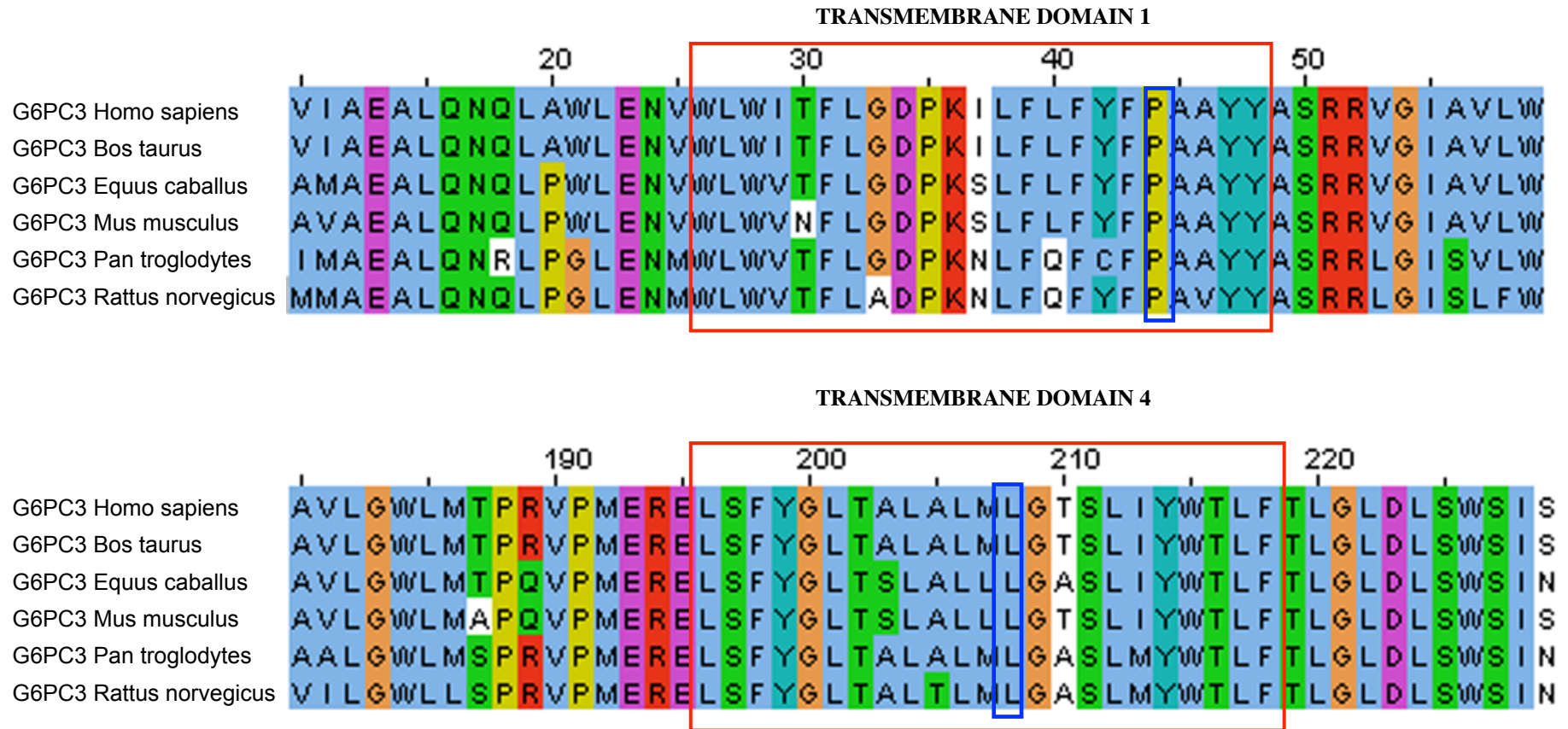


Supplementary Figure 1. Protein sequence alignment of G6PC3 in different species



G6PC3 amino acid residue homology between species with transmembrane domains 1 (residues 26-48) and 4 (residues 196-218) boxed in red. The positions of the p.Pro44Ser and p.Leu208Arg mutations are outlined in blue. Amino acid residues are 69% (16/23) and 79% (18/23) fully conserved between species in transmembrane domains 1 and 4 respectively. The proteins used for individual amino acid residue comparison and their corresponding RefSeq numbers include: Homo sapiens (NP_001073535), Bos taurus (NP_899208.2), Equus caballus (XP_001490866.1), Mus musculus (NM_175935.3), Pan troglodytes (XM_511541.2), Rattus norvegicus (NM_176077.3). The ClustalW method was used for sequence alignment.