

Appendix 4 Biological process (GO) enrichment analysis

Appendix 4.1 - Biological process (GO) enrichment analysis for breast cancer.

Category	Term	<i>p-value</i>	Genes	Rich-factor
Breast cancer	GO:0009953~dorsal/ventral pattern formation	0.000539379	LHX1, LHX2, TBX20, SP8	0.125
Breast cancer	GO:0007268~chemical synaptic transmission	0.007070558	GRM4, GRIN2B, SLC6A2, NPY2R, GABRA5, CHRNA6	0.025
Breast cancer	GO:0006810~transport	0.007959137	GRIN2B, GABRA4, SLC6A2, GABRA5, CACNG5, CHRNA6, TRPM1	0.020115
Breast cancer	GO:0034220~ion transmembrane transport	0.021093272	GRIN2B, GABRA4, SLC24A2, GABRA5, GABRQ	0.02381
Breast cancer	GO:0007417~central nervous system development	0.02230436	GABRA4, POU6F2, PDX1, TLX3	0.033333
Breast cancer	GO:0050900~leukocyte migration	0.023282782	APOB, F2, PROC, NKX2-3	0.032787
Breast cancer	GO:0007166~cell surface receptor signaling pathway	0.048566566	CRHR2, ADCYAP1R1, NPY2R, F2, PROKR1	0.018248
Breast cancer	GO:0007420~brain development	0.069907987	HMX2, FOXG1, GABRA5, NKX2-2	0.021053
Breast cancer	GO:0006355~regulation of transcription, DNA-templated	0.070533389	HMX2, POU6F2, HOXB13, MYT1, WT1, OTP, HOXC12, LHX1, LHX2, SP8, TLX3, TLX1, NKX2-3	0.008644
Breast cancer	GO:0007601~visual perception	0.079733988	RAX, SLC24A2, POU6F2, TRPM1	0.0199

Appendix 4.2 – Biological process (GO) enrichment analysis for colorectal cancer.

Category	Term	<i>p-value</i>	Genes	Rich-factor
Colorectal cancer	GO:0007268~chemical synaptic transmission	1.31E-10	GABRG1, OPRM1, HCRT, PLP1, SYT10, SLC6A2, NPY2R, KCNA1, GRIN2A, PCDH8, GRIA3, NRXN1, NPY5R, NPY, PENK, GRIA2, CHRNA4, NPFFR1, KCNQ2, GAD1, SST, HTR5A	0.091666667
Colorectal cancer	GO:0007218~neuropeptide signaling pathway	3.35186E-06	OPRM1, CALCA, HCRT, MCHR2, NPY, PENK, NPY2R, SORCS1, NPFFR1, NPY5R, SORCS3	0.108910891
Colorectal cancer	GO:0007417~central nervous system development	9.55498E-05	SH3GL3, PTRZ1, DNER, CHST8, CNTN2, DSCAML1, GRHL3, IL1RAPL2, NCAN, SNTG2	0.083333333
Colorectal cancer	GO:0007399~nervous system development	0.000142158	FGF19, SOX14, BEX1, NLGN1, CNTFR, ELAVL3, PCSK2, MYT1L, KIAA2022, CHRM2, ZIC5, GBX2, NRSN1, KCNQ2, GFRA3	0.052264808
Colorectal cancer	GO:0030154~cell differentiation	0.012012325	INA, SLCO4C1, ONECUT3, ADCYAP1R1, BEX1, PAX4, ELAVL3, NPAS4, ZIC1, SOHLH2, MYT1L, LECT1, ZIC5, HMX3, FGF3	0.032467532
Colorectal cancer	GO:0006366~transcription from RNA polymerase II promoter	0.012747964	PHOX2B, ONECUT3, OTX1, TBX20, PTF1A, GRHL3, NPAS4, ZIC1, WT1, SOHLH2, SALL4, SIX1, GBX2, TFAP2B, NEUROD1, MAFA	0.031189084
Colorectal cancer	GO:0007267~cell-cell signaling	0.016566019	CALCA, WNT2, BMP3, ADRB3, TBX5, PCDH8, CHST4, FGF20, SST, FGF3	0.039370079
Colorectal cancer	GO:0000165~MAPK cascade	0.01980359	FGF19, FGF8, MAPK4, GRIN2A, FGF10, IL5RA, FGF20, NEFL, FGF3, GFRA3	0.038167939
Colorectal cancer	GO:0006810~transport	0.042164235	ATCAY, CRABP1, SLC6A2, OBP2B, CACNG5, GRIN2A, GRIA3, PAEP, SEC14L4, CNGA3, CLVS2	0.031609195
Colorectal cancer	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	0.047063984	PHOX2B, NOS1, ONECUT3, TBX5, OTX1, TBX20, PTF1A, BEX1, FGF10, GRHL3, EN2, NPAS4, LMX1A, ZIC1, SOHLH2, WT1, WNT2, SALL4, SIX1, GBX2, TFAP2B, NEUROD1, MAFA	0.023445464

