



Supplementary Figure 1. Mapping of the 3D structure of the $\alpha\beta$ -tubulin heterodimer. A: 3D structure changes from the normal β -tubulin protein structure to the p.F341L mutation structure as indicated by SWISS-MODEL. SWISS-MODEL is a fully automated protein structure homology-modelling server. Arrows mean the position of 314. B: α -Tubulin is shown in green, and β -tubulin is shown in brown. The mutated residues are highlighted as blue spheres. Our mutation variant p.F341L is highlighted in red.