

Significant Genes and Enriched Pathways

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The genes included here are significantly conserved based on the conservation probability score derived from the posterior distribution of log sigmaP/sigmaT ratio (which will be high when tumor variability is lower than normal variability):

$$\text{score}_{\text{median}} = \text{Median}(\log \frac{\sigma_P}{\sigma_T})$$

We select significantly conserved genes based on the top 95th percentile of adjusted bootstrapped values.

Reactome Enriched Pathways

Begin reactome GSEA...

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user  system elapsed
16.351  1.540  19.448
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Total number of genes: 1660 Number of enrichment pathways: 54

score_median top enriched paths:

Table 1: Table continues below

Pathway	ngenes	padj
Antigen Presentation: Folding, assembly and peptide loading of class I MHC	14	1.072e-07
Nonsense-Mediated Decay (NMD)	30	1.072e-07
Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	30	1.072e-07
GTP hydrolysis and joining of the 60S ribosomal subunit	29	1.832e-07
Regulation of expression of SLITs and ROBOs	37	1.832e-07
L13a-mediated translational silencing of Ceruloplasmin expression	28	4.472e-07
Eukaryotic Translation Initiation	29	4.472e-07
Cap-dependent Translation Initiation	29	4.472e-07
Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	25	9.069e-07
Eukaryotic Translation Termination	24	2.253e-06
Influenza Life Cycle	31	2.253e-06
Signaling by ROBO receptors	39	7.365e-06
Eukaryotic Translation Elongation	23	8.8e-06
Influenza Infection	31	1.059e-05

Pathway	ngenes	padj
Selenoamino acid metabolism	26	1.285e-05
Peptide chain elongation	22	1.285e-05
Viral mRNA Translation	22	1.285e-05
Influenza Viral RNA Transcription and Replication	28	1.285e-05
Selenocysteine synthesis	22	2.63e-05
Formation of a pool of free 40S subunits	23	2.847e-05
Processing of Capped Intron-Containing Pre-mRNA	40	3.198e-05
SRP-dependent cotranslational protein targeting to membrane	24	4.801e-05
mRNA Splicing	33	8.672e-05
mRNA Splicing - Major Pathway	32	9.102e-05
Infectious disease	53	0.0001036
ER-Phagosome pathway	19	0.0001969
Mitochondrial protein import	16	0.0003217
Translation	42	0.0003721
Class I MHC mediated antigen processing & presentation	49	0.0007815
Interferon Signaling	31	0.001169
Metabolism of amino acids and derivatives	48	0.001416
Ribosomal scanning and start codon recognition	14	0.00153
Endosomal/Vacuolar pathway	6	0.001537
Antigen processing-Cross presentation	19	0.002128
Major pathway of rRNA processing in the nucleolus and cytosol	28	0.004005
rRNA processing in the nucleus and cytosol	29	0.004069
rRNA processing	30	0.004098
Translation initiation complex formation	13	0.005408
Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	13	0.006324
Protein localization	25	0.006445
snRNP Assembly	12	0.00779
Metabolism of non-coding RNA	12	0.00779
Mitotic Metaphase and Anaphase	28	0.01442
M Phase	46	0.01757
Interferon gamma signaling	16	0.0189
ATF6 (ATF6-alpha) activates chaperones	5	0.02375
Mitotic Prometaphase	27	0.02438
Separation of Sister Chromatids	26	0.02438
Mitotic Anaphase	27	0.02562
Deubiquitination	36	0.02847
Antiviral mechanism by IFN-stimulated genes	14	0.03289
ISG15 antiviral mechanism	13	0.03509
Cell Cycle Checkpoints	35	0.04015
Ub-specific processing proteases	28	0.0433

