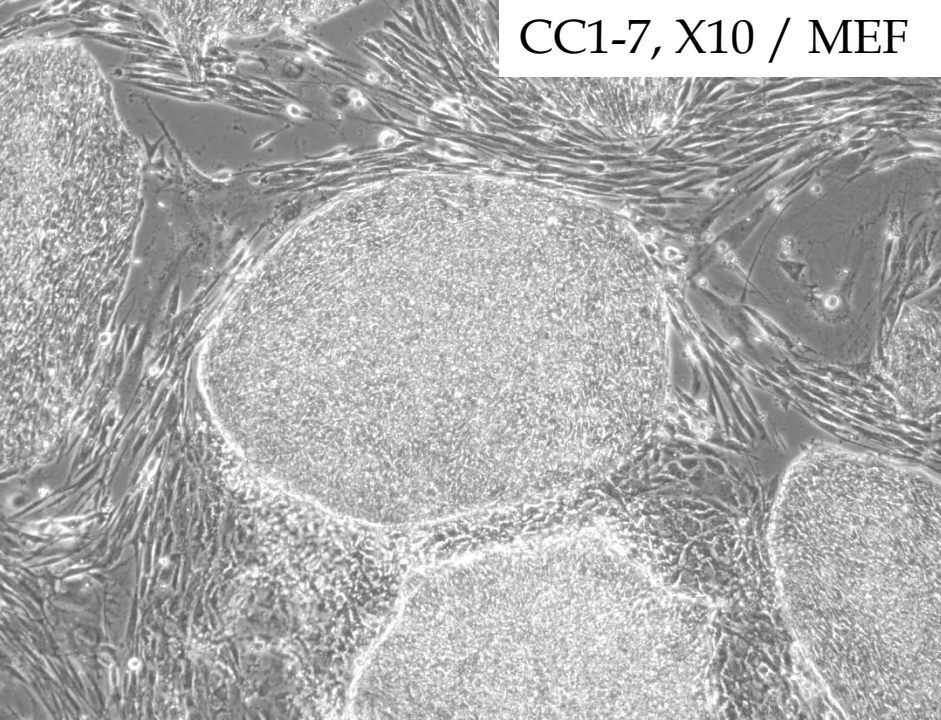
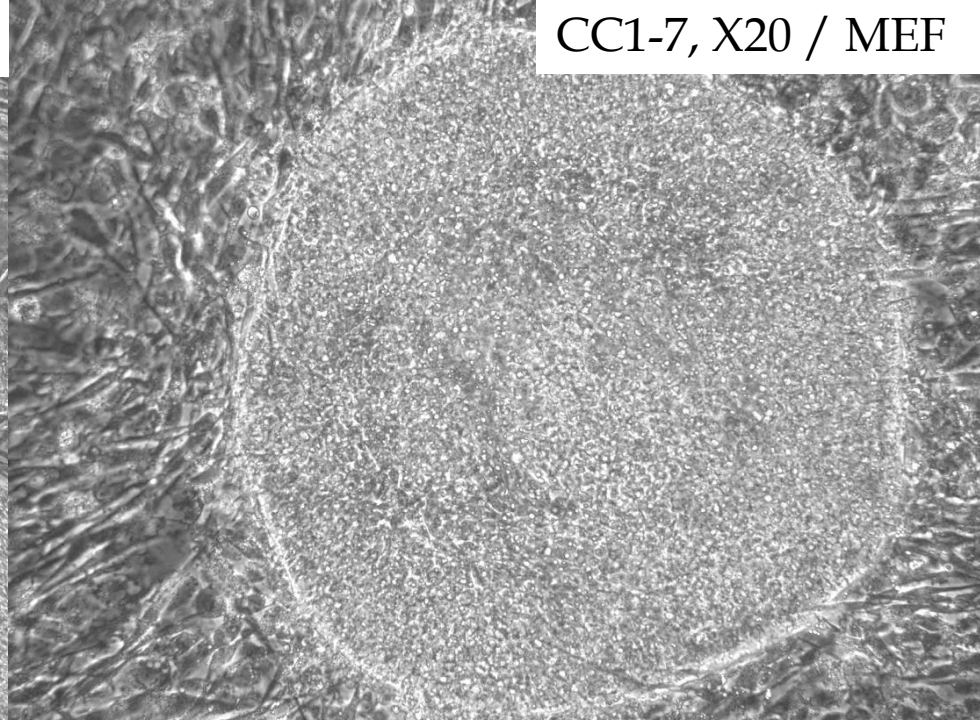


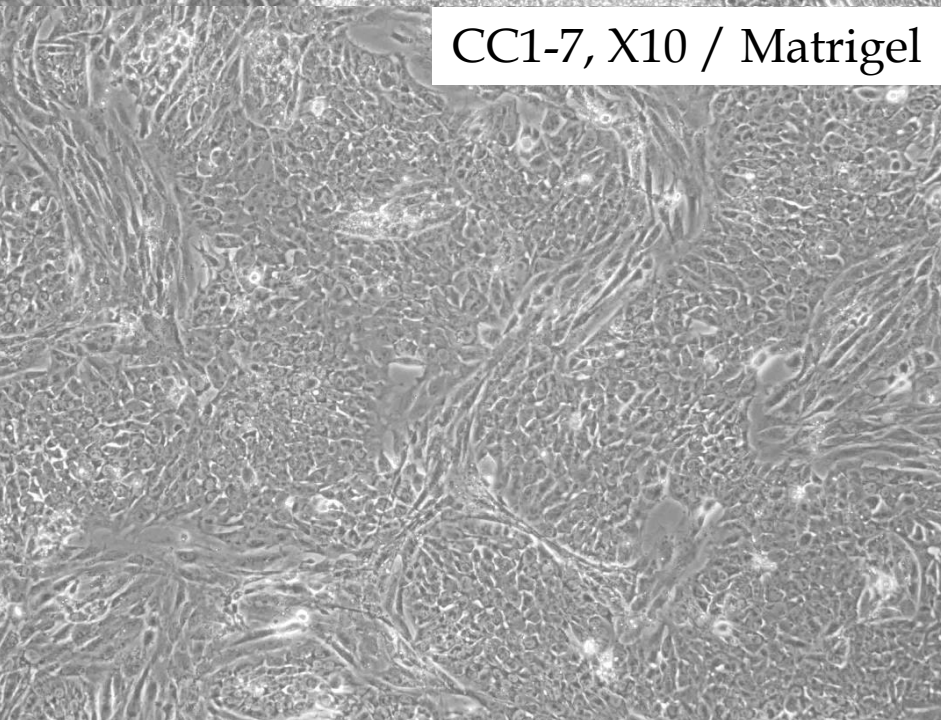
CC1-7, X10 / MEF



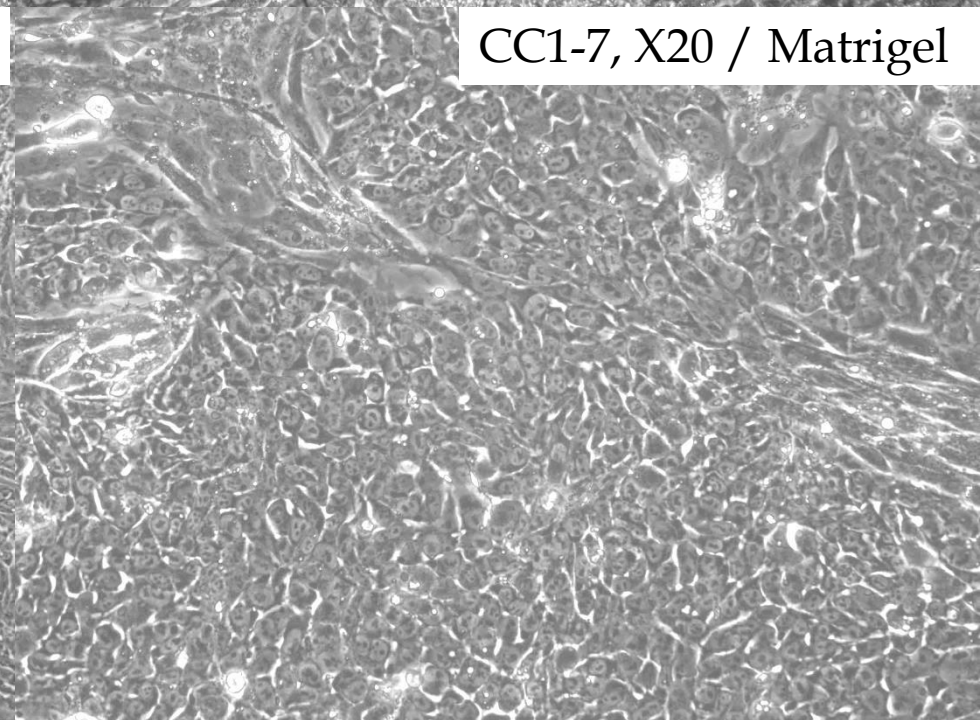
CC1-7, X20 / MEF



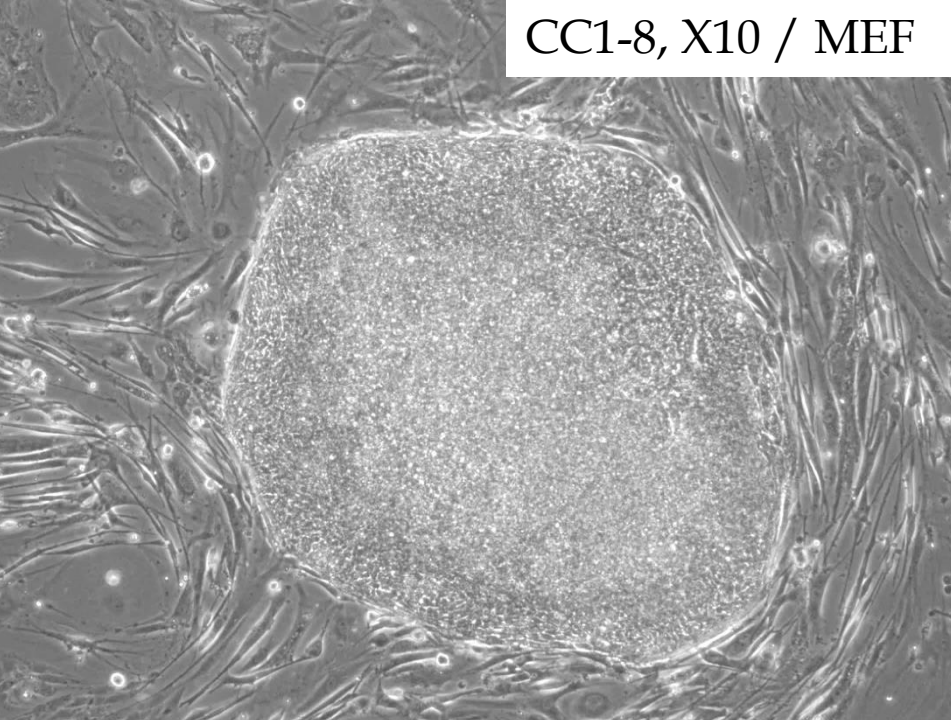
CC1-7, X10 / Matrigel



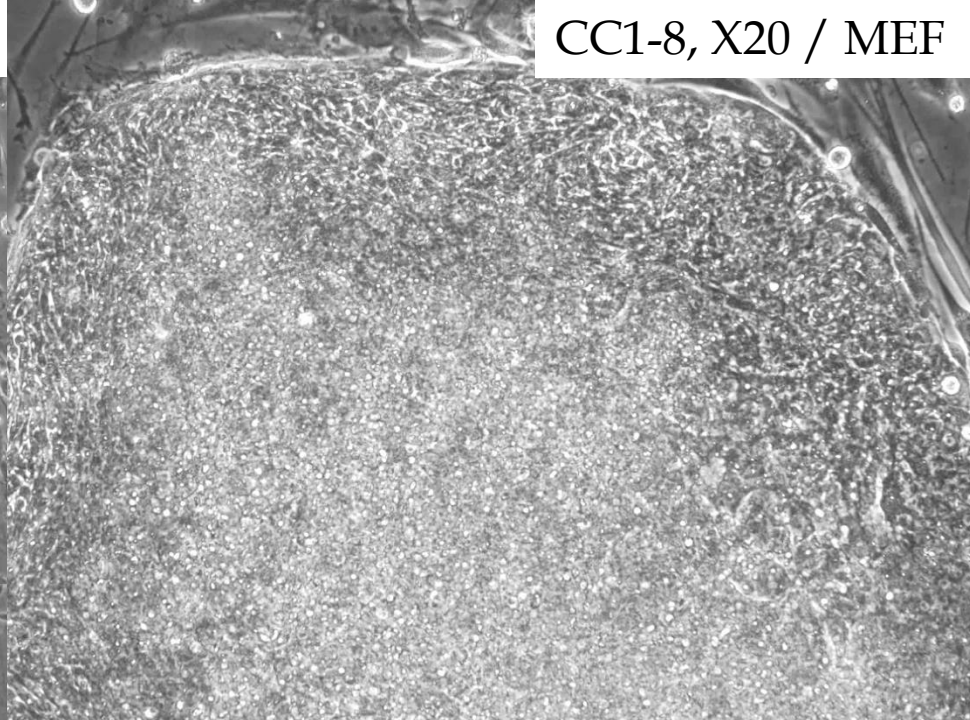
CC1-7, X20 / Matrigel



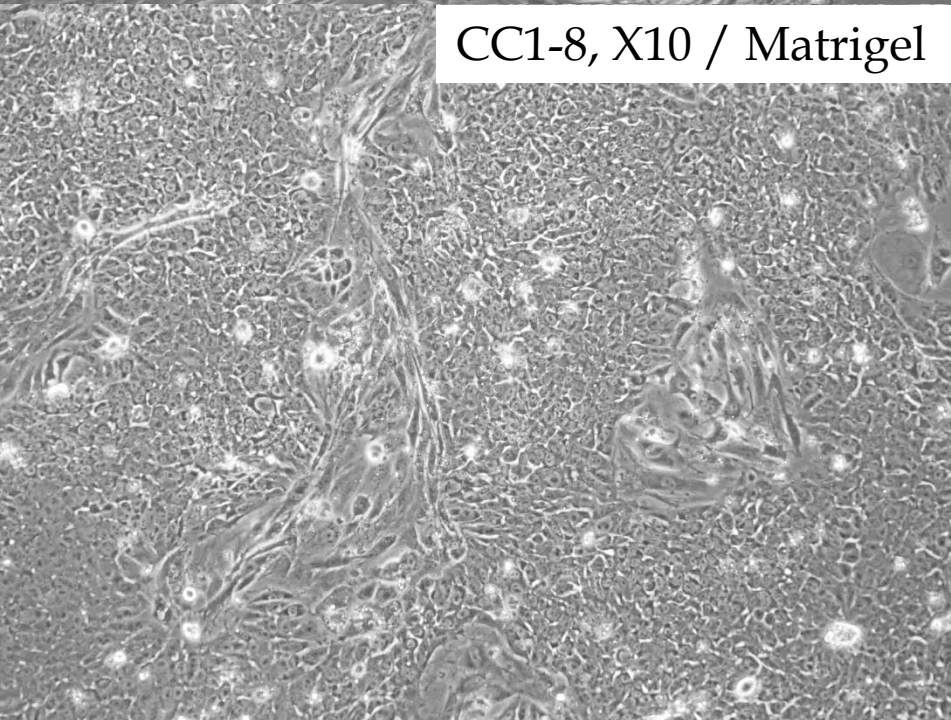
CC1-8, X10 / MEF



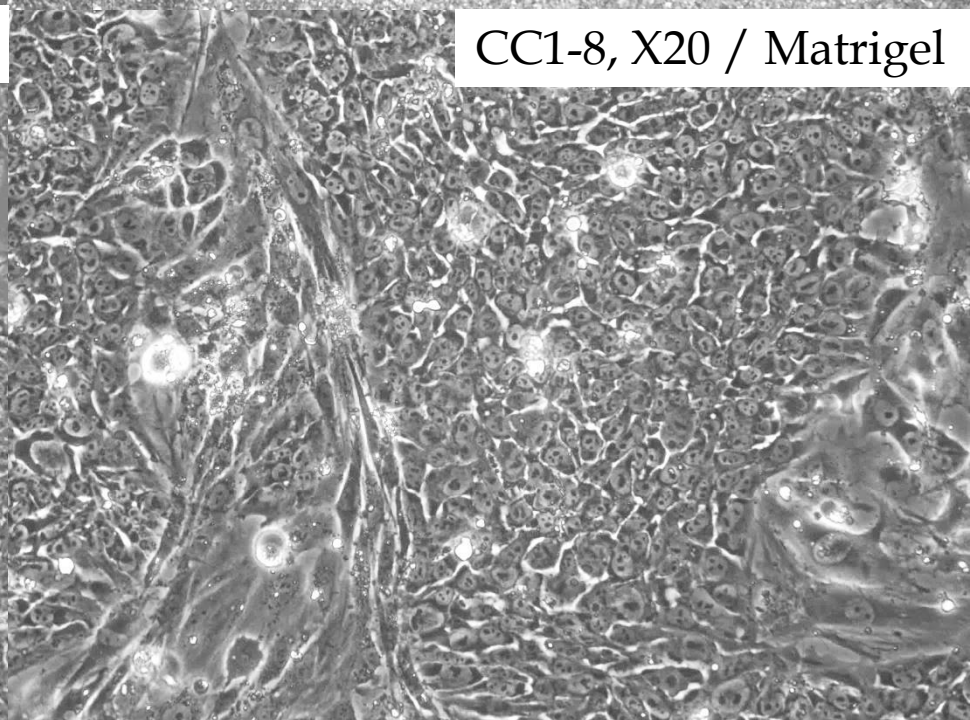
CC1-8, X20 / MEF

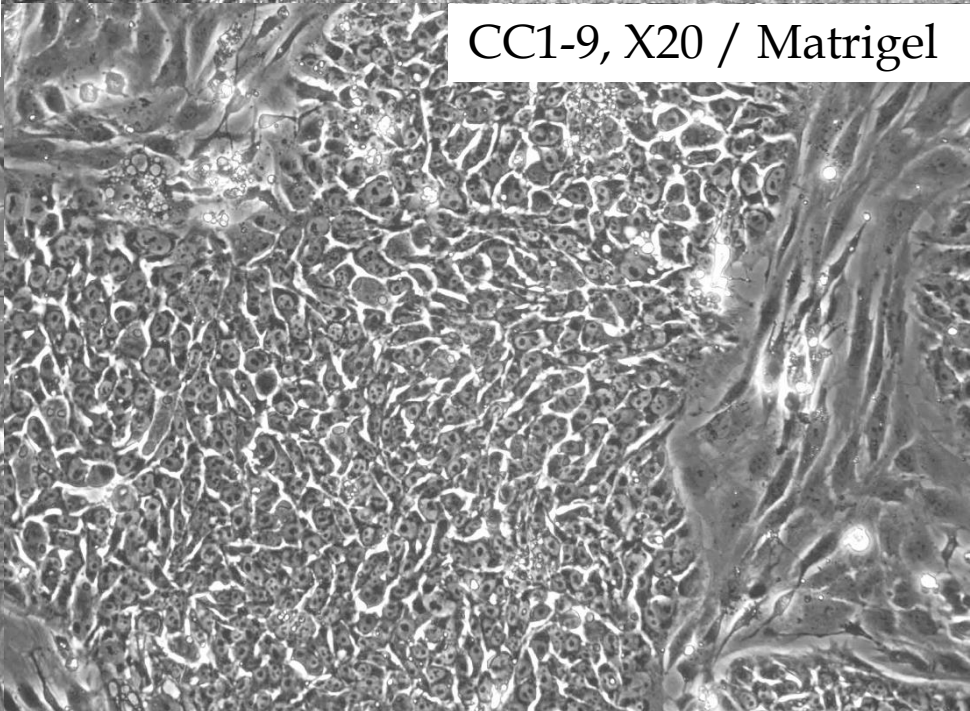
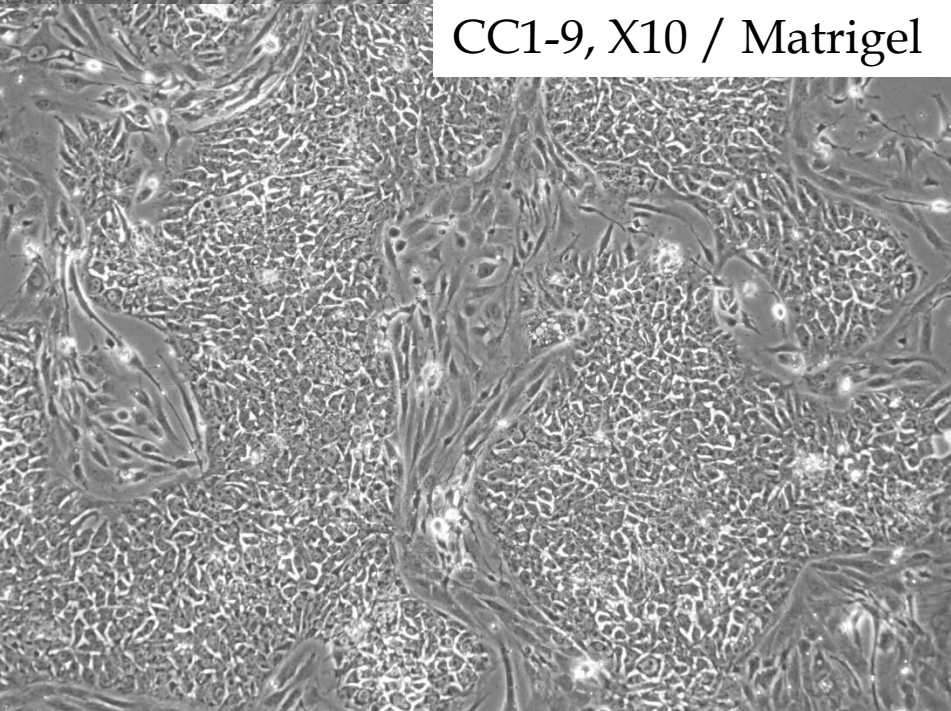
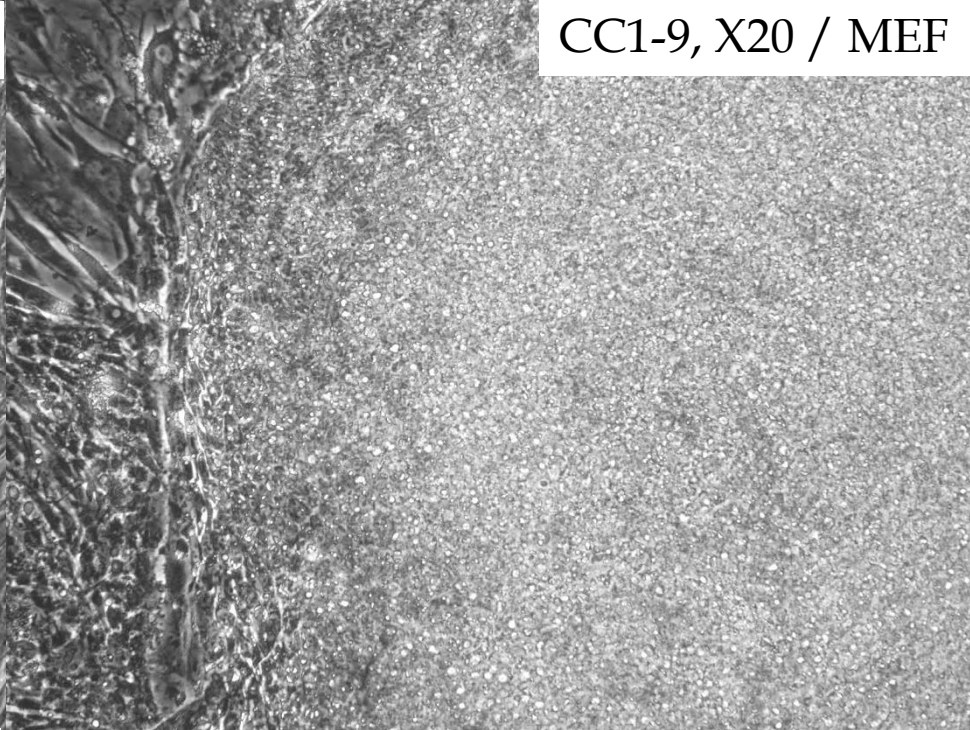
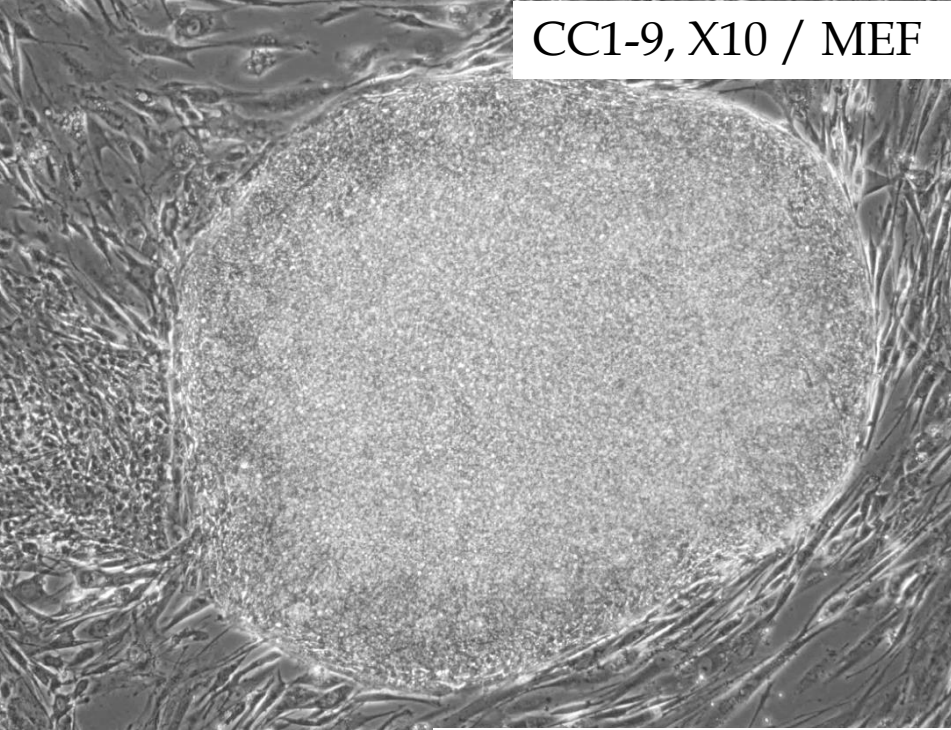


CC1-8, X10 / Matrigel

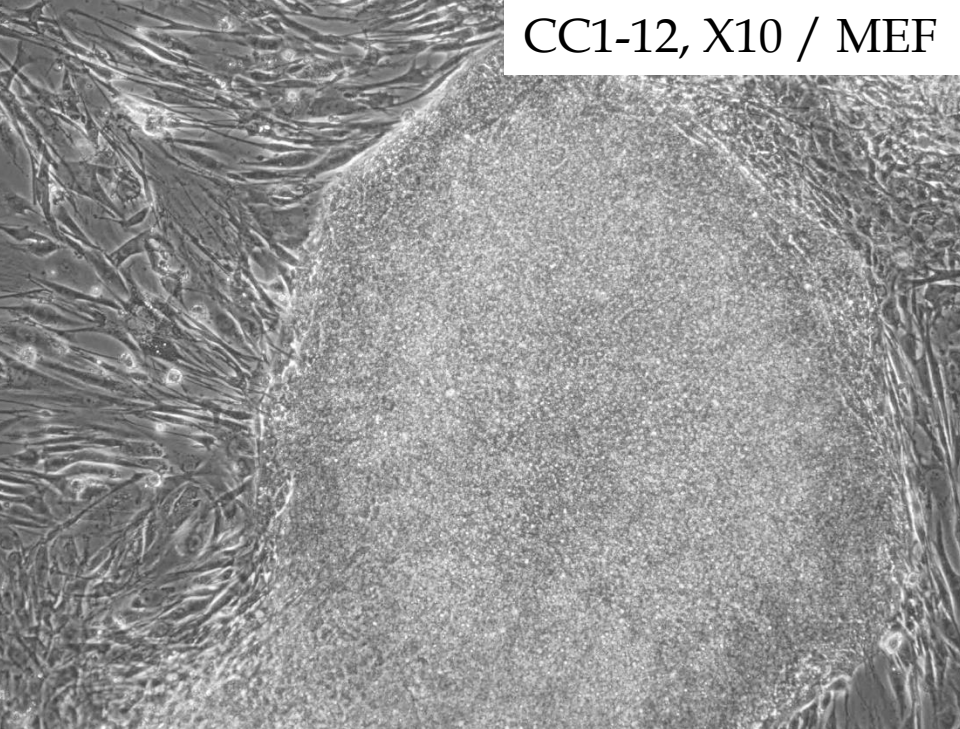


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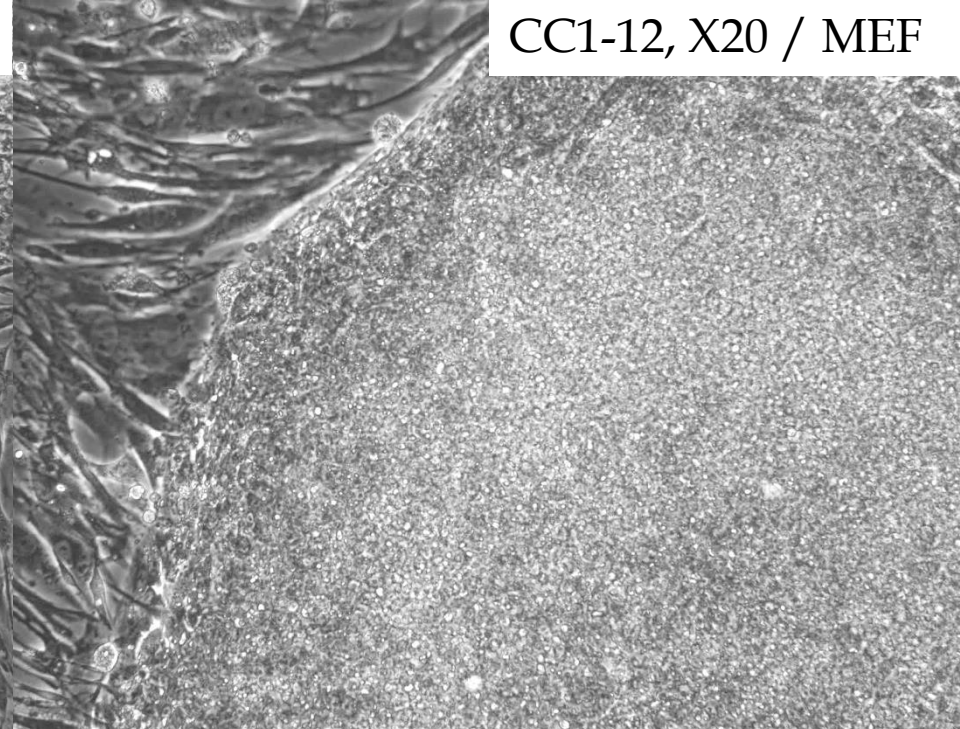




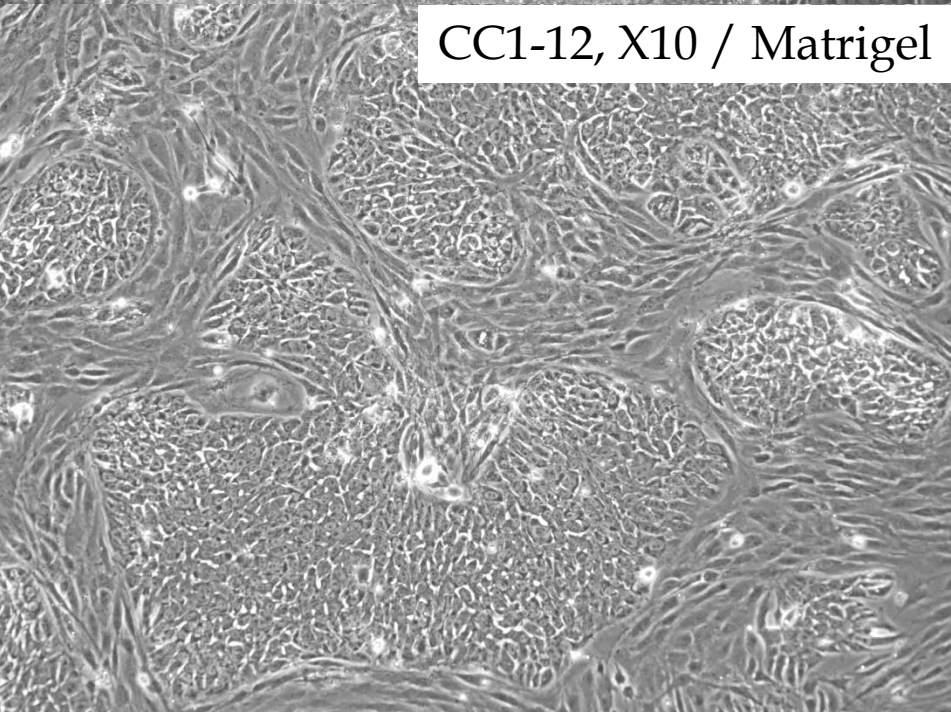
CC1-12, X10 / MEF



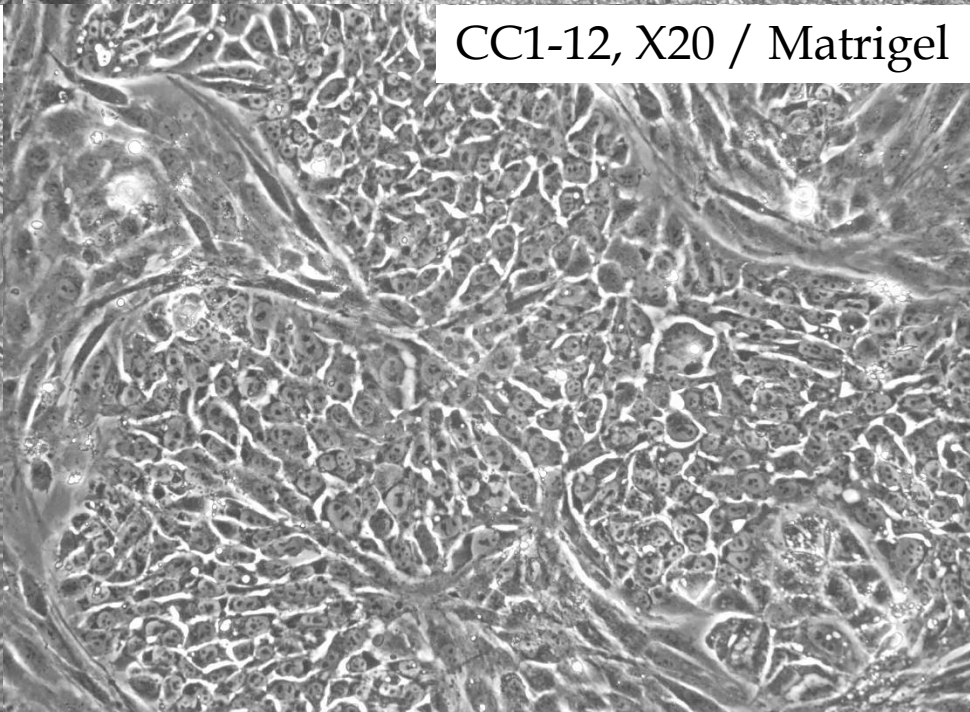
CC1-12, X20 / MEF



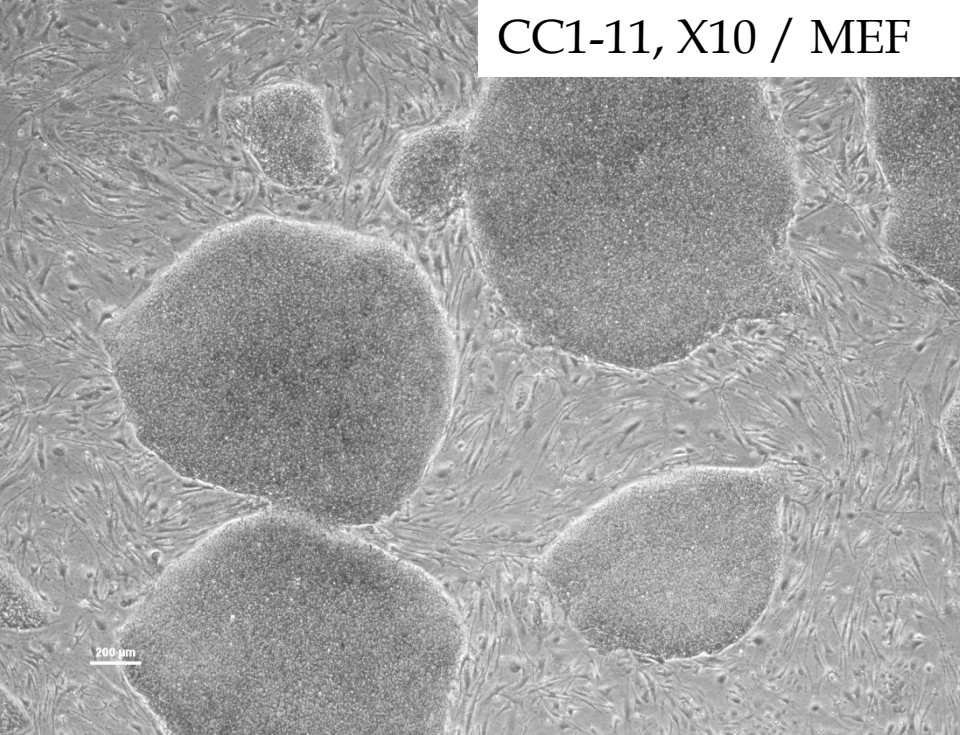
CC1-12, X10 / Matrigel



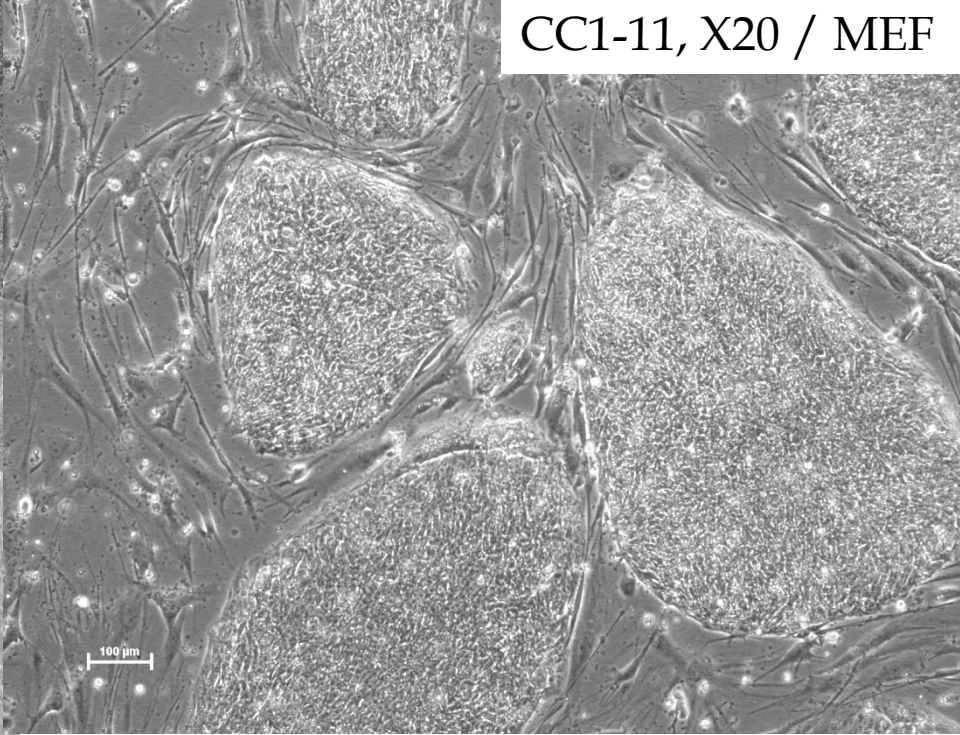
CC1-12, X20 / Matrigel



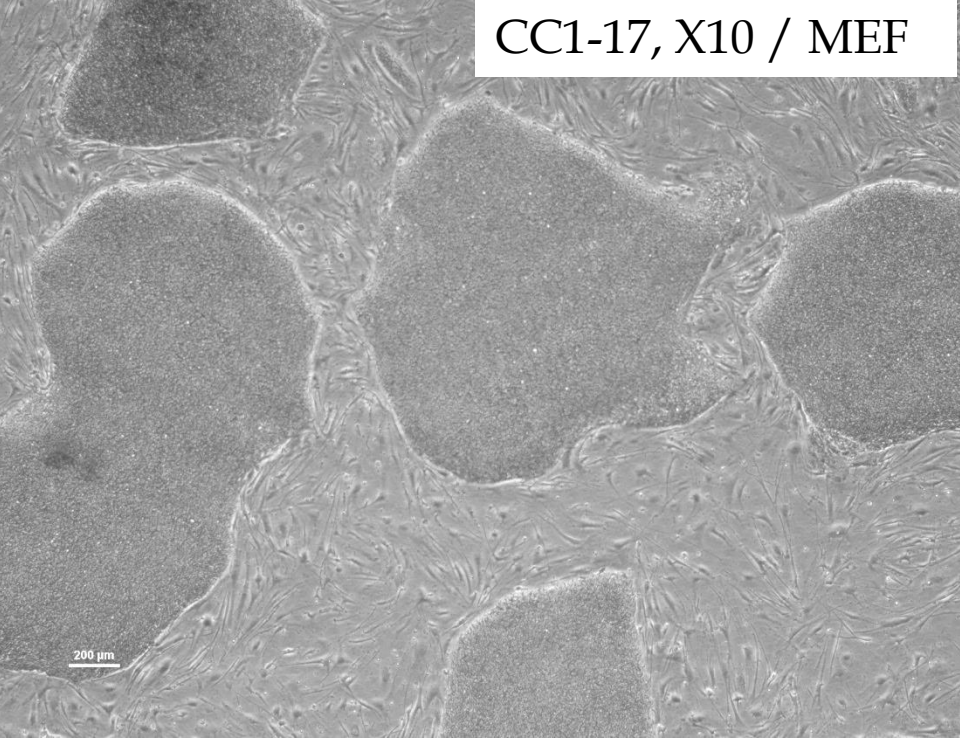
CC1-11, X10 / MEF



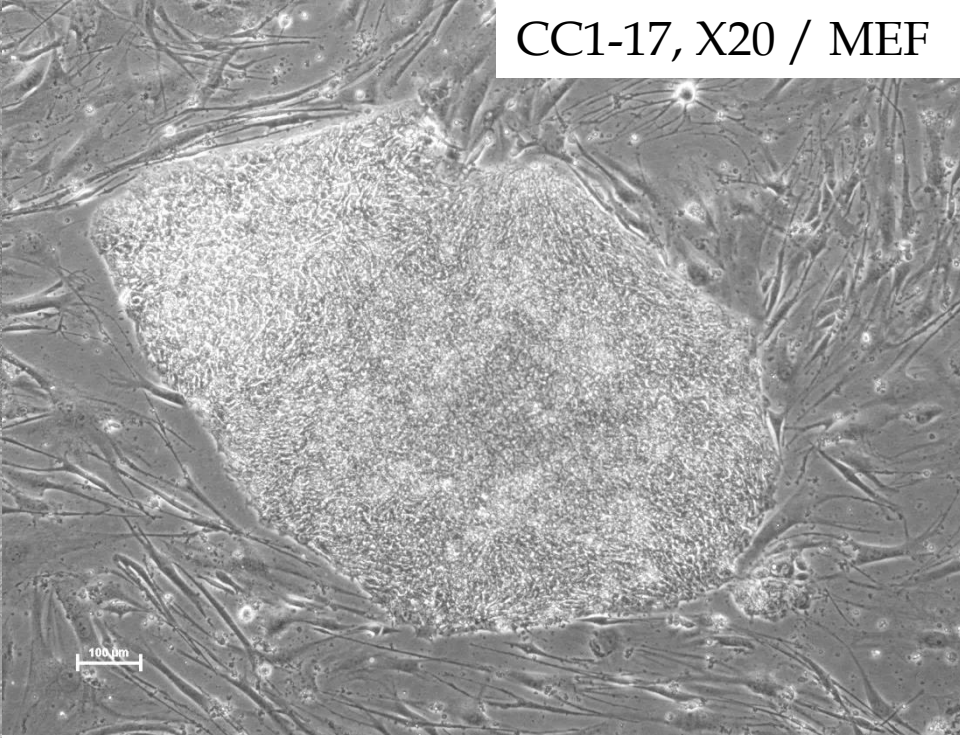
CC1-11, X20 / MEF



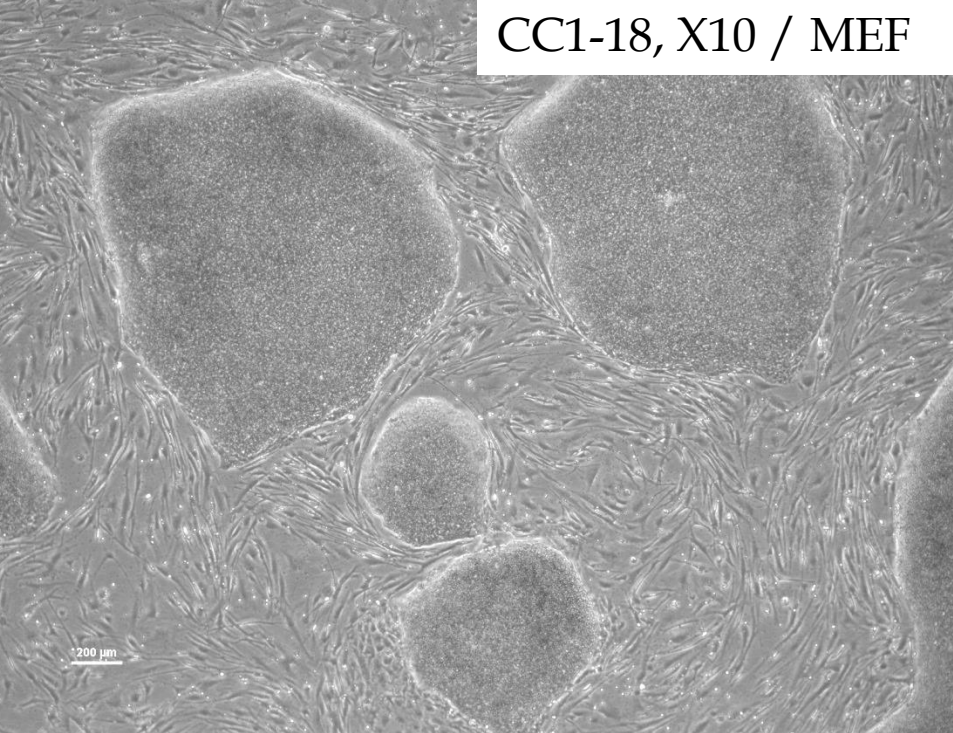
CC1-17, X10 / MEF



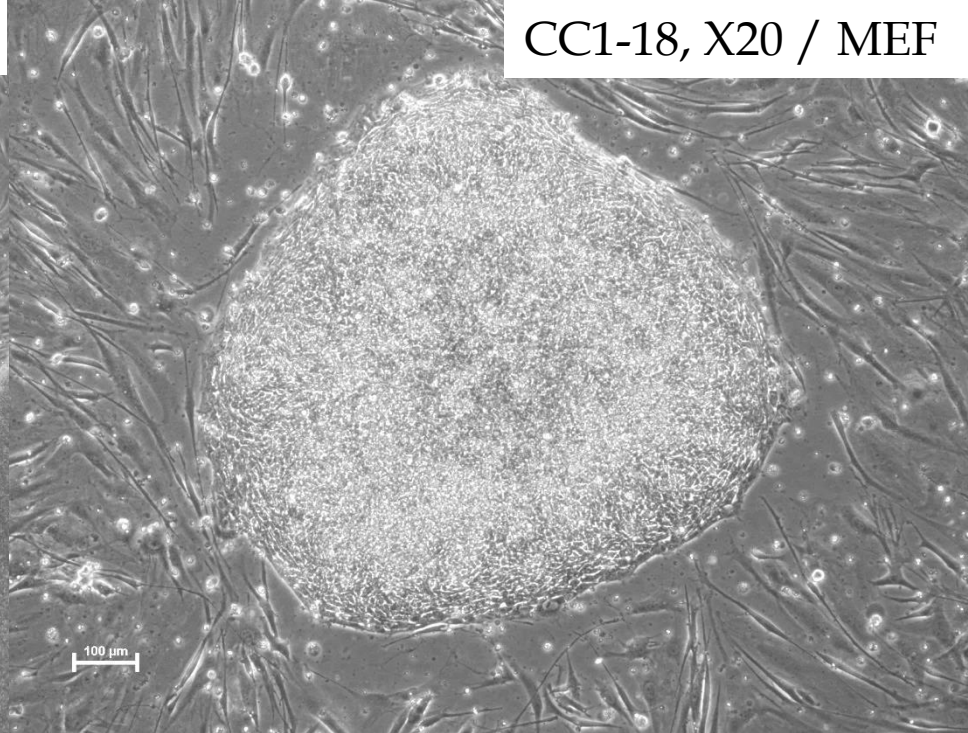
CC1-17, X20 / MEF



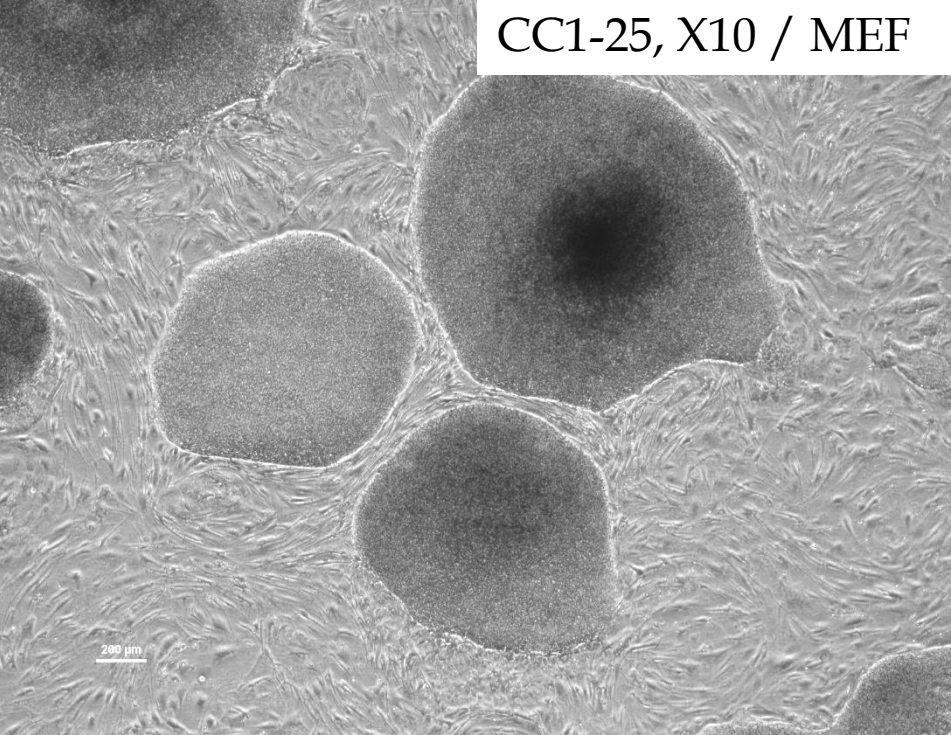
CC1-18, X10 / MEF



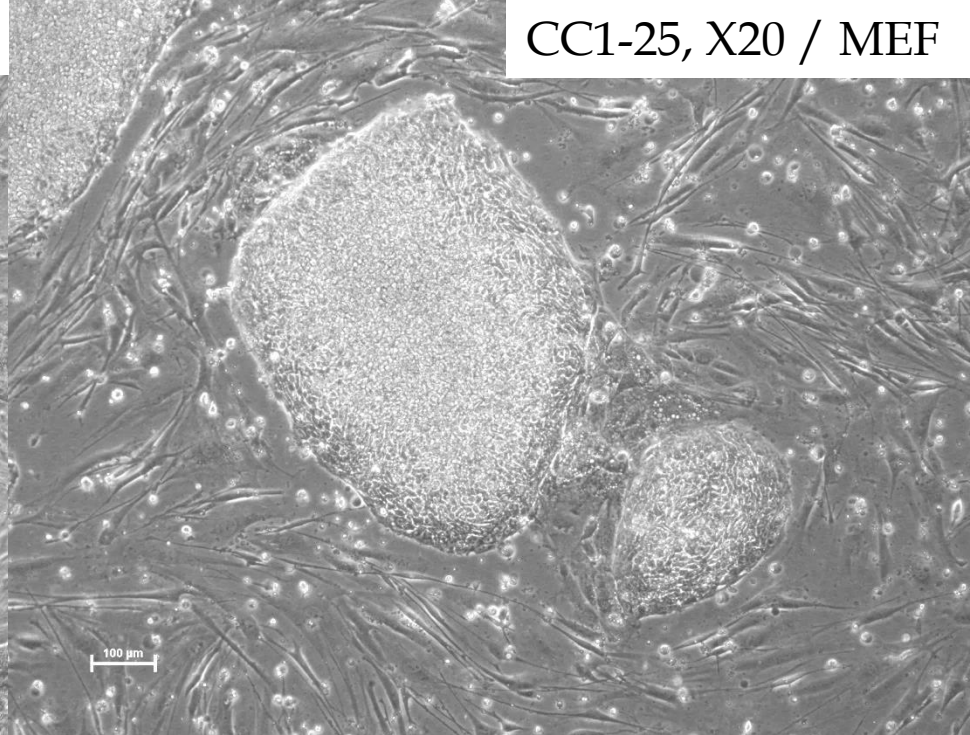
CC1-18, X20 / MEF



CC1-25, X10 / MEF



CC1-25, X20 / MEF



Supplemental Figure 1 Phase contrast micrographs of colon cancer tissue-derived iPSC lines. The human iPSC lines CC1-2, CC1-7, CC1-8, CC1-9, CC1-11, CC1-12, CC1-17, CC1-18, and CC1-25 were expanded with mitomycin C-treated mouse embryonic fibroblasts in gelatin-coated dishes (upper left panel: X10, upper right panel: X20). The human iPSC lines CC1-2, CC1-7, CC1-8, CC1-9, and CC1-12 were cultured with feeder-free mTeSR1 medium in BD Matrigel™ -coated dishes (lower left panel: X10, lower right panel: X20).

Supplemental Table 1 PCR Primer List				
Primer name	5'-sequence-3'	Tm	Primer Size	Product Size (bp)
GAPDH-F	ggcctccaaggagtaagacc	60.07	20	147
GAPDH-R	aggggtctacatggcaactg	59.99	20	
OCT3/4-F	agtgagaggcaacctggaga	59.99	20	110
OCT3/4-R	acactcggaccacatccttc	59.97	20	
SOX2-F	tggtagcgtaggagctttgc	60.27	20	80
SOX2-R	tttttcgtcgcttggagact	59.99	20	
NANOG-F	cagtctggacactggctgaa	60.02	20	149
NANOG-R	ctcgctgattaggctccaac	59.98	20	
ZFP42-F	gaaagcgcttctctctggac	59.31	20	150
ZFP42-R	tcgtatttgcacgcgttagg	59.72	20	

Supplemental Table 2 Real-time RT-PCR Cq values of ESC-enriched genes and GAPDH

iPSC lines	Cq (Ct)					
	SOX2	NANOG	OCT3/4	ZFP42	GAPDH	
CC1-1	19.79	21.28	17.22	22.8	15.08	
CC1-2	19.56	21.89	17.94	24.02	15.7	
CC1-7	19.24	21.15	17.33	23.07	15.27	
CC1-8	19.62	20.96	16.99	23.22	15.02	
CC1-9	19.12	21.23	17.04	23.56	15.08	
CC1-11	19.36	21.24	17.14	23.16	15.14	
CC1-12	19.47	21.78	16.82	23.15	15.19	
CC1-17	19.64	20.55	17.11	22.3	15.73	
CC1-18	19.55	22.12	18.12	25.57	16.26	
CC1-25	19.32	21.55	17.29	24.05	15.25	
201B7	19.57	21.44	17.42	25.45	17.07	

[illegible][illegible]

EPHB6
ERBB2
ERBB3
ERBB4
ERN1
ERN2
FASTK
FER
FES
FGFR1
FGFR2
FGFR3
FGFR4
FGR
FLJ25006
FLT1
FLT3
FLT4
FRK
FYN
GAK
GCK
GRK1
GRK4
GRK5
GRK6
GRK7
GSG2
GSK3A
GSK3B
GUCY2C
GUCY2D
GUCY2F
HCK
HIPK1
HIPK2
HIPK3
HIPK4
HSPB8
HUNK
ICK
IGF1R
IKBBK8
IKBKE
ILK
INSR
INSRR
IRAK1
IRAK2
IRAK3
IRAK4
ITK
JAK1
JAK2
JAK3
KALRN
KDR
KIAA1804
KIT
KSR1
KSR2
LATS1
LATS2
LCK
LIMK1
LIMK2
LMTK2
LMTK3
LRRK1
LRRK2
LTK
LYN
MAK
MAP2K1
MAP2K2
MAP2K3
MAP2K4
MAP2K5
MAP2K6
MAP2K7
MAP3K1
MAP3K10
MAP3K11
MAP3K12
MAP3K13
MAP3K14
MAP3K15
MAP3K2
MAP3K3
MAP3K4
MAP3K5
MAP3K6
MAP3K7
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MAPK14
MAPK15
MAPK3
MAPK4
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MAPK7
MAPK8
MAPK9
MAPKAPK2
MAPKAPK3
MAPKAPK5
MARK1
MARK2
MARK3
MARK4
MAST1
MAST2
MAST3
MAST4
MASTL
MATK
MELK
MERTK
MET
MGC42105
MINK1
MKNK1
MKNK2
MLK1
MOS
MST1R
MTOR
MUSK
MYLK
MYLK2
MYLK3
MYLK4
MYO3A
MYO3B
NEK1

NEK10
NEK11
NEK2
NEK3
NEK4
NEK5
NEK6
NEK7
NEK8
NEK9
NLK
NPR1
NPR2
NRBP1
NRBP2
NRK
NTRK1
NTRK2
NTRK3
NUAK1
NUAK2
OBSN
OXSRI
PAK1
PAK2
PAK3
PAK4
PAK6
PAK7
PAK8
PBK
PCTK1
PCTK2
PCTK3
PDGFRA
PDGFRB
PDK1L
PDK1
PDK2
PDK3
PDK4
PDPK1
PFTK1
PFTK2
PHKG1
PHKG2
PIM1
PIM2
PIM3
PINK1
PKLR
PKMYT1
PKN1
PKN2
PKN3
PLK1
PLK2
PLK3
PLK4
PNCK
PRAGMIN
PRKAA1
PRKAA2
PRKACA
PRKACB
PRKACG
PRKCA
PRKCB
PRKCD
PRKCE
PRKCG
PRKCH
PRKCI
PRKCQ
PRKCZ
PRKD1
PRKD2
PRKD3
PRKDC
PRKG1
PRKG2
PRKX
PRKY
PRPF4B
PSKH1
PSKH2
PTK2
PTK2B
PTK6
PTK7
PAK
RAC1
RAF1
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RET
RIOK1
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RNASEL
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ROR1
ROR2
ROSI
MST4
RPS6KA1
RPS6KA2
RPS6KA3
RPS6KA4
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RPS6KA6
RPS6KB1
RPS6KB2
RPS6KC1
RPS6KL1
RYK
SRK1
SRK2
SCYL1
SCYL2
SCYL3
SGK1
SGK196
SGK2
SGK269
SGK3
SGK493
SIK1
SIK2
SIK3
SLK
SMG1
SNRK
SPEG
SRC
SRM
SRM5
SRPK1
SRPK2
SRPK3
STK10

STK11
STK16
STK17A
STK17B
STK19
STK24
STK25
STK3
STK31
STK32A
STK32B
STK32C
STK33
STK35
STK36
STK38
STK38L
STK39
STK4
STK40
STRADA
STRADB
STYK1
SYK
TAF1
TAF1L
TAOK1
TAOK2
TAOK3
TBCK
TBK1
TEC
TEK
TESK1
TESK2
TEX14
TGFBFR1
TGFBFR2
TIE1
TILK1
TLK2
TNIK
TNK1
TNK2
TNNIBK
TP53RK
TRIB1
TRIB2
TRIB3
TRIM24
TRIM28
TRIM33
TRIO
TRPM6
TRPM7
TRRAP
TSSK1B
TSSK2
TSSK3
TSSK4
TSSK6
TTBK1
TTBK2
TTK
TTN
TXK
TYK2
TYRO3
UHMK1
ULK1
ULK2
ULK3
ULK4
VRK1
VRK2
VRK3
WEE1
WEE2
WNK1
WNK2
WNK3
WNK4
YES1
YSK4
ZAK
ZAP70

Supplemental Table 4 A comparison of the 378 non-synonymous SNVs with the hg19 genome

Chrom	Chrom Start	Chrom End	Reference	Alternatives	Type	Known/Novel	Gene	Function
chr1	1571841	1571841	A	C	SNV	Known	CDK11B.CDK11A	Missense
chr1	1575715	1575715	C	T	SNV	Novel	CDK11B.CDK11A	Missense
chr1	1575784	1575784	C	T	SNV	Known	CDK11B.CDK11A	Missense
chr1	1635011	1635011	A	G	SNV	Known	CDK11A.CDK11B	Missense
chr1	1638925	1638925	C	T	SNV	Novel	CDK11A.CDK11B	Missense
chr1	1638994	1638994	C	T	SNV	Known	CDK11A.CDK11B	Missense
chr1	9780196	9780196	A	G	SNV	Known	PIK3CD	Missense
chr1	22923873	22923873	G	C	SNV	Known	EPHA8	Missense
chr1	27688633	27688633	G	A	SNV	Known	MAP3K6	Missense
chr1	27942215	27942215	C	G	SNV	Novel	FGR	Missense
chr1	36807481	36807481	C	T	SNV	Known	STK40	Missense
chr1	38184063	38184063	C	A	SNV	Novel	EPHA10	Missense
chr1	38227086	38227086	A	T	SNV	Known	EPHA10	Missense
chr1	38227268	38227268	G	T	SNV	Known	EPHA10	Missense
chr1	46476587	46476587	T	G	SNV	Known	MAST2	Missense
chr1	46493460	46493460	T	G	SNV	Known	MAST2	Missense
chr1	46521559	46521559	A	T	SNV	Known	PIK3R3	Missense
chr1	64643277	64643277	C	T	SNV	Known	ROR1	Missense
chr1	92428495	92428495	C	A	SNV	Known	BRDT	Missense
chr1	92457843	92457843	C	T	SNV	Known	BRDT	Missense
chr1	114948281	114948281	A	G	SNV	Known	TRIM33	Missense
chr1	169823718	169823718	T	C	SNV	Known	SCYL3.C1orf112	Missense
chr1	182554557	182554557	C	T	SNV	Known	RNASEL	Missense
chr1	205130413	205130413	A	G	SNV	Known	DSTYK	Missense
chr1	205272918	205272918	G	A	SNV	Known	NUAK2	Missense
chr1	205500478	205500478	G	A	SNV	Known	CDK18	Missense
chr1	226923505	226923505	G	T	SNV	Known	ITPKB	Missense
chr1	227182033	227182033	G	A	SNV	Known	CDC42BPA	Missense
chr1	227216775	227216775	C	T	SNV	Known	CDC42BPA	Missense
chr1	228402121	228402121	A	G	SNV	Known	OBSCN.C1orf145	Missense
chr1	228444565	228444565	T	A	SNV	Known	OBSCN	Missense
chr1	228464248	228464248	T	G	SNV	Known	OBSCN.AL353593.1	Missense
chr1	228464276	228464276	T	C	SNV	Known	OBSCN.AL353593.1	Missense
chr1	228509589	228509589	G	A	SNV	Known	OBSCN	Missense
chr1	233497836	233497836	C	A	SNV	Novel	KIAA1804.RP5-862P8.2	Missense
chr1	233514934	233514934	G	A	SNV	Known	KIAA1804.RP5-862P8.2	Missense
chr1	233514975	233514975	G	T	SNV	Known	KIAA1804.RP5-862P8.2	Missense
chr1	233515102	233515102	T	G	SNV	Known	KIAA1804.RP5-862P8.2	Missense
chr2	11359120	11359120	G	T	SNV	Known	ROCK2	Missense
chr2	29416366	29416366	G	C	SNV	Known	ALK	Missense
chr2	29416481	29416481	T	C	SNV	Known	ALK	Missense
chr2	29416572	29416572	T	C	SNV	Known	ALK	Missense
chr2	29416635	29416635	C	A	SNV	Novel	ALK	Missense
chr2	29448410	29448410	T	G	SNV	Novel	ALK	Missense
chr2	37336419	37336419	C	T	SNV	Novel	EIF2AK2	Missense
chr2	42275664	42275664	T	C	SNV	Known	PKDCC	Missense
chr2	58316786	58316786	A	G	SNV	Known	VRK2	Missense
chr2	88913273	88913273	G	C	SNV	Known	EIF2AK3	Missense
chr2	99172244	99172244	A	G	SNV	Known	INPP4A	Missense
chr2	135744007	135744007	T	C	SNV	Known	YSK4	Missense
chr2	135744416	135744416	C	G	SNV	Known	YSK4	Missense
chr2	148676144	148676144	A	C	SNV	Novel	ACVR2A	Missense

chr2	158485099	158485099	C	A	SNV	Novel	ACVR1C.AC019186.1	Missense
chr2	171225841	171225841	A	G	SNV	Known	MYO3B	Missense
chr2	171260787	171260787	G	A	SNV	Known	MYO3B	Missense
chr2	171356274	171356274	G	A	SNV	Known	MYO3B	Missense
chr2	174128513	174128513	C	T	SNV	Known	ZAK.MLK7-AS1.AC013461.1.AC013461.2	Missense
chr2	179397561	179397561	C	T	SNV	Known	TTN.MIR548N.LOC100506866.AC009948.3	Missense
chr2	179406191	179406191	C	T	SNV	Known	TTN.MIR548N.LOC100506866.AC009948.3	Missense
chr2	179408086	179408086	A	G	SNV	Novel	TTN.MIR548N.LOC100506866.AC009948.3	Missense
chr2	179421694	179421694	A	G	SNV	Known	TTN.MIR548N.LOC100506866.AC009948.3	Missense
chr2	179425208	179425208	G	T	SNV	Known	TTN.MIR548N.LOC100506866.AC009948.3	Missense
chr2	179427536	179427536	T	C	SNV	Known	TTN.MIR548N.LOC100506866.AC009948.3	Missense
chr2	179430997	179430997	G	A	SNV	Known	TTN.MIR548N.LOC100506866.AC009948.3	Missense
chr2	179436020	179436020	G	A	SNV	Known	TTN.MIR548N.LOC100506866.AC009948.3	Missense
chr2	179444768	179444768	C	G	SNV	Known	TTN.MIR548N.LOC100506866.AC009948.3	Missense
chr2	179444939	179444939	C	T	SNV	Known	TTN.MIR548N.LOC100506866.AC009948.3	Missense
chr2	179451420	179451420	G	A	SNV	Known	TTN.MIR548N.LOC100506866.AC009948.3	Missense
chr2	179457147	179457147	G	A	SNV	Known	TTN.MIR548N.LOC100506866.AC009948.3	Missense
chr2	179458591	179458591	C	T	SNV	Known	TTN.MIR548N.LOC100506866.AC009948.3	Missense
chr2	179464527	179464527	T	C	SNV	Known	TTN.MIR548N.LOC100506866.AC009948.3	Missense
chr2	179474668	179474668	G	A	SNV	Known	TTN.MIR548N.LOC100506866	Missense
chr2	179515483	179515483	G	C	SNV	Known	TTN.MIR548N.AC010680.1	Missense
chr2	179558366	179558366	T	C	SNV	Known	TTN.AC010680.1	Missense
chr2	179579093	179579093	T	C	SNV	Known	TTN.AC010680.1	Missense
chr2	179582327	179582327	C	T	SNV	Known	TTN	Missense
chr2	179582537	179582537	G	T	SNV	Known	TTN	Missense
chr2	179583496	179583496	T	G	SNV	Known	TTN	Missense
chr2	179587130	179587130	C	G	SNV	Known	TTN	Missense
chr2	179589058	179589058	G	A	SNV	Known	TTN	Missense
chr2	179615887	179615887	T	C	SNV	Known	TTN	Missense
chr2	179615931	179615931	C	G	SNV	Known	TTN	Missense
chr2	179620951	179620951	C	T	SNV	Known	TTN	Missense
chr2	179621477	179621477	C	T	SNV	Known	TTN	Missense
chr2	179623758	179623758	C	T	SNV	Known	TTN	Missense
chr2	179629461	179629461	C	T	SNV	Known	TTN	Missense
chr2	179634421	179634421	T	G	SNV	Novel	TTN	Missense
chr2	179638072	179638072	C	T	SNV	Novel	TTN	Missense
chr2	179644035	179644035	G	A	SNV	Known	TTN	Missense
chr2	179659912	179659912	G	A	SNV	Known	TTN	Missense
chr2	209184980	209184980	G	A	SNV	Known	PIKFYVE	Missense
chr2	209190330	209190330	T	C	SNV	Known	PIKFYVE	Missense
chr2	209190519	209190519	A	T	SNV	Known	PIKFYVE	Missense
chr2	209190528	209190528	C	G	SNV	Known	PIKFYVE	Missense
chr2	209191082	209191082	C	A	SNV	Known	PIKFYVE	Missense
chr2	209195248	209195248	C	A	SNV	Novel	PIKFYVE	Missense
chr2	220337041	220337041	G	A	SNV	Known	SPEG.DNPEP	Missense
chr2	220354108	220354108	A	G	SNV	Known	SPEG.DNPEP.AC053503.11	Missense
chr2	242046785	242046785	A	C	SNV	Known	PASK	Missense
chr2	242054403	242054403	G	A	SNV	Known	PASK	Missense
chr2	242082262	242082262	T	C	SNV	Known	PASK	Missense
chr3	10276163	10276163	T	A	SNV	Known	IRAK2	Missense
chr3	27332820	27332820	A	G	SNV	Known	NEK10	Missense
chr3	41705179	41705179	A	C	SNV	Novel	ULK4	Missense
chr3	41841716	41841716	A	C	SNV	Known	ULK4	Missense
chr3	41925398	41925398	C	T	SNV	Known	ULK4	Missense
chr3	41960006	41960006	T	C	SNV	Known	ULK4	Missense

chr3	41996136	41996136	T	C	SNV	Known	ULK4	Missense
chr3	49928691	49928691	T	C	SNV	Known	MST1R	Missense
chr3	52797634	52797634	G	C	SNV	Known	NEK4	Missense
chr3	96585671	96585671	G	A	SNV	Known	EPHA6	Missense
chr3	123419573	123419573	G	T	SNV	Known	MYLK	Missense
chr3	123419733	123419733	A	G	SNV	Known	MYLK	Missense
chr3	123451773	123451773	G	C	SNV	Known	MYLK	Missense
chr3	123453061	123453061	A	G	SNV	Known	MYLK	Missense
chr3	123457893	123457893	G	A	SNV	Known	MYLK	Missense
chr3	123988019	123988019	C	A	SNV	Novel	KALRN	Missense
chr3	130947435	130947435	A	T	SNV	Known	NEK11	Missense
chr3	142281612	142281612	A	G	SNV	Known	ATR	Missense
chr3	185198262	185198262	G	A	SNV	Known	MAP3K13.TMEM41A	Missense
chr3	185990096	185990096	C	T	SNV	Known	DGKG	Missense
chr3	186006618	186006618	G	C	SNV	Known	DGKG	Missense
chr4	843498	843498	G	A	SNV	Known	GAK	Missense
chr4	2990499	2990499	G	T	SNV	Known	GRK4	Missense
chr4	3006043	3006043	C	T	SNV	Known	GRK4	Missense
chr4	5448429	5448429	A	G	SNV	Known	STK32B	Missense
chr4	25235801	25235801	G	A	SNV	Known	PI4K2B	Missense
chr4	55972974	55972974	T	A	SNV	Known	KDR	Missense
chr4	79786856	79786856	G	A	SNV	Known	BMP2K	Missense
chr4	107168431	107168431	G	C	SNV	Known	TBCK	Missense
chr4	113352397	113352397	G	A	SNV	Known	ALPK1	Missense
chr4	113352628	113352628	A	G	SNV	Known	ALPK1	Missense
chr4	113352899	113352899	G	A	SNV	Known	ALPK1	Missense
chr4	113353285	113353285	T	C	SNV	Known	ALPK1	Missense
chr4	128807219	128807219	T	A	SNV	Known	PLK4	Missense
chr4	151177340	151177340	C	T	SNV	Known	DCLK2	Missense
chr4	151177341	151177341	C	G	SNV	Known	DCLK2	Missense
chr4	170398454	170398454	T	C	SNV	Known	NEK1	Missense
chr5	56177443	56177443	G	A	SNV	Known	MAP3K1	Missense
chr5	56177743	56177743	G	A	SNV	Known	MAP3K1	Missense
chr5	66459878	66459878	G	C	SNV	Known	MAST4.AC044799.1	Missense
chr5	67588148	67588148	G	A	SNV	Known	PIK3R1	Missense
chr5	96503523	96503523	C	T	SNV	Known	RIOK2.CTD-2215E18.1	Missense
chr5	96513471	96513471	G	C	SNV	Known	RIOK2.CTD-2215E18.1.U1.72	Missense
chr5	96518792	96518792	T	G	SNV	Known	RIOK2.CTD-2215E18.1.RP11-155G15.2	Missense
chr5	112176756	112176756	T	A	SNV	Known	APC	Missense
chr5	112769527	112769527	C	T	SNV	Novel	MCC.TSSK1B.CTD-2201G3.1	Missense
chr5	149450132	149450132	T	C	SNV	Known	CSE1R	Missense
chr5	176516631	176516631	G	A	SNV	Known	FGFR4	Missense
chr5	176517797	176517797	C	T	SNV	Known	FGFR4	Missense
chr5	176520243	176520243	G	A	SNV	Known	FGFR4	Missense
chr5	180046344	180046344	G	C	SNV	Known	FLT4	Missense
chr5	180048626	180048626	C	T	SNV	Novel	FLT4	Missense
chr6	2679676	2679676	G	A	SNV	Known	MYLK4	Missense
chr6	4031998	4031998	A	G	SNV	Known	PRPF4B	Missense
chr6	31946695	31946695	C	G	SNV	Known	STK19.XXbac-BPG116M5.15	Missense
chr6	31947203	31947203	T	C	SNV	Novel	STK19.XXbac-BPG116M5.15	Missense
chr6	33690796	33690796	C	T	SNV	Known	IP6K3	Missense
chr6	33695975	33695975	G	A	SNV	Known	IP6K3	Missense
chr6	36489585	36489585	C	A	SNV	Novel	STK38	Missense
chr6	41903782	41903782	A	C	SNV	Known	CCND3	Missense
chr6	43111336	43111336	G	T	SNV	Novel	PTK7	Missense

chr6	43251912	43251912	A	G	SNV	Known	TTBK1	Missense
chr6	43252029	43252029	T	C	SNV	Known	TTBK1	Missense
chr6	44232920	44232920	A	G	SNV	Known	NFKBIE	Missense
chr6	44232977	44232977	G	A	SNV	Known	NFKBIE	Missense
chr6	110942394	110942394	G	T	SNV	Novel	CDK19	Missense
chr6	116325142	116325142	C	T	SNV	Known	FRK	Missense
chr6	117638325	117638325	C	T	SNV	Known	ROS1	Missense
chr6	136888782	136888782	T	C	SNV	Known	MAP3K5	Missense
chr6	161469774	161469774	G	A	SNV	Known	MAP3K4	Missense
chr6	167271711	167271711	T	C	SNV	Known	RPS6KA2.RP11-514O12.4	Missense
chr6	167271716	167271716	T	C	SNV	Known	RPS6KA2.RP11-514O12.4	Missense
chr7	23757162	23757162	G	C	SNV	Known	STK31	Missense
chr7	23775454	23775454	G	A	SNV	Known	STK31	Missense
chr7	23775477	23775477	G	T	SNV	Known	STK31	Missense
chr7	23808650	23808650	G	T	SNV	Novel	STK31	Missense
chr7	23811795	23811795	T	G	SNV	Known	STK31	Missense
chr7	23811800	23811800	G	T	SNV	Known	STK31	Missense
chr7	40027484	40027484	A	G	SNV	Known	CDK13	Missense
chr7	43635671	43635671	A	C	SNV	Known	STK17A	Missense
chr7	43664280	43664280	A	G	SNV	Known	STK17A	Missense
chr7	55229255	55229255	G	A	SNV	Known	EGFR	Missense
chr7	95216415	95216415	C	A	SNV	Novel	PDK4	Missense
chr7	97822115	97822115	T	A	SNV	Known	LMTK2	Missense
chr7	98490141	98490141	G	C	SNV	Novel	TRRAP	Missense
chr7	98547196	98547196	G	T	SNV	Novel	TRRAP	Missense
chr7	116340262	116340262	A	G	SNV	Known	MET	Missense
chr7	138145436	138145436	C	A	SNV	Novel	TRIM24	Missense
chr7	143088867	143088867	T	C	SNV	Known	EPHA1	Missense
chr7	143097100	143097100	A	G	SNV	Known	EPHA1	Missense
chr8	8176221	8176221	C	T	SNV	Known	SGK223.AC068353.1	Missense
chr8	8176554	8176554	C	T	SNV	Known	SGK223.AC068353.1	Missense
chr8	8234192	8234192	G	C	SNV	Known	SGK223.AC068353.1	Missense
chr8	8234219	8234219	G	A	SNV	Known	SGK223.AC068353.1	Missense
chr8	8234714	8234714	C	T	SNV	Known	SGK223.AC068353.1	Missense
chr8	8239069	8239069	C	A	SNV	Novel	SGK223.AC068353.1	Missense
chr8	11418773	11418773	C	T	SNV	Known	BLK.RP11-148O21.2	Missense
chr8	27308585	27308585	A	C	SNV	Known	PTK2B	Missense
chr8	38287238	38287238	G	A	SNV	Known	FGFR1	Missense
chr8	48719852	48719852	G	C	SNV	Known	PRKDC	Missense
chr8	87076520	87076520	C	A	SNV	Known	PSKH2	Missense
chr8	144800905	144800905	A	C	SNV	Novel	MAPK15.RP11-429J17.5	Missense
chr8	144802736	144802736	G	C	SNV	Known	MAPK15.RP11-429J17.5	Missense
chr8	145603114	145603114	A	C	SNV	Known	ADCK5	Missense
chr9	27168571	27168571	T	C	SNV	Known	TEK	Missense
chr9	27183463	27183463	A	C	SNV	Known	TEK	Missense
chr9	71628207	71628207	G	C	SNV	Known	PRKACG	Missense
chr9	77376647	77376647	T	C	SNV	Known	TRPM6	Missense
chr9	94486321	94486321	C	T	SNV	Known	ROR2	Missense
chr9	94495608	94495608	T	C	SNV	Known	ROR2	Missense
chr9	113457799	113457799	A	G	SNV	Known	MUSK	Missense
chr9	113538122	113538122	G	A	SNV	Known	MUSK	Missense
chr9	133759794	133759794	G	T	SNV	Known	ABL1	Missense
chr9	136268084	136268084	A	G	SNV	Known	C9orf96	Missense
chr10	6527143	6527143	G	A	SNV	Known	PRKCO	Missense
chr10	26355992	26355992	A	G	SNV	Known	MYO3A	Missense

chr10	26357748	26357748	G	A	SNV	Known	MYO3A	Missense
chr10	26463130	26463130	C	A	SNV	Known	MYO3A	Missense
chr10	26482157	26482157	A	G	SNV	Known	MYO3A	Missense
chr10	30728250	30728250	A	G	SNV	Known	MAP3K8	Missense
chr10	59956041	59956041	C	T	SNV	Known	IPMK	Missense
chr10	88635779	88635779	C	A	SNV	Known	BMPRI1A	Missense
chr10	99400747	99400747	C	A	SNV	Novel	PI4K2A.RP11-548K23.11	Missense
chr10	101977883	101977883	C	T	SNV	Known	CHUK	Missense
chr10	121196335	121196335	G	A	SNV	Known	GRK5	Missense
chr10	123310871	123310871	A	G	SNV	Known	FGFR2	Missense
chr11	46369267	46369267	G	A	SNV	Known	DGKZ	Missense
chr11	64597201	64597201	G	A	SNV	Known	CDC42BPG	Missense
chr11	108159732	108159732	C	T	SNV	Known	ATM	Missense
chr11	108183167	108183167	A	G	SNV	Known	ATM.C11orf65	Missense
chr11	111594312	111594312	C	A	SNV	Novel	SIK2	Missense
chr11	113266821	113266821	G	A	SNV	Known	ANKK1	Missense
chr11	113270015	113270015	G	C	SNV	Known	ANKK1	Missense
chr11	113270828	113270828	G	A	SNV	Known	ANKK1	Missense
chr11	125525195	125525195	A	G	SNV	Known	CHEK1	Missense
chr12	990912	990912	A	C	SNV	Known	WNK1	Missense
chr12	994487	994487	G	C	SNV	Known	WNK1	Missense
chr12	998365	998365	G	T	SNV	Known	WNK1	Missense
chr12	1009680	1009680	C	T	SNV	Novel	WNK1	Missense
chr12	10782115	10782115	T	C	SNV	Known	STYK1	Missense
chr12	14829893	14829893	A	C	SNV	Known	GUCY2C.RP11-174G6.1	Missense
chr12	18649057	18649057	C	T	SNV	Known	PIK3C2G	Missense
chr12	18719883	18719883	G	T	SNV	Known	PIK3C2G	Missense
chr12	40619082	40619082	G	A	SNV	Known	LRKK2.AC079630.3	Missense
chr12	40657700	40657700	C	G	SNV	Known	LRKK2	Missense
chr12	40702911	40702911	G	A	SNV	Known	LRKK2	Missense
chr12	48367976	48367976	C	T	SNV	Known	COL2A1	Missense
chr12	52306221	52306221	C	T	SNV	Known	ACVRL1	Missense
chr12	57919529	57919529	C	G	SNV	Known	MBD6	Missense
chr12	57994679	57994679	C	G	SNV	Known	PIP4K2C	Missense
chr12	66605228	66605228	A	G	SNV	Known	IRAK3	Missense
chr12	106460938	106460938	G	C	SNV	Known	NUAK1	Missense
chr12	118682751	118682751	C	T	SNV	Known	TAOK3	Missense
chr12	121691096	121691096	G	A	SNV	Known	CAMKK2.AC084018.1	Missense
chr12	132403161	132403161	A	G	SNV	Known	ULK1	Missense
chr12	132406666	132406666	G	C	SNV	Known	ULK1	Missense
chr13	21562832	21562832	C	T	SNV	Known	LATS2	Missense
chr13	21562948	21562948	G	A	SNV	Known	LATS2	Missense
chr13	28624294	28624294	G	A	SNV	Known	FLT3	Missense
chr13	32906480	32906480	A	C	SNV	Known	BRCA2	Missense
chr13	32911463	32911463	A	G	SNV	Known	BRCA2	Missense
chr13	32929387	32929387	T	C	SNV	Known	BRCA2	Missense
chr13	37679268	37679268	G	T	SNV	Known	CSNK1A1L	Missense
chr13	110434668	110434668	C	A	SNV	Novel	IRS2	Missense
chr13	110435231	110435231	C	T	SNV	Known	IRS2	Missense
chr13	110437802	110437802	A	C	SNV	Novel	IRS2	Missense
chr14	24808802	24808802	G	T	SNV	Novel	RIPK3	Missense
chr14	50798743	50798743	G	A	SNV	Known	CDKL1.ATP5S	Missense
chr14	50799126	50799126	G	C	SNV	Known	CDKL1.ATP5S	Missense
chr14	50901768	50901768	G	A	SNV	Known	MAP4K5	Missense
chr14	61924239	61924239	G	A	SNV	Known	PRKCH	Missense

chr14	75386576	75386576	G	A	SNV	Known	RPS6KL1	Missense
chr14	75388183	75388183	C	T	SNV	Known	RPS6KL1	Missense
chr14	75574087	75574087	C	T	SNV	Known	NEK9	Missense
chr14	93407062	93407062	A	G	SNV	Known	ITPK1	Missense
chr14	102695693	102695693	T	C	SNV	Known	MOKRAGE	Missense
chr14	103934488	103934488	T	C	SNV	Known	MARK3	Missense
chr15	40265799	40265799	A	G	SNV	Known	EIF2AK4	Missense
chr15	40477831	40477831	G	A	SNV	Known	BUB1B	Missense
chr15	40564576	40564576	C	T	SNV	Known	PAK6	Missense
chr15	43170793	43170793	A	G	SNV	Known	TTBK2	Missense
chr15	75130093	75130093	T	C	SNV	Known	ULK3	Missense
chr15	77450964	77450964	C	T	SNV	Known	PEAK1.AC087465.1	Missense
chr15	85383145	85383145	C	G	SNV	Known	ALPK3	Missense
chr15	85383640	85383640	G	A	SNV	Known	ALPK3	Missense
chr15	85401259	85401259	C	T	SNV	Known	ALPK3	Missense
chr15	85405995	85405995	T	C	SNV	Known	ALPK3	Missense
chr15	91436551	91436551	A	G	SNV	Novel	FES.AC068831.1	Missense
chr15	99250895	99250895	G	T	SNV	Novel	IGF1R	Missense
chr15	101606889	101606889	G	A	SNV	Known	LRRK1	Missense
chr15	101606890	101606890	C	A	SNV	Known	LRRK1	Missense
chr16	22269867	22269867	A	G	SNV	Known	EEF2K	Missense
chr16	23646191	23646191	T	C	SNV	Known	PALB2	Missense
chr16	23690401	23690401	C	T	SNV	Novel	PLK1	Missense
chr16	23711925	23711925	C	G	SNV	Known	ERN2	Missense
chr16	46744689	46744689	C	A	SNV	Known	MYLK3	Missense
chr16	46773999	46773999	C	A	SNV	Known	MYLK3	Missense
chr16	68732049	68732049	A	C	SNV	Known	CDH3	Missense
chr17	3627473	3627473	C	T	SNV	Known	ITGAE.GSG2	Missense
chr17	3627840	3627840	G	A	SNV	Known	ITGAE.GSG2	Missense
chr17	3628212	3628212	T	C	SNV	Known	ITGAE.GSG2	Missense
chr17	3628362	3628362	T	C	SNV	Known	ITGAE.GSG2	Missense
chr17	3775848	3775848	T	C	SNV	Known	CAMKK1	Missense
chr17	4796274	4796274	T	C	SNV	Known	MINK1	Missense
chr17	4796286	4796286	C	T	SNV	Known	MINK1	Missense
chr17	4797305	4797305	G	A	SNV	Known	MINK1	Missense
chr17	7292107	7292107	G	A	SNV	Known	TNK1	Missense
chr17	7579472	7579472	G	C	SNV	Known	TP53	Missense
chr17	7792326	7792326	C	T	SNV	Known	CHD3	Missense
chr17	7796794	7796794	A	C	SNV	Novel	CHD3	Missense
chr17	7796803	7796803	T	C	SNV	Novel	CHD3	Missense
chr17	7796815	7796815	G	C	SNV	Novel	CHD3	Missense
chr17	8108331	8108331	A	G	SNV	Known	AURKB	Missense
chr17	8789811	8789811	G	A	SNV	Novel	PIK3R5	Nonsense
chr17	19285705	19285705	G	A	SNV	Known	MAPK7	Missense
chr17	25909816	25909816	C	T	SNV	Known	KSR1	Missense
chr17	37879588	37879588	A	G	SNV	Known	ERBB2	Missense
chr17	37881392	37881392	A	G	SNV	Novel	ERBB2.MIR4728	Missense
chr17	37884037	37884037	C	G	SNV	Known	ERBB2	Missense
chr17	41223094	41223094	T	C	SNV	Known	BRCA1	Missense
chr17	41244000	41244000	T	C	SNV	Known	BRCA1	Missense
chr17	41244435	41244435	T	C	SNV	Known	BRCA1	Missense
chr17	41244936	41244936	G	A	SNV	Known	BRCA1	Missense
chr17	41245693	41245693	G	T	SNV	Novel	BRCA1	Missense
chr17	48265495	48265495	T	C	SNV	Known	COL1A1	Missense
chr17	56584508	56584508	T	C	SNV	Known	MTMR4	Missense

chr17	56659018	56659018	C	T	SNV	Known	TEX14	Missense
chr17	64783081	64783081	G	A	SNV	Known	PRKCA.MIR634	Missense
chr17	74381567	74381567	G	A	SNV	Known	SPHK1	Missense
chr17	79093822	79093822	A	G	SNV	Known	AATK	Missense
chr17	79095629	79095629	C	A	SNV	Known	AATK	Missense
chr18	18534948	18534948	G	C	SNV	Known	ROCK1	Missense
chr18	48190440	48190440	G	A	SNV	Known	MAPK4	Missense
chr18	53303101	53303101	C	G	SNV	Known	TCF4	Missense
chr18	56149099	56149099	T	C	SNV	Known	ALPK2	Missense
chr18	56203898	56203898	T	G	SNV	Known	ALPK2	Missense
chr18	56204250	56204250	A	C	SNV	Known	ALPK2	Missense
chr18	56204747	56204747	G	A	SNV	Known	ALPK2	Missense
chr18	56279025	56279025	T	G	SNV	Known	ALPK2	Missense
chr18	59854988	59854988	G	T	SNV	Novel	KIAA1468.PIGN	Missense
chr18	59919898	59919898	C	A	SNV	Novel	KIAA1468	Missense
chr19	2046399	2046399	G	A	SNV	Novel	MKNK2	Missense
chr19	10473048	10473048	G	A	SNV	Known	TYK2	Missense
chr19	10475652	10475652	C	A	SNV	Known	TYK2	Missense
chr19	14574897	14574897	C	A	SNV	Known	PKN1	Missense
chr19	14582468	14582468	G	A	SNV	Known	PKN1	Missense
chr19	17949138	17949138	C	A	SNV	Novel	JAK3	Missense
chr19	18255359	18255359	G	A	SNV	Known	MAST3	Missense
chr19	18273047	18273047	T	C	SNV	Known	PIK3R2	Missense
chr19	38896244	38896244	C	A	SNV	Known	FAM98C	Missense
chr19	40739513	40739513	A	G	SNV	Known	AKT2	Missense
chr19	41211056	41211056	T	C	SNV	Known	ADCK4	Missense
chr19	41743861	41743861	A	G	SNV	Known	AXL	Missense
chr19	46275976	46275976	G	C	SNV	Known	DMPK	Missense
chr19	47177913	47177913	A	G	SNV	Known	PRKD2.LOC100506068	Missense
chr19	47193933	47193933	G	T	SNV	Novel	PRKD2	Missense
chr19	56041255	56041255	C	G	SNV	Known	SBK2	Missense
chr19	56047448	56047448	A	G	SNV	Known	SBK2	Missense
chr19	56047544	56047544	G	T	SNV	Novel	SBK2	Missense
chr20	9543622	9543622	C	T	SNV	Known	PAK7	Missense
chr20	30407433	30407433	C	A	SNV	Known	MYLK2	Missense
chr20	54961463	54961463	T	C	SNV	Known	AURKA	Missense
chr20	54961541	54961541	A	T	SNV	Known	AURKA	Missense
chr21	33371123	33371123	C	T	SNV	Known	HUNK	Missense
chr21	43161357	43161357	T	C	SNV	Known	RIPK4.AP001615.9	Missense
chr21	44837555	44837555	G	A	SNV	Known	SIK1	Missense
chr21	45959312	45959312	C	T	SNV	Known	TSPEAR.KRTAP10-1	Missense
chr22	31673116	31673116	A	G	SNV	Known	LIMK2	Missense
chr22	50696678	50696678	G	A	SNV	Known	MAPK12	Missense
chr22	50705059	50705059	A	G	SNV	Known	MAPK11	Missense
chr22	50705304	50705304	C	T	SNV	Known	MAPK11	Nonsense
chrX	3631167	3631167	A	G	SNV	Known	PRKX	Missense
chrX	19482476	19482476	C	T	SNV	Known	MAP3K15	Missense
chrX	107976940	107976940	G	C	SNV	Known	IRS4	Missense
chrX	108708516	108708516	C	T	SNV	Known	GUCY2F	Missense
chrX	153278829	153278829	G	A	SNV	Known	IRAK1	Missense
chrX	153284192	153284192	A	G	SNV	Known	IRAK1	Missense

quality score: ≥ 30 ; depth: ≥ 8

Functions: non-synonymous (missense, nonsense or read-through)

novel genotypes (SNVs not reported in dbSNP135 data or Phase 1 of the 1000 Genomes data)

dbSNP
rs150949339 P=chr1:1571841 ST=+ AL=A/C
rs6658335 P=chr1:1575784 ST=+ AL=C/T
rs1059811 P=chr1:1635011 ST=+ AL=A/G
rs6658335 P=chr1:1638994 ST=+ AL=C/T rs139262276 P=chr1:1638994 ST=+ AL=C/T
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rs999765 P=chr1:22923873 ST=- AL=C/G
rs1138294 P=chr1:27688633 ST=- AL=C/T
rs3795498 P=chr1:36807481 ST=- AL=A/G
rs4653328 P=chr1:38227086 ST=+ AL=A/T
rs56276182 P=chr1:38227268 ST=+ AL=G/T
rs11211247 P=chr1:46476587 ST=+ AL=G/T
rs1707336 P=chr1:46493460 ST=+ AL=G/T
rs785467 P=chr1:46521559 ST=- AL=A/T
rs7527017 P=chr1:64643277 ST=+ AL=C/T
rs10783071 P=chr1:92428495 ST=+ AL=A/C
rs10747493 P=chr1:92457843 ST=+ AL=C/T
rs6537825 P=chr1:114948281 ST=+ AL=A/G
rs4656197 P=chr1:169823718 ST=+ AL=A/C/G/T
rs486907 P=chr1:182554557 ST=- AL=A/G
rs3851294 P=chr1:205130413 ST=+ AL=A/G
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rs77571454 P=chr1:205500478 ST=+ AL=A/G
rs708776 P=chr1:226923505 ST=- AL=A/C
rs2802269 P=chr1:227182033 ST=+ AL=A/C/G/T
rs1929860 P=chr1:227216775 ST=- AL=A/C/G/T
rs1771487 P=chr1:228402121 ST=- AL=C/T
rs7532342 P=chr1:228444565 ST=+ AL=A/T
rs1188721 P=chr1:228464248 ST=+ AL=G/T
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rs56249237 P=chr1:228509589 ST=+ AL=A/G
rs3795375 P=chr1:233514934 ST=- AL=C/T
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rs963981 P=chr1:233515102 ST=- AL=A/C
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rs1881421 P=chr2:29416366 ST=- AL=C/G
rs1881420 P=chr2:29416481 ST=- AL=A/G
rs1670283 P=chr2:29416572 ST=+ AL=C/T
rs187184761 P=chr2:42275664 ST=+ AL=C/T
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rs867529 P=chr2:88913273 ST=+ AL=C/G
rs2278206 P=chr2:99172244 ST=- AL=C/T
rs3905317 P=chr2:135744007 ST=- AL=A/G
rs1112542 P=chr2:135744416 ST=- AL=C/G

rs4668246 P=chr2:171225841 ST=+ AL=A/G
rs6736609 P=chr2:171260787 ST=+ AL=A/G
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rs3769148 P=chr2:174128513 ST=- AL=A/G
rs3829747 P=chr2:179397561 ST=- AL=A/G
rs3731749 P=chr2:179406191 ST=- AL=A/G

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rs3731746 P=chr2:179430997 ST=- AL=A/C/T
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rs2288569 P=chr2:179458591 ST=- AL=A/G
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rs72648960 P=chr2:179589058 ST=- AL=C/T
rs922984 P=chr2:179615887 ST=+ AL=C/T
rs922985 P=chr2:179615931 ST=+ AL=C/G
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rs6433728 P=chr2:179621477 ST=+ AL=C/T
rs2291310 P=chr2:179623758 ST=+ AL=C/T
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rs10932258 P=chr2:209184980 ST=+ AL=A/G
rs2363468 P=chr2:209190330 ST=+ AL=C/T
rs893254 P=chr2:209190519 ST=- AL=A/T
rs893253 P=chr2:209190528 ST=- AL=C/G
rs1529979 P=chr2:209191082 ST=- AL=G/T

rs116911250 P=chr2:220337041 ST=+ AL=A/G
rs55760516 P=chr2:220354108 ST=+ AL=A/G
rs1131293 P=chr2:242046785 ST=- AL=G/T
rs3815305 P=chr2:242054403 ST=+ AL=A/G
rs6709462 P=chr2:242082262 ST=+ AL=C/T
rs708035 P=chr3:10276163 ST=+ AL=A/T
rs10510592 P=chr3:27332820 ST=- AL=C/T

rs4973986 P=chr3:41841716 ST=+ AL=A/C
rs1052501 P=chr3:41925398 ST=- AL=A/G
rs1716975 P=chr3:41960006 ST=+ AL=A/C/G/T

