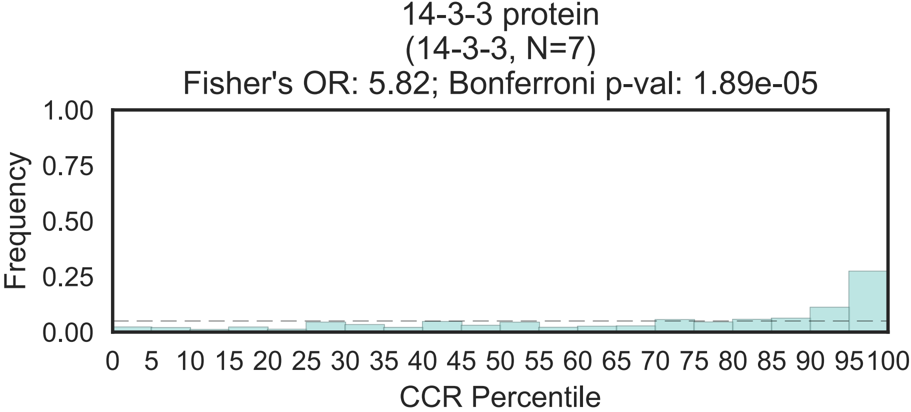
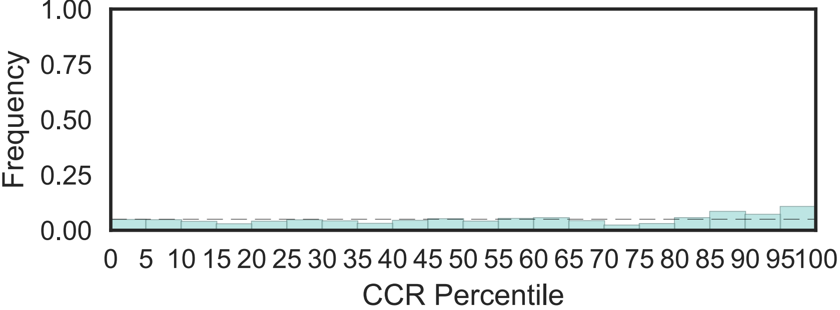
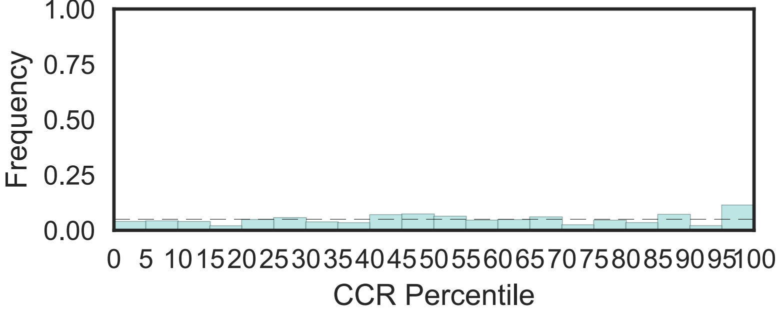
Supplementary Dataset 1.

The frequency represents the fraction of CCR base pairs that overlap an instance of the protein domain for each percentile bin (shown as 20 vigintiles). The first name is the full name of the domain, when applicable. The name in parentheses is the Pfam-A database name of the domain. The number after "N=" in parentheses represents the number of times the domain occurs throughout the genome. Statistics are not calculated if N<3. The dotted line represents the expectation of 0.05 frequency for each vigintile. The Fisher’s odds ratio is calculated using the number of intersections for the protein domain with the CCRs in the 95th percentile bin, and the number of intersections with other domains in that bin, as well as outside of that percentile bin for both the domain and other domains. The p-value is Bonferroni corrected across the 6,060 Pfam domains to show only the most significantly enriched domains genome-wide for constraint.

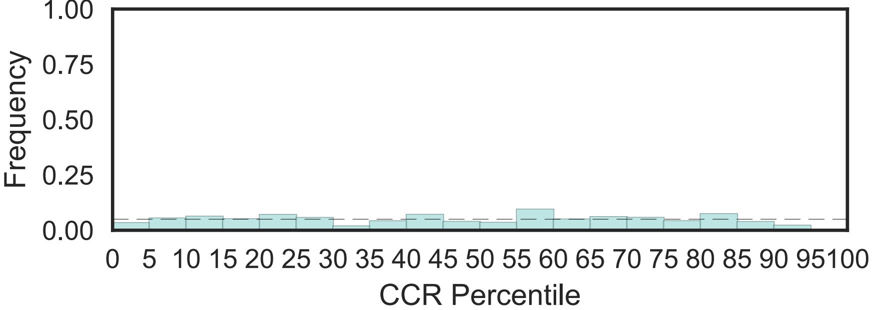

14-3-3 protein
(14-3-3, N=7)
Fisher's OR: 5.82; Bonferroni p-val: 1.89e-05
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



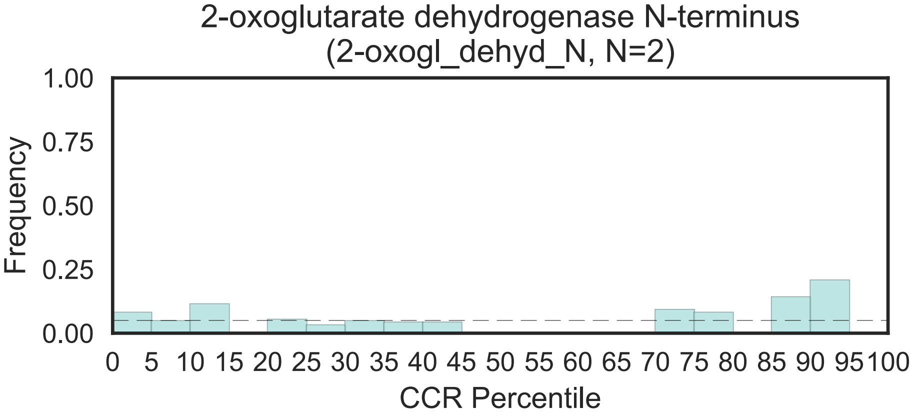
D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain
(2-Hacid_dh, N=4)
Fisher's OR: 1.43; Bonferroni p-val: 1

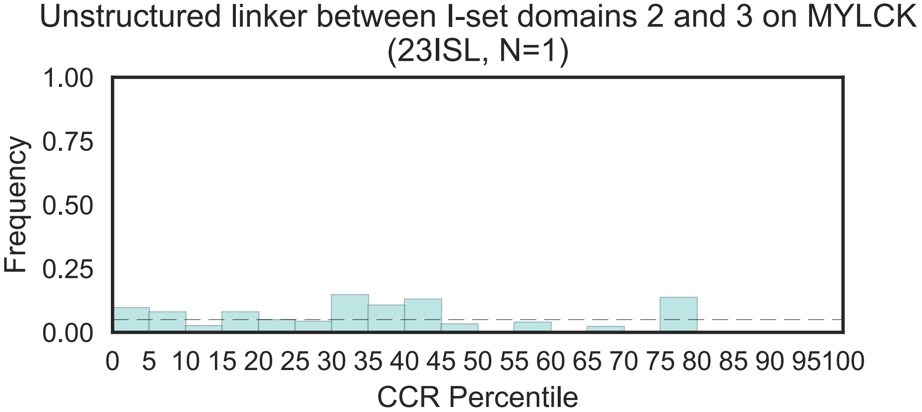


D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain
(2-Hacid_dh_C, N=8)
Fisher's OR: 1.39; Bonferroni p-val: 1

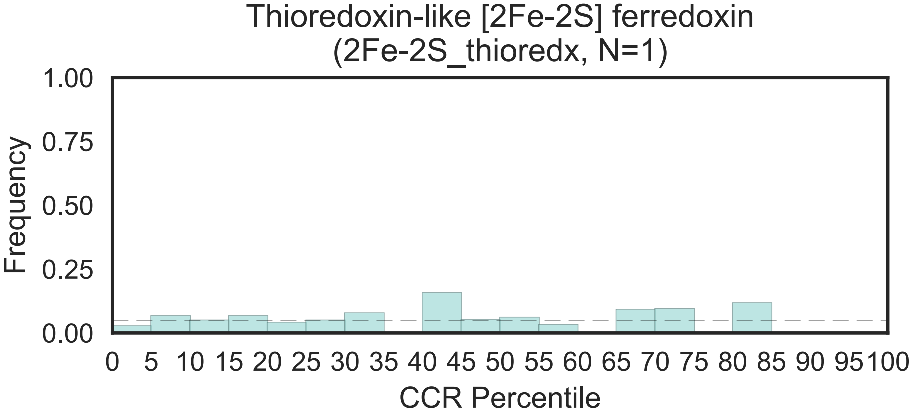


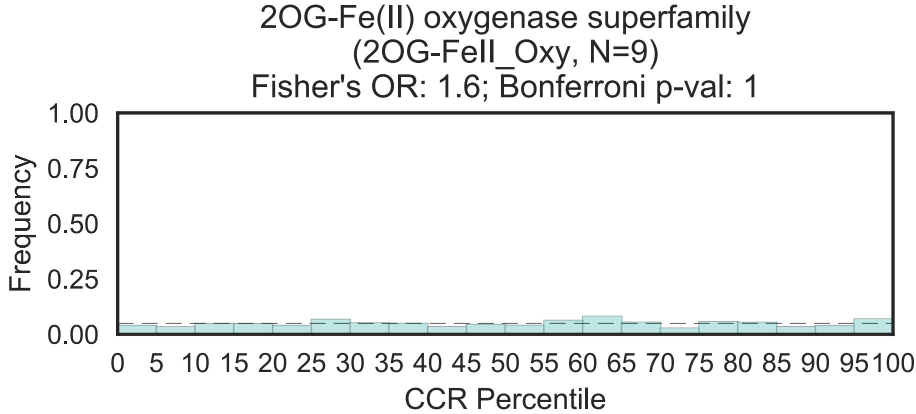
2-oxoacid dehydrogenases acyltransferase (catalytic domain)
(2-oxoacid_dh, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

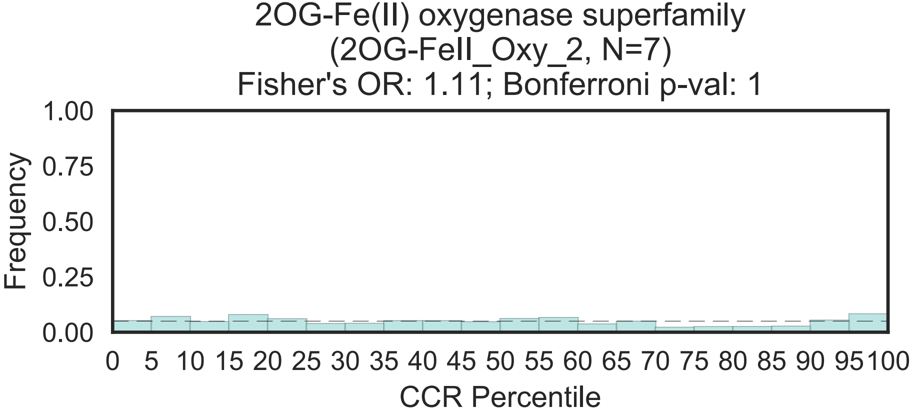

2-oxoglutarate dehydrogenase N-terminus
(2-oxogl_dehyd_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

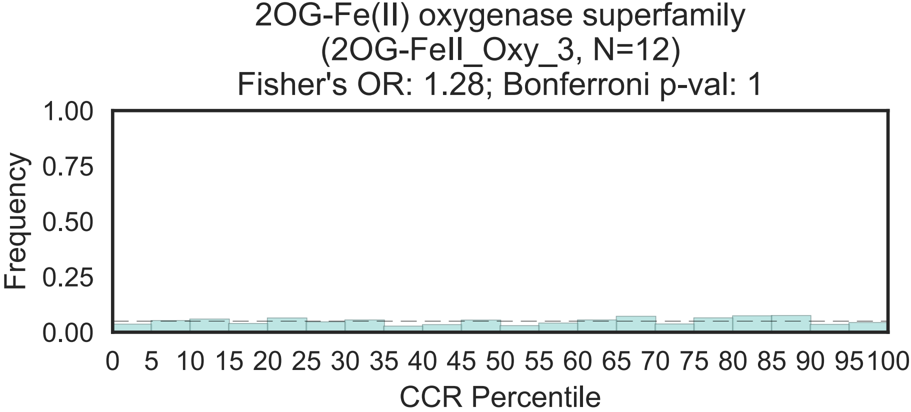


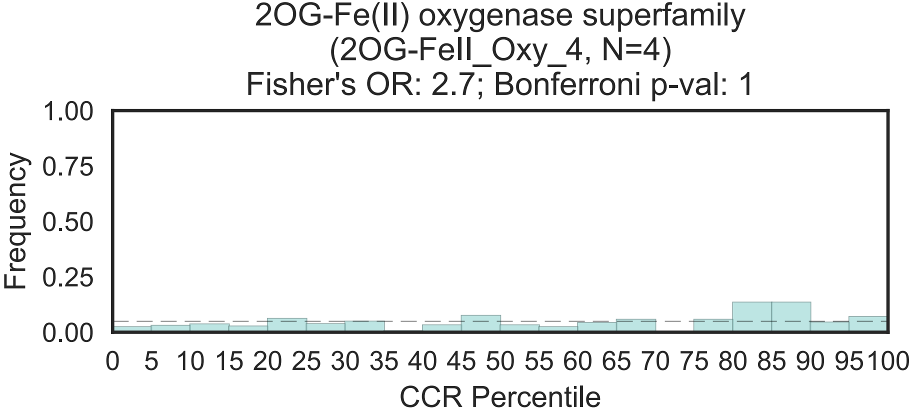
Unstructured linker between I-set domains 2 and 3 on MYLCK (23ISL, N=1)

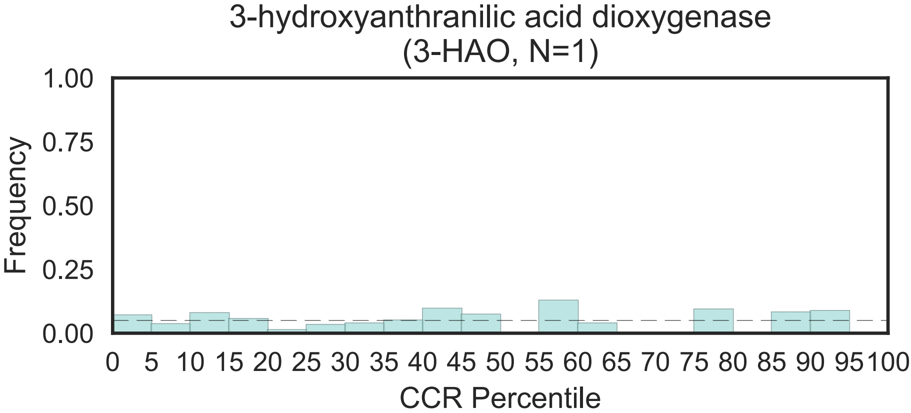

Thioredoxin-like [2Fe-2S] ferredoxin
(2Fe-2S_thioredx, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

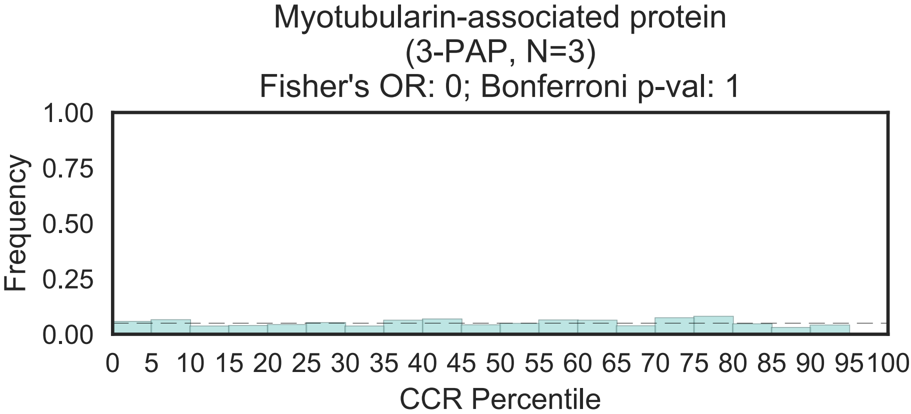

2OG-Fe(II) oxygenase superfamily
(2OG-FeII_Oxy, N=9)
Fisher's OR: 1.6; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

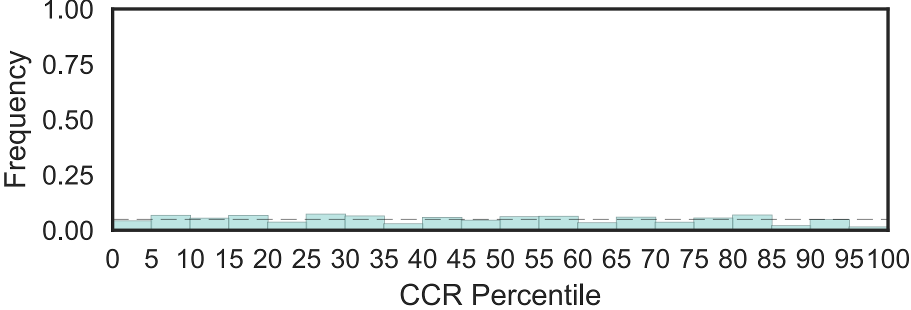

2OG-Fe(II) oxygenase superfamily
(2OG-FeII_Oxy_2, N=7)
Fisher's OR: 1.11; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

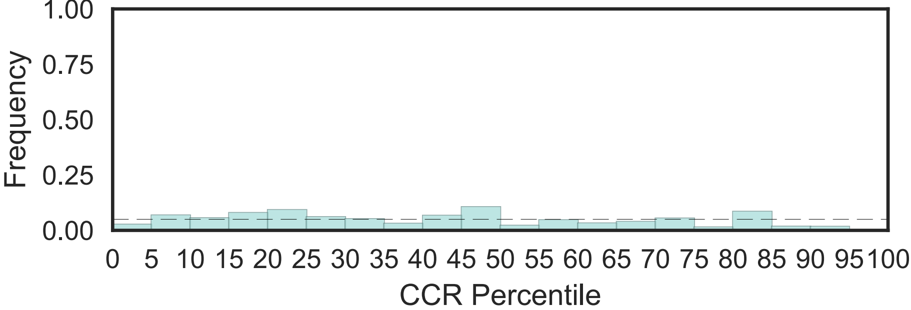

2OG-Fe(II) oxygenase superfamily
(2OG-FeII_Oxy_3, N=12)
Fisher's OR: 1.28; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


2OG-Fe(II) oxygenase superfamily
(2OG-FeII_Oxy_4, N=4)
Fisher's OR: 2.7; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

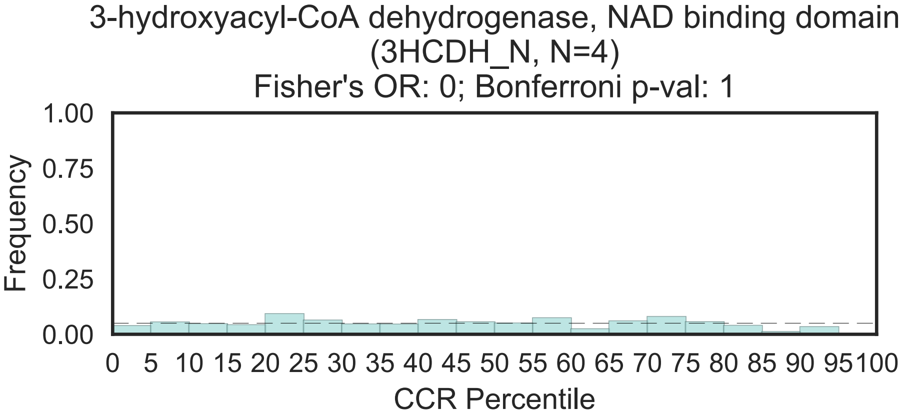

3-hydroxyanthranilic acid dioxygenase
(3-HAO, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Myotubularin-associated protein
(3-PAP, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

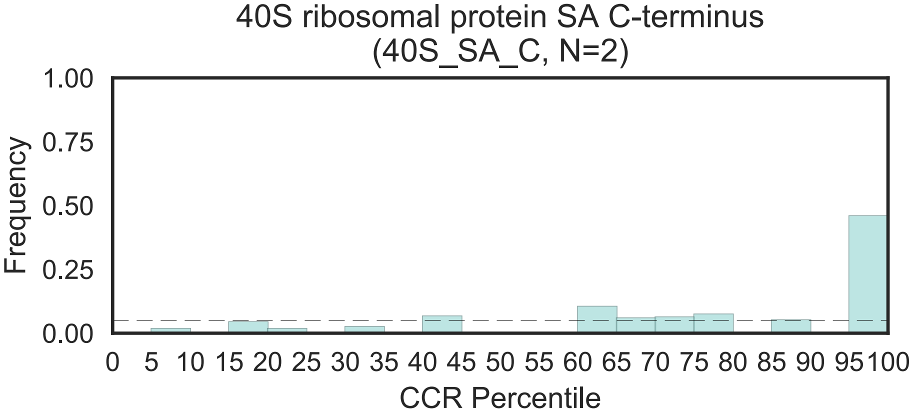

3-beta hydroxysteroid dehydrogenase/isomerase family
(3Beta_HSD, N=10)
Fisher's OR: 0.24; Bonferroni p-val: 1

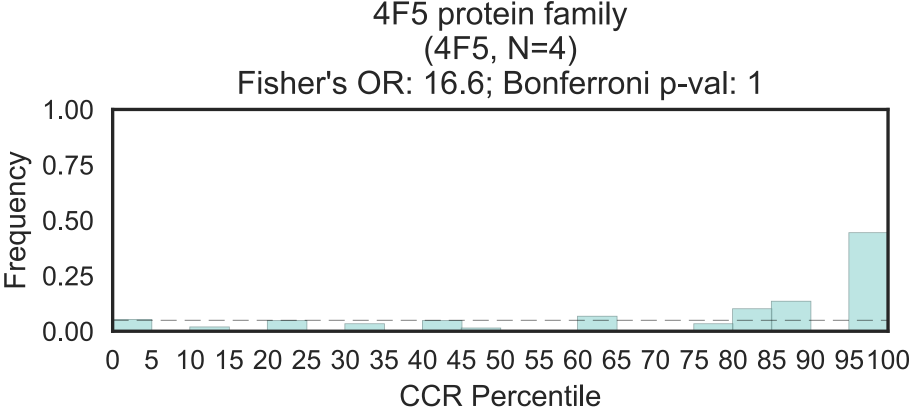


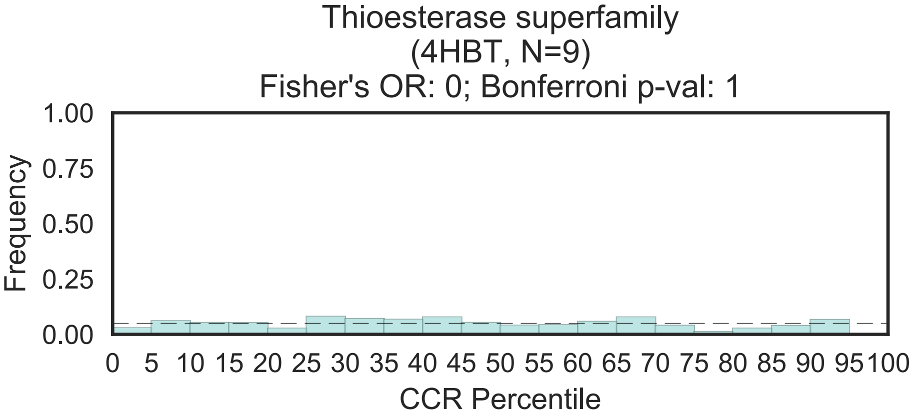
3-hydroxyacyl-CoA dehydrogenase, C-terminal domain
(3HCDH, N=6)
Fisher's OR: 0; Bonferroni p-val: 1

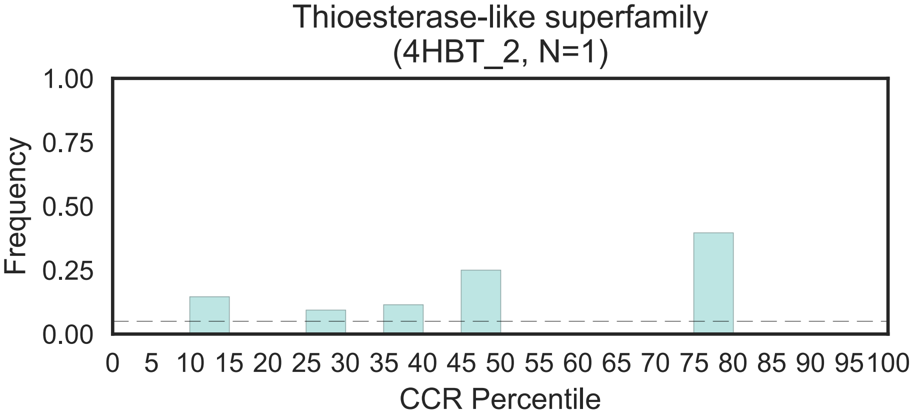


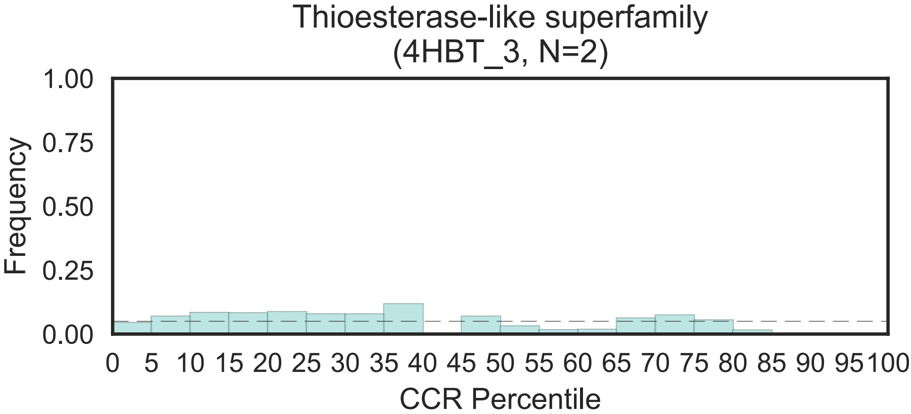
3-hydroxyacyl-CoA dehydrogenase, NAD binding domain
(3HCDH_N, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

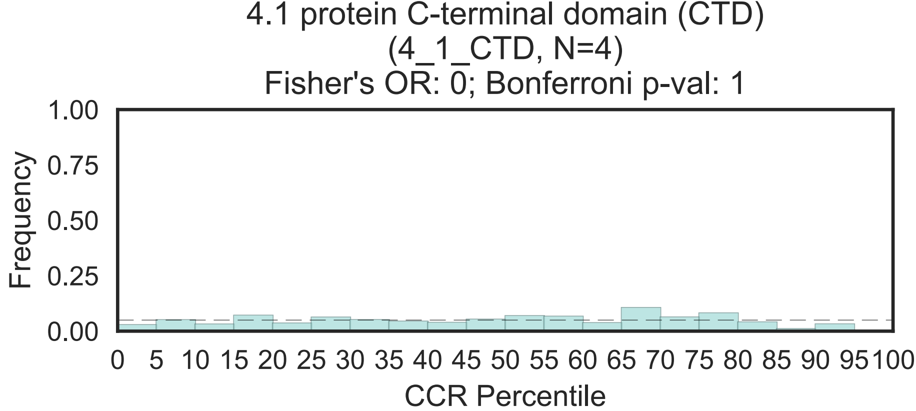

40S ribosomal protein SA C-terminus
(40S_SA_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

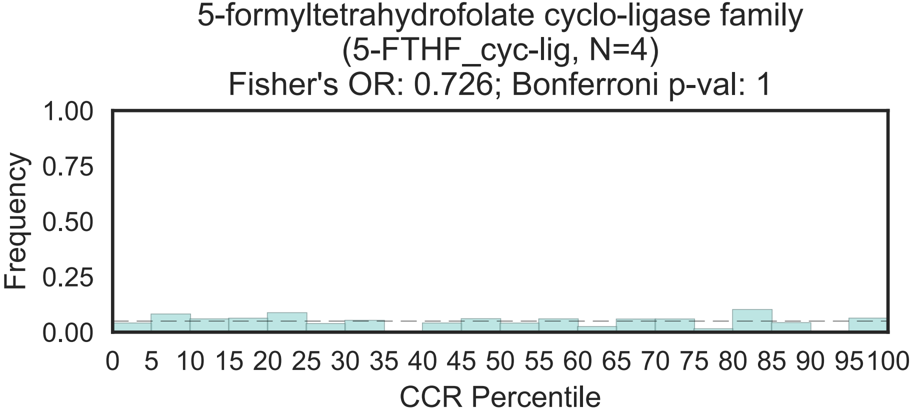

4F5 protein family
(4F5, N=4)
Fisher's OR: 16.6; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Thioesterase superfamily
(4HBT, N=9)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

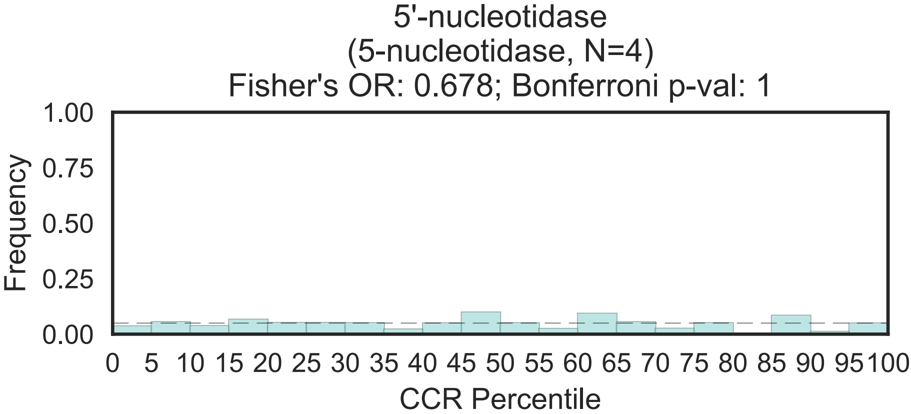

Thioesterase-like superfamily
(4HBT_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

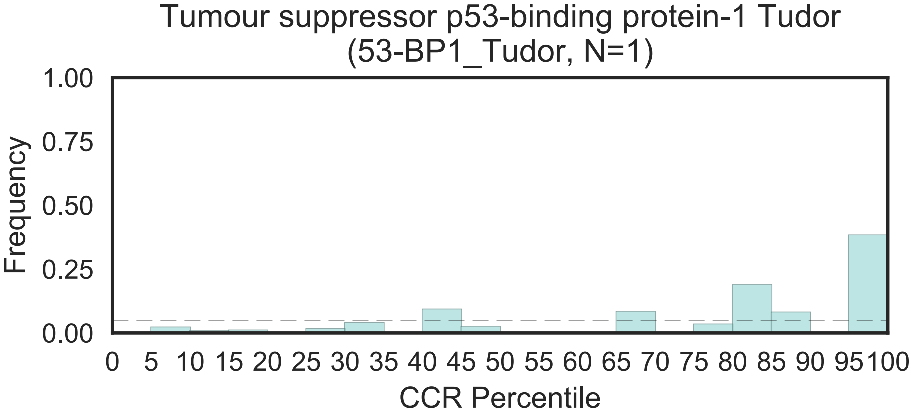

Thioesterase-like superfamily
(4HBT_3, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

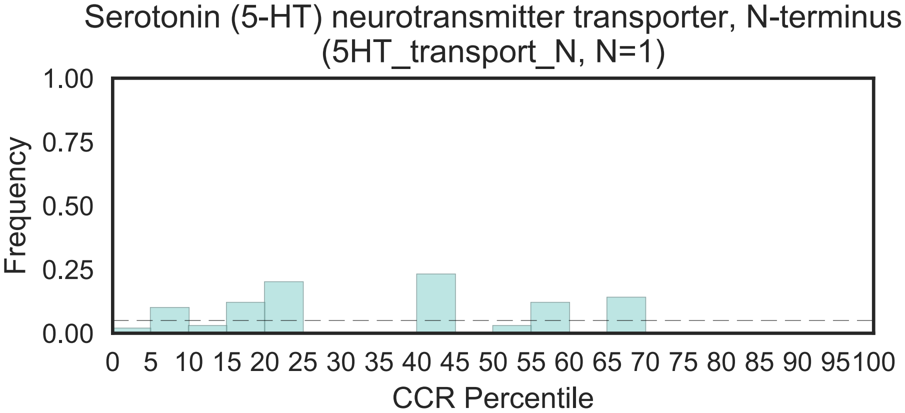

4.1 protein C-terminal domain (CTD)
(4_1_CTD, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

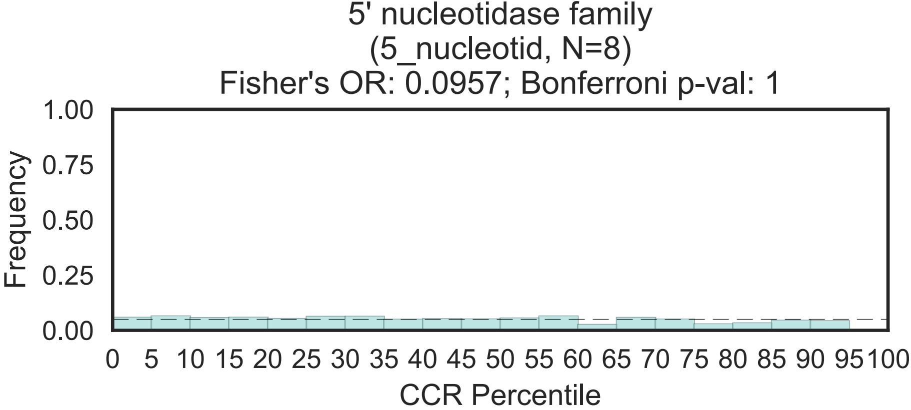


5-formyltetrahydrofolate cyclo-ligase family
(5-FTHF_cyc-lig, N=4)
Fisher's OR: 0.726; Bonferroni p-val: 1

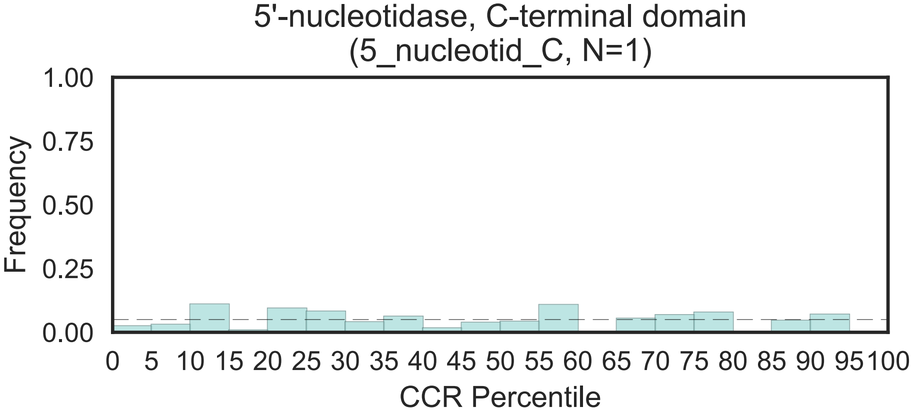

5'-nucleotidase
(5-nucleotidase, N=4)
Fisher's OR: 0.678; Bonferroni p-val: 1

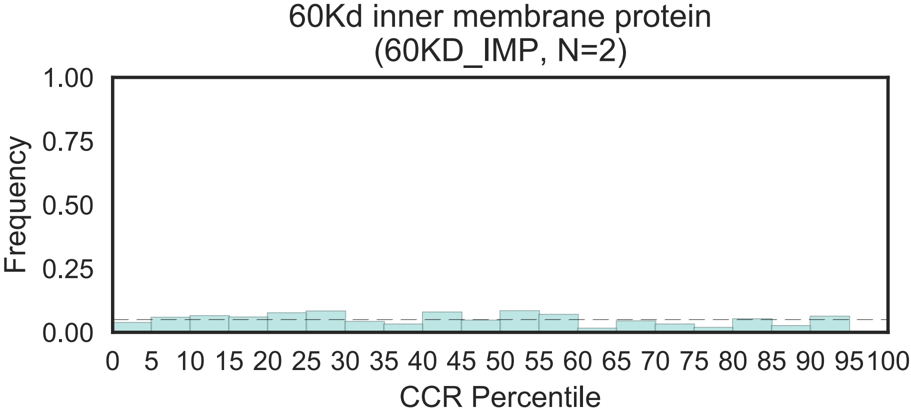

Tumour suppressor p53-binding protein-1 Tudor
(53-BP1_Tudor, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Serotonin (5-HT) neurotransmitter transporter, N-terminus
(5HT_transport_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

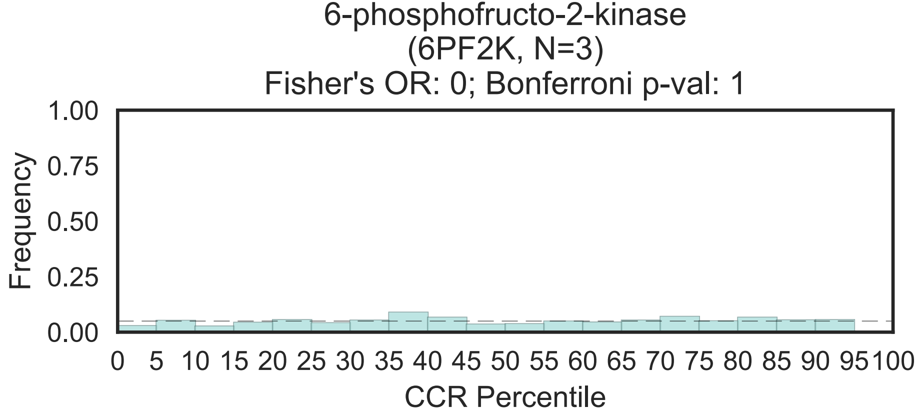


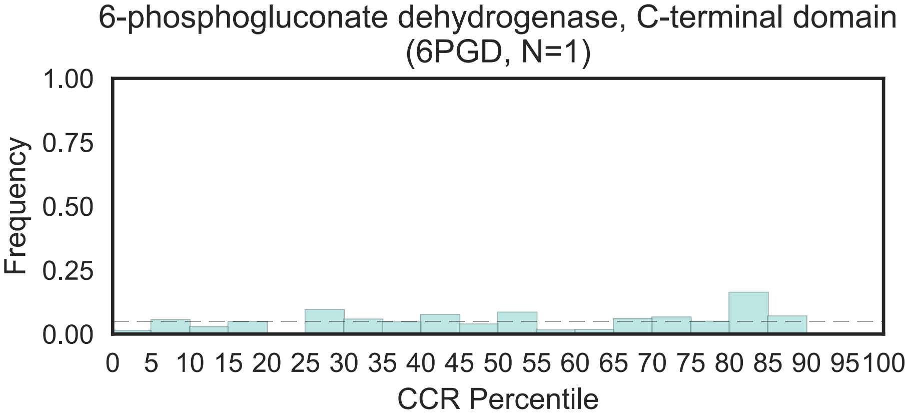
5' nucleotidase family
(5_nucleotid, N=8)
Fisher's OR: 0.0957; Bonferroni p-val: 1


5'-nucleotidase, C-terminal domain
(5_nucleotid_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

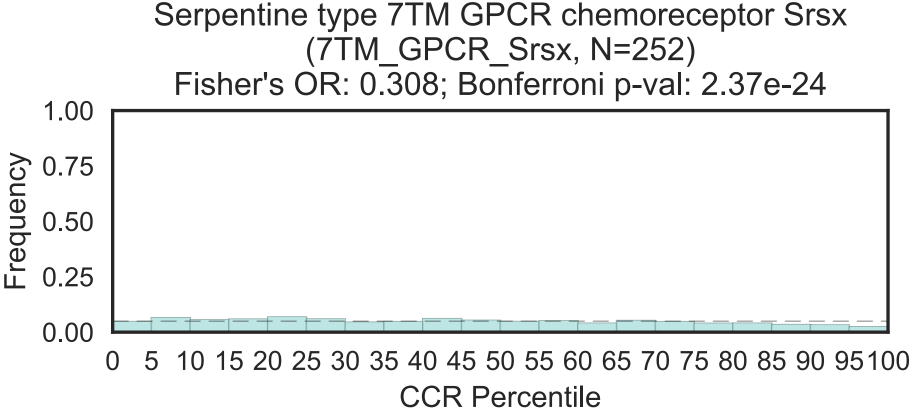


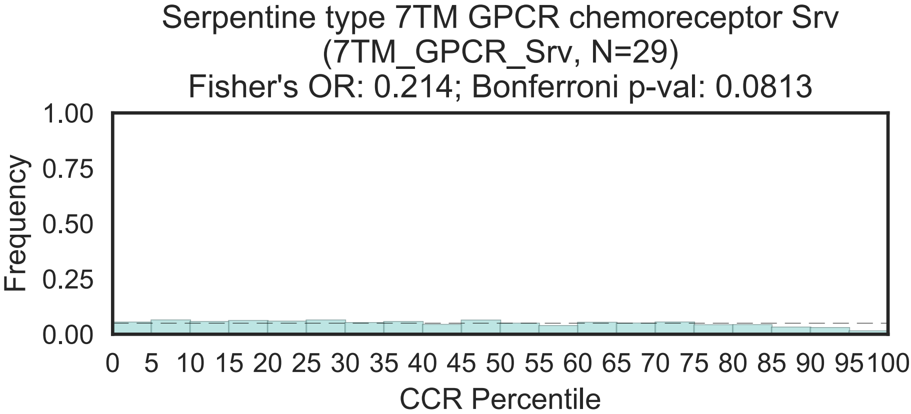
60Kd inner membrane protein
(60KD_IMP, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

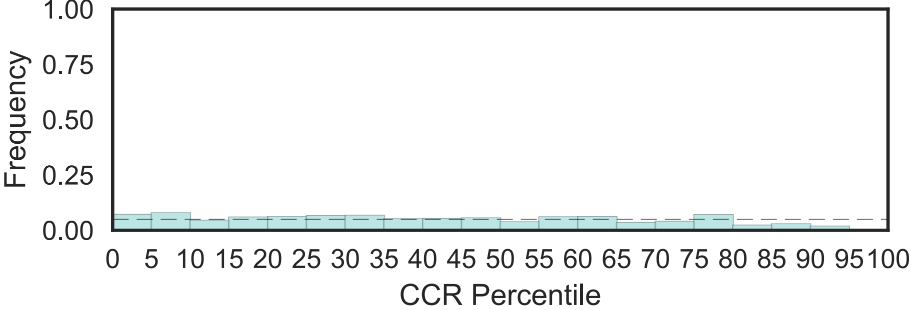

6-phosphofructo-2-kinase
(6PF2K, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



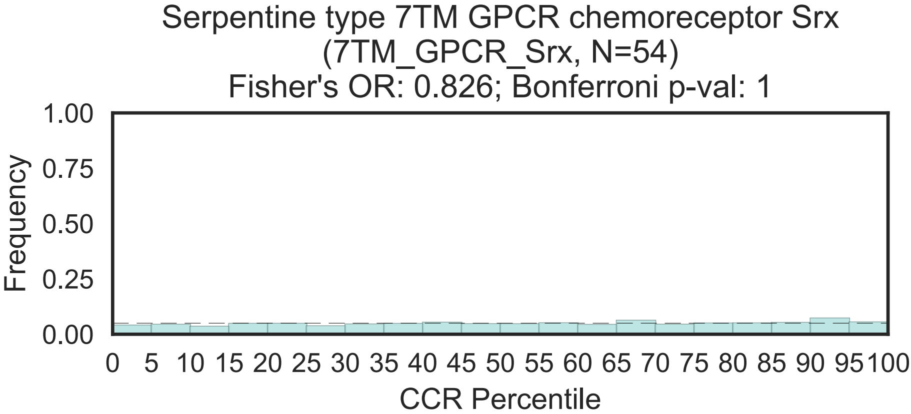
6-phosphogluconate dehydrogenase, C-terminal domain
(6PGD, N=1)

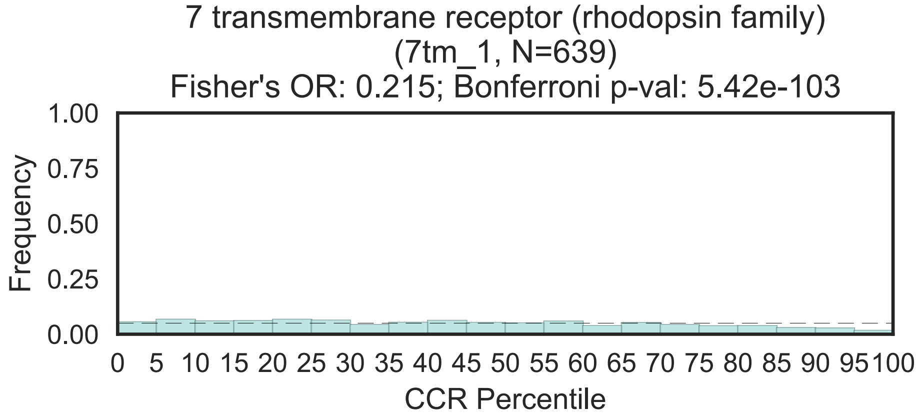

Serpentine type 7TM GPCR chemoreceptor Srsx
(7TM_GPCR_Srsx, N=252)
Fisher's OR: 0.308; Bonferroni p-val: 2.37e-24
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

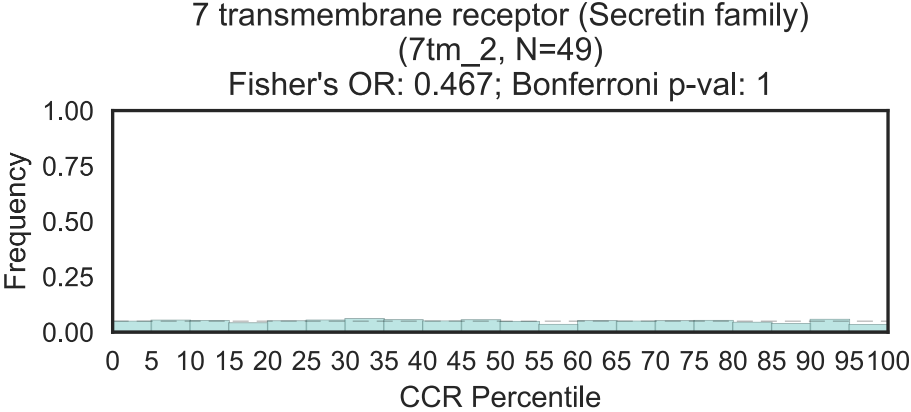

Serpentine type 7TM GPCR chemoreceptor Srv
(7TM_GPCR_Srv, N=29)
Fisher's OR: 0.214; Bonferroni p-val: 0.0813
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

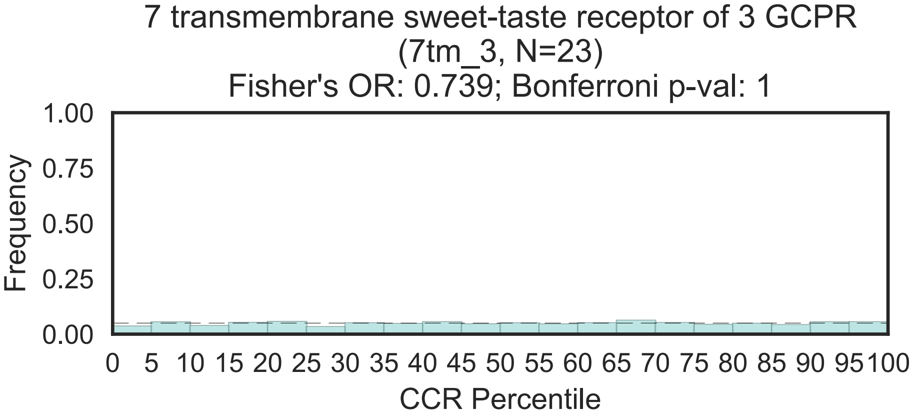


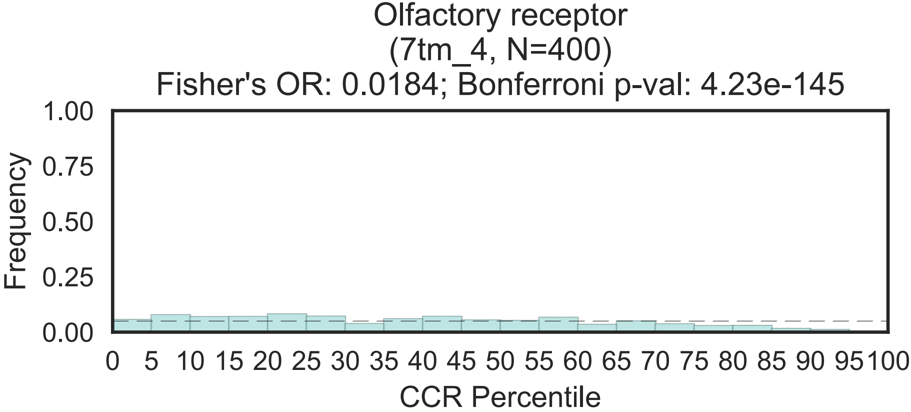
Serpentine type 7TM GPCR chemoreceptor Srw
(7TM_GPCR_Srw, N=8)
Fisher's OR: 0; Bonferroni p-val: 1

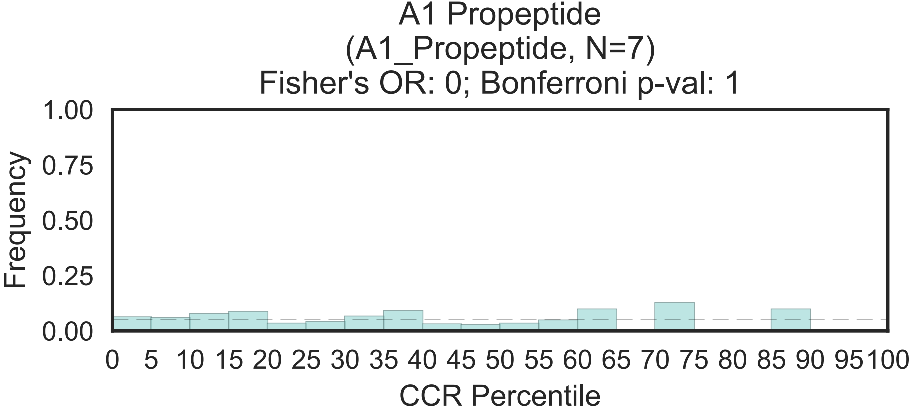

Serpentine type 7TM GPCR chemoreceptor Srx
(7TM_GPCR_Srx, N=54)
Fisher's OR: 0.826; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

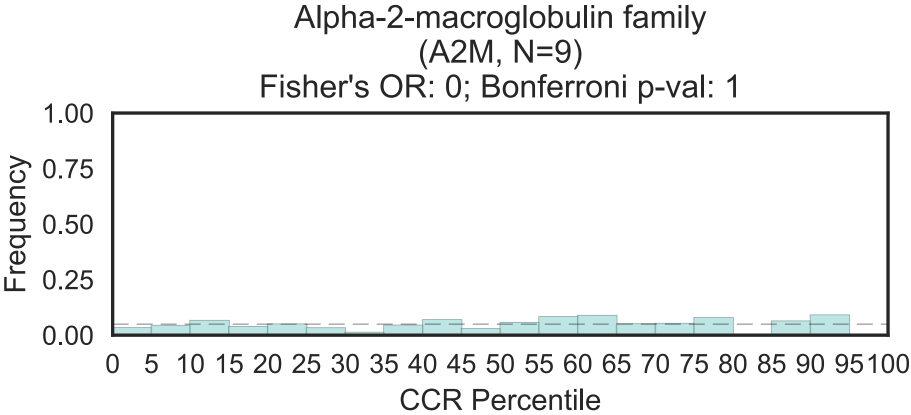

7 transmembrane receptor (rhodopsin family)
(7tm_1, N=639)
Fisher's OR: 0.215; Bonferroni p-val: 5.42e-103
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

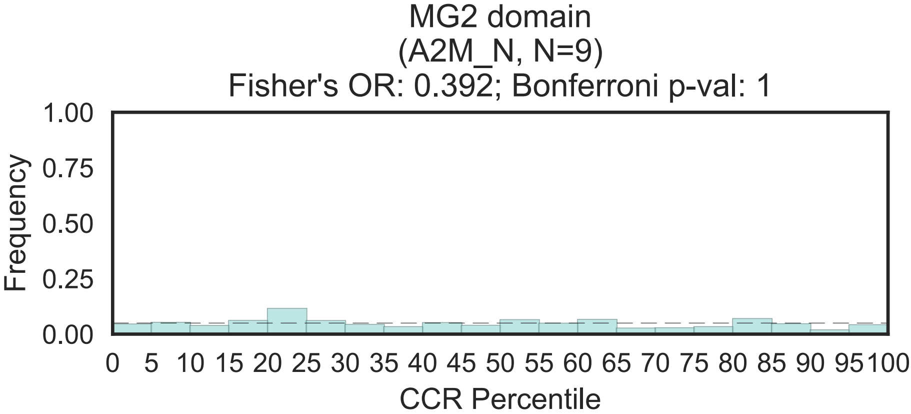

7 transmembrane receptor (Secretin family)
(7tm_2, N=49)
Fisher's OR: 0.467; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

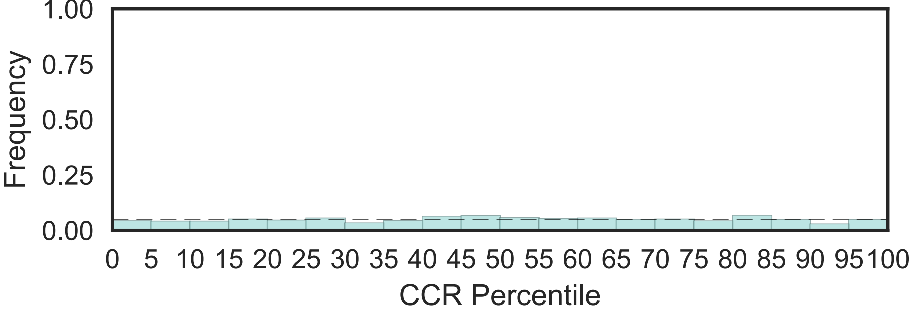

7 transmembrane sweet-taste receptor of 3 GCPR
(7tm_3, N=23)
Fisher's OR: 0.739; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Olfactory receptor
(7tm_4, N=400)
Fisher's OR: 0.0184; Bonferroni p-val: 4.23e-145
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

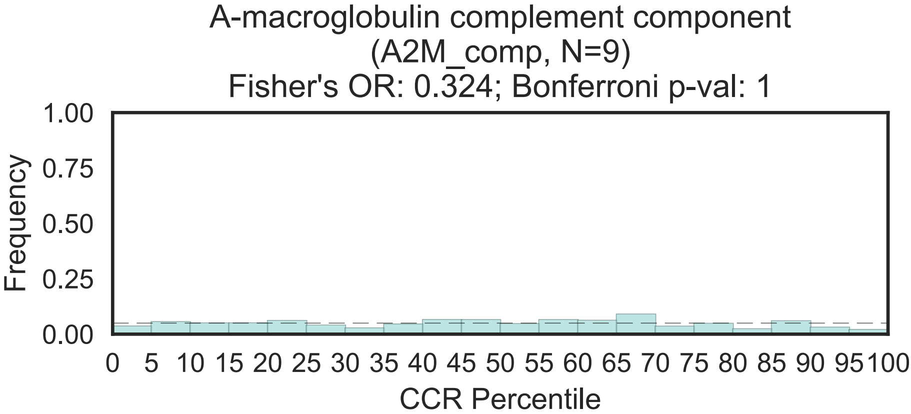

A1 Propeptide
(A1_Propeptide, N=7)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

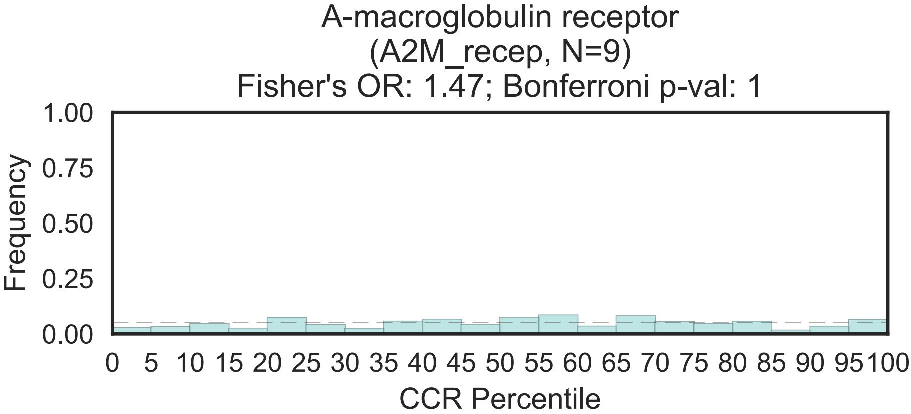

Alpha-2-macroglobulin family
(A2M, N=9)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


MG2 domain
(A2M_N, N=9)
Fisher's OR: 0.392; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

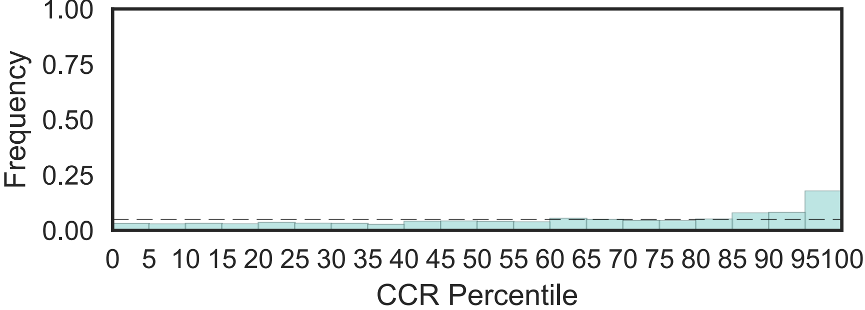


Alpha-2-macroglobulin family N-terminal region
(A2M_N_2, N=9)
Fisher's OR: 0.563; Bonferroni p-val: 1

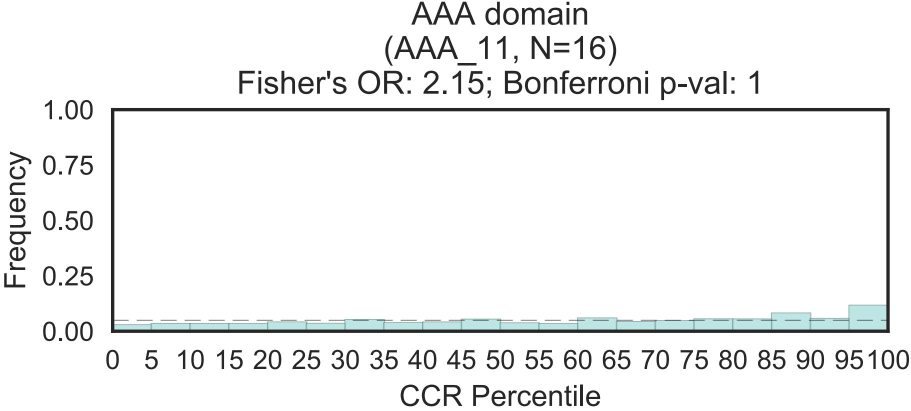

A-macroglobulin complement component
(A2M_comp, N=9)
Fisher's OR: 0.324; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

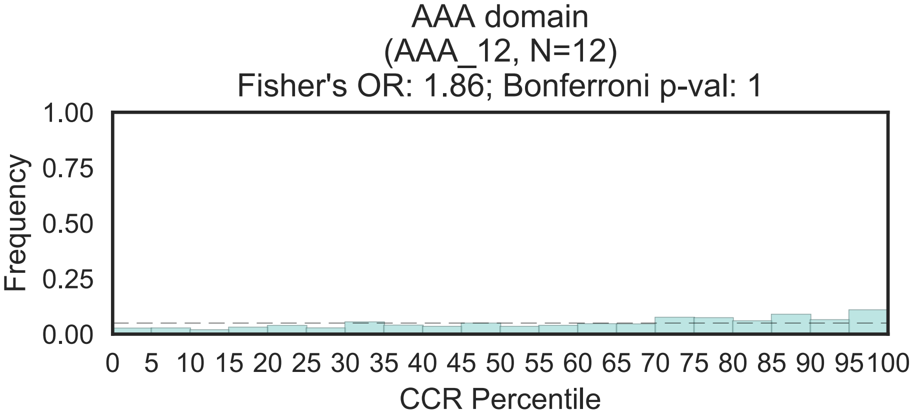


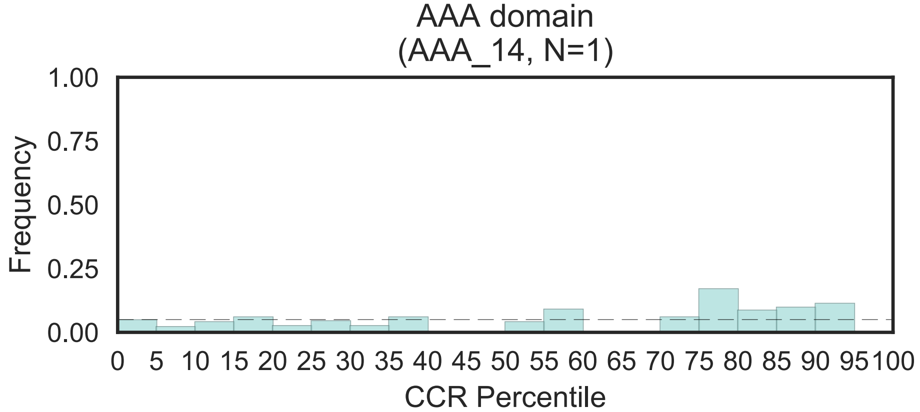
A-macroglobulin receptor
(A2M_recep, N=9)
Fisher's OR: 1.47; Bonferroni p-val: 1

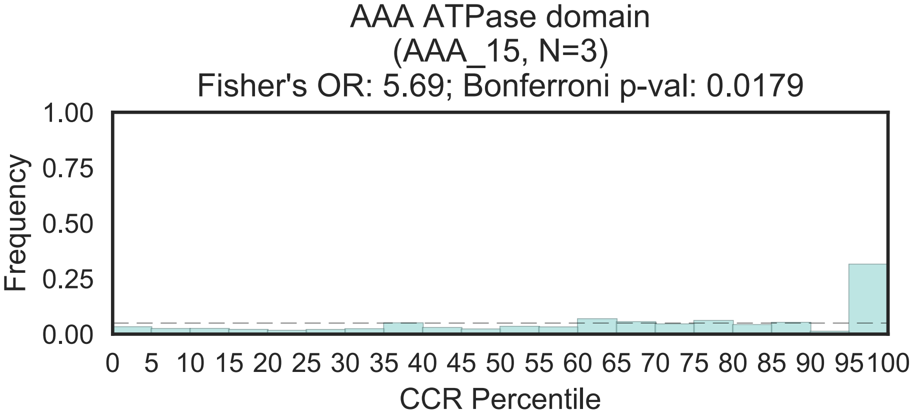


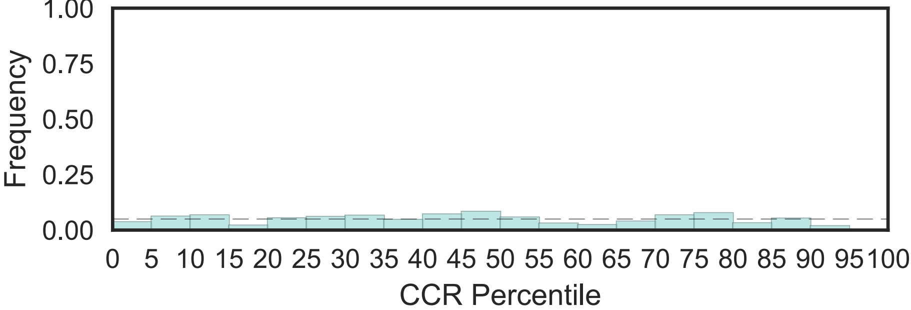
ATPase family associated with various cellular activities (AAA)
(AAA, N=64)
Fisher's OR: 2.88; Bonferroni p-val: 6.71e-08


AAA domain
(AAA_11, N=16)
Fisher's OR: 2.15; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

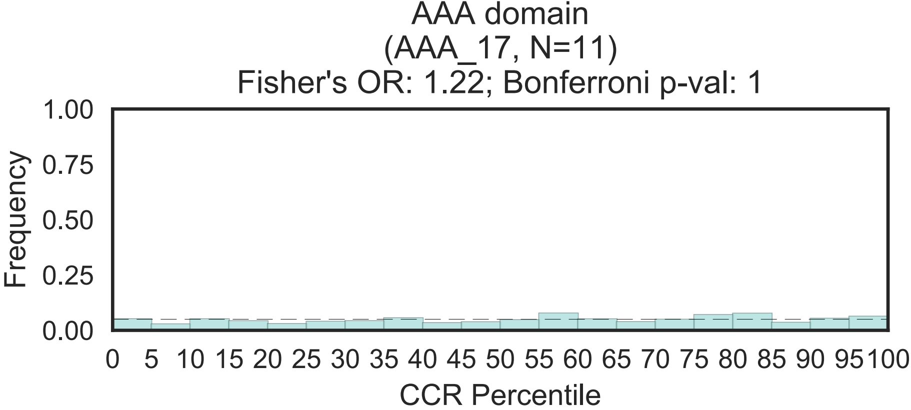

AAA domain
(AAA_12, N=12)
Fisher's OR: 1.86; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

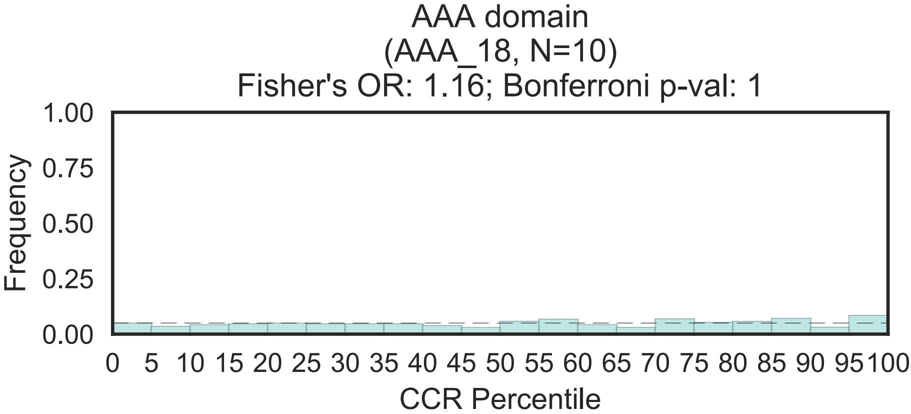

AAA domain
(AAA_14, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

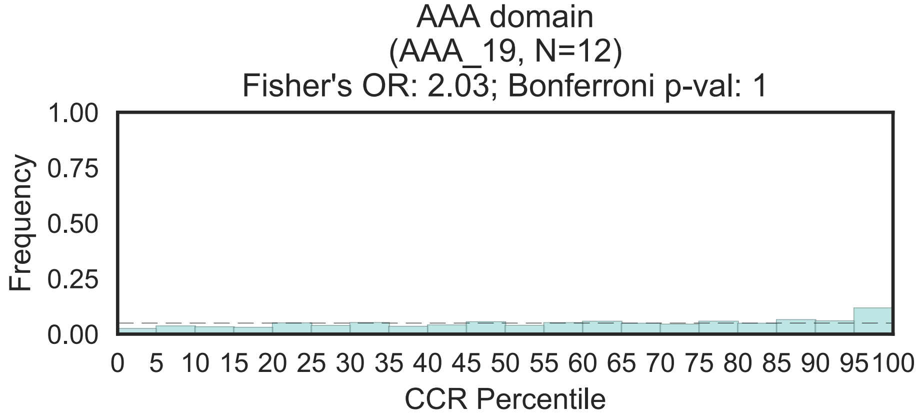

AAA ATPase domain
(AAA_15, N=3)
Fisher's OR: 5.69; Bonferroni p-val: 0.0179
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

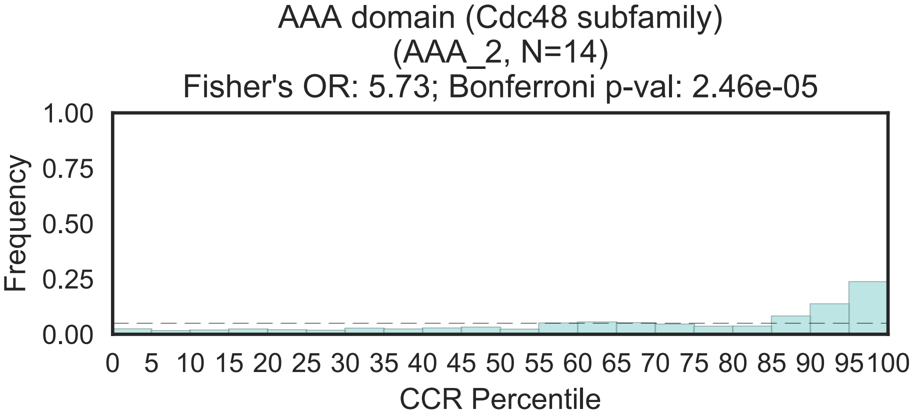


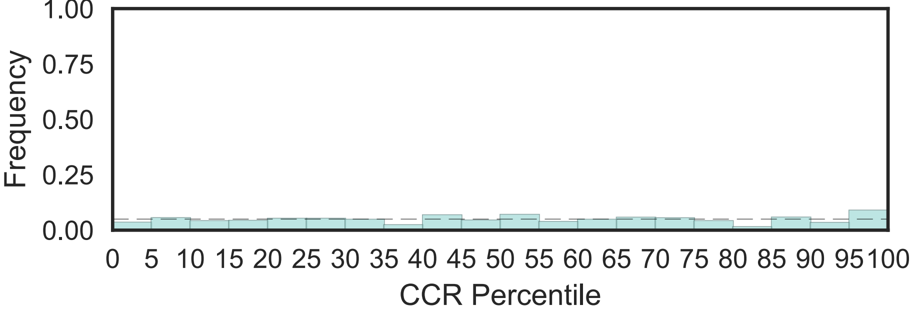
AAA ATPase domain
(AAA_16, N=4)
Fisher's OR: 0; Bonferroni p-val: 1


AAA domain
(AAA_17, N=11)
Fisher's OR: 1.22; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

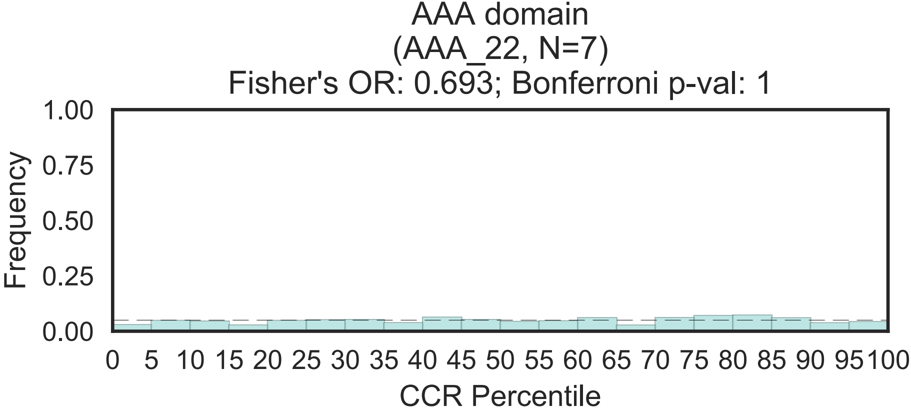

AAA domain
(AAA_18, N=10)
Fisher's OR: 1.16; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

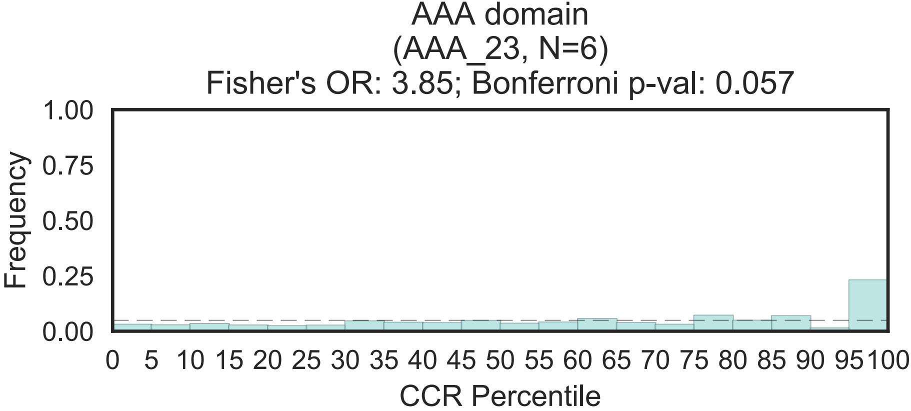

AAA domain
(AAA_19, N=12)
Fisher's OR: 2.03; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

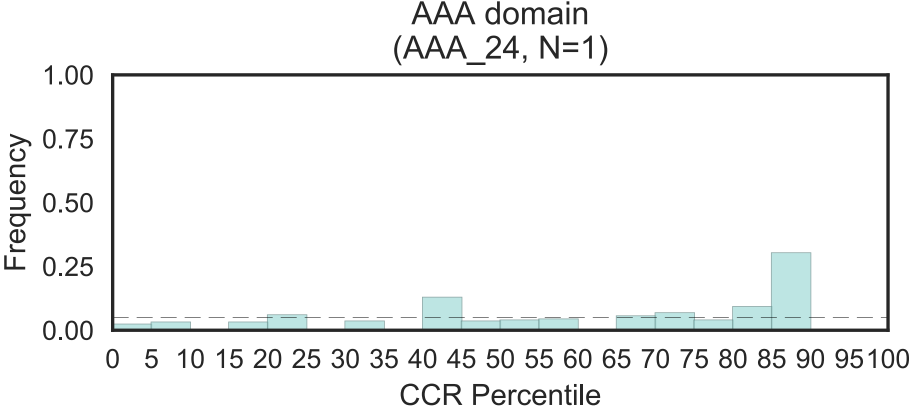

AAA domain (Cdc48 subfamily)
(AAA_2, N=14)
Fisher's OR: 5.73; Bonferroni p-val: 2.46e-05
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

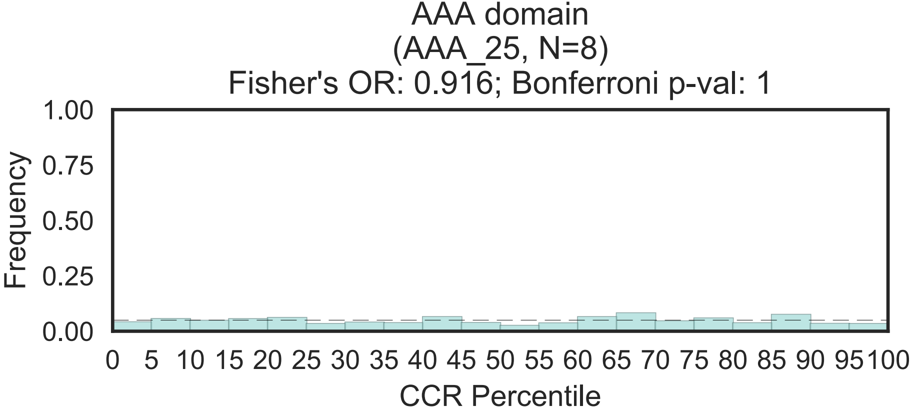


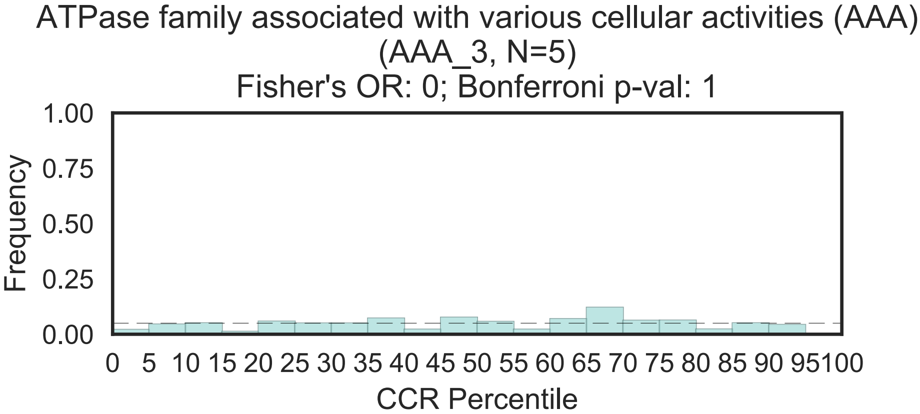
AAA domain, putative AbiEii toxin, Type IV TA system
(AAA_21, N=13)
Fisher's OR: 1.47; Bonferroni p-val: 1


AAA domain
(AAA_22, N=7)
Fisher's OR: 0.693; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

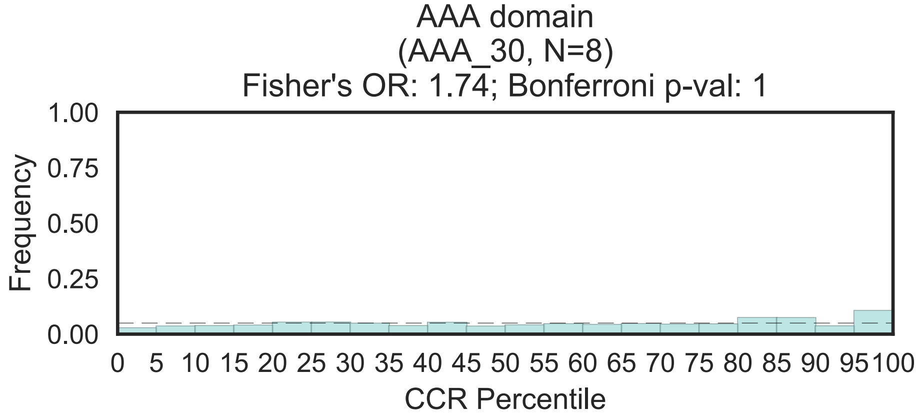

AAA domain
(AAA_23, N=6)
Fisher's OR: 3.85; Bonferroni p-val: 0.057
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


AAA domain
(AAA_24, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

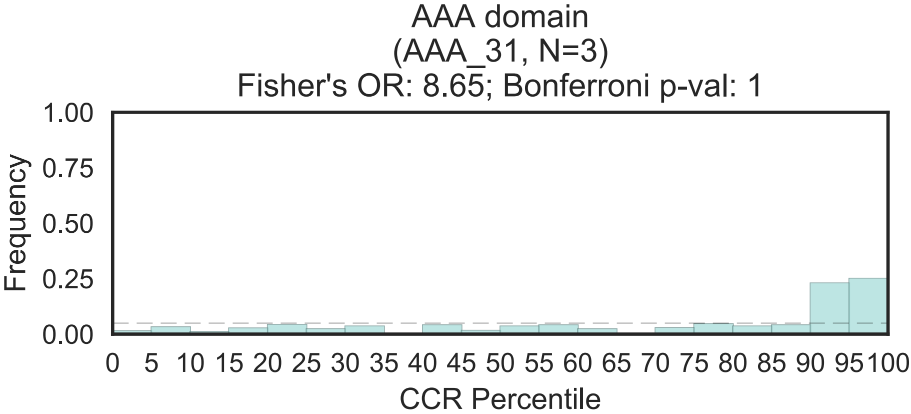

AAA domain
(AAA_25, N=8)
Fisher's OR: 0.916; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



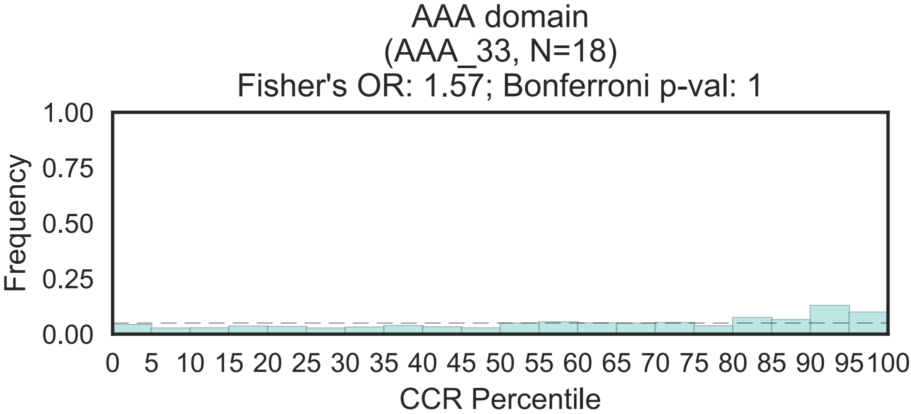
ATPase family associated with various cellular activities (AAA)
(AAA_3, N=5)
Fisher's OR: 0; Bonferroni p-val: 1

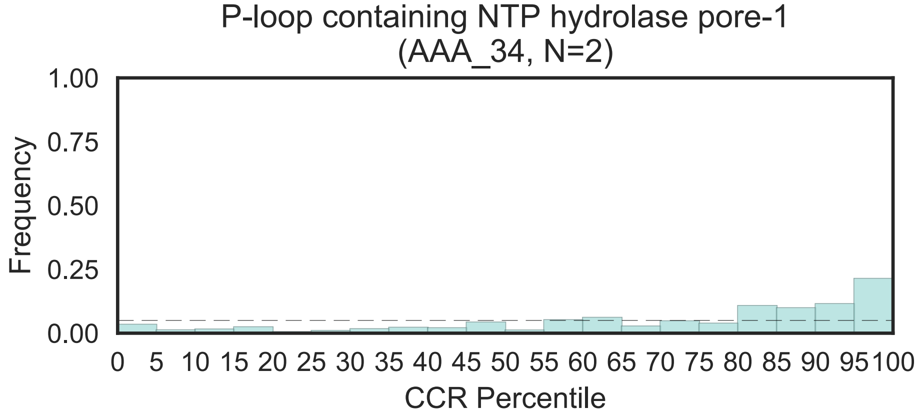


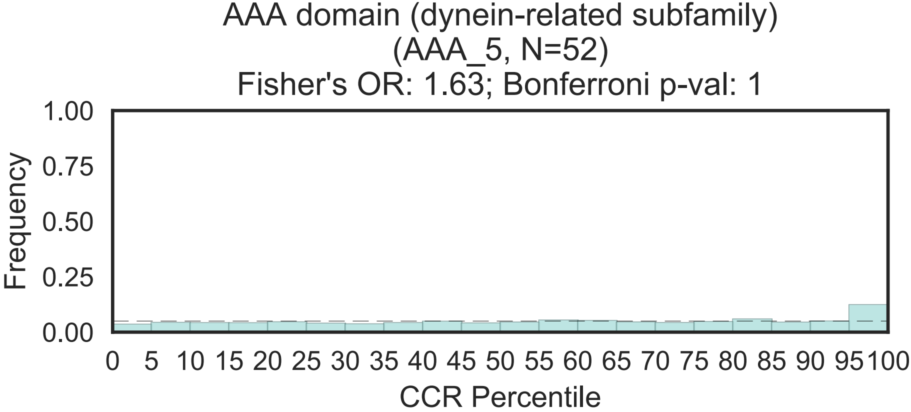
AAA domain
(AAA_30, N=8)
Fisher's OR: 1.74; Bonferroni p-val: 1

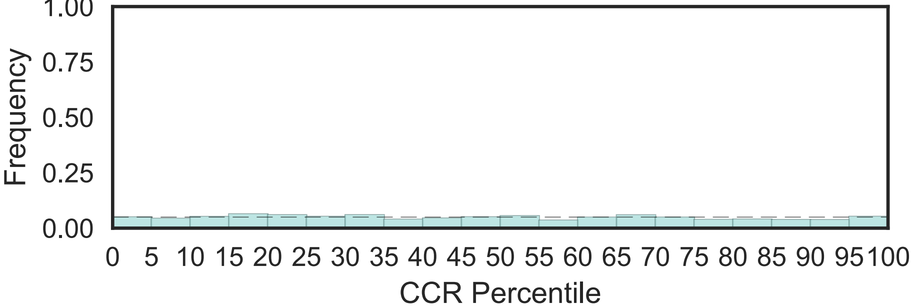


AAA domain
(AAA_31, N=3)
Fisher's OR: 8.65; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

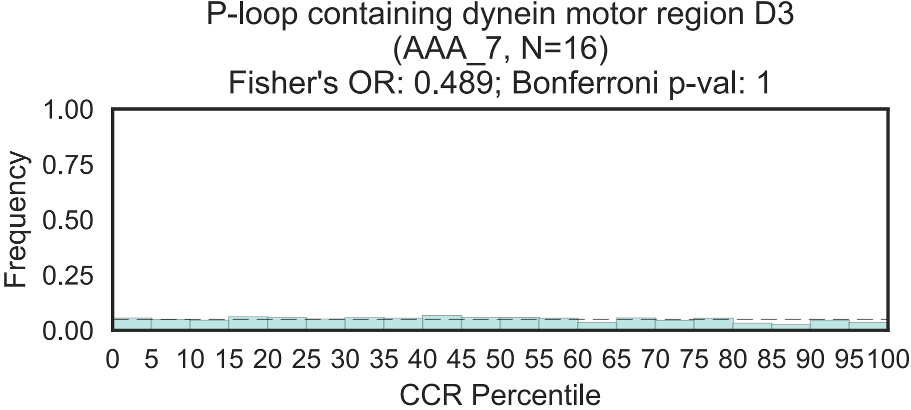

AAA domain
(AAA_33, N=18)
Fisher's OR: 1.57; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

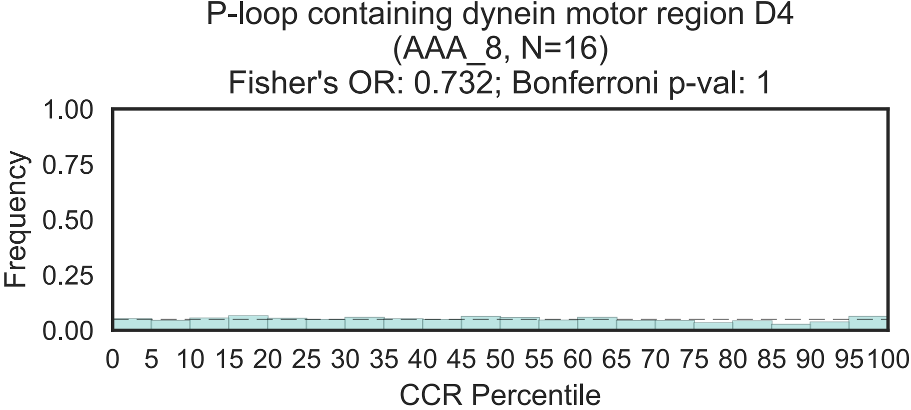

P-loop containing NTP hydrolase pore-1
(AAA_34, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

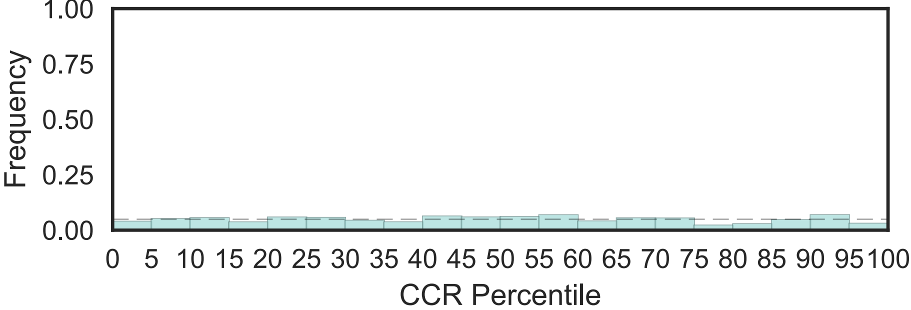

AAA domain (dynein-related subfamily)
(AAA_5, N=52)
Fisher's OR: 1.63; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



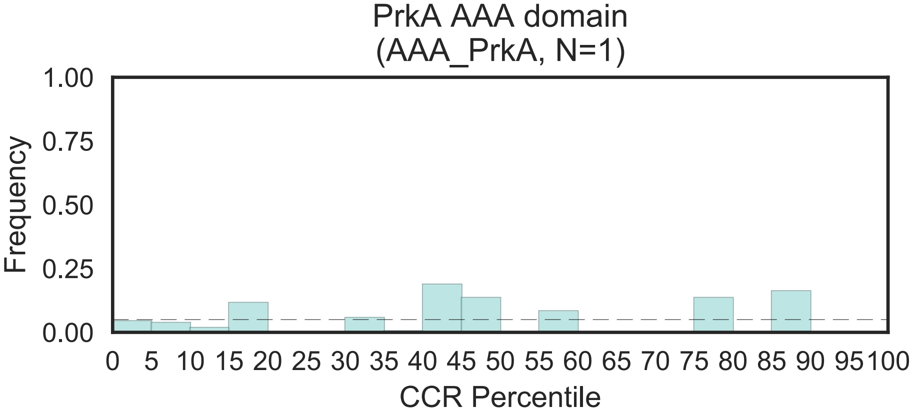
Hydrolytic ATP binding site of dynein motor region D1
(AAA_6, N=17)
Fisher's OR: 0.869; Bonferroni p-val: 1


P-loop containing dynein motor region D3
(AAA_7, N=16)
Fisher's OR: 0.489; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

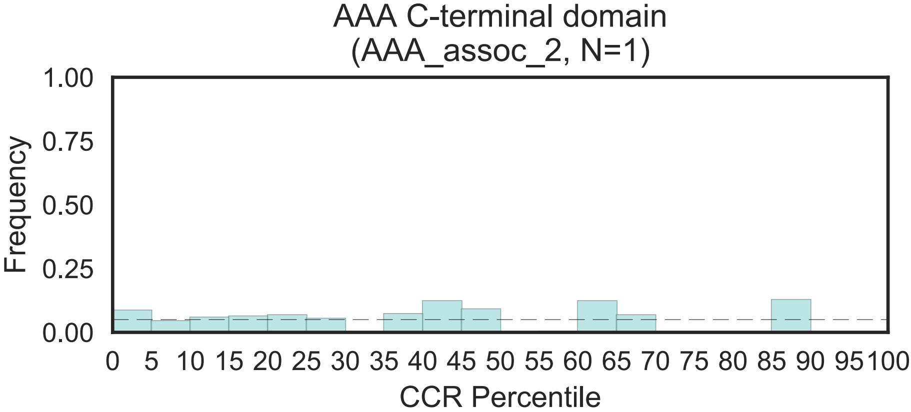

P-loop containing dynein motor region D4
(AAA_8, N=16)
Fisher's OR: 0.732; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

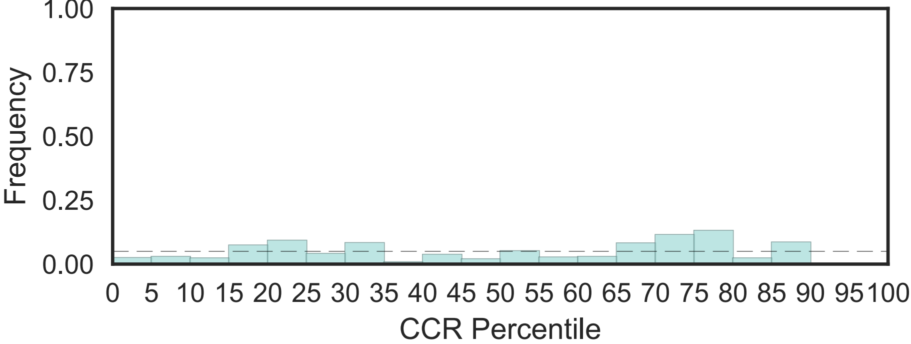


ATP-binding dynein motor region D5
(AAA_9, N=14)
Fisher's OR: 0.476; Bonferroni p-val: 1

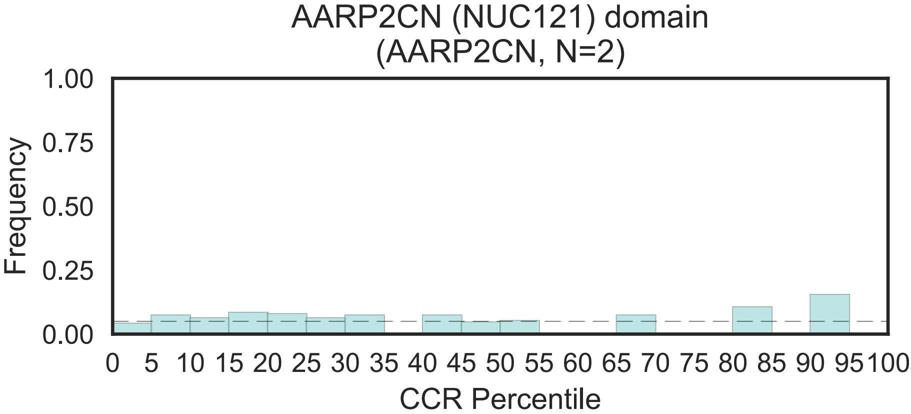


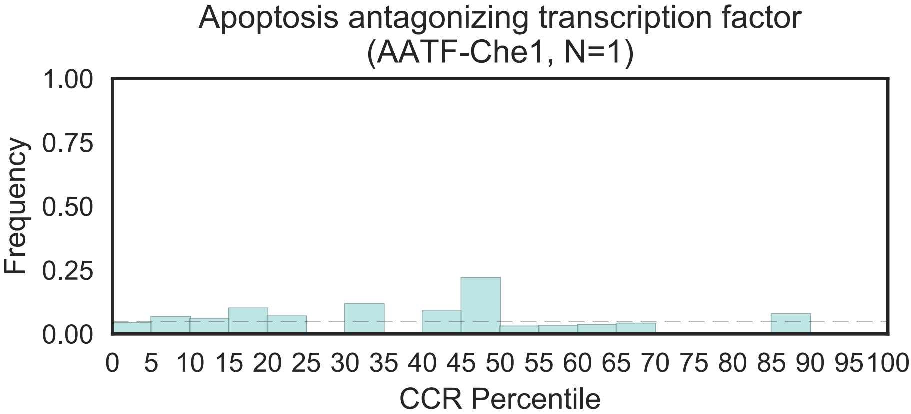
PrkA AAA domain
(AAA_PrkA, N=1)

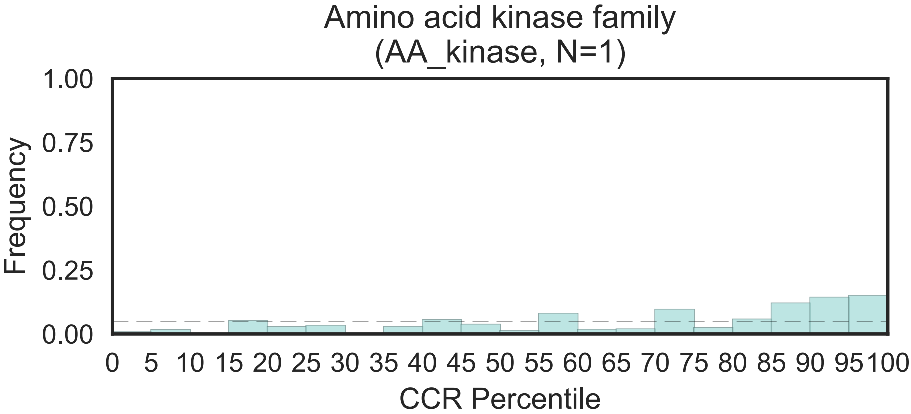

AAA C-terminal domain
(AAA_assoc_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

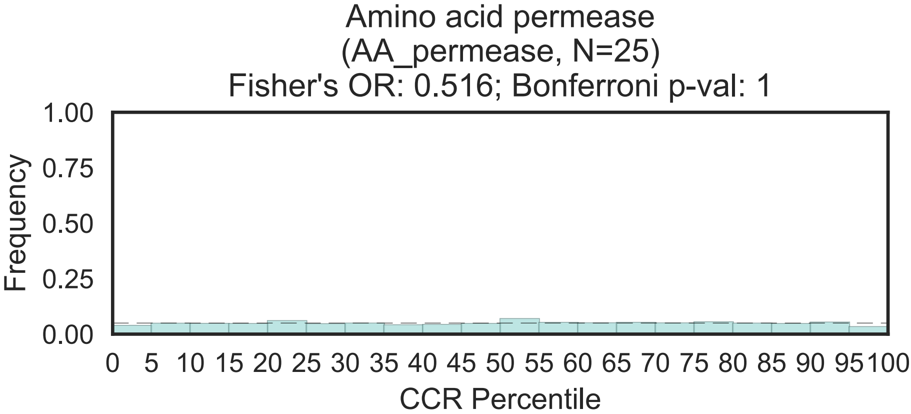


AAR2 protein
(AAR2, N=1)

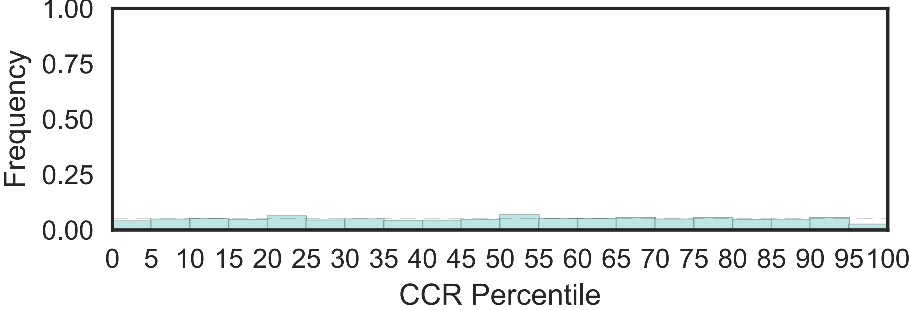

AARP2CN (NUC121) domain
(AARP2CN, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Apoptosis antagonizing transcription factor
(AATF-Che1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

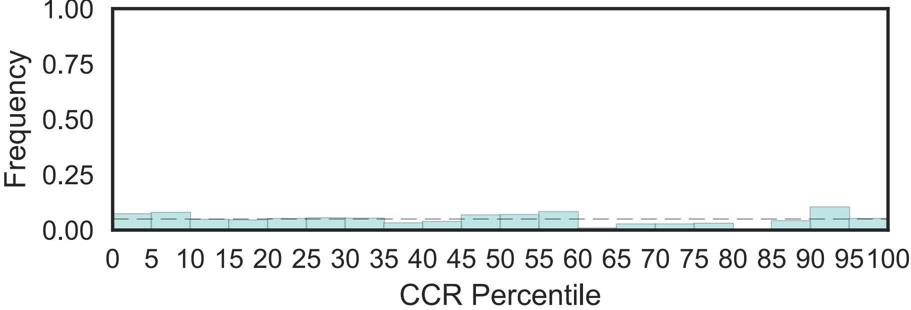

Amino acid kinase family
(AA_kinase, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

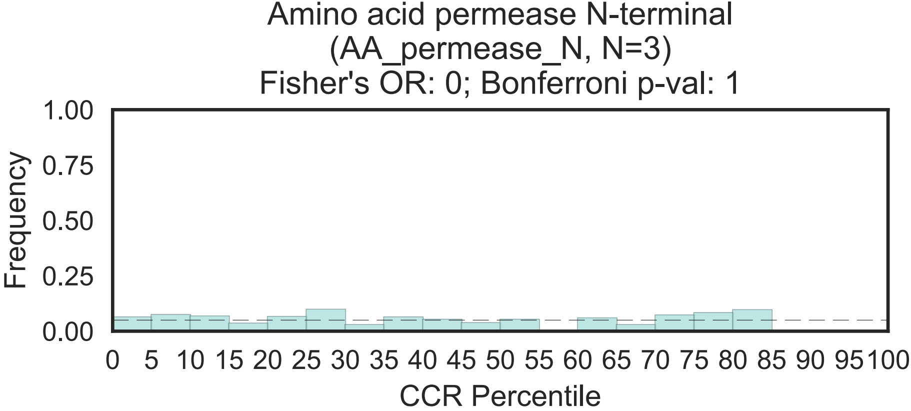

Amino acid permease
(AA_permease, N=25)
Fisher's OR: 0.516; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

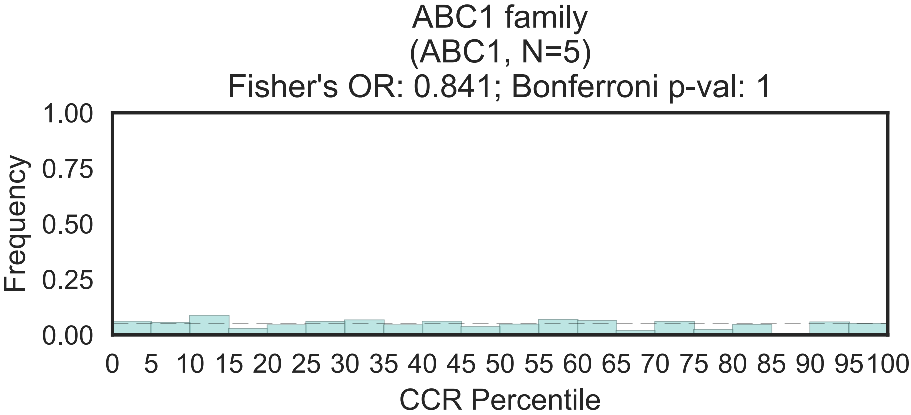
Amino acid permease (AA_permease_2, N=17) Fisher's OR: 0.413; Bonferroni p-val: 1

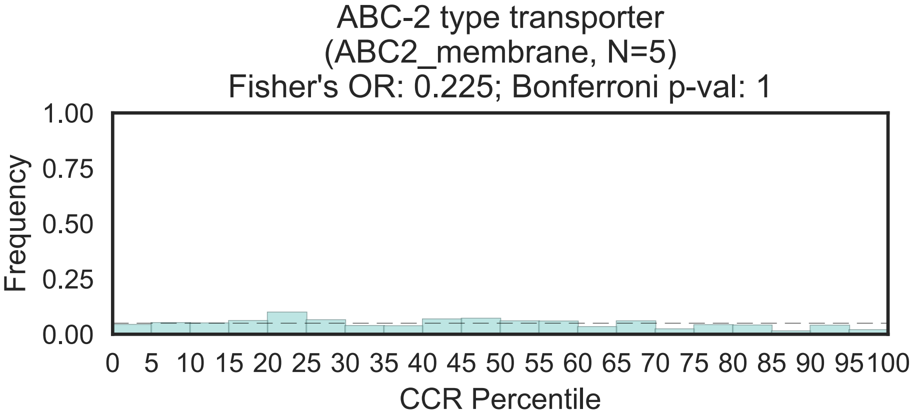


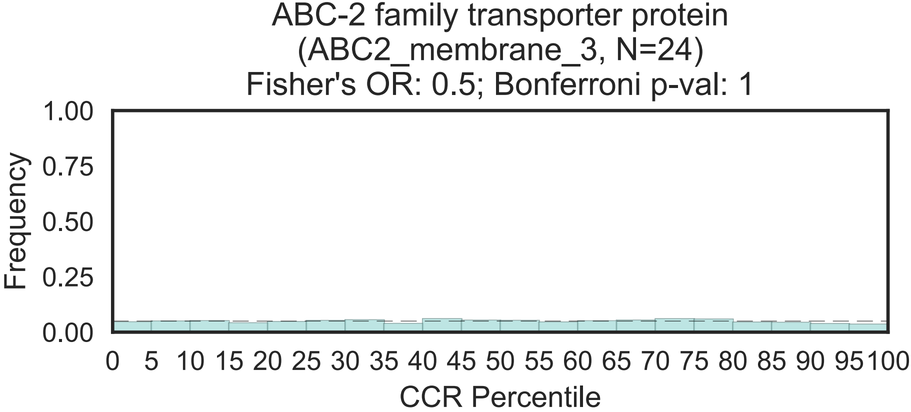
C-terminus of AA_permease
(AA_permease_C, N=5)
Fisher's OR: 1.11; Bonferroni p-val: 1

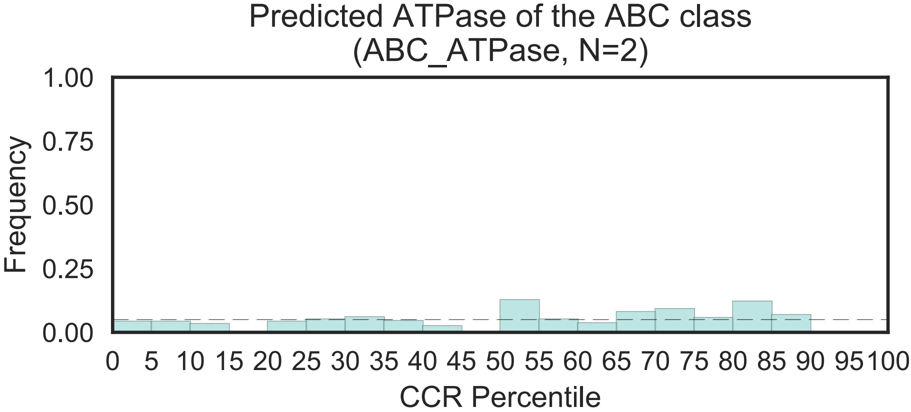


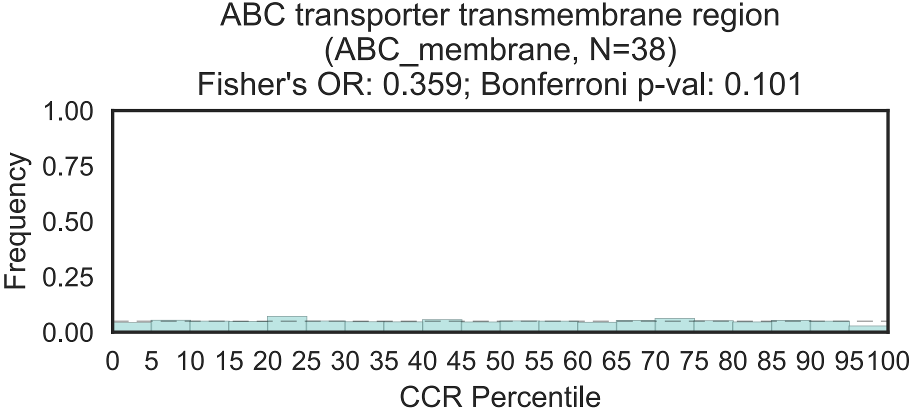

Amino acid permease N-terminal
(AA_permease_N, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

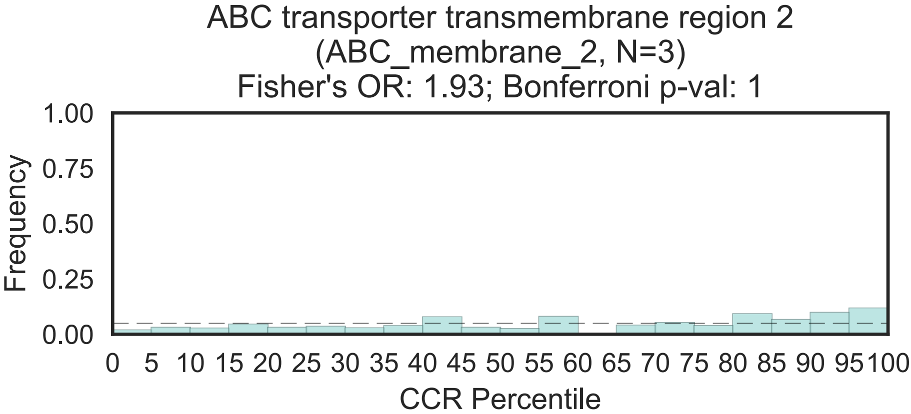

ABC1 family
(ABC1, N=5)
Fisher's OR: 0.841; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

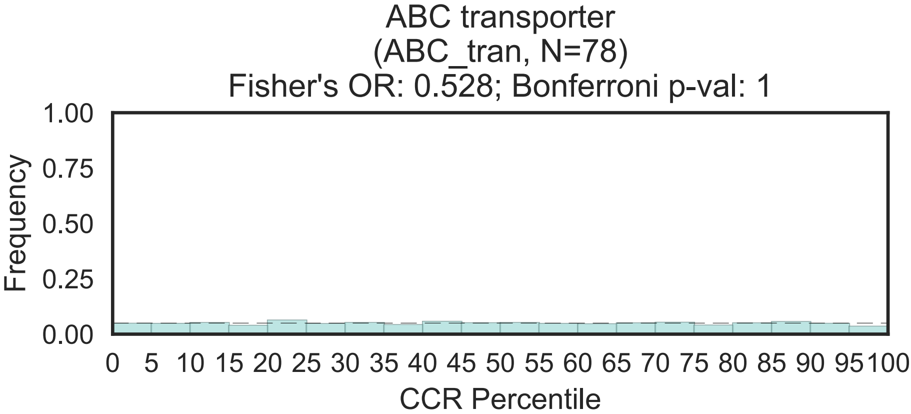

ABC-2 type transporter
(ABC2_membrane, N=5)
Fisher's OR: 0.225; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

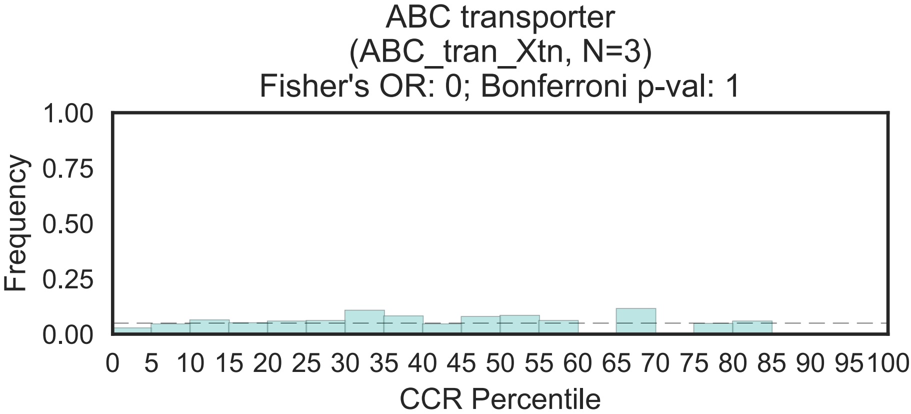

ABC-2 family transporter protein
(ABC2_membrane_3, N=24)
Fisher's OR: 0.5; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

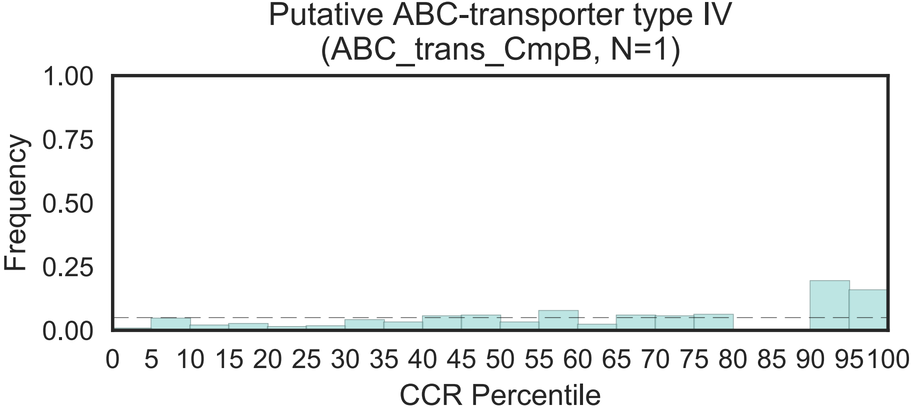

Predicted ATPase of the ABC class
(ABC_ATPase, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

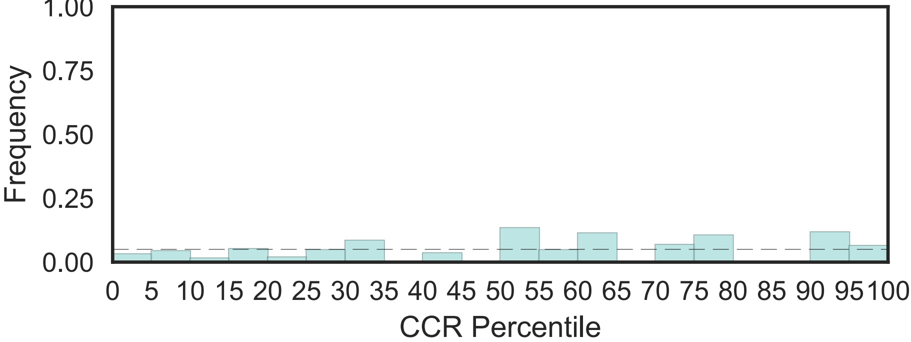

ABC transporter transmembrane region
(ABC_membrane, N=38)
Fisher's OR: 0.359; Bonferroni p-val: 0.101
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


ABC transporter transmembrane region 2
(ABC_membrane_2, N=3)
Fisher's OR: 1.93; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

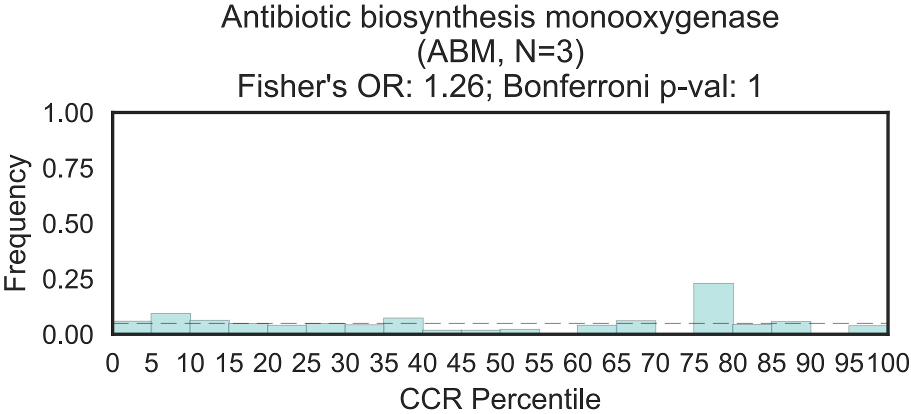

ABC transporter
(ABC_tran, N=78)
Fisher's OR: 0.528; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

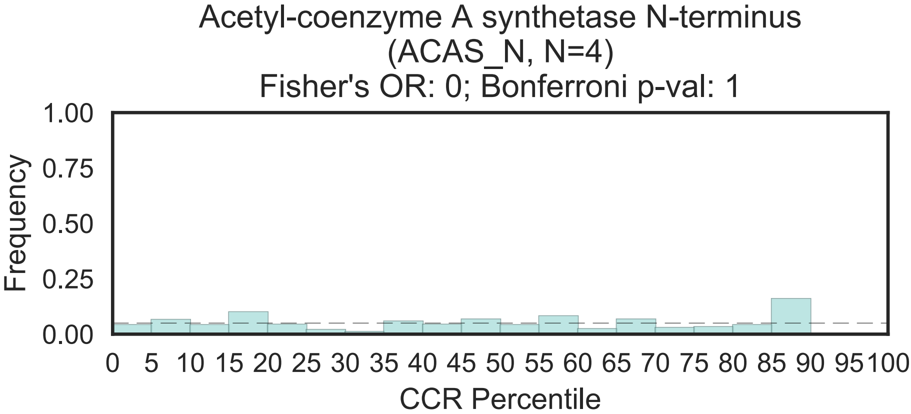

ABC transporter
(ABC_tran_Xtn, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

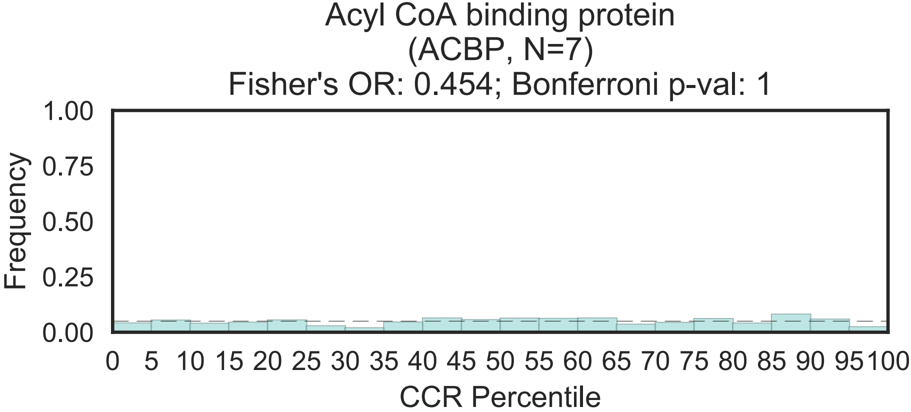

Putative ABC-transporter type IV
(ABC_trans_CmpB, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



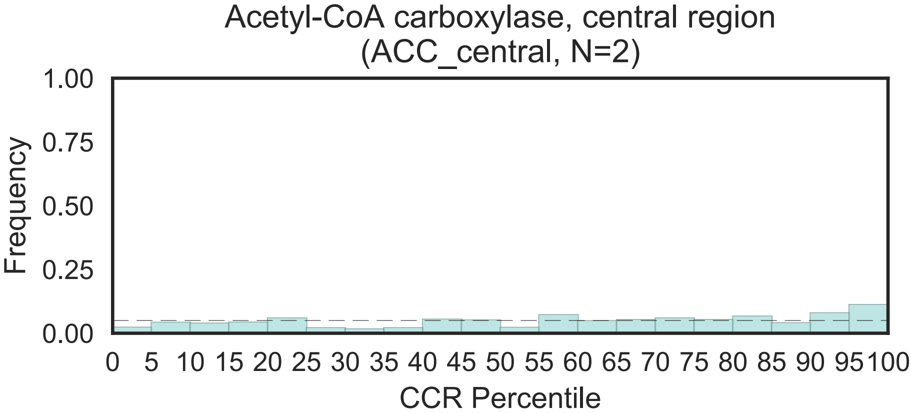
ABC-type uncharacterized transport system
(ABC_transp_aux, N=1)

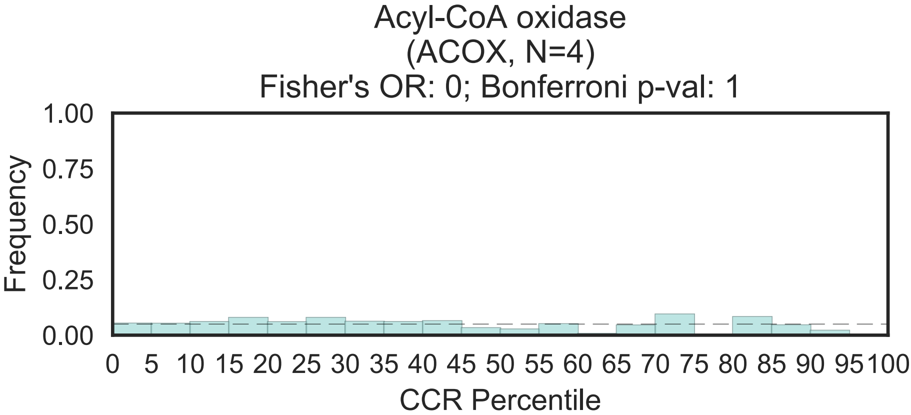

Antibiotic biosynthesis monooxygenase
(ABM, N=3)
Fisher's OR: 1.26; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

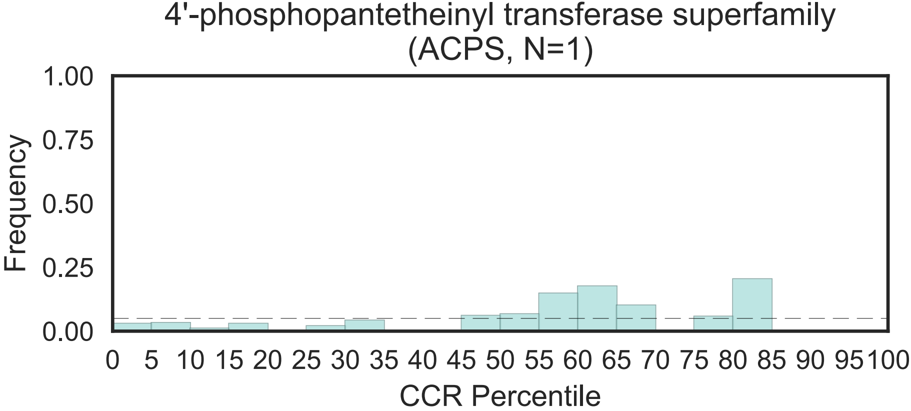

Acetyl-coenzyme A synthetase N-terminus
(ACAS_N, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

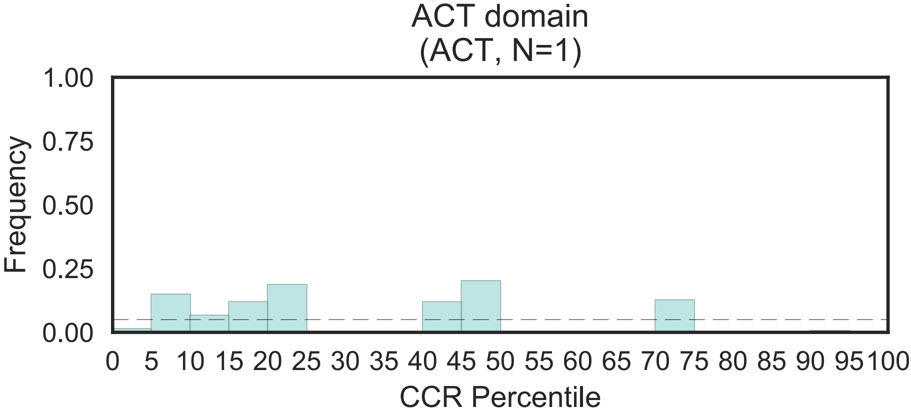


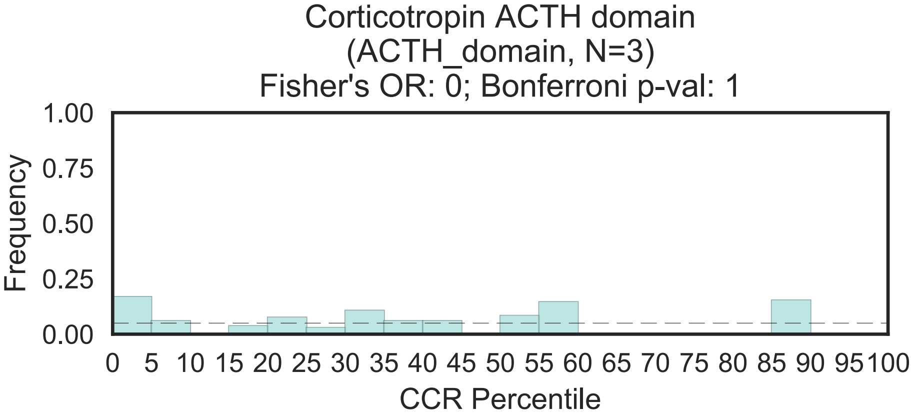
Acyl CoA binding protein
(ACBP, N=7)
Fisher's OR: 0.454; Bonferroni p-val: 1

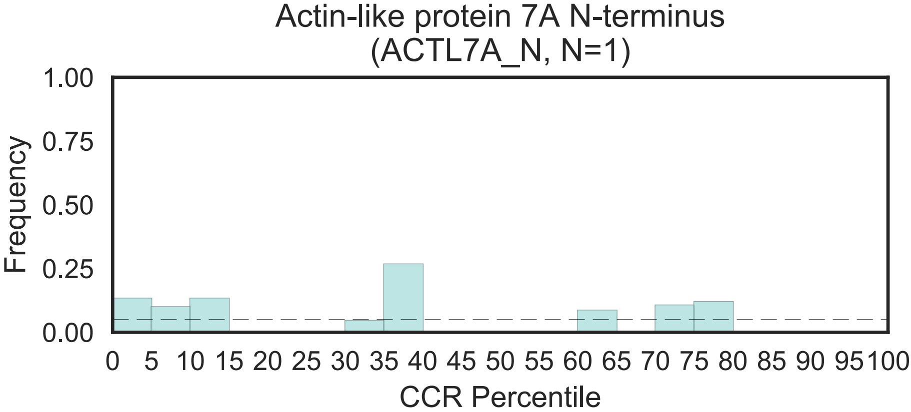

Acetyl-CoA carboxylase, central region
(ACC_central, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

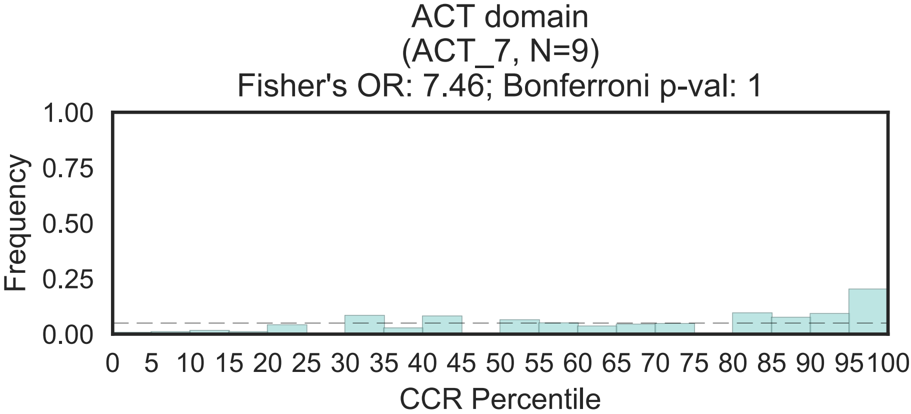

Acyl-CoA oxidase
(ACOX, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


4'-phosphopantetheinyl transferase superfamily
(ACPS, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

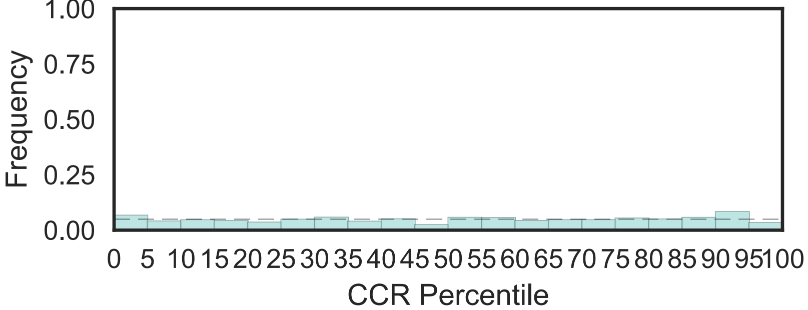

ACT domain
(ACT, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Corticotropin ACTH domain
(ACTH_domain, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

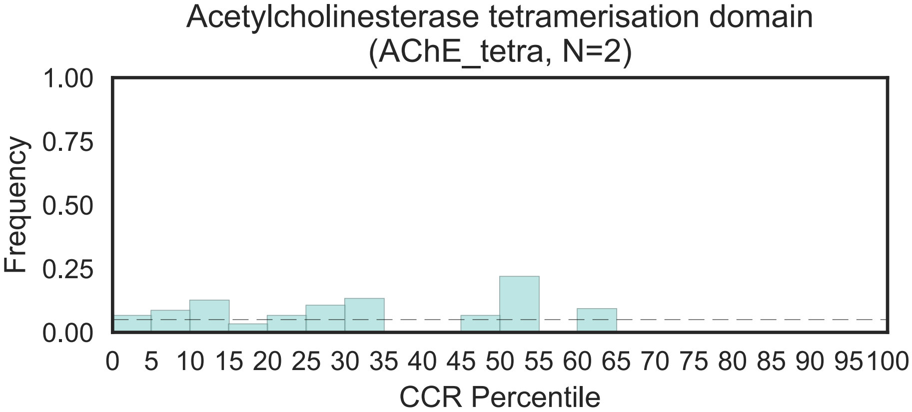

Actin-like protein 7A N-terminus
(ACTL7A_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

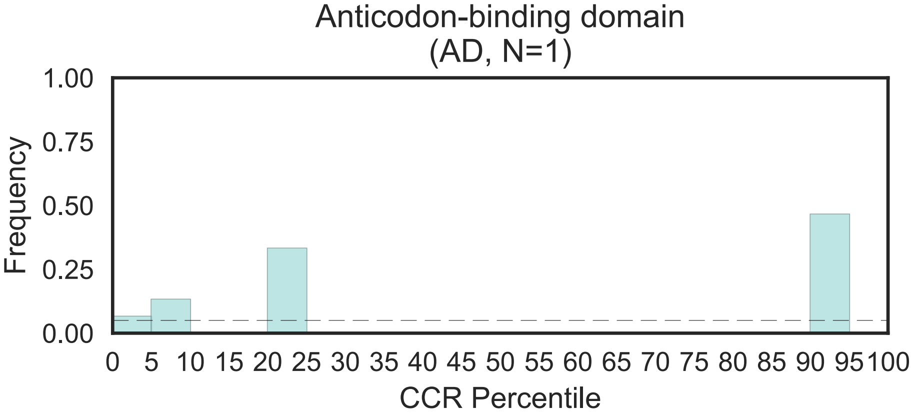


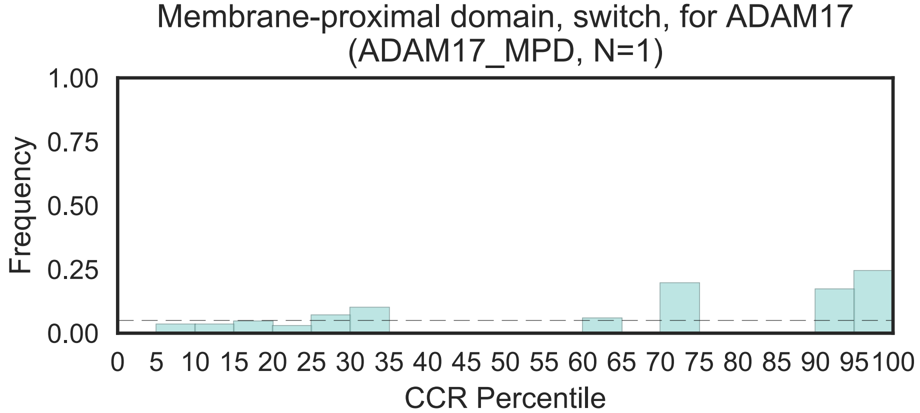
ACT domain
(ACT_7, N=9)
Fisher's OR: 7.46; Bonferroni p-val: 1

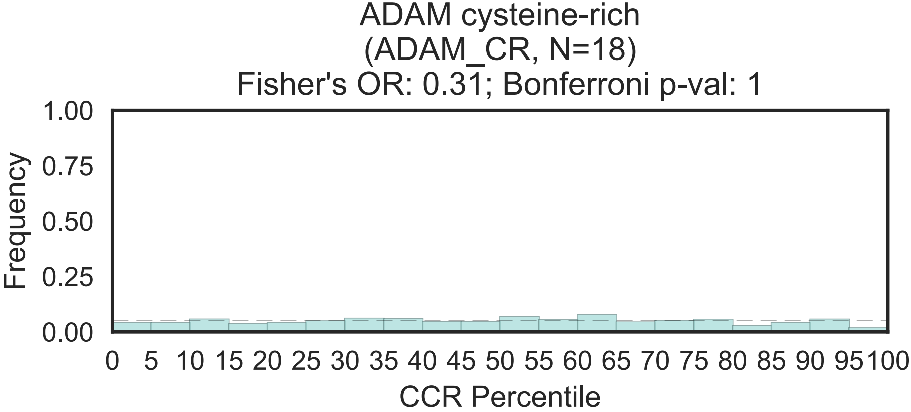


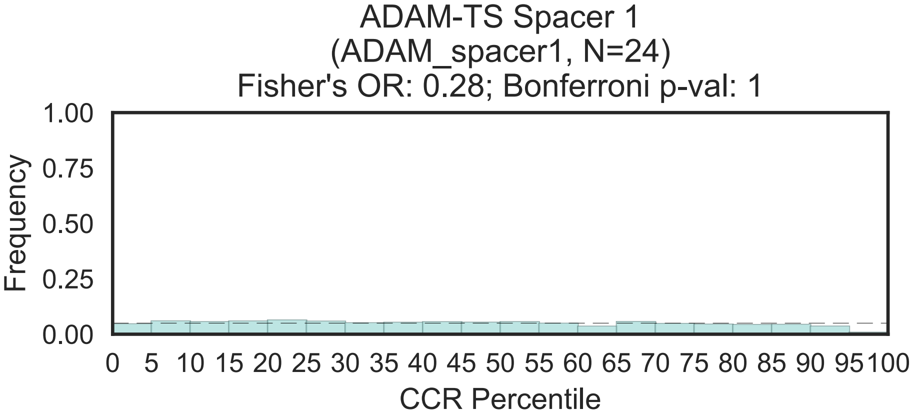
Adenylyl cyclase N-terminal extracellular and transmembrane region (AC_N, N=9)
Fisher's OR: 0.407; Bonferroni p-val: 1

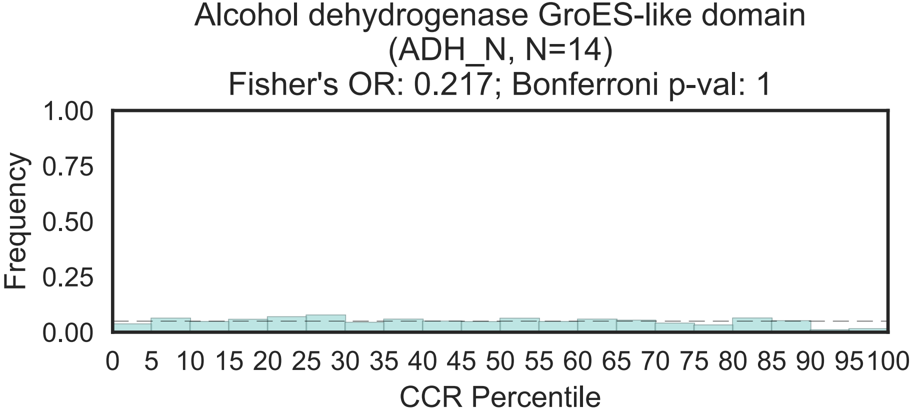

Acetylcholinesterase tetramerisation domain
(AChE_tetra, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

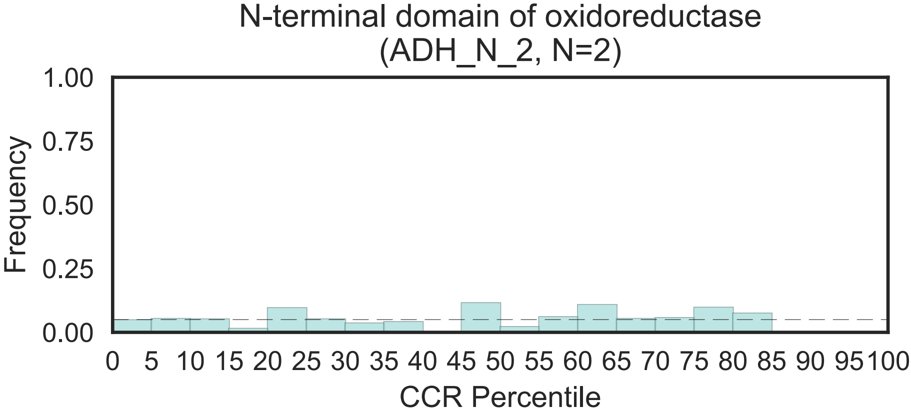

Anticodon-binding domain
(AD, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

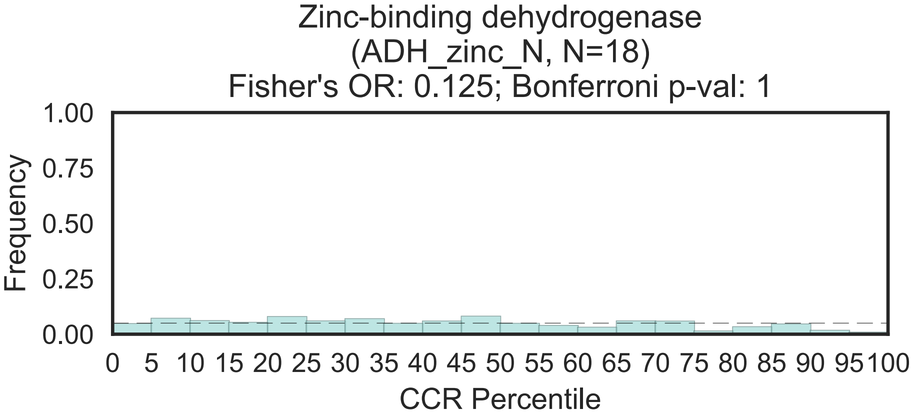

Membrane-proximal domain, switch, for ADAM17
(ADAM17_MPD, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

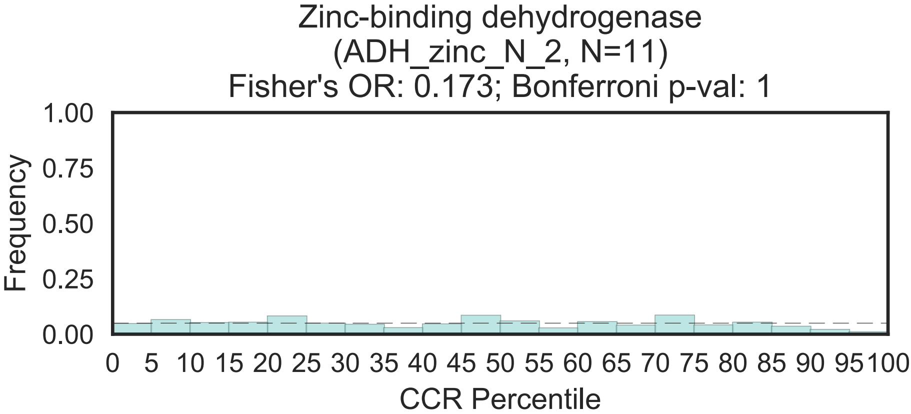
ADAM cysteine-rich
(ADAM_CR, N=18)
Fisher's OR: 0.31; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

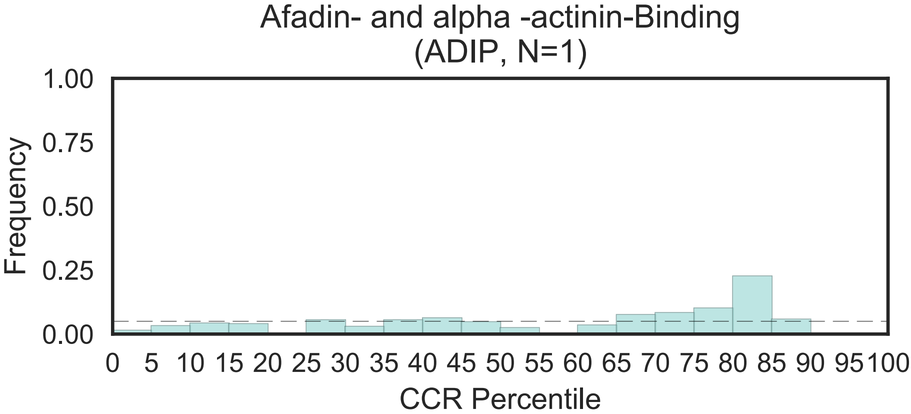

ADAM-TS Spacer 1
(ADAM_spacer1, N=24)
Fisher's OR: 0.28; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Alcohol dehydrogenase GroES-like domain
(ADH_N, N=14)
Fisher's OR: 0.217; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

