***Supplementary Results***

*Seasonal plasticity across the transcriptome: systemic and tissue-specific components*

Examining the seasonal plasticity programme in more detail revealed tissue-specific and systemic components, both at the level of individual genes, functional processes, and the whole transcriptome. A total of 2,093 genes showed the same response to the seasonal environment in both body parts, representing 14 and 17% of the abdomen and thorax transcriptome, respectively. This systemic plasticity programme is characterised by 89 enriched GO terms, which can be grouped into processes related to development, immunity, DNA methylation, cell division, translation, and DNA replication (Figure 2A; Supplementary Table S3; Supplementary Figure S5A, B).

In addition to the systemic plasticity genes, 4,767 genes were season-biased in the abdomen but not the thorax (Figure 2C), representing 32% of the abdomen transcriptome. These abdomen-specific plasticity genes were enriched for 155 GO terms, which could roughly be grouped into processes related to development, cell division, DNA replication, lipid metabolism, protein metabolism and phosphorylation, response to oxidative stress, and steroid hormone signalling (Supplementary Table S3; Supplementary Figure S5C, D).

Likewise, 3,752 genes were differentially expressed between the seasons only in the thorax, representing 30% of the thorax transcriptome. They showed significant enrichment for 189 GO terms, which roughly grouped into processes related to translation, cell division, methylation, steroid hormone and Notch signalling, and regulation of gene expression (Figure 2D; Supplementary Table S3; Supplementary Figure S5E, F).

Many of the overrepresented GO terms for seasonal plasticity identified separately in abdomen or thorax are shared, reflecting an additional systemic signature of adaptive plasticity that is only apparent at the level of functional processes, not individual genes. In particular, we identified 37 such shared GO terms showing the same pattern of seasonal bias between the thorax and abdomen (Supplementary Table S3). Together, these processes represent an additional 865 unique genes in the systemic plasticity programme that at the individual gene level appeared restricted in their plasticity response to either abdomen (398 genes) or thorax (467). Thus, while individual genes may be involved in plasticity in one body part and not the other, they may still contribute to functional processes that are shared between the body parts, and these genes can therefore be considered part of the systemic plasticity programme.

Interestingly, we also identified 718 individual genes that showed opposite patterns of season bias between the two body parts, i.e. their expression was wet season-biased in one body part and dry season-biased in the other body part. These genes were enriched for 37 GO terms (Figure 2E; Supplementary Table S3). In addition, the abdomen- and thorax-specific plasticity genes were enriched for 41 GO terms that overlapped but showed opposite patterns of seasonal response across the body parts. These processes are related to cell division, translation, chitin metabolism, and lipid metabolism, and their opposite patterns of season bias in abdomen and thorax likely reflect trade-offs between the body parts that differ across the seasons, for example in investment in growth and storage of resources.

*Depleted genetic variation for plasticity*

Expression of 1% of genes (160 and 146 genes in abdomens and thoraces, respectively, and 20 in both; Supplementary Table S4), was significantly affected (FDR < 0.05) by the interaction between seasonal environment and family, i.e. genotype-by-environment interaction (GxE).

*Developmental food stress*

Adults that were food-deprived for a limited period of larval development show significant differential expression in only 25 genes in abdomen and none in thorax (Supplementary Figure S1). Since the effect of developmental stress may be different in different seasons, we additionally tested the effect of food stress within each season separately. This revealed four stress-induced genes in the thorax, but only in the dry season, none in the wet season. In contrast, in the abdomen there were 19 genes affected by food stress, most of which in the wet season (Supplementary Table S5).

