Table SI. Differentially methylated genes associated with glioma (N=349).

ID	Gene name	adj.P.Val	P-value	t	B	logFC	Sequence
FZD9_E458_F	FZD9	1.26x10^{-12}	1.09x10^{-14}	9.1509	22.9269	0.7041	GCGGCTGCCGAGCTAGCGGAGTTCG[CG]CCGCTGGTGCAGTACGGCTGCC
HOXA11_P698_F	HOXA11	7.30x10^{-06}	3.01x10^{-07}	5.5147	6.0870	0.5690	TCATTCATGGTCACTTCCGAAG[CG]CTTTAGTGCCTTCCGTCCCTAAACC
TES_P182_F	TES	1.77x10^{-08}	2.82x10^{-10}	7.0532	12.9087	0.5577	GGCCCGTGGACGCCCAGAGAATCCCTT[CG]GAGACCAGGTCAGGGTCACTGAG
HOXA9_E252_R	HOXA9	3.33x10^{-04}	2.33x10^{-05}	4.4514	1.8825	0.5375	TGGGTTCCACGAGGCGCCAAACACCGT[CG]CCTTGGACTGGAAGCTGCACG
CD81_P272_R	CD81	1.45x10^{-07}	3.18x10^{-09}	6.5334	10.5300	0.5188	ACGCTGCATGCCTGTCCTCAGGCG[CG]GCCCTGCTGCCACCCCCTTGGG
TNFRSF10A_P171_F	TNFRSF10A	2.54x10^{-07}	6.07x10^{-09}	6.3925	9.8968	0.5030	TCGTTTTGCCACTTGGTCCCAG[CG]CCAGGCTTCTCGGTCGGGAGTTGACCT
TAL1_P594_F	TAL1	9.71x10^{-04}	9.10x10^{-05}	4.0883	0.5783	0.4672	TCACACATCGAAGTCTTGGATTAACTG[CG]AAGGCCTCCTTCTATTTGCCGCGGCTT
FLT3_E326_R	FLT3	3.36x10^{-03}	4.16x10^{-04}	3.6589	-0.8627	0.4583	CGCGGCCCGAGCCAGAGGAGAGACTT[CG]GAGAAGAGGGAAGAGGAC
AHR_P166_R	AHR	1.18x10^{-02}	2.08x10^{-03}	3.1656	-2.3667	0.4569	TTGCCTATGCACGAAGATGGCTACCGG[CG]GGGGGGGCGTCCTTACGTCCTACGTC
MEST_E150_F	MEST	5.63x10^{-04}	4.49x10^{-05}	4.2785	1.2523	0.4343	TCAGGAAGCGCATGCGCAACCGGTTCTC[CG]AAACATGGAGTCCTGTAGGCAAGG
IRAK3_E130_F	IRAK3	8.27x10^{-03}	1.29x10^{-03}	3.3171	-1.9228	0.4338	GCACACGCTGCTGTTCGACCTGCCGCCCG[CG]CTGCTCGGAGAGCTCTGCGCT
PENK_E26_F	PENK	4.33x10^{-03}	5.93x10^{-04}	3.5542	-1.1959	0.4330	TTCGAGCCTGCCTGGGCGCAGAA[CG]GGGTCCCTCGGCAGGACCCTC
MOS_E60_R	MOS	2.75x10^{-03}	3.10x10^{-04}	3.7441	-0.5860	0.4222	GAGGGACTGCTGCAGGGCCGCG[CG]TCCACCGATGGGGAAAACTCG
MYCL2_P19_F	MYCL2	6.35x10^{-03}	9.49x10^{-04}	3.4121	-1.6363	0.4182	GGAACTAGTCTGCTCCAGGTGGCAAGCTG[CG]TGAGCAAGCAAGCCAACATGGACCGCG
NEFL_P209_R	NEFL	9.76x10^{-03}	1.61x10^{-03}	3.2466	-2.1315	0.4178	GGGGCAGCGCGCTGCTGCAGCCAAGG[CG]AGGATTCTGCGCAAAAGGGA
NPY_P295_F	NPY	5.77x10^{-03}	8.35x10^{-04}	3.4511	-1.5170	0.3954	GAAGGAAAGAAGGAAAGCAGGGAT[CG]GGCACTGCCCGAGGGCAGATACT
GATA6_P726_F	GATA6	1.10x10^{-02}	1.87x10^{-03}	3.1998	-2.2681	0.3928	GGGACATCAAAAGTTGGAGAGCGTCCT[CG]GACACGACTGATGTGGAAGCC
TNFRSF10D_E27_F	TNFRSF10D	1.31x10^{-02}	2.38x10^{-03}	3.1224	-2.4901	0.3849	CAGAAATCGTCCCCGTAGTTTGTG[CG]CGTGCAAAGGTTCTCGCAGCTACACTGCCA
DSC2_E90_F	DSC2	1.21x10^{-02}	2.17x10^{-03}	3.1527	-2.4038	0.3824	CTGCGCAAGGTGTTTCTCACCAG[CG]GACGCCACCTATAAGGCCCATCTC
HOXA5_E187_F	HOXA5	5.79x10^{-03}	8.43x10^{-04}	3.4481	-1.5259	0.3789	CATTGTAGCCGTAGCCGTACCTGC[CG]GAGTGCATGCTCGCCGAGTCCCTGAATT
ALOX12_E85_R	ALOX12	1.32x10^{-02}	2.43x10^{-03}	3.1148	-2.5117	0.3712	GGGGCCTGGCTCTTCTCCGGGT[CG]TACAACCGCGTGCAGCTTTGGCTGGTCGG
ISL1_P379_F	ISL1	1.64x10^{-02}	3.49x10^{-03}	2.9961	-2.8434	0.3687	GCGGGGACCCCAGGAGCGCAGGG[CG]GAGGAGCAGCGCCACAGGAGGC
TFAP2C_P765_F	TFAP2C	2.34x10^{-02}	5.42x10^{-03}	2.8464	-3.2461	0.3683	GGCCCGCCAGAGGCAGCTGCAGAGCCGG[CG]TTCCGCAGGGCAGGGCAGGG
PCTK1_E77_R	PCTK1	2.27x10^{-07}	5.13x10^{-09}	6.4295	10.0626	0.3567	ATAACTCTTCAGGCTGCCTCTCCT[CG]AAAAGTCATCTTCTCGCGAACCTTTAA
GFI1_P45_R	GFI1	1.39x10^{-02}	2.66x10^{-03}	3.0864	-2.5921	0.3540	GCTCTCGACCGGGTCCGCTCAGCCTT[CG]ACTAATTTCCGGTGGTCGGA
DIO3_E230_R	DIO3	4.30x10^{-07}	1.18x10^{-08}	6.2476	9.2509	0.3489	GGCCTGCAGCCACCATGCTC[CG]CTCCCTGCTGCTTCACTCCTTGAGGCTC
DDIT3_P1313_R	DDIT3	1.71x10^{-03}	1.75x10^{-04}	3.9067	-0.0452	0.3427	GGGTCGAGATTTACAGCGGAGTCTCATCC[CG]GGACGTGTGAGTGCACTTCAGC
HTR1B_P107_F	HTR1B	5.24x10^{-06}	1.99x10^{-07}	5.6107	6.4908	0.3423	GGTTTGTCCCCAGTTGATAGTTC[CG]TGAGTTCCTCAATTATTCCTCCGC
IPF1_P750_F	IPF1	4.12x10^{-04}	3.09x10^{-05}	4.3769	1.6090	0.3338	CCTCGCTGTATTGGGAAGCTACGTTC[CG]GGCTGGCCAAATGGGCCC
TUSC3_E29_R	TUSC3	3.55x10^{-02}	9.93x10^{-03}	2.6310	-3.7948	0.3269	CAGGTCTTCTCCCGGTGAAC[CG]GATGCTCTGTCAGTCTCCTCCTCTGCGTC
BCR_P346_F	BCR	7.91x10^{-03}	1.21x10^{-03}	3.3372	-1.8627	0.3167	CTCTGACACGACGACTGGGCAGTGC[CG]GTGACGCTTATGGCACTGCGG
ZP3_E90_F	ZP3	3.48x10^{-02}	9.61x10^{-03}	2.6433	-3.7645	0.3107	CGCAGTGCACGTTGTCCAGCAGGATGTGTC[CG]GTGCCATAGCCGAAGAAGGCGTT
DNAJC15_P65_F	DNAJC15	1.22x10^{-05}	5.35x10^{-07}	5.3799	5.5263	0.2996	GTGGTAGAACTGTGGCATTAAACAGAAGTG[CG]AACAGAAGTTGAGAGTGGGAAG
PALM2-AKAP2_P420_R	PALM2-AKAP2	4.29x10^{-02}	1.31x10^{-02}	2.5287	-4.0424	0.2970	GGGTCCCACATTCGGTCAGA[CG]CCCCTCTCCACTGGCATCTGCCC
PRKCDBP_E206_F	PRKCDBP	2.85x10^{-02}	7.16x10^{-03}	2.7486	-3.4997	0.2905	GCCCAGGCCGCTCTGGATGCGG[CG]CACGGACCCTGCCAGGCCTCC
MYOD1_E156_F	MYOD1	2.94x10^{-02}	7.41x10^{-03}	2.7366	-3.5304	0.2827	TGGGCGAAGCCAGGACCGTGCCG[CG]CCACCGCCAGGATATGGAGCTACTGTC

Table SI. Continued.