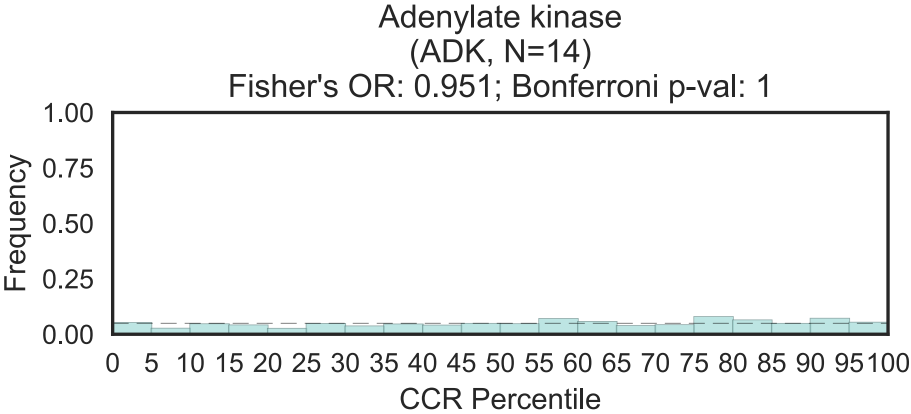

N-terminal domain of oxidoreductase
(ADH_N_2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Zinc-binding dehydrogenase
(ADH_zinc_N, N=18)
Fisher's OR: 0.125; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

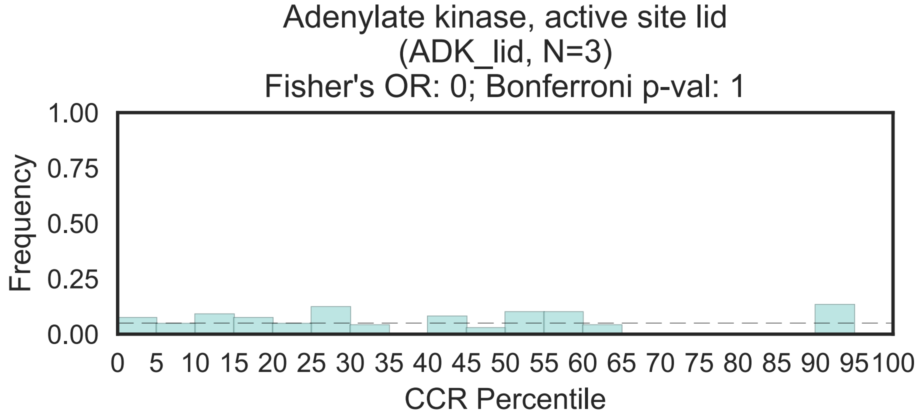

Zinc-binding dehydrogenase
(ADH_zinc_N_2, N=11)
Fisher's OR: 0.173; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

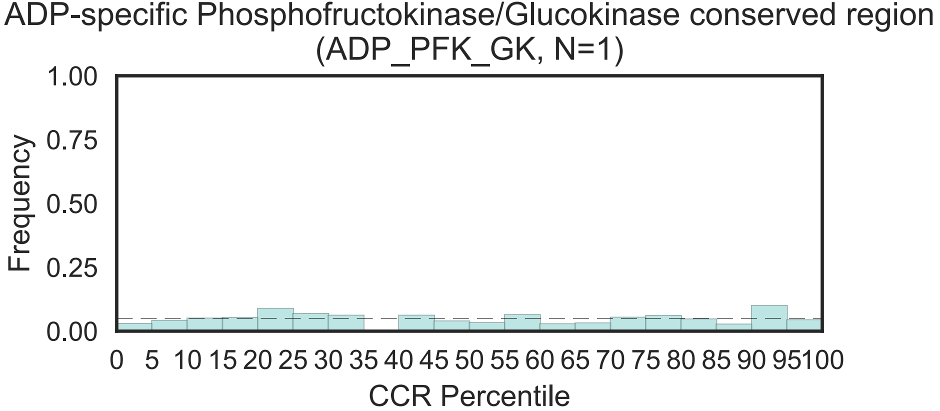


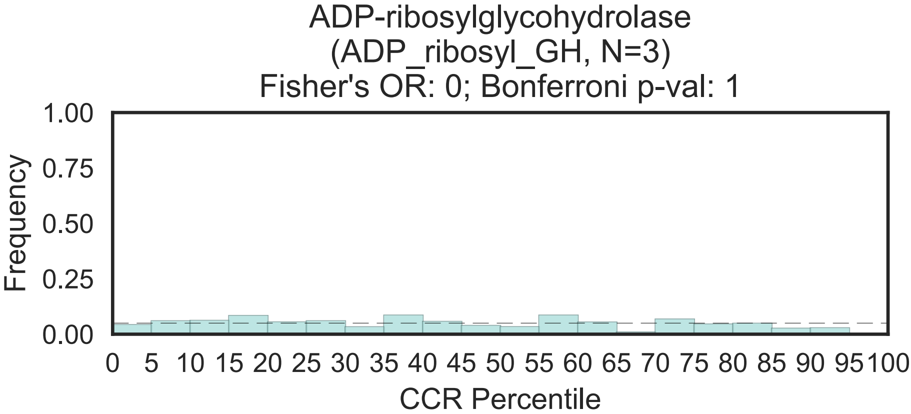
Afadin- and alpha -actinin-Binding
(ADIP, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

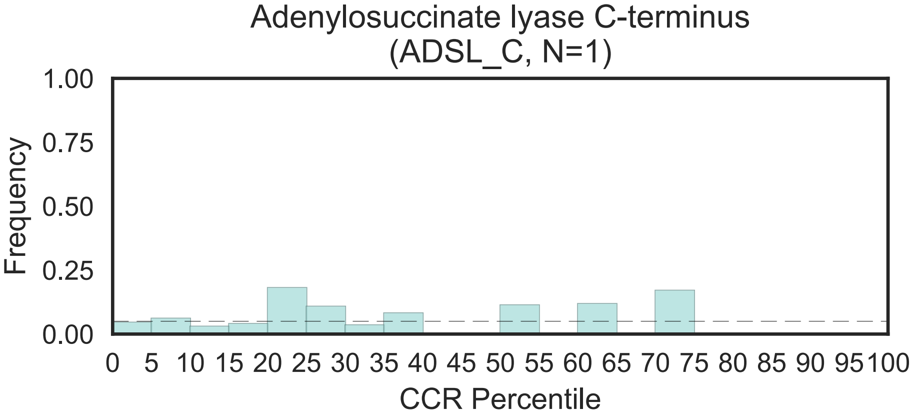


Adenylate kinase
(ADK, N=14)
Fisher's OR: 0.951; Bonferroni p-val: 1

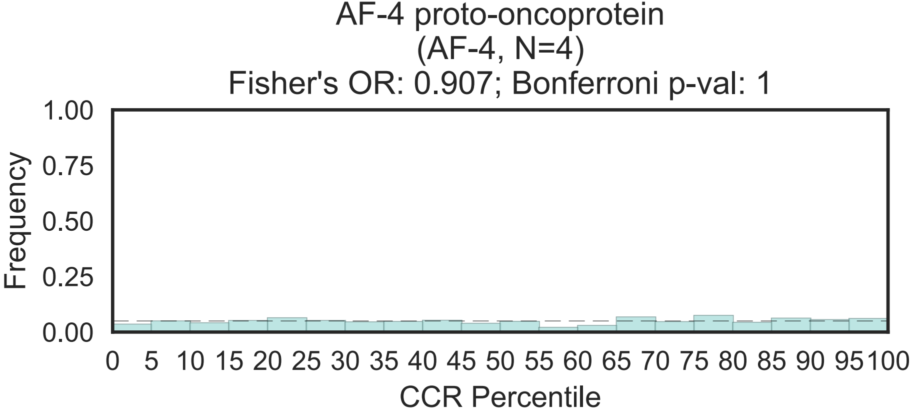

Adenylate kinase, active site lid
(ADK_lid, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

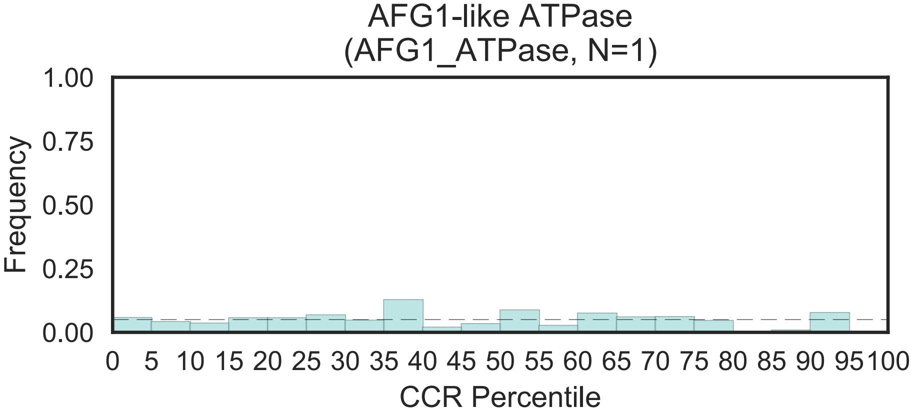

ADP-specific Phosphofructokinase/Glucokinase conserved region
(ADP_PFK_GK, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

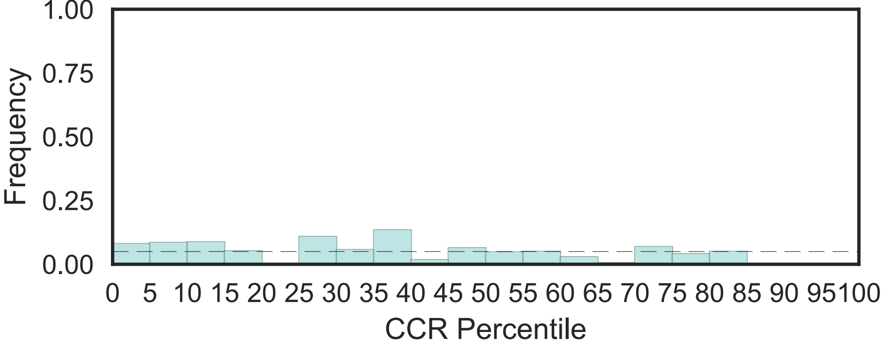

ADP-ribosylglycohydrolase
(ADP_ribosyl_GH, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

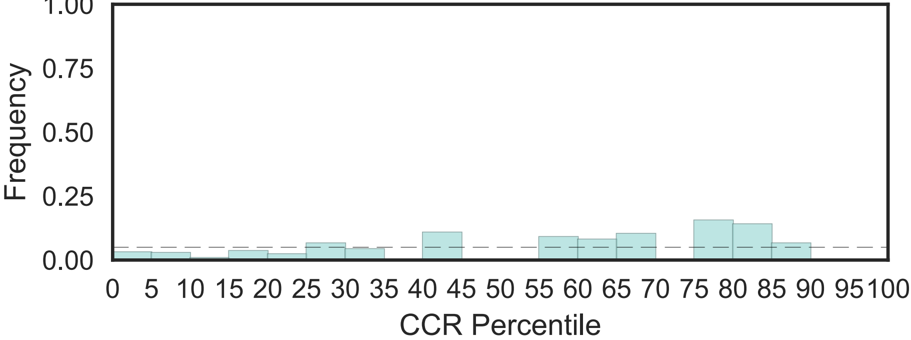


Adenylosuccinate lyase C-terminus
(ADSL_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

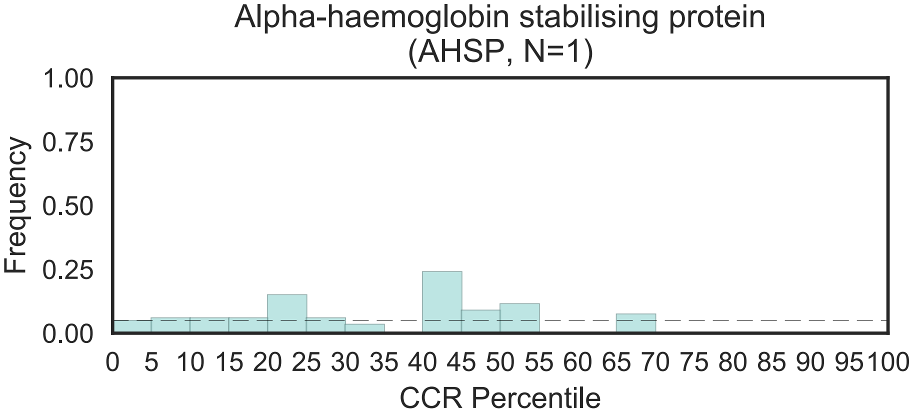

AF-4 proto-oncoprotein
(AF-4, N=4)
Fisher's OR: 0.907; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

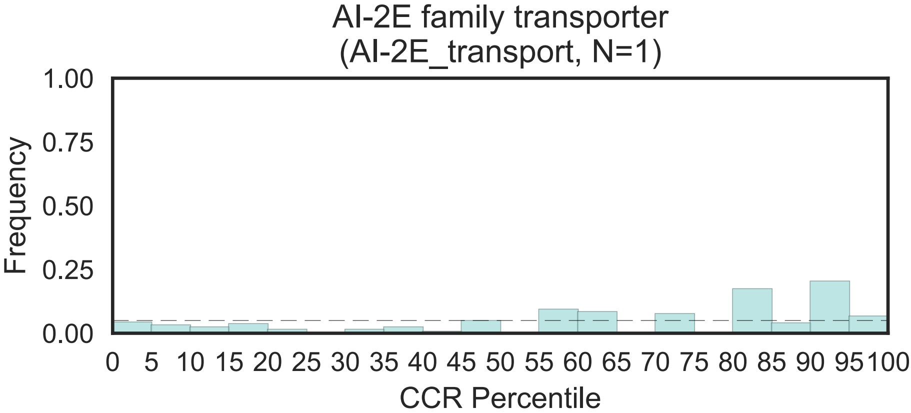

AFG1-like ATPase
(AFG1_ATPase, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

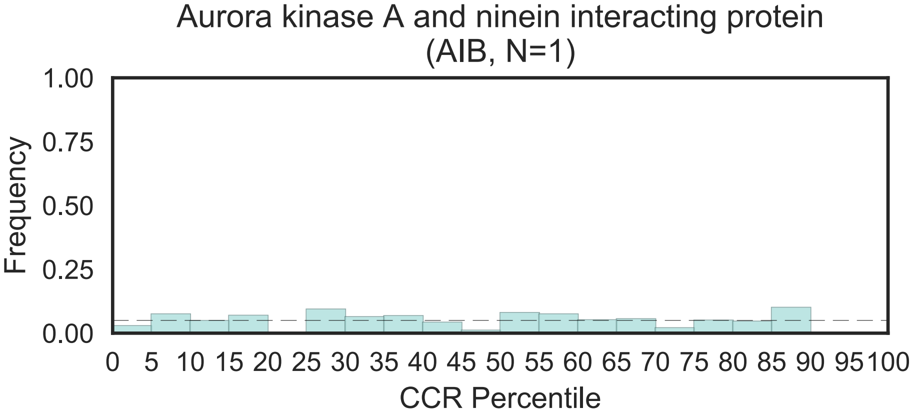

Angiotensin II, type I receptor-associated protein (AGTRAP)
(AGTRAP, N=1)

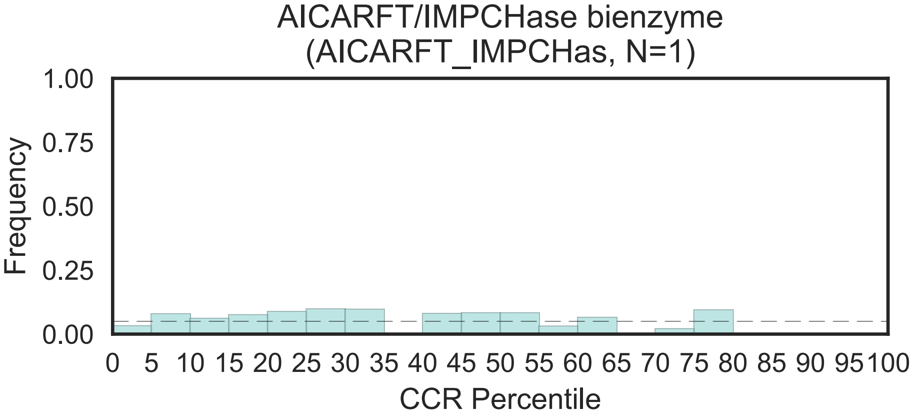


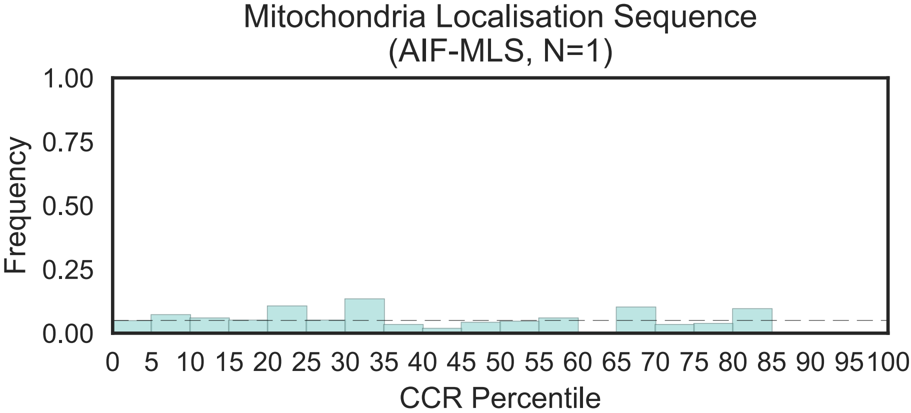
Activator of Hsp90 ATPase homolog 1-like protein
(AHSA1, N=1)

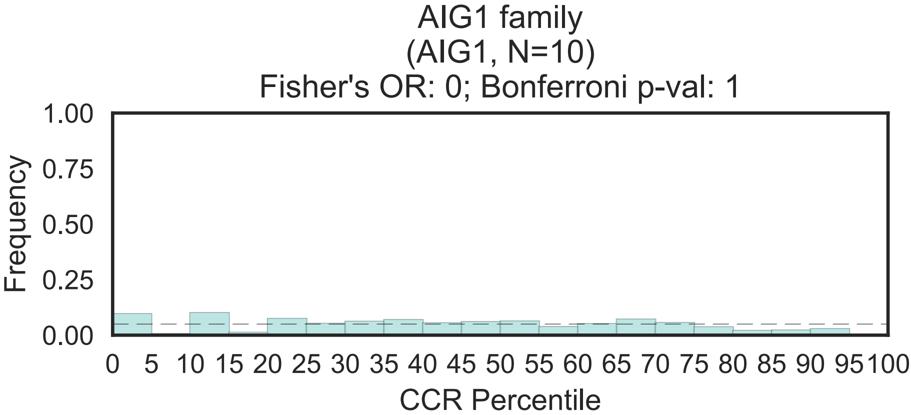

Alpha-haemoglobin stabilising protein
(AHSP, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

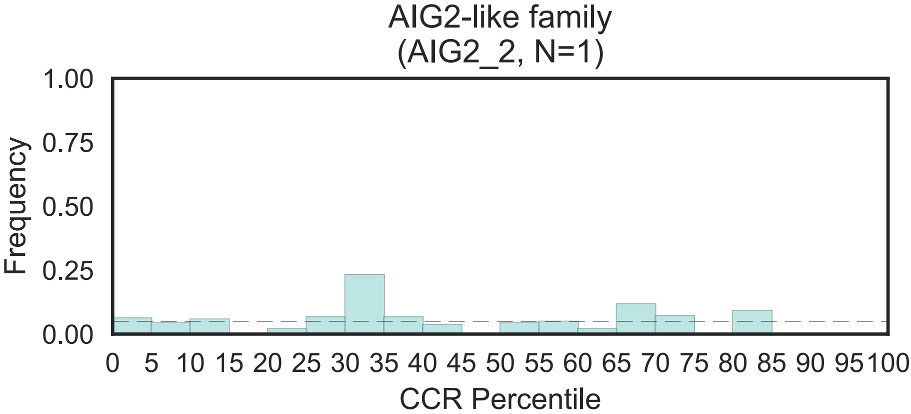

AI-2E family transporter
(AI-2E_transport, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

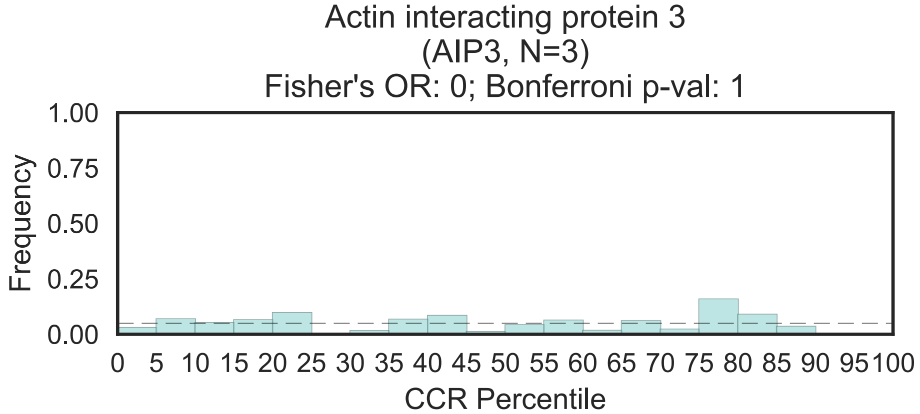

Aurora kinase A and ninein interacting protein
(AIB, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

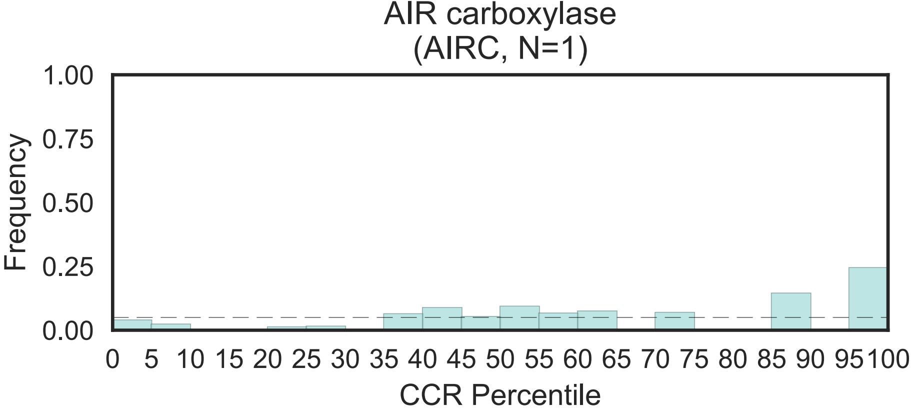

AICARFT/IMPCHase bienzyme
(AICARFT_IMPCHas, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

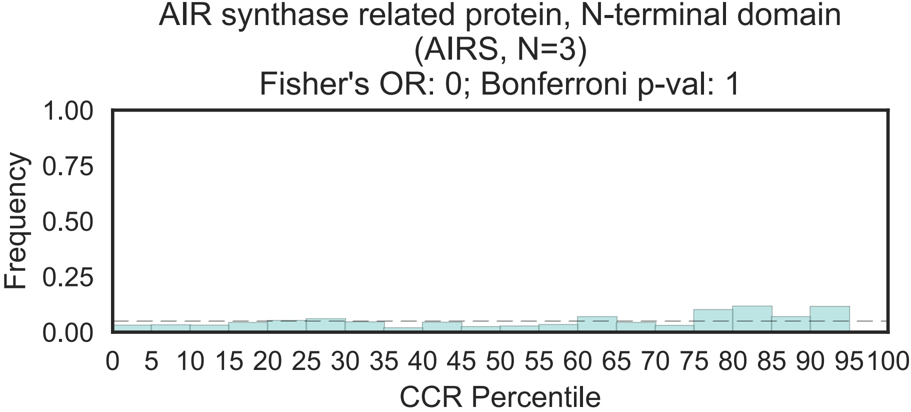

Mitochondria Localisation Sequence
(AIF-MLS, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


AIG1 family
(AIG1, N=10)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

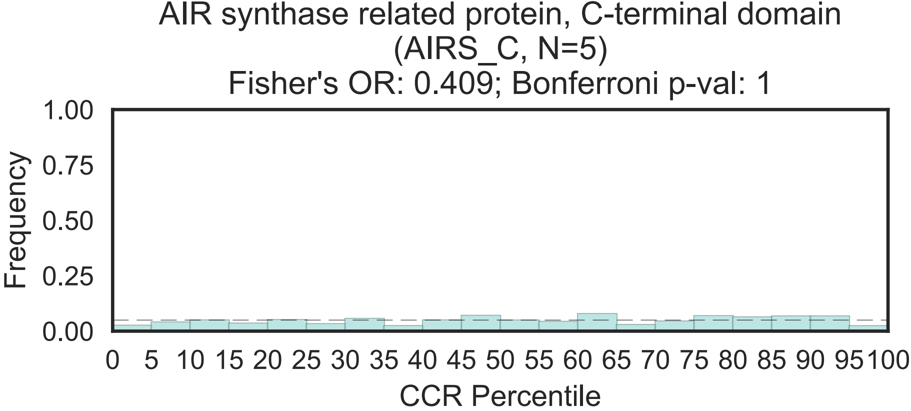

AIG2-like family
(AIG2_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

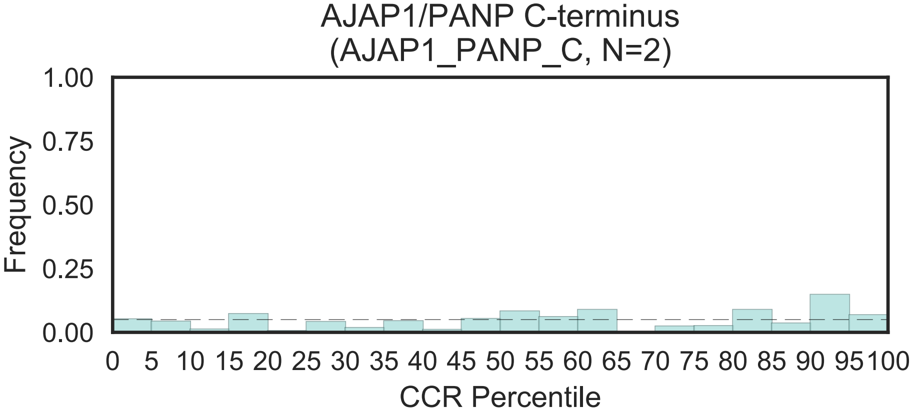

Actin interacting protein 3
(AIP3, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

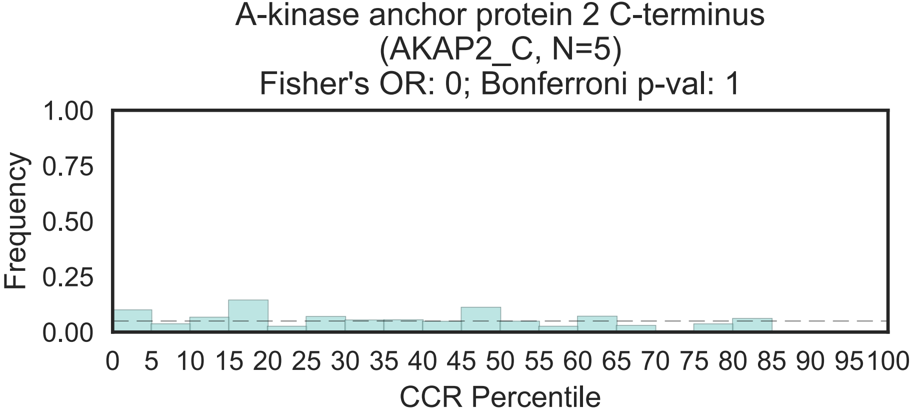

AIR carboxylase
(AIRC, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

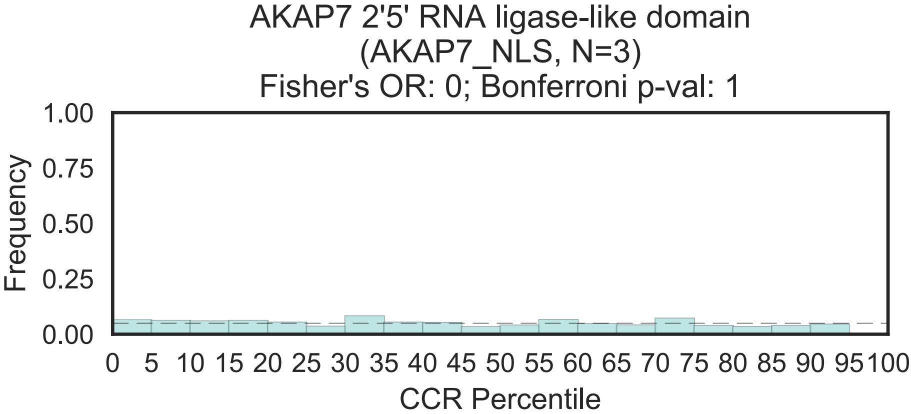


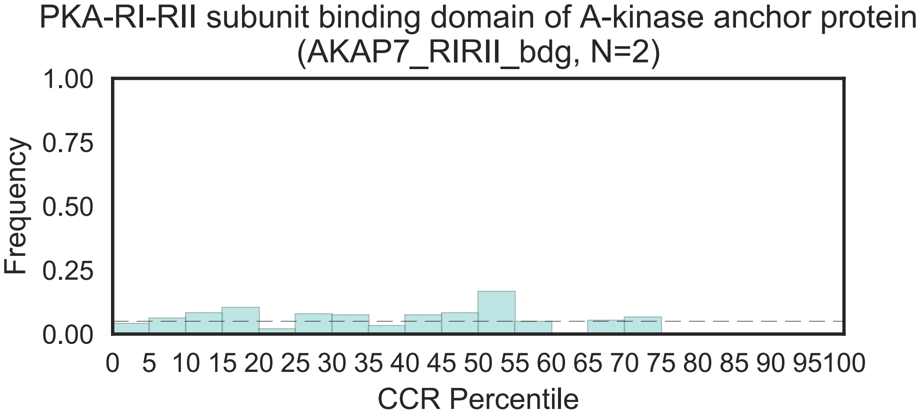
AIR synthase related protein, N-terminal domain
(AIRS, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

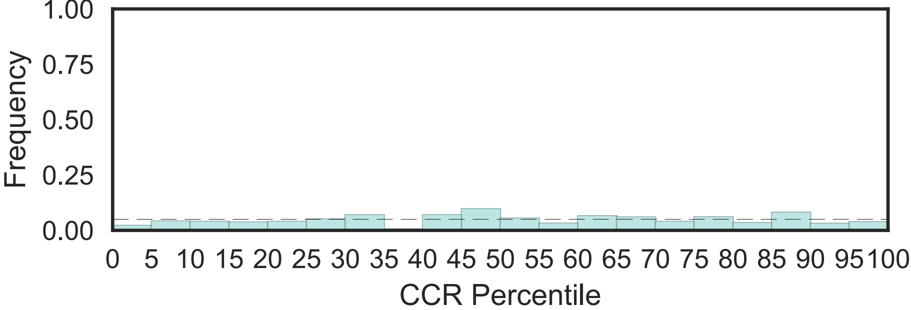

AIR synthase related protein, C-terminal domain
(AIRS_C, N=5)
Fisher's OR: 0.409; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


AJAP1/PANP C-terminus
(AJAP1_PANP_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

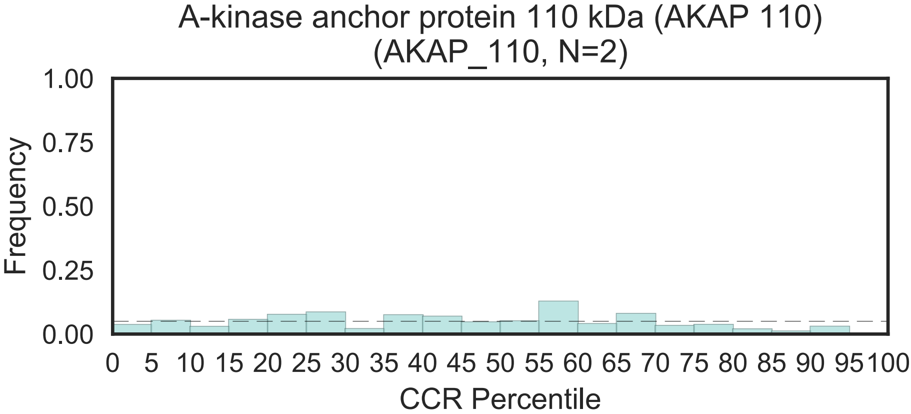

A-kinase anchor protein 2 C-terminus
(AKAP2_C, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


AKAP7 2'5' RNA ligase-like domain
(AKAP7_NLS, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

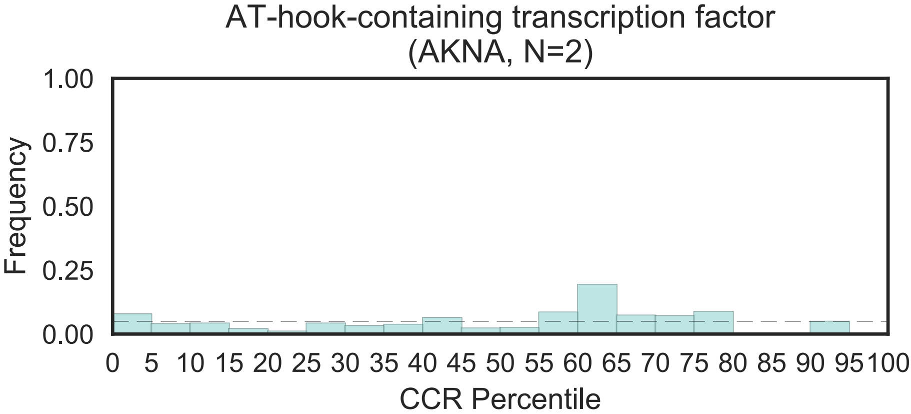

PKA-RI-RII subunit binding domain of A-kinase anchor protein
(AKAP7_RIRII_bdg, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

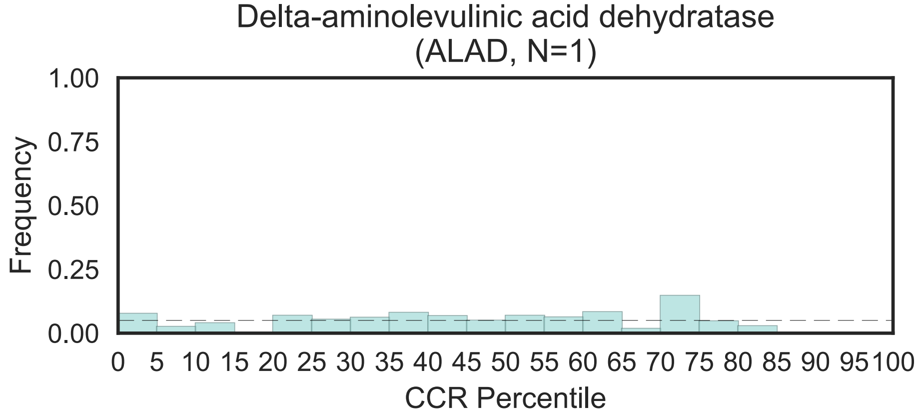


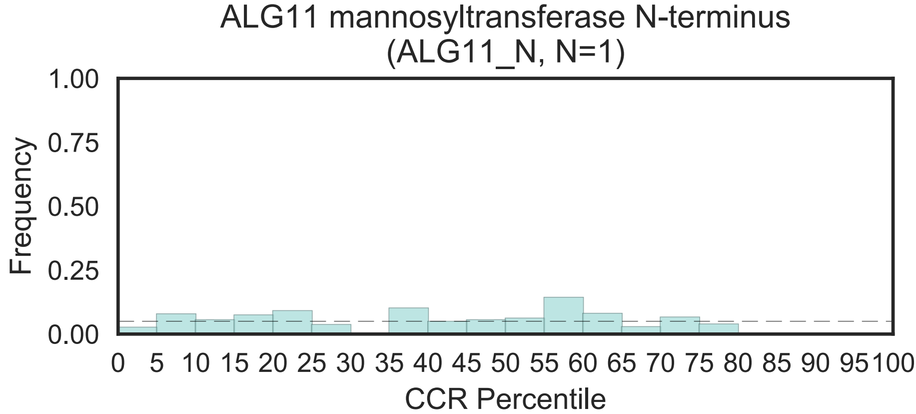
A-kinase anchoring protein 95 (AKAP95)
(AKAP95, N=3)
Fisher's OR: 0.647; Bonferroni p-val: 1



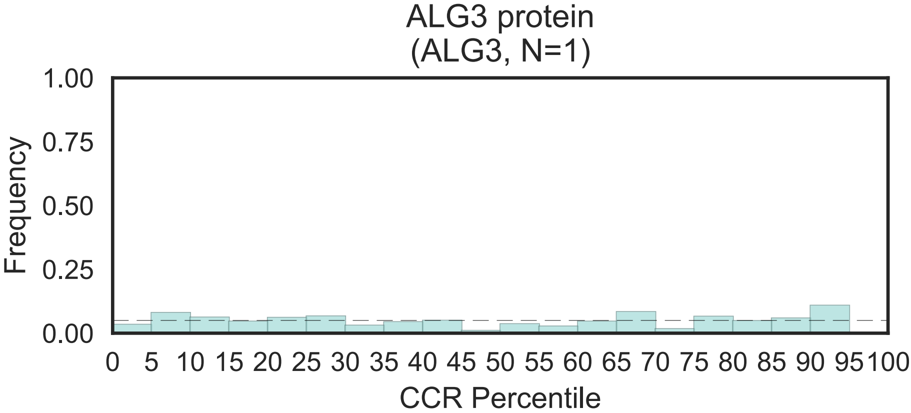
A-kinase anchor protein 110 kDa (AKAP 110)
(AKAP_110, N=2)

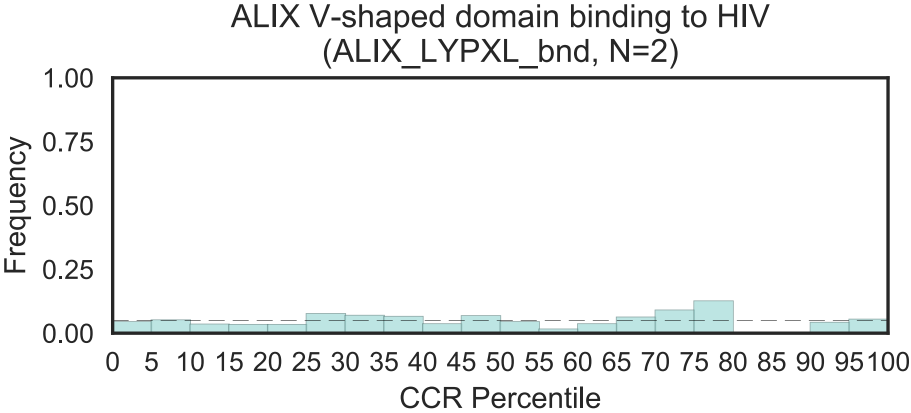

AT-hook-containing transcription factor
(AKNA, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Delta-aminolevulinic acid dehydratase
(ALAD, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

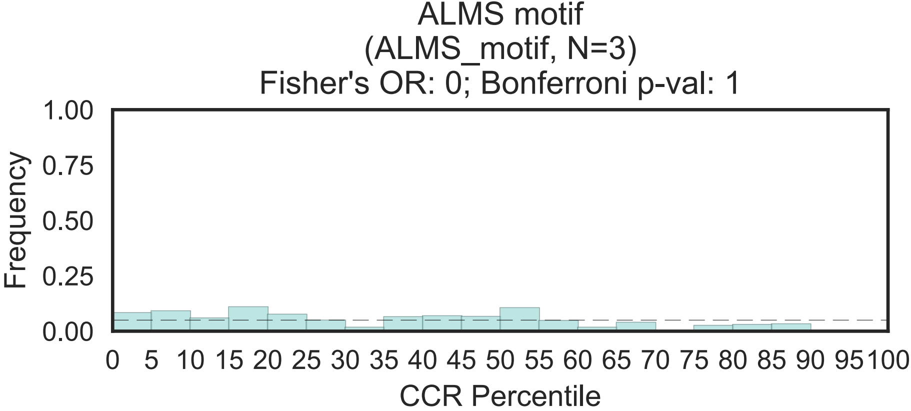


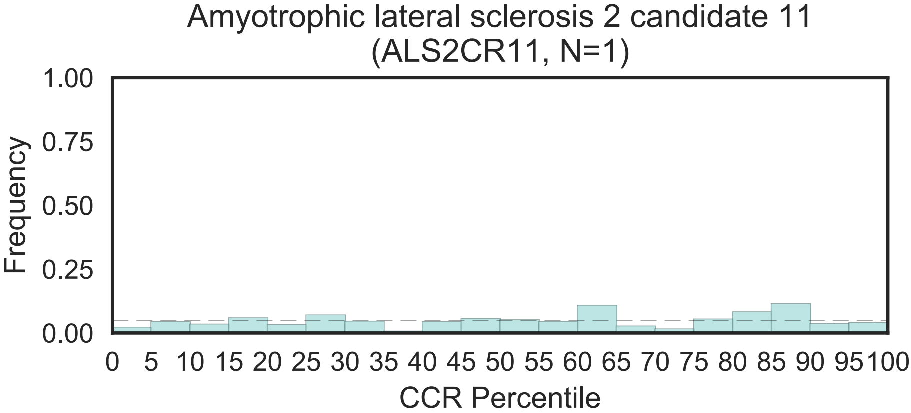
ALG11 mannosyltransferase N-terminus
(ALG11_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

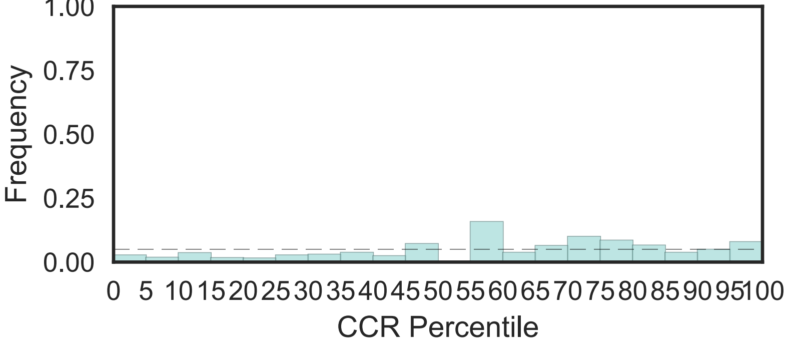

ALG3 protein
(ALG3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



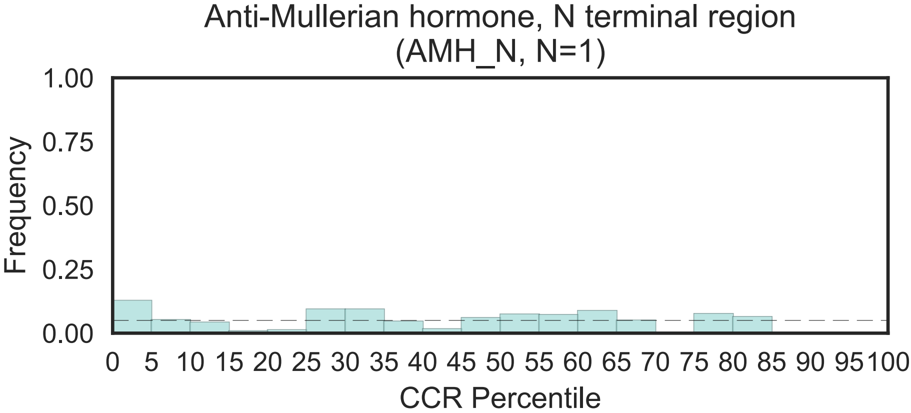
ALIX V-shaped domain binding to HIV
(ALIX_LYPXL_bnd, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

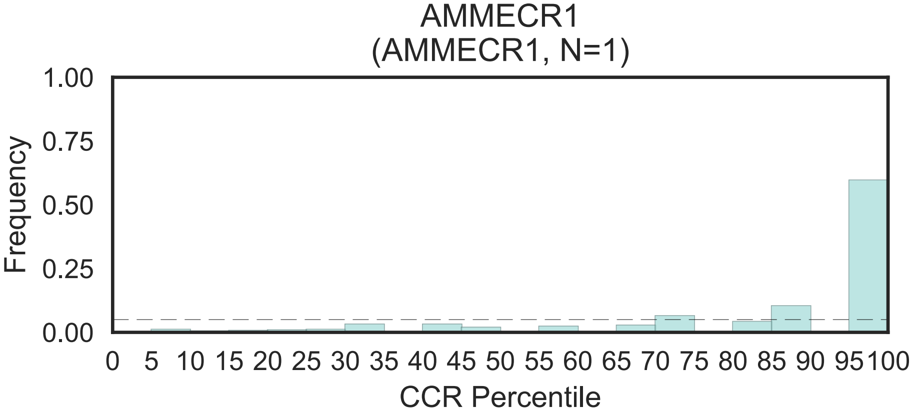

ALMS motif
(ALMS_motif, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

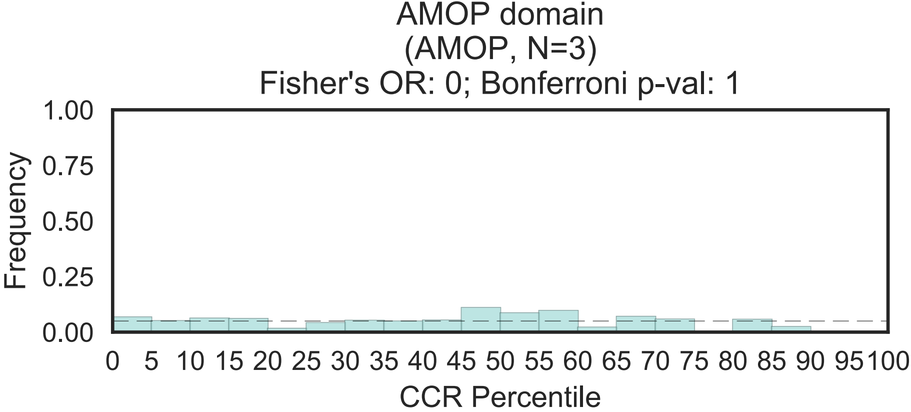

Amyotrophic lateral sclerosis 2 candidate 11
(ALS2CR11, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

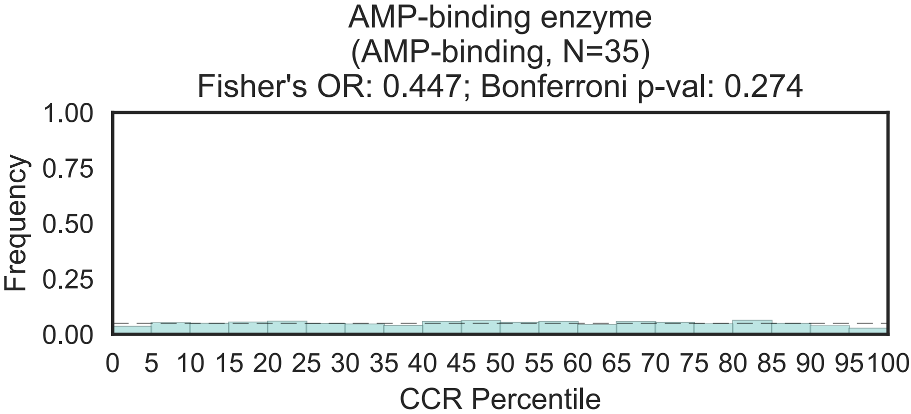


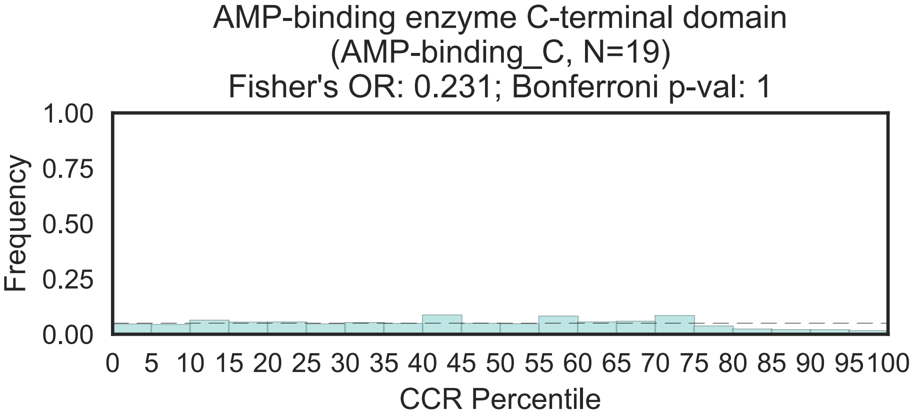
Amyotrophic lateral sclerosis 2 chromosomal region candidate gene 8 (ALS2CR8, N=1)

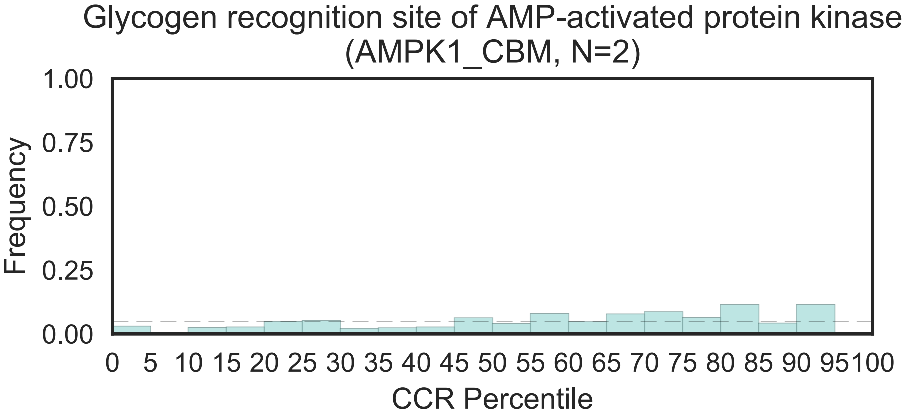

Anti-Mullerian hormone, N terminal region
(AMH_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

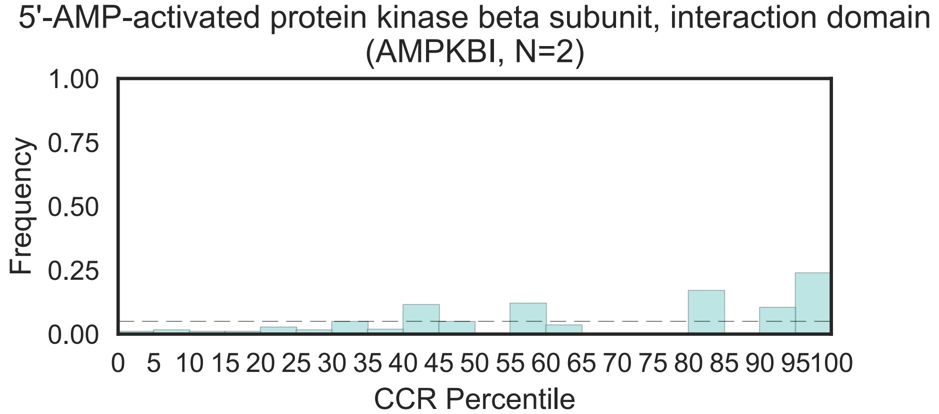

AMMECR1
(AMMECR1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

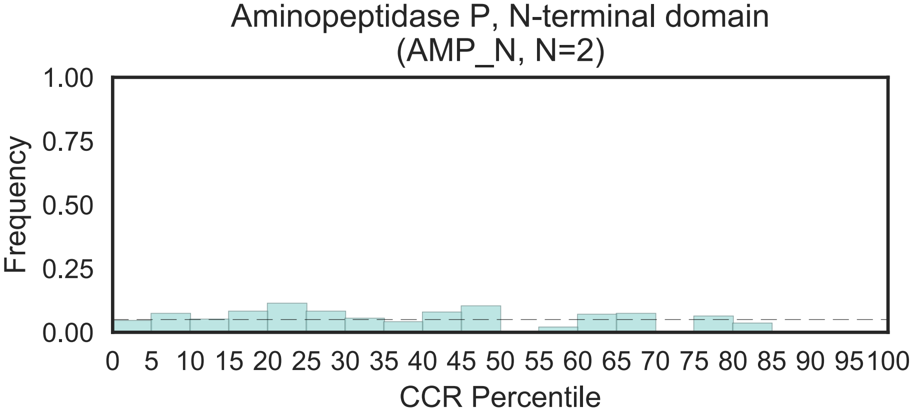

AMOP domain
(AMOP, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

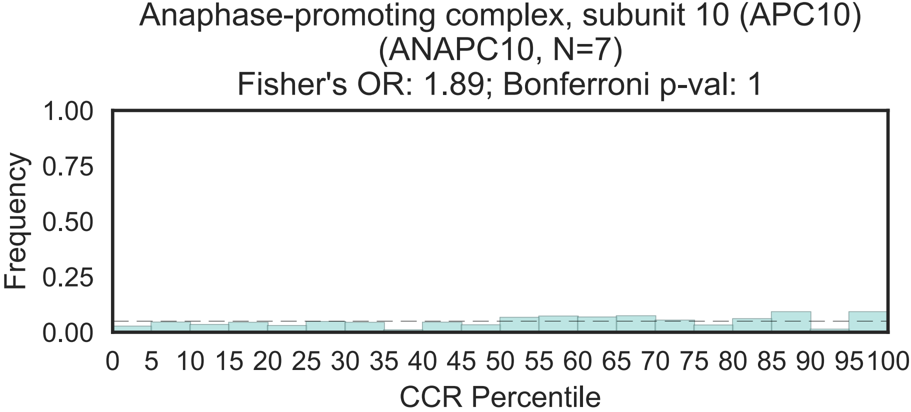

AMP-binding enzyme
(AMP-binding, N=35)
Fisher's OR: 0.447; Bonferroni p-val: 0.274
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

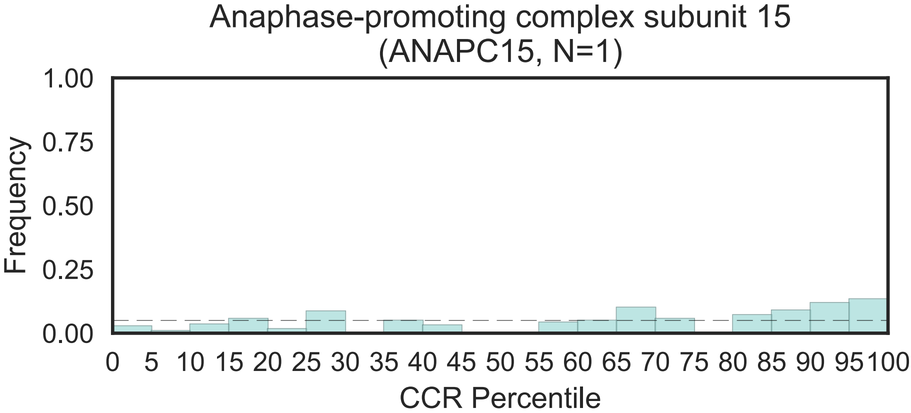

AMP-binding enzyme C-terminal domain
(AMP-binding_C, N=19)
Fisher's OR: 0.231; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

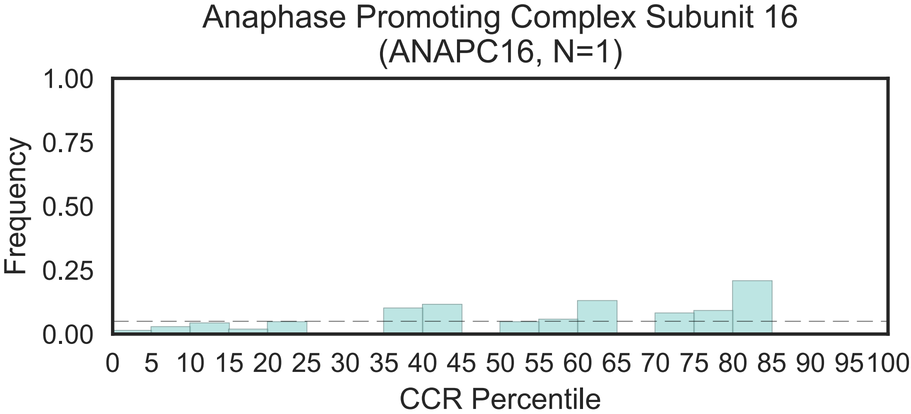

Glycogen recognition site of AMP-activated protein kinase
(AMPK1_CBM, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

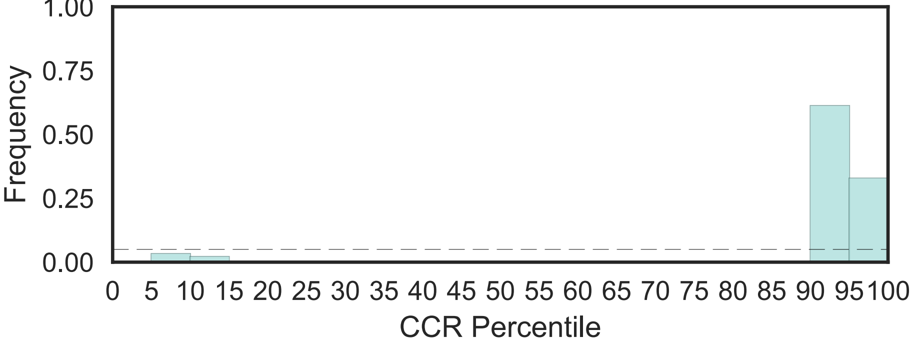

5'-AMP-activated protein kinase beta subunit, interaction domain
(AMPKBI, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Aminopeptidase P, N-terminal domain
(AMP_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

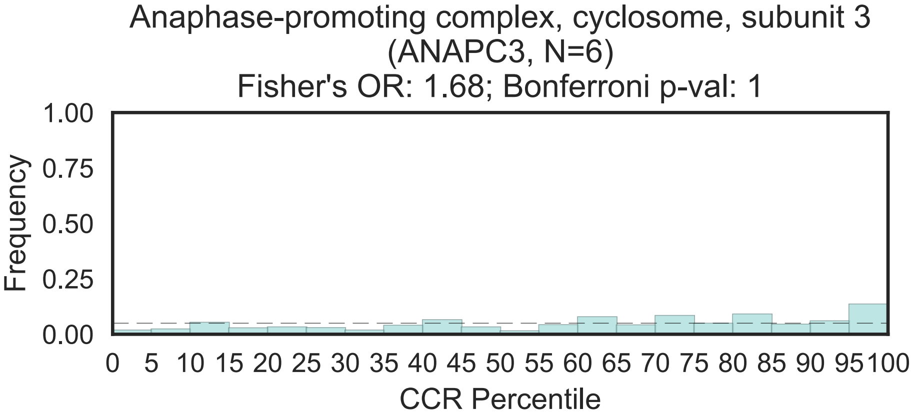

Anaphase-promoting complex, subunit 10 (APC10)
(ANAPC10, N=7)
Fisher's OR: 1.89; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

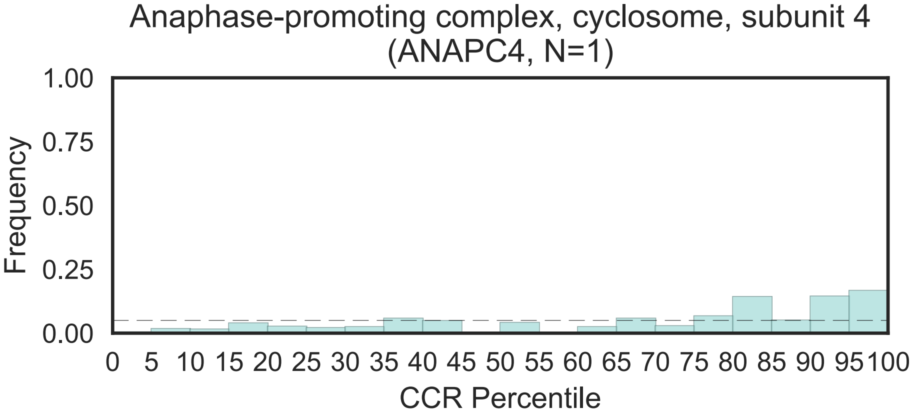

Anaphase-promoting complex subunit 15
(ANAPC15, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

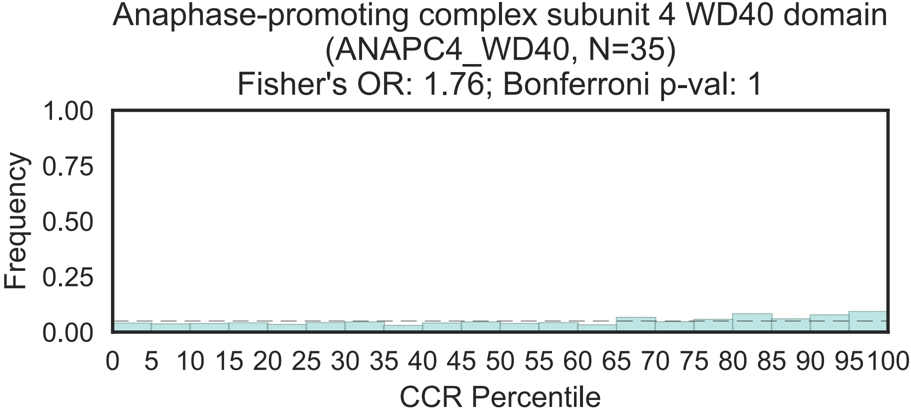

Anaphase Promoting Complex Subunit 16
(ANAPC16, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



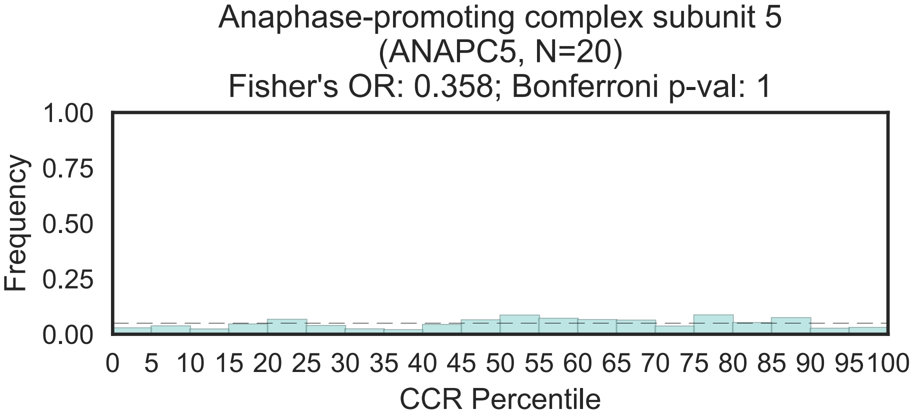
Anaphase promoting complex (APC) subunit 2 (ANAPC2, N=1)


Anaphase-promoting complex, cyclosome, subunit 3
(ANAPC3, N=6)
Fisher's OR: 1.68; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

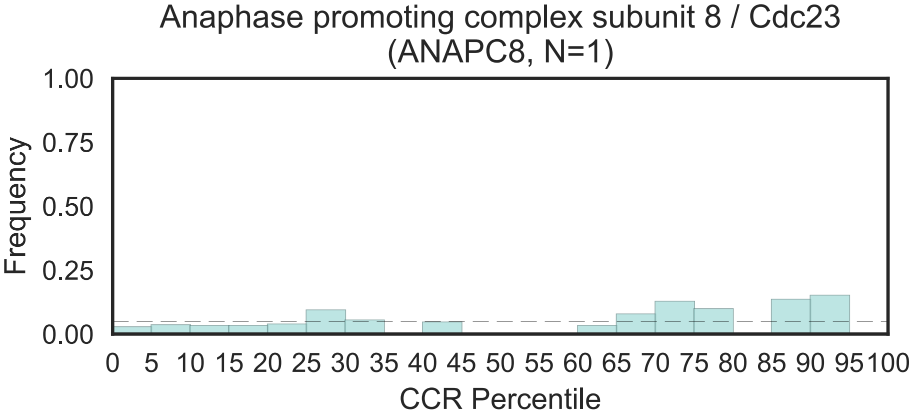

Anaphase-promoting complex, cyclosome, subunit 4
(ANAPC4, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

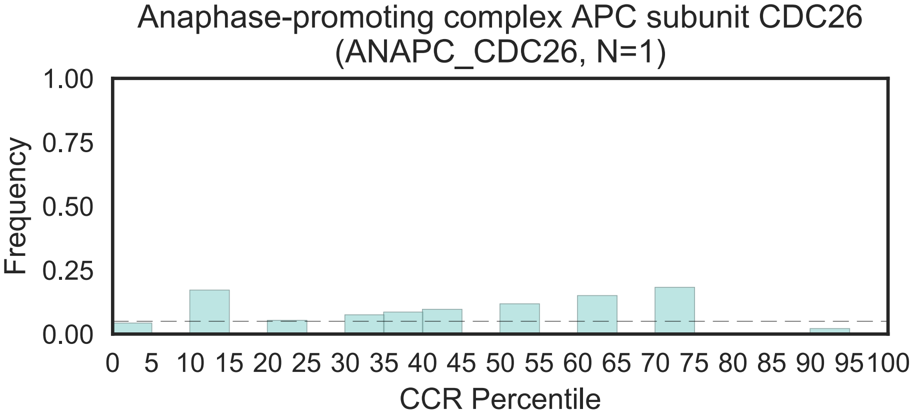


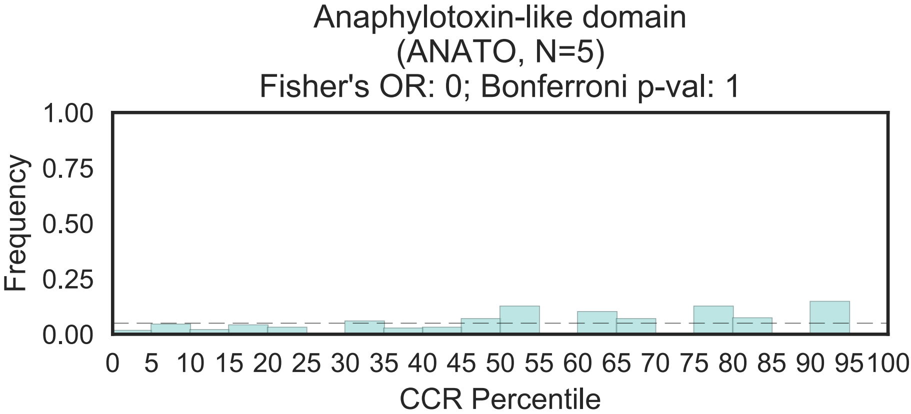
Anaphase-promoting complex subunit 4 WD40 domain
(ANAPC4_WD40, N=35)
Fisher's OR: 1.76; Bonferroni p-val: 1



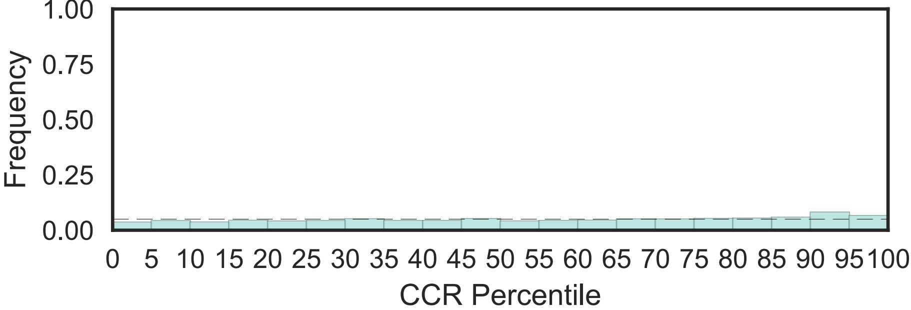
Anaphase-promoting complex subunit 5
(ANAPC5, N=20)
Fisher's OR: 0.358; Bonferroni p-val: 1

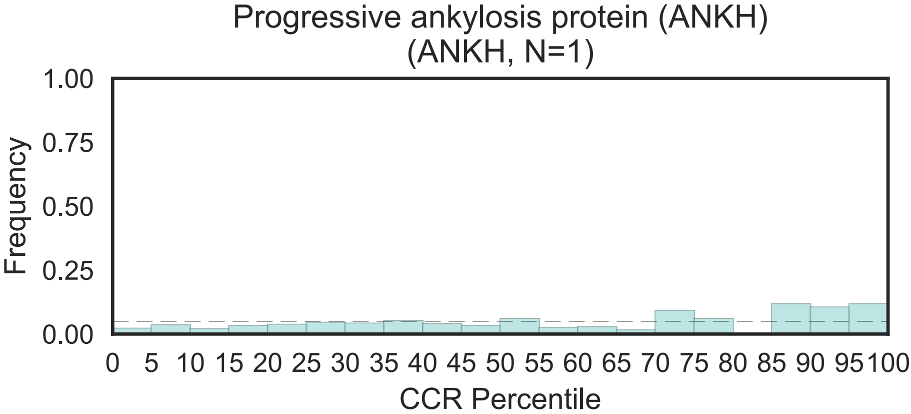

Anaphase promoting complex subunit 8 / Cdc23
(ANAPC8, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

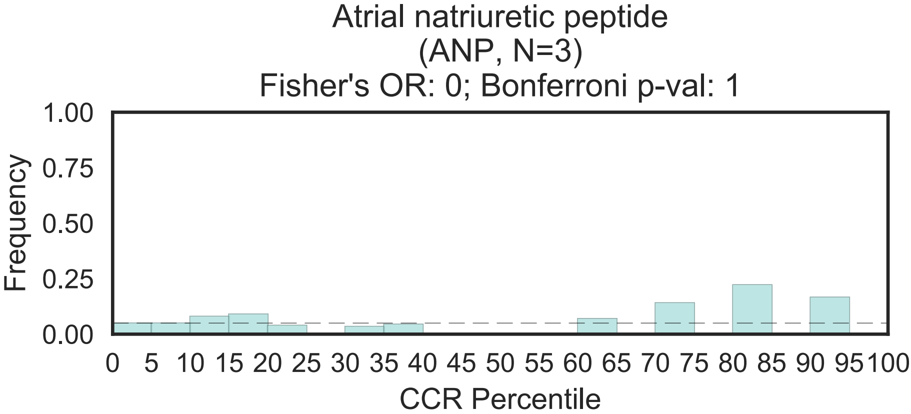

Anaphase-promoting complex APC subunit CDC26 (ANAPC_CDC26, N=1)

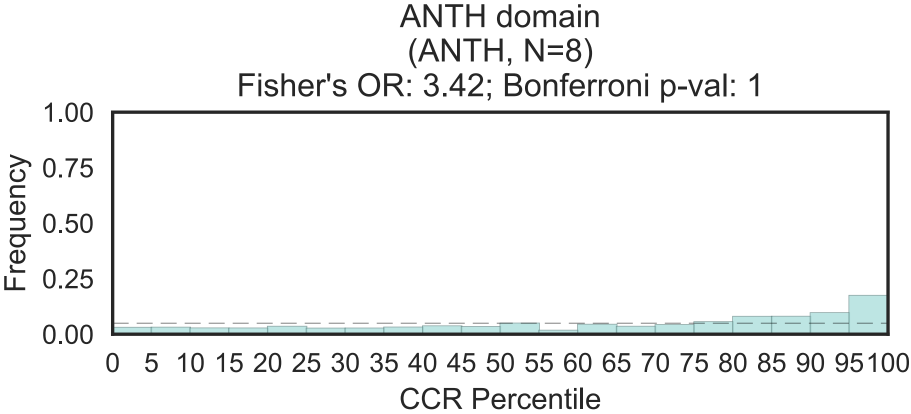

Anaphylotoxin-like domain
(ANATO, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

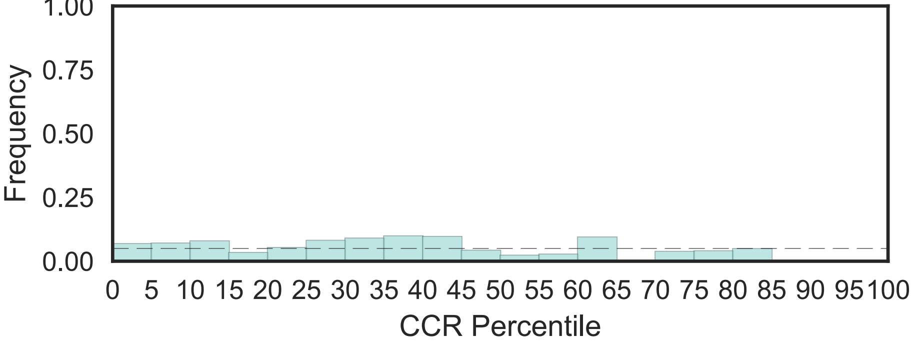
Receptor family ligand binding region
(ANF_receptor, N=37)
Fisher's OR: 1.01; Bonferroni p-val: 1



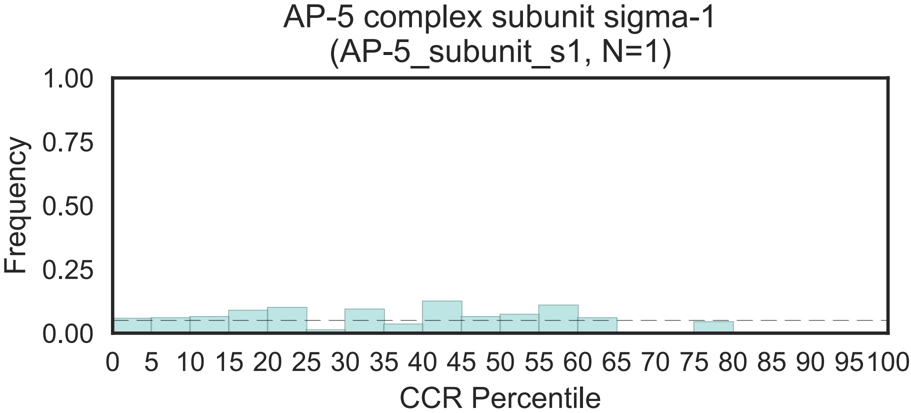

Progressive ankylosis protein (ANKH)
(ANKH, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

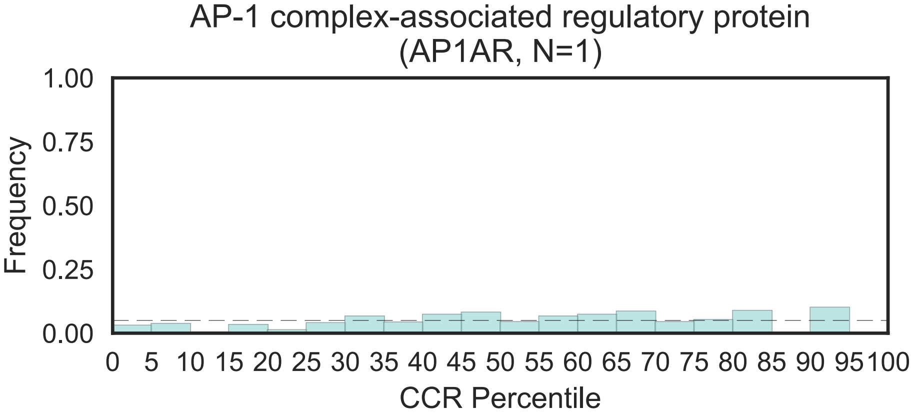

Atrial natriuretic peptide
(ANP, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

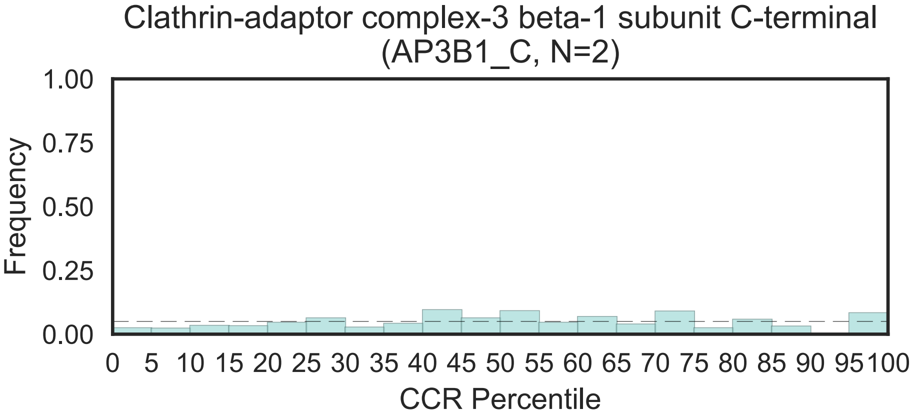

ANTH domain
(ANTH, N=8)
Fisher's OR: 3.42; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

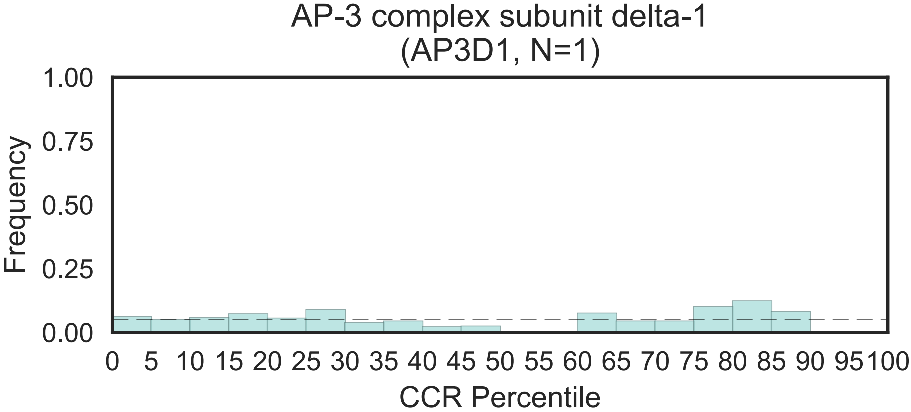


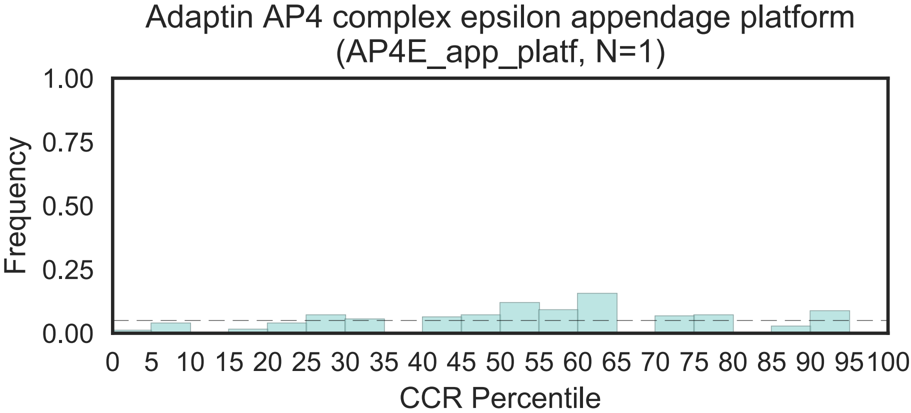
Annexin-2 receptor
(ANXA2R, N=1)

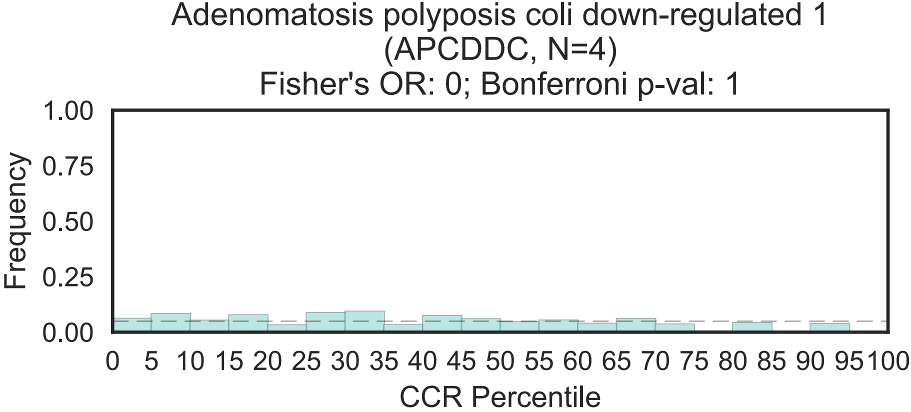

AP-5 complex subunit sigma-1
(AP-5_subunit_s1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

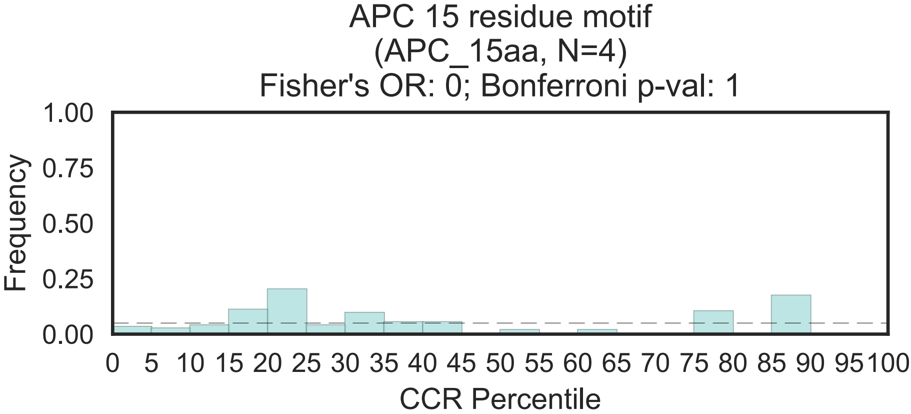

AP-1 complex-associated regulatory protein
(AP1AR, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Clathrin-adaptor complex-3 beta-1 subunit C-terminal
(AP3B1_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

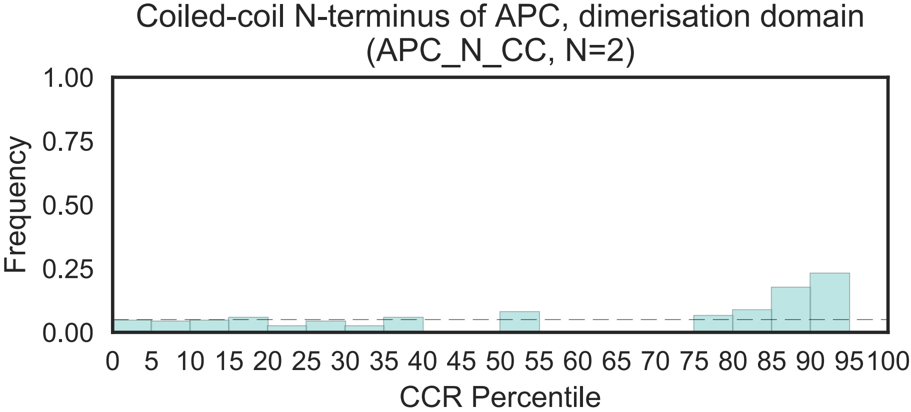

AP-3 complex subunit delta-1
(AP3D1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

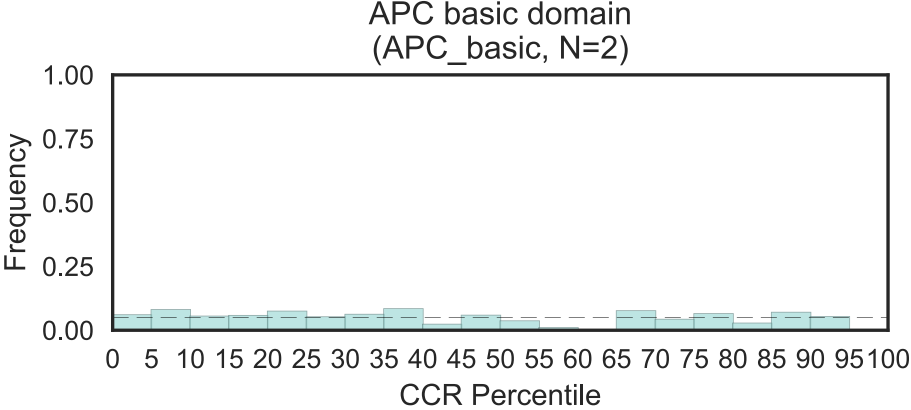

Adaptin AP4 complex epsilon appendage platform
(AP4E_app_platf, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

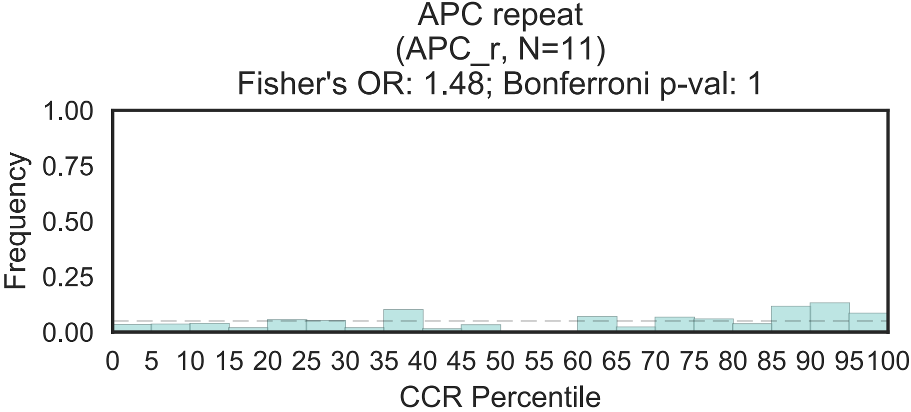

Adenomatosis polyposis coli down-regulated 1
(APCDDC, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

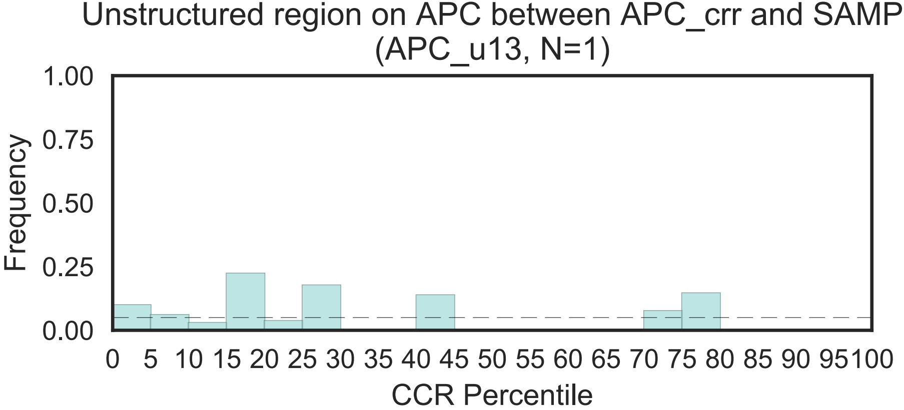


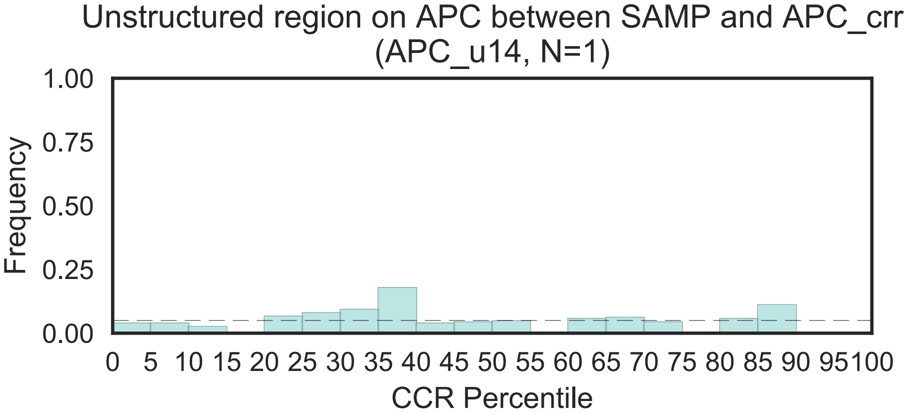
APC 15 residue motif
(APC_15aa, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

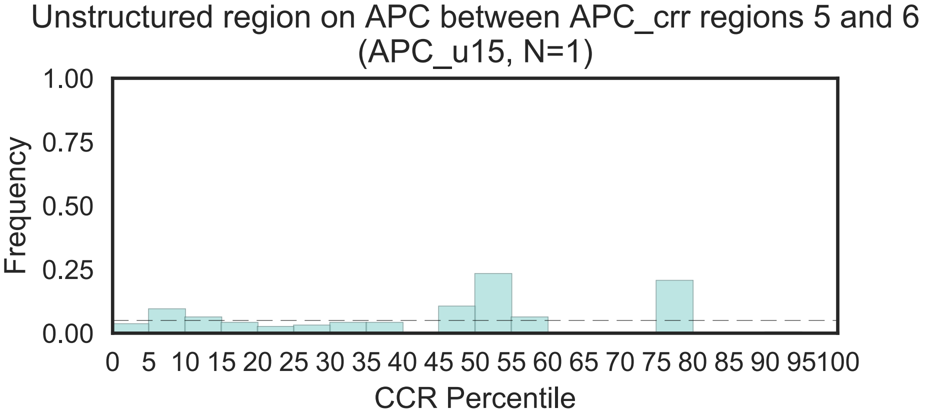

Coiled-coil N-terminus of APC, dimerisation domain
(APC_N_CC, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

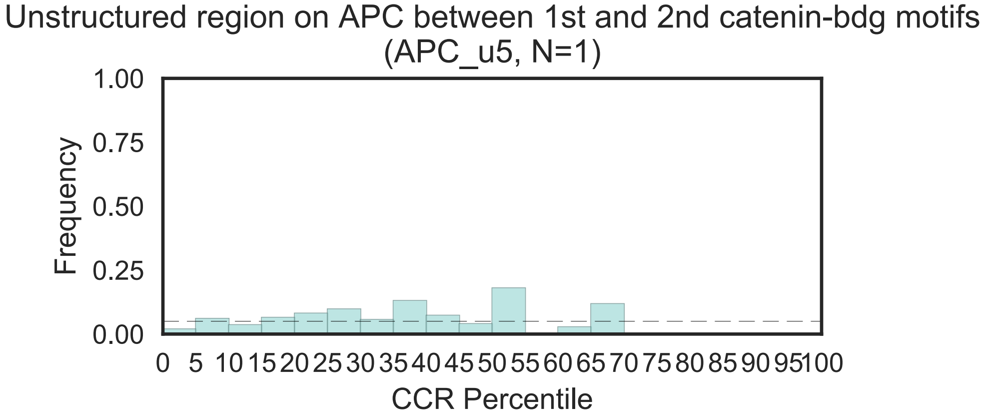

APC basic domain
(APC_basic, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

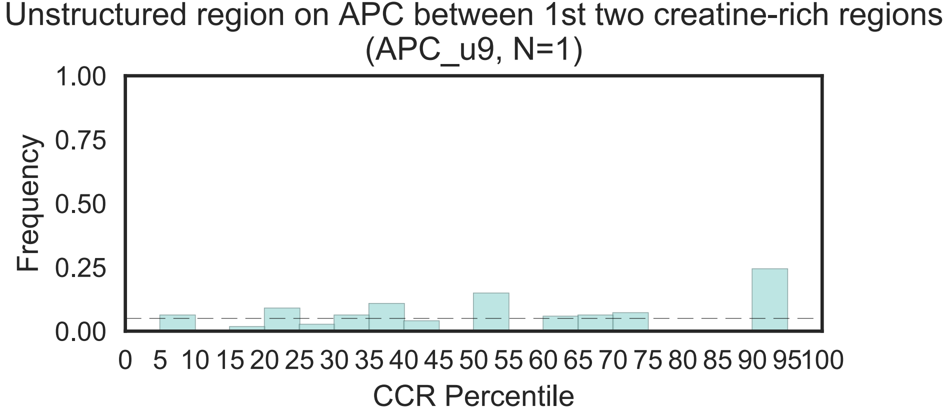

APC repeat
(APC_r, N=11)
Fisher's OR: 1.48; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

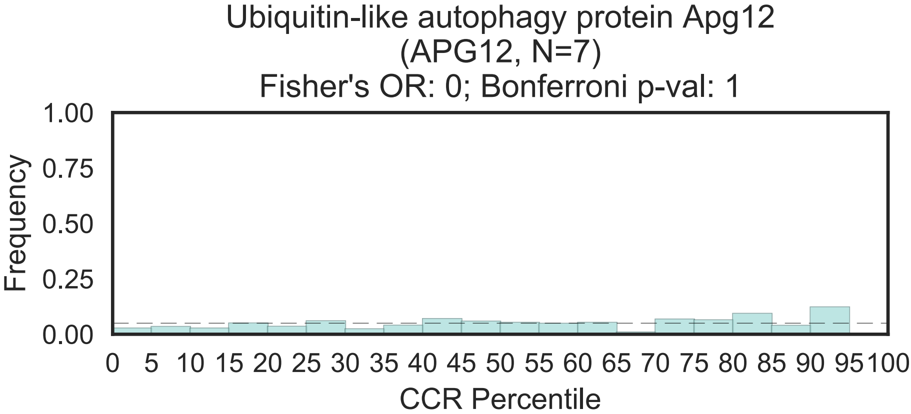

Unstructured region on APC between APC_crr and SAMP
(APC_u13, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

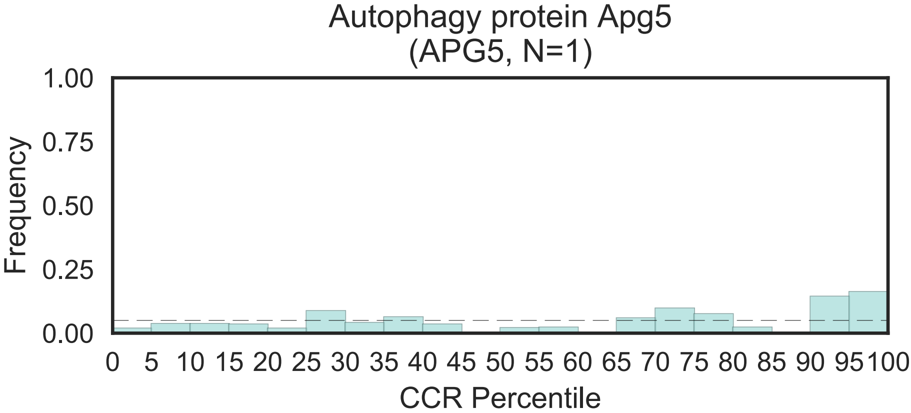

Unstructured region on APC between SAMP and APC_crr
(APC_u14, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

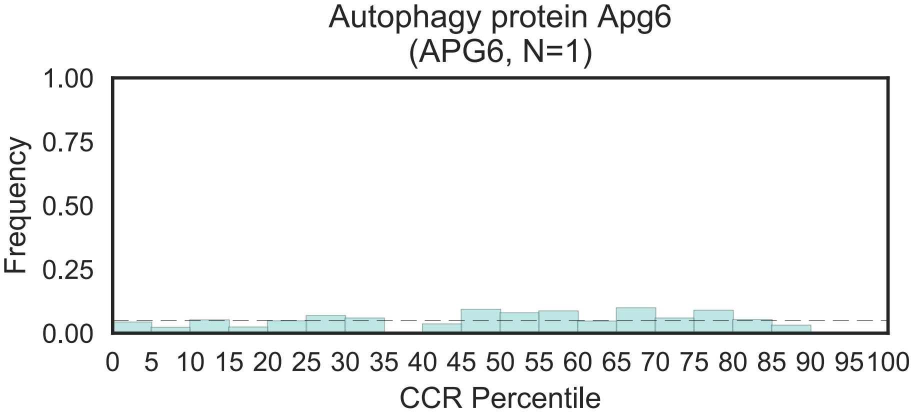

Unstructured region on APC between APC_crr regions 5 and 6
(APC_u15, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Unstructured region on APC between 1st and 2nd catenin-bdg motifs
(APC_u5, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

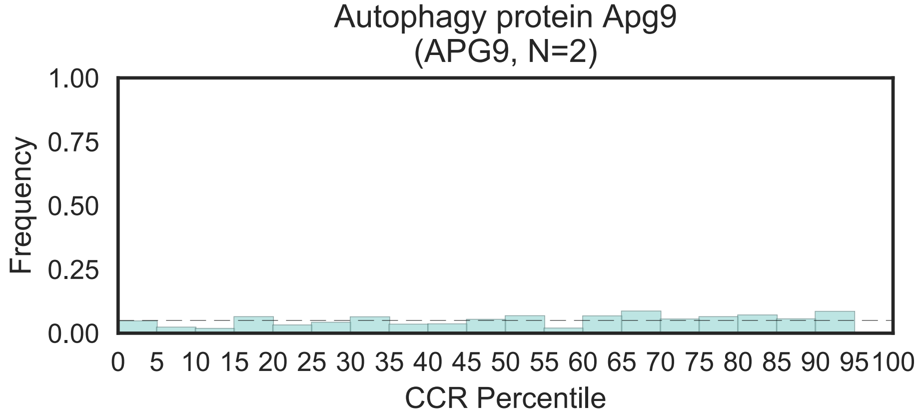

Unstructured region on APC between 1st two creatine-rich regions
(APC_u9, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

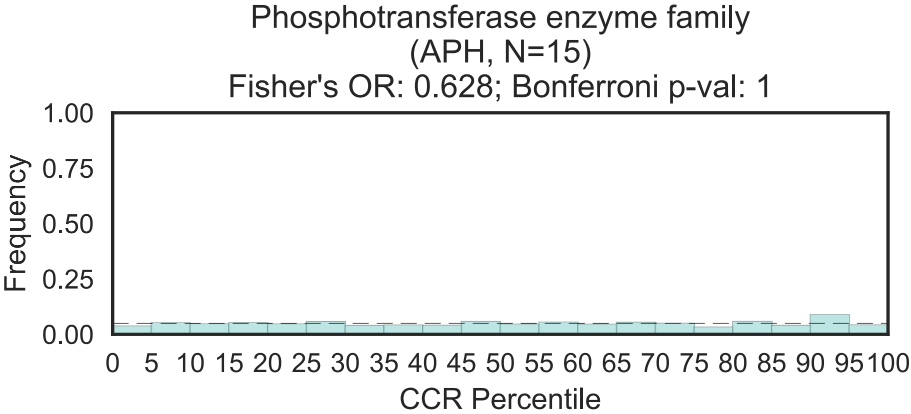

Ubiquitin-like autophagy protein Apg12
(APG12, N=7)
Fisher's OR: 0; Bonferroni p-val: 1


Autophagy protein Apg5
(APG5, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

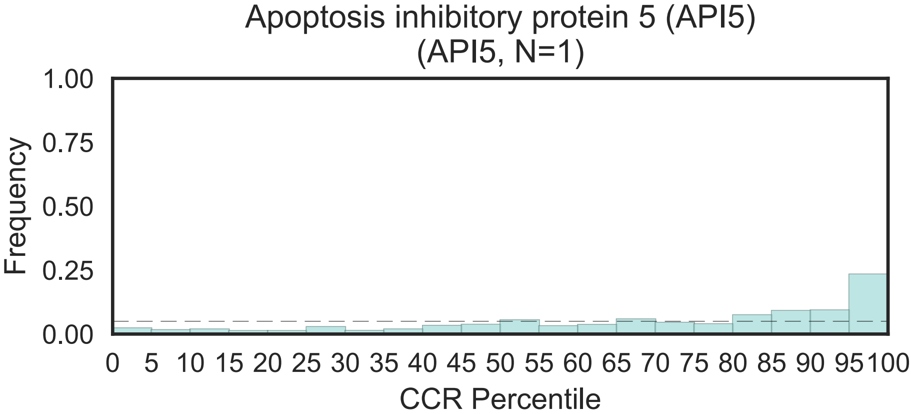


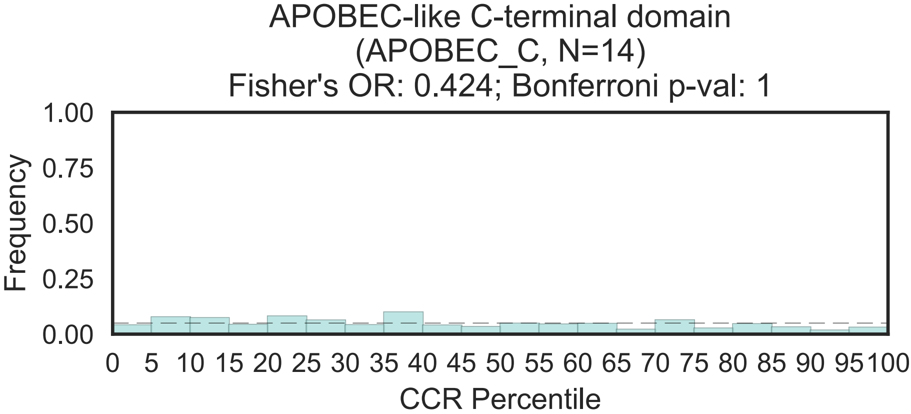
Autophagy protein Apg6
(APG6, N=1)

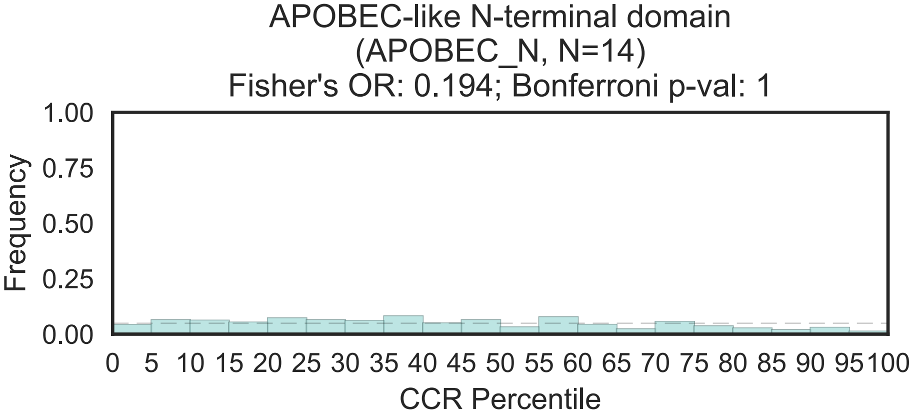

Autophagy protein Apg9
(APG9, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

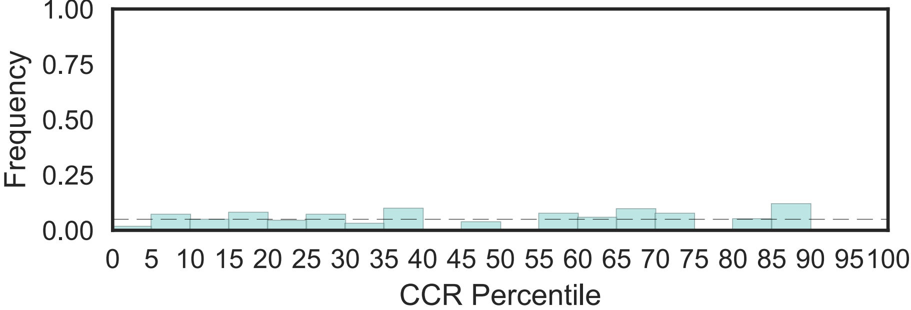


Phosphotransferase enzyme family
(APH, N=15)
Fisher's OR: 0.628; Bonferroni p-val: 1

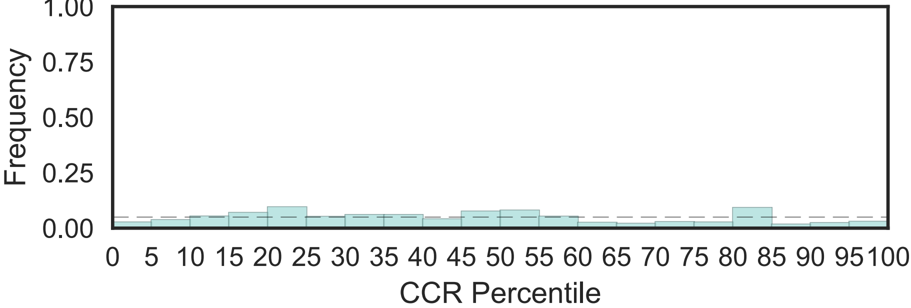

Apoptosis inhibitory protein 5 (API5)
(API5, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

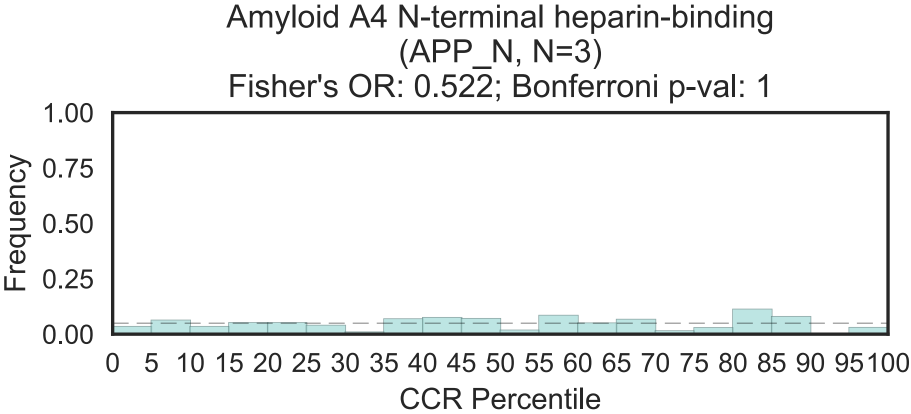

APOBEC-like C-terminal domain
(APOBEC_C, N=14)
Fisher's OR: 0.424; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

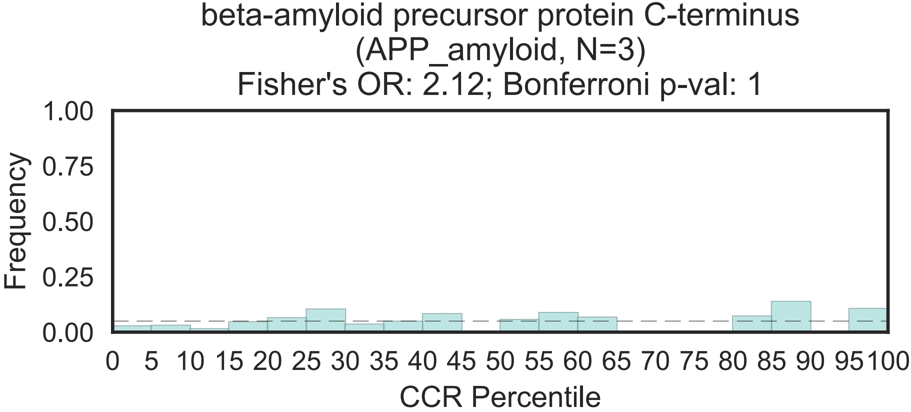

APOBEC-like N-terminal domain
(APOBEC_N, N=14)
Fisher's OR: 0.194; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

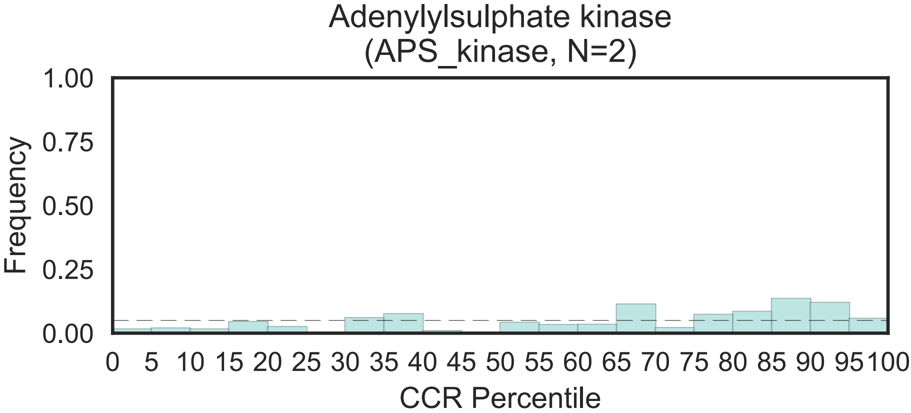


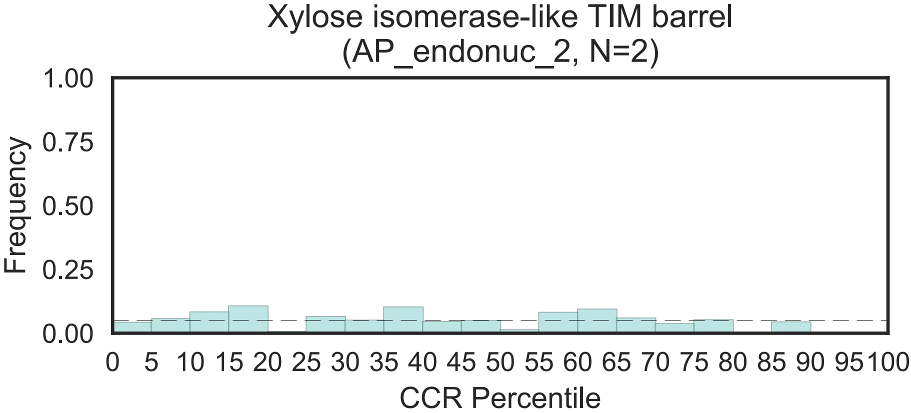
Copper-binding of amyloid precursor, CuBD
(APP_Cu_bd, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

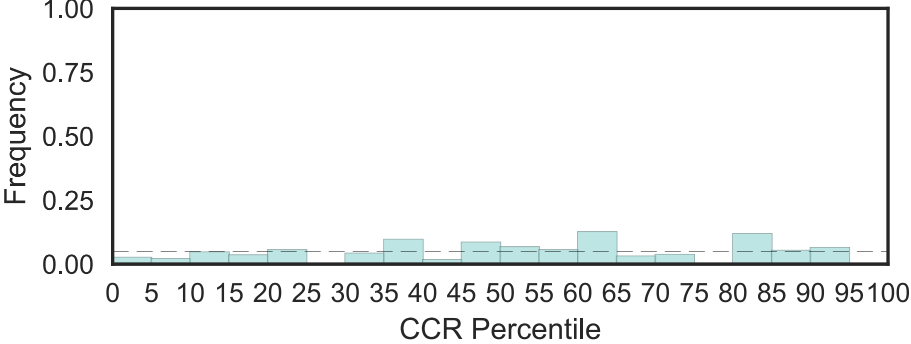

E2 domain of amyloid precursor protein
(APP_E2, N=3)
Fisher's OR: 0.48; Bonferroni p-val: 1


Amyloid A4 N-terminal heparin-binding
(APP_N, N=3)
Fisher's OR: 0.522; Bonferroni p-val: 1

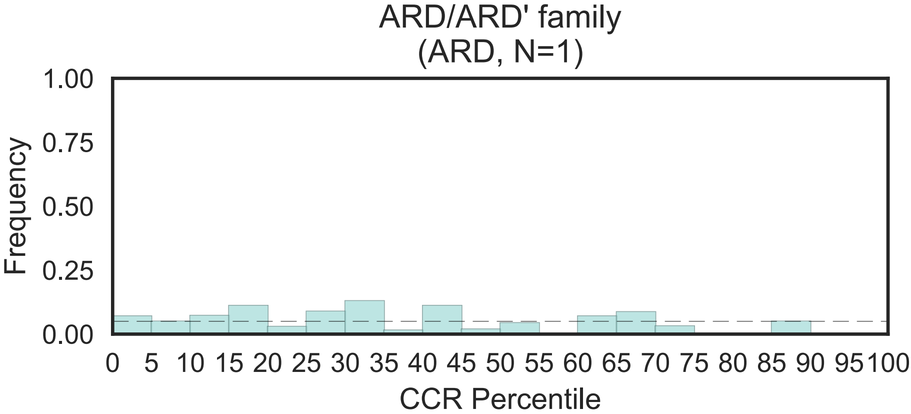

beta-amyloid precursor protein C-terminus
(APP_amyloid, N=3)
Fisher's OR: 2.12; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

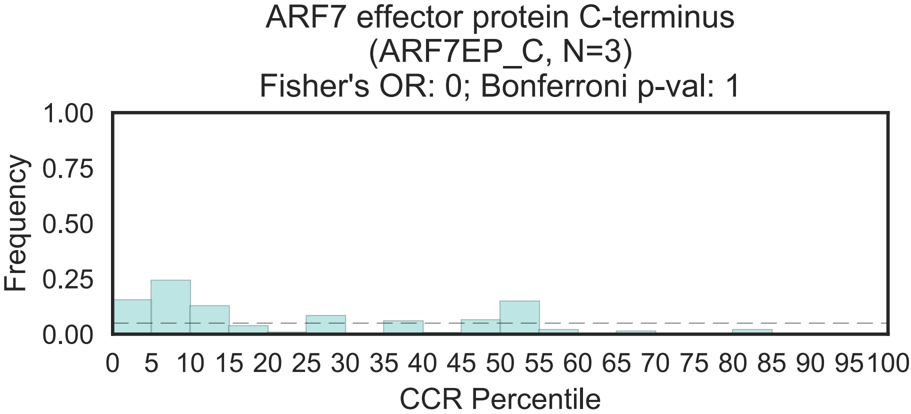

Adenylylsulphate kinase
(APS_kinase, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

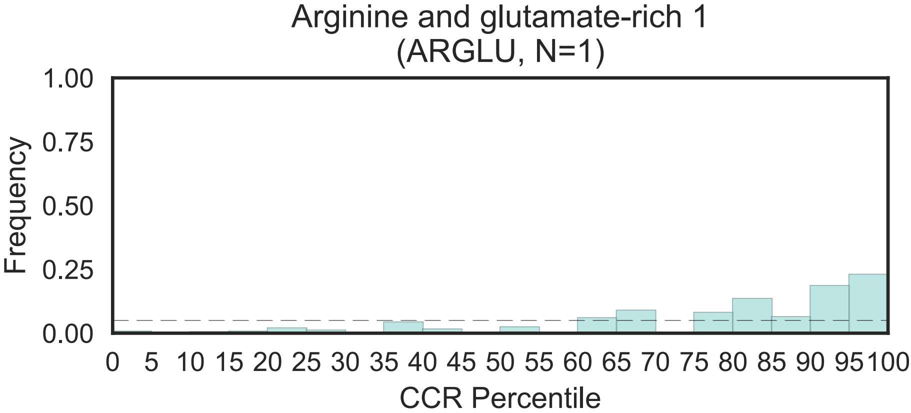

Xylose isomerase-like TIM barrel
(AP_endonuc_2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

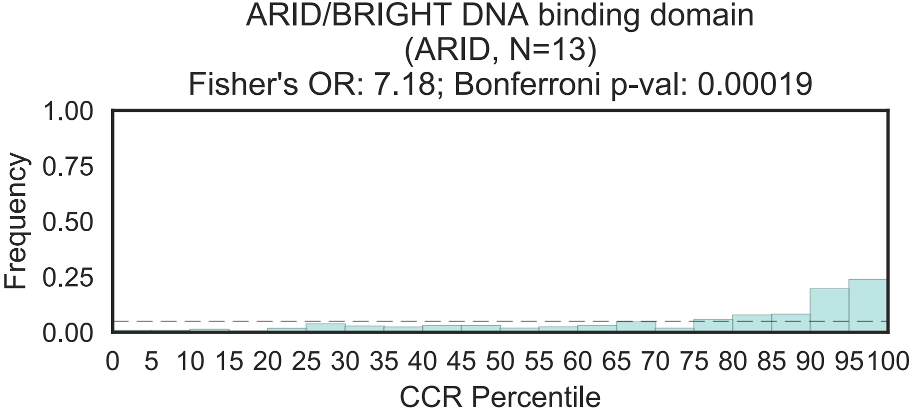


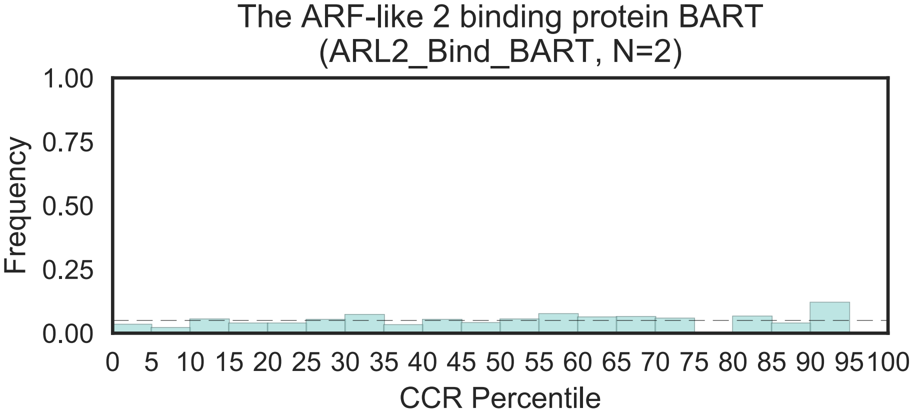
Nuclear coactivator
(ARA70, N=2)

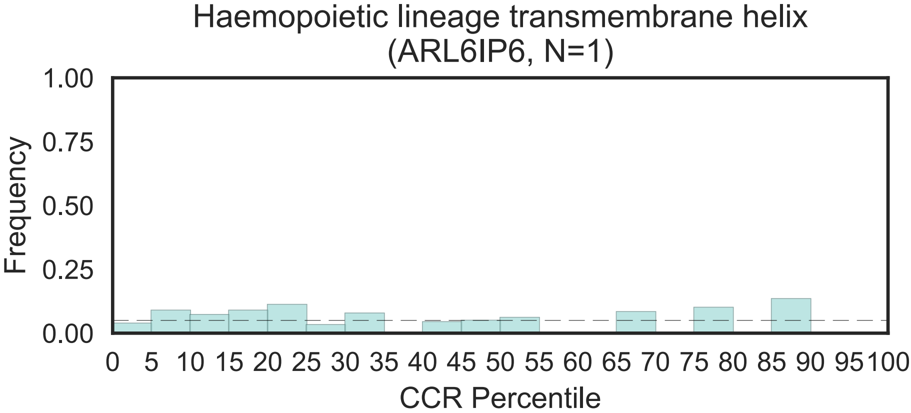

ARD/ARD' family
(ARD, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

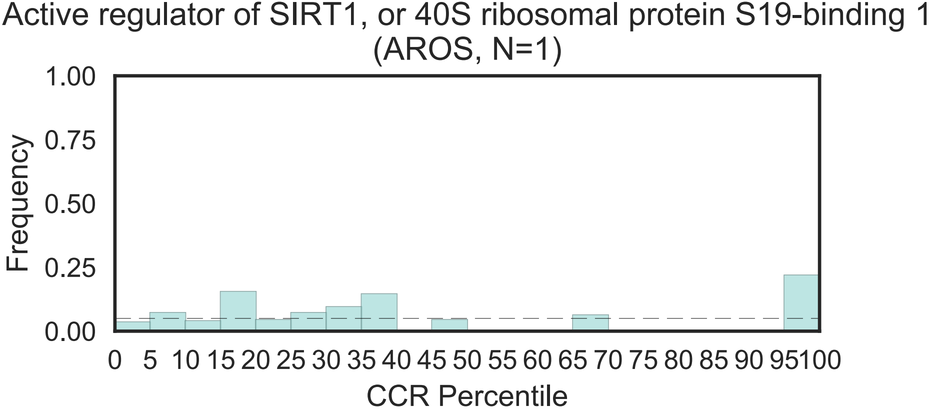

ARF7 effector protein C-terminus
(ARF7EP_C, N=3)
Fisher's OR: 0; Bonferroni p-val: 1


Arginine and glutamate-rich 1
(ARGLU, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

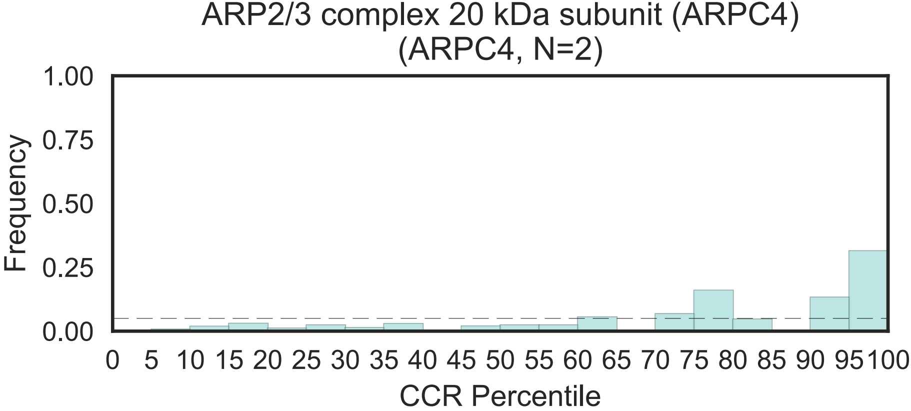

ARID/BRIGHT DNA binding domain
(ARID, N=13)
Fisher's OR: 7.18; Bonferroni p-val: 0.00019
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

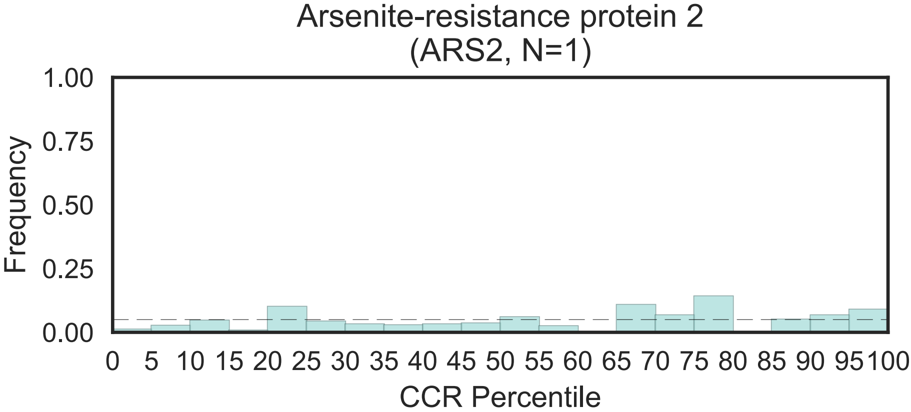

The ARF-like 2 binding protein BART
(ARL2_Bind_BART, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

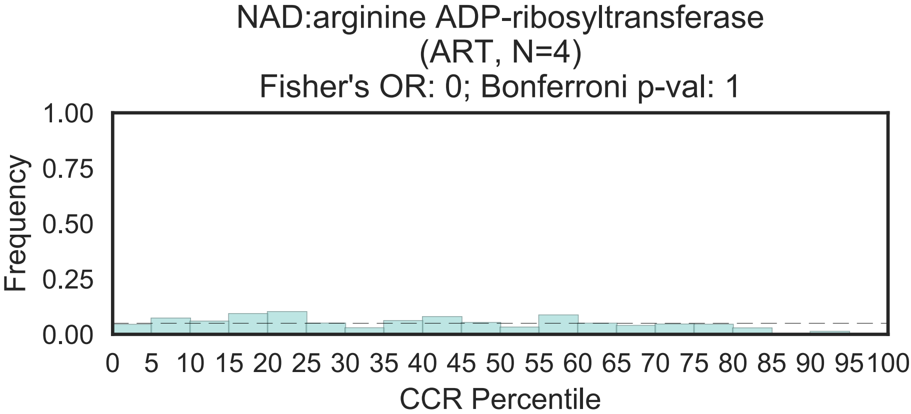

Haemopoietic lineage transmembrane helix
(ARL6IP6, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



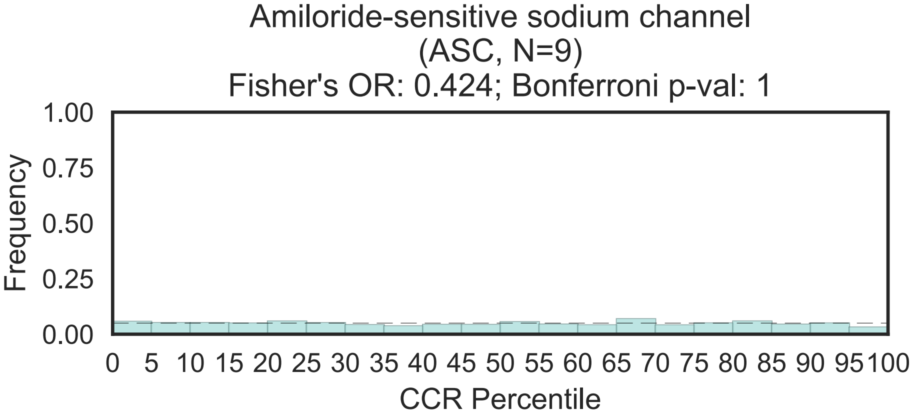
Active regulator of SIRT1, or 40S ribosomal protein S19-binding 1 (AROS, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

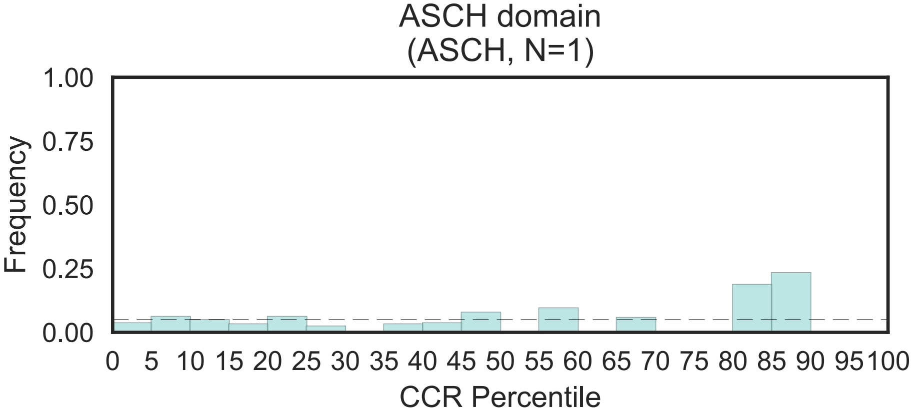

ARP2/3 complex 20 kDa subunit (ARPC4)
(ARPC4, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

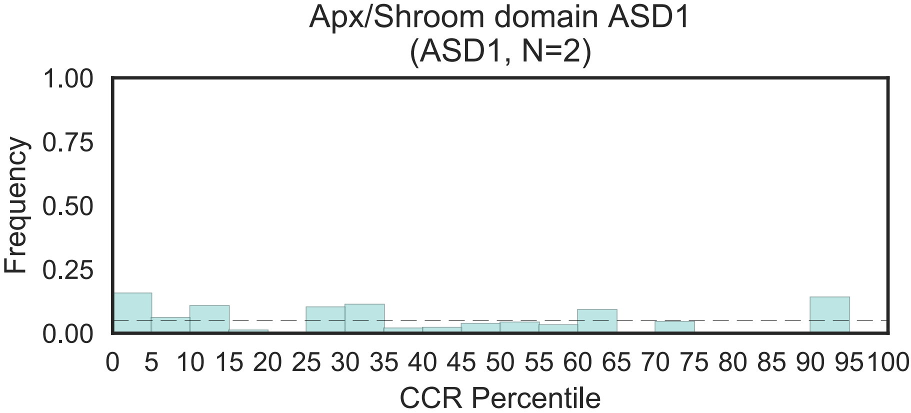

Arsenite-resistance protein 2
(ARS2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

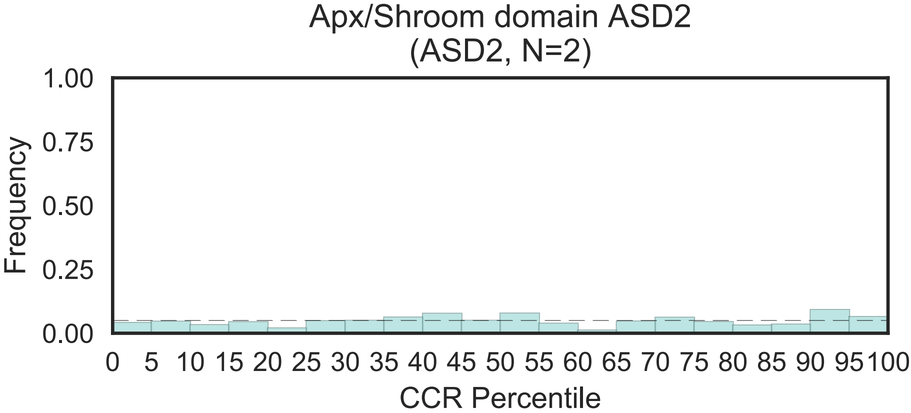


NAD:arginine ADP-ribosyltransferase
(ART, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

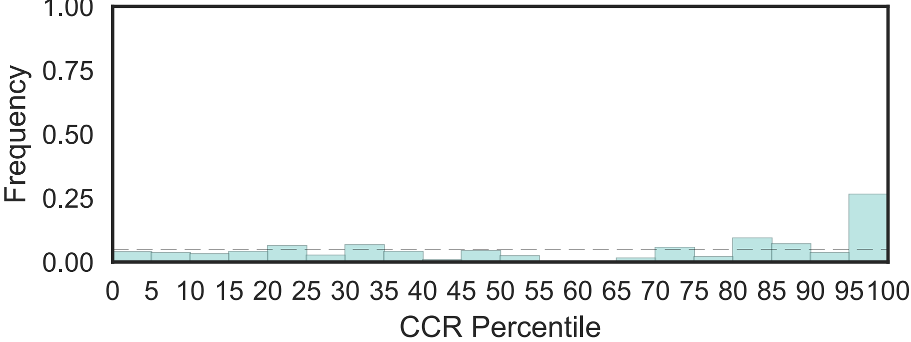

Amiloride-sensitive sodium channel
(ASC, N=9)
Fisher's OR: 0.424; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

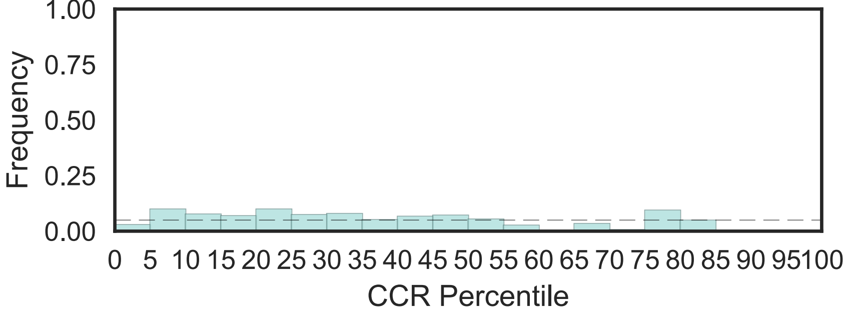

ASCH domain
(ASCH, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Apx/Shroom domain ASD1
(ASD1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

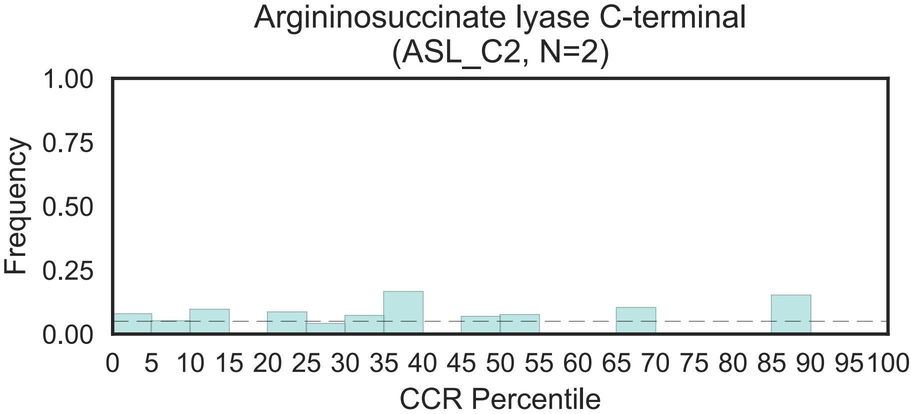

Apx/Shroom domain ASD2
(ASD2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

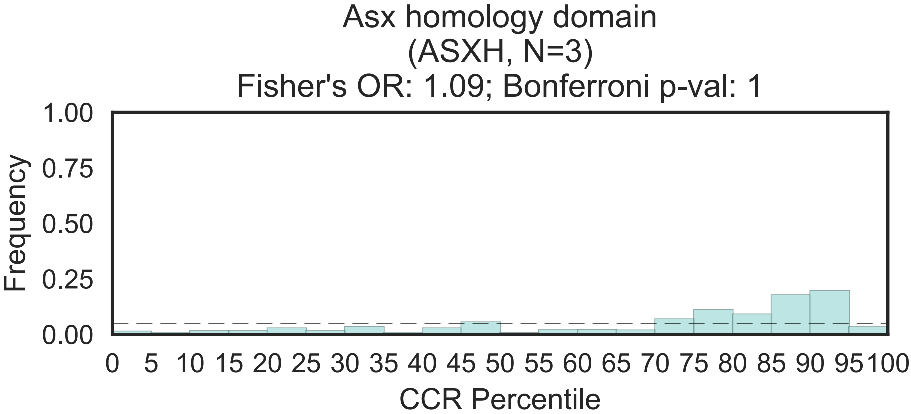
ASF1 like histone chaperone
(ASF1_hist_chap, N=2)

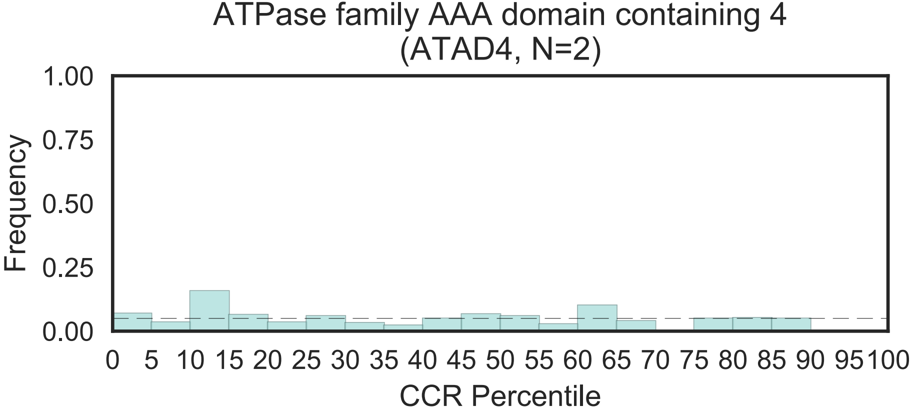


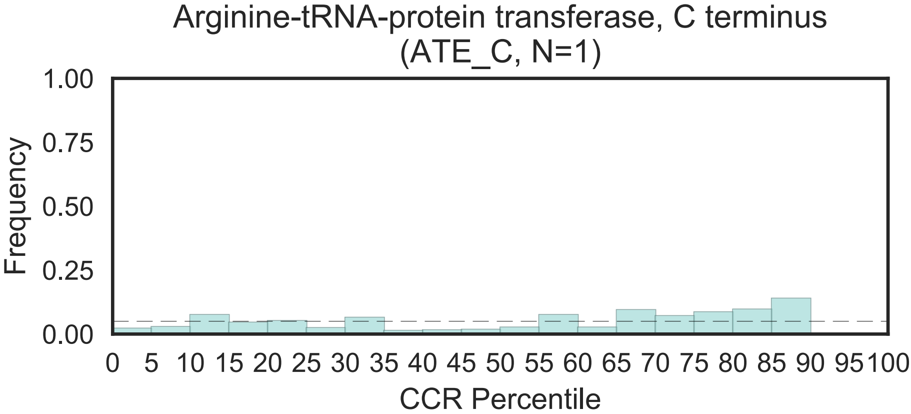


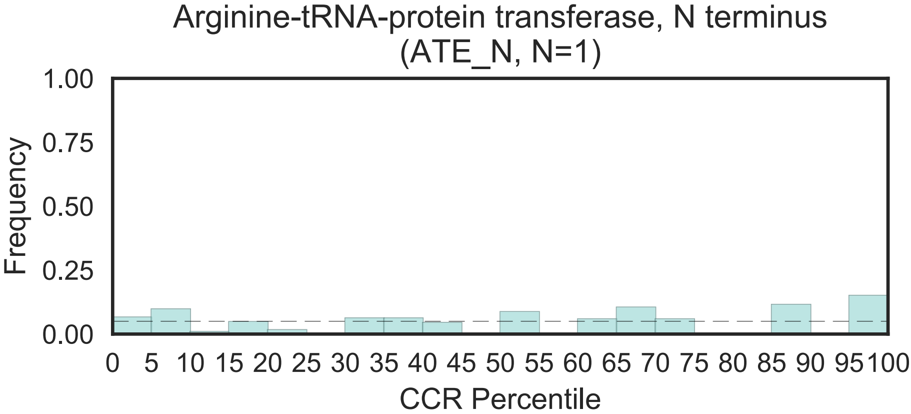
Abnormal spindle-like microcephaly-assoc'd, ASPM-SPD-2-Hydin
(ASH, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

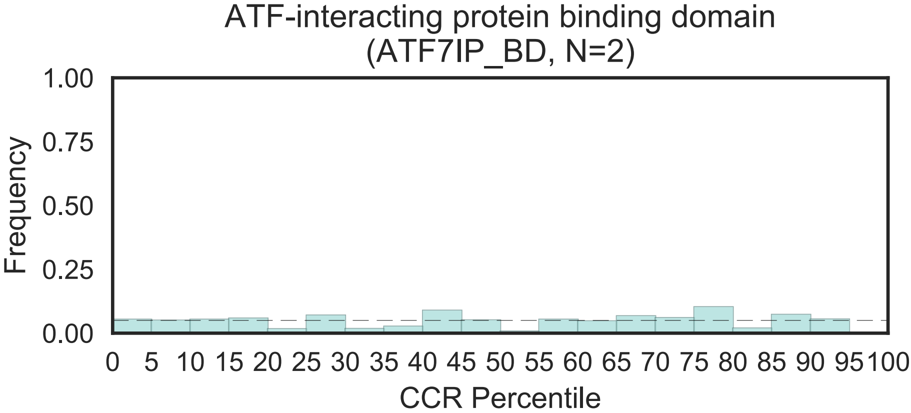

Argininosuccinate lyase C-terminal
(ASL_C2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

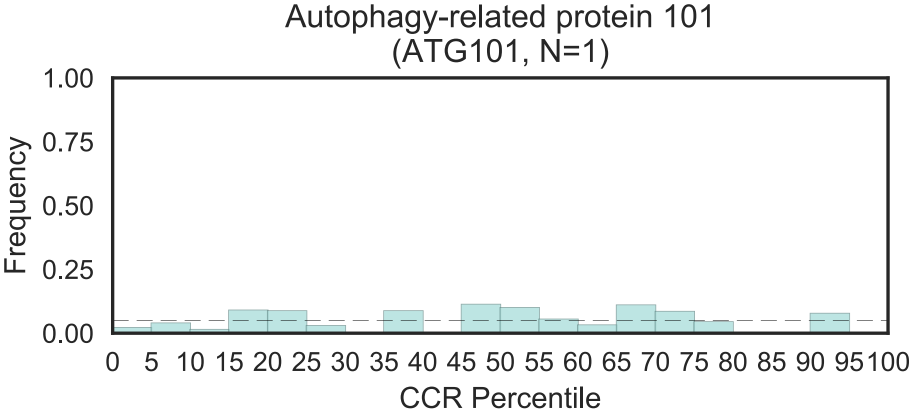

Asx homology domain
(ASXH, N=3)
Fisher's OR: 1.09; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

