

Supplementary information

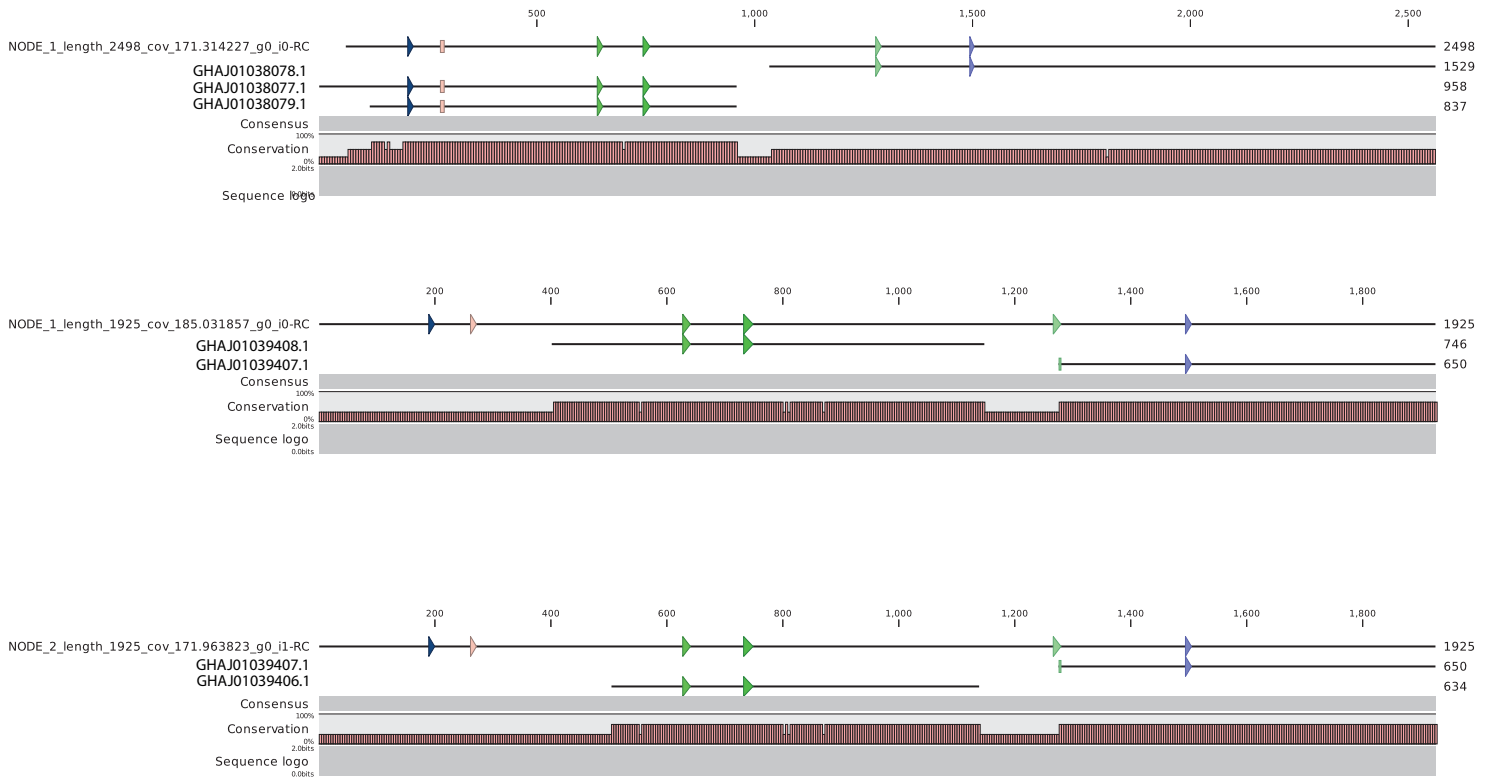






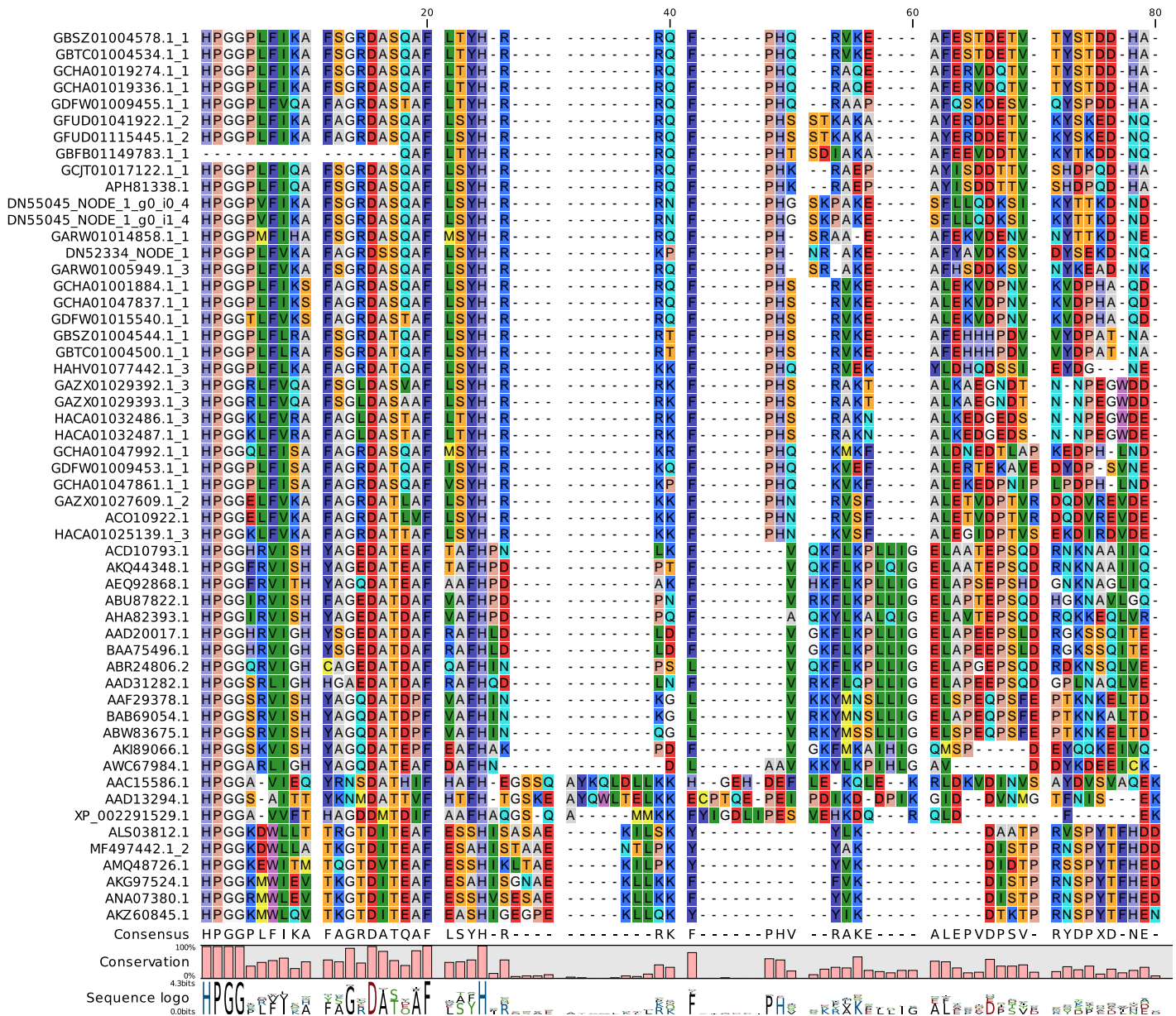


Figure S1. Aligning the nucleotide sequence of fragmented transcripts to complete genes.

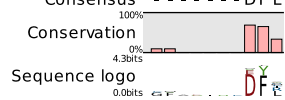
The three complete genes identified as putative front end desaturases were aligned to the initially identified fragmented genes from the GHAJ01 TSA assembly in CLCgenomics. For each complete gene, certain motifs were covered by the fragmented transcripts, but crucially, no fragment-ed gene covered all important front end desaturase motif. Notice that the fragmented isoforms and the complete genes do not share 100% sequence identity, likely because the assembly program faced with short reads with several SNPs had to chose a path through the variation. since Trinity was used for the initial assembly and SPAdes for the complete gene assemble, the results are not identical.