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rs7433231	P=chr3:49928691	ST=+	AL=C/T
rs1029871	P=chr3:52797634	ST=-	AL=C/G
rs142909067	P=chr3:96585671	ST=+	AL=A/G
rs3732487	P=chr3:123419573	ST=-	AL=A/C
rs3732486	P=chr3:123419733	ST=-	AL=C/T
rs9833275	P=chr3:123451773	ST=+	AL=C/G
rs3796164	P=chr3:123453061	ST=+	AL=A/G
rs9840993	P=chr3:123457893	ST=+	AL=A/C/G/T
rs3738000	P=chr3:130947435	ST=+	AL=A/T
rs2227928	P=chr3:142281612	ST=-	AL=C/T
rs3732576	P=chr3:185198262	ST=-	AL=C/T
rs2193587	P=chr3:185990096	ST=-	AL=A/G
rs1004588	P=chr3:186006618	ST=-	AL=C/G
rs142107211	P=chr4:843498	ST=+	AL=A/G
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rs1024323	P=chr4:3006043	ST=-	AL=A/G
rs3733182	P=chr4:5448429	ST=-	AL=C/T
rs10021593	P=chr4:25235801	ST=+	AL=A/G
rs1870377	P=chr4:55972974	ST=+	AL=A/T
rs2288255	P=chr4:79786856	ST=-	AL=C/T
rs3775091	P=chr4:107168431	ST=-	AL=C/G
rs2074388	P=chr4:113352397	ST=+	AL=A/G
rs13148353	P=chr4:113352628	ST=+	AL=A/G
rs2074379	P=chr4:113352899	ST=+	AL=A/G
rs11726117	P=chr4:113353285	ST=+	AL=C/T
rs3811740	P=chr4:128807219	ST=-	AL=A/T
rs13152819	P=chr4:151177340	ST=+	AL=C/T
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rs34099167	P=chr4:170398454	ST=+	AL=C/T
rs702689	P=chr5:56177443	ST=+	AL=A/G
rs832582	P=chr5:56177743	ST=+	AL=A/G
rs1705399	P=chr5:66459878	ST=-	AL=C/G
rs3730089	P=chr5:67588148	ST=+	AL=A/G
rs160632	P=chr5:96503523	ST=-	AL=A/G
rs2544773	P=chr5:96513471	ST=+	AL=C/G
rs3734010	P=chr5:96518792	ST=-	AL=A/C
rs459552	P=chr5:112176756	ST=-	AL=A/T
rs10079250	P=chr5:149450132	ST=+	AL=C/T
rs1966265	P=chr5:176516631	ST=+	AL=A/G
rs376618	P=chr5:176517797	ST=-	AL=A/G
rs351855	P=chr5:176520243	ST=-	AL=C/T
rs448012	P=chr5:180046344	ST=+	AL=C/G
rs12523992	P=chr6:2679676	ST=+	AL=A/G
rs9503893	P=chr6:4031998	ST=+	AL=A/G
rs149333646	P=chr6:31946695	ST=+	AL=C/G
rs4713668	P=chr6:33690796	ST=+	AL=C/T
rs139720178	P=chr6:33695975	ST=+	AL=A/G
rs1051130	P=chr6:41903782	ST=-	AL=A/C/G/T

rs3800297	P=chr6:43251912	ST=+	AL=A/G
rs3800298	P=chr6:43252029	ST=+	AL=C/T
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rs2233433	P=chr6:44232977	ST=-	AL=C/T
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rs3752566	P=chr6:117638325	ST=-	AL=A/G
rs35551087	P=chr6:136888782	ST=+	AL=C/T
rs4559074	P=chr6:161469774	ST=+	AL=A/G
rs943687	P=chr6:167271711	ST=+	AL=C/T
rs9347162	P=chr6:167271716	ST=+	AL=C/T
rs6945306	P=chr7:23757162	ST=+	AL=C/G
rs10264952	P=chr7:23775454	ST=+	AL=A/G
rs10264967	P=chr7:23775477	ST=+	AL=G/T
rs10263079	P=chr7:23811795	ST=+	AL=G/T
rs10247878	P=chr7:23811800	ST=+	AL=G/T
rs3735135	P=chr7:40027484	ST=-	AL=C/T
rs56286238	P=chr7:43635671	ST=+	AL=A/C
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rs11765552	P=chr7:97822115	ST=+	AL=A/T
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rs55793951	P=chr8:48719852	ST=+	AL=C/G
rs6998760	P=chr8:87076520	ST=+	AL=A/C
rs6420191	P=chr8:144802736	ST=+	AL=C/G
rs6599528	P=chr8:145603114	ST=+	AL=A/C
rs35969327	P=chr9:27168571	ST=+	AL=C/T
rs682632	P=chr9:27183463	ST=-	AL=G/T
rs3730386	P=chr9:71628207	ST=-	AL=C/G
rs2274924	P=chr9:77376647	ST=-	AL=A/G
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rs10820900	P=chr9:94495608	ST=+	AL=C/T
rs35176182	P=chr9:113457799	ST=+	AL=A/G
rs2274419	P=chr9:113538122	ST=-	AL=C/T
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rs3124747	P=chr9:136268084	ST=-	AL=C/T
rs2236379	P=chr10:6527143	ST=-	AL=C/T
rs3824699	P=chr10:26355992	ST=-	AL=C/T

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rs4783453 P=chr16:22269867 ST=+ AL=A/G
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rs9907144 P=chr17:3627473 ST=+ AL=C/T
rs220462 P=chr17:3627840 ST=- AL=C/T
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rs3809806 P=chr17:3628362 ST=- AL=A/G
rs7214723 P=chr17:3775848 ST=+ AL=C/T
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rs16942 P=chr17:41244000 ST=- AL=A/G
rs16941 P=chr17:41244435 ST=- AL=A/G
rs799917 P=chr17:41244936 ST=- AL=A/C/T
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rs7503604 P=chr17:79095629 ST=+ AL=A/C
rs2847092 P=chr18:18534948 ST=+ AL=C/G
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rs7240666 P=chr18:56149099 ST=+ AL=A/C/G/T
rs3809977 P=chr18:56203898 ST=- AL=A/C
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rs3826593 P=chr18:56204747 ST=- AL=C/T
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rs2304256 P=chr19:10475652 ST=+ AL=A/C
rs34309238 P=chr19:14574897 ST=+ AL=A/C
rs10846 P=chr19:14582468 ST=+ AL=A/G
rs8108738 P=chr19:18255359 ST=+ AL=A/G
rs1011320 P=chr19:18273047 ST=+ AL=C/T
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rs33933140 P=chr19:40739513 ST=+ AL=A/G
rs3865452 P=chr19:41211056 ST=+ AL=C/T
rs7249222 P=chr19:41743861 ST=+ AL=A/G
rs527221 P=chr19:46275976 ST=+ AL=C/G
rs314665 P=chr19:47177913 ST=- AL=C/T
rs620251 P=chr19:56041255 ST=- AL=C/G
rs310453 P=chr19:56047448 ST=- AL=C/T
rs2297345 P=chr20:9543622 ST=+ AL=C/T
rs192056427 P=chr20:30407433 ST=+ AL=A/C
rs1047972 P=chr20:54961463 ST=- AL=A/G
rs2273535 P=chr20:54961541 ST=+ AL=A/T
rs10775648 P=chr21:33371123 ST=+ AL=C/T
rs3746891 P=chr21:43161357 ST=+ AL=C/T
rs430554 P=chr21:44837555 ST=+ AL=A/G
rs233317 P=chr21:45959312 ST=- AL=A/G
rs3747154 P=chr22:31673116 ST=+ AL=A/G
rs34422484 P=chr22:50696678 ST=+ AL=A/G
rs742185 P=chr22:50705059 ST=+ AL=A/G
rs760747 P=chr22:50705304 ST=+ AL=C/T
rs3752362 P=chrX:3631167 ST=+ AL=A/G
rs5909299 P=chrX:19482476 ST=+ AL=C/T
rs1801164 P=chrX:107976940 ST=- AL=C/G/T
rs502209 P=chrX:108708516 ST=- AL=A/G
rs1059703 P=chrX:153278829 ST=- AL=C/T
rs1059702 P=chrX:153284192 ST=- AL=C/T

CCDS2205.1|GN=ACVR1|C|G|=130399|FC=Missense|CP=58|CF=0|AC=gCC->tCC|RP=20|RC=Ala|Ala->S|Ser||EN=179|DS=-41170|P=chr2:158390430-158485156|S

CCDS42773.1|GN=MYO3B|G|=140469|FC=Missense|CP=925|CF=0|AC=aAG->gAG|RP=309|RC=K|L|vs|>E|Glu||EN=9/35|DS=+110|P=chr2:171034798-171509631|S

CCDS42773.1|GN=MYO3B|G|=140469|FC=Missense|CP=2308|CF=0|AC=gTA->aTA|RP=770|RC=V|Val|>I|Ile||EN=20/35|DS=+31|P=chr2:171034798-171509631|S

CCDS42773.1|GN=MYO3B|G|=140469|FC=Missense|CP=3245|CF=1|AC=A-gG->AaG|RP=1082|RC=R|Arg|>K|L|vs|>E|Glu||EN=27/35|DS=+119|P=chr2:171034798-171509631|S

CCDS42777.1|GN=ZAK1|G|=51776|FC=Missense|CP=1592|CF=1|AC=TcG->TtG|RP=531|RC=S|Ser|>L|Leu||EN=18/19|DS=+41|P=chr2:173955760-174131478|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=96077|CF=1|AC=cGc->CaC|RP=32026|RC=R|Arg|>H|His||EN=306/311|DS=-2718|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=89909|CF=1|AC=Cgc->CaC|RP=29970|RC=R|Arg|>H|His||EN=298/311|DS=+121|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=88910|CF=1|AC=GtC->GcG|RP=29637|RC=V|Val|>A|Ala||EN=295/311|DS=+304|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=80483|CF=1|AC=AtC->AcC|RP=26828|RC=I|Ile|>T|Thr||EN=278/311|DS=+178|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=77947|CF=0|AC=cCA->aCA|RP=25983|RC=P|Pro|>T|Thr||EN=274/311|DS=-1844|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=75619|CF=0|AC=aTA->gTA|RP=25207|RC=I|Ile|>V|Val||EN=274/311|DS=-4172|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=72158|CF=1|AC=A-cG->AtG|RP=24053|RC=T|Thr|>M|Met||EN=274/311|DS=-7633|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=67135|CF=0|AC=cGC->TcG|RP=22379|RC=R|Arg|>C|Cys||EN=274/311|DS=+5124|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=59542|CF=0|AC=gCT->cCT|RP=19848|RC=A|Ala|>P|Pro||EN=266/311|DS=+189|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=59371|CF=0|AC=gTC->aTC|RP=19791|RC=V|Val|>I|Ile||EN=266/311|DS=+181|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=56504|CF=1|AC=A-cT->AtT|RP=18835|RC=T|Thr|>I|Ile||EN=256/311|DS=+115|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=51881|CF=1|AC=CcA->CtA|RP=17294|RC=P|Pro|>L|Leu||EN=249/311|DS=-1431|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=50732|CF=1|AC=Cgt->Cat|RP=16911|RC=R|Arg|>H|His||EN=246/311|DS=+41|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=48397|CF=0|AC=aAT->gAT|RP=16133|RC=N|Asn|>D|Asp||EN=237/311|DS=+511|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=43778|CF=1|AC=GcG->GtG|RP=14593|RC=A|Ala|>V|Val||EN=220/311|DS=+461|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=32402|CF=1|AC=CcA->CtA|RP=10801|RC=P|Pro|>R|Arg||EN=162/311|DS=+791|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=27832|CF=0|AC=aTT->gTT|RP=9278|RC=I|Ile|>V|Val||EN=115/311|DS=+511|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=22676|CF=1|AC=AaT->AgT|RP=7559|RC=N|Asn|>S|Ser||EN=87/311|DS=-1911|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=21542|CF=1|AC=A-gC->AaC|RP=7181|RC=S|Ser|>N|Asn||EN=83/311|DS=+211|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=21332|CF=1|AC=GcG->GaG|RP=7111|RC=A|Ala|>E|Glu||EN=83/311|DS=+11|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=20699|CF=1|AC=GaA->GcA|RP=6900|RC=E|Glu|>A|Ala||EN=80/311|DS=-1691|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=18652|CF=0|AC=gAT->cAT|RP=6218|RC=D|Asp|>H|His||EN=73/311|DS=+144|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=17312|CF=1|AC=GcA->GtA|RP=5771|RC=A|Ala|>V|Val||EN=68/311|DS=-1881|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Intron|EN=44:45/311|DS=+1964|P=chr2:179391739-179669369|S|T=-|C|=100272|CS=Public CCDS54422.1|GN=TTN|G|=7273|FC=Intron|EN=44:45/311|DS=+1920|P=chr2:179391739-179669369|S|T=-|C|=100272|CS=Public CCDS54422.1|GN=TTN|G|=7273|FC=Missense|CP=10739|CF=1|AC=Ggt->Gat|RP=3580|RC=G|Gly|>D|Asp||EN=43/191|DS=+574|P=chr2:179391739-179669369|S

CCDS54422.1|GN=TTN|G|=7273|FC=Missense|CP=10213|CF=0|AC=gCC->aCC|RP=3405|RC=A|Ala|>T|Thr||EN=43/191|DS=+481|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=10256|CF=1|AC=Agt->Aat|RP=3419|RC=S|Ser|>N|Asn||EN=43/311|DS=+1421|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=9781|CF=0|AC=gTG->aTG|RP=3261|RC=V|Val|>M|Met||EN=41/311|DS=+781|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=8887|CF=0|AC=aCC->cCC|RP=2963|RC=T|Thr|>P|Pro||EN=36/311|DS=+2461|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=7619|CF=1|AC=Cgt->Cat|RP=2540|RC=R|Arg|>H|His||EN=32/311|DS=+251|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=3884|CF=1|AC=TcA->tA|RP=1295|RC=S|Ser|>L|Leu||EN=22/311|DS=+1551|P=chr2:179391739-179669369|S

CCDS54424.1|GN=TTN|G|=7273|FC=Missense|CP=982|CF=0|AC=cGT->tGT|RP=328|RC=R|Arg|>C|Cys||EN=6/311|DS=+681|P=chr2:179391739-179669369|S

CCDS2382.1|GN=PIKEYVE|G|=200576|FC=Missense|CP=2087|CF=1|AC=AgT->AaT|RP=696|RC=S|Ser|>N|Asn||EN=16/41|DS=+51|P=chr2:209136244-209220029|S

CCDS2382.1|GN=PIKEYVE|G|=200576|FC=Missense|CP=2795|CF=1|AC=TtG->TcG|RP=932|RC=I|Ile|>S|Ser||EN=19/41|DS=+337|P=chr2:209136244-209220029|S

CCDS2382.1|GN=PIKEYVE|G|=200576|FC=Missense|CP=2984|CF=1|AC=CaG->CtG|RP=995|RC=Q|Gln|>L|Leu||EN=19/41|DS=+5261|P=chr2:209136244-209220029|S

CCDS2382.1|GN=PIKEYVE|G|=200576|FC=Missense|CP=2993|CF=1|AC=A-cT->AgT|RP=998|RC=T|Thr|>S|Ser||EN=19/41|DS=+5351|P=chr2:209136244-209220029|S

CCDS2382.1|GN=PIKEYVE|G|=200576|FC=Missense|CP=3547|CF=0|AC=cAA->aAA|RP=1183|RC=Q|Gln|>K|L|vs|>E|Glu||EN=19/41|DS=+10891|P=chr2:209136244-209220029|S

CCDS2382.1|GN=PIKEYVE|G|=200576|FC=Missense|CP=3793|CF=0|AC=cCT->aCT|RP=1265|RC=P|Pro|>T|Thr||EN=22/41|DS=+21|P=chr2:209136244-209220029|S

CCDS42824.1|GN=SPFG|G|=10290|FC=Missense|CP=3928|CF=0|AC=gAC->aAC|RP=1310|RC=D|Asp|>N|Asn||EN=15/41|DS=+931|P=chr2:220299700-220357508|S

CCDS42824.1|GN=SPFG|G|=10290|FC=Missense|CP=8368|CF=0|AC=aGG->gGG|RP=2790|RC=R|Arg|>G|Gly||EN=36/41|DS=+511|P=chr2:220299700-220357508|S

CCDS2545.1|GN=PASK|G|=23178|FC=Missense|CP=3797|CF=1|AC=TtT->TtG|RP=1266|RC=F|Phe|>C|Cys||EN=16/17|DS=+1301|P=chr2:242045981-242082447|S

CCDS2545.1|GN=PASK|G|=23178|FC=Intron|EN=13:14/17|DS=+551|P=chr2:242045981-242082447|S|T=-|C|=3972|CS=Public

CCDS2545.1|GN=PASK|G|=23178|FC=Synonymous-Coding|CP=186|CF=2|AC=ACa->ACg|RP=62|RC=T|Thr|>T|Thr||EN=1/17|DS=-20941|P=chr2:242045981-242082447|S

CCDS33697.1|GN=IRAK2|G|=3656|FC=Missense|CP=1293|CF=2|AC=Gat->Gaa|RP=431|RC=D|Asp|>E|Glu||EN=11/13|DS=+211|P=chr3:10206639-102839121|S

CCDS46781.1|GN=NEK10|G|=15210|FC=Missense|CP=1538|CF=1|AC=TtG->TcG|RP=513|RC=I|Ile|>S|Ser||EN=17/23|DS=+621|P=chr3:27257323-273943731|S

CCDS43071.1|GN=ULK4|G|=54986|FC=Missense|CP=2990|CF=1|AC=AtT->AgT|RP=997|RC=I|Ile|>S|Ser||EN=29/36|DS=+121|P=chr3:41288420-419962511|S|T=-|C|=10288420-419962511|S

CCDS43071.1|GN=ULK4|G|=54986|FC=Missense|CP=1918|CF=0|AC=tCC->gCC|RP=640|RC=S|Ser|>A|Ala||EN=19/36|DS=+701|P=chr3:41288420-419962511|S|T=-|C|=10288420-419962511|S

CCDS43071.1|GN=ULK4|G|=54986|FC=Missense|CP=1624|CF=0|AC=gCT->aCT|RP=542|RC=A|Ala|>T|Thr||EN=16/36|DS=+471|P=chr3:41288420-419962511|S|T=-|C|=10288420-419962511|S

CCDS43071.1|GN=ULK4|G|=54986|FC=Missense|CP=670|CF=0|AC=aTT->gTT|RP=224|RC=I|Ile|>V|Val||EN=6/36|DS=+271|P=chr3:41288420-419962511|S|T=-|C|=10288420-419962511|S

CCDS43071.1|GN=ULK4|GI=54986|FC=Missense|CP=116|CF=1|AC=AaA->AgA|RP=39|RC=KI|vs|->R|Arg||EN=1/36|DS=-16447|P=chr3:41288420-41996251|ST=-|C|=

CCDS2807.1|GN=MST1R|GI=4486|FC=Missense|CP=3583|CF=0|AC=aGC->gGC|RP=1195|RC=SI|Ser|->G|Glv||EN=17/20|DS=+49|P=chr3:49924740-49941042|ST=-|C|=

CCDS2863.1|GN=NEK4|GI=6787|FC=Missense|CP=673|CF=0|AC=cCA->gCA|RP=225|RC=PI|Pro|->A|Ala||EN=5/16|DS=+7|P=chr3:52745793-52804762|ST=-|C|=

CCDS46876.1|GN=EPHA6|GI=285220|FC=Missense|CP=388|CF=0|AC=gTC->aTC|RP=130|RC=V|Val|->M|Met||EN=2/18|DS=+3|P=chr3:96533468-97467545|ST=-|C|=

CCDS46896.1|GN=MYLK|GI=4638|FC=Missense|CP=2742|CF=2|AC=GAc->GAa|RP=914|RC=D|Asp|->E|Glu||EN=15/31|DS=+280|P=chr3:123332952-123512688|ST=-|C|=

CCDS46896.1|GN=MYLK|GI=4638|FC=Missense|CP=2582|CF=1|AC=CtA->CcA|RP=861|RC=I|Leu|->P|Pro||EN=15/31|DS=+120|P=chr3:123332952-123512688|ST=-|C|=

CCDS46896.1|GN=MYLK|GI=4638|FC=Missense|CP=1486|CF=0|AC=cTC->gTC|RP=496|RC=I|Leu|->V|Val||EN=8/31|DS=+177|P=chr3:123332952-123512688|ST=-|C|=

CCDS46896.1|GN=MYLK|GI=4638|FC=Missense|CP=782|CF=1|AC=GtG->GcG|RP=261|RC=V|Val|->A|Ala||EN=7/31|DS=+9|P=chr3:123332952-123512688|ST=-|C|=

CCDS46896.1|GN=MYLK|GI=4638|FC=Missense|CP=439|CF=0|AC=cCA->tCA|RP=147|RC=PI|Pro|->S|Ser||EN=4/31|DS=+17|P=chr3:123332952-123512688|ST=-|C|=

CCDS3027.1|GN=KALRN|GI=8997|FC=Missense|CP=880|CF=0|AC=cAC->aAC|RP=294|RC=HI|His|->N|Asn||EN=5/34|DS=+430|P=chr3:123813685-124237309|ST=-|C|=

CCDS3069.1|GN=NEK11|GI=79858|FC=Missense|CP=1463|CF=1|AC=GaA->GtA|RP=488|RC=EI|Glu|->V|Val||EN=13/16|DS=+64|P=chr3:130748553-131068620|ST=-|C|=

CCDS3124.1|GN=ATR|GI=545|FC=Missense|CP=632|CF=1|AC=AtG->AcG|RP=211|RC=M|Met|->T|Thr||EN=4/47|DS=+340|P=chr3:142168271-142297546|ST=-|C|=

CCDS3270.1|GN=MAP3K13|GI=9175|FC=Missense|CP=2744|CF=1|AC=Cgt->CaT|RP=915|RC=R|Arg|->H|His||EN=12/13|DS=+243|P=chr3:185146370-185200244|ST=-|C|=

CCDS3274.1|GN=DGKG|GI=1608|FC=Missense|CP=947|CF=1|AC=AgA->AaA|RP=316|RC=RI|Arg|->K|Lys||EN=10/24|DS=+37|P=chr3:185867879-186038248|ST=-|C|=

CCDS3274.1|GN=DGKG|GI=1608|FC=Missense|CP=425|CF=1|AC=AcC->AgC|RP=142|RC=TI|Thr|->S|Ser||EN=5/24|DS=+52|P=chr3:185867879-186038248|ST=-|C|=

CCDS3340.1|GN=GAK|GI=2580|FC=Missense|CP=3899|CF=1|AC=IcG->ItG|RP=1300|RC=SI|Ser|->L|Leu||EN=28/28|DS=+65|P=chr4:843461-925975|ST=-|C|=3

CCDS33946.1|GN=GRK4|GI=2868|FC=Missense|CP=194|CF=1|AC=Cgt->CtT|RP=65|RC=RI|Arg|->L|Leu||EN=3/16|DS=+46|P=chr4:2965798-3042352|ST=-|C|=

CCDS33946.1|GN=GRK4|GI=2868|FC=Missense|CP=425|CF=1|AC=GcC->GtC|RP=142|RC=A|Ala|->V|Val||EN=5/16|DS=+86|P=chr4:2965798-3042352|ST=-|C|=

CCDS3380.1|GN=STK32B|GI=55351|FC=Missense|CP=592|CF=0|AC=aGA->gGA|RP=198|RC=R|Arg|->G|Glv||EN=7/12|DS=+30|P=chr4:5053591-5500810|ST=-|C|=

CCDS3433.1|GN=PI4K2B|GI=55300|FC=Missense|CP=161|CF=0|AC=gAG->aAG|RP=6|RC=EI|Glu|->K|Lys||EN=1/10|DS=-18142|P=chr4:25235786-25278809|ST=-|C|=

CCDS3497.1|GN=KDR|GI=3791|FC=Missense|CP=1416|CF=2|AC=CAa->CaT|RP=472|RC=Q|Gln|->H|His||EN=11/30|DS=+4|P=chr4:55946108-55991460|ST=-|C|=

CCDS47083.1|GN=BMP2K|GI=55589|FC=Missense|CP=1213|CF=0|AC=gGT->aGT|RP=405|RC=GI|Glv|->S|Ser||EN=10/16|DS=+146|P=chr4:79697698-79833187|ST=-|C|=

CCDS54788.1|GN=TBCK1|GI=93627|FC=Missense|CP=796|CF=0|AC=cAA->gAA|RP=266|RC=Q|Gln|->E|Glu||EN=9/25|DS=+14|P=chr4:106967727-107230117|ST=-|C|=

CCDS3697.1|GN=ALPK1|GI=80216|FC=Missense|CP=1694|CF=1|AC=Ggt->GaT|RP=565|RC=G|Glv|->D|Asp||EN=9/14|DS=+794|P=chr4:113298934-113362366|ST=-|C|=

CCDS3697.1|GN=ALPK1|GI=80216|FC=Missense|CP=1925|CF=1|AC=Cat->Cgt|RP=642|RC=HI|His|->R|Arg||EN=9/14|DS=+1025|P=chr4:113298934-113362366|ST=-|C|=

CCDS3697.1|GN=ALPK1|GI=80216|FC=Missense|CP=2196|CF=2|AC=ATg->ATa|RP=732|RC=M|Met|->I|Ile||EN=9/14|DS=+1296|P=chr4:113298934-113362366|ST=-|C|=

CCDS3697.1|GN=ALPK1|GI=80216|FC=Missense|CP=2582|CF=1|AC=AtG->AcG|RP=861|RC=M|Met|->T|Thr||EN=9/14|DS=+1682|P=chr4:113298934-113362366|ST=-|C|=

CCDS3735.1|GN=PLK4|GI=10733|FC=Missense|CP=694|CF=0|AC=ctT->aCT|RP=232|RC=SI|Ser|->T|Thr||EN=5/16|DS=+357|P=chr4:128802290-128819696|ST=-|C|=

CCDS47142.2|GN=DCLK2|GI=166614|FC=Missense|CP=2293|CF=0|AC=cCT->tCT|RP=765|RC=PI|Pro|->S|Ser||EN=17/17|DS=+169|P=chr4:151000180-15117739|ST=-|C|=

CCDS47142.2|GN=DCLK2|GI=166614|FC=Missense|CP=2294|CF=1|AC=Cct->Cgt|RP=765|RC=PI|Pro|->R|Arg||EN=17/17|DS=+170|P=chr4:151000180-15117739|ST=-|C|=

CCDS56351.1|GN=NEK11|GI=4750|FC=Missense|CP=2255|CF=1|AC=GaA->GgA|RP=752|RC=EI|Glu|->G|Glv||EN=24/34|DS=+50|P=chr4:170315661-170523781|ST=-|C|=

CCDS43318.1|GN=MAP3K1|GI=4214|FC=Missense|CP=2416|CF=0|AC=gAT->aAT|RP=806|RC=D|Asp|->N|Asn||EN=14/20|DS=+47|P=chr5:56111401-56189507|ST=-|C|=

CCDS43318.1|GN=MAP3K1|GI=4214|FC=Missense|CP=2716|CF=0|AC=gTC->aTC|RP=906|RC=V|Val|->I|Ile||EN=14/20|DS=+347|P=chr5:56111401-56189507|ST=-|C|=

CCDS54861.1|GN=MAST4|GI=375449|FC=Missense|CP=4871|CF=1|AC=CgG->CcG|RP=1624|RC=RI|Arg|->P|Pro||EN=29/29|DS=+904|P=chr5:65892484-6646287|ST=-|C|=

CCDS3993.1|GN=PIK3R1|GI=5295|FC=Missense|CP=978|CF=2|AC=ATg->ATa|RP=326|RC=M|Met|->I|Ile||EN=7/15|DS=+62|P=chr5:67522504-67593429|ST=-|C|=

CCDS4089.1|GN=RIOK2|GI=55781|FC=Missense|CP=1045|CF=0|AC=gGG->aGG|RP=349|RC=G|Glv|->R|Arg||EN=8/10|DS=+173|P=chr5:96498765-96518895|ST=-|C|=

CCDS4089.1|GN=RIOK2|GI=55781|FC=Missense|CP=287|CF=1|AC=IcI->Igt|RP=96|RC=SI|Ser|->C|Cys||EN=3/10|DS=+82|P=chr5:96498765-96518895|ST=-|C|=

CCDS4089.1|GN=RIOK2|GI=55781|FC=Intron|EN=1/27|DS=+38|P=chr5:96498765-96518895|ST=-|C|=1659|CS=Public CCDS44884.1|GN=RIOK2|GI=55781|FC=

CCDS4107.1|GN=APC|GI=324|FC=Missense|CP=5465|CF=1|AC=GtC->GaC|RP=1822|RC=V|Val|->D|Asp||EN=15/15|DS=+3507|P=chr5:112090588-112179823|ST=-|C|=

CCDS4112.1|GN=TSK1B|GI=83942|FC=Missense|CP=1010|CF=1|AC=AgG->AaG|RP=337|RC=RI|Arg|->K|Lys||EN=1/17|P=chr5:112769433-112770536|ST=-|C|=

CCDS4302.1|GN=CSF1R|GI=1436|FC=Missense|CP=1085|CF=1|AC=CaC->CgC|RP=362|RC=HI|His|->R|Arg||EN=7/21|DS=+3|P=chr5:149433632-149465990|ST=-|C|=

CCDS4410.1|GN=FGFR4|GI=2264|FC=Missense|CP=28|CF=0|AC=gTC->aTC|RP=10|RC=V|Val|->I|Ile||EN=1/17|DS=-760|P=chr5:176516604-176524677|ST=-|C|=

CCDS4410.1|GN=FGFR4|GI=2264|FC=Missense|CP=407|CF=1|AC=CcC->CcT|RP=136|RC=PI|Pro|->L|Leu||EN=3/17|DS=+52|P=chr5:176516604-176524677|ST=-|C|=

CCDS4410.1|GN=FGFR4|GI=2264|FC=Missense|CP=1162|CF=0|AC=gGG->aGG|RP=388|RC=G|Glv|->R|Arg||EN=8/17|DS=+105|P=chr5:176516604-176524677|ST=-|C|=

CCDS4457.1|GN=FLT4|GI=2324|FC=Missense|CP=2670|CF=2|AC=CAc->CAg|RP=890|RC=HI|His|->Q|Gln||EN=19/30|DS=+23|P=chr5:180030192-180076545|ST=-|C|=

CCDS4457.1|GN=FLT4|GI=2324|FC=Missense|CP=1936|CF=0|AC=gAG->aAG|RP=646|RC=EI|Glu|->K|Lys||EN=13/30|DS=+279|P=chr5:180030192-180076545|ST=-|C|=

CCDS43330.1|GN=MYLK4|GI=340156|FC=Intron|EN=7/8/11|DS=-34|P=chr6:2671535-2749528|ST=-|C|=1167|CS=Public

CCDS4488.1|GN=PRPF4B|GI=8899|FC=Missense|CP=247|CF=0|AC=aTT->gTT|RP=83|RC=I|Leu|->V|Val||EN=2/15|DS=+206|P=chr6:4021660-4060850|ST=-|C|=3

CCDS4733.1|GN=STK19|GI=8859|FC=Missense|CP=583|CF=0|AC=cAG->gAG|RP=195|RC=Q|Gln|->E|Glu||EN=4/8|DS=+16|P=chr6:31939774-31948826|ST=-|C|=

CCDS4733.1|GN=STK19|GI=8859|FC=Missense|CP=688|CF=0|AC=tGT->cGT|RP=230|RC=C|Cys|->R|Arg||EN=5/8|DS=+13|P=chr6:31939774-31948826|ST=-|C|=

CCDS34435.1|GN=IP6K3|GI=117283|FC=Missense|CP=934|CF=0|AC=gTC->aTC|RP=312|RC=V|Val|->I|Ile||EN=5/5|DS=+169|P=chr6:33690497-33703253|ST=-|C|=

CCDS34435.1|GN=IP6K3|GI=117283|FC=Missense|CP=302|CF=1|AC=IcG->ItG|RP=101|RC=SI|Ser|->L|Leu||EN=2/5|DS=+103|P=chr6:33690497-33703253|ST=-|C|=

CCDS4822.1|GN=STK38|GI=11329|FC=Missense|CP=316|CF=0|AC=gTI->tTI|RP=106|RC=V|Val|->F|Phe||EN=4/13|DS=+10|P=chr6:36463561-36507979|ST=-|C|=

CCDS4863.1|GN=CCND3|GI=896|FC=Missense|CP=775|CF=0|AC=tCT->gCT|RP=259|RC=SI|Ser|->A|Ala||EN=5/5|DS=+64|P=chr6:41903678-41909387|ST=-|C|=

CCDS4884.1|GN=PTK7|GI=5754|FC=Missense|CP=2229|CF=2|AC=GAg->GAt|RP=743|RC=EI|Glu|->D|Asp||EN=14/20|DS=+182|P=chr6:43044227-43128619|ST=-|C|=

CCDS34455.1|GN=TTBK1|GI=84630|FC=Missense|CP=3434|CF=1|AC=AaG->AgG|RP=1145|RC=K|Lvs|>R|Arg|EN=13/14|DS=-809|P=chr6:43214399-43253114|
CCDS34455.1|GN=TTBK1|GI=84630|FC=Missense|CP=3551|CF=1|AC=TtG->TcG|RP=1184|RC=L|L|Leu|>S|Ser|EN=13/14|DS=-692|P=chr6:43214399-43253114|
CCDS34463.1|GN=NFKB1|GI=4794|FC=Missense|CP=581|CF=1|AC=GtC->GcC|RP=194|RC=V|Val|>A|Ala|EN=1/6|DS=-252|P=chr6:44226956-44233500|ST=-|CI|=|CS=Public
CCDS34463.1|GN=NFKB1|GI=4794|FC=Missense|CP=524|CF=1|AC=CcA->CtA|RP=175|RC=PI|Pro|>L|L|Leu|EN=1/6|DS=-2578|P=chr6:44226956-44233500|ST=-|CI|=|CS=Public
CCDS5085.1|GN=CDK19|GI=23097|FC=Missense|CP=1290|CF=2|AC=AGc->AGa|RP=430|RC=S|Ser|>R|Arg|EN=12/13|DS=+180|P=chr6:110935738-111136339|
CCDS5103.1|GN=FRK1|GI=2444|FC=Missense|CP=364|CF=0|AC=cGA->aGA|RP=122|RC=G|Glv|>R|Arg|EN=2/8|DS=+20|P=chr6:116263577-116381474|ST=-|CI|=|CS=Public
CCDS5116.1|GN=ROS1|GI=6098|FC=Missense|CP=6116|CF=1|AC=Cgt->Cat|RP=2039|RC=R|Arg|>H|His|EN=38/43|DS=+111|P=chr6:117609655-117746819|ST=-|CI|=|CS=Public
CCDS5179.1|GN=MAP3K5|GI=4217|FC=Missense|CP=3748|CF=0|AC=aTA->gTA|RP=1250|RC=I|Ile|>V|Val|EN=26/30|DS=+231|P=chr6:136878896-137113295|ST=-|CI|=|CS=Public
CCDS34565.1|GN=MAP3K4|GI=4216|FC=Missense|CP=470|CF=1|AC=Cgt->Cat|RP=157|RC=R|Arg|>H|His|EN=3/27|DS=+127|P=chr6:161412964-161537902|ST=-|CI|=|CS=Public
CCDS34570.1|GN=RPS6KA2|GI=6196|FC=Missense|CP=100|CF=0|AC=aCC->gCC|RP=34|RC=T|Thr|>A|Ala|EN=2/22|DS=+37|P=chr6:166826250-167275658|ST=-|CI|=|CS=Public
CCDS34570.1|GN=RPS6KA2|GI=6196|FC=Missense|CP=95|CF=1|AC=GaG->GgG|RP=32|RC=E|Glu|>G|Glv|EN=2/22|DS=+32|P=chr6:166826250-167275658|ST=-|CI|=|CS=Public
CCDS5386.1|GN=STK31|GI=56164|FC=Missense|CP=213|CF=2|AC=CAg->CAc|RP=71|RC=Q|Gln|>H|His|EN=4/24|DS=+63|P=chr7:23749905-23871985|ST=+|CI|=|CS=Public
CCDS5386.1|GN=STK31|GI=56164|FC=Missense|CP=781|CF=0|AC=aAG->aAG|RP=261|RC=E|Glu|>K|Lvs|EN=7/24|DS=+298|P=chr7:23749905-23871985|ST=+|CI|=|CS=Public
CCDS5386.1|GN=STK31|GI=56164|FC=Missense|CP=804|CF=2|AC=AAg->AAt|RP=268|RC=K|Lvs|>N|Asn|EN=7/24|DS=+321|P=chr7:23749905-23871985|ST=+|CI|=|CS=Public
CCDS5386.1|GN=STK31|GI=56164|FC=Missense|CP=1453|CF=0|AC=gCC->tCC|RP=485|RC=A|Ala|>S|Ser|EN=12/24|DS=+37|P=chr7:23749905-23871985|ST=+|CI|=|CS=Public
CCDS5386.1|GN=STK31|GI=56164|FC=Missense|CP=1863|CF=2|AC=AAt->AAg|RP=621|RC=N|Asn|>K|Lvs|EN=15/24|DS=+30|P=chr7:23749905-23871985|ST=+|CI|=|CS=Public
CCDS5386.1|GN=STK31|GI=56164|FC=Missense|CP=1868|CF=1|AC=aGT->AT|RP=623|RC=S|Ser|>I|Ile|EN=15/24|DS=+35|P=chr7:23749905-23871985|ST=+|CI|=|CS=Public
CCDS5461.1|GN=CDK13|GI=8621|FC=Missense|CP=1498|CF=0|AC=aCG->gCG|RP=500|RC=T|Thr|>A|Ala|EN=2/14|DS=+287|P=chr7:39990241-40134579|ST=+|CI|=|CS=Public
CCDS5470.1|GN=STK17A|GI=9263|FC=Missense|CP=378|CF=2|AC=GAa->GAc|RP=126|RC=E|Glu|>D|Asp|EN=2/7|DS=+172|P=chr7:43622843-43664441|ST=+|CI|=|CS=Public
CCDS5470.1|GN=STK17A|GI=9263|FC=Missense|CP=1084|CF=0|AC=aAG->gAG|RP=362|RC=K|Lvs|>E|Glu|EN=7/7|DS=+164|P=chr7:43622843-43664441|ST=+|CI|=|CS=Public
CCDS5514.1|GN=EGFR|GI=1956|FC=Missense|CP=1562|CF=1|AC=AgG->AaG|RP=521|RC=R|Arg|>K|Lvs|EN=13/28|DS=+64|P=chr7:55086971-55273310|ST=+|CI|=|CS=Public
CCDS5643.1|GN=PDK4|GI=5166|FC=Missense|CP=1002|CF=2|AC=TTg->Tt|RP=334|RC=L|L|Leu|>F|Phe|EN=10/11|DS=+21|P=chr7:95214953-95225605|ST=-|CI|=|CS=Public
CCDS5654.1|GN=LMTK2|GI=22853|FC=Missense|CP=2338|CF=0|AC=TTG->aTG|RP=780|RC=L|L|Leu|>P|Met|EN=11/14|DS=+1190|P=chr7:97736490-97834804|ST=-|CI|=|CS=Public
CCDS5659.1|GN=TRRAP1|GI=8295|FC=Missense|CP=356|CF=1|AC=CgC->CcC|RP=119|RC=R|Arg|>M|Met|EN=4/70|DS=+95|P=chr7:98478774-98609978|ST=+|CI|=|CS=Public
CCDS5659.1|GN=TRRAP1|GI=8295|FC=Missense|CP=4870|CF=0|AC=gCC->tCC|RP=1624|RC=A|Ala|>S|Ser|EN=33/70|DS=-87|P=chr7:98478774-98609978|ST=+|CI|=|CS=Public
CCDS47689.1|GN=MET1|GI=4233|FC=Missense|CP=1124|CF=1|AC=AaC->AgC|RP=375|RC=N|Asn|>S|Ser|EN=1/20|DS=-31460|P=chr7:116339139-116436178|ST=-|CI|=|CS=Public
CCDS5847.1|GN=TRIM24|GI=8805|FC=Missense|CP=143|CF=1|AC=CcC->GaC|RP=48|RC=A|Ala|>D|Asp|EN=1/19|DS=-43599|P=chr7:138145294-138269696|ST=-|CI|=|CS=Public
CCDS5884.1|GN=EPHA1|GI=2041|FC=Missense|CP=2698|CF=0|AC=aTG->gTG|RP=900|RC=M|Met|>V|Val|EN=17/18|DS=+2|P=chr7:143088550-143105898|ST=-|CI|=|CS=Public
CCDS5884.1|GN=EPHA1|GI=2041|FC=Missense|CP=479|CF=1|AC=GtG->GcG|RP=160|RC=V|Val|>A|Ala|EN=4/18|DS=+47|P=chr7:143088550-143105898|ST=-|CI|=|CS=Public
CCDS43706.1|GN=SGK223|GI=157285|FC=Missense|CP=3664|CF=0|AC=gGC->aGC|RP=1222|RC=G|Glv|>S|Ser|EN=5/5|DS=+598|P=chr8:8175676-8239257|ST=-|CI|=|CS=Public
CCDS43706.1|GN=SGK223|GI=157285|FC=Missense|CP=3331|CF=0|AC=gCC->aCC|RP=1111|RC=A|Ala|>T|Thr|EN=5/5|DS=+265|P=chr8:8175676-8239257|ST=-|CI|=|CS=Public
CCDS43706.1|GN=SGK223|GI=157285|FC=Missense|CP=1727|CF=1|AC=tcT->gt|RP=576|RC=S|Ser|>C|Cvs|EN=2/5|DS=+1397|P=chr8:8175676-8239257|ST=-|CI|=|CS=Public
CCDS43706.1|GN=SGK223|GI=157285|FC=Missense|CP=1700|CF=1|AC=CcG->CtG|RP=567|RC=PI|Pro|>L|L|Leu|EN=2/5|DS=+1370|P=chr8:8175676-8239257|ST=-|CI|=|CS=Public
CCDS43706.1|GN=SGK223|GI=157285|FC=Missense|CP=1205|CF=1|AC=CcG->CaG|RP=402|RC=R|Arg|>Q|Gln|EN=2/5|DS=+875|P=chr8:8175676-8239257|ST=-|CI|=|CS=Public
CCDS43706.1|GN=SGK223|GI=157285|FC=Missense|CP=189|CF=2|AC=AGg->AGt|RP=63|RC=R|Arg|>S|Ser|EN=1/5|DS=-3481|P=chr8:8175676-8239257|ST=-|CI|=|CS=Public
CCDS5982.1|GN=BLK|GI=640|FC=Intron|EN=9:10/12|DS=-38|P=chr8:11400734-11421617|ST=+|CI|=1518|CS=Public
CCDS6057.1|GN=PTK2B|GI=2185|FC=Missense|CP=2513|CF=1|AC=AaG->AcG|RP=838|RC=K|Lvs|>T|Thr|EN=25/30|DS=+26|P=chr8:27255102-27316026|ST=+|CI|=|CS=Public
CCDS55223.1|GN=EGFR|GI=2260|FC=Missense|CP=419|CF=1|AC=TcG->TtG|RP=140|RC=S|Ser|>L|L|Leu|EN=3/18|DS=+229|P=chr8:38271146-38318624|ST=-|CI|=|CS=Public
CCDS6240.1|GN=PSKH2|GI=85481|FC=Missense|CP=526|CF=0|AC=gCG->tCG|RP=176|RC=A|Ala|>S|Ser|EN=2/3|DS=+341|P=chr8:87060691-87081851|ST=-|CI|=|CS=Public
CCDS6409.2|GN=MAPK15|GI=225689|FC=Intron|EN=4:5/14|DS=-40|P=chr8:144798548-144804421|ST=+|CI|=1635|CS=Public
CCDS6409.2|GN=MAPK15|GI=225689|FC=Intron|EN=8:9/14|DS=-137|P=chr8:144798548-144804421|ST=+|CI|=1635|CS=Public
CCDS34965.1|GN=ADCK5|GI=203054|FC=Missense|CP=51|CF=2|AC=AGa->AGc|RP=17|RC=R|Arg|>S|Ser|EN=2/15|DS=+39|P=chr8:145597785-145618289|ST=-|CI|=|CS=Public
CCDS6519.1|GN=TEK1|GI=7010|FC=Missense|CP=443|CF=1|AC=AtT->AcT|RP=148|RC=I|Ile|>T|Thr|EN=3/23|DS=+79|P=chr9:27109589-27229230|ST=+|CI|=337|CS=Public
CCDS6519.1|GN=TEK1|GI=7010|FC=Missense|CP=1037|CF=1|AC=CaG->CcG|RP=346|RC=Q|Gln|>P|Pro|EN=8/23|DS=+7|P=chr9:27109589-27229230|ST=+|CI|=337|CS=Public
CCDS6625.1|GN=PRKACG|GI=5568|FC=Missense|CP=802|CF=0|AC=cAT->gAT|RP=268|RC=H|His|>D|Asp|EN=1/11|P=chr9:71627953-71629008|ST=-|CI|=1056|CS=Public
CCDS6647.1|GN=TRPM6|GI=140803|FC=Missense|CP=4750|CF=0|AC=aAG->aAG|RP=1584|RC=K|Lvs|>E|Glu|EN=27/39|DS=+78|P=chr9:77339529-77502772|ST=-|CI|=|CS=Public
CCDS6691.1|GN=ROR2|GI=4920|FC=Missense|CP=2455|CF=0|AC=gTC->aTC|RP=819|RC=V|Val|>I|Ile|EN=9/9|DS=+1069|P=chr9:94485944-94712245|ST=-|CI|=|CS=Public
CCDS6691.1|GN=ROR2|GI=4920|FC=Missense|CP=733|CF=0|AC=aCA->gCA|RP=245|RC=T|Thr|>A|Ala|EN=6/9|DS=+11|P=chr9:94485944-94712245|ST=-|CI|=|CS=Public
CCDS48005.1|GN=MUSK1|GI=4593|FC=Missense|CP=475|CF=0|AC=aGC->gGC|RP=159|RC=S|Ser|>G|Glv|EN=4/15|DS=+117|P=chr9:113431185-113563268|ST=-|CI|=|CS=Public
CCDS48005.1|GN=MUSK1|GI=4593|FC=Missense|CP=1239|CF=2|AC=ATg->ATa|RP=413|RC=M|Met|>I|Ile|EN=10/15|DS=+55|P=chr9:113431185-113563268|ST=-|CI|=|CS=Public
CCDS35165.1|GN=ABL1|GI=25|FC=Missense|CP=2174|CF=1|AC=Ggt->GtT|RP=725|RC=G|Glv|>V|Val|EN=11/11|DS=+439|P=chr9:133589707-133761070|ST=+|CI|=|CS=Public
CCDS35169.1|GN=C9orf96|GI=169436|FC=Missense|CP=1417|CF=0|AC=aAA->gAA|RP=473|RC=K|Lvs|>E|Glu|EN=14/18|DS=+78|P=chr9:136243345-13627054|ST=-|CI|=|CS=Public
CCDS7079.1|GN=PRKCA|GI=5588|FC=Missense|CP=989|CF=1|AC=CcG->CtG|RP=330|RC=PI|Pro|>L|L|Leu|EN=9/17|DS=+89|P=chr10:6470169-6557097|ST=-|CI|=|CS=Public
CCDS7148.1|GN=MYO3A|GI=53904|FC=Missense|CP=1042|CF=0|AC=aTT->gT|RP=348|RC=I|Ile|>V|Val|EN=9/33|DS=+89|P=chr10:26241040-26500892|ST=+|CI|=|CS=Public

CCDS7148.1|GN=MYO3A|GI=53904|FC=Missense|CP=1105|CF=0|AC=gTC->aT|CIRP=369|RC=V|Val|->|Ile|EN=10/33|DS=+52|P=chr10:26241040-26500892|ST=-|C|

CCDS7148.1|GN=MYO3A|GI=53904|FC=Missense|CP=3937|CF=0|AC=cGT->aG|TIRP=1313|RC=R|Arg|->S|Ser|EN=28/33|DS=+539|P=chr10:26241040-26500892|ST=-|C|

CCDS7148.1|GN=MYO3A|GI=53904|FC=Missense|CP=4462|CF=0|AC=aAA->gAA|IRP=1488|RC=K|Lys|->E|Glu|EN=30/33|DS=+24|P=chr10:26241040-26500892|ST=-|C|

CCDS7166.1|GN=MAP3K8|GI=1326|FC=Intron|EN=1:2/7|DS=+47|P=chr10:30727868-30749765|ST=-|C|

CCDS7250.1|GN=PMK1G|GI=253430|FC=Missense|CP=1047|CF=2|AC=ATg->ATa|IRP=349|RC=M|Met|->|Ile|EN=6/6|DS=+419|P=chr10:59955837-60027371|ST=-|C|

CCDS7378.1|GN=BMPT1A|GI=657|FC=Missense|CP=4|CF=0|AC=cCT->aCT|IRP=2|RC=P|Pro|->T|Thr|EN=1/11|DS=-14040|P=chr10:88635776-88683476|ST=-|C|

CCDS7469.1|GN=PI4K2A|GI=55361|FC=Missense|CP=248|CF=1|AC=GcT->GaT|IRP=83|RC=A|Ala|->D|Asp|EN=1/9|DS=-9951|P=chr10:99400500-99433499|ST=-|C|

CCDS7488.1|GN=CHUK1G|GI=1147|FC=Missense|CP=802|CF=0|AC=gTA->aT|IRP=268|RC=V|Val|->|Ile|EN=9/21|DS=+5|P=chr10:101949355-101989289|ST=-|C|

CCDS7612.1|GN=GRK5|GI=2869|FC=Missense|CP=911|CF=1|AC=CgT->CaT|IRP=304|RC=R|Arg|->H|His|EN=9/16|DS=+173|P=chr10:120967430-121214579|ST=-|C|

CCDS7620.2|GN=FGFR2|GI=2263|FC=Missense|CP=557|CF=1|AC=AtG->AcG|IRP=186|RC=M|Met|->T|Thr|EN=4/17|DS=+103|P=chr10:123239371-123353331|ST=-|C|

CCDS55757.1|GN=DGKZ|GI=8525|FC=Missense|CP=58|CF=0|AC=gCC->aCC|IRP=20|RC=A|Ala|->T|Thr|EN=1/31|DS=-19574|P=chr11:46369210-46401497|ST=-|C|

CCDS31601.1|GN=CDC42BP|GI=55561|FC=Missense|CP=3709|CF=0|AC=cGG->tGG|IRP=1237|RC=R|Arg|->W|Trp|EN=30/37|DS=+342|P=chr11:64591945-64611945|ST=-|C|

CCDS31669.1|GN=ATM|GI=472|FC=Missense|CP=4138|CF=0|AC=cAT->tAT|IRP=1380|RC=H|His|->Y|Tyr|EN=27/62|DS=+29|P=chr11:108098352-108236235|ST=-|C|

CCDS31669.1|GN=ATM|GI=472|FC=Missense|CP=5948|CF=1|AC=AaT->AgT|IRP=1983|RC=N|Asn|->S|Ser|EN=39/62|DS=+30|P=chr11:108098352-108236235|ST=-|C|

CCDS8347.1|GN=SIK2|GI=23235|FC=Missense|CP=2240|CF=1|AC=CcA->CaA|IRP=747|RC=P|Pro|->Q|Gln|EN=15/15|DS=+93|P=chr11:111473288-111594853|ST=-|C|

CCDS44734.1|GN=ANKK1|GI=255239|FC=Missense|CP=715|CF=0|AC=gCG->aCG|IRP=239|RC=A|Ala|->T|Thr|EN=5/8|DS=+33|P=chr11:113258607-113270989|ST=-|C|

CCDS44734.1|GN=ANKK1|GI=255239|FC=Missense|CP=1324|CF=0|AC=gGC->cGC|IRP=442|RC=G|Gly|->R|Arg|EN=8/8|DS=+330|P=chr11:113258607-113270989|ST=-|C|

CCDS44734.1|GN=ANKK1|GI=255239|FC=Missense|CP=2137|CF=0|AC=gAG->aAG|IRP=713|RC=E|Glu|->K|Lys|EN=8/8|DS=+143|P=chr11:113258607-113270989|ST=-|C|

CCDS8459.1|GN=CHK1|GI=1111|FC=Missense|CP=1411|CF=0|AC=aTT->gTT|IRP=471|RC=I|Ile|->V|Val|EN=12/12|DS=+76|P=chr11:125496664-125525215|ST=-|C|

CCDS53730.1|GN=WNK1|GI=65125|FC=Missense|CP=3946|CF=0|AC=aCC->cCC|IRP=1316|RC=T|Thr|->P|Pro|EN=13/28|DS=+55|P=chr12:862732-1017958|ST=-|C|

CCDS53730.1|GN=WNK1|GI=65125|FC=Missense|CP=5297|CF=1|AC=TgC->TcC|IRP=1766|RC=C|Cys|->S|Ser|EN=19/28|DS=+673|P=chr12:862732-1017958|ST=-|C|

CCDS53730.1|GN=WNK1|GI=65125|FC=Missense|CP=6204|CF=2|AC=ATg->ATt|IRP=2068|RC=M|Met|->|Ile|EN=21/28|DS=+60|P=chr12:862732-1017958|ST=-|C|

CCDS53730.1|GN=WNK1|GI=65125|FC=Missense|CP=7267|CF=0|AC=cCC->tCC|IRP=2423|RC=P|Pro|->S|Ser|EN=26/28|DS=+39|P=chr12:862732-1017958|ST=-|C|

CCDS8629.1|GN=STYK1|GI=55359|FC=Missense|CP=610|CF=0|AC=aGC->gGC|IRP=204|RC=S|Ser|->G|Gly|EN=4/9|DS=+159|P=chr12:10772743-10787217|ST=-|C|

CCDS8664.1|GN=GUCY2C|GI=2984|FC=Missense|CP=843|CF=2|AC=TtT->TtT|IRP=281|RC=F|Phe|->L|Leu|EN=7/27|DS=+13|P=chr12:14766051-14849382|ST=-|C|

CCDS44839.1|GN=PIK3C2G|GI=5288|FC=Missense|CP=2732|CF=1|AC=CcG->CcG|IRP=911|RC=P|Pro|->L|Leu|EN=19/31|DS=+62|P=chr12:18435016-188009621|ST=-|C|

CCDS44839.1|GN=PIK3C2G|GI=5288|FC=Missense|CP=3780|CF=2|AC=GAe->GA|IRP=1260|RC=E|Glu|->D|Asp|EN=27/31|DS=+11|P=chr12:18435016-188009621|ST=-|C|

CCDS31774.1|GN=LRRK2|GI=120892|FC=Missense|CP=149|CF=1|AC=CgC->CaC|IRP=50|RC=R|Arg|->H|His|EN=1/51|DS=-275|P=chr12:40618934-40761567|ST=-|C|

CCDS31774.1|GN=LRRK2|GI=120892|FC=Missense|CP=1653|CF=2|AC=AAc->AAg|IRP=551|RC=N|Asn|->K|Lys|EN=14/51|DS=+110|P=chr12:40618934-40761567|ST=-|C|

CCDS31774.1|GN=LRRK2|GI=120892|FC=Missense|CP=4193|CF=1|AC=CgT->CaT|IRP=1398|RC=R|Arg|->H|His|EN=30/51|DS=+4|P=chr12:40618934-40761567|ST=-|C|

CCDS41778.1|GN=COL2A1|GI=1280|FC=Missense|CP=4213|CF=0|AC=gGC->aGC|IRP=1405|RC=G|Gly|->S|Ser|EN=53/54|DS=+139|P=chr12:48367190-48398104|ST=-|C|

CCDS31804.1|GN=ACVR1|GI=94|FC=Upstream|DG=38|P=chr12:52306259-52314677|ST=-|C|

CCDS8944.1|GN=MBD6|GI=114785|FC=Missense|CP=778|CF=0|AC=cTC->gTC|IRP=260|RC=L|Leu|->V|Val|EN=4/11|DS=+399|P=chr12:57918087-57923017|ST=-|C|

CCDS8946.1|GN=PIP4K2C|GI=79837|FC=Missense|CP=899|CF=1|AC=GcG->GcG|IRP=300|RC=A|Ala|->G|Gly|EN=8/10|DS=+86|P=chr12:57985073-57995389|ST=-|C|

CCDS8975.1|GN=IRAK3|GI=11213|FC=Missense|CP=439|CF=0|AC=aTA->gTA|IRP=147|RC=I|Ile|->V|Val|EN=5/12|DS=+3|P=chr12:66583080-66641951|ST=-|C|

CCDS31892.1|GN=NUAK1|GI=9891|FC=Missense|CP=1628|CF=1|AC=CcT->CcT|IRP=543|RC=P|Pro|->R|Arg|EN=7/7|DS=+796|P=chr12:106460580-106532431|ST=-|C|

CCDS9188.1|GN=IAOK3|GI=51347|FC=Missense|CP=140|CF=1|AC=AgT->AaT|IRP=47|RC=S|Ser|->N|Asn|EN=2/19|DS=+20|P=chr12:118588802-118693372|ST=-|C|

CCDS9216.1|GN=CAMKK2|GI=10645|FC=Missense|CP=1087|CF=0|AC=cGC->tGC|IRP=363|RC=R|Arg|->C|Cys|EN=9/16|DS=+180|P=chr12:121678502-12171232|ST=-|C|

CCDS9274.1|GN=ULK1|GI=8408|FC=Missense|CP=2446|CF=0|AC=aCT->gCT|IRP=816|RC=T|Thr|->A|Ala|EN=23/28|DS=+120|P=chr12:132379547-132405906|ST=-|C|

CCDS9294.1|GN=LATS2|GI=26524|FC=Missense|CP=1087|CF=0|AC=gGC->aGC|IRP=363|RC=G|Gly|->S|Ser|EN=3/7|DS=+612|P=chr13:21549009-21620165|ST=-|C|

CCDS9294.1|GN=LATS2|GI=26524|FC=Missense|CP=971|CF=1|AC=GcG->GtG|IRP=324|RC=A|Ala|->V|Val|EN=3/7|DS=+496|P=chr13:21549009-21620165|ST=-|C|

CCDS31953.1|GN=FLT3|GI=2322|FC=Missense|CP=680|CF=1|AC=AcG->ATG|IRP=227|RC=T|Thr|->M|Met|EN=6/24|DS=+66|P=chr13:28578189-28674647|ST=-|C|

CCDS9344.1|GN=BRCA2|GI=675|FC=Missense|CP=865|CF=0|AC=aAT->aT|IRP=289|RC=N|Asn|->H|His|EN=9/26|DS=+72|P=chr13:32890598-32972907|ST=-|C|

CCDS9344.1|GN=BRCA2|GI=675|FC=Missense|CP=2971|CF=0|AC=aAC->gAC|IRP=991|RC=N|Asn|->D|Asp|EN=10/26|DS=+1062|P=chr13:32890598-32972907|ST=-|C|

CCDS9344.1|GN=BRCA2|GI=675|FC=Missense|CP=7397|CF=1|AC=GtA->GcA|IRP=2466|RC=V|Val|->A|Ala|EN=13/26|DS=+390|P=chr13:32890598-32972907|ST=-|C|

CCDS9363.1|GN=CSNK1A1|GI=12201|FC=Missense|CP=126|CF=2|AC=GAc->GAa|IRP=42|RC=D|Asp|->E|Glu|EN=1/1|P=chr13:37678380-37679393|ST=-|C|

CCDS9510.1|GN=IRS2|GI=8660|FC=Missense|CP=3733|CF=0|AC=gCC->tCC|IRP=1245|RC=A|Ala|->S|Ser|EN=1/2|DS=-26013|P=chr13:110408651-110438400|ST=-|C|

CCDS9510.1|GN=IRS2|GI=8660|FC=Missense|CP=3170|CF=1|AC=GcC->GaC|IRP=1057|RC=G|Gly|->D|Asp|EN=1/2|DS=-26576|P=chr13:110408651-110438400|ST=-|C|

CCDS9510.1|GN=IRS2|GI=8660|FC=Missense|CP=599|CF=1|AC=GtG->GgG|IRP=200|RC=V|Val|->G|Gly|EN=1/2|DS=-29147|P=chr13:110408651-110438400|ST=-|C|

CCDS9628.1|GN=IRPK3|GI=11035|FC=Missense|CP=22|CF=0|AC=cCC->aCC|IRP=8|RC=P|Pro|->T|Thr|EN=2/10|DS=+2|P=chr14:24805381-24809032|ST=-|C|

CCDS9699.1|GN=CDKL1|GI=8814|FC=Intron|EN=8:9/9|DS=+237|P=chr14:50796792-50862589|ST=-|C|

CCDS9699.1|GN=CDKL1|GI=8814|FC=Missense|CP=823|CF=0|AC=cAA->gAA|IRP=275|RC=Q|Gln|->E|Glu|EN=8/9|DS=+25|P=chr14:50796792-50862589|ST=-|C|

CCDS9752.1|GN=PRKCH|GI=5583|FC=Missense|CP=1120|CF=0|AC=gTA->aT|IRP=374|RC=V|Val|->|Ile|EN=9/14|DS=+16|P=chr14:61788820-62016549|ST=-|C|

CCDS9834.2|GN=RPS6K1|GI=83694|FC=Missense|CP=362|CF=1|AC=CcG->CtG|RP=121|RC=PI|Pro|->L|Leu||EN=2/10|DS=+97|P=chr14:75373717-75388244|ST=+|CI=2297|CS=Public

CCDS9834.2|GN=RPS6K1|GI=83694|FC=Missense|CP=62|CF=1|AC=CgA->CaA|RP=21|RC=RI|Arg|->Q|Gln||EN=1/10|DS=-151|P=chr14:75373717-75388244|ST=+|CI=2297|CS=Public

CCDS9839.1|GN=NEK9|GI=91754|FC=Missense|CP=1286|CF=1|AC=Cgt->CaT|RP=429|RC=RI|Arg|->H|His||EN=11/22|DS=+104|P=chr14:75551267-75593624|ST=+|CI=945|CS=Public

CCDS45157.1|GN=TPK1|GI=3705|FC=Intron|EN=9.10/10|DS=-219|P=chr14:93404828-93581508|ST=+|CI=945|CS=Public

CCDS9971.1|GN=MOKI|GI=5891|FC=Missense|CP=1193|CF=1|AC=CaG->CgG|RP=398|RC=Q|Gln|->R|Arg||EN=12/12|DS=+11|P=chr14:102695626-102771305|ST=+|CI=2297|CS=Public

CCDS45165.1|GN=MARK3|GI=4140|FC=Missense|CP=1229|CF=1|AC=TT->TcT|RP=410|RC=FI|Phe|->S|Ser||EN=12/18|DS=+119|P=chr14:103852367-103969564|ST=+|CI=2297|CS=Public

CCDS42016.1|GN=IF2AK4|GI=440275|FC=Missense|CP=1667|CF=1|AC=GaA->GgA|RP=556|RC=FI|Glu|->G|Glv||EN=11/39|DS=+7|P=chr15:40226397-40327285|ST=+|CI=2297|CS=Public

CCDS10053.1|GN=BUB1B|GI=701|FC=Missense|CP=1046|CF=1|AC=CgA->CaA|RP=349|RC=RI|Arg|->Q|Gln||EN=8/23|DS=+80|P=chr15:40453422-40512960|ST=+|CI=2297|CS=Public

CCDS10054.1|GN=PAK6|GI=56924|FC=Missense|CP=1010|CF=1|AC=CcG->CtG|RP=337|RC=PI|Pro|->L|Leu||EN=3/8|DS=+152|P=chr15:40556987-40568295|ST=+|CI=2297|CS=Public

CCDS42029.1|GN=TTBK2|GI=146057|FC=Missense|CP=23|CF=1|AC=CtG->CcG|RP=8|RC=L|Leu|->P|Pro||EN=1/14|DS=-5837|P=chr15:43037993-43170815|ST=+|CI=2297|CS=Public

CCDS45305.1|GN=ULK3|GI=25989|FC=Missense|CP=1334|CF=1|AC=AaG->AgG|RP=445|RC=K|Lys|->R|Arg||EN=14/16|DS=+47|P=chr15:75129569-75135446|ST=+|CI=2297|CS=Public

CCDS42062.1|GN=PEAK1|GI=79834|FC=Missense|CP=3212|CF=1|AC=AaG->AaG|RP=1071|RC=RI|Arg|->K|Lys||EN=2/4|DS=+75|P=chr15:77406498-77474268|ST=+|CI=2297|CS=Public

CCDS10333.1|GN=ALPK3|GI=57538|FC=Missense|CP=1241|CF=1|AC=Act->AgT|RP=414|RC=TI|Thr|->S|Ser||EN=5/14|DS=+213|P=chr15:85360078-85411687|ST=+|CI=2297|CS=Public

CCDS10333.1|GN=ALPK3|GI=57538|FC=Missense|CP=1736|CF=1|AC=GcG->GaG|RP=579|RC=G|Glv|->F|Glu||EN=5/14|DS=+708|P=chr15:85360078-85411687|ST=+|CI=2297|CS=Public

CCDS10333.1|GN=ALPK3|GI=57538|FC=Missense|CP=3896|CF=1|AC=Cct->CtT|RP=1299|RC=PI|Pro|->L|Leu||EN=6/14|DS=-1215|P=chr15:85360078-85411687|ST=+|CI=2297|CS=Public

CCDS10333.1|GN=ALPK3|GI=57538|FC=Missense|CP=4865|CF=1|AC=CtI->CcT|RP=1622|RC=L|Leu|->P|Pro||EN=10/14|DS=+130|P=chr15:85360078-85411687|ST=+|CI=2297|CS=Public

CCDS10365.1|GN=FES|GI=2242|FC=Missense|CP=1952|CF=1|AC=GaG->GgG|RP=651|RC=FI|Gln|->G|Glv||EN=15/18|DS=+31|P=chr15:91428276-91438788|ST=+|CI=2297|CS=Public

CCDS10378.1|GN=GFIR|GI=3480|FC=Missense|CP=199|CF=0|AC=gCC->tCC|RP=67|RC=A|Ala|->S|Ser||EN=2/21|DS=+105|P=chr15:99192811-99500671|ST=+|CI=2297|CS=Public

CCDS42086.1|GN=LRK1|GI=79705|FC=Missense|CP=5813|CF=1|AC=GcC->GaC|RP=1938|RC=G|Glv|->D|Asp||EN=32/33|DS=+45|P=chr15:101464838-1016090|ST=+|CI=2297|CS=Public

CCDS42086.1|GN=LRK1|GI=79705|FC=Synonymous-Coding|CP=5814|CF=2|AC=GcC->GgA|RP=1938|RC=G|Glv|->G|Glv||EN=32/33|DS=+46|P=chr15:101464838-1016090|ST=+|CI=2297|CS=Public

CCDS10604.1|GN=FEF2K|GI=29904|FC=Missense|CP=1082|CF=1|AC=CaA->CgA|RP=361|RC=Q|Gln|->R|Arg||EN=9/17|DS=+53|P=chr16:22237051-22295317|ST=+|CI=2297|CS=Public

CCDS32406.1|GN=PALB2|GI=79728|FC=Missense|CP=1676|CF=1|AC=CaA->CgA|RP=559|RC=Q|Gln|->R|Arg||EN=4/13|DS=+1465|P=chr16:23614780-23652478|ST=+|CI=2297|CS=Public

CCDS10616.1|GN=PLK1|GI=5347|FC=Missense|CP=148|CF=0|AC=cGG->tGG|RP=50|RC=RI|Arg|->W|Trop||EN=1/10|DS=-1004|P=chr16:23690254-23701384|ST=+|CI=2297|CS=Public

CCDS32407.1|GN=ERN2|GI=10595|FC=Missense|CP=1604|CF=1|AC=AgC->AcG|RP=535|RC=S|Ser|->T|Thr||EN=13/22|DS=+101|P=chr16:23702152-23724652|ST=+|CI=2297|CS=Public

CCDS10723.2|GN=MYLK3|GI=91807|FC=Missense|CP=2127|CF=2|AC=TTe->TTt|RP=709|RC=L|Leu|->F|Phe||EN=11/13|DS=+13|P=chr16:46741616-46782105|ST=+|CI=2297|CS=Public

CCDS10723.2|GN=MYLK3|GI=91807|FC=Missense|CP=538|CF=0|AC=gTG->tTG|RP=180|RC=V|Val|->L|Leu||EN=2/13|DS=+61|P=chr16:46741616-46782105|ST=+|CI=2297|CS=Public

CCDS10868.1|GN=CDH3|GI=1001|FC=Intron|EN=15.16/16|DS=-45|P=chr16:68679283-68732303|ST=+|CI=2297|CS=Public

CCDS11036.1|GN=GSG2|GI=83903|FC=Missense|CP=244|CF=0|AC=cGT->tGT|RP=82|RC=RI|Arg|->C|Cys||EN=1/7|P=chr17:3627230-3629626|ST=+|CI=2397|CS=Public

CCDS11036.1|GN=GSG2|GI=83903|FC=Missense|CP=611|CF=1|AC=GcC->GaC|RP=204|RC=G|Glv|->D|Asp||EN=1/1|P=chr17:3627230-3629626|ST=+|CI=2397|CS=Public

CCDS11036.1|GN=GSG2|GI=83903|FC=Missense|CP=983|CF=1|AC=AtA->AcA|RP=328|RC=I|Ile|->T|Thr||EN=1/7|P=chr17:3627230-3629626|ST=+|CI=2397|CS=Public

CCDS11036.1|GN=GSG2|GI=83903|FC=Missense|CP=1133|CF=1|AC=GtC->GcC|RP=378|RC=V|Val|->A|Ala||EN=1/1|P=chr17:3627230-3629626|ST=+|CI=2397|CS=Public

CCDS11039.1|GN=CAMKK1|GI=84254|FC=Missense|CP=1238|CF=1|AC=GaG->GgG|RP=413|RC=FI|Gln|->G|Glv||EN=12/15|DS=+74|P=chr17:3769198-3788981|ST=+|CI=2397|CS=Public

CCDS45588.1|GN=MINK1|GI=50488|FC=Missense|CP=2312|CF=1|AC=GtC->GcC|RP=771|RC=V|Val|->A|Ala||EN=20/32|DS=+1|P=chr17:4736879-4800582|ST=+|CI=2397|CS=Public

CCDS45588.1|GN=MINK1|GI=50488|FC=Missense|CP=2324|CF=1|AC=CcG->CtG|RP=775|RC=PI|Pro|->L|Leu||EN=20/32|DS=+13|P=chr17:4736879-4800582|ST=+|CI=2397|CS=Public

CCDS45588.1|GN=MINK1|GI=50488|FC=Missense|CP=2587|CF=0|AC=gTC->aTC|RP=863|RC=V|Val|->I|Ile||EN=22/32|DS=+23|P=chr17:4736879-4800582|ST=+|CI=2397|CS=Public

CCDS45602.1|GN=TNK1|GI=8711|FC=Missense|CP=1777|CF=0|AC=gTG->aTG|RP=593|RC=V|Val|->M|Met||EN=11/12|DS=+1|P=chr17:7286246-7292403|ST=+|CI=2397|CS=Public

CCDS11118.1|GN=TP53|GI=7157|FC=Missense|CP=215|CF=1|AC=CcC->CgC|RP=72|RC=PI|Pro|->R|Arg||EN=3/10|DS=+119|P=chr17:7572927-7579912|ST=+|CI=2397|CS=Public

CCDS32554.1|GN=CHD3|GI=1107|FC=Missense|CP=8|CF=1|AC=GcG->GtG|RP=3|RC=A|Ala|->V|Val||EN=1/40|DS=-656|P=chr17:7792319-7814903|ST=+|CI=2397|CS=Public

CCDS32553.2|GN=CHD3|GI=1107|FC=Missense|CP=877|CF=0|AC=aTA->ctA|RP=293|RC=I|Ile|->L|Leu||EN=5/40|DS=+191|P=chr17:7788125-7814903|ST=+|CI=2397|CS=Public

CCDS32553.2|GN=CHD3|GI=1107|FC=Missense|CP=886|CF=0|AC=tCC->cCC|RP=296|RC=S|Ser|->P|Pro||EN=5/40|DS=+200|P=chr17:7788125-7814903|ST=+|CI=2397|CS=Public

CCDS32553.2|GN=CHD3|GI=1107|FC=Missense|CP=898|CF=0|AC=gCC->cCC|RP=300|RC=A|Ala|->P|Pro||EN=5/40|DS=+212|P=chr17:7788125-7814903|ST=+|CI=2397|CS=Public

CCDS11134.1|GN=AURKB|GI=9212|FC=Missense|CP=893|CF=1|AC=AtG->AcG|RP=298|RC=M|Met|->T|Thr||EN=8/8|DS=+32|P=chr17:8108189-8113542|ST=+|CI=2397|CS=Public

CCDS11147.1|GN=PIK3R5|GI=23533|FC=Nonsense|CP=2017|CF=0|AC=cAA->tAA|RP=673|RC=Q|Gln|->Stop||EN=12/18|DS=+112|P=chr17:78783956-78814811|ST=+|CI=2397|CS=Public

CCDS11206.1|GN=MAPK7|GI=5598|FC=Missense|CP=2089|CF=0|AC=gGG->aGG|RP=697|RC=G|Glv|->R|Arg||EN=4/6|DS=-421|P=chr17:19282214-19286544|ST=+|CI=2397|CS=Public

CCDS32642.1|GN=ERBB2|GI=2064|FC=Missense|CP=1963|CF=0|AC=aTC->gTC|RP=655|RC=I|Ile|->V|Val||EN=17/27|DS=+17|P=chr17:37856492-37884297|ST=+|CI=2397|CS=Public

CCDS32642.1|GN=ERBB2|GI=2064|FC=Missense|CP=2584|CF=0|AC=aCA->gCA|RP=862|RC=TI|Thr|->A|Ala||EN=21/27|DS=+91|P=chr17:37856492-37884297|ST=+|CI=2397|CS=Public

CCDS32642.1|GN=ERBB2|GI=2064|FC=Missense|CP=3508|CF=0|AC=cCC->gCC|RP=1170|RC=PI|Pro|->A|Ala||EN=27/27|DS=+96|P=chr17:37856492-37884297|ST=+|CI=2397|CS=Public

CCDS11456.2|GN=BRCA1|GI=672|FC=Missense|CP=4900|CF=0|AC=aGT->gGT|RP=1634|RC=S|Ser|->G|Glv||EN=15/23|DS=+162|P=chr17:41197695-41276113|ST=+|CI=2397|CS=Public

CCDS11456.2|GN=BRCA1|GI=672|FC=Missense|CP=3548|CF=1|AC=AaA->AgA|RP=1183|RC=K|Lys|->R|Arg||EN=9/23|DS=-951|P=chr17:41197695-41276113|ST=+|CI=2397|CS=Public

CCDS11456.2|GN=BRCA1|GI=672|FC=Missense|CP=3113|CF=1|AC=GaA->GgA|RP=1038|RC=FI|Gln|->G|Glv||EN=9/23|DS=-1386|P=chr17:41197695-41276113|ST=+|CI=2397|CS=Public

CCDS11456.2|GN=BRCA1|GI=672|FC=Missense|CP=2612|CF=1|AC=CcG->CtG|RP=871|RC=PI|Pro|->L|Leu||EN=9/23|DS=-1887|P=chr17:41197695-41276113|ST=+|CI=2397|CS=Public

CCDS11456.2|GN=BRCA1|GI=672|FC=Missense|CP=1855|CF=0|AC=cAT->aAT|RP=619|RC=H|His|->N|Asn||EN=9/23|DS=+185|P=chr17:41197695-41276113|ST=+|CI=2397|CS=Public

CCDS11561.1|GN=COL1A1|GI=1277|FC=Missense|CP=3223|CF=0|AC=aCC->gCC|RP=1075|RC=TI|Thr|->A|Ala||EN=44/51|DS=+16|P=chr17:48262863-48278874|ST=+|CI=2397|CS=Public

CCDS11608.1|GN=MTMR4|GI=9110|FC=Missense|CP=838|CF=0|AC=aGC->gGC|RP=280|RC=S|Ser|->G|Glv||EN=8/18|DS=+173|P=chr17:56569024-56593943|ST=+|CI=2397|CS=Public

CCDS56042.1|GN=TEX14|GI=56155|FC=Missense|CP=3263|CF=1|AC=GgT->GaT|RP=1088|RC=GI|Givl->D|Asp||EN=19/32|DS=+74|P=chr17:56634372-56729362|I

CCDS11664.1|GN=PRKCA|GI=5578|FC=Missense|CP=1702|CF=0|AC=gTC->aTC|RP=568|RC=V|Val->I|Ile||EN=15/17|DS=+97|P=chr17:64298970-64800155|ST=-|C

CCDS11744.1|GN=SPHK1|GI=8877|FC=Missense|CP=100|CF=0|AC=gCA->aCA|RP=34|RC=A|Ala->T|Thr||EN=2/6|DS=+36|P=chr17:74381187-74383667|ST=+|C

CCDS45807.1|GN=AATK|GI=9625|FC=Missense|CP=3797|CF=1|AC=TtC->TcC|RP=1266|RC=F|Phe->S|Ser||EN=12/14|DS=+62|P=chr17:79092202-79139792|ST

CCDS45807.1|GN=AATK|GI=9625|FC=Missense|CP=2107|CF=0|AC=gGC->tGC|RP=703|RC=GI|Givl->C|Cys||EN=11/14|DS=+995|P=chr17:79092202-79139792|ST

CCDS11870.2|GN=ROCK1|GI=6093|FC=Missense|CP=3649|CF=0|AC=cAA->gAA|RP=1217|RC=Q|Gln->E|Gln||EN=31/33|DS=+58|P=chr18:18531345-18690871|IS

CCDS42437.1|GN=MAPK4|GI=5596|FC=Missense|CP=112|CF=0|AC=gTG->aTG|RP=38|RC=V|Val->M|Met||EN=1/5|DS=-51009|P=chr18:48190329-48256224|ST

CCDS11966.2|GN=ALPK2|GI=115701|FC=Missense|CP=6469|CF=0|AC=aTA->gTA|RP=2157|RC=I|Ile->V|Val||EN=12/12|DS=+173|P=chr18:56149055-56279029|S

CCDS11966.2|GN=ALPK2|GI=115701|FC=Missense|CP=3521|CF=1|AC=CaC->CcC|RP=1174|RC=H|His->P|Pro||EN=4/12|DS=+1559|P=chr18:56149055-5627902

CCDS11966.2|GN=ALPK2|GI=115701|FC=Missense|CP=3169|CF=0|AC=tTG->gTG|RP=1057|RC=L|Leu->V|Val||EN=4/12|DS=+1207|P=chr18:56149055-5627902

CCDS11966.2|GN=ALPK2|GI=115701|FC=Missense|CP=2672|CF=1|AC=AaC->AtC|RP=891|RC=T|Thr->I|Ile||EN=4/12|DS=+710|P=chr18:56149055-56279029|ST

CCDS11966.2|GN=ALPK2|GI=115701|FC=Missense|CP=5|CF=1|AC=AaA->AcA|RP=2|RC=K|Lys->T|Thr||EN=1/12|DS=-4354|P=chr18:56149055-56279029|ST=-

CCDS11979.2|GN=KIAA1468|GI=57614|FC=Missense|CP=250|CF=0|AC=gGC->tGC|RP=84|RC=GI|Givl->C|Cys||EN=1/29|DS=-23398|P=chr18:59854739-5997276

CCDS11979.2|GN=KIAA1468|GI=57614|FC=Missense|CP=1735|CF=0|AC=cAA->aAA|RP=579|RC=Q|Gln->K|Lys||EN=12/29|DS=+2|P=chr18:59854739-59972767

CCDS12080.1|GN=MKNK2|GI=2872|FC=Missense|CP=208|CF=0|AC=cGG->tGG|RP=70|RC=R|Arg->W|Trp||EN=3/13|DS=+69|P=chr19:2039612-2050850|ST=-|C

CCDS12236.1|GN=TYK2|GI=7297|FC=Missense|CP=1561|CF=0|AC=cGG->tGG|RP=521|RC=R|Arg->W|Trp||EN=9/23|DS=+85|P=chr19:10461510-10489082|ST=-

CCDS12236.1|GN=TYK2|GI=7297|FC=Missense|CP=1084|CF=0|AC=gTC->tTC|RP=362|RC=V|Val->F|Phe||EN=6/23|DS=+73|P=chr19:10461510-10489082|ST=-|

CCDS42514.1|GN=PKN1|GI=5585|FC=Missense|CP=1681|CF=0|AC=cTC->aTC|RP=561|RC=L|Leu->I|Ile||EN=12/22|DS=+26|P=chr19:14551103-14582596|ST=+|

CCDS42514.1|GN=PKN1|GI=5585|FC=Missense|CP=2719|CF=0|AC=gTC->aTC|RP=907|RC=V|Val->I|Ile||EN=22/22|DS=+76|P=chr19:14551103-14582596|ST=+|

CCDS12366.1|GN=JAK3|GI=3718|FC=Missense|CP=1503|CF=2|AC=CaG->CaT|RP=501|RC=Q|Gln->H|His||EN=10/23|DS=+62|P=chr19:17937552-17955226|ST

CCDS46014.1|GN=MAST3|GI=23031|FC=Missense|CP=2581|CF=0|AC=gGC->aGC|RP=861|RC=GI|Givl->S|Ser||EN=22/27|DS=+84|P=chr19:18208603-18260536|S

CCDS12371.1|GN=PIK3R2|GI=5296|FC=Missense|CP=937|CF=0|AC=tCC->cCC|RP=313|RC=S|Ser->P|Pro||EN=7/15|DS=+36|P=chr19:18266690-18280104|ST=-

CCDS42562.1|GN=FAM98|GI=147965|FC=Missense|CP=1719|CF=1|AC=AaC->AaA|RP=240|RC=T|Thr->K|Lys||EN=6/8|DS=+86|P=chr19:38893794-38899522|ST

CCDS12552.1|GN=AKT2|GI=208|FC=Downstream|DG=+266|P=chr19:40739779-40771174|ST=-|C|=1446|CS=Public

CCDS12562.1|GN=ADCK4|GI=79934|FC=Missense|CP=521|CF=1|AC=CaC->CcC|RP=174|RC=H|His->R|Arg||EN=6/14|DS=+31|P=chr19:41197940-41220537|ST

CCDS12575.1|GN=AXL|GI=558|FC=Missense|CP=796|CF=0|AC=aAC->gAC|RP=266|RC=N|Asn->D|Asp||EN=7/20|DS=+13|P=chr19:41725298-41765809|ST=+|C|

CCDS46119.1|GN=DMPK1|GI=1760|FC=Missense|CP=1297|CF=0|AC=cTG->gTG|RP=433|RC=L|Leu->V|Val||EN=9/14|DS=+35|P=chr19:46273746-46283317|ST=-

CCDS12689.1|GN=PRKD2|GI=25865|FC=Missense|CP=2504|CF=1|AC=GtG->GcG|RP=835|RC=V|Val->A|Ala||EN=18/18|DS=+80|P=chr19:47177780-47219627|S

CCDS12689.1|GN=PRKD2|GI=25865|FC=Missense|CP=1733|CF=1|AC=GcA->GaA|RP=578|RC=A|Ala->E|Glu||EN=13/18|DS=+31|P=chr19:47177780-47219627|S

CCDS42631.1|GN=SBK2|GI=646643|FC=Missense|CP=892|CF=0|AC=gCC->cCC|RP=298|RC=A|Ala->P|Pro||EN=3/3|DS=+436|P=chr19:56041100-56047661|ST

CCDS42631.1|GN=SBK2|GI=646643|FC=Missense|CP=214|CF=0|AC=tGC->cGC|RP=72|RC=C|Cys->R|Arg||EN=1/3|DS=-4736|P=chr19:56041100-56047661|ST

CCDS42631.1|GN=SBK2|GI=646643|FC=Missense|CP=118|CF=0|AC=cGC->aGC|RP=40|RC=R|Arg->S|Ser||EN=1/3|DS=-4832|P=chr19:56041100-56047661|ST

CCDS13107.1|GN=PAK7|GI=57144|FC=Missense|CP=1532|CF=1|AC=AgC->AaC|RP=511|RC=S|Ser->N|Asn||EN=4/8|DS=+50|P=chr20:9520109-9624976|ST=-|C

CCDS13191.1|GN=MYLK2|GI=85366|FC=Missense|CP=50|CF=1|AC=AaC->AaA|RP=17|RC=T|Thr->K|Lys||EN=1/12|DS=-496|P=chr20:30407384-30421600|ST=+

CCDS13451.1|GN=AURKA|GI=6790|FC=Missense|CP=169|CF=0|AC=aTT->gTT|RP=57|RC=I|Ile->V|Val||EN=2/8|DS=+127|P=chr20:54945214-54963253|ST=-|C|

CCDS13451.1|GN=AURKA|GI=6790|FC=Missense|CP=911|CF=0|AC=tTT->aTT|RP=311|RC=F|Phe->I|Ile||EN=2/8|DS=+49|P=chr20:54945214-54963253|ST=-|C|=1

CCDS13610.1|GN=HUNK1|GI=30811|FC=Missense|CP=1771|CF=0|AC=cGC->tGC|RP=591|RC=R|Arg->C|Cys||EN=11/11|DS=+285|P=chr21:33245988-33371497|S

CCDS13675.1|GN=RIPK4|GI=54101|FC=Missense|CP=1996|CF=0|AC=aTG->gTG|RP=666|RC=M|Met->V|Val||EN=8/8|DS=+801|P=chr21:43160998-43187201|ST

CCDS33575.1|GN=SIK1|GI=150094|FC=Missense|CP=1844|CF=1|AC=GcC->GtC|RP=615|RC=A|Ala->V|Val||EN=12/13|DS=+100|P=chr21:44836622-44846058|S

CCDS42954.1|GN=KRTAP10-1|GI=386677|FC=Missense|CP=722|CF=1|AC=CgG->CaG|RP=241|RC=R|Arg->Q|Gln||EN=1/1|P=chr21:45959185-45960033|ST=-|C

CCDS33637.1|GN=LIMK2|GI=3985|FC=Missense|CP=2051|CF=1|AC=CaG->CcG|RP=684|RC=Q|Gln->R|Arg||EN=15/15|DS=+342|P=chr22:31644703-31673126|S

CCDS14089.1|GN=MAPK12|GI=6300|FC=Missense|CP=308|CF=1|AC=AcG->AtG|RP=103|RC=T|Thr->M|Met||EN=3/12|DS=+53|P=chr22:50691830-50699938|ST

CCDS14090.1|GN=MAPK11|GI=5600|FC=Intron|EN=7:8/12|DS=-19|P=chr22:50703377-50708721|ST=-|C|=1095|CS=Public

CCDS14090.1|GN=MAPK11|GI=5600|FC=Intron|EN=7:8/12|DS=+59|P=chr22:50703377-50708721|ST=-|C|=1095|CS=Public

CCDS14125.1|GN=PRKXI|GI=5613|FC=Missense|CP=128|CF=1|AC=GtG->GcG|RP=43|RC=V|Val->A|Ala||EN=1/8|DS=-38360|P=chrX:3530241-3631294|ST=-|C|

CCDS14544.1|GN=IRS4|GI=8471|FC=Missense|CP=2635|CF=0|AC=cAT->gAT|RP=879|RC=H|His->D|Asp||EN=1/1|P=chrX:107975801-107979574|ST=-|C|=3774

CCDS14545.1|GN=GUCY2F1|GI=2986|FC=Missense|CP=887|CF=1|AC=CgG->CaG|RP=296|RC=R|Arg->Q|Gln||EN=2/18|DS=+157|P=chrX:108619128-108719165|I

CCDS14740.1|GN=IRAK1|GI=3654|FC=Missense|CP=1595|CF=1|AC=TcG->TtG|RP=532|RC=S|Ser->L|Leu||EN=12/14|DS=+56|P=chrX:153277310-153285263|ST

CCDS14740.1|GN=IRAK1|GI=3654|FC=Missense|CP=587|CF=1|AC=TtT->TcT|RP=196|RC=F|Phe->S|Ser||EN=5/14|DS=+47|P=chrX:153277310-153285263|ST=-

RefSeq Genes														
NM_033486.1	GN=CDK11B	GI=984	FC=Coding_synonymmv_unknown	EN=18/20	DS=+3	P=chr1:1571100-1655775	ST=-	IPD=	cvclin-dependent_kinase_11B_isoform_2					
NM_033486.1	GN=CDK11B	GI=984	FC=Coding_synonymmv_unknown	EN=11/20	DS=+99	P=chr1:1571100-1655775	ST=-	IPD=	cvclin-dependent_kinase_11B_isoform_2					
NM_033486.1	GN=CDK11B	GI=984	FC=Coding_synonymmv_unknown	EN=11/20	DS=+30	P=chr1:1571100-1655775	ST=-	IPD=	cvclin-dependent_kinase_11B_isoform_2					
NM_024011.2	GN=CDK11A	GI=728642	FC=Missense	CP=1964	CF=1	AC=GtA->GcA	IRP=655	RC=VlVal	->AlAla	EN=18/20	DS=+53	P=chr1:1634170-1655791	ST=	
NM_024011.2	GN=CDK11A	GI=728642	FC=Missense	CP=1168	CF=0	AC=gAC->aAG	IRP=390	RC=DlAsp	->NlAsn	EN=11/20	DS=+99	P=chr1:1634170-1655791	ST=	
NM_024011.2	GN=CDK11A	GI=728642	FC=Missense	CP=1099	CF=0	AC=gGG->aAG	IRP=367	RC=GlGlv	->RlArg	EN=11/20	DS=+30	P=chr1:1634170-1655791	ST=	
NM_005026.3	GN=PIK3CD1	GI=5293	FC=Missense	CP=1366	CF=0	AC=aCG->gCG	IRP=456	RC=TlThr	->AlAla	EN=11/24	DS=+27	P=chr1:9711790-9789172	ST=+	
NM_020526.3	GN=EPHA8	GI=2046	FC=Missense	CP=1834	CF=0	AC=gAA->cAA	IRP=612	RC=FlGlu	->QlGln	EN=10/17	DS=+69	P=chr1:22890004-22930087	ST=+	
NM_004672.3	GN=MAP3K6	GI=9064	FC=Missense	CP=1364	CF=1	AC=AcC->AtC	IRP=455	RC=TlThr	->Ille	EN=9/29	DS=+109	P=chr1:27681670-27693337	ST=-	
NM_005248.2	GN=GRIG1	GI=2268	FC=Missense	CP=823	CF=0	AC=gGG->cGG	IRP=275	RC=GlGlv	->RlArg	EN=8/13	DS=91	P=chr1:27938801-27961727	ST=-	ClE
NM_032017.1	GN=STK40	GI=83931	FC=Missense	CP=1183	CF=0	AC=gCC->aCC	IRP=395	RC=AlAla	->TlThr	EN=12/12	DS=+94	P=chr1:36805225-36851485	ST=	
NM_001099439.1	GN=EPHA10	GI=284656	FC=Missense	CP=3008	CF=1	AC=GgC->GtC	IRP=1003	RC=GlGlv	->VlVal	EN=17/17	DS=+96	P=chr1:38181646-382308		
NM_001099439.1	GN=EPHA10	GI=284656	FC=Missense	CP=841	CF=0	AC=tTC->aTC	IRP=281	RC=FlPhe	->Ille	EN=3/17	DS=+67	P=chr1:38181646-382308	24IS	
NM_001099439.1	GN=EPHA10	GI=284656	FC=Missense	CP=659	CF=1	AC=AcG->AaG	IRP=220	RC=TlThr	->KlLys	EN=3/17	DS=+488	P=chr1:38181646-382308	24IS	
NM_015112.2	GN=MAST2	GI=23139	FC=Missense	CP=1164	CF=2	AC=GAt->GAg	IRP=388	RC=DlAsp	->FlGlu	EN=10/29	DS=+186	P=chr1:46269285-46501796	ST=	
NM_015112.2	GN=MAST2	GI=23139	FC=Missense	CP=1977	CF=2	AC=ATt->ATg	IRP=659	RC=Ille	->MlMet	EN=17/29	DS=+58	P=chr1:46269285-46501796	ST=+	
NM_001114172.1	GN=PIK3R3	GI=8503	FC=Missense	CP=849	CF=2	AC=AAt->AAa	IRP=283	RC=NlAsn	->KlLys	EN=8/11	DS=+85	P=chr1:46505812-46598708	ST=	
NM_005012.2	GN=RORT1	GI=4919	FC=Missense	CP=1553	CF=1	AC=AcG->AtG	IRP=518	RC=TlThr	->MlMet	EN=9/9	DS=+167	P=chr1:64239690-64644707	ST=+	
NM_001242806.1	GN=BRDT1	GI=676	FC=Missense	CP=184	CF=0	AC=cAG->aAG	IRP=62	RC=QlGln	->KlLys	EN=2/19	DS=+221	P=chr1:92414928-92479985	ST=+	
NM_001242806.1	GN=BRDT1	GI=676	FC=Missense	CP=2099	CF=1	AC=CcG->CtG	IRP=700	RC=PlPro	->LlLeu	EN=14/19	DS=+23	P=chr1:92414928-92479985	ST=	
NM_015906.3	GN=TRIM3	GI=51592	FC=Missense	CP=2519	CF=1	AC=Att->Act	IRP=840	RC=Ille	->TlThr	EN=15/20	DS=+101	P=chr1:114935399-115053781	ST=	
NM_181093.2	GN=SCY1	GI=57147	FC=Missense	CP=1862	CF=1	AC=CaA->CgA	IRP=62	RC=QlGln	->RlArg	EN=13/14	DS=+388	P=chr1:169821804-169863076	ST=	
NM_021133.3	GN=RNASE1	GI=604	FC=Missense	CP=1385	CF=1	AC=CgA->CaA	IRP=462	RC=RlArg	->QlGln	EN=2/7	DS=-1256	P=chr1:182542769-182558394	ST=	
NM_015375.2	GN=DSTYK1	GI=25778	FC=Missense	CP=1921	CF=0	AC=tGT->cGT	IRP=64	RC=CiCvs	->RlArg	EN=7/13	DS=+103	P=chr1:205111631-205180727	ST=	
NM_030952.1	GN=NUAK2	GI=81788	FC=Missense	CP=1547	CF=1	AC=GcG->GtG	IRP=516	RC=AlAla	->VlVal	EN=7/7	DS=+724	P=chr1:205271191-205290883	ST=	
NM_212503.2	GN=CDK18	GI=5129	FC=Missense	CP=1487	CF=1	AC=GgG->GaG	IRP=496	RC=GlGlv	->FlGlu	EN=16/16	DS=+7	P=chr1:205473684-205501921	ST=	
NM_002221.3	GN=TPKB	GI=3707	FC=Missense	CP=1655	CF=1	AC=CcG->CaG	IRP=552	RC=PlPro	->QlGln	EN=2/8	DS=+1860	P=chr1:226819391-226926876	ST=	
NM_003607.3	GN=CDC42BPA	GI=8476	FC=Missense	CP=5096	CF=1	AC=GcT->GtT	IRP=1699	RC=AlAla	->VlVal	EN=36/36	DS=+68	P=chr1:227177566-2275058		
NM_003607.3	GN=CDC42BPA	GI=8476	FC=Missense	CP=3910	CF=0	AC=gTA->aTA	IRP=1304	RC=VlVal	->Ille	EN=29/36	DS=+177	P=chr1:227177566-2275058		
NM_001098623.1	GN=OBSCN1	GI=84033	FC=Missense	CP=1505	CF=1	AC=CaG->CgG	IRP=502	RC=QlGln	->RlArg	EN=4/105	DS=+247	P=chr1:228395861-22856		
NM_001098623.1	GN=OBSCN1	GI=84033	FC=Missense	CP=4523	CF=1	AC=GtC->GaC	IRP=1508	RC=VlVal	->DlAsp	EN=15/105	DS=+214	P=chr1:228395861-22856		
NM_001098623.1	GN=OBSCN1	GI=84033	FC=Missense	CP=6318	CF=2	AC=GAt->GAg	IRP=2106	RC=DlAsp	->FlGlu	EN=22/105	DS=+98	P=chr1:228395861-22856		
NM_001098623.1	GN=OBSCN1	GI=84033	FC=Missense	CP=6346	CF=0	AC=tTC->ctC	IRP=2116	RC=FlPhe	->LlLeu	EN=22/105	DS=+126	P=chr1:228395861-22856		
NM_001098623.1	GN=OBSCN1	GI=84033	FC=Missense	CP=15047	CF=1	AC=CgG->CaG	IRP=5016	RC=RlArg	->QlGln	EN=55/105	DS=+545	P=chr1:228395861-22856		
NM_032435.2	GN=KIAA1804	GI=84451	FC=Missense	CP=1349	CF=1	AC=GcT->GaT	IRP=450	RC=AlAla	->DlAsp	EN=5/10	DS=+38	P=chr1:233463514-233520894	ST=	
NM_032435.2	GN=KIAA1804	GI=84451	FC=Missense	CP=2182	CF=0	AC=gTC->aTC	IRP=728	RC=VlVal	->Ille	EN=9/10	DS=+258	P=chr1:233463514-233520894	ST=	
NM_032435.2	GN=KIAA1804	GI=84451	FC=Missense	CP=2223	CF=2	AC=GAg->GAT	IRP=741	RC=FlGlu	->DlAsp	EN=9/10	DS=+299	P=chr1:233463514-233520894	ST=	
NM_032435.2	GN=KIAA1804	GI=84451	FC=Missense	CP=2350	CF=0	AC=tGT->gGT	IRP=784	RC=CiCvs	->GlGlv	EN=9/10	DS=+426	P=chr1:233463514-233520894	ST=	
NM_004850.3	GN=ROCK2	GI=9475	FC=Missense	CP=1292	CF=1	AC=AcT->AaT	IRP=431	RC=TlThr	->NlAsn	EN=10/33	DS=+33	P=chr2:11321778-11484711	ST=	
NM_004304.4	GN=ALK1	GI=238	FC=Missense	CP=4587	CF=2	AC=GAc->GAg	IRP=1529	RC=DlAsp	->FlGlu	EN=29/29	DS=+423	P=chr2:29415640-30144477	ST=	
NM_004304.4	GN=ALK1	GI=238	FC=Missense	CP=4472	CF=1	AC=AaG->AgG	IRP=1491	RC=KlLys	->RlArg	EN=29/29	DS=+308	P=chr2:29415640-30144477	ST=-	
NM_004304.4	GN=ALK1	GI=238	FC=Missense	CP=4381	CF=0	AC=aTC->gTC	IRP=1461	RC=Ille	->VlVal	EN=29/29	DS=+217	P=chr2:29415640-30144477	ST=-	ClE
NM_004304.4	GN=ALK1	GI=238	FC=Missense	CP=4318	CF=0	AC=gCC->tCC	IRP=1440	RC=AlAla	->SlSer	EN=29/29	DS=+154	P=chr2:29415640-30144477	ST=-	
NM_004304.4	GN=ALK1	GI=238	FC=Missense	CP=3089	CF=1	AC=CaC->CcC	IRP=1030	RC=HlHis	->PlPro	EN=19/29	DS=+22	P=chr2:29415640-30144477	ST=-	ClE
NM_002759.3	GN=IF2AK2	GI=5610	FC=Missense	CP=1397	CF=1	AC=GgA->GaA	IRP=466	RC=GlGlv	->FlGlu	EN=15/17	DS=+20	P=chr2:37332284-37384190	ST=	
NM_138370.2	GN=PKDCC1	GI=91461	FC=Missense	CP=325	CF=0	AC=tCC->cCC	IRP=109	RC=SlSer	->PlPro	EN=1/7	DS=-4715	P=chr2:42275161-42285668	ST=	
NM_001130480.2	GN=VRK2	GI=7444	FC=Missense	CP=471	CF=2	AC=ATa->ATg	IRP=157	RC=Ille	->MlMet	EN=7/13	DS=+21	P=chr2:58273777-58387055	ST=+	
NM_004836.5	GN=IF2AK3	GI=9451	FC=Missense	CP=407	CF=1	AC=tCC->gCC	IRP=1360	RC=SlSer	->CtCvs	EN=2/17	DS=+99	P=chr2:88856259-88927094	ST=	
NM_001134224.1	GN=INPP4A	GI=3631	FC=Missense	CP=1810	CF=0	AC=aCT->gCT	IRP=604	RC=TlThr	->AlAla	EN=17/26	DS=+229	P=chr2:99061321-99207496	ST=	
NM_025052.3	GN=YSK4	GI=80122	FC=Missense	CP=2435	CF=1	AC=GaA->GgA	IRP=812	RC=FlGlu	->GlGlv	EN=7/10	DS=+1817	P=chr2:135722273-135782248	ST=	
NM_025052.3	GN=YSK4	GI=80122	FC=Missense	CP=2026	CF=0	AC=gAG->cAG	IRP=676	RC=FlGlu	->QlGln	EN=7/10	DS=+1408	P=chr2:135722273-135782248	ST=	
NM_001616.3	GN=ACVR2A	GI=92	FC=Missense	CP=945	CF=2	AC=AAa->AAc	IRP=315	RC=KlLys	->NlAsn	EN=7/11	DS=+129	P=chr2:148602570-148688393	ST=	

