

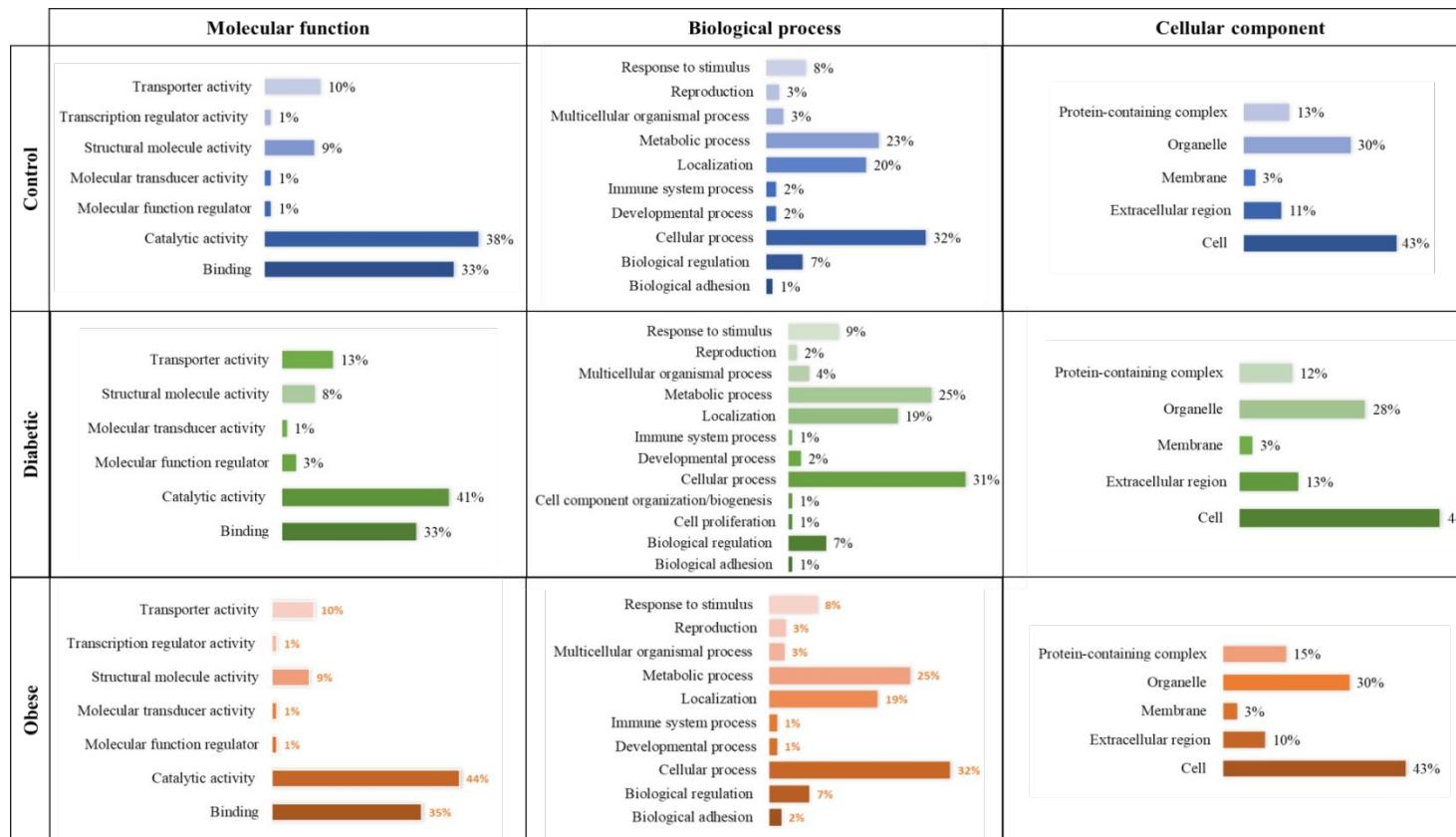
## Implications of Obesity and Diabetes on Sperm Cell Proteomic

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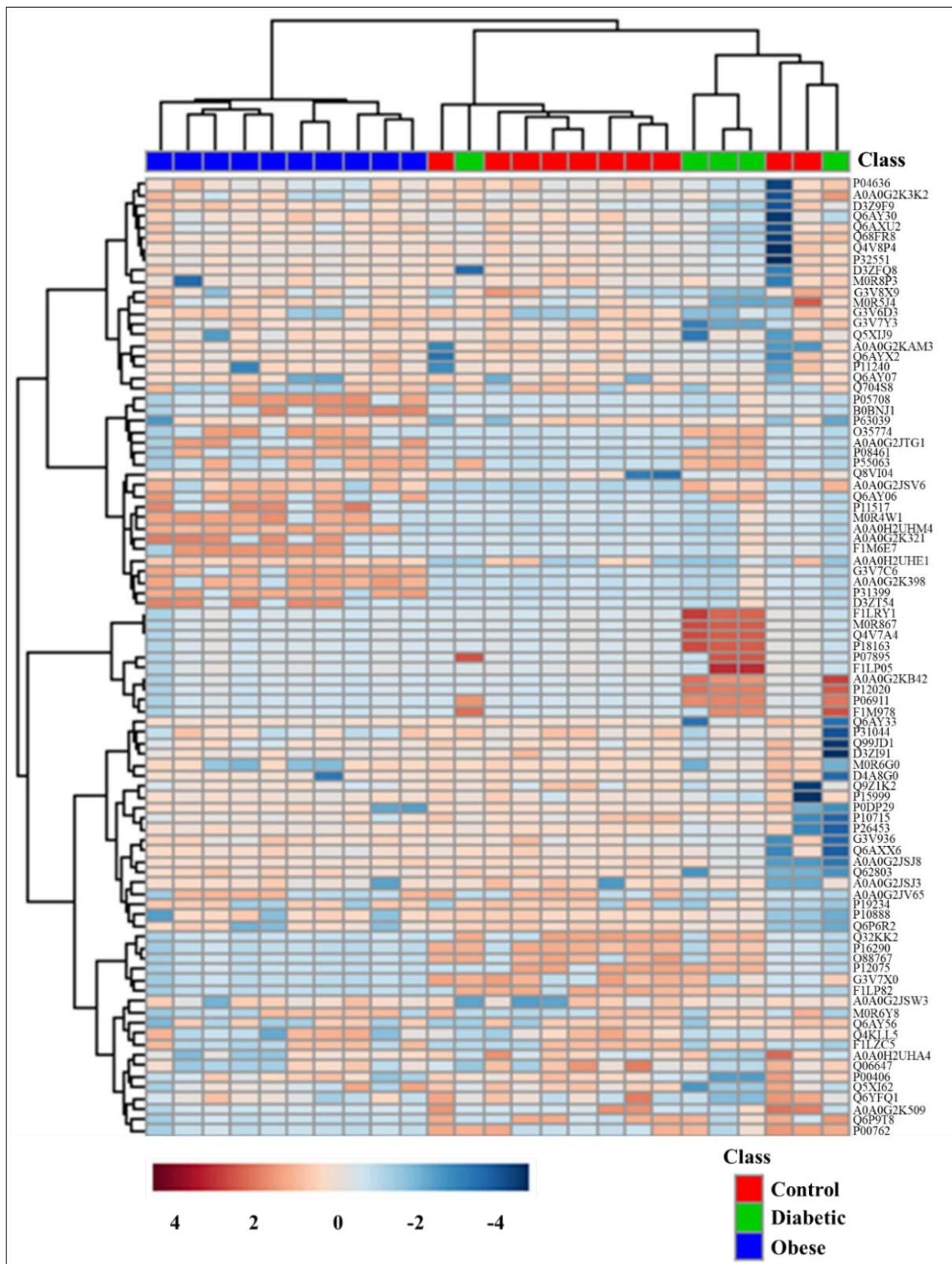
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## SUPPORTING INFORMATION FIGURES



**Supplemental Figure 1.** Gene ontology of the groups (control, diabetic and obese) considering molecular function, biological process and cell component.



**Supplemental Figure 2.** Non-hierarchical cluster analysis of samples according to the amount of differentially regulated protein in the control, diabetic and obese groups. Red color indicates increased and blue color decreased amount of protein.

## SUPPORTING INFORMATION TABLES

**Supplemental Table 1.**

Macronutrients and their caloric contributions of hyperglycemic diet (quantity to produce 100 g).

Ingredient	Macronutrient (g)			Calorie (kcal)
	Carbohydrate	Protein	Lipid	
Commercial food	28.64	9.34	1.82	162.96
Condensed milk	56.26	7.60	6.28	320.94
Sugar	9.60	0.03	0.00	37.30
Total em 100 g	94.50	16.97	8.10	521.20
Sucrose 5%*	--	--	--	200

\*50 g/L – 100 mL/24 h

**Supplemental Table 2.**

Gene ontology of proteins extracted from sperm cells of rats. Data obtained of UniprotKB ([www.uniprot.org](http://www.uniprot.org)).

Name protein	ID	Gene	Genetic ontology		
			Molecular function	Biological process	Cellular compartment
Tubulin beta-4B chain	Q6P9T8	Tubb4b	GTPase activity; GTP binding; structural constituent of cytoskeleton:	Microtubule-based process; microtubule cytoskeleton organization ; mitotic cell cycle	Cytoplasm, cytoskeleton, microtubule
ATP synthase subunit beta	G3V6D3	Atp5flb	Angiostatin binding; sATP binding; MHC class I protein binding; proton-transporting ATPase activity, rotational mechanism; proton-transporting ATP synthase activity, rotational mechanism	Angiogenesis; ATP synthesis coupled proton transport; cellular response to interleukin-7; lipid metabolic process; negative regulation of cell adhesion involved in substrate-bound cell migration; positive regulation of blood vessel endothelial cell migration; regulation of intracellular pH	Mitochondrion; mitochondrial nucleoid; mitochondrial; proton-transporting ATP synthase complex; plasma membrane; cell surface; proton-transporting; ATP synthase complex, catalytic core F(1)
Cytochrome c, testis-specific	P10715	Cyct	Electron transfer activity Source:; binding; metal ion binding	Apoptotic process; mitochondrial electron transport, cytochrome c to oxygen; mitochondrial electron transport, ubiquinol to cytochrome c	Mitochondrion,mitochondrial intermembrane; respirasome
Outer dense fiber protein 2	A0A0H2UHM 4	Odf2	--	--	--
Mitochondria-eating protein	A0A0H2UHA 4	Spata18	--	Cellular response to DNA damage stimulus; mitochondrial protein catabolic process, mitophagy by induced vacuole	Mitochondrion; mitochondrial outer membrane

				formation	
Phosphatidylethanolamine-binding protein 1	P31044	Pebp1	ATP binding; kinase binding; lipid binding; mitogen-activated protein kinase binding; protein kinase binding; receptor serine/threonine kinase binding; serine-type endopeptidase inhibitor activity; signaling receptor binding	Aging; eating behavior; hippocampus development; MAPK cascade; negative regulation of MAPK cascade negative regulation of protein phosphorylation; positive regulation of acetylcholine metabolic process; positive regulation of cAMP-mediated signaling; positive regulation of mitotic nuclear division; regulation of neurotransmitter levels; regulation of the force of heart contraction response to activity; response to calcium ion; response to cAMP; response to corticosterone; response to drug; response to electrical stimulus; response to ethanol; response to heat; response to organic cyclic compound; response to organic substance; response to organonitrogen compound response to oxidative stress; response to toxic substance; response to wounding; spermatid development ; sperm capacitation	Cytoplasm; membrane; peripheral membrane protein
Cytochrome c oxidase subunit 5A, mitochondrial	P11240	Cox5a	Cytochrome-c oxidase activity; metal ion binding	Mitochondrial electron transport, cytochrome c to oxygen	Mitochondrion; mitochondrion inner membrane
Globin a4	A0A0G2JSW3	Hbb	Heme binding; Metal ion binding; oxygen binding; oxygen carrier activity	Oxygen transport; transport; heme; iron; metal-binding	Cytosol; hemoglobin complex
Hemoglobin subunit alpha-1/2	P01946	Hba1	Amyloid-beta binding; heme binding; iron ion binding;	Cellular oxidant detoxification; hydrogen peroxide catabolic process; negative regulation of blood pressure; protein	Cytosol; hemoglobin complex; haptoglobin-hemoglobin complex;

			organic acid binding; oxygen binding; oxygen carrier activity	heterooligomerization; regulation of sensory perception of pain	synapse
Tubulin alpha-3 chain	Q68FR8	Tuba3a	GTPase activity; GTP binding; structural constituent of cytoskeleton	Microtubule-based process; microtubule cytoskeleton organization, mitotic cell cycle	Cytoskeleton; ciliary basal body; microtubule; cytoplasm
Sperm surface protein Sp17	Q9Z1K2	Spa17	Calmodulin binding	Binding of sperm to zona pellucida	Plasma Membrane; external side of plasma membrane; cilium; cytoplasm; sperm fibrous sheath; sperm principal piece
Malate dehydrogenase, mitochondrial	P04636	Mdh2	L-malate dehydrogenase activity; malate dehydrogenase (NADP+) activity; malate dehydrogenase activity; protein homodimerization activity; protein self-association	Carbohydrate metabolic process; internal protein amino acid acetylation; malate metabolic process; NADH metabolic process; oxaloacetate metabolic process; tricarboxylic acid cycle	Mitochondrion; mitochondrial matrix; mitochondrion; membrane
ATP synthase subunit delta, mitochondrial	G3V7Y3	Atp5fld	Proton-transporting ATP synthase activity, rotational mechanism	ATP synthesis coupled proton transport	Mitochondrion; mitochondrial proton-transporting ATP synthase complex; proton-transporting ATP synthase complex, catalytic core F(1)
Actin, cytoplasmic 1	A0A0G2K3K2	Actb	ATP binding; identical protein binding; kinesin binding; nitric-oxide synthase binding; protein	Cell motility; cellular response to cytochalasin B; negative regulation of protein binding; regulation of norepinephrine uptake; regulation of protein localization to plasma membrane;	Cytoskeleton; cortical cytoskeleton; postsynaptic actin cytoskeleton; cytosol; cytosol; Nucleus; nuA4 histone

