Supplementary Table 1: Forward (F) and reverse (R) sequences, melting temperature (MT) and amplicon size.

Region	Primers	MT (℃)	Amplicon
Exon 15	F- TGATTAGCTGTGTGGCTGAAA	59 ℃	571 bp
	R- CAATGAAGGGATGACCCG		

Table 2: Differentially Expressed (DE) genes when compared cell lines before and after *PIWIL1* knockout.

Probe Name	Gene Symbol	Fold-Change	P Value	P Adjusted
A_24_P215804	CKLF	0.2315	7.32E+09	0.0053
A_21_P0013109	XLOC_l2_013153	0.3181	0.0029	0.0324
A_21_P0010885	TMEM14B	228.738.161.870.967	0.0030	0.0328
A_33_P3228014	SCGB1D4	0.3190	0.0079	0.0395
A_24_P54390	RASGRP3	0.3250	0.0160	0.0488
A_24_P187056	ANKRD20A12P	0.3966	0.0013	0.0235
A_19_P00318261	SNORA26	0.4725	0.0052	0.0379
A_23_P146146	ATP6V0D2	0.3876	0.0007	0.0185
A_32_P57810	RNF157	0.3329	0.0020	0.0261
A_24_P11575	CRIM1	0.3190	0.0032	0.0334
A_32_P231086	GOLGA6L9	0.2961	0.0007	0.0185
A_33_P3337569	PRR27	0.4121	0.0162	0.0489
A_23_P22761	SHOX	0.4656	0.0136	0.0466
A_33_P3212188	LRP3	0.3826	0.0106	0.0431
A_23_P360990	DYDC1	0.2755	0.0008	0.0188
A_33_P3344690	PTGER4P2-CDK2AP2P2	0.3146	0.0052	0.0379
A_33_P3548190	LINC00347	0.4185	0.0166	0.0496
A_33_P3227842	EPB41	0.4498	0.0074	0.0391
A_23_P388124	ABCD2	0.4283	0.0121	0.0455
A_23_P42588	GIMAP5	0.4073	6.86E+09	0.0052
A_33_P3839897	RNU4ATAC	0.4883	0.0105	0.0431
A_33_P3383044	B9D1	0.4268	0.0144	0.0470
A_24_P358054	CTAGE10P	0.3231	0.0006	0.0167
A_33_P3259373	PWAR1	0.4143	0.0142	0.0468
A_33_P3413671	ABL2	0.2834	0.0008	0.0185
A_33_P3311493	TRHDE-AS1	0.3932	0.0018	0.0259
A_23_P2322	TSPAN19	0.3159	0.0021	0.0266
A_21_P0013552	XLOC_l2_014697	0.2845	7.97E+09	0.0054
A_21_P0000117	MID1	0.4333	0.0150	0.0478
A_33_P3285132	ZNF599	0.3649	0.0079	0.0395
A_21_P0000558	BRE-AS1	0.3975	0.0051	0.0379
A_33_P3260146	C9orf3	0.3746	0.0038	0.0344
A_24_P43144	PDE11A	0.4737	0.0082	0.0398
A_33_P3215676	MANSC4	0.4960	0.0127	0.0457
A_33_P3467872	LINC00343	0.4363	0.0077	0.0393
A_19_P00321316	LINC00882	0.4631	0.0044	0.0361
A_33_P3336484	NPIPA5	0.3706	0.0080	0.0395
A_33_P3405168	MMAA	0.4296	0.0051	0.0379

