

Figure S1. Exploration of the function of AC068643.1. (A-C) Pearson correlation analyses demonstrated that AC068643.1 was significantly positively correlated with (A) BMP2, (B) MSTN and (C) ATP13A5 in GBM samples from TCGA database. (D-E) Bioinformatic analyses revealed that (D) BMP2 and (E) MSTN were upregulated in *IDH^{MT}* compared with *IDH^{WT}* GBMs from the CGGA database. (F-G) Survival analyses demonstrated that high expression of (F) BMP2 and (G) MSTN predicted favorable prognosis for patients with GBM. ***P<0.001. GBM, glioblastoma; TCGA, The Cancer Genome Atlas; CGGA, Chinese Glioma Genome Atlas; HR, hazard ratio; CI, confidence interval; BMP2, Bone morphogenetic protein 2; MSTN, Myostatin; ATP13A5, ATPase 13 A5.

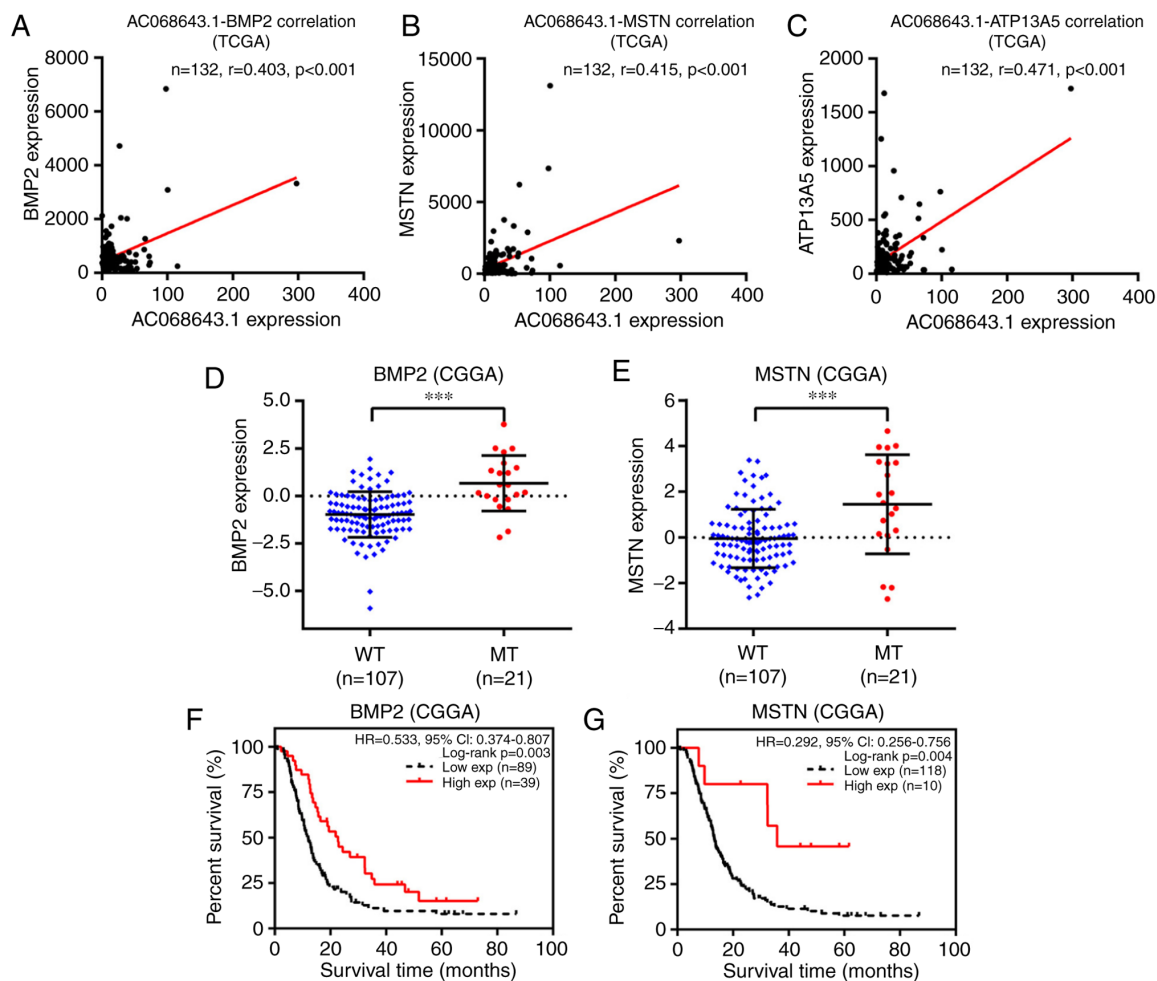


Figure S2. Functional analysis of AC068643.1. (A) KEGG and (B) GO gene enrichment analyses of the mRNAs co-expressed with AC068643.1. KEGG, Kyoto Encyclopedia of Genes and Genomes; GO, Gene Ontology.

