Interactome analysis of FGFR2 – a potential therapeutic target in breast cancer.

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Breast cancer (BC) is a leading cause of cancer death among women and results from multivariate factors of environmental and genetic origin. One of most consistent genetic risk factors for breast cancer is the single nucleotide polymorphism (SNP) rs2981582 that sits inside the intron 2 of the Fibroblast Growth Factor Receptor 2 (FGFR2) gene. The encoded protein, fgfr2, is a tyrosine kinase receptor that acts as a housekeeping molecule at the mammary tissue – amongst other tissues – and it is implicated in several cellular processes, such as cell cycle control, proliferation, migration, tissue repair and tumorigenesis. It has been demonstrated that the risk SNP rs2981582 is able to modulate the expression of the FGFR2 gene. However, the downstream effects in breast cancer at protein level are yet to be clarified. Here we used a data mining approach to reconstruct the fgfr2 interactome from a wide range of databases (STRING, HRPD, IntAct, BIOGRID, DIP, I2D and MINT). The resulting curated protein-protein interaction (PPI) network comprises the most significant proteins that establish interactions with the fgfr2 protein in several tissues and in non-tumor conditions. Along with previous studies, the fgfr2 PPI network might provide a rich groundwork to address systemic questions on how fgfr2 might affect signaling pathways related with breast cancer. Once we have concluded the curated PPI network, proper trimming will then be performed in order to map a mammary tissue specific fgfr2 PPI network, which will be validated through knockdown experimental data. We anticipate that this tissue-specific PPI network will allow us to exhaustively explore other relevant breast cancer risk SNPs in the context of fgfr2 signalling events.