

Figure S1 Upregulation of TRIM genes in HCC in ICGC cohort. Heatmap (A) and expression levels (B) of 62 TRIM genes. * $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$. TRIM, tripartite-motif; HCC, hepatocellular carcinoma; ICGC, International Cancer Genome Consortium.

Table S1 The expression of all *TRIM* genes in HCC

Gene	conMean	treatMean	logFC	pValue
<i>MID1</i>	2.3272	3.6603	0.6533	<0.0001
<i>MID2</i>	1.1669	2.0190	0.7910	<0.0001
<i>PML</i>	6.1567	8.8012	0.5155	<0.0001
<i>TRIM10</i>	1.6589	1.5359	-0.1112	0.0006
<i>TRIM11</i>	2.5510	6.4281	1.3333	<0.0001
<i>TRIM13</i>	1.8944	2.2073	0.2206	0.0001
<i>TRIM15</i>	13.4980	7.4353	-0.8603	<0.0001
<i>TRIM17</i>	0.1045	0.3931	1.9112	<0.0001
<i>TRIM2</i>	3.2447	3.2776	0.0146	0.0002
<i>TRIM21</i>	7.2214	8.9731	0.3133	<0.0001
<i>TRIM22</i>	21.7251	14.5495	-0.5784	<0.0001
<i>TRIM23</i>	2.7480	3.9504	0.5236	<0.0001
<i>TRIM24</i>	6.9237	15.8774	1.1974	<0.0001
<i>TRIM25</i>	9.4121	10.6317	0.1758	0.0008
<i>TRIM26</i>	17.6007	23.8897	0.4408	<0.0001
<i>TRIM27</i>	15.6307	25.1302	0.6850	<0.0001
<i>TRIM28</i>	20.1263	42.7724	1.0876	<0.0001
<i>TRIM3</i>	2.4164	3.7850	0.6474	<0.0001
<i>TRIM31</i>	1.9820	7.3746	1.8956	<0.0001
<i>TRIM32</i>	1.2058	2.2773	0.9174	<0.0001
<i>TRIM33</i>	3.5734	4.9978	0.4840	<0.0001
<i>TRIM34</i>	2.0262	2.6108	0.3657	<0.0001
<i>TRIM35</i>	4.7165	4.1282	-0.1922	<0.0001
<i>TRIM36</i>	0.1685	0.3419	1.0209	<0.0001
<i>TRIM37</i>	2.1983	4.8216	1.1331	<0.0001
<i>TRIM38</i>	6.4133	7.8524	0.2921	0.0009
<i>TRIM39</i>	3.2459	5.4129	0.7378	<0.0001
<i>TRIM4</i>	4.8269	7.8473	0.7011	<0.0001
<i>TRIM40</i>	0.4712	0.3437	-0.4550	0.5527
<i>TRIM41</i>	6.4748	10.8891	0.7500	<0.0001
<i>TRIM42</i>	0.0040	0.0090	1.1693	0.0193
<i>TRIM43</i>	0.0011	0.0067	2.5721	0.0004
<i>TRIM45</i>	0.5743	2.3532	2.0346	<0.0001
<i>TRIM46</i>	0.1212	0.3280	1.4361	<0.0001
<i>TRIM47</i>	4.8948	10.5915	1.1136	<0.0001
<i>TRIM48</i>	0.0013	0.0013	-0.0647	0.5072
<i>TRIM49</i>	0.0000	0.0035	Inf	0.0694
<i>TRIM5</i>	6.6641	7.1118	0.0938	0.1080
<i>TRIM50</i>	0.1675	3.0263	4.1756	0.0015
<i>TRIM52</i>	3.1569	6.2149	0.9772	<0.0001
<i>TRIM54</i>	0.0845	0.8949	3.4051	<0.0001
<i>TRIM55</i>	3.5903	17.7277	2.3038	<0.0001
<i>TRIM56</i>	1.8245	2.8449	0.6408	<0.0001
<i>TRIM58</i>	0.0689	0.0423	-0.7061	<0.0001
<i>TRIM6</i>	0.3605	1.2824	1.8309	<0.0001
<i>TRIM60</i>	0.0001	0.0508	8.5018	<0.0001
<i>TRIM61</i>	0.2178	0.1920	-0.1818	<0.0001
<i>TRIM62</i>	0.5455	0.9907	0.8609	<0.0001
<i>TRIM63</i>	0.0404	0.2764	2.7751	0.0124
<i>TRIM64</i>	0.0078	0.0017	-2.2199	0.9238
<i>TRIM65</i>	1.8777	4.5920	1.2902	<0.0001
<i>TRIM67</i>	0.0554	0.1652	1.5758	<0.0001
<i>TRIM68</i>	1.5532	2.7472	0.8227	<0.0001
<i>TRIM69</i>	0.9438	0.9485	0.0072	0.3320
<i>TRIM7</i>	0.2728	0.9631	1.8201	<0.0001
<i>TRIM71</i>	0.0074	0.3440	5.5479	<0.0001
<i>TRIM72</i>	0.0116	0.0673	2.5391	<0.0001
<i>TRIM73</i>	0.3637	0.3947	0.1179	0.2986
<i>TRIM74</i>	0.3637	0.3947	0.1179	0.2986
<i>TRIM8</i>	16.0656	24.6381	0.6169	<0.0001
<i>TRIM9</i>	0.1845	0.4125	1.1608	0.2852
<i>TRIML1</i>	0.0073	0.0134	0.8848	0.9188

Table S2 GSVA analysis to elucidate the potential regulatory mechanisms between the two subgroups

