

Supplemental Table S1. Average fold changes in JNK small molecule inhibitor treatments relative to untreated controls. All fold changes > 1.3 and p-value < 0.05.

Gene	Average fold change	P-value
ATF2	-1.84	0.04375
ATOH1	-3.86	0.00373
BARHL1	-1.59	0.00953
BRPF1	-1.48	0.02797
CDX1	-1.45	0.02563
CEBPG	-1.76	0.00474
DCP1A	2.15	0.00636
DLX6	-2.06	0.02448
E2F3	-1.61	0.04946
EN2	1.43	0.04134
EP300	-1.53	0.04926
ETV1	-1.84	0.01406
GFI1B	-1.8	0.0327
GORASP2	-2.03	0.01369
HEY2	1.52	0.04477
HOXB3	2.05	0.0159
HOXB8	1.36	0.0015
HSF2BP	-1.48	0.01955
ID3	-1.38	0.03158
KCNN2	1.61	0.01724
KIAA0161	-2.45	0.01336
LRP5	-1.52	0.00245
MEF2A	-1.68	0.00552
MEF2D	-1.63	0.0318
MLLT7	3	0.01889
MYH11	1.84	0.0392
NAP1L1	-1.97	0.01847
NFAT5	-1.68	0.00194
NR4A2	-1.56	0.03299
PMX2B	-1.67	0.00982
RXRA	-2.45	0.02784
SCPEP1	1.61	0.00229
SFRP4	2.55	0.03424
SMARCB1	-1.45	0.01814
SMARCE1	-1.42	0.0351
TAF-172	-2.12	0.00144
TFEC	-1.39	0.0323
THRA	1.59	0.04827
ZFAND6	1.4	0.04252
ZFX	3.8	0.02685

Supplemental Table S2. Average fold changes in JunD siRNA treatments relative to GFP siRNA treated controls. JunD knockdown was confirmed by end-point semi-quantitative PCR, all other fold changes are > 1.3 and p-value < 0.05.

Gene	Average fold change	P-value
ALDH3A2	-1.7	0.00709
BCL11A	2.56	0.00079
BLZF1	1.62	0.00618
BRD1	-1.9	0.0123
CEBPG	-2.22	0.011
DEAF1	-2.25	0.02818
ELF3	2.1	0.00369
EMX2	2.14	0.00169
EZH1	-1.38	0.00025
FAM48A	1.36	0.01181
FEZL	-2.12	0.01962
FOXP1	-1.92	0.02737
GATA3	1.65	0.0162
GTF2A1	1.3	0.00539
HEY2	1.6	0.01008
HOXA6	1.31	0.0011
HOXD8	1.58	0.0081
JIK	1.44	0.00009
KIAA0130	-1.81	0.03623
KLF5	-1.67	0.00434
LHX5	-2.04	0.01443
LHX6	-1.63	0.01008
LOC772263	1.61	0.0198
LRP5	-1.5	0.01779
MDN1	-1.46	0.00434
NEUROD6	-2.34	0.01428
NFE2L2	-1.36	0.01565
NR1I3	-1.68	0.03802
NR2E1	2.6	0.00067
PCMT1	-2.11	0.04481
PMX1	-1.75	0.00663
PRDM16	-1.72	0.00343
PRELP	-2.01	0.03844
PURA	-1.61	0.0129
RARA	-1.33	0.03953
SHH	-1.96	0.03742
SMARCA2	1.57	0.01549
SNAPC4	1.66	0.04773
SUPT4H1	-1.35	0.00736
TAF-172	-1.37	0.0061
TCF21	-1.36	0.0398
TFAP2B	-1.98	0.00208
TGIF	1.41	0.04588
WHSC1	1.39	0.00667
ZFP3	1.56	0.00096
ZIC4	1.3	0.04011
ZID	1.66	0.00032

ZNF143 -2.87 0.03757

Supplemental Table S3. Average fold changes in CEBPG siRNA treatments relative to GFP siRNA treated controls. All fold changes > 1.3 and p-value < 0.05.

GeneID	Average fold change	P- value
AEBP2	2.55	0.02715
ALDH3A2	-5.95	0.00182
ALDH4A1	-1.79	0.01266
ALX4	-5.96	0.02052
ARID1A	2.21	0.00772
ASCL1	-5.09	0.03264
ATF2	-4.4	0.01554
ATOH1	1.91	0.01676
BARHL1	-2.65	0.01138
BATF3	3.18	0.00206
BC052625	1.43	0.03388
BMI1	-2.55	0.02593
Bmp11	4.05	0.01105
Bmp3	2.48	0.01865
Bmp4	1.61	0.00082
Bmp8a	2.51	0.01818
Bmp9	1.69	0.01234
Bmpr1a	1.83	0.03068
Bmpr2	2.27	0.01001
BRD1	-8.18	0.01436
BRN-3A	2.05	0.02682
BRPF1	-2.09	0.03152
BRUNOL4	-2.3	0.01806
BTBD1	2.82	0.03384
BTBD14A	1.55	0.01718
CBFA2T3	2.1	0.04458
CDH23	3.34	0.01199
CDK9	-1.72	0.04315
CDKL2	1.53	0.02541
CEBPG	-3.92	0.0178
CHD1	-4.96	0.04074
CLDN14	1.61	0.04503
CLOCK	1.74	0.00412
CNOT4	-2.28	0.00543
CREB1	1.7	0.01312
CREB3L2	-4.3	0.04769
CSRP2	-2.55	0.01379
CTNNB1	2.68	0.03512
CYLD	-4.03	0.01772
DACH	3.14	0.01045
DAZAP1	-4.01	0.01811
DEAF1	-4.46	0.03461

