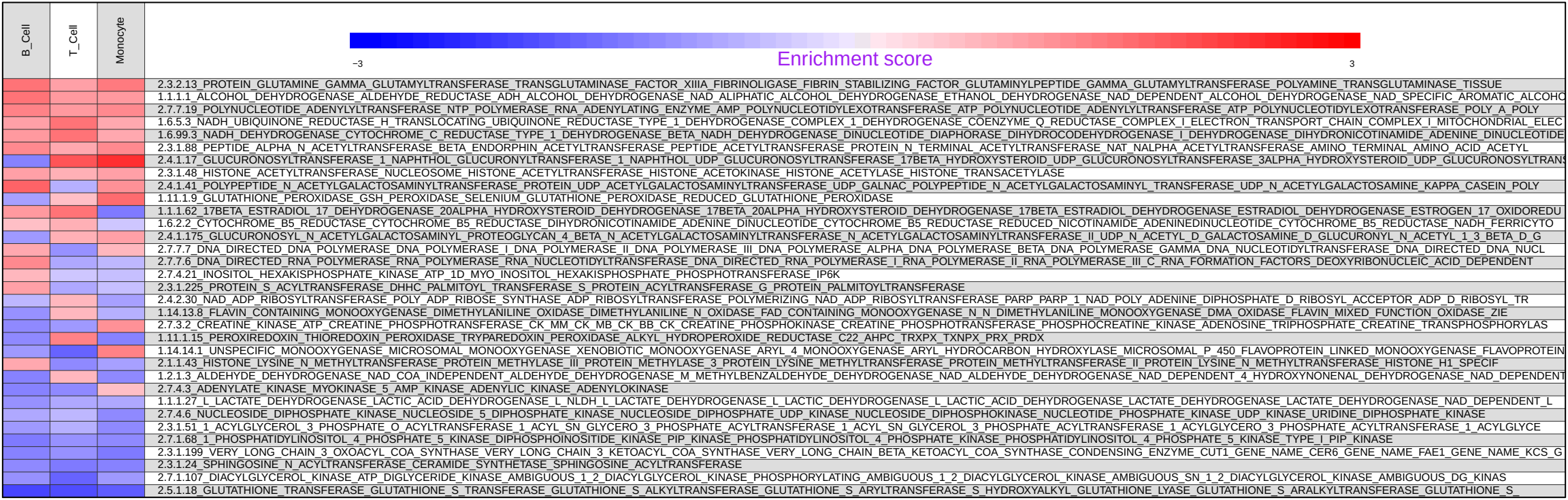
B_Cell
T_Cell
Monocyte
Enrichment score
−3
3
2.3.2.13_PROTEIN_GLUTAMINE_GAMMA_GLUTAMYLTRANSFERASE_TRANSGLUTAMINASE_FACTOR_XIIIA_FIBRINOLIGASE_FIBRIN_STABILIZING_FACTOR_GLUTAMINYLPEPTIDE_GAMMA_GLUTAMYLTRANSFERASE_POLYAMINE_TRANSGLUTAMINASE_TISSUE
1.1.1.1_ALCOHOL_DEHYDROGENASE_ALDEHYDE_REDUCTASE_ADH_ALCOHOL_DEHYDROGENASE_NAD_ALIPHATIC_ALCOHOL_DEHYDROGENASE_ETHANOL_DEHYDROGENASE_NAD_DEPENDENT_ALCOHOL_DEHYDROGENASE_NAD_SPECIFIC_AROMATIC_ALCOHO
2.7.7.19_POLYNUCLEOTIDE_ADENYLYLTRANSFERASE_NTP_POLYMERASE_RNA_ADENYLATING_ENZYME_AMP_POLYNUCLEOTIDYLEXOTRANSFERASE_ATP_POLYNUCLEOTIDE_ADENYLYLTRANSFERASE_ATP_POLYNUCLEOTIDYLEXOTRANSFERASE_POLY_A_POLY
1.6.5.3_NADH_UBIQUINONE_REDUCTASE_H_TRANSLOCATING_UBIQUINONE_REDUCTASE_TYPE_1_DEHYDROGENASE_COMPLEX_1_DEHYDROGENASE_COENZYME_Q_REDUCTASE_COMPLEX_I_ELECTRON_TRANSPORT_CHAIN_COMPLEX_I_MITOCHONDRIAL_ELEC
1.6.99.3_NADH_DEHYDROGENASE_CYTOCHROME_C_REDUCTASE_TYPE_1_DEHYDROGENASE_BETA_NADH_DEHYDROGENASE_DINUCLEOTIDE_DIAPHORASE_DIHYDROCODEHYDROGENASE_I_DEHYDROGENASE_DIHYDRONICOTINAMIDE_ADENINE_DINUCLEOTIDE
2.3.1.88_PEPTIDE_ALPHA_N_ACETYLTRANSFERASE_BETA_ENDORPHIN_ACETYLTRANSFERASE_PEPTIDE_ACETYLTRANSFERASE_PROTEIN_N_TERMINAL_ACETYLTRANSFERASE_NAT_NALPHA_ACETYLTRANSFERASE_AMINO_TERMINAL_AMINO_ACID_ACETYL
2.4.1.17_GLUCURONOSYLTRANSFERASE_1_NAPHTHOL_GLUCURONYLTRANSFERASE_1_NAPHTHOL_UDP_GLUCURONOSYLTRANSFERASE_17BETA_HYDROXYSTEROID_UDP_GLUCURONOSYLTRANSFERASE_3ALPHA_HYDROXYSTEROID_UDP_GLUCURONOSYLTRANS
2.3.1.48_HISTONE_ACETYLTRANSFERASE_NUCLEOSOME_HISTONE_ACETYLTRANSFERASE_HISTONE_ACETOKINASE_HISTONE_ACETYLASE_HISTONE_TRANSACETYLASE
2.4.1.41_POLYPEPTIDE_N_ACETYLGALACTOSAMINYLTRANSFERASE_PROTEIN_UDP_ACETYLGALACTOSAMINYLTRANSFERASE_UDP_GALNAC_POLYPEPTIDE_N_ACETYLGALACTOSAMINYL_TRANSFERASE_UDP_N_ACETYLGALACTOSAMINE_KAPPA_CASEIN_POLY
1.11.1.9_GLUTATHIONE_PEROXIDASE_GSH_PEROXIDASE_SELENIUM_GLUTATHIONE_PEROXIDASE_REDUCED_GLUTATHIONE_PEROXIDASE