A_23_P154784	BPIFB1	0.3620	0.0002	0.0094
A_33_P3393200	SRRM4	0.4686	0.0117	0.0455
A_33_P3387493	FTH1P18	0.3136	0.0002	0.0092
A_33_P3861634	LINC01305	0.4990	0.0101	0.0427
A_21_P0010488	ZNF605	0.4103	0.0051	0.0379
A_33_P3225535	OR10K2	0.4387	0.0115	0.0449
A_23_P31064	MOXD1	0.3839	0.0070	0.0389
A_33_P3375506	LINC01203	0.4358	3.48E+08	0.0016
A_33_P3246268	HOXD13	0.2687	0.0056	0.0379
A_33_P3255384	BPIFC	0.4614	0.0080	0.0395
A_33_P3383601	QRFP	0.4463	0.0038	0.0344
A_33_P3267989	CLNK	0.4025	0.0070	0.0389
A_32_P95960	CLEC2D	0.4298	0.0106	0.0431
A_23_P390148	RALGPS1	227.472.113.221.315	0.0059	0.0381
A_21_P0004143	LINC01335	0.4390	0.0090	0.0406
A_33_P3299066	NR4A2	0.4775	0.0137	0.0466
A_33_P3309911	PRAMEF5	0.4454	0.0103	0.0429
A_23_P218675	WFDC2	0.4787	0.0130	0.0464
A_33_P3347528	CHIAP2	0.4209	0.0001	0.0065
A_23_P212042	MFI2	0.3179	0.0029	0.0324
A_33_P3401556	CTLA4	0.4276	4.86E+08	0.0016
A_23_P217507	ZBED1	257.948.904.602.257	0.0096	0.0415
A_33_P3286536	FUT4	0.4820	0.0161	0.0489
A_33_P3408420	MDGA2	0.3470	0.0072	0.0389
A_23_P94762	ZNF354B	0.4901	0.0031	0.0331
A_23_P156824	HTR1B	239.937.085.039.903	0.0057	0.0379
A_23_P32577	DACH1	233.736.545.984.496	0.0061	0.0381
A_23_P419107	TCP11L2	232.350.395.892.368	0.0162	0.0489
A_24_P8075	KLHDC4	227.531.196.835.458	0.0089	0.0406
A_21_P0011389	XLOC_l2_005076	241.849.854.526.815	0.0060	0.0381
A_24_P89971	SURF4	209.000.357.924.191	0.0037	0.0344
A_33_P3327300	NUMBL	0.4328	9.75E+09	0.0063
A_33_P3263906	TUBE1	0.4903	0.0021	0.0266
A_24_P182892	SLC19A3	0.4390	0.0070	0.0389
A_24_P353905	MXRA8	0.3213	0.0144	0.0470
A_33_P3305243	PSMD5	0.4218	570019345.0720	0.0016
A_23_P84047	PABPC5	0.2679	0.0135	0.0466
A_21_P0007062	LINC00844	0.3525	0.0151	0.0478
A_33_P3793707	LINC00964	0.3792	0.0157	0.0488
A_32_P78681	GLP2R	0.4668	0.0084	0.0398
A_21_P0013210	XLOC_l2_013436	0.4251	0.0023	0.0273
A_23_P373724	PPFIBP1	0.3587	0.0042	0.0361
A_19_P00808461	ZNF37A	0.4825	0.0113	0.0444
A_21_P0010870	FAM21C	0.4970	0.0132	0.0465
A_23_P329261	KCNJ2	0.4844	6.58E+07	0.0016
A_24_P165205	MORN1	0.4445	0.0005	0.0162
A_33_P3299435	SART1	0.4873	0.0100	0.0423
A_23_P132826	SERPINI2	0.4693	0.0002	0.0079
A_33_P3374478	CASC4	0.4620	0.0002	0.0079
A_32_P485915	SLC9C2	0.4565	3.38E+09	0.0032
A_33_P3396886	C11orf52	0.4715	0.0119	0.0455
A_33_P3376379	CNST	0.4698	0.0033	0.0339
A_24_P378987	DHRSX	242.898.673.793.384	0.0069	0.0389
A_23_P148629	EIF1AY	200.273.907.748.429	0.0008	0.0185
A_24_P287189	TOLLIP	0.4632	0.0094	0.0411
A_33_P3422777	PRH2	0.4075	0.0023	0.0273
A_23_P904	BEND5	0.3056	1.49E+09	0.0027

