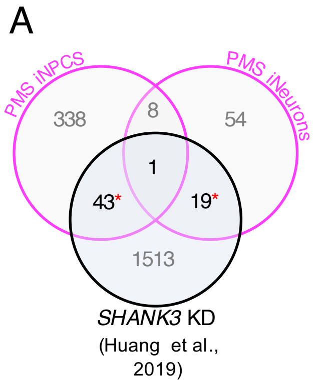
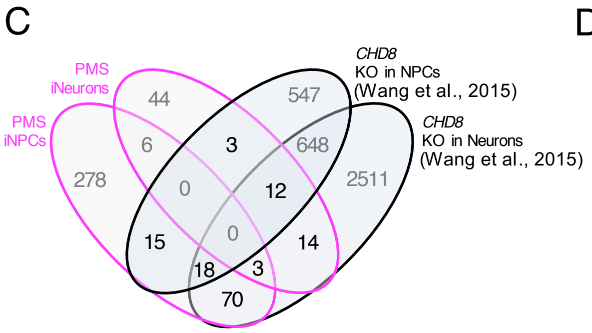


B

Enrichment based on overlapping features with *SHANK3* KD

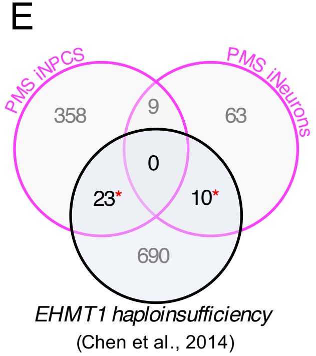
Gene set name	P-value	Adj. P-value
epithelial_cell_differentiation	9.56E-07	0.0100
cell_migration	2.98E-06	0.0116
canonical_Wnt_signaling_pathway	3.32E-06	0.0116
canonical_Wnt_signaling_pathway	6.78E-06	0.0178
endoplasmic_reticulum_lumen	6.73E-05	0.0191
smooth_endoplasmic_reticulum_lumen	6.73E-05	0.0191
cortical_endoplasmic_reticulum_lumen	7.31E-05	0.0191
perinuclear_endoplasmic_reticulum_lumen	7.77E-05	0.0191
rough_endoplasmic_reticulum_lumen	9.48E-05	0.0191
sarcoplasmic_reticulum_lumen	0.000104437	0.0191



D

Enrichment based on overlapping features with *CHD8* KO

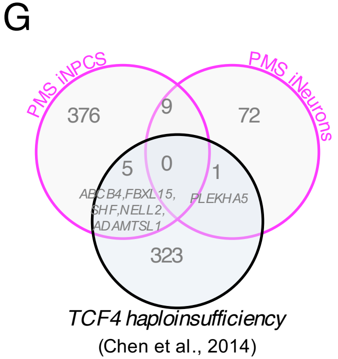
Gene set name	P-value	Adj. P-value
galactosaminoglycan/glycosaminoglycan/mucopolysaccharide metabolism	1.05E-08	2.77E-05
Golgi_lumen	1.52E-06	0.0016
trans-Golgi_network_transport_vesicle_lumen	2.92E-06	0.0016
multicellular_organism_development	2.04E-06	0.0019
lysosomal_matrix	8.16E-06	0.0022
cortical_endoplasmic_reticulum_lumen	2.44E-05	0.0032
perinuclear_endoplasmic_reticulum_lumen	2.66E-05	0.0032
endolysosome_lumen	2.25E-05	0.0032
proteinaceous_extracellular_matrix	0.000205759	0.0188
SMAD_protein_complex	0.000885591	0.0495
canonical_Wnt_signaling_pathway	0.000205759	0.0544