ID	logFC	AveExpr	P.Value	adj.P.Val
KEGG_LINOLEIC_ACID_METABOLISM	-0.4362	0.0560	<0.0001	<0.0001
KEGG_COMPLEMENT_AND_COAGULATION_CASCADES	-0.5351	0.0241	<0.0001	<0.0001
KEGG_HOMOLOGOUS_RECOMBINATION	0.4144	-0.0528	<0.0001	<0.0001
KEGG_PRIMARY_BILE_ACID_BIOSYNTHESIS	-0.6119	0.0168	<0.0001	<0.0001
KEGG_TRYPTOPHAN_METABOLISM	-0.4842	0.0175	<0.0001	<0.0001
KEGG_ABC_TRANSPORTERS	-0.3023	-0.0123	<0.0001	<0.0001
KEGG_BETA_ALANINE_METABOLISM	-0.4846	0.0198	<0.0001	<0.0001
KEGG_SPLICEOSOME	0.3668	-0.0469	<0.0001	<0.0001
KEGG_HISTIDINE_METABOLISM	-0.4064	0.0035	<0.0001	<0.0001
KEGG_DRUG_METABOLISM_CYTOCHROME_P450	-0.4921	0.0287	<0.0001	<0.0001
KEGG_ARACHIDONIC_ACID_METABOLISM	-0.2866	0.0366	<0.0001	<0.0001
KEGG_PHENYLALANINE_METABOLISM	-0.4250	0.0146	<0.0001	<0.0001
KEGG_PPAR_SIGNALING_PATHWAY	-0.3723	0.0278	<0.0001	<0.0001
KEGG_FATTY_ACID_METABOLISM	-0.5202	0.0120	<0.0001	<0.0001
KEGG_RETINOL_METABOLISM	-0.4790	0.0386	<0.0001	<0.0001
KEGG_PROPANOATE_METABOLISM	-0.4654	0.0061	<0.0001	<0.0001
KEGG_TYROSINE_METABOLISM	-0.3756	0.0143	<0.0001	<0.0001
KEGG_DNA_REPLICATION	0.4536	-0.0480	<0.0001	<0.0001
KEGG_GLYCINE_SERINE_AND_THREONINE_METABOLISM	-0.4740	0.0085	<0.0001	<0.0001
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION	-0.4999	0.0107	<0.0001	<0.0001
KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450	-0.4452	0.0278	<0.0001	<0.0001
KEGG_BUTANOATE_METABOLISM	-0.4414	0.0236	<0.0001	<0.0001
KEGG_STEROID_HORMONE_BIOSYNTHESIS	-0.4255	0.0340	<0.0001	<0.0001
KEGG_STARCH_AND_SUCROSE_METABOLISM	-0.3732	0.0159	<0.0001	<0.0001
KEGG_PYRUVATE_METABOLISM	-0.3380	0.0052	<0.0001	<0.0001
KEGG_ALANINE_ASPARTATE_AND_GLYTAMATE_METABOLISM	-0.3489	0.0130	<0.0001	<0.0001
KEGG_PEROXISOME	-0.3760	0.0035	<0.0001	<0.0001
KEGG_ARGININE_AND_PROLINE_METABOLISM	-0.3389	0.0119	<0.0001	<0.0001
KEGG_CELL_CYCLE	0.2833	-0.0425	<0.0001	<0.0001
KEGG_BASE_EXCISION_REPAIR	0.2861	-0.0547	<0.0001	<0.0001
KEGG_RNA_DEGRADATION	0.2455	-0.0447	<0.0001	<0.0001
KEGG_OLFACTORY_TRANSDUCTION	-0.1981	0.1215	<0.0001	<0.0001
KEGG_ASCORBATE_AND_ALDARATE_METABOLISM	-0.4993	0.0309	<0.0001	<0.0001
KEGG_NITROGEN_METABOLISM	-0.2892	0.0337	<0.0001	<0.0001
KEGG_DRUG_METABOLISM_OTHER_ENZYMES	-0.3605	0.0143	<0.0001	<0.0001
KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY	-0.1837	-0.0184	<0.0001	<0.0001
KEGG_PENTOSE_AND_GLYCUCURONATE_INTERCONVERSIONS	-0.4425	0.0253	<0.0001	<0.0001
KEGG_ALPHA_LINOLENIC_ACID_METABOLISM	-0.2423	0.0566	<0.0001	<0.0001
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	-0.1584	0.0431	<0.0001	<0.0001
KEGG_FOLATE_BIOSYNTHESIS	-0.3437	0.0017	<0.0001	<0.0001
KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION	-0.2409	0.0302	<0.0001	<0.0001
KEGG_MISMATCH_REPAIR	0.3222	-0.0470	<0.0001	<0.0001
KEGG_CYSTEINE_AND_METHIONINE_METABOLISM	-0.2067	-0.0193	<0.0001	<0.0001
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	0.1727	-0.0432	<0.0001	<0.0001
KEGG_NUCLEOTIDE_EXCISION_REPAIR	0.2386	-0.0505	<0.0001	<0.0001
KEGG_RENIN_ANGIOTENSIN_SYSTEM	-0.2404	0.0294	<0.0001	<0.0001
KEGG_RNA_POLYMERASE	0.2721	-0.0561	<0.0001	<0.0001
KEGG_PYRIMIDINE_METABOLISM	0.1930	-0.0445	<0.0001	<0.0001
KEGG_GLYCOLYSIS_GLUKONEOGENESIS	-0.2388	0.0118	<0.0001	<0.0001
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_KERATAN_SULFATE	0.2046	-0.0113	<0.0001	<0.0001
KEGG_PURINE_METABOLISM	0.1181	-0.0305	<0.0001	<0.0001
KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	-0.3215	-0.0056	<0.0001	<0.0001
KEGG_LYSINE_DEGRADATION	-0.2463	-0.0319	<0.0001	<0.0001
KEGG_OOCYTE_MEIOSIS	0.1546	-0.0246	<0.0001	<0.0001
KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS	-0.2928	-0.0033	<0.0001	<0.0001
KEGG_GLYCEROLIPID_METABOLISM	-0.1413	0.0045	<0.0001	<0.0001
KEGG_BLADDER_CANCER	0.1553	-0.0287	<0.0001	<0.0001
KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION	0.1656	-0.0266	<0.0001	<0.0001
KEGG_TAURINE_AND_HYPOTAUINE_METABOLISM	-0.1956	0.0123	<0.0001	<0.0001
KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	0.1904	-0.0226	<0.0001	<0.0001
KEGG_NICOTINATE_AND_NICOTINAMIDE_METABOLISM	-0.1734	-0.0065	<0.0001	<0.0001
KEGG_GLYOXYLATE_AND_DICARBOXYLATE_METABOLISM	-0.2582	-0.0179	<0.0001	<0.0001
KEGG_ENDOCYTOSIS	0.1132	-0.0290	<0.0001	<0.0001
KEGG_NOTCH_SIGNALING_PATHWAY	0.1637	-0.0331	<0.0001	<0.0001
KEGG_CHRONIC_MYELOID_LEUKEMIA	0.1469	-0.0356	<0.0001	<0.0001
KEGG_MATURITY_ONSET_DIABETES_OF_THE_YOUNG	-0.2106	0.0634	<0.0001	<0.0001
KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	0.1317	-0.0235	<0.0001	<0.0001
KEGG_VIBRIO_CHOLERAЕ_INFECTION	0.1555	-0.0246	<0.0001	<0.0001
KEGG_RIBOSOME	0.3317	-0.0444	<0.0001	<0.0001
KEGG_MTOR_SIGNALING_PATHWAY	0.1126	-0.0330	<0.0001	<0.0001
KEGG_CITRATE_CYCLE_TCA_CYCLE	-0.2601	-0.0140	<0.0001	<0.0001
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	0.1620	-0.0202	<0.0001	<0.0001
KEGG_PRION_DISEASES	-0.1604	-0.0142	<0.0001	<0.0001
KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION	-0.1090	0.0144	<0.0001	<0.0001
KEGG_CALCIIUM_SIGNALING_PATHWAY	-0.1111	0.0175	<0.0001	<0.0001
KEGG_PANCREATIC_CANCER	0.1387	-0.0314	<0.0001	<0.0001
KEGG_NON_HOMOLOGOUS_END_JOINING	0.1840	-0.0353	<0.0001	<0.0001
KEGG_THYROID_CANCER	0.1095	-0.0426	<0.0001	<0.0001
KEGG_NON_SMALL_CELL_LUNG_CANCER	0.1096	-0.0325	<0.0001	0.0001
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE	0.1164	0.0023	<0.0002	0.0001
KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	0.1118	-0.0292	0.0001	0.0002
KEGG_ERBB_SIGNALING_PATHWAY	0.1003	-0.0169	0.0001	0.0002
KEGG_BASAL_TRANSCRIPTION_FACTORS	0.1289	-0.0379	0.0001	0.0002
KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS	0.1491	-0.0471	0.0001	0.0002
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE	0.1576	-0.0157	0.0001	0.0003
KEGG_RENAL_CELL_CARCINOMA	0.1315	-0.0216	0.0002	0.0003
KEGG_PANTOTHENATE_AND_COA_BIOSYNTHESIS	-0.1478	-0.0195	0.0002	0.0005
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	-0.1909	-0.0013	0.0003	0.0006
KEGG_GLYTATHIONE_METABOLISM	-0.1349	-0.0093	0.0004	0.0009
KEGG_ONE_CARBON_POOL_BY_FOLATE	-0.1441	-0.0258	0.0005	0.0009
KEGG_GALACTOSE_METABOLISM	-0.1080	0.0034	0.0006	0.0011
KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	0.1004	-0.0327	0.0014	0.0027
KEGG_AUTOIMMUNE_THYROID_DISEASE	-0.1667	0.0217	0.0019	0.0035
KEGG_SULFUR_METABOLISM	-0.1121	-0.0188	0.0035	0.0062
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	-0.1077	0.0127	0.0058	0.0100
KEGG_CELL_ADHESION_MOLECULES_CAMS	-0.1107	0.0035	0.0060	0.0103
KEGG_RIBOFLAVIN_METABOLISM	0.1104	-0.0333	0.0062	0.0104
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	0.1325	-0.0469	0.0092	0.0146
KEGG_CIRCADIAN_RHYTHM_MAMMAL	-0.1121	-0.0384	0.0098	0.0153
KEGG_ASTHMA	-0.1477	0.0069	0.0103	0.0159
KEGG_GRAFT_VERSUS_HOST_DISEASE	-0.1461	-0.0085	0.0210	0.0309
KEGG_ALLOGRAFT_REJECTION	-0.1442	-0.0097	0.0256	0.0373