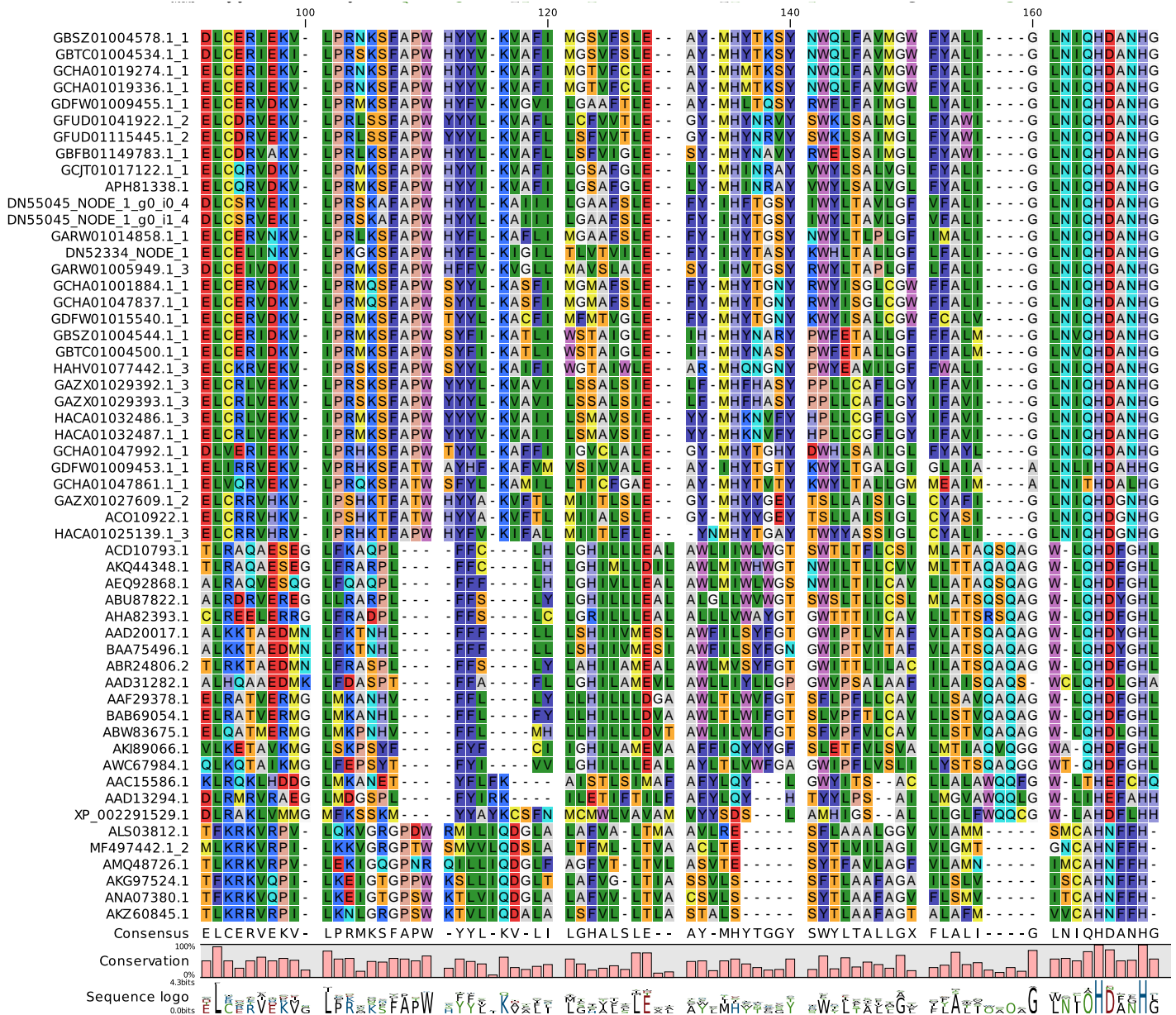
Annotation

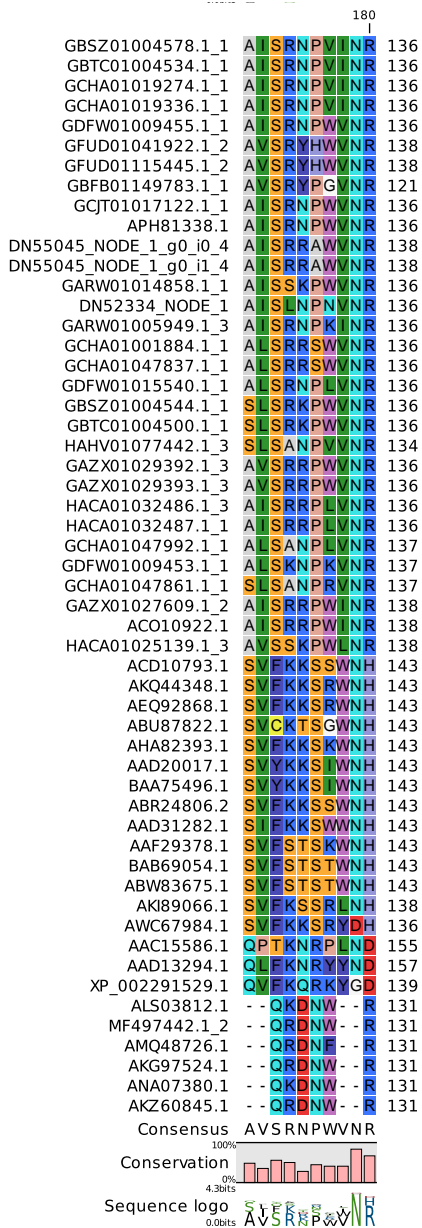
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-  Hisbox1 HDANH
-  Hisbox2 HVVQHH
-  Hisbox3 QIEHH
-  Stop codon site