NM 145259.2|GN=ACVR1C|GI=130399|FC=Missense|CP=58|CF=0|AC=gCC->tCC|RP=20|RC=A|Ala|>S|Ser||EN=1/9|DS=-41|70|P=chr2:158383279-158485399|S
 NM 138995.3|GN=MYO3B|GI=140469|FC=Missense|CP=925|CF=0|AC=aAG->gAG|RP=309|RC=K|Lys|>F|Glu||EN=9/35|DS=+110|P=chr2:171034655-171511674|S
 NM 138995.3|GN=MYO3B|GI=140469|FC=Missense|CP=2308|CF=0|AC=gTA->aTA|RP=770|RC=V|Val|>I|Ile||EN=20/35|DS=+31|P=chr2:171034655-171511674|S
 NM 138995.3|GN=MYO3B|GI=140469|FC=Missense|CP=3245|CF=1|AC=A-gC->A-aG|RP=1082|RC=R|Arg|>K|Lys||EN=27/35|DS=+119|P=chr2:171034655-171511674|S
 NM 016653.2|GN=ZAK1|GI=51776|FC=Missense|CP=1592|CF=1|AC=T-cG->T-tG|RP=531|RC=S|Ser|>L|Leu||EN=19/20|DS=+41|P=chr2:173940565-174132737|ST=I
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=96077|CF=1|AC=C-gC->C-aC|RP=32026|RC=R|Arg|>H|His||EN=307/312|DS=-27|18|P=chr2:179390718-179672150|S
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=89909|CF=1|AC=C-gC->C-aC|RP=29970|RC=R|Arg|>H|His||EN=299/312|DS=+121|P=chr2:179390718-179672150|S
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=88910|CF=1|AC=G-tG->G-cG|RP=29637|RC=V|Val|>A|Ala||EN=296/312|DS=+304|P=chr2:179390718-179672150|S
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=80483|CF=1|AC=A-tC->A-cC|RP=26828|RC=I|Ile|>T|Thr||EN=279/312|DS=+178|P=chr2:179390718-179672150|S
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=77947|CF=0|AC=cCA->aCA|RP=25983|RC=P|Pro|>T|Thr||EN=275/312|DS=-1844|P=chr2:179390718-179672150|S
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=75619|CF=0|AC=aTA->gTA|RP=25207|RC=I|Ile|>V|Val||EN=275/312|DS=-4172|P=chr2:179390718-179672150|S
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=72158|CF=1|AC=A-cG->A-tG|RP=24053|RC=T|Thr|>M|Met||EN=275/312|DS=-7633|P=chr2:179390718-179672150|S
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=67135|CF=0|AC=cGC->tGC|RP=22379|RC=R|Arg|>C|Cys||EN=275/312|DS=+5124|P=chr2:179390718-179672150|S
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=59542|CF=0|AC=gCT->cCT|RP=19848|RC=A|Ala|>P|Pro||EN=267/312|DS=+189|P=chr2:179390718-179672150|S
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=59371|CF=0|AC=gTC->aTC|RP=19791|RC=V|Val|>I|Ile||EN=267/312|DS=+18|P=chr2:179390718-179672150|S
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=56504|CF=1|AC=A-cT->A-tT|RP=18835|RC=T|Thr|>I|Ile||EN=257/312|DS=+115|P=chr2:179390718-179672150|S
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=51881|CF=1|AC=C-aP->C-aP|RP=17294|RC=P|Pro|>L|Leu||EN=250/312|DS=-143|P=chr2:179390718-179672150|S
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=50732|CF=1|AC=C-gT->C-aT|RP=16911|RC=R|Arg|>H|His||EN=247/312|DS=+4|P=chr2:179390718-179672150|S
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=48397|CF=0|AC=aAT->gAT|RP=16133|RC=N|Asn|>D|Asp||EN=238/312|DS=+51|P=chr2:179390718-179672150|S
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=43778|CF=1|AC=G-cG->G-tG|RP=14593|RC=A|Ala|>V|Val||EN=221/312|DS=+46|P=chr2:179390718-179672150|S
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=32402|CF=1|AC=C-aA->C-gA|RP=10801|RC=P|Pro|>R|Arg||EN=163/312|DS=+79|P=chr2:179390718-179672150|S
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=27832|CF=0|AC=aTT->gTT|RP=9278|RC=I|Ile|>V|Val||EN=116/312|DS=+51|P=chr2:179390718-179672150|ST=I
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=22676|CF=1|AC=A-aT->A-gT|RP=7559|RC=N|Asn|>S|Ser||EN=88/312|DS=-191|P=chr2:179390718-179672150|S
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=21542|CF=1|AC=A-gC->A-aC|RP=7181|RC=S|Ser|>N|Asn||EN=84/312|DS=+211|P=chr2:179390718-179672150|S
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=21332|CF=1|AC=G-cG->G-aC|RP=7111|RC=A|Ala|>E|Glu||EN=84/312|DS=+1|P=chr2:179390718-179672150|ST=I
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=20699|CF=1|AC=G-aA->G-cA|RP=6900|RC=E|Glu|>A|Ala||EN=81/312|DS=-169|P=chr2:179390718-179672150|S
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=18652|CF=0|AC=gAT->cAT|RP=6218|RC=D|Asp|>H|His||EN=74/312|DS=+144|P=chr2:179390718-179672150|S
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=17312|CF=1|AC=G-aA->G-tA|RP=5771|RC=A|Ala|>V|Val||EN=69/312|DS=-188|P=chr2:179390718-179672150|S
 NM 133379.3|GN=TTN|GI=7273|FC=Missense|CP=11240|CF=1|AC=G-aC->G-gC|RP=3747|RC=D|Asp|>G|Gly||EN=46/46|DS=+880|P=chr2:179610047-179672150|S
 NM 133379.3|GN=TTN|GI=7273|FC=Missense|CP=1196|CF=2|AC=TTG->TTG|RP=3732|RC=L|Leu|>F|Phe||EN=46/46|DS=+836|P=chr2:179610047-179672150|S
 NM 133437.3|GN=TTN|GI=7273|FC=Missense|CP=10739|CF=1|AC=G-gT->G-aT|RP=3580|RC=G|Gly|>D|Asp||EN=44/192|DS=+574|P=chr2:179390718-179672150|S
 NM 133437.3|GN=TTN|GI=7273|FC=Missense|CP=10213|CF=0|AC=gCC->aCC|RP=3405|RC=A|Ala|>T|Thr||EN=44/192|DS=+48|P=chr2:179390718-179672150|S
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=10256|CF=1|AC=A-gT->A-aT|RP=3419|RC=S|Ser|>N|Asn||EN=44/312|DS=+142|P=chr2:179390718-179672150|S
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=9781|CF=0|AC=gTG->aTG|RP=3261|RC=V|Val|>M|Met||EN=42/312|DS=+78|P=chr2:179390718-179672150|ST=I
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=8887|CF=0|AC=aCC->cCC|RP=2963|RC=T|Thr|>P|Pro||EN=37/312|DS=+246|P=chr2:179390718-179672150|S
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=7619|CF=1|AC=C-gT->C-aT|RP=2540|RC=R|Arg|>H|His||EN=33/312|DS=+25|P=chr2:179390718-179672150|ST=I
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=3884|CF=1|AC=T-cA->T-tA|RP=1295|RC=S|Ser|>L|Leu||EN=23/312|DS=+155|P=chr2:179390718-179672150|S
 NM 133378.4|GN=TTN|GI=7273|FC=Missense|CP=982|CF=0|AC=cGT->tGT|RP=328|RC=R|Arg|>C|Cys||EN=7/312|DS=+68|P=chr2:179390718-179672150|ST=I
 NM 015040.3|GN=PIKFYV|GI=200576|FC=Missense|CP=2087|CF=1|AC=A-gT->A-aT|RP=696|RC=S|Ser|>N|Asn||EN=17/42|DS=+5|P=chr2:209130991-20922347|S
 NM 015040.3|GN=PIKFYV|GI=200576|FC=Missense|CP=2795|CF=1|AC=T-tG->T-cG|RP=932|RC=L|Leu|>S|Ser||EN=20/42|DS=+337|P=chr2:209130991-20922347|S
 NM 015040.3|GN=PIKFYV|GI=200576|FC=Missense|CP=2984|CF=1|AC=C-aG->C-tG|RP=995|RC=Q|Gln|>L|Leu||EN=20/42|DS=+526|P=chr2:209130991-20922347|S
 NM 015040.3|GN=PIKFYV|GI=200576|FC=Missense|CP=2993|CF=1|AC=A-cT->A-gT|RP=998|RC=T|Thr|>S|Ser||EN=20/42|DS=+535|P=chr2:209130991-20922347|S
 NM 015040.3|GN=PIKFYV|GI=200576|FC=Missense|CP=3547|CF=0|AC=cAA->aAA|RP=1183|RC=Q|Gln|>K|Lys||EN=20/42|DS=+1089|P=chr2:209130991-20922347|S
 NM 015040.3|GN=PIKFYV|GI=200576|FC=Missense|CP=3793|CF=0|AC=cCT->aCT|RP=1265|RC=P|Pro|>T|Thr||EN=23/42|DS=+2|P=chr2:209130991-20922347|S
 NM 005876.4|GN=SPG|GI=10290|FC=Missense|CP=3928|CF=0|AC=gAC->aAC|RP=1310|RC=D|Asp|>N|Asn||EN=15/41|DS=+93|P=chr2:220299700-220358354|S
 NM 005876.4|GN=SPG|GI=10290|FC=Missense|CP=8368|CF=0|AC=aGG->gGG|RP=2790|RC=R|Arg|>G|Gly||EN=36/41|DS=+51|P=chr2:220299700-220358354|S
 NM 001252119.1|GN=PASK|GI=23178|FC=Missense|CP=3818|CF=1|AC=T-tT->T-gT|RP=1273|RC=F|Phe|>C|Cys||EN=17/18|DS=+130|P=chr2:242045514-24208891|S
 NM 001252124.1|GN=PASK|GI=23178|FC=Missense|CP=3888|CF=0|AC=cGG->tGG|RP=1130|RC=R|Arg|>W|Trp||EN=14/14|DS=+190|P=chr2:242053050-24208891|S
 NM 001252119.1|GN=PASK|GI=23178|FC=Synonymous-Coding|CP=186|CF=2|AC=ACa->ACg|RP=62|RC=T|Thr|>T|Thr||EN=2/18|DS=+228|P=chr2:242045514-24208891|S
 NM 001570.3|GN=IRAK2|GI=3656|FC=Missense|CP=1293|CF=2|AC=GAT->GAA|RP=431|RC=D|Asp|>E|Glu||EN=11/13|DS=+21|P=chr3:10206563-10285427|ST=I
 NM 199347.2|GN=NEK10|GI=152110|FC=Missense|CP=1538|CF=1|AC=T-tG->T-cG|RP=513|RC=L|Leu|>S|Ser||EN=19/25|DS=+62|P=chr3:27257097-27410912|ST=I
 NM 017886.2|GN=ULK4|GI=54986|FC=Missense|CP=2990|CF=1|AC=A-tT->A-gT|RP=997|RC=I|Ile|>S|Ser||EN=30/37|DS=+12|P=chr3:41288090-42003660|ST=I
 NM 017886.2|GN=ULK4|GI=54986|FC=Missense|CP=1918|CF=0|AC=TCC->gCC|RP=640|RC=S|Ser|>A|Ala||EN=20/37|DS=+70|P=chr3:41288090-42003660|ST=I
 NM 017886.2|GN=ULK4|GI=54986|FC=Missense|CP=1624|CF=0|AC=gCT->aCT|RP=542|RC=A|Ala|>T|Thr||EN=17/37|DS=+47|P=chr3:41288090-42003660|ST=I
 NM 017886.2|GN=ULK4|GI=54986|FC=Missense|CP=670|CF=0|AC=aTT->gTT|RP=224|RC=I|Ile|>V|Val||EN=7/37|DS=+27|P=chr3:41288090-42003660|ST=I

NM 017886.2|GN=ULK4|GI=54986|FC=Missense|CP=116|CF=1|AC=AaA->AgA|RP=39|RC=KI|vs|>R|Arg||EN=2/37|DS=+164|P=chr3:41288090-42003660|ST=-|CI=|
 NM 002447.2|GN=MST1R|GI=4486|FC=Missense|CP=3583|CF=0|AC=aGC->gGC|RP=1195|RC=SI|Ser|>G|Glv||EN=17/20|DS=+49|P=chr3:49924436-49941306|ST=-|CI=|
 NM 003157.4|GN=NEK4|GI=6787|FC=Missense|CP=673|CF=0|AC=cCA->gCA|RP=225|RC=PI|Pro|>A|Ala||EN=5/16|DS=+7|P=chr3:52744796-52804965|ST=-|CI=|
 NM 001080448.2|GN=EPHA6|GI=285220|FC=Missense|CP=388|CF=0|AC=gTC->aTC|RP=130|RC=VI|Val|>M|Met||EN=2/18|DS=+3|P=chr3:96533425-97467786|ST=-|CI=|
 NM 053025.3|GN=MYL K|GI=4638|FC=Missense|CP=2742|CF=2|AC=AGc->GAa|RP=914|RC=DI|Asp|>E|Glu||EN=18/34|DS=+280|P=chr3:123331143-123603149|ST=-|CI=|
 NM 053025.3|GN=MYL K|GI=4638|FC=Missense|CP=2582|CF=1|AC=CtA->CcA|RP=861|RC=LI|Leu|>P|Pro||EN=18/34|DS=+120|P=chr3:123331143-123603149|ST=-|CI=|
 NM 053025.3|GN=MYL K|GI=4638|FC=Missense|CP=1486|CF=0|AC=cTG->gTG|RP=496|RC=LI|Leu|>V|Val||EN=11/34|DS=+177|P=chr3:123331143-123603149|ST=-|CI=|
 NM 053025.3|GN=MYL K|GI=4638|FC=Missense|CP=782|CF=1|AC=CtG->CcG|RP=261|RC=VI|Val|>A|Ala||EN=10/34|DS=+9|P=chr3:123331143-123603149|ST=-|CI=|
 NM 053025.3|GN=MYL K|GI=4638|FC=Missense|CP=439|CF=0|AC=cCA->tCA|RP=147|RC=PI|Pro|>S|Ser||EN=7/34|DS=+17|P=chr3:123331143-123603149|ST=-|CI=|
 NM 001024660.3|GN=KALRN|GI=8997|FC=Missense|CP=880|CF=0|AC=cAC->aAC|RP=294|RC=HI|His|>N|Asn||EN=5/60|DS=+430|P=chr3:123813558-124440036|ST=-|CI=|
 NM 024800.4|GN=NEK11|GI=79858|FC=Missense|CP=1463|CF=1|AC=GaA->GtA|RP=488|RC=EI|Glu|>V|Val||EN=15/18|DS=+64|P=chr3:130745694-131069309|ST=-|CI=|
 NM 001184.3|GN=ATR|GI=545|FC=Missense|CP=632|CF=1|AC=AtG->AcG|RP=211|RC=M|Met|>T|Thr||EN=4/47|DS=+340|P=chr3:142168077-142297668|ST=-|CI=|
 NM 00124231.4|GN=MAP3K13|GI=9175|FC=Missense|CP=2744|CF=1|AC=CgT->CaT|RP=915|RC=R|Arg|>H|His||EN=14/15|DS=+243|P=chr3:185000729-185200729|ST=-|CI=|
 NM 001346.2|GN=DGKG|GI=1608|FC=Missense|CP=947|CF=1|AC=AgA->AaA|RP=316|RC=R|Arg|>K|Lys||EN=11/25|DS=+37|P=chr3:185864990-186080023|ST=-|CI=|
 NM 001346.2|GN=DGKG|GI=1608|FC=Missense|CP=425|CF=1|AC=AcC->AgC|RP=142|RC=T|Thr|>S|Ser||EN=6/25|DS=+52|P=chr3:185864990-186080023|ST=-|CI=|
 NM 005255.2|GN=GAK|GI=2580|FC=Missense|CP=3899|CF=1|AC=IcG->ItG|RP=1300|RC=SI|Ser|>L|Leu||EN=28/28|DS=+65|P=chr4:843065-926174|ST=-|CI=3|
 NM 182982.2|GN=GRK4|GI=2868|FC=Missense|CP=194|CF=1|AC=CgT->CtT|RP=65|RC=R|Arg|>L|Leu||EN=3/16|DS=+46|P=chr4:2965343-3042474|ST=+|CI=17|
 NM 182982.2|GN=GRK4|GI=2868|FC=Missense|CP=425|CF=1|AC=GcC->GtC|RP=142|RC=A|Ala|>V|Val||EN=5/16|DS=+86|P=chr4:2965343-3042474|ST=+|CI=1|
 NM 018401.1|GN=STK32B|GI=55351|FC=Missense|CP=592|CF=0|AC=aGA->gGA|RP=198|RC=R|Arg|>G|Glv||EN=7/12|DS=+30|P=chr4:5053527-5502725|ST=+|CI=|
 NM 018323.3|GN=PI4K2B|GI=55300|FC=Missense|CP=16|CF=0|AC=gAG->aAG|RP=6|RC=EI|Glu|>K|Lys||EN=1/10|DS=-18142|P=chr4:25235653-25280831|ST=+|CI=|
 NM 002253.2|GN=KDRIG|GI=3791|FC=Missense|CP=1416|CF=2|AC=CAa->CAa|RP=472|RC=Q|Gln|>H|His||EN=1/30|DS=+4|P=chr4:55944426-55991762|ST=-|CI=|
 NM 198892.1|GN=BMP2K|GI=55589|FC=Missense|CP=1213|CF=0|AC=gGT->aGT|RP=405|RC=G|Glv|>S|Ser||EN=10/16|DS=+146|P=chr4:79697532-79833341|ST=-|CI=|
 NM 001163436.1|GN=TBC1|GI=93627|FC=Missense|CP=796|CF=0|AC=cAA->gAA|RP=266|RC=Q|Gln|>E|Glu||EN=10/26|DS=+14|P=chr4:106967233-107237861|ST=-|CI=|
 NM 025144.3|GN=ALPK1|GI=80216|FC=Missense|CP=1694|CF=1|AC=GgT->GaT|RP=565|RC=G|Glv|>D|Asp||EN=11/16|DS=+794|P=chr4:113218499-113363764|ST=-|CI=|
 NM 025144.3|GN=ALPK1|GI=80216|FC=Missense|CP=1925|CF=1|AC=CaT->CgT|RP=642|RC=H|His|>R|Arg||EN=11/16|DS=+1025|P=chr4:113218499-113363764|ST=-|CI=|
 NM 025144.3|GN=ALPK1|GI=80216|FC=Missense|CP=2196|CF=2|AC=ATg->ATa|RP=732|RC=M|Met|>I|Ile||EN=11/16|DS=+1296|P=chr4:113218499-113363764|ST=-|CI=|
 NM 025144.3|GN=ALPK1|GI=80216|FC=Missense|CP=2582|CF=1|AC=AtG->AcG|RP=861|RC=M|Met|>T|Thr||EN=11/16|DS=+1682|P=chr4:113218499-113363764|ST=-|CI=|
 NM 014264.4|GN=PLK4|GI=10733|FC=Missense|CP=694|CF=0|AC=tCT->aCT|RP=232|RC=SI|Ser|>T|Thr||EN=5/16|DS=+357|P=chr4:128802016-128820377|ST=-|CI=|
 NM 001040261.4|GN=DCLK2|GI=166614|FC=Missense|CP=2293|CF=0|AC=cCT->tCT|RP=765|RC=PI|Pro|>S|Ser||EN=17/17|DS=+169|P=chr4:150999426-1511178|ST=-|CI=|
 NM 001040261.4|GN=DCLK2|GI=166614|FC=Missense|CP=2294|CF=1|AC=CcT->CgT|RP=765|RC=PI|Pro|>R|Arg||EN=17/17|DS=+170|P=chr4:150999426-1511178|ST=-|CI=|
 NM 001199397.1|GN=NEK11|GI=4750|FC=Missense|CP=2255|CF=1|AC=GaA->GgA|RP=752|RC=EI|Glu|>G|Glv||EN=26/36|DS=+50|P=chr4:170314421-170533778|ST=-|CI=|
 NM 005921.1|GN=MAP3K11|GI=4214|FC=Missense|CP=2416|CF=0|AC=gAT->aAT|RP=806|RC=DI|Asp|>N|Asn||EN=14/20|DS=+47|P=chr5:56110900-56191978|ST=-|CI=|
 NM 005921.1|GN=MAP3K11|GI=4214|FC=Missense|CP=2716|CF=0|AC=gTC->aTC|RP=906|RC=VI|Val|>I|Ile||EN=14/20|DS=+347|P=chr5:56110900-56191978|ST=-|CI=|
 NM 001164664.1|GN=MAST4|GI=375449|FC=Missense|CP=4871|CF=1|AC=CgG->CcG|RP=1624|RC=R|Arg|>P|Pro||EN=29/29|DS=+904|P=chr5:65892176-66465|ST=-|CI=|
 NM 181523.2|GN=PIK3R1|GI=5295|FC=Missense|CP=978|CF=2|AC=ATg->ATa|RP=326|RC=M|Met|>I|Ile||EN=8/16|DS=+62|P=chr5:67511584-67597649|ST=+|CI=|
 NM 018343.2|GN=RIOK2|GI=55781|FC=Missense|CP=1045|CF=0|AC=gGG->aGG|RP=349|RC=G|Glv|>R|Arg||EN=8/10|DS=+173|P=chr5:96496571-96519005|ST=-|CI=|
 NM 018343.2|GN=RIOK2|GI=55781|FC=Missense|CP=287|CF=1|AC=IcT->IcT|RP=96|RC=SI|Ser|>C|Cys||EN=3/10|DS=+82|P=chr5:96496571-96519005|ST=-|CI=|
 NM 000038.5|GN=APC|GI=324|FC=Missense|CP=5465|CF=1|AC=CtC->GaC|RP=1822|RC=VI|Val|>D|Asp||EN=16/16|DS=+3507|P=chr5:112073556-112181936|ST=-|CI=|
 NM 032028.3|GN=SSK1B|GI=83942|FC=Missense|CP=1010|CF=1|AC=AgG->AaG|RP=337|RC=R|Arg|>K|Lys||EN=1/1|P=chr5:112768251-112770728|ST=-|CI=|
 NM 005211.3|GN=CSF1R|GI=1436|FC=Missense|CP=1085|CF=1|AC=CaC->CcC|RP=362|RC=H|His|>R|Arg||EN=8/22|DS=+3|P=chr5:149432854-149492935|ST=-|CI=|
 NM 002011.3|GN=FGER4|GI=2264|FC=Missense|CP=28|CF=0|AC=gTC->aTC|RP=10|RC=VI|Val|>I|Ile||EN=2/18|DS=+81|P=chr5:176513921-176525126|ST=+|CI=|
 NM 002011.3|GN=FGER4|GI=2264|FC=Missense|CP=407|CF=1|AC=CcC->CcC|RP=136|RC=PI|Pro|>L|Leu||EN=4/18|DS=+52|P=chr5:176513921-176525126|ST=-|CI=|
 NM 002011.3|GN=FGER4|GI=2264|FC=Missense|CP=1162|CF=0|AC=gGG->aGG|RP=388|RC=G|Glv|>R|Arg||EN=9/18|DS=+105|P=chr5:176513921-176525126|ST=-|CI=|
 NM 182925.4|GN=FLT4|GI=2324|FC=Missense|CP=2670|CF=2|AC=CAc->CAg|RP=890|RC=H|His|>Q|Gln||EN=19/30|DS=+23|P=chr5:180028506-180076624|ST=-|CI=|
 NM 182925.4|GN=FLT4|GI=2324|FC=Missense|CP=1936|CF=0|AC=gAG->aAG|RP=646|RC=EI|Glu|>K|Lys||EN=13/30|DS=+279|P=chr5:180028506-180076624|ST=-|CI=|
 NM 001012418.3|GN=MYLK|GI=340156|FC=Intron|EN=8/9|DS=-34|P=chr6:2663863-2751154|ST=-|CI=1167|PD=mvosin light chain kinase family member 4|
 NM 003913.4|GN=PRPF4B|GI=8899|FC=Missense|CP=247|CF=0|AC=aTT->gTT|RP=83|RC=I|Ile|>V|Val||EN=2/15|DS=+206|P=chr6:4021569-4065217|ST=+|CI=3|
 NM 032454.1|GN=STK19|GI=8859|FC=Missense|CP=583|CF=0|AC=cAG->gAG|RP=195|RC=Q|Gln|>E|Glu||EN=4/8|DS=+16|P=chr6:31939646-31949223|ST=+|CI=|
 NM 032454.1|GN=STK19|GI=8859|FC=Missense|CP=688|CF=0|AC=tGT->cGT|RP=230|RC=C|Cys|>R|Arg||EN=5/8|DS=+13|P=chr6:31939646-31949223|ST=+|CI=|
 NM 054111.4|GN=IP6K3|GI=117283|FC=Missense|CP=934|CF=0|AC=gTC->aTC|RP=312|RC=VI|Val|>I|Ile||EN=6/6|DS=+169|P=chr6:33689443-33714762|ST=-|CI=|
 NM 054111.4|GN=IP6K3|GI=117283|FC=Missense|CP=302|CF=1|AC=IcG->ItG|RP=101|RC=SI|Ser|>L|Leu||EN=3/6|DS=+103|P=chr6:33689443-33714762|ST=-|CI=|
 NM 007271.2|GN=STK38|GI=11329|FC=Missense|CP=316|CF=0|AC=gTT->tTT|RP=106|RC=VI|Val|>F|Phe||EN=5/14|DS=+10|P=chr6:36461669-36515247|ST=-|CI=|
 NM 001760.3|GN=CCND3|GI=896|FC=Missense|CP=775|CF=0|AC=tCT->gCT|RP=259|RC=SI|Ser|>A|Ala||EN=5/5|DS=+64|P=chr6:41902671-41909552|ST=-|CI=|
 NM 002821.3|GN=PTK7|GI=5754|FC=Missense|CP=2229|CF=2|AC=GAg->GAt|RP=743|RC=EI|Glu|>D|Asp||EN=14/20|DS=+182|P=chr6:43044029-43129457|ST=+|CI=|

NM 032538.1|GN=TTBK1|GI=84630|FC=Missense|CP=3434|CF=1|AC=AaG->AgG|RP=1145|RC=K|Lvs|>R|Arg|LEN=14/15|DS=-809|P=chr6:43211222-43255997|S
 NM 032538.1|GN=TTBK1|GI=84630|FC=Missense|CP=3551|CF=1|AC=TtG->TcG|RP=1184|RC=L|L|Leu|>S|Ser|LEN=14/15|DS=-692|P=chr6:43211222-43255997|S
 NM 004556.2|GN=NFKB1|GI=4794|FC=Missense|CP=581|CF=1|AC=GtC->GcC|RP=194|RC=V|Val|>A|Ala|LEN=1/6|DS=-2521|P=chr6:44225903-44233525|ST=-|
 NM 004556.2|GN=NFKB1|GI=4794|FC=Missense|CP=524|CF=1|AC=CcA->CtA|RP=175|RC=P|Pro|>L|Leu|LEN=1/6|DS=-2578|P=chr6:44225903-44233525|ST=-|
 NM 015076.3|GN=CDK19|GI=23097|FC=Missense|CP=1290|CF=2|AC=AGc->AGa|RP=430|RC=S|Ser|>R|Arg|LEN=12/13|DS=+180|P=chr6:110931181-111136412|
 NM 002031.2|GN=FRK1|GI=2444|FC=Missense|CP=364|CF=0|AC=gGA->aGA|RP=122|RC=G|Glv|>R|Arg|LEN=2/8|DS=+20|P=chr6:116262693-116381921|ST=-|C|
 NM 002944.2|GN=ROS1|GI=6098|FC=Missense|CP=611|CF=1|AC=Cgt->Cat|RP=2039|RC=R|Arg|>H|His|LEN=38/43|DS=+111|P=chr6:117609530-117747018|S
 NM 005923.3|GN=MAP3K5|GI=4217|FC=Missense|CP=3748|CF=0|AC=aTA->gTA|RP=1250|RC=I|Ile|>V|Val|LEN=26/30|DS=+231|P=chr6:136878187-137113656|S
 NM 005922.2|GN=MAP3K4|GI=4216|FC=Missense|CP=470|CF=1|AC=Cgt->CAt|RP=157|RC=R|Arg|>H|His|LEN=3/27|DS=+127|P=chr6:161412822-161538417|ST
 NM 001006932.1|GN=RPS6KA2|GI=6196|FC=Missense|CP=100|CF=0|AC=aCC->gCC|RP=34|RC=T|Thr|>A|Ala|LEN=2/22|DS=+37|P=chr6:166822854-167275771|
 NM 001006932.1|GN=RPS6KA2|GI=6196|FC=Missense|CP=95|CF=1|AC=GaG->GgG|RP=32|RC=E|Glu|>G|Glv|LEN=2/22|DS=+32|P=chr6:166822854-167275771|S
 NM 031414.3|GN=STK31|GI=56164|FC=Missense|CP=213|CF=2|AC=CAg->CAG|RP=71|RC=Q|Gln|>H|His|LEN=4/24|DS=+63|P=chr7:23749838-23872127|ST=+|C|
 NM 031414.3|GN=STK31|GI=56164|FC=Missense|CP=781|CF=0|AC=gAG->aAG|RP=261|RC=E|Glu|>K|Lvs|LEN=7/24|DS=+298|P=chr7:23749838-23872127|ST=+|
 NM 031414.3|GN=STK31|GI=56164|FC=Missense|CP=804|CF=2|AC=AAg->AAt|RP=268|RC=K|Lvs|>N|Asn|LEN=7/24|DS=+321|P=chr7:23749838-23872127|ST=+|
 NM 031414.3|GN=STK31|GI=56164|FC=Missense|CP=1453|CF=0|AC=gCC->tCC|RP=485|RC=A|Ala|>S|Ser|LEN=12/24|DS=+37|P=chr7:23749838-23872127|ST=+|
 NM 031414.3|GN=STK31|GI=56164|FC=Missense|CP=1863|CF=2|AC=AAt->AAg|RP=621|RC=N|Asn|>K|Lvs|LEN=15/24|DS=+30|P=chr7:23749838-23872127|ST=+|
 NM 031414.3|GN=STK31|GI=56164|FC=Missense|CP=1868|CF=1|AC=gAG->aAG|RP=261|RC=E|Glu|>K|Lvs|LEN=7/24|DS=+298|P=chr7:23749838-23872127|ST=+|
 NM 003718.4|GN=CDK13|GI=8621|FC=Missense|CP=1498|CF=0|AC=aCG->gCG|RP=500|RC=T|Thr|>A|Ala|LEN=2/14|DS=+287|P=chr7:39989959-40136733|ST=+|
 NM 004760.2|GN=STK17A|GI=9263|FC=Missense|CP=378|CF=2|AC=GAa->GAc|RP=126|RC=E|Glu|>D|Asp|LEN=2/7|DS=+172|P=chr7:43622692-43666978|ST=+|
 NM 004760.2|GN=STK17A|GI=9263|FC=Missense|CP=1084|CF=0|AC=aAG->gAG|RP=362|RC=K|Lvs|>E|Glu|LEN=7/7|DS=+164|P=chr7:43622692-43666978|ST=+|
 NM 005228.3|GN=GFR1|GI=1956|FC=Missense|CP=1562|CF=1|AC=AgG->AaG|RP=521|RC=R|Arg|>K|Lvs|LEN=13/28|DS=+64|P=chr7:55086725-55275031|ST=+|
 NM 002612.3|GN=PDK4|GI=5166|FC=Missense|CP=1002|CF=2|AC=TTg->TtT|RP=334|RC=L|L|Leu|>F|Phe|LEN=10/11|DS=+21|P=chr7:95212809-95225925|ST=-|C|
 NM 014916.3|GN=MTK2|GI=22853|FC=Missense|CP=2338|CF=0|AC=TTG->aTG|RP=780|RC=L|L|Leu|>M|Met|LEN=11/14|DS=+190|P=chr7:97736197-97838944|S
 NM 001244580.1|GN=TRRAP1|GI=8295|FC=Missense|CP=356|CF=1|AC=CgC->CcC|RP=119|RC=R|Arg|>P|Pro|LEN=5/72|DS=+95|P=chr7:98476113-98610866|ST
 NM 001244580.1|GN=TRRAP1|GI=8295|FC=Missense|CP=4924|CF=0|AC=gCC->tCC|RP=1642|RC=A|Ala|>S|Ser|LEN=35/72|DS=-87|P=chr7:98476113-98610866|
 NM 001127500.1|GN=MET1|GI=4233|FC=Missense|CP=1124|CF=1|AC=AaC->AgC|RP=375|RC=N|Asn|>S|Ser|LEN=2/21|DS=+1138|P=chr7:116312459-116438440|
 NM 015905.2|GN=TRIM24|GI=8805|FC=Missense|CP=143|CF=1|AC=GcC->GaC|RP=48|RC=A|Ala|>D|Asp|LEN=1/19|DS=-43599|P=chr7:138145079-138270332|S
 NM 005232.4|GN=PHA1|GI=2041|FC=Missense|CP=2698|CF=0|AC=aTG->tG|RP=900|RC=M|Met|>V|Val|LEN=17/18|DS=+2|P=chr7:143088205-143105985|ST
 NM 005232.4|GN=PHA1|GI=2041|FC=Missense|CP=479|CF=1|AC=GtG->GcG|RP=160|RC=V|Val|>A|Ala|LEN=4/18|DS=+47|P=chr7:143088205-143105985|ST=-|
 NM 001080826.1|GN=SGK223|GI=157285|FC=Missense|CP=3664|CF=0|AC=gGC->aGC|RP=1222|RC=G|Glv|>S|Ser|LEN=5/5|DS=+598|P=chr8:8175258-8239257|
 NM 001080826.1|GN=SGK223|GI=157285|FC=Missense|CP=3331|CF=0|AC=gCG->aCG|RP=1111|RC=A|Ala|>T|Thr|LEN=5/5|DS=+265|P=chr8:8175258-8239257|
 NM 001080826.1|GN=SGK223|GI=157285|FC=Missense|CP=1727|CF=1|AC=TtC->TtT|RP=576|RC=S|Ser|>C|Cvs|LEN=2/5|DS=+1397|P=chr8:8175258-8239257|
 NM 001080826.1|GN=SGK223|GI=157285|FC=Missense|CP=1700|CF=1|AC=CcG->CtG|RP=567|RC=P|Pro|>L|Leu|LEN=2/5|DS=+1370|P=chr8:8175258-8239257|
 NM 001080826.1|GN=SGK223|GI=157285|FC=Missense|CP=1205|CF=1|AC=CgG->CaG|RP=402|RC=R|Arg|>Q|Gln|LEN=2/5|DS=+875|P=chr8:8175258-8239257|S
 NM 001080826.1|GN=SGK223|GI=157285|FC=Missense|CP=189|CF=2|AC=AGc->AGt|RP=63|RC=R|Arg|>S|Ser|LEN=1/5|DS=-3481|P=chr8:8175258-8239257|ST
 NM 001715.2|GN=BLK1|GI=640|FC=Intron|LEN=10:11/13|DS=-38|P=chr8:11351521-11422108|ST=+|C|=1518|PD=tyrosine-protein kinase Blk|OM=191305
 NM 173174.2|GN=PIK2B1|GI=2185|FC=Missense|CP=2513|CF=1|AC=AaG->AcG|RP=838|RC=K|Lvs|>T|Thr|LEN=31/36|DS=+26|P=chr8:27168999-27316908|ST=+|
 NM 001174067.1|GN=FGFR1|GI=2260|FC=Missense|CP=419|CF=1|AC=TcG->TtG|RP=140|RC=S|Ser|>L|Leu|LEN=4/19|DS=+229|P=chr8:38268656-38325363|ST
 NM 006904.6|GN=PRKDC1|GI=5591|FC=Coding synonvmv unknown|LEN=69/86|DS=+36|P=chr8:48685669-48872743|ST=-|PD=DNA-dependent protein kinase catal
 NM 033126.1|GN=PSKH2|GI=85481|FC=Missense|CP=526|CF=0|AC=gCG->tCG|RP=176|RC=A|Ala|>S|Ser|LEN=2/3|DS=+339|P=chr8:87060691-87081851|ST=-|C|
 NM 139021.2|GN=MAPK15|GI=225689|FC=Intron|LEN=4:5/14|DS=-40|P=chr8:144798507-144804633|ST=+|C|=1635|PD=mitogen-activated protein kinase 15
 NM 139021.2|GN=MAPK15|GI=225689|FC=Intron|LEN=8:9/14|DS=-137|P=chr8:144798507-144804633|ST=+|C|=1635|PD=mitogen-activated protein kinase 15
 NM 174922.3|GN=ADCK5|GI=203054|FC=Missense|CP=511|CF=2|AC=AGa->AGc|RP=17|RC=R|Arg|>S|Ser|LEN=2/15|DS=+39|P=chr8:145597731-145618453|ST=+|
 NM 000459.3|GN=TEK1|GI=7010|FC=Missense|CP=443|CF=1|AC=AtT->AcT|RP=148|RC=I|Ile|>T|Thr|LEN=3/23|DS=+79|P=chr9:27109147-27230172|ST=+|C|=33
 NM 000459.3|GN=TEK1|GI=7010|FC=Missense|CP=1037|CF=1|AC=CaG->CcG|RP=346|RC=Q|Gln|>P|Pro|LEN=8/23|DS=+7|P=chr9:27109147-27230172|ST=+|C|=33
 NM 002732.3|GN=PRKACG1|GI=5568|FC=Missense|CP=802|CF=0|AC=cAT->gAT|RP=268|RC=H|His|>D|Asp|LEN=1/11|P=chr9:71627449-71629039|ST=-|C|=1056
 NM 017662.4|GN=TRPM6|GI=140803|FC=Missense|CP=4750|CF=0|AC=aAG->aG|RP=1584|RC=K|Lvs|>E|Glu|LEN=27/39|DS=+78|P=chr9:7737411-77503010|S
 NM 004560.3|GN=ROR2|GI=4920|FC=Missense|CP=2455|CF=0|AC=gTC->aTC|RP=819|RC=V|Val|>I|Ile|LEN=9/9|DS=+1069|P=chr9:94484878-94712444|ST=-|C|
 NM 004560.3|GN=ROR2|GI=4920|FC=Missense|CP=733|CF=0|AC=aCA->gCA|RP=245|RC=T|Thr|>A|Ala|LEN=6/9|DS=+111|P=chr9:94484878-94712444|ST=-|C|
 NM 005592.3|GN=MUSK1|GI=4593|FC=Missense|CP=475|CF=0|AC=aCG->gCG|RP=159|RC=S|Ser|>G|Glv|LEN=4/14|DS=+117|P=chr9:113431051-113563278|ST=+|
 NM 005592.3|GN=MUSK1|GI=4593|FC=Missense|CP=1239|CF=2|AC=ATg->ATa|RP=413|RC=M|Met|>I|Ile|LEN=9/14|DS=+55|P=chr9:113431051-113563278|ST=+|
 NM 007313.2|GN=ABL1|GI=25|FC=Missense|CP=2174|CF=1|AC=Ggt->GtT|RP=725|RC=G|Glv|>V|Val|LEN=11/11|DS=+439|P=chr9:133589268-133763062|ST=+|
 NM 153710.3|GN=C9orf96|GI=169436|FC=Missense|CP=1417|CF=0|AC=aAA->gAA|RP=473|RC=K|Lvs|>E|Glu|LEN=14/18|DS=+78|P=chr9:136243284-136271220|
 NM 006257.3|GN=PRKCQ1|GI=5588|FC=Missense|CP=989|CF=1|AC=CcG->CtG|RP=330|RC=P|Pro|>L|Leu|LEN=10/18|DS=+89|P=chr10:6469105-6622254|ST=-|C|
 NM 017433.4|GN=MYO3A|GI=53904|FC=Missense|CP=1042|CF=0|AC=aTT->gtT|RP=348|RC=I|Ile|>V|Val|LEN=11/35|DS=+89|P=chr10:26223002-26501465|ST=+|

NM 017433.4|GN=MYO3A|GI=53904|FC=Missense|CP=1105|CF=0|AC=gTC->aTC|RP=369|RC=V|Val|>|Ile|EN=12/35|DS=+52|P=chr10:26223002-26501465|ST=|
 NM 017433.4|GN=MYO3A|GI=53904|FC=Missense|CP=3937|CF=0|AC=cGT->aGT|RP=1313|RC=R|Arg|>|Ser|EN=30/35|DS=+539|P=chr10:26223002-26501465|ST=|
 NM 017433.4|GN=MYO3A|GI=53904|FC=Missense|CP=4462|CF=0|AC=aAA->gAA|RP=1488|RC=K|Lys|>|Glu|EN=32/35|DS=+24|P=chr10:26223002-26501465|ST=|
 NM 005204.3|GN=MAP3K8|GI=1326|FC=Intron|EN=3:4/9|DS=+47|P=chr10:30722950-30750762|ST=+|C|EN=1404|PD=mitogen-activated protein kinase kinase kinase
 NM 152230.4|GN=PMK1|GI=253430|FC=Missense|CP=1047|CF=2|AC=ATg->A|RP=349|RC=M|Met|>|Ile|EN=6/6|DS=+419|P=chr10:59951278-60027694|ST=|
 NM 004329.2|GN=BMPRI|GI=657|FC=Missense|CP=4|CF=0|AC=cCT->aCT|RP=2|RC=P|Pro|>|Thr|EN=3/13|DS=+156|P=chr10:88516396-88684945|ST=+|C|EN=|
 NM 018425.2|GN=PI4K2A|GI=55361|FC=Missense|CP=248|CF=1|AC=GcT->G|RP=83|RC=A|Ala|>|Asp|EN=1/9|DS=-995|P=chr10:99400443-99436187|ST=|
 NM 001278.3|GN=CHUK1|GI=1147|FC=Missense|CP=802|CF=0|AC=gTA->aTA|RP=268|RC=V|Val|>|Ile|EN=9/21|DS=+5|P=chr10:101948124-101989344|ST=-|C|EN=|
 NM 005308.2|GN=GRK5|GI=2869|FC=Missense|CP=911|CF=1|AC=CgT->CaT|RP=304|RC=R|Arg|>|His|EN=9/16|DS=+173|P=chr10:120967197-121215131|ST=|
 NM 022970.3|GN=FGFR2|GI=2263|FC=Missense|CP=557|CF=1|AC=AtG->AcG|RP=186|RC=M|Met|>|Thr|EN=5/18|DS=+103|P=chr10:123237844-123357972|ST=|
 NM 001199266.1|GN=DGKZ|GI=8525|FC=Missense|CP=58|CF=0|AC=gCC->aCC|RP=20|RC=A|Ala|>|Thr|EN=1/31|DS=-19574|P=chr11:46368956-46402104|ST=|
 NM 017525.2|GN=CDC42BP|GI=55561|FC=Missense|CP=3709|CF=0|AC=cGG->tGG|RP=1237|RC=R|Arg|>|Tyr|EN=30/37|DS=+342|P=chr11:64591662-64611662|ST=|
 NM 000051.3|GN=ATM|GI=472|FC=Missense|CP=4138|CF=0|AC=cAT->tAT|RP=1380|RC=H|His|>|Arg|EN=28/63|DS=+29|P=chr11:108093559-108239826|ST=|
 NM 000051.3|GN=ATM|GI=472|FC=Missense|CP=5948|CF=1|AC=AaT->AgT|RP=1983|RC=N|Asn|>|Ser|EN=40/63|DS=+30|P=chr11:108093559-108239826|ST=|
 NM 015191.1|GN=SIK2|GI=23235|FC=Missense|CP=2240|CF=1|AC=CcA->CaA|RP=747|RC=P|Pro|>|Gln|EN=15/15|DS=+93|P=chr11:111473170-111597632|ST=|
 NM 178510.1|GN=ANKK1|GI=255239|FC=Missense|CP=715|CF=0|AC=gCG->aCG|RP=239|RC=A|Ala|>|Thr|EN=5/8|DS=+33|P=chr11:113258513-113271140|ST=|
 NM 178510.1|GN=ANKK1|GI=255239|FC=Missense|CP=324|CF=0|AC=gGC->cGC|RP=442|RC=G|Glu|>|Arg|EN=8/8|DS=+330|P=chr11:113258513-113271140|ST=|
 NM 178510.1|GN=ANKK1|GI=255239|FC=Missense|CP=2137|CF=0|AC=gAG->aAG|RP=713|RC=E|Glu|>|Lys|EN=8/8|DS=+143|P=chr11:113258513-113271140|ST=|
 NM 001114121.2|GN=CHK1|GI=1111|FC=Missense|CP=1411|CF=0|AC=aTT->gTT|RP=471|RC=I|Ile|>|Val|EN=13/14|DS=+76|P=chr11:125495031-125546150|ST=|
 NM 001184985.1|GN=WNK1|GI=65125|FC=Missense|CP=3946|CF=0|AC=aCC->cCC|RP=1316|RC=T|Thr|>|Pro|EN=13/28|DS=+55|P=chr12:862089-1020618|ST=|
 NM 001184985.1|GN=WNK1|GI=65125|FC=Missense|CP=5297|CF=1|AC=TgC->TcC|RP=1766|RC=C|Cys|>|Ser|EN=19/28|DS=+673|P=chr12:862089-1020618|ST=|
 NM 001184985.1|GN=WNK1|GI=65125|FC=Missense|CP=6204|CF=2|AC=ATg->ATt|RP=2068|RC=M|Met|>|Ile|EN=21/28|DS=+60|P=chr12:862089-1020618|ST=|
 NM 001184985.1|GN=WNK1|GI=65125|FC=Missense|CP=7267|CF=0|AC=cCC->tCC|RP=2423|RC=P|Pro|>|Ser|EN=26/28|DS=+39|P=chr12:862089-1020618|ST=|
 NM 018423.2|GN=STYK1|GI=55359|FC=Missense|CP=610|CF=0|AC=aGC->gGC|RP=204|RC=S|Ser|>|Glu|EN=6/11|DS=+159|P=chr12:10771538-10826891|ST=|
 NM 004963.3|GN=GUCY2C|GI=2984|FC=Missense|CP=843|CF=2|AC=TTt->TTg|RP=281|RC=E|Phe|>|Leu|EN=7/27|DS=+13|P=chr12:14765568-14849519|ST=|
 NM 004570.4|GN=PIK3C2G|GI=5288|FC=Missense|CP=2732|CF=1|AC=CcG->CcG|RP=911|RC=P|Pro|>|Leu|EN=20/32|DS=+62|P=chr12:18414474-18801352|ST=|
 NM 004570.4|GN=PIK3C2G|GI=5288|FC=Missense|CP=3780|CF=2|AC=GAg->GAt|RP=1260|RC=E|Glu|>|Asp|EN=28/32|DS=+1|P=chr12:18414474-18801352|ST=|
 NM 198578.3|GN=LRRK2|GI=120892|FC=Missense|CP=149|CF=1|AC=CgC->CaC|RP=50|RC=R|Arg|>|His|EN=1/51|DS=-275|P=chr12:40618813-40763086|ST=|
 NM 198578.3|GN=LRRK2|GI=120892|FC=Missense|CP=1653|CF=2|AC=AAc->AAg|RP=551|RC=N|Asn|>|Lys|EN=14/51|DS=+110|P=chr12:40618813-40763086|ST=|
 NM 198578.3|GN=LRRK2|GI=120892|FC=Missense|CP=4193|CF=1|AC=CgT->CaT|RP=1398|RC=R|Arg|>|His|EN=30/51|DS=+4|P=chr12:40618813-40763086|ST=|
 NM 001844.4|GN=COL2A1|GI=1280|FC=Missense|CP=4213|CF=0|AC=gGC->aGC|RP=1405|RC=G|Glu|>|Ser|EN=53/54|DS=+139|P=chr12:48366748-48398285|ST=|
 NM 001077401.1|GN=ACVR1|GI=94|FC=5' UTR|EN=179|DS=-662|P=chr12:52306113-52317145|ST=-|C|EN=1512|PD=serine/threonine-protein kinase receptor R3
 NM 052897.3|GN=MBD6|GI=114785|FC=Missense|CP=778|CF=0|AC=cTC->gTC|RP=260|RC=L|Leu|>|Val|EN=6/13|DS=+399|P=chr12:57916659-57923931|ST=|
 NM 024779.4|GN=PIP4K2C|GI=79837|FC=Missense|CP=899|CF=1|AC=GcG->GgG|RP=300|RC=A|Ala|>|Glu|EN=8/10|DS=+86|P=chr12:57984942-57997211|ST=|
 NM 007199.2|GN=IRAK3|GI=11213|FC=Missense|CP=439|CF=0|AC=aTA->gTA|RP=147|RC=I|Ile|>|Val|EN=5/12|DS=+3|P=chr12:66582978-66648394|ST=+|C|EN=|
 NM 014840.2|GN=NUAK1|GI=9891|FC=Missense|CP=1628|CF=1|AC=CcT->CgT|RP=543|RC=P|Pro|>|Arg|EN=7/7|DS=+796|P=chr12:106457125-106533811|ST=|
 NM 016281.3|GN=IAOK3|GI=51347|FC=Missense|CP=140|CF=1|AC=AgT->AaT|RP=47|RC=S|Ser|>|Asn|EN=4/21|DS=+20|P=chr12:118587606-118810750|ST=|
 NM 006549.3|GN=CAMKK2|GI=10645|FC=Missense|CP=1087|CF=0|AC=cGC->tGC|RP=363|RC=R|Arg|>|Cys|EN=10/17|DS=+180|P=chr12:121675495-121736173|ST=|
 NM 003565.2|GN=ULK1|GI=8408|FC=Missense|CP=2446|CF=0|AC=aCT->gCT|RP=816|RC=T|Thr|>|Ala|EN=23/28|DS=+120|P=chr12:132379279-132407707|ST=|
 NM 003565.2|GN=ULK1|GI=8408|FC=3' UTR|EN=28/28|DS=+816|P=chr12:132379279-132407707|ST=+|C|EN=3153|PD=serine/threonine-protein kinase ULK1|OM=6
 NM 014572.2|GN=LATS2|GI=26524|FC=Missense|CP=1087|CF=0|AC=gGC->aGC|RP=363|RC=G|Glu|>|Ser|EN=4/8|DS=+612|P=chr13:21547176-21635722|ST=|
 NM 014572.2|GN=LATS2|GI=26524|FC=Missense|CP=9711|CF=1|AC=GcG->GtG|RP=324|RC=A|Ala|>|Val|EN=4/8|DS=+496|P=chr13:21547176-21635722|ST=|
 NM 004119.2|GN=FLT3|GI=2322|FC=Missense|CP=680|CF=1|AC=AcG->AtG|RP=227|RC=T|Thr|>|Met|EN=6/24|DS=+66|P=chr13:28577411-28674729|ST=+|C|EN=|
 NM 000059.3|GN=BRCA2|GI=675|FC=Missense|CP=865|CF=0|AC=aAT->cAT|RP=289|RC=N|Asn|>|His|EN=10/27|DS=+72|P=chr13:32889617-32973809|ST=+|I|EN=|
 NM 000059.3|GN=BRCA2|GI=675|FC=Missense|CP=2971|CF=0|AC=aAC->gAC|RP=991|RC=N|Asn|>|Asp|EN=11/27|DS=+1062|P=chr13:32889617-32973809|ST=|
 NM 000059.3|GN=BRCA2|GI=675|FC=Missense|CP=7397|CF=1|AC=GtA->GcA|RP=2466|RC=V|Val|>|Ala|EN=14/27|DS=+390|P=chr13:32889617-32973809|ST=|
 NM 145203.5|GN=CSNK1A1|GI=122011|FC=Missense|CP=126|CF=2|AC=GAc->GA|RP=42|RC=D|Asp|>|Glu|EN=1/1|P=chr13:37677397-37679801|ST=-|C|EN=|
 NM 003749.2|GN=IRS2|GI=8660|FC=Missense|CP=3733|CF=0|AC=gCC->tCC|RP=1245|RC=A|Ala|>|Ser|EN=1/2|DS=-26013|P=chr13:110406184-110438914|ST=|
 NM 003749.2|GN=IRS2|GI=8660|FC=Missense|CP=3170|CF=1|AC=GcC->GaC|RP=1057|RC=G|Glu|>|Asp|EN=1/2|DS=-26576|P=chr13:110406184-110438914|ST=|
 NM 003749.2|GN=IRS2|GI=8660|FC=Missense|CP=599|CF=1|AC=GtG->GgG|RP=200|RC=V|Val|>|Glu|EN=1/2|DS=-29147|P=chr13:110406184-110438914|ST=|
 NM 006871.3|GN=RIPK3|GI=11035|FC=Missense|CP=22|CF=0|AC=cCC->aCC|RP=8|RC=P|Pro|>|Thr|EN=2/10|DS=+2|P=chr14:24805227-24809242|ST=-|C|EN=|
 NM 004196.3|GN=CDK1|GI=8814|FC=Intron|EN=8:9/9|DS=+237|P=chr14:50796720-50862617|ST=-|C|EN=1077|PD=cyclin-dependent kinase-like 1|OM=603441
 NM 004196.3|GN=CDK1|GI=8814|FC=Missense|CP=823|CF=0|AC=cAA->gAA|RP=275|RC=Q|Gln|>|Glu|EN=8/9|DS=+25|P=chr14:50796720-50862617|ST=-|C|EN=|
 NM 006575.4|GN=MAP4K5|GI=11183|FC=Missense|CP=1898|CF=1|AC=AcG->AtG|RP=633|RC=T|Thr|>|Met|EN=26/32|DS=+16|P=chr14:50885211-50999376|ST=|
 NM 006255.3|GN=PRKCH|GI=5583|FC=Missense|CP=1120|CF=0|AC=gTA->aTA|RP=374|RC=V|Val|>|Ile|EN=9/14|DS=+16|P=chr14:61788515-62017698|ST=+|C|EN=|

NM_031464.4|GN=RPS6K1|GI=83694|FC=Missense|CP=362|CF=1|AC=CcG->CtG|RP=121|RC=PIPro|>L|Leu||EN=3/11|DS=+97|P=chr14:75370657-75389145|ST=+
 NM_031464.4|GN=RPS6K1|GI=83694|FC=Missense|CP=62|CF=1|AC=CgA->CaA|RP=21|RC=RIArg|>Q|Gln||EN=2/11|DS=+82|P=chr14:75370657-75389145|ST=+
 NM_033116.4|GN=NFK91|GI=91754|FC=Missense|CP=1286|CF=1|AC=CgT->CaT|RP=429|RC=RIArg|>H|His||EN=1/122|DS=+104|P=chr14:75548818-75593778|ST=+
 NM_014216.4|GN=TPK1|GI=37051|FC=3' UTR|EN=11/11|DS=+1188|P=chr14:93406068-93582263|ST=+|C|=1245|PD=inositol-tetrakisphosphate 1-kinase isoform 4
 NM_014226.1|GN=MOK1|GI=58911|FC=Missense|CP=1193|CF=1|AC=CcG->CgG|RP=398|RC=Q|Gln|>R|Arg||EN=12/12|DS=+11|P=chr14:102695178-102771531|ST=+
 NM_001128918.1|GN=MARK3|GI=41401|FC=Missense|CP=1229|CF=1|AC=TTT->TcT|RP=410|RC=F|Phe|>S|Ser||EN=12/18|DS=+119|P=chr14:103851701-103970170|ST=+
 NM_001013703.2|GN=EIF2AK4|GI=440275|FC=Missense|CP=1667|CF=1|AC=GaA->GgA|RP=556|RC=F|Glu|>G|Gly||EN=11/39|DS=+7|P=chr15:40226347-403277170|ST=+
 NM_0012115|GN=BUB1B|GI=7011|FC=Missense|CP=1046|CF=1|AC=CgA->CaA|RP=349|RC=RIArg|>Q|Gln||EN=8/23|DS=+80|P=chr15:40453210-40513337|ST=+
 NM_001128628.1|GN=PAK6|GI=56924|FC=Missense|CP=1010|CF=1|AC=CcG->CtG|RP=337|RC=PIPro|>L|Leu||EN=6/11|DS=+152|P=chr15:40509629-40569688|ST=+
 NM_173500.3|GN=TBK2|GI=46057|FC=Missense|CP=231|CF=1|AC=CtG->CcG|RP=81|RC=L|Leu|>P|Pro||EN=2/15|DS=+90|P=chr15:43036542-43213007|ST=+
 NM_001099436.1|GN=ULK3|GI=25989|FC=Missense|CP=1334|CF=1|AC=AaG->AgG|RP=445|RC=K|Lys|>R|Arg||EN=14/16|DS=+47|P=chr15:75128459-75135552|ST=+
 NM_024776.3|GN=PEAK1|GI=79834|FC=Missense|CP=3212|CF=1|AC=AgG->AaG|RP=1071|RC=RIArg|>K|Lys||EN=6/8|DS=+75|P=chr15:77400498-77712446|ST=+
 NM_020778.4|GN=ALPK3|GI=57538|FC=Missense|CP=1241|CF=1|AC=AcT->AgT|RP=414|RC=T|Thr|>S|Ser||EN=5/14|DS=+213|P=chr15:85359911-85416713|ST=+
 NM_020778.4|GN=ALPK3|GI=57538|FC=Missense|CP=1736|CF=1|AC=GcG->GaG|RP=579|RC=G|Gly|>F|Glu||EN=5/14|DS=+708|P=chr15:85359911-85416713|ST=+
 NM_020778.4|GN=ALPK3|GI=57538|FC=Missense|CP=3896|CF=1|AC=CcT->CtT|RP=1299|RC=PIPro|>L|Leu||EN=6/14|DS=+1215|P=chr15:85359911-85416713|ST=+
 NM_020778.4|GN=ALPK3|GI=57538|FC=Missense|CP=4865|CF=1|AC=CtT->CcT|RP=1622|RC=L|Leu|>P|Pro||EN=10/14|DS=+130|P=chr15:85359911-85416713|ST=+
 NM_002005.3|GN=FFS1|GI=22421|FC=Missense|CP=1952|CF=1|AC=GaG->GgG|RP=651|RC=F|Glu|>G|Gly||EN=16/19|DS=+31|P=chr15:91427688-91439006|ST=+
 NM_000875.3|GN=IGF1R|GI=34801|FC=Missense|CP=1991|CF=0|AC=gCC->tcC|RP=67|RC=A|Ala|>S|Ser||EN=2/21|DS=+105|P=chr15:99192761-99507759|ST=+
 NM_024652.3|GN=RRK1|GI=79705|FC=Missense|CP=5813|CF=1|AC=GcC->CaC|RP=1938|RC=G|Gly|>D|Asp||EN=33/34|DS=+45|P=chr15:101459460-101610311|ST=+
 NM_024652.3|GN=RRK1|GI=79705|FC=Synonvmous-Coding|CP=5814|CF=2|AC=GGC->GGG|RP=1938|RC=G|Gly|>G|Gly||EN=33/34|DS=+46|P=chr15:101459460-101610311|ST=+
 NM_013302.3|GN=FFK1|GI=29904|FC=Missense|CP=1082|CF=1|AC=CaA->CgA|RP=361|RC=Q|Gln|>R|Arg||EN=10/18|DS=+53|P=chr16:22217592-22300661|ST=+
 NM_024675.3|GN=PALB2|GI=79728|FC=Missense|CP=1676|CF=1|AC=CaA->CgA|RP=559|RC=Q|Gln|>R|Arg||EN=4/13|DS=+1465|P=chr16:23614483-23652678|ST=+
 NM_005030.3|GN=PIK1|GI=5347|FC=Missense|CP=148|CF=0|AC=cGG->tGG|RP=50|RC=RIArg|>W|Trp||EN=1/10|DS=-1004|P=chr16:23690201-23701688|ST=+
 NM_033266.3|GN=ERN2|GI=10595|FC=Missense|CP=1604|CF=3|AC=AgC->AcC|RP=535|RC=S|Ser|>T|Thr||EN=13/22|DS=+101|P=chr16:23701626-23724821|ST=+
 NM_182493.2|GN=MYLK3|GI=91807|FC=Missense|CP=2127|CF=2|AC=TTG->TTT|RP=709|RC=L|Leu|>F|Phe||EN=11/13|DS=+13|P=chr16:46736194-46782221|ST=+
 NM_182493.2|GN=MYLK3|GI=91807|FC=Missense|CP=538|CF=0|AC=gTG->aTG|RP=180|RC=V|Val|>L|Leu||EN=2/3|DS=+61|P=chr16:46736194-46782221|ST=+
 NM_001793.4|GN=CDH3|GI=10011|FC=Intron|EN=15/16/16|DS=-45|P=chr16:68678151-68732957|ST=+|C|=2490|PD=cadherin-3 preproprotein|OM=114021
 NM_031965.2|GN=GS2|GI=83903|FC=Missense|CP=244|CF=0|AC=cGT->tGT|RP=82|RC=RIArg|>C|Cys||EN=1/1|P=chr17:3627197-3629992|ST=+|C|=2397|PD=3
 NM_031965.2|GN=GS2|GI=83903|FC=Missense|CP=611|CF=1|AC=GcC->GcC|RP=204|RC=G|Gly|>D|Asp||EN=1/1|P=chr17:3627197-3629992|ST=+|C|=2397|PD=3
 NM_031965.2|GN=GS2|GI=83903|FC=Missense|CP=983|CF=1|AC=AtA->AcA|RP=328|RC=L|Leu|>T|Thr||EN=1/1|P=chr17:3627197-3629992|ST=+|C|=2397|PD=3
 NM_031965.2|GN=GS2|GI=83903|FC=Missense|CP=1333|CF=1|AC=GtC->GcC|RP=378|RC=V|Val|>A|Ala||EN=1/1|P=chr17:3627197-3629992|ST=+|C|=2397|PD=3
 NM_172207.2|GN=CAMKK1|GI=84254|FC=Missense|CP=1238|CF=1|AC=CaG->CgG|RP=413|RC=F|Glu|>G|Gly||EN=13/16|DS=+74|P=chr17:3768451-3796337|ST=+
 NM_153827.4|GN=MINK1|GI=50488|FC=Missense|CP=2312|CF=1|AC=GtC->GcC|RP=771|RC=V|Val|>A|Ala||EN=20/32|DS=+11|P=chr17:4736635-4801356|ST=+
 NM_153827.4|GN=MINK1|GI=50488|FC=Missense|CP=2324|CF=1|AC=CcG->CtG|RP=775|RC=PIPro|>L|Leu||EN=20/32|DS=+13|P=chr17:4736635-4801356|ST=+
 NM_153827.4|GN=MINK1|GI=50488|FC=Missense|CP=2587|CF=0|AC=gTC->aTC|RP=863|RC=V|Val|>L|Leu||EN=22/32|DS=+23|P=chr17:4736635-4801356|ST=+
 NM_001251902.1|GN=TNK1|GI=87111|FC=Missense|CP=1792

NM 001201457.1|GN=TFX14|GI=56155|FC=Missense|CP=3263|CF=1|AC=GgT->GaT|RP=1088|RC=GI|Givl->DI|Asp|LEN=20/33|DS=+74|P=chr17:56634038-567694|
 NM 002737.2|GN=PRKCA|GI=5578|FC=Missense|CP=1702|CF=0|AC=gTC->aTC|RP=568|RC=VI|Val->I|Ile|LEN=15/17|DS=+97|P=chr17:64298926-64806862|ST=+|C|
 NM 182965.2|GN=SPHK1|GI=8877|FC=Missense|CP=100|CF=0|AC=gCA->aCA|RP=34|RC=AI|Ala->T|Thr|LEN=2/6|DS=+36|P=chr17:74380690-74383941|ST=+|C|
 NM 001080395.2|GN=AAATK|GI=9625|FC=Missense|CP=3797|CF=1|AC=tTC->TC|RP=1266|RC=FI|Phe->S|Ser|LEN=12/14|DS=+62|P=chr17:79091096-79139872|
 NM 001080395.2|GN=AAATK|GI=9625|FC=Missense|CP=2107|CF=0|AC=gGC->GC|RP=703|RC=GI|Gln->C|Cys|LEN=11/14|DS=+995|P=chr17:79091096-79139872|
 NM 005406.2|GN=ROCK1|GI=6093|FC=Missense|CP=3649|CF=0|AC=cAA->gAA|RP=1217|RC=QI|Gln->F|Gln|LEN=31/33|DS=+58|P=chr18:18529703-18691812|ST=+|C|
 NM 002747.3|GN=MAPK4|GI=5596|FC=Missense|CP=112|CF=0|AC=gTG->aTG|RP=38|RC=VI|Val->M|Met|LEN=2/6|DS=+982|P=chr18:48086484-48258196|ST=+|C|
 NM 001243226.1|GN=TCF4|GI=6925|FC=Missense|CP=28|CF=0|AC=gCA->cCA|RP=10|RC=AI|Ala->P|Pro|LEN=1/21|DS=-4482|P=chr18:52889562-53303188|ST=+|C|
 NM 052947.3|GN=ALPK2|GI=115701|FC=Missense|CP=6469|CF=0|AC=aTA->gTA|RP=2157|RC=II|Ile->V|Val|LEN=13/13|DS=+173|P=chr18:56148482-56296189|ST=+|C|
 NM 052947.3|GN=ALPK2|GI=115701|FC=Missense|CP=3521|CF=1|AC=CaC->CcC|RP=1174|RC=HI|His->P|Pro|LEN=5/13|DS=+1559|P=chr18:56148482-56296189|ST=+|C|
 NM 052947.3|GN=ALPK2|GI=115701|FC=Missense|CP=3169|CF=0|AC=tTG->gTG|RP=1057|RC=LI|Leu->V|Val|LEN=5/13|DS=+1207|P=chr18:56148482-56296189|ST=+|C|
 NM 052947.3|GN=ALPK2|GI=115701|FC=Missense|CP=2672|CF=1|AC=AcC->AtC|RP=891|RC=TI|Thr->I|Ile|LEN=5/13|DS=+710|P=chr18:56148482-56296189|ST=+|C|
 NM 052947.3|GN=ALPK2|GI=115701|FC=Missense|CP=5|CF=1|AC=AaA->AcA|RP=2|RC=KI|Lys->T|Thr|LEN=2/13|DS=+25|P=chr18:56148482-56296189|ST=-|C|
 NM 020854.3|GN=KIAA1468|GI=57614|FC=Missense|CP=250|CF=0|AC=gGC->gGC|RP=84|RC=GI|Givl->C|Cys|LEN=1/29|DS=-23398|P=chr18:59854524-59974355|
 NM 020854.3|GN=KIAA1468|GI=57614|FC=Missense|CP=1735|CF=0|AC=cAA->aAA|RP=579|RC=QI|Gln->K|Lys|LEN=12/29|DS=+2|P=chr18:59854524-59974355|
 NM 199054.2|GN=MKNK2|GI=2872|FC=Missense|CP=208|CF=0|AC=cGG->tGG|RP=70|RC=RI|Arg->W|Trp|LEN=4/14|DS=+69|P=chr19:2037470-2051243|ST=-|C|
 NM 003331.4|GN=TYK2|GI=7297|FC=Missense|CP=1561|CF=0|AC=cGG->tGG|RP=521|RC=RI|Arg->W|Trp|LEN=11/25|DS=+85|P=chr19:10461204-10491248|ST=-|C|
 NM 003331.4|GN=TYK2|GI=7297|FC=Missense|CP=1084|CF=0|AC=gTC->tTC|RP=362|RC=VI|Val->F|Phe|LEN=8/25|DS=+73|P=chr19:10461204-10491248|ST=-|C|
 NM 213560.1|GN=PKN1|GI=5585|FC=Missense|CP=1681|CF=0|AC=cTC->aTC|RP=561|RC=LI|Leu->I|Ile|LEN=12/22|DS=+26|P=chr19:14551086-14582679|ST=+|C|
 NM 213560.1|GN=PKN1|GI=5585|FC=Missense|CP=2719|CF=0|AC=gTC->aTC|RP=907|RC=VI|Val->I|Ile|LEN=22/22|DS=+76|P=chr19:14551086-14582679|ST=+|C|
 NM 000215.3|GN=JAK3|GI=3718|FC=Missense|CP=1503|CF=2|AC=CAg->CAr|RP=501|RC=QI|Gln->H|His|LEN=11/24|DS=+62|P=chr19:17935593-17958841|ST=-|C|
 NM 015016.1|GN=MAST3|GI=23031|FC=Missense|CP=2581|CF=0|AC=gGC->aGC|RP=861|RC=GI|Givl->S|Ser|LEN=22/27|DS=+84|P=chr19:18208603-18262499|ST=+|C|
 NM 005027.2|GN=PIK3R2|GI=5296|FC=Missense|CP=937|CF=0|AC=tCC->cCC|RP=313|RC=SI|Ser->P|Pro|LEN=8/16|DS=+36|P=chr19:18264016-18281343|ST=+|C|
 NM 174905.3|GN=MAP98C|GI=147965|FC=Missense|CP=719|CF=1|AC=AcA->AaA|RP=240|RC=TI|Thr->K|Lys|LEN=6/8|DS=+86|P=chr19:38893775-38899728|ST=+|C|
 NM 001626.4|GN=AKT2|GI=208|FC=3' UTR|LEN=14/14|DS=+346|P=chr19:40736224-40791302|ST=-|C|
 NM 024876.3|GN=ADCK4|GI=79934|FC=Missense|CP=521|CF=1|AC=CaC->CcC|RP=174|RC=HI|His->R|Arg|LEN=7/15|DS=+311|P=chr19:41197434-41222790|ST=-|C|
 NM 021913.3|GN=AXI1|GI=558|FC=Missense|CP=796|CF=0|AC=aAC->gAC|RP=266|RC=NI|Asn->D|Asp|LEN=7/20|DS=+13|P=chr19:41725108-41767671|ST=+|C|
 NM 001081563.1|GN=DMPK1|GI=1760|FC=Missense|CP=1297|CF=0|AC=cTG->gTG|RP=433|RC=LI|Leu->V|Val|LEN=9/14|DS=+35|P=chr19:46272976-46283861|ST=+|C|
 NM 016457.4|GN=PRKD2|GI=25865|FC=Missense|CP=2504|CF=1|AC=GtG->GcG|RP=835|RC=VI|Val->A|Ala|LEN=18/18|DS=+80|P=chr19:47177573-47220384|ST=+|C|
 NM 016457.4|GN=PRKD2|GI=25865|FC=Missense|CP=1733|CF=1|AC=GcA->GaA|RP=578|RC=AI|Ala->F|Gln|LEN=13/18|DS=+31|P=chr19:47177573-47220384|ST=+|C|
 NM 001101401.2|GN=SBK2|GI=646643|FC=Missense|CP=892|CF=0|AC=gCC->cCC|RP=298|RC=AI|Ala->P|Pro|LEN=4/4|DS=+436|P=chr19:56041100-56048435|ST=+|C|
 NM 001101401.2|GN=SBK2|GI=646643|FC=Missense|CP=214|CF=0|AC=tGC->cGC|RP=72|RC=C|Cys->R|Arg|LEN=2/4|DS=+214|P=chr19:56041100-56048435|ST=+|C|
 NM 001101401.2|GN=SBK2|GI=646643|FC=Missense|CP=118|CF=0|AC=cGC->aGC|RP=40|RC=RI|Arg->S|Ser|LEN=2/4|DS=+118|P=chr19:56041100-56048435|ST=+|C|
 NM 020341.3|GN=PAK7|GI=57144|FC=Missense|CP=1532|CF=1|AC=AgC->AaC|RP=511|RC=SI|Ser->N|Asn|LEN=7/11|DS=+50|P=chr20:9518037-9819687|ST=-|C|
 NM 033118.3|GN=MYLK2|GI=85366|FC=Missense|CP=501|CF=1|AC=AcA->AaA|RP=17|RC=TI|Thr->K|Lys|LEN=2/13|DS=+98|P=chr20:30407178-30422500|ST=+|C|
 NM 003600.2|GN=AURKA|GI=6790|FC=Missense|CP=169|CF=0|AC=aTT->gTT|RP=57|RC=II|Ile->V|Val|LEN=3/9|DS=+127|P=chr20:54944445-54967351|ST=-|C|
 NM 003600.2|GN=AURKA|GI=6790|FC=Missense|CP=911|CF=0|AC=tTT->aTT|RP=311|RC=FI|Phe->I|Ile|LEN=3/9|DS=+49|P=chr20:54944445-54967351|ST=-|C|
 NM 014586.1|GN=HUNK1|GI=30811|FC=Missense|CP=1771|CF=0|AC=cGC->tGC|RP=591|RC=RI|Arg->C|Cys|LEN=11/11|DS=+285|P=chr21:33245628-33376377|ST=+|C|
 NM 020639.2|GN=RIPK4|GI=54101|FC=Missense|CP=1996|CF=0|AC=aTG->gTG|RP=666|RC=M|Met->V|Val|LEN=8/8|DS=+801|P=chr21:43159529-43187249|ST=+|C|
 NM 173354.3|GN=SIK1|GI=150094|FC=Missense|CP=1844|CF=1|AC=GcC->GtC|RP=615|RC=AI|Ala->V|Val|LEN=13/14|DS=+100|P=chr21:44834398-44847002|ST=+|C|
 NM 198691.2|GN=KRTAP10-1|GI=386677|FC=Missense|CP=722|CF=1|AC=CgG->CaG|RP=241|RC=RI|Arg->Q|Gln|LEN=1/1|P=chr21:45959068-45960078|ST=-|C|
 NM 001031801.1|GN=LMK2|GI=3985|FC=Missense|CP=2051|CF=1|AC=CaG->CcG|RP=684|RC=QI|Gln->R|Arg|LEN=15/15|DS=+342|P=chr22:31644348-31673624|
 NM 002969.3|GN=MAPK12|GI=6300|FC=Missense|CP=308|CF=1|AC=AcG->AtG|RP=103|RC=TI|Thr->M|Met|LEN=3/12|DS=+53|P=chr22:50691331-50700089|ST=+|C|
 NM 002751.5|GN=MAPK11|GI=5600|FC=Intron|LEN=7:8/12|DS=-19|P=chr22:50702142-50708779|ST=-|C|
 NM 002751.5|GN=MAPK11|GI=5600|FC=Intron|LEN=7:8/12|DS=+59|P=chr22:50702142-50708779|ST=-|C|
 NM 005044.4|GN=PRKX|GI=5613|FC=Missense|CP=128|CF=1|AC=GtG->GcG|RP=43|RC=VI|Val->A|Ala|LEN=1/9|DS=-38360|P=chrX:3522384-3631675|ST=-|C|
 NM 001001671.3|GN=MAP3K15|GI=389840|FC=Missense|CP=574|CF=0|AC=gCT->aCT|RP=192|RC=AI|Ala->T|Thr|LEN=4/29|DS=+49|P=chrX:19378176-19533379|
 NM 003604.2|GN=IRS4|GI=8471|FC=Missense|CP=2635|CF=0|AC=cAT->gAT|RP=879|RC=HI|His->D|Asp|LEN=1/1|P=chrX:107975727-107979607|ST=-|C|
 NM 001522.2|GN=GLCY2F|GI=2986|FC=Missense|CP=887|CF=1|AC=CgG->CaG|RP=296|RC=RI|Arg->Q|Gln|LEN=3/20|DS=+157|P=chrX:108616135-108725285|ST=+|C|
 NM 001569.3|GN=IRAK1|GI=3654|FC=Missense|CP=1595|CF=1|AC=tCG->TtG|RP=532|RC=SI|Ser->L|Leu|LEN=12/14|DS=+56|P=chrX:15327597-153285342|ST=+|C|
 NM 001569.3|GN=IRAK1|GI=3654|FC=Missense|CP=587|CF=1|AC=TtT->TcT|RP=196|RC=FI|Phe->S|Ser|LEN=5/14|DS=+47|P=chrX:15327597-153285342|ST=-|C|

RefSeq Genes Product
cyclin-dependent kinase 11B isoform 2. cyclin-dependent kinase 11B isoform 3. cyclin-dependent kinase 11B isoform 4. cyclin-dependent kinase 11B isoform
cyclin-dependent kinase 11B isoform 2. cyclin-dependent kinase 11B isoform 3. cyclin-dependent kinase 11B isoform 4. cyclin-dependent kinase 11B isoform
cyclin-dependent kinase 11B isoform 2. cyclin-dependent kinase 11B isoform 3. cyclin-dependent kinase 11B isoform 4. cyclin-dependent kinase 11B isoform
cyclin-dependent kinase 11A isoform 1. cyclin-dependent kinase 11A isoform 4. cyclin-dependent kinase 11B isoform 2. cyclin-dependent kinase 11B isoform
cyclin-dependent kinase 11A isoform 1. cyclin-dependent kinase 11A isoform 4. cyclin-dependent kinase 11B isoform 2. cyclin-dependent kinase 11B isoform
cyclin-dependent kinase 11A isoform 1. cyclin-dependent kinase 11A isoform 4. cyclin-dependent kinase 11B isoform 2. cyclin-dependent kinase 11B isoform
phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit delta isoform
ephrin type-A receptor 8 isoform 1 precursor
mitogen-activated protein kinase kinase kinase 6
tyrosine-protein kinase Fgr
serine/threonine-protein kinase 40
ephrin type-A receptor 10 isoform 3
ephrin type-A receptor 10 isoform 3. ephrin type-A receptor 10 isoform 2 precursor
ephrin type-A receptor 10 isoform 3. ephrin type-A receptor 10 isoform 2 precursor
microtubule-associated serine/threonine-protein kinase 2
microtubule-associated serine/threonine-protein kinase 2
phosphatidylinositol 3-kinase regulatory subunit gamma
tyrosine-protein kinase transmembrane receptor ROR1 isoform 1
bromodomain testis-specific protein isoform a. bromodomain testis-specific protein isoform b. bromodomain testis-specific protein isoform c. bromodomain te
bromodomain testis-specific protein isoform a. bromodomain testis-specific protein isoform b. bromodomain testis-specific protein isoform c. bromodomain te
E3 ubiquitin-protein ligase TRIM33 isoform alpha. E3 ubiquitin-protein ligase TRIM33 isoform beta
protein-associating with the carboxyl-terminal
2-5A-dependent ribonuclease
dual serine/threonine and tyrosine protein kinase isoform 1. dual serine/threonine and tyrosine protein kinase isoform 2
NUAK family SNF1-like kinase 2
cyclin-dependent kinase 18 isoform a. cyclin-dependent kinase 18 isoform b
inositol-trisphosphate 3-kinase B
serine/threonine-protein kinase MRCK alpha isoform B. serine/threonine-protein kinase MRCK alpha isoform A
serine/threonine-protein kinase MRCK alpha isoform B. serine/threonine-protein kinase MRCK alpha isoform A
obscurin isoform b. obscurin isoform a
obscurin isoform b. obscurin isoform a
obscurin isoform b. obscurin isoform a
obscurin isoform b. obscurin isoform a
obscurin isoform b. obscurin isoform a
mitogen-activated protein kinase kinase kinase MLK4
mitogen-activated protein kinase kinase kinase MLK4
mitogen-activated protein kinase kinase kinase MLK4
mitogen-activated protein kinase kinase kinase MLK4
rho-associated protein kinase 2
ALK tyrosine kinase receptor precursor
ALK tyrosine kinase receptor precursor
ALK tyrosine kinase receptor precursor
ALK tyrosine kinase receptor precursor
ALK tyrosine kinase receptor precursor
interferon-induced, double-stranded RNA-activated protein kinase isoform a. interferon-induced, double-stranded RNA-activated protein kinase isoform b
protein kinase domain-containing protein, cytoplasmic precursor
serine/threonine-protein kinase VRK2 isoform 1. serine/threonine-protein kinase VRK2 isoform 2. serine/threonine-protein kinase VRK2 isoform 3
eukaryotic translation initiation factor 2-alpha kinase 3 precursor
type I inositol-3,4-bisphosphate 4-phosphatase isoform d. type I inositol-3,4-bisphosphate 4-phosphatase isoform c. type I inositol-3,4-bisphosphate 4-phosphatase isoform b
SPS1/STE20-related protein kinase YSK4 isoform 1. SPS1/STE20-related protein kinase YSK4 isoform 2
SPS1/STE20-related protein kinase YSK4 isoform 1. SPS1/STE20-related protein kinase YSK4 isoform 2
activin receptor type-2A precursor

[illegible]

serine/threonine-protein kinase ULK4
 macrophage-stimulating protein receptor isoform 1 preproprotein. macrophage-stimulating protein receptor isoform 2 precursor
 serine/threonine-protein kinase Nek4 isoform 1. serine/threonine-protein kinase Nek4 isoform 2
 ephrin type-A receptor 6 isoform a
 mvosin light chain kinase. smooth muscle isoform 1. mvosin light chain kinase. smooth muscle isoform 3A. mvosin light chain kinase. smooth muscle isoform 2.
 mvosin light chain kinase. smooth muscle isoform 1. mvosin light chain kinase. smooth muscle isoform 3A. mvosin light chain kinase. smooth muscle isoform 2.
 mvosin light chain kinase. smooth muscle isoform 1. mvosin light chain kinase. smooth muscle isoform 3A. mvosin light chain kinase. smooth muscle isoform 2.
 mvosin light chain kinase. smooth muscle isoform 1. mvosin light chain kinase. smooth muscle isoform 3A. mvosin light chain kinase. smooth muscle isoform 2.
 mvosin light chain kinase. smooth muscle isoform 1. mvosin light chain kinase. smooth muscle isoform 3A. mvosin light chain kinase. smooth muscle isoform 2.
 kalirin isoform 1. kalirin isoform 2
 serine/threonine-protein kinase Nek11 isoform 1. serine/threonine-protein kinase Nek11 isoform 3
 serine/threonine-protein kinase ATR
 mitogen-activated protein kinase kinase kinase 13 isoform 1. mitogen-activated protein kinase kinase kinase 13 isoform 2
 diacylglycerol kinase gamma isoform 1. diacylglycerol kinase gamma isoform 2. diacylglycerol kinase gamma isoform 3
 diacylglycerol kinase gamma isoform 1. diacylglycerol kinase gamma isoform 2. diacylglycerol kinase gamma isoform 3
 cyclin-G-associated kinase
 G protein-coupled receptor kinase 4 isoform alpha. G protein-coupled receptor kinase 4 isoform beta. G protein-coupled receptor kinase 4 isoform gamma
 G protein-coupled receptor kinase 4 isoform alpha. G protein-coupled receptor kinase 4 isoform beta. G protein-coupled receptor kinase 4 isoform gamma
 serine/threonine-protein kinase 32B
 phosphatidylinositol 4-kinase type 2-beta
 vascular endothelial growth factor receptor 2 precursor
 BMP-2-inducible protein kinase isoform a. BMP-2-inducible protein kinase isoform b
 TBC domain-containing protein kinase-like protein isoform a. TBC domain-containing protein kinase-like protein isoform b. TBC domain-containing protein kinase
 alpha-protein kinase 1
 alpha-protein kinase 1
 alpha-protein kinase 1
 alpha-protein kinase 1
 serine/threonine-protein kinase PLK4 isoform 1. serine/threonine-protein kinase PLK4 isoform 2. serine/threonine-protein kinase PLK4 isoform 3
 serine/threonine-protein kinase DCLK2 isoform b. serine/threonine-protein kinase DCLK2 isoform a
 serine/threonine-protein kinase DCLK2 isoform b. serine/threonine-protein kinase DCLK2 isoform a
 serine/threonine-protein kinase Nek1 isoform 1. serine/threonine-protein kinase Nek1 isoform 2. serine/threonine-protein kinase Nek1 isoform 3. serine/threonine-protein kinase Nek1 isoform 4
 mitogen-activated protein kinase kinase kinase 1
 mitogen-activated protein kinase kinase kinase 1
 microtubule-associated serine/threonine-protein kinase 4 isoform c. microtubule-associated serine/threonine-protein kinase 4 isoform a
 phosphatidylinositol 3-kinase regulatory subunit alpha isoform 1. phosphatidylinositol 3-kinase regulatory subunit alpha isoform 2. phosphatidylinositol 3-kinase regulatory subunit alpha isoform 3
 serine/threonine-protein kinase RIO2 isoform 1. serine/threonine-protein kinase RIO2 isoform 2
 serine/threonine-protein kinase RIO2 isoform 1. serine/threonine-protein kinase RIO2 isoform 2
 serine/threonine-protein kinase RIO2 isoform 1. serine/threonine-protein kinase RIO2 isoform 2
 adenomatous polyposis coli protein isoform b. adenomatous polyposis coli protein isoform a
 testis-specific serine/threonine-protein kinase 1. colorectal mutant cancer protein isoform 1
 macrophage colony-stimulating factor 1 receptor precursor
 fibroblast growth factor receptor 4 isoform 1 precursor. fibroblast growth factor receptor 4 isoform 2 precursor
 fibroblast growth factor receptor 4 isoform 1 precursor. fibroblast growth factor receptor 4 isoform 2 precursor
 fibroblast growth factor receptor 4 isoform 1 precursor. fibroblast growth factor receptor 4 isoform 2 precursor
 fibroblast growth factor receptor 4 isoform 1 precursor. fibroblast growth factor receptor 4 isoform 2 precursor
 vascular endothelial growth factor receptor 3 isoform 1 precursor. vascular endothelial growth factor receptor 3 isoform 2 precursor
 vascular endothelial growth factor receptor 3 isoform 1 precursor. vascular endothelial growth factor receptor 3 isoform 2 precursor
 mvosin light chain kinase family member 4
 serine/threonine-protein kinase PRP4 homolog
 serine/threonine-protein kinase 19 isoform 2. serine/threonine-protein kinase 19 isoform 1
 serine/threonine-protein kinase 19 isoform 2. serine/threonine-protein kinase 19 isoform 1
 inositol hexakisphosphate kinase 3
 inositol hexakisphosphate kinase 3
 serine/threonine-protein kinase 38
 G1/S-specific cyclin-D3 isoform 2. G1/S-specific cyclin-D3 isoform 3. G1/S-specific cyclin-D3 isoform 1. G1/S-specific cyclin-D3 isoform 4
 inactive tyrosine-protein kinase 7 isoform a precursor. inactive tyrosine-protein kinase 7 isoform b precursor. inactive tyrosine-protein kinase 7 isoform d precursor

tau-tubulin kinase 1
tau-tubulin kinase 1
NE-kappa-B inhibitor epsilon
NE-kappa-B inhibitor epsilon
cyclin-dependent kinase 19
tyrosine-protein kinase FRK
proto-oncogene tyrosine-protein kinase ROS precursor
mitogen-activated protein kinase kinase kinase 5
mitogen-activated protein kinase kinase 4 isoform a. mitogen-activated protein kinase kinase 4 isoform b
ribosomal protein S6 kinase alpha-2 isoform b
ribosomal protein S6 kinase alpha-2 isoform b
serine/threonine-protein kinase 31 isoform a. serine/threonine-protein kinase 31 isoform b
serine/threonine-protein kinase 31 isoform a. serine/threonine-protein kinase 31 isoform b
serine/threonine-protein kinase 31 isoform a. serine/threonine-protein kinase 31 isoform b
serine/threonine-protein kinase 31 isoform a. serine/threonine-protein kinase 31 isoform b
serine/threonine-protein kinase 31 isoform a. serine/threonine-protein kinase 31 isoform b
serine/threonine-protein kinase 31 isoform a. serine/threonine-protein kinase 31 isoform b
cyclin-dependent kinase 13 isoform 1. cyclin-dependent kinase 13 isoform 2
serine/threonine-protein kinase 17A
serine/threonine-protein kinase 17A
epidermal growth factor receptor isoform a precursor. epidermal growth factor receptor isoform d precursor. epidermal growth factor receptor isoform b precursor
pyruvate dehydrogenase kinase, isozyme 4
serine/threonine-protein kinase LMTK2 precursor
transformation/transcription domain-associated protein isoform 1. transformation/transcription domain-associated protein isoform 2
transformation/transcription domain-associated protein isoform 1. transformation/transcription domain-associated protein isoform 2
hepatocyte growth factor receptor isoform a precursor. hepatocyte growth factor receptor isoform b precursor
transcription intermediary factor 1-alpha isoform a. transcription intermediary factor 1-alpha isoform b
ephrin type-A receptor 1 precursor
ephrin type-A receptor 1 precursor
tyrosine-protein kinase Sgk223
tyrosine-protein kinase Sgk223
tyrosine-protein kinase Sgk223
tyrosine-protein kinase Sgk223
tyrosine-protein kinase Sgk223
tyrosine-protein kinase Sgk223
tyrosine-protein kinase Blk
protein-tyrosine kinase 2-beta isoform a. protein-tyrosine kinase 2-beta isoform b
fibroblast growth factor receptor 1 isoform 14 precursor. fibroblast growth factor receptor 1 isoform 1 precursor. fibroblast growth factor receptor 1 isoform 2
DNA-dependent protein kinase catalytic subunit isoform 1. DNA-dependent protein kinase catalytic subunit isoform 2
serine/threonine-protein kinase H2
mitogen-activated protein kinase 15
mitogen-activated protein kinase 15
uncharacterized aarF domain-containing protein kinase 5
angiopoietin-1 receptor precursor
angiopoietin-1 receptor precursor
cAMP-dependent protein kinase catalytic subunit gamma
transient receptor potential cation channel subfamily M member 6 isoform a. transient receptor potential cation channel subfamily M member 6 isoform b. transient receptor potential cation channel subfamily M member 6 isoform c
tyrosine-protein kinase transmembrane receptor ROR2 precursor
tyrosine-protein kinase transmembrane receptor ROR2 precursor
muscle, skeletal receptor tyrosine-protein kinase isoform 1. muscle, skeletal receptor tyrosine-protein kinase isoform 2. muscle, skeletal receptor tyrosine-protein kinase isoform 3
muscle, skeletal receptor tyrosine-protein kinase isoform 1. muscle, skeletal receptor tyrosine-protein kinase isoform 2. muscle, skeletal receptor tyrosine-protein kinase isoform 3
tyrosine-protein kinase ABL1 isoform b. tyrosine-protein kinase ABL1 isoform a
protein kinase-like protein Sgk071
protein kinase C theta type isoform 1. protein kinase C theta type isoform 2
myosin-IIIa

mvosin-IIIa
 mvosin-IIIa
 mvosin-IIIa
 mitogen-activated protein kinase kinase kinase 8
 inositol polyphosphate multikinase
 bone morphogenetic protein receptor type-1A precursor
 phosphatidylinositol 4-kinase type 2-alpha
 inhibitor of nuclear factor kappa-B kinase subunit alpha
 G protein-coupled receptor kinase 5
 fibroblast growth factor receptor 2 isoform 2 precursor. fibroblast growth factor receptor 2 isoform 1 precursor. fibroblast growth factor receptor 2 isoform 3 precursor
 diacylglycerol kinase zeta isoform 5. diacylglycerol kinase zeta isoform 2. diacylglycerol kinase zeta isoform 6. diacylglycerol kinase zeta isoform 7. diacylglycerol kinase zeta isoform 8
 serine/threonine-protein kinase MRCK gamma
 serine-protein kinase ATM
 serine-protein kinase ATM
 serine/threonine-protein kinase SIK2
 ankyrin repeat and protein kinase domain-containing protein 1
 ankyrin repeat and protein kinase domain-containing protein 1
 ankyrin repeat and protein kinase domain-containing protein 1
 serine/threonine-protein kinase Chk1 isoform 1. serine/threonine-protein kinase Chk1 isoform 2
 serine/threonine-protein kinase WNK1 isoform 4. serine/threonine-protein kinase WNK1 isoform 3. serine/threonine-protein kinase WNK1 isoform 1. serine/threonine-protein kinase WNK1 isoform 2
 serine/threonine-protein kinase WNK1 isoform 4. serine/threonine-protein kinase WNK1 isoform 3. serine/threonine-protein kinase WNK1 isoform 1. serine/threonine-protein kinase WNK1 isoform 2
 serine/threonine-protein kinase WNK1 isoform 4. serine/threonine-protein kinase WNK1 isoform 3. serine/threonine-protein kinase WNK1 isoform 1. serine/threonine-protein kinase WNK1 isoform 2
 serine/threonine-protein kinase WNK1 isoform 4. serine/threonine-protein kinase WNK1 isoform 3. serine/threonine-protein kinase WNK1 isoform 1. serine/threonine-protein kinase WNK1 isoform 2
 tyrosine-protein kinase STYK1
 heat-stable enterotoxin receptor precursor
 phosphatidylinositol-4-phosphate 3-kinase C2 domain-containing subunit gamma
 phosphatidylinositol-4-phosphate 3-kinase C2 domain-containing subunit gamma
 leucine-rich repeat serine/threonine-protein kinase 2
 leucine-rich repeat serine/threonine-protein kinase 2
 leucine-rich repeat serine/threonine-protein kinase 2
 collagen alpha-1(II) chain isoform 1 precursor. collagen alpha-1(II) chain isoform 2 precursor
 serine/threonine-protein kinase receptor R3 precursor
 methyl-CoG-binding domain protein 6
 phosphatidylinositol-5-phosphate 4-kinase type-2 gamma isoform a. phosphatidylinositol-5-phosphate 4-kinase type-2 gamma isoform b. phosphatidylinositol-5-phosphate 4-kinase type-2 gamma isoform c
 interleukin-1 receptor-associated kinase 3 isoform a. interleukin-1 receptor-associated kinase 3 isoform b
 NUA family SNF1-like kinase 1
 serine/threonine-protein kinase TAO3
 calcium/calmodulin-dependent protein kinase kinase 2 isoform 1. calcium/calmodulin-dependent protein kinase kinase 2 isoform 3. calcium/calmodulin-dependent protein kinase kinase 2 isoform 2
 serine/threonine-protein kinase ULK1
 serine/threonine-protein kinase ULK1
 serine/threonine-protein kinase LATS2
 serine/threonine-protein kinase LATS2
 receptor-type tyrosine-protein kinase FLT3
 breast cancer type 2 susceptibility protein
 breast cancer type 2 susceptibility protein
 breast cancer type 2 susceptibility protein
 casein kinase I isoform alpha-like
 insulin receptor substrate 2
 insulin receptor substrate 2
 insulin receptor substrate 2
 receptor-interacting serine/threonine-protein kinase 3
 cyclin-dependent kinase-like 1
 cyclin-dependent kinase-like 1
 mitogen-activated protein kinase kinase kinase kinase 5
 protein kinase C eta type

ribosomal protein S6 kinase-like 1
ribosomal protein S6 kinase-like 1
serine/threonine-protein kinase Nek9
inositol-tetrakisphosphate 1-kinase isoform a. inositol-tetrakisphosphate 1-kinase isoform b
MAPK/MAK/MRK overlapping kinase
MAP/microtubule affinity-regulating kinase 3 isoform a. MAP/microtubule affinity-regulating kinase 3 isoform b. MAP/microtubule affinity-regulating kinase 3 isoform c.
eukaryotic translation initiation factor 2-alpha kinase 4
mitotic checkpoint serine/threonine-protein kinase BUB1 beta
serine/threonine-protein kinase PAK 6
tau-tubulin kinase 2
serine/threonine-protein kinase ULK3
pseudopodium-enriched atypical kinase 1
alpha-protein kinase 3
alpha-protein kinase 3
alpha-protein kinase 3
alpha-protein kinase 3
tyrosine-protein kinase Fes/Fps isoform 1. tyrosine-protein kinase Fes/Fps isoform 2. tyrosine-protein kinase Fes/Fps isoform 3. tyrosine-protein kinase Fes/Fps isoform 4.
insulin-like growth factor 1 receptor precursor
leucine-rich repeat serine/threonine-protein kinase 1
leucine-rich repeat serine/threonine-protein kinase 1
eukaryotic elongation factor 2 kinase
partner and localizer of BRCA2
serine/threonine-protein kinase PLK1
serine/threonine-protein kinase/endoribonuclease
putative myosin light chain kinase 3
putative myosin light chain kinase 3
cadherin-3 preproprotein
serine/threonine-protein kinase haspin. integrin alpha-E precursor
serine/threonine-protein kinase haspin. integrin alpha-E precursor
serine/threonine-protein kinase haspin. integrin alpha-E precursor
serine/threonine-protein kinase haspin. integrin alpha-E precursor
calcium/calmodulin-dependent protein kinase kinase 1 isoform a. calcium/calmodulin-dependent protein kinase kinase 1 isoform b. calcium/calmodulin-dependent protein kinase kinase 1 isoform c.
misshapen-like kinase 1 isoform 3. misshapen-like kinase 1 isoform 4. misshapen-like kinase 1 isoform 2. misshapen-like kinase 1 isoform 1.
misshapen-like kinase 1 isoform 3. misshapen-like kinase 1 isoform 4. misshapen-like kinase 1 isoform 2. misshapen-like kinase 1 isoform 1.
misshapen-like kinase 1 isoform 3. misshapen-like kinase 1 isoform 4. misshapen-like kinase 1 isoform 2. misshapen-like kinase 1 isoform 1.
non-receptor tyrosine-protein kinase TNK1 isoform 1. non-receptor tyrosine-protein kinase TNK1 isoform 2.
cellular tumor antigen p53 isoform a. cellular tumor antigen p53 isoform c. cellular tumor antigen p53 isoform b. cellular tumor antigen p53 isoform d. cellular tumor antigen p53 isoform e.
chromodomain-helicase-DNA-binding protein 3 isoform 1. chromodomain-helicase-DNA-binding protein 3 isoform 2. chromodomain-helicase-DNA-binding protein 3 isoform 3.
chromodomain-helicase-DNA-binding protein 3 isoform 3. chromodomain-helicase-DNA-binding protein 3 isoform 1. chromodomain-helicase-DNA-binding protein 3 isoform 2.
chromodomain-helicase-DNA-binding protein 3 isoform 3. chromodomain-helicase-DNA-binding protein 3 isoform 1. chromodomain-helicase-DNA-binding protein 3 isoform 2.
chromodomain-helicase-DNA-binding protein 3 isoform 3. chromodomain-helicase-DNA-binding protein 3 isoform 1. chromodomain-helicase-DNA-binding protein 3 isoform 2.
aurora kinase B
phosphoinositide 3-kinase regulatory subunit 5 isoform 1. phosphoinositide 3-kinase regulatory subunit 5 isoform 2.
mitogen-activated protein kinase 7 isoform 1. mitogen-activated protein kinase 7 isoform 2.
kinase suppressor of Ras 1
receptor tyrosine-protein kinase erbB-2 isoform a precursor. receptor tyrosine-protein kinase erbB-2 isoform b.
receptor tyrosine-protein kinase erbB-2 isoform a precursor. receptor tyrosine-protein kinase erbB-2 isoform b.
receptor tyrosine-protein kinase erbB-2 isoform a precursor. receptor tyrosine-protein kinase erbB-2 isoform b.
breast cancer type 1 susceptibility protein isoform 2. breast cancer type 1 susceptibility protein isoform 1. breast cancer type 1 susceptibility protein isoform 3.
breast cancer type 1 susceptibility protein isoform 2. breast cancer type 1 susceptibility protein isoform 1. breast cancer type 1 susceptibility protein isoform 3.
breast cancer type 1 susceptibility protein isoform 2. breast cancer type 1 susceptibility protein isoform 1. breast cancer type 1 susceptibility protein isoform 3.
breast cancer type 1 susceptibility protein isoform 2. breast cancer type 1 susceptibility protein isoform 1. breast cancer type 1 susceptibility protein isoform 3.
breast cancer type 1 susceptibility protein isoform 2. breast cancer type 1 susceptibility protein isoform 1. breast cancer type 1 susceptibility protein isoform 3.
collagen alpha-1(I) chain preproprotein
microtubularin-related protein 4

testis-expressed protein 14 isoform c. testis-expressed protein 14 isoform a. testis-expressed protein 14 isoform b
 protein kinase C alpha type
 sphingosine kinase 1 isoform 2. sphingosine kinase 1 isoform 1. sphingosine kinase 1 isoform 3
 serine/threonine-protein kinase LMTK1 isoform 1. serine/threonine-protein kinase LMTK1 isoform 2
 serine/threonine-protein kinase LMTK1 isoform 1. serine/threonine-protein kinase LMTK1 isoform 2
 rho-associated protein kinase 1
 mitogen-activated protein kinase 4
 transcription factor 4 isoform c
 alpha-protein kinase 2
 alpha-protein kinase 2
 alpha-protein kinase 2
 alpha-protein kinase 2
 alpha-protein kinase 2
 IisH domain and HEAT repeat-containing protein KIAA1468. GPI ethanolamine phosphate transferase 1
 IisH domain and HEAT repeat-containing protein KIAA1468
 MAP kinase-interacting serine/threonine-protein kinase 2 isoform 2. MAP kinase-interacting serine/threonine-protein kinase 2 isoform 1
 non-receptor tyrosine-protein kinase TYK2
 non-receptor tyrosine-protein kinase TYK2
 serine/threonine-protein kinase N1 isoform 1. serine/threonine-protein kinase N1 isoform 2
 serine/threonine-protein kinase N1 isoform 1. serine/threonine-protein kinase N1 isoform 2
 tyrosine-protein kinase JAK3
 microtubule-associated serine/threonine-protein kinase 3
 phosphatidylinositol 3-kinase regulatory subunit beta
 protein FAM98C
 RAC-beta serine/threonine-protein kinase isoform 1. RAC-beta serine/threonine-protein kinase isoform 2
 uncharacterized aarF domain-containing protein kinase 4 isoform a. uncharacterized aarF domain-containing protein kinase 4 isoform b
 tyrosine-protein kinase receptor UFO isoform 1 precursor. tyrosine-protein kinase receptor UFO isoform 2 precursor
 mvotonin-protein kinase isoform 1. mvotonin-protein kinase isoform 2. mvotonin-protein kinase isoform 4. mvotonin-protein kinase isoform 3
 serine/threonine-protein kinase D2 isoform A. serine/threonine-protein kinase D2 isoform B
 serine/threonine-protein kinase D2 isoform A. serine/threonine-protein kinase D2 isoform B
 serine/threonine-protein kinase SBK2
 serine/threonine-protein kinase SBK2
 serine/threonine-protein kinase SBK2
 serine/threonine-protein kinase PAK 7
 mvosin light chain kinase 2. skeletal/cardiac muscle
 aurora kinase A
 aurora kinase A
 hormonally up-regulated neu tumor-associated kinase
 receptor-interacting serine/threonine-protein kinase 4
 serine/threonine-protein kinase SIK1
 keratin-associated protein 10-1. protein TSPEAR precursor
 LIM domain kinase 2 isoform 1. LIM domain kinase 2 isoform 2a. LIM domain kinase 2 isoform 2b
 mitogen-activated protein kinase 12
 mitogen-activated protein kinase 11
 mitogen-activated protein kinase 11
 cAMP-dependent protein kinase catalytic subunit PRKX
 mitogen-activated protein kinase kinase 15
 insulin receptor substrate 4
 retinal guanylyl cyclase 2
 interleukin-1 receptor-associated kinase 1 isoform 1. interleukin-1 receptor-associated kinase 1 isoform 3. interleukin-1 receptor-associated kinase 1 isoform
 interleukin-1 receptor-associated kinase 1 isoform 1. interleukin-1 receptor-associated kinase 1 isoform 2. interleukin-1 receptor-associated kinase 1 isoform