DII4	2.5	0.0197
DR1	4.48	0.01548
EEF1A1	-4.44	0.0407
EIF2B2	3.24	0.04663
ELAVL2	2.17	0.0335
ELL	-1.8	0.04875
ENO1	-2	0.00839
ETV4	2.69	0.01387
EYA4	-1.87	0.00219
FEZL	-4.81	0.01534
FEZL	-5.54	0.03053
Fgf12	-2.38	0.04495
Fgf13	-2.71	0.03439
Fgf16	-6.59	0.01411
Fgf20	6.04	0.04406
FHL2	-5.43	0.0167
FLJ11040	2.59	0.01738
FOG2	-4.13	0.01927
FOXA2	4.11	0.00877
FOXC2	-2.86	0.03208
FOXG1B	6.12	0.02161
FOXP1	-7.31	0.03633
FOXP4	2.32	0.01942
FREQ	3.33	0.03391
Fzd3	-1.63	0.03667
Fzd4	4.02	0.0175
GATA3	2.35	0.05068
GFI1B	3.96	0.02474
GORASP2	-1.75	0.04703
GPA33	1.82	0.03584
GSC	-1.69	0.02695
GTF2B	-1.67	0.02081
GTF2E2	-8.21	0.00048
H2AFY	2.57	0.01554
HES5	-3.78	0.03251
HES5	1.89	0.04241
HKR3	1.89	0.01581
HMG20A	4.46	0.01259
HOXA10	-3.04	0.00294
HOXA7	-5.78	0.02946
HOXC10	2.04	0.02496
HRY	-2.11	0.04924
HSPC063	1.42	0.03978
HSPX153	-3.26	0.00096
ID3	-5.09	0.02349
IFT172	-2.16	0.01046
IRF6	4.11	0.01029
Jag2	1.7	0.0426
JARID1A	-5.03	0.03911
KLF1	-3.69	0.02624

KLF15	2.83	0.00748
KLF5	-4.59	0.0257
KLHL1	2.66	0.03714
KLHL1	1.59	0.01457
KLHL25	2.75	0.02401
KRT12	1.49	0.01689
LARP1	-2.14	0.04177
Lfng	4.41	0.01572
LHX3	-2.46	0.01783
LHX8	-4.75	0.01002
LOC152485	-1.75	0.02303
LOC51652	2.55	0.00635
LOC771525	3.22	0.02052
LOC772263	1.84	0.03084
LRP5	-4.39	0.01861
MADH1	-3.3	0.01717
MADH2	1.95	0.02258
MADH5	-1.86	0.02175
MADH7	-3.89	0.0152
MAFG	-1.49	0.04327
MBNL2	-1.85	0.03537
Mfng	3.19	0.00244
MGC16733	-5.64	0.01322
MID2	-2.37	0.04879
MLL3	3.42	0.0408
MLLT10	-2.41	0.03251
MLLT6	-3.25	0.02008
MLLT7	-2	0.01936
MNT	5.03	0.01175
MORF4	-3.7	0.02657
MSX1	2.82	0.00959
MSX2	1.94	0.01357
MTF1	-3.04	0.03254
MTF2	-5.01	0.00154
MXD4	-1.85	0.02115
MXI1	-2.29	0.015
MYH11	1.88	0.01693
MYH9	4.11	0.01967
MYO6	-2.1	0.02708
MYOD1	-6.02	0.02566
MYT1	-3.99	0.03844
MYT1L	-4.38	0.00602
NCOA2	-7.18	0.00137
NCOR2	-4.85	0.01401
NEUROD6	-8.74	0.02847
NFE2L2	-9.83	0.00306
NFIC	-3.52	0.03787
NFKBIA	2.71	0.00146
NFYC	1.48	0.01901
NKRF	-1.67	0.05042

NKX6-2	1.83	0.0158
Nog	1.54	0.02221
NONO	2.7	0.01333
Notch1	1.59	0.00547
NR1D2	-2.75	0.02396
NR1I3	-6.65	0.0126
NUP153	-4.88	0.02545
OTOF	1.64	0.01307
OVOL2	-2.99	0.02102
PAX3	-2.18	0.0434
PAX6	3.36	0.00702
PCMT1	-6.91	0.01167
PLAG1	-1.76	0.02475
PMX2B	-7.6	0.01076
PPIB	3.78	0.01578
PRDM11	-1.56	0.02776
PRDM15	2.23	0.01135
PRPF4	2.82	0.04425
PSMC1	2.68	0.00879
QDPR	2.22	0.02796
R32184_3	1.71	0.01825
RAI15	-1.95	0.00404
RARA	-2.38	0.0442
RAX	-1.67	0.02078
REST	-2.05	0.03065
RFXANK	1.93	0.02546
RIC3	3.02	0.00105
RIP60	-2.95	0.01418
RNF12	-2.58	0.00181
Rxrg	-4.4	0.02716
SCA2	-3.24	0.03256
SETBP1	-2.78	0.0196
SHH	-4.35	0.02241
SIAH1	-7.05	0.01762
SIX1	2.24	0.02194
SIX3	1.76	0.03614
SMARCA2	-1.61	0.03791
SMARCA5	2.8	0.04924
SMARCC1	2.62	0.0346
SNW1	3.28	0.01118
SOX1	-2.81	0.02
SOX10	1.72	0.00146
SOX13	2.3	0.04484
SOX14	2.03	0.03133
SOX21	-3.01	0.02187
SOX7	2.95	0.04163
SPOP	-3.27	0.04332
STOML1	-3.9	0.02312
SURB7	2.41	0.00521
TAF-172	-2.02	0.05039

TAF2A	1.74	0.01574
TAF2B	2.39	0.02025
TAF3	-6.68	0.0209
TAL2	3.74	0.00717
TBP	-3.81	0.0434
TEAD3	2.06	0.01946
TGFBR3	-3.4	0.02431
TGIF	-3.55	0.03617
TIEG	1.93	0.04504
TITF1	-3.74	0.01405
TLE4	-2.37	0.0326
TMC1	3.36	0.01336
TNRC15	2.61	0.00243
TNRC9	-5.03	0.02731
TRAF5	-1.99	0.01569
TSC22D3	3.81	0.01305
UBC	2.57	0.0123
Wnt1	1.95	0.01061
Wnt16	2.93	0.01211
Wnt3	-5.35	0.01221
Wnt4	5.48	0.01669
Wnt7b	1.97	0.00196
Wnt8a	2.21	0.01298
Wnt9b	4.03	0.01186
ZBTB2	3.2	0.01141
ZBTB26	-4.13	0.04256
ZFP64	-1.48	0.04977
ZFPM1	1.76	0.01364
ZNF161	3.05	0.01979
ZNF503	-2.12	0.01954
ZYX	2.9	0.0317

Supplemental Table S4. Genes commonly up or down-regulated in CEBPG and LRP5 individual siRNA knockdowns. All fold changes > 1.3 and p-value < 0.05.

