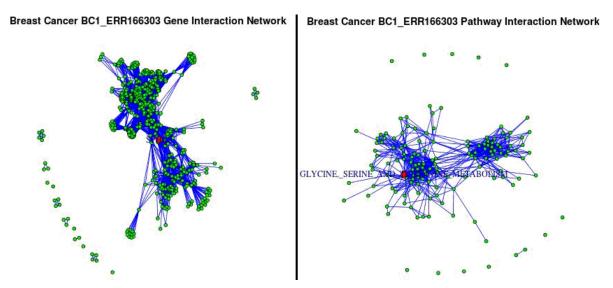
Analysis of Pathway and Gene interaction networks

Results of graph theory based analysis of 11 non-BRCA1/BRCA2 breast cancer patients are presented here. It has included all the genes in KEGG cancer pathways that have been mutated in various samples. The central pathways and genes (betweenness) measured through graph theory are also represented for each breast cancer sample. It also shows the pathway-pathway and the gene-gene graphs that have been constructed for 11 cancer patients. It is observed that the purine metabolism (BC2, BC6, BC11) and propanoate metabolism (BC5, BC10) pathways are most commonly affected and RAF1 (BC2, BC6, BC11) and PRKCA (BC5, BC10) are affected central genes.

ERR166303 (BC1)

Central Pathway = GLYCINE, _SERINE_AND_THREONINE_METABOLISM

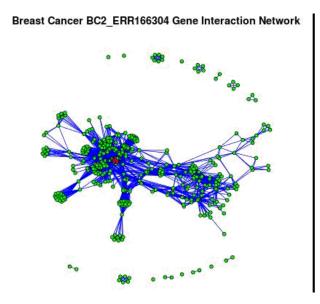
Central Gene = SPHK2

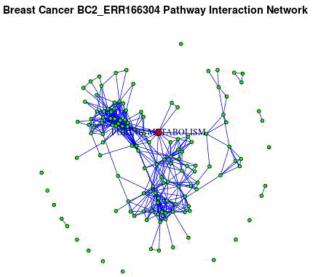


ERR166304 (BC2)

Central Pathway = PURINE_METABOLISM

Central Gene = RAF1

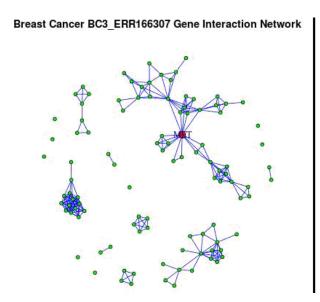


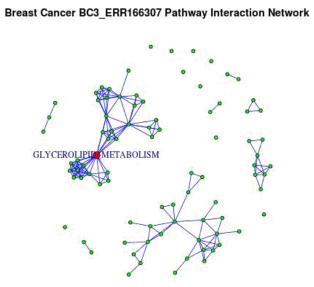


ERR166307 (BC3)

Central Pathway = GLYCEROLIPID_METABOLISM

Central Gene = MET

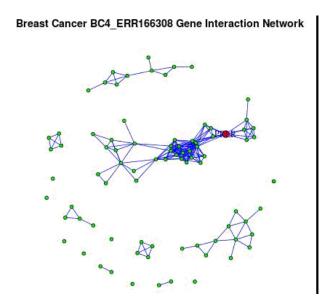


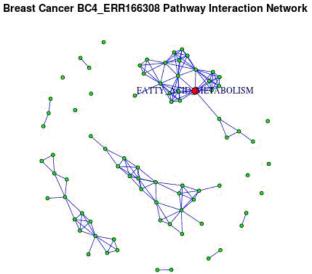


ERR166308 (BC4)

Central Pathway = FATTY_ACID_METABOLISM

Central Gene = PRLR

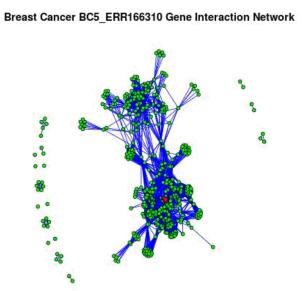


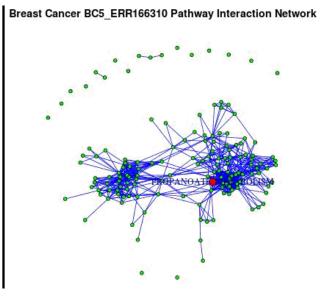


ERR166310 (BC5)

