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Abstract Topic: - Cancer

Abstract Title: - Data Exploration Analysis of Breast Oncogenomes

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Aims: - To explore mechanisms associated with BC, large-scale analyses are required focusing on gene mutation in cellular pathways

Methods: - Mutational data of 18,373 BC genes from 9,555 BC samples via cBioportal. BC genes with mutational count cut-off >40, 1,174 genes were obtained. It was further segregated into different BC-tiers based on mutational frequency. 1,174 BC genes were used for further analysis. Pathway enrichment analysis was carried out using EnrichR suite and protein-protein interaction was performed using STRING database

Results: - We have classified BC genes into five tiers based on mutational frequencies with tier I possessing 12 BC genes with mutational frequencies >5%. In BC tier-I five BC genes have >10% frequencies as PIK3CA (35.7%), TP53 (34.3%), GATA3 (11.5%), CDH1(11.4%) and MUC16 (11%). Next four BC tiers have mutational frequencies <5%, <2%, <1.5%, and <1% consisting of 56, 41, 118 and 947 BC genes, respectively. From pathway enrichment analysis we identified several other important pathways in which BC genes play a crucial role like developmental biology, and signal transduction. We have emphasized the importance of BC genes from all tiers and their role in BC. Using a confidence score of 0.700, we constructed PPIN and showed interactions between proteins of multiple pathways and their influence.

Conclusions: - To our best knowledge, this study is the most comprehensive data exploration analysis of BC with sample size of 9,555.

Keywords: - We have classified BC genes into five tiers based on mutational frequencies with tier I possessing 12 BC genes with mutational frequencies >5%. In BC tier-I five BC genes have >10% frequencies as PIK3CA (35.7%), TP53 (34.3%), GATA3 (11.5%), CDH1(11.4%) and MUC16 (11%). Next four BC tiers have mutational frequencies <5%, <2%, <1.5%, and <1% consisting of 56, 41, 118 and 947 BC genes, respectively. From pathway enrichment analysis we identified several other important pathways in which BC genes play a crucial role like developmental biology, and signal transduction. We have emphasized the importance of BC genes from all tiers and their role in BC. Using a confidence score of 0.700, we constructed PPIN and showed interactions between proteins of multiple pathways and their influence.