

1 **Lipid metabolism in *Calanus finmarchicus* is sensitive to variations in predation risk and**  
2 **food availability**

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25 Supplementary Table 1. Gene expression results of *ELOV* (elongation of very long chain fatty  
26 acids), *FABP* (a fatty acid binding protein), *ferritin*, *hsp22* and *torso-like* in *C. finmarchicus*  
27 copepods exposed to a combination of a predator cue and high or low food availability,  
28 compared to the reference group (*Calanus* spp. C5s in diapause). Hi-P=High food and no  
29 predator cue; Hi+P=High food and predator cue; Lo-P=Low food and no predator cue;  
30 Lo+P=Low food and predator cue. logCPM: log<sub>2</sub> counts per million. FDR: false discovery rate.  
31 (Submitted as Excel file).

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33 Supplementary Table 2. Gene expression of *ELOV* (elongation of very long chain fatty acids),  
34 *FABP* (a fatty acid binding protein), *ferritin*, *hsp22* and *torso-like* in *C. finmarchicus* copepods  
35 exposed to a combination of a predator cue and high or low food availability. The first group  
36 within each comparison is set as reference to the second group in each comparison, e.g. 4 genes  
37 upregulated in Lo+P vs Lo-P = 4 genes up in Lo+P and the same 4 genes down in Lo-P. Hi-  
38 P=High food and no predator cue; Hi+P=High food and predator cue; Lo-P=Low food and no  
39 predator cue; Lo+P=Low food and predator cue. logCPM: log<sub>2</sub> counts per million. FDR: false  
40 discovery rate. (Submitted as Excel file).

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42 Supplementary Table 3. Gene expression of lipid metabolism genes ( $P < 0.05$ ) previously  
43 identified by Lenz *et al.* (2014) and Tarrant *et al.* (2016) (desaturases, fatty acid synthetases,  
44 elongases and phospholipid acyltransferases) in *C. finmarchicus* copepods exposed to a  
45 combination of a predator cue and high or low food availability, compared to the reference group  
46 (*Calanus* spp. C5s in diapause). Hi-P=High food and no predator cue; Hi+P=High food and  
47 predator cue; Lo-P=Low food and no predator cue; Lo+P=Low food and predator cue. logCPM:

48 log<sub>2</sub> counts per million. FDR: false discovery rate. Note that the file contains one tab per  
49 stage/day. (Submitted as Excel file).

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51 Supplementary Table 4. Gene expression of  $\beta$ -oxidation genes ( $P < 0.05$ ) previously identified by  
52 Skottene *et al.* (2019) in *C. finmarchicus* copepods exposed to a combination of a predator cue  
53 and high or low food availability, compared to the reference group (C5s in diapause). Hi-P=High  
54 food and no predator cue; Hi+P=High food and predator cue; Lo-P=Low food and no predator  
55 cue; Lo+P=Low food and predator cue. logCPM: log<sub>2</sub> counts per million. FDR: false discovery  
56 rate. (Submitted as Excel file).

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58 Supplementary Table 5. Gene expression of  $\beta$ -oxidation genes ( $P < 0.05$ ) previously identified by  
59 Skottene *et al.* (2019) in *C. finmarchicus* copepods exposed to a combination of a predator cue  
60 and high or low food availability. The first group within each comparison is set as reference to  
61 the second group in each comparison, e.g. 4 genes upregulated in Lo+P vs Lo-P = 4 genes up in  
62 Lo+P and the same 4 genes down in Lo-P. Hi-P=High food and no predator cue; Hi+P=High  
63 food and predator cue; Lo-P=Low food and no predator cue; Lo+P=Low food and predator  
64 cue. logCPM: log<sub>2</sub> counts per million. FDR: false discovery rate. (Submitted as Excel file).

