

Supplementary Materials

Table of Contents

- Table S1. Genes demonstrating at least 2-fold difference in the transcription activity between lung cancer patients and healthy controls
- Figure S1. ATM Signaling pathway
- Figure S2. Role of BRCA1 in DNA Damage Response
- Figure S3. Base Excision Repair Pathway
- Figure S4. Role of CHK proteins in Cell Cycle Checkpoint Control
- Figure S5. Cell Cycle: G2/M DNA Damage Checkpoint Regulation
- Figure S6. DNA Double-Strand Break Repair by Non-Homologous End Joining
- Figure S7. Cyclins and Cell Cycle Regulation
- Figure S8. p53 Signaling
- Figure S9. Color and shape legends useful for IPA[®] pathway/network representation

Table S1. Genes demonstrating at least 2-fold difference in the transcription activity between lung cancer patients and healthy controls

Ingenuity Canonical Pathways	Molecules
ATM Signaling	ATM↓, CDC25A↑, CHEK1↑, MDC1↑, RAD51↑, RAD9A↑, RBBP8↑, RNF168↑, TP53↓, TP53BP1↑
Role of BRCA1 in DNA Damage Response	ATM↓, CHEK1↑, MDC1↑, MLH1↓, MSH2↓, RAD51↑, RBBP8↑, TP53↓
BER (Base Excision Repair) Pathway	APEX1↓, MPG↓, OGG1↓, PARP1↑, PNKP↑, TP53↓
Role of CHK Proteins in Cell Cycle Checkpoint Control	ATM↓, CDC25A↑, CHEK1↑, MDC1↑, RAD9A↑, TP53↓
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	ATM↓, CDK7↑, CHEK1↑, PRKDC↑, TP53↓
DNA Double-Strand Break Repair by Non-Homologous End Joining	ATM↓, PARP1↑, PRKDC↑
Cyclins and Cell Cycle Regulation	ATM↓, CHEK1↑, MDC1↑, MLH1↓, MSH2↓, RAD51↑, RBBP8↑, TP53↓
p53 Signaling	ATM↓, CHEK1↑, PRKDC↑, TP53↓
Mismatch Repair in Eukaryotes	EXO1↑, MLH1↓, MSH2↓
DNA Double-Strand Break Repair by Homologous Recombination	ATM↓, RAD51↑
NER (Nucleotide Excision Repair, Enhanced Pathway)	CDK7↑, DDB1↑, DDB2↑