Appendix 4.3 – Biological process (GO) enrichment analysis for head and neck cancer.

Category	Term	<i>p-value</i>	Genes	Rich-factor
Head and neck cancer	GO:0007268~chemical synaptic transmission	0.000158002	NPY, GRIA2, GRM7, NPY2R, NPFFR2, GRIA4, UNC13C, NPY5R	0.033333
Head and neck cancer	GO:0035235~ionotropic glutamate receptor signaling pathway	0.000203427	GRIA2, GRIK3, GRID2, GRIA4	0.166667
Head and neck cancer	GO:0034220~ion transmembrane transport	0.000529982	GABRG3, GRIA2, GABRA4, GABRB1, GRIK3, GRID2, GRIA4	0.033333
Head and neck cancer	GO:0009952~anterior/posterior pattern specification	0.000601578	HOXC11, HOXC9, LHX1, HOXD13, HOXB9	0.0625
Head and neck cancer	GO:0007218~neuropeptide signaling pathway	0.001438684	NPY, NPY2R, NPFFR2, PROKR2, NPY5R	0.049505
Head and neck cancer	GO:0071805~potassium ion transmembrane transport	0.020725116	KCNC2, HCN1, ABCC8, CNGB3	0.033058
Head and neck cancer	GO:0006810~transport	0.026449416	SYNPR, GABRA4, GABRB1, GRID2, GRIA4, CNGB3	0.017241
Head and neck cancer	GO:0007399~nervous system development	0.050008151	LHX1, CHRM1, ZIC5, GBX2, DSCAM	0.017422

Appendix 4.4 - Biological process (GO) enrichment analysis for kidney_R cancer.

Category	Term	PValue	Genes	Rich-factor
KidneyR cancer	GO:0007588~excretion	0.001902775	CLDN16, CLCNKA, KCNJ1, AQP2	0.108108
KidneyR cancer	GO:0006366~transcription from RNA polymerase II promoter	0.002267129	DLX2, OVOL2, LHX1, ELF5, TFAP2B, EHF, TFAP2C, GRHL2, FOXI1, ZIC3, TP73	0.021442
KidneyR cancer	GO:0034220~ion transmembrane transport	0.002839727	CLCN1, BSND, GABRA2, FXYD4, ATP4B, CLCNKA, AQP2	0.033333
KidneyR cancer	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	0.013616275	ESRRB, ELF5, EHF, GRHL2, TP73, ZIC3, DLX2, OVOL2, HES5, VGLL1, TFAP2B, TFAP2C, BMP7, FOXI1	0.014271
KidneyR cancer	GO:0006813~potassium ion transport	0.017473073	ATP4B, KCNA1, KCNA4, KCNJ1	0.04878
KidneyR cancer	GO:1902476~chloride transmembrane transport	0.02429721	CLCN1, BSND, GABRA2, CLCNKA	0.043011
KidneyR cancer	GO:0010468~regulation of gene expression	0.029287305	UMODL1, LHX1, F2, TP73	0.04
KidneyR cancer	GO:0071805~potassium ion transmembrane transport	0.047233998	FXYD4, KCNA1, KCNA4, KCNE1	0.033058
KidneyR cancer	GO:0006508~proteolysis	0.049982274	GGT6, CAPN8, OVCH2, F2, DPP10, TMPRSS12, PRSS22, TMPRSS4	0.016
KidneyR cancer	GO:0045893~positive regulation of transcription, DNA-templated	0.056837811	HES5, LHX1, TFAP2B, EHF, BMP7, ZIC3, TP73, TNNI2	0.015534
KidneyR cancer	GO:0007268~chemical synaptic transmission	0.076876756	NPY, KCNA1, CHRNA6, UNC13C, GRM1	0.020833
KidneyR cancer	GO:0007155~cell adhesion	0.08672939	TNFAIP6, OLFM4, HES5, ATP4B, LSAMP, GRHL2, CTNNA2	0.015251

Appendix 4.5 – Biological process (GO) enrichment analysis for kidneyP cancer.