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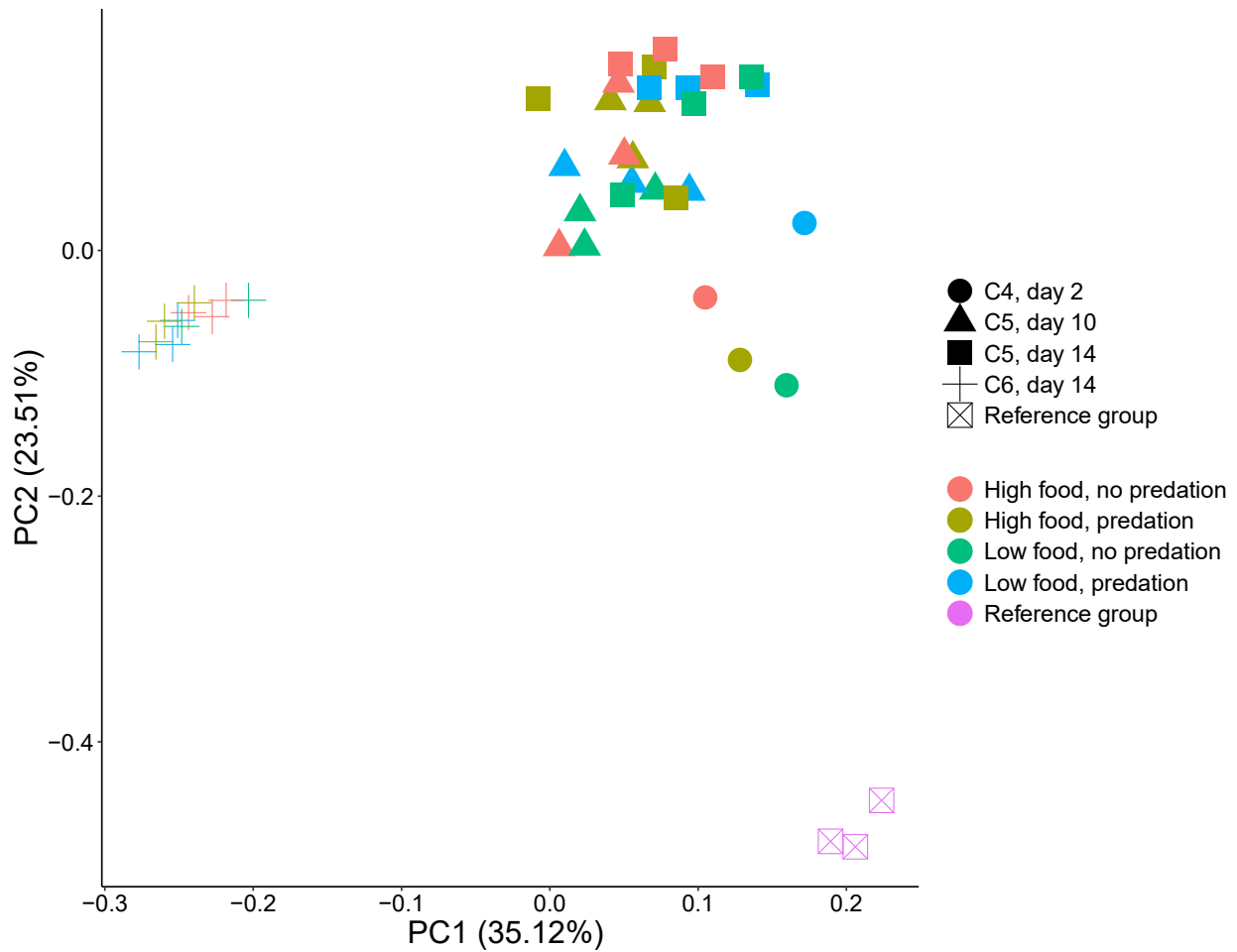
66 Supplementary Table 6. Results from the non-parametric two-sided Wilcoxon rank sum test of  
67 differences between treatments or stages. The file contains one tab per analysis: 1) Development  
68 stage per day and treatment; 2) Lipid fullness per day and stage; 3) Estimated wax ester (WE)  
69 content per day and stage; 4) Lipid fullness per day/stage and treatment; 5) WE per day/stage and  
70 treatment. In each table, the first row shows the mean values per stage, day and/or treatment

71 (indicated by column). The lower rows show the test statistic (W) and P-value from the  
72 Wilcoxon rank sum test of differences between the group indicated in the column and group  
73 indicated in the row. Hi-P=High food and no predator cue; Hi+P=High food and predator cue;  
74 Lo-P=Low food and no predator cue; Lo+P=Low food and predator cue. (Submitted as Excel  
75 file).

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77 Supplementary Table 7. Accession numbers and number of reads per library of *Calanus*

78 *finmarchicus*. (Submitted as Excel file).



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81 Supplementary Figure 1. Principal Component Analysis (PCA) plot of gene expression in all  
 82 *Calanus finmarchicus* samples. Colors indicate different treatments, symbol shape indicates stage.

83 The reference group (C5s in diapause) clustered together to the lower right, C6 (day 14) clustered  
 84 to the middle left. C4s (day 2) were closer to the reference group than the C5s (days 10 and 14),

85 which clustered between C4s and C6s. There was no clear pattern among treatment groups in the

86 PCA. Hi-P=High food and no predator cue; Hi+P=High food and predator cue; Lo-P=Low food

87 and no predator cue; Lo+P=Low food and predator cue.

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