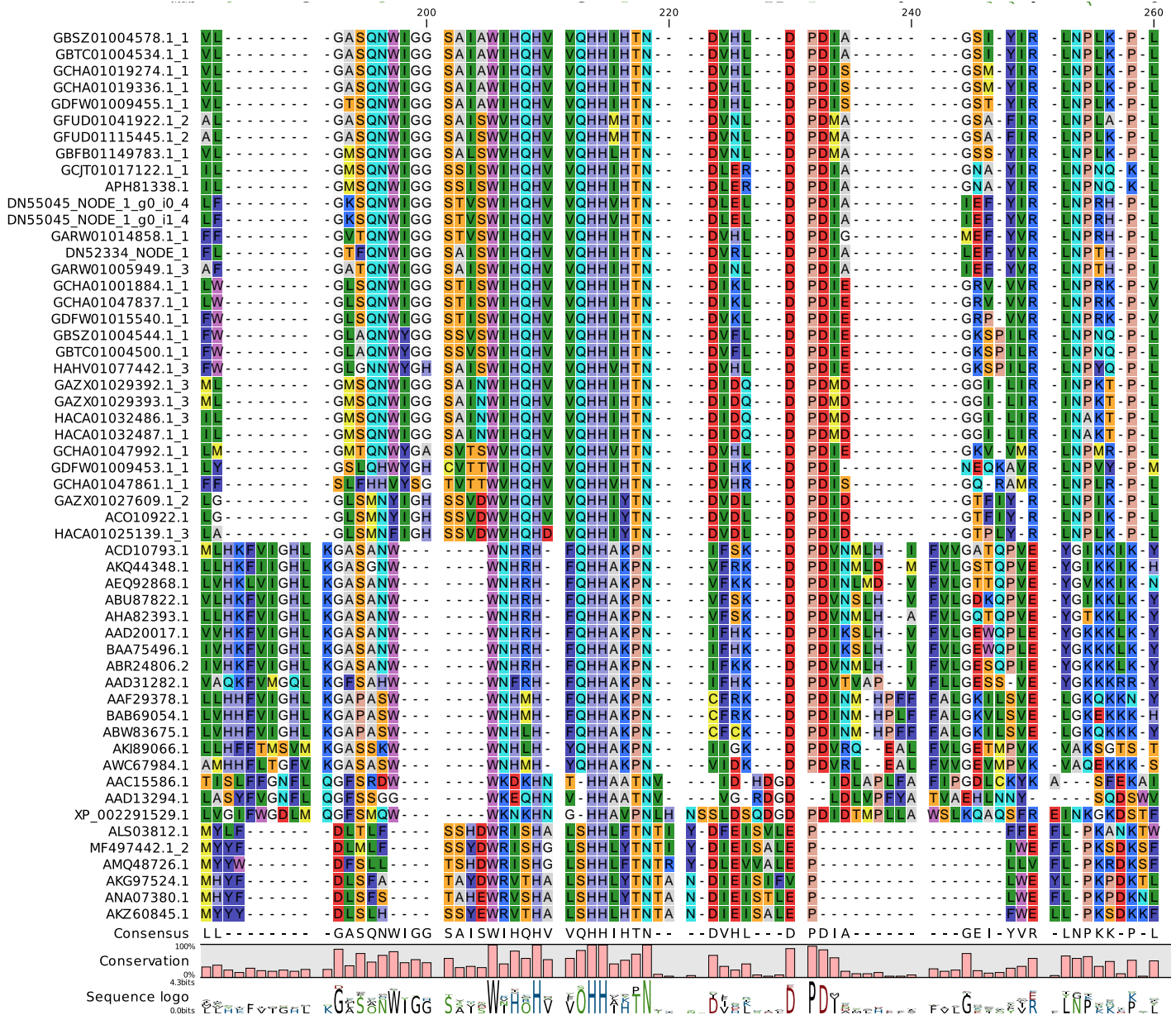


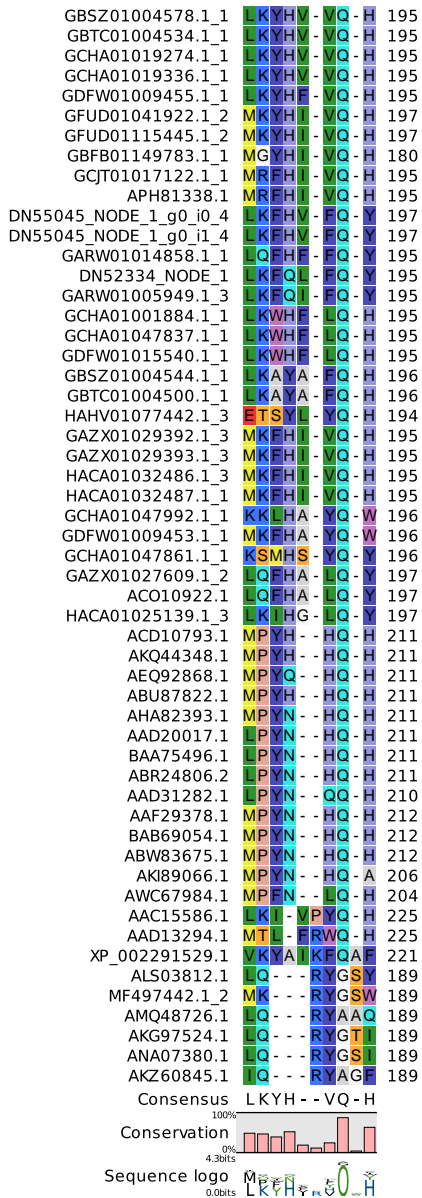