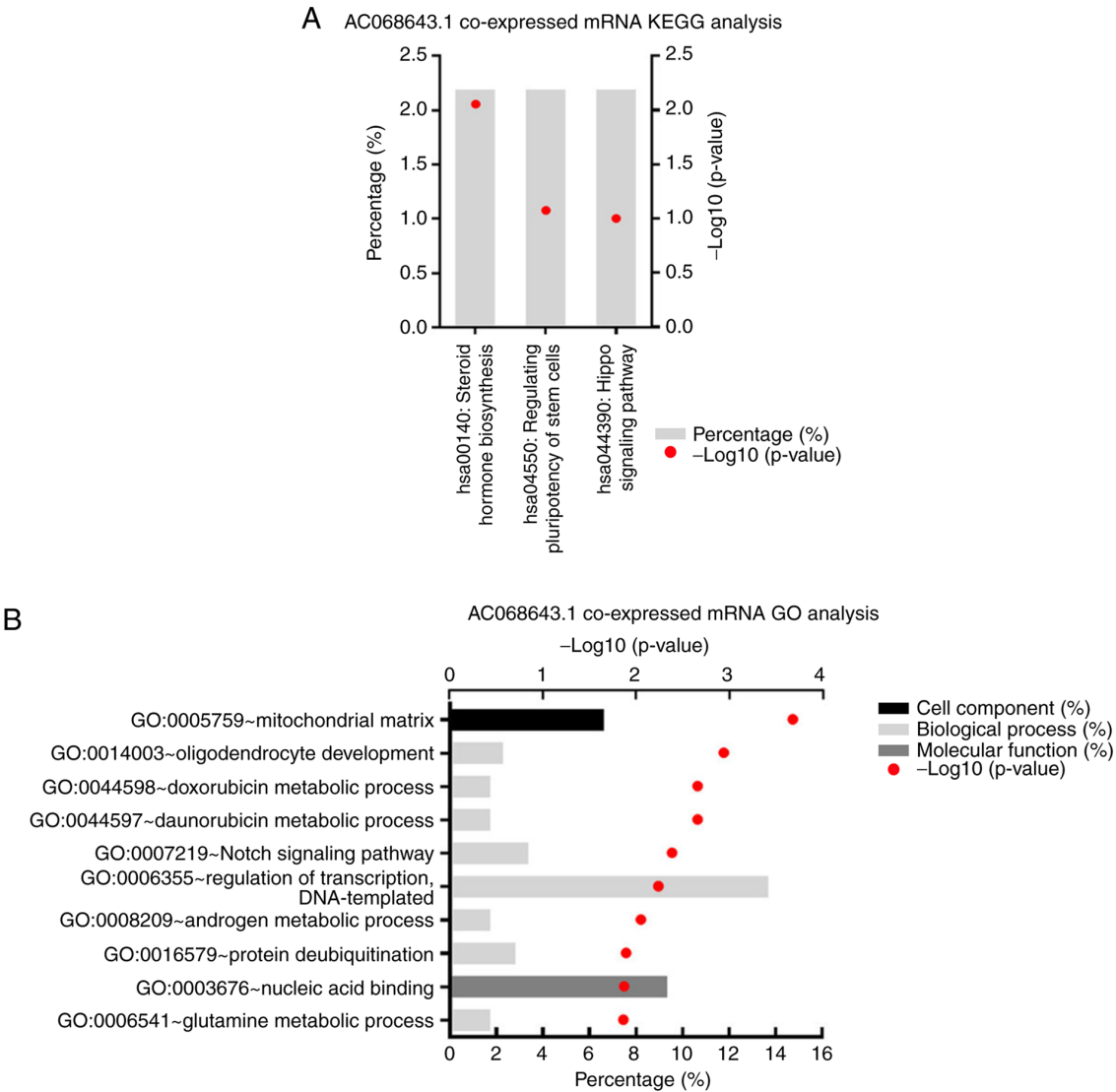


Table SI. Clinical characteristics of patients in TCGA and CGGA databases and the XQ Cohort.