Gencode													
ENST00000407249.3	GN=CDK11A	GI=ENSG000000008128.14	FC=Missense	CP=1929	CF=2	AC=GAt->GAG	IRP=643	RC=D	Asp->F	Glul	LEN=19/21	DS=+3	P=chr1:1
ENST00000407249.3	GN=CDK11A	GI=ENSG000000008128.14	FC=Missense	CP=1183	CF=0	AC=gAC->aAC	IRP=395	RC=D	Asp->N	Asn	LEN=12/21	DS=+99	P=chr1:1
ENST00000407249.3	GN=CDK11A	GI=ENSG000000008128.14	FC=Missense	CP=1114	CF=0	AC=gGG->aGG	IRP=372	RC=G	Glvl->R	Arg	LEN=12/21	DS=+30	P=chr1:1
ENST00000378633.1	GN=CDK11A	GI=ENSG000000008128.14	FC=Missense	CP=1973	CF=1	AC=GtA->GcA	IRP=658	RC=V	Val->A	Ala	LEN=18/20	DS=+53	P=chr1:1
ENST00000378633.1	GN=CDK11A	GI=ENSG000000008128.14	FC=Missense	CP=1177	CF=0	AC=gAC->aAC	IRP=393	RC=D	Asp->N	Asn	LEN=11/20	DS=+99	P=chr1:1
ENST00000378633.1	GN=CDK11A	GI=ENSG000000008128.14	FC=Missense	CP=1108	CF=0	AC=gGG->aGG	IRP=370	RC=G	Glvl->R	Arg	LEN=11/20	DS=+30	P=chr1:1
ENST00000536656.1	GN=PIK3CD1	GI=ENSG000000171608.9	FC=Missense	CP=1261	CF=0	AC=aCG->gCG	IRP=421	RC=T	Thr->A	Ala	LEN=11/24	DS=+27	P=chr1:9
ENST00000166244.3	GN=PHA8	GI=ENSG00000070886.6	FC=Missense	CP=1834	CF=0	AC=gAA->cAA	IRP=612	RC=F	Glul->Q	Gln	LEN=10/17	DS=+69	P=chr1:22
ENST00000493901.1	GN=MAP3K6	GI=ENSG000000142733.8	FC=Missense	CP=1364	CF=1	AC=AcC->AtC	IRP=455	RC=T	Thr->I	Ile	LEN=10/30	DS=+109	P=chr1:2
ENST00000374005.3	GN=FGRIG	GI=ENSG00000000938.7	FC=Missense	CP=823	CF=0	AC=gGG->cGG	IRP=275	RC=G	Glvl->R	Arg	LEN=8/13	DS=-9	P=chr1:27938
ENST00000373130.3	GN=STK40	GI=ENSG000000196182.6	FC=Missense	CP=1198	CF=0	AC=gCC->aCC	IRP=400	RC=A	Ala->T	Thr	LEN=11/11	DS=+94	P=chr1:36
ENST00000427468.2	GN=PHA10	GI=ENSG000000183317.1	FC=Missense	CP=3008	CF=1	AC=GgC->GtC	IRP=1003	RC=G	Glvl->V	Val	LEN=17/20	DS=+96	P=chr1:38
ENST00000427468.2	GN=PHA10	GI=ENSG000000183317.1	FC=Missense	CP=841	CF=0	AC=tIC->aIC	IRP=281	RC=F	Phe->I	Ile	LEN=3/20	DS=+67	P=chr1:38
ENST00000427468.2	GN=PHA10	GI=ENSG000000183317.1	FC=Missense	CP=659	CF=1	AC=AcG->AaG	IRP=220	RC=T	Thr->K	Lvs	LEN=3/20	DS=+488	P=chr1:3
ENST00000361297.2	GN=MAST2	GI=ENSG00000086015.13	FC=Missense	CP=1164	CF=2	AC=GAT->GAG	IRP=388	RC=D	Asp->F	Glul	LEN=10/29	DS=+186	P=chr1:1
ENST00000361297.2	GN=MAST2	GI=ENSG00000086015.13	FC=Missense	CP=1977	CF=2	AC=ATt->ATg	IRP=659	RC=I	Ile->M	Met	LEN=17/29	DS=+58	P=chr1:46
ENST00000540385.1	GN=PIK3R3	GI=ENSG000000117461.10	FC=Missense	CP=987	CF=2	AC=AAt->AAa	IRP=329	RC=N	Asn->K	Lvs	LEN=7/10	DS=+85	P=chr1:46
ENST00000371079.1	GN=ROR1	GI=ENSG000000185483.6	FC=Missense	CP=1553	CF=1	AC=AcC->AtC	IRP=518	RC=T	Thr->M	Met	LEN=9/9	DS=+167	P=chr1:642
ENST00000399546.2	GN=BRD1	GI=ENSG000000137948.12	FC=Missense	CP=184	CF=0	AC=cAG->aAG	IRP=62	RC=Q	Gln->K	Lvs	LEN=2/19	DS=+22	P=chr1:924
ENST00000399546.2	GN=BRD1	GI=ENSG000000137948.12	FC=Missense	CP=2087	CF=1	AC=CcG->CtG	IRP=696	RC=P	Pro->L	Leu	LEN=14/19	DS=+23	P=chr1:9
ENST00000358465.2	GN=TRIM33	GI=ENSG000000197323.6	FC=Missense	CP=2519	CF=1	AC=AtT->AcT	IRP=840	RC=I	Ile->T	Thr	LEN=15/20	DS=+101	P=chr1:11
ENST00000367772.4	GN=SCYL3	GI=ENSG00000000457.8	FC=Missense	CP=1862	CF=1	AC=CaA->CcA	IRP=621	RC=Q	Gln->R	Arg	LEN=13/14	DS=+388	P=chr1:1
ENST00000367559.3	GN=RNASEH1	GI=ENSG000000135828.6	FC=Missense	CP=1385	CF=1	AC=CgA->CaA	IRP=462	RC=R	Arg->Q	Gln	LEN=2/7	DS=-1256	P=chr1:1
ENST00000367162.3	GN=DSTYK1	GI=ENSG000000133059.11	FC=Missense	CP=1921	CF=0	AC=tGT->cGT	IRP=641	RC=C	Cys->R	Arg	LEN=7/13	DS=+103	P=chr1:1
ENST00000367157.3	GN=NUAK2	GI=ENSG000000163545.7	FC=Missense	CP=1547	CF=1	AC=GcG->GtG	IRP=516	RC=A	Ala->V	Val	LEN=7/7	DS=+724	P=chr1:205
ENST00000506784.1	GN=CDK18	GI=ENSG000000117266.10	FC=Missense	CP=1487	CF=1	AC=GgG->GaG	IRP=496	RC=G	Glvl->F	Glul	LEN=16/16	DS=+7	P=chr1:20
ENST00000429204.1	GN=TPKB1	GI=ENSG000000143772.5	FC=Missense	CP=1655	CF=1	AC=CcG->CaG	IRP=552	RC=P	Pro->Q	Gln	LEN=2/8	DS=+1860	P=chr1:22
ENST00000334218.5	GN=CDC42BPA	GI=ENSG000000143776.12	FC=Missense	CP=5282	CF=1	AC=GcT->GtT	IRP=1761	RC=A	Ala->V	Val	LEN=37/37	DS=+68	P=chr1:2
ENST00000334218.5	GN=CDC42BPA	GI=ENSG000000143776.12	FC=Missense	CP=3910	CF=0	AC=gTA->aTA	IRP=1304	RC=V	Val->I	Ile	LEN=29/37	DS=+177	P=chr1:2
ENST00000422127.1	GN=OBSCN1	GI=ENSG000000154358.13	FC=Missense	CP=1505	CF=1	AC=CaG->CcG	IRP=502	RC=Q	Gln->R	Arg	LEN=4/105	DS=+247	P=chr1:1
ENST00000422127.1	GN=OBSCN1	GI=ENSG000000154358.13	FC=Missense	CP=4523	CF=1	AC=GtC->GaC	IRP=1508	RC=V	Val->D	Asp	LEN=15/105	DS=+214	P=chr1:1
ENST00000422127.1	GN=OBSCN1	GI=ENSG000000154358.13	FC=Missense	CP=6318	CF=2	AC=GAT->GAG	IRP=2106	RC=D	Asp->F	Glul	LEN=22/105	DS=+98	P=chr1:1
ENST00000422127.1	GN=OBSCN1	GI=ENSG000000154358.13	FC=Missense	CP=6346	CF=0	AC=tTC->cTC	IRP=2116	RC=F	Phe->L	Leu	LEN=22/105	DS=+126	P=chr1:1
ENST00000422127.1	GN=OBSCN1	GI=ENSG000000154358.13	FC=Missense	CP=15047	CF=1	AC=CgG->CaG	IRP=5016	RC=R	Arg->Q	Gln	LEN=55/105	DS=+545	P=chr1:1
ENST00000366624.3	GN=RP5-862P8.2	GI=ENSG000000143674.6	FC=Missense	CP=1349	CF=1	AC=GcT->GaT	IRP=450	RC=A	Ala->D	Asp	LEN=5/10	DS=+38	P=chr1:1
ENST00000366624.3	GN=RP5-862P8.2	GI=ENSG000000143674.6	FC=Missense	CP=2182	CF=0	AC=gTC->aTC	IRP=728	RC=V	Val->I	Ile	LEN=9/10	DS=+258	P=chr1:1
ENST00000366624.3	GN=RP5-862P8.2	GI=ENSG000000143674.6	FC=Missense	CP=2223	CF=2	AC=GA->GAT	IRP=741	RC=F	Glul->D	Asp	LEN=9/10	DS=+299	P=chr1:1
ENST00000366624.3	GN=RP5-862P8.2	GI=ENSG000000143674.6	FC=Missense	CP=2350	CF=0	AC=tGT->gGT	IRP=784	RC=C	Cys->G	Glvl	LEN=9/10	DS=+426	P=chr1:1
ENST00000315872.6	GN=ROCK2	GI=ENSG000000134318.8	FC=Missense	CP=1292	CF=1	AC=Act->AaT	IRP=431	RC=T	Thr->N	Asn	LEN=10/33	DS=+33	P=chr2:1
ENST00000389048.3	GN=ALK1	GI=ENSG000000171094.11	FC=Missense	CP=4587	CF=2	AC=GAc->GAG	IRP=1529	RC=D	Asp->F	Glul	LEN=29/29	DS=+423	P=chr2:2
ENST00000389048.3	GN=ALK1	GI=ENSG000000171094.11	FC=Missense	CP=4472	CF=1	AC=AaG->AgG	IRP=1491	RC=K	Lvs->R	Arg	LEN=29/29	DS=+308	P=chr2:2
ENST00000389048.3	GN=ALK1	GI=ENSG000000171094.11	FC=Missense	CP=4381	CF=0	AC=aTC->gTC	IRP=1461	RC=I	Ile->V	Val	LEN=29/29	DS=+217	P=chr2:294
ENST00000389048.3	GN=ALK1	GI=ENSG000000171094.11	FC=Missense	CP=4318	CF=0	AC=gCC->tCC	IRP=1440	RC=A	Ala->S	Ser	LEN=29/29	DS=+154	P=chr2:2
ENST00000389048.3	GN=ALK1	GI=ENSG000000171094.11	FC=Missense	CP=3089	CF=1	AC=CaC->CcC	IRP=1030	RC=H	His->P	Pro	LEN=19/29	DS=+22	P=chr2:29
ENST00000233057.4	GN=IF2AK2	GI=ENSG00000055332.10	FC=Missense	CP=1397	CF=1	AC=GgA->GaA	IRP=466	RC=G	Glvl->F	Glul	LEN=15/17	DS=+20	P=chr2:1
ENST00000294964.5	GN=PKDCC1	GI=ENSG000000162878.8	FC=Missense	CP=325	CF=0	AC=tCC->cCC	IRP=109	RC=S	Ser->P	Pro	LEN=1/7	DS=-47	P=chr2:42
ENST00000435505.2	GN=VRK2	GI=ENSG00000028116.11	FC=Missense	CP=471	CF=2	AC=ATa->ATg	IRP=157	RC=I	Ile->M	Met	LEN=10/16	DS=+2	P=chr2:5813
ENST00000303236.3	GN=IF2AK3	GI=ENSG000000172071.6	FC=Missense	CP=407	CF=1	AC=tCC->gCC	IRP=136	RC=S	Ser->C	Cys	LEN=2/17	DS=+99	P=chr2:88
ENST00000074304.5	GN=INPP4A	GI=ENSG00000040933.10	FC=Missense	CP=1810	CF=0	AC=aCT->gCT	IRP=604	RC=T	Thr->A	Ala	LEN=17/26	DS=+229	P=chr2:1
ENST00000375845.3	GN=YSK4	GI=ENSG000000176601.7	FC=Missense	CP=2435	CF=1	AC=GaA->GgA	IRP=812	RC=F	Glul->G	Glvl	LEN=7/10	DS=+18	P=chr2:13
ENST00000375845.3	GN=YSK4	GI=ENSG000000176601.7	FC=Missense	CP=2026	CF=0	AC=gAG->cAG	IRP=676	RC=F	Glul->Q	Gln	LEN=7/10	DS=+1408	P=chr2:13
ENST00000241416.7	GN=ACVR2A	GI=ENSG000000121989.10	FC=Missense	CP=945	CF=2	AC=AAa->AAc	IRP=315	RC=K	Lvs->N	Asn	LEN=7/11	DS=+129	P=chr2:1

ENST00000243349.7|GN=ACVR1|GI=ENSG00000123612.10|FC=Missense|CP=58|CF=0|AC=gCC->tCC|RP=20|RC=A|Ala|>S|Ser||EN=1/9|DS=-41|70|P=chr2:1
 ENST00000334231.6|GN=MYO3B|GI=ENSG00000071909.12|FC=Missense|CP=952|CF=0|AC=aAG->gAG|RP=318|RC=K|Lys|>E|Glu||EN=9/35|DS=+110|P=chr2:1
 ENST00000334231.6|GN=MYO3B|GI=ENSG00000071909.12|FC=Missense|CP=2335|CF=0|AC=gTA->aTA|RP=779|RC=V|Val|>I|Ile||EN=20/35|DS=+31|P=chr2:17
 ENST00000334231.6|GN=MYO3B|GI=ENSG00000071909.12|FC=Missense|CP=3272|CF=1|AC=AaG->AaG|RP=1091|RC=R|Arg|>K|Lys||EN=27/35|DS=+119|P=chr2:1
 ENST00000375213.3|GN=AC013461.1|GI=ENSG000000091436.12|FC=Missense|CP=592|CF=1|AC=tCG->tG|RP=531|RC=S|Ser|>L|Leu||EN=19/20|DS=+41|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=96077|CF=1|AC=CgC->CaC|RP=32026|RC=R|Arg|>H|His||EN=307/312|DS=-27|18|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=89909|CF=1|AC=CgC->CaC|RP=29970|RC=R|Arg|>H|His||EN=299/312|DS=+121|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=88910|CF=1|AC=GtG->GcG|RP=29637|RC=V|Val|>A|Ala||EN=296/312|DS=+304|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=80483|CF=1|AC=AtC->AcC|RP=26828|RC=I|Ile|>T|Thr||EN=279/312|DS=+178|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=77947|CF=0|AC=cCA->aCA|RP=25983|RC=P|Pro|>T|Thr||EN=275/312|DS=-1844|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=75619|CF=0|AC=aTA->gTA|RP=25207|RC=I|Ile|>V|Val||EN=275/312|DS=-4172|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=72158|CF=1|AC=AcG->AtG|RP=24053|RC=T|Thr|>M|Met||EN=275/312|DS=-7633|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=67135|CF=0|AC=cGC->tGC|RP=22379|RC=R|Arg|>C|Cys||EN=275/312|DS=+51|24|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=59542|CF=0|AC=gCT->cCT|RP=19848|RC=A|Ala|>P|Pro||EN=267/312|DS=+189|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=59371|CF=0|AC=gTC->aTC|RP=19791|RC=V|Val|>I|Ile||EN=267/312|DS=+18|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=56504|CF=1|AC=AcT->AtT|RP=18835|RC=T|Thr|>I|Ile||EN=257/312|DS=+115|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=51881|CF=1|AC=CcA->CtA|RP=17294|RC=P|Pro|>L|Leu||EN=250/312|DS=-143|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=50732|CF=1|AC=Cgt->Cat|RP=16911|RC=R|Arg|>H|His||EN=247/312|DS=+4|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=48397|CF=0|AC=aAT->gAT|RP=16133|RC=N|Asn|>D|Asp||EN=238/312|DS=+51|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=43778|CF=1|AC=CcG->GtG|RP=14593|RC=A|Ala|>V|Val||EN=221/312|DS=+46|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=32402|CF=1|AC=GcA->CgA|RP=10801|RC=P|Pro|>R|Arg||EN=163/312|DS=+79|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=27832|CF=0|AC=aTT->gTT|RP=9278|RC=I|Ile|>V|Val||EN=116/312|DS=+51|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=22676|CF=1|AC=AaT->AgT|RP=7559|RC=N|Asn|>S|Ser||EN=88/312|DS=-191|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=21542|CF=1|AC=AgC->AaC|RP=7181|RC=S|Ser|>N|Asn||EN=84/312|DS=+211|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=21332|CF=1|AC=GcG->GcA|RP=7111|RC=A|Ala|>E|Glu||EN=84/312|DS=+1|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=20699|CF=1|AC=GaA->GcA|RP=6900|RC=E|Glu|>A|Ala||EN=81/312|DS=-169|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=18652|CF=0|AC=gAT->cAT|RP=6218|RC=D|Asp|>H|His||EN=74/312|DS=+144|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=17312|CF=1|AC=GcA->GtA|RP=5771|RC=A|Ala|>V|Val||EN=69/312|DS=-188|P=chr2:1
 ENST00000360870.4|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=11240|CF=1|AC=GaC->GcC|RP=3747|RC=D|Asp|>G|Gly||EN=46/46|DS=+880|P=chr2:1
 ENST00000360870.4|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=11196|CF=2|AC=TTG->TTc|RP=3732|RC=I|Ile|>F|Phe||EN=46/46|DS=+836|P=chr2:1
 ENST00000342175.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=10739|CF=1|AC=Ggt->Gat|RP=3580|RC=G|Gly|>D|Asp||EN=44/192|DS=+574|P=chr2:1
 ENST00000342175.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=10213|CF=0|AC=gCC->aCC|RP=3405|RC=A|Ala|>T|Thr||EN=44/192|DS=+48|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=10256|CF=1|AC=AgT->AaT|RP=3419|RC=S|Ser|>N|Asn||EN=44/312|DS=+142|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=9781|CF=0|AC=gTG->aTG|RP=3261|RC=V|Val|>M|Met||EN=42/312|DS=+78|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=8887|CF=0|AC=aCC->cCC|RP=2963|RC=T|Thr|>P|Pro||EN=37/312|DS=+246|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=7619|CF=1|AC=Cgt->Cat|RP=2540|RC=R|Arg|>H|His||EN=33/312|DS=+25|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=3884|CF=1|AC=tCA->tTA|RP=1295|RC=S|Ser|>L|Leu||EN=23/312|DS=+155|P=chr2:1
 ENST00000342992.6|GN=TTN|GI=ENSG00000155657.16|FC=Missense|CP=982|CF=0|AC=cGT->tGT|RP=328|RC=R|Arg|>C|Cys||EN=7/312|DS=+68|P=chr2:1793
 ENST00000264380.4|GN=PIKEYVE|GI=ENSG00000115020.11|FC=Missense|CP=2087|CF=1|AC=AgT->AaT|RP=696|RC=S|Ser|>N|Asn||EN=17/42|DS=+5|P=chr2:1
 ENST00000264380.4|GN=PIKEYVE|GI=ENSG00000115020.11|FC=Missense|CP=2795|CF=1|AC=TtC->TcC|RP=932|RC=I|Ile|>S|Ser||EN=20/42|DS=+337|P=chr2:1
 ENST00000264380.4|GN=PIKEYVE|GI=ENSG00000115020.11|FC=Missense|CP=2984|CF=1|AC=CaG->CtG|RP=995|RC=Q|Gln|>L|Leu||EN=20/42|DS=+526|P=chr2:1
 ENST00000264380.4|GN=PIKEYVE|GI=ENSG00000115020.11|FC=Missense|CP=2993|CF=1|AC=Act->AgT|RP=998|RC=T|Thr|>S|Ser||EN=20/42|DS=+535|P=chr2:1
 ENST00000264380.4|GN=PIKEYVE|GI=ENSG00000115020.11|FC=Missense|CP=3547|CF=0|AC=cAA->aAA|RP=1183|RC=Q|Gln|>K|Lys||EN=20/42|DS=+1089|P=chr2:1
 ENST00000264380.4|GN=PIKEYVE|GI=ENSG00000115020.11|FC=Missense|CP=3793|CF=0|AC=cCT->aCT|RP=1265|RC=P|Pro|>T|Thr||EN=23/42|DS=+2|P=chr2:1
 ENST00000312358.7|GN=SPFG|GI=ENSG00000072195.9|FC=Missense|CP=3928|CF=0|AC=gAC->aAC|RP=1310|RC=D|Asp|>N|Asn||EN=15/41|DS=+93|P=chr2:2
 ENST00000312358.7|GN=SPFG|GI=ENSG00000072195.9|FC=Missense|CP=8368|CF=0|AC=aGG->gGG|RP=2790|RC=R|Arg|>G|Gly||EN=36/41|DS=+51|P=chr2:2
 ENST00000358664.9|GN=PASKI|GI=ENSG00000115687.9|FC=Missense|CP=3818|CF=1|AC=ttt->tTt|RP=1273|RC=F|Phe|>C|Cys||EN=17/18|DS=+130|P=chr2:2
 ENST00000403638.3|GN=PASKI|GI=ENSG00000115687.9|FC=Missense|CP=3388|CF=0|AC=cGG->tGG|RP=1130|RC=R|Arg|>W|Trp||EN=14/14|DS=+190|P=chr2:2
 ENST00000544142.1|GN=PASKI|GI=ENSG00000115687.9|FC=Missense|CP=321|CF=1|AC=CaG->CgG|RP=11|RC=Q|Gln|>R|Arg||EN=1/15|DS=-4053|P=chr2:2420
 ENST00000256458.4|GN=IRAK2|GI=ENSG00000134070.4|FC=Missense|CP=1293|CF=2|AC=GA->GAa|RP=431|RC=D|Asp|>E|Glu||EN=11/13|DS=+21|P=chr3:10
 ENST00000396636.3|GN=NFK10|GI=ENSG00000163491.10|FC=Missense|CP=1538|CF=1|AC=tTG->tTG|RP=513|RC=I|Ile|>S|Ser||EN=19/24|DS=+62|P=chr3:2
 ENST00000301831.4|GN=ULK4|GI=ENSG00000168038.6|FC=Missense|CP=2990|CF=1|AC=AtT->AgT|RP=997|RC=I|Ile|>S|Ser||EN=30/37|DS=+12|P=chr3:41288
 ENST00000301831.4|GN=ULK4|GI=ENSG00000168038.6|FC=Missense|CP=1918|CF=0|AC=tCC->gCC|RP=640|RC=S|Ser|>A|Ala||EN=20/37|DS=+70|P=chr3:4128
 ENST00000301831.4|GN=ULK4|GI=ENSG00000168038.6|FC=Missense|CP=1624|CF=0|AC=gCT->aCT|RP=542|RC=A|Ala|>T|Thr||EN=17/37|DS=+47|P=chr3:4128
 ENST00000301831.4|GN=ULK4|GI=ENSG00000168038.6|FC=Missense|CP=670|CF=0|AC=aTT->gTT|RP=224|RC=I|Ile|>V|Val||EN=7/37|DS=+27|P=chr3:4128809

ENST00000301831.4|GN=ULK4|GIE=NSG00000168038.6|FC=Missense|CP=116|CF=1|AC=AaA->AgA|RP=39|RC=K|Vs|>R|Arg||EN=2/37|DS=+164|P=chr3:41288
 ENST00000296474.3|GN=MST1|RIGI=NSG00000164078.7|FC=Missense|CP=3583|CF=0|AC=aGC->gGC|RP=1195|RC=SI|Ser|>G|Giv||EN=17/20|DS=+49|P=chr3:41288
 ENST00000233027.5|GN=NEK4|GIE=NSG00000114904.8|FC=Missense|CP=673|CF=0|AC=cCA->gCA|RP=225|RC=PI|Pro|>A|Ala||EN=5/16|DS=+7|P=chr3:527448
 ENST00000389672.5|GN=PHA6|GIE=NSG00000080224.13|FC=Missense|CP=388|CF=0|AC=gTG->aTG|RP=130|RC=VI|Val|>M|Met||EN=2/18|DS=+3|P=chr3:965
 ENST00000360304.3|GN=MYL|KIGI=NSG00000065534.13|FC=Missense|CP=2742|CF=2|AC=GAc->GAa|RP=914|RC=DI|Asp|>E|Glu||EN=18/34|DS=+280|P=chr3:965
 ENST00000360304.3|GN=MYL|KIGI=NSG00000065534.13|FC=Missense|CP=2582|CF=1|AC=CtA->CcA|RP=861|RC=I|Leu|>P|Pro||EN=18/34|DS=+120|P=chr3:965
 ENST00000360304.3|GN=MYL|KIGI=NSG00000065534.13|FC=Missense|CP=1486|CF=0|AC=cTG->gTG|RP=496|RC=I|Leu|>V|Val||EN=11/34|DS=+177|P=chr3:965
 ENST00000360304.3|GN=MYL|KIGI=NSG00000065534.13|FC=Missense|CP=782|CF=1|AC=CtG->CcG|RP=261|RC=VI|Val|>A|Ala||EN=10/34|DS=+9|P=chr3:1233
 ENST00000360304.3|GN=MYL|KIGI=NSG00000065534.13|FC=Missense|CP=439|CF=0|AC=cCA->tCA|RP=147|RC=PI|Pro|>S|Ser||EN=7/34|DS=+17|P=chr3:1233
 ENST00000360013.3|GN=KAL|RNIGI=NSG00000160145.10|FC=Missense|CP=880|CF=0|AC=cAC->aAC|RP=294|RC=HI|His|>N|Asn||EN=5/60|DS=+430|P=chr3:1233
 ENST00000429253.2|GN=NEK1|TIGI=NSG00000114670.8|FC=Missense|CP=1463|CF=1|AC=GaA->GtA|RP=488|RC=EI|Glu|>V|Val||EN=14/17|DS=+64|P=chr3:130
 ENST00000350721.4|GN=ATR1|RIGI=NSG00000175054.9|FC=Missense|CP=632|CF=1|AC=AtG->AcG|RP=211|RC=M|Met|>T|Thr||EN=4/47|DS=+340|P=chr3:14216
 ENST00000424227.1|GN=MAP3K13|GIE=NSG00000073803.9|FC=Missense|CP=2744|CF=1|AC=CgT->CaT|RP=915|RC=RI|Arg|>H|His||EN=14/15|DS=+243|P=chr3:14216
 ENST00000265022.3|GN=DGKG|GIE=NSG00000058866.9|FC=Missense|CP=947|CF=1|AC=AaA->AaA|RP=316|RC=RI|Arg|>K|L|Vs||EN=11/25|DS=+37|P=chr3:1858
 ENST00000265022.3|GN=DGKG|GIE=NSG00000058866.9|FC=Missense|CP=425|CF=1|AC=AcC->AgC|RP=142|RC=TI|Thr|>S|Ser||EN=6/25|DS=+52|P=chr3:1858
 ENST00000314167.4|GN=GAKI|GIE=NSG00000178950.11|FC=Missense|CP=3899|CF=1|AC=TcG->TtG|RP=1300|RC=SI|Ser|>L|Leu||EN=28/28|DS=+65|P=chr4:84
 ENST00000398052.4|GN=GRK4|GIE=NSG00000125388.14|FC=Missense|CP=194|CF=1|AC=CgT->CtT|RP=65|RC=RI|Arg|>I|Leu||EN=3/16|DS=+46|P=chr4:29654
 ENST00000398052.4|GN=GRK4|GIE=NSG00000125388.14|FC=Missense|CP=425|CF=1|AC=GcC->GtC|RP=142|RC=A|Ala|>V|Val||EN=5/16|DS=+86|P=chr4:29654
 ENST00000282908.5|GN=STK32|BIGI=NSG00000152953.8|FC=Missense|CP=592|CF=0|AC=aGA->gGA|RP=198|RC=RI|Arg|>G|Giv||EN=7/12|DS=+30|P=chr4:503
 ENST00000264864.6|GN=PI4K2|BIGI=NSG00000038210.8|FC=Missense|CP=16|CF=0|AC=gAG->aAG|RP=6|RC=EI|Glu|>K|L|Vs||EN=1/10|DS=-18142|P=chr4:252
 ENST00000263923.4|GN=KDR1|GIE=NSG00000128052.8|FC=Missense|CP=1416|CF=2|AC=CAa->CaA|RP=472|RC=QI|Gln|>H|His||EN=11/30|DS=+4|P=chr4:55944
 ENST00000335016.5|GN=BMP2|KIGI=NSG00000138756.12|FC=Missense|CP=1213|CF=0|AC=gGT->aGT|RP=405|RC=G|Giv|>S|Ser||EN=10/16|DS=+146|P=chr4:106
 ENST00000273980.4|GN=TBC1|GIE=NSG00000145348.11|FC=Missense|CP=796|CF=0|AC=cAA->gAA|RP=266|RC=QI|Gln|>F|Glu||EN=11/27|DS=+14|P=chr4:106
 ENST00000458497.1|GN=ALPK1|TIGI=NSG00000073331.12|FC=Missense|CP=1694|CF=1|AC=GgT->GaT|RP=565|RC=G|Giv|>D|Asp||EN=11/16|DS=+794|P=chr4:106
 ENST00000458497.1|GN=ALPK1|TIGI=NSG00000073331.12|FC=Missense|CP=1925|CF=1|AC=CaT->CgT|RP=642|RC=HI|His|>R|Arg||EN=11/16|DS=+1025|P=chr4:106
 ENST00000458497.1|GN=ALPK1|TIGI=NSG00000073331.12|FC=Missense|CP=2196|CF=2|AC=ATg->ATa|RP=732|RC=M|Met|>I|Ile||EN=11/16|DS=+1296|P=chr4:106
 ENST00000458497.1|GN=ALPK1|TIGI=NSG00000073331.12|FC=Missense|CP=2582|CF=1|AC=AtG->AcG|RP=861|RC=M|Met|>T|Thr||EN=11/16|DS=+1682|P=chr4:106
 ENST00000270861.5|GN=PLK4|GIE=NSG00000142731.6|FC=Missense|CP=694|CF=0|AC=CT->aCT|RP=232|RC=SI|Ser|>T|Thr||EN=5/16|DS=+357|P=chr4:12880
 ENST00000302176.8|GN=DCLK2|GIE=NSG00000170390.10|FC=Missense|CP=2293|CF=0|AC=cCT->tCT|RP=765|RC=PI|Pro|>S|Ser||EN=17/17|DS=+169|P=chr4:12880
 ENST00000302176.8|GN=DCLK2|GIE=NSG00000170390.10|FC=Missense|CP=2294|CF=1|AC=CcT->CgT|RP=765|RC=PI|Pro|>R|Arg||EN=17/17|DS=+170|P=chr4:12880
 ENST00000507142.1|GN=NEK1|GIE=NSG00000137601.11|FC=Missense|CP=2255|CF=1|AC=GaA->GgA|RP=752|RC=EI|Glu|>G|Giv||EN=26/36|DS=+50|P=chr4:17
 ENST00000399503.3|GN=MAP3K1|GIE=NSG00000095015.5|FC=Missense|CP=2416|CF=0|AC=gAT->aAT|RP=806|RC=DI|Asp|>N|Asn||EN=14/20|DS=+47|P=chr5:56
 ENST00000399503.3|GN=MAP3K1|GIE=NSG00000095015.5|FC=Missense|CP=2716|CF=0|AC=gTC->aTC|RP=906|RC=VI|Val|>I|Ile||EN=14/20|DS=+347|P=chr5:56
 ENST00000404260.3|GN=MAST4|GIE=NSG00000069020.12|FC=Missense|CP=4880|CF=1|AC=CgG->CcG|RP=1627|RC=RI|Arg|>P|Pro||EN=29/29|DS=+904|P=chr5:56
 ENST00000396611.1|GN=PIK3R1|GIE=NSG00000145675.10|FC=Missense|CP=978|CF=2|AC=ATg->ATa|RP=326|RC=M|Met|>I|Ile||EN=7/15|DS=+62|P=chr5:6752
 ENST00000283109.3|GN=RIOK2|GIE=NSG00000058729.6|FC=Missense|CP=1045|CF=0|AC=gGG->aGG|RP=349|RC=G|Giv|>R|Arg||EN=8/10|DS=+173|P=chr5:96
 ENST00000283109.3|GN=RIOK2|GIE=NSG00000058729.6|FC=Missense|CP=287|CF=1|AC=TcT->TtT|RP=96|RC=SI|Ser|>C|Cys||EN=3/10|DS=+82|P=chr5:96496
 ENST00000509481.1|GN=CTD-2215F18.1|GIE=NSG00000251606.11|FC=Missense|CP=113|CF=1|AC=GtT->GgT|RP=38|RC=VI|Val|>G|Giv||EN=4/5|DS=+81|P=chr5:96496
 ENST00000457016.1|GN=APC|GIE=NSG00000134982.10|FC=Missense|CP=5465|CF=1|AC=CtG->GaC|RP=1822|RC=VI|Val|>D|Asp||EN=16/16|DS=+3507|P=chr5:96496
 ENST00000390666.3|GN=TSSK1|BIGI=NSG00000212122.3|FC=Missense|CP=1010|CF=1|AC=AaG->AaG|RP=337|RC=RI|Arg|>K|L|Vs||EN=1/11|P=chr5:112768251
 ENST00000286301.3|GN=CSF1|RIGI=NSG00000182578.8|FC=Missense|CP=1085|CF=1|AC=CaC->CcC|RP=362|RC=HI|His|>R|Arg||EN=8/22|DS=+3|P=chr5:1494
 ENST00000292408.4|GN=FGFR4|GIE=NSG00000160867.9|FC=Missense|CP=28|CF=0|AC=gTC->aTC|RP=10|RC=VI|Val|>I|Ile||EN=2/18|DS=+81|P=chr5:17651388
 ENST00000292408.4|GN=FGFR4|GIE=NSG00000160867.9|FC=Missense|CP=407|CF=1|AC=CcC->CcC|RP=136|RC=PI|Pro|>L|Leu||EN=9/18|DS=+52|P=chr5:17651388
 ENST00000292408.4|GN=FGFR4|GIE=NSG00000160867.9|FC=Missense|CP=1162|CF=0|AC=gGG->aGG|RP=388|RC=G|Giv|>R|Arg||EN=9/18|DS=+105|P=chr5:17651388
 ENST00000261937.6|GN=FLT4|GIE=NSG00000037280.10|FC=Missense|CP=2670|CF=2|AC=CAc->CAG|RP=890|RC=HI|His|>QI|Gln||EN=19/30|DS=+23|P=chr5:18
 ENST00000261937.6|GN=FLT4|GIE=NSG00000037280.10|FC=Missense|CP=1936|CF=0|AC=gAG->aAG|RP=646|RC=EI|Glu|>K|L|Vs||EN=13/30|DS=+279|P=chr5:18
 ENST00000268446.5|GN=MYL|K4|GIE=NSG00000145949.8|FC=Missense|CP=725|CF=1|AC=AcG->AtG|RP=242|RC=TI|Thr|>M|Met||EN=8/12|DS=+38|P=chr6:266
 ENST00000337659.6|GN=PRPF4|BIGI=NSG00000112739.11|FC=Missense|CP=247|CF=0|AC=aTT->gTT|RP=83|RC=I|Ile|>V|Val||EN=2/15|DS=+206|P=chr6:4021
 ENST00000375333.2|GN=STK19|GIE=NSG00000204344.9|FC=Missense|CP=583|CF=0|AC=cAG->gAG|RP=195|RC=QI|Gln|>E|Glu||EN=4/8|DS=+16|P=chr6:31939
 ENST00000375333.2|GN=STK19|GIE=NSG00000204344.9|FC=Missense|CP=688|CF=0|AC=tGT->gGT|RP=230|RC=C|Cys|>R|Arg||EN=5/8|DS=+13|P=chr6:31939
 ENST00000451316.1|GN=IP6K3|GIE=NSG00000161896.6|FC=Missense|CP=934|CF=0|AC=gTC->aTC|RP=312|RC=VI|Val|>I|Ile||EN=7/7|DS=+169|P=chr6:336894
 ENST00000451316.1|GN=IP6K3|GIE=NSG00000161896.6|FC=Missense|CP=302|CF=1|AC=TcG->TtG|RP=101|RC=SI|Ser|>L|Leu||EN=4/7|DS=+103|P=chr6:336894
 ENST00000229812.7|GN=STK38|GIE=NSG00000112079.8|FC=Missense|CP=316|CF=0|AC=gTT->tTT|RP=106|RC=VI|Val|>F|Phe||EN=5/14|DS=+10|P=chr6:336461
 ENST00000372991.4|GN=CCND3|GIE=NSG00000112576.8|FC=Missense|CP=775|CF=0|AC=tCT->gCT|RP=259|RC=SI|Ser|>A|Ala||EN=5/5|DS=+64|P=chr6:41902
 ENST00000481273.1|GN=PTK7|GIE=NSG00000112655.10|FC=Missense|CP=2253|CF=2|AC=GAg->GAt|RP=751|RC=EI|Glu|>D|Asp||EN=14/20|DS=+182|P=chr6:41902

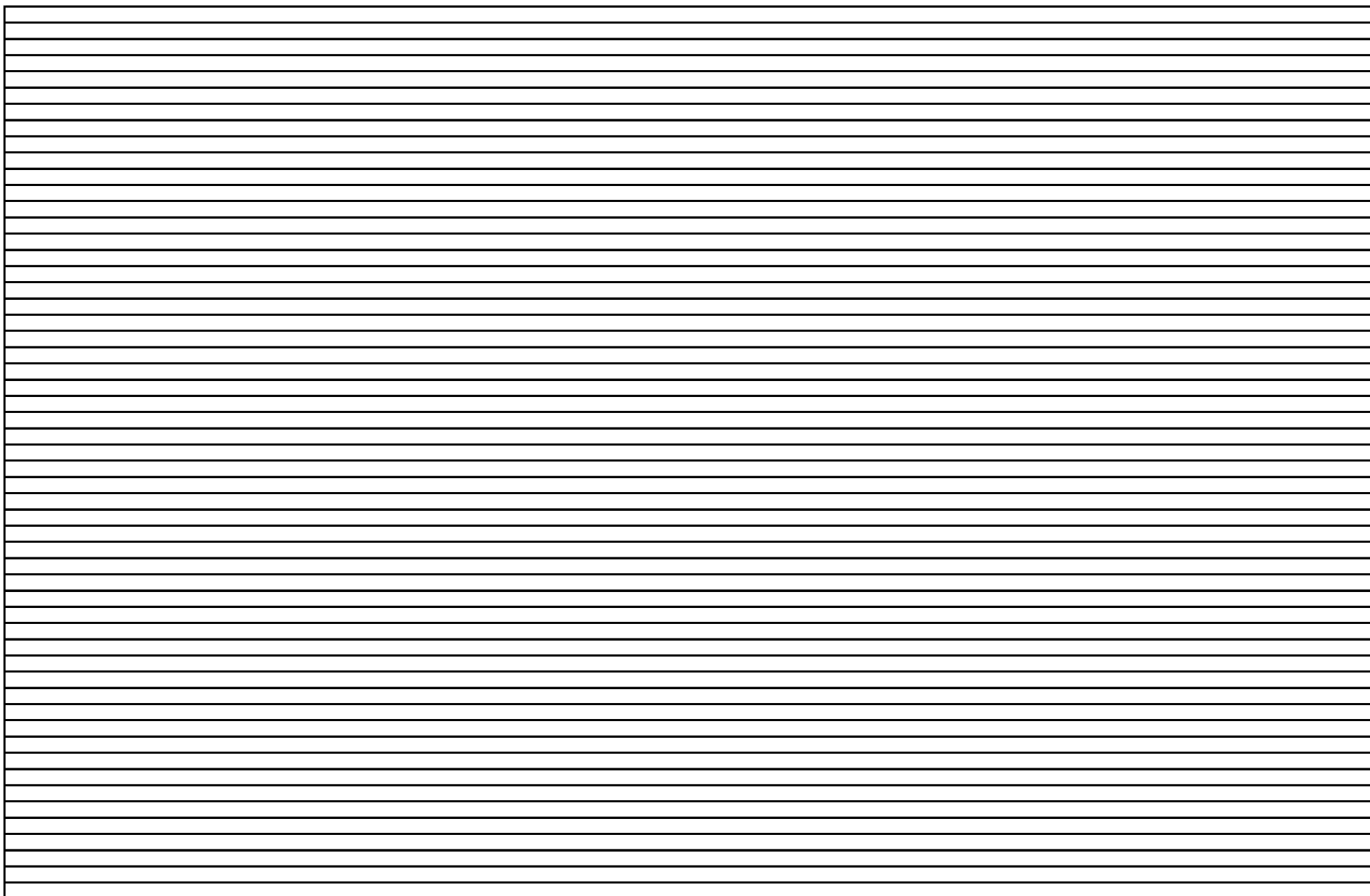
ENST00000259750.4|GN=TTBK1|GI=ENSG00000146216.5|FC=Missense|CP=3434|CF=1|AC=AaG->AgG|RP=1145|RC=K|LvsI->R|Arg|LEN=14/15|DS=-809|P=chr6
ENST00000259750.4|GN=TTBK1|GI=ENSG00000146216.5|FC=Missense|CP=3551|CF=1|AC=TtG->TcG|RP=1184|RC=L|L|LeuI->S|Ser|LEN=14/15|DS=-692|P=chr6
ENST00000275015.4|GN=NFKB1|GI=ENSG00000146232.8|FC=Missense|CP=581|CF=1|AC=GtC->GcC|RP=194|RC=V|ValI->A|Ala|LEN=1/6|DS=-2521|P=chr6:44
ENST00000275015.4|GN=NFKB1|GI=ENSG00000146232.8|FC=Missense|CP=524|CF=1|AC=CcA->CtA|RP=175|RC=P|ProI->L|Leu|LEN=1/6|DS=-2578|P=chr6:44
ENST00000368911.3|GN=CDK19|GI=ENSG00000155111.9|FC=Missense|CP=1290|CF=2|AC=AGc->AGa|RP=430|RC=S|SerI->R|Arg|LEN=12/13|DS=+180|P=chr6:1
ENST00000368626.3|GN=FRK1|GI=ENSG00000111816.5|FC=Missense|CP=364|CF=0|AC=gGA->aGA|RP=122|RC=G|GlvI->R|Arg|LEN=2/8|DS=+20|P=chr6:1162626
ENST00000368508.3|GN=ROS1|GI=ENSG00000047936.6|FC=Missense|CP=6116|CF=1|AC=CgtI->CatI|RP=2039|RC=R|ArgI->H|His|LEN=38/43|DS=+111|P=chr6:1
ENST00000359015.4|GN=MAP3K5|GI=ENSG00000197442.7|FC=Missense|CP=3748|CF=0|AC=aTA->gTA|RP=1250|RC=L|IleI->V|Val|LEN=26/30|DS=+231|P=chr6:1
ENST00000392142.4|GN=MAP3K4|GI=ENSG00000085511.14|FC=Missense|CP=470|CF=1|AC=CgtI->CaT|RP=157|RC=R|ArgI->H|His|LEN=3/27|DS=+127|P=chr6:1
ENST00000510118.1|GN=RPS6KA2|GI=ENSG00000071242.7|FC=Missense|CP=100|CF=0|AC=aCC->gCC|RP=34|RC=T|ThrI->A|Ala|LEN=2/23|DS=+37|P=chr6:166
ENST00000510118.1|GN=RPS6KA2|GI=ENSG00000071242.7|FC=Missense|CP=95|CF=1|AC=GaG->GgG|RP=32|RC=E|GluI->G|Glv|LEN=2/23|DS=+32|P=chr6:166
ENST00000355870.3|GN=STK31|GI=ENSG00000196335.8|FC=Missense|CP=213|CF=2|AC=CAg->CAc|RP=71|RC=Q|GlnI->H|His|LEN=4/24|DS=+63|P=chr7:23749
ENST00000355870.3|GN=STK31|GI=ENSG00000196335.8|FC=Missense|CP=781|CF=0|AC=gAG->aAG|RP=261|RC=F|GluI->K|LvsI|LEN=7/24|DS=+298|P=chr7:237
ENST00000355870.3|GN=STK31|GI=ENSG00000196335.8|FC=Missense|CP=804|CF=2|AC=AAg->AAt|RP=268|RC=K|LvsI->N|Asn|LEN=7/24|DS=+321|P=chr7:237
ENST00000355870.3|GN=STK31|GI=ENSG00000196335.8|FC=Missense|CP=1453|CF=0|AC=gCC->tCC|RP=485|RC=A|AlaI->S|Ser|LEN=12/24|DS=+37|P=chr7:23
ENST00000355870.3|GN=STK31|GI=ENSG00000196335.8|FC=Missense|CP=1863|CF=2|AC=AAt->AAg|RP=621|RC=N|AsnI->K|LvsI|LEN=15/24|DS=+30|P=chr7:23
ENST00000355870.3|GN=STK31|GI=ENSG00000196335.8|FC=Missense|CP=1868|CF=1|AC=AGt->AtT|RP=623|RC=S|SerI->L|Leu|LEN=15/24|DS=+35|P=chr7:2374
ENST00000181839.4|GN=CDK13|GI=ENSG00000065883.10|FC=Missense|CP=1498|CF=0|AC=aCG->gCG|RP=500|RC=T|ThrI->A|Ala|LEN=2/14|DS=+287|P=chr7:3
ENST00000319357.5|GN=STK17A|GI=ENSG00000164543.5|FC=Missense|CP=378|CF=2|AC=GAa->GAc|RP=126|RC=F|GluI->D|Asp|LEN=2/7|DS=+172|P=chr7:43
ENST00000319357.5|GN=STK17A|GI=ENSG00000164543.5|FC=Missense|CP=1084|CF=0|AC=aAG->gAG|RP=362|RC=K|LvsI->F|Glu|LEN=7/7|DS=+164|P=chr7:43
ENST00000275493.2|GN=EGFR|GI=ENSG00000146648.10|FC=Missense|CP=1562|CF=1|AC=AgG->AaG|RP=521|RC=R|ArgI->K|LvsI|LEN=13/28|DS=+64|P=chr7:5
ENST00000005178.5|GN=PDK4|GI=ENSG00000004799.6|FC=Missense|CP=1002|CF=2|AC=TTg->TtI|RP=334|RC=L|L|LeuI->F|Phe|LEN=10/11|DS=+21|P=chr7:952
ENST00000297293.5|GN=LMTK2|GI=ENSG00000164715.5|FC=Missense|CP=2338|CF=0|AC=tTG->atG|RP=780|RC=L|L|LeuI->M|Met|LEN=11/14|DS=+1190|P=chr7
ENST00000359863.4|GN=TRRAP1|GI=ENSG00000196367.7|FC=Missense|CP=356|CF=1|AC=CgC->CcC|RP=119|RC=R|ArgI->P|Pro|LEN=5/72|DS=+95|P=chr7:984
ENST00000359863.4|GN=TRRAP1|GI=ENSG00000196367.7|FC=Missense|CP=4924|CF=0|AC=gCC->tCC|RP=1642|RC=A|AlaI->S|Ser|LEN=35/72|DS=-87|P=chr7:9
ENST00000318493.6|GN=MET1|GI=ENSG00000105976.9|FC=Missense|CP=1124|CF=1|AC=AaC->AgC|RP=375|RC=N|AsnI->S|Ser|LEN=2/21|DS=+1138|P=chr7:11
ENST00000343526.4|GN=TRIM24|GI=ENSG00000122779.10|FC=Missense|CP=143|CF=1|AC=GcC->GaC|RP=48|RC=A|AlaI->D|Asp|LEN=1/19|DS=-43599|P=chr7
ENST00000275815.3|GN=EPHA1|GI=ENSG00000146904.4|FC=Missense|CP=2698|CF=0|AC=aTG->gTG|RP=900|RC=M|MetI->V|Val|LEN=17/18|DS=+2|P=chr7:14
ENST00000275815.3|GN=EPHA1|GI=ENSG00000146904.4|FC=Missense|CP=479|CF=1|AC=GtG->GcG|RP=160|RC=V|ValI->A|Ala|LEN=4/18|DS=+47|P=chr7:1430
ENST00000520004.1|GN=AC068353.1|GI=ENSG00000182319.5|FC=Missense|CP=3664|CF=0|AC=gGC->aGC|RP=1222|RC=G|GlvI->S|Ser|LEN=6/6|DS=+598|P=chr
ENST00000520004.1|GN=AC068353.1|GI=ENSG00000182319.5|FC=Missense|CP=3331|CF=0|AC=gCG->aCG|RP=1111|RC=A|AlaI->T|Thr|LEN=6/6|DS=+265|P=chr
ENST00000520004.1|GN=AC068353.1|GI=ENSG00000182319.5|FC=Missense|CP=1727|CF=1|AC=IcI->IgtI|RP=576|RC=C|CvsI|LEN=3/6|DS=+1397|P=chr
ENST00000520004.1|GN=AC068353.1|GI=ENSG00000182319.5|FC=Missense|CP=1700|CF=1|AC=CcG->CtG|RP=567|RC=P|ProI->L|Leu|LEN=3/6|DS=+1370|P=chr
ENST00000520004.1|GN=AC068353.1|GI=ENSG00000182319.5|FC=Missense|CP=1205|CF=1|AC=CgG->CaG|RP=402|RC=R|ArgI->Q|Gln|LEN=3/6|DS=+875|P=chr
ENST00000520004.1|GN=AC068353.1|GI=ENSG00000182319.5|FC=Missense|CP=189|CF=2|AC=AGg->AGt|RP=63|RC=R|ArgI->S|Ser|LEN=2/6|DS=+276|P=chr8:8
ENST00000526097.1|GN=BLK1|GI=ENSG00000136573.6|FC=Missense|CP=500|CF=1|AC=GcC->GtC|RP=167|RC=A|AlaI->V|Val|LEN=1/3|DS=-1715|P=chr8:11417
ENST00000397501.1|GN=PTK2B1|GI=ENSG00000120899.12|FC=Missense|CP=2513|CF=1|AC=AaG->AcG|RP=838|RC=K|LvsI->T|Thr|LEN=31/36|DS=+26|P=chr8:7
ENST00000425967.3|GN=EGFR1|GI=ENSG00000077782.14|FC=Missense|CP=419|CF=1|AC=TcG->TtG|RP=140|RC=S|SerI->L|L|LeuI|LEN=4/19|DS=+229|P=chr8:38
ENST00000314191.2|GN=PRKDC1|GI=ENSG00000253729.2|FC=Missense|CP=9590|CF=1|AC=AcC->AgC|RP=3197|RC=T|ThrI->S|Ser|LEN=70/87|DS=+36|P=chr8:8
ENST00000276616.2|GN=PSKH2|GI=ENSG00000147613.4|FC=Missense|CP=526|CF=0|AC=gCC->tCC|RP=176|RC=A|AlaI->S|Ser|LEN=2/3|DS=+341|P=chr8:8706
ENST00000395107.4|GN=MAPK15|GI=ENSG00000181085.10|FC=Missense|CP=298|CF=0|AC=aGC->gGC|RP=100|RC=S|SerI->R|Arg|LEN=5/8|DS=+12|P=chr8:14
ENST00000395108.2|GN=MAPK15|GI=ENSG00000181085.10|FC=Missense|CP=740|CF=1|AC=AGc->AGa|RP=247|RC=R|ArgI->T|Thr|LEN=8/8|DS=+19|P=chr8:14
ENST00000308860.6|GN=ADCK5|GI=ENSG00000173137.6|FC=Missense|CP=511|CF=2|AC=AGa->AGc|RP=17|RC=R|ArgI->S|Ser|LEN=2/15|DS=+39|P=chr8:14559
ENST00000380036.4|GN=TEK1|GI=ENSG00000120156.14|FC=Missense|CP=443|CF=1|AC=AtI->AcT|RP=148|RC=L|IleI->T|Thr|LEN=3/23|DS=+79|P=chr9:2710914
ENST00000380036.4|GN=TEK1|GI=ENSG00000120156.14|FC=Missense|CP=1037|CF=1|AC=CaG->CcG|RP=346|RC=Q|GlnI->P|Pro|LEN=8/23|DS=+7|P=chr9:27109
ENST00000377276.2|GN=PRKACG1|GI=ENSG00000165059.5|FC=Missense|CP=802|CF=0|AC=cAT->gAT|RP=268|RC=H|HisI->D|Asp|LEN=1/1|P=chr9:71627469-7
ENST00000457110.3|GN=TRPM6|GI=ENSG00000119121.15|FC=Missense|CP=4750|CF=0|AC=aAG->AGa|RP=1584|RC=K|LvsI->F|Glu|LEN=27/38|DS=+78|P=chr9
ENST00000375708.3|GN=ROR2|GI=ENSG00000169071.8|FC=Missense|CP=2455|CF=0|AC=gTC->aTC|RP=819|RC=V|ValI->L|Leu|LEN=9/9|DS=+1069|P=chr9:94484
ENST00000375708.3|GN=ROR2|GI=ENSG00000169071.8|FC=Missense|CP=733|CF=0|AC=aCA->gCA|RP=245|RC=T|ThrI->A|Ala|LEN=6/9|DS=+111|P=chr9:94484
ENST00000189978.4|GN=MUSK1|GI=ENSG00000030304.6|FC=Missense|CP=475|CF=0|AC=aGC->gGC|RP=159|RC=S|SerI->G|Glv|LEN=4/14|DS=+117|P=chr9:113
ENST00000189978.4|GN=MUSK1|GI=ENSG00000030304.6|FC=Missense|CP=1257|CF=2|AC=ATg->ATa|RP=419|RC=M|MetI->L|Leu|LEN=9/14|DS=+55|P=chr9:11343
ENST00000318560.5|GN=ABL1|GI=ENSG00000097007.11|FC=Missense|CP=2117|CF=1|AC=GgtI->GtT|RP=706|RC=G|GlvI->V|Val|LEN=11/11|DS=+439|P=chr9:11
ENST00000371957.3|GN=C9orf96|GI=ENSG00000198870.6|FC=Missense|CP=1471|CF=0|AC=aAA->gAA|RP=473|RC=K|LvsI->F|Glu|LEN=14/18|DS=+78|P=chr9:1
ENST00000263125.5|GN=PRKCA1|GI=ENSG00000065675.9|FC=Missense|CP=989|CF=1|AC=CcG->CtG|RP=330|RC=P|ProI->L|Leu|LEN=10/18|DS=+89|P=chr10:6
ENST00000265944.5|GN=MYO3A|GI=ENSG00000095777.10|FC=Missense|CP=1042|CF=0|AC=aTA->gTA|RP=348|RC=L|IleI->V|Val|LEN=11/35|DS=+89|P=chr10:26

ENST00000265944.5|GN=MYO3A|GI=ENSG00000095777.10|FC=Missense|CP=1105|CF=0|AC=gTC->aTC|IRP=369|RC=V|Val|>|Ile|EN=12/35|DS=+52|P=chr10:2|
ENST00000265944.5|GN=MYO3A|GI=ENSG00000095777.10|FC=Missense|CP=3937|CF=0|AC=cGT->aGT|IRP=1313|RC=R|Arg|>|S|Ser|EN=30/35|DS=+539|P=chr10:2|
ENST00000265944.5|GN=MYO3A|GI=ENSG00000095777.10|FC=Missense|CP=4462|CF=0|AC=aAA->gAA|IRP=1488|RC=K|Lys|>|E|Glu|EN=32/35|DS=+24|P=chr10:2|
ENST00000375322.1|GN=MAP3K8|GI=ENSG00000107968.4|FC=Missense|CP=383|CF=1|AC=TAc->TcC|IRP=128|RC=Y|Tyr|>|C|Cys|EN=3/3|DS=+406|P=chr10:3|
ENST00000373935.3|GN=IPMK|GI=ENSG00000151151.5|FC=Missense|CP=1047|CF=2|AC=ATg->ATA|IRP=349|RC=M|Met|>|Ile|EN=6/6|DS=+419|P=chr10:5995|
ENST00000224764.4|GN=BMPRI1A|GI=ENSG00000107779.5|FC=Missense|CP=4|CF=0|AC=cCT->aCT|IRP=2|RC=P|Pro|>|T|Thr|EN=3/13|DS=+156|P=chr10:8851|
ENST00000370631.3|GN=PI4K2A|GI=ENSG00000155252.10|FC=Missense|CP=248|CF=1|AC=GcI->GaT|IRP=83|RC=A|Ala|>|D|Asp|EN=1/9|DS=-995|P=chr10:9|
ENST00000370397.5|GN=CHUK1G|GI=ENSG00000213341.4|FC=Missense|CP=802|CF=0|AC=gTA->aTA|IRP=268|RC=V|Val|>|Ile|EN=9/21|DS=+51|P=chr10:1019480|
ENST00000392870.2|GN=GRK5|GI=ENSG00000198873.8|FC=Missense|CP=911|CF=1|AC=CgI->CaT|IRP=304|RC=R|Arg|>|H|His|EN=9/16|DS=+173|P=chr10:120|
ENST00000369062.3|GN=FGFR2|GI=ENSG00000066468.13|FC=Missense|CP=557|CF=1|AC=AtG->AcG|IRP=186|RC=M|Met|>|T|Thr|EN=5/19|DS=+103|P=chr10:10|
ENST00000527911.1|GN=DGKZ|GI=ENSG00000149091.10|FC=Missense|CP=58|CF=0|AC=cCC->aCC|IRP=20|RC=A|Ala|>|T|Thr|EN=1/31|DS=-19574|P=chr11:46|
ENST00000342711.5|GN=CDCA2BP|GI=ENSG00000171219.8|FC=Missense|CP=3709|CF=0|AC=cGG->tGG|IRP=1237|RC=R|Arg|>|W|Trp|EN=30/37|DS=+342|P=chr11:108|
ENST00000278616.4|GN=ATM|GI=ENSG00000149311.9|FC=Missense|CP=4138|CF=0|AC=cAT->tAT|IRP=1380|RC=H|His|>|Y|Tyr|EN=28/63|DS=+29|P=chr11:1108|
ENST00000278616.4|GN=ATM|GI=ENSG00000149311.9|FC=Missense|CP=5948|CF=1|AC=AaT->AgT|IRP=1983|RC=N|Asn|>|S|Ser|EN=40/63|DS=+30|P=chr11:1108|
ENST00000304987.3|GN=SIK2|GI=ENSG00000170145.4|FC=Missense|CP=2240|CF=1|AC=CcA->CaA|IRP=747|RC=P|Pro|>|Q|Gln|EN=15/15|DS=+93|P=chr11:111|
ENST00000303941.3|GN=ANKK1|GI=ENSG00000170209.4|FC=Missense|CP=715|CF=0|AC=gCG->aCG|IRP=239|RC=A|Ala|>|T|Thr|EN=5/8|DS=+33|P=chr11:1132|
ENST00000303941.3|GN=ANKK1|GI=ENSG00000170209.4|FC=Missense|CP=1324|CF=0|AC=gGC->cGC|IRP=442|RC=G|Gly|>|R|Arg|EN=8/8|DS=+330|P=chr11:1132|
ENST00000303941.3|GN=ANKK1|GI=ENSG00000170209.4|FC=Missense|CP=2137|CF=0|AC=gAG->aAG|IRP=713|RC=E|Glu|>|K|Lys|EN=8/8|DS=+1143|P=chr11:1132|
ENST00000427383.2|GN=CHK1|GI=ENSG00000149554.7|FC=Missense|CP=1459|CF=0|AC=aTT->gTT|IRP=487|RC=I|Ile|>|V|Val|EN=12/12|DS=+76|P=chr11:125|
ENST00000530271.2|GN=WNK1|GI=ENSG00000060237.10|FC=Missense|CP=4660|CF=0|AC=aCC->tCC|IRP=1554|RC=I|Ile|>|P|Pro|EN=15/30|DS=+55|P=chr12:8|
ENST00000530271.2|GN=WNK1|GI=ENSG00000060237.10|FC=Missense|CP=6011|CF=1|AC=ITg->ITcC|IRP=2004|RC=C|Cys|>|S|Ser|EN=21/30|DS=+673|P=chr12:8|
ENST00000530271.2|GN=WNK1|GI=ENSG00000060237.10|FC=Missense|CP=6918|CF=2|AC=ATg->ATt|IRP=2306|RC=M|Met|>|Ile|EN=23/30|DS=+60|P=chr12:8|
ENST00000530271.2|GN=WNK1|GI=ENSG00000060237.10|FC=Missense|CP=7981|CF=0|AC=cCC->tCC|IRP=2661|RC=P|Pro|>|S|Ser|EN=28/30|DS=+39|P=chr12:8|
ENST00000075503.3|GN=STYK1|GI=ENSG00000060140.4|FC=Missense|CP=610|CF=0|AC=aGC->gGC|IRP=204|RC=S|Ser|>|G|Gly|EN=6/11|DS=+159|P=chr12:10|
ENST00000261170.3|GN=GUCY2C|GI=ENSG00000070019.3|FC=Missense|CP=843|CF=2|AC=ITt->TTg|IRP=281|RC=F|Phe|>|L|Leu|EN=7/27|DS=+13|P=chr12:14|
ENST00000538779.1|GN=PIK3C2G|GI=ENSG00000139144.5|FC=Missense|CP=2855|CF=1|AC=CcG->CtG|IRP=952|RC=P|Pro|>|L|Leu|EN=20/32|DS=+62|P=chr12:14|
ENST00000538779.1|GN=PIK3C2G|GI=ENSG00000139144.5|FC=Missense|CP=3903|CF=2|AC=GAg->GAT|IRP=1301|RC=E|Glu|>|D|Asp|EN=28/32|DS=+11|P=chr12:14|
ENST00000298910.7|GN=LRRK2|GI=ENSG00000188906.9|FC=Missense|CP=149|CF=1|AC=CgC->CaC|IRP=501|RC=R|Arg|>|H|His|EN=1/51|DS=-275|P=chr12:406|
ENST00000298910.7|GN=LRRK2|GI=ENSG00000188906.9|FC=Missense|CP=1653|CF=2|AC=AAc->AAg|IRP=551|RC=N|Asn|>|K|Lys|EN=14/51|DS=+110|P=chr12:406|
ENST00000298910.7|GN=LRRK2|GI=ENSG00000188906.9|FC=Missense|CP=4193|CF=1|AC=CgT->CaT|IRP=1398|RC=R|Arg|>|H|His|EN=30/51|DS=+41|P=chr12:406|
ENST00000380518.3|GN=COL2A1|GI=ENSG00000139219.11|FC=Missense|CP=4213|CF=0|AC=gGC->aGC|IRP=1405|RC=G|Gly|>|S|Ser|EN=53/54|DS=+139|P=chr12:406|
ENST00000419526.2|GN=ACVR1|GI=ENSG00000139567.6|FC=Missense|CP=5|CF=1|AC=GcI->GtI|IRP=2|RC=A|Ala|>|V|Val|EN=1/6|DS=-2002|P=chr12:52306|
ENST00000431731.2|GN=MBD6|GI=ENSG00000166987.8|FC=Missense|CP=778|CF=0|AC=cTC->gTC|IRP=260|RC=L|Leu|>|V|Val|EN=6/15|DS=+399|P=chr12:579|
ENST00000354947.4|GN=PIP4K2C|GI=ENSG00000166908.11|FC=Missense|CP=899|CF=1|AC=GcG->GgG|IRP=300|RC=A|Ala|>|G|Gly|EN=8/10|DS=+86|P=chr12:579|
ENST00000261233.4|GN=IRAK3|GI=ENSG00000090376.4|FC=Missense|CP=439|CF=0|AC=aTA->gTA|IRP=147|RC=I|Ile|>|V|Val|EN=5/12|DS=+3|P=chr12:665826|
ENST00000261402.1|GN=NUAK1|GI=ENSG00000074590.7|FC=Missense|CP=1628|CF=1|AC=CcT->CgT|IRP=543|RC=P|Pro|>|R|Arg|EN=7/7|DS=+796|P=chr12:10|
ENST00000392533.3|GN=IAOK3|GI=ENSG00000135090.8|FC=Missense|CP=140|CF=1|AC=AgI->AaT|IRP=47|RC=S|Ser|>|N|Asn|EN=4/21|DS=+20|P=chr12:118|
ENST00000324774.5|GN=CAMKK2|GI=ENSG00000110931.12|FC=Missense|CP=1087|CF=0|AC=cGC->tGC|IRP=363|RC=R|Arg|>|C|Cys|EN=10/17|DS=+180|P=chr12:118|
ENST00000321867.3|GN=ULK1|GI=ENSG00000177169.3|FC=Missense|CP=2446|CF=0|AC=aCT->gCT|IRP=816|RC=T|Thr|>|A|Ala|EN=23/28|DS=+120|P=chr12:118|
ENST00000542419.1|GN=ULK1|GI=ENSG00000177169.3|FC=Missense|CP=406|CF=0|AC=gTA->cTA|IRP=136|RC=V|Val|>|L|Leu|EN=3/3|DS=+381|P=chr12:1324|
ENST00000382592.4|GN=LATS2|GI=ENSG00000150457.6|FC=Missense|CP=1087|CF=0|AC=gGC->aGC|IRP=363|RC=G|Gly|>|S|Ser|EN=4/8|DS=+612|P=chr13:21|
ENST00000382592.4|GN=LATS2|GI=ENSG00000150457.6|FC=Missense|CP=971|CF=1|AC=GcC->GtG|IRP=324|RC=A|Ala|>|V|Val|EN=4/8|DS=+496|P=chr13:21|
ENST00000380982.4|GN=FLN3|GI=ENSG00000122025.10|FC=Missense|CP=680|CF=1|AC=AcG->ATG|IRP=227|RC=T|Thr|>|M|Met|EN=6/24|DS=+66|P=chr13:285|
ENST00000544455.1|GN=BRCA2|GI=ENSG00000139618.9|FC=Missense|CP=865|CF=0|AC=aAT->cAT|IRP=289|RC=N|Asn|>|H|His|EN=10/28|DS=+72|P=chr13:32|
ENST00000544455.1|GN=BRCA2|GI=ENSG00000139618.9|FC=Missense|CP=2971|CF=0|AC=aAC->gAC|IRP=991|RC=N|Asn|>|D|Asp|EN=11/28|DS=+1062|P=chr13:32|
ENST00000544455.1|GN=BRCA2|GI=ENSG00000139618.9|FC=Missense|CP=7397|CF=1|AC=GtA->GcA|IRP=2466|RC=V|Val|>|A|Ala|EN=14/28|DS=+390|P=chr13:32|
ENST00000379800.3|GN=CSNK1A1|GI=ENSG00000180138.6|FC=Missense|CP=126|CF=2|AC=GAc->GAa|IRP=42|RC=D|Asp|>|E|Glu|EN=1/11|P=chr13:3767398|
ENST00000375856.3|GN=IRS2|GI=ENSG00000185950.7|FC=Missense|CP=3733|CF=0|AC=gCC->tCC|IRP=1245|RC=A|Ala|>|S|Ser|EN=1/2|DS=-26013|P=chr13:1|
ENST00000375856.3|GN=IRS2|GI=ENSG00000185950.7|FC=Missense|CP=3170|CF=1|AC=GcC->GaC|IRP=1057|RC=G|Gly|>|D|Asp|EN=1/2|DS=-26576|P=chr13:1|
ENST00000375856.3|GN=IRS2|GI=ENSG00000185950.7|FC=Missense|CP=599|CF=1|AC=GtG->GgG|IRP=200|RC=V|Val|>|G|Gly|EN=1/2|DS=-29147|P=chr13:1|
ENST00000216274.4|GN=PIPK3|GI=ENSG00000129465.10|FC=Missense|CP=22|CF=0|AC=cCC->aCC|IRP=8|RC=P|Pro|>|T|Thr|EN=2/10|DS=+21|P=chr14:248052|
ENST00000358473.1|GN=ATP5S1|GI=ENSG00000125375.9|FC=Missense|CP=490|CF=0|AC=gGA->aGA|IRP=164|RC=G|Gly|>|R|Arg|EN=5/6|DS=+4|P=chr14:50785|
ENST00000395834.1|GN=CDKL1|GI=ENSG00000100490.5|FC=Missense|CP=823|CF=0|AC=cAA->gAA|IRP=275|RC=Q|Gln|>|E|Glu|EN=8/9|DS=+25|P=chr14:5079|
ENST00000013125.3|GN=MAP4K5|GI=ENSG00000012983.5|FC=Missense|CP=1898|CF=1|AC=AcG->AtG|IRP=633|RC=T|Thr|>|M|Met|EN=26/32|DS=+16|P=chr14:5079|
ENST00000332981.4|GN=PRKCH1G|GI=ENSG00000027075.8|FC=Missense|CP=1120|CF=0|AC=gTA->aTA|IRP=374|RC=V|Val|>|Ile|EN=9/14|DS=+16|P=chr14:6178|

ENST00000358328.4|GN=RPS6K1|GI=ENSG00000198208.5|FC=Missense|CP=362|CF=1|AC=CcG->CtG|RP=121|RC=PIPro|>|L|Leu|EN=3/11|DS=+97|P=chr14:75
 ENST00000358328.4|GN=RPS6K1|GI=ENSG00000198208.5|FC=Missense|CP=62|CF=1|AC=CgA->CaA|RP=21|RC=RIArg|>Q|Gln|EN=2/11|DS=+82|P=chr14:75
 ENST00000238616.4|GN=NEK9|GI=ENSG00000119638.6|FC=Missense|CP=1286|CF=1|AC=CgT->CaT|RP=429|RC=RIArg|>H|His|EN=11/22|DS=+104|P=chr14:75
 ENST00000311458.6|GN=TPK1|GI=ENSG00000100605.9|FC=Missense|CP=1066|CF=0|AC=tGT->cGT|RP=356|RC=CI Cvs|>R|Arg|EN=13/13|DS=+55|P=chr14:9
 ENST00000361847.2|GN=RAGE|GI=ENSG00000080823.14|FC=Missense|CP=1193|CF=1|AC=CaG->CgG|RP=398|RC=Q|Gln|>R|Arg|EN=12/12|DS=+11|P=chr14:9
 ENST00000335102.4|GN=MARK3|GI=ENSG00000075413.10|FC=Missense|CP=1298|CF=1|AC=TtT->TcT|RP=433|RC=FI Phe|>S|Ser|EN=13/19|DS=+119|P=chr14:9
 ENST00000263791.4|GN=IF2AK4|GI=ENSG00000128829.5|FC=Missense|CP=1667|CF=1|AC=GaA->GgA|RP=556|RC=FI Gln|>G|Gly|EN=11/39|DS=+7|P=chr15:4
 ENST00000412359.2|GN=UBI1B|GI=ENSG00000156970.6|FC=Missense|CP=1088|CF=1|AC=CgA->CaA|RP=363|RC=RIArg|>Q|Gln|EN=8/23|DS=+80|P=chr15:4
 ENST00000441369.1|GN=PAK6|GI=ENSG00000137843.6|FC=Missense|CP=1010|CF=1|AC=CcG->CtG|RP=337|RC=PIPro|>|L|Leu|EN=6/11|DS=+152|P=chr15:4
 ENST00000267890.5|GN=TBK2|GI=ENSG00000128881.10|FC=Missense|CP=23|CF=1|AC=CtG->CcG|RP=8|RC=|L|Leu|>P|Pro|EN=2/15|DS=+90|P=chr15:4303
 ENST00000418051.2|GN=ULK3|GI=ENSG00000140474.6|FC=Missense|CP=1367|CF=1|AC=AaG->AgG|RP=456|RC=KI Lys|>R|Arg|EN=14/17|DS=+47|P=chr15:75
 ENST00000312493.4|GN=AC087465.1|GI=ENSG00000173517.4|FC=Missense|CP=3212|CF=1|AC=AgG->AaG|RP=1071|RC=RIArg|>K|Lys|EN=3/5|DS=+75|P=chr15:75
 ENST00000258888.5|GN=ALPK3|GI=ENSG00000136383.5|FC=Missense|CP=1241|CF=1|AC=ActT->AgT|RP=414|RC=TI Thr|>S|Ser|EN=5/14|DS=+213|P=chr15:8
 ENST00000258888.5|GN=ALPK3|GI=ENSG00000136383.5|FC=Missense|CP=1736|CF=1|AC=GgG->GaG|RP=579|RC=GI Gly|>FI Gln|EN=5/14|DS=+708|P=chr15:8
 ENST00000258888.5|GN=ALPK3|GI=ENSG00000136383.5|FC=Missense|CP=3896|CF=1|AC=CcT->CtT|RP=1299|RC=PIPro|>|L|Leu|EN=6/14|DS=-1215|P=chr15:8
 ENST00000258888.5|GN=ALPK3|GI=ENSG00000136383.5|FC=Missense|CP=4865|CF=1|AC=CtT->CcT|RP=1622|RC=|L|Leu|>P|Pro|EN=10/14|DS=+130|P=chr15:8
 ENST00000328850.3|GN=FEF3|GI=ENSG00000182511.6|FC=Missense|CP=1952|CF=1|AC=CcG->GgG|RP=651|RC=FI Gln|>G|Gly|EN=16/19|DS=+311|P=chr15:914
 ENST00000268035.6|GN=GF1R|GI=ENSG00000140443.8|FC=Missense|CP=199|CF=0|AC=gCC->tCC|RP=67|RC=AI Ala|>S|Ser|EN=2/21|DS=+105|P=chr15:9919
 ENST00000388948.3|GN=LRRK1|GI=ENSG00000154237.7|FC=Missense|CP=5813|CF=1|AC=GgC->GaC|RP=1938|RC=GI Gly|>D|Asp|EN=33/34|DS=+45|P=chr15:101
 ENST00000542170.1|GN=LRRK1|GI=ENSG00000154237.7|FC=Missense|CP=1475|CF=1|AC=CcG->GaG|RP=492|RC=AI Ala|>FI Gln|EN=8/9|DS=+41|P=chr15:101
 ENST00000263026.4|GN=FEF2K|GI=ENSG00000103319.6|FC=Missense|CP=1082|CF=1|AC=CaA->CgA|RP=361|RC=Q|Gln|>R|Arg|EN=10/18|DS=+53|P=chr16:2
 ENST00000261584.3|GN=PALB2|GI=ENSG00000083093.4|FC=Missense|CP=1676|CF=1|AC=CaA->CgA|RP=559|RC=Q|Gln|>R|Arg|EN=4/13|DS=+1465|P=chr16:2
 ENST00000300093.4|GN=PIK1|GI=ENSG00000166851.7|FC=Missense|CP=148|CF=0|AC=cGG->tGG|RP=50|RC=RIArg|>W|Tyr|EN=1/10|DS=-1004|P=chr16:236
 ENST00000256797.3|GN=ERN2|GI=ENSG00000134398.7|FC=Missense|CP=1604|CF=1|AC=AgC->AcC|RP=535|RC=SI Ser|>T|Thr|EN=13/22|DS=+101|P=chr16:2
 ENST00000394809.3|GN=MYLK3|GI=ENSG00000140795.7|FC=Missense|CP=2127|CF=2|AC=TtG->TtT|RP=709|RC=|L|Leu|>FI Phe|EN=11/13|DS=+13|P=chr16:4
 ENST00000394809.3|GN=MYLK3|GI=ENSG00000140795.7|FC=Missense|CP=538|CF=0|AC=gTG->tTG|RP=180|RC=VI Val|>|L|Leu|EN=2/13|DS=+61|P=chr16:467
 ENST00000429102.1|GN=CDH3|GI=ENSG00000062038.7|FC=Missense|CP=2334|CF=2|AC=AGa->AGc|RP=778|RC=RIArg|>S|Ser|EN=16/16|DS=+54|P=chr16:68
 ENST00000325418.4|GN=GS2|GI=ENSG00000177602.4|FC=Missense|CP=244|CF=0|AC=cGT->tGT|RP=82|RC=RIArg|>C|Cys|EN=1/11|P=chr17:3627211-36300
 ENST00000325418.4|GN=GS2|GI=ENSG00000177602.4|FC=Missense|CP=611|CF=1|AC=GgC->GaC|RP=204|RC=GI Gly|>D|Asp|EN=1/11|P=chr17:3627211-363
 ENST00000325418.4|GN=GS2|GI=ENSG00000177602.4|FC=Missense|CP=983|CF=1|AC=AtA->AcA|RP=328|RC=|I|Ile|>T|Thr|EN=1/11|P=chr17:3627211-36300
 ENST00000325418.4|GN=GS2|GI=ENSG00000177602.4|FC=Missense|CP=1133|CF=1|AC=GtC->GcC|RP=378|RC=VI Val|>AI Ala|EN=1/11|P=chr17:3627211-363
 ENST00000381771.2|GN=CAMKK1|GI=ENSG00000004660.9|FC=Missense|CP=1238|CF=1|AC=GaG->GgG|RP=413|RC=FI Gln|>G|Gly|EN=13/17|DS=+74|P=chr17:3
 ENST00000355280.5|GN=MINK1|GI=ENSG00000141503.9|FC=Missense|CP=2312|CF=1|AC=GtC->GcC|RP=771|RC=VI Val|>AI Ala|EN=20/32|DS=+11|P=chr17:474
 ENST00000355280.5|GN=MINK1|GI=ENSG00000141503.9|FC=Missense|CP=2324|CF=1|AC=CcG->CtG|RP=775|RC=PIPro|>|L|Leu|EN=20/32|DS=+13|P=chr17:4
 ENST00000355280.5|GN=MINK1|GI=ENSG00000141503.9|FC=Missense|CP=2587|CF=0|AC=gTC->aTC|RP=863|RC=VI Val|>|I|Ile|EN=22/32|DS=+23|P=chr17:473
 ENST00000311668.2|GN=TNK1|GI=ENSG00000174292.6|FC=Missense|CP=1777|CF=0|AC=gTG->aTG|RP=593|RC=VI Val|>M|Met|EN=12/13|DS=+11|P=chr17:728
 ENST00000269305.4|GN=TP53|GI=ENSG00000141510.8|FC=Missense|CP=215|CF=1|AC=CcC->CgC|RP=72|RC=PIPro|>R|Arg|EN=4/11|DS=+119|P=chr17:7571
 ENST00000330494.7|GN=CHD3|GI=ENSG00000170004.10|FC=Missense|CP=8|CF=1|AC=GcG->GtG|RP=3|RC=AI Ala|>VI Val|EN=1/40|DS=-656|P=chr17:779216
 ENST000003380358.4|GN=CHD3|GI=ENSG00000170004.10|FC=Missense|CP=877|CF=0|AC=aTA->cTA|RP=293|RC=|I|Ile|>|L|Leu|EN=5/40|DS=+191|P=chr17:778
 ENST000003380358.4|GN=CHD3|GI=ENSG00000170004.10|FC=Missense|CP=886|CF=0|AC=tCC->cCC|RP=296|RC=SI Ser|>P|Pro|EN=5/40|DS=+200|P=chr17:77
 ENST000003380358.4|GN=CHD3|GI=ENSG00000170004.10|FC=Missense|CP=898|CF=0|AC=gCC->cCC|RP=300|RC=AI Ala|>P|Pro|EN=5/40|DS=+212|P=chr17:77
 ENST00000316199.5|GN=AURKB|GI=ENSG00000178999.7|FC=Missense|CP=893|CF=1|AC=AtC->AcC|RP=298|RC=M|Met|>T|Thr|EN=9/9|DS=+32|P=chr17:810
 ENST00000447110.1|GN=PIK3R5|GI=ENSG00000141506.8|FC=Nonsense|CP=2017|CF=0|AC=cAA->tAA|RP=673|RC=Q|Gln|>S|Ser|EN=13/19|DS=+112|P=chr17:8
 ENST00000308406.5|GN=MAPK7|GI=ENSG00000166484.12|FC=Missense|CP=2089|CF=0|AC=gGG->aGG|RP=697|RC=GI Gly|>R|Arg|EN=5/7|DS=-42|P=chr17:7
 ENST00000319524.6|GN=KSR1|GI=ENSG00000141068.8|FC=Missense|CP=665|CF=1|AC=GcC->GtC|RP=222|RC=AI Ala|>VI Val|EN=4/21|DS=+145|P=chr17:257
 ENST00000269571.3|GN=ERBB2|GI=ENSG00000141736.7|FC=Missense|CP=1963|CF=0|AC=aTC->tTC|RP=655|RC=|I|Ile|>VI Val|EN=17/27|DS=+17|P=chr17:378
 ENST00000269571.3|GN=ERBB2|GI=ENSG00000141736.7|FC=Missense|CP=2584|CF=0|AC=aCA->gCA|RP=862|RC=TI Thr|>AI Ala|EN=21/27|DS=+91|P=chr17:3
 ENST00000269571.3|GN=ERBB2|GI=ENSG00000141736.7|FC=Missense|CP=3508|CF=0|AC=cCC->gCC|RP=1170|RC=PIPro|>AI Ala|EN=27/27|DS=+96|P=chr17:3
 ENST00000471181.1|GN=BRCA1|GI=ENSG0000012048.12|FC=Missense|CP=4903|CF=0|AC=aGT->gGT|RP=1635|RC=SI Ser|>G|Gly|EN=16/24|DS=+162|P=chr17:3
 ENST00000471181.1|GN=BRCA1|GI=ENSG0000012048.12|FC=Missense|CP=3548|CF=1|AC=AaA->AgA|RP=1183|RC=KI Lys|>R|Arg|EN=10/24|DS=-951|P=chr17:3
 ENST00000471181.1|GN=BRCA1|GI=ENSG0000012048.12|FC=Missense|CP=3113|CF=1|AC=GaA->GgA|RP=1088|RC=FI Gln|>G|Gly|EN=10/24|DS=-1386|P=chr17:3
 ENST00000471181.1|GN=BRCA1|GI=ENSG0000012048.12|FC=Missense|CP=2612|CF=1|AC=CcG->CtG|RP=871|RC=PIPro|>|L|Leu|EN=10/24|DS=-1887|P=chr17:3
 ENST00000471181.1|GN=BRCA1|GI=ENSG0000012048.12|FC=Missense|CP=1855|CF=0|AC=cAT->aAT|RP=619|RC=H|His|>N|Asn|EN=10/24|DS=+1185|P=chr17:3
 ENST00000225964.5|GN=COL1A1|GI=ENSG00000108821.7|FC=Missense|CP=3223|CF=0|AC=aCC->gCC|RP=1075|RC=TI Thr|>AI Ala|EN=44/51|DS=+16|P=chr17:3
 ENST00000323456.4|GN=MTMR4|GI=ENSG00000108389.4|FC=Missense|CP=838|CF=0|AC=aGC->gGC|RP=280|RC=SI Ser|>G|Gly|EN=9/19|DS=+173|P=chr17:5