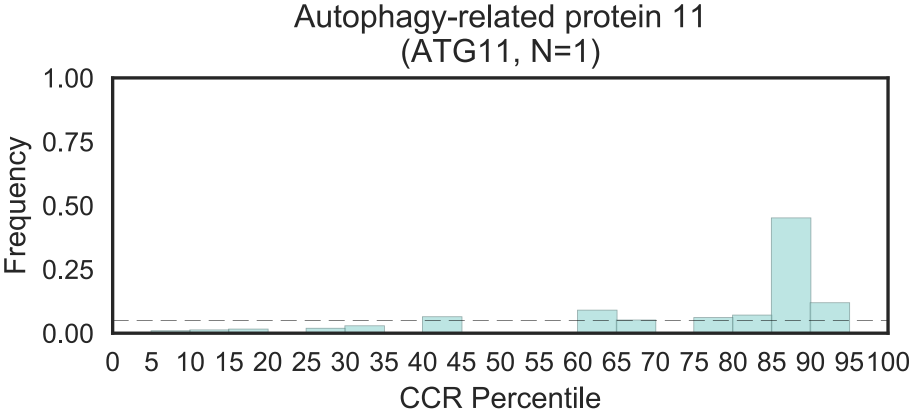

ATPase family AAA domain containing 4
(ATAD4, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

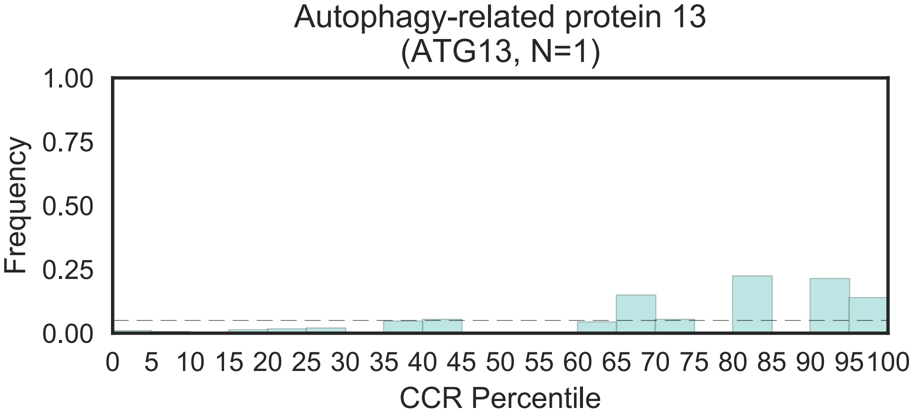

Arginine-tRNA-protein transferase, C terminus
(ATE_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

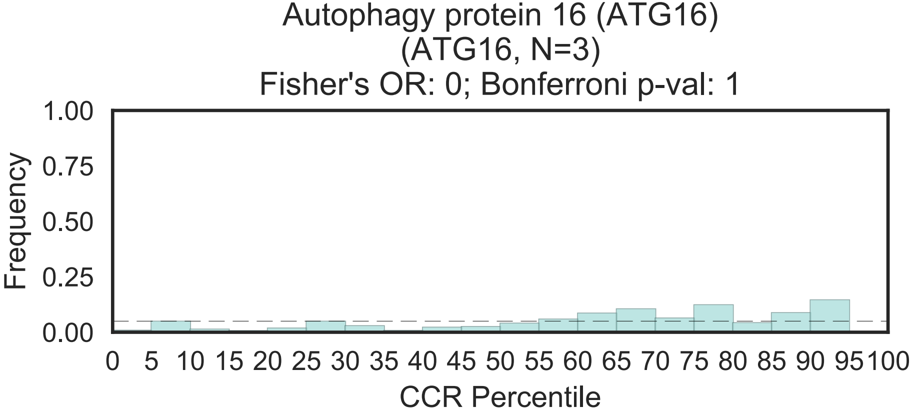

Arginine-tRNA-protein transferase, N terminus
(ATE_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

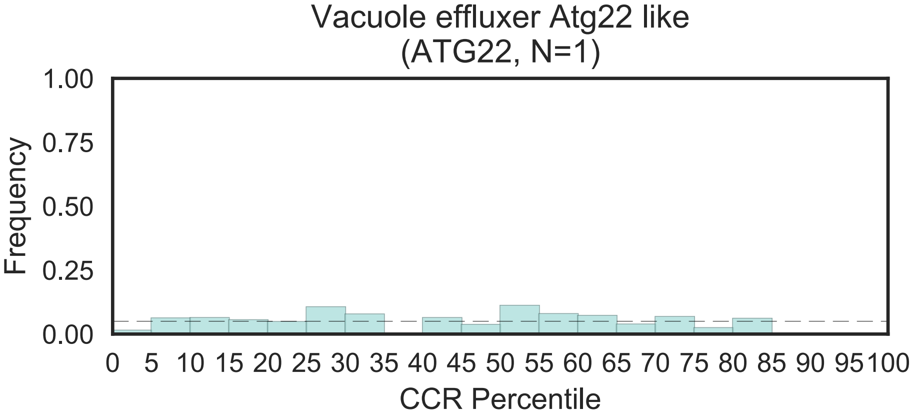

ATF-interacting protein binding domain
(ATF7IP_BD, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

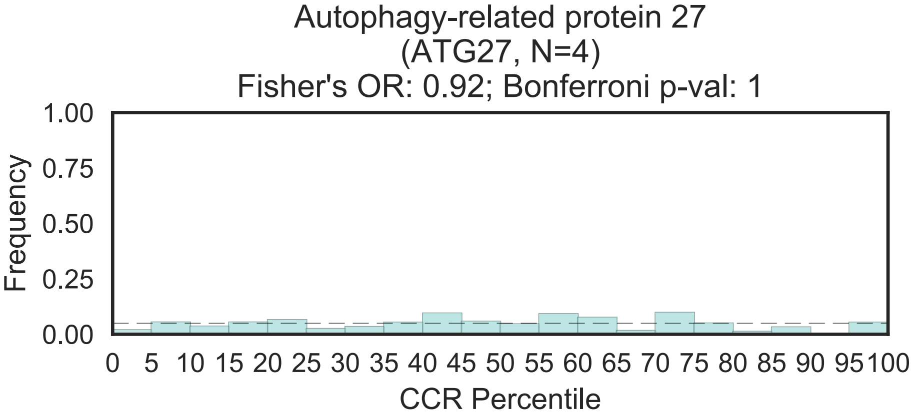

Autophagy-related protein 101
(ATG101, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

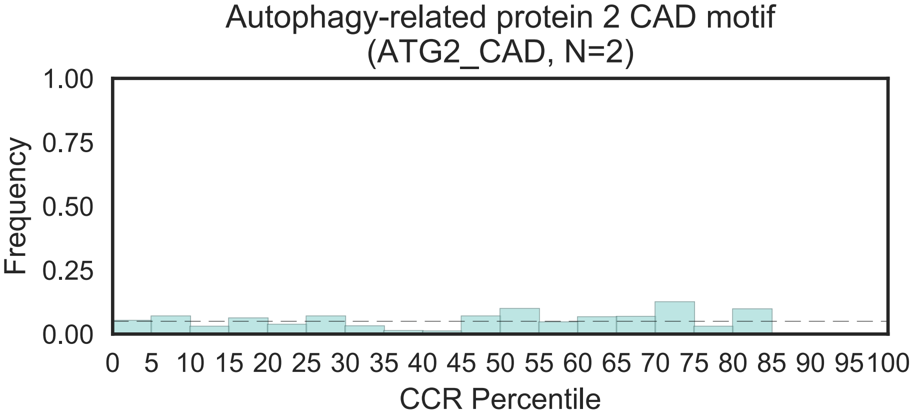

Autophagy-related protein 11
(ATG11, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

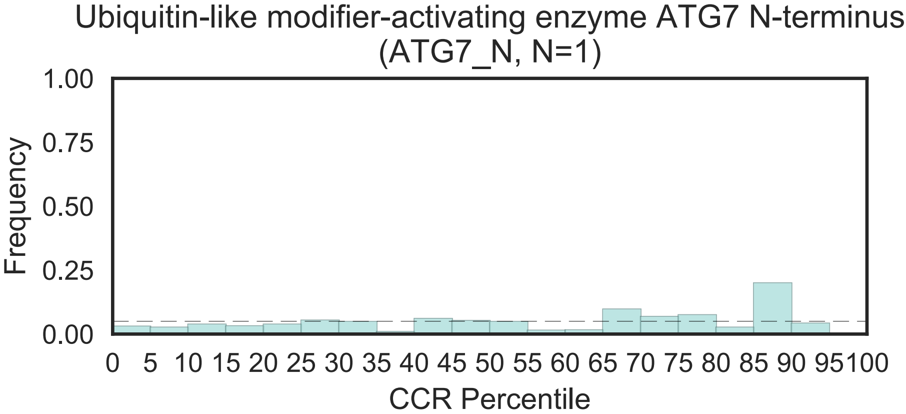

Autophagy-related protein 13
(ATG13, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Autophagy protein 16 (ATG16)
(ATG16, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Vacuole effluxer Atg22 like
(ATG22, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

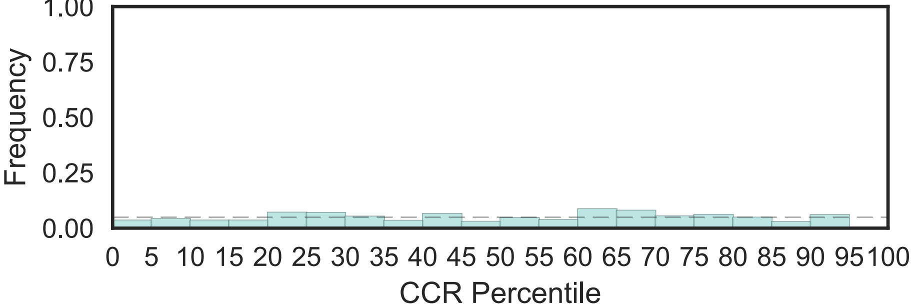

Autophagy-related protein 27
(ATG27, N=4)
Fisher's OR: 0.92; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

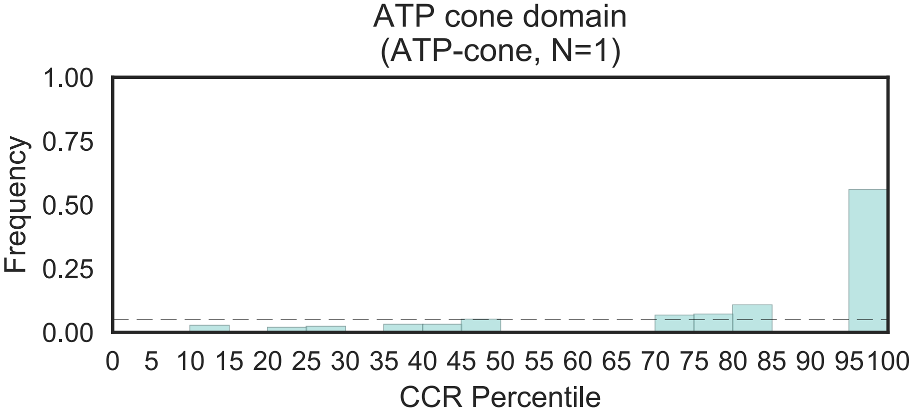

Autophagy-related protein 2 CAD motif
(ATG2_CAD, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

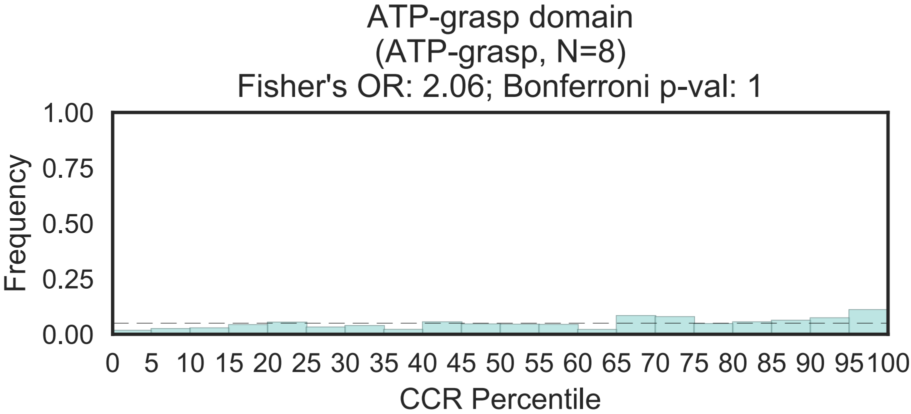

Ubiquitin-like modifier-activating enzyme ATG7 N-terminus
(ATG7_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

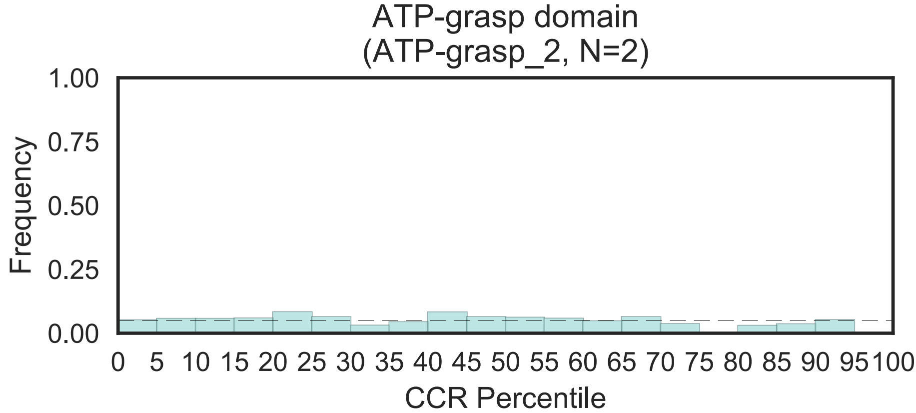
Autophagy-related protein C terminal domain (ATG_C, N=4)

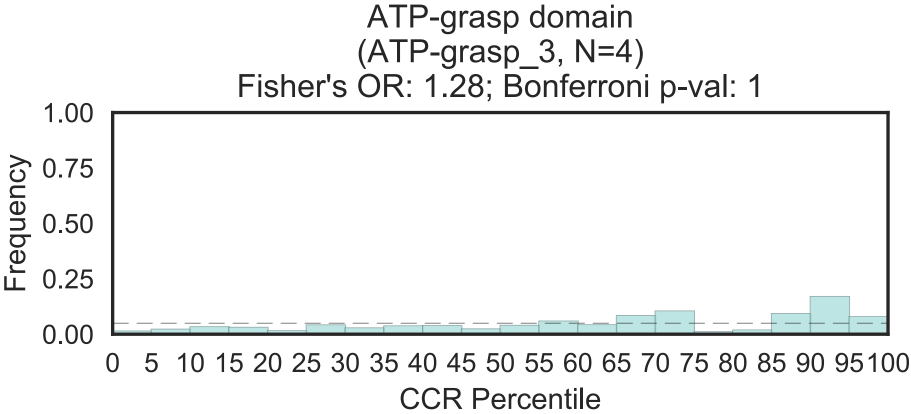
Fisher's OR: 0; Bonferroni p-val: 1

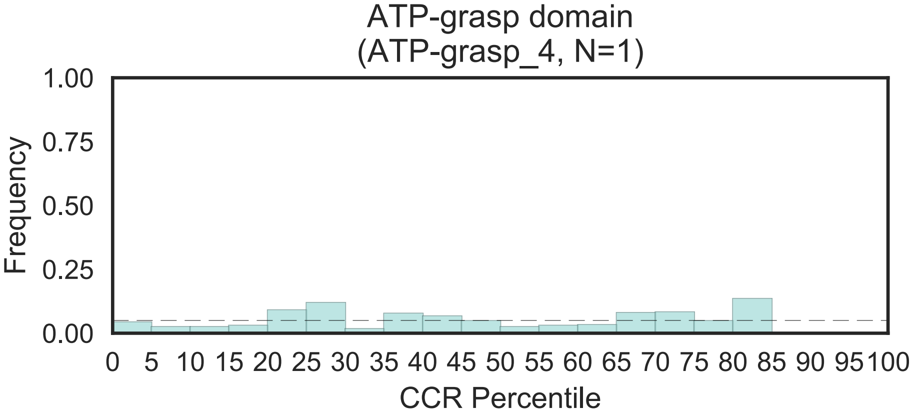


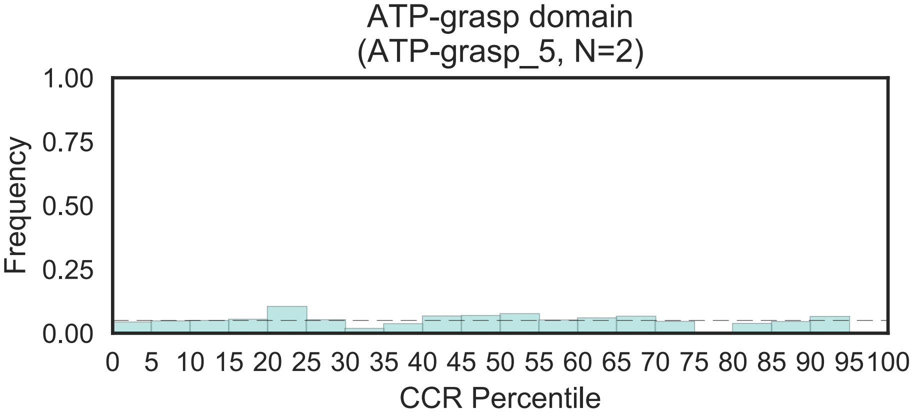

ATP cone domain
(ATP-cone, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

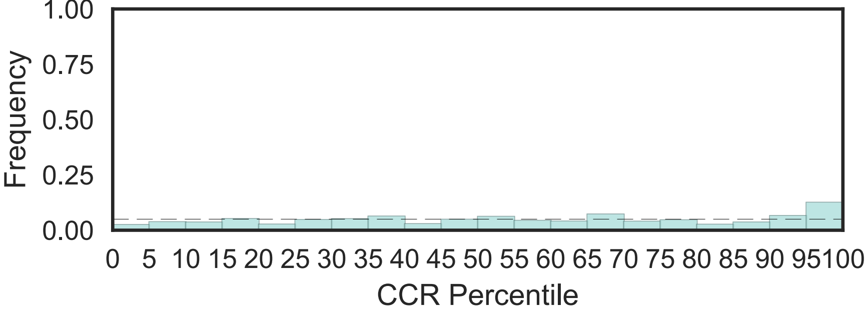

ATP-grasp domain
(ATP-grasp, N=8)
Fisher's OR: 2.06; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


ATP-grasp domain
(ATP-grasp_2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

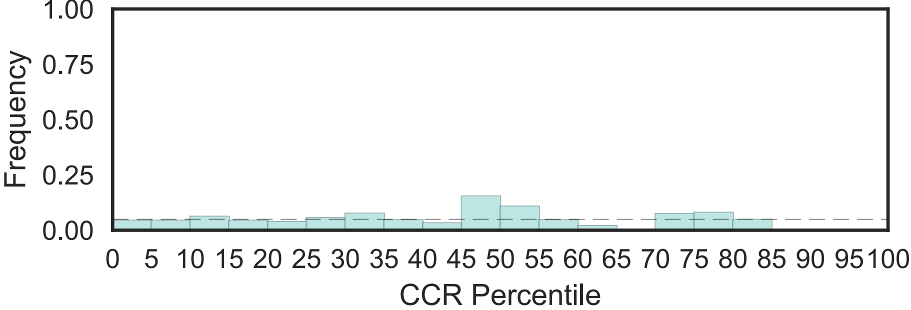

ATP-grasp domain
(ATP-grasp_3, N=4)
Fisher's OR: 1.28; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


ATP-grasp domain
(ATP-grasp_4, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

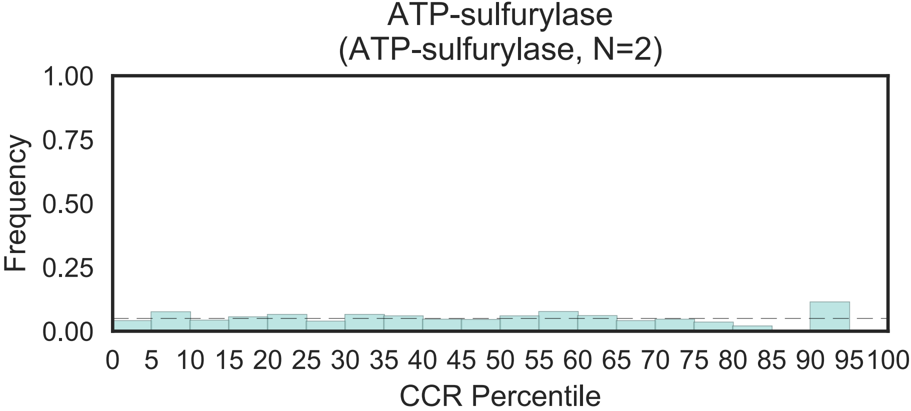

ATP-grasp domain
(ATP-grasp_5, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

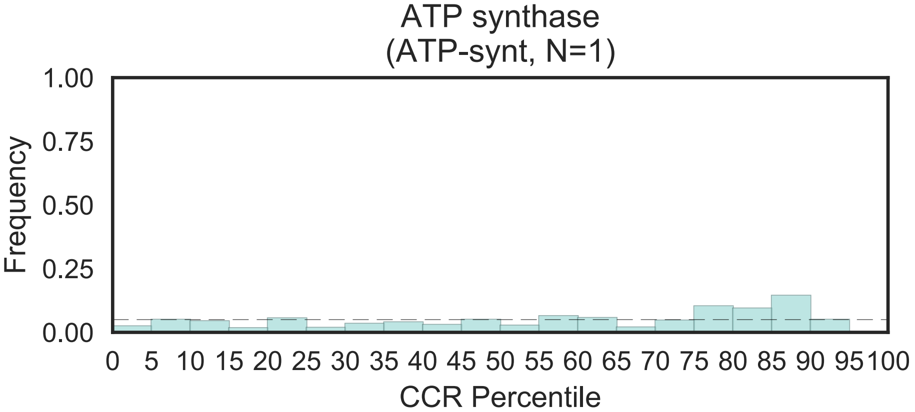


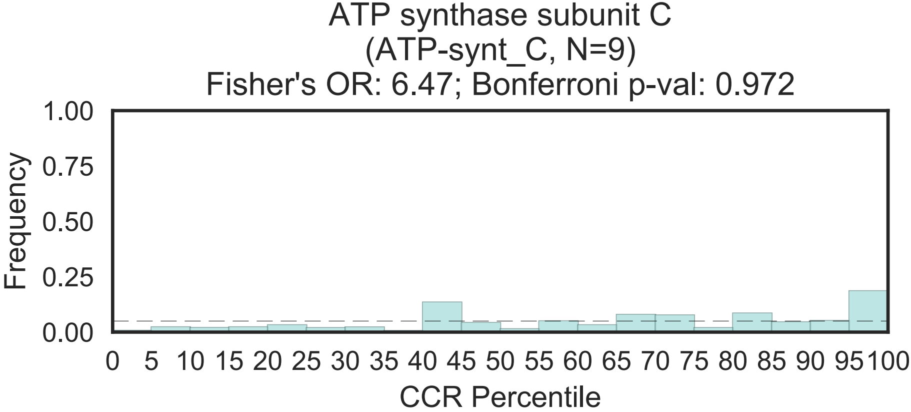
ATP:guanido phosphotransferase, C-terminal catalytic domain
(ATP-gua_Ptrans, N=5)
Fisher's OR: 2.14; Bonferroni p-val: 1



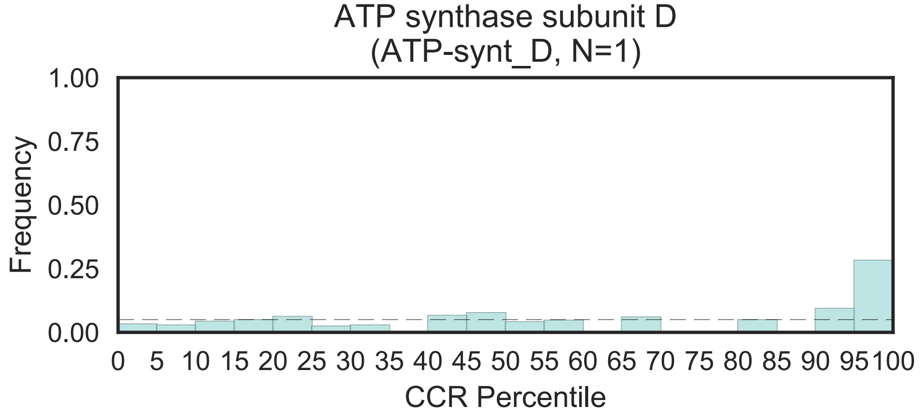
ATP:guanido phosphotransferase, N-terminal domain
(ATP-gua_PtransN, N=5)
Fisher's OR: 0; Bonferroni p-val: 1

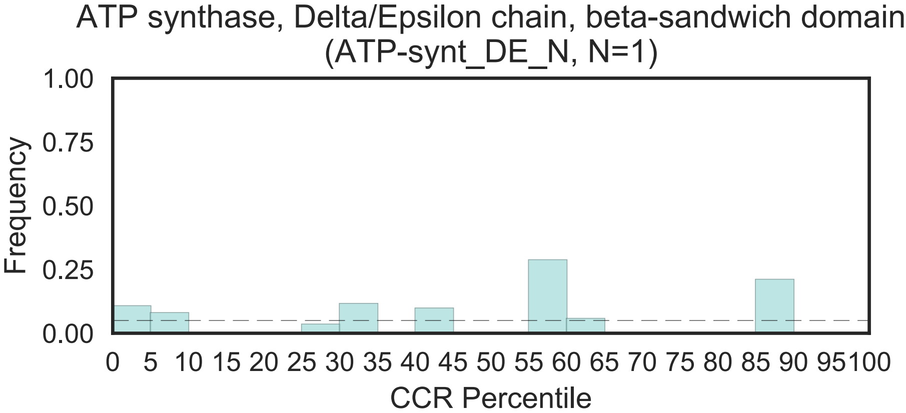

ATP-sulfurylase
(ATP-sulfurylase, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

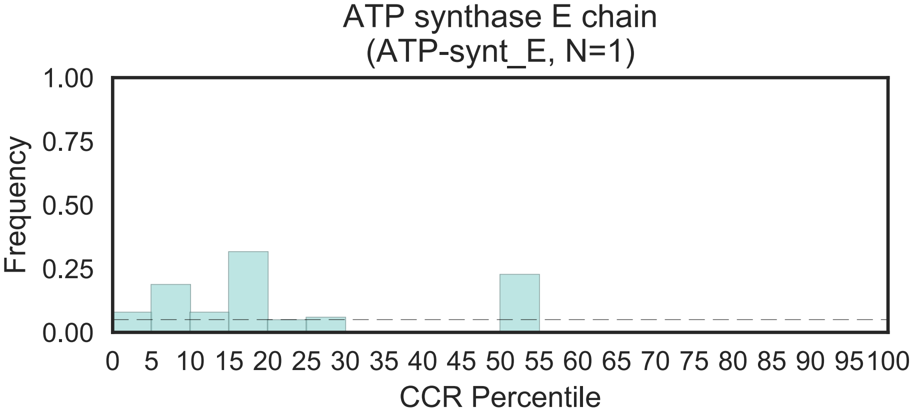

ATP synthase
(ATP-synt, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

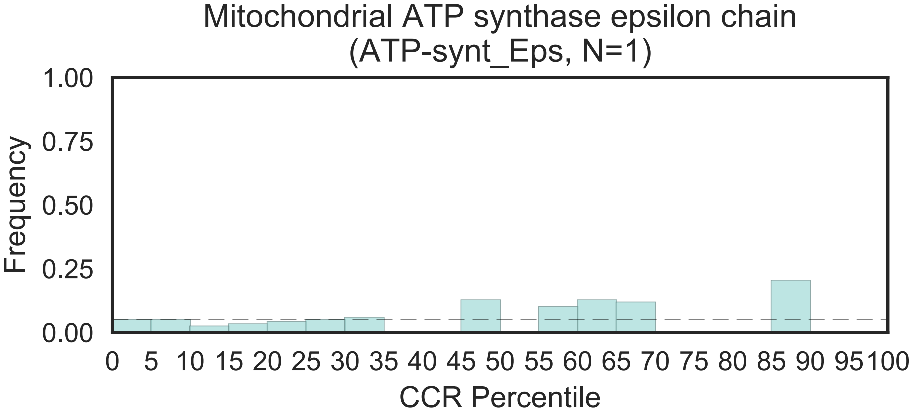


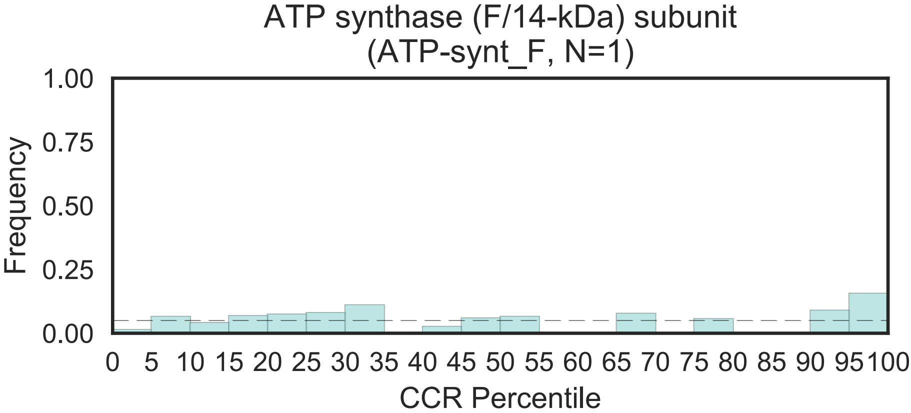
ATP synthase subunit C
(ATP-synt_C, N=9)
Fisher's OR: 6.47; Bonferroni p-val: 0.972

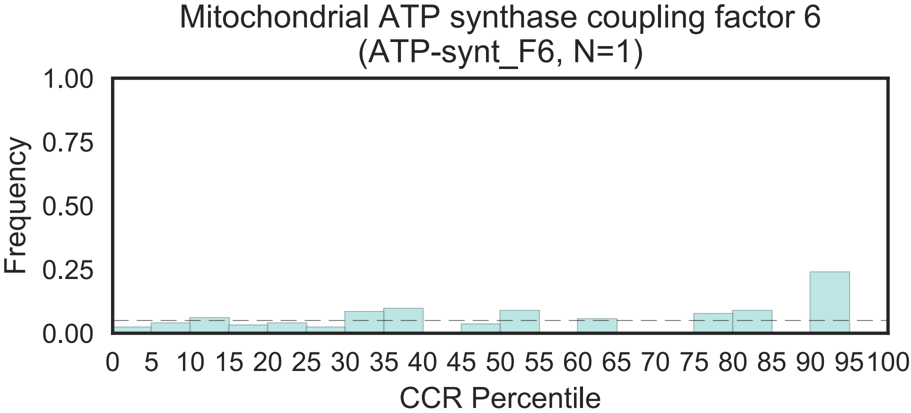

ATP synthase subunit D
(ATP-synt_D, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

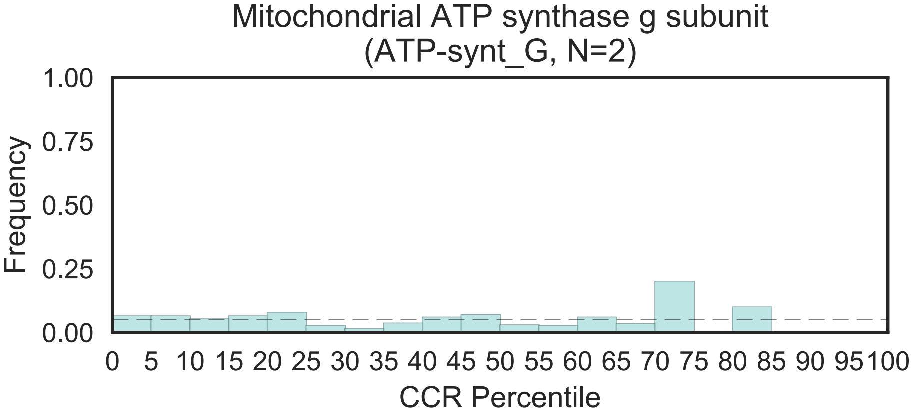

ATP synthase, Delta/Epsilon chain, beta-sandwich domain
(ATP-synt_DE_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

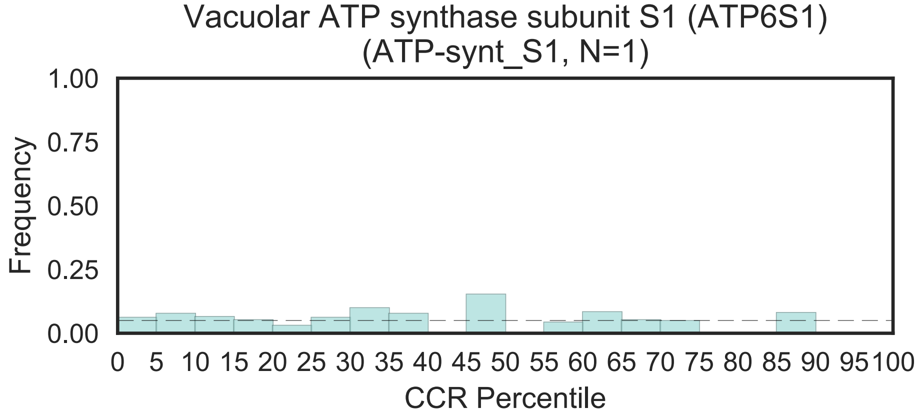

ATP synthase E chain
(ATP-synt_E, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

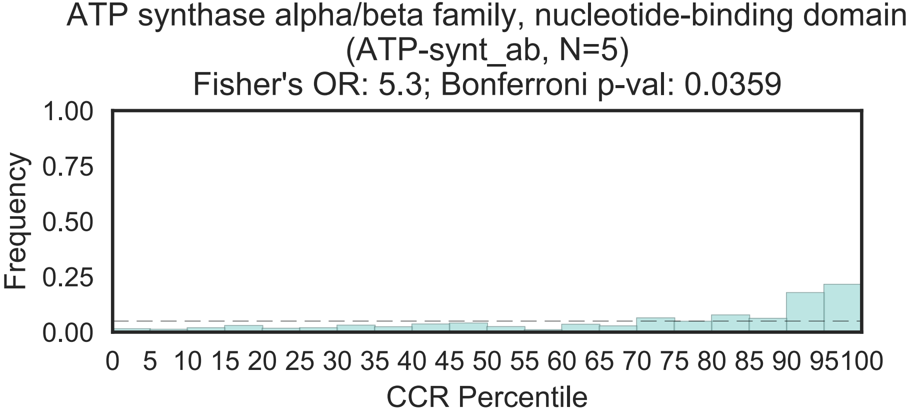

Mitochondrial ATP synthase epsilon chain
(ATP-synt_Eps, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

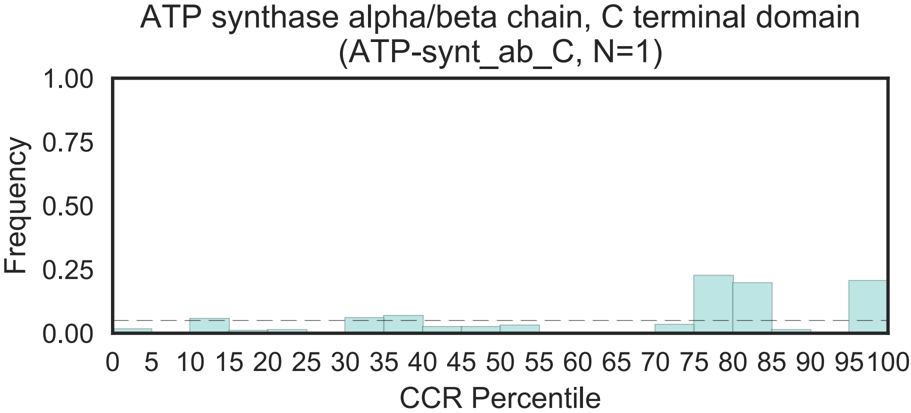

ATP synthase (F/14-kDa) subunit
(ATP-synt_F, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

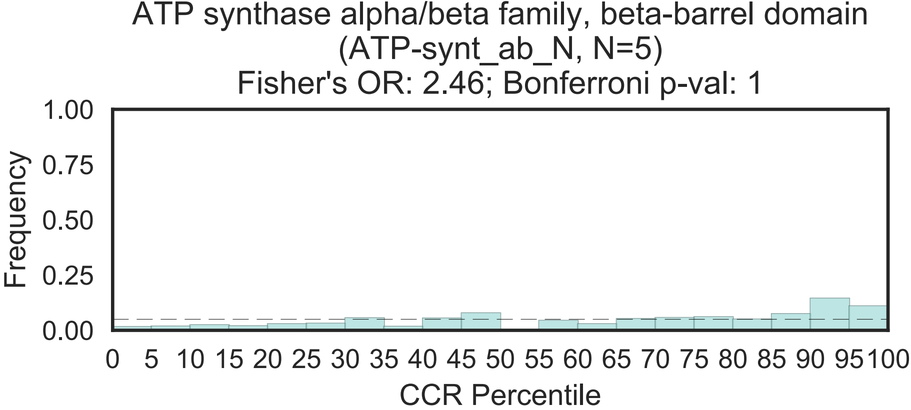

Mitochondrial ATP synthase coupling factor 6
(ATP-synt_F6, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Mitochondrial ATP synthase g subunit
(ATP-synt_G, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

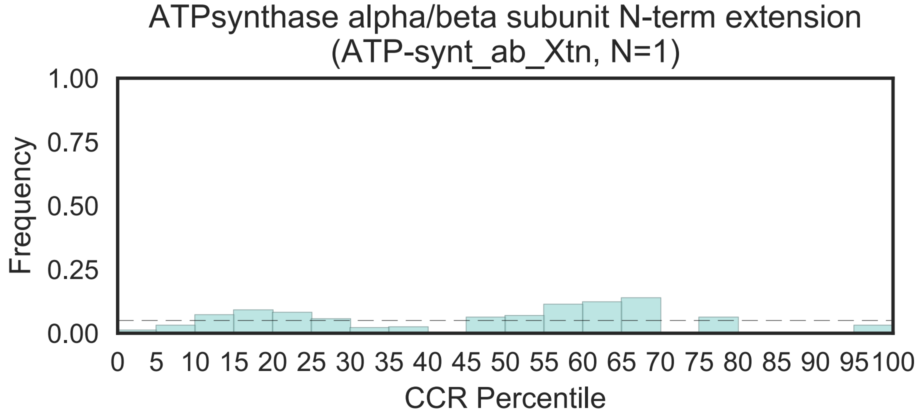

Vacuolar ATP synthase subunit S1 (ATP6S1)
(ATP-synt_S1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

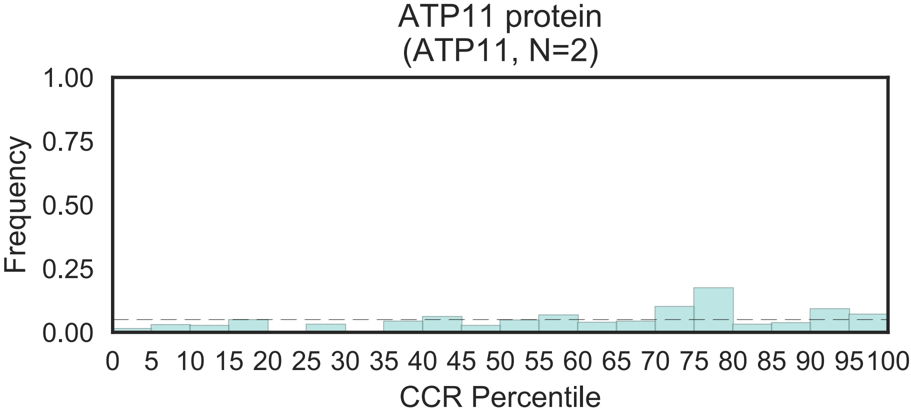

ATP synthase alpha/beta family, nucleotide-binding domain
(ATP-synt_ab, N=5)
Fisher's OR: 5.3; Bonferroni p-val: 0.0359
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

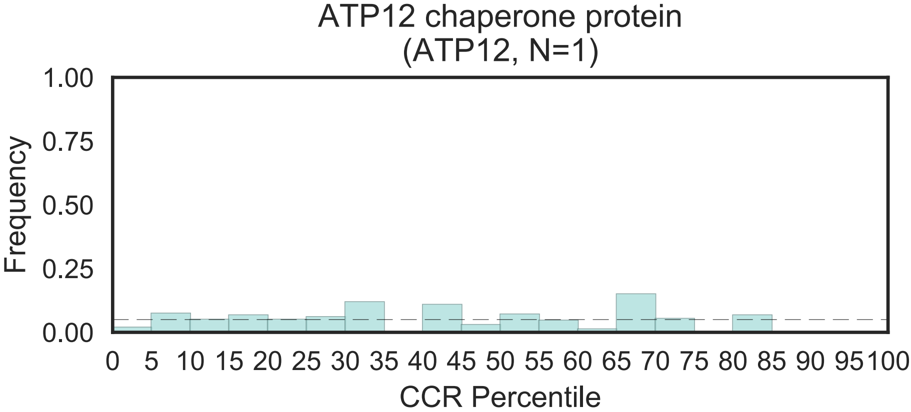

ATP synthase alpha/beta chain, C terminal domain
(ATP-synt_ab_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

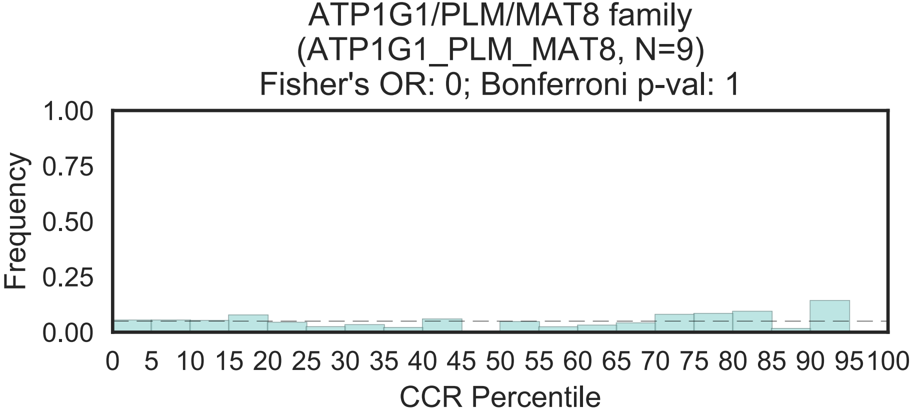


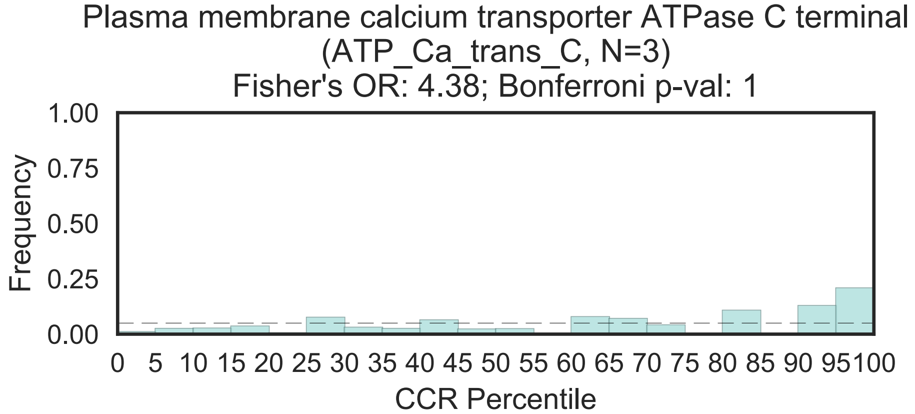
ATP synthase alpha/beta family, beta-barrel domain
(ATP-synt_ab_N, N=5)
Fisher's OR: 2.46; Bonferroni p-val: 1


ATPsynthase alpha/beta subunit N-term extension
(ATP-synt_ab_Xtn, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

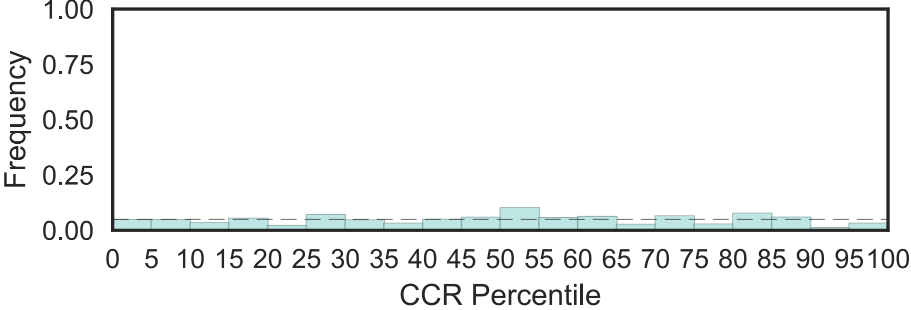

ATP11 protein
(ATP11, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

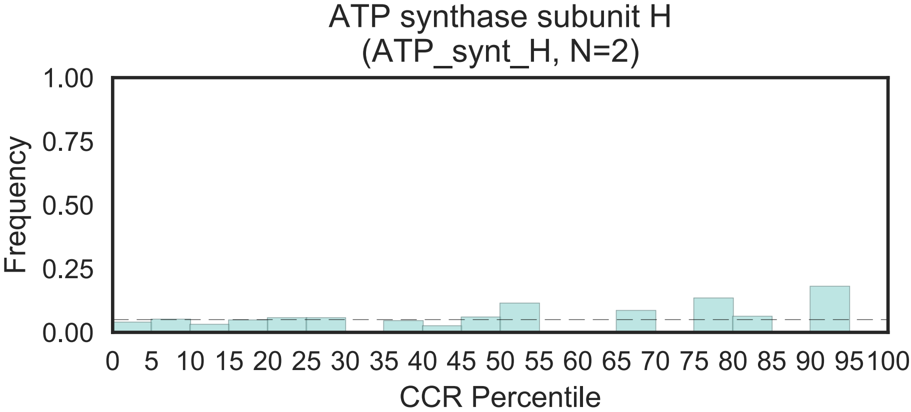

ATP12 chaperone protein
(ATP12, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

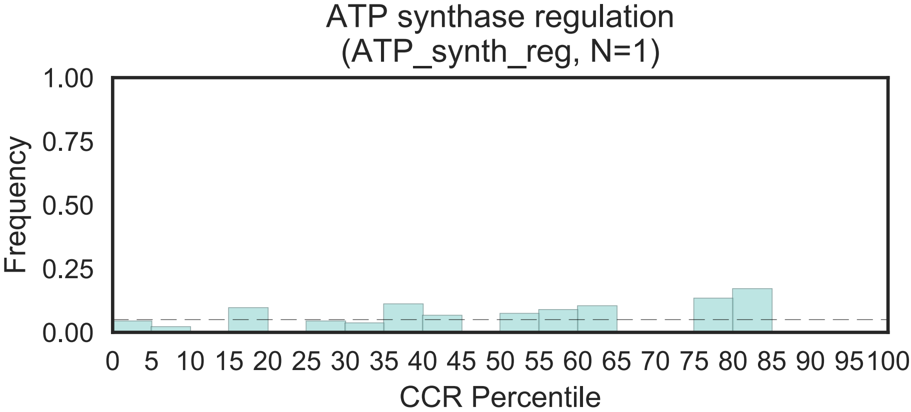

ATP1G1/PLM/MAT8 family
(ATP1G1_PLM_MAT8, N=9)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

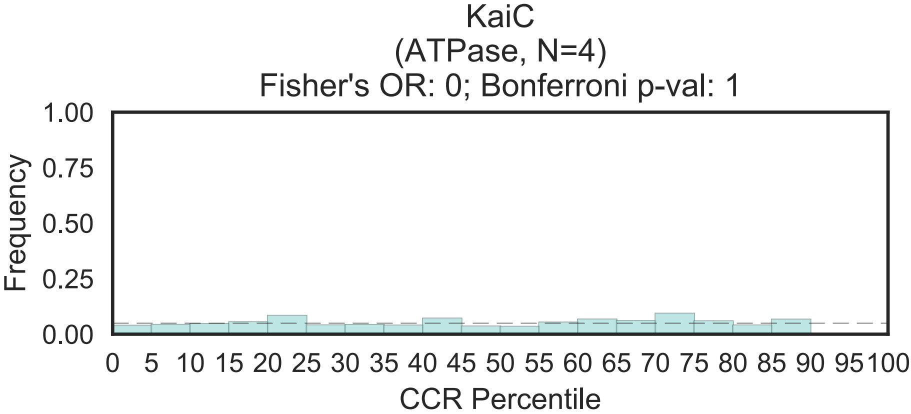

Plasma membrane calcium transporter ATPase C terminal
(ATP_Ca_trans_C, N=3)
Fisher's OR: 4.38; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

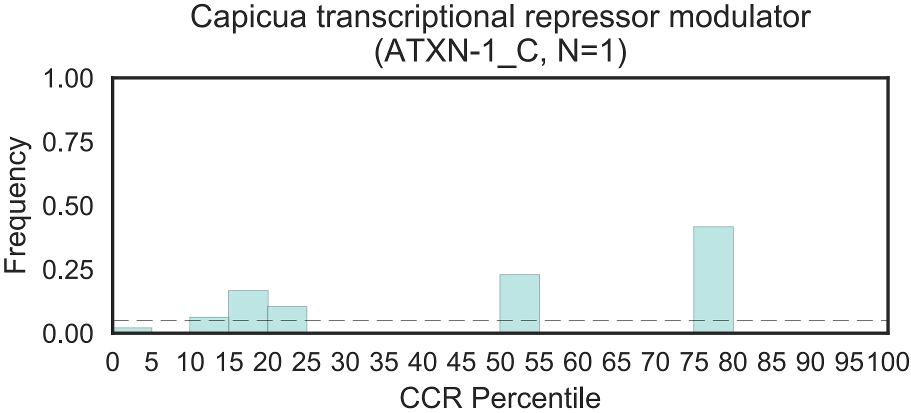
Conserved hypothetical ATP binding protein
(ATP_bind_1, N=4)
Fisher's OR: 0.353; Bonferroni p-val: 1

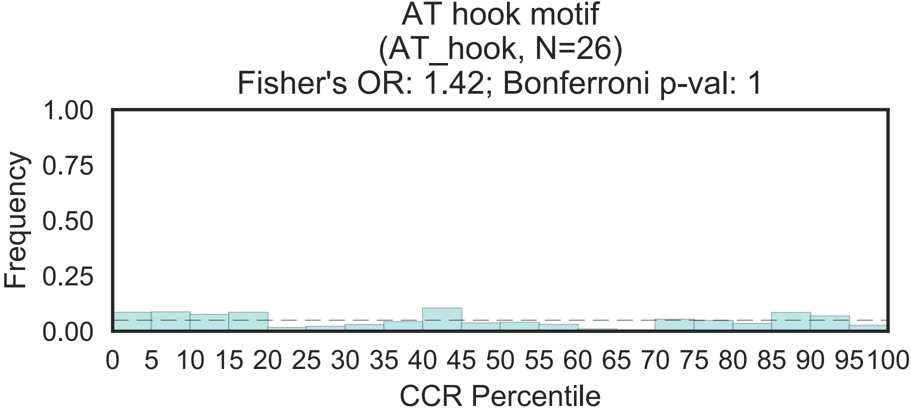


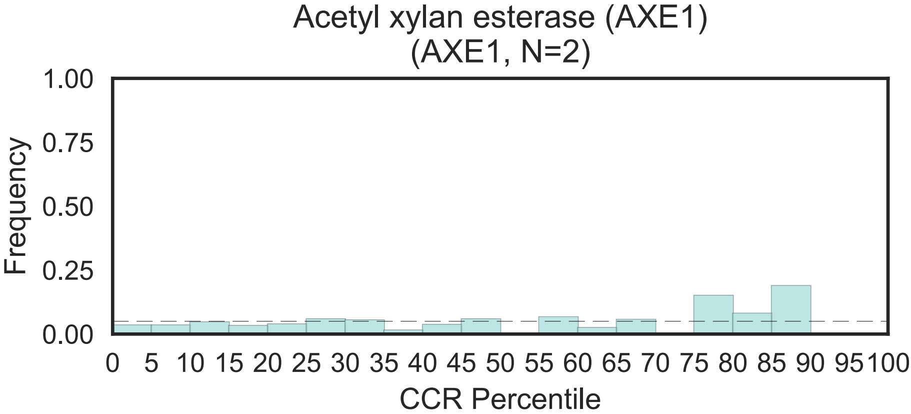

ATP synthase subunit H
(ATP_synt_H, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


ATP synthase regulation
(ATP_synth_reg, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

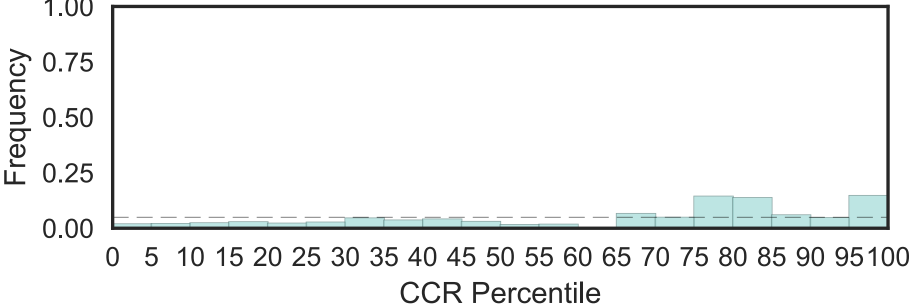

KaiC
(ATPase, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

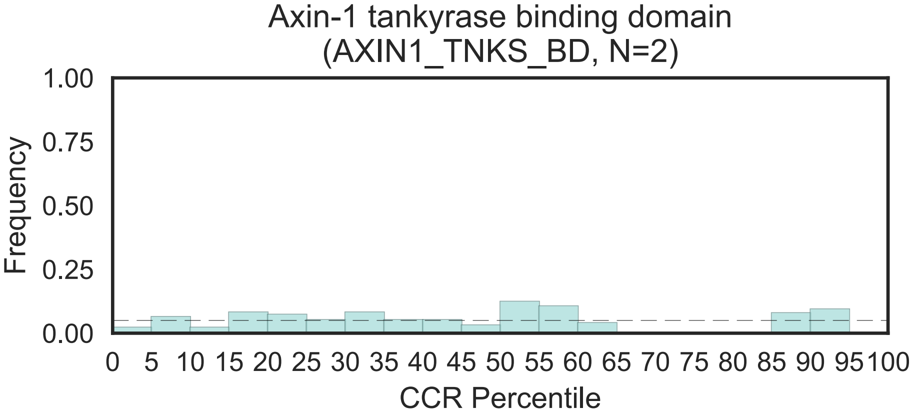

Capicua transcriptional repressor modulator
(ATXN-1_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

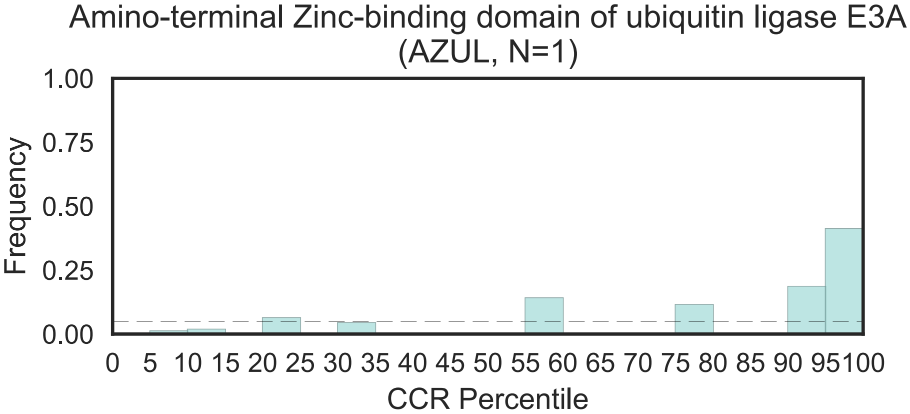

AT hook motif
(AT_hook, N=26)
Fisher's OR: 1.42; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

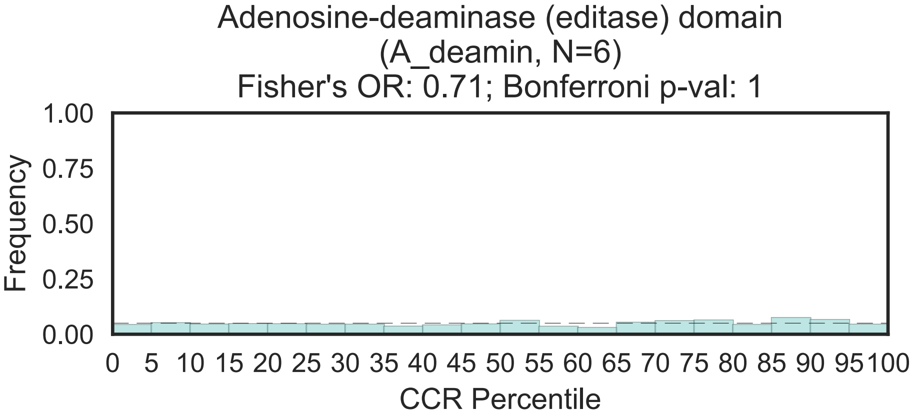

Acetyl xylan esterase (AXE1)
(AXE1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Ataxin-1 and HBP1 module (AXH) (AXH, N=3) Fisher's OR: 3.33; Bonferroni p-val: 1

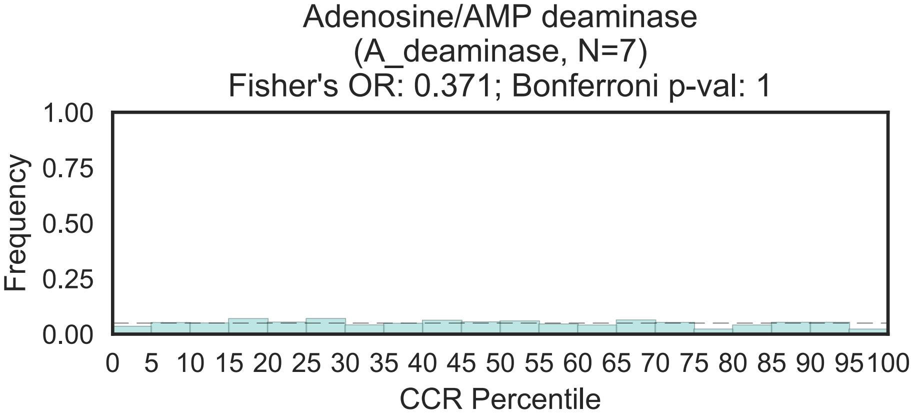


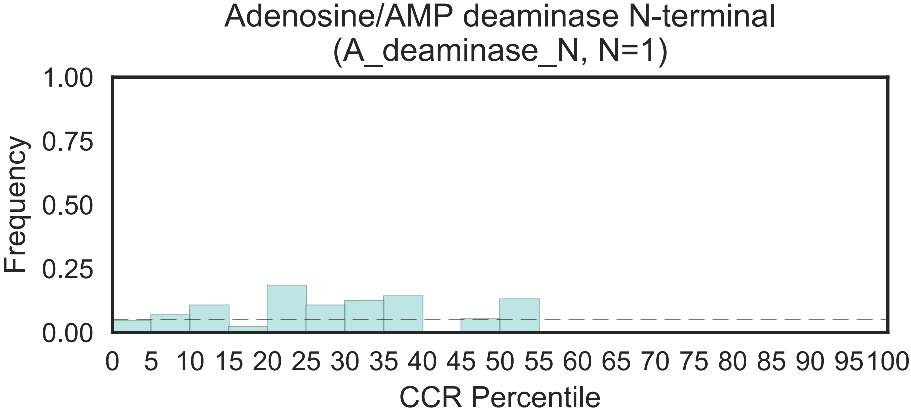

Axin-1 tankyrase binding domain
(AXIN1_TNKS_BD, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Amino-terminal Zinc-binding domain of ubiquitin ligase E3A
(AZUL, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

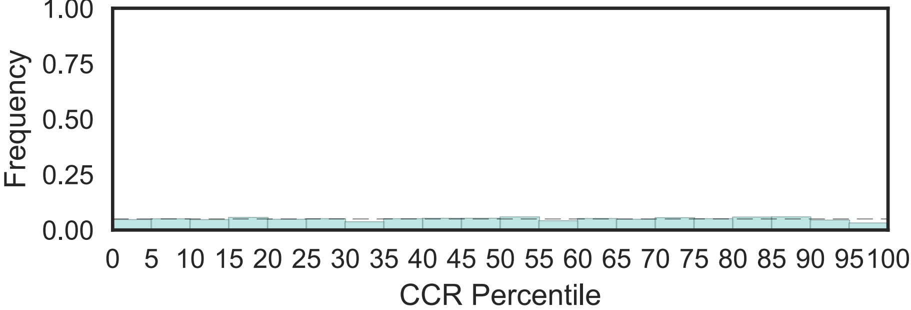


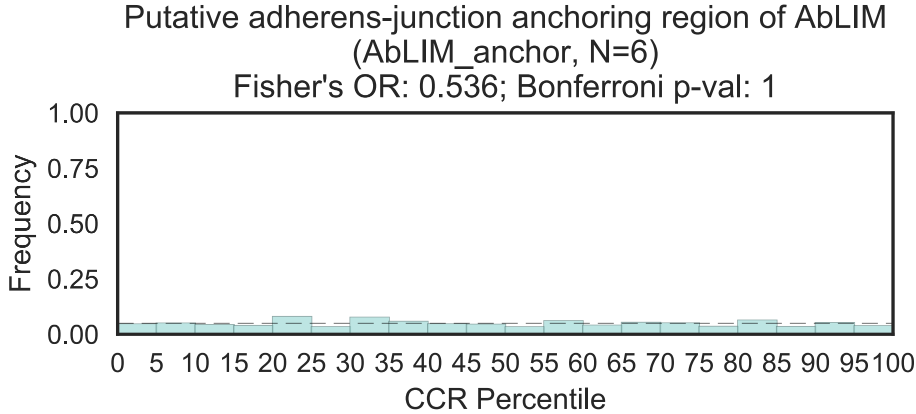
Adenosine-deaminase (editase) domain
(A_deamin, N=6)
Fisher's OR: 0.71; Bonferroni p-val: 1

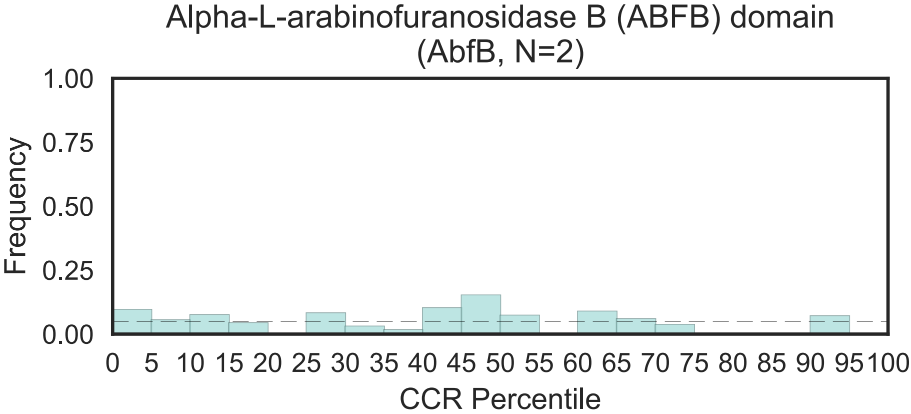

Adenosine/AMP deaminase
(A_deaminase, N=7)
Fisher's OR: 0.371; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

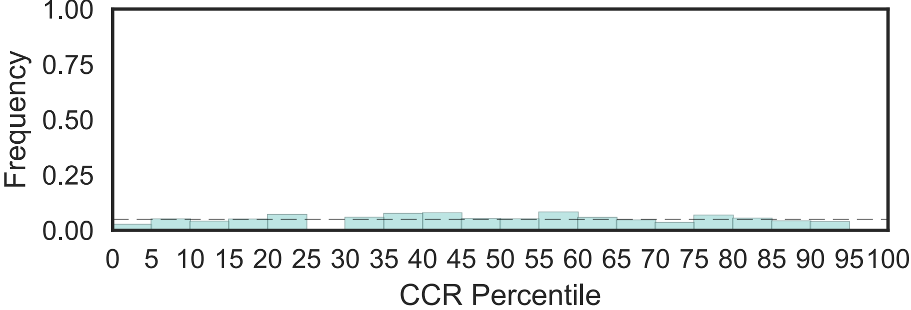

Adenosine/AMP deaminase N-terminal
(A_deaminase_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Transmembrane amino acid transporter protein (Aa_trans, N=18) Fisher's OR: 0.464; Bonferroni p-val: 1

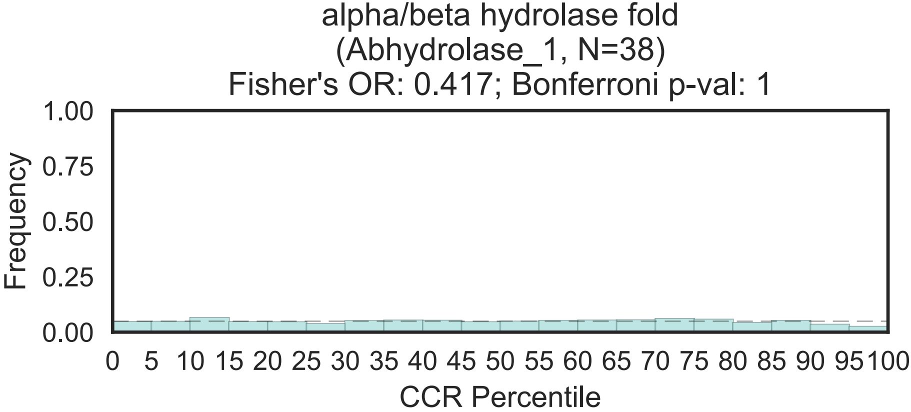



Putative adherens-junction anchoring region of AbLIM
(AbLIM_anchor, N=6)
Fisher's OR: 0.536; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

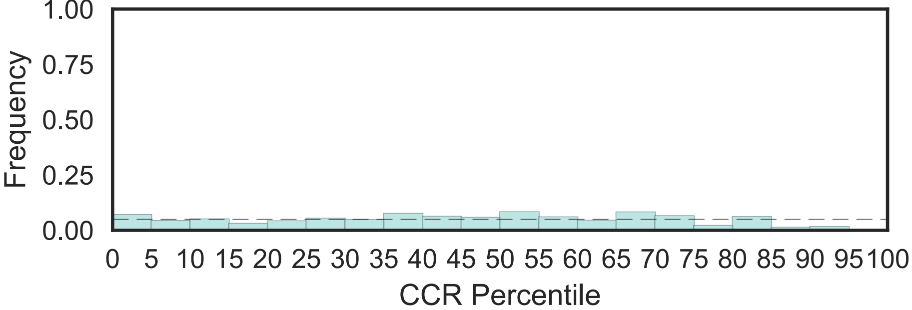

Alpha-L-arabinofuranosidase B (ABFB) domain
(AbfB, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

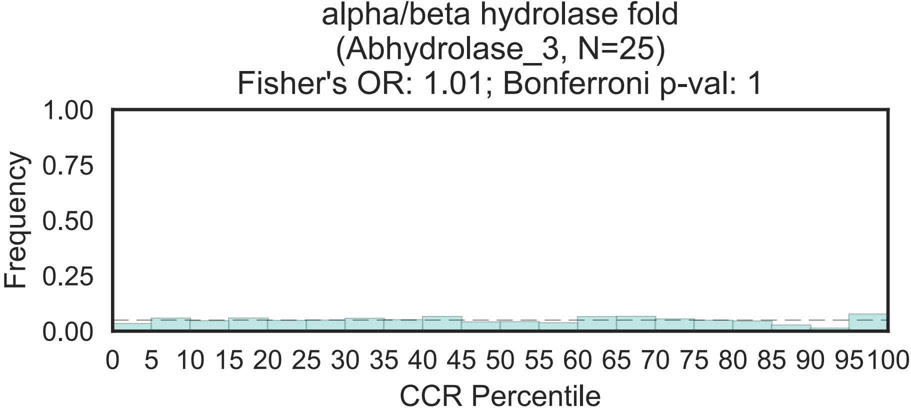


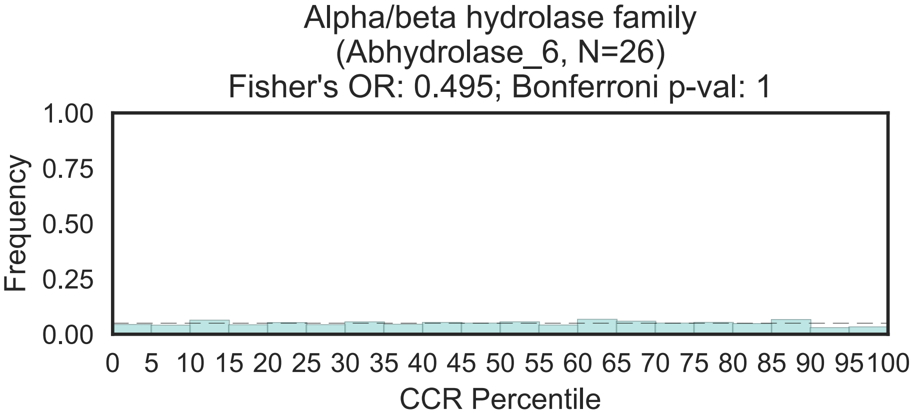
Partial alpha/beta-hydrolase lipase region
(Abhydro_lipase, N=10)
Fisher's OR: 0.118; Bonferroni p-val: 1

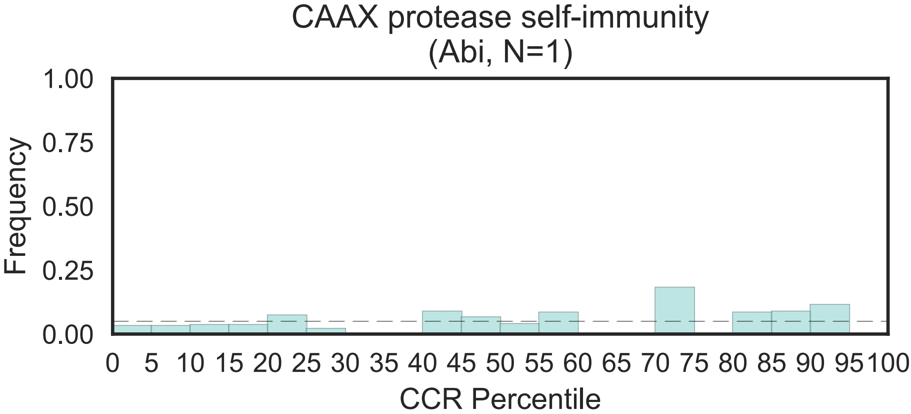


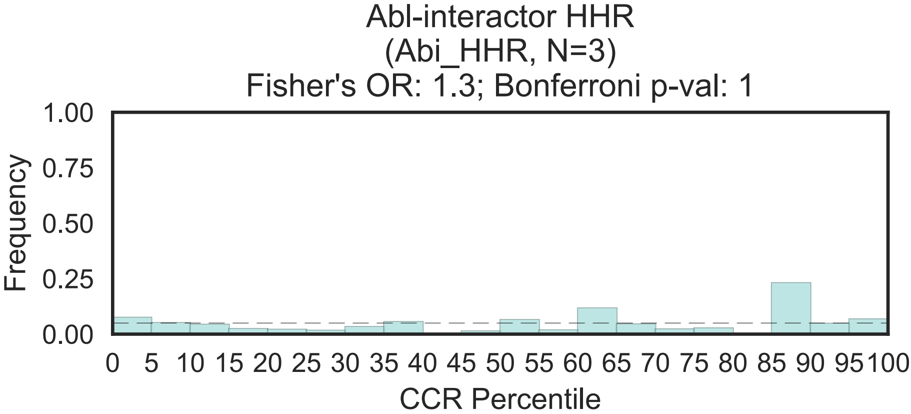
alpha/beta hydrolase fold
(Abhydrolase_1, N=38)
Fisher's OR: 0.417; Bonferroni p-val: 1

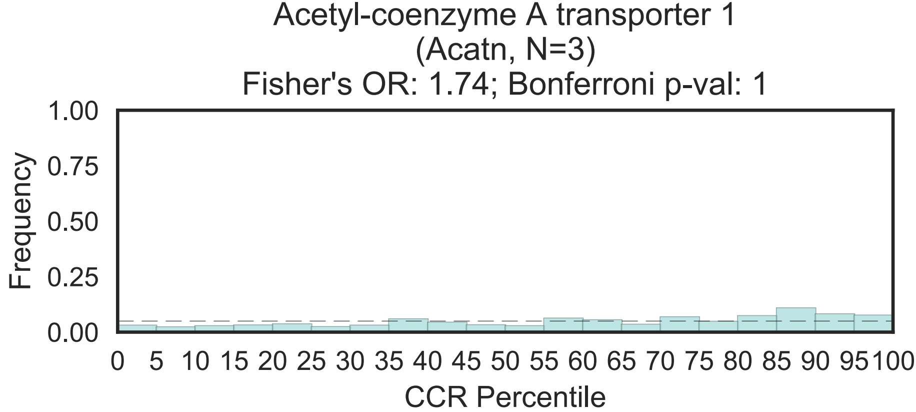

Phospholipase/Carboxylesterase
(Abhydrolase_2, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

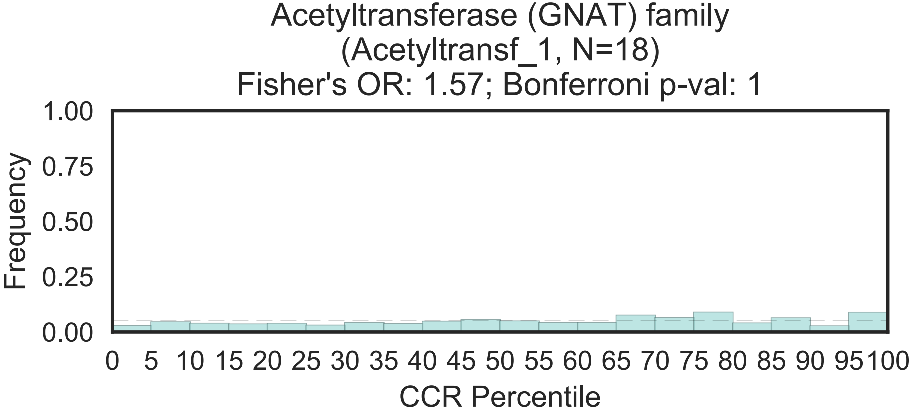

alpha/beta hydrolase fold
(Abhydrolase_3, N=25)
Fisher's OR: 1.01; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

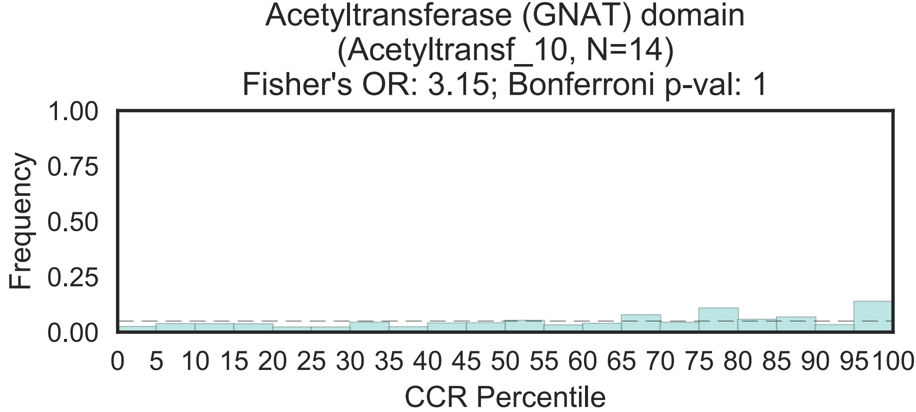

Alpha/beta hydrolase family
(Abhydrolase_6, N=26)
Fisher's OR: 0.495; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

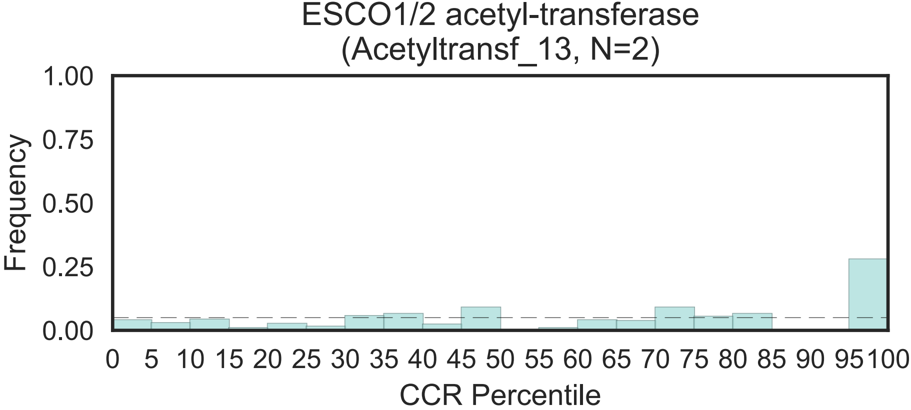

CAAX protease self-immunity
(Abi, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

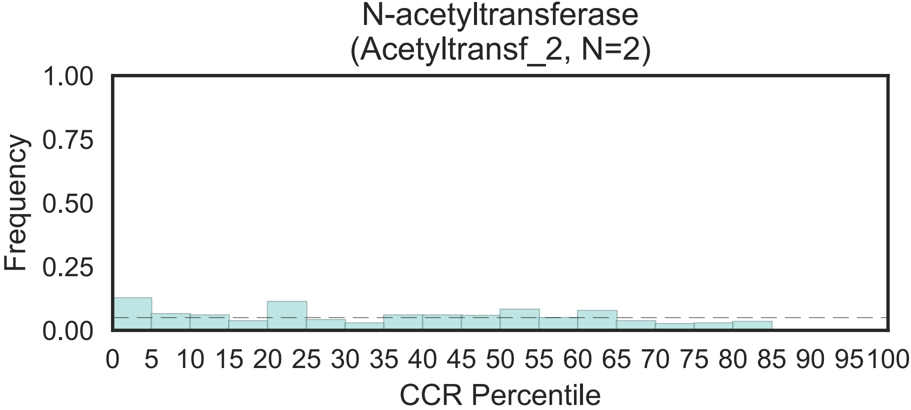

Abl-interactor HHR
(Abi_HHR, N=3)
Fisher's OR: 1.3; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

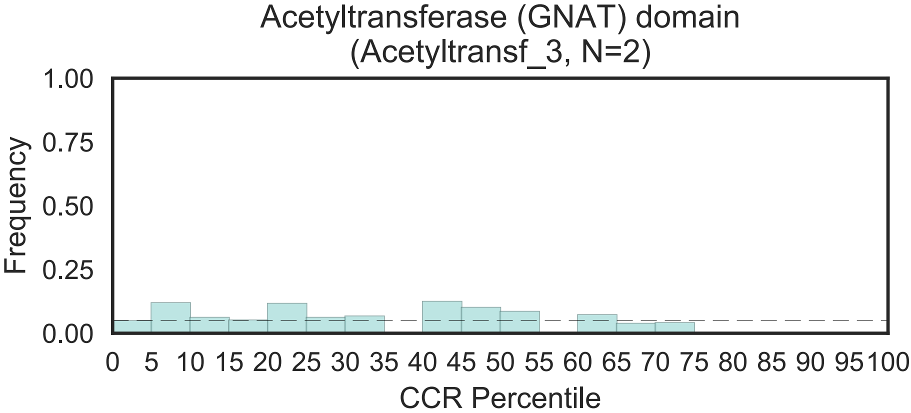

Acetyl-coenzyme A transporter 1
(Acatn, N=3)
Fisher's OR: 1.74; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

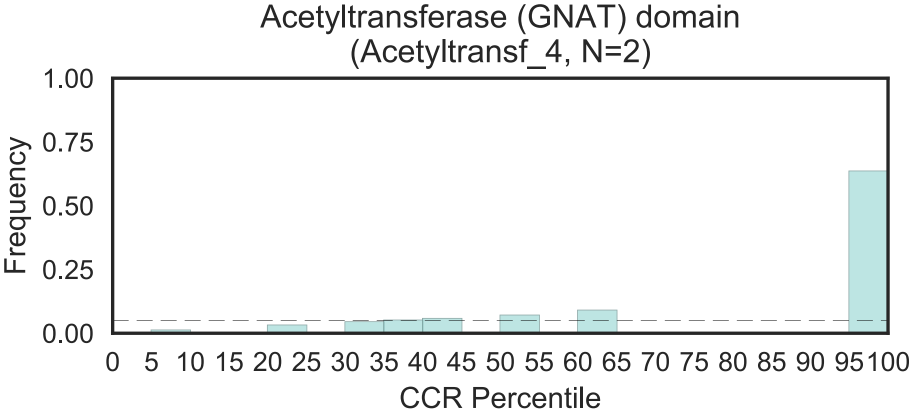

Acetyltransferase (GNAT) family
(Acetyltransf_1, N=18)
Fisher's OR: 1.57; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

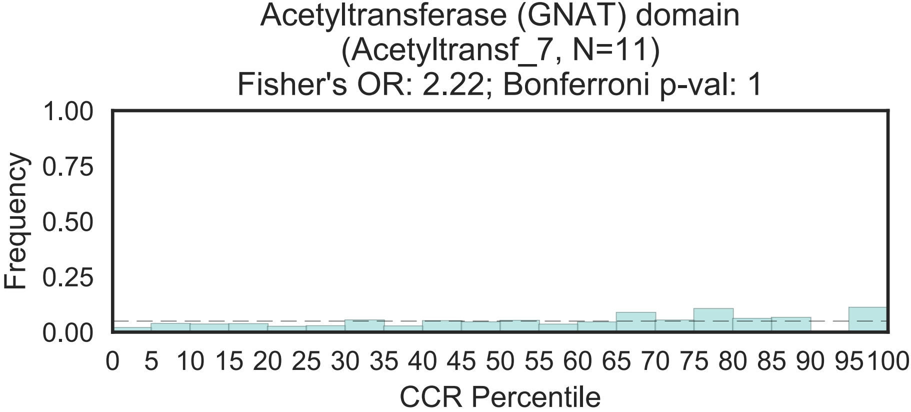

Acetyltransferase (GNAT) domain
(Acetyltransf_10, N=14)
Fisher's OR: 3.15; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


ESCO1/2 acetyl-transferase
(Acetyltransf_13, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

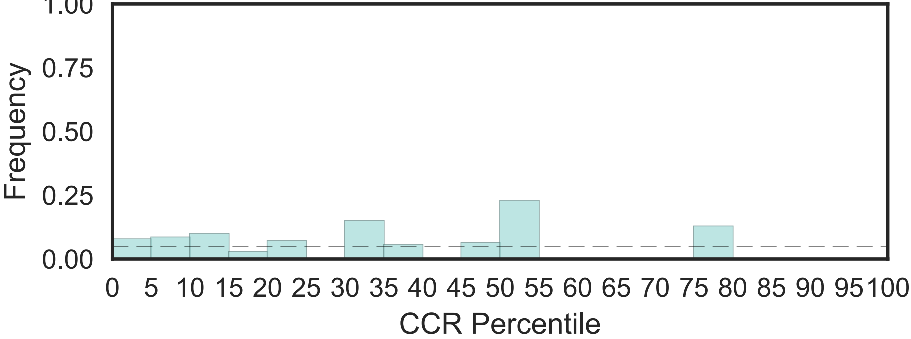

N-acetyltransferase
(Acetyltransf_2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

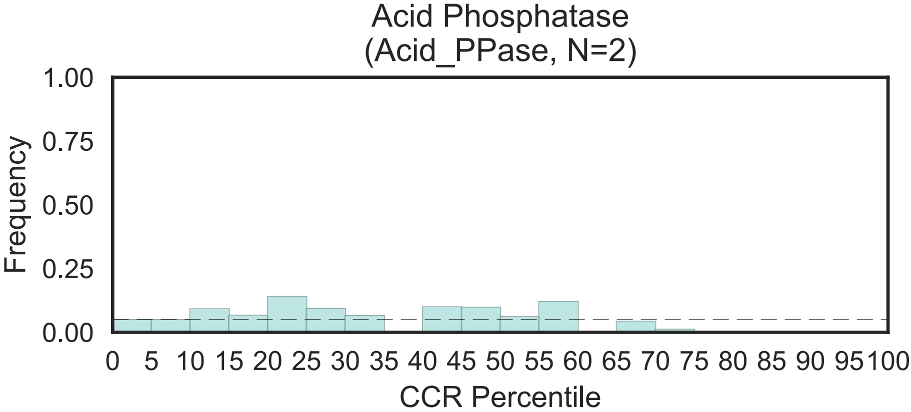

Acetyltransferase (GNAT) domain
(Acetyltransf_3, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

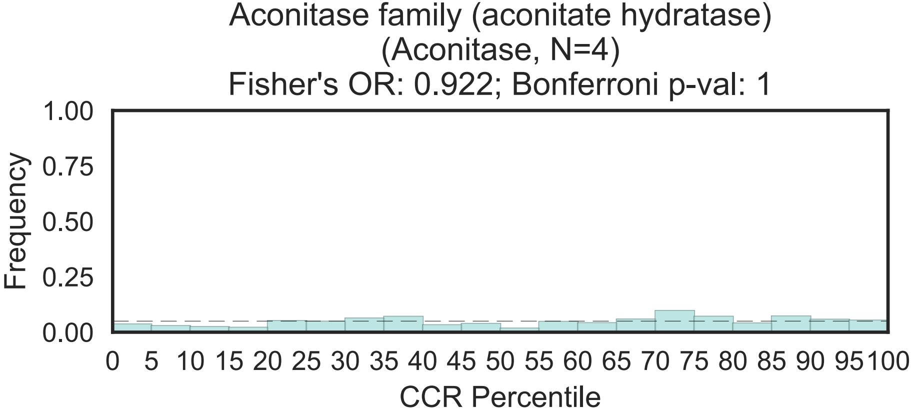

Acetyltransferase (GNAT) domain
(Acetyltransf_4, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

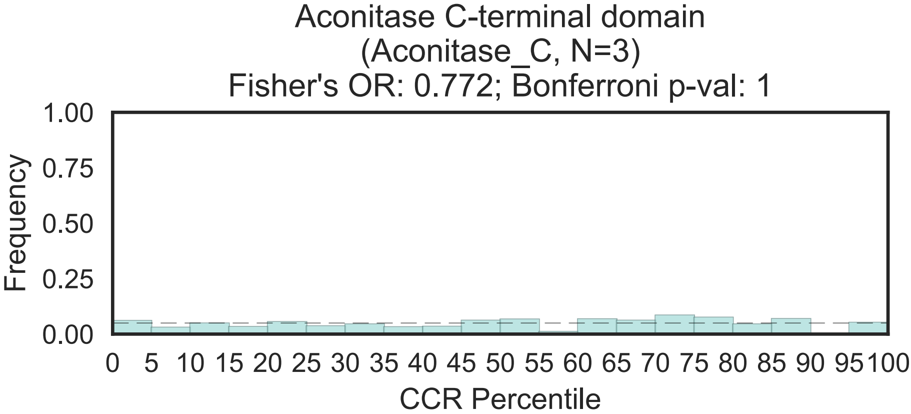

Acetyltransferase (GNAT) domain
(Acetyltransf_7, N=11)
Fisher's OR: 2.22; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

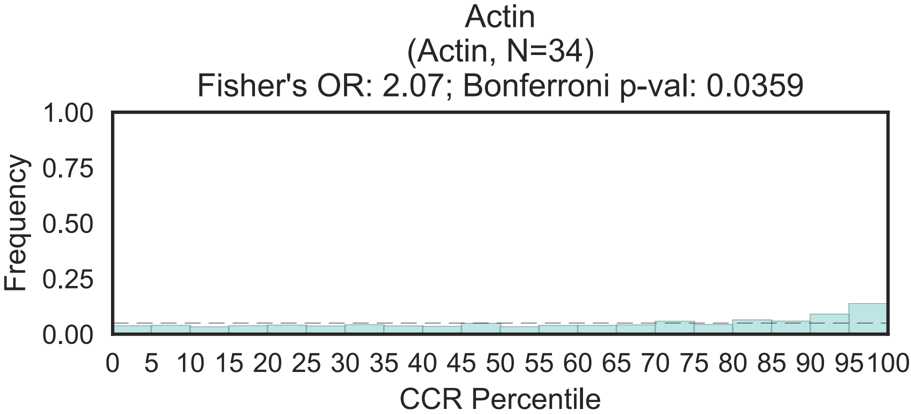
GCN5-related N-acetyl-transferase (Acetyltransf_CG, N=2)

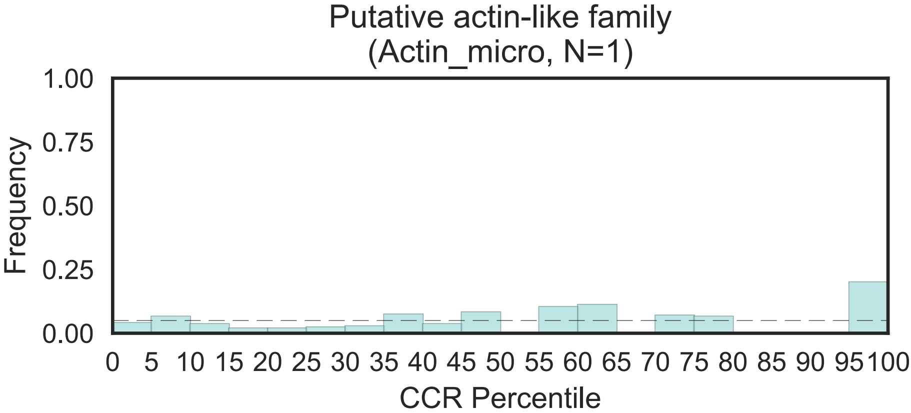


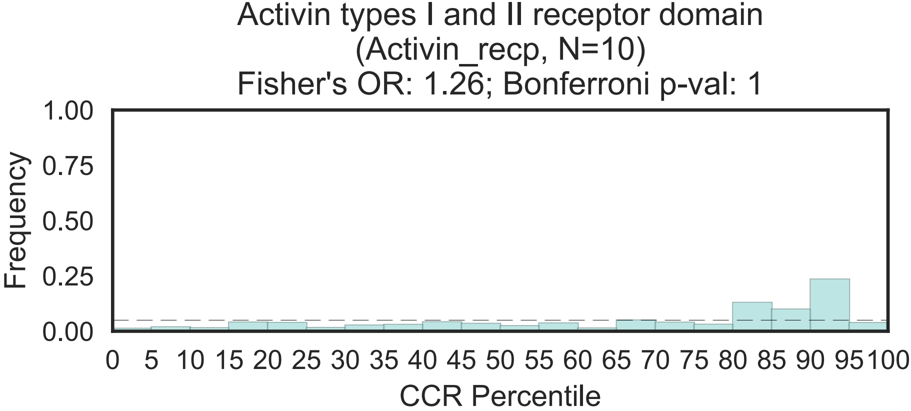

Acid Phosphatase
(Acid_PPase, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

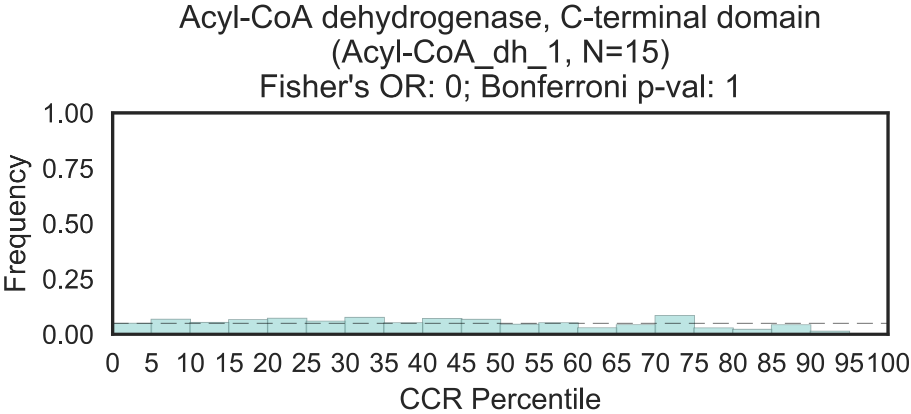

Aconitase family (aconitate hydratase)
(Aconitase, N=4)
Fisher's OR: 0.922; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Aconitase C-terminal domain
(Aconitase_C, N=3)
Fisher's OR: 0.772; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

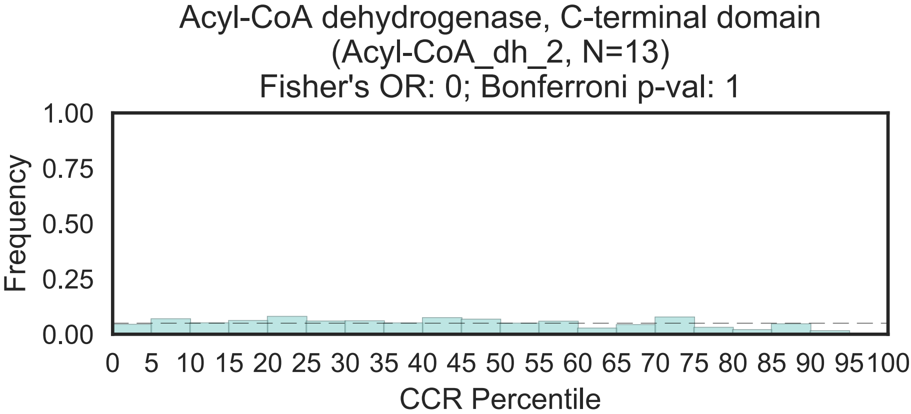

Actin
(Actin, N=34)
Fisher's OR: 2.07; Bonferroni p-val: 0.0359
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

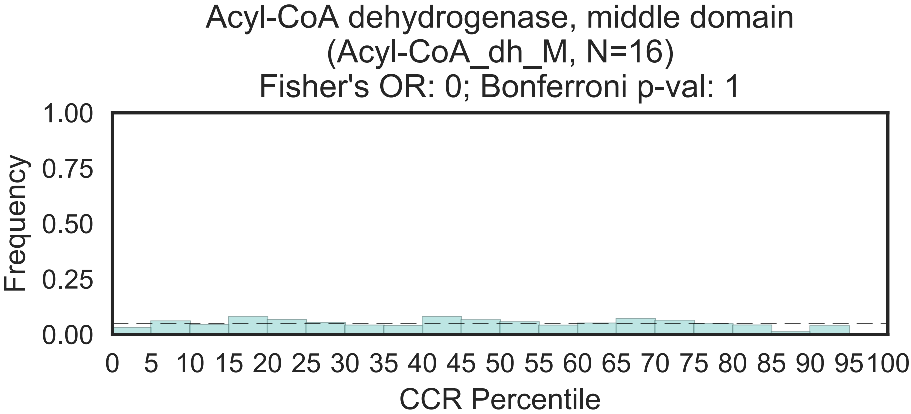

Putative actin-like family
(Actin_micro, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

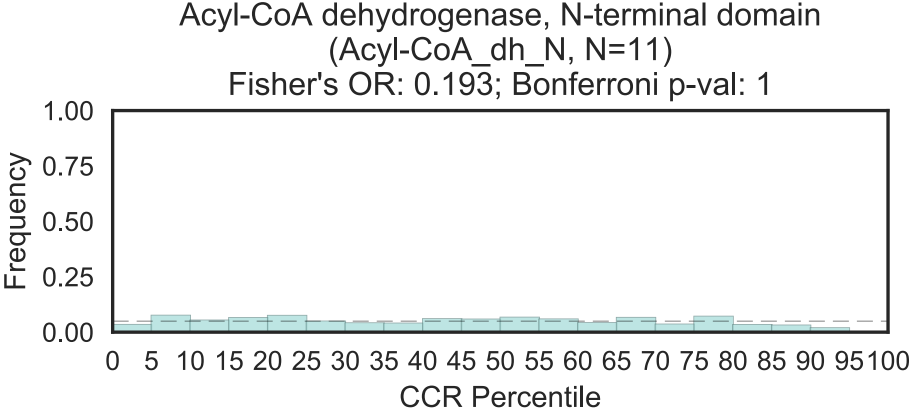

Activin types I and II receptor domain
(Activin_recp, N=10)
Fisher's OR: 1.26; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

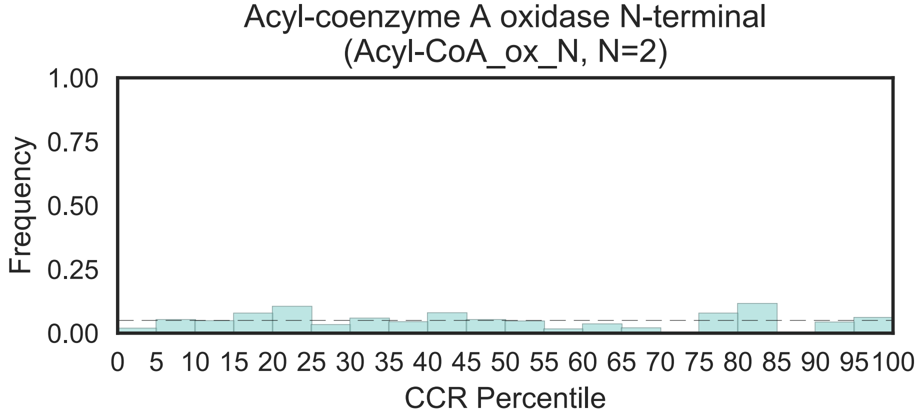


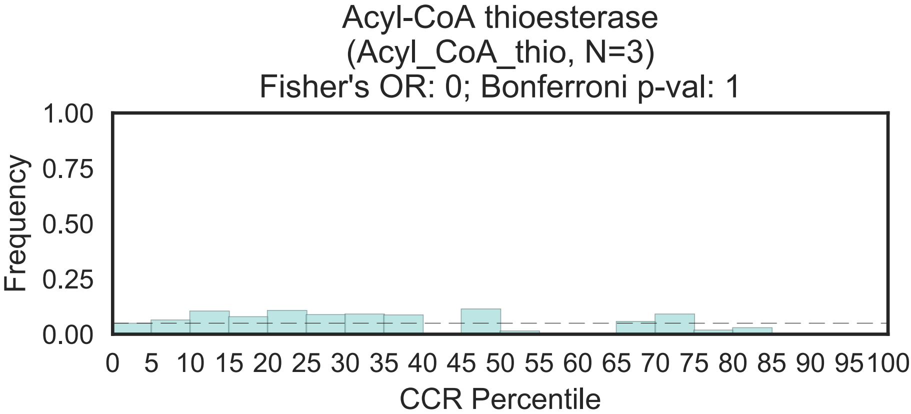
Acyl-CoA dehydrogenase, C-terminal domain
(Acyl-CoA_dh_1, N=15)
Fisher's OR: 0; Bonferroni p-val: 1

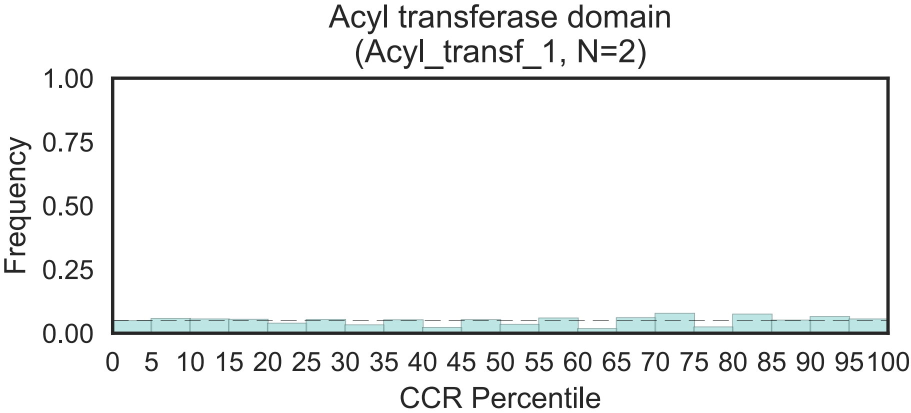

Acyl-CoA dehydrogenase, C-terminal domain
(Acyl-CoA_dh_2, N=13)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

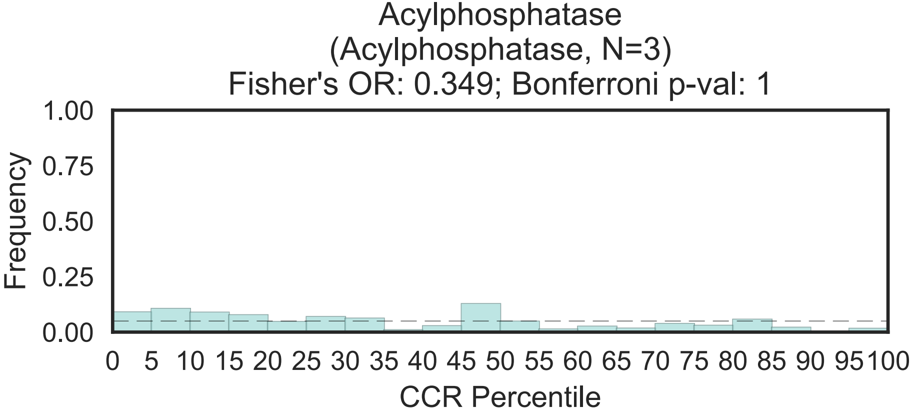

Acyl-CoA dehydrogenase, middle domain
(Acyl-CoA_dh_M, N=16)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

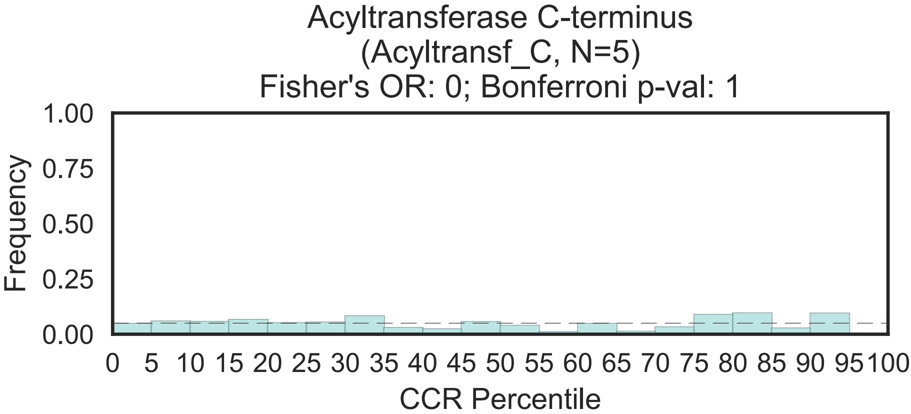

Acyl-CoA dehydrogenase, N-terminal domain
(Acyl-CoA_dh_N, N=11)
Fisher's OR: 0.193; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Acyl-coenzyme A oxidase N-terminal
(Acyl-CoA_ox_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

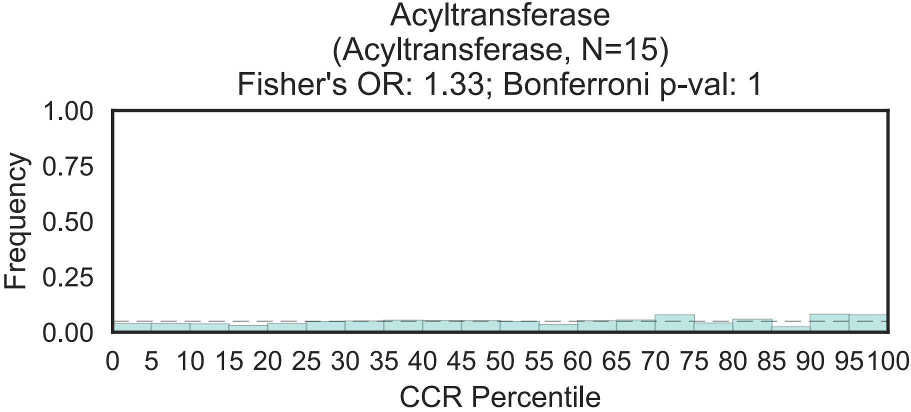

Acyl-CoA thioesterase
(Acyl_CoA_thio, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Acyl transferase domain
(Acyl_transf_1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

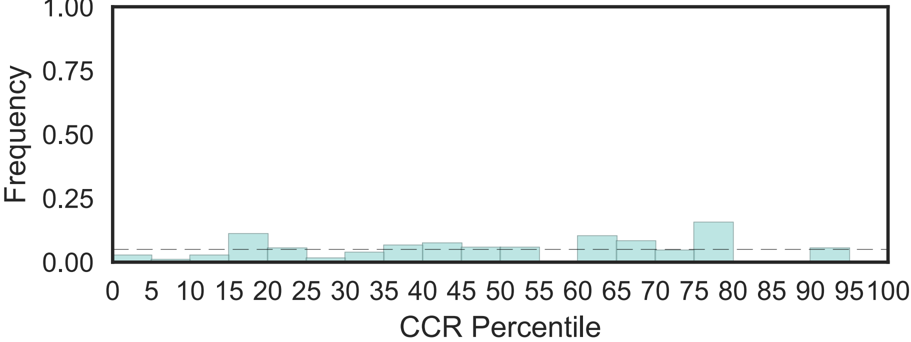

Acylphosphatase
(Acylphosphatase, N=3)
Fisher's OR: 0.349; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

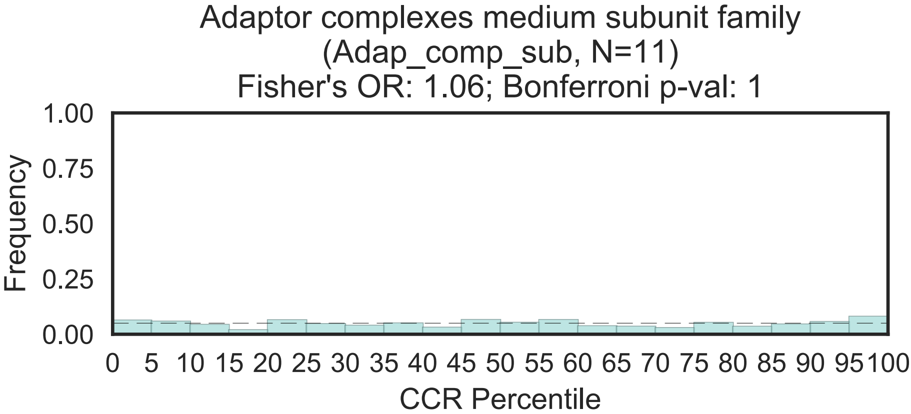


Acyltransferase C-terminus
(Acyltransf_C, N=5)
Fisher's OR: 0; Bonferroni p-val: 1

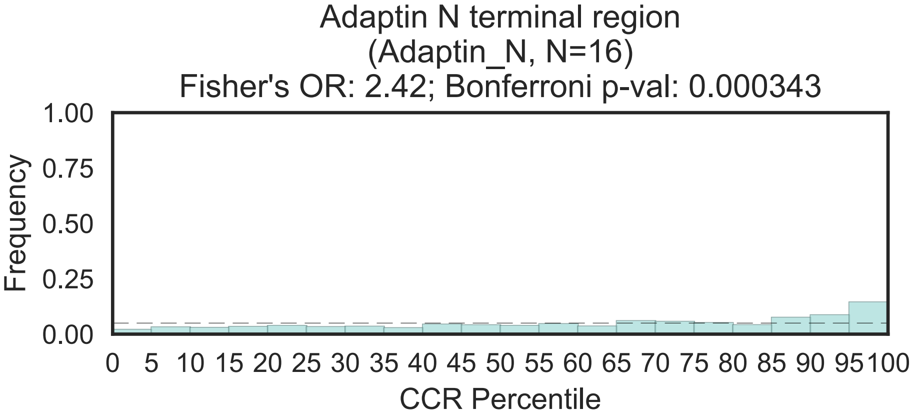

Acyltransferase
(Acyltransferase, N=15)
Fisher's OR: 1.33; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

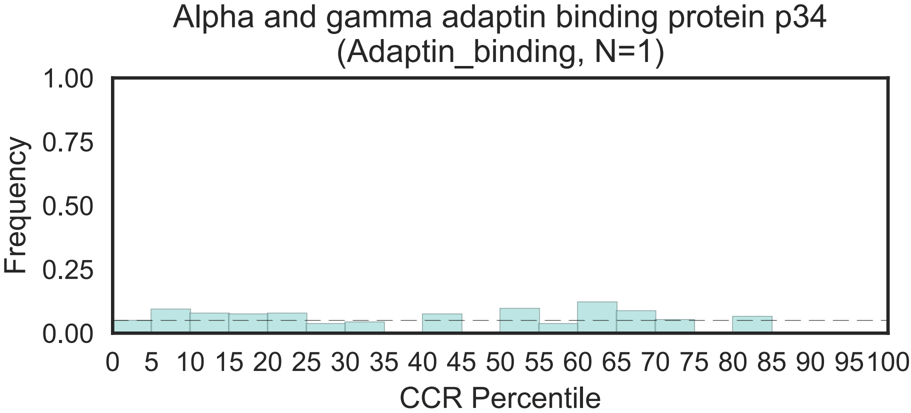
Histone acetyltransferases subunit 3
(Ada3, N=2)

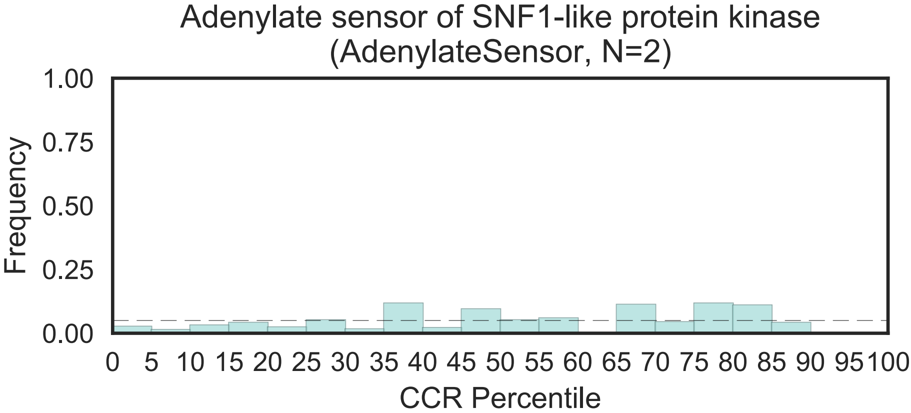


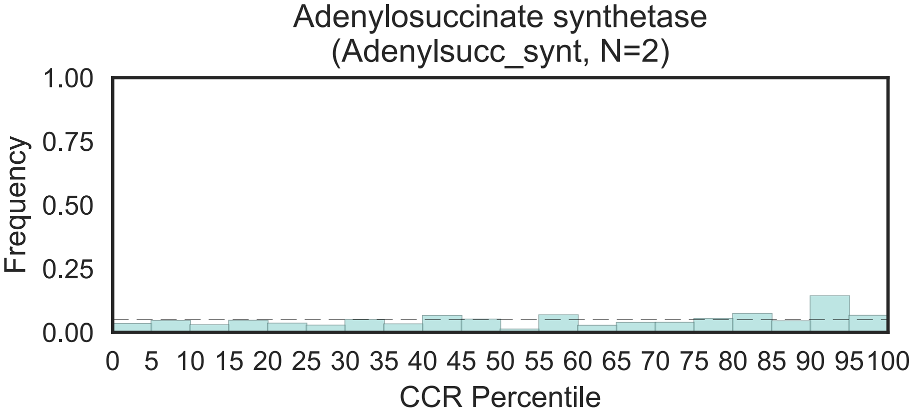


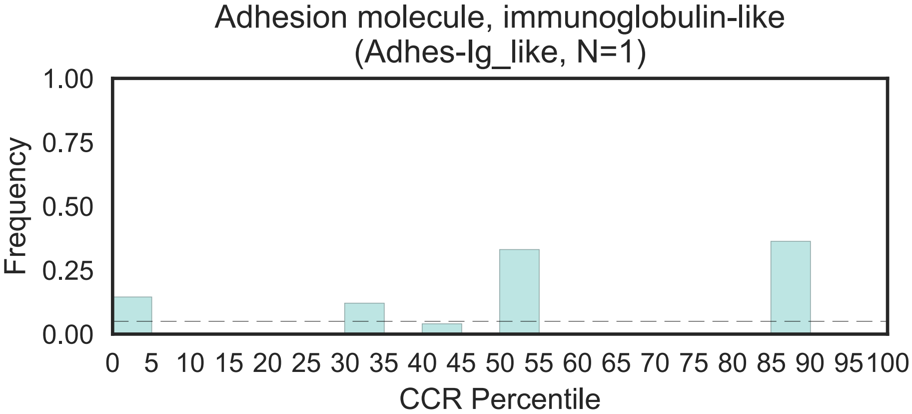
Adaptor complexes medium subunit family
(Adap_comp_sub, N=11)
Fisher's OR: 1.06; Bonferroni p-val: 1


Adaptin N terminal region
(Adaptin_N, N=16)
Fisher's OR: 2.42; Bonferroni p-val: 0.000343
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

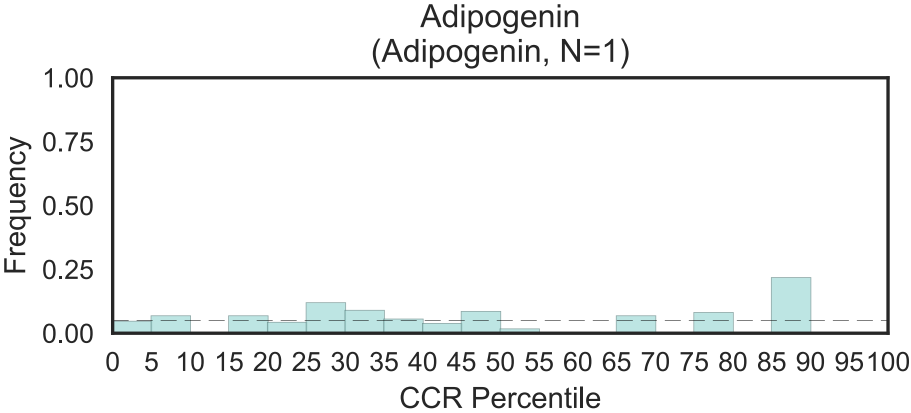

Alpha and gamma adaptin binding protein p34
(Adaptin_binding, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Adenylate sensor of SNF1-like protein kinase
(AdenylateSensor, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

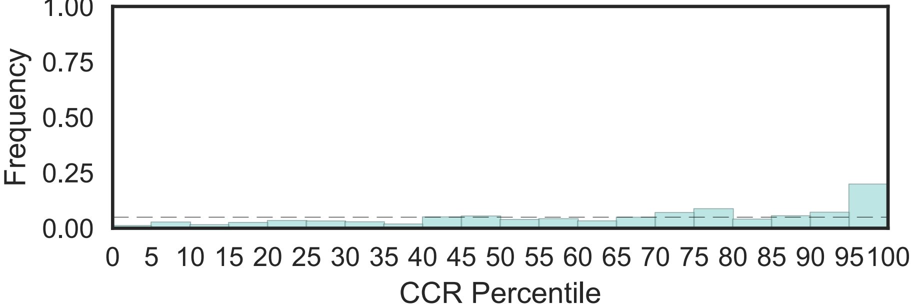

Adenylosuccinate synthetase
(Adenylsucc_synt, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

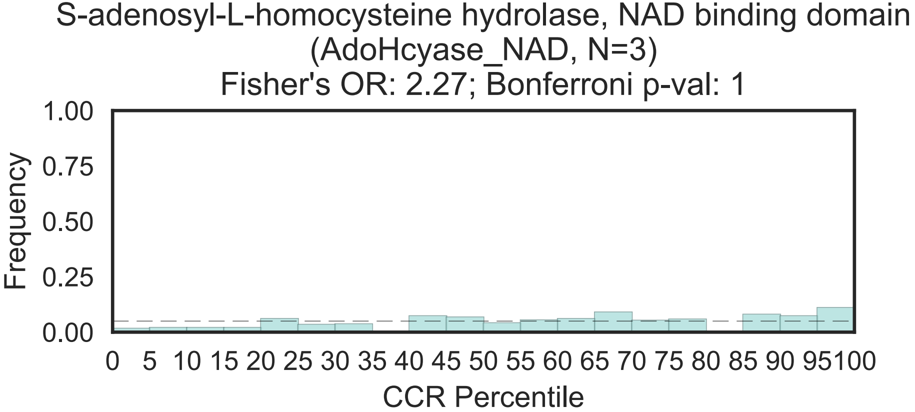


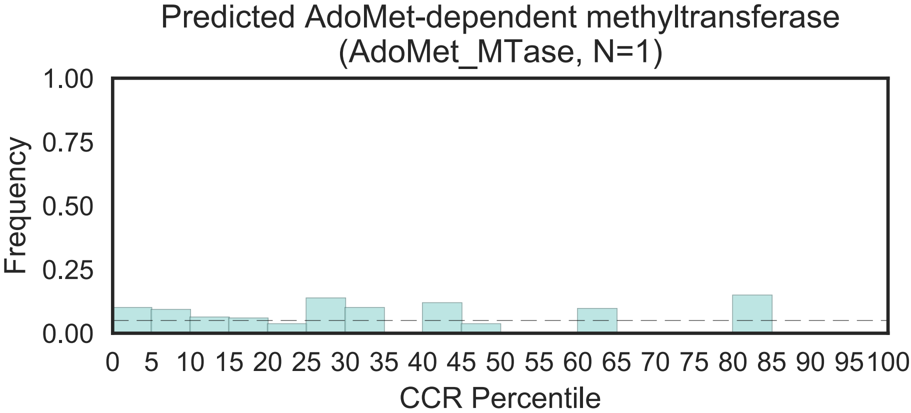
Adhesion molecule, immunoglobulin-like
(Adhes-Ig_like, N=1)

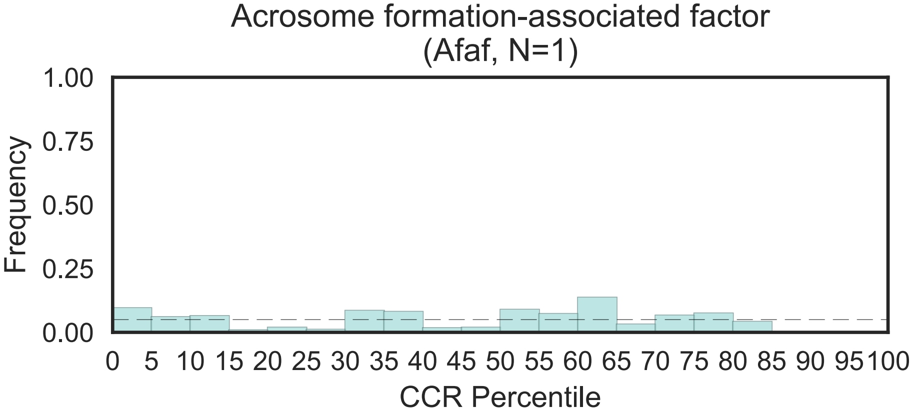

Adipogenin
(Adipogenin, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

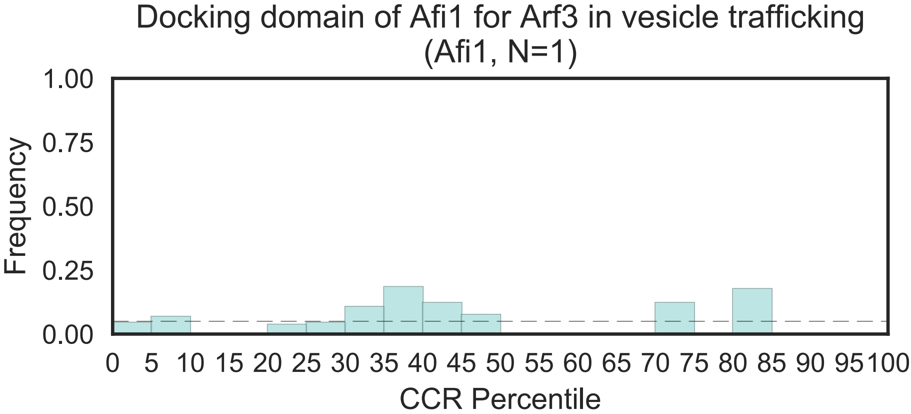
S-adenosyl-L-homocysteine hydrolase (AdoHcyase, N=4) Fisher's OR: 4.52; Bonferroni p-val: 0.0759

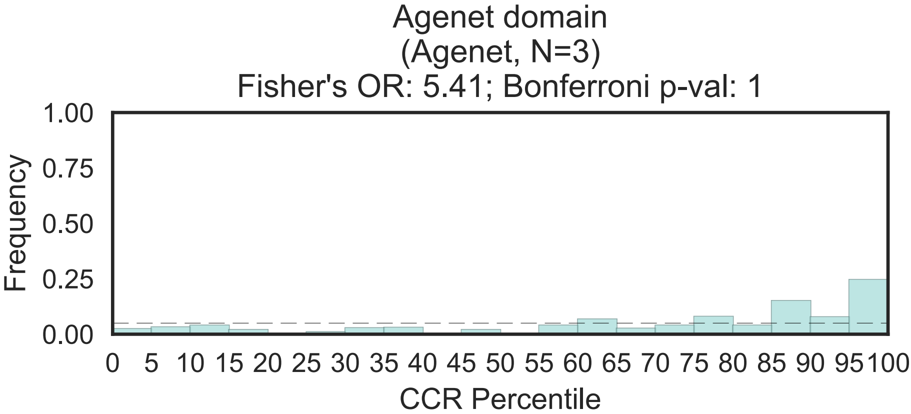


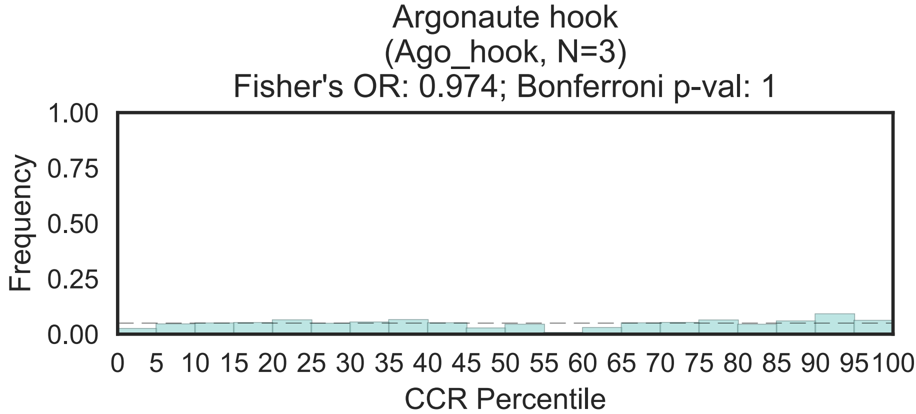

S-adenosyl-L-homocysteine hydrolase, NAD binding domain
(AdoHcyase_NAD, N=3)
Fisher's OR: 2.27; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

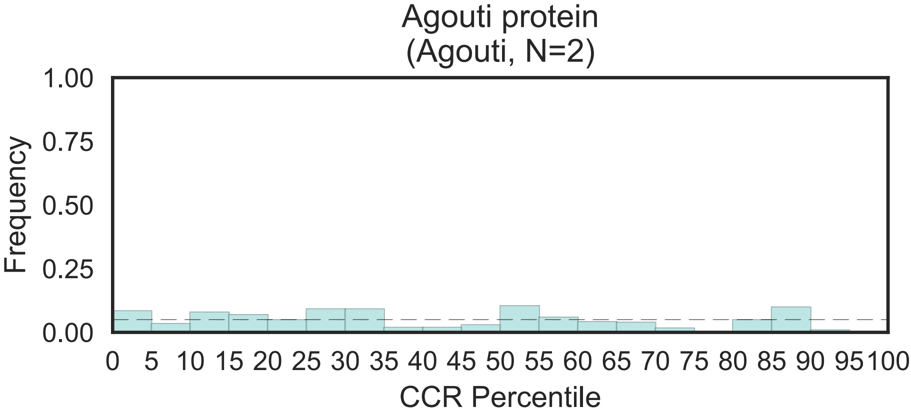

Predicted AdoMet-dependent methyltransferase
(AdoMet_MTase, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

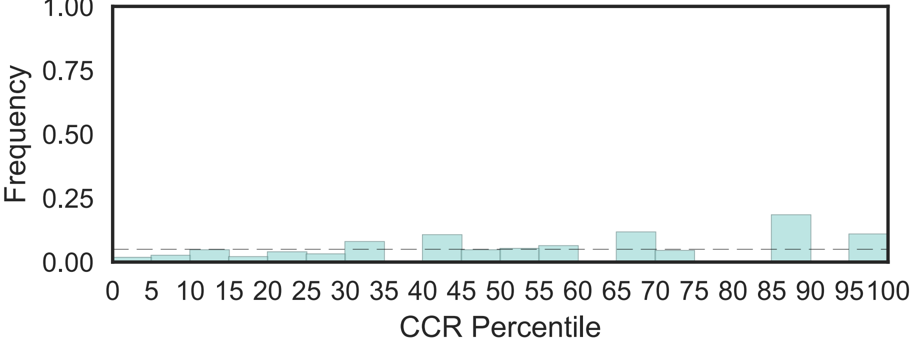

Acrosome formation-associated factor
(Afaf, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Docking domain of Afi1 for Arf3 in vesicle trafficking
(Afi1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

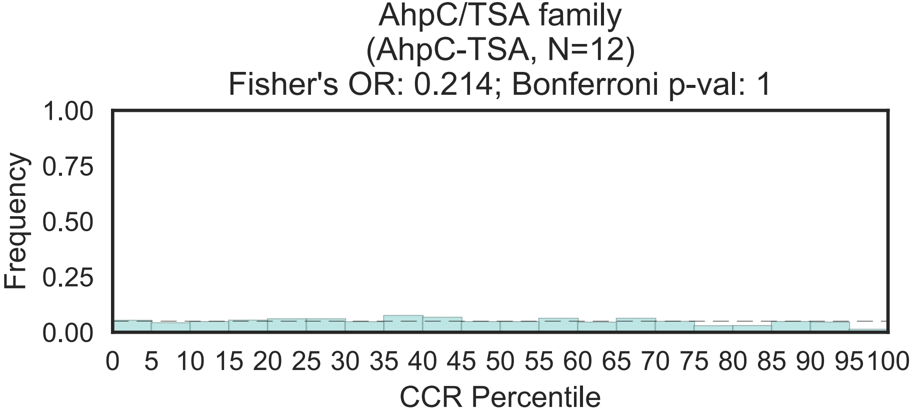

Agenet domain
(Agenet, N=3)
Fisher's OR: 5.41; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

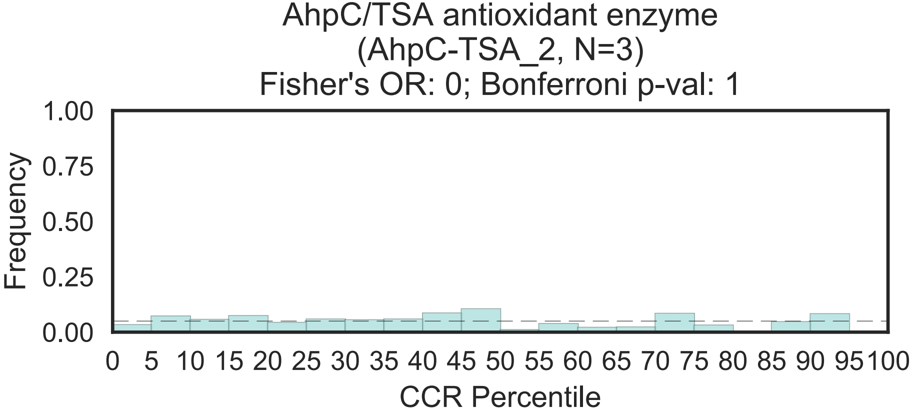

Argonaute hook
(Ago_hook, N=3)
Fisher's OR: 0.974; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Agouti protein
(Agouti, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

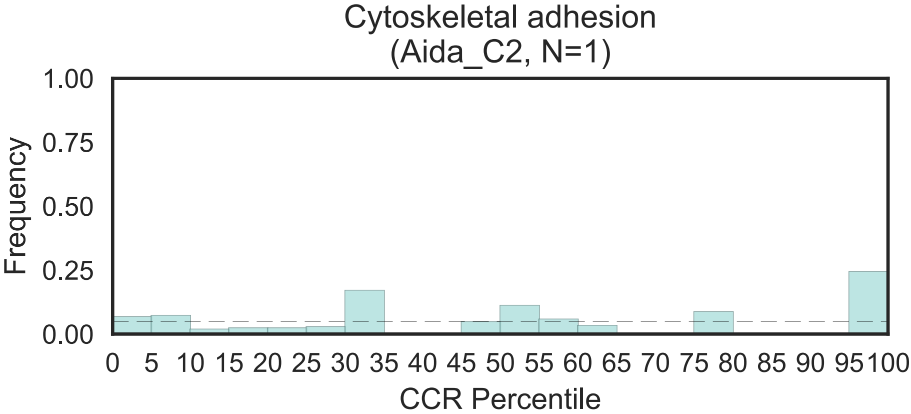


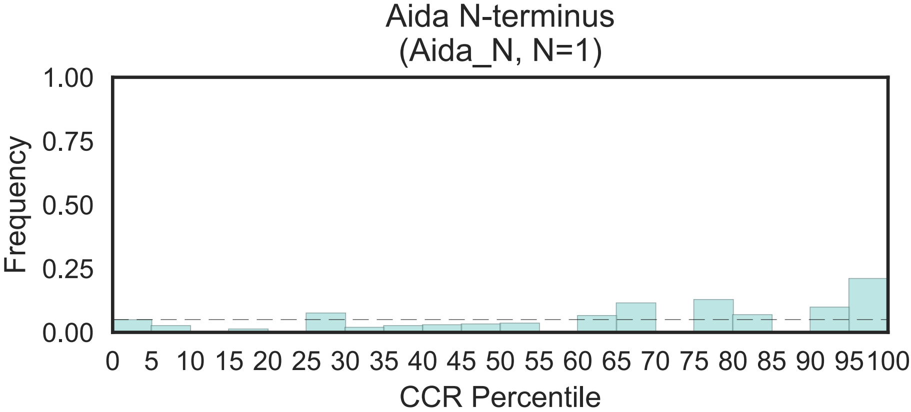
Activator of Hsp90 ATPase, N-terminal
(Aha1_N, N=1)

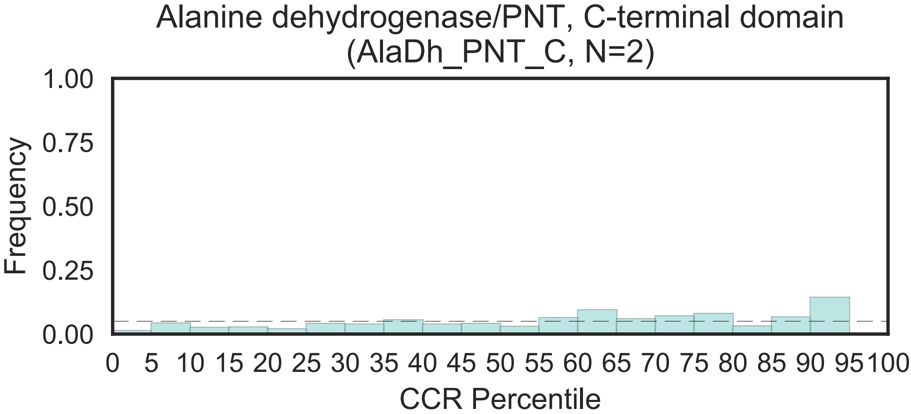

AhpC/TSA family
(AhpC-TSA, N=12)
Fisher's OR: 0.214; Bonferroni p-val: 1

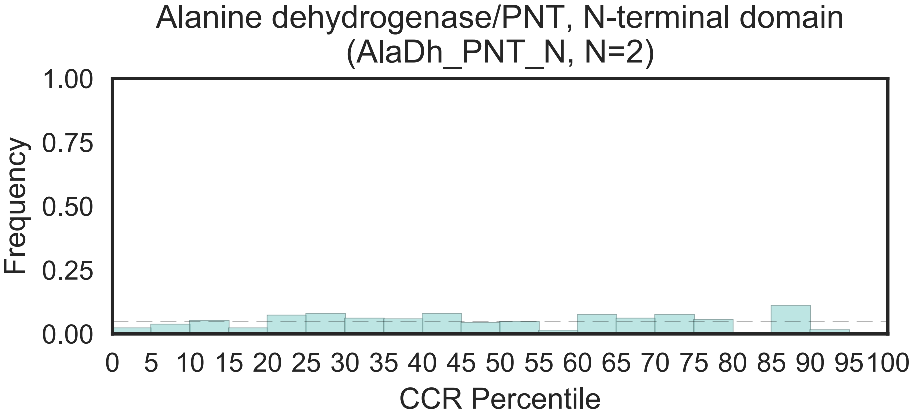


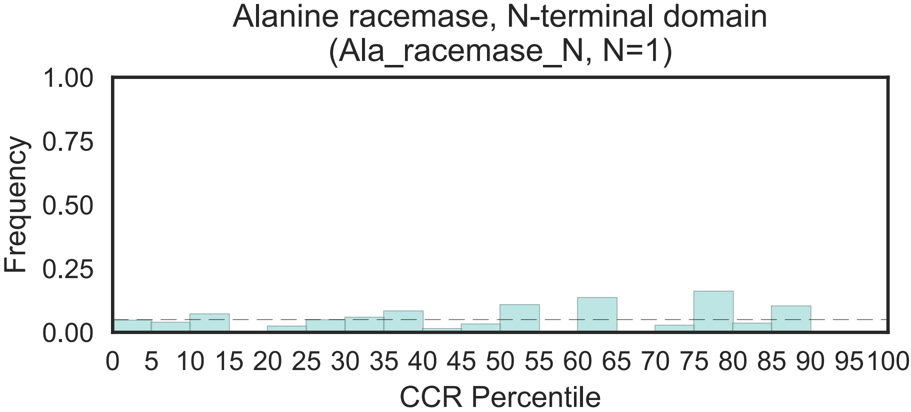
AhpC/TSA antioxidant enzyme
(AhpC-TSA_2, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

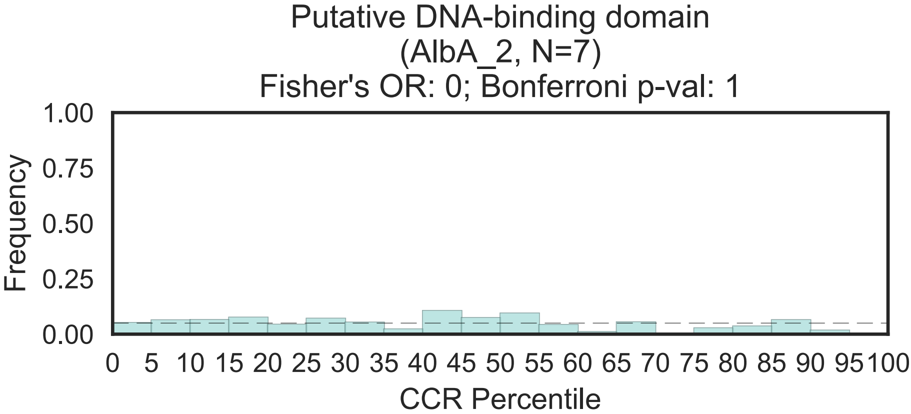

Cytoskeletal adhesion
(Aida_C2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

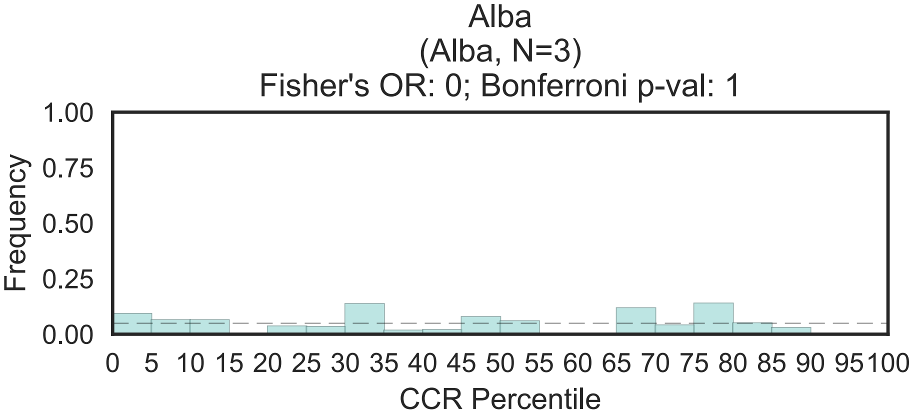

Aida N-terminus
(Aida_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

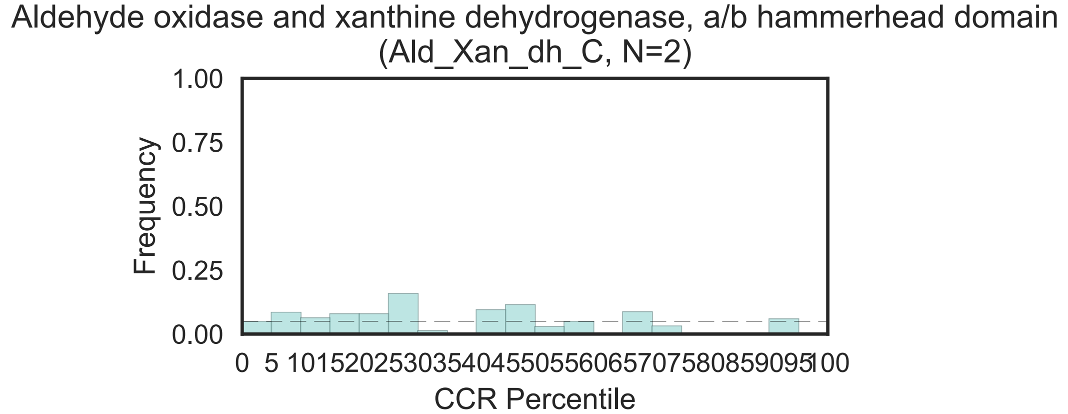

Alanine dehydrogenase/PNT, C-terminal domain
(AlaDh_PNT_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

