Table S1The signature riskScore composed of four immune-related lncRNAs combinations in the training dataset

id	futime	fustat	HAND2.AS1	MIR100HG	PCED1B.AS1	TRG.AS1	riskScore	risk
TCGA-A6-6141-01A-11R-1774-07	0.082192	1	2.341127	6.681211	7.012435	5.75259	2.418429	high
TCGA-AA-3955-01A-02R-1022-07	0.084932	1	0.306941	6.452967	5.347575	3.843713	3.674975	high
TCGA-CM-5344-01A-21R-1723-07	0.084932	1	4.964406	7.374239	5.075628	4.027594	2.578166	high
TCGA-CM-6674-01A-11R-1839-07	0.084932	0	5.647809	7.762888	6.786277	4.989306	2.027586	high
TCGA-AA-3663-01A-01R-1723-07	0.167123	1	0	5.267505	5.267516	4.116654	2.791774	high
TCGA-AA-3819-01A-01R-0905-07	0.167123	1	1.564065	5.951092	5.617789	4.675078	2.598187	high
TCGA-A6-2678-01A-01R-0821-07	0.246575	1	2.570301	6.737478	6.27731	5.130957	2.626693	high
TCGA-AZ-5403-01A-01R-1653-07	0.246575	0	5.583807	8.930038	5.867042	2.16548	3.403932	high
TCGA-CM-5860-01A-01R-1653-07	0.265753	1	5.209129	8.756005	6.487836	4.777376	3.194616	high
TCGA-CA-5255-01A-11R-1839-07	0.419178	1	3.435982	5.929415	4.972673	3.434886	1.999978	high
TCGA-AA-A010-01A-01R-A089-07	0.427397	1	0.648699	4.972039	5.833493	4.377553	2.054731	high
TCGA-CK-4947-01B-11R-1653-07	0.435616	1	3.604305	7.728765	7.006895	6.242811	2.799049	high
TCGA-D5-6541-01A-11R-1723-07	0.624658	1	5.528194	8.543207	7.532113	5.443845	2.504659	high
TCGA-DM-A28H-01A-11R-A16W-07	0.671233	0	0.449885	4.486153	4.996989	2.606427	2.005418	high
TCGA-AY-4070-01A-01R-1113-07	0.717808	1	1.614952	6.430057	6.857937	5.591844	2.563743	high
TCGA-AA-3660-01A-01R-1723-07	0.838356	1	3.040387	6.458419	6.029082	4.734333	2.265863	high
TCGA-AA-3842-01A-01R-1022-07	0.838356	0	4.607655	7.432402	5.763488	4.300734	2.542002	high
TCGA-AA-3673-01A-01R-0905-07	0.917808	0	4.003916	6.946001	6.385649	3.555129	2.15582	high
TCGA-AA-3860-01A-02R-0905-07	0.917808	0	3.385886	6.885436	7.061158	4.507178	2.131847	high
TCGA-CA-5256-01A-01R-1410-07	0.947945	0	2.208171	6.935365	6.232445	4.166484	2.972252	high
TCGA-AA-3509-01A-	0.978082	1	2.958351	6.455106	5.57744	3.710199	2.456298	high

01R-1410-07								
TCGA-A6-6137-01A-11R-1774-07	1.032877	0	1.833356	6.170593	6.588553	5.190585	2.335785	high
TCGA-A6-6651-01A-21R-1839-07	1.038356	0	9.106169	10.02068	8.192321	5.908097	2.035231	high
TCGA-CM-6167-01A-11R-1653-07	1.082192	0	9.036093	10.29472	6.711451	4.960252	2.82483	high
TCGA-A6-A56B-01A-31R-A28H-07	1.082192	0	4.327304	6.4024	4.052674	2.815366	2.354936	high
TCGA-A6-4107-01A-02R-1410-07	1.084932	0	3.724605	7.946961	7.292868	4.316288	2.839242	high
TCGA-AA-A017-01A-01R-A00A-07	1.084932	0	3.136288	6.451205	4.845852	4.04799	2.632408	high