Table S3 Prognostic nine TRIM genes

Gene	Coef
<i>MID1</i>	0.2666
<i>TRIM22</i>	-0.2776
<i>TRIM28</i>	0.0285
<i>TRIM31</i>	0.1564
<i>TRIM37</i>	0.5382
<i>TRIM38</i>	-0.1205
<i>TRIM47</i>	0.1407
<i>TRIM5</i>	-0.1805
<i>TRIM74</i>	-0.9219

Table S4 Risk score for all TCGA data

ID	Exclusion	Dysfunction	riskScore	Risk
TCGA-2Y-A9H3	-0.0474	0.1729	-49.3037	Low
TCGA-2Y-A9GU	-0.0283	-0.0595	-45.6506	Low
TCGA-FV-A3R3	0.0016	0.0780	-25.7199	Low
TCGA-2Y-A9GT	-0.1133	0.1553	-14.4872	Low
TCGA-RC-A75F	0.0027	-0.0308	-12.2966	Low
TCGA-5R-AA1C	0.0081	-0.1849	-11.2011	Low
TCGA-2Y-A9GZ	-0.0310	0.0087	-8.9811	Low
TCGA-ZS-A9CF	-0.0443	0.0566	-8.6015	Low
TCGA-ED-ASKG	-0.1825	0.2566	-7.1056	Low
TCGA-LG-A9QD	-0.0386	0.0088	-6.9790	Low
TCGA-G3-AAV3	-0.0393	0.0945	-5.0507	Low
TCGA-DD-AAV3	-0.0107	0.0569	-4.3457	Low
TCGA-ZS-A9CE	-0.0040	0.0088	-4.1545	Low
TCGA-K7-A5RF	-0.0908	0.2246	-4.0518	Low
TCGA-DD-A73G	0.0315	0.0656	-1.9289	Low
TCGA-WX-AA46	-0.0293	-0.0343	-1.6475	Low
TCGA-DD-AAE2	-0.0683	0.0630	-1.1195	Low
TCGA-DD-AAF1	-0.0923	-0.0071	-0.7051	Low
TCGA-UB-A7MF	-0.0987	0.1404	-0.1059	Low
TCGA-DD-AAE7	-0.0341	0.0628	-0.0399	Low
TCGA-EP-A12J	-0.0387	0.0018	-0.0217	Low
TCGA-DD-AAE4	-0.0108	0.0394	0.7199	High
TCGA-DD-AAJK	0.0292	0.0299	0.7691	High
TCGA-G3-A7M8	-0.0309	0.0196	0.8261	High
TCGA-ES-A2HS	0.0376	0.0594	1.3293	High
TCGA-UB-AA0V	-0.0022	0.0173	1.5663	High
TCGA-DD-AAAS	-0.0098	0.1034	1.7363	High
TCGA-DD-A113	-0.0018	-0.0684	2.2476	High
TCGA-UB-A7ME	-0.0416	0.0942	2.4707	High
TCGA-2Y-A9GW	-0.1168	0.0859	2.5219	High
TCGA-2Y-A9H1	0.0125	0.0484	2.7754	High
TCGA-DD-A73F	-0.1009	0.1551	2.9532	High
TCGA-2Y-A9H6	-0.0518	0.1375	3.0770	High
TCGA-DD-A4NL	-0.0425	0.0619	3.1210	High
TCGA-K7-A6G5	-0.0156	0.0430	3.1394	High
TCGA-LG-A6GG	-0.0199	-0.0384	3.2767	High
TCGA-G3-AAV0	0.0066	0.0990	3.4712	High
TCGA-ED-A82E	0.0374	-0.0066	3.8014	High
TCGA-DD-AAVX	-0.0609	0.0809	4.0699	High
TCGA-G3-A3CH	-0.0394	0.0582	4.1358	High
TCGA-G3-A5SK	-0.0617	-0.0617	4.1507	High
TCGA-BC-A10X	0.0040	-0.0119	4.3283	High
TCGA-MR-A520	-0.0346	-0.0784	4.3670	High
TCGA-EP-A26S	-0.0033	-0.0683	4.5219	High
TCGA-DD-A11C	0.0044	-0.0303	5.6144	High
TCGA-G3-A3CI	-0.0516	0.0535	5.8799	High
TCGA-DD-A73A	-0.0788	0.0224	5.9362	High
TCGA-DD-A11B	-0.0209	-0.1642	6.0507	High
TCGA-FV-A495	0.0461	0.1868	6.1468	High
TCGA-WQ-AB4B	0.0142	-0.0100	6.3425	High
TCGA-DD-A4ND	-0.0066	0.0436	6.4321	High
TCGA-ZS-A9CG	0.0049	-0.0553	6.5373	High
TCGA-ES-A2HT	0.0041	0.0666	6.5914	High
TCGA-2Y-A9GV	-0.0919	0.0599	6.7530	High
TCGA-DD-AAEG	0.0187	-0.0519	6.8438	High
TCGA-KR-A7K2	-0.0116	0.0542	7.0492	High
TCGA-DD-AAVR	-0.0418	0.0522	7.2502	High
TCGA-DD-AAJK	-0.0430	0.0197	7.5605	High
TCGA-PD-A5DF	0.0162	-0.0401	7.6052	High
TCGA-2Y-A9HB	-0.0880	0.0848	7.7086	High
TCGA-DD-A3A1	-0.0059	0.0065	8.1417	High
TCGA-FV-A3I0	0.0304	0.0477	8.1706	High
TCGA-DD-AAE3	0.0284	0.0006	8.4894	High
TCGA-G3-A6UC	-0.0475	-0.0144	8.7629	High
TCGA-5C-A9VG	0.0467	-0.1069	8.7828	High
TCGA-G3-A3CG	-0.0462	0.0066	9.0318	High
TCGA-2Y-A9H9	-0.0498	0.0371	9.1955	High
TCGA-EP-A3JL	-0.0205	0.0575	9.3135	High
TCGA-DD-AAKJ	-0.0127	-0.1191	9.3311	High
TCGA-ED-A4XI	-0.0559	0.1675	9.5345	High
TCGA-DD-AAED	-0.0236	-0.0681	9.6136	High
TCGA-DD-AAAC	-0.1869	0.2904	9.6498	High
TCGA-5R-AAAM	-0.0141	0.1120	9.7452	High
TCGA-DD-A39V	0.0321	0.0105	9.7919	High
TCGA-DD-A11D	-0.0371	0.0481	9.9768	High
TCGA-DD-AAAN	0.0165	-0.1350	10.0410	High
TCGA-5C-A9VH	0.0083	-0.0040	10.1745	High
TCGA-DD-AAAC	0.0164	0.0093	10.4713	High
TCGA-K7-A5RC	-0.1837	0.2402	10.6122	High
TCGA-DD-AAAD	0.0210	0.1095	10.7700	High
TCGA-DD-AAEK	-0.0931	0.1204	10.8463	High
TCGA-DD-A3A9	0.0527	0.0954	10.8841	High
TCGA-O8-A75V	-0.0335	0.0687	10.9630	High
TCGA-DD-AAUJ	-0.1064	0.2493	11.0546	High
TCGA-G3-AAUJ	0.0048	0.1033	11.1211	High
TCGA-DD-AAEH	-0.0626	0.0880	11.4667	High
TCGA-DD-A73B	0.0017	-0.1862	11.4723	High
TCGA-2Y-A9H5	-0.0277	0.0224	11.8374	High
TCGA-G3-A25T	0.0423	0.0380	12.2692	High
TCGA-DD-AAAZ	-0.0758	-0.0618	12.3836	High
TCGA-G3-A9DB	-0.0164	0.0513	12.4499	High
TCGA-G3-A3CK	-0.0302	-0.0706	12.5069	High
TCGA-DD-A1ED	-0.0614	0.0573	12.6590	High
TCGA-KR-A7K0	-0.0113	-0.0244	12.7702	High
TCGA-DD-AAAD	0.0098	0.0458	12.8558	High
TCGA-3K-AAZ8	-0.0510	0.0442	12.8906	High
TCGA-EP-A2KC	-0.0236	-0.0809	13.1717	High
TCGA-G3-AAV2	0.0261	0.0296	13.2008	High
TCGA-G3-AAV5	0.0352	-0.0780	13.2622	High
TCGA-2Y-A9H2	-0.0158	0.0491	13.2923	High
TCGA-XR-A8TD	-0.0864	0.0944	13.5165	High
TCGA-RC-A7S9	0.0146	-0.0440	13.5989	High
