

Table SVI. Enriched Kyoto Encyclopedia of Genes and Genomes pathways of hyperphosphorylation in myocardial ischemia-sudden cardiac death mice.

Term	P-value	Genes
mmu05415: Diabetic cardiomyopathy	6.0×10^{-40}	NDUFA13, NDUFB7, NDUFB11, COX4I1, ATP5A1, NDUFB3, ATP2A2, ATP5C1, ATP5J, PDHB, ATP5H, ATP5O, ATP5G1, COX5A, ATP5B, MPC1, ATP5E, CD36, CYC1, NDUFV3, CTSD, NDUFA9, NDUFA7, NDUFA6, NDUFA5, NDUFA4, ATP5PB, SDHD, COX6C, CPT1B, SDHB, MT-ATP8, COX6B1, NDUFS7, UQCRCQ, NDUFS6, NDUFAB1, PPIF, NDUFS3, VDAC3, VDAC2, MT-CO2, VDAC1, UQCRC2, SLC25A5, SLC25A4, GAPDH
mmu01100: Metabolic pathways	1.2×10^{-36}	NDUFA13, ACAA2, ATP5C1, ENO1, HADH, MCCC2, ACSL1, ACYP2, SDHD, MIF, SDHB, ATP5J2, COX6B1, MT-CO2, SUCLG1, UQCRC2, NDUFB11, AK2, ATP5J, AK4, ATP5H, ATP5O, ATP5L, ACAT1, ATP5B, LDHB, ATP5E, CYC1, NDUFV3, GOT1, IDH2, GOT2, PRDX6, CS, ALDH6A1, UQCRCQ, OGDH, CYCS, ACO2, ACADVL, COX4I1, ATP5G1, HK2, ACADL, ALDH2, AUH, DBT, DLAT, ACADM, ACADS, HIBCH, PGM1, IDH3A, ACAD8, TPI1, PGAM2, NME2, FH1, HADHB, HADHA, ALDH5A1, PKM, NDUFS7, BDH1, NDUFS6, IVD, ADSSL1, NDUFS3, ALDOA, DLD, GAPDH, BCAT2, ECHS1, NDUFB7, GSTP2, ATP5A1, NDUFB3, DLST, PDHB, COX5A, CKMT2, OXCT1, ACSS1, NDUFA9, NDUFA7, NDUFA6, MDH1, NDUFA5, CKM, MDH2, NDUFA4, ATP5PB, COX6C, MT-ATP8, SUCLA2, NDUFAB1, PFKM
mmu00190: Oxidative phosphorylation	1.8×10^{-34}	NDUFA13, NDUFB7, NDUFB11, COX4I1, ATP5A1, NDUFB3, ATP5C1, ATP5J, ATP5H, ATP5O, ATP5G1, COX5A, ATP5L, ATP5B, ATP5E, CYC1, NDUFV3, NDUFA9, NDUFA7, NDUFA6, NDUFA5, NDUFA4, ATP5PB, SDHD, COX6C, SDHB, MT-ATP8, ATP5J2, COX6B1, NDUFS7, UQCRCQ, NDUFS6, NDUFAB1, NDUFS3, CYCS, MT-CO2, UQCRC2
mmu05012: Parkinson disease	5.2×10^{-34}	NDUFA13, NDUFB7, NDUFB11, COX4I1, ATP5A1, NDUFB3, ATP5C1, ATP5J, PARK7, ATP5H, ATP5O, ATP5G1, COX5A, ATP5B, ATP5E, CYC1, NDUFV3, NDUFA9, NDUFA7, NDUFA6, NDUFA5, HSPA5, NDUFA4, ATP5PB, SDHD, COX6C, SDHB, TUBA4A, MT-ATP8, SOD1, COX6B1, NDUFS7, UQCRCQ, NDUFS6, NDUFAB1, PPIF, NDUFS3, VDAC3, CYCS, VDAC2, MT-CO2, VDAC1, UQCRC2, SLC25A5, SLC25A4, UBA52

mmu05208: Chemical carcinogenesis - reactive oxygen species	2.4×10^{-32}	NDUFA13, NDUFB7, NDUFB11, COX4I1, ATP5A1, NDUFB3, ATP5C1, ATP5J, ATP5H, ATP5O, ATP5G1, COX5A, ATP5B, ATP5E, CYC1, NDUFV3, NDUFA9, NDUFA7, NDUFA6, NDUFA5, NDUFA4, ATP5PB, SDHD, COX6C, SOD2, SDHB, MT-ATP8, SOD1, COX6B1, NDUFS7, UQCRCQ, NDUFS6, NDUFAB1, PPIF, NDUFS3, VDAC3, VDAC2, MT-CO2, VDAC1, UQCRC2, SLC25A5, SLC25A4
mmu05020 : Prion disease	2.7×10^{-31}	NDUFA13, NDUFB7, NDUFB11, COX4I1, ATP5A1, NDUFB3, ATP5C1, ATP5J, ATP5H, ATP5O, ATP5G1, COX5A, ATP5B, ATP5E, CYC1, NDUFV3, NDUFA9, NDUFA7, NDUFA6, NDUFA5, HSPA5, NDUFA4, ATP5PB, SDHD, COX6C, SDHB, TUBA4A, MT-ATP8, SOD1, COX6B1, NDUFS7, UQCRCQ, NDUFS6, NDUFAB1, PPIF, NDUFS3, VDAC3, CYCS, VDAC2, MT-CO2, VDAC1, UQCRC2, SLC25A5, SLC25A4
mmu01200: Carbon metabolism	4.5×10^{-29}	ECHS1, DLST, PDHB, ENO1, HK2, ACAT1, DLAT, ACSS1, ACADS, HIBCH, IDH3A, TPI1, MDH1, GOT1, MDH2, PGAM2, IDH2, GOT2, SDHD, SDHB, FH1, CS, ALDH6A1, SUCLA2, PKM, OGDH, SUCLG1, ACO2, ALDOA, DLD, PFKM, GAPDH
mmu05016: Huntington disease	4.7×10^{-29}	NDUFA13, NDUFB7, NDUFB11, COX4I1, ATP5A1, NDUFB3, ATP5C1, ATP5J, ATP5H, ATP5O, ATP5G1, COX5A, ATP5B, ATP5E, CYC1, NDUFV3, NDUFA9, NDUFA7, NDUFA6, NDUFA5, NDUFA4, ATP5PB, SDHD, COX6C, SOD2, SDHB, TUBA4A, MT-ATP8, SOD1, COX6B1, NDUFS7, UQCRCQ, NDUFS6, NDUFAB1, PPIF, NDUFS3, VDAC3, CYCS, VDAC2, MT-CO2, VDAC1, UQCRC2, SLC25A5, SLC25A4
mmu04714: Thermogenesis	8.5×10^{-27}	NDUFA13, NDUFB7, NDUFB11, COX4I1, ATP5A1, NDUFB3, ATP5C1, ATP5J, ATP5H, ATP5O, ATP5G1, COX5A, ATP5L, ATP5B, ATP5E, CYC1, NDUFV3, NDUFA9, NDUFA7, NDUFA6, NDUFA5, ACSL1, NDUFA4, ATP5PB, SDHD, COX6C, CPT1B, SDHB, MT-ATP8, ATP5J2, COX6B1, NDUFS7, UQCRCQ, NDUFS6, NDUFAB1, NDUFS3, MT-CO2, UQCRC2
mmu05022: Pathways of neurodegeneration - multiple diseases	6.7×10^{-25}	NDUFA13, NDUFB7, NDUFB11, COX4I1, ATP5A1, NDUFB3, ATP2A2, ATP5C1, ATP5J, PARK7, ATP5H, ATP5O, ATP5G1, COX5A, ATP5B, ATP5E, CYC1, NDUFV3, NDUFA9, NDUFA7, NDUFA6, NDUFA5, HSPA5, NDUFA4, ATP5PB, SDHD, COX6C, SDHB, TUBA4A, MT-ATP8, SOD1, COX6B1,

		NDUFS7, UQCRCQ, VAPB, NDUFS6, NDUFAB1, PPIF, NDUFS3, VDAC3, CYCS, VDAC2, MT-CO2, VDAC1, UQCRC2, SLC25A5, SLC25A4, UBA52
mmu05010: Alzheimer disease	9.4×10^{-25}	NDUFA13, NDUFB7, NDUFB11, COX4I1, ATP5A1, NDUFB3, ATP2A2, ATP5C1, ATP5J, ATP5H, ATP5O, ATP5G1, COX5A, ATP5B, ATP5E, CYC1, NDUFV3, NDUFA9, NDUFA7, NDUFA6, NDUFA5, NDUFA4, ATP5PB, SDHD, COX6C, SDHB, TUBA4A, MT-ATP8, COX6B1, NDUFS7, UQCRCQ, NDUFS6, NDUFAB1, PPIF, NDUFS3, VDAC3, CYCS, VDAC2, MT-CO2, VDAC1, UQCRC2, SLC25A5, SLC25A4, GAPDH
mmu05014: Amyotrophic lateral sclerosis	2.0×10^{-21}	NDUFA13, NDUFB7, NDUFB11, COX4I1, ATP5A1, NDUFB3, ATP5C1, ATP5J, ATP5H, ATP5O, ATP5G1, COX5A, ATP5B, ATP5E, CYC1, NDUFV3, NDUFA9, NDUFA7, NDUFA6, NDUFA5, HSPA5, NDUFA4, ATP5PB, SDHD, COX6C, SDHB, TUBA4A, MT-ATP8, SOD1, COX6B1, NDUFS7, UQCRCQ, VAPB, NDUFS6, NDUFAB1, NDUFS3, CYCS, MT-CO2, VDAC1, UQCRC2
mmu00020: Citrate cycle (TCA cycle)	4.1×10^{-19}	MDH1, MDH2, IDH2, DLST, PDHB, SDHD, SDHB, FH1, CS, SUCLA2, OGDH, SUCLG1, ACO2, DLAT, DLD, IDH3A
mmu00280: Valine, leucine and isoleucine degradation	5.3×10^{-19}	ACAD8, MCCC2, ECHS1, ACAA2, ACAT1, HADHB, HADHA, ALDH6A1, ALDH2, AUH, OXCT1, IVD, DBT, ACADM, HADH, DLD, ACADS, HIBCH, BCAT2
mmu04932: Non-alcoholic fatty liver disease	3.3×10^{-18}	NDUFA13, NDUFB7, NDUFB11, COX4I1, NDUFB3, COX5A, CYC1, NDUFV3, NDUFA9, NDUFA7, NDUFA6, NDUFA5, NDUFA4, ADIPOQ, SDHD, COX6C, SDHB, COX6B1, NDUFS7, UQCRCQ, NDUFS6, NDUFAB1, NDUFS3, CYCS, MT-CO2, UQCRC2
mmu04260: Cardiac muscle contraction	3.8×10^{-14}	TPM3, TNNC1, COX4I1, TPM1, ATP2A2, ATP1A1, COX6C, COX5A, COX6B1, ACTC1, ASPH, UQCRCQ, TNNT2, MYL2, MYL3, MT-CO2, CYC1, UQCRC2
mmu00071: Fatty acid degradation	1.5×10^{-12}	ACADVL, ECHS1, ACAA2, ACSL1, ECI1, CPT1B, ACAT1, HADHB, HADHA, ACADL, ALDH2, ACADM, HADH, ACADS
mmu00010: Glycolysis / Gluconeogenesis	2.9×10^{-12}	TPI1, PGAM2, PDHB, ENO1, HK2, LDHB, PKM, ALDH2, DLAT, ACSS1, ALDOA, GAPDH, DLD, PFKM, PGM1
mmu00640: Propanoate metabolism	3.7×10^{-11}	LDHB, HADHA, ALDH6A1, ECHS1, SUCLA2, DBT, SUCLG1, ACSS1, ACADS, DLD, HIBCH

mmu00620: Pyruvate metabolism	8.5×10^{-11}	LDHB, PKM, ALDH2, MDH1, MDH2, ACYP2, PDHB, DLAT, ACSS1, DLD, FH1, ACAT1
mmu01230: Biosynthesis of amino acids	4.2×10^{-10}	TPI1, GOT1, PGAM2, IDH2, GOT2, ENO1, CS, PKM, ACO2, ALDOA, GAPDH, PFKM, BCAT2, IDH3A
mmu01212: Fatty acid metabolism	4.3×10^{-9}	HADHB, HADHA, ACADVL, ECHS1, ACAA2, ACADL, ACSL1, ACADM, HADH, ACADS, CPT1B, ACAT1
mmu04723: Retrograde endocannabinoid signaling	1.3×10^{-7}	NDUFA9, NDUFA13, NDUFA7, NDUFB7, NDUFA6, NDUFA5, NDUFB11, NDUFA4, NDUFB3, NDUFS7, NDUFS6, GNB2, NDUFAB1, NDUFS3, NDUFV3
mmu00650: Butanoate metabolism	1.9×10^{-7}	HADHA, ALDH5A1, ECHS1, BDH1, OXCT1, HADH, ACADS, ACAT1
mmu01210: 2-Oxocarboxylic acid metabolism	5.9×10^{-7}	CS, GOT1, IDH2, GOT2, ACO2, BCAT2, IDH3A
mmu00630: Glyoxylate and dicarboxylate metabolism	1.1×10^{-5}	CS, MDH1, MDH2, ACO2, ACSS1, DLD, ACAT1
mmu00410: beta-Alanine metabolism	1.6×10^{-4}	HADHA, ALDH6A1, ECHS1, ALDH2, ACADS, HIBCH
mmu00380: Tryptophan metabolism	2.0×10^{-4}	HADHA, ECHS1, ALDH2, DLST, HADH, DLD, ACAT1
mmu00310: Lysine degradation	6.3×10^{-4}	HADHA, ECHS1, ALDH2, DLST, HADH, DLD, ACAT1
mmu03320: PPAR signaling pathway	6.5×10^{-4}	FABP3, FABP4, ACADL, ACSL1, ADIPOQ, ACADM, CD36, CPT1B
mmu05410: Hypertrophic cardiomyopathy	7.5×10^{-4}	ACTC1, TPM3, MYL2, TNNC1, TNNT2, TPM1, MYL3, ATP2A2
mmu05414: Dilated cardiomyopathy	9.1×10^{-4}	ACTC1, TPM3, MYL2, TNNC1, TNNT2, TPM1, MYL3, ATP2A2
mmu05230: Central carbon metabolism in cancer	9.4×10^{-4}	LDHB, PKM, IDH2, PGAM2, PDHB, PFKM, HK2
mmu00062: Fatty acid elongation	1.2×10^{-3}	HADHB, HADHA, ECHS1, ACAA2, HADH

mmu00270: Cysteine and methionine metabolism	1.9×10^{-3}	LDHB, MDH1, GOT1, MDH2, GOT2, BCAT2
mmu05017: Spinocerebellar ataxia	2.3×10^{-3}	AFG3L2, PPIF, VDAC3, ATP2A2, CYCS, VDAC2, VDAC1, SLC25A5, SLC25A4
mmu04066: HIF-1 signaling pathway	2.7×10^{-3}	LDHB, TRF, PDHB, ENO1, ALDOA, GAPDH, PFKM, HK2
mmu04146: Peroxisome	2.9×10^{-3}	PRDX5, ACSL1, PRDX1, ECH1, IDH2, SOD2, SOD1
mmu04261: Adrenergic signaling in cardiomyocytes	3.6×10^{-3}	ACTC1, TPM3, MYL2, TNNC1, TNNT2, TPM1, MYL3, ATP2A2, ATP1A1
mmu04979: Cholesterol metabolism	9.2×10^{-3}	VAPB, VDAC3, VDAC2, VDAC1, CD36
mmu00330: Arginine and proline metabolism	1.2×10^{-2}	CKMT2, ALDH2, CKM, GOT1, GOT2
mmu00051: Fructose and mannose metabolism	2.1×10^{-2}	TPI1, ALDOA, PFKM, HK2
mmu04022: cGMP-PKG signaling pathway	2.4×10^{-2}	PPIF, VDAC3, ATP2A2, VDAC2, VDAC1, ATP1A1, SLC25A5, SLC25A4
mmu00250: Alanine, aspartate and glutamate metabolism	2.6×10^{-2}	ALDH5A1, GOT1, GOT2, ADSSL1
mmu04216: Ferroptosis	2.8×10^{-2}	ACSL1, VDAC3, TRF, VDAC2
mmu04922: Glucagon signaling pathway	2.9×10^{-2}	LDHB, PKM, PGAM2, PDHB, PFKM, CPT1B
mmu01240: Biosynthesis of cofactors	4.0×10^{-2}	ALDH2, AK2, NME2, ADSSL1, AK4, DLD, BCAT2
mmu04020: Calcium signaling pathway	4.5×10^{-2}	ASPH, TNNC1, PPIF, VDAC3, ATP2A2, VDAC2, VDAC1, SLC25A5, SLC25A4

Table SVII. Enriched Kyoto Encyclopedia of Genes and Genomes pathways of hypophosphorylation in MI-SCD (myocardial ischemia-sudden cardiac death) mice.