1.1.1.62_17BETA_ESTRADIOL_17_DEHYDROGENASE_20ALPHA_HYDROXYSTEROID_DEHYDROGENASE_17BETA_20ALPHA_HYDROXYSTEROID_DEHYDROGENASE_17BETA_ESTRADIOL_DEHYDROGENASE_ESTRADIOL_DEHYDROGENASE_ESTROGEN_17_OXIDOREDU
1.6.2.2_CYTOCHROME_B5_REDUCTASE_CYTOCHROME_B5_REDUCTASE_DIHYDRONICOTINAMIDE_ADENINE_DINUCLEOTIDE_CYTOCHROME_B5_REDUCTASE_REDUCED_NICOTINAMIDE_ADENINEDINUCLEOTIDE_CYTOCHROME_B5_REDUCTASE_NADH_FERRICYTO
2.4.1.175_GLUCURONOSYL_N_ACETYLGALACTOSAMINYL_PROTEOGLYCAN_4_BETA_N_ACETYLGALACTOSAMINYLTRANSFERASE_N_ACETYLGALACTOSAMINYLTRANSFERASE_II_UDP_N_ACETYL_D_GALACTOSAMINE_D_GLUCURONYL_N_ACETYL_1_3_BETA_D_G
2.7.7.7_DNA_DIRECTED_DNA_POLYMERASE_DNA_POLYMERASE_I_DNA_POLYMERASE_II_DNA_POLYMERASE_III_DNA_POLYMERASE_ALPHA_DNA_POLYMERASE_BETA_DNA_POLYMERASE_GAMMA_DNA_NUCLEOTIDYLTRANSFERASE_DNA_DIRECTED_DNA_NUCL
2.7.7.6_DNA_DIRECTED_RNA_POLYMERASE_RNA_POLYMERASE_RNA_NUCLEOTIDYLTRANSFERASE_DNA_DIRECTED_RNA_POLYMERASE_I_RNA_POLYMERASE_II_RNA_POLYMERASE_III_C_RNA_FORMATION_FACTORS_DEOXYRIBONUCLEIC_ACID_DEPENDENT
2.7.4.21_INOSITOL_HEXAKISPHOSPHATE_KINASE_ATP_1D_MYO_INOSITOL_HEXAKISPHOSPHATE_PHOSPHOTRANSFERASE_IP6K
2.3.1.225_PROTEIN_S_ACYLTRANSFERASE_DHHC_PALMITOYL_TRANSFERASE_S_PROTEIN_ACYLTRANSFERASE_G_PROTEIN_PALMITOYLTRANSFERASE
2.4.2.30_NAD_ADP_RIBOSYLTRANSFERASE_POLY_ADP_RIBOSE_SYNTHASE_ADP_RIBOSYLTRANSFERASE_POLYMERIZING_NAD_ADP_RIBOSYLTRANSFERASE_PARP_PARP_1_NAD_POLY_ADENINE_DIPHOSPHATE_D_RIBOSYL_ACCEPTOR_ADP_D_RIBOSYL_TR
1.14.13.8_FLAVIN_CONTAINING_MONOOXYGENASE_DIMETHYLANILINE_OXIDASE_DIMETHYLANILINE_N_OXIDASE_FAD_CONTAINING_MONOOXYGENASE_N_N_DIMETHYLANILINE_MONOOXYGENASE_DMA_OXIDASE_FLAVIN_MIXED_FUNCTION_OXIDASE_ZIE
2.7.3.2_CREATINE_KINASE_ATP_CREATINE_PHOSPHOTRANSFERASE_CK_MM_CK_MB_CK_BB_CK_CREATINE_PHOSPHOKINASE_CREATINE_PHOSPHOTRANSFERASE_PHOSPHOCREATINE_KINASE_ADENOSINE_TRIPHOSPHATE_CREATINE_TRANSPHOSPHORYLAS
1.11.1.15_PEROXIREDOXIN_THIOREDOXIN_PEROXIDASE_TRYPAREDOXIN_PEROXIDASE_ALKYL_HYDROPEROXIDE_REDUCTASE_C22_AHPC_TRXPX_TXNPX_PRX_PRDX
1.14.14.1_UNSPECIFIC_MONOOXYGENASE_MICROSOMAL_MONOOXYGENASE_XENOBIOTIC_MONOOXYGENASE_ARYL_4_MONOOXYGENASE_ARYL_HYDROCARBON_HYDROXYLASE_MICROSOMAL_P_450_FLAVOPROTEIN_LINKED_MONOOXYGENASE_FLAVOPROTEIN
