

## List of gene sets significantly enriched among CMH-upregulated genes (based on definition A)

Databases: Kegg, Biocarta, GO biological processes, GO molecular functions

NAME	NES	NOM p-val	FDR q-val
GO_CILIUM_ORGANIZATION	3.80065	0	0
GO_CILIUM_MORPHOGENESIS	3.716047	0	0
GO_CILIUM_MOVEMENT	3.234982	0	0
GO_CELLULAR_COMPONENT_ASSEMBLY_INVOLVED_IN_MORPHOGENESIS	3.163264	0	0
GO_AXONEME_ASSEMBLY	3.116444	0	0
GO_CELL_PROJECTION_ASSEMBLY	2.965269	0	0
GO_ORGANELLE_ASSEMBLY	2.922216	0	0
GO_PROTEIN_TRANSPORT_ALONG_MICROTUBULE	2.922027	0	0
GO_INTRACILIARY_TRANSPORT	2.902845	0	0
GO_AXONEMAL_DYNEIN_COMPLEX_ASSEMBLY	2.902678	0	0
GO_MICROTUBULE_BUNDLE_FORMATION	2.862911	0	0
KEGG_PROTEASOME	2.761147	0	0
GO_NCRNA_TRANSCRIPTION	2.530663	0	3.13E-05
GO_RNA_SPLICING	2.53542	0	3.23E-05
GO_MICROTUBULE_BASED_PROCESS	2.543671	0	3.33E-05
GO_RNA_LOCALIZATION	2.543767	0	3.44E-05
GO_TRANSCRIPTION_COUPLED_NUCLEOTIDE_EXCISION_REPAIR	2.544786	0	3.56E-05
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	2.552915	0	3.69E-05
GO_ANAPHASE_PROMOTING_COMPLEX_DEPENDENT_CATABOLIC_PROCESS	2.56189	0	3.83E-05
GO_MRNA_PROCESSING	2.569639	0	3.97E-05
GO_CYSTEINE_TYPE_PEPTIDASE_ACTIVITY	2.571137	0	4.13E-05
GO_THIOL_DEPENDENT_UBIQUITIN_SPECIFIC_PROTEASE_ACTIVITY	2.5728	0	4.30E-05
GO_PROTEIN_COMPLEX_LOCALIZATION	2.586215	0	4.49E-05
KEGG_RNA_DEGRADATION	2.589887	0	4.69E-05
GO_POSITIVE_REGULATION_OF_LIGASE_ACTIVITY	2.600568	0	4.92E-05
GO_REGULATION_OF_LIGASE_ACTIVITY	2.455815	0	5.08E-05
GO_PROTEIN_POLYUBIQUITINATION	2.604567	0	5.16E-05
GO_RNA_PHOSPHODIESTER_BOND_HYDROLYSIS_EXONUCLEOLYTIC	2.457357	0	5.20E-05
GO_MICROTUBULE_CYTOSKELETON_ORGANIZATION	2.457578	0	5.34E-05
GO_MICROTUBULE_BASED_MOVEMENT	2.608739	0	5.44E-05
GO_NUCLEAR_EXPORT	2.472638	0	5.48E-05
GO_RIBONUCLEOPROTEIN_COMPLEX_SUBUNIT_ORGANIZATION	2.477872	0	5.63E-05
GO_RNA_SPLICING_VIA_TRANSESTERIFICATION_REACTIONS	2.613953	0	5.74E-05
GO_MULTIVESICULAR_BODY_ORGANIZATION	2.492811	0	5.78E-05
GO_LIGASE_ACTIVITY	2.516707	0	5.95E-05
GO_RIBONUCLEOPROTEIN_COMPLEX_BIOGENESIS	2.620134	0	6.08E-05
GO_REGULATION_OF_CENTROSOME_DUPLICATION	2.524993	0	6.12E-05

GO_NONMOTILE_PRIMARY_CILIUM_ASSEMBLY	2.630551	0	6.45E-05
GO_UBIQUITIN_LIKE_PROTEIN_SPECIFIC_PROTEASE_ACTIVITY	2.642457	0	6.89E-05
GO_REGULATION_OF_CELLULAR_RESPONSE_TO_HEAT	2.443078	0	6.99E-05
GO_EPITHELIAL_CILIUM_MOVEMENT	2.447186	0	7.16E-05
GO_PROTEASOMAL_PROTEIN_CATABOLIC_PROCESS	2.451657	0	7.33E-05
BIOCARTA_PROTEASOME_PATHWAY	2.693849	0	7.38E-05
GO_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_REMOVAL	2.708386	0	7.94E-05
GO_NUCLEOCYTOPLASMIC_TRANSPORTER_ACTIVITY	2.430321	0	9.16E-05
GO_NCRNA_METABOLIC_PROCESS	2.418559	0	1.09E-04
GO_RIBONUCLEOPROTEIN_COMPLEX_LOCALIZATION	2.422681	0	1.11E-04
