

Supplemental Table 1.

REAGENT/RESOURCE	SOURCE	IDENTIFIER
Slug (C19G7)	CST	Cat# 9585, RRID:AB 2239535
SNAI1 (L70G2)	CST	Cat# 3895s, RRID:AB 2191759
TWIST1 (3E11)	Callbiochem	Cat# DR1087, RRID:AB 10696455
PUMA	CST	Cat# 4976, RRID:AB 2064551
BIM (C34C5)	CST	Cat# 2933, RRID:AB 1030947
p53 (1C12)	CST	Cat# 2524, RRID:AB 331743
ZEB1 (D80D3)	CST	Cat# 3396, RRID:AB 1904164
phospho-CHEK1 (Ser345)	CST	Cat# 2341, RRID:AB 330023
CHEK1 (2G1D5)	CST	Cat# 2360, RRID:AB 2080320
phospho (Thr68) CHEK2	CST	Cat# 2661, RRID:AB 331479
CHEK2	CST	Cat# 2662, RRID:AB 2080793
BAX	CST	Cat# 2772, RRID:AB 10695870
BID (3C5)	CST	Cat# 8762, RRID:AB 11217434
BCL2 (124)	CST	Cat# 15071, RRID:AB 2744528
BCL-XL (54H6)	CST	Cat# 2764, RRID:AB 2228008
MCL-1 (D5V5L)	CST	Cat# 39224, RRID:AB 2799149
NOXA (114C307)	EMD	Cat# OP180, RRID:AB 2268468
BMF (E5U2J)	CST	Cat# 50542, RRID:AB 2892182
Flag	Sigma	Cat# F7425, RRID:AB 439687
PARP	CST	Cat# 9542, RRID:AB 2160739
Cleaved PARP (Asp214) (D64E10)	CST	Cat# 5625, RRID:AB 10699459
p16 INK4A (D7C1M)	CST	Cat# 80772, RRID:AB 2799960
p21 Waf1/Cip1 (DCS60)	CST	Cat# 2946, RRID:AB 2260325
Histone γ H2AX, phospho (Ser139)	Millipore	Cat# 05-636, RRID:AB 309864
α -Tubulin (DM1A)	Abcam	Cat# Ab7291, RRID:AB 2241126
β -Tubulin	Abcam	Cat# Ab6046, RRID:AB 2210370
HRP anti-rabbit	CST	Cat# 7074, RRID:AB 2099233
HRP anti-mouse	GE Healthcare	Cat# NA93IV, RRID:AB 772210
Ki67	Biocare Medical	Cat# CRM325, RRID:AB 2721189
Myogenin	Dako	Cat# M3559, RRID:AB 2250893
Myosin Heavy Chain (MF20)	DSHB	Cat# MF 20, RRID:AB 2147781
MEF2C (D80C1)	CST	Cat# 5030, RRID:AB 10548759
Alexa Flour 488 goat anti-mouse	Invitrogen	Cat# A11029, RRID:AB 138404
Alexa Fluor 594 goat anti-rabbit	Invitrogen	Cat# A11011, RRID:AB 143157

Supplemental Table 2.