Characteristic	TCGA			CGGA			XQ Cohort		
	Total	IDHwt	IDHmt	Total	IDHwt	IDHmt	Total	IDHwt	IDHmt
No. of patients	132	122	10	128	107	21	45	37	8
Age, years									
Median	59.8	61.5	39.2	46.7	48.3	39	50	52.3	40.9
Range	21-85	24-85	21-60	13-70	13-70	25-62	22-76	22-76	25-59
>40	121	116	5	91	81	10	31	28	3
≤40	11	6	5	37	26	11	14	9	5
Gender									
Male	86	78	8	80	67	13	28	23	5
Female	46	44	2	48	40	8	17	14	3
Male-to-Female ratio	1.87	1.77	4.00	1.67	1.68	1.63	1.65	1.64	1.67
KPS									
>70	79	73	6	-	-	-	27	22	5
≤70	30	30	0	-	-	-	18	15	3
N/A	33	19	4	-	-	-	-	-	-

TCGA, The Cancer Genome Atlas; CGGA, Chinese Glioma Genome Atlas; XQ, Xinqiao Hospital; IDHwt, isocitrate dehydrogenase wildtype; IDHmt, isocitrate dehydrogenase mutant; KPS, Karnofsky performance status; N/A, not available; ‘-’, no data.

Table SII. Univariate Cox analysis of differentially expressed long non-coding RNAs.

Gene	HR	z	P-value
AC068643.1	0.754	-3.720	0.001 ^a
AC022148.1	0.730	-3.408	0.001 ^a
LINC01776	1.234	3.338	0.001 ^a
LINC02036	1.385	3.311	0.001 ^a
AC005056.1	1.337	3.072	0.002
AL157700.1	0.760	-3.055	0.002
ANKRD62P1-PARP4P3	0.715	-2.968	0.003
AC093890.3	0.805	-2.949	0.003
AL353597.1	0.727	-2.882	0.004
AGAP2-AS1	1.170	2.875	0.004
LOXL1-AS1	1.197	2.787	0.005
AC093890.1	0.684	-2.677	0.007
AC243773.2	0.863	-2.653	0.008
LINC01124	1.216	2.647	0.008
TMEM220-AS1	1.268	2.635	0.008
AC007485.1	1.301	2.625	0.009
DBH-AS1	1.236	2.617	0.009
AC055874.1	1.150	2.572	0.010
LINC00683	1.244	2.557	0.011
AC025171.3	1.259	2.469	0.014
AC104090.1	0.839	-2.463	0.014
AC103718.1	0.794	-2.417	0.016
AC104407.1	1.123	2.412	0.016
AP002840.2	1.194	2.356	0.018
AC122108.2	0.726	-2.321	0.020
LINC00645	0.881	-2.318	0.020
AL161629.1	0.843	-2.278	0.023
AC096669.1	0.842	-2.224	0.026
AL512329.2	1.144	2.216	0.027
PAUPAR	1.162	2.189	0.029
AL162231.4	1.188	2.135	0.033
LINC00698	0.870	-2.130	0.033
AC005592.1	1.200	2.122	0.034
AC010729.1	1.160	2.116	0.034
CHL1-AS1	1.189	2.068	0.039
LINC00460	1.129	2.043	0.041
AC025154.2	1.156	2.020	0.043
CCDC26	0.864	-2.018	0.044
LINC01905	0.805	-2.003	0.045
LINC00601	1.171	1.977	0.048
AC131097.4	1.157	1.960	0.050
AC005225.2	1.214	1.938	0.053
AC103925.1	0.802	-1.922	0.055
LINC01842	1.136	1.899	0.058
LINC02086	1.151	1.887	0.059
AC005264.1	1.190	1.852	0.064
LINC01831	1.100	1.849	0.064
AP000289.1	0.856	-1.814	0.070
AC010754.1	1.108	1.794	0.073
CHL1-AS2	1.114	1.781	0.075
AL163636.1	1.133	1.769	0.077
AC022498.1	0.877	-1.763	0.078
AC015936.1	0.885	-1.738	0.082
AC068057.1	1.131	1.726	0.084
AC064875.1	1.099	1.718	0.086

Table SII. Continued.