			kinase binding; structural constituent of postsynaptic actin cytoskeleton; Tat protein binding	regulation of transmembrane transporter activity; synaptic vesicle endocytosis	acetyltransferase complex; calyx of Held; cytoplasmic ribonucleoprotein granule; glutamatergic synapse; schaffer collateral - CA1 synapse
Beta-defensin	Q99JD1	Defb22	--	Defense response to bacterium; innate immune response	Extracellular region or secreted
Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	P10888	Cox4i1	Cytochrome-c oxidase activity	Mitochondrial electron transport, cytochrome c to oxygen ; response to nutrient	Mitochondrion; mitochondrial respiratory chain complex IV; nucleus
Sperm acrosome-associated protein 9	Q4V8P4	Spaca9	Calcium-dependent protein binding	--	Cytoskeleton; ciliary basal body; cytoplasmic microtubule; nucleus; acrosomal vesicle; ciliary base; cytoplasm; sperm flagellum
Basigin	P26453	Bsg	Cell-cell adhesion mediator activity; mannose binding	Axon guidance; decidualization; dendrite self-avoidance; embryo implantation; homophilic cell adhesion via plasma membrane adhesion molecules; odontogenesis of dentin-containing tooth; protein localization to plasma membrane; response to cAMP; response to mercury ion; response to peptide hormone	Plasma membrane; single-pass type I membrane protein; melanosome
Calmodulin-1	P0DP29	Calm1	Adenylate cyclase activator activity; adenylate cyclase binding; calcium channel inhibitor activity; calcium channel regulator activity;	Activation of adenylate cyclase activity; calcium-mediated signaling; detection of calcium ion; establishment of protein localization to membrane; establishment of protein localization to mitochondrial membrane; G2/M transition of mitotic cell cycle; negative regulation of ryanodine-sensitive	Cytoskeleton; spindle; spindle pole

			calcium-dependent protein binding; calcium ion binding; disordered domain specific binding; ion channel binding; nitric-oxide synthase binding; nitric-oxide synthase regulator activity; N-terminal myristylation domain binding; phosphatidylinositol 3-kinase binding; protein domain specific binding; protein kinase binding; protein N-terminus binding; protein phosphatase activator activity; titin binding; type 3 metabotropic glutamate receptor binding	calcium-release channel activity; positive regulation by host of symbiont cAMP-mediated signal transduction; positive regulation of cyclic-nucleotide phosphodiesterase activity; positive regulation of DNA binding; positive regulation of nitric-oxide synthase activity; regulation of phosphoprotein phosphatase activity; positive regulation of ryanodine-sensitive calcium-release channel activity; regulation of cardiac muscle contraction; regulation of cytokinesis; regulation of heart rate; regulation of high voltage-gated calcium channel activity; regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum; regulation of ryanodine-sensitive calcium-release channel activity; regulation of store-operated calcium channel activity; regulation of synaptic vesicle endocytosis; regulation of synaptic vesicle exocytosis; response to amphetamine	
Succinyl-CoA:3-ketoacid coenzyme A transferase 2A, mitochondrial	Q5XIJ9	Oxct2a	3-oxoacid CoA-transferase activity	Ketone body catabolic process	Mitochondrion
Cytochrome b-c1 complex subunit 2, mitochondrial	P32551	Uqrc2	Metal ion binding; metalloendopeptidase activity; protein-containing complex	Oxidation-reduction process; protein processing involved in protein targeting to mitochondrion	Mitochondrion; mitochondrion inner membrane

			binding		
Citrate synthase	G3V936	Cs	Citrate (Si)-synthase activity	Carbohydrate metabolic process; tricarboxylic acid cycle	Mitochondrion; mitochondrial matrix
Keratin, type II cytoskeletal 5	A0A0G2K509	Krt5	Scaffold protein binding; structural molecule activity	--	Cytoskeleton; keratin filament; cytoplasm
Cytochrome c-1	D3ZFQ8	Cyc1	Electron transporter, transferring electrons within CoQH2-cytochrome c reductase complex activity; heme binding; metal ion binding	Mitochondrial ATP synthesis coupled proton transport; mitochondrial electron transport, ubiquinol to cytochrome c	Mitochondrion; mitochondrial respiratory chain complex III
Superoxide dismutase [Mn], mitochondrial	P07895	Sod2	DNA binding; enzyme binding; identical protein binding; manganese ion binding; metal ion binding; oxygen binding; superoxide dismutase activity	Acetylcholine-mediated vasodilation involved in regulation of systemic arterial blood pressure; age-dependent response to reactive oxygen species; aging; cellular response to ethanol; detection of oxygen; erythropoiesis; glutathione metabolic process; heart development; hemopoiesis; hydrogen peroxide biosynthetic; hydrogen peroxide metabolic process; intrinsic apoptotic signaling pathway in response to DNA damage; intrinsic apoptotic signaling pathway in response to oxidative stress; iron ion homeostasis; liver development; locomotory behavior; negative regulation of apoptotic process; negative regulation of fat cell differentiation; negative regulation of fibroblast proliferation; neuron development; positive regulation of nitric oxide biosynthetic process; post-	Mitochondrion; mitochondrial matrix

				embryonic development; protein homooligomerization; regulation of catalytic activity; regulation of mitochondrial membrane potential; regulation of transcription by RNA polymerase II; release of cytochrome c from mitochondria; removal of superoxide radicals; respiratory electron transport chain; response to activity; response to axon injury; response to cadmium ion; response to cold; response to drug; response to electrical stimulus; response to gamma radiation; response to hydrogen peroxide; response to hiperoxia; response to hipoxia; response to immobilization stress; response to isolation stress; response to L-ascorbic acid; response to lipopolysaccharide; response to magnetism; response to manganese ion; response to nutrient levels; response to oxidative stress; response to radiation; response to selenium ion; response to silicon dioxide; response to zinc ion; superoxide anion generation; superoxide metabolic process	
Fructose-bisphosphate aldolase	Q6AY07	Aldoart2	Fructose-bisphosphate aldolase activity	Glycolytic process	--
Isoaspartyl peptidase/L-asparaginase	Q8VI04	Asrgl1	Asparaginase activity; beta-aspartyl-peptidase activity; hydrolase activity	Asparagine catabolic process via L-aspartate; protein maturation	Cytoplasm Source; photoreceptor inner segment
Ropporin-1	Q4KLL5	Ropn1	--	Cilium organization; flagellated sperm motility; protein	Cytoplasm; sperm cytoplasmic droplet;

				localization to cilium; regulation of protein phosphorylation; sperm capacitation	sperm principal piece
Uncharacterized protein	F1LUD3	N/A	--	--	Costamere Source; cytoplasmic vesicle membrane; Z disc
Hypothetical LOC302884	M0R6G0	MGC105649	--	Response to bacterium	Nucleus
GLIPR1-like 1	D3ZI91	Glipr1ll	--	--	Extracellular region or secreted; extracellular space
Phosphoglycerate kinase	M0R6Y8	RGD1560402	ADP binding; ATP binding; phosphoglycerate kinase activity	Gluconeogenesis; glycolytic process; positive regulation of oxidative phosphorylation	Cytosol
Acrosin-binding protein	Q6AY33	Acrbp	--	--	Extracellular region or secreted; acrosomal membrane; acrosomal vesicle
Serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 16	G3V8X9	Serpina16	Serine-type endopeptidase inhibitor activity	Negative regulation of endopeptidase activity	Extracellular region or secreted
ATP synthase subunit d, mitochondrial	P31399	Atp5pd	Protein-containing complex binding; proton transmembrane transporter activity	ATP hydrolysis coupled cation transmembrane transport; ATP metabolic process; ATP synthesis coupled proton transport; cellular response to peptide	Mitochondrion; mitochondrial proton-transporting ATP synthase complex; mitochondrial proton-transferring ATP synthase complex, coupling factor F(o); mitochondrial proton-transferring ATP synthase, stator stalk

Anionic trypsin-1	P00762	Prss1	Metal ion binding; serine-type endopeptidase activity	Digestion; proteolysis; response to caffeine; response to nicotine; response to nutrient; response to organic substance	Extracellular region or secreted
Calcium-binding tyrosine phosphorylation-regulated	M0R8P3	Cabyr	Calcium ion binding	Sperm capacitation	Cytosol, nucleus; sperm fibrous sheath
Phosphoglycerate mutase 2	P16290	Pgam2	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase activity; bisphosphoglycerate mutase activity; cofactor binding; hydrolase activity; phosphoglycerate mutase activity	Gluconeogenesis; glycolytic process; Notch signaling pathway; response to inorganic substance; response to mercury ion; spermatogenesis; striated muscle contraction	Cytosol; nucleus
Alpha-amylase	E9PSQ1	Amy1a	Alpha-amylase activity; alpha-amylase activity (releasing maltohexaose); cation binding	Carbohydrate metabolic process; response to bacterium	Extracellular region or secreted
Protein MENT	Q5XI62	Ment	--	Regulation of cell population proliferation	Extracellular region or secreted
Cytochrome c oxidase subunit 5B, mitochondrial	P12075	Cox5b	Cytochrome-c oxidase activity; metal ion binding	Mitochondrial ATP synthesis coupled proton transport; mitochondrial electron transport, cytochrome c to oxygen; response to hormone; response to peptide hormone	Mitochondrion; mitochondrial inner membrane
Peroxiredoxin-like 2A	Q6AXX6	Prxl2a	Antioxidant activity	Oxidation-reduction process; regulation of osteoclast differentiation	Extracellular region or secreted; cytoplasm
Zona pellucida binding protein, isoform CRA_b	Q6AXU2	Zpbp	--	Binding of sperm to zona pellucida	Extracellular region or secreted; integral component of membrane

Slc25a17 protein	B2GUY8	Slc25a17	ADP transmembrane transporter activity; AMP transmembrane transporter activity; ATP transmembrane transporter activity; chaperone binding; coenzyme A transmembrane transporter activity; FAD transmembrane transporter activity; transmembrane transporter activity; NAD transmembrane transporter activity	Fatty acid beta-oxidation; fatty acid transport	Peroxisome; integral component of peroxisomal membrane
Saccharopine dehydrogenase-like oxidoreductase	Q6AY30	Sccpdh	Oxidoreductase activity	Glycolipid biosynthetic process	Mitochondrion;; plasma membrane; lipid droplet
Alpha-L-fucosidase	A0A0G2JSJ8	Fucal	Alpha-L-fucosidase activity	Fucose metabolic process; glycoside catabolic process	--
Dihydrolipoyl dehydrogenase, mitochondrial	Q6P6R2	Dld	dihydrolipoyl dehydrogenase activity; electron transfer activity; flavin adenine dinucleotide binding; lipoamide binding; NAD binding; pyruvate dehydrogenase (NAD+) activity	2-oxoglutarate metabolic process; acetyl-CoA biosynthetic process from pyruvate; aging; cell redox homeostasis; dihydrolipoamide metabolic; gastrulation; histone succinylation; lipoate metabolic process; mitochondrial electron transport, NADH to ubiquinone; proteolysis; regulation of membrane potential; sperm capacitation	Mitochondrion; mitochondrial matrix; mitochondrion;nucleus; nucleoplasm; nucleus; acrosomal matrix; motile cilium; oxoglutarate dehydrogenase complex; pyruvate dehydrogenase complex
5'-nucleotidase, cytosolic IB	A0A0G2JX78	Nt5c1b	5'-nucleotidase activity;	Adenosine metabolic process; nucleotide metabolic process	Cytosol

			magnesium ion binding; nucleotide binding		
Solute carrier family 2 (Facilitated glucose transporter), member 3	A0A0G2JSJ3	Slc2a3	Glucose transmembrane transporter activity	--	Integral component of membrane
14-3-3 protein zeta/delta	A0A0G2JV65	Ywhaz	Protein domain specific binding	Protein targeting; regulation of cell death; synaptic target recognition	Nucleus; hippocampal mossy fiber to CA3 synapse
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial	B2RYS8	Ndufb8	NADH dehydrogenase (ubiquinone) activity	Mitochondrial electron transport, NADH to ubiquinone	Mitochondrion; mitochondrion inner membrane
Fatty acid-binding protein 9	P55054	Fabp9	Lipid binding	Acrosome assembly	Acrosomal vesicle
Protein/nucleic acid deglycase DJ-1	O88767	Park7	Androgen receptor binding; copper ion binding; cupric ion binding; cuprous ion binding; cytokine binding; L-dopa decarboxylase activator activity; mercury ion binding; mRNA binding; peptidase activity; protein deglycase activity; protein homodimerization activity; repressing transcription	Aging; autophagy; cellular response to glyoxal; cellular response to hydrogen peroxide; cellular response to lipopolysaccharide; cellular response to oxidative stress; detoxification of copper ion; detoxification of mercury ion; DNA repair; fertilization; glucose homeostasis; glycolate biosynthetic process; guanine deglycation; guanine deglycation, glyoxal removal; guanine deglycation, methylglyoxal removal; hydrogen peroxide metabolic process; inflammatory response; insulin secretion; maternal process involved in female pregnancy; mitochondrion organization;	Cytosol; extracellular region or secreted; extracellular exosome; mitochondrion; nucleus; PMLbody; plasma membrane; axón; cytoplasm; membrane raft; sperm head

		factor binding; scaffold protein binding; signaling receptor binding; small protein activating enzyme binding; superoxide dismutase copper chaperone activity; transcription coactivator activity; transcription factor binding; tyrosine 3-monoxygenase activator activity; ubiquitin-like protein conjugating enzyme binding	negative regulation of cell death; negative regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway; negative regulation of extrinsic apoptotic signaling pathway; negative regulation of neuron apoptotic process; negative regulation of neuron death; negative regulation of NMDA glutamate receptor activity; negative regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway; negative regulation of protein acetylation; negative regulation of protein binding; negative regulation of protein export from nucleus; negative regulation of protein K48-linked deubiquitination; negative regulation of protein kinase activity; negative regulation of protein phosphorylation; negative regulation of protein sumoylation; negative regulation of protein ubiquitination; negative regulation of reactive oxygen species biosynthetic process; negative regulation of TRAIL-activated apoptotic signaling pathway; negative regulation of ubiquitin-specific protease activity; positive regulation of acute inflammatory response to antigenic stimulus; positive regulation of androgen receptor activity; positive regulation of dopamine biosynthetic process; positive regulation of fertilization; positive regulation of interleukin-8 production; positive regulation of L-dopa biosynthetic process; positive regulation of L-dopa	
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				decarboxylase activity; positive regulation of mitochondrial electron transport, NADH to ubiquinone; positive regulation of NAD(P)H oxidase activity; positive regulation of oxidative phosphorylation uncoupler activity; positive regulation of protein homodimerization activity; positive regulation of protein localization to nucleus; positive regulation of pyrroline-5-carboxylate reductase activity; positive regulation of superoxide dismutase activity; positive regulation of transcription by RNA polymerase II; positive regulation of tyrosine 3-monooxygenase activity; protein deglycation, glyoxal removal; protein deglycosylation; protein stabilization; regulation of androgen receptor signaling pathway; regulation of inflammatory response; regulation of mitochondrial membrane potential; regulation of neuron apoptotic process; response to drug; response to oxidative stress; single fertilization; spermatogenesis	
LSM12 homolog	D4A8G0	Lsm12	--	RNA metabolic process	--
Protein polyglycylase TTLL10	A0A0G2JX96	Ttll10	--	Cellular protein modification process	--
Similar to RIKEN cDNA 4930540L03 (Predicted)	D3Z9F9	Spaca1	--	Acrosome assembly	Acrosomal membrane; integral component of membrane
Hyaluronidase PH-20	Q62803	Spam1	Hyalurononoglucosaminidase activity	Carbohydrate metabolic process; cell adhesión; fusion of sperm to egg plasma membrane involved in single fertilization	Plasma membrane; anchored component of membrane