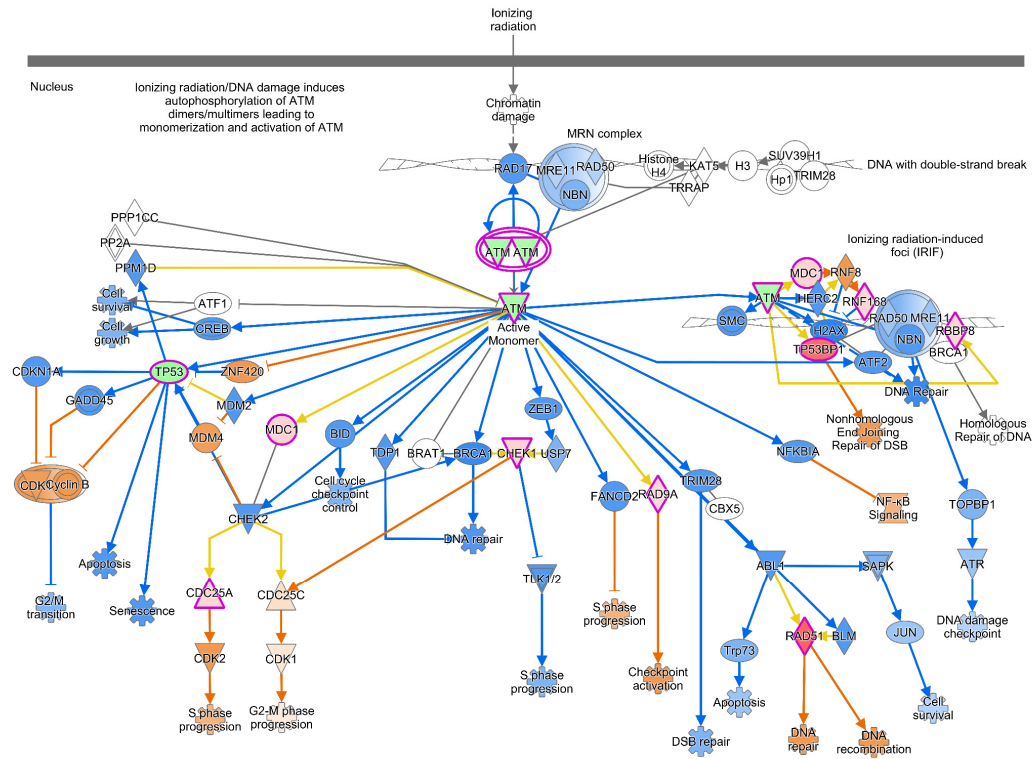


Figure S1. ATM Signaling pathway. Canonical pathways related to DNA damage response and repair from IPA® presenting statistically significant ($P < 0.05$) enrichment: ATM Signaling ($P = 3.03E-18$). Color and shape legends are presented in Figure S9.

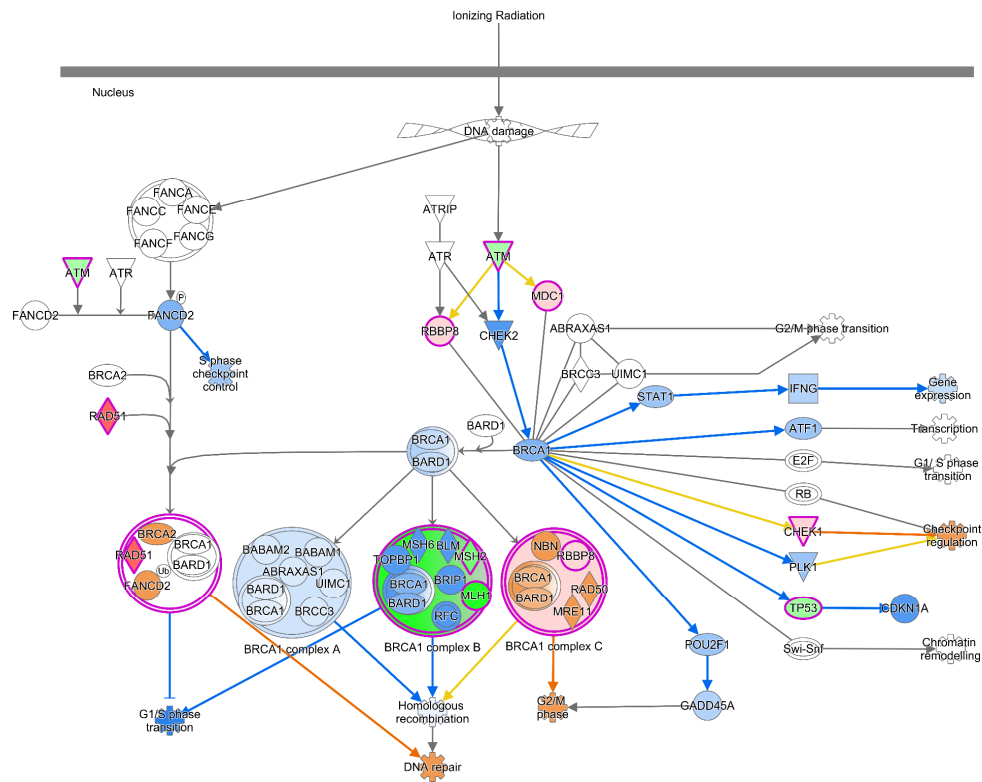


Figure S2. Role of BRCA1 in DNA Damage Response. Canonical pathways related to DNA damage response and repair from IPA[®] presenting statistically significant ($P < 0.05$) enrichment: Role of BRCA1 in DNA Damage Response ($P = 1.18 \times 10^{-14}$). Color and shape legends are presented in Figure S9.

