

CLUSTAL 2.1 multiple sequence alignment

[illegible]

Figure S2: Alignment of Wee1 amino acid sequences. Multiple sequence alignment using the ClustalW algorithm (<https://www.genome.jp/tools-bin/clustalw>) was performed using the following sequences: AAH70052.1 Wee1 homolog (*S. pombe*) [*Homo sapiens*]; NP_587933.1 protein kinase Wee1 [*Schizosaccharomyces pombe*]; KAF8293196.1 putative Wee1-like protein kinase [*Trypanosoma cruzi*].