

ProbeName	pvalues	foldchange	SI1_NS	SI2_NS	SI3_NS	SI1_flags	SI2_flags	SI3_flags
NC1_NS	NC2_NS	NC3_NS	NC1_flags	NC2_flags	NC3_flags	ProbeName.1	Type	
ProbeSeq	Accession	Source	Chromosome	Strand	Start	End	GeneSymbol	Gene_ID
Description	GO	Relation	Associated_gene	Associated_gene_description				
Associated_gene_strand	circRNA_ID	circ_chrom	Hsa_hg19_circRNA_start					
Hsa_hg19_circRNA_end	Hsa_hg19_circRNA_strand	genomic_length	spliced_seq_length					
LNCV6_54679_PI430048170	0.00000736099447		3.48267656	6.73247198	6.87016719			
6.74917073	P	P	P	4.96121830	5.05854957	4.93235146	P	P
LNCV6_54679_PI430048170	mRNA							
CCATGACACTCACAGAACATTACAACCTTTATTATGGGTGAGAGCTTCACTACAACCTTT	NM_001012758							
RefSeq chr1 + 145845632	145848575	NUDT17	NA	nudix (nucleoside diphosphate				
linked moiety X)-type motif 17	NA	.	NA	-	.	NA	NA	NA
NA	NA	NA						
LNCV6_141047_PI430048170	0.00000837684809		6.94283085	9.82414714	9.63306445			
9.81701041	P	P	P	6.83974790	7.08143479	6.96436885	P	P
LNCV6_141047_PI430048170	mRNA							
GGGCTTAAGATTCCAGACTCTGATTCACTAACTATAGTCACCCGTGTCCTGTGAAAAAA	NM_006744							
RefSeq chr10 - 93591835	93601236	RBP4	5950	"retinol binding protein 4, plasma"				
GO:0005515 GO:0060044 GO:0060065 GO:0007603 GO:0030324 GO:0001654 GO:0045471 GO:006006								
8 GO:0048706 GO:0016918 GO:0006094 GO:0007283 GO:0019841 GO:0005615 GO:0005829 GO:0007								
507 GO:0030277 GO:0050908 GO:0042574 GO:0042572 GO:0048807 GO:0032024 GO:0032526 GO.								
NA	-	.	NA	NA	NA	NA	NA	NA
LNCV6_135367_PI430048170	0.00001879954572		3.14282753	7.87009177	7.79376228			
7.86740375	P	P	P	6.24953778	6.20811409	6.11546151	P	P
LNCV6_135367_PI430048170	mRNA							
GTCTTGGTTGAGAGAATAACGTTGCAGTTCCACAGGGCATGTGACTTTGAAAGAGACTA	NM_001197247							
RefSeq chr6 + 26365158	26378320	BTN3A2	11118	"butyrophilin, subfamily 3,				
member A2, transcript variant 3"	GO:0072643 GO:0016020 GO:0005886 GO:0016021 GO:0002456							
NA	-	.	NA	NA	NA	NA	NA	NA
LNCV6_140877_PI430048170	0.00002004557190		2.04495827	9.27865160	9.28693835			
9.37290872	P	P	P	8.33604173	8.22526754	8.28074982	P	P
LNCV6_140877_PI430048170	mRNA							
AGGGACTTAGTTATATCTTCAGACCAGTGCAGCTGGTACACACAAAGTTCTCCTGTCTCA	NM_001081492							
RefSeq chr12 - 52168995	52192000	KRT80	144501	"keratin 80, type II, transcript				
variant 2"	GO:0030057 GO:0005882 GO:0005737 GO:0005198 GO:0045095							
NA	NA	NA	NA	NA	NA	NA	NA	NA
LNCV6_138728_PI430048170	0.00002629365452		2.77181996	9.24338740	9.26184125			
9.22766279	P	P	P	7.81528786	7.76765061	7.73656350	P	P
LNCV6_138728_PI430048170	mRNA							
GTAATTGTGGCTTGCTAGTATGTTTTATGATAATCTCGGGCATTGTTTGCATTGTGTTT	NM_013412							
RefSeq chr2 + 113627228	113643398	RABL2A	11159	"RAB, member of RAS oncogene				
family-like 2A, transcript variant 1"								
GO:0008152 GO:0003924 GO:0032482 GO:0019003 GO:0005525 GO:0006886 GO:0012505								
-	.	NA	NA	NA	NA	NA	NA	NA
LNCV6_135816_PI430048170	0.00003153981403		2.81025909	10.24318015	10.18940791			
10.11669989	P	P	P	8.65130940	8.71277637	8.71497813	P	P
LNCV6_135816_PI430048170	mRNA							
CCCGATGTTCTTGATTTTCCAGAGAAGCAAATAAACAGCGTGAACAGCCCCAGAAAAAA	NM_002579							
RefSeq chr19 + 708952	748330	PALM	5064	"paralemmin, transcript variant 1"				

GO:0005796|GO:0005578|GO:0016266|GO:0005615|GO:0031982|GO:0005176|GO:0006493|GO:0007160|GO:0016020|GO:0030197|GO:0030277|GO:0005887|GO:0044267|GO:0070062|GO:0043687 .
NA - . NA NA NA NA NA NA NA NA
LNCV6_138727_PI430048170 0.00003492589810 2.90419033 7.33781886 7.17727684
7.20231437 P P P 5.73615818 5.73840185 5.63108051 P P P
LNCV6_138727_PI430048170 mRNA
GTTAGGAATACACAAGCCGTAATCGAGTCCTTACAGCCATACCACAAGGTACGTCCAT NM_001130921
RefSeq chr22 - 50767491 50783659 RABL2B NA "RAB, member of RAS oncogene
family-like 2B, transcript variant 5" NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_142964_PI430048170 0.00003877028232 2.06451955 6.82802667 6.93983335
6.87807581 P P P 5.91156157 5.80851840 5.78753642 P P P
LNCV6_142964_PI430048170 mRNA
AGTTTTGGTGTGACTGGACATACTTGCTTCAATAAAAGAATACATCACTCCCCTCAAAAA NM_001282862
RefSeq chr10 - 43194532 43229739 RASGEF1A 221002 "RasGEF domain family,
member 1A, transcript variant 1"
GO:0005622|GO:0032320|GO:0016477|GO:0007264|GO:0046579|GO:0005088 . NA - .
NA NA NA NA NA NA NA NA NA NA
LNCV6_133029_PI430048170 0.00004916235966 2.42353898 6.23219270 6.34211435
6.38365684 P P P 5.13500339 5.02679143 4.96381588 P P P
LNCV6_133029_PI430048170 mRNA
AGCTTGACCTTTGACTTCTGACCCTCTCATCCTGGATGGTGTGTGGTGGCACAGGAACC NM_014266
RefSeq chr19 + 35902479 35904271 HCST 10870 "hematopoietic cell signal
transducer, transcript variant 1"
GO:0005515|GO:0009986|GO:0005886|GO:0050776|GO:0005102|GO:0014068|GO:0016021|GO:0043548 . NA - .
NA NA NA NA NA NA NA NA NA NA NA NA
LNCV6_135017_PI430048170 0.00005471680711 3.07537653 6.31480382 6.38948562
6.23337125 P P P 4.59918407 4.80683769 4.66571803 P P P
LNCV6_135017_PI430048170 mRNA
TTTTTAATTGCCAACTGCTCTCTTCATCAGCTCAGCACATGCTTTAAGAAAGCAAAACC NM_052854
RefSeq chr11 + 46277637 46321422 CREB3L1 90993 cAMP responsive element binding
protein 3-like 1
GO:0043565|GO:0030500|GO:0001077|GO:0035497|GO:0005783|GO:0045944|GO:0003682|GO:0005789|GO:0005634|GO:0016021|GO:0006351|GO:0030968 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_144719_PI430048170 0.00005536260418 2.41046192 5.62388056 5.59957940
5.47942864 P P P 4.35384609 4.29290884 4.25043575 P P P
LNCV6_144719_PI430048170 mRNA
ATGGAGGTGTAGGCTGGAGAGACATTGTGGGTGTGTATCTTCTTATCTCATTTTACAAGA NM_001271749
RefSeq chr19 + 47332146 47342015 C5AR2 27202 "complement component 5a
receptor 2, transcript variant 1"
GO:0005515|GO:0050679|GO:2000482|GO:0004944|GO:0005886|GO:0032720|GO:0045177|GO:0006954|GO:0009925|GO:1900165|GO:0006935|GO:0007186|GO:0090024|GO:0016021|GO:0070374 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133332_PI430048170 0.00006031310338 4.88644009 9.02245243 9.10719336
8.93433643 P P P 6.73833785 6.86148456 6.59024441 P P P
LNCV6_133332_PI430048170 mRNA
TTGTCGCTGCAGCCAACTTTGCCATTAAACTCTTTGCCAAAGTTTGCACCTGTAAAAAA NM_031297
RefSeq chr9 - 137220246 137221323 RNF208 727800 ring finger protein 208
GO:0005737|GO:0004842|GO:0008270|GO:0005654|GO:0051865 . NA - . NA NA
NA NA NA NA NA NA
LNCV6_130901_PI430048170 0.00007875732583 3.63439788 7.68098066 7.93061011
7.73792568 P P P 5.75791119 5.98702797 6.01773533 P P P
LNCV6_130901_PI430048170 mRNA
TACTTTTCTCCTAAGTCTACCCTGGACACTTTTTAGGGCACCTGGAGAGAACTTTCCTCT NM_178570
RefSeq chr11 + 57460536 57477539 RTN4RL2 349667 reticulon 4 receptor-like 2
GO:0031103|GO:0009986|GO:0045121|GO:0004872|GO:0046658|GO:0009897|GO:0070062 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_139260_PI430048170 0.00008002366530 6.57061212 7.39677544 7.61536566
7.77104251 P P P 5.04649473 4.64372259 4.93964699 P P P
LNCV6_139260_PI430048170 mRNA

CATGGGCAGGTACTGACTGAAGATGCAATCCAACCAAAGCCATTACATTTTTTTGAGTTAG NM_001860
RefSeq chr9 + 113150957 113164142 SLC31A2 1318 "solute carrier family 31 (copper transporter), member 2"
GO:0006878|GO:0005887|GO:0005770|GO:0005375|GO:0035434|GO:0055037|GO:0006825 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_94401_PI430048170 0.00008117463470 3.23980687 7.51799909 7.54181527
7.53708752 P P P 5.88597065 5.80139529 5.82055312 P P P
LNCV6_94401_PI430048170 mRNA
ACTGCGAGAACTGCAAGACCACTTTGGGCTGGAAATATGAACAGGCCTTTGAGAGCAGCC NM_031477
RefSeq chr16 - 30092313 30096200 YPEL3 83719 "yippee-like 3 (Drosophila), transcript variant 1"
GO:0005730 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_130913_PI430048170 0.00008288335245 3.98529463 6.77049150 6.76189192
6.58189276 P P P 4.60862190 4.87490186 4.63947732 P P P
LNCV6_130913_PI430048170 mRNA
AAATTGAGAGTGGCAGCTGCCTGCCAAATCTGTTCCGCTGTAAACAGAACTGAATTTGGA NM_004843
RefSeq chr19+ 14031739 14052905 IL27RA 9466 "interleukin 27 receptor, alpha"
GO:0048302|GO:0032729|GO:0006955|GO:0002829|GO:0050830|GO:0005887|GO:0002827|GO:0045509|GO:0007166|GO:0070106|GO:0004888 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_142490_PI430048170 0.00009706309111 3.25751641 8.71837419 8.87972915
8.67974862 P P P 6.96060299 7.20841939 6.99260676 P P P
LNCV6_142490_PI430048170 mRNA
TTCCTGGCTCTAAGGCTCGTCTGTGTAAACCCATAAAACCTGCTTTGATTCCAAAATGAGG NM_001271082
RefSeq chr5_KI270792v1_alt + 27468 57319 NKD285409 "naked cuticle homolog 2 (Drosophila), transcript variant 2"
GO:0005515|GO:0072661|GO:0005509|GO:0032436|GO:0031410|GO:0006887|GO:0016328|GO:0071944|GO:0016323|GO:0010954|GO:0019838|GO:0048210|GO:0016023|GO:0016055|GO:0090090|GO:0031625|GO:0090004 . NA - . NA NA NA NA NA NA NA NA
LNCV6_140478_PI430048170 0.00010502856772 2.73401476 4.00615512 3.89578134
4.02104377 P P P 2.41330071 2.53101479 2.62130476 A P P
LNCV6_140478_PI430048170 mRNA
TCAGAGAAATTATTGACCAGTTTGAGGAGAACATGCCTGTATTAAGGGCCGAGGTGGAAG NM_080571
RefSeq chr20- 270862 290778 C20orf96 140680 "chromosome 20 open reading frame 96, transcript variant 2" NA . NA - . NA NA NA NA NA NA NA NA
LNCV6_143952_PI430048170 0.00010510639277 2.33640759 7.65217981 7.84488901
7.70137000 P P P 6.59824008 6.49406988 6.43553734 P P P
LNCV6_143952_PI430048170 mRNA
GCTCATGCACAGTTTAGGCCATGTACAGCTGGCATCTAATAAATGTTTTTCATGAAAAAGA NM_181304
RefSeq chr14+ 22829882 22835037 MRPL52 122704 "mitochondrial ribosomal protein L52, transcript variant 4"
GO:0070124|GO:0070125|GO:0070126|GO:0032543|GO:0006996|GO:0003735|GO:0005743|GO:0006412|GO:0005762 . NA - . NA NA NA NA NA NA NA NA
LNCV6_59586_PI430048170 0.00010642287418 4.50292638 7.37775858 7.52215739
7.19842671 P P P 5.13633906 5.39474883 5.05014620 P P P
LNCV6_59586_PI430048170 mRNA
TGACTTATTTGACTGAGACTGGGGTCTCTACTTCACCAAACCTGGCCTCTATCCATACCAA NM_004658
RefSeq chr12- 113098818113136239RASAL1 8437 "RAS protein activator like 1 (GAP1 like), transcript variant 2"
GO:0035556|GO:0005099|GO:0046580|GO:0007165|GO:0005737|GO:0005543|GO:0032320|GO:0005886|GO:0031235|GO:0046872|GO:0005829 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130365_PI430048170 0.00011157126480 6.62140344 3.61731328 3.75533591
3.32674888 P P P 0.75953695 0.66570065 1.09010965 A A A
LNCV6_130365_PI430048170 mRNA
ATGGACTCCACATTTGAGCTCTGCAAGATCTGTGCTGAGAGCAACAAGGATGTGAAGATT NM_012116
RefSeq chr19+ 44777868 44800646 CBLC 23624 "Cbl proto-oncogene C, E3 ubiquitin protein ligase, transcript variant 1"
GO:0005154|GO:0017124|GO:0016567|GO:0016874|GO:0005509|GO:0042059|GO:0005634|GO:0042787|GO:0043407|GO:0007175|GO:0001784|GO:0008270|GO:0004871|GO:0007166|GO:0070062 . NA
- . NA NA NA NA NA NA NA NA NA

LNCV6_141579_PI430048170 0.00011284993251 7.83977617 3.60846311 3.45107335
3.25999539 P P P 0.53025198 0.36725913 0.52472183 A A A
LNCV6_141579_PI430048170 mRNA
ACTCCTGTGTACTTCACATCACTGAGCACTCATTTAGAAGTGAGGGAGACAGAAGTCTAG NM_001039803
RefSeq chr9 - 87966443 87974780 CDK20 23552 "cyclin-dependent kinase 20,
transcript variant 3"
GO:0005515|GO:0005929|GO:0007049|GO:0005737|GO:0051726|GO:0007275|GO:0006468|GO:000563
4|GO:0005524|GO:0051301|GO:0004693 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_133285_PI430048170 0.00011453519720 4.25561493 7.91852935 8.08683099
8.16022608 P P P 5.86599401 6.15644398 5.86564503 P P P
LNCV6_133285_PI430048170 mRNA
CTTGGCTGATGTTCTGTATCTTAACATGACCACAGTTTGTAAGTACAAAGGTAATTGGTA NM_152365
RefSeq chr1 - 26949555 26960410 KDF1 126695 keratinocyte differentiation factor 1
GO:0010839|GO:0060887|GO:0030054|GO:0010482|GO:0061436|GO:2000647|GO:0003334|GO:000573
7|GO:0045606|GO:0048589|GO:0016331|GO:0005938|GO:0031252 . NA - . NA NA
NA NA NA NA NA NA NA NA
LNCV6_130492_PI430048170 0.00011699533310 4.05249233 6.08463547 6.07859027
5.93408594 P P P 4.01245828 3.98267801 4.04993565 P P P
LNCV6_130492_PI430048170 mRNA
AGATGGGACTTCAGGGAGACCTGGCTTGGGCTAAAATCGAAATACAATATATATAGGCTG NM_001672
RefSeq chr20+ 34260364 34269342 ASIP 434 agouti signaling protein
GO:0008343|GO:0032438|GO:0005102|GO:0007267|GO:0006091|GO:0005615|GO:0032402|GO:004003
0|GO:0007165|GO:0009755|GO:0042438|GO:0071514|GO:0031781|GO:0031782 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136873_PI430048170 0.00011702556459 5.93632286 4.59181653 4.87270558
4.63063350 P P P 2.25084988 2.23740815 1.88567978 A A A
LNCV6_136873_PI430048170 mRNA
GAGGTTGAATAGGAGTTCTCCTGGAGCAACTTGAGGGTAATAATGATGATGATATAATAA NM_006179
RefSeq chr19- 49061139 49063867 NTF4 4909 neurotrophin 4
GO:0008344|GO:0061193|GO:0005166|GO:0042490|GO:0007616|GO:0007267|GO:0005576|GO:006038
4|GO:0043524|GO:0008052|GO:0008544|GO:0007402|GO:0048812|GO:0045664|GO:0005788|GO:0016
023|GO:0007169|GO:0008083 . NA - . NA NA NA NA NA NA NA NA
LNCV6_143586_PI430048170 0.00013485023826 16.34352716 7.14565012 7.75377589
7.25583477 P P P 3.75519222 3.18322466 3.11021414 P P P
LNCV6_143586_PI430048170 mRNA
AGGGACCGGCAGCCCTGGAAGGGGCACTTGATATTTTTCAATAAAAGCCTTTCGTTTTGC NM_001306
RefSeq chr7 - 73768996 73770270 CLDN3 1365 claudin 3
GO:0003382|GO:0007165|GO:0001666|GO:0016338|GO:0005887|GO:0005198|GO:0016021|GO:000592
3|GO:0016328|GO:0070062|GO:0042802|GO:0004888 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_143181_PI430048170 0.00014986941884 2.18171891 6.20990635 6.15800966
6.33520322 P P P 5.17859853 5.15484551 4.99201887 P P P
LNCV6_143181_PI430048170 mRNA
GAGTTGCTCCTTTGTTCCAAAATTAAATGTGTTAGATAAATTTGTGATTGTATGGGTGGC NM_002857
RefSeq chr1 - 160276808 160285151 PEX19 5824 "peroxisomal biogenesis factor 19,
transcript variant 1"
GO:0005515|GO:0006625|GO:0072663|GO:0005634|GO:0045046|GO:0031526|GO:0005829|GO:004323
1|GO:0005737|GO:0007031|GO:0051117|GO:0072321|GO:0016557|GO:0005778|GO:0016559|GO:0005
777|GO:0050821|GO:0055085|GO:0036105|GO:0043234|GO:1900131|GO:0047485|GO:0061077|GO.
NA - . NA NA NA NA NA NA NA NA
LNCV6_135234_PI430048170 0.00015174052117 4.47900207 4.70704506 4.60591968
4.32894044 P P P 2.57525819 2.25589814 2.32745456 P A P
LNCV6_135234_PI430048170 mRNA
TACTGTAATTGGCTCTTAAGGCTTGAAGTAACCTTATAGGTTACTCATAAGGCATATACA NM_000433
RefSeq chr1 - 183555561 183590604 NCF2 4688 "neutrophil cytosolic factor 2, transcript variant
1"
GO:0045730|GO:0005515|GO:0002474|GO:0006801|GO:0045777|GO:0032870|GO:0005829|GO:000573
7|GO:0043525|GO:0032496|GO:0032010|GO:0090382|GO:0042554|GO:0048010|GO:0014823|GO:0051
701|GO:0001669|GO:0042493|GO:0007568|GO:0005730|GO:0042590|GO:0009055|GO:0008022|GO.
NA - . NA NA NA NA NA NA NA NA

LNCV6_142969_PI430048170 0.00015712129624 3.03032534 8.29889601 8.41685635
 8.41786102 P P P 6.90642090 6.74161698 6.68082779 P P P
 LNCV6_142969_PI430048170 mRNA
 TTGCCATGGACTACCTTTGCTAAGAAAAGTCTGAATGAGAAGATGGCAGGACGTCTGAAA NM_138720
 RefSeq chr6 + 26158120 26171348 HIST1H2BD 3017 "histone cluster 1, H2bd, transcript
 variant 2"
 GO:0003674|GO:0046982|GO:0006325|GO:0005654|GO:0005634|GO:0000786|GO:0003677|GO:007006
 2 NA NA NA NA NA NA NA NA NA NA NA
 LNCV6_133741_PI430048170 0.00016135316658 2.16861479 6.10294232 6.10994432
 6.26454381 P P P 4.95056818 5.15321639 5.02180498 P P P
 LNCV6_133741_PI430048170 mRNA
 TGAATGTTAGAAGGGCATCTTGTACATCCACTGGGAATAAATTGCCTTGCCTTGGAAA NM_001258397
 RefSeq chr17+ 44899711 44903679 CCDC103 388389 "coiled-coil domain containing 103,
 transcript variant 4"
 GO:0060287|GO:0001947|GO:0036159|GO:0005737|GO:0031514|GO:0005930|GO:0030030|GO:003615
 8|GO:0003341|GO:0070286|GO:0071907|GO:0042803 NA NA NA NA NA NA NA NA
 NA NA NA NA
 LNCV6_136493_PI430048170 0.00016203419182 4.06632865 11.79082266 11.78665939
 11.85886233 P P P 9.69192540 9.89080743 9.77665148 P P P
 LNCV6_136493_PI430048170 mRNA
 GGGAGTGACCAGAAGAAATGACGCAGAAAGTGAAATGAACTTTTTATAAGCATTCTTTTAA NM_005218
 RefSeq chr8 - 6870575 6878007 DEFB1 1672 "defensin, beta 1"
 GO:0002526|GO:0005796|GO:0050830|GO:0005576|GO:0033574|GO:0005615|GO:0002227|GO:000961
 7|GO:0006955|GO:0006935|GO:0007186|GO:0045087|GO:0019731|GO:0070062 NA NA
 NA NA NA NA NA NA NA NA NA
 LNCV6_136530_PI430048170 0.00016481480158 2.54756315 5.01165374 5.23983386
 5.17135530 P P P 3.92721760 3.68661500 3.76043104 P P P
 LNCV6_136530_PI430048170 mRNA
 TACTGTTCTCTTTTCATATGTAGGAGGGTTTAAAAGTTCAGCGAATGGGCAAGGTACAAA NM_153376
 RefSeq chr4 - 7040849 7043001 CCDC96 257236 coiled-coil domain containing 96 NA
 NA NA NA NA NA NA NA NA NA
 LNCV6_138248_PI430048170 0.00017339728971 2.59650837 8.73817306 8.82628143
 8.63396267 P P P 7.37767891 7.46754822 7.21899342 P P P
 LNCV6_138248_PI430048170 mRNA
 GCTCTCTGAACAAGTTGAAAGTCCAAATAAACTTACCTGTTCCATCTGTGCTCAAAAAA NM_014726
 RefSeq chr17+ 47695263 47712063 TBKBP1 9755 TBK1 binding protein 1
 GO:0005515|GO:0045087 NA NA NA NA NA NA NA NA NA NA NA
 LNCV6_143991_PI430048170 0.00018232893488 2.77305803 8.94077959 9.14037977
 9.19661438 P P P 7.47457679 7.64612089 7.74234571 P P P
 LNCV6_143991_PI430048170 mRNA
 CAATCTCTAGTTGTCACCTTTCTCTTCCACTTTGATACCATTGGGTCATTGAATATAACT NM_001733
 RefSeq chr12- 7080210 7092447 C1R 715 "complement component 1, r subcomponent"
 GO:0005515|GO:0006956|GO:0006955|GO:0004252|GO:0045087|GO:0006958|GO:0005509|GO:000650
 8|GO:0008236|GO:0072562|GO:0005576|GO:0070062 NA NA NA NA NA NA NA NA
 NA NA NA NA
 LNCV6_141483_PI430048170 0.00019347208084 2.45023426 5.58129631 5.33355463
 5.47967638 P P P 4.23132552 4.04440825 4.24228009 P P P
 LNCV6_141483_PI430048170 mRNA
 GGAAAAATAAAAGTTGACTGTACTAAAAATGTATACTTGTTGCCAGGAAGGTGACCTCAA NM_000676
 RefSeq chr17+ 15944916 15975896 ADORA2B 136 adenosine A2b receptor
 GO:0032755|GO:0007588|GO:0005886|GO:0007254|GO:0032722|GO:0010575|GO:0060087|GO:004330
 6|GO:0000187|GO:0001609|GO:0007190|GO:0006968|GO:0001973|GO:0007186|GO:0005887|GO:0031
 668|GO:0031284|GO:0007189|GO:0002882 NA NA NA NA NA NA NA NA
 NA NA
 LNCV6_132186_PI430048170 0.00020209695913 3.51214004 4.09213949 3.74808799
 3.97202016 P P P 2.30941157 2.07718539 1.99033482 A A A
 LNCV6_132186_PI430048170 mRNA
 CCAAGGATGGAGAACAACCTTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAAT NM_017625
 RefSeq chr1 - 160876539160885170ITLN1 55600 intelectin 1 (galactofuranose binding)
 GO:0043235|GO:0046326|GO:0001934|GO:0030246|GO:0045121|GO:0031526|GO:0031225|GO:000962
 4|GO:0070062 NA NA NA NA NA NA NA NA NA NA

LNCV6_64717_PI430048170 0.00020360573148 8.41793723 9.18211170 9.34665973
9.29441379 P P P 6.39379217 6.16353422 6.02619531 P P P
LNCV6_64717_PI430048170 mRNA
AGCTATGTCAATGGTCTTCCCCAGTCTGATGTGTGTAATAAATGGTCACTGTCAAAGGA NM_001039876
RefSeq chr19- 36003099 36008770 SYNE4 163183 "spectrin repeat containing, nuclear
envelope family member 4, transcript variant 1" GO:0034993|GO:0031309|GO:0045198. NA -
. NA NA NA NA NA NA NA NA NA NA
LNCV6_127952_PI430048170 0.00020376133377 3.05147519 5.25855586 5.56203982
5.38468016 P P P 3.95223477 3.77360836 3.65112245 P P P
LNCV6_127952_PI430048170 mRNA
TTAAGCAGATAACCAAAGGGAGTTTCGTGATGGAGTGTACACGTTTATGCAGGTGTGTG NM_001286732
RefSeq chr13- 113324842 113364148 GRTP1 79774 "growth hormone regulated TBC
protein 1, transcript variant 2" GO:0032851|GO:0005097 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_144351_PI430048170 0.00022734017095 2.50868048 12.58773596 12.76001270
12.69734705 P P P 11.49651478 11.29117051 11.27089866 P P P
LNCV6_144351_PI430048170 mRNA
GAGAGAAAATTTTGTCTCTTGTCTTAGAGTTGTGTGTAAATCAAGGAAGCCATCATTA NM_001288565
RefSeq chr1 - 201134770 201154555 TMEM9 252839 "transmembrane protein 9, transcript
variant 3"
GO:0008150|GO:0003674|GO:0005770|GO:0031902|GO:0006810|GO:0016021|GO:0005765|GO:000576
4 . NA - . NA NA NA NA NA NA NA NA
LNCV6_139228_PI430048170 0.00022777076646 2.05854224 9.94477967 9.86925669
10.06497549 P P P 8.97924826 8.84223677 8.93606055 P P P
LNCV6_139228_PI430048170 mRNA
CAAGAAGAAATAGGCGAACGCCTACTTCTAAAACCCAAAAGGCTCTTTTCAGAGCCACCA NM_005319
RefSeq chr6 - 26055739 26056471 HIST1H1C 3006 "histone cluster 1, H1c"
GO:0005515|GO:0005719|GO:0006334|GO:0016584|GO:0005634|GO:0000786|GO:0031490 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_135996_PI430048170 0.00022778822786 5.12368600 4.23358210 4.67806843
4.37878684 P P P 2.29660341 2.08656158 1.83510645 A A A
LNCV6_135996_PI430048170 mRNA
AAGTGACTTTTTACAGAAGCCACTGAACCTGGTTATTTTGGCAAATCGTCCGTCTCGAGG NM_001284260
RefSeq chr7 - 151381120 151410038 WDR86 349136 "WD repeat domain 86, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA
LNCV6_81359_PI430048170 0.00023009386165 2.10277355 11.74336475 11.86058136
11.94033054 P P P 10.66071260 10.79140847 10.87407278 P P P
LNCV6_81359_PI430048170 mRNA
TTCTCCTAGACCCGTGACCTGAGATGTGTGATTTTTAGTCATTAAATGGAAGTGTCTGCC NM_004878
RefSeq chr9 - 129738335 129753065 PTGES 9536 prostaglandin E synthase
GO:0019369|GO:0019371|GO:0014070|GO:0048471|GO:0002526|GO:0006693|GO:0008285|GO:004428
1|GO:0002544|GO:0051592|GO:0007165|GO:0050220|GO:0043295|GO:0001516|GO:0016020|GO:0005
641|GO:0032496|GO:0005789|GO:0032526|GO:0016021|GO:0034097 . NA - . NA NA
NA NA NA NA NA NA NA NA
LNCV6_129854_PI430048170 0.00023720503444 5.66070774 6.67268003 6.56905114
6.21158084 P P P 4.19136801 3.89244316 3.88429688 P P P
LNCV6_129854_PI430048170 mRNA
CTCCTAAATCAAGCATCTTCTGTTACTGATGTTCAATAAAAGAATAGTTGCCAAGGCTG NM_001111035
RefSeq chr19- 11574659 11578986 ACP5 54 "acid phosphatase 5, tartrate resistant, transcript
variant 1"
GO:0050830|GO:0045453|GO:0003993|GO:0032691|GO:0032929|GO:0032720|GO:0006767|GO:004428
1|GO:0005764|GO:0008198|GO:0005829|GO:0008199|GO:0006771|GO:0045019|GO:0006766|GO:0032
695|GO:0060349|GO:0050728|GO:0016311|GO:0032496|GO:0016021|GO:0034097|GO:0070062 .
NA - . NA NA NA NA NA NA NA NA
LNCV6_109101_PI430048170 0.00024562047170 2.10271646 12.18860399 12.28933849
12.39169259 P P P 11.33647978 11.12233299 11.19288806 P P P
LNCV6_109101_PI430048170 mRNA
ATAAATTAGTCGACAGAACTCAGCACTGGGGACAGGATTGCAAAGTCGGGGACATAGAT NM_001010858
RefSeq chr1 + 228487366 228496188 RNF187 149603 ring finger protein 187
GO:0005515|GO:0008284|GO:0005737|GO:0004842|GO:0016874|GO:0043161|GO:0008270|GO:000565
4|GO:0005634|GO:0070936|GO:0045893|GO:0051865 . NA - . NA NA NA NA NA

NA	NA	NA
LNCV6_136335_PI430048170	0.00024806948299	2.81919146
6.65476912	P P P	5.08362055 5.35231415 5.22809787 P P P
LNCV6_136335_PI430048170	mRNA	
GAGGCTCTGCCTAATGTGAATTTATTATTTGTGAATAAACTGTACTGGTGTCAAGTTGGC	NM_018670	
RefSeq chr15-	89749866 89751309 MESP1	55897 mesoderm posterior basic helix-loop-helix transcription factor 1
GO:0090082 GO:0003700 GO:0003259 GO:0007369 GO:0044212 GO:0003236 GO:0003139 GO:0042662 GO:0005634 GO:0060913 GO:0042664 GO:0003143 GO:0001947 GO:0007219 GO:0008078 GO:0060975 GO:0045944 GO:0046983 GO:0051155 GO:0035481 GO:0045446 GO:0055007 GO:0003241 GO:		
NA - . NA NA NA NA NA NA NA NA NA NA		
LNCV6_94232_PI430048170	0.00025530765781	3.63202822 6.61702952 6.89229272
6.60153439	P P P	4.83836624 4.95089334 4.75123536 P P P
LNCV6_94232_PI430048170	mRNA	
CGTTATCACACAGAGCTATCTGCTTCACCTCAAATGCTTATTAAATTTCAATCTGAGACTC	NM_001007255	
RefSeq chr1 +	161098390161100348KLHDC9	126823 "kelch domain containing 9, transcript variant 2"
variant 2" NA . NA - . NA NA NA NA NA NA NA NA		
LNCV6_143670_PI430048170	0.00026689862709	2.03680983 3.83083199 3.63561000
3.71526009	P P P	2.82317577 2.65231443 2.62593198 P P P
LNCV6_143670_PI430048170	mRNA	
AACCCATCATCTATGTTTTCTTAACATAGCTGGCACAGGGTTTAACACATAATTGCCA	NM_021955	
RefSeq chr7 +	93906507 93911173 NGNT1	2792 "guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 1"
GO:0005886 GO:0007603 GO:0005834 GO:0003924 GO:0071456 GO:0007268 GO:0022400 GO:0001917 GO:0007165 GO:0008104 GO:0008152 GO:0010659 GO:0004871 GO:0042462 GO:0016056 . NA - . NA NA NA NA NA NA NA NA NA NA		
LNCV6_138686_PI430048170	0.00027155327116	2.14040527 10.69970474 10.57142369
10.47719649	P P P	9.36891539 9.59103289 9.49483359 P P P
LNCV6_138686_PI430048170	mRNA	
GGTTCATGTCCAATCTTGTTTCGATCACTAGATGATTCTAACATCGAAATAAACCTCTTTT	NM_014811	
RefSeq chr9 +	135479801135488893PPP1R26	9858 "protein phosphatase 1, regulatory subunit 26"
GO:0005515 GO:0019902 GO:0010923 GO:0004864 GO:0005730 GO:0005654 . NA - . NA NA NA NA NA NA NA NA		
LNCV6_64861_PI430048170	0.00028034018065	2.47764795 14.12622371 14.34059124
14.08455665	P P P	12.99987554 12.83400545 12.79559664 P P P
LNCV6_64861_PI430048170	mRNA	
GTCCCATCACAAGCCCCGGGGAGGGATCCCGCCTTTGAAAATAAAGCTGTTATGGGTGTCA	NM_006423	
RefSeq chr19-	41956680 41959376 RABAC1	10567 Rab acceptor 1 (prenylated)
GO:0005515 GO:0030054 GO:0005794 GO:0016020 GO:0005886 GO:0016021 GO:0008022 GO:0070064 GO:0042802 GO:0008021. NA - . NA NA NA NA NA NA NA NA		
LNCV6_133551_PI430048170	0.00029250646139	3.51442330 7.61732114 7.48544078
7.28657316	P P P	5.83417892 5.66324750 5.44488535 P P P
LNCV6_133551_PI430048170	mRNA	
CTCACAGGGCTCCCTCAGCCTGGGGAACATTAAAGGTTTTCTACAAATACAGTCAAAAAA	NM_016948	
RefSeq chr16+	67660947 67662778 PARDA6A	50855 "par-6 family cell polarity regulator alpha, transcript variant 1"
GO:0005515 GO:0005886 GO:0034329 GO:0045177 GO:0005634 GO:0001726 GO:0045216 GO:0045217 GO:0005829 GO:0043234 GO:0030742 GO:0007049 GO:0070830 GO:0005080 GO:0016032 GO:0007179 GO:0017048 GO:0005923 GO:0005938 GO:0051301 GO:0008134 . NA - . NA NA NA NA NA NA NA NA		
LNCV6_140879_PI430048170	0.00029897401175	2.95273998 11.52439218 11.49946017
11.64985081	P P P	9.96944003 10.02276436 9.99938604 P P P
LNCV6_140879_PI430048170	mRNA	
GCCTTCTCCTTTGTCTTTGTTTCACTCTGTGTTTCCAATAAACTCATTGTAGCGAATCAA	NM_002284	
RefSeq chr12+	52301864 52309163 KRT86	3892 "keratin 86, type II"
GO:0005198 GO:0045095 GO:0005615 GO:0070062 . NA - . NA NA NA NA NA NA		
LNCV6_131058_PI430048170	0.00030103806883	7.12908492 3.11055988 3.68736943
3.22762937	P P P	0.35567770 0.80284337 0.38784814 A A A
LNCV6_131058_PI430048170	mRNA	
AGTGTTTGGCTGAGCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCCACC CG NM	052863	

