

Male_Pos			
pathway	pval	padj	NES
GO_IMMUNOGLOBULIN_RECEPTOR_BINDING	2,17882E-06	0,00	2,32
REACTOME_OLFACTORY_SIGNALING_PATHWAY	3,11867E-06	0,00	1,96
chr22q11	2,91718E-06	0,00	1,88
KEGG_OLFACTORY_TRANSDUCTION	3,28815E-06	0,00	1,87
GO_OLFACTORY_RECEPTOR_ACTIVITY	3,34557E-06	0,00	1,99
GO_SENSORY_PERCEPTION_OF_CHEMICAL_STIMULUS	3,56356E-06	0,00	1,83
HALLMARK_HEME_METABOLISM	1,95937E-05	0,00	1,71
GO_ODORANT_BINDING	0,000151436	0,00	1,83
GO_AMIDE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0,000270048	0,01	2,03
GO_HUMORAL_IMMUNE_RESPONSE_MEDIATED_BY_CIRCULATING_IMMUNOGLOBULIN	0,000555136	0,01	1,84
GO_PROTEIN_ACTIVATION_CASCADE	0,000642848	0,01	1,75
GO_COMPLEMENT_ACTIVATION	0,001353477	0,02	1,74
GO_PHAGOCYTOSIS_ENGULFMENT	0,001518111	0,02	1,86
GO_PHAGOCYTOSIS_RECOGNITION	0,002333313	0,03	1,84
chr7q32	0,003338432	0,05	1,72
GO_UBIQUITIN_LIKE_PROTEIN_CONJUGATING_ENZYME_ACTIVITY	0,003625234	0,05	1,77
GO_RESPONSE_TO_MUSCLE_STRETCH	0,004634732	0,06	1,80
GO_CELLULAR_RESPONSE_TO_PROSTAGLANDIN_E_STIMULUS	0,004660445	0,06	1,81
GO_CARBOHYDRATE_TRANSMEMBRANE_TRANSPORT	0,006610624	0,08	1,73
GO_MEMBRANE_INVAGINATION	0,008134511	0,09	1,66
chr11q11	0,00942402	0,10	1,49
BIOCARTA_ARAP_PATHWAY	0,010040928	0,10	1,73
GO_LEUKOCYTE_APOPTOTIC_PROCESS	0,010021976	0,10	1,70
GO_ALCOHOL_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0,010236685	0,10	1,69
GO_T_CELL_APOPTOTIC_PROCESS	0,010596466	0,11	1,72
GO_CELLULAR_RESPONSE_TO_MECHANICAL_STIMULUS	0,010861203	0,11	1,52
GO_TRACHEA_DEVELOPMENT	0,013227112	0,12	1,67
chr1q44	0,015393836	0,14	1,48
GO_MESODERM_MORPHOGENESIS	0,015997903	0,14	1,50
REACTOME_FORMATION_OF_FIBRIN_CLOT_CLOTTING_CASCADE	0,017457791	0,15	1,59
GO_B_CELL_MEDIATED_IMMUNITY	0,020096929	0,16	1,44
GO_NEUTRAL_LIPID_CATABOLIC_PROCESS	0,021148684	0,17	1,59
GO_WATER_HOMEOSTASIS	0,021049276	0,17	1,46
chr6p23	0,021455099	0,17	1,62
BIOCARTA_RAS_PATHWAY	0,021410624	0,17	1,60
GO_RESPONSE_TO_PROSTAGLANDIN_E	0,022406467	0,17	1,59
GO_NEGATIVE_REGULATION_OF_POTASSIUM_ION_TRANSPORT	0,025780961	0,19	1,54
REACTOME_ACTIVATION_OF_BH3_ONLY_PROTEINS	0,026624625	0,19	1,60
GO_LYMPHOCYTE_APOPTOTIC_PROCESS	0,026779884	0,19	1,59
GO_HUMORAL_IMMUNE_RESPONSE	0,026714338	0,19	1,32
GO_T_CELL_LINEAGE_COMMITMENT	0,028720916	0,20	1,59
GO_REGULATION_OF_STEROL_TRANSPORT	0,02926375	0,20	1,50
GO_WATER_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	0,02974085	0,21	1,59
