



Figure S1 Evolutionary conservation of amino acids that are mutated in human LATS1 and LATS2. Human LATS1 (top) and LATS2 (bottom) protein sequences that cover several mutated amino acids are aligned and compared with homologous sequences from other vertebrates, Drosophila and nematode. For vertebrate Lats1, they include *H. sapiens* NP_004681.1, *P. troglodytes* XP_001173355.1, *M. musculus* NP_034820.1 and *G. gallus* XP_419666.2. Vertebrate Lats2 includes *H. sapiens* NP_055387.2, *P. troglodytes* XP_001149147.1, *M. musculus* NP_056586.2 and *G. gallus* XP_417143.3. For *D. melanogaster* Lats/Warts: NP_733403.1. For *C. elegans* Lats/Wts: NP_492699.1. Protein sequence alignment was performed by using MEGA 5.2.1 (TAMURA *et al.* 2011).

TAMURA, K., D. PETERSON, N. PETERSON, G. STECHER, M. NEI *et al.*, 2011 MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. *Mol. Biol. Evo.* **28**: 2731-2739.