Gene	HR	z	P-value
LINC01515	1.123	1.705	0.088
AP001269.2	1.127	1.689	0.091
PCOLCE-AS1	1.124	1.636	0.102
LINC02432	1.108	1.634	0.102
AC073486.1	0.872	-1.606	0.108
AC097641.1	0.831	-1.596	0.110
AC021218.1	1.089	1.595	0.111
HORMAD2-AS1	1.114	1.577	0.115
AC025035.1	0.885	-1.559	0.119
LINC01630	0.892	-1.558	0.119
LINC00028	0.868	-1.539	0.124
AC067735.1	1.100	1.538	0.124
LINC02058	0.899	-1.527	0.127
LINC01479	0.833	-1.526	0.127
AL035588.1	0.800	-1.521	0.128
AC022239.4	0.873	-1.496	0.135
AL049541.2	0.857	-1.466	0.143
MIR217HG	0.910	-1.449	0.147
VAV3-AS1	1.155	1.395	0.163
AP003032.1	1.099	1.392	0.164
LINC00960	0.898	-1.383	0.167
AL590560.2	1.107	1.357	0.175
AL121820.2	1.121	1.334	0.182
AL122019.1	0.931	-1.314	0.189
AL592494.3	1.084	1.307	0.191
AL139158.2	1.090	1.274	0.203
LINC01121	0.927	-1.268	0.205
AC004264.2	1.096	1.243	0.214
LINC01965	1.093	1.233	0.218
AL139231.1	0.935	-1.225	0.221
LINC00488	1.071	1.221	0.222
SPRY4-IT1	1.073	1.220	0.222
AL031283.3	1.115	1.192	0.233
AC025263.1	0.923	-1.169	0.242
AC022034.4	1.087	1.153	0.249
AC005550.3	1.086	1.139	0.255
LINC00470	0.900	-1.137	0.256
AC068768.2	0.888	-1.109	0.268
NPSR1-AS1	0.928	-1.054	0.292
AC084859.1	1.063	1.014	0.311
WASIR2	1.079	0.981	0.326
AL353597.2	0.921	-0.974	0.330
AC092535.4	1.081	0.963	0.336
AC092634.3	0.939	-0.949	0.343
FLJ16779	0.956	-0.912	0.362
DPP10-AS1	0.954	-0.884	0.376
LINC01711	1.072	0.877	0.380
AC022294.1	0.951	-0.874	0.382
AC131902.2	1.065	0.871	0.384
AC107464.1	1.057	0.870	0.384
AC024337.2	1.044	0.863	0.388
AC005383.1	0.938	-0.831	0.406
HOXB-AS3	1.039	0.811	0.418
AC027117.2	1.076	0.797	0.425
AL035425.1	0.953	-0.756	0.450
AC017002.1	1.079	0.736	0.461

Table SII. Continued.

Gene	HR	z	P-value
AC087477.2	1.037	0.676	0.499
AC009501.1	0.956	-0.647	0.517
AC021678.2	1.044	0.644	0.519
AC092675.2	1.042	0.637	0.524
AP000842.3	0.964	-0.632	0.528
MEIS1-AS2	1.048	0.626	0.532
AC016168.1	1.043	0.590	0.555
AL080312.2	1.033	0.569	0.569
AC138466.1	0.948	-0.537	0.591
ELOVL2-AS1	1.029	0.510	0.610
AC012409.3	1.032	0.501	0.616
AC026765.2	0.962	-0.496	0.620
AL445644.1	0.944	-0.460	0.645
AL359094.1	0.970	-0.432	0.665
AC148477.1	1.033	0.429	0.668
AC126614.1	0.966	-0.400	0.689
AC023301.1	1.018	0.383	0.702
AC003035.2	0.980	-0.327	0.744
AC131902.1	1.024	0.313	0.754
AL122034.1	0.979	-0.263	0.793
LINC01551	1.014	0.245	0.806
AC025031.2	1.021	0.198	0.843
AC092958.1	1.011	0.191	0.848
AC091138.1	0.993	-0.171	0.864
AC012213.4	1.006	0.083	0.934
AC073324.2	0.997	-0.076	0.939
AC018653.1	0.996	-0.053	0.958
AC090825.1	1.004	0.050	0.960
GDNF-AS1	1.000	-0.005	0.996

*P≤0.001. HR, hazard ratio.

