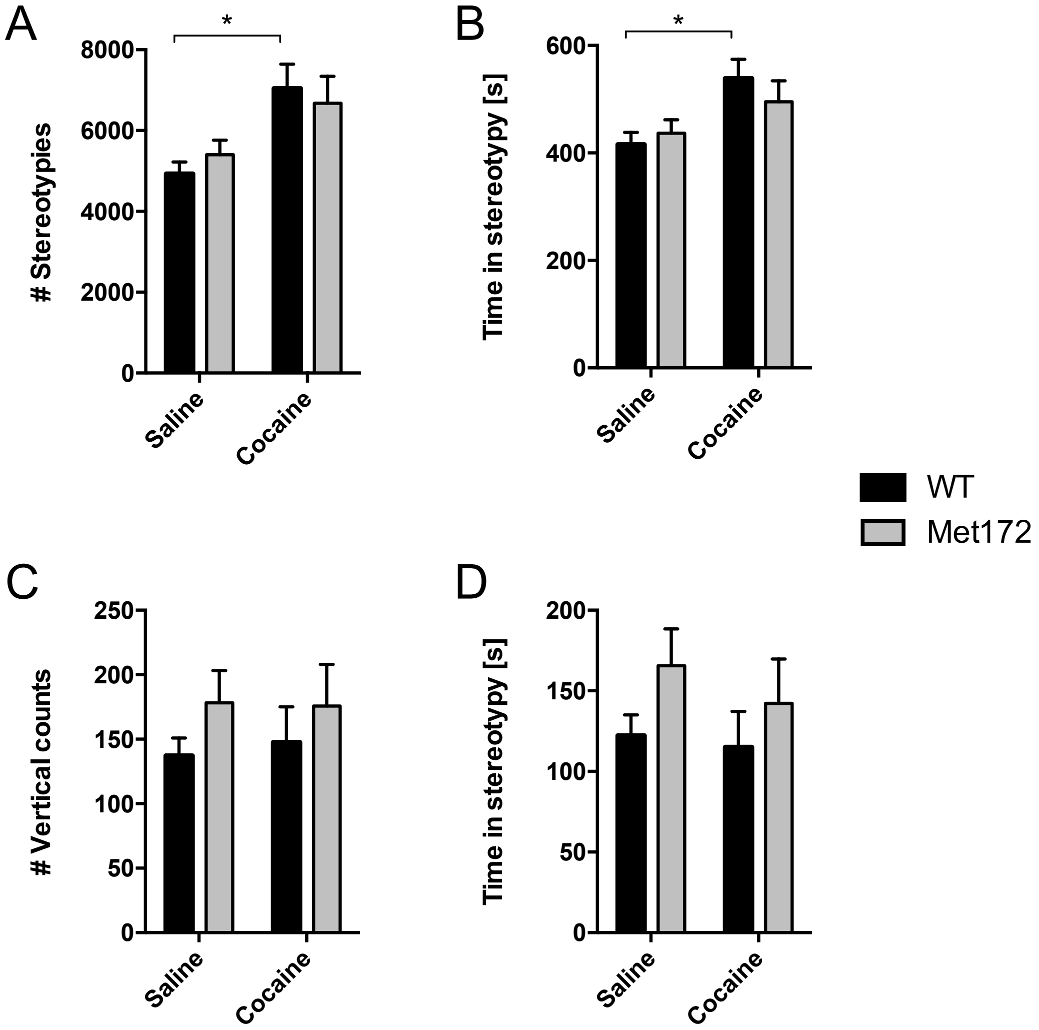
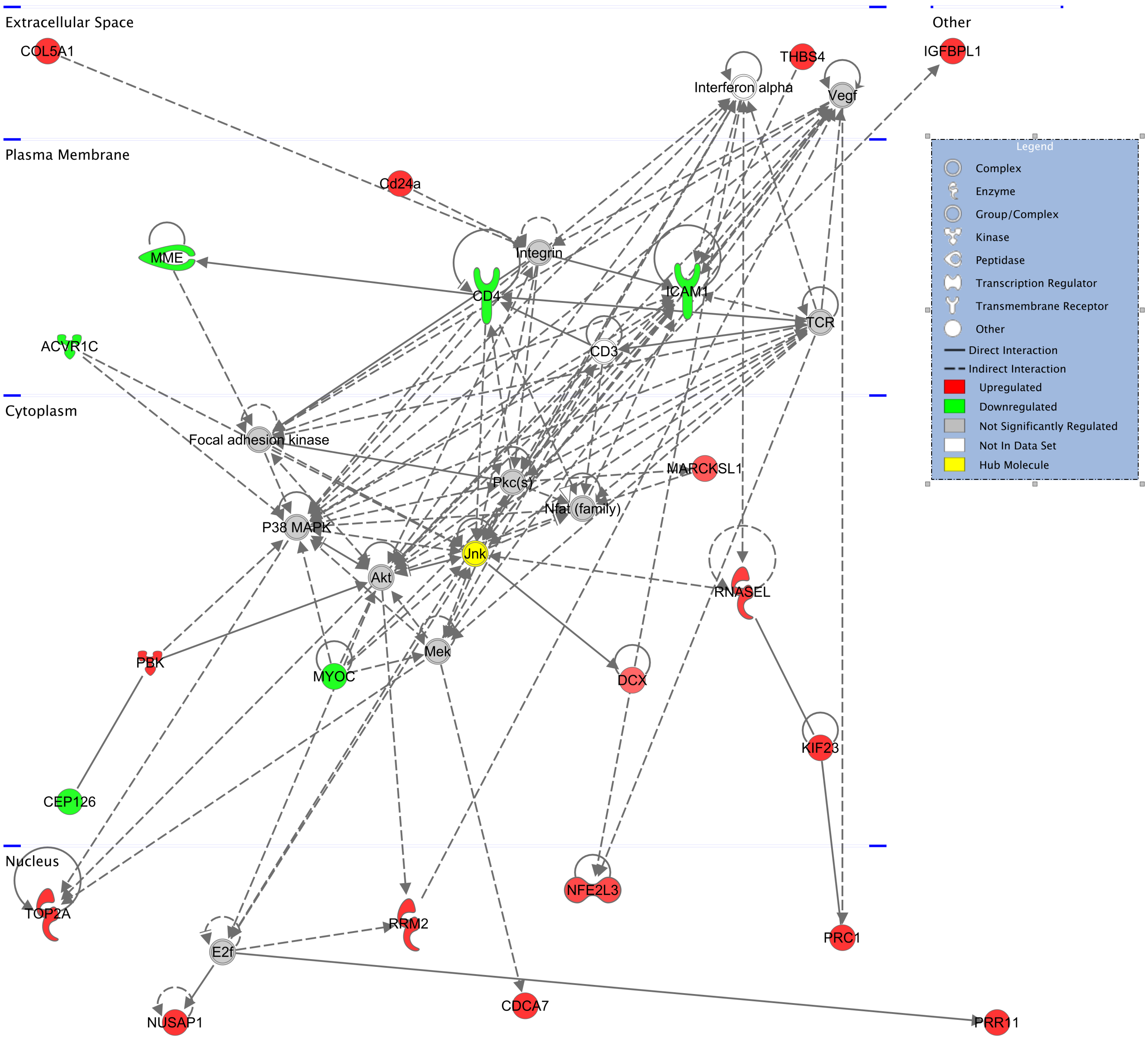


Figure S1: Stereotypies and vertical movements in the open field test in response to acute cocaine as a function of genotype. Number of stereotypies (A), time in stereotypy (B), number of vertical counts (C), and time vertical (D) during 50 min post injections. Saline (20 ml kg^{-1} i.p.) was administered in the first and cocaine (15 mg kg^{-1} cocaine i.p.) in the second session. Data represent mean ± S.E.M., n=28-31. Main treatment effect was significant in RM-2-way ANOVA. *P<0.05 in Sidak's post-hoc test.

Jnk hub network



Figures S2: Jnk related network, generated by IPA Path Designer (Qiagen). This gene network was significantly regulated ($P<0.05$ with the Fisher's Exact Test) in the NAc in response to acute cocaine (20 mg kg^{-1}, i.p.) in WT compared to SERT Met172 mice. Network is centered around the network hub gene Jnk. Seed molecules from the list of differentially regulated genes in WT compared to SERT Met172 mice are shown in the form of protein networks in red (upregulated in WT) and green (downregulated in WT), along with other molecules (gray and white) that connect smaller networks to make larger networks. Interaction or regulation between proteins or complexes is shown with arrows (activation) or blunt-ended lines (inhibition).

