

# Significant Genes and Enriched Pathways

Kevin Murgas

2020-08-24

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...

```
user  system elapsed
15.429  1.545  18.012
```

Total number of genes: 1660 Number of enrichment pathways: 54

score\_median top enriched paths:

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
Selenoamino acid metabolism	26	1.285e-05
Peptide chain elongation	22	1.285e-05

Pathway	ngenes	padj
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

## 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...

6.43 1.399 7.833 0 0

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

Shuffling 203 set-lengths: 1000x random shuffles (w/o replacement)

user	system	elapsed
228.341	106.041	335.946

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

score	pval	FDR	Ngene	GeneSet
0.471	0.000	0.000	49	KEGG_GLUTATHIONE_METABOLISM
0.498	0.000	0.000	30	KEGG_PROPANOATE_METABOLISM
0.552	0.000	0.000	86	KEGG_RIBOSOME
0.427	0.000	0.000	120	KEGG_SPLICEOSOME
0.479	0.000	0.000	67	KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION
0.411	0.000	0.000	97	KEGG_PARKINSONS_DISEASE
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
0.417	0.000	0.000	77	REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYTOPLASM
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
0.404	0.000	0.000	90	REACTOME_RECRUITMENT_OF_NUMA_TO_MITOTIC_CENTROSOMES
0.424	0.000	0.000	182	REACTOME_MRNA_SPLICING

0.541	0.000	0.000	28	REACTOME_PROCESSING_OF_CAPPED_INTRONLESS_PRE_MRNA
0.383	0.000	0.000	147	REACTOME_MITOTIC_G1_PHASE_AND_G1_S_TRANSITION
0.387	0.000	0.000	192	REACTOME_MITOTIC_G2_G2_M_PHASES
0.361	0.000	0.000	269	REACTOME_DNA_REPAIR
0.418	0.000	0.000	85	REACTOME_REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_B
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
0.380	0.000	0.000	297	REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION_PROTEASOME_DEG
0.410	0.000	0.000	129	REACTOME_G2_M_CHECKPOINTS
0.381	0.000	0.000	159	REACTOME_S_PHASE
0.648	0.000	0.000	23	REACTOME_CHOLESTEROL_BIOSYNTHESIS
0.460	0.000	0.000	46	REACTOME_APOPTOTIC_EXECUTION_PHASE
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
0.359	0.000	0.000	266	REACTOME_ORGANELLE_BIOGENESIS_AND_MAINTENANCE
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
0.420	0.000	0.000	77	REACTOME_TP53_REGULATES_METABOLIC_GENES
0.396	0.000	0.000	133	REACTOME_RHO_GTPASES_ACTIVATE_FORMINS
0.388	0.000	0.000	230	REACTOME_DEUBIQUITINATION
0.471	0.000	0.000	56	REACTOME_TRNA_PROCESSING_IN_THE_NUCLEUS
0.435	0.000	0.000	49	REACTOME_COMPLEX_I_BIOGENESIS
0.377	0.000	0.000	133	REACTOME_PTEN_REGULATION
0.423	0.000	0.000	339	REACTOME_M_PHASE
0.440	0.000	0.000	105	REACTOME_MITOTIC_SPINDLE_CHECKPOINT
0.421	0.000	0.000	100	REACTOME_TRNA_PROCESSING
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
0.453	0.000	0.000	63	REACTOME_PROTEIN_UBIQUITINATION
0.413	0.000	0.000	77	REACTOME_THE_ROLE_OF_GTSE1_IN_G2_M_PROGRESSION_AFTER_G2
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
0.382	0.000	0.000	155	REACTOME_PROTEIN_LOCALIZATION
0.553	0.000	0.000	93	REACTOME_EUKARYOTIC_TRANSLATION_ELONGATION
0.407	0.000	0.000	85	REACTOME_APC_C_MEDIATED_DEGRADATION_OF_CELL_CYCLE_PROTE
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
0.432	0.000	0.000	96	REACTOME_HCMV_INFECTION
0.424	0.000	0.000	72	REACTOME_HCMV_EARLY_EVENTS
0.464	0.000	0.000	52	REACTOME_HCMV_LATE_EVENTS
0.533	0.000	0.000	101	REACTOME_RESPONSE_OF EIF2AK4_GCN2_TO_AMINO_ACID_DEFICIENCY