1	Table SIII. Univariate Cox analysis of differentially expressed				Table SIII. Continued.				61
2	mRNAs								62
3									63
4	Gene	HR	z	P-value	Gene	HR	z	P-value	64
5					PDLIM4	1.165	2.498	0.013	65
6	LRRC61	1.262	3.941	0.001 ^a	TNFRSF11B	1.200	2.474	0.013	66
7	CBLN3	1.473	3.810	0.001 ^a	FABP5	1.201	2.451	0.014	67
8	PTX3	1.244	3.541	0.001 ^a	RANBP17	0.846	-2.444	0.015	68
9	ATP13A5	0.799	-3.470	0.001 ^a	PPL	1.161	2.442	0.015	69
10	WFDC2	1.339	3.391	0.001 ^a	FBXO39	1.203	2.438	0.015	70
11	EFEMP2	1.486	3.390	0.001 ^a	COL6A2	1.165	2.432	0.015	71
12	AEBP1	1.303	3.379	0.001 ^a	AC114296.1	1.219	2.426	0.015	72
13	CYGB	1.274	3.343	0.001 ^a	RBP3	0.875	-2.420	0.016	73
14	SLC16A11	1.284	3.324	0.001 ^a	IL9	0.794	-2.414	0.016	74
15	TIMP1	1.282	3.321	0.001 ^a	DIRAS3	1.188	2.402	0.016	75
16	DDIT4L	1.203	3.272	0.001 ^a	KHDRBS2	0.860	-2.398	0.016	76
17	VASN	1.316	3.253	0.001 ^a	SLC25A48	0.887	-2.390	0.017	77
18	CES1	1.179	3.236	0.001 ^a	RBP1	1.192	2.379	0.017	78
19	HIST3H2A	0.839	-3.236	0.001 ^a	RHOD	1.134	2.379	0.017	79
20	PODNL1	1.240	3.201	0.001 ^a	PRSS55	0.839	-2.379	0.017	80
21	FATE1	1.240	3.165	0.002	PNPLA4	1.238	2.378	0.017	81
22	ZNF560	0.843	-3.158	0.002	GJB2	1.133	2.372	0.018	82
23	GPR1	1.172	3.130	0.002	C10orf67	1.173	2.369	0.018	83
24	MTSN	0.857	-3.124	0.002	TRIM48	0.856	-2.364	0.018	84
25	RARRES1	1.185	3.105	0.002	EMP3	1.233	2.363	0.018	85
26	C9orf64	1.509	3.104	0.002	PQLC2L	1.160	2.347	0.019	86
27	RARRES2	1.201	3.044	0.002	TSPY2	0.760	-2.343	0.019	87
28	STEAP3	1.300	3.021	0.003	LGR6	1.117	2.316	0.021	88
29	TMEM61	1.229	2.982	0.003	GPX8	1.193	2.311	0.021	89
30	FBXO17	1.298	2.951	0.003	PTCHD4	1.210	2.295	0.022	90
31	ARSD	1.466	2.922	0.003	LGALS3	1.167	2.286	0.022	91
32	CHI3L1	1.145	2.883	0.004	RASSF9	1.120	2.283	0.022	92
33	PLA2R1	1.228	2.862	0.004	F3	1.211	2.283	0.022	93
34	AHNAK2	1.187	2.850	0.004	UBXN10	1.113	2.266	0.023	94
35	RAB36	1.279	2.838	0.005	ADAMTS20	0.872	-2.260	0.024	95
36	TEX26	1.198	2.825	0.005	RIN1	1.222	2.244	0.025	96
37	STAC2	1.179	2.765	0.006	ZNF729	0.852	-2.234	0.025	97
38	BMP2	0.769	-2.762	0.006	PCDHGB4	0.849	-2.214	0.027	98
39	TMEM100	0.826	-2.719	0.007	ARSI	1.133	2.207	0.027	99
40	AL162231.1	1.260	2.706	0.007	OPLAH	1.216	2.196	0.028	100
41	FOXE1	0.812	-2.689	0.007	PDGFRL	1.170	2.191	0.028	101
42	LOXL4	1.189	2.665	0.008	CRYAB	0.846	-2.185	0.029	102
43	DEFB124	0.820	-2.660	0.008	REM1	0.870	-2.176	0.030	103
44	PDPN	1.246	2.654	0.008	SCNN1G	1.101	2.172	0.030	104
45	FLNC	1.192	2.647	0.008	MT1M	1.171	2.152	0.031	105
46	SH2D4A	1.272	2.643	0.008	PLA2G5	1.119	2.145	0.032	106
47	FAM46B	1.211	2.634	0.008	MAOB	1.174	2.130	0.033	107
48	BANK1	1.196	2.621	0.009	COL8A1	1.118	2.128	0.033	108
49	FERMT1	0.855	-2.611	0.009	SLC2A10	1.250	2.126	0.033	109
50	CCDC8	1.196	2.610	0.009	PDGFA	1.193	2.117	0.034	110
51	OR10Q1	0.705	-2.606	0.009	LRRN4	0.827	-2.117	0.034	111
52	DES	1.152	2.598	0.009	TSHR	0.904	-2.114	0.035	112
53	NPY2R	1.124	2.569	0.010	AQP5	1.104	2.109	0.035	113
54	EDA2R	1.211	2.563	0.010	ARSJ	1.159	2.108	0.035	114
55	MEDAG	1.140	2.552	0.011	GRIK1	1.151	2.103	0.035	115
56	TNFRSF18	1.230	2.531	0.011	EMID1	1.225	2.101	0.036	116
57	KRT7	1.163	2.527	0.011	SYNPO2L	0.830	-2.090	0.037	117
58	TCEA3	1.225	2.520	0.012	TNFAIP6	1.157	2.090	0.037	118
59	AK7	1.159	2.515	0.012	ANKK1	1.132	2.059	0.039	119
60	COL5A1	1.170	2.498	0.012	TPPP3	1.154	2.059	0.040	120