GO_NUCLEUS_LOCALIZATION	0,029709247	0,21	1,58
REACTOME_RNA_POL_I_PROMOTER_OPENING	0,030635571	0,21	1,46
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	0,032088888	0,22	1,26
GO_TRIGLYCERIDE_CATABOLIC_PROCESS	0,033183578	0,22	1,54
GO_CHROMATIN_DISASSEMBLY	0,033250486	0,22	1,56
BIOCARTA_CCR3_PATHWAY	0,033612663	0,22	1,53

Male_Neg			
pathway	pval	padj	NES
HALLMARK_MYC_TARGETS_V1	1,56439E-06	0,00	-2,49
GO_TRANSLATIONAL_TERMINATION	1,66967E-06	0,00	-2,34
REACTOME_MRNA_SPLICING	1,65743E-06	0,00	-2,30
REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_MRNA	1,62196E-06	0,00	-2,30
GO_MITOCHONDRIAL_TRANSLATION	1,65149E-06	0,00	-2,27
GO_NUCLEAR_EXPORT	1,61547E-06	0,00	-2,26
GO_RNA_SPLICING_VIA_TRANSESTERIFICATION_REACTIONS	1,5167E-06	0,00	-2,25
GO_RIBONUCLEOPROTEIN_COMPLEX_LOCALIZATION	1,64735E-06	0,00	-2,24
KEGG_SPLICEOSOME	1,63082E-06	0,00	-2,24
GO_RIBONUCLEOPROTEIN_COMPLEX_BIOGENESIS	1,4358E-06	0,00	-2,21
REACTOME_MRNA_PROCESSING	1,60107E-06	0,00	-2,20
HALLMARK_MTORC1_SIGNALING	1,55481E-06	0,00	-2,19
GO_TERMINATION_OF_RNA_POLYMERASE_II_TRANSCRIPTION	1,73051E-06	0,00	-2,19
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION	1,76056E-06	0,00	-2,17
GO_RNA_LOCALIZATION	1,58345E-06	0,00	-2,17
GO_HELICASE_ACTIVITY	1,6037E-06	0,00	-2,17
HALLMARK_OXIDATIVE_PHOSPHORYLATION	1,5574E-06	0,00	-2,17
GO_REGULATION_OF_TRANSLATIONAL_INITIATION	1,70209E-06	0,00	-2,15
GO_RNA_3_END_PROCESSING	1,67451E-06	0,00	-2,14
REACTOME_SIGNALING_BY_WNT	1,72093E-06	0,00	-2,14
GO_CELLULAR_PROTEIN_COMPLEX_DISASSEMBLY	1,62994E-06	0,00	-2,14
GO_NUCLEIC_ACID_PHOSPHODIESTER_BOND_HYDROLYSIS	1,53968E-06	0,00	-2,13
REACTOME_METABOLISM_OF_RNA	1,51356E-06	0,00	-2,13
GO_RNA_SPLICING	1,46531E-06	0,00	-2,11
GO_NCRNA_PROCESSING	1,45872E-06	0,00	-2,11
GO_POSITIVE_REGULATION_OF_LIGASE_ACTIVITY	1,64614E-06	0,00	-2,11
GO_RIBOSOME_BIOGENESIS	1,49994E-06	0,00	-2,09
REACTOME_GENERIC_TRANSCRIPTION_PATHWAY	1,46237E-06	0,00	-2,07
GO_RNA_CATABOLIC_PROCESS	1,56189E-06	0,00	-2,05
GO_REGULATION_OF_LIGASE_ACTIVITY	1,62107E-06	0,00	-2,05
REACTOME_MITOTIC_M_M_G1_PHASES	1,5858E-06	0,00	-2,04
REACTOME_METABOLISM_OF_MRNA	1,54732E-06	0,00	-2,04
GO_NUCLEOBASE_CONTAINING_COMPOUND_TRANSPORT	1,57085E-06	0,00	-2,03
REACTOME_METABOLISM_OF_PROTEINS	1,42146E-06	0,00	-2,00
GO_RIBONUCLEOPROTEIN_COMPLEX_SUBUNIT_ORGANIZATION	1,5729E-06	0,00	-1,99
GO_PROTEIN_FOLDING	1,54732E-06	0,00	-1,99
