

Supplementary Table S4. Pathway analyses of GWAS datasets for sperm motility

Database	Pathway/Gene Set Name	<i>P</i> -value	FDR value
KEGG	Arrhythmogenic right ventricular cardiomyopathy arvc	0.001	0.0010
KEGG	Dilated cardiomyopathy	0.001	0.0010
KEGG	Glycosphingolipid biosynthesis lacto and neolacto series	0.001	0.0010
BioCarta	AT1R pathway	0.001	0.0010
BioCarta	FMLP pathway	0.001	0.0010
GO	Regulation of secretion	0.001	0.0010
GO	Glucose metabolic process	0.001	0.0010
GO	Di tri valent inorganic cation transport	0.001	0.0010
GO	Sulfur metabolic process	0.001	0.0010
GO	Striated muscle development	0.001	0.0010
GO	Bone remodeling	0.001	0.0010
GO	Neurogenesis	0.001	0.0010
GO	Neuron differentiation	0.001	0.0010
GO	Carbohydrate biosynthetic process	0.001	0.0010
GO	Potassium ion transport	0.001	0.0010
GO	Transmission of nerve impulse	0.001	0.0010
GO	Central nervous system development	0.001	0.0010
GO	RNA helicase activity	0.001	0.0010
GO	GTPase regulator activity	0.001	0.0010
GO	Voltage gated potassium channel activity	0.001	0.0010
GO	Amino acid transmembrane transporter activity	0.001	0.0010
GO	Substrate specific channel activity	0.001	0.0010
GO	Auxiliary transport protein activity	0.001	0.0010
GO	Metal ion transmembrane transporter activity	0.001	0.0010
GO	Ion channel activity	0.001	0.0010
GO	Guanyl nucleotide exchange factor activity	0.001	0.0010
GO	Chromatin	0.001	0.0010
GO	Voltage gated potassium channel complex	0.001	0.0010
GO	Cell projection	0.001	0.0010
GO	Receptor complex	0.001	0.0010
GO	Synapse organization and biogenesis	0.001	0.0010

GO	Nuclear chromosome part	0.001	0.0010
KEGG	Ascorbate and aldarate metabolism	0.001	0.0010
KEGG	Axon guidance	0.001	0.0010
KEGG	Calcium signaling pathway	0.001	0.0010
KEGG	Cardiac muscle contraction	0.001	0.0010
KEGG	ECM receptor interaction	0.001	0.0010
KEGG	Fructose and mannose metabolism	0.001	0.0010
KEGG	Hypertrophic cardiomyopathy HCM	0.001	0.0010
KEGG	JAK STAT signaling pathway	0.001	0.0010
KEGG	Pentose and glucuronate interconversions	0.001	0.0010
KEGG	Regulation of autophagy	0.001	0.0010
BioCarta	HDAC pathway	0.001	0.0010
BioCarta	PGC1A pathway	0.001	0.0010
GO	DNA repair	0.001	0.0010
GO	Muscle development	0.001	0.0010
GO	G protein signaling coupled to IP3 second messengerphospholipase C activating	0.001	0.0010
GO	Neurite development	0.001	0.0010
GO	Protein amino acid N linked glycosylation	0.001	0.0010
GO	Hemopoiesis	0.001	0.0010
GO	Immune system development	0.001	0.0010
GO	Axonogenesis	0.001	0.0010
GO	Protein DNA complex assembly	0.001	0.0010
GO	Calcium ion transport	0.001	0.0010
GO	Cellular morphogenesis during differentiation	0.001	0.0010
GO	Generation of neurons	0.001	0.0010
GO	Lipoprotein metabolic process	0.001	0.0010
GO	Organ morphogenesis	0.001	0.0010
GO	Alcohol metabolic process	0.001	0.0010
GO	Metal ion transport	0.001	0.0010
GO	Phosphoinositide mediated signaling	0.001	0.0010
GO	Hemopoietic or lymphoid organ development	0.001	0.0010
GO	Synaptic transmission	0.001	0.0010
GO	Synapse organization and biogenesis	0.001	0.0010

