Supplementary file S2

***Figure 1*.** Multiple sequence alignment of C6orf118 and orthologs. Conservation is indicated under the alignment. The Translin-associated factor X-interacting protein 1, N-terminal (IPR032755) domain is indicated with a red square, the coiled coil domains with green squares. The UniProt accession numbers of the sequences are as follows: *Alligator sinensis* A0A1U7RSV3*, Anas platyrhynchos* U3IR65*, Anolis carolinensis* H9G790*, Branchiostoma floridae* C3ZMD8*, Capitella teleta* R7VLG1*, Ciona intestinalis* F6QS01*, Homo sapiens* Q5T5N4*, Lottia gigantea* V4AD75*, Mus musculus* Q3TTN6*, Pelodiscus sinensis* K7FK90*, Salmo salar* A0A1S3NDW9*, Strongylocentrotus purpuratus* W4YG44*, Xenopus laevis* A0A1L8G278*, Xenopus tropicalis* Q0V9C4.

Figure 2. Multiple sequence alignment of C7orf25 and orthologs. Conservation is indicated under the alignment. Sequences are coloured by percentage of identity according to Jalview. Domains DUF5614 and DUF1308 are highlighted in green and red respectively. The positions of potentially phosphorylated residues in human C7orf25 are indicated by green circles. Position of the potential acidic catalytic residues are marked by red circles. Sequence accession numbers at UniProtB are the following: *Homo sapiens* Q9BPX7, *Mus Musculus* Q91WD4, Gallus gallus A0A1D5P7R3, *Danio rerio* Q803H0, *Xenopus tropicalis* Q5BKL1, Xenopus laevis Q08AW5, *Drosophila melanogaster* Q9W0M6, *Caenorabditis elegans* Q19987, *Arcella intermedia* A0A6B2L838, *Arabidopsis thaliana* A0A654EZB8, *Rhizopus microsporus* A0A1X0R3Z4, Trypanosome brucei Q387L1, *Tuber magnatum* A0A317T2G0, *Nostoc sp* K9QMI2, *Moumouvirus goulette* M1PC36.

Figure 3. **Sequence alignment analysis of CXorf58, MFI and orthologs. A**: Sequence alignment of human CXorf58 and human MFI proteins. Residues are colored according to Clustal default color scheme. Conservation is indicated under the alignment. **B**: Guide tree obtained from Clustal Omega alignment of CXorf58 and MFI orthologs **C:** Potential IQ domain magnification. Residues are colored according to Clustal default color scheme. **D:** Multiple sequence alignment of CXorf58 and MFI sequences. Conservation is indicated under the alignment. Sequences are coloured by percentage of identity according to Jalview. The position of the potential IQ domain is highlighted with a red box. UniProtKB accession numbers for CXorf58 are: *Homo sapiens* Q96LI9, *Mus musculus* A0A5F8MPE6, *Oncorhynchus_kisutch* A0A060WZF5, *Xenopus tropicalis* A8E5V6, *Octopus vulgaris* A0A0L8FJI4, *Amphimedon queenslandica* A0A1X7TW27, *Ciona intestinalis* F6PWJ2, *Stylophora pistillata* A0A2B4RI87, *Salpingoeca rosetta* F2U155, *Spizellomyces punctatus* A0A0L0HIZ9. UniProtKB or RefSeq

accession numbers for MFI are: *Homo sapiens:* Q8NCR3, *Amphimedon queenslandica:* A0A1X7VJ87, *Ciona intestinalis:* F6PP06, *Mytilus coruscus*: A0A0L8FYB0, *Xenopus tropicalis:* F7CTR5, *Danio rerio:* NP_001373428, *Paramecium tetraurelia:* A0CK10, *Tetrahymena thermophila:* XP_001030005, *Spizellomyces punctatus* A0A0L0HVN9.

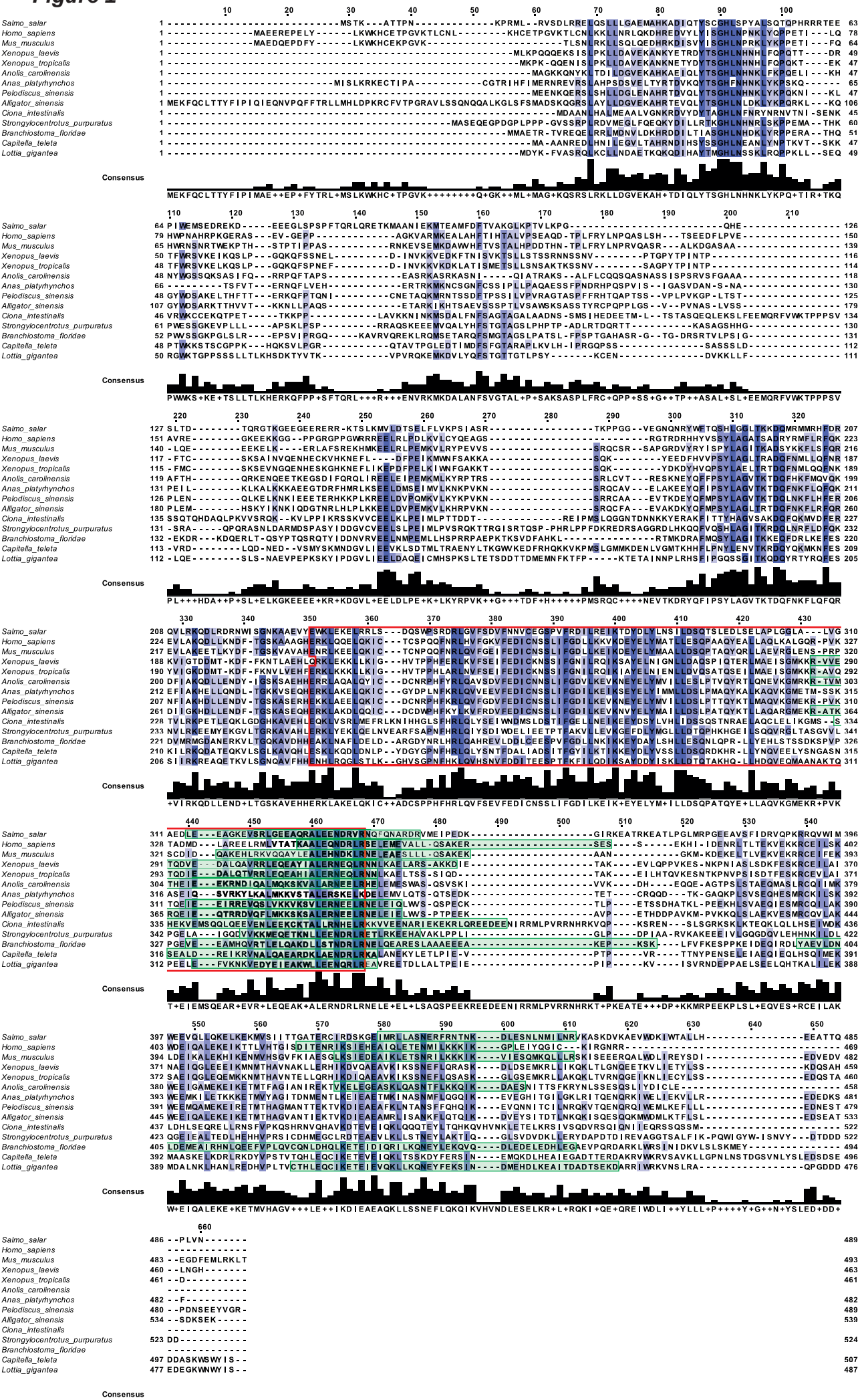
Figure 4. **Multiple sequence alignment of RSRP1 and orthologs**. Conservation is indicated under the alignment. Sequences are coloured by percentage of identity according to Jalview. The phosphorylated Ser in human and the Ser in the orthologs in this region are indicated with red squares. The UniProtKB or RefSeq sequence accession numbers are as follows: *Alligator sinensis* A0A1U7RG00, *Danio rerio* Q1ECZ9, *Gallus gallus* A0A1D5PEB7, *Homo sapiens* Q9BUV0*, Mus musculus* Q3UC65, *Nanorana parkeri* XP_018413522.1, *Pelodiscus sinensis* K7FY35, *Rattus norvegicus* Q5U2S0, *Rhincodon typus* XM_020518674.1.

