**Tab. S6:** Orthologous CHC biosynthesis candidate genes in the *Nasonia* species complex as well as two representative species from the two most closely related genera, *Trichomalopsis sarcophagae* and *Muscidifurax raptorellus* (see Fig. S1 for phylogeny). Genes with identified orthologs in all analyzed species were subjected to a dN/dS ratio analysis to screen for signatures of positive selection. Indicated are gene annotations and gene IDs obtained from the *N. vitripennis* reference genome, species IDs where no orthologous gene could be unambiguously identified, and Benjamini-Hochberg-corrected p-values from the BUSTED analysis for signatures of positive selection. Species abbreviations: MR: *M. raptorellus*, TS: *T. sarcophagae*, NG: *N. giraulti*, NO: *N. oneida*, NL: *N. longicornis*.

|  |  |  |  |
| --- | --- | --- | --- |
| Nv gene annotation | Nv gene ID | Positive selection (BUSTED, *p*-value) | Species with no identifiable ortholog |
| *acc* | 100123347 | 0.081 |  |
| *app* | 100121627 | 0.5 |  |
| *CG14688* | 100120956 |  | MR |
| *CG16979* | 100119053 | 0.283 |  |
| *CG5599* | 100122501 | 0.073 |  |
| *CG7724* | 100120136 | 0.5 |  |
| *Ndufs6* | 100119717 | 0.5 |  |
| *cyp4g44* | 100113546 | 0.5 |  |
| *desi* | 100115157 | 0.5 |  |
| ***fas1*** | **100121447** | **0.013** |  |
| *fas2* | 100122099 |  | MR |
| *fas3* | 100122083 | 0.5 |  |
| *fas4* | 100119597 |  | MR |
| *fas5* | 100678737 |  | TS, MR |
| *fatp1* | 100120211 |  | NG, MR |
| *hacd1* | 100119292 | 0.5 |  |
| *hacd2* | 100115280 |  | NO, NG, NL, TS, MR |
| *nrt* | 100121165 |  | NG, MR |
| *phgpx\_1* | 100677983 | 0.5 |  |
| *phgpx\_2* | 100114603 | 0.5 |  |
| *phgpx\_3* | 100123141 | 0.5 |  |
| *prx6005* | 100117827 | 0.363 |  |
| *pxd* | 100119885 | 0.5 |  |
| *pxn* | 100116337 | 0.071 |  |
| *sc2* | 107980451 | 0.363 |  |
| *spidey* | 100121752 | 0.5 |  |