Genes
EMD;STAG2;PSMD10;CETN2;PHF8;PSMD5;HIST1H2BK;ERCC6L;HDAC8;HAUS7;CDC20;TUBA3E;FBXO5;OFD1;TUBB;SMC1A;SEH1L;CENPK;CEP76;PLK4;DYNLL1;CENPA;STAG2;PSMD10;PSMD5;ERCC6L;HDAC8;CDC20;TUBA3E;PSMD13;SMC1A;SEH1L;CENPK;PSMA2;PSMA7;DYNLL1;CENPA;EMD;STAG2;PSMD10;PSMD5;ERCC6L;HDAC8;CDC20;TUBA3E;PSMD13;SMC1A;SEH1L;CENPK;PSMA2;PSMA7;DYNLL1;CENPA;IKBK;OTUD5;FOXO4;RNF128;HCFC1;PSMD10;BRCC3;TAF9B;OGT;PSMD5;HIST1H2BK;CDC20;TNIP2;HIST1H2AH;FLNA;EIF4E;SEH1L;EIF4A2;ARIH1;RANBP2;FLNB;EIF4E2;UBE2N;EIF4A3;EIF4A1;NUP37;NUP153;NUP160;EIF4E;SEH1L;EIF4A2;ARIH1;RANBP2;FLNB;EIF4E2;UBE2N;EIF4A3;EIF4A1;NUP37;NUP153;NUP160;PSMD10;BRCC3;PSMD5;HIST1H2BK;ERCC6L;CDC20;PSMD13;SEH1L;CENPK;CCNE1;PSMA2;RFC2;PSMA7;DYNLL1;IKBK;FOXO4;RNF128;PSMD10;TAF9B;PSMD5;HIST1H2BK;CDC20;HIST1H2AH;PSMD13;USP11;PSMA2;USP9X;TOM1

GSVA-type analysis

Evidence: conservation score rank

Ranked conservation scores



UBQLN2 ID1 CS IL7 C4B FLII CIC F7 F5 IL2 TTL MB C3 MIP F9

Begin calculating random-walk statistics...

7.36 1.516 8.911 0 0

Processed 23343 genes, 2232 pathways/genesets. Begin bootstrapping...

Shuffling 203 set-lengths: 5000x random shuffles (w/ replacement)

user	system	elapsed
1121.550	503.888	1635.062

111 significant pathways out of 1803 tested (429 excluded by size <10 | >500)

score	pval	FDR	Ngene	GeneSet
0.552	0.000	0.000	86	KEGG_RIBOSOME
0.427	0.000	0.000	120	KEGG_SPLICEOSOME
0.404	0.000	0.000	128	KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS
0.479	0.000	0.000	67	KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION
0.465	0.000	0.000	271	REACTOME_TRANSLATION
0.525	0.000	0.000	111	REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING
0.444	0.000	0.000	58	REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT
0.408	0.000	0.000	232	REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_MRNA
0.496	0.000	0.000	58	REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP
0.382	0.000	0.000	355	REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES
0.403	0.000	0.000	481	REACTOME_CELL_CYCLE_MITOTIC
0.414	0.000	0.000	246	REACTOME_CELL_CYCLE_CHECKPOINTS
0.424	0.000	0.000	182	REACTOME_MRNA_SPLICING
0.387	0.000	0.000	192	REACTOME_MITOTIC_G2_G2_M_PHASES
0.384	0.000	0.000	180	REACTOME_INTERFERON_SIGNALING
0.406	0.000	0.000	219	REACTOME_HIV_INFECTION
0.410	0.000	0.000	140	REACTOME_HIV_LIFE_CYCLE