ID	Gene name	adj.P.Val	P-value	t	B	logFC	Sequence
ICA1_P72_R	ICA1	4.29x10^{-02}	1.31x10^{-02}	2.5290	-4.0418	0.2791	CTCCGGCAGGTGTTCCACGTGGCCATAG[CG]TTTGCGTCACAATGACCTGGCGG
IGFBP1_P12_R	IGFBP1	3.99x10^{-02}	1.16x10^{-02}	2.5733	-3.9356	0.2723	CCTCCCACCAGCGGTTTG[CG]TAGGGCCTTGGGTGCACTAGCAAAACAAAC
RARA_P176_R	RARA	4.13x10^{-02}	1.24x10^{-02}	2.5486	-3.9950	0.2686	GAACTGTTCCTGTCCCCAGC[CG]ATGACCAGACGCCCATCTTTCTTC
WRN_P969_F	WRN	2.53x10^{-02}	6.11x10^{-03}	2.8045	-3.3557	0.2612	TTTCAGGACACTGTGAGGATGCTCTT[CG]GACCCCACCGAGACTGGTGG
TERT_P360_R	TERT	3.93x10^{-02}	1.13x10^{-02}	2.5828	-3.9125	0.2570	CGAGGGCCCCAGCGGAGAGAGGT[CG]AATCGGCCTAGGCTGTGGG
RARRES1_P426_R	RARRES1	2.39x10^{-02}	5.60x10^{-03}	2.8349	-3.2763	0.2465	CGGAGAAAGGGGCAGGCCGCAG[CG]GGCATTGATGGGGCTCCT
PGF_P320_F	PGF	3.65x10^{-02}	1.03x10^{-02}	2.6173	-3.8286	0.2408	CCAGGAGTCCAGCGTCAGC[CG]TCAAGGCTCATGATCTAACCGCCTCTGC
EFNB3_E17_R	EFNB3	1.20x10^{-06}	3.83x10^{-08}	5.9849	8.0960	0.2397	GACTGGTTTCCTCCCTTAGCC[CG]CTGCCCTCAATCCCAGCGAGGC
RAN_P581_R	RAN	4.26x10^{-02}	1.29x10^{-02}	2.5338	-4.0304	0.2393	GGGTGCATCCCTCTCTGGTTCCT[CG]CTCTCCAACTGGCCCTGGTCCTGGGG
HOXB2_P488_R	HOXB2	1.15x10^{-03}	1.10x10^{-04}	4.0358	0.3959	0.2385	AGGAAAAGATGAGTGAGGATCTCCG[CG]TTGGAGGAAGAGGGAGTC
GDF10_E39_F	GDF10	2.75x10^{-08}	4.58x10^{-10}	6.9503	12.4333	0.2316	GACCTCTGGGGCTGCAGCTGACAGGGT[CG]TCCCTGGCCCGGCTGCCGTGTGCGTGC
ELL_P693_F	ELL	2.64x10^{-02}	6.46x10^{-03}	2.7852	-3.4057	0.2305	ATCCCCACAGTCCCTGAG[CG]ATGGTGCAGTCCAGCTTCATTTTCCTATT
F2R_P839_F	F2R	1.49x10^{-02}	2.94x10^{-03}	3.0530	-2.6856	0.2278	CCAGGTAATCCGGAGGCTGGGG[CG]AAAGGGTGGCCTGAGCCAGG
PLSCR3_P751_R	PLSCR3	2.31x10^{-02}	5.32x10^{-03}	2.8530	-3.2285	0.2277	GTGGAAGCTGCGATTTGGCCCCA[CG]AGCAGCGAGGAGTCCACCGAGACATTT
BRCA1_P835_R	BRCA1	3.41x10^{-03}	4.26x10^{-04}	3.6517	-0.8857	0.2251	GCAATCGCCACCAGTCAATGGGGTGGT[CG]TTTTGAGGGACAAGTGGTAAGA
SNCG_E119_F	SNCG	6.35x10^{-03}	9.47x10^{-04}	3.4128	-1.6344	0.2184	GGAAAAGACCAAGCAGGGGGTGA[CG]GAAGCAGCTGAGAAGACCAAGGAG
CD40_P372_R	CD40	3.48x10^{-02}	9.60x10^{-03}	2.6435	-3.7640	0.2136	GGAACTTCCTCAGGCCTCTC[CG]CAGTGGAGCCTCTTTCGGTTCTGCCAGG
SOX17_P303_F	SOX17	3.45x10^{-02}	9.47x10^{-03}	2.6484	-3.7518	0.2125	GAATGGACGCTCGGTATGTTCATCTAAA[CG]ACCTTGGGCAAGTACGTCGATTC
FLT4_E206_F	FLT4	1.63x10^{-02}	3.43x10^{-03}	3.0019	-2.8273	0.2110	CGTGCTCCCCTCAGGCGTC[CG]CGCACCAGGGCCACCGTGTCCC
SLC6A8_P193_R	SLC6A8	1.45x10^{-04}	8.85x10^{-06}	4.6984	2.8111	0.2082	GTAGCAACCATCCTGCCTCC[CG]CTGGAGCGGCGTCTCCTCCCCG
RAD50_P191_F	RAD50	2.80x10^{-02}	6.95x10^{-03}	2.7595	-3.4718	0.2069	GAGTCCCAGGATCAAGCTTTGGGAAG[CG]CCATCCGTCACAGGTCTTGGTCTCC
LIMK1_P709_R	LIMK1	2.16x10^{-02}	4.88x10^{-03}	2.8828	-3.1496	0.2040	ACCACCCAATTCCTTTGGA[CG]CTTGACTCAGCCCAAACCCGTGCT
ERN1_P809_R	ERN1	2.03x10^{-02}	4.44x10^{-03}	2.9151	-3.0633	0.1978	GGATGTGAAGTTTGAGATGGTCTG[CG]TCACAACTCGTTGGAGGGAGTG
FGF9_P862_R	FGF9	3.51x10^{-08}	6.28x10^{-10}	6.8828	12.1226	0.1640	GACTCAGGGTTTCTTCCTCC[CG]CCTCTCGCAGTGCATCTTTCATTTGCTTTT
MAPK10_E26_F	MAPK10	2.98x10^{-02}	7.66x10^{-03}	2.7251	-3.5597	0.1606	AGCGGCAAAATCCCTCTGGGCT[CG]CTGGGTCCCCTGCCACGCCATTT
GNAS_E58_F	GNAS	2.34x10^{-02}	5.44x10^{-03}	2.8453	-3.2489	0.1561	GAGGACCGGCGGAGGCACCTCTCT[CG]AGTCTTAGGCTGCGGAATCTAAGA
AATK_P519_R	AATK	3.51x10^{-08}	6.30x10^{-10}	6.8820	12.1186	0.1446	GGGGACGTGCCCAGTGGGTCCT[CG]AAGAAGGCAGGACAGAAGGCGG
p16_seq_47_S85_F	CDKN2A	3.58x10^{-02}	1.00x10^{-02}	2.6277	-3.8030	0.1333	CGAAGGCTCCATGCTGCTCCC[CG]CCGCCGGCTCCATGCTGCTCCCC
SOD3_P460_R	SOD3	6.64x10^{-03}	1.00x10^{-03}	3.3957	-1.6864	0.1311	TAGCACAAGTCCTAGAATACCAGAA[CG]GAGACGTGCTTTCTTGGACCTTAAACGAAA
NGFB_P13_F	NGFB	4.94x10^{-02}	1.55x10^{-02}	2.4650	-4.1924	0.1295	CCAGCGCTCTCTGCTGTGCCGGAG[CG]CCGAGCTGCTCTCACACAGGCTTCTTGAA
WNT1_P79_R	WNT1	1.54x10^{-02}	3.14x10^{-03}	3.0307	-2.7476	0.1250	CCATTGTCTGCGCCCCTAAC[CG]GTGCGCCCTGGTGCCACAGTGCGGCC
THY1_P20_R	THY1	1.22x10^{-04}	6.98x10^{-06}	4.7582	3.0406	0.1150	CCGGTTGCTGCACCCAGCTCGGAGCC[CG]CAGTTTTCACCGGGGATGGAG
IRF5_E101_F	IRF5	2.83x10^{-03}	3.25x10^{-04}	3.7307	-0.6299	0.1106	TGCTCCCTGGCGCAGCCACGCAGGCGCAC[CG]CAGACAGGTGGGTCCCGGCC
BAX_E281_R	BAX	4.07x10^{-02}	1.21x10^{-02}	2.5590	-3.9699	0.1028	AGGTTCCTGGCTCTCTGATCCC[CG]TGTCCCGATCCCTGCCTCTCTGGC
IGF2R_P396_R	IGF2R	3.40x10^{-04}	2.44x10^{-05}	4.4392	1.8376	0.0898	CACGGATCCGCTGCCACTAGGCTGTG[CG]AAGGCATTTACCTCCCTGGCACTTTGAT
CREBBP_P712_R	CREBBP	5.47x10^{-06}	2.11x10^{-07}	5.5968	6.4323	0.0582	AGTGAGGGGGCCTCACGCCTGTT[CG]CATCCCAAGGCGGCAGGGCAGACACC

Table SI. Continued.