GO_DNA_REPAIR	2.397014	0	1.47E-04
GO_ENDOSOME_TO_LYSOSOME_TRANSPORT	2.398264	0	1.50E-04
KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS	2.380926	0	1.53E-04
GO_DNA_TEMPLATED_TRANSCRIPTION_TERMINATION	2.382359	0	1.56E-04
GO_POSITIVE_REGULATION_OF_TELOMERE_MAINTENANCE_VIA_TELOMERE_LENGTHENING	2.385475	0	1.59E-04
GO_REGULATION_OF_CENTROSOME_CYCLE	2.387777	0	1.62E-04
GO_PROTEIN_UBIQUITINATION_INVOLVED_IN_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS	2.388362	0	1.65E-04
GO_TRNA_TRANSPORT	2.377111	0	1.66E-04
GO_GDP_BINDING	2.377303	0	1.69E-04
GO_DNA_TEMPLATED_TRANSCRIPTION_ELONGATION	2.363932	0	1.78E-04
GO_REGULATION_OF_TELOMERE_MAINTENANCE	2.365428	0	1.81E-04
GO_EXONUCLEASE_ACTIVITY_ACTIVE_WITH_EITHER_RIBO_OR_DEOXYRIBONUCLEIC_ACIDS_AND_PRODUCING_5_PHOSPHOMONOESTERS	2.355031	0	1.89E-04
GO_UBIQUITIN_LIKE_PROTEIN_LIGASE_ACTIVITY	2.35571	0	1.92E-04
GO_TRNA_METABOLIC_PROCESS	2.346905	0	2.37E-04
GO_NUCLEOTIDE_EXCISION_REPAIR	2.344503	0	2.46E-04
GO_BASAL_TRANSCRIPTION_MACHINERY_BINDING	2.335392	0	2.46E-04
GO_MULTI_ORGANISM_TRANSPORT	2.337337	0	2.50E-04
GO_UBIQUITIN_LIKE_PROTEIN_BINDING	2.344837	0	2.50E-04
GO_EXORIBONUCLEASE_ACTIVITY	2.337556	0	2.54E-04
GO_ENDOSOME_ORGANIZATION	2.334043	0	2.58E-04
GO_THREONINE_TYPE_PEPTIDASE_ACTIVITY	2.341607	0	2.58E-04
GO_REGULATION_OF_ORGANELLE_ASSEMBLY	2.317524	0	2.94E-04
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I	2.318711	0	2.99E-04
GO_NCRNA_PROCESSING	2.290173	0	4.38E-04
GO_TRANSCRIPTION_FROM_RNA_POLYMERASE_III_PROMOTER	2.295359	0	4.44E-04
GO_LIGASE_ACTIVITY_FORMING_CARBON_NITROGEN_BONDS	2.295846	0	4.50E-04
GO_MULTI_ORGANISM_LOCALIZATION	2.281286	0	4.73E-04
KEGG_SPLICEOSOME	2.279663	0	4.81E-04
GO_POSITIVE_REGULATION_OF_TELOMERE_MAINTENANCE	2.266856	0	5.29E-04
GO_NLS_BEARING_PROTEIN_IMPORT_INTO_NUCLEUS	2.269684	0	5.30E-04
GO_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY	2.264687	0	5.35E-04
GO_REGULATION_OF_PROTEIN_UBIQUITINATION_INVOLVED_IN_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS	2.267378	0	5.36E-04

GO_NUCLEOTIDE_EXCISION_REPAIR_PREINCISION_COMPLEX_ASSEMBLY	2.260556	0	5.60E-04
GO_PROTEIN_LOCALIZATION_TO_CILIUM	2.259839	0	5.66E-04
GO_POSITIVE_REGULATION_OF_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CONJUGATION_OR_REMOVAL	2.261093	0	5.67E-04
GO_RNA_POLYMERASE_II_CORE_BINDING	2.256832	0	5.71E-04
GO_GPI_ANCHOR_METABOLIC_PROCESS	2.25532	0	6.13E-04
GO_TRANSCRIPTION_ELONGATION_FROM_RNA_POLYMERASE_II_PROMOTER	2.250078	0	6.79E-04
GO_SNRNA_METABOLIC_PROCESS	2.236979	0	7.49E-04
GO_SIGNAL_SEQUENCE_BINDING	2.242365	0	7.55E-04
GO_MRNA_CLEAVAGE	2.237301	0	7.58E-04
KEGG_RNA_POLYMERASE	2.234414	0	7.86E-04
GO_CYTOPLASMIC_MICROTUBULE_ORGANIZATION	2.229667	0	8.14E-04