1	Table SIII. Continued.				Table SIII. Continued.				61
2									62
3	Gene	HR	z	P-value	Gene	HR	z	P-value	63
4									64
5	ETV4	1.137	2.055	0.040	CNTNAP3B	1.124	1.617	0.106	65
6	FMOD	1.122	2.040	0.041	GATA3	1.110	1.613	0.107	66
7	SMCP	0.808	-2.040	0.041	POSTN	1.066	1.599	0.110	67
8	ZNF676	0.902	-2.011	0.044	RGS6	1.102	1.599	0.110	68
9	FREM3	0.927	-2.009	0.045	DSCAML1	0.915	-1.598	0.110	69
10	NPTX2	1.097	2.007	0.045	AC007906.2	1.132	1.583	0.113	70
11	IGFN1	0.919	-1.988	0.047	ESPNL	1.092	1.582	0.114	71
12	STEAP1	1.136	1.985	0.047	HOXB4	1.065	1.579	0.114	72
13	PGA3	0.818	-1.974	0.048	CSDC2	0.906	-1.573	0.116	73
14	SUSD5	0.904	-1.950	0.051	TLX3	0.860	-1.568	0.117	74
15	KCNN4	1.141	1.943	0.052	GPR157	1.148	1.543	0.123	75
16	NEUROD4	0.909	-1.943	0.052	ZNF98	0.921	-1.530	0.126	76
17	CPB1	0.880	-1.941	0.052	COL1A2	1.097	1.515	0.130	77
18	AC068775.2	0.851	-1.926	0.054	RD3	0.839	-1.514	0.130	78
19	RAB34	1.169	1.894	0.058	GADD45G	0.903	-1.514	0.130	79
20	CXCL14	1.093	1.892	0.058	ARSF	1.078	1.498	0.134	80
21	SSTR2	0.860	-1.879	0.060	KRT5	0.937	-1.498	0.134	81
22	ACSS3	1.137	1.876	0.061	SCG2	1.111	1.497	0.134	82
23	SSTR5	0.858	-1.876	0.061	VIPR2	0.941	-1.497	0.134	83
24	SYTL5	1.126	1.869	0.062	AGMO	1.109	1.496	0.135	84
25	GPR39	1.154	1.859	0.063	FGF17	0.930	-1.487	0.137	85
26	GALNT14	0.863	-1.856	0.063	OCIAD2	1.103	1.486	0.137	86
27	LHX1	0.922	-1.852	0.064	CHRN4	1.094	1.450	0.147	87
28	COL12A1	1.141	1.850	0.064	ANGPT4	0.903	-1.448	0.147	88
29	KLRC4	0.897	-1.849	0.064	PIK3CD	1.141	1.448	0.148	89
30	SLC25A21	0.896	-1.848	0.065	PGA5	0.918	-1.441	0.150	90
31	ARL9	1.127	1.836	0.066	MEOX2	1.065	1.441	0.150	91
32	CHRM3	1.104	1.822	0.069	HOXB13	1.055	1.428	0.153	92
33	KRT18	1.141	1.806	0.071	GALNT5	1.076	1.426	0.154	93
34	MTTP	1.128	1.800	0.072	C1QTNF3	0.870	-1.425	0.154	94
35	ABCC3	1.108	1.792	0.073	STAC	1.069	1.407	0.159	95
36	GLIS1	0.910	-1.792	0.073	TERT	1.070	1.400	0.161	96
37	FEZF1	1.081	1.780	0.075	KLRC3	0.933	-1.390	0.164	97
38	ADAM33	1.116	1.777	0.076	DPP10	0.938	-1.386	0.166	98
39	FBLN7	1.128	1.766	0.077	CNTN3	0.938	-1.385	0.166	99
40	CMYA5	1.136	1.753	0.080	LRRC26	0.900	-1.378	0.168	100
41	PGC	0.868	-1.753	0.080	HS3ST3B1	1.082	1.364	0.173	101
42	PPP1R36	1.144	1.752	0.080	GSDMC	0.926	-1.363	0.173	102
43	HOXB7	1.097	1.745	0.081	CARMIL1	1.124	1.360	0.174	103
44	APCDD1L	1.072	1.738	0.082	GLP1R	0.930	-1.352	0.176	104
45	DCHS2	1.131	1.725	0.085	TMEM221	1.107	1.350	0.177	105
46	LGALS12	1.135	1.716	0.086	C3orf22	0.894	-1.349	0.177	106
47	GPR3	1.175	1.685	0.092	C21orf62	1.103	1.340	0.180	107
48	OR4N2	0.933	-1.682	0.093	DAZ1	0.821	-1.336	0.181	108
49	ZNF728	0.884	-1.673	0.094	WNT16	1.058	1.315	0.188	109
50	EDN2	1.098	1.664	0.096	MOXD1	1.071	1.301	0.193	110
51	VAV3	1.124	1.663	0.096	ERICH3	1.080	1.298	0.194	111
52	TRPM3	1.150	1.660	0.097	PLAC1	0.879	-1.292	0.196	112
53	ZNF488	0.930	-1.659	0.097	PRAC2	1.048	1.266	0.205	113
54	HOXB3	1.077	1.659	0.097	PCDH15	0.951	-1.262	0.207	114
55	ZNF492	0.910	-1.650	0.099	LGI1	1.101	1.260	0.208	115
56	CHL1	1.127	1.634	0.102	LCN1	0.900	-1.256	0.209	116
57	TSTD1	1.103	1.633	0.102	SLC14A2	0.909	-1.250	0.211	117
58	SHROOM3	1.124	1.632	0.103	SRD5A2	0.930	-1.246	0.213	118
59	BMP5	1.063	1.619	0.106	NR2E1	1.099	1.236	0.217	119
60	CDH4	1.123	1.618	0.106	EGFR	0.942	-1.234	0.217	120