GO	Response to other organism	0.001	0.0010
GO	Vesicle mediated transport	0.001	0.0010
GO	Second messenger mediated signaling	0.001	0.0010
GO	Carbohydrate metabolic process	0.001	0.0010
GO	Cation transport	0.001	0.0010
GO	Neuron development	0.001	0.0010
GO	Innate immune response	0.001	0.0010
GO	DNA packaging	0.001	0.0010
GO	Cell migration	0.001	0.0010
GO	Cation transmembrane transporter activity	0.001	0.0010
GO	Hematopoietin interferon class d200 domain cytokine receptor binding	0.001	0.0010
GO	Cation channel activity	0.001	0.0010
GO	Hydrolase activity acting on carbon nitrogen not peptidebonds	0.001	0.0010
GO	Amine receptor activity	0.001	0.0010
GO	Single stranded DNA binding	0.001	0.0010
GO	Voltage gated channel activity	0.001	0.0010
GO	Gated channel activity	0.001	0.0010
GO	Amine transmembrane transporter activity	0.001	0.0010
GO	Protein tyrosine kinase activity	0.001	0.0010
GO	Potassium channel activity	0.001	0.0010
GO	G protein coupled receptor activity	0.001	0.0010
GO	Voltage gated cation channel activity	0.001	0.0010
GO	Transcription repressor activity	0.001	0.0010
GO	Serine hydrolase activity	0.001	0.0010
GO	Ligand gated channel activity	0.001	0.0010
GO	Calcium channel activity	0.001	0.0010
GO	Channel regulator activity	0.001	0.0010
GO	Cytokine activity	0.001	0.0010
GO	Chromosomal part	0.001	0.0010
KEGG	Vascular smooth muscle contraction	0.001	0.0010
KEGG	T cell receptor signaling pathway	0.001	0.0010
KEGG	Glycine serine and threonine metabolism	0.001	0.0010
BioCarta	NO1 pathway	0.001	0.0010

GO	Protein oligomerization	0.001	0.0010
GO	Organic acid transmembrane transporter activity	0.001	0.0010
KEGG	Starch and sucrose metabolism	0.001	0.0010
KEGG	Notch signaling pathway	0.001	0.0010
KEGG	Dorso ventral axis formation	0.001	0.0010
BioCarta	CCR3 pathway	0.001	0.0010
GO	Behavior	0.001	0.0010
GO	GTPase activator activity	0.001	0.0010
GO	Structure specific DNA binding	0.001	0.0010
GO	Serine type endopeptidase activity	0.001	0.0010
GO	Tissue remodeling	0.001	0.0010
GO	Cell junction	0.001	0.0010
GO	Immune effector process	0.001	0.0010
GO	Sequence specific DNA binding	0.001	0.0010
KEGG	Cytosolic DNA sensing pathway	0.001	0.0010
GO	Positive regulation of response to stimulus	0.001	0.0010
BioCarta	SPPA pathway	0.001	0.0010
GO	Leukocyte differentiation	0.001	0.0010
GO	Chromatin binding	0.001	0.0010
GO	Leading edge	0.001	0.0010
GO	Carboxylic acid transmembrane transporter activity	0.001	0.0010
GO	Neurotransmitter receptor activity	0.001	0.0010
GO	Transmembrane receptor protein tyrosine kinase activity	0.001	0.0010
GO	Negative regulation of catalytic activity	0.001	0.0010
GO	Hormone metabolic process	0.001	0.0010
BioCarta	BCR pathway	0.001	0.0010
GO	G protein signaling coupled to cyclic nucleotide second messenger	0.001	0.0010
GO	Transmembrane receptor protein tyrosine kinase signaling pathway	0.001	0.0010
GO	Regulation of anatomical structure morphogenesis	0.001	0.0010
GO	Glycoprotein biosynthetic process	0.001	0.0010
GO	Ion transport	0.001	0.0010
GO	Receptor mediated endocytosis	0.001	0.0010
GO	Enzyme linked receptor protein signaling pathway	0.001	0.0010

