

Table S4 The biological processes involved in the high-risk model

GO(BP)	Size	NES	NOM p
SPINDLE_LOCALIZATION	52	2.1736689	0
ESTABLISHMENT_OF_MITOTIC_SPINDLE_LOCALIZATION	33	2.0479047	0
NADPH_REGENERATION	18	2.0350494	0.003984064
MATURATION_OF_SSU_RRNA	50	2.011506	0
ESTABLISHMENT_OF_MITOTIC_SPINDLE_ORIENTATION	28	1.9801291	0.00204918
ESTABLISHMENT_OF_SPINDLE_ORIENTATION	34	1.9650413	0
MATURATION_OF_SSU_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_LSU_RRNA	37	1.9524888	0.00409836
REGULATION_OF_TRANSCRIPTION_BY_RNA_POLYMERASE_I	30	1.9517797	0.002109705
POSITIVE_REGULATION_OF_TRANSCRIPTION_BY_RNA_POLYMERASE_I	22	1.9514033	0.00204499
RRNA_TRANSCRIPTION	29	1.9328325	0.002141328
GLYCOLYTIC_PROCESS_THROUGH_FRUCTOSE_6_PHOSPHATE	29	1.932443	0.006382979
MATURATION_OF_LSU_RRNA	28	1.9166664	0.002061856
VIRAL_TRANSLATION	15	1.9137069	0
REGULATION_OF_TRANSLATIONAL_INITIATION_IN_RESPONSE_TO_STRESS	15	1.9111123	0
RIBOSOME_BIOGENESIS	299	1.9081647	0.004149378
GLUCOSE_CATABOLIC_PROCESS	35	1.8941289	0.004338395
MATURATION_OF_LSU_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_LSU_RRNA	15	1.8852247	0
LONG_CHAIN_FATTY_ACID_IMPORT_INTO_CELL	16	1.8688459	0.006160164
EPHRIN_RECEPTOR_SIGNALING_PATHWAY	86	1.8651295	0.004040404
ENDONUCLEOLYTIC_CLEAVAGE_INVOLVED_IN_RRNA_PROCESSING	15	1.8625565	0.002020202
NUCLEAR_MEMBRANE_ORGANIZATION	17	1.8617357	0.005988024
PSEUDOURIDINE_SYNTHESIS	18	1.8541995	0
RETROGRADE_VESICLE_MEDIATED_TRANSPORT_GOLGI_TO_ENDOPLASMIC_RETICULUM	87	1.8532321	0.003968254
NUCLEOBASE_METABOLIC_PROCESS	33	1.8517154	0.010121457
REGULATION_OF_SPINDLE_ASSEMBLY	25	1.84845	0.011857707
NUCLEOBASE_BIOSYNTHETIC_PROCESS	18	1.8398632	0.002141328
RRNA_METABOLIC_PROCESS	233	1.8289373	0.010373444
METAPHASE_PLATE_CONGRESSION	64	1.8287425	0.021052632
REGULATION_OF_MITOTIC_SPINDLE_ASSEMBLY	18	1.8181173	0.006072875
MITOTIC_METAPHASE_PLATE_CONGRESSION	50	1.8140993	0.027310925
CELL_DIFFERENTIATION_INVOLVED_IN_EMBRYONIC_PLACENTA_DEVELOPMENT	23	1.8134329	0.008230452
CYTOKINETIC_PROCESS	38	1.8106124	0.014583333
MATURATION_OF_5_8S_RRNA	35	1.8036094	0.006072875
MATURATION_OF_5_8S_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_LSU_RRNA	24	1.8014185	0.010245902
POSITIVE_REGULATION_OF_TELOMERASE_RNA_LOCALIZATION_TO_CAJAL_BODY	15	1.800732	0
RIBONUCLEOPROTEIN_COMPLEX_BIOGENESIS	432	1.7976259	0.012371134
RIBOSOMAL_LARGE_SUBUNIT_BIOGENESIS	71	1.7971251	0.012096774
CLEAVAGE_INVOLVED_IN_RRNA_PROCESSING	27	1.795943	0.01010101
REGULATION_OF_SPINDLE_ORGANIZATION	39	1.7930849	0.016771488
NEGATIVE_REGULATION_OF_CHONDROCYTE_	21	1.7902995	0.009920635

DIFFERENTIATION			
TELOMERASE_RNA_LOCALIZATION	19	1.7849377	0.004264392