Term	P-value	Genes
mmu04910: Insulin signaling pathway	1.2×10^{-8}	GSK3B, PRKAB2, PRKAA1, PRKAA2, PDPK1, ARAF, PHKB, SLC2A4, SORBS1, ACACB, PRKAB1, RPTOR, GYS1, PRKAR1A, TRIP10, EIF4EBP1, PRKACB
mmu03040: Spliceosome	3.6×10^{-7}	RBM17, HSPA8, HNRNPA3, RBM25, CCDC12, SRSF1, HNRNPU, SNW1, U2AF2, TRA2A, SRSF2, ACIN1, SRSF6, SRSF7, SRSF9
mmu04152: AMPK signaling pathway	7.3×10^{-6}	PRKAB2, PRKAA1, PRKAA2, PDPK1, PPP2R5A, SLC2A4, ACACB, PRKAB1, RPTOR, GYS1, STK11, PPP2R5E, EIF4EBP1
mmu04213: Longevity regulating pathway - multiple species	2.7×10^{-5}	RPTOR, HSPA8, PRKAB2, PRKAA1, HDAC2, ADCY9, PRKAA2, PRKAB1, PRKACB
mmu04931: Insulin resistance	6.0×10^{-5}	GYS1, GSK3B, PRKAB2, PRKAA1, PRKAA2, PDPK1, PRKCB, NOS3, SLC2A4, ACACB, PRKAB1
mmu05410: Hypertrophic cardiomyopathy	7.3×10^{-5}	CACNB2, RYR2, PRKAB2, PRKAA1, ACE, PRKAA2, LMNA, CACNA1C, PRKAB1, TTN
mmu04371: Apelin signaling pathway	8.1×10^{-5}	MEF2A, RYR2, PRKAB2, PRKAA1, ADCY9, PRKAA2, NOS3, RRAS2, PRKAB1, PRKACB, SLC9A1, MYLK
mmu05205: Proteoglycans in cancer	2.0×10^{-4}	CAV2, PDPK1, PRKCB, SDC2, ARAF, MSN, RRAS2, ANK2, HSPG2, SLC9A1, CTNNB1, FLNC, PRKACB, EIF4B
mmu04922: Glucagon signaling pathway	2.0×10^{-4}	GYS1, PRKAB2, PRKAA1, PDHA1, PRKAA2, GNAS, PHKB, ACACB, PRKAB1, PRKACB
mmu04211: Longevity regulating pathway	3.9×10^{-4}	RPTOR, PRKAB2, STK11, PRKAA1, ADCY9, PRKAA2, EIF4EBP1, PRKAB1, PRKACB
mmu05414: Dilated cardiomyopathy	5.2×10^{-4}	CACNB2, RYR2, PLN, ADCY9, LMNA, GNAS, CACNA1C, PRKACB, TTN
mmu05100: Bacterial invasion of epithelial cells	7.3×10^{-4}	SEPTIN2, CAV2, CTNNA1, CTNNB1, CTNNA3, DOCK1, VCL, DNM2

mmu05412: Arrhythmogenic right ventricular cardiomyopathy	7.9×10^{-4}	CACNB2, RYR2, GJA1, LMNA, CTNNA1, CTNNB1, CTNNA3, CACNA1C
mmu04261: Adrenergic signaling in cardiomyocytes	8.4×10^{-4}	CACNB2, RYR2, PLN, ADCY9, PPP2R5E, GNAS, PPP2R5A, CACNA1C, SCN5A, PRKACB, SLC9A1
mmu05213: Endometrial cancer	9.5×10^{-4}	GSK3B, PDPK1, CTNNA1, ARAF, CTNNB1, CTNNA3, MLH1
mmu04144: Endocytosis	9.8×10^{-4}	ARFGEF2, HSPA8, RAB5B, CAV2, SH3KBP1, VPS26B, IGF2R, PML, DNM2, EPN2, EPN3, EHD2, RABEP1, GIT1, RAB11FIP5
mmu04068: FoxO signaling pathway	1.1×10^{-3}	PRKAB2, STK11, PRKAA1, PRKAA2, PDPK1, BNIP3, ARAF, SLC2A4, CSNK1E, PRKAB1
mmu04530: Tight junction	1.7×10^{-3}	TJP1, PRKAB2, STK11, PRKAA1, PRKAA2, MSN, YBX3, BVES, PRKAB1, PRKACB, TJP2
mmu04141: Protein processing in endoplasmic reticulum	2.1×10^{-3}	PDIA3, HSPA8, VCP, BAG2, CANX, DNAJA2, RRBPI, STUB1, UBXN6, UBE2J1, SEC31A
mmu04114: Oocyte meiosis	2.7×10^{-3}	YWHAE, SLK, ADCY9, YWHAB, PPP2R5E, PPP2R5A, CPEB3, YWHAZ, PRKACB
mmu04920: Adipocytokine signaling pathway	2.7×10^{-3}	PRKAB2, STK11, PRKAA1, PRKAA2, SLC2A4, ACACB, PRKAB1
mmu04520: Adherens junction	2.7×10^{-3}	TJP1, CTNND1, CTNNA1, CTNNB1, CTNNA3, SORBS1, VCL
mmu04150: mTOR signaling pathway	3.9×10^{-3}	RPTOR, GSK3B, STK11, PRKAA1, PRKAA2, PDPK1, PRKCB, EIF4EBP1, GRB10, EIF4B
mmu04710: Circadian rhythm	4.3×10^{-3}	PRKAB2, PRKAA1, PRKAA2, CSNK1E, PRKAB1
mmu04140: Autophagy - animal	7.1×10^{-3}	RPTOR, STK11, PRKAA1, PRKAA2, PDPK1, BNIP3, RRAS2, WIPI2, PRKACB
mmu04919: Thyroid hormone signaling pathway	9.6×10^{-3}	GSK3B, HDAC2, PLN, PDPK1, PRKCB, CTNNB1, PRKACB, SLC9A1
mmu04962: Vasopressin-regulated water reabsorption	1.0×10^{-2}	RAB5B, ADCY9, GNAS, PRKACB, STX4A
mmu04151: PI3K-Akt signaling pathway	1.1×10^{-2}	YWHAE, GSK3B, PRKAA1, PRKAA2, YWHAB, PDPK1, NOS3, PPP2R5A, YWHAZ, RPTOR, GYS1, STK11, PPP2R5E, EIF4EBP1, EIF4B

mmu04810: Regulation of actin cytoskeleton	1.1×10^{-2}	CFL2, CFL1, ARAF, MSN, RRAS2, ARHGEF7, DOCK1, GIT1, VCL, SLC9A1, MYLK
mmu04971: Gastric acid secretion	1.6×10^{-2}	ADCY9, PRKCB, GNAS, PRKACB, SLC9A1, MYLK
mmu04714: Thermogenesis	1.6×10^{-2}	RPTOR, PRKAB2, PRKAA1, SMARCC1, ADCY9, PRKAA2, SMARCC2, GNAS, PRKAB1, PRKACB, COA6
mmu04020: Calcium signaling pathway	2.0×10^{-2}	RYR2, PLN, ADCY9, PDE1C, PRKCB, NOS3, GNAS, PHKB, CACNA1C, PRKACB, MYLK
mmu04936: Alcoholic liver disease	2.1×10^{-2}	GSK3B, PRKAB2, PRKAA1, PRKAA2, TRA2A, CTNNB1, ACACB, PRKAB1
mmu00640: Propanoate metabolism	2.2×10^{-2}	BCKDHA, ACSS2, PCCA, ACACB
mmu04270: Vascular smooth muscle contraction	2.4×10^{-2}	PPP1R14A, ADCY9, PRKCB, GNAS, ARAF, CACNA1C, PRKACB, MYLK
mmu04120: Ubiquitin mediated proteolysis	2.6×10^{-2}	HUWE1, FBXO4, TRIP12, BIRC6, STUB1, PML, UBE2M, UBE2J1
mmu04911: Insulin secretion	2.7×10^{-2}	RYR2, ADCY9, PRKCB, GNAS, CACNA1C, PRKACB
mmu04540: Gap junction	2.7×10^{-2}	TJP1, GJA1, ADCY9, PRKCB, GNAS, PRKACB
mmu04670: Leukocyte transendothelial migration	2.9×10^{-2}	PRKCB, CTNND1, CTNNA1, MSN, CTNNB1, CTNNA3, VCL
mmu04961: Endocrine and other factor-regulated calcium reabsorption	3.2×10^{-2}	ADCY9, PRKCB, GNAS, PRKACB, DNM2
mmu05134: Legionellosis	3.2×10^{-2}	HSPA8, BCL2L13, VCP, CR1L, BNIP3
mmu04390: Hippo signaling pathway	3.6×10^{-2}	YWHAE, GSK3B, YWHAB, CTNNA1, CTNNB1, CTNNA3, CSNK1E, YWHAZ
mmu04071: Sphingolipid signaling pathway	3.6×10^{-2}	ABCC1, PPP2R5E, PDPK1, PRKCB, NOS3, PPP2R5A, SGPP1
mmu04070: Phosphatidylinositol signaling system	4.1×10^{-2}	MTMR1, PIP4P2, PPIP5K2, PRKCB, PI4K2A, CDS2
mmu04713: Circadian entrainment	4.4×10^{-2}	RYR2, ADCY9, PRKCB, GNAS, CACNA1C, PRKACB

mmu04510: Focal adhesion	4.6×10^{-2}	GSK3B, CAV2, PDPK1, PRKCB, CTNNB1, FLNC, DOCK1, VCL, MYLK
mmu05031: Amphetamine addiction	4.7×10^{-2}	HDAC2, PRKCB, GNAS, CACNA1C, PRKACB
mmu04916: Melanogenesis	4.7×10^{-2}	GSK3B, ADCY9, PRKCB, GNAS, CTNNB1, PRKACB

Table SVIII. Enriched biological processes of hyperphosphorylation in myocardial ischemia-sudden cardiac death mice.

Term	P-value	Genes
GO: 0042776: mitochondrial ATP synthesis coupled proton transport	8.1×10^{-36}	NDUFA13, NDUFB7, NDUFB11, ATP5A1, NDUFB3, ATP5C1, ATP5J, ATP5H, ATP5O, ATP5L, ATP5B, ATP5E, NDUFV3, NDUFA9, NDUFA7, NDUFA6, NDUFA5, ATP5PB, SDHD, SDHB, MT-ATP8, ATP5J2, NDUFS7, NDUFS6, NDUFAB1, NDUFS3
GO: 0006099: tricarboxylic acid cycle	4.1×10^{-21}	MDH1, MDH2, IDH2, DLST, PDHB, SDHD, SDHB, FH1, CS, SUCLA2, OGDH, SUCLG1, ACO2, DLAT, IDH3A
GO: 0015986: ATP synthesis coupled proton transport	6.1×10^{-17}	ATP5B, ATP5PB, ATP5E, ATP5A1, ATP5J, ATP5C1, ATP5H, ATP5O, ATP5G1, MT-ATP8, ATP5L
GO: 0006635: fatty acid beta-oxidation	2.6×10^{-16}	ACADVL, ECHS1, ACAA2, ECI1, ECH1, ADIPOQ, CPT1B, ACAT1, HADHB, HADHA, AUH, ACADM, HADH, DECR1
GO: 0009060: aerobic respiration	1.3×10^{-15}	NDUFA9, NDUFA13, NDUFA7, NDUFB7, NDUFA6, NDUFA5, NDUFB11, MDH2, NDUFB3, SDHB, NDUFS7, NDUFS6, NDUFAB1, NDUFS3, NDUFV3
GO: 0006754: ATP biosynthetic process	4.3×10^{-15}	ATP5B, PKM, ATP5E, ATP5A1, ATP5C1, ATP5O, ALDOA, ATP5G1, MT-ATP8, ATP5L, ATP5J2
GO: 0006631: fatty acid metabolic process	1.5×10^{-14}	ACADVL, ECHS1, ACAA2, ACSL1, ECI1, ECH1, CPT1B, ACAT1, HADHB, HADHA, FABP3, FABP4, ACADL, NDUFS6, NDUFAB1, ACADM, CD36, HADH, ACADS, DECR1
GO: 0046034: ATP metabolic process	2.0×10^{-13}	ATP5B, ATP5E, ATP5A1, AK2, ATP5J, ATP5C1, AK4, ATP5H, ATP5O, ATP5G1, ATP5L, ATP5J2
GO: 0032981: mitochondrial respiratory chain complex I assembly	9.2×10^{-11}	NDUFA9, NDUFA13, NDUFB7, NDUFA6, NDUFA5, NDUFS7, NDUFB11, NDUFS6, NDUFAB1, NDUFB3, NDUFS3
GO: 0033539: fatty acid beta-oxidation using acyl-CoA dehydrogenase	3.0×10^{-10}	ACADVL, ACADL, IVD, ETFDH, ETFA, ACADM, ACADS

GO: 0009083: branched-chain amino acid catabolic process	5.6×10^{-10}	ACAD8, AUH, IVD, DBT, DLD, HIBCH, BCAT2
GO: 0006629: lipid metabolic process	5.6×10^{-10}	ACADVL, ECHS1, ACAA2, EC11, ATP5A1, ACAT1, ATP5B, HINT2, ACADL, OXCT1, PSAP, ACADM, HADH, ACSS1, ACADS, DECR1, ACAD8, ACSL1, ECH1, ACOT13, CPT1B, PRDX6, HADHB, HADHA, BDH1, NDUFAB1, BCAT2
GO: 0006096: glycolytic process	1.4×10^{-9}	TPI1, PKM, PGAM2, OGDH, ENO1, ALDOA, GAPDH, PFKM, HK2
GO: 0061621: canonical glycolysis	3.9×10^{-9}	TPI1, PKM, PGAM2, ENO1, ALDOA, GAPDH, PFKM
GO: 0006103: 2-oxoglutarate metabolic process	3.9×10^{-9}	GOT1, IDH2, GOT2, OGDH, DLST, DLD, IDH3A
GO: 0042744: hydrogen peroxide catabolic process	1.3×10^{-7}	PRDX3, PRDX2, PRDX5, PRDX1, HBB-B1, HBA-A1, PRDX6
GO: 0006979: Response to oxidative stress	3.7×10^{-7}	PRDX3, PRDX2, PRDX5, NDUFA6, PRDX1, ETFDH, PPIF, PARK7, SOD2, PRDX6, SOD1
GO: 0006107: oxaloacetate metabolic process	2.3×10^{-6}	CS, MDH1, GOT1, MDH2, GOT2
GO: 0006006: glucose metabolic process	6.2×10^{-6}	TPI1, PKM, ADIPOQ, PDHB, DLAT, GAPDH, PGM1, HK2
GO: 0006734: NADH metabolic process	6.3×10^{-6}	MDH1, MDH2, OGDH, DLST, IDH3A
GO: 0045454: cell redox homeostasis	8.1×10^{-6}	PRDX3, PRDX2, PRDX5, PRDX1, DLD, PRDX6
GO: 0006811: ion transport	1.4×10^{-5}	ATP5PB, ATP5A1, ATP2A2, ATP5C1, ATP5J, TRF, ATP1A1, ATP5H, ATP5O, ATP5G1, MT-ATP8, ATP5L, ATP5J2, ATP5B, ATP5E, VDAC3, VDAC2, VDAC1
GO: 0042542: response to hydrogen peroxide	1.5×10^{-5}	PRDX3, MB, HBA-A1, PARK7, SOD2, HSPD1, SOD1
GO: 0006105: succinate metabolic process	2.0×10^{-5}	ALDH5A1, SUCLA2, SUCLG1, SDHB
GO: 0006104: succinyl-CoA metabolic process	2.0×10^{-5}	SUCLA2, OGDH, DLST, SUCLG1
GO: 0009409: response to cold	2.7×10^{-5}	ACADVL, ACADL, MT-CO2, ACADM, SOD2, HSPD1