GeneID	CEBPG	P-value	LRP5	P-value
AEBP2	2.55	0.02715	2.72	0.04307
ALDH3A2	-5.95	0.00182	-5.08	0.01125
ALX4	-5.96	0.02052	-9.53	0.00017
ASCL1	-5.09	0.03264	-4.54	0.00225
ATOH1	1.91	0.01676	3.23	0.01383
BATF3	3.18	0.00206	2.86	0.007
BMI1	-2.55	0.02593	-1.87	0.00989
Bmp3	2.48	0.01865	3.48	0.01031
BRD1	-8.18	0.01436	-4.57	0.00571
CHD1	-4.96	0.04074	-8.75	0.00006
CREB3L2	-4.3	0.04769	-3.29	0.02514
CSRP2	-2.55	0.01379	-3.15	0.0047

CTNNB1	2.68	0.03512	3	0.01848
CYLD	-4.03	0.01772	-3.25	0.00989
DAZAP1	-4.01	0.01811	-8.49	0.00044
DEAF1	-4.46	0.03461	-5.48	0.00067
DII4	2.5	0.0197	3.34	0.00839
DR1	4.48	0.01548	4.27	0.00166
EEF1A1	-4.44	0.0407	-7.04	0.00292
ELAVL2	2.17	0.0335	2.23	0.04067
FEZL	-5.54	0.03053	-8.08	0.00069
FEZL	-4.81	0.01534	-3.47	0.03295
Fgf13	-2.71	0.03439	-7.15	0.00008
Fgf16	-6.59	0.01411	-8.65	0.00012
Fgf20	6.04	0.04406	3.33	0.00134
FHL2	-5.43	0.0167	-4.74	0.00113
FLJ11040	2.59	0.01738	4.34	0.00148
FOG2	-4.13	0.01927	-3.1	0.01669
FOXA2	4.11	0.00877	4.44	0.03313
FOXC2	-2.86	0.03208	-3.14	0.00345
FOXP1	-7.31	0.03633	-7.02	0.00362
FREQ	3.33	0.03391	4.2	0.02041
GATA3	2.35	0.05068	2.52	0.02665
HES5	1.89	0.04241	1.99	0.02062
HOXA7	-5.78	0.02946	-7.39	0.00383
ID3	-5.09	0.02349	-7.19	0.00029
IRF6	4.11	0.01029	3.02	0.00829
JARID1A	-5.03	0.03911	-6.81	0.0004
KLF1	-3.69	0.02624	-3.31	0.0008
KLF5	-4.59	0.0257	-3.01	0.00963
KLHL1	2.66	0.03714	3.12	0.00349
KLHL25	2.75	0.02401	3.91	0.00084
LOC51652	2.55	0.00635	2.94	0.00971
LRP5	-4.39	0.01861	-5.71	0.00035
MADH1	-3.3	0.01717	-3.46	0.03198
MADH7	-3.89	0.0152	-5.62	0.00209
MBNL2	-1.85	0.03537	-3.73	0.00118
MGC16733	-5.64	0.01322	-7.36	0.00152
MID2	-2.37	0.04879	-7.97	0.00542
MLLT6	-3.25	0.02008	-5.77	0.00013
MNT	5.03	0.01175	4.33	0.01327
MSX1	2.82	0.00959	5.83	0.00006
MTF1	-3.04	0.03254	-2.93	0.01283
MTF2	-5.01	0.00154	-2.95	0.01069
MXD4	-1.85	0.02115	-2.03	0.02043
MYH9	4.11	0.01967	3.8	0.0136
MYO6	-2.1	0.02708	-2.99	0.00612
MYOD1	-6.02	0.02566	-7.18	0.00812
MYT1	-3.99	0.03844	-3.01	0.01649
MYT1L	-4.38	0.00602	-4.05	0.00709
NCOA2	-7.18	0.00137	-5.16	0.00074
NEUROD6	-8.74	0.02847	-7.69	0.00011

NONO	2.7	0.01333	3.77	0.00351
NR1I3	-6.65	0.0126	-4.78	0.01252
NUP153	-4.88	0.02545	-6.9	0.01001
OVOL2	-2.99	0.02102	-6.13	0.04356
PAX3	-2.18	0.0434	-3.02	0.00159
PCMT1	-6.91	0.01167	-9.28	0.00059
PRPF4	2.82	0.04425	2.7	0.01283
PSMC1	2.68	0.00879	3	0.00294
R32184_3	1.71	0.01825	2.57	0.01586
RARA	-2.38	0.0442	-3.12	0.00287
RIP60	-2.95	0.01418	-3.13	0.00359
Rxrg	-4.4	0.02716	-7.28	0.00093
SCA2	-3.24	0.03256	-6.67	0.00041
SHH	-4.35	0.02241	-5.02	0.00269
SIAH1	-7.05	0.01762	-4.16	0.04671
SIX1	2.24	0.02194	2.98	0.00678
SIX3	1.76	0.03614	3.04	0.02718
SMARCA5	2.8	0.04924	10.48	0.00006
SNW1	3.28	0.01118	5.2	0.00071
SOX13	2.3	0.04484	3.91	0.00362
SPOP	-3.27	0.04332	-4.61	0.01417
STOML1	-3.9	0.02312	-4.85	0.00217
TAF2B	2.39	0.02025	3.81	0.00287
TAF3	-6.68	0.0209	-4.52	0.0109
TAL2	3.74	0.00717	3.16	0.00158
TBP	-3.81	0.0434	-5.96	0.02802
TGIF	-3.55	0.03617	-7.54	0.00563
TIEG	1.93	0.04504	3.72	0.02681
TITF1	-3.74	0.01405	-3.96	0.00124
TMC1	3.36	0.01336	3.98	0.00194
TNRC15	2.61	0.00243	3.44	0.00894
TNRC9	-5.03	0.02731	-7.67	0.00168
Wnt16	2.93	0.01211	2.28	0.00781
Wnt4	5.48	0.01669	4.16	0.03894
Wnt9b	4.03	0.01186	3.44	0.02481
ZBTB26	-4.13	0.04256	-7.75	0.00001
ZFPM1	1.76	0.01364	2.18	0.00425
ZNF161	3.05	0.01979	2.43	0.03695
ZNF503	-2.12	0.01954	-1.51	0.0222
ZYX	2.9	0.0317	5.03	0.00029

Supplemental Table S5. Average fold changes in LRP5 siRNA treatments relative to GFP siRNA treated controls. All fold changes > 1.3 and p-value < 0.05.

