Supplementary information S3 (Figure) | Structural variation in inactive AGC kinases

A) Structure of Akt2 in the active conformation (pdb-id 1o6k). The N-lobe and C-lobe of the kinase are coloured in shades of purple, the Activation-segment is shown in yellow, and the G-helix in salmon colours. pThr308 is shown in ball-and-stick representation with red oxygen atoms and purple phosphorous atoms, and the ATP analogue light blue with nitrogen and oxygen atoms indicated (blue and red respectively). The B and C helix and the activation segment are indicated. ’DFG-in’ denotes the active conformation of the DFG motif (black arrow). B) Structure of Akt2 in the inactive conformation (pdb id 1gzo). B and C helices are disordered, and the DFG-motif is in an unproductive conformation, in which the Phe residue occupies the position of the Adenine base (’DFG-out’). C) Structure of RSK1 in the inactive conformation (pdb id 2z7q). The B, C helices and activation segment are disordered, but the DFG motif is in an active conformation (’DFG-in’) and an ATP analogue is bound. D) Structure of MSK1 in the inactive conformation (pdb id 1vzo4). A three-stranded β-sheet (red circle), formed by the N-terminus, B/C helix residues and parts of the activation segment, occupies the position of the B and C helix in active AGC kinases. The ATP binding site is blocked. MSK1 needs to undergo major conformational changes in order to become active.