GO: 0061732: mitochondrial acetyl-CoA biosynthetic process from pyruvate	3.2×10^{-5}	MPC1, PDHB, DLAT, DLD
GO: 0006094: gluconeogenesis	3.4×10^{-5}	TPI1, MDH1, MDH2, PGAM2, ENO1, GAPDH
GO: 0008637: apoptotic mitochondrial changes	4.6×10^{-5}	PPIF, SOD2, SLC25A4, HK2, HSPD1
GO: 0042743: hydrogen peroxide metabolic process	4.8×10^{-5}	PRDX2, CYCS, PARK7, SOD2
GO: 0060048: cardiac muscle contraction	6.4×10^{-5}	ACTC1, MYL2, TNNC1, TNNT2, TPM1, MYL3
GO: 0006120: mitochondrial electron transport, NADH to ubiquinone	6.4×10^{-5}	NDUFA7, NDUFS7, NDUFS6, NDUFS3, DLD
GO: 0022904: respiratory electron transport chain	6.4×10^{-5}	NDUFA5, NDUFS6, ETFA, SOD2, SDHB
GO: 0005975: carbohydrate metabolic process	8.5×10^{-5}	CS, LDHB, TPI1, MDH1, MDH2, PDHB, DLAT, GAPDH, PGM1, HK2
GO: 0055010: ventricular cardiac muscle tissue morphogenesis	8.7×10^{-5}	MYL2, TNNC1, TNNT2, TPM1, MYL3
GO: 0042493: response to drug	1.0×10^{-4}	HADHA, FABP3, ACTC1, OXCT1, ACSL1, AK4, ATP1A1, UQCRC2, SOD2, HADH, HSPD1, SOD1
GO: 1902600: hydrogen ion transmembrane transport	1.4×10^{-4}	ATP5B, UQCRCQ, NDUFA4, ATP5A1, ATP1A1, ATP5G1

GO: 0006122: mitochondrial electron transport, ubiquinol to cytochrome c	1.6×10 ⁻⁴	UQCRCQ, CYCS, UQCRC2, CYC1
GO: 0019430: removal of superoxide radicals	1.6×10 ⁻⁴	PRDX2, PRDX1, SOD2, SOD1
GO: 0015909: Long-chain fatty acid transport	1.6×10 ⁻⁴	FABP3, FABP4, CD36, CPT1B
GO: 1904706: negative regulation of vascular smooth muscle cell proliferation	1.7×10 ⁻⁴	GSTP2, TPM1, ADIPOQ, PARK7, SOD2
GO: 0015908: fatty acid transport	1.9×10 ⁻⁴	FABP3, FABP4, ACSL1, GOT2, CD36
GO: 0019752: carboxylic acid metabolic process	3.7×10 ⁻⁴	LDHB, MDH1, MDH2, MIF
GO: 0050873: brown fat cell differentiation	3.9×10 ⁻⁴	ALDH6A1, FABP3, FABP4, MB, ADIPOQ
GO: 0045214: sarcomere organization	4.7×10 ⁻⁴	WDR1, ACTN2, TNNT2, TPM1, XIRP1
GO: 0022900: electron transport chain	5.2×10 ⁻⁴	NDUFA4, NDUFB3, ETFDH, MT-CO2
GO: 0006123: mitochondrial electron transport, cytochrome c to oxygen	6.1×10 ⁻⁴	COX4I1, CYCS, COX6C, COX5A
GO: 0006574: valine catabolic process	7.0×10 ⁻⁴	ACAD8, ALDH6A1, HIBCH
GO: 0034599: cellular response to oxidative stress	7.9×10 ⁻⁴	PRDX3, PRDX2, PRDX5, NME2, ATP2A2, PARK7
GO: 0045471: response to ethanol	8.6×10 ⁻⁴	ACTC1, OXCT1, ADIPOQ, GOT2, ATP5G1, TUFM, SOD1
GO: 0000302: response to reactive oxygen species	9.4×10 ⁻⁴	PRDX1, SOD2, PRDX6, SOD1

GO: 0002026: regulation of the force of heart contraction	9.4×10 ⁻⁴	MYL2, MYL3, ATP2A2, ATP1A1
GO: 0006086: acetyl-CoA biosynthetic process from pyruvate	1.0×10 ⁻³	PDHB, DLAT, DLD
GO: 0006531: aspartate metabolic process	1.0×10 ⁻³	GOT1, GOT2, ADSSL1
GO: 0060047: heart contraction	1.0×10 ⁻³	ACTC1, MYL2, ATP1A1, SOD1
GO: 0006102: isocitrate metabolic process	1.4×10 ⁻³	IDH2, ACO2, IDH3A
GO: 1901526: positive regulation of macromitophagy	1.4×10 ⁻³	VDAC1, SLC25A5, SLC25A4
GO: 0006552: leucine catabolic process	1.4×10 ⁻³	MCCC2, AUH, IVD
GO: 0006936: muscle contraction	1.4×10 ⁻³	ACTN2, TPM3, NDUFS6, TNNT2, TPM1
GO: 0014823: response to activity	1.5×10 ⁻³	OXCT1, ADIPOQ, SOD2, HADH, HSPD1
GO: 0001889: liver development	2.3×10 ⁻³	PKM, AK4, ACADM, ACO2, SOD2, ACAT1
GO: 0006108: malate metabolic process	2.4×10 ⁻³	MDH1, MDH2, FH1
GO: 2001243: negative regulation of intrinsic apoptotic signaling pathway	2.4×10 ⁻³	NDUFA13, PPIF, NDUFS3, VDAC2
GO: 0051881: Regulation of mitochondrial membrane potential	2.7×10 ⁻³	PRDX3, PARK7, SOD2, SOD1
GO: 0015671: oxygen transport	3.0×10 ⁻³	MB, HBB-B1, HBA-A1
GO: 0006749: glutathione metabolic process	3.4×10 ⁻³	EEF1G, GSTP2, HBB-B1, SOD2, SOD1
GO: 0043066: negative regulation of apoptotic process	4.2×10 ⁻³	HSPA5, NME2, MIF, PARK7, SOD2, SOD1, HSPD1, PRDX3, PRDX5, ACTC1, ALDH2, ALB, PPIF, VDAC1
GO: 1901029: negative regulation of mitochondrial outer membrane	4.4×10 ⁻³	ACAA2, SLC25A5, SLC25A4

permeabilization involved in apoptotic signaling pathway		
GO: 0034614: cellular response to reactive oxygen species	5.0×10^{-3}	PRDX3, PRDX5, TPM1, PARK7
GO: 0006536: glutamate metabolic process	5.2×10^{-3}	ALDH5A1, GOT1, GOT2
GO: 0042594: response to starvation	5.4×10^{-3}	OXCT1, ADSSL1, ACADM, ACAT1
GO: 0046902: regulation of mitochondrial membrane permeability	7.9×10^{-3}	PPIF, SLC25A5, SLC25A4
GO: 0098761: cellular response to interleukin-7	8.9×10^{-3}	ATP5B, ENO1, HSPD1
GO: 1903427: negative regulation of reactive oxygen species biosynthetic process	1.1×10^{-2}	PARK7, ATP5G1, HSPD1
GO: 0098869: cellular oxidant detoxification	1.2×10^{-2}	HBB-B1, HBA-A1, PRDX6
GO: 0007005: mitochondrion organization	1.3×10^{-2}	PRDX3, AFG3L2, PARK7, SOD2, NIPSNAP2
GO: 0043280: positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	1.3×10^{-2}	FIS1, NDUFA13, CYCS, CTSD
GO: 0002931: response to ischemia	1.4×10^{-2}	PPIF, CYCS, HK2, HSPD1
GO: 0009725: response to hormone	1.5×10^{-2}	OXCT1, MB, H3F3A, ACAT1
GO: 0006937: regulation of muscle contraction	1.6×10^{-2}	TNNC1, TNNT2, ATP2A2
GO: 0045321: leukocyte activation	1.6×10^{-2}	PRDX2, PRDX1

GO: 0006573: valine metabolic process	1.6×10 ⁻²	ALDH6A1, BCAT2
GO: 0032972: regulation of muscle filament sliding speed	1.6×10 ⁻²	TNNC1, TNNT2
GO: 0070994: detection of oxidative stress	1.6×10 ⁻²	ADIPOQ, PARK7
GO: 0019551: Glutamate catabolic process to 2-oxoglutarate	1.6×10 ⁻²	GOT1, GOT2
GO: 2000277: positive regulation of oxidative phosphorylation uncoupler activity	1.6×10 ⁻²	PARK7, SLC25A4
GO: 0019242: methylglyoxal biosynthetic process	1.6×10 ⁻²	TPI1, ALDOA
GO: 0070543: response to linoleic acid	1.6×10 ⁻²	ADIPOQ, CD36
GO: 0019550: glutamate catabolic process to aspartate	1.6×10 ⁻²	GOT1, GOT2
GO: 0006603: phosphocreatine metabolic process	1.6×10 ⁻²	CKMT2, CKM
GO: 0008152: metabolic process	1.9×10 ⁻²	HADHA, PKM, BDH1, PFKM, PRDX6, HK2
GO: 0045333: cellular respiration	2.0×10 ⁻²	UQCRCQ, UQCRC2, CYC1
GO: 0032496: response to lipopolysaccharide	2.1×10 ⁻²	PRDX3, PRDX2, ATP2A2, SOD2, ALDOA, HSPD1
GO: 0043524: negative regulation of neuron apoptotic process	2.2×10 ⁻²	PRDX3, PRDX2, PARK7, SOD2, HSPD1, SOD1
GO: 0046716: muscle cell cellular homeostasis	2.3×10 ⁻²	ALDOA, PFKM, SOD1
GO: 0007584: response to nutrient	2.4×10 ⁻²	OXCT1, ACSL1, COX4I1, ADIPOQ

GO: 0006532: aspartate biosynthetic process	2.5×10^{-2}	GOT1, GOT2
GO: 0019254: carnitine metabolic process, CoA-linked	2.5×10^{-2}	ACADL, ACADM
GO: 0006533: aspartate catabolic process	2.5×10^{-2}	GOT1, GOT2
GO: 0001819: positive regulation of cytokine production	2.9×10^{-2}	MIF, CD36, GAPDH, SOD1
GO: 0001666: response to hypoxia	3.1×10^{-2}	MB, ADIPOQ, SOD2, ALDOA, HK2, HSPD1
GO: 0014850: response to muscle activity	3.1×10^{-2}	GOT2, ADSSL1, ATP5J
GO: 0006172: ADP biosynthetic process	3.3×10^{-2}	AK2, AK4
GO: 1990544: mitochondrial ATP transmembrane transport	3.3×10^{-2}	SLC25A5, SLC25A4
GO: 1902177: positive regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	3.3×10^{-2}	PARK7, SOD1
GO: 0046952: ketone body catabolic process	3.3×10^{-2}	OXCT1, ACAT1
GO: 0015936: Coenzyme A metabolic process	3.3×10^{-2}	MCCC2, ACAT1
GO: 0046314: phosphocreatine biosynthetic process	3.3×10^{-2}	CKMT2, CKM
GO: 1902109: negative regulation of mitochondrial membrane permeability involved in apoptotic process	3.3×10^{-2}	ACAA2, SLC25A4

GO: 0043648: dicarboxylic acid metabolic process	3.3×10^{-2}	GOT1, GOT2
GO: 0055001: muscle cell development	3.5×10^{-2}	AFG3L2, ACTN2, MYL2
GO: 0032868: response to insulin	3.8×10^{-2}	HADHA, FABP3, GOT2, HADH
GO: 0007015: actin filament organization	3.9×10^{-2}	ACTC1, TPM3, TPM1, XIRP1, TRF
GO: 0009410: response to xenobiotic stimulus	4.0×10^{-2}	HADHA, ATP1A1, SOD2, HADH, SOD1
GO: 0000303: response to superoxide	4.1×10^{-2}	SOD2, SOD1
GO: 0006121: mitochondrial electron transport, succinate to ubiquinone	4.1×10^{-2}	SDHD, SDHB
GO: 0006550: isoleucine catabolic process	4.1×10^{-2}	BCAT2, ACAT1
GO: 0061615: glycolytic process through fructose-6-phosphate	4.1×10^{-2}	ALDOA, PFKM
GO: 0006101: citrate metabolic process	4.9×10^{-2}	CS, ACO2

Table SIX. Enriched biological processes of hypophosphorylation in myocardial ischemia-sudden cardiac death mice.

