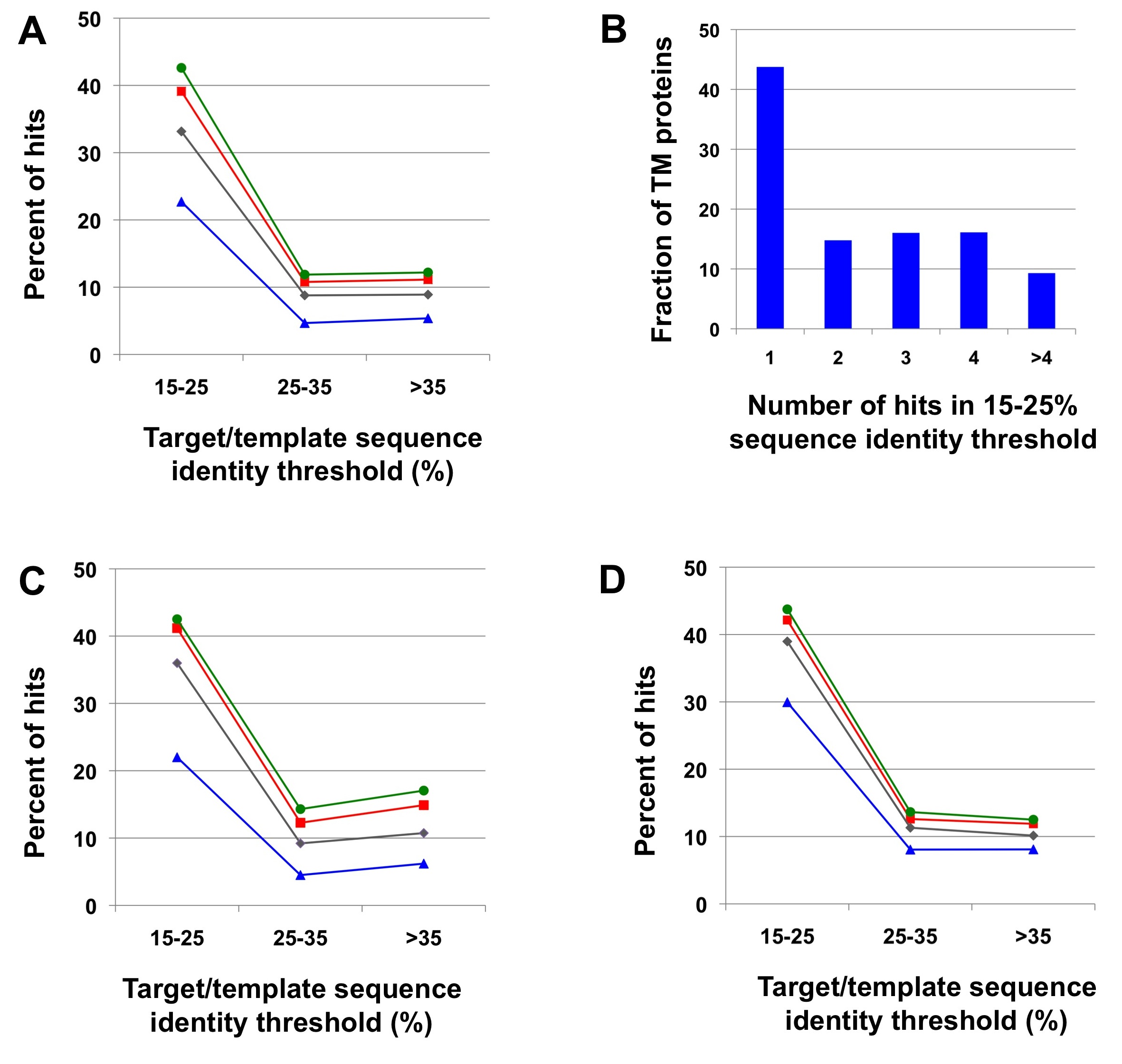
**Supporting Information**

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**Supplementary Figure 1. Homology modeling coverage for the human multi-pass TMH proteome.** **A.** Percent of hits (i.e. structural homologs) as calculated by HHpred [1](#_ENREF_1), [4](#_ENREF_4), [5](#_ENREF_5) for all full-length human multi-pass TMH proteins (3405 annotated sequences [6](#_ENREF_6)) split in three target/template sequence identity thresholds: distant (percent sequence identity between target and template between 15 and 25%: %ID 15-25), medium (%ID 25-35) and close homology (%ID >35) thresholds. The data is represented for four levels of target sequence length coverage by the template: 50% (green), 60% (red), 75% (grey) and 90% (blue). **B.** Distribution of hits in the distant homology (%ID 15-25) bin for all full-length human multi-pass TMH proteins. The fraction of transmembrane proteins for which 1, 2, 3, 4 or more than 4 distant homolog templates were identified by HHpred is represented for 75% target sequence length coverage by the template. **C, D.** Percent of hits (i.e. structural homologs) as calculated by HHpred [1](#_ENREF_1), [4](#_ENREF_4), [5](#_ENREF_5) for all full-length human multi-pass and single-pass TMH proteins (5818 annotated sequences, **C**) or for all TM domains (i.e. from the first to the last TMH residue) of all human multi-pass TMH proteins (3079 annotated sequences [6](#_ENREF_6), **D**), split in three target/template sequence identity thresholds: distant (percent sequence identity between target and template between 15 and 25%: %ID 15-25), medium (%ID 25-35) and close homology (%ID >35) thresholds. The data is represented for four levels of target sequence length coverage by the template: 50% (green), 60% (red), 75% (grey) and 90% (blue).

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