Adenylate cyclase	G3V9G1	Adcy5	Adenylate cyclase activity; adenylate cyclase binding; ATP binding; metal ion binding; protein heterodimerization activity; scaffold protein binding	Adenosine receptor signaling pathway; adenylate cyclase-activating dopamine receptor signaling pathway; adenylate cyclase-inhibiting dopamine receptor signaling pathway; cAMP biosynthetic process; cellular response to forskolin; locomotory behavior; neuromuscular process controlling balance; positive regulation of cytosolic calcium ion concentration; regulation of insulin secretion involved in cellular response to glucose stimulus	Cytoskeleton; intermediate filament cytoskeleton; plasma membrane; cilium; integral component of membrane
Tubulin alpha-1A chain	P68370	Tuba1a	GTPase activity; GTP binding; protein domain specific binding; protein heterodimerization activity; structural constituent of cytoskeleton	Microtubule-based; microtubule cytoskeleton organization; mitotic cell cycle; regulation of synapse organization	Cytoskeleton; cytoplasmic microtubule; microtubule; endosome; recycling endosome; cytoplasm; cytoplasmic ribonucleoprotein granule; membrane raft; myelin sheath; neuromuscular junction
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	A0A0G2KAM	Pdhb	Pyruvate dehydrogenase (NAD <sup>+</sup> ) activity	Tricarboxylic acid cycle	Mitochondrion; nucleus; nucleoplasm; pyruvate dehydrogenase complex
L-lactate dehydrogenase	Q6AYX2	Ldhc	L-lactate dehydrogenase activity	ATP biosynthetic process; carbohydrate metabolic process; flagellated sperm motility; lactate biosynthetic process from pyruvate; lactate oxidation	Cytoplasm; motile cilium
ATP synthase subunit alpha, mitochondrial	P15999	Atp5f1a	ADP binding; ATP binding; protease binding; proton-	Aging; apoptotic process; ATP biosynthetic process; ATP metabolic process; ATP synthesis coupled proton transport;	Mitochondrion; inner membrane; mitochondrial proton-transporting ATP

			transporting ATP synthase activity, rotational mechanism	cellular response to dexamethasone stimulus; cellular response to nitric oxide; electron transport chain; response to ethanol; response to muscle activity; response to oxidative stress	synthase complex; mitochondrial proton-transferring ATP synthase complex, catalytic core F(1); nucleus; plasma membrane; cell surface; membrane raft
Acrosin	A0A0G2K321	Acr	Serine-type endopeptidase activity	--	Acrosomal vesicle
Epididymal-specific lipocalin-5	P06911	Lcn5	Small molecule binding	--	Extracellular region or secreted
Carnitine O-acetyltransferase	A0A0H2UI21	Crat	Carnitine O-acetyltransferase activity; signaling receptor binding	Carnitine metabolic process, CoA-linked	Mitochondrion; peroxisome
Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	A0A0H2UHE1	Suclg1	Cofactor binding; nucleotide binding; succinate-CoA ligase (ADP-forming) activity; succinate-CoA ligase (GDP-forming) activity	Tricarboxylic acid cycle	Cytosol; mitochondrion; plasma membrane
CD177 antigen-like	M0R4W1	LOC100909620	--	--	--
NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	P19234	Ndufv2	2 iron, 2 sulfur cluster binding; metal ion binding; NADH dehydrogenase (ubiquinone) activity	Cardiac muscle tissue development; mitochondrial electron transport, NADH to ubiquinone; nervous system development	Mitochondrion; mitochondrial respiratory chain complex I

Ras-related protein Rab-2A	F1LP82	Rab2a	GDP binding; GTPase activity; GTP binding	Golgi organization	Golgi apparatus
Cytochrome c oxidase subunit 2	P00406	Mtco2	Copper ion binding; cytochrome-c oxidase activity	ATP synthesis coupled electron transport; lactation; positive regulation of ATP biosynthetic process; positive regulation of hydrogen peroxide biosynthetic process; positive regulation of necrotic cell death; response to cold	Mitochondrion; mitochondrial inner membrane; integral component of membrane; respiratory chain complex IV
Serum albumin	A0A0G2JSH5	Alb	Chaperone binding; DNA binding; exogenous protein binding; fatty acid binding; identical protein binding; metal ion binding; oxygen binding; pyridoxal phosphate binding; toxic substance binding	Cellular response to starvation; maintenance of mitochondrion location; negative regulation of apoptotic process; negative regulation of protein oligomerization	Endoplasmic reticulum; extracellular region or secreted; extracellular exosome; golgi apparatus; protein-containing complex
60 kDa heat shock protein, mitochondrial	P63039	Hspd1	ATP binding; hydrolase activity; insulin binding; lipopolysaccharide binding; modification-dependent protein binding; protease binding; protein-containing complex binding; protein heterodimerization activity; unfolded protein binding	'de novo' protein folding; apoptotic mitochondrial changes; cellular response to heat; cellular response to interleukin-7; mitochondrion organization; negative regulation of apoptotic process; negative regulation of apoptotic process in bone marrow cell; negative regulation of neuron apoptotic process; negative regulation of reactive oxygen species biosynthetic process; positive regulation of inflammatory response; positive regulation of interferon-alpha production; positive regulation of interferon-gamma production; positive	Cytosol; endoplasmic reticulum; rough endoplasmic reticulum; extracellular region or secreted; golgi apparatus; mitochondrion crista; mitochondrial inner membrane; mitochondrial matrix; peroxisome; peroxisomal matrix; plasma membrane; cell Surface; cytoplasm; membrane raft; protein-containing complex; secretory granule;

				regulation of interleukin-6 secretion; positive regulation of T cell activation; positive regulation of tumor necrosis factor secretion; protein import into mitochondrial intermembrane space; protein refolding; response to activity; response to ATP; response to cocaine; response to cold; response to drug; response to estrogen; response to glucocorticoid; response to heat; response to hydrogen peroxide; response to hypoxia; response to ischemia; response to lipopolysaccharide; response to organic cyclic compound; response to organic substance; T cell activation	zymogen granule
Dynein light chain 2, cytoplasmic	Q78P75	Dynll2	Dynein intermediate chain binding; dynein light intermediate chain binding; motor activity; protein heterodimerization activity; protein homodimerization activity; scaffold protein binding	microtubule-based process; positive regulation of ATP-dependent microtubule motor activity, plus-end-directed	Cytoskeleton; centrosome; cytoplasmic dynein complex; dynein complex; microtubule; myosin V complex; cytoplasm; glutamatergic synapse; postsynaptic density
Uncharacterized protein	F1MAE5	Prp211	--	--	Integral component of membrane
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	P08461	Dlat	Dihydrolipoyllysine-residue acetyltransferase activity; identical protein binding; nucleotide binding; pyruvate	Acetyl-CoA biosynthetic process from pyruvate; glucose metabolic process; sleep; tricarboxylic acid cycle	Mitochondrion; mitochondrial matrix; pyruvate dehydrogenase complex

			dehydrogenase (NAD+) activity		
Lysozyme c	F1M6E7	Spaca3	Lysozyme activity	Defense response to Gram-negative bacterium; defense response to Gram-positive bacterium; fusion of sperm to egg plasma membrane involved in single fertilization	Acrosomal matrix; acrosomal membrane
Heat shock 70 kDa protein 1-like	P55063	Hspall	ATPase activity; ATPase activity, coupled; ATP binding; heat shock protein binding; misfolded protein binding; protein folding chaperone; unfolded protein binding	Cellular response to heat; cellular response to unfolded protein; chaperone cofactor-dependent protein refolding; protein refolding; response to unfolded protein	Cytosol; mitochondrial matrix; mitochondrion; cytoplasm
Superoxide dismutase [Cu-Zn]	P07632	Sod1	Chaperone binding; copper ion binding; enzyme binding; identical protein binding; protein phosphatase 2B binding; Rac GTPase binding; superoxide dismutase activity; superoxide dismutase copper chaperone activity; zinc ion binding	Activation of MAPK activity; anterograde axonal transport; auditory receptor cell stereocilium organization; cell aging; cellular iron ion homeostasis; cellular response to ATP; cellular response to cadmium ion; cellular response to oxidative stress; cellular response to potassium ion; embryo implantation; glutathione metabolic process; heart contraction; hydrogen peroxide biosynthetic process; locomotory behavior; muscle cell cellular homeostasis; myeloid cell homeostasis; negative regulation of apoptotic process; negative regulation of cholesterol biosynthetic process; negative regulation of inflammatory response; negative regulation of neuron apoptotic process; neurofilament cytoskeleton organization;	Cytosol; extracellular region or secreted; extracellular space; lysosome; mitochondrion; mitochondrial intermembrane space; nucleus; nucleoplasm; peroxisome; plasma membrane; axon cytoplasm; cytoplasm; cytoplasmic vesicle; dendrite; dense core granule; neuron projection; neuronal cell body; protein-containing complex; secretory granule

				ovarian follicle development; peripheral nervous system myelin maintenance; positive regulation of catalytic activity; positive regulation of cytokine production; positive regulation of oxidative stress-induced intrinsic apoptotic signaling pathway; positive regulation of phagocytosis; positive regulation of superoxide anion generation; reactive oxygen species metabolic process; regulation of blood pressure; regulation of GTPase activity; regulation of mitochondrial membrane potential; regulation of multicellular organism growth; regulation of protein kinase activity; relaxation of vascular smooth muscle; removal of superoxide radicals; response to amphetamine; response to antibiotic; response to antipsychotic drug; response to axon injury; response to carbon monoxide; response to copper ion; response to drug; response to ethanol; response to heat; response to hydrogen peroxide; response to nutrient levels; response to organic substance; response to oxidative stress; response to superoxide; retina homeostasis; retrograde axonal transport; sensory perception of sound; spermatogenesis; superoxide anion generation; superoxide metabolic process; transmission of nerve impulse	
Inositol-1-monophosphatase	F1M978	Impa1	Inositol monophosphate 1-phosphatase activity; inositol	Inositol biosynthetic process; inositol phosphate dephosphorylation; phosphatidylinositol biosynthetic;	Cytoplasm

			monophosphate 3-phosphatase activity; inositol monophosphate 4-phosphatase activity; lithium ion binding; magnesium ion binding; manganese ion binding; protein homodimerization activity	phosphatidylinositol phosphorylation; signal transduction	
Cytochrome c oxidase subunit 6B2	Q6YFQ1	Cox6b2	--	--	Mitochondrion; mitochondrial crista
RCG44470	D3ZVR6	Slf1	Protein-containing complex binding; ubiquitin protein ligase binding	Cellular response to DNA damage stimulus; positive regulation of double-strand break repair; positive regulation of maintenance of mitotic sister chromatid cohesion; positive regulation of protein complex assembly; protein localization to site of double-strand break	Cytoskeleton; centrosome; nucleus; nuclear inclusion body; cytoplasm; nucleosome; site of double-strand break
Tubulin beta chain	G3V7C6	Tubb4b	Double-stranded RNA binding; GTPase activity; GTP binding; structural constituent of cytoskeleton	Microtubule-based process	Cytoskeleton; microtubule; cytoplasm
Tubulin alpha-8 chain	Q6AY56	Tuba8	GTPase activity; GTP binding; structural constituent of cytoskeleton	Microtubule-based process; microtubule cytoskeleton organization; mitotic cell cycle S	Cytoskeleton; microtubule; cytoplasm
Carnitine O-acetyltransferase	Q704S8	Crat	Carnitine O-acetyltransferase	Carnitine metabolic process, CoA-linked; fatty acid metabolic	Endoplasmic reticulum; mitochondrial

			activity	process	inner membrane; mitochondrion; peroxisome
Phosphoglycerate kinase	Q5XIV1	Pgk2	ADP binding; ATP binding; phosphoglycerate kinase activity	flagellated sperm motility; gluconeogenesis; glycolytic process; positive regulation of oxidative phosphorylation	Cytosol; sperm fibrous sheath
Hexokinase-1	P05708	Hk1	ATPase activity; ATP binding; fructokinase activity; glucokinase activity; glucose binding; hexokinase activity; mannokinase activity; protein-containing complex binding; protein homodimerization activity; protein kinase activity	Carbohydrate phosphorylation; cellular glucose homeostasis; glycolytic process; hexose metabolic process; negative regulation of apoptotic process; peptidyl-serine phosphorylation; peptidyl-threonine phosphorylation; peptidyl-tyrosine phosphorylation; protein autophosphorylation; protein phosphorylation; regulation of anion channel activity; response to brassinosteroid; response to hypoxia; response to ischemia; response to ketamine	Cytosol; mitochondrial outer membrane; mitochondrion; plasma membrane; caveola; protein-containing complex
Globin c2	A0A0G2JSV6	Hba-a2	Heme binding; iron ion binding; organic acid binding; oxygen binding; oxygen carrier activity	Cellular oxidant detoxification; hydrogen peroxide catabolic process; protein heterooligomerization; response to estradiol	Cytosol; hemoglobin complex; haptoglobin-hemoglobin complex
Izumo sperm-egg fusion protein 1	Q6AY06	Izumo1	Protein binding involved in heterotypic cell-cell adhesion; protein homodimerization activity; signaling receptor binding	Fusion of sperm to egg plasma membrane involved in single fertilization; heterotypic cell-cell adhesion; single fertilization; sperm-egg recognition	Plasma membrane; acrosomal membrane; integral component of membrane
Keratin, type II cytoskeletal 73	A0A0G2JXH6	Krt73	--	--	Cytoskeleton; keratin filament
Fibrous sheath CABYR-	Q4V7A4	Fscb	--	Negative regulation of protein sumoylation	Motile cilium

binding protein					
Fructose-bisphosphate aldolase A	P05065	Aldoa	Fructose-bisphosphate aldolase activity	Glycolytic; methylglyoxal biosynthetic process; protein homotetramerization; response to estrogen; response to heat; response to hipoxia; response to lipopolysaccharide; response to nicotine	Mitochondrion; nucleus; nuclear heterochromatin; cytoplasm; I band; M band
Equatorin	Q2LCV6	Eqtn	--	Acrosomal vesicle exocytosis; endocitosis; fusion of sperm to egg plasma membrane involved in single fertilization	Plasma membrane; acrosomal membrane; inner acrosomal membrane; integral component of membrane; outer acrosomal membrane
Translation initiation factor eIF-2B subunit beta	F7EVX2	Eif2b2	ATP binding; GTP binding; guanyl-nucleotide exchange factor activity; translation initiation factor activity	Myelination; oligodendrocyte development; ovarian follicle development; T cell receptor signaling pathway	Eukaryotic translation initiation factor 2B complex
Tensin 3	F1LN91	Tns3	Metal ion binding	Cell migration; intracellular signal transduction; lung alveolus development; positive regulation of cell population proliferation	Cytosol; ocal adhesion
Outer dense fiber protein 2	Q6AYX5-5	Odf2	--	Centriole-centriole cohesion; cilium organization; multicellular organism; protein localization; spermatid development	Cytoskeleton; centriole; centrosome; microtubule; outer dense fiber; spindle pole; centriolar subdistal appendage; ciliary transition fiber
Fc fragment of IgG-binding protein	D3ZJF8	Fcgbp	--	--	Extracellular region or secreted