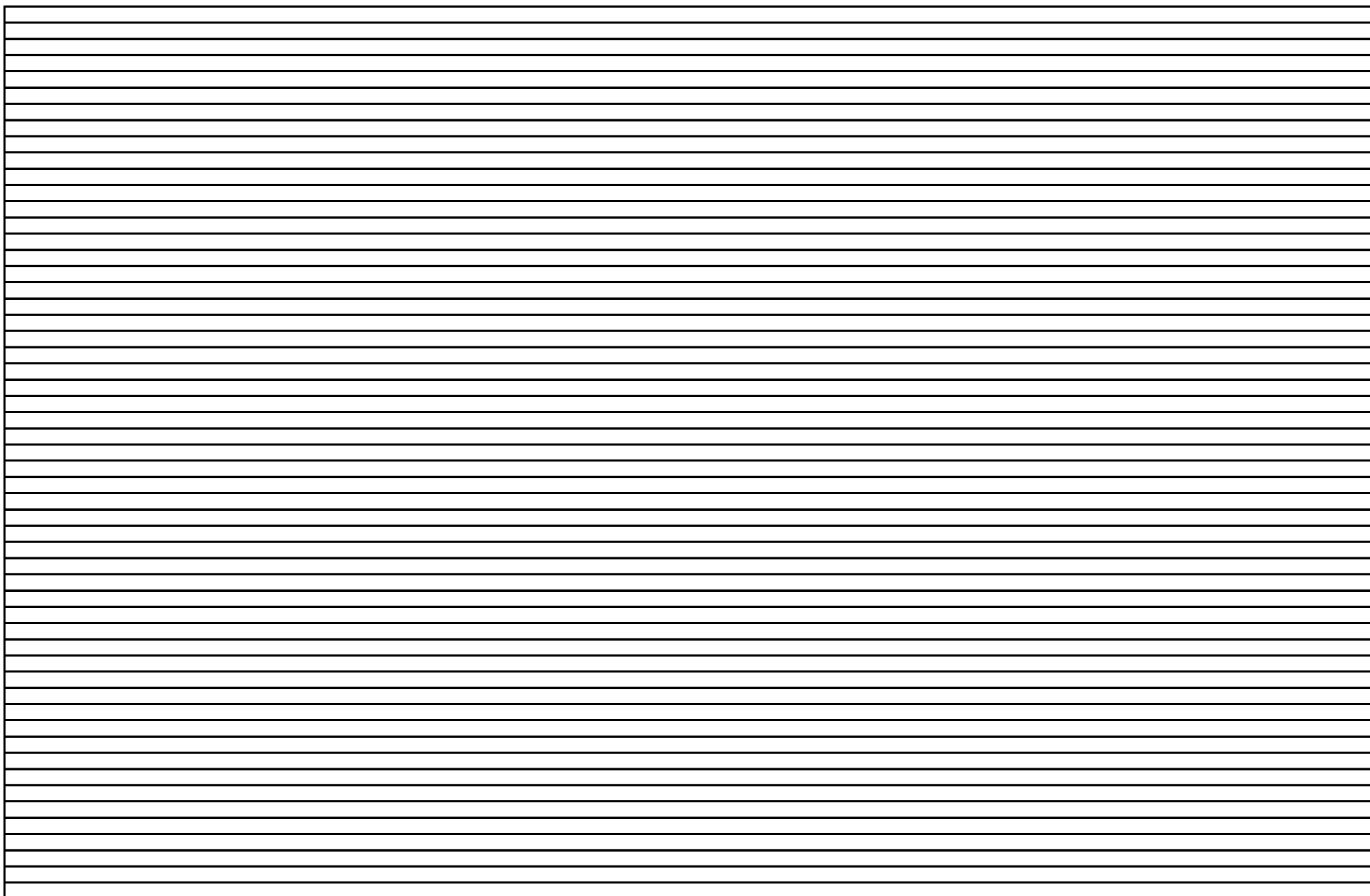
ENST00000240361.7|GN=TEX14|GI=ENSG00000121101.10|FC=Missense|CP=3263|CF=1|AC=GgT->GaT|RP=1088|RC=G|Glv|->D|Asp||EN=20/33|DS=+74|P=chr1
 ENST00000413366.2|GN=PRKCA|GI=ENSG00000154229.6|FC=Missense|CP=1702|CF=0|AC=gTC->aTC|RP=568|RC=V|Val|->I|Ile||EN=15/17|DS=+97|P=chr17:64
 ENST00000323374.3|GN=SPHK1|GI=ENSG00000176170.7|FC=Missense|CP=100|CF=0|AC=gCA->aCA|RP=34|RC=A|Ala|->T|Thr||EN=2/6|DS=+36|P=chr17:74380
 ENST00000326724.4|GN=AATK|GI=ENSG00000181409.6|FC=Missense|CP=3797|CF=1|AC=TtC->TcC|RP=1266|RC=F|Phe|->S|Ser||EN=12/14|DS=+62|P=chr17:7
 ENST00000326724.4|GN=AATK|GI=ENSG00000181409.6|FC=Missense|CP=2107|CF=0|AC=gGC->gC|RP=703|RC=G|Glv|->C|Cys||EN=11/14|DS=+995|P=chr17:7
 ENST00000399799.1|GN=ROCK1|GI=ENSG00000067900.4|FC=Missense|CP=3649|CF=0|AC=cAA->gAA|RP=1217|RC=Q|Gln|->F|Gln||EN=31/33|DS=+58|P=chr18
 ENST00000400384.1|GN=MAPK4|GI=ENSG00000141639.6|FC=Missense|CP=112|CF=0|AC=gTG->aTG|RP=38|RC=V|Val|->M|Met||EN=2/6|DS=+982|P=chr18:480
 ENST00000398339.1|GN=TCF4|GI=ENSG00000196628.6|FC=Missense|CP=28|CF=0|AC=gCA->cCA|RP=10|RC=A|Ala|->P|Pro||EN=1/21|DS=-4482|P=chr18:5289
 ENST00000361673.3|GN=ALPK2|GI=ENSG00000198796.5|FC=Missense|CP=6469|CF=0|AC=aTA->gTA|RP=2157|RC=I|Ile|->V|Val||EN=13/13|DS=+173|P=chr18:5
 ENST00000361673.3|GN=ALPK2|GI=ENSG00000198796.5|FC=Missense|CP=3521|CF=1|AC=CaC->CcC|RP=1174|RC=H|His|->P|Pro||EN=5/13|DS=+1559|P=chr18
 ENST00000361673.3|GN=ALPK2|GI=ENSG00000198796.5|FC=Missense|CP=3169|CF=0|AC=tTG->gTG|RP=1057|RC=L|Leu|->V|Val||EN=5/13|DS=+1207|P=chr18
 ENST00000361673.3|GN=ALPK2|GI=ENSG00000198796.5|FC=Missense|CP=2672|CF=1|AC=AcC->AtC|RP=891|RC=T|Thr|->I|Ile||EN=5/13|DS=+710|P=chr18:561
 ENST00000361673.3|GN=ALPK2|GI=ENSG00000198796.5|FC=Missense|CP=51CF=1|AC=AaA->AcA|RP=2|RC=K|Lys|->T|Thr||EN=2/13|DS=+25|P=chr18:5614847
 ENST00000256858.5|GN=KIAA1468|GI=ENSG00000134444.8|FC=Missense|CP=250|CF=0|AC=gGC->tGC|RP=84|RC=G|Glv|->C|Cys||EN=1/30|DS=-23398|P=chr18
 ENST00000256858.5|GN=KIAA1468|GI=ENSG00000134444.8|FC=Missense|CP=1735|CF=0|AC=cAA->aAA|RP=579|RC=Q|Gln|->K|Lys||EN=12/30|DS=+2|P=chr18
 ENST00000250896.3|GN=MKNK2|GI=ENSG00000099875.8|FC=Missense|CP=208|CF=0|AC=cGG->tGG|RP=70|RC=R|Arg|->W|Trp||EN=4/14|DS=+69|P=chr19:203
 ENST00000525621.1|GN=TYK2|GI=ENSG00000105397.7|FC=Missense|CP=1561|CF=0|AC=cGG->tGG|RP=521|RC=R|Arg|->W|Trp||EN=11/25|DS=+85|P=chr19:10
 ENST00000525621.1|GN=TYK2|GI=ENSG00000105397.7|FC=Missense|CP=1084|CF=0|AC=gTC->tTC|RP=362|RC=V|Val|->F|Phe||EN=8/25|DS=+73|P=chr19:104
 ENST00000342216.4|GN=PKN1|GI=ENSG00000123143.7|FC=Missense|CP=1681|CF=0|AC=cTC->aTC|RP=561|RC=L|Leu|->I|Ile||EN=12/22|DS=+26|P=chr19:145
 ENST00000342216.4|GN=PKN1|GI=ENSG00000123143.7|FC=Missense|CP=2719|CF=0|AC=gTC->aTC|RP=907|RC=V|Val|->I|Ile||EN=22/22|DS=+76|P=chr19:145
 ENST00000458235.1|GN=JAK3|GI=ENSG00000105639.13|FC=Missense|CP=1503|CF=2|AC=CaG->CaT|RP=501|RC=Q|Gln|->H|His||EN=11/24|DS=+62|P=chr19:1
 ENST00000262811.4|GN=MAST3|GI=ENSG00000099308.4|FC=Missense|CP=2581|CF=0|AC=gGC->aGC|RP=861|RC=G|Glv|->S|Ser||EN=22/27|DS=+84|P=chr19:1
 ENST00000222254.6|GN=PIK3R2|GI=ENSG00000105647.8|FC=Missense|CP=937|CF=0|AC=tCC->cCC|RP=313|RC=S|Ser|->P|Pro||EN=8/16|DS=+36|P=chr19:18
 ENST00000252530.4|GN=FAM98C|GI=ENSG00000130244.7|FC=Missense|CP=719|CF=1|AC=AcA->AaA|RP=240|RC=T|Thr|->K|Lys||EN=6/8|DS=+86|P=chr19:38
 ENST00000358335.4|GN=AKT2|GI=ENSG00000105221.9|FC=Missense|CP=407|CF=1|AC=AtT->AcT|RP=136|RC=I|Ile|->T|Thr||EN=6/7|DS=+84|P=chr19:4073824
 ENST00000324464.3|GN=ADCK4|GI=ENSG00000123815.6|FC=Missense|CP=521|CF=1|AC=CaC->CcC|RP=174|RC=H|His|->R|Arg||EN=7/15|DS=+31|P=chr19:41
 ENST00000301178.3|GN=AXIL|GI=ENSG00000167601.6|FC=Missense|CP=796|CF=0|AC=aAC->gAC|RP=266|RC=N|Asn|->D|Asp||EN=7/20|DS=+13|P=chr19:4172
 ENST00000342805.5|GN=DMPK|GI=ENSG00000104936.9|FC=Missense|CP=1345|CF=0|AC=cTG->gTG|RP=449|RC=L|Leu|->V|Val||EN=11/17|DS=+35|P=chr19:4
 ENST00000291281.3|GN=PRKD2|GI=ENSG00000105287.6|FC=Missense|CP=2504|CF=1|AC=GtG->GcG|RP=835|RC=V|Val|->A|Ala||EN=18/18|DS=+80|P=chr19:4
 ENST00000291281.3|GN=PRKD2|GI=ENSG00000105287.6|FC=Missense|CP=1733|CF=1|AC=GcA->GaA|RP=578|RC=A|Ala|->F|Gln||EN=13/18|DS=+31|P=chr19:4
 ENST00000413299.1|GN=SBK2|GI=ENSG00000187550.4|FC=Missense|CP=892|CF=0|AC=gCC->cCC|RP=298|RC=A|Ala|->P|Pro||EN=4/4|DS=+436|P=chr19:5604
 ENST00000413299.1|GN=SBK2|GI=ENSG00000187550.4|FC=Missense|CP=214|CF=0|AC=tGC->cGC|RP=72|RC=C|Cys|->R|Arg||EN=2/4|DS=+216|P=chr19:5604
 ENST00000413299.1|GN=SBK2|GI=ENSG00000187550.4|FC=Missense|CP=118|CF=0|AC=cGC->aGC|RP=40|RC=R|Arg|->S|Ser||EN=2/4|DS=+120|P=chr19:5604
 ENST00000378429.3|GN=PAK7|GI=ENSG00000101349.11|FC=Missense|CP=1532|CF=1|AC=AgC->AaC|RP=511|RC=S|Ser|->N|Asn||EN=7/11|DS=+50|P=chr20:9
 ENST00000375994.2|GN=MYLK2|GI=ENSG00000101306.6|FC=Missense|CP=50|CF=1|AC=AcA->AaA|RP=17|RC=T|Thr|->K|Lys||EN=1/12|DS=-496|P=chr20:3040
 ENST00000395913.3|GN=AURKA|GI=ENSG00000087586.13|FC=Missense|CP=169|CF=0|AC=aTT->gTT|RP=57|RC=I|Ile|->V|Val||EN=3/9|DS=+127|P=chr20:54944
 ENST00000395913.3|GN=AURKA|GI=ENSG00000087586.13|FC=Missense|CP=91|CF=0|AC=tTT->aTT|RP=31|RC=F|Phe|->I|Ile||EN=3/9|DS=+49|P=chr20:5494444
 ENST00000270112.2|GN=HUNK|GI=ENSG00000142149.4|FC=Missense|CP=1771|CF=0|AC=cGC->tGC|RP=591|RC=R|Arg|->C|Cys||EN=11/11|DS=+285|P=chr21:1
 ENST00000352483.2|GN=RIPK4|GI=ENSG00000183421.6|FC=Missense|CP=2140|CF=0|AC=aTG->gTG|RP=714|RC=M|Met|->V|Val||EN=9/9|DS=+801|P=chr21:43
 ENST00000270162.6|GN=SIK1|GI=ENSG00000142178.7|FC=Missense|CP=1844|CF=1|AC=CcC->GcC|RP=615|RC=A|Ala|->V|Val||EN=13/14|DS=+100|P=chr21:44
 ENST00000400375.1|GN=KRTAP10-1|GI=ENSG00000215455.3|FC=Missense|CP=722|CF=1|AC=CgG->CaG|RP=241|RC=R|Arg|->Q|Gln||EN=1/11|P=chr21:459588
 ENST00000340552.4|GN=LIMK2|GI=ENSG00000182541.12|FC=Missense|CP=2051|CF=1|AC=CaG->CcG|RP=684|RC=Q|Gln|->R|Arg||EN=15/15|DS=+342|P=chr21
 ENST00000215659.8|GN=MAPK12|GI=ENSG00000188130.8|FC=Missense|CP=308|CF=1|AC=AcG->ATG|RP=103|RC=T|Thr|->M|Met||EN=3/12|DS=+53|P=chr22:5
 ENST00000449719.2|GN=MAPK11|GI=ENSG00000185386.10|FC=Missense|CP=590|CF=1|AC=GtC->CcC|RP=197|RC=V|Val|->A|Ala||EN=6/6|DS=+419|P=chr22:5
 ENST00000449719.2|GN=MAPK11|GI=ENSG00000185386.10|FC=Nonsense|CP=345|CF=2|AC=TGg->TGA|RP=115|RC=W|Trp|->Stop||EN=6/6|DS=+174|P=chr22:5
 ENST00000262848.5|GN=PRKX|GI=ENSG00000183943.5|FC=Missense|CP=128|CF=1|AC=GtG->GcG|RP=43|RC=V|Val|->A|Ala||EN=1/9|DS=-38360|P=chrX:3522
 ENST00000338883.4|GN=MAP3K15|GI=ENSG00000180815.10|FC=Missense|CP=574|CF=0|AC=gCT->aCT|RP=192|RC=A|Ala|->T|Thr||EN=4/29|DS=+49|P=chrX:1
 ENST00000372129.2|GN=IRS4|GI=ENSG00000133124.10|FC=Missense|CP=2635|CF=0|AC=cAT->gAT|RP=879|RC=H|His|->D|Asp||EN=1/11|P=chrX:107975712-10
 ENST00000218006.2|GN=GUCY2F|GI=ENSG00000101890.4|FC=Missense|CP=887|CF=1|AC=CgG->CaG|RP=296|RC=R|Arg|->Q|Gln||EN=3/20|DS=+157|P=chrX:1
 ENST00000369980.3|GN=IRAK1|GI=ENSG00000184216.7|FC=Missense|CP=1595|CF=1|AC=TcG->tG|RP=532|RC=S|Ser|->L|Leu||EN=12/14|DS=+56|P=chrX:15
 ENST00000369980.3|GN=IRAK1|GI=ENSG00000184216.7|FC=Missense|CP=587|CF=1|AC=TtT->TcT|RP=196|RC=F|Phe|->S|Ser||EN=5/14|DS=+47|P=chrX:1532

[illegible]



[illegible]

[illegible]



ENST00000470049.1|GN=RP11-727C1.1|G=ENSG00000242320.1|P=chr18:53303078-53303545|ST=+|LV=2|GT=pseudogene|TT=processed_pseudogene

Gencode 2-wav Pseudogenes	Gencode PolyA	1K Genomes	1K Genomes All Alt Allele Freq
		P=chr1:9780196 REF=A ALT=G AC=26 AN=2184	0.0119
		P=chr1:22923873 REF=G ALT=C AC=217 AN=2184	0.0994
		P=chr1:27688633 REF=G ALT=A AC=714 AN=2184	0.3269
		P=chr1:36807481 REF=C ALT=T AC=376 AN=2184	0.1722
		P=chr1:38227086 REF=A ALT=T AC=785 AN=2184	0.3594
		P=chr1:38227268 REF=G ALT=T AC=224 AN=2184	0.1026
		P=chr1:46476587 REF=T ALT=G AC=1873 AN=2184	0.8576
		P=chr1:46493460 REF=T ALT=G AC=1012 AN=2184	0.4634
		P=chr1:46521559 REF=A ALT=T AC=1549 AN=2184	0.7092
		P=chr1:64643277 REF=C ALT=T AC=622 AN=2184	0.2848
		P=chr1:92428495 REF=C ALT=A AC=1677 AN=2184	0.7679
		P=chr1:92457843 REF=C ALT=T AC=1557 AN=2184	0.7129
		P=chr1:114948281 REF=A ALT=G AC=1832 AN=2184	0.8388
		P=chr1:169823718 REF=T ALT=C AC=1416 AN=2184	0.6484
		P=chr1:182554557 REF=C ALT=T AC=533 AN=2184	0.244
		P=chr1:205130413 REF=A ALT=G AC=2074 AN=2184	0.9496
		P=chr1:205272918 REF=G ALT=A AC=151 AN=2184	0.0691
		P=chr1:205500478 REF=G ALT=A AC=12 AN=2184	0.0055
		P=chr1:226923505 REF=G ALT=T AC=2125 AN=2184	0.973
		P=chr1:227182033 REF=G ALT=A AC=1958 AN=2184	0.8965
		P=chr1:227216775 REF=C ALT=T AC=727 AN=2184	0.3329
		P=chr1:228402121 REF=A ALT=G AC=1528 AN=2184	0.6996
		P=chr1:228444565 REF=T ALT=A AC=2184 AN=2184	1
		P=chr1:228464248 REF=T ALT=G AC=1578 AN=2184	0.7225
		P=chr1:228464276 REF=T ALT=C AC=1505 AN=2184	0.6891
		P=chr1:228509589 REF=G ALT=A AC=56 AN=2184	0.0256
		P=chr1:233514934 REF=G ALT=A AC=520 AN=2184	0.2381
		P=chr1:233514975 REF=G ALT=T AC=552 AN=2184	0.2527
		P=chr1:233515102 REF=T ALT=G AC=551 AN=2184	0.2523
		P=chr2:11359120 REF=G ALT=T AC=931 AN=2184	0.4263
		P=chr2:29416366 REF=G ALT=C AC=1235 AN=2184	0.5655
		P=chr2:29416481 REF=T ALT=C AC=863 AN=2184	0.3951
		P=chr2:29416572 REF=T ALT=C AC=2169 AN=2184	0.9931
		P=chr2:42275664 REF=T ALT=C AC=471 AN=2184	0.2157
		P=chr2:58316786 REF=A ALT=G AC=4 AN=2184	0.0018
		P=chr2:88913273 REF=G ALT=C AC=629 AN=2184	0.288
		P=chr2:99172244 REF=A ALT=G AC=601 AN=2184	0.2752
		P=chr2:135744007 REF=T ALT=C AC=237 AN=2184	0.1085
		P=chr2:135744416 REF=C ALT=G AC=298 AN=2184	0.1364

		P=chr2:171225841 REF=A ALT=G AC=703 AN=2184	0.3219
		P=chr2:171260787 REF=G ALT=A AC=1726 AN=2184	0.7903
		P=chr2:171356274 REF=G ALT=A AC=2003 AN=2184	0.9171
		P=chr2:174128513 REF=C ALT=T AC=615 AN=2184	0.2816
		P=chr2:179397561 REF=C ALT=T AC=414 AN=2184	0.1896
		P=chr2:179406191 REF=C ALT=T AC=415 AN=2184	0.19
		P=chr2:179421694 REF=A ALT=G AC=979 AN=2184	0.4483
		P=chr2:179425208 REF=G ALT=T AC=4 AN=2184	0.0018
		P=chr2:179427536 REF=T ALT=C AC=980 AN=2184	0.4487
		P=chr2:179430997 REF=G ALT=A AC=696 AN=2184	0.3187
		P=chr2:179436020 REF=G ALT=A AC=415 AN=2184	0.19
		P=chr2:179444768 REF=C ALT=G AC=2173 AN=2184	0.995
		P=chr2:179444939 REF=C ALT=T AC=710 AN=2184	0.3251
		P=chr2:179451420 REF=G ALT=A AC=977 AN=2184	0.4473
		P=chr2:179457147 REF=G ALT=A AC=425 AN=2184	0.1946
		P=chr2:179458591 REF=C ALT=T AC=423 AN=2184	0.1937
		P=chr2:179464527 REF=T ALT=C AC=996 AN=2184	0.456
		P=chr2:179474668 REF=G ALT=A AC=157 AN=2184	0.0719
		P=chr2:179515483 REF=G ALT=C AC=93 AN=2184	0.0426
		P=chr2:179558366 REF=T ALT=C AC=911 AN=2184	0.4171
		P=chr2:179579093 REF=T ALT=C AC=512 AN=2184	0.2344
		P=chr2:179582327 REF=C ALT=T AC=512 AN=2184	0.2344
		P=chr2:179582537 REF=G ALT=T AC=859 AN=2184	0.3933
		P=chr2:179583496 REF=T ALT=G AC=500 AN=2184	0.2289
		P=chr2:179587130 REF=C ALT=G AC=513 AN=2184	0.2349
		P=chr2:179589058 REF=G ALT=A AC=88 AN=2184	0.0403
		P=chr2:179615887 REF=T ALT=C AC=1696 AN=2184	0.7766
		P=chr2:179615931 REF=C ALT=G AC=2141 AN=2184	0.9803
		P=chr2:179620951 REF=C ALT=T AC=1828 AN=2184	0.837
		P=chr2:179621477 REF=C ALT=T AC=2183 AN=2184	0.9995
		P=chr2:179623758 REF=C ALT=T AC=1841 AN=2184	0.8429
		P=chr2:179629461 REF=C ALT=T AC=1833 AN=2184	0.8393
		P=chr2:179644035 REF=G ALT=A AC=2027 AN=2184	0.9281
		P=chr2:179659912 REF=G ALT=A AC=506 AN=2184	0.2317
		P=chr2:209184980 REF=G ALT=A AC=2169 AN=2184	0.9931
		P=chr2:209190330 REF=T ALT=C AC=2048 AN=2184	0.9377
		P=chr2:209190519 REF=A ALT=T AC=1994 AN=2184	0.913
		P=chr2:209190528 REF=C ALT=G AC=2045 AN=2184	0.9364
		P=chr2:209191082 REF=C ALT=A AC=2047 AN=2184	0.9373
		P=chr2:220337041 REF=G ALT=A AC=49 AN=2184	0.0224
		P=chr2:220354108 REF=A ALT=G AC=798 AN=2184	0.3654
		P=chr2:242046785 REF=A ALT=C AC=683 AN=2184	0.3127
		P=chr2:242054403 REF=G ALT=A AC=531 AN=2184	0.2431
		P=chr2:242082262 REF=T ALT=C AC=1303 AN=2184	0.5966
		P=chr3:10276163 REF=T ALT=A AC=1722 AN=2184	0.7885
		P=chr3:27332820 REF=A ALT=G AC=467 AN=2184	0.2138
		P=chr3:41841716 REF=A ALT=C AC=1870 AN=2184	0.8562
		P=chr3:41925398 REF=C ALT=T AC=1545 AN=2184	0.7074
		P=chr3:41960006 REF=T ALT=C AC=1513 AN=2184	0.6928

	P=chr3:41996136 REF=T ALT=C AC=1523 AN=2184	0.6973
	P=chr3:49928691 REF=T ALT=C AC=2184 AN=2184	1
	P=chr3:52797634 REF=G ALT=C AC=841 AN=2184	0.3851
	P=chr3:96585671 REF=G ALT=A AC=6 AN=2184	0.0027
	P=chr3:123419573 REF=G ALT=T AC=432 AN=2184	0.1978
	P=chr3:123419733 REF=A ALT=G AC=518 AN=2184	0.2372
	P=chr3:123451773 REF=G ALT=C AC=2182 AN=2184	0.9991
	P=chr3:123453061 REF=A ALT=G AC=535 AN=2184	0.245
	P=chr3:123457893 REF=G ALT=A AC=1924 AN=2184	0.881
	P=chr3:130947435 REF=A ALT=T AC=1054 AN=2184	0.4826
	P=chr3:142281612 REF=A ALT=G AC=1348 AN=2184	0.6172
	P=chr3:185198262 REF=G ALT=A AC=3 AN=2184	0.0014
	P=chr3:185990096 REF=C ALT=T AC=1785 AN=2184	0.8173
	P=chr3:186006618 REF=G ALT=C AC=1181 AN=2184	0.5408
	P=chr4:843498 REF=G ALT=A AC=2 AN=2184	0.0009
	P=chr4:2990499 REF=G ALT=T AC=736 AN=2184	0.337
	P=chr4:3006043 REF=C ALT=T AC=860 AN=2184	0.3938
	P=chr4:5448429 REF=A ALT=G AC=513 AN=2184	0.2349
	P=chr4:25235801 REF=G ALT=A AC=190 AN=2184	0.087
	P=chr4:55972974 REF=T ALT=A AC=513 AN=2184	0.2349
	P=chr4:79786856 REF=G ALT=A AC=180 AN=2184	0.0824
	P=chr4:107168431 REF=G ALT=C AC=2159 AN=2184	0.9886
	P=chr4:113352397 REF=G ALT=A AC=1393 AN=2184	0.6378
	P=chr4:113352628 REF=A ALT=G AC=1474 AN=2184	0.6749
	P=chr4:113352899 REF=G ALT=A AC=1394 AN=2184	0.6383
	P=chr4:113353285 REF=T ALT=C AC=1473 AN=2184	0.6745
	P=chr4:128807219 REF=T ALT=A AC=1548 AN=2184	0.7088
	P=chr4:151177340 REF=C ALT=T AC=1853 AN=2184	0.8484
	P=chr4:151177341 REF=C ALT=G AC=1842 AN=2184	0.8434
	P=chr4:170398454 REF=T ALT=C AC=249 AN=2184	0.114
	P=chr5:56177443 REF=G ALT=A AC=1096 AN=2184	0.5018
	P=chr5:56177743 REF=G ALT=A AC=1524 AN=2184	0.6978
	P=chr5:66459878 REF=G ALT=C AC=2070 AN=2184	0.9478
	P=chr5:67588148 REF=G ALT=A AC=475 AN=2184	0.2175
	P=chr5:96503523 REF=C ALT=T AC=1205 AN=2184	0.5517
	P=chr5:96513471 REF=G ALT=C AC=781 AN=2184	0.3576
	P=chr5:96518792 REF=T ALT=G AC=1144 AN=2184	0.5238
	P=chr5:112176756 REF=T ALT=A AC=1883 AN=2184	0.8622
	P=chr5:149450132 REF=T ALT=C AC=343 AN=2184	0.1571
	P=chr5:176516631 REF=G ALT=A AC=545 AN=2184	0.2495
	P=chr5:176517797 REF=C ALT=T AC=1779 AN=2184	0.8146
	P=chr5:176520243 REF=G ALT=A AC=661 AN=2184	0.3027
	P=chr5:180046344 REF=G ALT=C AC=1150 AN=2184	0.5266
	P=chr6:2679676 REF=G ALT=A AC=497 AN=2184	0.2276
	P=chr6:4031998 REF=A ALT=G AC=1554 AN=2184	0.7115
	P=chr6:31946695 REF=C ALT=G AC=2 AN=2184	0.0009
	P=chr6:33690796 REF=C ALT=T AC=896 AN=2184	0.4103
	P=chr6:33695975 REF=G ALT=A AC=11 AN=2184	0.005
	P=chr6:41903782 REF=A ALT=C AC=1275 AN=2184	0.5838

	P=chr6:43251912 REF=A ALT=G AC=735 AN=2184	0.3365
	P=chr6:43252029 REF=T ALT=C AC=773 AN=2184	0.3539
	P=chr6:44232920 REF=A ALT=G AC=162 AN=2184	0.0742
	P=chr6:44232977 REF=G ALT=A AC=137 AN=2184	0.0627
	P=chr6:116325142 REF=C ALT=T AC=996 AN=2184	0.456
	P=chr6:117638325 REF=C ALT=T AC=2 AN=2184	0.0009
	P=chr6:136888782 REF=T ALT=C AC=15 AN=2184	0.0069
	P=chr6:161469774 REF=G ALT=A AC=2132 AN=2184	0.9762
	P=chr6:167271711 REF=T ALT=C AC=2048 AN=2184	0.9377
	P=chr6:167271716 REF=T ALT=C AC=1398 AN=2184	0.6401
	P=chr7:23757162 REF=G ALT=C AC=552 AN=2184	0.2527
	P=chr7:23775454 REF=G ALT=A AC=232 AN=2184	0.1062
	P=chr7:23775477 REF=G ALT=T AC=243 AN=2184	0.1113
	P=chr7:23811795 REF=T ALT=G AC=284 AN=2184	0.13
	P=chr7:23811800 REF=G ALT=T AC=222 AN=2184	0.1016
	P=chr7:40027484 REF=A ALT=G AC=309 AN=2184	0.1415
	P=chr7:43635671 REF=A ALT=C AC=26 AN=2184	0.0119
	P=chr7:43664280 REF=A ALT=G AC=1729 AN=2184	0.7917
	P=chr7:55229255 REF=G ALT=A AC=652 AN=2184	0.2985
	P=chr7:97822115 REF=T ALT=A AC=613 AN=2184	0.2807
	P=chr7:116340262 REF=A ALT=G AC=46 AN=2184	0.0211
	P=chr7:143088867 REF=T ALT=C AC=2078 AN=2184	0.9515
	P=chr7:143097100 REF=A ALT=G AC=2029 AN=2184	0.929
	P=chr8:8176221 REF=C ALT=T AC=1129 AN=2184	0.5169
	P=chr8:8176554 REF=C ALT=T AC=686 AN=2184	0.3141
	P=chr8:8234192 REF=G ALT=C AC=950 AN=2184	0.435
	P=chr8:8234219 REF=G ALT=A AC=898 AN=2184	0.4112
	P=chr8:8234714 REF=C ALT=T AC=961 AN=2184	0.44
	P=chr8:11418773 REF=C ALT=T AC=1133 AN=2184	0.5188
	P=chr8:27308585 REF=A ALT=C AC=819 AN=2184	0.375
	P=chr8:38287238 REF=G ALT=A AC=13 AN=2184	0.006
	P=chr8:48719852 REF=G ALT=C AC=11 AN=2184	0.005
	P=chr8:87076520 REF=C ALT=A AC=713 AN=2184	0.3265
	P=chr8:144802736 REF=G ALT=C AC=597 AN=2184	0.2734
	P=chr8:145603114 REF=A ALT=C AC=1275 AN=2184	0.5838
	P=chr9:27168571 REF=T ALT=C AC=72 AN=2184	0.033
	P=chr9:27183463 REF=A ALT=C AC=2149 AN=2184	0.984
	P=chr9:71628207 REF=G ALT=C AC=599 AN=2184	0.2743
	P=chr9:77376647 REF=T ALT=C AC=544 AN=2184	0.2491
	P=chr9:94486321 REF=C ALT=T AC=1713 AN=2184	0.7843
	P=chr9:94495608 REF=T ALT=C AC=1366 AN=2184	0.6255
	P=chr9:113457799 REF=A ALT=G AC=261 AN=2184	0.1195
	P=chr9:113538122 REF=G ALT=A AC=224 AN=2184	0.1026
	P=chr9:133759794 REF=G ALT=T AC=4 AN=2184	0.0018
	P=chr9:136268084 REF=A ALT=G AC=1070 AN=2184	0.4899
	P=chr10:6527143 REF=G ALT=A AC=704 AN=2184	0.3223
	P=chr10:26355992 REF=A ALT=G AC=1455 AN=2184	0.6662

		P=chr10:26357748 REF=G ALT=A AC=1351 AN=2184	0.6186
		P=chr10:26463130 REF=C ALT=A AC=1348 AN=2184	0.6172
		P=chr10:26482157 REF=A ALT=G AC=22 AN=2184	0.0101
		P=chr10:30728250 REF=A ALT=G AC=962 AN=2184	0.4405
		P=chr10:59956041 REF=C ALT=T AC=237 AN=2184	0.1085
		P=chr10:88635779 REF=C ALT=A AC=990 AN=2184	0.4533
		P=chr10:101977883 REF=C ALT=T AC=1228 AN=2184	0.5623
		P=chr10:121196335 REF=G ALT=A AC=260 AN=2184	0.119
		P=chr10:123310871 REF=A ALT=G AC=263 AN=2184	0.1204
		P=chr11:46369267 REF=G ALT=A AC=800 AN=2184	0.3663
		P=chr11:64597201 REF=G ALT=A AC=96 AN=2184	0.044
		P=chr11:108159732 REF=C ALT=T AC=43 AN=2184	0.0197
		P=chr11:108183167 REF=A ALT=G AC=2184 AN=2184	1
		P=chr11:113266821 REF=G ALT=A AC=634 AN=2184	0.2903
		P=chr11:113270015 REF=G ALT=C AC=1204 AN=2184	0.5513
		P=chr11:113270828 REF=G ALT=A AC=648 AN=2184	0.2967
		P=chr11:125525195 REF=A ALT=G AC=2145 AN=2184	0.9821
		P=chr12:990912 REF=A ALT=C AC=1851 AN=2184	0.8475
		P=chr12:994487 REF=G ALT=C AC=2161 AN=2184	0.9895
		P=chr12:998365 REF=G ALT=T AC=843 AN=2184	0.386
		P=chr12:10782115 REF=T ALT=C AC=1351 AN=2184	0.6186
		P=chr12:14829893 REF=A ALT=C AC=2164 AN=2184	0.9908
		P=chr12:18649057 REF=C ALT=T AC=703 AN=2184	0.3219
		P=chr12:40619082 REF=G ALT=A AC=2127 AN=2184	0.9739
		P=chr12:40657700 REF=C ALT=G AC=221 AN=2184	0.1012
		P=chr12:40702911 REF=G ALT=A AC=218 AN=2184	0.0998
		P=chr12:48367976 REF=C ALT=T AC=428 AN=2184	0.196
		P=chr12:52306221 REF=C ALT=T AC=171 AN=2184	0.0783
		P=chr12:57919529 REF=C ALT=G AC=20 AN=2184	0.0092
		P=chr12:57994679 REF=C ALT=G AC=106 AN=2184	0.0485
		P=chr12:66605228 REF=A ALT=G AC=1569 AN=2184	0.7184
		P=chr12:106460938 REF=G ALT=C AC=507 AN=2184	0.2321
		P=chr12:118682751 REF=C ALT=T AC=1546 AN=2184	0.7079
		P=chr12:121691096 REF=G ALT=A AC=498 AN=2184	0.228
		P=chr12:132403161 REF=A ALT=G AC=2171 AN=2184	0.994
		P=chr12:132406666 REF=G ALT=C AC=587 AN=2184	0.2688
		P=chr13:21562832 REF=C ALT=T AC=1898 AN=2184	0.869
		P=chr13:21562948 REF=G ALT=A AC=1424 AN=2184	0.652
		P=chr13:28624294 REF=G ALT=A AC=1241 AN=2184	0.5682
		P=chr13:32906480 REF=A ALT=C AC=127 AN=2184	0.0582
		P=chr13:32911463 REF=A ALT=G AC=136 AN=2184	0.0623
		P=chr13:32929387 REF=T ALT=C AC=2135 AN=2184	0.9776
		P=chr13:37679268 REF=G ALT=T AC=1322 AN=2184	0.6053
		P=chr13:110435231 REF=C ALT=T AC=646 AN=2184	0.2958
		P=chr14:50798743 REF=G ALT=A AC=1214 AN=2184	0.5559
		P=chr14:50799126 REF=G ALT=C AC=1259 AN=2184	0.5765
		P=chr14:50901768 REF=G ALT=A AC=94 AN=2184	0.043
		P=chr14:61924239 REF=G ALT=A AC=137 AN=2184	0.0627

		P=chr14:75386576 REF=G ALT=A AC=757 AN=2184	0.3466
		P=chr14:75388183 REF=C ALT=T AC=828 AN=2184	0.3791
		P=chr14:75574087 REF=C ALT=T AC=1204 AN=2184	0.5513
		P=chr14:93407062 REF=A ALT=G AC=1542 AN=2184	0.706
		P=chr14:102695693 REF=T ALT=C AC=569 AN=2184	0.2605
		P=chr14:103934488 REF=T ALT=C AC=2184 AN=2184	1
		P=chr15:40265799 REF=A ALT=G AC=1880 AN=2184	0.8608
		P=chr15:40477831 REF=G ALT=A AC=1360 AN=2184	0.6227
		P=chr15:40564576 REF=C ALT=T AC=239 AN=2184	0.1094
		P=chr15:43170793 REF=A ALT=G AC=1047 AN=2184	0.4794
		P=chr15:75130093 REF=T ALT=C AC=880 AN=2184	0.4029
		P=chr15:77450964 REF=C ALT=T AC=499 AN=2184	0.2285
		P=chr15:85383145 REF=C ALT=G AC=359 AN=2184	0.1644
		P=chr15:85383640 REF=G ALT=A AC=359 AN=2184	0.1644
		P=chr15:85401259 REF=C ALT=T AC=1746 AN=2184	0.7995
		P=chr15:85405995 REF=T ALT=C AC=400 AN=2184	0.1832
		P=chr15:101606889 REF=G ALT=A AC=492 AN=2184	0.2253
		P=chr15:101606890 REF=C ALT=A AC=492 AN=2184	0.2253
		P=chr16:22269867 REF=A ALT=G AC=2182 AN=2184	0.9991
		P=chr16:23646191 REF=T ALT=C AC=320 AN=2184	0.1465
		P=chr16:23711925 REF=C ALT=G AC=892 AN=2184	0.4084
		P=chr16:46773999 REF=C ALT=A AC=1019 AN=2184	0.4666
		P=chr16:68732049 REF=A ALT=C AC=472 AN=2184	0.2161
		P=chr17:3627473 REF=C ALT=T AC=1080 AN=2184	0.4945
		P=chr17:3627840 REF=G ALT=A AC=500 AN=2184	0.2289
		P=chr17:3628212 REF=T ALT=C AC=494 AN=2184	0.2262
		P=chr17:3628362 REF=T ALT=C AC=1087 AN=2184	0.4977
		P=chr17:3775848 REF=T ALT=C AC=778 AN=2184	0.3562
		P=chr17:4796274 REF=T ALT=C AC=1462 AN=2184	0.6694
		P=chr17:4796286 REF=C ALT=T AC=1442 AN=2184	0.6603
		P=chr17:4797305 REF=G ALT=A AC=391 AN=2184	0.179
		P=chr17:7292107 REF=G ALT=A AC=1683 AN=2184	0.7706
		P=chr17:7579472 REF=G ALT=C AC=1317 AN=2184	0.603
		P=chr17:7792326 REF=C ALT=T AC=166 AN=2184	0.076
		P=chr17:8108331 REF=A ALT=G AC=1636 AN=2184	0.7491
		P=chr17:19285705 REF=G ALT=A AC=3 AN=2184	0.0014
		P=chr17:25909816 REF=C ALT=T AC=342 AN=2184	0.1566
		P=chr17:37879588 REF=A ALT=G AC=338 AN=2184	0.1548
		P=chr17:37884037 REF=C ALT=G AC=1071 AN=2184	0.4904
		P=chr17:41223094 REF=T ALT=C AC=715 AN=2184	0.3274
		P=chr17:41244000 REF=T ALT=C AC=708 AN=2184	0.3242
		P=chr17:41244435 REF=T ALT=C AC=662 AN=2184	0.3031
		P=chr17:41244936 REF=G ALT=A AC=1055 AN=2184	0.4831
		P=chr17:48265495 REF=T ALT=C AC=2132 AN=2184	0.9762
		P=chr17:56584508 REF=T ALT=C AC=602 AN=2184	0.2756

[illegible]

1K Genomes JPT Alt Allele Freq
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0.6629
0.1966
1
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0.0618
1
0.9045
0.3708
0.7921
1
0.809
0.809
0.0674
0.3708
0.3708
0.3708
0.3764
0.7022
0.7022
1
0.4157
0
0.427
0.2697
0.2809
0.2809

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0.4663
0.382
0.382
0.6011
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1
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0.764
0.809
0.5618
1
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0.927
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0.2809
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0.927
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0.8708

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0.4045
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0.1517
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0.5393
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0.0169
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0.0169
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0.3708
1
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1
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1
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0.1573
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0.5674
0.2135
1
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1
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1
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0.2022

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0.8146
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0.5393
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0.3764
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0.3764
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0.2472

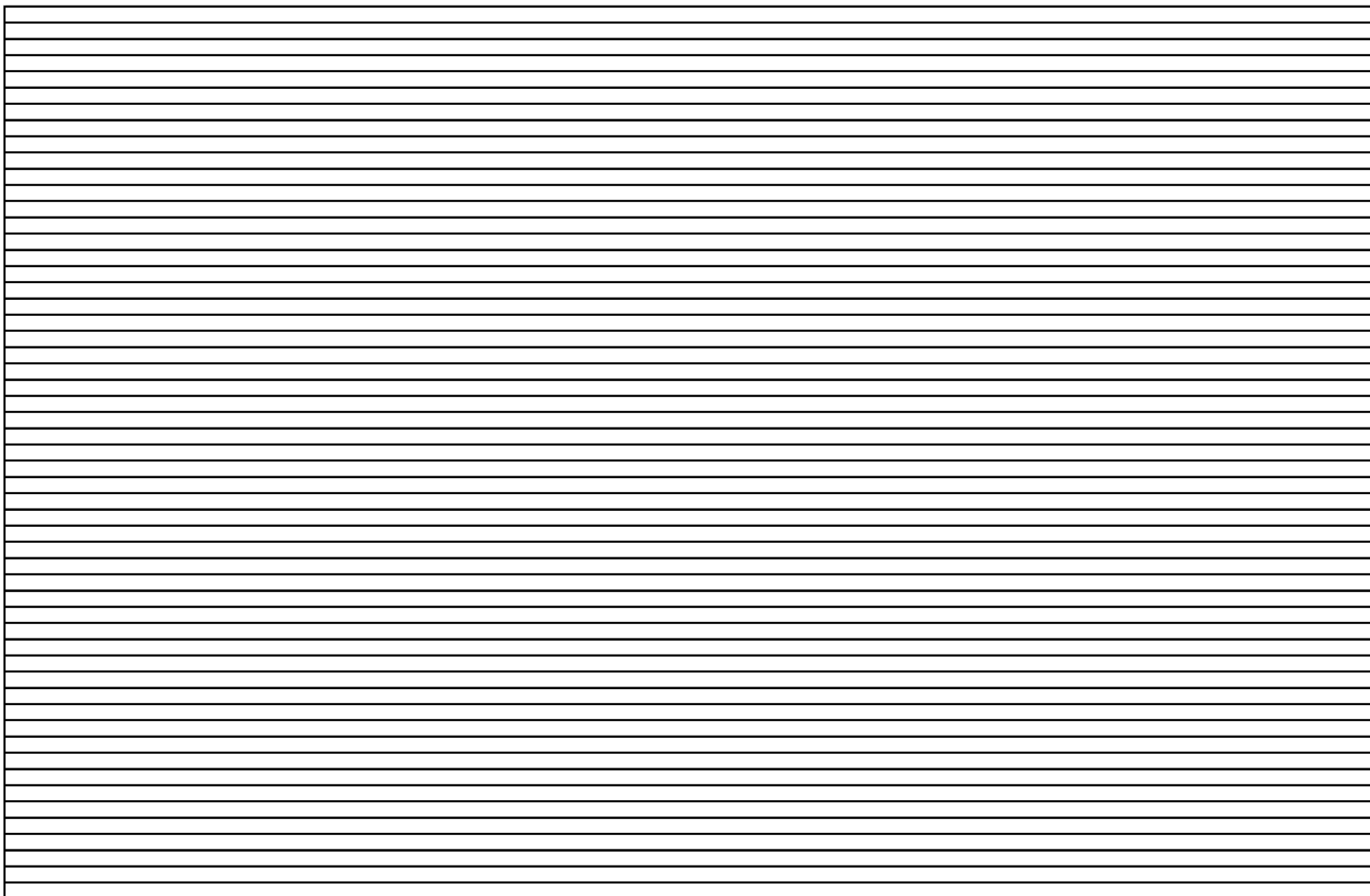
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1
0.1966
1
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0.5
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0.6798
0.2528

Segmental Duplications									
P=chr1:1567837-1584471	OP=chr1:1631056-1647700	ST=+	FM=0.9913	FMWI=0.9904					
P=chr1:1567837-1584471	OP=chr1:1631056-1647700	ST=+	FM=0.9913	FMWI=0.9904					
P=chr1:1567837-1584471	OP=chr1:1631056-1647700	ST=+	FM=0.9913	FMWI=0.9904					
P=chr1:1631056-1647700	OP=chr1:1567837-1584471	ST=+	FM=0.9913	FMWI=0.9904					
P=chr1:1631056-1647700	OP=chr1:1567837-1584471	ST=+	FM=0.9913	FMWI=0.9904					
P=chr1:1631056-1647700	OP=chr1:1567837-1584471	ST=+	FM=0.9913	FMWI=0.9904					

P=chr3:123415954-123427920|OP=chr3:75374980-75386568|ST=+|FM=0.9484|FMWI=0.9454

P=chr3:123415954-123427920|OP=chr3:75374980-75386568|ST=+|FM=0.9484|FMWI=0.9454

P=chr6:4031805-4032989|OP=chr9:117607930-117609091|ST=+|FM=0.9243|FMWI=0.9156



P=[chr10:59951278-59956460](#) | [OP=\[chr13:23406283-23411780\]\(#\)](#) | ST=+ | FM=0.952 | | FMW=0.9475. P=[chr10:59953327-59956460](#) | [OP=\[chr19:16018582-16022007\]\(#\)](#) | ST=+

[illegible]

[illegible]

P=chr18:18520340-18539808|OP=chr18:112547-131692|ST=-|FM=0.9900|FMWI=0.9887

P=chr21:45958346-45960058|OP=chr21:45998818-46000480|ST=+|FM=0.9319|FMWI=0.9257. P=chr21:45958351-45959931|OP=chr21:46032207-46033634|ST=-|

P=chrX:3617961-3634603|OP=chrY:7139241-7158907|ST=-|FM=0.9179|FMWI=0.9107

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

Primate Conserved Elements	Placental Mammal Conserved Elements
	P=chr1:1571812-1571845 od=60 SC=415
	P=chr1:1575696-1575715 od=24 SC=309
P=chr1:1575747-1575815 od=16 SC=239	P=chr1:1575757-1575815 od=76 SC=442
P=chr1:1638837-1639025 od=28 SC=322	P=chr1:1638906-1638949 od=22 SC=300
P=chr1:1638837-1639025 od=28 SC=322	P=chr1:1638967-1639025 od=61 SC=417
P=chr1:27688560-27688746 od=70 SC=458	P=chr1:27688570-27688746 od=417 SC=638
P=chr1:27941950-27942352 od=85 SC=487	P=chr1:27942192-27942242 od=116 SC=491
P=chr1:36807453-36807562 od=32 SC=342	P=chr1:36807441-36807487 od=70 SC=433
P=chr1:38184043-38184103 od=18 SC=257	P=chr1:38184043-38184103 od=89 SC=460
	P=chr1:38227074-38227089 od=32 SC=343
P=chr1:38227087-38227758 od=172 SC=592	
P=chr1:46476233-46476637 od=63 SC=443	P=chr1:46476576-46476601 od=67 SC=427
P=chr1:46493400-46493541 od=24 SC=300	P=chr1:46493401-46493537 od=324 SC=609
P=chr1:46521457-46521675 od=90 SC=496	P=chr1:46521461-46521675 od=538 SC=667
P=chr1:64643108-64643337 od=57 SC=428	P=chr1:64643135-64643313 od=369 SC=624
P=chr1:92428268-92428514 od=53 SC=417	
P=chr1:114948028-114948393 od=98 SC=508	P=chr1:114948188-114948395 od=469 SC=651
P=chr1:205130378-205130512 od=44 SC=389	P=chr1:205130378-205130440 od=125 SC=499
	P=chr1:205500465-205500508 od=63 SC=420
P=chr1:226923211-226923509 od=79 SC=476	
P=chr1:227181973-227182118 od=56 SC=425	
P=chr1:227216340-227216954 od=233 SC=637	P=chr1:227216612-227216953 od=780 SC=710
	P=chr1:228402115-228402133 od=32 SC=343
	P=chr1:228464243-228464259 od=32 SC=343
	P=chr1:228509559-228509610 od=71 SC=434
P=chr1:233497797-233498044 od=47 SC=399	P=chr1:233497835-233497851 od=38 SC=362
P=chr2:11359083-11359147 od=15 SC=230	P=chr2:11359117-11359147 od=67 SC=427
P=chr2:29416390-29416521 od=20 SC=272	
	P=chr2:29448398-29448417 od=27 SC=323
P=chr2:37336370-37336461 od=20 SC=272	P=chr2:37336392-37336423 od=52 SC=398
P=chr2:42275152-42275986 od=103 SC=516	
P=chr2:58316760-58316854 od=45 SC=393	P=chr2:58316762-58316842 od=198 SC=552
P=chr2:88913229-88913358 od=26 SC=311	P=chr2:88913236-88913376 od=268 SC=587
P=chr2:99172002-99172293 od=98 SC=508	P=chr2:99172210-99172286 od=150 SC=520
	P=chr2:135744409-135744418 od=17 SC=270
P=chr2:148676011-148676167 od=61 SC=438	P=chr2:148676009-148676166 od=362 SC=621

P=chr2:158485079-158485388 od=39 SC=372	P=chr2:158485081-158485102 od=31 SC=339
P=chr2:171225679-171225863 od=52 SC=414	P=chr2:171225823-171225890 od=124 SC=498
P=chr2:171356150-171356321 od=54 SC=420	P=chr2:171356204-171356301 od=217 SC=563
P=chr2:179396886-179397769 od=161 SC=582	P=chr2:179397507-179397577 od=172 SC=536
P=chr2:179405985-179406314 od=108 SC=523	P=chr2:179406140-179406314 od=392 SC=630
P=chr2:179407775-179408409 od=207 SC=619	P=chr2:179408044-179408129 od=167 SC=532
P=chr2:179421569-179421897 od=90 SC=496	
P=chr2:179424862-179426639 od=529 SC=758	P=chr2:179425165-179425247 od=128 SC=502
P=chr2:179426672-179435521 od=2691 SC=1000	P=chr2:179427514-179427703 od=280 SC=592
P=chr2:179426672-179435521 od=2691 SC=1000	P=chr2:179430877-179431046 od=297 SC=599
P=chr2:179435621-179436093 od=135 SC=556	P=chr2:179435941-179436047 od=179 SC=540
P=chr2:179444631-179444958 od=69 SC=456	
P=chr2:179444631-179444958 od=69 SC=456	P=chr2:179444920-179444959 od=83 SC=452
P=chr2:179451224-179451546 od=101 SC=513	P=chr2:179451306-179451424 od=283 SC=593
P=chr2:179457067-179457390 od=88 SC=492	P=chr2:179457103-179457274 od=469 SC=651
P=chr2:179458282-179458606 od=110 SC=525	P=chr2:179458543-179458597 od=153 SC=522
P=chr2:179464255-179464581 od=96 SC=505	P=chr2:179464523-179464579 od=138 SC=511
P=chr2:179474399-179474721 od=94 SC=502	P=chr2:179474668-179474716 od=110 SC=484
P=chr2:179558311-179558445 od=34 SC=351	P=chr2:179558328-179558372 od=110 SC=484
P=chr2:179579034-179579222 od=29 SC=328	P=chr2:179579040-179579172 od=201 SC=554
P=chr2:179582243-179582559 od=117 SC=534	P=chr2:179582244-179582390 od=341 SC=614
P=chr2:179582243-179582559 od=117 SC=534	P=chr2:179582492-179582549 od=160 SC=528
P=chr2:179583416-179583704 od=50 SC=408	
P=chr2:179586975-179587280 od=104 SC=517	P=chr2:179586978-179587220 od=510 SC=661
P=chr2:179588985-179589276 od=76 SC=470	P=chr2:179588980-179589065 od=181 SC=542
	P=chr2:179615886-179615893 od=15 SC=255
P=chr2:179620885-179621137 od=60 SC=435	P=chr2:179620931-179620955 od=19 SC=283
P=chr2:179621326-179621626 od=84 SC=485	P=chr2:179621441-179621567 od=143 SC=515
P=chr2:179623726-179623901 od=64 SC=445	
P=chr2:179629216-179629581 od=131 SC=551	P=chr2:179629349-179629494 od=350 SC=617
P=chr2:179634400-179634668 od=83 SC=484	P=chr2:179634400-179634553 od=405 SC=634
P=chr2:179637834-179638112 od=63 SC=443	
P=chr2:179643949-179644194 od=97 SC=507	P=chr2:179643952-179644035 od=196 SC=551
	P=chr2:209184966-209185049 od=216 SC=562
	P=chr2:209190326-209190360 od=51 SC=396
P=chr2:209190638-209191097 od=111 SC=527	P=chr2:209191080-209191094 od=30 SC=335
P=chr2:209195220-209195425 od=76 SC=470	P=chr2:209195235-209195425 od=490 SC=656
P=chr2:220336940-220337064 od=29 SC=328	P=chr2:220337020-220337062 od=81 SC=449
P=chr2:220354033-220354175 od=28 SC=322	P=chr2:220354094-220354153 od=139 SC=511
P=chr2:242046759-242046936 od=27 SC=317	P=chr2:242046784-242046804 od=38 SC=362
P=chr3:10276130-10276177 od=13 SC=209	P=chr3:10276161-10276168 od=17 SC=270
P=chr3:27332724-27333080 od=78 SC=474	P=chr3:27332799-27332885 od=169 SC=534
P=chr3:41841693-41841788 od=29 SC=328	P=chr3:41705176-41705193 od=34 SC=350
	P=chr3:41841700-41841719 od=51 SC=396
P=chr3:41959928-41960049 od=22 SC=287	

P=chr3:41996108-41996260 od=42 SC=383	P=chr3:41996108-41996173 od=149 SC=519
P=chr3:49928599-49928741 od=33 SC=347	P=chr3:49928625-49928691 od=161 SC=528
P=chr3:52797447-52797653 od=71 SC=460	P=chr3:52797463-52797652 od=315 SC=605
P=chr3:96585646-96585745 od=22 SC=287	P=chr3:96585658-96585744 od=190 SC=547
P=chr3:123419398-123419963 od=124 SC=543	P=chr3:123419499-123419581 od=183 SC=543
P=chr3:123419398-123419963 od=124 SC=543	P=chr3:123419667-123419760 od=133 SC=506
P=chr3:123451737-123451879 od=32 SC=342	P=chr3:123451754-123451779 od=44 SC=379
P=chr3:123987593-123988111 od=149 SC=570	P=chr3:123987947-123988107 od=456 SC=648
	P=chr3:130947419-130947459 od=73 SC=437
P=chr3:142281031-142281649 od=153 SC=574	P=chr3:142281553-142281647 od=177 SC=539
P=chr3:185198014-185198339 od=88 SC=492	P=chr3:185198255-185198271 od=32 SC=343
P=chr3:185990035-185990140 od=30 SC=333	P=chr3:185990072-185990138 od=141 SC=513
P=chr4:843468-843535 od=14 SC=220	P=chr4:843460-843508 od=65 SC=424
P=chr4:2990467-2990520 od=19 SC=265	P=chr4:2990492-2990517 od=46 SC=384
P=chr4:5448397-5448508 od=27 SC=317	P=chr4:5448397-5448445 od=86 SC=456
P=chr4:107168290-107168497 od=42 SC=383	
P=chr4:128806859-128807577 od=224 SC=631	P=chr4:128807039-128807403 od=511 SC=661
P=chr4:170398446-170398510 od=28 SC=322	P=chr4:170398436-170398508 od=139 SC=511
P=chr5:56177384-56177618 od=80 SC=478	P=chr5:56177394-56177642 od=453 SC=647
P=chr5:67588061-67588384 od=132 SC=552	P=chr5:67588084-67588196 od=322 SC=608
P=chr5:96513430-96513567 od=40 SC=375	P=chr5:96513427-96513563 od=284 SC=593
P=chr5:112176592-112176978 od=116 SC=533	P=chr5:112176593-112176759 od=258 SC=582
	P=chr5:176516626-176516635 od=13 SC=239
	P=chr5:176520229-176520250 od=26 SC=319
P=chr5:180046262-180046371 od=17 SC=248	P=chr5:180046342-180046371 od=54 SC=403
P=chr5:180048525-180048836 od=59 SC=433	P=chr5:180048537-180048668 od=185 SC=544
P=chr6:4031795-4032995 od=296 SC=672	
P=chr6:31946665-31946789 od=53 SC=417	P=chr6:31946671-31946708 od=82 SC=451
P=chr6:31947173-31947365 od=50 SC=408	P=chr6:31947189-31947216 od=49 SC=392
	P=chr6:33690777-33690796 od=36 SC=356
P=chr6:33695936-33696066 od=36 SC=360	P=chr6:33695975-33695979 od=16 SC=263
P=chr6:36489409-36489628 od=48 SC=402	P=chr6:36489504-36489596 od=290 SC=596
P=chr6:41903589-41903856 od=61 SC=438	
P=chr6:43111206-43111366 od=58 SC=430	P=chr6:43111325-43111363 od=104 SC=478

P=chr6:44232860-44232971 od=23 SC=293	
P=chr6:110942304-110942420 od=15 SC=230	
P=chr6:116325037-116325167 od=22 SC=287	P=chr6:116325117-116325168 od=115 SC=490
P=chr6:117638309-117638438 od=37 SC=364	P=chr6:117638310-117638437 od=254 SC=581
P=chr6:136888764-136889025 od=57 SC=428	P=chr6:136888775-136888800 od=71 SC=434
P=chr6:161469659-161470688 od=306 SC=677	P=chr6:161469763-161469779 od=26 SC=319
	P=chr7:23757160-23757203 od=79 SC=446
	P=chr7:23775451-23775457 od=15 SC=255
	P=chr7:23775464-23775484 od=19 SC=283
P=chr7:23808601-23808738 od=16 SC=239	P=chr7:23808626-23808661 od=82 SC=451
P=chr7:23811764-23811906 od=29 SC=328	P=chr7:23811763-23811906 od=248 SC=578
P=chr7:23811764-23811906 od=29 SC=328	P=chr7:23811763-23811906 od=248 SC=578
P=chr7:40027125-40027863 od=238 SC=640	P=chr7:40027461-40027543 od=148 SC=519
P=chr7:43635457-43635720 od=80 SC=478	P=chr7:43635494-43635719 od=373 SC=625
P=chr7:95216318-95216437 od=42 SC=383	P=chr7:95216338-95216420 od=225 SC=567
P=chr7:98489988-98490155 od=53 SC=417	P=chr7:98490044-98490155 od=296 SC=598
P=chr7:98547157-98547208 od=15 SC=230	P=chr7:98547157-98547207 od=142 SC=514
P=chr7:116340070-116340346 od=47 SC=399	P=chr7:116340231-116340345 od=259 SC=583
P=chr7:138145369-138145663 od=45 SC=393	P=chr7:138145369-138145583 od=211 SC=559
	P=chr7:143088863-143088874 od=25 SC=314
P=chr7:143096965-143097150 od=53 SC=417	
P=chr8:8176422-8176650 od=39 SC=372	
P=chr8:8238819-8239264 od=70 SC=458	P=chr8:8239067-8239119 od=54 SC=403
P=chr8:27308557-27308591 od=14 SC=220	P=chr8:27308545-27308591 od=77 SC=443
P=chr8:38287185-38287477 od=62 SC=440	P=chr8:38287191-38287332 od=366 SC=623
P=chr9:27168490-27168618 od=44 SC=389	P=chr9:27168489-27168609 od=306 SC=602
P=chr9:27183452-27183625 od=53 SC=417	P=chr9:27183454-27183615 od=305 SC=602
	P=chr9:77376634-77376647 od=17 SC=270
P=chr9:94486271-94486411 od=17 SC=248	P=chr9:94486317-94486411 od=197 SC=551
P=chr9:94495393-94495730 od=73 SC=464	P=chr9:94495472-94495668 od=458 SC=648
P=chr9:113457681-113457817 od=39 SC=372	
	P=chr9:113538121-113538154 od=23 SC=305
	P=chr10:26355962-26356008 od=86 SC=456

P=chr10:26357694-26357790 od=31 SC=337	P=chr10:26357695-26357820 od=192 SC=548
P=chr10:26482142-26482259 od=43 SC=386	P=chr10:26482127-26482161 od=42 SC=374
P=chr10:59955835-59956430 od=175 SC=594	P=chr10:59955907-59956127 od=441 SC=644
P=chr10:88635633-88635817 od=22 SC=287	P=chr10:88635771-88635785 od=41 SC=371
P=chr10:99400432-99400819 od=50 SC=408	P=chr10:99400457-99400832 od=564 SC=672
P=chr10:101977746-101977915 od=36 SC=360	P=chr10:101977783-101977905 od=275 SC=590
P=chr10:121196158-121196358 od=44 SC=389	P=chr10:121196325-121196358 od=62 SC=419
P=chr10:123310798-123310914 od=30 SC=333	P=chr10:123310800-123310914 od=161 SC=528
P=chr11:46368967-46369390 od=69 SC=456	P=chr11:46369117-46369390 od=628 SC=685
P=chr11:64597188-64597351 od=35 SC=355	P=chr11:64597188-64597228 od=67 SC=427
P=chr11:108159705-108159837 od=43 SC=386	P=chr11:108159701-108159837 od=256 SC=582
P=chr11:108183136-108183229 od=30 SC=333	
P=chr11:111594211-111594331 od=34 SC=351	P=chr11:111594269-111594343 od=140 SC=512
P=chr11:125525106-125525311 od=45 SC=393	P=chr11:125525118-125525215 od=259 SC=583
	P=chr12:990845-990915 od=86 SC=456
	P=chr12:994487-994562 od=109 SC=483
P=chr12:998302-998530 od=32 SC=342	
P=chr12:1009603-1009912 od=101 SC=513	P=chr12:1009639-1009707 od=146 SC=517
P=chr12:10782083-10782216 od=38 SC=368	P=chr12:10782087-10782127 od=118 SC=493
P=chr12:18648993-18649091 od=34 SC=351	P=chr12:18648994-18649091 od=225 SC=567
P=chr12:40618928-40619088 od=53 SC=417	P=chr12:18719881-18719956 od=118 SC=493
P=chr12:40702899-40703040 od=37 SC=364	P=chr12:40619072-40619088 od=22 SC=300
P=chr12:48367865-48368121 od=110 SC=525	P=chr12:40657693-40657705 od=35 SC=353
	P=chr12:40702906-40702949 od=69 SC=431
P=chr12:57919356-57920181 od=261 SC=653	P=chr12:48367900-48367976 od=216 SC=562
P=chr12:57994569-57994866 od=79 SC=476	P=chr12:57919335-57919751 od=763 SC=707
	P=chr12:57994571-57994679 od=210 SC=559
	P=chr12:106460913-106460941 od=64 SC=422
P=chr12:118682697-118682783 od=26 SC=311	P=chr12:118682697-118682773 od=182 SC=542
P=chr12:121691074-121691281 od=36 SC=360	P=chr12:121691070-121691099 od=62 SC=419
	P=chr13:28624229-28624301 od=96 SC=469
P=chr13:110434622-110434686 od=17 SC=248	
P=chr13:110437022-110438338 od=283 SC=665	P=chr13:110437466-110437894 od=605 SC=680
P=chr14:50901677-50901794 od=37 SC=364	P=chr14:50799116-50799152 od=80 SC=448
	P=chr14:50901677-50901789 od=293 SC=597
	P=chr14:61924233-61924264 od=39 SC=365

[illegible]

P=chr17:56658893-56659123 od=36 SC=360	
P=chr17:64782983-64783101 od=23 SC=293	P=chr17:64783078-64783098 od=52 SC=398
P=chr18:18534739-18535015 od=102 SC=514	P=chr18:18534739-18535015 od=686 SC=695
P=chr18:48190368-48190864 od=99 SC=510	
P=chr18:59854837-59855287 od=94 SC=502	
P=chr18:59919894-59919993 od=50 SC=408	P=chr18:59919891-59919911 od=43 SC=377
P=chr19:2046360-2046459 od=18 SC=257	P=chr19:2046395-2046435 od=57 SC=409
	P=chr19:14574883-14574898 od=24 SC=309
	P=chr19:14582456-14582538 od=119 SC=493
P=chr19:18255359-18255411 od=17 SC=248	
P=chr19:38896151-38896281 od=25 SC=306	
	P=chr19:41210996-41211095 od=177 SC=539
	P=chr19:46275969-46275994 od=55 SC=405
P=chr19:47177898-47177996 od=35 SC=355	P=chr19:47177898-47177953 od=98 SC=471
P=chr19:47193855-47193966 od=47 SC=399	P=chr19:47193933-47193966 od=73 SC=437
	P=chr19:56047423-56047469 od=69 SC=431
	P=chr19:56047522-56047574 od=74 SC=439
P=chr20:9543535-9543642 od=31 SC=337	P=chr20:9543610-9543675 od=165 SC=531
P=chr20:30407330-30407491 od=28 SC=322	P=chr20:30407430-30407454 od=57 SC=409
P=chr21:33370999-33371145 od=18 SC=257	
	P=chr22:50696667-50696733 od=72 SC=436
P=chrX:108708426-108708678 od=84 SC=485	P=chrX:108708513-108708619 od=196 SC=551

Vertebrate Conserved Elements	SIFT Input	PolyPhen-2 Input	Target Region	Filter
P=chr1:1571812-1571845 od=173 SC=520	1.1571841.1 A/C	chr1:1571841 A/C	Near	FilteredOut
P=chr1:1575696-1575721 od=75 SC=431	1.1575715.1 C/T	chr1:1575715 C/T	On	FilteredOut
P=chr1:1575757-1575784 od=109 SC=471	1.1575784.1 C/T	chr1:1575784 C/T	On	FilteredOut
P=chr1:1634913-1635012 od=337 SC=591	1.1635011.1 A/G	chr1:1635011 A/G	On	FilteredOut
P=chr1:1638906-1638949 od=68 SC=420	1.1638925.1 C/T	chr1:1638925 C/T	On	FilteredOut
P=chr1:1638955-1639037 od=228 SC=549	1.1638994.1 C/T	chr1:1638994 C/T	On	FilteredOut
P=chr1:9780181-9780200 od=112 SC=473	1.9780196.1 A/G	chr1:9780196 A/G	On	Retained
P=chr1:22923871-22923874 od=21 SC=295	1.22923873.1 G/C	chr1:22923873 G/C	On	Retained
	1.27688633.1 G/A	chr1:27688633 G/A	On	Retained
P=chr1:27942192-27942245 od=269 SC=567	1.27942215.1 C/G	chr1:27942215 C/G	On	FilteredOut
P=chr1:36807441-36807487 od=207 SC=539	1.36807481.1 C/T	chr1:36807481 C/T	On	Retained
P=chr1:38184043-38184082 od=192 SC=531	1.38184063.1 C/A	chr1:38184063 C/A	On	FilteredOut
P=chr1:38227074-38227089 od=66 SC=417	1.38227086.1 A/T	chr1:38227086 A/T	On	Retained
	1.38227268.1 G/T	chr1:38227268 G/T	On	Retained
P=chr1:46476576-46476601 od=164 SC=514	1.46476587.1 T/G	chr1:46476587 T/G	On	Retained
P=chr1:46493400-46493477 od=498 SC=633	1.46493460.1 T/G	chr1:46493460 T/G	On	Retained
P=chr1:46521460-46521661 od=1230 SC=730	1.46521559.1 A/T	chr1:46521559 A/T	On	Retained
P=chr1:64643267-64643298 od=180 SC=524	1.64643277.1 C/T	chr1:64643277 C/T	On	Retained
	1.92428495.1 C/A	chr1:92428495 C/A	On	Retained
	1.92457843.1 C/T	chr1:92457843 C/T	On	Retained
P=chr1:114948275-114948394 od=525 SC=639	1.114948281.1 A/G	chr1:114948281 A/G	On	Retained
	1.169823718.1 T/C	chr1:169823718 T/C	On	Retained
	1.182554557.1 C/T	chr1:182554557 C/T	On	Retained
P=chr1:205130377-205130422 od=245 SC=557	1.205130413.1 A/G	chr1:205130413 A/G	On	Retained
	1.205272918.1 G/A	chr1:205272918 G/A	On	Retained
P=chr1:205500469-205500508 od=132 SC=491	1.205500478.1 G/A	chr1:205500478 G/A	On	Retained
	1.226923505.1 G/T	chr1:226923505 G/T	On	Retained
	1.227182033.1 G/A	chr1:227182033 G/A	On	Retained
P=chr1:227216744-227216811 od=257 SC=562	1.227216775.1 C/T	chr1:227216775 C/T	On	Retained
P=chr1:228402114-228402133 od=92 SC=452	1.228402121.1 A/G	chr1:228402121 A/G	On	Retained
P=chr1:228444532-228444612 od=277 SC=570	1.228444565.1 T/A	chr1:228444565 T/A	On	Retained
P=chr1:228464243-228464252 od=57 SC=401	1.228464248.1 T/G	chr1:228464248 T/G	On	Retained
P=chr1:228464271-228464277 od=16 SC=265	1.228464276.1 T/C	chr1:228464276 T/C	On	Retained
P=chr1:228509573-228509597 od=56 SC=399	1.228509589.1 G/A	chr1:228509589 G/A	On	Retained
P=chr1:233497835-233497851 od=98 SC=459	1.233497836.1 C/A	chr1:233497836 C/A	On	FilteredOut
	1.233514934.1 G/A	chr1:233514934 G/A	On	Retained
P=chr1:233514973-233514977 od=25 SC=313	1.233514975.1 G/T	chr1:233514975 G/T	On	Retained
	1.233515102.1 T/G	chr1:233515102 T/G	On	Retained
P=chr2:11359114-11359155 od=111 SC=472	2.11359120.1 G/T	chr2:11359120 G/T	On	Retained
	2.29416366.1 G/C	chr2:29416366 G/C	On	Retained
P=chr2:29416479-29416491 od=27 SC=321	2.29416481.1 T/C	chr2:29416481 T/C	On	Retained
	2.29416572.1 T/C	chr2:29416572 T/C	On	Retained
	2.29416635.1 C/A	chr2:29416635 C/A	On	FilteredOut
P=chr2:29448398-29448411 od=64 SC=414	2.29448410.1 T/G	chr2:29448410 T/G	On	FilteredOut
P=chr2:37336392-37336423 od=71 SC=425	2.37336419.1 C/T	chr2:37336419 C/T	On	FilteredOut
P=chr2:42275663-42275688 od=22 SC=300	2.42275664.1 T/C	chr2:42275664 T/C	Near	FilteredOut
P=chr2:58316776-58316862 od=366 SC=600	2.58316786.1 A/G	chr2:58316786 A/G	On	Retained
P=chr2:88913237-88913274 od=247 SC=558	2.88913273.1 G/C	chr2:88913273 G/C	On	Retained
	2.99172244.1 A/G	chr2:99172244 A/G	On	Retained
P=chr2:135744004-135744029 od=43 SC=371	2.135744007.1 T/C	chr2:135744007 T/C	On	Retained
P=chr2:135744409-135744418 od=22 SC=300	2.135744416.1 C/G	chr2:135744416 C/G	On	Retained
P=chr2:148676098-148676146 od=255 SC=561	2.148676144.1 A/C	chr2:148676144 A/C	On	FilteredOut

P=chr2:158485081-158485102 od=44 SC=374	2.158485099.1.C/A	chr2:158485099 C/A	On	FilteredOut
P=chr2:171225824-171225863 od=139 SC=497	2.171225841.1.A/G	chr2:171225841 A/G	On	Retained
	2.171260787.1.G/A	chr2:171260787 G/A	On	Retained
P=chr2:171356237-171356301 od=294 SC=577	2.171356274.1.G/A	chr2:171356274 G/A	On	Retained
	2.174128513.1.C/T	chr2:174128513 C/T	On	Retained
P=chr2:179397531-179397570 od=265 SC=566	2.179397561.1.C/T	chr2:179397561 C/T	On	Retained
P=chr2:179406140-179406225 od=488 SC=631	2.179406191.1.C/T	chr2:179406191 C/T	On	Retained
P=chr2:179408050-179408089 od=178 SC=523	2.179408086.1.A/G	chr2:179408086 A/G	On	FilteredOut
P=chr2:179421637-179421767 od=724 SC=673	2.179421694.1.A/G	chr2:179421694 A/G	On	Retained
P=chr2:179425165-179425247 od=343 SC=593	2.179425208.1.G/T	chr2:179425208 G/T	On	Retained
P=chr2:179427514-179427650 od=703 SC=670	2.179427536.1.T/C	chr2:179427536 T/C	On	Retained
P=chr2:179430997-179431001 od=27 SC=321	2.179430997.1.G/A	chr2:179430997 G/A	On	Retained
P=chr2:179435974-179436047 od=338 SC=592	2.179436020.1.G/A	chr2:179436020 G/A	On	Retained
	2.179444768.1.C/G	chr2:179444768 C/G	On	Retained
P=chr2:179444902-179444939 od=157 SC=510	2.179444939.1.C/T	chr2:179444939 C/T	On	Retained
P=chr2:179451420-179451424 od=22 SC=300	2.179451420.1.G/A	chr2:179451420 G/A	On	Retained
P=chr2:179457102-179457274 od=897 SC=696	2.179457147.1.G/A	chr2:179457147 G/A	On	Retained
P=chr2:179458543-179458597 od=344 SC=593	2.179458591.1.C/T	chr2:179458591 C/T	On	Retained
P=chr2:179464517-179464557 od=235 SC=553	2.179464527.1.T/C	chr2:179464527 T/C	On	Retained
P=chr2:179474632-179474716 od=476 SC=628	2.179474668.1.G/A	chr2:179474668 G/A	On	Retained
	2.179515483.1.G/C	chr2:179515483 G/C	On	Retained
P=chr2:179558332-179558372 od=121 SC=482	2.179558366.1.T/C	chr2:179558366 T/C	On	Retained
P=chr2:179579040-179579118 od=316 SC=584	2.179579093.1.T/C	chr2:179579093 T/C	On	Retained
P=chr2:179582279-179582358 od=242 SC=556	2.179582327.1.C/T	chr2:179582327 C/T	On	Retained
P=chr2:179582492-179582549 od=239 SC=554	2.179582537.1.G/T	chr2:179582537 G/T	On	Retained
P=chr2:179583475-179583497 od=92 SC=452	2.179583496.1.T/G	chr2:179583496 T/G	On	Retained
P=chr2:179587054-179587138 od=250 SC=559	2.179587130.1.C/G	chr2:179587130 C/G	On	Retained
P=chr2:179588981-179589062 od=386 SC=606	2.179589058.1.G/A	chr2:179589058 G/A	On	Retained
	2.179615887.1.T/C	chr2:179615887 T/C	On	Retained
	2.179615931.1.C/G	chr2:179615931 C/G	On	Retained
P=chr2:179620931-179620955 od=77 SC=433	2.179620951.1.C/T	chr2:179620951 C/T	On	Retained
P=chr2:179621455-179621568 od=347 SC=594	2.179621477.1.C/T	chr2:179621477 C/T	On	Retained
	2.179623758.1.C/T	chr2:179623758 C/T	On	Retained
P=chr2:179629454-179629461 od=30 SC=333	2.179629461.1.C/T	chr2:179629461 C/T	On	Retained
P=chr2:179634400-179634424 od=165 SC=515	2.179634421.1.T/G	chr2:179634421 T/G	Near	FilteredOut
P=chr2:179638051-179638102 od=267 SC=566	2.179638072.1.C/T	chr2:179638072 C/T	On	Retained
P=chr2:179643952-179644035 od=439 SC=619	2.179644035.1.G/A	chr2:179644035 G/A	On	Retained
P=chr2:179659911-179659912 od=18 SC=278	2.179659912.1.G/A	chr2:179659912 G/A	On	Retained
P=chr2:209184970-209185088 od=744 SC=676	2.209184980.1.G/A	chr2:209184980 G/A	On	Retained
P=chr2:209190326-209190334 od=19 SC=284	2.209190330.1.T/C	chr2:209190330 T/C	On	Retained
P=chr2:209190515-209190519 od=17 SC=272	2.209190519.1.A/T	chr2:209190519 A/T	On	Retained
	2.209190528.1.C/G	chr2:209190528 C/G	On	Retained
	2.209191082.1.C/A	chr2:209191082 C/A	On	Retained
P=chr2:209195235-209195421 od=1204 SC=727	2.209195248.1.C/A	chr2:209195248 C/A	On	FilteredOut
P=chr2:220337020-220337064 od=156 SC=509	2.220337041.1.G/A	chr2:220337041 G/A	On	Retained
P=chr2:220354094-220354123 od=80 SC=437	2.220354108.1.A/G	chr2:220354108 A/G	On	Retained
	2.242046785.1.A/C	chr2:242046785 A/C	On	Retained
	2.242054403.1.G/A	chr2:242054403 G/A	Near	Retained
	2.242082262.1.T/C	chr2:242082262 T/C	On	Retained
P=chr3:10276161-10276168 od=20 SC=289	3.10276163.1.T/A	chr3:10276163 T/A	On	Retained
P=chr3:27332815-27332885 od=240 SC=555	3.27332820.1.A/G	chr3:27332820 A/G	On	Retained
P=chr3:41705176-41705193 od=37 SC=355	3.41705179.1.A/C	chr3:41705179 A/C	On	FilteredOut
P=chr3:41841700-41841719 od=77 SC=433	3.41841716.1.A/C	chr3:41841716 A/C	On	Retained
	3.41925398.1.C/T	chr3:41925398 C/T	On	Retained
	3.41960006.1.T/C	chr3:41960006 T/C	On	Retained

P=chr3:41996108-41996173 od=305 SC=581	3.41996136.1 T/C	chr3:41996136 T/C	On	Retained
P=chr3:49928625-49928691 od=429 SC=617	3.49928691.1 T/C	chr3:49928691 T/C	On	Retained
P=chr3:52797520-52797642 od=525 SC=639	3.52797634.1 G/C	chr3:52797634 G/C	On	Retained
P=chr3:96585654-96585744 od=334 SC=590	3.96585671.1 G/A	chr3:96585671 G/A	On	Retained
P=chr3:123419556-123419581 od=95 SC=456	3.123419573.1 G/T	chr3:123419573 G/T	On	Retained
P=chr3:123419733-123419746 od=26 SC=317	3.123419733.1 A/G	chr3:123419733 A/G	On	Retained
P=chr3:123451766-123451779 od=29 SC=329	3.123451773.1 G/C	chr3:123451773 G/C	On	Retained
	3.123453061.1 A/G	chr3:123453061 A/G	On	Retained
	3.123457893.1 G/A	chr3:123457893 G/A	On	Retained
P=chr3:123987956-123988095 od=990 SC=706	3.123988019.1 C/A	chr3:123988019 C/A	On	FilteredOut
P=chr3:130947419-130947459 od=108 SC=470	3.130947435.1 A/T	chr3:130947435 A/T	On	Retained
	3.142281612.1 A/G	chr3:142281612 A/G	On	Retained
P=chr3:185198255-185198262 od=41 SC=366	3.185198262.1 G/A	chr3:185198262 G/A	On	FilteredOut
P=chr3:185990055-185990135 od=339 SC=592	3.185990096.1 C/T	chr3:185990096 C/T	On	Retained
	3.186006618.1 G/C	chr3:186006618 G/C	On	Retained
P=chr4:843460-843547 od=405 SC=611	4.843498.1 G/A	chr4:843498 G/A	Near	FilteredOut
P=chr4:2990489-2990520 od=118 SC=479	4.2990499.1 G/T	chr4:2990499 G/T	On	Retained
	4.3006043.1 C/T	chr4:3006043 C/T	On	Retained
P=chr4:5448402-5448436 od=115 SC=476	4.5448429.1 A/G	chr4:5448429 A/G	On	Retained
	4.25235801.1 G/A	chr4:25235801 G/A	On	FilteredOut
	4.55972974.1 T/A	chr4:55972974 T/A	On	Retained
	4.79786856.1 G/A	chr4:79786856 G/A	On	Retained
P=chr4:107168430-107168431 od=13 SC=243	4.107168431.1 G/C	chr4:107168431 G/C	On	Retained
	4.113352397.1 G/A	chr4:113352397 G/A	On	Retained
	4.113352628.1 A/G	chr4:113352628 A/G	On	Retained
	4.113352899.1 G/A	chr4:113352899 G/A	On	Retained
	4.113353285.1 T/C	chr4:113353285 T/C	On	Retained
	4.128807219.1 T/A	chr4:128807219 T/A	On	FilteredOut
	4.151177340.1 C/T	chr4:151177340 C/T	On	Retained
	4.151177341.1 C/G	chr4:151177341 C/G	On	Retained
P=chr4:170398436-170398508 od=197 SC=534	4.170398454.1 T/C	chr4:170398454 T/C	On	Retained
P=chr5:56177391-56177465 od=355 SC=597	5.56177443.1 G/A	chr5:56177443 G/A	On	Retained
	5.56177743.1 G/A	chr5:56177743 G/A	Near	Retained
	5.66459878.1 G/C	chr5:66459878 G/C	On	Retained
P=chr5:67588107-67588186 od=503 SC=634	5.67588148.1 G/A	chr5:67588148 G/A	On	Retained
	5.96503523.1 C/T	chr5:96503523 C/T	On	Retained
P=chr5:96513430-96513563 od=651 SC=662	5.96513471.1 G/C	chr5:96513471 G/C	On	Retained
	5.96518792.1 T/G	chr5:96518792 T/G	Near	Retained
P=chr5:112176688-112176759 od=211 SC=541	5.112176756.1 T/A	chr5:112176756 T/A	On	Retained
	5.112769527.1 C/T	chr5:112769527 C/T	On	FilteredOut
P=chr5:149450126-149450136 od=18 SC=278	5.149450132.1 T/C	chr5:149450132 T/C	On	FilteredOut
P=chr5:176516626-176516639 od=17 SC=272	5.176516631.1 G/A	chr5:176516631 G/A	On	FilteredOut
	5.176517797.1 C/T	chr5:176517797 C/T	On	Retained
P=chr5:176520225-176520253 od=82 SC=440	5.176520243.1 G/A	chr5:176520243 G/A	On	Retained
P=chr5:180046342-180046371 od=173 SC=520	5.180046344.1 G/C	chr5:180046344 G/C	On	FilteredOut
P=chr5:180048550-180048665 od=417 SC=614	5.180048626.1 C/T	chr5:180048626 C/T	On	FilteredOut
	6.2679676.1 G/A	chr6:2679676 G/A	On	Retained
P=chr6:4031824-4031998 od=1018 SC=709	6.4031998.1 A/G	chr6:4031998 A/G	Near	Retained
P=chr6:31946671-31946744 od=202 SC=536	6.31946695.1 C/G	chr6:31946695 C/G	On	FilteredOut
P=chr6:31947189-31947210 od=36 SC=352	6.31947203.1 T/C	chr6:31947203 T/C	On	FilteredOut
P=chr6:33690777-33690796 od=74 SC=429	6.33690796.1 C/T	chr6:33690796 C/T	On	Retained
P=chr6:33695975-33695979 od=18 SC=278	6.33695975.1 G/A	chr6:33695975 G/A	On	Retained
P=chr6:36489507-36489598 od=641 SC=660	6.36489585.1 C/A	chr6:36489585 C/A	On	FilteredOut
	6.41903782.1 A/C	chr6:41903782 A/C	On	Retained
P=chr6:43111325-43111338 od=109 SC=471	6.43111336.1 G/T	chr6:43111336 G/T	On	FilteredOut

P=chr6:43251905-43251912 od=27 SC=321	6.43251912.1 A/G	chr6:43251912 A/G	On	Retained
	6.43252029.1 T/C	chr6:43252029 T/C	On	FilteredOut
	6.44232920.1 A/G	chr6:44232920 A/G	On	Retained
	6.44232977.1 G/A	chr6:44232977 G/A	On	Retained
P=chr6:110942392-110942395 od=20 SC=289	6.110942394.1 G/T	chr6:110942394 G/T	On	FilteredOut
P=chr6:116325117-116325167 od=209 SC=540	6.116325142.1 C/T	chr6:116325142 C/T	On	Retained
P=chr6:117638316-117638332 od=54 SC=395	6.117638325.1 C/T	chr6:117638325 C/T	On	Retained
P=chr6:136888775-136888803 od=162 SC=513	6.136888782.1 T/C	chr6:136888782 T/C	On	Retained
P=chr6:161469769-161469782 od=66 SC=417	6.161469774.1 G/A	chr6:161469774 G/A	On	Retained
	6.167271711.1 T/C	chr6:167271711 T/C	On	FilteredOut
	6.167271716.1 T/C	chr6:167271716 T/C	On	FilteredOut
P=chr7:23757160-23757203 od=101 SC=462	7.23757162.1 G/C	chr7:23757162 G/C	On	Retained
P=chr7:23775451-23775457 od=14 SC=251	7.23775454.1 G/A	chr7:23775454 G/A	On	Retained
	7.23775477.1 G/T	chr7:23775477 G/T	On	Retained
P=chr7:23808626-23808662 od=87 SC=446	7.23808650.1 G/T	chr7:23808650 G/T	On	FilteredOut
P=chr7:23811763-23811906 od=386 SC=606	7.23811795.1 T/G	chr7:23811795 T/G	On	Retained
P=chr7:23811763-23811906 od=386 SC=606	7.23811800.1 G/T	chr7:23811800 G/T	On	Retained
P=chr7:40027457-40027496 od=102 SC=463	7.40027484.1 A/G	chr7:40027484 A/G	Near	Retained
P=chr7:43635651-43635682 od=146 SC=502	7.43635671.1 A/C	chr7:43635671 A/C	On	Retained
	7.43664280.1 A/G	chr7:43664280 A/G	On	Retained
	7.55229255.1 G/A	chr7:55229255 G/A	On	FilteredOut
P=chr7:95216338-95216437 od=555 SC=645	7.95216415.1 C/A	chr7:95216415 C/A	On	FilteredOut
	7.97822115.1 T/A	chr7:97822115 T/A	On	Retained
P=chr7:98490116-98490154 od=266 SC=566	7.98490141.1 G/C	chr7:98490141 G/C	On	FilteredOut
P=chr7:98547157-98547207 od=334 SC=590	7.98547196.1 G/T	chr7:98547196 G/T	On	FilteredOut
P=chr7:116340255-116340307 od=227 SC=549	7.116340262.1 A/G	chr7:116340262 A/G	On	Retained
P=chr7:138145352-138145575 od=506 SC=635	7.138145436.1 C/A	chr7:138145436 C/A	Near	FilteredOut
P=chr7:143088860-143088876 od=45 SC=376	7.143088867.1 T/C	chr7:143088867 T/C	On	Retained
	7.143097100.1 A/G	chr7:143097100 A/G	On	Retained
	8.8176221.1 C/T	chr8:8176221 C/T	On	Retained
	8.8176554.1 C/T	chr8:8176554 C/T	On	Retained
	8.8234192.1 G/C	chr8:8234192 G/C	On	FilteredOut
	8.8234219.1 G/A	chr8:8234219 G/A	On	Retained
	8.8234714.1 C/T	chr8:8234714 C/T	On	FilteredOut
P=chr8:8239067-8239104 od=79 SC=436	8.8239069.1 C/A	chr8:8239069 C/A	On	FilteredOut
	8.11418773.1 C/T	chr8:11418773 C/T	On	FilteredOut
P=chr8:27308545-27308591 od=127 SC=487	8.27308585.1 A/C	chr8:27308585 A/C	On	Retained
P=chr8:38287238-38287269 od=157 SC=510	8.38287238.1 G/A	chr8:38287238 G/A	On	Retained
	8.48719852.1 G/C	chr8:48719852 G/C	On	Retained
	8.87076520.1 C/A	chr8:87076520 C/A	On	Retained
	8.144800905.1 A/C	chr8:144800905 A/C	On	FilteredOut
	8.144802736.1 G/C	chr8:144802736 G/C	Near	Retained
	8.145603114.1 A/C	chr8:145603114 A/C	On	Retained
P=chr9:27168490-27168609 od=418 SC=614	9.27168571.1 T/C	chr9:27168571 T/C	On	Retained
P=chr9:27183462-27183604 od=340 SC=592	9.27183463.1 A/C	chr9:27183463 A/C	On	Retained
P=chr9:71627993-71628306 od=599 SC=653	9.71628207.1 G/C	chr9:71628207 G/C	On	Retained
P=chr9:77376634-77376647 od=21 SC=295	9.77376647.1 T/C	chr9:77376647 T/C	On	Retained
P=chr9:94486317-94486330 od=74 SC=429	9.94486321.1 C/T	chr9:94486321 C/T	On	Retained
P=chr9:94495472-94495629 od=692 SC=668	9.94495608.1 T/C	chr9:94495608 T/C	On	Retained
	9.113457799.1 A/G	chr9:113457799 A/G	On	Retained
P=chr9:113538120-113538126 od=33 SC=343	9.113538122.1 G/A	chr9:113538122 G/A	On	Retained
	9.133759794.1 G/T	chr9:133759794 G/T	On	Retained
	9.136268084.1 A/G	chr9:136268084 A/G	On	Retained
	10.6527143.1 G/A	chr10:6527143 G/A	On	Retained
P=chr10:26355962-26356009 od=206 SC=539	10.26355992.1 A/G	chr10:26355992 A/G	On	Retained

P=chr10:26357709-26357773 lod=304 SC=580	10.26357748.1.G/A	chr10:26357748 G/A	On	Retained
	10.26463130.1.C/A	chr10:26463130 C/A	On	Retained
P=chr10:26482132-26482161 lod=52 SC=391	10.26482157.1.A/G	chr10:26482157 A/G	On	Retained
	10.30728250.1.A/G	chr10:30728250 A/G	Near	FilteredOut
P=chr10:59955907-59956067 lod=482 SC=629	10.59956041.1.C/T	chr10:59956041 C/T	On	Retained
P=chr10:88635769-88635785 lod=60 SC=407	10.88635779.1.C/A	chr10:88635779 C/A	On	FilteredOut
P=chr10:99400467-99400822 lod=1063 SC=714	10.99400747.1.C/A	chr10:99400747 C/A	Near	FilteredOut
P=chr10:101977844-101977890 lod=178 SC=523	10.101977883.1.C/T	chr10:101977883 C/T	On	Retained
P=chr10:121196331-121196335 lod=37 SC=355	10.121196335.1.G/A	chr10:121196335 G/A	On	Retained
	10.123310871.1.A/G	chr10:123310871 A/G	On	Retained
P=chr11:46369117-46369389 lod=811 SC=685	11.46369267.1.G/A	chr11:46369267 G/A	Near	FilteredOut
P=chr11:64597188-64597212 lod=79 SC=436	11.64597201.1.G/A	chr11:64597201 G/A	On	Retained
P=chr11:108159700-108159794 lod=456 SC=624	11.108159732.1.C/T	chr11:108159732 C/T	On	Retained
	11.108183167.1.A/G	chr11:108183167 A/G	On	Retained
	11.111594312.1.C/A	chr11:111594312 C/A	On	Retained
P=chr11:113266818-113266822 lod=17 SC=272	11.113266821.1.G/A	chr11:113266821 G/A	On	Retained
	11.113270015.1.G/C	chr11:113270015 G/C	On	FilteredOut
P=chr11:113270808-113270832 lod=58 SC=403	11.113270828.1.G/A	chr11:113270828 G/A	On	Retained
P=chr11:125525118-125525215 lod=402 SC=610	11.125525195.1.A/G	chr11:125525195 A/G	Near	Retained
P=chr12:990907-990919 lod=36 SC=352	12.990912.1.A/C	chr12:990912 A/C	On	Retained
	12.994487.1.G/C	chr12:994487 G/C	On	Retained
P=chr12:998301-998395 lod=396 SC=608	12.998365.1.G/T	chr12:998365 G/T	On	Retained
P=chr12:1009639-1009708 lod=312 SC=583	12.1009680.1.C/T	chr12:1009680 C/T	On	FilteredOut
P=chr12:10782087-10782127 lod=150 SC=505	12.10782115.1.T/C	chr12:10782115 T/C	On	Retained
	12.14829893.1.A/C	chr12:14829893 A/C	On	Retained
P=chr12:18648994-18649091 lod=371 SC=601	12.18649057.1.C/T	chr12:18649057 C/T	On	Retained
P=chr12:18719869-18719975 lod=174 SC=521	12.18719883.1.G/T	chr12:18719883 G/T	On	FilteredOut
	12.40619082.1.G/A	chr12:40619082 G/A	On	Retained
P=chr12:40657692-40657709 lod=48 SC=383	12.40657700.1.C/G	chr12:40657700 C/G	On	Retained
P=chr12:40702906-40702947 lod=204 SC=538	12.40702911.1.G/A	chr12:40702911 G/A	On	Retained
P=chr12:48367960-48367976 lod=137 SC=495	12.48367976.1.C/T	chr12:48367976 C/T		Retained
	12.52306221.1.C/T	chr12:52306221 C/T	On	Retained
P=chr12:57919357-57919798 lod=1011 SC=709	12.57919529.1.C/G	chr12:57919529 C/G		FilteredOut
P=chr12:57994584-57994679 lod=402 SC=610	12.57994679.1.C/G	chr12:57994679 C/G	On	Retained
	12.66605228.1.A/G	chr12:66605228 A/G	On	Retained
P=chr12:106460936-106460942 lod=34 SC=346	12.106460938.1.G/C	chr12:106460938 G/C	On	Retained
P=chr12:118682693-118682773 lod=484 SC=630	12.118682751.1.C/T	chr12:118682751 C/T	On	Retained
P=chr12:121691071-121691102 lod=144 SC=500	12.121691096.1.G/A	chr12:121691096 G/A	On	Retained
	12.132403161.1.A/G	chr12:132403161 A/G	On	Retained
	12.132406666.1.G/C	chr12:132406666 G/C	On	Retained
	13.21562832.1.C/T	chr13:21562832 C/T	On	Retained
	13.21562948.1.G/A	chr13:21562948 G/A	On	Retained
P=chr13:28624237-28624301 lod=138 SC=496	13.28624294.1.G/A	chr13:28624294 G/A	On	Retained
	13.32906480.1.A/C	chr13:32906480 A/C	On	Retained
	13.32911463.1.A/G	chr13:32911463 A/G	On	Retained
	13.32929387.1.T/C	chr13:32929387 T/C	On	Retained
P=chr13:37678232-37679393 lod=3056 SC=827	13.37679268.1.G/T	chr13:37679268 G/T	On	Retained
	13.110434668.1.C/A	chr13:110434668 C/A	Near	FilteredOut
	13.110435231.1.C/T	chr13:110435231 C/T	Near	Retained
P=chr13:110437613-110437827 lod=970 SC=704	13.110437802.1.A/C	chr13:110437802 A/C	Near	FilteredOut
	14.24808802.1.G/T	chr14:24808802 G/T	On	FilteredOut
	14.50798743.1.G/A	chr14:50798743 G/A		Retained
P=chr14:50799116-50799152 lod=197 SC=534	14.50799126.1.G/C	chr14:50799126 G/C	On	Retained
P=chr14:50901768-50901785 lod=117 SC=478	14.50901768.1.G/A	chr14:50901768 G/A	On	Retained
P=chr14:61924236-61924249 lod=31 SC=336	14.61924239.1.G/A	chr14:61924239 G/A	On	Retained

P=chr14:75386576-75386607 lod=163 SC=514	14.75386576.1.G/A	chr14:75386576 G/A	On	Retained
	14.75388183.1.C/T	chr14:75388183 C/T	On	Retained
	14.75574087.1.C/T	chr14:75574087 C/T	On	Retained
	14.93407062.1.A/G	chr14:93407062 A/G	Near	Retained
P=chr14:102695686-102695694 lod=16 SC=265	14.102695693.1.T/C	chr14:102695693 T/C	On	Retained
P=chr14:103934475-103934509 lod=195 SC=533	14.103934488.1.T/C	chr14:103934488 T/C	On	Retained
P=chr15:40265790-40265810 lod=69 SC=422	15.40265799.1.A/G	chr15:40265799 A/G	On	Retained
P=chr15:40477794-40477849 lod=189 SC=529	15.40477831.1.G/A	chr15:40477831 G/A	On	Retained
P=chr15:40564575-40564576 lod=14 SC=251	15.40564576.1.C/T	chr15:40564576 C/T	On	Retained
P=chr15:43170793-43170830 lod=217 SC=544	15.43170793.1.A/G	chr15:43170793 A/G	Near	Retained
P=chr15:75130090-75130142 lod=200 SC=535	15.75130093.1.T/C	chr15:75130093 T/C	On	Retained
	15.77450964.1.C/T	chr15:77450964 C/T	On	Retained
	15.85383145.1.C/G	chr15:85383145 C/G	On	Retained
	15.85383640.1.G/A	chr15:85383640 G/A	On	Retained
	15.85401259.1.C/T	chr15:85401259 C/T	On	Retained
	15.85405995.1.T/C	chr15:85405995 T/C	On	Retained
P=chr15:91436550-91436554 lod=39 SC=361	15.91436551.1.A/G	chr15:91436551 A/G	On	FilteredOut
P=chr15:99250802-99250956 lod=963 SC=703	15.99250895.1.G/T	chr15:99250895 G/T	On	FilteredOut
	15.101606889.1.G/A	chr15:101606889 G/A	On	Retained
	15.101606890.1.C/A	chr15:101606890 C/A	On	Retained
P=chr16:22269813-22269870 lod=285 SC=573	16.22269867.1.A/G	chr16:22269867 A/G	On	Retained
	16.23646191.1.T/C	chr16:23646191 T/C	Near	Retained
P=chr16:23690365-23690492 lod=475 SC=628	16.23690401.1.C/T	chr16:23690401 C/T	On	FilteredOut
	16.23711925.1.C/G	chr16:23711925 C/G	On	Retained
P=chr16:46744621-46744703 lod=533 SC=640	16.46744689.1.C/A	chr16:46744689 C/A	On	FilteredOut
	16.46773999.1.C/A	chr16:46773999 C/A	On	Retained
	16.68732049.1.A/C	chr16:68732049 A/C		Retained
P=chr17:3627466-3627477 lod=13 SC=243	17.3627473.1.C/T	chr17:3627473 C/T	On	FilteredOut
	17.3627840.1.G/A	chr17:3627840 G/A	On	Retained
	17.3628212.1.T/C	chr17:3628212 T/C	On	Retained
	17.3628362.1.T/C	chr17:3628362 T/C	On	Retained
P=chr17:3775842-3775852 lod=57 SC=401	17.3775848.1.T/C	chr17:3775848 T/C	On	Retained
P=chr17:4796270-4796343 lod=240 SC=555	17.4796274.1.T/C	chr17:4796274 T/C	On	Retained
P=chr17:4796270-4796343 lod=240 SC=555	17.4796286.1.C/T	chr17:4796286 C/T	On	Retained
P=chr17:4797277-4797330 lod=214 SC=543	17.4797305.1.G/A	chr17:4797305 G/A	On	Retained
P=chr17:7292105-7292113 lod=35 SC=349	17.7292107.1.G/A	chr17:7292107 G/A	On	Retained
	17.7579472.1.G/C	chr17:7579472 G/C	On	Retained
	17.7792326.1.C/T	chr17:7792326 C/T	On	Retained
P=chr17:7796785-7796801 lod=49 SC=385	17.7796794.1.A/C	chr17:7796794 A/C	Near	FilteredOut
	17.7796803.1.T/C	chr17:7796803 T/C	Near	Retained
	17.7796815.1.G/C	chr17:7796815 G/C	Near	FilteredOut
	17.8108331.1.A/G	chr17:8108331 A/G	On	Retained
P=chr17:8789798-8789823 lod=69 SC=422	17.8789811.1.G/A	chr17:8789811 G/A	On	FilteredOut
	17.19285705.1.G/A	chr17:19285705 G/A	On	Retained
	17.25909816.1.C/T	chr17:25909816 C/T	On	Retained
P=chr17:37879582-37879592 lod=42 SC=369	17.37879588.1.A/G	chr17:37879588 A/G	On	Retained
P=chr17:37881332-37881393 lod=348 SC=595	17.37881392.1.A/G	chr17:37881392 A/G	On	FilteredOut
P=chr17:37884023-37884098 lod=163 SC=514	17.37884037.1.C/G	chr17:37884037 C/G	On	Retained
	17.41223094.1.T/C	chr17:41223094 T/C	On	Retained
	17.41244000.1.T/C	chr17:41244000 T/C	On	Retained
	17.41244435.1.T/C	chr17:41244435 T/C	On	Retained
P=chr17:41244930-41244959 lod=56 SC=399	17.41244936.1.G/A	chr17:41244936 G/A	On	Retained
	17.41245693.1.G/T	chr17:41245693 G/T	On	FilteredOut
P=chr17:48265464-48265512 lod=253 SC=561	17.48265495.1.T/C	chr17:48265495 T/C	On	Retained
	17.56584508.1.T/C	chr17:56584508 T/C		Retained

	17.56659018.1.C/T	chr17:56659018 C/T	On	Retained
P=chr17:64783078-64783098 od=165 SC=515	17.64783081.1.G/A	chr17:64783081 G/A	On	Retained
	17.74381567.1.G/A	chr17:74381567 G/A	On	Retained
	17.79093822.1.A/G	chr17:79093822 A/G	On	Retained
	17.79095629.1.C/A	chr17:79095629 C/A	On	FilteredOut
P=chr18:18534821-18535008 od=1216 SC=728	18.18534948.1.G/C	chr18:18534948 G/C	On	FilteredOut
	18.48190440.1.G/A	chr18:48190440 G/A	On	Retained
	18.53303101.1.C/G	chr18:53303101 C/G		FilteredOut
	18.56149099.1.T/C	chr18:56149099 T/C	On	Retained
	18.56203898.1.T/G	chr18:56203898 T/G	On	Retained
	18.56204250.1.A/C	chr18:56204250 A/C	On	Retained
	18.56204747.1.G/A	chr18:56204747 G/A	On	Retained
P=chr18:56279022-56279042 od=50 SC=387	18.56279025.1.T/G	chr18:56279025 T/G	On	Retained
P=chr18:59854985-59854988 od=18 SC=278	18.59854988.1.G/T	chr18:59854988 G/T	On	FilteredOut
P=chr18:59919889-59919911 od=121 SC=482	18.59919898.1.C/A	chr18:59919898 C/A	On	FilteredOut
P=chr19:2046392-2046402 od=56 SC=399	19.2046399.1.G/A	chr19:2046399 G/A	On	FilteredOut
	19.10473048.1.G/A	chr19:10473048 G/A	On	Retained
	19.10475652.1.C/A	chr19:10475652 C/A	On	Retained
P=chr19:14574883-14574898 od=51 SC=389	19.14574897.1.C/A	chr19:14574897 C/A	On	Retained
P=chr19:14582456-14582493 od=146 SC=502	19.14582468.1.G/A	chr19:14582468 G/A	On	FilteredOut
	19.17949138.1.C/A	chr19:17949138 C/A	On	FilteredOut
	19.18255359.1.G/A	chr19:18255359 G/A	On	Retained
	19.18273047.1.T/C	chr19:18273047 T/C	On	Retained
	19.38896244.1.C/A	chr19:38896244 C/A		Retained
	19.40739513.1.A/G	chr19:40739513 A/G	On	Retained
P=chr19:41210996-41211088 od=521 SC=638	19.41211056.1.T/C	chr19:41211056 T/C	On	Retained
	19.41743861.1.A/G	chr19:41743861 A/G	On	Retained
P=chr19:46275969-46275994 od=56 SC=399	19.46275976.1.G/C	chr19:46275976 G/C	On	FilteredOut
P=chr19:47177898-47177953 od=298 SC=578	19.47177913.1.A/G	chr19:47177913 A/G	On	Retained
P=chr19:47193933-47193946 od=74 SC=429	19.47193933.1.G/T	chr19:47193933 G/T	On	FilteredOut
	19.56041255.1.C/G	chr19:56041255 C/G	On	Retained
P=chr19:56047438-56047469 od=105 SC=467	19.56047448.1.A/G	chr19:56047448 A/G	On	Retained
P=chr19:56047522-56047574 od=144 SC=500	19.56047544.1.G/T	chr19:56047544 G/T	On	Retained
P=chr20:9543610-9543632 od=189 SC=529	20.9543622.1.C/T	chr20:9543622 C/T	On	Retained
P=chr20:30407430-30407454 od=57 SC=401	20.30407433.1.C/A	chr20:30407433 C/A	On	FilteredOut
P=chr20:54961458-54961463 od=12 SC=235	20.54961463.1.T/C	chr20:54961463 T/C	On	Retained
	20.54961541.1.A/T	chr20:54961541 A/T	On	Retained
	21.33371123.1.C/T	chr21:33371123 C/T	On	Retained
P=chr21:43161353-43161363 od=34 SC=346	21.43161357.1.T/C	chr21:43161357 T/C	On	Retained
	21.44837555.1.G/A	chr21:44837555 G/A	On	Retained
	21.45959312.1.C/T	chr21:45959312 C/T		Retained
P=chr22:31672926-31673141 od=331 SC=589	22.31673116.1.A/G	chr22:31673116 A/G	On	FilteredOut
P=chr22:50696667-50696682 od=75 SC=431	22.50696678.1.G/A	chr22:50696678 G/A	On	Retained
	22.50705059.1.A/G	chr22:50705059 A/G	On	Retained
	22.50705304.1.C/T	chr22:50705304 C/T	Near	Retained
	X.3631167.1.A/G	chrX:3631167 A/G	On	FilteredOut
	X.19482476.1.C/T	chrX:19482476 C/T	On	Retained
	X.107976940.1.G/C	chrX:107976940 G/C	On	Retained
P=chrX:108708501-108708619 od=344 SC=593	X.108708516.1.C/T	chrX:108708516 C/T	On	Retained
	X.153278829.1.G/A	chrX:153278829 G/A	On	Retained
	X.153284192.1.A/G	chrX:153284192 A/G	On	Retained