Assessing the effect of food stress separately for specific gene repertoires revealed subtle stress-induced shifts in seasonal expression patterns, slightly decreasing transcriptional divergence between the seasons. In the abdomen, where the reproductive tissues are located, the typical dry season expression patterns became slightly less distinct under stress. Dry season genes, normally higher expressed in the dry season compared to wet (FDR < 0.05, fold change > 2), showed a stress-induced reduction in abdominal expression in the dry season, and wet season genes showed a stress-induced upregulation in the dry season (Supplementary Figure S6A, left panel; Wilcoxon signed rank test p < 0.0005). Thus, dry season butterflies under stress become more wet-season like in their abdominal transcriptional profile, potentially indicating a stress-induced terminal reproductive investment. In contrast, this response was absent for wet season butterflies (Supplementary Figure S6A, right panel), which presumably are already physiologically set up to reproduce maximally. We observe a similar down-regulation of dry season genes upon stress (p < 0.0005) but unlike in the abdomen there is no up-regulation of wet season genes, consistent with reproductive functions being restricted to the abdomen. The down-regulation of dry season genes in the thorax was also observed under wet season conditions, further decreasing their already low expression, although this response was not very pronounced (p < 0.05; Supplementary Figure S6B). Thus, stress pushed the typical dry season morph towards a slightly more wet season-like transcriptional profile, partly driven by a terminal reproductive investment in the abdomen but overall the reduction in transcriptional divergence between the seasons was quite modest (Supplementary Figure S6).

***Supplementary figure legends***

**Supplementary Figure S1. Pervasive seasonal plasticity and intra-population genetic variation but depleted genetic variation for plasticity across the transcriptome.** Differential expression analyses identify thousands of genes significantly affected by seasonal environment and genetic background, and relatively few genes affected by the gene-by-environment interaction. The vertical axis indicates numbers of significantly differentially expressed genes (FDR < 0.05) due to seasonal environment, food stress treatment, genetic background, or their interactions in edgeR general linear models, with genes affected in abdomen, thorax, and in both tissues indicated with blue, red, and orange bars, respectively. Numbers above each bar indicate the number of differentially expressed genes for that particular factor and body part. A total of 15,049 genes were expressed in abdomen, 12,567 in thorax, and 12,309 in both body parts.

**Supplementary Figure S2:** **Principal Components Analysis (PCA) reveals seasonal environment and genetic background as major drivers of whole-transcriptome expression profiles for abdomen (a-c) and thorax (d-f).** Individuals are plotted in Principal Component (PC) space for PC 1 through 6, with percentage variance explained by each PC indicated on the axes. Individuals reared in wet and dry season environments are represented by green circles and brown triangles, respectively, and individuals from different full-sib families have different colour shades and symbol sizes.

**Supplementary Figure S3. Significant associations of whole-transcriptome PCs with seasonal environment and genetic background but not genetic variation for plasticity. (a, e)** Percentage transcriptional variance explained by each of first 13 PCs is plotted for abdomen **(a)** and thorax **(e)**. **(b-d, f-h)** The seasonal environment and genetic background, but not their interaction, associate significantly with major PCs. P values (upper barplots) and F statistics (lower barplots) are shown on the vertical axes for two-way Anovas with seasonal environment **(**left panels **b, f)**, genetic background **(**middle panels **c, g)** and their interaction **(**right panels **d, h)** as fixed effects and PC 1 through 13 as dependent variables (plotted along each horizontal axis), for abdomen **(**upper panels **b-d)** and thorax **(**lower panels **f-h)**. Asterisks indicate a significant association (FDR < 0.05). In thorax, none of the first 13 Principal Components (together accounting for 62% of total variance) associated with the interaction between seasonal environment and genetic background (FDR > 0.49, F < 2.0), while in abdomen only PC 13 (accounting for 1.5% of total variance) was significantly affected by the interaction between seasonal environment and genetic background (FDR = 0.03, F = 3.9). In contrast, major PCs accounting for 15 to 56% of total variance are significantly (FDR < 0.05) associated with the seasonal environment or the genetic background.

**Supplementary Figure S4. Clustering of gene expression by seasonal environment and full-sib family.** **(a, b).** Neighbour joining trees from Euclidian distances of whole-transcriptome expression profiles for abdomen **(a)** and thorax **(b)** separate individuals reared in wet (green circles) or dry (brown triangles) season conditions, as well as individuals from different full-sib family (different colour shades and symbol sizes).

