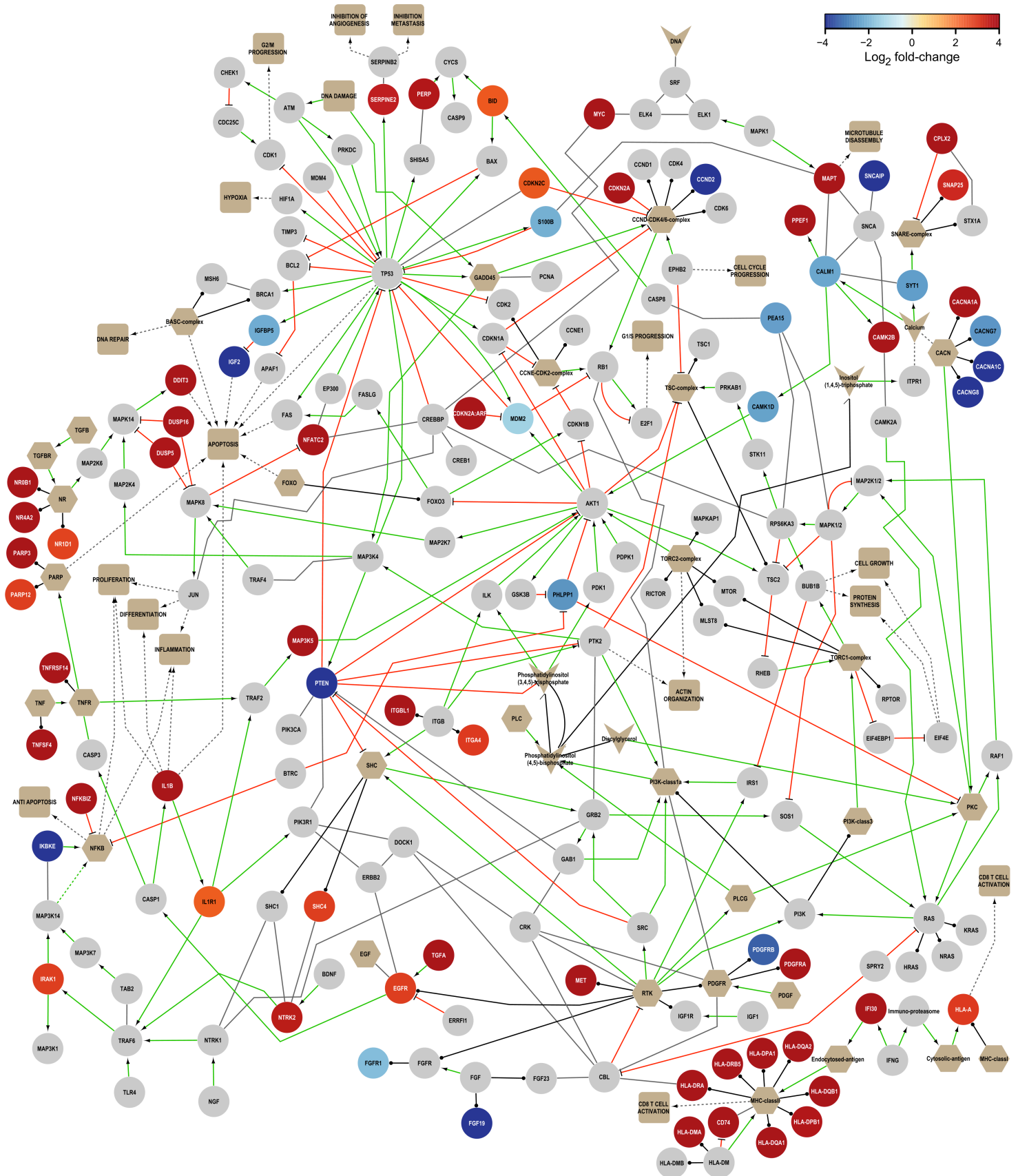




Integrated pathway map. *De novo* assembled pathway composed of 239 nodes, including known glioma-affected pathways as well as relevant proliferation, cell survival and apoptosis pathways. There are 182 nodes representing individual genes, depicted as circles and colored according to expression fold-change between the GNS and NS lines (see color key), or grey unless the expression difference was statistically significant at 10% FDR. Gene complexes and families (hexagons), small molecules (chevrons) and affected cellular processes (squares) are also included. Edges indicate *activation* (green), *inhibition* (red), *contains* (black with circular tip), *becomes* (black with half arrow) and other interactions (grey).