Term	P-value	Genes
GO: 0008380: RNA splicing	9.0×10^{-13}	RBM25, DHX9, SRSF1, HNRNPU, YBX1, CASC3, VIRMA, U2AF2, TRA2A, RALY, RBM10, SRRM2, RBM17, RBM39, HSPA8, HNRNPA3, ZRANB2, PRPF4B, SRRM1, SNW1, THRAP3, SRSF2, ACIN1, CD2BP2, RBM20, SREK1, SRSF6, SRSF7, SRSF9
GO: 0006397: mRNA processing	1.8×10^{-11}	RBM25, RBM26, DHX9, RNMT, SRSF1, HNRNPU, YBX1, CASC3, HNRNPLL, VIRMA, U2AF2, TRA2A, RALY, SRRM2, RBM17, RBM39, HSPA8, HNRNPA3, ZRANB2, PRPF4B, SRRM1, SNW1, THRAP3, SRSF2, ACIN1, CD2BP2, RBM20, SREK1, SRSF6, SRSF7, SRSF9
GO: 0045214: sarcomere organization	7.3×10^{-9}	CSRP3, PRKAR1A, SRF, CFL2, TCAP, LDB3, FLNC, MYOZ2, MYPN, TTN, LMOD2
GO: 0000398: mRNA splicing, via spliceosome	6.3×10^{-8}	SRRM2, RBM17, HSPA8, HNRNPA3, RBM15, MFAP1B, SRSF1, CASC3, HTATSF1, SRRM1, SNW1, U2AF2, TRA2A, SRSF2, SRSF6, SRSF7, RBM10, SRSF9
GO: 0006417: regulation of translation	1.8×10^{-7}	NIBAN1, DHX9, RPLP1, CASC3, PA2G4, BZW2, PUM2, FXR1, FXR2, LARP1, TCOF1, THRAP3, EIF4EBP1, CPEB3, EIF4G1, NCK1
GO: 0006897: endocytosis	1.6×10^{-6}	RAB5B, USP20, CAV2, SH3KBP1, FBNP1, ANK2, CSNK1E, FBNP1L, DNM2, EPN2, EPN3, EHD2, RABEP1, TRIP10, AAK1, PACSIN3, ESYT2
GO: 0071456: cellular response to hypoxia	8.2×10^{-6}	PRKAA1, BNIP3, MIEF1, SLC2A4, NDRG1, RTN4, SIRT2, SLC9A1, RPTOR, CR1L, LMNA, EIF4EBP1, STUB1
GO: 0000381: regulation of alternative mRNA splicing, via spliceosome	3.2×10^{-5}	FXR1, RBM25, RBM15, FXR2, THRAP3, SRSF2, HNRNPU, SRSF6, RBM10
GO: 0006468: protein phosphorylation	3.5×10^{-5}	GSK3B, PRKAA1, PRKAA2, ARAF, MYLK, TTN, STK11, SLK, TRIM28, CFL1, SPEG, PRKACB, PDPK1, PRKCB, CASK, DYRK1B, PHKB, PRPF4B, OXSR1, CSNK1E, TNNI3K, PRKAB1, YWHAZ, BCKDK, OBSCN, PRKAR1A, WNK1, PRKRA, SIK3, AAK1

GO: 0031669: Cellular response to nutrient levels	4.2×10^{-5}	RPTOR, PRKAB2, PRKAA1, PRKAA2, PRKAB1, EIF4G1
GO: 0055003: cardiac myofibril assembly	6.1×10^{-5}	CSRP3, SRF, CAVIN4, TCAP, TTN
GO: 0034605: cellular response to heat	7.0×10^{-5}	YWHAЕ, PDCL3, VCP, HDAC2, BAG3, DHX9, TPR, STUB1
GO: 0048025: negative regulation of mRNA splicing, via spliceosome	8.4×10^{-5}	U2AF2, ACIN1, SRSF6, SRSF7, RBM10, SRSF9
GO: 0070507: regulation of microtubule cytoskeleton organization	9.7×10^{-5}	GSK3B, PRKAA1, PRKAA2, MAPT, TPPP, CLASP1, BICD2
GO: 0003300: Cardiac muscle hypertrophy	1.2×10^{-4}	RYR2, CSRP3, HDAC2, TCAP, TTN
GO: 0090136: epithelial cell-cell adhesion	1.2×10^{-4}	SRF, CTNNA1, CTNNA3, BVES, VCL
GO: 0051028: mRNA transport	1.3×10^{-4}	HNRNPA3, THRAP3, DHX9, SRSF1, TPR, MAPT, CASC3, SRSF7, LRPPRC, BICD2
GO: 0030036: actin cytoskeleton organization	1.3×10^{-4}	SRF, LDB3, PDCL3, EHD2, CSRP3, ABLIM3, PALLD, EHBP1L1, TRIP10, FLNC, PDLIM5, DOCK1, PDLIM4, SPTBN1
GO: 0055013: Cardiac muscle cell development	1.8×10^{-4}	HDAC2, CXADR, TCAP, HNRNPU, SPEG, TTN
GO: 0061684: chaperone-mediated autophagy	2.4×10^{-4}	HSPA8, BAG3, SYNPO2, STUB1
GO: 0006413: translational initiation	2.6×10^{-4}	EIF5B, LARP1, EIF3G, EIF3C, EIF4B, EIF4G1, ABCF1, EIF3B
GO: 0031000: response to caffeine	2.7×10^{-4}	FKBP1A, RYR2, PRKAA1, HDAC2, PRKAA2
GO: 1904428: negative regulation of tubulin deacetylation	3.7×10^{-4}	PRKAA1, PRKAA2, MAPT, TPPP
GO: 0060048: cardiac muscle contraction	3.9×10^{-4}	RYR2, CSRP3, SRSF1, TCAP, ANK2, SCN5A, TTN

GO: 0046827: positive regulation of protein export from nucleus	4.3×10 ⁻⁴	YWHAE, GSK3B, BAG3, TPR, ANP32B
GO: 0016310: Phosphorylation	5.8×10 ⁻⁴	GSK3B, PRKAA1, PRKAA2, ARAF, MYLK, TTN, RPTOR, STK11, SLK, PPIP5K2, SPEG, PRKACB, PDPK1, PRKCB, CASK, DYRK1B, PRPF4B, OXSR1, CSNK1E, TNNI3K, BCKDK, OBSCN, WNK1, SIK3, AAK1, PI4K2A
GO: 0048255: mRNA stabilization	7.0×10 ⁻⁴	LARP1, THRAP3, SRSF1, HNRNPD, HNRNPU, YBX1
GO: 0007015: actin filament organization	7.1×10 ⁻⁴	SH3KBP1, RUFY3, SRF, CFL2, CFL1, CTNNA1, CTNNA3, SORBS2, SORBS3, NCK1, LMOD2
GO: 0051893: regulation of focal adhesion assembly	7.7×10 ⁻⁴	MACF1, SLK, LIMCH1, CLASP1, VCL
GO: 0048511: rhythmic process	8.3×10 ⁻⁴	GSK3B, PRKAA1, HDAC2, PRKAA2, THRAP3, DHX9, HUWE1, HNRNPD, HNRNPU, CSNK1E, PML
GO: 0006446: regulation of translational initiation	9.2×10 ⁻⁴	EIF5B, EIF4EBP1, BZW2, EIF4G1, EIF3B
GO: 0006915: apoptotic process	1.0×10 ⁻³	RBM25, SH3KBP1, FAF1, PDCD5, YBX3, AKAP1, BCL2L13, STK11, GJA1, BCLAF1, SLK, BAG3, CTNNA1, SUDS3, PEA15A, MEF2A, PRKCB, BNIP3, RMDN3, PML, PDCL3, RABEP1, ACIN1, BIRC6, MAPT, DOCK1
GO: 0010881: regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion	1.0×10 ⁻³	RYR2, PLN, ANK2, CACNA1C
GO: 1900152: Negative regulation of nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	1.0×10 ⁻³	DHX9, HNRNPD, HNRNPU, YBX1
GO: 0008104: Protein localization	1.1×10 ⁻³	YWHAE, MACF1, SEPTIN2, YWHAB, LMNA, CTNNA1, CTNNB1, CASK, ANK2, CSNK1E, YWHAZ, HSPG2

GO: 0098912: membrane depolarization during atrial cardiac muscle cell action potential	1.1×10 ⁻³	CACNB2, CACNA1C, SCN5A
GO: 0002027: regulation of heart rate	1.1×10 ⁻³	RYR2, ANK2, TNNT3, SCN5A, BVES, SNTA1
GO: 0008286: insulin receptor signaling pathway	1.1×10 ⁻³	GSK3B, CSRP3, SMARCC1, CAV2, EIF4EBP1, GRB10, SORBS1
GO: 0000380: alternative mRNA splicing, via spliceosome	1.2×10 ⁻³	RBM17, DHX9, SRSF1, SRSF6, SRSF9
GO: 0030953: astral microtubule organization	1.4×10 ⁻³	NUMA1, TPPP, TACC2, CLASP1
GO: 0046627: negative regulation of insulin receptor signaling pathway	1.4×10 ⁻³	PRKAA1, PRKCB, GRB10, YBX1, TNS2, NCK1
GO: 0006914: autophagy	1.4×10 ⁻³	STK11, VCP, PRKAA1, PRKAA2, USP10, TBC1D5, RAB12, FUNDC1, VPS13A, WIPI2, FBNP1L, SIRT2
GO: 0061025: membrane fusion	1.7×10 ⁻³	USO1, SNAP23, HUWE1, STX4A, DNM2
GO: 0045727: positive regulation of translation	1.7×10 ⁻³	FXR1, NIBAN1, FXR2, LARP1, HNRNPD, CPEB3, EIF3C, ABCF1
GO: 0070934: CRD-mediated mRNA stabilization	1.8×10 ⁻³	DHX9, HNRNPD, HNRNPU, YBX1
GO: 0051014: actin filament severing	1.8×10 ⁻³	SVIL, CFL2, CFL1, DSTN
GO: 0046716: muscle cell cellular homeostasis	1.9×10 ⁻³	CSRP3, PLN, BAG3, SRF, CFL2
GO: 0030512: negative regulation of transforming growth factor beta receptor signaling pathway	2.1×10 ⁻³	FKBP1A, HDAC2, CAV2, PDPK1, TGFB1I1, STUB1, SUDS3, DNM2

GO: 0007010: cytoskeleton organization	2.1×10 ⁻³	STRIP1, SVIL, GSK3B, STRIP2, ABLIM3, DST, SH3KBP1, CFL1, PACSIN3
GO: 0007507: heart development	2.1×10 ⁻³	MEF2A, CXADR, SRF, LDB3, CACNA1C, TTN, GYS1, GJA1, CSRP3, PRKAR1A, CTNNB1, RBM20, PDLIM5, PDLIM4, BVES
GO: 0035995: detection of muscle stretch	2.2×10 ⁻³	CSRP3, TCAP, TTN
GO: 0098904: regulation of AV node cell action potential	2.2×10 ⁻³	RYR2, CXADR, ANK2
GO: 0030043: actin filament fragmentation	2.2×10 ⁻³	CFL2, CFL1, DSTN
GO: 0097320: plasma membrane tubulation	2.2×10 ⁻³	EHD2, CAVIN2, PACSIN3, FBNP1L
GO: 0061337: cardiac conduction	3.3×10 ⁻³	MEF2A, GJA1, CACNA1C, SLC4A3
GO: 0001732: Formation of cytoplasmic translation initiation complex	3.3×10 ⁻³	EIF3G, EIF2S2, EIF3C, EIF3B
GO: 0086045: Membrane depolarization during AV node cell action potential	3.6×10 ⁻³	CACNB2, CACNA1C, SCN5A
GO: 0060789: hair follicle placode formation	3.6×10 ⁻³	HDAC2, GNAS, CTNNB1
GO: 0006281: DNA repair	3.8×10 ⁻³	VCP, DTX3L, USP10, HUWE1, DYRK1B, NUCKS1, PDS5B, MLH1, ALKBH3, VCPIP1, SFR1, TRIM28, JMY, STUB1, TRIP12, TRP53BP1, GTF2I
GO: 0086004: regulation of cardiac muscle cell contraction	4.0×10 ⁻³	PLN, FXDYD1, ANK2, SCN5A
GO: 2000767: positive regulation of cytoplasmic translation	4.0×10 ⁻³	DHX9, HNRNPD, HNRNPU, YBX1

GO: 0086005: ventricular cardiac muscle cell action potential	4.0×10 ⁻³	RYR2, ANK2, SCN5A, SNTA1
GO: 0033120: positive regulation of RNA splicing	4.0×10 ⁻³	U2AF2, SRSF1, RBM20, HNRNPLL
GO: 0048870: cell motility	4.5×10 ⁻³	DST, CFL2, CFL1, CTNNA1, DSTN
GO: 0043488: regulation of mRNA stability	4.5×10 ⁻³	FXR1, CARHSP1, FXR2, HNRNPD, PUM2
GO: 0007030: Golgi organization	5.1×10 ⁻³	VCPIP1, GOLPH3, USO1, HUWE1, TRAPPC12, ARHGEF7, CLASP1, PI4K2A
GO: 2000758: positive regulation of peptidyl-lysine acetylation	5.3×10 ⁻³	PRKAA1, PRKAA2, PML
GO: 0042981: regulation of apoptotic process	6.0×10 ⁻³	GSK3B, BCL2L13, GJA1, RBM25, SLK, TOMM70A, CTNNB1, ANK2, ANP32B, IGF2R, RBM10, PEA15A
GO: 2000059: negative regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process	6.4×10 ⁻³	PDCL3, ANKS1, SGTA, PML
GO: 0034613: cellular protein localization	6.5×10 ⁻³	GJA1, SEPTIN2, LMNA, CTNNA1, CTNNB1, ANK2, CSNK1E
GO: 0086091: regulation of heart rate by cardiac conduction	6.7×10 ⁻³	CACNB2, CTNNA3, ANK2, CACNA1C, SCN5A
GO: 0030032: lamellipodium assembly	6.7×10 ⁻³	GOLPH3, ABLIM3, ARHGEF7, VCL, NCK1
GO: 0006605: Protein targeting	7.3×10 ⁻³	YWHAE, YWHAB, SRPR, YWHAZ, PML
GO: 0010882: regulation of cardiac muscle contraction by calcium ion signaling	7.4×10 ⁻³	RYR2, ANK2, SLC9A1

GO: 0060307: Regulation of ventricular cardiac muscle cell membrane repolarization	7.4×10 ⁻³	GJA1, ANK2, SCN5A, SNTA1
GO: 0055117: regulation of cardiac muscle contraction	7.4×10 ⁻³	RYR2, RNF207, ANK2, TNNT3
GO: 0001701: in utero embryonic development	8.4×10 ⁻³	NOS3, SRF, SRSF1, YBX1, EIF2S2, YBX3, TTN, EPN2, RIC8A, GJA1, ADCY9, TRIM28, CR1L, CTNNA1, SPEG
GO: 1903829: positive regulation of cellular protein localization	9.7×10 ⁻³	PRKAA1, PRKAA2, MAPT
GO: 0044829: positive regulation by host of viral genome replication	9.7×10 ⁻³	HSPA8, STOM, NUCKS1
GO: 0030334: regulation of cell migration	9.8×10 ⁻³	MACF1, SLK, DPYSL3, LMNA, NEXN, RTN4, VCL, NCK1
GO: 0042752: regulation of circadian rhythm	1.0×10 ⁻²	GSK3B, PRKAA1, PRKAA2, HNRNPB, CSNK1E, PML
GO: 0045773: positive regulation of axon extension	1.1×10 ⁻²	MACF1, GSK3B, RUFY3, SRF, MAPT
GO: 0007029: endoplasmic reticulum organization	1.1×10 ⁻²	RETREG3, CAV2, LAMP1, RTN4, SEC31A
GO: 0006893: Golgi to plasma membrane transport	1.2×10 ⁻²	ARFGEF2, RABEP1, EXOC2, DNMT1
GO: 0045862: positive regulation of proteolysis	1.2×10 ⁻²	HSPA8, HDAC2, CFL1, STUB1
GO: 0030836: positive regulation of actin filament depolymerization	1.2×10 ⁻²	CFL2, CFL1, DSTN

GO: 0044794: positive regulation by host of viral process	1.2×10 ⁻²	CAV2, CFL1, IGF2R
GO: 0018107: peptidyl-threonine phosphorylation	1.3×10 ⁻²	GSK3B, STK11, WNK1, PDPK1, DYRK1B, OXSR1
GO: 0046777: protein autophosphorylation	1.3×10 ⁻²	HSPA8, GSK3B, STK11, SLK, OBSCN, TRIM28, WNK1, AAK1, DYRK1B, OXSR1
GO: 0045597: positive regulation of cell differentiation	1.3×10 ⁻²	GSK3B, SMARCC1, SMARCC2, SRF, CTNNB1, PA2G4
GO: 1902305: regulation of sodium ion transmembrane transport	1.5×10 ⁻²	WNK1, SCN5A, SNTA1
GO: 0035556: intracellular signal transduction	1.5×10 ⁻²	UNC13B, ARFGEF2, GSK3B, PRKAA1, PRKAA2, PDPK1, PRKCB, ARAF, OXSR1, SH3BP5L, ADCY9, WNK1, MCF2L, SIK3, ARHGEF7, TNS2, PEA15A
GO: 0016477: cell migration	1.6×10 ⁻²	GSK3B, PDPK1, SH3KBP1, SDC2, RRAS2, GOLPH3, STRIP2, PALLD, CTNNA1, CTNNA3, CD248, DOCK1, NCK1
GO: 0006511: ubiquitin-dependent protein catabolic process	1.6×10 ⁻²	RNF20, VCP, PSMA3, PPP1R11, DTX3L, USP20, USP10, FBXO4, 8030462N17RIK, TRIP12, BIRC6, STUB1
GO: 0034504: protein localization to nucleus	1.7×10 ⁻²	YWHAE, STK11, SRSF1, LMNA, HDGF
GO: 0043065: Positive regulation of apoptotic process	1.8×10 ⁻²	UNC13B, GSK3B, ACE, NOS3, BNIP3, PDCD5, IGF2R, SLC9A1, BCLAF1, SLK, JMY, CTNNB1, ACIN1, SUDS3, ARHGEF7
GO: 0072659: Protein localization to plasma membrane	1.8×10 ⁻²	EHD2, CACNB2, EFR3A, HECTD1, RAB12, TTC7B, CASK, ANK2, SPTBN1
GO: 0045216: cell-cell junction organization	1.8×10 ⁻²	TJP1, GJA1, CXADR, TJP2