Figure 5. **Multiple sequence alignment and conservation analysis of SMLR1 and ADIG sequences. A:** Multiple sequence alignment of SMLR1 and orthologs. Conservation is indicated under the alignment. Sequences are coloured by percentage of identity according to Jalview. The transmembrane domains (for human those annotated in neXtProt, for the rest of the species predicted by TMHMM2.0) are indicated with red squares and with a yellow square the alternative initiation Met. **B:** Multiple sequence alignment of SMLR1 and ADIG. Conservation is indicated under the alignment. Sequences coloured by percentage of identity according to Jalview. Red rectangles indicate the transmembrane domain of the human proteins. **C:** Guide tree performed with Clustal Omega. UniProtKB or RefSeq accession numbers for ADIG sequences are the following: *Alligator mississippiensis* XP_019340173.1*, Anas platyrhynchos XP_012947641.2, Chelonoidis abingdonii XP_032630224.1, Fumlmarus glacialis* XP_009574066.1*, Homo sapiens* Q0VDE8*, Lacerta agilis* XP_033009272.1, *Macaca mulatta* F7B4E4*, Meleagris gallopavo* XP_019477718.1, *Mus musculus* Q8R400*, Rattus norvegicus* XP_032758330*.1.* UniProtKB or RefSeq accession numbers for SMLR1 sequences are the following *Alligator mississippiensis* A0A151M398, *Amblyraja radiata* XR_004412037.1, *Anas platyrhynchos* XP_021126027.1, *Anguilla anguilla* XP_035277921.1, *Chelonoidis abingdonii* XP_032628575.1, *Cyprinus carpio* KTG25365.1, *Danio rerio* XR_222668.4, *Gallus gallus* XR_211919.3, *Homo sapiens* H3BR10, *Lacerta agilis* XP_033001307.1, *Macaca mulatta* G7MQD8, *Mus musculus* J3QMJ4, *Nanorana parkeri NW_017308262.1, Nipponia nippon* XP_009459104.1, *Paramormyrops kingsleyae* XP_023652802.1, *Rattus norvegicus* M0R807, *Rhinatrema bivittatum* XP_029450422*, Salmo salar* NC_027305.1, *Xenopus tropicalis* XR_208637.4. SMLR1 protein sequences of *Amblyraja radiata, Nanorana parkeri, Salmo salar, Xenopus tropicalis*, *Danio rerio* and *Gallus gallus* are the translations obtained as the result of tBLASTn.

Figure 6. Multiple sequence alignment of TMEM53. Conservation is indicated under the alignment. Sequences coloured by percentage of identity according to Jalview. The putative catalytic sites based on our HHPRED and SWISS-MODEL analyses are highlighted with red squares. In green squares the predicted transmembrane domains according to TMHMM. The UniProtKB accession numbers are the following: *Anolis carolinensis* G1KQB8*, Arabidopsis thaliana* A0A178VZN4*, Branchiostoma floridae* C3ZJ88*, Caenorhabditis elegans(1)* Q17846*, Caenorhabditis elegans(2)* Q22750*, Caenorhabditis elegans(3)* Q9TZH8*, Capitella teleta* R7TA92*, Ciona savignyi* H2Z7C5*, Danio rerio* Q6DHN0*, Dictyostelium discoideum(1)* Q54YR8*, Dictyostelium discoideum(2)* Q54N85*, Drosophila melanogaster* A1Z6G9*, Gallus gallus* A0A1L1RPU6*, Homo sapiens* Q6P2H8*, Mus musculus* Q9D0Z3*, Nematostella vectensis* A7SHF2*, Octopus bimaculoides* A0A0L8GWT2*, Oryza sativa subsp. Japonica* Q6Z6I1*, Penicillium chrysogenum* B6HTA6*, Salpingoeca rosetta F2U052, Strongylocentrotus purpuratus(1)* W4YNQ6*, Strongylocentrotus purpuratus(2)* W4Y103*, Xenopus laevis(1)* Q5PPS7*, Xenopus laevis(2)* A0A1L8GM57*, Xenopus tropicalis* A9JSB6*.*

Figure 7: Multiple sequence alignment of TMEM232 and orthologs. Conservation is indicated under the alignment. Sequences were coloured by percentage of identity according to Jalview. The transmembrane domains predicted by Phobius for the human and mouse proteins are indicated with red rectangles. The UniProtKB accession numbers are the following: *Homo sapiens* C9JQI7, *Mus musculus* Q5K6N0, *Alligator mississippiensis* A0A151PIJ1, *Anolis carolinensis* H9GC94, *Xenopus laevis* A0A1L8I1Q0, *Danio rerio* A5WVS1, *Capitella teleta* R7TJS3, *Branchiostoma floridae* C3YDS1, *Lottia gigantea* V3ZU21, *Ciona intestinalis* F6SFR5, *Macrostomum lignano* A0A267E638, *Trichoplax adhaerens* B3RTI4, *Nematostella vectensis* A7S2I4, *Amphimedon queenslandica* A0A1X7U5R7, *Strongylocentrotus purpuratus* W4Y6N3.

