

Supplementary Table 1 The analysis of GO and KEGG

ONTOLOG	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
Y									
GO									
BP	GO:0005996	monosaccharide metabolic process	26/111	292/18670	1.73E-23	4.15E-20	3.44E-20	FBP2/CYB5A/MPI/PGA M1/MDH1/ALDOB/ALD OA/GALE/PC/AKR1A1/ SLC37A4/ENO1/GOT1/I GFBP3/PKM/SLC25A13/ PDK3/HK2/RPE/PGK1/E NO2/PGM2/TALDO1/SL C25A10/GALK1/PFKP	26
BP	GO:0016051	carbohydrate biosynthetic process	22/111	214/18670	2.62E-21	2.80E-18	2.32E-18	FBP2/GYS2/PGAM1/MD H1/ALDOB/UGP2/ALDO A/PC/AKR1A1/SLC37A4 /ENO1/HS2ST1/GOT1/A GL/SLC25A13/GYS1/PG K1/ENO2/EXT1/PGM2/T ALDO1/SLC25A10	22
BP	GO:0019318	hexose metabolic process	23/111	249/18670	3.51E-21	2.80E-18	2.32E-18	FBP2/MPI/PGAM1/MDH 1/ALDOB/ALDOA/GAL E/PC/AKR1A1/SLC37A4 /ENO1/GOT1/IGFBP3/P KM/SLC25A13/PDK3/HK	23

								2/PGK1/ENO2/PGM2/SLC25A10/GALK1/PFKP	
BP	GO:0006006	glucose metabolic process	20/111	209/18670	8.36E-19	5.00E-16	4.15E-16	FBP2/PGAM1/MDH1/ALDOB/ALDOA/PC/AKR1A1/SLC37A4/ENO1/GOT1/IGFBP3/PKM/SLC25A13/PDK3/HK2/PGK1/ENO2/PGM2/SLC25A10/PFKP	20
BP	GO:0046365	monosaccharide catabolic process	14/111	67/18670	2.23E-18	1.07E-15	8.85E-16	PGAM1/ALDOB/ALDOA/GALE/AKR1A1/ENO1/PKM/HK2/RPE/PGK1/ENO2/PGM2/GALK1/PFKP	14
BP	GO:0046364	monosaccharide biosynthetic process	15/111	98/18670	1.87E-17	7.47E-15	6.20E-15	FBP2/PGAM1/MDH1/ALDOB/ALDOA/PC/AKR1A1/SLC37A4/ENO1/GOT1/SLC25A13/PGK1/ENO2/TALDO1/SLC25A10	15
BP	GO:0061615	glycolytic process through fructose-6-phosphate	10/111	28/18670	4.38E-16	1.31E-13	1.09E-13	PGAM1/ALDOB/ALDOA/ENO1/PKM/HK2/PGK1/ENO2/GALK1/PFKP	10
BP	GO:0061620	glycolytic process through	10/111	28/18670	4.38E-16	1.31E-13	1.09E-13	PGAM1/ALDOB/ALDOA/ENO1/PKM/HK2/PGK1	10

		glucose-6-phosphate						/ENO2/GALK1/PFKP	
BP	GO:00	hexose catabolic	12/111	57/18670	5.99E-16	1.59E-13	1.32E-13	PGAM1/ALDOB/ALDOA	12
	19320	process						/GALE/ENO1/PKM/HK2	
								/PGK1/ENO2/PGM2/GA	
								LK1/PFKP	
BP	GO:00	pyridine nucleotide	17/111	189/18670	1.18E-15	2.57E-13	2.14E-13	ME1/PGAM1/MDH1/AL	17
	19362	metabolic process						DOB/ALDOA/ENO1/ME	
								2/PKM/HK2/RPE/PGLS/	
								PGK1/ENO2/PGM2/TAL	
								DO1/GALK1/PFKP	
BP	GO:00	nicotinamide	17/111	189/18670	1.18E-15	2.57E-13	2.14E-13	ME1/PGAM1/MDH1/AL	17
	46496	nucleotide metabolic						DOB/ALDOA/ENO1/ME	
		process						2/PKM/HK2/RPE/PGLS/	
								PGK1/ENO2/PGM2/TAL	
								DO1/GALK1/PFKP	
BP	GO:00	pyridine-containing	17/111	195/18670	2.00E-15	3.99E-13	3.31E-13	ME1/PGAM1/MDH1/AL	17
	72524	compound metabolic						DOB/ALDOA/ENO1/ME	
		process						2/PKM/HK2/RPE/PGLS/	
								PGK1/ENO2/PGM2/TAL	
								DO1/GALK1/PFKP	
BP	GO:00	gluconeogenesis	13/111	89/18670	5.44E-15	9.30E-13	7.72E-13	FBP2/PGAM1/MDH1/AL	13
	06094							DOB/ALDOA/PC/SLC37	
								A4/ENO1/GOT1/SLC25A	
								13/PGK1/ENO2/SLC25A1	

								0	
BP	GO:0006733	oxidoreduction coenzyme metabolic process	17/111	207/18670	5.44E-15	9.30E-13	7.72E-13	ME1/PGAM1/MDH1/AL DOB/ALDOA/ENO1/ME 2/PKM/HK2/RPE/PGLS/ PGK1/ENO2/PGM2/TAL DO1/GALK1/PFKP	17
BP	GO:0019319	hexose biosynthetic process	13/111	92/18670	8.51E-15	1.36E-12	1.13E-12	FBP2/PGAM1/MDH1/AL DOB/ALDOA/PC/SLC37 A4/ENO1/GOT1/SLC25A 13/PGK1/ENO2/SLC25A1	13
								0	
BP	GO:0006090	pyruvate metabolic process	15/111	154/18670	1.92E-14	2.87E-12	2.38E-12	ME1/PGAM1/ALDOB/A LDOA/PC/ENO1/ME2/P KM/PDK3/HK2/SLC16A3 /PGK1/ENO2/GALK1/PF KP	15
BP	GO:0006732	coenzyme metabolic process	21/111	403/18670	2.43E-14	3.26E-12	2.70E-12	CYB5A/ME1/PGAM1/M DH1/ALDOB/ALDOA/P C/AKR1A1/ENO1/ME2/ PKM/PDK3/HK2/RPE/P GLS/PGK1/ENO2/PGM2 /TALDO1/GALK1/PFKP	21
BP	GO:0006734	NADH metabolic process	10/111	40/18670	2.66E-14	3.26E-12	2.70E-12	PGAM1/MDH1/ALDOB/ ALDOA/ENO1/PKM/HK	10

								2/PGK1/ENO2/PFKP	
BP	GO:00 06735	NADH regeneration	9/111	27/18670	2.86E-14	3.26E-12	2.70E-12	PGAM1/ALDOB/ALDOA /ENO1/PKM/HK2/PGK1 /ENO2/PFKP	9
BP	GO:00 61621	canonical glycolysis	9/111	27/18670	2.86E-14	3.26E-12	2.70E-12	PGAM1/ALDOB/ALDOA /ENO1/PKM/HK2/PGK1 /ENO2/PFKP	9
BP	GO:00 61718	glucose catabolic process to pyruvate	9/111	27/18670	2.86E-14	3.26E-12	2.70E-12	PGAM1/ALDOB/ALDOA /ENO1/PKM/HK2/PGK1 /ENO2/PFKP	9
BP	GO:00 16052	carbohydrate catabolic process	16/111	199/18670	5.08E-14	5.52E-12	4.58E-12	PGAM1/ALDOB/ALDOA /GALE/AKR1A1/ENO1/ AGL/PKM/HK2/RPE/PG K1/ENO2/PGM2/GALK1 /PFKP/PYGL	16
BP	GO:00 06007	glucose catabolic process	9/111	36/18670	5.49E-13	5.72E-11	4.74E-11	PGAM1/ALDOB/ALDOA /ENO1/PKM/HK2/PGK1 /ENO2/PFKP	9
BP	GO:00 30203	glycosaminoglycan metabolic process	14/111	160/18670	6.65E-13	6.64E-11	5.51E-11	DCN/HMMR/XYL2/CL N6/AGRN/SDC2/VCAN /HS2ST1/GPC4/CHPF/B 3GALT6/SDC3/SDC1/EX T1	14
BP	GO:00	aminoglycan	14/111	170/18670	1.53E-12	1.47E-10	1.22E-10	DCN/HMMR/XYL2/CL	14

	06022	metabolic process						N6/AGRN/SDC2/VCAN /HS2ST1/GPC4/CHPF/B 3GALT6/SDC3/SDC1/EX T1	
BP	GO:00	glycosaminoglycan	12/111	110/18670	2.30E-12	2.11E-10	1.75E-10	DCN/XYL2/ AGRN/SDC 2/VCAN/HS2ST1/GPC4/ CHPF/B3GALT6/SDC3/S DC1/EXT1	12
	06024	biosynthetic process							
BP	GO:00	aminoglycan	12/111	115/18670	3.93E-12	3.35E-10	2.78E-10	DCN/XYL2/ AGRN/SDC 2/VCAN/HS2ST1/GPC4/ CHPF/B3GALT6/SDC3/S DC1/EXT1	12
	06023	biosynthetic process							
BP	GO:00	response to hypoxia	18/111	359/18670	3.96E-12	3.35E-10	2.78E-10	CITED2/FAM162A/EGLN 3/ANG/AK4/ANGPTL4/ ENO1/CLDN3/NOL3/PK M/PSMC4/PDK3/PAM/P LOD1/HK2/VEGFA/PGK 1/STC1	18
	01666								
BP	GO:00	purine nucleoside	14/111	183/18670	4.20E-12	3.35E-10	2.78E-10	PGAM1/LHPP/ALDOB/ ALDOA/AK4/AK3/ENO1 /PKM/SLC25A13/HK2/P GK1/ENO2/GALK1/PFK P	14
	09127	monophosphate biosynthetic process							
BP	GO:00	purine	14/111	183/18670	4.20E-12	3.35E-10	2.78E-10	PGAM1/LHPP/ALDOB/	14