GO: 0061061: muscle structure development	1.8×10 ⁻²	LDB3, PDLIM5, PDLIM4
GO: 0035308: negative regulation of protein dephosphorylation	1.8×10 ⁻²	YWHAE, YWHAB, AKAP1
GO: 0071481: cellular response to X-ray	1.8×10 ⁻²	NUCKS1, TRP53BP1, DNM2
GO: 0098911: regulation of ventricular cardiac muscle cell action potential	1.8×10 ⁻²	RYR2, CTNNA3, CACNA1C
GO: 0098609: Cell-cell adhesion	1.9×10 ⁻²	TJP1, ARVCF, EFR3A, CXADR, SRF, CTNND1, CTNNA1, CTNNB1, CTNNA3, TJP2
GO: 0000165: MAPK cascade	2.0×10 ⁻²	YWHAE, MEF2A, IGHM, ARAF, CTNNB1, SORBS3, PEA15A
GO: 0030433: ubiquitin-dependent ERAD pathway	2.0×10 ⁻²	VCP, FAF1, SGTA, CANX, STUB1, UBE2J1
GO: 0043484: regulation of RNA splicing	2.1×10 ⁻²	RBM17, SRSF1, RBM20, HNRNPH2, HNRNPLL, RBM12
GO: 0051926: negative regulation of calcium ion transport	2.1×10 ⁻²	PLN, NOS3, PACSIN3
GO: 0033365: protein localization to organelle	2.1×10 ⁻²	CSRP3, AP3D1, ANK2, BICD2
GO: 0001944: vasculature development	2.1×10 ⁻²	RIC8A, STK11, CTNNB1, ANP32B
GO: 0032880: regulation of protein localization	2.2×10 ⁻²	FKBP1A, RALGAPB, SEPTIN2, TPR, SIK3, AAK1, CSNK1E
GO: 1903078: positive regulation of protein localization to plasma membrane	2.3×10 ⁻²	PGRMC1, PDPK1, SORBS1, STX4A, SPTBN1
GO: 0060038: cardiac muscle cell proliferation	2.3×10 ⁻²	HDAC2, CXADR, PRKAR1A, CTNNB1

GO: 0048709: oligodendrocyte differentiation	2.4×10 ⁻²	HDAC2, BNIP3, SRSF1, CTNNB1, TPPP
GO: 0006874: Cellular calcium ion homeostasis	2.4×10 ⁻²	RYR2, CSRP3, PLN, PRKCB, RMDN3, ANK2, CACNA1C
GO: 0034599: cellular response to oxidative stress	2.4×10 ⁻²	CHCHD2, PRKAA1, PRKAA2, PRKRA, STX4A, SIRT2
GO: 0071872: cellular response to epinephrine stimulus	2.5×10 ⁻²	RYR2, SIRT2, SLC9A1
GO: 2000637: positive regulation of gene silencing by miRNA	2.5×10 ⁻²	FXR1, DHX9, PUM2
GO: 0045947: negative regulation of translational initiation	2.5×10 ⁻²	LARP1, TPR, EIF4EBP1
GO: 0030042: actin filament depolymerization	2.5×10 ⁻²	CFL2, CFL1, DSTN
GO: 0014850: response to muscle activity	2.5×10 ⁻²	RYR2, PRKAA2, PERM1, TNS2
GO: 0015031: protein transport	2.6×10 ⁻²	ARFGEF2, RAB5B, RANBP3, DTX3L, USO1, SNAP23, AP3D1, VPS13A, ANK2, RRBP1, VPS26B, PEX1, BICD2, GOLPH3, RABEP1, TBC1D5, RAB12, TPR, EXOC2, SEC31A, RAB11FIP5
GO: 0097191: Extrinsic apoptotic signaling pathway	2.6×10 ⁻²	PDIA3, GSK3B, PDPK1, PML, SGPP1
GO: 0006936: muscle contraction	2.6×10 ⁻²	FKBP1A, MYOM1, MYH3, TTN, LMOD2
GO: 0043161: proteasome-mediated ubiquitin-dependent protein catabolic process	2.6×10 ⁻²	GSK3B, VCP, PSMA3, HECTD1, HUWE1, CTNNB1, TRIP12, STUB1, PML, SIRT2

GO: 0000226: microtubule cytoskeleton organization	2.7×10 ⁻²	DST, MAP7D1, SIK3, MAPT, TACC2, MAP4, EML1, CLASP1
GO: 0000209: protein polyubiquitination	2.7×10 ⁻²	RNF20, HECTD1, HUWE1, IRF2BP1, FBXO4, CTNNB1, TRIP12, STUB1, UBE2J1
GO: 0046907: intracellular transport	2.7×10 ⁻²	RANBP3, DST, AP3D1, MAPT
GO: 0006325: chromatin organization	2.8×10 ⁻²	RNF20, SMARCC1, HDAC2, PRKAA1, PRKAA2, SMARCC2, DTX3L, PRKCB, HNRNPU, NUCKS1, TRIM28, BANF1, SUDS3
GO: 0033673: negative regulation of kinase activity	2.9×10 ⁻²	WNK1, HNRNPU, MAPT
GO: 0045732: positive regulation of protein catabolic process	2.9×10 ⁻²	GSK3B, GJA1, VCP, FAF1, HUWE1, MSN
GO: 0050790: regulation of catalytic activity	3.0×10 ⁻²	PRKAB2, RANBP3, PRKAB1, TTN
GO: 0010608: posttranscriptional regulation of gene expression	3.0×10 ⁻²	LARP1, ACE, FBXO4, PUM2
GO: 0071277: cellular response to calcium ion	3.0×10 ⁻²	MEF2A, PRKAA1, PRKAA2, WNK1, SCN5A, MYLK
GO: 0017148: negative regulation of translation	3.2×10 ⁻²	FXR1, FXR2, LARP1, EIF4EBP1, YBX1, CPEB3
GO: 0032886: regulation of microtubule-based process	3.3×10 ⁻²	MACF1, GSK3B, TACC2
GO: 0010737: protein kinase A signaling	3.3×10 ⁻²	MYOM1, PRKACB, TTN
GO: 0061049: Cell growth involved in cardiac muscle cell development	3.3×10 ⁻²	GSK3B, SORBS2, PDLIM5

GO: 0071380: cellular response to prostaglandin E stimulus	3.3×10^{-2}	PRKAA1, PRKAA2, GNAS
GO: 2001022: positive regulation of response to DNA damage stimulus	3.3×10^{-2}	FXR1, BCLAF1, FXR2
GO: 0061077: chaperone-mediated protein folding	3.4×10^{-2}	FKBP1A, PDCL3, HSPA8, SGTA
GO: 0001578: microtubule bundle formation	3.4×10^{-2}	NUMA1, TPPP, MAP4, CLASP1
GO: 0017157: regulation of exocytosis	3.4×10^{-2}	SEPTIN2, RAB12, SNAP23, STX4A
GO: 0048026: positive regulation of mRNA splicing, via spliceosome	3.7×10^{-2}	HSPA8, SNW1, THRAP3, TRA2A
GO: 0030010: establishment of cell polarity	3.7×10^{-2}	GSK3B, STK11, CFL1, LMNA
GO: 0099003: vesicle-mediated transport in synapse	3.7×10^{-2}	SNAP23, AP3D1, STX4A
GO: 0010614: Negative regulation of cardiac muscle hypertrophy	3.7×10^{-2}	GSK3B, MLIP, AKAP1
GO: 0070885: negative regulation of calcineurin-NFAT signaling cascade	3.7×10^{-2}	GSK3B, CMYA5, MYOZ2
GO: 0032515: negative regulation of phosphoprotein phosphatase activity	3.7×10^{-2}	FKBP1A, PPP1R11, CMYA5
GO: 0055089: fatty acid homeostasis	3.7×10^{-2}	PRKAA1, PRKAA2, GPAM
GO: 0031647: regulation of protein stability	3.7×10^{-2}	HSPA8, LMNA, FBXO4, STUB1, ANK2, CDKN2AIP
GO: 0050821: protein stabilization	3.8×10^{-2}	PDCL3, BAG2, BAG3, PRKRA, CTNND1, AAK1, ANK2, PML, RTN4
GO: 0080090: regulation of primary metabolic process	3.8×10^{-2}	PRKAB2, PRKAB1

GO: 0086092: regulation of the force of heart contraction by cardiac conduction	3.8×10^{-2}	PLN, SLC9A1
GO: 0000961: Negative regulation of mitochondrial RNA catabolic process	3.8×10^{-2}	SLIRP, LRPPRC
GO: 1903645: negative regulation of chaperone-mediated protein folding	3.8×10^{-2}	PDCL3, PDCD5
GO: 0042593: glucose homeostasis	3.9×10^{-2}	CSRP3, STK11, PRKAA1, SLC16A1, PRKAA2, NUCKS1, CACNA1C, SLC2A4
GO: 0006974: cellular response to DNA damage stimulus	4.1×10^{-2}	VCP, DTX3L, USP10, HUWE1, DYRK1B, NUCKS1, MLH1, CDKN2AIP, RPTOR, ALKBH3, VCIPI1, STK11, SFR1, JMY, STUB1, TRIP12, TRP53BP1
GO: 0098761: cellular response to interleukin-7	4.2×10^{-2}	PDIA3, HDGF, YBX1
GO: 0007512: adult heart development	4.2×10^{-2}	GJA1, TCAP, TTN
GO: 0034394: protein localization to cell surface	4.2×10^{-2}	CTNNB1, ANK2, STX4A, VCL
GO: 0016055: Wnt signaling pathway	4.2×10^{-2}	MACF1, GSK3B, PRKAA1, PRKAA2, CCNY, TGFB1I1, CTNND1, CTNNB1, CSNK1E, NDRG2
GO: 0008285: negative regulation of cell proliferation	4.2×10^{-2}	CAV2, NOS3, SRF, PDCD5, PDS5B, NDRG1, PML, SIRT2, STK11, GJA1, NFIB, LMNA, CTNNB1, TNS2, RBM10
GO: 0016192: vesicle-mediated transport	4.3×10^{-2}	HSPA8, RABEP1, TRAPPC10, USO1, SNAP23, AP3D1, TRAPPC12, KIF1C, BVES, STX4A, SEC31A
GO: 0007399: nervous system development	4.7×10^{-2}	MEF2A, GSK3B, SMARCC1, SMARCC2, FNBP1, SDC2, VPS13A, NDRG2, RTN4, SIRT2, GAP43, RUFY3, DPYSL3, CTNNB1, ARHGEF7
GO: 0051592: response to calcium ion	4.9×10^{-2}	RYR2, PDE1C, HNRNPD, TTN, SEC31A

Table SX. Enriched biological process of hypophosphorylation in myocardial ischemia-sudden cardiac death mice.

Term	P-value	Genes
GO: 0005739: mitochondrion	1.2×10 ⁻⁹²	NDUFA13, ACAA2, ECI1, ATP5C1, PARK7, MPC1, HADH, MCCC2, ACSL1, ECH1, ACOT13, ACYP2, SDHD, CPT1B, SDHB, ATP5J2, TUFM, COX6B1, AFG3L2, VDAC3, PPIF, VDAC2, MT-CO2, VDAC1, SUCLG1, UQCRC2, ATP5MD, NDUFB11, AK2, ATP5J, AK4, ATP5H, ATP5O, ATP5L, ACAT1, PRDX3, PRDX2, ATP5B, LDHB, PRDX5, PRDX1, ATP5E, PSAP, GATD3A, CYC1, NDUFV3, DECR1, FIS1, HSPA5, IDH2, GOT2, PRDX6, CS, ALDH6A1, UQCRQ, OGDH, CYCS, ACO2, ACADVL, SLC25A3, COX4I1, ETFA, ATP5G1, CLYBL, HK2, HINT2, ACADL, ALDH2, AUH, DBT, DLAT, ACADM, CD36, ACADS, CTSD, HIBCH, IDH3A, ACAD8, NME2, FH1, NIPSNAP2, HADHB, HADHA, ALDH5A1, PKM, NDUFS7, BDH1, NDUFS6, IVD, NDUFS3, ALDOA, SLC25A5, SLC25A11, DLD, GAPDH, SLC25A4, BCAT2, ECHS1, NDUFB7, GSTP2, ATP5A1, NDUFB3, ETFDH, DLST, PDHB, COX5A, HSPD1, CKMT2, OXCT1, ACSS1, NDUFA9, NDUFA7, NDUFA6, MDH1, NDUFA5, MDH2, NDUFA4, ATP5PB, IMMT, COX6C, HSPE1, SOD2, MT-ATP8, SOD1, SUCLA2, NDUFAB1
GO: 0005743: mitochondrial inner membrane	1.2×10 ⁻⁵⁹	ACADVL, NDUFA13, SLC25A3, ACAA2, COX4I1, ECI1, ATP5C1, ATP5G1, MPC1, HADH, SDHD, SDHB, TUFM, ATP5J2, COX6B1, HADHB, HADHA, AFG3L2, NDUFS7, BDH1, NDUFS6, VDAC3, PPIF, NDUFS3, VDAC2, SUCLG1, MT-CO2, VDAC1, UQCRC2, SLC25A5, SLC25A11, SLC25A4, ATP5MD, NDUFB7, NDUFB11, ATP5A1, NDUFB3, ETFDH, AK2, ATP5J, ATP5H, ATP5O, COX5A, HSPD1, ATP5L, ACAT1, CKMT2, ATP5B, LDHB, ATP5E, CYC1, NDUFV3, NDUFA9, NDUFA7, NDUFA6, NDUFA5, MDH2, ATP5PB, NDUFA4, IDH2, GOT2, IMMT, SOD2, COX6C, UQCRQ, NDUFAB1

GO: 0043209: myelin sheath	5.0×10^{-57}	SLC25A3, WDR1, ATP5A1, DLST, HBB-B1, ATP5C1, HBA-A1, ATP1A1, ENO1, ATP5H, ATP5O, COX5A, HSPD1, PRDX3, LDHB, PRDX2, ATP5B, PRDX1, DLAT, IDH3A, MDH1, HSPA5, MDH2, ATP5PB, GOT2, NME2, IMMT, MIF, SOD2, TUFM, SOD1, SUCLA2, PKM, GNB2, ALB, EEF1A2, NDUFS3, CYCS, VDAC2, VDAC1, ACO2, UQCRC2, ALDOA, SLC25A5, DLD, SLC25A4, GAPDH, UBA52
GO: 0005759: Mitochondrial matrix	2.1×10^{-28}	ECHS1, ACAA2, ECI1, DLST, AK4, ETFA, PARK7, HSPD1, ACAT1, ALDH2, ACADL, OXCT1, PRDX1, DBT, DLAT, ACADM, HADH, ACSS1, ACADS, MCCC2, NDUFA9, MDH2, GOT2, ACOT13, HSPE1, SOD2, CS, BDH1, IVD, PPIF, OGDH, DLD
GO: 0070469: respiratory chain	1.3×10^{-23}	NDUFA9, NDUFA13, NDUFA7, NDUFB7, NDUFA6, NDUFA5, NDUFB11, NDUFA4, NDUFB3, NDUFS7, UQCRC2, NDUFS6, NDUFAB1, NDUFS3, CYCS, MT-CO2, CYC1, UQCRC2, NDUFV3
GO: 0005753: mitochondrial proton-transporting ATP synthase complex	1.0×10^{-21}	ATP5MD, ATP5PB, ATP5A1, ATP5C1, ATP5J, ATP5H, ATP5O, ATP5G1, MT-ATP8, ATP5L, ATP5J2, ATP5B, ATP5E
GO: 0031966: mitochondrial membrane	4.9×10^{-19}	NDUFA9, ACADVL, NDUFA13, NDUFA6, NDUFA4, COX4I1, NME2, ETFDH, COX6C, SDHB, COX5A, COX6B1, ATP5B, ACADL, IVD, OGDH, NDUFS3, VDAC2, MT-CO2, VDAC1, ACADM, ACADS
GO: 0005747: mitochondrial respiratory chain complex I	1.5×10^{-16}	NDUFA9, NDUFA13, NDUFA7, NDUFB7, NDUFA6, NDUFA5, NDUFB11, NDUFA4, NDUFB3, NDUFS7, NDUFS6, NDUFAB1, NDUFS3, NDUFV3
GO: 0000276: mitochondrial proton-transporting ATP synthase complex, coupling factor F(o)	1.6×10^{-12}	ATP5PB, ATP5J, ATP5H, ATP5O, ATP5G1, MT-ATP8, ATP5L, ATP5J2
GO: 0042645: mitochondrial nucleoid	1.6×10^{-10}	HADHB, ATP5B, HADHA, ACADVL, DBT, VDAC2, VDAC1, SOD2, SLC25A5, TUFM