Figure 1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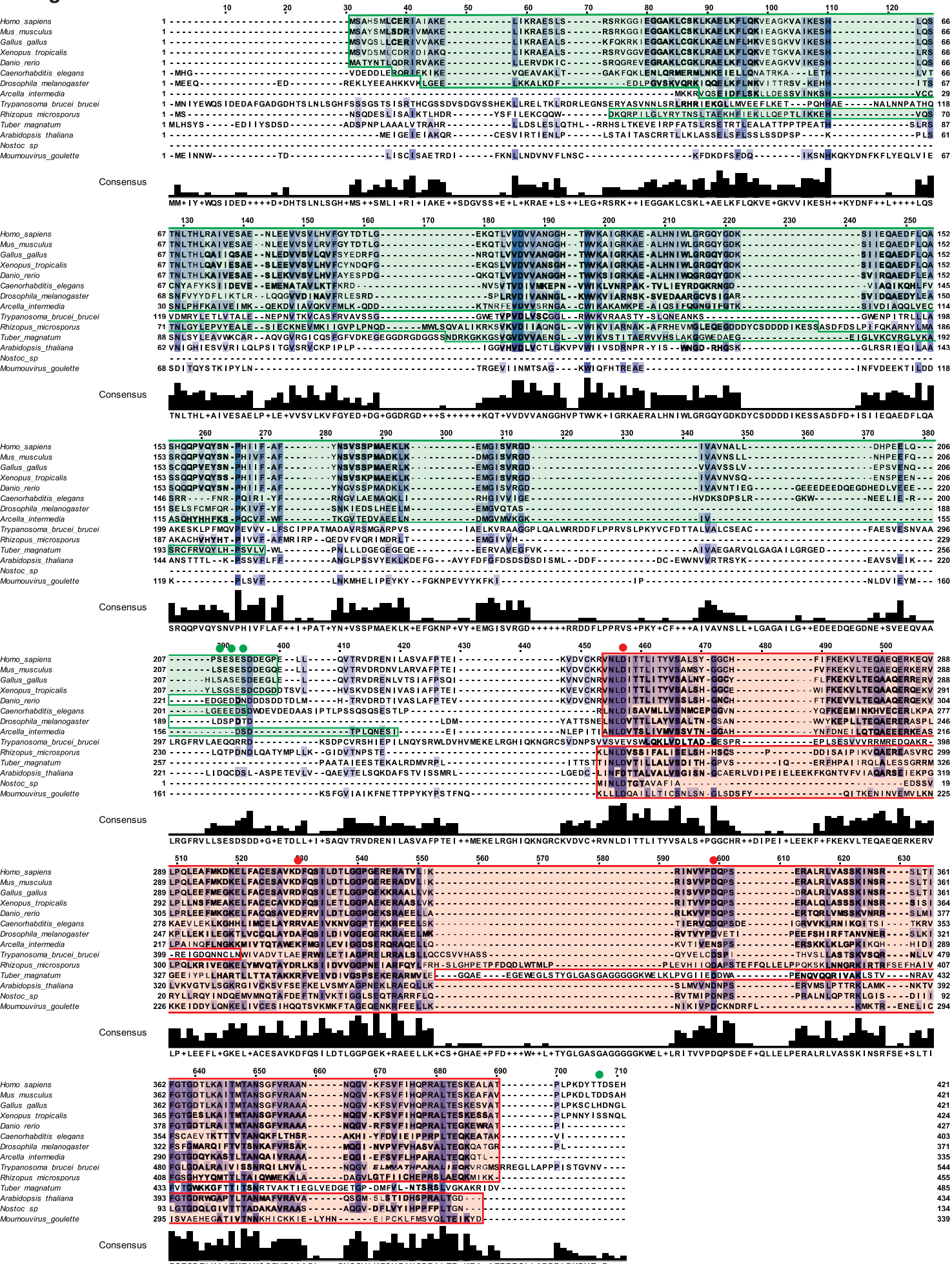
Consensus

