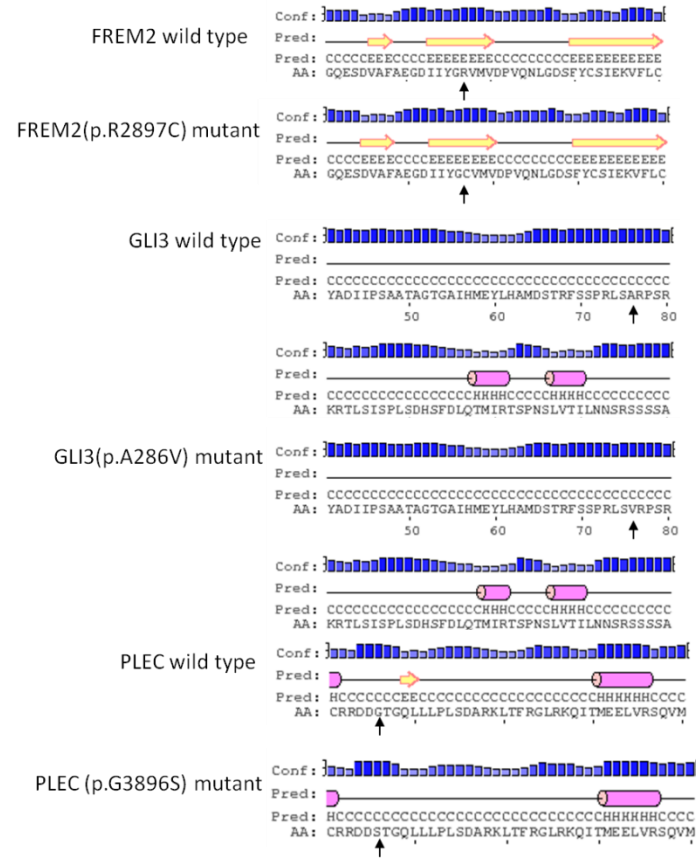
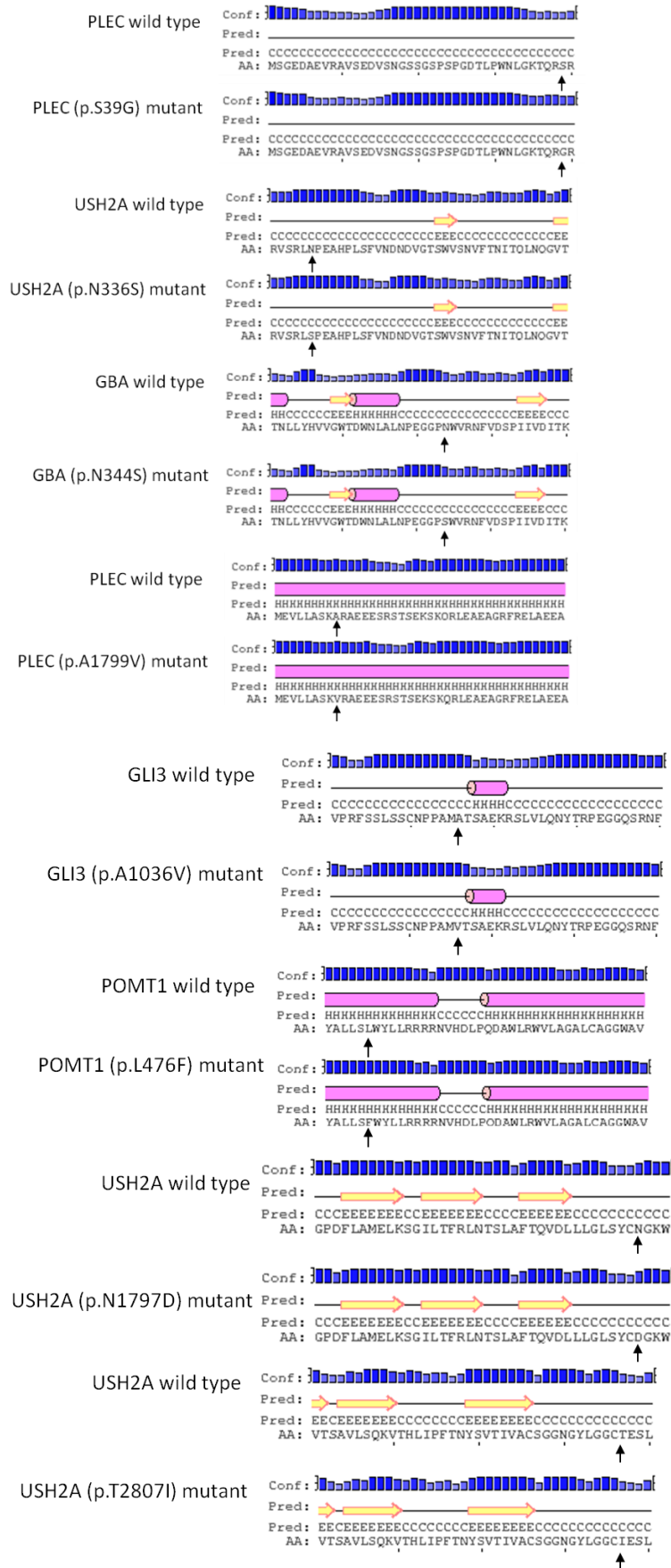