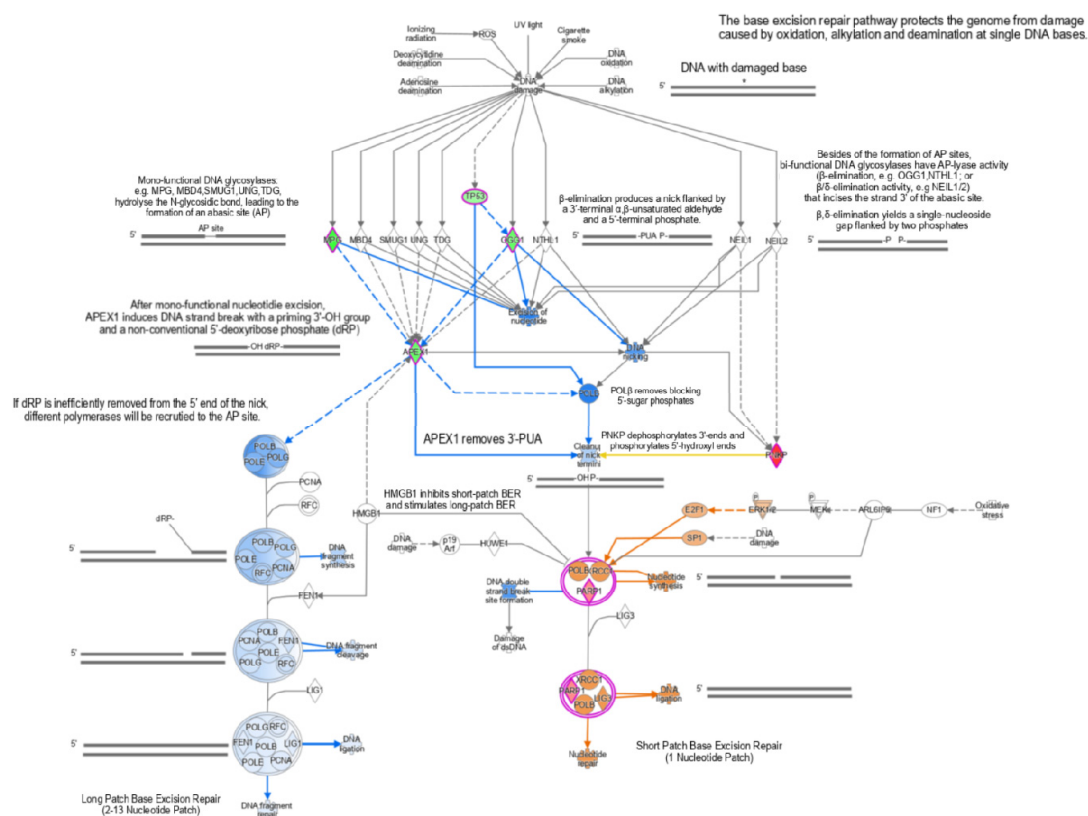


Figure S3. Base Excision Repair Pathway. Canonical pathways related to DNA damage response and repair from IPA® presenting statistically significant ($P<0.05$) enrichment: BER pathway ($P=4.84\text{E-}12$). Color and shape legends are presented in Figure S9.