GO_POST_GOLGI_VESICLE_MEDIATED_TRANSPORT	2.231024	0	8.23E-04
GO_TRANSLATION_INITIATION_FACTOR_ACTIVITY	2.228601	0	8.27E-04
GO_NUCLEAR_PORE_ORGANIZATION	2.226989	0	8.40E-04
GO_PROTEIN_LOCALIZATION_TO_CYTOSKELETON	2.222961	0	8.56E-04
GO_NUCLEAR_TRANSPORT	2.223043	0	8.65E-04
GO_NUCLEAR_ENVELOPE_ORGANIZATION	2.221268	0	8.70E-04
GO_POSTTRANSCRIPTIONAL_REGULATION_OF_GENE_EXPRESSION	2.221387	0	8.79E-04
GO_RNA_PHOSPHODIESTER_BOND_HYDROLYSIS	2.217704	0	8.95E-04
BIOCARTA_CDC42RAC_PATHWAY	2.218631	0	9.04E-04
GO_CELL_DIVISION	2.204946	0	0.001019179
GO_UBIQUITIN_LIKE_PROTEIN_TRANSFERASE_ACTIVITY	2.205904	0	0.001029171
GO_NUCLEUS_ORGANIZATION	2.2075	0	0.001029528
GO_PROTEIN_SUMOYLATION	2.207819	0	0.001039824
GO_REGULATION_OF_RNA_STABILITY	2.197219	0	0.001049283
GO_PROTEIN_LOCALIZATION_TO_CENTROSOME	2.197891	0	0.001049538
GO_NUCLEAR_IMPORT	2.198851	0	0.00105963
GO_NUCLEOBASE_CONTAINING_COMPOUND_TRANSPORT	2.193433	0	0.001126637
GO_HELICASE_ACTIVITY	2.191109	0	0.001153903
GO_PREASSEMBLY_OF_GPI_ANCHOR_IN_ER_MEMBRANE	2.187791	0	0.001177725
GO_REGULATION_OF_TELOMERE_MAINTENANCE_VIA_TELOMERE_LENGTHENING	2.18833	0	0.001179095
GO_CELL_CYCLE_G2_M_PHASE_TRANSITION	2.188855	0	0.001180898
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_DAMAGE_RECOGNITION	2.186847	0	0.001185944
GO_ESTABLISHMENT_OF_LOCALIZATION_BY_MOVEMENT_ALONG_MICROTUBULE	2.181576	0	0.001239547
GO_GOLGI_ORGANIZATION	2.180332	0	0.001273626
GO_POSTREPLICATION_REPAIR	2.177047	0	0.00129328
GO_RNA_CATABOLIC_PROCESS	2.177525	0	0.001304429
GO_MITOTIC_NUCLEAR_DIVISION	2.175021	0	0.001305978
GO_RIBOSOME_BIOGENESIS	2.175927	0	0.001308303
GO_REGULATION_OF_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CONJUGATION_OR_REMOVAL	2.178183	0	0.001315772
GO_POSITIVE_REGULATION_OF_CELLULAR_PROTEIN_CATABOLIC_PROCESS	2.170853	0	0.00138583
GO_NEGATIVE_REGULATION_OF_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CONJUGATION_OR_REMOVAL	2.171102	0	0.001388834

GO_RNA_CAPPING	2.163833	0	0.001456097
GO_RNA_POLYMERASE_III_ACTIVITY	2.165172	0	0.001459477
GO_RNA_POLYMERASE_CORE_ENZYME_BINDING	2.16162	0.002386635	0.001469182
GO_7_METHYLGUANOSINE_RNA_CAPPING	2.15116	0	0.00166955
GO_MITOCHONDRIAL_TRANSLATION	2.14965	0	0.001672959
GO_GLOBAL_GENOME_NUCLEOTIDE_EXCISION_REPAIR	2.148993	0	0.001675753
GO_MRNA_BINDING	2.148547	0	0.001678999
GO_FC_EPSILON_RECEPTOR_SIGNALING_PATHWAY	2.142	0	0.001804355
GO_EXONUCLEASE_ACTIVITY	2.143254	0	0.001808559
KEGG_BASAL_TRANSCRIPTION_FACTORS	2.142124	0	0.001818235
GO_CELLULAR_PROTEIN_COMPLEX_ASSEMBLY	2.139734	0	0.001821847
GO_REGULATION_OF_CHROMOSOME_SEGREGATION	2.138502	0	0.001823887
GO_PEPTIDYL_LYSINE_MODIFICATION	2.135335	0	0.001872082
GO_RRNA_METABOLIC_PROCESS	2.133801	0	0.001881295
