**Tab. S4**: Candidate genes for CHC biosynthesis and variation in *Nasonia vitripennis* based on orthology towards *Drosophila melanogaster,* where the impact on CHC profiles of the respective genes has been demonstrated through targeted knockdown studies. Indicated are the gene annotations, gene IDs obtained from RefSeq, descriptions of the gene function obtained from NCBI, linkage map positions (centimorgan (cM) on the respective chromosome (c)), recombination rates (Mb/cM), and evidence of orthology based on the three methods reciprocal blast search (RB), OrthoFinder (OF) and WaspAtlas (WA). Genes for which exactly one ortholog could be unambiguously identified are indicated with a ‘+’, in other cases the method(s) that have generated the most consistently reliable results in each case are shown. Genes that can clearly be assigned to a particular step in CHC biosynthesis (compare to Fig. 1) are indicated in bold.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Gene annotation |  RefSeq ID | Description NCBI | Linkage map position  | Recomb. rate (Mb/cM) | Evidence oforthology |
| ***acc*** | **100123347** | acetyl-CoA carboxylase | c1: 75.9 cM | 0.1114 | + |
| *app* | 100121627 | palmitoyltransferase ZDHHC18 | c2: 38 cM | 13.3806 | + |
| *CG14688* | 100120956 | phytanoyl-CoA dioxygenase | c1: 48.2 cM | 20.6198 | + |
| *CG16979* | 100119053 | ufm1-specific protease 2-like | c3: 64.2 cM | 0.1015 | + |
| *CG5599* | 100122501 | lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial | c4: 6.6 cM | 0.2967 | + |
| *CG7724* | 100120136 | 3 beta-hydroxysteroid dehydrogenase/Delta5-->4-isomerase type 4 | c2: 1.5 cM | 0.5931 | + |
| *Ndufs6* | 100119717 | NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase) | c2: 43.8 cM | 1.1653 | + |
| ***cyp4g44*** | **100113546** | cytochrome P450 4G44 | c1: 47.5 cM | 2.6119 | WA |
| *desi* | 100115157 | uncharacterized LOC100115157 | c4: 35.8 cM | 0.1267 | + |
| ***fas1*** | **100121447** | fatty acid synthase | c1: 60.6 cM | 0.3184 | OF |
| ***fas2*** | **100122099** | fatty acid synthase-like | c3: 5.8 cM | 0.556 | OF |
| ***fas3*** | **100122083** | fatty acid synthase-like | c3: 5.8 cM | 0.556 | OF |
| ***fas4*** | **100119597** | fatty acid synthase-like | c1: 49.6 cM | 20.78 | OF |
| ***fas5*** | **100678737** | fatty acid synthase-like | c5: 45.3 cM | 0.7646 | OF |
| ***fatp1*** | **100120211** | long-chain fatty acid transport protein 4- like | c2: 20.4 cM | 0.8866 | RB |
| ***hacd1*** | **100119292** | very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase hpo-8 | c4: 50.4 cM | 4.7456 | + |
| ***hacd2*** | **100115280** | very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase | c3: 38 cM | 11.8001 | + |
| *nrt* | 100121165 | neurotactin | c3: 73 cM | 0.1823 | + |
| *phgpx\_1* | 100677983 | probable phospholipid hydroperoxide glutathione peroxidase | c3: 38 cM | 11.8001 |  RB,WA |
| *phgpx\_2* | 100114603 | probable phospholipid hydroperoxide glutathione peroxidase | c4: 4.4 cM |  0.2203 |  RB,WA |
| *phgpx\_3* | 100123141 | phospholipid hydroperoxide glutathione peroxidase, mitochondrial-like | c4: 4.4 cM |  0.2203 |  RB,WA |
| *prx6005* | 100117827 | peroxiredoxin-6 | c2: 38 cM |  13.3806 | + |
| *pxd* | 100119885 | peroxidase | c3: 68.6 cM |  0.3195 |  OF,WA |
| *pxn* | 100116337 | peroxidasin | c1: 93.4 cM | 0.1259 | + |
| ***sc2*** | **107980451** | very-long-chain enoyl-CoA reductase | c4: 32.1 cM |  0.1186 | + |
| ***spidey*** | **100121752** | very-long-chain 3-oxoacyl-CoA reductase | c2: 52.6 cM |  0.3081 | + |