

Table S3. List of significant gene ontology (GO) terms enriched in the ALT-like group and non ALT group

Chromatin Decompaction Type	Prognosis	Category	Term	Description	LogP	Log(q-value)
High	Poor	GO Biological Processes	GO:0006397	mRNA processing	-10.589	-6.269871994
High	Poor	GO Biological Processes	GO:0016570	histone modification	-9.05492	-5.250122606
High	Poor	GO Biological Processes	GO:1902275	regulation of chromatin organization	-8.98277	-5.250122606
High	Poor	GO Biological Processes	GO:0044257	cellular protein catabolic process	-8.5671	-4.951781437
High	Poor	GO Biological Processes	GO:0006914	autophagy	-8.42579	-4.951781437
High	Poor	Reactome Gene Sets	R-HSA-3247509	Chromatin modifying enzymes	-7.62659	-4.483576345
High	Poor	GO Biological Processes	GO:0007017	microtubule-based process	-7.05963	-3.944639698
High	Poor	Reactome Gene Sets	R-HSA-983168	Antigen processing: Ubiquitination & F	-6.47015	-3.429800576
High	Poor	GO Biological Processes	GO:0071824	protein-DNA complex subunit organiz	-6.09352	-3.192262995
High	Poor	Reactome Gene Sets	R-HSA-69278	Cell Cycle, Mitotic	-6.0812	-3.192262995
High	Poor	GO Biological Processes	GO:0050657	nucleic acid transport	-5.83526	-3.022137766
High	Poor	GO Biological Processes	GO:0051640	organelle localization	-5.82829	-3.022137766
High	Poor	GO Biological Processes	GO:0010564	regulation of cell cycle process	-5.80317	-3.01554104
High	Poor	GO Biological Processes	GO:0022411	cellular component disassembly	-5.65267	-2.924632038
High	Poor	Reactome Gene Sets	R-HSA-9006925	Intracellular signaling by second mess	-5.57385	-2.871581804
High	Poor	KEGG Pathway	hsa01522	Endocrine resistance	-5.31032	-2.672456375
High	Poor	Reactome Gene Sets	R-HSA-5696399	Global Genome Nucleotide Excision R	-5.26521	-2.636301805
High	Poor	GO Biological Processes	GO:0010256	endomembrane system organization	-5.14237	-2.547540214
High	Poor	GO Biological Processes	GO:0007034	vacuolar transport	-5.07027	-2.502829784
Low	Good	GO Biological Processes	GO:0031349	positive regulation of defense respons	-11.3638	-7.04471182
Low	Good	GO Biological Processes	GO:0034123	positive regulation of toll-like receptor	-9.75064	-5.908659302
Low	Good	GO Biological Processes	GO:0002274	myeloid leukocyte activation	-9.05642	-5.515468777
Low	Good	GO Biological Processes	GO:0001819	positive regulation of cytokine product	-8.1197	-4.72885965
Low	Good	GO Biological Processes	GO:0002697	regulation of immune effector process	-7.55319	-4.322781154
Low	Good	GO Biological Processes	GO:0042110	T cell activation	-7.4357	-4.262718944
Low	Good	Reactome Gene Sets	R-HSA-1280218	Adaptive Immune System	-6.88873	-3.848382261
Low	Good	GO Biological Processes	GO:0034154	toll-like receptor 7 signaling pathway	-6.37842	-3.381533764
Low	Good	GO Biological Processes	GO:0032647	regulation of interferon-alpha producti	-6.09954	-3.227589884
Low	Good	GO Biological Processes	GO:0032103	positive regulation of response to exte	-5.71845	-2.955645623
Low	Good	GO Biological Processes	GO:0019221	cytokine-mediated signaling pathway	-5.52913	-2.812084855
Low	Good	GO Biological Processes	GO:0051345	positive regulation of hydrolase activit	-5.32993	-2.70979488
Low	Good	GO Biological Processes	GO:0009617	response to bacterium	-5.04979	-2.494112201

Low	Good	GO Biological Processes	GO:0002831	regulation of response to biotic stimuli	-5.00653	-2.465574516
Low	Good	GO Biological Processes	GO:0032760	positive regulation of tumor necrosis f	-4.54908	-2.146005969
Low	Good	GO Biological Processes	GO:0001909	leukocyte mediated cytotoxicity	-4.54083	-2.146005969
Low	Good	GO Biological Processes	GO:0033632	regulation of cell-cell adhesion mediat	-4.52092	-2.136316396
Low	Good	GO Biological Processes	GO:0072507	divalent inorganic cation homeostasis	-4.51208	-2.134368006
Low	Good	GO Biological Processes	GO:0034341	response to interferon-gamma	-4.11805	-1.836372035
Low	Good	GO Biological Processes	GO:0001821	histamine secretion	-4.05752	-1.7802587