**Supplementary Figure S5: Gene Set Enrichment (GSE) analysis of systemic and tissue-specific components of the seasonal plasticity programme.**

Gene Ontology (GO) terms enriched among genes differentially expressed between dry and wet season are plotted in semantic space, with more similar terms grouped closer together. Wet and dry season-biased GO terms are plotted in green and brown, respectively, with opacity proportional to the extent of enrichment. Analyses for systemic (shared), abdomen-specific, and thorax-specific plasticity genes are displayed in top **(a, b)**, middle **(c, d)** and bottom rows **(e, f)**, respectively. “Biological Process” (BP) and “Molecular Function” (MF) GO terms are in left **(a, c, e)** and right **(b, d, f)** panels, respectively, and names of selected GO terms are labelled. See Supplementary Table S3 for a full list of all GO terms.

**Figure S6: Developmental food stress induces limited reduction in transcriptional divergence between the seasons, but only in the dry season environment.** In the abdomen **(a)**, dry season genes (brown; normally having high expression in dry season and low expression in wet season) show downregulation upon stress in the dry season (left panel), but not in wet season (right panel). Wet season genes (green; normally having high expression in wet season and low expression in dry season) show upregulation in dry season (left panel), but not in wet season (right panel). Thus, in the dry season (left) the plasticity programme shifts towards wet season-like expression upon stress, while in the wet season this effect is absent. In the thorax **(B)**, a similar pattern is observed for dry season genes, which are downregulated upon stress in the dry season, but not for wet season genes, which are not upregulated upon stress in the dry season. Dry season and wet season genes were defined as genes differentially expressed between the seasonal environments (FDR < 0.05, Fold Change > 2). P-values above each boxplot are for Wilcoxon signed rank tests of log2 Fold Change for each group of genes for the effect of food stress within each seasonal environment differing from zero.

**Supplementary Figure S7. Temperature as a reliable cue for seasonal progression in *B. anynana*’s natural habitat makes seasonal transitions highly predictable.**

Monthly-averaged precipitation **(a)** and log10 of monthly-averaged precipitation **(b)** are highly correlated with monthly-averaged minimum temperature in the previous month (ρpearson = + 0.85 and + 0.92) in Nkhata Bay in Malawi, where the laboratory population originates. Each dot represents a month, with shades from brown to green representing dry to wet season months. Climate data is for 1901-2009 [1](#_ENREF_1), downloaded 12 Oct 2016 via http://www.globalspecies.org/weather\_stations/climate/429/157.

***Supplementary tables***

**Supplementary table S1. Sequencing information for all 144 sequenced RNA-seq libraries** (72 individuals, abdomen and thorax was sequenced for each individual).