UBC hub network

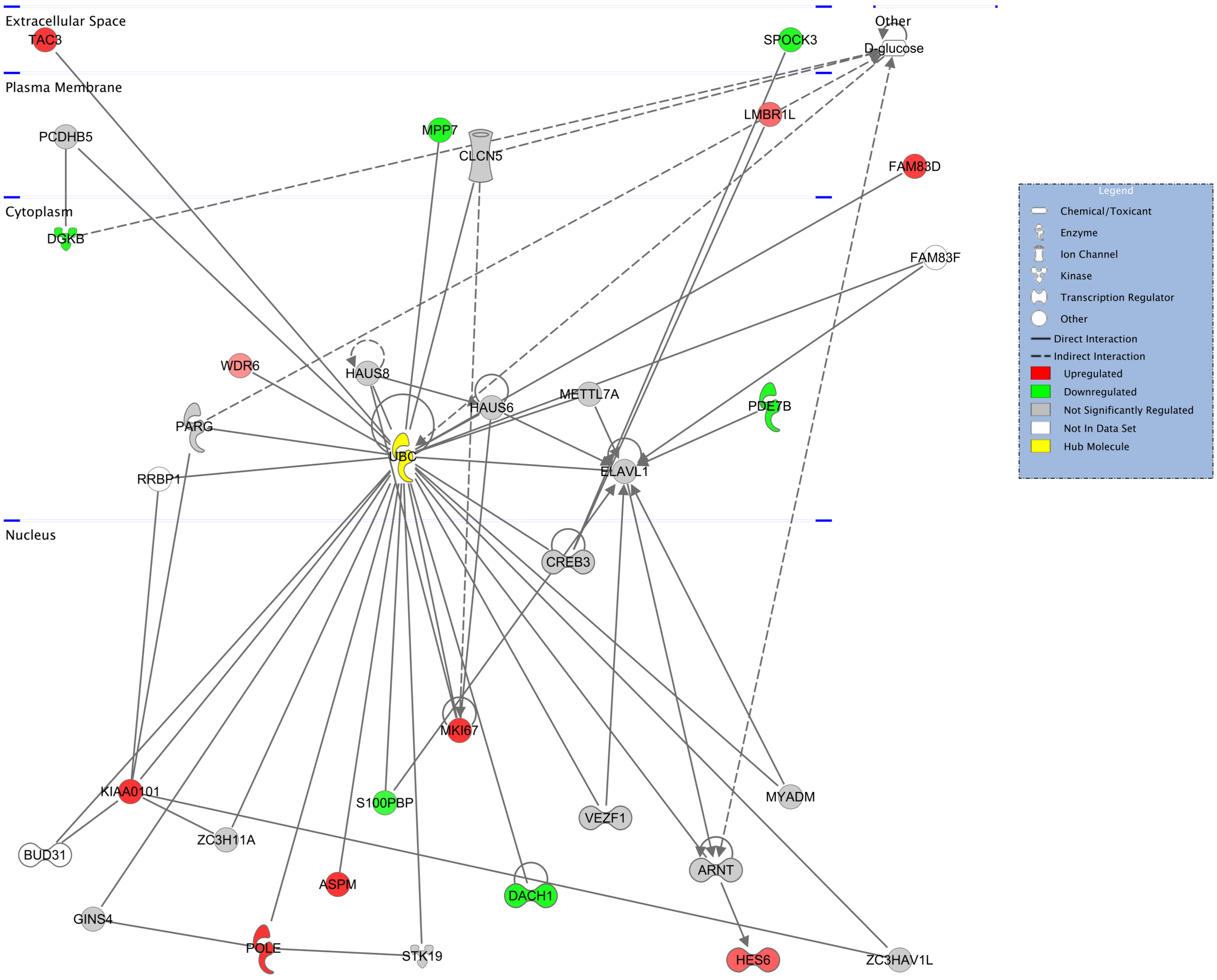


Figure S3: UBC related network, generated by IPA Path Designer (Qiagen). This gene network was significantly regulated (*P*<0.05 with the Fisher's Exact Test) in the NAc in response to acute cocaine (20 mg kg^{-1}, i.p.) in WT compared to SERT Met172 mice. Network is centered around the network hub gene UBC. Seed molecules from the list of differentially regulated genes in WT compared to SERT Met172 mice are shown in the form of protein networks in red (upregulated in WT) and green (downregulated in WT), along with other molecules (gray and white) that connect smaller networks to make larger networks. Interaction or regulation between proteins or complexes is shown with arrows (activation) or blunt-ended lines (inhibition).

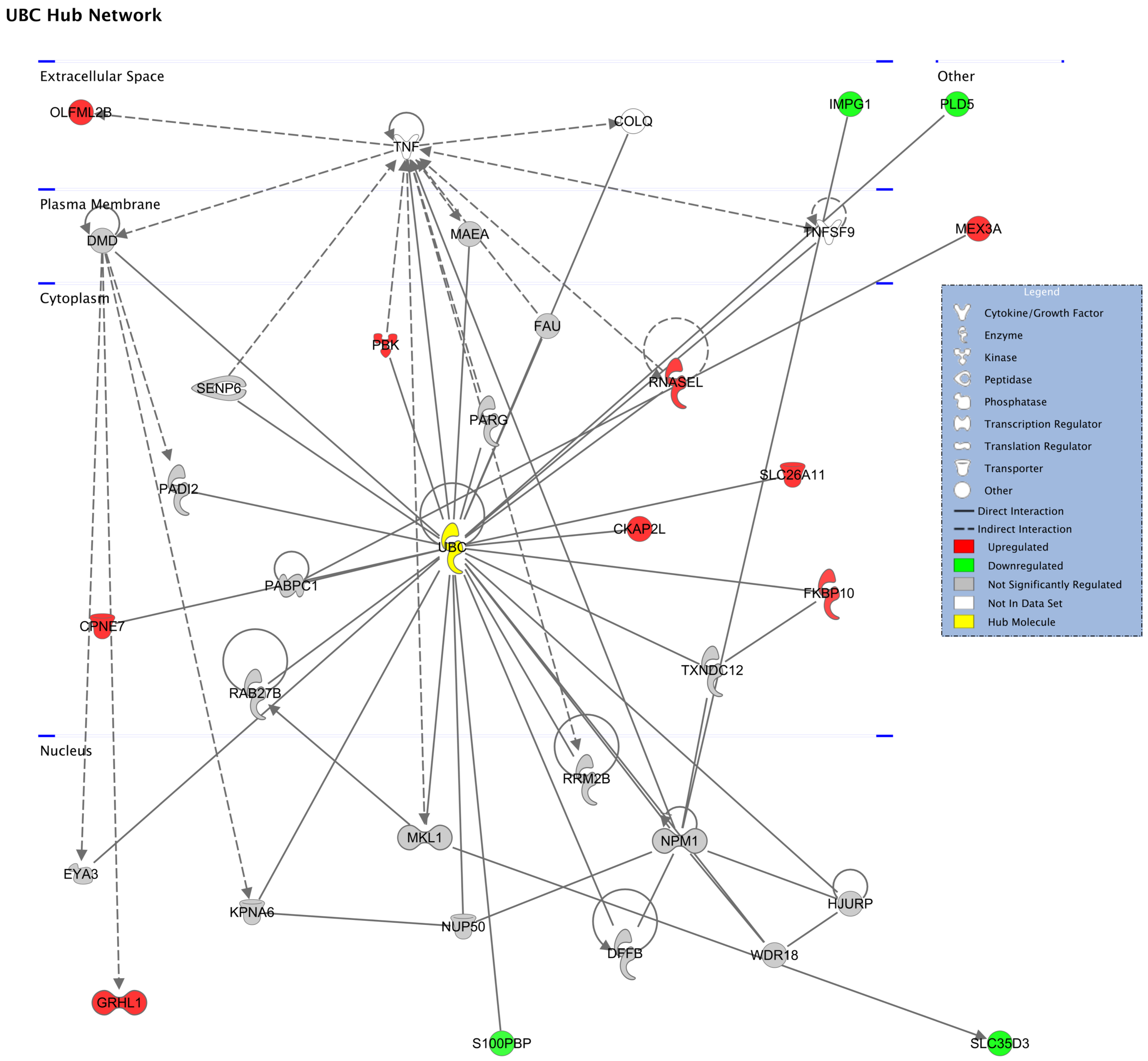


Figure S4: UBC related network, generated by IPA Path Designer (Qiagen). This gene network was significantly regulated ($P<0.05$ with the Fisher's Exact Test) in the NAc in response to acute cocaine (20 mg kg^{-1}, i.p.) in WT compared to SERT Met172 mice. Network is centered around the network hub gene UBC. Seed molecules from the list of differentially regulated genes in WT compared to SERT Met172 mice are shown in the form of protein networks in red (upregulated in WT) and green (downregulated in WT), along with other molecules (gray and white) that connect smaller networks to make larger networks. Interaction or regulation between proteins or complexes is shown with arrows (activation) or blunt-ended lines (inhibition).

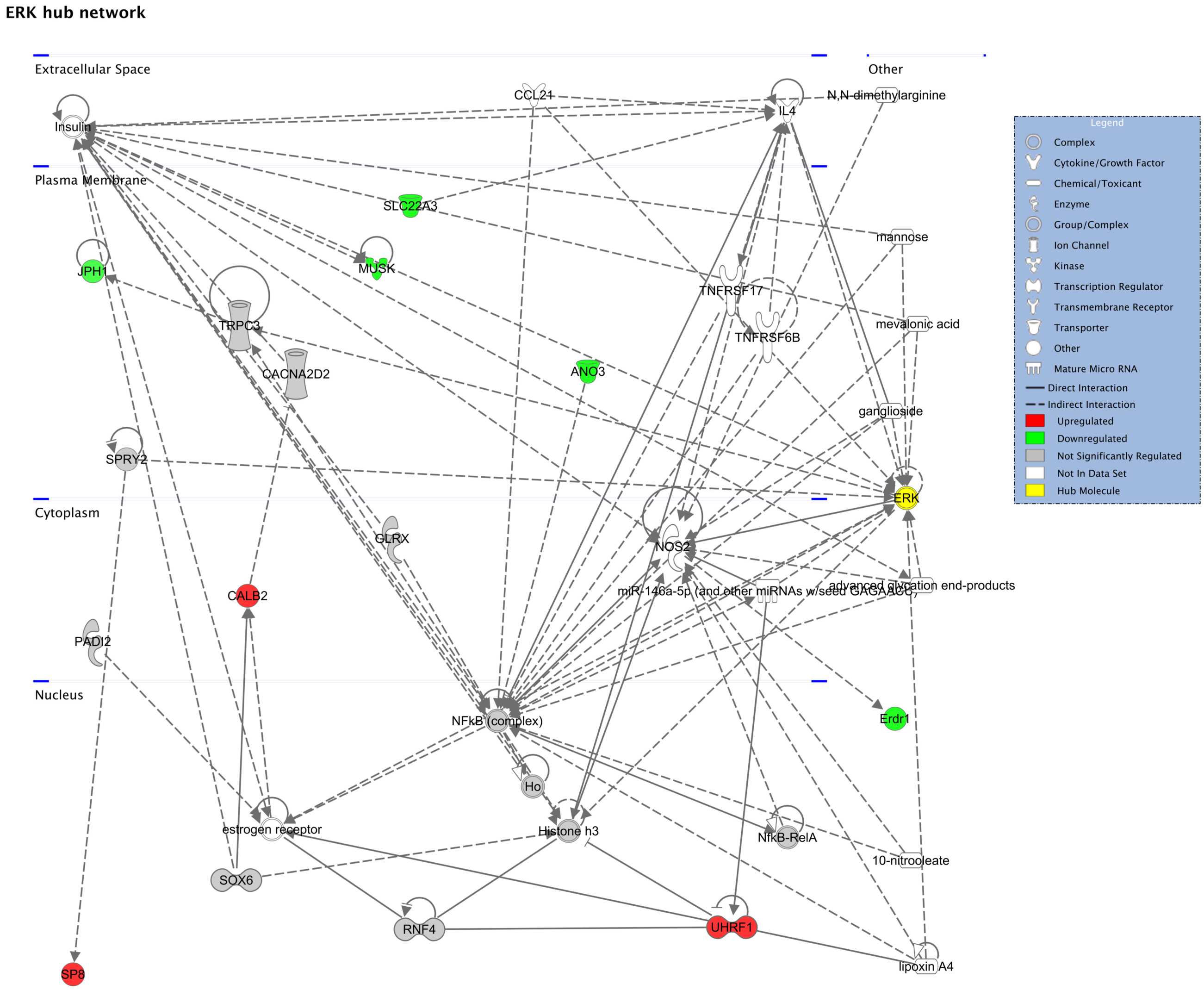


Figure S5: NFκB/ERK related network, generated by IPA Path Designer (Qiagen). This gene network was significantly regulated (*P*<0.05 with the Fisher's Exact Test) in response to acute cocaine (20 mg kg^{-1}, i.p.) in WT compared to SERT Met172 mice. Network is centered around the network hub genes NFκB and ERK. Seed molecules from the list of differentially regulated genes in WT compared to SERT Met172 mice are shown in the form of protein networks in red (upregulated in WT) and green (downregulated in WT), along with other molecules (gray and white) that connect smaller networks to make larger networks. Interaction or regulation between proteins or complexes is shown with arrows (activation) or blunt-ended lines (inhibition).

