

Suplimentary figures:

Table S1. Number of peaks detected per sample using MACS2.

Sample Name	# of peaks in rep 1	# of peaks in rep 2	# of peaks in rep 1
Pre-stress 18 °C Lab	104756	133764	112986
Pre-stress 18 °C Field	78973	68032	62041
Stress 37 °C Lab	41212	76922	83081
Stress 37 °C Field	55382	72263	115248
24h recovery 18 °C Lab	86776	84199	87249
24h recovery 18 °C Field	118525	89064	100770
48h recovery 18 °C Lab	80117	100069	121582
48h recovery 18 °C Field	78651	83962	73280

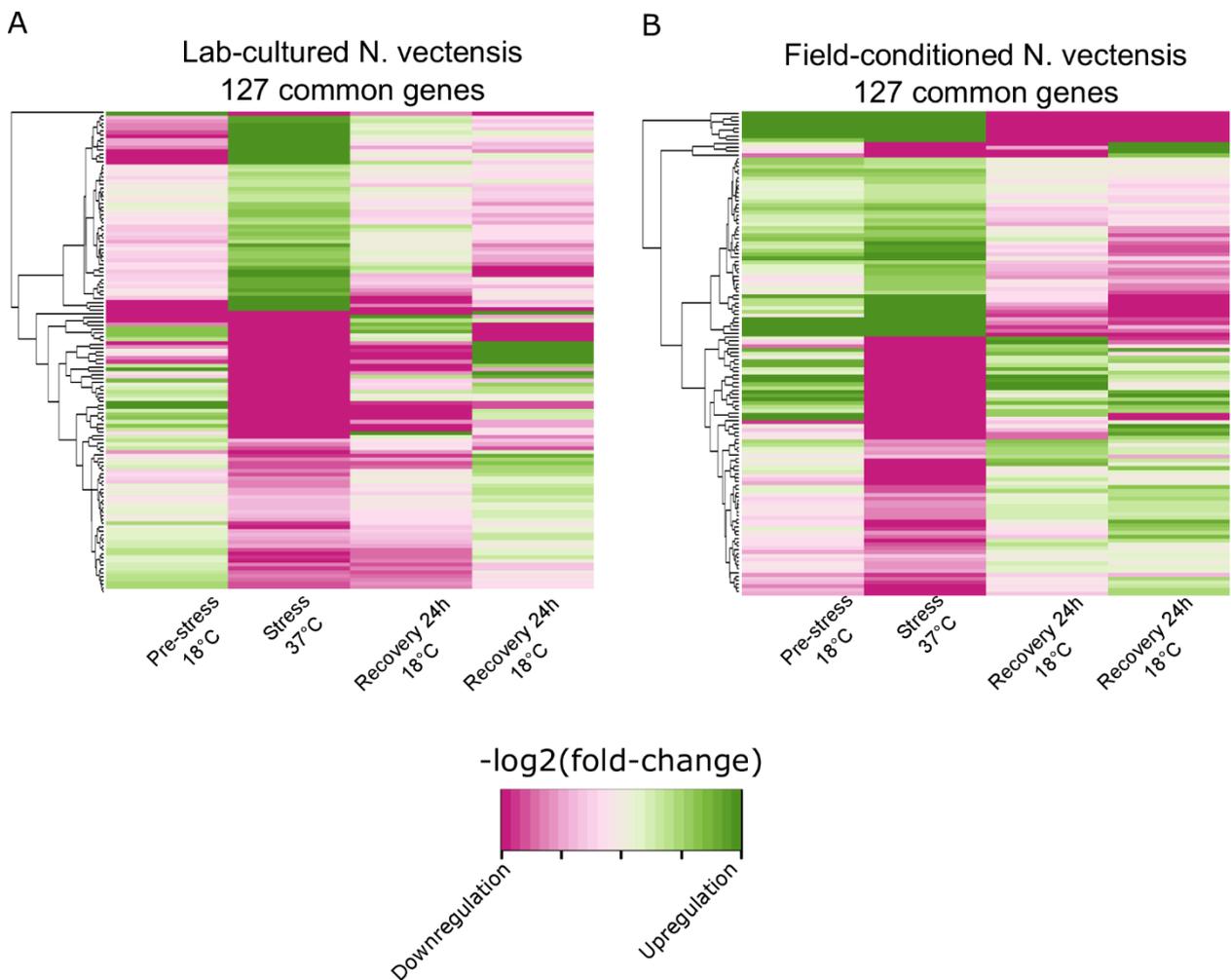


Figure S1: Rearing conditions effect transcriptional response during heat exposure. Heatmaps of $-\log_2(\text{fold-change})$ of RNA expression of *N. vectensis* 127 overlapping genes from lab-cultured and field-conditioned groups.

