

Table 4

The 10 most strongly enriched pathways in the set of genes common among all four groups described in table 3, as well as in the individual gene sets of each group.

Top ten pathways among Common Genes

pathway	<i>p</i> -value	overlap	all pathway genes
REACTOME_GENE_EXPRESSION	1.22E-35	235	425
REACTOME_DIABETES_PATHWAYS	1.91E-33	214	383
REACTOME_METABOLISM_OF_PROTEINS	9.48E-28	134	215
REACTOME_CELL_CYCLE_MITOTIC	7.34E-25	167	306
REACTOME_GLUCOSE_REGULATION_OF_INSULIN_SECRETION	1.24E-23	104	161
KEGG_HUNTINGTONS_DISEASE	3.16E-23	114	185
REACTOME_INTEGRATION_OF_ENERGY_METABOLISM	1.09E-21	130	229
REACTOME_ELECTRON_TRANSPORT_CHAIN	1.11E-21	60	75
REACTOME_RNA_POLYMERASE_I_III_AND_MITOCHONDRIAL_TRANSCRIPTION	2.72E-21	82	120
REACTOME_INFLUENZA_LIFE_CYCLE	1.11E-20	89	137

Top ten pathways among Group 1 Genes

pathway	<i>p</i> -value	overlap	all pathway genes
REACTOME_INORGANIC_CATION_ANION_SLC_TRANSPORTERS	0.00133586	7	94
KEGG_SMALL_CELL_LUNG_CANCER	0.00359651	6	84
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	0.00723812	6	97
KEGG_MATURITY_ONSET_DIABETES_OF_THE_YOUNG	0.00921957	3	25
REACTOME_AMINO_ACID_AND_OLIGOPEPTIDE_SLC_TRANSPORTERS	0.00984371	4	48
REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT	0.01009928	8	169
KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	0.01020969	5	75
KEGG_GLYCOBIPHENOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLACTO_SERIES	0.0102227	2	26

REGG_GETTINGLIPID_BIOSYNTHESIS_FACTO_AND_NEOFACTO_SERIES	0.0102007	3	20
REACTOME_NUCLEAR_RECEPTOR_TRANSCRIPTION_PATHWAY	0.01133769	4	50
REACTOME_CDC6_ASSOCIATION_WITH_THE_ORC:ORIGIN_COMPLEX	0.01516009	2	11

Top ten pathways among Group II Genes

pathway	p-value	overlap	all pathway genes
REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA_CELLS	0.00552	5	101
REACTOME_HDL_MEDIATED_LIPID_TRANSPORT	0.00637	2	11
REACTOME_GTP_HYDROLYSIS_AND_JOINING_OF_THE_60S_RIBOSOMAL_SUBUNIT	0.00675	5	106
REACTOME_FACILITATIVE_NA_INDEPENDENT_GLUCOSE_TRANSPORTERS	0.00759	2	12
REACTOME_REGULATION_OF_BETA_CELLDEVELOPMENT	0.00911	5	114
REACTOME_TRANSLATION	0.01121	5	120
REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECULES	0.01148	7	218
REACTOME_IRS_RELATED_EVENTS	0.01182	4	79
REACTOME_INFLUENZA_LIFE_CYCLE	0.01889	5	137
REACTOME_DEADENYLATION_OF_MRNA	0.02469	2	22

Top ten pathways among Group III Genes

pathway	p-value	overlap	all pathway genes
REACTOME_DOWN_STREAM_SIGNAL_TRANSDUCTION	0.00302075	5	35
REACTOME_GAB1_SIGNALOSOME	0.00324484	3	11
REACTOME_SIGNALING_IN_IMMUNE_SYSTEM	0.00470548	20	366
REACTOME_MITOTIC_PROMETAPHASE	0.00489389	8	92
REACTOME_INNATE_IMMUNITY_SIGNALING	0.00584887	10	136
REACTOME_SIGNALLING_TO_RAS	0.0060289	4	26
REACTOME_FORMATION_OF_PLATELET_PLUG	0.00753191	12	186

REACTOME_GRB2_SOS_PROVIDES_LINKAGE_TO_MAPK_SIGNALING_FOR_INTERGRINS	0.00821656	3	15
REACTOME_MYOGENESSIS	0.00895252	4	29
REACTOME_HEMOSTASIS	0.01301061	15	274

Top ten pathways among Group IV Genes

pathway	p-value	overlap	all pathway genes
REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	0.00059	12	173
REACTOME_GAP_JUNCTION_ASSEMBLY	0.00076	4	19
KEGG_CHEMOKINE_SIGNALING_PATHWAY	0.00133	12	190
REACTOME_GAP_JUNCTION_TRAFFICKING	0.00340	4	28
REACTOME_CHEMOKINE_RECEPTORS_BIND_CHEMOKINES	0.00787	5	55
REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS	0.00936	4	37
REACTOME_SIGNALING_IN_IMMUNE_SYSTEM	0.00943	16	366
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	0.01126	7	108
REACTOME_CELL_CYCLE_CHECKPOINTS	0.01237	7	110
KEGG_NATURAL_KILLER_CELL_MEDIATED_CYTOTOXICITY	0.01263	8	137

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