**Supplementary File 1:**

List of sequence reads in SRA datasets of Gadiformes published by Malmstrøm *et al.* that match with MHC class II system genes.

**Table of Contents Page**

1. Summary/Discussion 2

2. References used in this supplementary file 3

3. Read sequences 4

3.1 *MHC IIA* 4

3.2 *MHC IIB* 9

3.3 *CD4-2* 17

3.4 *CD74a* 18

3.5 *CD74b* 19

**1. Summary/Discussion**

This is a list of the MHC class II system gene matching nucleotide reads in FASTA format, except for those of *CD4-1*, which we found for gadiform fishes in the SRA datasets published by Malmstrøm *et al.*1. The list includes the SRA reads referred to in Table S1, plus all the additional ones that we found. Also the reads from the opposite ends of the same clones (paired reads) are included. Presented sequence orientations match the gene directions. In this list the MHC IIA and MHC IIB matching reads are not further separated into classical or nonclassical subcategories. Given that the reads may be contaminations, we feel that a detailed discussion of the reads in this article would probably be an overdiscussion. However, interested readers can contact us for such evidence, which includes facts like both read ends having the claimed gene features, the encoding of characteristic residues, and/or reciprocal top-matches.

*The coverage with reported reads of MHC class II system genes is much lower for the gadiform fishes than for the non-gadiform fishes.*

The coverage with the here listed reads per MHC class II system gene in gadiform fishes is generally low, with sometimes only one match per gene found, and did not result in assemblies into unitigs or scaffolds by Malmstrøm *et al.*1. In contrast, as shown in Supplementary File 2, for the investigated non-gadiform fishes Malmstrøm *et al.*1 found so many reads for the MHC class II system genes that they fulfilled their criteria for being assembled into unitigs and scaffolds. That is why we chose not to list all the individual matching SRAs for the non-gadiform fishes.

*The gadiform fish Melanonus zugmayeri should probably be investigated more intensively.*

With 60 reads (30 fragments with paired reads) matching to MHC class II system genes, the gadiform species *Melanonus zugmayeri* is most frequently represented in the here presented list. Although these reads are substantially less abundant than found for the non-gadiform fishes, we believe that they are nevertheless too many for reliably assuming absence of all (intact) MHC class II system genes. We recommend that Malmstrøm and co-workers do additional experiments for investigating whether all the MHC class II system matching reads in their *Melanonus zugmayeri* dataset do either belong to pseudogenes or are due to accidental contaminations. Such would very much help to reassure their claim that the MHC class II system genes were lost in all Gadiformes. Whether such analysis should also be done for *Merluccius merluccius* and *Merluccius capensis* is discussable.

*We do not analyze CD4-1 evolution.*

Malmstrøm and co-workers agree with us that in Gadiform fishes at least remnants of *CD4-1* gene can be found (see Star *et al.* 20132 and our on-line discussion at the article site of the respective journal; see also Fig. S1). We feel it is their task and not ours to analyze the development from intact *CD4-1* in non-gadiform fish into the form(s) found in Gadiformes, because it is they who claim the functional absence of CD4-1 in Gadiformes. Furthermore, a proper discussion would need full-length information of the *CD4-1* gene region (which is not available for all investigated fishes, for examples see Supplementary File 2) and analysis at the transcription level. Therefore, this supplementary file does not contain information on the *CD4-1* sequences found for Gadiformes.

*Organization of the list.*

The reads are listed per matching gene, and within these gene sections organized based on species phylogeny in the same order as is shown in Table S1 (for the species phylogeny see Malmstrøm *et al.*1). The species name is followed by the read name given in the SRA database (<https://www.ncbi.nlm.nih.gov/sra>) and, if applicable, the mentioning that in comparison to the read report the complementary strand is shown (com) and/or mentioning of the region of the molecule that is encoded. The encoded regions are distinguished as being part of MHC IIA 1 domain (alpha-1), MHC IIA 2 domain (alpha-2), MHC IIB 1 domain (beta-1), MHC IIB 2 domain (beta-2), MHC IIB transmembrane domain (TM), CD4-2 Ig-like domain 1 (Ig1), CD4-2 Ig-like domain 2 (Ig2), CD4-2 cytoplasmic tail (CY), CD74a or CD74b single-exon encoded region with transmembrane and amino-terminal part of CLIP regions (TM Nterm-CLIP), and CD74a or CD74b thyroglobulin type-1 domain (Thy).