TCGA-NH-A6GA-01A-11R-A37K-07	1.117808	0	3.893825	6.63703	5.620434	4.667536	2.19909	high
TCGA-CM-6679-01A-11R-1839-07	1.161644	1	5.720781	8.129352	7.255118	4.298018	2.154603	high
TCGA-A6-A5ZU-01A-11R-A28H-07	1.167123	1	3.230152	7.49905	6.582397	5.252839	2.906359	high
TCGA-AZ-4315-01A-01R-1410-07	1.252055	0	3.090597	6.919697	6.548942	4.129147	2.468247	high
TCGA-AA-3517-01A-01R-0821-07	1.252055	0	2.022179	5.833299	5.383352	4.610076	2.379594	high
TCGA-D5-5538-01A-01R-1653-07	1.252055	0	4.478833	7.636221	7.46589	4.767349	2.180915	high
TCGA-AD-6965-01A-11R-1928-07	1.369863	0	1.839181	6.232886	5.441672	4.042287	2.789506	high
TCGA-CM-4751-01A-02R-1839-07	1.380822	1	3.723715	7.57031	7.179472	5.425684	2.54786	high
TCGA-A6-3810-01A-01R-1022-07	1.4	1	4.827146	8.649857	6.027086	4.750148	3.426722	high
TCGA-A6-3810-01A-01R-A278-07	1.4	1	4.940482	8.161113	5.856138	4.179423	3.007724	high
TCGA-AA-3833-01A-01R-0905-07	1.419178	0	4.547807	7.335796	7.103475	4.851881	2.013727	high
TCGA-QG-A5YV-01A-11R-A28H-07	1.487671	0	0	5.144863	5.307107	4.279716	2.669992	high
TCGA-AA-3511-01A-21R-1839-07	1.487671	0	4.09293	7.110897	5.337578	3.919426	2.629478	high
TCGA-F4-6703-01A-11R-1839-07	1.50411	0	5.781407	9.033177	9.003118	7.009098	2.312099	high
TCGA-AA-3970-01A-01R-1022-07	1.515068	0	1.268387	5.963833	6.379468	4.895792	2.469953	high

TCGA-D5-6926-01A-11R-1928-07	1.520548	0	6.50851	8.053296	6.403514	4.416667	2.047011	high
TCGA-AA-3956-01A-02R-1022-07	1.610959	0	0.277482	6.824005	6.652359	4.241009	3.557481	high
TCGA-DM-A0XD-01A-12R-A155-07	1.610959	0	2.670316	6.128729	5.322296	2.922665	2.382242	high
TCGA-AA-A00Q-01A-01R-A002-07	1.668493	0	4.729586	7.041782	5.709955	4.246542	2.164562	high
TCGA-A6-6649-01A-11R-1774-07	1.690411	0	5.471285	7.778901	6.447229	4.756507	2.236251	high
TCGA-AA-A00L-01A-01R-A002-07	1.70137	0	0.160249	4.890353	4.493636	3.047814	2.661831	high
TCGA-AA-A00F-01A-01R-A002-07	1.747945	0	2.990823	8.335746	5.728456	5.07374	4.044443	high
TCGA-AY-6386-01A-21R-1723-07	1.761644	1	2.028831	5.891763	6.243279	5.203289	2.127207	high
TCGA-CM-6169-01A-11R-1653-07	1.786301	0	5.433238	8.872705	7.343306	5.987256	2.901531	high
TCGA-AA-3952-01A-01R-1022-07	1.832877	0	3.044944	7.035055	5.420855	3.195368	2.984223	high
TCGA-AA-A029-01A-01R-A00A-07	1.832877	0	0.587812	5.113186	5.703807	2.93652	2.250512	high
TCGA-CM-5349-01A-21R-1723-07	1.832877	0	6.832921	8.143417	6.144442	5.075081	2.077496	high
TCGA-AA-3655-01A-02R-1723-07	1.835616	1	3.187373	6.16331	5.575014	4.316548	2.101887	high
TCGA-AA-A01Z-01A-11R-A083-07	1.876712	0	2.647169	6.927947	3.702302	2.65139	3.662505	high