GeneID	Average fold change	P-value
ACVR1	2.64	0.04106
ACVR1C	2.8	0.00961
AEBP2	2.72	0.04307

ALDH3A2	-5.08	0.01125
ALX4	-9.53	0.00017
AMOT	-1.96	0.04339
ANP32A	2.02	0.01977
ARC	1.9	0.02585
ARF6	1.55	0.03909
ARNTL2	-3.23	0.00126
ARTN	-11.28	0.00001
ASCL1	-4.54	0.00225
ATOH1	3.23	0.01383
ATRX	4.16	0.00097
BATF3	2.86	0.007
BAZ2B	2.72	0.00454
BETA3	2.1	0.0207
BLZF1	9.14	0.00041
BMI1	-1.87	0.00989
Bmp2	2.03	0.01319
Bmp3	3.48	0.01031
BMP4	-11.43	0.00144
BRD1	-4.57	0.00571
BSX	2.07	0.03288
c14orf166	-3.52	0.04382
CATH1	7.24	0.00569
CCND3	-4.8	0.01255
CCNI	-21.3	0.00624
CDC2	2.1	0.00694
CDC2L5	-4.97	0.01608
CDK2	-7.83	0.00585
CDK8	-2.45	0.02345
CDKN2C	-3.26	0.00425
CHD1	-8.75	0.00006
CITED2	-6.73	0.00214
CKS1B	-11.9	0.03247
CREB3L2	-3.29	0.02514
CSRP2	-3.15	0.0047
CTNNB1	3	0.01848
CYLD	-3.25	0.00989
DAZAP1	-8.49	0.00044
DCP1A	6.21	0.02201
DEAF1	-5.48	0.00067
DKK3	-2.89	0.01078
DII4	3.34	0.00839
DPF3	1.36	0.01931
DR1	4.27	0.00166
EBF	-1.93	0.01492
EED	3.15	0.04982
EEF1A1	-7.04	0.00292
ELAVL2	2.23	0.04067
ELF3	9.39	0.00001
EP300	-2.94	0.00879

ETS1	-1.55	0.00004
EVX1	-4.98	0.01245
EYA1	1.8	0.00946
FAM48A	1.85	0.00125
FEZL	-3.47	0.03295
FEZL	-8.08	0.00069
Fgf10	3.21	0.01058
Fgf13	-7.15	0.00008
Fgf16	-8.65	0.00012
Fgf20	3.33	0.00134
Fgf4	-3.48	0.0136
FGFR1_exon13	2.21	0.00847
Fgfr4	-2.43	0.0098
FHL2	-4.74	0.00113
FKBP1A	2.68	0.00847
FLJ10300	-5.75	0.00179
FLJ10697	2.42	0.0287
FLJ11040	4.34	0.00148
FLJ36155	-4.72	0.00028
FMR2	-2.55	0.02594
FOG2	-3.1	0.01669
FOXA2	4.44	0.03313
FOXC2	-3.14	0.00345
FOXG1A	1.91	0.0354
FOXP1	-7.02	0.00362
FREQ	4.2	0.02041
GADD45	-5.44	0.01497
GATA3	2.52	0.02665
GDF1	3.48	0.01779
GDF8	-3.44	0.00982
GDNF	3.94	0.00519
GJA1	3.27	0.00044
GJB6	1.72	0.02614
GLI3	-3.43	0.03925
GPRC5C	5.49	0.00002
GTF3C1	-2.89	0.01911
HD	-9.82	0.00038
HES5	1.99	0.02062
HEY1	-2.94	0.02647
HEYL	-2.66	0.03782
HMGB3	2.6	0.01282
HMGIC	1.83	0.00173
HMGXB3	1.97	0.03002
HOXA3	7.86	0.00433
HOXA7	-7.39	0.00383
HOXA9	2.95	0.00017
HOXB3	2.97	0.01981
HOXC6	2.96	0.02211
HPCA	2.28	0.00685
HPCAL1	2.89	0.03793

HSF2BP	-3.56	0.02365
HSPA8	5.8	0.03527
HUMPPA	2.24	0.0009
ID2	-1.58	0.01516
ID3	-7.19	0.00029
IHH	2.42	0.02436
IRF2	-3.91	0.00051
IRF6	3.02	0.00829
IVNS1ABP	-7.08	0.00008
JARID1A	-6.81	0.0004
JUN	2.43	0.00097
KCNN2	6.52	0.03031
KIAA0130	-5.5	0.041
KIAA0293	-1.74	0.02188
KIAA1190	4.99	0.00682
KLF1	-3.31	0.0008
KLF5	-3.01	0.00963
KLHL1	3.12	0.00349
KLHL25	3.91	0.00084
KLHL3	-6.42	0.00438
KLHL9	3.87	0.0154
LAF4	-4.58	0.01076
LEF1	-1.47	0.03148
LHX5	-4.76	0.01065
LHX6	-2.41	0.01841
LHX8	2.43	0.00785
LHX9	-4.21	0.01238
LMO7	1.49	0.04261
LMX1B	-3.01	0.02745
LOC416414	3.85	0.03566
LOC51042	2.4	0.00843
LOC51131	3.25	0.01797
LOC51652	2.94	0.00971
LRP5	-5.71	0.00035
LRP6	4.42	0.00466
LZTS1	2.54	0.00499
MADH1	-3.46	0.03198
MADH1	2.47	0.02564
MADH3	-1.78	0.04044
MADH7	-5.62	0.00209
MADH9	2.29	0.00119
MBNL2	-3.73	0.00118
MEF2D	-2.68	0.01817
MGC16733	-7.36	0.00152
MIB1	1.53	0.01072
MID2	-7.97	0.00542
MLLT4	2.17	0.03512
MLLT6	-5.77	0.00013
MNT	4.33	0.01327
MSX1	5.83	0.00006