ID	Gene name	adj.P.Val	P-value	t	B	logFC	Sequence
APC_E117_R	APC	4.02x10^{-03}	5.26x10^{-04}	3.5898	-1.0835	0.0542	TTTCCCTCGCACTGTCTTAAAC[CG]ATGGCCTTTCCTTGGCACAGGGTCC
IL11_E232_F	IL11	7.62x10^{-04}	6.53x10^{-05}	4.1783	0.8944	0.0490	CCTGTCTCCGGGTCCCTCTCTGTG[CG]ACTCAGCGGGGTCTGCTCCCACC
CDKN2B_E220_F	CDKN2B	1.54x10^{-02}	3.13x10^{-03}	3.0323	-2.7432	0.0467	CTCAGCTTCATTACCCTCC[CG]TCGTCCTTCTGCGGCTTGGGGCCCC
MSH2_P1008_F	MSH2	1.32x10^{-02}	2.41x10^{-03}	3.1176	-2.5039	0.0456	ACTGGGATTATGGCGTGTGACACCA[CG]CCTGGCGTCAAACGTTTGTCTT
ALK_E183_R	ALK	2.54x10^{-07}	5.97x10^{-09}	6.3962	9.9135	0.0423	TTCGCAGGCACTGGAGCGGCCCCGG[CG]GCAGCAGCTGAGGGCGTTCAGG
FABP3_P598_F	FABP3	1.48x10^{-02}	2.89x10^{-03}	3.0591	-2.6687	0.0418	CCCTTCACTCTCACTGCCTGGTGG[CG]GAGACAGTCACCAGCGGCTCGGTCT
LAMC1_P808_F	LAMC1	2.52x10^{-04}	1.69x10^{-05}	4.5337	2.1883	0.0349	ACACAGTGGAAGAATTTCGCAGTGGGT[CG]TGCGTACCCAAGGGAAAAATTCATT
CDH11_P354_R	CDH11	1.36x10^{-02}	2.57x10^{-03}	3.0965	-2.5635	0.0342	TCAGGGCTCAGATGGAGTCTGGAG[CG]ACTGAAGTTGGGCTCCAGGG
JUNB_P1149_R	JUNB	1.01x10^{-02}	1.69x10^{-03}	3.2317	-2.1752	0.0342	GGCTGTTGCCACACTTCCTGCCTCTG[CG]CTCTTTCCCCAGCCTGTTTCTAAGG
LRP2_E20_F	LRP2	4.71x10^{-02}	1.45x10^{-02}	2.4893	-4.1356	0.0307	GCACCGGCAGCGCCTCTGCTAG[CG]AACGCTCCTTTAGGTCTGCACCTCCG
PLAU_P11_F	PLAU	8.67x10^{-11}	9.79x10^{-13}	8.2322	18.4847	0.0291	GCGGGCCCTGATATAGAGCAGGCGCCG[CG]GGTCGCAGCACAGTGCGGAGACC
CHFR_P635_R	CHFR	3.01x10^{-03}	3.54x10^{-04}	3.7062	-0.7098	0.0291	GAAAGAGGAGTAAAGACGGCGAGACG[CG]TCCACGCAGGGGGAGTCTGT
APBA1_P644_F	APBA1	8.65x10^{-04}	7.88x10^{-05}	4.1273	0.7147	0.0290	GAGTGACTCCCGAGCTTTCC[CG]CTTCCCAGGCCCCTTAGATATCG
IGSF4C_E65_F	IGSF4C	1.24x10^{-02}	2.23x10^{-03}	3.1429	-2.4316	0.0284	CAGCAGCAGCGGCCACTGGAAG[CG]CCGGGCCCGGCCCATGGTGCCG
CDKN1C_P6_R	CDKN1C	2.01x10^{-06}	6.96x10^{-08}	5.8504	7.5134	0.0261	TCGCTCAGGCCTGGCCGGCACCCCT[CG]AGCACAGCGCACTTGGCCTGTGGA
ENC1_P484_R	ENC1	1.54x10^{-02}	3.12x10^{-03}	3.0336	-2.7397	0.0255	ATGCTCTAAAAAGGGCTGCAAGGGG[CG]AGCTGGGTATCCGCAGGACAGG
CDK6_E256_F	CDK6	3.29x10^{-03}	3.98x10^{-04}	3.6718	-0.8210	0.0254	CGAAGTCCTCAACACAGACA[CG]ATTACATAGCCTCTGCCCAAGCGCGT
AKT1_P310_R	AKT1	1.09x10^{-05}	4.71x10^{-07}	5.4099	5.6504	0.0254	TGCCGTGACCCTAGCAGAAGGGGCC[CG]AGACAGGTCAGGGACGAATCCCG
ITGB1_P451_F	ITGB1	3.84x10^{-05}	1.89x10^{-06}	5.0797	4.3044	0.0239	CGTTTGTCCACTGATGTCCCGTTT[CG]AGCCCGGGAGATCCTGCATCTCGG
BCL2L2_P280_F	BCL2L2	1.38x10^{-02}	2.62x10^{-03}	3.0910	-2.5790	0.0223	CTGGAAAAGTTCAACAAGTGCATGGAACAT[CG]GAAACCTCCTGAAAATGCTAAATT
FHIT_P93_R	FHIT	1.77x10^{-04}	1.11x10^{-05}	4.6401	2.5890	0.0216	GGAGCGGAGGCCAATACGCGCAGAGCATG[CG]CCTACGCCGGGCCAATTGAAAGC
STK11_P295_R	STK11	9.88x10^{-03}	1.64x10^{-03}	3.2413	-2.1472	0.0215	CGAGGTCACAGCCGTGGCCT[CG]TCTCCCCATGCCTGCTTCCCG
FGF12_P210_R	FGF12	1.05x10^{-05}	4.48x10^{-07}	5.4215	5.6985	0.0210	AAACTAGAAAATGGATTGGACTAGTACTG[CG]TGCATCAGGACGAATTACTGAAGTCT
CCND3_P435_F	CCND3	2.22x10^{-03}	2.44x10^{-04}	3.8130	-0.3588	0.0209	ACTCACTACATCTTCACGAAAACT[CG]GAAACCGAGGCAACTGTCATTCAGTTGG
HHIP_E94_F	HHIP	1.65x10^{-03}	1.67x10^{-04}	3.9207	0.0022	0.0206	GGGGCGCGCTGTGGCAGCACCTCCC[CG]CGCGCTAGTTAAAAAGAAGAAGAAAAG
ID1_P880_F	ID1	6.89x10^{-04}	5.64x10^{-05}	4.2178	1.0347	0.0203	CTAACGGTCTGAGCCGCTGGTTCAGA[CG]CTGACACAGACCGGCCCGGGA
SMARCA3_P109_R	SMARCA3	4.70x10^{-04}	3.65x10^{-05}	4.3333	1.4502	0.0200	AGCACAGAAGGGAGGGCAACTCCGCCC[CG]CTGCCATTCAAAGACGGCGGG
KRAS_P651_F	KRAS	9.14x10^{-03}	1.49x10^{-03}	3.2710	-2.0596	0.0196	CACACCGGGGCTGTCTGATCGC[CG]CCCCGATTATTATCAGCCTCAGCAC
LAMB1_E144_R	LAMB1	3.83x10^{-02}	1.10x10^{-02}	2.5947	-3.8837	0.0190	GAACAGAGGGAGGCGCCTCTGCTCATG[CG]CATACGGAGAGCCGGGGCTG
ETV1_P515_F	ETV1	3.34x10^{-03}	4.09x10^{-04}	3.6641	-0.8460	0.0189	CACTTCCCCCTTGGAAGC[CG]AAAGCGCCTCTGACAGAGCTCAATTCG
IFNGR2_E164_F	IFNGR2	1.64x10^{-02}	3.47x10^{-03}	2.9975	-2.8394	0.0179	ACATTTCGACTAAAGGGGCGAATCCT[CG]AATTGTGCGATCAAGCACCCGAGAG
VAV2_E58_F	VAV2	7.97x10^{-05}	4.15x10^{-06}	4.8869	3.5409	0.0178	CACACCACCCGGTGGTTGGG[CG]GCAGGACCTTGCAATCGATGAGCCAG
E2F3_P840_R	E2F3	1.23x10^{-04}	7.37x10^{-06}	4.7445	2.9881	0.0171	CCTTTTGCACCTGCCAGACAT[CG]TCCGCATGGTCCAACTTGCCTTTGGCA
PCGF4_P760_R	PCGF4	2.90x10^{-03}	3.35x10^{-04}	3.7216	-0.6595	0.0168	GAAACGATGCGATCTCCTGGGTTTGT[CG]CAGACCCCTGCTTCGGGGCTCCG
BCL3_E71_F	BCL3	3.17x10^{-02}	8.43x10^{-03}	2.6903	-3.6473	0.0168	GGGGCCCGTGGACCTGCGCACC[CG]GCCCAAGGCCGCCGGACTCC
FAT_P279_R	FAT	3.16x10^{-02}	8.37x10^{-03}	2.6933	-3.6398	0.0164	AGGCTTGTGATGCCGAGGTTAGTTA[CG]GCCAGCCACAGGCGCTGTGCAAGGA

Table SI. Continued.

ID	Gene name	adj.P.Val	P-value	t	B	logFC	Sequence
CPNE1_P138_F	CPNE1	1.53x10^{-05}	6.93x10^{-07}	5.3191	5.2755	0.0162	ATTCAGTCCCTGCTTGCGACTGTTGG[CG]CACAGGACCGACCTTGGGCTAGTGGCC
TUBB3_P364_F	TUBB3	6.89x10^{-04}	5.63x10^{-05}	4.2182	1.0362	0.0161	GGCGTGGGGAAAAAAGACCCTC[CG]TACAAAGCCGCAGGGTGGGGC
WNT2B_P1195_F	WNT2B	5.97x10^{-08}	1.15x10^{-09}	6.7531	11.5278	0.0161	CTAGATTGGAAGCCATGTGGTTCTGA[CG]CCAAGGCCCGGCTGCAACGTGCC
CD34_E20_R	CD34	8.65x10^{-04}	7.93x10^{-05}	4.1257	0.7090	0.0156	TTAGGAGGGAGGCTGGGTTGC[CG]CCGTCGAGGCCAAAAAAGGTG
PDGFA_P78_F	PDGFA	2.06x10^{-02}	4.58x10^{-03}	2.9041	-3.0929	0.0156	CACCTGCCTGGACGCCTGGCC[CG]GCCCCGGCTGCGAGCTGCGAGCC
JAK2_P772_R	JAK2	2.23x10^{-05}	1.05x10^{-06}	5.2204	4.8722	0.0154	TCGCTAGGCCTTGTTGCCAACC[CG]CAGGCGGCTGGGCGCTTCATCCCAC
COL6A1_P425_F	COL6A1	1.87x10^{-04}	1.21x10^{-05}	4.6201	2.5135	0.0151	GAAGAGGCGAGTGAGCCTGCCCGTG[CG]TCCCGCATGGAGACGTCTGGA
MLH1_P381_F	MLH1	1.50x10^{-04}	9.36x10^{-06}	4.6843	2.7575	0.0151	GCGGGAGGCCACAAGAGCAGGGCCAA[CG]TTAGAAAGGCCGCAAGGGGAG
INHA_P1189_F	INHA	4.07x10^{-07}	1.08x10^{-08}	6.2659	9.3320	0.0150	GGTCAGCAGCAGGCCGTGCTCCGCGC[CG]TCCGCCGGGAAGCTCAGGC
DST_P262_R	DST	1.34x10^{-07}	2.84x10^{-09}	6.5582	10.6422	0.0146	GGACCGTGCGGCCAAGCACGCCCACCCC[CG]GACACTGGCTGCCCGGTCCC
PKD2_P336_R	PKD2	1.47x10^{-03}	1.45x10^{-04}	3.9595	0.1339	0.0143	ACCCAAGAGTTATCTCAGCGT[CG]GGCAGGCATCGACAGCTCCAGGAG
CDK10_E74_F	CDK10	8.13x10^{-04}	7.24x10^{-05}	4.1504	0.7958	0.0137	GGAGCCAGATCTGGAGTGCGAGCAGATC[CG]TCTGAAGTGTATTCGTAAGGAGG
MATK_P64_F	MATK	2.52x10^{-02}	6.02x10^{-03}	2.8099	-3.3417	0.0135	GGCCGACTTAACTCTTTGTCAGC[CG]GGCTGGTTTTCACCCACCTGGTGGCAG
DAB2IP_P9_F	DAB2IP	8.43x10^{-03}	1.33x10^{-03}	3.3083	-1.9492	0.0127	CTCAGCCGCCGCCTCAAGGGCTCCATCAAG[CG]CACCAAGAGCCAGCCCAAGCTGGACCG
BMPR1A_P956_F	BMPR1A	1.85x10^{-04}	1.18x10^{-05}	4.6261	2.5363	0.0122	TTTCCAAATGGACGGAATGAGCCTC[CG]GAGGGTACACGAGGTCACCAGCGT
COL4A3_P545_F	COL4A3	3.77x10^{-03}	4.84x10^{-04}	3.6146	-1.0044	0.0121	GGCGCCTTACCTGTGGGGACGCC[CG]CAGCGCCAGGAGCTGCCGCCTTG
EIF2AK2_E103_R	EIF2AK2	9.35x10^{-05}	4.97x10^{-06}	4.8426	3.3679	0.0120	GGGACGCAGGATTGGCGAGTCC[CG]CCCCGGCTGGGCCTGCAGCC
IGF1R_P325_R	IGF1R	4.44x10^{-04}	3.39x10^{-05}	4.3524	1.5197	0.0119	CAGGGCCGGGCTTGTTTTTCCT[CG]CCTAGGCAGATTTGGGCTTTGCCCCCT
WNT5A_E43_F	WNT5A	2.56x10^{-03}	2.87x10^{-04}	3.7662	-0.5135	0.0117	CAAGGGCAGGGCCTGGTCGGGG[CG]CAACTAGGGAGCCGCCGGTCCGGC
CASP3_P420_R	CASP3	2.70x10^{-02}	6.66x10^{-03}	2.7742	-3.4341	0.0117	CTCTGGGAAGAAGAGGAGCAGGC[CG]GGACGCCCACCGGTAATTTCTG
IGSF4_P454_F	IGSF4	1.23x10^{-04}	7.29x10^{-06}	4.7470	2.9978	0.0116	GCACACCGAGTGCATCTGGCCTAG[CG]AACCAGACGTTGCAAATTTCCGTCA
ERCC1_P354_F	ERCC1	3.77x10^{-03}	4.82x10^{-04}	3.6157	-1.0009	0.0115	TCCTCTCTTCCCGGTCCTGTG[CG]AGTCCGTGCTGGTGACACAGCAGTGACCA
CCKBR_P480_F	CCKBR	1.18x10^{-02}	2.08x10^{-03}	3.1656	-2.3668	0.0110	CGCAGCGAGGAGCTGCAGGGAACTA[CG]GTAGCAATAGTGTCACGGTCACTGCGG
MXI1_P75_R	MXI1	5.21x10^{-03}	7.38x10^{-04}	3.4887	-1.4006	0.0109	CCACCTTTTATTTTGACCGGTC[CG]ATGGCGACAGGCTCGCACTAGGACCC
MALT1_P406_R	MALT1	1.86x10^{-02}	4.03x10^{-03}	2.9474	-2.9763	0.0106	TGCCATACACATCTAACCCTAAAA[CG]AGGAAGCGTCCGCTGAGGTTGCCCAC
MAPK12_E165_R	MAPK12	2.67x10^{-02}	6.57x10^{-03}	2.7791	-3.4214	0.0101	CGGTAAAAGCCACTGCGGGCGGG[CG]GCGGAGAGCTCATGGCAGGCC
TK1_P62_R	TK1	1.54x10^{-02}	3.13x10^{-03}	3.0321	-2.7440	0.0101	CGTGCTGGCCAATCACGAGCCGGCCC[CG]CCGCCATGGGGCCAATCAGCGCCC
IGFBP6_P328_R	IGFBP6	2.65x10^{-02}	6.50x10^{-03}	2.7829	-3.4117	0.0099	CGGGTCCCTGCATGCCCCT[CG]TCGTCCTACACATACACACTAAGTGGATT
LIF_E208_F	LIF	2.22x10^{-03}	2.45x10^{-04}	3.8115	-0.3640	0.0098	CCCAGCGCCTCCGGTGGCTG[CG]CGGGCGCCCCAAGTGTTCGTGTGTCTGCG
TJP1_P326_R	TJP1	3.48x10^{-03}	4.37x10^{-04}	3.6445	-0.9090	0.0098	CATGCATGAGTGCGGCTGGAAAGGC[CG]GCAGAGCCGATACCCGACAGTTGTTT
LMO1_P169_F	LMO1	2.67x10^{-04}	1.81x10^{-05}	4.5167	2.1249	0.0091	CCTAGCTCGGTGAGCGTCTTTGCTC[CG]ATCCCAGGGTCGTGGTCTTCAATGATT
KLF5_P13_F	KLF5	4.06x10^{-02}	1.20x10^{-02}	2.5608	-3.9656	0.0091	AGTTGGGTGAAATAGAGGCGGG[CG]TCAAGTGTCAGTAGTCGCGGGGC
DUSP4_E61_F	DUSP4	2.36x10^{-02}	5.52x10^{-03}	2.8399	-3.2631	0.0090	CCTCCCGTGTATTTTTGCCGGT[CG]CGCGGCTCCTGTCGCCACTGGCGCC
PTEN_P438_F	PTEN	1.90x10^{-02}	4.13x10^{-03}	2.9390	-2.9989	0.0090	AAAGGAAAGAGCGAATGCAGTCCACGCCG[CG]GAAATCTAGGGGTAGAGGCAAG
TMEFF1_E180_R	TMEFF1	8.63x10^{-03}	1.38x10^{-03}	3.2956	-1.9870	0.0090	CTCCGCTCGCCTTCTGCTGCTACA[CG]TCGGTGCTTCTGCTCTTCGCCTTCTCTCT
HLF_E192_F	HLF	1.25x10^{-02}	2.27x10^{-03}	3.1378	-2.4463	0.0089	TGAACATTTTGCAAAACGAGGGGTT[CG]AGGCAGGTGAGAGCATCCTGCACGT

