

BRMS1 interacts with LSD1/CoREST complex

Table S1. Primers, shRNA and siRNA sequences used in this study

qChIP primers used in this study		
Gene	Strand	Sequence
Vimentin	F	CCGAATCTGAACACTCC
Vimentin	R	CACGGTGATTTGTCTGG
INSIG2	F	CTTATTGACAGCAGGAACCG
INSIG2	R	CTCCTCCACTCCCACAAC
KLK11	F	GACGTGGCTTTGTTCTAATA
KLK11	R	TCCTCCAGTTTCCCTTCA
MRPL33	F	GGGTCTAATGCAGGTGGTT
MRPL33	R	TCGTTCCCTCGGTTTCTCA
COL5A2	F	CTGTTATTAAGCCCCATCTATG
COL5A2	R	ATGCTGCCTCCACTTCTT
OLFML3	F	TCCTGCTTCCCTCCCTTCA
OLFML3	R	GCAAACGCCATTCTGT
SLC1A1	F	GGGCGGGACTCAGGGTTC
SLC1A1	R	GGCCAACCAGCGAGGAAG
GAPDH	F	TACTAGCGGTTTACGGGCG
GAPDH	R	TCGAACAGGAGGAGCAGAGAGCGA
Real-time quantitative primers		
Gene	Strand	Sequence
BRMS1	F	GCTAAAGGAGAAGTTGTTTCAG
BRMS1	R	GCTCACATTCGACTTATTCC
LSD1	F	GAATTTGCTAATGCCACACC
LSD1	R	GTATTCACAGCTATCACTTCA
INSIG2	F	CAGACATCTAGGAGAACCAC
INSIG2	R	CGAAATCCACTTTAGCACTG
KLK11	F	GCCAAACATCACCATCATTGAG
KLK11	R	TTTGCACTTTTCGTGTAGAC
MRPL33	F	GATCCAGTTGTGAAACAAAGAG
MRPL33	R	AGTGATTCCATGCCATTTCC
COL5A2	F	GTATTCAGCAAACCCATCCA
COL5A2	R	CATAAGCGAACTGAGACCCT
OLFML3	F	ACTGTACGTTTCTTCTACTC
OLFML3	R	GGATCTCAACCTCTAAAGCA
SLC1A1	F	TCATCACCATCAGTATCACGG
SLC1A1	R	TGAAACATCCATCTGCTCCA
Vimentin	F	ATTGAGATTGCCACCTACAG
Vimentin	R	ATCCAGATTAGTTTCCCTCAG
Fibronectin	F	TCAGGCGTCTGTAGAGGCTT
Fibronectin	R	ATGCACATCCTTCGATAAGACTG
E-cadherin	F	GAAATCACATCCTACTGCCC
E-cadherin	R	GTAGCAACTGGAGAACCATTGTC
α -catenin	F	ATGATCCCTGCTTCTGTG
α -catenin	R	GATACCATCTTCCACAACCTTTCAG
GAPAH	F	TCCTCCTGTTTCATCCAAGC
GAPDH	R	TAGTAGCCGGGCCCTACTTT
shRNA and siRNA sequences		
shSCR		TTCTCCGAACGTGTCACGT
shBRMS1 #1		GAGCTCCGAGATGGATGATGA
shBRMS1 #2		GCCCATACATCGGTACATGC
shLSD1 #1		GAGACAGACAATACTTGA
shLSD1 #2		CAATTAGAAGCACCTTATA
VIM siRNA		GAAAGTGTGGCTGCCAAGA

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Table S2. Detailed results of the mass spectrometry analysis

Accession	Description	Score	Coverage	# Proteins	# Unique Peptides	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pI
E9PJF5	Breast cancer metastasis-suppressor 1 (Fragment) OS=Homo sapiens GN=BRMS1 PE=4 SV=1 - [E9PJF5_HUMAN]	550.27	39.75	5	17	17	228	244	28.3	4.74
P08107	Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5 - [HSP71_HUMAN]	524.74	45.09	5	20	31	209	641	70.0	5.66
P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]	155.77	39.47	30	13	13	70	375	41.7	5.48
Q13547	Histone deacetylase 1 OS=Homo sapiens GN=HDAC1 PE=1 SV=1 - [HDAC1_HUMAN]	129.77	36.72	8	10	16	69	482	55.1	5.48
B3KRS5	Histone deacetylase OS=Homo sapiens GN=HDAC2 PE=1 SV=1 - [B3KRS5_HUMAN]	106.95	26.86	17	5	11	58	458	52.0	5.74
Q16531	DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1 - [DDB1_HUMAN]	89.34	22.02	17	20	20	37	1140	126.9	5.26
Q71U36-2	Isoform 2 of Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A - [TBA1A_HUMAN]	80.71	33.17	32	12	12	37	416	46.3	5.08
O60341	Lysine-specific histone demethylase 1A OS=Homo sapiens GN=KDM1A PE=1 SV=2 - [KDM1A_HUMAN]	29.71	11.15	5	8	8	11	852	92.8	6.52
Q9UKL0	REST corepressor 1 OS=Homo sapiens GN=RCOR1 PE=1 SV=1 - [RCOR1_HUMAN]	18.67	12.24	11	6	6	10	482	53.0	7.03
Q96ST3	Paired amphipathic helix protein Sin3a OS=Homo sapiens GN=SIN3A PE=1 SV=2 - [SIN3A_HUMAN]	6.40	2.04	1	3	3	3	1273	145.1	7.25