NCBI database accessions of the datasets that include the here listed reads are:

*Merluccius polli*: ERX1544994; *Merluccius merluccius*: ERX1544995, ERX1544996; *Merluccius capensis*: ERX1544997; *Melanonus zugmayeri*: ERX1544998, ERX1544999; *Muraenolepsis marmoratus*: ERX1545000; *Trachyrincus scabrus*: ERX1545001, ERX1545002; Trachyrincus murrayi: ERX1545003, ERX1545004, ERX1545005, ERX1545006; *Laemonema laureysi*: ERX1545009; *Bathygadus melanobranchus*: ERX1545010; *Malacocephalus occidentalis*: ERX1545013; *Phycis blennoides*: ERX1545014, ERX1545015, ERX1545016, ERX1545017; *Phycis phycis*: ERX1545018; *Lota lota*: ERX1545019, ERX1545020; *Theragra chalcogramma*: ERX1545033.

**2. References used in this supplementary file**

1) Malmstrøm, M., Matschiner, M., Tørresen, O.K., Star, B., Snipen, L.G., Hansen, T.F., Baalsrud, H.T., Nederbragt, A.J., Hanel, R., Salzburger, W., Stenseth, N.C., Jakobsen, K.S. & Jentoft, S. Evolution of the immune system influences speciation rates in teleost fishes. *Nat. Genet.* **48**, 1204-1210 (2016).

2) Star, B., Nederbragt, A.J., Jentoft, S., Grimholt, U., Malmstrøm, M., Gregers, T.F., Rounge, T.B., Paulsen, J., Solbakken, M.H., Sharma, A., Wetten, O.F., Lanzén, A., Winer, R., Knight, J.,Vogel, J.H., Aken, B., Andersen, O., Lagesen, K., Tooming-Klunderud, A., Edvardsen, R.B., Tina, K.G., Espelund, M., Nepal, C., Previti, C., Karlsen, B.O., Moum, T., Skage, M., Berg, P.R., Gjøen, T., Kuhl, H., Thorsen, J., Malde, K., Reinhardt, R., Du, L., Johansen, S.D., Searle, S., Lien, S., Nilsen, F., Jonassen, I., Omholt, S.W., Stenseth, N.C., Jakobsen, K.S. The genome sequence of Atlantic cod reveals a unique immune system. *Nature* **477**, 207-210 (2011).

**3. Read sequences**

**3.1 MHC IIA**

>Merluccius\_merluccius\_ERR1473848.13341992.1; alpha-2

GTAAAACACATTTATTTTAATTAGGCCTATTTTTAACATATTTCAATGTAACACAACTGA

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>Merluccius\_merluccius\_ERR1473848.13341992.2 com; alpha-2

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ATGCCCAATAATGACCAGACCTTCCATTGCTTCTCCACTCTCACGATCACGCCGGAGCAA

GGCGATGTGTACAGCTGCACAGTGGAGCAC

>Merluccius\_merluccius\_ERR1473848.13570169.1; alpha-2

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>Merluccius\_merluccius\_ERR1473848.23411049.1 com; alpha-2

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>Merluccius\_merluccius\_ERR1473849.12616696.1 com; alpha-2

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>Melanonus\_zugmayeri\_ERR1473851.34596639.1; alpha-2

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>Melanonus\_zugmayeri\_ERR1473852.5535820.1 com; alpha-1

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>Melanonus\_zugmayeri\_ERR1473851.28557328.1; alpha-1

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>Muraenolepis\_marmoratus\_ERR1473853.13532583.2; alpha-1

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>Muraenolepis\_marmoratus\_ERR1473853.35942289.1; alpha-2

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>Muraenolepis\_marmoratus\_ERR1473853.35942289.2 com; alpha-2

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>Phycis\_blennoides\_ERR1473867.1216359.1 com

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>Trachyrincus\_scabrus\_ERR1473854.42984801.1; alpha-2

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>Trachyrincus\_scabrus\_ERR1473855.24170403.2 com

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>Laemonema\_laureysi\_ERR1473862.17076666.1 com

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>Laemonema\_laureysi\_ERR1473862.17076666.2; alpha-2

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>Laemonema\_laureysi\_ERR1473862.20677118.1; alpha-1

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>Laemonema\_laureysi\_ERR1473862.20677118.2 com

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**3.3 CD4-2**

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**3.4 CD74a**

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**3.5 CD74b**

>Melanonus\_zugmayeri\_ERR1473851.26907834.1 com; Thy

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