MTA1	-3.62	0.00882
MTF1	-2.93	0.01283
MTF2	-2.95	0.01069
MXD4	-2.03	0.02043
MYH9	3.8	0.0136
MYNN	-2.71	0.0294
MYO6	-2.99	0.00612
MYOD1	-7.18	0.00812
MYT1	-3.01	0.01649
MYT1L	-4.05	0.00709
NCOA2	-5.16	0.00074
NEUROD6	-7.69	0.00011
NEUROG2	-2.56	0.01362
NKX2-5	2.28	0.03865
NKX2C	-1.93	0.03741
NNF1B	-1.81	0.00422
NONO	3.77	0.00351
NR1I3	-4.78	0.01252
NR2C2	-3.41	0.01038
NR2E1	7.54	0.00036
NRP1	3.57	0.00132
NUP153	-6.9	0.01001
OSR2	5.74	0.00175
OVOL2	-6.13	0.04356
p300/CBP	1.62	0.00955
PAX2	-3.39	0.0087
PAX3	-3.02	0.00159
PBX3	1.98	0.02499
PCMT1	-9.28	0.00059
PDEF	-2.33	0.03649
PGR	2.37	0.02879
PHF16	1.9	0.03335
PLTP	-10	0.00056
PME-1	5.02	0.00368
PMX1	-5.67	0.01022
PPARA	2.64	0.04734
PPARBP	4	0
PPP1R14C	2.9	0.00712
PRDM16	-2.73	0.03975
PRDM5	-2.52	0.00406
PRES	3.88	0.0293
PROP1	-5.57	0.04858
PRPF4	2.7	0.01283
PSIP1	5.3	0.04972
PSMC1	3	0.00294
PTX3	2.35	0.00055
R32184_3	2.57	0.01586
RARA	-3.12	0.00287
RBBP5	3.19	0.03419
RCOR1	1.67	0.01011

RERE	2.47	0.01007
RIP60	-3.13	0.00359
RNF24	2.48	0.02289
Rora	-4.56	0.00041
Rxrg	-7.28	0.00093
SCA2	-6.67	0.00041
SCML4	1.72	0.00785
SHH	-5.02	0.00269
SHH:	2.2	0.02928
SIAH1	-4.16	0.04671
SIX1	2.98	0.00678
SIX3	3.04	0.02718
SKIL	4.78	0.00017
SMARCA5	10.48	0.00006
SNW1	5.2	0.00071
SOX13	3.91	0.00362
SOX2	-2.7	0.01294
SOX4	2.71	0.0024
SOX4	3.26	0.02851
SPOP	-4.61	0.01417
STAT3	-3.79	0.01129
STOML1	-4.85	0.00217
SUB1	3.63	0.00305
SUPT4H1	-4.27	0.03636
SUV39H1	4.48	0.01877
TADA2L	-2.64	0.00338
TAF-172	2.24	0.04965
TAF2B	3.81	0.00287
TAF2C2	-5.59	0.00737
TAF3	-4.52	0.0109
TAF5L	3.45	0.02294
TAL2	3.16	0.00158
TBP	-5.96	0.02802
TBX2	-5.73	0.01713
TBX6	2.76	0.03092
TCF21	2.97	0.03116
TCF7	3.52	0.00178
TCFL1	-2.36	0.00676
TEAD1	-2.75	0.04778
TECPR1	-5.33	0.0013
TEK	4.75	0.00239
TGIF	-7.54	0.00563
TIE1	3.91	0.0164
TIEG	3.72	0.02681
TITF1	-3.96	0.00124
TMC1	3.98	0.00194
TNRC15	3.44	0.00894
TNRC6	3.61	0.00031
TNRC9	-7.67	0.00168
TSC22	-1.54	0.01957

VEGFC	-3.57	0.02917
VEGFR1	3.16	0.00204
VEGFR3	3.81	0.00672
WDR45L	3.66	0.0403
Wnt16	2.28	0.00781
Wnt4	4.16	0.03894
Wnt9b	3.44	0.02481
ZBTB26	-7.75	0.00001
ZFP276	1.94	0.0144
ZFP3	4.19	0.02637
ZFPM1	2.18	0.00425
ZFX	-1.55	0.02596
ZID	10.59	0.00002
ZNF161	2.43	0.03695
ZNF395	4.71	0.02937
ZNF503	-1.51	0.0222
ZYX	5.03	0.00029

Supplemental Table S6. Average fold changes in PAX2 siRNA treatments relative to GFP siRNA treated controls. All fold changes > 1.3 and p-value < 0.05.

Gene	Average fold change	P-value
BRD1	-1.34	0.03
CCNG1	-1.71	0.03232
CHKCHOX4D	1.49	0.00805
E2F4	1.36	0.00667
EGLN1	-1.48	0.04962
GTF2B	-1.64	0.02674
GTF2H3	1.44	0.03359
HIF1A	1.34	0.02088
HOXC11	1.36	0.03932
HOXD4	1.56	0.02156
KIAA1190	1.39	0.00187
KLF2	1.49	0.00585
LHX9	1.56	0.01101
MAFA	-1.49	0.011
MLLT1	1.57	0.00292
MYT1L	-1.51	0.00162
NFYC	1.35	0.00849
NPTXR	1.31	0.02901
PAX2	-1.61	0.00609
PKNOX1	-1.37	0.0315
SOX10	1.33	0.04559
TBX22	1.45	0.02754
TLE4	-1.35	0.04592
TNRC6	1.32	0.00481
Wnt4	1.34	0.04654
YBX1	1.32	0.00213

ZFAND6	-1.49	0.01723
ZMYND8	-1.56	0.03515

Supplemental Table S7. Average fold changes in PAX5 siRNA treatments relative to GFP siRNA treated controls. PAX5 knockdown were confirmed by end-point semi-quantitative PCR, all other fold changes are > 1.3 and p-value < 0.05.

