

Figure S1 Forest plot of the relationship of the genes with the survival of OS patients. P<0.05. OS, osteosarcoma.

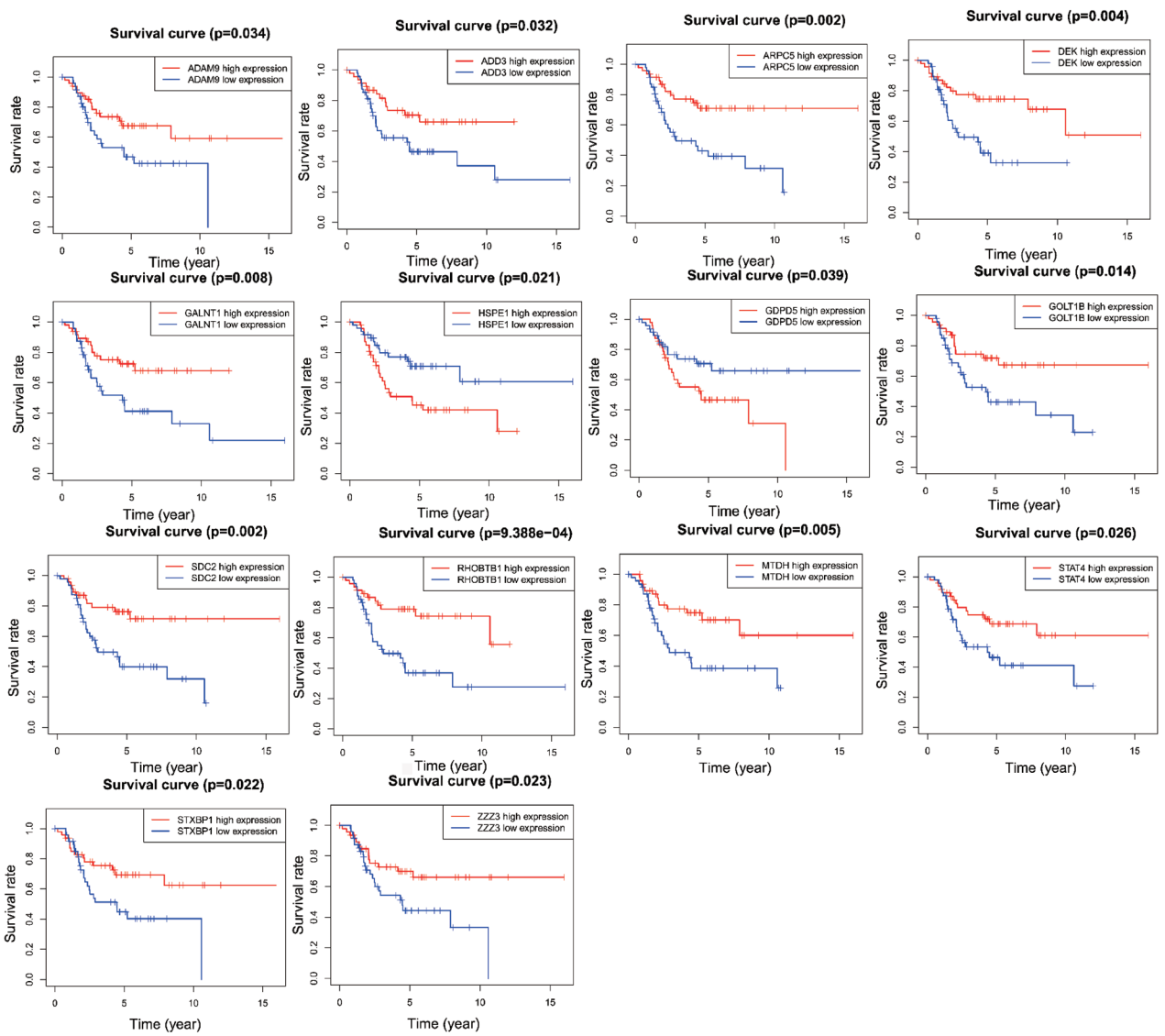


Figure S2 Survival curves of the high- and low-expression groups of 14 genes. $P < 0.05$.

Table S1 The signaling pathways enriched in the high- and low-risk groups

Group	Number	Pathway	Size	P value
Low-risk group	1	KEGG_MAPK_SIGNALING_PATHWAY	265	0.0315
	2	KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	212	0.0301
	3	KEGG_CALCIIUM_SIGNALING_PATHWAY	176	0.0386
	4	KEGG_ALZHEIMERS_DISEASE	156	0.0258
	5	KEGG_JAK_STAT_SIGNALING_PATHWAY	151	0.0216
	6	KEGG_WNT_SIGNALING_PATHWAY	149	0.0156
	7	KEGG_INSULIN_SIGNALING_PATHWAY	137	0.0037
	8	KEGG_TIGHT_JUNCTION	130	0.0344
	9	KEGG_AXON_GUIDANCE	127	0.0020
	10	KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	126	0.0019
	11	KEGG_GNRH_SIGNALING_PATHWAY	101	0.0075
	12	KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	101	0.0263
	13	KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	92	0.0132
	14	KEGG_GAP_JUNCTION	89	0.0399
	15	KEGG_ERBB_SIGNALING_PATHWAY	87	0
	16	KEGG_APOPTOSIS	86	0
	17	KEGG_TGF_BETA_SIGNALING_PATHWAY	85	0.0101
	18	KEGG_VEGF_SIGNALING_PATHWAY	75	0.0097
	19	KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC	74	0.0165
	20	KEGG_ADHERENS_JUNCTION	73	0.0019
	21	KEGG_CHRONIC_MYELOID_LEUKEMIA	73	0.0220
	22	KEGG_PANCREATIC_CANCER	70	0.0057
	23	KEGG_RENAL_CELL_CARCINOMA	70	0.0234
	24	KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY	67	0.0461
	25	KEGG_COLORECTAL_CANCER	62	0.0175
	26	KEGG_GLYCOLYSIS_GLUconeogenesis	61	0.0018
	27	KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	55	0.0298
	28	KEGG_NON_SMALL_CELL_LUNG_CANCER	54	0.0447
	29	KEGG_MTOR_SIGNALING_PATHWAY	52	0.0040
	30	KEGG_ENDOMETRIAL_CANCER	52	0.0301
	31	KEGG_NOTCH_SIGNALING_PATHWAY	47	0.0283
	32	KEGG_TYPE_II_DIABETES_MELLITUS	46	0.0153
	33	KEGG_GLYCEROLIPID_METABOLISM	42	0.0429
	34	KEGG_PROPANOATE_METABOLISM	32	0.0176
High-risk group	1	KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	54	0.0214

Size represented the number of genes enriched in the pathway. KEGG, Kyoto Encyclopedia of Genes and Genomes.