GO: 0045263: proton-transporting ATP synthase complex, coupling factor F(o)	4.3×10^{-10}	ATP5PB, ATP5J, ATP5H, ATP5G1, MT-ATP8, ATP5L, ATP5J2
GO: 0005751: mitochondrial respiratory chain complex IV	3.2×10^{-8}	NDUFA4, COX4I1, MT-CO2, UQCRC2, COX6C, COX5A, COX6B1
GO: 0045261: proton-transporting ATP synthase complex, catalytic core F(1)	6.3×10^{-8}	ATP5B, ATP5E, ATP5A1, ATP5C1, ATP5O
GO: 0000275: Mitochondrial proton-transporting ATP synthase complex, catalytic core F(1)	5.2×10^{-6}	ATP5B, ATP5E, ATP5A1, ATP5C1
GO: 0045121: membrane raft	1.4×10^{-5}	ATP5A1, PARK7, ENO1, ATP1A1, HSPD1, LDHB, ATP5B, VDAC2, VDAC1, CD36, SLC25A5, CTSD, SLC25A4
GO: 0005757: Mitochondrial permeability transition pore complex	1.8×10^{-5}	PPIF, VDAC1, SLC25A5, SLC25A4
GO: 0005741: mitochondrial outer membrane	2.3×10^{-5}	HADHB, FIS1, ACSL1, VDAC3, VDAC2, VDAC1, SLC25A4, CPT1B, HK2, NIPSNAP2
GO: 0032991: macromolecular complex	2.0×10^{-4}	FIS1, NDUFA5, HSPA5, H3F3A, TPM1, ADIPOQ, GOT2, ATP2A2, ATP1A1, SOD1, HSPD1, PRDX3, TTR, GNB2, ALB, PSAP, SUCLG1, VDAC1, CD36, ALDOA
GO: 0045252: oxoglutarate dehydrogenase complex	6.5×10^{-4}	OGDH, DLST, DLD
GO: 0016020: membrane	9.2×10^{-4}	ACADVL, NDUFA13, SLC25A3, COX4I1, TRF, ATP2A2, ATP5C1, PARK7, ENO1, ATP5G1, HK2, CAPZB, MPC1, CD36, ACSL1, SDHD, CPT1B, SDHB, NIPSNAP2, ATP5J2, COX6B1, HADHB, HADHA, AFG3L2, NDUFS7, ASPH, BDH1, NDUFS6, ADSSL1, VDAC3, NDUFS3, VDAC2, MT-CO2, VDAC1, UQCRC2, DSG4, ALDOA, SLC25A5, SLC25A11, SLC25A4, ATP5MD, NDUFB7, NDUFB11, ATP5A1, NDUFB3, ETFDH, ATP5J, ATP1A1, ATP5H, SRL, ATP5O, COX5A, HSPD1, ATP5L, CKMT2, ATP5B, LDHB, ATP5E, CYC1, NDUFV3, FIS1,

		NDUFA7, NDUFA6, NDUFA5, HSPA5, MDH2, ATP5PB, NDUFA4, GOT2, IMMT, COX6C, MT-ATP8, REEP5, UQCRCQ, VAPB, PFKM
GO: 0005967: mitochondrial pyruvate dehydrogenase complex	1.3×10^{-3}	PDHB, DLAT, DLD
GO: 0005758: mitochondrial intermembrane space	1.5×10^{-3}	NDUFB7, AK2, CYCS, IMMT, PARK7, SOD1
GO: 0045254: pyruvate dehydrogenase complex	1.7×10^{-3}	PDHB, DLAT, DLD
GO: 0016529: sarcoplasmic reticulum	2.8×10^{-3}	REEP5, ASPH, ATP2A2, SRL, HK2
GO: 0033017: sarcoplasmic reticulum membrane	3.3×10^{-3}	REEP5, ASPH, ATP2A2, SRL
GO: 0005750: mitochondrial respiratory chain complex III	4.1×10^{-3}	UQCRCQ, UQCRC2, CYC1
GO: 0046930: Pore complex	4.8×10^{-3}	VDAC3, VDAC2, VDAC1
GO: 0005777: Peroxisome	5.8×10^{-3}	FIS1, PRDX5, ACSL1, ECH1, IDH2, SOD1
GO: 0030017: sarcomere	6.2×10^{-3}	ACTC1, CAPZB, ACTN2, TNNT2
GO: 0016507: mitochondrial fatty acid beta-oxidation multienzyme complex	1.6×10^{-2}	HADHB, HADHA
GO: 0000274: mitochondrial proton-transporting ATP synthase, stator stalk	1.6×10^{-2}	ATP5H, ATP5O
GO: 0005782: peroxisomal matrix	2.1×10^{-2}	PRDX5, PRDX1, HSPD1
GO: 1990584: cardiac Troponin complex	2.4×10^{-2}	TNNC1, TNNT2
GO: 0017133: mitochondrial electron transfer flavoprotein complex	2.4×10^{-2}	ETFDH, ETFA
GO: 0045259: proton-transporting ATP synthase complex	3.2×10^{-2}	ATP5B, ATP5A1

GO: 0005749: mitochondrial respiratory chain complex II, succinate dehydrogenase complex (ubiquinone)	3.2×10^{-2}	SDHD, SDHB
GO: 0005947: mitochondrial alpha-ketoglutarate dehydrogenase complex	4.0×10^{-2}	DBT, DLD
GO: 0031305: integral component of mitochondrial inner membrane	4.0×10^{-2}	SLC25A3, MPC1, ETFDH

Table SXI. Enriched cellular components of hypophosphorylation in MI-SCD (myocardial ischemia-sudden cardiac death) mice.

Term	P-value	Genes
GO: 0005737: Cytoplasm	2.3x10 ⁻³⁷	HNRNPU, DCAF8, FNBP1L, MYLK, DCAF6, ALKBH3, GJA1, EFR3A, DPYSL3, FBXO4, MYOZ2, PRKACB, AGFG1, UNC13B, PRKAB2, SMARCC1, CXADR, LIMCH1, PRKCB, FNBP1, MTUS2, ANK2, CTPS, CSNK1E, PRKAB1, EML1, CARHSP1, CCNY, PRKAR1A, RUFY3, ZFYVE19, SIK3, CD2BP2, CFAP61, MTMR1, MACF1, DHX9, SLAIN2, VPS26B, FXR1, RIC8A, STRIP1, STRIP2, FXR2, LARP1, CMYA5, MAP4, STX4A, S100A11, SPTBN1, SEC31A, PEA15A, RAB11FIP5, ACE, STARD10, RMDN3, PRRC2C, IRF2BP2, PA2G4, GPN1, PUM2, EHD2, SNW1, WNK1, ETL4, HNRNPD, ANP32B, CPEB3, MYOM1, IGHM, RYR2, PPP1R11, SH3KBP1, RPLP1, FAF1, TGFB1I1, RPLP0, MYPN, RPTOR, AKAP12, GYS1, CSRP3, KIF1C, TNKS1BP1, NELFB, GIT1, UBXN6, PCYT1A, ZFR, SIRT2, PSMA3, CANX, MAPT, ARHGEF7, SYNPO2, GPS1, USO1, NEXN, ARVCF, BCLAF1, CTNNA1, CTNNA3, TRP53BP1, FLNC, FILIP1L, SVIL, RANBP3, CAVIN1, SEPTIN2, CAVIN2, TRAPPC10, RFTN1, CAVIN4, AP3D1, HUWE1, MIB2, SORBS2, SORBS1, SORBS3, LRPPRC, TJP1, FKBP1A, PDCL3, PRKRA, TRIP10, CTNNB1, TCAP, HDGF, TACC2, FHOD1, PDCD5, CTNND1, CPOX, NUCKS1, CASC3, BZW2, VIRMA, EDC4, STK11, SLK, PPIP5K2, CFL2, OSBP, CFL1, TRAPPC12, GRB10, BANF1, OSTF1, GTF2I, CAST, PDIA3, TTC7B, CASK, TNNI3K, OBSCN, MAP7D1, SRSF2, SRSF7, VCL, VCP, CACNA1C, NDRG2, NDRG1, RTN4, SLC9A1, VCPIP1, BAG3, G3BP1, TPR, EIF4EBP1, PACSIN3, TPPP, NIBAN1, HSPA8, CAV2, OSBPL3, DSTN, MSN, EIF2S2, SH3BP5L, JMY, GNAS, AAK1, EIF4G1, YWHAE, GSK3B, RBM25, NUMA1, YWHAB, SNAP23, LDB3, SLC2A4, YBX1, YBX3, BICD2, LMOD2, PPP2R5E, MCF2L, PGM5, SCN5A, NCK1, SNTA1, EIF5B, ABCC1, DST, DTX3L, PDPK1, SH2D3C, PPP2R5A, OXSR1, PEX1, YWHAZ, EPN2, DNM2, EPN3, GAP43, RABEP1, MYH3, EEF1D, PALLD, THRAP3, RNF207, BIRC6, DOCK1, PRKAA1, HDAC2, PRKAA2, ACSS2, SMPX, ANKS1, USP10, SRF, PERM1, SRSF1, TTN, PALMD, ABLIM3, STOM, TRIM47, PDLIM5, PDLIM4, CLASP1, ABCF1, ARFGEF2, PPP1R14A,

		HNRNPA3, PPP1R14C, USP20, TXNRD3, NOS3, BNIP3, SGTA, PTPN12, PML, 3425401B19RIK, DNAJA2, EIF3G, STUB1, CD248, SLIRP, EIF3C, SNTB2, EIF3B
GO: 0005829: cytosol	4.0×10 ⁻²³	FHOD1, PDCD5, CTNND1, ARAF, CPOX, HNRNPU, DCAF8, FBNP1L, VIRMA, DCAF6, ALKBH3, GJA1, STK11, EFR3A, PPIP5K2, OSBP, CFL1, DPYSL3, GRB10, BANF1, PRKACB, CAST, MEF2A, UNC13B, PRKAB2, PRKCB, TTC7B, CASK, CTPS, CSNK1E, PRKAB1, EML1, CARHSP1, OBSCN, RALGAPB, RUFY3, MAP7D1, SRSF2, CD2BP2, VCP, DHX9, SLAIN2, VPS26B, NDRG1, FXR1, RIC8A, STRIP1, STRIP2, FXR2, LARP1, BAG3, G3BP1, CMYA5, EIF4EBP1, PACSIN3, SUDS3, MAP4, TPPP, SPTBN1, SEC31A, PEA15A, NIBAN1, HSPA8, OSBPL8, CAV2, OSBPL3, STARD10, PRRC2C, MSN, GPN1, PUM2, EHD2, WNK1, GNAS, HNRNPD, CPEB3, EIF4G1, YWHAE, GSK3B, IGHM, NUMA1, YWHAB, FAF1, TGFB1I1, RPLP1, RPLP0, SLC2A4, YBX1, OSBPL11, YBX3, BICD2, RPTOR, AKAP12, GYS1, CSRP3, PPP2R5E, NELFB, PGM5, GIT1, UBXN6, NCK1, PCYT1A, DTX3L, DST, PDPK1, SH2D3C, PPP2R5A, WIPI2, OXSR1, PEX1, YWHAZ, SIRT2, DNMT2, GIGYF1, PSMA3, TBC1D5, EEF1D, PALLD, HNRNPH2, MAPT, ARHGEF7, DOCK1, PRKAA1, PRKAA2, ACSS2, ANKS1, USP10, GPS1, SYNPO2, USO1, TCOF1, LMNA, CTNNA1, TRIM47, CTNNA3, FLNC, PDLIM5, EIF4B, ABCF1, ARFGEF2, SVIL, TXNRD3, CAVIN1, CAVIN2, NOS3, TRAPPC10, SGTA, CAVIN4, HUWE1, PDAP1, PTPN12, SORBS1, PML, TJP1, FKBP1A, PDCL3, GOLPH3, PRKRA, DNAJA2, EIF3G, CTNNB1, ACIN1, STUB1, ESYT2, TACC2
GO: 0030018: Z disc	8.7×10 ⁻²³	RYR2, SYNPO2, NEXN, LDB3, CACNA1C, MYPN, TTN, STK11, CSRP3, JPH2, BAG3, CFL2, PGM5, SCN5A, FLNC, PDLIM5, PDLIM4, MYOZ2, DST, CAVIN4, PPP2R5A, SORBS2, ANK2, FKBP1A, OBSCN, PALLD, 3425401B19RIK, TCAP, CTNNB1, STUB1, VCL