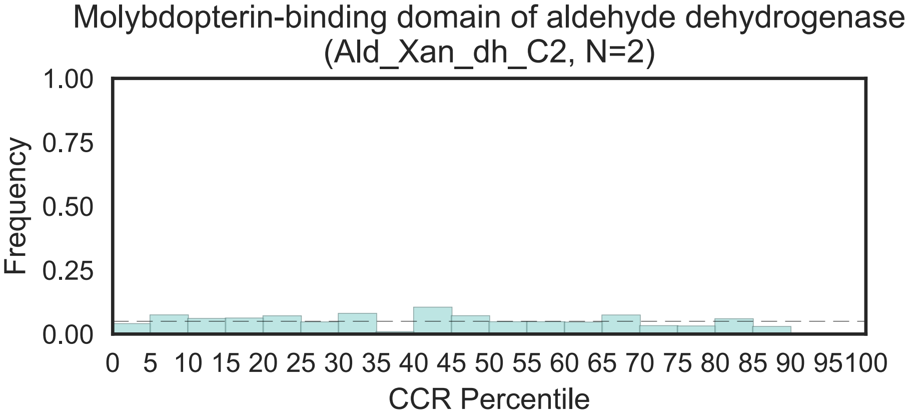

Alanine dehydrogenase/PNT, N-terminal domain
(AlaDh_PNT_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

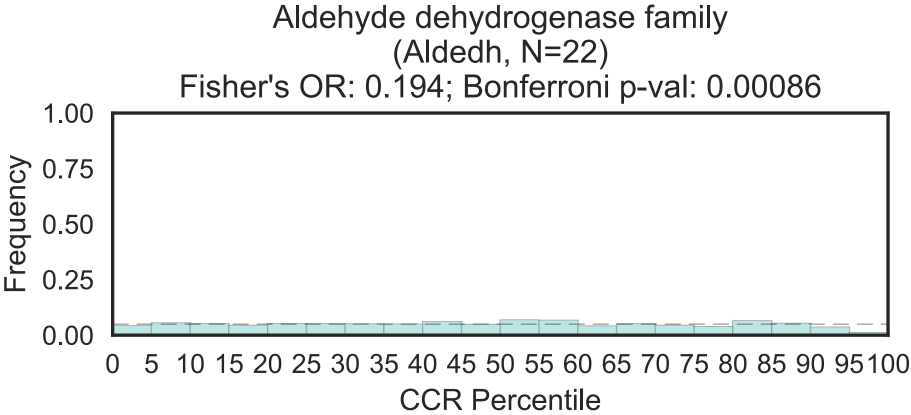

Alanine racemase, N-terminal domain
(Ala_racemase_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

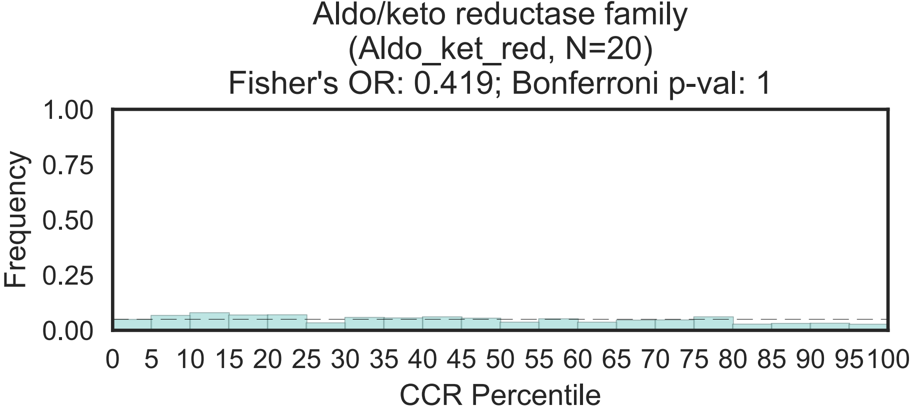

Putative DNA-binding domain
(AlbA_2, N=7)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

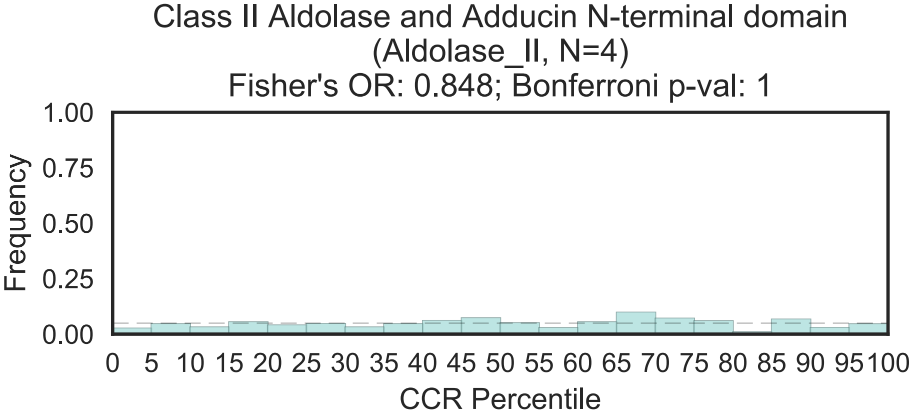

Alba
(Alba, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

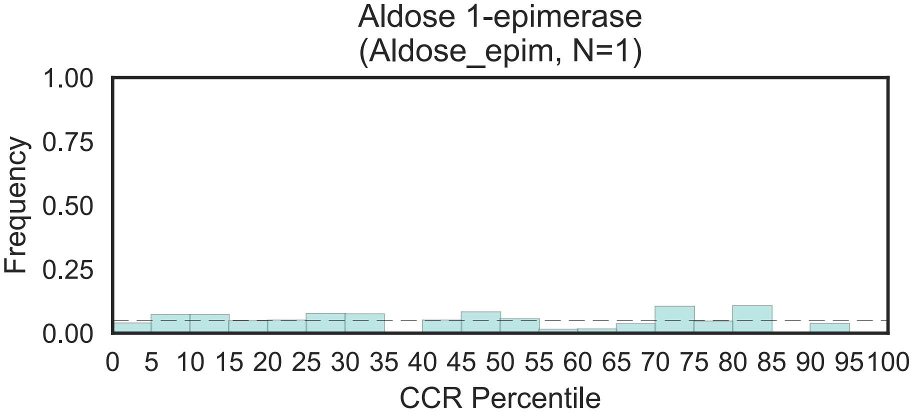

Aldehyde oxidase and xanthine dehydrogenase, a/b hammerhead domain
(Ald_Xan_dh_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

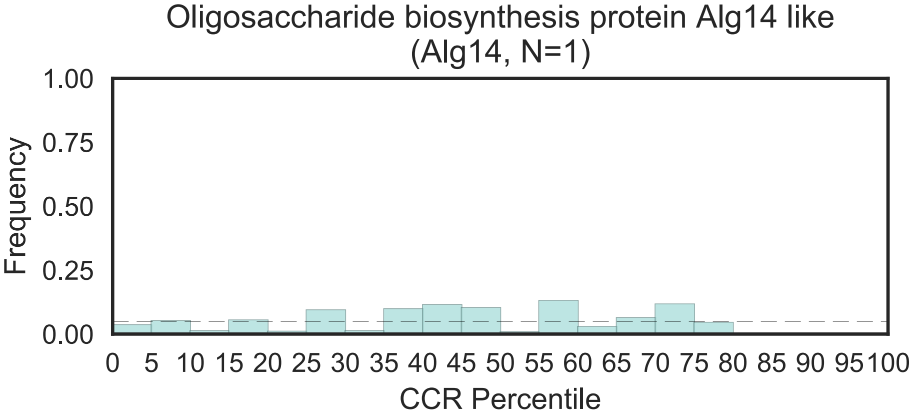

Molybdopterin-binding domain of aldehyde dehydrogenase
(Ald_Xan_dh_C2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

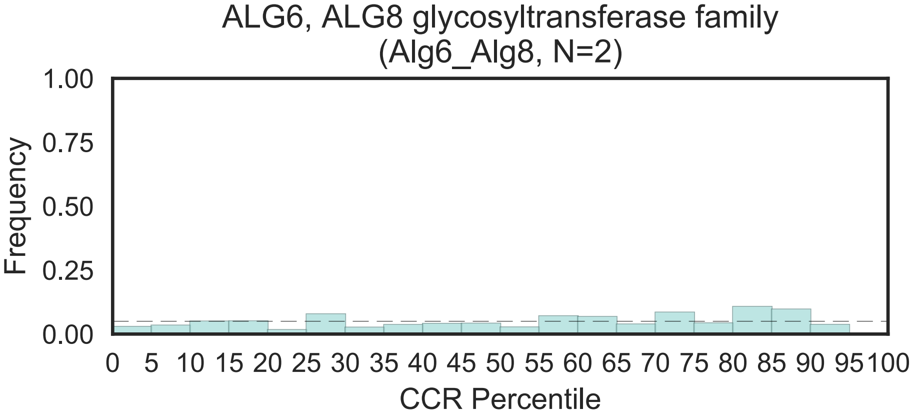

Aldehyde dehydrogenase family
(Aldedh, N=22)
Fisher's OR: 0.194; Bonferroni p-val: 0.00086
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

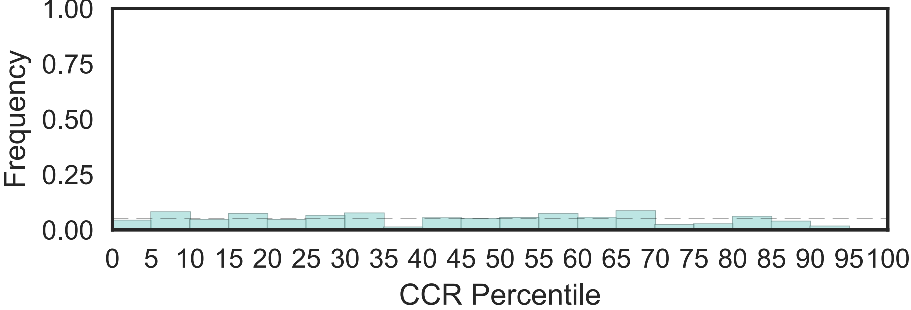

Aldo/keto reductase family
(Aldo_ket_red, N=20)
Fisher's OR: 0.419; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Class II Aldolase and Adducin N-terminal domain
(Aldolase_II, N=4)
Fisher's OR: 0.848; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

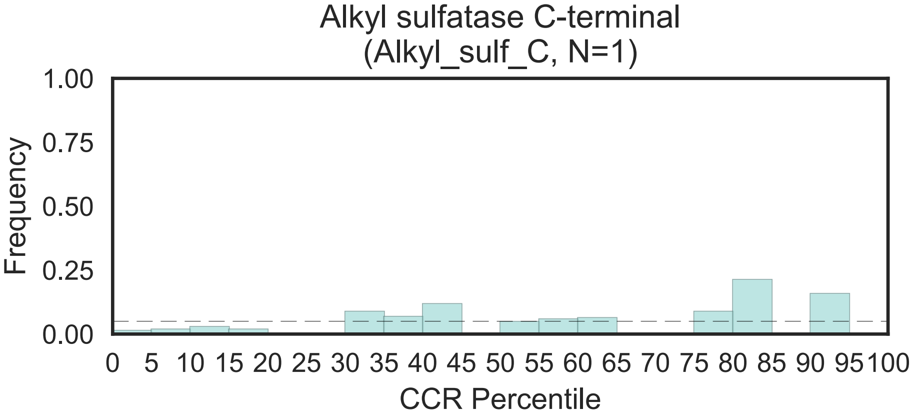

Aldose 1-epimerase
(Aldose_epim, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


Oligosaccharide biosynthesis protein Alg14 like
(Alg14, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

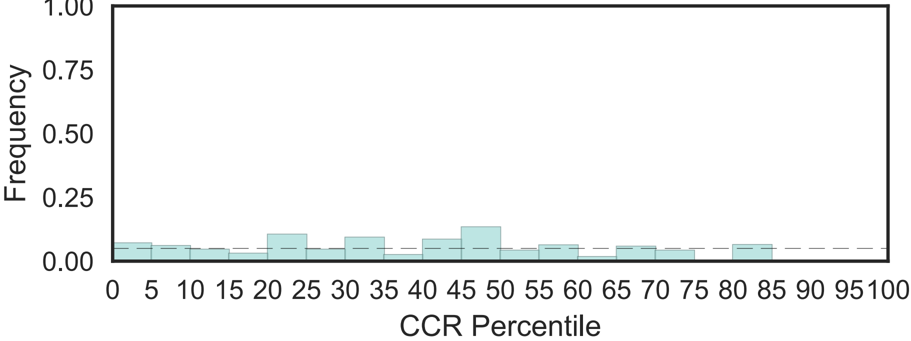

ALG6, ALG8 glycosyltransferase family
(Alg6_Alg8, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

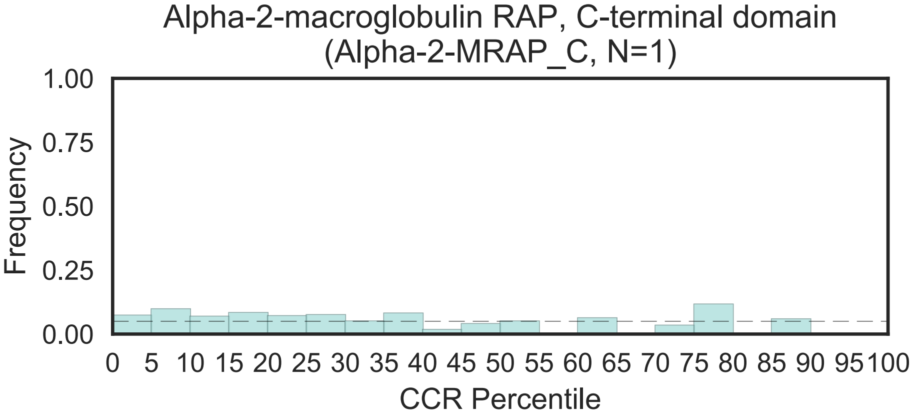


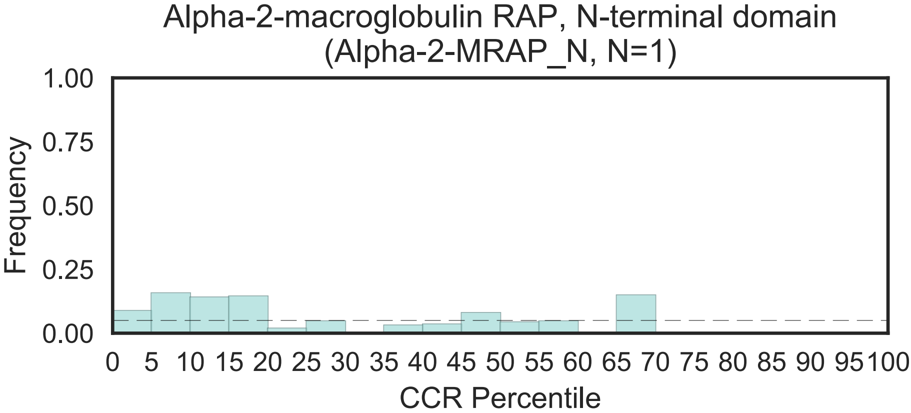
Alkaline phosphatase
(Alk_phosphatase, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

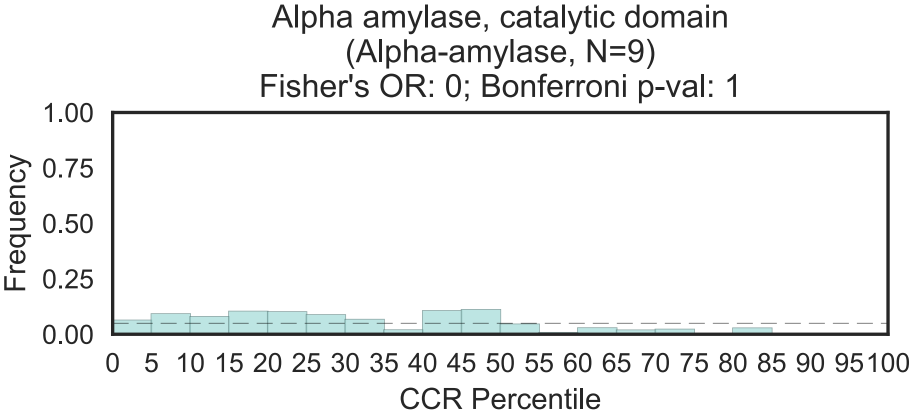

Alkyl sulfatase C-terminal
(Alkyl_sulf_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

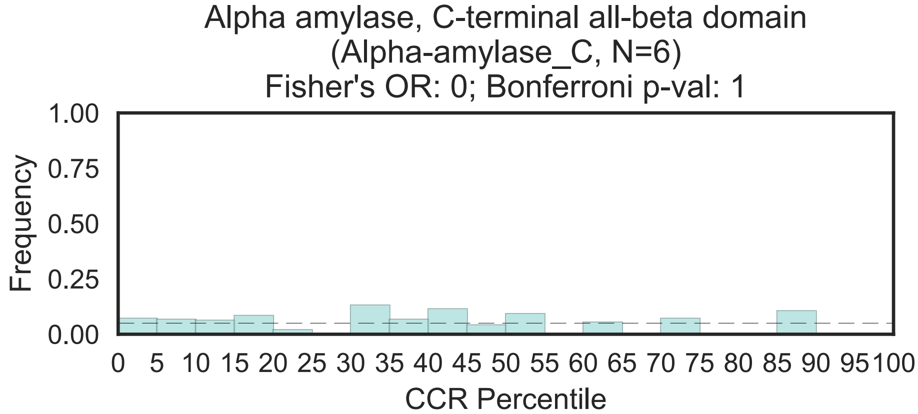
Allantoicase repeat
(Allantoicase, N=2)

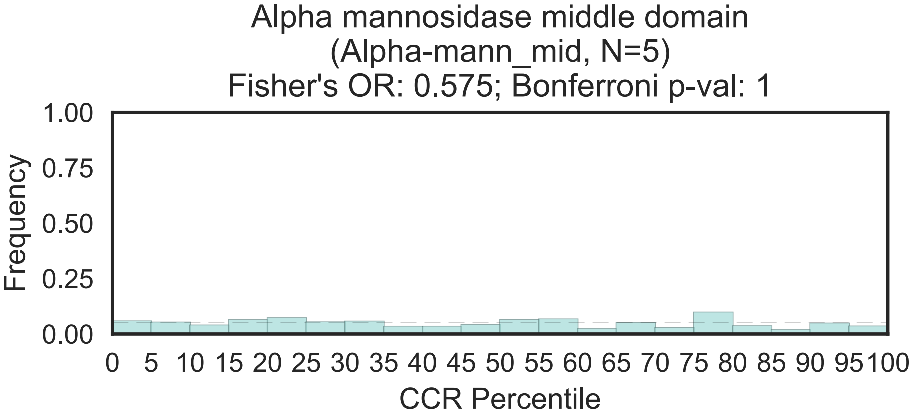



Alpha-2-macroglobulin RAP, C-terminal domain
(Alpha-2-MRAP_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

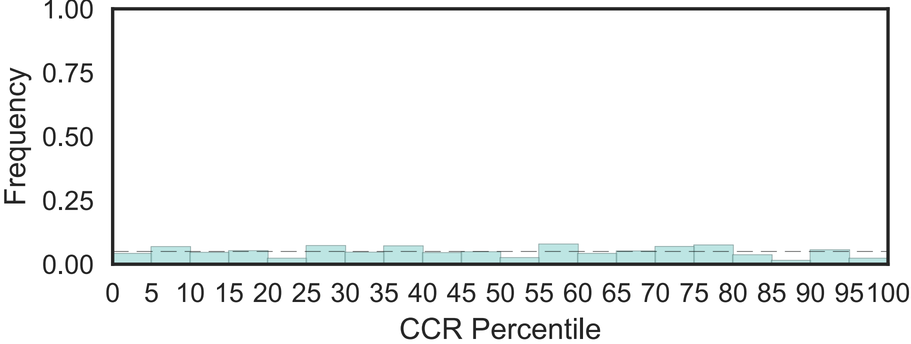

Alpha-2-macroglobulin RAP, N-terminal domain
(Alpha-2-MRAP_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

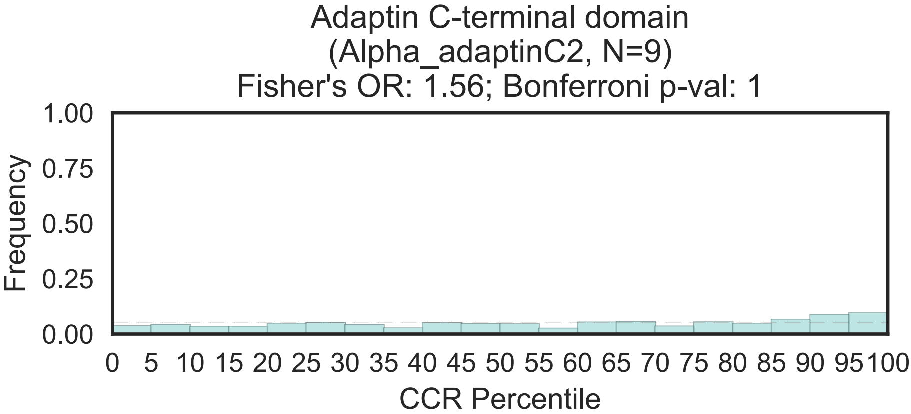

Alpha amylase, catalytic domain
(Alpha-amylase, N=9)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

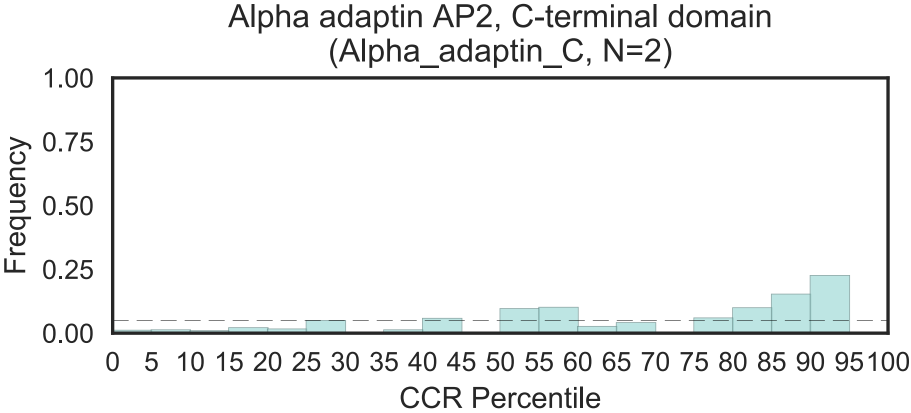

Alpha amylase, C-terminal all-beta domain
(Alpha-amylase_C, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

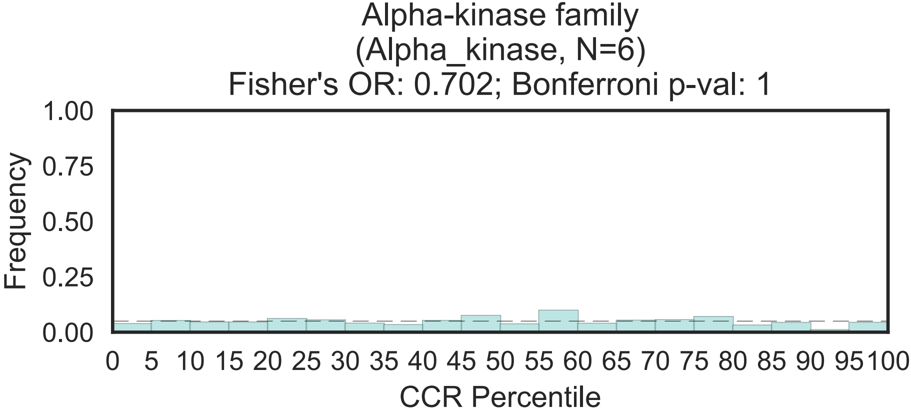

Alpha mannosidase middle domain
(Alpha-mann_mid, N=5)
Fisher's OR: 0.575; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

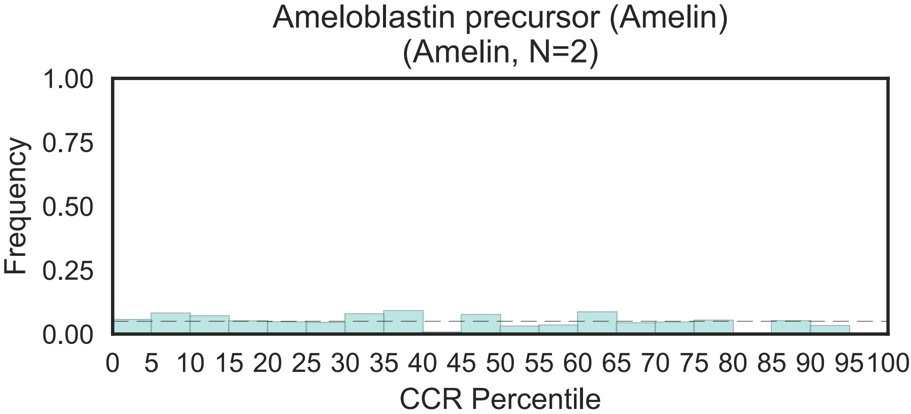
Alpha-L-fucosidase
(Alpha_L_fucos, N=2)

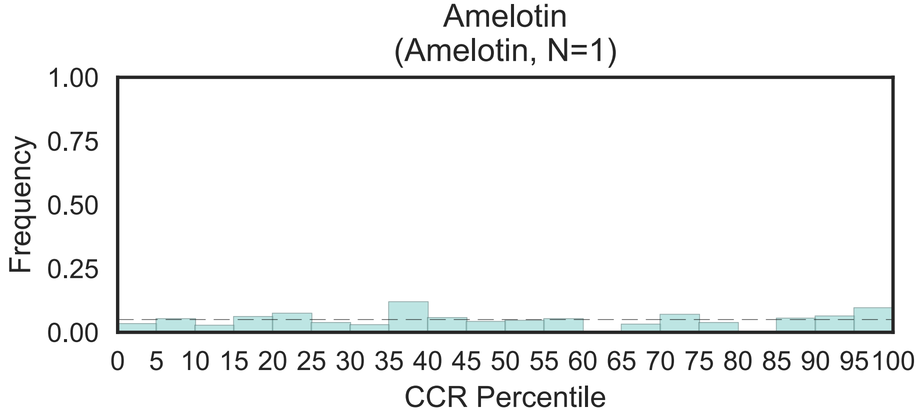


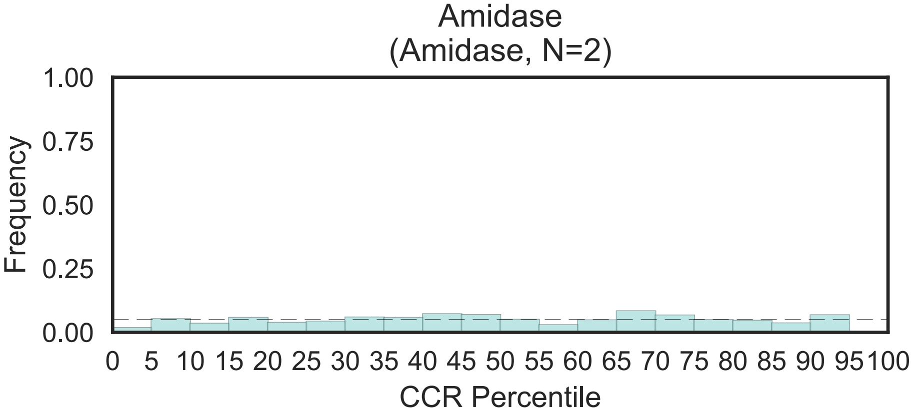

Adaptin C-terminal domain
(Alpha_adaptinC2, N=9)
Fisher's OR: 1.56; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Alpha adaptin AP2, C-terminal domain
(Alpha_adaptin_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

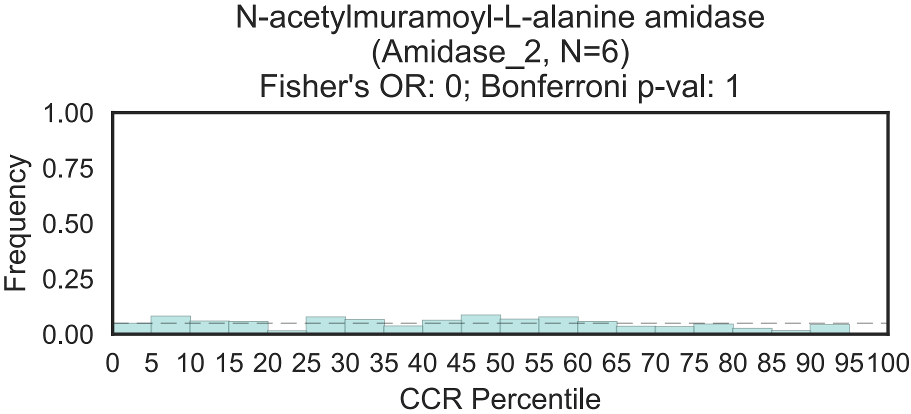

Alpha-kinase family
(Alpha_kinase, N=6)
Fisher's OR: 0.702; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

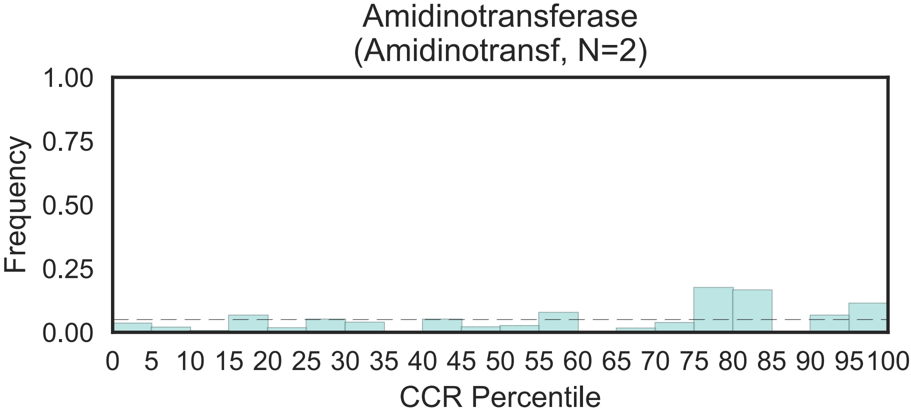

Ameloblastin precursor (Amelin)
(Amelin, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

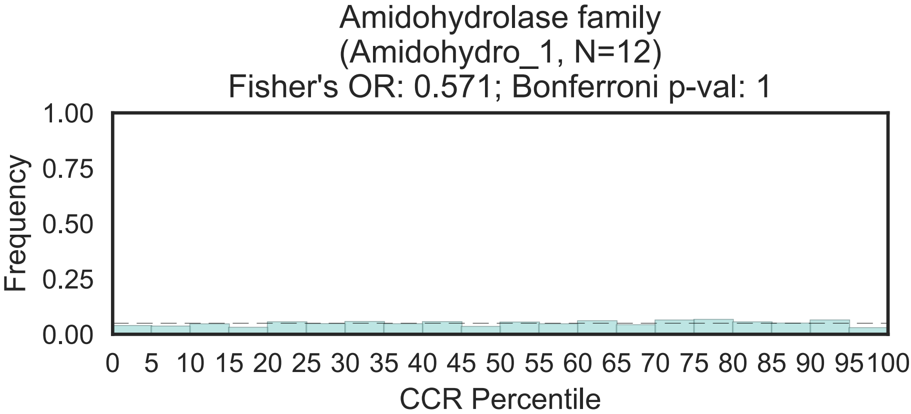

Amelotin
(Amelotin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

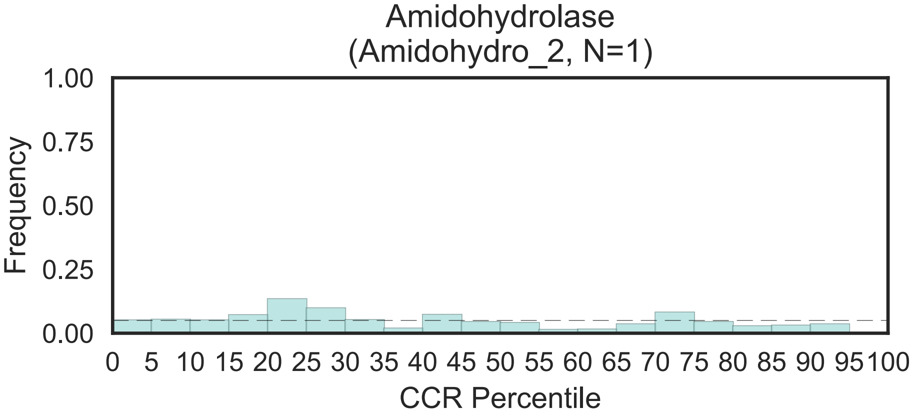


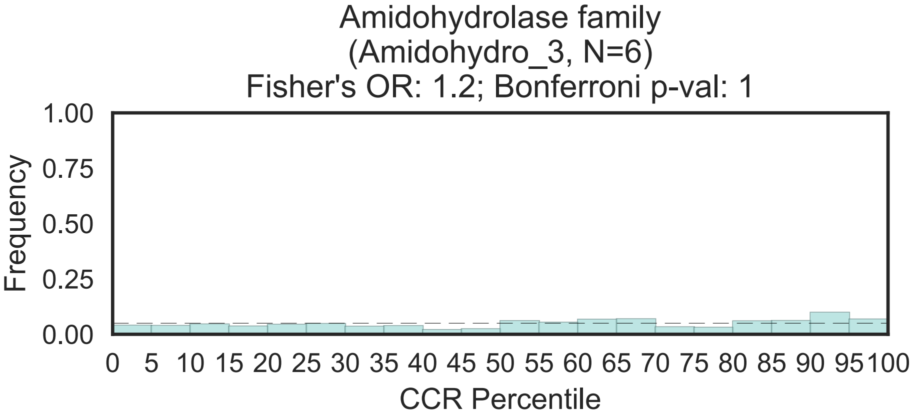
Amidase
(Amidase, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


N-acetylmuramoyl-L-alanine amidase
(Amidase_2, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

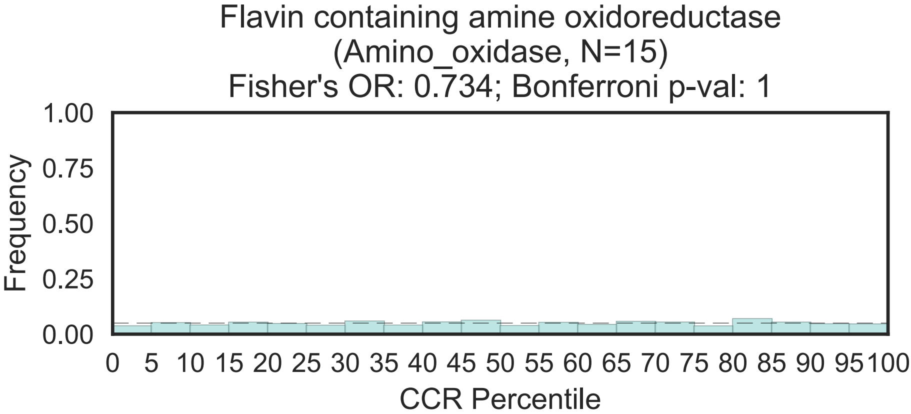

Amidinotransferase
(Amidinotransf, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Amidohydrolase family
(Amidohydro_1, N=12)
Fisher's OR: 0.571; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

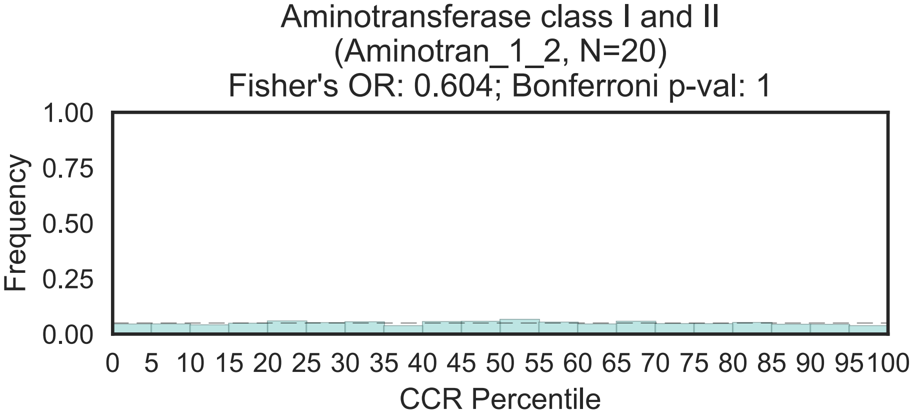

Amidohydrolase
(Amidohydro_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



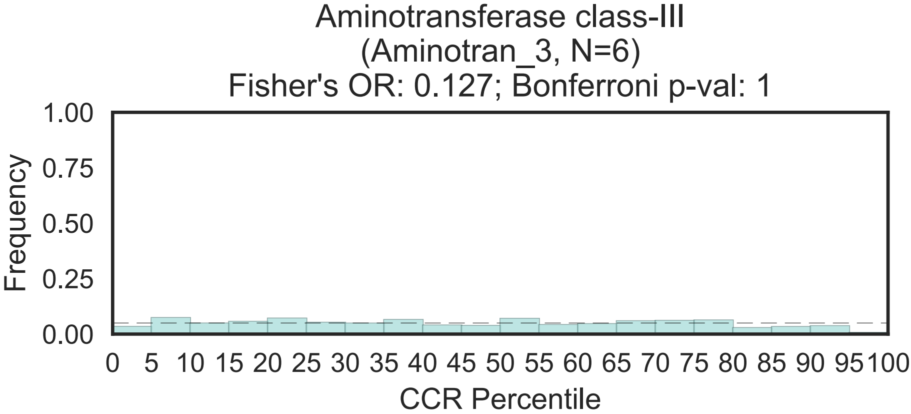
Amidohydrolase family
(Amidohydro_3, N=6)
Fisher's OR: 1.2; Bonferroni p-val: 1

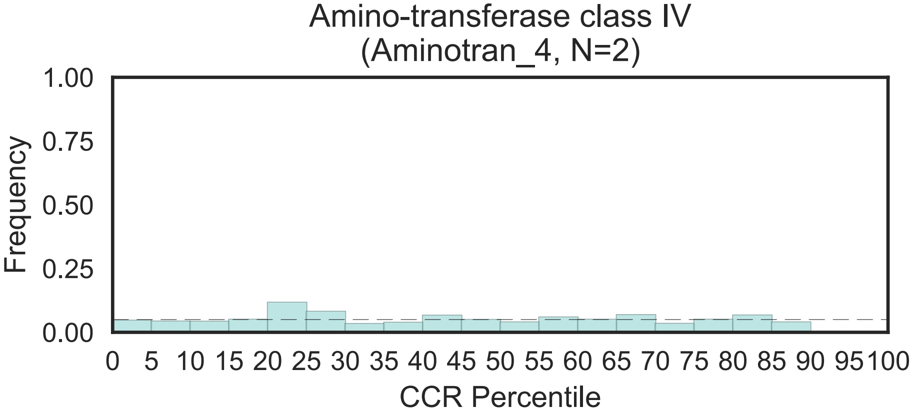


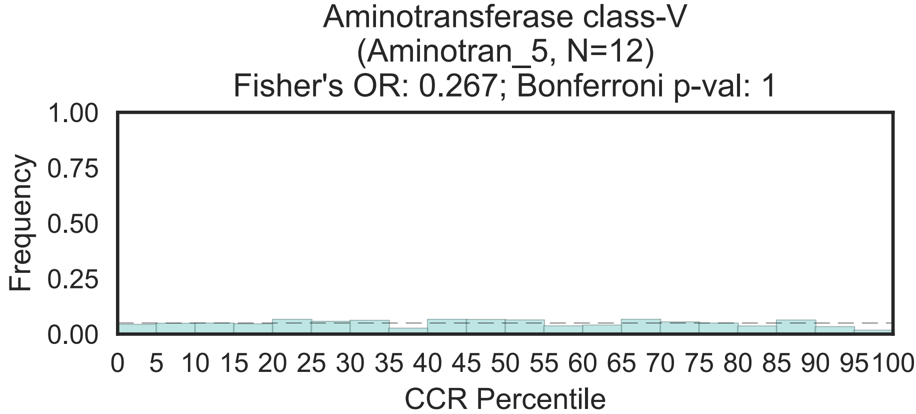
Flavin containing amine oxidoreductase
(Amino_oxidase, N=15)
Fisher's OR: 0.734; Bonferroni p-val: 1



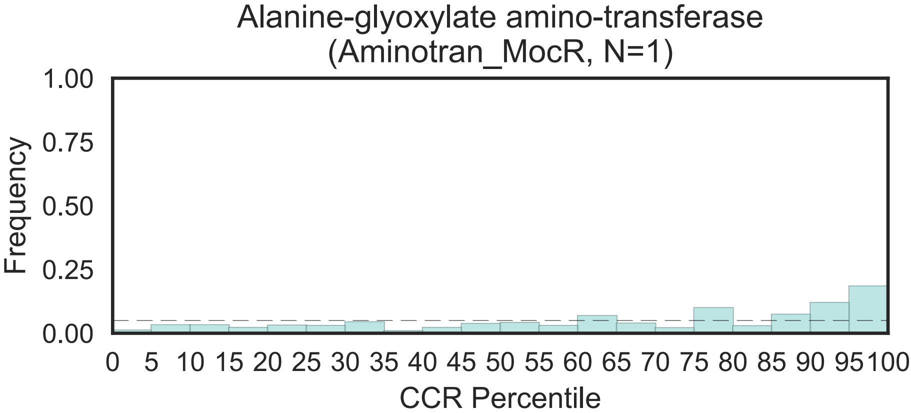
Aminotransferase class I and II
(Aminotran_1_2, N=20)
Fisher's OR: 0.604; Bonferroni p-val: 1

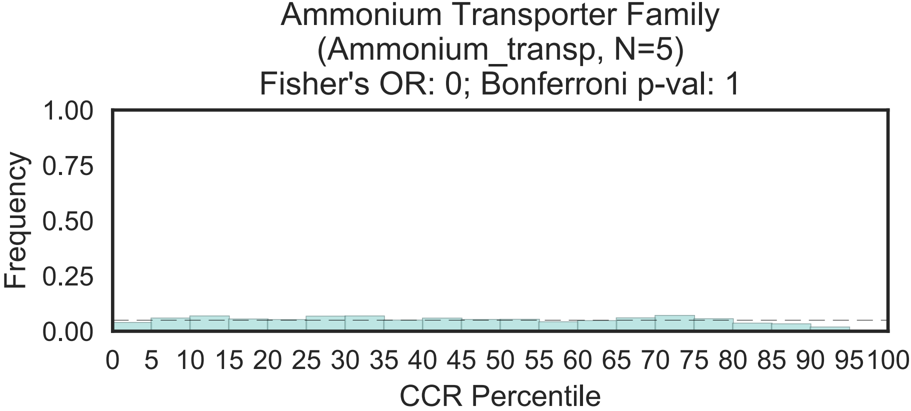

Aminotransferase class-III
(Aminotran_3, N=6)
Fisher's OR: 0.127; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

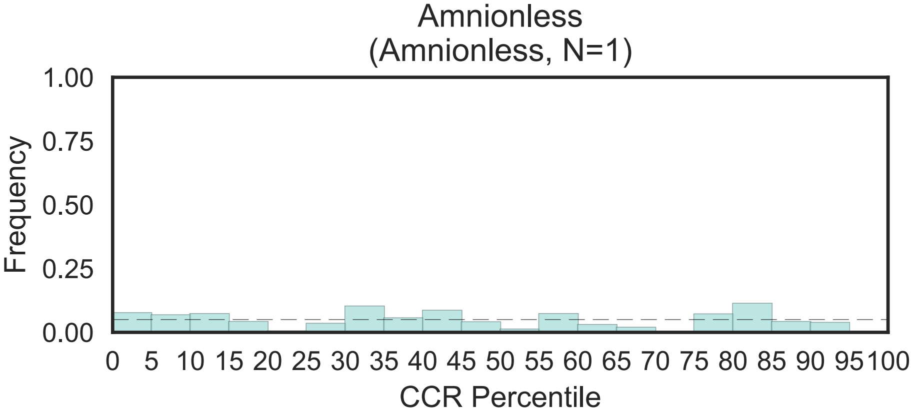

Amino-transferase class IV
(Aminotran_4, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

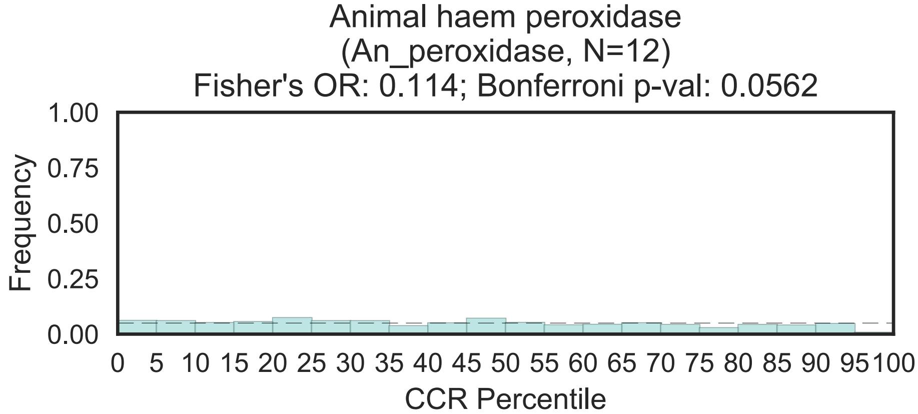


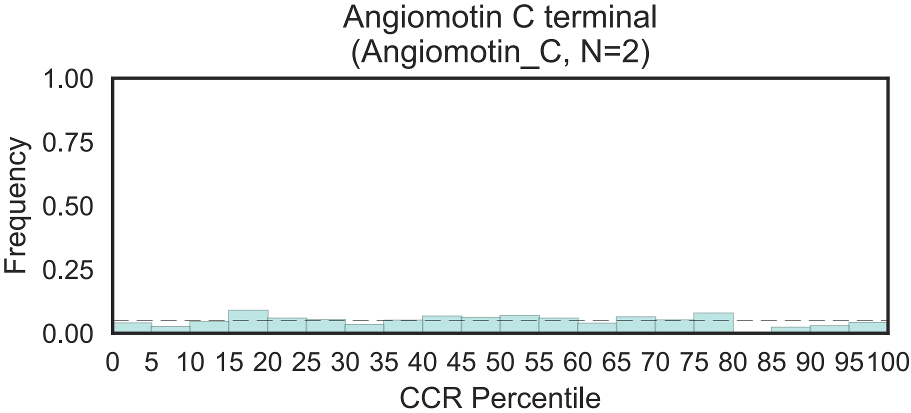
Aminotransferase class-V
(Aminotran_5, N=12)
Fisher's OR: 0.267; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

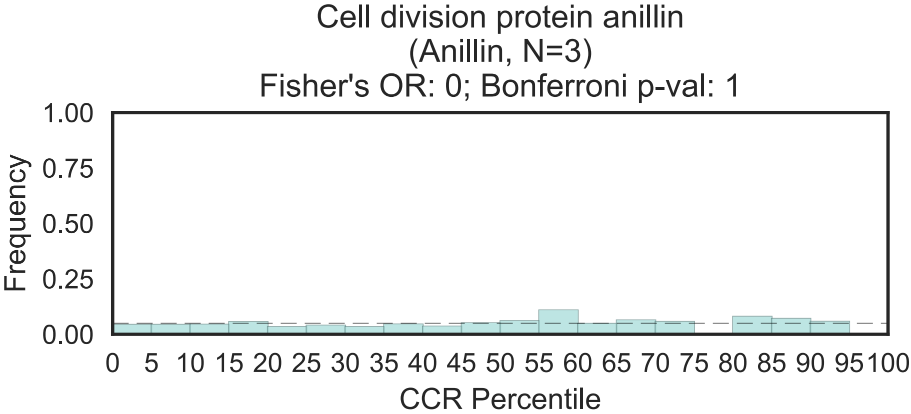

Alanine-glyoxylate amino-transferase
(Aminotran_MocR, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

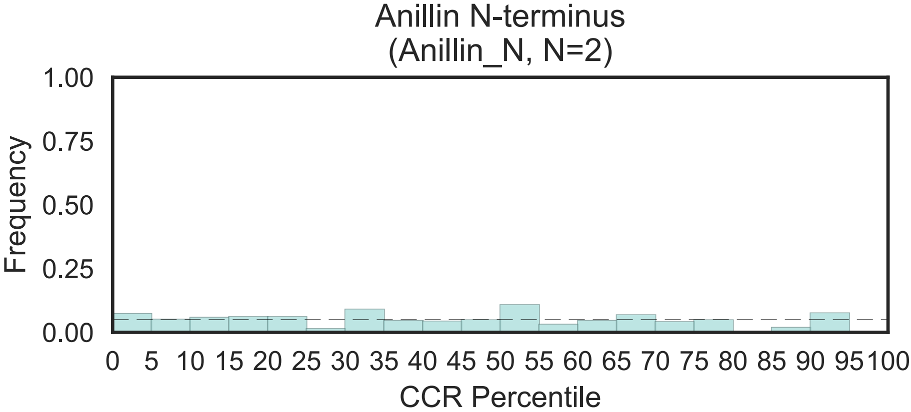

Ammonium Transporter Family
(Ammonium_transp, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

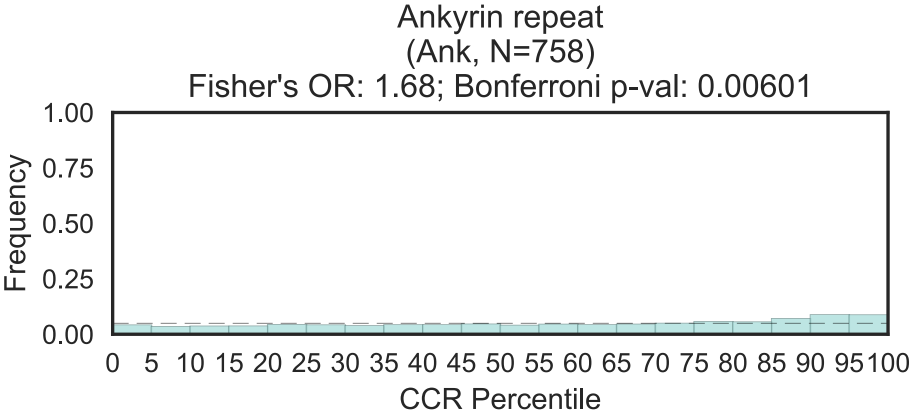

Amnionless
(Amnionless, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

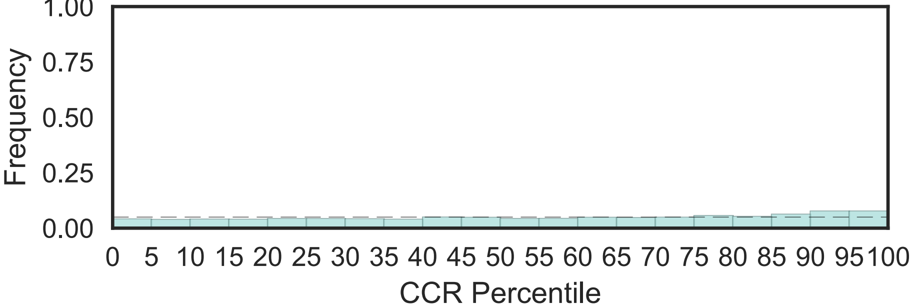

Animal haem peroxidase
(An_peroxidase, N=12)
Fisher's OR: 0.114; Bonferroni p-val: 0.0562


Angiomotin C terminal
(Angiomotin_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

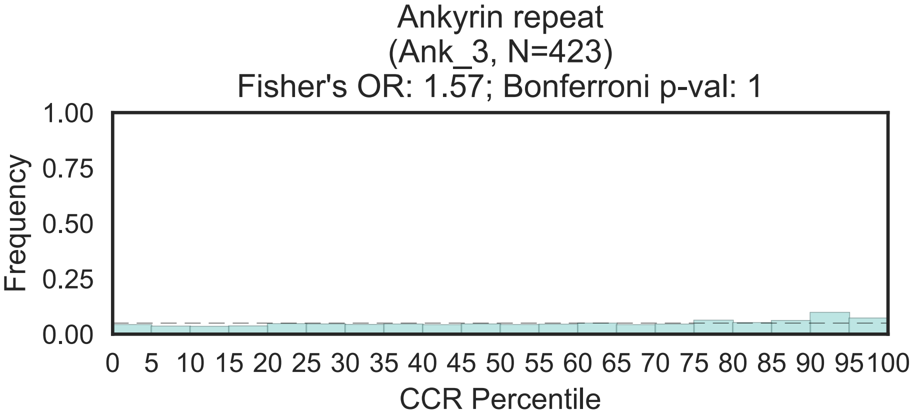

Cell division protein anillin
(Anillin, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

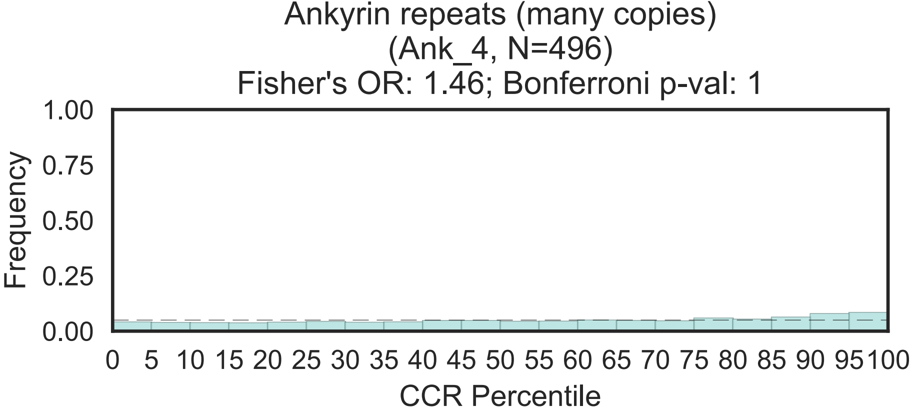

Anillin N-terminus
(Anillin_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ankyrin repeat
(Ank, N=758)
Fisher's OR: 1.68; Bonferroni p-val: 0.00601
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

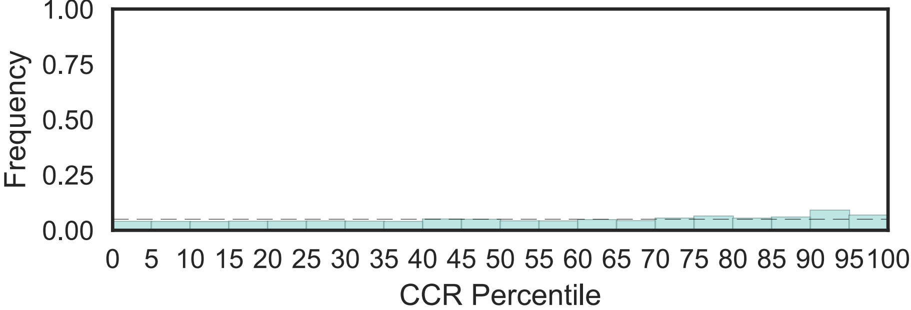


Ankyrin repeats (3 copies)
(Ank_2, N=490)
Fisher's OR: 1.24; Bonferroni p-val: 1

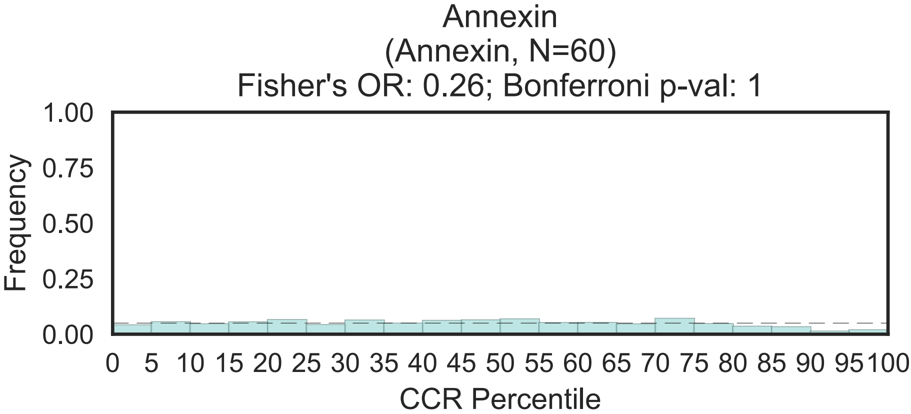

Ankyrin repeat
(Ank_3, N=423)
Fisher's OR: 1.57; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



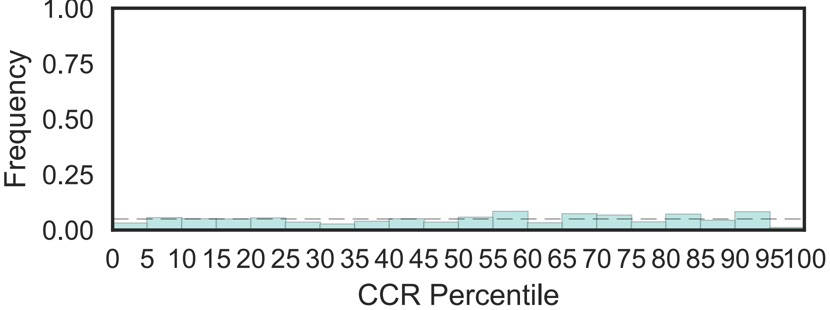
Ankyrin repeats (many copies)
(Ank_4, N=496)
Fisher's OR: 1.46; Bonferroni p-val: 1



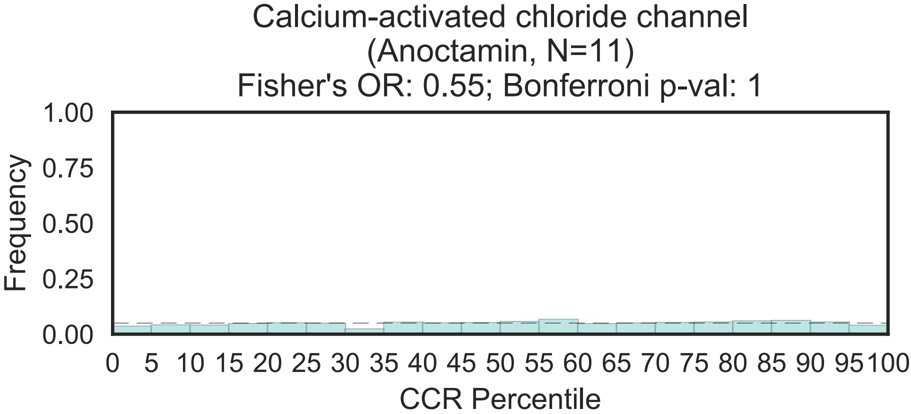
Ankyrin repeats (many copies)
(Ank_5, N=347)
Fisher's OR: 1.17; Bonferroni p-val: 1

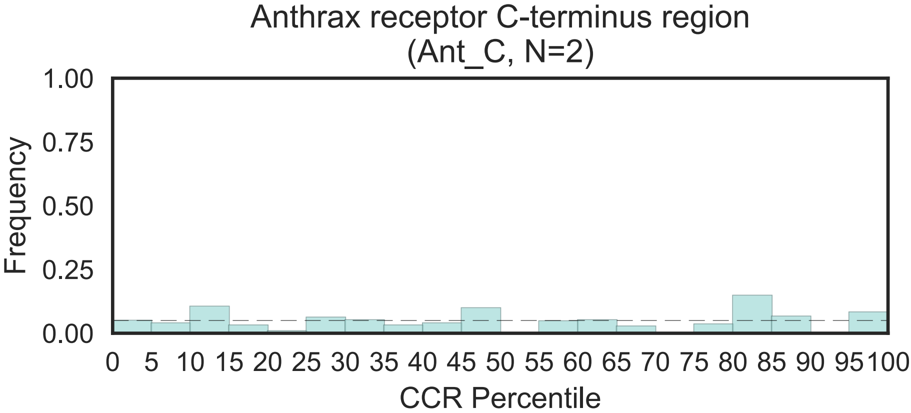


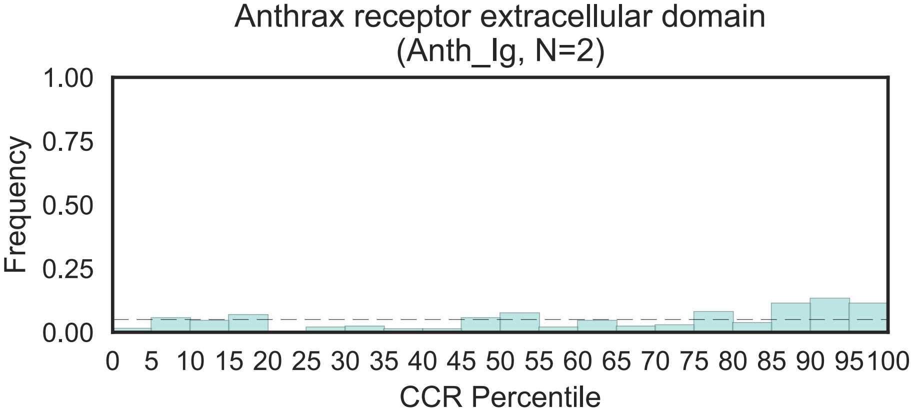
Annexin
(Annexin, N=60)
Fisher's OR: 0.26; Bonferroni p-val: 1

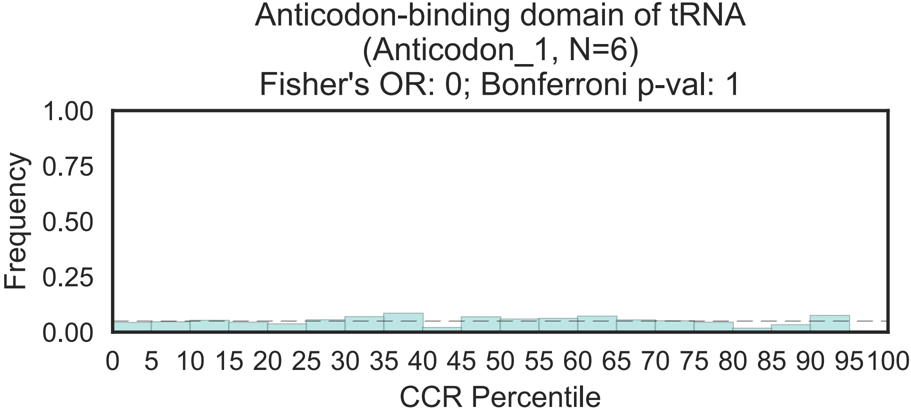


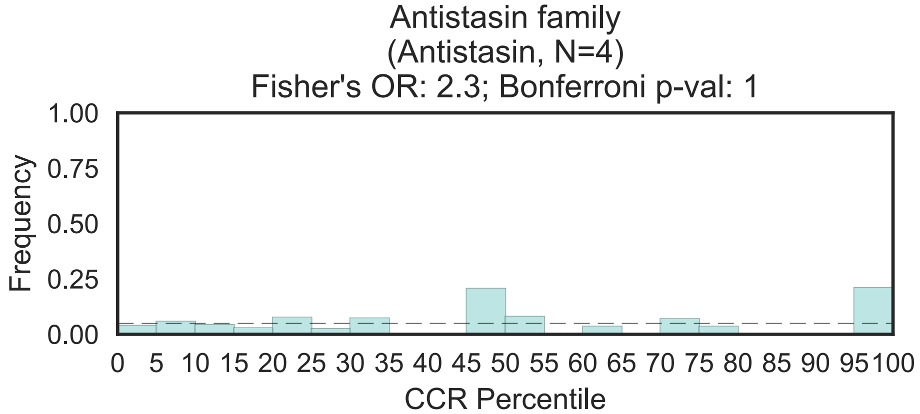
Dimerisation domain of Ca+-activated chloride-channel, anoctamin
(Anoct_dimer, N=7)
Fisher's OR: 0.172; Bonferroni p-val: 1


Calcium-activated chloride channel
(Anoctamin, N=11)
Fisher's OR: 0.55; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

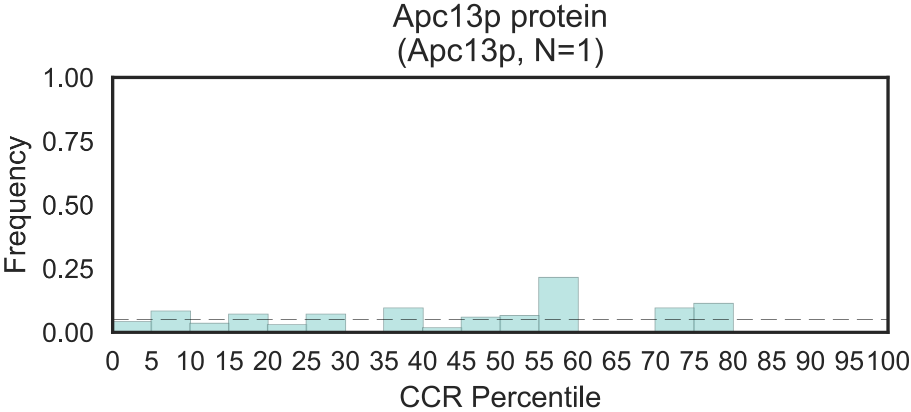

Anthrax receptor C-terminus region
(Ant_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

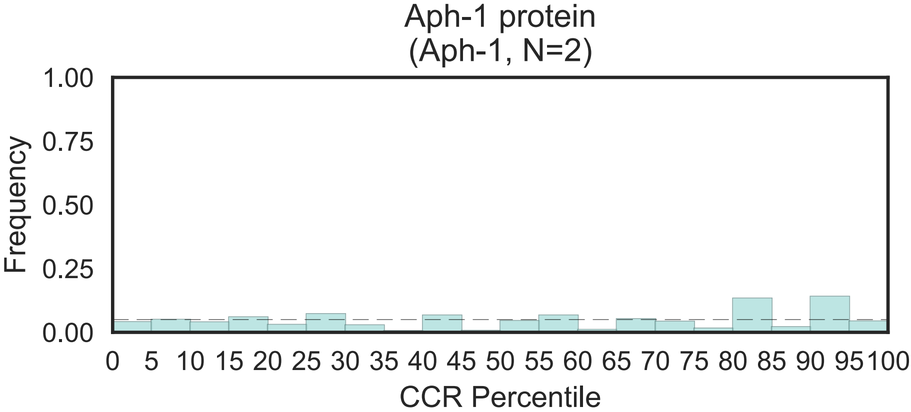

Anthrax receptor extracellular domain
(Anth_Ig, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

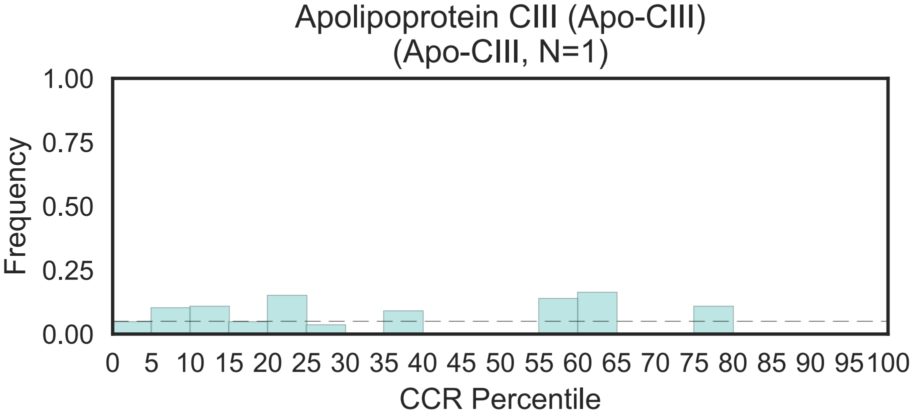

Anticodon-binding domain of tRNA
(Anticodon_1, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



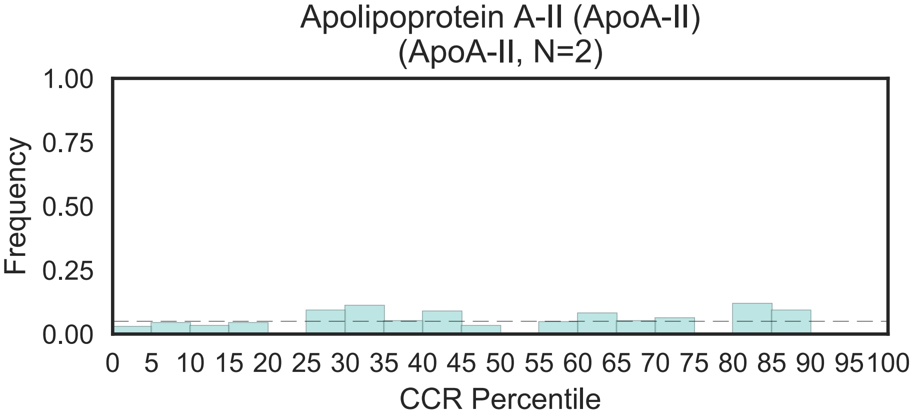
Antistasin family
(Antistasin, N=4)
Fisher's OR: 2.3; Bonferroni p-val: 1

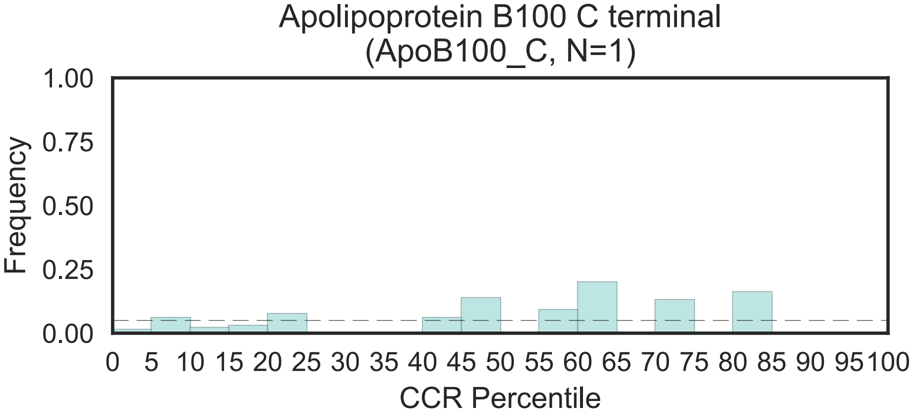

Apc13p protein
(Apc13p, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

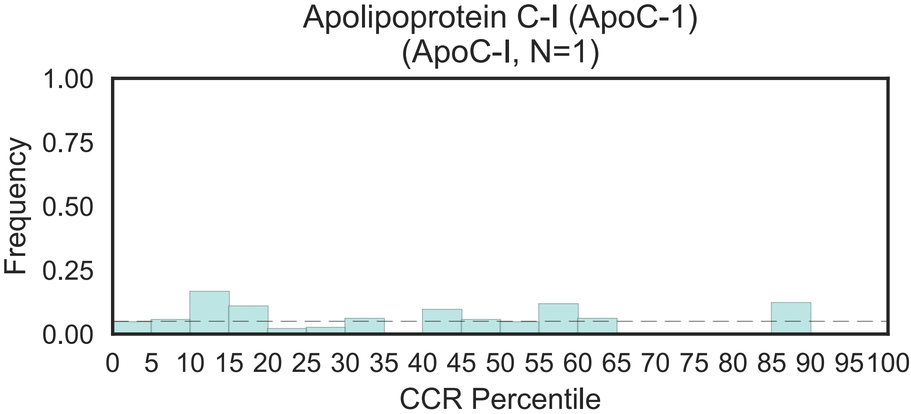

Aph-1 protein
(Aph-1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

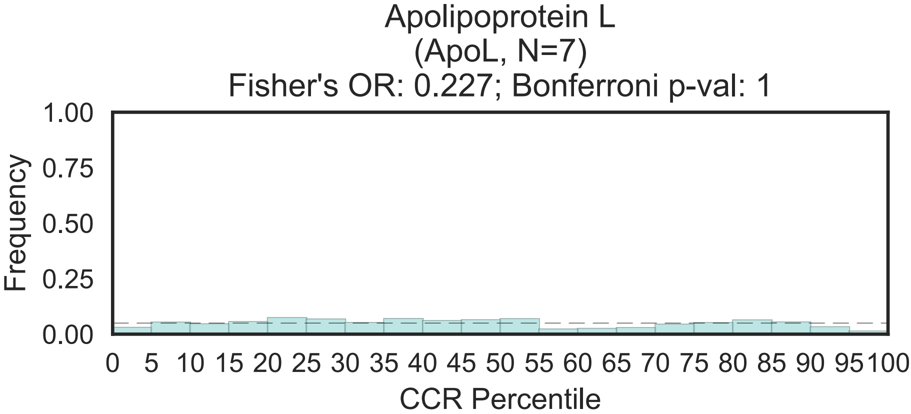


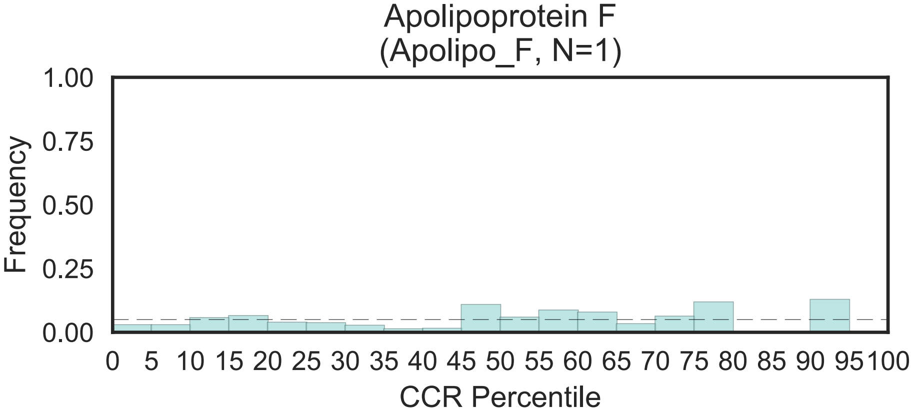
Apolipoprotein CIII (Apo-CIII)
(Apo-CIII, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

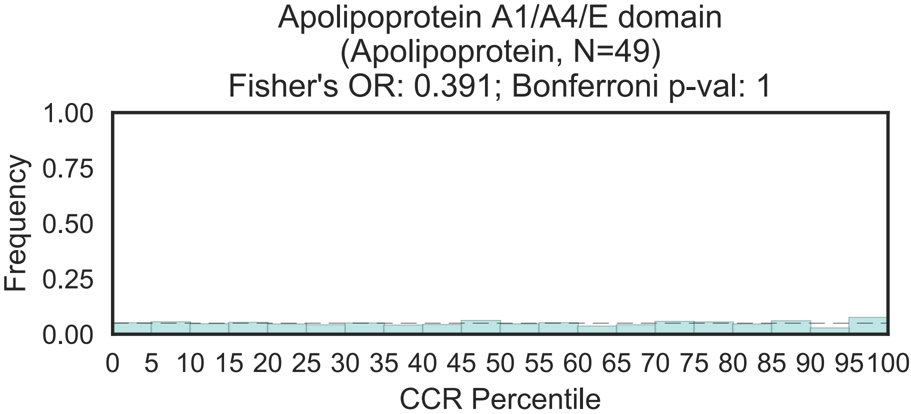

Apolipoprotein A-II (ApoA-II)
(ApoA-II, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

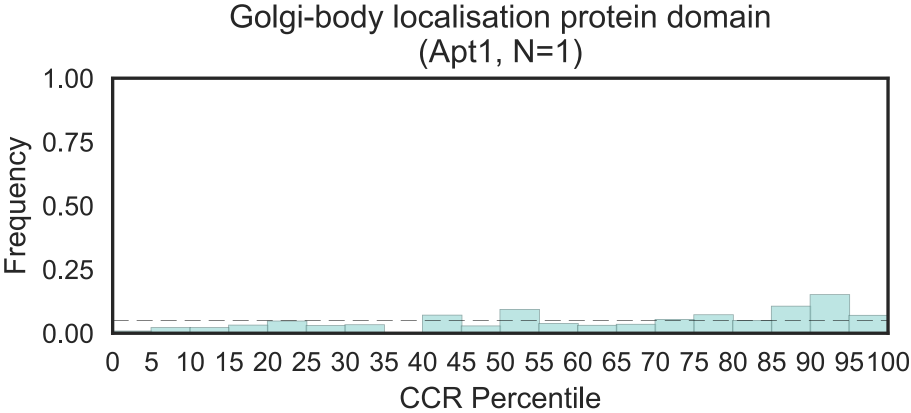

Apolipoprotein B100 C terminal
(ApoB100_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

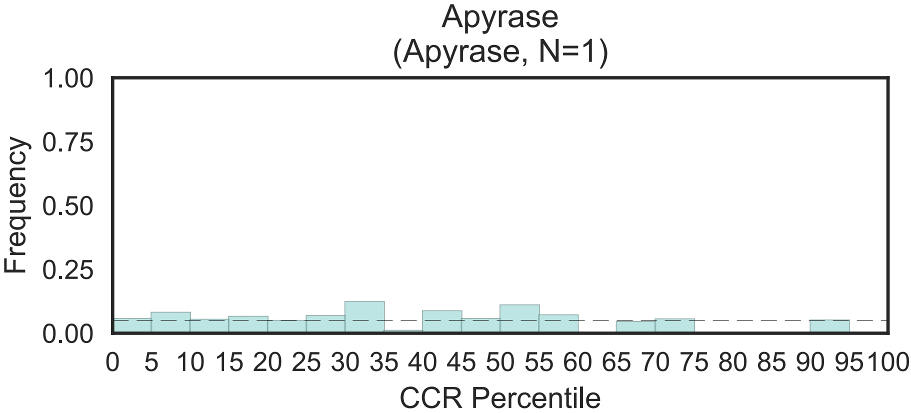

Apolipoprotein C-I (ApoC-1)
(ApoC-I, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

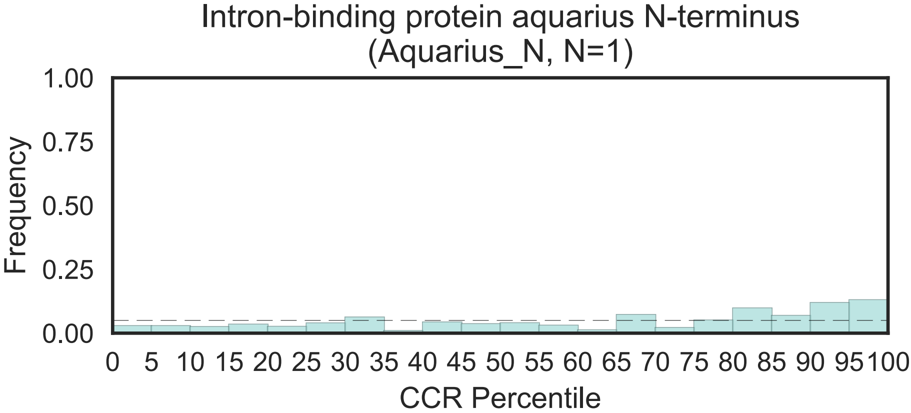

Apolipoprotein L
(ApoL, N=7)
Fisher's OR: 0.227; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

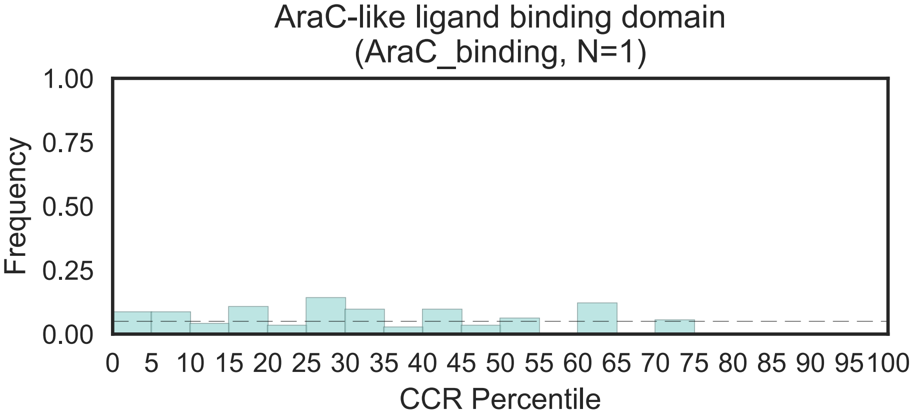

Apolipoprotein F
(Apolipo_F, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Apolipoprotein A1/A4/E domain
(Apolipoprotein, N=49)
Fisher's OR: 0.391; Bonferroni p-val: 1

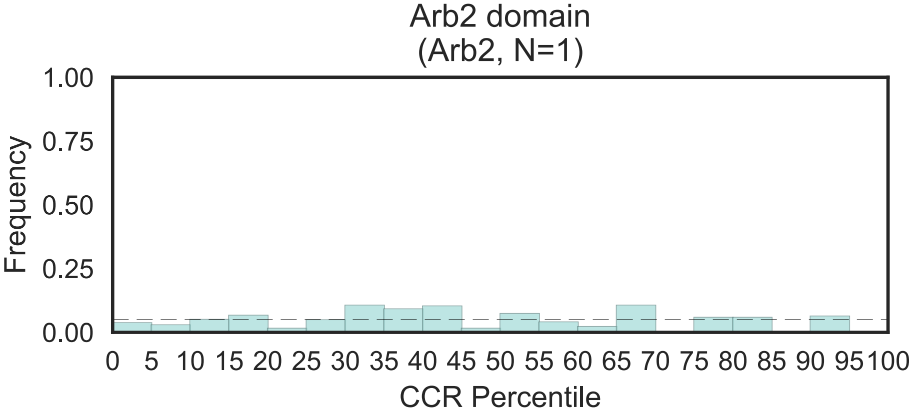

Golgi-body localisation protein domain
(Apt1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

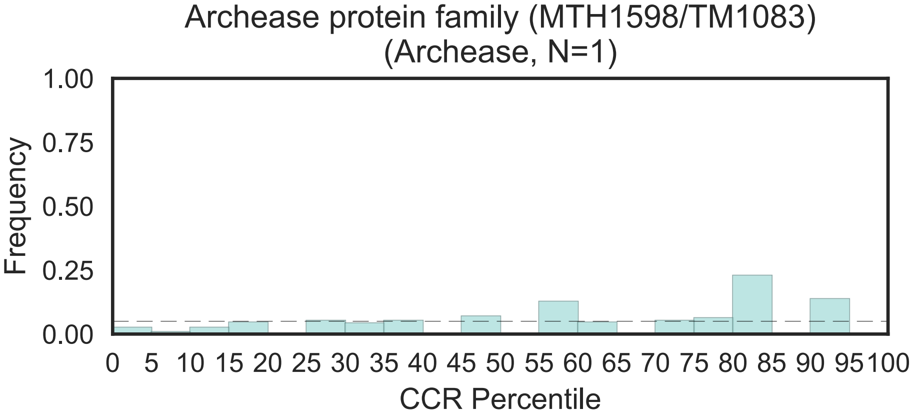

Apyrase
(Apyrase, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

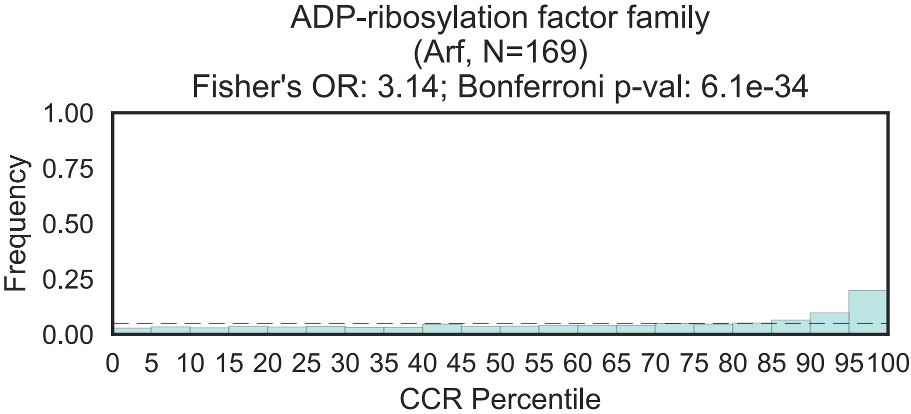

Intron-binding protein aquarius N-terminus
(Aquarius_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

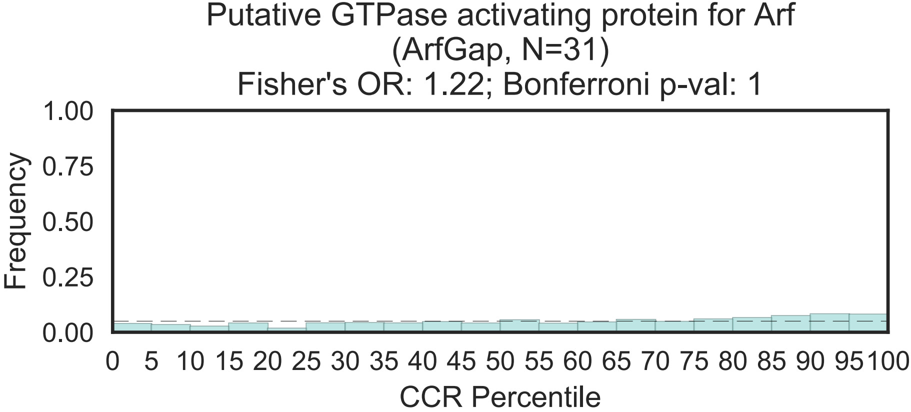


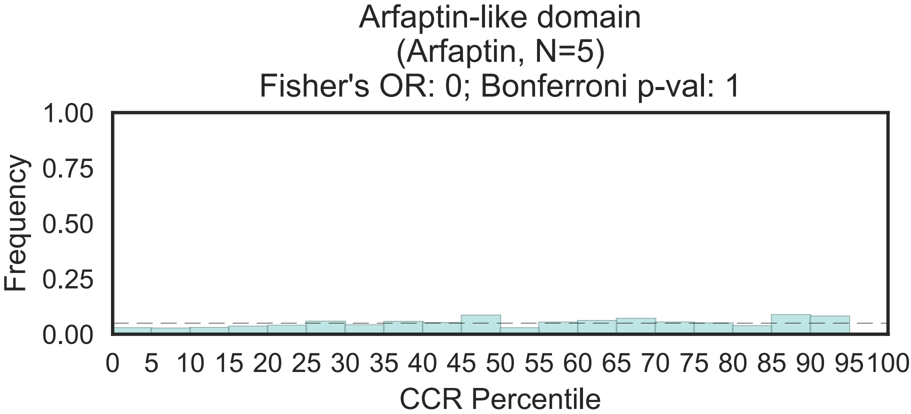
AraC-like ligand binding domain
(AraC_binding, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Arb2 domain
(Arb2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

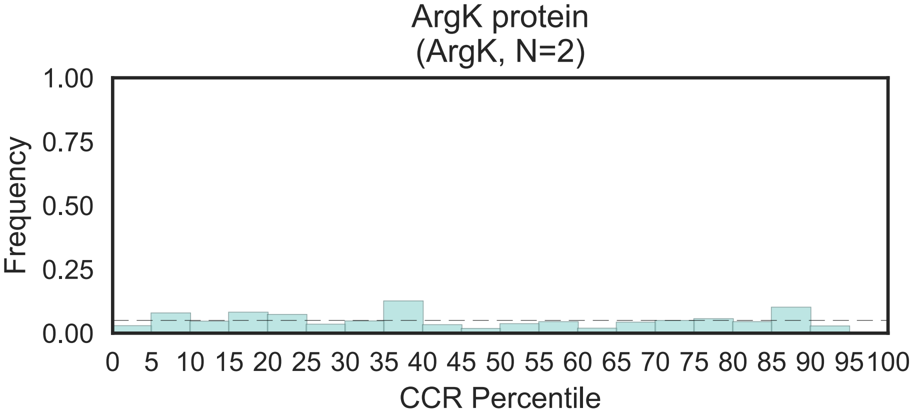

Archease protein family (MTH1598/TM1083)
(Archease, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

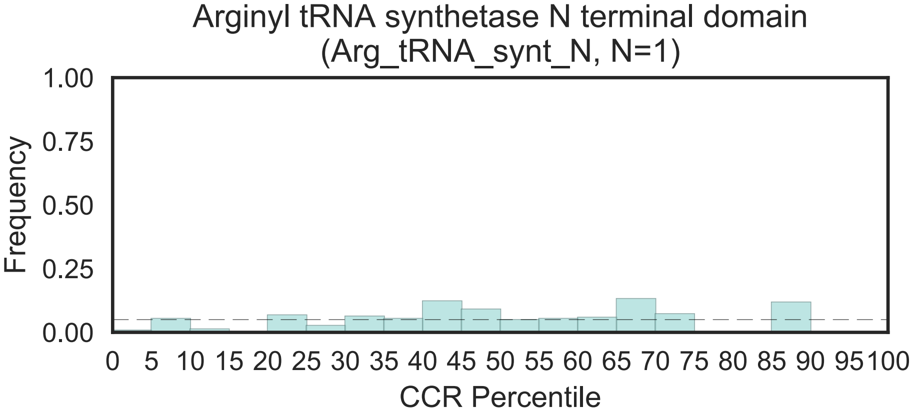

ADP-ribosylation factor family
(Arf, N=169)
Fisher's OR: 3.14; Bonferroni p-val: 6.1e-34
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Putative GTPase activating protein for Arf
(ArfGap, N=31)
Fisher's OR: 1.22; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

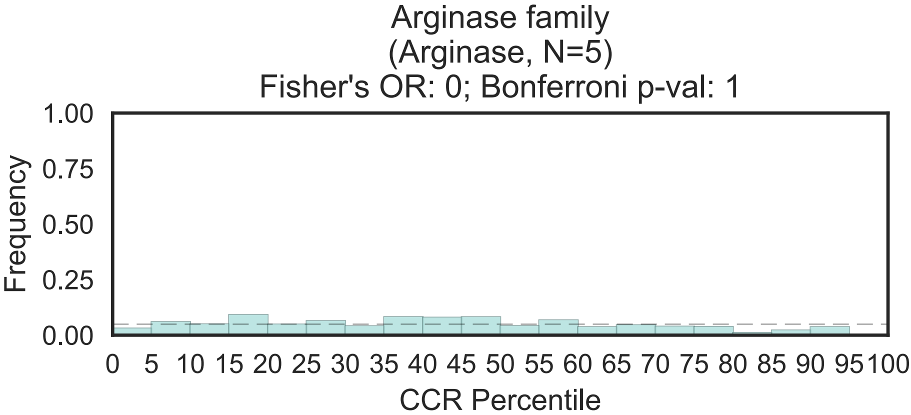


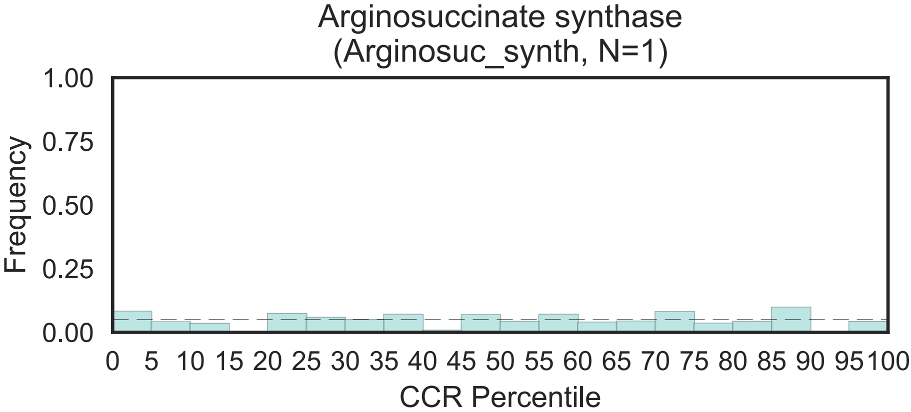
Arfaptin-like domain
(Arfaptin, N=5)
Fisher's OR: 0; Bonferroni p-val: 1

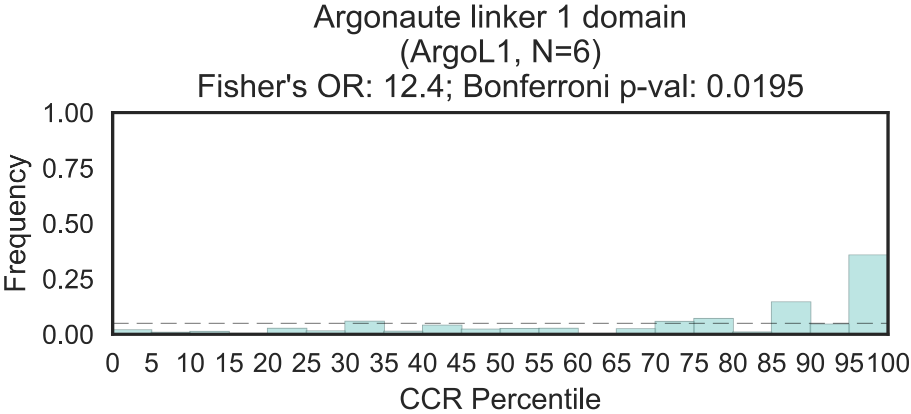

ArgK protein
(ArgK, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



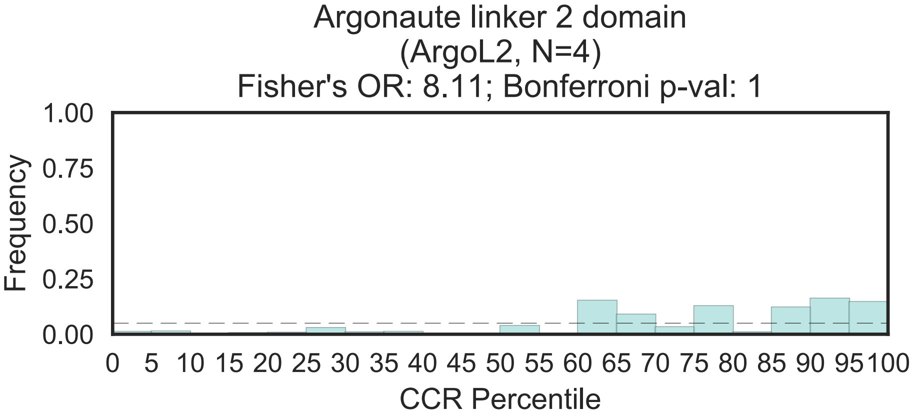
Arginyl tRNA synthetase N terminal domain
(Arg_tRNA_synt_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

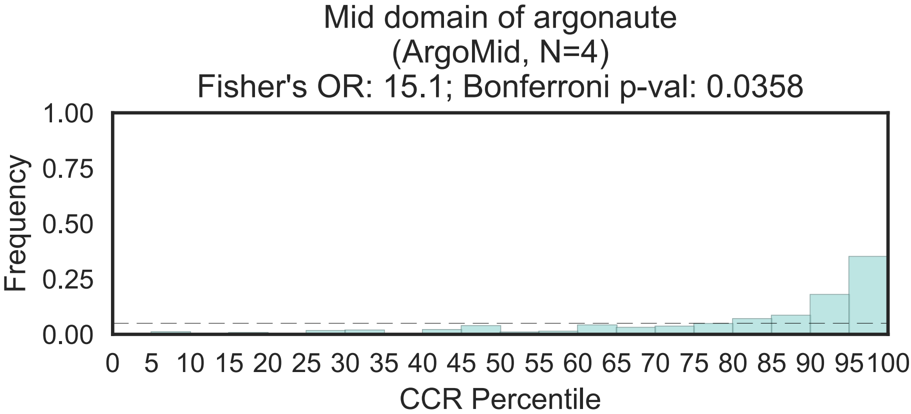

Arginase family
(Arginase, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

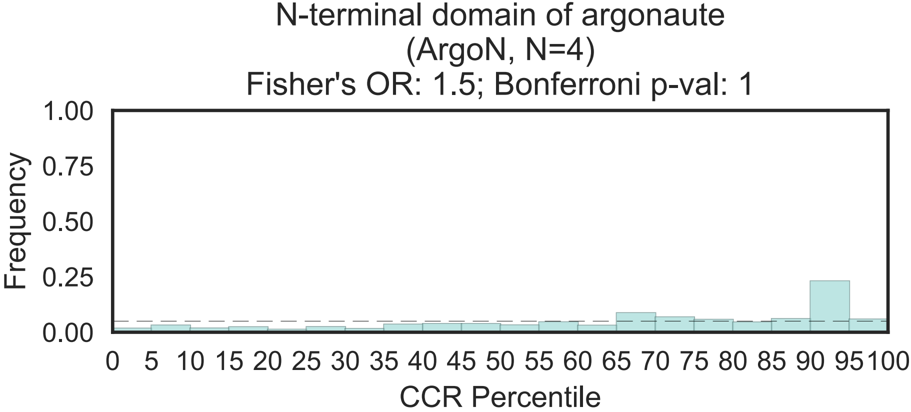

Arginosuccinate synthase
(Arginosuc_synth, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

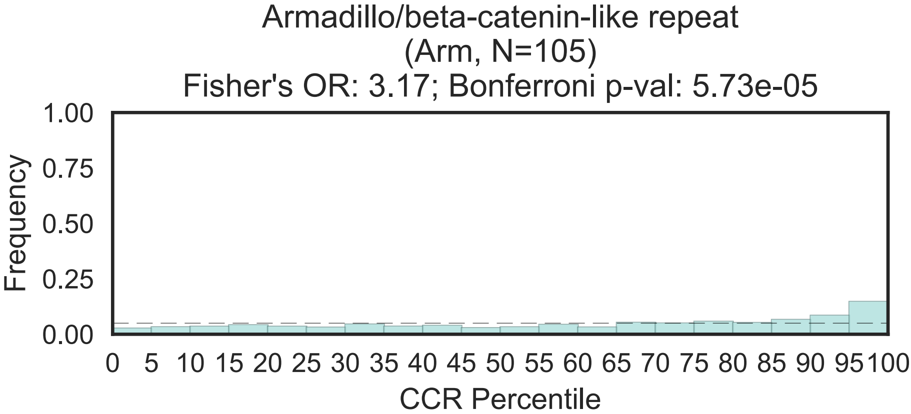


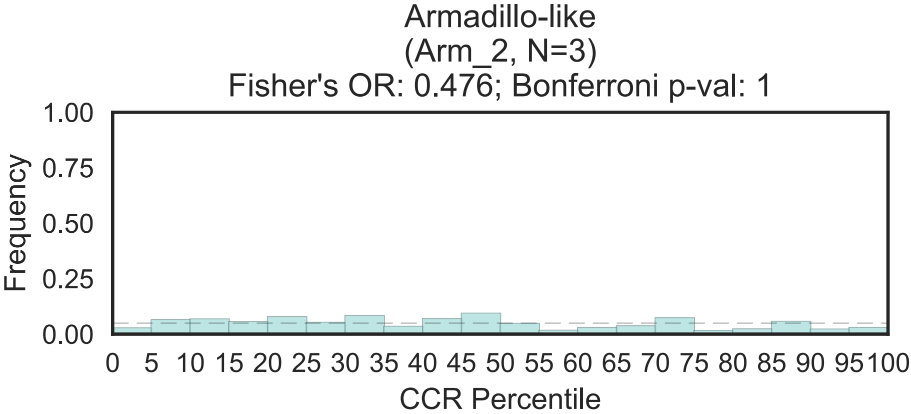
Argonaute linker 1 domain
(ArgoL1, N=6)
Fisher's OR: 12.4; Bonferroni p-val: 0.0195
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Argonaute linker 2 domain
(ArgoL2, N=4)
Fisher's OR: 8.11; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

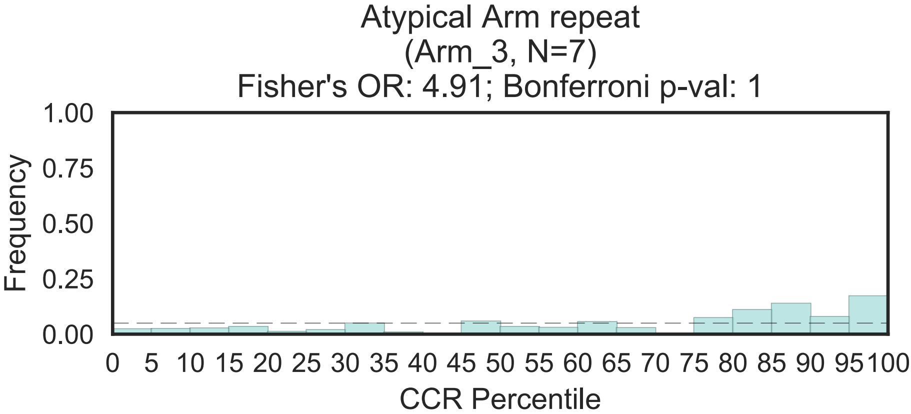

Mid domain of argonaute
(ArgoMid, N=4)
Fisher's OR: 15.1; Bonferroni p-val: 0.0358
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

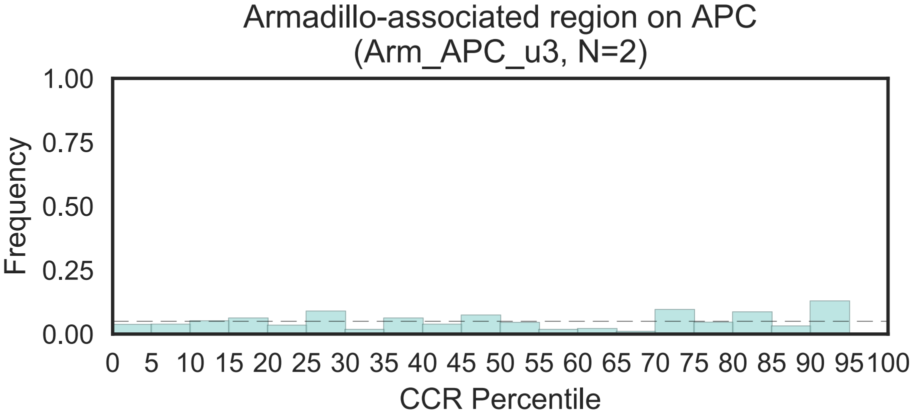

N-terminal domain of argonaute
(ArgoN, N=4)
Fisher's OR: 1.5; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

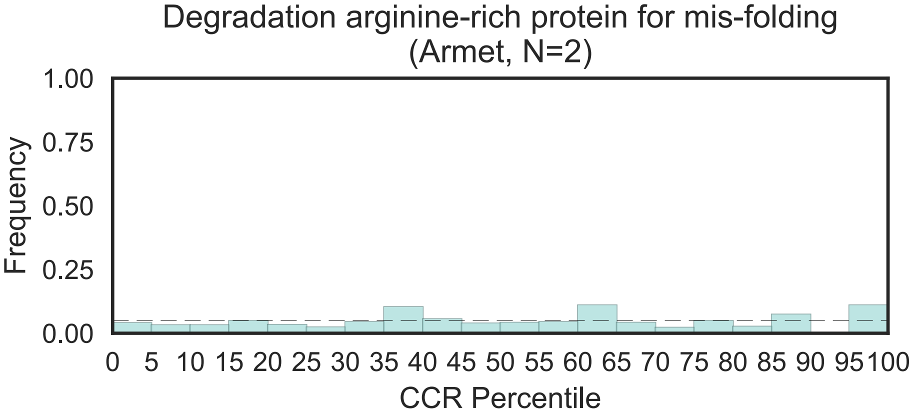

Armadillo/beta-catenin-like repeat
(Arm, N=105)
Fisher's OR: 3.17; Bonferroni p-val: 5.73e-05
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

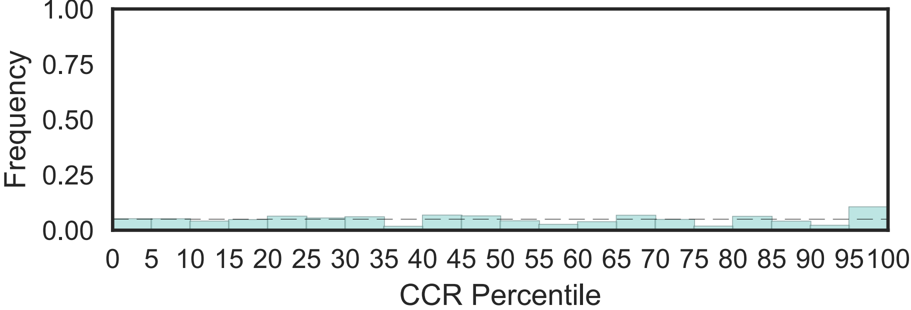


Armadillo-like
(Arm_2, N=3)
Fisher's OR: 0.476; Bonferroni p-val: 1


Atypical Arm repeat
(Arm_3, N=7)
Fisher's OR: 4.91; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

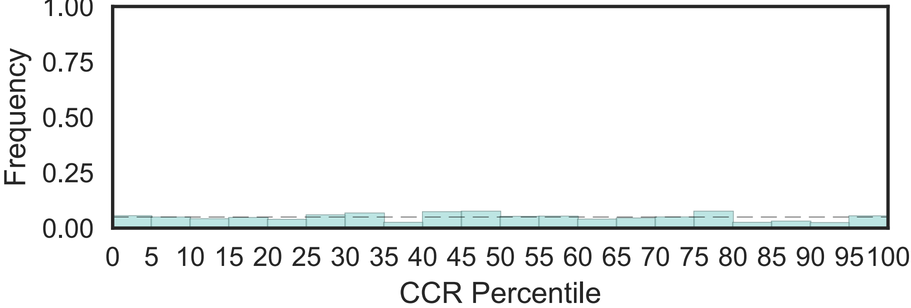

Armadillo-associated region on APC
(Arm_APC_u3, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

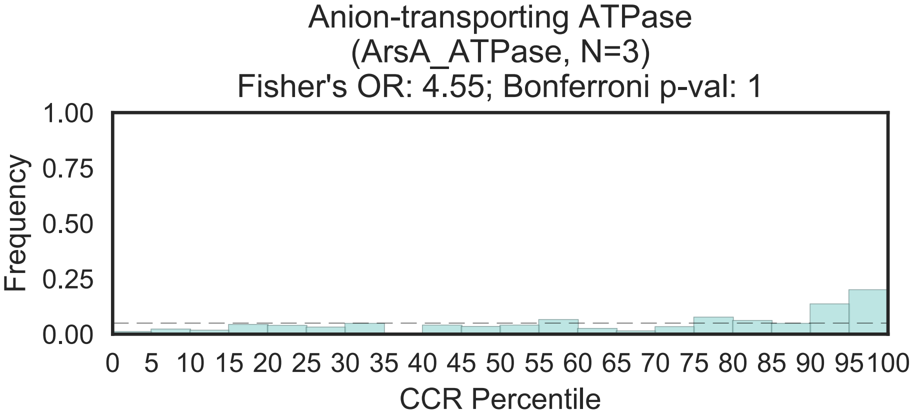

Degradation arginine-rich protein for mis-folding
(Armet, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

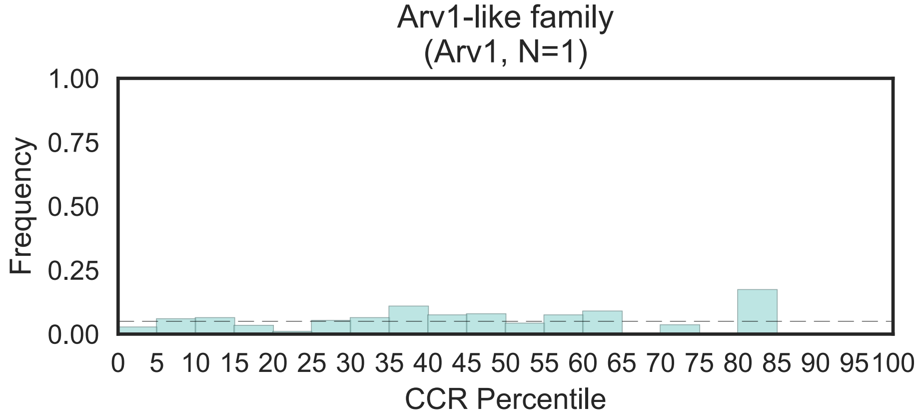


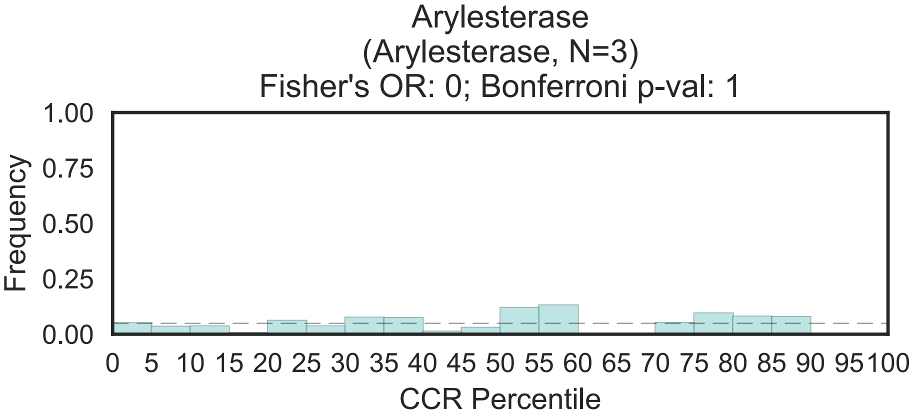
Arrestin (or S-antigen), C-terminal domain
(Arrestin_C, N=9)
Fisher's OR: 1.77; Bonferroni p-val: 1

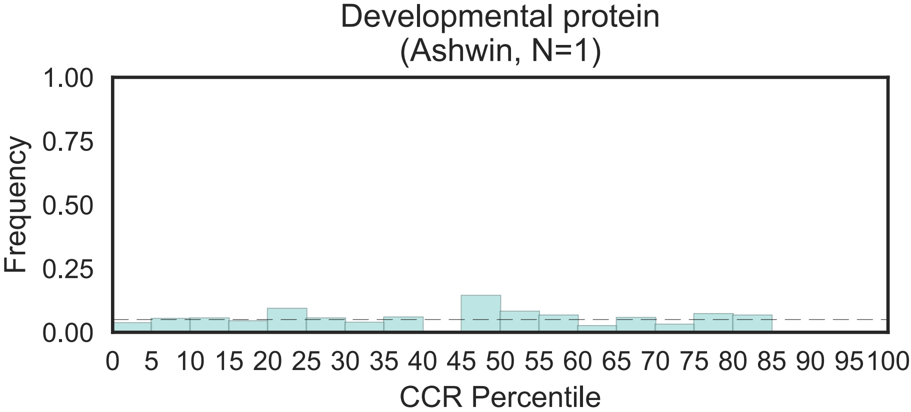
Arrestin (or S-antigen), N-terminal domain
(Arrestin_N, N=10)
Fisher's OR: 1.05; Bonferroni p-val: 1

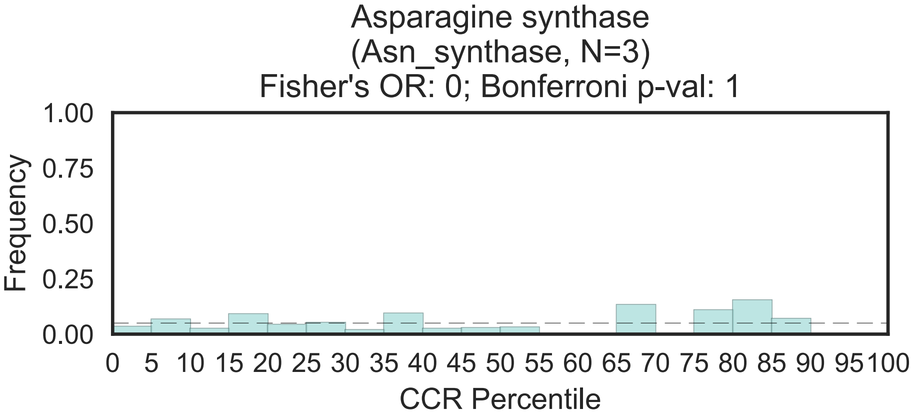



Anion-transporting ATPase
(ArsA_ATPase, N=3)
Fisher's OR: 4.55; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

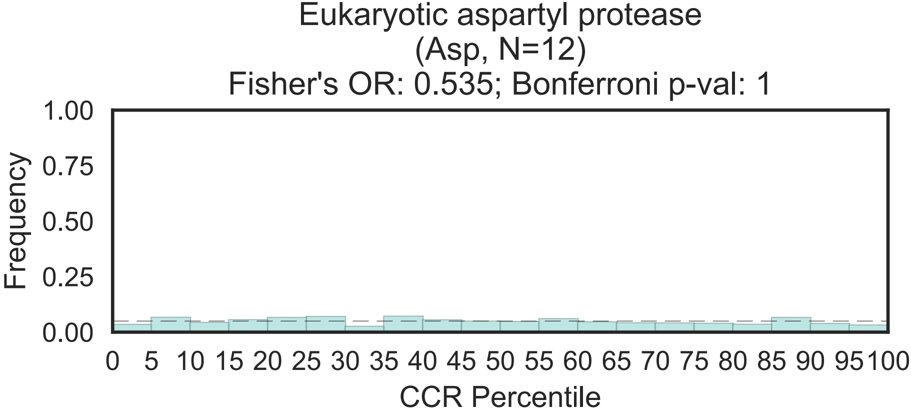

Arv1-like family
(Arv1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

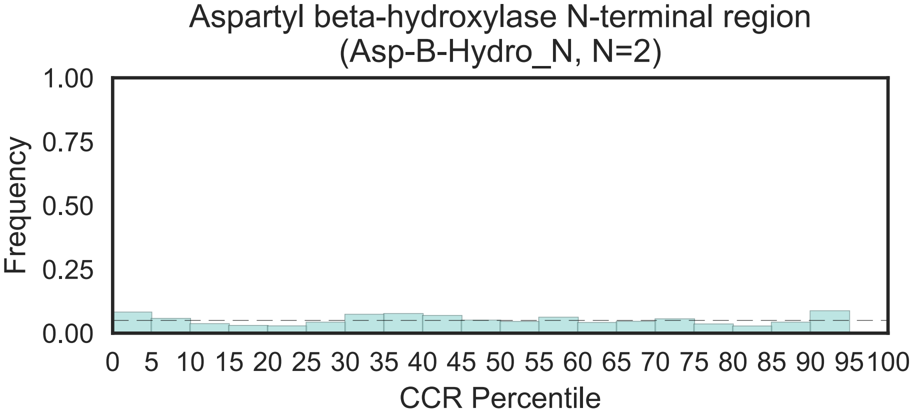

Arylesterase
(Arylesterase, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

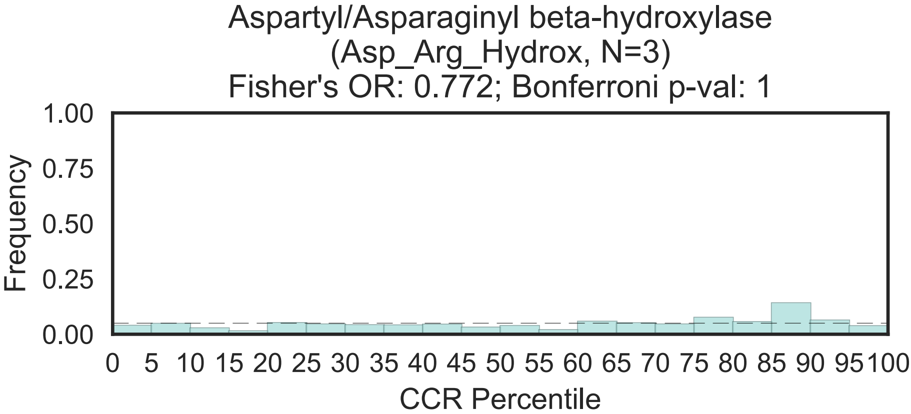

Developmental protein
(Ashwin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

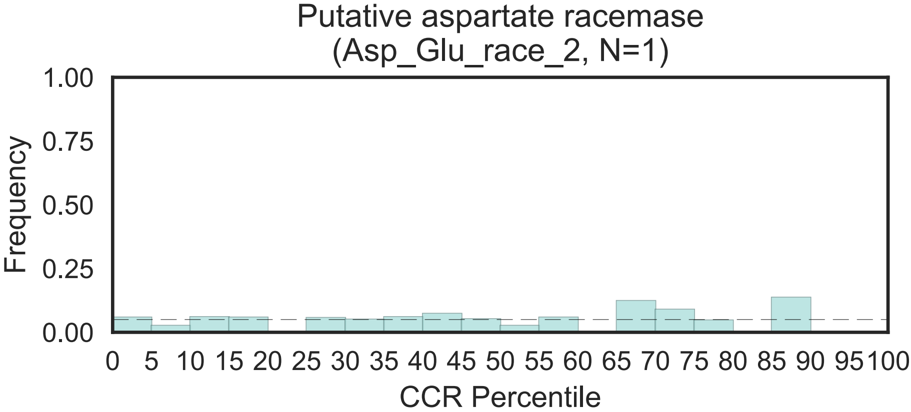


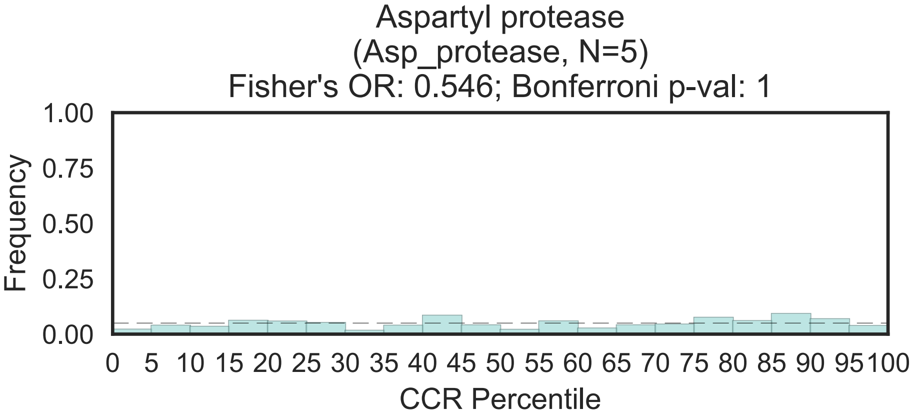
Asparagine synthase
(Asn_synthase, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

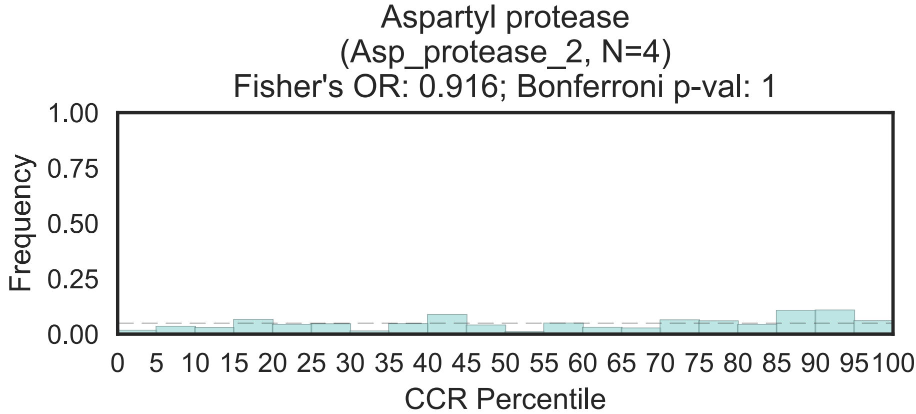

Eukaryotic aspartyl protease
(Asp, N=12)
Fisher's OR: 0.535; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Aspartyl beta-hydroxylase N-terminal region
(Asp-B-Hydro_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

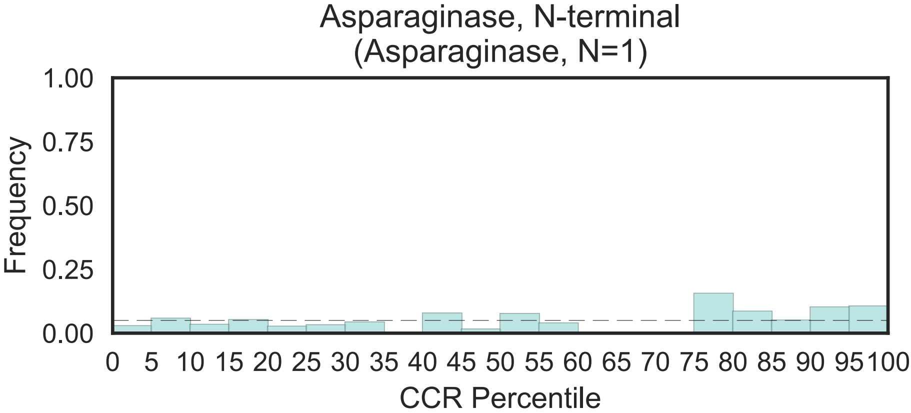

Aspartyl/Asparaginyl beta-hydroxylase
(Asp_Arg_Hydrox, N=3)
Fisher's OR: 0.772; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

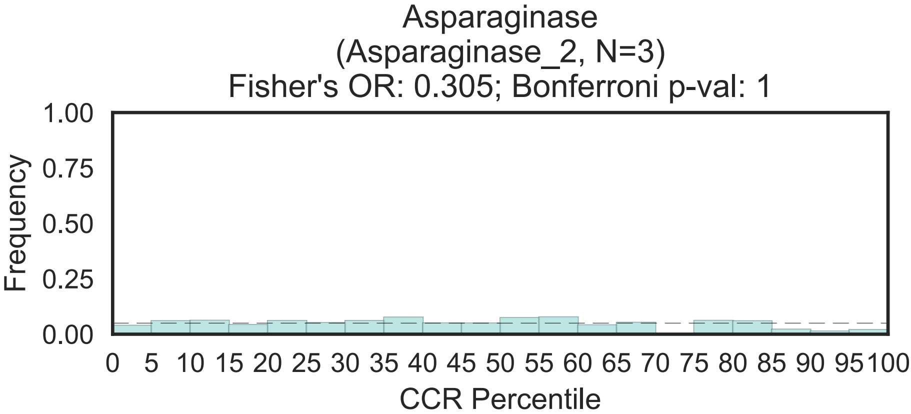

Putative aspartate racemase
(Asp_Glu_race_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

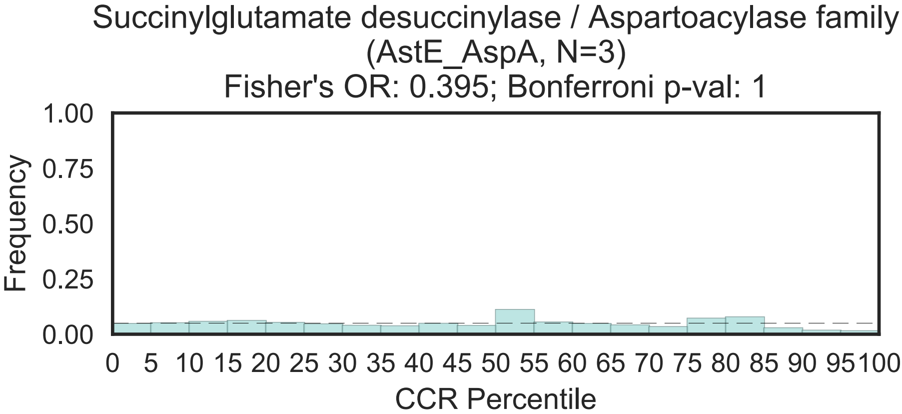

Aspartyl protease
(Asp_protease, N=5)
Fisher's OR: 0.546; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

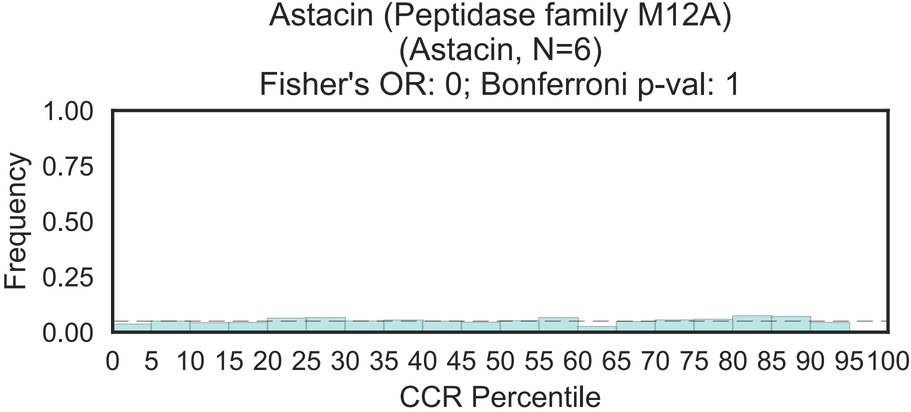


Aspartyl protease
(Asp_protease_2, N=4)
Fisher's OR: 0.916; Bonferroni p-val: 1

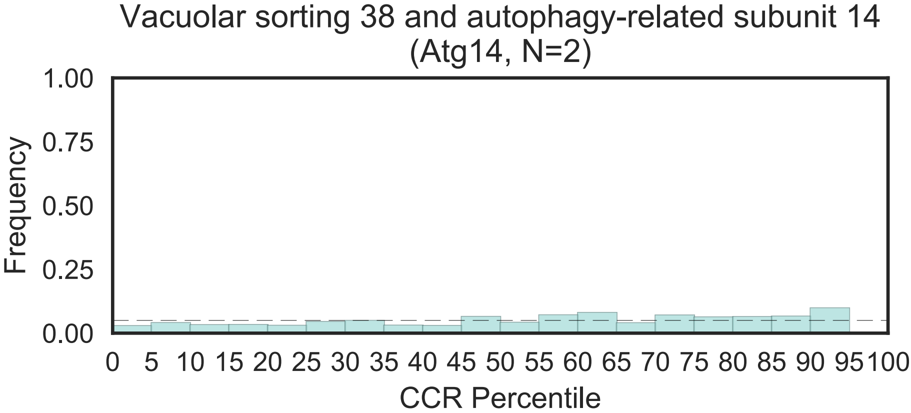

Asparaginase, N-terminal
(Asparaginase, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

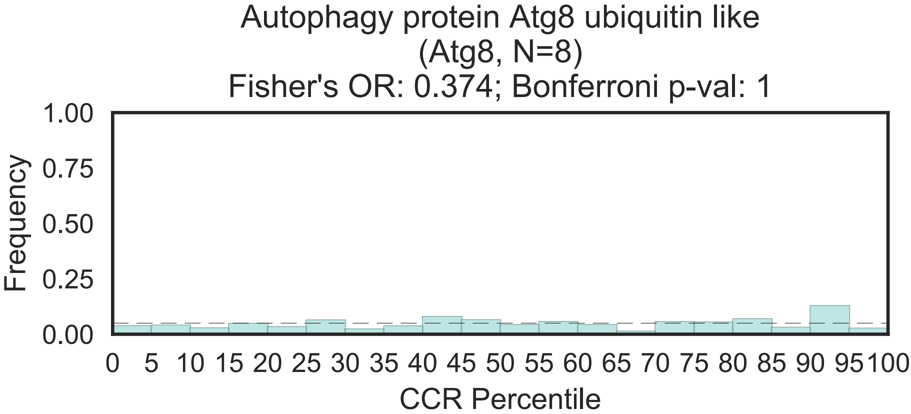

Asparaginase
(Asparaginase_2, N=3)
Fisher's OR: 0.305; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Succinylglutamate desuccinylase / Aspartoacylase family
(AstE_AspA, N=3)
Fisher's OR: 0.395; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

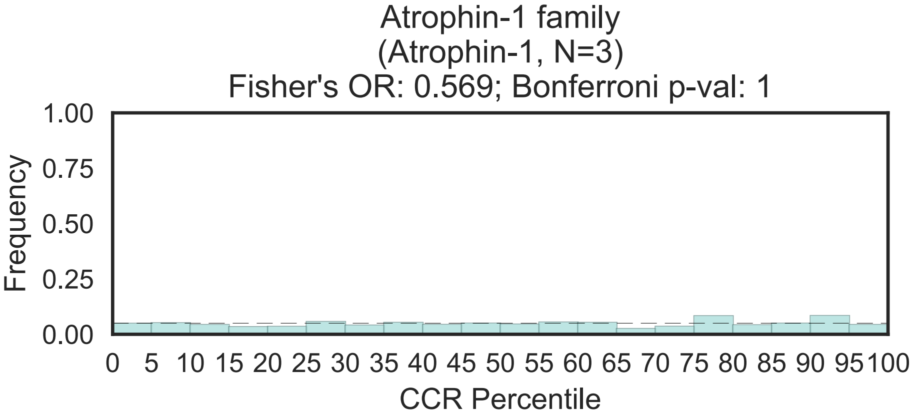


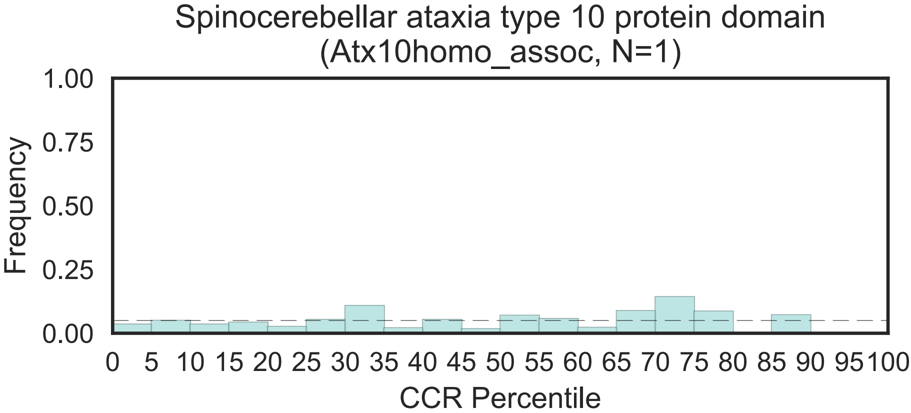
Astacin (Peptidase family M12A)
(Astacin, N=6)
Fisher's OR: 0; Bonferroni p-val: 1

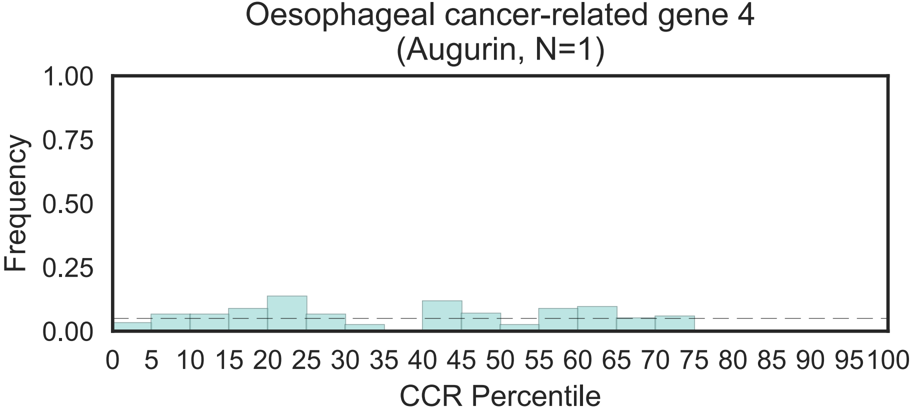

Vacuolar sorting 38 and autophagy-related subunit 14
(Atg14, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

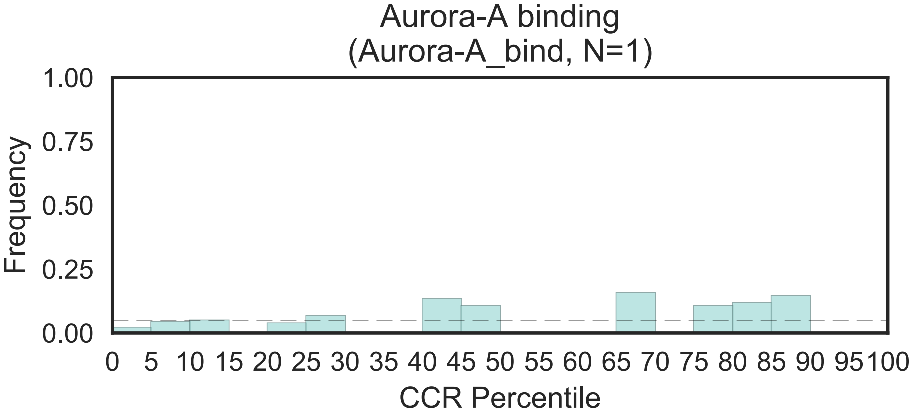


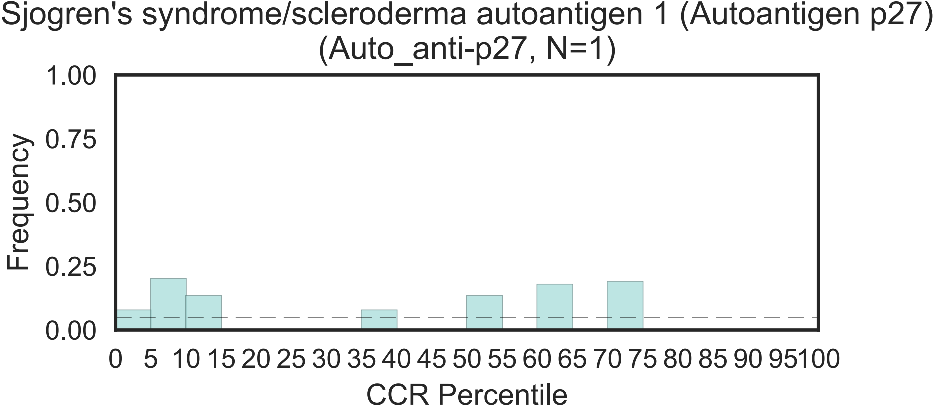
Autophagy protein Atg8 ubiquitin like
(Atg8, N=8)
Fisher's OR: 0.374; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

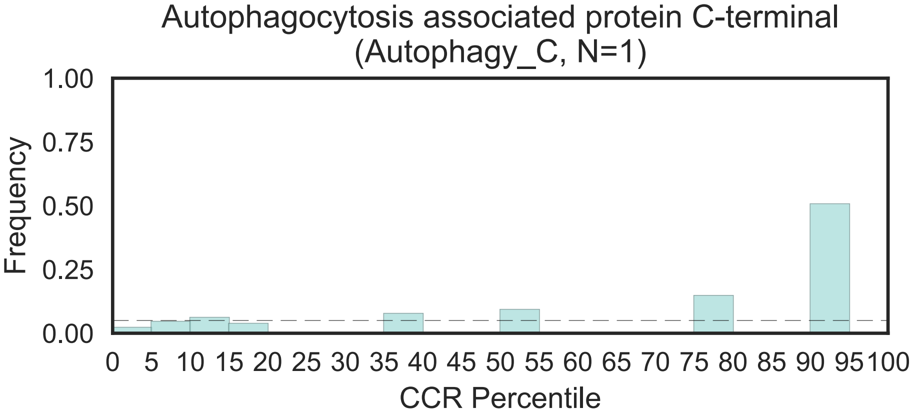

Atrophin-1 family
(Atrophin-1, N=3)
Fisher's OR: 0.569; Bonferroni p-val: 1

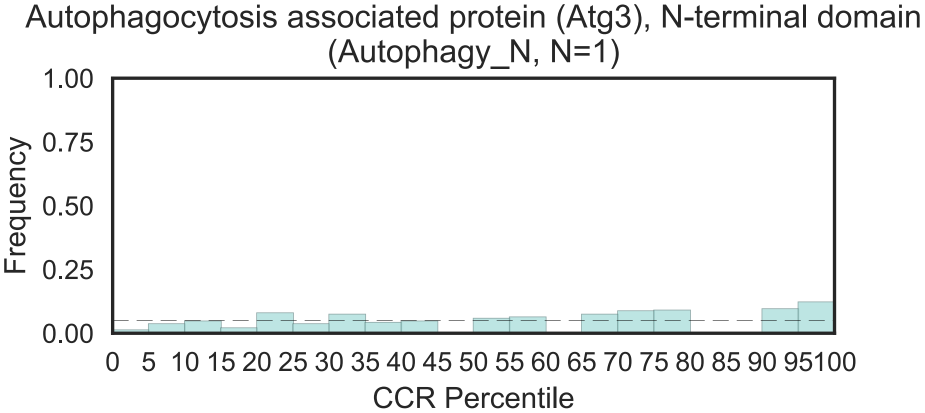

Spinocerebellar ataxia type 10 protein domain
(Atx10homo_assoc, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

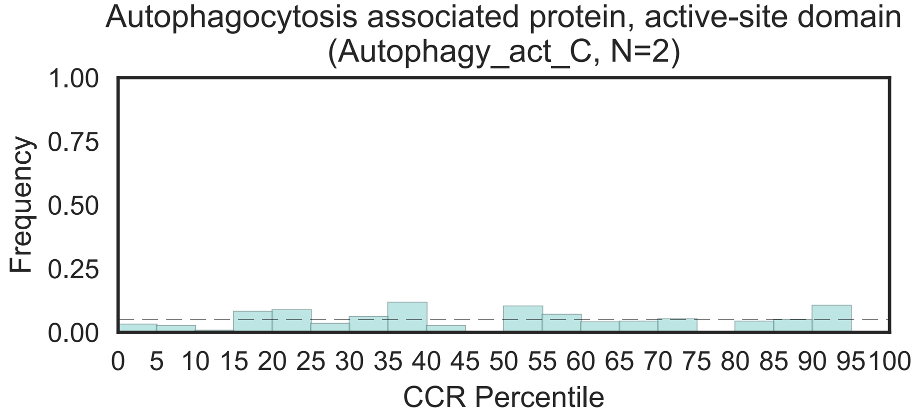

Oesophageal cancer-related gene 4
(Augurin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

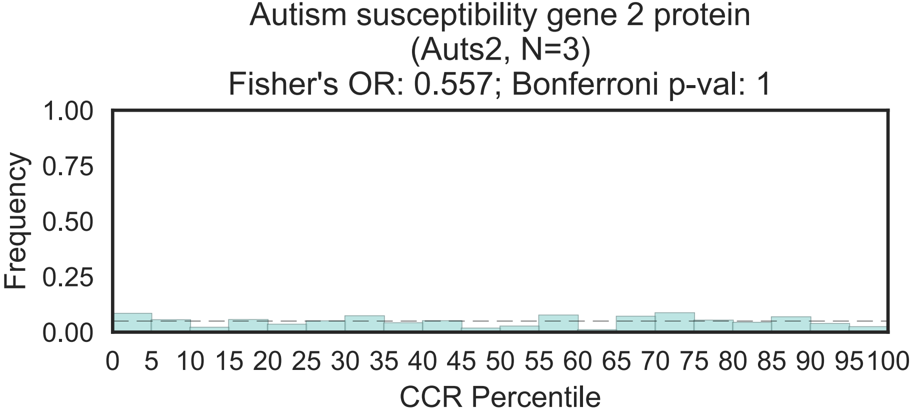

Aurora-A binding
(Aurora-A_bind, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

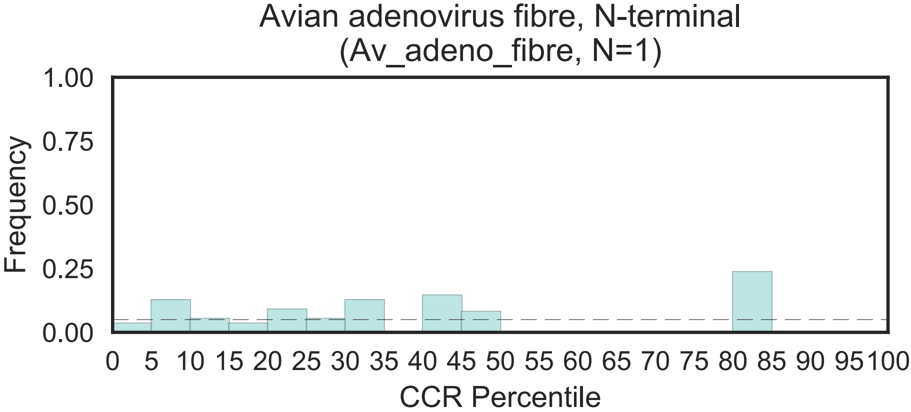

Sjogren's syndrome/scleroderma autoantigen 1 (Autoantigen p27)
(Auto_anti-p27, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Autophagocytosis associated protein C-terminal
(Autophagy_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