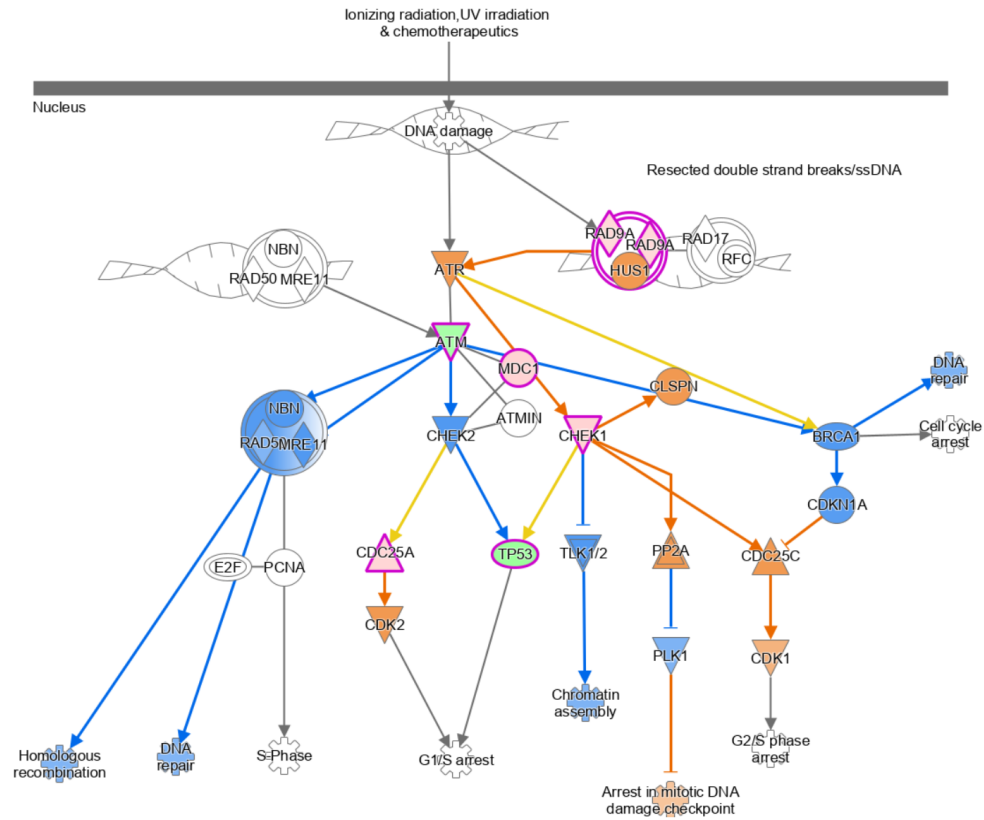


Figure S4. Role of CHK proteins in Cell Cycle Checkpoint Control. Canonical pathways related to DNA damage response and repair from IPA[®] presenting statistically significant ($P < 0.05$) enrichment: Role of CHK Proteins in Cell Cycle Checkpoint Control ($P = 2.46E-11$). Color and shape legends are presented in Figure S9.

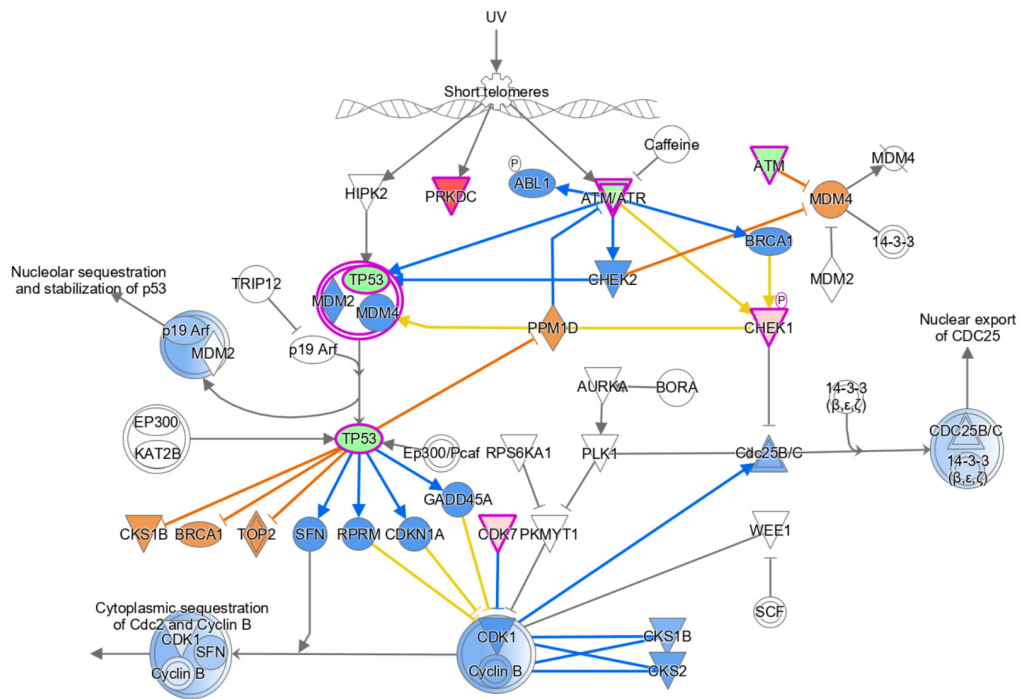


Figure S5. Cell Cycle: G2/M DNA Damage Checkpoint Regulation. Canonical pathways related to DNA damage response and repair from IPA® presenting statistically significant ($P < 0.05$) enrichment: Cell Cycle: G2/M DNA Damage Checkpoint Regulation ($P = 1.72 \times 10^{-9}$). Color and shape legends are presented in Figure S9.

