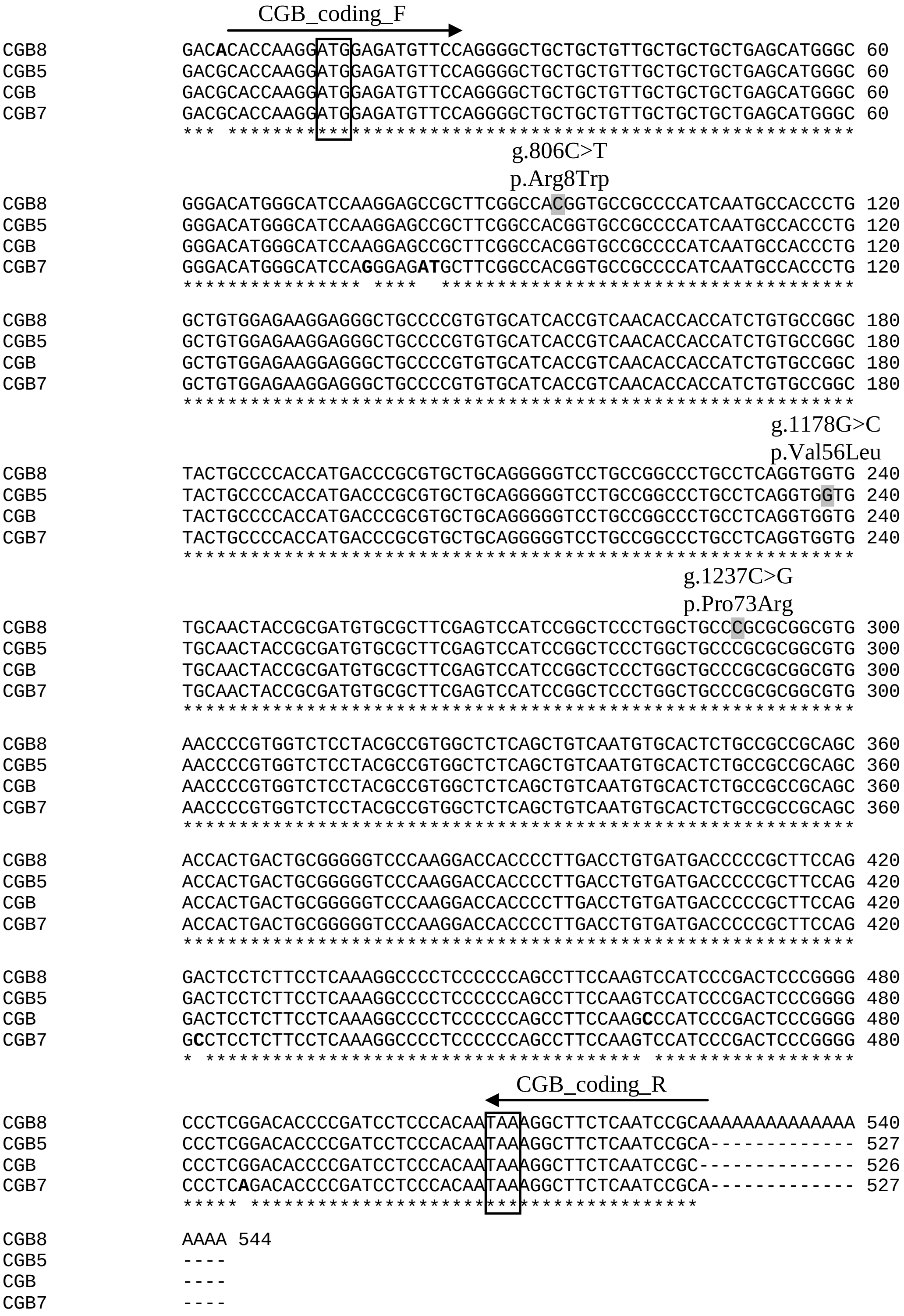
Figure S3. Alignment of the transcribed sequences of the *hCGβ* coding genes. Multiple sequence alignment has been performed with ClustalW2 alignment tool (http://www.ebi.ac.uk/Tools/msa/clustalw2/) and using mRNA sequence stretch from -12 nucleotides (relative to ATG) until the 3' end of the transcript (GenBank references: NM_033183.2 for *CGB8*, NM_033043.1 for *CGB5*, NM_000737.2 for *CGB*, NM_033142.1 for *CGB7*). Nucleotide differences between the aligned coding sequences are highlighted in bold; START (ATG) and STOP (TAA) codons are designated with frames. Primers used for the amplification of the *hCGβ* coding region and construction of the wild-type *hCGβ* plasmid are indicated by arrows. *hCGβ* mutations under study are highlighted in grey.