Gene	Average fold change	P-value
BMP4	-1.3	0.02255
BTF3	-1.32	0.0111
BUB3	-1.83	0.00815
CDC20	-1.42	0.04856
CDC25A	-1.35	0.02621
DCP1A	1.4	0.00117
EIFJ3	1.52	0.01814
ETV4	-1.31	0.00654
Fgf10	1.59	0.03598
FGF5	1.55	0.03268
FLJ31751	-1.34	0.04444
GAK	-1.34	0.03973
GCN5L2	-1.44	0.01275
GFI1B	-1.39	0.04111
HOXD4	-1.92	0.00128
IGHMBP2	-1.38	0.00337
KIAA1388	-1.33	0.03123
KLF15	-1.4	0.04076
KLHL1	-1.41	0.04846
LMX1A	1.4	0.0021
LOC51580	-1.74	0.0301
MED16	1.5	0.01025
MEF2D	-1.63	0.0138
MGC16733	-1.89	0.0252
MLLT1	-1.63	0.02207
MYT1L	-1.61	0.01409
Nog	-1.34	0.00048
NOS3	1.36	0.02308
ODD	-1.33	0.00169
p27KIP1	-1.46	0.00641
P2rx7-v1-2-3	-1.34	0.01505
PCAF	1.48	0.04489
PFKL	-1.38	0.01209
PKNOX1	1.69	0.03063
RBPJL	-1.37	0.01504
RCOR1	-1.38	0.03744
Sgk	1.44	0.04923

SNAPC1	-1.32	0.01579
SOX13	-1.37	0.0008
Sparcl1	-1.5	0.02325
STAT3	-1.34	0.01924
TBX2	-1.33	0.02284
TEAD3	-1.32	0.02935
TECPR1	-1.4	0.04376
TIEG	-1.38	0.00094
TP53mm1	1.55	0.00494
Wnt4	1.37	0.0071
YBX1	-1.5	0.02443

Supplemental Table S8. Average fold changes in WNT4 siRNA treatments relative to GFP siRNA treated controls. All fold changes > 1.5 and p-value < 0.05.

Gene	Average fold change	P-value
ALX4	2.18	0.00029
AMOT	-1.77	0.04323
ANAPC2	-2.26	0.00004
ANG1	1.84	0.02186
ARID1A	-1.52	0.0402
ARNT2	1.52	0.01731
ATRX	-1.56	0.02943
BACH2	-1.9	0.0001
BARX2	2.77	0.04025
BATF3	-2.64	0.02465
BC052269	-2.53	0.01787
BC052625	-2.06	0.0005
BCL6B	-1.73	0.00157
BETA3	1.65	0.00228
BHLHB2	-1.82	0.03654
Bmp11	-2.79	0.0002
Bmp15	-1.5	0.0073
BMP15	1.6	0.01594
Bmp6	-2.19	0.00427
Bmp8a	-1.61	0.00026
BRN-3A	-1.91	0.00396
BSX	-1.66	0.00504
BTBD14A	-1.74	0.00318
Calb2	2.64	0.00915
CALM3	1.99	0.00616
CCNB2	-1.7	0.01041
CCNB3	-1.74	0.00002
CCNE1	-1.66	0.02414
CCNL2	-2.51	0.01754
CDK11	-1.89	0.01698
CDKL2	-2.15	0.00013
CDKN2C	-2.5	0.00009

CHD1	-2.19	0.00999
CKS1B	-1.8	0.00723
CLDN14	-2.25	0.00672
Clorf78	-1.82	0.02775
Cnn1	-1.51	0.03096
CUTL1	-1.9	0.00725
DKK3	-2.01	0.00213
Dll1	1.6	0.00038
EGR2	-1.58	0.02791
EN2	-2.41	0.00338
ERK	-1.56	0.04275
EZH1	-1.83	0.00974
FBI1	1.71	0.03169
Fgf8	-1.58	0.04309
Fgfr3_UTR	-2.05	0.01167
FKBP1A	-1.63	0.00626
FKSG11	1.58	0.01361
FLJ11040	-1.54	0.0004
FLJ36155	-2.49	0.00001
FOG2	-5.9	0.01187
FOXD3	1.94	0.00238
FOXP4	-2.3	0.00002
FRZB	-2.78	0.00003
FUBP3	1.73	0.00436
GAK	-1.87	0.03287
GCN5L2	-1.71	0.01028
GDF1	-1.8	0.03196
GFI1B	-1.97	0.00905
GPA33	-2.18	0.00208
GSC	1.63	0.03557
GTF2F2	-1.7	0.04336
HAND1	2.34	0.00595
HAND2	-1.65	0.00028
HAS2	-2.05	0.01861
HAS2_UTR	-2.3	0.00037
HES6	1.61	0.00206
HEY2	-1.91	0.00169
HKR3	-4.44	0.02349
HMG1	2.57	0.0053
HMX2	-1.55	0.00169
HOX11	-2.22	0.0124
HOXA10	1.61	0.0197
HOXD8	2.35	0.02479
Hprt1	-1.67	0.04928
Hsp90ab1	1.65	0.02
HUMPPA	1.66	0.0016
IGHMBP2	-3.08	0.0317
IRF6	-1.85	0.04581
ISL1	1.66	0.04853
KLF15	-1.76	0.04501