Hemoglobin subunit beta-2	P11517	N/A	Heme binding; hemoglobin alpha binding; metal ion binding; organic acid binding; oxygen binding; oxygen carrier activity	Cellular oxidant detoxificationhydrogen peroxide catabolic process; protein heterooligomerization	Cytosol; hemoglobin complex
Arylsulfatase A	Q32KK2	Arsa	Arylsulfatase activity; cerebroside-sulfatase activity	Autophagy; binding of sperm to zona pellucida; central nervous system development; response to estrogen; response to ethanol; response to methylmercury; response to nutrient; response to pH	Endosome; extracellular region or secreted; lysosome; plasma membrane; extrinsic component of external side of plasma membrane; acrosomal vesicle; cytoplasm; integral component of membrane
ATP synthase subunit O, mitochondrial	Q06647	Atp5po	Protein-containing complex binding; proton-transporting; ATP synthase activity, rotational mechanism; steroid binding	ATP metabolic process; ATP synthesis coupled proton transport	Mitochondrion; mitochondrial proton-transporting ATP synthase complex; mitochondrial proton-transporting ATP synthase complex, coupling factor F(o)
Tektin-2	Q6AYM2	Tekt2	--	Cilium assembly; cilium movement involved in cell motility; flagellated sperm motility; inner dynein arm assembly	Cytoskeleton; microtubule; microtubule organizing center; cytoplasm; sperm flagellum
10 kDa heat shock protein, mitochondrial	A0A0G2JTG1	Hspel	ATP binding	Protein folding	Cytoplasm
Cytochrome b-c1 complex subunit 7	B2RYS2	Uqcrb	Protein-containing complex binding	Aerobic respiration; mitochondrial electron transport, ubiquinol to cytochrome c; mitochondrial respiratory chain complex III assembly; protein heterooligomerization	Mitochondrion; mitochondrial respiratory chain complex III

Serine/threonine-protein phosphatase	A0A0G2JVK2	Ppp1cc	Metal ion binding; protein serine/threonine phosphatase activity	--		Protein phosphatase type 1 complex
Nuclear receptor interacting protein 3 (Predicted), isoform CRA_a	D4A2K5	Nrip3	Aspartic-type endopeptidase activity	--	--	
ATP synthase F(0) complex subunit B1, mitochondrial	P19511	Atp5pb	Protein-containing complex binding; proton transmembrane transporter activity	ATP hydrolysis coupled cation transmembrane transport; ATP metabolic process; ATP synthesis coupled proton transport; cellular response to hypoxia	Mitochondrion; mitochondrial proton-transporting ATP synthase complex	mitochondrial proton-transferring ATP synthase complex, coupling factor F(o)
Uncharacterized protein	F1LZC5	N/A	--	--	--	
Vomeronasal type-2 receptor 116-like	A0A0G2JY7	LOC108348133	G protein-coupled receptor activity	--	Plasma membrane; integral component of membrane	
RCG22622	M0RAK2	LOC684270	Catalytic activity	--	Cytoplasm	
Tubulin beta chain	Q4QQV0	Tubb6	GTPase activity; GTP binding; structural constituent of cytoskeleton	Microtubule-based process; microtubule cytoskeleton organization; mitotic cell cycle	Cytoskeleton; microtubule; cytoplasm	
Outer dense fiber of sperm tails 2, isoform CRA_e	G3V7X0	Odf2	--	--	--	
Uncharacterized protein	M0R5J4	N/A	Magnesium ion binding; phosphopyruvate hydratase activity	Glycolytic process	Cytosol	

ATP synthase subunit alpha	F1LP05	Atp5fla	ATP binding; proton-transporting ATP synthase activity, rotational mechanism	ATP synthesis coupled proton transport; lipid metabolic process	Mitochondrion; proton-transporting ATP synthase complex, catalytic core F(1)	
Glyceraldehyde-3-phosphate dehydrogenase	B1WBQ8	Gapdhs	Glyceraldehyde-3-phosphate dehydrogenase (NAD <sup>+</sup> ) (phosphorylating) activity; NAD binding; NADP binding	glucose metabolic process; glycolytic process	--	
Glutathione peroxidase	A0A0G2K398	Gpx4	Glutathione peroxidase activity	Response to oxidative stress	--	
E3 ubiquitin-protein ligase RNF181	Q6AXU4	Rnf181	Metal ion binding; ubiquitin protein ligase activity	Protein autoubiquitination; protein ubiquitination	--	
Adenylate kinase isoenzyme 1	P39069	Ak1	Adenylate kinase activity; ATP binding; nucleoside diphosphate kinase activity	Adenine metabolic process; ADP biosynthetic process; AMP metabolic process; ATP metabolic process; cerebellum development; inosine biosynthetic process; muscle organ development; neuron differentiation; nucleoside diphosphate phosphorylation; nucleoside triphosphate biosynthetic process; olfactory bulb development; positive regulation of glucose transmembrane transpor; positive regulation of neuron maturation; response to activity; response to drug; response to estradiol; response to testosterone	Neuron projection; perinuclear region of cytoplasm; sarcomere	
Carnitine palmitoyltransferase 2, mitochondrial	O-2,	G3V7N5	Cpt2	Transferase activity, transferring acyl groups	Positive regulation of cold-induced thermogenesis	Mitochondrion; nucleolus; nucleoplasm

Adenylate kinase 2, mitochondrial	A0A0G2JSG6	Ak2	Adenylate kinase activity; ATP binding	ADP biosynthetic process; AMP metabolic process; ATP metabolic process	Mitochondrial intermembrane space; sperm mitochondrial sheath
Uncharacterized protein	D3ZE63	N/A	--	--	--
CDGSH iron-sulfur domain-containing protein 1	B0K020	Cisd1	2 iron, 2 sulfur cluster binding; identical protein binding ; metal ion binding	Regulation of cellular respiration	Mitochondrion; cytoplasmic side of mitochondrial outer membrane; integral component of membrane
3-hydroxyisobutyrate dehydrogenase, mitochondrial	P29266	Hibadh	3-hydroxyisobutyrate dehydrogenase activity; NAD binding; NADP binding; oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	Valine catabolic process	Mitochondrion
Axonemal dynein light intermediate polypeptide 1	Q4FZV3	Dnali1	Dynein heavy chain binding; motor activity	Inner dynein arm assembly	Cytoskeleton; axoneme; dynein complex; 9+2 motile cilium; cytoplasm; filopodium
ATP synthase-coupling factor 6, mitochondrial	P21571	Atp5pf	ATPase activity; protein-containing complex binding; proton transmembrane transporter activity	ATP metabolic process; ATP synthesis coupled proton transport; negative regulation of arachidonic acid secretion; negative regulation of prostaglandin secretion; positive regulation of blood pressure; positive regulation of heart rate; response to muscle activity	Extracellular region or secreted extracellular space; mitochondrion; mitochondrial proton-transporting ATP synthase complex; mitochondrial proton-transferring ATP synthase complex, coupling factor F(o); cell surface

Tripartite motif-containing 33	D3ZUK4	Trim33	co-SMAD binding; R-SMAD binding; zinc ion binding	Negative regulation of BMP signaling pathway; protein ubiquitination; regulation of transforming growth factor beta receptor signaling pathway	Nucleus
cAMP-dependent protein kinase type II-alpha regulatory subunit	P12368	Prkar2a	3',5'-cyclic-GMP phosphodiesterase activity; beta-2 adrenergic receptor binding; cAMP binding; cAMP-dependent protein kinase regulator activity; protein domain specific binding; protein homodimerization activity; protein kinase A catalytic subunit binding; small molecule binding	cGMP-mediated signaling; protein heterooligomerization; regulation of protein kinase activity; response to clozapine	Cytosol; plasma membrane T-tubule Source; cAMP-dependent protein kinase complex; cytoplasm; perinuclear region of cytoplasm; protein-containing complex
Histone H2A	M0RCL5	LOC100910554	DNA binding; protein heterodimerization activity	Chromatin organization	Nucleus; nuclear chromatin; nucleosome
Syntaxin-12	A0A0G2JVB6	Stx12	SNAP receptor activity	Autophagosome assembly; cholesterol efflux; intracellular protein transport; protein stabilization; vesicle-mediated transport	Cytosol; BLOC-1 complex; membrane raft; phagocytic vesicle; phagophore assembly site; SNARE complex
Signal-regulatory protein beta 3	A0A0G2JTD2	Sirpb3	--	--	Plasma membrane
Hexokinase-1	M0RAQ6	Hk1	ATP binding; glucose binding; hexokinase activity; identical	Cellular glucose homeostasis; establishment of protein localization to mitochondrion; glycolytic process;	Cytosol; mitochondrion; membrane raft

			protein binding; peptidoglycan binding	maintenance of protein location in mitochondrion; positive regulation of cytokine secretion involved in immune response; positive regulation of interleukin-1 beta secretion	
Beta-globin	A0A0G2JTW9	Hbb-b1	Heme binding; metal ion binding; oxygen binding; oxygen carrier activity	--	Cytosol; hemoglobin complex
Nuclear pore complex protein Nup85	Q4QQS8	Nup85	Structural constituent of nuclear pore	Lamellipodium assembly; macrophage chemotaxis; mRNA export from nucleus; positive regulation of transcription, DNA-templated; protein import into nucleus	Cytoskeleton; spindle; cytosol; nucleus; nuclear membrane; nuclear pore outer ring; condensed chromosome kinetochore
Heat shock 70 kDa protein 1A	P0DMW0	Hsp1a	ATPase activity; ATPase activity, coupled; ATP binding; heat shock protein binding; misfolded protein binding; protein folding chaperone; transcription corepressor activity; ubiquitin protein ligase binding; unfolded protein binding	Cellular response to heat; cellular response to unfolded protein; chaperone cofactor-dependent protein refolding; mRNA catabolic process; negative regulation of cell death; negative regulation of cell growth; negative regulation of cell population proliferation; negative regulation of transcription from RNA polymerase II promoter in response to stress; neuron differentiation; positive regulation of microtubule nucleation; positive regulation of neuron differentiation; positive regulation of proteasomal ubiquitin-dependent protein catabolic process; protein refolding; regulation of mitotic spindle assembly; response to etanol; response to ischemia; response to mechanical stimulus; response to radiation;	Cytoskeleton; centrosome; cytosol; nucleus; nuclear speck; nucleus; cytoplasm; membrane raft; perinuclear region of cytoplasm; protein-containing complex

				response to unfolded protein	
Uncharacterized protein	A0A0G2JUG1	N/A	Structural molecule activity	--	Cytoskeleton; keratin filament
Kazrin	Q5FWS6-2	Kazn	--	Keratinization	Cytoskeleton; nucleus; cell junction; cytoplasm
Septin-9	F1LN75	Sept9	GTP binding	Positive regulation of non-motile cilium assembly; protein heterooligomerization	Cytoskeleton; axoneme; microtubule ; septin complex; stress fiber; non-motile cilium; perinuclear region of cytoplasm
Long-chain-fatty-acid-CoA ligase 1	P18163	Acs1l	Acetate-CoA ligase activity; ATP binding; decanoate-CoA ligase activity; long-chain fatty acid-CoA ligase activity	Adiponectin-activated signaling pathway; fatty acid metabolic process; fatty acid transport; lipid metabolic process; long-chain fatty acid import into cell; long-chain fatty-acyl-CoA biosynthetic process; positive regulation of cold-induced thermogenesis; positive regulation of protein serine/threonine kinase activity; response to drug; response to nutrient; response to oleic acid; response to organic cyclic compound; response to organic substance; triglyceride biosynthetic process; xenobiotic catabolic process	Endoplasmic reticulum; reticulum membrane; mitochondrion; mitochondrial outer membrane; peroxisome; peroxisomal membrane; plasma membrane; integral component of membrane
A-kinase anchor protein 4	O35774	Akap4	Protein kinase A binding	Cell projection organization; flagellated sperm motility	--
Similar to chromosome 14 open reading frame 8 (Predicted)	D3ZCE7	Tppp2	Tubulin binding	Microtubule bundle formation; microtubule polymerization; positive regulation of protein polymerization	Cytosol
Clusterin	A0A0G2KB42	Clu	--	--	--
cAMP-dependent protein	A0A0G2K405	Prkar2a	cAMP binding; cAMP-	Negative regulation of cAMP-dependent protein kinase	Axoneme; centrosome; plasma