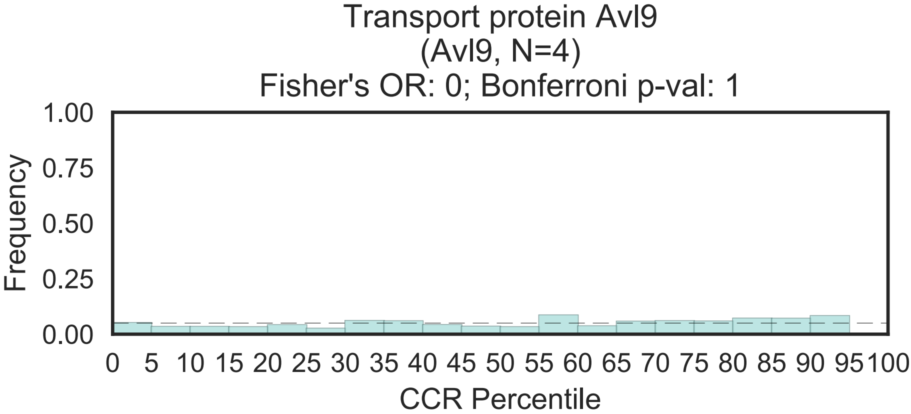

Autophagocytosis associated protein (Atg3), N-terminal domain
(Autophagy_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

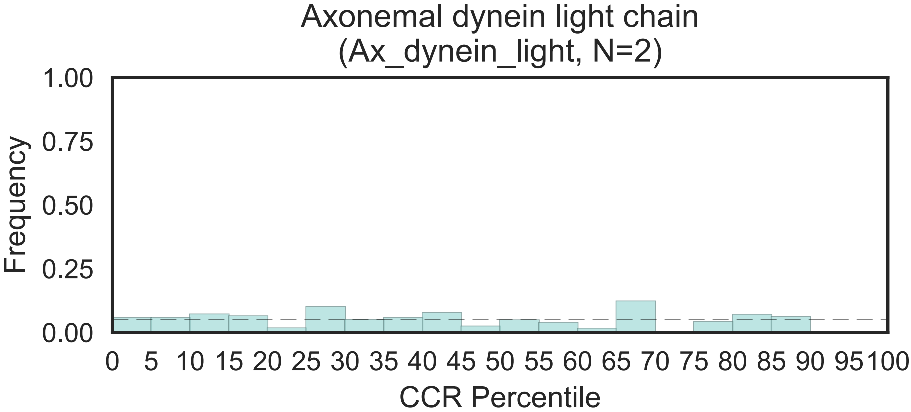

Autophagocytosis associated protein, active-site domain
(Autophagy_act_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

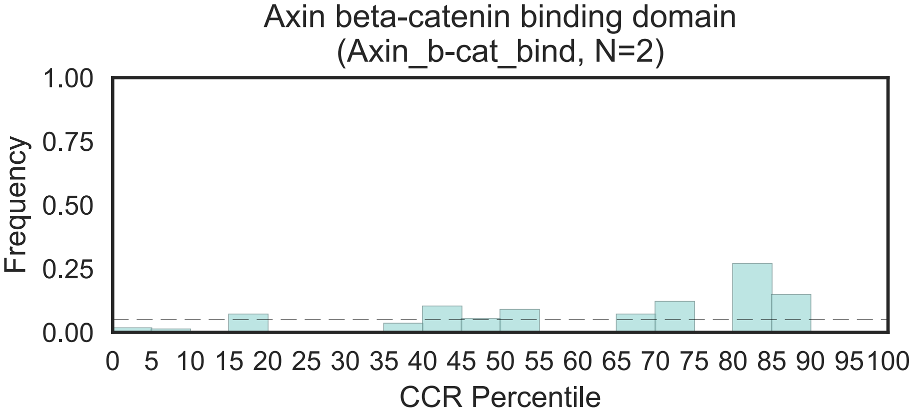

Autism susceptibility gene 2 protein
(Auts2, N=3)
Fisher's OR: 0.557; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

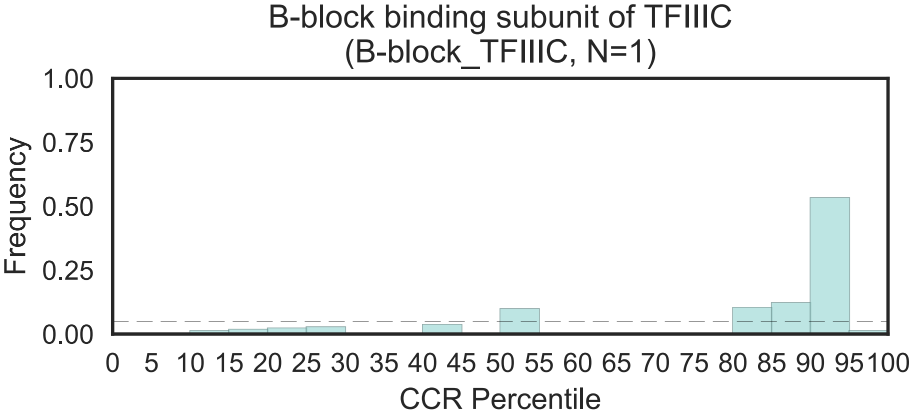


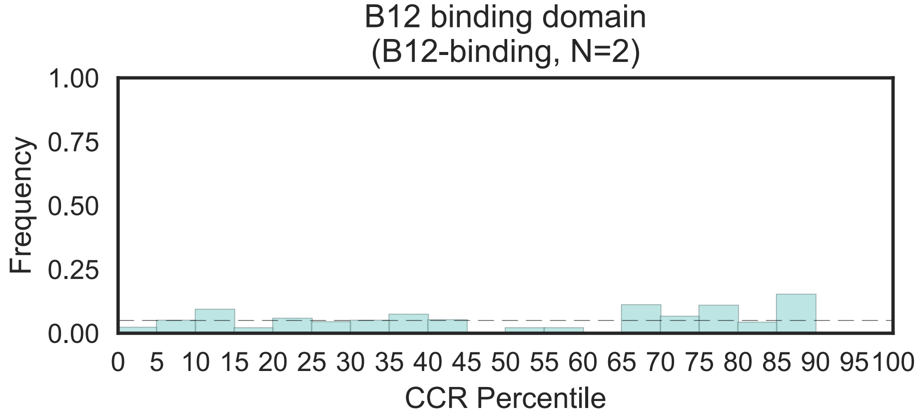
Avian adenovirus fibre, N-terminal
(Av_adeno_fibre, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

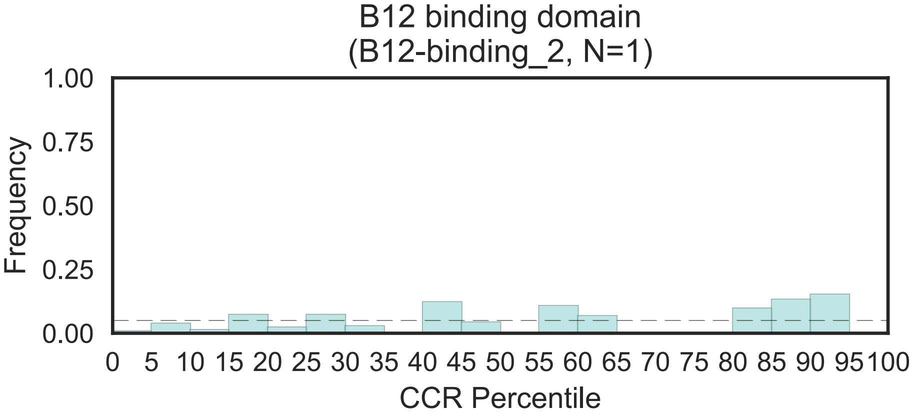

Transport protein Avl9
(Avl9, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

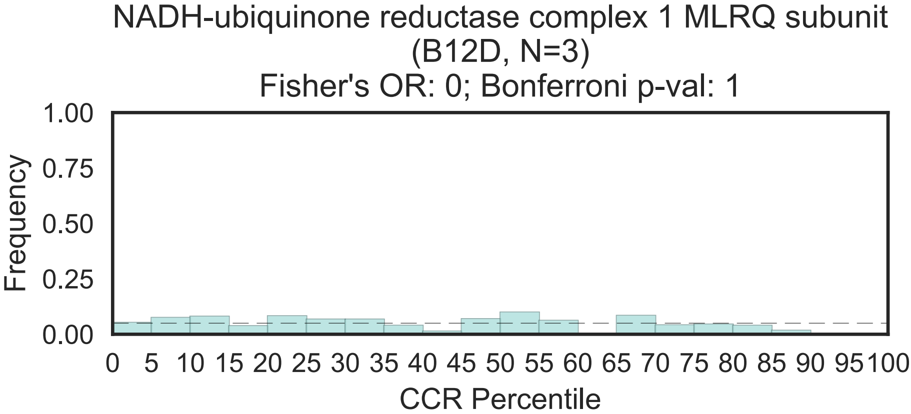

Axonemal dynein light chain
(Ax_dynein_light, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

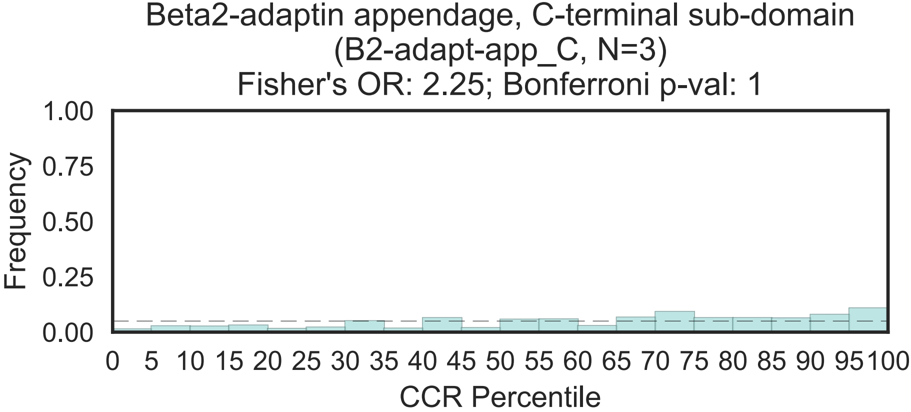

Axin beta-catenin binding domain
(Axin_b-cat_bind, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

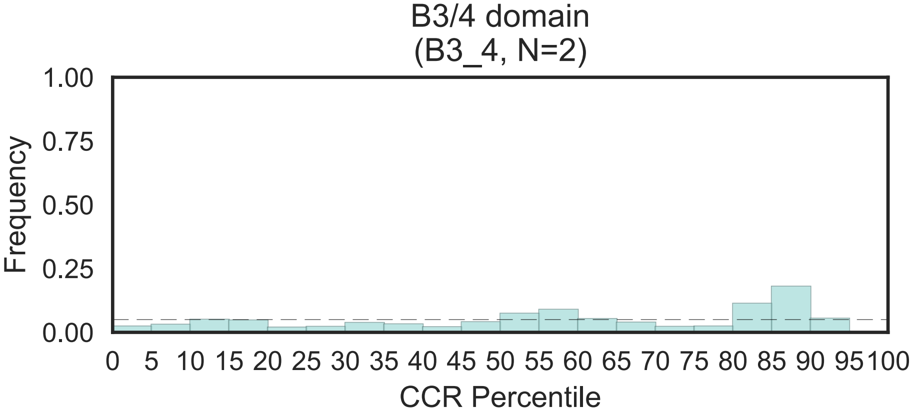

B-block binding subunit of TFIIIC
(B-block_TFIIIC, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

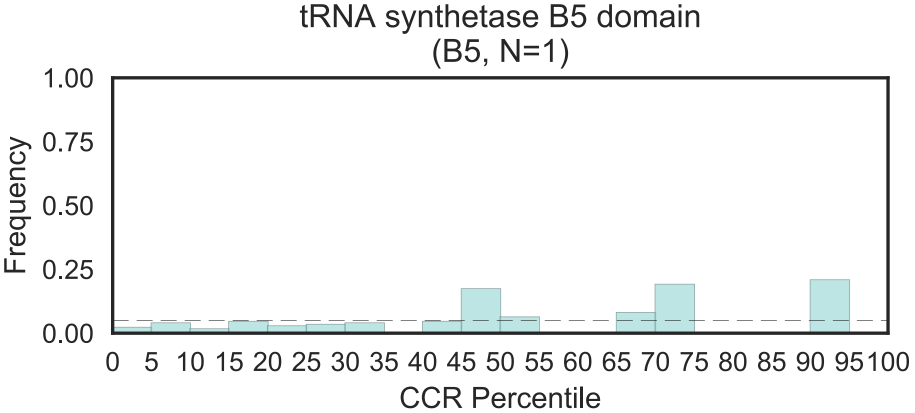

B12 binding domain
(B12-binding, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

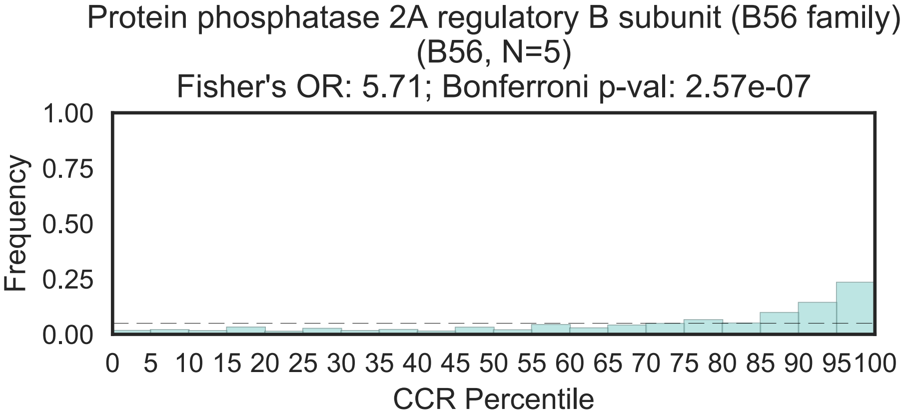

B12 binding domain
(B12-binding_2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

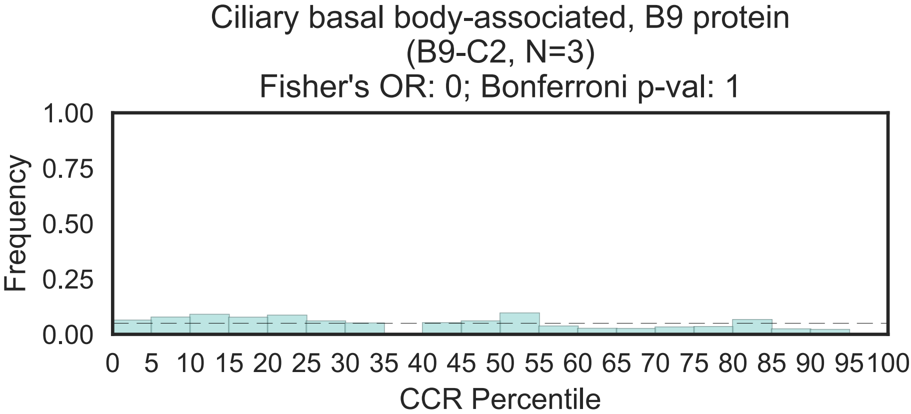

NADH-ubiquinone reductase complex 1 MLRQ subunit
(B12D, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

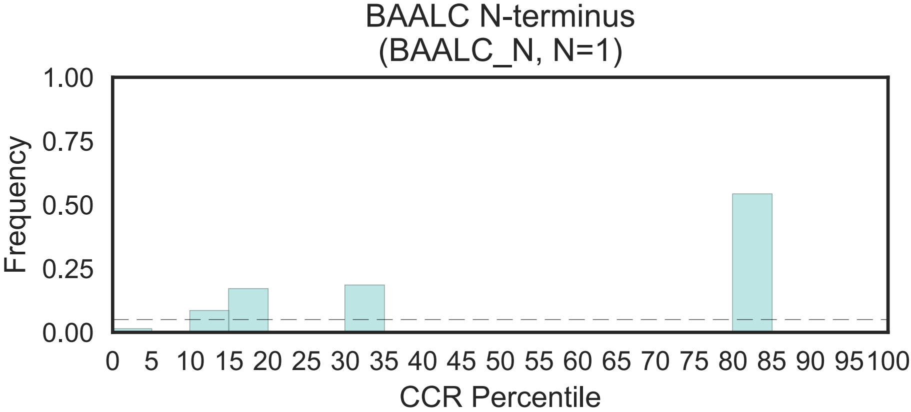

Beta2-adaptin appendage, C-terminal sub-domain
(B2-adapt-app_C, N=3)
Fisher's OR: 2.25; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

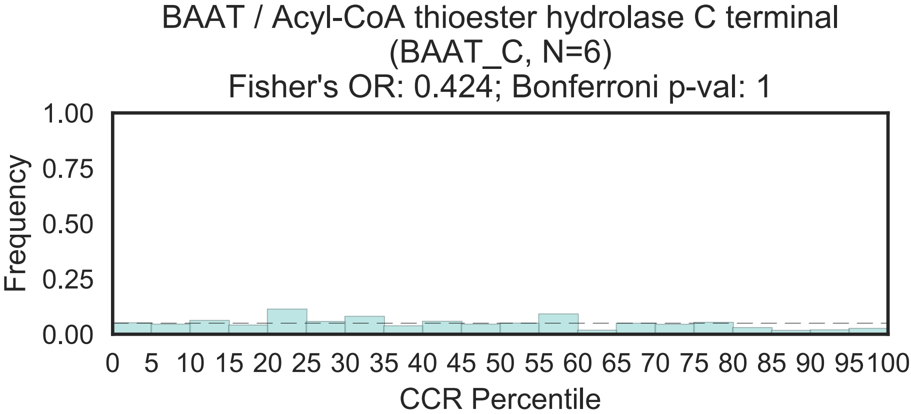

B3/4 domain
(B3_4, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

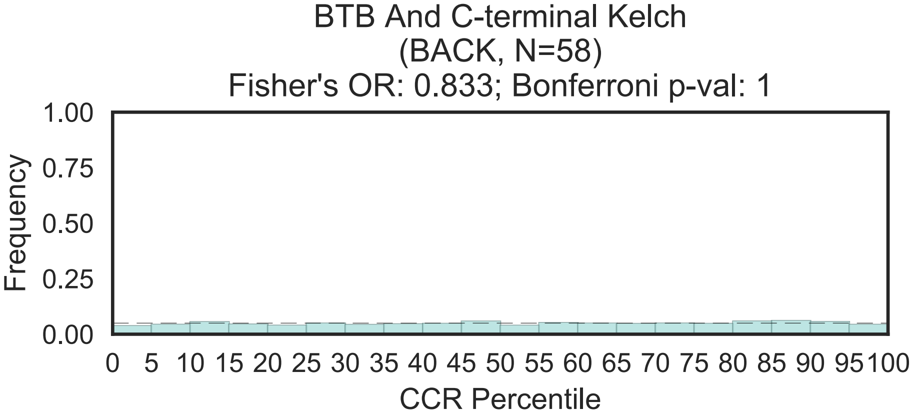

tRNA synthetase B5 domain
(B5, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

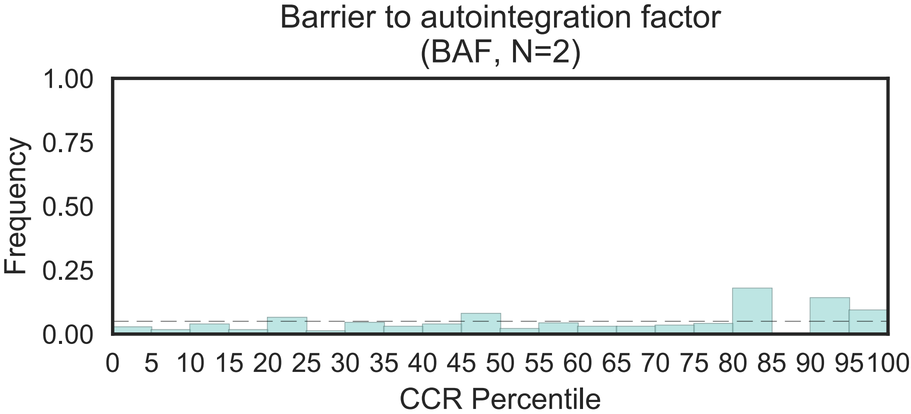

Protein phosphatase 2A regulatory B subunit (B56 family)
(B56, N=5)
Fisher's OR: 5.71; Bonferroni p-val: 2.57e-07
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

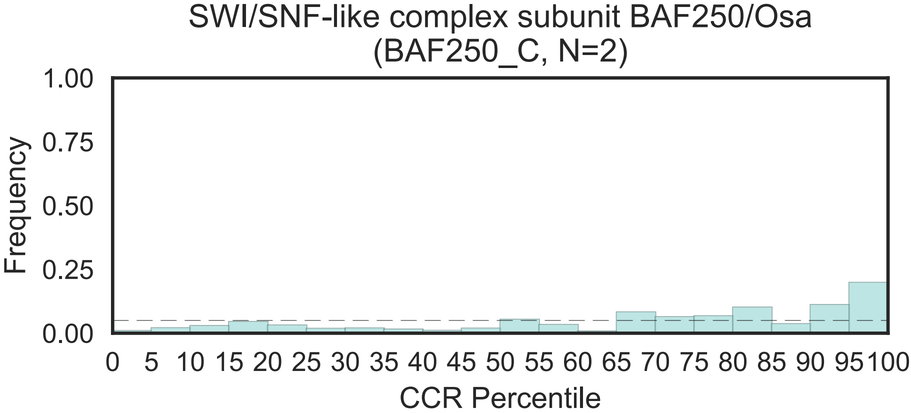

Ciliary basal body-associated, B9 protein
(B9-C2, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

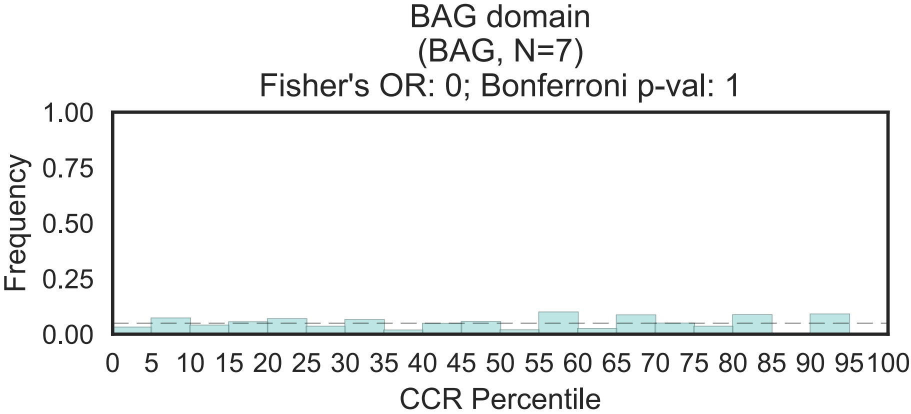

BAALC N-terminus
(BAALC_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

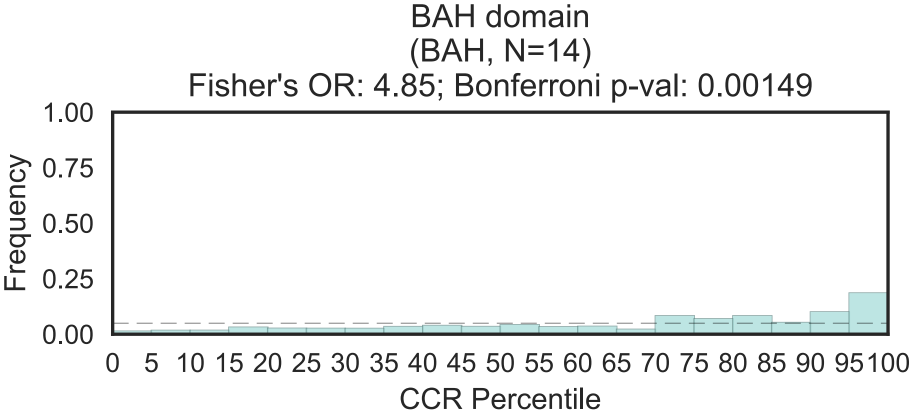
BAAT / Acyl-CoA thioester hydrolase C terminal
(BAAT_C, N=6)
Fisher's OR: 0.424; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


BTB And C-terminal Kelch
(BACK, N=58)
Fisher's OR: 0.833; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

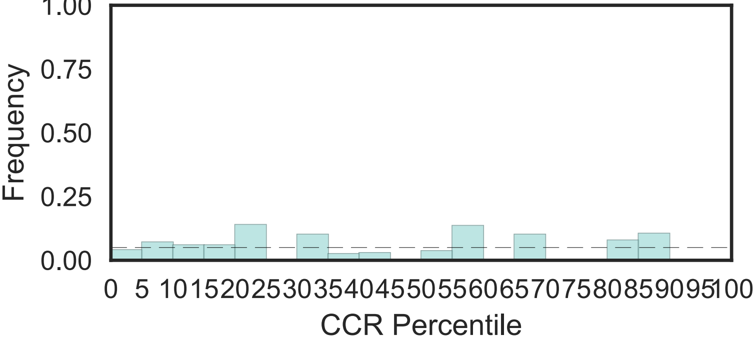

Barrier to autointegration factor
(BAF, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

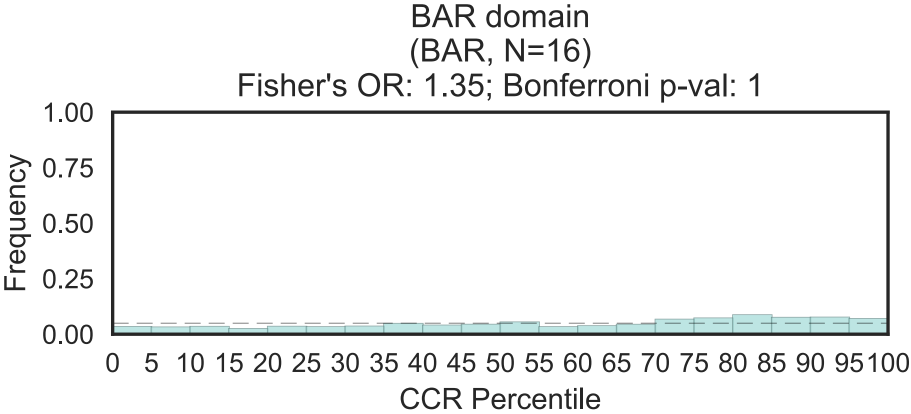

SWI/SNF-like complex subunit BAF250/Osa
(BAF250_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


BAG domain
(BAG, N=7)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

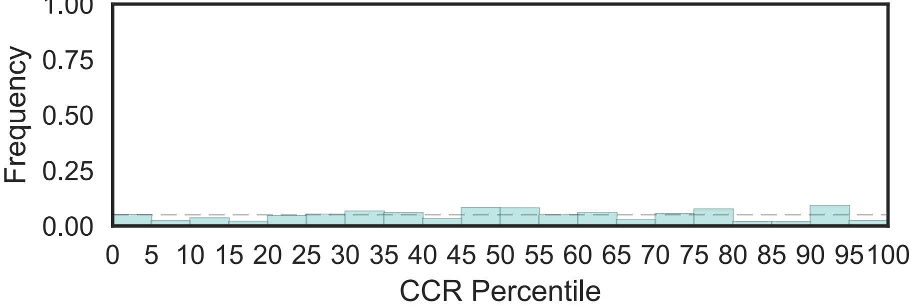

BAH domain
(BAH, N=14)
Fisher's OR: 4.85; Bonferroni p-val: 0.00149
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

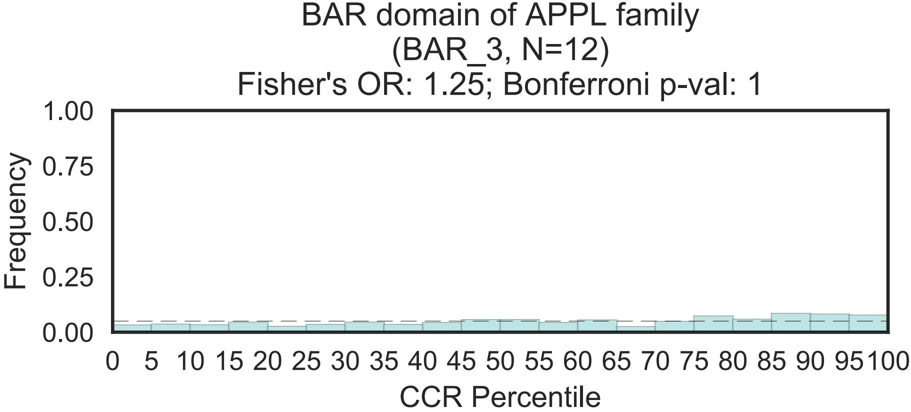
BMP and activin membrane-bound inhibitor (BAMBI) N-terminal domain (BAMBI, N=1)



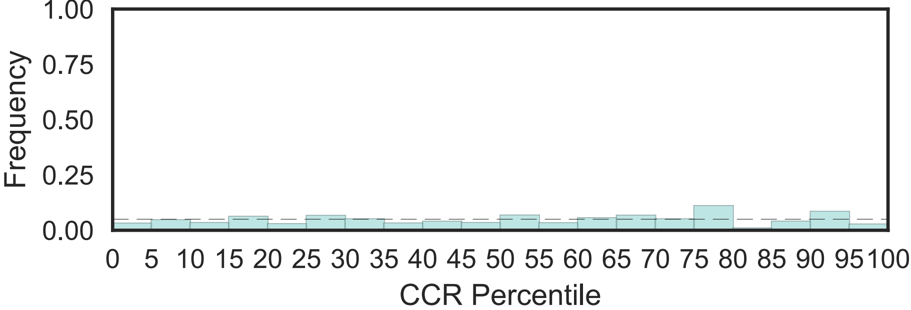

BAR domain
(BAR, N=16)
Fisher's OR: 1.35; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

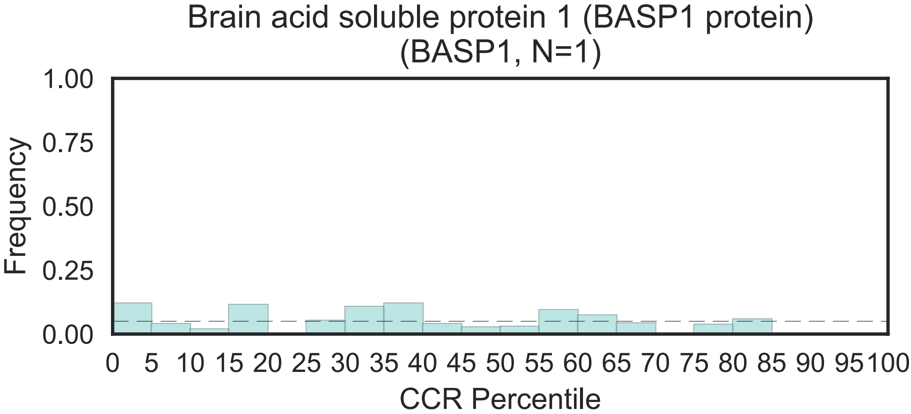
Bin/amphiphysin/Rvs domain for vesicular trafficking (BAR_2, N=4) Fisher's OR: 0.549; Bonferroni p-val: 1

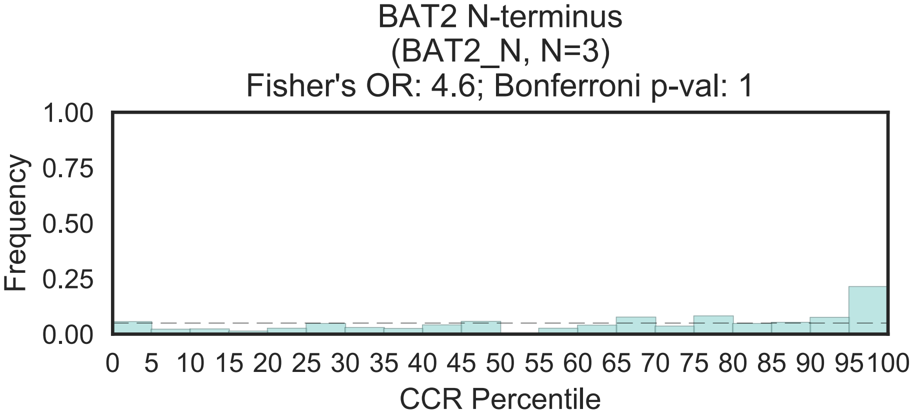


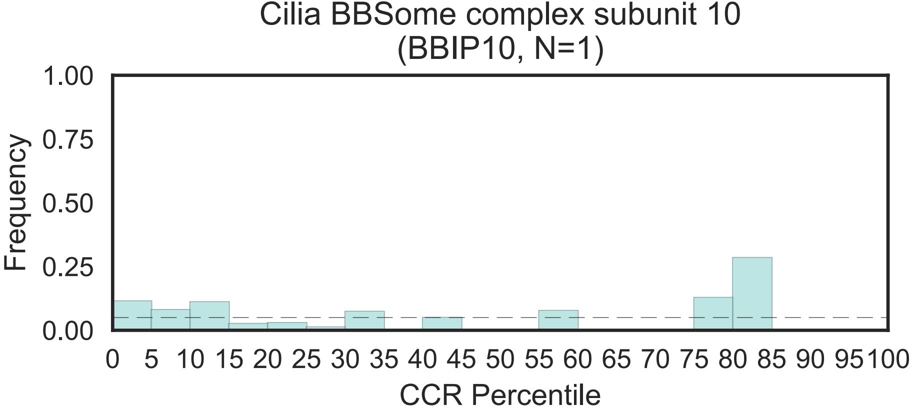

BAR domain of APPL family
(BAR_3, N=12)
Fisher's OR: 1.25; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

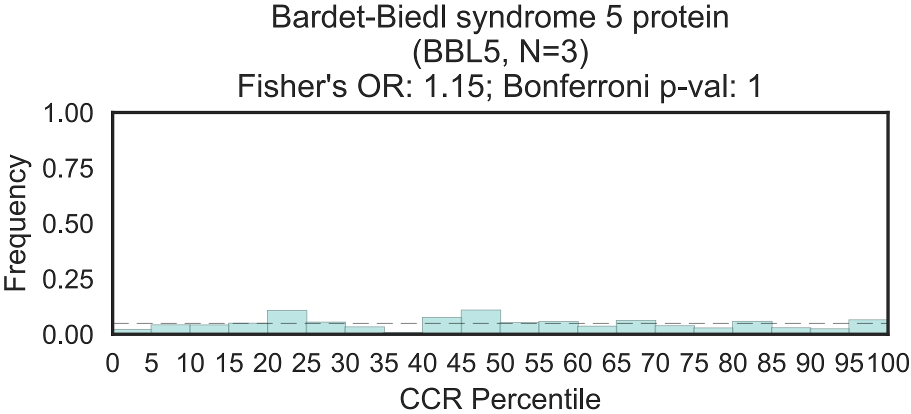
WASP-binding domain of Sorting nexin protein
(BAR_3_WASP_bdg, N=3)
Fisher's OR: 0.393; Bonferroni p-val: 1

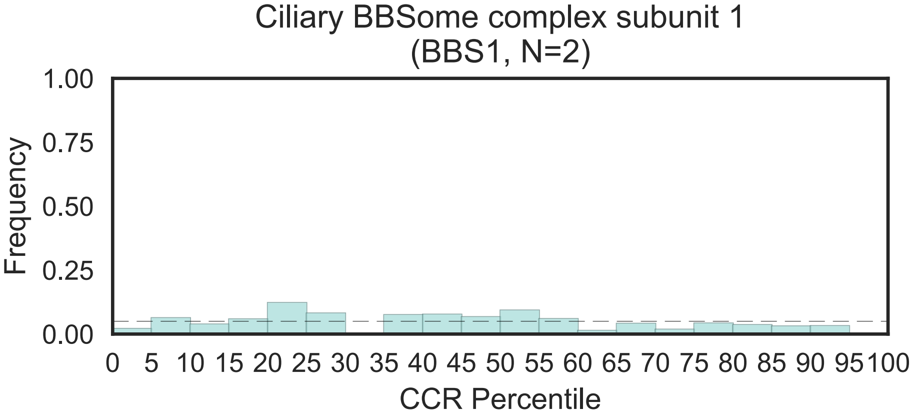


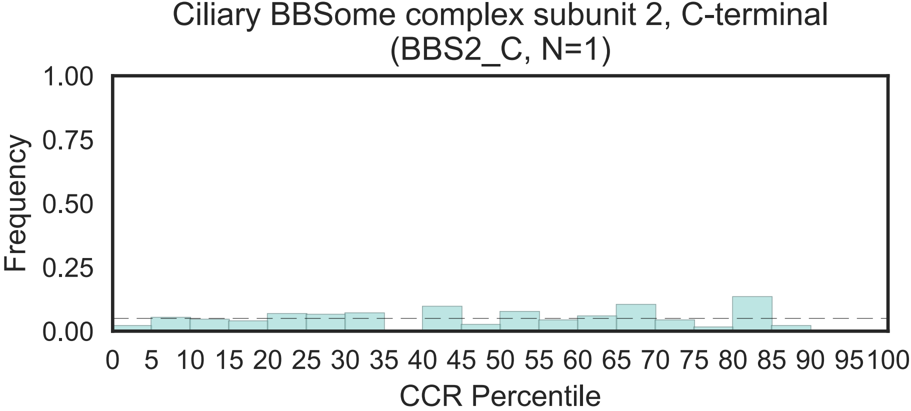

Brain acid soluble protein 1 (BASP1 protein)
(BASP1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


BAT2 N-terminus
(BAT2_N, N=3)
Fisher's OR: 4.6; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

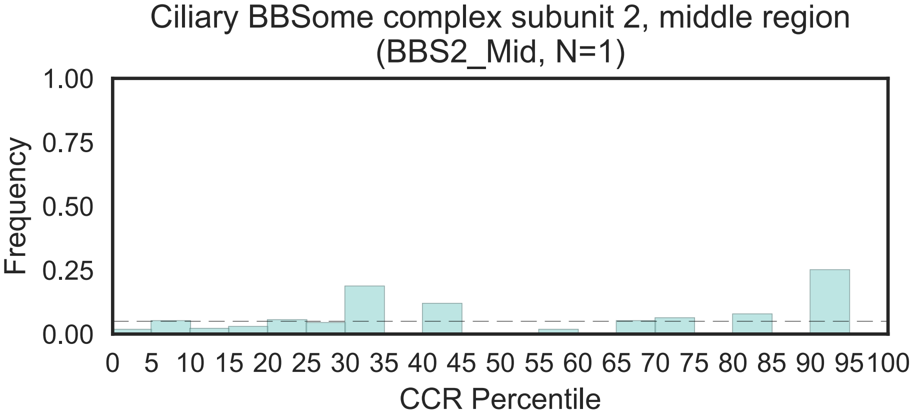

Cilia BBSome complex subunit 10
(BBIP10, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

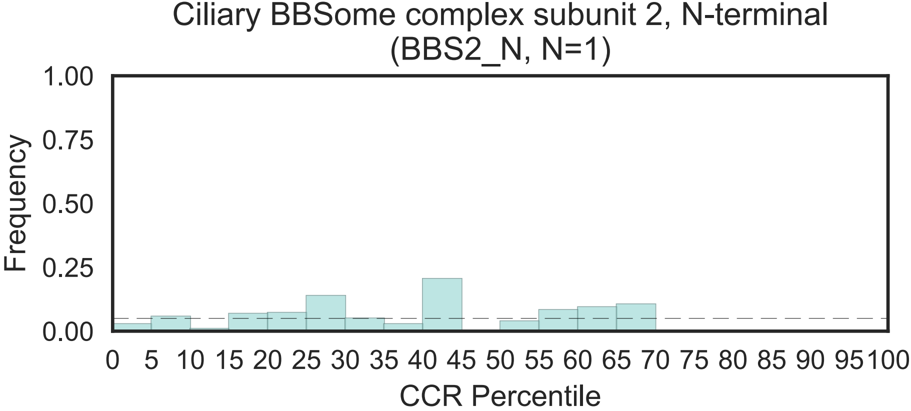

Bardet-Biedl syndrome 5 protein
(BBL5, N=3)
Fisher's OR: 1.15; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

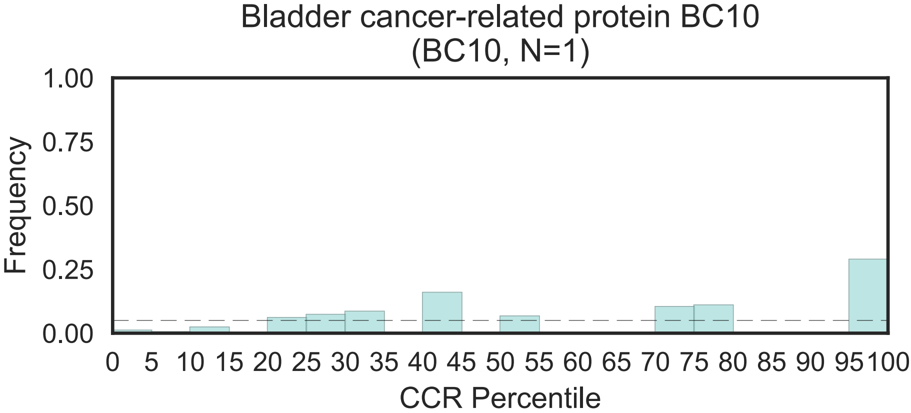

Ciliary BBSome complex subunit 1
(BBS1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

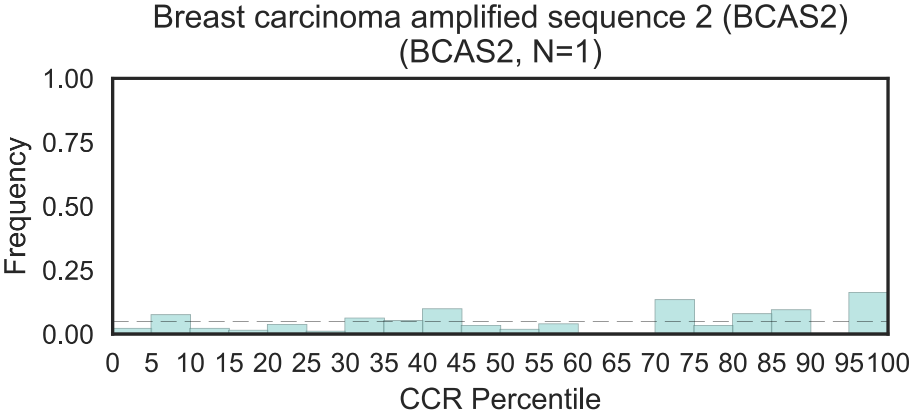


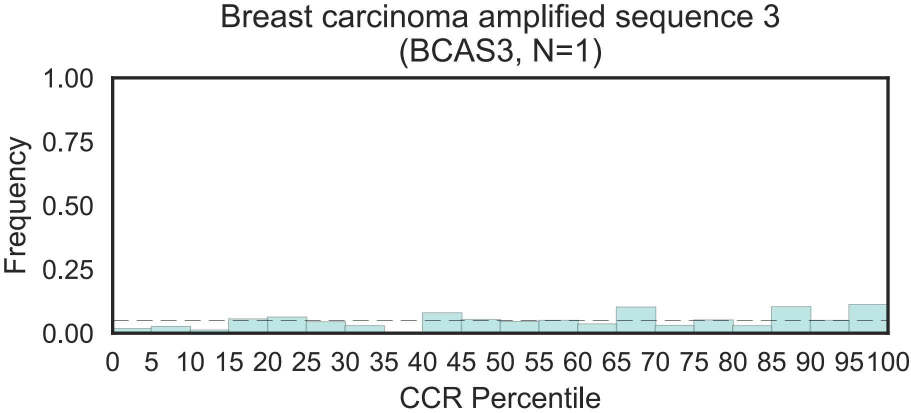
Ciliary BBSome complex subunit 2, C-terminal
(BBS2_C, N=1)


Ciliary BBSome complex subunit 2, middle region
(BBS2_Mid, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

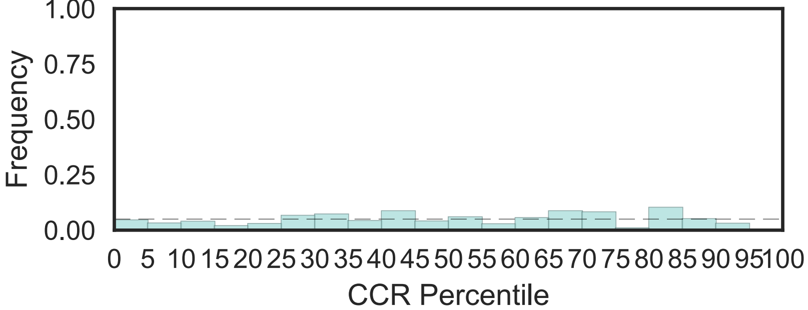

Ciliary BBSome complex subunit 2, N-terminal
(BBS2_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

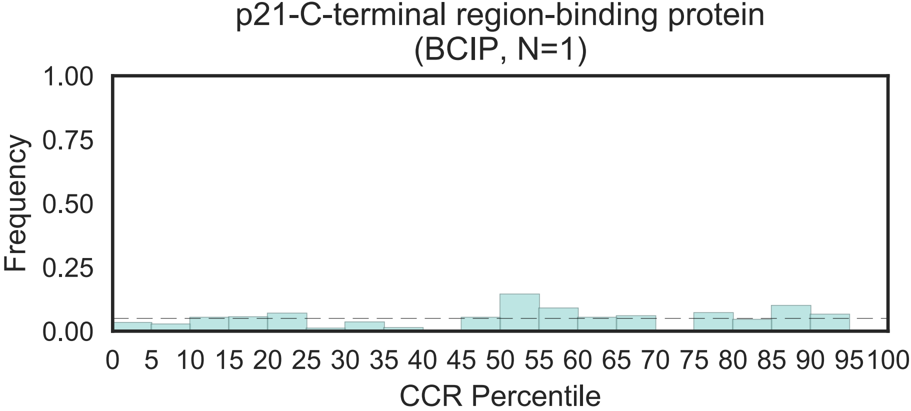

Bladder cancer-related protein BC10
(BC10, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

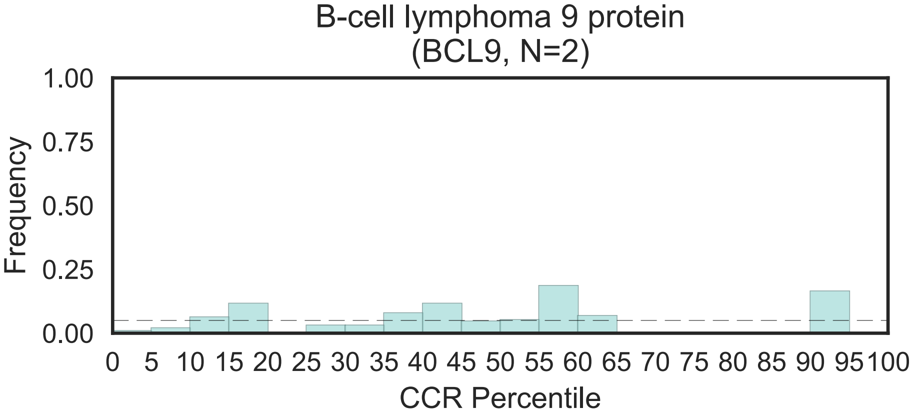

Breast carcinoma amplified sequence 2 (BCAS2)
(BCAS2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

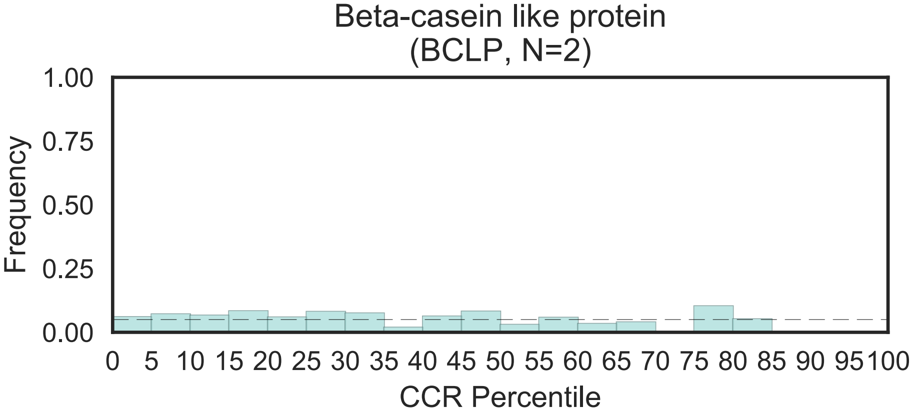

Breast carcinoma amplified sequence 3
(BCAS3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

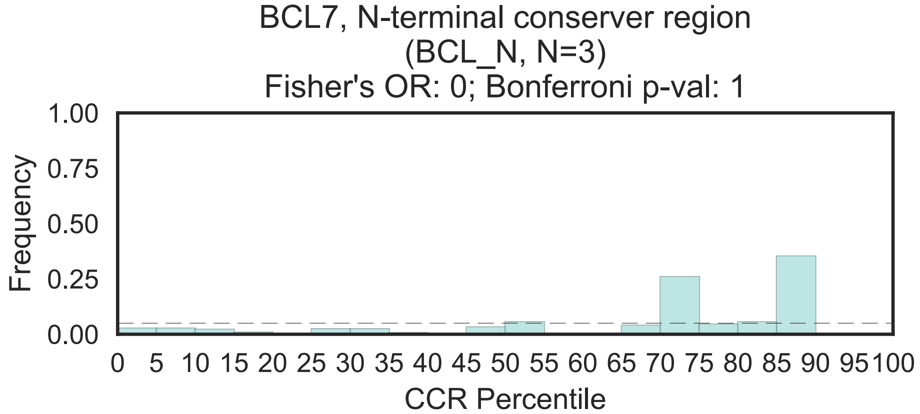
Mitochondrial branched-chain alpha-ketoacid dehydrogenase kinase
(BCDHK_Adom3, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

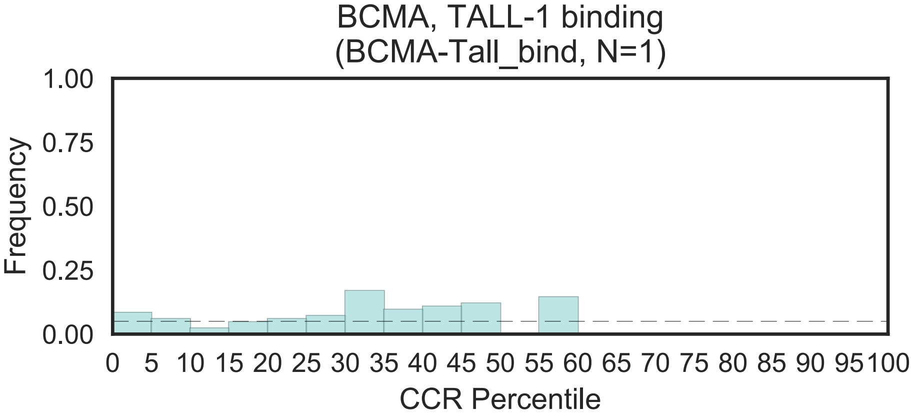


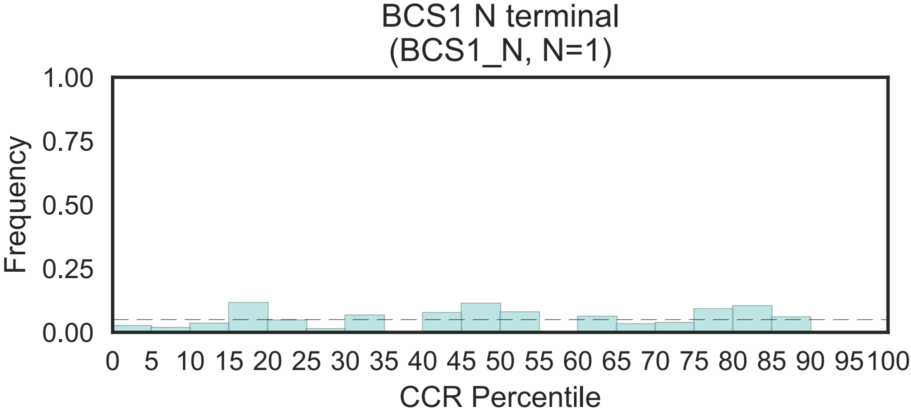

p21-C-terminal region-binding protein
(BCIP, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

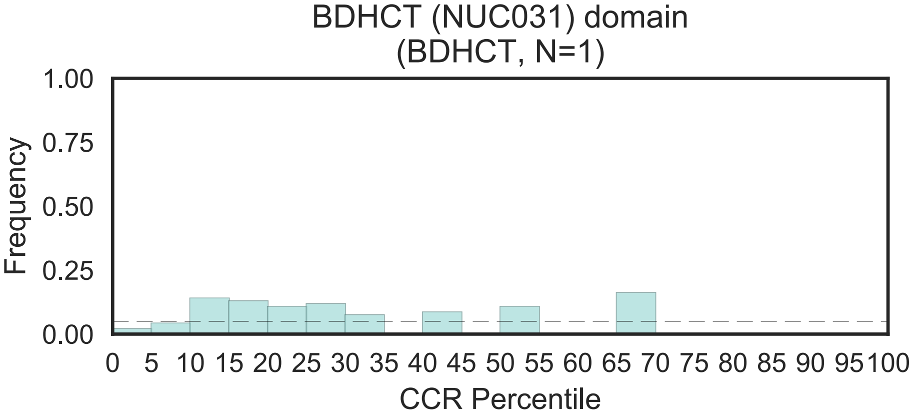

B-cell lymphoma 9 protein
(BCL9, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

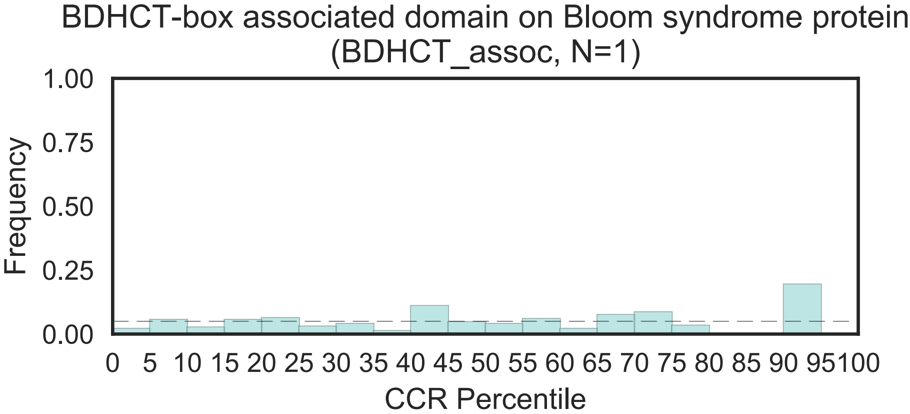

Beta-casein like protein
(BCLP, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


BCL7, N-terminal conserver region
(BCL_N, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

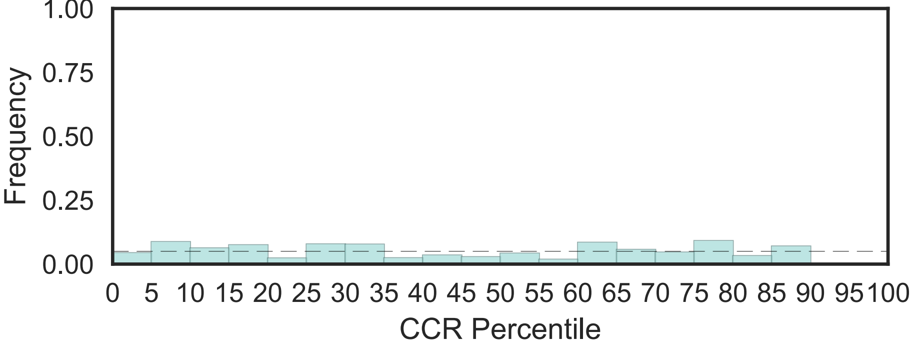

BCMA, TALL-1 binding
(BCMA-Tall_bind, N=1)

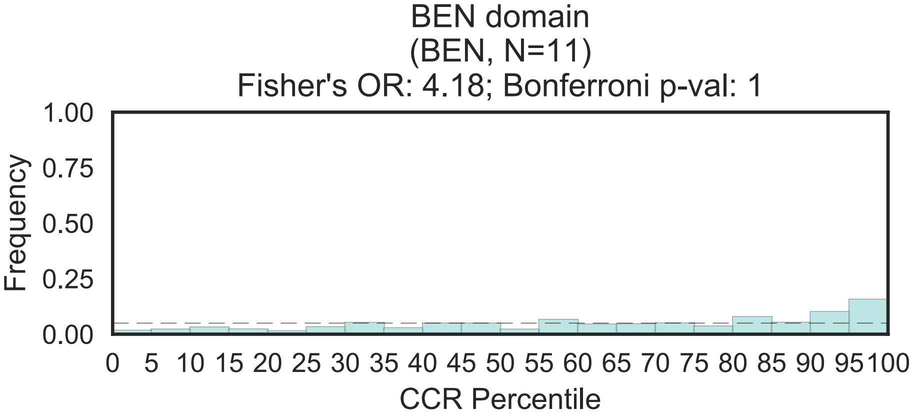

BCS1 N terminal
(BCS1_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

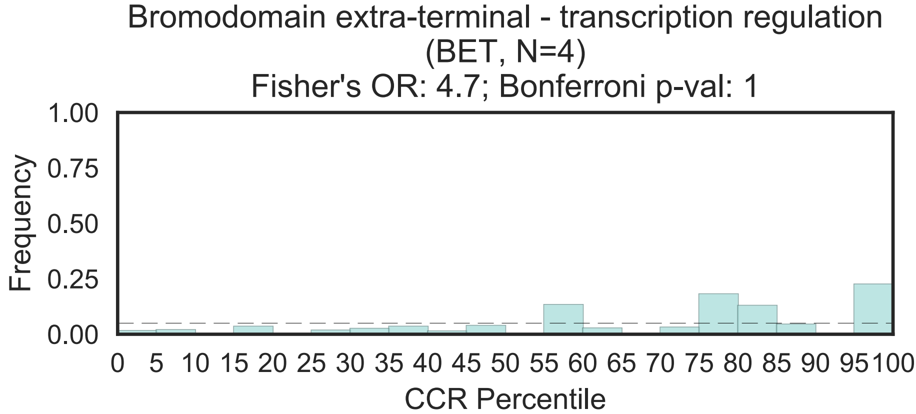

BDHCT (NUC031) domain
(BDHCT, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

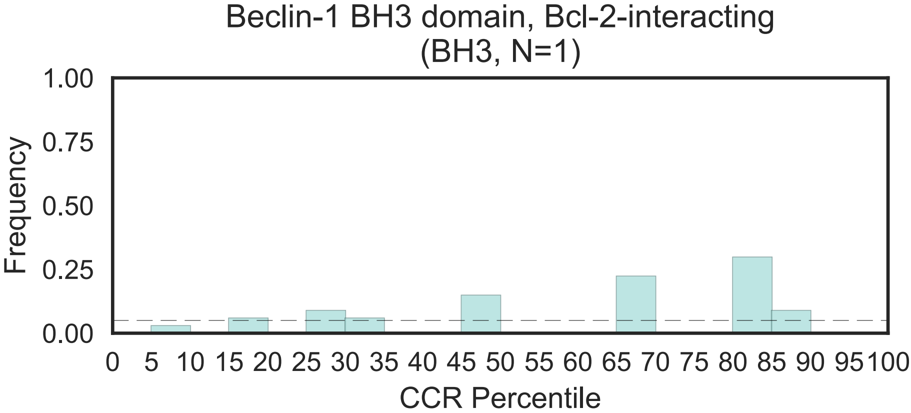

BDHCT-box associated domain on Bloom syndrome protein
(BDHCT_assoc, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95100
CCR Percentile

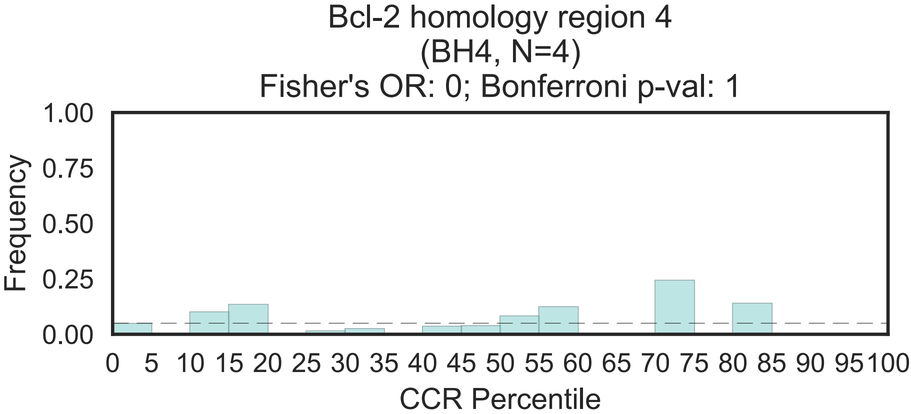
Borna disease virus P40 protein (BDV_P40, N=2)



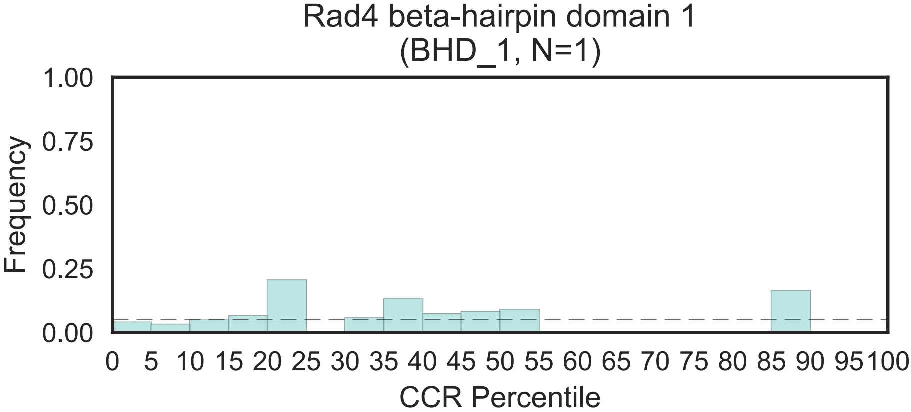

BEN domain
(BEN, N=11)
Fisher's OR: 4.18; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

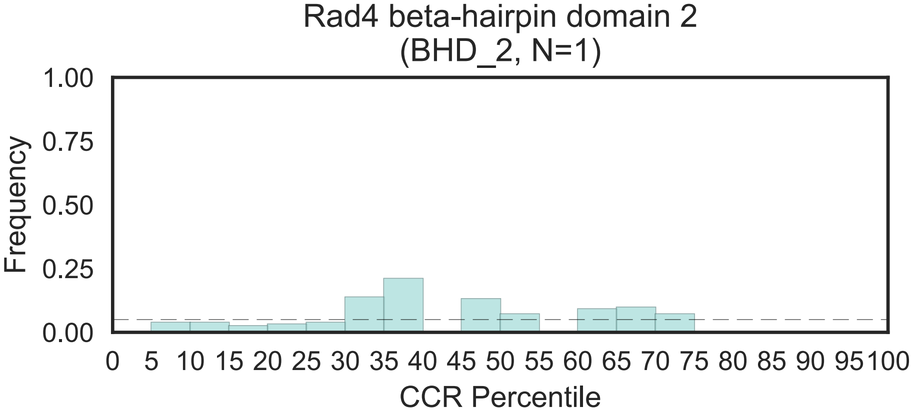

Bromodomain extra-terminal - transcription regulation
(BET, N=4)
Fisher's OR: 4.7; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

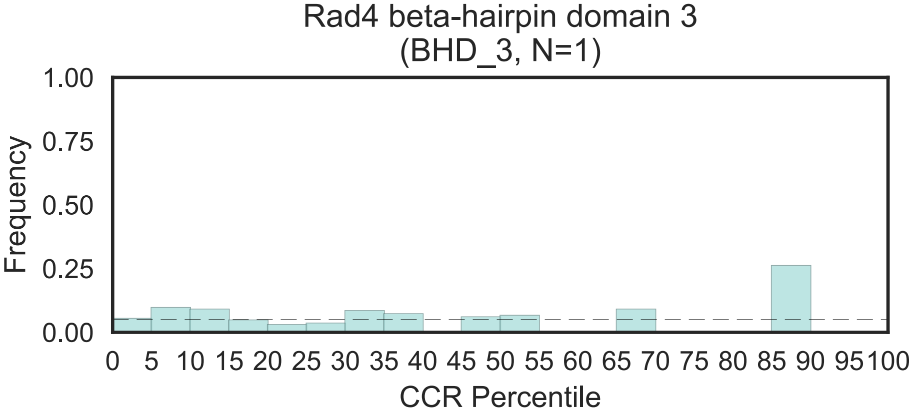

Beclin-1 BH3 domain, Bcl-2-interacting
(BH3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

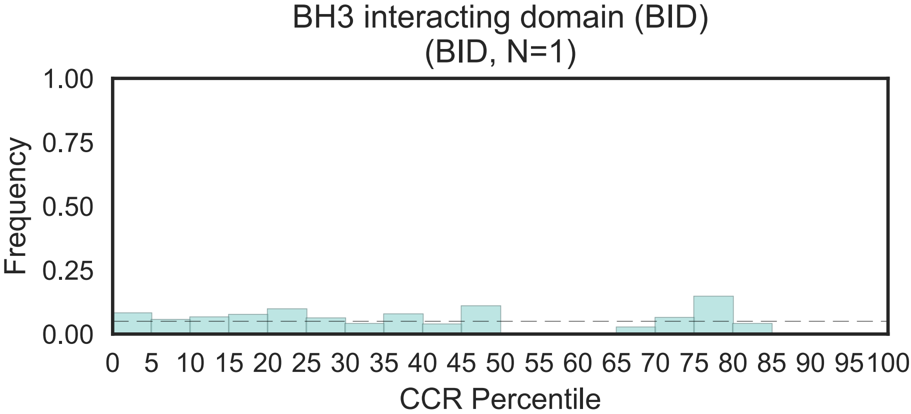


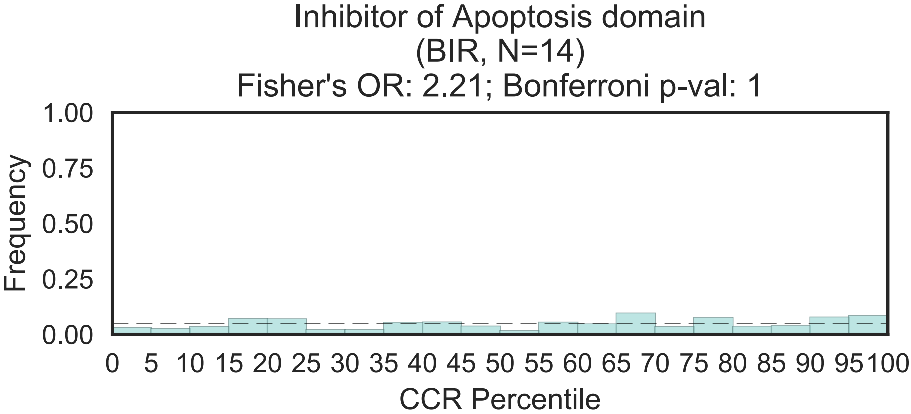
Bcl-2 homology region 4
(BH4, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

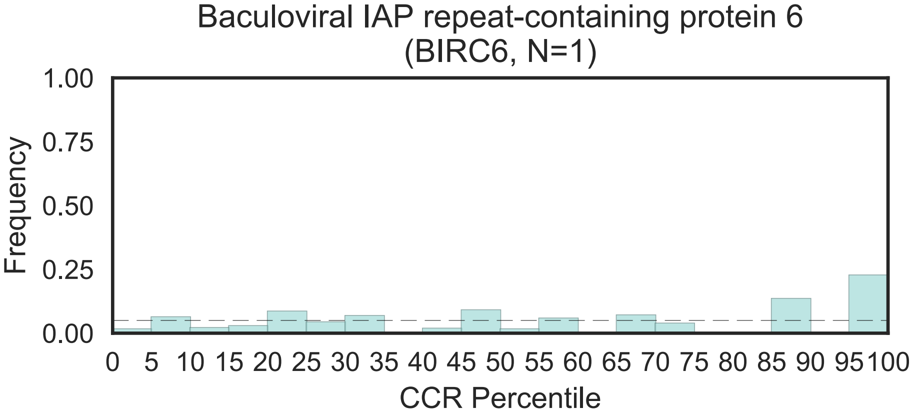

Rad4 beta-hairpin domain 1
(BHD_1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

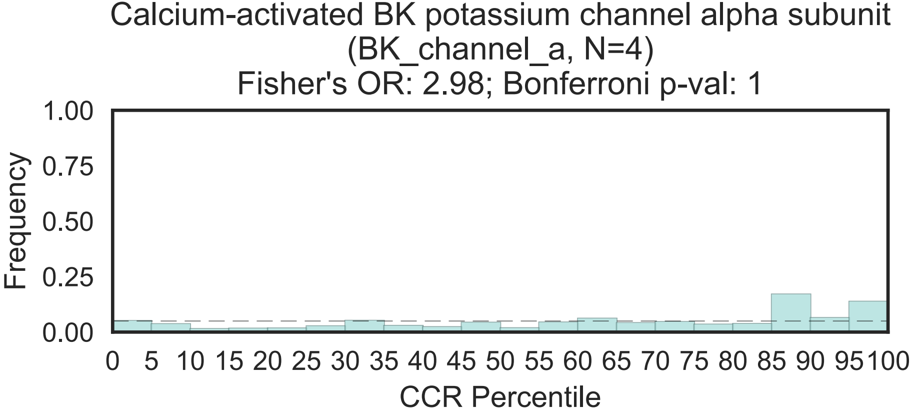

Rad4 beta-hairpin domain 2
(BHD_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

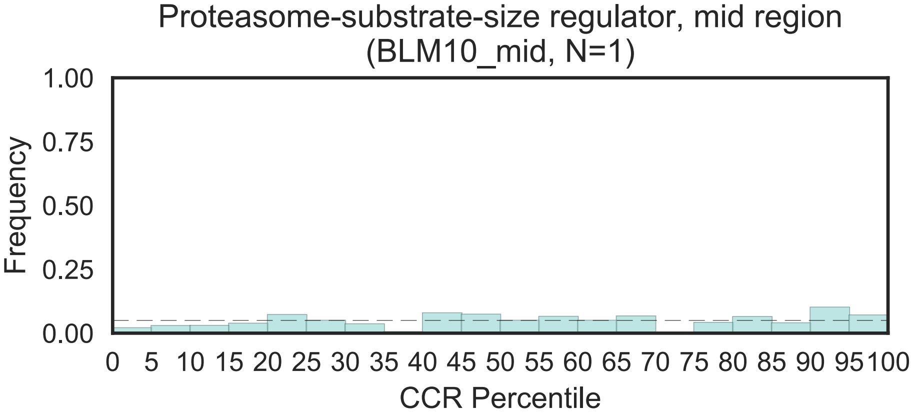

Rad4 beta-hairpin domain 3
(BHD_3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

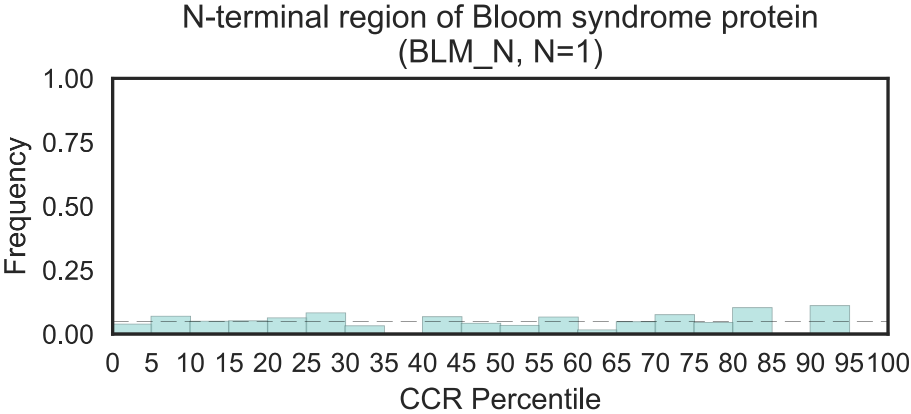
BH3 interacting domain (BID)
(BID, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

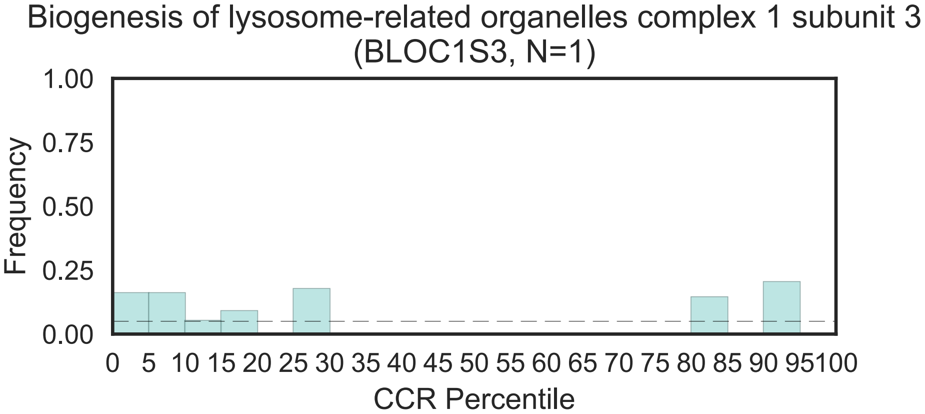

Inhibitor of Apoptosis domain
(BIR, N=14)
Fisher's OR: 2.21; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

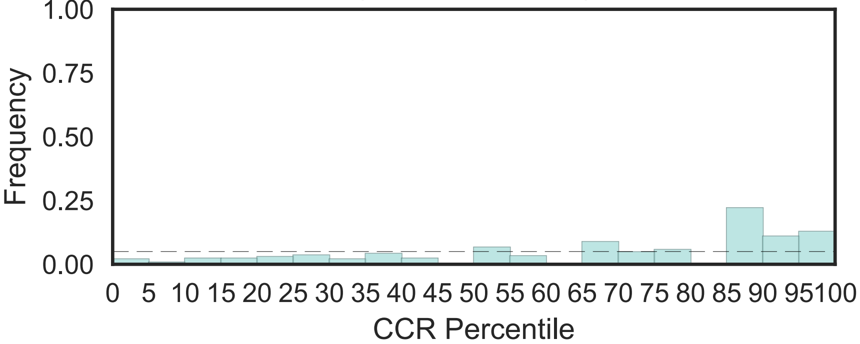

Baculoviral IAP repeat-containing protein 6
(BIRC6, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Calcium-activated BK potassium channel alpha subunit
(BK_channel_a, N=4)
Fisher's OR: 2.98; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

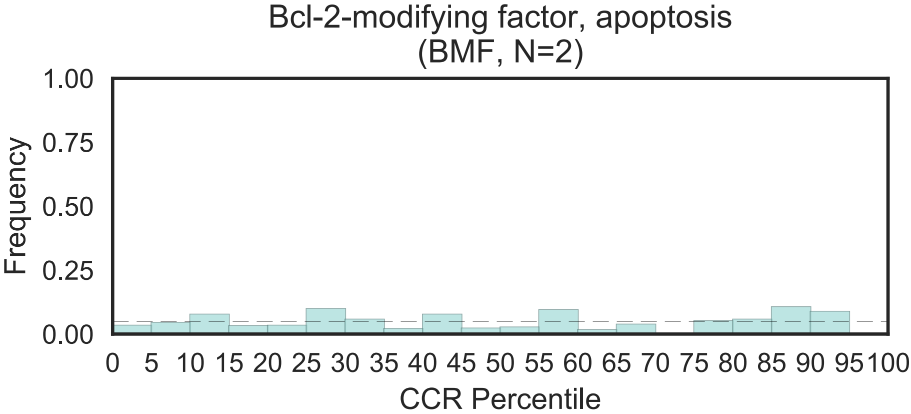

Proteasome-substrate-size regulator, mid region
(BLM10_mid, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

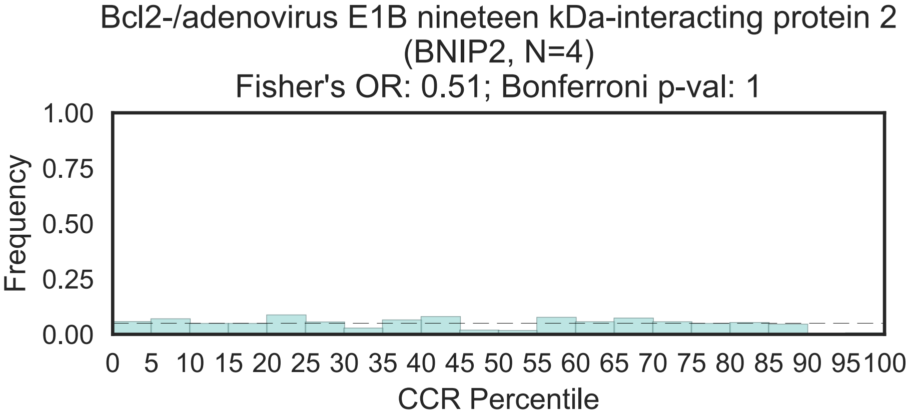

N-terminal region of Bloom syndrome protein
(BLM_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

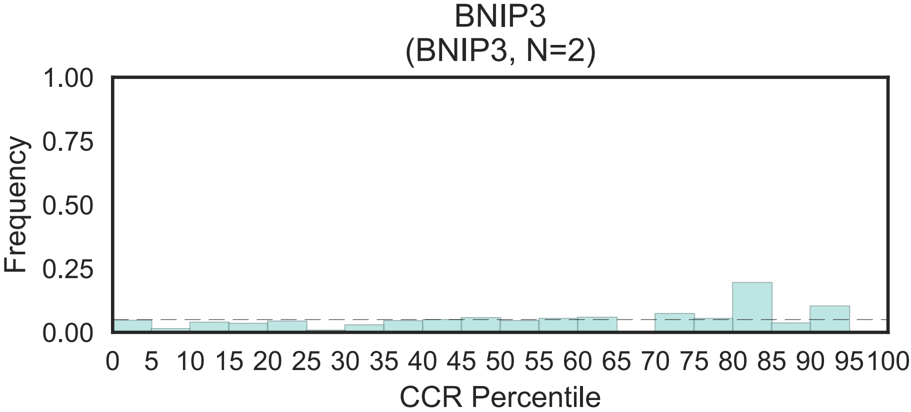

Biogenesis of lysosome-related organelles complex 1 subunit 3
(BLOC1S3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

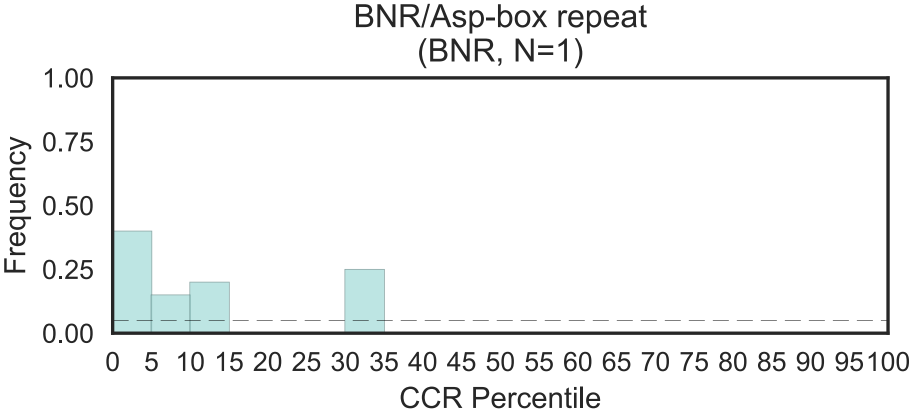


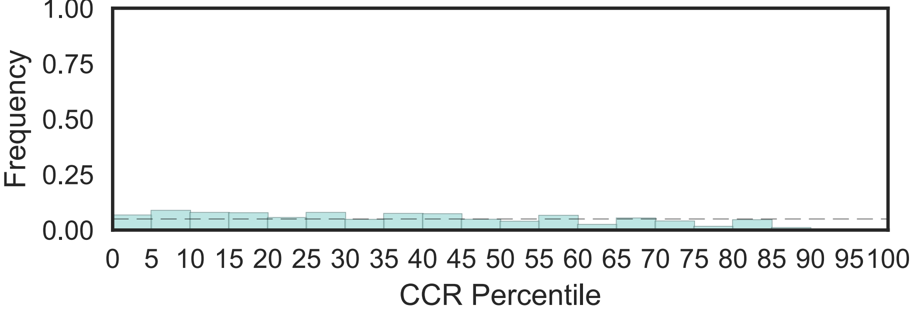
Biogenesis of lysosome-related organelles complex-1 subunit 2 (BLOC1_2, N=1)


Bcl-2-modifying factor, apoptosis
(BMF, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

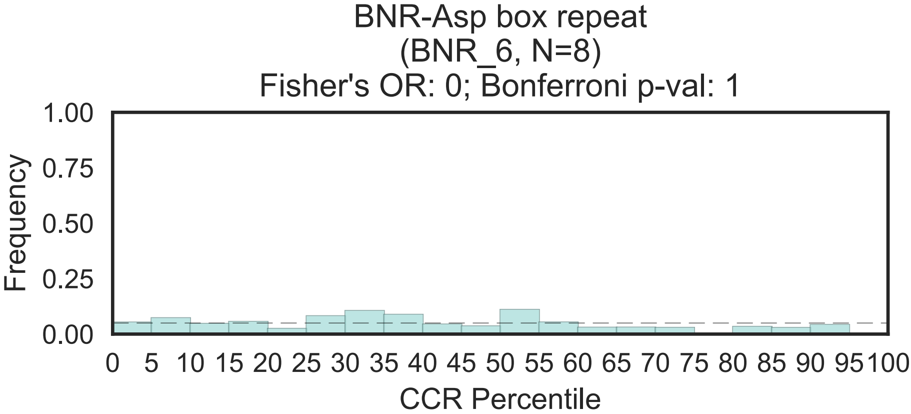

Bcl2-/adenovirus E1B nineteen kDa-interacting protein 2
(BNIP2, N=4)
Fisher's OR: 0.51; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

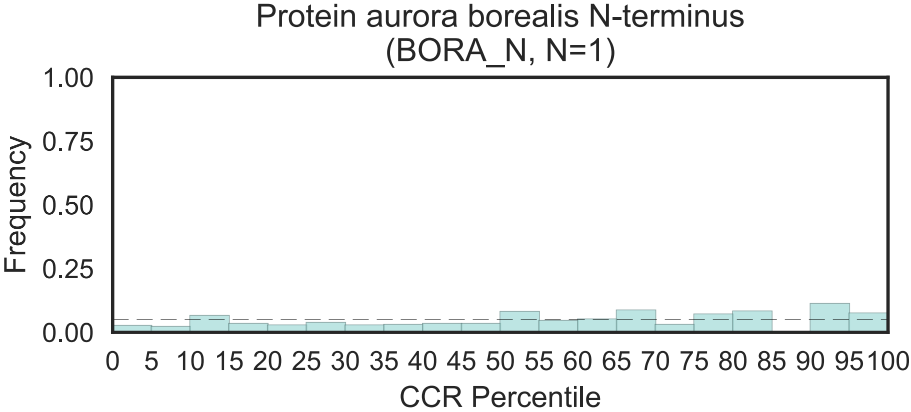

BNIP3
(BNIP3, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

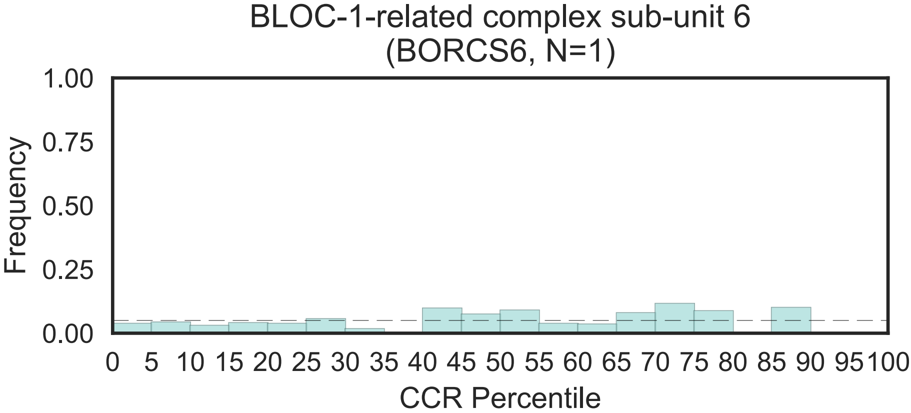

BNR/Asp-box repeat
(BNR, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

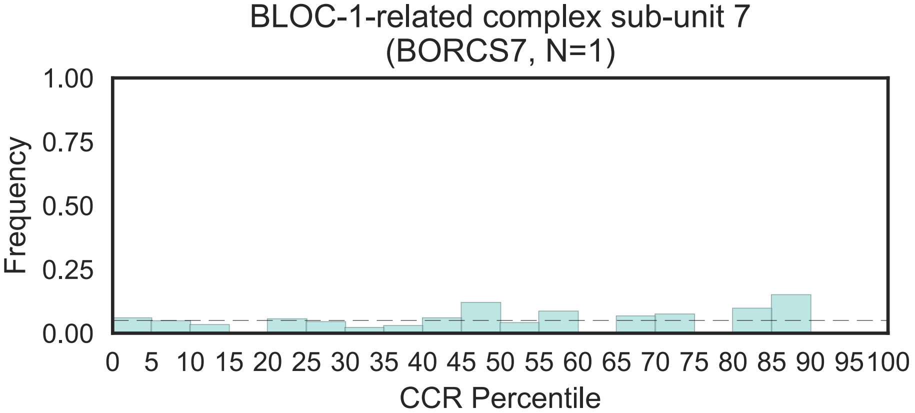


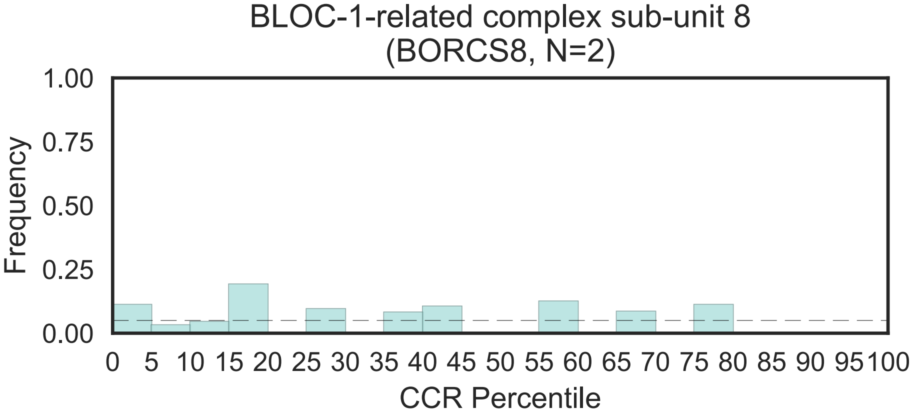
BNR repeat-like domain
(BNR_2, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

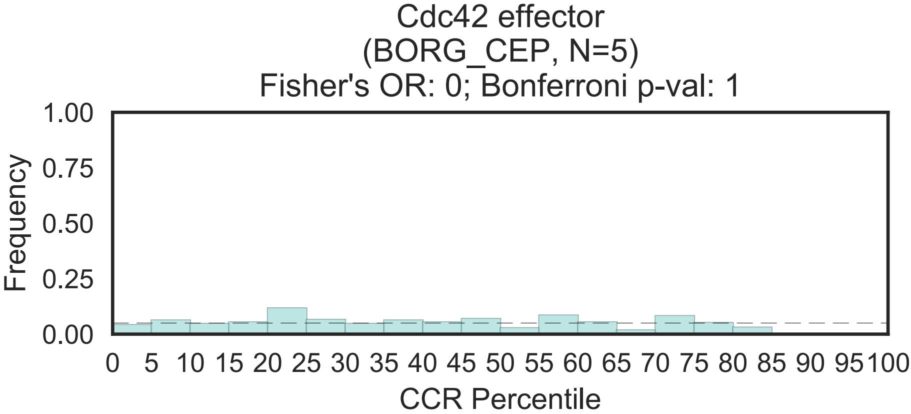

BNR-Asp box repeat
(BNR_6, N=8)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

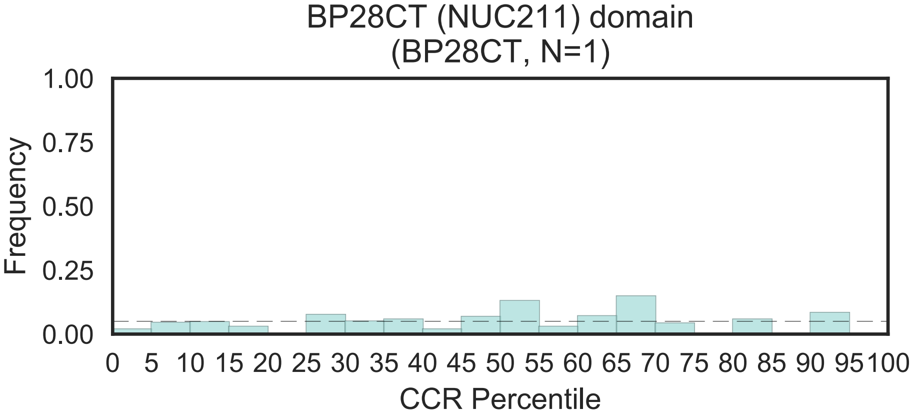

Protein aurora borealis N-terminus
(BORA_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

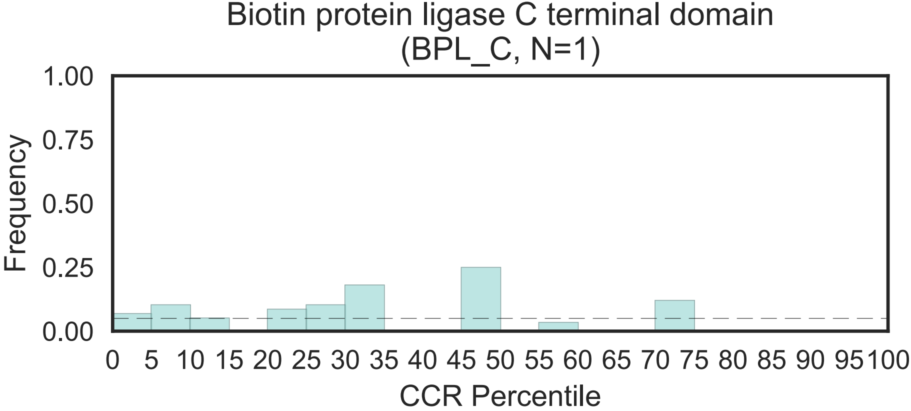

BLOC-1-related complex sub-unit 6
(BORCS6, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

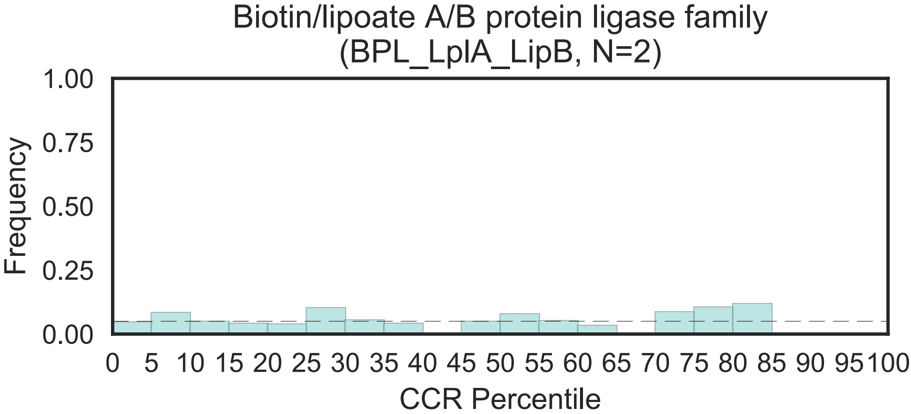

BLOC-1-related complex sub-unit 7
(BORCS7, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

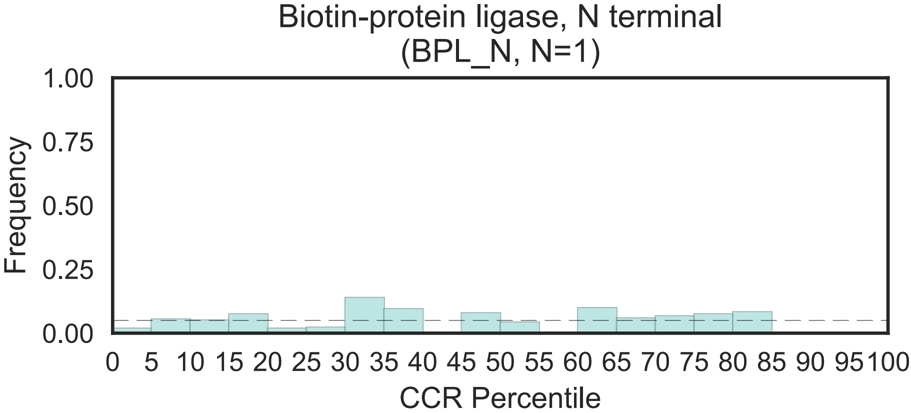

BLOC-1-related complex sub-unit 8
(BORCS8, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

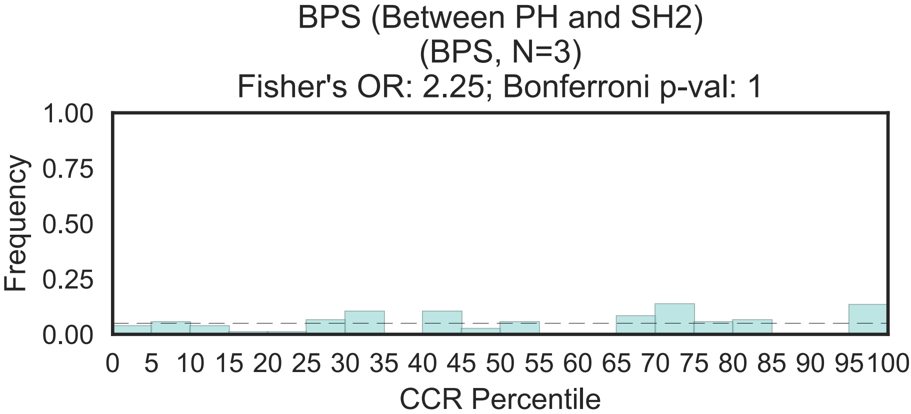

Cdc42 effector
(BORG_CEP, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

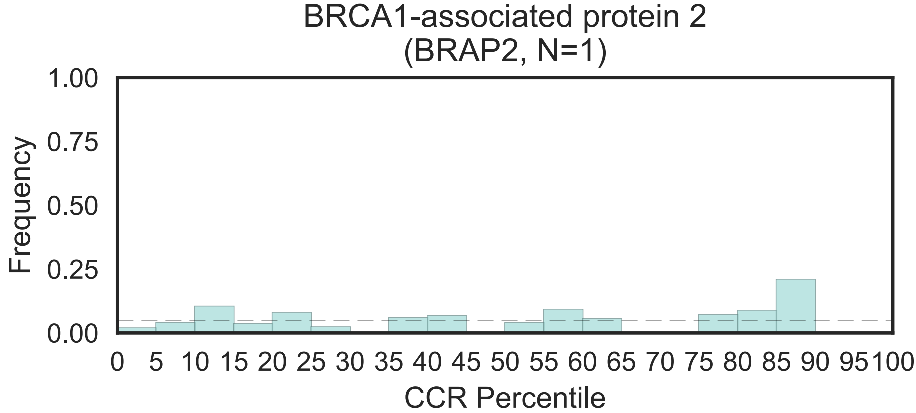

BP28CT (NUC211) domain
(BP28CT, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

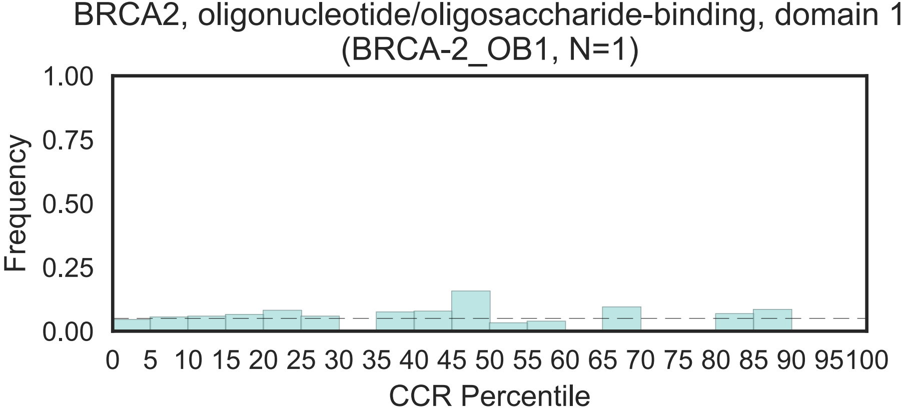

Biotin protein ligase C terminal domain
(BPL_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

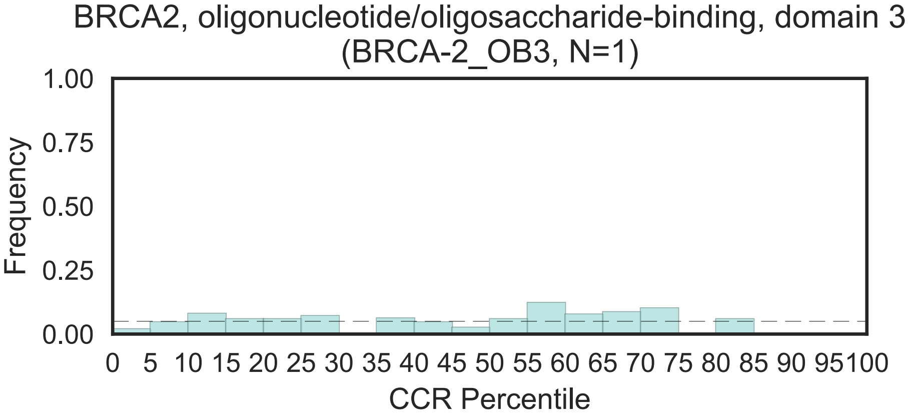

Biotin/lipoate A/B protein ligase family
(BPL_LplA_LipB, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

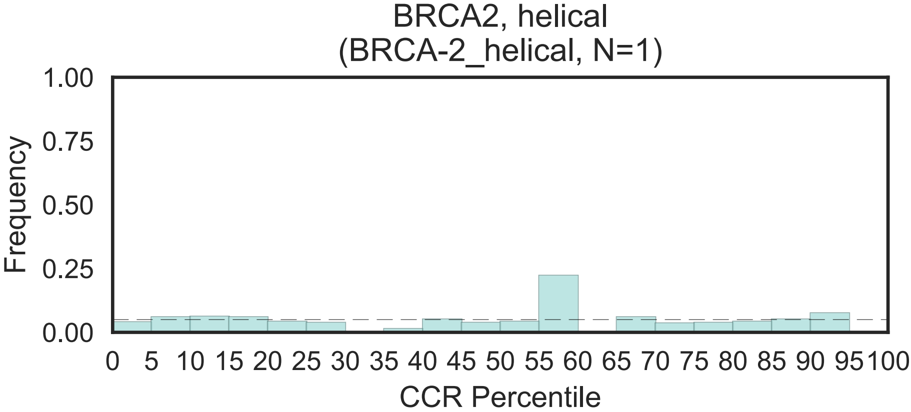

Biotin-protein ligase, N terminal
(BPL_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

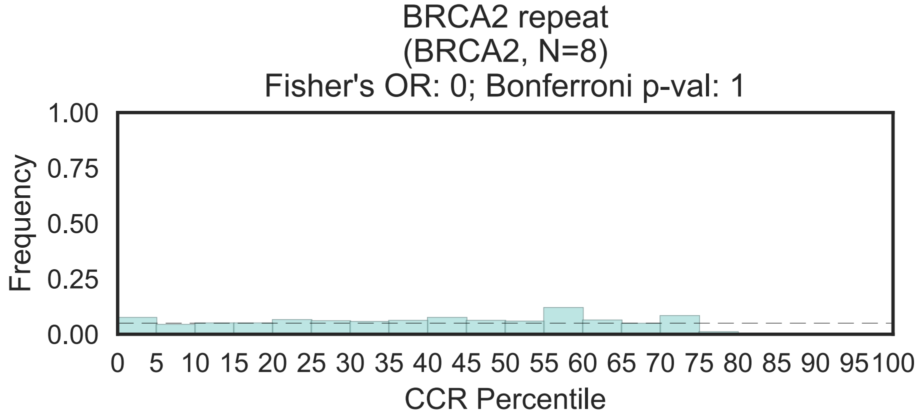

BPS (Between PH and SH2)
(BPS, N=3)
Fisher's OR: 2.25; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

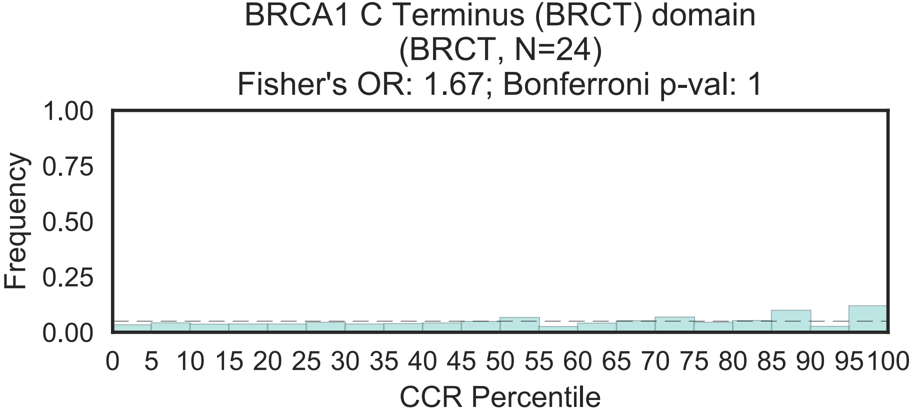

BRCA1-associated protein 2
(BRAP2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

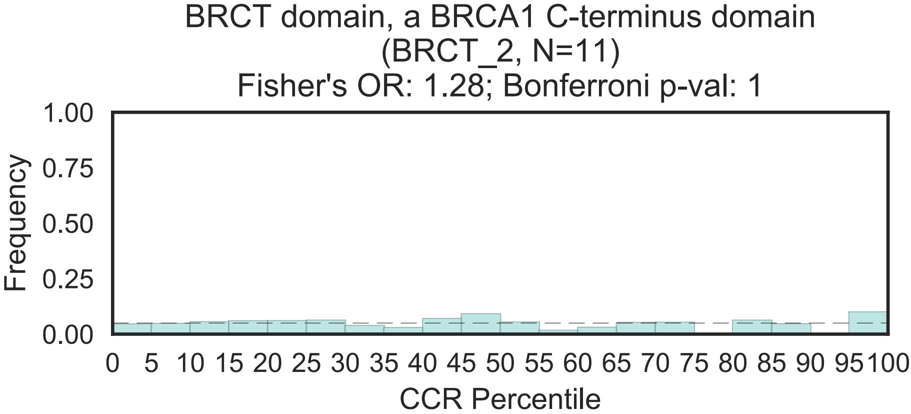

BRCA2, oligonucleotide/oligosaccharide-binding, domain 1
(BRCA-2_OB1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


BRCA2, oligonucleotide/oligosaccharide-binding, domain 3 (BRCA-2_OB3, N=1)

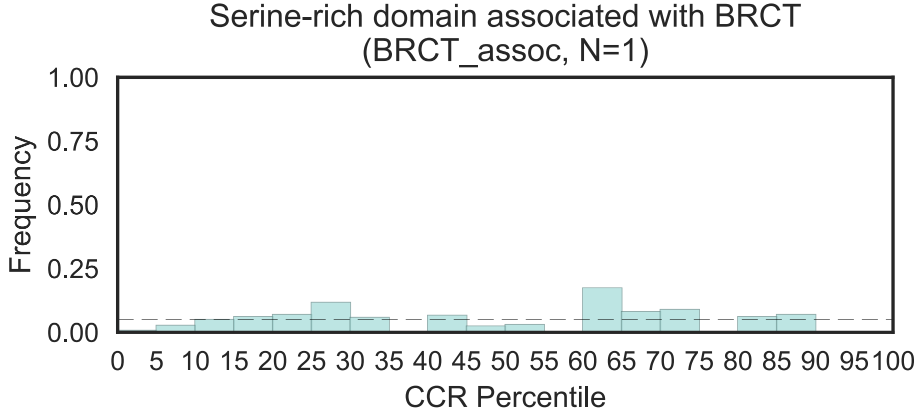

BRCA2, helical
(BRCA-2_helical, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


BRCA2 repeat
(BRCA2, N=8)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

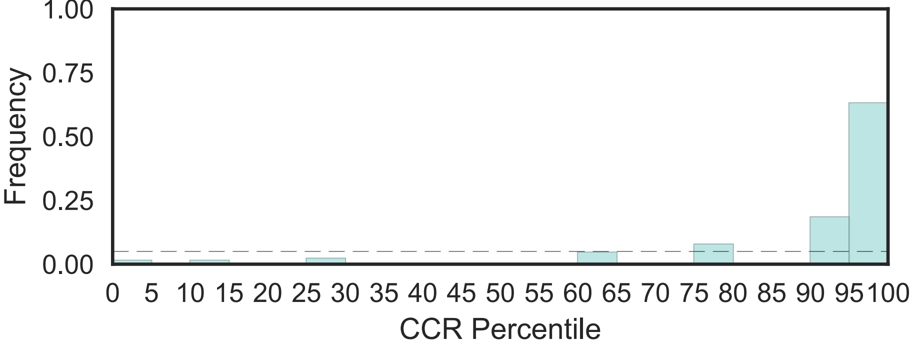

BRCA1 C Terminus (BRCT) domain
(BRCT, N=24)
Fisher's OR: 1.67; Bonferroni p-val: 1



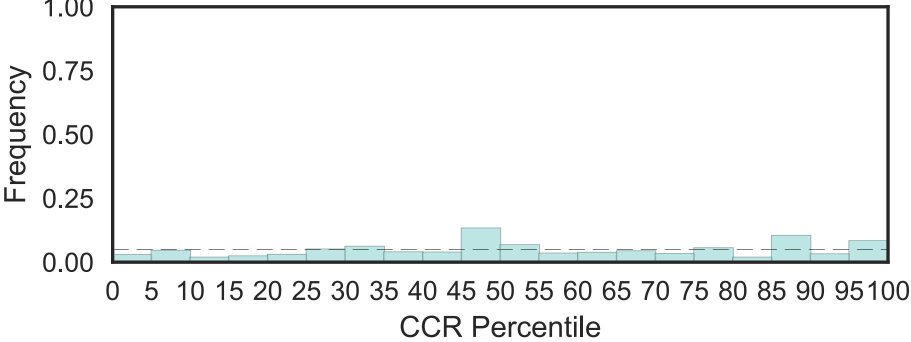
BRCT domain, a BRCA1 C-terminus domain
(BRCT_2, N=11)
Fisher's OR: 1.28; Bonferroni p-val: 1

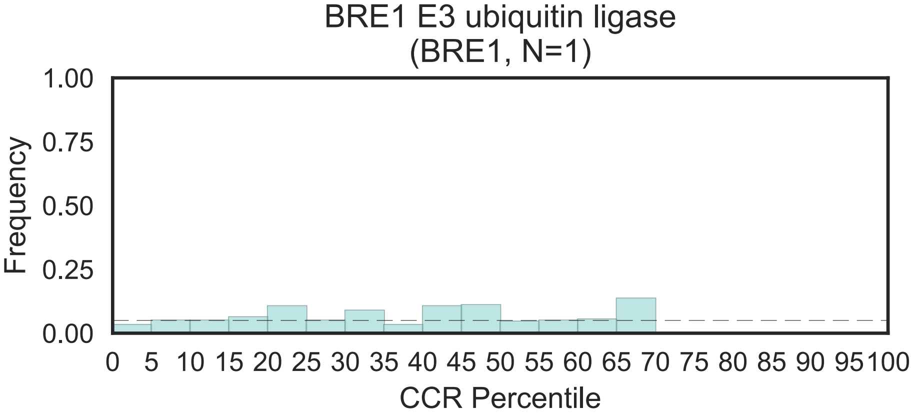

Serine-rich domain associated with BRCT
(BRCT_assoc, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

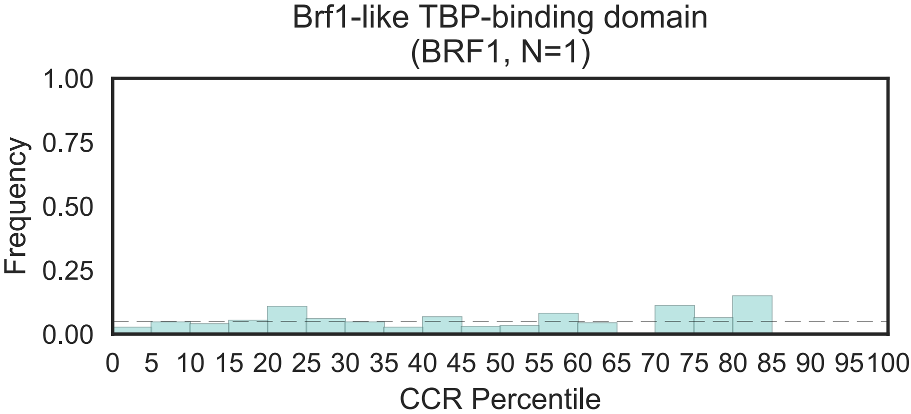
C-terminal domain of bromodomain protein 4 (BRD4_CDT, N=2)

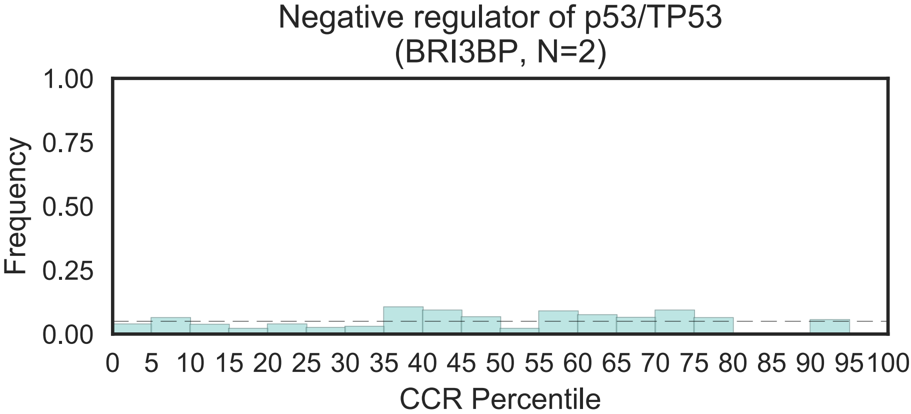


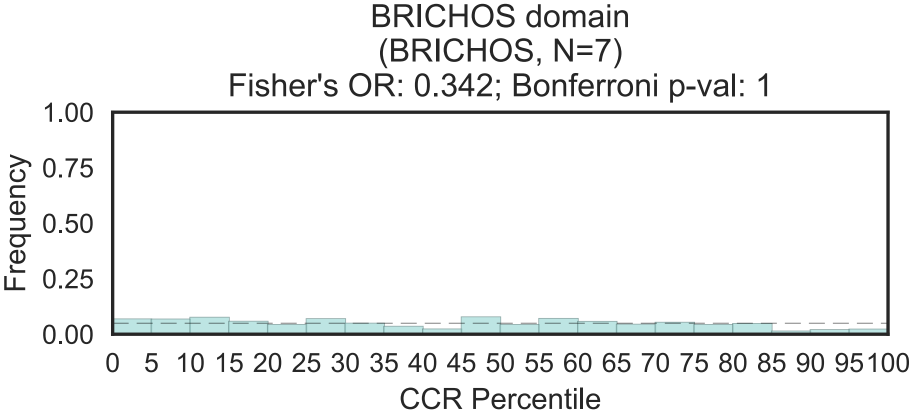
Brain and reproductive organ-expressed protein (BRE)
(BRE, N=1)

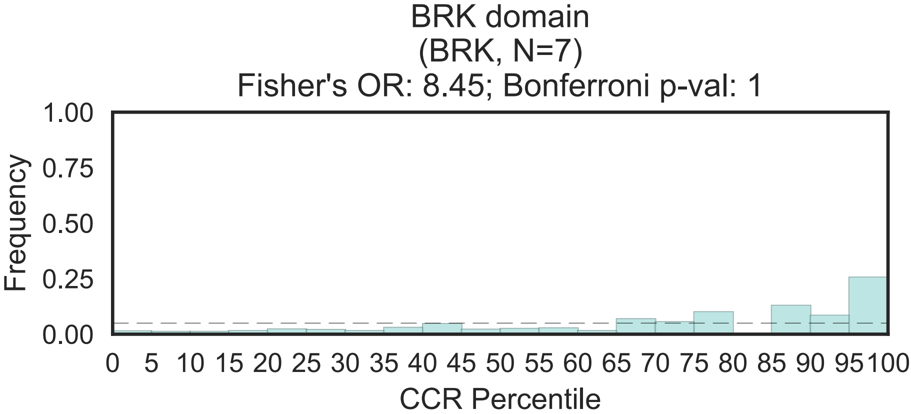


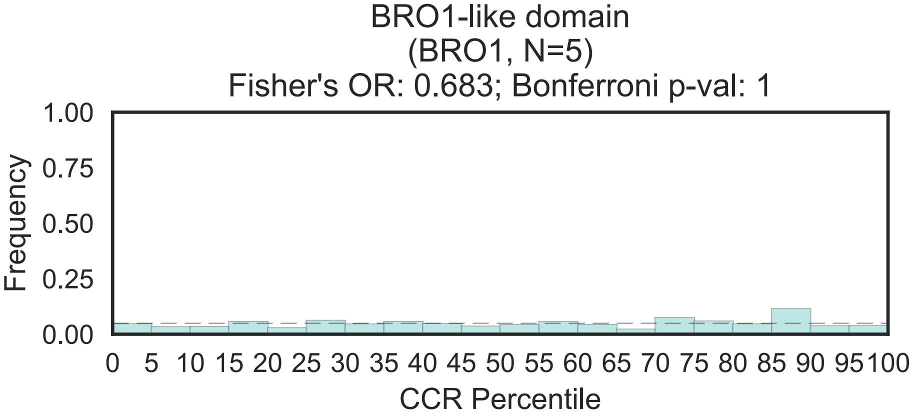

BRE1 E3 ubiquitin ligase
(BRE1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

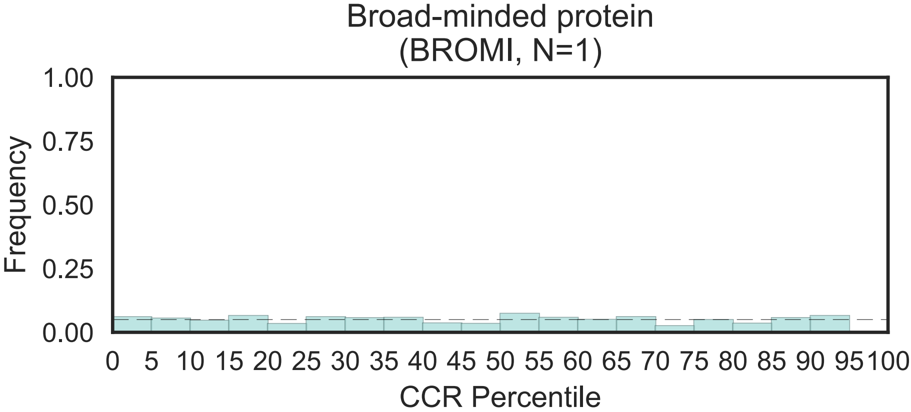

Brf1-like TBP-binding domain
(BRF1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Negative regulator of p53/TP53
(BRI3BP, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

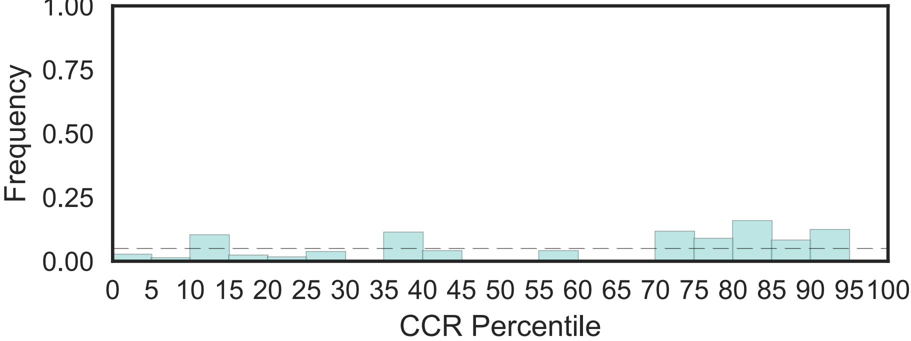

BRICHOS domain
(BRICHOS, N=7)
Fisher's OR: 0.342; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

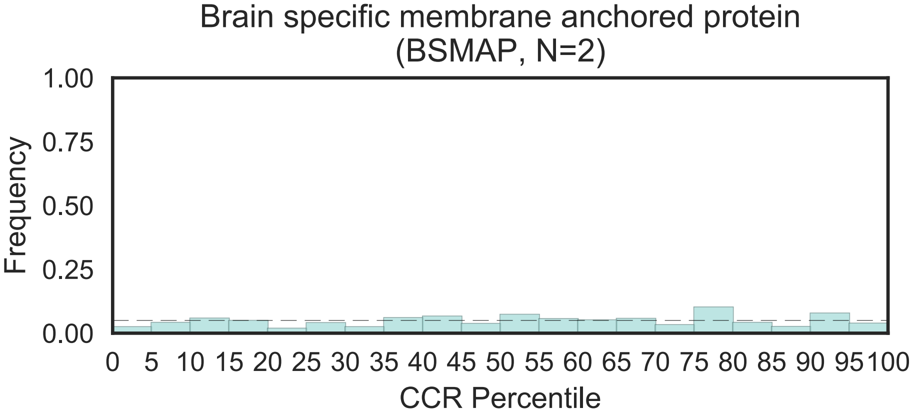

BRK domain
(BRK, N=7)
Fisher's OR: 8.45; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

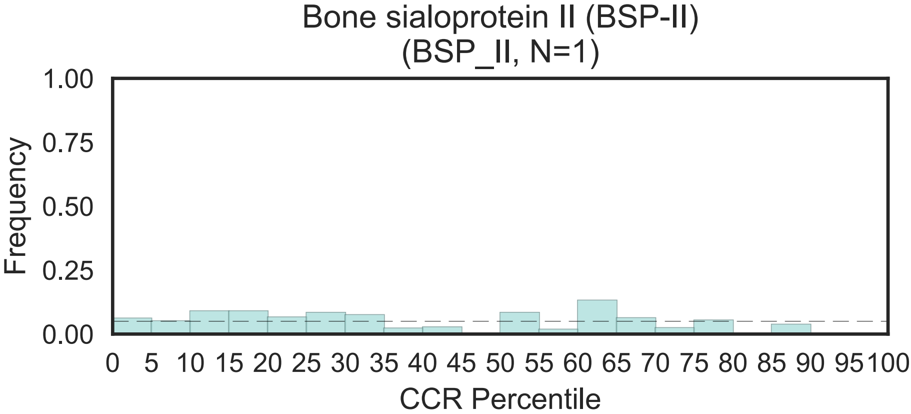

BRO1-like domain
(BRO1, N=5)
Fisher's OR: 0.683; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

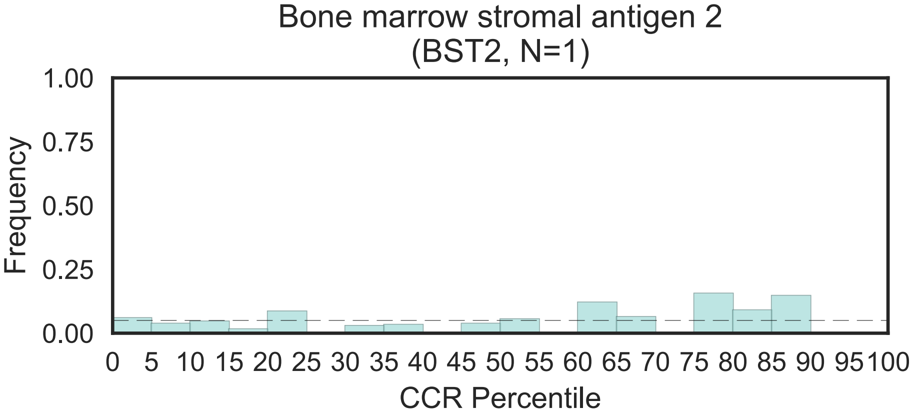

Broad-minded protein
(BROMI, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

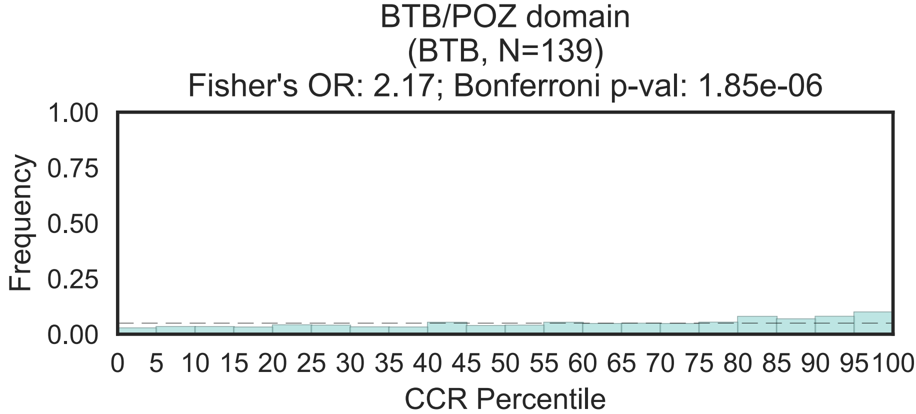
BSD domain
(BSD, N=2)

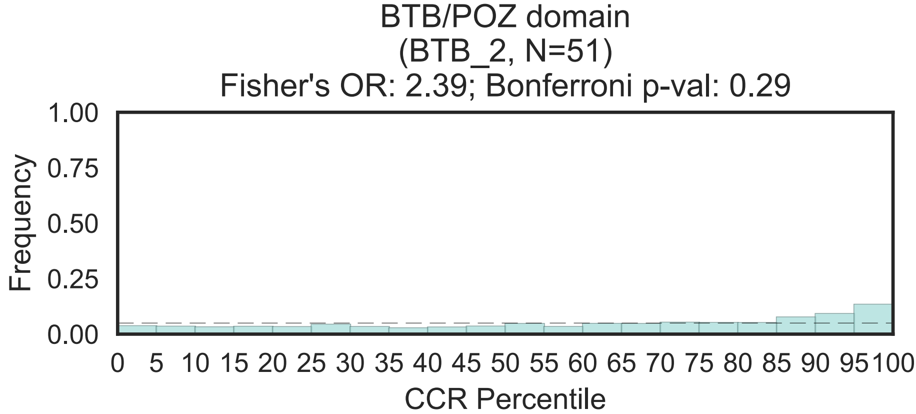


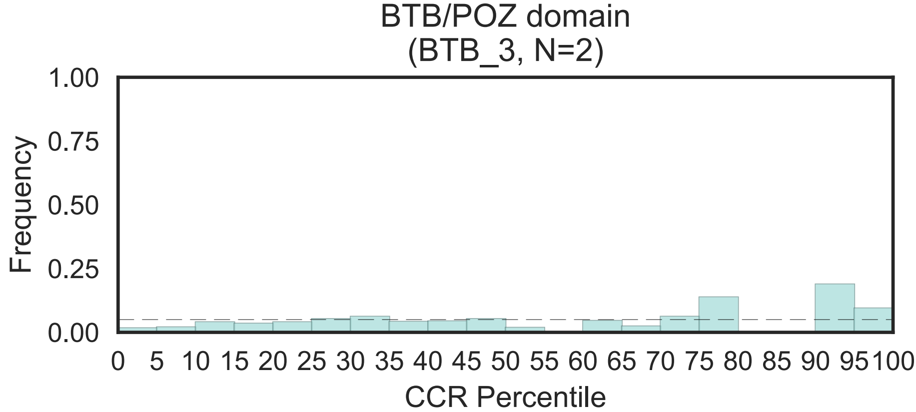

Brain specific membrane anchored protein
(BSMAP, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

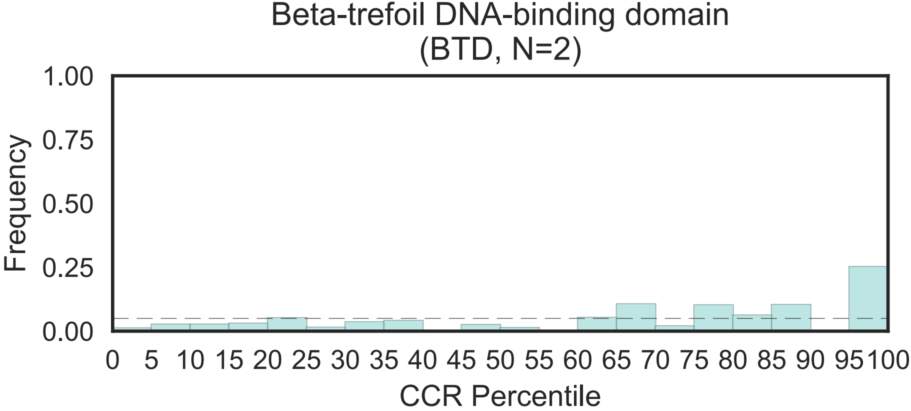

Bone sialoprotein II (BSP-II)
(BSP_II, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

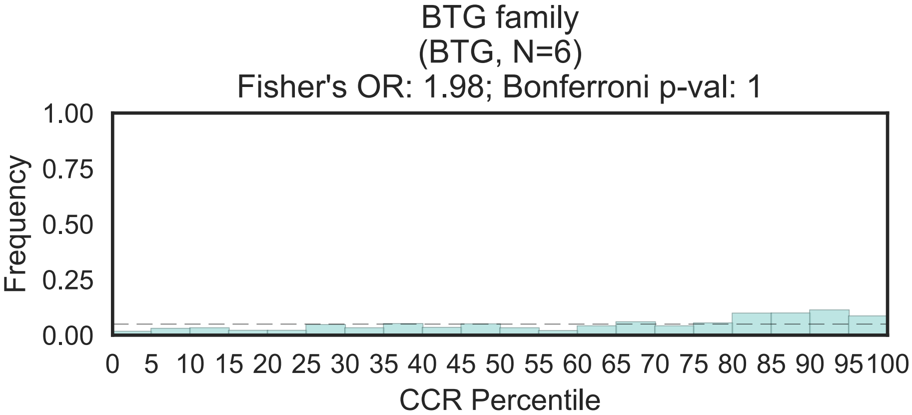

Bone marrow stromal antigen 2
(BST2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

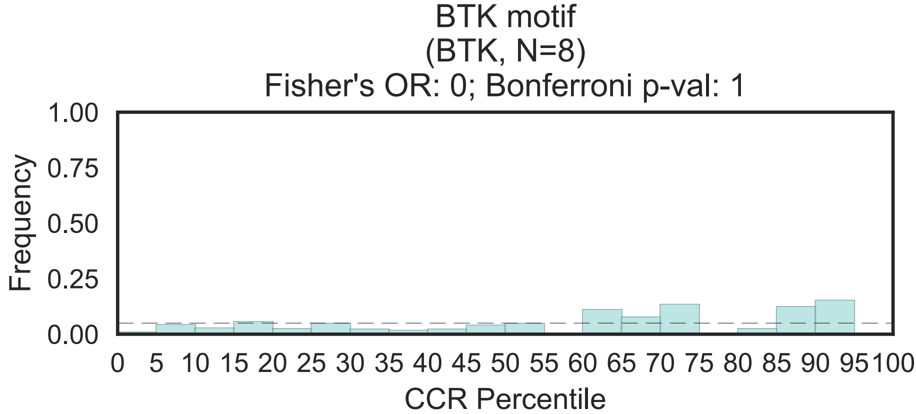

BTB/POZ domain
(BTB, N=139)
Fisher's OR: 2.17; Bonferroni p-val: 1.85e-06
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

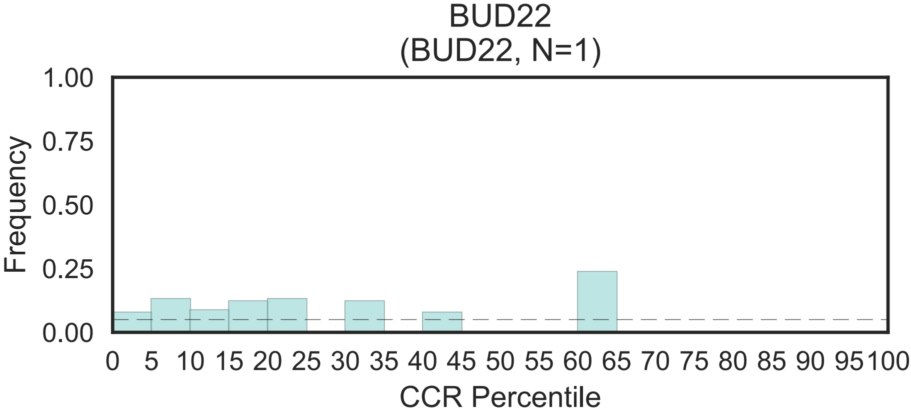

BTB/POZ domain
(BTB_2, N=51)
Fisher's OR: 2.39; Bonferroni p-val: 0.29
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

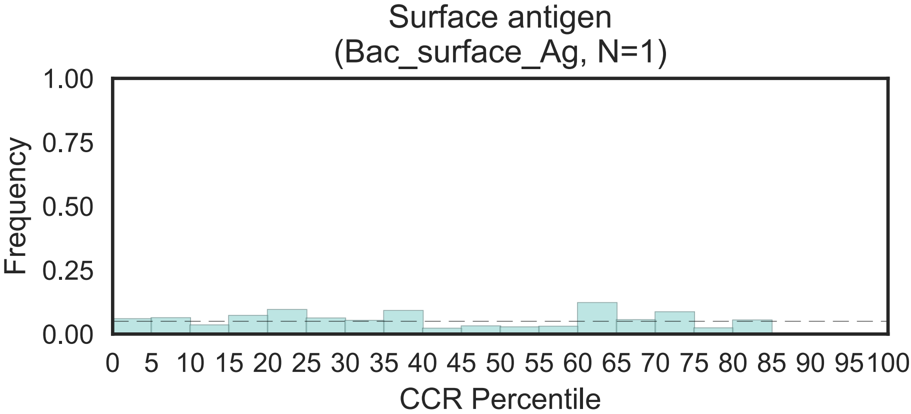

BTB/POZ domain
(BTB_3, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

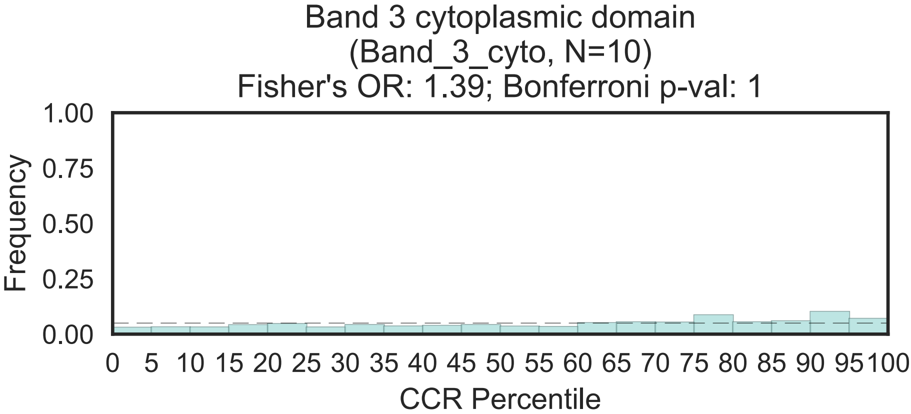

Beta-trefoil DNA-binding domain
(BTD, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


BTG family
(BTG, N=6)
Fisher's OR: 1.98; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

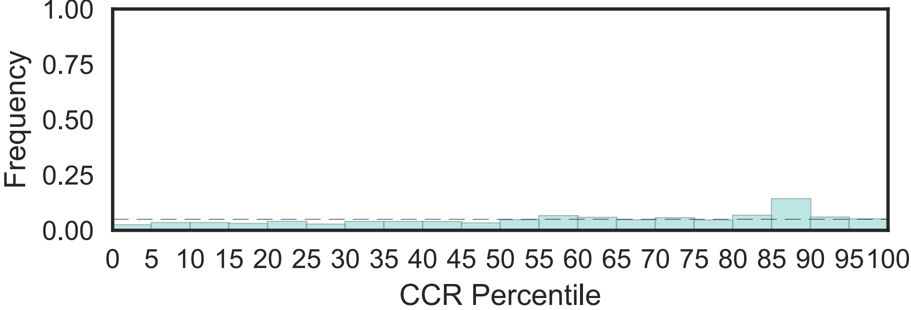

BTK motif
(BTK, N=8)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

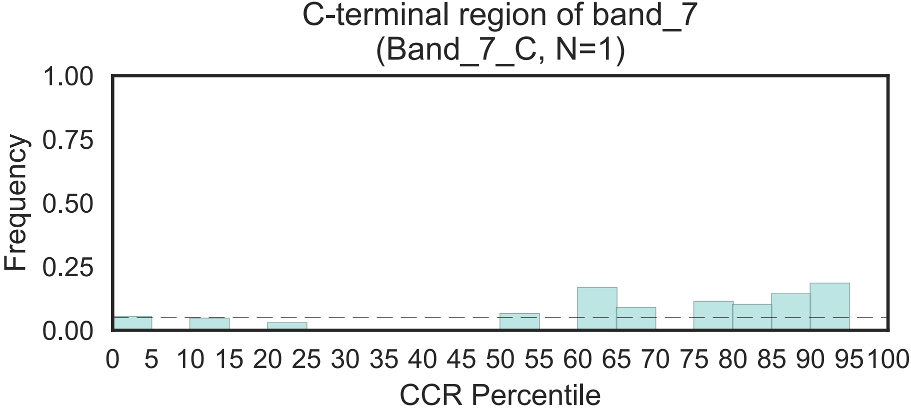

BUD22
(BUD22, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

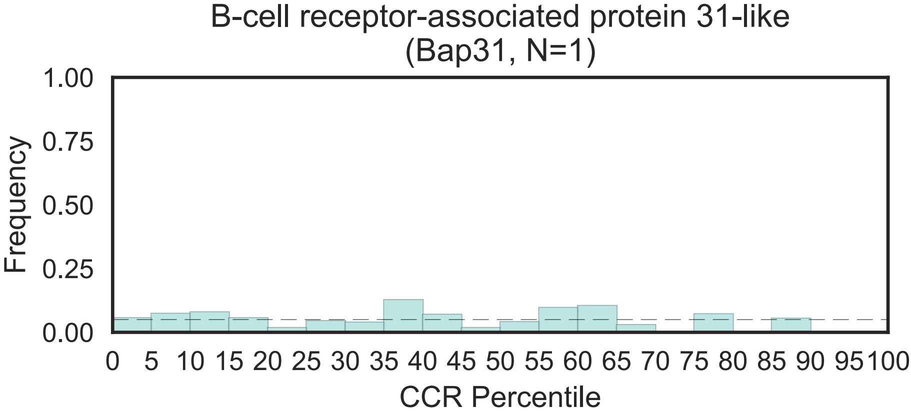

Surface antigen
(Bac_surface_Ag, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

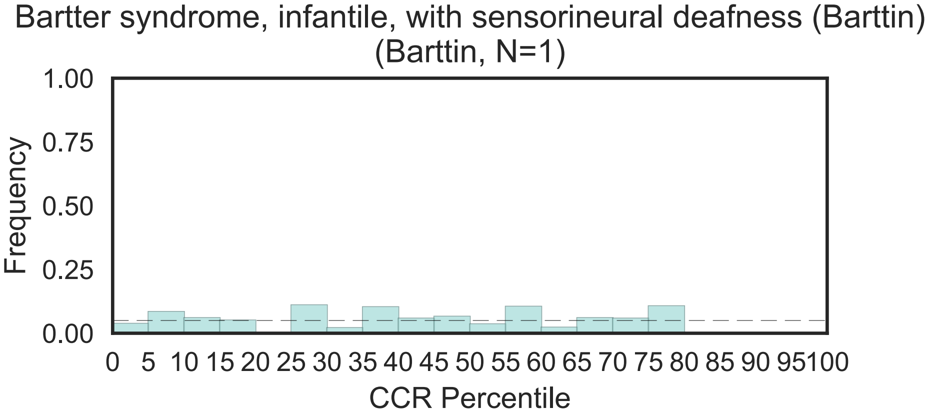

Band 3 cytoplasmic domain
(Band_3_cyto, N=10)
Fisher's OR: 1.39; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

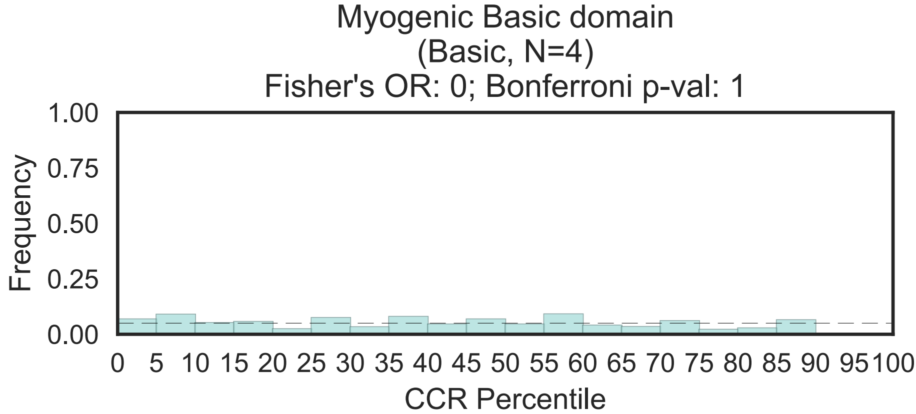
SPFH domain / Band 7 family
(Band_7, N=13)
Fisher's OR: 1.05; Bonferroni p-val: 1