TCGA-AA-3666-01A-02R-0905-07	1.915068	0	1.626765	5.35523	5.473691	5.051006	2.097302	high
TCGA-DM-A0XF-01A-11R-A155-07	1.920548	0	3.137325	6.223762	5.247466	3.993978	2.291247	high
TCGA-D5-6529-01A-11R-1774-07	2.010959	0	5.000015	7.926137	8.128339	5.907584	1.980075	high
TCGA-NH-A50V-01A-11R-A28H-07	2.035616	1	3.875752	7.780594	6.372689	4.914092	2.949908	high
TCGA-AA-3685-01A-02R-A32Z-07	2.057534	0	3.389898	7.181775	7.288942	5.609015	2.311176	high
TCGA-CM-6172-01A-11R-1653-07	2.167123	0	2.408313	6.488557	4.94025	4.614987	2.945268	high
TCGA-F4-6855-01A-11R-1928-07	2.167123	0	5.067099	8.357051	6.755469	3.745411	2.810938	high
TCGA-AA-3864-01A-01R-1022-07	2.252055	0	1.56672	7.086269	5.614572	4.979615	3.597127	high

TCGA-AA-3548-01A-01R-1873-07	2.252055	0	1.485789	6.156853	6.774825	4.554612	2.407953	high
TCGA-AA-3560-01A-01R-0821-07	2.257534	0	1.840582	6.526046	6.952581	4.74671	2.518067	high
TCGA-AA-3561-01A-01R-0821-07	2.284932	0	1.534544	6.307125	5.88761	3.85134	2.829752	high
TCGA-CM-5348-01A-21R-1723-07	2.419178	0	5.750793	8.504626	6.814179	5.098925	2.626267	high
TCGA-A6-3808-01A-01R-1022-07	2.432877	0	6.904642	9.099094	7.222066	4.713432	2.510484	high
TCGA-A6-5660-01A-01R-1653-07	2.50137	0	3.20939	7.970167	5.905637	3.083352	3.566736	high
TCGA-G4-6320-01A-11R-1723-07	2.506849	0	1.212867	5.072011	4.911293	3.703646	2.222884	high
TCGA-D5-6536-01A-11R-1723-07	2.583562	0	4.472969	6.824048	5.332831	3.377754	2.215295	high
TCGA-D5-5540-01A-01R-1653-07	2.589041	0	2.348316	6.653787	5.713776	2.923297	2.845735	high
TCGA-AA-A01K-01A-01R-A00A-07	2.663014	1	3.890264	8.232896	6.924109	4.433367	3.148697	high
TCGA-AA-3846-01A-01R-1022-07	2.668493	0	2.449831	6.391795	6.143599	5.048333	2.421093	high
TCGA-AA-3851-01A-01R-1022-07	2.70411	0	2.89217	7.022244	7.072181	4.612061	2.460678	high
TCGA-CM-6165-01A-11R-1653-07	2.747945	0	5.631016	7.969542	6.499295	4.895813	2.317108	high
TCGA-A6-2676-01A-01R-0826-07	2.753425	0	0.284866	7.018888	6.918123	5.729784	3.632786	high
TCGA-D5-6531-01A-11R-1723-07	2.832877	0	4.44326	7.250192	6.522609	3.983976	2.186654	high
TCGA-DM-A28G-01A-11R-A16W-07	2.835616	0	3.630753	6.445725	5.671647	4.156256	2.125937	high
TCGA-5M-AATE-01A-11R-A41B-07	2.917808	0	2.111947	6.026578	5.009858	3.471871	2.641802	high
TCGA-AA-3697-01A-01R-1723-07	3.079452	0	1.875888	5.660423	6.156495	5.140022	2.019767	high
TCGA-AA-3534-01A-01R-0821-07	3.084932	1	3.987034	6.749362	5.709505	4.107841	2.226687	high
TCGA-AZ-6605-01A-11R-1839-07	3.084932	0	5.255204	8.317549	7.512553	5.571164	2.430312	high
TCGA-AA-3844-01A-01R-1022-07	3.087671	0	1.291034	5.403805	5.57306	5.035471	2.249633	high