	09168	ribonucleoside monophosphate biosynthetic process						ALDOA/AK4/AK3/ENO1 /PKM/SLC25A13/HK2/P GK1/ENO2/GALK1/PFK P	
BP	GO:00 36293	response to decreased oxygen levels	18/111	370/18670	6.55E-12	5.06E-10	4.20E-10	CITED2/FAM162A/EGLN 3/ANG/AK4/ANGPTL4/ ENO1/CLDN3/NOL3/PK M/PSMC4/PDK3/PAM/P LOD1/HK2/VEGFA/PGK 1/STC1	18
BP	GO:00 09156	ribonucleoside monophosphate biosynthetic process	14/111	197/18670	1.14E-11	8.52E-10	7.07E-10	PGAM1/LHPP/ALDOB/ ALDOA/AK4/AK3/ENO1 /PKM/SLC25A13/HK2/P GK1/ENO2/GALK1/PFK P	14
BP	GO:00 46031	ADP metabolic process	12/111	126/18670	1.18E-11	8.52E-10	7.07E-10	PGAM1/ALDOB/ALDOA /AK4/AK3/ENO1/PKM/ HK2/PGK1/ENO2/GALK 1/PFKP	12
BP	GO:00 44262	cellular carbohydrate metabolic process	16/111	286/18670	1.34E-11	9.41E-10	7.81E-10	FBP2/GYS2/PGAM1/UGP 2/HS2ST1/GOT1/AGL/I GFBP3/PDK3/HK2/RPE/ GYS1/EXT1/PGM2/GAL K1/PYGL	16

BP	GO:0009167	purine ribonucleoside monophosphate metabolic process	17/111	340/18670	1.73E-11	1.18E-09	9.82E-10	NDUFV3/PGAM1/LHPP/ALDOB/CDK1/SDHC/ALDOA/AK4/AK3/ENO1/PKM/SLC25A13/HK2/PK1/ENO2/GALK1/PFKP	17
BP	GO:0009126	purine nucleoside monophosphate metabolic process	17/111	341/18670	1.81E-11	1.20E-09	9.97E-10	NDUFV3/PGAM1/LHPP/ALDOB/CDK1/SDHC/ALDOA/AK4/AK3/ENO1/PKM/SLC25A13/HK2/PK1/ENO2/GALK1/PFKP	17
BP	GO:0070482	response to oxygen levels	18/111	394/18670	1.86E-11	1.20E-09	9.97E-10	CITED2/FAM162A/EGLN3/ANG/AK4/ANGPTL4/ENO1/CLDN3/NOL3/PKM/PSMC4/PDK3/PAM/PLOD1/HK2/VEGFA/PKG1/STC1	18
BP	GO:0006081	cellular aldehyde metabolic process	10/111	74/18670	1.91E-11	1.20E-09	9.98E-10	PGAM1/CACNA1H/ALDOB/ALDH9A1/AKR1A1/ALDH7A1/RPE/PGLS/PGM2/TALDO1	10
BP	GO:0009124	nucleoside monophosphate biosynthetic process	14/111	208/18670	2.38E-11	1.46E-09	1.21E-09	PGAM1/LHPP/ALDOB/ALDOA/AK4/AK3/ENO1/PKM/SLC25A13/HK2/PK1/ENO2/GALK1/PFK	14

								P	
BP	GO:0019674	NAD metabolic process	10/111	76/18670	2.51E-11	1.50E-09	1.25E-09	PGAM1/MDH1/ALDOB/ALDOA/ENO1/PKM/HK2/PGK1/ENO2/PFKP	10
BP	GO:0009161	ribonucleoside monophosphate metabolic process	17/111	354/18670	3.26E-11	1.90E-09	1.58E-09	NDUFV3/PGAM1/LHPP/ALDOB/CDK1/SDHC/ALDOA/AK4/AK3/ENO1/PKM/SLC25A13/HK2/PGK1/ENO2/GALK1/PFKP	17
BP	GO:0009135	purine nucleoside diphosphate metabolic process	12/111	138/18670	3.46E-11	1.93E-09	1.60E-09	PGAM1/ALDOB/ALDOA/AK4/AK3/ENO1/PKM/HK2/PGK1/ENO2/GALK1/PFKP	12
BP	GO:0009179	purine ribonucleoside diphosphate metabolic process	12/111	138/18670	3.46E-11	1.93E-09	1.60E-09	PGAM1/ALDOB/ALDOA/AK4/AK3/ENO1/PKM/HK2/PGK1/ENO2/GALK1/PFKP	12
BP	GO:0009435	NAD biosynthetic process	9/111	56/18670	4.01E-11	2.18E-09	1.81E-09	PGAM1/ALDOB/ALDOA/ENO1/PKM/HK2/PGK1/ENO2/PFKP	9
BP	GO:0009185	ribonucleoside diphosphate metabolic process	12/111	140/18670	4.11E-11	2.18E-09	1.81E-09	PGAM1/ALDOB/ALDOA/AK4/AK3/ENO1/PKM/HK2/PGK1/ENO2/GALK1/PFKP	12

BP	GO:0009123	nucleoside monophosphate metabolic process	17/111	375/18670	8.03E-11	4.18E-09	3.47E-09	NDUFV3/PGAM1/LHPP/ ALDOB/CDK1/SDHC/A LDOA/AK4/AK3/ENO1/ PKM/SLC25A13/HK2/PG K1/ENO2/GALK1/PFKP	17
BP	GO:0044282	small molecule catabolic process	18/111	445/18670	1.36E-10	6.93E-09	5.75E-09	PGAM1/ALDOB/HMMR /ALDOA/GALE/AKR1A1 /ENO1/GOT1/ALDH7A1 /PKM/GNPDA1/HK2/RP E/PGK1/ENO2/PGM2/G ALK1/PFKP	18
BP	GO:0009205	purine ribonucleoside triphosphate metabolic process	16/111	335/18670	1.41E-10	7.03E-09	5.84E-09	NDUFV3/PGAM1/ALDO B/CDK1/SDHC/ALDOA /AK4/AK3/ENO1/PKM/ SLC25A13/HK2/PGK1/E NO2/GALK1/PFKP	16
BP	GO:0009132	nucleoside diphosphate metabolic process	12/111	158/18670	1.70E-10	8.29E-09	6.88E-09	PGAM1/ALDOB/ALDOA /AK4/AK3/ENO1/PKM/ HK2/PGK1/ENO2/GALK 1/PFKP	12
BP	GO:0009199	ribonucleoside triphosphate metabolic process	16/111	341/18670	1.83E-10	8.77E-09	7.28E-09	NDUFV3/PGAM1/ALDO B/CDK1/SDHC/ALDOA /AK4/AK3/ENO1/PKM/ SLC25A13/HK2/PGK1/E	16

								NO2/GALK1/PFKP	
BP	GO:00	purine nucleoside	16/111	342/18670	1.91E-10	8.98E-09	7.45E-09	NDUFV3/PGAM1/ALDO	16
	09144	triphosphate						B/CDK1/SDHC/ALDOA	
		metabolic process						/AK4/AK3/ENO1/PKM/ SLC25A13/HK2/PGK1/E	
								NO2/GALK1/PFKP	
BP	GO:00	ATP biosynthetic	12/111	160/18670	1.97E-10	9.05E-09	7.51E-09	PGAM1/ALDOB/ALDOA	12
	06754	process						/AK4/ENO1/PKM/SLC25	
								A13/HK2/PGK1/ENO2/ GALK1/PFKP	
BP	GO:00	ribose phosphate	15/111	300/18670	2.95E-10	1.33E-08	1.11E-08	PGAM1/ALDOB/ALDOA	15
	46390	biosynthetic process						/AK4/AK3/ENO1/PKM/ SLC25A13/PDK3/HK2/P	
								GK1/ENO2/GALK1/PFK P/PYGL	
BP	GO:00	ATP metabolic	15/111	305/18670	3.71E-10	1.64E-08	1.36E-08	NDUFV3/PGAM1/ALDO	15
	46034	process						B/CDK1/SDHC/ALDOA	
								/AK4/ENO1/PKM/SLC25	
								A13/HK2/PGK1/ENO2/ GALK1/PFKP	
BP	GO:00	purine	12/111	171/18670	4.25E-10	1.85E-08	1.54E-08	PGAM1/ALDOB/ALDOA	12
	09206	ribonucleoside						/AK4/ENO1/PKM/SLC25	
		triphosphate						A13/HK2/PGK1/ENO2/ GALK1/PFKP	
		biosynthetic process							