KLF2	-1.69	0.01722
KLHL14	1.69	0.00775
KRML	-1.74	0.01049
LAF4	-2.05	0.00543
LHX3	1.97	0.00003
LHX8	1.74	0.02232
LMX1A	2.14	0.00075
LOC152485	2.17	0.00399
LOC771525	-1.74	0.00638
MADH9	2.88	0.00496
MED14	1.73	0.01796
MED16	1.87	0.00008
Mfng	-2.39	0.00027
MLLT1	-1.68	0.00761
MLLT4	-1.75	0.02114
MLLT7	1.83	0.00015
MSX2	-2.39	0.00367
MYC	-2.64	0.01802
MYH9	-2.15	0.00664
MYNN	-2.11	0.00052
MYT1	-1.55	0.02223
NAB1	-2.55	0.00014
NFE2L1	-1.79	0.03015
NKRF	1.69	0.00838
NKX2-5	2.05	0.00246
NKX6-2	-3.36	0.02093
Notch1	-1.85	0.00001
Notch2	-1.82	0.00121
NRP1	-2.36	0.02026
NUCKS	-2.12	0.01804
Otog	-1.83	0.04318
p21	-3.37	0.02447
P2ry4	-1.84	0.01216
p300/CBP	-2.1	0.03698
PARD3	1.75	0.00264
PAX6	-1.87	0.00107
PCQAP	1.66	0.03955
PGR	1.92	0.03528
PITX3	1.71	0.01013
PLRG1	1.54	0.04161
PME-1	2.33	0.00008
POU4F2	-1.91	0.00753
PPARBP	-3.32	0.00017
PRDM15	-1.65	0.00047
PRDM16	-2.62	0.00042
PRDM5	-1.67	0.00414
PSIP1	1.64	0.00228
PTX3	-1.52	0.03467
RBPJL	-1.97	0.00297
RELB	-2	0.00771

RFX5	1.59	0.00692
RIC3	-1.74	0.00948
RIP60	2.07	0.00136
Rora	-1.74	0.00671
RYBP	-1.81	0.00201
SATB2	-1.79	0.00136
SHH	1.71	0.00549
SIX1	-2.3	0.00239
SIX6	-1.71	0.0363
SKP1	1.82	0.00431
Slc18a1	1.57	0.02583
SMARCC1	-1.87	0.04588
Smo	-1.78	0.01981
SON	2.05	0.00015
SOX10	-2.87	0.00012
SOX13	-1.63	0.03549
SOX8	1.61	0.0491
SPOP	2.15	0.04223
SPRY4	-2.05	0.01979
SRF	-2.63	0.02924
STT3A	-1.93	0.01513
SUB1	-1.86	0.03622
TAF4	-2.77	0.01191
TAL2	-2.29	0.03779
TBX2	-1.58	0.00274
TCEB1	-3.22	0.01058
TCF15	2.14	0.00413
TCF7	-2.17	0.03236
TFAP2A	-3	0.0001
TLX3	1.87	0.00308
Tnf	-1.64	0.03914
TP63	1.68	0.03256
TSC22	-2.59	0.00311
USF2	2.5	0.02211
VSX	-2.04	0.0077
Wnt16	-3.07	0.02395
Wnt4	-2.27	0.00885
Wnt6	-2.04	0.00001
Wnt7b	-1.62	0.00598
Wnt9a	-1.54	0.03195
Wnt9b	-2.59	0.00007
ZDHHC17	1.7	0.02356
ZFP276	-1.91	0.02169
ZNF238	1.97	0.00991

Supplemental Table S9. Average fold changes in BTAF1 siRNA treatments relative to GFP siRNA treated controls. All fold changes > 1.3 and p-value < 0.05.

Gene	Average fold	P-value
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	change		
ARNTL	-1.66	0.02824	
ASCL1	1.47	0.00156	
Atp1b2	-1.31	0.03605	
Atp2b2	-1.31	0.02807	
BANP	-1.32	0.02394	
BATF3	-1.38	0.027	
BC052269	-1.47	0.04729	
Bmp3	-1.35	0.02365	
Bmp4	1.79	0.02849	
BRD1	3.7	0.0167	
BRN-3A	-1.46	0.00223	
BTAF1	-1.57	0.00185	
Calr	-1.3	0.00171	
CART1	1.43	0.02321	
CBX4	-1.49	0.00962	
CDK2	10.03	0.01323	
CEBPB	-1.34	0.0447	
CEBPG	-1.5	0.01825	
CNNM4	-1.44	0.00103	
COL5A1	-1.38	0.01428	
CSRP2	-1.38	0.0422	
CTNNB1	-2.1	0.00012	
CUTL1	-1.38	0.01135	
Dlx5- exon2	-1.48	0.02285	
ENG	-1.3	0.01444	
EYA4	-1.32	0.03376	
EZH2	-1.43	0.02372	
FBXO3	-1.43	0.00142	
FKHL18	-1.68	0.03499	
FLJ11040	-1.97	0.01685	
FOSL2	-1.3	0.00931	
FOXA2	-1.5	0.00823	
FOXN4	-1.5	0.00189	
FOXP1	4.69	0.01984	
GCN5L2	-1.59	0.00177	
GTF3C1	-1.7	0.00566	
Gusb	-1.48	0.02619	
HDAC1	1.35	0.01932	
HDAC2	-1.32	0.02186	
HEYL	1.4	0.0202	
HMG1	1.45	0.00358	
HOXB13	-1.76	0.0054	
HPCA	-1.76	0.02741	
HUMPPA	1.58	0.00997	
ID2	-2.41	0.042	
ID3	4.49	0.01481	
IFT172	-1.36	0.02401	
IVNS1ABP	2.28	0.00241	
KCNIP4	1.38	0.02154	