TCGA-CM-6680-01A-11R-1839-07	3.169863	0	3.547795	7.156739	6.307294	4.497353	2.564825	high

TCGA-AA-3818-01A-01R-0905-07	3.169863	0	3.756097	6.898358	6.384854	3.601566	2.220734	high
TCGA-DM-A28A-01A-21R-A32Y-07	3.249315	1	3.559578	6.267433	4.764166	2.714392	2.317265	high
TCGA-A6-4105-01A-02R-1774-07	3.287671	0	3.836127	7.725654	6.753044	4.748457	2.785476	high
TCGA-A6-5664-01A-21R-1839-07	3.693151	1	6.125525	8.739707	7.310606	5.427881	2.498255	high
TCGA-A6-5661-01B-05R-2302-07	3.723288	0	2.369394	5.674804	5.348526	5.339399	2.103004	high
TCGA-A6-5661-01A-01R-1653-07	3.723288	0	1.541526	5.687099	6.464252	4.806617	2.079303	high
TCGA-AU-3779-01A-01R-1723-07	3.742466	0	3.400594	6.905486	6.61336	5.312845	2.299896	high
TCGA-CK-5914-01A-11R-1653-07	3.920548	1	2.973607	6.020148	5.282235	4.686607	2.170297	high
TCGA-A6-2686-01A-01R-A32Z-07	3.950685	1	4.242575	7.78303	7.919373	5.993653	2.252979	high
TCGA-A6-6782-01A-11R-1839-07	4.416438	0	4.729785	8.178856	7.290851	5.037931	2.611788	high
TCGA-CM-5341-01A-01R-1410-07	4.586301	1	4.918805	9.359666	7.567927	5.319159	3.472645	high
TCGA-AA-3862-01A-01R-1022-07	4.660274	0	3.666441	6.769772	6.473886	5.451546	2.11497	high
TCGA-AA-3562-01A-02R-0821-07	4.865753	0	1.973492	6.775466	6.556835	4.539545	2.818916	high
TCGA-AA-A00O-01A-02R-A089-07	5.065753	0	4.17279	7.212469	5.395305	4.324828	2.664316	high
TCGA-AA-3939-01A-01R-1022-07	5.153425	0	2.820969	7.190303	6.166301	4.594032	2.956245	high
TCGA-D5-6927-01A-21R-1928-07	0.082192	0	5.218596	6.852269	7.245744	5.524597	1.24999	low
TCGA-G4-6307-01A-11R-1723-07	0.084932	0	1.741489	4.235959	4.149175	2.568241	1.526593	low
TCGA-G4-6309-01A-21R-1839-07	0.117808	1	1.82986	4.445101	6.138609	4.804129	0.976336	low
TCGA-A6-5667-01A-21R-1723-07	0.134247	1	7.03809	7.318283	4.955018	3.044604	1.679454	low
TCGA-F4-6461-01A-11R-1774-07	0.167123	1	4.67856	7.344377	7.13179	4.999467	1.955145	low
TCGA-CA-5254-01A-21R-1839-07	0.167123	1	5.052615	7.299443	6.921461	3.554462	1.828374	low
TCGA-CM-6164-01A-11R-1653-07	0.419178	1	5.660344	7.096807	5.768289	4.699727	1.792341	low

TCGA-CA-6718-01A-11R-1839-07	0.471233	1	5.032189	6.690554	7.593514	6.926336	1.066116	low
TCGA-AZ-4308-01A-01R-1410-07	0.515068	1	3.539084	5.372523	5.997853	0.273809	1.106766	low
TCGA-AA-A01Q-01A-01R-A002-07	0.564384	1	3.188886	5.166185	6.194235	5.100412	1.007039	low
TCGA-A6-2685-01A-01R-1410-07	0.580822	0	8.256732	8.714723	7.567677	4.958118	1.469874	low
TCGA-AA-A00U-01A-01R-A002-07	0.627397	0	2.223757	4.922157	5.339149	4.183509	1.506581	low
TCGA-F4-6460-01A-11R-1774-07	0.753425	0	7.61314	7.673804	5.88867	4.093974	1.418263	low