Figure 2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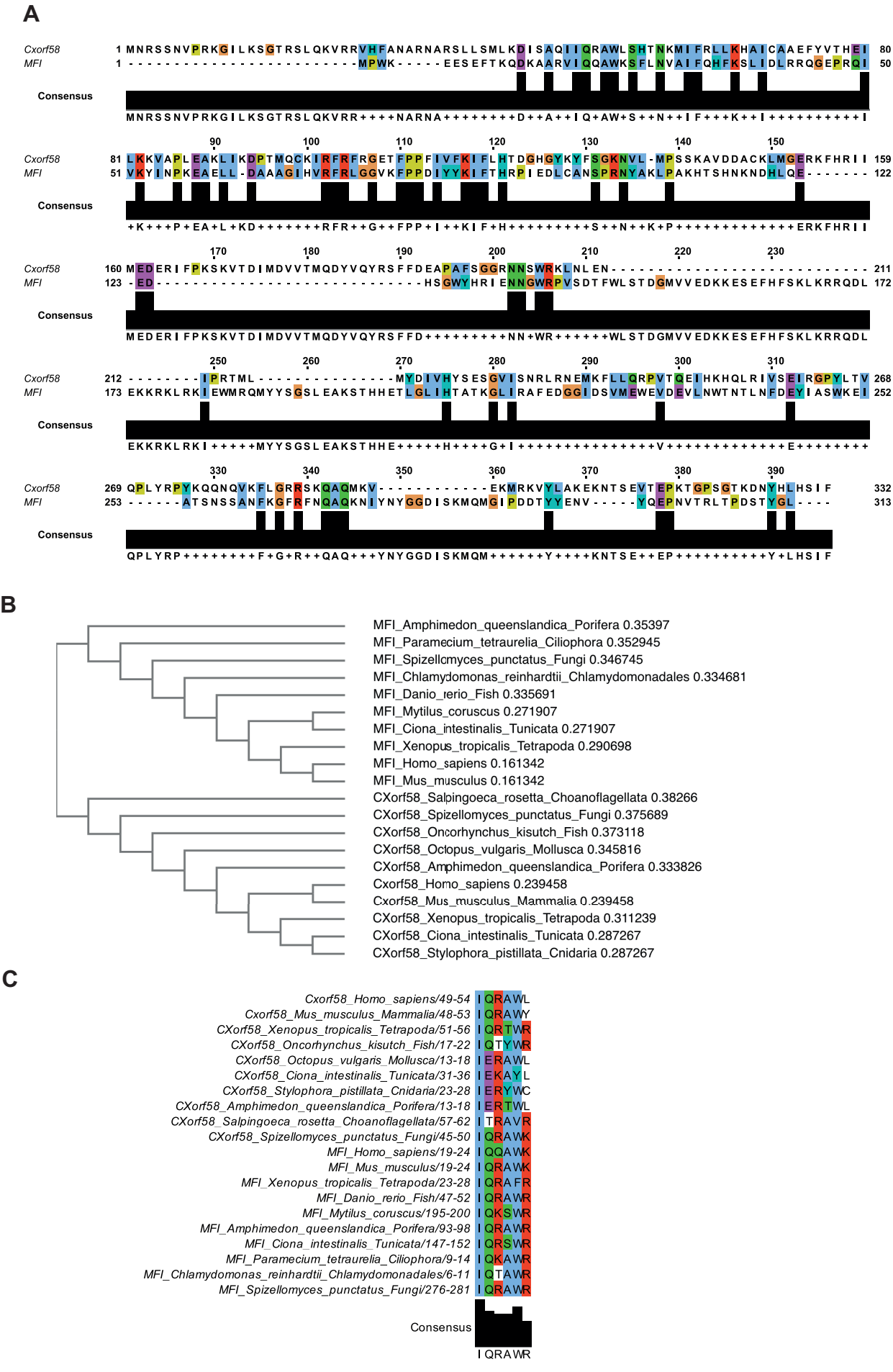
Consensus

Figure 3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MFI
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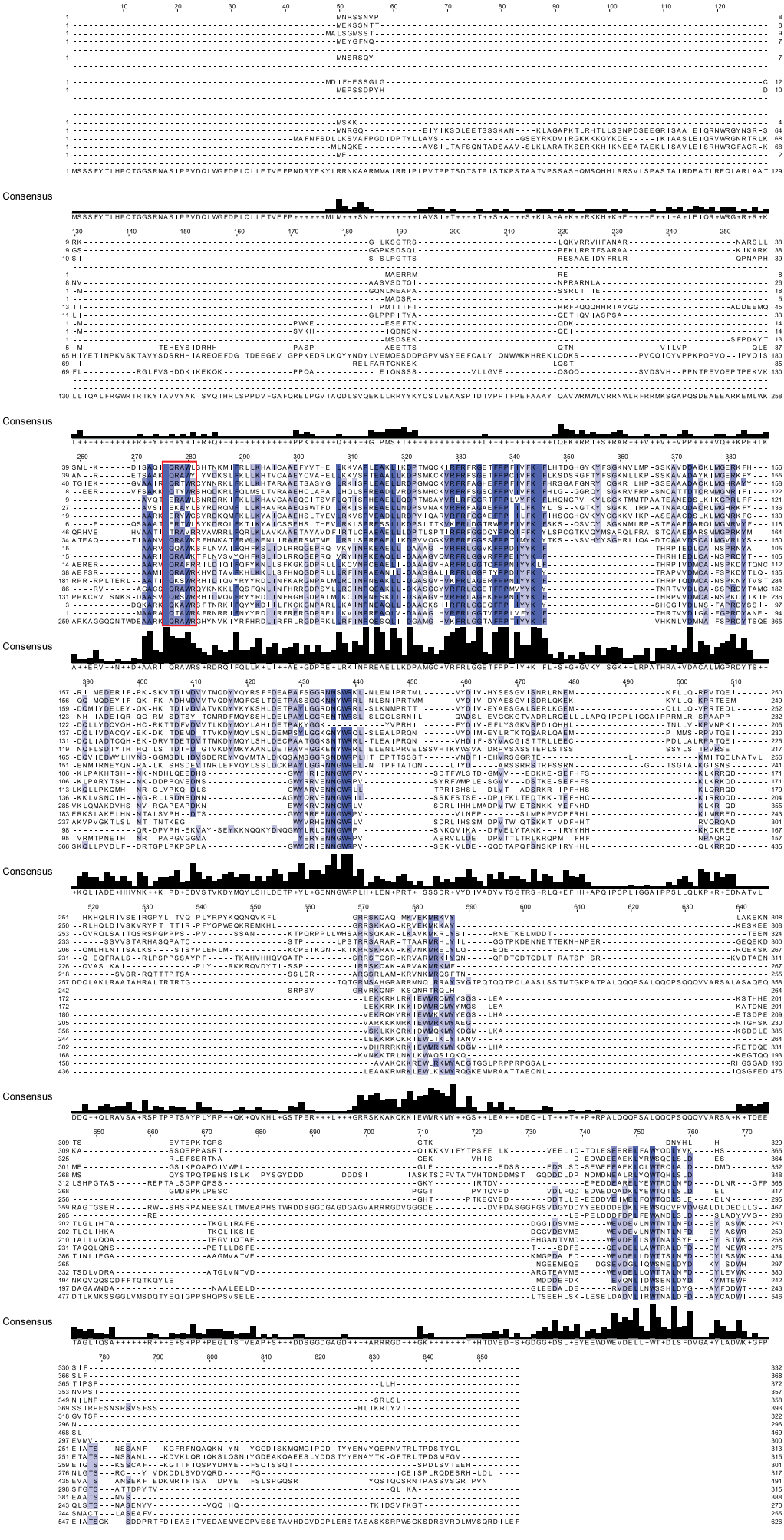
Consensus
IQRAWR