BP	GO:00	nucleoside	16/111	362/18670	4.40E-10	1.86E-08	1.54E-08	NDUFV3/PGAM1/ALDO	16
	09141	triphosphate						B/CDK1/SDHC/ALDOA	
		metabolic process						/AK4/AK3/ENO1/PKM/ SLC25A13/HK2/PGK1/E NO2/GALK1/PFKP	
BP	GO:00	nucleoside	11/111	134/18670	4.42E-10	1.86E-08	1.54E-08	PGAM1/ALDOB/ALDOA	11
	06165	diphosphate						/AK4/ENO1/PKM/HK2/ PGK1/ENO2/GALK1/PF	
		phosphorylation						KP	
BP	GO:00	purine nucleoside	12/111	172/18670	4.55E-10	1.88E-08	1.56E-08	PGAM1/ALDOB/ALDOA	12
	09145	triphosphate						/AK4/ENO1/PKM/SLC25	
		biosynthetic process						A13/HK2/PGK1/ENO2/ GALK1/PFKP	
BP	GO:00	nucleotide	11/111	136/18670	5.19E-10	2.10E-08	1.75E-08	PGAM1/ALDOB/ALDOA	11
	46939	phosphorylation						/AK4/ENO1/PKM/HK2/ PGK1/ENO2/GALK1/PF	
								KP	
BP	GO:00	ribonucleoside	12/111	177/18670	6.33E-10	2.52E-08	2.10E-08	PGAM1/ALDOB/ALDOA	12
	09201	triphosphate						/AK4/ENO1/PKM/SLC25	
		biosynthetic process						A13/HK2/PGK1/ENO2/ GALK1/PFKP	
BP	GO:00	NADP metabolic	7/111	32/18670	6.46E-10	2.53E-08	2.10E-08	ME1/PGAM1/ME2/RPE/	7
	06739	process						PGLS/PGM2/TALDO1	
BP	GO:00	purine ribonucleotide	14/111	280/18670	1.21E-09	4.66E-08	3.87E-08	PGAM1/ALDOB/ALDOA	14

	09152	biosynthetic process						/AK4/AK3/ENO1/PKM/ SLC25A13/PDK3/HK2/P GK1/ENO2/GALK1/PFK P	
BP	GO:00	nucleoside	12/111	188/18670	1.26E-09	4.80E-08	3.99E-08	PGAM1/ALDOB/ALDOA	12
	09142	triphosphate biosynthetic process						/AK4/ENO1/PKM/SLC25 A13/HK2/PGK1/ENO2/ GALK1/PFKP	
BP	GO:19	nucleoside phosphate	16/111	390/18670	1.30E-09	4.84E-08	4.02E-08	ME1/PGAM1/LHPP/ALD	16
	01293	biosynthetic process						OB/ALDOA/AK4/AK3/E NO1/PKM/SLC25A13/PD K3/HK2/PGK1/ENO2/G ALK1/PFKP	
BP	GO:00	glycolytic process	10/111	115/18670	1.62E-09	5.96E-08	4.94E-08	PGAM1/ALDOB/ALDOA	10
	06096							/ENO1/PKM/HK2/PGK1 /ENO2/GALK1/PFKP	
BP	GO:00	fructose 6-phosphate	5/111	10/18670	1.67E-09	6.05E-08	5.02E-08	FBP2/MPI/GFPT1/TALD	5
	06002	metabolic process						O1/PFKP	
BP	GO:00	ATP generation from	10/111	116/18670	1.76E-09	6.29E-08	5.22E-08	PGAM1/ALDOB/ALDOA	10
	06757	ADP						/ENO1/PKM/HK2/PGK1 /ENO2/GALK1/PFKP	
BP	GO:00	glyceraldehyde-3-ph	6/111	21/18670	1.94E-09	6.81E-08	5.65E-08	PGAM1/ALDOB/RPE/P	6
	19682	osphate metabolic process						LS/PGM2/TALDO1	

BP	GO:0046394	carboxylic acid biosynthetic process	17/111	462/18670	1.96E-09	6.81E-08	5.65E-08	PGAM1/DCN/ALDOB/U GP2/ALDOA/VCAN/AK R1A1/ENO1/GOT1/PKM /PLOD1/HK2/MIF/PGK1 /ENO2/GALK1/PFKP	17
BP	GO:0016053	organic acid biosynthetic process	17/111	463/18670	2.03E-09	6.93E-08	5.75E-08	PGAM1/DCN/ALDOB/U GP2/ALDOA/VCAN/AK R1A1/ENO1/GOT1/PKM /PLOD1/HK2/MIF/PGK1 /ENO2/GALK1/PFKP	17
BP	GO:0034637	cellular carbohydrate biosynthetic process	9/111	86/18670	2.10E-09	7.07E-08	5.87E-08	FBP2/GYS2/UGP2/HS2ST 1/GOT1/AGL/GYS1/EXT 1/PGM2	9
BP	GO:0009260	ribonucleotide biosynthetic process	14/111	293/18670	2.17E-09	7.21E-08	5.98E-08	PGAM1/ALDOB/ALDOA /AK4/AK3/ENO1/PKM/ SLC25A13/PDK3/HK2/P GK1/ENO2/GALK1/PFK P	14
BP	GO:0042866	pyruvate biosynthetic process	10/111	119/18670	2.26E-09	7.42E-08	6.16E-08	PGAM1/ALDOB/ALDOA /ENO1/PKM/HK2/PGK1 /ENO2/GALK1/PFKP	10
BP	GO:0006027	glycosaminoglycan catabolic process	8/111	61/18670	2.74E-09	8.86E-08	7.36E-08	DCN/HMMR/AGRN/SD C2/VCAN/GPC4/SDC3/S DC1	8

BP	GO:0006164	purine nucleotide biosynthetic process	14/111	300/18670	2.94E-09	9.38E-08	7.78E-08	PGAM1/ALDOB/ALDOA/ AK4/ AK3/ ENO1/ PKM/ SLC25A13/ PDK3/ HK2/ P GK1/ ENO2/ GALK1/ PFK P	14
BP	GO:0006026	aminoglycan catabolic process	8/111	65/18670	4.61E-09	1.45E-07	1.20E-07	DCN/HMMR/ AGRN/ SD C2/ VCAN/ GPC4/ SDC3/ S DC1	8
BP	GO:0007252	purine-containing compound biosynthetic process	14/111	313/18670	5.06E-09	1.57E-07	1.30E-07	PGAM1/ALDOB/ALDOA/ AK4/ AK3/ ENO1/ PKM/ SLC25A13/ PDK3/ HK2/ P GK1/ ENO2/ GALK1/ PFK P	14
BP	GO:00051156	glucose 6-phosphate metabolic process	6/111	25/18670	6.22E-09	1.91E-07	1.59E-07	PGAM1/ HK2/ RPE/ PGLS / PGM2/ TALDO1	6
BP	GO:0009165	nucleotide biosynthetic process	15/111	386/18670	9.21E-09	2.79E-07	2.32E-07	ME1/ PGAM1/ ALDOB/ A LDOA/ AK4/ AK3/ ENO1/ PKM/ SLC25A13/ PDK3/ H K2/ PGK1/ ENO2/ GALK1 / PFKP	15
BP	GO:0015980	energy derivation by oxidation of organic compounds	13/111	285/18670	1.47E-08	4.40E-07	3.65E-07	NDUFV3/ GYS2/ MDH1/ U GP2/ CDK1/ SDHC/ GFPT1 / AGL/ ME2/ SLC25A13/ G YS1/ PGM2/ PYGL	13

BP	GO:00	nicotinamide	10/111	147/18670	1.76E-08	5.13E-07	4.26E-07	PGAM1/ALDOB/ALDOA	10
	19359	nucleotide						/ENO1/PKM/HK2/PGK1	
		biosynthetic process						/ENO2/GALK1/PFKP	
BP	GO:00	pyridine nucleotide	10/111	147/18670	1.76E-08	5.13E-07	4.26E-07	PGAM1/ALDOB/ALDOA	10
	19363	biosynthetic process						/ENO1/PKM/HK2/PGK1	
								/ENO2/GALK1/PFKP	
BP	GO:00	pentose-phosphate	5/111	15/18670	1.94E-08	5.60E-07	4.65E-07	PGAM1/RPE/PGLS/PGM	5
	06098	shunt						2/TALDO1	
BP	GO:00	pyridine-containing	10/111	150/18670	2.14E-08	6.08E-07	5.05E-07	PGAM1/ALDOB/ALDOA	10
	72525	compound						/ENO1/PKM/HK2/PGK1	
		biosynthetic process						/ENO2/GALK1/PFKP	
BP	GO:00	cellular response to	11/111	207/18670	4.29E-08	1.21E-06	1.00E-06	CITED2/FAM162A/EGLN	11
	71456	hypoxia						3/AK4/ENO1/NOL3/PS	
								MC4/PDK3/VEGFA/PGK	
								1/STC1	
BP	GO:00	coenzyme	12/111	261/18670	5.01E-08	1.39E-06	1.16E-06	PGAM1/ALDOB/ALDOA	12
	09108	biosynthetic process						/AKR1A1/ENO1/PKM/P	
								DK3/HK2/PGK1/ENO2/	
								GALK1/PFKP	
BP	GO:00	cellular response to	11/111	217/18670	6.95E-08	1.91E-06	1.59E-06	CITED2/FAM162A/EGLN	11
	36294	decreased oxygen						3/AK4/ENO1/NOL3/PS	
		levels						MC4/PDK3/VEGFA/PGK	
								1/STC1	
BP	GO:00	cofactor biosynthetic	13/111	326/18670	7.15E-08	1.94E-06	1.61E-06	PGAM1/ALDOB/ALDOA	13