NFkB hub network

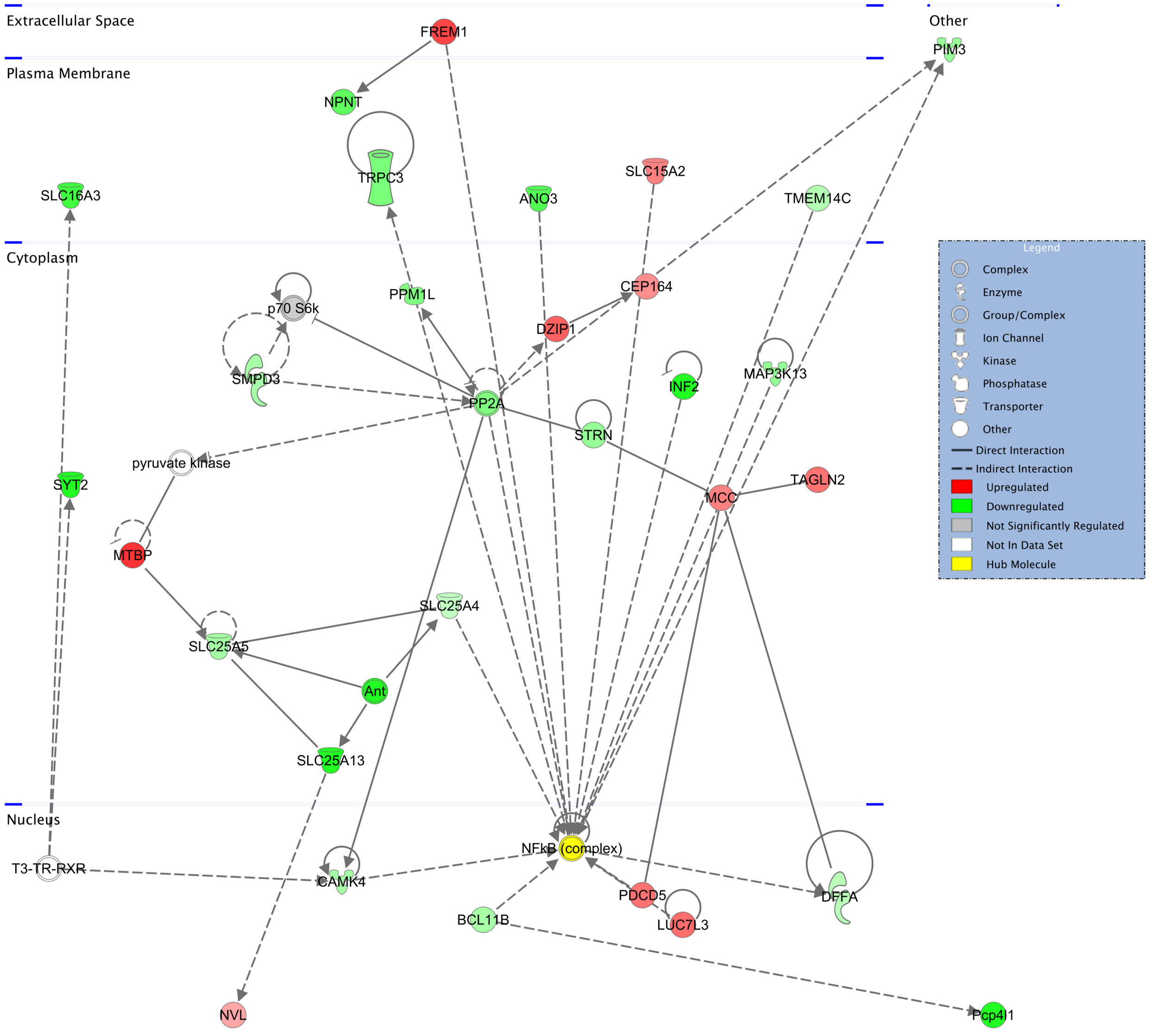


Figure S6: NFκB related network, generated by IPA Path Designer (Qiagen). This gene network was significantly regulated (*P*<0.05 with the Fisher's Exact Test) in the PrL in response to acute cocaine (20 mg kg^{-1}, i.p.) in WT compared to SERT Met172 mice. Network is centered around the network hub genes NFκB. Seed molecules from the list of differentially regulated genes in WT compared to SERT Met172 mice are shown in the form of protein networks in red (upregulated in WT) and green (downregulated in WT), along with other molecules (gray and white) that connect smaller networks to make larger networks. Interaction or regulation between proteins or complexes is shown with arrows (activation) or blunt-ended lines (inhibition).

Akt hub network

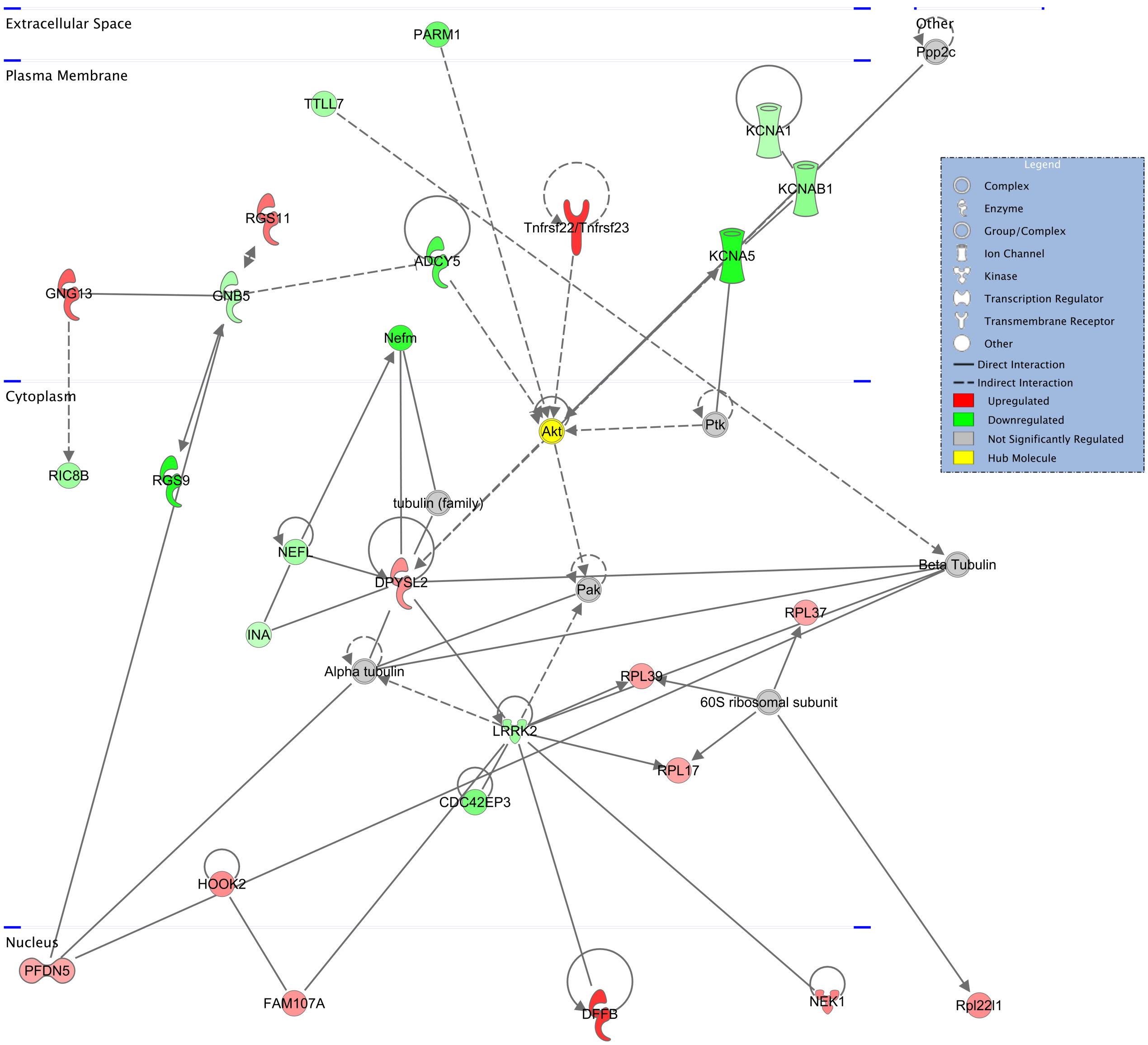
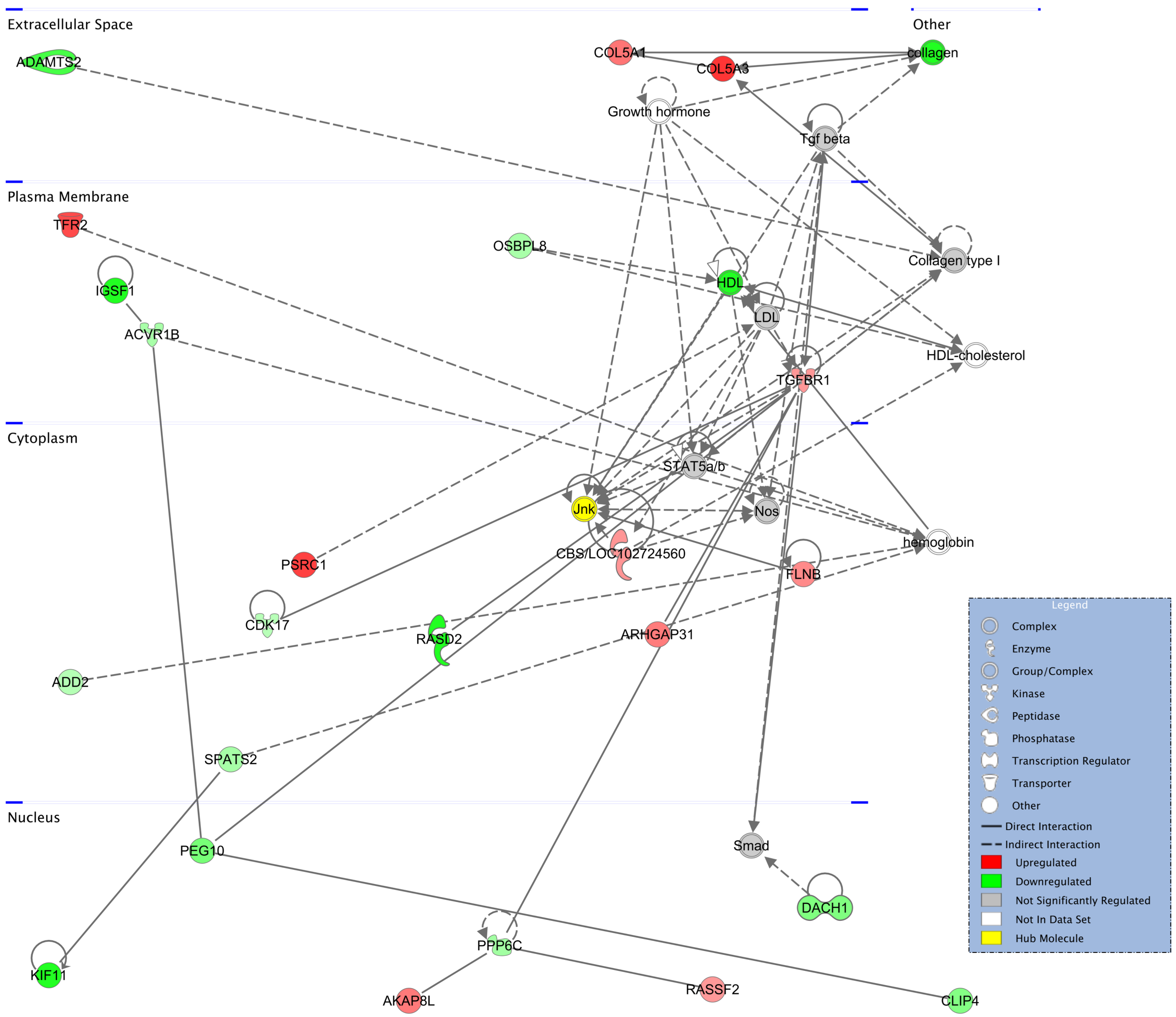


Figure S7: Akt related network, generated by IPA Path Designer (Qiagen). This gene network was significantly regulated (*P*<0.05 with the Fisher's Exact Test) in the PrL in response to acute cocaine (20 mg kg^{-1}, i.p.) in WT compared to SERT Met172 mice. Network is centered around the network hub genes Akt. Seed molecules from the list of differentially regulated genes in WT compared to SERT Met172 mice are shown in the form of protein networks in red (upregulated in WT) and green (downregulated in WT), along with other molecules (gray and white) that connect smaller networks to make larger networks. Interaction or regulation between proteins or complexes is shown with arrows (activation) or blunt-ended lines (inhibition).