Figure 3

D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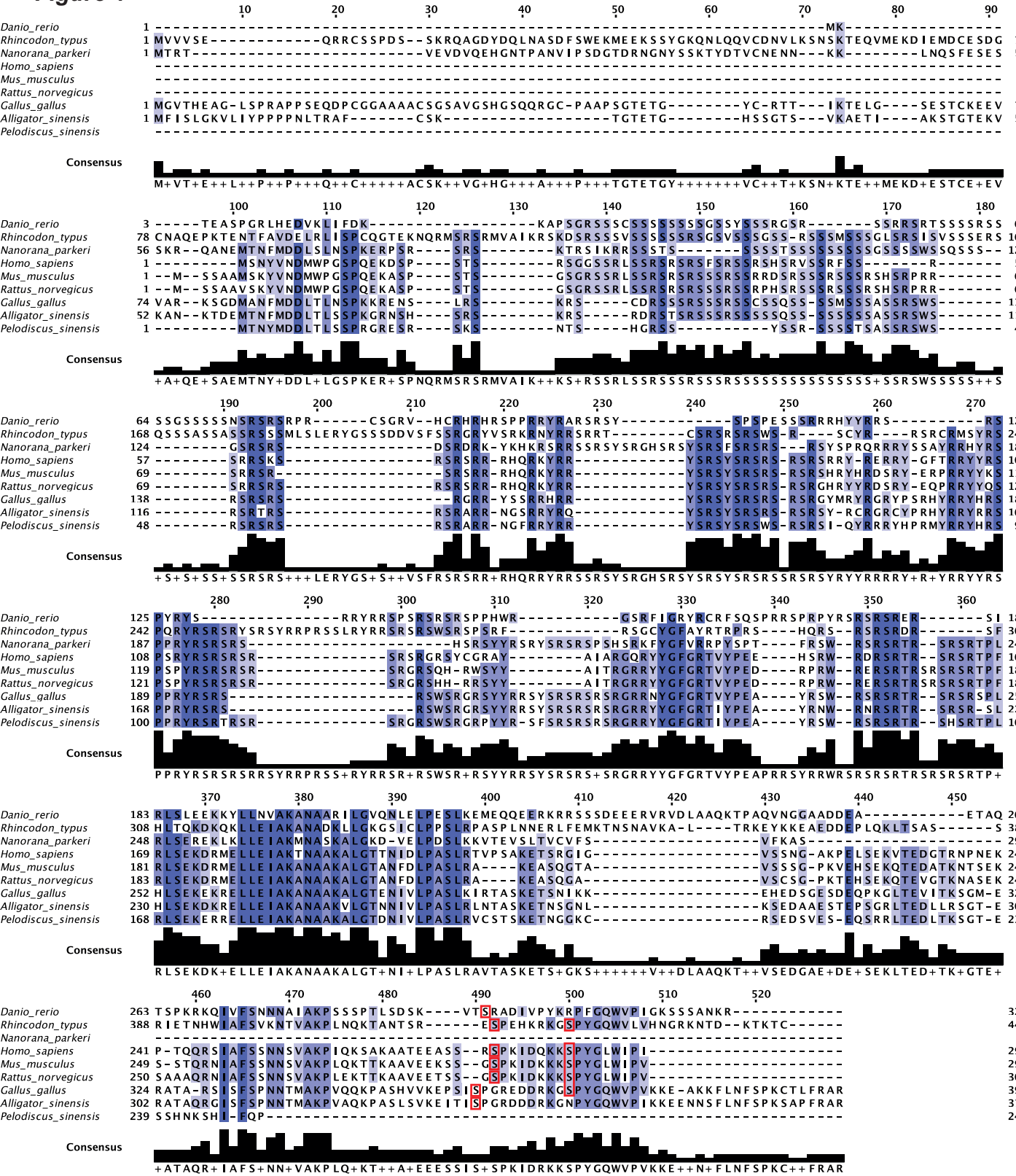
Consensus

Figure 4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Consensus

Figure 5

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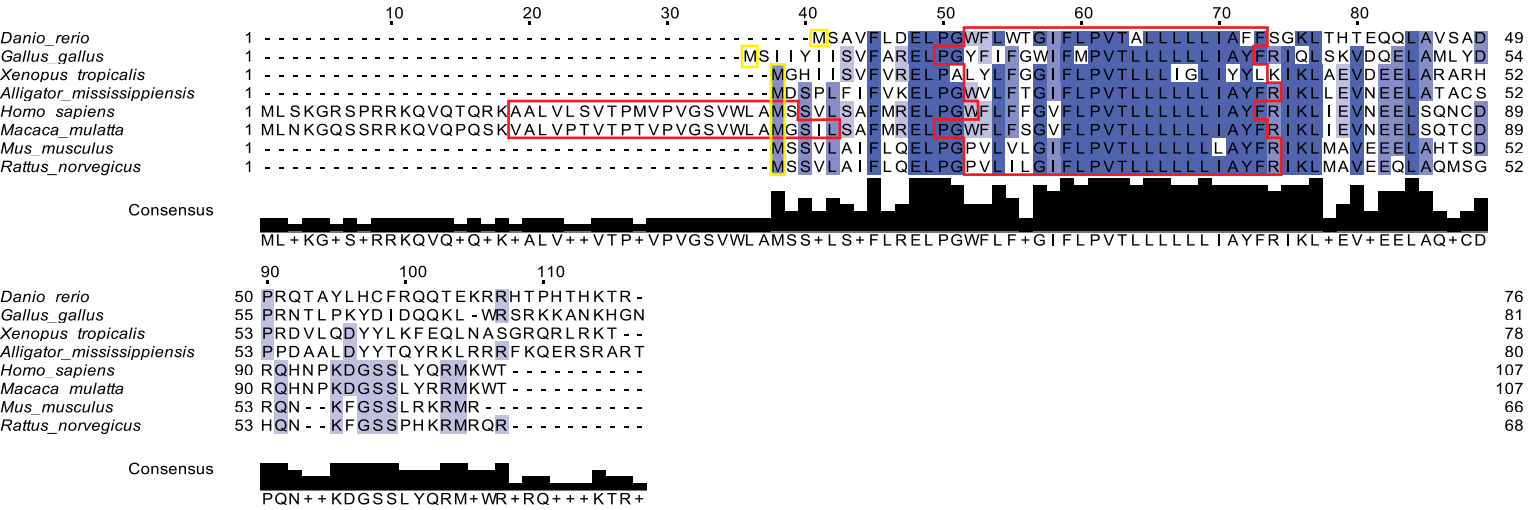
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Consensus

