Fig. S3

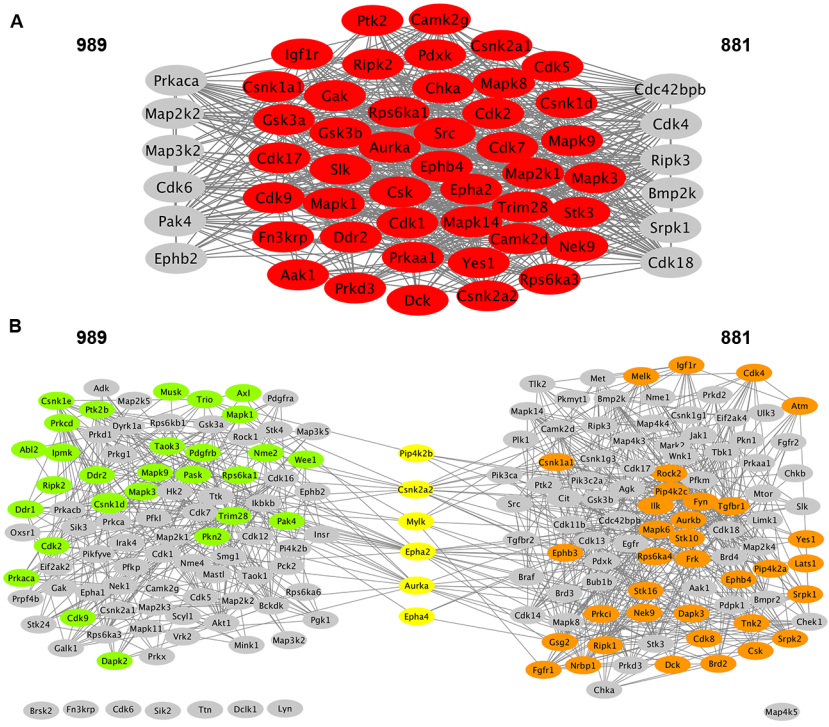

Fig. S3 Protein-protein interaction networks of 989 and 881 *Nf1* mutant kinomes. A. Multiplexed Inhibitor Beads (MIB) and quantitative mass spectrometry (MS) used to compare the kinomes of two parental *Nf1* mutant cell lines 989 and 881 grown under standard conditions. Protein interaction networks were visualized using Cytoscape software integrated with Genemania. The kinases associated with the 50 highest Log2LFQs of 989 were compared with the Log2LFQs of the highest 50 Log2LFQs of 881. Red shaded kinases represent common kinases with the highest MIB binding. B. The 100 kinases with the greatest Log2LFQs in 989 were divided by Log2LFQ values of the corresponding 100 kinases in 881. Similarly, the 100 greatest Log2LFQs of 881 were divided by Log2LFQs of the respective kinases in 989. Yellow shaded kinases are in common; green shading highlights kinases in 989 that demonstrate direct physical interaction with the common kinases; orange shading denotes kinases demonstrating direct physical interaction with common kinases in 881. C. Cell proliferation of parental cell lines 989 and 881 treated with Aurora inhibitors MLN8237, AZD1152 and VX680 was measured by MTS assay. Cell viability was assessed after 72 hours of exposure (*P<0.05; **P<0.01; ns, not significant). D. Western blot analysis evaluating the phosphorylation of Aurora A, B and C in response to Aurora inhibitors MLN8237, AZD1152 and VX680.