Jnk hub network



Figures **S8:** Jnk related network, generated by IPA Path Designer (Qiagen). This gene network was significantly regulated (*P*<0.05 with the Fisher's Exact Test) in the PrL in response to acute cocaine (20 mg kg^{-1}, i.p.) in WT compared to SERT Met172 mice. Network is centered around the network hub genes Jnk. Seed molecules from the list of differentially regulated genes in WT compared to SERT Met172 mice are shown in the form of protein networks in red (upregulated in WT) and green (downregulated in WT), along with other molecules (gray and white) that connect smaller networks to make larger networks. Interaction or regulation between proteins or complexes is shown with arrows (activation) or blunt-ended lines (inhibition).

ERK1/2 hub network

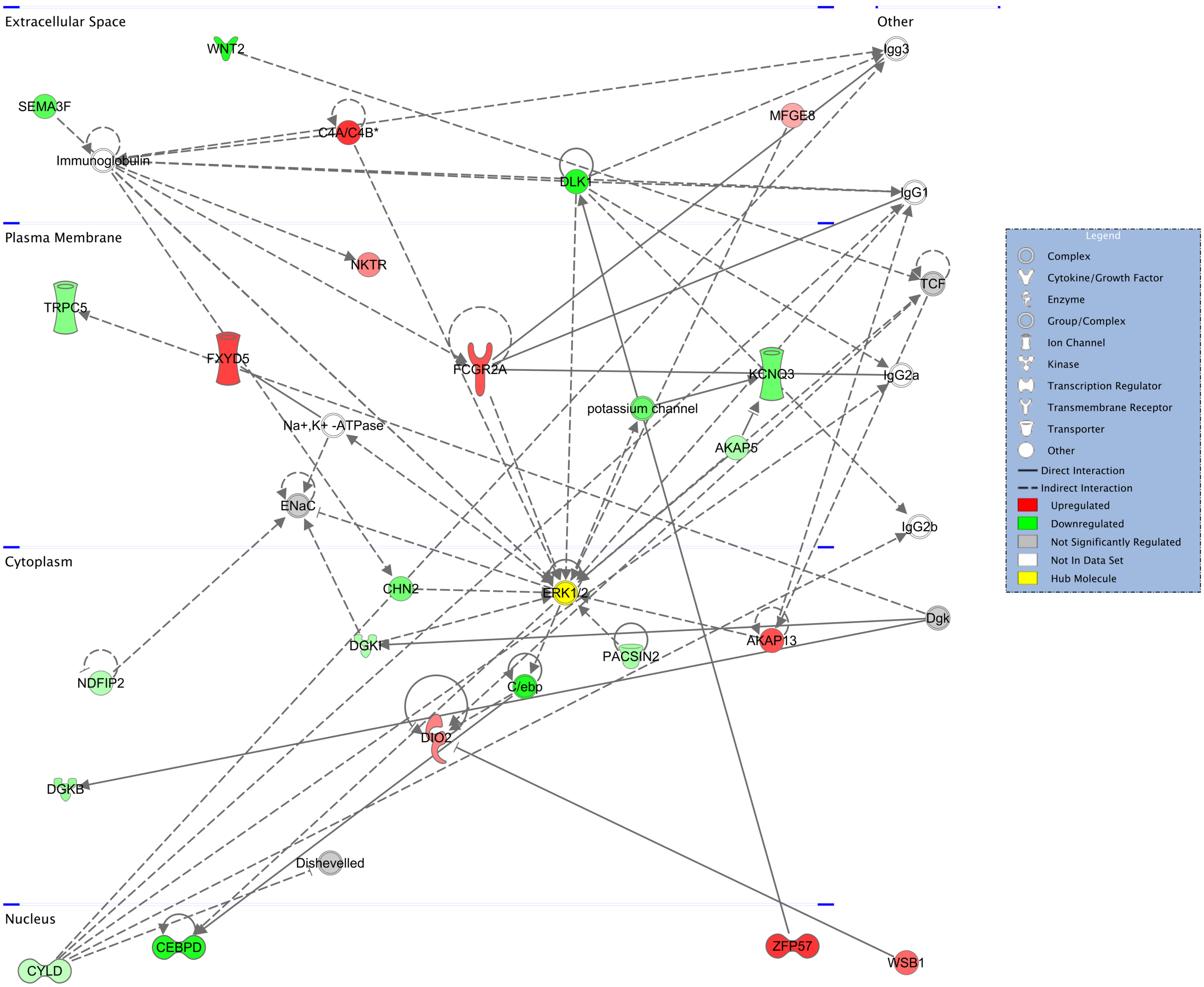


Figure S9: ERK1/2 related network, generated by IPA Path Designer (Qiagen). This gene network was significantly regulated (*P*<0.05 with the Fisher's Exact Test) in the PrL in response to acute cocaine (20 mg kg^{-1}, i.p.) in WT compared to SERT Met172 mice. Network is centered around the network hub genes ERK1/2. Seed molecules from the list of differentially regulated genes in WT compared to SERT Met172 mice are shown in the form of protein networks in red (upregulated in WT) and green (downregulated in WT), along with other molecules (gray and white) that connect smaller networks to make larger networks. Interaction or regulation between proteins or complexes is shown with arrows (activation) or blunt-ended lines (inhibition).