B

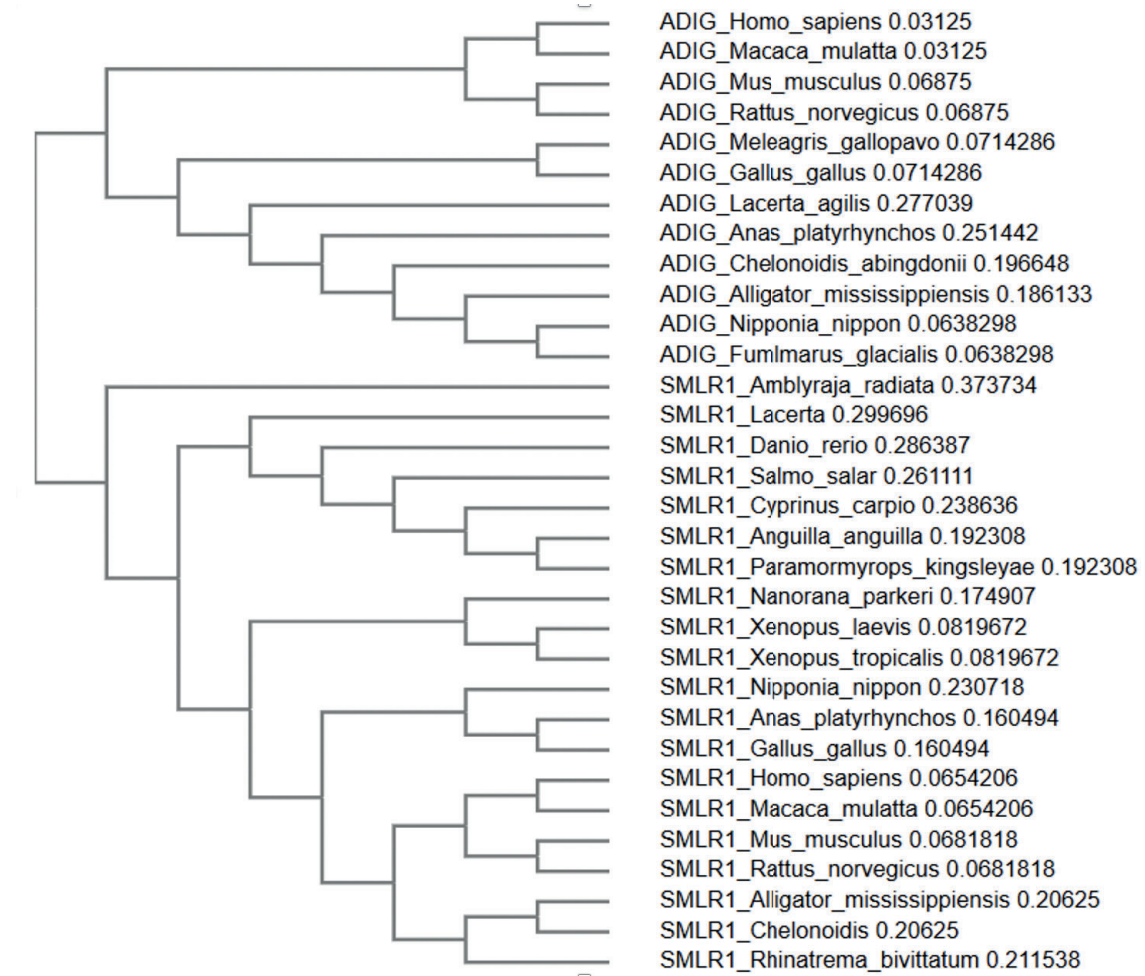
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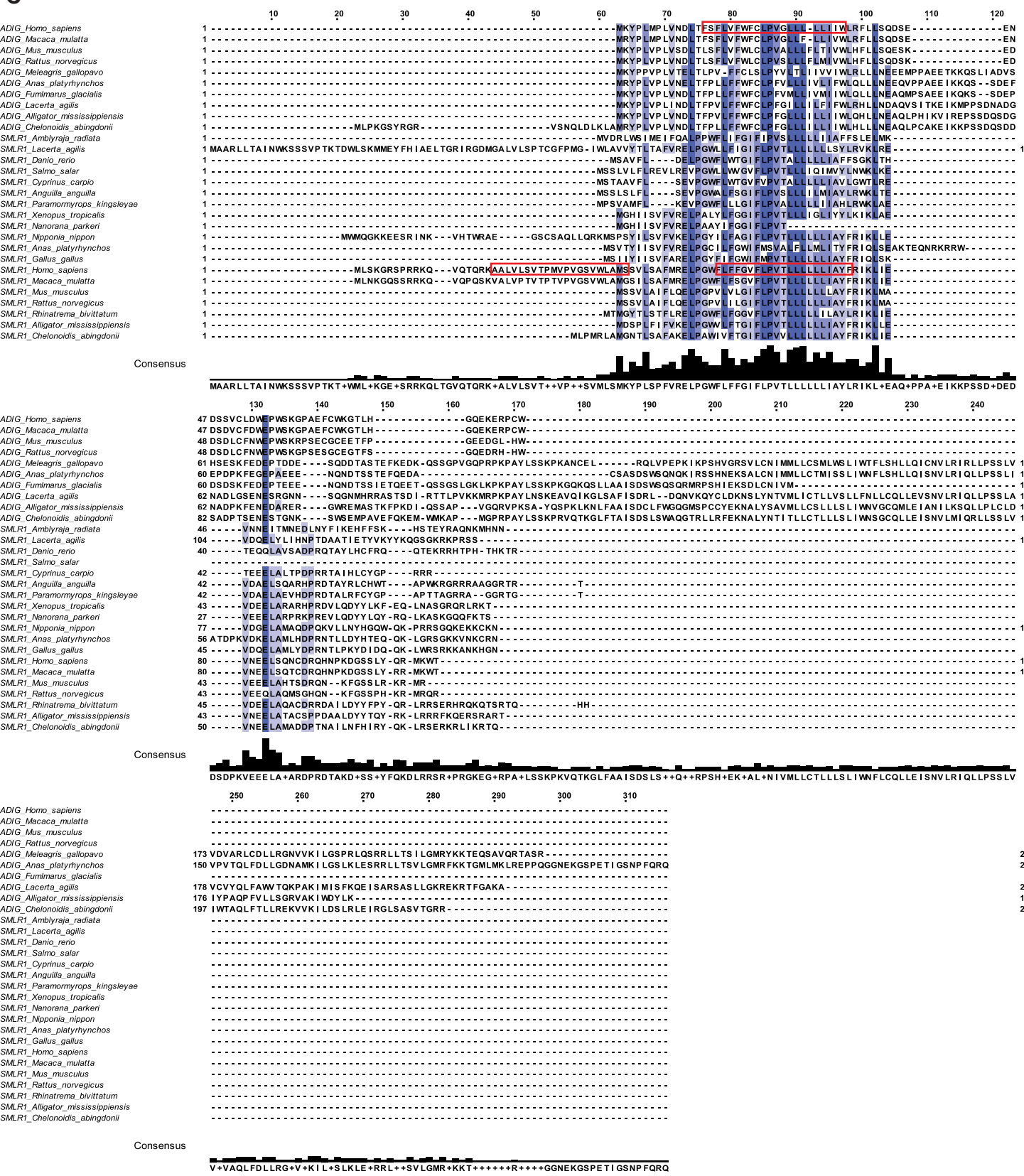
Figure 5