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Individual** | **Season** | **Food treatment** | **Family** | **Body part** | **Raw reads (x 106)** | **Trimmed reads (%)** | **Mapped reads (%)** |
| 1\_4 | dry | control | 21 | abdomen | 15.5 | 5 | 85 |
| 1\_4 | dry | control | 21 | thorax | 16.1 | 6 | 72 |
| 4\_4 | dry | control | 21 | abdomen | 15.7 | 6 | 84 |
| 4\_4 | dry | control | 21 | thorax | 15.2 | 7 | 84 |
| 2\_6 | dry | control | 29 | abdomen | 16.0 | 6 | 83 |
| 2\_6 | dry | control | 29 | thorax | 15.5 | 10 | 81 |
| 3\_5 | dry | control | 29 | abdomen | 15.1 | 5 | 82 |
| 3\_5 | dry | control | 29 | thorax | 15.7 | 6 | 76 |
| 5\_6 | dry | control | 29 | abdomen | 12.4 | 8 | 89 |
| 5\_6 | dry | control | 29 | thorax | 15.0 | 8 | 83 |
| 1\_8 | dry | control | 30 | abdomen | 15.3 | 4 | 83 |
| 1\_8 | dry | control | 30 | thorax | 15.8 | 7 | 78 |
| 4\_9 | dry | control | 30 | abdomen | 15.8 | 7 | 85 |
| 4\_9 | dry | control | 30 | thorax | 15.1 | 8 | 85 |
| 5\_10 | dry | control | 30 | abdomen | 15.7 | 8 | 83 |
| 5\_10 | dry | control | 30 | thorax | 16.0 | 7 | 78 |
| 2\_12 | dry | control | 37 | abdomen | 15.7 | 6 | 85 |
| 2\_12 | dry | control | 37 | thorax | 15.8 | 9 | 79 |
| 3\_13 | dry | control | 37 | abdomen | 15.4 | 5 | 86 |
| 3\_13 | dry | control | 37 | thorax | 15.7 | 6 | 64 |
| 5\_13 | dry | control | 37 | abdomen | 15.8 | 6 | 87 |
| 5\_13 | dry | control | 37 | thorax | 15.7 | 7 | 77 |
| 2\_16 | dry | control | 53 | abdomen | 15.8 | 6 | 90 |
| 2\_16 | dry | control | 53 | thorax | 16.2 | 8 | 74 |
| 3\_16 | dry | control | 53 | abdomen | 14.4 | 10 | 82 |
| 3\_16 | dry | control | 53 | thorax | 15.2 | 7 | 77 |
| 1\_19 | dry | control | 60 | abdomen | 15.1 | 5 | 90 |
| 1\_19 | dry | control | 60 | thorax | 16.0 | 10 | 80 |
| 2\_20 | dry | control | 60 | abdomen | 15.1 | 6 | 89 |
| 2\_20 | dry | control | 60 | thorax | 16.0 | 8 | 74 |
| 4\_21 | dry | control | 60 | abdomen | 14.2 | 14 | 90 |
| 4\_21 | dry | control | 60 | thorax | 15.9 | 7 | 77 |
| 1\_23 | dry | control | 63 | abdomen | 15.1 | 5 | 88 |
| 1\_23 | dry | control | 63 | thorax | 15.2 | 10 | 82 |
| 3\_22 | dry | control | 63 | abdomen | 15.6 | 8 | 88 |
| 3\_22 | dry | control | 63 | thorax | 16.2 | 7 | 71 |
| 2\_4 | dry | stress | 21 | abdomen | 15.0 | 5 | 84 |
| 2\_4 | dry | stress | 21 | thorax | 15.1 | 9 | 77 |
| 4\_5 | dry | stress | 21 | abdomen | 15.8 | 7 | 84 |
| 4\_5 | dry | stress | 21 | thorax | 16.1 | 7 | 81 |
| 1\_6 | dry | stress | 29 | abdomen | 16.0 | 6 | 84 |
| 1\_6 | dry | stress | 29 | thorax | 15.9 | 6 | 73 |
| 3\_6 | dry | stress | 29 | abdomen | 15.0 | 5 | 83 |
| 3\_6 | dry | stress | 29 | thorax | 15.8 | 7 | 78 |
| 5\_7 | dry | stress | 29 | abdomen | 12.6 | 8 | 94 |
