Figure S1. Structural conservation of sequences in NDR kinases.

a.The N-terminal regulatory domain (NTR) has been shown to interact with MOB proteins in mammals, trypanosome and yeast[4,22,51,123]. Residues shown to be required for human MOB1A-binding are numbered and framed in red[22,51] (Hergovich *et al*. unpublished data). Phosphorylation of Thr74/75 in human NDR1/2 is required for kinase activity and probably also MOB1A-binding[22,26,30,31]. However, this phosphorylation site is not present in some yeast NDR kinases, but appears to be conserved in higher eukaryotes. **b.** The insert that separates the kinase subdomains VII and VIII ranges in size from 30 to 60 amino acids and it does not appear to be well conserved at the amino-acid level. However, it comprises a stretch rich in positively charged residues at its C terminus (marked in red). These residues have been shown to function as autoinhibitory sequence (AIS) in the case of human NDR1/2 (REF. 22). **c.** The hydrophobic motif (HM). The consensus sequence of the HM, a common and invariant regulatory feature of AGC kinases, is almost completely conserved within the entire NDR kinase family. The different levels of residue conservation are shown in graded tones of blue, where dark blue represents complete, and light blue moderate conservation.

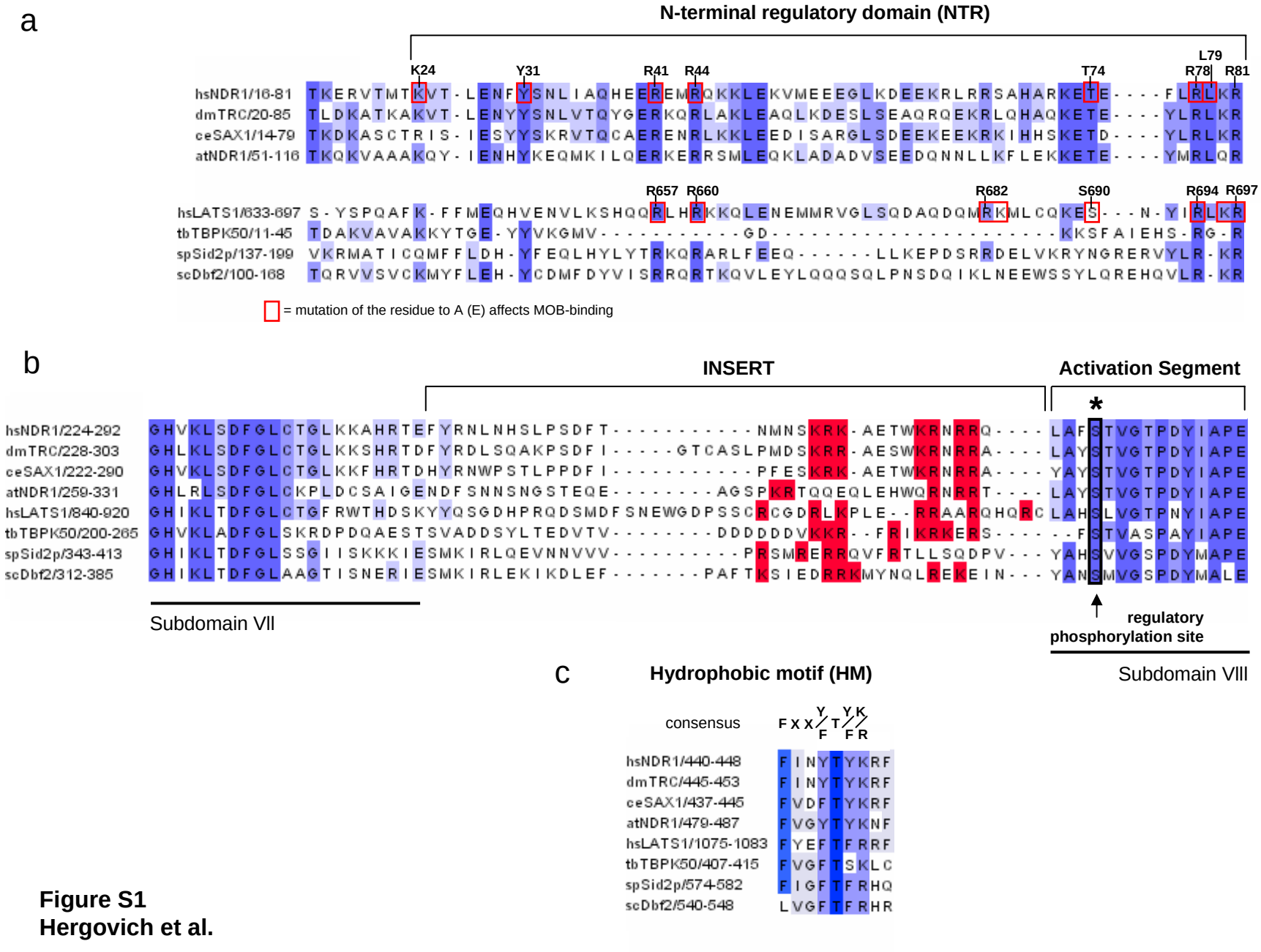

Figure S1
Hergovich et al.