TCGA-ED-A627	-0.0212	0.2243	13.6795	High
TCGA-DD-AAAD	-0.0228	-0.0528	13.6966	High
TCGA-DD-AAAD	-0.0408	-0.0407	13.6971	High
TCGA-XR-A8TG	-0.0113	-0.0581	13.9032	High
TCGA-DD-AAAC	0.0194	-0.0051	13.9748	High
TCGA-DD-A4NS	0.0179	0.1750	14.0901	High
TCGA-2Y-A9GX	-0.0399	0.1317	14.1431	High
TCGA-YA-A8S7	-0.0327	0.0863	14.6573	High
TCGA-DD-AAAF	0.0171	-0.0235	14.7114	High
TCGA-CC-5260	0.0270	0.0650	14.9802	High
TCGA-BC-A69I	0.0211	0.0915	14.9951	High
TCGA-G3-A25V	-0.0369	0.1178	15.1010	High
TCGA-DD-AAAP	0.0198	0.0001	15.1884	High
TCGA-FV-A2QR	0.0009	-0.0206	15.3318	High
TCGA-DD-A1EE	-0.0298	-0.0888	15.3649	High
TCGA-DD-A3A5	0.0143	0.0626	15.3840	High
TCGA-DD-AAW1	-0.0282	-0.0241	15.5194	High
TCGA-DD-AAAN	0.0525	-0.0546	15.6017	High
TCGA-DD-AAVV	-0.0175	-0.0118	15.7967	High
TCGA-BC-A5W4	0.0425	0.0174	16.1183	High
TCGA-DD-AAAC	0.0163	-0.0488	16.1690	High
TCGA-UB-AAOU	0.0107	-0.0400	16.1917	High
TCGA-DD-AAAY	-0.0233	0.0078	16.3513	High
TCGA-DD-AAAC	0.0336	-0.0660	16.3846	High
TCGA-KR-A7K8	-0.0538	0.1509	16.4430	High
TCGA-G3-A3OU	-0.2045	0.2154	16.5132	High
TCGA-DD-A1EB	-0.0438	0.0155	16.5358	High
TCGA-DD-AAAY	0.0026	-0.0949	16.5388	High
TCGA-LG-A9QC	-0.0105	-0.0263	16.7782	High
TCGA-DD-AAAD	-0.0171	0.1293	16.8467	High
TCGA-FV-A3R2	-0.0092	-0.0088	16.8733	High
TCGA-DD-AAVY	-0.0192	-0.0819	17.0350	High
TCGA-DD-AAAF	-0.0650	0.0275	17.2182	High
TCGA-DD-AAAN	-0.0016	-0.0828	17.4766	High
TCGA-DD-AAAJ	-0.0408	-0.0589	17.6363	High
TCGA-CC-A8HS	0.0254	-0.1110	17.6735	High
TCGA-HP-A5M2	-0.0402	0.0823	17.7588	High
TCGA-DD-A11A	-0.0296	-0.1176	17.8499	High
TCGA-DD-A3A8	0.0292	-0.0196	17.8818	High
TCGA-DD-AAAC	-0.0195	0.0035	18.0012	High
TCGA-DD-AAAC	-0.0112	0.0560	18.1104	High
TCGA-MI-A75C	0.0056	0.0004	18.1866	High
TCGA-G3-A7M7	0.0087	-0.0180	18.2393	High
TCGA-ZS-A9CD	-0.0124	0.0705	18.3647	High
TCGA-DD-AAEI	-0.0240	0.0392	18.3789	High
TCGA-DD-AAAD	0.0171	-0.0497	18.4240	High
TCGA-DD-A73C	-0.0261	-0.0161	18.5181	High
TCGA-BC-4073	-0.0804	-0.0009	18.5490	High
TCGA-DD-A3A6	0.0724	0.1434	18.5962	High
TCGA-DD-A1E9	-0.0380	0.0294	18.6194	High
TCGA-MI-A75E	-0.0103	0.1863	18.7210	High
TCGA-4R-A78I	-0.0474	-0.0195	19.0536	High
TCGA-RC-A7SH	-0.0142	0.0613	19.0774	High
TCGA-DD-AAAR	-0.1546	0.2374	19.1824	High
TCGA-CC-A9FS	-0.0061	-0.0708	19.2683	High
TCGA-DD-AAAM	0.0485	-0.0364	19.2798	High
TCGA-UB-A7MD	-0.0492	0.0982	19.3661	High
TCGA-DD-AAAD	0.0164	-0.0124	19.4552	High
TCGA-DD-AAAD	-0.0050	-0.0781	19.5100	High
TCGA-DD-A1EC	-0.1259	0.1826	19.5392	High
TCGA-DD-A73E	0.0212	-0.0072	19.7399	High
TCGA-FV-A496	-0.0267	-0.0554	19.8703	High
TCGA-CC-5261	-0.0072	0.0137	19.8791	High
TCGA-CC-A3M9	0.0365	0.1520	19.9448	High
TCGA-RC-A6M4	0.0256	-0.0504	19.9468	High
TCGA-DD-AAE1	-0.0093	-0.0723	20.0012	High
TCGA-DD-AAAD	0.0107	-0.0028	20.0163	High
TCGA-2Y-A9H4	0.0037	0.0098	20.0555	High
TCGA-G3-AAV4	0.0085	-0.0376	20.1092	High
TCGA-5C-AAAP	-0.0332	0.1339	20.1679	High
TCGA-DD-A115	0.0042	0.1068	20.2658	High
TCGA-G3-A25Y	0.0284	-0.0204	20.2727	High
TCGA-DD-AAEA	-0.0119	0.0390	20.3918	High
TCGA-K7-AAU7	0.0321	0.0047	20.4091	High
TCGA-BW-A5U0	-0.0080	-0.0106	20.6713	High
TCGA-DD-A1EK	-0.0513	0.0568	20.7388	High
TCGA-ED-A7XP	-0.0294	-0.1107	20.7799	High
TCGA-FV-A2QQ	-0.0130	-0.0072	20.8270	High
TCGA-DD-A4N0	-0.0081	-0.0432	21.1019	High
TCGA-DD-AAAD	-0.0059	-0.0688	21.1156	High
TCGA-DD-AAAD	0.0047	-0.0233	21.1901	High
TCGA-DD-A1EI	0.0441	-0.0705	21.2066	High
TCGA-ED-A7XO	0.0071	0.1014	21.2980	High
TCGA-EP-A3RK	-0.0419	0.0989	21.5279	High
TCGA-ED-A7XP	0.0458	0.0165	21.5419	High
TCGA-DD-A39W	-0.0084	-0.0197	21.6860	High
TCGA-G3-A5SM	-0.0369	0.0954	21.8444	High
TCGA-BC-ASBY	-0.0609	-0.0283	21.9492	High
TCGA-WX-AA44	0.0176	-0.0447	22.5134	High
TCGA-ED-A97K	0.0002	0.0556	22.5578	High
TCGA-DD-A118	-0.0012	-0.0115	22.5898	High
TCGA-CC-5262	0.0543	0.0823	22.6086	High
TCGA-DD-A1E9	0.0284	0.0755	22.6417	High
TCGA-DD-AAE9	0.0195	-0.0532	22.8720	High
TCGA-BD-A3ER	-0.0281	0.0665	22.9885	High
TCGA-CC-5258	0.0434	-0.1473	23.0318	High
TCGA-DD-A3A2	-0.0154	-0.0245	23.5287	High
TCGA-G3-A5SL	0.0122	-0.1855	23.6051	High
TCGA-G3-A3CJ	0.0216	-0.0260	23.6632	High
TCGA-DD-AAAC	-0.0095	0.1043	23.7211	High
TCGA-DD-A1EF	-0.0063	-0.0685	23.9588	High
TCGA-BC-A216	-0.0206	-0.0046	24.0985	High
TCGA-DD-A119	0.0377	-0.1074	24.1091	High
TCGA-DD-AA1H	-0.0330	-0.0339	24.3243	High
TCGA-DD-AAAC	-0.0002	-0.0405	24.3873	High
TCGA-DD-AAV2	-0.0338	-0.1349	24.4536	High
TCGA-FV-A3I1	-0.0415	0.0878	24.5146	High
TCGA-CC-A7IH	-			