Table SIII. Continued.

Gene	HR	z	P-value
C9orf24	1.066	1.224	0.221
IRS4	0.914	-1.210	0.226
HTR1D	1.079	1.202	0.229
RIPK4	0.928	-1.188	0.235
VSX1	1.074	1.183	0.237
DBX2	1.071	1.180	0.238
DNAH8	0.925	-1.171	0.242
GPR50	0.891	-1.168	0.243
THBS4	1.078	1.165	0.244
MAB21L1	1.083	1.146	0.252
RASSF10	1.050	1.132	0.258
DMRTA2	1.053	1.127	0.260
VEPH1	0.941	-1.118	0.263
SSTR1	0.946	-1.113	0.266
KDELR3	1.081	1.113	0.266
CLDN10	1.080	1.096	0.273
C11orf52	0.883	-1.093	0.275
CREB3L1	1.065	1.085	0.278
CHRNA6	1.077	1.077	0.281
GDF15	1.065	1.064	0.287
PLCZ1	0.908	-1.063	0.288
LRAT	1.063	1.060	0.289
KCNE4	1.079	1.060	0.289
RYR3	1.068	1.059	0.290
PCDH11Y	0.948	-1.056	0.291
GABRP	0.905	-1.038	0.299
CPNE8	1.076	1.037	0.300
RPRM	0.954	-1.034	0.301
SMOC1	0.957	-1.033	0.301
SLFNL1	0.916	-1.022	0.307
RPH3A	1.051	1.022	0.307
EPHB1	0.946	-1.020	0.308
KRT6B	1.075	1.003	0.316
FZD8	1.075	0.975	0.330
ZNF804A	0.945	-0.973	0.331
WISP1	1.054	0.961	0.337
LCE1D	0.908	-0.956	0.339
SPRY4	1.069	0.954	0.340
DAPL1	0.955	-0.943	0.346
PSG1	0.906	-0.933	0.351
ACRV1	0.933	-0.923	0.356
CAPZA3	0.903	-0.919	0.358
CNGA3	1.053	0.917	0.359
ELOVL2	1.051	0.910	0.363
HSPB3	0.952	-0.900	0.368
KLRC2	0.968	-0.880	0.379
SLC7A10	1.046	0.874	0.382
PABPC5	0.962	-0.860	0.390
GSX2	1.035	0.851	0.395
MYOD1	0.921	-0.848	0.397
NMUR2	0.947	-0.844	0.399
FAM19A3	1.051	0.827	0.408
IL1RAP	1.067	0.816	0.414
AKR1C4	0.912	-0.814	0.416
OSBPL10	1.073	0.804	0.422
FAM133A	0.950	-0.786	0.432

Table SIII. Continued.