TCGA-F4-6807-01A-11R-1839-07	0.756164	0	7.079522	8.600611	8.019198	5.426594	1.717624	low
TCGA-G4-6317-01A-11R-1723-07	0.827397	1	2.021025	3.984156	4.245498	2.848096	1.151093	low
TCGA-A6-3807-01A-01R-1022-07	0.923288	0	4.175725	6.378525	5.34067	4.7311	1.948306	low
TCGA-AY-A69D-01A-11R-A37K-07	1.041096	0	1.760304	5.242861	6.062793	4.56452	1.734809	low
TCGA-QG-A5YW-01A-11R-A28H-07	1.049315	0	2.023574	5.703284	6.53375	5.599755	1.861941	low
TCGA-CA-5797-01A-01R-1653-07	1.079452	0	5.20541	7.168753	6.169887	4.328691	1.910716	low
TCGA-F4-6805-01A-11R-1839-07	1.087671	0	8.069972	8.213397	7.346684	5.392612	1.186362	low
TCGA-CK-5913-01A-11R-1653-07	1.147945	0	4.463798	6.597027	6.597075	5.612031	1.576974	low
TCGA-AA-3971-01A-01R-1022-07	1.161644	0	3.888768	5.929881	6.424313	5.117906	1.297615	low
TCGA-G4-6588-01A-11R-1774-07	1.167123	0	3.525093	6.20663	5.722106	4.405441	1.943307	low
TCGA-CM-4752-01A-01R-1410-07	1.167123	0	3.386331	6.595729	7.188705	4.997498	1.832072	low
TCGA-AA-3856-01A-01R-0905-07	1.208219	0	3.418178	6.643088	7.287483	5.383474	1.825482	low
TCGA-AY-6197-01A-11R-1723-07	1.249315	0	1.046769	4.747107	5.49411	4.470701	1.804406	low
TCGA-G4-6321-01A-11R-1723-07	1.249315	0	3.598351	4.987092	6.990996	5.330174	0.394501	low
TCGA-D5-6532-01A-11R-1723-07	1.252055	0	3.445557	4.912312	4.847983	1.519969	1.144451	low
TCGA-AA-3678-01A-01R-0905-07	1.252055	0	0.996772	4.165264	6.224037	4.243267	1.058407	low

TCGA-F4-6459-01A-11R-1774-07	1.328767	0	7.266955	8.111647	6.022106	4.281476	1.905721	low
TCGA-QG-A5YX-01A-11R-A28H-07	1.336986	0	0.585856	3.070301	4.665685	3.610346	0.816957	low
TCGA-AA-3554-01A-01R-0826-07	1.339726	0	4.728036	6.702175	7.490001	5.434363	1.243358	low
TCGA-A6-6140-01A-11R-1774-07	1.358904	1	1.170221	3.861776	5.545772	4.117182	0.954147	low
TCGA-DM-A28M-01A-12R-A16W-07	1.419178	0	1.514645	3.946371	4.372634	3.435569	1.291087	low
TCGA-D5-5541-01A-01R-1653-07	1.427397	0	5.076947	7.312119	6.813426	4.923077	1.866878	low
TCGA-AA-3519-01A-02R-0821-07	1.438356	0	1.707064	5.175492	5.450995	3.176237	1.912547	low
TCGA-AA-3532-01A-01R-0821-07	1.463014	0	4.798408	7.216487	7.370734	5.609297	1.707436	low
TCGA-AA-A01T-01A-21R-A16W-07	1.479452	0	1.580097	2.691474	4.343683	3.534167	0.168766	low
TCGA-CM-5861-01A-01R-1653-07	1.484932	0	3.667047	5.816935	5.0498	2.467321	1.774643	low
TCGA-D5-6537-01A-11R-1723-07	1.487671	0	0.806923	3.715848	5.168263	3.718886	1.114078	low
TCGA-AA-A00E-01A-01R-A002-07	1.50411	0	2.397644	4.865224	6.492244	5.27621	0.978125	low
TCGA-A6-5657-01A-01R-A32Z-07	1.586301	0	6.727154	8.255949	7.536165	5.250705	1.734901	low