OLIGONUCLEOTIDES	
GAPDH Fwd	GGTGGTCTCCTCTGACTTCAACA
GAPDH Rev	GTTGCTGTAGCCAAATTCGTTGT
SNAI2_Fwd	CAGACCCTGGTTGCTTCAA
SNAI2_Reverse	TGACCTGTCTGCAAATGCTC
23-Fwd hBIM	TAAGTTCTGAGTGTGACCGAGA
118-Rev hBIM	GCTCTGTCTGTAGGGAGGTAGG
CDKN1A Forward	TGTCCGTCAGAACCCATGC
CDKN1A Reverse	AAAGTCGAAGTCCATCGCTC
69-Fwd DAP	AATGCGAATTGTGCAGAAACAC
149-Rev DAP	GGGCTTTCCCATTCCTGGTC
661-Fwd FDXR	CTGAGGCAGAGTCGAGTGAAG
745-Rev FDXR	CCCGAAGCTCCTTAATGGTGA
492-Fwd F2R	CGGCAGTGATTGGCAGTTTG
577-Rev F2R	TGAGCAAGATAGAGGCGTACA
390-Fwd PDGFRB	TGATGCCGAGGA ACTATTCATCT
492-Rev PDGFRB	TTTCTTCTCGTGCAGTGTCAC
104-Fwd CLU	CCAATCAGGGAAGTAAGTACGTC
204-Rev CLU	CTTGCGCTCTTCGTTTGTTTT
183-Fwd IER3	CAGCCGCAGGGTTCTCTAC
294-Rev IER3	GATCTGGCAGAAGACGATGGT
576-Fwd TAP1	CTGGGGAAGTCACCCTACC
662-Rev TAP1	CAGAGGCTCCCGAGTTTGTG
Hs_sgSnai1-1 top	caccgAGAGCGCGGCATAGTGGTCG
Hs_sgSnai1-1 bottom	aaacCGACCACTATGCCGCGCTCTc
Hs_sgSnai1-2 top	caccgGCCTAACTACAGCGAGCTGC
Hs_sgSnai1-2 bottom	aaacGCAGCTCGCTGTAGTTAGGCc
BCL2L11 p1 Fwd	CACTTGGGTGGGGAGTTGTG
BCL2L11 p1 Rev	TTTGGGTGACCCCTTTGACC
BCL2L11 p2 Fwd	CAGCAGGGCAGCACTGTTTC
BCL2L11 p2 Rev	GCAGGGCACACATGGGTAAT
NEG_CTL Fwd	AGGGAGTTTTTATGAGCATTCCA
NEG_CTL Rev	AGCAGGTAAAGGTCCATATTCA



Supplemental Table 3.

RMS Cell Line	Oncogene	TP53 Status
ERMS		
RD	Q61H mutation of NRAS (50), 51-hyperdiploid, MYC amplification (22)	R248W mutation (35)
Rh18	Amplification of MDM2 (22)	Wild-type (51,52)
JR-1	Near tetraploid (22), Q61L mutation of NRAS (Sanger sequencing)	R248W mutation (52)
Rh36	Q61K mutation of HRAS (53)	Wild-type (52)
SMS-CTR	Q61K mutation of HRAS (50); Hypertriploid (22)	4bp deletion at codons 219/220, ΔNt 1236-1239 (35,52)
ARMS		
Rh30	PAX3-FOXO1 fusion (22)	R273C mutation; heterozygous (51,52)
Rh41	t(2;13) (22)	ΔNt 1001 – 1013 (52)
Rh28	Near tetraploid (22)	Wild-type (52)

Supplemental Table 4. Correlation between *SNAI2* and pro-apoptotic genes in RMS.