MICROTUBULE_CYTOSKELETON_ORGANIZATION _INVOLVED_IN_MITOSIS	141	1.7827733	0.015021459
NUCLEAR_ENVELOPE_REASSEMBLY	18	1.7792196	0.012345679
NADH_METABOLIC_PROCESS	42	1.7713242	0.02244898
CELLULAR_RESPONSE_TO_ARSENIC_CONTAINING_SUBSTANCE	18	1.7704316	0.014522822
PROTEIN_INSERTION_INTO_ER_MEMBRANE	17	1.7594883	0.014705882
GLUCOSE_6_PHOSPHATE_METABOLIC_PROCESS	25	1.7594767	0.012793177
TRANSCRIPTION_BY_RNA_POLYMERASE_I	60	1.7591196	0.014198783
RIBOSOMAL_SMALL_SUBUNIT_BIOGENESIS	73	1.7576888	0.016129032
RNA_DEPENDENT_DNA_BIOSYNTHETIC_PROCESS	69	1.7576473	0.015686275
RRNA_CONTAINING_RIBONUCLEOPROTEIN_ COMPLEX_EXPORT_FROM_NUCLEUS	15	1.7550685	0.006036217
DNA_UNWINDING_INVOLVED_IN_DNA_REPLICATION	16	1.7548027	0.006224067
MITOTIC_SPINDLE_ASSEMBLY	64	1.7539581	0.025210084
REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_ IN_RESPONSE_TO_STRESS	115	1.7462771	0.010288066
ENTRY_OF_BACTERIUM_INTO_HOST_CELL	15	1.7449327	0.006072875
AMINO_ACID_ACTIVATION	30	1.7416078	0.023715414
RESPONSE_TO_ARSENIC_CONTAINING_SUBSTANCE	30	1.7405218	0.010416667
INCLUSION_BODY_ASSEMBLY	23	1.7399479	0.014344262
CHROMOSOME_LOCALIZATION	80	1.7389088	0.025917927
FORMATION_OF_CYTOPLASMIC_TRANSLATION_ INITIATION_COMPLEX	16	1.7337966	0.016666668
CYTOSKELETON_DEPENDENT_CYTOKINESIS	85	1.7262726	0.012269938
PROTEIN_LOCALIZATION_TO_CHROMOSOME_ TELOMERIC_REGION	29	1.723966	0.026530612
MITOTIC_SPINDLE_ORGANIZATION	116	1.7182591	0.029661017
RNA_5_END_PROCESSING	22	1.7170882	0.014344262
TRNA_TRANSPORT	36	1.7154179	0.022774328
NCRNA_EXPORT_FROM_NUCLEUS	37	1.7147744	0.028688524
ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_TELOMERE	18	1.7133894	0.029227557
MAMMARY_GLAND_EPITHELIAL_CELL_PROLIFERATION	24	1.711685	0.010615711
ZINC_ION_TRANSPORT	27	1.7115198	0.011650485
CELLULAR_RESPONSE_TO_HEAT	115	1.7111329	0.01632653
MITOTIC_CYTOKINESIS	69	1.7079787	0.012422361
REGULATION_OF_UBIQUITIN_PROTEIN_LIGASE_ACTIVITY	23	1.7074962	0.018480493
MONOSACCHARIDE_CATABOLIC_PROCESS	61	1.700879	0.017621145
OLIGOSACCHARIDE_LIPID_INTERMEDIATE_ BIOSYNTHETIC_PROCESS	21	1.6938397	0.023109244
LIPID_IMPORT_INTO_CELL	33	1.6914728	0.020325202
REGULATION_OF_CELLULAR_RESPONSE_TO_HEAT	78	1.6901805	0.031185031
CYTOPLASMIC_TRANSLATIONAL_INITIATION	34	1.6900403	0.032719836
REGULATION_OF_INCLUSION_BODY_ASSEMBLY	16	1.688101	0.022540983
REGULATION_OF_TRANSLATION_IN_RESPONSE_TO_STRESS	21	1.6872149	0.020120725
NEGATIVE_REGULATION_OF_DNA_TEMPLATED_ TRANSCRIPTION_ELONGATION	17	1.6852261	0.016597511
POSITIVE_REGULATION_OF_TELOMERASE_ACTIVITY	33	1.679867	0.030107526
DNA_REPLICATION_INITIATION	40	1.6758078	0.019565217
ASYMMETRIC_CELL_DIVISION	17	1.6711833	0.009708738