GO	Helicase activity	0.001	0.0010
GO	Cytoplasmic membrane bound vesicle	0.001	0.0010
GO	Active transmembrane transporter activity	0.001	0.0010
GO	Cellular carbohydrate metabolic process	0.001	0.0010
KEGG	Snare interactions in vesicular transport	0.001	0.0010
GO	Positive regulation of transport	0.001	0.0010
GO	Neurotransmitter binding	0.001	0.0010
GO	Cell surface	0.001	0.0010
GO	Regulation of immune response	0.001	0.0010
GO	Cell matrix adhesion	0.001	0.0010
GO	Cyclic nucleotide mediated signaling	0.001	0.0010
GO	Response to biotic stimulus	0.001	0.0010
GO	Serine type peptidase activity	0.001	0.0010
GO	Regulation of response to stimulus	0.001	0.0010
GO	Transmembrane receptor protein kinase activity	0.001	0.0010
BioCarta	NKT pathway	0.001	0.0010
BioCarta	ALK pathway	0.001	0.0010
GO	Response to bacterium	0.001	0.0010
KEGG	N glycan biosynthesis	0.001	0.0010
GO	Metalloendopeptidase activity	0.001	0.0010
KEGG	Adipocytokine signaling pathway	0.001	0.0010
GO	Multi organism process	0.001	0.0011
GO	Positive regulation of immune response	0.001	0.0011
KEGG	Porphyrin and chlorophyll metabolism	0.001	0.0011
GO	Monovalent inorganic cation transport	0.001	0.0011
KEGG	Gap junction	0.001	0.0011
KEGG	Retinol metabolism	0.001	0.0011
KEGG	Long term potentiation	0.001	0.0011
GO	Protein amino acid dephosphorylation	0.001	0.0011
BioCarta	Myosin pathway	0.001	0.0011
GO	Glycoprotein metabolic process	0.001	0.0011
GO	Regulation of transport	0.001	0.0011
GO	Regulation of cell differentiation	0.001	0.0011

GO	Positive regulation of multicellular organismal process	0.001	0.0011
GO	Intercellular junction	0.001	0.0011
GO	Structural constituent of muscle	0.001	0.0011
BioCarta	PAR1 pathway	0.001	0.0011
GO	Phosphoric ester hydrolase activity	0.001	0.0011
GO	Ribonucleoprotein complex	0.001	0.0011
GO	Ruffle	0.001	0.0011
GO	Ligand dependent nuclear receptor activity	0.001	0.0011
GO	Secretion by cell	0.001	0.0011
GO	Lamellipodium	0.001	0.0011
GO	Membrane bound vesicle	0.001	0.0011
GO	Exocytosis	0.001	0.0011
KEGG	Pyruvate metabolism	0.002	0.0011
GO	Endonuclease activity	0.001	0.0011
GO	Endopeptidase activity	0.001	0.0011
KEGG	Natural killer cell mediated cytotoxicity	0.001	0.0011
KEGG	Pentose phosphate pathway	0.001	0.0012
GO	Nucleoplasm part	0.001	0.0012
GO	Rhodopsin like receptor activity	0.001	0.0012
KEGG	ABC Transporters	0.001	0.0012
GO	Generation of a signal involved in cell cell signaling	0.001	0.0012
GO	Intermediate filament cytoskeleton	0.001	0.0012
GO	Intermediate filament cytoskeleton	0.001	0.0012
GO	Positive regulation of cell proliferation	0.001	0.0012
GO	Peptide receptor activity	0.001	0.0012
GO	Brain development	0.001	0.0012
GO	RAS GTPase activator activity	0.001	0.0012
GO	Amino acid transport	0.001	0.0012
GO	Cell cycle phase	0.001	0.0012
KEGG	Ether lipid metabolism	0.001	0.0012
BioCarta	RHO pathway	0.001	0.0012
GO	Extracellular structure organization and biogenesis	0.001	0.0012
GO	Sulfotransferase activity	0.001	0.0012