C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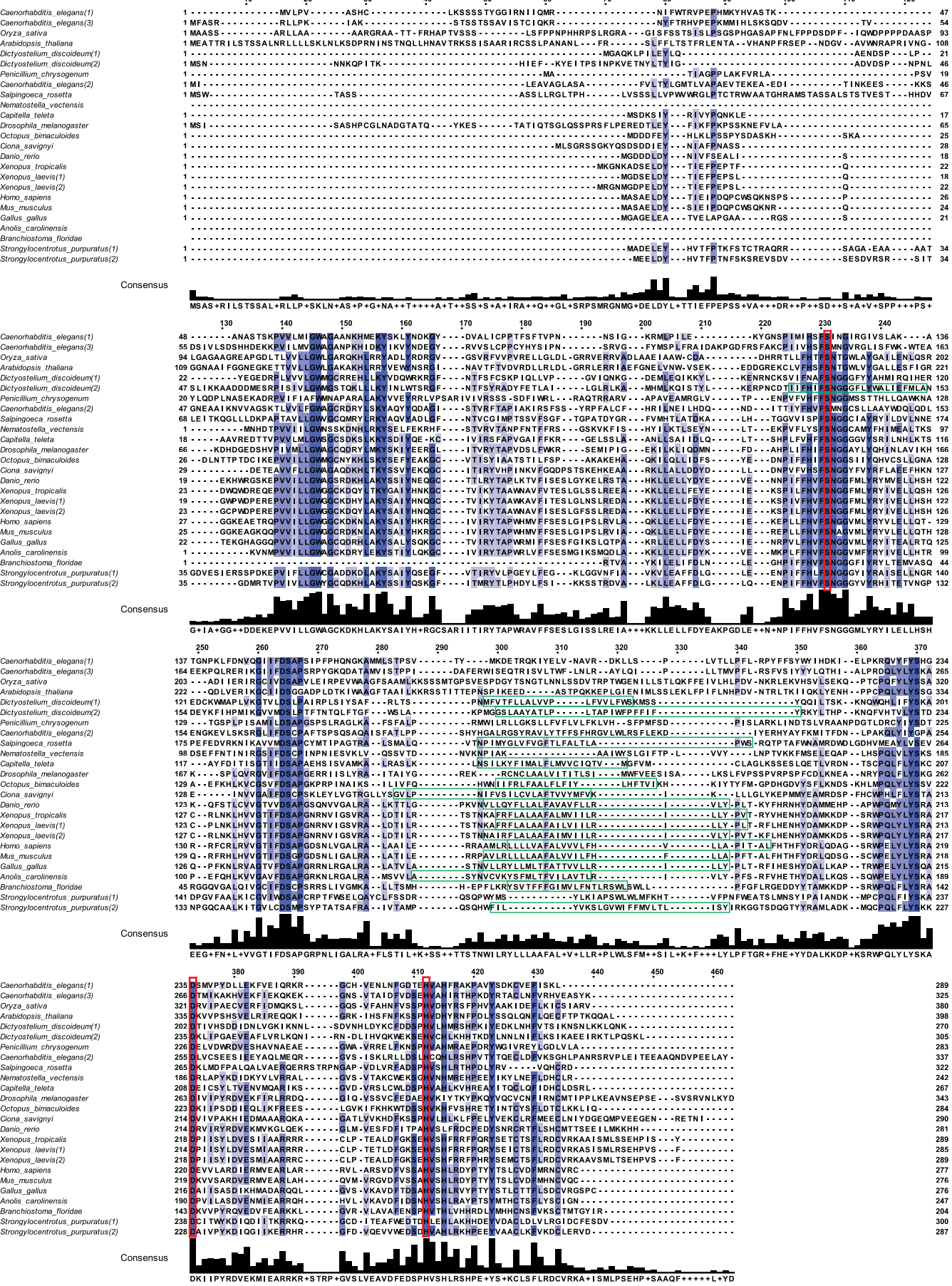
Consensus

