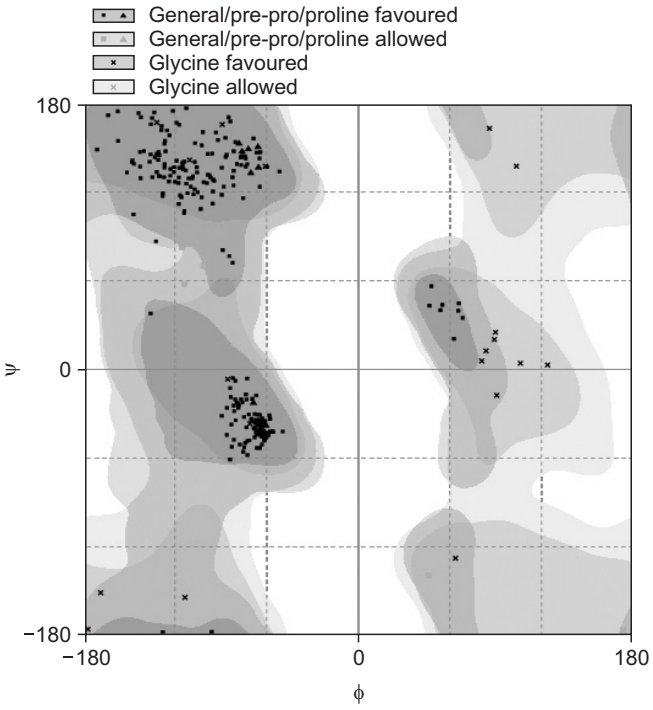

Residue [19: LEU] (−101.37, 69.86) in allowed region
Residue [48: MET] (−115.46, 82.42) in allowed region
Residue [127: SER] (45.86,−139.21) in allowed region
Residue [148: CYS] (173.47,−176.45) in allowed region
Residue [177: ASN] (−113.65, 57.73) in allowed region
Number of residues in favoured region (~98.0% expected): 283 (98.3%)
Number of residues in allowed region (~2.0% expected): 5 (1.7%)
Number of residues in outlier region: 0 (0.0%)

Supplementary Figure S4. Ramachandran plot and evaluation of residues for MT model of NAT2 of human. MT: mutant; NAT2: *N*-acetyl transferase.