

Supplementary material for the manuscript:

**SFPQ rescues F508del-CFTR expression and function in cystic fibrosis
bronchial epithelial cells**

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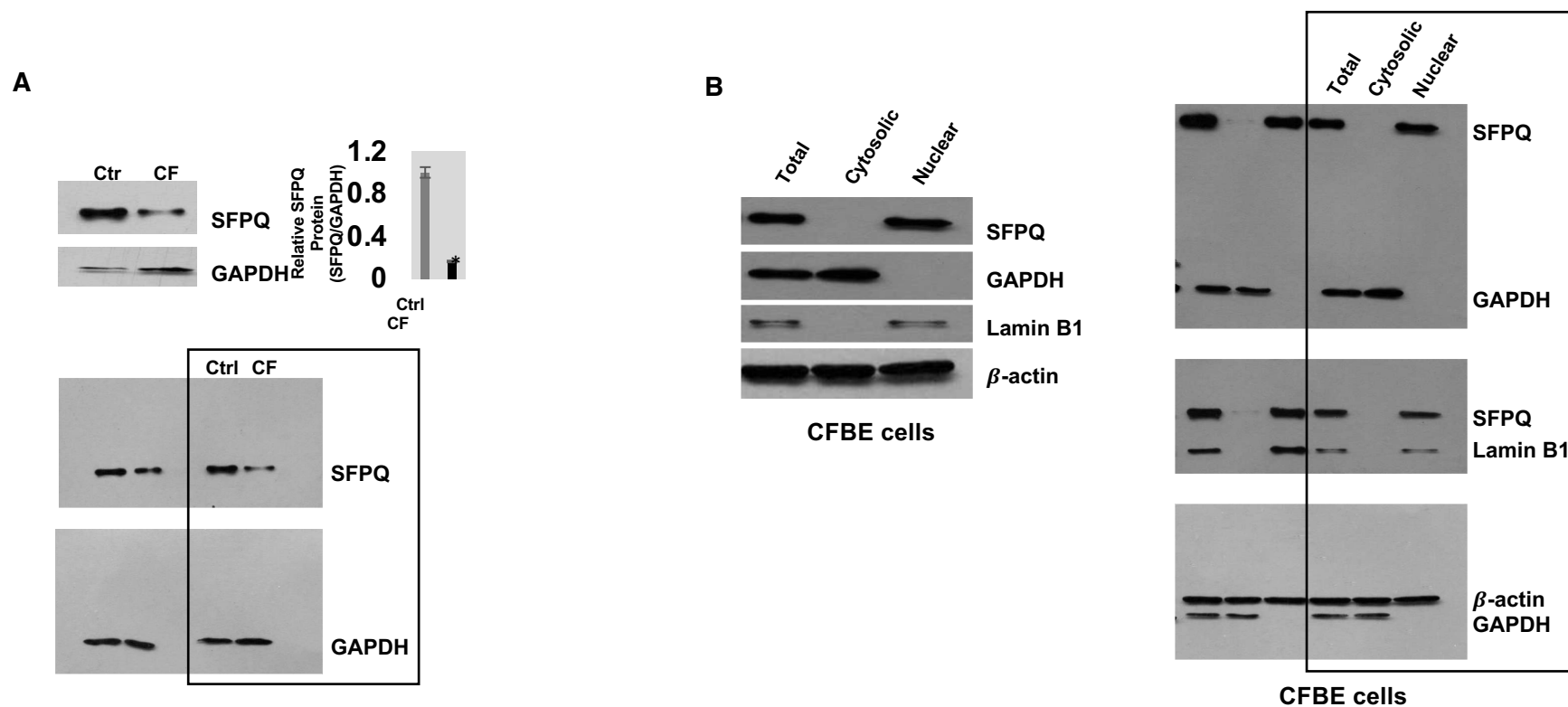


Figure S1: Expression of SFPQ protein in CF lung cells. (A) SFPQ protein was analyzed by immunoblot in CF and control cells and normalized to GAPDH protein levels. (B) Localization of SFPQ protein was analyzed by immunoblot CFBE cells containing the F508del mutation. The controls are indicated. The same blots were probed with multiple antibodies for normalization (endogenous controls) as well as subcellular fractionation (GAPDH is in the cytosolic fraction while Lamin B1 is exclusive to the nuclear fraction).