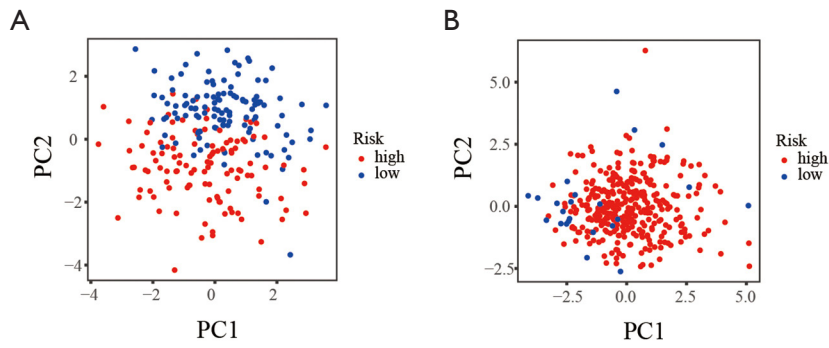


Figure S2 Principal component analysis of the total mRNA expression profile in patients with HCC. (A) ICGC dataset (231), (B) TCGA dataset (370). HCC, hepatocellular carcinoma; ICGC, International Cancer Genome Consortium; TCGA, The Cancer Genome Atlas.

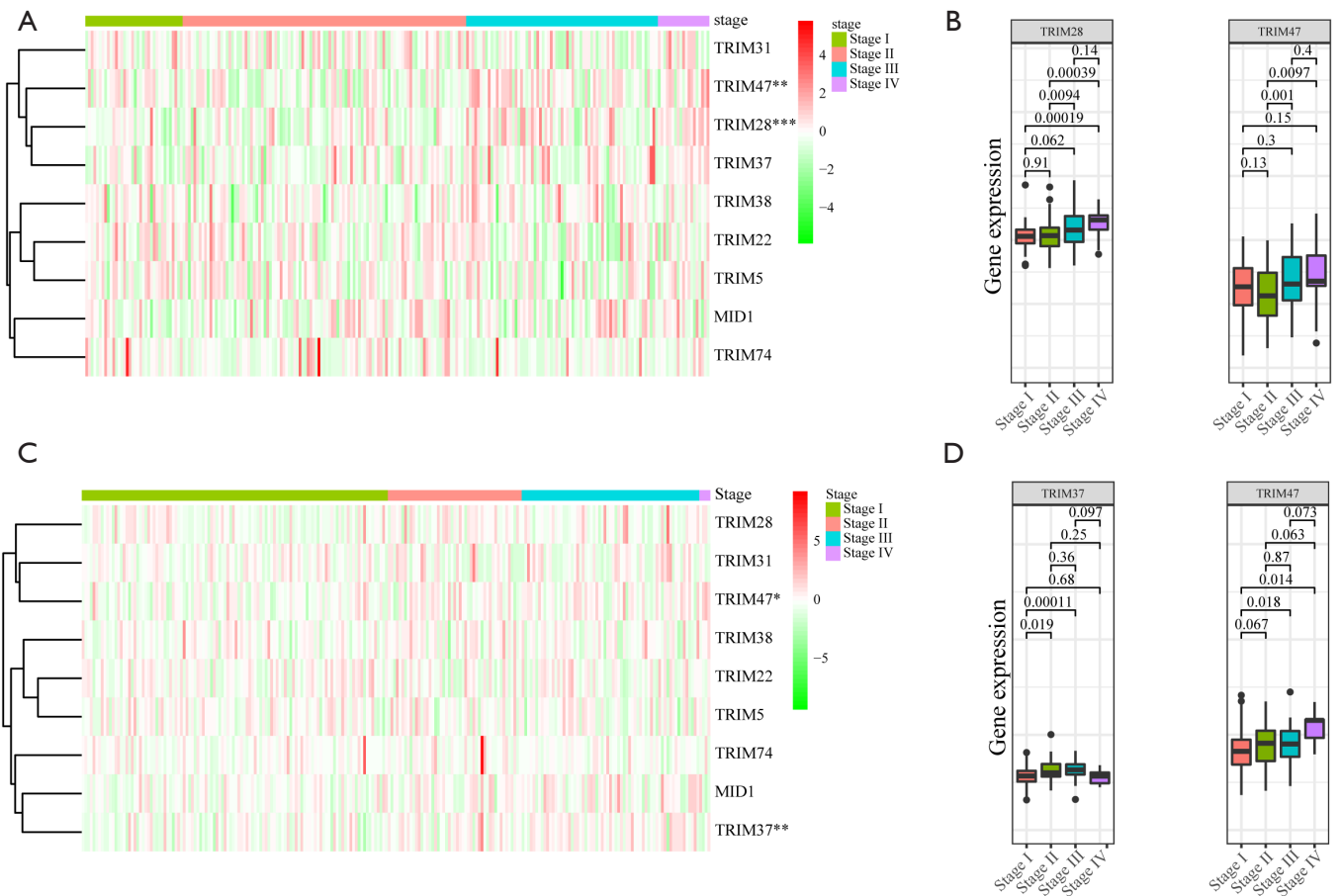


Figure S3 Expression of 9 prognostic TRIM genes in different TNM stages. (A,B) ICGC dataset; (C,D) TCGA dataset. * $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$. TRIM, tripartite-motif; ICGC, International Cancer Genome Consortium; TCGA, The Cancer Genome Atlas.