Gene	HR	z	P-value
PIPOX	1.058	0.786	0.432
SLITRK1	0.965	-0.781	0.435
ZNF727	0.961	-0.770	0.441
SLC6A11	1.049	0.764	0.445
ZNF860	1.061	0.740	0.459
MYOT	0.959	-0.729	0.466
PAX5	1.037	0.722	0.471
KCNJ6	1.041	0.716	0.474
ZNF99	0.959	-0.709	0.479
AL591806.3	1.056	0.705	0.481
HIST1H3G	1.055	0.704	0.481
SEC61G	1.035	0.699	0.484
CBLN1	0.970	-0.689	0.491
ANGPT1	1.047	0.683	0.495
C6orf141	1.032	0.680	0.497
ZAR1	1.053	0.675	0.499
PIWIL1	0.930	-0.674	0.501
MIPOL1	0.962	-0.670	0.503
PCDHGA3	0.954	-0.665	0.506
LHX5	0.968	-0.658	0.511
OTX1	0.966	-0.658	0.511
DPP4	1.035	0.650	0.516
HOXB8	1.023	0.646	0.518
KCTD4	0.967	-0.637	0.524
INHBC	0.964	-0.634	0.526
JPH1	1.045	0.624	0.533
HGD	0.966	-0.621	0.535
FABP7	1.037	0.619	0.536
PRG4	1.038	0.610	0.542
IGF2	1.037	0.576	0.564
CPNE4	1.024	0.542	0.588
PRRX2	1.030	0.534	0.593
MYH11	1.039	0.531	0.596
ALDH1A3	1.024	0.526	0.599
FOXA1	1.027	0.526	0.599
PRLHR	0.970	-0.512	0.608
CNMD	1.026	0.490	0.624
ZIC5	1.033	0.488	0.626
NR0B1	0.983	-0.476	0.634
AKR1C3	0.970	-0.452	0.651
LRTM2	0.977	-0.443	0.658
CHODL	1.021	0.426	0.670
FGFR3	1.025	0.424	0.671
SLC1A6	0.982	-0.407	0.684
KCNF1	1.022	0.405	0.685
VAX1	0.980	-0.404	0.686
RASEF	1.019	0.365	0.715
ACOT12	1.026	0.354	0.724
ADGRG7	0.984	-0.351	0.725
PCDH11X	0.986	-0.346	0.729
ENTPD2	1.020	0.337	0.736
RAB27B	1.019	0.312	0.755
SALL4	1.017	0.295	0.768
NTN4	0.981	-0.286	0.775
TACR1	0.988	-0.277	0.782
AKR1C1	0.984	-0.275	0.784

Table SIII. Continued.

Gene	HR	z	P-value
TFAP2D	0.974	-0.261	0.794
EYA2	1.017	0.259	0.796
AKR1B15	0.984	-0.256	0.798
DMRT1	1.023	0.255	0.799
METTL7B	1.016	0.255	0.799
MAP1LC3C	1.016	0.251	0.802
CTAGE1	0.980	-0.248	0.804
SP7	0.981	-0.238	0.812
C6orf15	1.008	0.232	0.817
FOXD3	0.989	-0.209	0.834
CAPN6	0.991	-0.172	0.864
OBP2A	1.010	0.169	0.865
KLK4	1.011	0.158	0.875
ZC3H12B	0.991	-0.157	0.875
HMX1	1.005	0.144	0.885
HOPX	1.006	0.118	0.906
ZNF208	0.993	-0.115	0.908
UGT2B7	0.994	-0.086	0.931
NPSR1	0.996	-0.085	0.932
ZDHHC23	1.006	0.080	0.936
NOS2	0.997	-0.071	0.944
PATE2	1.005	0.062	0.951
NETO1	1.002	0.050	0.960
TFCP2L1	1.000	0.009	0.993
CDH18	1.000	-0.002	0.998

^aP≤0.001. HR, hazard ratio.