



**Supplementary Figure 5:** Boxplots showing the spatial distribution of MSP1 (Z9-14:OH) and fold change expression of candidate genes  $\Delta$ 9- and  $\Delta$ 11-desaturase across the *B. anynana* body. A) Amount of MSP1 (in ng/individual) with, from left to right, male wings, female wings and male heads. Data modified after Heuskin et al. (2014 Front Ecol Evol: Table S1). B, C) RT-qPCR of  $\Delta$ 9- and  $\Delta$ 11-desaturase genes with, from left to right, male androconial wing tissues, male control wing tissues, female wings and male heads. The  $\Delta$ 9-desaturase gene showed overall significant variation in transcript abundance across tissues that correlated with the distribution pattern of MSP1 (nested ANOVA,  $n = 24$  samples with 3 biological replicates and 2 technical replicates;  $F_{3,6} = 883.5$ ;  $p$ -value  $< 0.01$ ). Specifically,  $\Delta$ 9-desaturase was found to be significantly expressed in male wing parts containing the androconia that produce MSP1, compared to remaining male wing tissues (nested ANOVA;  $F_{1,4} = 1,814.0$ ;  $p$ -value  $< 0.01$ ) and female wings (nested ANOVA;  $F_{1,4} = 50.5$ ;  $p$ -value  $< 0.01$ ). Moreover,  $\Delta$ 9-desaturase gene expression was also found to be significantly expressed in male head tissue containing MSP1. No such match between gene expression and MSP1 abundance was found for the  $\Delta$ 11-desaturase gene, which showed no significant variation in transcript abundance across tissues known to contain MSP1 (nested ANOVA,  $F_{3,6} = 0.07$ ;  $p$ -value  $< 0.01$ ).