TCGA-CA-6716-01A-11R-1839-07	1.589041	0	5.575981	6.503474	3.963869	2.419817	1.938031	low
TCGA-A6-6654-01A-21R-1839-07	1.589041	0	7.106888	8.562142	7.86158	5.953077	1.72717	low
TCGA-AA-3815-01A-01R-1022-07	1.589041	0	2.25329	6.041235	7.617213	6.42819	1.681347	low
TCGA-G4-6304-01A-11R-1928-07	1.665753	0	0.04974	3.862334	5.210206	4.067174	1.553894	low
TCGA-AA-3841-01A-01R-0905-07	1.682192	0	2.183506	5.658699	7.258624	4.615892	1.500229	low
TCGA-AA-3831-01A-01R-0905-07	1.750685	0	2.613963	5.716719	6.434108	4.77839	1.654771	low
TCGA-4N-A93T-01A-11R-A37K-07	1.780822	0	1.353964	3.451149	4.623309	3.624308	0.836649	low
TCGA-AA-3522-01A-01R-0821-07	1.813699	0	3.209862	5.920357	5.881229	5.664081	1.771243	low
TCGA-DM-A1DB-01A-11R-A155-07	1.835616	0	0.932879	2.898113	5.363706	4.730313	0.271905	low

TCGA-D5-6924-01A-11R-1928-07	1.841096	0	5.612499	7.204308	7.323304	5.143397	1.363261	low
TCGA-AZ-6601-01A-11R-1774-07	1.958904	1	5.241539	7.022406	7.691625	6.155855	1.233786	low
TCGA-A6-2677-01A-01R-0821-07	1.989041	0	3.17918	5.25782	4.533348	3.179244	1.673163	low
TCGA-CM-4743-01A-01R-1723-07	2	0	1.901416	4.408974	6.187013	4.885032	0.896834	low
TCGA-AA-3542-01A-02R-1873-07	2.00274	0	1.856334	5.10466	5.273499	1.859388	1.848153	low
TCGA-G4-6299-01A-11R-1774-07	2.00274	0	5.15115	7.234923	7.235422	4.883795	1.61934	low
TCGA-D5-6932-01A-11R-1928-07	2.032877	0	4.964166	6.577454	6.004888	4.575017	1.551857	low
TCGA-A6-6650-01A-11R-1774-07	2.084932	0	0.613234	3.982995	5.061738	3.799275	1.469737	low
TCGA-G4-6295-01A-11R-1723-07	2.09863	0	3.116247	5.563937	7.232497	5.913137	1.024904	low
TCGA-AA-A00Z-01A-01R-A002-07	2.123288	0	2.40821	4.954505	4.739928	3.793355	1.665459	low
TCGA-AA-3510-01A-01R-1410-07	2.180822	0	3.594721	5.98452	6.838502	5.201904	1.327172	low
TCGA-NH-A6GB-01A-11R-A37K-07	2.205479	1	2.718768	4.453072	5.942692	4.70265	0.669691	low
TCGA-AA-A01F-01A-01R-A002-07	2.252055	1	1.628889	4.522865	4.134515	2.295628	1.832619	low
TCGA-DM-A1DA-01A-11R-A155-07	2.252055	0	1.17747	4.368335	4.94795	2.829519	1.60604	low
TCGA-A6-2680-01A-01R-1410-07	2.416438	0	3.154099	5.06705	5.517895	4.68773	1.171478	low
TCGA-AA-3861-01A-01R-1022-07	2.421918	0	3.079364	4.873298	7.031447	5.633359	0.503369	low
TCGA-AD-6888-01A-11R-1928-07	2.50411	0	1.58367	2.984746	3.901268	1.886881	0.580155	low
TCGA-A6-2679-01A-02R-1410-07	2.50411	0	0.796185	3.369945	8.294784	5.44992	-0.27998	low
TCGA-DM-A28F-01A-11R-A32Y-07	2.536986	0	1.716996	4.649526	5.643975	3.28725	1.377883	low
TCGA-A6-2681-01A-01R-1410-07	2.583562	0	6.288261	7.763123	7.597634	4.624644	1.468424	low
TCGA-G4-6586-01A-11R-1774-07	2.608219	0	1.433565	3.845859	6.655199	5.471307	0.438603	low