kinase type II-alpha regulatory subunit			dependent inhibitor activity; cAMP-dependent protein kinase regulator activity; protein domain specific binding; protein kinase A catalytic subunit binding; ubiquitin protein ligase binding	activity	membrane raft; cAMP-dependent protein kinase complex; nucleotide-activated protein kinase complex
Type II keratin Kb15	A0A0G2JVA8	Kb15	Structural molecule activity	--	Cytoskeleton; keratin filament
Transitional endoplasmic reticulum ATPase	P46462	Vcp	ADP binding; ATPase activity; ATP binding; BAT3 complex binding; deubiquitinase activator activity; identical protein binding; K48-linked polyubiquitin modification-dependent protein binding; lipid binding; MHC class I protein binding; polyubiquitin modification-dependent protein binding; protein-containing complex binding; protein domain specific binding; protein phosphatase binding; signaling	Activation of cysteine-type endopeptidase activity involved in apoptotic process; aggresome assembly; ATP metabolic process; autophagosome maturation; autophagy; cellular response to arsenite ion; cellular response to DNA damage stimulus; cellular response to heat; double-strand break repair; endoplasmic reticulum stress-induced pre-emptive quality control; endoplasmic reticulum to Golgi vesicle-mediated transport; endosome to lysosome transport via multivesicular body sorting pathway; ERAD pathway; ER-associated misfolded protein catabolic process; flavin adenine dinucleotide catabolic process; macroautophagy; itotic spindle disassembly; NADH metabolic process; positive regulation of ATP biosynthetic process; positive regulation of canonical Wnt signaling pathway; positive regulation of Lys63-specific	Cytosol; endoplasmic reticulum; derlin-1 retrotranslocation complex; endoplasmic; VCP-NPL4-UFD1 AAA ATPase complex; nucleus; nucleoplasm; ATPase complex; cytoplasm; cytoplasmic stress granule; glutamatergic synapse; intracellular membrane-bounded organelle; lipid droplet; perinuclear region of cytoplasm; proteasome complex; site of double-strand break; VCP-NSFL1C complex

			receptor binding; ubiquitin-protein ligase binding; ubiquitin-specific protease binding	deubiquitinase activity; positive regulation of mitochondrial membrane potential; positive regulation of oxidative phosphorylation; positive regulation of proteasomal ubiquitin-dependent protein catabolic process; positive regulation of protein complex assembly; proteasomal protein catabolic process; proteasome-mediated ubiquitin-dependent protein catabolic process; protein hexamerization; protein homooligomerization; protein N-linked glycosylation via asparagine; protein ubiquitination; regulation of aerobic respiration; regulation of synapse organization; retrograde protein transport, ER to cytosol; stress granule disassembly; translesion synthesis; ubiquitin-dependent ERAD pathway; viral genome replication	
Aspartyl aminopeptidase	Q4V8H5	Dnpep	Metalloaminopeptidase activity; zinc ion binding	--	Cytosol; extracellular region or secreted; cytoplasm
Ubiquitin-40S ribosomal protein S27a	P62982	Rps27a	Metal ion binding; protein tag; structural constituent of ribosome; ubiquitin protein ligase binding	Modification-dependent protein catabolic process; protein ubiquitination; translation	Cytosol; cytosolic small ribosomal subunit; nucleus; cytoplasm
Glucose-6-phosphate isomerase	Q6P6V0	Gpi	Cytokine activity; glucose-6-phosphate isomerase activity; growth factor activity;	Aldehyde catabolic process; carbohydrate metabolic process; erythrocyte homeostasis; gluconeogenesis; glucose 6-phosphate metabolic process; glucose homeostasis; glycolytic	Cytosol; extracellular region or secreted; extracellular space; nucleus; nucleoplasm; plasma membrane; ciliary

			intramolecular transferase activity; monosaccharide binding; ubiquitin protein ligase binding	process; in utero embryonic development; learning or memory; mesoderm formation; methylglyoxal biosynthetic process; negative regulation of cysteine-type endopeptidase activity involved in apoptotic process; negative regulation of neuron apoptotic process; positive regulation of endothelial cell migration; positive regulation of immunoglobulin secretion; response to cadmium ion; response to estradiol; response to immobilization stress; response to morphine; response to muscle stretch; response to progesterone; response to testosterone	membrane; cytoplasm; neuron projection
RAD23 homolog A, nucleotide excision repair protein	A0A0G2K7M	Rad23a	Damaged DNA binding; kinase binding; polyubiquitin modification-dependent protein binding; proteasome binding; ubiquitin binding; ubiquitin-specific protease binding	Nucleotide-excision repair; positive regulation of cell cycle; positive regulation of proteasomal ubiquitin-dependent protein catabolic process; positive regulation of viral genome replication; proteasome-mediated ubiquitin-dependent protein catabolic process; protein destabilization	Cytoskeleton; microtubule organizing center; cytosol; nucleus; nucleoplasm; proteasome complex
DOP1 leucine zipper-like protein A	D4A0Y2	Dopla	--	Golgi to endosome transport	Cytosol; endosome; Golgi apparatus; trans-Golgi network
Jumonji domain-containing 7	D3ZZV5	Jmjd7	2-oxoglutarate-dependent dioxygenase activity	--	--
Coiled-coil domain-containing protein 63	F1LTP5	Ccdc63	--	--	--

ERCC excision repair 6-like 2	D3ZPU4	Ercc6l2	ATP binding	--	--
Radial spoke head 3 homolog	F1LRY1	Rspf3	--	--	Cilium
Tektin-3	Q4V8G8	Tkt3	--	Cilium assembly; cilium movement involved in cell motility; flagellated sperm motility; regulation of brood size	Acrosomal membrane; outer acrosomal membrane; sperm flagellum
Keratin 79	A0A0G2JW69	Krt79	Enzyme binding; structural molecule activity	--	Cytoskeleton; keratin filament
RCG60210	B0BMZ4	Spatc1	--	--	Cytoskeleton; centrosome
Cytochrome b-c1 complex subunit 1, mitochondrial	Q68FY0	Uqrc1	Catalytic activity; metal ion binding; protein-containing complex binding; ubiquitin protein ligase binding	Mitochondrial electron transport, ubiquinol to cytochrome c; response to activity; response to alkaloid	Cytosol; mitochondrion; mitochondrial inner membrane; mitochondrial respiratory chain complex III
Sperm mitochondrial-associated cysteine-rich protein	Q64298	Smcp	--	Flagellated sperm motility; single fertilization	Mitochondrion; mitochondrial membrane; cytoplasm
Similar to testes development-related NYD-SP22 isoform 1	D4A9U1	RGD1561916	Alpha-tubulin binding	Cellular protein-containing complex assembly	Cytoskeleton; manchette; nucleus; perinuclear region of cytoplasm
Conserved helix-loop-helix ubiquitous kinase	G3V926	Chuk	ATP binding; IkappaB kinase activity; protein heterodimerization activity; protein homodimerization activity; protein serine/threonine kinase activity; scaffold protein	Cellular response to cadmium ion; cellular response to reactive oxygen species; cellular response to virus; negative regulation of NF-kappaB transcription factor activity; NIK/NF-kappaB signaling; peptidyl-serine phosphorylation; positive regulation of I-kappaB kinase/NF-kappaB signaling; positive regulation of interferon-alpha secretion; positive regulation of NF-	Cytosol; IkappaB kinase complex; nucleus; nucleoplasm; intracellular membrane-bounded organelle

			binding	kappaB transcription factor activity; positive regulation of transcription by RNA polymerase II; response to acetate; response to amino acid; response to cholecystokinin; response to drug; response to hydroperoxide; response to lipopolysaccharide; response to organic substance; response to toxic substance; Rho protein signal transduction; skeletal muscle contraction; striated muscle cell differentiation; tumor necrosis factor-mediated signaling pathway	
Similar to BC049730 protein	M0R867	LOC102553892	--	--	--
Solute carrier family 15 member 3	Q924V4	Slc15a3	Oligopeptide transmembrane transporter activity; peptide:proton symporter activity; peptide transmembrane transporter activity; proton-dependent oligopeptide secondary active transmembrane transporter activity	Protein catabolic process; protein transport	Lysosome; lysosomal membrane; integral component of membrane
MICOS complex subunit MIC60	A0A0G2JVH4	Immt	--	Ristae formation; mitochondrial calcium ion homeostasis	Mitochondrion; MICOS complex
Similar to EF hand calcium-binding domain 1	F1LX06	LOC500007	Calcium ion binding	--	--
NME/NM23 family member 5	D3ZH90	Nme5	Nucleoside diphosphate kinase	Cilium assembly; CTP biosynthetic process; epithelial cilium	Sperm flagellum

			activity	movement; GTP biosynthetic process; negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway; spermatid development; UTP biosynthetic process; ventricular system development	
Sodium channel protein	F1LX08	Scn3a	Voltage-gated ion channel activity; voltage-gated sodium channel activity	Regulation of ion transmembrane transport	Plasma membrane; voltage-gated sodium channel complex; cytoplasm
ATP-sensitive inward rectifier potassium channel 11	P70673	Kcnj11	Ankyrin binding; ATP-activated inward rectifier potassium channel activity; ATP binding; heat shock protein binding; inward rectifier potassium channel activity; ion channel binding; protein C-terminus binding	Cellular response to glucose stimulus; cellular response to nicotine ; cellular response to tumor necrosis factor; glucose metabolic process; negative regulation of insulin secretion ; nervous system process; positive regulation of cation channel activity; positive regulation of protein localization to plasma membrane; potassium ion import across plasma membrane; potassium ion transport; regulation of membrane potential; response to ATP; response to drug; response to estradiol; response to ischemia; response to testosterone	Cytosol; endoplasmic reticulum; endosome; mitochondrion; nucleus; nuclear envelope; plasma membrane axolemma; inward rectifying potassium channel; plasma membrane; sarcolemma; T-tubule; acrosomal; cell body fiber; intercalated disc; intracellular membrane-bounded organelle; myelin sheath; neuronal cell body
Clusterin	G3V836	Clu	Amyloid-beta binding; low-density lipoprotein particle receptor binding; misfolded protein binding; protein-containing complex binding; tau protein binding; ubiquitin protein	Cell morphogenesis; central nervous system myelin maintenance; chaperone-mediated protein complex assembly; chaperone-mediated protein foldin; microglial cell activation; microglial cell proliferation; negative regulation of amyloid-beta formation; negative regulation of amyloid fibril formation; negative regulation of cellular response to	Cytoskeleton; cytosol; endoplasmic reticulum; perinuclear endoplasmic reticulum lumen; extracellular region or secreted; spherical high-density lipoprotein particle; mitochondrion; mitochondrial inner membrane;

			ligase binding	thapsigargin; negative regulation of cellular response to tunicamycin; negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage; negative regulation of protein homooligomerization; negative regulation of response to endoplasmic reticulum stress; positive regulation of amyloid-beta formation; positive regulation of apoptotic process; positive regulation of neurofibrillary tangle assembly; positive regulation of neuron death; positive regulation of NF-kappaB transcription factor activity; positive regulation of nitric oxide biosynthetic process; positive regulation of proteasomal ubiquitin-dependent protein catabolic process; positive regulation of protein homooligomerization; positive regulation of receptor-mediated endocitosis; positive regulation of tau-protein kinase activity; positive regulation of tumor necrosis factor production; protein import; protein stabilization; regulation of amyloid-beta clearance; regulation of cell population proliferation; regulation of neuronal signal transduction; response to misfolded protein; response to virus	nucleus; apical dendrite; cell periphery; cell surface; neurofibrillary tangle; synapse
NPC intracellular cholesterol transporter 2	F7FJQ3	Npc2	Cholesterol binding; cholesterol transporter activity; enzyme binding	Cholesterol efflux; cholesterol homeostasis; intracellular cholesterol transport; response to virus	Extracellular region or secreted; extracellular space; lysosome

Heat shock-related 70 kDa protein 2	A0A0G2JUT0	Hspa2	ATP binding	--	--
Cysteine-rich secretory protein 1	P12020	Crisp1	--	--	Extracellular region or secreted; extracellular space; specific granule
Galactosidase, beta 1-like	B1WBS6	Glb1l	Beta-galactosidase activity	Carbohydrate metabolic process	Vacuole
Transforming growth factor beta-1 proprotein	P17246	Tgfb1	Antigen binding; cytokine activity; enzyme binding; growth factor activity; protein heterodimerization activity; protein homodimerization activity; protein N-terminus binding; protein serine/threonine kinase activator activity; transforming growth factor beta receptor binding; type III transforming growth factor beta receptor binding; type II transforming growth factor beta receptor binding; type I transforming growth factor beta receptor binding	Adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains; aging; animal organ regeneration; aortic valve morphogenesis; ATP biosynthetic process; branch elongation involved in mammary gland duct branching; cell-cell junction organization; cell cycle arrest; cell development; cell migration; cellular calcium ion homeostasis; cellular response to dexamethasone stimulus; cellular response to insulin-like growth factor stimulus; cellular response to ionizing radiation; cellular response to mechanical stimulus; cellular response to organic cyclic compound; cellular response to transforming growth factor beta stimulus; chondrocyte differentiation; common-partner SMAD protein phosphorylation; defense response to fungus, incompatible interaction; digestive tract development; embryonic liver development; endoderm development; epidermal growth factor receptor signaling pathway; epithelial to mesenchymal transition; evasion or	Extracellular region or secreted; blood microparticle; collagen-containing extracellular matrix; extracellular space; nucleus; axón; cell Surface; cytoplasm; microvillus; neuronal cell body; secretory granule