GO	Transferase activity transferring glycosyl groups	0.001	0.0012
GO	Dephosphorylation	0.001	0.0013
GO	Hydrolase activity acting on acid anhydrides catalyzing transmembrane movement of substance	0.001	0.0013
GO	Primary active transmembrane transporter activity	0.001	0.0013
KEGG	Tryptophan metabolism	0.001	0.0013
GO	Membrane organization and biogenesis	0.001	0.0013
GO	INTERPHASE OF MITOTIC CELL CYCLE	0.002	0.0013
GO	Chromosome	0.001	0.0013
GO	Skeletal muscle development	0.001	0.0013
GO	GTP binding	0.001	0.0013
GO	Vesicle	0.001	0.0013
KEGG	Cell adhesion molecules	0.001	0.0013
GO	Cell substrate adhesion	0.001	0.0013
GO	Transcription corepressor activity	0.001	0.0014
KEGG	RIG I like receptor signaling pathway	0.001	0.0014
KEGG	Drug metabolism other enzymes	0.001	0.0014
GO	ATPase activity coupled to movement of substances	0.001	0.0014
GO	Secretion by cell	0.001	0.0014
GO	Spliceosome	0.001	0.0014
BioCarta	NFAT pathway	0.001	0.0014
GO	Transcription factor complex	0.001	0.0014
GO	Lipoprotein biosynthetic process	0.001	0.0014
GO	ATPase activity	0.001	0.0014
KEGG	Chemokine signaling pathway	0.001	0.0015
GO	Regulation of hydrolase activity	0.001	0.0015
GO	Actin cytoskeleton	0.001	0.0015
GO	Steroid metabolic process	0.001	0.0015
GO	Cation binding	0.001	0.0015
GO	Cell cell adhesion	0.001	0.0015
GO	Transferase activity transferring sulfur containing groups	0.001	0.0015
GO	Aromatic compound metabolic process	0.001	0.0015
GO	Cytoskeletal protein binding	0.001	0.0015
GO	Membrane fusion	0.002	0.0015

GO	Regulation of intracellular transport	0.001	0.0016
GO	Mitotic cell cycle	0.001	0.0016
GO	Positive regulation of transcription DNA dependent	0.001	0.0016
GO	Cytoplasmic vesicle	0.001	0.0016
GO	Skeletal development	0.001	0.0016
GO	Response to virus	0.002	0.0016
GO	Pattern binding	0.001	0.0017
GO	Cytoskeleton organization and biogenesis	0.001	0.0017
GO	Vasculature development	0.001	0.0017
GO	Embryonic development	0.001	0.0017
GO	DNA directed RNA polymeraseii holoenzyme	0.002	0.0017
GO	Adherens junction	0.002	0.0017
GO	Positive regulation of lymphocyte activation	0.001	0.0017
GO	Zinc ion binding	0.001	0.0018
GO	Negative regulation of cell differentiation	0.001	0.0018
GO	Electron carrier activity	0.001	0.0018
GO	Regulation of multicellular organismal process	0.001	0.0018
GO	Peptide binding	0.002	0.0018
GO	Cytoplasmic vesicle membrane	0.001	0.0018
GO	Cytoplasmic vesicle part	0.001	0.0018
GO	Glycosaminoglycan binding	0.001	0.0018
GO	Regulation of immune system process	0.002	0.0018
GO	Transport vesicle	0.001	0.0018
GO	Locomotory behavior	0.002	0.0019
BioCarta	ERK pathway	0.001	0.0019
GO	Calcium ion binding	0.001	0.0019
GO	Soluble fraction	0.001	0.0019
GO	Negative regulation of nucleobasenucleosidenucleotide and nucleic acid metabolic process	0.001	0.0019
GO	Regulation of T cell activation	0.001	0.0019
GO	RAS GTPase binding	0.001	0.0019
GO	Phosphoric monoester hydrolase activity	0.001	0.0019
GO	Polysaccharide binding	0.001	0.0020
GO	Leukocyte activation	0.001	0.0020

GO	Peptidase activity	0.001	0.0020
GO	Structural constituent of ribosome	0.005	0.0021
GO	Lymphocyte activation	0.001	0.0021
GO	Integrin binding	0.002	0.0021
KEGG	FC gamma R mediated phagocytosis	0.001	0.0021
GO	Energy derivation by oxidation of organic compounds	0.001	0.0021
KEGG	Long term depression	0.001	0.0022
GO	Extrinsic to membrane	0.003	0.0022
KEGG	Protein export	0.001	0.0022
GO	Myeloid cell differentiation	0.001	0.0022
GO	Clathrin coated vesicle	0.001	0.0022
KEGG	B cell receptor signaling pathway	0.001	0.0023
GO	Regulation of lymphocyte activation	0.001	0.0023
GO	Cell activation	0.001	0.0023
GO	Lytic vacuole	0.002	0.0023
GO	Lysosome	0.002	0.0023
GO	Negative regulation of transcription	0.002	0.0023
BioCarta	EIF4 pathway	0.002	0.0023
GO	Transcription activator activity	0.001	0.0023
GO	ATPase activity coupled to movement of substances	0.001	0.0024
GO	Phosphoprotein phosphatase activity	0.001	0.0025
GO	Nuclear chromosome	0.001	0.0027
GO	Sensory perception	0.002	0.0027
GO	Digestion	0.001	0.0027
KEGG	Nucleotide excision repair	0.004	0.0027
GO	Small GTPase binding	0.002	0.0028
BioCarta	Integrin pathway	0.002	0.0030
GO	Response to endogenous stimulus	0.002	0.0030
GO	Guanyl nucleotide binding	0.001	0.0031
GO	RNA polymerase II transcription factor activity	0.001	0.0031
GO	Positive regulation of cell differentiation	0.001	0.0031
GO	T cell activation	0.002	0.0031
KEGG	Regulation of actin cytoskeleton	0.003	0.0031