REACTOME_DNA_REPLICATION	1,56678E-06	0,00	-1,97
GO_POSTTRANSCRIPTIONAL_REGULATION_OF_GENE_EXPRESSION	1,43003E-06	0,00	-1,95
GO_MRNA_PROCESSING	1,43703E-06	0,00	-1,95
GO_REGULATION_OF_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CONJUGATION_OR_REMOVAL	1,50412E-06	0,00	-1,94
REACTOME_CELL_CYCLE_MITOTIC	1,47705E-06	0,00	-1,91
GO_NCRNA_METABOLIC_PROCESS	1,39947E-06	0,00	-1,91
GO_TRNA_METABOLIC_PROCESS	1,58448E-06	0,00	-1,91
GO_ORGANIC_CYCLIC_COMPOUND_CATABOLIC_PROCESS	1,44036E-06	0,00	-1,91
GO_POSITIVE_REGULATION_OF_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CONJUGATION_OR_REMOVAL	1,56321E-06	0,00	-1,90
GO_REGULATION_OF_CELLULAR_AMIDE_METABOLIC_PROCESS	1,47567E-06	0,00	-1,89
GO_MACROMOLECULAR_COMPLEX_DISASSEMBLY	1,5718E-06	0,00	-1,89
GO_RRNA_METABOLIC_PROCESS	1,53369E-06	0,00	-1,89
REACTOME_HIV_INFECTION	1,56189E-06	0,00	-1,89

Female_Pos			
pathway	pval	padj	NES
REACTOME_PEPTIDE_CHAIN_ELONGATION	1,58E-06	0,00	2,79
REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION	1,56E-06	0,00	2,70
REACTOME_INFLUENZA_VIRAL_RNA_TRANSCRIPTION_AND_REPLICATION	1,56E-06	0,00	2,69
KEGG_RIBOSOME	1,62E-06	0,00	2,60
REACTOME_SRP_DEPENDENT_COTRANSLATIONAL_PROTEIN_TARGETING_TO_MEMBRANE	1,55E-06	0,00	2,57
REACTOME_NONSENSE_MEDIATED_DECAY_ENHANCED_BY_THE_EXON_JUNCTION_COMPLEX	1,56E-06	0,00	2,53
REACTOME_INFLUENZA_LIFE_CYCLE	1,52E-06	0,00	2,44
REACTOME_TRANSLATION	1,51E-06	0,00	2,41
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	1,59E-06	0,00	2,39
GO_TRANSLATIONAL_INITIATION	1,54E-06	0,00	2,26
GO_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	1,47E-06	0,00	2,24
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	1,57E-06	0,00	2,21
REACTOME_ACTIVATION_OF_THE_MRNA_UPON_BINDING_OF_THE_CAP_BINDING_COMPLEX_AND_EIFS_AND_SUBSEQUENT_BINDING_TO_43S	1,65E-06	0,00	2,20
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_BY_UNCOUPLING_PROTEINS_	1,59E-06	0,00	2,20
REACTOME_FORMATION_OF_THE_TERNARY_COMPLEX_AND_SUBSEQUENTLY_THE_43S_COMPLEX	3,32E-06	0,00	2,19
GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	1,57E-06	0,00	2,16
GO_MULTI_ORGANISM_METABOLIC_PROCESS	1,55E-06	0,00	2,14
KEGG_OXIDATIVE_PHOSPHORYLATION	1,54E-06	0,00	2,04
KEGG_PARKINSONS_DISEASE	1,54E-06	0,00	1,98
REACTOME_METABOLISM_OF_MRNA	1,45E-06	0,00	1,95
REACTOME_METABOLISM_OF_RNA	1,42E-06	0,00	1,94
REACTOME_METABOLISM_OF_PROTEINS	2,65E-06	0,00	1,66