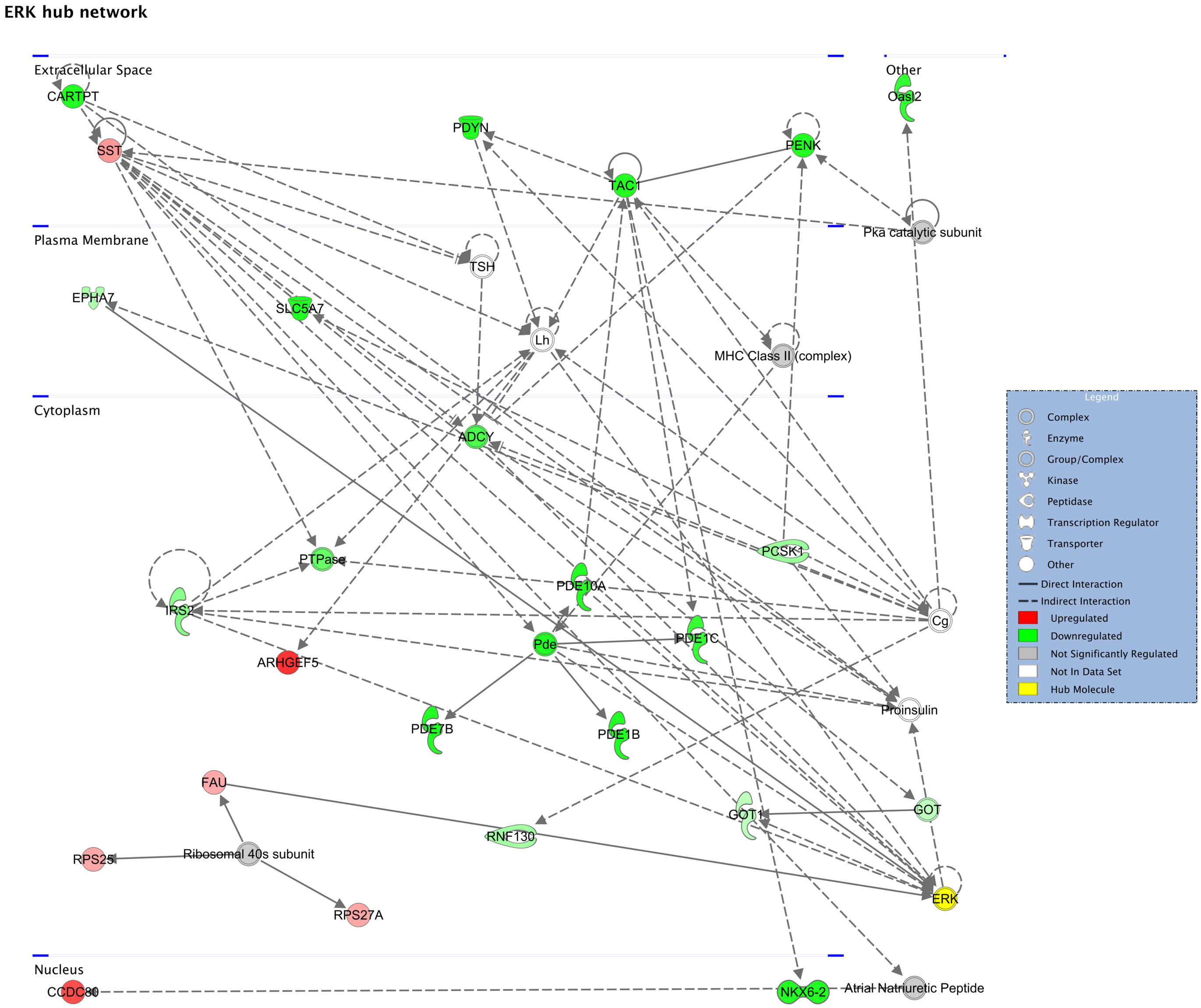
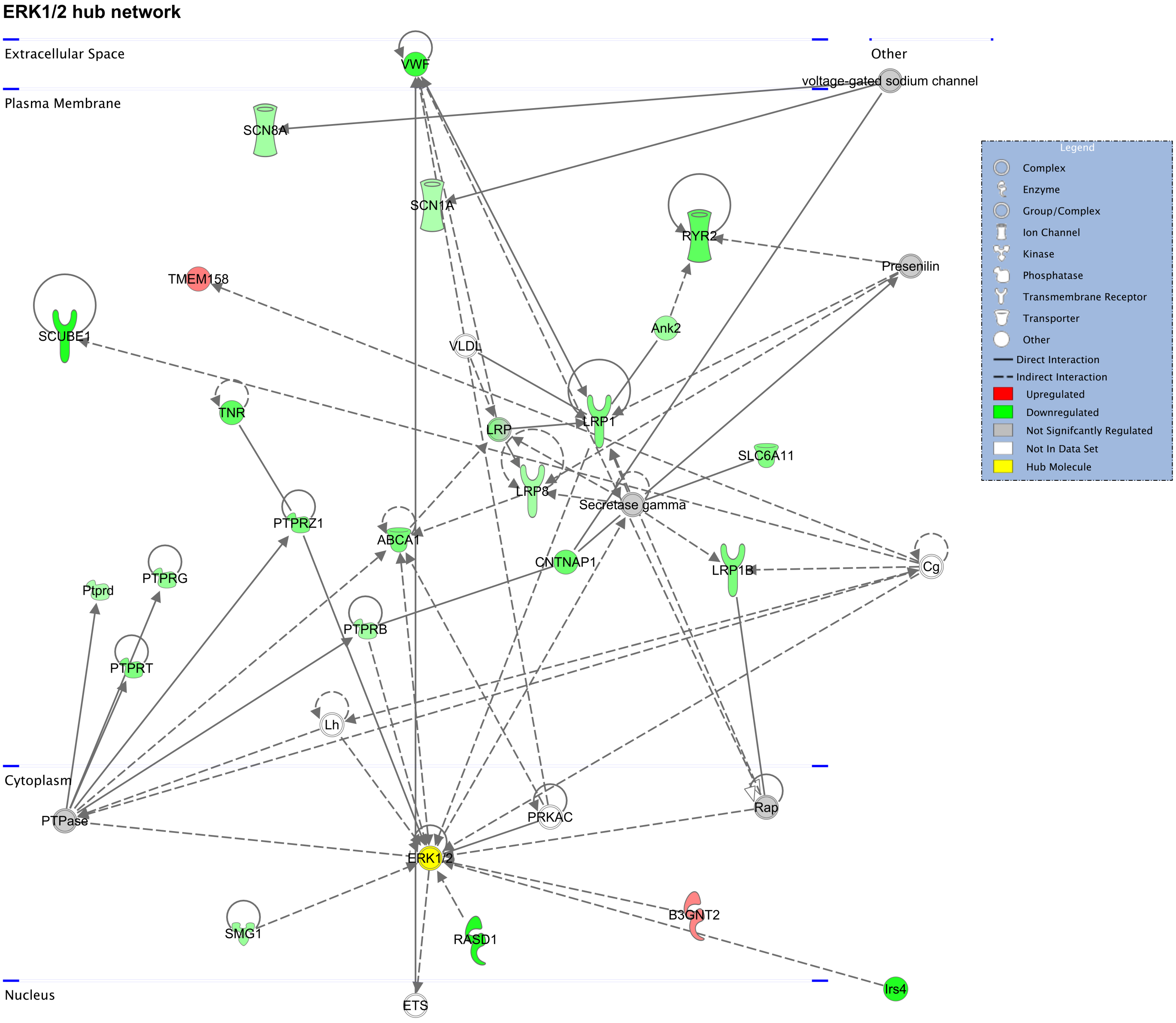
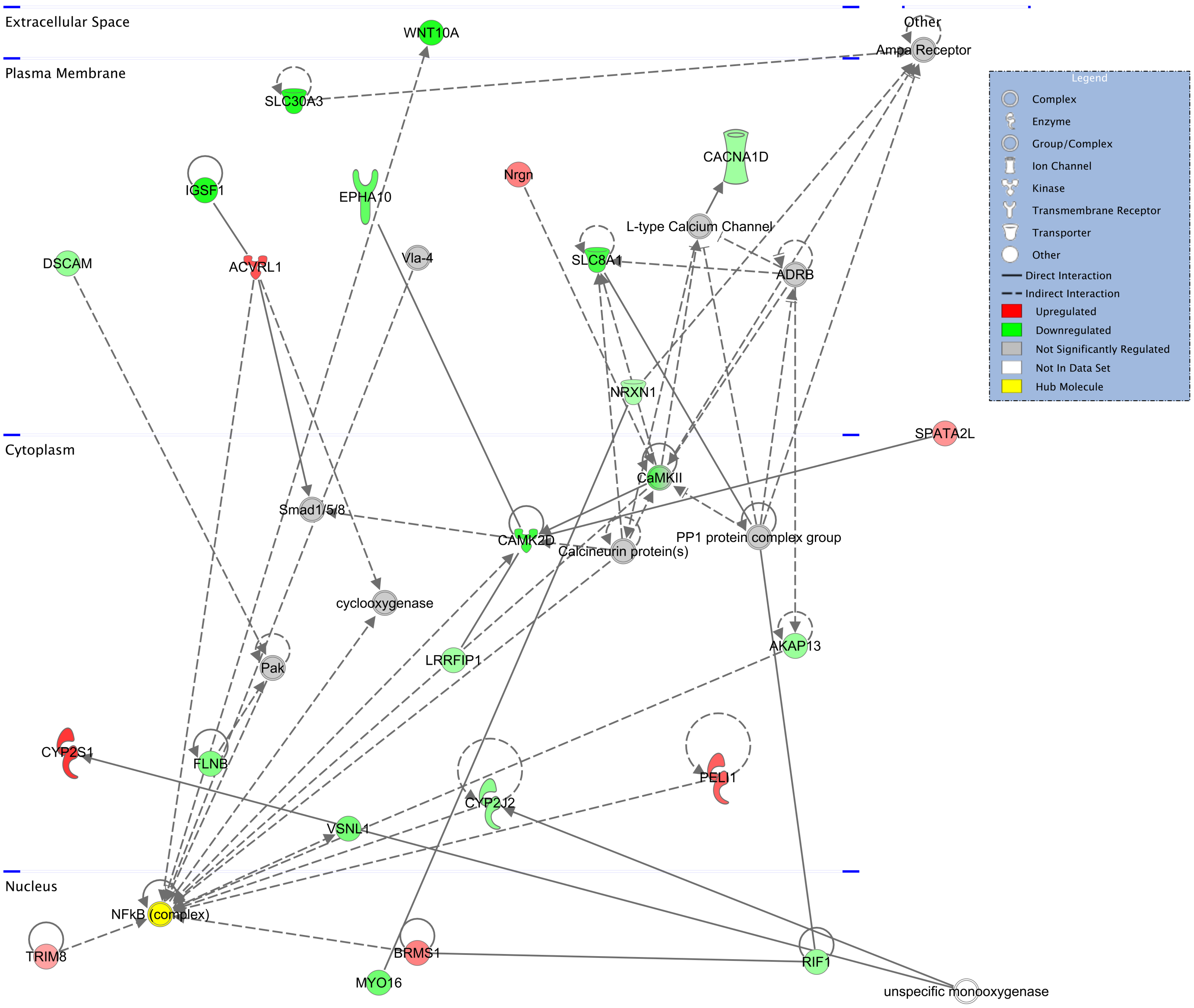


Figure S10: ERK related network, generated by IPA Path Designer (Qiagen). This gene network was significantly regulated ($P<0.05$ with the Fisher's Exact Test) in the PrL in response to acute cocaine (20 mg kg^{-1}, i.p.) in WT compared to SERT Met172 mice. Network is centered around the network hub genes ERK. Seed molecules from the list of differentially regulated genes in WT compared to SERT Met172 mice are shown in the form of protein networks in red (upregulated in WT) and green (downregulated in WT), along with other molecules (gray and white) that connect smaller networks to make larger networks. Interaction or regulation between proteins or complexes is shown with arrows (activation) or blunt-ended lines (inhibition).

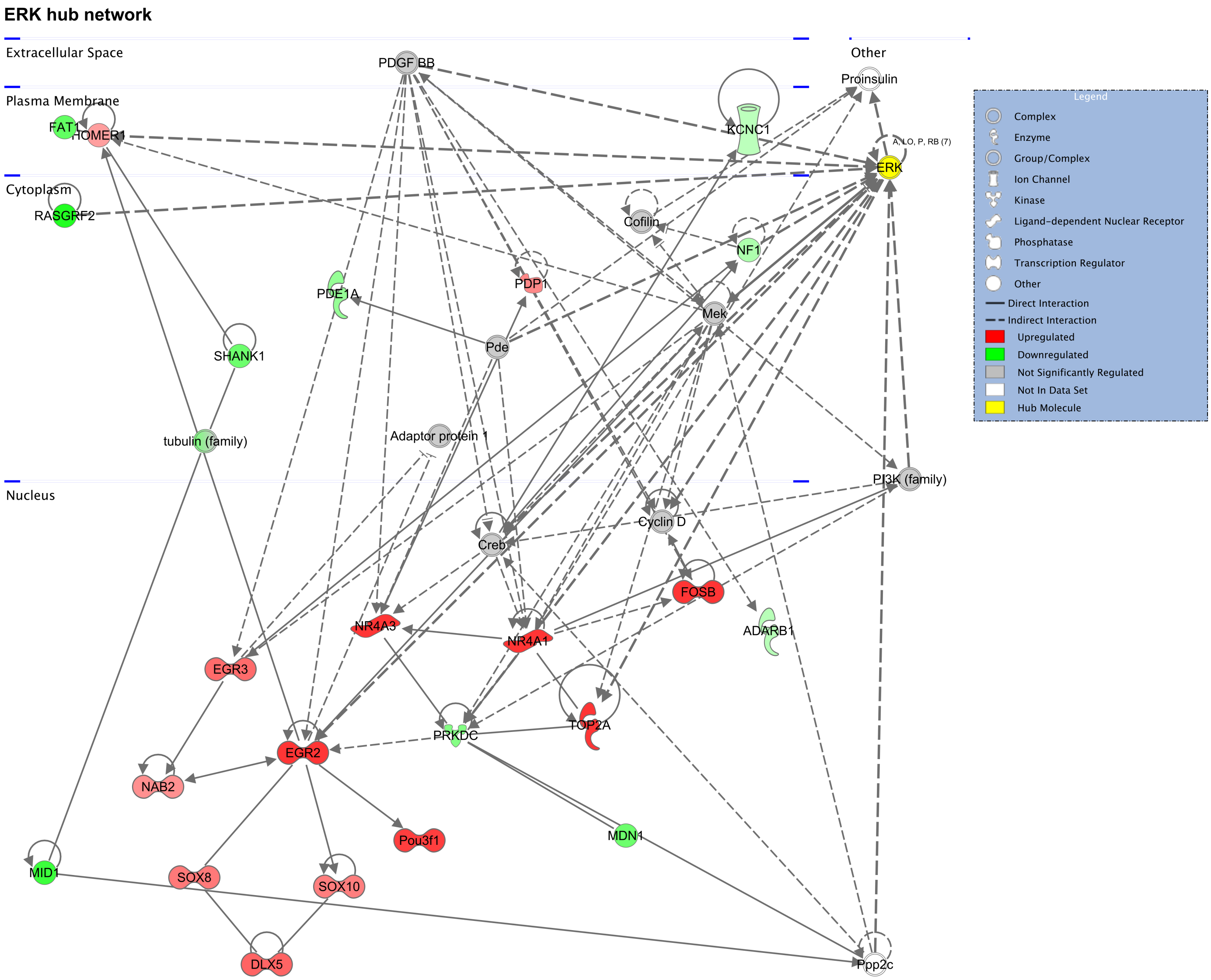


Figures S11: ERK1/2 related network, generated by IPA Path Designer (Qiagen). This gene network was significantly regulated ($P<0.05$ with the Fisher's Exact Test) in the NAc in response to chronic cocaine (15 mg kg^{-1}, i.p. for five days) in WT compared to SERT Met172 mice. Network is centered around the network hub gene ERK1/2. Seed molecules from the list of differentially regulated genes in WT compared to SERT Met172 mice are shown in the form of protein networks in red (upregulated in WT) and green (downregulated in WT), along with other molecules (gray and white) that connect smaller networks to make larger networks. Interaction or regulation between proteins or complexes is shown with arrows (activation) or blunt-ended lines (inhibition).