	51188	process						/SOD1/AKR1A1/ENO1/P KM/PDK3/HK2/PGK1/E NO2/GALK1/PFKP	
BP	GO:00	monocarboxylic acid	13/111	343/18670	1.29E-07	3.46E-06	2.88E-06	PGAM1/DCN/ALDOB/A LDOA/VCAN/ENO1/PK M/HK2/MIF/PGK1/ENO 2/GALK1/PFKP	13
	72330	biosynthetic process							
BP	GO:00	nucleotide catabolic	10/111	182/18670	1.33E-07	3.54E-06	2.94E-06	PGAM1/ALDOB/ALDOA /ENO1/PKM/HK2/PGK1 /ENO2/GALK1/PFKP	10
	09166	process							
BP	GO:00	cellular response to	11/111	234/18670	1.49E-07	3.92E-06	3.26E-06	CITED2/FAM162A/EGLN 3/AK4/ENO1/NOL3/PS MC4/PDK3/VEGFA/PGK 1/STC1	11
	71453	oxygen levels							
BP	GO:00	proteoglycan	7/111	69/18670	1.73E-07	4.49E-06	3.73E-06	DCN/XYL2/VCAN/HS2 ST1/CHPF/B3GALT6/EX T1	7
	30166	biosynthetic process							
BP	GO:00	cellular	8/111	103/18670	1.80E-07	4.59E-06	3.81E-06	GYS2/UGP2/HS2ST1/AG L/GYS1/EXT1/PGM2/PY GL	8
	44264	polysaccharide metabolic process							
BP	GO:19	nucleoside phosphate	10/111	188/18670	1.80E-07	4.59E-06	3.81E-06	PGAM1/ALDOB/ALDOA /ENO1/PKM/HK2/PGK1 /ENO2/GALK1/PFKP	10
	01292	catabolic process							
BP	GO:00	nucleotide-sugar	5/111	23/18670	2.10E-07	5.26E-06	4.36E-06	MPI/UGP2/GMPPB/GFP	5

	09226	biosynthetic process						T1/GNPDA1	
BP	GO:00	cellular	7/111	71/18670	2.11E-07	5.26E-06	4.36E-06	GYS2/UGP2/HS2ST1/AG	7
	33692	polysaccharide						L/GYS1/EXT1/PGM2	
		biosynthetic process							
BP	GO:19	carbohydrate	10/111	192/18670	2.19E-07	5.41E-06	4.49E-06	DCN/HMMR/AGRN/SD	10
	01136	derivative catabolic						C2/VCAN/GPC4/GNPD	
		process						A1/SDC3/SDC1/PGM2	
BP	GO:00	fructose	4/111	10/18670	2.42E-07	5.90E-06	4.90E-06	FBP2/ALDOB/ALDOA/P	4
	30388	1,6-bisphosphate						FKP	
		metabolic process							
BP	GO:00	organophosphate	11/111	248/18670	2.68E-07	6.47E-06	5.37E-06	PGAM1/ALDOB/ALDOA	11
	46434	catabolic process						/ENO1/PKM/HK2/PGK1	
								/ENO2/PGM2/GALK1/P	
								FKP	
BP	GO:00	polysaccharide	8/111	114/18670	3.95E-07	9.45E-06	7.84E-06	GYS2/UGP2/HS2ST1/AG	8
	05976	metabolic process						L/GYS1/EXT1/PGM2/PY	
								GL	
BP	GO:00	chondroitin sulfate	5/111	26/18670	4.04E-07	9.50E-06	7.88E-06	DCN/XYLT2/VCAN/CH	5
	30206	biosynthetic process						PF/B3GALT6	
BP	GO:00	polysaccharide	7/111	78/18670	4.05E-07	9.50E-06	7.88E-06	GYS2/UGP2/HS2ST1/AG	7
	00271	biosynthetic process						L/GYS1/EXT1/PGM2	
BP	GO:00	energy reserve	7/111	87/18670	8.57E-07	1.99E-05	1.65E-05	GYS2/UGP2/GFPT1/AGL	7
	06112	metabolic process						/GYS1/PGM2/PYGL	
BP	GO:00	nucleobase-containin	10/111	226/18670	9.82E-07	2.26E-05	1.88E-05	PGAM1/ALDOB/ALDOA	10

	34404	g small molecule biosynthetic process						/ENO1/PKM/HK2/PGK1 /ENO2/GALK1/PFKP	
BP	GO:0050650	chondroitin sulfate proteoglycan biosynthetic process	5/111	31/18670	1.02E-06	2.32E-05	1.93E-05	DCN/XYLT2/VCAN/CH PF/B3GALT6	5
BP	GO:0006029	proteoglycan metabolic process	7/111	94/18670	1.45E-06	3.28E-05	2.72E-05	DCN/XYLT2/VCAN/HS2 ST1/CHPF/B3GALT6/EX T1	7
BP	GO:0022900	electron transport chain	9/111	186/18670	1.68E-06	3.76E-05	3.12E-05	CYB5A/ME1/NDUFV3/G LRX/CDK1/SDHC/AKR1 A1/ME2/SLC25A13	9
BP	GO:0006140	regulation of nucleotide metabolic process	8/111	146/18670	2.58E-06	5.72E-05	4.75E-05	ME1/PGAM1/CDK1/AK4 /ENO1/ME2/PDK3/PGK 1	8
BP	GO:0009225	nucleotide-sugar metabolic process	5/111	38/18670	2.91E-06	6.39E-05	5.31E-05	MPI/UGP2/GMPPB/GFP T1/GNPDA1	5
BP	GO:0030204	chondroitin sulfate metabolic process	5/111	39/18670	3.32E-06	7.23E-05	6.00E-05	DCN/XYLT2/VCAN/CH PF/B3GALT6	5
BP	GO:0007548	sex differentiation	10/111	270/18670	4.84E-06	0.000104338	8.66E-05	CITED2/SOX9/ANG/SOD 1/NASP/HSPA5/FKBP4/ SDC1/BIK/VEGFA	10
BP	GO:0005977	glycogen metabolic process	6/111	74/18670	5.14E-06	0.000109836	9.12E-05	GYS2/UGP2/AGL/GYS1/ PGM2/PYGL	6
BP	GO:0005977	cellular glucan	6/111	75/18670	5.56E-06	0.000116729	9.69E-05	GYS2/UGP2/AGL/GYS1/	6

	06073	metabolic process						PGM2/PYGL	
BP	GO:0044042	glucan metabolic process	6/111	75/18670	5.56E-06	0.000116729	9.69E-05	GYS2/UGP2/AGL/GYS1/PGM2/PYGL	6
BP	GO:0008406	gonad development	9/111	217/18670	5.94E-06	0.000123651	0.000102637	CITED2/SOX9/ANG/SOD1/NASP/HSPA5/SDC1/BIK/VEGFA	9
BP	GO:0050654	chondroitin sulfate proteoglycan metabolic process	5/111	44/18670	6.12E-06	0.000126349	0.000104876	DCN/XYLT2/VCAN/CHPF/B3GALT6	5
BP	GO:0009101	glycoprotein biosynthetic process	11/111	348/18670	7.24E-06	0.000148035	0.000122877	MPI/DCN/XYLT2/VCAN/HS2ST1/GFPT1/CHPF/B3GALT6/GAL3ST1/EXT1/CHST4	11
BP	GO:0045137	development of primary sexual characteristics	9/111	223/18670	7.41E-06	0.000150237	0.000124704	CITED2/SOX9/ANG/SOD1/NASP/HSPA5/SDC1/BIK/VEGFA	9
BP	GO:0005978	glycogen biosynthetic process	5/111	46/18670	7.66E-06	0.000152711	0.000126758	GYS2/UGP2/AGL/GYS1/PGM2	5
BP	GO:0009250	glucan biosynthetic process	5/111	46/18670	7.66E-06	0.000152711	0.000126758	GYS2/UGP2/AGL/GYS1/PGM2	5
BP	GO:0048608	reproductive structure development	12/111	431/18670	9.86E-06	0.000194902	0.000161779	CITED2/DCN/SOX9/ANG/SOD1/NASP/HSPA5/FKBP4/SDC1/BIK/VEGFA/STC1	12

BP	GO:0048732	gland development	12/111	434/18670	1.06E-05	0.00020553	0.000170601	CITED2/SOX9/AK4/SOD1/AURKA/PKM/PAM/ELF3/HK2/FKBP4/VEGFA/MET	12
BP	GO:0061458	reproductive system development	12/111	434/18670	1.06E-05	0.00020553	0.000170601	CITED2/DCN/SOX9/ANG/SOD1/NASP/HSPA5/FKBP4/SDC1/BIK/VEGFA/STC1	12
BP	GO:0006790	sulfur compound metabolic process	11/111	372/18670	1.35E-05	0.000261061	0.000216694	DCN/XYL2/PC/VCAN/SOD1/AKR1A1/CHPF/B3GALT6/PDK3/CHST4/SLC25A10	11
BP	GO:0015012	heparan sulfate proteoglycan biosynthetic process	4/111	32/18670	3.74E-05	0.000716473	0.00059471	XYLT2/HS2ST1/B3GALT6/EXT1	4
BP	GO:0009100	glycoprotein metabolic process	11/111	419/18670	4.04E-05	0.000766719	0.000636417	MPI/DCN/XYLT2/VCAN/HS2ST1/GFPT1/CHPF/B3GALT6/GAL3ST1/EXT1/CHST4	11
BP	GO:0003510	mucopolysaccharide metabolic process	6/111	112/18670	5.53E-05	0.001042002	0.000864917	DCN/HMMR/XYLT2/VCAN/CHPF/B3GALT6	6
BP	GO:0006012	galactose metabolic process	3/111	13/18670	5.60E-05	0.00104716	0.000869198	GALE/PGM2/GALK1	3
BP	GO:0006012	response to metal ion	10/111	364/18670	6.31E-05	0.001169888	0.000971069	CYB5A/CACNA1H/CDK	10