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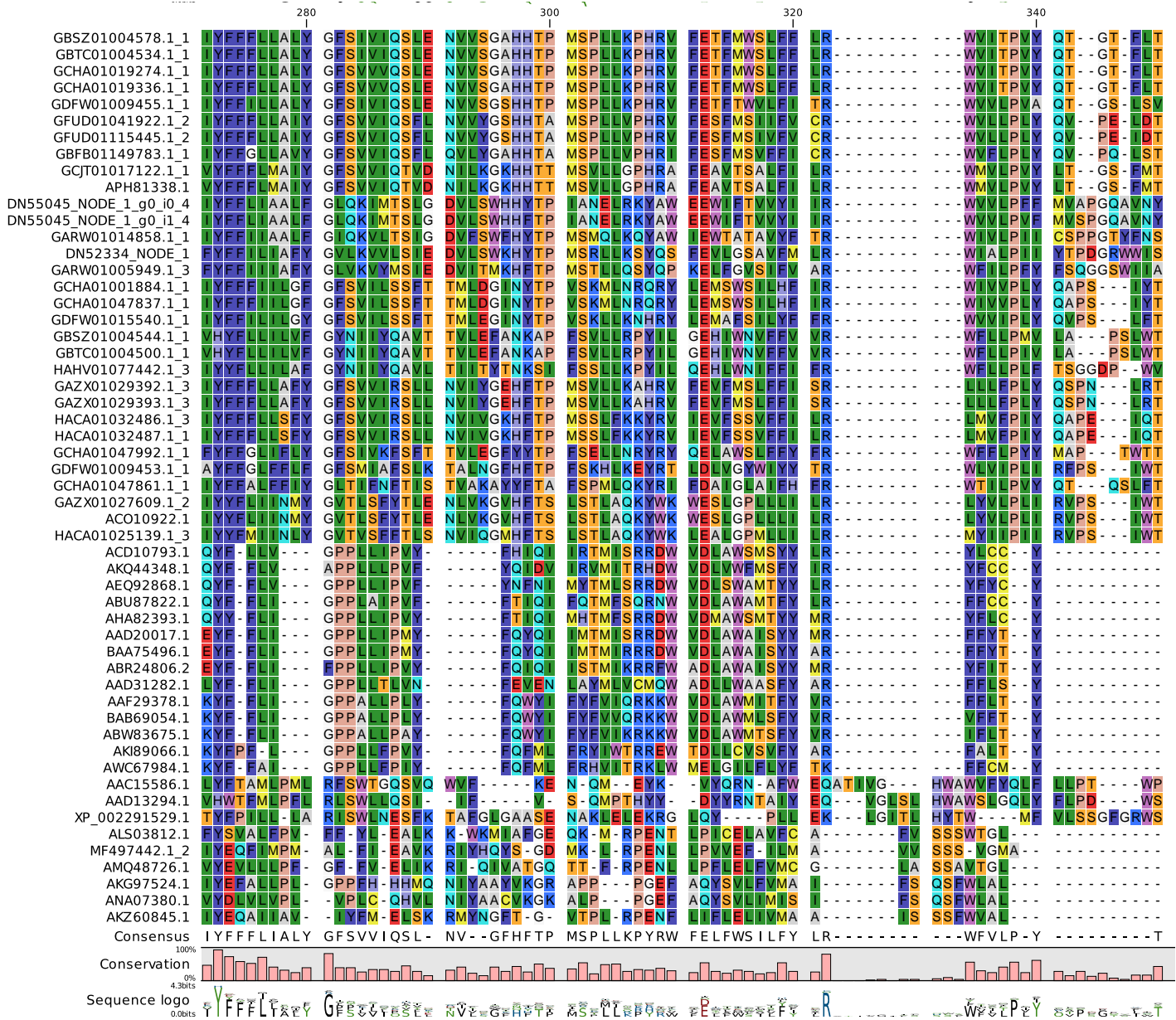