Table SI. Continued.

ID	Gene name	adj.P.Val	P-value	t	B	logFC	Sequence
LIG4_P194_F	LIG4	3.57x10^{-03}	4.50x10^{-04}	3.6357	-0.9371	0.0089	GAGTACACACGGCTCCTATTGGCCT[CG]GCAGCAGATGCTCTCTGCAAGCAGTTGATC
MCM6_E136_F	MCM6	2.36x10^{-02}	5.51x10^{-03}	2.8408	-3.2607	0.0087	TCTGGCACTTCTCGGCCACCT[CG]TCGCGGACCTCCAGGTGCTGGCTGCCG
HDAC11_P556_F	HDAC11	2.71x10^{-02}	6.71x10^{-03}	2.7718	-3.4404	0.0087	GTCTTCGCCGGGAGTGCTTGTCC[CG]GAGCTGCTCGCAGACTGGGC
ABCA1_E120_R	ABCA1	2.31x10^{-02}	5.32x10^{-03}	2.8525	-3.2301	0.0087	ACCGGGGAAAAAACAAGGAGCAAAG[CG]CCCTGAGAACCGGCTCTGTTG
APP_E8_F	APP	2.28x10^{-02}	5.23x10^{-03}	2.8585	-3.2142	0.0087	GCGGCGGGGCTCAGAGCCAGG[CG]AGTCAGCTGATCCGGCCCACCC
GSTP1_seq_38_S153_R	GSTP1	1.33x10^{-02}	2.49x10^{-03}	3.1073	-2.5331	0.0084	CCGTGACTCAGCACTGGGGCGGAG[CG]GGGCGGGACCACCCTTATAAGGCTCG
EPM2A_P64_R	EPM2A	6.61x10^{-03}	9.93x10^{-04}	3.3981	-1.6790	0.0084	TCATAAGGAAGGGAATGACCTCTAGACAGC[CG]CCTTCTAATTGTGAAACGGGG
CSTB_E410_F	CSTB	8.34x10^{-03}	1.31x10^{-03}	3.3128	-1.9359	0.0079	CCGGGCTATCAATTCCCACT[CG]CCCTTGCTGTATTCAGCGGAGCCCAA
RASA1_E107_F	RASA1	2.03x10^{-02}	4.46x10^{-03}	2.9131	-3.0688	0.0078	GCGGGCAGGGTAGGGCAGAGTAGAG[CG]GGCTTCAACATGATGGCGGCC
TIMP2_E394_R	TIMP2	9.00x10^{-03}	1.45x10^{-03}	3.2799	-2.0335	0.0072	TGCAAAACGCCTGTTGCGGGTGCAC[CG]GGGAGCAGCTGCAGGCGTCG
ASCL1_E24_F	ASCL1_	2.06x10^{-02}	4.61x10^{-03}	2.9022	-3.0980	0.0072	TCTGGCCAGGGAACGTGGAAGG[CG]CACCGACAGGGATCCGGCCAGG
NQO1_E74_R	NQO1	2.58x10^{-02}	6.23x10^{-03}	2.7977	-3.3732	0.0069	CGGCTGCAACCTTGTGGGAGTCG[CG]TGTGTAGTGCACGGTGCATTCTCT
UNG_P170_F	UNG	3.16x10^{-02}	8.35x10^{-03}	2.6939	-3.6383	0.0067	AGCAGAGGTGGGCTGAAGGCACAAAG[CG]AATGAAAGAATAGGCCCCCGG
PAX6_E129_F	PAX6	1.52x10^{-02}	3.03x10^{-03}	3.0428	-2.7142	0.0067	CGCTCCTCACTGGCCCATTAG[CG]AAGCCTGACCTCTGTCATCATCCTCC
PCDH1_E22_F	PCDH1	4.47x10^{-03}	6.15x10^{-04}	3.5434	-1.2298	0.0066	GCTCCGGCTCCGGCTGGCTCTGGG[CG]CAGCAGCCCGGCGGCTTTGCGTCC
TNC_P57_F	TNC	4.80x10^{-02}	1.49x10^{-02}	2.4799	-4.1576	0.0065	TCCTTCCTCTGTAATGGGACGCCT[CG]CCTCCAGACATCCTTTCCCAC
PTK2B_P673_R	PTK2B	4.01x10^{-02}	1.18x10^{-02}	2.5684	-3.9473	0.0063	AAATCGCTGCTCTTACCCGAAAGT[CG]TGGGCAGTGTCCTTCACCGGCTGCAC
ERBB2_P59_R	ERBB2	1.18x10^{-02}	2.10x10^{-03}	3.1631	-2.3738	0.0063	AGCTTCCACTTCCGGAGTAAC[CG]GAAGTTCCTGTGTTCTTTATTCTACTCTCC
PTPRO_E56_F	PTPRO	1.06x10^{-02}	1.78x10^{-03}	3.2159	-2.2213	0.0059	GGGACTGGAAAGGCAGCATGCGCT[CG]CCAGGAGCAACCTCGGCGCCCAGG
EPHB2_E297_F	EPHB2	3.77x10^{-02}	1.07x10^{-02}	2.6030	-3.8636	0.0055	GCTGATTGACTGTGCCAGGAGGAGG[CG]AAGGGACCATCTTGCCGAGGC
PTCH_E42_F	PTCH	3.39x10^{-02}	9.22x10^{-03}	2.6580	-3.7280	0.0055	GCAGGCTGCTCGGGCTCGGGCTC[CG]GTTGACAGACCAGCCGCTGCTGCTGCTCA
GAS1_P754_R	GAS1	3.98x10^{-02}	1.15x10^{-02}	2.5766	-3.9277	0.0054	AAGGAGGCTCGGATATGCAGCCCCAGCT[CG]CGCACAGAACCAGCGGGCAGGGCT
PTPNS1_P301_R	PTPNS1	3.28x10^{-02}	8.80x10^{-03}	2.6752	-3.6852	0.0053	GGCCTCTGGGCAGCCCCGG[CG]GCGCTTCCAGTGCCTTCCAGCC
VEGFB_P658_F	VEGFB	1.84x10^{-02}	3.94x10^{-03}	-2.9549	-2.9558	-0.0117	CGGCTAGGGCAGCGGCAGCCGCCACCATC[CG]AGCCAACCCAAGGCCCCGAGATCGT
GNG7_E310_R	GNG7	2.43x10^{-02}	5.76x10^{-03}	-2.8255	-3.3008	-0.0138	AGGCCAGACGCTGAGAGAGAAAAACACTG[CG]TAATCCCACGTATTGTGGAGTCCAAAA
IGFBP5_P9_R	IGFBP5	8.04x10^{-03}	1.24x10^{-03}	-3.3283	-1.8896	-0.0161	GAAGTTTCCAAAGAGACTACGGGGCTC[CG]GGAGAGCAGGCGCTTTTAAATAGC
CTAG1B_P77_F	CTAG1B	2.53x10^{-02}	6.06x10^{-03}	-2.8075	-3.3479	-0.0179	CCGGGATCCTCAGGGCGCCTG[CG]CACAGGGGCCCTACTTCCGGCCC
XRCC2_P1077_F	XRCC2	8.13x10^{-04}	7.18x10^{-05}	-4.1526	0.8035	-0.0205	CCTTGGCCTCTTCTCTACGTAGGGCTG[CG]GGCCCGTATCTGAAACATTAACAACCA
UGT1A7_P751_R	UGT1A7	7.94x10^{-03}	1.22x10^{-03}	-3.3351	-1.8693	-0.0216	CGCTAAGACCCTTGCTCTCTTTC[CG]TCGAACATGAGATGCCAATTTCTTTCTGGG
THPO_P585_R	THPO	1.48x10^{-02}	2.91x10^{-03}	-3.0566	-2.6756	-0.0223	TGTCAGGTGCGGGGCACATGTATGTG[CG]CACACGTGCACTGGGTTAAGCCTGAG
NTRK2_P10_F	NTRK2	3.36x10^{-03}	4.17x10^{-04}	-3.6579	-0.8657	-0.0227	TGACTGCGGAAAAACAGATTCCGAGC[CG]CAAAAGGGAAGACGGATTCTCAG
CPA4_P1265_R	CPA4	5.28x10^{-03}	7.54x10^{-04}	-3.4819	-1.4217	-0.0239	CACTGATCCTCTCTGTTTTCTTTGC[CG]TATTCAGTGTTAAGCACAGTAAGTCTTTCC
FGR_P39_F	FGR	5.58x10^{-03}	8.00x10^{-04}	-3.4641	-1.4768	-0.0239	GGCGGAACTGGGCCACCTACTGTAC[CG]TTCAGTCTGCCTCACAGTATGTCCCC
HDAC9_E38_F	HDAC9	3.98x10^{-04}	2.96x10^{-05}	-4.3884	1.6511	-0.0246	GAGGCACAGACACAGATAGGAGAAGGGCAC[CG]GCTGGAGCCACTTGCAGGACTG

Table SI. Continued.

