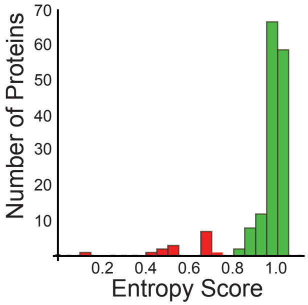
A

No.	Feature	Description
i	**NWD Score**	*Primary CompPASS Score: incorporates total spectral counts, frequency of observation, and reproducibility across replicates*
ii	**Z Score**	*Secondary CompPASS Score: Z-score transformation of a protein's average PSM's compared to its abundance in all other IP's.*
iii	**Plate Z Score**	*Z-score transformation of a protein's average PSM's compared to its abundance in all other IPs on the same plate.*
iv	**Entropy**	*Detects LC carry-over and other inconsistent proteins*
v	**Unique Peptide Bins**	*Unique Peptide Count (binned). A single bin is used for 10+ peptides.*
vi	**Ratio**	*Fraction of IP's in which a given protein was detected*
vii	**Total PSMs**	*Sum of PSM's observed for a given protein across ALL IP's.*
viii	**Ratio Total PSM's**	*For a given protein, the ratio of observed PSM's within a single IP to the total PSM's across all IP's.*
ix	**Unique:Total Peptide Ratio**	*Ratio of unique to total peptide counts.*

B

$$s_E = p_A \log_2(p_A) + p_B \log_2(p_B)$$

$$p_A = \frac{PSM_A + 0.5}{PSM_A + PSM_B + 1.0}$$



CDK19 PSMs across Runs

Entropy	Rep. A	Rep. B	Bait
0.41	0	5	**CDKL5**
0.54	0	3	**RCAN2**
0.34	0	7	**C1orf49**
0.18	0	17	**PON2**
0.98	508	353	**CDK19**
0.1	107	1	**UQCRB**
0.14	24	0	**FAM177A1**
0.21	14	0	**PPP1R1A**
0.41	5	0	**CDK5**
0.47	4	0	**PRG2**

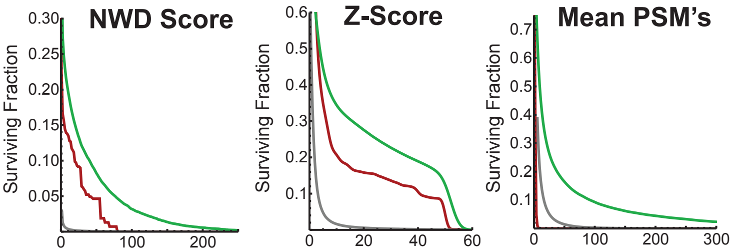
Run Order ↓

Run Order ↑

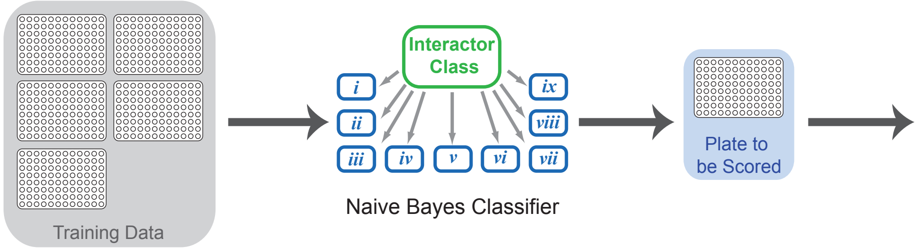
C

Initial Training Data

Class	Description	Percent
Likely Wrong ID	*Modeled by distribution of decoy prey ID's.*	0.05
Non-Interaction	*Bait-prey pairs not reported in STRING/GeneMania*	98.6
Likely Interaction	*Bait-prey pairs confirmed by STRING/GeneMania.*	1.35



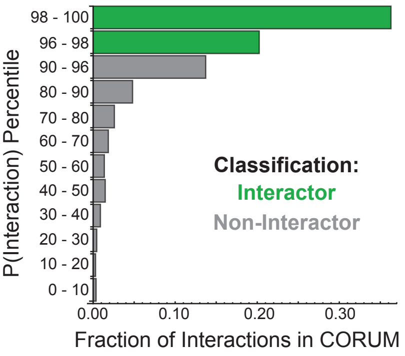
D



Bait	Prey	P(Wrong)	P(NoInt)	P(Int)
FBXO6	FBXO6	0	0	**1**
FBXO6	UBB	0	0	**1**
FBXO6	CUL1	0	0.002	**0.998**
FBXO6	COPS2	0	0.121	**0.879**
FBXO6	HSPA8	0	**0.974**	0.026
FBXO6	PSMD2	0	**0.986**	0.014
FBXO6	SLC25A6	0	**0.995**	0.005
FBXO6	TMEM30A	0.258	**0.738**	0.004
FBXO6	PLA2G15	**0.999**	0	0.001

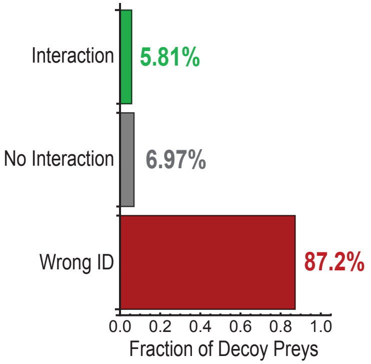
E

CORUM Comparison



F

Decoy Prey Classifications



G