A_32_P100258	FLJ37453	261.439.515.682.183	0.0149	0.0478
A_24_P408704	DOCK2	0.3989	0.0037	0.0344
A_33_P3263867	P2RX7	0.4894	0.0075	0.0391
A_33_P3556532	DNAH17	0.4725	0.0148	0.0477
A_32_P96000	ETV3L	0.4919	0.0076	0.0391
A_24_P940135	CTBS	0.4883	0.0083	0.0398
A_23_P329353	CNRIP1	562.111.664.539.578	0.0141	0.0466
A_23_P4714	MIA	25.557.836.842.375	0.0072	0.0389
A_23_P363778	FRZB	0.3747	0.0059	0.0381
A_33_P3336622	ALDH3A2	0.4271	0.0043	0.0361
A_32_P183218	ZNF367	0.4598	0.0100	0.0423
A_21_P0010980	MALAT1	0.4995	0.0159	0.0488
A_21_P0011744	LINC00665	0.4015	0.0062	0.0382
A_21_P0004602	OSTM1-AS1	0.4881	0.0011	0.0213
A_23_P58538	EPB41L4A-AS1	0.4450	3.34E+09	0.0032
A_32_P171181	NBPF10	0.4671	0.0065	0.0388
A_33_P3320772	ATXN1	241.262.550.757.345	0.0084	0.0398
A_33_P3415551	GPAT2	0.3903	0.0005	0.0162
A_21_P0000702	STX18-AS1	0.4048	0.0004	0.0136
A_21_P0011825	XLOC_l2_007449	0.3220	0.0013	0.0235
A_21_P0013633	XLOC_l2_015174	0.4479	0.0103	0.0429
A_32_P4018	ROR1	209.471.242.431.168	0.0043	0.0361
A_19_P00320274	ZMIZ1-AS1	247.147.261.007.869	0.0039	0.0344
A_23_P35883	FOXRED1	225.117.526.651.875	0.0020	0.0262
A_19_P00802872	XIST	31.994.851.869.667	0.0157	0.0488
A_24_P58501	OR4F4	0.4951	0.0091	0.0406
A_19_P00321129	TSIX	320.070.484.723.775	0.0023	0.0277
A_33_P3369401	CYP24A1	228.002.503.108.971	0.0073	0.0389
A_24_P203106	PFKFB1	239.308.418.243.043	0.0033	0.0339
A_24_P105391	ERMAP	222.428.151.416.224	0.0061	0.0381
A_33_P3404316	MIR100HG	0.4148	0.0150	0.0478
A_24_P307580	HTATIP2	0.2971	5.65E+08	0.0016
A_23_P401700	APBB1IP	221.062.196.465.168	0.0058	0.0381
A_33_P3254082	SPATA6L	0.4469	0.0088	0.0406
A_23_P422245	KIAA0825	0.4245	0.0068	0.0389
A_21_P0013192	7/set	0.3977	0.0119	0.0455
A_23_P214533	ZSCAN31	210.944.376.103.009	0.0117	0.0455
A_33_P3221648	XLOC_l2_010328	0.3856	0.0166	0.0496
A_33_P3216232	ITGB1BP1	201.975.833.333.702	0.0109	0.0433
A_23_P141802	SERPINB7	0.4387	0.0040	0.0352
A_33_P3332018	FGL2	0.4741	0.0056	0.0379
A_33_P3213508	C7orf72	0.4364	0.0090	0.0406
A_23_P356494	SPINK5	0.4280	0.0119	0.0455
A_23_P170186	OPLAH	0.4671	0.0031	0.0330
A_33_P3380867	STAT5B	263.605.790.194.262	0.0039	0.0344
A_24_P136029	SLC12A1	0.3525	0.0054	0.0379
A_21_P0013560	XLOC_l2_014757	226.353.903.304.204	0.0110	0.0435
A_23_P149858	ELOVL3	546.951.058.273.017	0.0107	0.0431
A_21_P0005159	LINC00581	0.3758	0.0037	0.0344
A_19_P00318183	LINC01197	0.3818	0.0044	0.0361
A_32_P221958	AGAP9	0.4735	0.0076	0.0391
A_23_P217704	GYG2	222.806.714.133.915	0.0056	0.0379
A_33_P3482417	ANKRD26P3	0.4621	2.89E+09	0.0032
A_24_P225635	HNRNPLL	0.3815	0.0023	0.0273
A_23_P252471	PECAM1	0.4664	0.0149	0.0478
A_24_P282416	ABL1	0.4531	0.0145	0.0470
A_33_P3383326	LPAR1	0.4802	0.0159	0.0488