RefSeq chr5 - 180590104180591487SCGB3A1 92304 "secretoglobin, family 3A, member 1"
 GO:0030308|GO:0042127|GO:0005615|GO:0005125|GO:0070062 . NA - . NA NA NA
 NA NA NA NA NA NA
 LNCV6_138481_PI430048170 0.00031423824452 6.40317649 5.15033735 5.15781378
 5.32052409 P P P 2.32772396 2.72864296 2.51449561 A P P
 LNCV6_138481_PI430048170 mRNA
 GCTGGAGGAGGACGGCTTACATGTTTGTCTGTAGAAAATAAACTGAGCTACGAAAAA NM_001327
 RefSeq chrX - 154617608154619271CTAG1B NA cancer/testis antigen 1B NA . NA
 - . NA NA NA NA NA NA NA NA NA
 LNCV6_129001_PI430048170 0.00032046388714 3.26193443 8.36571543 8.59221196
 8.42936057 P P P 6.95284103 6.65028729 6.65526760 P P P
 LNCV6_129001_PI430048170 mRNA
 GAAACAAGACAAGCTCCTCCCTTGAGAATTCCTGTGGATTTTTAAAACAGATATTATTT NM_003809
 RefSeq chr17+ 7549057 7557890 TNFSF12 8742 "tumor necrosis factor (ligand) superfamily,
 member 12, transcript variant 1"
 GO:0005515|GO:0005164|GO:2001238|GO:0048471|GO:0045732|GO:0005102|GO:0006915|GO:000152
 5|GO:0097190|GO:0005125|GO:0005615|GO:0045766|GO:0030154|GO:0007165|GO:0006955|GO:0001
 938|GO:0005887|GO:0043542 . NA - . NA NA NA NA NA NA NA NA NA
 LNCV6_64365_PI430048170 0.00032242296541 2.86253429 5.10422580 5.30473474
 5.33222934 P P P 3.68474133 3.80653682 3.70563294 P P P
 LNCV6_64365_PI430048170 mRNA
 TCAAGAAACTCTTGAACAAGACCAACAAGAAGGCAGCGGAGTCCTGAAGGCCCCGTGCTC NM_020428
 RefSeq chr19+ 10625494 10644559 SLC44A2 57153 "solute carrier family 44 (choline
 transporter), member 2, transcript variant 1"
 GO:0015220|GO:0005886|GO:0015871|GO:0044281|GO:0005765|GO:0055085|GO:0007165|GO:000487
 1|GO:0016021|GO:0006644|GO:0043123|GO:0070062|GO:0006656|GO:0046474 . NA - .
 NA NA NA NA NA NA NA NA NA NA
 LNCV6_127149_PI430048170 0.00032609799325 2.60086265 5.69934109 5.90307713
 5.60734452 P P P 4.49536301 4.36210993 4.21806881 P P P
 LNCV6_127149_PI430048170 mRNA
 GAAAATGCCAGCCTAGTGTTTACAGTTTTTCGCCACAACATGAAGAGCAGCAATGACTTC NM_016524
 RefSeq chr16+ 19168212 19268334 SYT17 51760 synaptotagmin XVII
 GO:0005802|GO:0005215|GO:0016020|GO:0006887|GO:0008021 . NA - . NA NA NA
 NA NA NA NA NA NA
 LNCV6_129493_PI430048170 0.00032761765432 4.61879979 4.87281407 5.35595612
 5.15376137 P P P 3.14221679 2.76093247 2.87002578 P P P
 LNCV6_129493_PI430048170 mRNA
 TCATGCAGATGCAGTCTGAATTCCTTGCTGAATTAAATTTATGTATCCTCTCCAAAAA NM_001166663
 RefSeq chr1 - 160830159160862902CD244 51744 "CD244 molecule, natural killer cell
 receptor 2B4, transcript variant 2"
 GO:0005515|GO:0007165|GO:0005886|GO:0007596|GO:0004872|GO:0016021|GO:0050900|GO:000989
 7 . NA - . NA NA NA NA NA NA NA NA NA
 LNCV6_139667_PI430048170 0.00033151177968 2.48184434 6.74425694 6.71658292
 6.65583568 P P P 5.33197333 5.34083124 5.50442781 P P P
 LNCV6_139667_PI430048170 mRNA
 GGGAGGTGCTGCCCTTAACCATGACACCATTGTAAGAGCTGTCCACATTTGTATGTTGTG NM_004823
 RefSeq chr19+ 38319843 38329009 KCNK6 9424 "potassium channel, two pore domain
 subfamily K, member 6"
 GO:0005242|GO:0005886|GO:0008076|GO:0007268|GO:0034765|GO:0060075|GO:0006813|GO:000308
 5|GO:0071805 . NA - . NA NA NA NA NA NA NA NA NA
 LNCV6_137804_PI430048170 0.00034075516324 2.45595753 13.49276539 13.22368552
 13.42599855 P P P 11.96731549 12.13994395 12.15242450 P P P
 LNCV6_137804_PI430048170 mRNA
 TACCAAAGAAGAGTTTACAGACAATAAAATGGAAAGGTCCTGCTGTGGAAACTTACCCAA NM_001740
 RefSeq chr16+ 71358712 71390438 CALB2 794 "calbindin 2, transcript variant CALB2"
 GO:0005737|GO:0051480|GO:0005509|GO:0005921|GO:0005634 . NA - . NA NA NA
 NA NA NA NA NA NA
 LNCV6_133107_PI430048170 0.00034335600375 2.02684360 8.58345371 8.73675954
 8.72687503 P P P 7.75733133 7.53834209 7.69011522 P P P
 LNCV6_133107_PI430048170 mRNA
 CAGCTTCATACTTCATGAAATCCTGGGTTTTCTTAACCATCTTTTCTCATTTTCAATGG NM_005423

RefSeq chr21- 42346357 42351099 TFF2 7032 trefoil factor 2
GO:0005515|GO:0030334|GO:0008284|GO:0019722|GO:0070098|GO:0043031|GO:0007586|GO:0005615|GO:0031723|GO:0050728|GO:0060455|GO:0070374|GO:0070062 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_133390_PI430048170 0.00034703884108 7.70990785 9.16825826 9.59618395
9.32219534 P P P 6.73650742 6.35732350 6.11724503 P P P
LNCV6_133390_PI430048170 mRNA
TTTTGAGCAGGTGGCTTTTGACGAAACCAAGAATGTGTTTGTCAAGTTCTATGCCCCGTG NM_006849
RefSeq chr16+ 283117 287209 PDIA2 64714 "protein disulfide isomerase family A, member 2"
GO:0031545|GO:0005515|GO:0034976|GO:0006457|GO:0005783|GO:0005788|GO:0003756|GO:0045454|GO:0019511|GO:0006621|GO:0005496 . NA - . NA NA NA NA NA NA NA NA
NA NA
LNCV6_99138_PI430048170 0.00034843598163 3.20326673 6.76522774 6.70735497
7.04691481 P P P 5.18773813 5.32739995 4.96632410 P P P
LNCV6_99138_PI430048170 mRNA
CTGGAAGATAAGGGAAGCCAGGAAAAGCAGGGCAAGTCCGAAGGTGAGGGCAAGCCACAANM_001006938
RefSeq chrX - 102139960102142416TCEAL6 158931 transcription elongation factor A (SII)-like 6
GO:0006355|GO:0005634|GO:0006351. NA - . NA NA NA NA NA NA NA
NA NA NA
LNCV6_134500_PI430048170 0.00035500377169 5.19932748 5.38179660 5.76499509
5.47948965 P P P 2.86758783 3.38241989 3.22229669 P P P
LNCV6_134500_PI430048170 mRNA
ATGAGATCCGTGCTTTTATCTTGTCTCAGACTCCCAATGATAGGCACATACTCTCCTCTG NM_001294306
RefSeq chr19+ 36773117 36777078 LOC728485 728485 uncharacterized LOC728485 NA
. NA - . NA NA NA NA NA NA NA NA
LNCV6_131303_PI430048170 0.00035972690644 2.80055625 9.36802144 9.34685730
9.12406409 P P P 7.84701213 7.92489780 7.60314759 P P P
LNCV6_131303_PI430048170 mRNA
GTGTCATCTTACCCTTTACAGAGAAATTAATGGCCTTGGTGGGACCAAATGGGAAAAAA NM_001303439
RefSeq chr17+ 45160173 45170040 HEXIM2 124790 "hexamethylene bis-acetamide inducible 2, transcript variant 1"
GO:0005515|GO:0005737|GO:0045736|GO:0004861|GO:0017069|GO:0005654|GO:0005634|GO:0000122|GO:0045892|GO:0006351. NA - . NA NA NA NA NA NA NA NA
LNCV6_130055_PI430048170 0.00036264481219 6.81042393 9.00118560 9.61946052
9.21932170 P P P 6.33153191 6.83641398 6.38279007 P P P
LNCV6_130055_PI430048170 mRNA
TTCCCCAGAATGGATGGTATTGAATCTCAGCCACATGCAACACTGTGTCCAGCATTCTTT NM_004567
RefSeq chr3 - 48517683 48556794 PFKFB4 5210 "6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4"
GO:0005975|GO:0044281|GO:0005524|GO:0006096|GO:0005829|GO:0004331|GO:0016311|GO:0009405|GO:0006006|GO:0046835|GO:0006003|GO:0003873|GO:0006000 . NA - . NA NA
NA NA NA NA NA NA NA NA
LNCV6_130258_PI430048170 0.00036857637002 2.75716726 10.43605857 10.43036351
10.34388542 P P P 9.06459948 8.89584547 8.85338275 P P P
LNCV6_130258_PI430048170 mRNA
AGCCCAGTTAGCAAGGTGCCGGGTACCCCTGCAGGTTCCCATAAAAACGATTTGCAGCCA NM_016246
RefSeq chr19- 48813016 48836677 HSD17B14 51171 hydroxysteroid (17-beta) dehydrogenase 14
GO:0005515|GO:0006706|GO:0004303|GO:0047045|GO:0055114|GO:0005829
. NA - . NA NA NA NA NA NA NA NA
LNCV6_135779_PI430048170 0.00037311547549 2.78160628 4.85562375 5.01822652
4.84121745 P P P 3.58902583 3.40134305 3.28754107 P P P
LNCV6_135779_PI430048170 mRNA
AAGGTGCATTGTCTTCCAGTATCTACAGCTTCAGACTTGAGCTAAGTAAATGCTTCAAAG NM_033467
RefSeq chr1_KI270762v1_alt - 141831 184229 MMEL1 79258 membrane metallo-endopeptidase-like 1
GO:0005794|GO:0005783|GO:0006508|GO:0008270|GO:0016021|GO:0004222|GO:0005615 . NA
- . NA NA NA NA NA NA NA NA
LNCV6_134787_PI430048170 0.00038878535266 2.52300110 8.45406126 8.74294005
8.68448647 P P P 7.30177160 7.40983810 7.17040098 P P P
LNCV6_134787_PI430048170 mRNA

AGGACACACATATGCTTACACCTACCTTTATCACCATTTCGTTTCATGAATCATGCCTAGCT NM_173546
RefSeq chr3 + 49171584 49176486 KLHDC8B 200942 kelch domain containing 8B
GO:0005737 . NA - . NA NA NA NA NA NA NA NA
LNCV6_127090_PI430048170 0.00039249940206 0.18938304 1.39598033 1.44385035
1.88285828 A A A 3.78992222 4.17663926 3.98359516 P P P
LNCV6_127090_PI430048170 mRNA
ATGTCTATAGTGTCTTTAAATTATTGTGACCTACACTGGGTACCGGAGAGGGGGATGGCT NM_058238
RefSeq chr22- 45920365 45977128 WNT7B 7477 "wingless-type MMTV integration site
family, member 7B"
GO:0060710|GO:0072236|GO:0070307|GO:0071300|GO:0046330|GO:0005615|GO:0005109|GO:001605
5|GO:0060033|GO:0005796|GO:0072089|GO:0051384|GO:0072207|GO:0072205|GO:0001701|GO:0021
871|GO:0045165|GO:0050808|GO:0005788|GO:0060484|GO:0060535|GO:0032364|GO:0060482|GO.
NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_142877_PI430048170 0.00042970527887 2.06330397 11.65840713 11.85482950
11.63753991 P P P 10.66932210 10.79234308 10.55454537 P P P
LNCV6_142877_PI430048170 mRNA
CCCCACCTAAAAAGACCAAGCATTGATGCCCAAGTTTTGGAAATATTCTGTTTTAAAAAG NM_003730
RefSeq chr6 - 166929515 166956589 RNASET2 8635 ribonuclease T2
GO:0003723|GO:0033897|GO:0005788|GO:0005576|GO:0004540|GO:0005764|GO:0005615|GO:007006
2|GO:0043202|GO:0006401. NA - . NA NA NA NA NA NA NA NA
LNCV6_126937_PI430048170 0.00044730141407 4.61362856 7.86731179 8.29602746
7.91005894 P P P 6.11546151 5.71372665 5.61642137 P P P
LNCV6_126937_PI430048170 mRNA
CTTCAGCTTGGGTACACACACAGAGGAGACCTCAGCCTCACACCAGAAATATTATTTTTT NM_206539
RefSeq chr6 - 43450351 43456632 DLK2 65989 "delta-like 2 homolog (Drosophila),
transcript variant 2"
GO:0045746|GO:0046982|GO:0045598|GO:0005509|GO:0016021|GO:0042803|GO:0070062 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_140866_PI430048170 0.00044980133354 2.31019624 7.47666480 7.54029378
7.41640868 P P P 6.36418273 6.29764442 6.14116088 P P P
LNCV6_140866_PI430048170 mRNA
GGATACAGAACACAAGTCTTGGCACATATGTGATGGAAATAAAGTGTTTTGCAATCTTTA NM_138456
RefSeq chr11- 64987944 64997045 BATF2 116071 "basic leucine zipper transcription
factor, ATF-like 2, transcript variant 1"
GO:0043565|GO:0005515|GO:0003700|GO:0006357|GO:0042832|GO:0005634|GO:0043011|GO:000635
1 . NA - . NA NA NA NA NA NA NA NA
LNCV6_133590_PI430048170 0.00046256965298 4.10341048 7.96359531 8.05563755
8.33075199 P P P 5.98955122 6.19214451 6.07637424 P P P
LNCV6_133590_PI430048170 mRNA
TTTTAAGTGATTCTCAGTGCTGAAAAGCCTGTCCAGGTTTCCTTCCCTTTCCCAAGCCT NM_015993
RefSeq chr16- 57256096 57284672 PLLP 51090 plasmolipin
GO:0043218|GO:0042552|GO:0009611|GO:0045121|GO:0016021|GO:0070062|GO:0006811 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_108277_PI430048170 0.00046260567416 2.90080968 8.49510404 8.39484379
8.52468366 P P P 7.03676742 6.98142336 6.77754294 P P P
LNCV6_108277_PI430048170 mRNA
AGTCCCCTGTGAATCAAGATTTGGGCATGTTCTTGGTCACCATTTCTGCTACACCAGAG NM_001122955
RefSeq chr11- 62690261 62707707 BSCL2 26580 "Berardinelli-Seip congenital
lipodystrophy 2 (seipin), transcript variant 1"
GO:0016042|GO:0003674|GO:0050995|GO:0019915|GO:0045444|GO:0030176|GO:0034389 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_137044_PI430048170 0.00046455824128 4.98110179 5.06035397 4.91724031
4.74240951 P P P 2.47001796 2.40363617 2.86924209 A A P
LNCV6_137044_PI430048170 mRNA
TCCCACGCCAGGCCCAAGAGAGATTCTATGACATATATTATAGAGAGAATTCTATATCAA NM_001031690
RefSeq chr7 - 143353399 143362747 FAM131B 9715 "family with sequence similarity 131,
member B, transcript variant a" GO:0005737|GO:0005654 . NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_145639_PI430048170 0.00046523819670 2.23604930 6.28538138 6.39124067
6.56057366 P P P 5.37327195 5.21926541 5.16720409 P P P
LNCV6_145639_PI430048170 mRNA

ACATAAAAAATGAAGGGCTCGCATCATCCAGGAAAGAATTTCAGCAGAAGTTCACTTTTTT NM_016608
RefSeq chrX + 101550530101554692ARMCX1 51309 "armadillo repeat containing, X-linked
1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA
LNCV6_142189_PI430048170 0.00048310488940 2.48725185 6.33836659 6.64561134
6.46455936 P P P 4.99340023 5.28947593 5.22221401 P P P
LNCV6_142189_PI430048170 mRNA
TGCCAACTTGGTTTTTAACTCCTCTCACCTGTTAGCTCTGATTAACAACTGCAACC NM_030765
RefSeq chr12+ 122203680122207537B3GNT4 79369 "UDP-GlcNAc:betaGal beta-1,3-N-
acetylglucosaminyltransferase 4"
GO:0005975|GO:0030311|GO:0016266|GO:0044281|GO:0008378|GO:0042339|GO:0008532|GO:000013
9|GO:0006493|GO:0018146|GO:0009405|GO:0016021|GO:0044267|GO:0030203|GO:0043687 . NA
- . NA NA NA NA NA NA NA NA NA NA
LNCV6_135542_PI430048170 0.00049473802043 2.79616782 7.07486575 6.91244912
7.17420382 P P P 5.77244505 5.47850512 5.44962591 P P P
LNCV6_135542_PI430048170 mRNA
AAGTAGCAAGAAGCTACATCCCTCAAACCTTCGGCAATGAAAATAAAGTTTGAGAAGCTGA NM_032461
RefSeq chrX + 141002590141003706SPANXB1 728695 "SPANX family, member B1"
GO:0003674|GO:0005737|GO:0007286|GO:0005634 . NA - . NA NA NA NA NA NA
NA NA NA NA
LNCV6_139123_PI430048170 0.00050063766758 3.24711501 4.47040953 4.76572471
4.84622618 P P P 2.90375224 2.93887100 3.15566605 P P P
LNCV6_139123_PI430048170 mRNA
ATCTCAACCCGGGCTTTGAAATGTGTTTGTTCACATAATTGTCCATTACCCATCCTTCCT NM_001256272
RefSeq chr20- 25070885 25082379 VSX1 30813 "visual system homeobox 1, transcript
variant 4"
GO:0043565|GO:0006355|GO:0003700|GO:0060040|GO:0042551|GO:0005634|GO:0005575|GO:000760
1|GO:0050896|GO:0006351. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139654_PI430048170 0.00050168872720 2.14576268 6.08751493 6.06467185
6.11257827 P P P 4.97561505 5.06147092 4.92007674 P P P
LNCV6_139654_PI430048170 mRNA
ACAGTGACTTTCTCAGAGGTGACAGAGATGATGGATGAGCAGCTGGATTTTCGTGATGAA NM_001099335
RefSeq chr8 - 22219702 22232338 PHYHIP 9796 "phytanoyl-CoA 2-hydroxylase interacting
protein, transcript variant 1"NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_143723_PI430048170 0.00051212411568 7.73758017 3.10838946 3.74087684
3.35803346 P P P 0.35519453 0.35186228 0.68906264 A A A
LNCV6_143723_PI430048170 mRNA
TCAGAGCCACATTGAGTTGCTTTTTCTGGGATGAGGAAGTAGGGTTAACTCCCCAGTTT NM_024046
RefSeq chr3 - 49857988 49869936 CAMKV 79012 CaM kinase-like vesicle-associated
GO:0005516|GO:0004672|GO:0005886|GO:0006468|GO:0005524|GO:0030659 . NA - .
NA NA NA NA NA NA NA NA NA NA
LNCV6_135262_PI430048170 0.00052917461540 2.27003467 8.20313997 8.26099188
8.46572713 P P P 7.26880708 6.97700748 7.13454731 P P P
LNCV6_135262_PI430048170 mRNA
GCATTGTTCTTTAGTTGGAGTTCTCATTCTTATTCTCCAGTACTGACTTGTGGGGAAAGC NM_001142648
RefSeq chr10- 70150204 70170529 SAR1A 56681 "secretion associated, Ras related
GTPase 1A, transcript variant 1"
GO:0016529|GO:0005794|GO:0016192|GO:0005525|GO:0006886|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA NA
LNCV6_142767_PI430048170 0.00054242839566 3.30091624 6.68330375 6.61287297
6.28653672 P P P 5.01879357 4.78815861 4.60787769 P P P
LNCV6_142767_PI430048170 mRNA
GAGGGGGCGCTGGAGCTTCCAACCCGAGGCAATAAAAGAAATGTTGCGTAACTCAAAAAA NM_002256
RefSeq chr1 - 204190340204196491KISS1 3814 KiSS-1 metastasis-suppressor
GO:0005515|GO:0007010|GO:0005576. NA - . NA NA NA NA NA NA NA NA NA
NA
LNCV6_142929_PI430048170 0.00054597880749 2.05344784 11.25928475 11.41424813
11.29026772 P P P 10.31258856 10.29393724 10.24704423 P P P
LNCV6_142929_PI430048170 mRNA
GTGGCTGCAGAAGGGGCCACCCTAGCCTTTTAACTGCTTTGTCAAATTAACATTTTGTA NM_032140
RefSeq chr16- 67662946 67666725 ENKD1 84080 enkurin domain containing 1
GO:0005881|GO:0015630 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_143514_PI430048170 0.00054732159702 4.77989748 8.02483687 8.38011476
 7.81774103 P P P 5.69482096 6.11297294 5.65479459 P P P
 LNCV6_143514_PI430048170 mRNA
 AAGGAGGCCTCTGTCATTTTAAAGACTCGTGTTTACAGTTTTGTATCCAAGGCCAAAAAA NM_025268
 RefSeq chr14+ 105526615 105530202 TMEM121 80757 transmembrane protein 121
 GO:0008150|GO:0003674|GO:0016021|GO:0005575 . NA - . NA NA NA NA NA
 NA NA NA NA
 LNCV6_129304_PI430048170 0.00056919377906 8.53686187 8.15947244 8.14013522
 8.30857612 P P P 4.93923089 5.37042430 4.98325525 P P P
 LNCV6_129304_PI430048170 mRNA
 AAGATGAAAACCTTTATGAAGGCCTGAACCTGGACGACTGCTCCATGTATGAGGACATCT NM_001783
 RefSeq chr19+ 41877119 41881372 CD79A 973 "CD79a molecule, immunoglobulin-
 associated alpha, transcript variant 1"
 GO:0050853|GO:0042113|GO:0019815|GO:0005886|GO:0042100|GO:0005771|GO:0030183|GO:004512
 1|GO:0016021|GO:0009897|GO:0004888 . NA - . NA NA NA NA NA NA NA
 NA NA
 LNCV6_133216_PI430048170 0.00057382586486 3.11654862 9.42025662 9.57971355
 9.47570527 P P P 7.81594884 8.02046414 7.70617838 P P P
 LNCV6_133216_PI430048170 mRNA
 CCTTGCCACCCGTGGTTGGATCTTGTTTTATATCTGCAAATAAATAGCTTGTTTGGAAGC NM_030812
 RefSeq chr1 + 17755312 17827063 ACTL8 81569 actin-like 8
 GO:0005737|GO:0030855|GO:0005856. NA - . NA NA NA NA NA NA NA NA
 NA
 LNCV6_131503_PI430048170 0.00061024899484 3.16921255 8.83054378 8.93491579
 8.64212687 P P P 7.35944811 7.09323003 6.94697981 P P P
 LNCV6_131503_PI430048170 mRNA
 AGGAAACTTGTAACCACCCTTTTCTAACAGCAATAAAGAGGTGTCCTTGTCGCCGAAAAAA NM_003793
 RefSeq chr11- 66563463 66568576 CTSF 8722 cathepsin F
 GO:0004197|GO:0019886|GO:0006508|GO:0031982|GO:0005764|GO:0070062|GO:0043202 . NA
 - . NA NA NA NA NA NA NA NA NA
 LNCV6_128071_PI430048170 0.00062626158130 3.62298710 6.59191566 6.85201607
 7.00747738 P P P 5.23455867 4.85418429 4.77880949 P P P
 LNCV6_128071_PI430048170 mRNA
 CCCACAGGCAATGGGTTTATAGACATTATGTGAGTTTCCTGCTATATTAACATCATCTTA NM_001772
 RefSeq chr19+ 51225078 51240019 CD33 945 "CD33 molecule, transcript variant 1"
 GO:0005515|GO:0007165|GO:0008285|GO:0005886|GO:0005887|GO:0007267|GO:0030246|GO:000487
 2|GO:0007155|GO:0009897|GO:0070062 . NA - . NA NA NA NA NA NA NA
 NA NA
 LNCV6_68839_PI430048170 0.00062660133443 2.12404347 4.82044416 4.74132109
 5.01733298 P P P 3.88199883 3.78836554 3.65335029 P P P
 LNCV6_68839_PI430048170 mRNA
 AAGCACGGTCACGGGAAGTTGTTATTTAAAGATGGCAGTTATTACGAAGGGGCGTTTGTG NM_024848
 RefSeq chr1 - 2321252 2391751 MORN1 79906 "MORN repeat containing 1, transcript
 variant 1" NA . NA - . NA NA NA NA NA NA NA NA
 LNCV6_128716_PI430048170 0.00063694878185 3.25417004 6.51290724 6.82742896
 6.92951798 P P P 5.26181756 4.83566634 5.06605359 P P P
 LNCV6_128716_PI430048170 mRNA
 TGCAGCTGAGTGAATCAGGAAGTGACAGTGATGACTGAAGAAATATTTAGCTATAAATAA NM_018456
 RefSeq chr3 + 121835186 121886526 EAF2 55840 ELL associated factor 2
 GO:0060770|GO:0005515|GO:0030308|GO:0000977|GO:0016607|GO:0045944|GO:0032783|GO:000691
 5|GO:0001228|GO:0008023|GO:0006351 . NA - . NA NA NA NA NA NA NA
 NA NA
 LNCV6_133184_PI430048170 0.00066246760152 2.03139279 7.48075857 7.71429796
 7.53801700 P P P 6.47962392 6.63102447 6.56143261 P P P
 LNCV6_133184_PI430048170 mRNA
 GGCTCGGGACGCTCATGTAAATTTGGTTTTGGTGCTCAAGGGTTCTTTCCTCCCAGGGGC NM_005975
 RefSeq chr20- 63528422 63537370 PTK6 5753 "protein tyrosine kinase 6, transcript variant 1"
 GO:0005515|GO:0042506|GO:0030036|GO:0042503|GO:0071300|GO:0061099|GO:0005634|GO:004280
 2|GO:0060575|GO:0005737|GO:0046777|GO:0042127|GO:0038083|GO:0045926|GO:0005102|GO:0005
 524|GO:0001726|GO:0031234|GO:0016477|GO:0045087|GO:0010976|GO:0006468|GO:0005654|GO.
 NA - . NA NA NA NA NA NA NA NA NA

LNCV6_127786_PI430048170	0.0006654866462	2.96887713	9.60425725	9.52829782
9.34109008 P P P	7.69011522	8.06075411	7.99893637 P	P P
LNCV6_127786_PI430048170	mRNA			
GCCTGGCTCTGTTATTTACCGTGTATCATATGTAAATATCGACAGAACTTCAATAAACT	NM_031896			
RefSeq chr19+ 53912736 53943715 CACNG7 59284	"calcium channel, voltage-dependent, gamma subunit 7"			
GO:0005245 GO:0032281 GO:2000311 GO:0070588 GO:0006816 GO:0005891				
NA - NA NA NA NA NA NA NA NA NA				
LNCV6_132199_PI430048170	0.00068982608666	2.49148986	6.45543773	6.46979271
6.53287080 P P P	5.27572666	5.16362264	5.06090016 P	P P
LNCV6_132199_PI430048170	mRNA			
GTGCTTTTTTGTCTTTTGTATTTTTGGTTGGGTGGGTGGGAAGGTCTCTTTAAATG	NM_005704			
RefSeq chr1 + 29236515 29326813 PTPRU 10076	"protein tyrosine phosphatase, receptor type, U, transcript variant 3"			
GO:0005515 GO:0030336 GO:0008285 GO:0005886 GO:0008013 GO:0031100 GO:0051384 GO:0035335 GO:0030154 GO:0034109 GO:0016337 GO:0006470 GO:0005001 GO:0005887 GO:0005911 GO:0034394 GO:0007185 GO:0007155 GO:0060070 GO:0004725	NA - NA NA NA NA			
LNCV6_128615_PI430048170	0.00069152642296	6.77481470	5.58365156	5.46542089
5.73058580 P P P	2.90444097	2.51297409	3.04310249 P	P P
LNCV6_128615_PI430048170	mRNA			
TGTCGCTGGAGGAGGACGGCTTACATGTTTGTCTGTAGAAAATAAACTGAGCTACGA	NM_139250			
RefSeq chrX - 154617608 154619271 CTAG1A 246100	cancer/testis antigen 1A			
GO:0005515 GO:0005737	NA - NA NA NA NA NA NA NA NA			
LNCV6_59436_PI430048170	0.00069609377953	2.03870833	10.20667741	10.31676195
10.47621222 P P P	9.44327218	9.18540518	9.28907068 P	P P
LNCV6_59436_PI430048170	mRNA			
TATGTAGTAGACAGTTGTGACCGAGACCGAATTGGCATTTCCAAATCAGAGTTAGTTGCC	NM_001177			
RefSeq chr12- 101393119 101407820 ARL1 400	"ADP-ribosylation factor-like 1, transcript variant 1"			
GO:0005802 GO:0031584 GO:0005794 GO:0007264 GO:0019904 GO:0003924 GO:0005525 GO:0046872 GO:0006184 GO:0005737 GO:0000139 GO:0034067 GO:0007030 GO:0042147 GO:0048193 GO:0009404 GO:0008047 GO:0070062	NA - NA NA NA NA NA NA NA NA			
LNCV6_134000_PI430048170	0.00070162510457	4.11521098	3.60264678	3.88947046
3.95316372 P P P	1.78877214	1.69466219	1.85791805 A	A A
LNCV6_134000_PI430048170	mRNA			
CGTGTGAGGCTGTGTAGAGTGCAATTGTACAGCATATTTTCATGAATAAAATTGTTTTAA	NM_001291281			
RefSeq chr1 + 41361930 41383591 FOXO6 NA	forkhead box O6 NA			
NA NA NA NA NA NA NA NA NA				
LNCV6_128263_PI430048170	0.00071521425046	2.73677328	7.58252125	7.68013620
7.60191573 P P P	6.03019182	6.18710162	6.28069401 P	P P
LNCV6_128263_PI430048170	mRNA			
TGGACTGGGATATCATCTCTACAGCCTGCAAATAAACCAGACAACTTACCAACGTCAAA	NM_001185095			
RefSeq chr9 + 131096475 131123152 AIF1L 83543	"allograft inflammatory factor 1-like, transcript variant 3"			
GO:0005737 GO:0051015 GO:0005884 GO:0005509 GO:0032587 GO:0015629 GO:0005925 GO:0070062	NA - NA NA NA NA NA NA NA NA			
LNCV6_129359_PI430048170	0.00071897487217	2.50429114	6.86388955	7.07540534
7.15372040 P P P	5.90888951	5.63590188	5.56730708 P	P P
LNCV6_129359_PI430048170	mRNA			
CAGCCCCTGAGCAGGGAGAGAGAAGTTTTGTTGGCATAGGTTTGCTTAGGTAGCCGGCTT	NM_012168			
RefSeq chr1 - 11648360 11654831 FBXO2 26232	F-box protein 2			
GO:0004842 GO:0008285 GO:0016567 GO:0005783 GO:0031146 GO:0030433 GO:0005829 GO:0001540 GO:0001948 GO:0043197 GO:0031090 GO:0006508 GO:0006516 GO:0030246 GO:0031396 GO:0006464 GO:0019005 GO:0070062	NA - NA NA NA NA NA NA NA NA			
LNCV6_138733_PI430048170	0.00073579257205	2.66631827	7.00855100	7.03580937
7.15025367 P P P	5.69229932	5.76688311	5.47967638 P	P P
LNCV6_138733_PI430048170	mRNA			
AAAGAGTTTTGTAACCTTCAAGTGCTGTTCAGCTGCGGGGATTTAGCACAGGAGACTCTA	NM_019118			
RefSeq chr1 - 32216196 32222325 TMEM234 56063	transmembrane protein 234			
GO:0016021	NA - NA NA NA NA NA NA NA NA			
LNCV6_127248_PI430048170	0.00074187881059	3.58849057	3.88105799	3.91199335

4.12520832 P P P 2.18358041 2.30766303 1.87579533 A A A
LNCV6_127248_PI430048170 mRNA
GCGTGTGTAACATCCCATGTGCCTCACCTAATAAAATGGCTCTTCTTCTGCATCAAAAAA NM_130852
RefSeq chr20+ 33235995 33243309 BPIFA1 51297 "BPI fold containing family A, member
1, transcript variant 2"
GO:0003674|GO:0050828|GO:0050891|GO:0045087|GO:1900229|GO:0019731|GO:0005576|GO:000561
5|GO:0008289 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144628_PI430048170 0.00077164180491 2.49354816 3.90844674 4.23188228
4.11142227 P P P 2.59285613 2.74418733 2.95533674 A P P
LNCV6_144628_PI430048170 mRNA
ATACCAGGGTACTGGGGGCAATGCTATGATTAAGTTGCTTCAAATAAAAAGTTCCCGCC NM_139278
RefSeq chr8 - 22146829 22156831 LGI3 203190 "leucine-rich repeat LGI family, member 3"
GO:0043005|GO:0030054|GO:0017157|GO:0008152|GO:0005576|GO:0006887|GO:0003824|GO:000802
1 . NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_129819_PI430048170 0.00078391712563 2.34704601 7.94083175 7.66007222
7.77599144 P P P 6.36506183 6.69075713 6.62236720 P P P
LNCV6_129819_PI430048170 mRNA
ATGGAACTTGCAACTGGCATCCGAAAGAAAACTGTTTTATCCTGTTGTACAAATACA NM_001258376
RefSeq chr19- 16400630 16472012 EPS15L1 58513 "epidermal growth factor receptor
pathway substrate 15-like 1, transcript variant 4"
GO:0005515|GO:0005905|GO:0016020|GO:0007173|GO:0005886|GO:0005509|GO:0042059|GO:000563
4|GO:0006897 . NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_9470_PI430048170 0.00078684965239 6.63545947 4.16824315 4.01052191
3.44618903 P P P 0.78427182 1.35159950 1.32591414 A A A
LNCV6_9470_PI430048170 mRNA
TTCTGCACAACTAGATTCTGGACACCAGTGTGCGGAAATGCTTCTGCTACATTTTTAGG NM_032413
RefSeq chr15+ 45430528 45433449 C15orf48 84419 "chromosome 15 open reading frame
48, transcript variant 2" GO:0005739|GO:0005634 . NA - . NA NA NA NA NA NA
NA NA NA NA
LNCV6_132795_PI430048170 0.00082307236080 2.31532764 9.61194765 9.79054345
9.94378005 P P P 8.75592813 8.49571401 8.46171940 P P P
LNCV6_132795_PI430048170 mRNA
CCATCTTGAGATTGTTTGCCTATCTCATAATACAGTTTTATGCAGAAAGGTTGAAACT NM_016097
RefSeq chr18- 47155018 47176374 IER3IP1 51124 immediate early response 3
interacting protein 1 GO:0005794|GO:0016020|GO:0005783|GO:2000269|GO:0005789|GO:0016021
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130012_PI430048170 0.00083386388398 2.55327336 6.07985957 6.07314174
5.84121066 P P P 4.52443410 4.85758652 4.54283604 P P P
LNCV6_130012_PI430048170 mRNA
CTGTTAGAATGAAATGGTTCCCATAAATAAGGGGCATGAGCCCTTCCTCACGACAAAAAA NM_016582
RefSeq chr11- 60937082 60951785 SLC15A3 51296 "solute carrier family 15 (oligopeptide
transporter), member 3, transcript variant 1"
GO:0015833|GO:0016021|GO:0015031|GO:0005765|GO:0055085|GO:0043231|GO:0015293|GO:000681
1 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_66504_PI430048170 0.00083417002070 2.90896542 7.06041133 7.24334395
6.90134984 P P P 5.67057822 5.62758889 5.27387329 P P P
LNCV6_66504_PI430048170 mRNA
GCAGACCTGGTGTGTTGTTGTTGGGCTCACGCTTGACAATGAAGGCTTGTTACACAAC NM_001161404
RefSeq chr2 - 127638420 127681786 LIMS2 55679 "LIM and senescent cell antigen-like
domains 2, transcript variant 5"
GO:2001046|GO:0043066|GO:0016337|GO:2000178|GO:0005886|GO:0034329|GO:2000346|GO:000827
0|GO:0005634|GO:0005925|GO:0045216|GO:0005829 . NA - . NA NA NA NA NA NA
NA NA NA NA
LNCV6_145163_PI430048170 0.00083573822545 2.30133474 8.59173158 8.74694533
8.43156537 P P P 7.46899337 7.42927478 7.27454231 P P P
LNCV6_145163_PI430048170 mRNA
CAAGCTAGGGCAGAAGAGGGGTGTCAAGCTCCTCAATAAACTTGTCTCCACTTCAAAAAA NM_003782
RefSeq chr6_GL000255v2_alt + 4471559 4473245 B3GALT4 8705 "UDP-Gal:betaGlcNAc beta
1,3-galactosyltransferase, polypeptide 4"
GO:0000139|GO:0008499|GO:0047915|GO:0006486|GO:0016021 . NA - . NA NA NA
NA NA NA NA NA NA