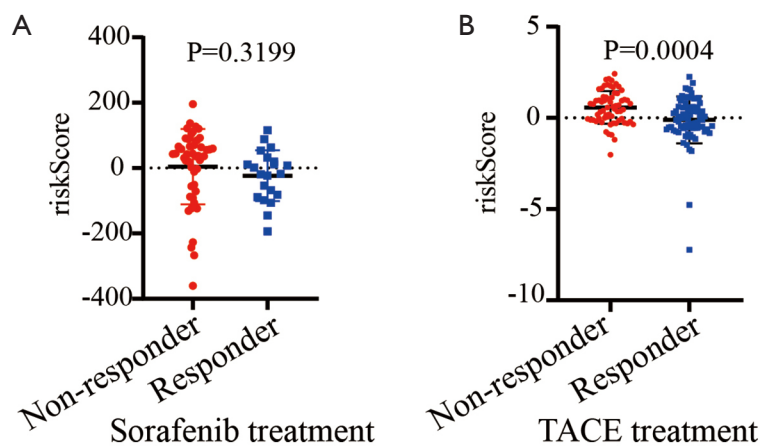


Figure S4 Prognostic risk scores correlated with sorafenib treatment and TACE treatment. (A) Sorafenib treatment; (B) TACE treatment. TACE, transarterial chemotherapy embolization.

Table S5 Prognostic risk scores correlated with sorafenib treatment

ID	riskScore	Risk	Response
GSM2935384	-360.5127	Low	Non-responder
GSM2935326	-266.9720	Low	Non-responder
GSM2935402	-242.7517	Low	Non-responder
GSM2935416	-226.8208	Low	Non-responder
GSM2935378	-130.6702	Low	Non-responder
GSM2935395	-123.8420	Low	Non-responder
GSM2935362	-123.5592	Low	Non-responder
GSM2935304	-106.2238	Low	Non-responder
GSM2935355	-91.8073	Low	Non-responder
GSM2935397	-87.6133	Low	Non-responder
GSM2935380	-70.9621	Low	Non-responder
GSM2935292	-55.8145	Low	Non-responder
GSM2935350	-50.8004	Low	Non-responder
GSM2935340	-10.8910	Low	Non-responder
GSM2935389	-2.3515	Low	Non-responder
GSM2935414	2.0936	High	Non-responder
GSM2935297	20.2977	High	Non-responder
GSM2935351	23.0205	High	Non-responder
GSM2935323	24.3236	High	Non-responder
GSM2935328	30.6782	High	Non-responder
GSM2935307	36.0293	High	Non-responder
GSM2935353	36.1191	High	Non-responder
GSM2935407	37.9594	High	Non-responder
GSM2935338	42.4778	High	Non-responder
GSM2935370	43.1468	High	Non-responder
GSM2935342	44.0766	High	Non-responder
GSM2935360	44.5883	High	Non-responder
GSM2935356	55.4280	High	Non-responder
GSM2935296	56.8567	High	Non-responder
GSM2935401	58.0768	High	Non-responder
GSM2935403	59.7852	High	Non-responder
GSM2935320	63.6101	High	Non-responder
GSM2935303	65.7638	High	Non-responder
GSM2935386	66.0764	High	Non-responder
GSM2935331	70.3566	High	Non-responder
GSM2935289	85.0381	High	Non-responder
GSM2935330	88.0587	High	Non-responder
GSM2935314	90.7093	High	Non-responder
GSM2935317	92.2376	High	Non-responder
GSM2935365	104.9897	High	Non-responder
GSM2935327	110.6924	High	Non-responder
GSM2935305	120.1545	High	Non-responder
GSM2935301	121.9265	High	Non-responder
GSM2935302	126.8631	High	Non-responder
GSM2935311	136.7348	High	Non-responder
GSM2935329	195.8208	High	Non-responder
GSM2935313	-193.8786	Low	Responder
GSM2935279	-144.9182	Low	Responder
GSM2935394	-106.0342	Low	Responder
GSM2935288	-98.4313	Low	Responder
GSM2935280	-89.0318	Low	Responder
GSM2935406	-81.4792	Low	Responder
GSM2935385	-67.9112	Low	Responder
GSM2935411	-53.9916	Low	Responder
GSM2935281	-22.7166	Low	Responder
GSM2935333	-19.0166	Low	Responder
GSM2935310	-17.8325	Low	Responder
GSM2935413	1.9529	High	Responder
GSM2935415	7.8781	High	Responder
GSM2935282	10.8473	High	Responder
GSM2935361	11.4204	High	Responder
GSM2935285	19.6260	High	Responder
GSM2935396	32.1272	High	Responder
GSM2935392	53.3647	High	Responder
GSM2935409	62.7018	High	Responder
GSM2935300	88.6393	High	Responder
GSM2935405	115.5827	High	Responder

Table S6 Prognostic risk scores correlated with Sorafenib treatment and TACE treatment