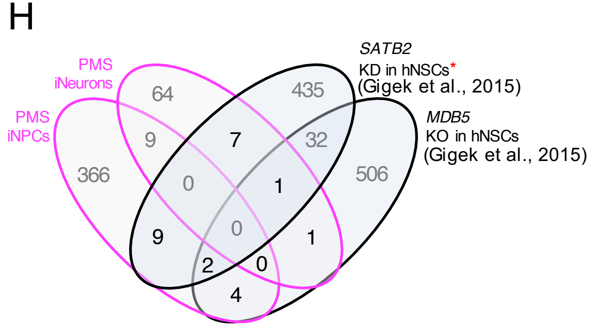


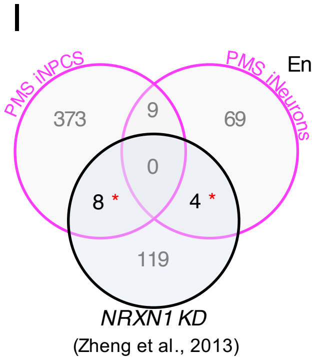
F

Enrichment based on overlapping features with *EHMT1* haploinsufficiency

Gene set name	P-value	Adj. P-value
Golgi_lumen	9.77E-06	0.00770
trans-Golgi_network_transport_vesicle_lumen	1.43E-05	0.0077
hyaluronic_acid_binding	3.10E-06	0.0106
galactosaminoglycan/glycosaminoglycan/mucopolysaccharide metabolism	7.58E-06	0.0197
biofilm_matrix_organization	4.32E-05	0.0292
cellulose_microfibril_organization	4.32E-05	0.0292
extracellular_matrix_organization	4.32E-05	0.0292
basement_membrane_organization	4.44E-05	0.0292
fibronectin_fibril_organization	4.44E-05	0.0292
extracellular_matrix_assembly	5.07E-05	0.0296
collagen_fibril_organization	5.77E-05	0.0319
central_nervous_system_neuron_differentiation	6.53E-05	0.0343
chondroitin_sulfate_biosynthetic_process	7.31E-05	0.0366



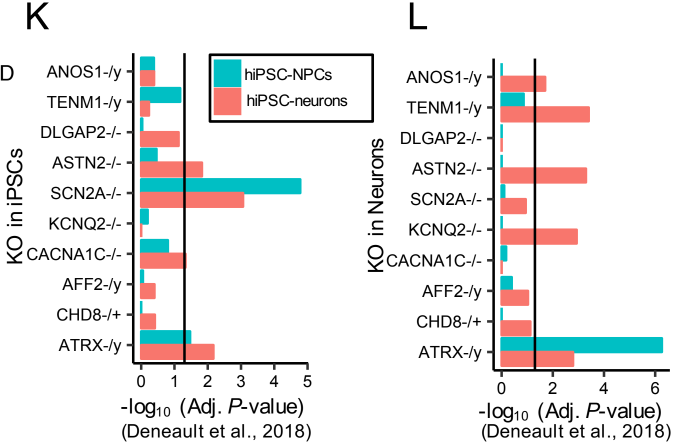




J

Enrichment based on overlapping features with NRXN1 KD

Gene set term	P-value	Adj. P-value
canonical_Wnt_signaling_pathway	0.0003	0.4296
beta-catenin_destruction_complex_disassembly	0.0005	0.4296
receptor_internalization_involved_in_Wnt signaling	0.0011	0.756
Golgi_lumen	0.0014	0.7816
trans-Golgi_network_transport_vesicle_lumen	0.0017	0.7816
L-glutamate_import	0.0034	1
central_nervous_system_neuron_differentiation	0.0037	1
L-glutamate_import	0.0046	1
ion_channel_complex	0.0052	1



M

Enrichment based on overlapping features with ATRX-/y

Gene set name	P-value	Adj. P-value
cell_migration_involved_in_sprouting_angiogenesis	0.0001	0.6967
cerebellar_granule_cell_differentiation	0.0002	0.4866
positive_regulation_of_Wnt_signaling_pathway	0.0002	0.8067
glutamate_receptor_activity	0.0003	0.4866
contractile_vacuole_discharge	0.0004	0.8067
regulated_exocytosis	0.0004	0.4866
ionotropic_glutamate_receptor_activity	0.0005	0.4866
endocytic_vesicle_membrane	0.0006	0.0904
synapse_assembly	0.0009	0.6358
calcium_ion_regulated_exocytosis	0.0011	0.8067
NMDA_glutamate_receptor_activity	0.0012	0.8067