LNCV6_128623_PI430048170	0.00085087199073	3.72969865	6.57020776	6.74394494
6.36251212 P P P	4.92744368	4.62811119	4.40038252 P	P P
LNCV6_128623_PI430048170	mRNA			
CTCCACACAGAAAATCTTCTTGATTCTATAGAGACTTAATCATGCCTATGGCTTTGAATA	NM_024693			
RefSeq chr10+ 11742356 11764066 ECHDC3 79746	enoyl CoA hydratase domain			
containing 3 GO:0005739 GO:0008152 GO:0003824.	NA - .	NA NA NA NA NA		
NA NA NA NA				
LNCV6_136525_PI430048170	0.00087283835569	3.87218960	5.25205379	5.24159171
4.86173764 P P P	3.11936929	3.30632393	3.09399456 P	P P
LNCV6_136525_PI430048170	mRNA			
CCCAGAGCAGCTCCACGTGAGAGCATTAAAGATGTAATGAAGATGTTTACATGGAAAAA	NM_016210			
RefSeq chr3 - 50558024 50567792 C3orf18 51161	"chromosome 3 open reading frame			
18, transcript variant 1" GO:0016021 .	NA - .	NA NA NA NA NA NA NA		
NA NA				
LNCV6_107928_PI430048170	0.00090667365593	2.07541193	6.14370191	6.37359958
6.12589971 P P P	5.32745043	5.03351375	5.11947944 P	P P
LNCV6_107928_PI430048170	mRNA			
AAGAGAGGGACTTCCTGCGGTGCCAGCTGGACAAATTCATCTCTTCTGCTCGGATGGAGG	NM_013301			
RefSeq chr19+ 55647587 55653160 CCDC106 29903	coiled-coil domain containing 106			
GO:0005515 GO:0005737 GO:0005730 GO:0005654 GO:0005634 .	NA - .	NA NA NA		
NA NA NA NA NA NA				
LNCV6_114489_PI430048170	0.00091722466168	2.14691527	4.46857072	4.58943073
4.73690121 P P P	3.52117611	3.32213107	3.63967774 P	P P
LNCV6_114489_PI430048170	mRNA			
GCAAGAGACTTAAATGACTGATAAGAACCGTGAGAAACATGTTGCTTCCAGGCTTGATTT	NM_000405			
RefSeq chr5 + 151253051 151270392 GM2A 2760	"GM2 ganglioside activator, transcript			
variant 1"				
GO:0006665 GO:0009313 GO:0032428 GO:0051345 GO:0006687 GO:0019915 GO:0006689 GO:004428				
1 GO:0005739 GO:0016004 GO:0045179 GO:0005889 GO:0006869 GO:0050885 GO:0007611 GO:0009				
898 GO:0005319 GO:0070062 GO:0043202 .	NA - .	NA NA NA NA NA NA NA		
NA NA				
LNCV6_128003_PI430048170	0.00092201630883	2.58620570	9.40286238	9.22859209
9.27124042 P P P	8.09112874	7.92677365	7.75896026 P	P P
LNCV6_128003_PI430048170	mRNA			
TTCCAGAGCCCCAGTTTGTAAATGAACCTGTGTCACATTTGATAAACACTATCCTGGGCG	NM_001042576			
RefSeq chr20- 17613677 17682283 RRP1 6238	"ribosome binding protein 1, transcript			
variant 1"				
GO:0016020 GO:0005783 GO:0005840 GO:0030176 GO:0004872 GO:0015031 GO:0006412 GO:000164				
9 .	NA - .	NA NA NA NA NA NA NA NA		
LNCV6_134813_PI430048170	0.00092255203861	2.79046004	6.55063249	6.63421977
6.72129988 P P P	4.95574165	5.26022380	5.23442174 P	P P
LNCV6_134813_PI430048170	mRNA			
GTTAGCGAGCACCTTTTGACCAGTAATAAAAAACCTTGGCTTTGGAGTTTTCCACTGAAA	NM_030758			
RefSeq chr22+ 30694805 30907824 OSBP2 23762	"oxysterol binding protein 2,			
transcript variant 1" GO:0016020 GO:0015485 GO:0006869.	NA - .	NA NA NA NA		
NA NA NA NA NA				
LNCV6_128330_PI430048170	0.00096173924146	2.40697131	8.98565450	9.14791325
9.08654464 P P P	7.92269321	7.85438959	7.63002766 P	P P
LNCV6_128330_PI430048170	mRNA			
AAGTCCTGACCTTTGTTCTCTTGACGGAATAAAAGCTTGCTTATCCTTATACTTACCAAA	NM_018381			
RefSeq chr19+ 10086118 10093252 C19orf66 55337	chromosome 19 open reading frame			
66 NA .	NA - .	NA NA NA NA NA NA NA NA		
LNCV6_129541_PI430048170	0.00096515921102	2.13937421	5.65388296	5.64099080
5.57027155 P P P	4.53490907	4.62392362	4.40802148 P	P P
LNCV6_129541_PI430048170	mRNA			
TTCAATCTTCTCCTGCTGGTGCTGGTGCTAGGGACCATCTTGCTACCCGCTGTCACCATG	NM_203411			
RefSeq chr17+ 7855065 7856099 TMEM88 92162	transmembrane protein 88			
GO:0005886 GO:0007275 GO:0016021 GO:0016055 .	NA - .	NA NA NA NA NA		
NA NA NA NA				
LNCV6_141699_PI430048170	0.00098651285593	2.93914231	5.52547524	5.69263405
5.48103975 P P P	4.23234609	3.90080725	3.88086605 P	P P

LNCV6_141699_PI430048170 mRNA
GGAGGGTCTCTGGCTTTATTTTTCTGCTGTGCAGAATCCTATTTTATATTTTTTAAAGTC NM_003745
RefSeq chr16- 11254416 11256182 SOCS1 8651 suppressor of cytokine signaling 1
GO:0005515|GO:0016567|GO:0005159|GO:0019221|GO:0005634|GO:0060397|GO:0005829|GO:0060334|GO:0005737|GO:0060337|GO:0060338|GO:0071230|GO:0045444|GO:0060333|GO:0042518|GO:0019901|GO:0019210|GO:0046627|GO:0007259|GO:0046426|GO:0016023|GO:0004860|GO:0001932|GO.NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_139794_PI430048170 0.00104549087853 2.08333729 3.90198785 3.71608842
3.75316789 P P P 2.74047278 2.57317959 2.87219452 P P P
LNCV6_139794_PI430048170 mRNA
TGGCTCTGTCACTCGAAGCCAGGCTTGATCAATAAACACAATGGTATTCCACGTCAAA NM_032206
RefSeq chr16+ 57017073 57083524 NLRC5 84166 "NLR family, CARD domain containing 5"
GO:0005515|GO:0005634|GO:0032088|GO:0000979|GO:0005524|GO:0005829|GO:0060335|GO:0005737|GO:0051607|GO:0060339|GO:0045345|GO:0045087|GO:0045944|GO:0060340|GO:0032480|GO:0043549 . NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_139562_PI430048170 0.00106688968297 2.10177895 6.88914412 6.84084226
7.14113404 P P P 5.74370623 6.02844483 5.88845663 P P P
LNCV6_139562_PI430048170 mRNA
TGAATTTCTGCTTTCTGTTGAATTTTCTACTGTTTCACGTGGTGTAACCCTAGACTG NM_001134647
RefSeq chr4 - 7758712 7939926 AFAP1 60312 "actin filament associated protein 1, transcript variant A" GO:0005737|GO:0051493|GO:0003779|GO:0009966|GO:0015629|GO:0005925
. NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_140359_PI430048170 0.00106889666268 3.03522268 3.77090585 3.32664242
3.39066383 P P P 1.79426003 1.79092610 2.11421681 A A A
LNCV6_140359_PI430048170 mRNA
CAGTTCGGTGAGGAAAGAAACCAAGCTATTTTCTCTTTTCCTCATGAACATTATATTTAG NM_001243531
RefSeq chr15+ 84172489 84182233 UBE2Q2L 100505679 ubiquitin-conjugating enzyme E2Q family member 2-like NA . NA - . NA NA NA NA NA NA NA NA
LNCV6_130823_PI430048170 0.00107593774079 6.19623590 5.08741433 5.21839048
5.20844800 P P P 2.78948729 2.42212982 2.37552363 P P P
LNCV6_130823_PI430048170 mRNA
CCAGTCTATTCACAGAAGTGTTAACTTTTCTAACAGAAAGCATGATTTTGATTGCTTACC NM_006207
RefSeq chr8 + 17576432 17643133 PDGFR1 5157 platelet-derived growth factor receptor-like GO:0008150|GO:0005019|GO:0004992|GO:0007186|GO:0035791|GO:0005576|GO:0005575 . NA - . NA NA NA NA NA NA NA NA
LNCV6_136654_PI430048170 0.00108680543999 2.60161012 6.78086564 6.91837812
6.86179935 P P P 5.37692089 5.64617024 5.38655479 P P P
LNCV6_136654_PI430048170 mRNA
ACAAAGGCTTTGATATCAGAATGAACTGTCAAGGGAGGTGCTGGAGAGGGATTAACCTGT NM_178422
RefSeq chr1 - 25861483 25871253 PAQR7 164091 progesterin and adipoQ receptor family member VII
GO:0048477|GO:0005886|GO:0043401|GO:0003707|GO:0007275|GO:0016021|GO:0048545|GO:0005496 . NA - . NA NA NA NA NA NA NA NA
LNCV6_108135_PI430048170 0.00109338240666 2.43393741 9.48107642 9.48660253
9.56810582 P P P 8.11671078 8.19597065 8.36375551 P P P
LNCV6_108135_PI430048170 mRNA
GGGTTCTGATTTCTGTATACATGTAGCTTTGCCAGATATGTACTTAGTAATATAAACTG NM_005552
RefSeq chr14+ 103629187103686231KLC1 3831 "kinesin light chain 1, transcript variant 1" GO:0005515|GO:0030424|GO:0005871|GO:0005874|GO:0035418|GO:0003777|GO:0035617|GO:0006886|GO:0030426|GO:0005829|GO:0019886|GO:0003774|GO:0015631|GO:0016020|GO:0007596|GO:0035253|GO:0008152|GO:0043025|GO:0016032|GO:0016023|GO:0008088|GO:0007018 . NA - . NA NA NA NA NA NA NA NA
LNCV6_137601_PI430048170 0.00111013533601 2.09252096 12.35322615 12.28291114
12.04379321 P P P 11.29415490 11.18193004 11.01215683 P P P
LNCV6_137601_PI430048170 mRNA
TTGTCAGGATTACCTCGGGCTAAAGAGGAAAAATAAAGATGTTGAGCTACCACTCTGGA NM_033518
RefSeq chrX - 48458536 48470256 SLC38A5 92745 "solute carrier family 38, member 5" GO:0015816|GO:0005886|GO:0005887|GO:0006865|GO:0015187|GO:0055085|GO:0003333|GO:0006811 . NA - . NA NA NA NA NA NA NA NA
LNCV6_131312_PI430048170 0.00111029010367 2.06816754 10.97727587 11.13986840

11.13013561	P	P	P	9.88193615	10.17519988	10.03590023	P	P	P
LNCV6_131312_PI430048170 mRNA									
GGTCCAGCTACTTCCTTTTGAACCTTAAATAGAATGGGTGTTGGTTGATTAATTTTATT NM_006397									
RefSeq chr19+ 12806613 12813648 RNASEH2A 10535 "ribonuclease H2, subunit A"									
GO:0032299 GO:0006260 GO:0004523 GO:0003723 GO:0005634 GO:0004540 GO:0006298 GO:0046872 GO:0006401 . NA - . NA NA NA NA NA NA NA NA NA									
LNCV6_132189_PI430048170				0.00111319674307	2.13303811	4.52856621		4.77834290	
4.51639217	P	P	P	3.34137733	3.67390500	3.52558871	P	P	P
LNCV6_132189_PI430048170 mRNA									
AGGCTGGGCCCAGGGCAGGACACCAGTCCTGATGTCCACCTTGATGTCTACCTTAACCCT NM_080669									
RefSeq chr17- 28394641 28406212 SLC46A1 113235 "solute carrier family 46 (folate transporter), member 1, transcript variant 1"									
GO:0015886 GO:0005886 GO:0009986 GO:0015232 GO:0015884 GO:0006767 GO:0044281 GO:0031526 GO:0008517 GO:0055085 GO:0006879 GO:0016324 GO:0005542 GO:0005737 GO:0006766 GO:0046655 GO:0016021 GO:0015350 GO:0051958 . NA - . NA NA NA NA NA NA NA NA									
LNCV6_135714_PI430048170				0.00112237624099	2.41268724	12.38716977		12.72889337	
12.55763202	P	P	P	11.38976531	11.18976939	11.29552473	P	P	P
LNCV6_135714_PI430048170 mRNA									
TAATCACGGAGGGAAGTGGCTGCCCCCTTAACACACCTTTAATAAACAGTCTACAGACCC NM_007108									
RefSeq chr16- 2771413 2777296 TCEB2 6923 "transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B), transcript variant 1"									
GO:0005515 GO:0070449 GO:0010467 GO:0006368 GO:0016567 GO:0006366 GO:0071456 GO:0061418 GO:0005829 GO:0050434 GO:0006461 GO:0016032 GO:0031462 GO:0005654 GO:0031466 GO:0031625 GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA									
LNCV6_135791_PI430048170				0.00114402974629	4.51434757	7.49369550		7.65244419	
7.35713526	P	P	P	5.44738606	5.50090597	4.99513307	P	P	P
LNCV6_135791_PI430048170 mRNA									
GTAAAGGTTATCTGTCCATTGCCTTGACGAAAGTCTCAAGAAAAGTCTACATCTTAAAA NM_015672									
RefSeq chr22- 18606126 18611919 RIMBP3 85376 RIMS binding protein 3 NA .									
NA - . NA NA NA NA NA NA NA NA NA									
LNCV6_128271_PI430048170				0.00116177818892	2.32469946	5.01973608		5.38027207	
5.23979390	P	P	P	3.85383916	4.08574983	4.06069608	P	P	P
LNCV6_128271_PI430048170 mRNA									
TAGGAGCAGTGAGTGACAAAGCCTCTGAAAGATGCATCATCTCTTCCTCACACCCATTTA NM_005631									
RefSeq chr7 + 129188871129213544SMO 6608 "smoothened, frizzled class receptor"									
GO:0005515 GO:0017147 GO:0034504 GO:0060248 GO:0021696 GO:0001755 GO:0007228 GO:0005113 GO:0007224 GO:0031069 GO:0043231 GO:0001947 GO:0021794 GO:0071397 GO:0060644 GO:0003140 GO:0048589 GO:0070062 GO:0060684 GO:0050679 GO:0005794 GO:0001708 GO:0004930 GO: NA - . NA NA NA NA NA NA NA NA NA									
LNCV6_34277_PI430048170				0.00117030669551	2.67770564	9.56369946		9.87187704	
9.54307839	P	P	P	8.31787595	8.28481292	8.13014220	P	P	P
LNCV6_34277_PI430048170 mRNA									
GCACCTGGCTTTATTTCTGGTGCACCTCTCCTGAGAGTGTAGACCAAGGTTGCCTAAT NM_001242313									
RefSeq chr22+ 18527801 18530573 TMEM191B728229 transmembrane protein 191B									
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA									
LNCV6_128696_PI430048170				0.00117766801680	2.67180372	7.15216077		7.00877664	
7.21766566	P	P	P	5.55939106	5.91799450	5.63011051	P	P	P
LNCV6_128696_PI430048170 mRNA									
CTAAAGTATTTTATCCAAATTCGAATAAATTTTCCCAACAACCTTGCAGCGGGTGGAATGT NM_001048265									
RefSeq chr9 - 135495179135499915 C9orf116 138162 "chromosome 9 open reading frame 116, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA									
LNCV6_144304_PI430048170				0.00118921505348	2.85746865	6.45588213		6.50666123	
6.07571770	P	P	P	4.63926487	5.03461088	4.83030435	P	P	P
LNCV6_144304_PI430048170 mRNA									
CTTGTAGCCCTTTCCAAGCTTCTAGAAGGTGCTTAGTAAATACTTGATAAGCCCCACGTG NM_007101									
RefSeq chr9 - 133663561 133739955 SARDH 1757 "sarcosine dehydrogenase, transcript variant 1" GO:0005739 GO:0005759 GO:0055114 GO:0008480 . NA - . NA NA NA NA NA NA NA									
LNCV6_131287_PI430048170				0.00119079043493	2.01238357	13.27070097		13.35306316	

13.40776279	P	P	P	12.48079264	12.27568324	12.23972278	P	P	P
LNCV6_131287_PI430048170	mRNA								
TTCAAGCTCAAACACCACCTCCCTTATTCAGGACCGGCACTTCTTAATGTTTGTGGCTTT NM_007278									
RefSeq chr17 - 7240418 7242434 GABARAP 11337 GABA(A) receptor-associated protein									
GO:0005515 GO:0008017 GO:0008625 GO:0048471 GO:0005886 GO:0007268 GO:0050811 GO:0006605 GO:0015629 GO:0005764 GO:0005829 GO:0061025 GO:0000045 GO:0005776 GO:0000422 GO:0005875 GO:0005930 GO:0005874 GO:0000421 GO:0048487 GO:0000226 GO:0000407 GO:0031410 GO:NA									
LNCV6_138822_PI430048170				0.00119495146685	2.25587057	4.97239107	4.94655223		
4.65544934	P	P	P	3.61321430	3.55735505	3.88238709	P	P	P
LNCV6_138822_PI430048170	mRNA								
CCTGGGTTTCTCTTACTCAATCCCTGGAGTGTAAGCATTTGGATTGTGTCACAGATTACC NM_024709									
RefSeq chr1 + 220690285 220699157 C1orf115 79762 chromosome 1 open reading									
frame 115 GO:0016021 . NA - . NA NA NA NA NA NA NA NA									
LNCV6_134531_PI430048170				0.00119640377930	5.72116475	6.99518547	6.88954651		
6.80559836	P	P	P	4.51956486	4.07727776	4.50833167	P	P	P
LNCV6_134531_PI430048170	mRNA								
TGTGGGTTCTGCCGGTGGGGCTTCAGGAGTAATAAAGTGTCCACCTATCCTTGTAATAAAAA NM_014427									
RefSeq chr16 + 89575767 89597246 CPNE7 27132 "copine VII, transcript variant 2"									
GO:0006629 GO:0005215 GO:0006810 GO:0070062 . NA - . NA NA NA NA NA									
LNCV6_126720_PI430048170				0.00120237727230	2.46607964	6.07023825	5.90317810		
5.69107781	P	P	P	4.49304149	4.72962573	4.54931728	P	P	P
LNCV6_126720_PI430048170	mRNA								
TGAGAAAGACTCCAACCTCCAGAACCCATTTAAAATCGACCGCACAGAGTTCATTCCCAG NM_024821									
RefSeq chr22 + 41800621 41826299 CCDC134 79879 "coiled-coil domain containing 134, transcript variant 1" GO:0016020 GO:0005576 . NA - . NA NA NA									
LNCV6_137899_PI430048170				0.00120345546617	2.30063581	4.62870264	4.29328403		
4.33346238	P	P	P	3.36035313	3.26892050	3.02311915	P	P	P
LNCV6_137899_PI430048170	mRNA								
ATGCAGAAAGCCGAAGAGTTAGAACTTTTGGATACAGCAGAAGAAACAGCGGCTCCACTA NM_145641									
RefSeq chr22 - 36140322 36166177 APOL3 80833 "apolipoprotein L, 3, transcript variant beta/a"									
GO:0007165 GO:0005737 GO:0006954 GO:0016020 GO:0006869 GO:0042157 GO:0005576 GO:0004871 GO:0043123 GO:0005319 GO:0008289 . NA - . NA NA NA NA NA									
LNCV6_145003_PI430048170				0.00121255150973	3.12594701	8.84792730	8.60619667		
8.48663105	P	P	P	7.19732057	7.07954772	6.71150785	P	P	P
LNCV6_145003_PI430048170	mRNA								
TGTGAATGCCGCGTCTGTCTGGTGACAGGAGAACAAATGTTGGTGAACGTCGCAAAAAA NM_001009939									
RefSeq chr22 + 19718434 19723322 SEPT5 NA "septin 5, transcript variant 2" NA									
. NA - . NA NA NA NA NA NA NA NA									
LNCV6_131927_PI430048170				0.00123193279844	2.09008486	9.63651518	9.51267463		
9.38975422	P	P	P	8.61209326	8.44681430	8.28091441	P	P	P
LNCV6_131927_PI430048170	mRNA								
CTTAGCCCAAGGGAGAGGCAATAAAGAACACAAAGCTGTTCCCGTCTGCTGAGTAAAAA NM_138493									
RefSeq chr6 - 37482920 37499924 CCDC167 154467 coiled-coil domain containing 167									
GO:0016021 . NA - . NA NA NA NA NA NA NA NA									
LNCV6_139542_PI430048170				0.00123494409069	2.32580168	9.26084369	9.56482186		
9.45500446	P	P	P	8.42590711	8.07225170	8.11945466	P	P	P
LNCV6_139542_PI430048170	mRNA								
AATCTATATGTTTCAAACCACTTGCCATCCTGTTAGATTGCCAGTTCCTGGGACCAGGC NM_198183									
RefSeq chr11- 57551654 57568330 UBE2L6 9246 "ubiquitin-conjugating enzyme E2L 6, transcript variant 2"									
GO:0005515 GO:0004842 GO:0016567 GO:0032020 GO:0045087 GO:0019941 GO:0016874 GO:0019221 GO:0032480 GO:0006464 GO:0042296 GO:0005829 . NA - . NA NA NA NA NA									
LNCV6_142117_PI430048170				0.00125511692607	2.53919565	5.70942450	5.49990641		
5.58158620	P	P	P	4.45604310	4.10227725	4.18299389	P	P	P

LNCV6_142117_PI430048170 mRNA
AGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAATA NM_138455
RefSeq chr8 + 103371514103383004CTHRC1 115908 "collagen triple helix repeat
containing 1, transcript variant 1"
GO:0017147|GO:0005581|GO:0043932|GO:0060122|GO:0005578|GO:0090177|GO:0005615|GO:003209
2|GO:0005109|GO:0045669|GO:0005737|GO:0016477|GO:0090103|GO:0033690|GO:0090090|GO:0060
071 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_132472_PI430048170 0.00125986319613 10.96122004 5.57223445 5.58827664
5.32402821 P P P 1.64043661 2.02131348 2.38049872 A A P
LNCV6_132472_PI430048170 mRNA
CCCACTAAGTATGCTTCTTTAAAGAGACTGGGAAATGTTTTAAGCAAATCTAGTTTTGT NM_001287005
RefSeq chr9 + 93058687 93085136 SUSD3 203328 "sushi domain containing 3, transcript
variant 2" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142563_PI430048170 0.00127346753420 3.74582331 11.22969066 11.33264631
11.02531124 P P P 9.31778635 9.32116296 9.24844557 P P P
LNCV6_142563_PI430048170 mRNA
GAGATAGCGAAGGGTCTGGCCTCGCTGTGATCTGATTTGGGATTAAAGGTTTGGAAATTT NM_145814
RefSeq chr19+ 53992287 54012666 CACNG6 59285 "calcium channel, voltage-dependent,
gamma subunit 6, transcript variant 1" GO:0005245|GO:0070588|GO:0034765|GO:0006816|GO:0005891
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_89109_PI430048170 0.00128702117855 3.62968872 8.72087451 8.72748803
8.75397696 P P P 6.77386561 7.01396951 6.82390959 P P P
LNCV6_89109_PI430048170 mRNA
TTATTCCTGCTGCCCGAAGACATAGGTCTTGGAAATAAAATGGCTGGTTCTTTTGTTC NM_021175
RefSeq chr19+ 35282506 35285142 HAMP 57817 hepcidin antimicrobial peptide
GO:0006879|GO:0006955|GO:0045179|GO:0005179|GO:0050832|GO:0031640|GO:0005576|GO:004274
2 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_135325_PI430048170 0.00130281004808 2.29102407 7.04091379 6.95284103
6.80862509 P P P 5.94018629 5.65180715 5.60890153 P P P
LNCV6_135325_PI430048170 mRNA
CCCCAAGACAAACGCTGATGTATCCCCGAATAAATAAAGACATCTTACATCTTCAAAAAA NM_014475
RefSeq chr19+ 48933681 48944969 DHDH 27294 dihydrodiol dehydrogenase (dimeric)
GO:0005975|GO:0047837|GO:0047115|GO:0008746|GO:0009055|GO:0042843|GO:0055114 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_138935_PI430048170 0.00130550289927 2.08458042 8.59615558 8.29011134
8.41107395 P P P 7.28598319 7.47532637 7.36705955 P P P
LNCV6_138935_PI430048170 mRNA
GGAGTGGCTGTTTTTATAAGTTGTTTTACAGATACGGAAACAGTCCAAAATGGGATTTA NM_206967
RefSeq chr16- 85707517 85751083 C16orf74 404550 chromosome 16 open reading frame
74 NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140176_PI430048170 0.00132344283147 4.51930598 5.57887729 6.06587209
6.25028297 P P P 4.06838763 3.51884179 3.80782132 P P P
LNCV6_140176_PI430048170 mRNA
ATTTTCTTCCTGGGATTGGGGAGGGGATGATTCAGACCCACATGGCCTCCAACCTTGGC NM_000453
RefSeq chr19+ 17871972 17895174 SLC5A5 6528 "solute carrier family 5 (sodium/iodide
cotransporter), member 5"
GO:0005886|GO:0008507|GO:0005634|GO:0044281|GO:0015111|GO:0055085|GO:0031982|GO:003464
1|GO:0071371|GO:0006810|GO:0006590|GO:0035725|GO:0016021|GO:0071320|GO:0015705|GO:0070
062|GO:0006811 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92065_PI430048170 0.00132525443955 2.49409705 6.41173262 6.77005616
6.61312053 P P P 5.35099533 5.17111800 5.33275835 P P P
LNCV6_92065_PI430048170 mRNA
AATTGATGGGTGAAGACACTGAAGAGTCATGAGCAGGCTCCATTAAAGCTCTTTTCTTGC NM_024643
RefSeq chr14+ 75069576 75079987 ZC2HC1C 79696 "zinc finger, C2HC-type containing
1C, transcript variant 1" GO:0046872 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_135127_PI430048170 0.00137932653533 4.77992848 3.69001977 3.94133328
3.41486925 P P P 1.81329626 1.30296219 1.11341813 A A A
LNCV6_135127_PI430048170 mRNA
CTCCAGTCTGATTTTATAAAGTGCTGACGAGATTGGGAATAAAGAGGCATAAAGAAAAA NM_182847
RefSeq chr2 + 219514169219538772ASIC4 55515 acid sensing (proton gated) ion

channel family member 4
GO:0034220|GO:0005887|GO:0005272|GO:0006810|GO:0035725|GO:0015081|GO:0005216 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_65225_PI430048170 0.00143486212038 2.31390518 12.36337703 12.50173740
12.11117208 P P P 11.11601325 10.95460916 11.28281237 P P P
LNCV6_65225_PI430048170 mRNA
GGGTTTAAGGGACTTGGGGAGCCACTGGAAGAATAATAAAAGTGTTGCTCTTTATCATCT NM_012267
RefSeq chr19- 55262222 55280383 HSPBP1 23640 "HSPA (heat shock 70kDa) binding
protein, cytoplasmic cochaperone 1, transcript variant 1"
GO:0005515|GO:0004857|GO:0006457|GO:0032436|GO:0031398|GO:0043086 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_143565_PI430048170 0.00149641286854 5.58231231 7.91797748 8.04167010
7.80682831 P P P 5.69217581 5.12078233 5.46409159 P P P
LNCV6_143565_PI430048170 mRNA
GTCTCCTAAACCAATTATGCTGTGCCTGGGAACGAAATACTGTGTCTAAGTCTCAAAAAA NM_001145536
RefSeq chr17+ 4899652 4902932 C17orf107 NA chromosome 17 open reading frame 107
NA . NA - . NA NA NA NA NA NA NA NA
LNCV6_128402_PI430048170 0.00150634298835 2.15770979 12.79289533 13.13182468
12.93851958 P P P 11.96604839 11.82297759 11.75791304 P P P
LNCV6_128402_PI430048170 mRNA
CAACCCTGACCGTGACCGTTTGCTATATTCCTTTTTCTATGAAATAATGTGAATGATAAT NM_005953
RefSeq chr16+ 56608565 56609497 MT2A 4502 metallothionein 2A
GO:0071294|GO:0005515|GO:0048471|GO:0019221|GO:0005634|GO:0035690|GO:0036016|GO:000582
9|GO:0036018|GO:0005737|GO:0006878|GO:0008144|GO:0008270|GO:0045926|GO:0060333 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_55339_PI430048170 0.00151105851206 2.45880284 7.19766475 7.42422173
7.50681005 P P P 6.07648819 6.28636539 5.85768977 P P P
LNCV6_55339_PI430048170 mRNA
TTTAACTGCGAGTTCTTCACCTTCTGCTGCGGGACCTGCTACCATCGGTACTGCTGCAGG NM_198149
RefSeq chr1 + 201888676 201892587 SHISA4 149345 "shisa family member 4, transcript
variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA
LNCV6_129443_PI430048170 0.00151588906103 3.55741350 4.95251739 5.31019001
5.40150583 P P P 3.38761303 3.68399656 3.07387952 P P P
LNCV6_129443_PI430048170 mRNA
AACAGTTTTGCCAGAGCAAGAACTCCCAGAGAATAAATGTATCCCCATCTGCCTCTAAA NM_182504
RefSeq chr7 + 73861158 73865893 WBSCR28 135886 Williams-Beuren syndrome
chromosome region 28 GO:0016021 . NA - . NA NA NA NA NA NA NA NA
NA NA
LNCV6_144822_PI430048170 0.00151984997011 2.49845390 5.77218184 5.90771943
6.18400960 P P P 4.42434537 4.63366389 4.84337037 P P P
LNCV6_144822_PI430048170 mRNA
GCAGTCACCCATCAGAGAAAATAAAAATGGAAACCACGTTACAGCATTTTAAAAGTTTT NM_033201
RefSeq chr16_KI270853v1_alt+ 1092444 1246252 C16orf45 89927 "chromosome 16
open reading frame 45, transcript variant 1" GO:0021822|GO:0015630|GO:0007026. NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_138075_PI430048170 0.00153506591965 2.67300974 7.33828772 7.30445963
7.24426297 P P P 6.03279120 5.75342626 5.83241646 P P P
LNCV6_138075_PI430048170 mRNA
TCCTTACAGGACTGACACCCTAATGCCAATAAAAGTTGCTCATTATGGACTGCTACAAAG NM_032211
RefSeq chr10- 98247685 98268250 LOXL4 84171 lysyl oxidase-like 4
GO:0043235|GO:0005515|GO:0016020|GO:0005507|GO:0004720|GO:0005615|GO:0006898|GO:007006
2|GO:0055114|GO:0005044. NA - . NA NA NA NA NA NA NA NA
LNCV6_134413_PI430048170 0.00161614729061 2.50511555 8.36063167 8.45666948
8.05542245 P P P 6.83907852 7.21610317 6.83888649 P P P
LNCV6_134413_PI430048170 mRNA
CTGCTGTAGAGCTGAAGCTGAACATGTGTTTGCTAAATAAAGATTCCCATTCTAGCGCA NM_194312
RefSeq chr2 + 238100309 238133287 ESPNL 339768 espin-like NA . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_144762_PI430048170 0.00164577471274 2.25281260 5.43499044 5.27211709
5.06578497 P P P 4.23883436 3.86707047 4.14982460 P P P
LNCV6_144762_PI430048170 mRNA

TAAATGGGGGCTCCATTAGTTCTGCTGCCGAGACTAATAAAGATTTGGTTGGCTCTAGCA NM_021200
RefSeq chr11+ 73646177 73662819 PLEKHB1 58473 "pleckstrin homology domain
containing, family B (evectins) member 1, transcript variant 1"
GO:0005515|GO:0005737|GO:0045595|GO:0007275|GO:0016021|GO:0004871|GO:0008022|GO:000760
2|GO:0042803 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141702_PI430048170 0.00165689405227 2.14014077 8.31764279 8.65062307
8.57403381 P P P 7.54744482 7.34426128 7.36953323 P P P
LNCV6_141702_PI430048170 mRNA
AAGAGTTTCAATCAGACATGACTGTGACGTGCATCCTCAATTAGAATTAAAGTGATGTAT NM_001128592
RefSeq chr6 + 3258927 3268066 PSMG4 NA "proteasome (prosome, macropain)
assembly chaperone 4, transcript variant 1" NA . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_138570_PI430048170 0.00166714810087 6.32213110 5.19271305 5.23236976
4.86687782 P P P 2.42515544 2.47278014 2.43950209 A P P
LNCV6_138570_PI430048170 mRNA
GTGATGAACGCTCTGAACCCCTATAAAAAATGTGCATGTAAATATATACTCTCAACATT NM_144613
RefSeq chr19- 55349701 55354814 COX6B2 125965 cytochrome c oxidase subunit VIb
polypeptide 2 (testis) GO:0005758|GO:0004129|GO:0030061. NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_133510_PI430048170 0.00167682090513 4.45414131 5.41870877 5.52751939
5.29277249 P P P 3.13344316 3.55288135 3.04416954 P P P
LNCV6_133510_PI430048170 mRNA
GTCAAGACAATCCATTCCATTCAAGACCAATTTACTCTCAAATTTTGCCAACACAGAAAT NM_152421
RefSeq chr9 + 136712571 136724718 FAM69B 138311 "family with sequence similarity 69,
member B"GO:0005789|GO:0016021 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_91166_PI430048170 0.00172090837800 3.47949706 4.31552723 4.08409574
4.38376926 P P P 2.41157164 2.74290045 2.19594650 A P A
LNCV6_91166_PI430048170 mRNA
AGCAATAATTACCTGACCAAGGAGGAGTGCCTCAAGAAATGTGCCACTGTCACAGAGAAT NM_021102
RefSeq chr19+ 38264457 38292614 SPINT2 10653 "serine peptidase inhibitor, Kunitz
type, 2, transcript variant a"
GO:0010951|GO:0005737|GO:0004866|GO:0004867|GO:0006928|GO:0005576|GO:0016021 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_134559_PI430048170 0.00175051697653 2.37581487 7.25224738 7.50079303
7.46307733 P P P 5.91844813 6.30768723 6.22833406 P P P
LNCV6_134559_PI430048170 mRNA
TTTAAATAAGGTTGGAGATGTCAAGTTGGGTTCACTTGCCATGCAGGAAGAGGCCCACTA NM_174963
RefSeq chr1 + 43707532 43931165 ST3GAL3 6487 "ST3 beta-galactoside alpha-2,3-
sialyltransferase 3, transcript variant 1"
GO:0005975|GO:0016266|GO:0005576|GO:0044281|GO:0003836|GO:0042339|GO:0030173|GO:000013
9|GO:0006493|GO:0008118|GO:0018146|GO:0032580|GO:0009405|GO:0006488|GO:0044267|GO:0030
203|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA
LNCV6_144168_PI430048170 0.00178353404698 2.03973841 5.57259226 5.33374853
5.64496150 P P P 4.54412770 4.55429046 4.37917640 P P P
LNCV6_144168_PI430048170 mRNA
TTAAGCAGTAATCCTACTTCATTAAGCCTTCCTGGGGTGCGGTACACACCGTTAATTTCAG NM_018242
RefSeq chr17+ 19533853 19579033 SLC47A1 55244 "solute carrier family 47 (multidrug
and toxin extrusion), member 1"
GO:0015695|GO:0005886|GO:0006855|GO:0031988|GO:0005451|GO:0016021|GO:0055085|GO:001523
8 . NA - . NA NA NA NA NA NA NA NA
LNCV6_97152_PI430048170 0.00181223922476 4.03454387 8.80675110 8.88053881
9.19452652 P P P 6.55430898 7.10754194 7.14106914 P P P
LNCV6_97152_PI430048170 mRNA
AGTCAAAGTCGAGGATATTTTTTATTTCAGGCCACGGAATGGAAGAAGGTCAGCAGGGTTC NM_006681
RefSeq chr4 - 55595228 55636298 NMU 10874 "neuromedin U, transcript variant 1"
GO:0007586|GO:0005102|GO:0005576|GO:0009648|GO:0006940|GO:0001696|GO:0019233|GO:000716
5|GO:0007186|GO:0045987|GO:0007218|GO:0050806|GO:0043195|GO:0046887|GO:0042922|GO:0042
755 . NA - . NA NA NA NA NA NA NA NA
LNCV6_138038_PI430048170 0.00181862826598 3.70937942 10.76104407 10.89662745
11.09491396 P P P 9.31860242 8.73035578 8.98922952 P P P

LNCV6_138038_PI430048170 mRNA
GTTTGCAGTCTTCAGTTGTGTTCTTATGCTTCAGTGTCACATTTTCATTTGAAACT NM_013338
RefSeq chr13- 36949770 36999367 ALG5 29880 "ALG5, dolichyl-phosphate beta-glucosyltransferase, transcript variant 1"
GO:0004581|GO:0004576|GO:0007368|GO:0016020|GO:0005789|GO:0006486|GO:0016021|GO:0006488|GO:0044267|GO:0043687|GO:0018279 . NA - . NA NA NA NA NA NA NA NA
LNCV6_140876_PI430048170 0.00188160381509 4.32662606 9.12108652 9.47785161
9.27248088 P P P 7.53482720 6.99541121 6.94723861 P P P
LNCV6_140876_PI430048170 mRNA
TCGCTGGCTTTTCCCCTTGTGTTCTGAGAATACACCATCGGCTCATTCCCACCAGCGGCT NM_002282
RefSeq chr12- 52314300 52321398 KRT83 3889 "keratin 83, type II"
GO:0042633|GO:0008544|GO:0005198|GO:0007568|GO:0045095|GO:0005615 . NA - .
NA NA NA NA NA NA NA NA NA NA
LNCV6_125055_PI430048170 0.00190659918652 2.40780240 5.90416180 5.59113583
5.72198263 P P P 4.22840070 4.50378186 4.66576577 P P P
LNCV6_125055_PI430048170 mRNA
AAGATGCCAAAGCTTCGCTTTGCCAGTAGAATCCGGAATAATTCGGAAGAAGCAATTTTAA NM_006528
RefSeq chr7 - 93885396 93890991 TFPI2 7980 "tissue factor pathway inhibitor 2, transcript variant 1"
GO:0010951|GO:0007596|GO:0004867|GO:0005578|GO:0005634|GO:0005201 . NA - .
NA NA NA NA NA NA NA NA NA NA
LNCV6_128667_PI430048170 0.00190984927953 6.02021268 4.04174485 4.89615436
4.64939693 P P P 1.55378358 2.40900472 1.84948792 A P A
LNCV6_128667_PI430048170 mRNA
CTGTCTTGGCTTTCATGTTATTAAACGTATGCATGTGAAGAAAGGGTGTTTTTCTGTTTT NM_004233
RefSeq chr6 + 14117633 14136917 CD83 9308 "CD83 molecule, transcript variant 1"
GO:0014070|GO:0007165|GO:0032733|GO:0005886|GO:0032743|GO:0005887|GO:0043372|GO:0006959|GO:0032713|GO:0006952|GO:0009897 . NA - . NA NA NA NA NA NA NA NA
NA NA
LNCV6_134793_PI430048170 0.00197678640248 2.31205050 6.91368364 6.84417064
6.55478007 P P P 5.46988858 5.80439182 5.40250492 P P P
LNCV6_134793_PI430048170 mRNA
AGTCCCACTTAGCTTGGGGTCAGAACCAAGGGGTTTAATAAATAACCCTTGAAAAGTGGGA NM_052972
RefSeq chr19- 4537214 4540024 LRG1 116844 leucine-rich alpha-2-glycoprotein 1
GO:0008150|GO:0003674|GO:0016020|GO:0001938|GO:0050873|GO:0005576|GO:0005615|GO:0005160|GO:0045766|GO:0070062|GO:0030511 . NA - . NA NA NA NA NA NA NA NA
NA NA
LNCV6_136792_PI430048170 0.00197731620854 2.32779153 3.58820398 3.19110587
3.34286191 P P P 1.91157341 2.24021672 2.31093288 A A A
LNCV6_136792_PI430048170 mRNA
GTCTACATTTGATTGTACGTAGAATGTTTAAAAGTCAGTTATAAGCCATCTCATCCCATC NM_032146
RefSeq chr3 + 97764520 97798535 ARL6 84100 "ADP-ribosylation factor-like 6, transcript variant 1"
GO:0005515|GO:0060170|GO:0051258|GO:0007368|GO:0005886|GO:0007264|GO:0030117|GO:0032402|GO:0046872|GO:0005829|GO:0005737|GO:0005543|GO:0006612|GO:0005879|GO:0045444|GO:0016055|GO:0070062|GO:0034464|GO:0006996|GO:0005930|GO:0046909|GO:0010842|GO:0072372|GO: .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142225_PI430048170 0.00199958964508 2.28003310 9.83668162 10.09914279
9.95950770 P P P 8.76818460 8.82613066 8.74459617 P P P
LNCV6_142225_PI430048170 mRNA
TGCACTCACAGGATCCTGAGCTGCACTTACCTGTGAGAGTCTTCAAACCTTTTAAACCTTG NM_002872
RefSeq chr22- 37225260 37244299 RAC2 5880 "ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)"
GO:0008284|GO:0005886|GO:0007264|GO:0005884|GO:0010810|GO:0045453|GO:0003924|GO:0060263|GO:0005635|GO:0005829|GO:0010592|GO:0007411|GO:0010310|GO:0007015|GO:0070062|GO:0051056|GO:0030168|GO:0005525|GO:0030027|GO:0071593|GO:0006184|GO:0007165|GO:0007186|GO: .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127913_PI430048170 0.00203124297571 3.63412956 4.23673471 4.73667026
4.23159036 P P P 2.48266477 2.73679361 2.44316295 A P P
LNCV6_127913_PI430048170 mRNA
ATAGTAAATGTTTTATTTCGGGTGTATCATTTCATACAGTAAAGACACCAATCTTCAGAGGC NM_001290212