	10038							1/PPP2CB/SOD1/GOT1/ HSPA5/SLC25A13/PAM/ SDC1	
BP	GO:0030201	heparan sulfate proteoglycan metabolic process	4/111	37/18670	6.72E-05	0.001236662	0.001026495	XYLT2/HS2ST1/B3GALT6 /EXT1	4
BP	GO:0006000	fructose metabolic process	3/111	15/18670	8.83E-05	0.001613726	0.001339477	FBP2/ALDOB/ALDOA	3
BP	GO:0062012	regulation of small molecule metabolic process	11/111	459/18670	9.14E-05	0.001656586	0.001375054	ME1/PGAM1/CDK1/AK4 /SOD1/ENO1/ME2/IGFB P3/PSMC4/PDK3/PGK1	11
BP	GO:0044275	cellular carbohydrate catabolic process	4/111	45/18670	0.000146118	0.002629017	0.002182222	PGAM1/AGL/PGM2/PY GL	4
BP	GO:0044272	sulfur compound biosynthetic process	7/111	192/18670	0.000150356	0.002685094	0.002228769	DCN/XYLT2/VCAN/AK R1A1/CHPF/B3GALT6/P DK3	7
BP	GO:0001889	liver development	6/111	135/18670	0.00015549	0.002756201	0.002287792	CITED2/SOX9/AK4/AUR KA/PKM/MET	6
BP	GO:0035722	interleukin-12-mediated signaling pathway	4/111	47/18670	0.00017333	0.003049839	0.002531527	SOD1/MIF/PPIA/TALDO 1	4
BP	GO:0061008	hepaticobiliary system development	6/111	138/18670	0.000175309	0.003062152	0.002541747	CITED2/SOX9/AK4/AUR KA/PKM/MET	6
BP	GO:0071349	cellular response to interleukin-12	4/111	49/18670	0.000204023	0.003525544	0.002926387	SOD1/MIF/PPIA/TALDO 1	4

BP	GO:19 00542	regulation of purine nucleotide metabolic process	6/111	142/18670	0.000204785	0.003525544	0.002926387	PGAM1/CDK1/AK4/EN O1/PDK3/PGK1	6
BP	GO:00 43062	extracellular structure organization	10/111	422/18670	0.000211418	0.003613737	0.002999592	DCN/SOX9/AGRN/VCA N/QSOX1/P4HA1/COL5 A1/ELF3/PLOD1/SDC1	10
BP	GO:00 70671	response to interleukin-12	4/111	50/18670	0.000220754	0.003746559	0.003109841	SOD1/MIF/PPIA/TALDO 1	4
BP	GO:00 02064	epithelial cell development	7/111	207/18670	0.000238626	0.004021358	0.003337938	SOX9/SOD1/CLDN3/SD C1/VEGFA/MET/STC1	7
BP	GO:00 51260	protein homooligomerization	9/111	351/18670	0.00024851	0.004158639	0.003451889	ALDOA/ALDH9A1/ANG PTL4/CLDN3/PKM/PAM /MIF/BIK/PFKP	9
BP	GO:00 16999	antibiotic metabolic process	6/111	151/18670	0.000285434	0.004743363	0.00393724	MDH1/SDHC/SOD1/AK R1A1/ME2/GNPDA1	6
BP	GO:00 05980	glycogen catabolic process	3/111	22/18670	0.000290066	0.004787094	0.003973539	AGL/PGM2/PYGL	3
BP	GO:00 09251	glucan catabolic process	3/111	23/18670	0.000332136	0.00544384	0.004518673	AGL/PGM2/PYGL	3
BP	GO:00 30198	extracellular matrix organization	9/111	368/18670	0.00035158	0.005723335	0.004750669	DCN/SOX9/AGRN/VCA N/QSOX1/P4HA1/COL5 A1/ELF3/PLOD1	9
BP	GO:00 18208	peptidyl-proline modification	4/111	57/18670	0.000366737	0.005929741	0.004921997	EGLN3/P4HA1/FKBP4/P PIA	4

BP	GO:00	protein	3/111	24/18670	0.000377945	0.006069945	0.005038374	EGLN3/P4HA1/PLOD1	3
		18126 hydroxylation							
BP	GO:00	male sex	6/111	160/18670	0.000389165	0.006194848	0.00514205	CITED2/SOX9/NASP/FK	6
		46661 differentiation						BP4/SDC1/BIK	
BP	GO:00	retinoid metabolic	5/111	104/18670	0.000390899	0.006194848	0.00514205	AGRN/SDC2/GPC4/SDC	5
		01523 process						3/SDC1	
BP	GO:00	maintenance of	5/111	105/18670	0.000408521	0.006431513	0.005338494	MXI1/SPAG4/HSPA5/HK	5
		45185 protein location						2/KDEL3	
BP	GO:00	cellular	3/111	25/18670	0.000427629	0.00668834	0.005551674	AGL/PGM2/PYGL	3
		44247 polysaccharide							
		catabolic process							
BP	GO:00	diterpenoid	5/111	110/18670	0.000505787	0.007859404	0.006523718	AGRN/SDC2/GPC4/SDC	5
		16101 metabolic process						3/SDC1	
BP	GO:00	response to cadmium	4/111	63/18670	0.000538114	0.008270417	0.006864881	CYB5A/CDK1/SOD1/GO	4
		46686 ion						T1	
BP	GO:00	polysaccharide	3/111	27/18670	0.00053915	0.008270417	0.006864881	AGL/PGM2/PYGL	3
		00272 catabolic process							
BP	GO:00	terpenoid metabolic	5/111	120/18670	0.000751468	0.011453906	0.009507344	AGRN/SDC2/GPC4/SDC	5
		06721 process						3/SDC1	
BP	GO:20	positive regulation of	4/111	69/18670	0.000759931	0.011509587	0.009553563	CITED2/CACNA1H/SOX	4
		00243 reproductive process						9/AURKA	
BP	GO:00	regulation of	6/111	182/18670	0.000767668	0.011553652	0.009590139	DCN/FAM162A/HAX1/N	6
		10821 mitochondrion						OL3/HK2/BIK	
		organization							

BP	GO:0043618	regulation of transcription from RNA polymerase II promoter in response to stress	5/111	121/18670	0.000780192	0.011668742	0.00968567	CITED2/EGLN3/HSPA5/PSMC4/VEGFA	5
BP	GO:1903578	regulation of ATP metabolic process	5/111	122/18670	0.000809728	0.012029154	0.00998483	PGAM1/CDK1/AK4/ENO1/PGK1	5
BP	GO:0002082	regulation of oxidative phosphorylation	3/111	31/18670	0.000814343	0.012029154	0.00998483	CDK1/AK4/PGK1	3
BP	GO:0008637	apoptotic mitochondrial changes	5/111	124/18670	0.000871294	0.012791448	0.010617575	FAM162A/PPP2CB/NOL3/HK2/BIK	5
BP	GO:0043620	regulation of DNA-templated transcription in response to stress	5/111	127/18670	0.000970099	0.014155162	0.011749529	CITED2/EGLN3/HSPA5/PSMC4/VEGFA	5
BP	GO:0032507	maintenance of protein location in cell	4/111	74/18670	0.000988703	0.014339186	0.011902278	SPAG4/HSPA5/HK2/KDELR3	4
BP	GO:0045333	cellular respiration	6/111	193/18670	0.001040757	0.015003209	0.012453452	NDUFV3/MDH1/CDK1/SDFHC/ME2/SLC25A13	6
BP	GO:0003382	epithelial cell morphogenesis	3/111	34/18670	0.001070151	0.015243282	0.012652726	CLDN3/MET/STC1	3

BP	GO:00	tricarboxylic acid 06099 cycle	3/111	34/18670	0.001070151	0.015243282	0.012652726	MDH1/SDHC/ME2	3
BP	GO:00	regulation of 61418 transcription from RNA polymerase II promoter in response to hypoxia	4/111	77/18670	0.001147084	0.016242441	0.01348208	CITED2/EGLN3/PSMC4/ VEGFA	4
BP	GO:00	citrate metabolic 06101 process	3/111	35/18670	0.001165439	0.016405262	0.01361723	MDH1/SDHC/ME2	3
BP	GO:00	cellular modified 06575 amino acid metabolic process	6/111	202/18670	0.001315193	0.018405011	0.015277126	EGLN3/ALDH9A1/SOD1 /P4HA1/ALDH7A1/PLO D1	6
BP	GO:00	male gonad 08584 development	5/111	138/18670	0.001404783	0.019544453	0.016222923	CITED2/SOX9/NASP/SD C1/BIK	5
BP	GO:00	isoprenoid metabolic 06720 process	5/111	139/18670	0.001450397	0.019947121	0.016557159	AGRN/SDC2/GPC4/SDC 3/SDC1	5
BP	GO:00	development of 46546 primary male sexual characteristics	5/111	139/18670	0.001450397	0.019947121	0.016557159	CITED2/SOX9/NASP/SD C1/BIK	5
BP	GO:00	amino sugar 06040 metabolic process	3/111	38/18670	0.001482853	0.020276949	0.016830934	GFPT1/GNPDA1/CHST4	3
BP	GO:00	cellular response to 35865 potassium ion	2/111	10/18670	0.001528036	0.0206587	0.017147807	CACNA1H/SOD1	2
BP	GO:19	positive regulation of	2/111	10/18670	0.001528036	0.0206587	0.017147807	CDK1/PGK1	2