				tolerance of host defenses by virus; extracellular matrix assembly; extrinsic apoptotic signaling pathway; face morphogenesis; female pregnancy; frontal suture morphogenesis; germ cell migration; hematopoietic progenitor cell differentiation; hyaluronan catabolic process; inflammatory response; inner ear development; lens fiber cell differentiation; lipopolysaccharide-mediated signaling pathway; liver regeneration; lung development; lymph node development; mammary gland branching involved in thelarche; MAPK cascade; membrane protein intracellular domain proteolysis; mitotic cell cycle checkpoint; mononuclear cell proliferation; morphogenesis of a branching structure; myelination; myeloid dendritic cell differentiation; negative regulation of biomineral tissue development; negative regulation of blood vessel endothelial cell migration; negative regulation of cell-cell adhesión; negative regulation of cell cycle; negative regulation of cell growth; negative regulation of cell population proliferation; negative regulation of cytolysis; negative regulation of epithelial cell proliferation; negative regulation of fat cell differentiation; negative regulation of gene expression; negative regulation of hyaluronan biosynthetic process; negative regulation of immune response; negative regulation of interleukin-17	
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				production; negative regulation of macrophage cytokine production; negative regulation of mitotic cell cycle; negative regulation of myoblast differentiation; negative regulation of neuroblast proliferation; negative regulation of ossification; negative regulation of phagocytosis; negative regulation of production of miRNAs involved in gene silencing by miRNA; negative regulation of protein localization to plasma membrane; negative regulation of protein phosphorylation; negative regulation of release of sequestered calcium ion into cytosol; negative regulation of skeletal muscle tissue development; negative regulation of T cell proliferation; negative regulation of transcription, DNA-templated; negative regulation of transcription by RNA polymerase II; neural tube closure; Notch signaling pathway; oligodendrocyte development; ossification involved in bone remodeling; osteoclast differentiation; pathway-restricted SMAD protein phosphorylation; phosphate-containing compound metabolic process; positive regulation of apoptotic process; positive regulation of blood vessel endothelial cell migration; positive regulation of bone mineralization; positive regulation of branching involved in ureteric bud morphogenesis; positive regulation of cardiac muscle cell differentiation; positive regulation of cell cycle arrest; positive regulation of cell	
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				división; positive regulation of cell migration; positive regulation of cell population proliferation; positive regulation of cellular protein metabolic process; positive regulation of chemotaxis; positive regulation of collagen biosynthetic process; positive regulation of epithelial cell proliferation; positive regulation of epithelial to mesenchymal transition; positive regulation of ERK1 and ERK2 cascade; positive regulation of exit from mitosis; positive regulation of fibroblast migration; positive regulation of fibroblast proliferation; positive regulation of gene expression; positive regulation of histone acetylation; positive regulation of histone deacetylation; positive regulation of interleukin-17 production; positive regulation of isotype switching to IgA isotypes; positive regulation of MAP kinase activity; positive regulation of microglia differentiation; positive regulation of mononuclear cell migration; positive regulation of NAD <sup>+</sup> ADP-ribosyltransferase activitypositive regulation of NF-kappaB transcription factor activity; positive regulation of odontogenesis; positive regulation of pathway-restricted SMAD protein phosphorylation; positive regulation of peptidyl-serine phosphorylation; positive regulation of peptidyl-threonine phosphorylation; positive regulation of peptidyl-tyrosine phosphorylation; positive regulation of	
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			phosphatidylinositol 3-kinase activity; positive regulation of pri-miRNA transcription by RNA polymerase II; positive regulation of production of miRNAs involved in gene silencing by miRNA; positive regulation of protein complex assembly; positive regulation of protein dephosphorylation; positive regulation of protein import into nucleus; positive regulation of protein kinase B signaling; positive regulation of protein phosphorylation; positive regulation of protein secretion; positive regulation of receptor clustering; positive regulation of regulatory T cell differentiation; positive regulation of SMAD protein signal transduction; positive regulation of smooth muscle cell differentiation; positive regulation of superoxide anion generation; positive regulation of transcription, DNA-templated; positive regulation of transcription by RNA polymerase II; positive regulation of transcription regulatory region DNA binding; positive regulation of vascular permeability; protein export from nucleus; protein kinase B signaling; protein phosphorylation; receptor catabolic process; regulation of actin cytoskeleton reorganization; regulation of apoptotic process; regulation of branching involved in mammary gland duct morphogenesis; regulation of cartilage development; regulation of cell growth; regulation of cell population proliferation; regulation of	
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				interleukin-23 production; regulation of MAPK cascade; regulation of SMAD protein signal transduction; regulation of sodium ion transport; regulation of transforming growth factor beta receptor signaling pathway; regulatory T cell differentiation; response to cholesterol; response to drug; response to estradiol; response to glucose; response to hipoxia; response to immobilization stress; response to laminar fluid shear stress; response to organic cyclic compound; response to organic substance; response to progesterone; response to radiation; response to salt; response to vitamin D; response to wounding; salivary gland morphogenesis; SMAD protein complex assembly; SMAD protein signal transduction; T cell homeostasis; tolerance induction to self-antigen; transforming growth factor beta receptor signaling pathway; transforming growth factor beta receptor signaling pathway involved in heart development; ureteric bud development; vasculogenesis; ventricular cardiac muscle tissue morphogenesis; wound healing	
Thymosin beta	A0A0G2K7A1	LOC100361139	Actin monomer binding	Actin filament organization; regulation of cell migration; sequestering of actin monomers	Cytoskeleton; cytoplasm
Keratin, type II cytoskeletal 1	A0A0G2JST3	Krt1	Carbohydrate binding; protein heterodimerization; structural	complement activation, lectin pathway; establishment of skin barrier; negative regulation of inflammatory response; peptide	Cytoskeleton; keratin filament; plasma membrane; cornified envelope

			constituent of epidermis	cross-linking; protein heterotetramerization	
A-kinase anchor protein 4	F1LMR8	Akap4	Protein kinase A binding	Establishment of protein localization; flagellated sperm motility; motile cilium assembly; transmembrane receptor protein serine/threonine kinase signaling pathway	Perinuclear region of cytoplasm; sperm fibrous sheath; sperm principal piece; Z disc
Glutathione S-transferase Mu 5	Q9Z1B2	Gstm5	Glutathione transferase activity; protein homodimerization activity	Glutathione metabolic process	Cytoplasm
Pyruvate dehydrogenase E1 component subunit alpha, testis-specific form, mitochondrial	Q06437	Pdha2	Pyruvate dehydrogenase (acetyl-transferring) activity; pyruvate dehydrogenase (NAD+) activity	Acetyl-CoA biosynthetic process from pyruvate; glucose metabolic process; pyruvate metabolic process; tricarboxylic acid cycle	Mitochondrion; nucleolus; pyruvate dehydrogenase complex
Isocitrate dehydrogenase [NAD] subunit, mitochondrial	F1LNF7	Idh3a	Isocitrate dehydrogenase (NAD+) activity; magnesium ion binding; NAD binding	Tricarboxylic acid cycle	Mitochondrion
Collagen type XVIII alpha 1 chain	F1LR02	Col18a1	Extracellular matrix structural constituent	Angiogenesis; endothelial cell morphogenesis; extracellular matrix organization; response to drug; response to hydrostatic pressure	Extracellular region or secreted; collagen type XVIII trimer; extracellular matrix; extracellular space
LOC683667 protein	B0BNJ1	Sri	Calcium ion binding; protease binding; protein heterodimerization activity; repressing transcription factor binding	Calcium ion transport; cytoplasmic sequestering of transcription factor; heart development; negative regulation of cardiac muscle contraction; negative regulation of heart rate; negative regulation of ryanodine-sensitive calcium-release channel activity; negative regulation of transcription	Cytosol; endoplasmic reticulum; endoplasmic reticulum membrane; smooth endoplasmic reticulum; extracellular region or secreted; extracellular exosome; mitochondrion;

				regulatory region DNA binding; positive regulation of insulin secretion involved in cellular response to glucose stimulus; positive regulation of release of sequestered calcium ion into cytosol Source: Ensembl regulation of cardiac muscle cell contraction; regulation of cell communication by electrical coupling involved in cardiac conduction; regulation of high voltage-gated calcium channel activity; regulation of relaxation of muscle	nucleus; nucleoplasm; plasma membrane; T-tubule; axón; axon terminus; chromaffín granule membrane; dendritic spine neck; Z disc
Outer dense fiber of sperm tails 3	D3ZE94	Odf3	--	--	Cytoskeleton; outer dense fiber
WD repeat domain 72	A0A0G2K3H7	Wdr72	--	--	Cytoplasm
RNA-binding motif protein 39	Q5BJP4	Rbm39	RNA binding	mRNA processing	Nucleus
Park7 protein	Q5BKC3	Park7	Androgen receptor binding; cupric ion binding; cuprous ion binding; cytokine binding; kinase binding; L-dopa decarboxylase activator activity; mercury ion binding; mRNA binding; oxidoreductase activity, acting on peroxide as acceptor; peptidase activity; protein deglycase activity; protein	cellular response to glyoxal; cellular response to hydrogen peroxide; detoxification of copper ion; detoxification of mercury ion; DNA repair; glutathione deglycation; guanine deglycation, glyoxal removal; guanine deglycation, methylglyoxal removal; hydrogen peroxide metabolic process; negative regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway; negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway; negative regulation of gene expression; negative regulation of hydrogen peroxide-induced neuron	Cytosol; mitochondrion; mitochondrial respiratory chain complex I; nucleus; PML body; chromatin; perinuclear region of cytoplasm

		homodimerization activity; repressing transcription factor binding; scaffold protein binding; small protein activating enzyme binding; superoxide dismutase copper chaperone activity; transcription coactivator activity; tyrosine 3-monooxygenase activator activity; ubiquitin-like protein conjugating enzyme binding; ubiquitin-specific protease binding	intrinsic apoptotic signaling pathway; negative regulation of nitrosative stress-induced intrinsic apoptotic signaling pathway; negative regulation of proteasomal ubiquitin-dependent protein catabolic process; negative regulation of protein acetylation; negative regulation of protein binding; negative regulation of protein export from nucleus; negative regulation of protein K48-linked deubiquitination; negative regulation of protein kinase activity; negative regulation of protein sumoylation; negative regulation of TRAIL-activated apoptotic signaling pathway; negative regulation of ubiquitin-protein transferase activity; negative regulation of ubiquitin-specific protease activity; peptidyl-arginine deglycation; peptidyl-cysteine deglycation; peptidyl-lysine deglycation; positive regulation of androgen receptor activity; positive regulation of dopamine biosynthetic process; positive regulation of interleukin-8 production; positive regulation of L-dopa biosynthetic process; positive regulation of mitochondrial electron transport, NADH to ubiquinone; positive regulation of peptidyl-serine phosphorylation; positive regulation of protein homodimerization activity; positive regulation of protein localization to nucleus; positive regulation of pyrroline-5-carboxylate reductase activity; positive regulation of superoxide dismutase activity; positive	
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				regulation of transcription by RNA polymerase II; positive regulation of transcription regulatory region DNA binding; protein deglycation, glyoxal removal; protein deglycation, methylglyoxal removal; protein deglycosylation; protein stabilization; regulation of androgen receptor signaling pathway; regulation of mitochondrial membrane potential	
Tektin 5	Q6AYH7	Tekt5	--	Cilium assembly; cilium movement involved in cell motility; flagellated sperm motility	Sperm flagellum
Aconitate hydratase, mitochondrial	Q9ER34	Aco2	3 iron, 4 sulfur cluster binding; 4 iron, 4 sulfur cluster binding; aconitate hydratase activity; iron ion binding	Citrate metabolic process; isocitrate metabolic process; liver development; response to isolation stress; tricarboxylic acid cycle	Cytosol; mitochondrion
Fructose-bisphosphate aldolase	Q6AY07	Aldoart2	Fructose-bisphosphate aldolase activity	Glycolytic process	--
Histone H2B	A0A0G2JXE0	LOC102549061	DNA binding; protein heterodimerization activity	Nucleosome assembly	Nucleus; chromosome
Keratin, type II cytoskeletal 8	Q10758	Krt8	Protein-containing complex binding; scaffold protein binding; structural molecule activity	Cell differentiation involved in embryonic placenta development; extrinsic apoptotic signaling pathway; hepatocyte apoptotic process; response to hydrostatic pressure; response to other organism; sarcomere organization; tumor necrosis factor-mediated signaling pathway	Cytoskeleton; keratin filament; nucleus; nuclear matrix; nucleoplasm; plasma membrane; apicolateral plasma membrane; dystrophin-associated glycoprotein complex; sarcolema; cell-cell junction; costamere; Z disc

Keratin, type I cytoskeletal 19	Q63279	Krt19	Protein-containing complex binding; structural constituent of muscle	Cell differentiation involved in embryonic placenta development; Notch signaling pathway; response to estrogen; sarcomere organization	Cytoskeleton; intermediate filament; terminal web; plasma membrane; apicolateral plasma membrane; dystrophin-associated glycoprotein complex; sarcolemma; costamere; Z disc
Glycerol kinase	A0A0G2K785	Gk	Glycerol kinase activity	Glucose homeostasis; glycerol-3-phosphate metabolic process; glycerol metabolic process; regulation of fatty acid metabolic process	--
Alpha-mannosidase	Q6P762	Man2b1	Alpha-mannosidase activity; mannose binding; metal ion binding	Learning or memory; mannose metabolic process; protein deglycosylation	Lysosome; vacuolar membrane
Apolipoprotein E	A0A0G2K151	Apoe	Amyloid-beta binding; antioxidant activity; heparan sulfate proteoglycan binding; heparin binding; lipid transporter activity; low-density lipoprotein particle receptor binding; metal chelating activity; phosphatidylcholine-sterol O-acyltransferase activator activity; phospholipid binding; protein-containing complex binding;	AMPA glutamate receptor clustering; amyloid precursor protein metabolic process; cGMP-mediated signaling; cholesterol efflux; cholesterol homeostasis; cholesterol metabolic process; chylomicron remnant clearance; fatty acid homeostasis; G protein-coupled receptor signaling pathway; high-density lipoprotein particle assembly; high-density lipoprotein particle clearance; high-density lipoprotein particle remodeling; intermediate-density lipoprotein particle clearance; lipoprotein biosynthetic process; locomotory exploration behavior; long-chain fatty acid transport; long-term memory; negative regulation of amyloid-beta formation;	Endoplasmic reticulum; extracellular region or secreted; chylomicron; extracellular matrix; high-density lipoprotein particle; intermediate-density lipoprotein particle; low-density lipoprotein particle; synaptic cleft; very-low-density lipoprotein particle; Golgi apparatus; plasma membran; glutamatergic synapse