0.419	0.000	0.000	124	REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS
0.435	0.000	0.000	94	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY
0.421	0.000	0.000	192	REACTOME_MITOTIC_PROMETAPHASE
0.638	0.000	0.000	25	REACTOME_ANTIGEN_PRESENTATION_FOLDING_ASSEMBLY_AND_PEPTID
0.387	0.000	0.000	356	REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRESENTA
0.410	0.000	0.000	129	REACTOME_G2_M_CHECKPOINTS
0.648	0.000	0.000	23	REACTOME_CHOLESTEROL_BIOSYNTHESIS
0.422	0.000	0.000	143	REACTOME_THE_CITRIC_ACID_TCA_CYCLE_AND_RESPIRATORY_ELECTR
0.474	0.000	0.000	152	REACTOME_INFLUENZA_INFECTION
0.369	0.000	0.000	252	REACTOME_RHO_GTPASE_EFFECTORS
0.498	0.000	0.000	108	REACTOME_SELENOAMINO_ACID_METABOLISM
0.434	0.000	0.000	119	REACTOME_RESOLUTION_OF_SISTER_CHROMATID_COHESION
0.440	0.000	0.000	226	REACTOME_MITOTIC_METAPHASE_AND_ANAPHASE
0.469	0.000	0.000	74	REACTOME_NUCLEAR_ENVELOPE_NE_REASSEMBLY
0.370	0.000	0.000	339	REACTOME_TRANSCRIPTIONAL_REGULATION_BY_TP53
0.407	0.000	0.000	211	REACTOME_SIGNALING_BY_ROBO_RECEPTORS
0.371	0.000	0.000	172	REACTOME_PROGRAMMED_CELL_DEATH
0.388	0.000	0.000	230	REACTOME_DEUBIQUITINATION
0.423	0.000	0.000	339	REACTOME_M_PHASE
0.440	0.000	0.000	105	REACTOME_MITOTIC_SPINDLE_CHECKPOINT
0.450	0.000	0.000	190	REACTOME_RRNA_PROCESSING
0.508	0.000	0.000	118	REACTOME_EUKARYOTIC_TRANSLATION_INITIATION
0.474	0.000	0.000	63	REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_TERMINATION
0.461	0.000	0.000	168	REACTOME_REGULATION_OF_EXPRESSION_OF_SLITS_AND_ROBOS
0.527	0.000	0.000	115	REACTOME_NONSENSE_MEDIATED_DECAY_NMD
0.553	0.000	0.000	93	REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION
0.499	0.000	0.000	51	REACTOME_SNRNP_ASSEMBLY
0.432	0.000	0.000	182	REACTOME_SEPARATION_OF_SISTER_CHROMATIDS
0.371	0.000	0.000	187	REACTOME_CHROMATIN_MODIFYING_ENZYMES
0.533	0.000	0.000	101	REACTOME_RESPONSE_OF_EIF2AK4_GCN2_TO_AMINO_ACID_DEFICIENCY
0.471	0.000	0.006	49	KEGG_GLUTATHIONE_METABOLISM
0.481	0.000	0.006	44	PID_PLK1_PATHWAY
0.426	0.000	0.006	95	REACTOME_ANTIGEN_PROCESSING_CROSS_PRESENTATION
0.429	0.000	0.006	88	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT
0.380	0.000	0.006	297	REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION_PROTEASOME_DEGR
0.359	0.000	0.006	266	REACTOME_ORGANELLE_BIOGENESIS_AND_MAINTENANCE
0.448	0.000	0.006	59	REACTOME_SCF_SKP2_MEDIATED_DEGRADATION_OF_P27_P21
0.414	0.000	0.006	83	REACTOME_UCH_PROTEINASES
0.379	0.000	0.006	158	REACTOME_UB_SPECIFIC_PROCESSING_PROTEASES
0.409	0.000	0.006	89	REACTOME_SWITCHING_OF_ORIGINS_TO_A_POST_REPLICATIVE_STATE
0.382	0.000	0.006	155	REACTOME_PROTEIN_LOCALIZATION
0.432	0.000	0.006	96	REACTOME_HCMV_INFECTION
0.541	0.000	0.010	28	REACTOME_PROCESSING_OF_CAPPED_INTRONLESS_PRE_MRNA
0.383	0.000	0.010	147	REACTOME_MITOTIC_G1_PHASE_AND_G1_S_TRANSITION
0.381	0.000	0.010	159	REACTOME_S_PHASE
0.404	0.000	0.010	93	REACTOME_TOLL LIKE RECEPTOR_9_TLR9_CASCADE
0.396	0.000	0.010	133	REACTOME_RHO_GTPASES_ACTIVATE_FORMINS
0.471	0.000	0.010	56	REACTOME_TRNA_PROCESSING_IN_THE_NUCLEUS
0.421	0.000	0.010	100	REACTOME_TRNA_PROCESSING
0.453	0.000	0.010	63	REACTOME_PROTEIN_UBIQUITINATION
0.414	0.000	0.010	82	REACTOME_TOLL LIKE RECEPTOR_10_TLR10_CASCADE
0.464	0.000	0.010	52	REACTOME_HCMV_LATE_EVENTS
0.411	0.001	0.015	97	KEGG_PARKINSONS_DISEASE
0.361	0.001	0.015	269	REACTOME_DNA_REPAIR

