

Supplementary Table 1. Details of cluster analysis of dysregulated DEGs

Contrasts	Clusters and seeds	Genes
LLW vs LD	14 seeds in 20 clusters	<i>zgc:56596 (UBL4A)</i> , <i>atp5f1</i> , <i>zp2.6</i> , <i>DBF4B</i> , <i>pigx</i> , <i>brca2</i> , <i>cops8</i> , <i>MRPS36</i> , <i>rbc3</i> , <i>setd2</i> , <i>mgst2</i> , <i>wu:fe01c10</i> , <i>itgb1b</i> , <i>ENSDARP00000080968 (atp10a)</i>
LLM vs LD	20 seeds in 21 clusters	<i>zgc:56596 (UBL4A)</i> , <i>ndufa7</i> , <i>zp2.6</i> , <i>trmt112</i> , <i>hace1</i> , <i>ncaph</i> , <i>supt4h1</i> , <i>ssr1</i> , <i>sod1</i> , <i>itsn2b</i> , <i>gpt2</i> , <i>plk1</i> , <i>map3k1</i> , <i>grna</i> , <i>bbs12</i> , <i>cmss1</i> , <i>prtfcd1</i> , <i>nr1d2a</i> , <i>mfsd8</i> , <i>efna3a</i>
LLY vs LD	13 seeds in 18 clusters	<i>rps23</i> , <i>polr3b</i> , <i>setd1a</i> , <i>ncapg</i> , <i>polr2d</i> , <i>C2CD3</i> , <i>cept1a</i> , <i>s100a1</i> , <i>rad18</i> , <i>ptbp1b</i> , <i>frya</i> , <i>ENSDARP00000079424 (gnb1b)</i>
Total	47 seeds (40 unique, 0 common)	

Supplementary Table 2. Pathway enrichment of top two clusters of significant dysregulated DEGs of each contrast, other clusters didn't enrich any pathways

Contrasts	Cluster	Score	Enriched pathway	No of genes
LLW vs LD	1	34.8	1. Ribosome 2. Protein export	30 2
	2	18.3	3. Oxidative phosphorylation 4. Metabolic pathways 5. Cardiac muscle contraction	17 17 4
LLM vs LD	1	31.18	1. Ribosome 2. Protein export	26 2
	2	17.7	3. Oxidative phosphorylation 4. Metabolic pathways 5. Cardiac muscle contraction	16 16 4
LLY vs LD	1	31.097	1. Ribosome	27
	2	10.625	2. Oxidative phosphorylation 3. Metabolic pathways 4. <i>RNA polymerase</i> 5. Cardiac muscle contraction 6. <i>Cytosolic DNA-sensing pathway</i>	11 11 3 3 2