A_23_P142075	ACP5	0.4037	0.0007	0.0185
A_33_P3391039	PRR27	0.3662	0.0133	0.0466
A_19_P00317168	XLOC_l2_002160	0.4815	0.0132	0.0466
A_21_P0011299	XLOC_l2_004595	0.4874	0.0151	0.0478
A_24_P192988	CCDC89	0.3456	0.0093	0.0410
A_23_P502081	MAGEC3	0.4331	0.0123	0.0455
A_23_P128974	BATF	0.4931	0.0123	0.0455
A_19_P00321148	LINC01127	0.4417	0.0088	0.0406
A_33_P3380457	GPR88	0.4516	0.0095	0.0415
A_24_P218006	DNAJC30	0.3820	0.0085	0.0401
A_32_P163247	CD8A	0.4407	0.0011	0.0210
A_24_P355267	SLC25A25	0.4431	0.0147	0.0477
A_21_P0002781	LINC01213	0.3793	0.0043	0.0361
A_24_P324368	DNAJC14	0.4240	0.0103	0.0429
A_23_P329835	UTY	0.4832	0.0158	0.0488
A_21_P0000545	OR5E1P	0.3217	0.0044	0.0361
A_21_P0001612	LINC00303	0.4302	0.0040	0.0350
A_19_P00318370	LINC00883	0.4883	0.0048	0.0370
A_23_P7901	TTLL2	0.3387	0.0094	0.0411
A_32_P140489	GDF6	0.4679	0.0006	0.0167
A_21_P0013896	TTTY14	0.4533	0.0075	0.0391
A_21_P0009555	SMAD2	0.4626	0.0138	0.0466
A_24_P214552	LINC01565	0.4366	0.0061	0.0381
A_24_P176079	WASF3	0.4537	0.0008	0.0185
A_24_P111406	CFHR5	0.4664	0.0061	0.0381
A_33_P3241388	SLC4A5	0.4290	0.0140	0.0466
A_21_P0000614	LINC00254	0.3837	0.0037	0.0344
A_33_P3276653	SPANXN1	0.4538	3.00E+09	0.0032
A_32_P212095	C17orf105	0.3412	0.0096	0.0415
A_23_P63521	LCE2C	0.4621	0.0002	0.0092
A_23_P132341	C22orf46	0.4358	0.0081	0.0396
A_23_P364324	ABCA13	0.3581	0.0017	0.0259
A_23_P57658	HRASLS	0.3726	0.0100	0.0423
A_21_P0012471	XLOC_l2_010451	0.4752	0.0123	0.0455
A_33_P3249489	WDR89	0.3448	0.0029	0.0324
A_33_P3319870	GREM1	0.3785	0.0095	0.0413
A_21_P0012424	XLOC_l2_010056	0.4935	0.0127	0.0457
A_24_P176493	ATMIN	0.4982	0.0077	0.0393
A_23_P257111	FBP1	0.4487	0.0139	0.0466
A_32_P46214	SLC9A9	0.4617	0.0054	0.0379
A_23_P145376	MAPK13	0.3207	0.0003	0.0106
A_33_P3323904	WTH3DI	0.3614	0.0124	0.0455
A_24_P38081	FKBP5	0.4297	0.0151	0.0478
A_21_P0013742	LINC01509	0.3400	0.0069	0.0389
A_23_P161940	SCGB2A2	0.3922	0.0059	0.0381
A_21_P0006771	ZNF503	0.4531	0.0049	0.0372
A_21_P0013029	XLOC_l2_012614	0.4506	0.0073	0.0389
A_21_P0012764	LINC01262	0.4163	0.0070	0.0389
A_24_P12059	GYPA	0.4426	0.0063	0.0382
A_21_P0013164	LPAL2	0.4825	0.0038	0.0344
A_33_P3408152	NEFH	0.4982	0.0046	0.0368
A_21_P0011571	XLOC_l2_006003	0.4365	0.0083	0.0398
A_33_P3281308	FIRRE	0.4802	0.0044	0.0361
A_23_P311010	SPRY3	0.4689	0.0124	0.0455
A_33_P3306307	KRT26	0.4371	0.0140	0.0466
A_33_P3334679	SNCAIP	0.3970	0.0159	0.0488
A_33_P3367247	CNTLN	0.4596	0.0126	0.0457