GO_PROTEIN_TARGETING_TO_MEMBRANE	4,56E-06	0,00	1,92
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	4,84E-06	0,00	2,07
GO_OXIDATIVE_PHOSPHORYLATION	8,01E-06	0,00	2,03
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H_QUINONE_OR_SIMILAR_COMPOUND_AS_ACCEPTOR	1,66E-05	0,00	2,08
GO_HYDROGEN_ION_TRANSMEMBRANE_TRANSPORT	1,72E-05	0,00	1,90
chr21q21	3,41E-05	0,00	2,07
REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_TRANSPORT	4,92E-05	0,00	1,83
GO_ELECTRON_TRANSPORT_CHAIN	5,08E-05	0,00	1,92
GO_CYTOPLASMIC_TRANSLATION	5,25E-05	0,00	2,04
GO_HYDROGEN_TRANSPORT	6,41E-05	0,00	1,80
GO_AMIDE_BIOSYNTHETIC_PROCESS	0,00015819	0,01	1,49
GO_RNA_CATABOLIC_PROCESS	0,00016564	0,01	1,67
GO_ORGANIC_CYCLIC_COMPOUND_CATABOLIC_PROCESS	0,00044558	0,01	1,48
KEGG_HUNTINGTONS_DISEASE	0,00048172	0,01	1,63
GO_CXCR_CHEMOKINE_RECEPTOR_BINDING	0,00052677	0,01	1,93
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MIGRATION	0,00053367	0,01	1,71
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_HEME_GROUP_OF_DONORS	0,00058662	0,01	1,91
GO_RRNA_METABOLIC_PROCESS	0,00060965	0,02	1,56
GO_HEPARIN_BINDING	0,00094291	0,02	1,61
GO_VIRAL_LIFE_CYCLE	0,00094396	0,02	1,52
GO_OXYGEN_BINDING	0,00109407	0,02	1,81
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_MEMBRANE	0,00113097	0,02	1,52
GO_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_ACTIVITY	0,00116237	0,02	1,83
GO_RIBOSOMAL_LARGE_SUBUNIT_BIOGENESIS	0,00115931	0,02	1,81
KEGG_ALZHEIMERS_DISEASE	0,00196055	0,03	1,56
REACTOME_POST_CHAPERONIN_TUBULIN_FOLDING_PATHWAY	0,00233481	0,04	1,83
chr14q22	0,0023447	0,04	1,72

Female_Neg			
pathway	pval	padj	NES
GO_COMPLEMENT_ACTIVATION	2,58E-06	0,00	-2,62
GO_B_CELL_MEDIATED_IMMUNITY	2,69E-06	0,00	-2,50
GO_HUMORAL_IMMUNE_RESPONSE_MEDIATED_BY_CIRCULATING_IMMUNOGLOBULIN	2,54E-06	0,00	-2,46
GO_PROTEIN_ACTIVATION_CASCADE	2,70E-06	0,00	-2,46
GO_ANTIGEN_BINDING	2,73E-06	0,00	-2,44
chr2p11	2,91E-06	0,00	-2,39
GO_REGULATION_OF_TELOMERE_MAINTENANCE	2,56E-06	0,00	-2,26
GO_ADAPTIVE_IMMUNE_RESPONSE_BASED_ON_SOMATIC_RECOMBINATION_OF_IMMUNE_RECEPTORS_BUILT_FROM_IMMUNE_RECEPTOR_GENE	2,94E-06	0,00	-2,24
GO_PURINE_NTP_DEPENDENT_HELICASE_ACTIVITY	2,73E-06	0,00	-2,21
GO_FC_GAMMA_RECEPTOR_SIGNALING_PATHWAY	2,69E-06	0,00	-2,20
GO_HELICASE_ACTIVITY	2,95E-06	0,00	-2,16
GO_LYMPHOCYTE_MEDIATED_IMMUNITY	2,90E-06	0,00	-2,10
chr14q11	3,27E-06	0,00	-2,08
GO_ACTIVATION_OF_IMMUNE_RESPONSE	4,02E-06	0,00	-2,06