| 5\_7 | dry | stress | 29 | thorax | 15.7 | 7 | 80 |
| 2\_10 | dry | stress | 30 | abdomen | 15.3 | 5 | 85 |
| 2\_10 | dry | stress | 30 | thorax | 15.3 | 9 | 78 |
| 3\_10 | dry | stress | 30 | abdomen | 15.9 | 8 | 78 |
| 3\_10 | dry | stress | 30 | thorax | 15.4 | 7 | 77 |
| 4\_10 | dry | stress | 30 | abdomen | 15.8 | 8 | 83 |
| 4\_10 | dry | stress | 30 | thorax | 15.6 | 7 | 77 |
| 1\_12 | dry | stress | 37 | abdomen | 16.2 | 4 | 82 |
| 1\_12 | dry | stress | 37 | thorax | 15.9 | 7 | 76 |
| 4\_12 | dry | stress | 37 | abdomen | 15.2 | 8 | 90 |
| 4\_12 | dry | stress | 37 | thorax | 15.5 | 7 | 80 |
| 5\_14 | dry | stress | 37 | abdomen | 15.0 | 7 | 85 |
| 5\_14 | dry | stress | 37 | thorax | 15.9 | 7 | 81 |
| 1\_15 | dry | stress | 53 | abdomen | 15.9 | 5 | 83 |
| 1\_15 | dry | stress | 53 | thorax | 15.0 | 7 | 75 |
| 5\_16 | dry | stress | 53 | abdomen | 16.1 | 5 | 82 |
| 5\_16 | dry | stress | 53 | thorax | 15.5 | 7 | 81 |
| 1\_20 | dry | stress | 60 | abdomen | 15.0 | 5 | 89 |
| 1\_20 | dry | stress | 60 | thorax | 15.8 | 10 | 80 |
| 3\_19 | dry | stress | 60 | abdomen | 14.2 | 8 | 87 |
| 3\_19 | dry | stress | 60 | thorax | 16.1 | 7 | 97 |
| 5\_21 | dry | stress | 60 | abdomen | 15.8 | 6 | 87 |
| 5\_21 | dry | stress | 60 | thorax | 15.8 | 8 | 74 |
| 2\_23 | dry | stress | 63 | abdomen | 15.8 | 6 | 86 |
| 2\_23 | dry | stress | 63 | thorax | 15.8 | 7 | 76 |
| 3\_23 | dry | stress | 63 | abdomen | 15.7 | 8 | 85 |
| 3\_23 | dry | stress | 63 | thorax | 15.9 | 7 | 77 |
| 3\_4 | wet | control | 21 | abdomen | 16.2 | 6 | 86 |
| 3\_4 | wet | control | 21 | thorax | 15.6 | 6 | 75 |
| 5\_4 | wet | control | 21 | abdomen | 15.0 | 8 | 87 |
| 5\_4 | wet | control | 21 | thorax | 15.6 | 7 | 80 |
| 2\_7 | wet | control | 29 | abdomen | 16.1 | 5 | 89 |
| 2\_7 | wet | control | 29 | thorax | 16.6 | 8 | 77 |
| 3\_7 | wet | control | 29 | abdomen | 15.8 | 5 | 83 |
| 3\_7 | wet | control | 29 | thorax | 15.0 | 7 | 84 |
| 5\_8 | wet | control | 29 | abdomen | 14.2 | 11 | 93 |
| 5\_8 | wet | control | 29 | thorax | 15.4 | 7 | 80 |
| 1\_9 | wet | control | 30 | abdomen | 15.9 | 4 | 87 |
| 1\_9 | wet | control | 30 | thorax | 15.1 | 7 | 80 |
| 2\_11 | wet | control | 30 | abdomen | 15.2 | 5 | 93 |
| 2\_11 | wet | control | 30 | thorax | 15.9 | 8 | 83 |
| 3\_11 | wet | control | 30 | abdomen | 15.0 | 5 | 89 |
| 3\_11 | wet | control | 30 | thorax | 16.2 | 7 | 76 |
| 2\_14 | wet | control | 37 | abdomen | 15.2 | 5 | 93 |
| 2\_14 | wet | control | 37 | thorax | 15.7 | 9 | 83 |
| 3\_14 | wet | control | 37 | abdomen | 14.7 | 8 | 87 |
| 3\_14 | wet | control | 37 | thorax | 15.3 | 7 | 79 |
| 5\_15 | wet | control | 37 | abdomen | 15.9 | 7 | 90 |
| 5\_15 | wet | control | 37 | thorax | 15.4 | 7 | 79 |
| 4\_17 | wet | control | 53 | abdomen | 14.6 | 8 | 93 |