A_23_P46584	C1orf105	0.4630	0.0022	0.0266
A_23_P37410	CYP19A1	0.4975	0.0137	0.0466
A_21_P0006456	XIST	245.683.205.873.009	0.0107	0.0431
A_33_P3235531	CD1D	0.3872	0.0019	0.0261
A_21_P0000043	KRTAP21-3	0.4999	0.0004	0.0128
A_24_P153831	CTNNA3	0.3771	0.0068	0.0389
A_33_P3354607	CCL4L2	326.462.786.883.446	0.0086	0.0401
A_24_P124988	GOLGA6A	0.4383	0.0140	0.0466
A_23_P163227	CKMT1A	0.3685	0.0093	0.0411
A_21_P0013561	XLOC_l2_014757	0.4287	0.0127	0.0457
A_33_P3274691	SCART1	0.4215	0.0123	0.0455
A_21_P0010549	XLOC_l2_000384	0.4466	0.0064	0.0385
A_33_P3232498	C2orf71	0.4339	0.0048	0.0370
A_33_P3280317	C1orf137	0.4534	0.0012	0.0213
A_32_P152767	SKIDA1	218.191.970.012.065	0.0136	0.0466
A_33_P3285420	LINC01020	0.4724	0.0083	0.0398
A_19_P00324839	MALAT1	0.4644	0.0048	0.0370
A_24_P274795	CDCA7L	0.4789	0.0014	0.0239
A_33_P3284108	NSF	0.4088	0.0117	0.0455
A_23_P397208	GSTM2	0.4712	0.0015	0.0246
A_24_P319942	SSR3	20.004.869.951.758	0.0106	0.0431
A_33_P3389649	PDE4D	0.3525	0.0161	0.0489
A_23_P94782	CAPN8	209.979.600.208.782	0.0071	0.0389
A_33_P3736691	ZNF430	234.278.480.913.037	0.0090	0.0406
A_23_P162300	IRAK3	251.309.135.760.067	0.0019	0.0261
A_33_P3391905	SMEK3P	0.4882	0.0127	0.0457
A_33_P3851023	NRXN3	0.4731	0.0054	0.0379
A_23_P373541	DSPP	0.4296	0.0016	0.0255
A_23_P15678	TEKT1	0.4975	0.0073	0.0389
A_23_P114585	PCNXL2	0.3763	0.0006	0.0167
A_23_P13102	CASP12	285.961.311.304.283	0.0057	0.0380
A_19_P00316324	LINC01132	329.589.428.688.704	0.0024	0.0278
A_33_P3417950	AKAP8	208.300.268.063.925	0.0121	0.0455
A_24_P133162	STPG1	21.435.761.924.329	0.0018	0.0261
A_33_P3260445	DYNLT1	0.3427	0.0084	0.0398
A_24_P285501	UBR3	244.140.845.915.473	0.0119	0.0455
A_33_P3215043	HEPHL1	0.4947	0.0074	0.0390
A_23_P217384	AP1S2	0.4893	0.0040	0.0353
A_33_P3341601	WDR86	396.843.744.975.867	0.0141	0.0466
A_33_P3280405	OR7E37P	0.4439	0.0139	0.0466
A_21_P0011611	DNAH17	0.4613	0.0150	0.0478
A_33_P3243069	KIAA0040	0.3351	0.0076	0.0391

Supplementary Table 3: Differentially expressed genes involved in invasion and migration cellular processes when comparing cell lines before and after *PIWIL1* knockout.

Genes	Regulation
DACH1, ITGB1BP1, RALGPS1, ROR1, STAT5B	Up
ABL1, ABL2, B9D1, CD8A, CTNNA3, FRZB, GREM1, GSTM2, HOXD13, DOCK2, SMAD2, WASF3, CTLA4, SART1, BATF, CD1C, NR4A2, MXRA8, KCNJ2, KRT26, KRTAP21-3,	Down