Supplementary Fig. 3 Predicted secondary structures of the wild and mutant protein sequences flanking the remaining candidate rare mutations. The diagrams show the protein sequences with their secondary structures and their confidence values at the aligned positions. The secondary structure is annotated as follows: pink cylinder (alpha-helix); yellow arrow (beta-sheet); black line (coil); Conf, confidence; Pred, predict; H in Pred line (Helix); C in Pred line (coil); E in Pred line (sheet); AA, amino acid; ↑, mutant amino acid.





Conf: 
 Pred: 
 Pred: EEEEEEECCEEEEEECCCCCEEECCCCCEEEEEEE
 AA: KEYQIRQVGGLIHDTDDRQKTVTGLQPYTNYSTLTA



Conf: 
 Pred: 
 Pred: EEEEEEECEEEEEEECCCCCEEECCCCCEEEEEEE
 AA: KEYRIQVGKGLINTDTTDRRQHTVTGLQPYTNYSFTLT



Conf: 
 Pred: 
 Pred: CCEEEEEEEECCECCCCCEEEECCECCCCCCCCCE
 AA: YTNYSFTLTACTSAGCTSSPEFLGQTLQAPEGVWVTPRH



Conf:
 Pred:
 Pred: CCCEEEEEEECCCECCCCCEEEECCECCCCCEEE
 AA: YTSYSFTLTACTSAGCTSSPEFLGQTLQAPEGVWVTPR



Conf:
 Pred: 
 Pred: CCCCCCEEEEECCCEEEEECCCCCCCCEEEEEEEC
 AA: PEGVWTPRHIIINSTTVELYWSLPEKPNGLVSOYOLSRN

Conf: 
 Pred: 
 Pred: CCCCCCEEEEECEEEEECECCCCCEEEEEEEEC
 AA: PEGVWTPRHIIINSTVELYWSLPEKLNGLYSOYLSRN

Conf: 
 Pred: 
 Pred: EEEEEEEEEECCECCCCCEEEEEEEEECCCCCEEEEC
 AA: SGLNRFQFLFRRLDPFTLYTLTLEACTRAGCAHSAPOPLWT

Conf: 
 Pred: 
 Pred: EEEEEEEECCECCCCCEEEEEEEECCECCCCCEEEEC
 AA: SGLNHOLFRRLOPFTLYTLTLEACTRAGCAHSAPOPLWT

Conf: 
 Pred: 
 Pred: CCCCCCCCCCEEEEECEEEEEEECCCCCEEEEE
 AA: TLEAAPSEVSPDLWAVSAQMNVCWSPPTVQNGKITKYL

Conf: 
Pred: 
Pred: CCCCCCCCCCEEECCCEEEEEEECCCCCEEEEE
AA: TLEAAPSEVSPDNLWAVSATQNMVCWSPTTQNKGTTKYL