

## Supplementary Material

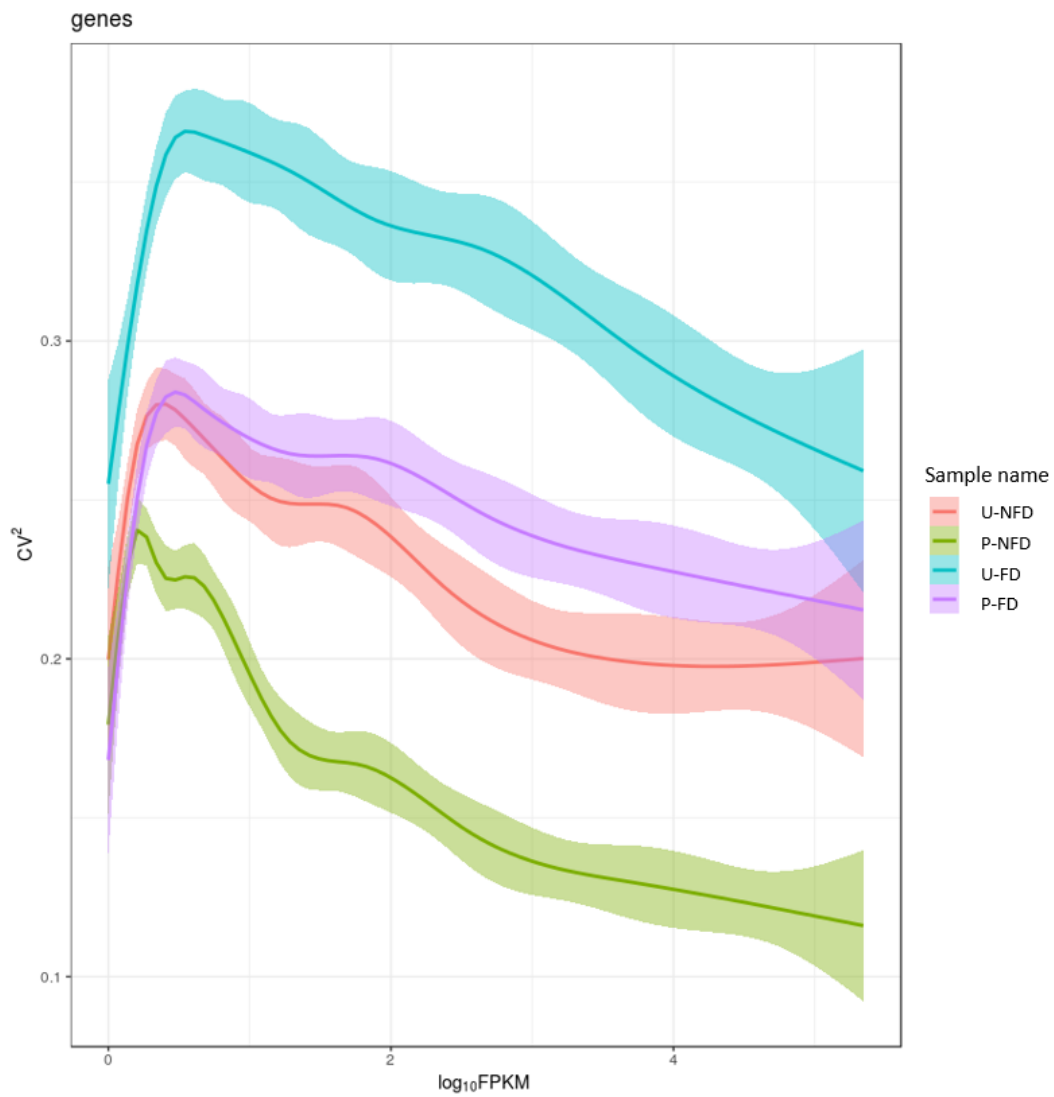
### Gene expression in diapausing rotifer eggs in response to divergent environmental predictability regimes