| 4\_17 | wet | control | 53 | thorax | 15.8 | 7 | 80 |
| 5\_17 | wet | control | 53 | abdomen | 15.7 | 8 | 92 |
| 5\_17 | wet | control | 53 | thorax | 15.7 | 8 | 81 |
| 1\_21 | wet | control | 60 | abdomen | 15.3 | 5 | 90 |
| 1\_21 | wet | control | 60 | thorax | 15.6 | 10 | 84 |
| 2\_21 | wet | control | 60 | abdomen | 15.8 | 6 | 92 |
| 2\_21 | wet | control | 60 | thorax | 15.5 | 7 | 72 |
| 3\_20 | wet | control | 60 | abdomen | 15.2 | 8 | 91 |
| 3\_20 | wet | control | 60 | thorax | 15.6 | 7 | 86 |
| 1\_24 | wet | control | 63 | abdomen | 15.9 | 5 | 90 |
| 1\_24 | wet | control | 63 | thorax | 15.6 | 9 | 82 |
| 3\_24 | wet | control | 63 | abdomen | 15.4 | 8 | 91 |
| 3\_24 | wet | control | 63 | thorax | 15.5 | 7 | 83 |
| 4\_6 | wet | stress | 21 | abdomen | 15.3 | 7 | 89 |
| 4\_6 | wet | stress | 21 | thorax | 15.0 | 7 | 87 |
| 5\_5 | wet | stress | 21 | abdomen | 14.5 | 8 | 92 |
| 5\_5 | wet | stress | 21 | thorax | 15.1 | 7 | 86 |
| 1\_7 | wet | stress | 29 | abdomen | 16.0 | 4 | 87 |
| 1\_7 | wet | stress | 29 | thorax | 15.6 | 5 | 72 |
| 3\_8 | wet | stress | 29 | abdomen | 15.1 | 5 | 86 |
| 3\_8 | wet | stress | 29 | thorax | 15.8 | 7 | 82 |
| 5\_9 | wet | stress | 29 | abdomen | 15.0 | 7 | 89 |
| 5\_9 | wet | stress | 29 | thorax | 15.2 | 7 | 81 |
| 3\_12 | wet | stress | 30 | abdomen | 15.0 | 5 | 84 |
| 3\_12 | wet | stress | 30 | thorax | 16.0 | 7 | 77 |
| 4\_11 | wet | stress | 30 | abdomen | 13.8 | 13 | 89 |
| 4\_11 | wet | stress | 30 | thorax | 15.5 | 8 | 79 |
| 5\_12 | wet | stress | 30 | abdomen | 15.9 | 8 | 85 |
| 5\_12 | wet | stress | 30 | thorax | 15.0 | 7 | 82 |
| 1\_14 | wet | stress | 37 | abdomen | 15.0 | 4 | 88 |
| 1\_14 | wet | stress | 37 | thorax | 15.3 | 7 | 81 |
| 3\_15 | wet | stress | 37 | abdomen | 15.7 | 7 | 85 |
| 3\_15 | wet | stress | 37 | thorax | 15.0 | 7 | 77 |
| 4\_14 | wet | stress | 37 | abdomen | 14.6 | 7 | 93 |
| 4\_14 | wet | stress | 37 | thorax | 15.0 | 7 | 83 |
| 1\_16 | wet | stress | 53 | abdomen | 15.5 | 4 | 88 |
| 1\_16 | wet | stress | 53 | thorax | 15.7 | 7 | 77 |
| 3\_17 | wet | stress | 53 | abdomen | 14.3 | 8 | 90 |
| 3\_17 | wet | stress | 53 | thorax | 15.9 | 7 | 80 |
| 1\_22 | wet | stress | 60 | abdomen | 15.1 | 6 | 92 |
| 1\_22 | wet | stress | 60 | thorax | 16.0 | 10 | 84 |
| 2\_22 | wet | stress | 60 | abdomen | 16.1 | 5 | 89 |
| 2\_22 | wet | stress | 60 | thorax | 16.0 | 8 | 73 |
| 5\_22 | wet | stress | 60 | abdomen | 15.6 | 5 | 80 |
| 5\_22 | wet | stress | 60 | thorax | 16.6 | 8 | 75 |
| 2\_24 | wet | stress | 63 | abdomen | 15.0 | 5 | 91 |
| 2\_24 | wet | stress | 63 | thorax | 15.1 | 7 | 79 |
| 4\_24 | wet | stress | 63 | abdomen | 14.0 | 15 | 98 |
| 4\_24 | wet | stress | 63 | thorax | 16.2 | 7 | 82 |