```
                          CGB_coding_F
CGB8           GACACACCAAGGATGGAGATGTTCCAGGGGCTGCTGCTGTTGCTGCTGCTGAGCATGGGC 60
CGB5           GACGCACCAAGGATGGAGATGTTCCAGGGGCTGCTGCTGTTGCTGCTGCTGAGCATGGGC 60
CGB            GACGCACCAAGGATGGAGATGTTCCAGGGGCTGCTGCTGTTGCTGCTGCTGAGCATGGGC 60
CGB7           GACGCACCAAGGATGGAGATGTTCCAGGGGCTGCTGCTGTTGCTGCTGCTGAGCATGGGC 60
               *** ********************************************************
                                              g.806C>T
                                              p.Arg8Trp
CGB8           GGGACATGGGCATCCAAGGAGCCGCTTCGGCCACGGTGCCGCCCCATCAATGCCACCCTG 120
CGB5           GGGACATGGGCATCCAAGGAGCCGCTTCGGCCACGGTGCCGCCCCATCAATGCCACCCTG 120
CGB            GGGACATGGGCATCCAAGGAGCCGCTTCGGCCACGGTGCCGCCCCATCAATGCCACCCTG 120
CGB7           GGGACATGGGCATCCAGGGAGATGCTTCGGCCACGGTGCCGCCCCATCAATGCCACCCTG 120
               **************** ****  *************************************

CGB8           GCTGTGGAGAAGGAGGGCTGCCCCGTGTGCATCACCGTCAACACCACCATCTGTGCCGGC 180
CGB5           GCTGTGGAGAAGGAGGGCTGCCCCGTGTGCATCACCGTCAACACCACCATCTGTGCCGGC 180
CGB            GCTGTGGAGAAGGAGGGCTGCCCCGTGTGCATCACCGTCAACACCACCATCTGTGCCGGC 180
CGB7           GCTGTGGAGAAGGAGGGCTGCCCCGTGTGCATCACCGTCAACACCACCATCTGTGCCGGC 180
               ************************************************************
                                                                    g.1178G>C
                                                                    p.Val56Leu
CGB8           TACTGCCCCACCATGACCCGCGTGCTGCAGGGGGTCCTGCCGGCCCTGCCTCAGGTGGTG 240
CGB5           TACTGCCCCACCATGACCCGCGTGCTGCAGGGGGTCCTGCCGGCCCTGCCTCAGGTGGTG 240
CGB            TACTGCCCCACCATGACCCGCGTGCTGCAGGGGGTCCTGCCGGCCCTGCCTCAGGTGGTG 240
CGB7           TACTGCCCCACCATGACCCGCGTGCTGCAGGGGGTCCTGCCGGCCCTGCCTCAGGTGGTG 240
               ************************************************************
                                                             g.1237C>G
                                                             p.Pro73Arg
CGB8           TGCAACTACCGCGATGTGCGCTTCGAGTCCATCCGGCTCCCTGGCTGCCCGCGCGGCGTG 300
CGB5           TGCAACTACCGCGATGTGCGCTTCGAGTCCATCCGGCTCCCTGGCTGCCCGCGCGGCGTG 300
CGB            TGCAACTACCGCGATGTGCGCTTCGAGTCCATCCGGCTCCCTGGCTGCCCGCGCGGCGTG 300
CGB7           TGCAACTACCGCGATGTGCGCTTCGAGTCCATCCGGCTCCCTGGCTGCCCGCGCGGCGTG 300
               ************************************************************

CGB8           AACCCCGTGGTCTCCTACGCCGTGGCTCTCAGCTGTCAATGTGCACTCTGCCGCCGCAGC 360
CGB5           AACCCCGTGGTCTCCTACGCCGTGGCTCTCAGCTGTCAATGTGCACTCTGCCGCCGCAGC 360
CGB            AACCCCGTGGTCTCCTACGCCGTGGCTCTCAGCTGTCAATGTGCACTCTGCCGCCGCAGC 360
CGB7           AACCCCGTGGTCTCCTACGCCGTGGCTCTCAGCTGTCAATGTGCACTCTGCCGCCGCAGC 360
               ************************************************************

CGB8           ACCACTGACTGCGGGGGTCCCAAGGACCACCCCTTGACCTGTGATGACCCCCGCTTCCAG 420
CGB5           ACCACTGACTGCGGGGGTCCCAAGGACCACCCCTTGACCTGTGATGACCCCCGCTTCCAG 420
CGB            ACCACTGACTGCGGGGGTCCCAAGGACCACCCCTTGACCTGTGATGACCCCCGCTTCCAG 420
CGB7           ACCACTGACTGCGGGGGTCCCAAGGACCACCCCTTGACCTGTGATGACCCCCGCTTCCAG 420
               ************************************************************

CGB8           GACTCCTCTTCCTCAAAGGCCCCTCCCCCAGCCTTCCAAGTCCATCCCGACTCCCGGGG 480
CGB5           GACTCCTCTTCCTCAAAGGCCCCTCCCCCAGCCTTCCAAGTCCATCCCGACTCCCGGGG 480
CGB            GACTCCTCTTCCTCAAAGGCCCCTCCCCCAGCCTTCCAAGCCCATCCCGACTCCCGGGG 480
CGB7           GCCTCCTCTTCCTCAAAGGCCCCTCCCCCAGCCTTCCAAGTCCATCCCGACTCCCGGGG 480
               * ************************************** *******************
                                                 CGB_coding_R
CGB8           CCCTCGGACACCCCGATCCTCCCACAATAAAGGCTTCTCAATCCGCAAAAAAAAAAAAAA 540
CGB5           CCCTCGGACACCCCGATCCTCCCACAATAAAGGCTTCTCAATCCGCA------------- 527
CGB            CCCTCGGACACCCCGATCCTCCCACAATAAAGGCTTCTCAATCCGC-------------- 526
CGB7           CCCTCAGACACCCCGATCCTCCCACAATAAAGGCTTCTCAATCCGCA------------- 527
               ***** ****************************************

CGB8           AAAA 544
CGB5           ----
CGB            ----
CGB7           ----
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