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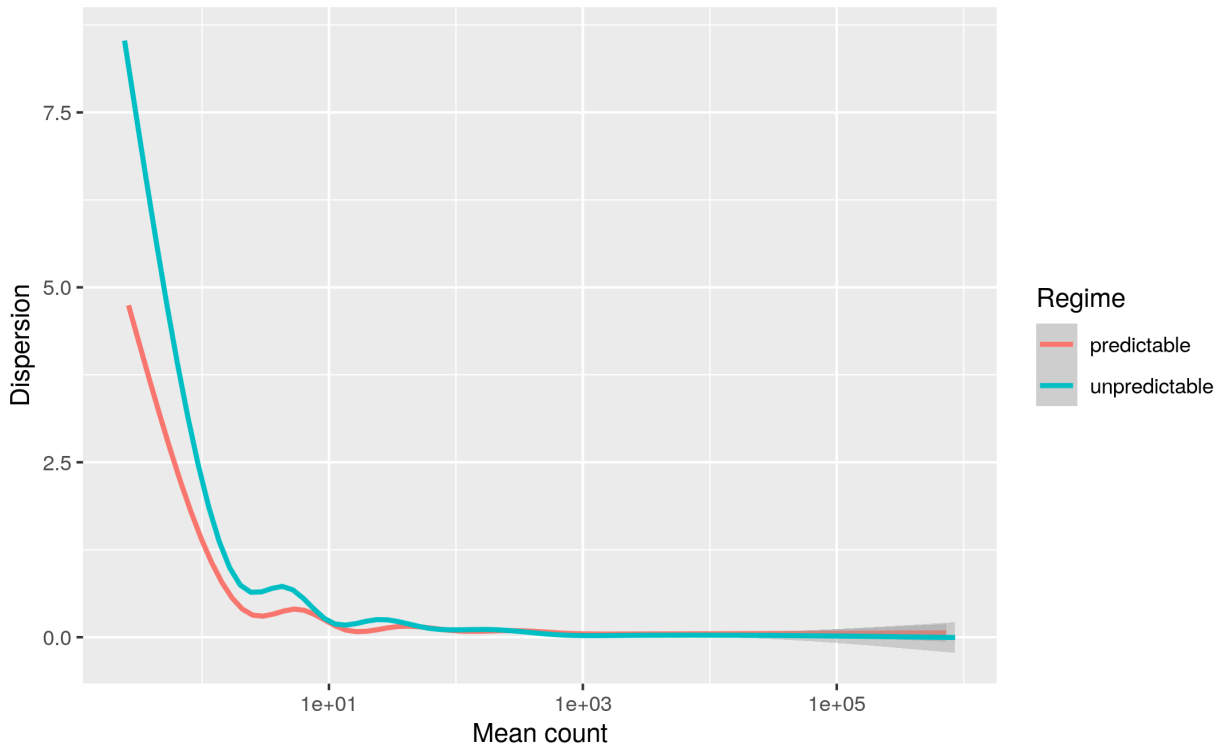
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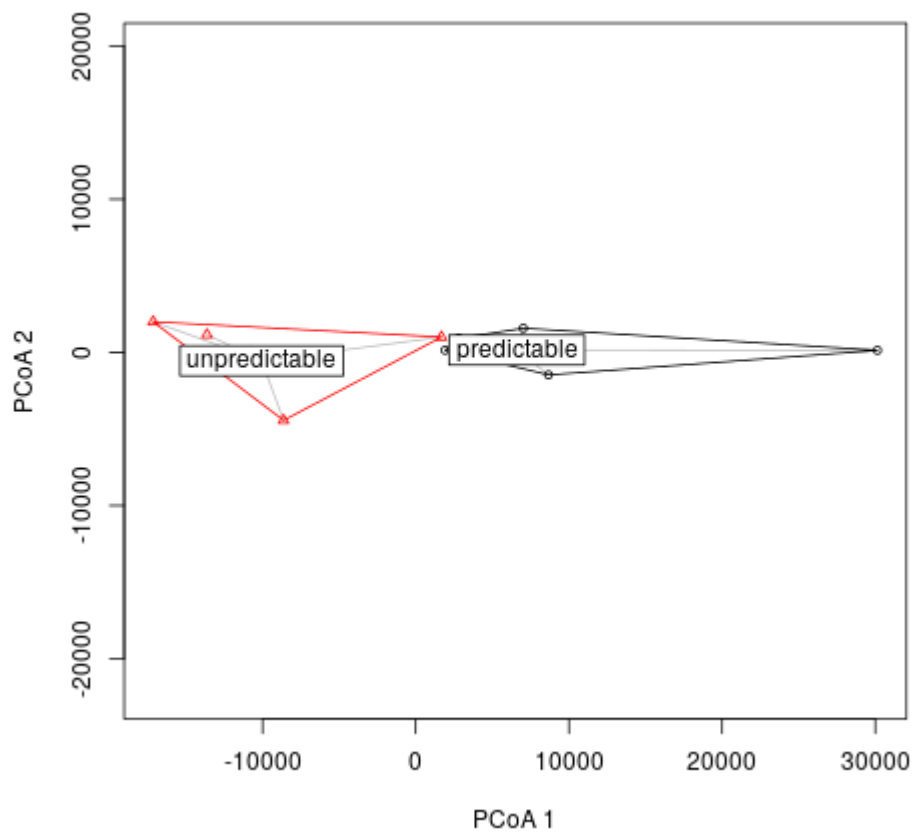
§ Both authors contributed equally to this work.