GO	Cell cycle process	0.002	0.0031
BioCarta	Carm ER pathway	0.001	0.0032
GO	Phosphoric diester hydrolase activity	0.003	0.0033
KEGG	mTOR signaling pathway	0.003	0.0033
GO	Secretory pathway	0.001	0.0033
GO	Carboxylic acid transport	0.001	0.0036
GO	Response to DNA damage stimulus	0.001	0.0036
KEGG	ERBB signaling pathway	0.001	0.0037
GO	Transcription initiation	0.003	0.0037
GO	Microtubule cytoskeleton organization and biogenesis	0.003	0.0037
GO	Nuclear organization and biogenesis	0.003	0.0037
GO	Anatomical structure formation	0.003	0.0037
GO	Protein amino acid autophosphorylation	0.001	0.0039
GO	ATP dependent helicase activity	0.006	0.0040
GO	Pattern specification process	0.002	0.0040
GO	Nuclear transport	0.001	0.0041
GO	Nucleocytoplasmic transport	0.001	0.0041
BioCarta	CHREBP2 pathway	0.002	0.0041
KEGG	O glycan biosynthesis	0.001	0.0043
GO	Coated vesicle	0.004	0.0046
GO	Coagulation	0.004	0.0046
GO	GTPase binding	0.004	0.0050
GO	Chromatin assembly or disassembly	0.004	0.0050
GO	Growth factor activity	0.005	0.0055
BioCarta	VEGF pathway	0.003	0.0056
KEGG	Melanogenesis	0.001	0.0057
GO	Negative regulation of developmental process	0.001	0.0058
GO	Regulation of heart contraction	0.002	0.0060
GO	Secondary metabolic process	0.004	0.0060
GO	Organic acid transport	0.004	0.0061
GO	Positive Regulation of immune system process	0.002	0.0062
GO	Development of primary sexual characteristics	0.003	0.0062
GO	Serine type endopeptidase inhibitor activity	0.003	0.0068

GO	Interphase of mitotic cell cycle	0.002	0.0070
GO	Anion transmembrane transporter activity	0.004	0.0072
GO	Protein C terminus binding	0.002	0.0076
GO	Organelle localization	0.008	0.0078
GO	Vesicle membrane	0.001	0.0080
GO	Activation of protein kinase activity	0.003	0.0084
GO	Protein secretion	0.006	0.0085
GO	Protein processing	0.005	0.0087
KEGG	Hedgehog signaling pathway	0.005	0.0087
KEGG	TGF beta signaling pathway	0.005	0.0094
GO	Protein homodimerization activity	0.005	0.0094
GO	Apical junction complex	0.006	0.0096
GO	Apicolateral plasma membrane	0.006	0.0096
GO	Vacuole	0.005	0.0101
BioCarta	TCR pathway	0.008	0.0102
GO	Sexual reproduction	0.005	0.0104
GO	Hemostasis	0.005	0.0105
BioCarta	Inflam pathway	0.007	0.0108
KEGG	Aldosterone regulated sodium reabsorption	0.004	0.0108
GO	Protein folding	0.005	0.0109
GO	Transition metal ion binding	0.005	0.0111
GO	Protein autoprocessing	0.007	0.0117
GO	Spindle	0.006	0.0117
GO	Protein serine threonine phosphatase activity	0.006	0.0121
GO	Cellular homeostasis	0.005	0.0125
GO	Lymphocyte differentiation	0.007	0.0126
GO	Proteinaceous extracellular matrix	0.005	0.0137
GO	Nitrogen compound biosynthetic process	0.008	0.0139
GO	Homeostatic process	0.007	0.0140
BioCarta	EDG1 pathway	0.006	0.0142
GO	Blood coagulation	0.007	0.0142
GO	Gamete generation	0.008	0.0143
GO	Hydrolase activity hydrolyzing O glycosyl compounds	0.006	0.0145

