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		DEG	> 2-fold	UP	GENE ONTOLOGY / *KEGG PATHWAYS / GENE NAMES
3dpf	GFQ vs. NMQ	1,874	90 (5%)	961 (51%)	lipid metabolic process (81), single-organism process (655), transmembrane transport (77), ion homeostasis (1)
	SFQ vs. NMQ	1,948	94 (5%)	990 (51%)	metabolic pathways (139), organic acid metabolic process (73), transmembrane transport (76), lipid metabolic process (79), single-organism process (667), cytoplasmic translation (31), *citrate cycle (13)
	GFQ vs. SFQ	1	0	0	<i>Slit homolog 1 protein</i>
25dpf	GFQ vs. NMQ	2,169	107 (5%)	1,036 (48%)	single-organism process (754), *metabolic pathways (168), transmembrane transport (86), lipid metabolic process (84), ion transport (79), carboxylic acid metabolic process (67), purine nucleotide metabolic process (60), *ribosome (51), small molecule biosynthetic process (35), microtubule organizing center organization (34), anion transport (27), gluconeogenesis (16), regulation of pH (13), *metabolism of xenobiotics by cytochrome P450 (7)
	large	2,208	90 (4%)	1,003 (45%)	
	small	1,449	86 (6%)	694 (48%)	
	SFQ vs. NMQ	2,763	136 (5%)	1,254 (45%)	cellular process (914), transport (278), carboxylic acid metabolic process (82), microtubule cytoskeleton organization (80), *ribosome (66), ribosome biogenesis (66), *oxidative phosphorylation (62), centrosome organization (50), small molecule biosynthetic process (43), *carbon metabolism (40), anion transport (30), hydrogen transport (23), ATP biosynthetic process (15), carbohydrate catabolic process (15), isoprenoid biosynthetic process (11), glycolytic process (10)
	GFQ vs. SFQ	659	17 (3%)	482 (73%)	oxidation-reduction process (46), fatty acid metabolic process (16), translation (46), centrosome duplication (14)
	GFQlarge vs. GFQsmall	5	0	3	<i>Translocase of the inner mitochondrial membrane 17b, two ribosomal proteins (RpL9 and RpS30) and two uncharacterized genes</i>