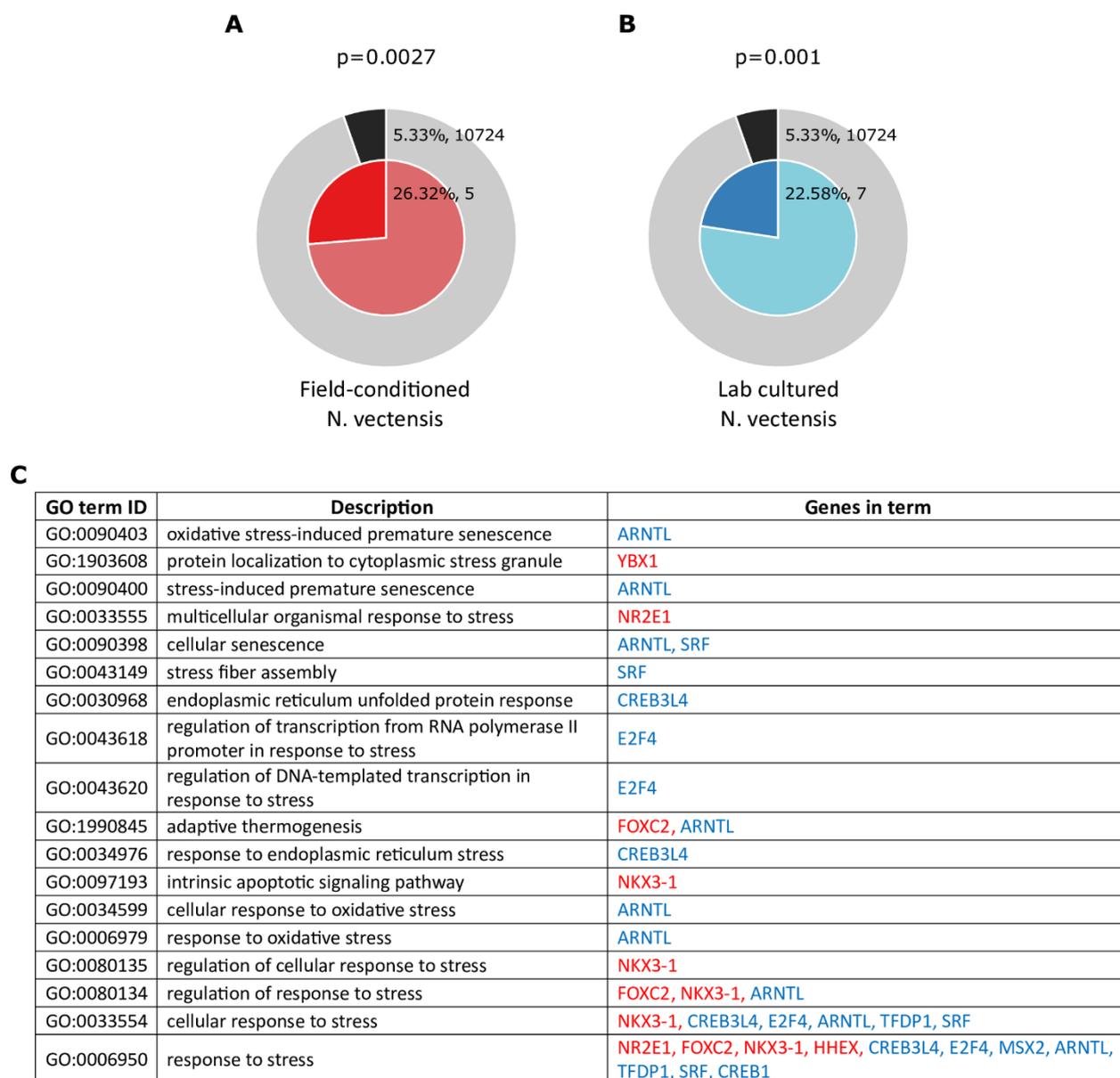


Figure S2: Rearing conditions effect TF enrichment and transcriptional response during heat exposure. (A and B) Enrichment of motifs for stress-responsive transcription factors in promoters of differentially expressed genes. The outer pie chart shows the number and the percentage of genes in the background (the total number of genes in all terms) that are associated with the stress related terms (in black); the inner pie chart shows the number and the percentage of genes in the individual input gene list (genes corresponding to TF motifs that are enriched in promoters of differentially expressed genes) that are associated with the stress related terms. The p -value indicates whether the stress membership is statistically significantly enriched in the list. GO term IDs, descriptions, and TF gene names are detailed in (C). Gene names in red are enriched in field-conditioned animals, and those in blue are enriched in lab-cultured animals.

Table S4: pathway enrichment statistics—Annotations (Excel file).

Table S5: pathway enrichment statistics—enrichment (Excel file)

Table S6. ATAC-seq primer sequences used to label libraries.

Primer index	Primer barcode	Primer forward sequence
Global for primer	Ad1 noMX:	AATGATACGGCGACCACCGAGATCTACACTCGTCGGCAGCGTCAGATGTG
A	Ad2.1_TAAGGCGA	CAAGCAGAAGACGGCATAACGAGATTCGCCTTAGTCTCGTGGGCTCGGAGATGT
B	Ad2.2_CGTACTAG	CAAGCAGAAGACGGCATAACGAGATCTAGTACGGTCTCGTGGGCTCGGAGATGT
C	Ad2.3_AGGCAGAA	CAAGCAGAAGACGGCATAACGAGATTTCTGCCTGTCTCGTGGGCTCGGAGATGT