	03862	oxidative phosphorylation							
BP	GO:0072350	tricarboxylic acid metabolic process	3/111	39/18670	0.001599515	0.021383458	0.017749394	MDH1/SDHC/ME2	3
BP	GO:0072595	maintenance of protein localization in organelle	3/111	39/18670	0.001599515	0.021383458	0.017749394	HSPA5/HK2/KDELR3	3
BP	GO:0030879	mammary gland development	5/111	143/18670	0.001643835	0.021853875	0.018139865	SOX9/PAM/ELF3/HK2/V EGFA	5
BP	GO:0006119	oxidative phosphorylation	5/111	145/18670	0.001747364	0.023101895	0.019175787	NDUFV3/CDK1/SDHC/ AK4/PGK1	5
BP	GO:0042542	response to hydrogen peroxide	5/111	146/18670	0.001800887	0.023549297	0.019547155	CDK1/PPP2CB/SOD1/SD C1/MET	5
BP	GO:0051384	response to glucocorticoid	5/111	146/18670	0.001800887	0.023549297	0.019547155	GOT1/AGL/PAM/SDC1/ STC1	5
BP	GO:0006048	UDP-N-acetylglucosamine biosynthetic process	2/111	11/18670	0.001860356	0.023806586	0.019760717	GFPT1/GNPDA1	2
BP	GO:0015014	heparan sulfate proteoglycan biosynthetic process, polysaccharide chain biosynthetic process	2/111	11/18670	0.001860356	0.023806586	0.019760717	HS2ST1/EXT1	2
BP	GO:0000000	L-ascorbic acid	2/111	11/18670	0.001860356	0.023806586	0.019760717	CYB5A/AKR1A1	2

	19852	metabolic process							
BP	GO:19	positive regulation of	2/111	11/18670	0.001860356	0.023806586	0.019760717	CITED2/SOX9	2
	05941	gonad development							
BP	GO:19	alpha-amino acid	6/111	222/18670	0.002121018	0.026880576	0.022312291	EGLN3/P4HA1/GOT1/G	6
	01605	metabolic process						FPT1/ALDH7A1/PLOD1	
BP	GO:00	regulation of cardiac	3/111	43/18670	0.002123038	0.026880576	0.022312291	DSC2/PKP2/STC1	3
	86004	muscle cell							
		contraction							
BP	GO:00	dermatan sulfate	2/111	12/18670	0.002223772	0.027572472	0.022886601	DCN/VCAN	2
	30208	biosynthetic process							
BP	GO:00	maintenance of	2/111	12/18670	0.002223772	0.027572472	0.022886601	HSPA5/KDEL3	2
	35437	protein localization in							
		endoplasmic							
		reticulum							
BP	GO:00	thrombin-activated	2/111	12/18670	0.002223772	0.027572472	0.022886601	STMN1/MET	2
	70493	receptor signaling							
		pathway							
BP	GO:19	regulation of GTP	2/111	12/18670	0.002223772	0.027572472	0.022886601	STMN1/MET	2
	04424	binding							
BP	GO:00	response to copper	3/111	44/18670	0.002268596	0.027983248	0.023227567	CDK1/SOD1/PAM	3
	46688	ion							
BP	GO:00	protein	4/111	94/18670	0.002392955	0.029365851	0.0243752	ALDOA/ALDH9A1/PKM	4
	51289	homotetramerization						/PFKP	
BP	GO:00	neutrophil	9/111	485/18670	0.002433203	0.029707418	0.024658719	PGAM1/ALDOA/QSOX1	9

	43312	degranulation						/AGL/PKM/MIF/PPIA/P GM2/PYGL	
BP	GO:00	regulation of	4/111	95/18670	0.002486846	0.030055672	0.024947788	ME1/PGAM1/ME2/PDK3	4
	51196	coenzyme metabolic process							
BP	GO:00	maintenance of	4/111	95/18670	0.002486846	0.030055672	0.024947788	SPAG4/HSPA5/HK2/KD ELR3	4
	51651	location in cell							
BP	GO:00	neutrophil activation	9/111	488/18670	0.002535713	0.030492266	0.025310184	PGAM1/ALDOA/QSOX1 /AGL/PKM/MIF/PPIA/P GM2/PYGL	9
	02283	involved in immune response							
BP	GO:00	female gonad	4/111	96/18670	0.002583241	0.030559317	0.02536584	ANG/SOD1/HSPA5/VEG FA	4
	08585	development							
BP	GO:00	endothelial cell	2/111	13/18670	0.002617911	0.030559317	0.02536584	MET/STC1	2
	01886	morphogenesis							
BP	GO:00	peptidyl-proline	2/111	13/18670	0.002617911	0.030559317	0.02536584	EGLN3/P4HA1	2
	19511	hydroxylation							
BP	GO:00	dermatan sulfate	2/111	13/18670	0.002617911	0.030559317	0.02536584	DCN/VCAN	2
	30205	metabolic process							
BP	GO:00	negative regulation	2/111	13/18670	0.002617911	0.030559317	0.02536584	STMN1/FKBP4	2
	31115	of microtubule polymerization							
BP	GO:00	amino sugar	2/111	13/18670	0.002617911	0.030559317	0.02536584	GFPT1/GNPDA1	2
	46349	biosynthetic process							
BP	GO:19	regulation of actin	3/111	47/18670	0.002741889	0.031697299	0.026310424	DSC2/PKP2/STC1	3

	03115	filament-based movement							
BP	GO:19	positive regulation of	3/111	47/18670	0.002741889	0.031697299	0.026310424	CDK1/ENO1/PGK1	3
	03580	ATP metabolic process							
BP	GO:00	response to	5/111	162/18670	0.002830296	0.032562014	0.027028183	GOT1/AGL/PAM/SDC1/ STC1	5
	31960	corticosteroid							
BP	GO:00	dicarboxylic acid	4/111	99/18670	0.002887774	0.032871393	0.027284984	ME1/MDH1/GOT1/ME2	4
	43648	metabolic process							
BP	GO:00	neutrophil activation	9/111	498/18670	0.00290248	0.032871393	0.027284984	PGAM1/ALDOA/QSOX1 /AGL/PKM/MIF/PPIA/P GM2/PYGL	9
	42119								
BP	GO:00	lactation	3/111	48/18670	0.002912133	0.032871393	0.027284984	PAM/HK2/VEGFA	3
	07595								
BP	GO:00	regulation of release	3/111	48/18670	0.002912133	0.032871393	0.027284984	FAM162A/NOL3/BIK	3
	90199	of cytochrome c from mitochondria							
BP	GO:00	neutrophil mediated	9/111	499/18670	0.002941354	0.033045356	0.027429383	PGAM1/ALDOA/QSOX1 /AGL/PKM/MIF/PPIA/P GM2/PYGL	9
	02446	immunity							
BP	GO:00	chondroitin sulfate	2/111	14/18670	0.003042399	0.033244115	0.027594363	DCN/VCAN	2
	30207	catabolic process							
BP	GO:00	phosphate ion	2/111	14/18670	0.003042399	0.033244115	0.027594363	SLC37A4/SLC25A10	2
	35435	transmembrane							

		transport							
BP	GO:0046033	AMP metabolic process	2/111	14/18670	0.003042399	0.033244115	0.027594363	AK4/AK3	2
BP	GO:0046940	nucleoside monophosphate phosphorylation	2/111	14/18670	0.003042399	0.033244115	0.027594363	AK4/AK3	2
BP	GO:0060009	Sertoli cell development	2/111	14/18670	0.003042399	0.033244115	0.027594363	SOX9/SDC1	2
BP	GO:0086069	bundle of His cell to Purkinje myocyte communication	2/111	14/18670	0.003042399	0.033244115	0.027594363	DSC2/PKP2	2
BP	GO:0046545	development of primary female sexual characteristics	4/111	101/18670	0.003103914	0.033762124	0.028024338	ANG/SOD1/HSPA5/VEGFA	4
BP	GO:0018209	peptidyl-serine modification	7/111	322/18670	0.003129234	0.033883512	0.028125096	DCN/CDK1/HAX1/AURKA/PDK3/MIF/VEGFA	7
BP	GO:0031113	regulation of microtubule polymerization	3/111	50/18670	0.003271813	0.035109633	0.029142841	STMN1/FKBP4/MET	3
BP	GO:0042398	cellular modified amino acid biosynthetic process	3/111	50/18670	0.003271813	0.035109633	0.029142841	ALDH9A1/ALDH7A1/PLOD1	3
BP	GO:0032091	negative regulation of protein binding	4/111	103/18670	0.003330852	0.035583616	0.029536271	STMN1/AURKA/HSPA5/MET	4