Figure 6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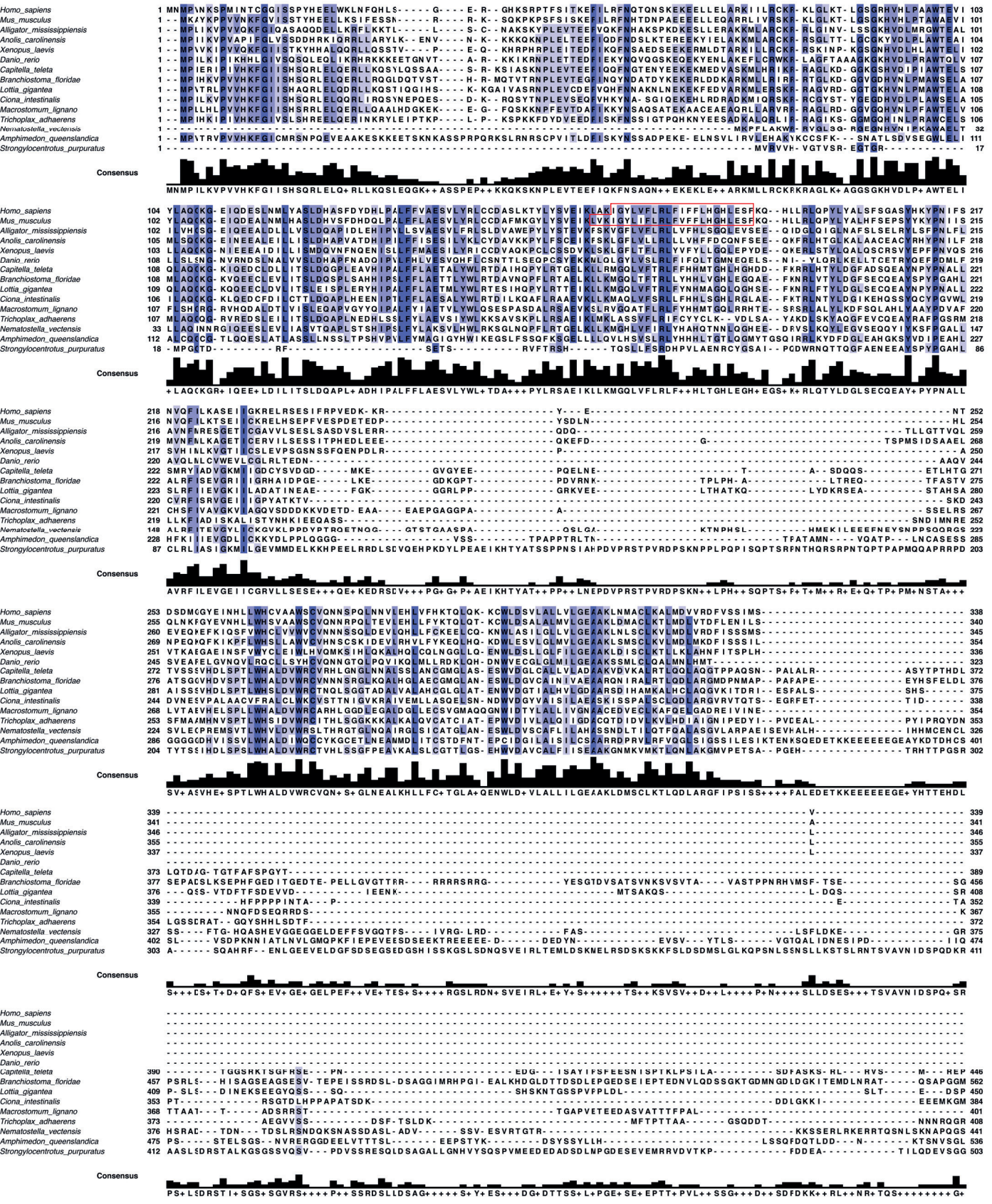
Consensus

Figure 7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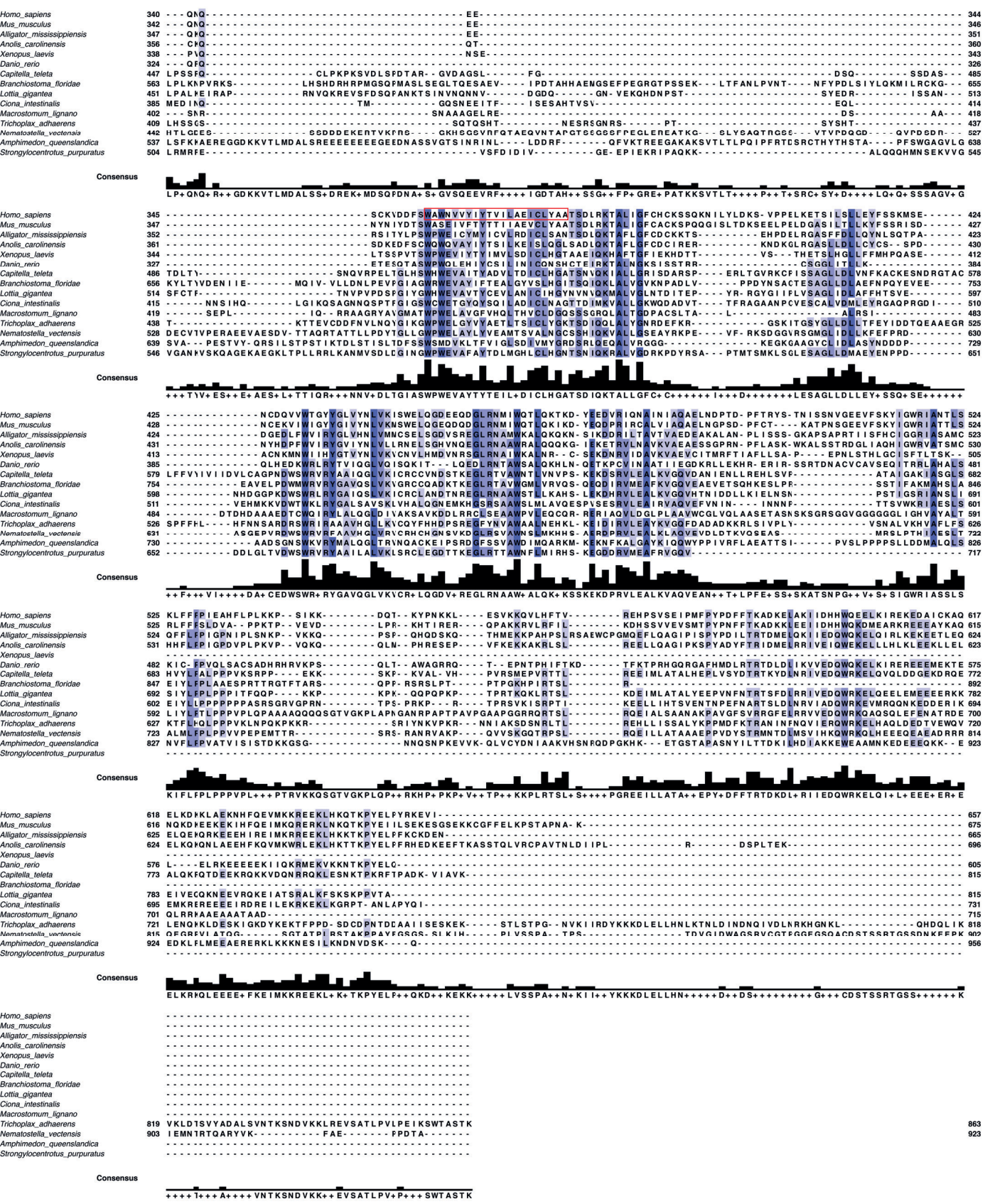
Consensus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Consensus