		protein homodimerization activity; tau protein binding; very-low-density lipoprotein particle receptor binding	negative regulation of blood vessel endothelial cell migration; negative regulation of canonical Wnt signaling pathway; negative regulation of cholesterol biosynthetic process; negative regulation of endothelial cell proliferation; negative regulation of long-term synaptic potentiation; negative regulation of MAP kinase activity; negative regulation of neuron death; negative regulation of neuron projection development; negative regulation of platelet activation; negative regulation of presynaptic membrane organization; neuron projection development; nitric oxide mediated signal transduction; NMDA glutamate receptor clustering; phospholipid efflux; positive regulation by host of viral process; positive regulation of cholesterol efflux; positive regulation of cholesterol esterification; positive regulation of dendritic spine development; positive regulation of dendritic spine maintenance; positive regulation of endocitosis; positive regulation of ERK1 and ERK2 cascade; positive regulation of heparan sulfate binding; positive regulation of heparan sulfate proteoglycan binding; positive regulation of lipid biosynthetic process; positive regulation of lipid transport across blood-brain barrier; positive regulation of low-density lipoprotein particle receptor catabolic process; positive regulation of membrane protein ectodomain proteolysis; positive regulation	
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				of nitric-oxide synthase activity; positive regulation of phospholipid efflux; positive regulation of postsynaptic membrane organization; positive regulation of transcription, DNA-templated; protein import; receptor-mediated endocitosis; regulation of amyloid-beta clearance; regulation of amyloid fibril formation; regulation of behavioral fear response; regulation of Cdc42 protein signal transduction; regulation of cellular response to very-low-density lipoprotein particle stimulus; regulation of proteasomal protein catabolic process; regulation of protein homooligomerization; response to caloric restriction; reverse cholesterol transport; triglyceride metabolic proces; very-low-density lipoprotein particle clearance; very-low-density lipoprotein particle remodeling; virion assembly	
Copper-transporting ATPase 2	A0A0G2JWJ5	Atp7b	ATP binding; copper-exporting ATPase activity; copper ion binding	Cellular copper ion homeostasis; cellular zinc ion homeostasis; copper ion import; lactation; protein maturation by copper ion transfer; response to copper ion; sequestering of calcium ion	Endosome; late endosome; Golgi apparatus; trans-Golgi network membrane; plasma membrane; basolateral plasma membrane; integral component of membrane; perinuclear region of cytoplasm
Cell division cycle 25 homolog A ( <i>S. cerevisiae</i> ),	G3V8T0	Cdc25a	Chaperone binding; protein kinase binding; protein tyrosine	Cell division; cellular response to UV; positive regulation of cell cycle G2/M phase transition	Nucleus; cytoplasm

isoform CRA_a			phosphatase activity		
Phosphatase and actin regulator	M0R7T1	Phactr4	Actin binding; protein phosphatase 1 binding; protein phosphatase inhibitor activity	--	--
L-lactate dehydrogenase A chain	P04642	Ldha	Identical protein binding; kinase binding; lactate dehydrogenase activity; L-lactate dehydrogenase activity; NAD binding	Carbohydrate metabolic; lactate metabolic process; NAD metabolic process; positive regulation of apoptotic process; post-embryonic animal organ development; response to Camp; response to drug; response to estrogen; response to glucose; response to hydrogen peroxide; response to hipoxia; response to nutrient; response to organic cyclic compound	cytoplasm
Zona pellucida 3 receptor, isoform CRA_a	G3V902	Zp3r	--	--	--
Protein FAM221A	Q4V8D7	Fam221a	--	--	--
Testis-specific gene 10 protein	Q9Z220	Tsga10	Structural molecule activity	Spermatogenesis	Cytoskeleton; centriole; cytoplasm
14-3-3 protein theta	P68255	Ywhaq	14-3-3 protein binding; identical protein binding; ion channel binding; protein C-terminus binding; protein domain specific binding; protein N-terminus binding	Negative regulation of ion transmembrane transport; negative regulation of transcription, DNA-templated	--
Annexin A1	P07150	Anxa1	Calcium-dependent phospholipid binding; calcium-dependent	Actin cytoskeleton reorganization; adaptive immune response; alpha-beta T cell differentiation; arachidonic acid secretion;	Cytoskeleton; actin filament; cytosol; endosome; early endosome membrane;

		<p>protein binding; calcium ion binding; DNA/DNA annealing activity; double-stranded DNA-dependent ATPase activity; phospholipase A2 inhibitor activity; phospholipid binding; protein binding, bridging; protein homodimerization activity; single-stranded DNA binding; structural molecule activity</p>	<p>cell surface receptor signaling pathway; cellular response to glucocorticoid stimulus; cellular response to hydrogen peroxide; cellular response to vascular endothelial growth factor stimulus; DNA duplex unwinding; endocrine pancreas development; estrous cycle; gliogenesis; G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second Messenger; granulocyte chemotaxis; hepatocyte differentiation; inflammatory response; innate immune response; insulin secretion; keratinocyte differentiation; monocyte chemotaxis; myoblast migration involved in skeletal muscle regeneration; negative regulation of exocytosis; negative regulation of interleukin-8 secretion; negative regulation of phospholipase A2 activity; negative regulation of protein secretion; negative regulation of T-helper 2 cell differentiation; neutrophil clearance; peptide cross-linking; phagocytosis; positive regulation of apoptotic process; positive regulation of cell migration involved in sprouting angiogenesis; positive regulation of G1/S transition of mitotic cell cycle; positive regulation of interleukin-2 production; positive regulation of neutrophil apoptotic process; positive regulation of prostaglandin biosynthetic process; positive regulation of T cell proliferation; positive regulation of T-helper 1 cell differentiation; positive regulation of vesicle</p>	<p>extrinsic component of endosome membrane; extracellular region or secreted; extracellular exosome; extracellular space; lysosome; mast cell granule; mitochondrion; mitochondrial membrane, nucleus; nucleoplasm; nucleus; plasma membrane; apical plasma membrane; basolateral plasma membrane; cornified envelope; extrinsic component of external side of plasma membrane; lateral plasma membrane; phagocytic cup; plasma membrane; sarcolemma; synaptic membrane; cytoplasm; cytoplasmic vesicle membrane; motile cilium; protein-containing complex</p>
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				fusión; positive regulation of wound healing; prolactin secretion; prostate gland development; regulation of cell population proliferation; regulation of cell shape; regulation of hormone secretion; regulation of inflammatory response; regulation of interleukin-1 production; regulation of leukocyte migration; response to corticosteroid; response to drug; response to estradiol; response to glucocorticoi; response to hormone; response to interleukin-1; response to organic cyclic compound; response to peptide hormone; response to X-ray	
RCG63538	D3ZT54	Spaca4	--	--	--
Normal mucosa of esophagus-specific gene 1 protein	Q5RK28	Nmes1	--	Electron transport chain; proton transmembrane transport	Mitochondrion; mitochondrial respiratory chain complex; nucleus
Tekton-4	Q6AXV2	Tekt4	--	Cilium assembly; cilium movement involved in cell motility; flagellated sperm motility	Sperm flagellum
Tekton-1	Q99JD2	Tekt1	--	Cilium assembly; cilium movement involved in cell motility; flagellated sperm motility	Cytoskeleton; microtubule; cytoplasm; sperm flagellum
IZUMO family member 4	D4ABT2	Izumo4	--	--	--
Cylicin 1	A0A0G2K3Y3	Cycl1	Structural constituent of cytoskeleton	--	--
Transmembrane protein 42	D3Z8L0	Tmem42	--	--	Integral component of membrane
Radial spoke head 6 homolog A	Q4V8E8	Rspn6a	--	--	--

Triosephosphate isomerase	A0A0G2JWU 1	N/A	Triose-phosphate isomerase activity	Gluconeogenesis; glyceraldehyde-3-phosphate biosynthetic process; glycerol catabolic process; glycolytic process	Cytosol
FERM domain-containing 7	A0A096MJB8	Frmld7	--	--	Cytoskeleton
Actin, aortic smooth muscle	A0A0G2K4M 6	Acta2	ATP binding; protein kinase binding	Glomerular mesangial cell development; regulation of blood pressure; response to virus; vascular smooth muscle contraction	Cytoskeleton; actin cytoskeleton; protein-containing complex; smooth muscle contractile fiber
Keratin, type I cytoskeletal 14	A0A0G2JXJ9	Krt14	Structural molecule activity	--	Cytoskeleton; intermediate filament
von Willebrand factor D and EGF domains	D4AEB5	Vwde	--	--	--
ATP synthase subunit e, mitochondrial	P29419	Atp5me	ATPase activity; protein-containing complex binding; proton transmembrane transporter activity	ATP metabolic process; ATP synthesis coupled proton transport	Mitochondrion; mitochondrial proton-transporting ATP synthase complex; mitochondrial proton-transporting ATP synthase complex, coupling factor F(o)
Erythroblast membrane-associated protein	D3Z9R6	Ermap	Signaling receptor binding	Regulation of immune response; T cell receptor signaling pathway	Plasma Membrane; external side of plasma membrane ; integral component of membrane
39S ribosomal protein L17, mitochondrial	Q6PDW6	Mrpl17	Protein domain specific binding; structural constituent of ribosome	Translation	Mitochondrion; mitochondrial large ribosomal subunit
Tumor necrosis factor receptor superfamily member 11B	O08727	Tnfrsf11b	Cytokine activity	Apoptotic process; extracellular matrix organization; negative regulation of bone resorption; negative regulation of odontogenesis of dentin-containing tooth; response to arsenic-containing substance; response to drug; response to estrogen;	Extracellular region or secreted; extracellular matrix; extracellular space

				response to inorganic substance; response to magnesium ion; response to nutrient; signal transduction	
Similar to TDPOZ2	A0A0G2JZT4	RGD1566337	Ubiquitin protein ligase binding	Proteasome-mediated ubiquitin-dependent protein catabolic process; regulation of proteolysis; ubiquitin-dependent protein catabolic process	Nucleus; cytoplasm
Lysine demethylase 5B	A0A0G2K3N6	Kdm5b	DNA binding; histone demethylase activity; histone demethylase activity (H3-trimethyl-K4 specific); metal ion binding	Cellular response to fibroblast growth factor stimulus; chromatin remodeling; lens fiber cell differentiation; response to fungicide	Nucleus; histone methyltransferase complex
NADH:ubiquinone oxidoreductase subunit B10	D4A0T0	Ndufb10	--	Mitochondrial respiratory chain complex I assembly	Mitochondrion; mitochondrial respiratory chain complex I
Tubulin gamma chain	F1LUW9	Tubg2	GTPase activity; GTP binding; structural constituent of cytoskeleton	Cytoplasmic microtubule organization; meiotic spindle organization; microtubule-based process; microtubule cytoskeleton organization; microtubule nucleation; mitotic cell cycle; mitotic sister chromatid segregation; mitotic spindle organization	Cytoskeleton; centrosome; cytoplasmic microtubule; gamma-tubulin complex; microtubule; pericentriolar material; spindle; spindle microtubule; nucleus; cytoplasm
Nucleoporin 210-like	D3Z8Z6	Nup210l	--	Sertoli cell development; spermatid development	Nucleus; nuclear pore; integral component of membrane
Maestro heat-like repeat-containing protein family member 7	A2RUW0	Mroh7	--	--	Integral component of membrane

Myelin regulatory factor	D4A352	Myrf	DNA-binding transcription factor activity; sequence-specific DNA binding	Central nervous system myelination; central nervous system myelin maintenance; positive regulation of myelination; positive regulation of transcription, DNA-templated	Cytosol; Golgi apparatus; nucleus Nucleoplasm; cytoplasm
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**Supplemental Table 3.**

Proteins extracted from sperm cells of rats identified in the control, diabetic and obese groups.

Name protein	ID	Gene	Group		
			Control	Diabetic	Obese
10 kDa heat shock protein, mitochondrial	A0A0G2JTG1	Hspe1	X	X	X
14-3-3 protein theta	P68255	Ywhaq			X
14-3-3 protein zeta/delta	A0A0G2JV65	Ywhaz	X	X	X
39S ribosomal protein L17, mitochondrial	Q6PDW6	Mrpl17			X
3-hydroxyisobutyrate dehydrogenase, mitochondrial	P29266	Hibadh	X	X	
5'-nucleotidase, cytosolic IB	A0A0G2JX78	Nt5c1b	X	X	X
60 kDa heat shock protein, mitochondrial	P63039	Hspd1	X	X	
Aconitate hydratase, mitochondrial	Q9ER34	Aco2		X	
Acrosin	A0A0G2K321	Acr	X	X	X
Acrosin-binding protein	Q6AY33	Acrbp	X	X	X
Actin, aortic smooth muscle	A0A0G2K4M6	Acta2			X
Actin, cytoplasmic 1	A0A0G2K3K2	Actb	X	X	X
Adenylate cyclase	G3V9G1	Adcy5	X	X	X
Adenylate kinase 2, mitochondrial	A0A0G2JSG6	Ak2	X		X
Adenylate kinase isoenzyme 1	P39069	Ak1	X		
A-kinase anchor protein 4	O35774	Akap4	X	X	X
A-kinase anchor protein 4	F1LMR8	Akap4		X	
Alpha-amylase	E9PSQ1	Amy1a	X		
Alpha-L-fucosidase	A0A0G2JSJ8	Fuca1	X	X	X
Alpha-mannosidase	Q6P762	Man2b1		X	
Anionic trypsin-1	P00762	Prss1	X	X	X
Annexin A1	P07150	Anxa1			X
Apolipoprotein E	A0A0G2K151	Apoe		X	
Arylsulfatase A	Q32KK2	Arsa	X	X	X
Aspartyl aminopeptidase	Q4V8H5	Dnpep	X	X	
ATP synthase F(0) complex subunit B1, mitochondrial	P19511	Atp5pb	X	X	X
ATP synthase subunit alpha	F1LP05	Atp5f1a	X	X	X
ATP synthase subunit alpha, mitochondrial	P15999	Atp5f1a	X	X	X

ATP synthase subunit beta	G3V6D3	Atp5f1b	X	X	X
ATP synthase subunit d, mitochondrial	P31399	Atp5pd	X	X	X
ATP synthase subunit delta, mitochondrial	G3V7Y3	Atp5f1d	X	X	X
ATP synthase subunit e, mitochondrial	P29419	Atp5me			X
ATP synthase subunit O, mitochondrial	Q06647	Atp5po	X	X	X
ATP synthase-coupling factor 6, mitochondrial	P21571	Atp5pf	X	X	
ATP-sensitive inward rectifier potassium channel 11	P70673	Kcnj11		X	
Axonemal dynein light intermediate polypeptide 1	Q4FZV3	Dnali1	X		
Basigin	P26453	Bsg	X	X	X
Beta-defensin	Q99JD1	Defb22	X	X	X
Beta-globin	A0A0G2JTW9	Hbb-b1	X		X
Calcium-binding tyrosine phosphorylation-regulated	M0R8P3	Cabyr	X	X	X
Calmodulin-1	P0DP29	Calm1	X	X	X
cAMP-dependent protein kinase type II-alpha regulatory subunit	P12368	Prkar2a	X		
cAMP-dependent protein kinase type II-alpha regulatory subunit	A0A0G2K405	Prkar2a	X	X	
Carnitine O-acetyltransferase	A0A0H2UI21	Crat	X	X	X
Carnitine O-acetyltransferase	Q704S8	Crat	X	X	X
Carnitine O-palmitoyltransferase 2, mitochondrial	G3V7N5	Cpt2	X		
CD177 antigen-like	M0R4W1	LOC100909620	X	X	X
CDGSH iron-sulfur domain-containing protein 1	B0K020	Cisd1	X		X
Cell division cycle 25 homolog A ( <i>S. cerevisiae</i> ), isoform CRA_a	G3V8T0	Cdc25a		X	
Citrate synthase	G3V936	Cs	X	X	X
Clusterin	A0A0G2KB42	Clu	X	X	X
Clusterin	G3V836	Clu		X	X
Coiled-coil domain-containing protein 63	F1LTP5	Ccde63	X		
Collagen type XVIII alpha 1 chain	F1LR02	Col18a1		X	X
Conserved helix-loop-helix ubiquitous kinase	G3V926	Chuk	X		
Copper-transporting ATPase 2	A0A0G2JWJ5	Atp7b		X	
Cylicin 1	A0A0G2K3Y3	Cyclc1		X	X
Cysteine-rich secretory protein 1	P12020	Crisp1		X	