D	Ad2.4_TCCTGAGC	CAAGCAGAAGACGGCATAACGAGATGCTCAGGAGTCTCGTGGGCTCGGAGATGT
E	Ad2.5_GGACTCCT	CAAGCAGAAGACGGCATAACGAGATAGGAGTCCGTCTCGTGGGCTCGGAGATGT
F	Ad2.6_TAGGCATG	CAAGCAGAAGACGGCATAACGAGATCATGCCTAGTCTCGTGGGCTCGGAGATGT
G	Ad2.7_CTCTCTAC	CAAGCAGAAGACGGCATAACGAGATGTAGAGAGGTCTCGTGGGCTCGGAGATGT
H	Ad2.8_CAGAGAGG	CAAGCAGAAGACGGCATAACGAGATCCTCTCTGGTCTCGTGGGCTCGGAGATGT
I	Ad2.9_GCTACGCT	CAAGCAGAAGACGGCATAACGAGATAGCGTAGCGTCTCGTGGGCTCGGAGATGT
J	Ad2.10_CGAGGCTG	CAAGCAGAAGACGGCATAACGAGATCAGCCTCGGTCTCGTGGGCTCGGAGATGT
K	Ad2.11_AAGAGGCA	CAAGCAGAAGACGGCATAACGAGATTGCCTCTTGTCTCGTGGGCTCGGAGATGT
L	Ad2.12_GTAGAGGA	CAAGCAGAAGACGGCATAACGAGATTCCTCTACGTCTCGTGGGCTCGGAGATGT
M	Ad2.13_GTCGTGAT	CAAGCAGAAGACGGCATAACGAGATATCACGACGTCTCGTGGGCTCGGAGATGT
N	Ad2.14_ACCACTGT	CAAGCAGAAGACGGCATAACGAGATACAGTGGTGTCTCGTGGGCTCGGAGATGT
O	Ad2.15_TGGATCTG	CAAGCAGAAGACGGCATAACGAGATCAGATCCAGTCTCGTGGGCTCGGAGATGT
P	Ad2.16_CCGTTTGT	CAAGCAGAAGACGGCATAACGAGATACAAACGGGTCTCGTGGGCTCGGAGATGT
Q	Ad2.17_TGCTGGGT	CAAGCAGAAGACGGCATAACGAGATACCCAGCAGTCTCGTGGGCTCGGAGATGT
R	Ad2.18_GAGGGGT	CAAGCAGAAGACGGCATAACGAGATAACCCCTCGTCTCGTGGGCTCGGAGATGT
S	Ad2.19_AGGTTGGG	CAAGCAGAAGACGGCATAACGAGATCCCAACCTGTCTCGTGGGCTCGGAGATGT
T	Ad2.20_GTGTGGTG	CAAGCAGAAGACGGCATAACGAGATCACCACACGTCTCGTGGGCTCGGAGATGT
U	Ad2.21_TGGTTTC	CAAGCAGAAGACGGCATAACGAGATGAAACCCAGTCTCGTGGGCTCGGAGATGT
V	Ad2.22_TGGTCACA	CAAGCAGAAGACGGCATAACGAGATTGTGACCAGTCTCGTGGGCTCGGAGATGT
W	Ad2.23_TTGACCCT	CAAGCAGAAGACGGCATAACGAGATAGGGTCAAGTCTCGTGGGCTCGGAGATGT
X	Ad2.24_CCACTCCT	CAAGCAGAAGACGGCATAACGAGATAGGAGTGGGTCTCGTGGGCTCGGAGATGT

