

Table S3: GeneCodis analysis

GO biological process

all signature genes

Genes	NGR	TNGR	NG	TNG	Hyp	Hyp*	Annotations
13 genes	136	34208		13	341	0,000123	0,124843 GO:0006805: xenobiotic metabolic process (BP)
9 genes	56	34208		9	341	0,000439	0,222782 GO:0007586: digestion (BP)
24 genes	630	34208		24	341	0,002805	0,948987 GO:0055085: transmembrane transport (BP)
13 genes	181	34208		13	341	0,003935	0,998436 GO:0019221: cytokine-mediated signaling pathway (BP)
20 genes	549	34208		20	341	0,082354	0,0001671 GO:0006811: ion transport (BP)
30 genes	1176	34208		30	341	0,299356	0,0005064 GO:0007165: signal transduction (BP)
7 genes	75	34208		7	341	1,02096	0,0012953 GO:0060337: type I interferon-mediated signaling pathway (BP)
9 genes	136	34208		9	341	0,965131	0,0013994 GO:0032496: response to lipopolysaccharide (BP)
3 genes	6	34208		3	341	1,92057	0,0021659 GO:0046483: heterocycle metabolic process (BP)
7 genes	88	34208		7	341	2,92364	0,0029675 GO:0008202: steroid metabolic process (BP)

downregulated signature genes

Genes	NGR	TNGR	NG	TNG	Hyp	Hyp*	Annotations
12 genes	136	34208		12	225	1,21E-05	0,004089 GO:0006805: xenobiotic metabolic process (BP)
9 genes	56	34208		9	225	1,14E-05	0,007686 GO:0007586: digestion (BP)
21 genes	630	34208		21	225	0,00015	0,033903 GO:0055085: transmembrane transport (BP)
19 genes	549	34208		19	225	0,000513	0,086713 GO:0006811: ion transport (BP)
7 genes	88	34208		7	225	0,195953	0,0002649 GO:0008202: steroid metabolic process (BP)
3 genes	6	34208		3	225	0,553433	0,0006235 GO:0046483: heterocycle metabolic process (BP)
4 genes	20	34208		4	225	0,081281	0,0006868 GO:0017144: drug metabolic process (BP)
5 genes	41	34208		5	225	0,727521	0,0007025 GO:0006865: amino acid transport (BP)
2 genes	2	34208		2	225	4,30713	0,0032351 GO:0046485: ether lipid metabolic process (BP)
8 genes	200	34208		8	225	5,77955	0,0039069 GO:0034641: cellular nitrogen compound metabolic process (BP)

upregulated signature genes

Genes	NGR	TNGR	NG	TNG	Hyp	Hyp*	Annotations
7 genes	181	34208		7	116	0,296553	0,0015450 GO:0019221: cytokine-mediated signaling pathway (BP)
8 genes	341	34208		8	116	2,24209	0,0058406 GO:0008285: negative regulation of cell proliferation (BP)
14 genes	1176	34208		14	116	4,62423	0,0080307 GO:0007165: signal transduction (BP)
3 genes	23	34208		3	116	6,40348	0,0083405 GO:0002504: antigen processing and presentation of peptide or polysaccharide antigen via MHC class II (BP)
5 genes	136	34208		5	116	0,0001038	0,0108246 GO:0032496: response to lipopolysaccharide (BP)
4 genes	93	34208		4	116	0,0002904	0,0116398 GO:0006414: translational elongation (BP)
4 genes	82	34208		4	116	0,0001790	0,0116601 GO:0060333: interferon-gamma-mediated signaling pathway (BP)
4 genes	82	34208		4	116	0,0001790	0,0116601 GO:0019083: viral transcription (BP)
4 genes	92	34208		4	116	0,0002786	0,0120989 GO:0045471: response to ethanol (BP)
2 genes	7	34208		2	116	0,0002367	0,0123351 GO:0019886: antigen processing and presentation of exogenous peptide antigen via MHC class II (BP)