Gene	Alternatively spliced Transcript ID	Pearson Correlation	P-value	Protein (Amino acid)	Uniprot family and/or domains	Significance
<i>BCL2L11</i>	ENST00000438054	-0.321	0.000139	96	BIM	***
<i>BCL2L11</i>	ENST00000308659	-0.148	0.084985	138	BH3	
<i>BCL2L11</i>	ENST00000393252	-0.052	0.551543	71	BIM	
<i>BCL2L11</i>	ENST00000405953	-0.047	0.585795	112	BH3	
<i>BCL2L11</i>	ENST00000432179	0.109	0.207174	122	BIM	
<i>BCL2L11</i>	ENST00000337565	0.128	0.136278	112	BH3	
<i>BCL2L11</i>	ENST00000393256	0.212	0.013071	198	BH3	*
<i>BMF</i>	ENST00000561360	-0.052	0.549257	184	BH3	
<i>BMF</i>	ENST00000561282	0.028	0.748620	184	BH3	
<i>BMF</i>	ENST00000559701	0.044	0.613513	129	BH3	
<i>BMF</i>	ENST00000431415	0.064	0.458153	163	BH3	
<i>BMF</i>	ENST00000557870	0.095	0.272875	61	BMF	
<i>BMF</i>	ENST00000354670	0.166	0.053532	184	BH3	
<i>BMF</i>	ENST00000558774	0.170	0.047850	129	BH3	*
<i>BMF</i>	ENST00000560430	0.192	0.025198	13	none	*
<i>BMF</i>	ENST00000397573	0.216	0.011625	184	BH3	*
<i>BBC3</i>	ENST00000300880	-0.053	0.541170	101	BBC3	
<i>BBC3</i>	ENST00000449228	0.108	0.209177	261	BBC3	
<i>BBC3</i>	ENST00000439096	0.212	0.013187	193	BH3	*
<i>BBC3</i>	ENST00000341983	0.213	0.012902	131	BH3	*
<i>BAX</i>	ENST00000391871	0.055	0.521069	175	BAX	
<i>BAX</i>	ENST00000539787	0.060	0.488773	140	BAX	
<i>BAX</i>	ENST00000354470	0.139	0.107790	143	BH3, BH1, BH2	
<i>BAX</i>	ENST00000415969	0.165	0.054501	179	BH3, BH1, BH2	
<i>BAX</i>	ENST00000293288	0.185	0.031002	218	BH3, BH1, BH2	*
<i>BAX</i>	ENST00000345358	0.214	0.012513	192	BH3, BH1, BH2	*
<i>BAX</i>	ENST00000506183	0.248	0.003534	126	BAX	**
<i>BAD</i>	ENST00000544785	-0.119	0.166228	157	BAD	
<i>BAD</i>	ENST00000493798	0.016	0.854734	64	BAD	
<i>BAD</i>	ENST00000394531	0.063	0.466894	163	BAD	
<i>BAD</i>	ENST00000492141	0.089	0.303797	51	BAD	
<i>BAD</i>	ENST00000394532	0.133	0.121317	168	BAD	
<i>BAD</i>	ENST00000309032	0.253	0.002998	168	BAD	**
<i>HRK</i>	ENST00000257572	0.100	0.248959	91	BH3	
<i>HRK</i>	ENST00000550505	0.102	0.237747	18	none	
<i>BID</i>	ENST00000342111	-0.137	0.112815	137	BH3	
<i>BID</i>	ENST00000317361	-0.112	0.196201	241	BH3	
<i>BID</i>	ENST00000551952	-0.013	0.880903	195	BH3	
<i>BID</i>	ENST00000399767	0.065	0.454731	99	BH3	
<i>BID</i>	ENST00000399765	0.183	0.033199	99	BH3	*
<i>PMAIP1</i>	ENST00000316660	-0.190	0.026852	54	BH3	*
<i>PMAIP1</i>	ENST00000269518	-0.186	0.030234	136	BH3	*



*p<0.05, **p<0.005, ***p<0.0005

	Blue: Positively Correlated, Red: Negatively Correlated
	Significance <0.05

Supplemental Table 5. Correlation between *SNAI2* and anti-apoptotic genes in RMS.

Gene	Alternatively spliced Transcript ID	Pearson Correlation	P-value	Protein (Amino acid)	Uniprot family and/or domains	Significance
<i>BCL2</i>	ENST00000333681	-0.393	0.000002	239	BH4, BH3, BH1, BH2	***
<i>BCL2</i>	ENST00000590515	-0.130	0.130980	46	none	
<i>BCL2</i>	ENST00000398117	-0.025	0.771852	239	BH4, BH3, BH1, BH2	
<i>BCL2</i>	ENST00000589955	0.061	0.482746	205	BH4, BH3, BH1, BH2	
<i>BCL2L1</i>	ENST00000434194	-0.246	0.003938	233	BH4	**
<i>BCL2L1</i>	ENST00000439267	-0.174	0.043232	233	BH4	*
<i>BCL2L1</i>	ENST00000422920	-0.104	0.227766	170	BH4	
<i>BCL2L1</i>	ENST00000450273	-0.095	0.272018	307	BH4	
<i>BCL2L1</i>	ENST00000307677	-0.078	0.367356	233	BH4, BH3, BH1, BH2	
<i>BCL2L1</i>	ENST00000376062	-0.072	0.406773	233	BH4, BH3, BH1, BH2	
<i>BCL2L1</i>	ENST00000456404	-0.065	0.453711	233	BH4	
<i>BCL2L1</i>	ENST00000420488	-0.034	0.694000	233	BH4	
<i>BCL2L1</i>	ENST00000376055	0.070	0.418254	170	BH4, BH3, BH1, BH2	
<i>MCL1</i>	ENST00000307940	0.121694088	0.158145	271	BH3, BH1, BH2	
<i>MCL1</i>	ENST00000369026	0.262012971	0.002060	350	BH3, BH1, BH2	**

*p<0.05, **p<0.005, ***p<0.0005

	Blue: Positively Correlated, Red: Negatively Correlated
	Significance <0.05