

## Appendix 6 Pathways enrichment analysis (Reactome) for specific gene patterns

Appendix 6.1 – Pathways enrichment analysis (Reactome) for specific gene pattern of each cohort. Breast and thyroid have no significant functions.

Cohort	Term	Count	p-value	Genes
TCGA-COAD/READ	R-HSA-5673001: RAF/MAP kinase cascade	8	8.01E-05	FGF19, FGF8, GRIN2A, IL5RA, FGF20, NEFL, FGF3, GFRA3
TCGA-COAD/READ	R-HSA-109704: PI3K Cascade	4	0.004096	FGF19, FGF8, FGF20, FGF3
TCGA-COAD/READ	R-HSA-373760: L1CAM interactions	3	0.004208	CNTN2, CNTN1, NCAN
TCGA-HNSC	R-HSA-977441: GABA A receptor activation	2	0.026896	GABRG3, GABRB1
TCGA-HNSC	R-HSA-112314: Neurotransmitter receptors and postsynaptic signal transmission	2	0.028936	GABRG3, GABRB1
TCGA-HNSC	R-HSA-3772470: Negative regulation of TCF-dependent signaling by WNT ligand antagonists	2	0.030972	SOST, WIF1
TCGA-HNSC	R-HSA-416476: G alpha (q) signalling events	3	0.045894	NPFFR2, PROKR2, TRH
TCGA-LUAD	R-HSA-375276: Peptide ligand-binding receptors	4	0.006942	SSTR4, EDN3, NPBWR1, OPRD1
TCGA-LUAD	R-HSA-73728: RNA Polymerase I Promoter Opening	3	0.023072	HIST1H2BI, HIST1H3B, HIST1H4E
TCGA-LUAD	R-HSA-5334118: DNA methylation	3	0.024459	HIST1H2BI, HIST1H3B, HIST1H4E
TCGA-LUAD	R-HSA-5625886: Activated PKN1 stimulates transcription of AR (androgen receptor) regulated genes KLK2 and KLK3	3	0.025879	HIST1H2BI, HIST1H3B, HIST1H4E
TCGA-LUAD	R-HSA-427359: SIRT1 negatively regulates rRNA expression	3	0.026601	HIST1H2BI, HIST1H3B, HIST1H4E
TCGA-LUAD	R-HSA-212300: PRC2 methylates histones and DNA	3	0.030335	HIST1H2BI, HIST1H3B, HIST1H4E
TCGA-LUAD	R-HSA-2299718: Condensation of Prophase Chromosomes	3	0.031105	HIST1H2BI, HIST1H3B, HIST1H4E

<b>TCGA-LUAD</b>	R-HSA-912446: Meiotic recombination	3	0.041 806	HIST1H2BI, HIST1H3B, HIST1H4E
<b>TCGA-LUAD</b>	R-HSA-201722: Formation of the beta-catenin:TCF transactivating complex	3	0.042 679	HIST1H2BI, HIST1H3B, HIST1H4E
<b>TCGA-LUAD</b>	R-HSA-73777: RNA Polymerase I Chain Elongation	3	0.044 447	HIST1H2BI, HIST1H3B, HIST1H4E
<b>TCGA-LUAD</b>	R-HSA-5250924: B-WICH complex positively regulates rRNA expression	3	0.045 341	HIST1H2BI, HIST1H3B, HIST1H4E
<b>TCGA-LUAD</b>	R-HSA-3214815: HDACs deacetylate histones	3	0.048 063	HIST1H2BI, HIST1H3B, HIST1H4E
<b>TCGA-KIRC</b>	R-HSA-420029: Tight junction interactions	2	0.097 71	CLDN16, CLDN19
<b>TCGA-KIRP</b>	R-HSA-5578775: Ion homeostasis	3	0.015 509	FXYD3, CAMK2A, CASQ2
<b>TCGA-LIHC</b>	R-HSA-1650814: Collagen biosynthesis and modifying enzymes	4	0.031 157	COL6A6, COL25A1, COL2A1, COL24A1
<b>TCGA-LIHC</b>	R-HSA-420092: Glucagon-type ligand receptors	3	0.037 531	GLP2R, GLP1R, GHRHR
<b>TCGA-LIHC</b>	R-HSA-418990: Adherens junctions interactions	3	0.042 236	CDH8, CDH9, CDH10
<b>TCGA-LIHC</b>	R-HSA-186797: Signaling by PDGF	3	0.042 236	COL6A6, COL2A1, THBS4