RefSeq chr17+ 81637170 81648755 TSPAN10 83882 "tetraspanin 10, transcript variant 1"
GO:0072594|GO:0016021|GO:0019899. NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_128346_PI430048170 0.00204812935434 3.55412322 5.32265179 5.95911368
5.73873857 P P P 3.79649514 3.57312240 4.16927043 P P P
LNCV6_128346_PI430048170 mRNA
CAAGTTTGTAGAATAAACACTGGTTTCCTAGCCATCCTCTGAAAACAGTATGAAACATGA NM_022147
RefSeq chr3 + 187368379 187371581 RTP4 64108 receptor (chemosensory) transporter
protein 4 GO:0005515|GO:0005737|GO:0006612|GO:0016021|GO:0001580 . NA - . NA
NA NA NA NA NA NA NA NA NA
LNCV6_102887_PI430048170 0.00206540956319 10.87487059 3.51060945 4.01917556
4.45088626 P P P 0.38805376 0.80807060 0.57586445 A A A
LNCV6_102887_PI430048170 mRNA
AAGGAATGTTATCAGTATTAAGCTAATGGTCCTGTTATGTCATTGTGTTTGTGTGCTGTT NM_005025
RefSeq chr3 + 167735722 167825569 SERPINI1 5274 "serpin peptidase inhibitor, clade I
(neuroserpin), member 1, transcript variant 1"
GO:0010951|GO:0004867|GO:0007422|GO:0007417|GO:0030155|GO:0005615|GO:0070062 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_139323_PI430048170 0.00208045600011 2.40927587 5.33165041 5.69123511
5.40972334 P P P 3.95623171 4.24709266 4.41237993 P P P
LNCV6_139323_PI430048170 mRNA
TGTGGGTGGGGGACTAACTGCGCAATGTAGTTAGGTGCTCAATAAACGGAGTTGCCGCTG NM_001301159
RefSeq chr16+ 566994 569495 NHLRC4 283948 "NHL repeat containing 4, transcript
variant 1" NA . NA - . NA NA NA NA NA NA NA NA
LNCV6_132915_PI430048170 0.00210433068382 3.09572408 9.81989188 10.14646676
10.21096825 P P P 8.50060456 8.46840723 8.34233955 P P P
LNCV6_132915_PI430048170 mRNA
GCTTCTGTGTTGTGATTCCCTTCTCTTCAACGGTTTCAGTACATATCTCTCTTCAATAAA NM_032882
RefSeq chrX + 153072413 153075019 PNMA6A 84968 paraneoplastic Ma antigen family
member 6A NA . NA - . NA NA NA NA NA NA NA NA
LNCV6_127242_PI430048170 0.00212342907127 2.21720798 6.46789740 6.77903668
6.60663410 P P P 5.55008846 5.42458684 5.44640970 P P P
LNCV6_127242_PI430048170 mRNA
CCACCCACCTGGATTCCCTGTTCTTTGAAGTGGCACCTAATAAGAAATAATACCCTGCC NM_002686
RefSeq chr17+ 39668452 39670475 PNMT 5409 "phenylethanolamine N-methyltransferase,
transcript variant 1"
GO:0034641|GO:0004603|GO:0042418|GO:0044281|GO:0032259|GO:0042423|GO:0005829 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_130787_PI430048170 0.00219586681696 2.19955839 9.31721018 9.36207020
9.15533013 P P P 8.30312728 8.17289866 7.93061011 P P P
LNCV6_130787_PI430048170 mRNA
CGTCCTCCTGGGGTGGACCCTAGTTTAAATAAAGATTCACCAAGTTTCACGCATCAAAAAA NM_001302688
RefSeq chr19+ 44905748 44909395 APOE348 "apolipoprotein E, transcript variant 1"
GO:0005515|GO:0010468|GO:0006707|GO:0007603|GO:0005764|GO:0002021|GO:0005615|GO:003436
1|GO:0034365|GO:0034364|GO:0034363|GO:0034362|GO:0019433|GO:0034447|GO:0033344|GO:0032
868|GO:0005794|GO:0016209|GO:0007568|GO:0031232|GO:0006898|GO:0007271|GO:0034372|GO.
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_126900_PI430048170 0.00221233289933 2.73240885 7.06654256 7.08120521
6.93598430 P P P 5.66658278 5.69934109 5.34594754 P P P
LNCV6_126900_PI430048170 mRNA
ATTTATTTGTTTCAAGAATACATTGGCAGCTGCTAGTGGTTTCCCTGGAAGTGGCAGCAGCA NM_001080496
RefSeq chr9 + 35749279 35753267 RGP19827 RGP1 retrograde golgi transport homolog (S.
cerevisiae)
GO:0005515|GO:0043234|GO:0017112|GO:0017137|GO:0016020|GO:0034066|GO:0042147|GO:003285
1|GO:0005829 . NA - . NA NA NA NA NA NA NA NA
LNCV6_141068_PI430048170 0.00236725846226 6.97034631 4.03334194 3.80571258
3.35682740 P P P 0.30814666 1.22478037 1.16979098 A A A
LNCV6_141068_PI430048170 mRNA
GATAGAGTTGAGGAGTGTGAGGCTGTTAGACTGTTAGATTTAAATGTATATTGATGAGAT NM_000557
RefSeq chr20- 35433348 35438190 GDF58200 growth differentiation factor 5
GO:0005515|GO:0035137|GO:0035136|GO:0005886|GO:0050680|GO:0007267|GO:0030326|GO:006039

5|GO:0005615|GO:0042802|GO:0043524|GO:0030198|GO:0002062|GO:0040014|GO:0043408|GO:0007179|GO:0032332|GO:0048468|GO:0010862|GO:0005576|GO:0042981|GO:0030509|GO:0005160|GO.NA - . NA NA NA NA NA NA NA NA
LNCV6_130943_PI430048170 0.00240241542587 2.32369985 10.25433797 10.19052733
10.34756139 P P P 8.83756439 9.12710122 9.16141447 P P P
LNCV6_130943_PI430048170 mRNA
CTGCCCTGTTTGAACCTCCTGTTTGACAATGTTTGCTGTTGATTTTTTTGTTCAATAAAGA NM_144569
RefSeq chr1 - 31790421 31816051 SPOCD1 90853 "SPOC domain containing 1, transcript variant 1" GO:0010923|GO:0006351 . NA - . NA NA NA NA NA NA NA NA
LNCV6_134021_PI430048170 0.00243764225619 2.61000642 4.54685763 4.99201887
4.94515679 P P P 3.39460661 3.62419342 3.33689295 P P P
LNCV6_134021_PI430048170 mRNA
TGAAGGAAACAACACATTTATACGGATTTCATATTTCTACCCGCCTTTCCTGACTCTGTG NM_001405
RefSeq chr19+ 1286153 1301430 EFNA2 1943 ephrin-A2
GO:0031594|GO:0048013|GO:0046875|GO:0046849|GO:0021772|GO:0005886|GO:0007411|GO:0030316|GO:0007267|GO:0043204|GO:0005576|GO:0031225 . NA - . NA NA NA NA NA NA
LNCV6_110416_PI430048170 0.00247755985624 2.37789268 5.55150417 5.82198949
5.50855521 P P P 4.51417877 4.50227734 4.09964672 P P P
LNCV6_110416_PI430048170 mRNA
CTTGCGAGGCGTCCAATAAGCACGGCCATGCGAGGGCGCTCTACGTACTTGTGGTCTACG NM_145296
RefSeq chr19- 43622369 43639839 CADM4 199731 cell adhesion molecule 4
GO:0016021|GO:0007155|GO:0070062. NA - . NA NA NA NA NA NA NA NA
LNCV6_131374_PI430048170 0.00248775081537 2.72847501 7.30198357 7.11439132
7.22716570 P P P 5.77827246 5.96109198 5.53458598 P P P
LNCV6_131374_PI430048170 mRNA
TTCCATCTAGCTGCTAATGCCAAGTGTCCCTAAAGATGGAGGAATAAAGCCACCAATTCT NM_004143
RefSeq chrX - 72301637 72306987 CITED1 4435 "Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 1, transcript variant 1"
GO:0001656|GO:0005515|GO:0001658|GO:0043627|GO:0060711|GO:0003700|GO:0044212|GO:0060712|GO:0051591|GO:0042803|GO:0043524|GO:0000578|GO:0042438|GO:0032496|GO:0070670|GO:0007179|GO:0071107|GO:0032868|GO:0071104|GO:0071105|GO:0003713|GO:0060231|GO:0001890|GO.NA - . NA NA NA NA NA NA NA NA
LNCV6_141836_PI430048170 0.00259959197069 2.92017371 3.88164553 4.26608838
4.45239468 P P P 2.90934382 2.36969861 2.68985991 P A P
LNCV6_141836_PI430048170 mRNA
GGGTGCACTGACAAAGTATAGAAGGTTCTAGGTATCTTAATGTGTGGATATTCTTAATTA NM_012240
RefSeq chr12+ 120302320120313242SIRT4 23409 sirtuin 4
GO:0005515|GO:0006342|GO:0034983|GO:0046322|GO:0070403|GO:0006974|GO:0003950|GO:0034979|GO:0005739|GO:0006471|GO:0046889|GO:0072350|GO:0005759|GO:0008270|GO:0046676|GO:0006541 . NA - . NA NA NA NA NA NA NA NA
LNCV6_141209_PI430048170 0.00261216351340 2.25195579 7.61272060 7.50809332
7.26485197 P P P 6.37944529 6.45216460 6.02752023 P P P
LNCV6_141209_PI430048170 mRNA
ATGGAGAAAGCCACAGTTAGAAGTGTGGATACAGGAGAAGAAACAGCGGCTCCACTAAA NM_030643
RefSeq chr22- 36189127 36204833 APOL4 80832 "apolipoprotein L, 4, transcript variant a" GO:0006629|GO:0003674|GO:0006869|GO:0042157|GO:0005575|GO:0005615|GO:0008289 .
LNCV6_11336_PI430048170 0.00267253686214 2.24034299 5.55141517 5.96212208
5.91359662 P P P 4.43644183 4.68605962 4.82128554 P P P
LNCV6_11336_PI430048170 mRNA
TAGACCGGGAGTCTGGACTTGGAGCGTGAAGTCTCACCCGAGCCGGTCCCCTTACAAC NM_001270945
RefSeq chr1 + 111990567111998841LOC643355 643355 uncharacterized LOC643355 NA
LNCV6_73389_PI430048170 0.00268755700526 2.09600703 4.21291609 4.22445323
4.57755914 P P P 3.44818332 3.11908208 3.25623864 P P P
LNCV6_73389_PI430048170 mRNA
ATTGGAAAAGCTCAACTTGAAGCTTTCTTGCCTGCAGTGAAGCAGAGAGATAGATATTAT NM_212543
RefSeq chr3 - 119211741119240905B4GALT4 8702 "UDP-Gal:betaGlcNAc beta 1,4-

galactosyltransferase, polypeptide 4, transcript variant 1"
GO:0005975|GO:0044281|GO:0008378|GO:0046872|GO:0042339|GO:0000139|GO:0003945|GO:0018146|GO:0032580|GO:0009405|GO:0016021|GO:0044267|GO:0030203|GO:0006643|GO:0018279|GO:0043687 . NA - . NA NA NA NA NA NA NA NA
LNCV6_143450_PI430048170 0.00268833412424 2.05245827 4.99216091 5.32265179
4.96850230 P P P 4.11273321 3.90331405 4.16962655 P P P
LNCV6_143450_PI430048170 mRNA
AATTACAAGTCAGGGTCTGAACCCAGTGTGATGGGGGGAGTCTCTGGGGCCCTGAGTTCA NM_032129
RefSeq chr1 + 966496 975104 PLEKHN1 84069 "pleckstrin homology domain
containing, family N member 1, transcript variant 1" GO:0005886 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_136213_PI430048170 0.00269429424844 5.18144011 4.16302540 3.79688444
3.79113041 P P P 1.09983649 1.54488924 1.90704114 A A A
LNCV6_136213_PI430048170 mRNA
GCTTCTCAAGCTGACAATTCTCACTTTGCAATAAATAGTCCAGTGTTCCTTCCAAAAA NM_001169
RefSeq chr16+ 25216963 25228932 AQP8343 aquaporin 8
GO:0005886|GO:0046691|GO:0009992|GO:0045177|GO:0055085|GO:0043231|GO:0034220|GO:0005887|GO:0015250|GO:0015722|GO:0015793|GO:0006810|GO:0006833|GO:0015254|GO:0071320|GO:0000302 . NA - . NA NA NA NA NA NA NA NA
LNCV6_130876_PI430048170 0.00272203551696 3.91949717 6.59285077 6.85316660
6.74161698 P P P 5.08618393 4.54770040 4.58907932 P P P
LNCV6_130876_PI430048170 mRNA
GGGCTCTGGAATCCCTTTGTAAATAGGTGTGTTGAATTTGTTTTGAAGTGAATAAAATTC NM_018088
RefSeq chr12- 8221259 8227618 FAM90A1 55138 "family with sequence similarity 90,
member A1" GO:0008270|GO:0003676 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_138976_PI430048170 0.00278983879254 3.00332030 8.99248663 9.18958339
8.81507353 P P P 7.09993792 7.69570551 7.40497293 P P P
LNCV6_138976_PI430048170 mRNA
CATTTTTGAAGCACCTGCTCCTTTTCTTGCACTGTATTTTCTACAACCAGATTGTATTAA NM_018419
RefSeq chr20- 64047725 64049626 SOX18 54345 SRY (sex determining region Y)-box
18
GO:0000790|GO:0044212|GO:0005634|GO:0060836|GO:0048866|GO:0001947|GO:0001946|GO:0061028|GO:0045944|GO:0060956|GO:0042789|GO:0048469|GO:0001942|GO:0001944|GO:0035050|GO:0046982|GO:0060214|GO:0001525|GO:0000122|GO:0000978|GO:0001701|GO:0003151|GO:0022405|GO:NA - . NA NA NA NA NA NA NA NA
LNCV6_142526_PI430048170 0.00279122090526 2.19021359 12.23163556 12.63525498
12.31201442 P P P 11.36575240 11.33245070 11.10625910 P P P
LNCV6_142526_PI430048170 mRNA
GCCTGGAAACGTGCCAGGACACTGTCCTGGTGCCCAGCCCAACGTGGTCCAACGTTTTTT NM_002513
RefSeq chr16- 1770319 1771709 NME3 4832 NME/NM23 nucleoside diphosphate kinase
3
GO:0006241|GO:0004550|GO:0006915|GO:0042981|GO:0006220|GO:0009142|GO:0005524|GO:0046872|GO:0005829|GO:0005739|GO:0006165|GO:0006228|GO:0006183|GO:0006163|GO:0070062 . NA
- . NA NA NA NA NA NA NA NA
LNCV6_139423_PI430048170 0.00280822288129 2.38097694 5.79889387 5.74124989
5.69189326 P P P 4.35748960 4.66989105 4.43329544 P P P
LNCV6_139423_PI430048170 mRNA
GGGATGTCCGCTATATCCAAAATTACAGCTATTGGCAAATAAACGAGATGGATAAAGGTG NM_005167
RefSeq chr1 - 112709993112715328PPM1J 333926 "protein phosphatase, Mg2+/Mn2+
dependent, 1J" GO:0006470|GO:0004722 . NA - . NA NA NA NA NA NA
NA NA
LNCV6_134610_PI430048170 0.00280884860291 3.20194504 9.91923372 10.43462892
10.24720076 P P P 8.61973170 8.58288049 8.39829977 P P P
LNCV6_134610_PI430048170 mRNA
ACAGACATGGTTTGTCACTGTTGAGCTTCTGTTCTAGAGAATCCTAGAGGCTTGATTGG NM_024827
RefSeq chr3 + 13480214 13506424 HDAC11 79885 "histone deacetylase 11, transcript
variant 1"
GO:0032041|GO:0070932|GO:0070933|GO:0006355|GO:0016575|GO:0005886|GO:0005634|GO:0046970|GO:0006351|GO:0000118|GO:0014003|GO:0004407|GO:0046969|GO:0070062|GO:0008134|GO:0016568 . NA - . NA NA NA NA NA NA NA NA

LNCV6_116939_PI430048170 0.00284792979236 2.07262711 4.74155220 5.04790957
 5.13724290 P P P 3.95057713 4.08011655 3.75201457 P P P
 LNCV6_116939_PI430048170 mRNA
 TTGACATTTGAATAGGATCCGAGATGTTCTGCTTTTATCCCGGGCAGCCCTGATATGTCA NM_004980
 RefSeq chr1 - 111775831 111989155 KCND3 3752 "potassium channel, voltage gated Shal
 related subfamily D, member 3, transcript variant 1"
 GO:0005251|GO:0005515|GO:0005250|GO:0005886|GO:0007268|GO:0097038|GO:0030425|GO:004687
 2|GO:0044325|GO:0042383|GO:0071435|GO:0086009|GO:0008076|GO:0043025|GO:0051260|GO:0034
 765|GO:0006813 . NA - . NA NA NA NA NA NA NA NA
 LNCV6_141741_PI430048170 0.00287900775982 2.95813003 5.71642372 5.92693094
 6.28538138 P P P 4.27838528 4.37556531 4.61741555 P P P
 LNCV6_141741_PI430048170 mRNA
 CCTACTGTTTGTATTTGCAAACTGAGCTTGTTGGAGGGAAGGCATTATTTTTTAAAATAC NM_003645
 RefSeq chr15+ 50182195 50236392 SLC27A2 11001 "solute carrier family 27 (fatty acid
 transporter), member 2, transcript variant 1"
 GO:0001676|GO:0006699|GO:0070251|GO:0097089|GO:0030176|GO:0044281|GO:0005739|GO:000156
 1|GO:0050197|GO:0008206|GO:0031957|GO:0005779|GO:0044539|GO:0005778|GO:0042760|GO:0044
 255|GO:0070062|GO:0015245|GO:0006635|GO:0005102|GO:0005524|GO:0004467|GO:0005789|GO.
 NA - . NA NA NA NA NA NA NA NA NA NA
 LNCV6_140004_PI430048170 0.00290516106162 2.48998436 9.14366603 9.15771666
 9.01186398 P P P 7.55850005 7.93176223 7.85280913 P P P
 LNCV6_140004_PI430048170 mRNA
 TCAGAGGCGTACAACCTAGTTGGCGATTAGACTTGTTATGTGATGTTACCAGCCTGAAATG NM_022463
 RefSeq chr17- 799312 979758 NXN 64359 "nucleoredoxin, transcript variant 1"
 GO:0030178|GO:0004791|GO:0005634|GO:0031397|GO:0072358|GO:0016055|GO:0047134|GO:003015
 4|GO:0055114|GO:0005829. NA - . NA NA NA NA NA NA NA NA NA
 LNCV6_132798_PI430048170 0.00292018910791 2.42847646 9.04630943 9.13762669
 8.98528216 P P P 7.62175739 7.98377905 7.70209059 P P P
 LNCV6_132798_PI430048170 mRNA
 TACTGGAATAGATTCCGAGGAGCAGGAGTGCTCAATAAAATGTTGGTTTCCAGCAAAAAA NM_001197
 RefSeq chr22+ 43110747 43129712 BIK 638 BCL2-interacting killer (apoptosis-inducing)
 GO:0032464|GO:0005515|GO:0051400|GO:0031966|GO:0008637|GO:0046982|GO:0090200|GO:000691
 5|GO:0016021|GO:0007283|GO:0008584|GO:0012505 . NA - . NA NA NA NA NA NA
 NA NA NA NA
 LNCV6_129333_PI430048170 0.00293676705592 2.18488683 8.12108251 8.28414988
 7.85245544 P P P 6.82551946 7.11900231 6.94784233 P P P
 LNCV6_129333_PI430048170 mRNA
 CAGCAGAGACTTGGGACATTGCCTTTTCTAGCCCGAATACAAACACCTGGACTTAAAAAA NM_001099786
 RefSeq chr17- 64002594 64020634 ICAM2 3384 "intercellular adhesion molecule 2,
 transcript variant 1"
 GO:0016337|GO:0005178|GO:0016020|GO:0005886|GO:0030198|GO:0005887|GO:0050776|GO:000193
 1|GO:0007155|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
 LNCV6_132187_PI430048170 0.00301095090874 5.06316148 5.86084426 5.09185996
 5.47316168 P P P 3.37299810 3.08068282 3.02972935 P P P
 LNCV6_132187_PI430048170 mRNA
 TTGGAGACGGAAAACTGGAATTCTAACAAGGAGGAGAGGAGACTAAATCACATCAATTT NM_080878
 RefSeq chr1 - 160945025 160954799 ITLN2 142683 intelectin 2 GO:0030246|GO:0005576
 . NA - . NA NA NA NA NA NA NA NA NA
 LNCV6_135329_PI430048170 0.00304643444042 3.31822323 5.08692972 5.59546830
 5.43604793 P P P 3.23626121 3.75238823 3.90311092 P P P
 LNCV6_135329_PI430048170 mRNA
 TGGTCGAGCAGGGCAGTACTGGACCAGGTCTACGTCAGCATTTCAGGTTCAATGGGGACAC NM_001197237
 RefSeq chr6 + 26383210 26394872 BTN2A2 10385 "butyrophilin, subfamily 2, member
 A2, transcript variant 3" GO:0031324|GO:0046007|GO:0016021|GO:0050710|GO:0070062 . NA
 - . NA NA NA NA NA NA NA NA NA
 LNCV6_131340_PI430048170 0.00305163088453 2.30090021 5.03015109 4.59181653
 4.94080423 P P P 3.81622303 3.51740255 3.64303194 P P P
 LNCV6_131340_PI430048170 mRNA
 TGAATCCACATCCTGAAGGGAGGCTACAACCTGGAATAAAAATAAGAAAGCTTTCAAAAAA NM_153608
 RefSeq chr19+ 48270098 48287608 ZNF114 163071 "zinc finger protein 114, transcript
 variant 1"

GO:0008150|GO:0003674|GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_137293_PI430048170 0.00305585884267 2.47565045 9.60650049 9.29310229

9.08391504 P P P 7.93904258 8.26832148 7.86885557 P P P

LNCV6_137293_PI430048170 mRNA

ACCTGCCAGGGAGACAGAGCTCACAATAAAATGGCTCAGATGCCACTTCAAAGAAAAAA NM_001771

RefSeq chr19+ 35329168 35347361 CD22933 "CD22 molecule, transcript variant 1"

GO:0005515|GO:0005887|GO:0030246|GO:0007155|GO:0009897|GO:0070062 . NA - .

NA NA NA NA NA NA NA NA NA NA

LNCV6_129332_PI430048170 0.00306548882636 2.47966303 9.85813401 9.92485038

9.94625455 P P P 8.54885741 8.77570481 8.45677898 P P P

LNCV6_129332_PI430048170 mRNA

TCAACGTAACACATAATGGTACTTATCAGTGCCAAGCGTCCAGCTCACGAGGCAAATACA NM_002162

RefSeq chr19- 10333775 10339669 ICAM3 3385 intercellular adhesion molecule 3

GO:0005515|GO:0016337|GO:0005178|GO:0005886|GO:0030198|GO:0005887|GO:0050776|GO:0005102|GO:0007155|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA

LNCV6_136496_PI430048170 0.00309010911337 2.22768392 5.25485566 5.39726533

4.94839472 P P P 4.01504910 4.26984331 3.85399265 P P P

LNCV6_136496_PI430048170 mRNA

TAAACAACACACAGAGCACAAATATGCTCCTGACGGACTCAGGAAAATGCCAACAGCAGA NM_203297

RefSeq chr5 - 181193923 181200930 TRIM7 81786 "tripartite motif containing 7, transcript variant 2"

GO:0005737|GO:0008270|GO:0005634. NA - . NA NA NA NA

NA NA NA NA NA

LNCV6_83706_PI430048170 0.00310891047603 2.50907773 7.50553688 8.02631650

7.75308044 P P P 6.64280151 6.31264799 6.37324100 P P P

LNCV6_83706_PI430048170 mRNA

GATGATTTAAACATGAAAGTGTATTGTTGTCACTGTGGTAATTTCTTGCCAGTTTCTG NM_001285486

RefSeq chr2 - 96497642 96505385 NEURL3 93082 "neuralized E3 ubiquitin protein ligase 3, transcript variant 2"

GO:0004842|GO:0016567|GO:0016874|GO:0008270 . NA - . NA

NA NA NA NA NA NA NA NA

LNCV6_139062_PI430048170 0.00313874800922 2.09136446 5.21256895 5.29920906

5.28448107 P P P 4.32441352 4.22476100 4.04105618 P P P

LNCV6_139062_PI430048170 mRNA

AACAAGTTACTTGAAAGAGTGTACCAATAATCATTAAGTACGGCAGGCTGAACCTTCA NM_001291774

RefSeq chr19- 55132697 55149354 TNNT1 7138 "troponin T type 1 (skeletal, slow), transcript variant 4"

GO:0031014|GO:0045932|GO:0030049|GO:0005861|GO:0003009|GO:0031444|GO:0005523|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_49628_PI430048170 0.00315560313427 4.35612908 7.37912129 7.31157956

7.39349614 P P P 5.47810167 5.18913704 5.01009443 P P P

LNCV6_49628_PI430048170 mRNA

CCAGTGGCCACACTGGGATAGGGTGGGGAGGCTGGCAGCCCTCTTTTATAAATATTATAC NM_006841

RefSeq chr3 + 50205245 50220979 SLC38A3 10991 "solute carrier family 38, member 3"

GO:0005290|GO:0005886|GO:0006865|GO:0055085|GO:0015180|GO:0015297|GO:0005887|GO:0006867|GO:0006868|GO:0015182|GO:0015186|GO:0006814|GO:0015817|GO:0015808|GO:0006811|GO:0015293 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_135925_PI430048170 0.00315561902782 4.02430832 5.97427167 6.29376272

5.93907605 P P P 4.44610423 3.92165277 3.74533290 P P P

LNCV6_135925_PI430048170 mRNA

GATGCTTCTGAATAGAAATAAAGTGGGTTTTCCCTGGAGGTACCCAGCAGCCTGAAAAAA NM_139317

RefSeq chr20+ 63235882 63240507 BIRC7 79444 "baculoviral IAP repeat containing 7, transcript variant 1"

GO:0005515|GO:0043066|GO:0004842|GO:0004869|GO:0005794|GO:0016567|GO:0016874|GO:0070247|GO:0005634|GO:0007257|GO:0009966|GO:0005737|GO:0042127|GO:0005876|GO:0008270|GO:0090307|GO:0019899|GO:0043027 . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_143872_PI430048170 0.00320617142230 2.05868768 6.91400916 7.04078177

7.22424435 P P P 5.77126861 6.09917508 6.16985327 P P P

LNCV6_143872_PI430048170 mRNA

GTTCAGTAACCCTATGTGAATCAGATGTCTCCTGGATAACATTAAAGCCATGTCTTTGTC NM_152331

RefSeq chr14+ 73591705 73595766 ACOT4 122970 acyl-CoA thioesterase 4

GO:0052689|GO:0000038|GO:0004778|GO:0006637|GO:0001676|GO:0046459|GO:0043648|GO:001629

0|GO:0043649|GO:0005102|GO:0047617|GO:0032789|GO:0032788|GO:0006104|GO:0019605|GO:0005777 . NA - . NA NA NA NA NA NA NA NA
 LNCV6_129113_PI430048170 0.00323330309033 2.61811354 8.03377923 8.47450270
 8.33576631 P P P 7.20740891 6.65990727 6.78726017 P P P
 LNCV6_129113_PI430048170 mRNA
 CATATCAGCCCCTTCATTCCATGTATTCCAGTTGTAAAACAAGTATCAAAATATTGGGAA NM_001004323
 RefSeq chr7 - 100456614100464271C7orf61 402573 chromosome 7 open reading frame
 61 GO:0005634 . NA - . NA NA NA NA NA NA NA NA
 LNCV6_130326_PI430048170 0.00324641050177 2.28559078 7.67135848 7.67481242
 7.61800783 P P P 6.55741777 6.52011587 6.29604167 P P P
 LNCV6_130326_PI430048170 mRNA
 TCATCCTTCTTCAATAAATGCTGAATGACATTCAAGCTGATTTTCTAGACCACTGAGAAA NM_003498
 RefSeq chr16+ 11668432 11679161 SNN 8303 stannin
 GO:0009628|GO:0006950|GO:0005741|GO:0016021 . NA - . NA NA NA NA NA
 NA NA NA NA
 LNCV6_127388_PI430048170 0.00329456541128 2.23475168 12.76001270 13.04589660
 12.92387947 P P P 12.00247739 11.65125056 11.57272004 P P P
 LNCV6_127388_PI430048170 mRNA
 AAGTCTCTGGCCTCATAAAAGGTGGCTGTGGGTCGTCAGGAATCTGCGCCATCTTCCTGG NM_016535
 RefSeq chr19+ 55643619 55645623 ZNF581 51545 zinc finger protein 581
 GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA
 NA NA NA NA NA NA
 LNCV6_141213_PI430048170 0.00331411415482 2.61595129 9.80736933 10.32147662
 10.13648903 P P P 8.85172239 8.72868561 8.55359115 P P P
 LNCV6_141213_PI430048170 mRNA
 TTGATGTCCTTCCAAGAATAAAGTCTTCCCTGGTGATGGTCTCTCGCTCTGTCTTTCCA NM_145637
 RefSeq chr22- 36226208 36239954 APOL2 23780 "apolipoprotein L, 2, transcript variant beta"
 GO:0006629|GO:0008035|GO:0060135|GO:0005102|GO:0005576|GO:0007275|GO:0006953|GO:0008289|GO:0016020|GO:0006869|GO:0005789|GO:0042157|GO:0008203 . NA - . NA NA
 NA NA NA NA NA NA NA NA
 LNCV6_92423_PI430048170 0.00337587413193 2.27672360 6.48617895 6.73031443
 6.80662255 P P P 5.36147028 5.31819462 5.75945370 P P P
 LNCV6_92423_PI430048170 mRNA
 GTTGCGAGAAATTCCACAAGCCTCTTGCAACTTTTTCCTTTGCAAACACACGATCCAGAT NM_001127395
 RefSeq chr2 - 207609114207625331METTL21A 151194 "methyltransferase like 21A, transcript variant 2"
 GO:0005515|GO:0018022|GO:0005737|GO:0043462|GO:0006479|GO:0051117|GO:0030544|GO:0016279 . NA - . NA NA NA NA NA NA
 LNCV6_144482_PI430048170 0.00342884162472 2.12353070 7.50816174 7.46320038
 7.52506724 P P P 6.51734809 6.44977917 6.25826583 P P P
 LNCV6_144482_PI430048170 mRNA
 TAAAGGCTCTAATACAACCTATAAGGACTGCAAAGTATGGCCAGGGGGTAGTCGGACTT NM_024684
 RefSeq chr11+ 77821161 77872352 AAMDC 28971 "adipogenesis associated, Mth938 domain containing"
 GO:0043066|GO:0005737|GO:0045944|GO:0045600 . NA - . NA
 NA NA NA NA NA NA NA NA
 LNCV6_130700_PI430048170 0.00354432586996 2.88845320 7.49015011 7.75352988
 7.46852087 P P P 6.04934346 6.03874169 6.05098872 P P P
 LNCV6_130700_PI430048170 mRNA
 TGGCGCTTGATCTGGGGTGGGAGTAACAGGGCAGAAATGATTAAAATGTTTGAGCACAA NM_002773
 RefSeq chr16- 31131432 31135830 PRSS8 5652 "protease, serine, 8"
 GO:0005515|GO:0005886|GO:0004252|GO:0010765|GO:0006508|GO:0008236|GO:0005576|GO:0016021|GO:0005615|GO:0070062. NA - . NA NA NA NA NA NA NA NA
 LNCV6_142821_PI430048170 0.00359729653914 3.90334941 4.00180660 3.85791549
 3.37975019 P P P 1.29234053 1.92659985 2.08222701 A A A
 LNCV6_142821_PI430048170 mRNA
 CTTTGGCCCTGAGAAGGTTTTTAAATGTGTTATTTACTTCTCTAAACATGACGATTGCTA NM_001024401
 RefSeq chr16+ 28292518 28323849 SBK1 388228 SH3 domain binding kinase 1
 GO:0005737|GO:0004674|GO:0006468|GO:0005524 . NA - . NA NA NA NA NA
 NA NA NA NA
 LNCV6_127595_PI430048170 0.00365256423333 3.69008116 7.46397469 8.07473582

8.13780397 P P P 6.26554976 5.81826819 5.99726798 P P P
LNCV6_127595_PI430048170 mRNA
CGTATAACATTGTCAAGTGGAAACATGCTGAAATCTATTAAACCATCTTTGTTTGTGGAA NM_000961
RefSeq chr20- 49503873 49568170 PTGIS 5740 prostaglandin I2 (prostacyclin) synthase
GO:0005515|GO:0019369|GO:0006805|GO:0005783|GO:0019674|GO:0006767|GO:0005634|GO:000676
9|GO:0044281|GO:0005615|GO:0006690|GO:0004497|GO:0035360|GO:0001516|GO:0045019|GO:0071
354|GO:0019371|GO:0005506|GO:0071456|GO:0032088|GO:0097190|GO:0045766|GO:0006766|GO.
NA - NA NA NA NA NA NA NA NA NA NA
LNCV6_120535_PI430048170 0.00389492714413 3.97099660 5.26037255 5.49837183
6.08477456 P P P 3.22841814 3.75252115 3.93336412 P P P
LNCV6_120535_PI430048170 mRNA
TGCACACCCTCCAGAGACAACAGGTAAAACAGGGCCACATAGATGCTGATGGAGCCTTCC NM_000499
RefSeq chr15- 74719541 74725536 CYP1A1 1543 "cytochrome P450, family 1, subfamily A,
polypeptide 1"
GO:0019369|GO:0046685|GO:0006805|GO:0017144|GO:0017143|GO:0033189|GO:0009792|GO:001004
1|GO:0016711|GO:0032496|GO:0070576|GO:0044255|GO:0046677|GO:0005506|GO:0070330|GO:0042
359|GO:0007568|GO:0060137|GO:0009635|GO:0006778|GO:0097267|GO:0055093|GO:0016491|GO.
NA - NA NA NA NA NA NA NA NA NA NA
LNCV6_136347_PI430048170 0.00391821157086 2.19767461 8.11580612 7.82810919
7.62843533 P P P 6.56357636 6.94444182 6.67117210 P P P
LNCV6_136347_PI430048170 mRNA
CCTCTCGATCTGTATATCCTCCAGTCCAAGATTAAAGAGGCGGACTGTGGCCTGAAAAAA NM_001099781
RefSeq chr22- 24219653 24245142 GGT52687 "gamma-glutamyltransferase 5, transcript variant
1"
GO:0019369|GO:0006520|GO:0019370|GO:0005886|GO:0006749|GO:0044281|GO:0006691|GO:003136
2|GO:0006954|GO:0003840|GO:0006750|GO:0006508|GO:0016021 . NA - . NA NA
NA NA NA NA NA NA NA NA
LNCV6_128240_PI430048170 0.00394871812958 4.30290464 8.17379446 8.77421673
8.66610491 P P P 6.58077472 6.39020075 6.38662732 P P P
LNCV6_128240_PI430048170 mRNA
CTTCTCAACAAGAAAACTTAAATCCGTCGTGCCCAAATATAGTTGTGCTTTTATTTCCA NM_004283
RefSeq chr19- 11322045 11339668 RAB3D 9545 "RAB3D, member RAS oncogene family"
GO:0030133|GO:0009306|GO:0005886|GO:0003924|GO:0005525|GO:0072659|GO:0006886|GO:001607
9|GO:0006904|GO:0008021|GO:0042588|GO:0005739|GO:0031489|GO:0018125|GO:0051020|GO:0017
157|GO:0032482|GO:0019003|GO:0070062|GO:0030667|GO:0005768 . NA - . NA NA
NA NA NA NA NA NA NA NA
LNCV6_75093_PI430048170 0.00398232892984 3.25640471 7.17254102 7.79351856
7.62500035 P P P 6.00582741 5.85081392 5.67468883 P P P
LNCV6_75093_PI430048170 mRNA
AGCAAAAGTTGGAAGCCTGGAGTGCCTAAGCCTGCTTGTAGCCAGTGATGCCCAAATTGA NM_181726
RefSeq chr4 + 185396685 185400236 ANKRD37 353322 ankyrin repeat domain 37
GO:0005737|GO:0005634 . NA - . NA NA NA NA NA NA NA NA
LNCV6_134700_PI430048170 0.00403727655198 4.18983523 5.85064909 5.92141292
5.69456776 P P P 3.89746940 3.94857095 3.35848582 P P P
LNCV6_134700_PI430048170 mRNA
TATCATGGTGGTGTCTGTCATCTGCTGGAGCCCAATGCTGGTGTGTTGGTGGCGCTGGCCGT NM_000955
RefSeq chr19- 14472465 14475362 PTGER1 5731 "prostaglandin E receptor 1 (subtype EP1),
42kDa" GO:0007186|GO:0005886|GO:0005887|GO:0032496|GO:0004957 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_126803_PI430048170 0.00414929714542 2.02622789 7.33147921 7.65237953
7.54695309 P P P 6.72547887 6.28092013 6.45111350 P P P
LNCV6_126803_PI430048170 mRNA
TACTGTACTCAGAATCACGACATTCTTCCCTACCAAGGCCACTTCTATTTTTTTGAGGCT NM_024119
RefSeq chr17- 42101405 42112733 DHX58 79132 DEXH (Asp-Glu-X-His) box
polypeptide 58
GO:0003725|GO:0005515|GO:0003727|GO:0004386|GO:1900246|GO:1900245|GO:0039534|GO:000961
5|GO:0003677|GO:0005524|GO:0051607|GO:0005737|GO:0045087|GO:0045088|GO:0039536|GO:0008
152|GO:0016032|GO:0008270|GO:0032481|GO:0032480|GO:0045824 . NA - . NA NA
NA NA NA NA NA NA NA NA
LNCV6_108302_PI430048170 0.00419814778097 2.44067112 4.05783119 3.55628181
3.91001833 P P P 2.78031538 2.63178999 2.24330857 P P A