ID	Gene name	adj.P.Val	P-value	t	B	logFC	Sequence
CDH17_P532_F	CDH17	3.63x10^{-02}	1.02x10^{-02}	-2.6214	-3.8183	-0.0254	CCAAAGTCTGCAAGAAACAAC[CG]ATAGCAAATTTCCCCCAAACAC
SLC22A2_E271_R	SLC22A2	1.18x10^{-02}	2.10x10^{-03}	-3.1633	-2.3732	-0.0254	CCAGGAAGACGATGCCCACGTAGATGGG[CG]CGAAGGTAGCCGAGAGCAGAGCCAAG
BCL2A1_P1127_R	BCL2A1	3.57x10^{-03}	4.53x10^{-04}	-3.6340	-0.9424	-0.0257	TGGGTGGCAGAGAACAGGGCCTCT[CG]AGGTGACTCTGGCAGTACCGCCC
IL1A_E113_R	IL1A	4.33x10^{-03}	5.91x10^{-04}	-3.5550	-1.1933	-0.0265	TTCTGTAGAAGAAGGTGTGTGCAAGCCC[CG]GGAGGTATGCGTAAGGCCTCAG
CTLA4_E176_R	CTLA4	4.00x10^{-03}	5.20x10^{-04}	-3.5931	-1.0730	-0.0293	AAGCCATGGCTTGCCTTGGATTTCAG[CG]GCACAAGGCTCAGCTGAACCTGGCTACC
THBS2_E129_F	THBS2	1.84x10^{-02}	3.96x10^{-03}	-2.9532	-2.9605	-0.0295	CTGTGCAGGGCTGTCAATCAGACACA[CG]AGGAAGCACGTTTAATTCATTCCTTCG
IL3_P556_F	IL3	3.40x10^{-04}	2.42x10^{-05}	-4.4409	1.8440	-0.0302	CCAGAAACAAAGTGTCAAGGAGAAGCTGCC[CG]AAGCCCATGGGACAAACCACTGG
USP29_P282_R	USP29	8.39x10^{-04}	7.52x10^{-05}	-4.1400	0.7592	-0.0303	TTTCTCTGAACCCTAACTCCTGC[CG]TTACGCCCCACCAGCTCTAGGCC
SEMA3B_P110_R	SEMA3B	1.48x10^{-02}	2.91x10^{-03}	-3.0563	-2.6764	-0.0314	CTTGTGCCCATTCCACTCC[CG]CCTGGCTGCCGTCTCCAGCTGGTCCC
DMP1_E194_F	DMP1	3.81x10^{-03}	4.90x10^{-04}	-3.6105	-1.0175	-0.0314	ATACCATGTAGAGAGAGATGGGAGAGCTG[CG]CTTTGGGTAAAAACAGTTCCTATTT
MKRN4_P1320_R	MKRN4	2.98x10^{-02}	7.62x10^{-03}	-2.7267	-3.5555	-0.0333	CAGCTGCTGCATCTCCCTCTCTTT[CG]CTTCTAGTCGCTCAGTAAGCCTCTCAATT
SRC_E100_R	SRC	2.08x10^{-03}	2.27x10^{-04}	-3.8342	-0.2885	-0.0340	CCTCTAGCCTCAGTTTATCAC[CG]CAAGAGCTACCATTCATCTAGCACAACC
NCL_P1102_F	NCL	9.05x10^{-04}	8.36x10^{-05}	-4.1113	0.6586	-0.0340	TAAAAATCACCTCAGGCCGGG[CG]CGGTGGCTCAGATCCGCAATCCCA
EPS8_P437_F	EPS8	1.40x10^{-02}	2.69x10^{-03}	-3.0822	-2.6039	-0.0346	CACCCAGTCTGGCTGCACAGCT[CG]TAACCCCTGCCCTTTGGCGGCAA
TIMP3_P1114_R	TIMP3	1.08x10^{-06}	3.30x10^{-08}	-6.0179	8.2401	-0.0368	GAATCTCTCAAATTCCACCA[CG]TATGCCCTCATTCAACCTGGATCCT
EDNRB_P148_R	EDNRB	6.98x10^{-05}	3.57x10^{-06}	-4.9243	3.6874	-0.0386	ATACCGAATTAAAGAAAGAAGAGGTTTATT[CG]GCCAGAAGCATCGGCAAGACTCCTG
ITGA6_P718_R	ITGA6	3.11x10^{-03}	3.71x10^{-04}	-3.6921	-0.7555	-0.0395	TTAAACAACCCATCCTTGACTTG[CG]TGACTTCTTCCACAAGCTCTCCTGGT
SHB_P473_R	SHB	4.51x10^{-09}	6.89x10^{-11}	-7.3503	14.2941	-0.0402	TGAGGAGGGAGAGTGGATTAACA[CG]GAACCTGTCTAGTTTACAGCGTGGC
AFF3_P808_F	AFF3	4.31x10^{-02}	1.32x10^{-02}	-2.5270	-4.0465	-0.0411	CCATACTCTCCTGGTTTTTGTCAGG[CG]GTCTCTCACACTGGCAGGCTTCCATT
ACTG2_P455_R	ACTG2	6.90x10^{-04}	5.73x10^{-05}	-4.2135	1.0195	-0.0437	GCACGCAGGATTTCTTTCCTGGGTA[CG]GAAGGCATTTCTCTTCAGCTTTCATTGG
PWCR1_E81_R	PWCR1	3.37x10^{-02}	9.12x10^{-03}	-2.6622	-3.7177	-0.0460	GAGAACTCATAACGTCATTCTCAT[CG]GAACTGAGGTCCAGCATGTTGCTTCCTCT
FGF6_E294_F	FGF6	6.67x10^{-06}	2.66x10^{-07}	-5.5431	6.2061	-0.0461	CGTTGCAGTAGAGCCTCCGCTGC[CG]CTTGATCCCCACCAAATAGCCA
LCK_E28_F	LCK	1.42x10^{-02}	2.73x10^{-03}	-3.0776	-2.6168	-0.0468	GTGAATGGGGCCAGAGGGCTCC[CG]GGCTGGGCAGGTAAGGAG
NOTCH1_E452_R	NOTCH1	5.76x10^{-13}	4.59x10^{-15}	-9.3261	23.7781	-0.0481	GGCGAAGAAGAAAGAAGATAAATGGCC[CG]GAGAAGCAACAGGAAACCAAAACCGA
TNF_P1084_F	TNF	4.62x10^{-02}	1.43x10^{-02}	-2.4968	-4.1179	-0.0483	ATGTGATGGACTCACCAGGTGAGGC[CG]CCAGACTGCTGCAGGGGAAGCAA
ABCC2_P88_F	ABCC2	1.54x10^{-02}	3.14x10^{-03}	-3.0311	-2.7466	-0.0487	GTTGGGATGAAAGGTCATCCTTTA[CG]GAGAACATCAGAATGGTAGATAATTCC
CSF2_E248_R	CSF2	3.50x10^{-02}	9.68x10^{-03}	-2.6404	-3.7715	-0.0493	CAGCTGGCCCCTGACTGGCCA[CG]CCTGTCAGCTTGATAACATGACATTTTCCT
FGF7_P610_F	FGF7	4.03x10^{-02}	1.19x10^{-02}	-2.5658	-3.9536	-0.0511	TGAGACTCTGGAACAGCAGGTAACTTGCC[CG]AAGTCATACTGGTCATTAGTGGTCCAA
SMO_P455_R	SMO	2.34x10^{-05}	1.12x10^{-06}	-5.2056	4.8120	-0.0511	CCGAGTCTCTCCTTGCAGGTC[CG]GCCCACGATTTCCACTCATCTC
LRRK1_P39_F	LRRK1	4.15x10^{-02}	1.25x10^{-02}	-2.5456	-4.0022	-0.0516	TTACCTGCGTGCTCAGCTGCGGAAAG[CG]GAAAAGTGCAAGCTGATGAAGAT
CSF1_P217_F	CSF1	3.98x10^{-06}	1.46x10^{-07}	-5.6822	6.7935	-0.0541	TTTGCTGAAGGCTTGGAAGTGCAG[CG]CAGAAGACAGAGGGTGACTAGGAA
IL13_E75_R	IL13	1.49x10^{-02}	2.95x10^{-03}	-3.0516	-2.6897	-0.0543	GGCCTCATGGCGCTTTTGTTGACCA[CG]GTCATTGCTCTCACTTGCCTTGGCGGCTTT
IL18BP_E285_F	IL18BP	3.94x10^{-02}	1.14x10^{-02}	-2.5810	-3.9169	-0.0548	TGGGAAAGGCCAGGATGTGGA[CG]GACTGGTATGGCATTGAGCCTG

Table SI. Continued.