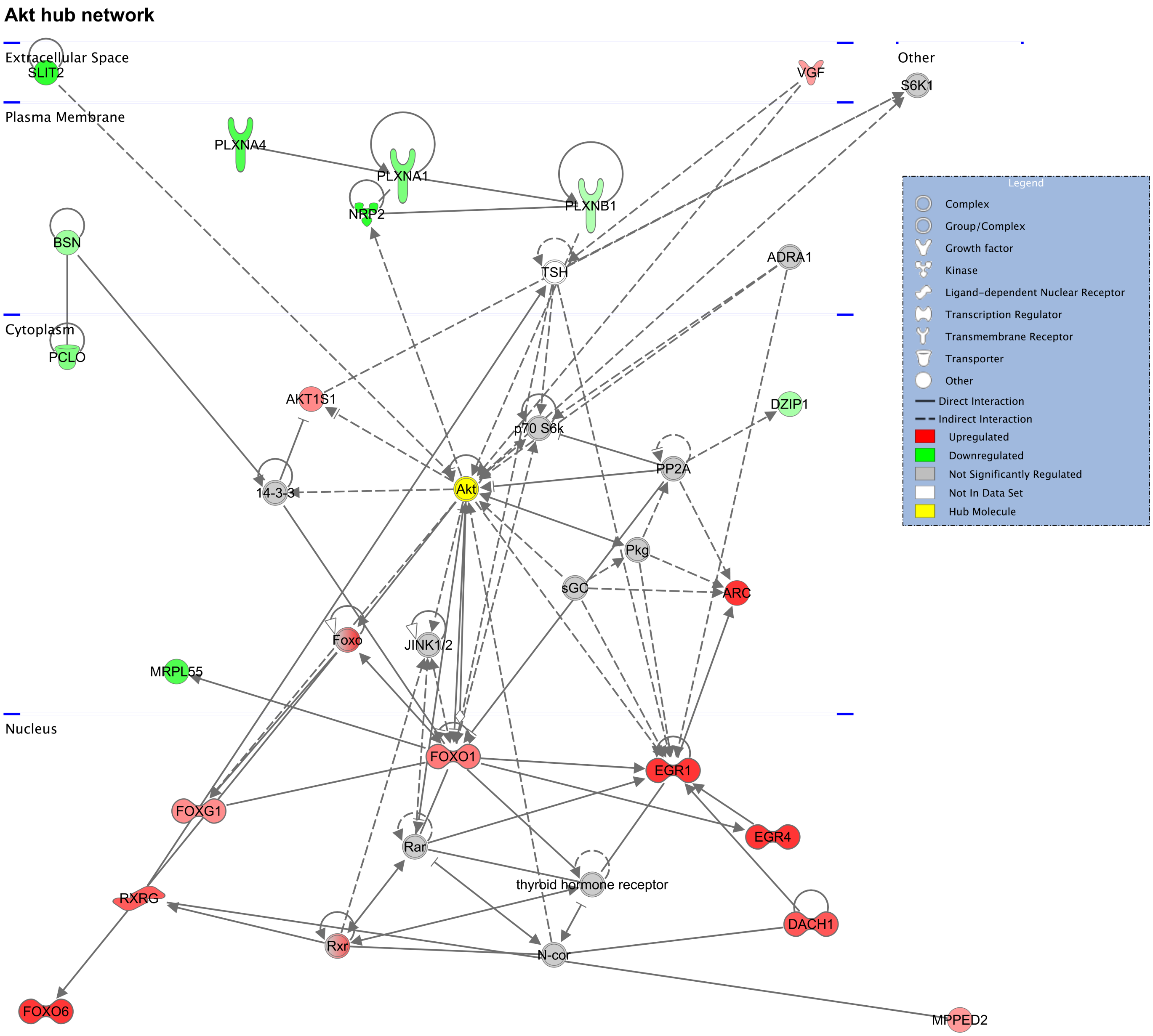
NFκB hub network



Figures S12: NFκB related network, generated by IPA Path Designer (Qiagen). This gene network was significantly regulated ($P<0.05$ with the Fisher's Exact Test) in the NAc in response to chronic cocaine (15 mg kg^{-1}, i.p. for five days) in WT compared to SERT Met172 mice. Network is centered around the network hub gene NFκB. Seed molecules from the list of differentially regulated genes in WT compared to SERT Met172 mice are shown in the form of protein networks in red (upregulated in WT) and green (downregulated in WT), along with other molecules (gray and white) that connect smaller networks to make larger networks. Interaction or regulation between proteins or complexes is shown with arrows (activation) or blunt-ended lines (inhibition).

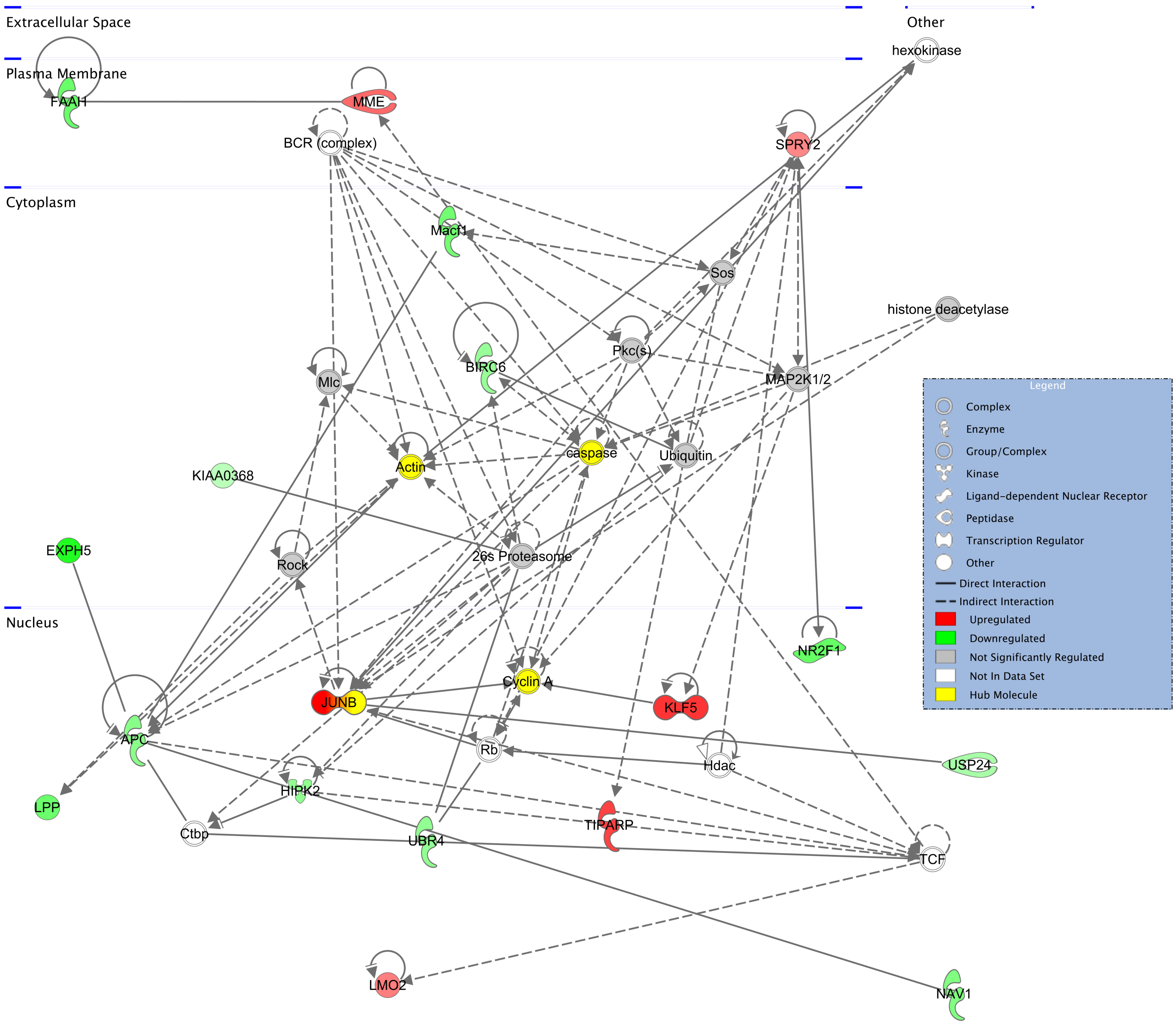


Figures S13: ERK related network, generated by IPA Path Designer (Qiagen). This gene network was significantly regulated ($P<0.05$ with the Fisher's Exact Test) in the NAc in response to chronic cocaine (15 mg kg^{-1}, i.p. for five days) in WT compared to SERT Met172 mice. Network is centered around the network hub gene ERK. Seed molecules from the list of differentially regulated genes in WT compared to SERT Met172 mice are shown in the form of protein networks in red (upregulated in WT) and green (downregulated in WT), along with other molecules (gray and white) that connect smaller networks to make larger networks. Interaction or regulation between proteins or complexes is shown with arrows (activation) or blunt-ended lines (inhibition).