LNCV6_108302_PI430048170 mRNA
ATGCGGTGCCATCAACAAAAATGGTCTTCAAGCCTCAAGCTGTGAAGTTCCTTTACTG NM_005810
RefSeq chr12+ 8989624 9010744 KLRG1 10219 "killer cell lectin-like receptor
subfamily G, member 1"
GO:0006968|GO:0006954|GO:0005886|GO:0045087|GO:0050776|GO:0030246|GO:0004872|GO:001602
1|GO:0007166 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127438_PI430048170 0.00420904264932 3.16373089 4.88909221 5.15989104
5.00152702 P P P 2.99030523 3.53054702 3.49690076 P P P
LNCV6_127438_PI430048170 mRNA
TGGAGGAACCACTGAATTCTTTCCTGGCATTAAACGCATTCTGTACAGTCCCCATTCC NM_001008223
RefSeq chr12- 49332416 49337188 C1QL4 NA "complement component 1, q
subcomponent-like 4" NA . NA - . NA NA NA NA NA NA NA NA
LNCV6_145423_PI430048170 0.00422843232667 2.92064628 9.27474881 9.55989318
9.39845830 P P P 8.18055269 7.74749348 7.61873384 P P P
LNCV6_145423_PI430048170 mRNA
CTGGCGCCACCGAACCTGCACATCTCAACTTGTAACATAACAGAAAGTGACAATCGG NM_024527
RefSeq chr19- 17292130 17303473 ABHD8 79575 abhydrolase domain containing 8
GO:0016787|GO:0008152|GO:0070062. NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_140341_PI430048170 0.00429570314406 2.20500868 5.25056940 5.54884102
5.46312047 P P P 4.29932257 4.31125400 4.24484584 P P P
LNCV6_140341_PI430048170 mRNA
GGTCAGCCTTGTAATCTTAGGTAAGGATCAAAGAAATGATTCTTTGCCACTAACTTG NM_001865
RefSeq chr6 - 75237674 75243928 COX7A2 1347 "cytochrome c oxidase subunit VIIa
polypeptide 2 (liver), transcript variant 1" GO:0005746|GO:0004129|GO:0070062. NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135924_PI430048170 0.00431368343612 2.33008542 9.49126090 9.49090251
9.42948175 P P P 8.05655210 8.35335851 8.32336039 P P P
LNCV6_135924_PI430048170 mRNA
AGGCTGTCGCCATGTGGAAAGAGTAACACCAATTGCCAATAAAGTCTCATGTGGTTTTTA NM_001012271
RefSeq chr17+ 78214195 78225635 BIRC5 332 "baculoviral IAP repeat containing 5,
transcript variant 3"
GO:0008017|GO:0005515|GO:0004842|GO:0042803|GO:0042802|GO:0000910|GO:0043027|GO:004803
7|GO:0046982|GO:0005814|GO:0005819|GO:0031536|GO:0030496|GO:0051303|GO:0045931|GO:0000
777|GO:0008270|GO:0000278|GO:0019899|GO:0045892|GO:0000775|GO:0051301|GO:0005881|GO.
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136355_PI430048170 0.00431574109095 2.04204664 10.26947722 10.37203159
10.02551297 P P P 8.94652243 9.40566333 9.20995652 P P P
LNCV6_136355_PI430048170 mRNA
CCCCATCCAGTGTCCAGCACTGGAGTCGAACACAGTAATAAAGATGCTGAGAAAAAGTCA NM_001136485
RefSeq chr11+ 66975282 66977008 C11orf86 254439 chromosome 11 open reading frame
86 NA . NA - . NA NA NA NA NA NA NA NA
LNCV6_143330_PI430048170 0.00437983283884 2.10945533 11.14412563 11.16015705
11.09094360 P P P 10.22264268 9.97090819 9.95612569 P P P
LNCV6_143330_PI430048170 mRNA
GGAATTGTTTACACATGACCTACATTTTGGACGGTTTATCAATAAACATGTGTGAACAAC NM_013321
RefSeq chr7 - 2251769 2314475 SNX8 29886 sorting nexin 8
GO:0005515|GO:0016050|GO:0034498|GO:0031901|GO:0035091|GO:0006886|GO:0043231|GO:004280
2|GO:0030904|GO:0019898|GO:0006897 . NA - . NA NA NA NA NA NA NA NA
NA NA
LNCV6_129467_PI430048170 0.00438123206788 2.16376291 10.17735201 10.29870518
10.18591072 P P P 9.29810176 9.06969774 8.93294753 P P P
LNCV6_129467_PI430048170 mRNA
TTGCTGTTTGTCTTCTAGTTAAGGCTCTTTATAAAGAGCTTGTTCTTCATGTTTTAAGC NM_015470
RefSeq chr2 - 73073381 73113018 RAB11FIP5 26056 RAB11 family interacting protein 5
(class I)
GO:0005515|GO:0017137|GO:0005794|GO:0005815|GO:0043015|GO:0005741|GO:0071468|GO:001503
1|GO:2000008|GO:0043231|GO:0045055|GO:0000139|GO:0031901|GO:0035773|GO:0055037|GO:0030
141|GO:0055038|GO:0005769|GO:0030658 . NA - . NA NA NA NA NA NA NA NA
NA NA
LNCV6_141681_PI430048170 0.00441725341483 9.57963527 6.71389705 7.05573379

6.76351130	P	P	P	4.09116807	3.03257913	3.45432671	P	P	P
LNCV6_141681_PI430048170	mRNA								
AAGGTTTGAAGGTTACGGCTCAGGGCTGCCCCATTAAAGTCAGTGTTGTGTTCTAAAAAA NM_015417									
RefSeq	chr20-	3777503	3781455	SPEF1	25876	sperm flagellar 1			
GO:0008150 GO:0003674 GO:0031514 GO:0005930 GO:0005575 GO:0005856	.	NA	-	.					
NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LNCV6_116008_PI430048170	0.00444802266648			2.76243675	8.13359221	8.21799210			
8.25791689	P	P	P	6.94552415	6.72903281	6.50659890	P	P	P
LNCV6_116008_PI430048170	mRNA								
GCGGAAGATATAACCTTATATTTGGTAAGTGTTTCTTGTGCTATTTTATCACGTGACCTG NM_153350									
RefSeq	chr16-	692499	705825	FBXL16	146330	F-box and leucine-rich repeat protein			
16	GO:0005737	.	NA	-	NA	NA	NA	NA	NA
LNCV6_129909_PI430048170	0.00445482726605			2.28770630	9.70172416	9.88129460			
9.56022264	P	P	P	8.21640919	8.62112555	8.69725893	P	P	P
LNCV6_129909_PI430048170	mRNA								
CTGGGTATGTGCCTACCGATGACAATGTGTAAATAAATGCGTGTTACACCCACAAAAAA NM_006876									
RefSeq	chr11-	66345371	66347690	B4GAT1	11041	"beta-1,4-glucuronyltransferase 1"			
GO:0005794 GO:0005975 GO:0030311 GO:0015020 GO:0044281 GO:0046872 GO:0035269 GO:0042339 GO:0030173 GO:0008532 GO:0000139 GO:0018146 GO:0007411 GO:0009405 GO:0030203 GO:0070062	.	NA	-	NA	NA	NA	NA	NA	NA
LNCV6_112413_PI430048170	0.00448993706839			2.78510292	6.82050285	6.48729618			
6.80993986	P	P	P	5.24440278	5.26378305	5.19982380	P	P	P
LNCV6_112413_PI430048170	mRNA								
GTGATCTTGGAACCTTCATGATTATCCACTTAAAGATCAAAGTATTATATGCTGTGTGCT NM_012106									
RefSeq	chr16+	57245125	57253633	ARL2BP	23568	ADP-ribosylation factor-like 2 binding protein			
GO:0005515 GO:0005813 GO:0042517 GO:0003713 GO:0005819 GO:0030496 GO:0005634 GO:0005758 GO:0005929 GO:0007165 GO:0005083 GO:0050790 GO:0051457	.	NA	-	.	NA	NA			
NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LNCV6_133404_PI430048170	0.00454744117561			2.23848401	3.63399433	3.27979098			
3.25497527	P	P	P	2.32941153	2.23519808	2.14249959	A	A	A
LNCV6_133404_PI430048170	mRNA								
CCTGGGGCCTTGATGGTGAAAATGCACCCCAAATGAAAAATAATTATTAATAAATGATCTT NM_144672									
RefSeq	chr16+	21678513	21760729	OTOA	146183	"otoancorin, transcript variant 1"			
GO:0016324 GO:0007160 GO:0007605 GO:0005578 GO:0031225 GO:0019226	.	NA	-	.					
NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LNCV6_141783_PI430048170	0.00456688066212			2.64185306	6.46929751	7.03217433			
6.54370435	P	P	P	5.30901140	5.55903618	4.98217692	P	P	P
LNCV6_141783_PI430048170	mRNA								
CCCAGGACTTGCGGTCTGAGCCTTTTTGGATAATTAATAAATATTTTACACAGCAAAAAA NM_001278720									
RefSeq	chr16+	675665	678268	RHBDL1	9028	"rhomboid, veinlet-like 1 (Drosophila), transcript variant 1"			
GO:0007165 GO:0016020 GO:0004252 GO:0005887 GO:0006508	.	NA	-	.					
NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LNCV6_139926_PI430048170	0.00473535685718			6.02392673	5.63293962	5.90736905			
5.30928140	P	P	P	3.51290264	3.00446804	2.41773700	P	P	A
LNCV6_139926_PI430048170	mRNA								
CCCTGTGCTGTAGCTTCTTTCCAGGCCTTTCCCAAGGAGTAGCTGAAAGGAAGACGCGAT NM_206818									
RefSeq	chr19_KI270938v1_alt-	69045	77107	OSCAR	126014	"osteoclast associated, immunoglobulin-like receptor, transcript variant 1"			
GO:0005886 GO:0016021 GO:0070062	.	NA	-	.	NA	NA			
NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LNCV6_143106_PI430048170	0.00484973730995			2.84545354	4.04156293	4.11792329			
4.43217651	P	P	P	2.89024994	2.28772297	2.84385990	P	A	P
LNCV6_143106_PI430048170	mRNA								
TGCCTCCTCAGGTATGGCAGTGACTCACCTGGTTTTAATAAAACAACCTGCAACATCTCA NM_203377									
RefSeq	chr22-	35606763	35623354	MB	4151	"myoglobin, transcript variant 2"			
GO:0001666 GO:0042542 GO:0005506 GO:0043353 GO:0015671 GO:0007507 GO:0019825 GO:0050873 GO:0005344 GO:0031444 GO:0009725 GO:0020037 GO:0070062	.	NA	-	.	NA	NA			
NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
LNCV6_90907_PI430048170	0.00501137872430			3.37552808	5.14037887	4.89873955			
5.27043413	P	P	P	3.69928380	2.96720572	3.30902124	P	P	P
LNCV6_90907_PI430048170	mRNA								

TTCAACATCACAGATGAAATCATGTCTCAGTTCCCATCTAGCAAGGTGGCTTCAGGAGAG NM_001042454
RefSeq chr16+ 31472154 31477960 TGFBI1 7041 "transforming growth factor beta 1 induced
transcript 1, transcript variant 1"
GO:0005515|GO:0008285|GO:0009408|GO:0006366|GO:0045599|GO:0010718|GO:0050681|GO:004849
5|GO:0016363|GO:0005622|GO:0005737|GO:0030855|GO:0016055|GO:0007155|GO:0005856|GO:0030
579|GO:0030512|GO:0030511|GO:0003713|GO:0070411|GO:0031012|GO:0045165|GO:0016331|GO.
NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_129744_PI430048170 0.00502894172732 2.17452153 6.89522059 6.99039106
7.11844417 P P P 5.61426558 5.95476459 6.04665457 P P P
LNCV6_129744_PI430048170 mRNA
CTGTTGTCTCTTTTCAAACCAAATTGGGAGAATTGTTGCAAAGTAGTGAATGGCAAATAA NM_015941
RefSeq chr8 - 53715542 53843311 ATP6V1H 51606 "ATPase, H+ transporting, lysosomal
50/57kDa, V1 subunit H, transcript variant 1"
GO:0005515|GO:0008286|GO:0051701|GO:0005886|GO:0005765|GO:0055085|GO:0050690|GO:000582
9|GO:0006897|GO:0006879|GO:0033572|GO:0000221|GO:0050790|GO:0046961|GO:0007035|GO:0008
152|GO:0015991|GO:0016032|GO:0030234|GO:0090382|GO:0016887|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA NA
LNCV6_142197_PI430048170 0.00507756248708 4.03258772 3.85257903 4.36411259
4.20103379 P P P 2.58031576 1.69894468 2.00813253 A A A
LNCV6_142197_PI430048170 mRNA
ACAACCAGAGGTCTCATCTCTGAACCTTCTTGCCTACTGATTACATGAGTCTTTGGAGTC NM_001105248
RefSeq chr16+ 19410734 19499112 TMC5 79838 "transmembrane channel-like 5,
transcript variant 1" GO:0016021|GO:0070062|GO:0006811. NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_121181_PI430048170 0.00508377099405 2.39155688 7.26580224 7.42868720
7.38381012 P P P 6.26723611 6.16877657 5.83938589 P P P
LNCV6_121181_PI430048170 mRNA
CCGCAAGCCCCCGGTATGAGATTGTCATCATCACTGTGGTAGCAGCCGCAGTCATAATGG NM_000201
RefSeq chr19+ 10270840 10286615 ICAM1 3383 intercellular adhesion molecule 1
GO:0005515|GO:0014070|GO:0008360|GO:0007605|GO:0019221|GO:0050731|GO:0050900|GO:000561
5|GO:0030155|GO:0030838|GO:1900027|GO:0001618|GO:0030198|GO:0071356|GO:0031669|GO:0051
926|GO:0070374|GO:0070062|GO:0060333|GO:0009986|GO:0007569|GO:0071312|GO:0005178|GO.
NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_127696_PI430048170 0.00509969223914 2.35393038 6.36705932 6.32172021
6.32935628 P P P 5.24645452 5.12852795 4.91956573 P P P
LNCV6_127696_PI430048170 mRNA
ATTGGTTGAGGTGACACCATCTGTTGTAACAGATAAACCCCGAAATCCCAGTGCTGAACT NM_030907
RefSeq chr1 - 16231686 16237164 RSG179363 REM2 and RAB-like small GTPase 1
GO:0042384|GO:0005737|GO:0007264|GO:0017157|GO:0005654|GO:0034613|GO:0015031|GO:000688
7|GO:0005525|GO:0036064|GO:0031338 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_143894_PI430048170 0.00511075759461 2.83539856 6.00327743 6.52915102
5.97129454 P P P 5.04021183 4.57159400 4.36737107 P P P
LNCV6_143894_PI430048170 mRNA
CTGGGGATTTTTCAACATGAAAGGTACCGAGTCTCCAAATGCTGGTTGTAGGGCCTAAAA NM_001242854
RefSeq chr11- 6474682 6481479 ARFIP2 23647 "ADP-ribosylation factor interacting
protein 2, transcript variant 1"
GO:0005515|GO:0030036|GO:0005886|GO:0007264|GO:0019904|GO:0030032|GO:0070273|GO:000692
8|GO:0005525|GO:0032588|GO:0001726|GO:0031529|GO:0048365|GO:0005737|GO:0030742|GO:0005
938 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_82921_PI430048170 0.00512926001691 2.35164995 7.02724696 7.24525352
6.94869755 P P P 5.75368681 6.12820059 5.60315625 P P P
LNCV6_82921_PI430048170 mRNA
TGTGCCTGATGCCAGGACAGCTGTGCTCTCAGATGTAAATAGAGCAACCTATATAAACCT NM_005952
RefSeq chr16+ 56682469 56684196 MT1X4501 metallothionein 1X
GO:0071294|GO:0048471|GO:0007263|GO:0006882|GO:0005634|GO:0046872|GO:0036018|GO:001027
3|GO:0005737|GO:0010038|GO:0008270|GO:0071276|GO:0045926 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_126201_PI430048170 0.00522216668409 6.81776126 6.30347501 6.25429581
6.23727734 P P P 3.07379539 3.53697415 3.78865404 P P P
LNCV6_126201_PI430048170 mRNA

GGTGAGTTCTTCTGTCCAGCGTCAGTATTTTATGTTGGCTTTAGACTTGCCAGATAACA NM_001288747
RefSeq chrX + 154762741 154777689 DKC1 1736 "dyskeratosis congenita 1, dyskerin, transcript variant 3"
GO:0009982|GO:0005515|GO:0006396|GO:0005697|GO:0015030|GO:0008283|GO:0003720|GO:0003723|GO:0006364|GO:0005730|GO:0005634|GO:0001522|GO:0005737|GO:0000723|GO:0005654|GO:0007004 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133712_PI430048170 0.00524287297073 2.69455717 5.58212697 6.06033736
5.61632593 P P P 3.93767427 4.41081516 4.59427444 P P P
LNCV6_133712_PI430048170 mRNA
CCTGGTTCCTTCGCTTGTGTTTCTGTACTTACCAAAAATCTACCATTTCATAAATTTTG NM_177551
RefSeq chr12- 122701292 122703357 HCAR2 338442 hydroxycarboxylic acid receptor 2
GO:0001781|GO:0050995|GO:0070165|GO:0007186|GO:0005886|GO:0016021|GO:0070553|GO:0033031 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136762_PI430048170 0.00527492817130 2.43855277 5.11794697 4.81317115
5.37252167 P P P 3.49994757 3.86799939 4.07410477 P P P
LNCV6_136762_PI430048170 mRNA
GCCACGTACTCAGAGTATAACAATGTGTTCTCATTAATAAATACATCCCACGGAAACCTC NM_001204375
RefSeq chr5 + 32711331 32791724 NPR3 4883 "natriuretic peptide receptor 3, transcript variant 1"
GO:0033688|GO:0048015|GO:0042562|GO:0007200|GO:0008528|GO:0048662|GO:0030157|GO:0007194|GO:0007193|GO:0042803|GO:0001501|GO:0016941|GO:0051000|GO:0005887|GO:0008217|GO:0002158|GO:0017046|GO:0035810|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133835_PI430048170 0.00530736253433 2.65340165 9.34843228 9.33970031
9.28311637 P P P 7.76175377 8.13345102 7.82539355 P P P
LNCV6_133835_PI430048170 mRNA
TTTCTTCACGGTCACTATTTATTCTTTGTTCTTTTCTTTTGTAAAGAAACATTTCACAA NM_001258320
RefSeq chr11- 44932347 44950208 TP53 111 9537 "tumor protein p53 inducible protein 11, transcript variant 1" GO:0008285|GO:0006950|GO:0016021. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138500_PI430048170 0.00543775218651 2.93238218 7.17831511 6.66546265
6.70059226 P P P 4.97083740 5.69522481 5.18219807 P P P
LNCV6_138500_PI430048170 mRNA
TGTAAGTGTATGTTTCTCTACTGTATGGAAAATAAAGTTTACAAGCACACGGTTCTCAGCC NM_053044
RefSeq chr4 + 8269764 8307111 HTRA3 94031 "HtrA serine peptidase 3, transcript variant 1"
GO:0030514|GO:0005515|GO:0004252|GO:0004175|GO:0006508|GO:0008236|GO:0005576|GO:0001558|GO:0030512|GO:0005520. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137621_PI430048170 0.00548197539279 2.68390992 4.00000616 4.56216416
4.58071352 P P P 3.29691325 2.70591684 2.87312574 P P P
LNCV6_137621_PI430048170 mRNA
GCTTTGTACGAGGCTTAGTATTTAGACATGATGTACATTTTTTACAGTGCATACTACTCA NM_172341
RefSeq chr19+ 35745576 35747155 PSENEN 55851 "presenilin enhancer gamma secretase subunit, transcript variant 1"
GO:0042987|GO:0005515|GO:0048011|GO:0043065|GO:0005794|GO:0007220|GO:0070765|GO:0048013|GO:0005886|GO:0005783|GO:0031293|GO:0043085|GO:0097190|GO:0007219|GO:0005887|GO:0007411|GO:0016485|GO:0032580|GO:0005789|GO:0006509 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_90848_PI430048170 0.00553739657676 2.18997555 4.21813845 3.81275063
4.32195154 P P P 2.74741261 3.10802636 3.12281198 A P P
LNCV6_90848_PI430048170 mRNA
GGTATACTGGCAGACATCTTTGTTTCCATGAGCAAGAACGATTATGAAAAGTTTAAAAAC NM_025144
RefSeq chr4 + 112297342 112442608 ALPK1 80216 "alpha-kinase 1, transcript variant 1"
GO:0004674|GO:0006468|GO:0005524. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131133_PI430048170 0.00565457478349 7.47690151 3.19362655 4.22543651
3.05746477 P P P 1.08120599 0.44272839 0.44780239 A A A
LNCV6_131133_PI430048170 mRNA
TCTTTGACAACAGCGACAACGTGGTGCTGCGGCAGTATGAGGACATGGTGGTGGACGAGT NM_021267
RefSeq chr19- 18868545 18896144 CERS1 NA "ceramide synthase 1, transcript variant 1"
NA . NA - . NA NA NA NA NA NA NA NA NA

LNCV6_127813_PI430048170 0.00577727437181 2.28219860 4.68544226 4.20833309
4.35989840 P P P 3.11850497 3.34483323 3.25200864 P P P
LNCV6_127813_PI430048170 mRNA
CTAGAAATGGCCAGAGTTTTTGACAGACAGAGTGTAGTCTCCTTATTAGAAGAAAGGAAA NM_145235
RefSeq chr10+ 125896538 126009592 FANK1 92565 fibronectin type III and ankyrin
repeat domains 1 GO:0005737|GO:0005654 . NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_139850_PI430048170 0.00578260979213 2.59710900 7.93287536 7.87258501
8.29485766 P P P 6.26087720 6.84664606 6.82623061 P P P
LNCV6_139850_PI430048170 mRNA
CAGCATGGAGGACACAGATGACTCTTTGGTGTGGTCTTTTGTCTGCAGTGAATGTTCA NM_001018111
RefSeq chr7 - 131500261 131556617 PODXL 5420 "podocalyxin-like, transcript variant 1"
GO:0005515|GO:0022408|GO:0030335|GO:0072015|GO:0005886|GO:0032534|GO:0031528|GO:003017
5|GO:0050900|GO:0033634|GO:0001726|GO:0005615|GO:0044297|GO:0030027|GO:0072175|GO:0005
737|GO:0007162|GO:0016324|GO:0016477|GO:0005887|GO:0036057|GO:0045121|GO:0007155|GO.
NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_141010_PI430048170 0.00580124931954 2.32235735 7.01324031 7.27303451
6.86805999 P P P 6.14704085 5.75985557 5.56895975 P P P
LNCV6_141010_PI430048170 mRNA
AGGATCTTCTGAGCAGAAGCCCAGGCGGGCCCGGGGCCTTGGCTGGCAAATAAAGCGTTA NM_002307
RefSeq chr19- 38770967 38773517 LGALS7 3963 "lectin, galactoside-binding, soluble, 7" NA
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131465_PI430048170 0.00586594980821 2.14679740 5.26074099 4.92765788
5.00213406 P P P 4.00588410 3.97801147 3.92031474 P P P
LNCV6_131465_PI430048170 mRNA
ATAGCTTGAAAGGCCTGGCCAGGGGAGGAGCACAGATATTTTCCTGTATAATTCCAGAAT NM_001134387
RefSeq chr7 + 6577433 6588979 ZDHHC4 55146 "zinc finger, DHHC-type containing 4,
transcript variant 1" GO:0005794|GO:0008152|GO:0008270|GO:0016021|GO:0019706 . NA -
. NA NA NA NA NA NA NA NA NA NA
LNCV6_126752_PI430048170 0.00586911565008 2.00883349 6.60075315 6.47768720
6.44971769 P P P 5.42049503 5.71915678 5.34640280 P P P
LNCV6_126752_PI430048170 mRNA
TTTCTTCTCTGGCTAAAAATTTTAAATTGGATGTGTTTGGGGGCGGGGGGATGGAAGTGA NM_001661
RefSeq chr17+ 43398984 43401136 ARL4D 379 ADP-ribosylation factor-like 4D
GO:0005515|GO:0005737|GO:0009306|GO:0005886|GO:0007264|GO:0008152|GO:0005730|GO:000392
4|GO:0005525 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133652_PI430048170 0.00590008474706 2.40288274 3.32221697 3.38093579
3.72349376 P P P 1.84911116 2.32939201 2.42398538 A A P
LNCV6_133652_PI430048170 mRNA
ACATTCAATTCCATCACTTCTCTCGGAGGAAGCCCTGCAGAAGGTCAAGTACTTTGTAG NM_001162530
RefSeq chr1 + 36306392 36321347 SH3D21 79729 "SH3 domain containing 21, transcript
variant 1" GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141190_PI430048170 0.00596093435708 3.14340134 8.49571401 8.62130874
8.62463062 P P P 7.22832488 6.75035136 6.75577518 P P P
LNCV6_141190_PI430048170 mRNA
TCCCCTCTACTTGGCAAGTGGTTGTCAAGTTCTAGTTGTTCAATAAATGTGTTAATAATG NM_006994
RefSeq chr6 + 26440471 26453415 BTN3A3 10384 "butyrophilin, subfamily 3, member
A3, transcript variant 1"
GO:0005737|GO:0005794|GO:0016020|GO:0005886|GO:0005730|GO:0016021|GO:0002456 . NA
- . NA NA NA NA NA NA NA NA NA NA
LNCV6_142488_PI430048170 0.00609776402840 3.05952830 4.01159359 3.66586040
4.00938629 P P P 2.18699336 1.93214302 2.65857144 A A P
LNCV6_142488_PI430048170 mRNA
TCTTGAGGTCCTAAAGGTATGATTCAGACCTTTCAGCCCTTTCAGAACTTTGACCCTCT NM_032316
RefSeq chr3 - 49422332 49429324 NICN1 84276 nicotin 1 GO:0005874|GO:0005634
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_138869_PI430048170 0.00613813242586 2.38224274 6.22466355 6.52940200
6.43591104 P P P 5.44927182 4.89339045 5.04871231 P P P
LNCV6_138869_PI430048170 mRNA
AGATACAGCAGAGCTCACAGTGAGTCAGAAAGTCTCCACTTTCTGAACATAGCTCTATAA NM_017881
RefSeq chr9 - 75061199 75088217 NMRK1 54981 "nicotinamide riboside kinase 1,

transcript variant 1" GO:0016310|GO:0050262|GO:0009435|GO:0005524|GO:0046872 . NA -
. NA NA NA NA NA NA NA NA NA
LNCV6_145102_PI430048170 0.00620789626411 2.93449021 8.72310708 8.80699587
8.57715329 P P P 7.27197558 7.34034299 6.78368037 P P P
LNCV6_145102_PI430048170 mRNA
TTCAGTCTGGCTTCAAATTTGGGGATGTAAATGAGGGTCCTCTGGTTTTTGGTAACCAGG NM_152911
RefSeq chr10 + 133379236 133391696 PAOX 196743 "polyamine oxidase (exo-N4-
amino), transcript variant 1"
GO:0052901|GO:0006805|GO:0052902|GO:0005782|GO:0052903|GO:0052904|GO:0005102|GO:004428
1|GO:0046592|GO:0034641|GO:0006598|GO:0006596|GO:0052899|GO:0006595|GO:0009446|GO:0046
208|GO:0046203|GO:0009447|GO:0055114 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_128092_PI430048170 0.00623523275818 2.90033568 3.24386433 3.57064075
3.36717811 P P P 1.49516940 2.17067234 1.84770921 A A A
LNCV6_128092_PI430048170 mRNA
ACTATGTTGAGCTAACACAGACCTGCTGAATCAGCTTCTTTCTGAGCTGCCAGAAGTACA NM_001006114
RefSeq chr21 + 46286352 46292197 YBEY 54059 "ybeY metalloproteinase (putative),
transcript variant 2"
GO:0005739|GO:0006364|GO:0006508|GO:0005654|GO:0005634|GO:0004222|GO:0046872 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_145330_PI430048170 0.00629341606008 2.52224701 9.37592104 9.25891970
9.10396148 P P P 7.94856240 8.15683116 7.58531424 P P P
LNCV6_145330_PI430048170 mRNA
CTGACTCATGCCTTGAGTACATACCATACAGCAAATAAATGGTAGCAAAACATTCTAAAA NM_005165
RefSeq chr17 - 28573114 28576933 ALDOC 230 "aldolase C, fructose-bisphosphate"
GO:0005515|GO:0008092|GO:0014070|GO:0030424|GO:0031100|GO:0006094|GO:0051290|GO:004428
1|GO:0006096|GO:0005829|GO:0005739|GO:0004332|GO:0051289|GO:0030855|GO:0006006|GO:0005
856|GO:0006000|GO:0070062|GO:0001666|GO:0005975|GO:0007568|GO:0006915|GO:0010243|GO .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_144398_PI430048170 0.00637522508717 2.13819557 6.19791171 6.68410175
6.38590846 P P P 5.32233037 5.47124730 5.21578025 P P P
LNCV6_144398_PI430048170 mRNA
TTTGATGTGATCTCATTGATGTACACAACCAAGTTCCAATAAAGTGCTAGAATGTGCAAA NM_032947
RefSeq chr5 + 150777945 150796736 SMIM3 85027 small integral membrane protein 3
GO:0016021 . NA - . NA NA NA NA NA NA NA NA
LNCV6_139721_PI430048170 0.00645951378053 2.42122368 9.92832260 10.35270575
10.07084151 P P P 8.91829469 8.81139739 8.82537606 P P P
LNCV6_139721_PI430048170 mRNA
TATGATCTAATTGAAACAAGACTGAAGGATCAATAAACAGCCATCTGCCCCTTCAAAAA NM_004585
RefSeq chr11 + 63536800 63546458 RARRES3 5920 retinoic acid receptor responder
(tazarotene induced) 3 GO:0016042|GO:0005515|GO:0008285|GO:0004623|GO:0016021|GO:0006644
. NA - . NA NA NA NA NA NA NA NA
LNCV6_128258_PI430048170 0.00657029909952 2.02150573 7.29310957 7.27988261
7.35958325 P P P 6.46870652 6.12703705 6.27132043 P P P
LNCV6_128258_PI430048170 mRNA
TAAACAGTATCTCGGAGAAGCCTGGGATGAGAAAATGAGGAGGATGGGTCCAAGAAACAT NM_021944
RefSeq chr14 - 22986900 23010201 C14orf93 60686 "chromosome 14 open
reading frame 93, transcript variant 1" GO:0005576 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_129151_PI430048170 0.00663199157982 4.72294455 4.66188534 4.33650704
4.72012430 P P P 1.84528289 2.22539150 2.79671908 A A P
LNCV6_129151_PI430048170 mRNA
ACTCAATATTGGGTGAGTTGGTCTGAACAAGGTGGGGATAAAGTAGAGTGGAAATAATGT NM_015253
RefSeq chr17 + 6070613 6124427 WSCD1 23302 WSC domain containing 1
GO:0008152|GO:0008146|GO:0016021 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_136229_PI430048170 0.00668293231175 3.11399610 4.32717764 3.80813583
3.93960350 P P P 2.54309964 2.65990405 1.89662739 A A A
LNCV6_136229_PI430048170 mRNA
ACACCAGTGACGCCGCTGTGTGTCTTAGCATGGAAATAAATAACCTGAATGTACGTGCT NM_172367
RefSeq chr17_KI270862v1_alt + 240267 243012 TUSC5 286753 tumor suppressor candidate 5

GO:0009607|GO:0016021 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_143901_PI430048170 0.00674461862630 2.01799973 4.89624052 4.66071265
5.08877220 P P P 3.59598000 4.10642077 3.89120303 P P P
LNCV6_143901_PI430048170 mRNA
AGAACACCAGGAGTATGATTCTGTTTCTGAAAGGTGAGTGGTGTATTGCTGTCATTGGGC NM_005982
RefSeq chr14 - 60644698 60649437 SIX1 6495 SIX homeobox 1
GO:0005515|GO:0007389|GO:0001657|GO:0001658|GO:0034504|GO:0003700|GO:0044212|GO:000760
5|GO:0048538|GO:0048704|GO:0001759|GO:0030878|GO:0048701|GO:0072075|GO:0043524|GO:0090
191|GO:2001014|GO:0030910|GO:0050678|GO:0048839|GO:0042472|GO:0072107|GO:0000122|GO .
NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_134935_PI430048170 0.00682386108038 4.45869954 6.58028181 6.56419785
7.08466792 P P P 4.77539063 3.95051352 4.92032483 P P P
LNCV6_134935_PI430048170 mRNA
TTTGAAGACTTACTGTTGGCCATAGTTAATTGTGTGAGGAACACGCCGGCCTTTTGTAGCC NM_005139
RefSeq chr4 + 78551587 78610451 ANXA3 306 annexin A3
GO:0006909|GO:0005886|GO:0043312|GO:0005509|GO:0042581|GO:0019834|GO:0043086|GO:004576
6|GO:0005544|GO:0010595|GO:0051091|GO:0005737|GO:0016020|GO:0030670|GO:0042742|GO:0070
062|GO:0048306 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145594_PI430048170 0.00683415712397 4.03083985 4.10426606 4.60925716
4.67349367 P P P 2.97942109 2.23840907 2.01704950 P A A
LNCV6_145594_PI430048170 mRNA
GTATTGTCAGAGTTGAATATCACCTCTCAAAGCATCACCTCTATCTGCCTCATCTCACA NM_000928
RefSeq chr12- 120322110120327789PLA2G1B 5319 "phospholipase A2, group IB (pancreas)"
GO:0032052|GO:0050830|GO:0010524|GO:0044240|GO:0050714|GO:0048146|GO:0044281|GO:000561
5|GO:0032431|GO:0035556|GO:0000187|GO:0051092|GO:0015758|GO:0045944|GO:0047498|GO:0004
623|GO:0007015|GO:0006633|GO:0030141|GO:0006654|GO:0050482|GO:0019370|GO:0032869|GO .
NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_135485_PI430048170 0.00703981476802 2.28426145 5.35432491 5.52937980
5.12826666 P P P 4.17493580 4.18737411 4.10079015 P P P
LNCV6_135485_PI430048170 mRNA
GTTTGCCGCTTCATCATTGTCTGTTGATTTTCTTCAAAGAAGAGGTTTTGAGCATTGGA NM_001291516
RefSeq chr9 - 136280941136306901MGC50722 399693 "uncharacterized MGC50722,
transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110337_PI430048170 0.00706403266367 2.29701899 3.51459696 3.70441921
3.58741512 P P P 2.32434273 2.18183373 2.66402607 A A P
LNCV6_110337_PI430048170 mRNA
ATATTTGGGAATTAGTGGAGTGATCTCTGAAGACCTAGGGCTATGATCTGGAGCTGCTGT NM_198536
RefSeq chr19- 11342775 11346305 TMEM205 374882 "transmembrane protein 205,
transcript variant 1" GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA NA
LNCV6_88442_PI430048170 0.00708496492789 4.46633852 3.93014910 3.58664002
3.67390500 P P P 1.02028587 1.87763930 1.70376149 A A A
LNCV6_88442_PI430048170 mRNA
AGGGGAGAGGTCCTTACCTCTGATCCACTTAGAGCAATAACCACTTTTTAAATGTAAAAT NM_001171941
RefSeq chr1 - 32862267 32872492 FNDC5 252995 "fibronectin type III domain
containing 5, transcript variant 1"
GO:0008150|GO:0003674|GO:0005886|GO:0005179|GO:0014850|GO:0005783|GO:0005576|GO:001602
1|GO:0090336|GO:0005778. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_140978_PI430048170 0.00709589088373 6.09842929 4.60235651 4.73131016
5.07825864 P P P 2.71293417 2.12409296 1.56691303 A A A
LNCV6_140978_PI430048170 mRNA
AACAAATGCTTGTTGGGCAAGAATGGGATTGAGGATTATCTTCTCTCAGAAAGGCATTGT NM_021181
RefSeq chr1 + 160739056160754818SLAMF7 57823 "SLAM family member 7, transcript
variant 1" GO:0030101|GO:0042267|GO:0004872|GO:0016021|GO:0007155 . NA - . NA
NA NA NA NA NA NA NA NA NA
LNCV6_108015_PI430048170 0.00711043113619 4.27810468 7.09890305 7.23182518
7.16537166 P P P 4.90017173 5.43591779 4.78569056 P P P
LNCV6_108015_PI430048170 mRNA
TGTGATTCTCTGCTTGCCTGGAGACGTGGAACCTCTGTCTCATCCTCCTGGAACCTTGC NM_001975
RefSeq chr12+ 6914449 6923696 ENO22026 "enolase 2 (gamma, neuronal)"

