

**Supplementary Table 9. The list of hypoxia-related genes.**

<b>Gene</b>
VEGFA
SLC2A1
PGAM1
ENO1
LDHA
TPI1
P4HA1
MRPS17
CDKN3
ADM
NDRG1
TUBB6
ALDOA
MIF
ACOT7

**Supplementary Table 10. The list of immune checkpoint genes.**

<b>Gene</b>
CD274
CTLA4
IDO1
LAG3
CD276
VTCN1
CD70
HAVCR2
CD40
CD47
TNFRSF18
TNFSF14
TIGIT
PVR
NECTIN2
CD226

**Supplementary Table 11. Cancer-related Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways associated with risk group based on a gene set enrichment analysis.**

	Enrichment in phenotype: C1 GS	ES	NES	NOM p- val	FDR q-val	FWER p-val
1	KEGG_PEROXISOME	-0.66	-2.24	0	0.001	0.001
2	KEGG_CITRATE_CYCLE_TCA_CYCLE	-0.81	-2.23	0	0	0.001
3	KEGG_PROPANOATE_METABOLISM	-0.73	-2.15	0	0.003	0.009
4	KEGG_HUNTINGTONS_DISEASE	-0.58	-2.14	0	0.002	0.01
5	KEGG_ALZHEIMERS_DISEASE	-0.57	-2.12	0	0.003	0.013
6	KEGG_VALINE_LEUCINE_AND_Isoleucine_DEGRADATION	-0.72	-2.05	0.002	0.007	0.028
7	KEGG_PYRUVATE_METABOLISM	-0.64	-2.04	0	0.007	0.031
8	KEGG_PROTEASOME	-0.76	-2.04	0	0.007	0.035
9	KEGG_PARKINSONS_DISEASE	-0.63	-1.98	0.008	0.012	0.061
10	KEGG_PYRIMIDINE_METABOLISM	-0.54	-1.97	0.008	0.014	0.073
11	KEGG_CELL_CYCLE	-0.59	-1.95	0.012	0.014	0.079
12	KEGG_OXIDATIVE_PHOSPHORYLATION	-0.64	-1.94	0.01	0.013	0.083
13	KEGG_OOCYTE_MEIOSIS	-0.52	-1.94	0.002	0.013	0.088
14	KEGG_NUCLEOTIDE_EXCISION_REPAIR	-0.64	-1.91	0.01	0.016	0.115
15	KEGG_BUTANOATE_METABOLISM	-0.61	-1.85	0.008	0.026	0.174
16	KEGG_FATTY_ACID_METABOLISM	-0.59	-1.84	0.01	0.031	0.211
17	KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	-0.54	-1.84	0.004	0.029	0.214
18	KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	-0.5	-1.83	0.013	0.028	0.217
19	KEGG_PROTEIN_EXPORT	-0.72	-1.82	0.014	0.029	0.227
20	KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	-0.65	-1.82	0.021	0.029	0.239
21	KEGG_PURINE_METABOLISM	-0.43	-1.8	0.008	0.032	0.262
22	KEGG_GLUTATHIONE_METABOLISM	-0.52	-1.8	0.002	0.031	0.266
23	KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS	-0.62	-1.78	0.01	0.034	0.3
24	KEGG_DNA_REPLICATION	-0.72	-1.77	0.02	0.037	0.323
25	KEGG_BASAL_TRANSCRIPTION_FACTORS	-0.59	-1.77	0.023	0.036	0.325
26	KEGG_MISMATCH_REPAIR	-0.69	-1.73	0.018	0.049	0.401