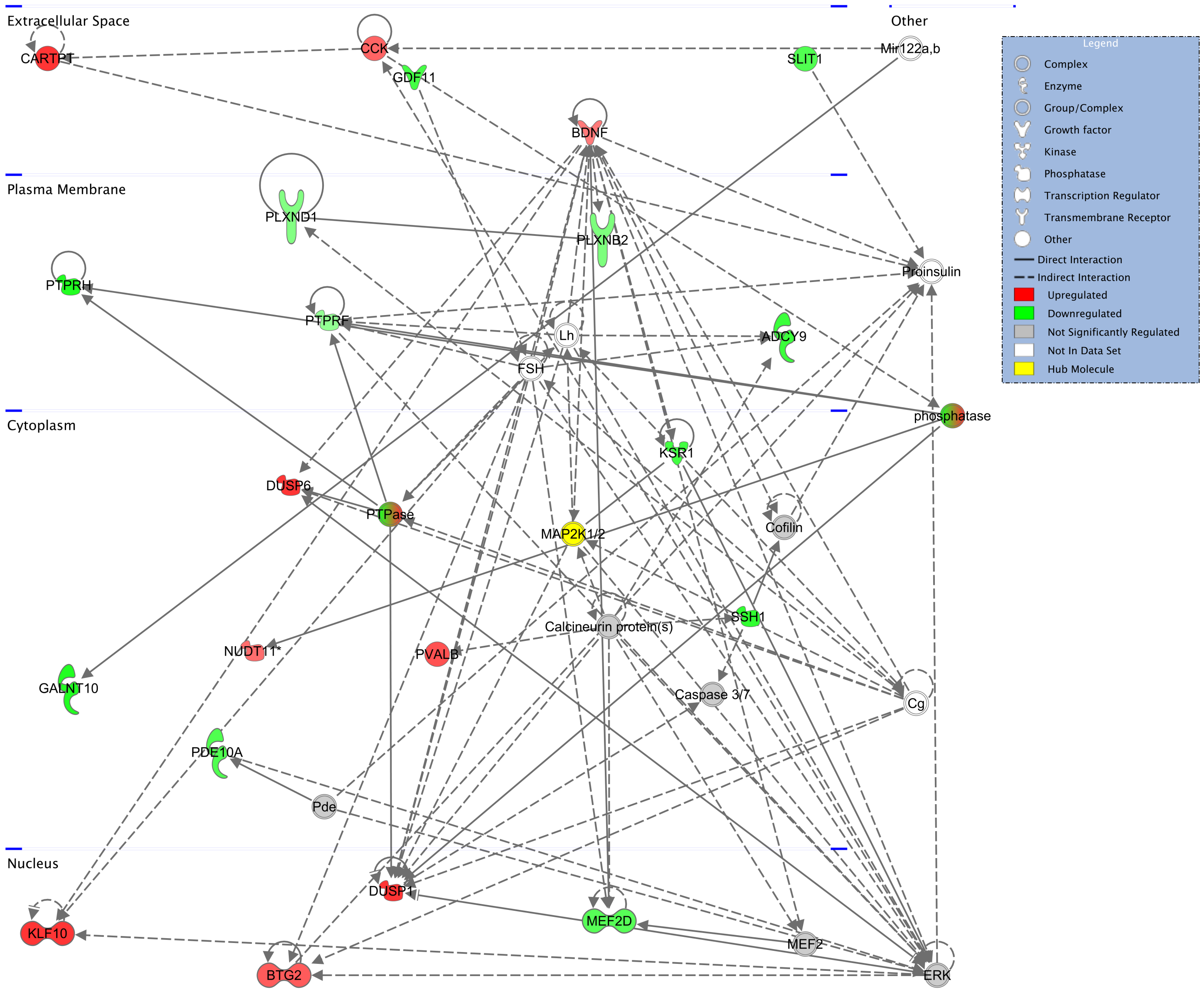
Figures S14: Akt related network, generated by IPA Path Designer (Qiagen). This gene network was significantly regulated ($P<0.05$ with the Fisher's Exact Test) in the NAc in response to chronic cocaine (15 mg kg^{-1}, i.p. for five days) in WT compared to SERT Met172 mice. Network is centered around the network hub gene Akt. Seed molecules from the list of differentially regulated genes in WT compared to SERT Met172 mice are shown in the form of protein networks in red (upregulated in WT) and green (downregulated in WT), along with other molecules (gray and white) that connect smaller networks to make larger networks. Interaction or regulation between proteins or complexes is shown with arrows (activation) or blunt-ended lines (inhibition).

JUNB hub network



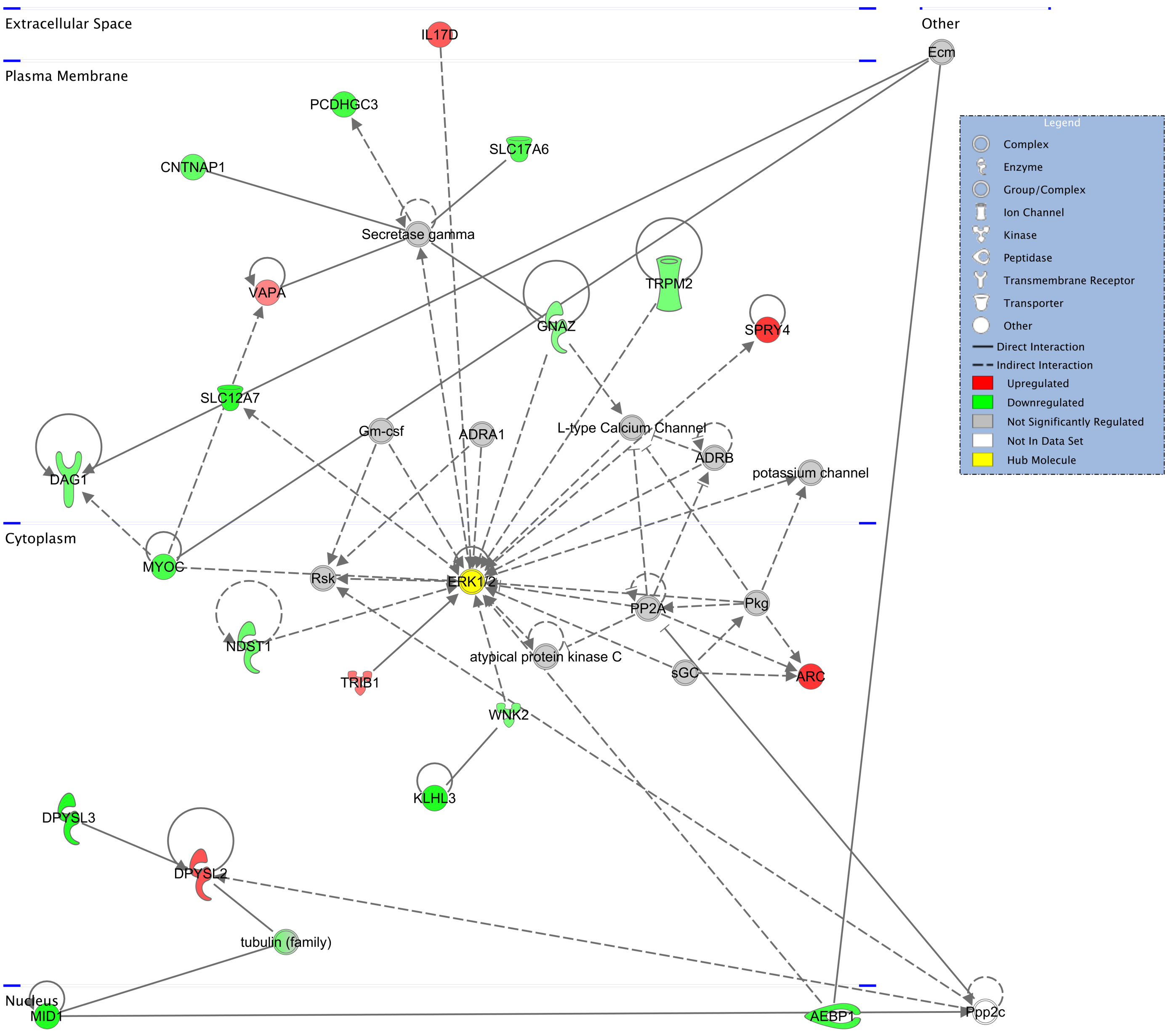
Figures S15: JUNB related network, generated by IPA Path Designer (Qiagen). This gene network was significantly regulated (*P*<0.05 with the Fisher's Exact Test) in the NAc in response to chronic cocaine (15 mg kg^{-1}, i.p. for five days) in WT compared to SERT Met172 mice. Network is centered around the network hub gene JUNB, but also actin, caspase, and cyclin A. Seed molecules from the list of differentially regulated genes in WT compared to SERT Met172 mice are shown in the form of protein networks in red (upregulated in WT) and green (downregulated in WT), along with other molecules (gray and white) that connect smaller networks to make larger networks. Interaction or regulation between proteins or complexes is shown with arrows (activation) or blunt-ended lines (inhibition).

MAP2K1/2 hub network

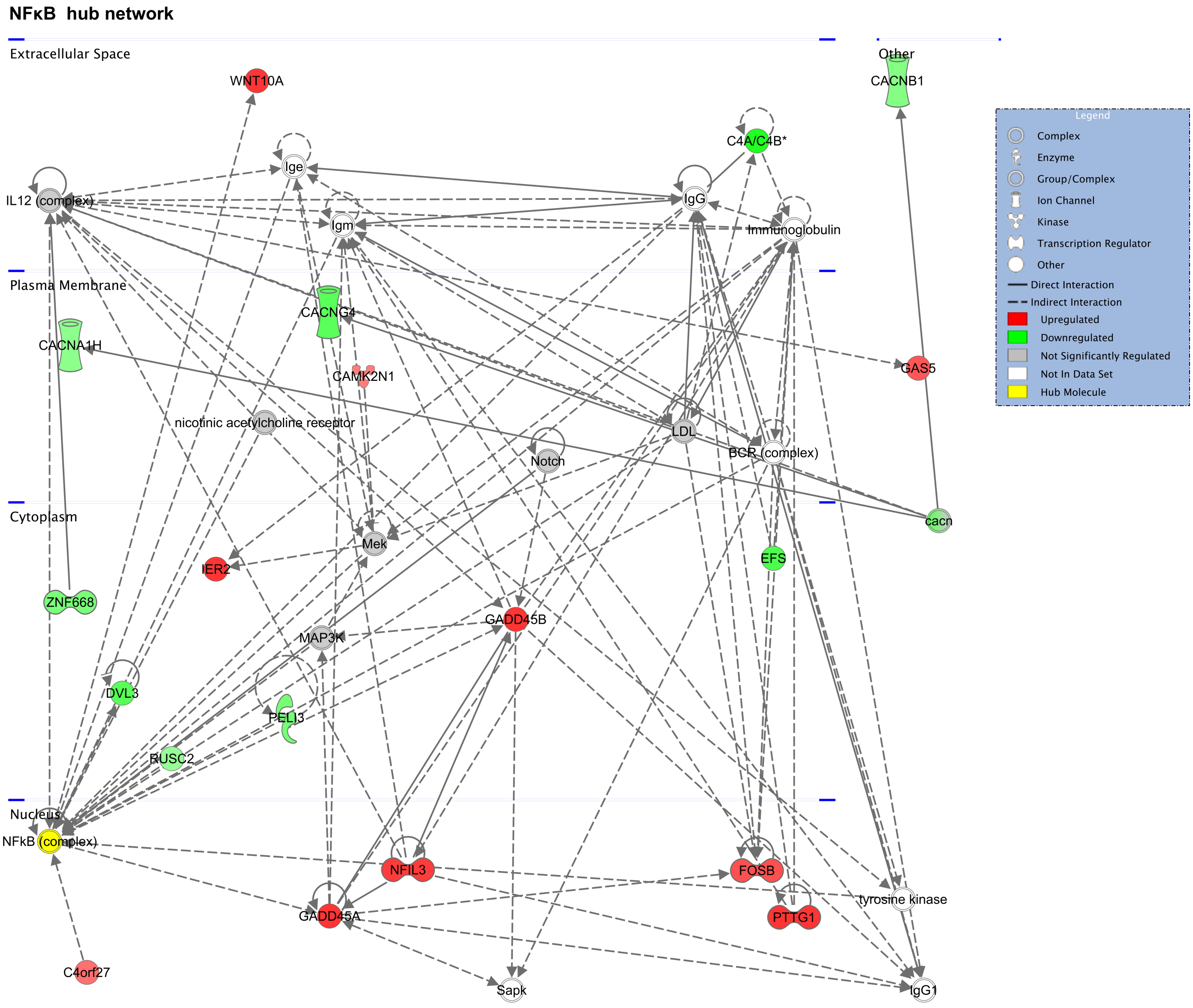


Figures S16: MAP2K1/2 related network, generated by IPA Path Designer (Qiagen). This gene network was significantly regulated ($P<0.05$ with the Fisher's Exact Test) in the PrL in response to chronic cocaine (15 mg kg^{-1}, i.p. for five days) in WT compared to SERT Met172 mice. Network is centered around the network hub gene MAP2K1/2. Seed molecules from the list of differentially regulated genes in WT compared to SERT Met172 mice are shown in the form of protein networks in red (upregulated in WT) and green (downregulated in WT), along with other molecules (gray and white) that connect smaller networks to make larger networks. Interaction or regulation between proteins or complexes is shown with arrows (activation) or blunt-ended lines (inhibition).