GO:0000287|GO:0005886|GO:0005975|GO:0006094|GO:0044281|GO:0005615|GO:0004634|GO:0006096|GO:0005829|GO:0001917|GO:0009405|GO:0006006|GO:0043204|GO:0000015|GO:0070062 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_142936_PI430048170 0.00711729564723 2.81449774 6.84469093 7.60536333
7.25747648 P P P 6.05552666 5.73385088 5.48097972 P P P
LNCV6_142936_PI430048170 mRNA
ATGTTCTGTGAGGCCCAAGAGAACACATGGAGTCTTAGCAAATGCACTAATGTATTCCGG NM_007021
RefSeq chr10- 44976260 44978882 C10orf10 11067 chromosome 10 open reading frame
10 GO:0005739 . NA - . NA NA NA NA NA NA NA NA
LNCV6_143059_PI430048170 0.00712993737331 5.17387529 8.49859574 8.79647489
8.25986995 P P P 6.61241028 6.16025557 5.51496737 P P P
LNCV6_143059_PI430048170 mRNA
AGGGCTCTCGGAGAAAGTGTGTGTATTCTTTCTTAATAAAGTGTGGACTGAACAAAAA NM_014370
RefSeq chrX + 153781000 153785732 SRPK3 26576 "SRF protein kinase 3, transcript
variant 1"
GO:0005515|GO:0007519|GO:0004674|GO:0060537|GO:0006468|GO:0005575|GO:0005524|GO:0030154
4 . NA - . NA NA NA NA NA NA NA NA
LNCV6_33426_PI430048170 0.00719876866881 2.84647741 4.31583416 4.64943928
4.99207448 P P P 3.52062467 3.13660965 2.74903401 P P P
LNCV6_33426_PI430048170 mRNA
TCTCTAAGGGATCTCTGTTGCTTGAGAGAATAAACCTCGGATTCCTTCCTTGGCTCTCGG NM_001278655
RefSeq chr20+ 50267485 50279795 LINC01272 NA long intergenic non-protein coding RNA
1272 NA . NA - . NA NA NA NA NA NA NA NA
LNCV6_130782_PI430048170 0.00722039093254 3.06215576 3.00304667 2.90975170
3.65844191 P P P 1.56310353 1.95591938 1.23953888 A A A
LNCV6_130782_PI430048170 mRNA
AAAGATTGCCAAATCATGTTTGGTAGGAGGACTTTTGAGGTAGCTTTTGAACAAATGTTT NM_020682
RefSeq chr10+ 102869452 102901898 AS3MT 57412 arsenite methyltransferase
GO:0030791|GO:0005739|GO:0030792|GO:0005737|GO:0008757|GO:0009404|GO:0032259|GO:0018872|GO:0005829 . NA - . NA NA NA NA NA NA NA NA
LNCV6_130125_PI430048170 0.00725963050127 4.32940599 3.27150541 3.91595871
3.88223871 P P P 1.65082674 1.65524618 1.50235674 A A A
LNCV6_130125_PI430048170 mRNA
TTTACAAGGGACGGATGGACACAAGGCTGCCAGGCATCCTCCGAAAAGACAGCTCAGGGA NM_032134
RefSeq chr17- 76274048 76307680 QRICH2 84074 "glutamine rich 2, transcript variant
1" NA . NA - . NA NA NA NA NA NA NA NA
LNCV6_142015_PI430048170 0.00732122176205 2.01366413 12.11861810 12.09409677
11.73821572 P P P 10.89277161 11.06678211 10.98714532 P P P
LNCV6_142015_PI430048170 mRNA
TTTTGCACATGTCATGCAGCTCAGCTGGGAGCTGCTTAGGTGGAAACTCCAAATAAAGT NM_001458
RefSeq chr7 + 128830428 128859274 FLNC 2318 "filamin C, gamma, transcript variant 1"
GO:0005515|GO:0008092|GO:0030018|GO:0005886|GO:0034329|GO:0030506|GO:0005829|GO:0048747|GO:0042383|GO:0005737|GO:0016528|GO:0051015|GO:0043034|GO:0005856|GO:0005925 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_32949_PI430048170 0.00759168393842 2.86314250 7.65856057 7.51466383
7.45580242 P P P 6.30606452 6.01966545 5.69353686 P P P
LNCV6_32949_PI430048170 mRNA
GAGAAGCCTCCCTCATTCCTCCCAGGAATTAATAATGTGAAGAGAGGCTCTGTTTAAAA NM_130786
RefSeq chr19- 58346805 58353499 A1BG1 alpha-1-B glycoprotein
GO:0008150|GO:0003674|GO:0072562|GO:0005576|GO:0005615|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141472_PI430048170 0.00762387897944 3.70137323 5.17203700 4.72062715
4.59707295 P P P 2.91330129 2.99870773 2.97751287 P P P
LNCV6_141472_PI430048170 mRNA
AGAGGGTGCCCATTTGGACCTTTGGCACTGGATGAGCCAATAAACCAAACTCTGGCACCTC NM_001271803
RefSeq chr5 + 138439000 138446969 REEP2 51308 "receptor accessory protein 2,
transcript variant 1"
GO:0005881|GO:0032386|GO:0050913|GO:0005887|GO:0005783|GO:0071786|GO:0031883|GO:0005789|GO:0050916|GO:0032596|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_129847_PI430048170 0.00764209514434 2.37957164 7.39747356 8.02002236

7.69079211	P	P	P	6.25298525	6.58546951	6.56173930	P	P	P
LNCV6_129847_PI430048170 mRNA									
AAAGTGATCAACCACTGTTCTTCTATGGGGCTCTTGCTCTAGTGTCTATGGTGAGAACA NM_001304771									
RefSeq chr16- 19858970 19885634 GPRC5B 51704 "G protein-coupled receptor, class C, group 5, member B, transcript variant 2"									
GO:0001664 GO:0005886 GO:0009986 GO:0019901 GO:0004930 GO:0061098 GO:0090263 GO:0005730 GO:0005634 GO:0042593 GO:0030295 GO:0005615 GO:0043231 GO:0007186 GO:0045666 GO:0050729 GO:0010976 GO:0060907 GO:0045121 GO:0007626 GO:0016021 GO:0043123 GO:0030659 GO:NA - . NA NA NA NA NA NA NA NA NA NA									
LNCV6_132835_PI430048170				0.00785374773801	3.56043065	3.94157101		4.48376624	
4.54363177	P	P	P	2.55967694	2.56514139	2.41578868	A	P	P
LNCV6_132835_PI430048170 mRNA									
TGCTTTCTGGCCTCAGCTATGTAATTAAACGCCCGAAGTAAAATGGCCTTCTCCAAAAA NM_032805									
RefSeq chr16- 3088890 3099317 ZSCAN10 84891 "zinc finger and SCAN domain containing 10, transcript variant 1"									
GO:0043565 GO:0006355 GO:0003700 GO:0005654 GO:0005634 GO:0045892 GO:0035019 GO:0046872 GO:0006351 . NA - . NA NA NA NA NA NA NA NA NA NA									
LNCV6_141358_PI430048170				0.00788640164323	2.12444509	7.96276301		7.99131020	
7.98554236	P	P	P	6.81938447	7.08238770	6.75555953	P	P	P
LNCV6_141358_PI430048170 mRNA									
TGCAGAAACCGCTGGGTGGAGAAGAAGCCGATAAAGTCTATGAATCAACCTGCCAAAAA NM_016339									
RefSeq chr17+ 40177988 40195656 RAPGEFL1 51195 "Rap guanine nucleotide exchange factor (GEF)-like 1, transcript variant 3"									
GO:0043547 GO:0005085 GO:0016020 GO:0007186 GO:0007264 GO:0007399 . NA - . NA NA NA NA NA NA NA NA NA NA									
LNCV6_141440_PI430048170				0.00800677234042	2.19331393	7.58637495		7.58073405	
7.20138277	P	P	P	6.65727219	6.19644384	6.08190406	P	P	P
LNCV6_141440_PI430048170 mRNA									
CTGAGCGAGTCTGTTGTGGAGAAGAACTTTTTGTAGTAATTTACTAGGAAAAATTCTGAA NM_031308									
RefSeq chr8 - 143857318 143878464 EPPK1 83481 epiplakin 1									
GO:0008150 GO:0005737 GO:0005856. NA - . NA NA NA NA NA NA NA NA NA NA									
LNCV6_142897_PI430048170				0.00812047100202	2.12254409	9.14854683		9.20393907	
9.08171661	P	P	P	8.22729368	8.10631464	7.81534615	P	P	P
LNCV6_142897_PI430048170 mRNA									
AAGTAACTTTTTGTATAAATAAAAAGAAAATGGGACGTGTCCCAGCTCCAGGGGTAAAAA NM_004444									
RefSeq chr7 - 100802564 100827521 EPHB4 2050 EPH receptor B4									
GO:0005515 GO:0048013 GO:0005886 GO:0002042 GO:0018108 GO:0005576 GO:0001525 GO:0005524 GO:0005829 GO:0003007 GO:0046777 GO:0005003 GO:0005887 GO:0007411 GO:0004714 GO:0007155 GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA NA									
LNCV6_129134_PI430048170				0.00818159775630	2.16306396	8.45565484		9.01117851	
8.89046929	P	P	P	7.75869215	7.82888044	7.46194963	P	P	P
LNCV6_129134_PI430048170 mRNA									
TTGTAACCAGAGAACTATTACTAGGCCTTGAAGAACCTGTCTAACTGGATGCTCATTGCC NM_013332									
RefSeq chr7 + 128455829 128458418 HILPDA 29923 "hypoxia inducible lipid droplet-associated, transcript variant 1"									
GO:0005811 GO:0005515 GO:0008284 GO:0009986 GO:0006950 GO:0005102 GO:0010884 GO:0035425 GO:0016021 GO:0001819 GO:0030141 GO:0005615 . NA - . NA NA NA NA NA NA NA NA NA NA									
LNCV6_115721_PI430048170				0.00821016163336	2.11887417	4.58275278		4.69344003	
4.99500784	P	P	P	4.00148596	3.47194200	3.51836041	P	P	P
LNCV6_115721_PI430048170 mRNA									
CGGACGACGCGGCCTTCCGGGAGCGCGCGCGTTGCTGGCCGCCCTCGAGCGCCGCCACTNM_178449									
RefSeq chr19- 49422413 49423441 PTH2 113091 parathyroid hormone 2									
GO:0007218 GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA NA									
LNCV6_145528_PI430048170				0.00825077479540	2.34915296	4.20381664		4.65844344	
4.75910123	P	P	P	3.25816487	3.00541945	3.64663691	P	P	P
LNCV6_145528_PI430048170 mRNA									
TTCTACTTTGATTTTATTGTTAGTGCATTGTCGTTCTTGTGTCAGTAGCAAGTTTCAGTG NM_005275									
RefSeq chr6_GL000251v2_alt - 2021095 2037314 GNL1 2794 guanine nucleotide binding protein-like 1									

GO:0007165|GO:0005198|GO:0042254|GO:0008152|GO:0003924|GO:0005634|GO:0005525|GO:0005615|GO:0006974|GO:0002456. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137456_PI430048170 0.00843208184084 2.36726134 8.01430610 8.56640293
8.22013443 P P P 6.94532972 7.17015174 7.00072299 P P P
LNCV6_137456_PI430048170 mRNA
CTTTTGATTGCACAAGCCTTTGTTTCAGTCCTAGTGAATAAAGTTGTGTTTTCTGGAAA NM_014353
RefSeq chr16+ 2148649 2154140 RAB26 25837 "RAB26, member RAS oncogene family"

GO:0005515|GO:0009306|GO:0005886|GO:0043001|GO:0031226|GO:0003924|GO:0005525|GO:0006904|GO:0006184|GO:0045055|GO:0000139|GO:0035272|GO:0017157|GO:0032482|GO:0019003|GO:0019002|GO:0030667|GO:0005768|GO:0030658 . NA - . NA NA NA NA NA NA NA NA
NA NA
LNCV6_129586_PI430048170 0.00851939393142 2.67447977 8.05228265 8.11255184
8.15947244 P P P 6.39454575 6.90623194 6.72205862 P P P
LNCV6_129586_PI430048170 mRNA
TCCGCAGTGC GGATAAAAATTGGACTCGAATAAAACCCTTGTTGCCCGGATGGTAAAAAA NM_001291831
RefSeq chr7 + 76201892 76287292 SRRM3 222183 "serine/arginine repetitive matrix 3, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA
LNCV6_141995_PI430048170 0.00866791984122 2.15161674 7.61029256 8.14886311
8.04759673 P P P 7.08644322 6.87044836 6.53588385 P P P
LNCV6_141995_PI430048170 mRNA
ATATTATGTCCATCAGATGGACAATGCGCAGGACCTGCTTTCCTTTGGTGGTCTTCAAGT NM_001037633
RefSeq chr5 - 138946720139198376SIL1 64374 "SIL1 nucleotide exchange factor, transcript variant 1" GO:0006457|GO:0005783|GO:0005788|GO:0051082|GO:0006886|GO:0005615 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_145650_PI430048170 0.00867483482205 2.38218245 8.09112874 8.28886415
8.27561891 P P P 7.26908896 6.73031443 6.85079553 P P P
LNCV6_145650_PI430048170 mRNA
TGACTACCTTGACTTGAAATGCTCTTTTGCACAAGGAAATAAAGCGTCCTCTCAGTAATG NM_003561
RefSeq chr16_KI270853v1_alt- 245406 267531 PLA2G10 8399 "phospholipase A2, group X"

GO:0019369|GO:0051977|GO:0043030|GO:0044281|GO:0043433|GO:0007411|GO:0004623|GO:0006654|GO:0042632|GO:0010744|GO:0036149|GO:0005509|GO:0036148|GO:0090238|GO:0010884|GO:0005576|GO:0004620|GO:0016042|GO:0032270|GO:0036150|GO:0090370|GO:0032308|GO:0006644|GO. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141211_PI430048170 0.00886662940622 3.00537691 6.46129824 6.68558511
6.64045987 P P P 5.33055858 4.98030610 4.64144430 P P P
LNCV6_141211_PI430048170 mRNA
ACTGGAGAGTGTGGGAATGGGAAGAAGCAGTTTACTTTAGACTAAAGAATATATTGGGG NM_145343
RefSeq chr22+ 36253070 36267531 APOL1 8542 "apolipoprotein L, 1, transcript variant 2"

GO:0005515|GO:0006821|GO:0072562|GO:0005576|GO:0031224|GO:0005254|GO:0005615|GO:0006898|GO:0008289|GO:0034361|GO:0034364|GO:0045087|GO:0006869|GO:0019835|GO:0042157|GO:0031640|GO:0008203 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129971_PI430048170 0.00894014456749 2.11189743 5.63637129 5.91215092
5.53694462 P P P 4.59446375 4.66590464 4.61517447 P P P
LNCV6_129971_PI430048170 mRNA
AGGTCACACAGCCTAGAAGCTAGAGCAGTGCAGAGTCTGCAAATAAAACCTTAAGTCTGT NM_133639
RefSeq chr15- 40872213 40874289 RHOV 171177 ras homolog family member V

GO:0005515|GO:0051056|GO:0005886|GO:0007264|GO:0005525|GO:0046872|GO:0010008|GO:0005829 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136045_PI430048170 0.00899687508794 3.07912185 6.03786977 5.82654938
6.02690070 P P P 4.63965433 3.94157101 4.36825582 P P P
LNCV6_136045_PI430048170 mRNA
CTGCTGTTGTGTGAAGATTGACATTTACCATGATTTTCCTTAGTTACTGCAGAACATAGA NM_014061
RefSeq chrX + 55452088 55453568 MAGEH1 28986 melanoma antigen family H1

GO:0005737|GO:0006915 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134411_PI430048170 0.00910096150019 2.11769484 4.53220089 4.39295676
4.29032020 P P P 3.57551755 3.30953112 3.04445865 P P P
LNCV6_134411_PI430048170 mRNA
TATTTATTCCCTCACCTTCTGCAGGGCTCCGTGCGGGCTGAAATTAAAGATTTCTTAGAG NM_002068
RefSeq chr19+ 3136031 3163769 GNA15 2769 "guanine nucleotide binding protein (G

protein), alpha 15 (Gq class)"
GO:0001664|GO:0005886|GO:0005834|GO:0003924|GO:0030168|GO:0007202|GO:0031683|GO:0005525|GO:0007204|GO:0046872|GO:0006184|GO:0007596|GO:0060158|GO:0007207|GO:0007188|GO:0004871 . NA - . NA NA NA NA NA NA NA NA
LNCV6_124586_PI430048170 0.00910631014442 2.33435167 7.53052092 7.42754095
7.56785799 P P P 6.41727470 5.98253507 6.41845928 P P P
LNCV6_124586_PI430048170 mRNA
CTCTTATGATGAGATTTCTGGTCAAGGAGCGAGCTCTCAGGATACGAAGACATTTGACGT NM_007028
RefSeq chr6_GL000256v2_alt - 1401828 1412013 TRIM31 11074 tripartite motif
containing 31
GO:0005739|GO:0051091|GO:0016567|GO:0046597|GO:0045087|GO:0016874|GO:0019221|GO:0032897|GO:0008270|GO:0060333|GO:0005829 . NA - . NA NA NA NA NA NA NA NA
NA NA
LNCV6_74519_PI430048170 0.00918556146826 2.47685616 3.32433539 3.31884785
3.60188983 P P P 2.42432872 1.76136797 2.07619279 A A A
LNCV6_74519_PI430048170 mRNA
GATCAAGAGTGCACCTTCTTTTCAACTTCAAAGTGGCACAAACACTGTGCTTTCCATCT NM_004354
RefSeq chr4 + 77157203 77170060 CCNG2 901 cyclin G2
GO:0007067|GO:0005737|GO:0051726|GO:0000075|GO:0051301 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_140936_PI430048170 0.00924788717183 2.00705716 6.59904280 7.13454731
6.84870756 P P P 5.99223922 5.68376143 5.92305352 P P P
LNCV6_140936_PI430048170 mRNA
TTCAGAGCCACCCACCTTTTCTGTAAAGTGCTGGAATACACATACGATGCCTGAAATCTC NM_021052
RefSeq chr6 + 26216919 26217483 HIST1H2AE 3012 "histone cluster 1, H2ae"
GO:0008150|GO:0046982|GO:0005634|GO:0000786|GO:0003677|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_127018_PI430048170 0.00925537562733 2.11717930 4.67770818 5.08411211
5.09832642 P P P 3.53650989 3.91764625 4.13544649 P P P
LNCV6_127018_PI430048170 mRNA
AGCTGCCTGTGATCTTCTTAGGTTATAGCCAAGTCAGCAACATAATTCCTCTAAATAAAA NM_003649
RefSeq chr6 - 110392179110415550DDO 8528 "D-aspartate oxidase, transcript variant 1"
GO:0005515|GO:0007320|GO:0048037|GO:0006531|GO:0006533|GO:0005102|GO:0042445|GO:0007625|GO:0019478|GO:0055114|GO:0008445|GO:0005777 . NA - . NA NA NA NA NA NA
NA NA NA NA
LNCV6_93773_PI430048170 0.00926056299515 3.58161201 3.68478022 3.36487555
3.91952108 P P P 2.28584714 1.74866503 1.29559197 A A A
LNCV6_93773_PI430048170 mRNA
TCGTGGTAGCAACTCTTCCACAATTAAAGTTCCTCTTTAGAGAGCAAAGACCACCTACAG NM_012472
RefSeq chr8 - 132571952132675617LRRC6 23639 "leucine rich repeat containing 6,
transcript variant 1"
GO:0060287|GO:0044458|GO:0005515|GO:0036159|GO:0005929|GO:0003674|GO:0005737|GO:0036158|GO:0003341|GO:0030317|GO:0008584 . NA - . NA NA NA NA NA NA NA NA
NA NA
LNCV6_135451_PI430048170 0.00928922350962 2.15259590 7.76593559 7.89336949
7.73016838 P P P 6.79623585 6.84299142 6.39689209 P P P
LNCV6_135451_PI430048170 mRNA
TATCACTCTCCCCAACACCTAGATGTGAAAACAGAATAAACTTCACCCAGAAAACACTT NM_022873
RefSeq chr1 - 27666060 27672213 IFI6 2537 "interferon, alpha-inducible protein 6, transcript
variant 3"
GO:0005739|GO:0005515|GO:0006955|GO:0060337|GO:0005886|GO:0051902|GO:0019221|GO:2001240|GO:0001836|GO:0016021|GO:0043154 . NA - . NA NA NA NA NA NA NA NA
NA NA
LNCV6_128481_PI430048170 0.00937392540941 4.27187636 6.82417424 6.65893041
6.79821390 P P P 4.93455692 4.79011378 4.16867305 P P P
LNCV6_128481_PI430048170 mRNA
GGAACCTCTGGTTATTATGGTGTAGTTATCGAATAAAAACGACTTCAGAATGCAGCTAAA NM_001100876
RefSeq chr9 + 128920894128942041PHYHD1 254295 "phytanoyl-CoA dioxygenase domain
containing 1, transcript variant 1" GO:0051213|GO:0046872|GO:0055114. NA - . NA NA
NA NA NA NA NA NA NA NA
LNCV6_129511_PI430048170 0.00941446647786 3.39069849 5.63392031 5.75524145

5.63086119 P P P 3.68080443 4.27693320 3.69807491 P P P
LNCV6_129511_PI430048170 mRNA
GACAAGGTCAGCATCATTTGCTCTCCTGAATTTATGAGGTTTATTTATTTTCTCTTTCC NM_004573
RefSeq chr15- 40287896 40307973 PLCB2 5330 "phospholipase C, beta 2, transcript variant 1"
GO:0043647|GO:0005509|GO:0007268|GO:0007202|GO:0044281|GO:0005829|GO:0016042|GO:0035556|GO:0004629|GO:0050913|GO:0004435|GO:0008152|GO:0004871|GO:0006644 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_132657_PI430048170 0.00971414593262 5.20244831 6.26774315 6.58627098
6.27314553 P P P 4.46215498 3.96748282 3.38698541 P P P
LNCV6_132657_PI430048170 mRNA
TGACTGTTTCTCATGCCTTTATGTTCTTCATGTAAGTAAAGTGGACCTTTGTGCTCAAA NM_024320
RefSeq chr17- 47951967 47957877 PRR15L 79170 proline rich 15-like NA . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_145428_PI430048170 0.00994710960004 2.14018171 5.38016925 5.89317053
5.76137273 P P P 4.83733434 4.65364869 4.23393253 P P P
LNCV6_145428_PI430048170 mRNA
GAGGAGCTTGAAACCCGTGGCGCTTTCTGCAGTTTGCAGGTTATCATTGTGAACTTTTTT NM_001671
RefSeq chr17- 7173430 7179564 ASGR1 432 "asialoglycoprotein receptor 1, transcript variant 1"
GO:0005515|GO:0005887|GO:0031668|GO:0030246|GO:0004873|GO:0005576|GO:0046872|GO:0042803|GO:0006898 . NA - . NA NA NA NA NA NA NA NA
LNCV6_134703_PI430048170 0.01005854186666 3.53578095 3.02783542 3.70568012
3.54528785 P P P 2.04689420 1.00651335 1.65871397 A A A
LNCV6_134703_PI430048170 mRNA
AAGACAGAGGAAGGAGATTGATGCCAGAGAACACAAACGCTTCAGGAGAAATTCAAGCCT NM_173855
RefSeq chr12- 121651386121669654MORN3 283385 MORN repeat containing 3
GO:0005634 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_137567_PI430048170 0.01034682983923 2.26705092 4.91272889 4.85469895
4.68333985 P P P 3.51661146 3.39262919 3.94823686 P P P
LNCV6_137567_PI430048170 mRNA
ACTACCTCTGTGCCTTGCCACATTAAATTGATAACATGGAAATGAGATGCAACCCAACAA NM_016602
RefSeq chr17- 42679401 42681827 CCR10 2826 chemokine (C-C motif) receptor 10
GO:0006955|GO:0070098|GO:0009986|GO:0007186|GO:0006935|GO:0005886|GO:0005887|GO:0004930|GO:0016493|GO:0007204. NA - . NA NA NA NA NA NA NA NA
LNCV6_137896_PI430048170 0.01035916711676 3.13768724 5.79921914 6.00769209
6.23764733 P P P 3.86023812 4.40159031 4.73579148 P P P
LNCV6_137896_PI430048170 mRNA
CCTTAGTCAACACCAGAGAATTCACATGAGGGGAAAACCTATTAATGTAAGGAACTTAAAT NM_003447
RefSeq chr6 + 28080703 28089562 ZNF165 7718 zinc finger protein 165
GO:0005515|GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA
- . NA NA NA NA NA NA NA NA NA NA
LNCV6_134709_PI430048170 0.01079795395647 12.39460324 4.74193163 5.00004373
4.98642922 P P P 1.89303202 1.18190570 0.39552817 A A A
LNCV6_134709_PI430048170 mRNA
CTGTAGTTCTAGAACCTGATTTTAACTCAGGAATAAAGACTTTCTGCGGTCAGTGGCAAA NM_198469
RefSeq chr9 + 122159907122200088MORN5 254956 "MORN repeat containing 5, transcript variant 1" NA . NA - . NA NA NA NA NA NA NA NA
LNCV6_127429_PI430048170 0.01111796983766 2.73205175 8.59899178 9.32219534
8.62448934 P M P 7.69894550 7.37594561 7.19766475 P P P
LNCV6_127429_PI430048170 mRNA
CAGATTACTGAGATTGGGGATTGTAACCTCTGACTTGCCAAACAACTGCTGCCTCATAAA NM_001035235
RefSeq chr5 - 140550066140558093SRA1 10011 "steroid receptor RNA activator 1, transcript variant 1"
GO:0005515|GO:0006355|GO:0005886|GO:0008283|GO:0003713|GO:0006915|GO:0042981|GO:0005634|GO:2000273|GO:0006351|GO:0030154|GO:0045171|GO:0005737|GO:0030374|GO:0030529|GO:0015630|GO:0005654 . NA - . NA NA NA NA NA NA NA NA
LNCV6_123694_PI430048170 0.01113080343601 2.35024411 9.24486225 9.51980000
9.33869598 P P P 8.47906332 7.87054576 7.99511409 P P P
LNCV6_123694_PI430048170 mRNA
GGCCCGCAGTATGGCTCCGAGGGCAGGTTCACTTTCCTTCCCATACCCCTGAGAGTTC NM_017510

RefSeq chr5 + 177592211 177596098 TMED9 54732 transmembrane emp24 protein
transport domain containing 9
GO:0005515|GO:0019905|GO:0005793|GO:0005794|GO:0005783|GO:0048205|GO:0010638|GO:000013
9|GO:0034498|GO:0033116|GO:0005789|GO:0007030|GO:0032527|GO:0016021|GO:0030140|GO:0070
062 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_133462_PI430048170 0.01125494283083 6.09600352 4.51071438 3.84759293
4.42626755 P P P 1.37405932 0.93016532 2.35909395 A A P
LNCV6_133462_PI430048170 mRNA
GAGGACGGCTTACATGTTTGTCTGTAGAAAATAAAGCTGAGCTACGATTCCGAAAAA NM_020994
RefSeq chrX - 154651971 154653579 CTAG2 30848 "cancer/testis antigen 2, transcript
variant 2" GO:0008150|GO:0003674|GO:0005813. NA - . NA NA NA NA NA NA
NA NA NA
LNCV6_90487_PI430048170 0.01127639126311 7.88664411 4.38778115 4.99216091
5.08364313 P P P 2.54184586 1.71908003 0.90609208 P A A
LNCV6_90487_PI430048170 mRNA
AATGTGGAGCTCAAATATGCCTTATTTTGCACAAAAGACTGCCAAGGACATGACCAGCAG NM_001013398
RefSeq chr7 - 45912244 45921272 IGFBP3 3486 "insulin-like growth factor binding protein
3, transcript variant 1"
GO:0005515|GO:0008285|GO:0031994|GO:0031995|GO:0005634|GO:0005615|GO:0001558|GO:004687
2|GO:0010906|GO:0014912|GO:0008160|GO:0044342|GO:0009968|GO:0001968|GO:0070062|GO:0005
520|GO:0043065|GO:0006915|GO:0048662|GO:0005576|GO:0043085|GO:0001649|GO:0016942|GO.
NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_134267_PI430048170 0.01145437262822 2.10574162 5.07188706 4.46768401
4.72658702 P P P 3.96523141 3.69709527 3.38744636 P P P
LNCV6_134267_PI430048170 mRNA
GATCAGAAGCTCAGCATGGCCATTATGCCTAGTTTTGATGAATAAACATGGGAAAGCCAT NM_021916
RefSeq chr22- 23741583 23751092 ZNF70 7621 zinc finger protein 70
GO:0006355|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_100510_PI430048170 0.01145768449191 3.12324147 5.97968729 5.98811431
5.87129835 P P P 4.53479964 4.40990671 3.89080222 P P P
LNCV6_100510_PI430048170 mRNA
AGGACATGGCACATCAAGTCCAAGAGTTGTTTAGAACCCGTCAGGTGGTGAAGAAGTACT NM_032795
RefSeq chr11- 126202093 126211692 RPUSD4 84881 "RNA pseudouridylate synthase
domain containing 4, transcript variant 1" GO:0009982|GO:0005739|GO:0005515|GO:0001522 .
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_141451_PI430048170 0.01174605601012 2.22561597 15.54923151 15.57208856
15.55903476 P P P 14.14694410 14.57653749 14.46087799 P P P
LNCV6_141451_PI430048170 mRNA
GAAAGAGTGTGTTGGTGTGCTGGGGTGTCAATAAAGCTGTGCTTGGGGTCGCTGAAAAA NM_002178
RefSeq chr12+ 53097651 53102344 IGFBP6 3489 insulin-like growth factor binding protein 6
GO:0007165|GO:0008285|GO:0005794|GO:0043567|GO:0031994|GO:0031995|GO:0005576|GO:004426
7|GO:0005615|GO:0001558|GO:0070062 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_127759_PI430048170 0.01195591540367 2.00309751 13.10868113 13.52748605
13.39322278 P P P 12.40575824 12.33017102 12.31626941 P P P
LNCV6_127759_PI430048170 mRNA
CTTGCCTTGGCTCTTTGAGCTCCCTTTTGCTTAATTACTGGGTTTTCTGGGCAGTTTTTT NM_152766
RefSeq chr17- 7402973 7404131 TMEM256 254863 transmembrane protein 256
GO:0008150|GO:0003674|GO:0016021|GO:0070062 . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_110165_PI430048170 0.01216871127249 2.02056383 9.76464832 9.79796773
10.05563617 P P P 9.17997306 8.63138189 8.71837419 P P P
LNCV6_110165_PI430048170 mRNA
ACTTTGGTCTTCATTCAATGTGTGATCAATGCTGTGTTTGCCAAGATCTGGTGGATCGTA NM_005827
RefSeq chr17- 49700933 49707951 SLC35B1 10237 "solute carrier family 35, member B1,
transcript variant 1" GO:0072334|GO:0006810|GO:0005789|GO:0016021|GO:0005459|GO:0043231
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_136823_PI430048170 0.01226489210200 2.08957548 9.28006112 9.67292133
9.66847726 P P P 8.50582809 8.52320248 8.43544608 P P P
LNCV6_136823_PI430048170 mRNA

AGAAGGTAAAGAAGAGGCATGTCCAGTATGCTTTGCAGGGTGTGTTTGCTCTTTTCCATG NM_017836
RefSeq chr3 - 126006356|126084291|SLC41A3 54946 "solute carrier family 41, member 3,
transcript variant 2" GO:0005886|GO:0008324|GO:0016021. NA - . NA NA NA NA
NA NA NA NA NA
LNCV6_142837_PI430048170 0.01240826445997 2.52571357 8.25440130 8.57532922
8.89414703 P P P 7.38118313 7.19867340 7.19667687 P P P
LNCV6_142837_PI430048170 mRNA
AACAAAGTTTGTGATGATGCATTGGAAGCAAAGACATTCACGCAGCCGTCCTTATCCTGTG NM_153333
RefSeq chrX - 103252994|103255193|TCEAL8 90843 "transcription elongation factor A
(SII)-like 8, transcript variant 1" GO:0006355|GO:0005634|GO:0006351. NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_137693_PI430048170 0.01252074329069 2.09402371 5.61447630 5.18139718
5.21553404 P P P 3.96308165 4.61378210 4.20078119 P P P
LNCV6_137693_PI430048170 mRNA
TGGAGCATATGACCCGTCACCTGGAGGAGAGTGAGAAGGCCATGCAGGAGCGGGTGCAGANM_144999
RefSeq chr17+ 82023301 82031151 LRRC45 201255 leucine rich repeat containing 45
GO:0005813|GO:0005737 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_110344_PI430048170 0.01271121285917 2.24834067 5.74833335 6.30729573
5.82164011 P P P 5.18561220 4.64489965 4.51570110 P P P
LNCV6_110344_PI430048170 mRNA
ACCTGCTGCACCAGCAGCTGCAGGAGCTGCACGCCACGTGGTGCTTCCCGACCCGGCGG NM_002741
RefSeq chr19+ 14433353 14471867 PKN1 5585 "protein kinase N1, transcript variant 2"
GO:0005515|GO:0042826|GO:0005886|GO:2000145|GO:0005634|GO:0050681|GO:0032154|GO:004239
3|GO:0005737|GO:0030374|GO:0005080|GO:0006357|GO:0030496|GO:0007257|GO:0035407|GO:0006
972|GO:0005524|GO:0006351|GO:0035402|GO:0048365|GO:0007165|GO:0004672|GO:0004674|GO.
NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_133317_PI430048170 0.01297252091195 2.48008149 7.25594474 7.22016773
7.16515272 P P P 5.63555044 6.19144438 5.82847977 P P P
LNCV6_133317_PI430048170 mRNA
TGGACAGATGGGTAGATGTGGCAGGCATGTCATCGACAGCACAGAAGGGCTGTCCTGTGT NM_002236
RefSeq chr2 + 10911936 10914225 KCNF1 3754 "potassium channel, voltage gated modifier
subfamily F, member 1"
GO:0005251|GO:0005886|GO:0008076|GO:0007268|GO:0005267|GO:0051260|GO:0034765|GO:001602
1|GO:0006813|GO:0071805. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134323_PI430048170 0.01303979983037 4.05888740 6.85556434 6.82226387
6.90262970 P P P 4.88328983 5.17317402 4.34305255 P P P
LNCV6_134323_PI430048170 mRNA
AGAATGAGTTTAATATCAAAGTGTAAGCTTACTTTCCATCCCCAAGCCAGCCTGCCCCCT NM_001288708
RefSeq chr16- 90004864 90020131 DBNDD1 79007 "dysbindin (dystrobrein binding
protein 1) domain containing 1, transcript variant 3" GO:0005737 . NA - . NA NA
NA NA NA NA NA NA NA
LNCV6_133622_PI430048170 0.01336942789827 2.05601025 9.34650254 9.63225058
9.89550230 P P P 8.68382936 8.47479017 8.63974967 P P P
LNCV6_133622_PI430048170 mRNA
GCCTTTTTTAAGAAATAAATTTTTTTGTTACATGACCAAAGCCCCTCCTGTGTGTGTTAA NM_203462
RefSeq chr4 - 6707700 6709879 MRFAP1L1 114932 Morf4 family associated protein 1-like
1 GO:0005515 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_131828_PI430048170 0.01348617241473 4.46416525 4.28586048 4.08857329
4.67490474 P P P 1.40546182 2.57625325 2.40316027 A P P
LNCV6_131828_PI430048170 mRNA
CAGTCTGACAAAAGTCTATGGTTCCTAAATATGACATCAGTGTTGCCAATAAAATGTTTC NM_004411
RefSeq chr7 + 95772505 96098424 DYNC1I1 1780 "dynein, cytoplasmic 1, intermediate chain
1, transcript variant 1"
GO:0005515|GO:0008017|GO:0048471|GO:0005874|GO:0030507|GO:0003777|GO:0031982|GO:000582
9|GO:0019886|GO:0000922|GO:0003774|GO:0047496|GO:0008152|GO:0000777|GO:0000776|GO:0005
868|GO:0055037 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_130177_PI430048170 0.01362517448927 2.31299667 4.31198028 4.61436091
4.97701983 P P P 3.83379146 3.29287996 3.12660952 P P P
LNCV6_130177_PI430048170 mRNA
CACCCCTTCTCTACAATTTTGTGAACATTTATGCTCCAGTGGCATTCACTGGTTGTTTCAT NM_001143962
RefSeq chr1 - 223541608|223665734|CAPN8 388743 calpain 8