GO_REGULATION_OF_CELLULAR_PROTEIN_CATABOLIC_PROCESS	2.129684	0	0.001935054
GO_REGULATION_OF_TRANSLATIONAL_INITIATION	2.126419	0	0.001966588
GO_PROTEIN_EXPORT_FROM_NUCLEUS	2.120131	0	0.002177942
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_CH_GROUP_OF_DONORS_NAD_OR_NADP_AS_ACCEPTOR	2.118121	0	0.002192004
GO_MULTI_ORGANISM_MEMBRANE_BUDDING	2.111513	0	0.002366943
GO_ACTIN_NUCLEATION	2.109234	0	0.002423629
GO_INNATE_IMMUNE_RESPONSE_ACTIVATING_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY	2.104032	0	0.00257233
GO_REGULATION_OF_SPINDLE_ORGANIZATION	2.100814	0	0.002655916
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_EXONUCLEOLYTIC	2.097056	0.002421308	0.002754136
GO_REGULATION_OF_SISTER_CHROMATID_COHESION	2.097572	0	0.002766242
GO_DNA_GEOMETRIC_CHANGE	2.094713	0	0.002798952
GO_MULTI_ORGANISM_ORGANELLE_ORGANIZATION	2.093369	0.002288329	0.002822134
GO_REGULATION_OF_TELOMERASE_RNA_LOCALIZATION_TO_CAJAL_BODY	2.090587	0	0.002914545
GO_NUCLEOTIDYLTRANSFERASE_ACTIVITY	2.089346	0	0.002915729
GO_RAN_GTPASE_BINDING	2.083351	0	0.003087527
GO_DAMAGED_DNA_BINDING	2.080593	0	0.003149295
GO_CELL_SEPARATION_AFTER_CYTOKINESIS	2.079632	0	0.003162176
GO_RNA_POLYADENYLATION	2.076454	0	0.003243079
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ORGANELLE	2.073881	0	0.003382922
GO_POSITIVE_REGULATION_OF_TELOMERASE_RNA_LOCALIZATION_TO_CAJAL_BODY	2.063795	0	0.003751751
GO_VACUOLAR_TRANSPORT	2.053152	0	0.004077421
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_DUPLEX_UNWINDING	2.051477	0	0.004116688
GO_FC_RECEPTOR_SIGNALING_PATHWAY	2.044436	0	0.004388112
KEGG_NUCLEOTIDE_EXCISION_REPAIR	2.043304	0	0.004397876
GO_INTRA_GOLGI_VESICLE_MEDIATED_TRANSPORT	2.041553	0	0.004399377
GO_REGULATION_OF_TELOMERE_CAPPING	2.044603	0	0.004409445
GO_NUCLEAR_LOCALIZATION_SEQUENCE_BINDING	2.041829	0	0.004413869
GO_TRNA_AMINOACYLATION	2.042616	0	0.004415465

GO_UBIQUITIN_LIKE_PROTEIN_LIGASE_BINDING	2.040527	0	0.00441661
GO_AEROBIC_RESPIRATION	2.043506	0	0.004418832
GO_REGULATION_OF_EXOSOMAL_SECRETION	2.038348	0.002192983	0.004450532
GO_ATPASE_ACTIVITY	2.039052	0	0.004458885
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_DEADENYLATION_DEPENDENT_DECAY	2.038142	0	0.00446079
GO_POSITIVE_REGULATION_OF_CHROMOSOME_ORGANIZATION	2.035747	0	0.004562443
GO_PROTEIN_TARGETING	2.030701	0	0.004681019
GO_SISTER_CHROMATID_SEGREGATION	2.02643	0	0.004802016
GO_GLUTATHIONE_DERIVATIVE_BIOSYNTHETIC_PROCESS	2.025566	0	0.004804031
GO_SPLICEOSOMAL_SNRNP_ASSEMBLY	2.027133	0	0.004811891
GO_PROTEIN_LOCALIZATION_TO_NUCLEUS	2.027428	0	0.004822127
GO_LYSOSOMAL_TRANSPORT	2.024744	0	0.004835687
GO_GLUTATHIONE_DERIVATIVE_METABOLIC_PROCESS	2.018585	0	0.005130293
GO_REGULATION_OF_MRNA_METABOLIC_PROCESS	2.015402	0	0.005256963