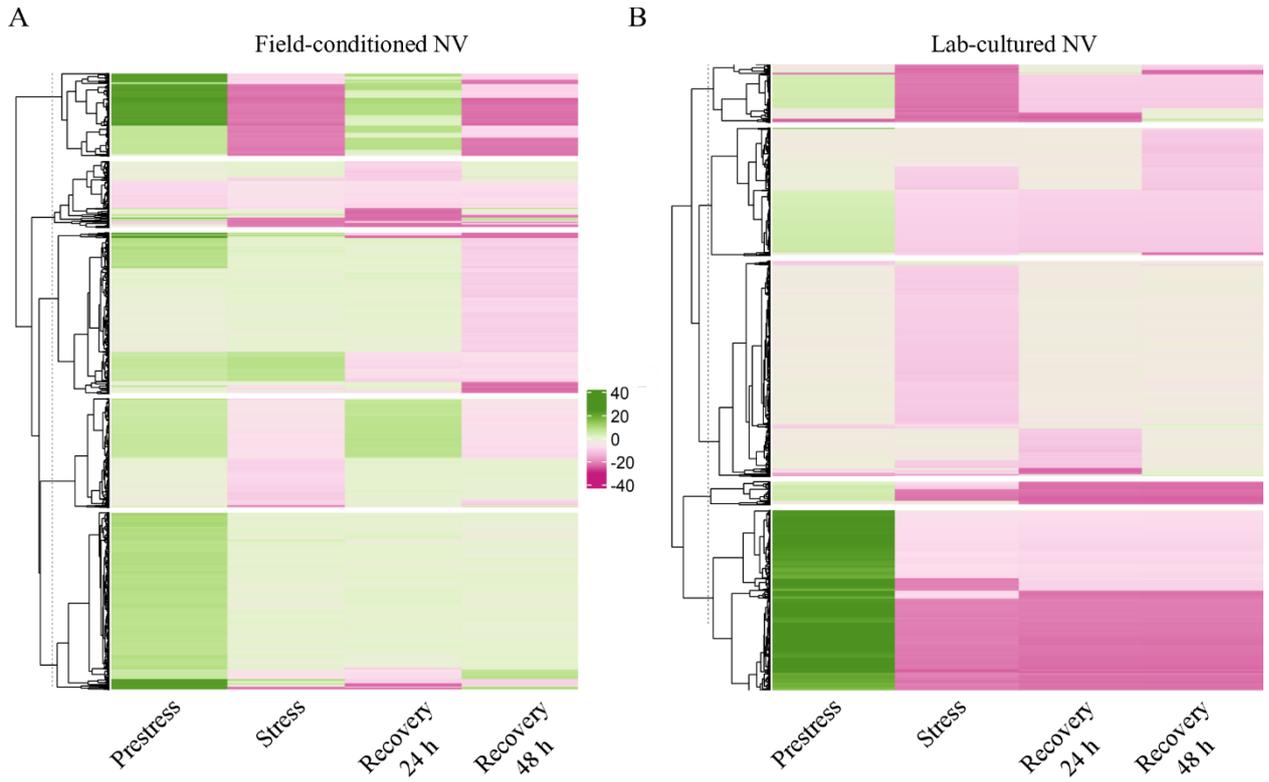


Figure S3: Dynamic chromatin changes during heat exposure in field-conditions and lab-cultured *N. vectensis* promoters. (A) 4462 differentially accessible promoters of field-conditioned *N. vectensis*. (B) 4633 differentially accessible promoters of lab-cultured *N. vectensis*.