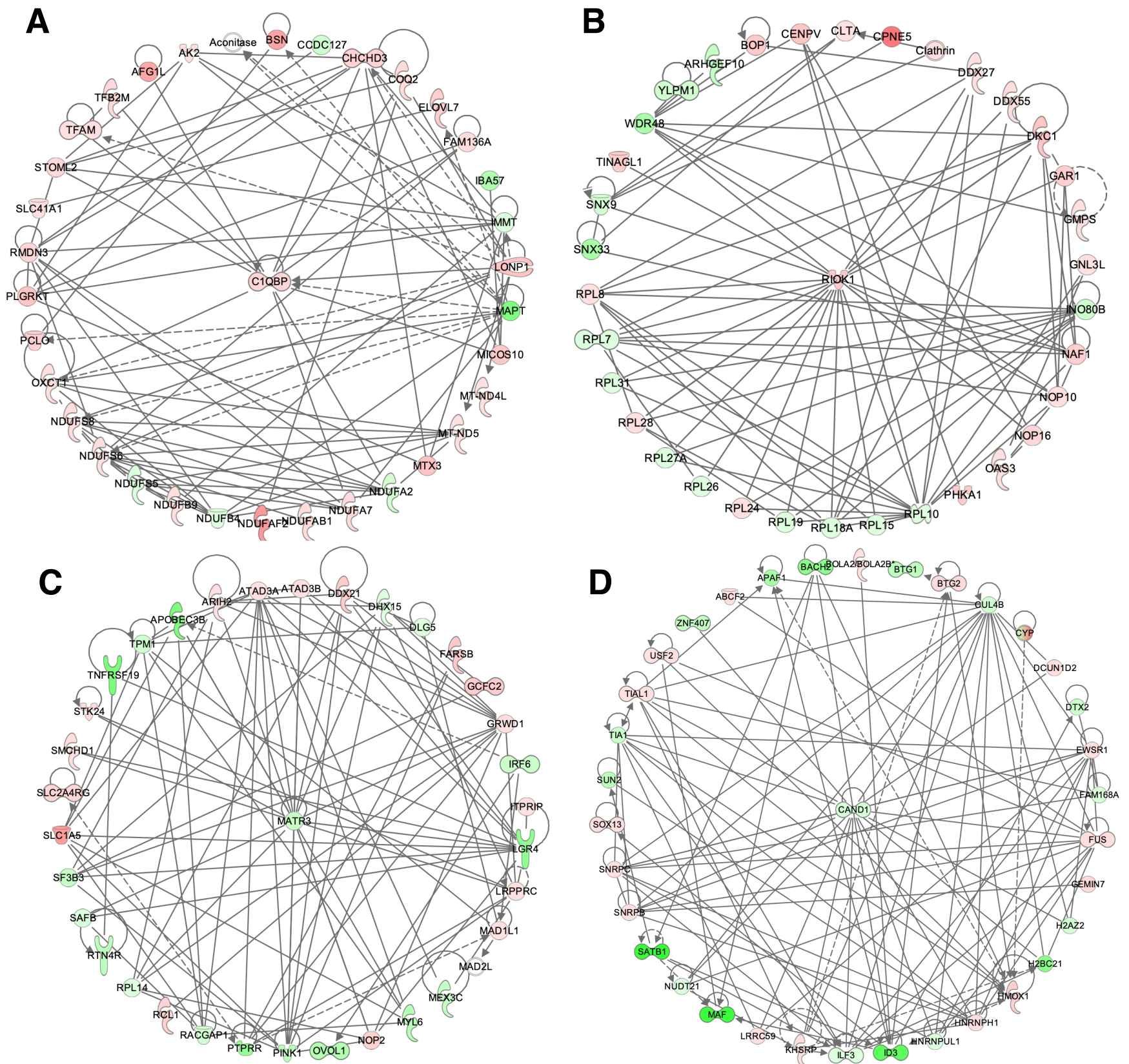


Figure S2. Ingenuity Pathway Analysis gene networks. The radial representations indicate the most enriched networks in SFPQ over-expressed and control CFBE41o- cells. **(A)** Network 5: cell signaling, post-translational modification, protein synthesis; **(B)** Network 6: protein synthesis, RNA damage and repair, RNA post-transcriptional modification; **(C)** Network 7: cell cycle, organismal injury and abnormalities, RNA post-transcriptional modification; **(D)** Network 8: cell cycle, post-translational modification, RNA post-transcriptional modification. Green color denotes down regulation, red color denotes