

Supplementary Information

Figure S1. Protein structure predictions of OrufRPK1, OsI219RPK1, OsI9311RPK1 and OsJNipponRPK1. The 3D protein structure predictions of (A) OrufRPK1; (B) OsI219RPK1; (C) OsI9311RPK1 and (D) OsJNipponRPK1. LRR domain (red), kinase domain (green) and transmembrane helix (yellow).

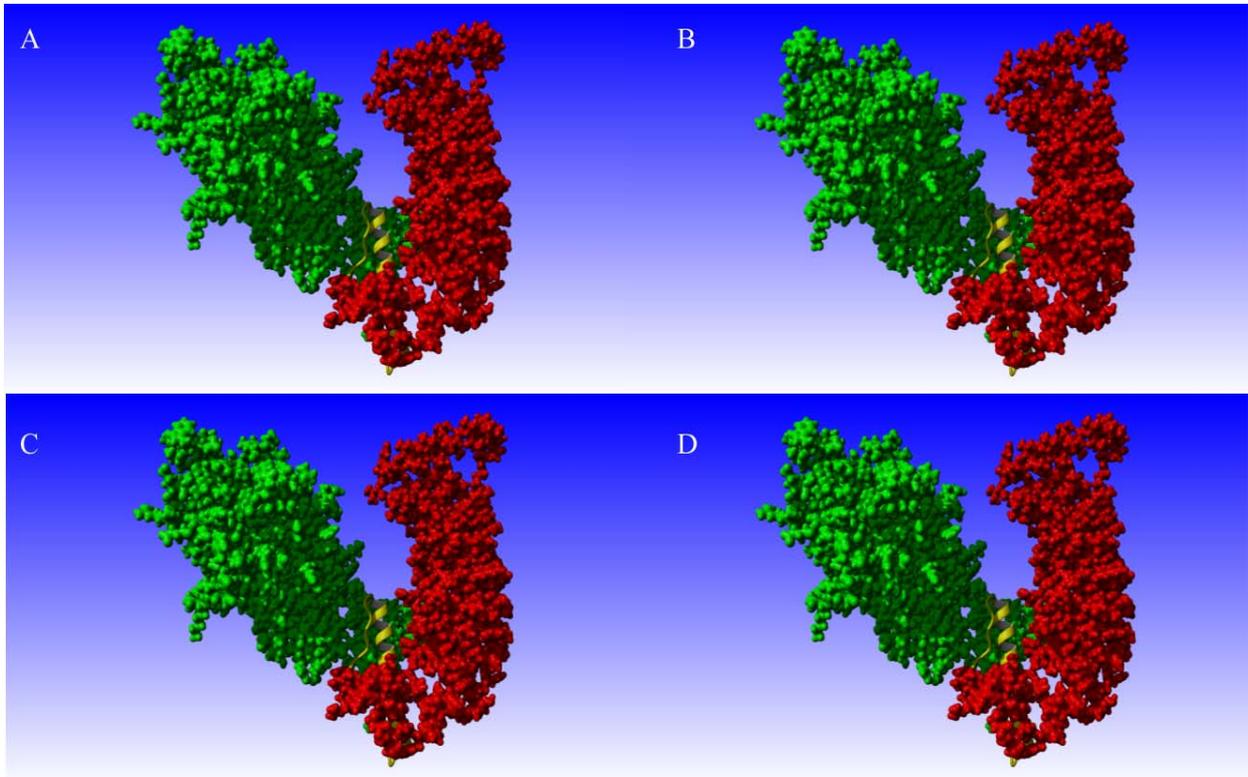


Figure S2. Structural superimposition of kinase domain of OrufRPK1 protein. Superimposition of (A) DFC-DFG motifs and (B) HRD-HGN motifs in kinase domain VII and kinase domain VIb respectively were analyzed. The DFG motif was selected from 2CPK.pdb; the HRD motif was selected from IHCL.pdb.

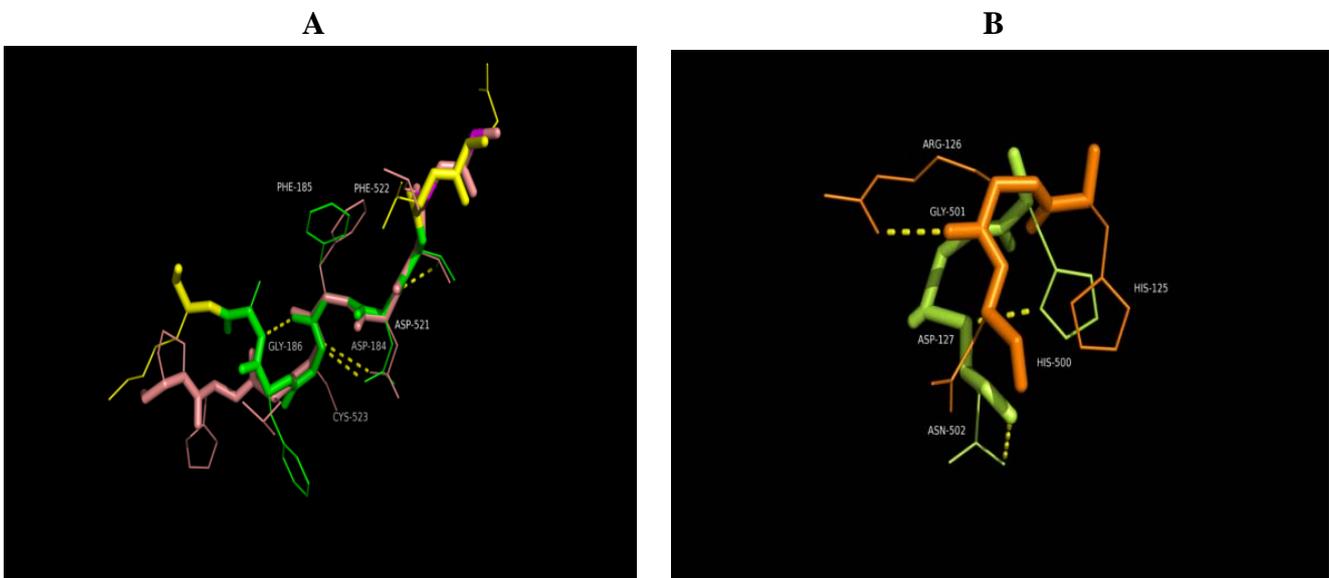


Figure S3. JCoDA output using sliding window analysis of pairwise dN/dS between *OrufRPK1*, *OsI219RPK1*, *OsI9311RPK1* and *OsNipponRPK1*. Adaptive selection dominates between amino acid 200 to 230 amino acid residues (*OsNipponRPK1* versus *OrufRPK1*) which are overlapped with a LRR domain (amino acid 192-214). *OsI219* = *OsI219RPK1*; *OsJNippo* = *OsNipponRPK1*; *OsI9311* = *OsI9311RPK1* and *Oruf* = *OrufRPK1*. All pairwise comparisons were performed using a window 200 and jump of 25.