id	riskScore	risk	responder
GSM2803756	-2.0163	low	non-responder
GSM2803739	-1.1911	low	non-responder
GSM2803800	-0.9370	low	non-responder
GSM2803752	-0.8942	low	non-responder
GSM2803747	-0.7745	low	non-responder
GSM2803792	-0.3672	low	non-responder
GSM2803738	-0.3559	low	non-responder
GSM2803786	-0.3010	low	non-responder
GSM2803765	-0.2988	low	non-responder
GSM2803788	-0.2933	low	non-responder
GSM2803742	-0.2682	low	non-responder
GSM2803768	-0.2405	low	non-responder
GSM2803780	-0.2104	low	non-responder
GSM2803784	-0.1980	low	non-responder
GSM2803791	-0.1464	low	non-responder
GSM2803759	-0.1228	low	non-responder
GSM2803736	-0.1119	low	non-responder
GSM2803745	-0.0562	low	non-responder
GSM2803776	-0.0407	low	non-responder
GSM2803771	-0.0290	low	non-responder
GSM2803777	0.0099	low	non-responder
GSM2803764	0.0515	low	non-responder
GSM2803772	0.0981	low	non-responder
GSM2803744	0.1543	low	non-responder
GSM2803783	0.1767	low	non-responder
GSM2803775	0.1945	low	non-responder
GSM2803794	0.3324	low	non-responder
GSM2803767	0.3550	low	non-responder
GSM2803751	0.3713	low	non-responder
GSM2803797	0.3890	low	non-responder
GSM2803793	0.4574	low	non-responder
GSM2803770	0.4944	low	non-responder
GSM2803760	0.5732	high	non-responder
GSM2803748	0.6140	high	non-responder
GSM2803779	0.6665	high	non-responder
GSM2803750	0.6906	high	non-responder
GSM2803740	0.7522	high	non-responder
GSM2803749	0.7751	high	non-responder
GSM2803746	0.7779	high	non-responder
GSM2803782	0.8685	high	non-responder
GSM2803773	0.8790	high	non-responder
GSM2803741	0.9386	high	non-responder
GSM2803753	0.9496	high	non-responder
GSM2803766	0.9600	high	non-responder
GSM2803755	0.9653	high	non-responder
GSM2803801	0.9665	high	non-responder
GSM2803761	1.0067	high	non-responder
GSM2803799	1.0301	high	non-responder
GSM2803798	1.1131	high	non-responder
GSM2803737	1.1334	high	non-responder
GSM2803778	1.1620	high	non-responder
GSM2803754	1.3480	high	non-responder
GSM2803758	1.3742	high	non-responder
GSM2803795	1.5149	high	non-responder
GSM2803790	1.5834	high	non-responder
GSM2803762	1.6215	high	non-responder
GSM2803785	1.6765	high	non-responder
GSM2803757	1.7183	high	non-responder
GSM2803796	1.7663	high	non-responder
GSM2803774	1.7796	high	non-responder
GSM2803743	1.8133	high	non-responder
GSM2803763	1.8644	high	non-responder
GSM2803769	2.0558	high	non-responder
GSM2803781	2.1016	high	non-responder
GSM2803789	2.1436	high	non-responder
GSM2803787	2.4178	high	non-responder
GSM2803709	-7.2321	low	responder
GSM2803734	-4.7626	low	responder
GSM2803655	-1.8194	low	responder
GSM2803695	-1.7293	low	responder
GSM2803679	-1.4777	low	responder
GSM2803715	-1.3736	low	responder
GSM2803682	-1.1624	low	responder
GSM2803704	-1.0597	low	responder
GSM2803674	-1.0376	low	responder
GSM2803721	-0.9981	low	responder
GSM2803670	-0.9307	low	responder
GSM2803671	-0.8857	low	responder
GSM2803723	-0.8292	low	responder
GSM2803705	-0.7900	low	responder
GSM2803689	-0.7610	low	responder
GSM2803688	-0.7389	low	responder
GSM2803664	-0.6850	low	responder
GSM2803728	-0.6304	low	responder
GSM2803696	-0.6146	low	responder
GSM2803673	-0.5658	low	responder
GSM2803724	-0.5632	low	responder
GSM2803719	-0.5481	low	responder
GSM2803720	-0.5407	low	responder
GSM2803702	-0.5404	low	responder
GSM2803676	-0.5136	low	responder
GSM2803732	-0.5046	low	responder
GSM2803685	-0.4953	low	responder
GSM2803686	-0.4770	low	responder
GSM2803662	-0.4727	low	responder
GSM2803735	-0.4581	low	responder
GSM2803693	-0.4477	low	responder
GSM2803717	-0.4018	low	responder
GSM2803678	-0.3976	low	responder
GSM2803700	-0.3152	low	responder
GSM2803697	-0.2857	low	responder
GSM2803680	-0.2494	low	responder
GSM2803716	-0.2079	low	responder
GSM2803672	-0.1175	low	responder
GSM2803690	-0.1055	low	responder
GSM2803657	-0.0843	low	responder
GSM2803667	-0.0118	low	responder
GSM2803718	-0.0029	low	responder
GSM2803698	-0.0011	low	responder
GSM2803733	0.0595	low	responder
GSM2803687	0.0664	low	responder
GSM2803681	0.0781	low	responder
GSM2803684	0.1246	low	responder
GSM2803710	0.1591	low	responder
GSM2803669	0.1761	low	responder
GSM2803729	0.2021	low	responder
GSM2803722	0.2509	low	responder
GSM2803701	0.3419	low	responder
GSM2803677	0.3516	low	responder
GSM2803711	0.3664	low	responder
GSM2803694	0.3712	low	responder
GSM2803691	0.3879	low	responder
GSM2803675	0.4749	low	responder
GSM2803713	0.5477	low	responder
GSM2803666	0.5613	low	responder
GSM2803714	0.5724	high	responder
GSM2803663	0.5818	high	responder
GSM2803661	0.5962	high	responder
GSM2803656	0.6022	high	responder
GSM2803692	0.6147	high	responder
GSM2803727	0.8035	high	responder
GSM2803726	0.8210	high	responder
GSM2803668	0.9388	high	responder
GSM2803707	1.0595	high	responder
GSM2803660	1.0819	high	responder
GSM2803659	1.0863	high	responder
GSM2803708	1.1031	high	responder
GSM2803658	1.1051	high	responder
GSM2803683	1.1233	high	responder
GSM2803725	1.1621	high	responder
GSM2803712	1.2094	high	responder
GSM2803731	1.3620	high	responder
GSM2803706	1.5474	high	responder
GSM2803730	1.5793	high	responder
GSM2803665	1.6264	high	responder
GSM2803699	1.9248	high	responder
GSM2803703	2.2595	high	responder

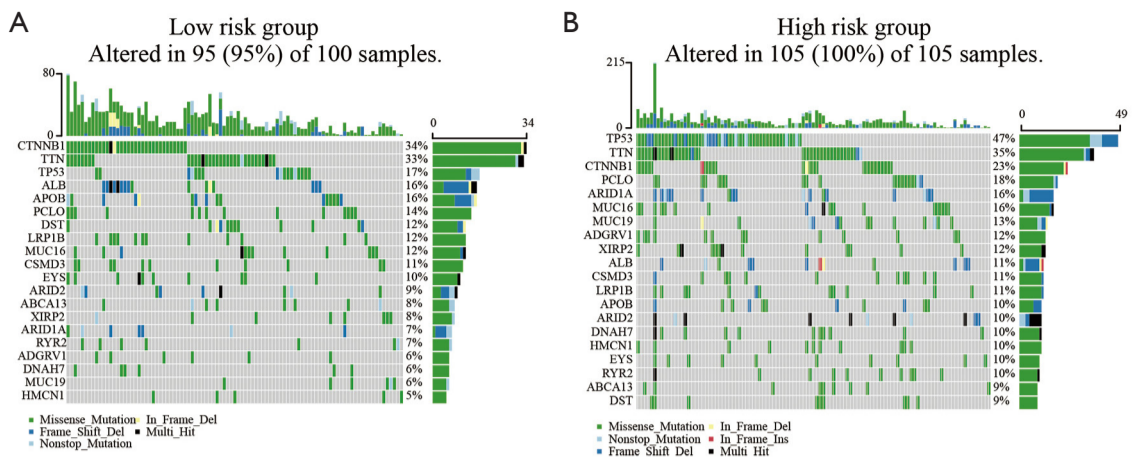


Figure S5 Landscape of mutation information of high- and low-risk HCC sample in waterfall plot. (A) Low-risk; (B) high-risk. HCC, hepatocellular carcinoma.