KEGG pathways

all signature genes

Genes	NGR	TNGR	NG	TNG	Hyp	Hyp*	Annotations
11 genes	68	34208		11	341	7,6E-06	0,001102 (KEGG) 00980: Metabolism of xenobiotics by cytochrome P450
9 genes	70	34208		9	341	0,003334	0,024172 (KEGG) 00982: Drug metabolism - cytochrome P450
7 genes	61	34208		7	341	0,252841	0,0001222 (KEGG) 00830: Retinol metabolism
6 genes	52	34208		6	341	1,29913	0,0004709 (KEGG) 00140: Steroid hormone biosynthesis
4 genes	26	34208		4	341	0,0001219	0,0035366 (KEGG) 00053: Ascorbate and aldarate metabolism
6 genes	84	34208		6	341	0,0001985	0,0035992 (KEGG) 05323: Rheumatoid arthritis
5 genes	51	34208		5	341	0,0001541	0,0037253 (KEGG) 04978: Mineral absorption
4 genes	29	34208		4	341	0,0001892	0,0039198 (KEGG) 00591: Linoleic acid metabolism
7 genes	125	34208		7	341	0,0002683	0,0043236 (KEGG) 04514: Cell adhesion molecules (CAMs)
8 genes	172	34208		8	341	0,0003515	0,0050971 (KEGG) 05152: Tuberculosis

downregulated signature genes

Genes	NGR	TNGR	NG	TNG	Hyp	Hyp*	Annotations
9 genes	68	34208		9	225	6,91E-05	0,000705 (KEGG) 00980: Metabolism of xenobiotics by cytochrome P450
7 genes	70	34208		7	225	0,040902	2,08599 (KEGG) 00982: Drug metabolism - cytochrome P450
4 genes	29	34208		4	225	3,80365	0,0012932 (KEGG) 00591: Linoleic acid metabolism
5 genes	61	34208		5	225	5,19025	0,0013235 (KEGG) 00830: Retinol metabolism
3 genes	23	34208		3	225	0,0004511	0,0076700 (KEGG) 00910: Nitrogen metabolism
4 genes	52	34208		4	225	0,0003851	0,0078574 (KEGG) 00140: Steroid hormone biosynthesis
4 genes	62	34208		4	225	0,0007539	0,0109867 (KEGG) 00010: Glycolysis / Gluconeogenesis
4 genes	70	34208		4	225	0,0011895	0,0151669 (KEGG) 03320: PPAR signaling pathway
3 genes	39	34208		3	225	0,0021548	0,0244212 (KEGG) 00620: Pyruvate metabolism
3 genes	53	34208		3	225	0,0051633	0,0438887 (KEGG) 00590: Arachidonic acid metabolism

upregulated signature genes

Genes	NGR	TNGR	NG	TNG	Hyp	Hyp*	Annotations
6 genes	172	34208		6	116	2,78101	0,0026697 (KEGG) 05152: Tuberculosis
4 genes	66	34208		4	116	7,69183	0,0036920 (KEGG) 05140: Leishmaniasis
4 genes	86	34208		4	116	0,0002151	0,0041303 (KEGG) 03010: Ribosome
3 genes	34	34208		3	116	0,0002105	0,0050534 (KEGG) 04940: Type I diabetes mellitus
3 genes	46	34208		3	116	0,0005185	0,0055313 (KEGG) 05150: Staphylococcus aureus infection
4 genes	102	34208		4	116	0,0004129	0,0056631 (KEGG) 05142: Chagas disease (American trypanosomiasis)
3 genes	45	34208		3	116	0,0004859	0,0058312 (KEGG) 00514: Other types of O-glycan biosynthesis
4 genes	113	34208		4	116	0,0006080	0,0058371 (KEGG) 04670: Leukocyte transendothelial migration
4 genes	84	34208		4	116	0,0001964	0,0062875 (KEGG) 05323: Rheumatoid arthritis
4 genes	101	34208		4	116	0,0003977	0,0063644 (KEGG) 04620: Toll-like receptor signaling pathway

NGR = Number of annotated genes in the reference list;

TNGR = Total number of genes in the reference list;

NG = Number of annotated genes in the input list;

TNG = Total number of genes in the input list;

Hyp = Hypergeometric pValue; Hyp* = Corrected hypergeometric pValue

Tabas-Madrid D, Nogales-Cadenas R, Pascual-Montano A: GeneCodis3: a non-redundant and modular enrichment analysis tool for functional genomics.

Nucleic Acids Research 2012; doi: 10.1093/nar/gks402

Nogales-Cadenas R, Carmona-Saez P, Vazquez M, Vicente C, Yang X, Tirado F, Carazo JM, Pascual-Montano A:

GeneCodis: interpreting gene lists through enrichment analysis and integration of diverse biological information. Nucleic Acids Research 2009; doi: 10.1093/nar/gkp416

Carmona-Saez P, Chagoyen M, Tirado F, Carazo JM, Pascual-Montano A: GENECODIS: A web-based tool for finding significant concurrent annotations in gene lists.

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