upregulation whereas grey color denotes those present within our data set but not changed significantly. Solid arrows represent the genes that interact directly, while dotted arrows represent indirect interactions between genes.

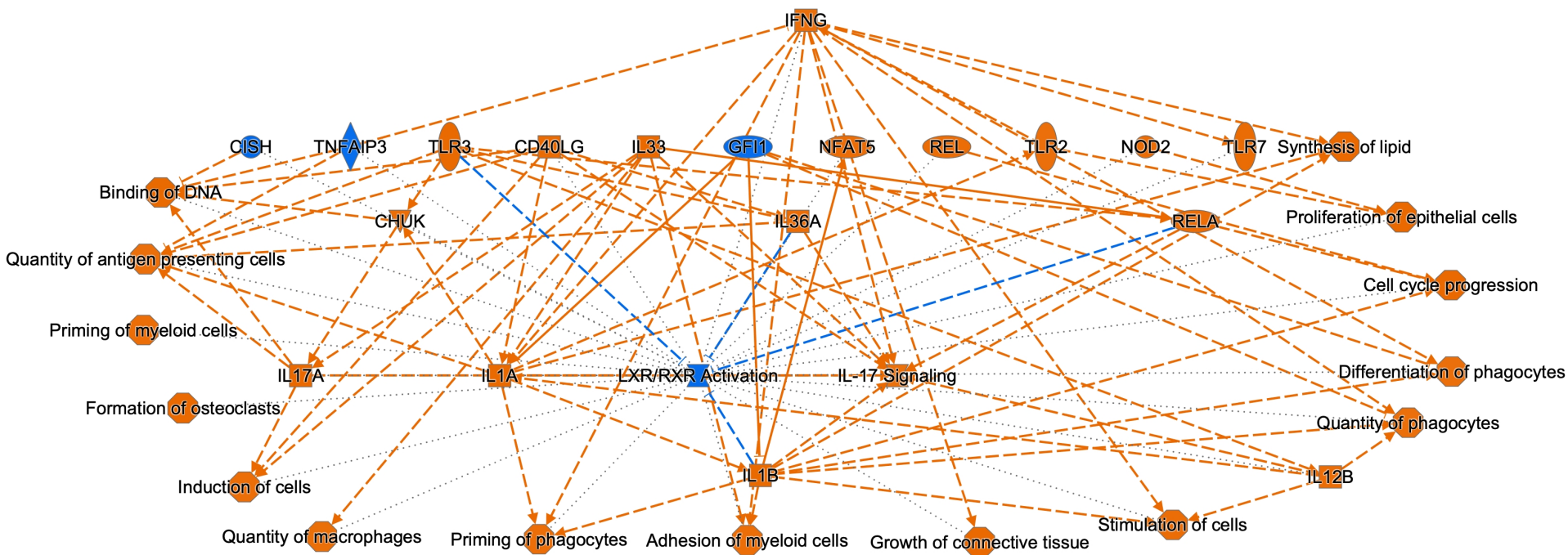


Figure S3. Graphical summary. The predicted key functions that are altered in SFPQ overexpressed versus control CFBE41o⁻ cells are indicated. Orange circles represent predicted activation of functions, blue circles represent predicted inhibition of functions. Solid arrows represent the genes that interact directly, while dotted arrows represent indirect interactions between genes.