**Supplementary Table S2.** Summary of contrasts used in edgeR general linear models. Analyses for abdomen and thorax were performed separately.

|  |  |  |  |
| --- | --- | --- | --- |
| **Factor** | **Number of  groups compared** | **Number of  orthogonal contrasts** | **Number of  individuals per group** |
| Seasonal environment | 2 (wet vs. dry) | 1 | 36 |
| Food treatment | 2 (control vs. stress) | 1 | 36 |
| Family | 7 (families 1 through 7) | 6 | 8 or 12 |
| Season by family | 14 | 6 | 4 or 6 |
| Food by family | 14 | 6 | 4 or 6 |
| Season by food | 4 | 1 | 18 |
| Season by food by family | 28 | 6 | 2 or 3 |

**Supplementary Table S3.** Gene Set Enrichment analyses for the systemic, abdomen-specific and thorax-specific plasticity programme, as well as discordant genes showing opposite patterns of season bias between the two body parts. See Supplementary Figure S5 for a visualisation and grouping of these terms. Supplementary Table S3 is available at Figshare (doi: 10.6084/m9.figshare.4834031).

**Table S4.** Twenty genes showing a significant effect (FDR < 0.05) of the interaction between seasonal environment and family (i.e. genotype-by-environment interaction) in both thorax and abdomen. An additional 140 and 126 genes showed such an effect in either abdomen or thorax only but not in both tissues.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **gene** | **Uniref90 protein name** | **mean Fold Change (2log)** | **p value in abdomen \*)** | **p value in thorax \*)** |
| evgtrinc226369\_g1\_i2 | Putative WD repeat domain 66 | 0.47 | 0.00001 | 0.00001 |
| evgtrinc263124\_g1\_i1 | Uncharacterized protein | 0.44 | 0.00320 | 0.00612 |
| evgtrinc209424\_g1\_i1 | NA | 0.41 | 0.00601 | 0.02510 |
| evgtrinc284430\_g1\_i1 | Polyprotein | 0.38 | 0.00123 | 0.00028 |
| evgtrinc286162\_g2\_i1 | NA | 0.35 | 0.00137 | 0.00206 |
| evgtrinc281265\_g2\_i1 | NA | 0.33 | 0.03629 | < 0.00001 |
| evgtrinc283752\_g1\_i1 | NA | 0.30 | 0.03521 | 0.03990 |
| evgtrinc282076\_g2\_i1 | NA | 0.29 | 0.02454 | 0.00335 |
| evgtrinc287665\_g3\_i3 | Uncharacterized protein | 0.26 | 0.02642 | 0.00052 |
| evgtrinc286241\_g2\_i2 | Putative tick transposon | 0.24 | 0.00804 | 0.01685 |
| evgtrinc287665\_g3\_i6 | Uncharacterized protein | 0.23 | 0.03807 | 0.00068 |
| evgtrinc287644\_g1\_i4 | SMC domain protein | 0.22 | 0.00001 | 0.00148 |
| evgtrinc346736\_g1\_i1 | Uncharacterized protein | 0.19 | 0.02494 | 0.03207 |
| evgtrinc288929\_g1\_i1 | NA | 0.15 | 0.00106 | 0.00969 |
| evgtrinc285360\_g1\_i10 | Uncharacterized protein | 0.14 | 0.03990 | 0.03374 |
| evgtrinc118669\_g1\_i1 | Retrotransposable element | 0.11 | 0.00002 | 0.00166 |
| evgtrinc285478\_g1\_i2 | NA | 0.10 | 0.00644 | 0.00001 |
| evgtrinc282066\_g1\_i1 | Carboxylic ester hydrolase | 0.09 | 0.00577 | 0.03535 |
| evgtrinc277738\_g2\_i8 | NA | 0.09 | 0.02416 | 0.03592 |
| evgtrinc288093\_g2\_i1 | Uncharacterized protein | 0.06 | 0.00110 | 0.00391 |