GO: 0005634: nucleus	1.9×10 ⁻¹⁸	HNRNPU, DCAF8, DCAF6, ALKBH3, GJA1, TRIM28, PRKACB, AGFG1, TMPO, SRRM2, MEF2A, PRKAB2, SMARCC1, CXADR, SMARCC2, PRKCB, MTUS2, CSNK1E, PRKAB1, SRRM1, CCNY, CD2BP2, DHX9, HTATSF1, HNRNPLL, CDKN2AIP, UBE2J1, FXR1, STRIP1, FXR2, CMYA5, RBM12, RBM10, S100A11, SPTBN1, ZRANB2, IRF2BP1, RMDN3, IRF2BP2, PA2G4, GPN1, SNW1, HNRNPD, OGDH, ANP32B, CPEB3, PPP1R11, FAF1, TGFB1I1, RPLP0, MYPN, CSRP3, JPH2, TNKS1BP1, NELFB, UBXN6, PCYT1A, ZFR, SIRT2, PSMA3, HNRNPH2, MAPT, RNMT, SYNPO2, GPS1, PURB, ARVCF, BCLAF1, TCOF1, LMNA, TRP53BP1, FILIP1L, SVIL, RANBP3, CAVIN1, SEPTIN2, MFAP1B, HUWE1, SORBS1, MLH1, SORBS3, GATAD2B, LRPPRC, TJP1, NFIB, PRKRA, CTNNB1, TCEA1, TRIP12, HDGF, TACC2, TJP2, FHOD1, PDCD5, CTNND1, NUCKS1, CASC3, VIRMA, EDC4, CHCHD2, STK11, CFL2, CFL1, TRAPPC12, BANF1, GTF2I, CAST, PDIA3, MLIP, CASK, DYRK1B, PRPF4B, TNNI3K, OBSCN, HNRNPUL1, HNRNPUL2, SRSF2, SREK1, SRSF6, SRSF7, SRSF9, VCP, PDS5B, NDRG2, NDRG1, ACACB, TOR1AIP1, VCPIP1, BAG3, G3BP1, TPR, EIF4EBP1, TPPP, SUDS3, HSPA8, OSBPL8, CAV2, OSBPL3, IGF2R, ZC3HC1, JMY, GNAS, UBE2M, EIF4G1, YWHAE, GSK3B, RBM25, RBM26, NUMA1, YWHAB, ZFP768, YBX1, YBX3, BICD2, SFR1, PPP2R5E, SPEG, NCK1, RBM17, RBM15, DST, DTX3L, PDPK1, ELAC2, PPP2R5A, SAFB, YWHAZ, DNM2, EPN3, EEF1D, PALLD, THRAP3, RBM20, BIRC6, PRKAA1, HDAC2, PRKAA2, SMPX, USP10, SRF, PERM1, SRSF1, TTN, U2AF2, TRA2A, TRIM47, RALY, PDLIM4, ABCF1, RNF20, RBM39, HNRNPA3, TXNRD3, NOS3, BNIP3, SGTA, PTPN12, KLF3, PML, DNAJA2, EIF3G, ACIN1, STUB1, SLIRP
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GO: 0048471: perinuclear region of cytoplasm	4.3×10 ⁻¹⁴	IGHM, GSK3B, YWHAB, FAF1, LDB3, CASC3, SLC2A4, YBX1, SLK, OSBP, TRAPPC12, SCN5A, PRKACB, DST, CASK, ANK2, EML1, YWHAZ, SIRT2, DNM2, EPN3, RNF207, VCP, USO1, NDRG2, NDRG1, SLC9A1, FXR1, LMNA, CMYA5, STOM, TPPP, STX4A, PDLIM4, SEC31A, ARFGEF2, HSPA8, USP20, SEPTIN2, CAV2, MSN, SORBS2, IGF2R, LRPPRC, PUM2, PDCL3, EHD2, PRKRA, GNAS, EIF3G, CTNNB1, SLIRP
GO: 0005856: cytoskeleton	6.0×10 ⁻¹³	MYOM1, NUMA1, SH3KBP1, TGFB1I1, FHOD1, HNRNPU, LDB3, FNBP1L, BICD2, MYLK, LMOD2, AKAP12, CSRP3, CFL2, CFL1, TNKS1BP1, KIF1C, PGM5, GIT1, UBXN6, SNTA1, DST, LIMCH1, FNBP1, MTUS2, ANK2, EML1, SIRT2, DNM2, PALLD, ZFYVE19, MAP7D1, BIRC6, MAPT, VCL, CFAP61, MACF1, DHX9, NEXN, SLAIN2, NDRG1, TPR, CTNNA1, STOM, CTNNA3, FLNC, MAP4, TPPP, PDLIM4, SPTBN1, CLASP1, ARFGEF2, SVIL, USP20, NOS3, SEPTIN2, MSN, RMDN3, SORBS2, SORBS1, SORBS3, LRPPRC, CR1L, JMY, TRIP10, CTNNB1, TACC2, SNTB2
GO: 0042383: sarcolemma	1.4×10 ⁻¹²	RYR2, MLIP, DST, CAV2, NOS3, CAVIN4, ANK2, CACNA1C, SLC2A4, SLC9A1, CACNB2, OBSCN, FXYD1, GNAS, PGM5, SCN5A, FLNC, STX4A, BVES, VCL, SNTA1
GO: 0005654: nucleoplasm	7.6×10 ⁻¹¹	FHOD1, HNRNPU, DCAF8, NUCKS1, VIRMA, DCAF6, EDC4, ALKBH3, GJA1, STK11, TRIM28, OSBP, TRAPPC12, BANF1, GTF2I, MEF2A, PRKAB2, SMARCC1, CXADR, SMARCC2, PRKCB, DYRK1B, CSNK1E, HNRNPUL1, HNRNPUL2, SIK3, SRSF2, CD2BP2, SREK1, SRSF7, SRSF9, VCP, DHX9, PDS5B, HTATSF1, CDKN2AIP, SLC9A1, RBM12, PEA15A, ZRANB2, DENND4B, IRF2BP1, IRF2BP2, GPN1, ZC3HC1, SNW1, HNRNPD, ANP32B, CPEB3, GSK3B, NUMA1, FAF1, SNAP23, OSBPL11, RPTOR, CSRP3, NELFB, SCN5A, COA6, RBM17, RBM15, DTX3L, DST, ELAC2, WIPI2, SAFB, EPN3, PSMA3, EEF1D, THRAP3, HNRNPH2, DOCK1, HDAC2, PRKAA2, ACSS2, ANKS1, RNMT, USP10, SRF, GPS1, SYNPO2, PERM1, SRSF1, PURB, BCLAF1, TCOF1, LMNA, TRA2A, TRP53BP1, LNPB, ABCF1, RNF20, RBM39, HNRNPA3, RANBP3, TXNRD3, SEPTIN2, CAVIN2, BNIP3, MFAP1B, HUWE1, MLH1, KLF3, GATAD2B, PML, LRPPRC, PDCL3, NFIB, PRKRA, TRIP10, TCEA1, ACIN1, TRIP12, HDGF, STUB1, TACC2, SNTB2

GO: 0014704: intercalated disc	1.0×10^{-10}	CXADR, DST, FHOD1, ANK2, SLC9A1, TJP1, GJA1, OBSCN, FXYD1, CTNNA1, CTNNB1, PGM5, SCN5A, VCL
GO: 0016607: Nuclear speck	1.3×10^{-10}	RBM25, PRKAA1, PRKAA2, SRSF1, HNRNPU, CASC3, VIRMA, BCLAF1, HECTD1, U2AF2, LMNA, CMYA5, RBM10, SRRM2, FBNP4, RBM39, RBM15, PRPF4B, GATAD2B, SRRM1, SNW1, THRAP3, SRSF2, ACIN1, CD2BP2, TRIP12, MAPT, SREK1, SRSF6, SRSF7, DOCK1, SRSF9
GO: 0032991: macromolecular complex	1.9×10^{-10}	GSK3B, RYR2, RETREG3, NUMA1, YWHAB, HNRNPU, STK11, GJA1, TRIM28, GRB10, UBXN6, SNTA1, RBM17, CXADR, DTX3L, CASK, WIP1, PRKAB1, YWHAZ, DNM2, GIGYF1, RABEP1, PRKAR1A, CANX, ARHGEF7, VCL, PI4K2A, PRKAA1, HDAC2, VCP, PRKAA2, DHX9, USP10, CACNA1C, RTN4, PLN, EIF4EBP1, SPTBN1, RBM10, RBM39, HSPA8, CAVIN1, CAV2, RFTN1, TJP1, PDCL3, WNK1, CTNNB1, SNTB2
GO: 0005925: focal adhesion	1.1×10^{-9}	DST, CAV2, PDPK1, SH3KBP1, TGFB1I1, SYNPO2, MSN, NEXN, SORBS2, PTPN12, SORBS1, SORBS3, DCAF6, PALLD, CFL1, PGM5, ARHGEF7, GIT1, CLASP1, TNS2, VCL
GO: 0030054: cell junction	3.3×10^{-9}	SH3KBP1, TGFB1I1, SYNPO2, SNAP23, CTNND1, NEXN, CACNA1C, RTN4, GJA1, ARVCF, PALMD, OSBP, CTNNA1, PGM5, PDLIM5, PDLIM4, BVES, GIT1, SPTBN1, TNS2, SNTA1, ATAD1, UNC13B, SVIL, ARFGEF2, SLC16A1, CXADR, DST, PDPK1, SORBS2, ANK2, PTPN12, SORBS1, SORBS3, DNM2, TJP1, GAP43, PALLD, RUFY3, AAK1, CTNNB1, CPEB3, ARHGEF7, VCL, PI4K2A, SNTB2, TJP2
GO: 0005912: adherens junction	8.4×10^{-9}	CXADR, CTNND1, SNAP23, MSN, NEXN, LDB3, SORBS1, NDRG1, TJP1, ARVCF, CTNNA1, CTNNB1, TNKS1BP1, CTNNA3, PGM5, PDLIM5, PDLIM4, VCL
GO: 0001725: stress fiber	1.1×10^{-8}	DST, LIMCH1, SYNPO2, FHOD1, LDB3, SORBS1, MYLK, ABLIM3, PALLD, BAG3, PGM5, PDLIM5, PDLIM4, VCL
GO: 0031430: M band	1.6×10^{-8}	MYOM1, OBSCN, SMPX, CMYA5, PPP2R5A, ANK2, SPTBN1, TTN, LMOD2

GO: 0014069: postsynaptic density	2.6×10^{-8}	MACF1, GSK3B, RPLP0, CACNA1C, RTN4, FXR1, FXR2, MAP4, PDLIM5, GIT1, SPTBN1, CAST, HSPA8, HNRNPA3, DST, PDPK1, BNIP3, CASK, SORBS2, ANK2, YWHAZ, DNM2, GAP43, HNRNPH2, MAPT, CPEB3
GO: 0005768: Endosome	9.1×10^{-8}	RAB5B, USP10, GOLIM4, VPS26B, SLC2A4, OSBPL11, PIP4P2, GJA1, PACSIN3, PDLIM4, STX4A, GIT1, UBXN6, RAB11FIP5, SEC31A, ARFGEF2, ACE, DTX3L, RFTN1, VPS13A, MIB2, ANK2, IGF2R, PML, EPN2, DNM2, EPN3, EHD2, GOLPH3, RABEP1, TBC1D5, RAB12, EHBP1L1, GNAS, OCIAD1, BIRC6, PI4K2A
GO: 0015629: actin cytoskeleton	3.2×10^{-7}	MACF1, SVIL, DST, SEPTIN2, DHX9, SYNPO2, NEXN, DSTN, MYLK, ABLIM3, PALLD, CFL2, CFL1, CTNNA1, TNKS1BP1, FLNC, PDLIM5, PDLIM4, MYOZ2, VCL
GO: 0045202: synapse	3.8×10^{-7}	YWHAZ, VCP, SH3KBP1, SDC2, SNAP23, CTNND1, RPLP0, CACNA1C, VCPIP1, PGRMC1, ABLIM3, PALMD, DPYSL3, PDLIM5, PDLIM4, STX4A, GIT1, SNTA1, ATAD1, UNC13B, ARFGEF2, SLC16A1, SEPTIN2, CAV2, CASK, SORBS2, ANK2, SORBS1, DNM2, FKBP1A, PSMA3, GAP43, PRKAR1A, EEF1D, AAK1, HNRNPD, CTNNB1, CPEB3, PI4K2A, EIF3B, SNTB2
GO: 0043034: costamere	9.2×10^{-7}	FXR1, SVIL, SMPX, CMYA5, PGM5, ANK2, VCL
GO: 0030027: lamellipodium	1.1×10^{-6}	CTNND1, SORBS2, MYLK, DNM2, ABLIM3, PALLD, RUFY3, MCF2L, DPYSL3, CFL1, CTNNA1, CTNNB1, CTNNA3, ARHGEF7, PDLIM4, STX4A, GIT1
GO: 0098978: glutamatergic synapse	2.2×10^{-6}	YWHAZ, GSK3B, VCP, SNAP23, CTNND1, CACNA1C, NDRG2, NDRG1, RTN4, FXR1, FXR2, ABLIM3, P2RY2, CFL1, EIF4EBP1, STX4A, GIT1, SPTBN1, ATAD1, UNC13B, HSPA8, AP3D1, YWHAZ, SIRT2, DNM2, PRKAR1A, EEF1D, CANX
GO: 0016020: membrane	4.4×10^{-6}	RETREG3, CTNND1, GOLIM4, CPOX, SLC4A3, FNBP1L, GJA1, STK11, EFR3A, OSBP, CFL1, CAR14, BVES, PRKACB, TNS2, BORCS6, TMPO, CAST, UNC13B, MLIP, CXADR, FNBP1, TTC7B, CASK, ANK2, HSPG2, AFG3L1, CACNB2, BCAM, OBSCN, ADCY9, CCNY, TMX1, PRKAR1A, RUFY3, VCL, PI4K2A, MTMR1, MACF1, RAB5B, SDC2, CACNA1C, VPS26B, NDRG1, TOR1AIP1, RTN4, SLC9A1, UBE2J1, FXR1, RIC8A, BCL2L13, TMEM245, FXR2,

		BAG3, TPR, PACSIN3, STX4A, SPTBN1, SEC31A, RAB11FIP5, NIBAN1, HSPA8, OSBPL8, ACE, CAV2, OSBPL3, STARD10, MSN, RMDN3, PHKB, IGF2R, EHD2, ARMC10, WNK1, FXYD1, JMY, GNAS, AAK1, CDS2, GSK3B, IGHM, RYR2, NUMA1, SH3KBP1, RPLP0, SRPR, SNAP23, MIA2, SLC2A4, OSBPL11, AKAP12, PIP4P2, MFSD6, JPH2, MCF2L, FUNDC1, SCN5A, UBXN6, SNTA1, ABCC1, RBM15, PCYT1A, DTX3L, DST, PDPK1, SH2D3C, VPS13A, PPP2R5A, RRAS2, WIPI2, PEX1, SIRT2, DNM2, GAP43, TBC1D5, CANX, BIRC6, MAPT, DOCK1, SLC20A2, USO1, RRBPI, MIEF1, AKAP1, PGRMC1, PLN, PALMD, P2RY2, CTNNA1, STOM, FLNC, PDLIM5, FILIP1L, PDLIM4, LNPKE, GPR157, ATAD1, ARFGEF2, SVIL, SLC16A1, PPP1R14C, CAVIN1, SEPTIN2, CAVIN2, CMTM4, NOS3, BNIP3, SGTA, RFTN1, CAVIN4, AP3D1, SORBS2, SORBS1, SGPP1, PML, LRPPRC, TJP1, FKBP1A, GOLPH3, GPAM, CR1L, TOMM70A, RAB12, DNAJA2, TRIP10, CTNNB1, CD248, ESYT2, TJP2, SNTB2
GO: 0005681: spliceosomal complex	6.2×10^{-6}	SRRM2, RBM17, HSPA8, HNRNPA3, SRSF1, HNRNPU, PRPF4B, CASC3, SRRM1, SNW1, U2AF2, TRA2A, SRSF2, RALY, SREK1
GO: 0016363: nuclear matrix	6.8×10^{-6}	SMARCC1, SMARCC2, NUMA1, TGFB1I1, HNRNPU, CASK, SORBS1, PML, SRRM1, SNW1, CFL2, LMNA, CFL1
GO: 1990904: ribonucleoprotein complex	1.1×10^{-5}	HSPA8, GSK3B, DHX9, RPLP0, HNRNPU, CASC3, CSNK1E, YBX1, PA2G4, LRPPRC, G3BP1, HNRNPD, HNRNPH2, SLIRP, RBM12
GO: 0030426: growth cone	2.0×10^{-5}	GSK3B, CXADR, CTNND1, CSNK1E, NDRG2, SIRT2, DNM2, FXR1, FXR2, PALLD, RUFY3, DPYSL3, CFL1, MAPT, ARHGEF7
GO: 0098794: postsynapse	2.4×10^{-5}	ATAD1, HSPA8, SNAP23, RPLP0, AP3D1, FXR1, FXR2, ARHGEF7, CPEB3, STX4A, GIT1, SPTBN1, EIF4B, EIF4G1
GO: 0010494: cytoplasmic stress granule	3.3×10^{-5}	RPTOR, VCP, LARP1, PRKAA2, G3BP1, PRRC2C, YBX1, CASC3, PUM2, EIF4G1
GO: 0031588: nucleotide-activated protein kinase complex	3.6×10^{-5}	PRKAB2, PRKAA1, PRKAA2, PRKAR1A, PRKAB1