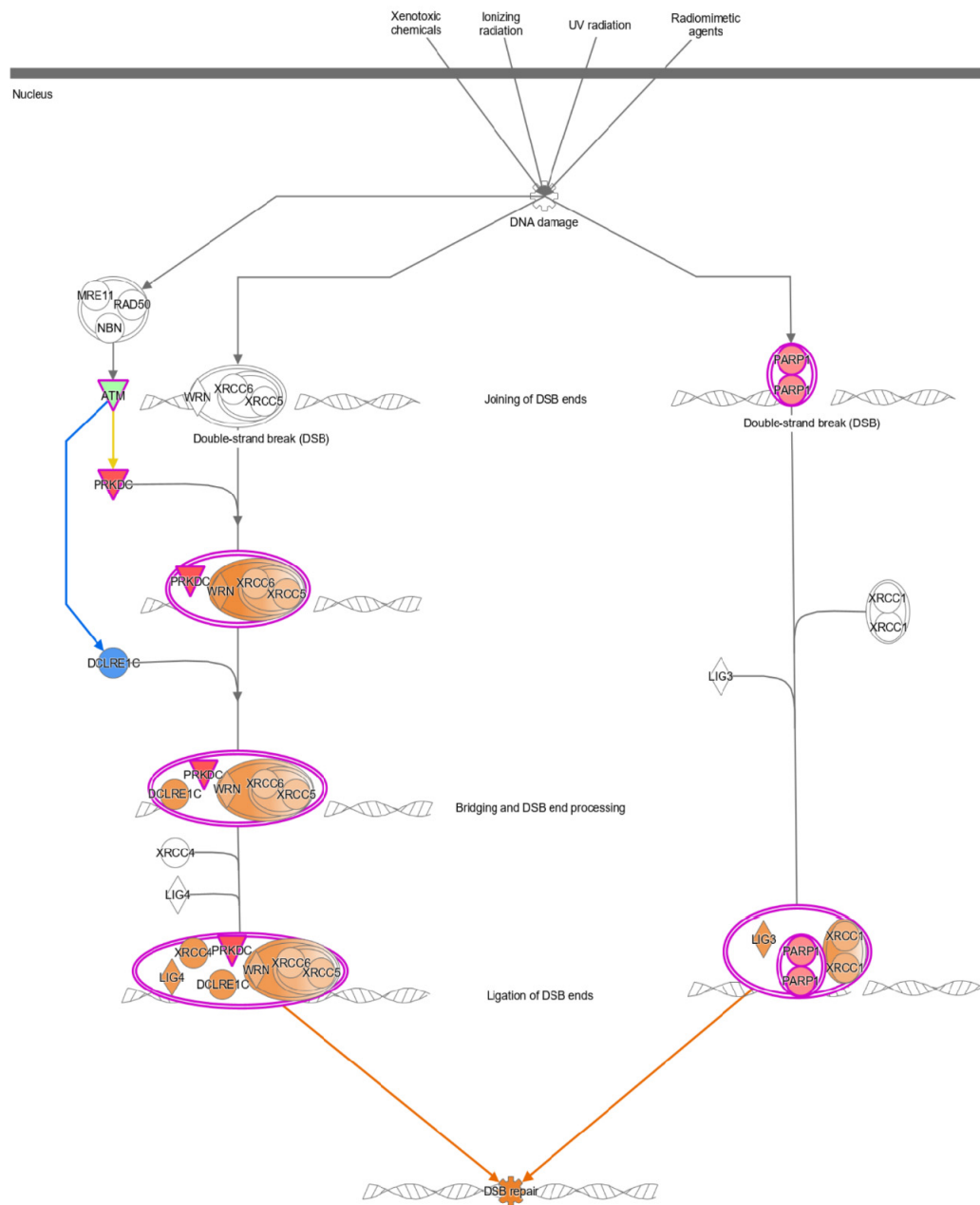


Figure S6. DNA Double-Strand Break Repair by Non-Homologous End Joining. Canonical pathways related to DNA damage response and repair from IPA® presenting statistically significant ($P < 0.05$) enrichment: DNA Double-Strand Break Repair by Non-Homologous End Joining ($P = 3.7E-07$). Color and shape legends are presented in Figure S9.