GO:0005737|GO:0005794|GO:0004198|GO:0007586|GO:0005509|GO:0006508 . NA - .
NA NA NA NA NA NA NA NA
LNCV6_129461_PI430048170 0.01401222780334 16.53555950 8.19929952 10.14048537
9.28291146 P P P 5.64888377 5.95277001 3.53537459 P P P
LNCV6_129461_PI430048170 mRNA
CTCTGCTTTTCCTGTCTGTATATAACTTATTTGCCCTAAGAACTTTGAGAATCCCAATTA NM_001956
RefSeq chr1 - 41478774 41484683 EDN21907 "endothelin 2, transcript variant 1"
GO:0008284|GO:0001659|GO:0019722|GO:0019221|GO:0007204|GO:0005615|GO:0019229|GO:0001516|GO:0045987|GO:0042310|GO:0003100|GO:0014824|GO:0014826|GO:0048286|GO:0030593|GO:0048016|GO:0005576|GO:0060585|GO:0002690|GO:0097009|GO:0005179|GO:0003058|GO:0042116|GO: NA - . NA NA NA NA NA NA NA NA NA
LNCV6_100530_PI430048170 0.01426757333679 2.05371712 4.28219773 4.43612630
4.43835784 P P P 3.59389445 3.05190989 3.35104424 P P P
LNCV6_100530_PI430048170 mRNA
GTTTCAGGGACTGGAATTGCAAGAGTATTTTCATGCGTGTTGAAGATGAACTGGAAATCCC NM_021908
RefSeq chr7 + 116953326117223907ST7 7982 "suppression of tumorigenicity 7, transcript variant b" GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_92677_PI430048170 0.01436401166276 2.13447005 5.03127439 5.09682744
4.54407596 P P P 3.89159109 3.66652218 3.88199883 P P P
LNCV6_92677_PI430048170 mRNA
TTCCGCCATGCTCAGCTTCTGGACGCAGCAAAGCAGGTGGTGAGTTCTTGCTGCGGTAT NM_002910
RefSeq chrX - 153935268153944780RENBP 5973 renin binding protein
GO:0010951|GO:0004866|GO:0050121|GO:0006051|GO:0008217|GO:0006044|GO:0019262|GO:0005524|GO:0042803|GO:0070062. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_103281_PI430048170 0.01444777119592 2.07509493 5.72995685 6.15003373
6.24462278 P P P 4.78847665 4.77796898 5.36697853 P P P
LNCV6_103281_PI430048170 mRNA
TTTTTGAATTTTCGTAAGGCAAGAAGTGACATGCTTCTCTCCAGGAAGAATCAGCTCCTG NM_001483
RefSeq chr7 + 55964576 56000182 GBAS2631 "glioblastoma amplified sequence, transcript variant 1" GO:0005739|GO:0005515|GO:0006754|GO:2000984|GO:0016020|GO:0005887|GO:0006119 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_145169_PI430048170 0.01456310875279 5.10097139 3.27826954 4.12244053
3.03882917 P P P 0.86450207 0.40952997 1.91785505 A A A
LNCV6_145169_PI430048170 mRNA
AGATTTGCATCTTTACAACCAGAAGCTCAGGGAGAAGTTGAAGGAGGAGGAGAACACAGT NM_022158
RefSeq chr17+ 82735575 82751197 FN3K64122 fructosamine 3 kinase
GO:0016310|GO:0030387|GO:0030389|GO:0030855|GO:0005575|GO:0030393 . NA - .
NA NA NA NA NA NA NA NA NA NA
LNCV6_133940_PI430048170 0.01511110768304 2.23104331 4.42076107 4.56445540
4.70018306 P P P 3.74209876 3.07702042 3.32734780 P P P
LNCV6_133940_PI430048170 mRNA
GTGTTTGTCTTCTTTGAATGTCTTGCCACTGGTTGCAGTAAAAGTGTCTGTATTCATT NM_145051
RefSeq chr9 - 113297092113299040RNF183 138065 ring finger protein 183
GO:0008270|GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134690_PI430048170 0.01522634091335 2.59713590 3.00132511 3.74581351
3.71983399 P P P 2.55291263 2.02717670 1.75600076 A A A
LNCV6_134690_PI430048170 mRNA
AGGCATTCCTTCAGTCCCCTGGGGAGGTTTCAGATGCTCAGACTCCCTGATACCACCTTTC NM_018280
RefSeq chr22- 46050458 46054144 PRR34 55267 proline rich 34 NA . NA -
. NA NA NA NA NA NA NA NA NA NA
LNCV6_143560_PI430048170 0.01530143492510 2.28326120 6.71032803 7.04122947
7.42996586 P P P 5.84527514 5.72956170 6.09845549 P P P
LNCV6_143560_PI430048170 mRNA
CCCCTGTATAGAATTGAAAGGATCCAAAGGATTATTGCACATTTTCTACATTCCAAGGAG NM_015364
RefSeq chr8 + 73991328 74029072 LY96 23643 "lymphocyte antigen 96, transcript variant 1"
GO:0005515|GO:0034142|GO:0005886|GO:0007249|GO:0001875|GO:0005615|GO:0002756|GO:0006954|GO:0002755|GO:0031666|GO:0032496|GO:0032497|GO:0031663|GO:0034138|GO:0046696|GO:0038124|GO:0038123|GO:0034134|GO:0015026|GO:0002224|GO:0006968|GO:0045087|GO:0035666|GO: NA - . NA NA NA NA NA NA NA NA NA
LNCV6_142436_PI430048170 0.01582015641918 2.08818914 9.30498550 9.38606977

9.34486433 P P P 7.99668212 8.31742075 8.49309555 P P P
 LNCV6_142436_PI430048170 mRNA
 AGATGAAGTAAATGCAGTGTCTACTGCCTGATGTGAAAGAGAGCTATGTATGATAATTA NM_018140
 RefSeq chr5 + 612289 653551 CEP72 55722 centrosomal protein 72kDa
 GO:0005515|GO:0005813|GO:0006996|GO:0000086|GO:0007051|GO:0000278|GO:0033566|GO:004280
 2|GO:0005829 . NA - . NA NA NA NA NA NA NA NA
 LNCV6_132598_PI430048170 0.01623726868415 10.78094090 10.16009542 10.73954717
 10.59377719 P P P 7.97421218 6.36270027 6.21541078 P P P
 LNCV6_132598_PI430048170 mRNA
 AAGAAAGTTTCTCAAACAGGGAGTACTTCAAGATCACCTCTACGGGAGAACCAAGGAG NM_005564
 RefSeq chr9 + 128149452 128153455 LCN2 3934 lipocalin 2
 GO:0005215|GO:0070301|GO:0002020|GO:0005615|GO:0042803|GO:0005829|GO:0006879|GO:007020
 7|GO:0031669|GO:0071356|GO:0015891|GO:0006811|GO:0070062|GO:0005506|GO:0042493|GO:0036
 094|GO:0009635|GO:0005576|GO:0009615|GO:0055085|GO:0097192|GO:0010628|GO:0071222|GO.
 NA - . NA NA NA NA NA NA NA NA NA NA
 LNCV6_126726_PI430048170 0.01644519661870 2.45855860 5.69693540 5.85907148
 5.50591231 P P P 3.94329171 4.73790791 4.40077437 P P P
 LNCV6_126726_PI430048170 mRNA
 GCAGGGATTTTGACTTTGGATGACAAGGCTTTATTTGTAAATATGCTCTTAATATGCAAC NM_001039570
 RefSeq chr22+ 29073077 29146820 KREMEN1 83999 "kringle containing transmembrane
 protein 1, transcript variant 3"
 GO:0005515|GO:0007154|GO:0016020|GO:0016021|GO:0016055|GO:0060828 . NA - .
 NA NA NA NA NA NA NA NA NA NA
 LNCV6_112398_PI430048170 0.01669942595953 2.15001359 3.65017993 3.52724720
 3.97272880 P P P 2.27179751 2.50590172 2.99911897 A P P
 LNCV6_112398_PI430048170 mRNA
 TTGAGAGGAGACTTACTGAATATATTCATTGTTTGCAACCTGCTACTGGACGCTGGAGAA NM_153261
 RefSeq chr16+ 50025205 50037088 CNEP1R1 255919 "CTD nuclear envelope phosphatase 1
 regulatory subunit 1, transcript variant 1"
 GO:0007077|GO:0006629|GO:0005515|GO:0034504|GO:0031965|GO:0005737|GO:0010867|GO:003530
 7|GO:0071595|GO:0016021|GO:0005635|GO:0000278 . NA - . NA NA NA NA NA NA
 NA NA NA NA
 LNCV6_144954_PI430048170 0.01698007723225 2.32532533 4.85257104 4.88767644
 5.47640118 P P P 4.02731081 3.75106518 3.86109634 P P P
 LNCV6_144954_PI430048170 mRNA
 TTCCAATGAATGAAAGTCATGCACCTTATTTATAGGCTCTATGTTTTGGCTTCTGCAGTA NM_198827
 RefSeq chr12+ 130953906 131141463 ADGRD1 NA adhesion G protein-coupled receptor D1
 NA . NA - . NA NA NA NA NA NA NA NA
 LNCV6_140227_PI430048170 0.01702429383219 2.62207790 7.29630307 7.33728680
 7.55250875 P P P 5.51461565 6.16197788 6.24593066 P P P
 LNCV6_140227_PI430048170 mRNA
 GTTCTTTTGTAAAGAAATAGCCTAATGGTCCAACCTTGTCTGTCTTCTTCAAATGTTT NM_001004298
 RefSeq chr10- 126425004 126521441 C10orf90 118611 chromosome 10 open reading frame
 90
 GO:0007095|GO:0030308|GO:0005813|GO:0005737|GO:0042826|GO:0010212|GO:0050821|GO:001562
 9|GO:0009411 . NA - . NA NA NA NA NA NA NA NA
 LNCV6_145147_PI430048170 0.01706074327337 2.55571677 3.32672105 3.37275578
 3.66728529 P P P 2.41714419 2.19309065 1.60218541 A A A
 LNCV6_145147_PI430048170 mRNA
 AATCAGGTAACCTACCAGACCAGCCTTGAATCTATCAAATCTAACTGCTGAGCTACCCA NM_002562
 RefSeq chr12+ 121132827 121186551 P2RX7 5027 "purinergic receptor P2X, ligand gated ion
 channel, 7, transcript variant 1"
 GO:0005515|GO:0032755|GO:0006649|GO:0043132|GO:0031594|GO:0010524|GO:0034405|GO:004870
 5|GO:0006900|GO:0010043|GO:0042803|GO:0019228|GO:0006884|GO:0016485|GO:0031668|GO:0043
 025|GO:0032496|GO:0033198|GO:0001614|GO:0006509|GO:0043029|GO:0000287|GO:0030501|GO.
 NA - . NA NA NA NA NA NA NA NA NA
 LNCV6_129102_PI430048170 0.01714622709218 5.01459262 3.82931801 4.88423728
 4.54149729 P P P 2.19089268 2.19474105 2.07862697 A A A
 LNCV6_129102_PI430048170 mRNA
 CAAAATCAAGTGGATAAACTTTTTAGCGCTTGGATGCAGCATGCTTGGTGGGTCCTTGAA NM_031916
 RefSeq chr5 + 10441861 10465026 ROPN1L 83853 "rhopilin associated tail protein 1-

like, transcript variant 1"
GO:0005515|GO:0005737|GO:0003351|GO:0031514|GO:0001932|GO:0030317|GO:0048240 . NA
- . NA NA NA NA NA NA NA NA
LNCV6_140501_PI430048170 0.01722671238564 2.60019705 3.43081254 4.34078110
3.83501082 P P P 2.85945888 2.42162511 2.26708559 A A A
LNCV6_140501_PI430048170 mRNA
GTACCACTAGCATCTATATGACTTTTGTGTAATTTTCTCTCTTGAAGCTCTGGTGCTGTTT NM_021221
RefSeq chr6_GL000253v2_alt + 2975997 2977497 LY6G5B 58496 "lymphocyte antigen
6 complex, locus G5B" GO:0008150|GO:0003674|GO:0005576|GO:0005575 . NA - . NA
NA NA NA NA NA NA NA NA
LNCV6_129927_PI430048170 0.01754366373995 2.34825900 4.35620862 4.36079337
4.69966869 P P P 2.75652996 3.49459302 3.39345684 P P P
LNCV6_129927_PI430048170 mRNA
GGGATGGAGTTAGAACCTTAATGATAATTTCTTTCGTTTGGTGTAGGTTTTAGAGATTTTG NM_012244
RefSeq chr14- 23125294 23183660 SLC7A8 23428 "solute carrier family 7 (amino acid
transporter light chain, L system), member 8, transcript variant 1"
GO:0005515|GO:0019534|GO:0006520|GO:0015695|GO:0005886|GO:0006865|GO:0009636|GO:005090
0|GO:0055085|GO:0015101|GO:0055065|GO:0016323|GO:0015804|GO:0005737|GO:0015171|GO:0005
887|GO:0007596|GO:0042605|GO:0006810|GO:0015175|GO:0015179|GO:0070062|GO:0006811 .
NA - . NA NA NA NA NA NA NA NA
LNCV6_130937_PI430048170 0.01760602482300 2.27914757 5.64491560 5.73602262
5.47518451 P P P 4.12008205 4.80260322 4.28984577 P P P
LNCV6_130937_PI430048170 mRNA
CTAGGGCCCTCCAAAAGAGTCCTTTTAAATAAATGAGCTATTTAGGTGCTGTGATTGTG NM_004750
RefSeq chr19- 18593224 18606850 CRLF1 9244 cytokine receptor-like factor 1
GO:0005515|GO:0001657|GO:0008284|GO:0046982|GO:0042517|GO:2000672|GO:0005125|GO:000561
5|GO:0005127|GO:0097058|GO:0043524|GO:0019955|GO:0004872 . NA - . NA NA
NA NA NA NA NA NA NA NA
LNCV6_137742_PI430048170 0.01767120900653 2.55905331 7.30684702 7.25312198
7.27979349 P P P 5.54340205 6.18507684 5.97293473 P P P
LNCV6_137742_PI430048170 mRNA
GTCCGGACAGCCCTGCTCGAAGATATAGAAAGAGTGACCTGCACAACTTGGAATTTTTT NM_005946
RefSeq chr16+ 56638665 56640088 MT1A 4489 metallothionein 1A
GO:0071294|GO:0005515|GO:0048471|GO:0005737|GO:0008270|GO:0005634|GO:0071276|GO:004592
6 . NA - . NA NA NA NA NA NA NA NA
LNCV6_128160_PI430048170 0.01769130813859 2.01211241 6.59948287 7.18415381
6.87786151 P P P 6.23474933 5.81311680 5.56642937 P P P
LNCV6_128160_PI430048170 mRNA
TGAAGAAAAAGTTTATGCGAGTACATGATGCGGAGTCCTCCGATGAAGACGGCTATGACT NM_001267560
RefSeq chr19+ 3708336 3750813 TJP3 27134 "tight junction protein 3, transcript variant
1" GO:0005515|GO:0016324|GO:0030054|GO:0005654|GO:0005634|GO:0005923|GO:2000045 .
NA - . NA NA NA NA NA NA NA NA
LNCV6_135459_PI430048170 0.01770610402902 2.40117701 9.92537020 9.84181547
9.81888309 P P P 8.94116712 8.43818007 8.34375957 P P P
LNCV6_135459_PI430048170 mRNA
CTCACTCTATATTTATGGGAGGAAAAGTGAAGATTAAATCCCAAGTTGTGCGTGTGTCT NM_198447
RefSeq chr1 - 204198159204214092 GOLT1A 127845 golgi transport 1A
GO:0006629|GO:0000139|GO:0016021|GO:0016192|GO:0015031|GO:0016298 . NA - .
NA NA NA NA NA NA NA NA
LNCV6_136160_PI430048170 0.01818139033378 2.98019935 3.95443938 4.35762648
4.31583416 P P P 2.64701642 3.06077169 2.05510528 P P A
LNCV6_136160_PI430048170 mRNA
GCACTCAGCTTCCCAGGCAATAACAGCCGTGGGGTAATAAATGGTCTCTGCACACCTGCA NM_178310
RefSeq chr16- 88677681 88686474 SNAI3 333929 snail family zinc finger 3
GO:0005667|GO:0003700|GO:0006357|GO:0005507|GO:0005634|GO:0003677|GO:0006351 . NA
- . NA NA NA NA NA NA NA NA
LNCV6_136169_PI430048170 0.01820756719039 2.40793350 3.75671945 3.64145150
2.98796493 P P P 2.22082568 2.57137412 1.80137191 A A A
LNCV6_136169_PI430048170 mRNA
TATGGTGCGATTCAATGACTGACTCATTTAATCAAGTGGGGACCTGTCTGTCTGTGCCTT NM_024825
RefSeq chr19- 13931186 13938476 PODNL1 79883 "podocan-like 1, transcript variant 1"

GO:0005578 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_134302_PI430048170 0.01848741397245 2.58014211 7.67682756 7.94446376
7.56287725 P P P 6.81360541 6.20031474 5.95523196 P P P
LNCV6_134302_PI430048170 mRNA
CAAAACCCTCCCAGTGTGTGTCCGTCTCTCATCTCAATAAAAGAATTTATTTTATTCTGA NM_024877
RefSeq chr19- 40222207 40226690 CNTD2 79935 cyclin N-terminal domain containing 2
NA . NA - . NA NA NA NA NA NA NA NA
LNCV6_134252_PI430048170 0.01852331879281 3.16809513 4.96469373 5.96621922
5.80854762 P P P 4.51643282 3.65748513 3.55777706 P P P
LNCV6_134252_PI430048170 mRNA
TAAATTGGAGATTCTCTACATTTCACTTGCAGTTTCCTGTTCTCCTCATTGCCTGCCTTC NM_080832
RefSeq chrX + 91434597 91438584 PABPC5 140886 "poly(A) binding protein, cytoplasmic
5" GO:0000166|GO:0005759|GO:0003723. NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_144375_PI430048170 0.01855573504690 5.26304782 4.62775059 4.56941220
4.53220089 P P P 2.65400560 1.46162102 2.18796142 P A A
LNCV6_144375_PI430048170 mRNA
GTATTTAGTTGTGATTACTGATTGCCTGATTTTAAAATGTTGCCTTCTGGGACATCTTCT NM_001033081
RefSeq chr1 - 39895423 39902015 MYCL4610 "v-myc avian myelocytomatosis viral oncogene
lung carcinoma derived homolog, transcript variant 1"
GO:0006355|GO:0003700|GO:0046983|GO:0005634|GO:0003677 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_143026_PI430048170 0.01908366599129 2.18935850 7.78063676 8.05797323
7.69781632 P P P 6.28969758 7.04588395 6.73637142 P P P
LNCV6_143026_PI430048170 mRNA
CTTCTCTTGCCGACATGTTTTTGTAAAGGCTGGTAAATAAATTATTTTGGACAAACTGG NM_018957
RefSeq chr22+ 37639676 37656043 SH3BP1 23616 SH3-domain binding protein 1
GO:0043547|GO:0007165|GO:0017124|GO:0005737|GO:0005096 . NA - . NA NA NA
NA NA NA NA NA NA
LNCV6_131399_PI430048170 0.01936790717301 3.13172051 3.33806361 4.34174065
3.95236681 P P P 2.18669815 2.79041299 1.66712104 A P A
LNCV6_131399_PI430048170 mRNA
TATATTCTGCCAGGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTT NM_014400
RefSeq chr19- 43460793 43465679 LYPD3 27076 LY6/PLAUR domain containing 3
GO:0007160|GO:0043236|GO:0006928|GO:0016021|GO:0046658|GO:0005615 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_141616_PI430048170 0.01947058018283 2.25490314 11.34192637 11.52910507
11.64489095 P P P 10.68762967 9.93623076 10.29106717 P P P
LNCV6_141616_PI430048170 mRNA
TCTGTATAAAAGGGAACAGTGTGGAGATGTTTTGTCTTGTTCCAAATAAAAGATTCACCA NM_033280
RefSeq chr18+ 59139856 59158837 SEC11C 90701 SEC11 homolog C (S. cerevisiae)
GO:0010467|GO:0050796|GO:0006614|GO:0006508|GO:0005789|GO:0008236|GO:0016021|GO:004426
7|GO:0006412|GO:0006465. NA - . NA NA NA NA NA NA NA NA
LNCV6_128787_PI430048170 0.01947617803261 2.28797595 4.25517376 4.11634701
4.87345371 P P P 3.36586155 3.50169384 2.82820996 P P P
LNCV6_128787_PI430048170 mRNA
TGCTTCGACAACAGGTGGAAGATCTTAAAAACAAGAATCTGCTGCTTCGAGCTCAGTTGC NM_007122
RefSeq chr1 - 161039250161045979USF1 7391 "upstream transcription factor 1, transcript
variant 1"
GO:0005515|GO:0006366|GO:0042826|GO:0003705|GO:0005634|GO:0045990|GO:0042803|GO:000369
0|GO:0045944|GO:0006006|GO:0000432|GO:0009411|GO:0005667|GO:0001666|GO:0032869|GO:0019
086|GO:0006357|GO:0019901|GO:0046982|GO:0055088|GO:0051918|GO:0043425|GO:0042593|GO.
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_129896_PI430048170 0.01953342627184 2.92506426 6.64177822 7.43931603
7.34330358 P P P 5.66289368 5.48654041 5.74124989 P P P
LNCV6_129896_PI430048170 mRNA
AAGCTAAGCGACTGTACGTGCTACTAAAAATGTCTGACACTGAAATAATTTTACTCAACT NM_138448
RefSeq chr2 + 54115272 54305298 ACYP2 98 "acylphosphatase 2, muscle type"
GO:0005739|GO:0003998|GO:0006796. NA - . NA NA NA NA NA NA NA
NA
LNCV6_127080_PI430048170 0.01964061944267 5.44151084 3.69062065 3.50218155

4.29808286 P P P 2.18234382 0.50389602 1.07955993 A A A
 LNCV6_127080_PI430048170 mRNA
 CTGTAAGTTTTCTGTCAGAAGAGGACTTTCATCAACTTTCATGGAAAGATGTTTATTGC NM_001159560
 RefSeq chrX - 102153706 102155790 BEX5 340542 "brain expressed, X-linked 5, transcript
 variant 2" GO:0005737|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
 NA
 LNCV6_127464_PI430048170 0.01967955493956 2.02397569 3.76180190 4.12100227
 3.90965407 P P P 2.49290377 3.06663062 3.12384363 A P P
 LNCV6_127464_PI430048170 mRNA
 TCAGCCACTGGTACTACGAGAATGTTTGTATTACCCACATTTGAAATGATTGCTATGAT NM_006308
 RefSeq chr5 + 54455600 54456384 HSPB3 8988 heat shock 27kDa protein 3
 GO:0006986|GO:0005737|GO:0005634. NA - . NA NA NA NA NA NA NA NA
 NA
 LNCV6_78925_PI430048170 0.01976130320548 2.03069713 7.48790875 7.45690661
 7.40795870 P P P 6.35423742 6.70571822 6.17701446 P P P
 LNCV6_78925_PI430048170 mRNA
 ATTCCCAGCCACTATGATGTCCAGGACCGCTTCCGCATTGAGCTGTCTGAGGAAGGAGCT NM_023948
 RefSeq chr7 + 100612490 100615377 MOSPD3 64598 "motile sperm domain containing 3,
 transcript variant 1" GO:0007507|GO:0016021 . NA - . NA NA NA NA NA NA NA
 NA NA NA
 LNCV6_136573_PI430048170 0.01979364432512 3.18164823 4.32468833 3.38571317
 3.98560532 P P P 2.21510218 2.16439037 2.44259623 A A P
 LNCV6_136573_PI430048170 mRNA
 AGGCCTCAAAAACATACGTAACGAAAAGGCCTAGCGAGGCAAATTCTGATTGATTTGAAT NM_139072
 RefSeq chr2 - 229357628 229714570 DNER 92737 delta/notch-like EGF repeat
 containing
 GO:0005515|GO:0007220|GO:0005886|GO:0005509|GO:0048741|GO:0005112|GO:0007417|GO:000741
 6|GO:0030425|GO:0006897|GO:0007219|GO:0030276|GO:0043025|GO:0010001|GO:0016021|GO:0001
 764|GO:0005769|GO:0004888 . NA - . NA NA NA NA NA NA NA NA NA
 LNCV6_95074_PI430048170 0.01982708150872 2.05491127 5.98436160 5.78537068
 5.77254297 P P P 4.45956987 5.10810260 4.79487503 P P P
 LNCV6_95074_PI430048170 mRNA
 AGTTGTCAGCAAGAAAGCCCCAGGGCTGAAGTCCAAGTCCGTCGGGAACATGCCAGCTAA NM_007137
 RefSeq chrX + 47836901 47922256 ZNF81 347344 zinc finger protein 81
 GO:0006355|GO:0003700|GO:0005634|GO:0003677|GO:0046872|GO:0006351 . NA - .
 NA NA NA NA NA NA NA NA NA
 LNCV6_127613_PI430048170 0.01986992599446 2.24308005 4.92801533 4.44833275
 4.40161829 P P P 3.28970391 3.87124289 3.05557404 P P P
 LNCV6_127613_PI430048170 mRNA
 AAAGTGTGCTCGTGGCGGGATAAGAATTCGGCGGCATGTGTGGTGTACGAGGACATGTCTG NM_006137
 RefSeq chr17- 82314869 82317604 CD7 924 CD7 molecule
 GO:0042110|GO:0006955|GO:0048873|GO:0016020|GO:0005886|GO:0004872|GO:0016021|GO:000716
 9|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
 LNCV6_130900_PI430048170 0.01990211280223 6.82839206 4.16016536 4.71940753
 4.12550164 P P P 1.81341161 2.06780172 0.40623732 A A A
 LNCV6_130900_PI430048170 mRNA
 TTTCTGTGAAATAAAGACTTTTTGTATTTCTGGGGCTGAGGCTCAGCAACAGCCCCTCAG NM_005764
 RefSeq chr1 - 47183588 47190099 PDZK1IP1 10158 PDZK1 interacting protein 1
 GO:0016021|GO:0070062 . NA - . NA NA NA NA NA NA NA NA NA
 LNCV6_144617_PI430048170 0.02019356254463 6.46665436 6.20595123 6.10561914
 6.20297949 P P P 2.60687193 4.01211884 3.48922646 A P P
 LNCV6_144617_PI430048170 mRNA
 GCCTTGAAATCCAGATCTTTAAAATTTTATGTATTTATTAACATCGCCATTGGACCCCA NM_139155
 RefSeq chr10+ 70672802 70762439 ADAMTS14 140766 "ADAM metalloproteinase with
 thrombospondin type 1 motif, 14, transcript variant 1"
 GO:0030198|GO:0030199|GO:0030574|GO:0006508|GO:0005578|GO:0008270|GO:0005576|GO:000422
 2 . NA - . NA NA NA NA NA NA NA NA NA
 LNCV6_101686_PI430048170 0.02042947232293 2.53350486 4.55628185 4.37458917
 4.74023770 P P P 3.66501882 3.06502359 2.80120692 P P P
 LNCV6_101686_PI430048170 mRNA
 TCGGCATCATTTGGGGAAGAGTCCACTCCAGGCCAGACTAACTCAGAGACAGCTGTGGTG NM_006044

RefSeq chrX + 48802079 48824970 HDAC6 10013 histone deacetylase 6
GO:0008017|GO:0005515|GO:0032418|GO:0070301|GO:0010469|GO:0051354|GO:0008013|GO:004559
8|GO:0051879|GO:0006886|GO:0051787|GO:0034605|GO:0051788|GO:0070201|GO:0031625|GO:0000
209|GO:0006996|GO:0034983|GO:0060765|GO:0048487|GO:0009636|GO:0001047|GO:0070848|GO.
NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_140600_PI430048170 0.02081985409732 2.05957176 7.93904258 7.90781763
7.84248790 P P P 6.84417064 7.11756259 6.54594706 P P P
LNCV6_140600_PI430048170 mRNA
GGGCTCCTCCCGCGCGGGGCTTGCCAAAGCTTTCTTAATAAAATGCCTTTCCCCTCAAA NM_153334
RefSeq chr22- 20424583 20437859 SCARF2 91179 "scavenger receptor class F, member
2, transcript variant 1"GO:0005515|GO:0016021|GO:0005925|GO:0007157|GO:0006898|GO:0005044
. NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_77141_PI430048170 0.02089034829974 2.55832131 3.87065093 4.61325552
4.32926594 P P P 3.20546326 3.15413058 2.32646472 P P A
LNCV6_77141_PI430048170 mRNA
AAACTTTGGTGTAATAATCCACCAGTTTCCAGCCACCTTCCTGACTTCTATCTGGGCTTG NM_025262
RefSeq chr6_GL000256v2_alt - 2975967 2979658 LY6G5C 80741 "lymphocyte antigen
6 complex, locus G5C"GO:0005576 . NA - . NA NA NA NA NA NA NA NA NA
NA
LNCV6_134291_PI430048170 0.02126670940682 2.68626558 11.41989822 11.50121470
11.44520052 P P P 10.43826200 9.78174766 9.76377367 P P P
LNCV6_134291_PI430048170 mRNA
AGGGCCACCTGTGACGTCTGCATCTTCTTGGAGAGAGAATAAAGTTTGTATTTAAGTGGT NM_178545
RefSeq chr1 - 1917589 1919301 TMEM52 339456 transmembrane protein 52
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139623_PI430048170 0.02133430485071 5.10965115 3.67648049 3.96558452
3.26810517 P P P 0.84634394 0.51875065 2.07538778 A A A
LNCV6_139623_PI430048170 mRNA
TTTGGCCATTAGCATTTTCATGTCTTTCCCAAATGAAGATGCCCTGCAAAGGGCAGTAAC NM_012396
RefSeq chr1 - 201465493201469171PHLDA3 23612 "pleckstrin homology-like domain,
family A, member 3, transcript variant 1"
GO:0051898|GO:0043065|GO:0005886|GO:0043325|GO:0005547|GO:0080025|GO:0005546|GO:003226
6|GO:0009653|GO:0042771|GO:0005737|GO:0010314|GO:0070062 . NA - . NA NA
NA NA NA NA NA NA NA NA
LNCV6_92670_PI430048170 0.02168187410953 2.04744523 4.80221562 5.28197730
5.53224261 P P P 4.27030791 4.39964713 3.89030271 P P P
LNCV6_92670_PI430048170 mRNA
TATGGCCTCATTTTAGCTGCTTCAGTGTGTTGGAGCTGTTACTTGCTCCTTCATTTCTG NM_001267782
RefSeq chr11- 46396411 46594069 AMBRA1 55626 "autophagy/beclin-1 regulator 1,
transcript variant 1"
GO:0005515|GO:0005776|GO:0008285|GO:0005930|GO:0006914|GO:0030154|GO:0005829|GO:004323
1|GO:0045335|GO:0005739|GO:0005737|GO:0043524|GO:0043552|GO:2000785|GO:0021915|GO:0031
625 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127406_PI430048170 0.02182994621407 7.19154402 5.76039484 6.13678350
5.96427266 P P P 3.79082763 2.08123144 2.98757063 P A P
LNCV6_127406_PI430048170 mRNA
GTGTGCTGGGGGACTTTTGCCTTGTTTGTAAAGTTTTTGTACATTGAGAATA NM_153274
RefSeq chr1 - 44783584 44787754 BEST4 266675 bestrophin 4
GO:0008150|GO:0003674|GO:0005886|GO:0034707|GO:0005254 . NA - . NA NA NA
NA NA NA NA NA NA NA
LNCV6_129842_PI430048170 0.02188922996199 2.14709779 11.53943220 11.58987122
11.75487769 P P P 10.88800827 10.21397547 10.39747891 P P P
LNCV6_129842_PI430048170 mRNA
CTTCCACCCAAGTCCGCATCTGTGTGTATCATCAATAAAGTTGTGTGCTTTGATTGGCAG NM_001184768
RefSeq chrX - 101615117101618001ARMCX6 54470 "armadillo repeat containing, X-linked
6, transcript variant 3"GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
NA
LNCV6_131832_PI430048170 0.02249482337130 2.07363423 5.09021195 4.92229253
5.07870084 P P P 4.32650511 3.82574747 3.71194838 P P P
LNCV6_131832_PI430048170 mRNA
AGTTATCAGCCAGCAGAAACAGATCTTCAGGAATCACATGTCTGACTTCCGGATCCAGAA NM_194296

RefSeq chr5 - 139396766139404087SPATA24 202051 spermatogenesis associated 24
GO:0006355|GO:0005737|GO:0005730|GO:0007275|GO:0005654|GO:0005634|GO:0007283|GO:0003677|GO:0042803|GO:0030154|GO:0006351 . NA - . NA NA NA NA NA NA NA NA
NA NA
LNCV6_127867_PI430048170 0.02257109862967 5.43484813 3.35357546 3.53749750
3.74355662 P P P 1.82128462 0.75052047 0.33968358 A A A
LNCV6_127867_PI430048170 mRNA
ATTACAAATGAGCCCGAATCATGACAGTCAGCAACATGATACCTGGATCCAGCCATTCCT NM_003332
RefSeq chr19- 35904400 35908309 TYROBP 7305 "TYRO protein tyrosine kinase binding protein, transcript variant 1"
GO:0005515|GO:0005886|GO:0009986|GO:2001204|GO:0005102|GO:0042802|GO:0035556|GO:0007165|GO:0006968|GO:0002281|GO:0005887|GO:0007229|GO:0007411|GO:0045087|GO:0050776|GO:0002283|GO:0005057 . NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_140136_PI430048170 0.02298410839776 3.05944405 3.13253903 3.23564076
3.17404836 P P P 1.90579232 1.64185573 1.01975872 A A A
LNCV6_140136_PI430048170 mRNA
AGCCTGCAGTTTGATCTGGTGAAGAATGGCGAATCCATTGCCTCTTTCTTCCAGTTTTTC NM_031433
RefSeq chr11- 119338933119346673MFRP83552 membrane frizzled-related protein
GO:0003674|GO:0016324|GO:0016021|GO:0009790 . NA - . NA NA NA NA NA NA
NA NA NA NA
LNCV6_109979_PI430048170 0.02304928146505 2.08882593 8.13676286 8.14133929
8.33842077 P P P 7.48470812 6.79713495 7.07202199 P P P
LNCV6_109979_PI430048170 mRNA
CACTAACACCTGTAATAAATATGGAGTCAGTGGATATCCAACCCTGAAGATATTTAGAGA NM_005313
RefSeq chr15+ 43746391 43772606 PDIA3 2923 "protein disulfide isomerase family A, member 3"
GO:0005515|GO:0002474|GO:2001238|GO:0034976|GO:0005783|GO:0005634|GO:0006606|GO:0004629|GO:0006457|GO:0006508|GO:0018279|GO:0070062|GO:0042470|GO:0009986|GO:0042590|GO:0003756|GO:0005790|GO:0004197|GO:0007165|GO:0005788|GO:0002479|GO:0045454|GO:0006621|GO. NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_59157_PI430048170 0.02340733668695 2.05500744 7.49807132 7.97762748
7.61634287 P P P 7.05187488 6.59100025 6.26720002 P P P
LNCV6_59157_PI430048170 mRNA
AAATCCTAGGGGGTGTGGACTCTTCTTTAGCTTTACAGAGATCCTTGGTGTGGCTAG NM_005981
RefSeq chr12+ 57745000 57748243 TSPAN31 6302 tetraspanin 31
GO:0008284|GO:0016020|GO:0005887. NA - . NA NA NA NA NA NA NA NA NA
NA
LNCV6_138669_PI430048170 0.02373852348755 4.17484771 5.04378762 5.25824472
5.25458724 P P P 3.75609298 2.66569728 2.66817137 P P P
LNCV6_138669_PI430048170 mRNA
CCATCTCACTGTAAATAAGTCTCTGTTCTGTAAATAGATGTACAGAAGCCATGTTATTTTC NM_170600
RefSeq chr9 - 127738316127778769SH2D3C 10044 "SH2 domain containing 3C, transcript variant 1"
GO:0043547|GO:0005515|GO:0005085|GO:0005737|GO:0016020|GO:0007264|GO:0005070|GO:0007254|GO:0009967 . NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_127989_PI430048170 0.02426677470220 2.50565326 9.49637273 9.50403004
9.85564439 P P P 7.71429796 8.44227513 8.60716143 P P P
LNCV6_127989_PI430048170 mRNA
TTCACCTTCACATAGATGTCCCTTTCTTGCCAGTTATCCCTTCCTTTTAGCCTAGTTCA NM_001145031
RefSeq chr10+ 73911103 73917500 PLAUI 5328 "plasminogen activator, urokinase, transcript variant 2"
GO:0005515|GO:0033628|GO:0001666|GO:0010469|GO:0004252|GO:0005886|GO:0009986|GO:0014910|GO:0014909|GO:0005576|GO:2000097|GO:0005615|GO:0061041|GO:0007165|GO:0006935|GO:0007596|GO:0042127|GO:0006508|GO:0042730|GO:0005925|GO:0070062 . NA - . NA NA NA NA NA NA NA NA
LNCV6_79933_PI430048170 0.02473456924817 2.43175453 5.21786492 5.74547440
6.09991881 P P P 4.58127652 4.20867982 4.53250877 P P P
LNCV6_79933_PI430048170 mRNA
ACAATATTTCTCAGAGGATAGCCTTTCACTTATTCATCTGTCCAGCATGACTCATCCCCG NM_019607
RefSeq chr8 + 66667551 66681142 C8orf44 56260 chromosome 8 open reading frame 44
GO:0005654 . NA - . NA NA NA NA NA NA NA NA NA NA