LCE2C, *LPAR1*, *P2RX7*, *PDE4D*, *PSMD5*, *SLC4A5*, *SPINK5*, *TOLLIP*, *ZNF503*

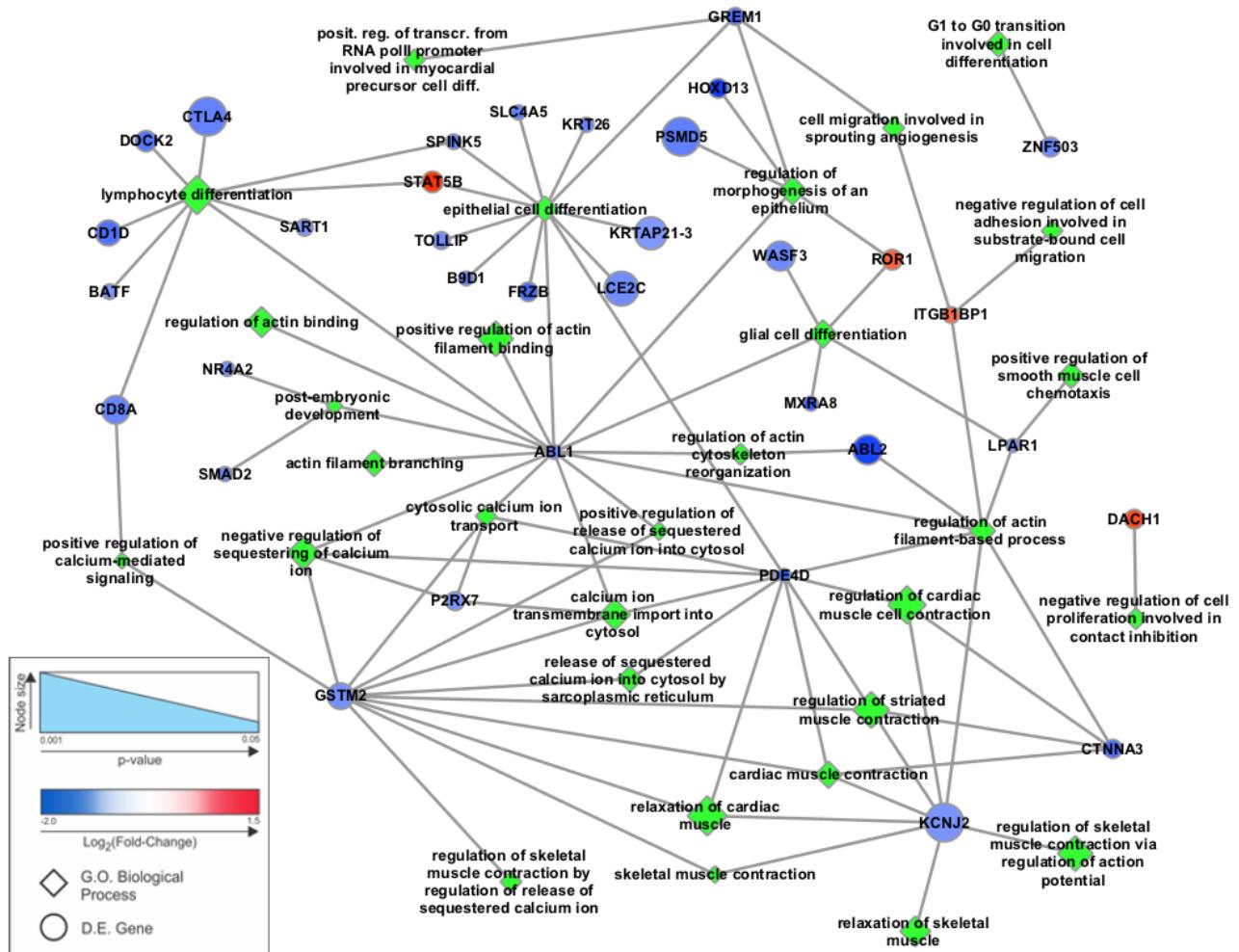Supplementary Table 4: Gene Ontology (GO) enrichment of Differentially Expressed (DE) genes.