Cytochrome b-c1 complex subunit 1, mitochondrial	Q68FY0	Uqcrc1	X	X	X
Cytochrome b-c1 complex subunit 2, mitochondrial	P32551	Uqcrc2	X	X	X
Cytochrome b-c1 complex subunit 7	B2RYS2	Uqcrb	X	X	X
Cytochrome c oxidase subunit 2	P00406	Mtco2	X	X	X
Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	P10888	Cox4i1	X	X	X
Cytochrome c oxidase subunit 5A, mitochondrial	P11240	Cox5a	X	X	X
Cytochrome c oxidase subunit 5B, mitochondrial	P12075	Cox5b	X	X	X
Cytochrome c oxidase subunit 6B2	Q6YFQ1	Cox6b2	X	X	X
Cytochrome c, testis-specific	P10715	Cyct	X	X	X
Cytochrome c-1	D3ZFQ8	Cyc1	X	X	X
Dihydrolipoyl dehydrogenase, mitochondrial	Q6P6R2	Dld	X	X	X
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	P08461	Dlat	X	X	X
DOP1 leucine zipper-like protein A	D4A0Y2	Dop1a	X		
Dynein light chain 2, cytoplasmic	Q78P75	Dynll2	X		
E3 ubiquitin-protein ligase RNF181	Q6AXU4	Rnf181	X		X
Epididymal-specific lipocalin-5	P06911	Lcn5	X	X	X
Equatorin	Q2LCV6	Eqtn	X	X	
ERCC excision repair 6-like 2	D3ZPU4	Ercce6l2	X	X	
Erythroblast membrane-associated protein	D3Z9R6	Ermap			X
Fatty acid-binding protein 9	P55054	Fabp9	X		
Fc fragment of IgG-binding protein	D3ZJF8	Fcgbp	X		
FERM domain-containing 7	A0A096MJB8	Frmd7			X
Fibrous sheath CABYR-binding protein	Q4V7A4	Fscb	X	X	
Fructose-bisphosphate aldolase	Q6AY07	Aldoart2	X	X	X
Fructose-bisphosphate aldolase	Q6AY07	Aldoa	X	X	X
Fructose-bisphosphate aldolase A	P05065	Glb1l	X	X	X
Galactosidase, beta 1-like	B1WBS6	Glipr111		X	X
GLIPR1-like 1	D3ZI91	Hbb	X	X	X
Globin a4	A0A0G2JSW3	Hba-a2	X	X	X
Globin c2	A0A0G2JSV6	Gpi	X	X	X
Glucose-6-phosphate isomerase	Q6P6V0	Gpx4	X		
Glutathione peroxidase	A0A0G2K398	Gstm5	X		X

Glutathione S-transferase Mu 5	Q9Z1B2	Gapdhs		X	
Glyceraldehyde-3-phosphate dehydrogenase	B1WBQ8	Gk	X	X	X
Glycerol kinase	A0A0G2K785	Hspala		X	
Heat shock 70 kDa protein 1A	P0DMW0	Hspa11	X	X	
Heat shock 70 kDa protein 1-like	P55063	Hspa2	X	X	X
Heat shock-related 70 kDa protein 2	A0A0G2JUT0	Hba1		X	
Hemoglobin subunit alpha-1/2	P01946	N/A	X	X	X
Hemoglobin subunit beta-2	P11517	Hk1	X	X	X
Hexokinase-1	P05708	Hk1	X	X	X
Hexokinase-1	M0RAQ6	LOC100910554	X	X	X
Histone H2A	M0RCL5	LOC102549061	X	X	
Histone H2B	A0A0G2JXE0	Spam1		X	X
Hyaluronidase PH-20	Q62803	MGC105649	X	X	X
Hypothetical LOC302884	M0R6G0	Impa1	X	X	X
Inositol-1-monophosphatase	F1M978	Asrgl1	X	X	X
Isoaspartyl peptidase/L-asparaginase	Q8VI04	Idh3a	X	X	X
Isocitrate dehydrogenase [NAD] subunit, mitochondrial	F1LNF7	Izumo4		X	X
IZUMO family member 4	D4ABT2	Izumo1			X
Izumo sperm-egg fusion protein 1	Q6AY06	Jmjd7	X	X	X
Jumonji domain-containing 7	D3ZZV5	Kazn	X		
Kazrin	Q5FWS6-2	Krt79	X	X	
Keratin 79	A0A0G2JW69	Krt14	X		
Keratin, type I cytoskeletal 14	A0A0G2JXJ9	Krt19			X
Keratin, type I cytoskeletal 19	Q63279	Krt1		X	
Keratin, type II cytoskeletal 1	A0A0G2JST3	Krt5		X	
Keratin, type II cytoskeletal 5	A0A0G2K509	Krt73	X	X	X
Keratin, type II cytoskeletal 73	A0A0G2JXH6	Krt8	X		X
Keratin, type II cytoskeletal 8	Q10758	Ldhc		X	
L-lactate dehydrogenase	Q6AYX2	Ldha	X	X	X
L-lactate dehydrogenase A chain	P04642	Sri		X	X
LOC683667 protein	B0BNJ1	Acs11		X	X
Long-chain-fatty-acid--CoA ligase 1	P18163	Lsm12	X	X	X
LSM12 homolog	D4A8G0	Kdm5b	X	X	X

Lysine demethylase 5B	A0A0G2K3N6	Spaca3			X
Lysozyme c	F1M6E7	Mroh7	X	X	X
Maestro heat-like repeat-containing protein family member 7	A2RUW0	Mdh2			X
Malate dehydrogenase, mitochondrial	P04636	Immt	X	X	X
MICOS complex subunit MIC60	A0A0G2JVH4	Spata18		X	X
Mitochondria-eating protein	A0A0H2UHA4	Myrf	X	X	X
Myelin regulatory factor	D4A352	Ndufb8			X
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial	B2RYS8	Ndufv2	X	X	X
NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	P19234	Ndufb10	X	X	X
NADH:ubiquinone oxidoreductase subunit B10	D4A0T0	Nme5			X
NME/NM23 family member 5	D3ZH90	Nmes1		X	
Normal mucosa of esophagus-specific gene 1 protein	Q5RK28	Npc2			X
NPC intracellular cholesterol transporter 2	F7FJQ3	Nup85		X	X
Nuclear pore complex protein Nup85	Q4QQS8	Nrip3	X		X
Nuclear receptor interacting protein 3 (Predicted), isoform CRA_a	D4A2K5	Nup210l	X		X
Nucleoporin 210-like	D3Z8Z6	Odf2			X
Outer dense fiber of sperm tails 2, isoform CRA_e	G3V7X0	Odf3	X	X	X
Outer dense fiber of sperm tails 3	D3ZE94	Odf2		X	X
Outer dense fiber protein 2	A0A0H2UHM4	Odf2	X	X	X
Outer dense fiber protein 2	Q6AYX5-5	Park7	X	X	X
Park7 protein	Q5BKC3	Prxl2a		X	
Peroxiredoxin-like 2A	Q6AXX6	Phactr4	X	X	X
Phosphatase and actin regulator	M0R7T1	Pebp1		X	
Phosphatidylethanolamine-binding protein 1	P31044	RGD1560402	X	X	X
Phosphoglycerate kinase	M0R6Y8	Pgk2	X	X	X
Phosphoglycerate kinase	Q5XIV1	Pgam2	X	X	X
Phosphoglycerate mutase 2	P16290	Fam221a	X	X	X
Protein FAM221A	Q4V8D7	Ment		X	
Protein MENT	Q5XI62	Ttll10	X	X	X

Protein polyglycylase TTLL10	A0A0G2JX96	Park7	X		
Protein/nucleic acid deglycase DJ-1	Park7	Pdha2	X	X	X
Pyruvate dehydrogenase E1 component subunit alpha, testis-specific form, mitochondrial	Q06437	Pdhb		X	X
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	A0A0G2KAM3	Rad23a	X	X	X
RAD23 homolog A, nucleotide excision repair protein	A0A0G2K7M2	Rspn3	X		
Radial spoke head 3 homolog	F1LRY1	Rspn6a	X	X	X
Radial spoke head 6 homolog A	Q4V8E8	Rab2a			X
Ras-related protein Rab-2A	F1LP82	LOC684270	X	X	X
RCG22622	M0RAK2	Slf1	X	X	
RCG44470	D3ZVR6	Spatc1	X		
RCG60210	B0BMZ4	Spaca4	X	X	
RCG63538	D3ZT54	Rbm39			X
RNA-binding motif protein 39	Q5BJP4	Ropn1		X	
Ropporin-1	Q4KLL5	Sccpdh	X	X	X
Saccharopine dehydrogenase-like oxidoreductase	Q6AY30	Sept9	X	X	X
Septin-9	F1LN75	Serpina16	X		
Serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 16	G3V8X9	Ppp1cc	X	X	X
Serine/threonine-protein phosphatase	A0A0G2JVK2	Alb	X	X	X
Serum albumin	A0A0G2JSH5	Sirpb3	X	X	X
Signal-regulatory protein beta 3	A0A0G2JTD2	LOC102553892	X	X	X
Similar to BC049730 protein	M0R867	Tppp2		X	X
Similar to chromosome 14 open reading frame 8 (Predicted)	D3ZCE7		X		
Similar to EF hand calcium-binding domain 1	F1LX06	LOC500007		X	
Similar to RIKEN cDNA 4930540L03 (Predicted)	D3Z9F9	Spaca1	X		
Similar to TDPOZ2	A0A0G2JZT4	RGD1566337			X
Similar to testes development-related NYD-SP22 isoform 1	D4A9U1	RGD1561916	X	X	X
Slc25a17 protein	B2GUY8	Slc25a17	X	X	X
Sodium channel protein	F1LX08	Scn3a		X	
Solute carrier family 15 member 3	Q924V4	Slc15a3		X	
Solute carrier family 2 (Facilitated glucose transporter),	A0A0G2JSJ3	Slc2a3	X	X	X

member 3					
Sperm acrosome-associated protein 9	Q4V8P4	Spaca9	X	X	X
Sperm mitochondrial-associated cysteine-rich protein	Q64298	Smcp	X	X	X
Sperm surface protein Sp17	Q9Z1K2	Spa17	X	X	X
Succinate--CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	A0A0H2UHE1	Suclg1	X	X	X
Succinyl-CoA:3-ketoacid coenzyme A transferase 2A, mitochondrial	Q5XIJ9	Oxct2a	X	X	X
Superoxide dismutase [Cu-Zn]	P07632	Sod1	X	X	X
Superoxide dismutase [Mn], mitochondrial	P07895	Sod2	X	X	X
Syntaxin-12	A0A0G2JVB6	Stx12	X		
Tektin 5	Q6AYH7	Tekt5		X	X
Tektin-1	Q99JD2	Tekt1		X	X
Tektin-2	Q6AYM2	Tekt2	X	X	
Tektin-3	Q4V8G8	Tekt3	X	X	X
Tektin-4	Q6AXV2	Tekt4			X
Tensin 3	F1LN91	Tns3	X		
Testis-specific gene 10 protein	Q9Z220	Tsga10		X	X
Thymosin beta	A0A0G2K7A1	LOC100361139		X	X
Transforming growth factor beta-1 proprotein	P17246	Tgfb1		X	
Transitional endoplasmic reticulum ATPase	P46462	Vcp	X		X
Translation initiation factor eIF-2B subunit beta	F7EVX2	Eif2b2	X		
Transmembrane protein 42	D3Z8L0	Tmem42			X
Triosephosphate isomerase	A0A0G2JWU1	N/A			X
Tripartite motif-containing 33	D3ZUK4	Trim33	X	X	X
Tubulin alpha-1A chain	P68370	Tuba1a	X		X
Tubulin alpha-3 chain	Q68FR8	Tuba3a	X	X	X
Tubulin alpha-8 chain	Q6AY56	Tuba8	X	X	X
Tubulin beta chain	G3V7C6	Tubb4b	X	X	X
Tubulin beta chain	Q4QQV0	Tubb6	X		
Tubulin beta-4B chain	Q6P9T8	Tubb4b	X	X	X
Tubulin gamma chain	F1LUW9	Tubg2			X
Tumor necrosis factor receptor superfamily member 11B	O08727	Tnfrsf11b			X

Type II keratin Kb15	A0A0G2JVA8	Kb15	X		
Ubiquitin-40S ribosomal protein S27a	P62982	Rps27a	X	X	
Uncharacterized protein	F1LUD3	N/A	X	X	X
Uncharacterized protein	F1MAE5	Prp211	X	X	
Uncharacterized protein	F1LZC5	N/A	X	X	X
Uncharacterized protein	M0R5J4	N/A	X	X	X
Uncharacterized protein	D3ZE63	N/A	X	X	
Uncharacterized protein	A0A0G2JUG1	N/A	X	X	
Vomeronasal type-2 receptor 116-like	A0A0G2JVY7	LOC108348133	X		
von Willebrand factor D and EGF domains	D4AEB5	Vwde			X
WD repeat domain 72	A0A0G2K3H7	Wdr72		X	
Zona pellucida 3 receptor, isoform CRA_a	G3V902	Zp3r		X	X
Zona pellucida binding protein, isoform CRA_b	Q6AXU2	Zpbp	X	X	X