**Supplementary Figure 2: Multiple translation alignment of the NCBI annotated non ‘low-quality protein’ (LQ) tagged DRD5 coding sequences, including the manually predicted DRD5 coding sequence of *Hippopotamus amphibius* (hippopotamus)and excluding the NCBI DRD5 annotated coding sequence of *Tursiops truncatus* (common bottlenose dolphin).**

An alignment identity graph is presented above the alignment and *Homo sapiens* (human) DRD5 coding sequence is set as reference. Greenish colors represent very high alignment identity values, followed by yellowish (mid to high alignment identity values) and finally reddish colors, indicating a very low alignment identity value. Results show an average pairwise alignment identity of 83.6%.