GO_COVALENT_CHROMATIN_MODIFICATION	3,67E-06	0,00	-2,00
GO_PHAGOCYTOSIS	3,09E-06	0,00	-1,98
GO_POSITIVE_REGULATION_OF_CHROMOSOME_ORGANIZATION	2,93E-06	0,00	-1,97
GO_LEUKOCYTE_MEDIATED_IMMUNITY	3,08E-06	0,00	-1,96
GO_REGULATION_OF_CHROMOSOME_ORGANIZATION	3,44E-06	0,00	-1,96
GO_TRANSCRIPTIONAL_REPRESSOR_ACTIVITY_RNA_POLYMERASE_II_TRANSCRIPTION_REGULATORY_REGION_SEQUENCE_SPECIFIC	3,04E-06	0,00	-1,94
chr14q32	3,49E-06	0,00	-1,90
GO_IMMUNE_RESPONSE_REGULATING_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY	3,60E-06	0,00	-1,89
GO_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	3,12E-06	0,00	-1,88
GO_CHROMATIN_BINDING	4,04E-06	0,00	-1,87
GO_ADAPTIVE_IMMUNE_RESPONSE	3,46E-06	0,00	-1,86
GO_ATPASE_ACTIVITY_COUPLED	3,61E-06	0,00	-1,81
GO_POSITIVE_REGULATION_OF_CELL_ACTIVATION	3,58E-06	0,00	-1,74
GO_REGULATION_OF_CELLULAR_PROTEIN_CATABOLIC_PROCESS	3,44E-06	0,00	-1,74
GO_REGULATION_OF_DNA_METABOLIC_PROCESS	3,68E-06	0,00	-1,73
GO_LYMPHOCYTE_ACTIVATION	3,73E-06	0,00	-1,73
GO_REGULATION_OF_INNATE_IMMUNE_RESPONSE	3,80E-06	0,00	-1,71
GO_ATPASE_ACTIVITY	4,06E-06	0,00	-1,70
GO_LIGASE_ACTIVITY	3,96E-06	0,00	-1,70
GO_LEUKOCYTE_ACTIVATION	4,02E-06	0,00	-1,70
GO_REGULATION_OF_PROTEIN_CATABOLIC_PROCESS	3,90E-06	0,00	-1,68
GO_ORGANELLE_LOCALIZATION	3,97E-06	0,00	-1,66
GO_POSITIVE_REGULATION_OF_CATABOLIC_PROCESS	3,94E-06	0,00	-1,65
GO_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	4,05E-06	0,00	-1,60
GO_ENDOCYTOSIS	4,34E-06	0,00	-1,77
GO_IMMUNE_EFFECTOR_PROCESS	4,25E-06	0,00	-1,71
GO_REGULATION_OF_CELL_ACTIVATION	4,28E-06	0,00	-1,61
GO_CHROMATIN_MODIFICATION	4,44E-06	0,00	-1,76
GO_B_CELL_RECEPTOR_SIGNALING_PATHWAY	4,97E-06	0,00	-2,31
GO_TRANSCRIPTIONAL_REPRESSOR_ACTIVITY_RNA_POLYMERASE_II_CORE_PROMOTER_PROXIMAL_REGION_SEQUENCE_SPECIFIC	5,54E-06	0,00	-2,11
GO_CORE_PROMOTER_BINDING	5,91E-06	0,00	-1,92
GO_POSITIVE_REGULATION_OF_TELOMERE_MAINTENANCE	7,38E-06	0,00	-2,29
GO_RNA_HELICASE_ACTIVITY	7,77E-06	0,00	-2,14
GO_RECEPTOR_MEDIATED_ENDOCYTOSIS	9,77E-06	0,00	-1,78
GO_REGULATION_OF_INFLAMMATORY_RESPONSE	1,05E-05	0,00	-1,66

Supplementary table 1

Top down- or up-regulated Gene ontology gene sets from female and male samples. Male_pos are the most upregulated gene sets in men. Male_neg are the most downregulated gene sets in men. Female_pos are the most upregulated gene sets in women. Female_neg are the most downregulated gene sets in women.