Table SI. Hypoxia- and glycolysis-associated genes.

No.	Gene symbol
1	CLSTN1
2	ATP2A2
3	FAT2
4	COL7A1
5	SLC2A1
6	PTGFRN
7	DYNC1H1
8	HSPG2
9	DSG2
10	NFE2L1
11	PTK7
12	ITPR3
13	IGSF3
14	VEGFA
15	RRBP1
16	PLXNA1
17	AHNAK2
18	GANAB
19	FAM120A
20	GALNT2
21	LAMP2
22	MYOF
23	GJA1
24	FAM83H
25	CLPTM1L
26	TLN1
27	COL4A5
28	CERS6
29	STT3B
30	HYOU1
31	ESYT2
32	IMPAD1
33	KIF13A
34	PURB
35	KIAA0930
36	TANC2
37	KPNA6
38	NCOA6
39	NOMO1
40	TNRC18
41	PAM
42	KIAA2013
43	DUS1L
44	SDK2
45	YTHDF1
46	CRIM1
47	CLOCK
48	MYO5A

49	CSNK2A2
50	NUMBL
51	LAMC2
52	LAMB3
53	COL17A1
54	FLNA
55	ITGA6
56	ITGB1
57	ITGB4
58	APP
59	LAMA3
60	ITGA3
61	TNC
62	ACTN1
63	KTN1
64	SERPINE1
65	CD44
66	CDH3
67	APLP2
68	PTHLH
69	ITGB6
70	MSN
71	MYO1B
72	MT-ND6
73	PDPN
74	LAMC1
75	DUSP6
76	ITGA5
77	TENM2
78	CALD1
79	LTBP1
80	GLG1
81	FST
82	DKK3
83	COL5A1
84	PXN
85	SLC16A1
86	COL12A1
87	MYO10
88	MAP4K4
89	PCDH7
90	ARHGAP21
91	TIMP3
92	TRIO
93	HEG1
94	COL5A2
95	NRG1
96	TGFBR1
97	EXT2
98	EHD2

99	MXRA5
100	KDM1A
101	OLFML2A
102	IRS1
103	PDE7A
104	FOXC2

Table SII. Hazard ratios of critical hypoxia- and glycolysis-associated genes.

Gene	**Hazard ratio (95% confidence interval)**		**P-value**	
	TCGA-OSCC	**GSE65858**	**TCGA-OSCC**	**GSE65858**
HSPG2	1.64 (1.01-2.67)	1.31 (0.98-1.75)	<0.05	<0.05
IGSF3	0.73 (0.53-1.00)	0.77 (0.57-1.03)	<0.001	<0.001
DUS1L	0.51 (0.22-1.16)	0.52 (0.31-0.89)	<0.05	<0.001
DYNC1H1	2.02 (1.31-3.11)	1.32 (0.98-1.78)	<0.001	<0.05

TCGA, The Cancer Genome Atlas; OSCC, oral squamous cell carcinoma; HSPG2, heparan sulfate proteoglycan 2; IGSF3, immunoglobulin superfamily member 3; DUS1L, dihydrouridine synthase 1 like; DYNC1H1, dynein cytoplasmic 1 heavy chain 1.