0.581	0.001	0.021	15	KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS
0.373	0.001	0.021	123	KEGG_CELL_CYCLE
0.404	0.001	0.021	128	KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS
0.476	0.001	0.021	30	PID_HDAC_CLASSII_PATHWAY
0.397	0.001	0.021	73	PID_E2F_PATHWAY
0.393	0.001	0.021	101	PID_ERBB1_DOWNSTREAM_PATHWAY
0.426	0.001	0.021	95	REACTOME_ANTIGEN_PROCESSING_CROSS_PRESENTATION
0.404	0.001	0.021	77	REACTOME_RECRUITMENT_OF_MITOTIC_CENTROSOME_PROTEINS_AND
0.429	0.001	0.021	88	REACTOME_RESPIRATORY_ELECTRON_TRANSPORT
0.380	0.001	0.021	126	REACTOME_DNA_REPLICATION
0.489	0.001	0.021	34	REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_CELLULAR_PROTEINS
0.448	0.001	0.021	59	REACTOME_SCF_SKP2_MEDIATED_DEGRADATION_OF_P27_P21
0.379	0.001	0.021	158	REACTOME_UB_SPECIFIC_PROCESSING_PROTEASES
0.440	0.001	0.021	53	REACTOME_RRNA_MODIFICATION_IN_THE_NUCLEUS_AND_CYTOSOL
0.409	0.001	0.021	89	REACTOME_SWITCHING_OF_ORIGINS_TO_A_POST_REPLICATIVE_STATE
0.406	0.001	0.021	84	REACTOME_CYCLIN_A_CDK2_ASSOCIATED_EVENTS_AT_S_PHASE_ENTRY
0.361	0.002	0.032	157	KEGG_HUNTINGTONS_DISEASE
0.475	0.002	0.032	35	KEGG_ALLOGRAFT_REJECTION
0.481	0.002	0.032	44	PID_PLK1_PATHWAY
0.653	0.002	0.032	11	REACTOME_ENDOSOMAL_VACUOLAR_PATHWAY
0.423	0.002	0.032	79	REACTOME_ANTIVIRAL_MECHANISM_BY_IFN_STIMULATED_GENES
0.497	0.002	0.032	33	REACTOME_FANCONI_ANEMIA_PATHWAY
0.412	0.002	0.032	67	REACTOME_ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX
0.425	0.002	0.032	71	REACTOME_APC_C_CDH1_MEDIATED_DEGRADATION_OF_CDC20_AND_O
0.506	0.002	0.032	29	REACTOME_G1_S_SPECIFIC_TRANSCRIPTION
0.446	0.002	0.032	57	REACTOME_G2_M_DNA_DAMAGE_CHECKPOINT
0.590	0.002	0.032	14	BIOCARTA_SM_PATHWAY
0.404	0.002	0.032	93	REACTOME_TOLL LIKE RECEPTOR_9_TLR9_CASCADE
0.402	0.002	0.032	95	REACTOME_TOLL LIKE RECEPTOR_TLR1_TLR2_CASCADE
0.464	0.002	0.032	35	REACTOME_INTERACTIONS_OF_REV_WITH_HOST_CELLULAR_PROTEINS
0.386	0.002	0.032	85	REACTOME_EPIGENETIC_REGULATION_OF_GENE_EXPRESSION
0.394	0.002	0.032	85	REACTOME_REGULATION_OF_PLK1_ACTIVITY_AT_G2_M_TRANSITION
0.370	0.002	0.032	165	REACTOME_SUMOYLATION
0.394	0.002	0.032	93	REACTOME_MITOCHONDRIAL_TRANSLATION
0.428	0.002	0.032	60	REACTOME_PROCESSING_OF_DNA_DOUBLE_STRAND_BREAK_ENDS
0.326	0.002	0.032	466	REACTOME_NEUTROPHIL_DEGRANULATION
0.394	0.002	0.032	90	REACTOME_REGULATION_OF_TP53_ACTIVITY_THROUGH_PHOSPHORYLA
0.406	0.002	0.032	78	REACTOME_MITOTIC_PROPHASE
0.418	0.002	0.032	71	REACTOME_AURKA_ACTIVATION_BY_TPX2
0.414	0.002	0.032	82	REACTOME_TOLL LIKE RECEPTOR_10_TLR10_CASCADE
0.516	0.002	0.032	25	REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAINING_NUCLEOSOMES
0.432	0.003	0.044	54	KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION
0.535	0.003	0.044	19	REACTOME_PROCESSING_OF_INTRONLESS_PRE_MRNAS
0.406	0.003	0.044	67	REACTOME_CHROMOSOME_MAINTENANCE
0.406	0.003	0.044	64	REACTOME_TRANSCRIPTION_OF_THE_HIV_GENOME
0.393	0.003	0.044	74	REACTOME_SUMOYLATION_OF_DNA_DAMAGE_RESPONSE_AND_REPAIR
0.394	0.003	0.044	96	REACTOME_CELLULAR_RESPONSE_TO_HEAT_STRESS
0.440	0.003	0.044	54	REACTOME_AUF1_HNRNP_D0_BINDS_AND_DESTABILIZES_MRNA
0.371	0.003	0.044	172	REACTOME_PROGRAMMED_CELL_DEATH
0.348	0.003	0.044	194	REACTOME_CILIUM_ASSEMBLY
0.414	0.003	0.044	83	REACTOME_UCH_PROTEINASES