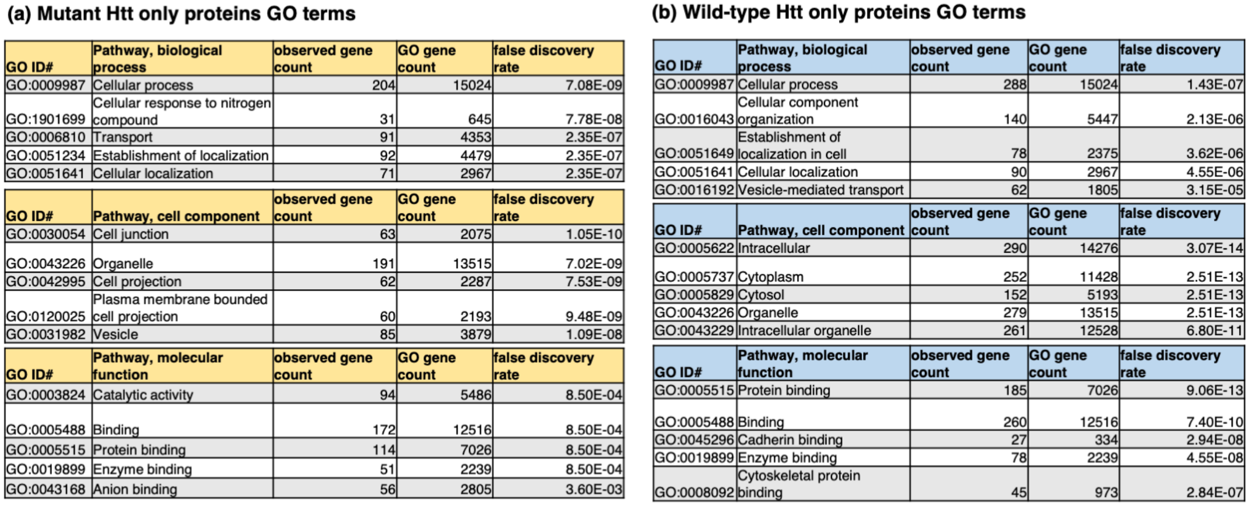
Supplemental Material

Mutant Huntingtin Protein Interaction Map Implicates Dysregulation of Multiple Cellular Pathways in Neurodegeneration of Huntington's Disease

Supplementary Figure 1. Gene ontology analysis of proteins interacting exclusively with mutant Htt, and those interacting exclusively with wild-type Htt. Gene ontology (GO) analysis of biological functions of proteins that interact only with mutant Htt is illustrated in (a). GO analysis proteins interacting only with wild-type Htt are shown in (b).



(a) Mutant Htt only proteins GO terms

GO ID#	Pathway, biological process	observed gene count	GO gene count	false discovery rate
GO:0009987	Cellular process	204	15024	7.08E-09
GO:1901699	Cellular response to nitrogen compound	31	645	7.78E-08
GO:0006810	Transport	91	4353	2.35E-07
GO:0051234	Establishment of localization	92	4479	2.35E-07
GO:0051641	Cellular localization	71	2967	2.35E-07

GO ID#	Pathway, cell component	observed gene count	GO gene count	false discovery rate
GO:0030054	Cell junction	63	2075	1.05E-10
GO:0043226	Organelle	191	13515	7.02E-09
GO:0042995	Cell projection	62	2287	7.53E-09
GO:0120025	Plasma membrane bounded cell projection	60	2193	9.48E-09
GO:0031982	Vesicle	85	3879	1.09E-08

GO ID#	Pathway, molecular function	observed gene count	GO gene count	false discovery rate
GO:0003824	Catalytic activity	94	5486	8.50E-04
GO:0005488	Binding	172	12516	8.50E-04
GO:0005515	Protein binding	114	7026	8.50E-04
GO:0019899	Enzyme binding	51	2239	8.50E-04
GO:0043168	Anion binding	56	2805	3.60E-03

(b) Wild-type Htt only proteins GO terms

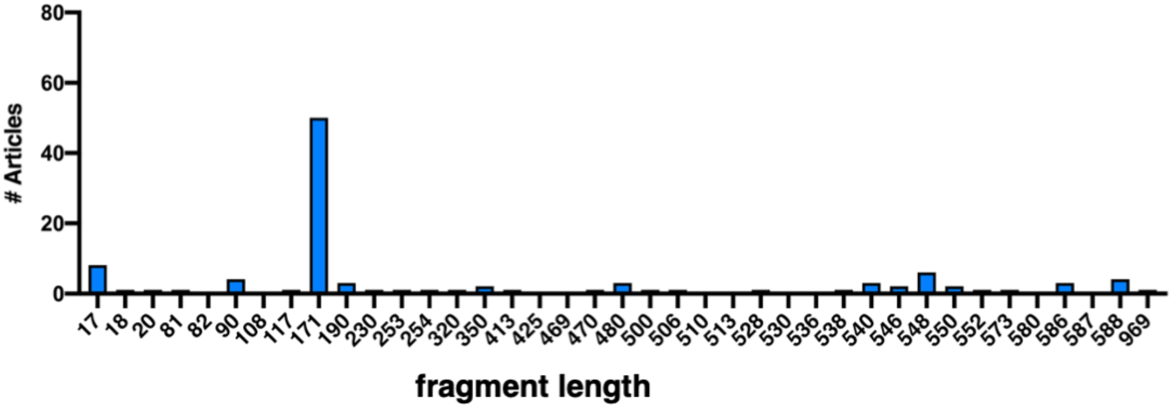
GO ID#	Pathway, biological process	observed gene count	GO gene count	false discovery rate
GO:0009987	Cellular process	288	15024	1.43E-07
GO:0016043	Cellular component organization	140	5447	2.13E-06
GO:0051649	Establishment of localization in cell	78	2375	3.62E-06
GO:0051641	Cellular localization	90	2967	4.55E-06
GO:0016192	Vesicle-mediated transport	62	1805	3.15E-05

GO ID#	Pathway, cell component	observed gene count	GO gene count	false discovery rate
GO:0005622	Intracellular	290	14276	3.07E-14
GO:0005737	Cytoplasm	252	11428	2.51E-13
GO:0005829	Cytosol	152	5193	2.51E-13
GO:0043226	Organelle	279	13515	2.51E-13
GO:0043229	Intracellular organelle	261	12528	6.80E-11

GO ID#	Pathway, molecular function	observed gene count	GO gene count	false discovery rate
GO:0005515	Protein binding	185	7026	9.06E-13
GO:0005488	Binding	260	12516	7.40E-10
GO:0045296	Cadherin binding	27	334	2.94E-08
GO:0019899	Enzyme binding	78	2239	4.55E-08
GO:0008092	Cytoskeletal protein binding	45	973	2.84E-07

Supplementary Figure 2. N-terminal fragment lengths of wt Htt and mutant Htt used to identify interacting proteins. The number of published articles reporting use of N-terminal Htt fragments of various lengths is illustrated for studies of wt Htt interactors (a) and mutant Htt interactors (b).

(a) N-terminal fragment lengths of wild-type Htt



(b) N-terminal fragment lengths of mutant Htt