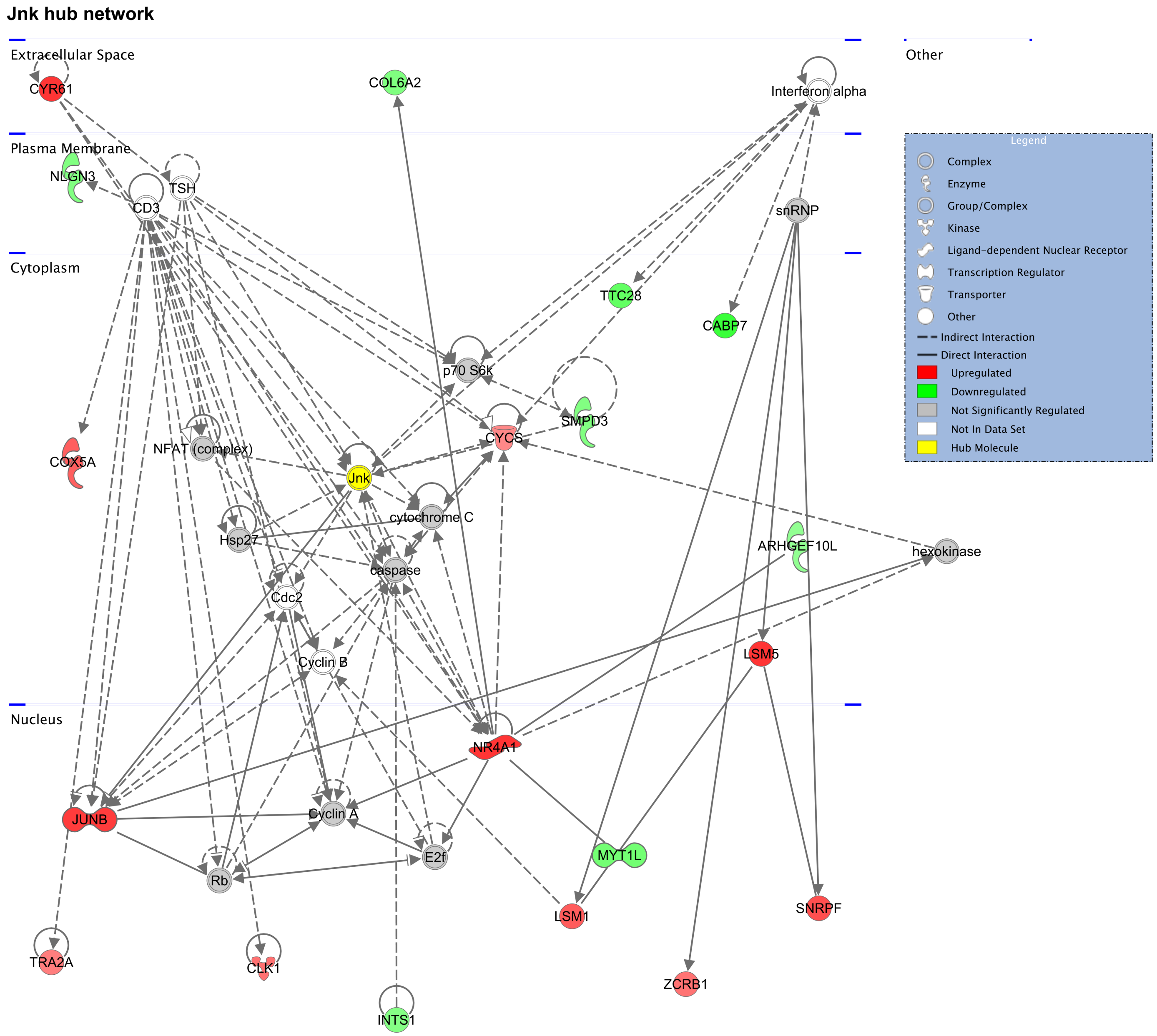
ERK1/2 hub network



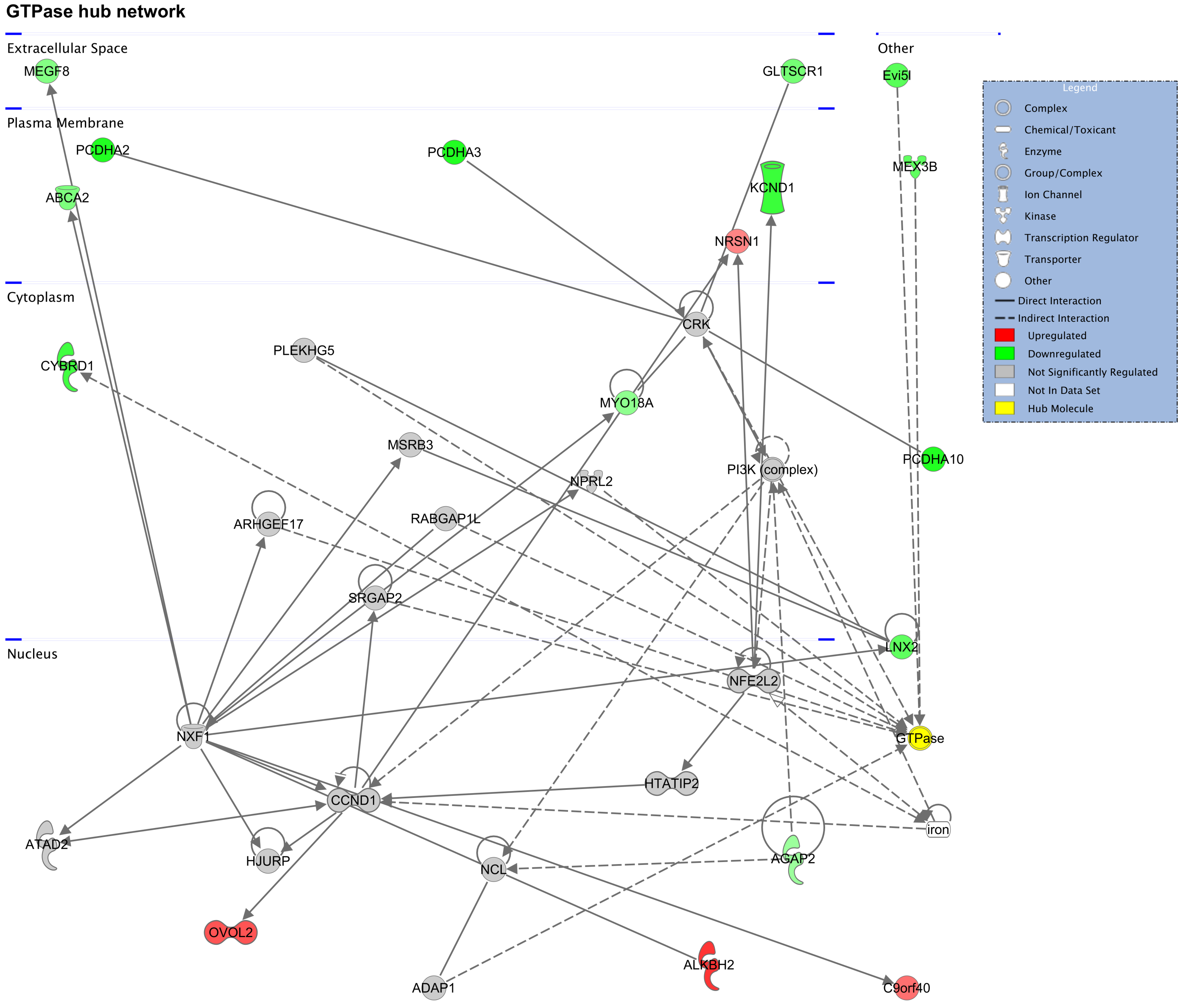
Figures S17: ERK1/2 related network, generated by IPA Path Designer (Qiagen). This gene network was significantly regulated ($P<0.05$ with the Fisher's Exact Test) in the PrL in response to chronic cocaine (15 mg kg^{-1}, i.p. for five days) in WT compared to SERT Met172 mice. Network is centered around the network hub gene ERK1/2. Seed molecules from the list of differentially regulated genes in WT compared to SERT Met172 mice are shown in the form of protein networks in red (upregulated in WT) and green (downregulated in WT), along with other molecules (gray and white) that connect smaller networks to make larger networks. Interaction or regulation between proteins or complexes is shown with arrows (activation) or blunt-ended lines (inhibition).



Figures S18: NFκB related network, generated by IPA Path Designer (Qiagen). This gene network was significantly regulated (*P*<0.05 with the Fisher's Exact Test) in the PrL in response to chronic cocaine (15 mg kg^{-1}, i.p. for five days) in WT compared to SERT Met172 mice. Network is centered around the network hub gene NFκB. Seed molecules from the list of differentially regulated genes in WT compared to SERT Met172 mice are shown in the form of protein networks in red (upregulated in WT) and green (downregulated in WT), along with other molecules (gray and white) that connect smaller networks to make larger networks. Interaction or regulation between proteins or complexes is shown with arrows (activation) or blunt-ended lines (inhibition).


Jnk hub network

Figures S19: Jnk related network, generated by IPA Path Designer (Qiagen). This gene network was significantly regulated ($P<0.05$ with the Fisher's Exact Test) in the PrL in response to chronic cocaine (15 mg kg^{-1}, i.p. for five days) in WT compared to SERT Met172 mice. Network is centered around the network hub gene Jnk. Seed molecules from the list of differentially regulated genes in WT compared to SERT Met172 mice are shown in the form of protein networks in red (upregulated in WT) and green (downregulated in WT), along with other molecules (gray and white) that connect smaller networks to make larger networks. Interaction or regulation between proteins or complexes is shown with arrows (activation) or blunt-ended lines (inhibition).



Figures S20: GTPase related network, generated by IPA Path Designer (Qiagen). This gene network was significantly regulated ($P<0.05$ with the Fisher's Exact Test) in the PrL in response to chronic cocaine (15 mg kg^{-1}, i.p. for five days) in WT compared to SERT Met172 mice. Network is centered around the network hub gene GTPase, but also actin, caspase, and cyclin A. Seed molecules from the list of differentially regulated genes in WT compared to SERT Met172 mice are shown in the form of protein networks in red (upregulated in WT) and green (downregulated in WT), along with other molecules (gray and white) that connect smaller networks to make larger networks. Interaction or regulation between proteins or complexes is shown with arrows (activation) or blunt-ended lines (inhibition).