REGULATION_OF_HAIR_CYCLE	26	1.6677923	0.014056225
POSITIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_NUCLEUS	85	1.6673682	0.017429193
DE_NOVO_PROTEIN_FOLDING	40	1.6645352	0.026
RESPONSE_TO_SALT	16	1.663192	0.023809524
POSITIVE_REGULATION_OF_TELOMERE_MAINTENANCE_VIA_TELOMERE_LENGTHENING	36	1.659336	0.039014373
ATTACHMENT_OF_MITOTIC_SPINDLE_MICROTUBULES_TO_KINETOCHORE	15	1.6573994	0.046653144
BLASTOCYST_GROWTH	19	1.6528047	0.026476579
DNA_STRAND_ELONGATION	26	1.6527267	0.030800821
POSITIVE_REGULATION_OF_DNA_REPLICATION	37	1.6503004	0.03448276
POSITIVE_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_INITIATION	35	1.6502596	0.016096579
NEGATIVE_REGULATION_OF_CARTILAGE_DEVELOPMENT	25	1.641633	0.030674847
NCRNA_PROCESSING	388	1.640707	0.044176705
PYRIMIDINE_NUCLEOBASE_METABOLIC_PROCESS	16	1.6391147	0.03168317
ALDITOL_METABOLIC_PROCESS	23	1.6353346	0.030927835
PYRUVATE_METABOLIC_PROCESS	149	1.6308068	0.006289308
CELLULAR_RESPONSE_TO_GAMMA_RADIATION	27	1.629843	0.030674847
NCRNA_METABOLIC_PROCESS	463	1.6240171	0.04684318
TELOMERE_MAINTENANCE_VIA_TELOMERE_LENGTHENING	79	1.6232336	0.035714287
ADHERENS_JUNCTION_ORGANIZATION	66	1.6231241	0.024242423
REGULATION_OF_CHOLESTEROL_BIOSYNTHETIC_PROCESS	43	1.6213636	0.039748956
RRNA_MODIFICATION	37	1.6155937	0.047325104
ENDOPLASMIC_RETICULUM_TUBULAR_NETWORK_ORGANIZATION	18	1.6128219	0.02834008
RESPONSE_TO_X_RAY	31	1.6108366	0.035940804
POSITIVE_REGULATION_OF_TELOMERE_MAINTENANCE	51	1.6060848	0.03950104
PYRIMIDINE_RIBONUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROCESS	17	1.6025511	0.037475344
PROTEIN_IMPORT	193	1.5973465	0.022633744
CENTROSOME_SEPARATION	15	1.5962898	0.04
RNA_LOCALIZATION	230	1.5930654	0.044210527
REGULATION_OF_CELL_AGING	47	1.5920178	0.035343036
REGULATION_OF_MRNA_CATABOLIC_PROCESS	210	1.5893779	0.027777778
NUCLEOBASE_CONTAINING_SMALL_MOLECULE_INTERCONVERSION	27	1.5869205	0.035051547
CELLULAR_RESPONSE_TO_IONIZING_RADIATION	64	1.5843478	0.028806584
MONOSACCHARIDE_BIOSYNTHETIC_PROCESS	95	1.5815395	0.020746889
REGULATION_OF_TELOMERASE_ACTIVITY	47	1.5795172	0.033126295
POSITIVE_REGULATION_OF_TRANSLATION	129	1.5790343	0.018181818
CELLULAR_CARBOHYDRATE_CATABOLIC_PROCESS	45	1.578003	0.006060606
PROTEIN_HYDROXYLATION	27	1.5775561	0.047034767
REGULATION_OF_PROTEIN_LOCALIZATION_TO_NUCLEUS	129	1.5706551	0.023605151
POSITIVE_REGULATION_OF_SODIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	16	1.5704399	0.04112554
NAD_METABOLIC_PROCESS	50	1.5698129	0.04347826
DNA_STRAND_ELONGATION_INVOLVED_IN_DNA_REPLICATION	19	1.5674301	0.04
CHAPERONE_COFACTOR_DEPENDENT_PROTEIN_REFOLDING	31	1.5668992	0.04527559