GO	Positive regulation of nucleobasenucleosidenucleotide and nucleic acid metabolic process	0.004	0.0151
GO	Protein complex assembly	0.01	0.0154
BioCarta	HER2 pathway	0.007	0.0157
GO	Protein domain specific binding	0.005	0.0157
GO	Protein import into nucleus	0.01	0.0157
GO	Regulation of mitotic cell cycle	0.008	0.0164
GO	Positive regulation of developmental process	0.007	0.0172
KEGG	VEGF signaling pathway	0.006	0.0172
GO	Extracellular matrix	0.005	0.0173
GO	Regulation of cell adhesion	0.006	0.0174
GO	Positive regulation of transcription DNA dependent	0.004	0.0175
BioCarta	GPCR pathway	0.01	0.0178
GO	Nuclear export	0.009	0.0184
GO	Metallopeptidase activity	0.012	0.0192
GO	Muscle cell differentiation	0.01	0.0195
GO	Positive regulation of protein modification process	0.011	0.0212
GO	Regulation of body fluid levels	0.01	0.0212
GO	Protein tyrosine phosphatase activity	0.006	0.0215
BioCarta	mTOR pathway	0.008	0.0216
KEGG	GnRH signaling pathway	0.013	0.0224
GO	G protein signaling coupled to camp nucleotide second messenger	0.008	0.0225
GO	Response to abiotic stimulus	0.008	0.0225
GO	Purine nucleotide binding	0.015	0.0226
BioCarta	ECM pathway	0.011	0.0231
BioCarta	VIP pathway	0.009	0.0232
GO	Wound healing	0.015	0.0237
GO	Structural constituent of cytoskeleton	0.01	0.0246
GO	Positive regulation of hydrolase activity	0.014	0.0262
GO	Microtubule based process	0.012	0.0273
GO	Cytosol	0.012	0.0300
GO	inorganic cation transmembrane transporter activity	0.015	0.0306
GO	Enzyme activator activity	0.007	0.0306
GO	Cofactor binding	0.018	0.0316

BioCarta	AGR pathway	0.011	0.0320
GO	Phosphatase regulator activity	0.017	0.0320
GO	Lipid biosynthetic process	0.014	0.0320
BioCarta	PYK2 pathway	0.014	0.0320
GO	Cell cortex part	0.011	0.0321
GO	Lipid transport	0.018	0.0324
GO	Negative regulation of cell proliferation	0.018	0.0331
KEGG	Insulin signaling pathway	0.014	0.0345
GO	Negative regulation of translation	0.019	0.0350
GO	Negative regulation of programmed cell death	0.018	0.0352
GO	Peptidyl amino acid modification	0.016	0.0357
GO	Negative regulation of multicellular organismal process	0.017	0.0376
GO	Condensed chromosome	0.021	0.0378
GO	Tight junction	0.02	0.0380
KEGG	Glycosaminoglycan biosynthesis heparan sulfate	0.012	0.0390
KEGG	Focal adhesion	0.018	0.0405
GO	Amine transport	0.015	0.0409
GO	Nuclear import	0.022	0.0418
GO	Purine ribonucleotide binding	0.022	0.0419
GO	Basement membrane	0.018	0.0428
BioCarta	Proteasome pathway	0.024	0.0437
GO	Positive regulation of RNA metabolic process	0.008	0.0443
KEGG	Steroid hormone biosynthesis	0.02	0.0456
GO	Negative regulation of apoptosis	0.026	0.0458
GO	Specific RNA polymerase II transcription factor activity	0.031	0.0463
GO	G protein signaling adenylate cyclase activating pathway	0.024	0.0484
GO	Hormone activity	0.019	0.0487

Pathway analyses were conducted using i-GSEA4GWAS v2 (<http://gesa4gwas-v2.psych.ac.cn/>).

The gene set/pathway databases were from KEGG (<http://www.genome.jp/kegg/>), BioCarta (<http://www.biocarta.com>) and GO (<http://www.geneontology.org>).

The threshold of $FDR < 0.05$ is statistical significance in this analysis.

Abbreviat Abbreviation: FDR, false discovery rate.