			(V	0.1
			ulfur compound metabolic process (GO:0006790)	<u> </u>
			egulation of sister chromatid cohesion (GO:0007063)	
			egulation of MHC class II biosynthetic process (GO:0045346)	<u> </u>
			ost-embryonic development (GO:0009791)	0.08
			poyte development (GO:0048599)	<u></u>
			egative regulation of intrinsic apoptotic signaling pathway by p53 class mediator (GO:1902254)	<u></u>
			acrophage differentiation (GO:0030225)	_ ^ ^ ^
			noleic acid metabolic process (GO:0043651)	0.06
			stone H4 deacetylation (GO:0070933)	<u></u>
		-	ranulocyte differentiation (GO:0030851)	
			tty acid beta-oxidation using acyl-CoA oxidase (GO:0033540)	0.04
			mbryo development (GO:0009790)	0.04
			pha-linolenic acid metabolic process (GO:0036109)	<u></u>
			natomical structure arrangement (GO:0048532)	<u></u>
			ridine nucleotide metabolic process (GO:0019362)	0.02
			cotinamide nucleotide metabolic process (GO:0046496)	0.02
		me	onosaccharide catabolic process (GO:0046365)	<u></u>
			exose catabolic process (GO:0019320)	
			exose biosynthetic process (GO:0019319)	0
		gly	ycolytic process (GO:0006096)	U
		ce	ellular aldehyde metabolic process (GO:0006081)	ŀ
		glı	uconeogenesis (GO:0006094)	ļ
			vnaptic vesicle maturation (GO:0016188)	ŀ
			rotein palmitoylation (GO:0018345)	ŀ
			entose-phosphate shunt (GO:0006098)	ŗ
		•	ADPH regeneration (GO:0006740)	ŗ
			ucose catabolic process (GO:0006007)	ļ
			ADP metabolic process (GO:0006739)	ŗ
			idbrain development (GO:0030901)	ŗ
			rebrain morphogenesis (GO:0048853)	ŗ
			teral ventricle development (GO:0021670)	ľ
			roteolysis involved in cellular protein catabolic process (GO:0051603)	ŀ
		·	piquitin-dependent protein catabolic process (GO:0006511)	I
			odification-dependent macromolecule catabolic process (GO:0043632)	ļ
			odification-dependent macromolecule catabolic process (GO:0043632)	
			ulticellular organismal development (GO:0007275)	
			egulation of Rho GTPase activity (GO:0032319)	
			opodium assembly (GO:0046847)	
			egulation of Cdc42 GTPase activity (GO:0043088)	
			positive regulation of GTP catabolic process (GO:0033126)	
.		·	ositive regulation of GTP catabolic process (GO:0033126) positive regulation of GTPase activity (GO:0043547)	
			egulation of small GTPase mediated signal transduction (GO:0051056)	
			mall GTPase mediated signal transduction (GO:0007264)	
, , , , , , , , , , , , , , , , , , ,			sulin secretion (GO:0030073)	
		_	gnal release (GO:0023061)	
			egulation of peptide secretion (GO:0002791)	
			egulation of peptide hormone secretion (GO:0090276)	
			egulation of insulin secretion (GO:0050796)	
			arbohydrate homeostasis (GO:0033500)	
		_	ucose homeostasis (GO:0042593)	
			mide transport (GO:0042886)	
		•	eptide transport (GO:0015833)	
		-	eptide secretion (GO:0002790)	
		-	eptide hormone secretion (GO:0030072)	
			ormone secretion (GO:0046879)	
		ho	ormone transport (GO:0009914)	
		en	nergy derivation by oxidation of organic compounds (GO:0015980)	
		en	nergy reserve metabolic process (GO:0006112)	
<u>5</u>		S		
IsMale	ls10ppm	IsCd		
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