0.418	0.001	0.015	85	REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_B
0.380	0.001	0.015	126	REACTOME_DNA_REPLICATION
0.393	0.001	0.018	101	PID_ERBB1_DOWNSTREAM_PATHWAY
0.423	0.001	0.018	79	REACTOME_ANTIVIRAL_MECHANISM_BY_IFN_STIMULATED_GENES
0.404	0.001	0.018	90	REACTOME_RECRUITMENT_OF_NUMA_TO_MITOTIC_CENTROSOMES
0.370	0.001	0.018	165	REACTOME_SUMOYLATION
0.326	0.001	0.018	466	REACTOME_NEUTROPHIL_DEGRANULATION
0.377	0.001	0.018	133	REACTOME_PTEN_REGULATION
0.424	0.001	0.018	72	REACTOME_HCMV_EARLY_EVENTS
0.425	0.001	0.021	71	REACTOME_APC_C_CDH1_MEDIATED_DEGRADATION_OF_CDC20_AND_O
0.446	0.001	0.021	57	REACTOME_G2_M_DNA_DAMAGE_CHECKPOINT
0.394	0.001	0.021	93	REACTOME_MITOCHONDRIAL_TRANSLATION
0.420	0.001	0.021	77	REACTOME_TP53_REGULATES_METABOLIC_GENES
0.653	0.001	0.025	11	REACTOME_ENDOSOMAL_VACUOLAR_PATHWAY
0.417	0.001	0.025	77	REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYTOPLASM
0.394	0.001	0.028	96	REACTOME_CELLULAR_RESPONSE_TO_HEAT_STRESS
0.440	0.001	0.028	53	REACTOME_RRNA_MODIFICATION_IN_THE_NUCLEUS_AND_CYTOSOL
0.394	0.001	0.028	90	REACTOME_REGULATION_OF_TP53_ACTIVITY_THROUGH_PHOSPHORYLA
0.413	0.001	0.028	77	REACTOME_THE_ROLE_OF_GTSE1_IN_G2_M_PROGRESSION_AFTER_G2
0.407	0.001	0.028	85	REACTOME_APC_C_MEDIATED_DEGRADATION_OF_CELL_CYCLE_PROTE
0.460	0.002	0.030	46	REACTOME_APOPTOTIC_EXECUTION_PHASE
0.402	0.002	0.030	95	REACTOME_TOLL LIKE RECEPTOR_TLR1_TLR2_CASCADE
0.406	0.002	0.030	84	REACTOME_CYCLIN_A_CDK2_ASSOCIATED_EVENTS_AT_S_PHASE_ENTR
0.418	0.002	0.030	71	REACTOME_AURKA_ACTIVATION_BY_TPX2
0.373	0.002	0.034	123	KEGG_CELL_CYCLE
0.412	0.002	0.035	79	REACTOME_DOWNSTREAM_SIGNALING_EVENTS_OF_B_CELL_RECEPTOR
0.497	0.002	0.035	33	REACTOME_FANCONI_ANEMIA_PATHWAY
0.489	0.002	0.035	34	REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_CELLULAR_PROTEINS
0.398	0.002	0.035	82	REACTOME_DEGRADATION_OF_BETA_CATENIN_BY_THE_DESTRUCTION
0.445	0.002	0.035	44	REACTOME_SUMOYLATION_OF_DNA_REPLICATION_PROTEINS
0.428	0.002	0.035	60	REACTOME_PROCESSING_OF_DNA_DOUBLE_STRAND_BREAK_ENDS
0.350	0.002	0.035	198	REACTOME_INTRA_GOLGI_AND_RETROGRADE_GOLGI_TO_ER_TRAFFIC
0.406	0.002	0.035	78	REACTOME_MITOTIC_PROPHASE
0.344	0.003	0.045	227	REACTOME_NEDDYLATION
0.404	0.003	0.047	77	REACTOME_RECRUITMENT_OF_MITOTIC_CENTROSOME_PROTEINS_AND
0.440	0.003	0.047	54	REACTOME_AUF1_HNRNP_D0_BINDS_AND_DESTABILIZES_MRNA
0.475	0.003	0.049	35	KEGG_ALLOGRAFT_REJECTION
0.506	0.003	0.049	29	REACTOME_G1_S_SPECIFIC_TRANSCRIPTION
0.390	0.003	0.049	91	REACTOME_UNFOLDED_PROTEIN_RESPONSE_UPR
0.435	0.003	0.049	49	REACTOME_COMPLEX_I_BIOGENESIS

Warning in write.csv(enrichedGenes, here("significantgenes_filtered.csv"), :
attempt to set 'col.names' ignored

Warning in write.csv(GSEA_df %>% arrange(FDR) %>% filter(FDR < 0.05) %>% :
attempt to set 'col.names' ignored