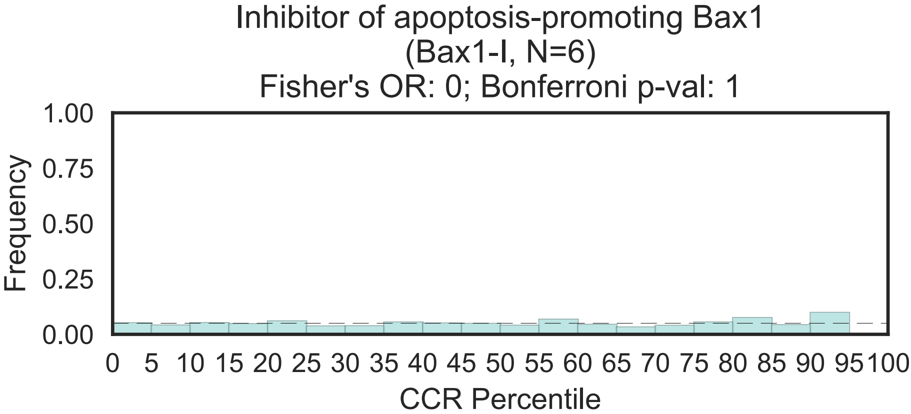


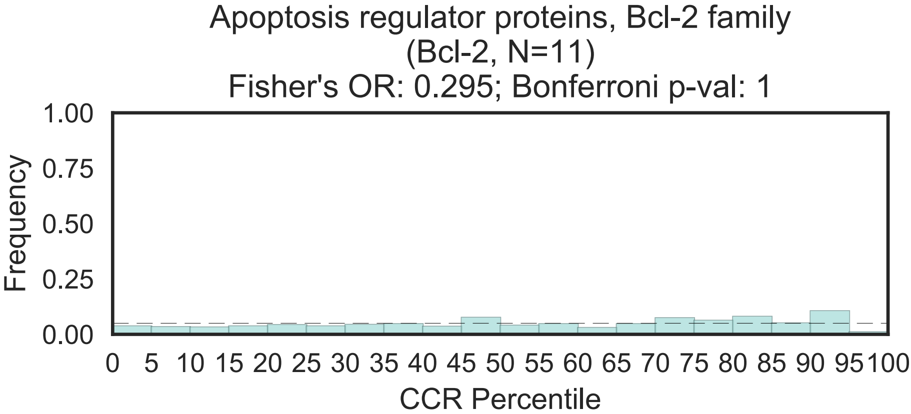

C-terminal region of band_7
(Band_7_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

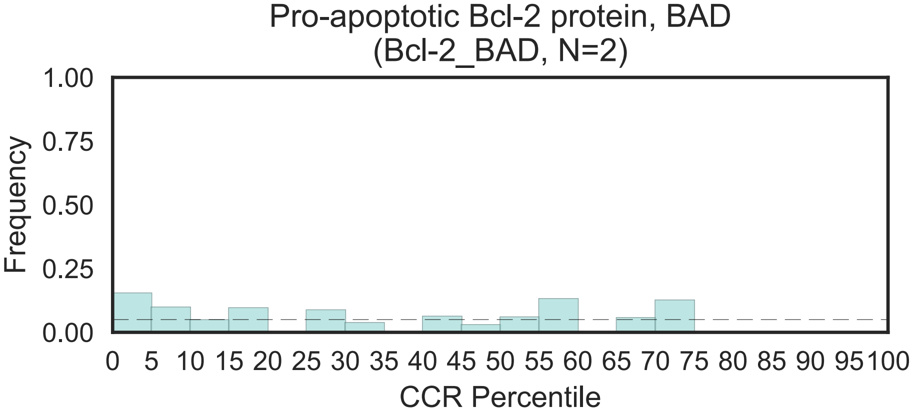

B-cell receptor-associated protein 31-like
(Bap31, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

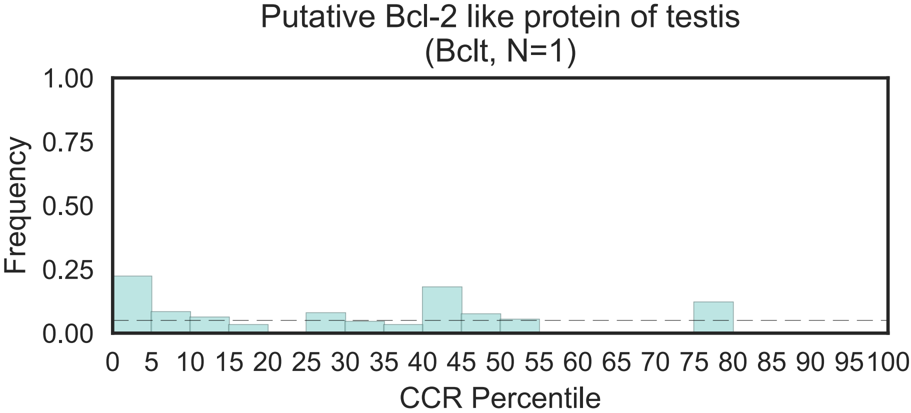

Bartter syndrome, infantile, with sensorineural deafness (Barttin)
(Barttin, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

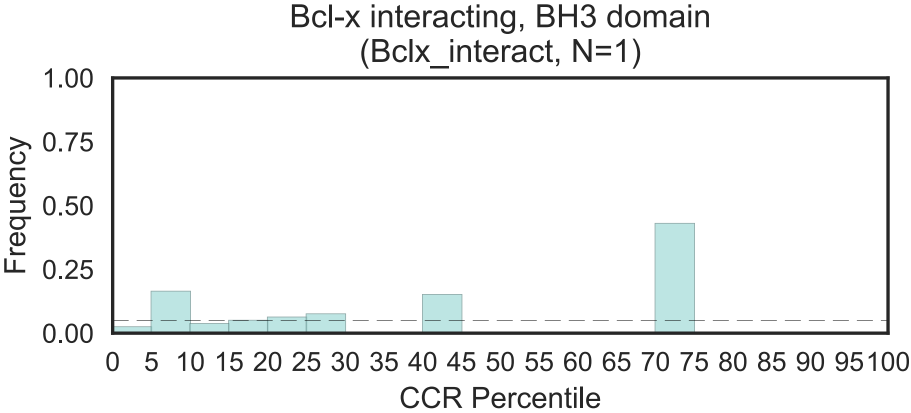

Myogenic Basic domain
(Basic, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

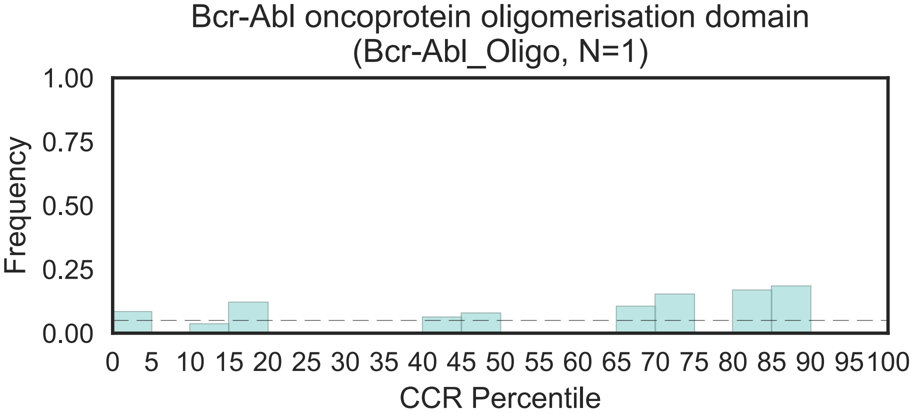

Inhibitor of apoptosis-promoting Bax1
(Bax1-I, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

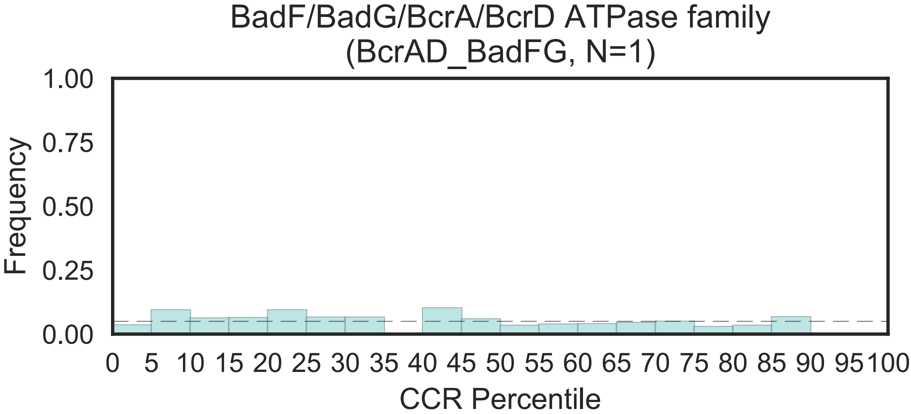

Apoptosis regulator proteins, Bcl-2 family
(Bcl-2, N=11)
Fisher's OR: 0.295; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

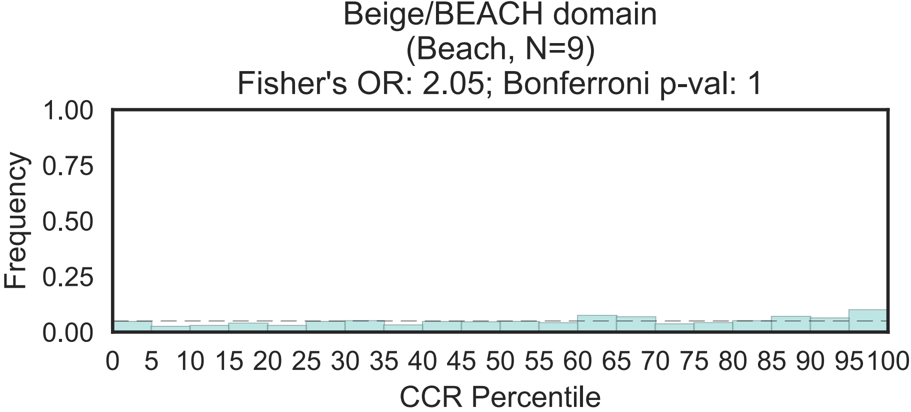

Pro-apoptotic Bcl-2 protein, BAD
(Bcl-2_BAD, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

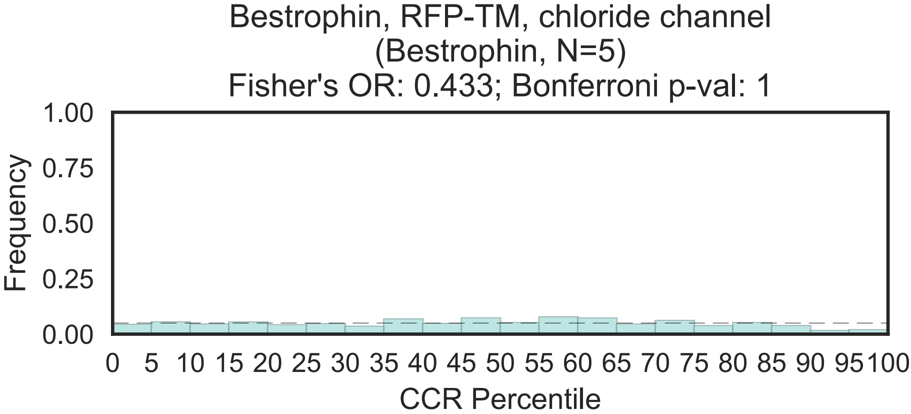

Putative Bcl-2 like protein of testis
(Bclt, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

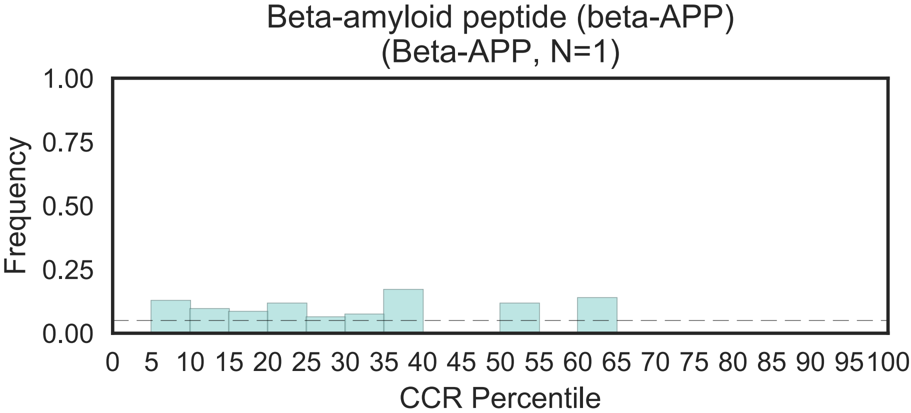

Bcl-x interacting, BH3 domain
(Bclx_interact, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

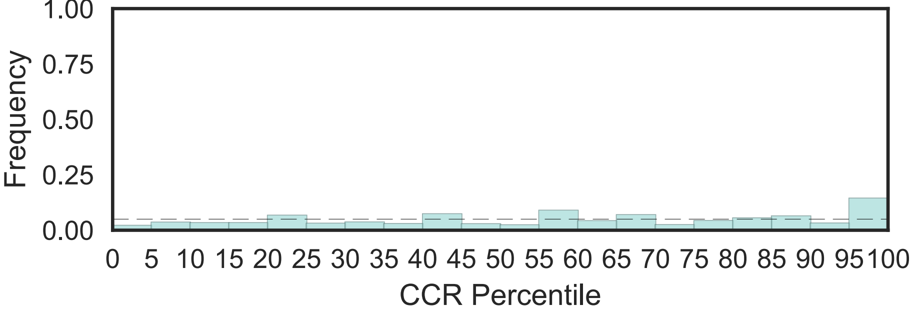

Bcr-Abl oncoprotein oligomerisation domain
(Bcr-Abl_Oligo, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


BadF/BadG/BcrA/BcrD ATPase family
(BcrAD_BadFG, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

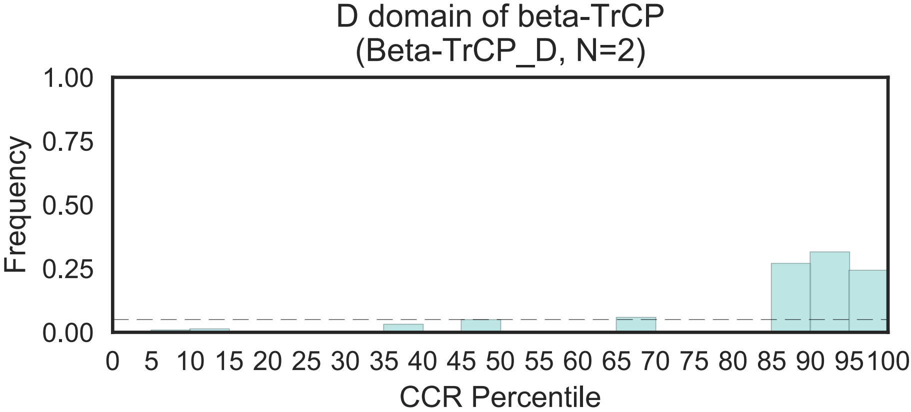

Beige/BEACH domain
(Beach, N=9)
Fisher's OR: 2.05; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

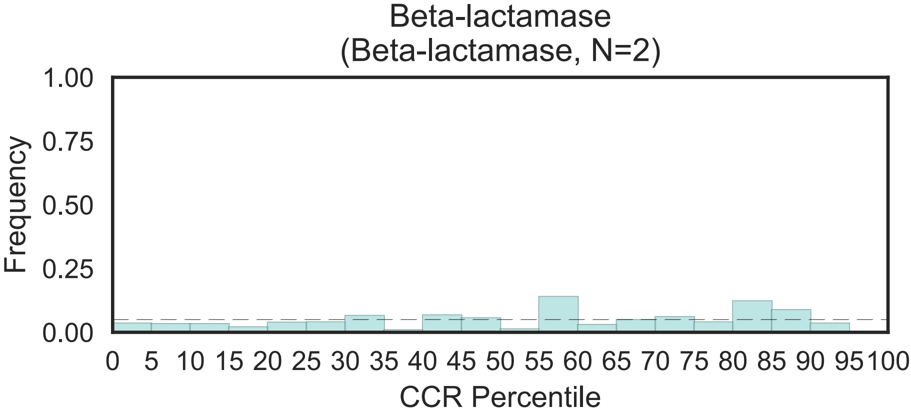

Bestrophin, RFP-TM, chloride channel
(Bestrophin, N=5)
Fisher's OR: 0.433; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

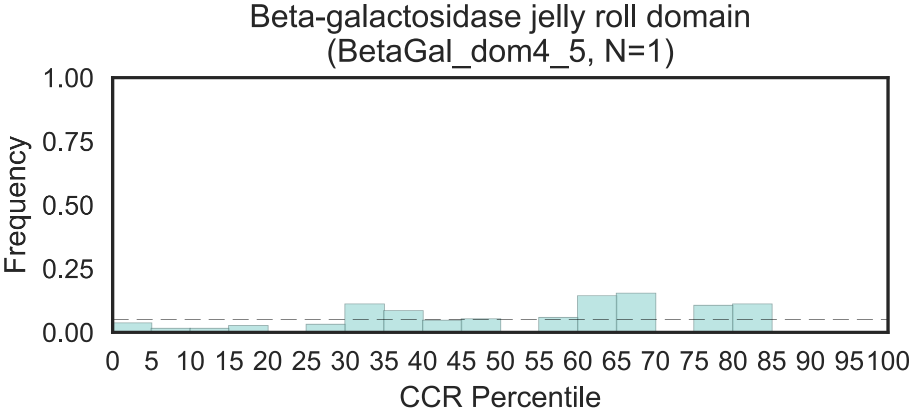

Beta-amyloid peptide (beta-APP)
(Beta-APP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

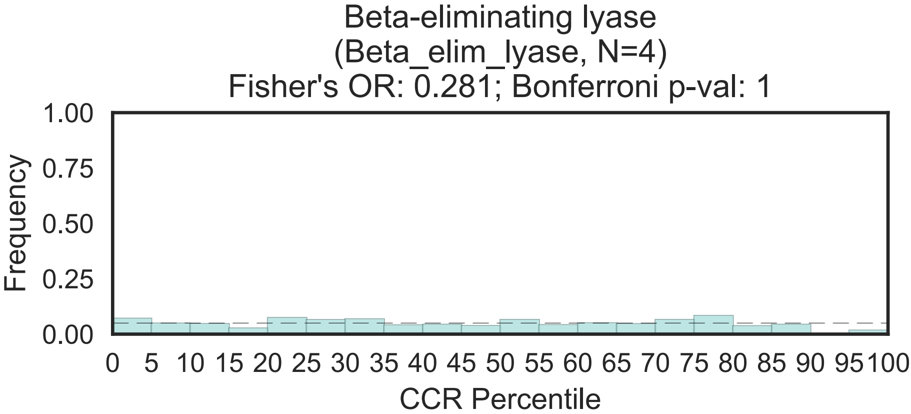


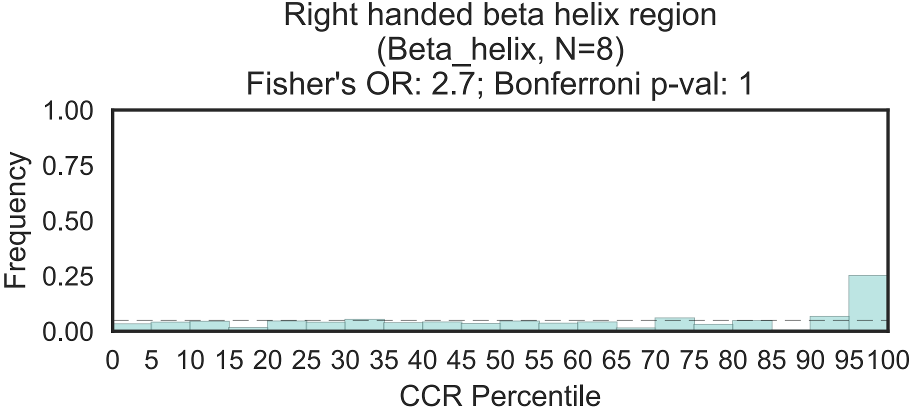
Beta-Casp domain
(Beta-Casp, N=4)
Fisher's OR: 2.12; Bonferroni p-val: 1

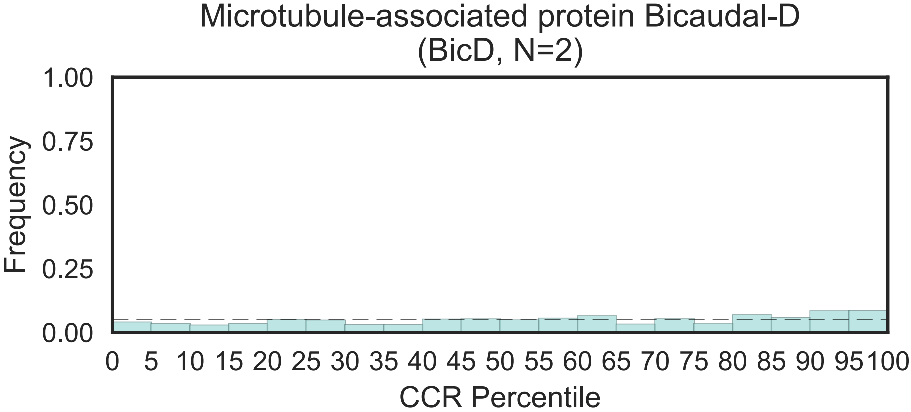

D domain of beta-TrCP
(Beta-TrCP_D, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

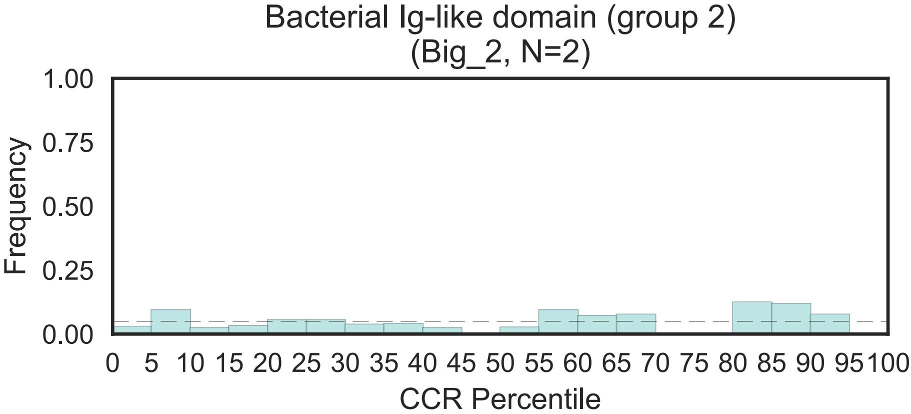

Beta-lactamase
(Beta-lactamase, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

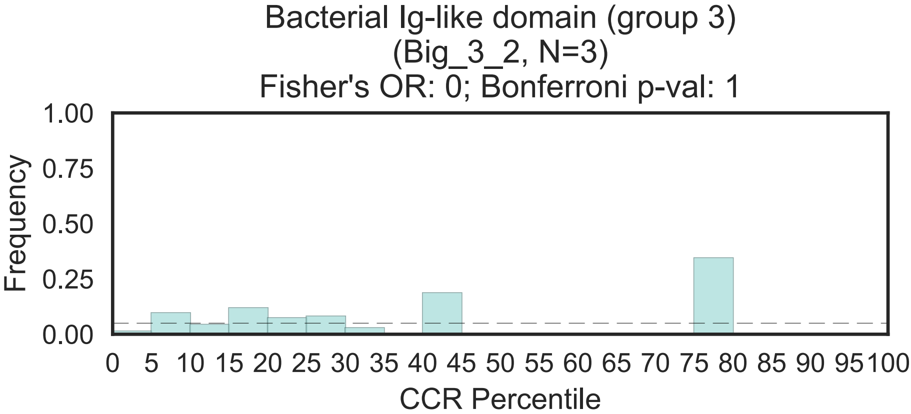

Beta-galactosidase jelly roll domain
(BetaGal_dom4_5, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

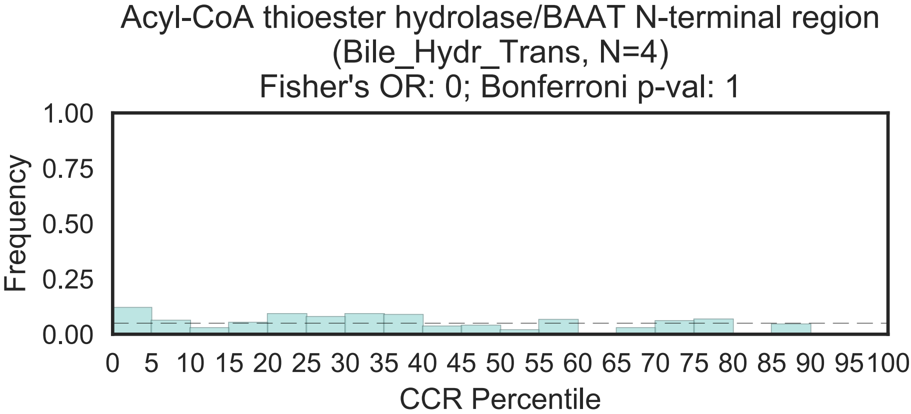

Beta-eliminating lyase
(Beta_elim_lyase, N=4)
Fisher's OR: 0.281; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Right handed beta helix region
(Beta_helix, N=8)
Fisher's OR: 2.7; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

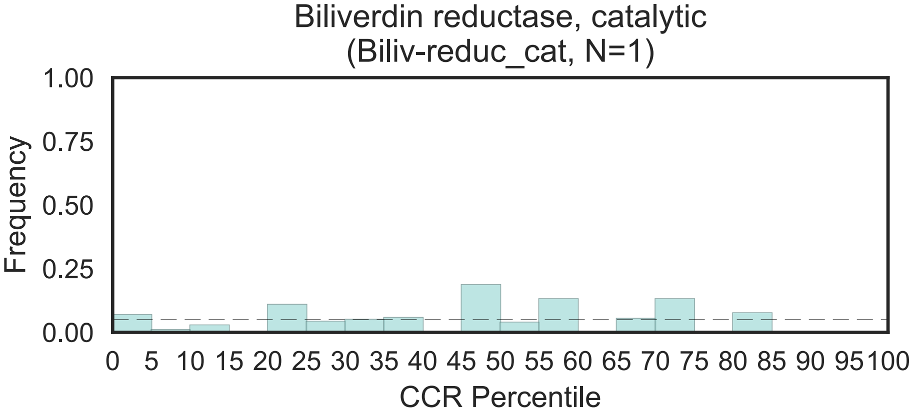

Microtubule-associated protein Bicaudal-D
(BicD, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

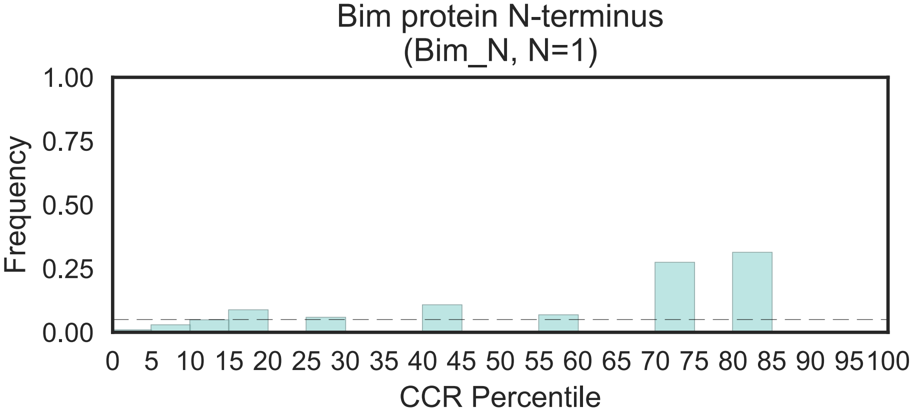

Bacterial Ig-like domain (group 2)
(Big_2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Bacterial Ig-like domain (group 3)
(Big_3_2, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

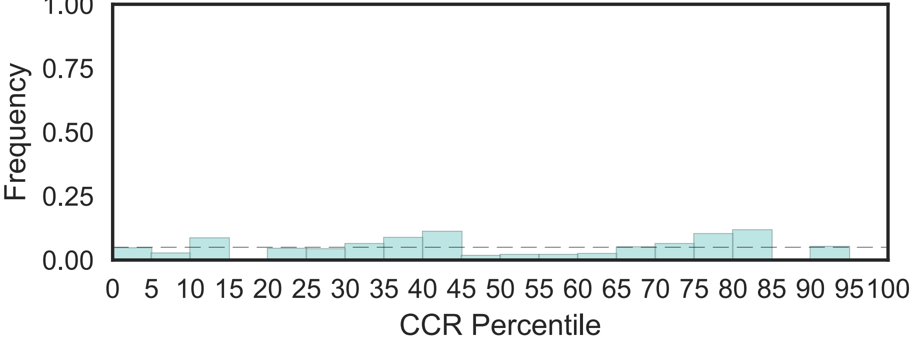


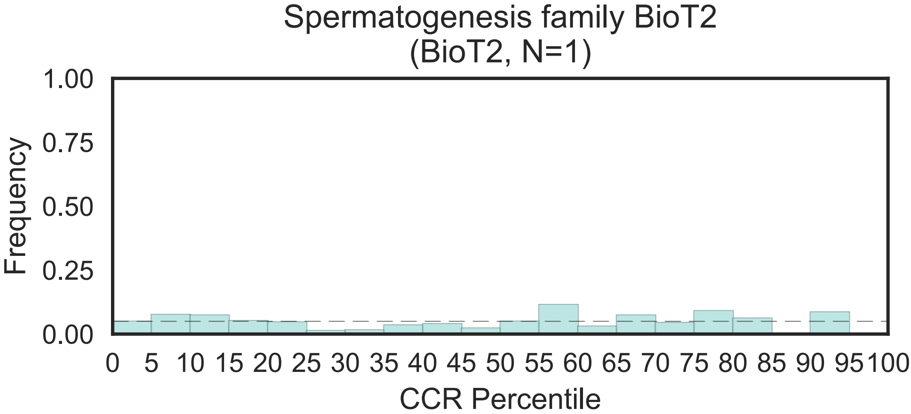
Acyl-CoA thioester hydrolase/BAAT N-terminal region
(Bile_Hydr_Trans, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

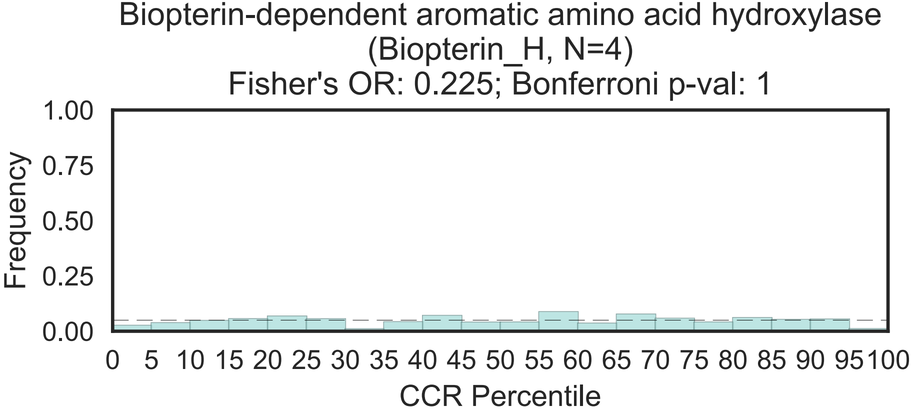


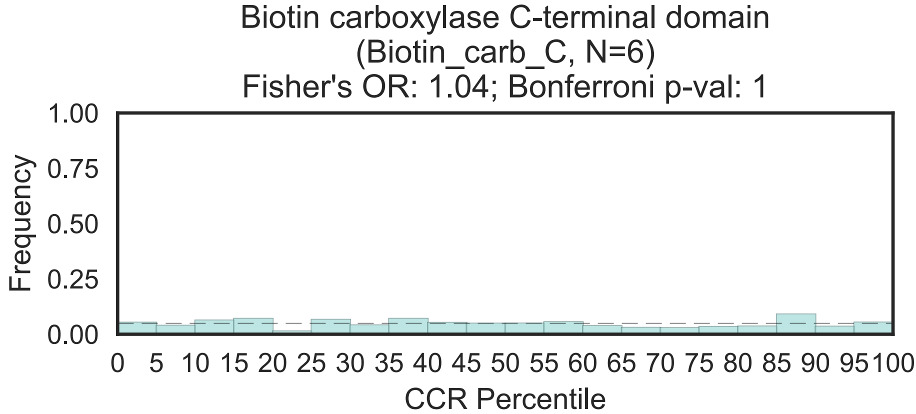

Bim protein N-terminus
(Bim_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

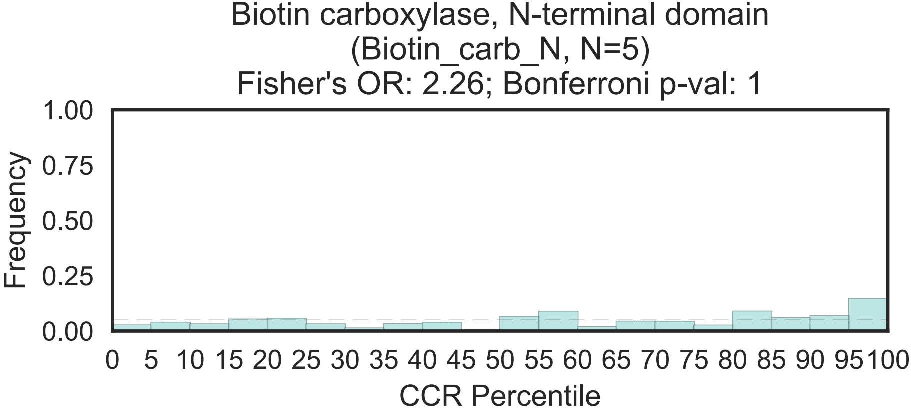
Bicoid-interacting protein 3 (Bin3)
(Bin3, N=2)

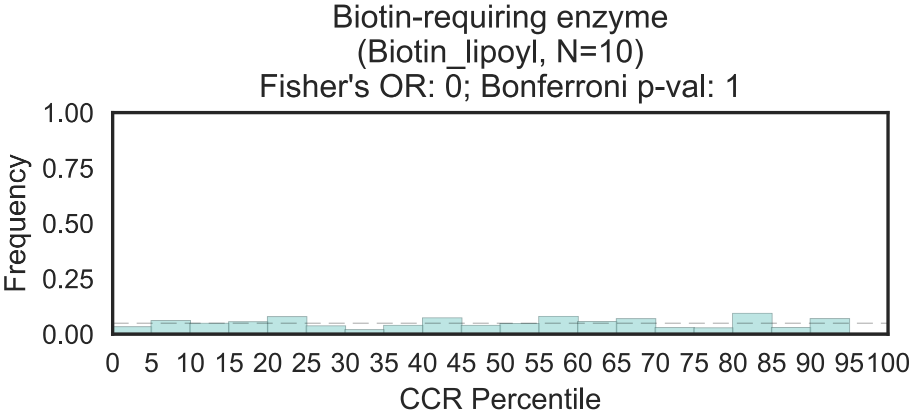


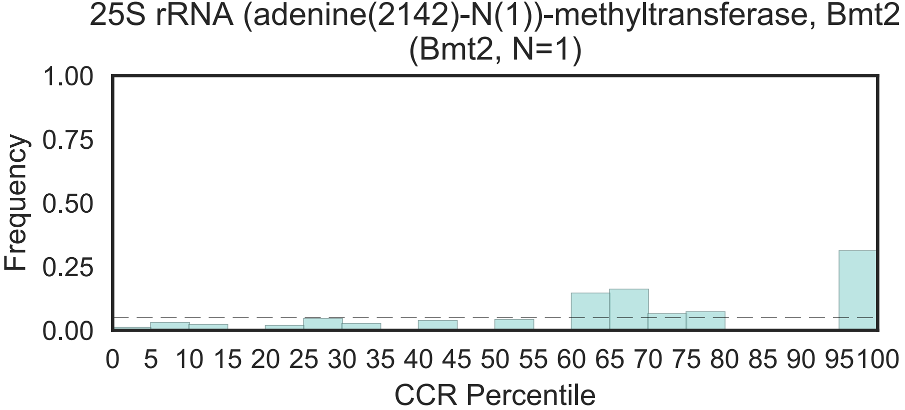

Spermatogenesis family BioT2
(BioT2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

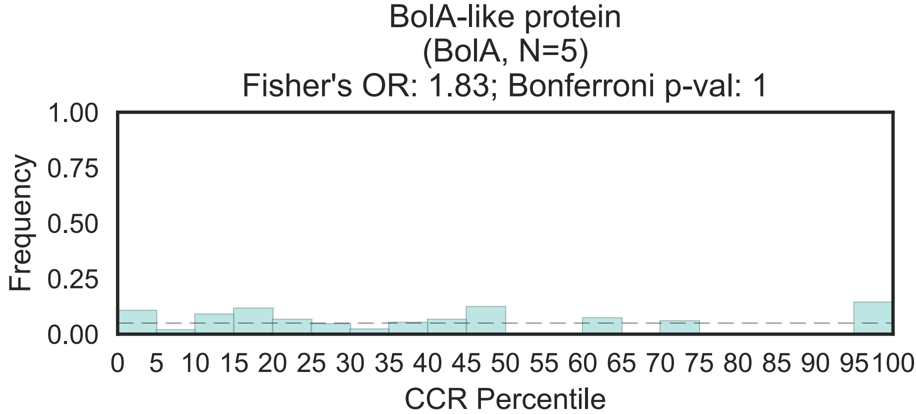

Biopterin-dependent aromatic amino acid hydroxylase
(Biopterin_H, N=4)
Fisher's OR: 0.225; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

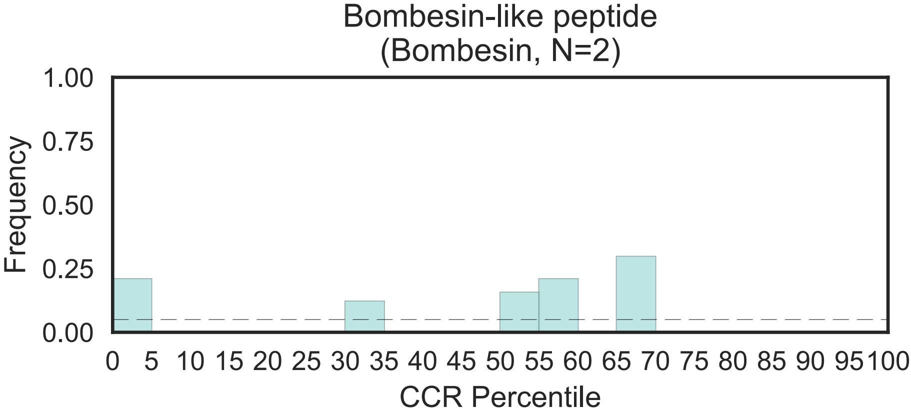

Biotin carboxylase C-terminal domain
(Biotin_carb_C, N=6)
Fisher's OR: 1.04; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

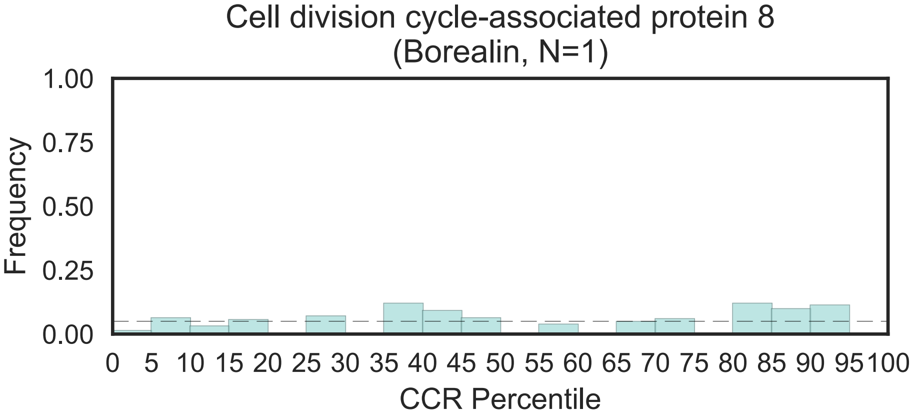
Biotin carboxylase, N-terminal domain
(Biotin_carb_N, N=5)
Fisher's OR: 2.26; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

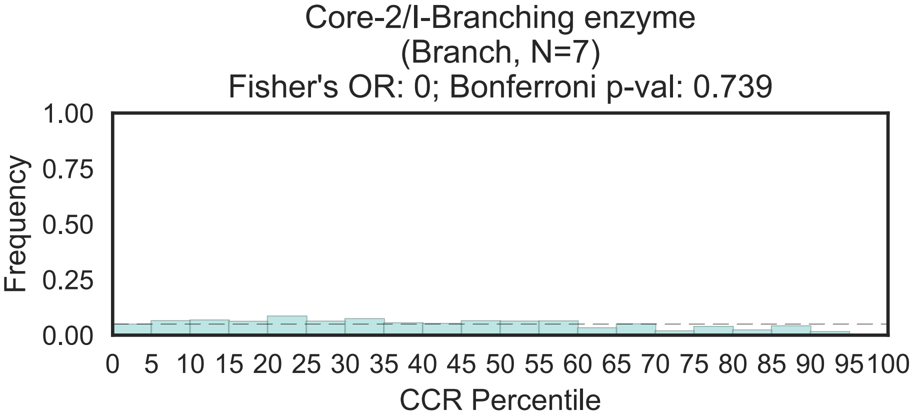

Biotin-requiring enzyme
(Biotin_lipoyl, N=10)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

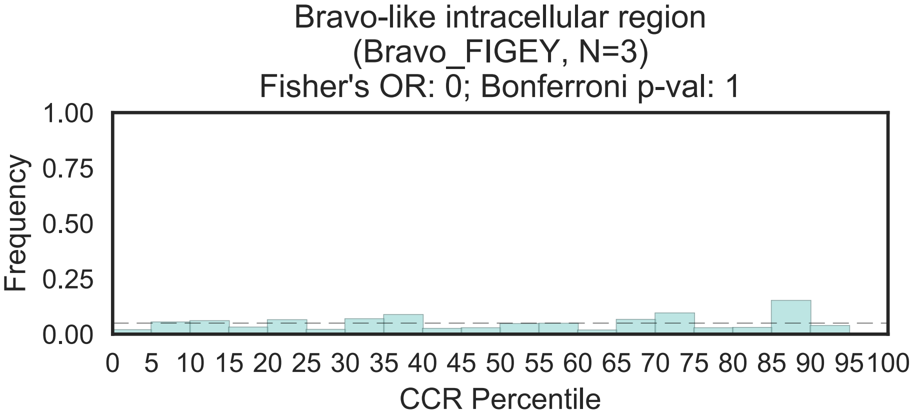

25S rRNA (adenine(2142)-N(1))-methyltransferase, Bmt2
(Bmt2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

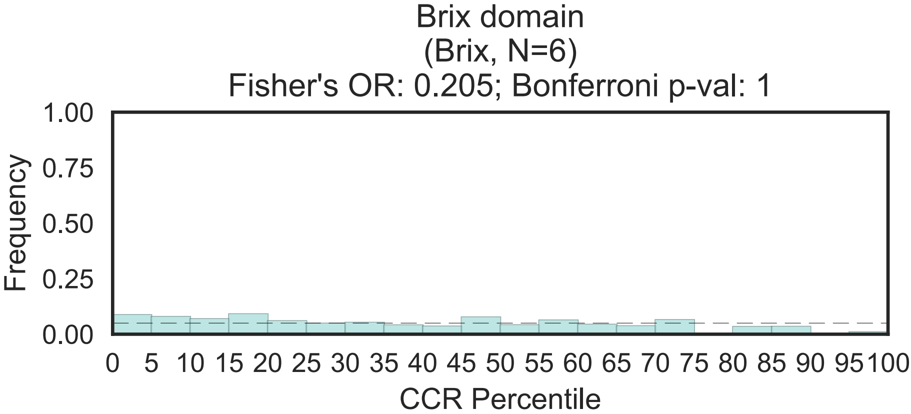

BolA-like protein
(BolA, N=5)
Fisher's OR: 1.83; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

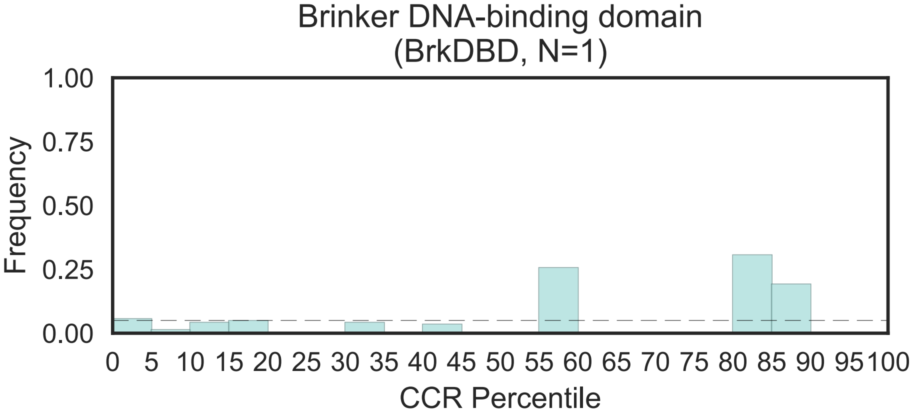

Bombesin-like peptide
(Bombesin, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

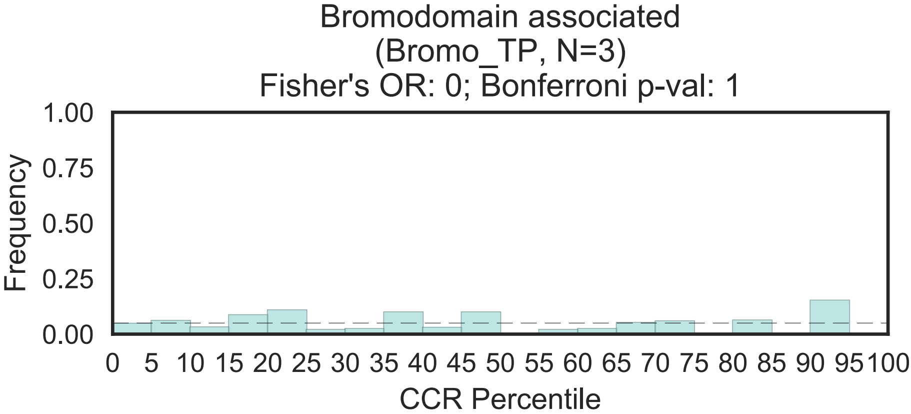

Cell division cycle-associated protein 8
(Borealin, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

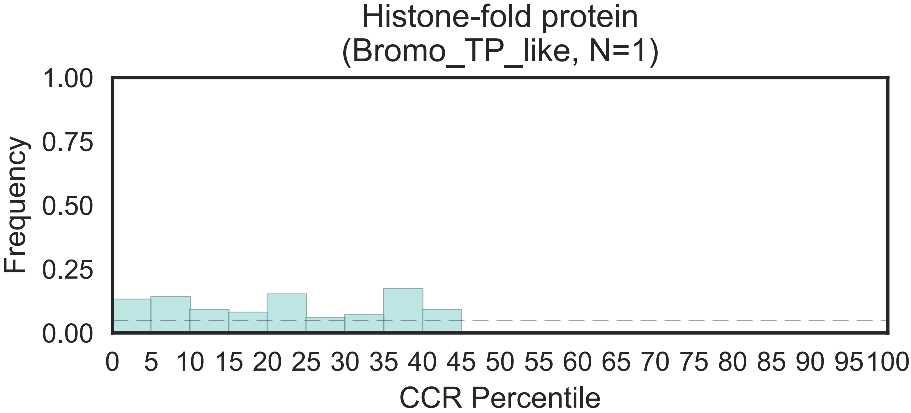

Core-2/I-Branching enzyme
(Branch, N=7)
Fisher's OR: 0; Bonferroni p-val: 0.739
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

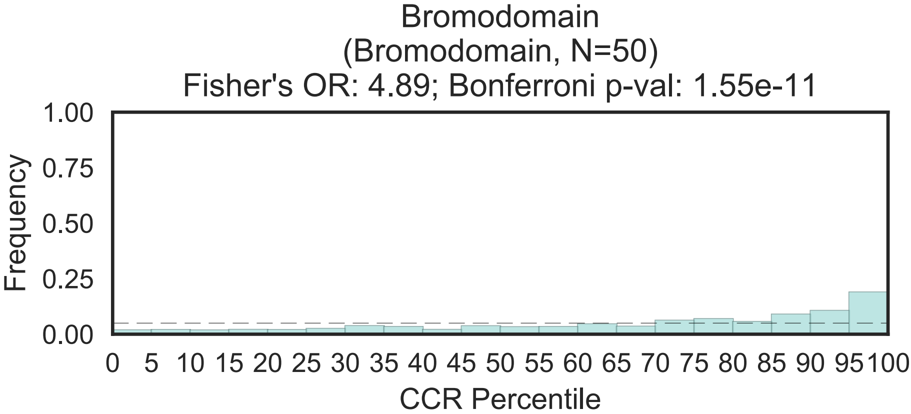

Bravo-like intracellular region
(Bravo_FIGEY, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

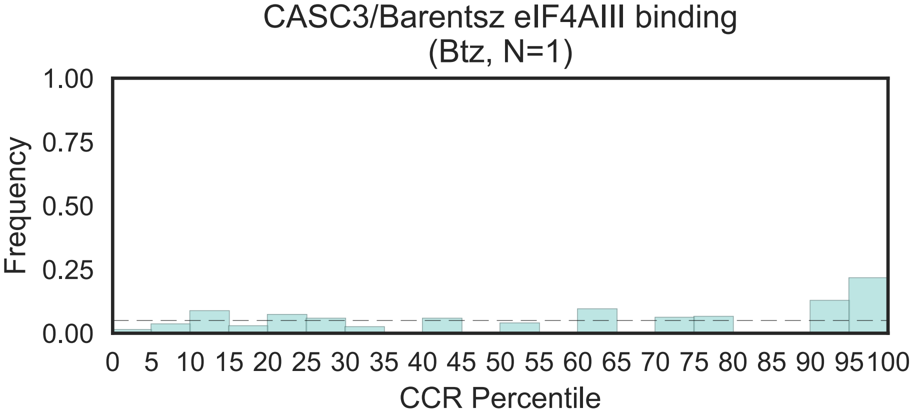

Brix domain
(Brix, N=6)
Fisher's OR: 0.205; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

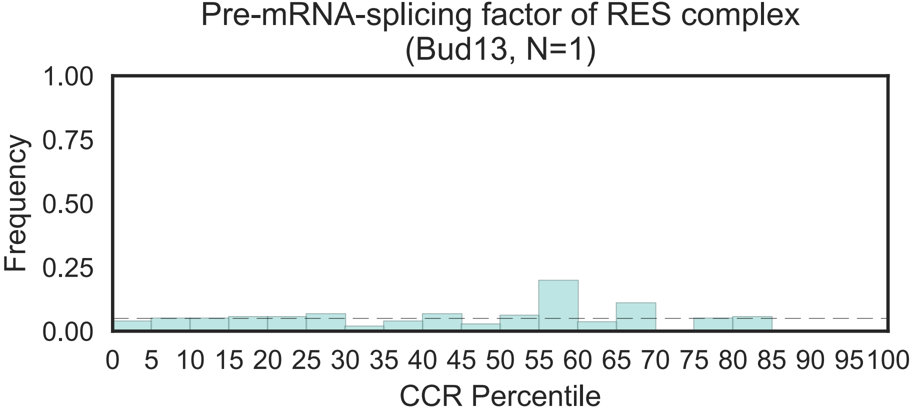

Brinker DNA-binding domain
(BrkDBD, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

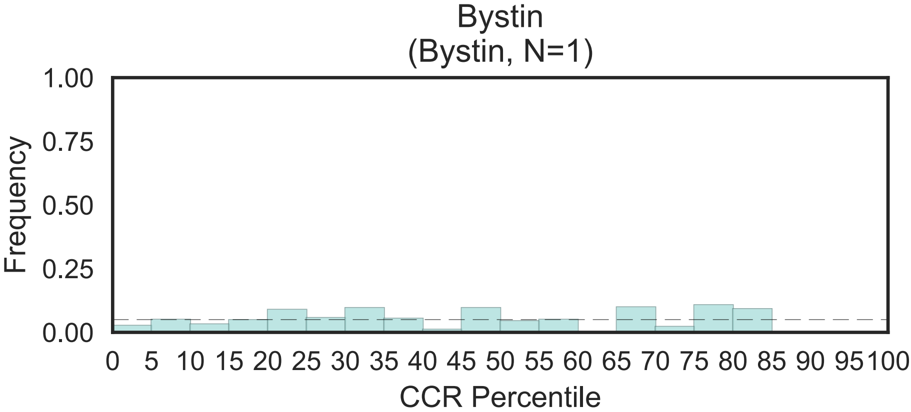

Bromodomain associated
(Bromo_TP, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

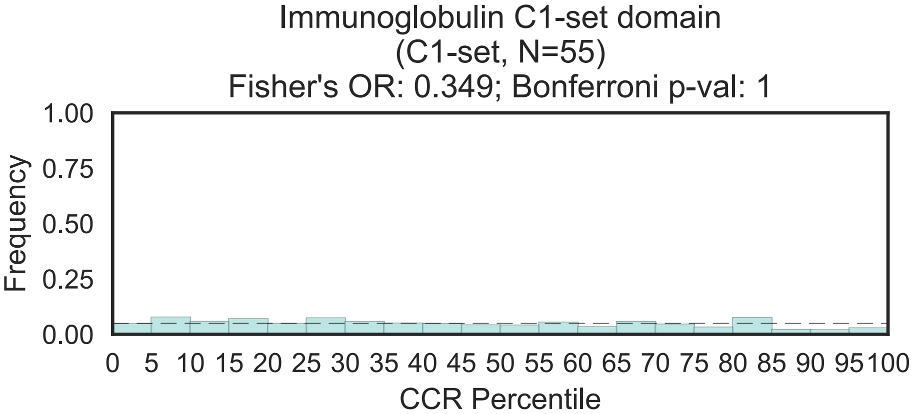

Histone-fold protein
(Bromo_TP_like, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

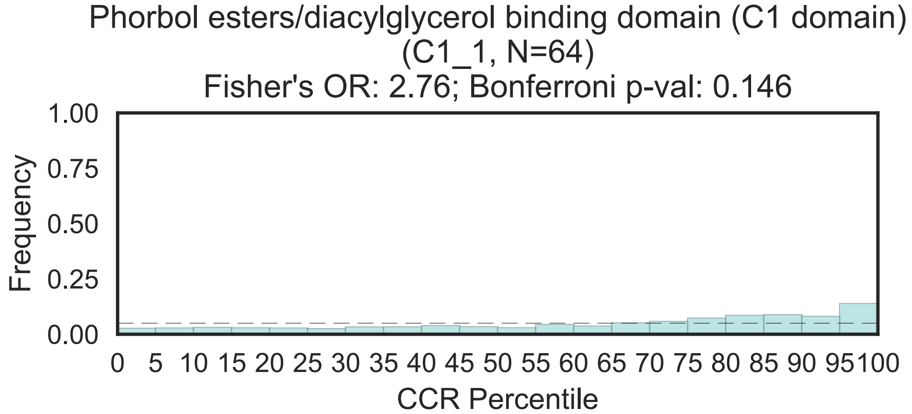

Bromodomain
(Bromodomain, N=50)
Fisher's OR: 4.89; Bonferroni p-val: 1.55e-11
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

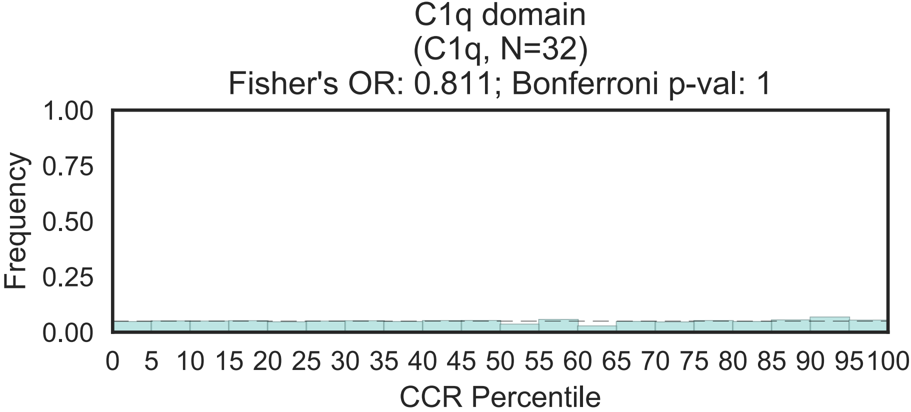

CASC3/Barentsz eIF4AIII binding
(Btz, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

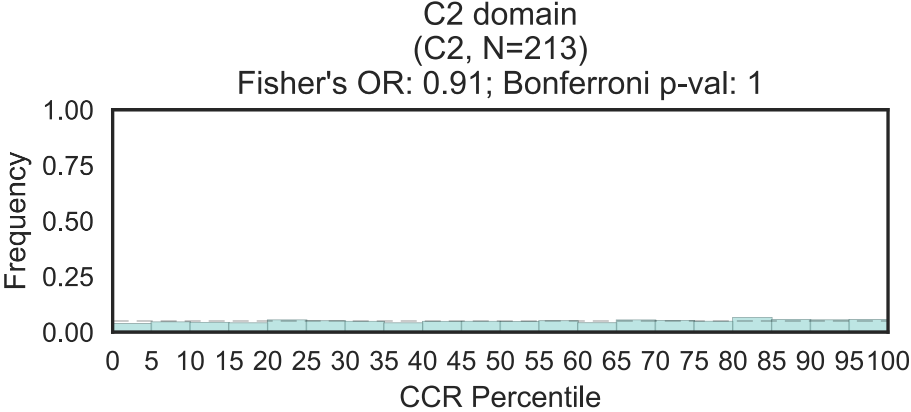

Pre-mRNA-splicing factor of RES complex
(Bud13, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

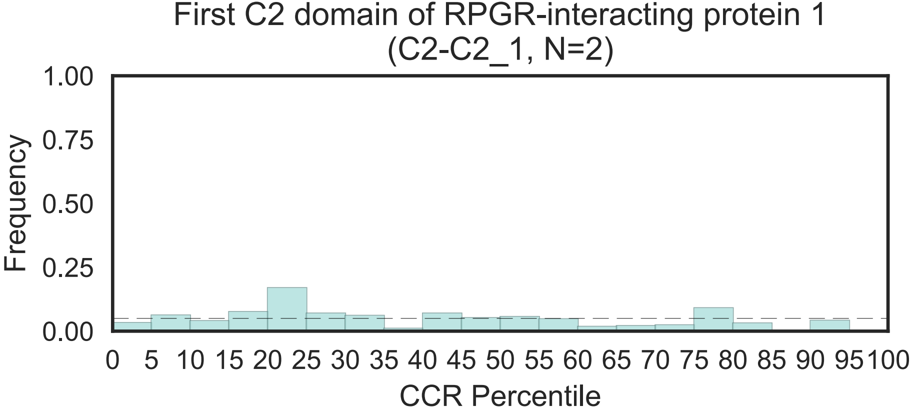

Bystin
(Bystin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

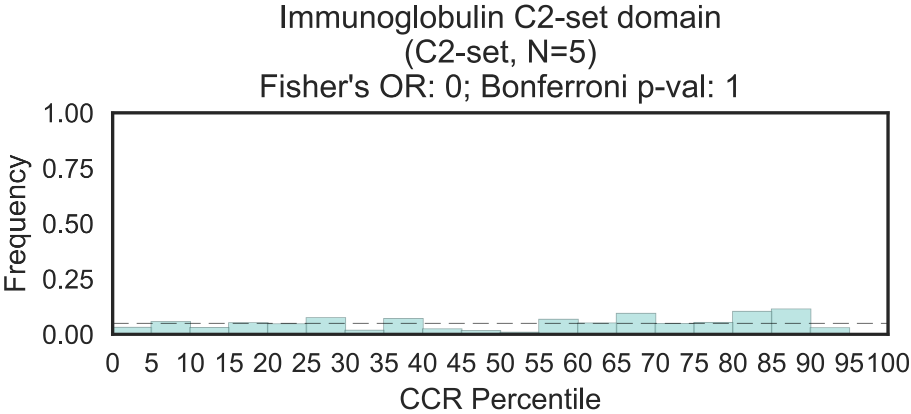

Immunoglobulin C1-set domain
(C1-set, N=55)
Fisher's OR: 0.349; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

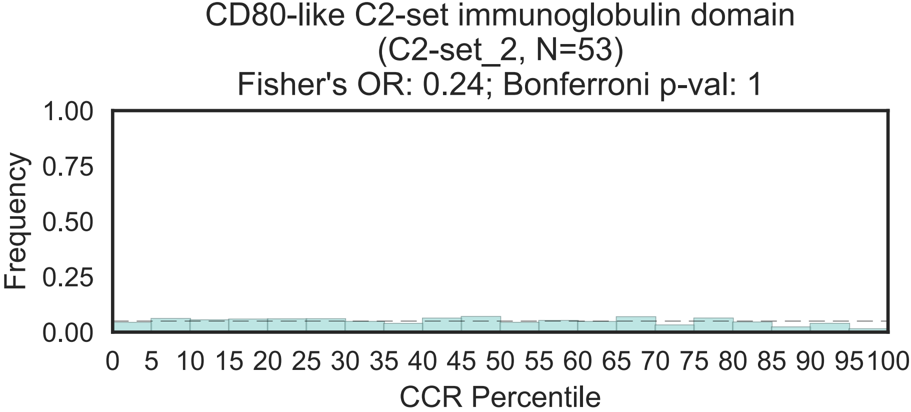

Phorbol esters/diacylglycerol binding domain (C1 domain)
(C1_1, N=64)
Fisher's OR: 2.76; Bonferroni p-val: 0.146
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

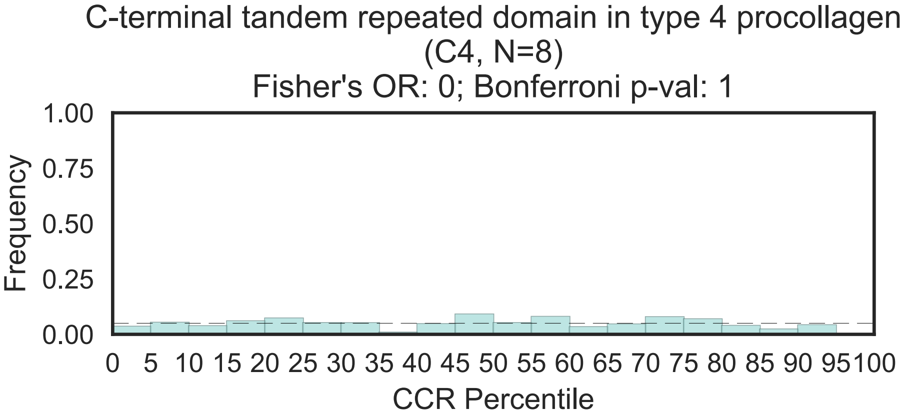

C1q domain
(C1q, N=32)
Fisher's OR: 0.811; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

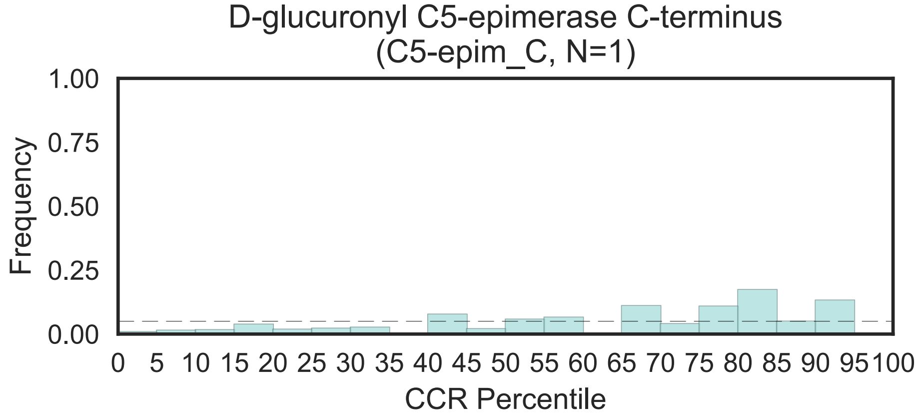

C2 domain
(C2, N=213)
Fisher's OR: 0.91; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

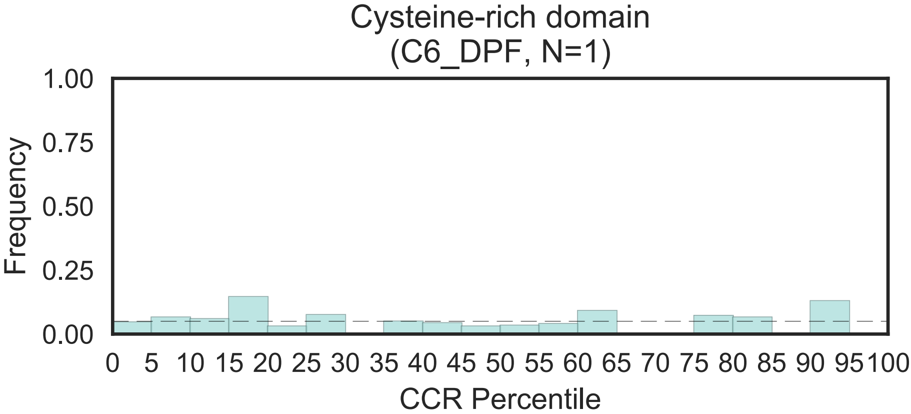

First C2 domain of RPGR-interacting protein 1
(C2-C2_1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

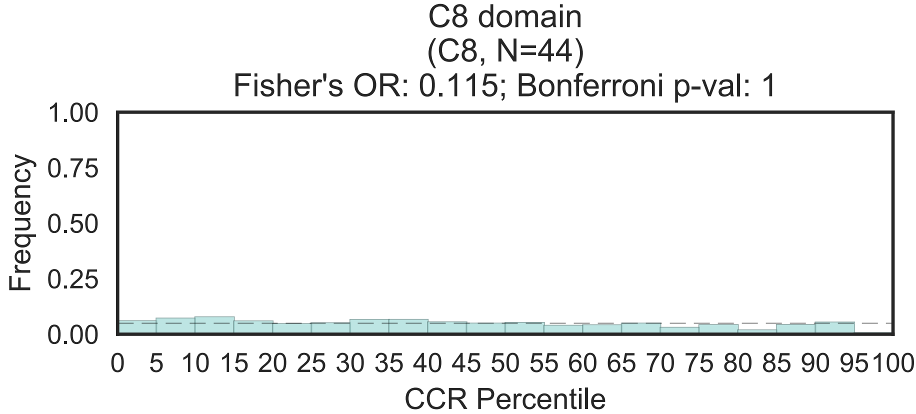

Immunoglobulin C2-set domain
(C2-set, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

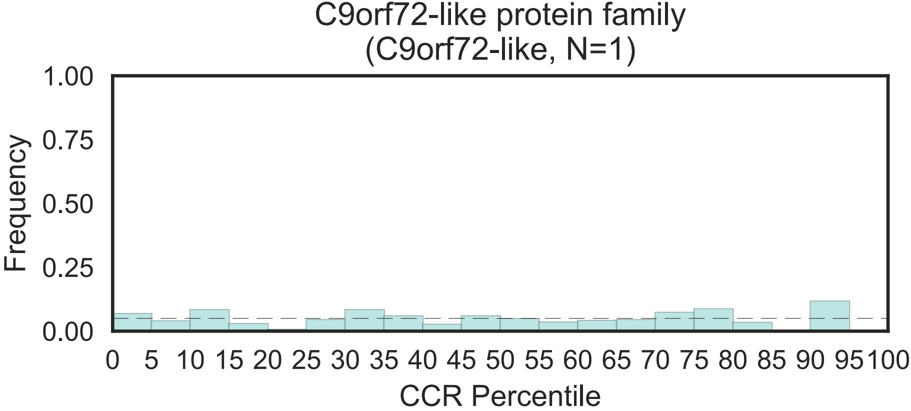

CD80-like C2-set immunoglobulin domain
(C2-set_2, N=53)
Fisher's OR: 0.24; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

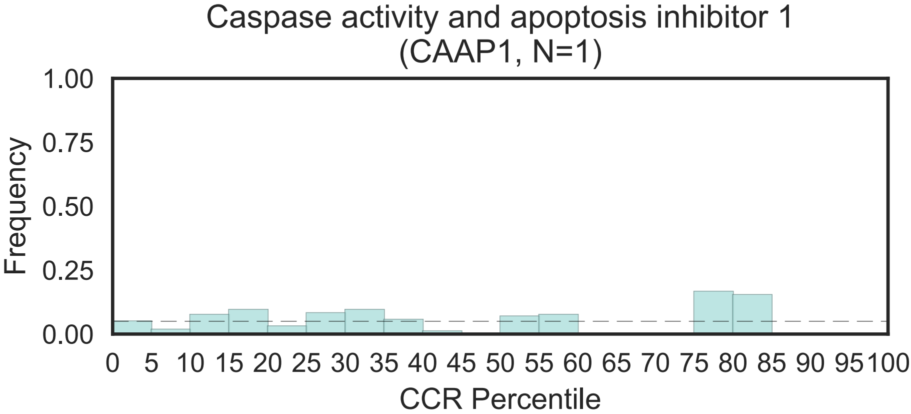

C-terminal tandem repeated domain in type 4 procollagen
(C4, N=8)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

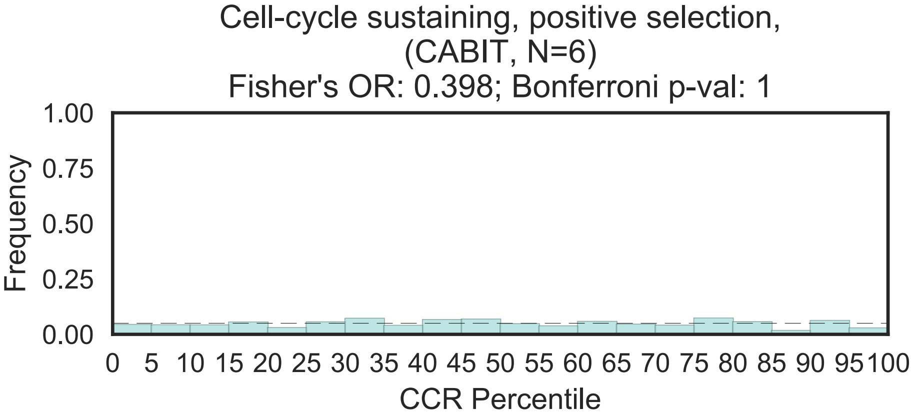

D-glucuronyl C5-epimerase C-terminus
(C5-epim_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Cysteine-rich domain
(C6_DPF, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

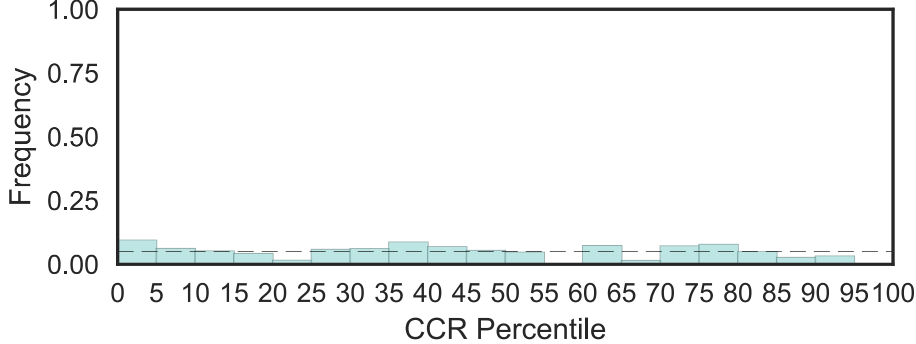

C8 domain
(C8, N=44)
Fisher's OR: 0.115; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

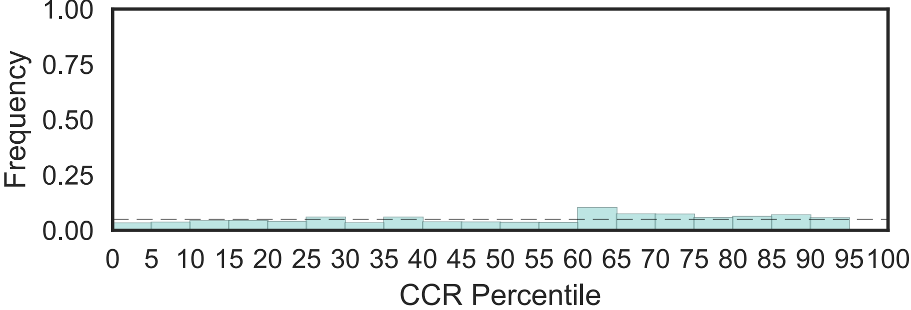

C9orf72-like protein family
(C9orf72-like, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


Caspase activity and apoptosis inhibitor 1
(CAAP1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

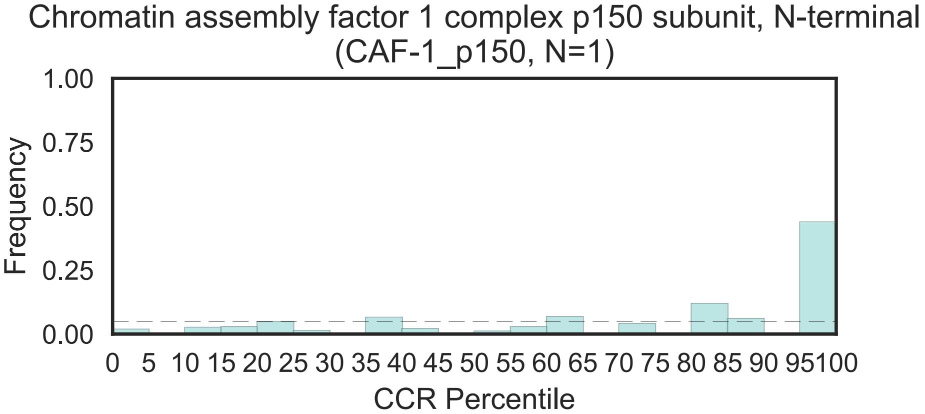

Cell-cycle sustaining, positive selection,
(CABIT, N=6)
Fisher's OR: 0.398; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

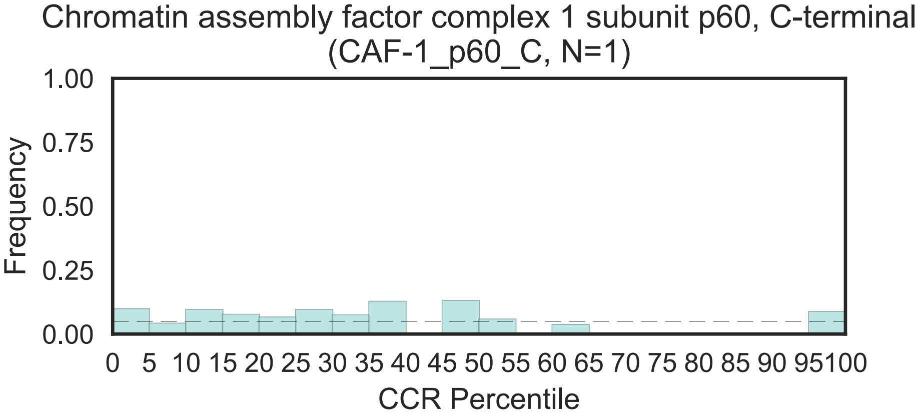
Calcium-binding and spermatid-specific protein 1 (CABS1, N=1)

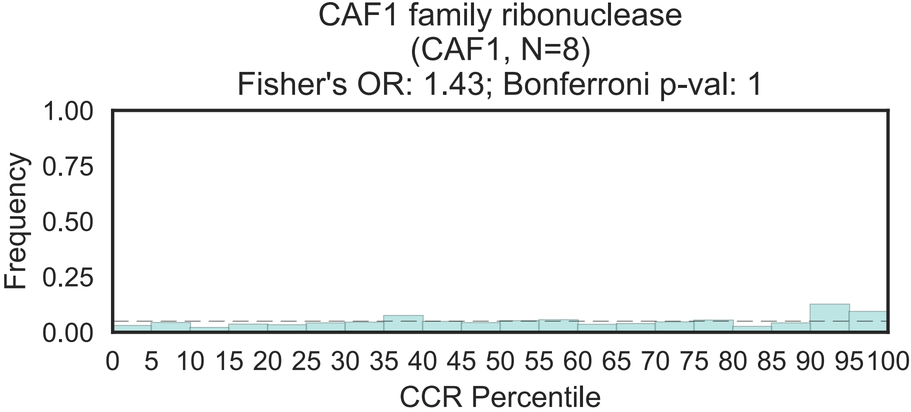


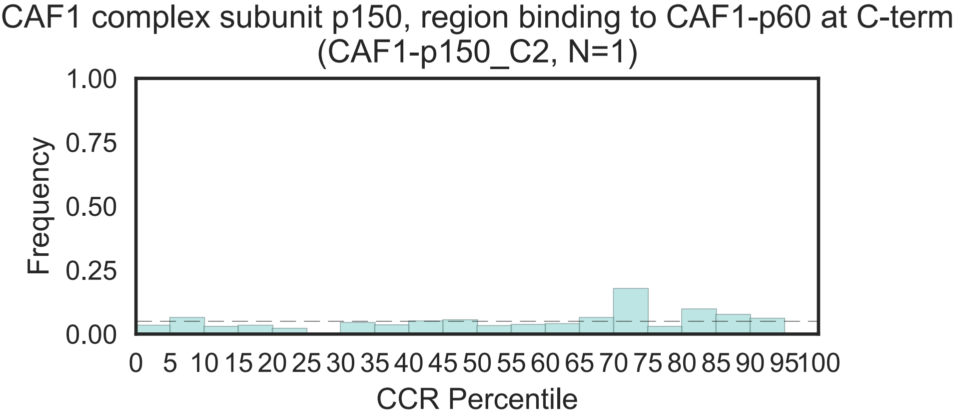


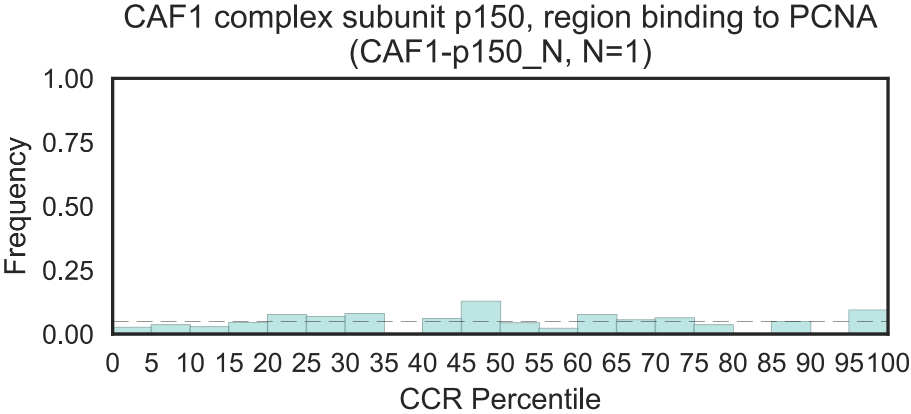
Voltage-gated calcium channel subunit alpha, C-term
(CAC1F_C, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

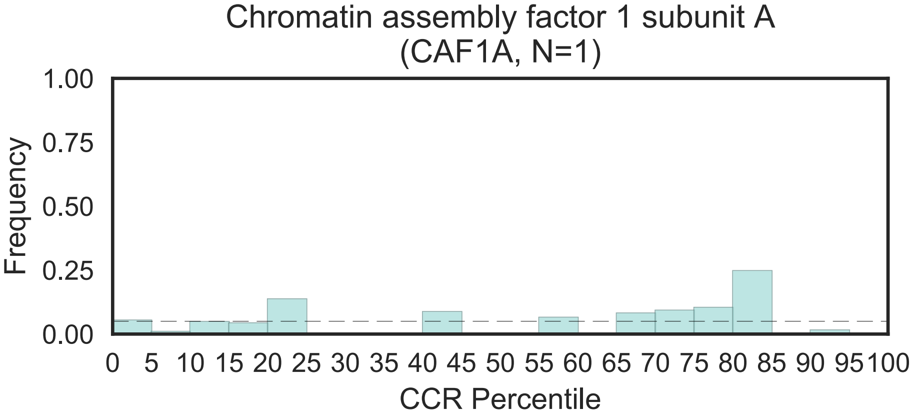

Chromatin assembly factor 1 complex p150 subunit, N-terminal
(CAF-1_p150, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

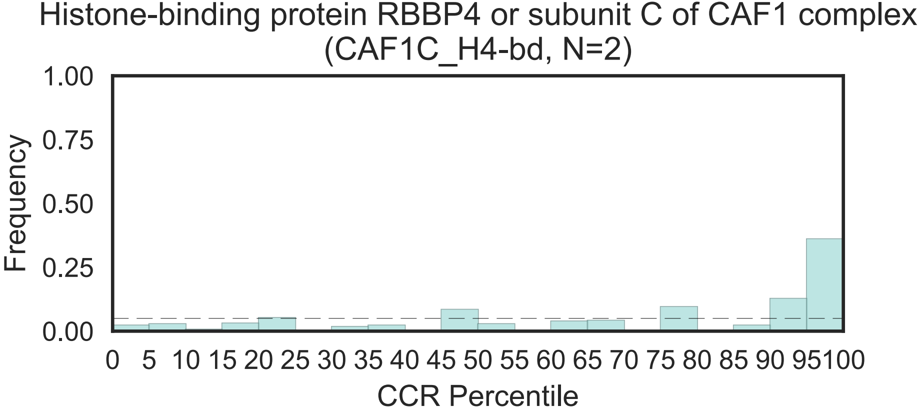

Chromatin assembly factor complex 1 subunit p60, C-terminal
(CAF-1_p60_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

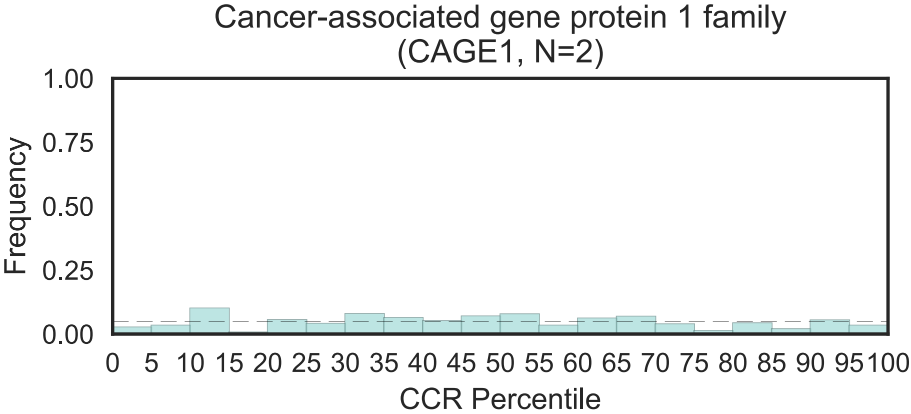

CAF1 family ribonuclease
(CAF1, N=8)
Fisher's OR: 1.43; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

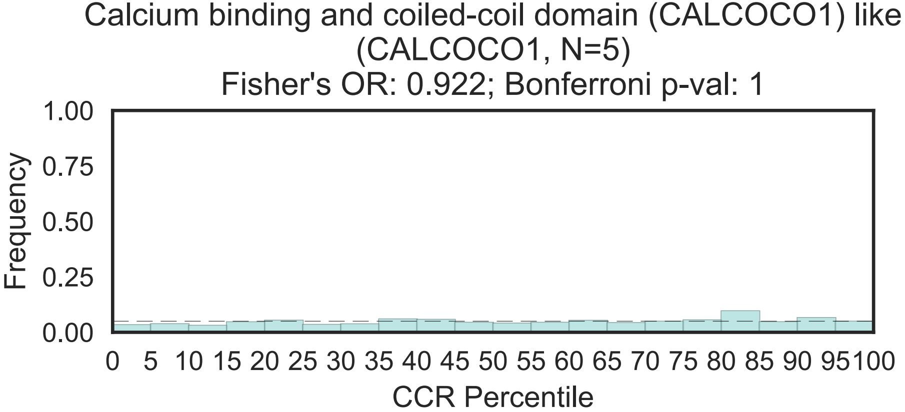

CAF1 complex subunit p150, region binding to CAF1-p60 at C-term
(CAF1-p150_C2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

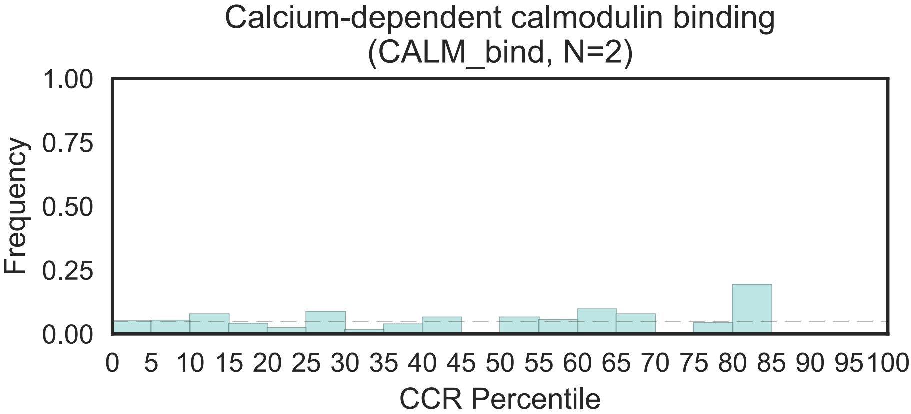

CAF1 complex subunit p150, region binding to PCNA
(CAF1-p150_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

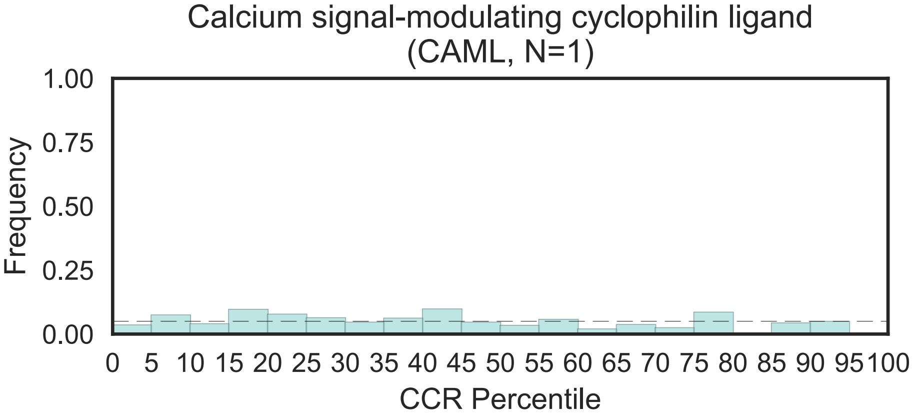

Chromatin assembly factor 1 subunit A
(CAF1A, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Histone-binding protein RBBP4 or subunit C of CAF1 complex
(CAF1C_H4-bd, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

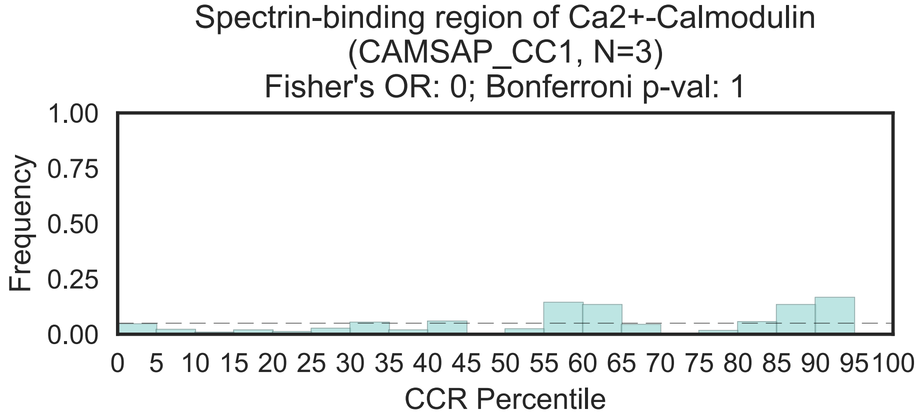

Cancer-associated gene protein 1 family
(CAGE1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

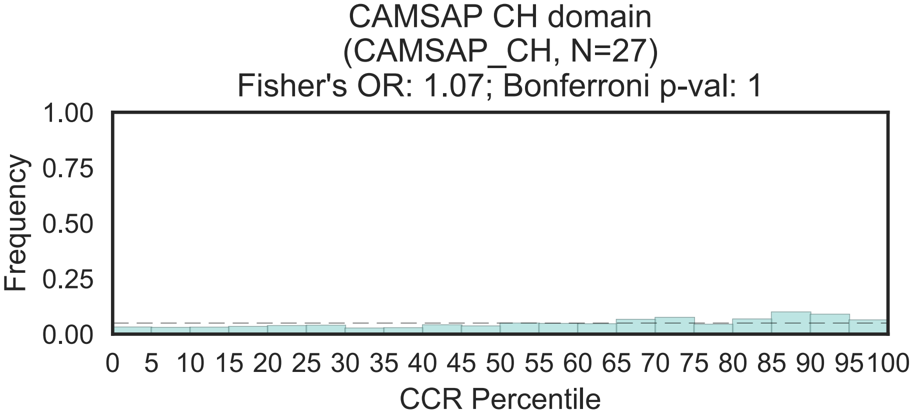

Calcium binding and coiled-coil domain (CALCOCO1) like
(CALCOCO1, N=5)
Fisher's OR: 0.922; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

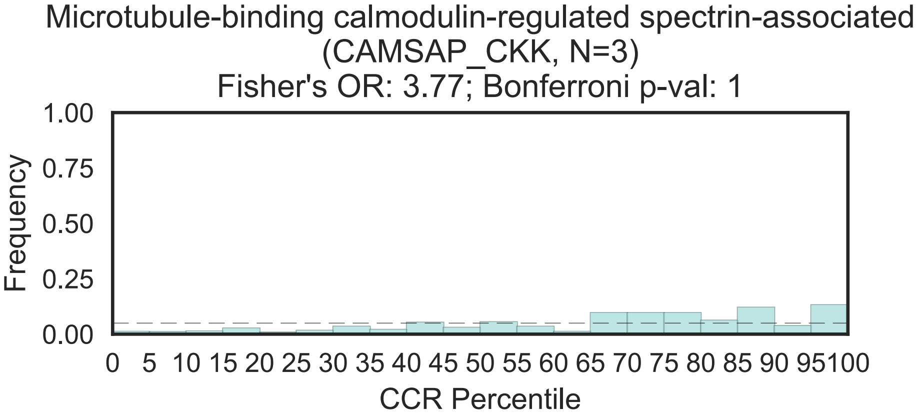

Calcium-dependent calmodulin binding
(CALM_bind, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

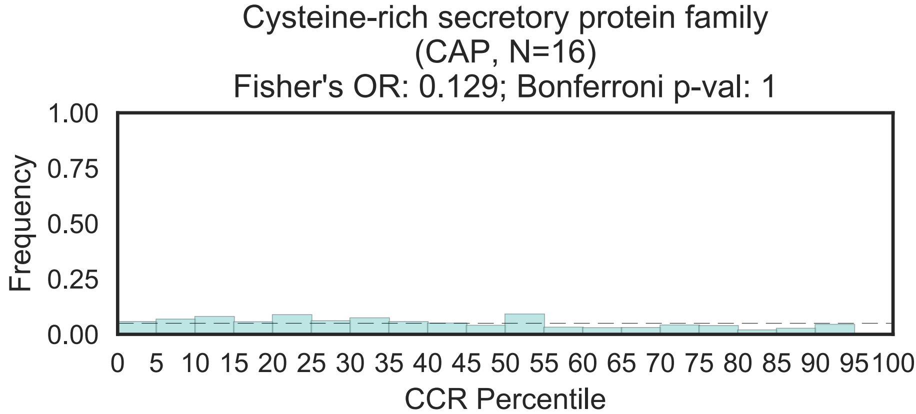


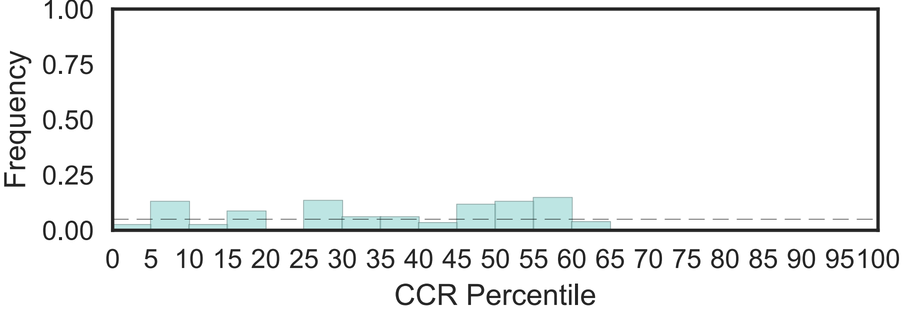
Calcium signal-modulating cyclophilin ligand (CAML, N=1)

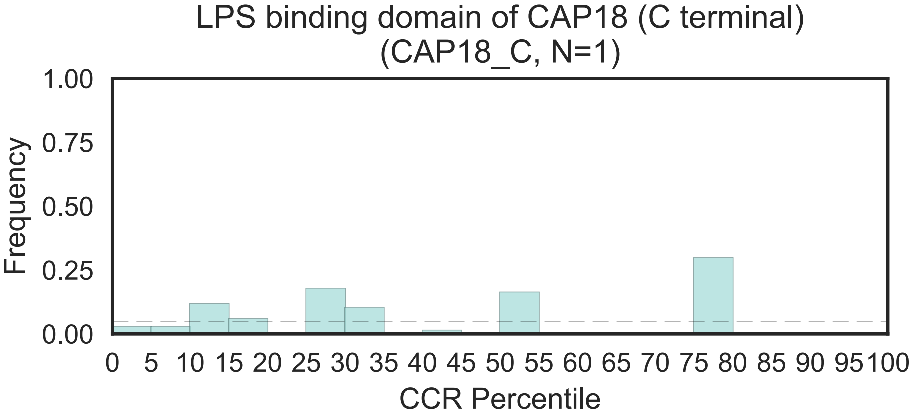

Spectrin-binding region of Ca2+-Calmodulin
(CAMSAP_CC1, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

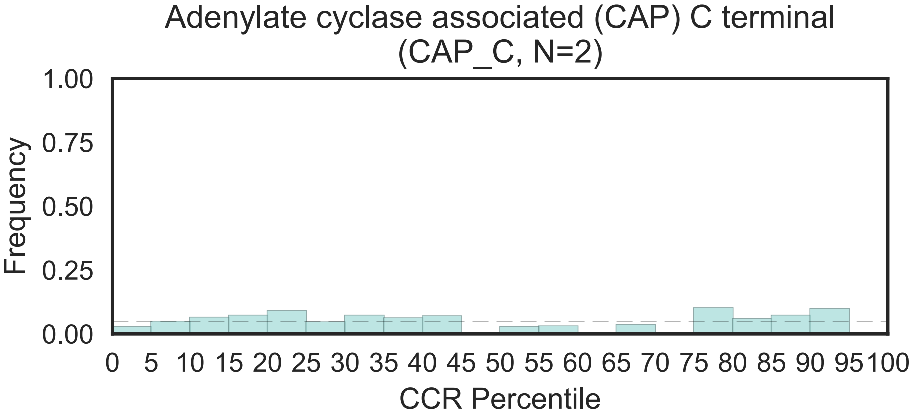
CAMSAP CH domain
(CAMSAP_CH, N=27)
Fisher's OR: 1.07; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

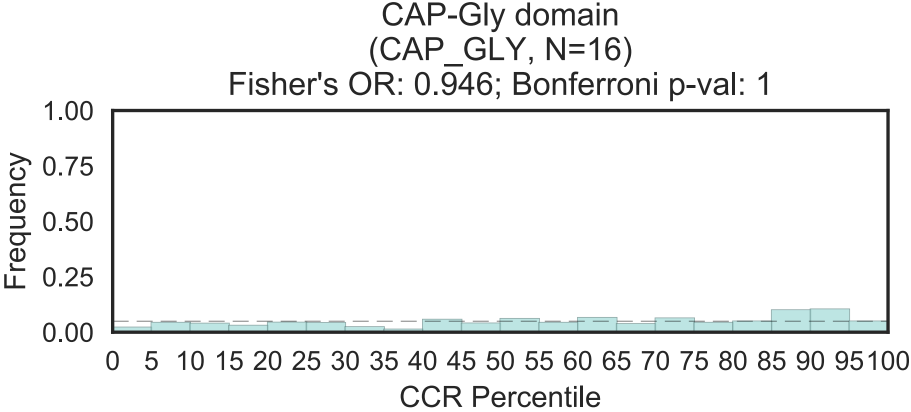

Microtubule-binding calmodulin-regulated spectrin-associated
(CAMSAP_CKK, N=3)
Fisher's OR: 3.77; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

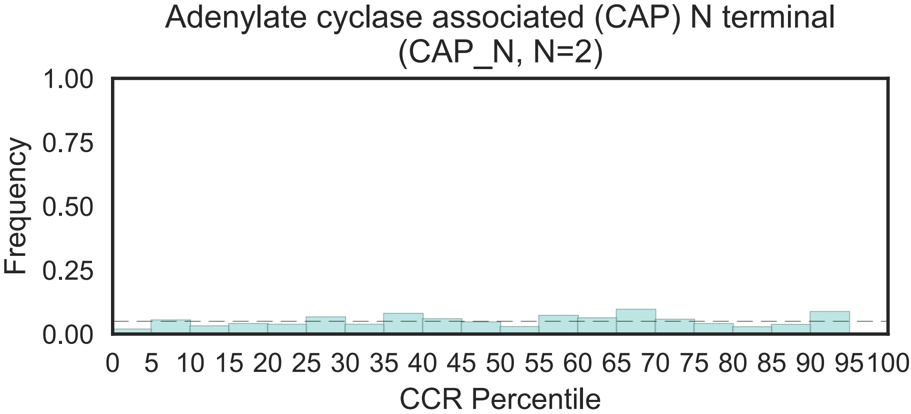

Cysteine-rich secretory protein family
(CAP, N=16)
Fisher's OR: 0.129; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

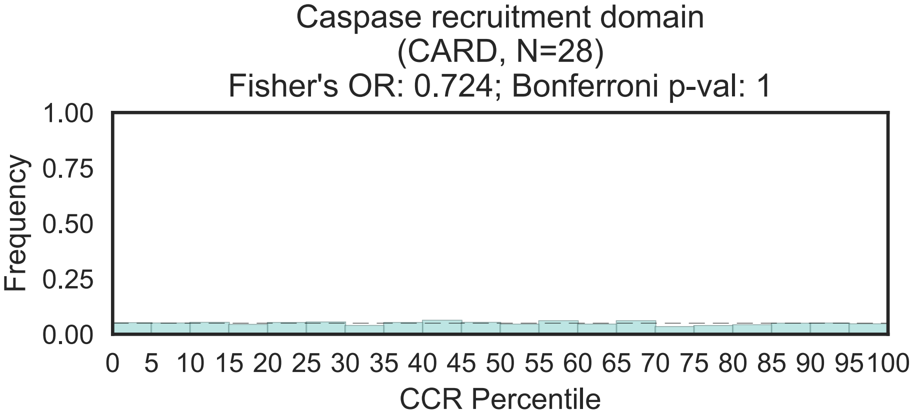

WASH complex subunit CAP-Z interacting, central region
(CAP-ZIP_m, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

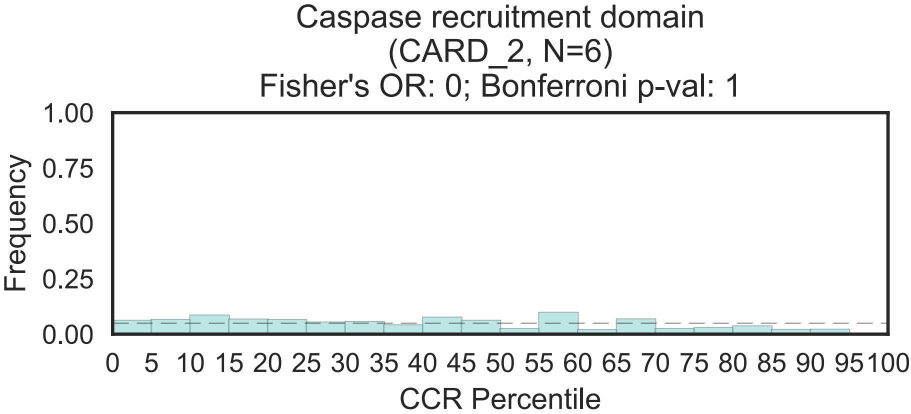

LPS binding domain of CAP18 (C terminal)
(CAP18_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

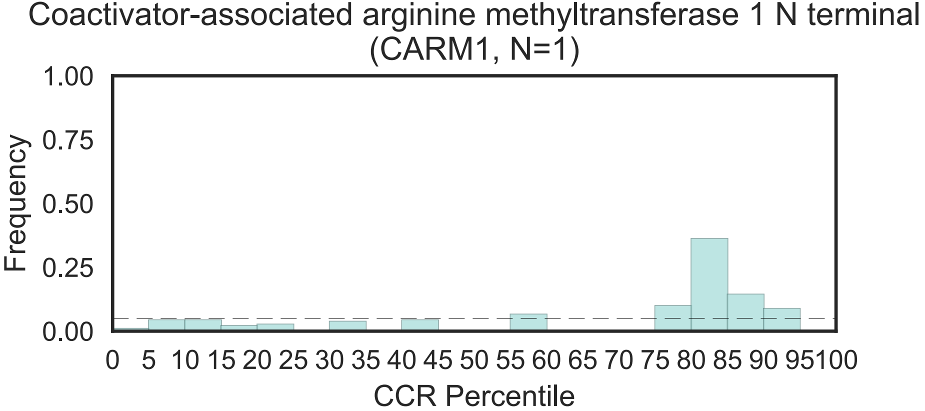

Adenylate cyclase associated (CAP) C terminal (CAP_C, N=2)

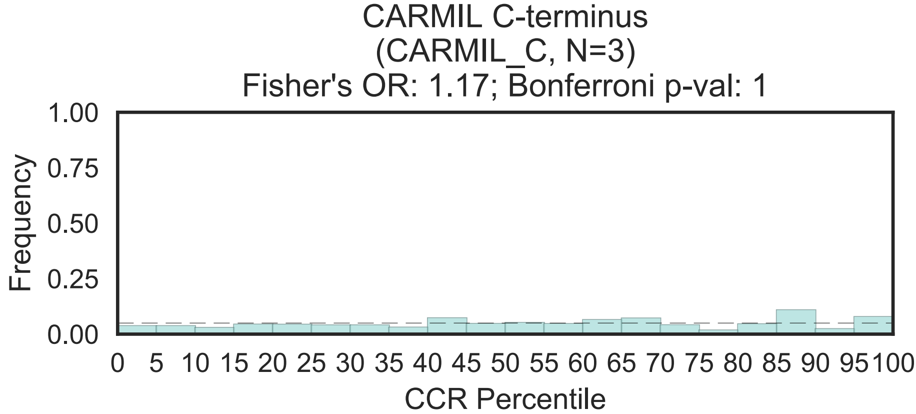

CAP-Gly domain
(CAP_GLY, N=16)
Fisher's OR: 0.946; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

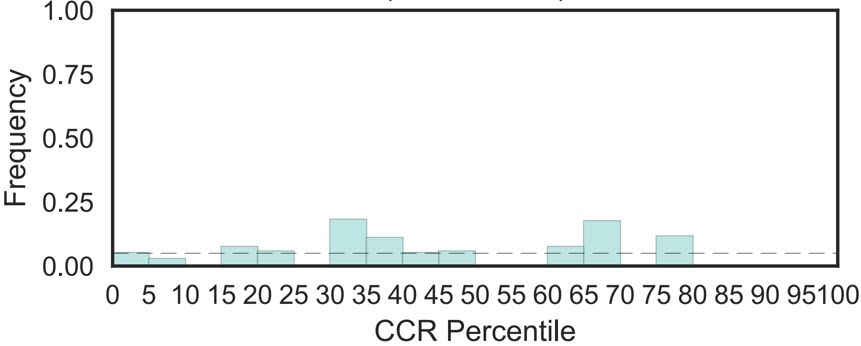

Adenylate cyclase associated (CAP) N terminal
(CAP_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Caspase recruitment domain
(CARD, N=28)
Fisher's OR: 0.724; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

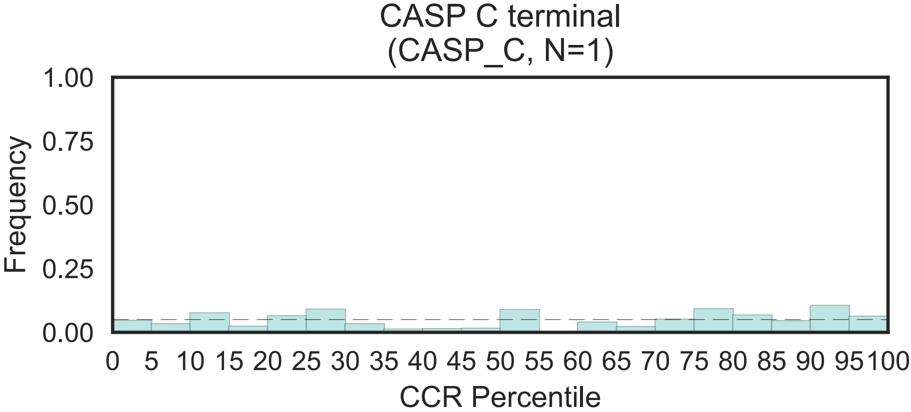

Caspase recruitment domain
(CARD_2, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

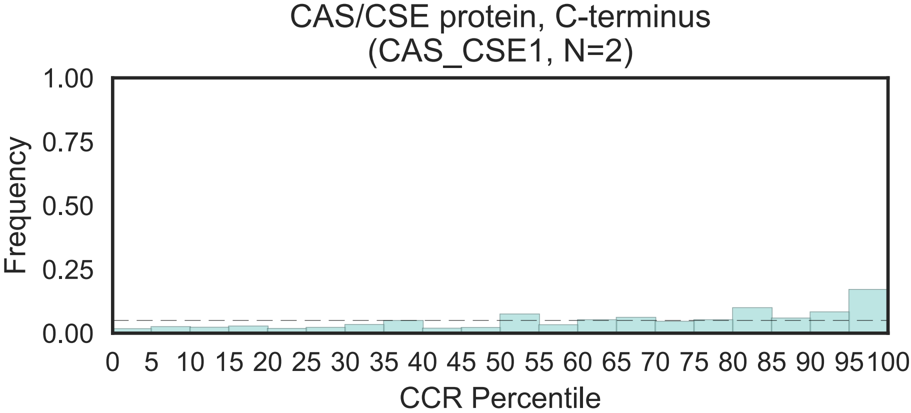

Coactivator-associated arginine methyltransferase 1 N terminal
(CARM1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

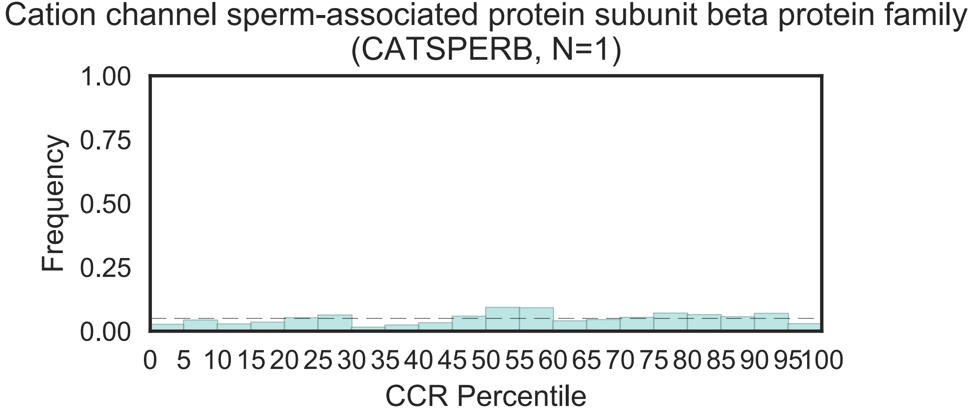

CARMIL C-terminus
(CARMIL_C, N=3)
Fisher's OR: 1.17; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



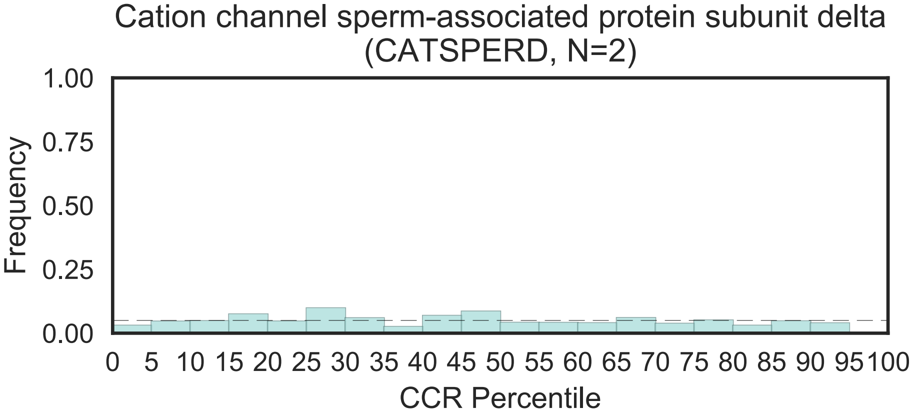
Cocaine and amphetamine regulated transcript protein (CART) (CART, N=1)

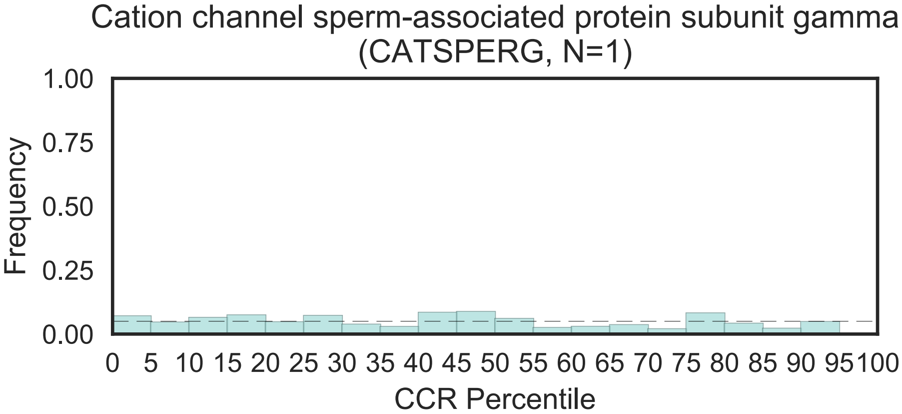

CASP C terminal
(CASP_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

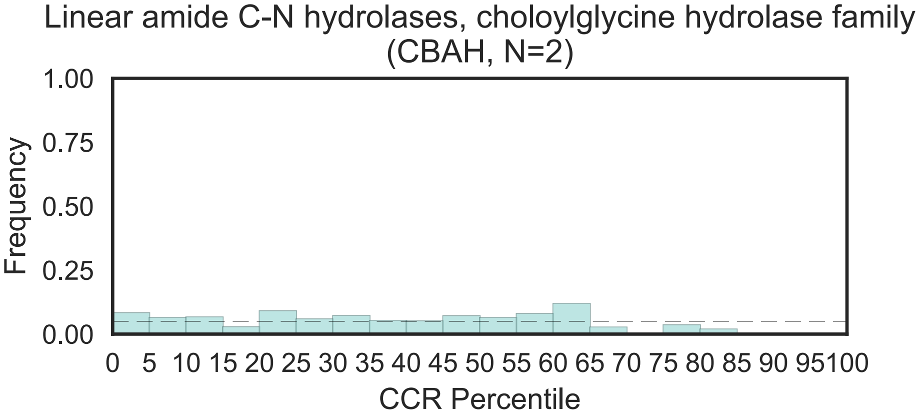

CAS/CSE protein, C-terminus
(CAS_CSE1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



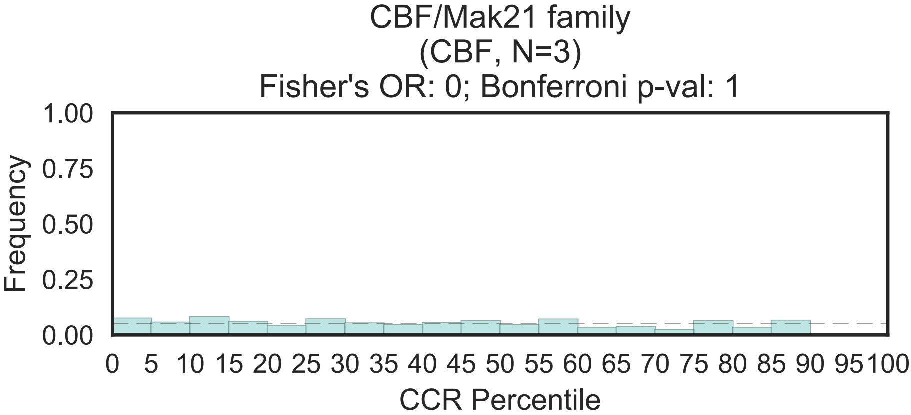
Cation channel sperm-associated protein subunit beta protein family
(CATSPERB, N=1)

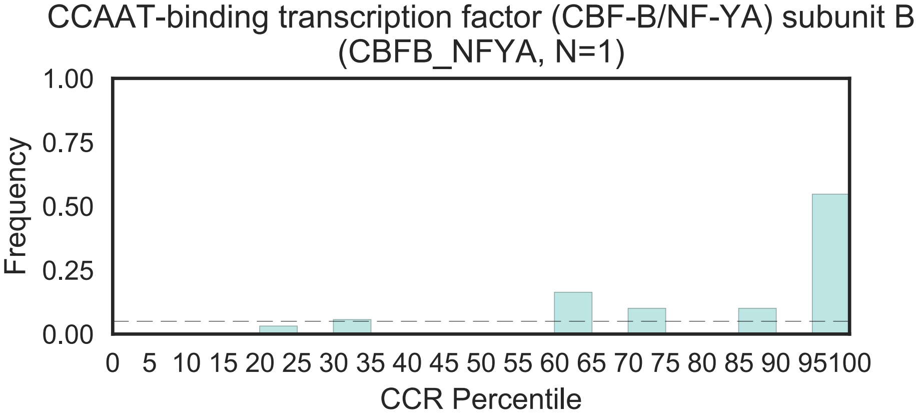

Cation channel sperm-associated protein subunit delta
(CATSPERD, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

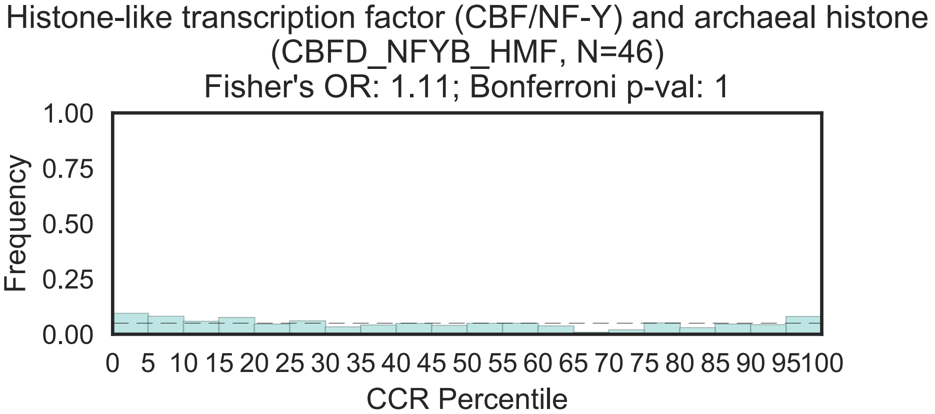

Cation channel sperm-associated protein subunit gamma
(CATSPERG, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

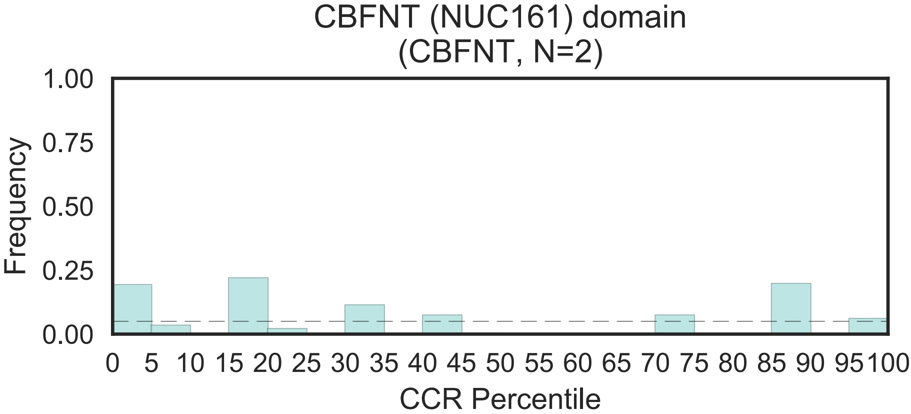


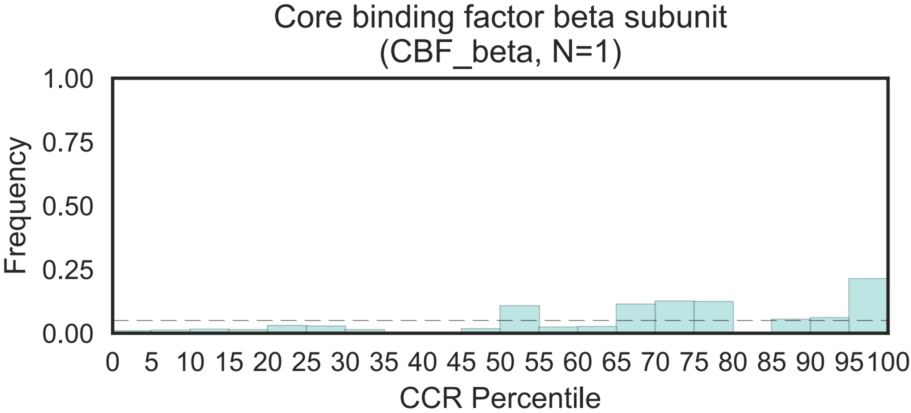
Linear amide C-N hydrolases, choloylglycine hydrolase family
(CBAH, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

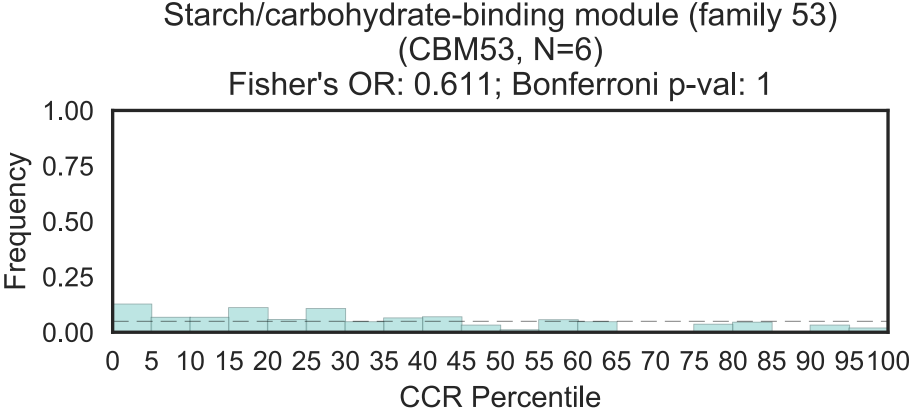

CBF/Mak21 family
(CBF, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

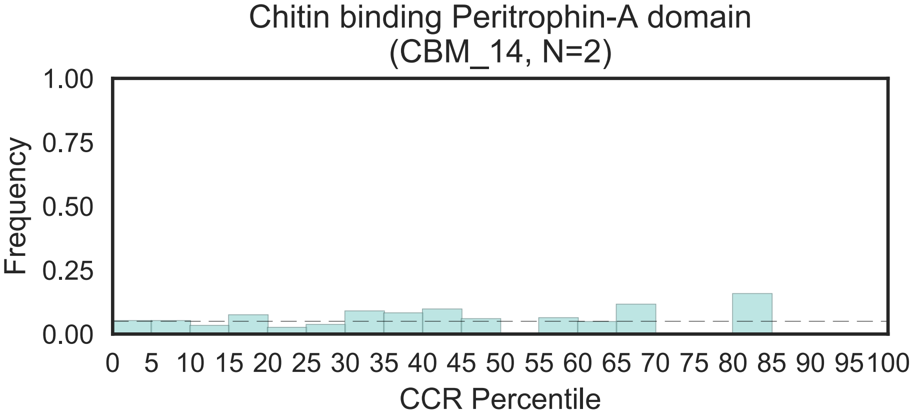

CCAAT-binding transcription factor (CBF-B/NF-YA) subunit B
(CBFB_NFYA, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

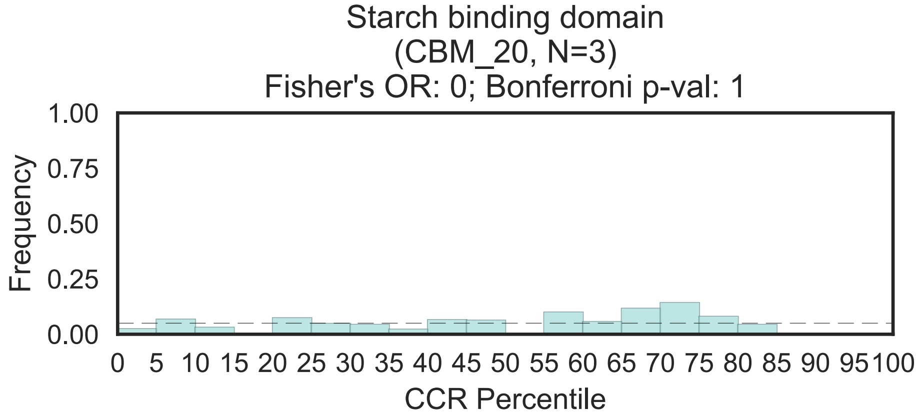

Histone-like transcription factor (CBF/NF-Y) and archaeal histone
(CBFD_NFYB_HMF, N=46)
Fisher's OR: 1.11; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

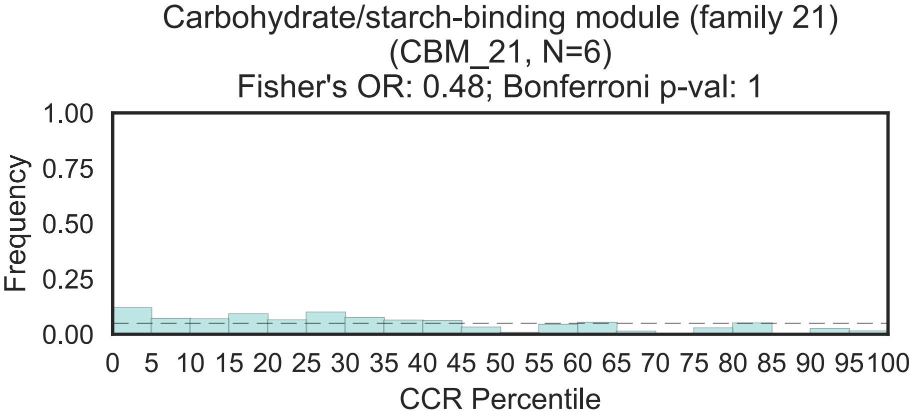

CBFNT (NUC161) domain
(CBFNT, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

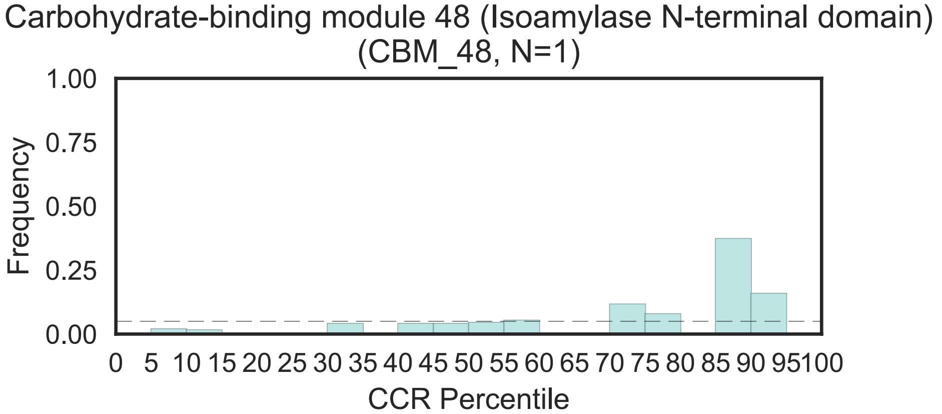

Core binding factor beta subunit
(CBF_beta, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

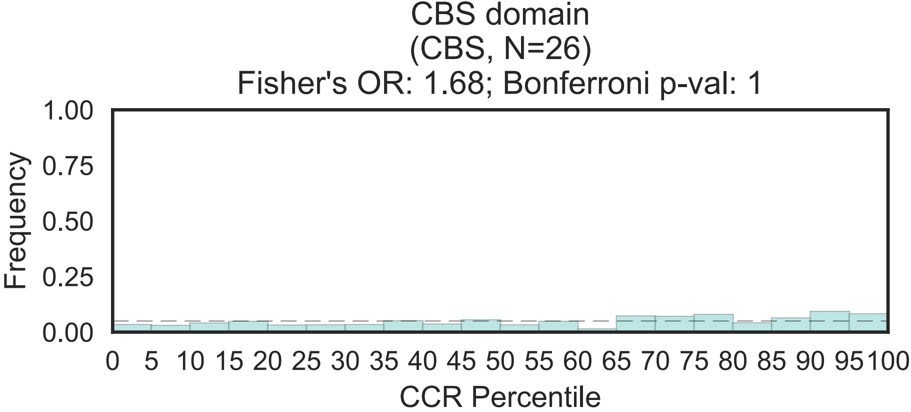

Starch/carbohydrate-binding module (family 53)
(CBM53, N=6)
Fisher's OR: 0.611; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

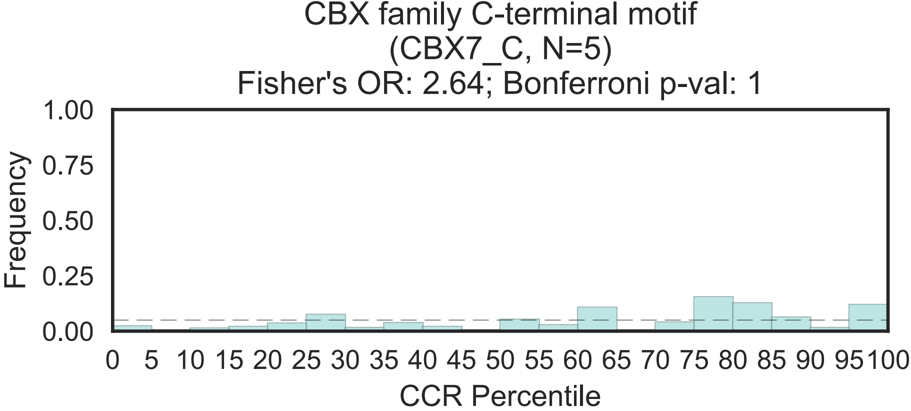

Chitin binding Peritrophin-A domain
(CBM_14, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

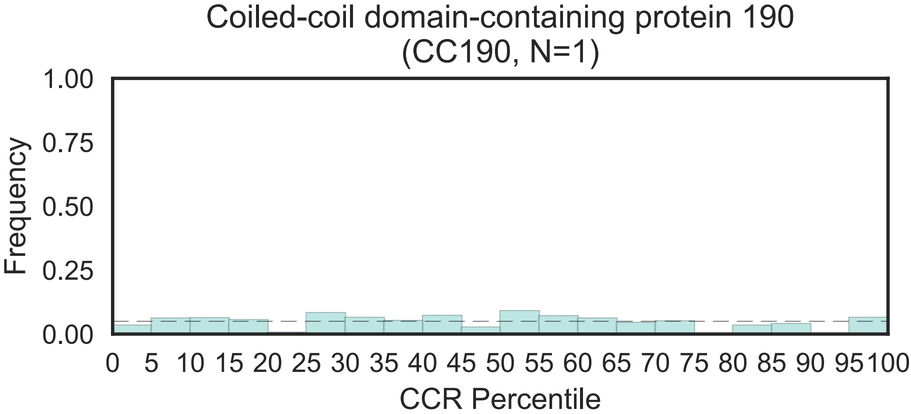

Starch binding domain
(CBM_20, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

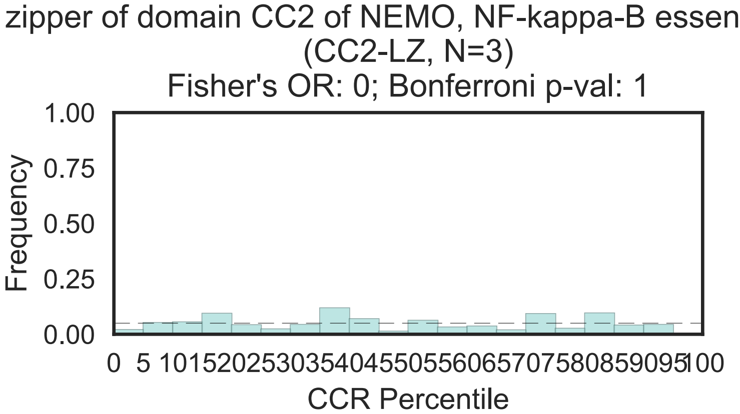

Carbohydrate/starch-binding module (family 21)
(CBM_21, N=6)
Fisher's OR: 0.48; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

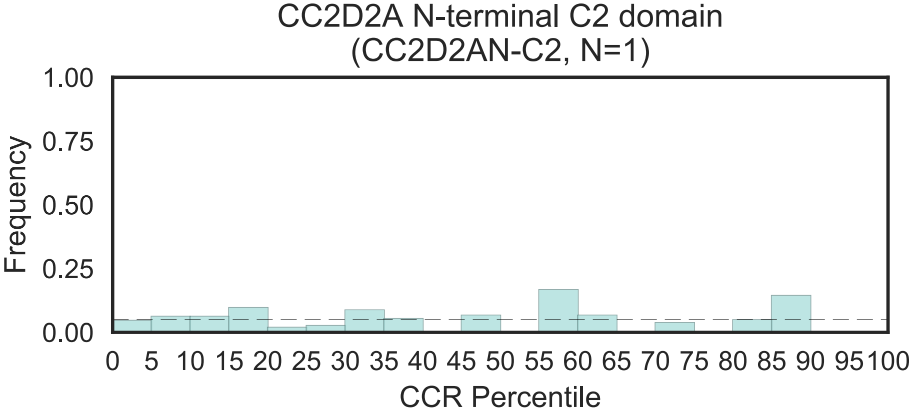

Carbohydrate-binding module 48 (Isoamylase N-terminal domain)
(CBM_48, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

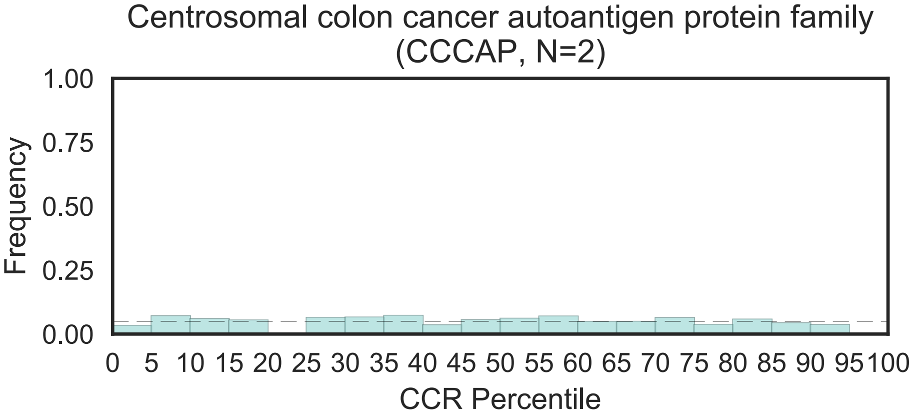

CBS domain
(CBS, N=26)
Fisher's OR: 1.68; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

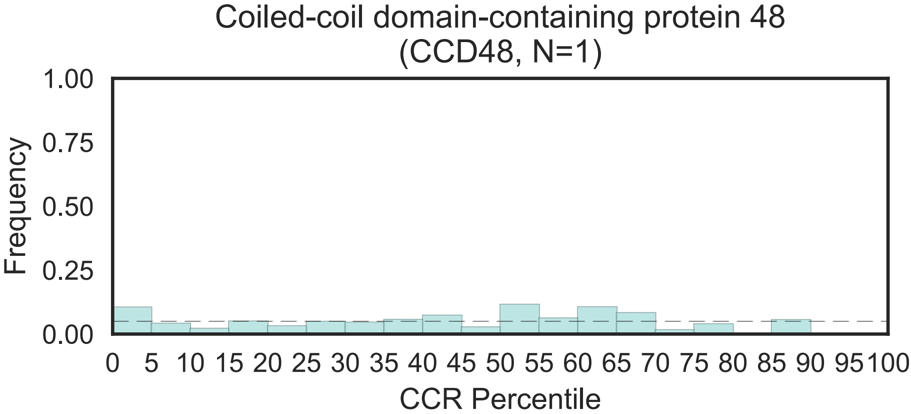

CBX family C-terminal motif
(CBX7_C, N=5)
Fisher's OR: 2.64; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Coiled-coil domain-containing protein 190
(CC190, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

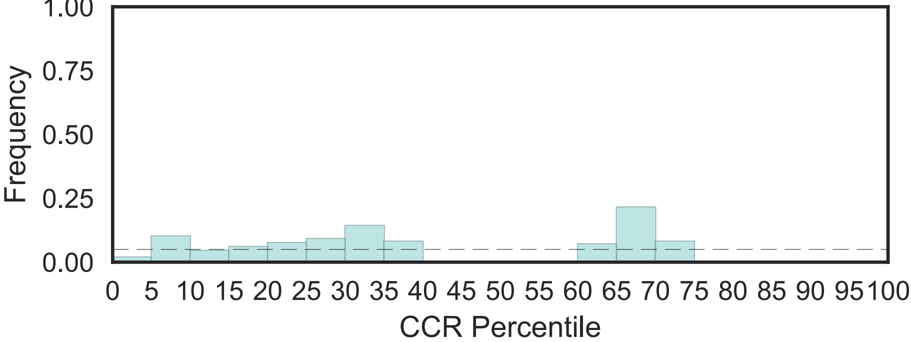

Leucine zipper of domain CC2 of NEMO, NF-kappa-B essential modulator
(CC2-LZ, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

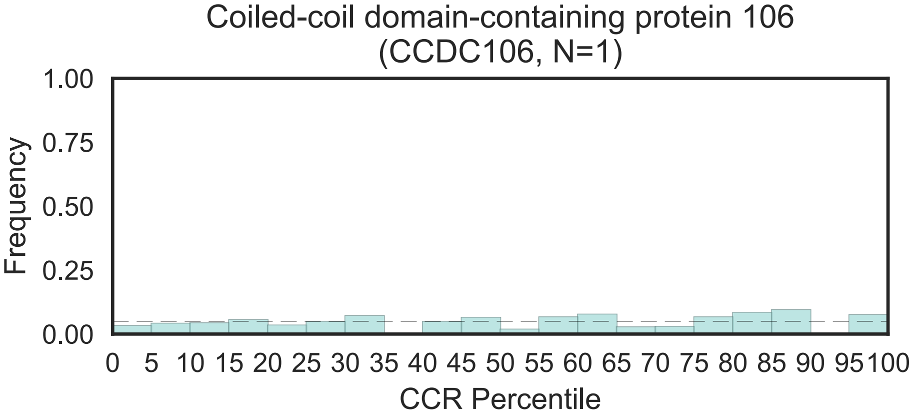

CC2D2A N-terminal C2 domain
(CC2D2AN-C2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Centrosomal colon cancer autoantigen protein family
(CCCAP, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

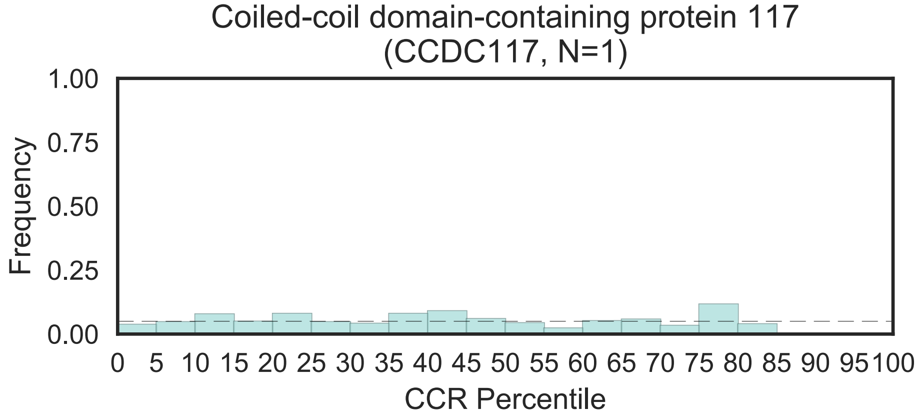

Coiled-coil domain-containing protein 48
(CCD48, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

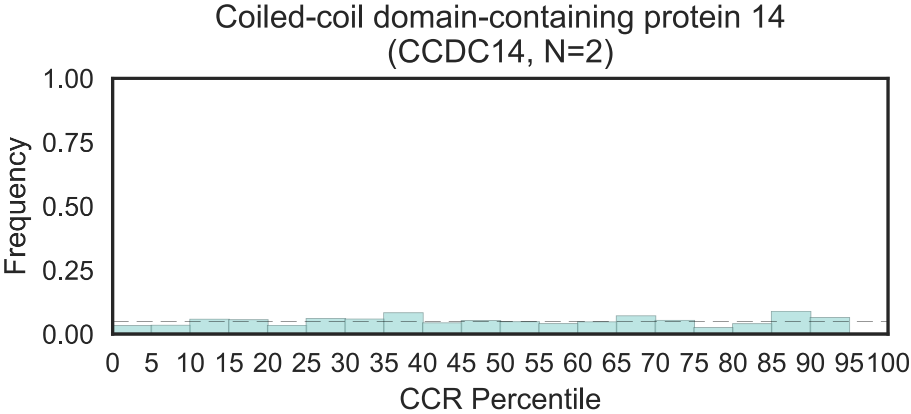
Coiled-coil domain-containing protein 167
(CCDC-167, N=1)