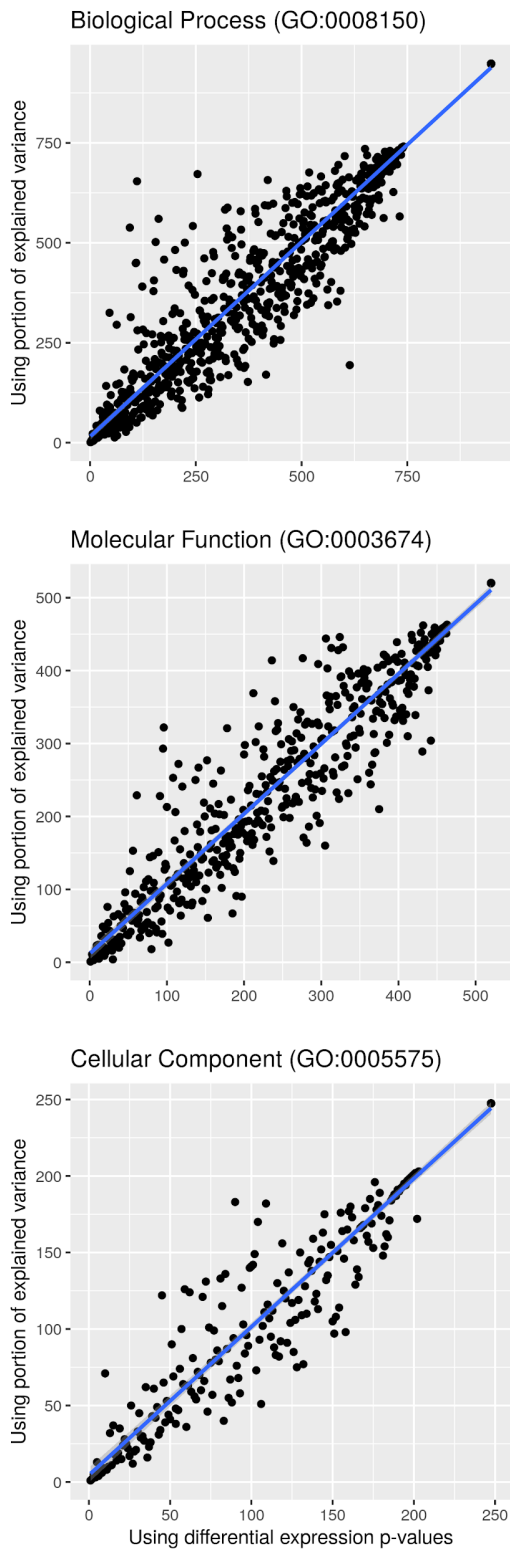
**Figure S1.** RPKM density distribution plot (the squared coefficient of variation ( $CV^2$ ) vs  $\log_{10}$ FPKM) per selective regime and diapause condition.



**Figure S2.** Estimated relationship between biological variation in gene expression between replicates (dispersion) and average level of expression among replicates, measured by a normalized number of counts. Estimates of gene-wise dispersions were obtained using the *estimateDispersion()* function of the *DESeq2* package, separately for samples from the two selective regimes.



**Figure S3.** Principal coordinates of gene expression profiles based on Poisson distances. Distances of samples to their regime-specific centroid are not significantly different between selective regimes ( $p$ -value = 0.883).



**Figure S4.** Ordination of gene ontology (GO) terms according to their significance in the enrichment analyses based on either the differential expression  $p$ -values or the portion of variance explained by regime.

**Table S1.** Gene Ontology (GO) specific terms for biological process (GO:0008150) significantly associated with selective regime according to all three algorithms used in enrichment analysis. *p*-values are derived from Kolmogorov-Smirnov tests.