**Supplementary Table S5.** Genes significantly affected by food stress, analysed separately for each tissue for each seasonal environment.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **gene** | **stress effect** | **season** | **body part** | **Fold Change (2log)** | **p value \*)** | **Uniref90 protein name** |
| evgtrinc269331\_g1\_i4 | up | dry | abdomen | 2.6 | 0.04936 | Trypsin AiT9 |
| evgtrinc273562\_g2\_i1 | up | dry | abdomen | 1.5 | 0.04936 | Beta-fructofuranosidase 2 |
| evgtrinc281022\_g4\_i1 | up | dry | abdomen | 1.1 | 0.00898 | Sugar transporter 12 |
| evgtrinc279897\_g1\_i2 | up | dry | both | 2.3 | 0.01768 | NA |
| evgtrinc288360\_g3\_i1 | up | dry | thorax | 2.0 | 0.03438 | NA |
| evgtrinc287818\_g3\_i2 | up | dry | thorax | 1.9 | 0.03438 | NA |
| evgtrinc289482\_g5\_i1 | up | wet | abdomen | 4.0 | 0.00084 | NA |
| evgtrinc290184\_g2\_i2 | up | wet | abdomen | 2.4 | 0.01513 | Uncharacterized protein |
| evgtrinc284646\_g1\_i3 | up | wet | abdomen | 2.4 | 0.03299 | NA |
| evgtrinc286859\_g1\_i4 | up | wet | abdomen | 2.4 | 0.03800 | p260 |
| evgtrinc244065\_g1\_i1 | up | wet | abdomen | 1.9 | 0.02135 | NA |
| evgtrinc286931\_g1\_i3 | up | wet | abdomen | 0.7 | 0.03299 | Putative reverse transcriptase |
| evgtrinc278939\_g1\_i1 | up | wet | abdomen | 0.5 | 0.01954 | Putative uncharacterized protein |
| evgtrinc283258\_g1\_i1 | down | both | abdomen | 1.8 | 0.00003 | Uncharacterized protein |
| evgtrinc212398\_g1\_i1 | down | both | abdomen | 1.3 | 0.00006 | Bombyrin |
| evgtrinc288751\_g1\_i1 | down | dry | thorax | 1.1 | 0.03438 | Putative monocarboxylate transporter |
| evgtrinc401477\_g1\_i1 | down | wet | abdomen | 1.9 | 0.02518 | NA |
| evgtrinc274166\_g1\_i1 | down | wet | abdomen | 1.7 | < 0.00001 | Uncharacterized protein |
| evgtrinc286831\_g2\_i1 | down | wet | abdomen | 1.4 | < 0.00001 | Moderately methionine rich storage protein |
| evgtrinc281179\_g1\_i1 | down | wet | abdomen | 1.3 | 0.00010 | Methionine-rich storage protein |
| evgtrinc286831\_g3\_i2 | down | wet | abdomen | 1.2 | 0.00029 | Moderately methionine rich storage protein |
| evgtrinc287884\_g3\_i1 | down | wet | abdomen | 0.9 | 0.00322 | Arylphorin-type storage protein |

\* Corrected for multiple testing using Benjamini and Hochberg’s multiple comparisons correction (false discovery rate).

**Literature cited**

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