GO_VITAMIN_D_RECEPTOR_BINDING	2.013185	0.002352941	0.005324259
GO_MRNA_3_END_PROCESSING	2.013781	0	0.005325303
GO_CHROMOSOME_SEGREGATION	2.010806	0	0.005425776
GO_POSITIVE_REGULATION_OF_DNA_REPAIR	2.010808	0	0.005450068
GO_PORE_COMPLEX_ASSEMBLY	2.005998	0.002309469	0.005585594
GO_TBP_CLASS_PROTEIN_BINDING	2.00524	0.002304148	0.005594318
GO_CYTOSKELETON_DEPENDENT_CYTOKINESIS	2.004525	0	0.005603486
GO_MODULATION_BY_VIRUS_OF_HOST_MORPHOLOGY_OR_PHYSIOLOGY	2.006047	0.00257732	0.005616284
GO_TRNA_METHYLATION	2.000622	0.002427185	0.005811726
GO_REGULATION_OF_CELLULAR_AMIDE_METABOLIC_PROCESS	1.998937	0	0.00586873
GO_VIRAL_BUDDING	1.991583	0.002364066	0.005977449
GO_CYTOSKELETON_DEPENDENT_INTRACELLULAR_TRANSPORT	1.996337	0	0.005979083
GO_SPLICEOSOMAL_COMPLEX_ASSEMBLY	1.991708	0	0.006008103
GO_REGULATION_OF_CILIUM_ASSEMBLY	1.994417	0	0.006025642
GO_REGULATION_OF_SISTER_CHROMATID_SEGREGATION	1.993845	0	0.006031918
GO_AMINO_ACID_ACTIVATION	1.992045	0	0.006039072
KEGG_PEROXISOME	1.995065	0	0.006040672
GO_REGULATION_OF_INTRACELLULAR_ESTROGEN_RECEPTOR_SIGNALING_PATHWAY	1.994496	0	0.006052177
GO_RNA_SECONDARY_STRUCTURE_UNWINDING	1.989683	0	0.006062082
GO_TRANSLATIONAL_TERMINATION	1.992108	0	0.006070362
GO_MICROTUBULE_MOTOR_ACTIVITY	1.984118	0	0.006320398
GO_MITOCHONDRIAL_TRANSPORT	1.985134	0	0.006342388
GO_VACUOLE_ORGANIZATION	1.984283	0	0.006347037
GO_REGULATION_OF_CELLULAR_AMINO_ACID_METABOLIC_PROCESS	1.981582	0	0.006417877
GO_PROTEIN_IMPORT	1.97818	0	0.006531867
GO_3_5_EXONUCLEASE_ACTIVITY	1.978205	0.002450981	0.006564203
GO_POSITIVE_REGULATION_OF_HISTONE_H3_K4_METHYLATION	1.974726	0.00234192	0.006742995
GO_REGULATION_OF_MICROTUBULE_BASED_PROCESS	1.971852	0	0.006881181

GO_DOUBLE_STRAND_BREAK_REPAIR	1.970927	0	0.006922801
GO_REGULATION_OF_RESPONSE_TO_DNA_DAMAGE_STIMULUS	1.970017	0	0.00693973
GO_ATPASE_ACTIVITY_COUPLED	1.969025	0	0.006965593
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H_QUINONE_OR_SIMILAR_COMPOUND_AS_ACCEPTOR	1.967072	0	0.007074927
GO_TRANSCRIPTION_FROM_RNA_POLYMERASE_I_PROMOTER	1.963294	0	0.00732527
GO_NUCLEAR_ENVELOPE_DISASSEMBLY	1.958186	0	0.007647388
GO_LIGASE_ACTIVITY_FORMING_CARBON_OXYGEN_BONDS	1.949941	0.002512563	0.008265242
GO_PROTEIN_K48_LINKED_UBIQUITINATION	1.942777	0	0.008885002
GO_MEMBRANE_DISASSEMBLY	1.940524	0	0.009063603
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_INCISION_3_TO_LESION	1.93743	0	0.009313379
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_VACUOLE	1.935876	0	0.009413272
GO_MRNA_3_UTR_BINDING	1.935042	0	0.009416682
GO_TRNA_PROCESSING	1.935435	0	0.009421908
GO_TRNA_METHYLTRANSFERASE_ACTIVITY	1.934207	0	0.009424865
GO_PROTEIN_TRANSPORTER_ACTIVITY	1.934512	0	0.00944424