Central Pathway = PROPANOATE_METABOLISM

Central Gene = PRKCA

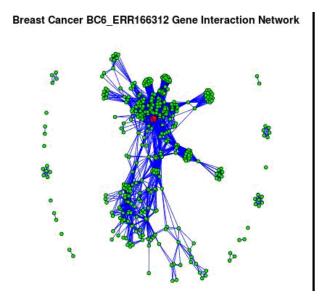


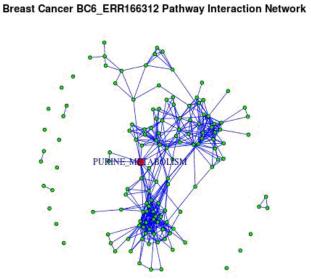


ERR166312 (BC6)

Central Pathway = PURINE_METABOLISM

Central Gene = RAF1

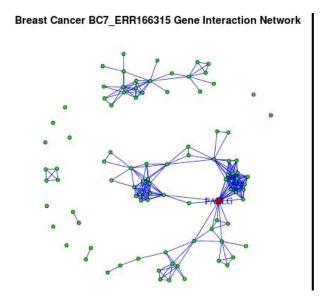


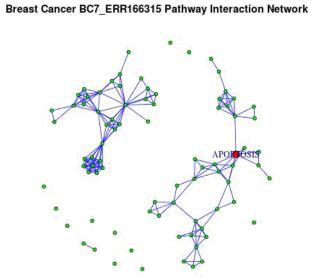


ERR166315 (BC7)

Central Pathway = APOPTOSIS

Central Gene = FASLG

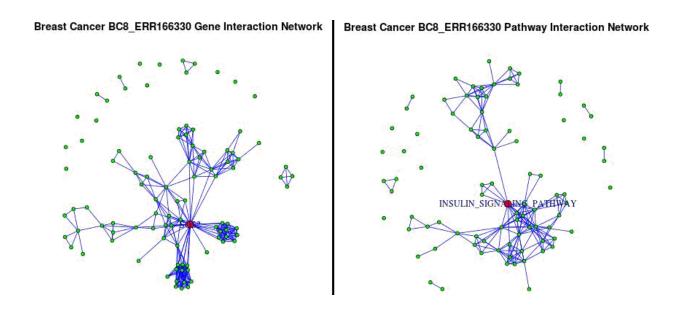




ERR166330 (BC8)

Central Pathway = INSULIN_SIGNALING_PATHWAY

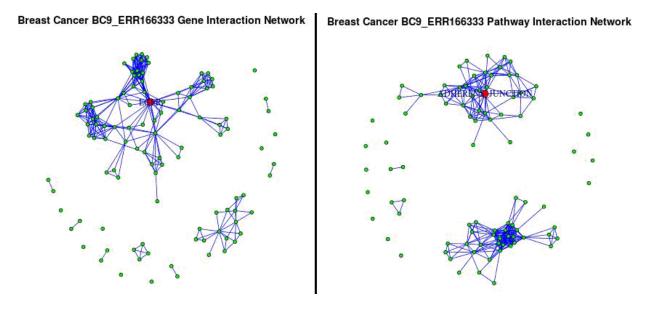
Central Gene = SOS2



ERR166333 (BC9)

Central Pathway = ADHERENS_JUNCTION

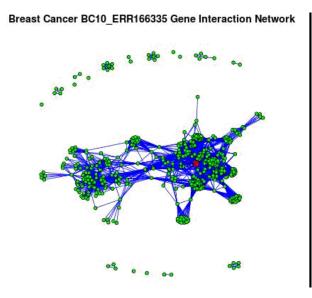
Central Gene = EGFR

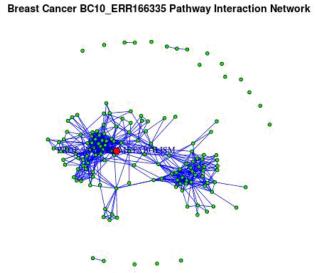


ERR166335 (BC10)

Central Pathway = PROPANOATE_METABOLISM

Central Gene = PRKCA





ERR166336 (BC11)

Central Pathway = PURINE_METABOLISM

Central Gene = RAF1