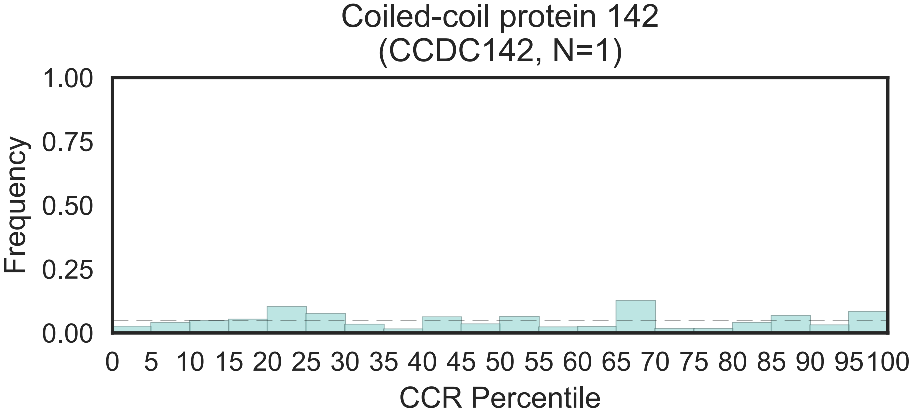


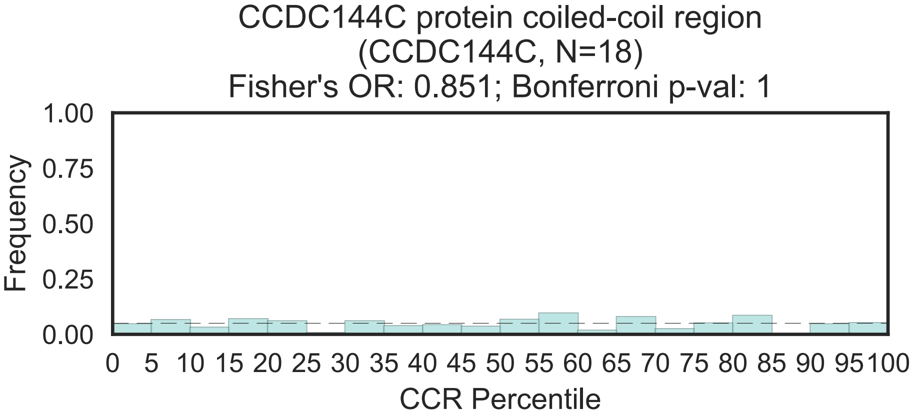


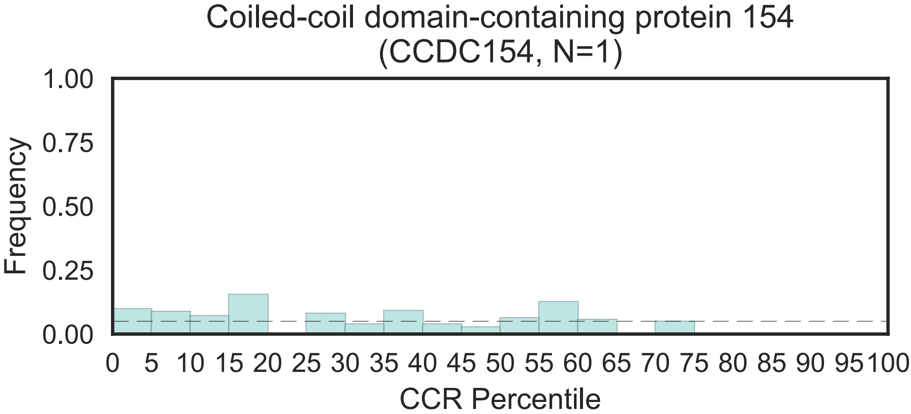
Coiled-coil domain-containing protein 106
(CCDC106, N=1)

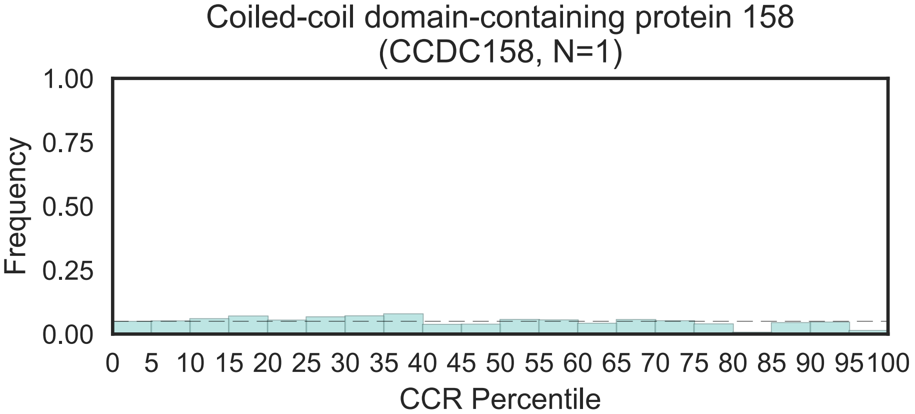

Coiled-coil domain-containing protein 117
(CCDC117, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

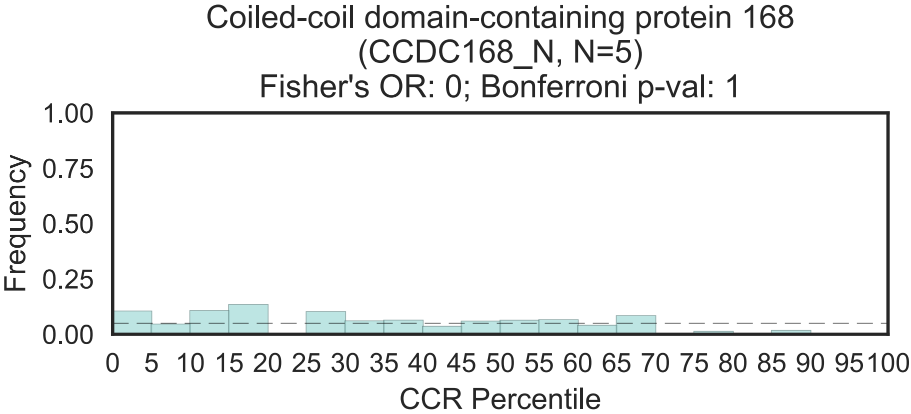

Coiled-coil domain-containing protein 14
(CCDC14, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

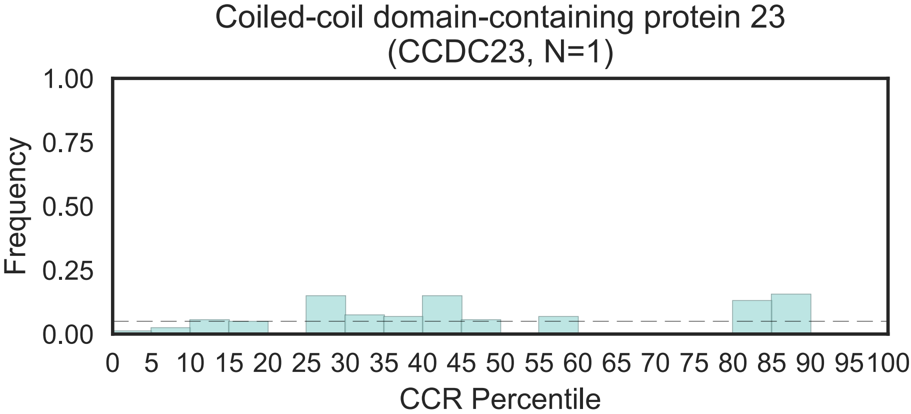

Coiled-coil protein 142
(CCDC142, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

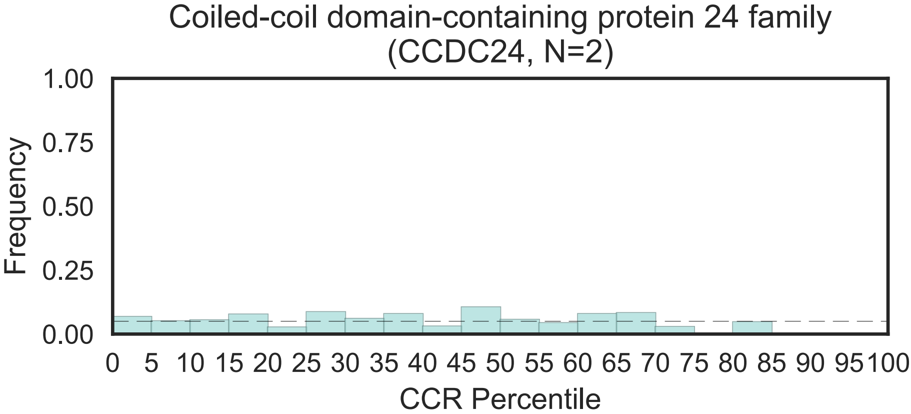

CCDC144C protein coiled-coil region
(CCDC144C, N=18)
Fisher's OR: 0.851; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

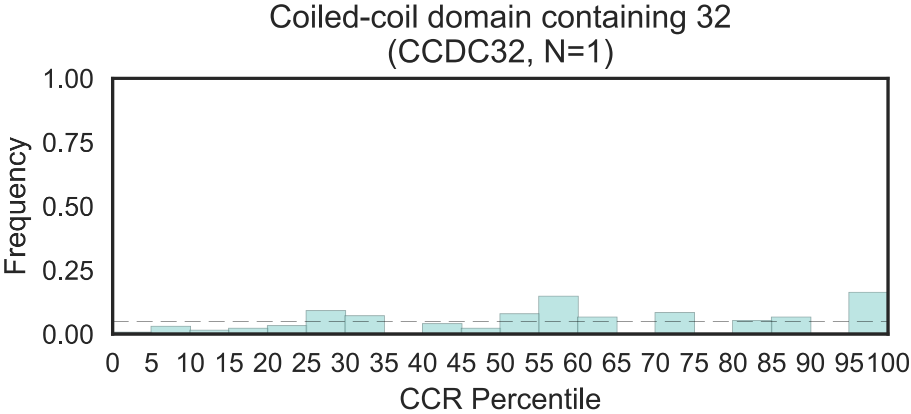

Coiled-coil domain-containing protein 154
(CCDC154, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

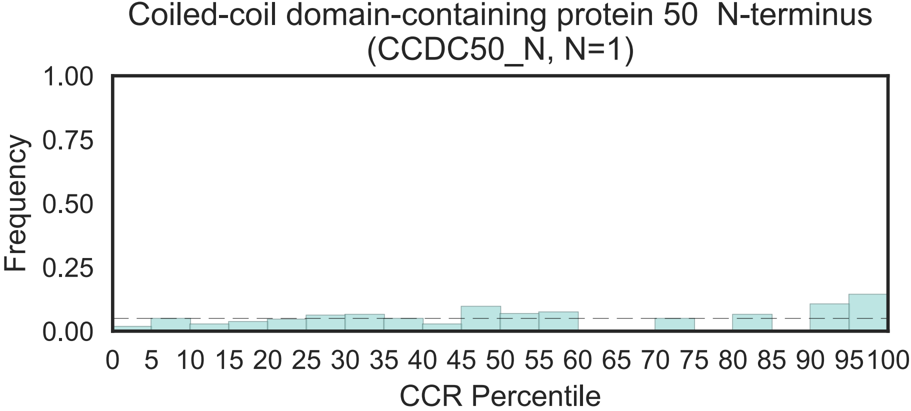

Coiled-coil domain-containing protein 158
(CCDC158, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

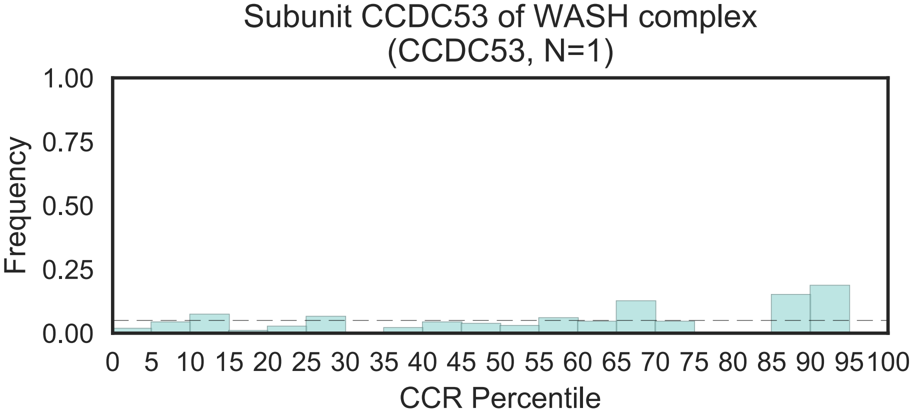

Coiled-coil domain-containing protein 168
(CCDC168_N, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Coiled-coil domain-containing protein 23
(CCDC23, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

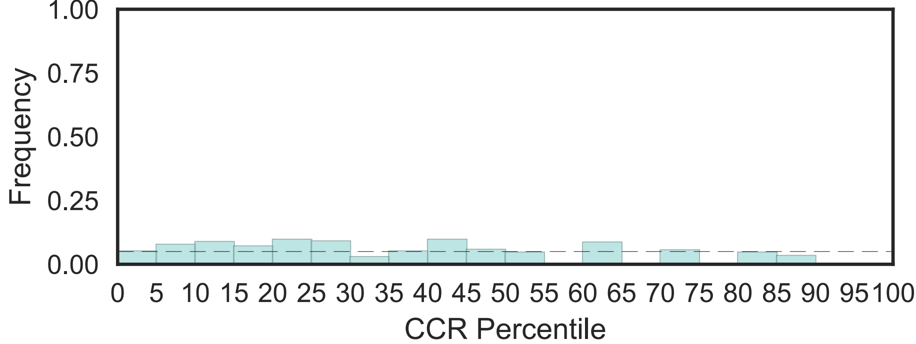

Coiled-coil domain-containing protein 24 family
(CCDC24, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

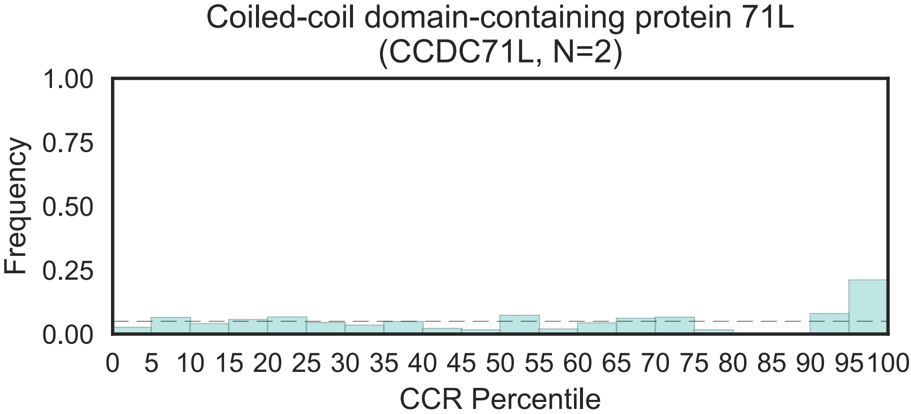

Coiled-coil domain containing 32
(CCDC32, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

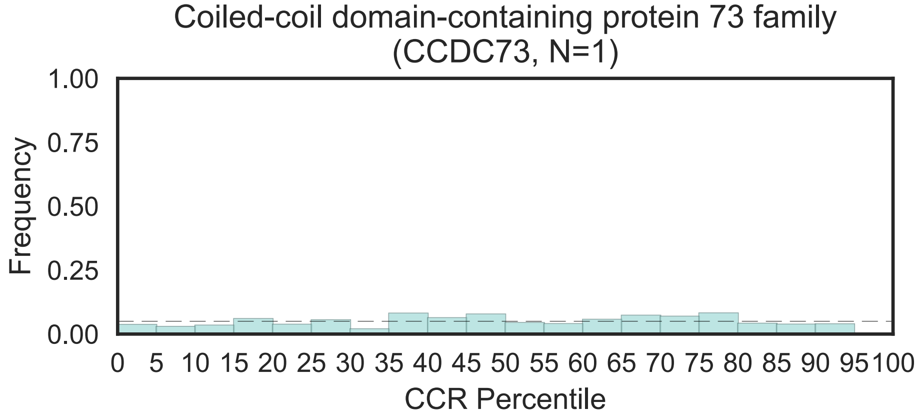

Coiled-coil domain-containing protein 50 N-terminus
(CCDC50_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

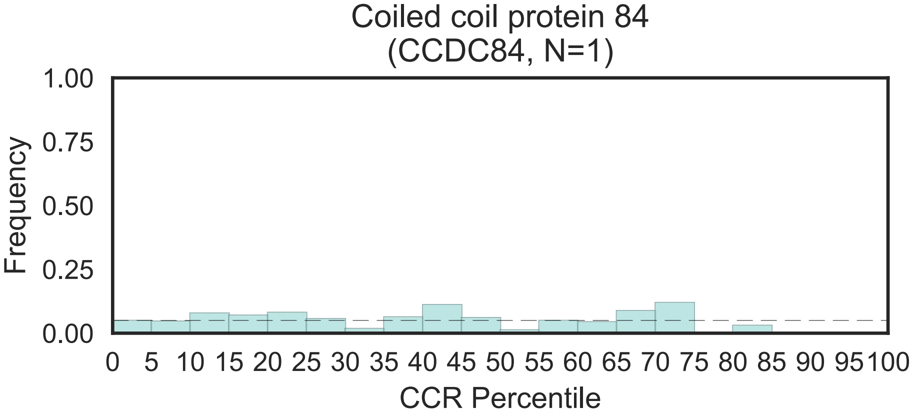

Subunit CCDC53 of WASH complex
(CCDC53, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

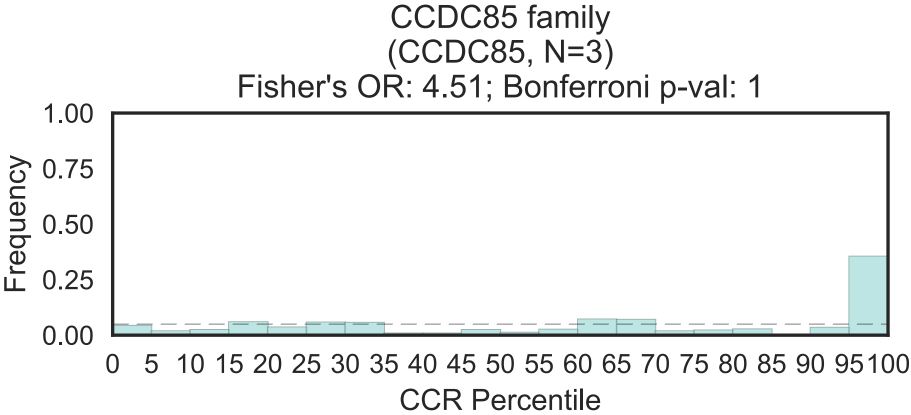
Coiled-coil domain-containing protein 66 (CCDC66, N=2)

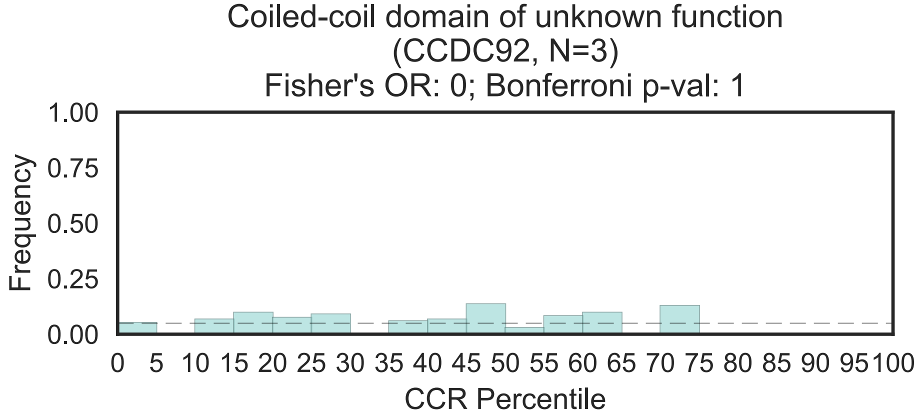


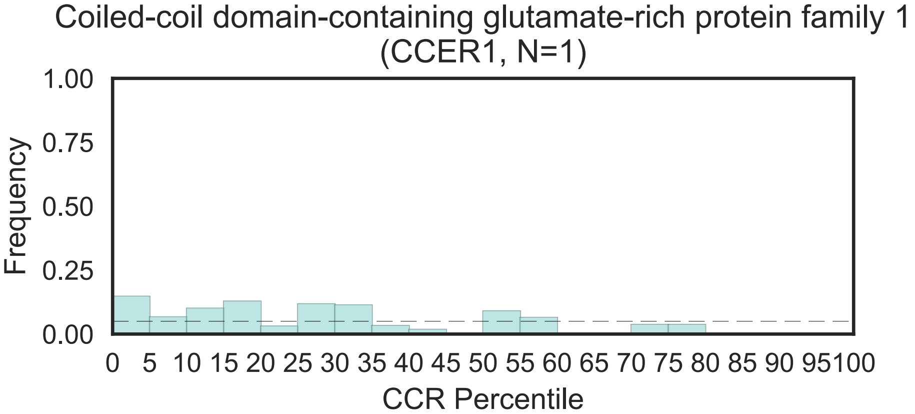

Coiled-coil domain-containing protein 71L
(CCDC71L, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

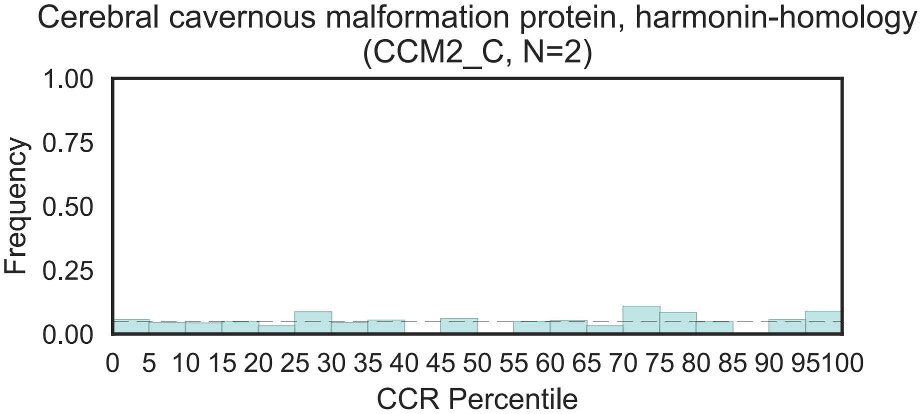

Coiled-coil domain-containing protein 73 family
(CCDC73, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

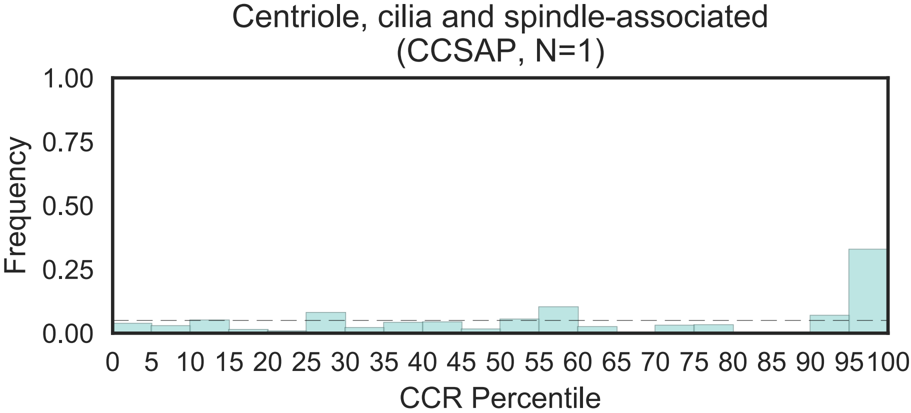

Coiled coil protein 84
(CCDC84, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

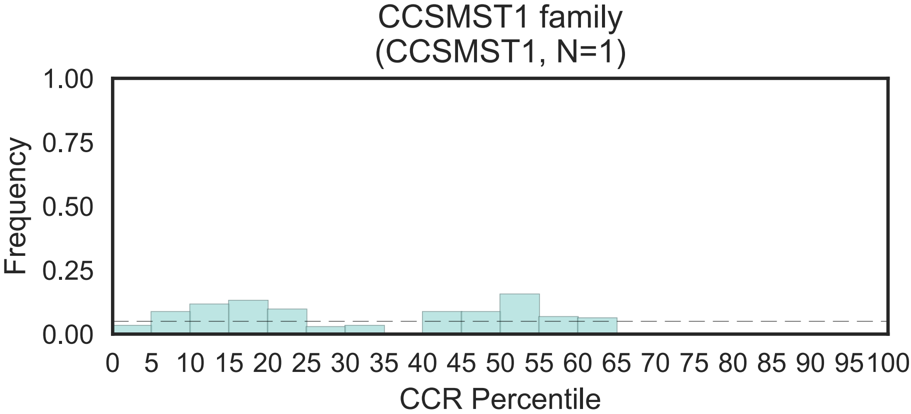

CCDC85 family
(CCDC85, N=3)
Fisher's OR: 4.51; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

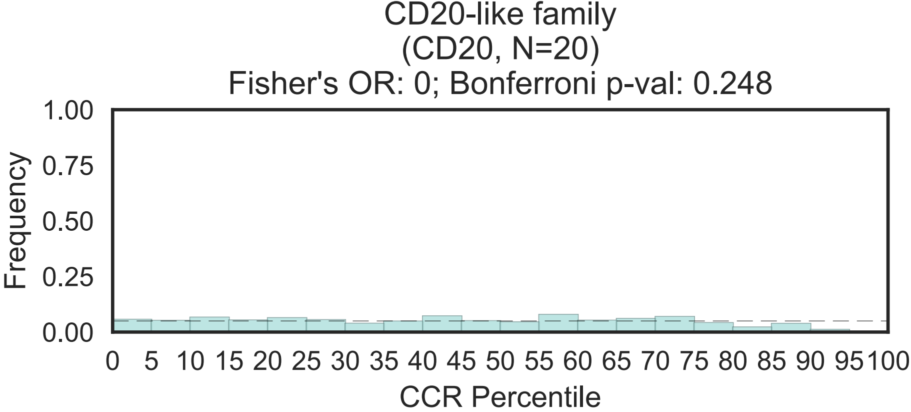

Coiled-coil domain of unknown function
(CCDC92, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

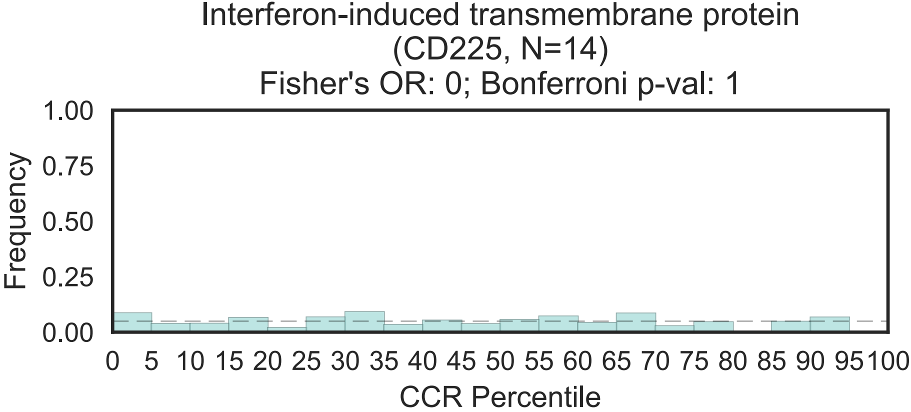

Coiled-coil domain-containing glutamate-rich protein family 1
(CCER1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

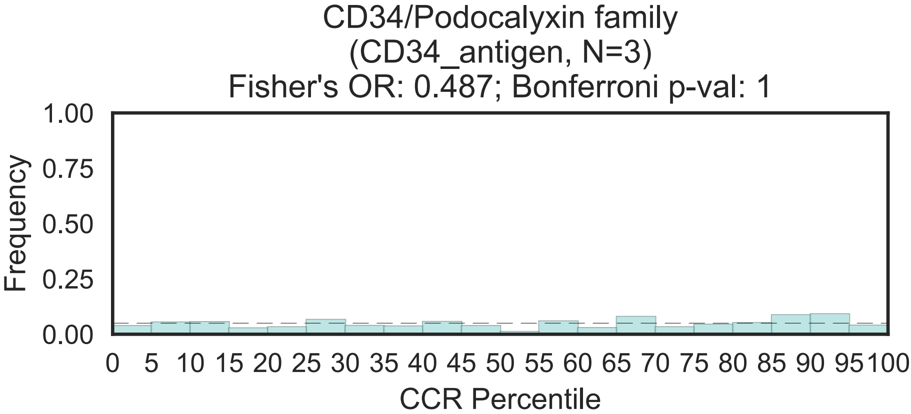

Cerebral cavernous malformation protein, harmonin-homology
(CCM2_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

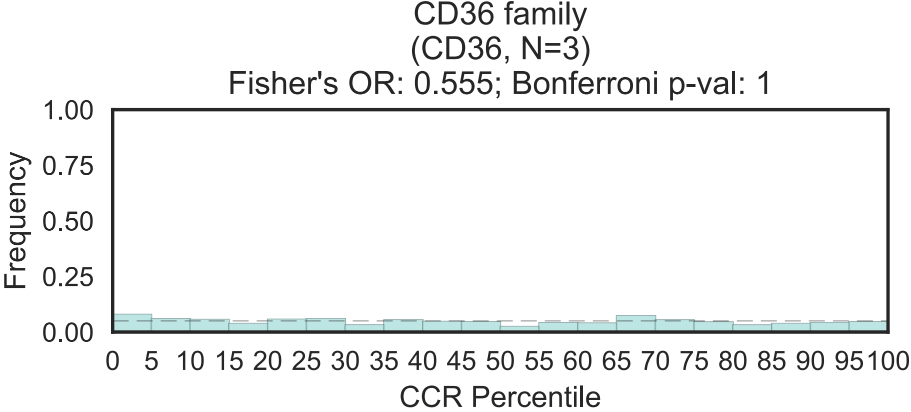

Centriole, cilia and spindle-associated
(CCSAP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

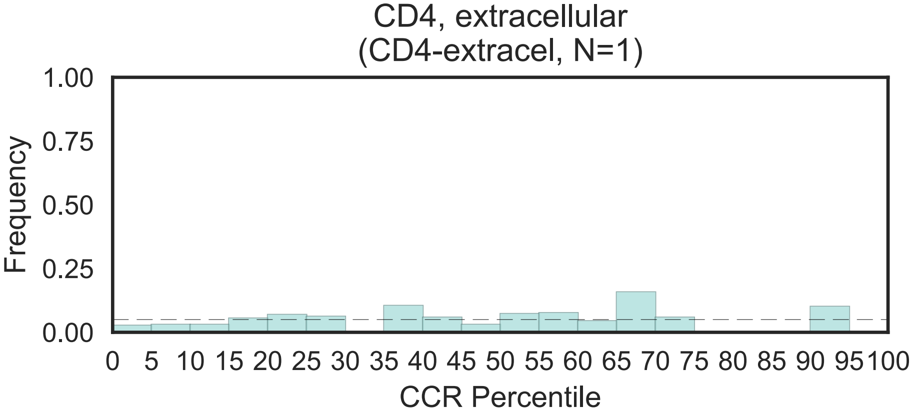

CCSMST1 family
(CCSMST1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

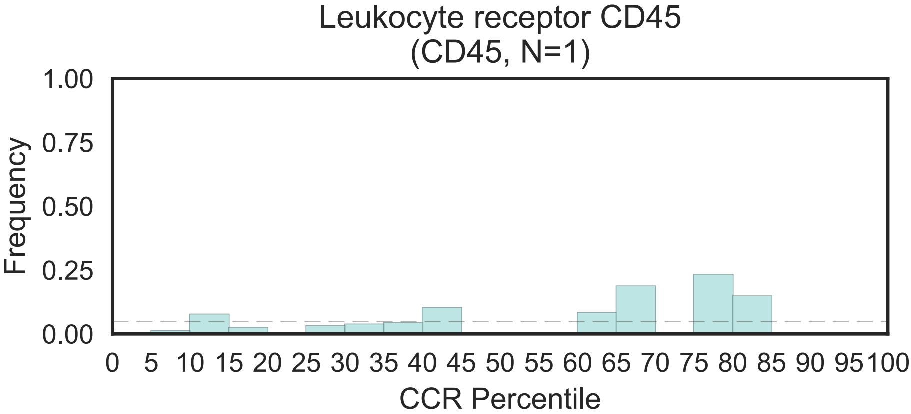

CD20-like family
(CD20, N=20)
Fisher's OR: 0; Bonferroni p-val: 0.248
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

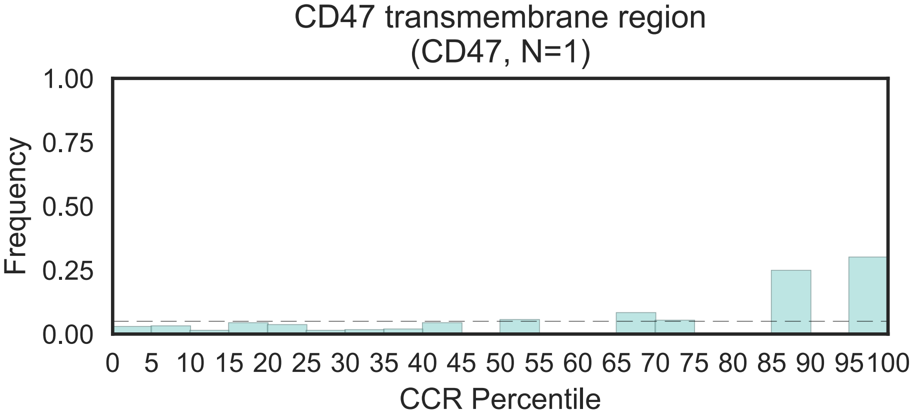

Interferon-induced transmembrane protein
(CD225, N=14)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

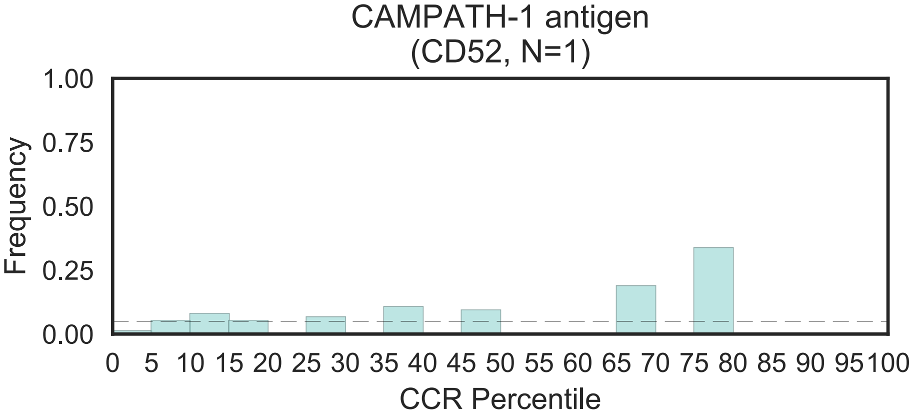

CD34/Podocalyxin family
(CD34_antigen, N=3)
Fisher's OR: 0.487; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

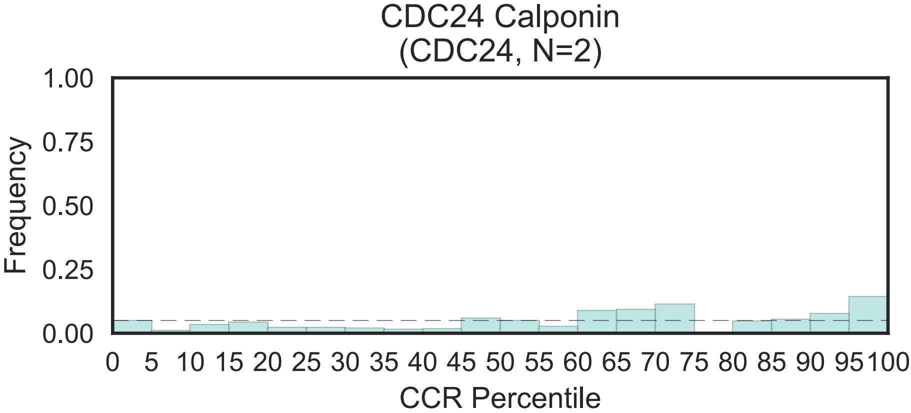

CD36 family
(CD36, N=3)
Fisher's OR: 0.555; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

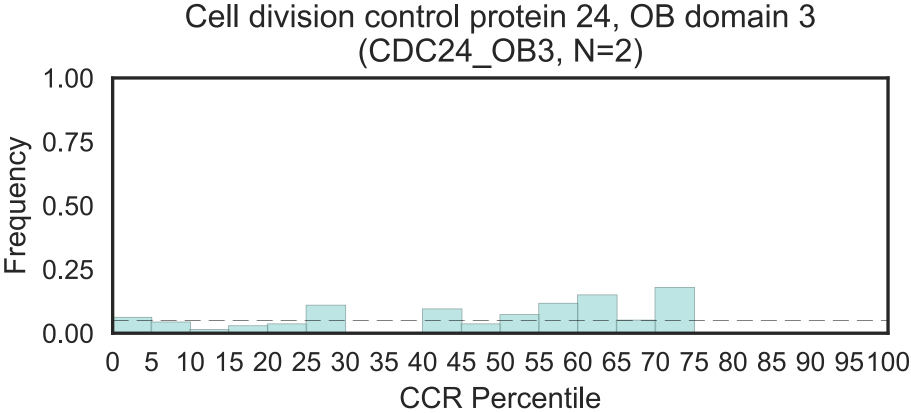

CD4, extracellular
(CD4-extracel, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

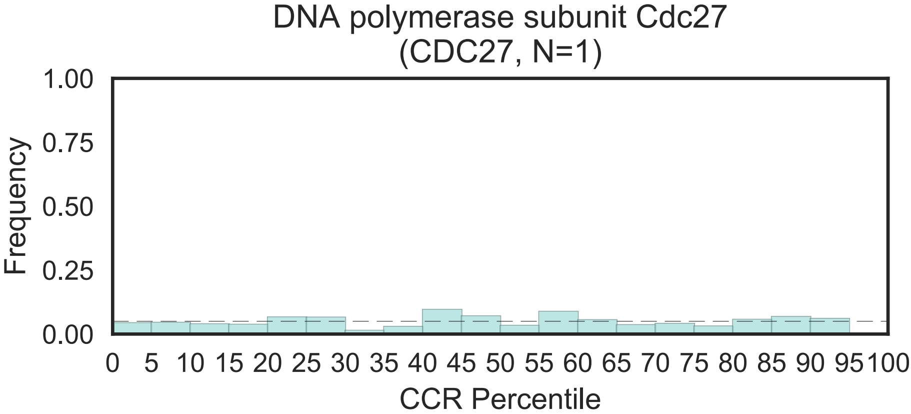

Leukocyte receptor CD45
(CD45, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

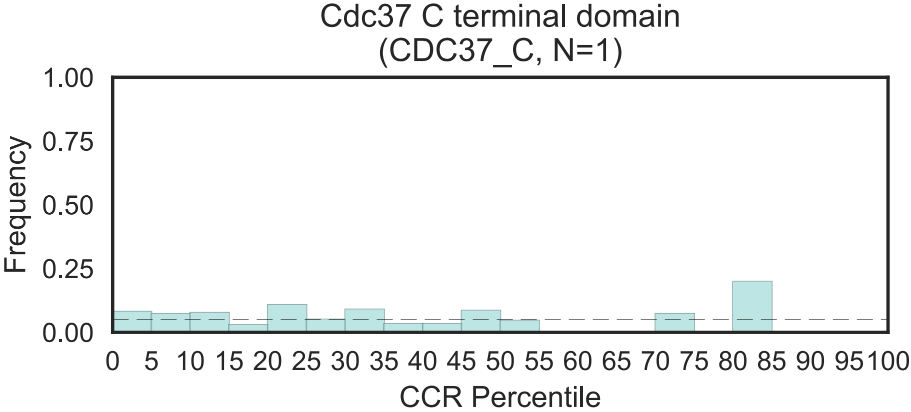

CD47 transmembrane region
(CD47, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

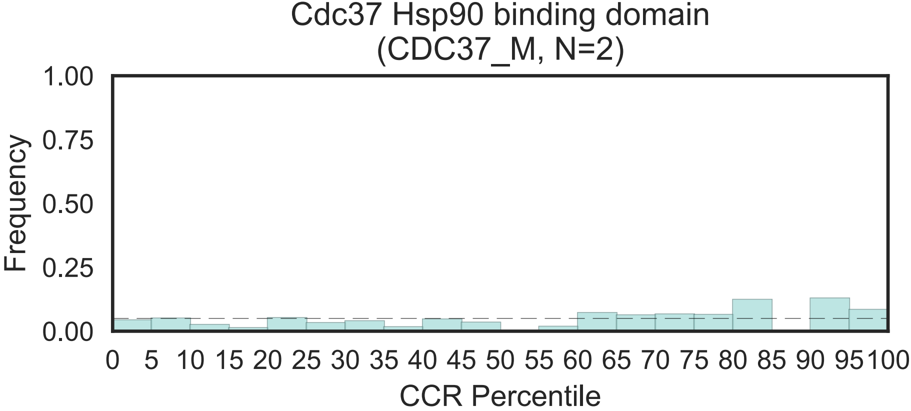

CAMPATH-1 antigen
(CD52, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


CDC24 Calponin
(CDC24, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

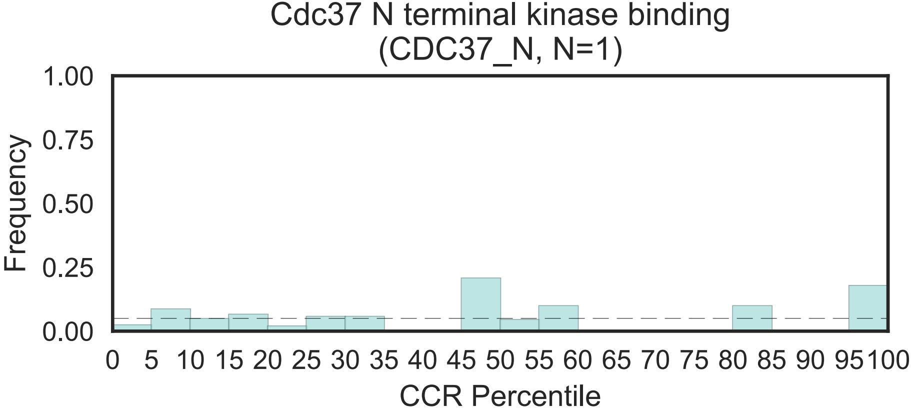

Cell division control protein 24, OB domain 3
(CDC24_OB3, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

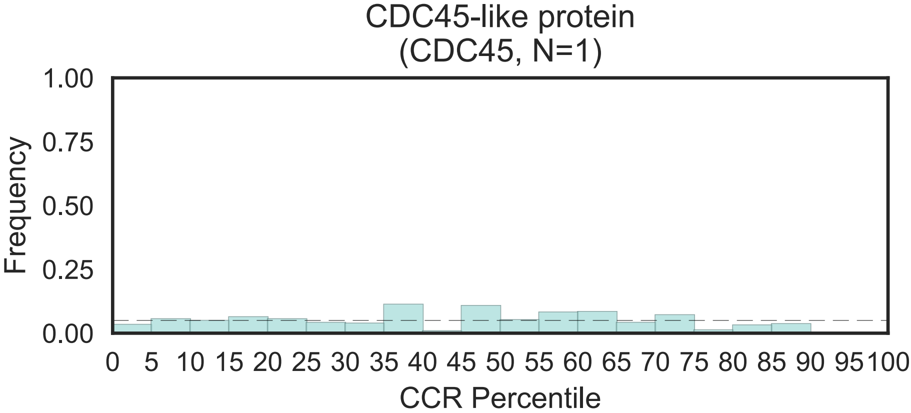

DNA polymerase subunit Cdc27
(CDC27, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

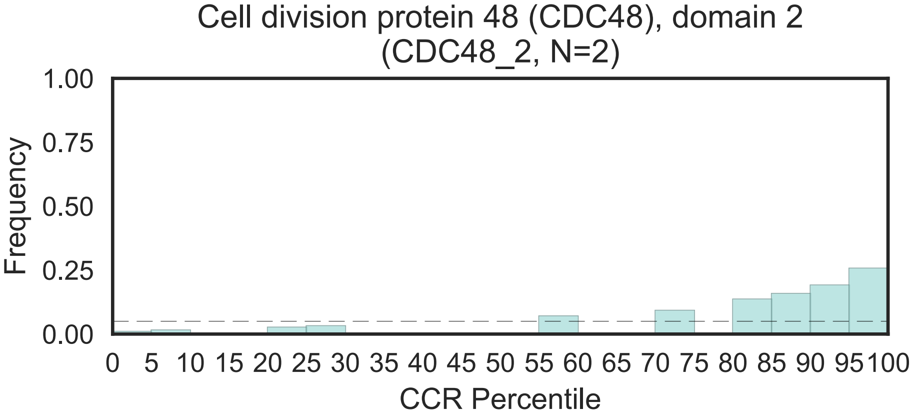

Cdc37 C terminal domain
(CDC37_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

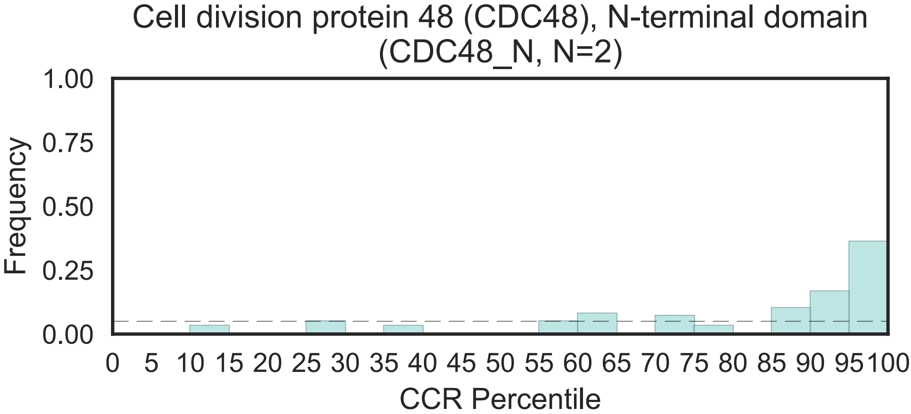


Cdc37 Hsp90 binding domain
(CDC37_M, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Cdc37 N terminal kinase binding
(CDC37_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

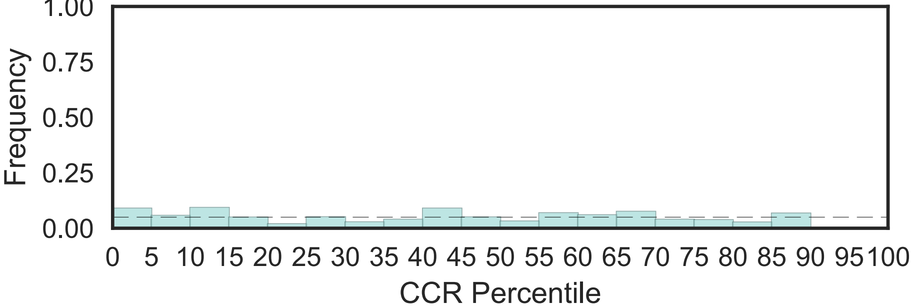

CDC45-like protein
(CDC45, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

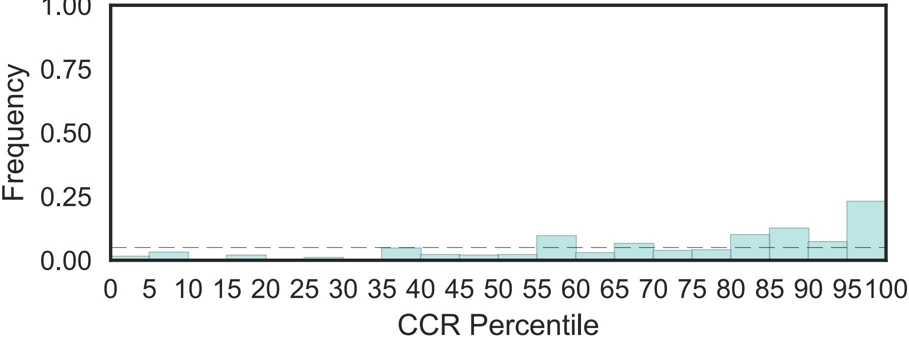

Cell division protein 48 (CDC48), domain 2
(CDC48_2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Cell division protein 48 (CDC48), N-terminal domain
(CDC48_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

LEM3 (ligand-effect modulator 3) family / CDC50 family (CDC50, N=3)

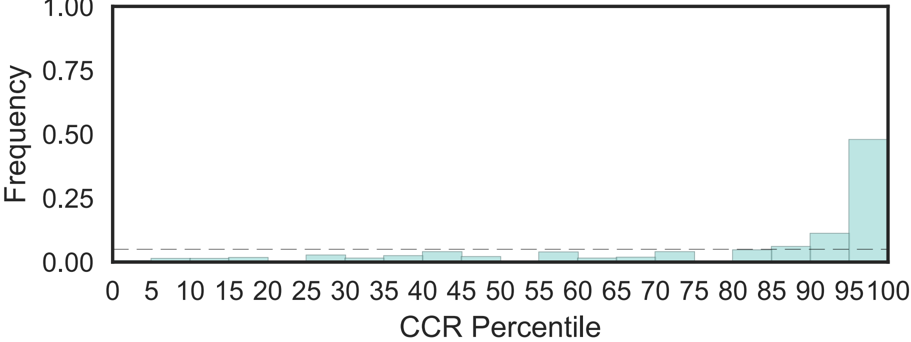
Fisher's OR: 0; Bonferroni p-val: 1

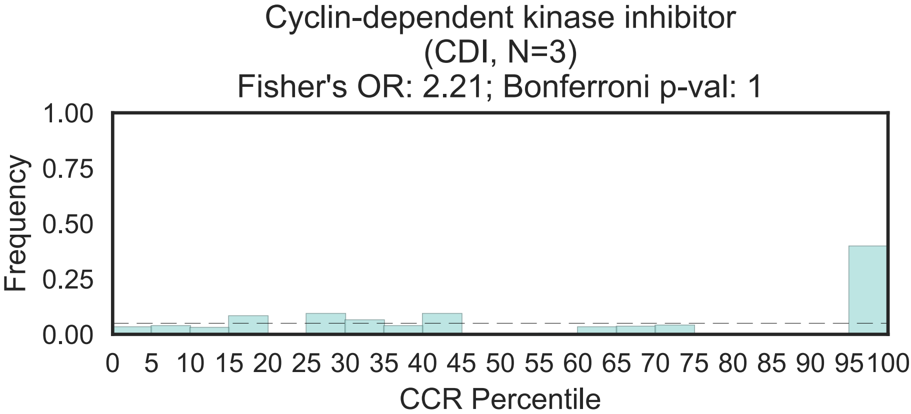


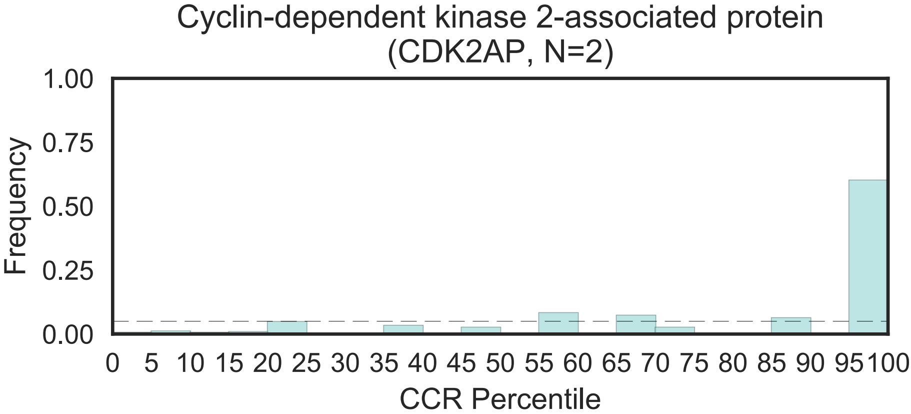


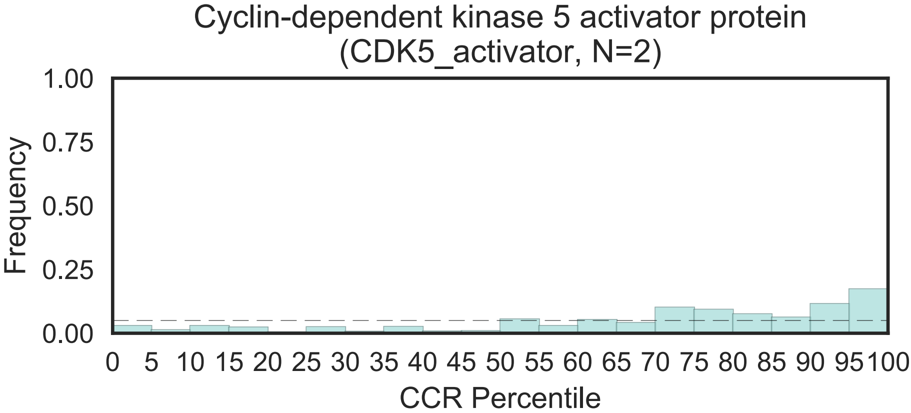
RNA pol II accessory factor, Cdc73 family, C-terminal (CDC73_C, N=1)

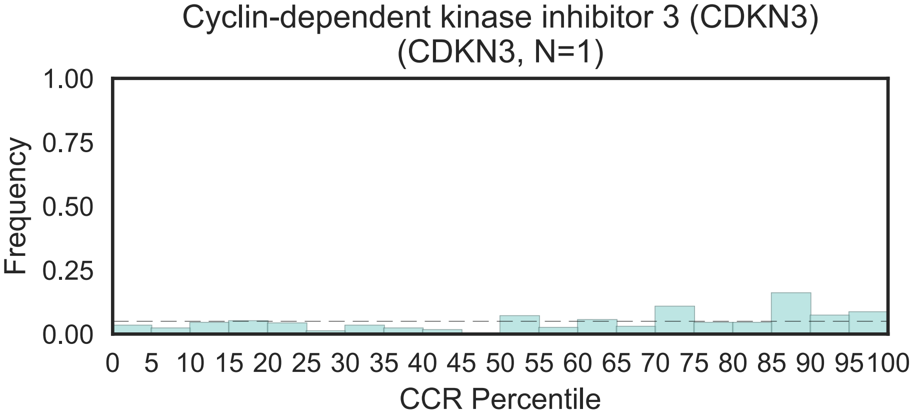
Paf1 complex subunit CDC73 N-terminal (CDC73_N, N=1)

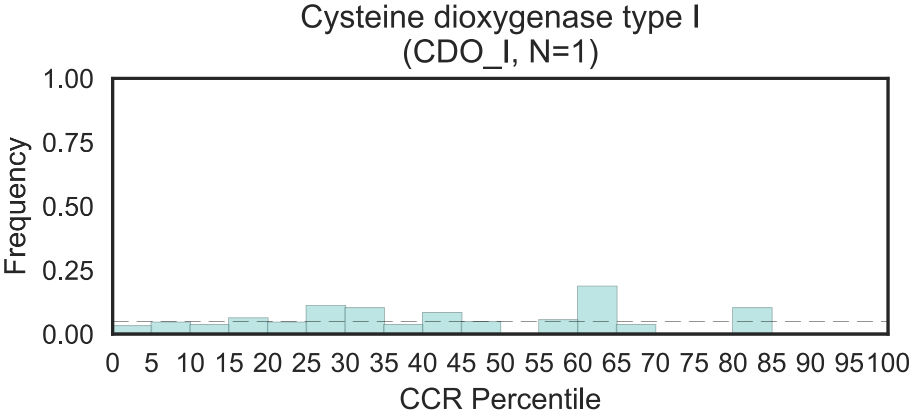


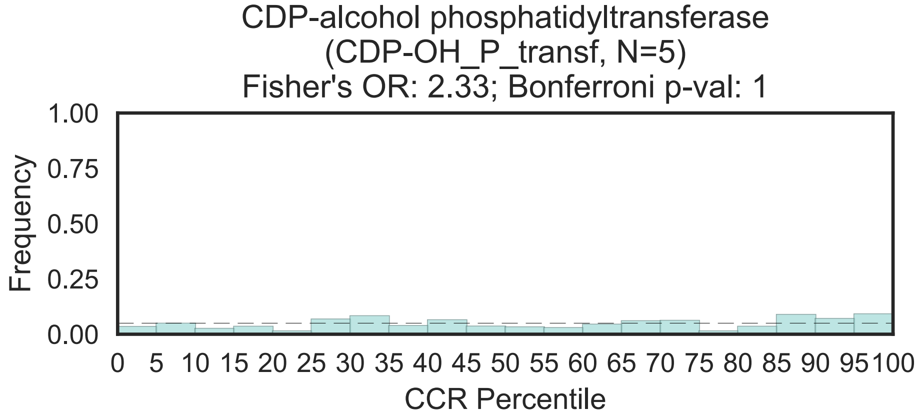

Cyclin-dependent kinase inhibitor
(CDI, N=3)
Fisher's OR: 2.21; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

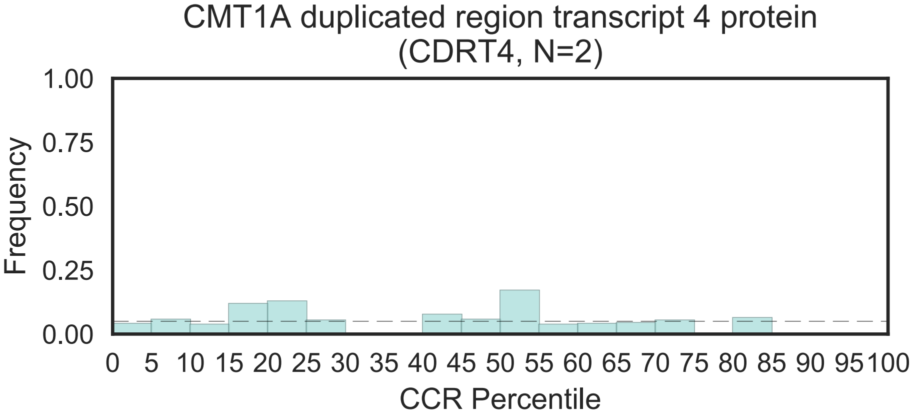

Cyclin-dependent kinase 2-associated protein
(CDK2AP, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

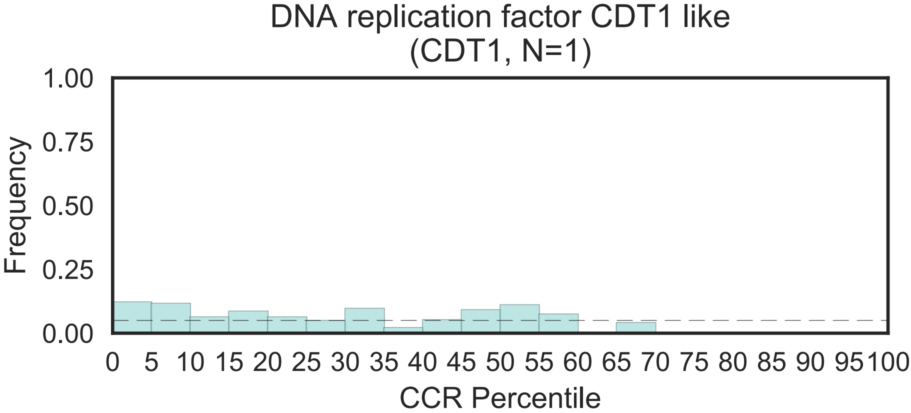

Cyclin-dependent kinase 5 activator protein
(CDK5_activator, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

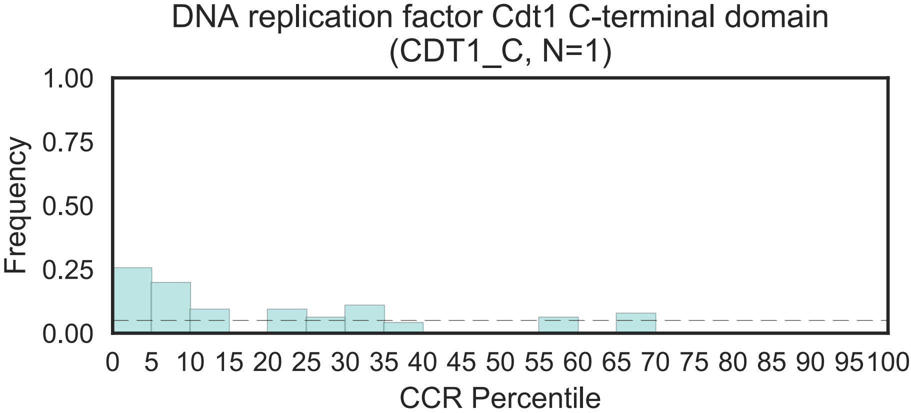

Cyclin-dependent kinase inhibitor 3 (CDKN3)
(CDKN3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Cysteine dioxygenase type I
(CDO_I, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

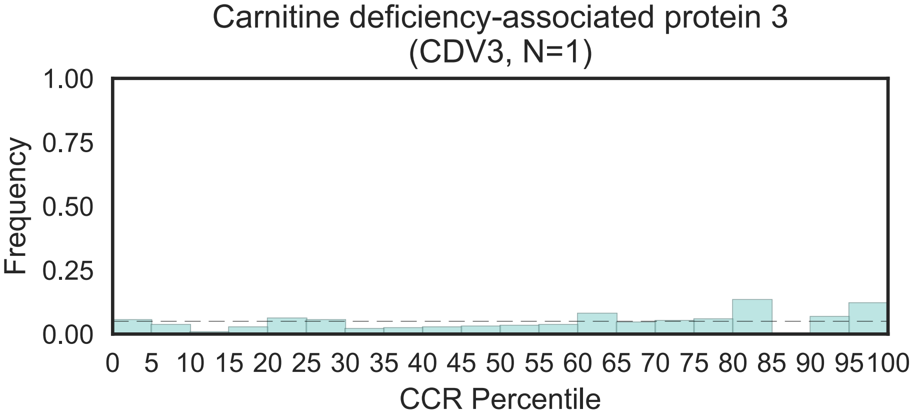

CDP-alcohol phosphatidyltransferase
(CDP-OH_P_transf, N=5)
Fisher's OR: 2.33; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


CMT1A duplicated region transcript 4 protein
(CDRT4, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

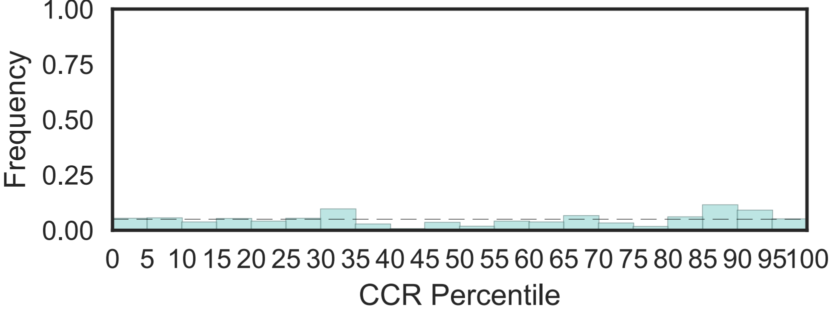
DNA replication factor CDT1 like
(CDT1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

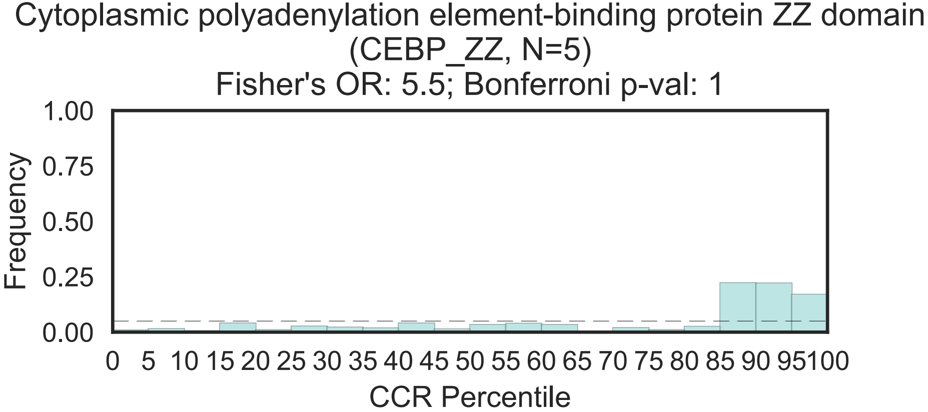


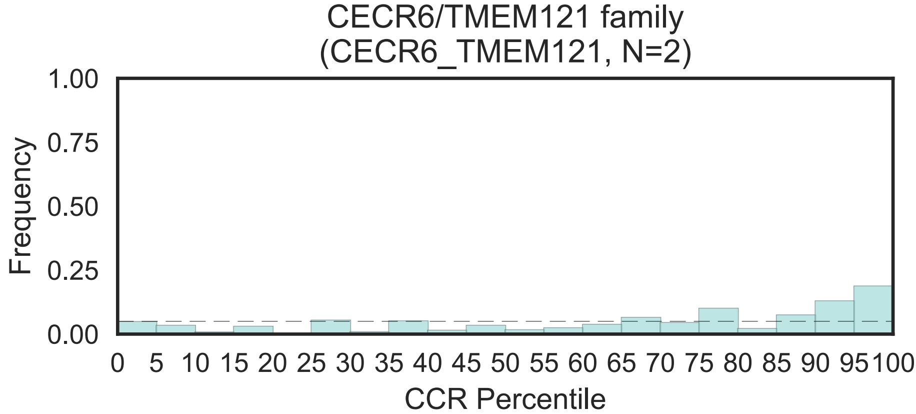
DNA replication factor Cdt1 C-terminal domain
(CDT1_C, N=1)

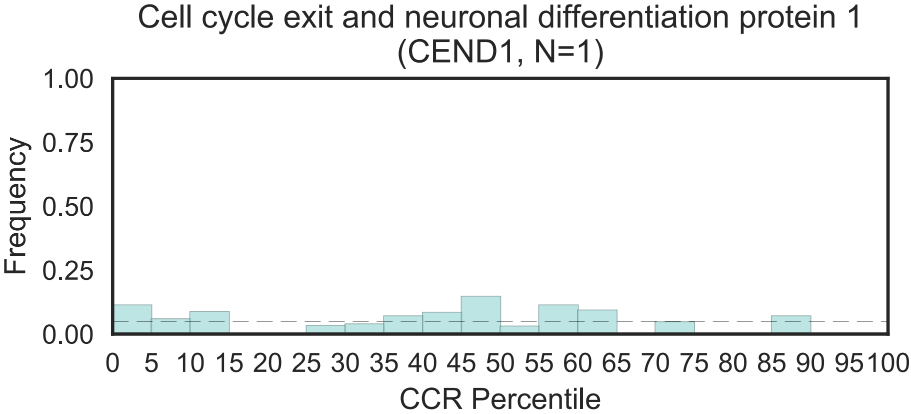

Carnitine deficiency-associated protein 3
(CDV3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

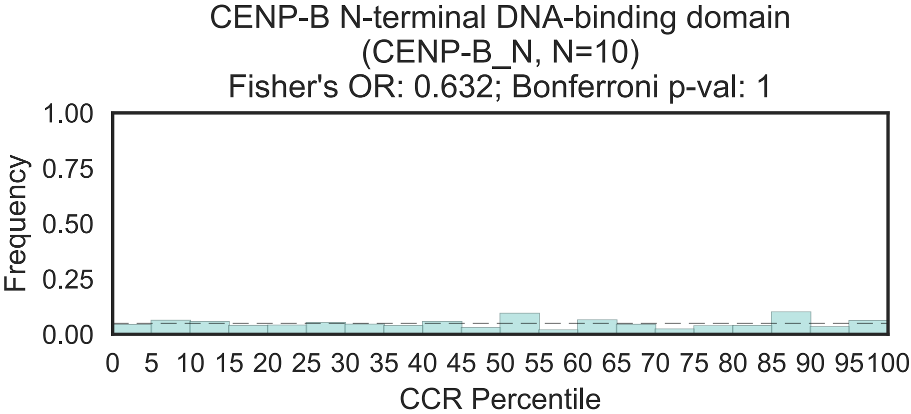
Cytoplasmic polyadenylation element-binding protein 1 N-terminus
(CEBP1_N, N=3)
Fisher's OR: 0.735; Bonferroni p-val: 1

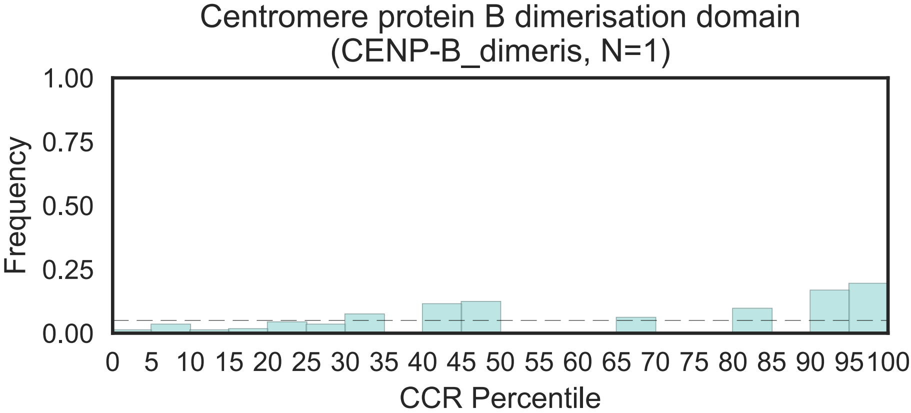


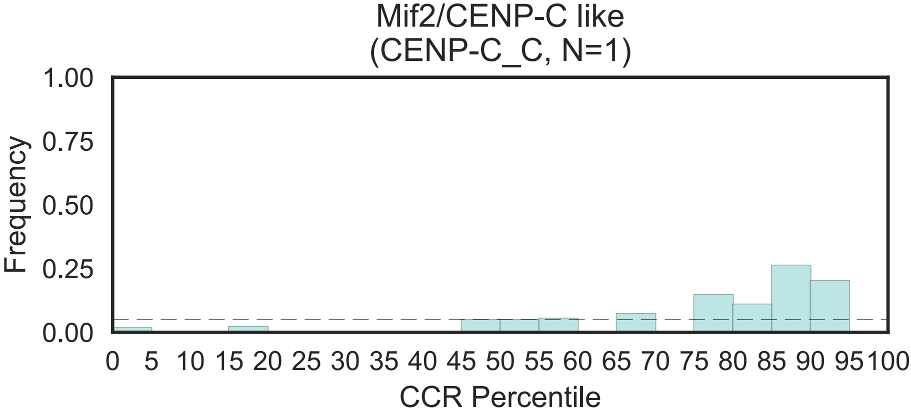

Cytoplasmic polyadenylation element-binding protein ZZ domain
(CEBP_ZZ, N=5)
Fisher's OR: 5.5; Bonferroni p-val: 1

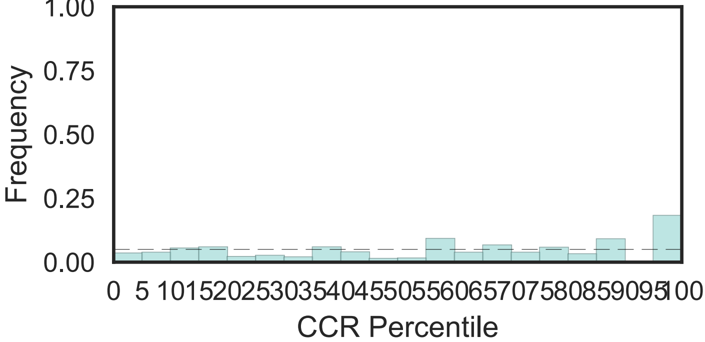

CECR6/TMEM121 family
(CECR6_TMEM121, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Cell cycle exit and neuronal differentiation protein 1
(CEND1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

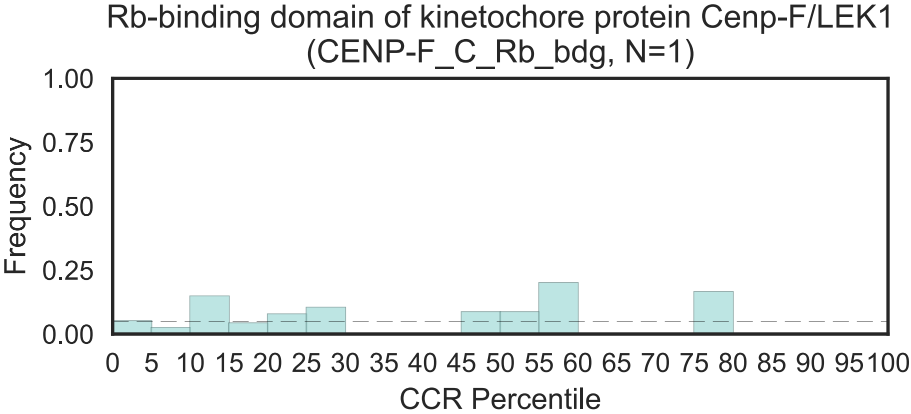

CENP-B N-terminal DNA-binding domain
(CENP-B_N, N=10)
Fisher's OR: 0.632; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

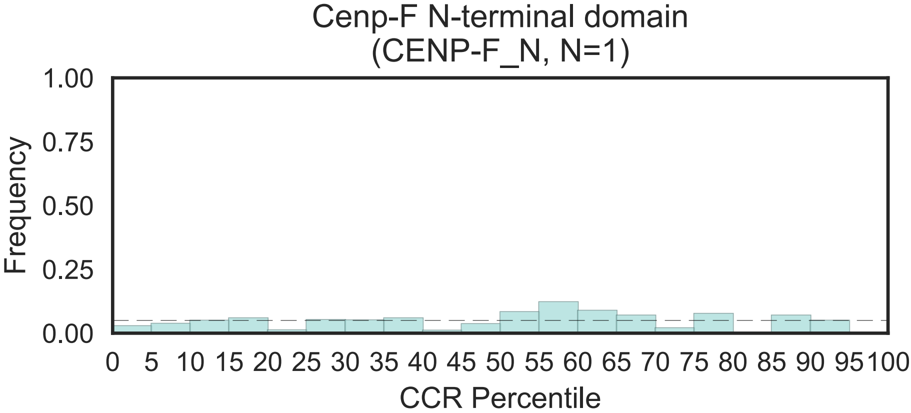

Centromere protein B dimerisation domain
(CENP-B_dimeris, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

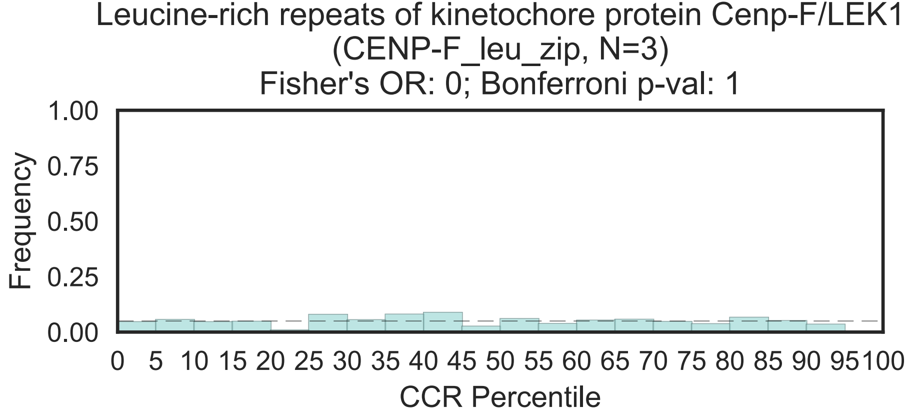

Mif2/CENP-C like
(CENP-C_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile



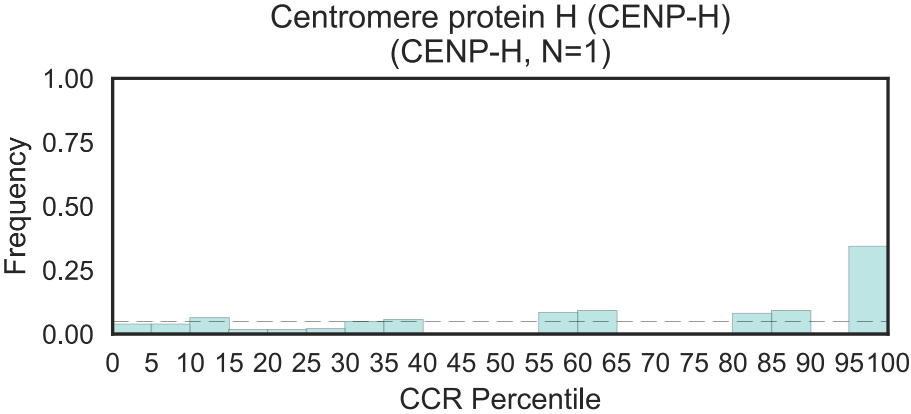
Centromere assembly component CENP-C middle DNMT3B-binding region (CENP-C_mid, N=1)

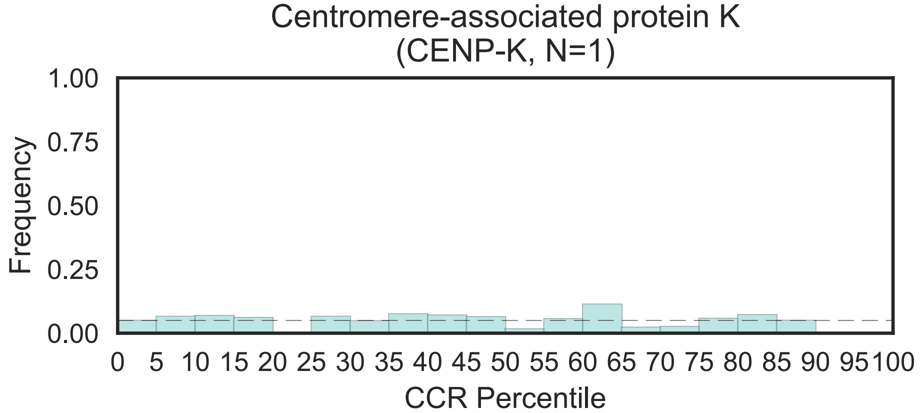

Rb-binding domain of kinetochore protein Cenp-F/LEK1
(CENP-F_C_Rb_bdg, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

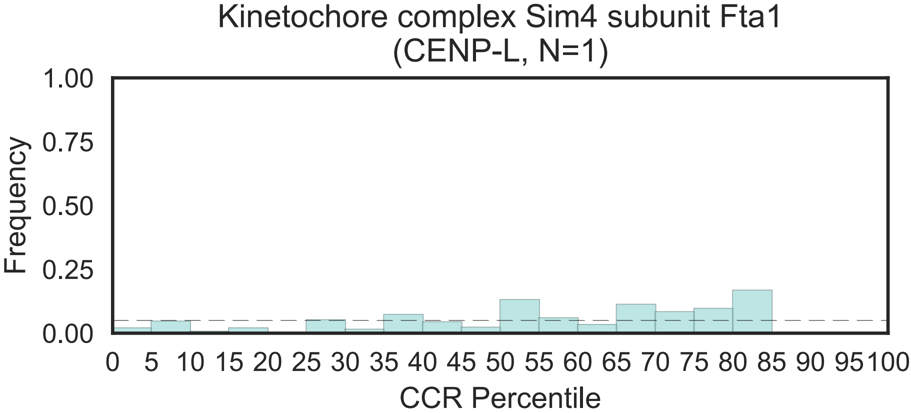

Cenp-F N-terminal domain
(CENP-F_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



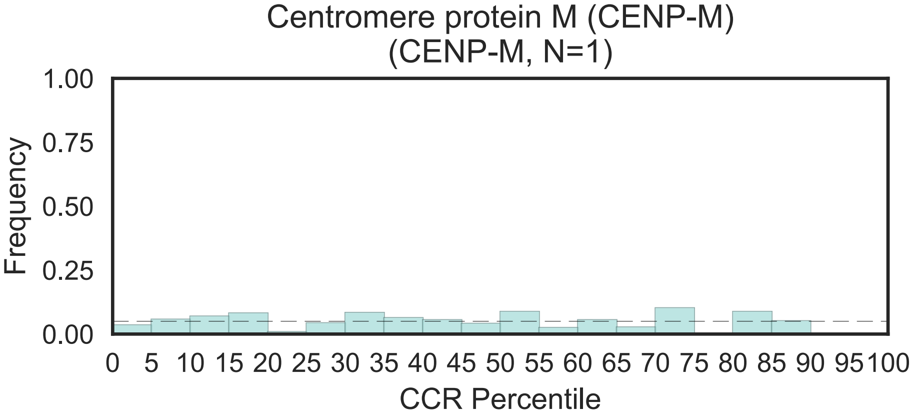
Leucine-rich repeats of kinetochore protein Cenp-F/LEK1
(CENP-F_leu_zip, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

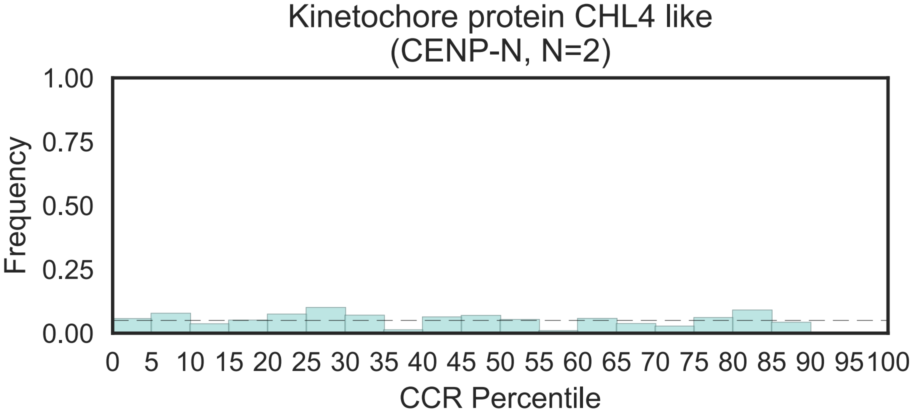

Centromere protein H (CENP-H)
(CENP-H, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

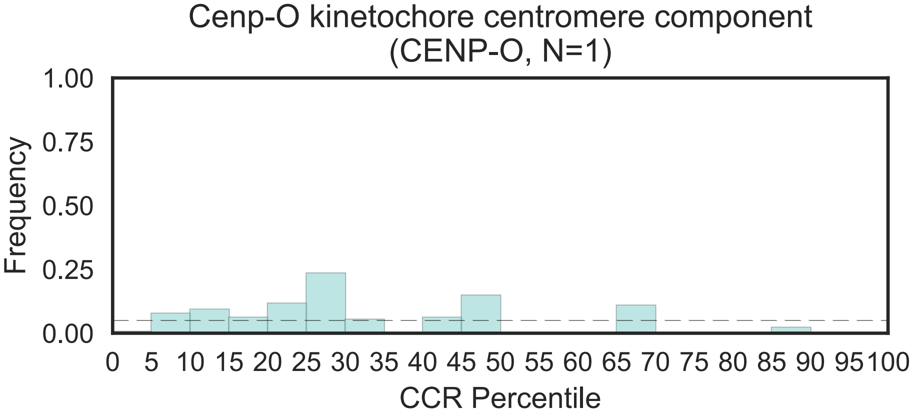

Centromere-associated protein K
(CENP-K, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

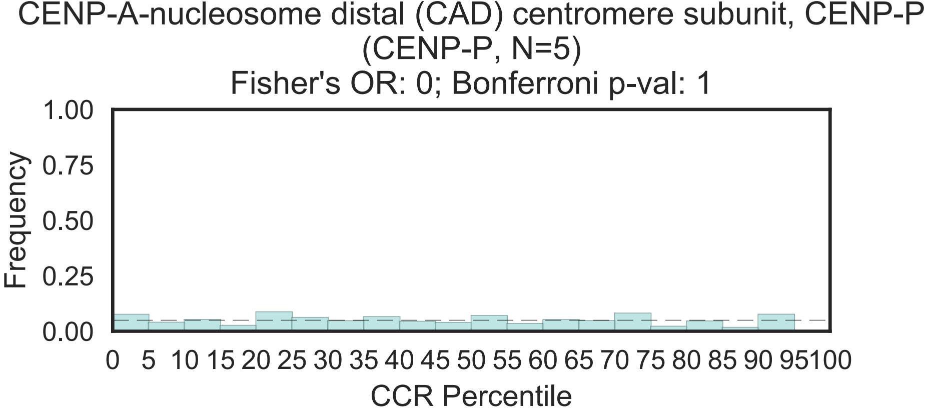


Kinetochore complex Sim4 subunit Fta1
(CENP-L, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

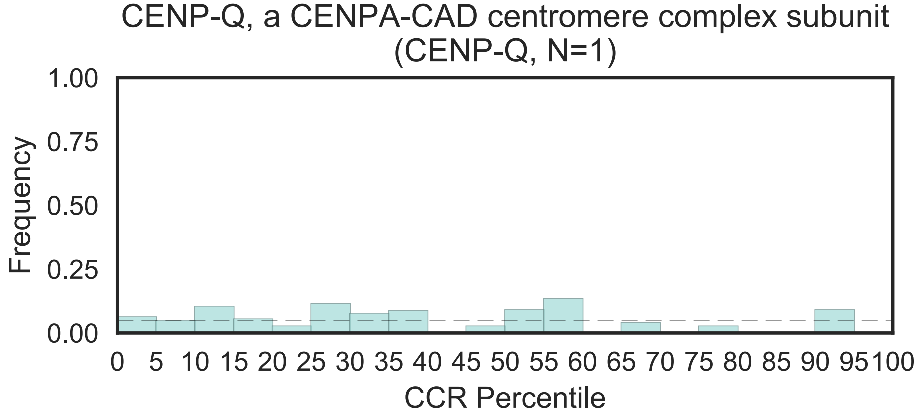

Centromere protein M (CENP-M)
(CENP-M, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

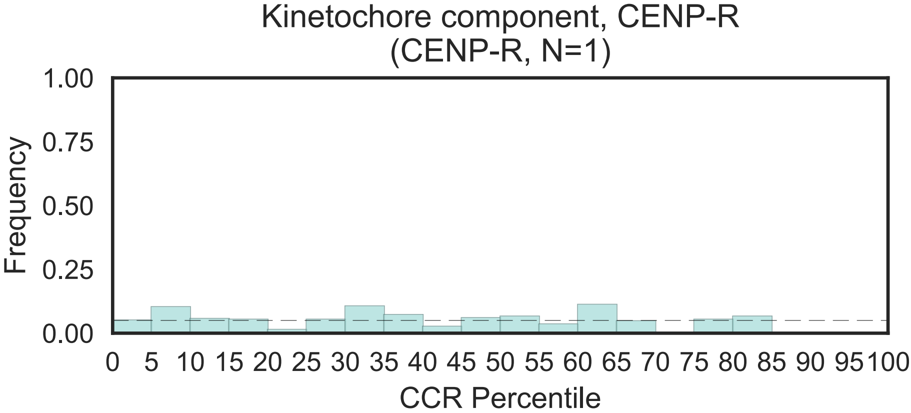

Kinetochore protein CHL4 like
(CENP-N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

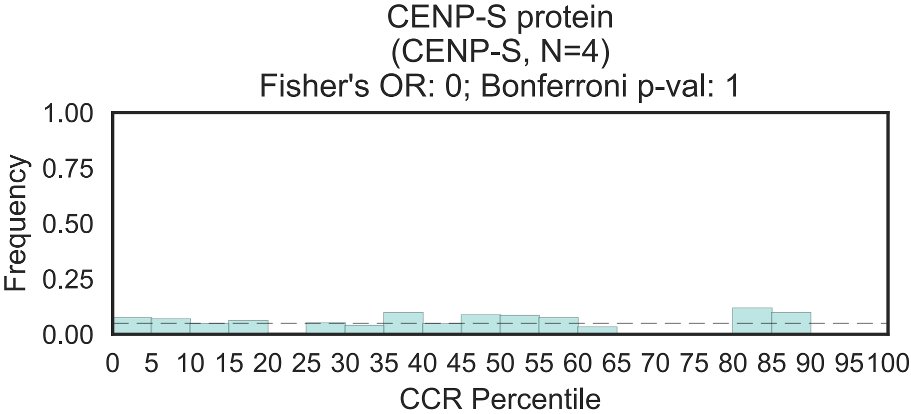

Cenp-O kinetochore centromere component
(CENP-O, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

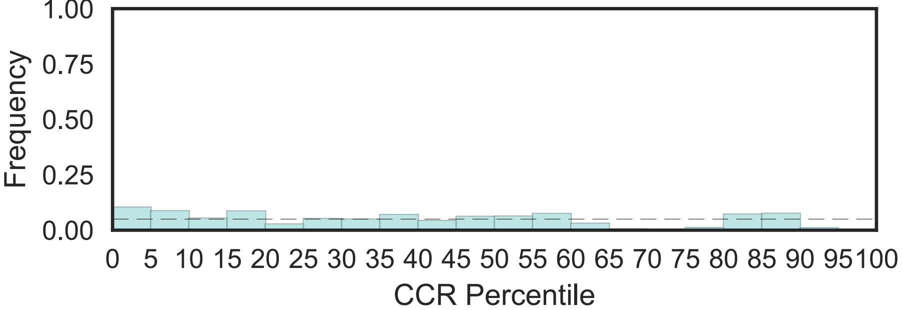


CENP-A-nucleosome distal (CAD) centromere subunit, CENP-P
(CENP-P, N=5)
Fisher's OR: 0; Bonferroni p-val: 1

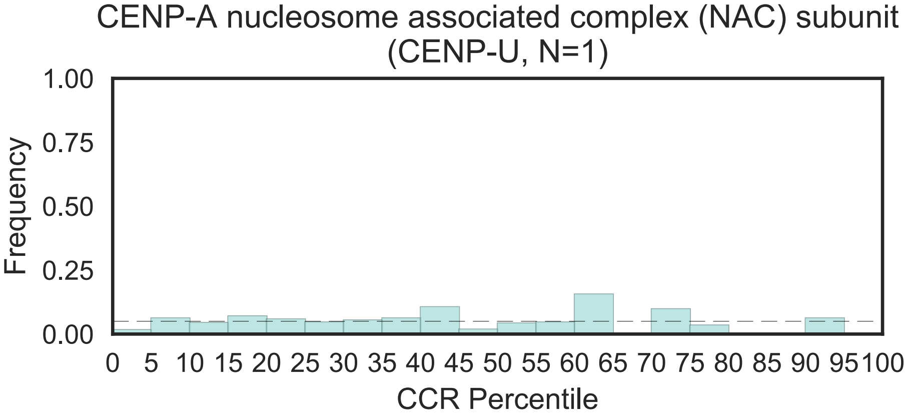

CENP-Q, a CENPA-CAD centromere complex subunit
(CENP-Q, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

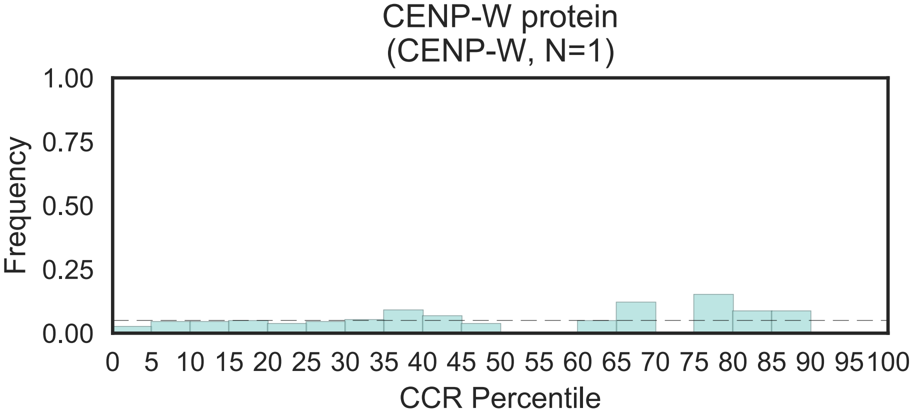

Kinetochore component, CENP-R
(CENP-R, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

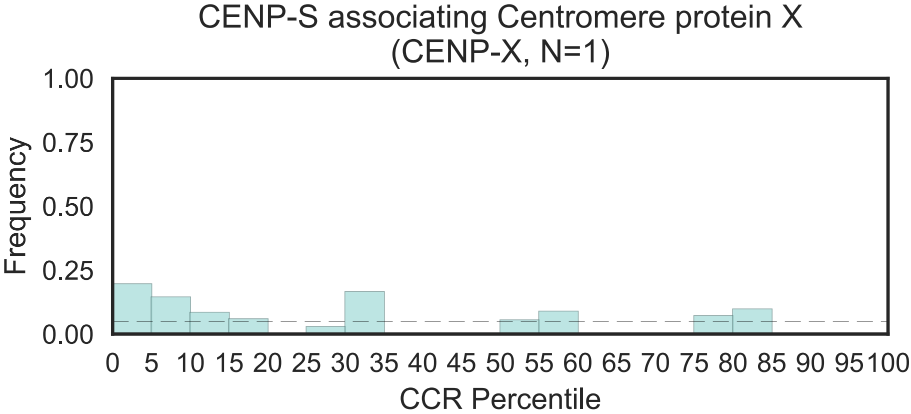

CENP-S protein
(CENP-S, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

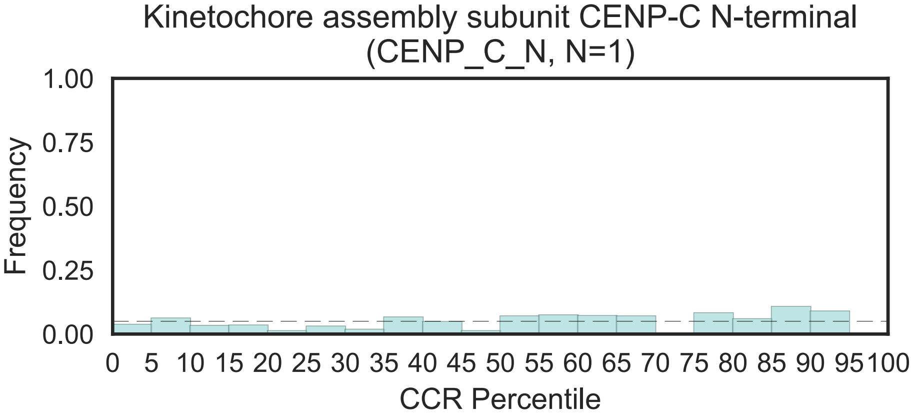


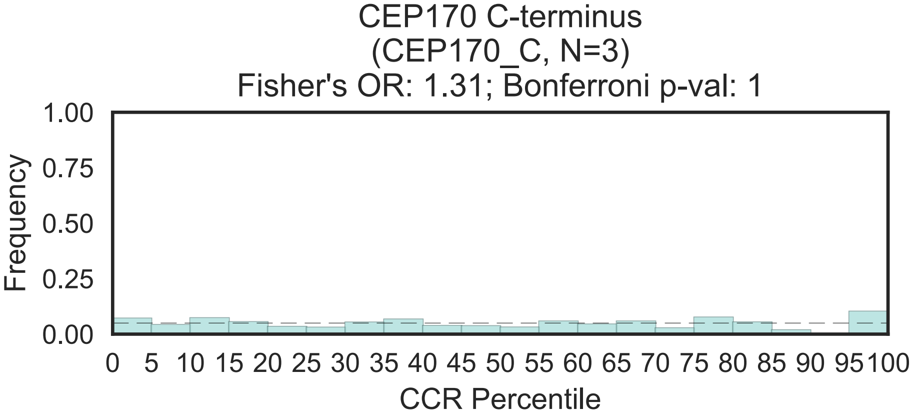
Centromere kinetochore component CENP-T histone fold
(CENP-T_C, N=18)
Fisher's OR: 0; Bonferroni p-val: 1


CENP-A nucleosome associated complex (NAC) subunit
(CENP-U, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

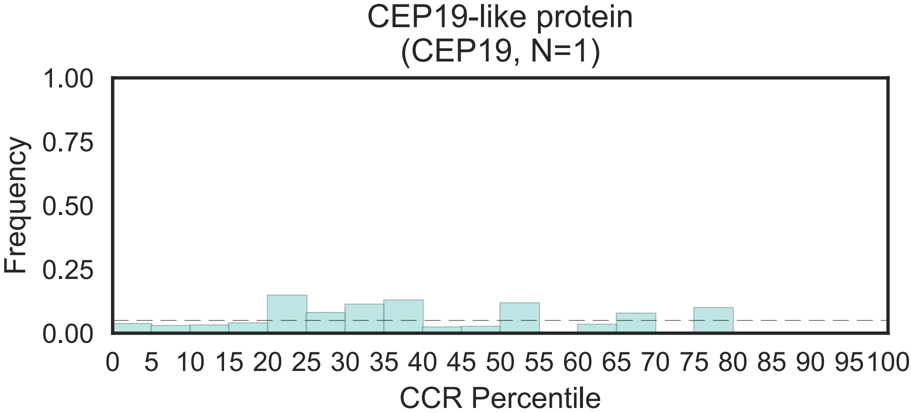

CENP-W protein
(CENP-W, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

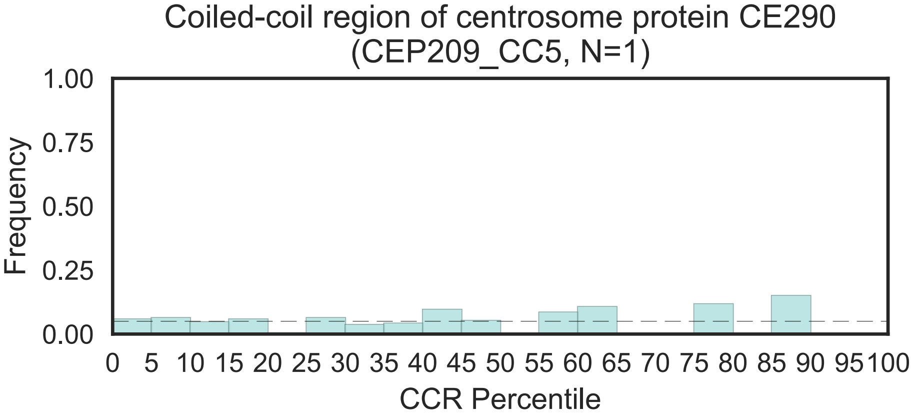

CENP-S associating Centromere protein X
(CENP-X, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

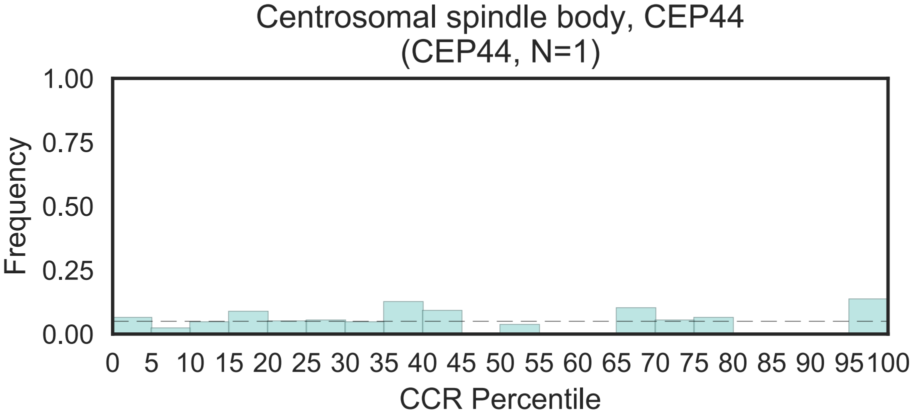

Kinetochore assembly subunit CENP-C N-terminal
(CENP_C_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

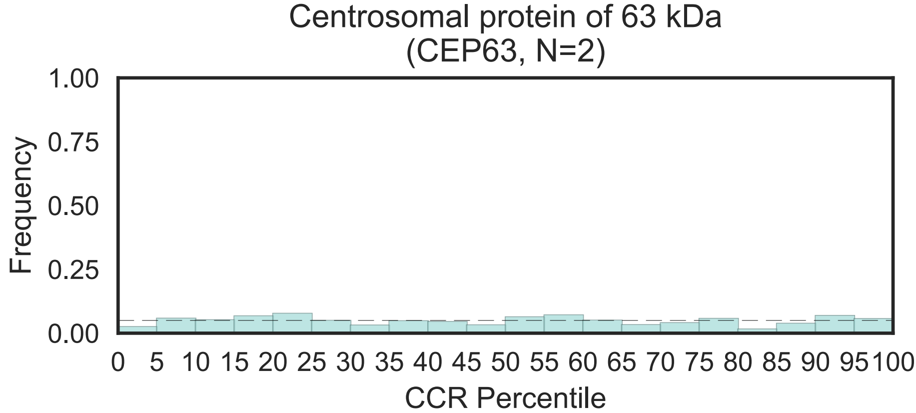


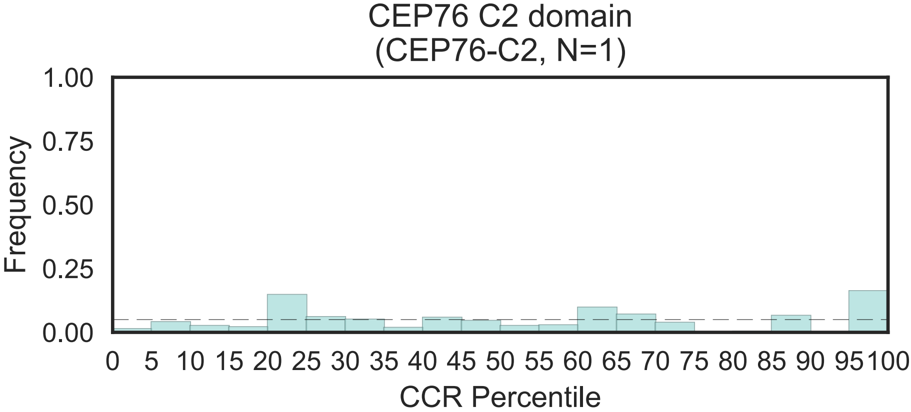
CEP170 C-terminus
(CEP170_C, N=3)
Fisher's OR: 1.31; Bonferroni p-val: 1

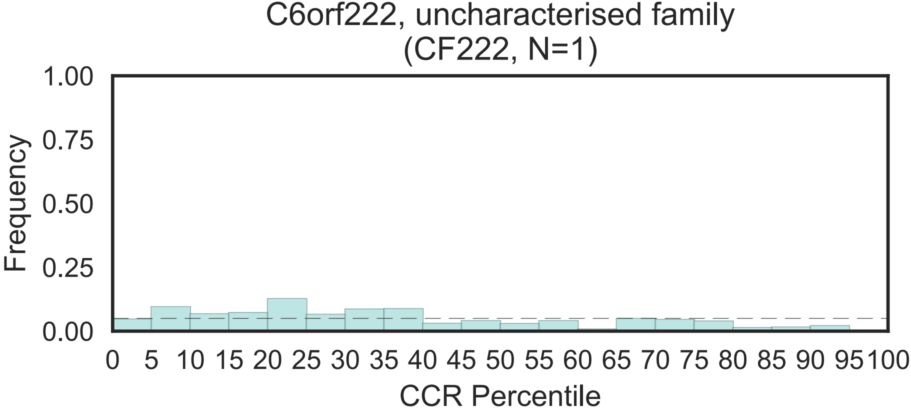

CEP19-like protein
(CEP19, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

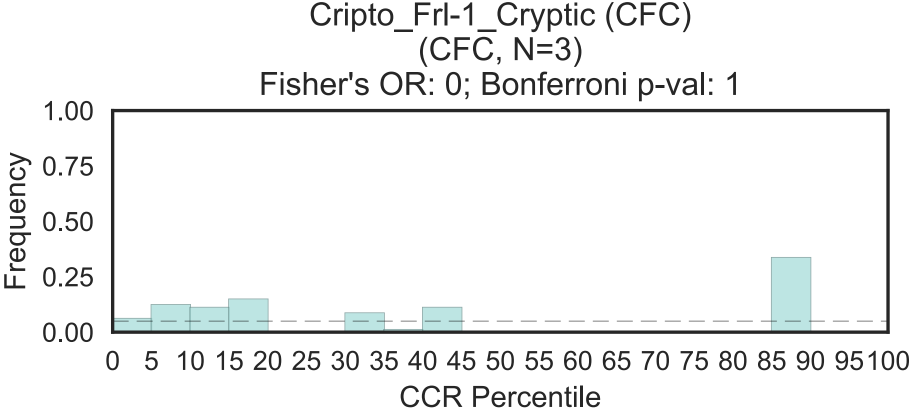

Coiled-coil region of centrosome protein CE290
(CEP209_CC5, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

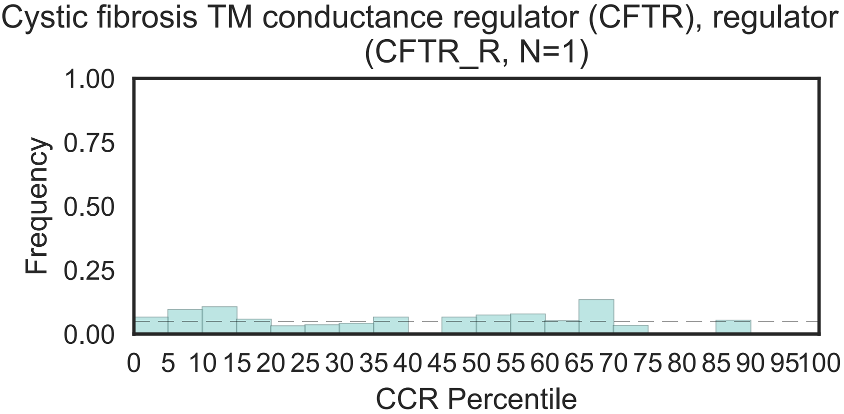

Centrosomal spindle body, CEP44
(CEP44, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

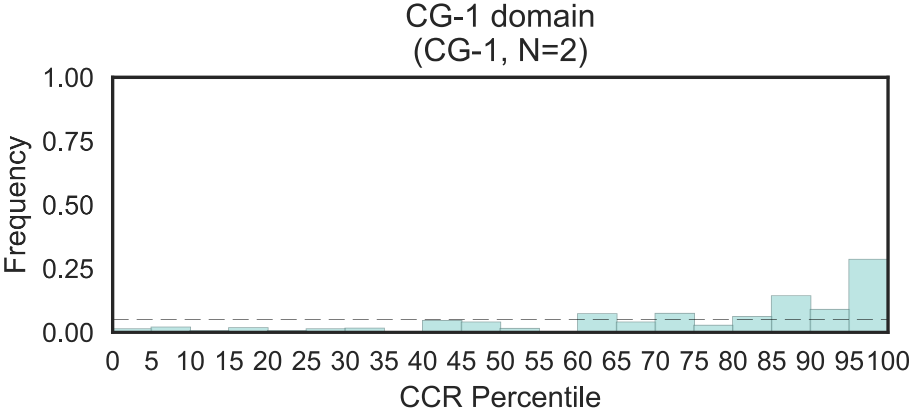

Centrosomal protein of 63 kDa
(CEP63, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


CEP76 C2 domain
(CEP76-C2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

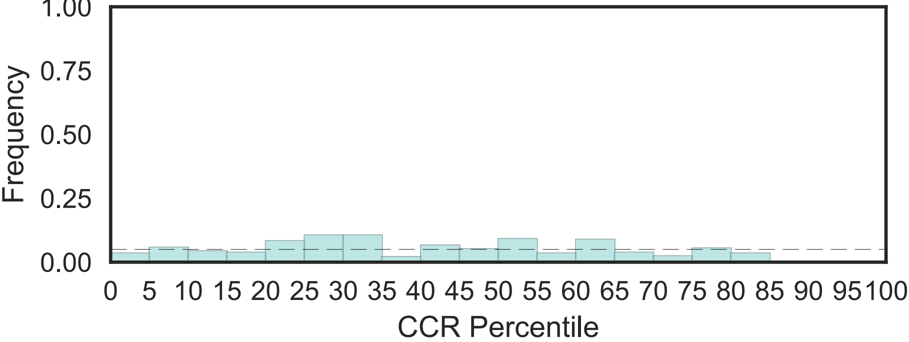

C6orf222, uncharacterised family
(CF222, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

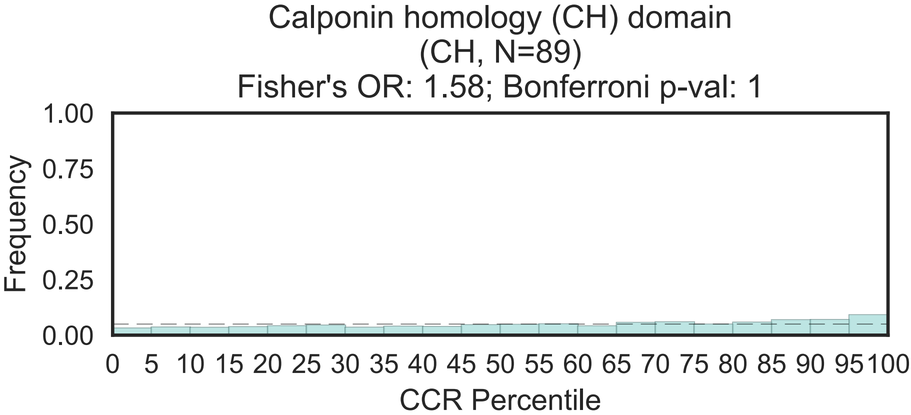

Cripto_Frl-1_Cryptic (CFC)
(CFC, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

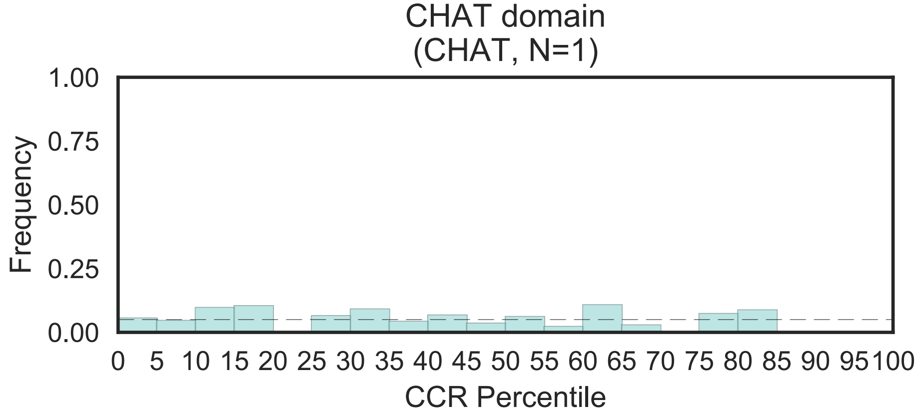

Cystic fibrosis TM conductance regulator (CFTR), regulator domain
(CFTR_R, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

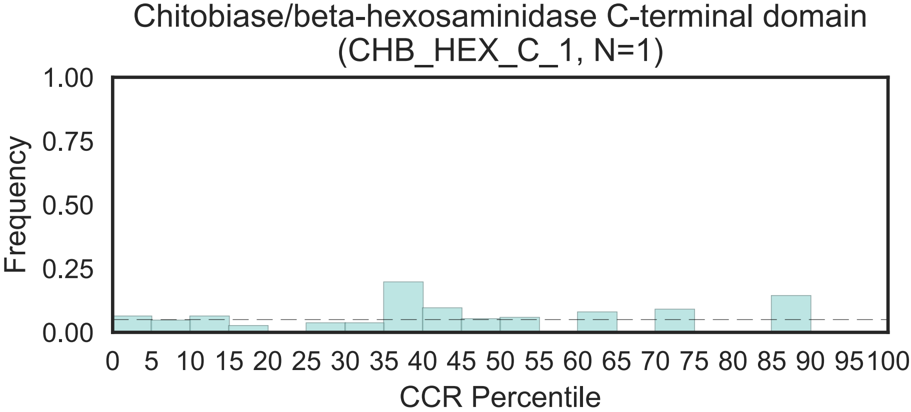

CG-1 domain
(CG-1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

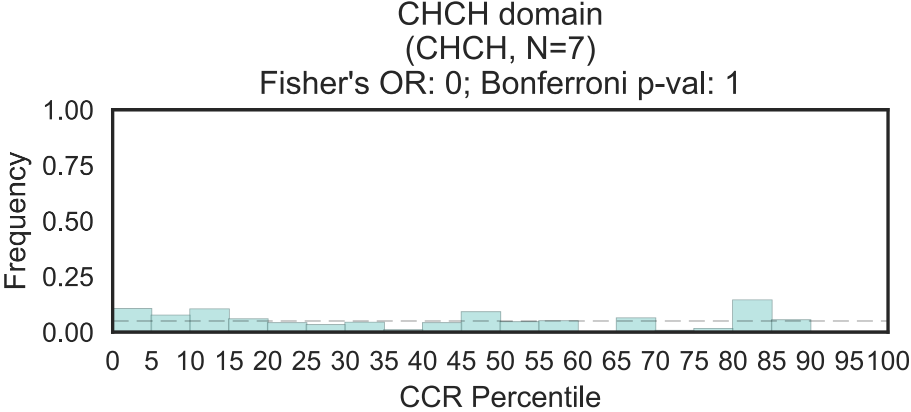
Kinase binding protein CGI-121
(CGI-121, N=1)

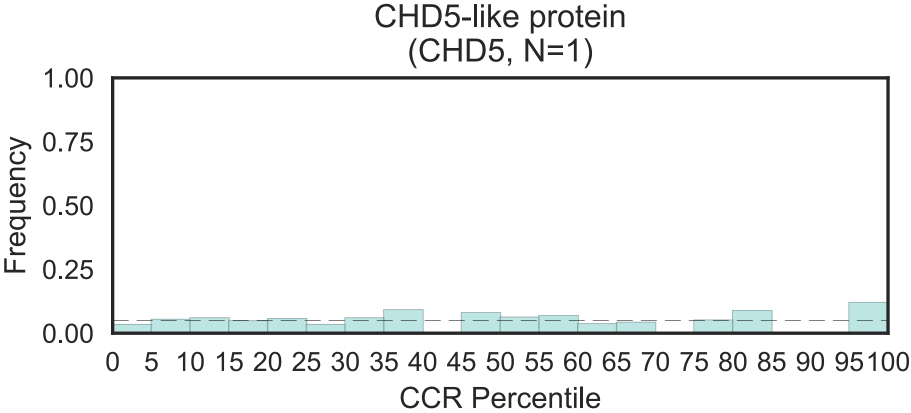


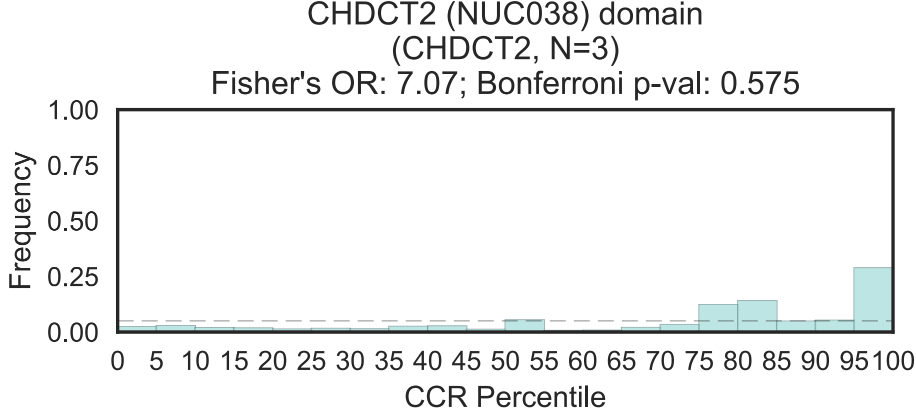

Calponin homology (CH) domain
(CH, N=89)
Fisher's OR: 1.58; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

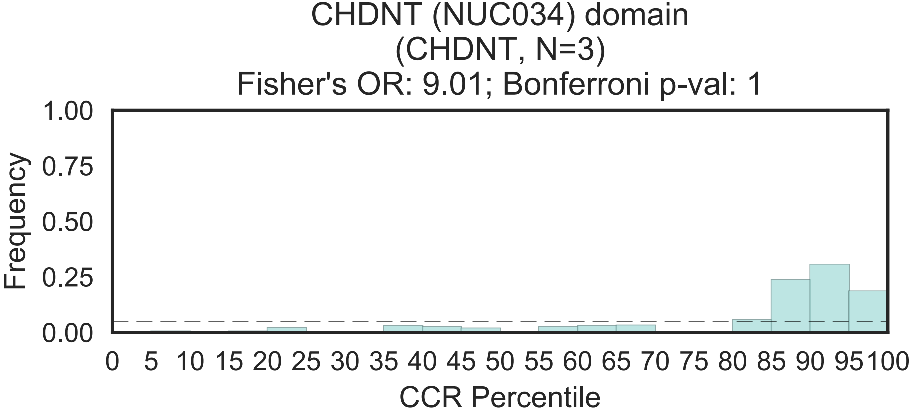

CHAT domain
(CHAT, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

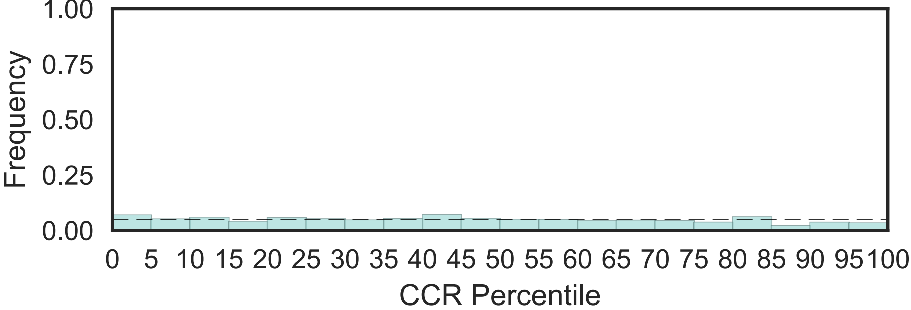

Chitobiase/beta-hexosaminidase C-terminal domain
(CHB_HEX_C_1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


CHCH domain
(CHCH, N=7)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

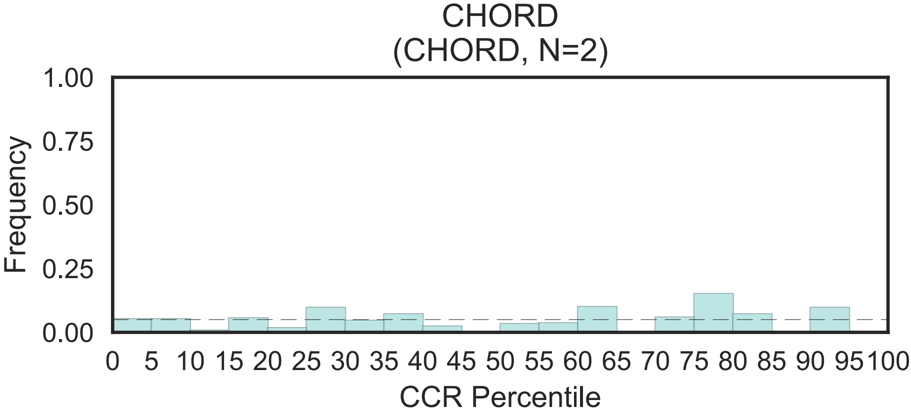

CHD5-like protein
(CHD5, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

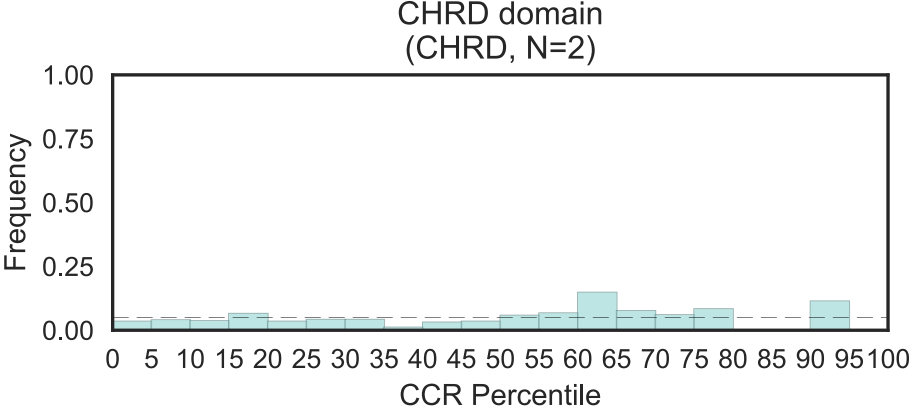

CHDCT2 (NUC038) domain
(CHDCT2, N=3)
Fisher's OR: 7.07; Bonferroni p-val: 0.575
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

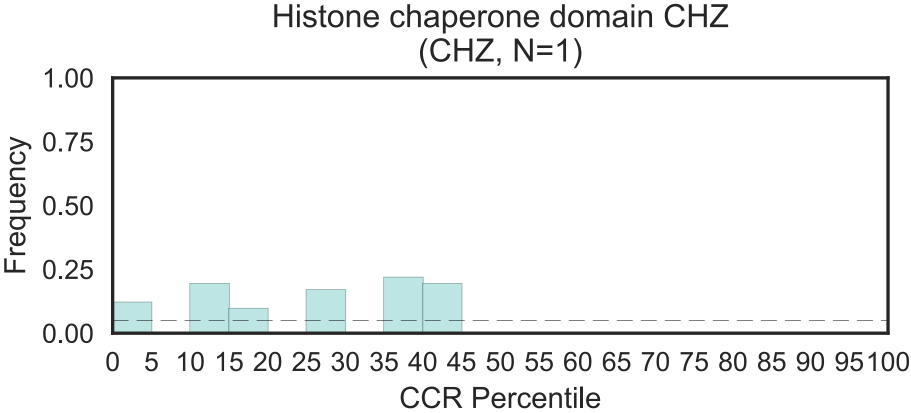

CHDNT (NUC034) domain
(CHDNT, N=3)
Fisher's OR: 9.01; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

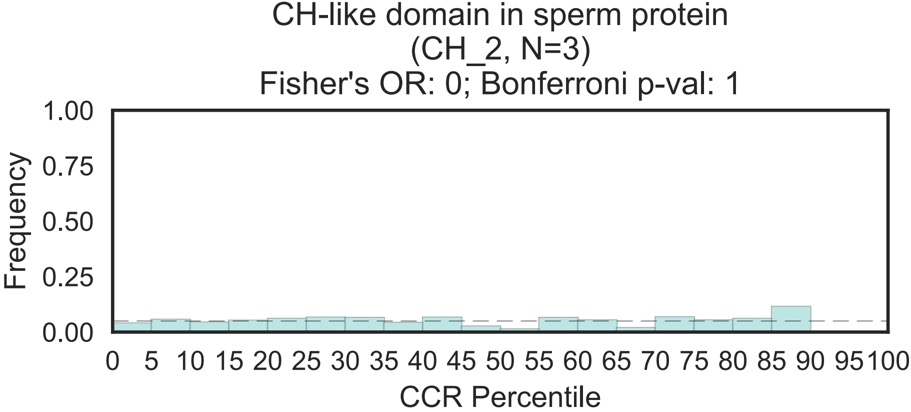


Chondroitin N-acetylgalactosaminyltransferase
(CHGN, N=8)
Fisher's OR: 0.368; Bonferroni p-val: 1

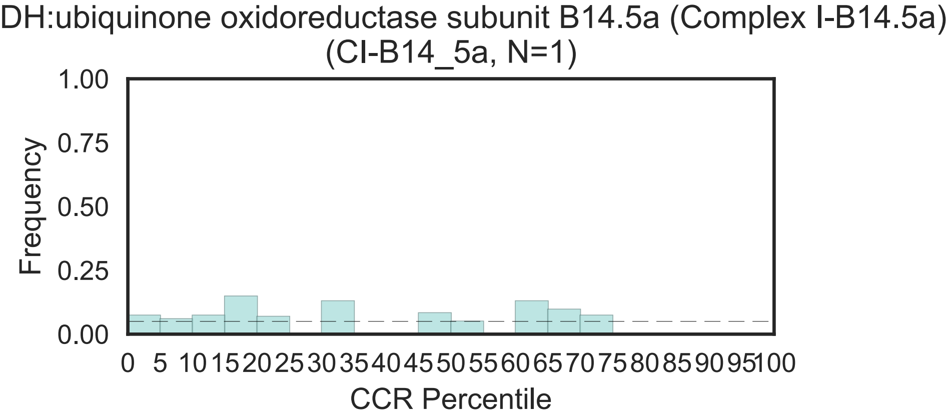

CHORD
(CHORD, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


CHRD domain
(CHRD, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

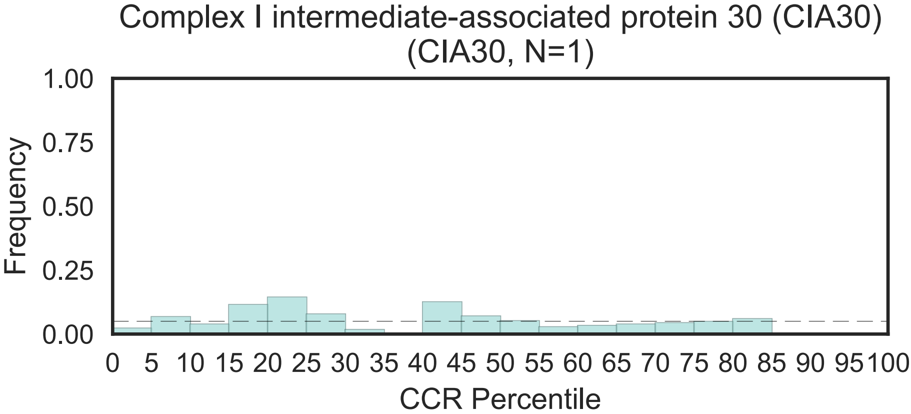

Histone chaperone domain CHZ
(CHZ, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

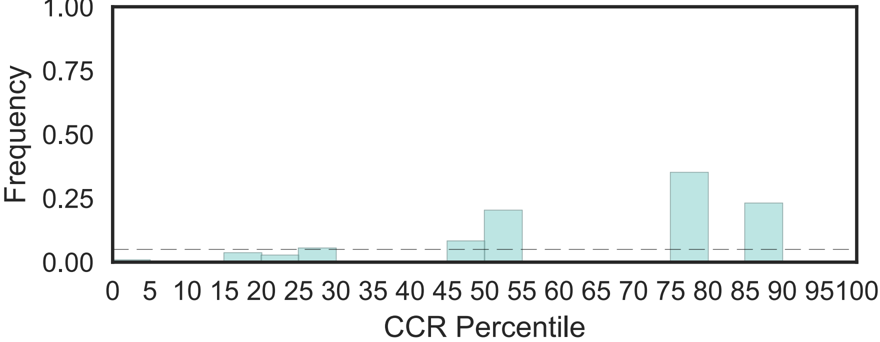


CH-like domain in sperm protein
(CH_2, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

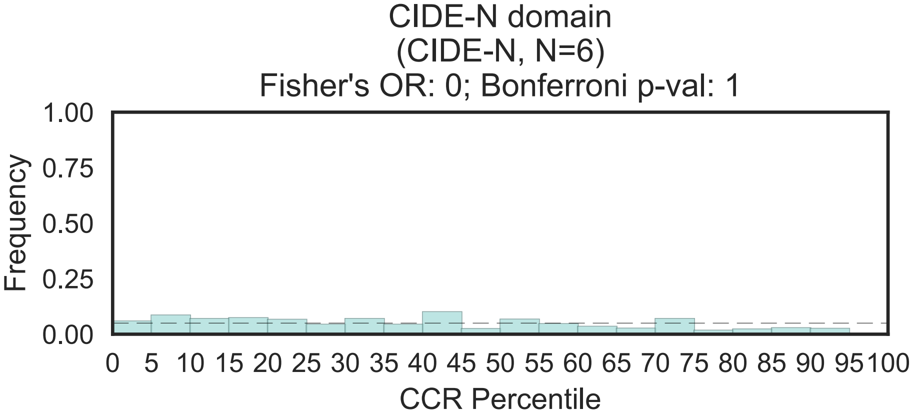


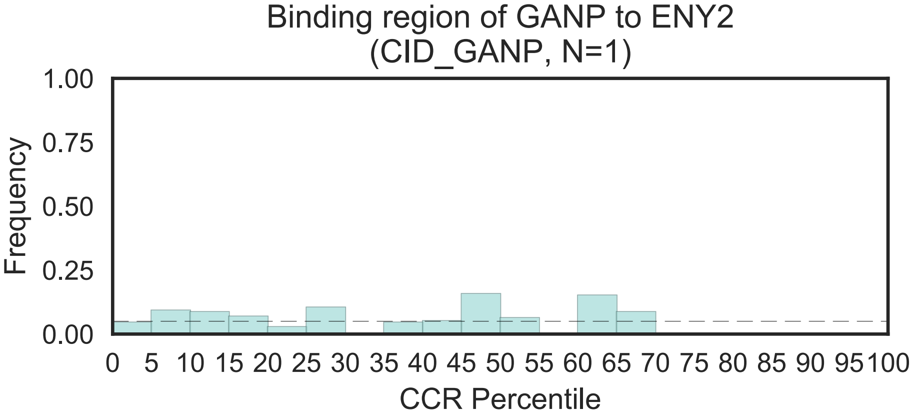
NADH:ubiquinone oxidoreductase subunit B14.5a (Complex I-B14.5a)
(CI-B14_5a, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

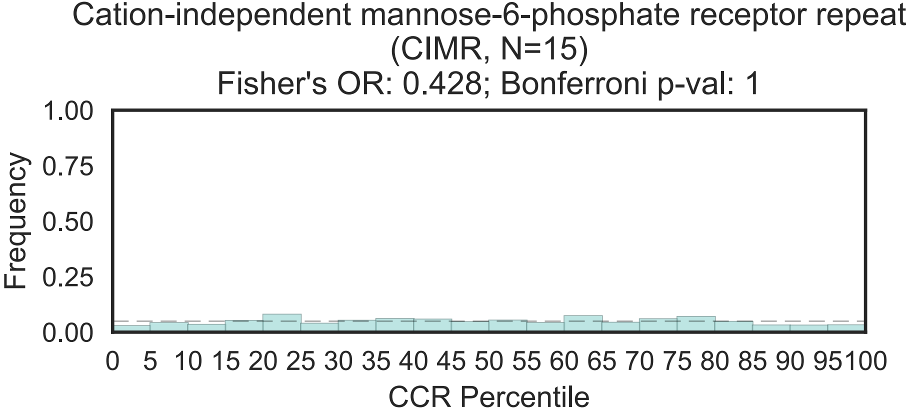

Complex I intermediate-associated protein 30 (CIA30)
(CIA30, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

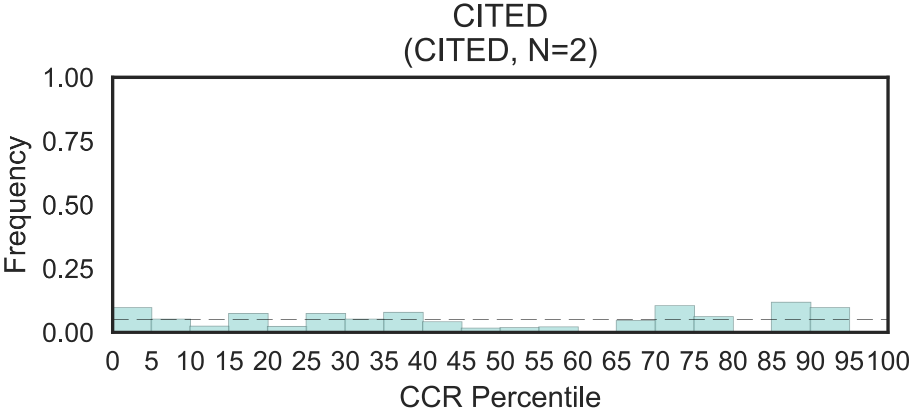


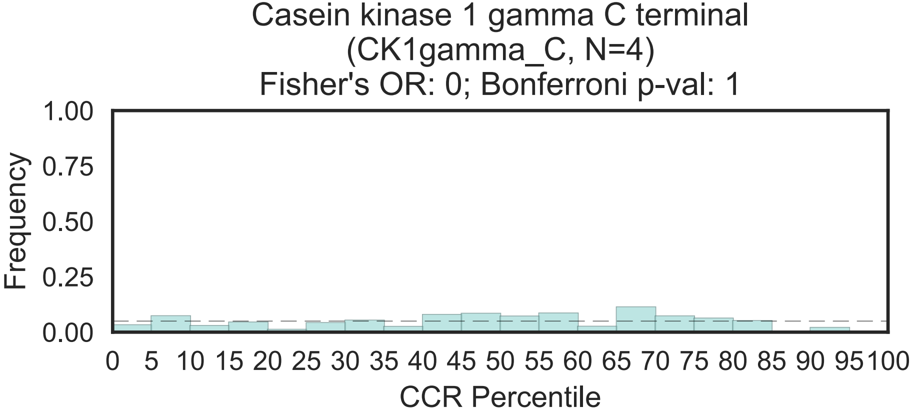
Cytokine-induced anti-apoptosis inhibitor 1, Fe-S biogenesis (CIAPIN1, N=2)

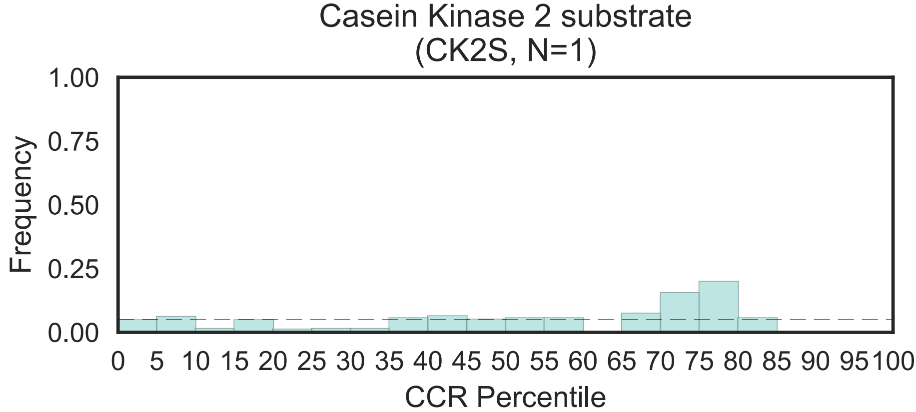

CIDE-N domain
(CIDE-N, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Binding region of GANP to ENY2
(CID_GANP, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

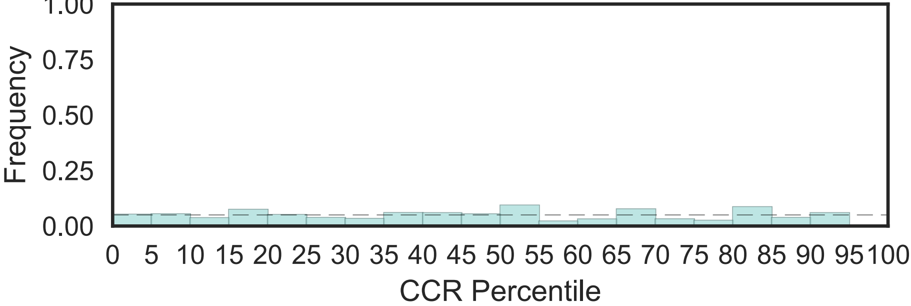

Cation-independent mannose-6-phosphate receptor repeat
(CIMR, N=15)
Fisher's OR: 0.428; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

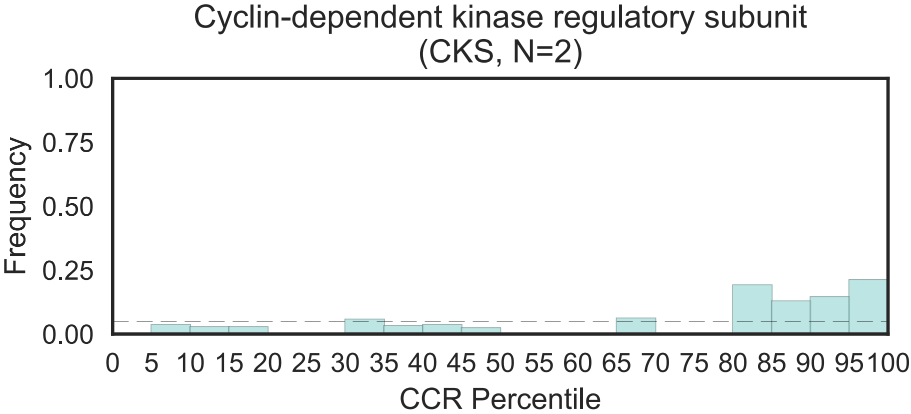

CITED
(CITED, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

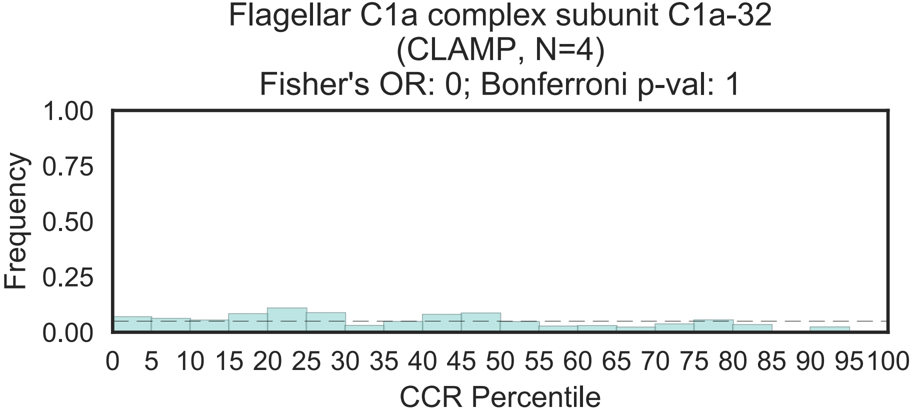

Casein kinase 1 gamma C terminal
(CK1gamma_C, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

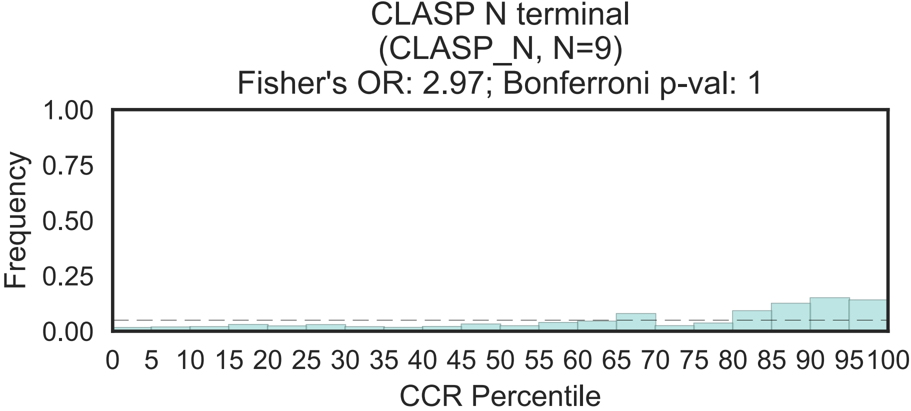

Casein Kinase 2 substrate
(CK2S, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