LNCV6_134896_PI430048170 0.02478593268106 2.61583721 5.96898191 6.62073079
 6.18279951 P P P 5.44995259 4.50927526 4.51430461 P P P
 LNCV6_134896_PI430048170 mRNA
 GGCTCTTTTGTAAAGTTTTTGTAGTGATTTTTATGCCACCTGAATAAAGAATGAATGGGC NM_001165920
 RefSeq chr17_KI270861v1_alt+ 171977 184214 SERPINF2 5345 "serpin peptidase inhibitor,
 clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 2, transcript variant 2"
 GO:0005515|GO:0004866|GO:0004867|GO:0045597|GO:0046330|GO:0048514|GO:2000049|GO:007256
 2|GO:0002020|GO:0005615|GO:0042803|GO:0071636|GO:0030199|GO:0045944|GO:0031093|GO:0070
 374|GO:0070062|GO:0010033|GO:0009986|GO:0051918|GO:0005577|GO:0002034|GO:0030168|GO.
 NA - . NA NA NA NA NA NA NA NA NA
 LNCV6_141425_PI430048170 0.02501428423426 2.02931594 3.45236452 4.09601750
 4.03264381 P P P 2.53937763 2.72658228 3.24088086 P P P
 LNCV6_141425_PI430048170 mRNA
 AGGGCCTTAGAAATGTCAATGGGGCAGGAAGAAAACACAATTTCTAACTGCCTGTTTTTG NM_003462
 RefSeq chr1 + 37556918 37566857 DNALI1 7802 "dynein, axonemal, light intermediate chain
 1"
 GO:0007338|GO:0005515|GO:0045504|GO:0005737|GO:0005930|GO:0008152|GO:0006928|GO:000585
 8|GO:0030175|GO:0003777. NA - . NA NA NA NA NA NA NA NA
 LNCV6_127747_PI430048170 0.02510313232361 2.32954392 5.50055112 5.79543246
 5.59233125 P P P 4.85809467 4.16298165 4.09336073 P P P
 LNCV6_127747_PI430048170 mRNA
 CAAGCATACTTCTTTTGCCTATTATGTTTAACTCACAAAACAAAGCTCATCATGCGTTTG NM_001304579
 RefSeq chr1 + 27934954 27959157 SMPDL3B 27293 "sphingomyelin phosphodiesterase,
 acid-like 3B, transcript variant 3"
 GO:0008150|GO:0003674|GO:0006685|GO:0016798|GO:0004767|GO:0005615|GO:0070062 . NA
 - . NA NA NA NA NA NA NA NA NA
 LNCV6_131774_PI430048170 0.02511150126453 2.27123921 3.69367958 3.01858827
 3.47271159 P P P 2.69657282 2.06618709 1.80014227 P A A
 LNCV6_131774_PI430048170 mRNA
 CCAGGCTATTACACAGGCCACAGCAGAAAAGAGAGCACCTGTGAAGAAATAAATACCAT NM_015077
 RefSeq chr17+ 28371661 28401038 SARM1 23098 sterile alpha and TIR motif containing
 1
 GO:0030424|GO:0030054|GO:0034142|GO:0005874|GO:0045202|GO:0042981|GO:0002224|GO:003042
 5|GO:0005829|GO:0009749|GO:0048814|GO:0005739|GO:0002756|GO:0005737|GO:0031315|GO:0045
 087|GO:0034138 . NA - . NA NA NA NA NA NA NA NA
 LNCV6_127692_PI430048170 0.02594929523620 2.57600543 3.18261712 4.06847549
 3.88266913 P P P 2.83182442 2.35216745 1.82297863 P A A
 LNCV6_127692_PI430048170 mRNA
 ATTTCTGGCTTTGCAGGACTCTTACCATGGCCAGGCATTCTGCCAGCCTTTACCTCCT NM_001005922
 RefSeq chr11_KI270903v1_alt- 60878 61820 KRTAP5-1 NA keratin associated protein
 5-1 NA . NA - . NA NA NA NA NA NA NA NA
 LNCV6_139392_PI430048170 0.02613849898692 2.52908899 12.95490597 13.31757139
 13.27339054 P P P 11.24695639 11.98689790 12.16795587 P P P
 LNCV6_139392_PI430048170 mRNA
 CTGGCCCTCTAGCTTCTACCCTTTGTCCCTGTAGCCTATACAGTTTAGAATATTTATTTG NM_001878
 RefSeq chr1 - 156699607156705667CRABP2 1382 "cellular retinoic acid binding protein 2,
 transcript variant 1"
 GO:0005215|GO:0006355|GO:0005783|GO:0016918|GO:0055085|GO:0019841|GO:0005829|GO:000716
 5|GO:0005737|GO:0008544|GO:0042573|GO:0001972|GO:0005501|GO:0005654|GO:0035115|GO:0070
 062 . NA - . NA NA NA NA NA NA NA NA
 LNCV6_144588_PI430048170 0.02671219569509 3.00346648 3.58846831 4.01136324
 4.07055491 P P P 2.36007566 2.77083560 1.58956289 A P A
 LNCV6_144588_PI430048170 mRNA
 CTCTTCAACGTTTTCTAGTACGTGTTTCTCTTCAATAAACTTCATTTCAGTGTTCCAGCCGG NM_013364
 RefSeq chrX + 153056408153060467PNMA3 29944 "paraneoplastic Ma antigen 3,
 transcript variant 1" GO:0043065|GO:0005730|GO:0008270|GO:0003676 . NA - . NA
 NA NA NA NA NA NA NA NA
 LNCV6_135994_PI430048170 0.02773686546279 4.95045224 3.54490541 3.44360800
 3.52055486 P P P 1.63662052 0.27425474 1.35325073 A A A
 LNCV6_135994_PI430048170 mRNA
 GGACAACTGCCAGACTTGAGCCCAATTAAATTTTATTTTGTCTGGTTTTGAATGAAAA NM_138805

RefSeq chr3 - 58633942 58666834 FAM3D 131177 "family with sequence similarity 3, member D" GO:0005576|GO:0046676|GO:0005125. NA - . NA NA NA NA NA NA NA NA NA NA

LNCV6_137766_PI430048170 0.02785475207979 2.38267049 3.97440618 3.45293874
4.15426995 P P P 2.14664170 3.13760656 2.44292820 A P P

LNCV6_137766_PI430048170 mRNA
ATGTCCTTCCATTACATCTCAATGGGAGACTGCATAGGATGGCTTGAGGACTTCTTGATG NM_130900

RefSeq chr6 - 150020129150025532RAET1L NA retinoic acid early transcript 1L NA .
NA - . NA NA NA NA NA NA NA NA NA NA

LNCV6_72199_PI430048170 0.02800702685890 4.18613110 6.29302598 6.58062653
6.44677840 P P P 5.05688789 3.77973441 3.94602166 P P P

LNCV6_72199_PI430048170 mRNA
ATCCTACCCATGACCCCTACTTGGGGCAGAAAAAACCCATCCTAAAGGCTGGGCCCATGC NM_198440

RefSeq chr22_KI270879v1_alt - 70864 75374 DERL3 91319 "derlin 3, transcript variant 3" GO:0005515|GO:0030176|GO:0030433|GO:0030968|GO:0018279 . NA - . NA NA
NA NA NA NA NA NA NA NA

LNCV6_72969_PI430048170 0.02838277070533 2.02202723 6.55708223 6.50853036
6.50976970 P P P 5.17827078 5.80629643 5.47553614 P P P

LNCV6_72969_PI430048170 mRNA
AGATGATGGTGAGCTCAGGAGATAAGATGGAAGATGCAACAGCCAATGGTCAAGAAGACT NM_001040454

RefSeq chr3 - 48625722 48633846 SLC26A6 65010 "solute carrier family 26 (anion exchanger), member 6, transcript variant 4" GO:0005515|GO:0015562|GO:0019531|GO:0019532|GO:0015660|GO:0031526|GO:0005254|GO:0015797|GO:0015659|GO:0070633|GO:0030165|GO:0038166|GO:0015499|GO:0071346|GO:0005887|GO:0008272|GO:0051454|GO:0015701|GO:0008271|GO:0051453|GO:0048240|GO:2001150|GO:0006820|GO .
NA - . NA NA NA NA NA NA NA NA NA NA

LNCV6_138507_PI430048170 0.02847330536970 2.05349567 5.77563727 5.95416040
5.58827664 P P P 4.33402020 5.13190291 4.64764933 P P P

LNCV6_138507_PI430048170 mRNA
ATTTACTTAGCTCAAGTCTGAAGCTGTAGATACTGGAAGACAATGCACCTTGGAGGGTGG NM_001195736

RefSeq chr1_KI270762v1_alt + 137939 142659 FAM213B 127281 "family with sequence similarity 213, member B, transcript variant 1" GO:0019371|GO:0019369|GO:0005737|GO:0001516|GO:0005783|GO:0043209|GO:0047017|GO:0044281|GO:0070062|GO:0055114|GO:0016616|GO:0005829 . NA - . NA NA NA
NA NA NA NA NA NA

LNCV6_140221_PI430048170 0.02855215324477 2.15922501 3.51178223 4.04518170
3.94297875 P P P 2.26493606 2.64381929 3.16915683 A P P

LNCV6_140221_PI430048170 mRNA
ATGCATTTGCATTGACTATGGGAGAAAAATTAGGGGGGAAATGACAGTCATGGTGTTTTTT NM_001143912

RefSeq chr1 + 27725978 27762912 FAM76A 199870 "family with sequence similarity 76, member A, transcript variant 1" NA . NA - . NA NA NA NA NA
NA NA NA NA

LNCV6_68250_PI430048170 0.02864592529405 2.05652084 6.20861506 5.56797980
6.15448144 P P P 4.82625678 5.01892358 5.03894057 P P P

LNCV6_68250_PI430048170 mRNA
TACACTTGTGAGGAGCCATATTACTACATGGAAAATGGAGGAGGTGGGGAGTATCACTGT NM_201442

RefSeq chr12 + 7060675 7071031 C1S 716 "complement component 1, s subcomponent, transcript variant 1" GO:0005515|GO:0006956|GO:0004252|GO:0045087|GO:0006958|GO:0005509|GO:0006508|GO:0072562|GO:0005576|GO:0070062|GO:0042802 . NA - . NA NA NA NA NA
NA NA NA NA

LNCV6_141055_PI430048170 0.02948863283430 2.43500803 4.93134220 5.07217685
4.80977276 P P P 3.73738554 3.99262056 3.10590398 P P P

LNCV6_141055_PI430048170 mRNA
TGTTGGCCTGCTGTGTTTATTGTAGAGACACTGTTTTAGTAAACATGCTGAGCATTCAAA NM_001127582

RefSeq chr12 - 6650537 6663142 ING4 51147 "inhibitor of growth family, member 4, transcript variant 9" GO:0005515|GO:0043065|GO:0008285|GO:0003713|GO:0006325|GO:0006915|GO:0005634|GO:0035064|GO:0043981|GO:0006260|GO:0043983|GO:0043982|GO:0043966|GO:0043984|GO:0000123|GO:0005654|GO:0007050|GO:0008270|GO:0006978|GO:0045892|GO:0045926|GO:0006473 . NA - .
NA NA NA NA NA NA NA NA NA NA

LNCV6_139734_PI430048170 0.02965718017563 2.38244135 6.74659355 6.55012828
 6.59055182 P P P 4.90737991 5.77211061 5.32904572 P P P
 LNCV6_139734_PI430048170 mRNA
 CTGGGTGACGCATGCCTCTGGTCTAATAAACTGGGTTTCAACCATCTCCTCTTCAAAAAA NM_020039
 RefSeq chr12 + 50057636 50083622 ASIC1 41 "acid sensing (proton gated) ion
 channel 1, transcript variant 1"
 GO:0005515|GO:0005886|GO:0050915|GO:0055085|GO:0071467|GO:0070207|GO:0007165|GO:001528
 0|GO:0034220|GO:0005887|GO:0006810|GO:0006816|GO:0035725|GO:0006814|GO:0009268 .
 NA - NA NA NA NA NA NA NA NA NA
 LNCV6_128911_PI430048170 0.03095857005535 2.44867655 3.63004805 3.95600382
 3.88316102 P P P 1.93831158 2.88529611 2.63197507 A P P
 LNCV6_128911_PI430048170 mRNA
 GATCTCCTGCTGCCTTTTCTGGAGTTTGTAAAATTGTTCTGAATACAAGCCTATGCGTG NM_003881
 RefSeq chr20 + 44715243 44727811 WISP2 8839 WNT1 inducible signaling pathway
 protein 2
 GO:0007165|GO:0005178|GO:0005886|GO:0060548|GO:0007267|GO:0005578|GO:0007155|GO:000820
 1|GO:0005615|GO:0001558|GO:0070062|GO:0005520 . NA - NA NA NA
 NA NA NA NA NA NA
 LNCV6_133314_PI430048170 0.03098469034715 2.03376984 6.85189247 6.92766128
 6.94926176 P P P 6.15414017 5.93914330 5.48688928 P P P
 LNCV6_133314_PI430048170 mRNA
 ATGTTATTGGAGCTATTTTGTAAAGGTCCCACATTTGACCAAGGAGTGCCTGGTAGCGTTG NM_183239
 RefSeq chr10 + 104268872 104299418 GSTO2 119391 "glutathione S-transferase
 omega 2, transcript variant 1"
 GO:0006805|GO:0006767|GO:0044281|GO:0004364|GO:0045174|GO:0005829|GO:0019852|GO:005061
 0|GO:0006766|GO:0016491|GO:0071243|GO:0055114|GO:0070062 . NA - NA NA
 NA NA NA NA NA NA NA
 LNCV6_128223_PI430048170 0.03135867048108 4.10536663 4.69266041 4.50276276
 4.32505775 P P P 1.80714001 2.01870716 3.19407392 A A P
 LNCV6_128223_PI430048170 mRNA
 CTTCCAAGCTGCCTAAAGCGCTGTTTATAGGTTCAATTTATTTTATTATGTTTCAGAAGCATC NM_019043
 RefSeq chr10 + 26438336 26567803 APBB1IP 54518 "amyloid beta (A4) precursor
 protein-binding, family B, member 1 interacting protein"
 GO:0005515|GO:0007165|GO:0005886|GO:0007596|GO:0030168|GO:0005856|GO:0005925|GO:003002
 7|GO:0005829 . NA - NA NA NA NA NA NA NA NA
 LNCV6_63310_PI430048170 0.03176499904577 4.62121372 3.64199503 3.94078356
 3.82899522 P P P 0.58128600 2.03671273 1.80756211 A A A
 LNCV6_63310_PI430048170 mRNA
 TTTAAGAGCAAAGGCAACTACGACGAGGGGTTTGGCCGCAAGCAGCACAAGGAGCTCTGG NM_030576
 RefSeq chr17 - 63695888 63700159 LIMD2 80774 LIM domain containing 2
 GO:0008270 . NA - NA NA NA NA NA NA NA NA
 LNCV6_137995_PI430048170 0.03187126708057 2.39334544 6.46434883 6.60335244
 6.62478074 P P P 5.70196456 5.26271972 4.82308814 P P P
 LNCV6_137995_PI430048170 mRNA
 ACACAGTCATGCTTCCTGGATTTTGGAGTCGAGGCTTTCTACAGAAAAGAAAGTTCTGAT NM_001193532
 RefSeq chr1 + 28592494 28594576 RAB42 115273 "RAB42, member RAS oncogene
 family, transcript variant 1"
 GO:0006184|GO:0005794|GO:0016020|GO:0003924|GO:0032482|GO:0019003|GO:0005525|GO:000688
 6 . NA - NA NA NA NA NA NA NA NA
 LNCV6_111113_PI430048170 0.03223929158851 2.94651545 3.87864590 4.28063642
 4.19582382 P P P 3.14291331 1.94087611 2.36046055 P A A
 LNCV6_111113_PI430048170 mRNA
 CTTGCTGGAGAATGACCCAGATGTCCCAGGTGCAGGAGCTCTTCCATGAGGCAGCCCAGC NM_024628
 RefSeq chr3 - 125082635125212765SLC12A8 84561 "solute carrier family 12, member 8,
 transcript variant 1" GO:0016021|GO:0055085|GO:0006813|GO:0015293 . NA - NA
 NA NA NA NA NA NA NA NA
 LNCV6_128690_PI430048170 0.03231879642097 4.91115968 3.89407076 3.98593147
 3.50866050 P P P 0.44182340 2.20279205 1.38352422 A A A
 LNCV6_128690_PI430048170 mRNA
 ACCCCCAAATTTGACTCTGGGAGACTCAGCCAAATCCTATCTGGTAATAAAATTTCTTTT NM_001166215
 RefSeq chr19- 10512741 10517992 S1PR5 53637 "sphingosine-1-phosphate receptor 5,

transcript variant 2" GO:0005886|GO:0045664|GO:0003376|GO:0016021|GO:0038036 . NA -
NA NA NA NA NA NA NA NA NA NA
LNCV6_133138_PI430048170 0.03244441226119 3.62574424 3.46429245 4.86698560
3.75351861 P P P 1.75526376 2.69526007 2.31027952 A P P
LNCV6_133138_PI430048170 mRNA
CAGCCTTACTGGTACTTTTTCTCATGTATCACAGGTTACTTCTTATGTATATTAAAGTGG NM_001105576
RefSeq chrX + 119758612119760202SOWAHD 347454 sosondowah ankyrin repeat domain
family member D NA . NA - . NA NA NA NA NA NA NA NA
LNCV6_23518_PI430048170 0.03255330624480 3.46534730 3.81937440 3.64735041
3.68632945 P P P 2.45215642 1.85843144 1.20547791 A A A
LNCV6_23518_PI430048170 mRNA
ATGCTTGGGTTTTGTCTTTAACCTTGTAACGCTTGCAATCCCAATAAAGCATTAAAAGTC NM_000612
RefSeq chr11- 2129111 2138974 IGF2 3481 "insulin-like growth factor 2, transcript variant 1"
GO:0005515|GO:0005159|GO:0005158|GO:0050731|GO:0005615|GO:0009887|GO:0031667|GO:000761
3|GO:0032355|GO:0070062|GO:2000467|GO:0007565|GO:0030168|GO:0007275|GO:0045840|GO:0038
028|GO:0043085|GO:0001649|GO:0001501|GO:0005179|GO:0030546|GO:0043539|GO:0008083|GO.
NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_101405_PI430048170 0.03255386230485 2.12166432 4.35272181 4.38742217
4.77998710 P P P 2.87620482 3.74623178 3.54622541 P P P
LNCV6_101405_PI430048170 mRNA
TGAAAAAGTCTGTCTGATTCCAGGGTGTTCCTGGGTTTCATCATCAGGTACCTCCTC NM_001440
RefSeq chr8 + 28701472 28753690 EXTL3 2137 "exostosin-like glycosyltransferase 3,
transcript variant 1"
GO:0001888|GO:0030307|GO:0005783|GO:0005789|GO:0016021|GO:0015012|GO:0006987|GO:004426
7|GO:0046872|GO:0006024|GO:0030968 . NA - . NA NA NA NA NA NA NA NA
NA NA
LNCV6_129838_PI430048170 0.03269021918608 3.54690955 3.69887151 3.83235722
4.25757868 P P P 2.84837977 1.56616326 1.53950022 P A A
LNCV6_129838_PI430048170 mRNA
CCTGTCCATTATGAATGGCCTACTGTTCTATTATTTGTTTTGACTTGAATTTATCCACCA NM_177949
RefSeq chrX - 101655280101659891ARMCX2 9823 "armadillo repeat containing, X-linked 2,
transcript variant 1" GO:0016021 . NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_61137_PI430048170 0.03295662192801 3.85321351 3.37049987 3.27107016
3.07217330 P P P 0.46572081 1.88879993 1.19399867 A A A
LNCV6_61137_PI430048170 mRNA
TCTGCACTGTGTGCCGGTGGAGACGGCCAATGTCACCATGCACTCCTAAAGATCCGTTCT NM_002632
RefSeq chr14- 74941829 74955764 PGF 5228 "placental growth factor, transcript variant 1"
GO:0005515|GO:0048010|GO:0001666|GO:0001658|GO:0007565|GO:0008284|GO:0046982|GO:004249
3|GO:0031100|GO:0007267|GO:0002040|GO:0005576|GO:0060688|GO:0005615|GO:0045766|GO:0042
803|GO:0032870|GO:0030154|GO:0007165|GO:0016020|GO:0001938|GO:0051781|GO:0008083|GO.
NA - . NA NA NA NA NA NA NA NA NA NA
LNCV6_135553_PI430048170 0.03383461062141 3.37256173 5.25763594 5.67896805
5.23170677 P P P 4.22971865 3.57018339 2.81481204 P P P
LNCV6_135553_PI430048170 mRNA
GCACGCAGTGATGGGCAAACCAATTGCTGCCCATCTGGCCTGTGTGCCCATCTTTTTCTG NM_152891
RefSeq chr16- 2783952 2786707 PRSS33 260429 "protease, serine, 33"
GO:0004252|GO:0006508|GO:0005615. NA - . NA NA NA NA NA NA NA NA
NA
LNCV6_93231_PI430048170 0.03399922124336 6.67387548 4.49940201 4.75963869
5.04689946 P P P 2.83664114 0.69776404 1.86224143 P A A
LNCV6_93231_PI430048170 mRNA
AATGATGCTAGCTGCCCTTAAATTCCTTCAGATTTGGAAGTGTATCTGTATGGAAACAA NM_001139488
RefSeq chr2 + 33476253 33564731 RASGRP3 25780 "RAS guanyl releasing protein 3
(calcium and DAG-regulated), transcript variant 1"
GO:0048471|GO:0005886|GO:0007264|GO:0005509|GO:0007265|GO:0032854|GO:0019992|GO:004354
7|GO:0005085|GO:0046582|GO:0000165|GO:0005887|GO:0004871|GO:0019900|GO:0017016|GO:0005
088|GO:0032045 . NA - . NA NA NA NA NA NA NA NA
LNCV6_145574_PI430048170 0.03401684650769 2.12213638 3.13709238 3.86340659
3.35002231 P P P 2.87246474 2.02037567 2.14695282 P A A
LNCV6_145574_PI430048170 mRNA

AGAACATCTTCTTCATGAGCAAAGTCACCAATCCCAAGCAAGCCTAGAGCTTGCCATCAA NM_001085
RefSeq chr14+ 94612376 94624053 SERPINA3 12 "serpin peptidase inhibitor, clade A (alpha-1
antiproteinase, antitrypsin), member 3"
GO:0005515|GO:0004867|GO:0072562|GO:0005576|GO:0005634|GO:0006953|GO:0003677|GO:000561
5|GO:0019216|GO:0005622|GO:0010951|GO:0006954|GO:0030277|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_136134_PI430048170 0.03402332780636 2.00711156 5.79578331 5.92543156
5.55427275 P P P 4.87680988 5.04257474 4.25024118 P P P
LNCV6_136134_PI430048170 mRNA
TGGGTCTTGCAGTTTTTCAGGAGGCCTTGATTAAAATGCAAATACTTGTCTGAGAAAAAA NM_153006
RefSeq chr17+ 44004663 44009068 NAGS162417 N-acetylglutamate synthase
GO:0034641|GO:0006536|GO:0005759|GO:0006526|GO:0000050|GO:0044281|GO:0004042 . NA
- . NA NA NA NA NA NA NA NA NA
LNCV6_133998_PI430048170 0.03568071733201 2.65977268 6.14209535 6.12448434
6.21043670 P P P 5.24900730 4.28359920 4.53108509 P P P
LNCV6_133998_PI430048170 mRNA
GGAGTGGGGAAGTGTGTCAAATCAATAAATGAATAAATTCAATAAATGCCTATAACCAGC NM_005938
RefSeq chrX + 71096148 71103534 FOXO4 4303 "forkhead box O4, transcript variant 1"
GO:0007095|GO:0005515|GO:0008286|GO:0003700|GO:0008285|GO:0006366|GO:0000981|GO:000563
4|GO:0005829|GO:0005737|GO:0007173|GO:0007050|GO:0048011|GO:0006355|GO:0006357|GO:0051
151|GO:0048015|GO:0070317|GO:0003677|GO:0048863|GO:0043565|GO:0007517|GO:0008543|GO.
NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139268_PI430048170 0.03600869187723 2.08586011 8.12304225 8.02368108
8.11847420 P P P 6.62122986 7.38552537 6.97728567 P P P
LNCV6_139268_PI430048170 mRNA
AAATATTAGTAAGTATGACTGACGTCCCCAGAAGTTTCTGGGTCTACCACACTCCCCAAC NM_002084
RefSeq chr5 + 151020437151028993GPX3 2878 glutathione peroxidase 3
GO:0004602|GO:0008430|GO:0006982|GO:0051289|GO:0005576|GO:0042744|GO:0005615|GO:000030
2|GO:0070062|GO:0055114|GO:0008134 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_130346_PI430048170 0.03622498962441 2.08338164 8.05038941 8.15491083
8.02932091 P P P 6.56515876 7.32785081 7.06717583 P P P
LNCV6_130346_PI430048170 mRNA
TTTTCTTTTTTGGGGTGGGGGGATTGGTTTGTA AAAATTCTCTACTCTTTTGGAATGTGA NM_080627
RefSeq chr20- 36783774 36863684 SOGA1 140710 "suppressor of glucose, autophagy
associated 1, transcript variant 1"
GO:0045721|GO:0008286|GO:0003674|GO:0010506|GO:0005615|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_135244_PI430048170 0.03640191396934 2.20155786 5.16726238 5.88478744
5.79947073 P P P 4.58167010 4.49640461 4.45565534 P P P
LNCV6_135244_PI430048170 mRNA
CTCCAGTCAAGAATGTCACTGGTTGGCATGATATTCTTAGTTCTATTTTTCCTTCTTTAA NM_024074
RefSeq chr19+ 16661126 16689005 TMEM38A 79041 transmembrane protein 38A
GO:0031965|GO:0033017|GO:0005267|GO:0016021|GO:0071805|GO:0070062 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_134137_PI430048170 0.03666944031705 2.53775467 3.47766153 3.76961784
3.13313964 P P P 1.44565326 2.64614518 2.08314170 A P A
LNCV6_134137_PI430048170 mRNA
GCTGGCCCCGCTGGGCCCCGTGGCCACGGGGCGCGAGGAGGCTGTGGGGCTCACAATAA
NM_001195135 RefSeq chr19+ 58396089 58397079 RNF225 NA ring finger protein 225NA
. NA - . NA NA NA NA NA NA NA NA NA
LNCV6_127630_PI430048170 0.03672691445389 3.07174291 3.17997170 4.21889235
4.09200258 P P P 2.61035958 2.56020776 1.35606190 A A A
LNCV6_127630_PI430048170 mRNA
GAGTCTGTTTGACTAGTGCTAAAGGAAACAATTCATGCGGATGTATAAACTCGCTCTTT NM_012263
RefSeq chr22- 43039515 43089428 TTLL1 25809 "tubulin tyrosine ligase-like family
member 1, transcript variant 1"
GO:0018095|GO:0005737|GO:0035082|GO:0003351|GO:0005874|GO:0070740 . NA - .
NA NA NA NA NA NA NA NA NA
LNCV6_145583_PI430048170 0.03749393860005 9.12458162 4.46739427 4.85965231
4.82160750 P P P 0.33873027 2.61397477 0.39933737 A P A

LNCV6_145583_PI430048170 mRNA
TGACATGTAAATGCACCTGCACCGTTTCTGAGCCGGGAGAGTGTTTACTTAAAATCATGC NM_144727
RefSeq chr7 - 151428831151440170CRYGN 155051 "crystallin, gamma N" NA NA
- NA NA NA NA NA NA NA NA
LNCV6_93252_PI430048170 0.03765207208865 2.07894258 4.15802862 4.07656508
3.97775845 P P P 3.44610053 2.74041118 2.74413798 P P P
LNCV6_93252_PI430048170 mRNA
TGTTAAGATTCCAGTGAGAAACCATGGGATCCTGATGGAGACCCACAAAGAACTGAAACC NM_152449
RefSeq chr15- 99727400 99733444 LYSMD4 145748 "LysM, putative peptidoglycan-
binding, domain containing 4, transcript variant 1" GO:0016021 NA NA NA NA
NA NA NA NA NA NA
LNCV6_140322_PI430048170 0.03806742239410 3.83411971 3.63498291 4.18299389
3.67271065 P P P 2.54447055 1.86175578 0.87597320 P A A
LNCV6_140322_PI430048170 mRNA
TCGGGGGACCTGAAGAATCAATCTGTGTGAGTCTGTTTTTCAAATGAAATAAACACAC NM_012261
RefSeq chr20+ 9514357 9530524 LAMP5 24141 "lysosomal-associated membrane
protein family, member 5, transcript variant 1"
GO:0032590|GO:0005886|GO:0033116|GO:0031901|GO:0032584|GO:0016021|GO:0055038|GO:003065
9|GO:0030425|GO:0010008. NA - NA NA NA NA NA NA NA NA
LNCV6_140078_PI430048170 0.03971839916033 2.12027041 5.66317129 5.93287563
6.47095594 P P P 4.96169455 4.86941025 5.09411528 P P P
LNCV6_140078_PI430048170 mRNA
GCAGGGCACTTACTAGCATAAGAATTGGTTTGGGATTTAAGTGTATGAAGCTAACTTG NM_004374
RefSeq chr8 - 99877994 99894014 COX6C 1345 cytochrome c oxidase subunit VIc
GO:0022904|GO:0005739|GO:0004129|GO:0005743|GO:0044281|GO:0016021|GO:0006091|GO:005508
5|GO:0044237 NA - NA NA NA NA NA NA NA NA
LNCV6_88836_PI430048170 0.04022839155723 2.20607417 10.63503938 11.48271193
10.91702230 P P P 10.03132468 9.80674532 9.89550230 P P P
LNCV6_88836_PI430048170 mRNA
GGACGGGGATGTCAGGGAGGCAAGTGTGTTGTGTTACTGTGTCAATAAACTGATTTAAAG NM_002537
RefSeq chr15- 64687573 64703281 OAZ24947 "ornithine decarboxylase antizyme 2, transcript
variant 1"
GO:0005515|GO:0034641|GO:0008073|GO:0045732|GO:0006596|GO:0006521|GO:0006595|GO:000563
4|GO:0090316|GO:0044281|GO:0043086|GO:0005829 NA - NA NA NA NA NA
NA NA NA NA
LNCV6_142643_PI430048170 0.04063220293739 2.56026812 3.82098596 3.92062805
3.32012942 P P P 1.57149868 2.43832732 2.79568685 A P P
LNCV6_142643_PI430048170 mRNA
GAGGGGGAAATTTGTATATTAGAACTTATTCATCCCACTCAGGACAATAAAAACGAATG NM_022468
RefSeq chr16+ 3046680 3060723 MMP25 64386 matrix metalloproteinase 25
GO:0006954|GO:0016020|GO:0005886|GO:0005509|GO:0006508|GO:0005578|GO:0008270|GO:003122
5|GO:0016021|GO:0004222|GO:0060022 NA - NA NA NA NA NA NA
NA NA
LNCV6_135173_PI430048170 0.04123931705514 2.04226761 3.49713925 4.16076062
3.43729504 P P P 2.79797207 2.74167587 2.57235411 A P P
LNCV6_135173_PI430048170 mRNA
TGAATTGTCTTTATTAACAAACAGGATATCCAAGGCCACTACATTGAGGAGGGGTGGGGG NM_000080
RefSeq chr17- 4897768 4903074 CHRNE 1145 "cholinergic receptor, nicotinic, epsilon
(muscle)"
GO:0030054|GO:0005886|GO:0008324|GO:0007268|GO:0005892|GO:0007271|GO:0007165|GO:000693
6|GO:0005887|GO:0045211|GO:0015464|GO:0042391|GO:0006810|GO:0004889 NA -
NA NA NA NA NA NA NA NA
LNCV6_125571_PI430048170 0.04146649575134 2.09092229 6.63952717 7.48679213
6.98358021 P P P 6.16859206 5.97405220 5.88749968 P P P
LNCV6_125571_PI430048170 mRNA
ATGTCTCGGGAGATGCAGGATGTAGACCTCGCTGAGGTGAAGCCTTTGGTGGAGAAAGGGNM_001135242
RefSeq chr8 - 133237170133297304NDRG1 10397 "N-myc downstream regulated 1,
transcript variant 1"
GO:0005515|GO:0008017|GO:0048471|GO:0045576|GO:0005813|GO:0017137|GO:0045296|GO:004301
5|GO:0005886|GO:0030330|GO:0005874|GO:0071456|GO:0005634|GO:0032287|GO:0090232|GO:0005
829|GO:0005737|GO:0005913|GO:0010038|GO:0015630|GO:0055038|GO:0070062 NA -

NA NA NA NA NA NA NA NA NA
LNCV6_57149_PI430048170 0.04253495313959 2.50169449 4.01497176 3.65298201
3.73573950 P P P 1.79154801 2.50604865 2.93986841 A P P
LNCV6_57149_PI430048170 mRNA
TGACTTATCTCCTGCAACTGACTCATCTGCAACATTCACACCATTGCTTCCTTGTGGTTT NM_021616
RefSeq chr11+ 5624976 5644395 TRIM34 53840 "tripartite motif containing 34,
transcript variant 1"
GO:0003674|GO:0070206|GO:0051091|GO:0005737|GO:0019221|GO:0008270|GO:0060333|GO:000582
9 NA - NA NA NA NA NA NA NA NA
LNCV6_140996_PI430048170 0.04481703483854 2.71494936 3.60609581 4.02925601
3.85286995 P P P 2.25416558 2.97560598 1.67114834 A P A
LNCV6_140996_PI430048170 mRNA
TTGCTTGGGGAATGTTGTTTTCTGACTAGGCTGATCATTATCTAAAGAATCTAATTCTGT NM_000053
RefSeq chr13- 51932670 52011494 ATP7B 540 "ATPase, Cu++ transporting, beta
polypeptide, transcript variant 1"
GO:0005802|GO:0005515|GO:0048471|GO:0006882|GO:0015680|GO:0005739|GO:0016323|GO:000687
8|GO:0034220|GO:0015677|GO:0060003|GO:0051208|GO:0005770|GO:0005507|GO:0005524|GO:0055
085|GO:0004008|GO:0007595|GO:0000139|GO:0016020|GO:0005887|GO:0008152|GO:0016023|GO.
NA - NA NA NA NA NA NA NA NA NA
LNCV6_127035_PI430048170 0.04497262926766 2.01286032 7.41881455 7.55822911
7.50795555 P P P 6.92339357 6.17256719 6.23958768 P P P
LNCV6_127035_PI430048170 mRNA
GTTGAAGGCAAAATTGTTGTAACACTACAGCTGAGCAGATGTAATAGAAATAAACCTATG NM_000716
RefSeq chr1 + 207089238 207099992 C4BPB 725 "complement component 4 binding protein,
beta, transcript variant 1"
GO:0044216|GO:0005515|GO:0030449|GO:0045732|GO:0005886|GO:0007596|GO:0045087|GO:000695
8|GO:0045959|GO:0005576|GO:0005615 NA - NA NA NA NA NA NA NA
NA NA
LNCV6_135871_PI430048170 0.04570906194186 2.97521010 5.77126861 5.56547588
5.33903884 P P P 4.65401252 3.24205599 3.72692965 P P P
LNCV6_135871_PI430048170 mRNA
TACCCAGAGACAGACTCTTTTGTAAAGATTTTGTAAATAAAACACTGAACTTCCTGGA NM_015193
RefSeq chr8 - 142611043 142614472 ARC 23237 activity-regulated cytoskeleton-associated
protein
GO:0030054|GO:0001669|GO:0005886|GO:0014069|GO:0009952|GO:0015629|GO:0006897|GO:000573
7|GO:0048168|GO:0043197|GO:0007492|GO:0016477|GO:0045211|GO:0007010|GO:0022604|GO:0007
612|GO:0005768 NA - NA NA NA NA NA NA NA NA
LNCV6_131814_PI430048170 0.04705259766384 2.31961944 9.49838764 9.56645440
9.41946940 P P P 8.80666062 7.97209955 7.87650897 P P P
LNCV6_131814_PI430048170 mRNA
TTTTCTAAGAGTCTGTGAACCCAGGAGCCTCTCGCTCTGGCTTTAAGATGCTATGACTAA NM_001242348
RefSeq - - 0 0 --- NA - NA . NA - . NA NA NA NA NA
NA NA NA NA
LNCV6_108891_PI430048170 0.04748759962781 2.27924044 3.70469254 3.48261582
3.60200835 P P P 2.59878688 2.70179222 1.76063215 A P A
LNCV6_108891_PI430048170 mRNA
AAGCGACACTGGGTTGGAAACACTTGGCTCTCTCATGAGTATTAATAAATTCTATTTCAATC NM_130897
RefSeq chr16+ 80540951 80550809 DYNLRB2 83657 "dynein, light chain, roadblock-type 2,
transcript variant 1"
GO:0006996|GO:0008152|GO:0005874|GO:0006810|GO:0072372|GO:0005868|GO:0003777|GO:007006
2|GO:0007018 NA - NA NA NA NA NA NA NA NA
LNCV6_109977_PI430048170 0.04751819773942 2.98428379 4.80872097 4.82522806
4.61407993 P P P 3.74484550 2.37636091 3.08717405 P A P
LNCV6_109977_PI430048170 mRNA
TTTCTCTATAAAGCCTCAGCGTATAGAACAGATTTACATGCCAGAGGCTGTTGAGCAG NM_172095
RefSeq chr15- 43630561 43648841 CATSPER2 117155 "cation channel, sperm associated 2,
transcript variant 2"
GO:0005515|GO:0035036|GO:0086010|GO:0005245|GO:0005886|GO:0031514|GO:0036128|GO:000727
5|GO:0007283|GO:0030317|GO:0030154|GO:0007338|GO:0070509|GO:0070588|GO:0034765|GO:0005
227|GO:0032504 NA - NA NA NA NA NA NA NA NA
LNCV6_140816_PI430048170 0.04769799266802 2.11004181 3.98326909 3.56427938

3.15495223 P P P 2.49595281 2.57969785 2.51187959 A P P
LNCV6_140816_PI430048170 mRNA
ACAGCAGCAGATGGCTCCGAAGAAGTGGAGCGTTTTTCATCAGGTTCAACTTTGAAACCTC NM_001282670
RefSeq chr1 - 2189548 2212720 C1orf86 199990 "chromosome 1 open reading frame
86, transcript variant 6"
GO:0005515|GO:0043130|GO:0030054|GO:0005694|GO:0005654|GO:0019985|GO:0070530|GO:004687
2|GO:0006974|GO:0043240|GO:0031593 . NA - . NA NA NA NA NA NA NA
NA NA
LNCV6_93747_PI430048170 0.04824337458988 2.73486478 4.81285458 4.52737472
4.78083133 P P P 2.42979666 3.64246447 3.44426738 A P P
LNCV6_93747_PI430048170 mRNA
TTTGTCTCAGTGTACAAGATCAACAAAATGGCCTTCTGGGTCGGAGAGACAGTGTTTCTC NM_024789
RefSeq chr10+ 102461412102477045TMEM180 79847 transmembrane protein 180
GO:0016021 . NA - . NA NA NA NA NA NA NA NA NA
LNCV6_139499_PI430048170 0.04830426212934 11.91618879 8.82652863 8.42472331
8.18598693 P P P 6.19791171 3.40032545 2.88887950 P P P
LNCV6_139499_PI430048170 mRNA
GACAGCAACCTCCTGGGTAAATCTGAATGAAAAACGTGCTAGTCTCTTTCATGCAAAAAA NM_004933
RefSeq chr16+ 89171754 89195492 CDH15 1013 "cadherin 15, type 1, M-cadherin
(myotubule)"
GO:0031594|GO:0005886|GO:0034329|GO:0005509|GO:0045216|GO:0042692|GO:0051149|GO:000590
1|GO:0016021|GO:0007155|GO:0007156|GO:0034332|GO:0070062 . NA - . NA NA
NA NA NA NA NA NA NA NA
LNCV6_133711_PI430048170 0.04986657312849 2.37962175 3.90805790 5.05601799
4.57547793 P P P 3.53521857 2.71696855 3.60168667 P P P
LNCV6_133711_PI430048170 mRNA
AGGATAGAAAGCTGTTTCCACCTGTTTGCTTTTACCATTAAAAGGGAAACGTGCCTCTG NM_006018
RefSeq chr12- 122714755122716892HCAR3 8843 hydroxycarboxylic acid receptor 3
GO:0007186|GO:0005886|GO:0005887|GO:0004930 . NA - . NA NA NA NA NA
NA NA NA NA