ID	Gene name	adj.P.Val	P-value	t	B	logFC	Sequence
FANCA_P1006_R	FANCA	3.99x10^{-02}	1.17x10^{-02}	-2.5723	-3.9378	-0.0581	CCTCTGGCAGTGGCCTTGGAACCAC[CG]AAGGGATTCAGCCGAAGGGC
PTHR1_E36_R	PTHR1	3.55x10^{-02}	9.93x10^{-03}	-2.6311	-3.7946	-0.0606	GGGACTATCCATGGCCTCCC[CG]TGGCCAACTTGAGTCTGCTCTGCAGCTTTA
APBA2_P305_R	APBA2	1.23x10^{-04}	7.30x10^{-06}	-4.7467	2.9963	-0.0612	AGCATGCAGCTCTGCTACCTGTGGCC[CG]AAATCATTAGTTGTCCATACTCACTGACCT
TMPRSS4_E83_F	TMPRSS4	2.95x10^{-02}	7.51x10^{-03}	-2.7318	-3.5425	-0.0635	TTGCTCAGCGGACAAGGATGCTGGG[CG]TGAGGGACCAAGGCCTGCCC
ITK_E166_R	ITK	4.81x10^{-02}	1.50x10^{-02}	-2.4784	-4.1611	-0.0652	TCTCCCTCGAACTTTAAAGTC[CG]CTTCTTTGTGTTAACCAAAGCCAGCCT
B3GALT5_P330_F	B3GALT5	1.55x10^{-02}	3.23x10^{-03}	-3.0222	-2.7713	-0.0654	GGGGGCAGTGACCTAGGCAGAGGG[CG]GGAGCCAGCAGATGGGATACACTCAG
FGFR4_P610_F	FGFR4	2.46x10^{-04}	1.63x10^{-05}	-4.5428	2.2224	-0.0658	GAGTAGCAGGGTGGGAGCCAGGAGG[CG]TGGGTCATGGCAATCTATGTATAAAG
ZIM3_P718_R	ZIM3	2.64x10^{-02}	6.44x10^{-03}	-2.7861	-3.4034	-0.0658	CCTCCCAGGAGAAGAGGTATCCAAAGAT[CG]TATTAGCAAATGACCCTTGGCGGTG
PLG_P370_F	PLG	1.43x10^{-04}	8.62x10^{-06}	-4.7049	2.8362	-0.0662	GAAGCTTGAGGGAGGCTATGGA[CG]TGCAGCGCTTGGCAGAGGGTCT
PTHLH_P757_F	PTHLH	2.27x10^{-02}	5.18x10^{-03}	-2.8621	-3.2045	-0.0684	CCAAGCTGCCCTGTTTATTACTTTC[CG]TAGAAATTCTCCTCAATATATACCCA
CD1A_P414_R	CD1A	3.44x10^{-02}	9.40x10^{-03}	-2.6510	-3.7454	-0.0724	AACATTGAAGTCAAAATTCTGGGCTGG[CG]TACATTAGTTAGGAGCCCCCATTTTAG
LTA_P214_R	LTA	4.57x10^{-02}	1.41x10^{-02}	-2.5021	-4.1055	-0.0767	CCTTTCCCAGAACTCAGT[CG]CCTGAACCCCCAGCCTGTGGTTCTC
MAS1_P657_R	MAS1	3.99x10^{-02}	1.16x10^{-02}	-2.5730	-3.9363	-0.0770	CCACACATCAATGGCTTGCCTGGCTTA[CG]TAGTCTGAGCAGGTGCCCAGCTTTGTCGC
S100A4_P194_R	S100A4	4.13x10^{-02}	1.24x10^{-02}	-2.5498	-3.9922	-0.0771	CCCGTGGGTAACGGGTAAGCCCTAG[CG]GTTACTAGCAGGGGACTGGAT
BTK_E64_R	BTK	3.55x10^{-02}	9.92x10^{-03}	-2.6317	-3.7931	-0.0773	CAGGACTTGGAAGGTGGGACT[CG]ATCGCAGCAGACACTGGCCCTGGAG
ABCB4_P51_F	ABCB4	3.12x10^{-02}	8.16x10^{-03}	-2.7024	-3.6170	-0.0799	TCTGTCCTTTCCTCCTCTTC[CG]CCTTTGTCCATTGTCAAAAGCATGGCCTGG
RHOC_P536_F	RHOC	8.20x10^{-19}	3.84x10^{-21}	-12.1965	37.6132	-0.0811	TCCTAGGATCGTACAGCCCAA[CG]TCATCCCCCAAACTTGAAGACC
MAGEL2_P170_R	MAGEL2	1.16x10^{-02}	2.02x10^{-03}	-3.1759	-2.3372	-0.0817	AGATGATGGAAGGGCAGTGCACAGCCTG[CG]GGGCAGACAGTGGGGCAGACA
PRDM2_P1340_R	PRDM2	2.85x10^{-02}	7.14x10^{-03}	-2.7500	-3.4961	-0.0826	AGAAGTGGACTTCAGGTCTGTCCA[CG]TTCCTTTCCACCTTTGGTTTTGTGACTT
HLA-DPA1_E35_R	HLA-DPA1	3.36x10^{-03}	4.16x10^{-04}	-3.6588	-0.8628	-0.0828	CTCTGATATGGAACATTCTGTCTTCAGGG[CG]CATGTTGTGGGGTCTATAATTGA
CHI3L2_P226_F	CHI3L2	4.05x10^{-02}	1.20x10^{-02}	-2.5626	-3.9613	-0.0894	TGATGAGGAAGGAGATTCAGGGC[CG]AGGGTGATACCAGGAGGCAGA
FANCE_P356_R	FANCE	3.88x10^{-02}	1.11x10^{-02}	-2.5889	-3.8978	-0.0904	CATGACAAGCAACATGCCGTCAG[CG]TAAATACAGCGCGGGTCCTCTAGCACA
MMP2_P197_F	MMP2	2.73x10^{-02}	6.78x10^{-03}	-2.7683	-3.4493	-0.0952	GCGAGAGAGGCAAGTGGGGTGA[CG]AGGTCGTGCACTGAGGGTG
CSF3_E242_R	CSF3	3.08x10^{-02}	7.96x10^{-03}	-2.7110	-3.5953	-0.0964	GGAACAGCATGTCTCCTGAGCC[CG]CTCTGTCCCCAGCCCTGCAGCTGCT
IL10_P348_F	IL10	4.29x10^{-02}	1.31x10^{-02}	-2.5299	-4.0395	-0.0971	ATTCGCGTGTTCCTAGGTCACAGTGA[CG]TGGACAAATTGCCCATTCCAGAATAC
PEG3_E496_F	PEG3	1.54x10^{-02}	3.13x10^{-03}	-3.0326	-2.7424	-0.0980	CATTGGTGTCGACCTTGCTGGACTTGC[CG]TGGCAGAGCCCCCGGCTGTCTGCC
PDGFRB_P273_F	PDGFRB	6.89x10^{-04}	5.67x10^{-05}	-4.2160	1.0284	-0.0997	CTTAGAAATTCCACAGCCCA[CG]CCAGCCGCCAGCTGCTGAGTCACTTTT
GUCY2F_P255_F	GUCY2F	1.70x10^{-02}	3.63x10^{-03}	-2.9826	-2.8803	-0.1008	CCATTCTGTCTAATAACCACCAAT[CG]CCCTTTCTCCAGGACAGTTCTAAATGC
TNFRSF1A_P678_F	TNFRSF1A	2.23x10^{-02}	5.04x10^{-03}	-2.8713	-3.1803	-0.1077	TCCTGGCTCTGCCACCAATCATG[CG]ACATCAGGCAACTCCTCTCCTAAGC
ARHGAP9_P260_F	ARHGAP9	3.65x10^{-02}	1.03x10^{-02}	-2.6178	-3.8272	-0.1080	TAAGGTCCCTGTCTTGCAGCTGGATAG[CG]GCAACTACCTCTTCTCCACTAGTGCAATC
PXN_P308_F	PXN	5.26x10^{-10}	6.64x10^{-12}	-7.8378	16.5980	-0.1158	TCAAAGTCACTTGCCTGACCCTG[CG]GATGACAAATCCGTCCACAGTCAGC
MFAP4_P197_F	MFAP4	3.72x10^{-04}	2.75x10^{-05}	-4.4080	1.7228	-0.1169	GACCACCTGTGTCTCATTAGTCCTGT[CG]GGCAAAGTACTGCAGACGTTAACTCCCTGC
AXL_P223_R	AXL	8.01x10^{-03}	1.23x10^{-03}	-3.3309	-1.8816	-0.1172	GCCAGTAGCATGCCCCTGCC[CG]TCTGGGTCCCTCTGCGTGTCTCTGCTTGTC
HLA-DOB_E432_R	HLA-DOB	2.06x10^{-02}	4.55x10^{-03}	-2.9062	-3.0871	-0.1189	AGGCTCGAACCCAAGCCAAGGCCTTCAACA[CG]CCCAGGCACTGACTGAGGTTGAT

Table SI. Continued.

ID	Gene name	adj.P.Val	P-value	t	B	logFC	Sequence
MMP14_P208_R	MMP14	3.33x10^{-04}	2.35x10^{-05}	-4.4490	1.8737	-0.1223	CTACAGCCCCCTGCTGTCCAT[CG]CGGCCTCAACCCCTGCAGATGGCA
LMTK2_P1034_F	LMTK2	4.13x10^{-04}	3.13x10^{-05}	-4.3739	1.5981	-0.1251	TCTGTGTGTCCAGTGCTGTGTTAACATCAT[CG]ACAGCTGGCATTTAGGATGGACATTT
ZAP70_P220_R	ZAP70	1.17x10^{-02}	2.03x10^{-03}	-3.1732	-2.3449	-0.1268	GGTATGCAGGCTTCCTCCCTTCTGA[CG]GTTCCTGCTGCTGGAGTCGTCCTTCCTGA
EGF_P242_R	EGF	1.35x10^{-02}	2.54x10^{-03}	-3.1003	-2.5528	-0.1277	CATAGCCAATATTTAGCAGTTCC[CG]CCATTCACCATGAGCACCTCCAC
SFTPC_E13_F	SFTPC	4.08x10^{-02}	1.22x10^{-02}	-2.5560	-3.9773	-0.1300	CTCACAGGGGGCTTATCTGGGCTT[CG]GTTCTGGAGGGCCAGGAACA
KLK11_P1290_F	KLK11	4.79x10^{-03}	6.68x10^{-04}	-3.5186	-1.3076	-0.1340	GGTCAGTTGTTCCTCATGATCATC[CG]GATCCAGTCCACATACTTGCAAATATAG
UGT1A1_P564_R	UGT1A1	3.88x10^{-02}	1.12x10^{-02}	-2.5878	-3.9005	-0.1372	TCTGGCTCACCTCATGGCGCGTGCT[CG]TGTGGTGGGCTCTGCTGCAGCCTCAAGACC
KRT13_P676_F	KRT13	1.08x10^{-02}	1.83x10^{-03}	-3.2062	-2.2494	-0.1442	GAAGTGGCCCTGTCCATTATCATAG[CG]AATATTCTCCGAGCCCTCACCATA
GABRA5_P1016_F	GABRA5	4.96x10^{-02}	1.56x10^{-02}	-2.4624	-4.1983	-0.1444	TGGTAGAGAAATGAAAGCACCACAGTGTGG[CG]GCTCTGGGAGTGCACTGGC
AIM2_E208_F	AIM2	2.33x10^{-02}	5.38x10^{-03}	-2.8491	-3.2389	-0.1445	GGTGCTTACCTCCTGATCCCTGGGG[CG]ATCAGCAAACCGGGTCTGCCACC
IL1B_P829_F	IL1B	1.43x10^{-02}	2.78x10^{-03}	-3.0716	-2.6337	-0.1502	CAAGAGTTATCAGTTTCTCTTTAAC[CG]AGACACCAGCAAAGTGCCTGCTCCA
SLC14A1_E295_F	SLC14A1	4.25x10^{-02}	1.28x10^{-02}	-2.5361	-4.0247	-0.1515	TCCTGGAAGCTCAAAGGCATGCCTTTATT[CG]TGATTTCTGAAGCAAGGTGCATGC
TFDP1_P543_R	TFDP1	7.91x10^{-04}	6.84x10^{-05}	-4.1656	0.8494	-0.1534	TAGTGCACACACCAGTCCC[CG]CTCCCTCACGTGCACATGCACTAGTGCA
TFF2_P178_F	TFF2	3.81x10^{-02}	1.08x10^{-02}	-2.5987	-3.8738	-0.1550	GCCAGGGTGACTCTCTCCCTGCT[CG]GTGATACCTCTTCCTGCCCTGGACAGA
MMP7_P613_F	MMP7	9.05x10^{-03}	1.47x10^{-03}	-3.2760	-2.0451	-0.1560	TGTGTCCCCTCACCTTCCA[CG]TCCCTTAGCAGAGCAGTGATAATTCCC
APOC2_P377_F	APOC2	7.97x10^{-05}	4.19x10^{-06}	-4.8851	3.5336	-0.1587	GGGAAGGAAGAGTAGGGAGGT[CG]GGAAGGGTATCAAGGAATAACACC
KLK10_P268_R	KLK10	4.01x10^{-02}	1.18x10^{-02}	-2.5684	-3.9472	-0.1607	AACAGAAACAAGGAAAAAGGGAAACCCA[CG]CCCACTCTGTGGCCGTGAGTGA
FLJ20712_P984_R	FLJ20712	3.08x10^{-02}	7.98x10^{-03}	-2.7101	-3.5977	-0.1623	ACTGCTTTGTTGAGCCCCAGAAC[CG]GCAGCGGATACTCCCTGCCAATCAC
CD82_P557_R	CD82	2.46x10^{-04}	1.63x10^{-05}	-4.5437	2.2257	-0.1630	AAAGTTCCTGGGCCCAGGC[CG]CCTCCTGATAGAGGCCCCGACTTAGG
LAT_E46_F	LAT	2.53x10^{-02}	6.09x10^{-03}	-2.8059	-3.3521	-0.1635	GGGTCCTGGATATGGAGGCCA[CG]GCTGCCAGCTGGCAGGTGGC
OSM_P188_F	OSM	3.99x10^{-02}	1.16x10^{-02}	-2.5745	-3.9326	-0.1637	CGCTCCTCCTCCTGTTTTCTT[CG]AATTCGTTCTTCGAGGTCAGCCCTAC
PADI4_E24_F	PADI4	3.07x10^{-02}	7.91x10^{-03}	-2.7133	-3.5895	-0.1643	TCCTACAGCCAGAGGGACGAGCTAGCCCGA[CG]ATGGCCCAGGGGACATTGATC
TFF1_P180_R	TFF1	2.35x10^{-03}	2.60x10^{-04}	-3.7946	-0.4200	-0.1677	ATGGAAGGATTTGCTGATAGACAGAGA[CG]ACATGTGGTGAGGTCATCTTGG
NOTCH4_P938_F	NOTCH4	3.44x10^{-02}	9.39x10^{-03}	-2.6516	-3.7440	-0.1681	CCTGAGAGCCTTCCCCTAC[CG]GGGAATATACTTCACCAGCACCACTTT
CCL3_P543_R	CCL3	3.27x10^{-03}	3.93x10^{-04}	-3.6755	-0.8090	-0.1681	ATGTAGTGACTAGGGCGCTGTGTTAAA[CG]CTAGTTGTGGATCATAAAAATACTTT
LCN2_P86_R	LCN2	4.43x10^{-02}	1.36x10^{-02}	-2.5148	-4.0755	-0.1725	GCAGAAATCTTGCCAAGTGTTTC[CG]CAGGAGTTGCTGGCAATTGCCTCACATTCC
CSF3R_P472_F	CSF3R	1.91x10^{-02}	4.16x10^{-03}	-2.9366	-3.0054	-0.1734	CTCACTGCTCCCCTCTTCATTA[CG]TATTCTGTGCATTGCCCATAGACCAGGCA
CD2_P68_F	CD2	4.81x10^{-02}	1.50x10^{-02}	-2.4772	-4.1638	-0.1740	TGTAAAGAGAGGCACGTGGTTAAGCTCT[CG]GGGTGTGGACTCCACCAGTC
MC2R_P1025_F	MC2R	3.54x10^{-02}	9.84x10^{-03}	-2.6347	-3.7857	-0.1776	AACATGCCCTGCAGCTGAAACC[CG]GCGTTCCACAGGCCTCTTTCC
CREB1_P819_F	CREB1	1.53x10^{-05}	7.03x10^{-07}	-5.3156	5.2615	-0.1799	TGTAGAAAACAGGCTGAGGAAAGAAAG[CG]ACACAGGATGTTGTCTGGAGAAA
PTPRH_E173_F	PTPRH	3.41x10^{-02}	9.29x10^{-03}	-2.6555	-3.7343	-0.1802	CAGCACCTACTTCCTCAAGAT[CG]AGGTGCAGGCACCCAGCTCCTTCT
PYCARD_P393_F	PYCARD	8.63x10^{-03}	1.38x10^{-03}	-3.2957	-1.9867	-0.1805	CCAGCATAACATGGCCAACC[CG]ATGGCTCCCGAAACCTTGCCAGATGC
KRT5_P308_F	KRT5	4.17x10^{-03}	5.48x10^{-04}	-3.5775	-1.1223	-0.1827	GAGTATTGACAACCATCCCAGTA[CG]GTACATGCTGAGCACCTGCCCTTCCAG
VAMP8_P241_F	VAMP8	3.11x10^{-02}	8.11x10^{-03}	-2.7045	-3.6116	-0.1832	ATCAGGAGGTCCAGCCTCTGGAAACCT[CG]GAGGGCTGCTTGATCTTT
SFTPA1_P421_F	SFTPA1	1.52x10^{-02}	3.01x10^{-03}	-3.0447	-2.7087	-0.1847	TGGGGCTCATGGCTGAGCCAGGT[CG]CAGGACAGACAAGTTGGCCTGGA
IL16_P93_R	IL16	2.42x10^{-02}	5.72x10^{-03}	-2.8277	-3.2952	-0.1854	CTCATATTCAAATACTCCCAGC[CG]AGAAGCTGCCATCGATCCTCCCATG