BP	GO:0046677	response to antibiotic	7/111	327/18670	0.003406094	0.036069005	0.02993917	CDK1/PPP2CB/SOD1/HS PA5/CLDN3/SDC1/MET	7
BP	GO:0007566	embryo implantation	3/111	51/18670	0.003461398	0.036069005	0.02993917	SOD1/FKBP4/STC1	3
BP	GO:0019321	pentose metabolic process	2/111	15/18670	0.00349687	0.036069005	0.02993917	RPE/TALDO1	2
BP	GO:0019471	4-hydroxyproline metabolic process	2/111	15/18670	0.00349687	0.036069005	0.02993917	EGLN3/P4HA1	2
BP	GO:0035864	response to potassium ion	2/111	15/18670	0.00349687	0.036069005	0.02993917	CACNA1H/SOD1	2
BP	GO:0050651	dermatan sulfate proteoglycan biosynthetic process	2/111	15/18670	0.00349687	0.036069005	0.02993917	DCN/VCAN	2
BP	GO:1900037	regulation of cellular response to hypoxia	2/111	15/18670	0.00349687	0.036069005	0.02993917	ENO1/NOL3	2
BP	GO:2001028	positive regulation of endothelial cell chemotaxis	2/111	15/18670	0.00349687	0.036069005	0.02993917	VEGFA/MET	2
BP	GO:0006937	regulation of muscle contraction	5/111	171/18670	0.003568137	0.036646145	0.030418226	DSC2/SOD1/ENO1/PKP2 /STC1	5
BP	GO:0046580	negative regulation of Ras protein signal transduction	3/111	52/18670	0.003657577	0.037248062	0.030917849	PPP2CB/STMN1/MET	3
BP	GO:00	protein	5/111	172/18670	0.003657875	0.037248062	0.030917849	ME1/ALDOA/ALDH9A1	5

	51262	tetramerization						/PKM/PFKP	
BP	GO:00	UDP-N-acetylglucosa	2/111	16/18670	0.003980957	0.040027021	0.033224532	GFPT1/GNPDA1	2
	06047	mine metabolic process							
BP	GO:00	hepatocyte growth	2/111	16/18670	0.003980957	0.040027021	0.033224532	STMN1/MET	2
	48012	factor receptor signaling pathway							
BP	GO:00	dermatan sulfate	2/111	16/18670	0.003980957	0.040027021	0.033224532	DCN/VCAN	2
	50655	proteoglycan metabolic process							
BP	GO:00	aspartate family	3/111	54/18670	0.004069993	0.040581222	0.033684548	GOT1/ALDH7A1/PLOD1	3
	09066	amino acid metabolic process							
BP	GO:00	collagen fibril	3/111	54/18670	0.004069993	0.040581222	0.033684548	P4HA1/COL5A1/PLOD1	3
	30199	organization							
BP	GO:00	ovarian follicle	3/111	55/18670	0.004286365	0.042561293	0.03532811	ANG/SOD1/VEGFA	3
	01541	development							
BP	GO:00	protein glycosylation	6/111	258/18670	0.004445659	0.043779674	0.036339431	MPI/GFPT1/B3GALT6/G	6
	06486							AL3ST1/EXT1/CHST4	
BP	GO:00	macromolecule	6/111	258/18670	0.004445659	0.043779674	0.036339431	MPI/GFPT1/B3GALT6/G	6
	43413	glycosylation						AL3ST1/EXT1/CHST4	
BP	GO:00	microtubule	4/111	112/18670	0.004492485	0.043897391	0.036437142	STMN1/FKBP4/KIF2A/M	4
	31109	polymerization or depolymerization						ET	

BP	GO:0006577	amino-acid betaine metabolic process	2/111	17/18670	0.0044943	0.043897391	0.036437142	ALDH9A1/ALDH7A1	2
BP	GO:0090257	regulation of muscle system process	6/111	259/18670	0.004529527	0.044061621	0.036573461	DSC2/SOD1/ENO1/NOL3/PKP2/STC1	6
BP	GO:0045981	positive regulation of nucleotide metabolic process	3/111	57/18670	0.004739758	0.045734846	0.037962326	CDK1/ENO1/PGK1	3
BP	GO:1900544	positive regulation of purine nucleotide metabolic process	3/111	57/18670	0.004739758	0.045734846	0.037962326	CDK1/ENO1/PGK1	3
BP	GO:0046660	female sex differentiation	4/111	115/18670	0.004933348	0.047411651	0.039354163	ANG/SOD1/HSPA5/VEGFA	4
BP	GO:0051058	negative regulation of small GTPase mediated signal transduction	3/111	58/18670	0.004976903	0.047638913	0.039542802	PPP2CB/STMN1/MET	3
BP	GO:0090190	positive regulation of branching involved in ureteric bud morphogenesis	2/111	18/18670	0.00503654	0.04801769	0.039857207	SOX9/VEGFA	2
BP	GO:0001836	release of cytochrome c from mitochondria	3/111	59/18670	0.005221091	0.049008455	0.040679594	FAM162A/NOL3/BIK	3
BP	GO:0001885	endothelial cell development	3/111	59/18670	0.005221091	0.049008455	0.040679594	VEGFA/MET/STC1	3

BP	GO:0010822	positive regulation of mitochondrion organization	4/111	117/18670	0.00524286	0.049008455	0.040679594	DCN/FAM162A/HK2/BIK	4
BP	GO:0022904	respiratory electron transport chain	4/111	117/18670	0.00524286	0.049008455	0.040679594	NDUFV3/CDK1/SDHC/SLC25A13	4
BP	GO:0000371	regulation of purine nucleotide biosynthetic process	4/111	117/18670	0.00524286	0.049008455	0.040679594	PGAM1/AK4/ENO1/PDK3	4
BP	GO:0043902	positive regulation of multi-organism process	5/111	188/18670	0.005323539	0.049568985	0.041144863	CACNA1H/PC/AURKA/MIF/PPIA	5
CC	GO:0004813	ficolin-1-rich granule lumen	8/111	124/19717	5.01E-07	0.000128229	0.000117578	PGAM1/ALDOA/AGL/PKM/MIF/PPIA/PGM2/PYGL	8
CC	GO:0043202	lysosomal lumen	7/111	95/19717	1.09E-06	0.000139308	0.000127737	DCN/AGRN/SDC2/VCAN/GPC4/SDC3/SDC1	7
CC	GO:0005796	Golgi lumen	7/111	102/19717	1.76E-06	0.000150275	0.000137793	DCN/AGRN/SDC2/VCAN/GPC4/SDC3/SDC1	7
CC	GO:0001002	ficolin-1-rich granule	8/111	185/19717	1.00E-05	0.000640245	0.000587067	PGAM1/ALDOA/AGL/PKM/MIF/PPIA/PGM2/PYGL	8
CC	GO:0034774	secretory granule lumen	10/111	321/19717	1.37E-05	0.000702114	0.000643797	PGAM1/ALDOA/QSOX1/AGL/PKM/MIF/VEGFA/PPIA/PGM2/PYGL	10

CC	GO:0060205	cytoplasmic vesicle lumen	10/111	338/19717	2.14E-05	0.000801664	0.000735078	PGAM1/ALDOA/QSOX1 /AGL/PKM/MIF/VEGFA /PPIA/PGM2/PYGL	10
CC	GO:0031983	vesicle lumen	10/111	339/19717	2.19E-05	0.000801664	0.000735078	PGAM1/ALDOA/QSOX1 /AGL/PKM/MIF/VEGFA /PPIA/PGM2/PYGL	10
CC	GO:0005775	vacuolar lumen	7/111	172/19717	5.39E-05	0.001725899	0.001582547	DCN/AGRN/SDC2/VCA N/GPC4/SDC3/SDC1	7
CC	GO:0005788	endoplasmic reticulum lumen	8/111	309/19717	0.000362964	0.010324315	0.009466785	CLN6/SDC2/VCAN/QSO X1/P4HA1/HSPA5/IGFB P3/COL5A1	8
CC	GO:0062023	collagen-containing extracellular matrix	9/111	406/19717	0.000484042	0.012391464	0.011362239	DCN/AGRN/ANG/SDC2 /VCAN/GPC4/PKM/CO L5A1/SDC3	9
CC	GO:0016529	sarcoplasmic reticulum	4/111	71/19717	0.000691535	0.016093913	0.014757165	HAX1/AGL/NOL3/HK2	4
CC	GO:0016528	sarcoplasm	4/111	80/19717	0.001082856	0.023100919	0.021182175	HAX1/AGL/NOL3/HK2	4
CC	GO:0005759	mitochondrial matrix	9/111	469/19717	0.001339129	0.026370537	0.024180221	CDK1/AK4/PC/SOD1/A K3/ALDH7A1/ME2/CHP F/PDK3	9
MF	GO:0048029	monosaccharide binding	13/111	75/17697	1.03E-15	3.61E-13	2.99E-13	ALDOB/UGP2/ALDOA/ EGLN3/P4HA1/PAM/PL OD1/HK2/GYS1/TALDO	13