TCGA-AA-3664-01A-01R-0905-07	2.753425	0	1.973699	4.550252	5.467399	4.03375	1.241942	low

TCGA-AA-3531-01A-01R-0821-07	2.756164	0	2.190799	3.865171	4.882686	2.979075	0.750366	low
TCGA-CM-6677-01A-11R-1839-07	2.778082	0	4.57836	7.067358	6.962954	5.009274	1.813547	low
TCGA-AA-3489-01A-21R-1839-07	2.794521	0	5.743244	8.335968	8.662713	6.242403	1.834107	low
TCGA-AA-3982-01A-02R-1022-07	2.805479	0	4.178157	6.970989	6.798248	5.240509	1.958476	low
TCGA-AA-A01C-01A-01R-A00A-07	2.838356	0	3.907048	6.362349	5.640548	1.922389	1.944644	low
TCGA-D5-6922-01A-11R-1928-07	2.915068	0	7.170813	7.743822	5.749281	4.729378	1.718865	low
TCGA-AA-A004-01A-01R-A00A-07	2.920548	0	0.514978	2.085732	6.080578	3.252073	-0.5142	low
TCGA-D5-6920-01A-11R-1928-07	2.983562	0	0.635825	4.779494	6.681781	5.007959	1.593926	low
TCGA-G4-6625-01A-21R-1774-07	2.994521	0	4.724079	6.867093	7.490737	6.270668	1.38993	low
TCGA-AZ-6598-01A-11R-1774-07	2.99726	1	2.135933	5.595278	6.326334	4.251676	1.791176	low
TCGA-D5-6931-01A-11R-1928-07	3.00274	0	3.982919	6.413429	7.15291	5.774275	1.427643	low
TCGA-CA-6719-01A-11R-1839-07	3.043836	0	7.501162	8.501862	6.727341	4.917627	1.901569	low
TCGA-AA-3681-01A-01R-0905-07	3.084932	0	2.726775	5.201494	6.518742	5.326884	1.123242	low
TCGA-AA-A00K-01A-02R-A002-07	3.413699	0	5.283	6.166093	5.669697	3.806363	1.170078	low
TCGA-D5-6535-01A-11R-1723-07	3.50137	0	3.160723	6.223397	6.529587	5.180135	1.832123	low
TCGA-AA-A01X-01A-21R-A083-07	3.523288	0	5.215491	6.106613	5.271421	2.567082	1.286162	low
TCGA-G4-6311-01A-11R-1723-07	3.564384	0	4.5043	6.755097	6.589673	4.748646	1.701251	low
TCGA-DM-A1D4-01A-21R-A155-07	3.646575	0	0	2.216128	4.57435	4.616808	0.34917	low
TCGA-AA-A00A-01A-01R-A002-07	3.783562	0	3.567287	5.931902	6.779006	5.111533	1.313488	low
TCGA-AA-3710-01A-01R-1022-07	3.8	0	3.741696	6.30466	7.7023	6.815644	1.243366	low
TCGA-AA-A01P-01A-21R-A083-07	3.917808	0	5.879153	7.380526	8.43613	7.120048	1.014182	low
TCGA-AA-3518-01A-02R-0826-07	4.169863	0	2.357382	5.049695	6.053577	5.04702	1.311305	low

TCGA-AA-3812-01A-01R-0905-07	4.276712	0	5.561413	6.677958	7.281324	3.782852	0.936732	low
TCGA-T9-A92H-01A-11R-A37K-07	4.550685	0	0.528557	4.002962	4.79438	3.079988	1.617294	low
TCGA-AA-3848-01A-01R-0905-07	4.673973	0	0.257217	4.453051	6.123382	4.051275	1.664898	low
TCGA-A6-2672-01B-03R-2302-07	4.835616	0	3.800627	6.286045	5.521813	5.113011	1.964815	low
TCGA-A6-2672-01A-01R-0826-07	4.835616	0	4.330162	6.944747	7.150914	5.985004	1.746588	low
TCGA-AA-3496-01A-21R-1839-07	5.084932	0	3.482926	6.329834	6.581261	5.62994	1.769154	low