Category	Term	PValue	Genes	Rich-factor
KidneyP cancer	GO:0034220~ion transmembrane transport	0.0005659 49	BSND, FXYD3, GABRR1, FXYD4, CASQ2, AQP2, HTR3D	0.033333
KidneyP cancer	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	0.0027824 22	CSF3, CGA, UCN, LMX1B, ELF5, GRHL2, WT1, MYOCD, GATA5, EBF2, TFAP2A, ALX4, BMP5	0.013252
KidneyP cancer	GO:0006366~transcription from RNA polymerase II promoter	0.0035354 53	GATA5, MYOCD, LHX1, EBF2, ELF5, TFAP2A, ALX4, GRHL2, WT1	0.017544
KidneyP cancer	GO:0001822~kidney development	0.0085859 56	LHX1, TFAP2A, STRA6, WT1	0.046512
KidneyP cancer	GO:0007218~neuropeptide signaling pathway	0.0132718 51	HCRTR1, NXPH2, UCN, PYY	0.039604

Appendix 4.6 – Biological process (GO) enrichment analysis for liver cancer.

Category	Term	PValue	Genes	Rich-factor
Liver cancer	GO:0034765~regulation of ion transmembrane transport	1.33188E-05	KCNJ16, KCNU1, HCN1, KCNK16, TRPM5, KCNJ9, KCNH7, CACNA1E, KCNG3, CACNA1S, CACNA1B	0.099099
Liver cancer	GO:0007601~visual perception	0.000114605	MYO3A, POU6F2, TH, OPN1MW, KRT12, BFSP2, RCVRN, COL2A1, VSX2, CNGB3, ZIC2, RDH8, SLITRK6	0.064677
Liver cancer	GO:0007269~neurotransmitter secretion	0.000170379	GRM4, HRH3, NRXN1, DGKI, SLC5A7, GAD1, CACNA1B	0.137255
Liver cancer	GO:0071805~potassium ion transmembrane transport	0.003638388	KCNU1, HCN1, KCNK16, TRPM5, KCNK9, KCNH7, KCNG3, CNGB3	0.066116
Liver cancer	GO:1902476~chloride transmembrane transport	0.004092465	GABRD, GABRR3, GABRA4, GABRA3, GABRA5, CFTR, GABRQ	0.075269
Liver cancer	GO:0007268~chemical synaptic transmission	0.006034193	GABRD, GABRR3, GRM4, PLP1, GRIN1, GABRA5, MYCBPAP, CACNA1E, NRXN1, GAD1, CACNA1B	0.045833
Liver cancer	GO:0007605~sensory perception of sound	0.006088072	SLC17A8, MYO3A, SRRM4, SIX1, GABRA5, TH, COL2A1, SLITRK6	0.06015
Liver cancer	GO:0007155~cell adhesion	0.018372906	BMP10, MAG, CNTNAP4, CHST4, CLDN10, STAB2, TINAG, CTNNA2, CDH8, COL6A6, TNFR, NPHS1, KIRREL2, DSCAM, THBS4	0.03268
Liver cancer	GO:0007275~multicellular organism development	0.024212614	HIFNT, CRABP1, POU6F2, OTX1, TBX4, NXF5, RTL1, VSX2, WNT2, REG3A, DACH2, HOXD4, MYCBPAP, HOXA10, SPRED3, PAEP	0.03071
Liver cancer	GO:0001501~skeletal system development	0.0245762	SOX11, DLX5, HOXA10, NKX3-2, COL2A1, PITX1, BMP5	0.051095
Liver cancer	GO:0006810~transport	0.027451372	GABRD, CRABP1, GABRA4, GABRA3, GABRA5, CACNA1E, CFTR, PAEP, SLC7A4, PMP2, CNGB3, CACNA1B	0.034483
Liver cancer	GO:0007399~nervous system development	0.045482951	PCSK2, CPLX2, ERBB4, SRRM4, CHRM2, DLX5, ZIC5, DPYSL5, NEUROD6, DSCAM	0.034843
Liver cancer	GO:0007411~axon guidance	0.045684983	DCC, ZNF280A, TNFR, WNT3A, DLX5, DPYSL5, NRXN1	0.044025

Appendix 4.7 – Biological process (GO) enrichment analysis for lung cancer.