GOBPID	p Value	Count	Size	Process	Genes
GO:0086004	0.0036	3	35	Regulation of cardiac muscle cell contraction	*KCNJ2, CTNNA3, PDE4D*
GO:0006942	0.0069	4	85	Regulation of striated muscle contraction	*KCNJ2, CTNNA3, GSTM2, PDE4D*
GO:0055119	0.0004	3	17	Relaxation of cardiac muscle	*KCNJ2, GSTM2, PDE4D*
GO:0014861	0.0089	1	1	Regulation of skeletal muscle contraction via regulation of action potential	*KCNJ2*
GO:1904531	0.0089	1	1	Positive regulation of actin filament binding	*ABL1*
GO:0051283	0.0134	4	103	Negative regulation of sequestering of calcium ion	*P2RX7, ABL1, GSTM2, PDE4D*
GO:0097553	0.0162	4	109	Calcium ion transmembrane import into cytosol	*P2RX7, ABL1, GSTM2, PDE4D*
GO:0090076	0.0177	1	2	Relaxation of skeletal muscle	*KCNJ2*
GO:1904616	0.0177	1	2	Regulation of actin binding	*ABL1*
GO:1905330	0.0218	5	179	Regulation of morphogenesis of an epithelium	*HOXD13, PSMD5, ROR1, ABL1, GREM1*
GO:0060048	0.0247	4	124	Cardiac muscle contraction	*KCNJ2, CTNNA3, GSTM2, PDE4D*
GO:0032485	0.0264	1	3	Regulation of Ral protein signal transduction	*RALGPS1*
GO:0070315	0.0264	1	3	G1 to G0 transition involved in cell differentiation	*ZNF503*
GO:0071673	0.0264	1	3	Positive regulation of smooth muscle cell chemotaxis	*LPAR1*
GO:0090135	0.0264	1	3	Actin filament branching	*ABL1*
GO:0032970	0.0265	7	326	Regulation of actin filament-based process	*ABL2, KCNJ2, ITGB1BP1, ABL1, LPAR1, CTNNA3, PDE4D*
GO:0030855	0.0268	12	720	Epithelial cell differentiation	*B9D1, TOLLIP, FRZB, SPINK5, STAT5B, ABL1, SLC4A5, LCE2C, GREM1, KRT26, KRTAP21-3, PDE4D*
GO:0014808	0.0272	2	29	Release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	*GSTM2, PDE4D*
GO:0002042	0.0345	2	33	Cell migration involved in sprouting angiogenesis	*ITGB1BP1, GREM1*
GO:2000249	0.0345	2	33	Regulation of actin cytoskeleton reorganization	*ABL2, ABL1*
GO:0003257	0.0350	1	4	Posit. reg. of transcr. from RNA polII promoter involved in myocardial precursor cell diff.	*GREM1*
GO:0006933	0.0350	1	4	Negative regulation of cell	*ITGB1BP1*

GO:0014809	0.0350	1	4	adhesion involved in substrate-bound cell migration Regulation of skeletal muscle contraction by regulation of release of sequestered calcium ion	*GSTM2*
GO:0060244	0.0350	1	4	Negative regulation of cell proliferation involved in contact inhibition	*DACH1*
GO:0060401	0.0354	4	139	Cytosolic calcium ion transport	*P2RX7, ABL1, GSTM2, PDE4D*
GO:0051281	0.0405	2	36	Positive regulation of release of sequestered calcium ion into cytosol	*ABL1, GSTM2*
GO:0003009	0.0426	2	37	Skeletal muscle contraction	*KCNJ2, GSTM2*
GO:0050850	0.0447	2	38	Positive regulation of calcium-mediated signaling	*CD8A, GSTM2*
GO:0030098	0.0020	9	316	Lymphocyte differentiation	*CTLA4, SART1, DOCK2, SPINK5, STAT5B, ABL1, BATF, CD8A, CD1D*
GO:0009791	0.0448	3	89	Post-embryonic development	*NR4A2, ABL1, SMAD2*
GO:0010001	0.0223	5	180	Glial cell differentiation	*MXRA8, ROR1, ABL1, LPAR1, WASF3*

Supplementary Table 5: Epithelial-mesenchymal transition proteins status when comparing cell lines before and after *PIWIL1* knockout.

	Before knockout	After knockout
Present	ACTN4, AGO2, ALDH1A1, CALM1, CBR1, CUL4B, DDX5, EHD1, FGFR1, GELSOLIN, LRP5, MAP3K11, MSI2, PCBP2, PCNA, PRMT1, RPS6KA5, TRAP1, TUBB3, TXNRD1, TYRO3, UBE2N	ACSM3, ADGRG1, ANPEP, NKX2.5, RAD50, SLIT3
Absent	ACSM3, ADGRG1, ANPEP, NKX2.5, RAD50, SLIT3	ACTN4, AGO2, ALDH1A1, CALM1, CBR1, CUL4B, DDX5, EHD1, FGFR1, GELSOLIN, LRP5, MAP3K11, MSI2, PCBP2, PCNA, PRMT1, RPS6KA5, TRAP1, TUBB3, TXNRD1,

Supplementary Figure 1: Gene ontology enrichment of DE mRNAs. Processes involved in cellular invasion and migration.