Supplementary information, Figure S2

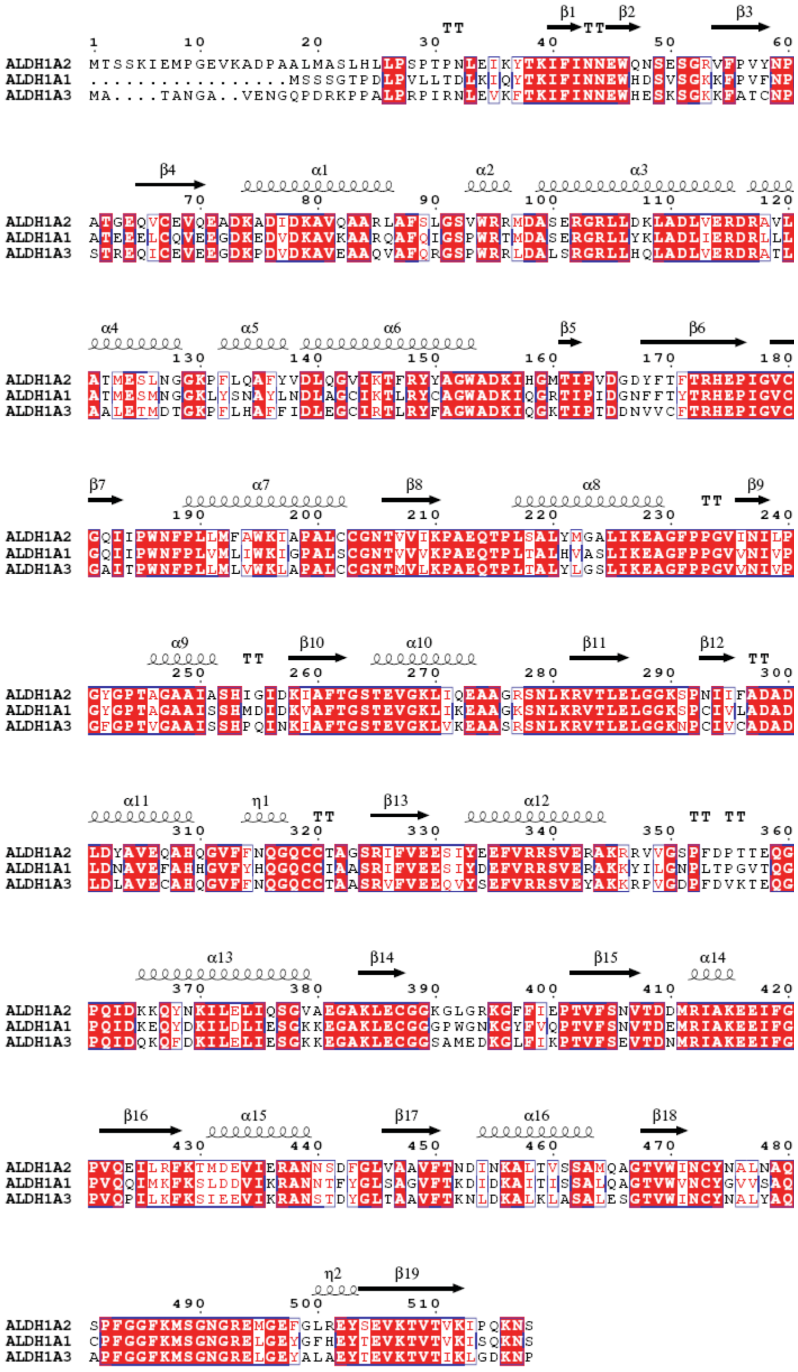

Figure S2 The members of mammalian ALDH1A family proteins are highly conserved in both amino acid sequences and secondary structures. The amino acid sequence alignments among ALDH1A1, 2 and 3 family members were performed using Clustal Omega, while the secondary structure alignments using ESPript 3.0. Here, the secondary structure of ALDH1A2 was presented above the alignments, according to the reported protein structures (PDB code: 4X2Q; also Moretti A *et al*. Sci Rep 6, 35710 (2016)). α-helices were displayed as squiggles, β-strands as strands, and β-turns as TT letters. Identical sequences among family members were depicted in white with a red background; while non-identical residues with similarity above 70%, were colored in red, and framed in blue.