Detected Information

QUA=18429.82:BaseQRankSum=15.241:Dels=0.00:FS=113.274:HRun=0:HaplotvpeScore=6.2764:MQ=44.62:MQ0=119:QD=6.25:ReadPosRankSum=-2.596:SB=-495
 QUA=573.31:BaseQRankSum=5.294:Dels=0.00:FS=265.947:HRun=1:HaplotvpeScore=6.0799:MQ=29.71:MQ0=443:QD=0.46:ReadPosRankSum=-8.798:SB=-5.80:cul
 QUA=18700.11:BaseQRankSum=21.759:Dels=0.00:FS=77.695:HRun=0:HaplotvpeScore=6.1077:MQ=29.70:MQ0=250:QD=6.23:ReadPosRankSum=-0.274:SB=-7925
 QUA=10899.43:BaseQRankSum=1.575:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=0.6942:MQ=22.65:MQ0=191:QD=17.84:ReadPosRankSum=1.460:SB=-939.21
 QUA=67725.38:BaseQRankSum=1.261:Dels=0.00:FS=1.885:HRun=1:HaplotvpeScore=4.9434:MQ=30.58:MQ0=468:QD=22.80:ReadPosRankSum=1.924:SB=-32154.2
 QUA=32995.64:BaseQRankSum=1.659:Dels=0.00:FS=5.907:HRun=0:HaplotvpeScore=4.1021:MQ=19.15:MQ0=1292:QD=11.88:ReadPosRankSum=1.164:SB=-1638.1
 QUA=23825.95:BaseQRankSum=-6.727:Dels=0.00:FS=11.386:HRun=0:HaplotvpeScore=3.8923:MQ=59.86:MQ0=0:QD=13.66:ReadPosRankSum=-0.065:SB=-13239
 QUA=34656.85:BaseQRankSum=-3.051:Dels=0.00:FS=11.231:HRun=0:HaplotvpeScore=7.2085:MQ=59.87:MQ0=0:QD=13.39:ReadPosRankSum=0.796:SB=-10898.6
 QUA=42408.69:BaseQRankSum=-27.304:Dels=0.00:FS=0.134:HRun=0:HaplotvpeScore=6.1972:MQ=59.87:MQ0=0:QD=14.14:ReadPosRankSum=-1.164:SB=-17549
 QUA=31961.02:BaseQRankSum=0.782:Dels=0.00:FS=42.033:HRun=1:HaplotvpeScore=6.5129:MQ=59.92:MQ0=0:QD=12.70:ReadPosRankSum=0.279:SB=-14304.70
 QUA=22772.06:BaseQRankSum=-7.859:Dels=0.00:FS=6.742:HRun=0:HaplotvpeScore=3.2781:MQ=59.85:MQ0=0:QD=12.92:ReadPosRankSum=0.666:SB=-10778.67
 QUA=2623.94:BaseQRankSum=-19.759:Dels=0.00:FS=729.607:HRun=0:HaplotvpeScore=5.8688:MQ=59.83:MQ0=0:QD=1.06:ReadPosRankSum=6.142:SB=-0.02:cul
 QUA=42277.71:BaseQRankSum=-17.691:Dels=0.00:FS=1.367:HRun=0:HaplotvpeScore=7.8711:MQ=59.73:MQ0=0:QD=14.71:ReadPosRankSum=0.521:SB=-18748.9
 QUA=40402.61:BaseQRankSum=21.404:Dels=0.00:FS=17.328:HRun=1:HaplotvpeScore=7.3416:MQ=59.89:MQ0=0:QD=16.11:ReadPosRankSum=0.786:SB=-16352
 QUA=111710.53:BaseQRankSum=2.375:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=4.8561:MQ=59.90:MQ0=0:QD=37.42:ReadPosRankSum=-1.436:SB=-43896.3
 QUA=41429.56:BaseQRankSum=16.189:Dels=0.00:FS=1.947:HRun=2:HaplotvpeScore=5.0968:MQ=59.87:MQ0=0:QD=15.69:ReadPosRankSum=-0.212:SB=-9841.93
 QUA=47070.70:BaseQRankSum=5.995:Dels=0.00:FS=15.579:HRun=2:HaplotvpeScore=4.7459:MQ=59.66:MQ0=0:QD=15.72:ReadPosRankSum=-0.189:SB=-19527.5
 QUA=44178.66:BaseQRankSum=16.115:Dels=0.00:FS=0.403:HRun=0:HaplotvpeScore=4.2421:MQ=59.89:MQ0=0:QD=14.76:ReadPosRankSum=0.187:SB=-21069.08
 QUA=80096.39:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=4.3485:MQ=59.90:MQ0=0:QD=36.78:SB=-14419.86:culprit=HaplotvpeScore:
 QUA=104968.49:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=3.8403:MQ=59.39:MQ0=0:QD=35.57:SB=-45125.50:culprit=HaplotvpeScore:
 QUA=112858.50:BaseQRankSum=1.710:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=6.7774:MQ=59.82:MQ0=0:QD=37.64:ReadPosRankSum=-1.258:SB=-42528.7
 QUA=43607.83:BaseQRankSum=-19.070:Dels=0.00:FS=0.133:HRun=0:HaplotvpeScore=6.5974:MQ=59.78:MQ0=0:QD=14.66:ReadPosRankSum=-1.490:SB=-20009
 QUA=43129.33:BaseQRankSum=11.555:Dels=0.00:FS=0.699:HRun=3:HaplotvpeScore=5.0664:MQ=59.84:MQ0=0:QD=14.86:ReadPosRankSum=-2.000:SB=-21421.2
 QUA=87861.92:BaseQRankSum=1.641:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=4.6493:MQ=59.87:MQ0=0:QD=34.00:ReadPosRankSum=1.150:SB=-37622.23
 QUA=48186.75:BaseQRankSum=3.850:Dels=0.00:FS=1.325:HRun=0:HaplotvpeScore=5.4494:MQ=59.82:MQ0=0:QD=16.07:ReadPosRankSum=1.359:SB=-24447.46
 QUA=28116.40:BaseQRankSum=-16.346:Dels=0.00:FS=8.292:HRun=0:HaplotvpeScore=3.1569:MQ=59.91:MQ0=0:QD=13.49:ReadPosRankSum=-0.855:SB=-5845.1
 QUA=97169.84:BaseQRankSum=1.731:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=6.1472:MQ=59.84:MQ0=0:QD=35.13:ReadPosRankSum=1.347:SB=-42877.82
 QUA=105906.71:Dels=0.00:FS=0.000:HRun=2:HaplotvpeScore=5.8553:MQ=59.87:MQ0=0:QD=35.34:SB=-33175.21:culprit=HaplotvpeScore:
 QUA=46166.94:BaseQRankSum=14.943:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=6.5660:MQ=59.77:MQ0=0:QD=15.41:ReadPosRankSum=-0.199:SB=-23342.5
 QUA=86959.47:BaseQRankSum=1.712:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=4.8802:MQ=59.83:MQ0=0:QD=33.27:ReadPosRankSum=1.148:SB=-31537.90
 QUA=93985.45:BaseQRankSum=1.685:Dels=0.00:FS=3.211:HRun=0:HaplotvpeScore=5.9771:MQ=59.75:MQ0=0:QD=33.08:ReadPosRankSum=-0.306:SB=-44512.83
 QUA=25511.80:BaseQRankSum=8.510:Dels=0.00:FS=5.030:HRun=2:HaplotvpeScore=3.3681:MQ=59.83:MQ0=0:QD=12.58:ReadPosRankSum=-0.455:SB=-11495.91
 QUA=29754.80:BaseQRankSum=9.181:Dels=0.00:FS=3.707:HRun=0:HaplotvpeScore=4.1284:MQ=59.80:MQ0=0:QD=12.62:ReadPosRankSum=-1.005:SB=-15039.56
 QUA=41833.21:BaseQRankSum=13.474:Dels=0.00:FS=0.745:HRun=0:HaplotvpeScore=6.0025:MQ=59.83:MQ0=0:QD=15.50:ReadPosRankSum=-2.253:SB=-16868.3
 QUA=524.79:BaseQRankSum=-18.279:Dels=0.00:FS=309.258:HRun=0:HaplotvpeScore=4.9625:MQ=59.83:MQ0=0:QD=0.79:ReadPosRankSum=-0.468:SB=0.02:cul
 QUA=47174.19:BaseQRankSum=5.656:Dels=0.00:FS=2.073:HRun=0:HaplotvpeScore=6.8506:MQ=59.79:MQ0=0:QD=15.86:ReadPosRankSum=-0.172:SB=-18018.63
 QUA=43803.06:BaseQRankSum=-13.850:Dels=0.00:FS=1.410:HRun=0:HaplotvpeScore=5.5799:MQ=59.86:MQ0=0:QD=14.89:ReadPosRankSum=1.296:SB=-15244.4
 QUA=35546.31:BaseQRankSum=-14.806:Dels=0.00:FS=13.692:HRun=1:HaplotvpeScore=8.3614:MQ=59.80:MQ0=0:QD=14.59:ReadPosRankSum=-0.839:SB=-1703
 QUA=46067.74:BaseQRankSum=-6.831:Dels=0.00:FS=5.704:HRun=3:HaplotvpeScore=2.9816:MQ=59.82:MQ0=0:QD=15.44:ReadPosRankSum=-0.652:SB=-23723.2
 QUA=39764.64:BaseQRankSum=2.006:Dels=0.00:FS=3.048:HRun=0:HaplotvpeScore=6.5726:MQ=59.87:MQ0=0:QD=14.92:ReadPosRankSum=0.617:SB=-16824.28
 QUA=41121.19:BaseQRankSum=-1.497:Dels=0.00:FS=0.000:HRun=2:HaplotvpeScore=7.5293:MQ=59.75:MQ0=0:QD=14.56:ReadPosRankSum=-0.751:SB=-21010.1
 QUA=104218.73:BaseQRankSum=1.703:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=4.5642:MQ=59.84:MQ0=0:QD=36.14:ReadPosRankSum=0.034:SB=-46903.60
 QUA=332.51:BaseQRankSum=-20.745:Dels=0.00:FS=337.780:HRun=1:HaplotvpeScore=5.1619:MQ=59.89:MQ0=0:QD=0.33:ReadPosRankSum=1.660:SB=-9.26:cul
 QUA=979.74:BaseQRankSum=-17.907:Dels=0.00:FS=1898.288:HRun=2:HaplotvpeScore=4.4822:MQ=59.40:MQ0=0:QD=1.13:ReadPosRankSum=-19.617:SB=4.95:cul
 QUA=3709.37:BaseQRankSum=-12.727:Dels=0.00:FS=2.030:HRun=3:HaplotvpeScore=3.8031:MQ=59.87:MQ0=0:QD=14.84:ReadPosRankSum=-0.449:SB=-1464.96
 QUA=5503.45:BaseQRankSum=2.204:Dels=0.00:FS=3.019:HRun=2:HaplotvpeScore=0.6592:MQ=59.84:MQ0=0:QD=15.00:ReadPosRankSum=-0.677:SB=-0.02:cul
 QUA=45406.81:BaseQRankSum=30.973:Dels=0.00:FS=4.312:HRun=0:HaplotvpeScore=5.0792:MQ=59.90:MQ0=0:QD=15.16:ReadPosRankSum=-0.491:SB=-15847.8
 QUA=108343.40:BaseQRankSum=1.697:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=4.6189:MQ=59.89:MQ0=0:QD=36.37:ReadPosRankSum=1.583:SB=-48025.6
 QUA=37763.88:BaseQRankSum=-11.523:Dels=0.00:FS=0.553:HRun=0:HaplotvpeScore=6.0305:MQ=59.86:MQ0=0:QD=12.60:ReadPosRankSum=0.093:SB=-18296.2
 QUA=48107.38:BaseQRankSum=18.938:Dels=0.00:FS=7.322:HRun=1:HaplotvpeScore=5.8617:MQ=59.88:MQ0=0:QD=16.07:ReadPosRankSum=0.281:SB=-24947.93
 QUA=48481.88:BaseQRankSum=2.207:Dels=0.00:FS=7.300:HRun=0:HaplotvpeScore=4.2620:MQ=59.91:MQ0=0:QD=16.16:ReadPosRankSum=-1.397:SB=-23195.10
 QUA=4287.54:BaseQRankSum=-38.865:Dels=0.00:FS=1530.408:HRun=2:HaplotvpeScore=41.7032:MQ=59.38:MQ0=0:QD=1.48:ReadPosRankSum=-10.239:SB=-0.0

QUAL=421.85:BaseQRankSum=-25.438:Dels=0.00:FS=707.699:HRun=0:HaplotvpeScore=4.8344:MQ=59.88:MQ0=0:QD=0.39:ReadPosRankSum=4.943:SB=-1.54:culpr

QUAL=44271.86:BaseQRankSum=-7.047:Dels=0.00:FS=2.011:HRun=0:HaplotvpeScore=5.8531:MQ=59.85:MQ0=0:QD=14.79:ReadPosRankSum=-1.324:SB=-18172.3

QUAL=46705.49:BaseQRankSum=-15.908:Dels=0.00:FS=3.801:HRun=0:HaplotvpeScore=5.0990:MQ=59.85:MQ0=0:QD=15.57:ReadPosRankSum=-1.472:SB=-22230

QUAL=108859.25:BaseQRankSum=1.731:Dels=0.00:FS=0.000:HRun=4:HaplotvpeScore=4.9031:MQ=58.91:MQ0=0:QD=37.08:ReadPosRankSum=1.267:SB=-34336.97

QUAL=43898.55:BaseQRankSum=3.848:Dels=0.00:FS=3.610:HRun=2:HaplotvpeScore=5.1677:MQ=59.88:MQ0=0:QD=15.69:ReadPosRankSum=-1.491:SB=-14436.62

QUAL=107594.28:BaseQRankSum=3.601:Dels=0.00:FS=2.038:HRun=0:HaplotvpeScore=6.9386:MQ=59.85:MQ0=1:QD=35.86:ReadPosRankSum=-1.198:SB=-53778.2

QUAL=85602.13:BaseQRankSum=1.142:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=5.4791:MQ=59.80:MQ0=0:QD=34.31:ReadPosRankSum=0.280:SB=-33505.337

QUAL=3677.47:BaseQRankSum=-1.663:Dels=0.00:FS=4.002:HRun=0:HaplotvpeScore=5.7074:MQ=59.82:MQ0=0:QD=14.71:ReadPosRankSum=-0.900:SB=-1670.157

QUAL=112036.56:BaseQRankSum=1.681:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=4.8486:MQ=59.85:MQ0=0:QD=38.20:ReadPosRankSum=0.481:SB=-56284.43

QUAL=48519.11:BaseQRankSum=-26.976:Dels=0.00:FS=9.524:HRun=0:HaplotvpeScore=6.1948:MQ=59.89:MQ0=0:QD=16.21:ReadPosRankSum=1.166:SB=-18066.3

QUAL=101778.59:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=6.5249:MQ=59.90:MQ0=0:QD=34.74:SB=-52867.39:culpritr=HaplotvpeScore:

QUAL=112152.32:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=4.0559:MQ=59.83:MQ0=0:QD=37.48:SB=-47444.17:culpritr=HaplotvpeScore:

QUAL=107728.05:BaseQRankSum=2.414:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=4.7728:MQ=59.77:MQ0=0:QD=37.58:ReadPosRankSum=0.410:SB=-54877.60

QUAL=113405.03:BaseQRankSum=0.472:Dels=0.00:FS=3.285:HRun=1:HaplotvpeScore=5.4109:MQ=59.90:MQ0=0:QD=37.89:ReadPosRankSum=-0.039:SB=-55925.7

QUAL=109417.79:BaseQRankSum=1.690:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=5.0504:MQ=59.86:MQ0=0:QD=37.13:ReadPosRankSum=1.680:SB=-45324.94

QUAL=110421.17:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=5.0385:MQ=59.84:MQ0=0:QD=36.94:SB=-47905.41:culpritr=HaplotvpeScore:

QUAL=113813.60:BaseQRankSum=1.897:Dels=0.00:FS=2.934:HRun=0:HaplotvpeScore=4.1685:MQ=59.84:MQ0=0:QD=37.94:ReadPosRankSum=1.731:SB=-52936.87

QUAL=110101.19:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=11.1232:MQ=59.80:MQ0=0:QD=36.72:SB=-52843.15:culpritr=HaplotvpeScore:

QUAL=102884.66:BaseQRankSum=1.075:Dels=0.00:FS=4.064:HRun=0:HaplotvpeScore=4.3454:MQ=59.84:MQ0=0:QD=34.82:ReadPosRankSum=-1.386:SB=-44613.8

QUAL=44799.44:BaseQRankSum=0.262:Dels=0.00:FS=1.589:HRun=0:HaplotvpeScore=3.5598:MQ=59.84:MQ0=0:QD=15.26:ReadPosRankSum=0.748:SB=-16242.747

QUAL=37586.74:BaseQRankSum=-15.092:Dels=0.00:FS=2.406:HRun=0:HaplotvpeScore=4.1523:MQ=59.89:MQ0=0:QD=13.04:ReadPosRankSum=-0.744:SB=-11773

QUAL=44108.22:BaseQRankSum=-11.521:Dels=0.00:FS=1.642:HRun=0:HaplotvpeScore=3.7664:MQ=59.85:MQ0=0:QD=14.76:ReadPosRankSum=-1.906:SB=-20614

QUAL=46678.42:BaseQRankSum=8.743:Dels=0.00:FS=5.458:HRun=0:HaplotvpeScore=6.2900:MQ=59.91:MQ0=0:QD=15.59:ReadPosRankSum=0.382:SB=-22172.367

QUAL=47597.89:BaseQRankSum=-10.608:Dels=0.00:FS=5.712:HRun=1:HaplotvpeScore=5.1515:MQ=59.84:MQ0=0:QD=15.90:ReadPosRankSum=0.204:SB=-22154.8

QUAL=47852.03:BaseQRankSum=11.557:Dels=0.00:FS=0.846:HRun=0:HaplotvpeScore=5.8020:MQ=59.81:MQ0=0:QD=15.95:ReadPosRankSum=-0.190:SB=-21609.8

QUAL=48904.62:BaseQRankSum=19.860:Dels=0.00:FS=0.837:HRun=0:HaplotvpeScore=5.0859:MQ=59.86:MQ0=0:QD=16.40:ReadPosRankSum=1.097:SB=-24308.66

QUAL=48567.91:BaseQRankSum=19.284:Dels=0.00:FS=5.493:HRun=1:HaplotvpeScore=3.5296:MQ=59.84:MQ0=0:QD=16.19:ReadPosRankSum=-0.722:SB=-21489.5

QUAL=47603.66:BaseQRankSum=-28.100:Dels=0.00:FS=11.167:HRun=0:HaplotvpeScore=4.9762:MQ=59.86:MQ0=0:QD=16.01:ReadPosRankSum=-1.051:SB=-2321

QUAL=116045.57:BaseQRankSum=2.605:Dels=0.00:FS=0.000:HRun=2:HaplotvpeScore=4.8290:MQ=59.84:MQ0=0:QD=38.68:ReadPosRankSum=1.370:SB=-52586.29

QUAL=117804.87:BaseQRankSum=1.718:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=5.3190:MQ=59.79:MQ0=0:QD=39.28:ReadPosRankSum=-0.728:SB=-54826.7

QUAL=109745.13:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=4.3400:MQ=59.84:MQ0=0:QD=36.58:SB=-22119.50:culpritr=HaplotvpeScore:

QUAL=107163.86:BaseQRankSum=3.865:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=4.7141:MQ=59.84:MQ0=0:QD=35.86:ReadPosRankSum=0.833:SB=-42052.70

QUAL=110728.29:BaseQRankSum=2.431:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=3.9979:MQ=59.81:MQ0=0:QD=36.97:ReadPosRankSum=-1.103:SB=-47538.4

QUAL=97118.66:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=5.1341:MQ=59.82:MQ0=0:QD=34.69:SB=-40958.21:culpritr=HaplotvpeScore:

QUAL=706.07:BaseQRankSum=-14.922:Dels=0.00:FS=2.107:HRun=3:HaplotvpeScore=4.4521:MQ=59.71:MQ0=0:QD=1.13:ReadPosRankSum=1.953:SB=-0.02:culpritr

QUAL=43778.29:BaseQRankSum=21.939:Dels=0.00:FS=4.243:HRun=0:HaplotvpeScore=4.5024:MQ=59.88:MQ0=0:QD=14.59:ReadPosRankSum=0.113:SB=-15680.87

QUAL=112199.56:BaseQRankSum=1.616:Dels=0.00:FS=3.091:HRun=2:HaplotvpeScore=3.6977:MQ=59.86:MQ0=0:QD=37.47:ReadPosRankSum=-1.647:SB=-56612.2

QUAL=42598.52:BaseQRankSum=7.443:Dels=0.00:FS=6.256:HRun=0:HaplotvpeScore=6.6863:MQ=59.85:MQ0=0:QD=14.28:ReadPosRankSum=1.290:SB=-22121.337

QUAL=112344.56:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=2.7950:MQ=59.80:MQ0=0:QD=37.45:SB=-19192.35:culpritr=HaplotvpeScore:

QUAL=97153.52:BaseQRankSum=2.959:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=7.1212:MQ=59.70:MQ0=0:QD=34.16:ReadPosRankSum=0.781:SB=-42095.917

QUAL=111458.76:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=5.2454:MQ=59.67:MQ0=0:QD=37.24:SB=-48793.43:culpritr=HaplotvpeScore:

QUAL=110468.79:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=5.6031:MQ=59.62:MQ0=0:QD=37.43:SB=-47045.60:culpritr=HaplotvpeScore:

QUAL=105270.73:Dels=0.00:FS=0.000:HRun=2:HaplotvpeScore=7.3214:MQ=59.60:MQ0=0:QD=36.30:SB=-52808.07:culpritr=HaplotvpeScore:

QUAL=1517.36:BaseQRankSum=-22.562:Dels=0.00:FS=522.570:HRun=0:HaplotvpeScore=5.3091:MQ=59.47:MQ0=0:QD=0.76:ReadPosRankSum=4.049:SB=2.32:culpr

QUAL=27136.96:BaseQRankSum=-11.393:Dels=0.00:FS=7.641:HRun=1:HaplotvpeScore=5.5271:MQ=59.83:MQ0=0:QD=13.71:ReadPosRankSum=-0.551:SB=-10161

QUAL=43306.26:BaseQRankSum=-5.451:Dels=0.00:FS=6.133:HRun=2:HaplotvpeScore=7.9031:MQ=59.88:MQ0=0:QD=14.84:ReadPosRankSum=-0.330:SB=-14955.6

QUAL=73649.52:BaseQRankSum=2.975:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=4.3260:MQ=59.86:MQ0=0:QD=34.02:ReadPosRankSum=0.377:SB=-25396.867

QUAL=66669.86:BaseQRankSum=2.314:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=3.3418:MQ=59.84:MQ0=0:QD=35.96:ReadPosRankSum=0.472:SB=-10828.827

QUAL=95530.81:BaseQRankSum=1.713:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=5.1383:MQ=59.84:MQ0=0:QD=34.31:ReadPosRankSum=-1.665:SB=-24038.70

QUAL=103615.33:BaseQRankSum=1.715:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=6.0490:MQ=59.90:MQ0=0:QD=34.92:ReadPosRankSum=-1.480:SB=-49394.9

QUAL=106982.87:BaseQRankSum=2.429:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=5.2327:MQ=59.89:MQ0=0:QD=35.68:ReadPosRankSum=-1.067:SB=-53330.4

QUAL=3364.89:BaseQRankSum=5.867:Dels=0.00:FS=8.801:HRun=0:HaplotvpeScore=3.7408:MQ=59.92:MQ0=0:QD=14.14:ReadPosRankSum=1.991:SB=-828.14:culpr

QUAL=47258.88:BaseQRankSum=24.333:Dels=0.00:FS=0.130:HRun=1:HaplotvpeScore=3.6220:MQ=59.89:MQ0=0:QD=15.80:ReadPosRankSum=0.061:SB=-22418.14

QUAL=92431.82:BaseQRankSum=1.681:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=4.2488:MQ=56.10:MQ0=0:QD=33.49:ReadPosRankSum=0.831:SB=-37289.787

QUAL=103739.61:BaseQRankSum=1.679:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=4.5410:MQ=57.88:MQ0=0:QD=35.83:ReadPosRankSum=1.130:SB=-39399.93

QUAL=112198.81:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=5.3076:MQ=59.85:MQ0=0:QD=37.54:SB=-57216.97:culprit=HaplotvpeScore:
QUAL=103214.45:BaseQRankSum=-0.198:Dels=0.00:FS=2.819:HRun=1:HaplotvpeScore=5.6985:MQ=59.80:MQ0=0:QD=34.83:ReadPosRankSum=-0.132:SB=-39909
QUAL=35340.52:BaseQRankSum=2.346:Dels=0.00:FS=1.998:HRun=0:HaplotvpeScore=5.1712:MQ=59.79:MQ0=0:QD=12.38:ReadPosRankSum=-0.050:SB=-13733.54
QUAL=42816.39:BaseQRankSum=-27.822:Dels=0.00:FS=1.058:HRun=0:HaplotvpeScore=3.9323:MQ=59.91:MQ0=0:QD=14.44:ReadPosRankSum=0.560:SB=-9930.16
QUAL=101300.90:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=5.0325:MQ=59.57:MQ0=1:QD=35.17:SB=-48666.54:culprit=HaplotvpeScore:
QUAL=68117.26:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=5.3228:MQ=55.13:MQ0=2:QD=35.04:SB=-35769.77:culprit=HaplotvpeScore:
QUAL=82870.90:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=3.7610:MQ=59.87:MQ0=0:QD=34.95:SB=-38501.88:culprit=HaplotvpeScore:
QUAL=89662.51:BaseQRankSum=-0.115:Dels=0.00:FS=3.745:HRun=0:HaplotvpeScore=5.4534:MQ=59.83:MQ0=0:QD=33.01:ReadPosRankSum=-0.874:SB=-38308.6
QUAL=103200.92:BaseQRankSum=1.691:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=5.6094:MQ=59.85:MQ0=0:QD=34.67:ReadPosRankSum=-0.937:SB=-49631.4
QUAL=259.36:BaseQRankSum=-18.377:Dels=0.00:FS=560.007:HRun=1:HaplotvpeScore=3.4076:MQ=59.80:MQ0=0:QD=0.48:ReadPosRankSum=0.921:SB=-9.16:culp
QUAL=104145.50:BaseQRankSum=1.727:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=6.4531:MQ=59.84:MQ0=0:QD=35.28:ReadPosRankSum=0.835:SB=-19435.16
QUAL=44235.79:BaseQRankSum=-13.253:Dels=0.00:FS=0.685:HRun=0:HaplotvpeScore=4.2779:MQ=59.90:MQ0=0:QD=14.75:ReadPosRankSum=-1.566:SB=-21914
QUAL=46290.90:BaseQRankSum=11.639:Dels=0.00:FS=1.649:HRun=0:HaplotvpeScore=4.6901:MQ=59.83:MQ0=0:QD=15.44:ReadPosRankSum=3.555:SB=-22502.06
QUAL=109879.68:Dels=0.00:FS=0.000:HRun=3:HaplotvpeScore=5.1063:MQ=59.91:MQ0=0:QD=37.05:SB=-45160.52:culprit=HaplotvpeScore:
QUAL=100125.42:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=7.9508:MQ=59.84:MQ0=0:QD=33.96:SB=-50016.50:culprit=HaplotvpeScore:
QUAL=6602.36:BaseQRankSum=3.556:Dels=0.00:FS=0.393:HRun=1:HaplotvpeScore=1.0639:MQ=59.90:MQ0=0:QD=16.03:ReadPosRankSum=-0.410:SB=-1956.25:cul
QUAL=115173.05:BaseQRankSum=1.731:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=3.1447:MQ=58.54:MQ0=0:QD=38.39:ReadPosRankSum=0.699:SB=-52458.78
QUAL=76428.99:BaseQRankSum=1.709:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=3.6675:MQ=59.87:MQ0=0:QD=34.18:ReadPosRankSum=1.703:SB=-24421.32
QUAL=59481.03:BaseQRankSum=1.530:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=3.4244:MQ=59.40:MQ0=0:QD=33.06:ReadPosRankSum=-1.483:SB=-28050.36
QUAL=15482.91:BaseQRankSum=13.106:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=2.0414:MQ=59.88:MQ0=0:QD=13.63:ReadPosRankSum=-0.278:SB=-6222.52
QUAL=44765.92:BaseQRankSum=-21.769:Dels=0.00:FS=4.281:HRun=0:HaplotvpeScore=4.1205:MQ=59.86:MQ0=0:QD=14.94:ReadPosRankSum=-0.674:SB=-16272
QUAL=114480.15:BaseQRankSum=0.429:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=4.3238:MQ=59.86:MQ0=0:QD=38.36:ReadPosRankSum=1.659:SB=-32250.02
QUAL=108722.53:BaseQRankSum=2.947:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=5.8725:MQ=59.77:MQ0=0:QD=36.92:ReadPosRankSum=-1.049:SB=-38319.6
QUAL=109452.93:BaseQRankSum=1.729:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=4.9585:MQ=59.81:MQ0=0:QD=36.94:ReadPosRankSum=0.522:SB=-44505.46
QUAL=101497.82:BaseQRankSum=0.806:Dels=0.00:FS=4.158:HRun=0:HaplotvpeScore=6.2780:MQ=59.77:MQ0=0:QD=33.87:ReadPosRankSum=1.057:SB=-43571.61
QUAL=110354.40:BaseQRankSum=0.309:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=5.2945:MQ=59.76:MQ0=0:QD=37.28:ReadPosRankSum=-0.047:SB=-34998.2
QUAL=62321.05:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=2.7096:MQ=59.85:MQ0=0:QD=34.45:SB=-22292.61:culprit=HaplotvpeScore:
QUAL=46394.60:BaseQRankSum=3.272:Dels=0.00:FS=24.270:HRun=1:HaplotvpeScore=4.0820:MQ=59.88:MQ0=0:QD=15.46:ReadPosRankSum=1.057:SB=-19632.14
QUAL=36805.04:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=3.6628:MQ=59.11:MQ0=0:QD=33.58:SB=-9244.50:culprit=HaplotvpeScore:
QUAL=37279.14:BaseQRankSum=1.424:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=3.6628:MQ=59.11:MQ0=0:QD=34.01:ReadPosRankSum=-0.008:SB=-9202.49
QUAL=44955.73:BaseQRankSum=23.875:Dels=0.00:FS=1.024:HRun=1:HaplotvpeScore=4.2961:MQ=59.85:MQ0=0:QD=15.33:ReadPosRankSum=-0.500:SB=-18694.4
QUAL=47138.60:BaseQRankSum=-21.397:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=5.0226:MQ=59.92:MQ0=0:QD=15.72:ReadPosRankSum=-1.241:SB=-24002
QUAL=25079.68:BaseQRankSum=-8.777:Dels=0.00:FS=2.475:HRun=1:HaplotvpeScore=3.5405:MQ=59.86:MQ0=0:QD=15.32:ReadPosRankSum=-0.837:SB=-4888.15
QUAL=44369.37:BaseQRankSum=1.724:Dels=0.00:FS=0.000:HRun=2:HaplotvpeScore=3.0168:MQ=59.84:MQ0=0:QD=32.48:ReadPosRankSum=1.156:SB=-14599.65
QUAL=40199.54:BaseQRankSum=-17.207:Dels=0.00:FS=0.137:HRun=0:HaplotvpeScore=3.1434:MQ=59.92:MQ0=0:QD=14.55:ReadPosRankSum=0.282:SB=-17947.8
QUAL=114324.43:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=4.1598:MQ=59.87:MQ0=0:QD=38.11:SB=-55228.35:culprit=HaplotvpeScore:
QUAL=46524.77:BaseQRankSum=-3.426:Dels=0.00:FS=0.401:HRun=0:HaplotvpeScore=3.6003:MQ=59.87:MQ0=0:QD=15.57:ReadPosRankSum=0.708:SB=-22221.56
QUAL=38088.68:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=2.3119:MQ=59.80:MQ0=0:QD=36.38:SB=-9172.74:culprit=HaplotvpeScore:
QUAL=109943.96:BaseQRankSum=1.370:Dels=0.00:FS=3.642:HRun=0:HaplotvpeScore=3.8377:MQ=59.83:MQ0=0:QD=36.67:ReadPosRankSum=1.659:SB=-49390.03
QUAL=4121.43:BaseQRankSum=3.171:Dels=0.00:FS=5.506:HRun=1:HaplotvpeScore=8.3345:MQ=59.87:MQ0=0:QD=16.49:ReadPosRankSum=-1.713:SB=-1960.66:cul
QUAL=9834.93:BaseQRankSum=-11.173:Dels=0.00:FS=1.510:HRun=0:HaplotvpeScore=2.2121:MQ=59.75:MQ0=0:QD=11.61:ReadPosRankSum=-3.814:SB=-3539.83
QUAL=43258.25:BaseQRankSum=-21.800:Dels=0.00:FS=32.957:HRun=0:HaplotvpeScore=5.7557:MQ=59.88:MQ0=0:QD=14.67:ReadPosRankSum=0.795:SB=-16960
QUAL=109663.45:BaseQRankSum=1.730:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=5.8425:MQ=59.90:MQ0=0:QD=36.58:ReadPosRankSum=-0.048:SB=-57237.8
QUAL=41515.20:BaseQRankSum=18.653:Dels=0.00:FS=0.281:HRun=0:HaplotvpeScore=8.0105:MQ=59.75:MQ0=0:QD=15.26:ReadPosRankSum=2.768:SB=-18865.64
QUAL=17800.06:BaseQRankSum=-1.164:Dels=0.00:FS=38.938:HRun=0:HaplotvpeScore=2.6233:MQ=56.91:MQ0=0:QD=13.78:ReadPosRankSum=1.772:SB=-7996.15
QUAL=2409.09:BaseQRankSum=3.178:Dels=0.00:FS=1.381:HRun=1:HaplotvpeScore=4.6499:MQ=59.90:MQ0=0:QD=15.64:ReadPosRankSum=0.444:SB=-1156.64:cul
QUAL=48122.84:BaseQRankSum=4.025:Dels=0.00:FS=1.278:HRun=0:HaplotvpeScore=5.4517:MQ=59.91:MQ0=0:QD=16.46:ReadPosRankSum=-2.412:SB=-15481.79
QUAL=49887.70:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=1.7027:MQ=59.70:MQ0=0:QD=39.78:SB=-244.94:culprit=HaplotvpeScore:
QUAL=17079.81:BaseQRankSum=1.587:Dels=0.00:FS=17.489:HRun=1:HaplotvpeScore=1.8153:MQ=59.79:MQ0=0:QD=14.16:ReadPosRankSum=-0.676:SB=-5428.24
QUAL=3109.97:BaseQRankSum=-6.300:Dels=0.00:FS=7.552:HRun=2:HaplotvpeScore=5.4507:MQ=58.27:MQ0=0:QD=12.64:ReadPosRankSum=-0.041:SB=-1112.18
QUAL=101090.76:BaseQRankSum=2.441:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=5.7259:MQ=59.45:MQ0=0:QD=36.81:ReadPosRankSum=0.161:SB=-43102.68
QUAL=39919.41:BaseQRankSum=23.854:Dels=0.00:FS=4.930:HRun=1:HaplotvpeScore=4.9538:MQ=59.93:MQ0=0:QD=14.67:ReadPosRankSum=1.492:SB=-7662.19
QUAL=3870.21:BaseQRankSum=-20.116:Dels=0.00:FS=1941.557:HRun=2:HaplotvpeScore=33.1896:MQ=59.85:MQ0=0:QD=1.41:ReadPosRankSum=-27.603:SB=2.16
QUAL=98807.45:BaseQRankSum=3.769:Dels=0.00:FS=3.300:HRun=0:HaplotvpeScore=5.5169:MQ=59.89:MQ0=0:QD=33.28:ReadPosRankSum=0.350:SB=-46339.20
QUAL=2641.01:BaseQRankSum=-15.961:Dels=0.00:FS=550.825:HRun=0:HaplotvpeScore=2.9503:MQ=59.90:MQ0=0:QD=1.55:ReadPosRankSum=2.210:SB=-0.02:cul

QUAL=13685.41:BaseQRankSum=-0.389:Dels=0.00:FS=0.922:HRun=1:HaplotvpeScore=1.4805:MQ=59.24:MQ0=0:QD=14.54:ReadPosRankSum=-1.089:SB=-2961.89
QUAL=23838.10:BaseQRankSum=-10.929:Dels=0.00:FS=2.743:HRun=0:HaplotvpeScore=4.2517:MQ=57.30:MQ0=0:QD=11.47:ReadPosRankSum=0.845:SB=-11959.4
QUAL=29259.46:BaseQRankSum=14.239:Dels=0.00:FS=1.702:HRun=1:HaplotvpeScore=4.4363:MQ=59.84:MQ0=0:QD=14.39:ReadPosRankSum=-0.803:SB=-11855.5
QUAL=22386.65:BaseQRankSum=-0.864:Dels=0.00:FS=1.117:HRun=0:HaplotvpeScore=3.5054:MQ=59.88:MQ0=0:QD=14.47:ReadPosRankSum=-0.960:SB=-5847.80
QUAL=2446.12:BaseQRankSum=-22.611:Dels=0.00:FS=782.038:HRun=0:HaplotvpeScore=5.0001:MQ=59.89:MQ0=0:QD=11.23:ReadPosRankSum=7.995:SB=4.61:culp
QUAL=47620.45:BaseQRankSum=20.078:Dels=0.00:FS=4.101:HRun=0:HaplotvpeScore=6.2255:MQ=59.91:MQ0=0:QD=15.96:ReadPosRankSum=0.458:SB=-20297.91
QUAL=45078.37:BaseQRankSum=13.967:Dels=0.00:FS=0.264:HRun=0:HaplotvpeScore=5.2248:MQ=59.88:MQ0=0:QD=15.09:ReadPosRankSum=0.455:SB=-22640.93
QUAL=45644.55:BaseQRankSum=4.226:Dels=0.00:FS=3.476:HRun=0:HaplotvpeScore=4.9098:MQ=59.87:MQ0=0:QD=15.32:ReadPosRankSum=-0.886:SB=-19108.55
QUAL=109643.22:BaseQRankSum=1.731:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=4.7864:MQ=59.82:MQ0=0:QD=36.65:ReadPosRankSum=0.805:SB=-48538.14
QUAL=38814.83:BaseQRankSum=-12.809:Dels=0.00:FS=2.405:HRun=0:HaplotvpeScore=9.5549:MQ=59.65:MQ0=0:QD=12.94:ReadPosRankSum=-8.447:SB=-18238
QUAL=37442.15:BaseQRankSum=-2.079:Dels=0.00:FS=117.260:HRun=2:HaplotvpeScore=10.2656:MQ=59.67:MQ0=0:QD=12.68:ReadPosRankSum=-6.429:SB=-881
QUAL=27016.25:BaseQRankSum=-18.780:Dels=0.00:FS=1.780:HRun=0:HaplotvpeScore=3.6228:MQ=59.93:MQ0=0:QD=12.40:ReadPosRankSum=0.839:SB=-15575.3
QUAL=42878.05:BaseQRankSum=-13.936:Dels=0.00:FS=10.359:HRun=1:HaplotvpeScore=4.8936:MQ=59.83:MQ0=0:QD=14.58:ReadPosRankSum=-0.559:SB=-1394
QUAL=40386.96:BaseQRankSum=-17.730:Dels=0.00:FS=4.258:HRun=0:HaplotvpeScore=4.2373:MQ=59.79:MQ0=0:QD=14.39:ReadPosRankSum=0.845:SB=-11766.3
QUAL=3227.04:BaseQRankSum=-9.916:Dels=0.00:FS=7.553:HRun=0:HaplotvpeScore=5.4329:MQ=59.86:MQ0=0:QD=13.06:ReadPosRankSum=-2.052:SB=-1496.81
QUAL=45901.03:BaseQRankSum=19.985:Dels=0.00:FS=4.753:HRun=0:HaplotvpeScore=2.6006:MQ=59.80:MQ0=0:QD=15.31:ReadPosRankSum=0.737:SB=-11963.55
QUAL=45376.22:BaseQRankSum=-9.872:Dels=0.00:FS=10.004:HRun=1:HaplotvpeScore=2.7549:MQ=59.83:MQ0=0:QD=15.17:ReadPosRankSum=0.273:SB=-12498.9
QUAL=15082.19:BaseQRankSum=-10.735:Dels=0.00:FS=0.241:HRun=0:HaplotvpeScore=1.9412:MQ=59.86:MQ0=0:QD=14.19:ReadPosRankSum=-0.684:SB=-5106.5
QUAL=41047.80:BaseQRankSum=-28.668:Dels=0.00:FS=1.697:HRun=0:HaplotvpeScore=4.4882:MQ=59.90:MQ0=0:QD=13.75:ReadPosRankSum=0.469:SB=-18627.2
QUAL=106989.71:BaseQRankSum=1.629:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=3.6283:MQ=59.86:MQ0=0:QD=35.66:ReadPosRankSum=0.933:SB=-51916.01
QUAL=28412.59:BaseQRankSum=1.728:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=0.8409:MQ=59.88:MQ0=0:QD=34.36:ReadPosRankSum=1.673:SB=-12119.88
QUAL=67.61:BaseQRankSum=-13.302:Dels=0.00:FS=365.410:HRun=2:HaplotvpeScore=13.6931:MQ=59.57:MQ0=1:QD=0.18:ReadPosRankSum=-7.862:SB=-9.10:cul
QUAL=46468.25:BaseQRankSum=-24.048:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=4.9060:MQ=59.90:MQ0=0:QD=15.52:ReadPosRankSum=0.680:SB=-23875.9
QUAL=3633.19:BaseQRankSum=9.265:Dels=0.00:FS=6.118:HRun=1:HaplotvpeScore=4.3811:MQ=59.85:MQ0=0:QD=14.83:ReadPosRankSum=1.320:SB=-896.31:culp
QUAL=2691.66:BaseQRankSum=-24.019:Dels=0.00:FS=1056.787:HRun=0:HaplotvpeScore=5.1094:MQ=59.81:MQ0=0:QD=0.98:ReadPosRankSum=-0.061:SB=1.78:cul
QUAL=47349.76:BaseQRankSum=9.106:Dels=0.00:FS=4.509:HRun=0:HaplotvpeScore=4.9369:MQ=59.83:MQ0=0:QD=15.78:ReadPosRankSum=0.820:SB=-20544.55
QUAL=136.48:BaseQRankSum=-9.911:Dels=0.00:FS=94.576:HRun=0:HaplotvpeScore=3.5123:MQ=59.58:MQ0=0:QD=0.50:ReadPosRankSum=2.269:SB=-9.59:culpriti
QUAL=107028.61:BaseQRankSum=0.754:Dels=0.00:FS=4.037:HRun=2:HaplotvpeScore=5.7447:MQ=59.76:MQ0=0:QD=36.29:ReadPosRankSum=-0.808:SB=-43531.3
QUAL=96923.90:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=6.6251:MQ=59.81:MQ0=0:QD=32.34:SB=-32718.50:culpriti=HaplotvpeScore:
QUAL=41415.98:BaseQRankSum=24.148:Dels=0.00:FS=6.192:HRun=0:HaplotvpeScore=7.8238:MQ=59.86:MQ0=0:QD=14.23:ReadPosRankSum=2.768:SB=-7982.51
QUAL=16207.61:BaseQRankSum=-10.723:Dels=0.00:FS=4.523:HRun=0:HaplotvpeScore=1.8692:MQ=59.78:MQ0=0:QD=12.60:ReadPosRankSum=-1.807:SB=-6528.6
QUAL=40832.66:BaseQRankSum=3.701:Dels=0.00:FS=8.462:HRun=0:HaplotvpeScore=6.8037:MQ=59.49:MQ0=0:QD=13.64:ReadPosRankSum=-3.633:SB=-15604.58
QUAL=40051.60:BaseQRankSum=12.048:Dels=0.00:FS=2.792:HRun=0:HaplotvpeScore=5.8756:MQ=59.70:MQ0=0:QD=13.40:ReadPosRankSum=1.992:SB=-20341.80
QUAL=44994.74:BaseQRankSum=7.116:Dels=0.00:FS=8.003:HRun=0:HaplotvpeScore=6.6111:MQ=58.92:MQ0=0:QD=15.29:ReadPosRankSum=1.055:SB=-18118.98
QUAL=1360.21:BaseQRankSum=-22.932:Dels=0.00:FS=1180.475:HRun=0:HaplotvpeScore=4.9479:MQ=59.90:MQ0=0:QD=0.61:ReadPosRankSum=4.587:SB=2.96:cul
QUAL=22809.09:BaseQRankSum=2.442:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=0.9198:MQ=59.85:MQ0=0:QD=33.20:ReadPosRankSum=1.357:SB=-4793.44:cul
QUAL=62892.89:BaseQRankSum=1.714:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=2.7309:MQ=59.89:MQ0=0:QD=32.59:ReadPosRankSum=-1.653:SB=-33282.11
QUAL=45406.66:BaseQRankSum=14.684:Dels=0.00:FS=3.602:HRun=1:HaplotvpeScore=6.8972:MQ=59.87:MQ0=0:QD=15.21:ReadPosRankSum=-0.832:SB=-22880.3
QUAL=47225.80:BaseQRankSum=1.590:Dels=0.00:FS=3.954:HRun=0:HaplotvpeScore=4.9181:MQ=59.76:MQ0=0:QD=15.90:ReadPosRankSum=0.348:SB=-18807.52
QUAL=45549.35:BaseQRankSum=-19.857:Dels=0.00:FS=3.600:HRun=1:HaplotvpeScore=5.8617:MQ=59.85:MQ0=0:QD=15.41:ReadPosRankSum=-1.928:SB=-22506
QUAL=42.73:BaseQRankSum=-6.493:Dels=0.01:FS=106.584:HRun=7:HaplotvpeScore=13.4301:MQ=57.81:MQ0=0:QD=0.40:ReadPosRankSum=-2.113:SB=-14.83:cul
QUAL=3897.19:BaseQRankSum=0.086:Dels=0.00:FS=3.278:HRun=0:HaplotvpeScore=0.6432:MQ=59.00:MQ0=0:QD=17.09:ReadPosRankSum=0.609:SB=-236.51:culp
QUAL=104581.72:BaseQRankSum=1.989:Dels=0.00:FS=3.224:HRun=0:HaplotvpeScore=4.9599:MQ=59.93:MQ0=0:QD=36.66:ReadPosRankSum=0.652:SB=-52845.34
QUAL=49690.41:BaseQRankSum=4.438:Dels=0.00:FS=7.343:HRun=0:HaplotvpeScore=4.6059:MQ=59.87:MQ0=0:QD=16.62:ReadPosRankSum=-0.564:SB=-18923.34
QUAL=107666.31:BaseQRankSum=2.819:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=5.0900:MQ=59.88:MQ0=0:QD=35.97:ReadPosRankSum=1.841:SB=-26949.20
QUAL=43250.11:BaseQRankSum=1.410:Dels=0.00:FS=1.198:HRun=1:HaplotvpeScore=5.3566:MQ=59.86:MQ0=0:QD=15.51:ReadPosRankSum=0.813:SB=-22518.99
QUAL=41317.48:BaseQRankSum=8.809:Dels=0.00:FS=10.892:HRun=0:HaplotvpeScore=4.2008:MQ=59.76:MQ0=0:QD=13.78:ReadPosRankSum=0.144:SB=-14433.21
QUAL=75515.39:BaseQRankSum=0.345:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=5.7610:MQ=59.76:MQ0=0:QD=33.77:ReadPosRankSum=0.349:SB=-29660.16
QUAL=44397.32:BaseQRankSum=7.989:Dels=0.00:FS=0.557:HRun=2:HaplotvpeScore=4.6068:MQ=59.92:MQ0=0:QD=14.81:ReadPosRankSum=-1.243:SB=-19408.58
QUAL=42404.65:BaseQRankSum=-14.932:Dels=0.00:FS=16.525:HRun=1:HaplotvpeScore=3.6677:MQ=59.90:MQ0=0:QD=14.81:ReadPosRankSum=-0.367:SB=-1302
QUAL=90549.63:BaseQRankSum=1.715:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=4.6967:MQ=59.92:MQ0=0:QD=34.47:ReadPosRankSum=1.589:SB=-49814.59
QUAL=29661.05:BaseQRankSum=-12.662:Dels=0.00:FS=7.321:HRun=1:HaplotvpeScore=3.1927:MQ=59.92:MQ0=0:QD=15.42:ReadPosRankSum=-2.093:SB=-9965.5
QUAL=26236.70:BaseQRankSum=-5.022:Dels=0.00:FS=6.295:HRun=0:HaplotvpeScore=2.9188:MQ=59.90:MQ0=0:QD=14.96:ReadPosRankSum=-0.874:SB=-8742.57
QUAL=46278.98:BaseQRankSum=23.648:Dels=0.00:FS=4.382:HRun=0:HaplotvpeScore=5.7625:MQ=59.90:MQ0=0:QD=15.49:ReadPosRankSum=0.649:SB=-16741.34
QUAL=109659.39:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=3.3998:MQ=59.91:MQ0=0:QD=36.97:SB=-36971.29:culpriti=HaplotvpeScore:

QUAL=109068.39:BaseQRankSum=1.724:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=3.7957:MQ=59.86:MQ0=0:QD=36.48:ReadPosRankSum=-1.367:SB=-51495.2
QUAL=108220.01:BaseQRankSum=1.398:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=6.1812:MQ=59.87:MQ0=0:QD=36.87:ReadPosRankSum=0.599:SB=-53673.96
QUAL=46634.48:BaseQRankSum=0.942:Dels=0.00:FS=1.495:HRun=0:HaplotvpeScore=4.2935:MQ=59.92:MQ0=0:QD=15.54:ReadPosRankSum=1.023:SB=-20231.04:
QUAL=30465.24:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=1.4335:MQ=59.83:MQ0=0:QD=39.41:SB=-753.62:culprit=HaplotvpeScore:
QUAL=48596.24:BaseQRankSum=-20.161:Dels=0.00:FS=0.685:HRun=0:HaplotvpeScore=3.4941:MQ=59.56:MQ0=0:QD=16.20:ReadPosRankSum=0.386:SB=-23613.1
QUAL=40590.63:BaseQRankSum=-27.815:Dels=0.00:FS=0.133:HRun=0:HaplotvpeScore=3.2039:MQ=54.59:MQ0=1:QD=13.58:ReadPosRankSum=-0.708:SB=-1703
QUAL=520.95:BaseQRankSum=-13.560:Dels=0.00:FS=42.685:HRun=0:HaplotvpeScore=1.8147:MQ=59.84:MQ0=0:QD=0.80:ReadPosRankSum=3.026:SB=-0.42:culpr
QUAL=47395.35:BaseQRankSum=-6.210:Dels=0.00:FS=2.935:HRun=1:HaplotvpeScore=4.3096:MQ=59.82:MQ0=0:QD=15.84:ReadPosRankSum=-0.824:SB=-16801.3
QUAL=22937.52:BaseQRankSum=3.449:Dels=0.00:FS=0.856:HRun=0:HaplotvpeScore=3.5903:MQ=59.86:MQ0=0:QD=14.75:ReadPosRankSum=1.550:SB=-6993.99:c
QUAL=42384.63:BaseQRankSum=-19.630:Dels=0.00:FS=1.482:HRun=0:HaplotvpeScore=5.4289:MQ=59.76:MQ0=0:QD=14.16:ReadPosRankSum=0.736:SB=-21496.0
QUAL=34.46:BaseQRankSum=1.900:Dels=0.00:FS=28.294:HRun=0:HaplotvpeScore=0.2791:MQ=53.17:MQ0=2:QD=0.60:ReadPosRankSum=-1.144:SB=-43.63:culprit
QUAL=20685.58:BaseQRankSum=13.629:Dels=0.00:FS=2.961:HRun=0:HaplotvpeScore=2.9537:MQ=59.51:MQ0=0:QD=17.01:ReadPosRankSum=1.106:SB=-5958.59:
QUAL=45939.74:BaseQRankSum=-23.706:Dels=0.00:FS=6.751:HRun=1:HaplotvpeScore=3.9810:MQ=58.79:MQ0=0:QD=15.31:ReadPosRankSum=-0.359:SB=-21255
QUAL=109509.88:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=3.4566:MQ=59.86:MQ0=1:QD=36.63:SB=-56391.80:culprit=HaplotvpeScore:
QUAL=43849.67:BaseQRankSum=-1.625:Dels=0.00:FS=4.006:HRun=2:HaplotvpeScore=6.7764:MQ=59.87:MQ0=0:QD=14.89:ReadPosRankSum=-0.732:SB=-13928.5
QUAL=39829.99:BaseQRankSum=-15.069:Dels=0.00:FS=1.170:HRun=0:HaplotvpeScore=6.1945:MQ=59.77:MQ0=0:QD=13.69:ReadPosRankSum=3.500:SB=-19796.4
QUAL=21004.61:BaseQRankSum=3.958:Dels=0.00:FS=20.661:HRun=1:HaplotvpeScore=3.7037:MQ=59.80:MQ0=0:QD=14.11:ReadPosRankSum=0.907:SB=-7514.51:
QUAL=34342.81:BaseQRankSum=3.573:Dels=0.00:FS=2.478:HRun=1:HaplotvpeScore=4.4449:MQ=59.86:MQ0=0:QD=14.60:ReadPosRankSum=1.576:SB=-12361.09:
QUAL=80254.04:BaseQRankSum=1.718:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=3.8487:MQ=59.78:MQ0=0:QD=37.22:ReadPosRankSum=1.639:SB=-11263.13:
QUAL=107868.62:BaseQRankSum=2.416:Dels=0.00:FS=3.351:HRun=3:HaplotvpeScore=4.4676:MQ=59.88:MQ0=0:QD=36.27:ReadPosRankSum=0.694:SB=-54187.91
QUAL=113728.52:BaseQRankSum=2.533:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=4.5125:MQ=59.82:MQ0=0:QD=38.09:ReadPosRankSum=0.299:SB=-53799.05
QUAL=46060.18:BaseQRankSum=-24.351:Dels=0.00:FS=4.391:HRun=1:HaplotvpeScore=4.7593:MQ=59.87:MQ0=0:QD=15.36:ReadPosRankSum=-0.972:SB=-18195
QUAL=435.27:BaseQRankSum=0.964:Dels=0.00:FS=4.690:HRun=0:HaplotvpeScore=7.7385:MQ=59.80:MQ0=0:QD=1.74:ReadPosRankSum=-2.318:SB=-11.17:culprit
QUAL=37959.62:BaseQRankSum=-14.606:Dels=0.00:FS=9.394:HRun=1:HaplotvpeScore=5.1464:MQ=59.92:MQ0=0:QD=13.43:ReadPosRankSum=0.145:SB=-11309.2
QUAL=79220.22:BaseQRankSum=2.255:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=2.7673:MQ=59.87:MQ0=0:QD=35.73:ReadPosRankSum=-1.122:SB=-34579.00
QUAL=44625.74:BaseQRankSum=22.108:Dels=0.00:FS=7.241:HRun=0:HaplotvpeScore=4.5507:MQ=59.90:MQ0=0:QD=15.11:ReadPosRankSum=-0.610:SB=-19851.3
QUAL=42637.45:BaseQRankSum=-22.498:Dels=0.00:FS=23.845:HRun=3:HaplotvpeScore=2.6953:MQ=59.92:MQ0=0:QD=14.21:ReadPosRankSum=0.635:SB=-10951
QUAL=104204.98:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=4.1552:MQ=59.85:MQ0=0:QD=35.75:SB=-41343.58:culprit=HaplotvpeScore:
QUAL=31863.59:BaseQRankSum=-6.074:Dels=0.00:FS=12.927:HRun=0:HaplotvpeScore=3.5973:MQ=59.90:MQ0=0:QD=13.82:ReadPosRankSum=-0.796:SB=-6323.8
QUAL=45804.29:BaseQRankSum=16.657:Dels=0.00:FS=0.719:HRun=0:HaplotvpeScore=4.3194:MQ=59.78:MQ0=0:QD=15.30:ReadPosRankSum=0.073:SB=-18032.72
QUAL=15585.59:BaseQRankSum=-1.682:Dels=0.00:FS=1.952:HRun=0:HaplotvpeScore=2.4794:MQ=59.89:MQ0=0:QD=13.13:ReadPosRankSum=-1.139:SB=-7778.50
QUAL=44127.48:BaseQRankSum=-8.116:Dels=0.00:FS=0.264:HRun=1:HaplotvpeScore=8.0281:MQ=59.84:MQ0=0:QD=14.75:ReadPosRankSum=-0.439:SB=-20415.6
QUAL=2250.23:BaseQRankSum=0.792:Dels=0.00:FS=5.281:HRun=0:HaplotvpeScore=0.1831:MQ=59.73:MQ0=0:QD=13.39:ReadPosRankSum=0.731:SB=-87.58:culpr
QUAL=107724.09:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=5.2216:MQ=59.82:MQ0=0:QD=36.00:SB=-49123.09:culprit=HaplotvpeScore:
QUAL=110278.69:BaseQRankSum=2.312:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=4.4651:MQ=59.86:MQ0=0:QD=36.93:ReadPosRankSum=0.468:SB=-39213.91
QUAL=66754.83:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=5.3659:MQ=59.79:MQ0=0:QD=33.77:SB=-32854.62:culprit=HaplotvpeScore:
QUAL=42619.34:BaseQRankSum=-5.098:Dels=0.00:FS=2.738:HRun=1:HaplotvpeScore=6.4926:MQ=59.70:MQ0=0:QD=14.67:ReadPosRankSum=-2.689:SB=-12540.1
QUAL=31997.99:BaseQRankSum=21.652:Dels=0.00:FS=9.430:HRun=0:HaplotvpeScore=4.3081:MQ=59.78:MQ0=0:QD=15.41:ReadPosRankSum=-1.104:SB=-6061.59
QUAL=101620.24:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=6.7705:MQ=57.12:MQ0=0:QD=33.90:SB=-50040.49:culprit=HaplotvpeScore:
QUAL=47059.47:BaseQRankSum=3.712:Dels=0.00:FS=5.044:HRun=0:HaplotvpeScore=7.4792:MQ=59.88:MQ0=0:QD=15.70:ReadPosRankSum=0.582:SB=-20586.27:
QUAL=105107.01:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=7.6180:MQ=59.78:MQ0=0:QD=35.62:SB=-48598.35:culprit=HaplotvpeScore:
QUAL=101888.01:BaseQRankSum=1.724:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=5.9318:MQ=59.82:MQ0=0:QD=34.80:ReadPosRankSum=1.024:SB=-50829.87
QUAL=46771.81:BaseQRankSum=16.804:Dels=0.00:FS=2.370:HRun=0:HaplotvpeScore=4.2656:MQ=59.92:MQ0=0:QD=15.63:ReadPosRankSum=-0.845:SB=-23754.8
QUAL=49041.52:BaseQRankSum=12.167:Dels=0.00:FS=5.354:HRun=0:HaplotvpeScore=5.2291:MQ=59.91:MQ0=0:QD=16.77:ReadPosRankSum=0.131:SB=-20973.43
QUAL=48361.67:BaseQRankSum=20.321:Dels=0.00:FS=3.351:HRun=1:HaplotvpeScore=4.3693:MQ=59.90:MQ0=0:QD=16.12:ReadPosRankSum=0.767:SB=-23560.33
QUAL=114886.21:BaseQRankSum=2.334:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=3.6938:MQ=59.85:MQ0=0:QD=38.33:ReadPosRankSum=-0.484:SB=-50570.3
QUAL=50119.26:BaseQRankSum=17.985:Dels=0.00:FS=4.856:HRun=1:HaplotvpeScore=4.7080:MQ=59.87:MQ0=0:QD=16.82:ReadPosRankSum=0.906:SB=-18188.64
QUAL=811.33:BaseQRankSum=-12.398:Dels=0.00:FS=419.375:HRun=1:HaplotvpeScore=1.8012:MQ=59.86:MQ0=0:QD=1.48:ReadPosRankSum=3.689:SB=2.45:culpr
QUAL=4751.24:BaseQRankSum=-9.537:Dels=0.00:FS=0.667:HRun=0:HaplotvpeScore=1.2606:MQ=59.71:MQ0=0:QD=13.02:ReadPosRankSum=0.967:SB=-483.97:cul
QUAL=41.85:BaseQRankSum=-11.301:Dels=0.00:FS=31.152:HRun=2:HaplotvpeScore=3.0669:MQ=59.70:MQ0=0:QD=1.05:ReadPosRankSum=5.846:SB=-22.01:culpr
QUAL=123.76:BaseQRankSum=-18.862:Dels=0.00:FS=90.892:HRun=0:HaplotvpeScore=6.2487:MQ=59.86:MQ0=0:QD=0.68:ReadPosRankSum=2.859:SB=-18.23:culpr
QUAL=4254.74:BaseQRankSum=-7.903:Dels=0.00:FS=2.040:HRun=0:HaplotvpeScore=0.5352:MQ=59.51:MQ0=0:QD=17.23:ReadPosRankSum=0.824:SB=-115.55:cul
QUAL=48093.80:BaseQRankSum=0.429:Dels=0.00:FS=1.489:HRun=0:HaplotvpeScore=5.2807:MQ=59.89:MQ0=0:QD=16.05:ReadPosRankSum=-0.928:SB=-20690.64
QUAL=46849.93:BaseQRankSum=7.571:Dels=0.00:FS=6.964:HRun=0:HaplotvpeScore=4.4961:MQ=59.85:MQ0=0:QD=15.67:ReadPosRankSum=-0.143:SB=-16575.69
QUAL=44347.16:BaseQRankSum=-2.869:Dels=0.00:FS=17.085:HRun=1:HaplotvpeScore=4.2425:MQ=59.75:MQ0=0:QD=14.79:ReadPosRankSum=-0.229:SB=-19398

QUAL=70146.04:BaseQRankSum=1.720:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=5.5932:MQ=59.88:MQ0=0:QD=34.20:ReadPosRankSum=0.744:SB=-37438.96:
QUAL=108393.84:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=5.8595:MQ=59.85:MQ0=0:QD=36.59:SB=-47064.70:culprit=HaplotvpeScore:
QUAL=46871.53:BaseQRankSum=20.905:Dels=0.00:FS=1.232:HRun=0:HaplotvpeScore=4.8797:MQ=59.88:MQ0=0:QD=15.65:ReadPosRankSum=1.459:SB=-15838.62:
QUAL=5948.43:BaseQRankSum=-1.947:Dels=0.00:FS=0.822:HRun=0:HaplotvpeScore=1.1956:MQ=59.56:MQ0=0:QD=14.20:ReadPosRankSum=-0.407:SB=-1665.01:
QUAL=43020.18:BaseQRankSum=-17.729:Dels=0.00:FS=0.543:HRun=1:HaplotvpeScore=5.5685:MQ=59.94:MQ0=0:QD=14.35:ReadPosRankSum=0.153:SB=-20573.5:
QUAL=106932.92:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=5.1252:MQ=59.07:MQ0=0:QD=35.92:SB=-51484.94:culprit=HaplotvpeScore:
QUAL=46769.34:BaseQRankSum=21.890:Dels=0.00:FS=0.400:HRun=1:HaplotvpeScore=6.0353:MQ=59.91:MQ0=0:QD=15.61:ReadPosRankSum=-0.219:SB=-22920.0:
QUAL=43432.49:BaseQRankSum=7.503:Dels=0.00:FS=3.311:HRun=1:HaplotvpeScore=5.3881:MQ=59.87:MQ0=0:QD=14.52:ReadPosRankSum=1.047:SB=-16120.20:
QUAL=31048.29:BaseQRankSum=7.739:Dels=0.00:FS=0.948:HRun=0:HaplotvpeScore=3.5587:MQ=59.81:MQ0=0:QD=15.47:ReadPosRankSum=-0.848:SB=-9355.23:
QUAL=37490.52:BaseQRankSum=-31.508:Dels=0.00:FS=2.439:HRun=1:HaplotvpeScore=5.6420:MQ=59.80:MQ0=0:QD=12.61:ReadPosRankSum=-0.089:SB=-5683.7:
QUAL=41125.08:BaseQRankSum=-6.729:Dels=0.00:FS=12.135:HRun=2:HaplotvpeScore=9.0411:MQ=59.85:MQ0=0:QD=13.75:ReadPosRankSum=-0.320:SB=-17681:
QUAL=45633.72:BaseQRankSum=-0.416:Dels=0.00:FS=9.800:HRun=1:HaplotvpeScore=5.5130:MQ=59.89:MQ0=0:QD=15.21:ReadPosRankSum=-2.150:SB=-23062.9:
QUAL=39961.67:BaseQRankSum=1.693:Dels=0.00:FS=3.949:HRun=0:HaplotvpeScore=6.3709:MQ=59.83:MQ0=0:QD=15.07:ReadPosRankSum=0.951:SB=-16297.68:
QUAL=30285.68:BaseQRankSum=-3.895:Dels=0.00:FS=4.073:HRun=0:HaplotvpeScore=6.3681:MQ=59.94:MQ0=0:QD=14.46:ReadPosRankSum=-1.938:SB=-11533.1:
QUAL=61293.89:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=3.6564:MQ=59.67:MQ0=0:QD=37.51:SB=-27641.97:culprit=HaplotvpeScore:
QUAL=31931.70:BaseQRankSum=-7.872:Dels=0.00:FS=7.938:HRun=2:HaplotvpeScore=7.2818:MQ=59.80:MQ0=0:QD=14.86:ReadPosRankSum=0.411:SB=-12301.33:
QUAL=191.39:BaseQRankSum=-11.495:Dels=0.00:FS=202.191:HRun=5:HaplotvpeScore=3.4566:MQ=59.51:MQ0=0:QD=0.92:ReadPosRankSum=-12.001:SB=0.04:culp
QUAL=514.21:BaseQRankSum=-25.735:Dels=0.00:FS=609.721:HRun=0:HaplotvpeScore=5.4206:MQ=59.78:MQ0=0:QD=0.31:ReadPosRankSum=6.571:SB=-0.50:culp
QUAL=27515.38:BaseQRankSum=-8.288:Dels=0.00:FS=5.120:HRun=0:HaplotvpeScore=3.8907:MQ=59.78:MQ0=0:QD=14.38:ReadPosRankSum=-1.453:SB=-14669.9:
QUAL=28677.26:BaseQRankSum=19.332:Dels=0.00:FS=3.416:HRun=0:HaplotvpeScore=3.9141:MQ=59.87:MQ0=0:QD=15.00:ReadPosRankSum=-1.676:SB=-15310.2:
QUAL=93733.95:BaseQRankSum=1.728:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=5.2178:MQ=59.85:MQ0=0:QD=33.16:ReadPosRankSum=0.692:SB=-47250.87:
QUAL=67576.56:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=3.4581:MQ=59.79:MQ0=0:QD=39.33:SB=-629.76:culprit=HaplotvpeScore:
QUAL=3664.75:BaseQRankSum=7.793:Dels=0.00:FS=3.463:HRun=0:HaplotvpeScore=4.4405:MQ=59.89:MQ0=0:QD=15.27:ReadPosRankSum=0.388:SB=-1489.82:cul
QUAL=42298.61:BaseQRankSum=3.803:Dels=0.00:FS=3.210:HRun=2:HaplotvpeScore=9.8651:MQ=59.91:MQ0=0:QD=14.23:ReadPosRankSum=0.340:SB=-21344.35:
QUAL=286.56:BaseQRankSum=-23.290:Dels=0.00:FS=1622.388:HRun=2:HaplotvpeScore=76.8262:MQ=59.53:MQ0=0:QD=0.29:ReadPosRankSum=-14.603:SB=-11.3:
QUAL=107420.85:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=5.4284:MQ=59.89:MQ0=0:QD=35.93:SB=-39751.54:culprit=HaplotvpeScore:
QUAL=4108.69:BaseQRankSum=2.937:Dels=0.00:FS=4.060:HRun=0:HaplotvpeScore=1.4867:MQ=59.72:MQ0=0:QD=16.63:ReadPosRankSum=-0.286:SB=-156.62:cul
QUAL=33380.49:BaseQRankSum=7.916:Dels=0.00:FS=15.338:HRun=0:HaplotvpeScore=4.8200:MQ=59.89:MQ0=0:QD=13.46:ReadPosRankSum=2.119:SB=-11199.11:
QUAL=40715.93:BaseQRankSum=-22.626:Dels=0.00:FS=3.867:HRun=0:HaplotvpeScore=9.1379:MQ=59.84:MQ0=0:QD=13.70:ReadPosRankSum=-0.249:SB=-18929:
QUAL=43678.44:BaseQRankSum=16.869:Dels=0.00:FS=0.866:HRun=0:HaplotvpeScore=5.7324:MQ=59.87:MQ0=1:QD=14.89:ReadPosRankSum=-1.178:SB=-18706.2:
QUAL=46189.98:BaseQRankSum=19.430:Dels=0.00:FS=2.759:HRun=1:HaplotvpeScore=5.2022:MQ=59.87:MQ0=0:QD=15.52:ReadPosRankSum=-1.309:SB=-16664.6:
QUAL=24040.95:BaseQRankSum=4.389:Dels=0.00:FS=4.819:HRun=2:HaplotvpeScore=4.2758:MQ=59.89:MQ0=0:QD=12.98:ReadPosRankSum=-2.082:SB=-7760.69:
QUAL=59225.45:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=3.6541:MQ=58.38:MQ0=0:QD=33.33:SB=-24403.14:culprit=HaplotvpeScore:
QUAL=61792.76:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=3.2260:MQ=58.48:MQ0=0:QD=33.17:SB=-27146.05:culprit=HaplotvpeScore:
QUAL=30845.12:BaseQRankSum=14.742:Dels=0.00:FS=1.417:HRun=0:HaplotvpeScore=4.0136:MQ=59.91:MQ0=0:QD=14.49:ReadPosRankSum=-2.101:SB=-14150.5:
QUAL=62712.98:BaseQRankSum=1.346:Dels=0.00:FS=5.180:HRun=0:HaplotvpeScore=5.4849:MQ=59.76:MQ0=0:QD=36.27:ReadPosRankSum=-0.510:SB=-19231.30:
QUAL=99181.29:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=5.2407:MQ=57.11:MQ0=0:QD=33.41:SB=-25141.29:culprit=HaplotvpeScore:
QUAL=44767.71:BaseQRankSum=4.451:Dels=0.00:FS=1.168:HRun=0:HaplotvpeScore=6.4804:MQ=59.89:MQ0=0:QD=15.03:ReadPosRankSum=0.646:SB=-22919.74:
QUAL=3021.35:BaseQRankSum=-5.460:Dels=0.00:FS=276.438:HRun=5:HaplotvpeScore=62.1076:MQ=52.43:MQ0=0:QD=1.98:ReadPosRankSum=3.736:SB=-0.02:cul
QUAL=72.41:BaseQRankSum=-15.750:Dels=0.00:FS=114.046:HRun=3:HaplotvpeScore=84.4069:MQ=52.72:MQ0=0:QD=0.10:ReadPosRankSum=7.617:SB=-8.26:culp
QUAL=6298.44:BaseQRankSum=-14.632:Dels=0.00:FS=1180.964:HRun=6:HaplotvpeScore=51.6034:MQ=54.51:MQ0=0:QD=3.01:ReadPosRankSum=-4.577:SB=-0.02:
QUAL=38340.06:BaseQRankSum=-2.340:Dels=0.00:FS=12.733:HRun=0:HaplotvpeScore=5.3269:MQ=59.77:MQ0=0:QD=13.84:ReadPosRankSum=0.492:SB=-13459.7:
QUAL=2382.70:BaseQRankSum=-7.417:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=6.5280:MQ=59.88:MQ0=0:QD=13.02:ReadPosRankSum=0.150:SB=-1305.44:cul
QUAL=46189.10:BaseQRankSum=18.520:Dels=0.00:FS=3.924:HRun=0:HaplotvpeScore=6.2444:MQ=59.92:MQ0=0:QD=15.40:ReadPosRankSum=0.197:SB=-11722.47:
QUAL=18512.22:BaseQRankSum=-12.493:Dels=0.00:FS=2.099:HRun=0:HaplotvpeScore=4.9777:MQ=59.90:MQ0=0:QD=13.91:ReadPosRankSum=0.980:SB=-9344.80:
QUAL=38494.06:BaseQRankSum=-9.477:Dels=0.00:FS=0.558:HRun=0:HaplotvpeScore=4.4789:MQ=59.85:MQ0=0:QD=13.39:ReadPosRankSum=1.005:SB=-17608.64:
QUAL=1151.76:BaseQRankSum=4.379:Dels=0.00:FS=3.137:HRun=0:HaplotvpeScore=7.2119:MQ=59.86:MQ0=0:QD=4.61:ReadPosRankSum=0.374:SB=-617.79:culpr
QUAL=27124.19:BaseQRankSum=-2.211:Dels=0.00:FS=3.579:HRun=2:HaplotvpeScore=5.1444:MQ=59.80:MQ0=0:QD=15.14:ReadPosRankSum=0.856:SB=-13263.70:
QUAL=112251.27:BaseQRankSum=1.662:Dels=0.00:FS=3.340:HRun=1:HaplotvpeScore=3.8552:MQ=59.82:MQ0=0:QD=37.58:ReadPosRankSum=1.257:SB=-54746.39:
QUAL=114493.20:BaseQRankSum=2.707:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=4.2124:MQ=59.87:MQ0=0:QD=38.20:ReadPosRankSum=-1.138:SB=-53624.6:
QUAL=114852.41:BaseQRankSum=0.054:Dels=0.00:FS=3.287:HRun=1:HaplotvpeScore=3.9481:MQ=59.86:MQ0=0:QD=38.41:ReadPosRankSum=-0.001:SB=-55787.0:
QUAL=115114.31:BaseQRankSum=1.730:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=4.6494:MQ=59.91:MQ0=0:QD=38.40:ReadPosRankSum=0.261:SB=-53211.60:
QUAL=266.51:BaseQRankSum=-26.169:Dels=0.00:FS=1003.928:HRun=1:HaplotvpeScore=4.1925:MQ=59.92:MQ0=0:QD=0.27:ReadPosRankSum=2.767:SB=-10.70:cul
QUAL=41819.16:BaseQRankSum=-1.469:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=2.8258:MQ=59.91:MQ0=0:QD=33.32:ReadPosRankSum=1.591:SB=-8601.59:
QUAL=6789.43:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=0.1444:MQ=59.89:MQ0=0:QD=32.49:SB=-1318.77:culprit=HaplotvpeScore:

QUA1=89491.27:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=2.4222:MQ=59.86:MQ0=0:QD=34.27:SB=-41116.22:culpritr=HaplotvpeScore:
 QUA1=102640.18:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=3.7703:MQ=59.84:MQ0=0:QD=35.69:SB=-29277.89:culpritr=HaplotvpeScore:
 QUA1=29419.01:BaseQRankSum=1.403:Dels=0.00:FS=3.217:HRun=0:HaplotvpeScore=1.2652:MQ=59.91:MQ0=0:QD=35.36:ReadPosRankSum=0.046:SB=-14486.71:
 QUA1=8946.99:BaseQRankSum=6.567:Dels=0.00:FS=2.431:HRun=2:HaplotvpeScore=1.9742:MQ=59.81:MQ0=0:QD=14.20:ReadPosRankSum=-0.694:SB=-4453.21:
 QUA1=18462.35:BaseQRankSum=9.364:Dels=0.00:FS=0.216:HRun=0:HaplotvpeScore=2.1172:MQ=59.89:MQ0=0:QD=16.01:ReadPosRankSum=-0.547:SB=-10051.10:
 QUA1=1475.66:BaseQRankSum=-0.511:Dels=0.00:FS=734.419:HRun=0:HaplotvpeScore=4.2547:MQ=38.42:MQ0=17:QD=0.99:ReadPosRankSum=2.008:SB=2.01:cul
 QUA1=28489.79:BaseQRankSum=10.634:Dels=0.00:FS=2.876:HRun=0:HaplotvpeScore=4.9978:MQ=59.94:MQ0=0:QD=14.90:ReadPosRankSum=-0.691:SB=-14204.9
 QUA1=43523.88:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=1.4507:MQ=59.94:MQ0=0:QD=35.13:SB=-22060.82:culpritr=HaplotvpeScore:
 QUA1=113519.65:BaseQRankSum=-1.655:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=4.7497:MQ=59.79:MQ0=0:QD=37.84:ReadPosRankSum=1.574:SB=-50856.2
 QUA1=112946.27:BaseQRankSum=2.858:Dels=0.00:FS=0.000:HRun=3:HaplotvpeScore=6.7451:MQ=59.52:MQ0=0:QD=37.86:ReadPosRankSum=1.314:SB=-51666.92
 QUA1=112461.96:BaseQRankSum=2.431:Dels=0.00:FS=0.000:HRun=1:HaplotvpeScore=4.3591:MQ=59.83:MQ0=0:QD=37.56:ReadPosRankSum=0.563:SB=-43375.29
 QUA1=111127.28:BaseQRankSum=2.210:Dels=0.00:FS=3.075:HRun=0:HaplotvpeScore=4.9863:MQ=59.84:MQ0=0:QD=37.04:ReadPosRankSum=0.149:SB=-56514.97
 QUA1=87791.35:BaseQRankSum=7.546:Dels=0.00:FS=2.889:HRun=0:HaplotvpeScore=7.4569:MQ=59.88:MQ0=0:QD=32.95:ReadPosRankSum=0.332:SB=-39000.96:
 QUA1=41937.14:BaseQRankSum=-18.411:Dels=0.00:FS=4.693:HRun=0:HaplotvpeScore=8.4020:MQ=59.83:MQ0=0:QD=14.63:ReadPosRankSum=-1.305:SB=-16863
 QUA1=2777.74:BaseQRankSum=-22.110:Dels=0.00:FS=840.263:HRun=3:HaplotvpeScore=3.1785:MQ=59.91:MQ0=0:QD=0.93:ReadPosRankSum=6.516:SB=-0.03:cul
 QUA1=68.79:BaseQRankSum=2.086:Dels=0.00:FS=1.190:HRun=0:HaplotvpeScore=3.1083:MQ=59.93:MQ0=0:QD=0.68:ReadPosRankSum=-1.209:SB=-36.49:culpritr=
 QUA1=15770.76:BaseQRankSum=10.237:Dels=0.00:FS=2.079:HRun=0:HaplotvpeScore=2.1605:MQ=59.89:MQ0=0:QD=14.17:ReadPosRankSum=-1.557:SB=-7042.98
 QUA1=17327.75:BaseQRankSum=1.304:Dels=0.00:FS=5.382:HRun=1:HaplotvpeScore=4.2558:MQ=59.83:MQ0=0:QD=13.51:ReadPosRankSum=2.195:SB=-8312.42:c
 QUA1=34214.54:BaseQRankSum=-9.003:Dels=0.00:FS=10.347:HRun=0:HaplotvpeScore=4.4466:MQ=59.89:MQ0=0:QD=14.84:ReadPosRankSum=0.975:SB=-18087.7
 QUA1=18211.52:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=1.1530:MQ=59.81:MQ0=0:QD=33.35:SB=-8427.10:culpritr=HaplotvpeScore:
 QUA1=16311.40:BaseQRankSum=-12.436:Dels=0.00:FS=0.231:HRun=0:HaplotvpeScore=2.3139:MQ=59.93:MQ0=0:QD=13.41:ReadPosRankSum=-1.062:SB=-5280.1
 QUA1=28272.94:BaseQRankSum=23.847:Dels=0.00:FS=10.944:HRun=0:HaplotvpeScore=4.0938:MQ=59.83:MQ0=0:QD=14.64:ReadPosRankSum=1.120:SB=-5907.43
 QUA1=32284.36:Dels=0.00:FS=0.000:HRun=2:HaplotvpeScore=2.4472:MQ=59.66:MQ0=0:QD=34.94:SB=-15378.97:culpritr=HaplotvpeScore:
 QUA1=3356.80:BaseQRankSum=-2.382:Dels=0.00:FS=3.165:HRun=1:HaplotvpeScore=0.3182:MQ=59.68:MQ0=0:QD=14.99:ReadPosRankSum=-1.467:SB=-1243.38:
 QUA1=24150.59:BaseQRankSum=-1.464:Dels=0.00:FS=2.736:HRun=0:HaplotvpeScore=5.7849:MQ=59.73:MQ0=0:QD=13.98:ReadPosRankSum=1.056:SB=-8405.88:
 QUA1=76307.82:BaseQRankSum=-0.148:Dels=0.00:FS=3.262:HRun=0:HaplotvpeScore=4.0390:MQ=59.88:MQ0=0:QD=31.74:ReadPosRankSum=0.293:SB=-34160.00
 QUA1=106132.63:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=6.5807:MQ=59.93:MQ0=0:QD=35.59:SB=-42323.20:culpritr=HaplotvpeScore:
 QUA1=32685.50:BaseQRankSum=3.319:Dels=0.00:FS=25.342:HRun=0:HaplotvpeScore=6.2587:MQ=59.87:MQ0=0:QD=13.27:ReadPosRankSum=0.155:SB=-10542.22
 QUA1=94769.57:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=5.3080:MQ=59.88:MQ0=0:QD=32.37:SB=-43723.21:culpritr=HaplotvpeScore:
 QUA1=242.23:BaseQRankSum=-21.822:Dels=0.00:FS=577.877:HRun=1:HaplotvpeScore=5.7474:MQ=59.84:MQ0=0:QD=0.42:ReadPosRankSum=5.095:SB=-10.40:cul
 QUA1=68874.25:BaseQRankSum=1.690:Dels=0.00:FS=0.000:HRun=2:HaplotvpeScore=3.7216:MQ=59.71:MQ0=0:QD=34.33:ReadPosRankSum=1.376:SB=-37273.00:
 QUA1=36809.25:BaseQRankSum=-20.852:Dels=0.00:FS=2.237:HRun=0:HaplotvpeScore=5.8560:MQ=59.87:MQ0=0:QD=12.47:ReadPosRankSum=-0.533:SB=-18785
 QUA1=40877.54:BaseQRankSum=1.392:Dels=0.00:FS=7.042:HRun=0:HaplotvpeScore=5.3135:MQ=59.90:MQ0=0:QD=14.86:ReadPosRankSum=-0.239:SB=-17555.37
 QUA1=41622.36:BaseQRankSum=-7.417:Dels=0.00:FS=20.513:HRun=1:HaplotvpeScore=4.7671:MQ=59.84:MQ0=0:QD=13.96:ReadPosRankSum=1.246:SB=-16711.4
 QUA1=23527.37:BaseQRankSum=-10.921:Dels=0.00:FS=11.312:HRun=2:HaplotvpeScore=3.7568:MQ=59.87:MQ0=0:QD=12.98:ReadPosRankSum=-1.711:SB=-6862
 QUA1=71891.02:BaseQRankSum=1.532:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=4.5357:MQ=59.68:MQ0=0:QD=33.74:ReadPosRankSum=-0.300:SB=-34826.57
 QUA1=89011.84:BaseQRankSum=1.578:Dels=0.00:FS=0.000:HRun=2:HaplotvpeScore=3.7256:MQ=59.78:MQ0=0:QD=34.77:ReadPosRankSum=-1.907:SB=-47072.87
 QUA1=41266.92:BaseQRankSum=15.018:Dels=0.00:FS=8.379:HRun=1:HaplotvpeScore=5.8265:MQ=59.88:MQ0=0:QD=15.28:ReadPosRankSum=2.226:SB=-19953.11
 QUA1=73663.37:BaseQRankSum=1.726:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=4.9911:MQ=59.84:MQ0=0:QD=33.79:ReadPosRankSum=-0.901:SB=-38578.01
 QUA1=42521.08:BaseQRankSum=-1.732:Dels=0.00:FS=3.430:HRun=0:HaplotvpeScore=4.4026:MQ=59.52:MQ0=0:QD=32.14:ReadPosRankSum=1.489:SB=-20956.43
 QUA1=4567.55:BaseQRankSum=1.604:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=0.3524:MQ=56.93:MQ0=0:QD=33.58:ReadPosRankSum=-1.373:SB=-2343.73:c
 QUA1=20743.35:BaseQRankSum=-13.154:Dels=0.00:FS=1.103:HRun=1:HaplotvpeScore=4.0765:MQ=59.15:MQ0=1:QD=10.97:ReadPosRankSum=0.812:SB=-9563.41
 QUA1=20551.83:BaseQRankSum=10.925:Dels=0.00:FS=1.019:HRun=0:HaplotvpeScore=3.3561:MQ=59.91:MQ0=0:QD=13.61:ReadPosRankSum=0.832:SB=-10340.71
 QUA1=11060.19:BaseQRankSum=7.596:Dels=0.00:FS=1.485:HRun=4:HaplotvpeScore=2.1499:MQ=59.90:MQ0=0:QD=13.18:ReadPosRankSum=-0.309:SB=-4646.42:
 QUA1=39678.91:BaseQRankSum=-21.335:Dels=0.00:FS=1.286:HRun=0:HaplotvpeScore=5.4849:MQ=59.89:MQ0=0:QD=15.37:ReadPosRankSum=-0.114:SB=-1485.6
 QUA1=18733.42:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=0.7026:MQ=59.84:MQ0=0:QD=32.13:SB=-8580.45:culpritr=HaplotvpeScore:
 QUA1=65001.98:BaseQRankSum=2.393:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=3.8870:MQ=59.87:MQ0=0:QD=35.44:ReadPosRankSum=0.567:SB=-15100.94:
 QUA1=106503.27:BaseQRankSum=4.179:Dels=0.00:FS=3.105:HRun=0:HaplotvpeScore=5.7627:MQ=59.83:MQ0=0:QD=36.67:ReadPosRankSum=-0.194:SB=-55430.5
 QUA1=99835.42:BaseQRankSum=1.705:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=6.0638:MQ=59.88:MQ0=0:QD=36.89:ReadPosRankSum=0.257:SB=-50944.62:
 QUA1=41096.22:BaseQRankSum=1.724:Dels=0.00:FS=0.000:HRun=2:HaplotvpeScore=4.0470:MQ=59.81:MQ0=0:QD=33.55:ReadPosRankSum=0.487:SB=-20493.13:
 QUA1=35262.96:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=2.1567:MQ=59.86:MQ0=0:QD=35.09:SB=-14652.08:culpritr=HaplotvpeScore:

[illegible]

[illegible]

[illegible]

A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	01	01	01
T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	01	01	01
A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	01	01	01
G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	01	01	01
G/T	G/T	G/T	G/G	G/T	G/T	G/G	G/T	G/T	G/T	G/T	G/G	01	01	01
C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	01	01	01
C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	01	01	01
T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	01	01	01
A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	11	11	11
T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	01	01	01
T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	01	01	01
G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	01	01	01
G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	01	01	01
G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	01	01	01
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/T	G/G	G/G	G/G	G/G	00	00	00
T/G	T/G	T/G	T/G	T/G	T/G	T/G	T/G	T/G	T/G	T/G	T/G	01	01	01
G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	01	01	01
A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	01	01	01
A/C	A/C	A/C	A/C	A/C	A/C	A/C	A/C	A/C	A/C	A/C	A/C	01	01	01
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	11	11	11
A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	11	11	11
C/C	C/C	C/A	C/A	C/A	C/C	C/A	C/C	C/C	C/C	C/C	C/C	00	00	01
T/A	T/A	T/A	T/A	T/A	T/A	T/A	T/A	T/A	T/A	T/A	T/A	01	01	01
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/C	G/G	G/G	G/G	00	00	00
G/T	G/G	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	01	00	01
A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	01	01	01
C/C	C/A	C/A	C/C	C/A	C/C	C/C	C/A	C/C	C/C	C/C	C/A	00	01	01
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	11	11	11
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	11	11	11
C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	01	01	01
C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	01	01	01
G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	01	01	01
G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	01	01	01
C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	01	01	01
C/A	G/A	C/A	C/A	C/A	C/A	C/A	C/A	G/A	C/A	C/A	C/C	01	01	01
T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	11	11	11
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	11	11	11
G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	01	01	01
G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	01	01	01
C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	01	01	01
A/A	A/C	A/A	A/C	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/C	00	01	00
G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	01	01	01
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	11	11	11
T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	01	01	01
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	11	11	11
G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	01	01	01
T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	01	01	01
T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	11	11	11
T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	01	01	01
A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	01	01	01
A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	11	11	11
G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	01	01	01
A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	01	01	01
G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	01	01	01
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	11	11	11

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A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	11	11	11
T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	11	11	11
C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	01	01	01
A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	01	01	01
T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	01	01	01
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	11	11	11
A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	01	01	01
G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	01	01	01
C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	01	01	01
A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	01	01	01
T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	01	01	01
C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	01	01	01
C/G	C/G	C/G	C/G	C/G	C/G	C/G	C/G	C/G	C/G	C/G	C/G	01	01	01
G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	01	01	01
T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	11	11	11
T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	01	01	01
A/A	A/A	A/G	A/A	A/A	A/G	A/A	A/G	A/A	A/G	A/G	A/A	010	010	01
G/T	G/G	G/T	G/G	G/T	G/G	G/T	G/G	G/T	G/T	G/T	G/G	01	010	01
G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	01	01	01
C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	01	01	01
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	11	11	11
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	11	11	11
C/C	C/C	C/C	C/T	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	010	010	010
C/G	C/G	C/G	C/G	C/G	C/G	C/G	C/G	C/G	C/G	C/G	C/G	01	01	01
C/A	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/A	C/C	C/A	C/A	01	010	010
A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	11	11	11
A/C	A/C	A/C	A/C	A/C	A/C	A/C	A/C	A/C	A/C	A/C	A/C	01	01	01
C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	01	01	01
G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	01	01	01
T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	01	01	01
T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	T/C	01	01	01
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	11	11	11
T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	11	11	11
G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	01	01	01
A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	11	11	11
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	11	11	11
C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	01	01	01
A/C	A/C	A/C	A/C	A/C	A/C	A/C	A/C	A/C	A/C	A/C	A/C	01	01	01
T/C	T/T	T/T	T/C	T/T	T/C	T/C	T/C	T/T	T/T	T/T	T/T	01	010	010
G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	01	01	01
A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	01	01	01
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/A	010	010	010
G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	G/A	01	01	01
C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	01	01	01
A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	01	01	01
A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	010	01	010
C/G	C/G	C/G	C/G	C/G	C/G	C/G	C/G	C/G	C/G	C/G	C/G	01	01	01
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	11	11	11
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	11	11	11
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	11	11	11
A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	11	11	11
G/G	G/T	G/T	G/G	G/T	G/G	G/T	G/G	G/G	G/G	G/G	G/G	010	01	01
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	11	11	11

[illegible]

Alleles	Alleles	Alleles	Alleles	Alleles	Alleles	Alleles	Alleles	Alleles	Depth	Depth	Depth	Depth	Depth	Depth	Depth	Depth	Depth
CC1-2	CC1-7	CC1-8	CC1-9	CC1-11	CC1-12	CC1-17	CC1-18	CC1-25	NCC1	CC1	CC1-1	CC1-2	CC1-7	CC1-8	CC1-9	CC1-11	CC1-12
01	01	01	01	01	01	01	01	01	250	236	250	247	244	250	246	249	243
01	00	01	01	00	01	00	01	00	250	250	250	250	250	250	250	250	250
01	01	01	01	01	01	01	01	01	250	250	250	250	250	250	250	250	250
11	11	11	11	11	11	11	11	11	53	41	58	43	45	55	66	36	67
11	11	11	11	11	11	11	11	11	238	250	250	243	247	250	248	248	247
11	11	11	11	11	11	11	11	11	235	194	225	238	248	237	236	225	240
01	01	01	01	01	01	01	01	01	149	128	95	151	141	147	176	147	150
01	01	01	01	01	01	01	01	01	250	174	179	242	223	216	237	169	223
01	01	01	01	01	01	01	01	01	250	250	249	250	250	250	250	250	250
01	01	01	01	01	01	01	01	01	250	176	165	228	208	236	234	173	203
01	01	01	01	01	01	01	01	01	160	129	136	159	144	155	137	110	155
01	01	01	01	01	01	01	01	01	225	184	163	210	209	222	244	204	205
01	01	01	01	01	01	01	01	01	250	239	241	237	237	247	235	236	235
01	01	01	01	01	01	01	01	01	239	183	185	214	228	230	191	159	234
11	11	11	11	11	11	11	11	11	250	250	250	250	250	249	250	242	250
01	01	01	01	01	01	01	01	01	243	193	207	212	190	249	206	186	244
01	01	01	01	01	01	01	01	01	250	250	250	250	249	250	250	246	250
01	01	01	01	01	01	01	01	01	250	243	250	250	250	250	250	250	250
11	11	11	11	11	11	11	11	11	175	171	192	203	173	186	182	163	206
11	11	11	11	11	11	11	11	11	250	250	250	250	250	249	250	250	250
11	11	11	11	11	11	11	11	11	250	250	250	250	250	250	250	250	250
01	01	01	01	01	01	01	01	01	250	250	250	247	248	250	245	250	240
01	01	01	01	01	01	01	01	01	250	234	241	248	213	247	250	235	249
11	11	11	11	11	11	11	11	11	222	193	216	228	228	231	228	179	221
01	01	01	01	01	01	01	01	01	250	250	250	250	249	250	250	250	250
01	01	01	01	01	01	01	01	01	204	163	141	179	139	186	190	163	167
11	11	11	11	11	11	11	11	11	241	218	195	250	209	246	244	213	247
11	11	11	11	11	11	11	11	11	248	250	250	250	250	249	250	250	250
01	01	01	01	01	01	01	01	01	250	250	249	249	250	250	250	249	248
11	11	11	11	11	11	11	11	11	215	224	199	205	202	230	232	217	218
11	11	11	11	11	11	11	11	11	250	238	208	225	240	235	250	208	250
01	01	01	01	01	01	01	01	01	174	153	117	186	154	176	159	151	198
01	01	01	01	01	01	01	01	01	213	200	122	210	193	218	179	176	226
01	01	01	01	01	01	01	01	01	220	213	208	220	241	232	227	212	233
01	01	01	00	00	01	00	00	00	144	125	111	150	139	142	121	124	146
01	01	01	01	01	01	01	01	01	247	250	250	250	250	247	250	249	250
01	01	01	01	01	01	01	01	01	250	250	247	244	245	242	239	245	247
01	01	01	01	01	01	01	01	01	237	191	202	182	241	220	220	181	189
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11	11	11	11	11	11	11	11	11	250	249	202	249	247	250	250	231	250
010	01	010	010	010	010	010	010	010	220	206	163	223	201	223	205	232	221
11	11	11	11	11	11	11	11	11	199	123	126	181	161	182	160	126	190
01	01	01	01	01	01	01	01	01	246	247	227	250	250	246	246	248	246
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Depth	Depth	Depth	AllelicDepth	AllelicDepth	AllelicDepth	AllelicDepth	AllelicDepth	AllelicDepth	AllelicDepth	AllelicDepth	AllelicDepth	AllelicDepth
CC1-17	CC1-18	CC1-25	NCC1	CC1	CC1-1	CC1-2	CC1-7	CC1-8	CC1-9	CC1-11	CC1-12	CC1-17
238	250	244	178172	165171	158192	157189	156188	163187	167178	155194	161182	152186
250	250	250	193156	193155	189161	198150	189161	182167	190160	200150	192158	208142
250	249	250	164186	145105	162188	157191	151199	148102	157193	157192	151199	163187
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250	250	250	221216	161234	171233	241219	211226	311218	171230	191229	211226	221228
228	233	239	421192	401154	401185	681170	451203	541181	381198	431182	501190	431185
127	178	155	68181	48180	39156	75176	78163	84162	96180	74173	66184	76151
216	250	210	133117	90184	94185	116126	113110	103113	119118	109160	119104	116199
250	249	250	127123	136114	124125	131119	138111	125124	134114	114136	118132	112138
216	248	180	145105	103173	90175	135193	108100	137198	121113	91181	95108	118197
145	189	144	92168	60169	73162	90169	80164	85170	57180	50160	78176	73172
200	222	180	168157	136148	121142	163147	166143	169152	191153	160144	155149	148152
241	240	236	123127	108129	119122	114123	126111	131115	104131	122114	118117	128113
230	210	205	118121	83100	81103	99115	103125	113117	87104	88171	101132	106124
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191	169	166	01175	01170	01192	01203	01173	01186	01182	01163	01206	01191
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209	208	221	01222	01193	01216	01227	01226	01231	01228	01179	01221	01209
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185	191	176	100103	85178	70171	93186	75164	102184	100188	106157	85182	99185
240	233	230	01241	01218	01193	01250	01209	01246	01244	01213	11246	01240
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239	222	211	11214	01224	01198	01205	01201	01229	01232	01217	01218	11238
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178	206	176	98176	94159	55162	105181	96158	101175	86173	94157	106192	111167
211	211	199	120193	112188	56166	118191	117176	125193	96182	104172	128198	127183
235	236	222	125195	111102	96112	101119	128113	116116	113114	106105	131101	111124
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247	243	243	120129	133117	107140	132112	127118	111130	127112	119126	131116	129118
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241	246	228	01237	01240	01241	01236	01250	01250	01249	01215	11248	01241
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246	250	250	127	123	128	120	125	125	103	147	126	123	114	136	125	125	120	130	127	123	106	139
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243	245	246	0	2	4	5	0	2	4	9	0	2	3	4	0	2	5	0	0	2	4	8
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158	193	162	0 200	2 153	0 132	0 200	0 155	0 178	0 191	1 147	0 174	0 158
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228	246	201	1 28 122	96 87	97 113	115 102	116 103	134 96	119 130	90 89	113 122	121 107
165	216	149	1 16 101	81 81	82 92	97 98	83 66	106 73	78 84	77 59	86 102	100 65
136	155	95	0 154	0 96	0 116	0 154	0 130	0 172	0 160	0 116	0 148	0 136
167	199	186	1 03 102	101 64	68 78	89 96	92 91	83 93	84 86	91 75	117 83	85 82
43	45	36	47 7	33 5	29 10	42 8	44 5	43 12	33 7	19 7	46 5	33 10
228	244	246	1 88 59	187 57	188 58	203 37	185 51	194 46	197 47	211 36	199 39	197 31
148	189	125	88 86	59 56	66 85	72 84	100 76	93 82	98 79	62 75	75 115	72 76
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245	240	248	1 88 58	201 38	215 35	193 49	199 46	204 44	198 50	204 39	198 50	204 38
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204	217	178	1 24 94	87 96	81 80	96 121	114 97	119 124	112 121	81 85	118 115	97 106
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164	187	130	1 26 75	72 66	57 55	77 71	96 65	73 80	96 65	93 52	80 72	105 59
144	194	148	0 172	0 105	0 112	0 159	0 142	0 163	0 141	0 139	0 155	0 144
145	201	156	0 199	0 114	0 114	0 173	0 151	0 172	0 144	0 141	0 149	0 145
157	217	176	98 111	70 63	63 77	86 105	103 78	94 115	104 78	66 74	101 91	66 91
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142	143	116	1 13 44	76 25	68 28	75 35	80 35	91 36	94 39	85 40	122 34	103 39
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206	185	159	1 54 63	102 33	102 42	130 45	106 48	115 60	138 58	114 39	133 56	136 70
224	244	222	1 21 117	119 77	127 103	117 122	112 111	120 123	140 106	124 96	109 137	112 112
182	233	183	246 1	172 0	181 0	208 0	209 0	198 0	189 0	175 0	244 0	182 0
250	250	250	1 34 115	113 136	118 132	123 126	118 131	135 115	105 145	118 131	111 139	126 122
100	120	84	67 67	49 46	45 34	65 65	60 70	50 69	78 48	45 38	73 58	50 50
243	237	235	1 05 120	144 92	115 122	130 120	119 128	126 109	115 119	122 124	132 115	128 115
250	250	250	249 1	195 54	241 0	249 0	249 0	249 1	249 0	250 0	249 0	250 0
122	161	133	91 102	81 63	74 73	66 67	80 73	93 86	75 75	59 46	86 83	64 58
250	250	250	0 250	0 249	0 237	0 250	0 250	1 249	0 250	0 250	0 250	0 249
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250	250	250	0 249	0 249	0 249	0 245	0 249	0 250	2 246	0 249	0 250	0 250
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97	141	91	0 120	0 73	0 71	0 106	0 116	0 112	1 111	0 81	0 134	0 97
141	16	17	0 19	0 13	0 10	0 18	0 20	0 22	0 17	0 17	0 26	0 14

