Table S1 Fifty-two differentially expressed glycolysis-related genes

Gene	conMean	treatMean	logFC	P value
AC016586.1	0.541199	0.252303	–1.101	4.06E-14
ACTN3	0.05002	0.015548	–1.68578	1.12E-15
AGRN	22.1092	46.1904	1.062946	5.30E-27
ANGPTL4	8.47078	22.02692	1.378701	1.44E-10
B3GAT1	1.056808	4.091612	1.952957	1.29E-23
B3GNT3	0.343202	18.62594	5.762113	1.45E-18
CD44	23.64155	55.27598	1.225328	8.79E-24
CHST2	5.880716	25.84026	2.135557	1.19E-25
CHST6	0.036072	0.21004	2.541727	1.62E-17
CITED2	221.0603	68.17017	–1.69723	2.54E-26
CLDN9	1.030933	6.584371	2.675096	3.18E-20
COL5A1	2.005016	7.003881	1.804541	9.28E-08
CTH	5.16804	1.626699	–1.66767	3.30E-26
DCN	33.77995	8.477774	–1.99441	7.23E-25
DPYSL4	0.31194	0.944202	1.597825	0.037904
DSC2	1.184663	2.625639	1.148192	5.75E-08
EFNA3	0.706924	1.521173	1.105558	3.36E-20
ELF3	1.867485	7.641938	2.032842	1.70E-14
ENO4	0.437242	0.171567	–1.34966	1.14E-25
FBP2	0.098322	0.021292	–2.20719	9.49E-10
GALE	2.196281	18.68538	3.088775	8.78E-29
GCKR	0.02943	0.157077	2.416115	4.27E-14
GPC3	7.262081	0.815459	–3.1547	2.32E-32
GPR87	0.024971	0.420158	4.072619	2.33E-13
GYS2	0.096623	0.033104	–1.54537	9.34E-20
HDAC4	2.713549	1.10965	–1.29008	6.08E-27
HKDC1	4.254272	1.696967	–1.32595	4.16E-20
HS6ST2	0.321417	3.755313	3.546417	2.90E-07
HTR2A	0.050591	0.018263	–1.46996	2.90E-15
IGFBP3	8.277112	26.33518	1.669792	1.55E-10
INSR	6.885022	14.03193	1.027181	5.50E-26
KDELR3	4.718449	12.77691	1.437154	9.74E-23
MET	11.81067	69.16071	2.549862	4.53E-24
MIOX	9.232944	3.455103	–1.41806	8.10E-23
MLXIPL	0.744173	2.654179	1.834555	4.71E-14
NT5E	9.665598	26.37453	1.448214	7.61E-11
OGDHL	15.59248	5.8479	–1.41486	5.80E-22
P4HA2	2.849222	10.59953	1.895361	6.93E-32
PC	4.044894	11.66517	1.528034	1.09E-24
PFKFB1	0.405589	0.143794	–1.49602	2.64E-25
PFKFB2	18.7996	8.333122	–1.17377	1.99E-23
PKP2	0.244379	0.829063	1.762359	1.52E-09
PPARGC1A	8.456713	2.259498	–1.90409	1.31E-26
QSOX1	6.222757	18.44137	1.56732	3.62E-22
SDC1	22.69221	46.84309	1.045639	1.03E-17
SDC2	177.716	86.774	–1.03424	1.56E-23
SDC3	7.684957	19.25227	1.32492	5.21E-22
TFF3	802.1512	86.20233	–3.21808	6.66E-32
TGFA	3.401024	19.52026	2.520931	9.18E-28
TGFBI	4.196403	14.60663	1.799399	2.39E-17
TKTL1	0.029211	0.014387	–1.02176	2.49E-08
VCAN	0.912372	3.25451	1.834746	8.05E-05