Category	Term	PValue	Genes	Rich-factor
Lung cancer	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	1.2474E-07	ONECUT2, HOXD13, FGF10, NR2E1, GDNF, BARX1, LHX2, PAX7, POU4F1, PITX1, FOXD3, ALX1, PITX2, PHOX2A, FOXL2, NOS1, OTX1, SOX11, OTX2, DMRT1, GRHL3, EN2, TBR1, NKX6-1, HOXC11, HOXC13, SALL1, TFAP2D, HOXB9	0.029562
Lung cancer	GO:0006366~transcription from RNA polymerase II promoter	3.65588E-07	FOXL2, CDX2, SOX11, OTX1, ONECUT2, OTX2, DMRT1, HOXD13, GRHL3, NKX6-1, SALL3, BARX1, HOXC11, HOXC13, NKX3-2, POU4F1, PITX1, FOXE3, PITX2, ALX1	0.038986
Lung cancer	GO:0009952~anterior/posterior pattern specification	8.39868E-07	HOXC10, BARX1, HOXC11, HOXC13, OTX1, HOXA11, HOXD13, HOXB9, ALX1	0.1125
Lung cancer	GO:0007275~multicellular organism development	0.000413974	EDN3, CDX2, CRABP1, OTX1, HOXA11, OTX2, HOXD13, EN2, BOLL, TAF7L, C14ORF39, SPATA19, SPRED3, TLX1, ALX1	0.028791
Lung cancer	GO:0000122~negative regulation of transcription from RNA polymerase II promoter	0.001256859	FOXL2, CDX2, SOX11, DMRT1, MAGEA2, NR2E1, NKX6-1, FEZF1, T, DLX1, SALL1, FOXE1, NKX3-2, POU4F1, PITX2, ALX1, FOXD3	0.023611
Lung cancer	GO:0043524~negative regulation of neuron apoptotic process	0.001559435	DLX1, POU4F1, PRKCG, TFAP2D, EN2, GDNF, TERT	0.05303
Lung cancer	GO:0006357~regulation of transcription from RNA polymerase II promoter	0.003074679	SRY, BARX1, FOXI3, MNX1, FOXE1, POU4F1, UCPI, SIM1, FOXE3, NKX6-1, PITX2, TAF7L	0.027211
Lung cancer	GO:0045893~positive regulation of transcription, DNA-templated	0.00350027	FOXL2, NOS1, CDX2, SOX11, HOXA11, OTX2, FGF10, FEZF1, SRY, SALL1, LHX2, FOXE1, ALX1	0.025243
Lung cancer	GO:0030154~cell differentiation	0.00436224	SRY, HMX2, FOXL2, CDX2, ADCYAP1R1, ZIC5, ONECUT2, SPATA19, BRDT, SIM1, BOLL, TAF7L	0.025974
Lung cancer	GO:0007268~chemical synaptic transmission	0.007703478	SSTR4, NPBWR1, CRH, CHRNA4, PRKCG, GAD1, NPY5R, OPRD1	0.033333
Lung cancer	GO:0007399~nervous system development	0.019023147	BARX1, FUT9, CHRM2, CHRM1, ZIC5, GDNF, NR2E1, SIM1	0.027875
Lung cancer	GO:0006351~transcription, DNA-templated	0.026126765	HMX2, HOXA11, MAGEA2, HOXB13, NR2E1, HOXD11, SRY, T, LHX2, PAX7, TLX2, SIM1, FOXD3, PHOX2A, DMRT3, TBR1, VSX1, FEZF1, HOXC10, FOXI3, SALL1, MNX1, FOXE1, BRDT, TFAP2D, HOXB9, SP8, FOXE3	0.014322
Lung cancer	GO:0008284~positive regulation of cell proliferation	0.032329124	HOXC10, EDN3, T, HMX2, CDX2, REG1A, SOX11, CHRM1, CRH, GDNF	0.021459

Lung cancer	GO:0007186~G-protein coupled receptor signaling pathway	0.044258577	OR5P3, OR10A3, OR5P2, OR2B11, ADCYAP1R1, NPBWR1, OR2W3, NPY5R, SSTR4, CHRM2, CHRM1, OR6K3, GPR50, OR6N1, OPRD1	0.016685
Lung cancer	GO:0006810~transport	0.046626806	SYNPR, GABRA1, CRABP1, GABRA4, GABRA3, GRID2, CNGA3, TRPM1	0.022989