250	250	194	0	249	0	199	0	152	0	199	0	208	0	237	0	211	0	226	0	235	0	250
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65	99	63	0	178	0	43	0	62	0	88	0	58	1	66	0	60	0	52	0	97	0	65
54	57	25	3	427	2	022	2	7131	3	3325	2	1129	3	3228	3	3631	1	7116	3	35127	3	34119
81	122	81	5	458	3	545	3	3238	4	868	4	4049	4	755	4	767	5	344	4	4344	3	3348
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177	167	148	6	599	7	567	9	069	8	581	6	066	7	5110	8	680	5	76	7	7474	9	087
136	117	88	0	97	0	100	0	87	0	108	0	90	0	102	0	110	0	92	0	111	0	136
250	250	250	0	250	0	250	0	250	0	250	0	250	0	250	0	250	0	250	0	249	0	250
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229	216	204	3	228	4	208	0	209	2	215	4	227	1	234	1	240	1	198	4	234	0	229
249	246	205	1	27120	1	26119	1	18116	1	13130	1	07130	1	26123	1	28122	1	05105	1	15131	1	20129
246	250	250	1	82168	1	8070	1	87160	1	94156	1	95155	1	85165	2	1732	2	0446	1	92158	1	91155
111	142	90	1	3710	9	110	7	90	1	3110	1	0210	1	0310	1	0310	8	310	1	0610	1	1110
104	105	93	4	6153	3	538	4	826	5	339	4	052	5	144	4	955	3	748	4	849	5	549
114	137	89	6	7181	4	543	3	244	4	856	6	557	5	847	5	941	4	742	5	060	5	5559
181	226	172	1	14122	7	084	8	1174	9	5100	9	674	1	03118	9	899	7	676	1	14129	9	883
47	75	30	0	49	0	41	0	42	0	40	0	50	0	41	0	52	0	36	0	43	0	47
116	114	90	6	243	5	225	3	844	5	854	4	646	6	039	6	459	5	038	6	453	5	066
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63	80	71	0	118	0	58	0	67	0	90	0	74	0	80	0	93	0	54	0	75	0	63
19	31	18	1	319	9	12	1	19	1	510	1	36	1	214	8	14	6	6	6	3	8	11
128	174	119	9	8175	7	658	7	061	7	2165	8	072	7	6178	7	8173	6	853	7	5178	6	6563
183	224	200	3	247	0	171	0	141	1	230	0	184	0	201	0	233	1	195	1	189	1	182
250	250	241	0	248	0	247	0	250	0	250	0	248	0	250	0	250	0	246	0	250	0	250
201	250	210	1	0191	1	494	1	0688	1	4188	1	0693	1	0795	1	1273	1	0692	9	897	1	1190
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237	193	207	1	8930	1	5848	1	2736	1	8537	1	5843	1	9527	1	8223	2	1022	1	8535	2	0334
192	197	169	0	199	0	123	0	125	0	181	0	161	0	182	1	159	0	126	0	189	0	192
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246	237	220	1	17119	9	2109	1	03101	1	25119	1	12120	1	05123	1	16114	1	17117	1	02134	1	11134
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154	163	137	9	7193	7	7178	7	056	7	667	9	056	9	690	9	272	6	346	8	157	8	272
186	218	152	0	177	1	177	2	150	0	180	0	193	0	199	0	184	0	154	0	157	0	186
242	249	159	0	222	0	248	1	151	1	199	0	207	0	243	0	214	0	212	0	211	0	242
207	250	182	1	18132	1	05104	1	0894	1	29121	9	9105	1	12134	1	02127	1	24107	1	12125	1	1790
196	222	152	0	196	0	167	0	156	0	166	0	193	0	210	0	185	0	142	0	193	0	196
85	144	93	1	130	0	82	1	189	1	115	2	120	0	112	1	127	0	106	1	109	1	183
15	9	14	0	14	0	9	1	10	0	10	0	8	0	11	0	11	0	13	0	10	0	15
152	196	147	1	0185	8	945	9	161	8	044	7	459	1	0967	9	671	8	564	9	975	9	854
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64	76	69	4	263	3	525	2	626	4	228	2	933	4	529	3	537	3	120	3	642	3	628
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41	67	32	0	65	0	52	0	44	0	64	0	38	0	50	0	52	0	37	0	41	0	41
164	217	140	0	157	0	107	0	128	0	154	0	140	0	175	0	147	0	160	0	140	2	162
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241	241	212	0	245	0	209	0	182	0	226	0	225	0	247	0	232	1	198	0	244	0	241
96	101	85	1	124	0	113	0	84	0	100	0	91	0	115	0	114	0	84	0	115	0	94
74	107	78	0	114	0	78	0	60	0	80	0	71	0	87	0	91	0	67	0	97	0	74

AllelicDepth	AllelicDepth	GenotypeQuality	GenotypeQuality	GenotypeQuality	GenotypeQuality	GenotypeQuality	GenotypeQuality	GenotypeQuality
CC1-18	CC1-25	NCC1	CC1	CC1-1	CC1-2	CC1-7	CC1-8	CC1-9
166 84	162 81	99	99	99	99	99	99	99
191 59	185 64	53.64	27.35	38	72.84	2	99	99
152 95	150 100	99	99	99	99	99	99	99
145	0 47	87.25	60.16	93.24	51.14	69.19	99	99
19 231	26 223	99	99	99	99	99	99	99
36 196	63 176	99	99	99	99	99	99	99
88 90	48 107	99	99	99	99	99	99	99
139 111	102 107	99	99	99	99	99	99	99
125 124	133 117	99	99	99	99	99	99	99
133 114	96 84	99	99	99	99	99	99	99
100 89	78 66	99	99	99	99	99	99	99
167 54	133 47	99	99	99	99	99	99	99
104 134	128 108	99	99	99	99	99	99	99
110 100	97 108	99	99	99	99	99	99	99
0 247	0 246	99	99	99	99	99	99	99
127 119	113 106	99	99	99	99	99	99	99
143 107	121 129	99	99	99	99	99	99	99
136 114	143 107	99	99	99	99	99	99	99
0 169	0 166	99	99	99	99	99	99	99
0 249	0 202	99	99	99	99	99	99	99
0 248	0 250	99	99	99	99	99	99	99
137 113	120 130	99	99	99	99	99	99	99
139 111	125 111	99	99	99	99	99	99	99
0 208	1 220	99	99	99	99	99	99	99
114 136	122 127	99	99	99	99	99	99	99
107 84	95 81	99	99	99	99	99	99	99
0 233	1 229	99	99	99	99	99	99	99
0 250	0 249	99	99	99	99	99	99	99
125 125	115 135	99	99	99	99	99	99	99
0 220	0 211	99	99	99	99	99	99	99
0 250	0 250	99	99	99	99	99	99	99
112 94	99 77	99	99	99	99	99	99	99
112 98	106 93	99	99	99	99	99	99	99
130 106	106 116	99	99	99	99	99	99	99
123 21	83 23	48.18	21.41	99	99	99	29.63	22.04
130 118	123 108	99	99	99	99	99	99	99
137 106	122 121	99	99	99	99	99	99	99
103 123	80 82	99	99	99	99	99	99	99
124 125	125 112	99	99	99	99	99	99	99
130 119	115 96	99	99	99	99	99	99	99
127 123	99 113	99	99	99	99	99	99	99
0 245	0 228	99	99	99	99	99	99	99
221 29	208 41	78.41	99	40.41	99	99	99	48.32
120 24	68 18	99	26.72	99	99	32.5	74.69	46.29
129 121	250 0	99	99	99	99	99	99	99
131 6	131 0	99	99	99	99	99	99	99
140 110	125 121	99	99	99	99	99	99	99
0 250	0 244	99	99	99	99	99	99	99
132 118	131 118	99	99	99	99	99	99	99
118 132	123 127	99	99	99	99	99	99	99
123 127	127 123	99	99	99	99	99	99	99
153 92	153 86	99	99	99	99	99	99	99

194151	148140	99	99	6.21	62.21	90.36	66.4	99
122128	133117	99	99	99	99	99	99	99
126124	122128	99	99	99	99	99	99	99
01245	01237	99	99	99	99	99	99	99
128120	89109	99	99	99	99	99	99	99
11249	11248	99	99	99	99	99	99	99
01250	11194	99	99	99	99	99	99	99
25010	24410	99	99	99	99	99	99	99
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122128	125125	99	99	99	99	99	99	99
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01250	01250	99	99	99	99	99	99	99
01247	01226	99	99	99	99	99	99	99
01250	01248	99	99	99	99	99	99	99
01249	01250	99	99	99	99	99	99	99
01249	01250	99	99	99	99	99	99	99
01250	01250	99	99	99	99	99	99	99
134113	129121	99	99	99	99	99	99	99
121126	105191	99	99	99	99	99	99	99
122128	117133	99	99	99	99	99	99	99
132117	131118	99	99	99	99	99	99	99
127122	123127	99	99	99	99	99	99	99
125125	129121	99	99	99	99	99	99	99
111131	115128	99	99	99	99	99	99	99
118132	126124	99	99	99	99	99	99	99
108141	127122	99	99	99	99	99	99	99
21247	01250	99	99	99	99	99	99	99
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01250	01250	99	99	99	99	99	99	99
11249	01249	99	99	99	99	99	99	99
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30131	28120	70.41	44.09	99	51.41	95.08	82.82	85.83
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01236	01213	99	99	99	99	99	99	99
01246	01249	99	99	99	99	99	99	99
01249	01241	99	99	99	99	99	99	99
01250	01215	99	99	99	99	99	99	99
224123	197153	99	99	99	30.44	99	67.31	99
891110	82173	99	99	99	99	99	99	99
132111	137111	99	99	99	99	99	99	99
01235	11169	99	99	99	99	99	99	99
11186	01142	99	99	99	99	99	99	99
01250	01199	99	99	99	99	99	99	99
01250	01250	99	99	99	99	99	99	99
11249	01250	99	99	99	99	99	99	99
24510	132106	99	99	99	99	99	99	99
130120	125125	99	99	99	99	99	99	99
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0 250	0 250	99	99	99	99	99	99	99	99
1 249	0 250	99	99	99	99	99	99	99	99
155 95	132 95	99	99	99	99	99	99	99	99
143 107	103 112	99	99	99	99	99	99	99	99
0 237	0 249	99	99	99	99	99	99	99	99
0 190	0 159	99	99	99	99	99	99	99	99
0 250	0 187	99	99	99	99	99	99	99	99
0 247	0 218	99	99	99	99	99	99	99	99
0 243	0 250	99	99	99	99	99	99	99	99
121 35	88 20	73.74	99	81.74	77.49	3.89	18.31	65.29	99
0 250	0 250	99	99	99	99	99	99	99	99
137 113	133 116	99	99	99	99	99	99	99	99
118 132	124 126	99	99	99	99	99	99	99	99
0 249	0 249	99	99	99	99	99	99	99	99
0 248	0 248	99	99	99	99	99	99	99	99
19 13	10 13	99	99	99	99	99	99	99	99
0 250	0 250	99	99	99	99	99	99	99	99
0 213	0 182	99	99	99	99	99	99	99	99
0 177	0 125	99	99	99	99	99	99	99	99
67 61	40 40	99	99	99	99	99	99	99	99
131 119	125 124	99	99	99	99	99	99	99	99
1 248	0 250	99	99	99	99	99	99	99	99
1 247	0 246	99	99	99	99	99	99	99	99
0 249	0 250	99	99	99	99	99	99	99	99
0 248	0 250	99	99	99	99	99	99	99	99
0 250	0 250	99	99	99	99	99	99	99	99
0 200	0 116	99	99	99	99	99	99	99	99
130 120	126 124	99	99	99	99	99	99	99	99
0 103	0 85	99	99	99	99	99	99	99	99
0 104	0 83	99	99	99	99	99	99	99	99
132 118	121 119	99	99	99	99	99	99	99	99
114 136	125 124	99	99	99	99	99	99	99	99
67 80	50 53	99	99	99	99	99	99	99	99
0 118	0 93	99	99	99	99	99	99	99	99
118 104	119 113	99	99	99	99	99	99	99	99
0 249	0 250	99	99	99	99	99	99	99	99
120 129	118 132	99	99	99	99	99	99	99	99
0 109	0 64	99	99	99	99	99	99	99	99
0 250	0 250	99	99	99	99	99	99	99	99
250 0	249 0	99	99	99	99	99	99	99	99
34 46	32 25	99	99	99	99	99	99	99	99
135 108	126 114	99	99	99	99	99	99	99	99
0 249	0 248	99	99	99	99	99	99	99	99
119 131	119 106	99	99	99	99	99	99	99	99
57 75	52 43	99	99	99	99	99	99	99	99
207 0	179 0	99	99	99	99	99	99	99	99
119 131	111 127	99	99	99	99	99	99	99	99
0 83	0 91	99	99	99	99	99	99	99	99
44 66	56 48	99	99	99	99	99	99	99	99
250 0	249 0	99	99	99	99	99	99	99	99
1 246	1 192	99	99	99	99	99	99	99	99
143 107	110 103	99	99	99	99	99	99	99	99
179 70	186 63	99	99	18.41	99	99	99	99	99
1 244	1 248	99	99	99	99	99	99	99	99
129 42	107 39	99	99	99	99	99	99	99	99

51 49	39 36	99	99	99	99	99	99	99	99
119 115	84 88	99	99	99	99	99	99	99	99
87 96	81 89	99	99	99	99	99	99	99	99
70 56	60 55	99	99	99	99	99	99	99	99
191 52	161 32	99	99	99	99	99	99	51.03	45.95
130 120	110 125	99	99	99	99	99	99	99	99
122 127	147 102	99	99	99	99	99	99	99	99
117 125	126 124	99	99	99	99	99	99	99	99
0 250	0 250	99	99	99	99	99	99	99	99
135 115	135 115	99	99	99	99	99	99	99	99
139 111	134 116	99	99	99	99	99	99	99	99
102 122	86 77	99	99	99	99	99	99	99	99
128 119	113 117	99	99	99	99	99	99	99	99
129 118	108 106	99	99	99	99	99	99	99	99
250 0	246 1	99	99	99	99	99	99	99	99
127 123	127 123	99	99	99	99	99	99	99	99
124 126	127 122	99	99	99	99	99	99	99	99
46 36	43 39	99	99	99	99	99	99	99	99
144 106	115 134	99	99	99	99	99	99	99	99
0 250	1 249	99	99	99	99	99	99	99	99
0 88	0 52	99	99	99	99	99	99	99	99
110 20	77 12	57.7	99	11.46	10.29	46.1	99	61.68	99
110 140	133 117	99	99	99	99	99	99	99	99
247 0	241 0	99	99	99	99	99	99	99	99
207 43	198 52	67.67	11.5	99	99	99	99	99	99
116 134	126 124	99	99	99	99	99	99	99	99
56 10	38 7	16.91	89.69	59.58	9.05	6.43	1.08	60.07	99
1 248	0 234	99	99	99	99	99	99	99	99
0 250	0 249	99	99	99	99	99	99	99	99
128 120	138 104	99	99	99	99	99	99	99	99
72 58	50 55	99	99	99	99	99	99	99	99
140 110	135 115	99	99	99	99	99	99	99	99
139 111	137 110	99	99	99	99	99	99	99	99
127 123	118 123	99	99	99	99	99	99	99	99
198 52	179 37	55.76	99	99	99	99	99	8.38	99
0 56	0 53	99	99	99	99	99	99	99	99
0 217	0 121	99	99	99	99	99	99	99	99
125 125	124 123	99	99	99	99	99	99	99	99
117 133	116 126	99	99	99	99	99	99	99	99
108 142	106 122	99	99	99	99	99	99	99	99
32 8	20 9	38.82	7	43.52	66.66	91.09	99	74.32	99
8 10	10 7	99	99	99	99	82.33	99	99	99
0 246	0 231	99	99	99	99	99	99	99	99
127 123	113 137	99	99	99	99	99	99	99	99
0 250	1 248	99	99	99	99	99	99	99	99
117 129	110 120	99	99	99	99	99	99	99	99
131 119	131 118	99	99	99	99	99	99	99	99
0 200	0 162	99	99	99	99	99	99	99	99
132 118	123 127	99	99	99	99	99	99	99	99
134 100	131 106	99	99	99	99	99	99	99	99
0 243	0 192	99	99	99	99	99	99	99	99
89 77	74 73	99	99	99	99	99	99	99	99
93 93	54 72	99	99	99	99	99	99	99	99
125 124	116 132	99	99	99	99	99	99	99	99
0 247	0 249	99	99	99	99	99	99	99	99

0 250	0 248	99	99	99	99	99	99	99	99
2 248	0 241	99	99	99	99	99	99	99	99
140 109	128 122	99	99	99	99	99	99	99	99
0 80	0 57	99	99	99	99	99	99	99	99
113 137	124 126	99	99	99	99	99	99	99	99
128 122	120 127	99	99	99	99	99	99	99	99
75 24	69 22	3.16	99	57.12	19.58	35.47	18.77	79.57	99
119 131	117 133	99	99	99	99	99	99	99	99
75 76	56 64	99	99	99	99	99	99	99	99
122 128	119 125	99	99	99	99	99	99	99	99
13 5	12 0	7.16	48.11	42.09	66.14	63.13	3.38	41.39	99
46 53	31 47	99	99	99	99	99	99	99	99
137 113	137 113	99	99	99	99	99	99	99	99
0 250	0 244	99	99	99	99	99	99	99	99
129 121	142 108	99	99	99	99	99	99	99	99
123 127	139 103	99	99	99	99	99	99	99	99
80 65	48 52	99	99	99	99	99	99	99	99
114 111	82 67	99	99	99	99	99	99	99	99
0 182	0 142	99	99	99	99	99	99	99	99
0 250	0 249	99	99	99	99	99	99	99	99
2 247	0 249	99	99	99	99	99	99	99	99
119 131	143 107	99	99	99	99	99	99	99	99
250 0	249 0	99	99	99	99	99	99	99	99
147 102	102 104	99	99	99	99	99	99	99	99
0 189	0 189	99	99	99	99	99	99	99	99
134 116	122 126	99	99	99	99	99	99	99	99
137 113	135 115	99	99	99	99	99	99	99	99
0 237	0 244	99	99	99	99	99	99	99	99
109 104	97 74	99	99	99	99	99	99	99	99
138 112	114 136	99	99	99	99	99	99	99	99
70 48	55 40	99	99	99	99	99	99	99	99
123 127	126 124	99	99	99	99	99	99	99	99
7 5	6 6	99	99	99	84.17	99	99	99	99
0 248	0 250	99	99	99	99	99	99	99	99
0 250	0 250	99	99	99	99	99	99	99	99
0 199	0 122	99	99	99	99	99	99	99	99
135 115	121 89	99	99	99	99	99	99	99	99
94 111	102 83	99	99	99	99	99	99	99	99
0 250	0 249	99	99	99	99	99	99	99	99
130 120	131 117	99	99	99	99	99	99	99	99
1 245	0 250	99	99	99	99	99	99	99	99
1 242	0 246	99	99	99	99	99	99	99	99
124 126	130 120	99	99	99	99	99	99	99	99
117 131	95 106	99	99	99	99	99	99	99	99
112 138	128 122	99	99	99	99	99	99	99	99
0 250	0 250	99	99	99	99	99	99	99	99
114 136	111 139	99	99	99	99	99	99	99	99
42 23	34 8	58.19	99	85.13	62.35	21.37	32.15	24.38	99
13 12	12 17	99	99	99	99	99	99	99	99
25 15	25 10	89.32	71.01	51.04	39.86	28.73	32.88	14.01	99
174 28	183 21	2.23	99	99	99	99	99	37.2	99
5 6	6 12	99	99	99	99	99	99	99	99
113 136	136 113	99	99	99	99	99	99	99	99
134 115	114 136	99	99	99	99	99	99	99	99
127 123	131 119	99	99	99	99	99	99	99	99

01192	11160	99	99	99	99	99	99	99	99
01250	01248	99	99	99	99	99	99	99	99
1271123	135115	99	99	99	99	99	99	99	99
1915	9122	99	99	99	99	99	99	99	99
1211129	1171132	99	99	99	99	99	99	99	99
01250	01247	99	99	99	99	99	99	99	99
1261124	1271123	99	99	99	99	99	99	99	99
159191	1181132	99	99	99	99	99	99	99	99
931113	76182	99	99	99	99	99	99	99	99
1371113	1221128	99	99	99	99	99	99	99	99
1381110	1321116	99	99	99	99	99	99	99	99
1131137	1391111	99	99	99	99	99	99	99	99
1281118	103198	99	99	99	99	99	99	99	99
1141102	82167	99	99	99	99	99	99	99	99
01155	0194	99	99	99	99	99	99	99	99
101198	98188	99	99	99	99	99	99	99	99
3916	3115	99	24.33	84.15	30.31	51.45	53.19	69.02	
201143	202144	99	28.22	62.6	99	99	99	23.2	
93195	65160	99	99	99	99	99	99	99	
94197	65160	99	99	99	99	99	99	99	
01244	01231	99	99	99	99	99	99	99	
01154	01126	99	99	99	99	99	99	99	
24910	17410	99	99	99	99	99	99	99	
150199	1201129	99	99	99	99	99	99	99	
191149	206142	99	99	99	15.14	33.07	99	59.77	
01249	01250	99	99	99	99	99	99	99	
1519	11116	99	99	99	99	99	99	99	
126190	85192	99	99	99	99	99	99	99	
1231124	1291118	99	99	99	99	99	99	99	
1141131	1411109	99	99	99	99	99	99	99	
1351115	1451105	99	99	99	99	99	99	99	
95192	63167	99	99	99	99	99	99	99	
01194	01148	99	99	99	99	99	99	99	
01199	01156	99	99	99	99	99	99	99	
1041113	96180	99	99	99	99	99	99	99	
01158	01137	99	99	99	99	99	99	99	
01250	01250	99	99	99	99	99	99	99	
1151134	1261124	99	99	99	99	99	99	99	
99144	81135	99	99	99	99	99	92.61	99	
103146	91136	1.68	14.9	6.58	72.3	11.2	7.86	25.19	
136149	109150	99	99	99	99	99	99	99	
1241120	1131108	99	99	99	99	99	99	99	
23310	95187	99	99	99	99	99	99	99	
1221128	1311118	99	99	99	99	99	99	99	
65155	44140	99	99	99	99	99	99	99	
1141123	1171118	99	99	99	99	99	99	99	
24911	25010	99	99	99	99	99	99	99	
67193	68165	99	99	99	99	99	99	99	
01250	01250	99	99	99	99	99	99	99	
01250	01250	99	99	99	99	99	99	99	
01250	01250	99	99	99	99	99	99	99	
11249	01250	99	99	99	99	99	99	99	
215135	205144	73.5	99	4.18	17.87	99	50.14	8.39	
01141	0191	99	99	99	99	99	99	99	
0116	0117	48.14	39.11	27.08	51.13	54.13	66.15	48.14	

0 249	0 194	99	99	99	99	99	99	99	99
0 245	0 244	99	99	99	99	99	99	99	99
0 99	0 63	99	99	99	99	99	99	99	99
28 29	12 13	99	99	99	99	99	99	99	99
54 68	37 44	99	99	99	99	99	99	99	99
230 20	218 28	99	99	99	99	99	99	99	59.59
80 87	82 66	99	99	99	99	99	99	99	99
0 117	0 88	99	99	99	99	99	99	99	99
0 250	0 250	99	99	99	99	99	99	99	99
0 250	1 242	99	99	99	99	99	99	99	99
0 250	0 247	99	99	99	99	99	99	99	99
0 250	0 250	99	99	99	99	99	99	99	99
1 214	1 203	99	99	99	99	99	99	99	99
141 105	98 106	99	99	99	99	99	99	99	99
199 51	183 67	99	99	99	54.36	99	99	99	22.15
142 0	90 0	99	99	99	99	99	99	99	99
55 50	56 37	99	99	99	99	99	99	99	99
75 62	46 42	99	99	99	99	99	99	99	99
93 133	90 82	99	99	99	99	99	99	99	99
0 75	0 30	99	96.29	99	99	99	99	99	99
51 63	41 49	99	99	99	99	99	99	99	99
109 108	70 79	99	99	99	99	99	99	99	99
0 80	0 71	99	99	99	99	99	99	99	99
12 19	6 12	99	42.82	9.04	99	99	99	99	99
82 92	62 57	99	99	99	99	99	99	99	99
0 223	0 199	99	99	99	99	99	99	99	99
0 250	0 241	99	99	99	99	99	99	99	99
131 119	114 96	99	99	99	99	99	99	99	99
0 249	0 250	99	99	99	99	99	99	99	99
160 33	178 29	99	20.17	94.29	63.84	99	99	99	99
0 197	0 168	99	99	99	99	99	99	99	99
140 108	134 115	99	99	99	99	99	99	99	99
115 122	109 111	99	99	99	99	99	99	99	99
141 105	124 120	99	99	99	99	99	99	99	99
89 74	84 53	99	99	99	99	99	99	99	99
0 217	0 152	99	99	99	99	99	99	99	99
0 249	0 159	99	99	99	99	99	99	99	99
115 135	92 90	99	99	99	99	99	99	99	99
1 220	0 152	99	99	99	99	99	99	99	99
0 143	0 93	99	99	99	99	99	99	99	99
0 9	0 14	36.11	21.07	8.4	24.06	24.07	30.1	30.09	99
115 81	91 56	99	99	99	99	99	99	99	99
89 81	60 65	99	99	99	99	99	99	99	99
41 35	31 38	99	99	99	99	99	99	99	99
122 120	124 102	99	99	99	99	99	99	99	99
0 67	0 32	99	99	99	99	99	99	99	99
0 217	0 140	99	99	99	99	99	99	99	99
1 249	0 237	99	99	99	99	99	99	99	99
0 241	0 212	99	99	99	99	99	99	99	99
0 100	0 85	99	99	99	99	99	99	99	99
0 107	0 77	99	99	99	99	99	99	99	99

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

Supplemental Table 5 The 50 novel SNVs not reported in dbSNP135 or 1000 Genomes

Chrom	Chrom Start	Chrom End	Reference	Alternatives	Type	Known/Novel	Gene	Function	dbSNP
chr1	1575715	1575715	C	T	SNV	Novel	CDK11B.CDK11A	Missense	
chr1	1638925	1638925	C	T	SNV	Novel	CDK11A.CDK11B	Missense	
chr1	27942215	27942215	C	G	SNV	Novel	FGR	Missense	
chr1	38184063	38184063	C	A	SNV	Novel	EPHA10	Missense	
chr1	233497836	233497836	C	A	SNV	Novel	KIAA1804.RP5-862P8.2	Missense	
chr2	29416635	29416635	C	A	SNV	Novel	ALK	Missense	
chr2	29448410	29448410	T	G	SNV	Novel	ALK	Missense	
chr2	37336419	37336419	C	T	SNV	Novel	EIF2AK2	Missense	
chr2	148676144	148676144	A	C	SNV	Novel	ACVR2A	Missense	
chr2	158485099	158485099	C	A	SNV	Novel	ACVR1C.AC019186.1	Missense	
chr2	179408086	179408086	A	G	SNV	Novel	TTN.MIR548N.LOC100506866.AC009948.3	Missense	
chr2	179634421	179634421	T	G	SNV	Novel	TTN	Missense	
chr2	179638072	179638072	C	T	SNV	Novel	TTN	Missense	
chr2	209195248	209195248	C	A	SNV	Novel	PIKFYVE	Missense	
chr3	41705179	41705179	A	C	SNV	Novel	ULK4	Missense	
chr3	123988019	123988019	C	A	SNV	Novel	KALRN	Missense	
chr5	112769527	112769527	C	T	SNV	Novel	MCC.TSSK1B.CTD-2201G3.1	Missense	
chr5	180048626	180048626	C	T	SNV	Novel	FLT4	Missense	
chr6	31947203	31947203	T	C	SNV	Novel	STK19.XXbac-BPG116M5.15	Missense	
chr6	36489585	36489585	C	A	SNV	Novel	STK38	Missense	
chr6	43111336	43111336	G	T	SNV	Novel	PTK7	Missense	
chr6	110942394	110942394	G	T	SNV	Novel	CDK19	Missense	
chr7	23808650	23808650	G	T	SNV	Novel	STK31	Missense	
chr7	95216415	95216415	C	A	SNV	Novel	PDK4	Missense	
chr7	98490141	98490141	G	C	SNV	Novel	TRRAP	Missense	
chr7	98547196	98547196	G	T	SNV	Novel	TRRAP	Missense	
chr7	138145436	138145436	C	A	SNV	Novel	TRIM24	Missense	
chr8	8239069	8239069	C	A	SNV	Novel	SGK223.AC068353.1	Missense	
chr8	144800905	144800905	A	C	SNV	Novel	MAPK15.RP11-429J17.5	Missense	
chr10	99400747	99400747	C	A	SNV	Novel	PI4K2A.RP11-548K23.11	Missense	
chr11	111594312	111594312	C	A	SNV	Novel	SIK2	Missense	
chr12	1009680	1009680	C	T	SNV	Novel	WNK1	Missense	
chr13	110434668	110434668	C	A	SNV	Novel	IRS2	Missense	
chr13	110437802	110437802	A	C	SNV	Novel	IRS2	Missense	
chr14	24808802	24808802	G	T	SNV	Novel	RIPK3	Missense	
chr15	91436551	91436551	A	G	SNV	Novel	FES.AC068831.1	Missense	
chr15	99250895	99250895	G	T	SNV	Novel	IGF1R	Missense	
chr16	23690401	23690401	C	T	SNV	Novel	PLK1	Missense	
chr17	7796794	7796794	A	C	SNV	Novel	CHD3	Missense	
chr17	7796803	7796803	T	C	SNV	Novel	CHD3	Missense	
chr17	7796815	7796815	G	C	SNV	Novel	CHD3	Missense	
chr17	8789811	8789811	G	A	SNV	Novel	PIK3R5	Nonsense	
chr17	37881392	37881392	A	G	SNV	Novel	ERBB2.MIR4728	Missense	
chr17	41245693	41245693	G	T	SNV	Novel	BRCA1	Missense	
chr18	59854988	59854988	G	T	SNV	Novel	KIAA1468.PIGN	Missense	
chr18	59919898	59919898	C	A	SNV	Novel	KIAA1468	Missense	
chr19	2046399	2046399	G	A	SNV	Novel	MKNK2	Missense	
chr19	17949138	17949138	C	A	SNV	Novel	JAK3	Missense	
chr19	47193933	47193933	G	T	SNV	Novel	PRKD2	Missense	
chr19	56047544	56047544	G	T	SNV	Novel	SBK2	Missense	

CCDS

CCDS44042.1|GN=CDK11A|GI=728642|FC=Missense|CP=1168|CF=0|AC=gAC->aAC|RP=390|RC=D|Asp|I->N|Asn|LEN=10/19|DS=-99|P=chr1:1634346-1654257|S
CCDS305.1|GN=FGR|GI=2268|FC=Missense|CP=823|CF=0|AC=gGG->cGG|RP=275|RC=G|Glv|I->R|Arg|LEN=6/11|DS=-91|P=chr1:27939425-27950427|S=-|C|=1
CCDS41305.1|GN=EPHA10|GI=284656|FC=Missense|CP=3008|CF=1|AC=GgC->GtC|RP=1003|RC=G|Glv|I->V|Val|LEN=17/17|DS=-96|P=chr1:38184044-38230738
CCDS1598.1|GN=KIAA1804|GI=84451|FC=Missense|CP=1349|CF=1|AC=GcT->GaT|RP=450|RC=A|Ala|I->D|Asp|LEN=5/10|DS=-38|P=chr1:233463775-233518457|S
CCDS33172.1|GN=ALK|GI=238|FC=Missense|CP=4318|CF=0|AC=gCC->tCC|RP=1440|RC=A|Ala|I->S|Ser|LEN=29/29|DS=-154|P=chr2:29416090-30143525|S=-|C|=1
CCDS33172.1|GN=ALK|GI=238|FC=Missense|CP=3089|CF=1|AC=cAc->CcC|RP=1030|RC=H|His|I->P|Pro|LEN=19/29|DS=-22|P=chr2:29416090-30143525|S=-|C|=1
CCDS1786.1|GN=EIF2AK2|GI=5610|FC=Missense|CP=1397|CF=1|AC=GgA->GaA|RP=466|RC=G|Glv|I->E|Glu|LEN=13/15|DS=-20|P=chr2:37334416-37374949|S
CCDS33301.1|GN=ACVR2A|GI=92|FC=Missense|CP=945|CF=2|AC=AAa->AAc|RP=315|RC=K|Lys|I->N|Asn|LEN=7/11|DS=-129|P=chr2:148602722-148684843|S
CCDS2205.1|GN=ACVR1C|GI=130399|FC=Missense|CP=58|CF=0|AC=gCC->tCC|RP=20|RC=A|Ala|I->S|Ser|LEN=1/9|DS=-41|P=chr2:158390430-158485156|S
CCDS54424.1|GN=TTN|GI=7273|FC=Missense|CP=88910|CF=1|AC=GtG->GcG|RP=29637|RC=V|Val|I->A|Ala|LEN=295/311|DS=-304|P=chr2:179391739-1796693
CCDS54424.1|GN=TTN|GI=7273|FC=Missense|CP=8887|CF=0|AC=aCC->cCC|RP=2963|RC=T|Thr|I->P|Pro|LEN=36/311|DS=-246|P=chr2:179391739-179669369|S
CCDS54424.1|GN=TTN|GI=7273|FC=Missense|CP=7619|CF=1|AC=CgT->CaT|RP=2540|RC=R|Arg|I->H|His|LEN=32/311|DS=-25|P=chr2:179391739-179669369|S
CCDS2382.1|GN=PIKEYV|GI=200576|FC=Missense|CP=3793|CF=0|AC=cCT->aCT|RP=1265|RC=P|Pro|I->T|Thr|LEN=22/41|DS=-2|P=chr2:209136244-20922002
CCDS43071.1|GN=ULK4|GI=54986|FC=Missense|CP=2990|CF=1|AC=AtT->AgT|RP=997|RC=I|Ile|I->S|Ser|LEN=29/36|DS=-12|P=chr3:41288420-41996251|S=-|C|=1
CCDS3027.1|GN=KALRN|GI=8997|FC=Missense|CP=880|CF=0|AC=cAc->aAC|RP=294|RC=H|His|I->N|Asn|LEN=5/34|DS=-430|P=chr3:123813685-124237309|S
CCDS4112.1|GN=TSSK1B|GI=83942|FC=Missense|CP=1010|CF=1|AC=AgG->AaG|RP=337|RC=R|Arg|I->K|Lys|LEN=1/11|P=chr5:112769433-112770536|S=-|C|=1
CCDS4457.1|GN=FLT4|GI=2324|FC=Missense|CP=1936|CF=0|AC=gAG->aAG|RP=646|RC=E|Glu|I->K|Lys|LEN=13/30|DS=-279|P=chr5:180030192-180076545|S
CCDS4733.1|GN=STK19|GI=8859|FC=Missense|CP=688|CF=0|AC=tGT->cGT|RP=230|RC=C|Cys|I->R|Arg|LEN=5/8|DS=-13|P=chr6:31939774-31948826|S=-|C|=1
CCDS4822.1|GN=STK38|GI=11329|FC=Missense|CP=316|CF=0|AC=gTT->tTT|RP=106|RC=V|Val|I->F|Phe|LEN=4/13|DS=-10|P=chr6:36463561-36507979|S=-|C|=1
CCDS4884.1|GN=PTK7|GI=5754|FC=Missense|CP=2229|CF=2|AC=GAg->GAt|RP=743|RC=E|Glu|I->D|Asp|LEN=14/20|DS=-182|P=chr6:43044227-43128619|S=-|C|=1
CCDS5085.1|GN=CDK19|GI=23097|FC=Missense|CP=1290|CF=2|AC=AGc->AGa|RP=430|RC=S|Ser|I->R|Arg|LEN=12/13|DS=-180|P=chr6:110935738-111136339|S
CCDS5386.1|GN=STK31|GI=56164|FC=Missense|CP=1453|CF=0|AC=gCC->tCC|RP=485|RC=A|Ala|I->S|Ser|LEN=12/24|DS=-37|P=chr7:23749905-23871985|S
CCDS5643.1|GN=PKD4|GI=5166|FC=Missense|CP=1002|CF=2|AC=TTg->TTt|RP=334|RC=L|Leu|I->F|Phe|LEN=10/11|DS=-21|P=chr7:95214953-95225605|S=-|C|=1
CCDS5659.1|GN=TRRAP1G|8295|FC=Missense|CP=356|CF=1|AC=CgC->CcC|RP=119|RC=R|Arg|I->P|Pro|LEN=4/70|DS=-95|P=chr7:98478774-98609978|S=-|C|=1
CCDS5659.1|GN=TRRAP1G|8295|FC=Missense|CP=4870|CF=0|AC=gCC->tCC|RP=1624|RC=A|Ala|I->S|Ser|LEN=33/70|DS=-87|P=chr7:98478774-98609978|S
CCDS5847.1|GN=TRIM24|GI=8805|FC=Missense|CP=143|CF=1|AC=GcC->GaC|RP=48|RC=A|Ala|I->D|Asp|LEN=1/19|DS=-43599|P=chr7:138145294-138269696|S
CCDS43706.1|GN=SGK23|GI=157285|FC=Missense|CP=189|CF=2|AC=AGg->AGt|RP=63|RC=R|Arg|I->S|Ser|LEN=1/5|DS=-3481|P=chr8:8175676-8239257|S=-|C|=1
CCDS6409.2|GN=MAPK15|GI=225689|FC=Intron|LEN=4/5/14|DS=-40|P=chr8:144798548-144804421|S=-|C|=1635|CS=Public
CCDS7469.1|GN=PI4K2A|GI=55361|FC=Missense|CP=248|CF=1|AC=GcT->GaT|RP=83|RC=A|Ala|I->D|Asp|LEN=1/9|DS=-9951|P=chr10:99400500-99433499|S
CCDS8347.1|GN=SIK2|GI=23235|FC=Missense|CP=2240|CF=1|AC=CcA->CaA|RP=747|RC=P|Pro|I->Q|Gln|LEN=15/15|DS=-93|P=chr11:111473288-111594853|S
CCDS53730.1|GN=WNK1|GI=65125|FC=Missense|CP=7267|CF=0|AC=cCC->tCC|RP=2423|RC=P|Pro|I->S|Ser|LEN=26/28|DS=-39|P=chr12:862732-1017958|S
CCDS9510.1|GN=IRS2|GI=8660|FC=Missense|CP=3733|CF=0|AC=gCC->tCC|RP=1245|RC=A|Ala|I->S|Ser|LEN=5/12|DS=-26013|P=chr13:110408651-110438400|S
CCDS9510.1|GN=IRS2|GI=8660|FC=Missense|CP=599|CF=1|AC=GtG->GgG|RP=200|RC=V|Val|I->G|Glv|LEN=1/2|DS=-29147|P=chr13:110408651-110438400|S
CCDS9628.1|GN=RIPK3|GI=11035|FC=Missense|CP=221|CF=0|AC=cCC->aCC|RP=8|RC=P|Pro|I->T|Thr|LEN=2/10|DS=-2|P=chr14:24805381-24809032|S=-|C|=1
CCDS10365.1|GN=FES|GI=2242|FC=Missense|CP=1952|CF=1|AC=GAg->GgG|RP=651|RC=E|Glu|I->G|Glv|LEN=15/18|DS=-31|P=chr15:91428276-91438788|S=-|C|=1
CCDS10378.1|GN=GFTR|GI=3480|FC=Missense|CP=199|CF=0|AC=gCC->tCC|RP=67|RC=A|Ala|I->S|Ser|LEN=2/21|DS=-105|P=chr15:99192811-99500671|S=-|C|=1
CCDS10616.1|GN=PLK1|GI=5347|FC=Missense|CP=148|CF=0|AC=cGG->tGG|RP=50|RC=R|Arg|I->W|Trp|LEN=1/10|DS=-1004|P=chr16:23690254-23701384|S=-|C|=1
CCDS32553.2|GN=CHD3|GI=1107|FC=Missense|CP=877|CF=0|AC=aTA->cTA|RP=293|RC=L|Leu|I->L|Leu|LEN=5/40|DS=-191|P=chr17:7788125-7814903|S=-|C|=1
CCDS32553.2|GN=CHD3|GI=1107|FC=Missense|CP=886|CF=0|AC=tCC->cCC|RP=296|RC=S|Ser|I->P|Pro|LEN=5/40|DS=-200|P=chr17:7788125-7814903|S=-|C|=1
CCDS32553.2|GN=CHD3|GI=1107|FC=Missense|CP=898|CF=0|AC=gCC->tCC|RP=300|RC=L|Leu|I->P|Pro|LEN=5/40|DS=-212|P=chr17:7788125-7814903|S=-|C|=1
CCDS11147.1|GN=PIK3R5|GI=23533|FC=Nonsense|CP=2017|CF=0|AC=cAA->tAA|RP=673|RC=Q|Gln|I->Stop|LEN=12/18|DS=-112|P=chr17:8783956-8814811|S
CCDS32642.1|GN=ERBB2|GI=2064|FC=Missense|CP=2584|CF=0|AC=cAc->gCA|RP=862|RC=T|Thr|I->A|Ala|LEN=21/27|DS=-91|P=chr17:37856492-37884297|S
CCDS11456.2|GN=BRCA1|GI=672|FC=Missense|CP=1855|CF=0|AC=cAT->aAT|RP=619|RC=H|His|I->N|Asn|LEN=9/23|DS=-1185|P=chr17:41197695-41276113|S
CCDS11979.2|GN=KIAA1468|GI=57614|FC=Missense|CP=250|CF=0|AC=gGC->tGC|RP=84|RC=G|Glv|I->C|Cys|LEN=1/29|DS=-23398|P=chr18:59854739-5997276
CCDS11979.2|GN=KIAA1468|GI=57614|FC=Missense|CP=1735|CF=0|AC=cAA->aAA|RP=579|RC=Q|Gln|I->K|Lys|LEN=12/29|DS=-2|P=chr18:59854739-59972767
CCDS12080.1|GN=MKNK2|GI=2872|FC=Missense|CP=208|CF=0|AC=cGG->tGG|RP=70|RC=R|Arg|I->W|Trp|LEN=3/13|DS=-69|P=chr19:2039612-2050850|S=-|C|=1
CCDS12366.1|GN=JAK3|GI=3718|FC=Missense|CP=1503|CF=2|AC=CAg->CAT|RP=501|RC=Q|Gln|I->H|His|LEN=10/23|DS=-62|P=chr19:17937552-17955226|S
CCDS12689.1|GN=PRKD2|GI=25865|FC=Missense|CP=1733|CF=1|AC=GcA->GaA|RP=578|RC=A|Ala|I->E|Glu|LEN=13/18|DS=-31|P=chr19:47177780-47219627|S
CCDS42631.1|GN=SBK2|GI=646643|FC=Missense|CP=118|CF=0|AC=cGC->aGC|RP=40|RC=R|Arg|I->S|Ser|LEN=1/3|DS=-4832|P=chr19:56041100-56047661|S

RefSeq Genes	
NM_033486.1	GN=CDK11B GI=984 FC=Coding_synonym EN=11/20 DS=+99 P=chr1:1571100-1655775 ST=- PD=cyclin-dependent kinase 11B isoform 2
NM_024011.2	GN=CDK11A GI=728642 FC=Missense CP=1168 CF=0 AC=gAC->aAC RP=390 RC=D Asp ->N Asn EN=11/20 DS=+99 P=chr1:1634170-1655791 ST=
NM_005248.2	GN=FGR GI=2268 FC=Missense CP=823 CF=0 AC=gCG->cGG RP=275 RC=G Glv ->R Arg EN=8/13 DS=-91 P=chr1:27938801-27961727 ST=- C =
NM_001099439.1	GN=EPHA10 GI=284656 FC=Missense CP=3008 CF=1 AC=GgC->GtC RP=1003 RC=G Glv ->V Val EN=17/17 DS=+96 P=chr1:38181646-382308
NM_032435.2	GN=KIAA1804 GI=84451 FC=Missense CP=1349 CF=1 AC=GcT->GaT RP=450 RC=A Ala ->D Asp EN=5/10 DS=+38 P=chr1:233463514-233520894
NM_004304.4	GN=ALK GI=238 FC=Missense CP=4318 CF=0 AC=gCC->tCC RP=1440 RC=A Ala ->S Ser EN=29/29 DS=+154 P=chr2:29415640-30144477 ST=- C =
NM_004304.4	GN=ALK GI=238 FC=Missense CP=3089 CF=1 AC=CaC->CcC RP=1030 RC=H His ->P Pro EN=19/29 DS=+22 P=chr2:29415640-30144477 ST=- C =
NM_002759.3	GN=EIF2AK2 GI=5610 FC=Missense CP=1397 CF=1 AC=GgA->GaA RP=466 RC=G Glv ->E Glu EN=15/17 DS=+20 P=chr2:37332284-37384190 ST=
NM_001616.3	GN=ACVR2A GI=92 FC=Missense CP=945 CF=2 AC=AAa->AAc RP=315 RC=K Lys ->N Asn EN=7/11 DS=+129 P=chr2:148602570-148688393 ST=
NM_145259.2	GN=ACVR1C GI=130399 FC=Missense CP=58 CF=0 AC=gCC->tCC RP=20 RC=A Ala ->S Ser EN=1/9 DS=-41170 P=chr2:158383279-158485399 S
NM_133378.4	GN=TTN GI=7273 FC=Missense CP=88910 CF=1 AC=GtG->GcG RP=29637 RC=V Val ->A Ala EN=296/312 DS=+304 P=chr2:179390718-17967215
NM_133378.4	GN=TTN GI=7273 FC=Missense CP=8887 CF=0 AC=aCC->cCC RP=2963 RC=T Thr ->P Pro EN=37/312 DS=+246 P=chr2:179390718-179672150 S
NM_133378.4	GN=TTN GI=7273 FC=Missense CP=7619 CF=1 AC=CgT->CaT RP=2540 RC=R Arg ->H His EN=33/312 DS=+25 P=chr2:179390718-179672150 ST=
NM_015040.3	GN=PIKFYVE GI=200576 FC=Missense CP=3793 CF=0 AC=cCT->aCT RP=1265 RC=P Pro ->T Thr EN=23/42 DS=+2 P=chr2:209130991-20922347
NM_017886.2	GN=ULK4 GI=54986 FC=Missense CP=2990 CF=1 AC=AtT->AgT RP=997 RC=I Ile ->S Ser EN=30/37 DS=+12 P=chr3:41288090-42003660 ST=- C =
NM_001024660.3	GN=KALRN GI=8997 FC=Missense CP=880 CF=0 AC=cAC->aAC RP=294 RC=H His ->N Asn EN=5/60 DS=+430 P=chr3:123813558-124440036
NM_032028.3	GN=SSK1B GI=83942 FC=Missense CP=1010 CF=1 AC=AgG->AaG RP=337 RC=R Arg ->K Lys EN=1/11 P=chr5:112768251-112770728 ST=- C =
NM_182925.4	GN=FLT4 GI=2324 FC=Missense CP=1936 CF=0 AC=gAG->aAG RP=646 RC=E Glu ->K Lys EN=13/30 DS=+279 P=chr5:180028506-180076624 ST=
NM_032454.1	GN=STK19 GI=8859 FC=Missense CP=688 CF=0 AC=tGT->cGT RP=230 RC=C Cys ->R Arg EN=5/8 DS=+13 P=chr6:31939646-31949223 ST=+ C =
NM_007271.2	GN=STK38 GI=11329 FC=Missense CP=887 CF=0 AC=gTT->tTT RP=106 RC=V Val ->F Phe EN=5/14 DS=+10 P=chr6:36461669-36515247 ST=- C =
NM_002821.3	GN=PTK7 GI=5754 FC=Missense CP=2229 CF=2 AC=GAg->GAt RP=743 RC=E Glu ->D Asp EN=14/20 DS=+182 P=chr6:43044029-43129457 ST=+
NM_015076.3	GN=CDK19 GI=23097 FC=Missense CP=1290 CF=2 AC=AGc->AGa RP=430 RC=S Ser ->R Arg EN=12/13 DS=+180 P=chr6:110931181-111136412
NM_031414.3	GN=STK31 GI=56164 FC=Missense CP=1453 CF=0 AC=gCC->tCC RP=485 RC=A Ala ->S Ser EN=12/24 DS=+37 P=chr7:23749838-23872127 ST=
NM_002612.3	GN=PDK4 GI=5166 FC=Missense CP=1002 CF=2 AC=TTg->TTt RP=334 RC=L Leu ->F Phe EN=10/11 DS=+21 P=chr7:95212809-9525925 ST=- C =
NM_001244580.1	GN=TRRAP1 GI=8295 FC=Missense CP=356 CF=1 AC=CgC->CcC RP=119 RC=R Arg ->P Pro EN=5/72 DS=+95 P=chr7:98476113-98610866 ST=
NM_001244580.1	GN=TRRAP1 GI=8295 FC=Missense CP=4924 CF=0 AC=gCC->tCC RP=1642 RC=A Ala ->S Ser EN=35/72 DS=-87 P=chr7:98476113-98610866
NM_015905.2	GN=TRIM24 GI=8805 FC=Missense CP=143 CF=1 AC=GcC->GaC RP=48 RC=A Ala ->D Asp EN=1/19 DS=-43599 P=chr7:138145079-138270332 S
NM_001080826.1	GN=SGK223 GI=157285 FC=Missense CP=189 CF=2 AC=AGg->AGt RP=63 RC=R Arg ->S Ser EN=1/5 DS=-3481 P=chr8:8175258-8239257 ST=
NM_139021.2	GN=MAPK15 GI=225689 FC=Intron EN=4:5/14 DS=-40 P=chr8:144798507-144804633 ST=+ C =1635 PD=mitogen-activated protein kinase 15
NM_018425.2	GN=PI4K2A GI=55361 FC=Missense CP=248 CF=1 AC=GcT->GaT RP=83 RC=A Ala ->D Asp EN=1/9 DS=-9951 P=chr10:99400443-99436187 ST=
NM_015191.1	GN=SIK2 GI=23235 FC=Missense CP=2240 CF=1 AC=CcA->CaA RP=747 RC=P Pro ->Q Gln EN=15/15 DS=+93 P=chr11:111473170-111597632 S
NM_001184985.1	GN=WNK1 GI=65125 FC=Missense CP=7267 CF=0 AC=cCC->tCC RP=2423 RC=P Pro ->S Ser EN=26/28 DS=+39 P=chr12:862089-1020618 ST=
NM_003749.2	GN=IRS2 GI=8660 FC=Missense CP=3733 CF=0 AC=gCC->tCC RP=1245 RC=A Ala ->S Ser EN=1/2 DS=-26013 P=chr13:110406184-110438914 S
NM_003749.2	GN=IRS2 GI=8660 FC=Missense CP=599 CF=1 AC=GtG->GgG RP=200 RC=V Val ->G Glv EN=1/2 DS=-29147 P=chr13:110406184-110438914 ST=
NM_006871.3	GN=RIPK3 GI=11035 FC=Missense CP=22 CF=0 AC=cCC->aCC RP=8 RC=P Pro ->T Thr EN=2/10 DS=+2 P=chr14:24805227-24809242 ST=- C =
NM_002005.3	GN=FEI3 GI=2242 FC=Missense CP=1952 CF=1 AC=GaG->GgG RP=651 RC=E Glu ->G Glv EN=16/19 DS=+31 P=chr15:91427688-91439006 ST=+ C =
NM_000875.3	GN=GEI1 GI=3480 FC=Missense CP=199 CF=0 AC=gCC->tCC RP=67 RC=A Ala ->S Ser EN=2/21 DS=+105 P=chr15:99192761-99507759 ST=+ C =
NM_005030.3	GN=PLK1 GI=5347 FC=Missense CP=148 CF=0 AC=cGG->tGG RP=50 RC=R Arg ->W Trp EN=1/10 DS=-1004 P=chr16:23690201-23701688 ST=+
NM_001005271.2	GN=CHD3 GI=1107 FC=Missense CP=877 CF=0 AC=aTA->cTA RP=293 RC=L Leu ->L Leu EN=5/40 DS=+191 P=chr17:7788123-7816075 ST=+ C =
NM_001005271.2	GN=CHD3 GI=1107 FC=Missense CP=886 CF=0 AC=tCC->cCC RP=296 RC=S Ser ->P Pro EN=5/40 DS=+200 P=chr17:7788123-7816075 ST=
NM_001005271.2	GN=CHD3 GI=1107 FC=Missense CP=898 CF=0 AC=gCC->cCC RP=300 RC=A Ala ->P Pro EN=5/40 DS=+212 P=chr17:7788123-7816075 ST=
NM_001142633.2	GN=PIK3R5 GI=23533 FC=Nonsense CP=2017 CF=0 AC=cAA->tAA RP=673 RC=Q Gln ->Stop EN=13/19 DS=+112 P=chr17:8782233-8869029 S
NM_004448.2	GN=RB2 GI=2064 FC=Missense CP=2584 CF=0 AC=aCA->gCA RP=862 RC=T Thr ->A Ala EN=21/27 DS=+91 P=chr17:37856254-37884915 ST=
NM_007300.3	GN=BRCA1 GI=672 FC=Missense CP=1855 CF=0 AC=cAT->aAT RP=619 RC=H His ->N Asn EN=10/24 DS=+1185 P=chr17:41196312-41277500 ST=
NM_020854.3	GN=KIAA1468 GI=57614 FC=Missense CP=250 CF=0 AC=gGC->tGC RP=84 RC=G Glv ->C Cys EN=1/29 DS=-23398 P=chr18:59854524-59974355 S
NM_020854.3	GN=KIAA1468 GI=57614 FC=Missense CP=1735 CF=0 AC=cAA->aAA RP=579 RC=Q Gln ->K Lys EN=12/29 DS=+2 P=chr18:59854524-59974355 S
NM_199054.2	GN=MKNK2 GI=2872 FC=Missense CP=208 CF=0 AC=cGG->tGG RP=70 RC=R Arg ->W Trp EN=4/14 DS=+69 P=chr19:2037470-2051243 ST=- C =
NM_000215.3	GN=JAK3 GI=3718 FC=Missense CP=1503 CF=2 AC=CAg->CAT RP=501 RC=Q Gln ->H His EN=11/24 DS=+62 P=chr19:17935593-17958841 ST=-
NM_016457.4	GN=PRKD2 GI=25865 FC=Missense CP=1733 CF=1 AC=GcA->GaA RP=578 RC=A Ala ->E Glu EN=13/18 DS=+31 P=chr19:47177573-47220384 ST=
NM_001101401.2	GN=SBK2 GI=646643 FC=Missense CP=118 CF=0 AC=cGC->aGC RP=40 RC=R Arg ->S Ser EN=2/4 DS=+118 P=chr19:56041100-56048435 ST=

RefSeq Genes Product
<p> cyclin-dependent kinase 11B isoform 2. cyclin-dependent kinase 11B isoform 3. cyclin-dependent kinase 11B isoform 4. cyclin-dependent kinase 11B isoform cyclin-dependent kinase 11A isoform 1. cyclin-dependent kinase 11A isoform 4. cyclin-dependent kinase 11B isoform 2. cyclin-dependent kinase 11B isoform tyrosine-protein kinase Fgr ephrin type-A receptor 10 isoform 3 mitogen-activated protein kinase kinase kinase MLK4 ALK tyrosine kinase receptor precursor ALK tyrosine kinase receptor precursor interferon-induced, double-stranded RNA-activated protein kinase isoform a. interferon-induced, double-stranded RNA-activated protein kinase isoform b activin receptor type-2A precursor activin receptor type-1C isoform 1. activin receptor type-1C isoform 3 precursor. activin receptor type-1C isoform 4 precursor titin isoform N2-A. titin isoform novex-2. titin isoform novex-1. titin isoform N2-B titin isoform N2-A. titin isoform novex-2. titin isoform novex-1. titin isoform N2-B. titin isoform novex-3 titin isoform N2-A. titin isoform novex-2. titin isoform novex-1. titin isoform N2-B. titin isoform novex-3 1-phosphatidylinositol-3-phosphate 5-kinase isoform 2 serine/threonine-protein kinase ULK4 kalirin isoform 1. kalirin isoform 2 testis-specific serine/threonine-protein kinase 1. colorectal mutant cancer protein isoform 1 vascular endothelial growth factor receptor 3 isoform 1 precursor. vascular endothelial growth factor receptor 3 isoform 2 precursor serine/threonine-protein kinase 19 isoform 2. serine/threonine-protein kinase 19 isoform 1 serine/threonine-protein kinase 38 inactive tyrosine-protein kinase 7 isoform a precursor. inactive tyrosine-protein kinase 7 isoform b precursor. inactive tyrosine-protein kinase 7 isoform d prec cyclin-dependent kinase 19 serine/threonine-protein kinase 31 isoform a. serine/threonine-protein kinase 31 isoform b pyruvate dehydrogenase kinase. isozyme 4 transformation/transcription domain-associated protein isoform 1. transformation/transcription domain-associated protein isoform 2 transformation/transcription domain-associated protein isoform 1. transformation/transcription domain-associated protein isoform 2 transcription intermediary factor 1-alpha isoform a. transcription intermediary factor 1-alpha isoform b tyrosine-protein kinase Sgk223 mitogen-activated protein kinase 15 phosphatidylinositol 4-kinase type 2-alpha serine/threonine-protein kinase SIK2 serine/threonine-protein kinase WNK1 isoform 4. serine/threonine-protein kinase WNK1 isoform 3. serine/threonine-protein kinase WNK1 isoform 1. serine/th insulin receptor substrate 2 insulin receptor substrate 2 receptor-interacting serine/threonine-protein kinase 3 tyrosine-protein kinase Fes/Fps isoform 1. tyrosine-protein kinase Fes/Fps isoform 2. tyrosine-protein kinase Fes/Fps isoform 3. tyrosine-protein kinase Fes insulin-like growth factor 1 receptor precursor serine/threonine-protein kinase PLK1 chromodomain-helicase-DNA-binding protein 3 isoform 3. chromodomain-helicase-DNA-binding protein 3 isoform 1. chromodomain-helicase-DNA-binding pro chromodomain-helicase-DNA-binding protein 3 isoform 3. chromodomain-helicase-DNA-binding protein 3 isoform 1. chromodomain-helicase-DNA-binding pro chromodomain-helicase-DNA-binding protein 3 isoform 3. chromodomain-helicase-DNA-binding protein 3 isoform 1. chromodomain-helicase-DNA-binding pro phosphoinositide 3-kinase regulatory subunit 5 isoform 1. phosphoinositide 3-kinase regulatory subunit 5 isoform 2 receptor tyrosine-protein kinase erbB-2 isoform a precursor. receptor tyrosine-protein kinase erbB-2 isoform b breast cancer type 1 susceptibility protein isoform 2. breast cancer type 1 susceptibility protein isoform 1. breast cancer type 1 susceptibility protein isoform 3 lisH domain and HEAT repeat-containing protein KIAA1468. GPI ethanolamine phosphate transferase 1 lisH domain and HEAT repeat-containing protein KIAA1468 MAP kinase-interacting serine/threonine-protein kinase 2 isoform 2. MAP kinase-interacting serine/threonine-protein kinase 2 isoform 1 tyrosine-protein kinase JAK3 serine/threonine-protein kinase D2 isoform A. serine/threonine-protein kinase D2 isoform B serine/threonine-protein kinase SBK2 </p>

Gencode													
ENST00000407249.3	GN=CDK11A	GI=ENSG000000008128.14	FC=Missense	CP=1183	CF=0	AC=gAC->aAC	IRP=395	RC=D	Asp->N	Asn	LEN=12/21	DS=+99	P=chr
ENST00000378633.1	GN=CDK11A	GI=ENSG000000008128.14	FC=Missense	CP=1177	CF=0	AC=gAC->aAC	IRP=393	RC=D	Asp->N	Asn	LEN=11/20	DS=+99	P=chr
ENST00000374005.3	GN=FRG1	GI=ENSG00000000938.7	FC=Missense	CP=823	CF=0	AC=gGC->cG	IRP=275	RC=G	Glv->R	Arg	LEN=8/13	DS=-91	P=chr1:27938
ENST00000427468.2	GN=PHA10	GI=ENSG00000018331.7	FC=Missense	CP=3008	CF=1	AC=GgC->GtC	IRP=1003	RC=G	Glv->V	Val	LEN=17/20	DS=+96	P=chr
ENST00000366624.3	GN=RP5-862P8.2	GI=ENSG00000014367.4	FC=Missense	CP=1349	CF=1	AC=GcT->GaT	IRP=450	RC=A	Ala->D	Asp	LEN=5/10	DS=+38	P=chr
ENST00000389048.3	GN=ALK1	GI=ENSG000000171094.11	FC=Missense	CP=4318	CF=0	AC=gCC->tCC	IRP=1440	RC=A	Ala->S	Ser	LEN=29/29	DS=+154	P=chr2:29
ENST00000389048.3	GN=ALK1	GI=ENSG000000171094.11	FC=Missense	CP=3089	CF=1	AC=CaC->CcC	IRP=1030	RC=H	His->P	Pro	LEN=19/29	DS=+22	P=chr2:29
ENST00000233057.4	GN=EIF2AK2	GI=ENSG000000055332.10	FC=Missense	CP=1397	CF=1	AC=GgA->GaA	IRP=466	RC=G	Glv->F	Glu	LEN=15/17	DS=+20	P=chr2
ENST00000241416.7	GN=ACVR2A	GI=ENSG000000121989.10	FC=Missense	CP=945	CF=2	AC=AAa->AAc	IRP=315	RC=K	Ivs->N	Asn	LEN=7/11	DS=+129	P=chr2
ENST00000243349.7	GN=ACVR1C	GI=ENSG000000123612.10	FC=Missense	CP=58	CF=0	AC=gCC->tCC	IRP=20	RC=A	Ala->S	Ser	LEN=1/9	DS=-41	P=chr2:1
ENST00000342992.6	GN=TTN1	GI=ENSG000000155657.16	FC=Missense	CP=88910	CF=1	AC=GtG->GcG	IRP=29637	RC=V	Val->A	Ala	LEN=296/312	DS=+304	P=chr
ENST00000342992.6	GN=TTN1	GI=ENSG000000155657.16	FC=Missense	CP=8887	CF=0	AC=aCC->cCC	IRP=2963	RC=T	Thr->P	Pro	LEN=37/312	DS=+246	P=chr2
ENST00000342992.6	GN=TTN1	GI=ENSG000000155657.16	FC=Missense	CP=7619	CF=1	AC=CgT->CaT	IRP=2540	RC=R	Arg->H	His	LEN=33/312	DS=+25	P=chr2:1
ENST00000264380.4	GN=PIKFYV	GI=ENSG000000115020.11	FC=Missense	CP=3793	CF=0	AC=cCT->aCT	IRP=1265	RC=P	Pro->T	Thr	LEN=23/42	DS=+2	P=chr2
ENST00000301831.4	GN=ULK4	GI=ENSG000000168038.6	FC=Missense	CP=2990	CF=1	AC=AtT->AgT	IRP=997	RC=I	Ile->S	Ser	LEN=30/37	DS=+12	P=chr3:41288
ENST00000360013.3	GN=KALRN1	GI=ENSG000000160145.10	FC=Missense	CP=880	CF=0	AC=cAC->aAC	IRP=294	RC=H	His->N	Asn	LEN=5/60	DS=+430	P=chr3:1
ENST00000390666.3	GN=TSK1B1	GI=ENSG000000212122.3	FC=Missense	CP=1010	CF=1	AC=AgG->AaG	IRP=337	RC=R	Arg->K	Ivs	LEN=1/11	P=chr5:112768251	
ENST00000261937.6	GN=FLT4	GI=ENSG000000037280.10	FC=Missense	CP=1936	CF=0	AC=gAG->aAG	IRP=646	RC=E	Glu->K	Ivs	LEN=13/30	DS=+279	P=chr5:1
ENST00000375333.2	GN=STK19	GI=ENSG000000204344.9	FC=Missense	CP=688	CF=0	AC=gGT->cGT	IRP=230	RC=C	Cys->R	Arg	LEN=5/8	DS=+13	P=chr6:31939
ENST00000229812.7	GN=STK38	GI=ENSG000000112079.8	FC=Missense	CP=316	CF=0	AC=gTT->tTT	IRP=106	RC=V	Val->F	Phe	LEN=5/14	DS=+10	P=chr6:36461
ENST00000481273.1	GN=PTK7	GI=ENSG000000112655.10	FC=Missense	CP=2253	CF=2	AC=GAg->GAt	IRP=751	RC=E	Glu->D	Asp	LEN=14/20	DS=+182	P=chr6:4
ENST00000368911.3	GN=CDK19	GI=ENSG000000155111.9	FC=Missense	CP=1290	CF=2	AC=AGc->AGa	IRP=430	RC=S	Ser->R	Arg	LEN=12/13	DS=+180	P=chr6:1
ENST00000355870.3	GN=STK31	GI=ENSG000000196335.8	FC=Missense	CP=1453	CF=0	AC=gCC->tCC	IRP=485	RC=A	Ala->S	Ser	LEN=12/24	DS=+37	P=chr7:23
ENST00000005178.5	GN=PDK4	GI=ENSG00000004799.6	FC=Missense	CP=1002	CF=2	AC=TTg->TTl	IRP=334	RC=L	Ile->F	Phe	LEN=10/11	DS=+21	P=chr7:952
ENST00000359863.4	GN=TRRAP1	GI=ENSG000000196367.7	FC=Missense	CP=356	CF=1	AC=CgC->CcC	IRP=119	RC=R	Arg->P	Pro	LEN=5/72	DS=+95	P=chr7:984
ENST00000359863.4	GN=TRRAP1	GI=ENSG000000196367.7	FC=Missense	CP=4924	CF=0	AC=gCC->tCC	IRP=1642	RC=A	Ala->S	Ser	LEN=35/72	DS=-87	P=chr7:9
ENST00000343526.4	GN=TRIM24	GI=ENSG000000122779.10	FC=Missense	CP=143	CF=1	AC=GcC->GaC	IRP=48	RC=A	Ala->D	Asp	LEN=1/19	DS=-43599	P=chr7
ENST00000520004.1	GN=AC068353.1	GI=ENSG000000182319.5	FC=Missense	CP=189	CF=2	AC=AGg->AGt	IRP=63	RC=R	Arg->S	Ser	LEN=2/6	DS=+12	P=chr8:8
ENST00000395107.4	GN=MAPK15	GI=ENSG000000181085.10	FC=Missense	CP=298	CF=0	AC=aGC->cGC	IRP=100	RC=S	Ser->R	Arg	LEN=5/8	DS=+18	P=chr8:14
ENST00000370631.3	GN=PI4K2A	GI=ENSG000000155252.10	FC=Missense	CP=248	CF=1	AC=GcT->GaT	IRP=83	RC=A	Ala->D	Asp	LEN=1/9	DS=-995	P=chr10:9
ENST00000304987.3	GN=SIK2	GI=ENSG000000170145.4	FC=Missense	CP=2240	CF=1	AC=CcA->CaA	IRP=747	RC=P	Pro->Q	Gln	LEN=15/15	DS=+93	P=chr11:11
ENST00000530271.2	GN=WNK1	GI=ENSG000000060237.10	FC=Missense	CP=7981	CF=0	AC=cCC->tCC	IRP=2661	RC=P	Pro->S	Ser	LEN=28/30	DS=+39	P=chr12
ENST00000375856.3	GN=IRS2	GI=ENSG000000185950.7	FC=Missense	CP=3733	CF=0	AC=gCC->tCC	IRP=1245	RC=A	Ala->S	Ser	LEN=1/2	DS=-260	P=chr13:1
ENST00000375856.3	GN=IRS2	GI=ENSG000000185950.7	FC=Missense	CP=599	CF=1	AC=GtG->GgG	IRP=200	RC=V	Val->G	Glv	LEN=1/2	DS=-29147	P=chr13:110
ENST00000216274.4	GN=RIPK3	GI=ENSG000000129465.10	FC=Missense	CP=22	CF=0	AC=cCC->aCC	IRP=8	RC=P	Pro->T	Thr	LEN=2/10	DS=+2	P=chr14:248052
ENST00000328850.3	GN=FEI3	GI=ENSG000000182511.6	FC=Missense	CP=1952	CF=1	AC=GAg->GgG	IRP=651	RC=E	Glu->G	Glv	LEN=16/19	DS=+3	P=chr15:914
ENST00000268035.6	GN=IGF1R1	GI=ENSG000000140443.8	FC=Missense	CP=199	CF=0	AC=gCC->tCC	IRP=67	RC=A	Ala->S	Ser	LEN=2/21	DS=+105	P=chr15:9919
ENST00000300093.4	GN=PLK1	GI=ENSG000000166851.7	FC=Missense	CP=148	CF=0	AC=cGG->tGG	IRP=50	RC=R	Arg->W	Tro	LEN=1/10	DS=-1004	P=chr16:236
ENST00000380358.4	GN=CHD3	GI=ENSG000000170004.10	FC=Missense	CP=877	CF=0	AC=aTA->cTA	IRP=293	RC=L	Ile->L	Ileu	LEN=5/40	DS=+191	P=chr17:778
ENST00000380358.4	GN=CHD3	GI=ENSG000000170004.10	FC=Missense	CP=886	CF=0	AC=tCC->cCC	IRP=296	RC=S	Ser->P	Pro	LEN=5/40	DS=+200	P=chr17:77
ENST00000380358.4	GN=CHD3	GI=ENSG000000170004.10	FC=Missense	CP=898	CF=0	AC=gCC->cCC	IRP=300	RC=A	Ala->P	Pro	LEN=5/40	DS=+212	P=chr17:77
ENST00000447110.1	GN=PIK3R5	GI=ENSG000000141506.8	FC=Nonsense	CP=2017	CF=0	AC=cAA->tAA	IRP=673	RC=Q	Gln->Stop		LEN=13/19	DS=+112	P=chr17:8
ENST00000269571.3	GN=ERBB2	GI=ENSG000000141736.7	FC=Missense	CP=2584	CF=0	AC=aCA->gCA	IRP=862	RC=T	Thr->A	Ala	LEN=21/27	DS=+91	P=chr17:3
ENST00000471181.1	GN=BRCA1	GI=ENSG00000012048.12	FC=Missense	CP=1855	CF=0	AC=cAT->aAT	IRP=619	RC=H	His->N	Asn	LEN=10/24	DS=+1185	P=chr
ENST00000256858.5	GN=KIAA1468	GI=ENSG000000134444.8	FC=Missense	CP=250	CF=0	AC=gGC->tGC	IRP=84	RC=G	Glv->C	Cys	LEN=1/30	DS=-23398	P=chr
ENST00000256858.5	GN=KIAA1468	GI=ENSG000000134444.8	FC=Missense	CP=1735	CF=0	AC=cAA->aAA	IRP=579	RC=Q	Gln->K	Ivs	LEN=12/30	DS=+2	P=chr18
ENST00000250896.3	GN=MKNK2	GI=ENSG000000099875.8	FC=Missense	CP=208	CF=0	AC=cGG->tGG	IRP=70	RC=R	Arg->W	Tro	LEN=4/14	DS=+69	P=chr19:203
ENST00000458235.1	GN=JAK3	GI=ENSG000000105639.13	FC=Missense	CP=1503	CF=2	AC=CAg->CAt	IRP=501	RC=Q	Gln->H	His	LEN=11/24	DS=+62	P=chr19:1
ENST00000291281.3	GN=PRKD2	GI=ENSG000000105287.6	FC=Missense	CP=1733	CF=1	AC=GcA->GaA	IRP=578	RC=A	Ala->F	Glu	LEN=13/18	DS=+31	P=chr19:4
ENST00000413299.1	GN=SBK2	GI=ENSG000000187550.4	FC=Missense	CP=118	CF=0	AC=cGC->aGC	IRP=40	RC=R	Arg->S	Ser	LEN=2/4	DS=+120	P=chr19:5604

Gencode Pseudogenes

ENST00000513088.1|GN=AL691432.2|G=ENSG00000248333.1|P=chr1:1571126-1588935|ST=-|LV=2|GT=pseudogene|TT=unprocessed pseudogene

[illegible]

[illegible]

Primate Conserved Elements	Placental Mammal Conserved Elements	Vertebrate Conserved Elements
P=chr1:1638837-1639025 od=28 SC=322	P=chr1:1575696-1575715 od=24 SC=309	P=chr1:1575696-1575721 od=75 SC=431
P=chr1:27941950-27942352 od=85 SC=487	P=chr1:1638906-1638949 od=22 SC=300	P=chr1:1638906-1638949 od=68 SC=420
P=chr1:38184043-38184103 od=18 SC=257	P=chr1:27942192-27942242 od=116 SC=491	P=chr1:27942192-27942245 od=269 SC=567
P=chr1:233497797-233498044 od=47 SC=399	P=chr1:38184043-38184103 od=89 SC=460	P=chr1:38184043-38184082 od=192 SC=531
	P=chr1:233497835-233497851 od=38 SC=362	P=chr1:233497835-233497851 od=98 SC=459
P=chr2:37336370-37336461 od=20 SC=272	P=chr2:29448398-29448417 od=27 SC=323	P=chr2:29448398-29448411 od=64 SC=414
P=chr2:148676011-148676167 od=61 SC=438	P=chr2:37336392-37336423 od=52 SC=398	P=chr2:37336392-37336423 od=71 SC=425
P=chr2:158485079-158485388 od=39 SC=372	P=chr2:148676009-148676166 od=362 SC=621	P=chr2:148676098-148676146 od=255 SC=561
P=chr2:179407775-179408409 od=207 SC=619	P=chr2:158485081-158485102 od=31 SC=339	P=chr2:158485081-158485102 od=44 SC=374
P=chr2:179634400-179634668 od=83 SC=484	P=chr2:179408044-179408129 od=167 SC=532	P=chr2:179408050-179408089 od=178 SC=523
P=chr2:179637834-179638112 od=63 SC=443	P=chr2:179634400-179634553 od=405 SC=634	P=chr2:179634400-179634424 od=165 SC=515
P=chr2:209195220-209195425 od=76 SC=470		P=chr2:179638051-179638102 od=267 SC=566
	P=chr2:209195235-209195425 od=490 SC=656	P=chr2:209195235-209195421 od=1204 SC=727
	P=chr3:41705176-41705193 od=34 SC=350	P=chr3:41705176-41705193 od=37 SC=355
P=chr3:123987593-123988111 od=149 SC=570	P=chr3:123987947-123988107 od=456 SC=648	P=chr3:123987956-123988095 od=990 SC=706
P=chr5:180048525-180048836 od=59 SC=433	P=chr5:180048537-180048668 od=185 SC=544	P=chr5:180048550-180048665 od=417 SC=614
P=chr6:31947173-31947365 od=50 SC=408	P=chr6:31947189-31947216 od=49 SC=392	P=chr6:31947189-31947210 od=36 SC=352
P=chr6:36489409-36489628 od=48 SC=402	P=chr6:36489504-36489596 od=290 SC=596	P=chr6:36489507-36489598 od=641 SC=660
P=chr6:43111206-43111366 od=58 SC=430	P=chr6:43111325-43111363 od=104 SC=478	P=chr6:43111325-43111338 od=109 SC=471
P=chr6:110942304-110942420 od=15 SC=230		P=chr6:110942392-110942395 od=20 SC=289
P=chr7:23808601-23808738 od=16 SC=239	P=chr7:23808626-23808661 od=82 SC=451	P=chr7:23808626-23808662 od=87 SC=446
P=chr7:95216318-95216437 od=42 SC=383	P=chr7:95216338-95216420 od=225 SC=567	P=chr7:95216338-95216437 od=555 SC=645
P=chr7:98489988-98490155 od=53 SC=417	P=chr7:98490044-98490155 od=296 SC=598	P=chr7:98490116-98490154 od=266 SC=566
P=chr7:98547157-98547208 od=15 SC=230	P=chr7:98547157-98547207 od=142 SC=514	P=chr7:98547157-98547207 od=334 SC=590
P=chr7:138145369-138145663 od=45 SC=393	P=chr7:138145369-138145583 od=211 SC=559	P=chr7:138145352-138145575 od=506 SC=635
P=chr8:8238819-8239264 od=70 SC=458	P=chr8:8239067-8239119 od=54 SC=403	P=chr8:8239067-8239104 od=79 SC=436
P=chr10:99400432-99400819 od=50 SC=408	P=chr10:99400457-99400832 od=564 SC=672	P=chr10:99400467-99400822 od=1063 SC=714
P=chr11:111594211-111594331 od=34 SC=351	P=chr11:111594269-111594343 od=140 SC=512	
P=chr12:1009603-1009912 od=101 SC=513	P=chr12:1009639-1009707 od=146 SC=517	P=chr12:1009639-1009708 od=312 SC=583
P=chr13:110434622-110434686 od=17 SC=248		
P=chr13:110437022-110438338 od=283 SC=665	P=chr13:110437466-110437894 od=605 SC=680	P=chr13:110437613-110437827 od=970 SC=704
P=chr15:91436518-91436649 od=27 SC=317	P=chr15:91436550-91436554 od=18 SC=276	P=chr15:91436550-91436554 od=39 SC=361
P=chr15:99250772-99251370 od=137 SC=558	P=chr15:99250802-99250974 od=468 SC=651	P=chr15:99250802-99250956 od=963 SC=703
P=chr16:23690362-23690671 od=86 SC=489	P=chr16:23690365-23690666 od=483 SC=654	P=chr16:23690365-23690492 od=475 SC=628
P=chr17:7796480-7796893 od=137 SC=558	P=chr17:7796740-7796813 od=176 SC=538	P=chr17:7796785-7796801 od=49 SC=385
P=chr17:7796480-7796893 od=137 SC=558	P=chr17:7796740-7796813 od=176 SC=538	
P=chr17:7796480-7796893 od=137 SC=558		
	P=chr17:8789792-8789879 od=71 SC=434	P=chr17:8789798-8789823 od=69 SC=422
P=chr17:37881293-37881459 od=37 SC=364	P=chr17:37881332-37881441 od=242 SC=575	P=chr17:37881332-37881393 od=348 SC=595
P=chr17:41245643-41245801 od=24 SC=300		
P=chr18:59854837-59855287 od=94 SC=502		P=chr18:59854985-59854988 od=18 SC=278
P=chr18:59919894-59919993 od=50 SC=408	P=chr18:59919891-59919911 od=43 SC=377	P=chr18:59919889-59919911 od=121 SC=482
P=chr19:2046360-2046459 od=18 SC=257	P=chr19:2046395-2046435 od=57 SC=409	P=chr19:2046392-2046402 od=56 SC=399
P=chr19:47193855-47193966 od=47 SC=399	P=chr19:47193933-47193966 od=73 SC=437	P=chr19:47193933-47193946 od=74 SC=429
	P=chr19:56047522-56047574 od=74 SC=439	P=chr19:56047522-56047574 od=144 SC=500

SIFT Input	PolyPhen-2 Input	Target Region	Filter
1.1575715.1.C/T	chr1:1575715 C/T	On	FilteredOut
1.1638925.1.C/T	chr1:1638925 C/T	On	FilteredOut
1.27942215.1.C/G	chr1:27942215 C/G	On	FilteredOut
1.38184063.1.C/A	chr1:38184063 C/A	On	FilteredOut
1.233497836.1.C/A	chr1:233497836 C/A	On	FilteredOut
2.29416635.1.C/A	chr2:29416635 C/A	On	FilteredOut
2.29448410.1.T/G	chr2:29448410 T/G	On	FilteredOut
2.37336419.1.C/T	chr2:37336419 C/T	On	FilteredOut
2.148676144.1.A/C	chr2:148676144 A/C	On	FilteredOut
2.158485099.1.C/A	chr2:158485099 C/A	On	FilteredOut
2.179408086.1.A/G	chr2:179408086 A/G	On	FilteredOut
2.179634421.1.T/G	chr2:179634421 T/G	Near	FilteredOut
2.179638072.1.C/T	chr2:179638072 C/T	On	Retained
2.209195248.1.C/A	chr2:209195248 C/A	On	FilteredOut
3.41705179.1.A/C	chr3:41705179 A/C	On	FilteredOut
3.123988019.1.C/A	chr3:123988019 C/A	On	FilteredOut
5.112769527.1.C/T	chr5:112769527 C/T	On	FilteredOut
5.180048626.1.C/T	chr5:180048626 C/T	On	FilteredOut
6.31947203.1.T/C	chr6:31947203 T/C	On	FilteredOut
6.36489585.1.C/A	chr6:36489585 C/A	On	FilteredOut
6.43111336.1.G/T	chr6:43111336 G/T	On	FilteredOut
6.110942394.1.G/T	chr6:110942394 G/T	On	FilteredOut
7.23808650.1.G/T	chr7:23808650 G/T	On	FilteredOut
7.95216415.1.C/A	chr7:95216415 C/A	On	FilteredOut
7.98490141.1.G/C	chr7:98490141 G/C	On	FilteredOut
7.98547196.1.G/T	chr7:98547196 G/T	On	FilteredOut
7.138145436.1.C/A	chr7:138145436 C/A	Near	FilteredOut
8.8239069.1.C/A	chr8:8239069 C/A	On	FilteredOut
8.144800905.1.A/C	chr8:144800905 A/C	On	FilteredOut
10.99400747.1.C/A	chr10:99400747 C/A	Near	FilteredOut
11.111594312.1.C/A	chr11:111594312 C/A	On	Retained
12.1009680.1.C/T	chr12:1009680 C/T	On	FilteredOut
13.110434668.1.C/A	chr13:110434668 C/A	Near	FilteredOut
13.110437802.1.A/C	chr13:110437802 A/C	Near	FilteredOut
14.24808802.1.G/T	chr14:24808802 G/T	On	FilteredOut
15.91436551.1.A/G	chr15:91436551 A/G	On	FilteredOut
15.99250895.1.G/T	chr15:99250895 G/T	On	FilteredOut
16.23690401.1.C/T	chr16:23690401 C/T	On	FilteredOut
17.7796794.1.A/C	chr17:7796794 A/C	Near	FilteredOut
17.7796803.1.T/C	chr17:7796803 T/C	Near	Retained
17.7796815.1.G/C	chr17:7796815 G/C	Near	FilteredOut
17.8789811.1.G/A	chr17:8789811 G/A	On	FilteredOut
17.37881392.1.A/G	chr17:37881392 A/G	On	FilteredOut
17.41245693.1.G/T	chr17:41245693 G/T	On	FilteredOut
18.59854988.1.G/T	chr18:59854988 G/T	On	FilteredOut
18.59919898.1.C/A	chr18:59919898 C/A	On	FilteredOut
19.2046399.1.G/A	chr19:2046399 G/A	On	FilteredOut
19.17949138.1.C/A	chr19:17949138 C/A	On	FilteredOut
19.47193933.1.G/T	chr19:47193933 G/T	On	FilteredOut
19.56047544.1.G/T	chr19:56047544 G/T	On	Retained

Detected Information

QUAL=573.31:BaseQRankSum=5.294:Dels=0.00:FS=265.947:HRun=1:HaplotvpeScore=6.0799:MQ=29.71:MQ0=443:QD=0.46:ReadPosRankSum=-8.798:SB=-5.80:cul
 QUAL=67725.38:BaseQRankSum=1.261:Dels=0.00:FS=1.885:HRun=1:HaplotvpeScore=4.9434:MQ=30.58:MQ0=468:QD=22.80:ReadPosRankSum=1.924:SB=-32154.2
 QUAL=31961.02:BaseQRankSum=0.782:Dels=0.00:FS=42.033:HRun=1:HaplotvpeScore=6.5129:MQ=59.92:MQ0=0:QD=12.70:ReadPosRankSum=0.279:SB=-14304.70
 QUAL=2623.94:BaseQRankSum=-19.759:Dels=0.00:FS=729.607:HRun=0:HaplotvpeScore=5.8688:MQ=59.83:MQ0=0:QD=1.06:ReadPosRankSum=6.142:SB=-0.02:cul
 QUAL=524.79:BaseQRankSum=-18.279:Dels=0.00:FS=309.258:HRun=0:HaplotvpeScore=4.9625:MQ=59.83:MQ0=0:QD=0.79:ReadPosRankSum=-0.468:SB=0.02:cul
 QUAL=332.51:BaseQRankSum=-20.745:Dels=0.00:FS=337.780:HRun=1:HaplotvpeScore=5.1619:MQ=59.89:MQ0=0:QD=0.33:ReadPosRankSum=1.660:SB=-9.26:cul
 QUAL=979.74:BaseQRankSum=-17.907:Dels=0.00:FS=1898.288:HRun=2:HaplotvpeScore=4.4822:MQ=59.40:MQ0=0:QD=1.13:ReadPosRankSum=-19.617:SB=4.95:c
 QUAL=3709.37:BaseQRankSum=-12.727:Dels=0.00:FS=2.030:HRun=3:HaplotvpeScore=3.8031:MQ=59.87:MQ0=0:QD=14.84:ReadPosRankSum=-0.449:SB=-1464.96
 QUAL=4287.54:BaseQRankSum=-38.865:Dels=0.00:FS=1530.408:HRun=2:HaplotvpeScore=41.7032:MQ=59.38:MQ0=0:QD=1.48:ReadPosRankSum=-10.239:SB=-0.0
 QUAL=421.85:BaseQRankSum=-25.438:Dels=0.00:FS=707.699:HRun=0:HaplotvpeScore=4.8344:MQ=59.88:MQ0=0:QD=0.39:ReadPosRankSum=4.943:SB=-1.54:cul
 QUAL=3677.47:BaseQRankSum=-1.663:Dels=0.00:FS=4.002:HRun=0:HaplotvpeScore=5.7074:MQ=59.82:MQ0=0:QD=14.71:ReadPosRankSum=-0.900:SB=-1670.15
 QUAL=706.07:BaseQRankSum=-14.922:Dels=0.00:FS=2.107:HRun=3:HaplotvpeScore=4.4521:MQ=59.71:MQ0=0:QD=1.13:ReadPosRankSum=1.953:SB=-0.02:cul
 QUAL=43778.29:BaseQRankSum=21.939:Dels=0.00:FS=4.243:HRun=0:HaplotvpeScore=4.5024:MQ=59.88:MQ0=0:QD=14.59:ReadPosRankSum=0.113:SB=-15680.87
 QUAL=1517.36:BaseQRankSum=-22.562:Dels=0.00:FS=522.570:HRun=0:HaplotvpeScore=5.3091:MQ=59.47:MQ0=0:QD=0.76:ReadPosRankSum=4.049:SB=2.32:cul
 QUAL=3364.89:BaseQRankSum=5.867:Dels=0.00:FS=8.801:HRun=0:HaplotvpeScore=3.7408:MQ=59.92:MQ0=0:QD=14.14:ReadPosRankSum=1.991:SB=-828.14:cul
 QUAL=259.36:BaseQRankSum=-18.377:Dels=0.00:FS=560.007:HRun=1:HaplotvpeScore=3.4076:MQ=59.80:MQ0=0:QD=0.48:ReadPosRankSum=0.921:SB=-9.16:cul
 QUAL=4121.43:BaseQRankSum=3.171:Dels=0.00:FS=5.506:HRun=1:HaplotvpeScore=8.3345:MQ=59.87:MQ0=0:QD=16.49:ReadPosRankSum=-1.713:SB=-1960.66:c
 QUAL=2409.09:BaseQRankSum=3.178:Dels=0.00:FS=1.381:HRun=1:HaplotvpeScore=4.6499:MQ=59.90:MQ0=0:QD=15.64:ReadPosRankSum=0.444:SB=-1156.64:cul
 QUAL=3109.97:BaseQRankSum=-6.300:Dels=0.00:FS=7.552:HRun=2:HaplotvpeScore=5.4507:MQ=58.27:MQ0=0:QD=12.64:ReadPosRankSum=-0.041:SB=-1112.18
 QUAL=3870.21:BaseQRankSum=-20.116:Dels=0.00:FS=1941.557:HRun=2:HaplotvpeScore=33.1896:MQ=59.85:MQ0=0:QD=1.41:ReadPosRankSum=-27.603:SB=2.16
 QUAL=2641.01:BaseQRankSum=-15.961:Dels=0.00:FS=550.825:HRun=0:HaplotvpeScore=2.9503:MQ=59.90:MQ0=0:QD=1.55:ReadPosRankSum=2.210:SB=-0.02:cul
 QUAL=2446.12:BaseQRankSum=-22.611:Dels=0.00:FS=782.038:HRun=0:HaplotvpeScore=5.0001:MQ=59.89:MQ0=0:QD=1.23:ReadPosRankSum=7.995:SB=4.61:cul
 QUAL=3227.04:BaseQRankSum=-9.916:Dels=0.00:FS=7.553:HRun=0:HaplotvpeScore=5.4329:MQ=59.86:MQ0=0:QD=13.06:ReadPosRankSum=-2.052:SB=-1496.81
 QUAL=67.61:BaseQRankSum=-13.302:Dels=0.00:FS=365.410:HRun=2:HaplotvpeScore=13.6931:MQ=59.57:MQ0=1:QD=0.18:ReadPosRankSum=-7.862:SB=-9.10:cul
 QUAL=3633.19:BaseQRankSum=9.265:Dels=0.00:FS=6.118:HRun=1:HaplotvpeScore=4.3811:MQ=59.85:MQ0=0:QD=14.83:ReadPosRankSum=1.320:SB=-896.31:cul
 QUAL=2691.66:BaseQRankSum=-24.019:Dels=0.00:FS=1056.787:HRun=0:HaplotvpeScore=5.1094:MQ=59.81:MQ0=0:QD=0.98:ReadPosRankSum=-0.061:SB=1.78:c
 QUAL=136.48:BaseQRankSum=-9.911:Dels=0.00:FS=94.576:HRun=0:HaplotvpeScore=3.5123:MQ=59.58:MQ0=0:QD=0.50:ReadPosRankSum=2.269:SB=-9.59:cul
 QUAL=1360.21:BaseQRankSum=-22.932:Dels=0.00:FS=1180.475:HRun=0:HaplotvpeScore=4.9479:MQ=59.90:MQ0=0:QD=0.61:ReadPosRankSum=4.587:SB=2.96:cul
 QUAL=42.73:BaseQRankSum=-6.493:Dels=0.01:FS=106.584:HRun=7:HaplotvpeScore=13.4301:MQ=57.81:MQ0=0:QD=0.40:ReadPosRankSum=2.113:SB=-14.83:cul
 QUAL=520.95:BaseQRankSum=-13.560:Dels=0.00:FS=42.685:HRun=0:HaplotvpeScore=1.8147:MQ=59.84:MQ0=0:QD=0.80:ReadPosRankSum=3.026:SB=-0.42:cul
 QUAL=43849.67:BaseQRankSum=-1.625:Dels=0.00:FS=4.006:HRun=2:HaplotvpeScore=6.7764:MQ=59.87:MQ0=0:QD=14.89:ReadPosRankSum=-0.732:SB=-13928.5
 QUAL=435.27:BaseQRankSum=0.964:Dels=0.00:FS=4.690:HRun=0:HaplotvpeScore=7.7385:MQ=59.80:MQ0=0:QD=1.74:ReadPosRankSum=-2.318:SB=-11.17:cul
 QUAL=811.33:BaseQRankSum=-12.398:Dels=0.00:FS=419.375:HRun=1:HaplotvpeScore=1.8012:MQ=59.86:MQ0=0:QD=1.48:ReadPosRankSum=3.689:SB=2.45:cul
 QUAL=41.85:BaseQRankSum=-11.301:Dels=0.00:FS=31.152:HRun=2:HaplotvpeScore=3.0669:MQ=59.70:MQ0=0:QD=1.05:ReadPosRankSum=5.846:SB=-22.01:cul
 QUAL=123.76:BaseQRankSum=-18.862:Dels=0.00:FS=90.892:HRun=0:HaplotvpeScore=6.2487:MQ=59.86:MQ0=0:QD=0.68:ReadPosRankSum=2.859:SB=-18.23:cul
 QUAL=191.39:BaseQRankSum=-11.495:Dels=0.00:FS=202.191:HRun=5:HaplotvpeScore=3.4566:MQ=59.51:MQ0=0:QD=0.92:ReadPosRankSum=-12.001:SB=0.04:cul
 QUAL=514.21:BaseQRankSum=-25.735:Dels=0.00:FS=609.721:HRun=0:HaplotvpeScore=5.4206:MQ=59.78:MQ0=0:QD=0.31:ReadPosRankSum=6.571:SB=-0.50:cul
 QUAL=3664.75:BaseQRankSum=7.793:Dels=0.00:FS=3.463:HRun=0:HaplotvpeScore=4.4405:MQ=59.89:MQ0=0:QD=15.27:ReadPosRankSum=0.388:SB=-1489.82:cul
 QUAL=3021.35:BaseQRankSum=-5.460:Dels=0.00:FS=276.438:HRun=5:HaplotvpeScore=62.1076:MQ=52.43:MQ0=0:QD=1.98:ReadPosRankSum=3.736:SB=-0.02:cul
 QUAL=72.41:BaseQRankSum=-15.750:Dels=0.00:FS=114.046:HRun=3:HaplotvpeScore=84.4069:MQ=52.72:MQ0=0:QD=0.10:ReadPosRankSum=7.617:SB=-8.26:cul
 QUAL=6298.44:BaseQRankSum=-14.632:Dels=0.00:FS=1180.964:HRun=6:HaplotvpeScore=51.6034:MQ=54.51:MQ0=0:QD=3.01:ReadPosRankSum=4.577:SB=-0.02
 QUAL=2382.70:BaseQRankSum=-7.417:Dels=0.00:FS=0.000:HRun=0:HaplotvpeScore=6.5280:MQ=59.88:MQ0=0:QD=13.02:ReadPosRankSum=0.150:SB=-1305.44:c
 QUAL=1151.76:BaseQRankSum=4.379:Dels=0.00:FS=3.137:HRun=0:HaplotvpeScore=7.2119:MQ=59.86:MQ0=0:QD=4.61:ReadPosRankSum=0.374:SB=-617.79:cul
 QUAL=266.51:BaseQRankSum=-26.169:Dels=0.00:FS=1003.928:HRun=1:HaplotvpeScore=4.1925:MQ=59.92:MQ0=0:QD=0.27:ReadPosRankSum=2.767:SB=-10.70:c
 QUAL=41937.14:BaseQRankSum=-18.411:Dels=0.00:FS=4.693:HRun=0:HaplotvpeScore=8.4020:MQ=59.83:MQ0=0:QD=14.63:ReadPosRankSum=-1.305:SB=-16863
 QUAL=2777.74:BaseQRankSum=-22.110:Dels=0.00:FS=840.263:HRun=3:HaplotvpeScore=3.1785:MQ=59.91:MQ0=0:QD=0.93:ReadPosRankSum=6.516:SB=-0.03:cul
 QUAL=68.79:BaseQRankSum=2.086:Dels=0.00:FS=1.190:HRun=0:HaplotvpeScore=3.1083:MQ=59.93:MQ0=0:QD=0.68:ReadPosRankSum=-1.209:SB=-36.49:cul
 QUAL=16311.40:BaseQRankSum=-12.436:Dels=0.00:FS=0.231:HRun=0:HaplotvpeScore=2.3139:MQ=59.93:MQ0=0:QD=13.41:ReadPosRankSum=-1.062:SB=-5280.1
 QUAL=242.23:BaseQRankSum=-21.822:Dels=0.00:FS=577.877:HRun=1:HaplotvpeScore=5.7474:MQ=59.84:MQ0=0:QD=0.42:ReadPosRankSum=5.095:SB=-10.40:cul
 QUAL=40877.54:BaseQRankSum=1.392:Dels=0.00:FS=7.042:HRun=0:HaplotvpeScore=5.3135:MQ=59.90:MQ0=0:QD=14.86:ReadPosRankSum=-0.239:SB=-17555.37