POSITIVE_REGULATION_OF_TRANSCRIPTION_INITIATION	28	1.5662723	0.032520324

FROM_RNA_POLYMERASE_II_PROMOTER			
POSITIVE_REGULATION_OF_DENDRITIC_SPINE_MORPHOGENESIS	18	1.565656	0.04
CELL_CELL_JUNCTION_ORGANIZATION	206	1.5643792	0.019493178
NUCLEOTIDE_PHOSPHORYLATION	131	1.5642219	0.023305085
HEPATOCTE_DIFFERENTIATION	16	1.5634693	0.046184737
NEGATIVE_REGULATION_OF_HORMONE_SECRETION	59	1.5576938	0.016913319
PROTEIN_LOCALIZATION_TO_NUCLEUS	273	1.554413	0.03877551
POSITIVE_REGULATION_OF_CELL_AGING	15	1.5501387	0.04109589
NEGATIVE_REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY	215	1.5447297	0.008196721
REGULATION_OF_TRANSLATIONAL_INITIATION	80	1.5412967	0.043933053
ENDODERM_DEVELOPMENT	75	1.5409527	0.044660196
REGULATION_OF_MAMMARY_GLAND_EPITHELIAL_CELL_PROLIFERATION	15	1.5406914	0.034858387
UTERUS_DEVELOPMENT	18	1.539906	0.049689442
ENDOPLASMIC_RETICULUM_ORGANIZATION	81	1.5398483	0.031185031
CELLULAR_RESPONSE_TO_OXYGEN_LEVELS	219	1.5376254	0.01629328
BLASTOCYST_FORMATION	35	1.5360253	0.044989776
BINDING_OF_SPERM_TO_ZONA_PELLUCIDA	43	1.5347697	0.026584867
POSITIVE_REGULATION_OF_PROTEIN_MATURATION	26	1.5177819	0.042682927
REGULATION_OF_BRANCHING_INVOLVED_IN_URETERIC_BUD_MORPHOGENESIS	20	1.5164241	0.04821803
PROTEIN_FOLDING	219	1.5150144	0.036960986
REGULATION_OF_UBIQUITIN_PROTEIN_TRANSFERASE_ACTIVITY	53	1.5106783	0.044585988
EPITHELIAL_CELL_MATURATION	15	1.4893361	0.04329897
NUCLEOSIDE_DIPHOSPHATE_METABOLIC_PROCESS	154	1.4851787	0.023060797
REGULATION_OF_MITOCHONDRIAL_MEMBRANE_PERMEABILITY	71	1.4851401	0.041841004
INTESTINAL_EPITHELIAL_CELL_DIFFERENTIATION	21	1.4807682	0.044715445
REGULATION_OF_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPREADING	57	1.4704218	0.048732944
PLACENTA_DEVELOPMENT	133	1.4691668	0.034907598
POSITIVE_REGULATION_OF_CELLULAR_AMIDE_METABOLIC_PROCESS	157	1.4592147	0.030241935
CELLULAR_RESPONSE_TO_DEXAMETHASONE_STIMULUS	29	1.4477022	0.047904193
POSITIVE_REGULATION_OF_CELLULAR_PROTEIN_LOCALIZATION	291	1.4383585	0.044585988
CARBOHYDRATE_BIOSYNTHETIC_PROCESS	207	1.4322413	0.030107526
SKIN_EPIDERMIS_DEVELOPMENT	84	1.4316211	0.048681542
POST_TRANSLATIONAL_PROTEIN_MODIFICATION	358	1.4224731	0.028455285
NEGATIVE_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	90	1.4218748	0.049281314
NEGATIVE_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	100	1.4203365	0.042168673
CELLULAR_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	86	1.4181676	0.034764826
MONOSACCHARIDE_METABOLIC_PROCESS	269	1.4140674	0.01724138
RESPONSE_TO_OXYGEN_LEVELS	372	1.4086951	0.020576132
GLUCOSE_METABOLIC_PROCESS	207	1.3864388	0.029535865
REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY	332	1.3318124	0.046938777