2.1.1.43_HISTONE_LYSINE_N_METHYLTRANSFERASE_PROTEIN_METHYLASE_III_PROTEIN_METHYLASE_3_PROTEIN_LYSINE_METHYLTRANSFERASE_PROTEIN_METHYLTRANSFERASE_II_PROTEIN_LYSINE_N_METHYLTRANSFERASE_HISTONE_H1_SPECIF
1.2.1.3_ALDEHYDE_DEHYDROGENASE_NAD_COA_INDEPENDENT_ALDEHYDE_DEHYDROGENASE_M_METHYLBENZALDEHYDE_DEHYDROGENASE_NAD_ALDEHYDE_DEHYDROGENASE_NAD_DEPENDENT_4_HYDROXYNONENAL_DEHYDROGENASE_NAD_DEPENDENT
2.7.4.3_ADENYLATE_KINASE_MYOKINASE_5_AMP_KINASE_ADENYLIC_KINASE_ADENYLOKINASE
1.1.1.27_L_LACTATE_DEHYDROGENASE_LACTIC_ACID_DEHYDROGENASE_L_NLDH_L_LACTATE_DEHYDROGENASE_L_LACTIC_DEHYDROGENASE_L_LACTIC_ACID_DEHYDROGENASE_LACTATE_DEHYDROGENASE_LACTATE_DEHYDROGENASE_NAD_DEPENDENT_L
2.7.4.6_NUCLEOSIDE_DIPHOSPHATE_KINASE_NUCLEOSIDE_5_DIPHOSPHATE_KINASE_NUCLEOSIDE_DIPHOSPHATE_UDP_KINASE_NUCLEOSIDE_DIPHOSPHOKINASE_NUCLEOTIDE_PHOSPHATE_KINASE_UDP_KINASE_URIDINE_DIPHOSPHATE_KINASE
2.3.1.51_1_ACYLGLYCEROL_3_PHOSPHATE_O_ACYLTRANSFERASE_1_ACYL_SN_GLYCERO_3_PHOSPHATE_ACYLTRANSFERASE_1_ACYL_SN_GLYCEROL_3_PHOSPHATE_ACYLTRANSFERASE_1_ACYLGLYCERO_3_PHOSPHATE_ACYLTRANSFERASE_1_ACYLGLYCE
2.7.1.68_1_PHOSPHATIDYLINOSITOL_4_PHOSPHATE_5_KINASE_DIPHOSPHOINOSITIDE_KINASE_PIP_KINASE_PHOSPHATIDYLINOSITOL_4_PHOSPHATE_KINASE_PHOSPHATIDYLINOSITOL_4_PHOSPHATE_5_KINASE_TYPE_I_PIP_KINASE
2.3.1.199_VERY_LONG_CHAIN_3_OXOACYL_COA_SYNTHASE_VERY_LONG_CHAIN_3_KETOACYL_COA_SYNTHASE_VERY_LONG_CHAIN_BETA_KETOACYL_COA_SYNTHASE_CONDENSING_ENZYME_CUT1_GENE_NAME_CER6_GENE_NAME_FAE1_GENE_NAME_KCS_G
2.3.1.24_SPHINGOSINE_N_ACYLTRANSFERASE_CERAMIDE_SYNTHETASE_SPHINGOSINE_ACYLTRANSFERASE
2.7.1.107_DIACYLGLYCEROL_KINASE_ATP_DIGLYCERIDE_KINASE_AMBIGUOUS_1_2_DIACYLGLYCEROL_KINASE_PHOSPHORYLATING_AMBIGUOUS_1_2_DIACYLGLYCEROL_KINASE_AMBIGUOUS_SN_1_2_DIACYLGLYCEROL_KINASE_AMBIGUOUS_DG_KINAS
2.5.1.18_GLUTATHIONE_TRANSFERASE_GLUTATHIONE_S_TRANSFERASE_GLUTATHIONE_S_ALKYLTRANSFERASE_GLUTATHIONE_S_ARYLTRANSFERASE_S_HYDROXYALKYL_GLUTATHIONE_LYASE_GLUTATHIONE_S_ARALKYLTRANSFERASE_GLUTATHIONE_S_