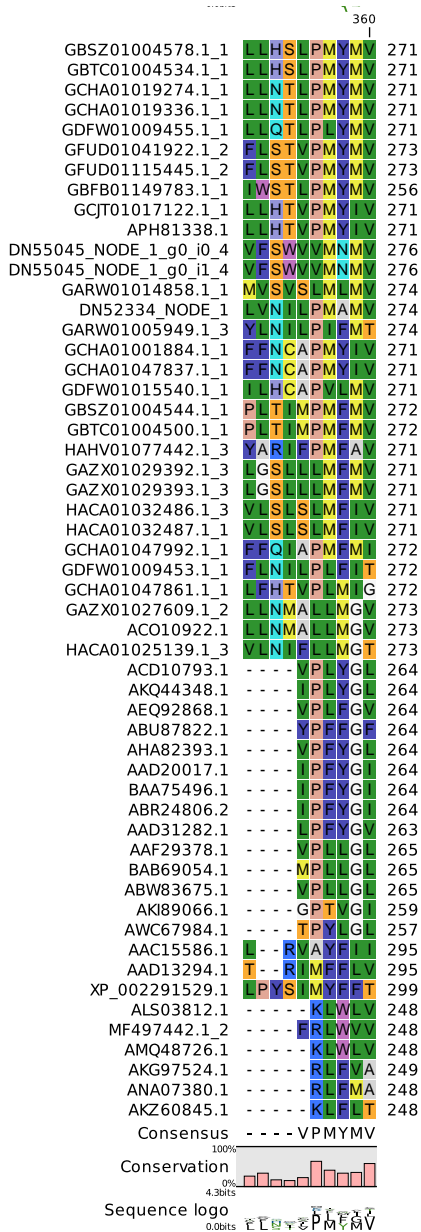


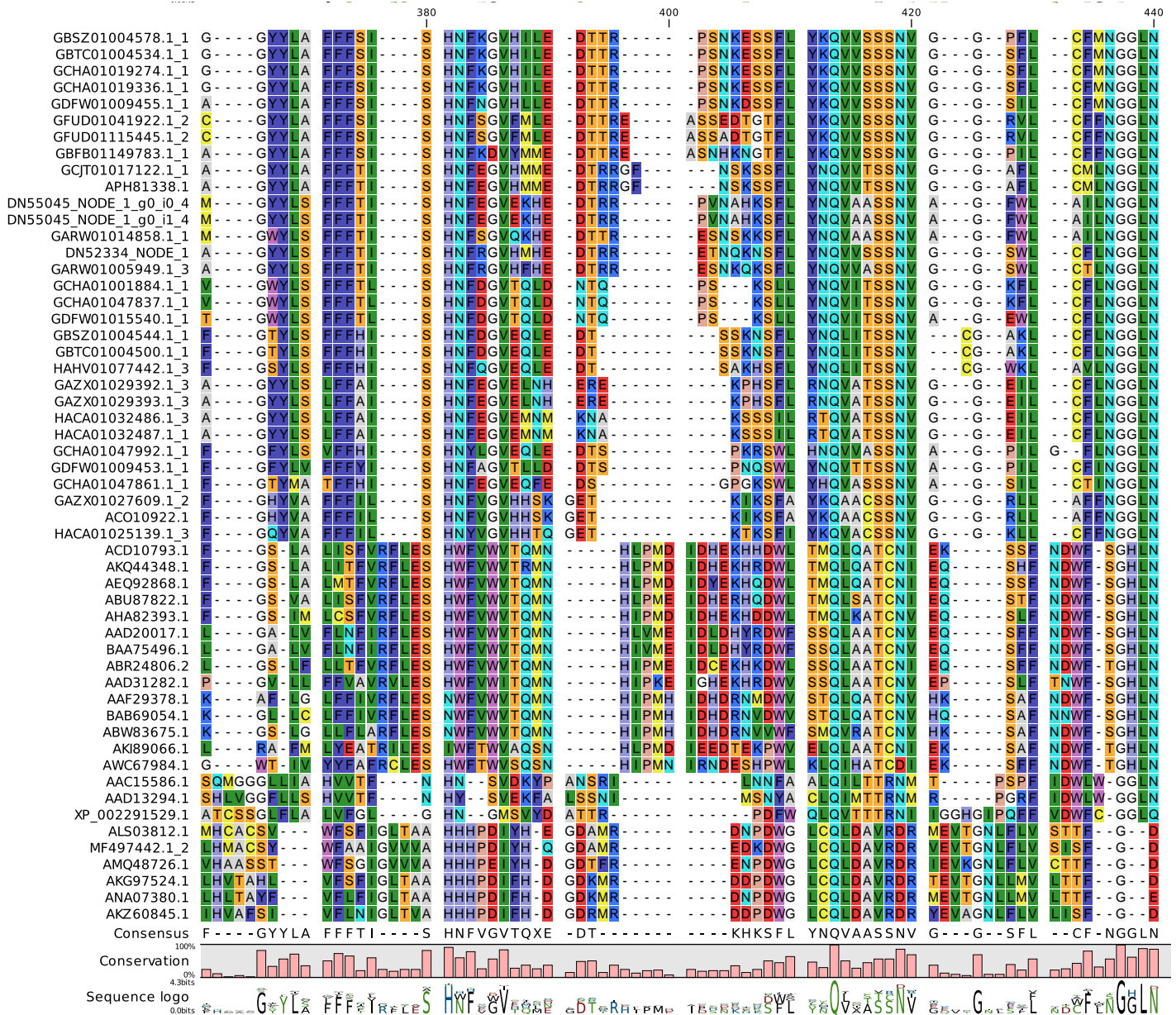












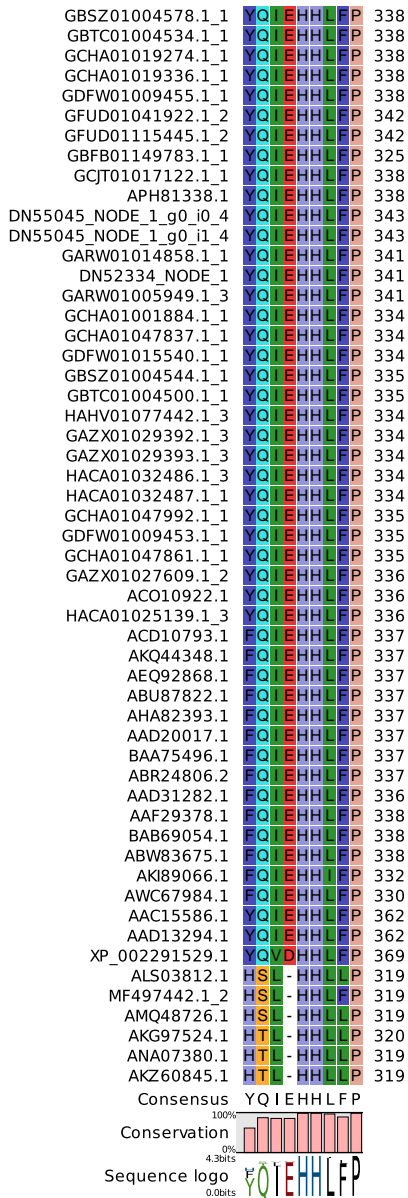


Figure S2. txt overview of identified copepod desaturase genes including AA sequence.

Table S1. Fasta nt sequence of differently expressed desaturase genes.

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Table S2. Datasets used for FA desaturase and elongase identification.

