

Table S4. Gene Set Enrichment Analysis results for genes associated most significantly with patient survival.

	Gene set collection	Gene set	Normalized enrichment score	False discovery rate q-value
Genes associated with short survival	HALLMARK	EPITHELIAL_MESENCHYMAL_TRANSITION	3.454	0.000
		COAGULATION	2.882	0.000
		COMPLEMENT	2.083	0.015
	KEGG	FOCAL_ADHESION	2.316	0.008
		ECM_RECEPTOR_INTERACTION	2.314	0.004
		LYSOSOME	2.038	0.011
		REGULATION_OF_ACTIN_CYTOSKELETON	1.920	0.016
	REACTOME	EXTRACELLULAR_MATRIX_ORGANIZATION	3.125	0.000
		COLLAGEN_FORMATION	2.668	0.001
		DIABETES_PATHWAYS	2.638	0.000
		METABOLISM_OF_CARBOHYDRATES	2.571	0.000
		PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION	2.328	0.002
		RESPONSE_TO_ELEVATED_PLATELET_CYTOSOLIC_CA2	2.154	0.009
		HEMOSTASIS	1.896	0.038
		INTEGRIN_CELL_SURFACE_INTERACTIONS	1.837	0.050
	GO BIOLOGICAL PROCESS	ANGIOGENESIS	2.817	0.002
		PLATELET_DEGRANULATION	2.790	0.002
		SINGLE_ORGANISM_CATABOLIC_PROCESS	2.687	0.003
		EXTRACELLULAR_STRUCTURE_ORGANIZATION	2.589	0.004
		MULTICELLULAR_ORGANISM_METABOLIC_PROCESS	2.505	0.007
MULTICELLULAR_ORGANISMAL_MACROMOLECULE_METABOLIC_PROCESS		2.443	0.011	
BLOOD_VESSEL_MORPHOGENESIS		2.404	0.014	
RESPONSE_TO_TOPOLOGICALLY_INCORRECT_PROTEIN		2.341	0.021	
REGENERATION		2.311	0.024	
REGULATED_EXOCYTOSIS		2.286	0.025	
RECEPTOR_MEDIATED_ENDOCYTOSIS		2.215	0.039	
EXOCYTOSIS		2.207	0.037	
Genes associated with long survival	HALLMARK	ADIPOGENESIS	-2.037	0.039
	GO BIOLOGICAL PROCESS	EPIDERMAL_CELL_DIFFERENTIATION	-2.751	0.002
		SKIN_DEVELOPMENT	-2.683	0.002
		EPIDERMIS_DEVELOPMENT	-2.681	0.001
		KERATINOCYTE_DIFFERENTIATION	-2.681	0.001
		PROTEIN_LOCALIZATION_TO_CELL_PERIPHERY	-2.320	0.021
		POSITIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER	-2.233	0.032