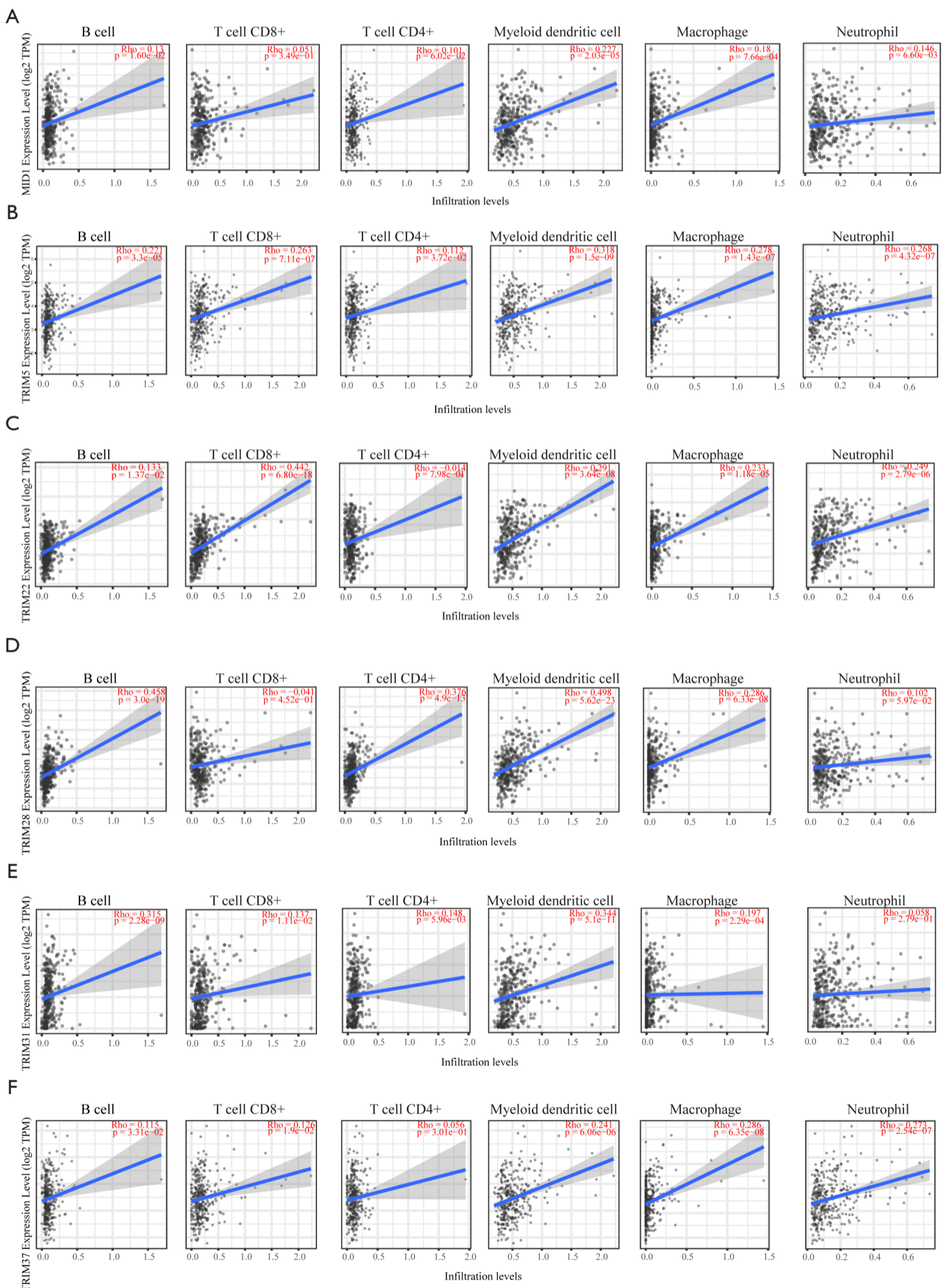


Figure S6 Relationship of the 9 TRIM genes with infiltration levels of 6 immune cell types. (A) MID1, (B) TRIM5, (C) TRIM22, (D) TRIM28, (E) TRIM31, (F) TRIM37. TRIM, tripartite-motif.

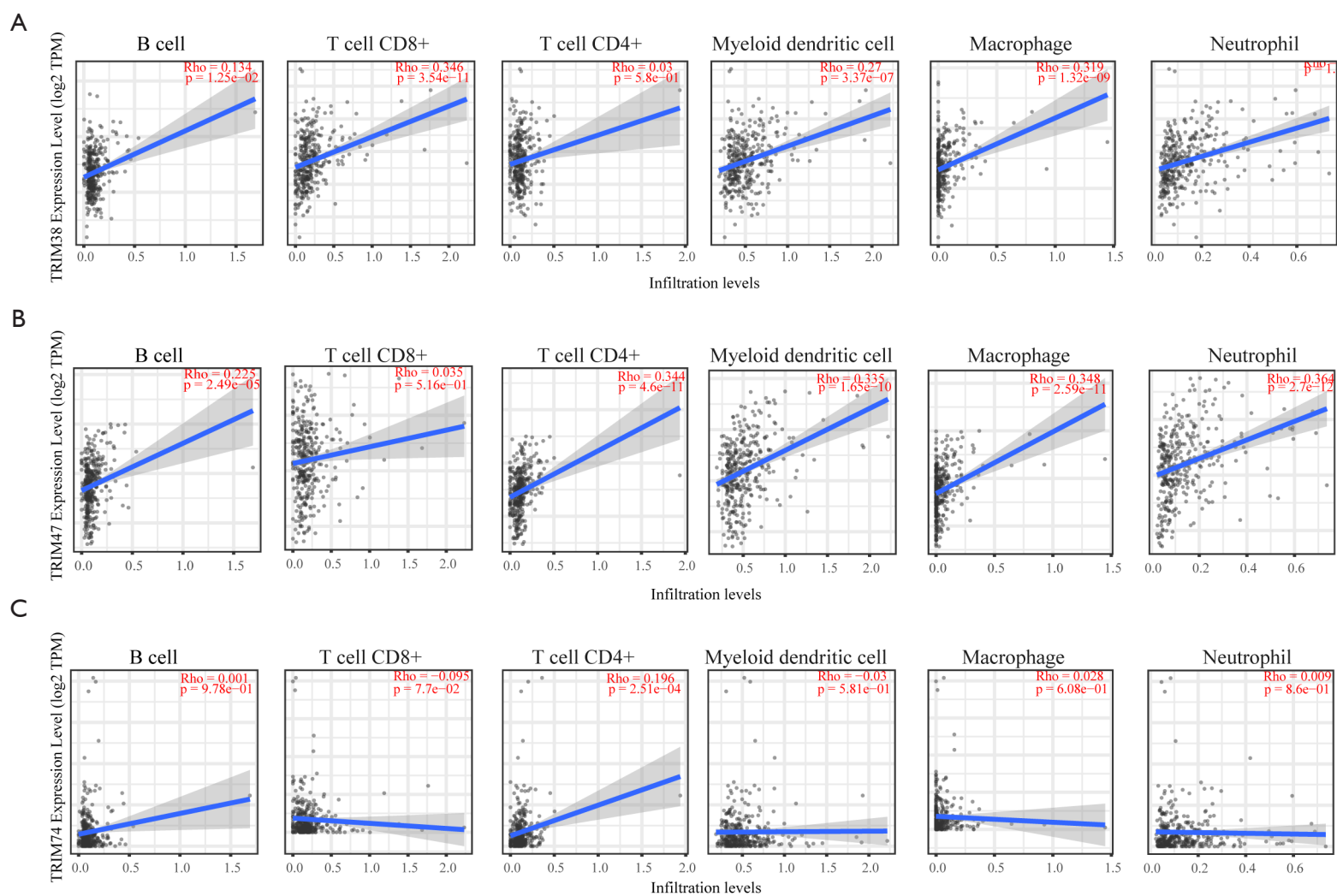


Figure S7 Relationship of the 9 TRIM genes with infiltration levels of 6 immune cell types. (A) TRIM38, (B) TRIM47, and (C) TRIM74. TRIM, tripartite-motif.