GO ID	GO Term	<i>p</i> -value
<a href="#">GO:0055085</a>	transmembrane transport	< 0.001
<a href="#">GO:0006508</a>	proteolysis	< 0.001
<a href="#">GO:0055114</a>	oxidation-reduction process	< 0.001
<a href="#">GO:0007186</a>	G protein-coupled receptor signalling pathway	< 0.001
<a href="#">GO:0006468</a>	protein phosphorylation	< 0.001
<a href="#">GO:0006813</a>	potassium ion transport	< 0.001
<a href="#">GO:0006355</a>	regulation of transcription, DNA-templated	< 0.001
<a href="#">GO:0006289</a>	nucleotide-excision repair	< 0.001
<a href="#">GO:0034220</a>	ion transmembrane transport	0.001
<a href="#">GO:0006470</a>	protein dephosphorylation	0.001
<a href="#">GO:0006812</a>	cation transport	0.002
<a href="#">GO:0003341</a>	cilium movement	0.002
<a href="#">GO:0060271</a>	cilium assembly	0.002
<a href="#">GO:0005992</a>	trehalose biosynthetic process	0.003
<a href="#">GO:0007018</a>	microtubule-based movement	0.003
<a href="#">GO:0006367</a>	transcription initiation from RNA polymerase II promoter	0.004
<a href="#">GO:0046039</a>	GTP metabolic process	0.004
<a href="#">GO:0046129</a>	purine ribonucleoside biosynthetic process	0.004
<a href="#">GO:0007160</a>	cell-matrix adhesion	0.005
<a href="#">GO:0070836</a>	caveola assembly	0.006
<a href="#">GO:0006821</a>	chloride transport	0.007
<a href="#">GO:0006979</a>	response to oxidative stress	0.007
<a href="#">GO:0043161</a>	proteasome-mediated ubiquitin-dependent protein catabolic process	0.008
<a href="#">GO:0051260</a>	protein homooligomerization	0.008
<a href="#">GO:0008272</a>	sulphate transport	0.009

**Table S2.** Gene ontology (GO) specific terms for molecular function (GO:0003674) significantly associated with selective regime according to all three algorithms used in enrichment analysis. *p*-values are derived from Kolmogorov-Smirnov tests.

GO ID	GO Term	<i>p</i> -value
<a href="#">GO:0005515</a>	protein binding	< 0.001
<a href="#">GO:0005509</a>	calcium ion binding	< 0.001
<a href="#">GO:0003774</a>	motor activity	< 0.001
<a href="#">GO:0004930</a>	G protein-coupled receptor activity	< 0.001
<a href="#">GO:0004252</a>	serine-type endopeptidase activity	< 0.001
<a href="#">GO:0005524</a>	ATP binding	< 0.001
<a href="#">GO:0004672</a>	protein kinase activity	< 0.001
<a href="#">GO:0022857</a>	transmembrane transporter activity	< 0.001
<a href="#">GO:0042626</a>	ATPase activity, coupled to transmembrane movement of substances	0.001
<a href="#">GO:0004198</a>	calcium-dependent cysteine-type endopeptidase activity	0.001
<a href="#">GO:0005525</a>	GTP binding	0.001
<a href="#">GO:0061630</a>	ubiquitin protein ligase activity	0.001
<a href="#">GO:0004181</a>	metallocarboxypeptidase activity	0.001
<a href="#">GO:0005230</a>	extracellular ligand-gated ion channel activity	0.002
<a href="#">GO:0005249</a>	voltage-gated potassium channel activity	0.002
<a href="#">GO:0005507</a>	copper ion binding	0.003
<a href="#">GO:0051015</a>	actin filament binding	0.003
<a href="#">GO:0016840</a>	carbon-nitrogen lyase activity	0.004
<a href="#">GO:0004550</a>	nucleoside diphosphate kinase activity	0.005
<a href="#">GO:0004601</a>	peroxidase activity	0.005
<a href="#">GO:0030246</a>	carbohydrate binding	0.005
<a href="#">GO:0005200</a>	structural constituent of cytoskeleton	0.006
<a href="#">GO:0016491</a>	oxidoreductase activity	0.007
<a href="#">GO:0003777</a>	microtubule motor activity	0.008
<a href="#">GO:0047631</a>	ADP-ribose diphosphatase activity	0.008

**Table S3.** Gene ontology (GO) specific terms for cellular component (GO:0005575) significantly associated with selective regime according to all three algorithms used in enrichment analysis. *p*-values are derived from Kolmogorov-Smirnov tests.

GO ID	GO Term	<i>p</i> -value
<a href="#">GO:0016020</a>	membrane	< 0.001
<a href="#">GO:0016459</a>	myosin complex	< 0.001
<a href="#">GO:0008076</a>	voltage-gated potassium channel complex	< 0.001
<a href="#">GO:0005887</a>	integral component of plasma membrane	0.001
<a href="#">GO:0005576</a>	extracellular region	0.001
<a href="#">GO:0090575</a>	RNA polymerase II transcription factor complex	0.001
<a href="#">GO:0005634</a>	nucleus	0.003
<a href="#">GO:0005886</a>	plasma membrane	0.003
<a href="#">GO:0005743</a>	mitochondrial inner membrane	0.004
<a href="#">GO:0005929</a>	cilium	0.004
<a href="#">GO:0005741</a>	mitochondrial outer membrane	0.009