								1/GALK1/PFKP/PYGL	
MF	GO:00	carbohydrate binding	15/111	271/17697	1.48E-10	2.59E-08	2.15E-08	ALDOB/UGP2/ALDOA/ EGLN3/VCAN/P4HA1/A GL/PAM/PLOD1/HK2/G YS1/TALDO1/GALK1/PF KP/PYGL	15
		30246							
MF	GO:00	isomerase activity	10/111	158/17697	5.75E-08	6.69E-06	5.55E-06	MPI/PGAM1/GALE/QSO X1/GNPDA1/RPE/FKBP4 /MIF/PPIA/PGM2	10
		16853							
MF	GO:00	carboxylic acid binding	10/111	193/17697	3.74E-07	3.26E-05	2.71E-05	HMMR/EGLN3/AGRN/P C/VCAN/P4HA1/GOT1/ PAM/PLOD1/PYGL	10
		31406							
MF	GO:00	glucose binding	4/111	11/17697	4.68E-07	3.26E-05	2.71E-05	UGP2/HK2/GYS1/PYGL	4
		05536							
MF	GO:00	organic acid binding	10/111	205/17697	6.52E-07	3.79E-05	3.14E-05	HMMR/EGLN3/AGRN/P C/VCAN/P4HA1/GOT1/ PAM/PLOD1/PYGL	10
		43177							
MF	GO:00	coenzyme binding	11/111	291/17697	2.17E-06	0.000108135	8.97E-05	ME1/MDH1/EGLN3/PC/ QSOX1/P4HA1/GOT1/M E2/PAM/PLOD1/PYGL	11
		50662							
MF	GO:00	L-ascorbic acid binding	4/111	20/17697	6.57E-06	0.000286737	0.00023783	EGLN3/P4HA1/PAM/PL OD1	4
		31418							
MF	GO:00	carbon-carbon lyase activity	5/111	51/17697	1.66E-05	0.0006418	0.000532333	ME1/ALDOB/ALDOA/G OT1/ME2	5
		16830							

MF	GO:0016829	lyase activity	8/111	187/17697	2.34E-05	0.000815347	0.000676279	ME1/ALDOB/ALDOA/E NO1/GOT1/ME2/PAM/E NO2	8
MF	GO:0019842	vitamin binding	7/111	138/17697	2.60E-05	0.000825913	0.000685044	EGLN3/PC/P4HA1/GOT 1/PAM/PLOD1/PYGL	7
MF	GO:0016758	transferase activity, transferring hexosyl groups	8/111	216/17697	6.51E-05	0.00189201	0.001569304	GYS2/XYL2/AGL/CHPF /B3GALT6/GYS1/EXT1/P YGL	8
MF	GO:0009055	electron transfer activity	6/111	114/17697	8.18E-05	0.002196268	0.001821667	CYB5A/ME1/GLRX/SDH C/AKR1A1/ME2	6
MF	GO:0016860	intramolecular oxidoreductase activity	4/111	47/17697	0.000212402	0.005294881	0.004391773	MPI/QSOX1/GNPDA1/M IF	4
MF	GO:0019200	carbohydrate kinase activity	3/111	21/17697	0.000294158	0.006844075	0.005676733	HK2/GALK1/PFKP	3
MF	GO:0008194	UDP-glycosyltransfer ase activity	6/111	151/17697	0.000378761	0.007888414	0.006542947	GYS2/XYL2/CHPF/B3G ALT6/GYS1/EXT1	6
MF	GO:0016757	transferase activity, transferring glycosyl groups	8/111	280/17697	0.000384249	0.007888414	0.006542947	GYS2/XYL2/AGL/CHPF /B3GALT6/GYS1/EXT1/P YGL	8
MF	GO:0005539	glycosaminoglycan binding	7/111	229/17697	0.000602242	0.0116768	0.009685176	DCN/HMMR/AGRN/AN G/VCAN/COL5A1/VEGF A	7
MF	GO:00	carboxy-lyase activity	3/111	35/17697	0.001358073	0.024945663	0.020690868	ME1/GOT1/ME2	3

	16831								
MF	GO:00	ADP binding	3/111	38/17697	0.001726732	0.030131476	0.024992176	ME1/PKM/PGK1	3
	43531								
MF	GO:00	aldehyde-lyase	2/111	11/17697	0.002066568	0.031357929	0.026009442	ALDOB/ALDOA	2
	16832	activity							
MF	GO:00	intramolecular	2/111	11/17697	0.002066568	0.031357929	0.026009442	PGAM1/PGM2	2
	16868	transferase activity, phosphotransferases							
MF	GO:00	UDP-glucosyltransfer	2/111	11/17697	0.002066568	0.031357929	0.026009442	GYS2/GYS1	2
	35251	ase activity							
MF	GO:00	magnesium ion	6/111	213/17697	0.002248727	0.032700245	0.027122809	LHPP/XYLT2/ENO1/PK	6
	00287	binding						M/ENO2/PGM2	
MF	GO:00	racemase and	2/111	12/17697	0.002469742	0.033151532	0.027497124	GALE/RPE	2
	16857	epimerase activity, acting on carbohydrates and derivatives							
MF	GO:00	peptidyl-proline	2/111	12/17697	0.002469742	0.033151532	0.027497124	EGLN3/P4HA1	2
	31543	dioxygenase activity							
MF	GO:00	oxidoreductase	3/111	45/17697	0.002813615	0.034982512	0.029015807	EGLN3/P4HA1/PLOD1	3
	16706	activity, acting on paired donors, with incorporation or reduction of							

molecular oxygen,
 2-oxoglutarate as one
 donor, and
 incorporation of one
 atom each of oxygen
 into both donors

MF	GO:00	AMP binding	2/111	13/17697	0.002906856	0.034982512	0.029015807	PFKP/PYGL	2
		16208							
MF	GO:00	protein binding	2/111	13/17697	0.002906856	0.034982512	0.029015807	DSC2/PKP2	2
		86080							
		involved in							
		heterotypic cell-cell							
		adhesion							
MF	GO:00	C4-dicarboxylate	2/111	14/17697	0.003377478	0.038023868	0.031538422	SLC25A13/SLC25A10	2
		15556							
		transmembrane							
		transporter activity							
MF	GO:00	glucosidase activity	2/111	14/17697	0.003377478	0.038023868	0.031538422	LCT/AGL	2
		15926							
MF	GO:00	aldehyde	2/111	15/17697	0.003881178	0.042329096	0.035109339	ALDH9A1/ALDH7A1	2
		04029							
		dehydrogenase							
		(NAD) activity							
MF	GO:00	sulfotransferase	3/111	52/17697	0.004245173	0.044895924	0.037238363	HS2ST1/GAL3ST1/CHST4	3
		08146							
		activity							
KEGG									
	hsa012	Carbon metabolism	19/89	118/8081	1.46E-17	2.07E-15	1.69E-15	8789/4199/5223/4190/229	19

00							/6391/226/5091/2023/280	
							5/4200/5315/3099/6120/2	
							5796/5230/2026/6888/521	
							4	
hsa000	Glycolysis /	14/89	67/8081	8.19E-15	5.81E-13	4.74E-13	8789/5223/229/226/223/1	14
10	Gluconeogenesis						0327/2023/501/5315/3099	
							/5230/2026/55276/5214	
hsa012	Biosynthesis of	12/89	75/8081	2.21E-11	1.05E-09	8.53E-10	5223/229/226/5091/2023/	12
30	amino acids						2805/5315/6120/5230/202	
							6/6888/5214	
hsa000	Pentose phosphate	8/89	30/8081	7.55E-10	2.68E-08	2.19E-08	8789/229/226/6120/25796	8
30	pathway						/55276/6888/5214	
hsa005	Amino sugar and	9/89	48/8081	1.86E-09	5.29E-08	4.32E-08	4351/7360/29925/2582/26	9
20	nucleotide sugar						73/10007/3099/55276/258	
	metabolism						4	
hsa000	Galactose metabolism	7/89	31/8081	3.28E-08	7.77E-07	6.34E-07	7360/3938/2582/3099/552	7
52							76/2584/5214	
hsa000	Fructose and	7/89	33/8081	5.24E-08	1.06E-06	8.67E-07	8789/4351/229/226/29925	7
51	mannose metabolism						/3099/5214	
hsa005	Starch and sucrose	7/89	36/8081	9.97E-08	1.77E-06	1.44E-06	2998/7360/178/3099/2997	7
00	metabolism						/55276/5836	
hsa006	Pyruvate metabolism	7/89	39/8081	1.79E-07	2.82E-06	2.30E-06	4199/4190/223/5091/501/	7
20							4200/5315	
hsa040	HIF-1 signaling	9/89	109/8081	2.74E-06	3.89E-05	3.17E-05	229/226/112399/2023/309	9

66	pathway						9/7422/5230/2026/5214	
hsa052	Central carbon	6/89	70/8081	0.000112191	0.001448285	0.001180959	5223/5315/3099/9123/423	6
30	metabolism in cancer						3/5214	
hsa005	Glycosaminoglycan	4/89	24/8081	0.000123443	0.001460739	0.001191114	64132/9653/126792/2131	4
34	biosynthesis - heparan sulfate / heparin							
hsa049	Glucagon signaling	7/89	107/8081	0.000165549	0.001808305	0.001474526	8789/2998/5223/5315/299	7
22	pathway						7/5214/5836	
hsa005	Glycosaminoglycan	3/89	20/8081	0.001285542	0.013039072	0.010632305	64132/79586/126792	3
32	biosynthesis - chondroitin sulfate / dermatan sulfate							
hsa012	Biosynthesis of	7/89	156/8081	0.001599922	0.015145932	0.012350278	4351/7360/29925/205/508	7
40	cofactors						08/10327/5315	
hsa003	Arginine and proline	4/89	51/8081	0.002315227	0.020547636	0.01675493	223/5033/2805/501	4
30	metabolism							
hsa000	Citrate cycle (TCA	3/89	30/8081	0.004228925	0.03336152	0.027203612	4190/6391/5091	3
20	cycle)							
hsa000	Ascorbate and	3/89	30/8081	0.004228925	0.03336152	0.027203612	223/10327/501	3
53	aldarate metabolism							

hsa000	Pentose and	3/89	34/8081	0.006038794	0.045132039	0.036801514	7360/10327/6120	3
40	glucuronate							
	interconversions							