Accession number	Data type	Species
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GFWY01	TSA	<i>Acartia tonsa</i>
HAGX01	TSA	<i>Acartia tonsa</i>
GAXK01	TSA	<i>Calanus finmarchicus</i>
GBFB01	TSA	<i>Calanus finmarchicus</i>
GBXU01	TSA	<i>Calanus finmarchicus</i>
GBXT01	TSA	<i>Calanus glacialis</i>
HACJ01	TSA	<i>Calanus glacialis</i>
GAZX01	TSA	<i>Caligus rogercresseyi</i>
GFUA01	TSA	<i>Epischura baikalensis</i>
GARW01	TSA	<i>Eucyclops serrulatus</i>
GBGO01	TSA	<i>Eurytemora affinis</i>
GEAN01	TSA	<i>Eurytemora affinis</i>
GFWO01	TSA	<i>Labidocera madurae</i>
HACA01	TSA	<i>Lepeophtheirus salmonis</i>
GFUD01	TSA	<i>Neocalanus flemingeri</i>
GCJT01	TSA	<i>Paracyclops nana</i>
GFCI01	TSA	<i>Pleuromamma xiphias</i>
GBSZ01	TSA	<i>Tigriopus californicus</i>
GBTC01	TSA	<i>Tigriopus californicus</i>
GCHA01	TSA	<i>Tigriopus japonicus</i>
GDFW01	TSA	<i>Tigriopus sp.</i>
HAHV01	TSA	<i>Tisbe holothuriae</i>

Table S3. CLC alignment of all identified sequences with database versions.

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>GBFB01149783.1_Calanus_finmarchicus_comp270289_c0_seq6_1_reverse
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>GBSZ01004544.1_Tigriopus_californicus_SD_As4_Contig22385_1_forward
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SVLLRPYILGEHIWNVFFVVRWFLLPMLVAPSLWPTLTPMFMVFGTYLSFFFHISHNFDGVEQLEDTSSKNSFLYNQLITSSN
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>GBSZ01004578.1_Tigriopus_californicus_SD_As4_Contig8388_1_forward
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>GBTC01004500.1_Tigriopus_californicus_SCN_Contig_30034_1_forward
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SVLLRPYILGEHIWNVFFVVRWFLLPIVLAPSLWPTLTPMFMVFGTYLSFFFHISHNFDGVEQLEDTSSKNSFLYNQLITSSNVC
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>GBTC01004534.1_Tigriopus_californicus_SCN_Contig_11004_1_forward
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PVYQTGTFTLLHSLPMYVGGYYLAFFFSISHNFKGVHILEDTRPSNKESFLYKQVSSSNVGGPFLCFMNGGLNYQIEHHLF
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>GCHA01001884.1_Tigriopus_japonicus_TJ_CDS_01884_1_forward

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>GCHA01019274.1_Tigriopus_japonicus_TJ_CDS_19276_1_forward

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>GCHA01019336.1_Tigriopus_japonicus_TJ_CDS_19338_1_forward

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>GCHA01047837.1_Tigriopus_japonicus_TJ_CDS_47840_1_forward

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>GCHA01047861.1_Tigriopus_japonicus_TJ_CDS_47864_1_forward

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>GCHA01047992.1_Tigriopus_japonicus_TJ_CDS_47995_1_forward

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>GCJT01017122.1_Paracyclopsina_nana_Pnana_mRNA_18686_1_forward

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TMSVLLGPHRAFEAVTSALFILRWMVLPVYLTGSFMTLLHTVPMYIVAGYLAFFFTISHNFEGVHMMEDTRRGFNKSSFLYN
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>GDFW01009453.1_Tigriopus_sp._1_SL-2012_Tk_CDS_08242-1_1_forward

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>GDFW01009455.1_Tigriopus_sp._1_SL-2012_Tk_CDS_08243-1_1_forward

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AH*

>GDFW01015540.1_Tigriopus_sp._1_SL-2012_Tk_CDS_13549-1_1_forward

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DGV TQLD
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>GFUD01041922.1_Neocalanus_flemingeri_Contig41928_2_forward

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>GFUD01115445.1_Neocalanus_flemingeri_W4a28933:c0_g1_i2_2_forward

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AGYYLSFFFTISHNFRGVHMHEDTRRETnQNSFLYNQVSSSNVGGSWLcFLNGGLNYQIEHHLFPRINHTHYPTIAPHVKKF
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*EDSLEFSKILLRETKSEIFNYF*STSIS*LLNRIEGY*LKWQVLRs*LQFSF*N*FLLCLISTYI*CSNPMQCKTIKCFYCVFIRVLGI
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>NA_Apocyclops_royi_NODE_2_length_1925_cov_171.963823_g0_i1_complete_gene_1_reverse

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