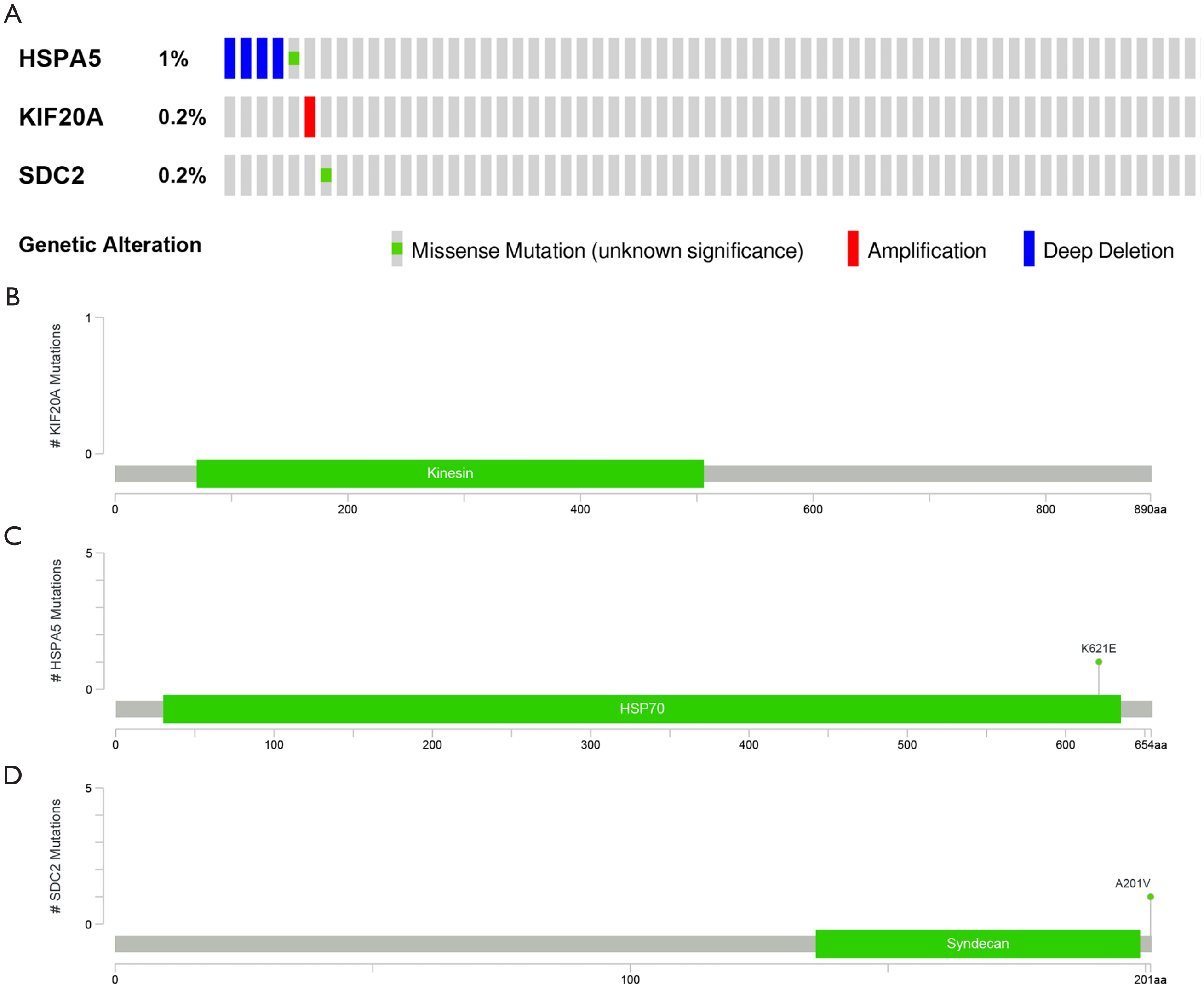

Figure S1 Identification of mutations in model genes.

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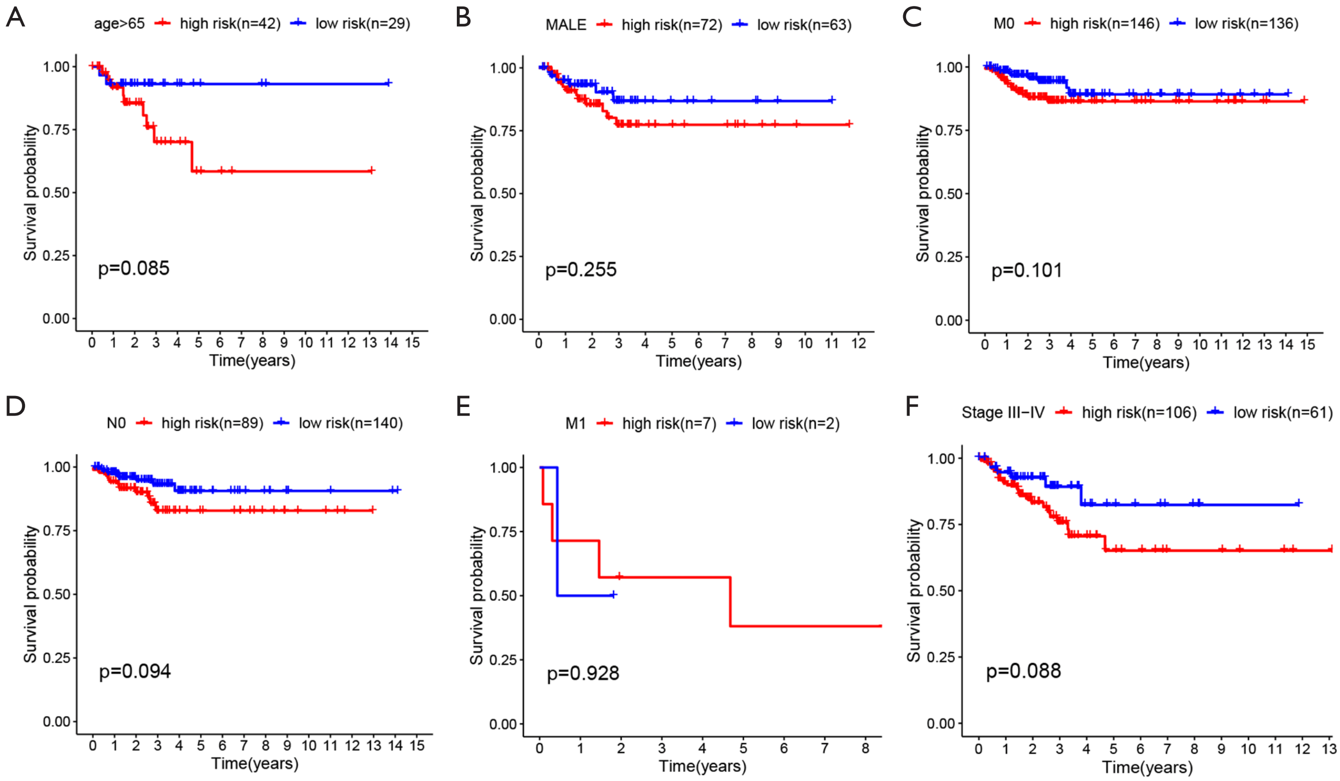

Figure S2 Relationship between survival probability and clinical features of thyroid cancer patients (P>0.05).