Table SI. Continued.

ID	Gene name	adj.P.Val	P-value	t	B	logFC	Sequence
PTK6_E50_F	PTK6	$3.02\text{x}10^{-02}$	$7.76\text{x}10^{-03}$	-2.7201	-3.5723	-0.1862	GGCCCAGGTGAGCCTGGTCC[CG]GGACACCATGGCGGGCGGGCGCAGC
MPL_P62_F	MPL	$2.06\text{x}10^{-02}$	$4.59\text{x}10^{-03}$	-2.9035	-3.0945	-0.1866	AGGGGCAGGGACAGGGACAGGA[CG]TGGGGCTGTATCTGACAGGA
SPARC_P195_F	SPARC	$1.65\text{x}10^{-03}$	$1.66\text{x}10^{-04}$	-3.9223	0.0076	-0.1891	ACCCTGCCTGCCTCATCTGTTC[CG]GGGCTGCTGCCTAAACCGACTCACAGAG
SPI1_P48_F	SPI1	$4.11\text{x}10^{-02}$	$1.23\text{x}10^{-02}$	-2.5526	-3.9852	-0.1917	GTCCCCTTGGGGTGACATCAC[CG]CCCCAACCCGTTTGCATAAATCTC
CASP8_E474_F	CASP8	$6.12\text{x}10^{-03}$	$9.03\text{x}10^{-04}$	-3.4274	-1.5895	-0.1952	CCTTGCCCAGAGGCTGCGGGCTG[CG]GGTCAAGACATCAGTAGAAGGAGG
LEFTY2_P719_F	LEFTY2	$3.37\text{x}10^{-02}$	$9.10\text{x}10^{-03}$	-2.6628	-3.7160	-0.2000	CTCTCCCCAGTGAGCTGGCTGGC[CG]GTTCATGCCACCAGCACTCAGCTGG
IL6_P213_R	IL6	$4.76\text{x}10^{-02}$	$1.47\text{x}10^{-02}$	-2.4843	-4.1472	-0.2023	TCTGCTTCTTAGCGCTAGCCTCAATGA[CG]ACCTAAGCTGCACTTTTCCCCCTAG
PSCA_P135_F	PSCA	$2.21\text{x}10^{-02}$	$4.99\text{x}10^{-03}$	-2.8749	-3.1706	-0.2053	AAGGGAGAGGGAGGTGCAGGT[CG]CTCAGGGAGGAGACTCGGAC
SFTPB_P689_R	SFTPB	$4.67\text{x}10^{-03}$	$6.48\text{x}10^{-04}$	-3.5276	-1.2795	-0.2063	GGTAGGGGCTGGGGCATAGCTG[CG]ATGGTTCAGCAGAAAGAAACTGTCC
MMP19_P306_F	MMP19	$4.82\text{x}10^{-02}$	$1.51\text{x}10^{-02}$	-2.4753	-4.1683	-0.2087	CCTGGGCCAGCAAATCACTC[CG]CCCCTACCTTTGAGTCTCCCTAGAA
MAGEC3_E307_F	MAGEC3	$2.51\text{x}10^{-02}$	$5.98\text{x}10^{-03}$	-2.8120	-3.3361	-0.2123	TCCCTTGGTTGCAGTAGCCTGTGGT[CG]CTCATGTCTGAATCTCCAGGGAA
NAT2_P11_F	NAT2	$3.36\text{x}10^{-02}$	$9.04\text{x}10^{-03}$	-2.6652	-3.7103	-0.2130	AACTAGACTCTGGTGTCAGGGTGATA[CG]GAATTCCAGTGAGATCACTTCCCT
ZNFN1A1_E102_F	ZNFN1A1	$3.81\text{x}10^{-02}$	$1.09\text{x}10^{-02}$	-2.5972	-3.8775	-0.2133	GGAGGATTTACGAATGCTTGATGCCT[CG]GGAGAGAAAATGAATGGCT
LMO2_E148_F	LMO2	$3.38\text{x}10^{-02}$	$9.17\text{x}10^{-03}$	-2.6603	-3.7224	-0.2152	CGGAGCCTTCACCCTTGCAG[CG]AGCTCTCTCACACCAGATGTGCTCTGCGT
GLI2_E90_F	GLI2	$2.95\text{x}10^{-02}$	$7.47\text{x}10^{-03}$	-2.7340	-3.5370	-0.2172	AAGAAAGTGATGATGCGATGTCTAAAA[CG]TTCAAGGCACCGCATCTGTGATCAAGA
SERPINE1_E189_R	SERPINE1	$7.11\text{x}10^{-06}$	$2.88\text{x}10^{-07}$	-5.5246	6.1285	-0.2174	CGCTATTCCTCTATTTTCTTTTCCT[CG]GACCTGCAGCCTTGGGTCGACCCTGC
MMP9_E88_R	MMP9	$2.64\text{x}10^{-02}$	$6.41\text{x}10^{-03}$	-2.7877	-3.3993	-0.2176	CTGCTTTGCTGCCCCCAGACAG[CG]CCAGTCCACCCTTGTGCTCTTCCC
MUC1_P191_F	MUC1	$1.54\text{x}10^{-02}$	$3.18\text{x}10^{-03}$	-3.0272	-2.7575	-0.2190	CTCAACCCCCTGACTACC[CG]TTTGTTCTCCAGCTGGCCTCCCC
SLC22A18_P216_R	SLC22A18	$4.13\text{x}10^{-02}$	$1.24\text{x}10^{-02}$	-2.5480	-3.9964	-0.2200	GTCAGCCTGGATCCTCTCATC[CG]GCAGAACTGTCGCCTTGCTTCTCTGAAGCG
MBD2_P233_F	MBD2	$5.59\text{x}10^{-03}$	$8.05\text{x}10^{-04}$	-3.4621	-1.4829	-0.2214	GGGGTGATAGCCCCTTTTCC[CG]CCCCTCTGCACAAAGCTTGCAGGGGA
C4B_P191_F	C4B	$6.12\text{x}10^{-03}$	$9.03\text{x}10^{-04}$	-3.4274	-1.5896	-0.2220	CTCAGGCACTGGAATGAGAGGAGTTAA[CG]GGGAAGGACAGGGTTATTT
TRPM5_P721_F	TRPM5	$3.12\text{x}10^{-02}$	$8.20\text{x}10^{-03}$	-2.7006	-3.6216	-0.2234	GGCTCATGTCTCCCAGCTGCC[CG]GTGAGGTCGGGCATCTCAGCCCCT
HBII-52_E142_F	HBII-52	$3.24\text{x}10^{-02}$	$8.65\text{x}10^{-03}$	-2.6814	-3.6696	-0.2258	GGCCCCCGACGGGGCCACTGTATTT[CG]GGCTGCAGACCTAGAGGCCCTG
WNT8B_E487_F	WNT8B	$9.17\text{x}10^{-03}$	$1.50\text{x}10^{-03}$	-3.2688	-2.0662	-0.2301	GGGGTAAATGGACAGCAGCCCTTTTCA[CG]AAATCCTGATGTCAGCATTGTAGAGAG
SPP1_P647_F	SPP1	$1.73\text{x}10^{-02}$	$3.71\text{x}10^{-03}$	-2.9756	-2.8993	-0.2317	GGGAACAAGGATAGGTAGGCTGGG[CG]ATTTGCCCAAGGTTGCACAGGTCAGCA
MMP3_P55_F	MMP3	$1.90\text{x}10^{-03}$	$1.99\text{x}10^{-04}$	-3.8702	-0.1680	-0.2331	AGAGTGACAGTGTTTGTTTGGATCACC[CG]CAGCTTGACTCATCCTTGCTTTCATCC
IL12B_E25_F	IL12B	$4.47\text{x}10^{-03}$	$6.17\text{x}10^{-04}$	-3.5422	-1.2337	-0.2352	GAAGTGCTTACCTTGCTCTGGGCAGGA[CG]GAGAGTCCAATGGCCCTGAAACAGAT
HLA-DQA2_E93_F	HLA-DQA2	$4.43\text{x}10^{-02}$	$1.36\text{x}10^{-02}$	-2.5156	-4.0735	-0.2373	AGCTCTGCTGCTGGGGGCCCT[CG]CCCTGACTGCCGTGATGAGCCC
IFNG_P188_F	IFNG	$3.77\text{x}10^{-02}$	$1.07\text{x}10^{-02}$	-2.6043	-3.8601	-0.2376	CCTTTAGACTCCTTGGGTCCTTTGA[CG]ATGAGACAGACCCATTATGCCCACC
EMR3_P1297_R	EMR3	$1.33\text{x}10^{-02}$	$2.51\text{x}10^{-03}$	-3.1050	-2.5396	-0.2379	TGATTTACACAGGAACCGAGAGATTGGT[CG]GACTGGGTGTGCTGTTTG
IRF7_E236_R	IRF7	$4.28\text{x}10^{-08}$	$7.96\text{x}10^{-10}$	-6.8320	11.8892	-0.2396	CGTCAGGGGCGGGTCAGGCTCC[CG]GGAAAGCGAAACCTAAACAGTGG
AGXT_P180_F	AGXT	$7.12\text{x}10^{-03}$	$1.08\text{x}10^{-03}$	-3.3725	-1.7566	-0.2429	GAGCTAAGCAGAATAAGAGGGGCTGGA[CG]TGCAGGACTCAGAGTGGGAGCG
NGFR_P355_F	NGFR	$2.94\text{x}10^{-03}$	$3.41\text{x}10^{-04}$	-3.7166	-0.6758	-0.2439	CTCCAGGGAGAAGGTGAAGCCAGAGG[CG]GAGGAAGATGGGTAAGAGA
CDK2_P330_R	CDK2	$1.87\text{x}10^{-26}$	$2.49\text{x}10^{-29}$	-16.3381	56.2196	-0.2453	AGGCCCAGGATTCCTTTGCAA[CG]AGATTCCCGGCTTCCTGGTTTCCA
MKRN3_P108_F	MKRN3	$2.82\text{x}10^{-02}$	$7.02\text{x}10^{-03}$	-2.7560	-3.4807	-0.2515	AAGACCAAAAGAAACGGCGCCTTGTCAAC[CG]AACGAATTGAAAAAAGCTTCCTG
MMP8_E89_R	MMP8	$1.24\text{x}10^{-02}$	$2.23\text{x}10^{-03}$	-3.1437	-2.4295	-0.2545	CTGCACATGGAGTAAGAGCAGAAATGGAAG[CG]TCTTCAGGGAGAACATGATCTTCT
AOC3_P890_R	AOC3	$1.17\text{x}10^{-02}$	$2.04\text{x}10^{-03}$	-3.1720	-2.3484	-0.2568	AATCCTGTGGCCTGCCTCCC[CG]ACCTGGCAGCCTGTGTCCCGGACTTAC