KLF15	-1.34	0.02901
KLF7	-1.55	0.00865
KLHL1	-1.59	0.02272
KRML	-1.45	0.0245
LHX5	-1.54	0.01711
LHX6	-1.4	0.01723
LRP5	1.4	0.00675
LRP5_2	-1.44	0.02223
MADH5	2.2	0.01321
Mfng	-1.31	0.0017
MLL3	-1.38	0.03292
MNT	-1.42	0.0323
MSX1	-1.33	0.0036
MYO5A	-1.56	0.00054
MYT1L	1.87	0.02871
NCOA2	1.68	0.03353
NFE2L2	7.41	0.01504
NFKBIA	-1.54	0.01004
NNF1B	-1.91	0.00278
Nog	-1.34	0.00164
NR2F2	-1.75	0.00481
NR5A2	1.9	0.04283
NUP153	1.39	0.01928
OVOL2	-1.5	0.01145
PCGF3	-1.38	0.00028
PCMT1	5.63	0.01401
PCSK6	-1.35	0.00244
PDX1	-1.37	0.03395
Penk1	1.44	0.00942
PGR	1.41	0.0009
PPIB	-1.6	0.01093
PRDM5	1.35	0.02742
PROX1	-1.36	0.01243
PSIP1	1.96	0.00498
RALGDS	-1.46	0.01745
RCOR1	2.25	0.0366
RIP60	1.67	0.02657
RIPX	-1.38	0.04041
RUNX1T1	2.37	0.03541
RUNX2	-1.66	0.01747
RXR	-1.38	0.00795
S100a9	-1.47	0.02575
SAFB	-1.37	0.02966
SATB2	-1.3	0.0043
SCML4	-1.44	0.03003
SNW1	-1.31	0.00545
SOX1	1.73	0.01092
SOX10	-1.45	0.00293
SOX9	-1.74	0.03898
SRF	-1.38	0.01785

TAF2D	-1.35	0.03415
TAL2	-1.48	0.01534
TBP	1.85	0.03976
TBX22	1.61	0.0094
TCEB1	-1.92	0.04614
TCF1	1.31	0.01141
TCF7L2	-1.63	0.01806
TEAD3	-1.34	0.02092
THRA	-1.33	0.03067
Wnt1	-1.39	0.00306
Wnt16	-1.67	0.00082
Wnt5a	-1.51	0.00442
Wnt7b	-1.42	0.00275
Wnt9b	-1.39	0.02715
ZBTB20	-1.64	0.02039
ZFP276	-1.71	0.04442
ZFX	-1.5	0.0368
ZHX1	-1.58	0.03711
ZNF384	-1.34	0.02363
ZNF703	-1.38	0.01542

Supplemental Table S10. Primer sequences for *in vitro* dicer products and chemically synthesized dicer substrate RNA (DsiRNA) target sequences.

Accession	siRNA Target	Forward Primer	Reverse Primer
NM_206859	CEBPG	AGCAAGCAGGGAAAGAAGAA	TTTGAGCTGGGTGACCCTTT
X60063	JUND	ATCGATATGGACACGCAGGA	CTGAGCACCTTCTGCTTGAG
XM_421689	TAF172	TCGAAAACCTTGGAGAACTATGG	TCCCCCGTGAGACAGGTGAC
NM_001012897	LRP5	CTTATTCAGGGCCATCTGGA	AGCAGCACAGCCACATCTAA
XM_001237023	RARA	TCCGCAATGACCGCAATAAGAAG	GTCGGCGATGGTGAGCGTGGTGAA
NM_204793	PAX2	CACCTCTGCTAACCCAGACC	AGTGCCACCATCTCTGCTCT
NM_204424	PAX5	GGG AGC ATT AAG CCT GGA GT	GTG TCG TTA TCG CAC ACT CG
XM_425393	CUTL1	GCAGCACTCACCGCCCCTTTCGTC	GGCGTCCCCTTCCGTGGCAGAGTT
NM_204590	ID1	ACATGAAGGGCTGCTACTCG	TCTCTCTCAGCGGCACAGTA
NM_204269	PAX3	CTCAGCCTCTCCCTCCAAG	CAGGGTTCATGGGATTTGAG
NM_205065	PAX7	AGCAACCGACGAGCAAGAT	AAATGGTGGTGGTTGGGTAG
NM_204256	CDKN1B	GGAGGCGCGGCAGTCGGAGTA	CGTCGGCGGCAGGTCTTTTC
NM_204642	CBX4	CAAACGGGAGCAAGAATCAC	AGGAGGAGGAGGCTGAAGG
XM_418879	EZH2	TGCAATCGCCAGACTAATTG	TTTTGGCATTCTGAGCTGCA
NM_001031031	BCL11A	TGTCACCAGCACACCTGTTT	TGGAAGTGGAAACAGCAACA
NM_001031596	TRIP15	CAAAGGGCAGTTAATGACCAG	TTGCTGCTTGAACCTAAGTGA
NM_205081	CTNNB1	CTGCGGGTGTACTTTGTGAA	CTAGGATCATCTGGGCGGTA
NM_003920	TIME	GAGAGCGTGAAGGATCTGAT	GAACGCCTCTTTGTACGCCT
NM_001006457	PPARGC1	GTGTGCTGAGACCACTGCAT	CAGCCAGTACAGCAATGAGC

Accession	siRNA Target	siRNA Source	Target Sequence
NM_206859	CEBPG	Ambion	AATAAGTGCAGATCGAAATCC
X60063	JUND	IDT	CCATGTTCCCTGAATGCGATATATGCG
XM_421689	BTA1F1	IDT	ATTGTAATCTTGCTCTCTCTGTAGGAG
NM_001012897	LRP5	IDT	ATCCACTTCATCAGATTTATCTTGCA
NM_204536	RARA	IDT	TGCTGATGAAGATCACAGAT
NM_204793	PAX2	IDT	TAACAGAAAGTCACTTGGTCCTTCTCT
NM_204424	PAX5	IDT	CAGGAGTCGTTGTACGTTGAGTACTGT
NM_204783	WNT4	IDT	TCC CTG CAG CGT CTG GGT CGT TTG CTC
NM_204783	WNT4	IDT	GTT CAA GAC GTG CTG GAA AGC CAT G
XM_425393	CUX1	IDT	ACATTCATCTGTTACTGATT
NM_204643	CBX3	IDT	TGCAAACAATTATTGTGCTTCATCTTC
NM_001005848	HES1 (HRY)	Ambion	TGAGTGCATGAACGAGGTG
XM_419932	MYT1L	IDT	ACATCTAATTGGCTCTTGGTCTTCTTT
NM_205081	CTNNB1	IDT	GTCGAGGAGTAATAATACAAATGGATT
NM_205081	CTNNB1	IDT	GAGGACCTACACTTATGAGAACTATT
NM_205081	CTNNB1	IDT	AAACTGTTGAATGATGAGGACCAGGTG