GO: 0043025: neuronal cell body	3.7×10 ⁻⁵	GSK3B, PRKAA1, PRKAA2, NUMA1, PDE1C, SDC2, CACNA1C, YBX1, RTN4, RPTOR, AKAP12, FXR1, PGRMC1, FXR2, CFL1, EIF4B, AGFG1, HSPA8, CASK, SORBS2, CSNK1E, PUM2, PALLD, RUFY3, CANX, GNAS, MAPT, ARHGEF7, PI4K2A
GO: 0005635: nuclear envelope	3.8×10 ⁻⁵	RYR2, MLIP, PCYT1A, DST, CAV2, FAF1, BNIP3, TOR1AIP1, RTN4, BICD2, LMNA, TPR, BANF1, ABCF1, TMPO
GO: 0045121: membrane raft	4.4×10 ⁻⁵	HSPA8, GSK3B, CXADR, CAVIN1, CAVIN2, CAV2, NOS3, RFTN1, CASK, ANK2, SLC2A4, SORBS1, SLC9A1, GJA1, GNAS, STOM, MAPT, VCL, PI4K2A
GO: 0042995: cell projection	4.6×10 ⁻⁵	CFAP61, MACF1, FHOD1, LDB3, CACNA1C, CASC3, NDRG2, RTN4, MYLK, PALMD, CFL1, DPYSL3, PDLIM5, PDLIM4, STX4A, GIT1, SPTBN1, GPR157, AGFG1, SVIL, ARFGEF2, DST, SEPTIN2, PDPK1, OSBPL3, STARD10, SH2D3C, MSN, SORBS2, PTPN12, SIRT2, DNM2, GAP43, PALLD, RUFY3, TRIP10, AAK1, GNAS, CTNNB1, MAPT, CPEB3, ARHGEF7, PI4K2A
GO: 0005874: microtubule	6.1×10 ⁻⁵	MACF1, HSPA8, GSK3B, NUMA1, DST, RMDN3, MTUS2, NDRG1, EML1, LRPPRC, SIRT2, DNM2, BAG2, TRIP10, KIF1C, MAPT, TPPP, MAP4, CLASP1, SNTB2
GO: 0030425: dendrite	9.4×10 ⁻⁵	GSK3B, PRKAA1, PRKAA2, NUMA1, RPLP0, CACNA1C, YBX1, CASC3, RPTOR, FXR1, FXR2, BAG2, PALMD, KIF1C, EIF4B, HSPA8, BNIP3, CASK, SORBS2, PUM2, GAP43, ADCY9, RUFY3, GNAS, MAPT, CPEB3, PI4K2A
GO: 0005741: Mitochondrial outer membrane	2.2×10 ⁻⁴	ATAD1, BNIP3, VPS13A, RMDN3, MIEF1, AKAP1, PGRMC1, GJA1, GPAM, FUNDC1, TOMM70A, NELFB, RAB11FIP5
GO: 0015630: microtubule cytoskeleton	2.9×10 ⁻⁴	MACF1, RBM39, DST, SEPTIN2, MTUS2, SLAIN2, NDRG1, EML1, DNM2, EHD2, MAP7D1, MAPT, MAP4, CLASP1
GO: 0005739: mitochondrion	3.5×10 ⁻⁴	YWHAE, GSK3B, SNAP23, ARAF, DCAF8, CPOX, ALKBH3, STK11, GJA1, CHCHD2, FUNDC1, GIT1, COA6, BCKDHA, PDIA3, EIF5B, ELAC2, VPS13A, ANK2, YWHAZ, SIRT2, AFG3L1, PCCA, PALLD, PI4K2A, MIEF1, ACACB, SLC9A1, AKAP1, BCL2L13, PGRMC1, PLN, P2RY2, STOM, TPPP, RAB11FIP5, ATAD1, SLC16A1, PDHA1, TXNRD3, CAVIN1, NOS3, BNIP3,

		HUWE1, RMDN3, COQ9, GPN1, LRPPRC, BCKDK, GOLPH3, MTRES1, ARMC10, GPAM, TOMM70A, OGDH, OCIAD1, SLIRP
GO: 0005901: caveola	4.1×10 ⁻⁴	EHD2, CAVIN1, CAVIN2, CAV2, NOS3, CAVIN4, FXYD1, SCN5A, BVES
GO: 0030055: cell-substrate junction	5.0×10 ⁻⁴	NEXN, PGM5, SORBS1, SORBS3
GO: 0030424: axon	5.7×10 ⁻⁴	YWHAE, HSPA8, GSK3B, PRKAA1, PRKAA2, DST, SH2D3C, AP3D1, NEXN, MYPN, DNM2, FXR1, GAP43, FXR2, ADCY9, BAG2, PALLD, RUFY3, CANX, KIF1C, MAPT, MAP4
GO: 0098793: presynapse	6.1×10 ⁻⁴	FXR1, UNC13B, CACNB2, HSPA8, FXR2, SGTA, SNAP23, AP3D1, AAK1, SLC2A4, PDLIM5, DNM2
GO: 0016600: flotillin complex	7.1×10 ⁻⁴	CTNND1, CTNNA1, CTNNB1, SORBS1
GO: 0005813: centrosome	7.5×10 ⁻⁴	GSK3B, SLC16A1, NUMA1, USP20, DHX9, PRKCB, MFAP1B, PPP2R5A, HNRNPU, MTUS2, SLAIN2, SORBS1, NDRG1, BICD2, SIRT2, DNM2, PRKAR1A, ZFYVE19, CTNNB1, ARHGEF7, PRKACB, GIT1, CLASP1
GO: 0031674: I band	1.1×10 ⁻³	TJP1, CFL2, TCAP, MYPN, TTN
GO: 0030315: T-tubule	1.3×10 ⁻³	FXYD1, MSN, ANK2, CACNA1C, SLC2A4, SCN5A, SLC9A1
GO: 0005911: cell-cell junction	1.5×10 ⁻³	CXADR, SH3KBP1, CTNND1, CASK, MYLK, TJP1, GJA1, CFL1, CTNNA1, CTNNB1, VCL, TJP2, NCK1
GO: 0005916: fascia adherens	1.6×10 ⁻³	GJA1, CTNNB1, CTNNA3, VCL
GO: 0031965: nuclear membrane	2.3×10 ⁻³	OSBPL8, RBM15, OSBPL3, CASC3, YBX1, TOR1AIP1, PML, PUM2, ZC3HC1, LMNA, TPR, CTNNB1, TMPO
GO: 0042470: Melanosome	2.4×10 ⁻³	YWHAE, PDIA3, HSPA8, RAB5B, YWHAB, CANX, STOM, YWHAZ
GO: 1990124: messenger ribonucleoprotein complex	2.5×10 ⁻³	HSPA8, HNRNPA3, YBX1, CPEB3
GO: 0005938: cell cortex	2.6×10 ⁻³	EPN3, MACF1, NUMA1, DST, SEPTIN2, FNBP1, TRIP10, CTNNB1, FNBP1L, ARHGEF7, CLASP1
GO: 0071013: catalytic step 2 spliceosome	2.7×10 ⁻³	SRRM2, HNRNPA3, SNW1, SRSF1, HNRNPU, RALY, PRPF4B, SRRM1

GO: 0016328: lateral plasma membrane	3.4×10^{-3}	GJA1, ABCC1, SLC16A1, NUMA1, CTNNB1, SCN5A, BVES
GO: 0043209: myelin sheath	3.4×10^{-3}	PDIA3, HSPA8, VCP, PDHA1, SEPTIN2, CANX, MSN, TPPP, NDRG1, RTN4, SIRT2
GO: 0012505: endomembrane system	4.3×10^{-3}	PGRMC1, RAB5B, PPP1R14C, TMX1, RUFY3, MCF2L, SLC2A4, STX4A, SPTBN1
GO: 0036464: cytoplasmic ribonucleoprotein granule	4.6×10^{-3}	FXR1, EDC4, FXR2, DHX9, RPLP0, HNRNPU, MAPT
GO: 0070937: CRD-mediated mRNA stability complex	5.0×10^{-3}	DHX9, HNRNPU, YBX1
GO: 0031941: filamentous actin	5.4×10^{-3}	DPYSL3, EHBP1L1, LDB3, PDLIM5, PDLIM4
GO: 0005783: endoplasmic reticulum	5.9×10^{-3}	RYR2, VCP, RETREG3, FAF1, SRPR, USO1, RPLP0, MIA2, RRBP1, YBX1, RTN4, SLC9A1, UBE2J1, AKAP1, VCIPI1, PGRMC1, GJA1, JPH2, PLN, OSBP, STOM, SCN5A, LNPB, SEC31A, NCK1, CAST, PDIA3, OSBPL8, PCYT1A, DST, CAVIN1, TXNRD3, CAV2, BNIP3, OSBPL3, VPS13A, PML, SGPP1, PDCL3, ARMC10, TMX1, EEF1D, CANX, ESYT2, STUB1, CDS2
GO: 0097431: mitotic spindle pole	6.5×10^{-3}	NUMA1, RMDN3, ARHGEF7, EML1, GIT1
GO: 0043197: dendritic spine	6.6×10^{-3}	FXR1, HSPA8, ARFGEF2, GSK3B, FXR2, PALMD, CTNND1, CFL1, CANX, PDLIM4, STX4A
GO: 0005915: zonula adherens	6.9×10^{-3}	CTNND1, CTNNA1, VCL
GO: 0043005: neuron projection	7.7×10^{-3}	HSPA8, RYR2, HNRNPA3, CXADR, ANKS1, SH3KBP1, SNAP23, ANK2, CSNK1E, RTN4, PGRMC1, BAG3, CFL1, CTNNB1, MAPT, MAP4, ARHGEF7, CPEB3, PDLIM4, GIT1, PI4K2A
GO: 0035145: exon-exon junction complex	7.7×10^{-3}	THRAP3, SRSF1, ACIN1, CASC3
GO: 0101031: chaperone complex	8.7×10^{-3}	HSPA8, BAG2, BAG3, STUB1
GO: 0005769: early endosome	1.0×10^{-2}	RAB5B, DTX3L, USP10, RFTN1, AP3D1, MIB2, ANK2, VPS26B, IGF2R, EHD2, GJA1, RABEP1, P2RY2, RAB11FIP5
GO: 0030017: sarcomere	1.0×10^{-2}	MYOM1, RYR2, OBSCN, TTN, LMOD2
GO: 0016327: apicolateral plasma membrane	1.1×10^{-2}	TJP1, CXADR, CTNND1, CTNNB1
GO: 0016529: Sarcoplasmic reticulum	1.1×10^{-2}	FKBP1A, RYR2, JPH2, PLN, CMYA5, SLC2A4

GO: 0005844: polysome	1.1×10 ⁻²	FXR1, FXR2, LARP1, DHX9, EIF4G1
GO: 0005952: cAMP-dependent protein kinase complex	1.1×10 ⁻²	PRKAB2, PRKAR1A, PRKACB
GO: 0019898: extrinsic component of membrane	1.2×10 ⁻²	EHD2, MCF2L, TPR, VPS13A, WIPI2, UBXN6
GO: 0070160: occluding junction	1.3×10 ⁻²	TJP1, GJA1, CTNNB1, TJP2
GO: 0016323: basolateral plasma membrane	1.3×10 ⁻²	TJP1, ABCC1, SLC16A1, CXADR, CR1L, P2RY2, MSN, CTNNB1, CASK, ANK2, STX4A, SLC9A1
GO: 0016324: apical plasma membrane	1.4×10 ⁻²	PDIA3, PRKAB2, ABCC1, PRKAA1, PRKAA2, SLC16A1, MSN, SORBS2, SLC9A1, TJP1, GJA1, P2RY2, FXYD1, GNAS, CTNNB1, STX4A
GO: 0031252: cell leading edge	1.4×10 ⁻²	SLK, DST, JMY, CFL1, AAK1, YWHAZ
GO: 0030496: midbody	1.5×10 ⁻²	SVIL, SEPTIN2, ZFYVE19, CTNND1, HNRNPU, BIRC6, SAFB, CPEB3, SIRT2, DNM2
GO: 0072686: mitotic spindle	1.6×10 ⁻²	NUMA1, TPR, HNRNPU, TPPP, MAP4, EML1, CLASP1, SIRT2
GO: 0005921: gap junction	2.1×10 ⁻²	TJP1, GJA1, YBX3, TJP2
GO: 0043231: intracellular membrane-bounded organelle	2.1×10 ⁻²	RAB5B, VCP, ACSS2, SYNPO2, YBX1, SLC2A4, OSBPL11, PGRMC1, GJA1, OSBP, TRA2A, CMYA5, CTNNA1, RAB11FIP5, AGFG1, SEC31A, OSBPL8, ARFGEF2, SLC16A1, PDHA1, CAVIN1, TXNRD3, FNBP1, OSBPL3, EPN2, EPN3, FKBP1A, EHD2, GOLPH3, RABEP1, TBC1D5, RAB12, TRIP10, PI4K2A
GO: 0005622: intracellular	2.2×10 ⁻²	HSPA8, EFR3A, SMARCC1, PRKRA, DHX9, RRAS2, SNTA1, SNTB2
GO: 0005802: trans-Golgi network	2.2×10 ⁻²	ARFGEF2, GOLPH3, OSBP, AP3D1, BIRC6, SLC2A4, STX4A, IGF2R, PI4K2A, DNM2
GO: 0002102: podosome	2.3×10 ⁻²	SVIL, PALLD, PTPN12, VCL
GO: 0000776: kinetochore	2.8×10 ⁻²	SMARCC1, SMARCC2, SEPTIN2, TPR, TRAPPC12, HNRNPU, TRP53BP1, CLASP1
GO: 1990023: mitotic spindle midzone	3.1×10 ⁻²	NUMA1, HNRNPU, EML1
GO: 0033290: eukaryotic 48S preinitiation complex	3.1×10 ⁻²	EIF3G, EIF3C, EIF3B

GO: 0033017: sarcoplasmic reticulum membrane	3.1×10^{-2}	FKBP1A, RYR2, JPH2, PLN
GO: 0000792: heterochromatin	3.2×10^{-2}	HDAC2, TRIM28, TNKS1BP1, PML, SIRT2
GO: 0016010: dystrophin-associated glycoprotein complex	3.5×10^{-2}	PGM5, SNTA1, SNTB2
GO: 0005852: eukaryotic translation initiation factor 3 complex	3.5×10^{-2}	EIF3G, EIF3C, EIF3B
GO: 0005905: clathrin-coated pit	3.7×10^{-2}	EPN3, FBNP1, AAK1, SLC2A4, DNM2
GO: 1990733: Titin-telethonin complex	3.7×10^{-2}	TCAP, TTN
GO: 0016282: eukaryotic 43S preinitiation complex	3.9×10^{-2}	EIF3G, EIF3C, EIF3B
GO: 0005876: spindle microtubule	4.1×10^{-2}	NUMA1, SEPTIN2, RMDN3, CLASP1
GO: 0031966: mitochondrial membrane	4.1×10^{-2}	BCL2L13, PLN, GPAM, BNIP3, CFL1, OGDH, VPS13A, DNM2
GO: 0030139: endocytic vesicle	4.2×10^{-2}	EHD2, RAB5B, RABEP1, SH3KBP1, IGF2R
GO: 0031410: cytoplasmic vesicle	4.3×10^{-2}	SH3KBP1, SNAP23, FBNP1L, BICD2, PIP4P2, STOM, RAB11FIP5, AGFG1, SEC31A, ARFGEF2, DST, DENND4B, CAV2, PDPK1, FBNP1, VPS13A, DNM2, EPN3, RABEP1, TBC1D5, RAB12, JMY, GNAS, PI4K2A, SNTB2
GO: 0098831: presynaptic active zone cytoplasmic component	4.8×10^{-2}	UNC13B, CTNND1, CTNNB1
GO: 0043292: Contractile fiber	4.8×10^{-2}	GJA1, MYH3, SMPX
GO: 0005684: U2-type spliceosomal complex	4.8×10^{-2}	CCDC12, MFAP1B, HTATSF1