Genotype	Genotype	Genotype	Genotype	Genotype	Genotype	Genotype	Genotype	Genotype	Genotype	Genotype	Genotype	Alleles	Alleles	Alleles
NCC1	CC1	CC1-1	CC1-2	CC1-7	CC1-8	CC1-9	CC1-11	CC1-12	CC1-17	CC1-18	CC1-25	NCC1	CC1	CC1-1
C/C	C/C	C/C	C/T	C/C	C/T	C/T	C/C	C/T	C/C	C/T	C/C	0/0	0/0	0/0
T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	1/1	1/1	1/1
C/G	C/G	C/G	C/G	C/G	C/G	C/G	C/G	C/G	C/G	C/G	C/G	0/1	0/1	0/1
C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	0/1	0/1	0/1
C/A	C/C	C/C	C/A	C/A	C/C	C/C	C/A	C/C	C/C	C/C	C/A	0/1	0/0	0/0
C/A	C/C	C/A	C/C	C/A	C/C	C/C	C/C	C/C	C/C	C/C	C/A	0/1	0/0	0/1
T/G	T/G	T/G	T/G	T/T	T/T	T/G	T/G	T/T	T/T	T/G	T/G	0/1	0/1	0/1
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	0/0	0/0	0/0
A/C	A/C	A/C	A/C	A/C	A/C	A/C	A/C	A/C	A/C	A/C	A/C	0/1	0/1	0/1
C/C	C/A	C/C	C/C	C/A	C/C	C/A	C/C	C/A	C/C	C/C	C/A	0/0	0/1	0/0
A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	0/0	0/0	0/0
T/T	T/G	T/G	T/G	T/G	T/G	T/G	T/G	T/G	T/T	T/G	T/G	0/0	0/1	0/1
C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	C/T	0/1	0/1	0/1
C/A	C/A	C/A	C/C	C/A	C/C	C/A	C/C	C/A	C/A	C/C	C/A	0/1	0/1	0/1
A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/C	0/0	0/0	0/0
C/A	C/A	C/C	C/C	C/A	C/C	C/C	C/C	C/C	C/C	C/C	C/A	0/1	0/1	0/0
C/C	C/C	C/C	C/C	C/C	C/T	C/C	C/C	C/C	C/C	C/C	C/C	0/0	0/0	0/0
C/C	C/C	C/T	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	0/0	0/0	0/1
T/T	T/T	T/T	T/C	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	0/0	0/0	0/0
C/A	C/A	C/C	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	0/1	0/1	0/0
G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	0/1	0/1	0/1
G/T	G/T	G/T	G/G	G/T	G/T	G/G	G/T	G/T	G/T	G/T	G/G	0/1	0/1	0/1
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/T	G/G	G/G	G/G	G/G	0/0	0/0	0/0
C/C	C/C	C/A	C/A	C/A	C/C	C/A	C/C	C/C	C/C	C/C	C/C	0/0	0/0	0/1
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/C	G/G	G/G	G/G	0/0	0/0	0/0
G/T	G/G	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	0/1	0/0	0/1
C/C	C/A	C/A	C/C	C/A	C/C	C/C	C/A	C/C	C/C	C/C	C/A	0/0	0/1	0/1
C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/C	0/1	0/1	0/1
A/A	A/C	A/A	A/C	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/C	0/0	0/1	0/0
C/C	C/A	C/A	C/A	C/A	C/C	C/C	C/C	C/C	C/A	C/A	C/A	0/0	0/1	0/1
C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	0/1	0/1	0/1
C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C	C/C	C/C	C/C	C/C	0/0	0/0	0/0
C/A	C/A	C/A	C/A	C/A	C/A	C/C	C/A	C/A	C/A	C/A	C/A	0/1	0/1	0/1
A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/C	A/A	0/0	0/0	0/0
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/T	G/G	G/G	G/G	G/G	0/0	0/0	0/0
A/A	A/A	A/G	A/A	A/A	A/G	A/A	A/G	A/A	A/G	A/G	A/A	0/0	0/0	0/1
G/T	G/G	G/T	G/G	G/T	G/G	G/T	G/G	G/T	G/T	G/T	G/G	0/1	0/0	0/1
C/C	C/C	C/C	C/T	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	0/0	0/0	0/0
A/C	A/C	A/C	A/C	A/C	A/C	A/C	A/C	A/C	A/C	A/C	A/C	0/1	0/1	0/1
T/C	T/T	T/T	T/C	T/T	T/C	T/C	T/C	T/T	T/T	T/T	T/T	0/1	0/0	0/0
G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	G/C	0/1	0/1	0/1
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/A	0/0	0/0	0/0
A/A	A/G	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	0/0	0/1	0/0
G/G	G/T	G/T	G/G	G/T	G/G	G/T	G/G	G/G	G/G	G/G	G/G	0/0	0/1	0/1
G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	0/1	0/1	0/1
C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	0/1	0/1	0/1
G/G	G/A	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	0/0	0/1	0/0
C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	0/1	0/1	0/1
G/G	G/T	G/T	G/G	G/T	G/G	G/G	G/G	G/G	G/G	G/G	G/G	0/0	0/1	0/1
G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	0/1	0/1	0/1

Alleles	Alleles	Alleles	Alleles	Alleles	Alleles	Alleles	Alleles	Alleles	Depth	Depth	Depth	Depth	Depth	Depth	Depth	Depth	Depth
CC1-2	CC1-7	CC1-8	CC1-9	CC1-11	CC1-12	CC1-17	CC1-18	CC1-25	NCC1	CC1	CC1-1	CC1-2	CC1-7	CC1-8	CC1-9	CC1-11	CC1-12
011	010	011	011	010	011	010	011	010	250	250	250	250	250	250	250	250	250
111	111	111	111	111	111	111	111	111	238	250	250	243	247	250	248	248	247
011	011	011	011	011	011	011	011	011	250	176	165	228	208	236	234	173	203
011	011	011	011	011	011	011	011	011	225	184	163	210	209	222	244	204	205
011	011	010	010	011	010	010	010	011	144	125	111	150	139	142	121	124	146
010	011	010	010	010	010	010	010	011	250	250	245	246	249	250	245	248	250
011	010	010	011	011	010	010	011	011	127	98	95	99	102	100	117	102	101
010	010	010	010	010	010	010	010	011	250	246	232	250	250	250	250	248	250
011	011	011	011	011	011	011	011	011	242	247	235	248	246	246	238	227	237
010	011	010	011	010	011	010	010	011	248	183	188	244	246	232	232	159	239
010	010	010	011	010	010	010	010	010	250	240	240	248	250	250	250	248	242
011	011	011	011	011	011	011	011	011	69	61	49	70	59	72	80	49	76
011	011	011	011	011	011	011	011	011	250	250	250	250	250	250	250	250	250
010	011	010	011	010	011	011	010	011	250	250	249	250	250	250	250	250	248
010	010	010	010	010	010	010	010	010	246	249	249	239	246	248	233	241	239
010	011	010	010	010	010	010	010	010	165	129	117	122	135	123	123	112	120
010	010	011	010	010	010	010	010	010	250	239	243	248	245	250	250	237	250
010	010	010	010	010	010	010	010	010	217	150	154	190	184	180	201	131	176
011	010	010	010	010	010	010	010	010	249	239	250	246	250	250	242	250	250
011	011	011	011	011	011	011	011	011	250	249	250	250	244	250	250	250	248
011	011	011	011	011	011	011	011	011	160	107	101	151	128	156	150	113	173
010	011	011	010	011	011	011	011	010	215	214	228	207	204	237	211	179	235
010	010	010	010	011	010	010	010	010	250	248	250	250	245	246	245	247	250
011	011	010	010	011	010	010	010	010	86	73	83	88	93	87	108	89	113
010	010	010	010	010	011	010	010	010	233	242	243	250	247	242	247	248	245
011	011	011	011	011	011	011	011	011	250	250	250	250	250	250	250	250	250
010	011	010	010	011	010	010	010	010	69	61	51	52	72	67	58	46	66
011	011	011	011	011	011	011	011	011	236	175	204	214	240	250	246	205	218
011	010	010	010	010	010	010	010	011	56	22	27	57	54	49	43	40	46
011	011	010	010	010	010	011	011	011	117	75	87	119	85	106	114	64	99
011	011	011	011	011	011	011	011	011	250	250	241	250	248	229	243	250	250
010	010	011	010	010	010	010	010	010	250	250	250	250	249	250	245	250	250
011	011	011	010	011	011	011	011	011	54	73	47	37	55	55	59	34	42
010	010	010	010	010	010	010	011	010	55	45	25	37	38	43	41	29	51
010	010	010	010	011	010	010	010	010	216	172	194	183	219	228	217	182	226
010	010	011	010	011	010	011	011	010	54	38	39	50	49	55	40	26	51
010	011	010	011	010	011	011	011	010	247	244	246	240	236	242	244	248	239
011	010	010	010	010	010	010	010	010	247	177	188	240	198	244	241	176	221
011	011	011	011	011	011	011	011	011	157	101	96	110	115	127	133	125	156
011	010	011	011	011	010	010	010	010	176	108	108	127	119	144	149	124	166
011	011	011	011	011	011	011	011	011	219	135	144	175	154	175	196	153	189
010	010	010	010	010	010	010	010	011	247	172	182	208	210	198	189	175	244
010	010	010	010	010	010	010	010	010	250	250	241	249	250	250	250	250	250
010	011	010	011	010	010	010	010	010	250	250	250	249	250	249	250	249	250
011	011	011	011	011	011	011	011	011	249	246	234	243	238	249	250	210	247
011	011	011	011	011	011	011	011	011	250	250	247	250	250	250	250	250	250
010	010	010	010	010	010	010	010	010	137	101	79	131	102	103	103	84	106
011	011	011	011	011	011	011	011	011	105	77	82	112	92	100	123	88	117
010	011	010	010	010	010	010	010	010	220	206	163	223	201	223	205	232	221
011	011	011	011	011	011	011	011	011	236	201	204	244	233	228	230	234	236

Depth	Depth	Depth	AllelicDepth	AllelicDepth	AllelicDepth	AllelicDepth	AllelicDepth	AllelicDepth	AllelicDepth	AllelicDepth	AllelicDepth	AllelicDepth
CC1-17	CC1-18	CC1-25	NCC1	CC1	CC1-1	CC1-2	CC1-7	CC1-8	CC1-9	CC1-11	CC1-12	CC1-17
250	250	250	193 56	193 55	189 61	198 50	189 61	182 67	190 60	200 50	192 58	208 42
250	250	250	22 216	16 234	17 233	24 219	21 226	31 218	17 230	19 229	21 226	22 228
216	248	180	145 105	103 73	90 75	135 93	108 100	137 98	121 113	91 81	95 108	118 97
200	222	180	168 57	136 48	121 42	163 47	166 43	169 52	191 53	160 44	155 49	148 52
125	146	106	113 31	101 24	94 17	117 33	111 27	119 23	105 16	101 21	120 23	102 20
243	250	249	212 37	223 27	213 32	223 23	201 48	220 30	211 33	216 31	225 24	213 30
90	144	86	96 31	73 25	72 23	81 18	89 13	90 10	93 24	82 20	83 18	74 16
250	250	250	250 0	246 0	232 0	250 0	250 0	250 0	250 0	248 0	250 0	250 0
239	248	245	137 103	160 87	149 81	137 111	149 96	135 110	148 90	139 85	150 86	135 101
220	245	188	191 57	144 39	150 38	203 41	191 55	180 52	183 49	131 28	195 44	188 32
250	250	244	249 0	240 0	240 0	248 0	248 1	250 0	129 121	248 0	242 0	250 0
55	61	49	36 32	37 24	32 17	34 36	33 25	39 32	44 36	28 21	42 32	32 23
250	250	250	118 132	148 102	130 119	145 105	134 116	130 119	126 124	138 112	142 108	132 118
250	247	250	194 56	204 46	197 52	214 36	193 57	218 32	202 48	217 33	194 54	197 53
241	245	238	246 0	247 2	249 0	238 1	246 0	248 0	233 0	241 0	238 1	241 0
144	156	108	140 25	97 32	103 14	101 21	110 25	106 16	108 15	97 15	102 18	118 26
250	250	249	250 0	239 0	243 0	248 0	245 0	120 129	250 0	236 0	250 0	250 0
221	207	180	216 0	150 0	75 79	189 0	184 0	180 0	200 1	131 0	176 0	221 0
250	250	250	249 0	238 0	250 0	132 114	250 0	250 0	242 0	248 0	248 0	250 0
250	249	249	189 61	203 46	199 51	186 63	190 54	195 55	189 61	189 61	198 49	182 68
152	171	146	103 57	69 38	68 33	114 37	90 38	116 40	120 30	87 26	138 35	120 32
237	246	193	162 53	159 55	171 57	172 35	140 64	196 41	182 29	136 43	181 54	179 58
250	250	247	250 0	248 0	250 0	250 0	245 0	246 0	245 0	135 111	249 0	250 0
99	130	90	73 13	66 7	71 12	75 13	74 19	80 7	91 17	80 9	99 14	87 10
241	249	241	233 0	240 1	243 0	250 0	245 0	242 0	247 0	248 0	132 113	240 1
250	250	250	202 47	200 50	187 63	181 69	189 60	195 55	190 59	191 59	189 61	198 50
43	66	45	56 13	41 20	36 12	43 8	55 17	52 14	49 8	34 11	47 17	36 7
236	250	217	183 53	136 39	156 46	177 36	194 45	206 44	211 35	165 39	181 37	191 44
47	40	29	44 12	18 4	25 2	39 18	49 5	43 4	38 5	36 4	39 7	40 7
96	99	91	84 33	56 19	67 20	96 23	64 21	86 20	92 22	59 5	81 18	63 33
233	250	250	131 119	126 124	117 124	125 125	130 117	124 105	121 122	128 122	125 125	124 109
250	250	250	249 0	246 2	250 0	250 0	249 0	220 30	244 0	249 0	250 0	249 1
44	65	42	42 12	51 22	32 15	25 12	42 13	39 16	46 13	27 7	28 13	31 13
40	40	35	42 13	32 12	18 7	26 11	27 11	33 9	29 12	24 4	43 8	27 13
212	202	204	185 31	148 24	162 31	167 16	200 19	206 22	186 30	148 34	204 22	189 23
43	45	36	47 7	33 5	29 10	42 8	44 5	43 12	33 7	19 7	46 5	33 10
228	244	246	188 59	187 57	188 58	203 37	185 51	194 46	197 47	211 36	199 39	197 31
226	249	174	247 0	177 0	188 0	119 121	198 0	244 0	241 0	176 0	221 0	224 0
142	143	116	113 44	76 25	68 28	75 35	80 35	91 36	94 39	85 40	122 34	103 39
161	151	128	125 50	74 32	71 36	92 35	89 30	108 36	110 38	93 31	122 43	117 43
206	185	159	154 63	102 33	102 42	130 45	106 48	115 60	138 58	114 39	133 56	136 70
182	233	183	246 1	172 0	181 0	208 0	209 0	198 0	189 0	175 0	244 0	182 0
250	250	250	249 1	195 54	241 0	249 0	249 0	249 1	249 0	250 0	249 0	250 0
250	250	249	206 43	199 51	202 48	207 42	202 48	207 42	204 45	213 36	217 33	201 48
249	246	205	127 120	126 119	118 116	113 130	107 130	126 123	128 122	105 105	115 131	120 129
246	250	250	182 68	180 70	187 60	194 56	195 55	185 65	217 32	204 46	192 58	191 55
111	142	90	137 0	91 10	79 0	131 0	102 0	103 0	103 0	83 0	106 0	111 0
116	114	90	62 43	52 25	38 44	58 54	46 46	60 39	64 59	50 38	64 53	50 66
237	193	207	189 30	158 48	127 36	185 37	158 43	195 27	182 23	210 22	185 35	203 34
246	237	220	117 119	92 109	103 101	125 119	112 120	105 123	116 114	117 117	102 134	111 134

AllelicDepth CC1-18	AllelicDepth CC1-25	GenotypeQuality NCC1	GenotypeQuality CC1	GenotypeQuality CC1-1	GenotypeQuality CC1-2	GenotypeQuality CC1-7	GenotypeQuality CC1-8	GenotypeQuality CC1-9
191 59	185 64	53.64	27.35	38	72.84	2	99	99
19 231	26 223	99	99	99	99	99	99	99
133 114	96 84	99	99	99	99	99	99	99
167 54	133 47	99	99	99	99	99	99	99
123 21	83 23	48.18	21.41	99	99	99	29.63	22.04
221 29	208 41	78.41	99	40.41	99	99	99	48.32
120 24	68 18	99	26.72	99	99	32.5	74.69	46.29
129 121	250 0	99	99	99	99	99	99	99
153 92	153 86	99	99	99	99	99	99	99
194 51	148 40	99	99	6.21	62.21	90.36	66.4	99
250 0	244 0	99	99	99	99	99	99	99
30 31	28 20	70.41	44.09	99	51.41	95.08	82.82	85.83
141 109	136 114	99	99	99	99	99	99	99
224 23	197 53	99	99	99	30.44	99	67.31	99
245 0	132 106	99	99	99	99	99	99	99
121 35	88 20	73.74	99	81.74	77.49	3.89	18.31	65.29
250 0	249 0	99	99	99	99	99	99	99
207 0	179 0	99	99	99	99	99	99	99
250 0	249 0	99	99	99	99	99	99	99
179 70	186 63	99	99	18.41	99	99	99	99
129 42	107 39	99	99	99	99	99	99	99
191 52	161 32	99	99	99	99	99	51.03	45.95
250 0	246 1	99	99	99	99	99	99	99
110 20	77 12	57.7	99	11.46	10.29	46.1	99	61.68
247 0	241 0	99	99	99	99	99	99	99
207 43	198 52	67.67	11.5	99	99	99	99	99
56 10	38 7	16.91	89.69	59.58	9.05	6.43	1.08	60.07
198 52	179 37	55.76	99	99	99	99	99	8.38
32 8	20 9	38.82	7	43.52	66.66	91.09	99	74.32
75 24	69 22	3.16	99	57.12	19.58	35.47	18.77	79.57
129 121	142 108	99	99	99	99	99	99	99
250 0	249 0	99	99	99	99	99	99	99
42 23	34 8	58.19	99	85.13	62.35	21.37	32.15	24.38
25 15	25 10	89.32	71.01	51.04	39.86	28.73	32.88	14.01
174 28	183 21	2.23	99	99	99	99	99	37.2
39 6	31 5	99	24.33	84.15	30.31	51.45	53.19	69.02
201 43	202 44	99	28.22	62.6	99	99	99	23.2
249 0	174 0	99	99	99	99	99	99	99
99 44	81 35	99	99	99	99	99	92.61	99
103 46	91 36	1.68	14.9	6.58	72.3	11.2	7.86	25.19
136 49	109 50	99	99	99	99	99	99	99
233 0	95 87	99	99	99	99	99	99	99
249 1	250 0	99	99	99	99	99	99	99
215 35	205 44	73.5	99	4.18	17.87	99	50.14	8.39
141 105	98 106	99	99	99	99	99	99	99
199 51	183 67	99	99	99	54.36	99	99	22.15
142 0	90 0	99	99	99	99	99	99	99
51 63	41 49	99	99	99	99	99	99	99
160 33	178 29	99	20.17	94.29	63.84	99	99	99
115 122	109 111	99	99	99	99	99	99	99

GenotypeQuality CC1-11	GenotypeQuality CC1-12	GenotypeQuality CC1-17	GenotypeQuality CC1-18	GenotypeQuality CC1-25
99	35.3	99	99	74.33
99	99	99	99	99
99	99	99	99	99
99	99	99	99	99
99	43.11	59.9	87.85	17.88
99	99	99	99	99
99	37.11	6.24	99	99
99	99	99	99	99
70.09	99	99	99	99
9.72	83.09	99	99	52.28
99	99	99	99	99
66.88	61.16	32.55	99	56.12
99	99	99	99	99
99	99	99	99	99
99	99	99	99	99
99	4.79	82.5	13.4	99
99	99	99	99	99
99	99	99	99	99
99	99	99	99	99
99	99	99	99	99
73.66	99	25.72	99	99
99	99	99	99	99
99	99	99	99	99
99	88.14	99	34.27	87.47
99	99	99	99	99
99	99	93.38	99	99
36.56	69.16	14.39	45.71	6.8
59.52	19.72	99	99	48.87
37.09	43.79	87.39	52.11	24.51
67.76	87.23	99	93.77	99
99	99	99	99	99
99	99	99	99	99
36.22	91	59.85	99	21.92
10.65	14.08	59.46	82.56	53.46
99	99	99	99	91.63
71.96	65.3	23.85	26.31	15.34
55.28	10.23	0.71	52.97	99
99	99	99	99	99
99	99	99	99	99
26.1	64.6	34.09	3.53	59.18
99	99	99	99	99
99	99	99	99	99
99	99	99	99	99
99	99	60.28	50.65	99
99	99	99	99	99
83.98	99	99	99	99
99	99	99	99	99
99	99	99	99	99
99	94.35	99	53.03	38.86
99	99	99	99	99

Supplemental Table 6 The 40 distinct genotypes among the twelve samples

Chrom	Chrom Start	Chrom End	Reference	Alternatives	Type	Known/Novel	Gene	Function
chr1	1575715	1575715	C	T	SNV	Novel	CDK11B,CDK11A	Missense
chr1	233497836	233497836	C	A	SNV	Novel	KIAA1804,RP5-862P8.2	Missense
chr2	29416635	29416635	C	A	SNV	Novel	ALK	Missense
chr2	29448410	29448410	T	G	SNV	Novel	ALK	Missense
chr2	37336419	37336419	C	T	SNV	Novel	EIF2AK2	Missense
chr2	158485099	158485099	C	A	SNV	Novel	ACVR1C,AC019186.1	Missense
chr2	179408086	179408086	A	G	SNV	Novel	TTN,MIR548N,LOC100506866,AC009948.3	Missense
chr2	179634421	179634421	T	G	SNV	Novel	TTN	Missense
chr2	209195248	209195248	C	A	SNV	Novel	PIKFYVE	Missense
chr3	41705179	41705179	A	C	SNV	Novel	ULK4	Missense
chr3	123988019	123988019	C	A	SNV	Novel	KALRN	Missense
chr5	112769527	112769527	C	T	SNV	Novel	MCC,TSSK1B,CTD-2201G3.1	Missense
chr5	180048626	180048626	C	T	SNV	Novel	FLT4	Missense
chr6	31947203	31947203	T	C	SNV	Novel	STK19,XXbac-BPG116M5.15	Missense
chr6	36489585	36489585	C	A	SNV	Novel	STK38	Missense
chr6	110942394	110942394	G	T	SNV	Novel	CDK19	Missense
chr7	23808650	23808650	G	T	SNV	Novel	STK31	Missense
chr7	95216415	95216415	C	A	SNV	Novel	PKD4	Missense
chr7	98490141	98490141	G	C	SNV	Novel	TRRAP	Missense
chr7	98547196	98547196	G	T	SNV	Novel	TRRAP	Missense
chr7	138145436	138145436	C	A	SNV	Novel	TRIM24	Missense
chr8	8239069	8239069	C	A	SNV	Novel	SGK223,AC068353.1	Missense
chr8	144800905	144800905	A	C	SNV	Novel	MAPK15,RP11-429J17.5	Missense
chr10	99400747	99400747	C	A	SNV	Novel	PI4K2A,RP11-548K23.11	Missense
chr11	46369267	46369267	G	A	SNV	Known	DGKZ	Missense
chr12	1009680	1009680	C	T	SNV	Novel	WNK1	Missense
chr13	110434668	110434668	C	A	SNV	Novel	IRS2	Missense
chr13	110437802	110437802	A	C	SNV	Novel	IRS2	Missense
chr14	24808802	24808802	G	T	SNV	Novel	RIPK3	Missense
chr15	91436551	91436551	A	G	SNV	Novel	FES,AC068831.1	Missense
chr15	99250895	99250895	G	T	SNV	Novel	IGF1R	Missense
chr16	23690401	23690401	C	T	SNV	Novel	PLK1	Missense
chr16	46744689	46744689	C	A	SNV	Known	MYLK3	Missense
chr17	7796803	7796803	T	C	SNV	Novel	CHD3	Missense
chr17	8789811	8789811	G	A	SNV	Novel	PIK3R5	Nonsense
chr17	37881392	37881392	A	G	SNV	Novel	ERBB2,MIR4728	Missense
chr17	41245693	41245693	G	T	SNV	Novel	BRCA1	Missense
chr18	18534948	18534948	G	C	SNV	Known	ROCK1	Missense
chr19	2046399	2046399	G	A	SNV	Novel	MKNK2	Missense
chr19	47193933	47193933	G	T	SNV	Novel	PRKD2	Missense

[illegible]

CCDS

CCDS1598.1	GN=KIAA1804	GI=84451	FC=Missense	CP=1349	CF=1	AC=GcT->GaT	RP=450	RC=A[Ala]->D[Asp]	EN=5/10	DS=+38	P=chr1:233463775-233518457	
CCDS33172.1	GN=ALK	GI=238	FC=Missense	CP=4318	CF=0	AC=gCC->tCC	RP=1440	RC=A[Ala]->S[Ser]	EN=29/29	DS=+154	P=chr2:29416090-30143525	ST=-
CCDS33172.1	GN=ALK	GI=238	FC=Missense	CP=3089	CF=1	AC=CaC->CcC	RP=1030	RC=H[His]->P[Pro]	EN=19/29	DS=+22	P=chr2:29416090-30143525	ST=-
CCDS1786.1	GN=EIF2AK2	GI=5610	FC=Missense	CP=1397	CF=1	AC=GgA->GaA	RP=466	RC=G[Gly]->E[Glu]	EN=13/15	DS=+20	P=chr2:37334416-37374949	ST=
CCDS2205.1	GN=ACVR1C	GI=130399	FC=Missense	CP=58	CF=0	AC=gCC->tCC	RP=20	RC=A[Ala]->S[Ser]	EN=1/9	DS=-41170	P=chr2:158390430-158485156	S
CCDS54424.1	GN=TTN	GI=7273	FC=Missense	CP=88910	CF=1	AC=GtG->GcG	RP=29637	RC=V[Val]->A[Ala]	EN=295/311	DS=+304	P=chr2:179391739-1796693	
CCDS54424.1	GN=TTN	GI=7273	FC=Missense	CP=8887	CF=0	AC=aCC->cCC	RP=2963	RC=T[Thr]->P[Pro]	EN=36/311	DS=+246	P=chr2:179391739-179669369	
CCDS2382.1	GN=PIKFYVE	GI=200576	FC=Missense	CP=3793	CF=0	AC=cCT->aCT	RP=1265	RC=P[Pro]->T[Thr]	EN=22/41	DS=+2	P=chr2:209136244-20922002	
CCDS43071.1	GN=ULK4	GI=54986	FC=Missense	CP=2990	CF=1	AC=AtT->AgT	RP=997	RC=I[Ile]->S[Ser]	EN=29/36	DS=+12	P=chr3:41288420-41996251	ST=-
CCDS3027.1	GN=KALRN	GI=8997	FC=Missense	CP=880	CF=0	AC=cAC->aAC	RP=294	RC=H[His]->N[Asn]	EN=5/34	DS=+430	P=chr3:123813685-124237309	ST=
CCDS4112.1	GN=TSSK1B	GI=83942	FC=Missense	CP=1010	CF=1	AC=AgG->AaG	RP=337	RC=R[Arg]->K[Lys]	EN=1/1	P=chr5:112769433-112770536	ST=-	CL=1
CCDS4457.1	GN=FLT4	GI=2324	FC=Missense	CP=1936	CF=0	AC=gAG->aAG	RP=646	RC=E[Glu]->K[Lys]	EN=13/30	DS=+279	P=chr5:180030192-180076545	ST=
CCDS4733.1	GN=STK19	GI=8859	FC=Missense	CP=688	CF=0	AC=tGT->cGT	RP=230	RC=C[Cys]->R[Arg]	EN=5/8	DS=+13	P=chr6:31939774-31948826	ST=+
CCDS4822.1	GN=STK38	GI=11329	FC=Missense	CP=316	CF=0	AC=gTT->tTT	RP=106	RC=V[Val]->F[Phe]	EN=4/13	DS=+10	P=chr6:36463561-36507979	ST=-
CCDS5085.1	GN=CDK19	GI=23097	FC=Missense	CP=1290	CF=2	AC=AGc->AGa	RP=430	RC=S[Ser]->R[Arg]	EN=12/13	DS=+180	P=chr6:110935738-111136339	
CCDS5386.1	GN=STK31	GI=56164	FC=Missense	CP=1453	CF=0	AC=gCC->tCC	RP=485	RC=A[Ala]->S[Ser]	EN=12/24	DS=+37	P=chr7:23749905-23871985	ST=-
CCDS5643.1	GN=PKD4	GI=5166	FC=Missense	CP=1002	CF=2	AC=TTg->TTt	RP=334	RC=L[Leu]->F[Phe]	EN=10/11	DS=+21	P=chr7:95214953-95225605	ST=-
CCDS5659.1	GN=TRRAP	GI=8295	FC=Missense	CP=356	CF=1	AC=CgC->CcC	RP=119	RC=R[Arg]->P[Pro]	EN=4/70	DS=+95	P=chr7:98478774-98609978	ST=+
CCDS5659.1	GN=TRRAP	GI=8295	FC=Missense	CP=4870	CF=0	AC=gCC->tCC	RP=1624	RC=A[Ala]->S[Ser]	EN=33/70	DS=-87	P=chr7:98478774-98609978	ST=
CCDS5847.1	GN=TRIM24	GI=8805	FC=Missense	CP=143	CF=1	AC=GcC->GaC	RP=48	RC=A[Ala]->D[Asp]	EN=1/19	DS=-43599	P=chr7:138145294-138269696	S
CCDS43706.1	GN=SGK223	GI=157285	FC=Missense	CP=189	CF=2	AC=AGg->AGt	RP=63	RC=R[Arg]->S[Ser]	EN=1/5	DS=-3481	P=chr8:8175676-8239257	ST=-
CCDS6409.2	GN=MAPK15	GI=225689	FC=Intron	EN=4:5/14	DS=-40	P=chr8:144798548-144804421	ST=+	CL=1635	CS=Public			
CCDS7469.1	GN=PI4K2A	GI=55361	FC=Missense	CP=248	CF=1	AC=GcT->GaT	RP=83	RC=A[Ala]->D[Asp]	EN=1/9	DS=-9951	P=chr10:99400500-99433499	ST=-
CCDS55757.1	GN=DGKZ	GI=8525	FC=Missense	CP=58	CF=0	AC=gCC->aCC	RP=20	RC=A[Ala]->T[Thr]	EN=1/31	DS=-19574	P=chr11:46369210-46401497	ST=+
CCDS53730.1	GN=WNK1	GI=65125	FC=Missense	CP=7267	CF=0	AC=cCC->tCC	RP=2423	RC=P[Pro]->S[Ser]	EN=26/28	DS=+39	P=chr12:862732-1017958	ST=+
CCDS9510.1	GN=IRS2	GI=8660	FC=Missense	CP=3733	CF=0	AC=gCC->tCC	RP=1245	RC=A[Ala]->S[Ser]	EN=1/2	DS=-26013	P=chr13:110408651-110438400	S
CCDS9510.1	GN=IRS2	GI=8660	FC=Missense	CP=599	CF=1	AC=GtG->GgG	RP=200	RC=V[Val]->G[Gly]	EN=1/2	DS=-29147	P=chr13:110408651-110438400	ST=
CCDS9628.1	GN=RIPK3	GI=11035	FC=Missense	CP=22	CF=0	AC=cCC->aCC	RP=8	RC=P[Pro]->T[Thr]	EN=2/10	DS=+2	P=chr14:24805381-24809032	ST=-
CCDS10365.1	GN=FES	GI=2242	FC=Missense	CP=1952	CF=1	AC=GaG->GgG	RP=651	RC=E[Glu]->G[Gly]	EN=15/18	DS=+31	P=chr15:91428276-91438788	ST=+
CCDS10378.1	GN=IGF1R	GI=3480	FC=Missense	CP=199	CF=0	AC=gCC->tCC	RP=67	RC=A[Ala]->S[Ser]	EN=2/21	DS=+105	P=chr15:99192811-99500671	ST=+
CCDS10616.1	GN=PLK1	GI=5347	FC=Missense	CP=148	CF=0	AC=cGG->tGG	RP=50	RC=R[Arg]->W[Trp]	EN=1/10	DS=-1004	P=chr16:23690254-23701384	ST=+
CCDS10723.2	GN=MYLK3	GI=91807	FC=Missense	CP=2127	CF=2	AC=TTg->TTt	RP=709	RC=L[Leu]->F[Phe]	EN=11/13	DS=+13	P=chr16:46741616-46782105	S
CCDS32553.2	GN=CHD3	GI=1107	FC=Missense	CP=886	CF=0	AC=tCC->cCC	RP=296	RC=S[Ser]->P[Pro]	EN=5/40	DS=+200	P=chr17:7788125-7814903	ST=+
CCDS11147.1	GN=PIK3R5	GI=23533	FC=Nonsense	CP=2017	CF=0	AC=cAA->tAA	RP=673	RC=Q[Gln]->Stop	EN=12/18	DS=+112	P=chr17:8783956-8814811	ST=
CCDS32642.1	GN=ERBB2	GI=2064	FC=Missense	CP=2584	CF=0	AC=aCA->gCA	RP=862	RC=T[Thr]->A[Ala]	EN=21/27	DS=+91	P=chr17:37856492-37884297	ST=
CCDS11456.2	GN=BRCA1	GI=672	FC=Missense	CP=1855	CF=0	AC=cAT->aAT	RP=619	RC=H[His]->N[Asn]	EN=9/23	DS=+1185	P=chr17:41197695-41276113	ST=
CCDS11870.2	GN=ROCK1	GI=6093	FC=Missense	CP=3649	CF=0	AC=cAA->gAA	RP=1217	RC=Q[Gln]->E[Glu]	EN=31/33	DS=+58	P=chr18:18531345-18690871	S
CCDS12080.1	GN=MKNK2	GI=2872	FC=Missense	CP=208	CF=0	AC=cGG->tGG	RP=70	RC=R[Arg]->W[Trp]	EN=3/13	DS=+69	P=chr19:2039612-2050850	ST=-
CCDS12689.1	GN=PRKD2	GI=25865	FC=Missense	CP=1733	CF=1	AC=GcA->GaA	RP=578	RC=A[Ala]->E[Glu]	EN=13/18	DS=+31	P=chr19:47177780-47219627	S

RefSeq Genes													
NM_033486.1	GN=CDK11B	GI=984	FC=Coding synonymy unknown	EN=11/20	DS=+99	P=chr1:1571100-1655775	ST=-	PD=cyclin-dependent kinase 11B isoform 2					
NM_032435.2	GN=KIAA1804	GI=84451	FC=Missense	CP=1349	CF=1	AC=GcT->GaT	RP=450	RC=A[Ala]->D[Asp]	EN=5/10	DS=+38	P=chr1:233463514-233520894		
NM_004304.4	GN=ALK	GI=238	FC=Missense	CP=4318	CF=0	AC=gCC->tCC	RP=1440	RC=A[Ala]->S[Ser]	EN=29/29	DS=+154	P=chr2:29415640-30144477	ST=-	CL=C
NM_004304.4	GN=ALK	GI=238	FC=Missense	CP=3089	CF=1	AC=CaC->CcC	RP=1030	RC=H[His]->P[Pro]	EN=19/29	DS=+22	P=chr2:29415640-30144477	ST=-	CL=C
NM_002759.3	GN=EIF2AK2	GI=5610	FC=Missense	CP=1397	CF=1	AC=GgA->GaA	RP=466	RC=G[Gly]->E[Glu]	EN=15/17	DS=+20	P=chr2:37332284-37384190	ST=-	CL=C
NM_145259.2	GN=ACVR1C	GI=130399	FC=Missense	CP=58	CF=0	AC=gCC->tCC	RP=20	RC=A[Ala]->S[Ser]	EN=1/9	DS=-41170	P=chr2:158383279-158485399	ST=-	CL=C
NM_133378.4	GN=TTN	GI=7273	FC=Missense	CP=88910	CF=1	AC=GtG->GcG	RP=29637	RC=V[Val]->A[Ala]	EN=296/312	DS=+304	P=chr2:179390718-17967215	ST=-	CL=C
NM_133378.4	GN=TTN	GI=7273	FC=Missense	CP=8887	CF=0	AC=aCC->cCC	RP=2963	RC=T[Thr]->P[Pro]	EN=37/312	DS=+246	P=chr2:179390718-179672150	ST=-	CL=S
NM_015040.3	GN=PIKFYVE	GI=200576	FC=Missense	CP=3793	CF=0	AC=cCT->aCT	RP=1265	RC=P[Pro]->T[Thr]	EN=23/42	DS=+2	P=chr2:209130991-20922347	ST=-	CL=C
NM_017886.2	GN=ULK4	GI=54986	FC=Missense	CP=2990	CF=1	AC=AtT->AgT	RP=997	RC=I[Ile]->S[Ser]	EN=30/37	DS=+12	P=chr3:41288090-42003660	ST=-	CL=C
NM_001024660.3	GN=KALRN	GI=8997	FC=Missense	CP=880	CF=0	AC=cAC->aAC	RP=294	RC=H[His]->N[Asn]	EN=5/60	DS=+430	P=chr3:123813558-124440036	ST=-	CL=C
NM_032028.3	GN=TSSK1B	GI=83942	FC=Missense	CP=1010	CF=1	AC=AgG->AaG	RP=337	RC=R[Arg]->K[Lys]	EN=1/1	P=chr5:112768251-112770728	ST=-	CL=C	
NM_182925.4	GN=FLT4	GI=2324	FC=Missense	CP=1936	CF=0	AC=gAG->aAG	RP=646	RC=E[Glu]->K[Lys]	EN=13/30	DS=+279	P=chr5:180028506-180076624	ST=-	CL=C
NM_032454.1	GN=STK19	GI=8859	FC=Missense	CP=688	CF=0	AC=tGT->cGT	RP=230	RC=C[Cys]->R[Arg]	EN=5/8	DS=+13	P=chr6:31939646-31949223	ST=+	CL=C
NM_007271.2	GN=STK38	GI=11329	FC=Missense	CP=316	CF=0	AC=gTT->tTT	RP=106	RC=V[Val]->F[Phe]	EN=5/14	DS=+10	P=chr6:36461669-36515247	ST=-	CL=C
NM_015076.3	GN=CDK19	GI=23097	FC=Missense	CP=1290	CF=2	AC=AGc->AGa	RP=430	RC=S[Ser]->R[Arg]	EN=12/13	DS=+180	P=chr6:110931181-111136412	ST=-	CL=C
NM_031414.3	GN=STK31	GI=56164	FC=Missense	CP=1453	CF=0	AC=gCC->tCC	RP=485	RC=A[Ala]->S[Ser]	EN=12/14	DS=+37	P=chr7:23749838-23872127	ST=-	CL=C
NM_002612.3	GN=PDK4	GI=5166	FC=Missense	CP=1002	CF=2	AC=TTg->TTt	RP=334	RC=L[Leu]->F[Phe]	EN=10/11	DS=+21	P=chr7:95212809-95225925	ST=-	CL=C
NM_001244580.1	GN=TRRAP	GI=8295	FC=Missense	CP=356	CF=1	AC=CgC->CcC	RP=119	RC=R[Arg]->P[Pro]	EN=5/72	DS=+95	P=chr7:98476113-98610866	ST=-	CL=C
NM_001244580.1	GN=TRRAP	GI=8295	FC=Missense	CP=4924	CF=0	AC=gCC->tCC	RP=1642	RC=A[Ala]->S[Ser]	EN=35/72	DS=-87	P=chr7:98476113-98610866	ST=-	CL=C
NM_015905.2	GN=TRIM24	GI=8805	FC=Missense	CP=143	CF=1	AC=GcC->GaC	RP=48	RC=A[Ala]->D[Asp]	EN=1/19	DS=-43599	P=chr7:138145079-138270332	ST=-	CL=C
NM_001080826.1	GN=SGK223	GI=157285	FC=Missense	CP=189	CF=2	AC=AGg->AGt	RP=63	RC=R[Arg]->S[Ser]	EN=1/5	DS=-3481	P=chr8:8175258-8239257	ST=-	CL=C
NM_139021.2	GN=MAPK15	GI=225689	FC=Intron	EN=4/5/14	DS=-40	P=chr8:144798507-144804633	ST=+	CL=1635	PD=mitogen-activated protein kinase 15				
NM_018425.2	GN=PI4K2A	GI=55361	FC=Missense	CP=248	CF=1	AC=GcT->GaT	RP=83	RC=A[Ala]->D[Asp]	EN=1/9	DS=-9951	P=chr10:99400443-99436187	ST=-	CL=C
NM_001199266.1	GN=DGKZ	GI=8525	FC=Missense	CP=58	CF=0	AC=gCC->aCC	RP=20	RC=A[Ala]->T[Thr]	EN=1/31	DS=-19574	P=chr11:46368956-46402104	ST=-	CL=C
NM_001184985.1	GN=WNK1	GI=65125	FC=Missense	CP=7267	CF=0	AC=cCC->tCC	RP=2423	RC=P[Pro]->S[Ser]	EN=26/28	DS=+39	P=chr12:862089-1020618	ST=-	CL=C
NM_003749.2	GN=IRS2	GI=8660	FC=Missense	CP=3733	CF=0	AC=gCC->tCC	RP=1245	RC=A[Ala]->S[Ser]	EN=1/2	DS=-26013	P=chr13:110406184-110438914	ST=-	CL=C
NM_003749.2	GN=IRS2	GI=8660	FC=Missense	CP=599	CF=1	AC=GtG->GgG	RP=200	RC=V[Val]->G[Gly]	EN=1/2	DS=-29147	P=chr13:110406184-110438914	ST=-	CL=C
NM_006871.3	GN=RIPK3	GI=11035	FC=Missense	CP=22	CF=0	AC=cCC->aCC	RP=8	RC=P[Pro]->T[Thr]	EN=2/10	DS=+2	P=chr14:24805227-24809242	ST=-	CL=C
NM_002005.3	GN=FES	GI=2242	FC=Missense	CP=1952	CF=1	AC=GaG->GgG	RP=651	RC=E[Glu]->G[Gly]	EN=16/19	DS=+31	P=chr15:91427688-91439006	ST=+	CL=C
NM_000875.3	GN=IGF1R	GI=3480	FC=Missense	CP=199	CF=0	AC=gCC->tCC	RP=67	RC=A[Ala]->S[Ser]	EN=2/21	DS=+105	P=chr15:99192761-99507759	ST=+	CL=C
NM_005030.3	GN=PLK1	GI=5347	FC=Missense	CP=148	CF=0	AC=cGG->tGG	RP=50	RC=R[Arg]->W[Trp]	EN=1/10	DS=-1004	P=chr16:23690201-23701688	ST=+	CL=C
NM_182493.2	GN=MYLK3	GI=91807	FC=Missense	CP=2127	CF=2	AC=TTg->TTt	RP=709	RC=L[Leu]->F[Phe]	EN=11/13	DS=+13	P=chr16:46736194-46782221	ST=-	CL=C
NM_001005271.2	GN=CHD3	GI=1107	FC=Missense	CP=886	CF=0	AC=tCC->cCC	RP=296	RC=S[Ser]->P[Pro]	EN=5/40	DS=+200	P=chr17:7788123-7816075	ST=-	CL=C
NM_001142633.2	GN=PIK3R5	GI=23533	FC=Nonsense	CP=2017	CF=0	AC=cAA->tAA	RP=673	RC=Q[Gln]->Stop	EN=13/19	DS=+112	P=chr17:8782233-8869029	ST=-	CL=C
NM_004448.2	GN=ERBB2	GI=2064	FC=Missense	CP=2584	CF=0	AC=aCA->gCA	RP=862	RC=T[Thr]->A[Ala]	EN=21/27	DS=+91	P=chr17:37856254-37884915	ST=-	CL=C
NM_007300.3	GN=BRCA1	GI=672	FC=Missense	CP=1855	CF=0	AC=cAT->aAT	RP=619	RC=H[His]->N[Asn]	EN=10/24	DS=+1185	P=chr17:41196312-41277500	ST=-	CL=C
NM_005406.2	GN=ROCK1	GI=6093	FC=Missense	CP=3649	CF=0	AC=cAA->gAA	RP=1217	RC=Q[Gln]->E[Glu]	EN=31/33	DS=+58	P=chr18:18529703-18691812	ST=-	CL=C
NM_199054.2	GN=MKNK2	GI=2872	FC=Missense	CP=208	CF=0	AC=cGG->tGG	RP=70	RC=R[Arg]->W[Trp]	EN=4/14	DS=+69	P=chr19:2037470-2051243	ST=-	CL=C
NM_016457.4	GN=PRKD2	GI=25865	FC=Missense	CP=1733	CF=1	AC=GcA->GaA	RP=578	RC=A[Ala]->E[Glu]	EN=13/18	DS=+31	P=chr19:47177573-47220384	ST=-	CL=C

RefSeq Genes Product
cyclin-dependent kinase 11B isoform 2, cyclin-dependent kinase 11B isoform 3, cyclin-dependent kinase 11B isoform 4, cyclin-dependent kinase 11B isoform
mitogen-activated protein kinase kinase MLK4
ALK tyrosine kinase receptor precursor
ALK tyrosine kinase receptor precursor
interferon-induced, double-stranded RNA-activated protein kinase isoform a, interferon-induced, double-stranded RNA-activated protein kinase isoform b
activin receptor type-1C isoform 1, activin receptor type-1C isoform 3 precursor, activin receptor type-1C isoform 4 precursor
titin isoform N2-A, titin isoform novex-2, titin isoform novex-1, titin isoform N2-B
titin isoform N2-A, titin isoform novex-2, titin isoform novex-1, titin isoform N2-B, titin isoform novex-3
1-phosphatidylinositol-3-phosphate 5-kinase isoform 2
serine/threonine-protein kinase ULK4
kalirin isoform 1, kalirin isoform 2
testis-specific serine/threonine-protein kinase 1, colorectal mutant cancer protein isoform 1
vascular endothelial growth factor receptor 3 isoform 1 precursor, vascular endothelial growth factor receptor 3 isoform 2 precursor
serine/threonine-protein kinase 19 isoform 2, serine/threonine-protein kinase 19 isoform 1
serine/threonine-protein kinase 38
cyclin-dependent kinase 19
serine/threonine-protein kinase 31 isoform a, serine/threonine-protein kinase 31 isoform b
pyruvate dehydrogenase kinase, isozyme 4
transformation/transcription domain-associated protein isoform 1, transformation/transcription domain-associated protein isoform 2
transformation/transcription domain-associated protein isoform 1, transformation/transcription domain-associated protein isoform 2
transcription intermediary factor 1-alpha isoform a, transcription intermediary factor 1-alpha isoform b
tyrosine-protein kinase SgK223
mitogen-activated protein kinase 15
phosphatidylinositol 4-kinase type 2-alpha
diacylglycerol kinase zeta isoform 5, diacylglycerol kinase zeta isoform 2, diacylglycerol kinase zeta isoform 6, diacylglycerol kinase zeta isoform 7, diacylglycerol kinase zeta isoform 8
serine/threonine-protein kinase WNK1 isoform 4, serine/threonine-protein kinase WNK1 isoform 3, serine/threonine-protein kinase WNK1 isoform 1, serine/threonine-protein kinase WNK1 isoform 2
insulin receptor substrate 2
insulin receptor substrate 2
receptor-interacting serine/threonine-protein kinase 3
tyrosine-protein kinase Fes/Fps isoform 1, tyrosine-protein kinase Fes/Fps isoform 2, tyrosine-protein kinase Fes/Fps isoform 3, tyrosine-protein kinase Fes/Fps isoform 4
insulin-like growth factor 1 receptor precursor
serine/threonine-protein kinase PLK1
putative myosin light chain kinase 3
chromodomain-helicase-DNA-binding protein 3 isoform 3, chromodomain-helicase-DNA-binding protein 3 isoform 1, chromodomain-helicase-DNA-binding protein 3 isoform 2
phosphoinositide 3-kinase regulatory subunit 5 isoform 1, phosphoinositide 3-kinase regulatory subunit 5 isoform 2
receptor tyrosine-protein kinase erbB-2 isoform a precursor, receptor tyrosine-protein kinase erbB-2 isoform b
breast cancer type 1 susceptibility protein isoform 2, breast cancer type 1 susceptibility protein isoform 1, breast cancer type 1 susceptibility protein isoform 3
rho-associated protein kinase 1
MAP kinase-interacting serine/threonine-protein kinase 2 isoform 2, MAP kinase-interacting serine/threonine-protein kinase 2 isoform 1
serine/threonine-protein kinase D2 isoform A, serine/threonine-protein kinase D2 isoform B

Gencode											
ENST00000407249.3	GN=CDK11A	GI=ENSG00000008128.14	FC=Missense	CP=1183	CF=0	AC=gAC->aAC	RP=395	RC=D[Asp]->N[Asn]	EN=12/21	DS=+99	P=chr
ENST00000366624.3	GN=RP5-862P8.2	GI=ENSG00000143674.6	FC=Missense	CP=1349	CF=1	AC=GcT->GaT	RP=450	RC=A[Ala]->D[Asp]	EN=5/10	DS=+38	P=chr
ENST00000389048.3	GN=ALK	GI=ENSG00000171094.11	FC=Missense	CP=4318	CF=0	AC=gCC->tCC	RP=1440	RC=A[Ala]->S[Ser]	EN=29/29	DS=+154	P=chr2:29
ENST00000389048.3	GN=ALK	GI=ENSG00000171094.11	FC=Missense	CP=3089	CF=1	AC=CaC->CcC	RP=1030	RC=H[His]->P[Pro]	EN=19/29	DS=+22	P=chr2:29
ENST00000233057.4	GN=EIF2AK2	GI=ENSG00000055332.10	FC=Missense	CP=1397	CF=1	AC=GgA->GaA	RP=466	RC=G[Gly]->E[Glu]	EN=15/17	DS=+20	P=chr2
ENST00000243349.7	GN=ACVR1C	GI=ENSG00000123612.10	FC=Missense	CP=58	CF=0	AC=gCC->tCC	RP=20	RC=A[Ala]->S[Ser]	EN=1/9	DS=-41170	P=chr2:15
ENST00000342992.6	GN=TTN	GI=ENSG00000155657.16	FC=Missense	CP=88910	CF=1	AC=GtG->GcG	RP=29637	RC=V[Val]->A[Ala]	EN=296/312	DS=+304	P=chr
ENST00000342992.6	GN=TTN	GI=ENSG00000155657.16	FC=Missense	CP=8887	CF=0	AC=aCC->cCC	RP=2963	RC=T[Thr]->P[Pro]	EN=37/312	DS=+246	P=chr2
ENST00000264380.4	GN=PIKFYVE	GI=ENSG00000115020.11	FC=Missense	CP=3793	CF=0	AC=cCT->aCT	RP=1265	RC=P[Pro]->T[Thr]	EN=23/42	DS=+2	P=chr2
ENST00000301831.4	GN=ULK4	GI=ENSG00000168038.6	FC=Missense	CP=2990	CF=1	AC=AtT->AgT	RP=997	RC=I[Ile]->S[Ser]	EN=30/37	DS=+12	P=chr3:41288
ENST00000360013.3	GN=KALRN	GI=ENSG00000160145.10	FC=Missense	CP=880	CF=0	AC=cAC->aAC	RP=294	RC=H[His]->N[Asn]	EN=5/60	DS=+430	P=chr3:1
ENST00000390666.3	GN=TSSK1B	GI=ENSG00000212122.3	FC=Missense	CP=1010	CF=1	AC=AgG->AaG	RP=337	RC=R[Arg]->K[Lys]	EN=1/1	P=chr5:112768251	
ENST00000261937.6	GN=FLT4	GI=ENSG00000037280.10	FC=Missense	CP=1936	CF=0	AC=gAG->aAG	RP=646	RC=E[Glu]->K[Lys]	EN=13/30	DS=+279	P=chr5:1
ENST00000375333.2	GN=STK19	GI=ENSG00000204344.9	FC=Missense	CP=688	CF=0	AC=tGT->cGT	RP=230	RC=C[Cys]->R[Arg]	EN=5/8	DS=+13	P=chr6:31939
ENST00000229812.7	GN=STK38	GI=ENSG00000112079.8	FC=Missense	CP=316	CF=0	AC=gTT->tTT	RP=106	RC=V[Val]->F[Phe]	EN=5/14	DS=+10	P=chr6:36461
ENST00000368911.3	GN=CDK19	GI=ENSG00000155111.9	FC=Missense	CP=1290	CF=2	AC=AGc->AGa	RP=430	RC=S[Ser]->R[Arg]	EN=12/13	DS=+180	P=chr6:1
ENST00000355870.3	GN=STK31	GI=ENSG00000196335.8	FC=Missense	CP=1453	CF=0	AC=gCC->tCC	RP=485	RC=A[Ala]->S[Ser]	EN=12/24	DS=+37	P=chr7:23
ENST00000005178.5	GN=PDK4	GI=ENSG00000004799.6	FC=Missense	CP=1002	CF=2	AC=TTg->TTt	RP=334	RC=L[Leu]->F[Phe]	EN=10/11	DS=+21	P=chr7:952
ENST00000359863.4	GN=TRRAP	GI=ENSG00000196367.7	FC=Missense	CP=356	CF=1	AC=CgC->CcC	RP=119	RC=R[Arg]->P[Pro]	EN=5/72	DS=+95	P=chr7:984
ENST00000359863.4	GN=TRRAP	GI=ENSG00000196367.7	FC=Missense	CP=4924	CF=0	AC=gCC->tCC	RP=1642	RC=A[Ala]->S[Ser]	EN=35/72	DS=-87	P=chr7:9
ENST00000343526.4	GN=TRIM24	GI=ENSG00000122779.10	FC=Missense	CP=143	CF=1	AC=GcC->GaC	RP=48	RC=A[Ala]->D[Asp]	EN=1/19	DS=-43599	P=chr7
ENST00000520004.1	GN=AC068353.1	GI=ENSG00000182319.5	FC=Missense	CP=189	CF=2	AC=AGg->AGt	RP=63	RC=R[Arg]->S[Ser]	EN=2/6	DS=+276	P=chr8:8
ENST00000395107.4	GN=MAPK15	GI=ENSG00000181085.10	FC=Missense	CP=298	CF=0	AC=aGC->cGC	RP=100	RC=S[Ser]->R[Arg]	EN=5/8	DS=+12	P=chr8:14
ENST00000370631.3	GN=PI4K2A	GI=ENSG00000155252.10	FC=Missense	CP=248	CF=1	AC=GcT->GaT	RP=83	RC=A[Ala]->D[Asp]	EN=1/9	DS=-9951	P=chr10:9
ENST00000527911.1	GN=DGKZ	GI=ENSG00000149091.10	FC=Missense	CP=58	CF=0	AC=gCC->aCC	RP=20	RC=A[Ala]->T[Thr]	EN=1/31	DS=-19574	P=chr11:46
ENST00000530271.2	GN=WNK1	GI=ENSG00000060237.10	FC=Missense	CP=7981	CF=0	AC=cCC->tCC	RP=2661	RC=P[Pro]->S[Ser]	EN=28/30	DS=+39	P=chr12
ENST00000375856.3	GN=IRS2	GI=ENSG00000185950.7	FC=Missense	CP=3733	CF=0	AC=gCC->tCC	RP=1245	RC=A[Ala]->S[Ser]	EN=1/2	DS=-26013	P=chr13:1
ENST00000375856.3	GN=IRS2	GI=ENSG00000185950.7	FC=Missense	CP=599	CF=1	AC=GtG->GgG	RP=200	RC=V[Val]->G[Gly]	EN=1/2	DS=-29147	P=chr13:110
ENST00000216274.4	GN=RIPK3	GI=ENSG00000129465.10	FC=Missense	CP=22	CF=0	AC=cCC->aCC	RP=8	RC=P[Pro]->T[Thr]	EN=2/10	DS=+2	P=chr14:248052
ENST00000328850.3	GN=FES	GI=ENSG00000182511.6	FC=Missense	CP=1952	CF=1	AC=GaG->GgG	RP=651	RC=E[Glu]->G[Gly]	EN=16/19	DS=+31	P=chr15:914
ENST00000268035.6	GN=IGF1R	GI=ENSG00000140443.8	FC=Missense	CP=199	CF=0	AC=gCC->tCC	RP=67	RC=A[Ala]->S[Ser]	EN=2/21	DS=+105	P=chr15:9919
ENST00000300093.4	GN=PLK1	GI=ENSG00000166851.7	FC=Missense	CP=148	CF=0	AC=cGG->tGG	RP=50	RC=R[Arg]->W[Trp]	EN=1/10	DS=-1004	P=chr16:236
ENST00000394809.3	GN=MYLK3	GI=ENSG00000140795.7	FC=Missense	CP=2127	CF=2	AC=TTg->TTt	RP=709	RC=L[Leu]->F[Phe]	EN=11/13	DS=+13	P=chr16:4
ENST00000380358.4	GN=CHD3	GI=ENSG00000170004.10	FC=Missense	CP=886	CF=0	AC=tCC->cCC	RP=296	RC=S[Ser]->P[Pro]	EN=5/40	DS=+200	P=chr17:77
ENST00000447110.1	GN=PIK3R5	GI=ENSG00000141506.8	FC=Nonsense	CP=2017	CF=0	AC=cAA->tAA	RP=673	RC=Q[Gln]->Stop	EN=13/19	DS=+112	P=chr17:8
ENST00000269571.3	GN=ERBB2	GI=ENSG00000141736.7	FC=Missense	CP=2584	CF=0	AC=aCA->gCA	RP=862	RC=T[Thr]->A[Ala]	EN=21/27	DS=+91	P=chr17:3
ENST00000471181.1	GN=BRCA1	GI=ENSG00000012048.12	FC=Missense	CP=1855	CF=0	AC=cAT->aAT	RP=619	RC=H[His]->N[Asn]	EN=10/24	DS=+1185	P=chr
ENST00000399799.1	GN=ROCK1	GI=ENSG00000067900.4	FC=Missense	CP=3649	CF=0	AC=cAA->gAA	RP=1217	RC=Q[Gln]->E[Glu]	EN=31/33	DS=+58	P=chr18
ENST00000250896.3	GN=MKNK2	GI=ENSG00000099875.8	FC=Missense	CP=208	CF=0	AC=cGG->tGG	RP=70	RC=R[Arg]->W[Trp]	EN=4/14	DS=+69	P=chr19:203
ENST00000291281.3	GN=PRKD2	GI=ENSG00000105287.6	FC=Missense	CP=1733	CF=1	AC=GcA->GaA	RP=578	RC=A[Ala]->E[Glu]	EN=13/18	DS=+31	P=chr19:4

Gencode Pseudogenes

ENST00000513088.1	GN=AL691432.2	GI=ENSG00000248333.1	P=chr1:1571126-1588935	ST=-	LV=2	GT=pseudogene	TT=unprocessed pseudogene
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[illegible]

Repeat Masker	Primate Conserved Elements	Placental Mammal Conserved Elements
		P=chr1:1575696-1575715 lod=24 SC=309
	P=chr1:233497797-233498044 lod=47 SC=399	P=chr1:233497835-233497851 lod=38 SC=362
		P=chr2:29448398-29448417 lod=27 SC=323
	P=chr2:37336370-37336461 lod=20 SC=272	P=chr2:37336392-37336423 lod=52 SC=398
	P=chr2:158485079-158485388 lod=39 SC=372	P=chr2:158485081-158485102 lod=31 SC=339
	P=chr2:179407775-179408409 lod=207 SC=619	P=chr2:179408044-179408129 lod=167 SC=532
	P=chr2:179634400-179634668 lod=83 SC=484	P=chr2:179634400-179634553 lod=405 SC=634
	P=chr2:209195220-209195425 lod=76 SC=470	P=chr2:209195235-209195425 lod=490 SC=656
		P=chr3:41705176-41705193 lod=34 SC=350
	P=chr3:123987593-123988111 lod=149 SC=570	P=chr3:123987947-123988107 lod=456 SC=648
	P=chr5:180048525-180048836 lod=59 SC=433	P=chr5:180048537-180048668 lod=185 SC=544
	P=chr6:31947173-31947365 lod=50 SC=408	P=chr6:31947189-31947216 lod=49 SC=392
	P=chr6:36489409-36489628 lod=48 SC=402	P=chr6:36489504-36489596 lod=290 SC=596
	P=chr6:110942304-110942420 lod=15 SC=230	
	P=chr7:23808601-23808738 lod=16 SC=239	P=chr7:23808626-23808661 lod=82 SC=451
	P=chr7:95216318-95216437 lod=42 SC=383	P=chr7:95216338-95216420 lod=225 SC=567
	P=chr7:98489988-98490155 lod=53 SC=417	P=chr7:98490044-98490155 lod=296 SC=598
	P=chr7:98547157-98547208 lod=15 SC=230	P=chr7:98547157-98547207 lod=142 SC=514
	P=chr7:138145369-138145663 lod=45 SC=393	P=chr7:138145369-138145583 lod=211 SC=559
	P=chr8:8238819-8239264 lod=70 SC=458	P=chr8:8239067-8239119 lod=54 SC=403
	P=chr10:99400432-99400819 lod=50 SC=408	P=chr10:99400457-99400832 lod=564 SC=672
	P=chr11:46368967-46369390 lod=69 SC=456	P=chr11:46369117-46369390 lod=628 SC=685
	P=chr12:1009603-1009912 lod=101 SC=513	P=chr12:1009639-1009707 lod=146 SC=517
	P=chr13:110434622-110434686 lod=17 SC=248	
	P=chr13:110437022-110438338 lod=283 SC=665	P=chr13:110437466-110437894 lod=605 SC=680
	P=chr15:91436518-91436649 lod=27 SC=317	P=chr15:91436550-91436554 lod=18 SC=276
	P=chr15:99250772-99251370 lod=137 SC=558	P=chr15:99250802-99250974 lod=468 SC=651
	P=chr16:23690362-23690671 lod=86 SC=489	P=chr16:23690365-23690666 lod=483 SC=654
	P=chr16:46744545-46744700 lod=62 SC=440	P=chr16:46744621-46744703 lod=215 SC=561
	P=chr17:7796480-7796893 lod=137 SC=558	P=chr17:7796740-7796813 lod=176 SC=538
		P=chr17:8789792-8789879 lod=71 SC=434
	P=chr17:37881293-37881459 lod=37 SC=364	P=chr17:37881332-37881441 lod=242 SC=575
	P=chr17:41245643-41245801 lod=24 SC=300	
	P=chr18:18534739-18535015 lod=102 SC=514	P=chr18:18534739-18535015 lod=686 SC=695
	P=chr19:2046360-2046459 lod=18 SC=257	P=chr19:2046395-2046435 lod=57 SC=409
	P=chr19:47193855-47193966 lod=47 SC=399	P=chr19:47193933-47193966 lod=73 SC=437

Vertebrate Conserved Elements	SIFT Input	PolyPhen-2 Input	Target Region	Filter
P=chr1:1575696-1575721 lod=75 SC=431	1,1575715,1,C/T	chr1:1575715 C/T	On	FilteredOut
P=chr1:233497835-233497851 lod=98 SC=459	1,233497836,1,C/A	chr1:233497836 C/A	On	FilteredOut
	2,29416635,1,C/A	chr2:29416635 C/A	On	FilteredOut
P=chr2:29448398-29448411 lod=64 SC=414	2,29448410,1,T/G	chr2:29448410 T/G	On	FilteredOut
P=chr2:37336392-37336423 lod=71 SC=425	2,37336419,1,C/T	chr2:37336419 C/T	On	FilteredOut
P=chr2:158485081-158485102 lod=44 SC=374	2,158485099,1,C/A	chr2:158485099 C/A	On	FilteredOut
P=chr2:179408050-179408089 lod=178 SC=523	2,179408086,1,A/G	chr2:179408086 A/G	On	FilteredOut
P=chr2:179634400-179634424 lod=165 SC=515	2,179634421,1,T/G	chr2:179634421 T/G	Near	FilteredOut
P=chr2:209195235-209195421 lod=1204 SC=727	2,209195248,1,C/A	chr2:209195248 C/A	On	FilteredOut
P=chr3:41705176-41705193 lod=37 SC=355	3,41705179,1,A/C	chr3:41705179 A/C	On	FilteredOut
P=chr3:123987956-123988095 lod=990 SC=706	3,123988019,1,C/A	chr3:123988019 C/A	On	FilteredOut
	5,112769527,1,C/T	chr5:112769527 C/T	On	FilteredOut
P=chr5:180048550-180048665 lod=417 SC=614	5,180048626,1,C/T	chr5:180048626 C/T	On	FilteredOut
P=chr6:31947189-31947210 lod=36 SC=352	6,31947203,1,T/C	chr6:31947203 T/C	On	FilteredOut
P=chr6:36489507-36489598 lod=641 SC=660	6,36489585,1,C/A	chr6:36489585 C/A	On	FilteredOut
P=chr6:110942392-110942395 lod=20 SC=289	6,110942394,1,G/T	chr6:110942394 G/T	On	FilteredOut
P=chr7:23808626-23808662 lod=87 SC=446	7,23808650,1,G/T	chr7:23808650 G/T	On	FilteredOut
P=chr7:95216338-95216437 lod=555 SC=645	7,95216415,1,C/A	chr7:95216415 C/A	On	FilteredOut
P=chr7:98490116-98490154 lod=266 SC=566	7,98490141,1,G/C	chr7:98490141 G/C	On	FilteredOut
P=chr7:98547157-98547207 lod=334 SC=590	7,98547196,1,G/T	chr7:98547196 G/T	On	FilteredOut
P=chr7:138145352-138145575 lod=506 SC=635	7,138145436,1,C/A	chr7:138145436 C/A	Near	FilteredOut
P=chr8:8239067-8239104 lod=79 SC=436	8,8239069,1,C/A	chr8:8239069 C/A	On	FilteredOut
	8,144800905,1,A/C	chr8:144800905 A/C	On	FilteredOut
P=chr10:99400467-99400822 lod=1063 SC=714	10,99400747,1,C/A	chr10:99400747 C/A	Near	FilteredOut
P=chr11:46369117-46369389 lod=811 SC=685	11,46369267,1,G/A	chr11:46369267 G/A	Near	FilteredOut
P=chr12:1009639-1009708 lod=312 SC=583	12,1009680,1,C/T	chr12:1009680 C/T	On	FilteredOut
	13,110434668,1,C/A	chr13:110434668 C/A	Near	FilteredOut
P=chr13:110437613-110437827 lod=970 SC=704	13,110437802,1,A/C	chr13:110437802 A/C	Near	FilteredOut
	14,24808802,1,G/T	chr14:24808802 G/T	On	FilteredOut
P=chr15:91436550-91436554 lod=39 SC=361	15,91436551,1,A/G	chr15:91436551 A/G	On	FilteredOut
P=chr15:99250802-99250956 lod=963 SC=703	15,99250895,1,G/T	chr15:99250895 G/T	On	FilteredOut
P=chr16:23690365-23690492 lod=475 SC=628	16,23690401,1,C/T	chr16:23690401 C/T	On	FilteredOut
P=chr16:46744621-46744703 lod=533 SC=640	16,46744689,1,C/A	chr16:46744689 C/A	On	FilteredOut
	17,7796803,1,T/C	chr17:7796803 T/C	Near	Retained
P=chr17:8789798-8789823 lod=69 SC=422	17,8789811,1,G/A	chr17:8789811 G/A	On	FilteredOut
P=chr17:37881332-37881393 lod=348 SC=595	17,37881392,1,A/G	chr17:37881392 A/G	On	FilteredOut
	17,41245693,1,G/T	chr17:41245693 G/T	On	FilteredOut
P=chr18:18534821-18535008 lod=1216 SC=728	18,18534948,1,G/C	chr18:18534948 G/C	On	FilteredOut
P=chr19:2046392-2046402 lod=56 SC=399	19,2046399,1,G/A	chr19:2046399 G/A	On	FilteredOut
P=chr19:47193933-47193946 lod=74 SC=429	19,47193933,1,G/T	chr19:47193933 G/T	On	FilteredOut

Detected Information
QUAL=573.31;BaseQRankSum=5.294;Dels=0.00;FS=265.947;HRun=1;HaplotypeScore=6.0799;MQ=29.71;MQ0=443;QD=0.46;ReadPosRankSum=-8.798;SB=-5.80;culpr
QUAL=524.79;BaseQRankSum=-18.279;Dels=0.00;FS=309.258;HRun=0;HaplotypeScore=4.9625;MQ=59.83;MQ0=0;QD=0.79;ReadPosRankSum=-0.468;SB=0.02;culpr
QUAL=332.51;BaseQRankSum=-20.745;Dels=0.00;FS=337.780;HRun=1;HaplotypeScore=5.1619;MQ=59.89;MQ0=0;QD=0.33;ReadPosRankSum=1.660;SB=-9.26;culpr
QUAL=979.74;BaseQRankSum=-17.907;Dels=0.00;FS=1898.288;HRun=2;HaplotypeScore=4.4822;MQ=59.40;MQ0=0;QD=1.13;ReadPosRankSum=-19.617;SB=4.95;culpr
QUAL=3709.37;BaseQRankSum=-12.727;Dels=0.00;FS=2.030;HRun=3;HaplotypeScore=3.8031;MQ=59.87;MQ0=0;QD=14.84;ReadPosRankSum=-0.449;SB=-1464.96
QUAL=421.85;BaseQRankSum=-25.438;Dels=0.00;FS=707.699;HRun=0;HaplotypeScore=4.8344;MQ=59.88;MQ0=0;QD=0.39;ReadPosRankSum=4.943;SB=-1.54;culpr
QUAL=3677.47;BaseQRankSum=-1.663;Dels=0.00;FS=4.002;HRun=0;HaplotypeScore=5.7074;MQ=59.82;MQ0=0;QD=14.71;ReadPosRankSum=-0.900;SB=-1670.15;
QUAL=706.07;BaseQRankSum=-14.922;Dels=0.00;FS=2.107;HRun=3;HaplotypeScore=4.4521;MQ=59.71;MQ0=0;QD=1.13;ReadPosRankSum=1.953;SB=-0.02;culpr
QUAL=1517.36;BaseQRankSum=-22.562;Dels=0.00;FS=522.570;HRun=0;HaplotypeScore=5.3091;MQ=59.47;MQ0=0;QD=0.76;ReadPosRankSum=4.049;SB=2.32;culpr
QUAL=3364.89;BaseQRankSum=5.867;Dels=0.00;FS=8.801;HRun=0;HaplotypeScore=3.7408;MQ=59.92;MQ0=0;QD=14.14;ReadPosRankSum=1.991;SB=-828.14;culpr
QUAL=259.36;BaseQRankSum=-18.377;Dels=0.00;FS=560.007;HRun=1;HaplotypeScore=3.4076;MQ=59.80;MQ0=0;QD=0.48;ReadPosRankSum=0.921;SB=-9.16;culpr
QUAL=4121.43;BaseQRankSum=3.171;Dels=0.00;FS=5.506;HRun=1;HaplotypeScore=8.3345;MQ=59.87;MQ0=0;QD=16.49;ReadPosRankSum=-1.713;SB=-1960.66;culpr
QUAL=2409.09;BaseQRankSum=3.178;Dels=0.00;FS=1.381;HRun=1;HaplotypeScore=4.6499;MQ=59.90;MQ0=0;QD=15.64;ReadPosRankSum=0.444;SB=-1156.64;culpr
QUAL=3109.97;BaseQRankSum=-6.300;Dels=0.00;FS=7.552;HRun=2;HaplotypeScore=5.4507;MQ=58.27;MQ0=0;QD=12.64;ReadPosRankSum=-0.041;SB=-1112.18;
QUAL=3870.21;BaseQRankSum=-20.116;Dels=0.00;FS=1941.557;HRun=2;HaplotypeScore=33.1896;MQ=59.85;MQ0=0;QD=1.41;ReadPosRankSum=-27.603;SB=2.16
QUAL=2446.12;BaseQRankSum=-22.611;Dels=0.00;FS=782.038;HRun=0;HaplotypeScore=5.0001;MQ=59.89;MQ0=0;QD=1.23;ReadPosRankSum=7.995;SB=4.61;culpr
QUAL=3227.04;BaseQRankSum=-9.916;Dels=0.00;FS=7.553;HRun=0;HaplotypeScore=5.4329;MQ=59.86;MQ0=0;QD=13.06;ReadPosRankSum=-2.052;SB=-1496.81;
QUAL=67.61;BaseQRankSum=-13.302;Dels=0.00;FS=365.410;HRun=2;HaplotypeScore=13.6931;MQ=59.57;MQ0=1;QD=0.18;ReadPosRankSum=-7.862;SB=-9.10;culpr
QUAL=3633.19;BaseQRankSum=9.265;Dels=0.00;FS=6.118;HRun=1;HaplotypeScore=4.3811;MQ=59.85;MQ0=0;QD=14.83;ReadPosRankSum=1.320;SB=-896.31;culpr
QUAL=2691.66;BaseQRankSum=-24.019;Dels=0.00;FS=1056.787;HRun=0;HaplotypeScore=5.1094;MQ=59.81;MQ0=0;QD=0.98;ReadPosRankSum=-0.061;SB=1.78;culpr
QUAL=136.48;BaseQRankSum=-9.911;Dels=0.00;FS=94.576;HRun=0;HaplotypeScore=3.5123;MQ=59.58;MQ0=0;QD=0.50;ReadPosRankSum=2.269;SB=-9.59;culpr
QUAL=1360.21;BaseQRankSum=-22.932;Dels=0.00;FS=1180.475;HRun=0;HaplotypeScore=4.9479;MQ=59.90;MQ0=0;QD=0.61;ReadPosRankSum=4.587;SB=2.96;culpr
QUAL=42.73;BaseQRankSum=-6.493;Dels=0.01;FS=106.584;HRun=7;HaplotypeScore=13.4301;MQ=57.81;MQ0=0;QD=0.40;ReadPosRankSum=-2.113;SB=-14.83;culpr
QUAL=520.95;BaseQRankSum=-13.560;Dels=0.00;FS=42.685;HRun=0;HaplotypeScore=1.8147;MQ=59.84;MQ0=0;QD=0.80;ReadPosRankSum=3.026;SB=-0.42;culpr
QUAL=34.46;BaseQRankSum=1.900;Dels=0.00;FS=28.294;HRun=0;HaplotypeScore=0.2791;MQ=53.17;MQ0=2;QD=0.60;ReadPosRankSum=-1.144;SB=-43.63;culpr
QUAL=435.27;BaseQRankSum=0.964;Dels=0.00;FS=4.690;HRun=0;HaplotypeScore=7.7385;MQ=59.80;MQ0=0;QD=1.74;ReadPosRankSum=-2.318;SB=-11.17;culpr
QUAL=811.33;BaseQRankSum=-12.398;Dels=0.00;FS=419.375;HRun=1;HaplotypeScore=1.8012;MQ=59.86;MQ0=0;QD=1.48;ReadPosRankSum=3.689;SB=2.45;culpr
QUAL=41.85;BaseQRankSum=-11.301;Dels=0.00;FS=31.152;HRun=2;HaplotypeScore=3.0669;MQ=59.70;MQ0=0;QD=1.05;ReadPosRankSum=5.846;SB=-22.01;culpr
QUAL=123.76;BaseQRankSum=-18.862;Dels=0.00;FS=90.892;HRun=0;HaplotypeScore=6.2487;MQ=59.86;MQ0=0;QD=0.68;ReadPosRankSum=2.859;SB=-18.23;culpr
QUAL=191.39;BaseQRankSum=-11.495;Dels=0.00;FS=202.191;HRun=5;HaplotypeScore=3.4566;MQ=59.51;MQ0=0;QD=0.92;ReadPosRankSum=-12.001;SB=0.04;culpr
QUAL=514.21;BaseQRankSum=-25.735;Dels=0.00;FS=609.721;HRun=0;HaplotypeScore=5.4206;MQ=59.78;MQ0=0;QD=0.31;ReadPosRankSum=6.571;SB=-0.50;culpr
QUAL=3664.75;BaseQRankSum=7.793;Dels=0.00;FS=3.463;HRun=0;HaplotypeScore=4.4405;MQ=59.89;MQ0=0;QD=15.27;ReadPosRankSum=0.388;SB=-1489.82;culpr
QUAL=286.56;BaseQRankSum=-23.290;Dels=0.00;FS=1622.388;HRun=2;HaplotypeScore=76.8262;MQ=59.53;MQ0=0;QD=0.29;ReadPosRankSum=-14.603;SB=-11.3
QUAL=72.41;BaseQRankSum=-15.750;Dels=0.00;FS=114.046;HRun=3;HaplotypeScore=84.4069;MQ=52.72;MQ0=0;QD=0.10;ReadPosRankSum=7.617;SB=-8.26;culpr
QUAL=2382.70;BaseQRankSum=-7.417;Dels=0.00;FS=0.000;HRun=0;HaplotypeScore=6.5280;MQ=59.88;MQ0=0;QD=13.02;ReadPosRankSum=0.150;SB=-1305.44;culpr
QUAL=1151.76;BaseQRankSum=4.379;Dels=0.00;FS=3.137;HRun=0;HaplotypeScore=7.2119;MQ=59.86;MQ0=0;QD=4.61;ReadPosRankSum=0.374;SB=-617.79;culpr
QUAL=266.51;BaseQRankSum=-26.169;Dels=0.00;FS=1003.928;HRun=1;HaplotypeScore=4.1925;MQ=59.92;MQ0=0;QD=0.27;ReadPosRankSum=2.767;SB=-10.70;culpr
QUAL=1475.66;BaseQRankSum=-0.511;Dels=0.00;FS=734.419;HRun=0;HaplotypeScore=4.2547;MQ=38.42;MQ0=17;QD=0.99;ReadPosRankSum=2.008;SB=

Genotype	Genotype	Genotype	Genotype	Genotype	Genotype	Genotype	Genotype	Genotype	Genotype	Genotype	Genotype	Genotype	Alleles	Alleles	Alleles
NCC1	CC1	CC1-1	CC1-2	CC1-7	CC1-8	CC1-9	CC1-11	CC1-12	CC1-17	CC1-18	CC1-25	NCC1	CC1	CC1-1	
C/C	C/C	C/C	C/T	C/C	C/T	C/T	C/C	C/T	C/C	C/T	C/C	00	00	00	
C/A	C/C	C/C	C/A	C/A	C/C	C/C	C/A	C/C	C/C	C/C	C/A	01	00	00	
C/A	C/C	C/A	C/C	C/A	C/C	C/C	C/C	C/C	C/C	C/C	C/A	01	00	01	
T/G	T/G	T/G	T/G	T/T	T/T	T/G	T/G	T/T	T/T	T/G	T/G	01	01	01	
C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C	00	00	00	
C/C	C/A	C/C	C/C	C/A	C/C	C/A	C/C	C/A	C/C	C/C	C/A	00	01	00	
A/A	A/A	A/A	A/A	A/A	A/A	A/G	A/A	A/A	A/A	A/A	A/A	00	00	00	
T/T	T/G	T/G	T/G	T/G	T/G	T/G	T/G	T/G	T/T	T/G	T/G	00	01	01	
C/A	C/A	C/A	C/C	C/A	C/C	C/A	C/C	C/A	C/A	C/C	C/A	01	01	01	
A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/C	00	00	00	
C/A	C/A	C/C	C/C	C/A	C/C	C/C	C/C	C/C	C/C	C/C	C/A	01	01	00	
C/C	C/C	C/C	C/C	C/C	C/T	C/C	C/C	C/C	C/C	C/C	C/C	00	00	00	
C/C	C/C	C/T	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	00	00	01	
T/T	T/T	T/T	T/C	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T	00	00	00	
C/A	C/A	C/C	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	C/A	01	01	00	
G/T	G/T	G/T	G/G	G/T	G/T	G/G	G/T	G/T	G/T	G/T	G/G	01	01	01	
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/T	G/G	G/G	G/G	G/G	00	00	00	
C/C	C/C	C/A	C/A	C/A	C/C	C/A	C/C	C/C	C/C	C/C	C/C	00	00	01	
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/C	G/G	G/G	G/G	00	00	00	
G/T	G/G	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	01	00	01	
C/C	C/A	C/A	C/C	C/A	C/C	C/C	C/A	C/C	C/C	C/C	C/A	00	01	01	
C/A	C/A	C/A	C/A	C/A	C/A	C/C	C/A	C/A	C/A	C/A	C/C	01	01	01	
A/A	A/C	A/A	A/C	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/C	00	01	00	
C/C	C/A	C/A	C/A	C/A	C/C	C/C	C/C	C/C	C/A	C/A	C/A	00	01	01	
G/A	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/A	G/G	G/A	G/G	01	00	00	
C/C	C/C	C/C	C/C	C/C	C/T	C/C	C/C	C/C	C/C	C/C	C/C	00	00	00	
C/A	C/A	C/A	C/A	C/A	C/A	C/C	C/A	C/A	C/A	C/A	C/A	01	01	01	
A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/C	A/A	00	00	00	
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/T	G/G	G/G	G/G	G/G	00	00	00	
A/A	A/A	A/G	A/A	A/A	A/G	A/A	A/G	A/A	A/G	A/G	A/A	00	00	01	
G/T	G/G	G/T	G/G	G/T	G/G	G/T	G/G	G/T	G/T	G/T	G/G	01	00	01	
C/C	C/C	C/C	C/T	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	00	00	00	
C/A	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/A	C/C	C/A	C/A	01	00	00	
T/C	T/T	T/T	T/C	T/T	T/C	T/C	T/C	T/T	T/T	T/T	T/T	01	00	00	
G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/A	00	00	00	
A/A	A/G	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A	00	01	00	
G/G	G/T	G/T	G/G	G/T	G/G	G/T	G/G	G/G	G/G	G/G	G/G	00	01	01	
G/G	G/C	G/C	G/C	G/G	G/G	G/G	G/C	G/G	G/C	G/G	G/C	00	01	01	
G/G	G/A	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	00	01	00	
G/G	G/T	G/T	G/G	G/T	G/G	G/G	G/G	G/G	G/G	G/G	G/G	00	01	01	

Alleles	Alleles	Alleles	Alleles	Alleles	Alleles	Alleles	Alleles	Alleles	Depth	Depth	Depth	Depth	Depth	Depth	Depth	Depth	Depth
CC1-2	CC1-7	CC1-8	CC1-9	CC1-11	CC1-12	CC1-17	CC1-18	CC1-25	NCC1	CC1	CC1-1	CC1-2	CC1-7	CC1-8	CC1-9	CC1-11	CC1-12
01	00	01	01	00	01	00	01	00	250	250	250	250	250	250	250	250	250
01	01	00	00	01	00	00	00	01	144	125	111	150	139	142	121	124	146
00	01	00	00	00	00	00	00	01	250	250	245	246	249	250	245	248	250
01	00	00	01	01	00	00	01	01	127	98	95	99	102	100	117	102	101
00	00	00	00	00	00	00	01	00	250	246	232	250	250	250	250	248	250
00	01	00	01	00	01	00	00	01	248	183	188	244	246	232	232	159	239
00	00	00	01	00	00	00	00	00	250	240	240	248	250	250	250	248	242
01	01	01	01	01	01	00	01	01	69	61	49	70	59	72	80	49	76
00	01	00	01	00	01	01	00	01	250	250	249	250	250	250	250	250	248
00	00	00	00	00	00	00	00	01	246	249	249	239	246	248	233	241	239
00	01	00	00	00	00	00	00	01	165	129	117	122	135	123	123	112	120
00	00	01	00	00	00	00	00	00	250	239	243	248	245	250	250	237	250
00	00	00	00	00	00	00	00	00	217	150	154	190	184	180	201	131	176
01	00	00	00	00	00	00	00	00	249	239	250	246	250	250	242	250	250
01	01	01	01	01	01	01	01	01	250	249	250	250	244	250	250	250	248
00	01	01	00	01	01	01	01	00	215	214	228	207	204	237	211	179	235
00	00	00	00	01	00	00	00	00	250	248	250	250	245	246	245	247	250
01	01	00	01	00	00	00	00	00	86	73	83	88	93	87	108	89	113
00	00	00	00	00	01	00	00	00	233	242	243	250	247	242	247	248	245
01	01	01	01	01	01	01	01	01	250	250	250	250	250	250	250	250	250
00	01	00	00	01	00	00	00	01	69	61	51	52	72	67	58	46	66
01	01	01	00	01	01	01	01	00	236	175	204	214	240	250	246	205	218
01	00	00	00	00	00	00	00	01	56	22	27	57	54	49	43	40	46
01	01	00	00	00	00	01	01	01	117	75	87	119	85	106	114	64	99
00	00	00	00	00	01	00	01	00	27	21	15	27	21	17	24	10	12
00	00	01	00	00	00	00	00	00	250	250	250	250	249	250	245	250	250
01	01	01	00	01	01	01	01	01	54	73	47	37	55	55	59	34	42
00	00	00	00	00	00	00	01	00	55	45	25	37	38	43	41	29	51
00	00	00	00	01	00	00	00	00	216	172	194	183	219	228	217	182	226
00	00	01	00	01	00	01	01	00	54	38	39	50	49	55	40	26	51
00	01	00	01	00	01	01	01	00	247	244	246	240	236	242	244	248	239
01	00	00	00	00	00	00	00	00	247	177	188	240	198	244	241	176	221
00	00	00	00	00	01	00	01	01	247	240	250	243	245	248	248	243	248
01	00	01	01	01	00	00	00	00	176	108	108	127	119	144	149	124	166
00	00	00	00	00	00	00	00	01	247	172	182	208	210	198	189	175	244
00	00	00	00	00	00	00	00	00	250	250	241	249	250	250	250	250	250
00	01	00	01	00	00	00	00	00	250	250	250	249	250	249	250	249	250
01	00	00	00	01	00	01	00	01	250	250	250	250	250	250	250	250	247
00	00	00	00	00	00	00	00	00	137	101	79	131	102	103	103	84	106
00	01	00	00	00	00	00	00	00	220	206	163	223	201	223	205	232	221

Depth	Depth	Depth	AllelicDepth	AllelicDepth	AllelicDepth	AllelicDepth	AllelicDepth	AllelicDepth	AllelicDepth	AllelicDepth	AllelicDepth	AllelicDepth	AllelicDepth
CC1-17	CC1-18	CC1-25	NCC1	CC1	CC1-1	CC1-2	CC1-7	CC1-8	CC1-9	CC1-11	CC1-12	CC1-17	
250	250	250	193 56	193 55	189 61	198 50	189 61	182 67	190 60	200 50	192 58	208 42	
125	146	106	113 31	101 24	94 17	117 33	111 27	119 23	105 16	101 21	120 23	102 20	
243	250	249	212 37	223 27	213 32	223 23	201 48	220 30	211 33	216 31	225 24	213 30	
90	144	86	96 31	73 25	72 23	81 18	89 13	90 10	93 24	82 20	83 18	74 16	
250	250	250	250 0	246 0	232 0	250 0	250 0	250 0	250 0	248 0	250 0	250 0	
220	245	188	191 57	144 39	150 38	203 41	191 55	180 52	183 49	131 28	195 44	188 32	
250	250	244	249 0	240 0	240 0	248 0	248 1	250 0	129 121	248 0	242 0	250 0	
55	61	49	36 32	37 24	32 17	34 36	33 25	39 32	44 36	28 21	42 32	32 23	
250	247	250	194 56	204 46	197 52	214 36	193 57	218 32	202 48	217 33	194 54	197 53	
241	245	238	246 0	247 2	249 0	238 1	246 0	248 0	233 0	241 0	238 1	241 0	
144	156	108	140 25	97 32	103 14	101 21	110 25	106 16	108 15	97 15	102 18	118 26	
250	250	249	250 0	239 0	243 0	248 0	245 0	120 129	250 0	236 0	250 0	250 0	
221	207	180	216 0	150 0	75 79	189 0	184 0	180 0	200 1	131 0	176 0	221 0	
250	250	250	249 0	238 0	250 0	132 114	250 0	250 0	242 0	248 0	248 0	250 0	
250	249	249	189 61	203 46	199 51	186 63	190 54	195 55	189 61	189 61	198 49	182 68	
237	246	193	162 53	159 55	171 57	172 35	140 64	196 41	182 29	136 43	181 54	179 58	
250	250	247	250 0	248 0	250 0	250 0	245 0	246 0	245 0	135 111	249 0	250 0	
99	130	90	73 13	66 7	71 12	75 13	74 19	80 7	91 17	80 9	99 14	87 10	
241	249	241	233 0	240 1	243 0	250 0	245 0	242 0	247 0	248 0	132 113	240 1	
250	250	250	202 47	200 50	187 63	181 69	189 60	195 55	190 59	191 59	189 61	198 50	
43	66	45	56 13	41 20	36 12	43 8	55 17	52 14	49 8	34 11	47 17	36 7	
236	250	217	183 53	136 39	156 46	177 36	194 45	206 44	211 35	165 39	181 37	191 44	
47	40	29	44 12	18 4	25 2	39 18	49 5	43 4	38 5	36 4	39 7	40 7	
96	99	91	84 33	56 19	67 20	96 23	64 21	86 20	92 22	59 5	81 18	63 33	
20	18	12	24 3	21 0	15 0	27 0	21 0	15 2	23 1	10 0	9 3	19 1	
250	250	250	249 0	246 2	250 0	250 0	249 0	220 30	244 0	249 0	250 0	249 1	
44	65	42	42 12	51 22	32 15	25 12	42 13	39 16	46 13	27 7	28 13	31 13	
40	40	35	42 13	32 12	18 7	26 11	27 11	33 9	29 12	24 4	43 8	27 13	
212	202	204	185 31	148 24	162 31	167 16	200 19	206 22	186 30	148 34	204 22	189 23	
43	45	36	47 7	33 5	29 10	42 8	44 5	43 12	33 7	19 7	46 5	33 10	
228	244	246	188 59	187 57	188 58	203 37	185 51	194 46	197 47	211 36	199 39	197 31	
226	249	174	247 0	177 0	188 0	119 121	198 0	244 0	241 0	176 0	221 0	224 0	
245	240	248	188 58	201 38	215 35	193 49	199 46	204 44	198 50	204 39	198 50	204 38	
161	151	128	125 50	74 32	71 36	92 35	89 30	108 36	110 38	93 31	122 43	117 43	
182	233	183	246 1	172 0	181 0	208 0	209 0	198 0	189 0	175 0	244 0	182 0	
250	250	250	249 1	195 54	241 0	249 0	249 0	249 1	249 0	250 0	249 0	250 0	
250	250	249	206 43	199 51	202 48	207 42	202 48	207 42	204 45	213 36	217 33	201 48	
250	250	248	232 18	217 33	220 29	217 33	230 19	231 19	229 20	215 34	226 20	220 30	
111	142	90	137 0	91 10	79 0	131 0	102 0	103 0	103 0	83 0	106 0	111 0	
237	193	207	189 30	158 48	127 36	185 37	158 43	195 27	182 23	210 22	185 35	203 34	

AllelicDepth	AllelicDepth	GenotypeQuality	GenotypeQuality	GenotypeQuality	GenotypeQuality	GenotypeQuality	GenotypeQuality	GenotypeQuality
CC1-18	CC1-25	NCC1	CC1	CC1-1	CC1-2	CC1-7	CC1-8	CC1-9
191 59	185 64	53.64	27.35	38	72.84	2	99	99
123 21	83 23	48.18	21.41	99	99	99	29.63	22.04
221 29	208 41	78.41	99	40.41	99	99	99	48.32
120 24	68 18	99	26.72	99	99	32.5	74.69	46.29
129 121	250 0	99	99	99	99	99	99	99
194 51	148 40	99	99	6.21	62.21	90.36	66.4	99
250 0	244 0	99	99	99	99	99	99	99
30 31	28 20	70.41	44.09	99	51.41	95.08	82.82	85.83
224 23	197 53	99	99	99	30.44	99	67.31	99
245 0	132 106	99	99	99	99	99	99	99
121 35	88 20	73.74	99	81.74	77.49	3.89	18.31	65.29
250 0	249 0	99	99	99	99	99	99	99
207 0	179 0	99	99	99	99	99	99	99
250 0	249 0	99	99	99	99	99	99	99
179 70	186 63	99	99	18.41	99	99	99	99
191 52	161 32	99	99	99	99	99	51.03	45.95
250 0	246 1	99	99	99	99	99	99	99
110 20	77 12	57.7	99	11.46	10.29	46.1	99	61.68
247 0	241 0	99	99	99	99	99	99	99
207 43	198 52	67.67	11.5	99	99	99	99	99
56 10	38 7	16.91	89.69	59.58	9.05	6.43	1.08	60.07
198 52	179 37	55.76	99	99	99	99	99	8.38
32 8	20 9	38.82	7	43.52	66.66	91.09	99	74.32
75 24	69 22	3.16	99	57.12	19.58	35.47	18.77	79.57
13 5	12 0	7.16	48.11	42.09	66.14	63.13	3.38	41.39
250 0	249 0	99	99	99	99	99	99	99
42 23	34 8	58.19	99	85.13	62.35	21.37	32.15	24.38
25 15	25 10	89.32	71.01	51.04	39.86	28.73	32.88	14.01
174 28	183 21	2.23	99	99	99	99	99	37.2
39 6	31 5	99	24.33	84.15	30.31	51.45	53.19	69.02
201 43	202 44	99	28.22	62.6	99	99	99	23.2
249 0	174 0	99	99	99	99	99	99	99
191 49	206 42	99	99	99	15.14	33.07	99	59.77
103 46	91 36	1.68	14.9	6.58	72.3	11.2	7.86	25.19
233 0	95 87	99	99	99	99	99	99	99
249 1	250 0	99	99	99	99	99	99	99
215 35	205 44	73.5	99	4.18	17.87	99	50.14	8.39
230 20	218 28	99	99	99	99	99	99	59.59
142 0	90 0	99	99	99	99	99	99	99
160 33	178 29	99	20.17	94.29	63.84	99	99	99

GenotypeQuality CC1-11	GenotypeQuality CC1-12	GenotypeQuality CC1-17	GenotypeQuality CC1-18	GenotypeQuality CC1-25
99	35.3	99	99	74.33
99	43.11	59.9	87.85	17.88
99	99	99	99	99
99	37.11	6.24	99	99
99	99	99	99	99
9.72	83.09	99	99	52.28
99	99	99	99	99
66.88	61.16	32.55	99	56.12
99	99	99	99	99
99	99	99	99	99
99	4.79	82.5	13.4	99
99	99	99	99	99
99	99	99	99	99
99	99	99	99	99
99	99	99	99	99
99	99	99	99	99
99	88.14	99	34.27	87.47
99	99	99	99	99
99	99	93.38	99	99
36.56	69.16	14.39	45.71	6.8
59.52	19.72	99	99	48.87
37.09	43.79	87.39	52.11	24.51
67.76	87.23	99	93.77	99
24.05	51.13	20.98	31.34	27.05
99	99	99	99	99
36.22	91	59.85	99	21.92
10.65	14.08	59.46	82.56	53.46
99	99	99	99	91.63
71.96	65.3	23.85	26.31	15.34
55.28	10.23	0.71	52.97	99
99	99	99	99	99
99	16.6	99	99	0.58
26.1	64.6	34.09	3.53	59.18
99	99	99	99	99
99	99	99	99	99
99	99	60.28	50.65	99
99	84.15	99	99	99
99	99	99	99	99
99	94.35	99	53.03	38.86