Table SI. Continued.

ID	Gene name	adj.P.Val	P-value	t	B	logFC	Sequence
KRT1_P798_R	KRT1	2.83x10^{-03}	3.24x10^{-04}	-3.7315	-0.6271	-0.2611	TTGAGTGAAAAAGCCCACAGAGCAGTGAGA[CG]AGTAAATAGAAGCTCTAGGACATTTTG
CCR5_P630_R	CCR5	2.14x10^{-05}	9.93x10^{-07}	-5.2337	4.9264	-0.2620	ACTTCTAAACACCATTACATTGGGATT[CG]AATTTCAACATGAATTTTTGGGGAACACAA
LTB4R_E64_R	LTB4R	4.31x10^{-03}	5.79x10^{-04}	-3.5615	-1.1730	-0.2663	CCTGAACTCTGACTTCAGTTCTTGCTG[CG]GTTTCTGCCCATTTTTTTCATATCCT
ACVR1_P983_F	ACVR1	1.54x10^{-02}	3.18x10^{-03}	-3.0268	-2.7586	-0.2692	GTAAGCACTGGCCTCTCTCGGGTCT[CG]CCTTTCTATTGTCCCACCCTGCAGGG
MPO_E302_R	MPO	9.55x10^{-03}	1.57x10^{-03}	-3.2546	-2.1079	-0.2701	GGAGCAGCACCTTCAGAGGGCTGGGG[CG]TGGCCAGAATGGCCAGGAGCCC
PI3_P1394_R	PI3	8.63x10^{-03}	1.38x10^{-03}	-3.2956	-1.9868	-0.2706	AAAGGCTTCCACAGTCTGACATT[CG]TTTATGTCTCCCTCAGTTTCAGGCTTGG
GSTM2_P453_R	GSTM2	9.03x10^{-08}	1.86x10^{-09}	-6.6496	11.0563	-0.2783	CCTTGCCTGTGTTGTCCTTCCCA[CG]TTAGGTCTGTCATGCCACGTATGTCCGCAG
TJP2_P518_F	TJP2	1.14x10^{-04}	6.30x10^{-06}	-4.7837	3.1394	-0.2810	GCTGAGAAATGTGGGGTACAAGGC[CG]TGTATGTGTTGGTTAGCCGGG
TNFSF8_P184_F	TNFSF8	1.06x10^{-02}	1.79x10^{-03}	-3.2136	-2.2278	-0.2833	CACACACAAAGCAACTTCTGTTT[CG]TTTAGACTCTGCCACAAAACGCCTTC
PGR_P790_F	PGR	1.33x10^{-02}	2.47x10^{-03}	-3.1105	-2.5240	-0.2838	CACTAGCAGTTATTCCACATTTC[CG]CCTAAATCTCCCAGCAGCCACTAATAT
FAS_P322_R	FAS	1.41x10^{-06}	4.70x10^{-08}	-5.9389	7.8964	-0.2901	CATATGGTTAACTGTCCATTCCAGAAA[CG]TCTGTGAGCCTCTCATGTTGCAGCCACAAC
HLA-DPB1_E2_R	HLA-DPB1	1.33x10^{-02}	2.49x10^{-03}	-3.1080	-2.5312	-0.2957	TTCAAACAGGAGCTCCCTTTAG[CG]AGTCCTTCTTTTCCTGACTGCAGCTCTTT
DSG1_P159_R	DSG1	1.32x10^{-02}	2.43x10^{-03}	-3.1152	-2.5105	-0.2992	CCCATCACCTGTATAACCCT[CG]GTATTTCTGTTCACTTTAAGAGCCTGCCAC
VAV1_P317_F	VAV1	8.49x10^{-03}	1.34x10^{-03}	-3.3047	-1.9599	-0.3057	TGGAGTCAGAAGACCAGCTGAGTGATGA[CG]GGGCTGGACCAGACAGAGGA
STAT5A_E42_F	STAT5A	1.38x10^{-02}	2.64x10^{-03}	-3.0888	-2.5853	-0.3072	TGCTGTGGCAAGGCCTGTAGAGAGTTT[CG]AAGTTAGGAGGACTCAAGACGGT
SPDEF_P6_R	SPDEF	7.91x10^{-04}	6.89x10^{-05}	-4.1638	0.8433	-0.3131	TGTGCTGGGAGGAAGTCAGACAGCCG[CG]AGATGAAGAGTTGGCCAGGGC
FGFR2_P460_R	FGFR2	1.68x10^{-06}	5.71x10^{-08}	-5.8951	7.7067	-0.3150	GAGACTTTAAAATGCGCCTGCTTGATACTG[CG]GGGAGGGTTGCCAGGCAG
NOS2A_P288_R	NOS2A	1.78x10^{-03}	1.84x10^{-04}	-3.8938	-0.0888	-0.3166	AGGGTGGCTGCTAAGATAGAGGCACCA[CG]GAGCCAGGTTTTATTTGGCCAAGCC
CD86_P3_F	CD86	4.24x10^{-03}	5.63x10^{-04}	-3.5695	-1.1477	-0.3284	AAGTTAGCTGGGTAGGTATACAGTCATTGC[CG]AGGAAGGCTTGCACAGGGTG
GFAP_P1214_F	GFAP	1.86x10^{-03}	1.94x10^{-04}	-3.8779	-0.1421	-0.3368	CCTGGAGACTTCAGGTCCATCTA[CG]CCCTCCACTCTGGTCCCACAGG
RIPK3_P24_F	RIPK3	1.12x10^{-02}	1.92x10^{-03}	-3.1911	-2.2931	-0.3633	TCCGGGTTGTTACCCTTTTTC[CG]AGTTGACTGAACAACTTCCCTTATAGGCGC
ALPL_P433_F	ALPL	6.02x10^{-11}	6.40x10^{-13}	-8.3193	18.9031	-0.3641	GAGAGACAGGGACACGTGGGCAGAGA[CG]GATAAAGACAGAGACCCAGAGAAAGCC
CASP10_E139_F	CASP10	1.50x10^{-04}	9.38x10^{-06}	-4.6837	2.7552	-0.3692	TTTGTTTTCAGGCAATTTCCCTGAGAAC[CG]TTTACTTCCAGAAGATTGGTGGAG
HDAC1_P414_R	HDAC1	3.54x10^{-04}	2.59x10^{-05}	-4.4237	1.7804	-0.3798	CCTCCTTTGCGGCCACAAACT[CG]CTTTCTAACCCAGGTTCAGCCCT
PRSS1_P1249_R	PRSS1	1.30x10^{-03}	1.27x10^{-04}	-3.9955	0.2572	-0.3830	TAGCCCCCTGGCCAGGTC[CG]ATTTCAACACCAAGTTTCTGAGCTTTT
SH3BP2_E18_F	SH3BP2	6.75x10^{-22}	1.79x10^{-24}	-13.8286	45.1908	-0.3868	GGGTCCAGCCGGGTGACCCAGGC[CG]AGGCCGGCAGAAGACAGCCTGAT
S100A2_P1186_F	S100A2	2.09x10^{-04}	1.36x10^{-05}	-4.5893	2.3973	-0.3932	TCTACACCTTGGCACAGCCAC[CG]AGTGTCCCTTGCTCCCCTCAGTACTT
TNFSF10_P2_R	TNFSF10	8.60x10^{-04}	7.77x10^{-05}	-4.1311	0.7279	-0.4161	TCTTTTATAGTCAGTGAGGAAATGAAAG[CG]AATGAGTTGTTTTTCTGGGT
TRIP6_P1090_F	TRIP6	1.24x10^{-09}	1.73x10^{-11}	-7.6396	15.6571	-0.4211	AAGGGGACTTTGTGAACAGTGGG[CG]GGGAGACGCAGAGGCAGAGG
JAK3_P1075_R	JAK3	1.00x10^{-06}	2.93x10^{-08}	-6.0449	8.3583	-0.4220	GGACAGGCACAGACTGGAACTTGGACC[CG]AGGCAGGACAGGGAGCTGGC
IL8_P83_F	IL8	1.30x10^{-03}	1.26x10^{-04}	-3.9985	0.2675	-0.4397	AGGGGATGGGCCATCAGTTGCAAAT[CG]TGGAATTTCCTCTGACATAATGAAA

adj.P.Val, adjusted P-value; t, the t value of the expression values of the two groups to be compared after t test; B, the logarithmic value of the standard deviation obtained by Bayesian adjustment.