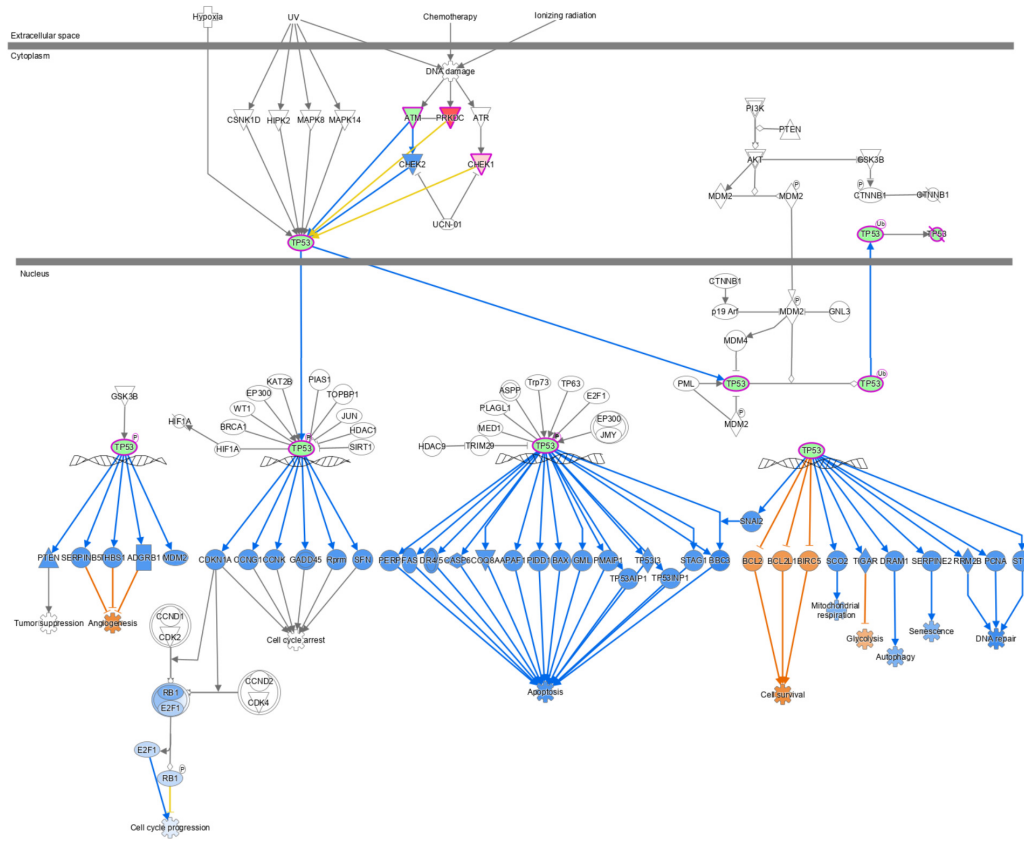


Figure S8. p53 Signaling. Canonical pathways related to DNA damage response and repair from IPA[®] presenting statistically significant ($P < 0.05$) enrichment: p53 Signaling ($P = 3.2E-06$). Color and shape legends are presented in Figure S9.

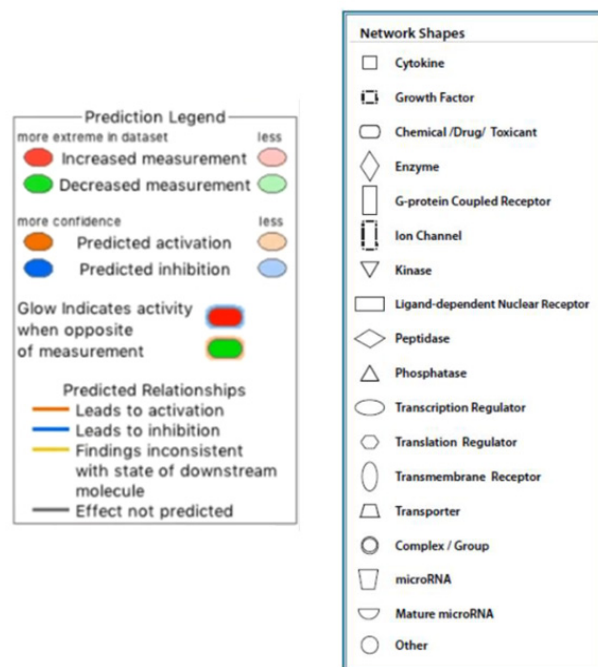


Figure S9. Color and shape legends useful for IPA[®] pathway/network representation.