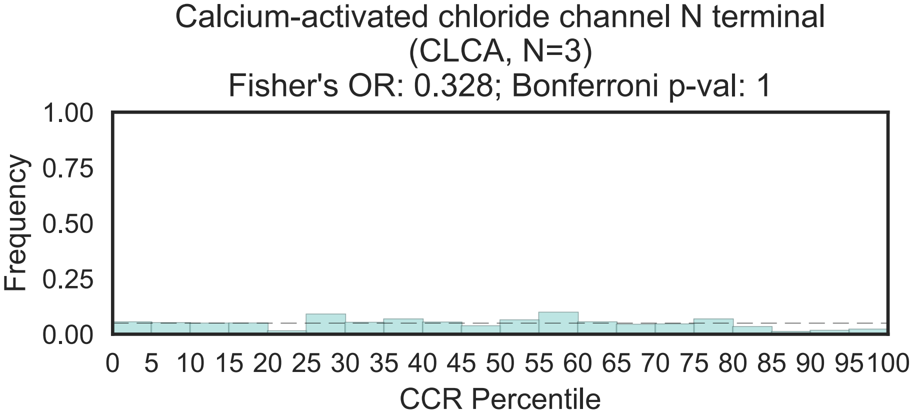
Cytoskeleton-associated protein 2 C-terminus
(CKAP2_C, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

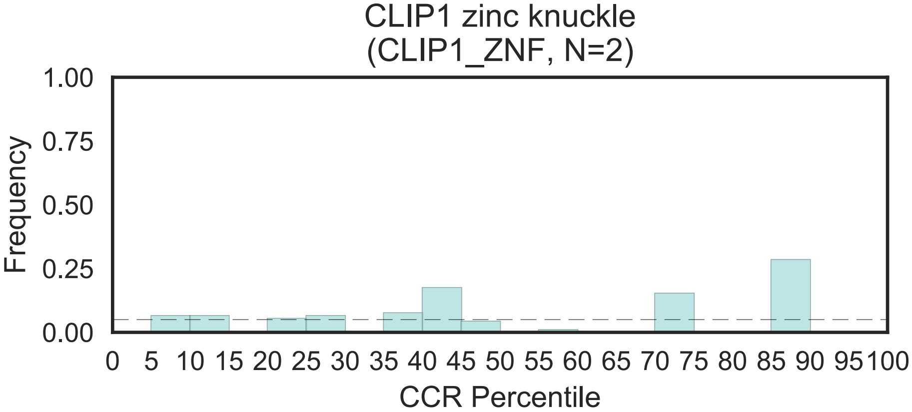


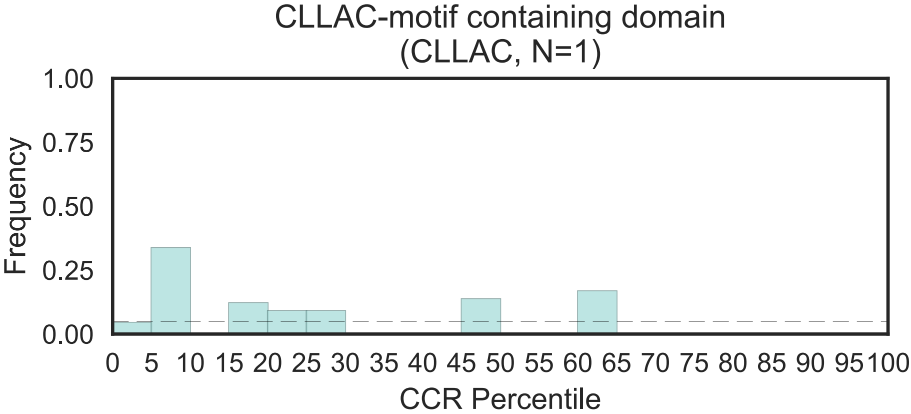

Cyclin-dependent kinase regulatory subunit
(CKS, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

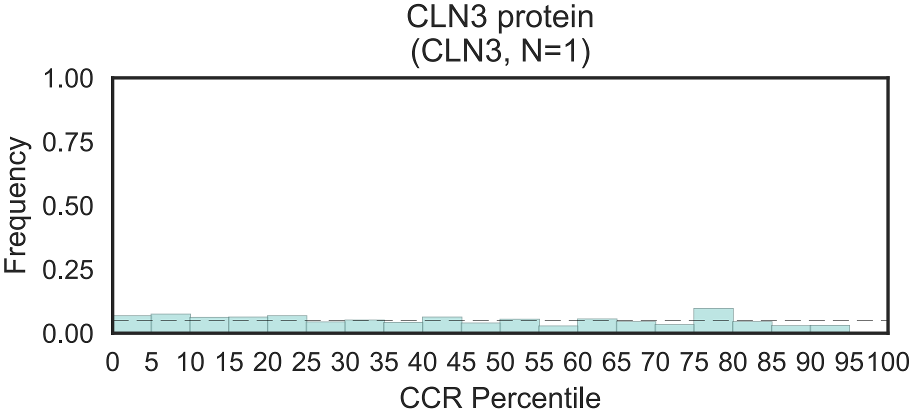

Flagellar C1a complex subunit C1a-32
(CLAMP, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

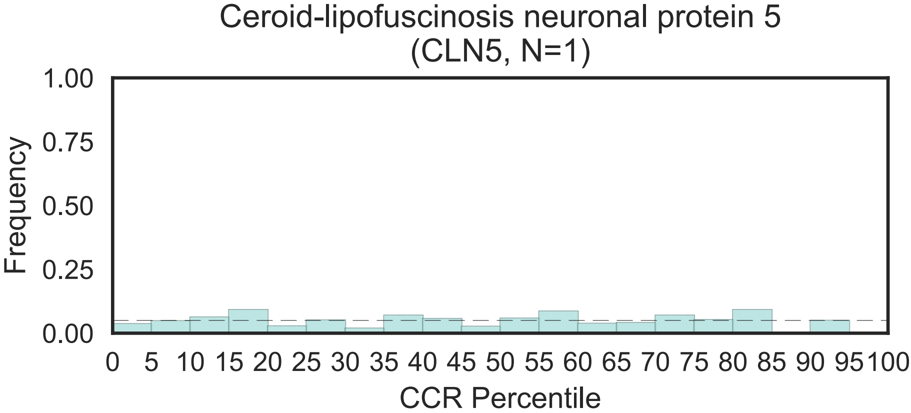

CLASP N terminal
(CLASP_N, N=9)
Fisher's OR: 2.97; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

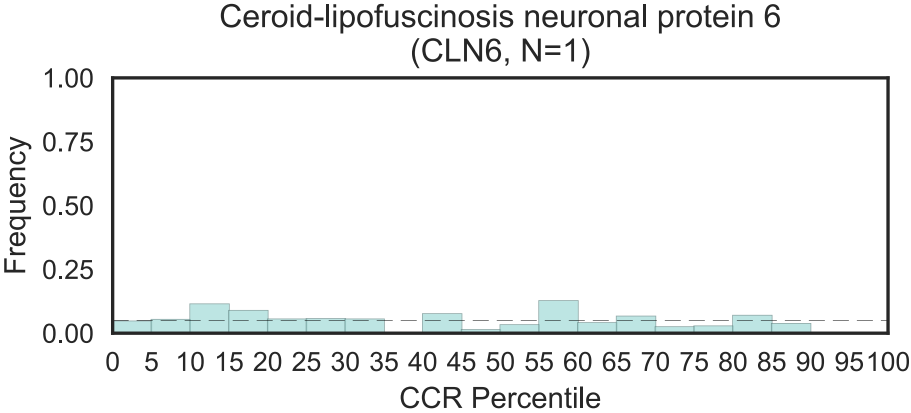

Calcium-activated chloride channel N terminal
(CLCA, N=3)
Fisher's OR: 0.328; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


CLIP1 zinc knuckle
(CLIP1_ZNF, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

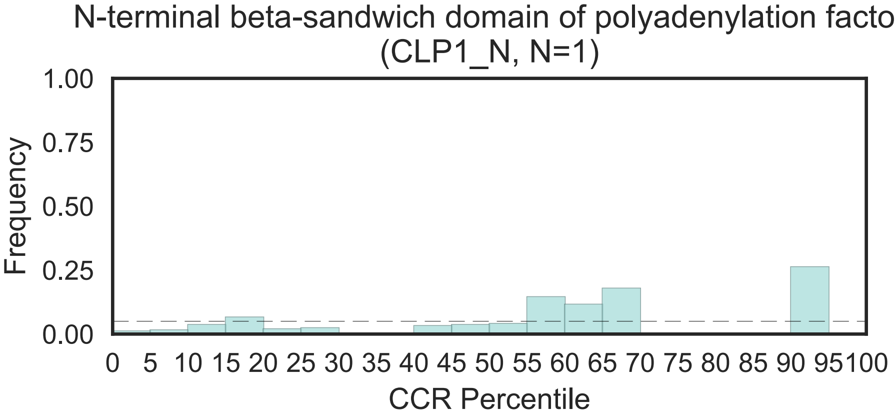

CLLAC-motif containing domain
(CLLAC, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

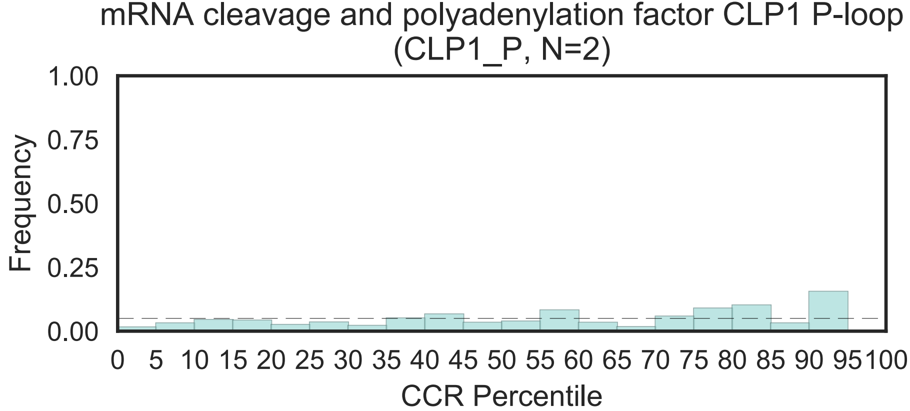

CLN3 protein
(CLN3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ceroid-lipofuscinosis neuronal protein 5
(CLN5, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

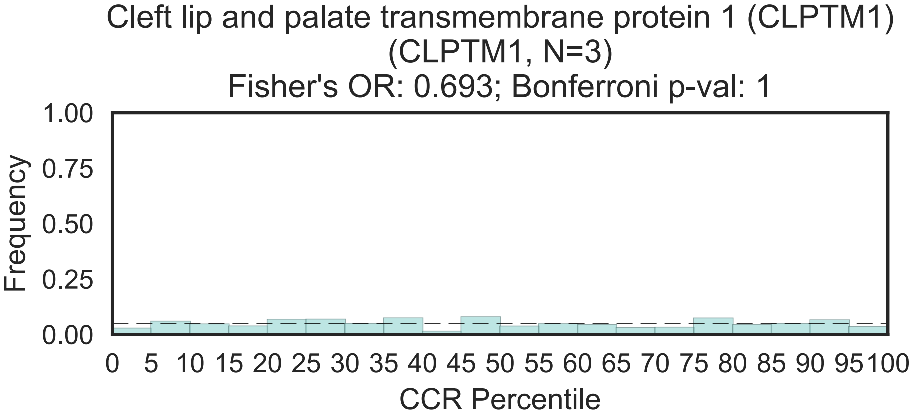


Ceroid-lipofuscinosis neuronal protein 6
(CLN6, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


N-terminal beta-sandwich domain of polyadenylation factor
(CLP1_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

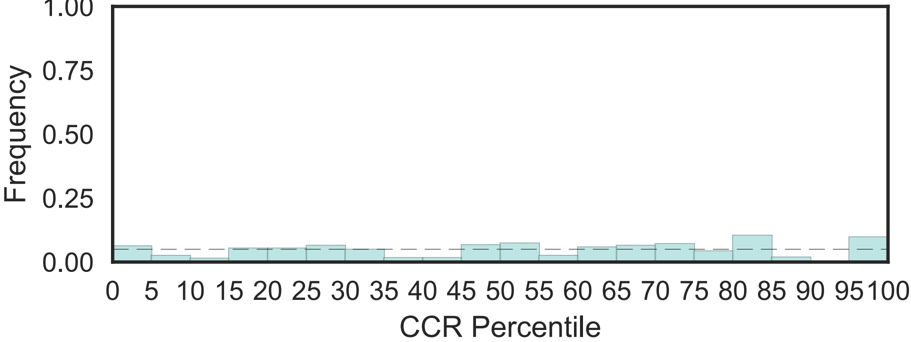


mRNA cleavage and polyadenylation factor CLP1 P-loop (CLP1_P, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

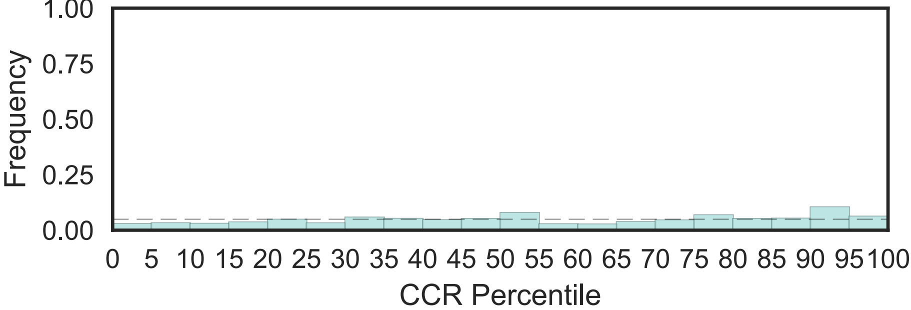


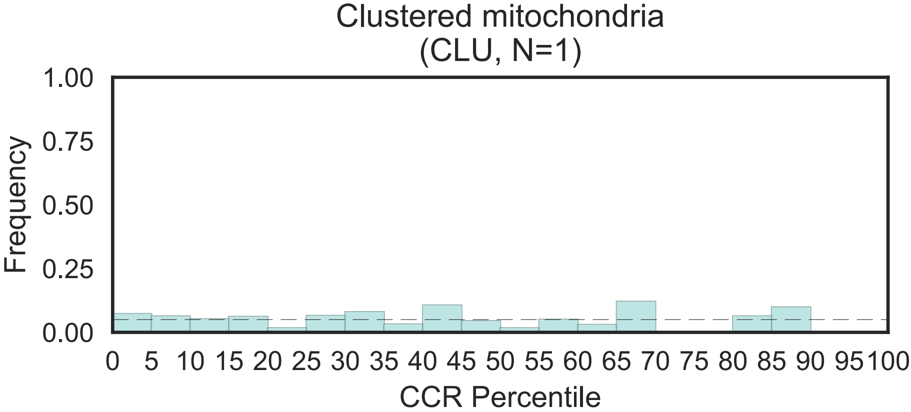
Cleft lip and palate transmembrane protein 1 (CLPTM1)
(CLPTM1, N=3)
Fisher's OR: 0.693; Bonferroni p-val: 1

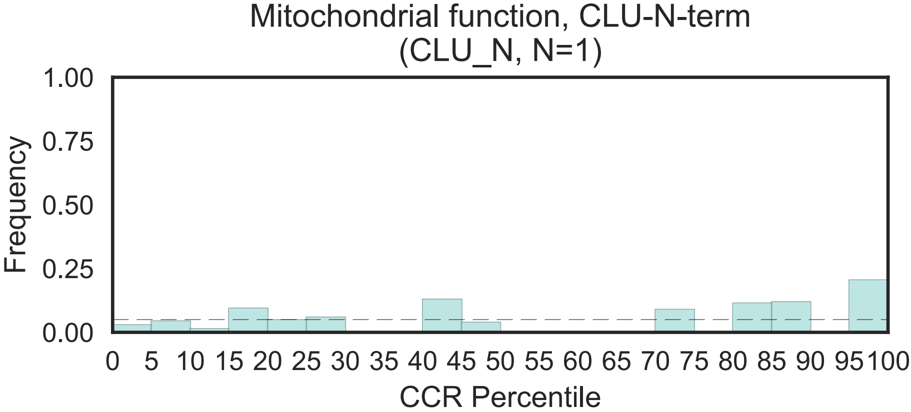
Clp protease
(CLP_protease, N=1)

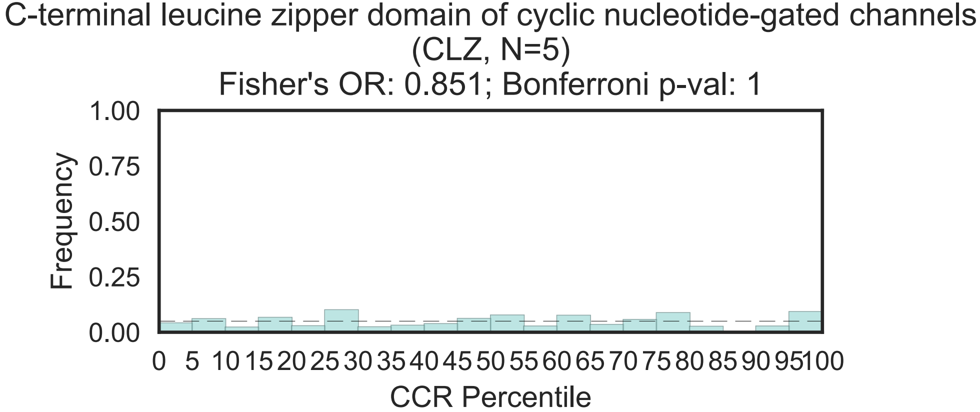


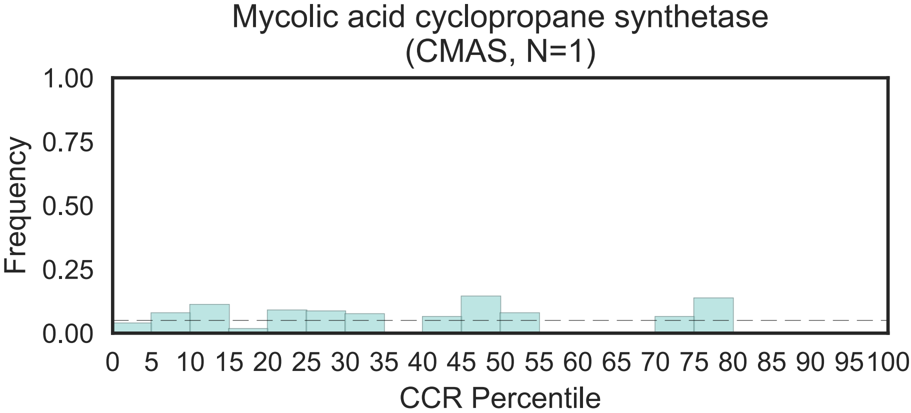
CTLH/CRA C-terminal to LisH motif domain (CLTH, N=6) Fisher's OR: 1.04; Bonferroni p-val: 1

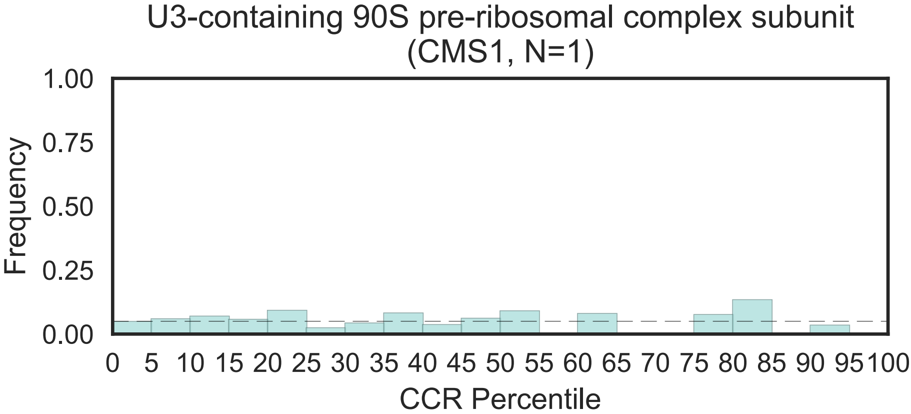


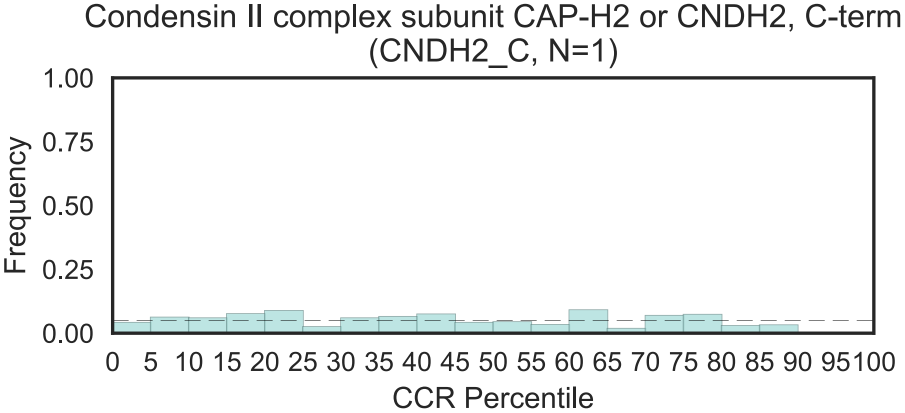

Clustered mitochondria
(CLU, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

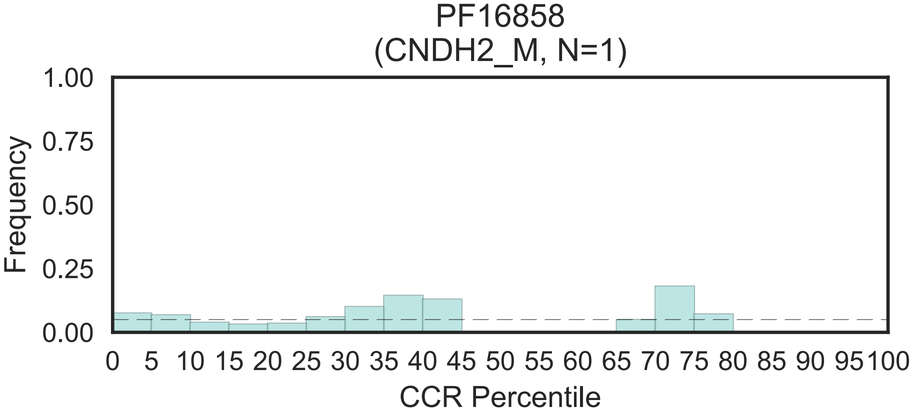

Mitochondrial function, CLU-N-term
(CLU_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

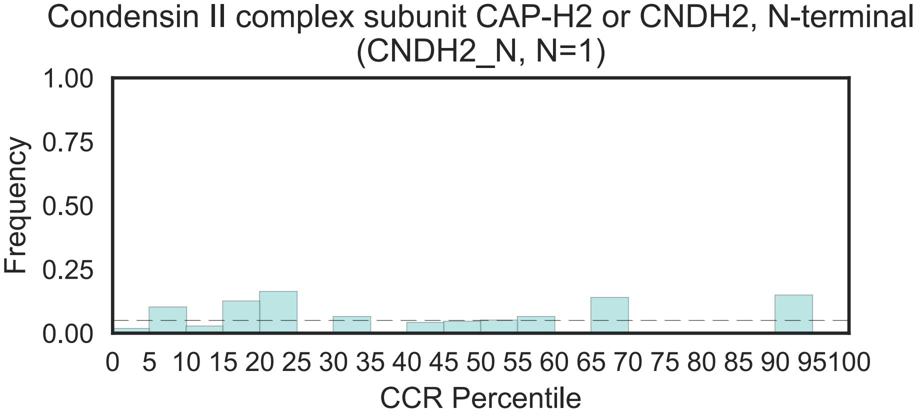

C-terminal leucine zipper domain of cyclic nucleotide-gated channels
(CLZ, N=5)
Fisher's OR: 0.851; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Mycolic acid cyclopropane synthetase
(CMAS, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

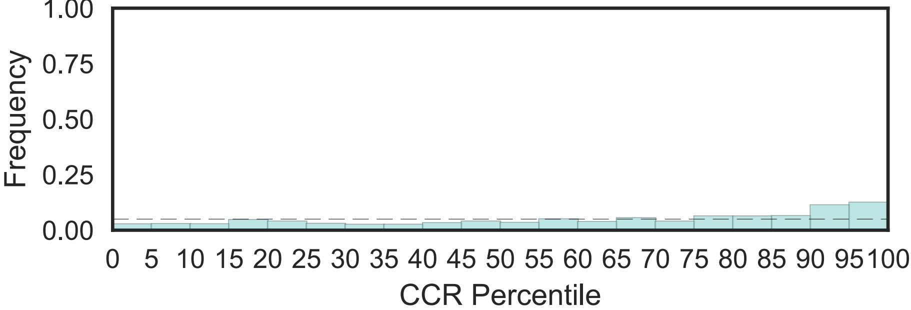

U3-containing 90S pre-ribosomal complex subunit
(CMS1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

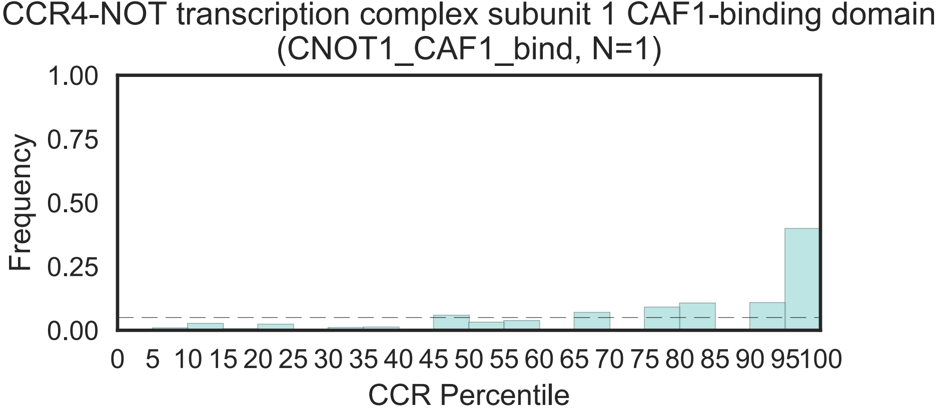

Condensin II complex subunit CAP-H2 or CNDH2, C-term
(CNDH2_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


PF16858
(CNDH2_M, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

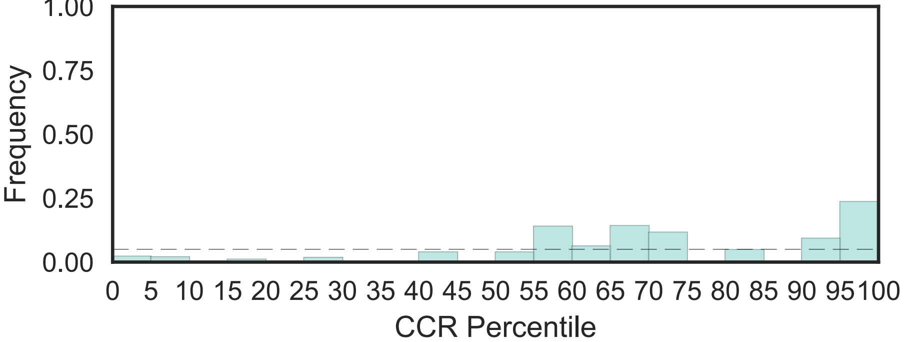

Condensin II complex subunit CAP-H2 or CNDH2, N-terminal
(CNDH2_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95100
CCR Percentile

CNH domain
(CNH, N=15)
Fisher's OR: 2.3; Bonferroni p-val: 1

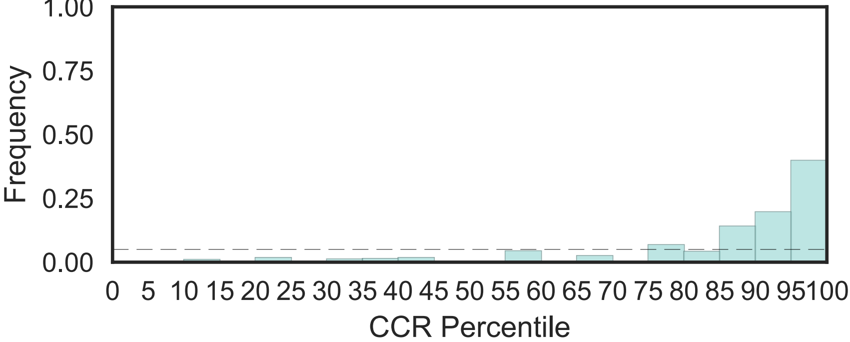


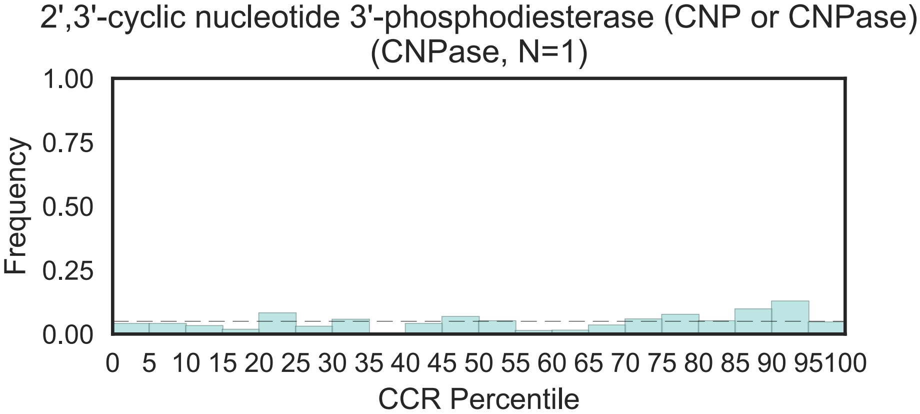

CCR4-NOT transcription complex subunit 1 CAF1-binding domain
(CNOT1_CAF1_bind, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

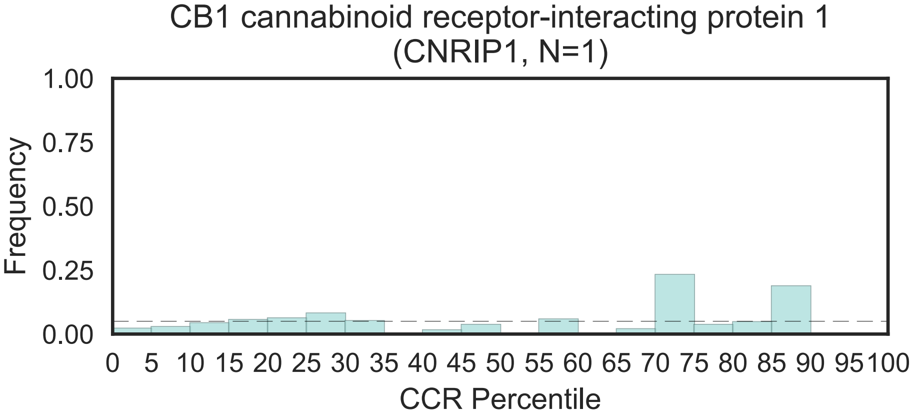
CCR4-NOT transcription complex subunit 1 HEAT repeat (CNOT1_HEAT, N=1)

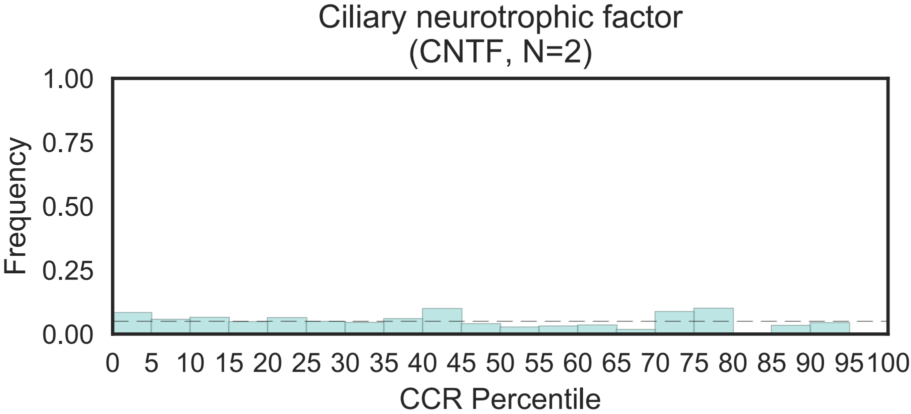


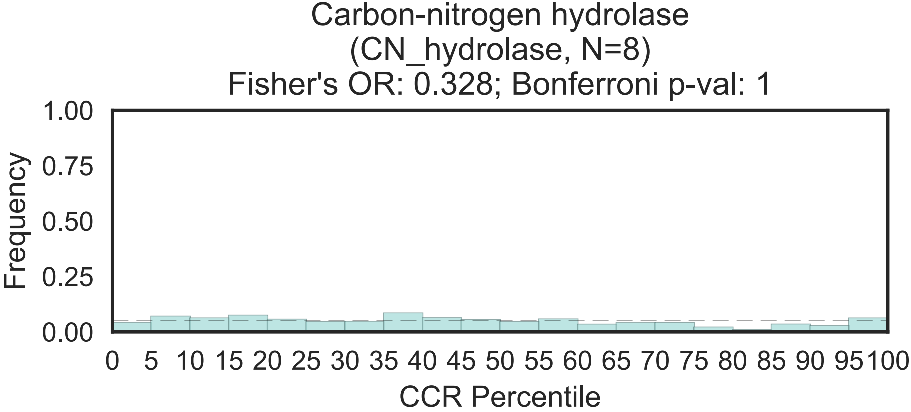
CCR4-NOT transcription complex subunit 1 TTP binding domain (CNOT1_TTP_bind, N=1)

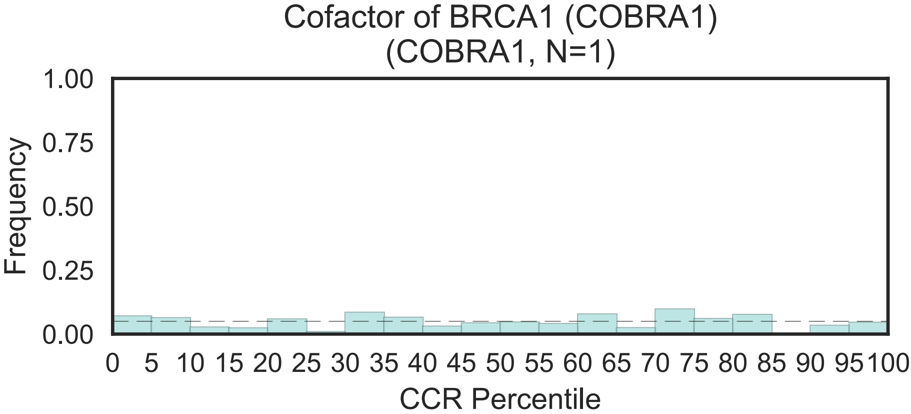


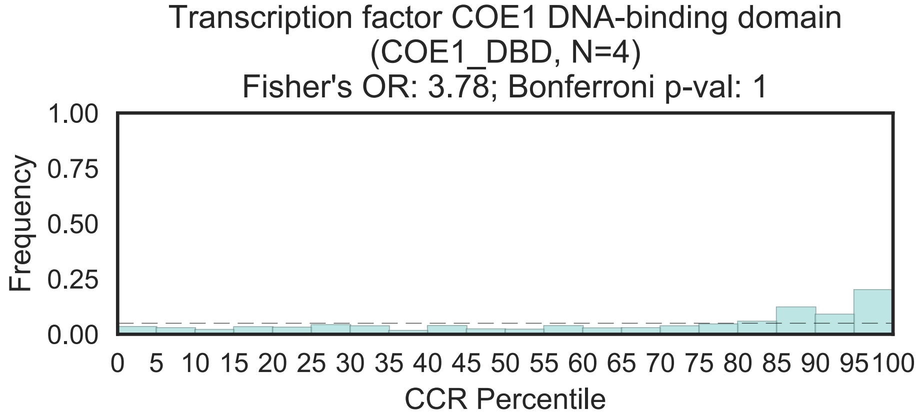

2',3'-cyclic nucleotide 3'-phosphodiesterase (CNP or CNPase)
(CNPase, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

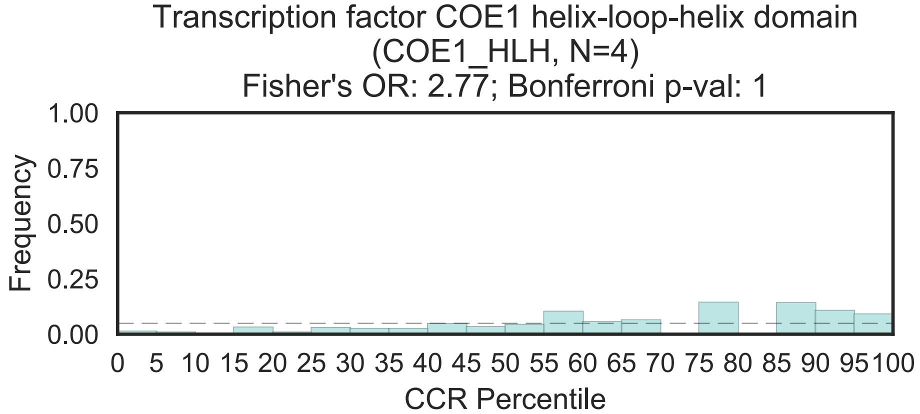

CB1 cannabinoid receptor-interacting protein 1
(CNRIP1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

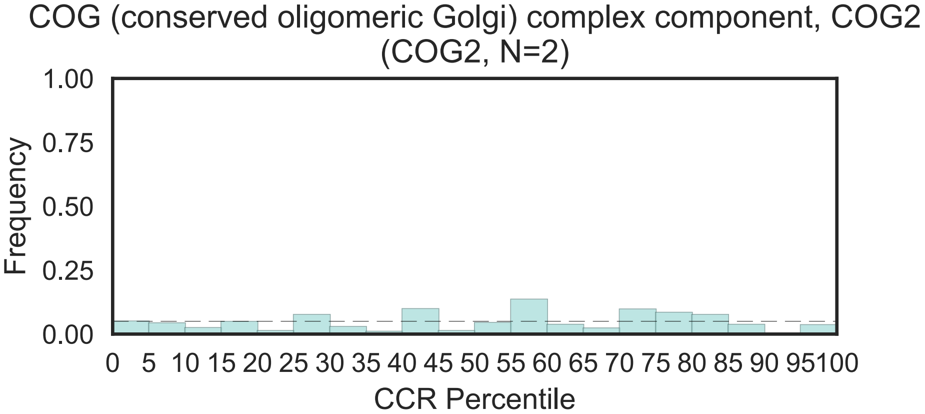

Ciliary neurotrophic factor
(CNTF, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Carbon-nitrogen hydrolase
(CN_hydrolase, N=8)
Fisher's OR: 0.328; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

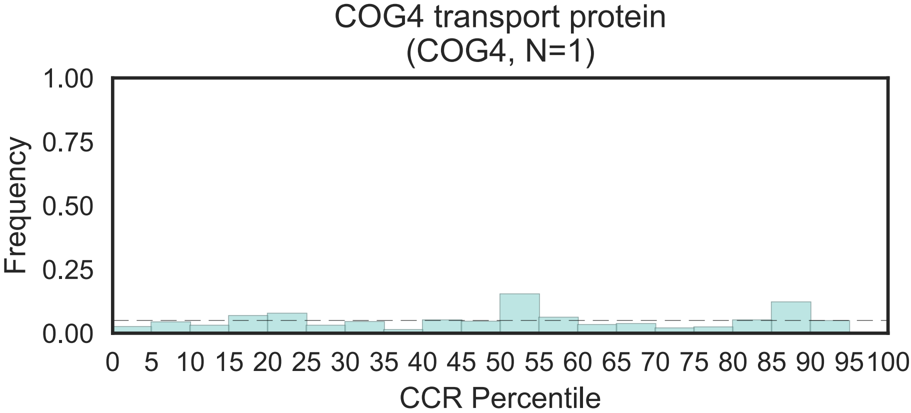

Cofactor of BRCA1 (COBRA1)
(COBRA1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

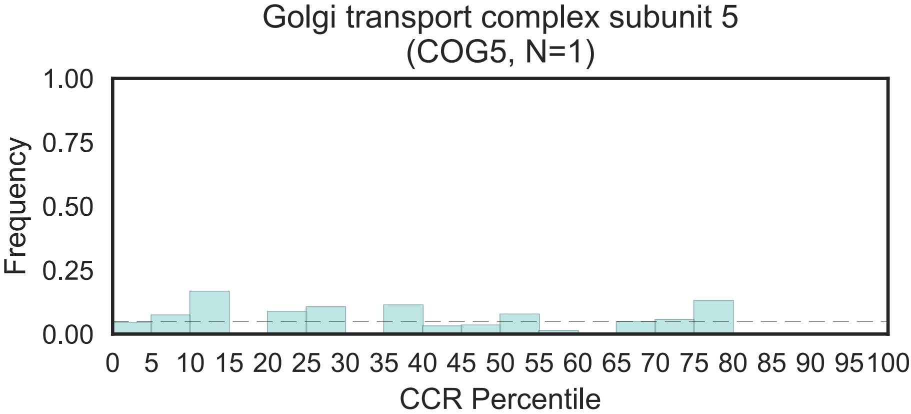

Transcription factor COE1 DNA-binding domain
(COE1_DBD, N=4)
Fisher's OR: 3.78; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

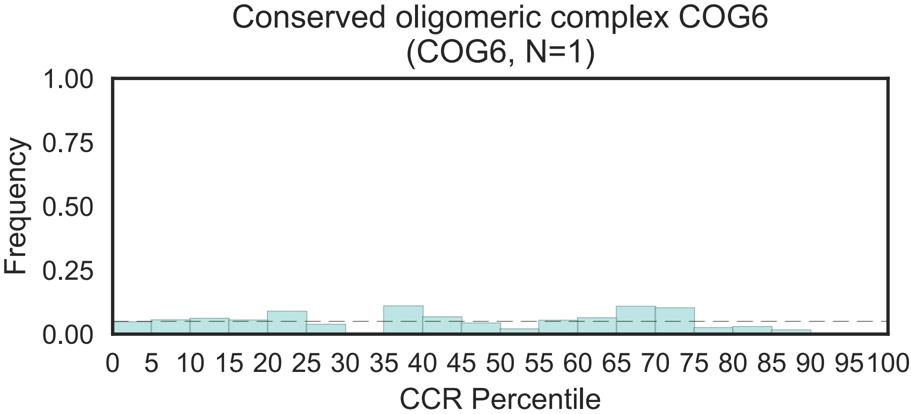

Transcription factor COE1 helix-loop-helix domain
(COE1_HLH, N=4)
Fisher's OR: 2.77; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

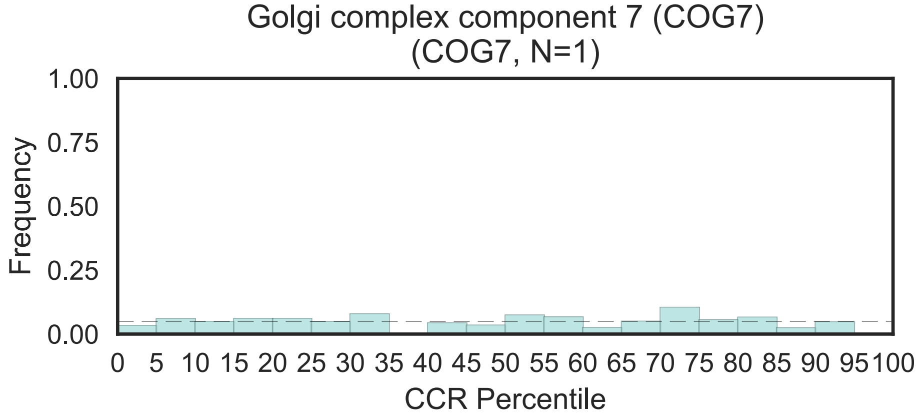


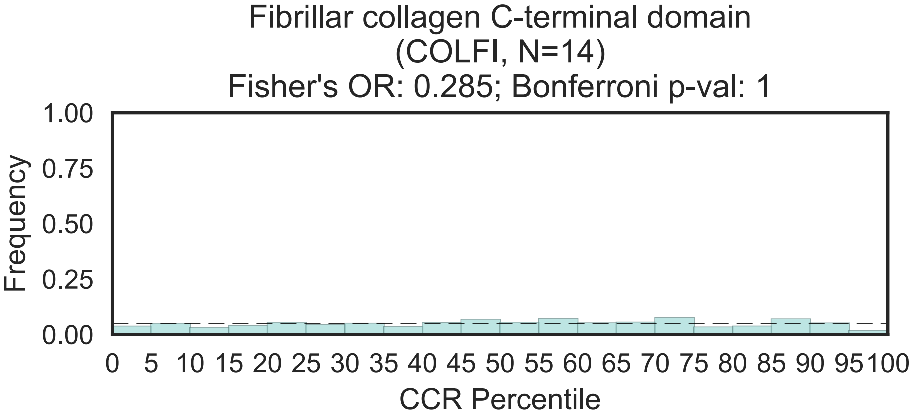
COG (conserved oligomeric Golgi) complex component, COG2
(COG2, N=2)

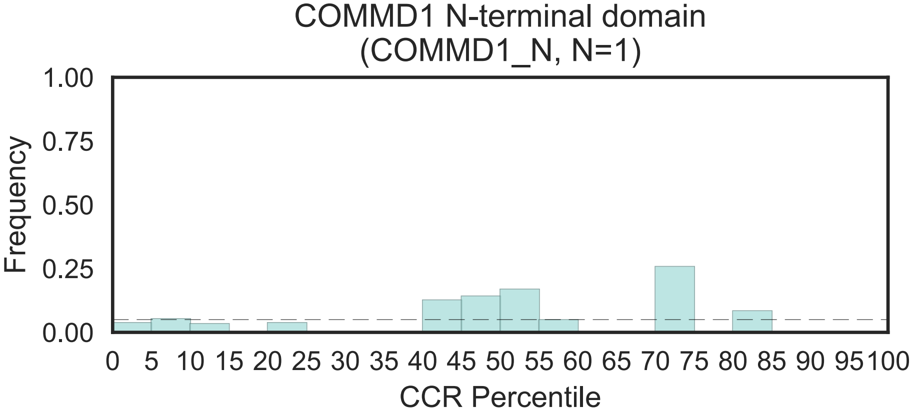

COG4 transport protein
(COG4, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

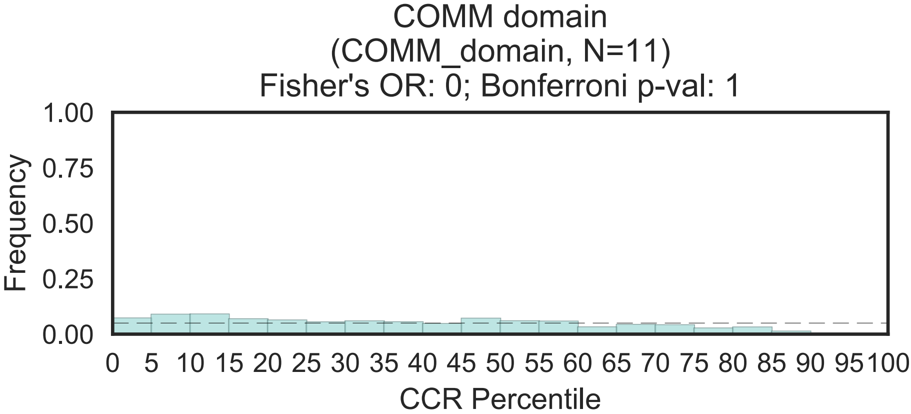

Golgi transport complex subunit 5
(COG5, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

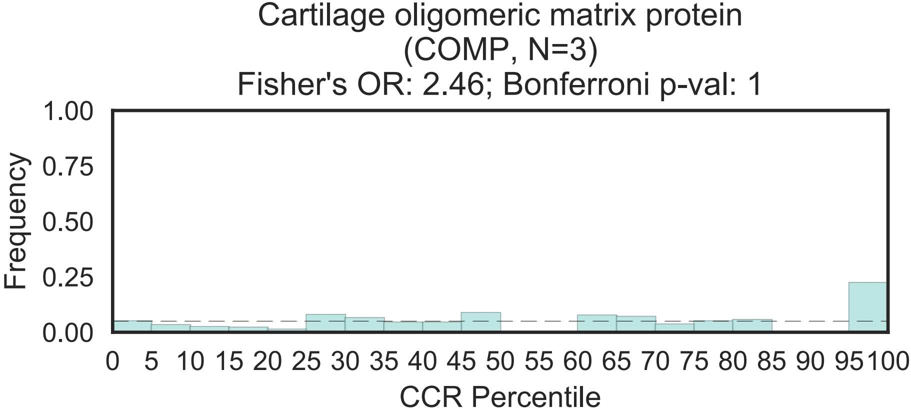

Conserved oligomeric complex COG6
(COG6, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


Golgi complex component 7 (COG7)
(COG7, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

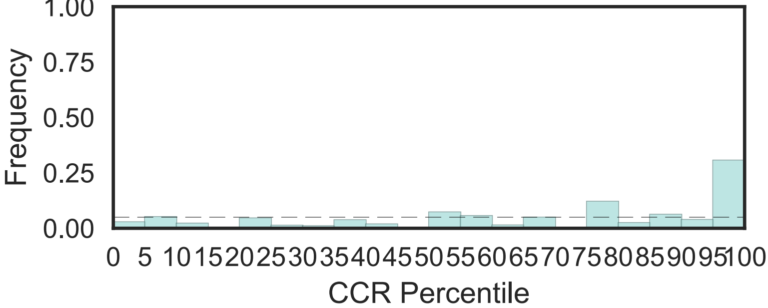

Fibrillar collagen C-terminal domain
(COLFI, N=14)
Fisher's OR: 0.285; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

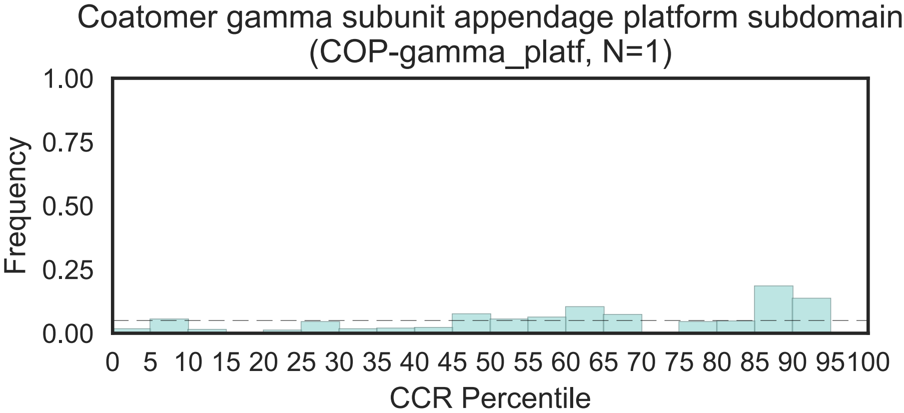

COMMD1 N-terminal domain
(COMMD1_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

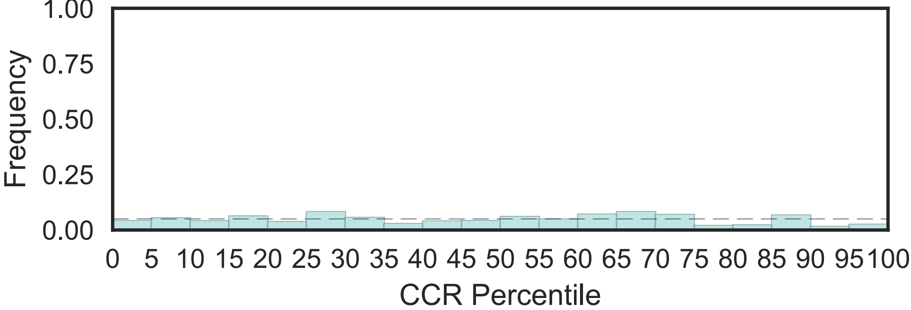

COMM domain
(COMM_domain, N=11)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Cartilage oligomeric matrix protein
(COMP, N=3)
Fisher's OR: 2.46; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

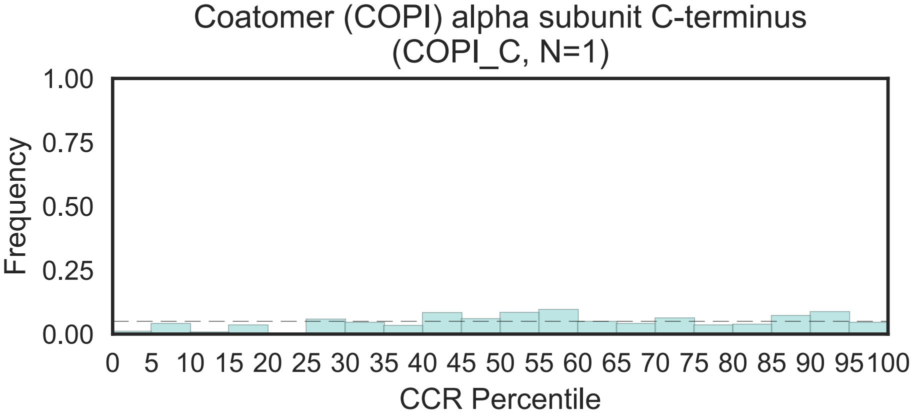
COMPASS (Complex proteins associated with Set1p) component shg1
(COMPASS-Shg1, N=3)
Fisher's OR: 6.59; Bonferroni p-val: 1

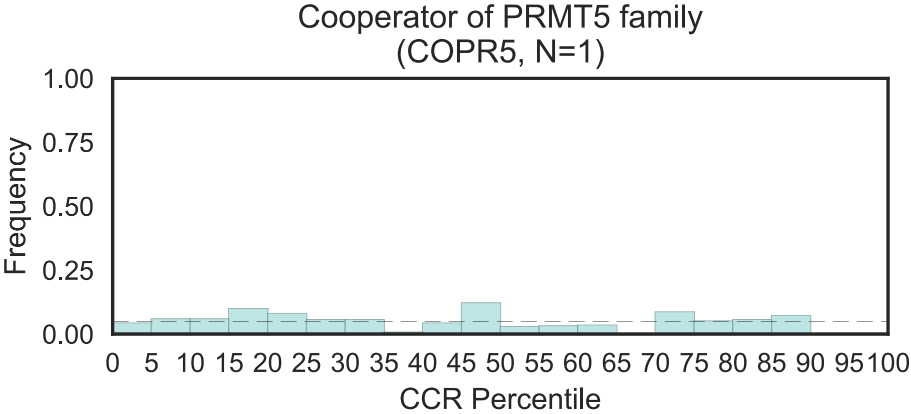


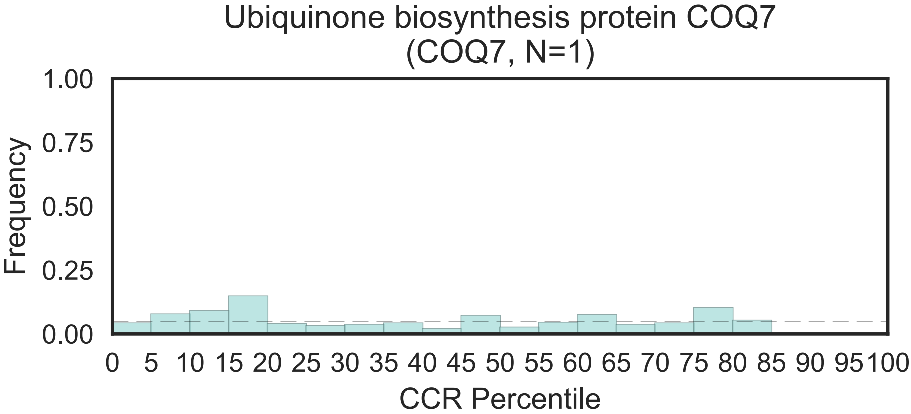

Coatomer gamma subunit appendage platform subdomain
(COP-gamma_platf, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

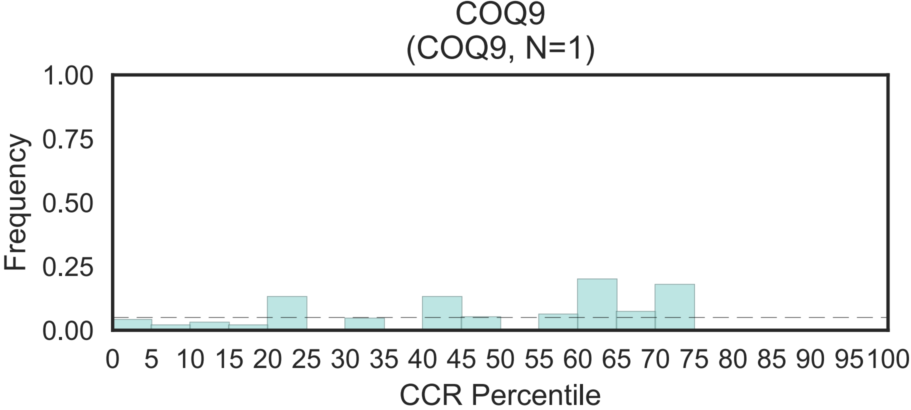


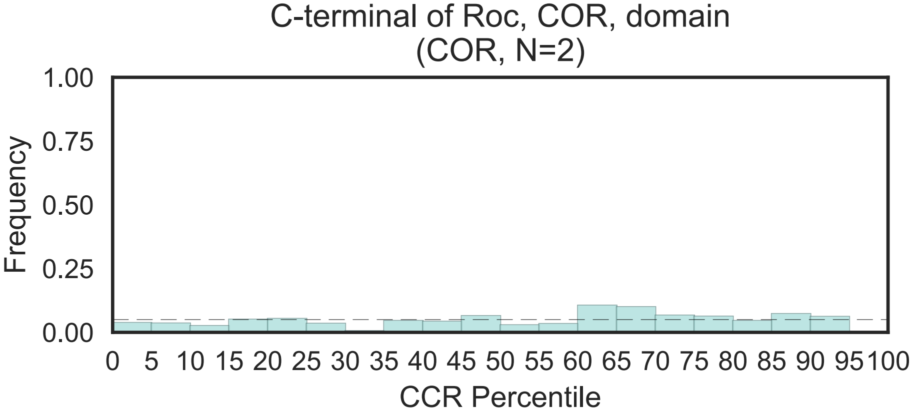
Endoplasmic reticulum vesicle transporter
(COPIIcoated_ERV, N=3)
Fisher's OR: 0.778; Bonferroni p-val: 1

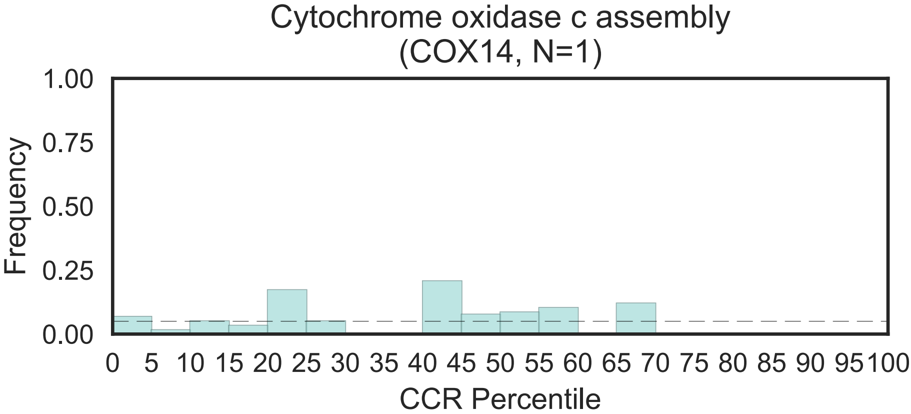

Coatomer (COPI) alpha subunit C-terminus
(COPI_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

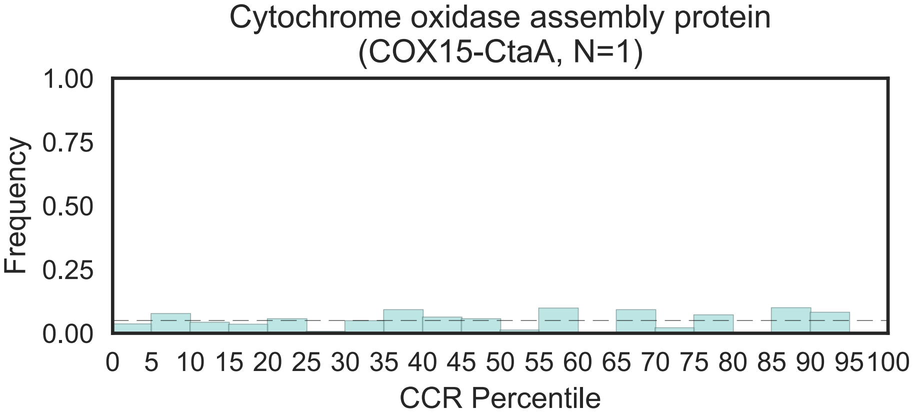

Cooperator of PRMT5 family
(COPR5, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

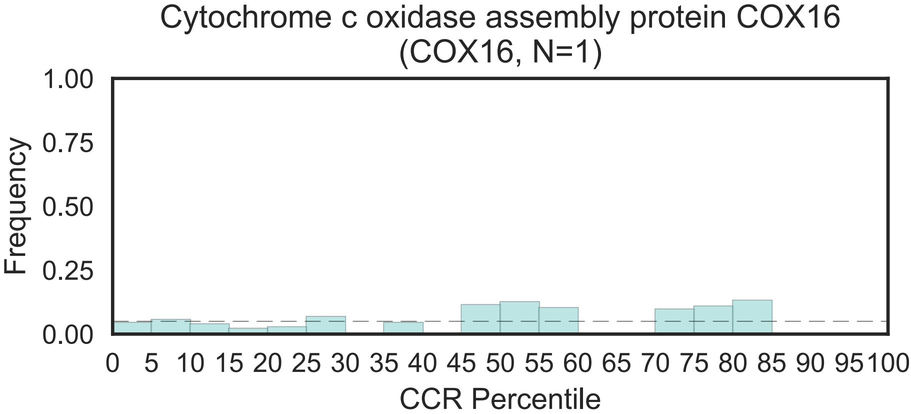

Ubiquinone biosynthesis protein COQ7
(COQ7, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


COQ9
(COQ9, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

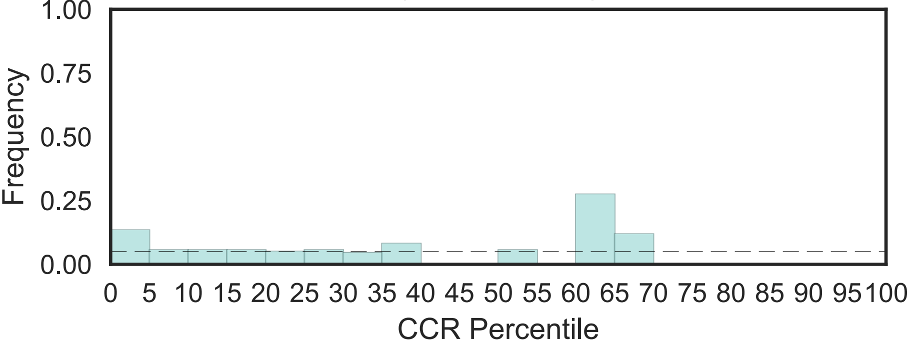

C-terminal of Roc, COR, domain
(COR, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

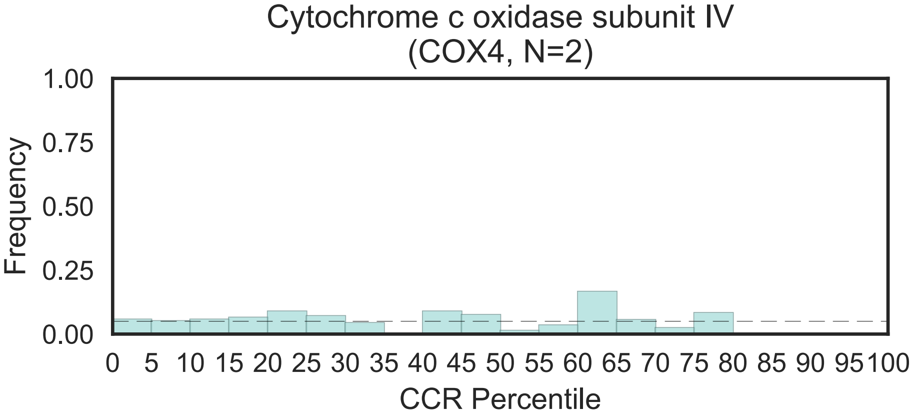

Cytochrome oxidase c assembly
(COX14, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

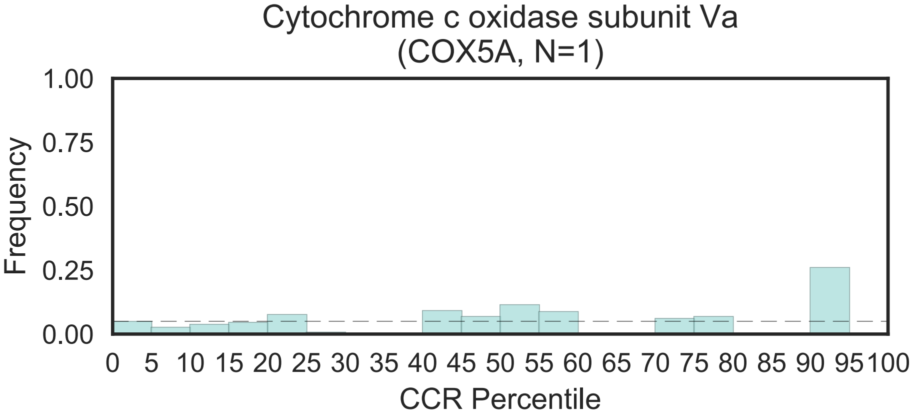

Cytochrome oxidase assembly protein
(COX15-CtaA, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

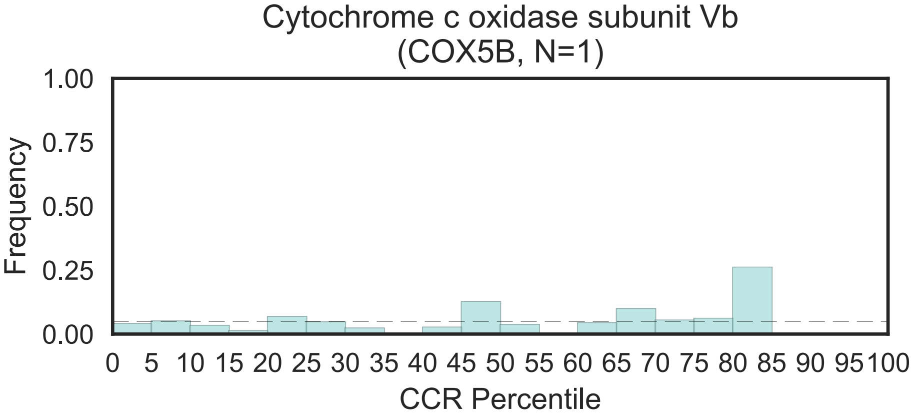

Cytochrome c oxidase assembly protein COX16
(COX16, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

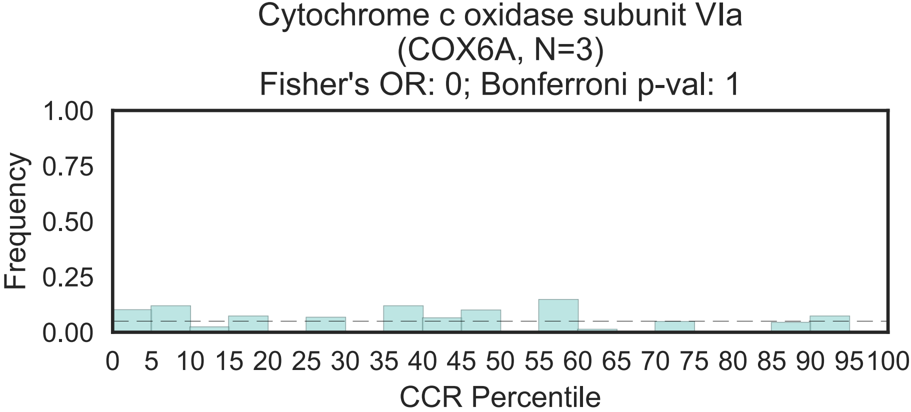
Cytochrome C oxidase copper chaperone (COX17)
(COX17, N=1)

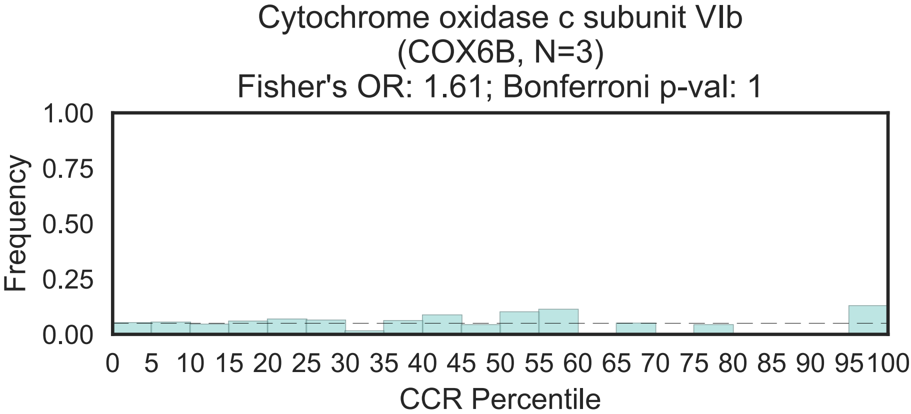


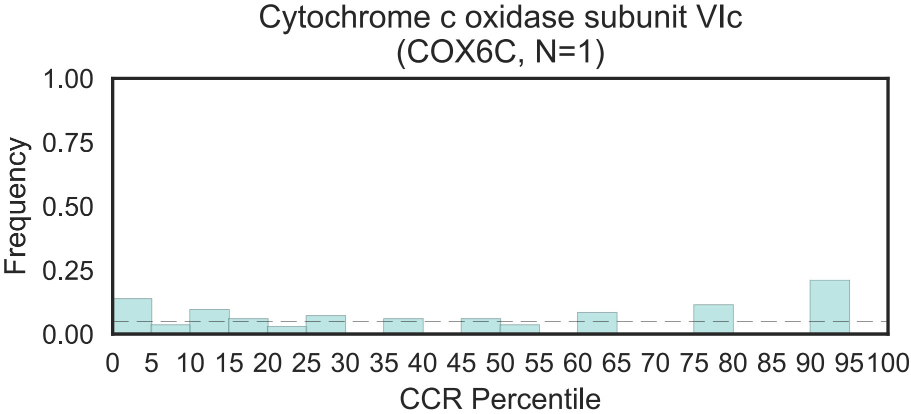

Cytochrome c oxidase subunit IV
(COX4, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

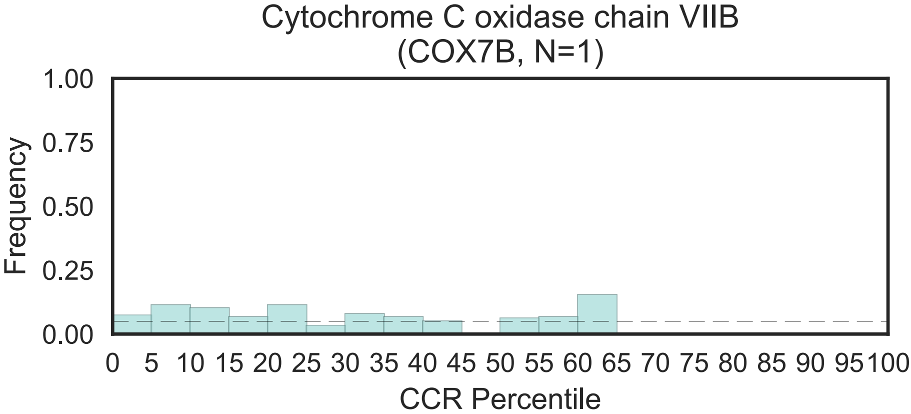

Cytochrome c oxidase subunit Va
(COX5A, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

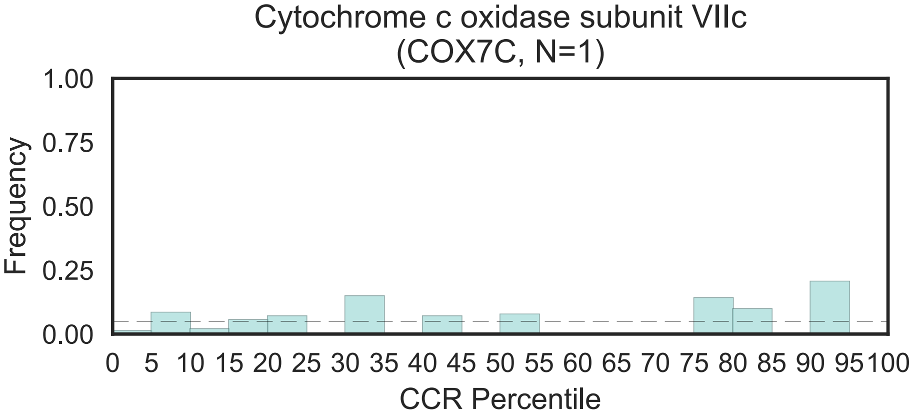

Cytochrome c oxidase subunit Vb
(COX5B, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

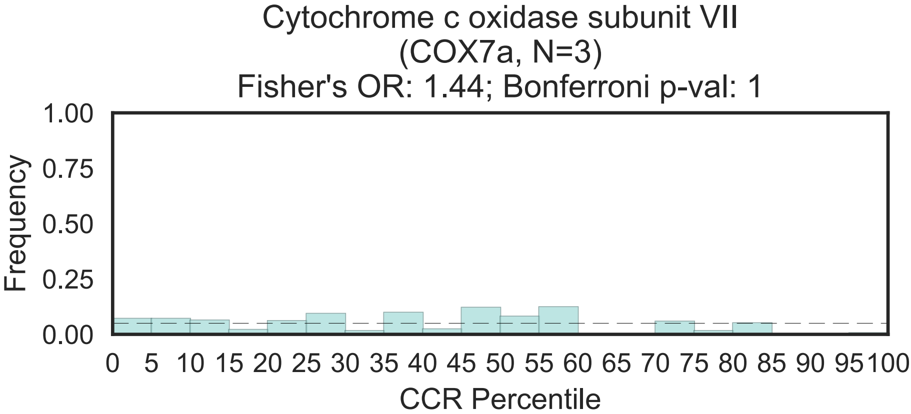

Cytochrome c oxidase subunit VIa
(COX6A, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

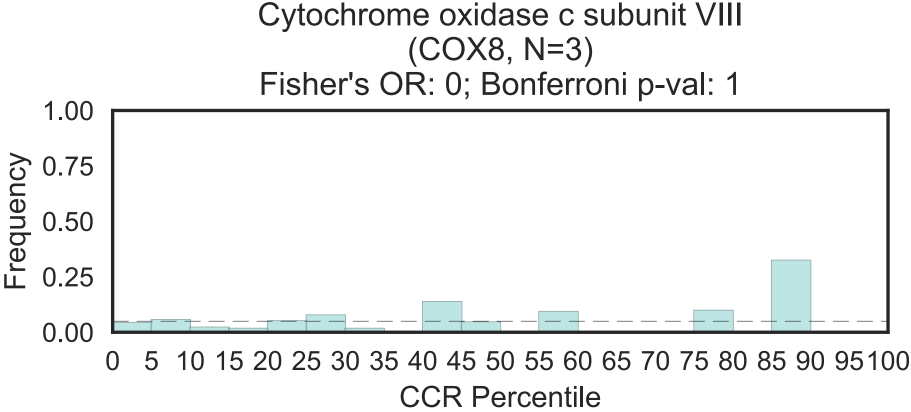

Cytochrome oxidase c subunit VIb
(COX6B, N=3)
Fisher's OR: 1.61; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

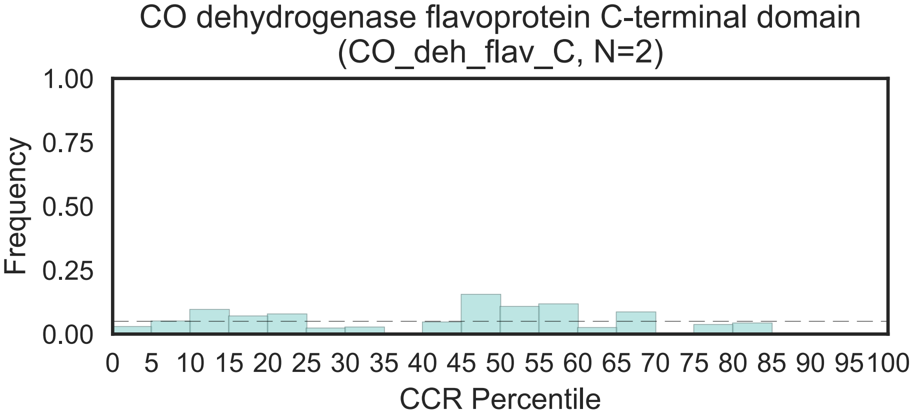

Cytochrome c oxidase subunit VIc
(COX6C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

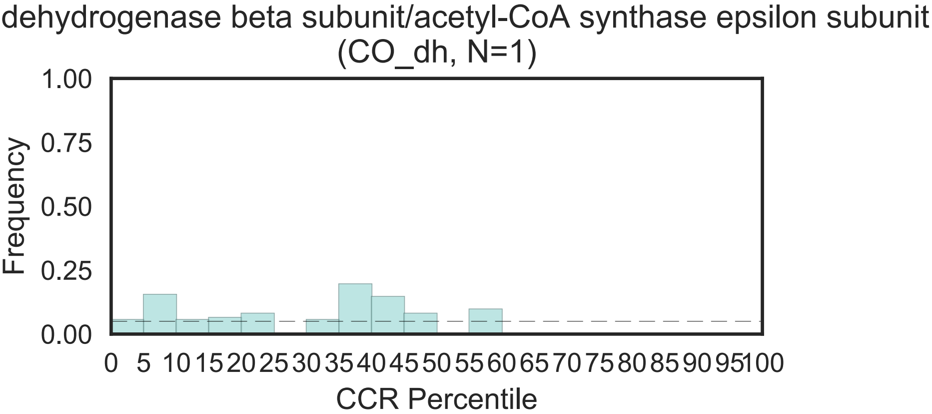

Cytochrome C oxidase chain VIIB
(COX7B, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Cytochrome c oxidase subunit VIIc
(COX7C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

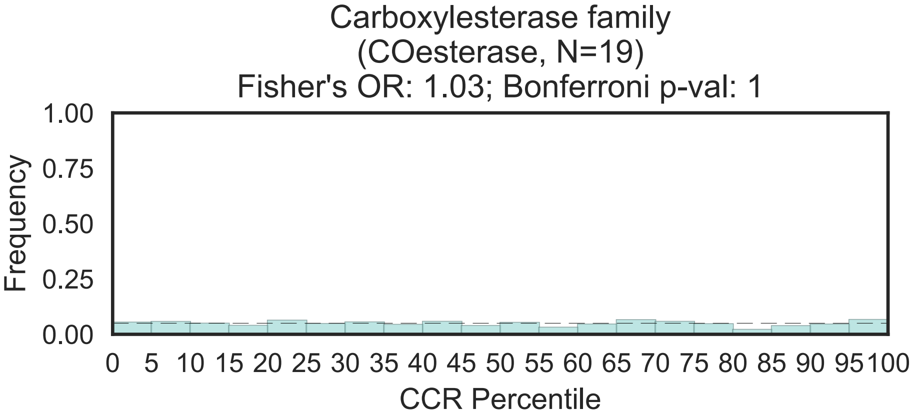

Cytochrome c oxidase subunit VII
(COX7a, N=3)
Fisher's OR: 1.44; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

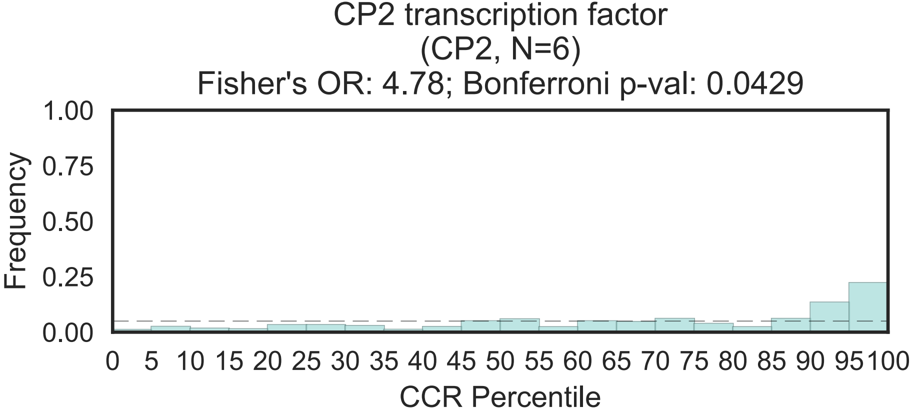

Cytochrome oxidase c subunit VIII
(COX8, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


CO dehydrogenase flavoprotein C-terminal domain
(CO_deh_flav_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

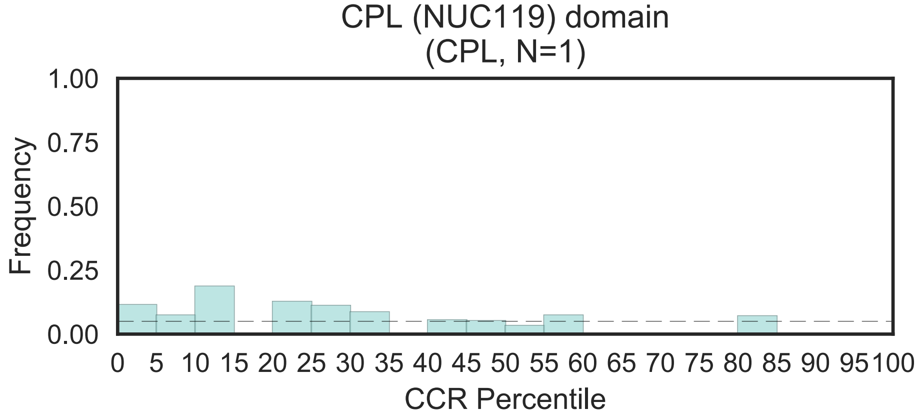


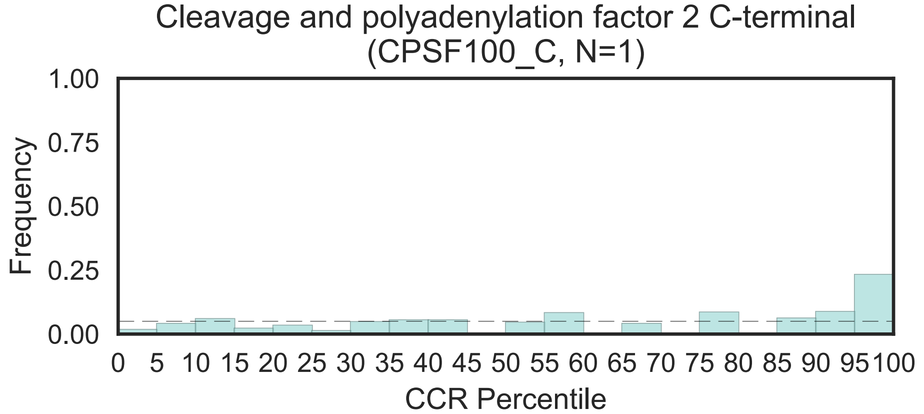
CO dehydrogenase beta subunit/acetyl-CoA synthase epsilon subunit
(CO_dh, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Carboxylesterase family
(COesterase, N=19)
Fisher's OR: 1.03; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

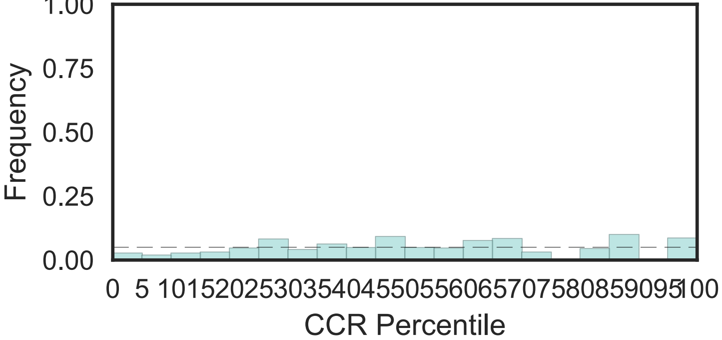


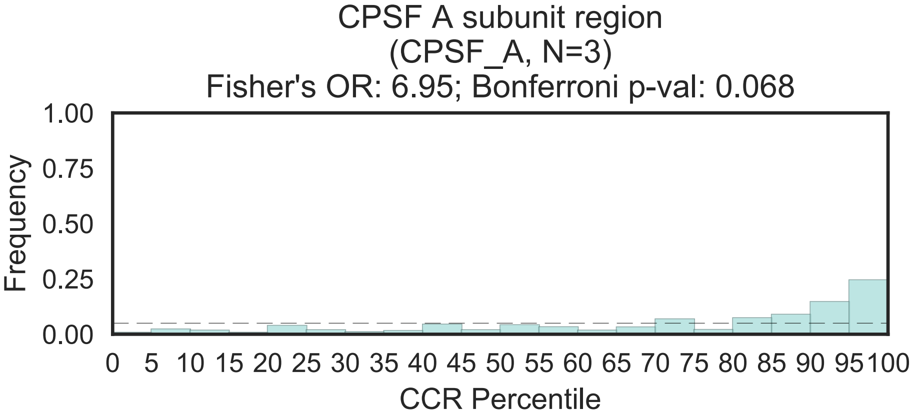
CP2 transcription factor
(CP2, N=6)
Fisher's OR: 4.78; Bonferroni p-val: 0.0429


CPL (NUC119) domain
(CPL, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

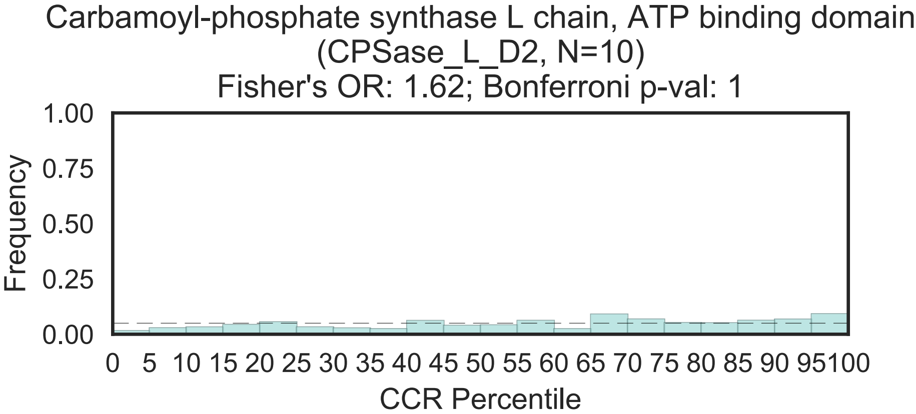

Cleavage and polyadenylation factor 2 C-terminal
(CPSF100_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

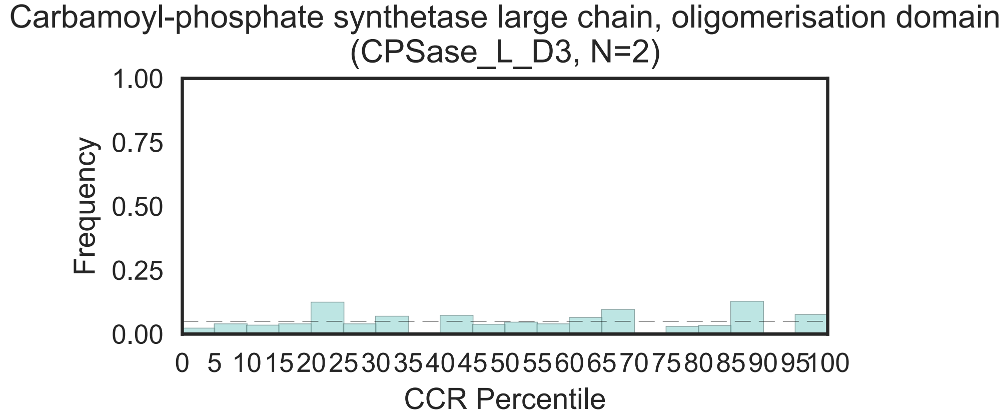
Pre-mRNA 3'-end-processing endonuclease polyadenylation factor C-term (CPSF73-100_C, N=1)

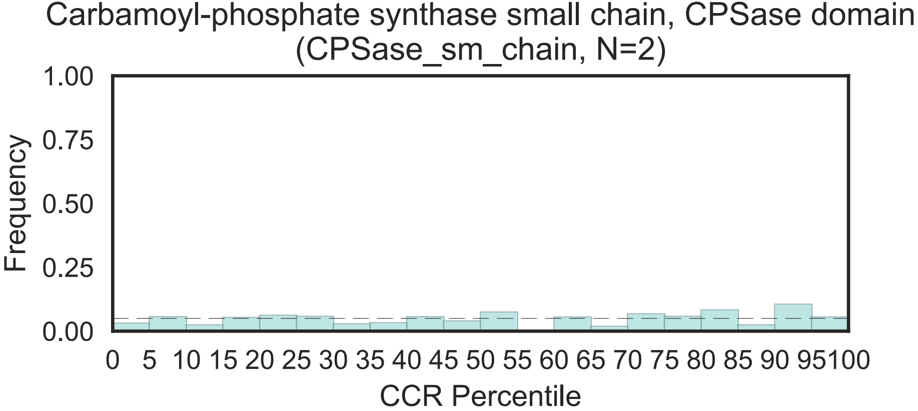


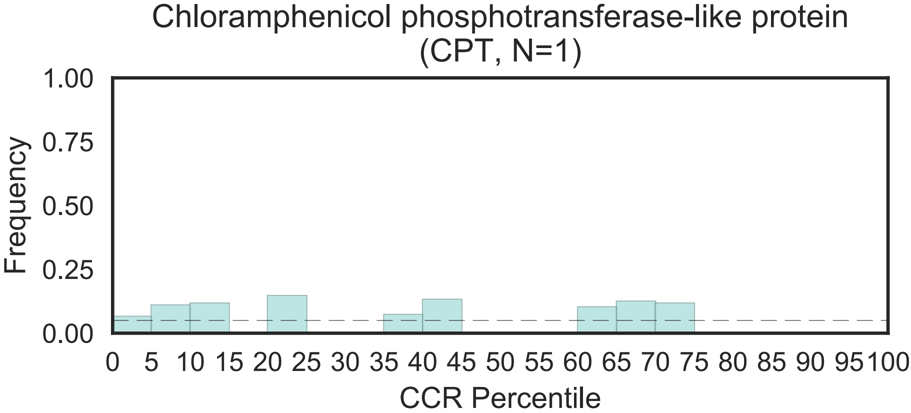


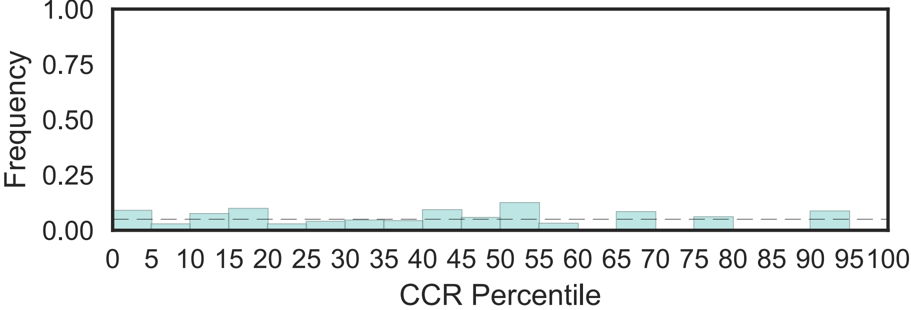
CPSF A subunit region
(CPSF_A, N=3)
Fisher's OR: 6.95; Bonferroni p-val: 0.068


Carbamoyl-phosphate synthase L chain, ATP binding domain
(CPSase_L_D2, N=10)
Fisher's OR: 1.62; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Carbamoyl-phosphate synthetase large chain, oligomerisation domain
(CPSase_L_D3, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

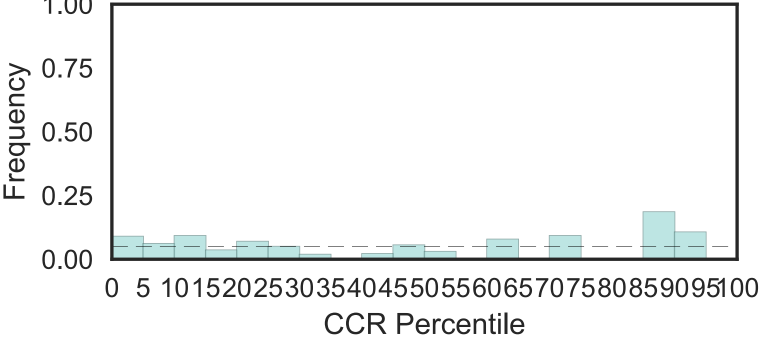

Carbamoyl-phosphate synthase small chain, CPSase domain
(CPSase_sm_chain, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

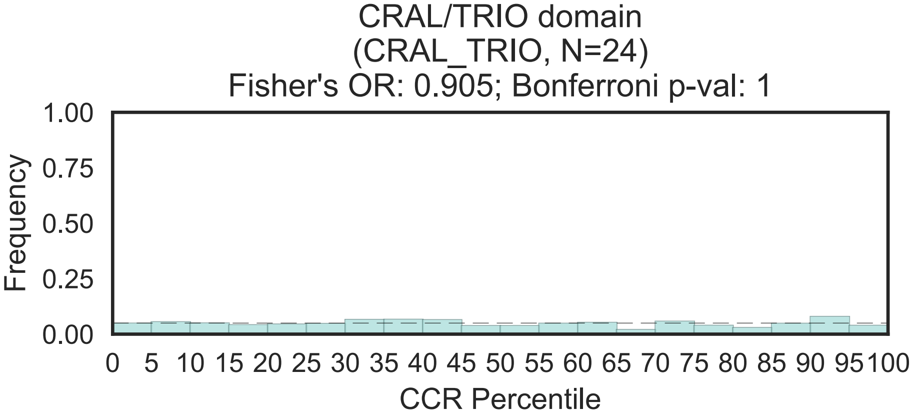

Chloramphenicol phosphotransferase-like protein
(CPT, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

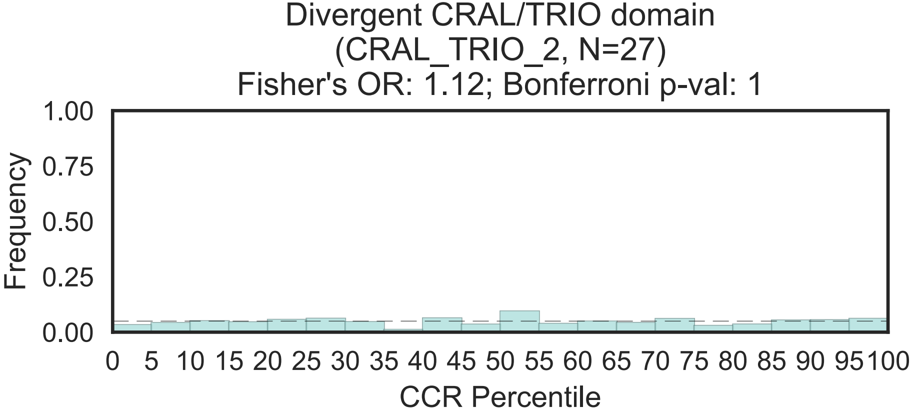


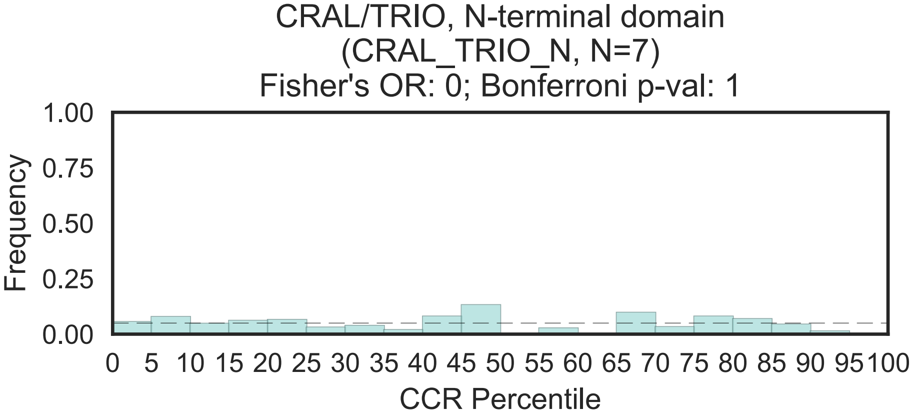
Carnitine O-palmitoyltransferase N-terminus
(CPT_N, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

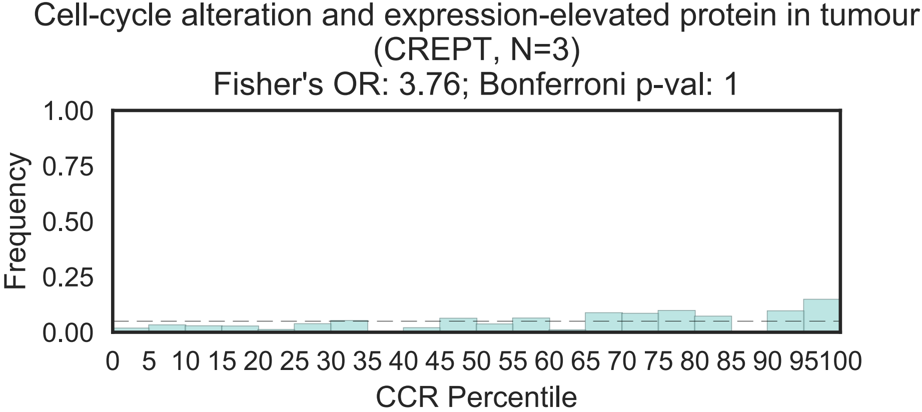
Growth arrest and DNA-damage-inducible proteins-interacting protein 1 (CR6_interact, N=1)

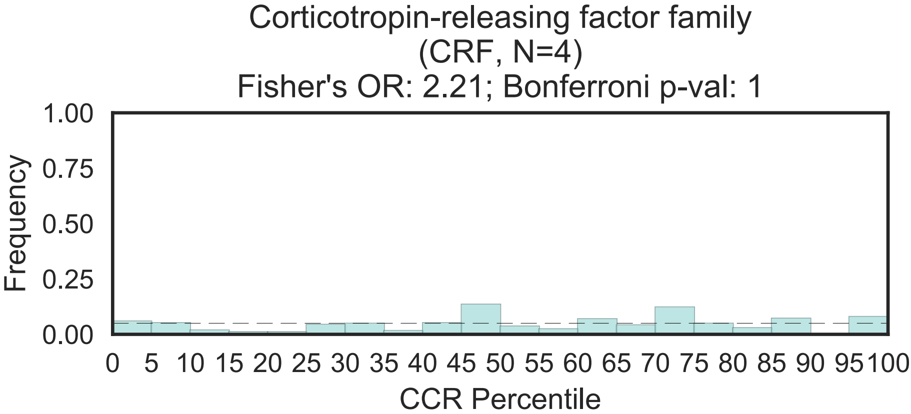


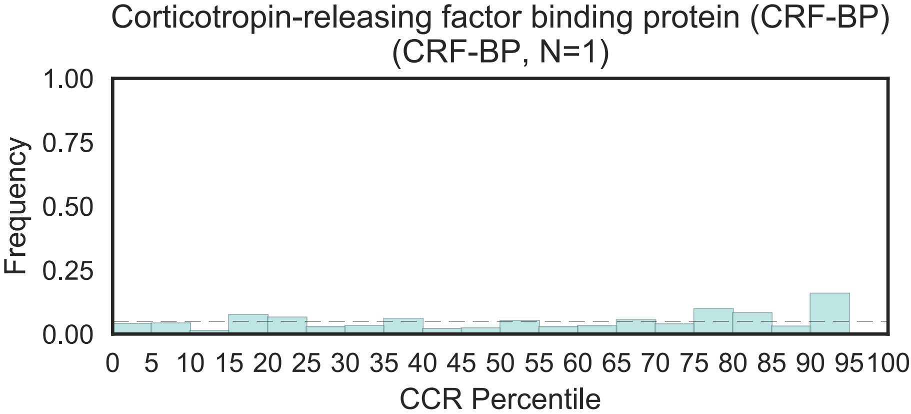

CRAL/TRIO domain
(CRAL_TRIO, N=24)
Fisher's OR: 0.905; Bonferroni p-val: 1

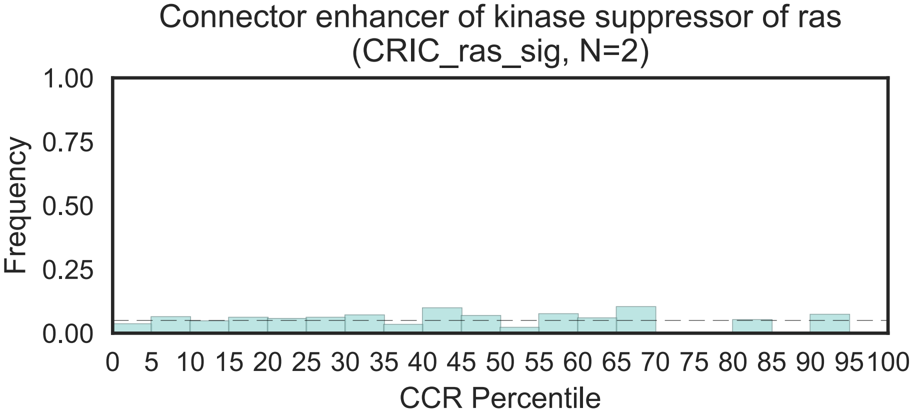

Divergent CRAL/TRIO domain
(CRAL_TRIO_2, N=27)
Fisher's OR: 1.12; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

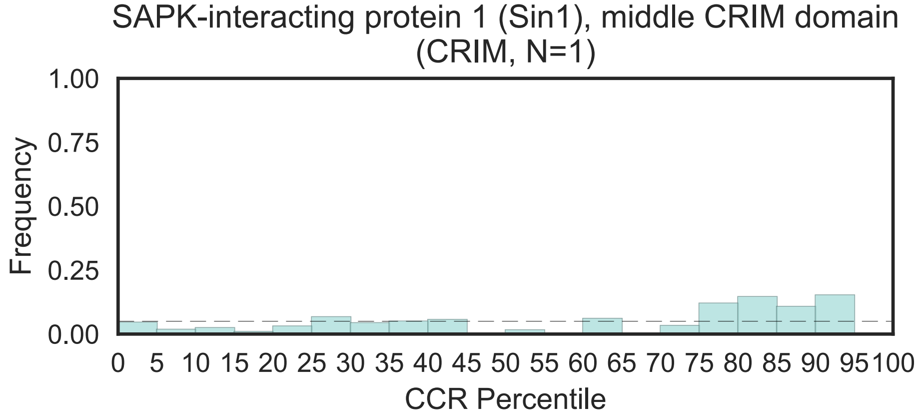

CRAL/TRIO, N-terminal domain
(CRAL_TRIO_N, N=7)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

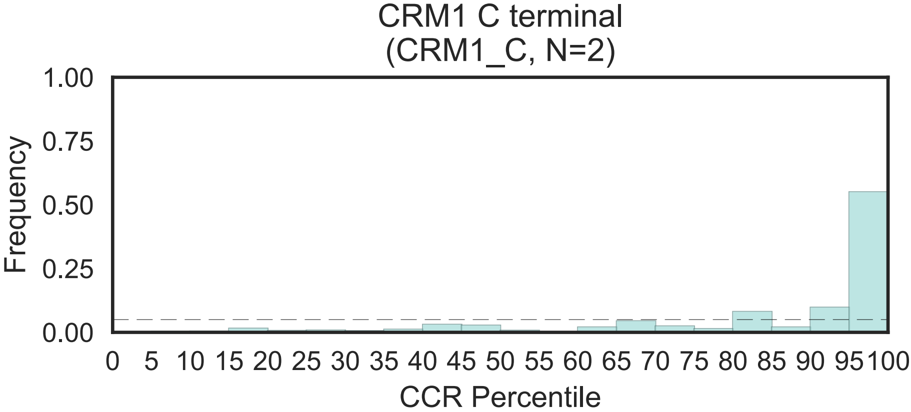

Cell-cycle alteration and expression-elevated protein in tumour
(CREPT, N=3)
Fisher's OR: 3.76; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

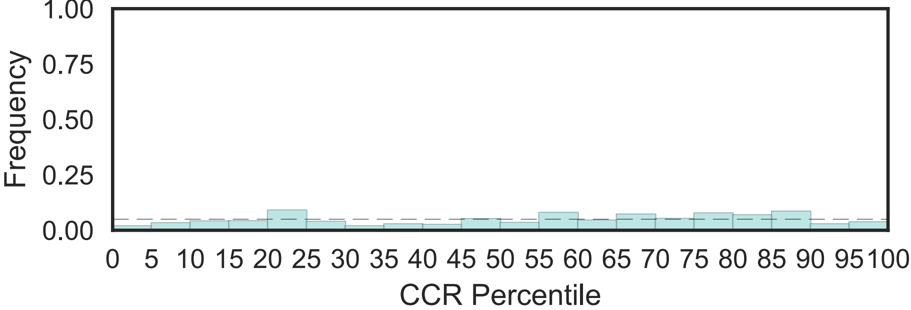

Corticotropin-releasing factor family
(CRF, N=4)
Fisher's OR: 2.21; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Corticotropin-releasing factor binding protein (CRF-BP)
(CRF-BP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

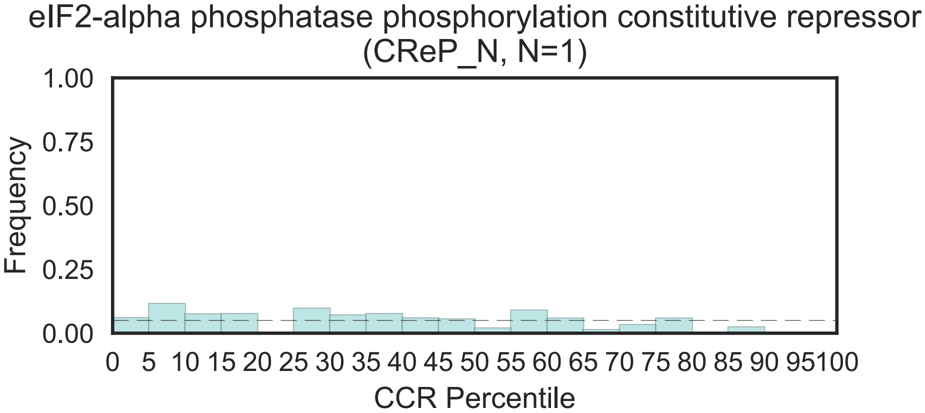

Connector enhancer of kinase suppressor of ras
(CRIC_ras_sig, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

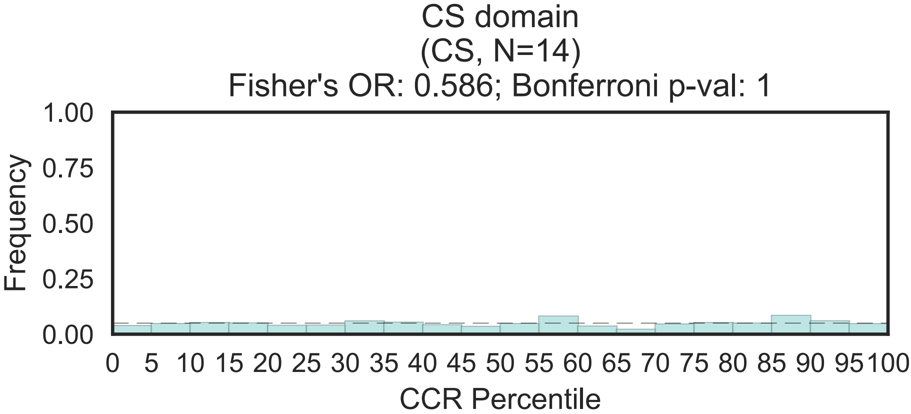

SAPK-interacting protein 1 (Sin1), middle CRIM domain
(CRIM, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

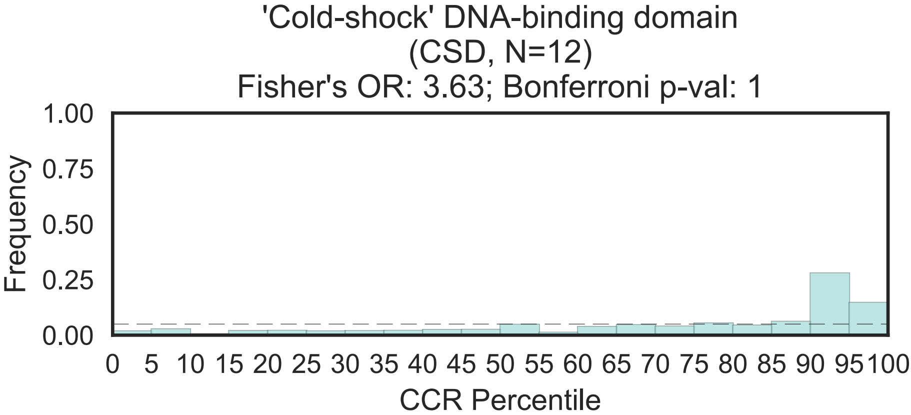

CRM1 C terminal
(CRM1_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

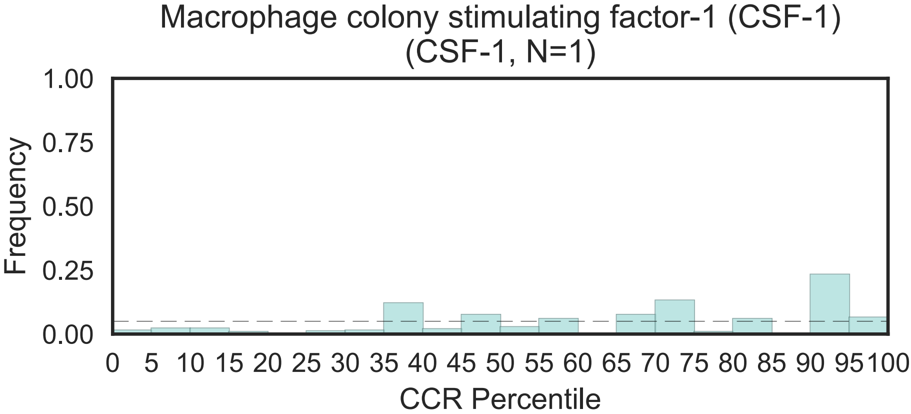


CRT-like, chloroquine-resistance transporter-like
(CRT-like, N=3)
Fisher's OR: 0.651; Bonferroni p-val: 1

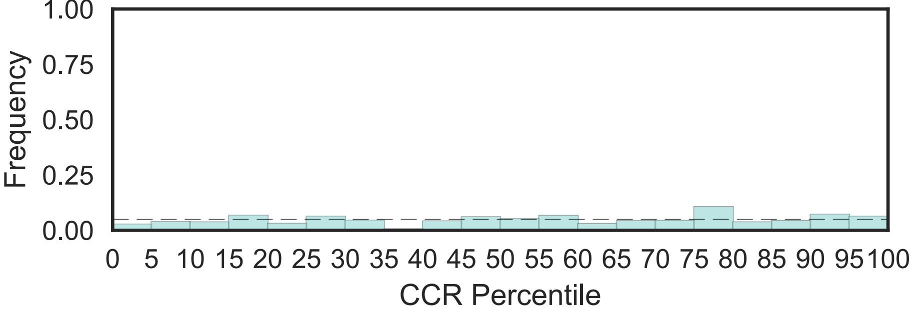

eIF2-alpha phosphatase phosphorylation constitutive repressor
(CReP_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

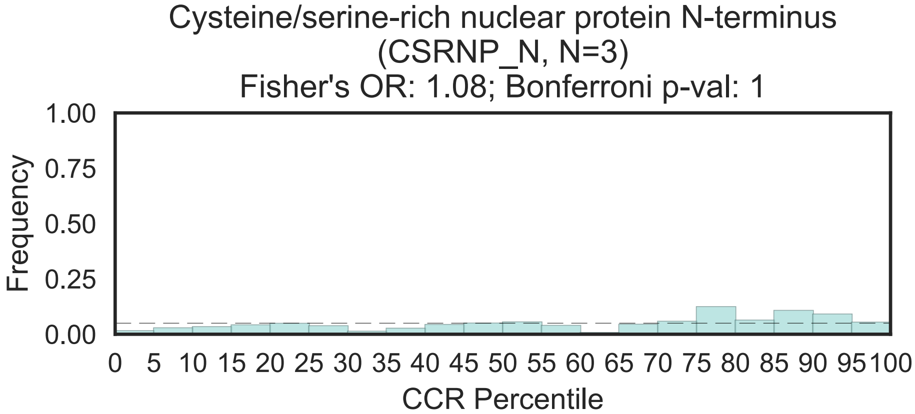

CS domain
(CS, N=14)
Fisher's OR: 0.586; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

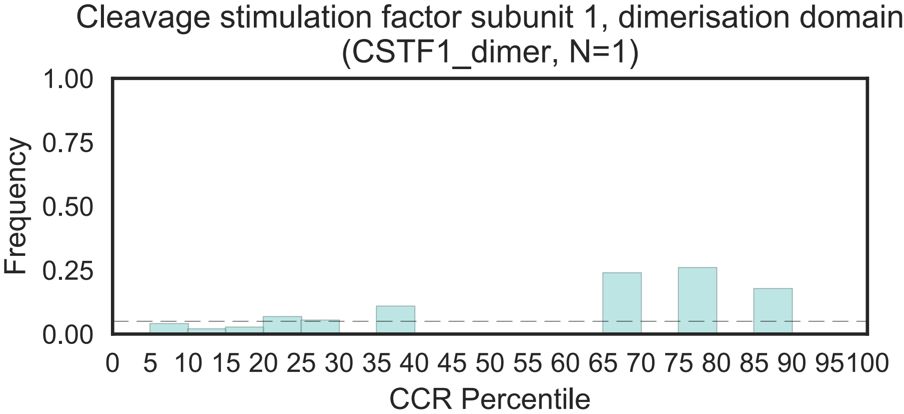

'Cold-shock' DNA-binding domain
(CSD, N=12)
Fisher's OR: 3.63; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

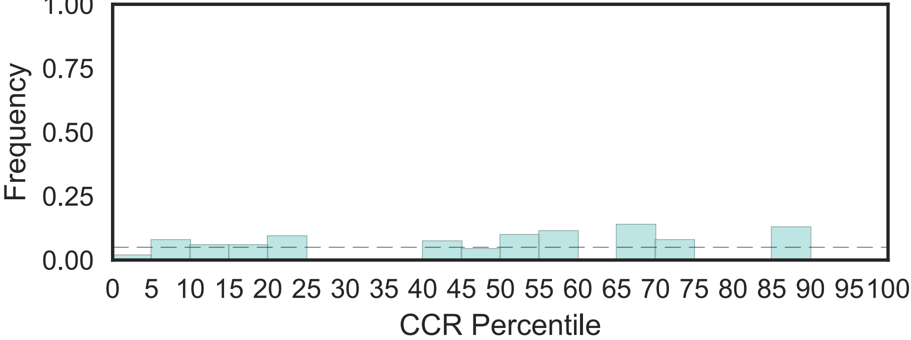

Macrophage colony stimulating factor-1 (CSF-1)
(CSF-1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

CSN8/PSMD8/EIF3K family
(CSN8_PSD8_EIF3K, N=3)
Fisher's OR: 0.73; Bonferroni p-val: 1

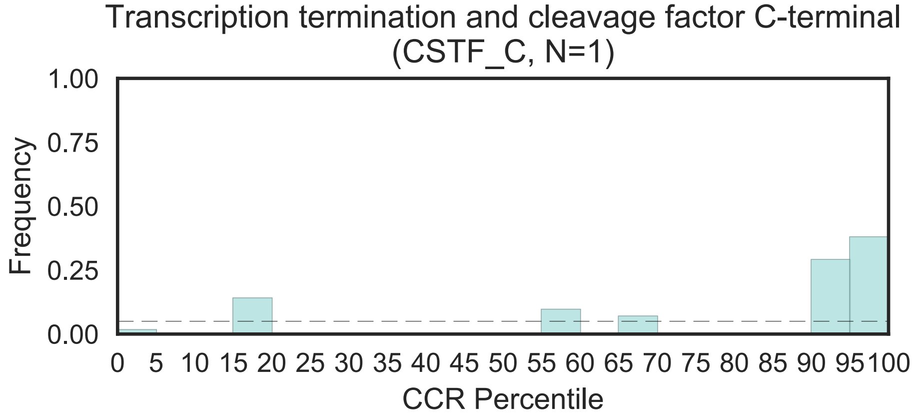



Cysteine/serine-rich nuclear protein N-terminus
(CSRNP_N, N=3)
Fisher's OR: 1.08; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

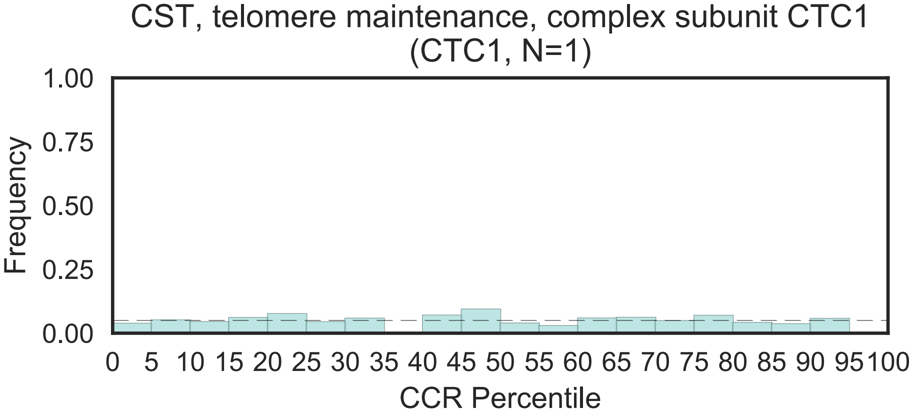

Cleavage stimulation factor subunit 1, dimerisation domain
(CSTF1_dimer, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

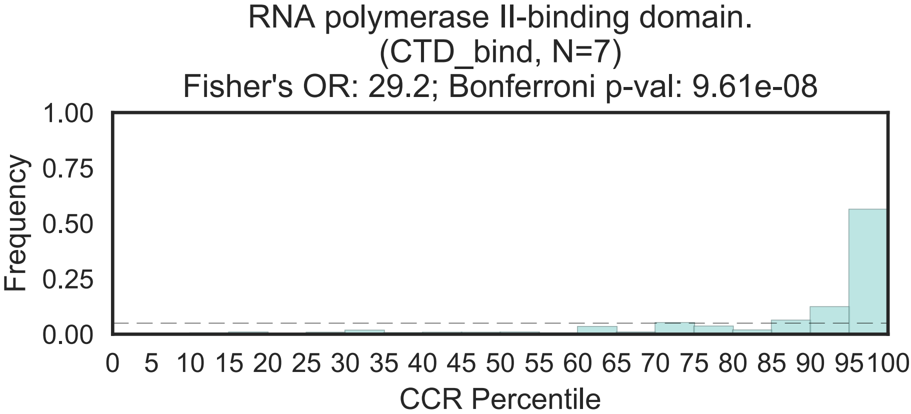


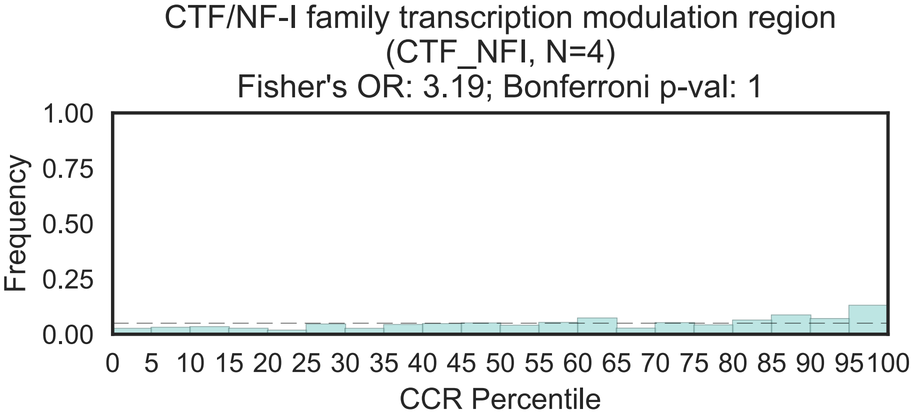
Hinge domain of cleavage stimulation factor subunit 2
(CSTF2_hinge, N=1)

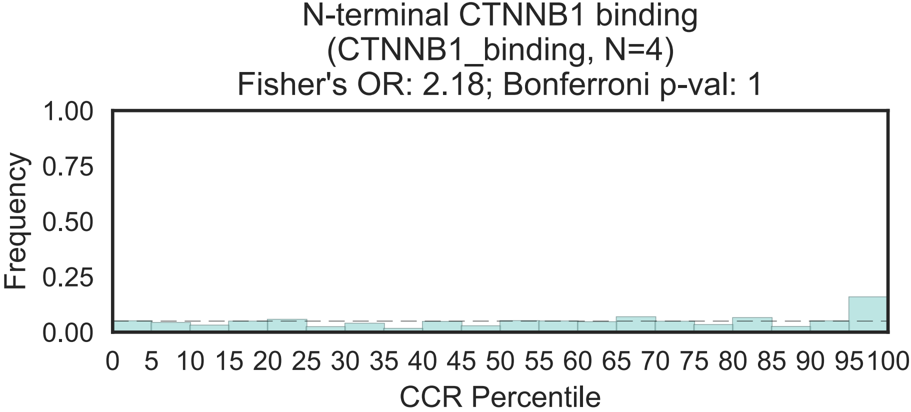


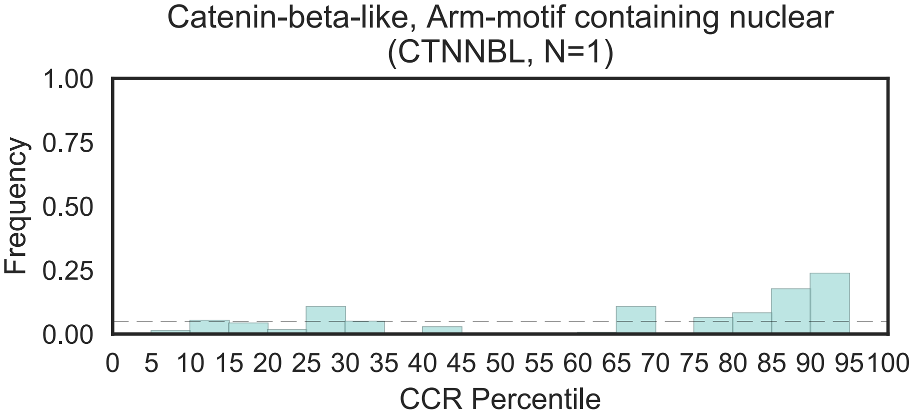
Transcription termination and cleavage factor C-terminal
(CSTF_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

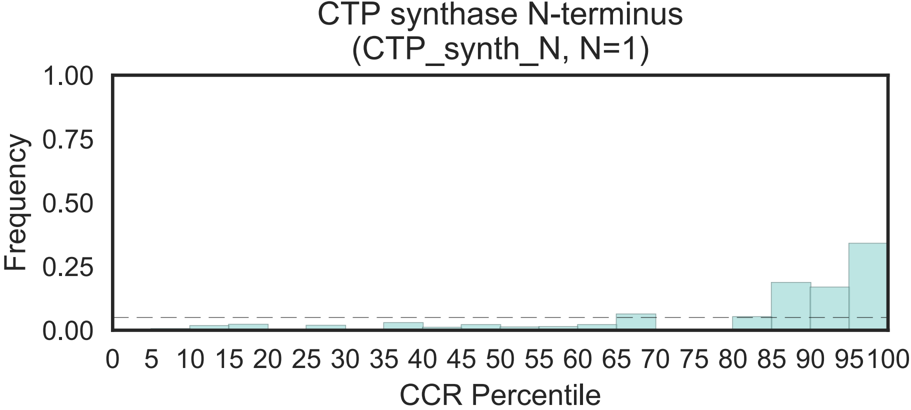

CST, telomere maintenance, complex subunit CTC1
(CTC1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

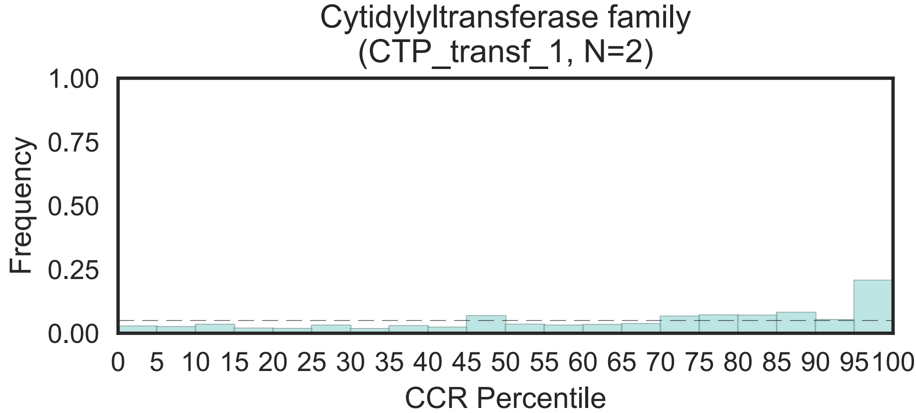

RNA polymerase II-binding domain.
(CTD_bind, N=7)
Fisher's OR: 29.2; Bonferroni p-val: 9.61e-08
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

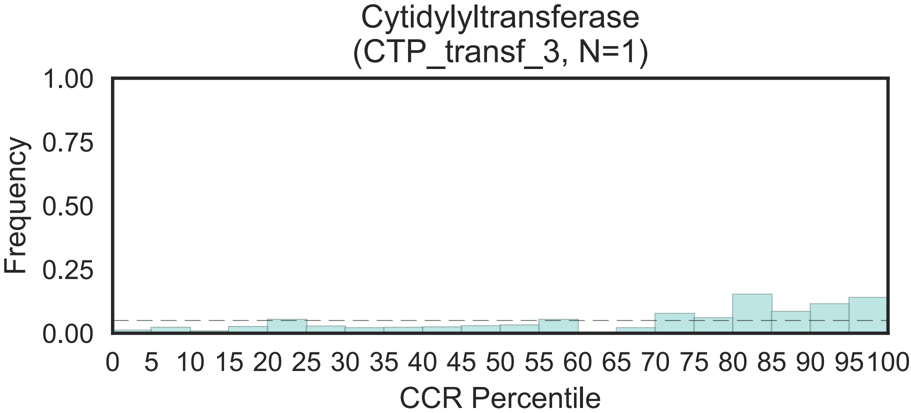

CTF/NF-I family transcription modulation region
(CTF_NFI, N=4)
Fisher's OR: 3.19; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

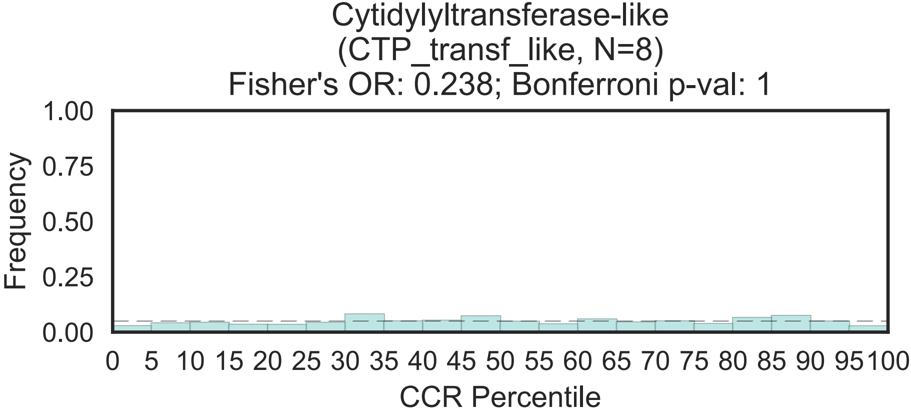

N-terminal CTNNB1 binding
(CTNNB1_binding, N=4)
Fisher's OR: 2.18; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

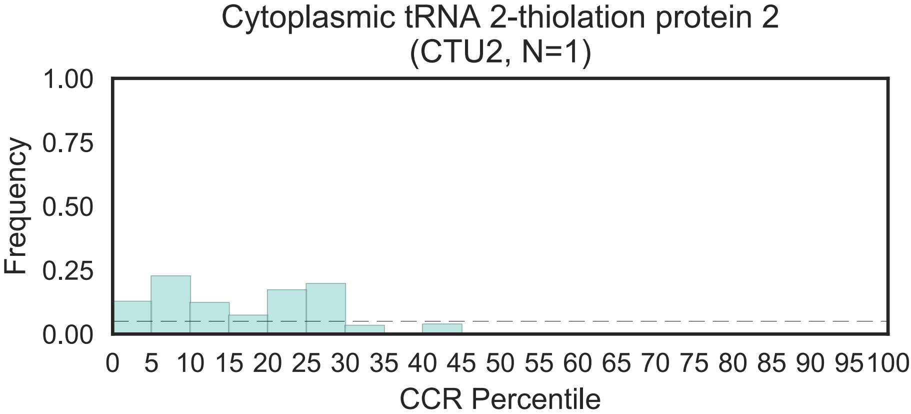

Catenin-beta-like, Arm-motif containing nuclear
(CTNNBL, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

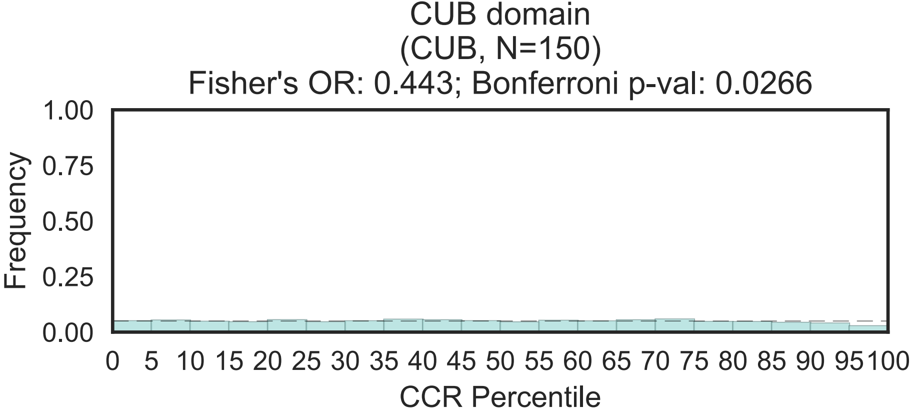

CTP synthase N-terminus
(CTP_synth_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

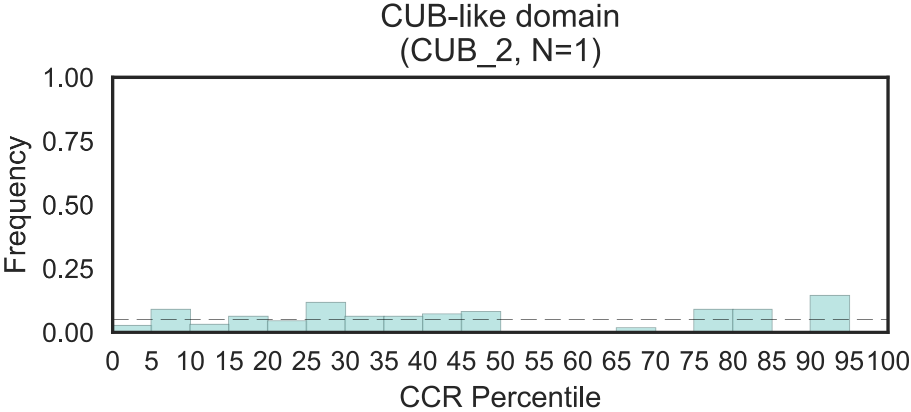

Cytidylyltransferase family
(CTP_transf_1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

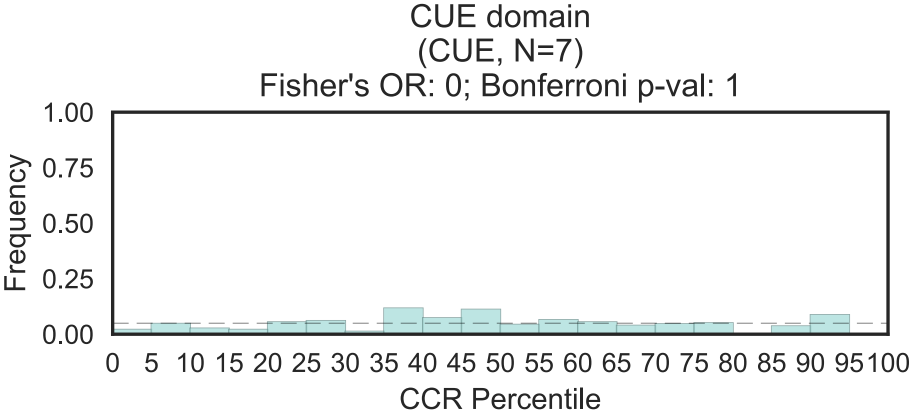

Cytidylyltransferase
(CTP_transf_3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

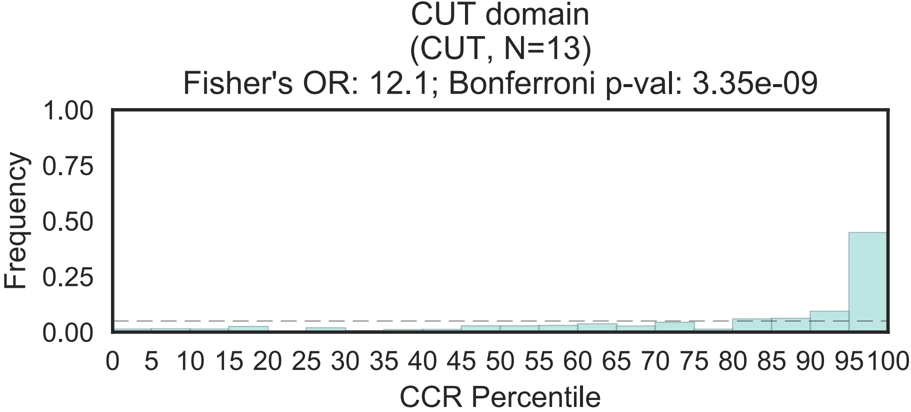

Cytidylyltransferase-like
(CTP_transf_like, N=8)
Fisher's OR: 0.238; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

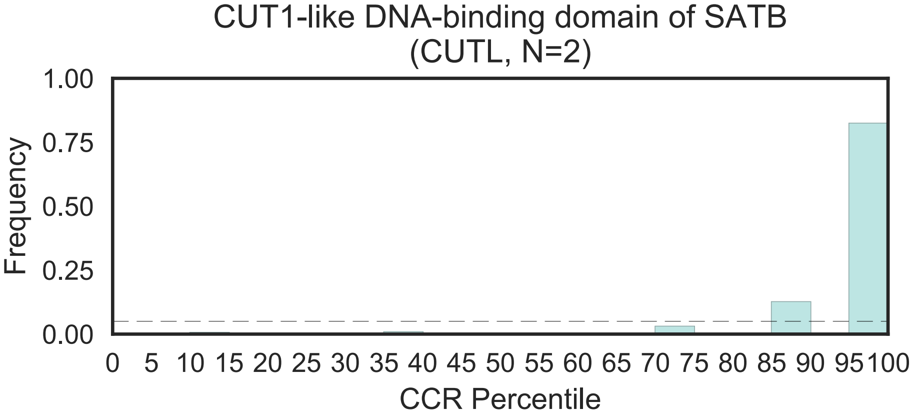

Cytoplasmic tRNA 2-thiolation protein 2
(CTU2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

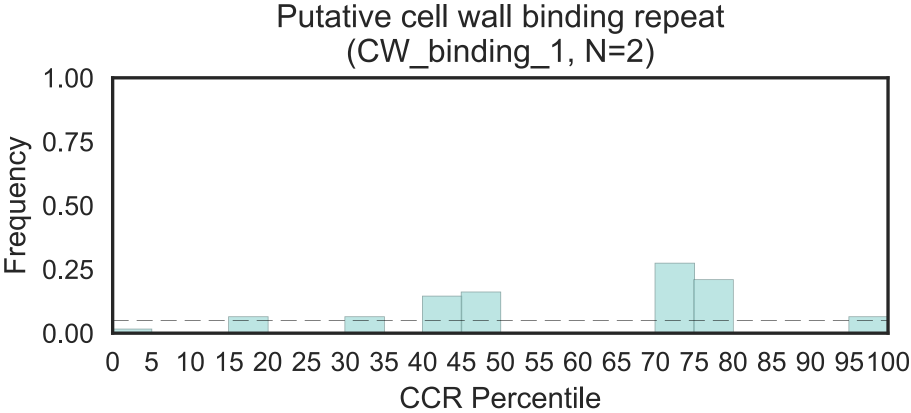

CUB domain
(CUB, N=150)
Fisher's OR: 0.443; Bonferroni p-val: 0.0266
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

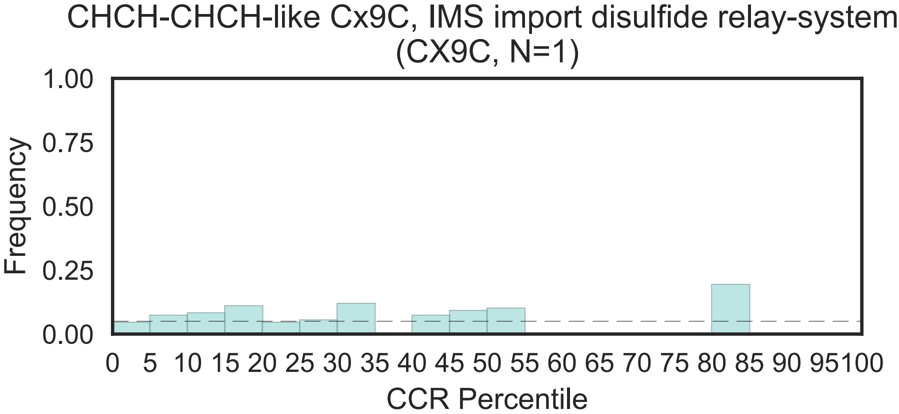

CUB-like domain
(CUB_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

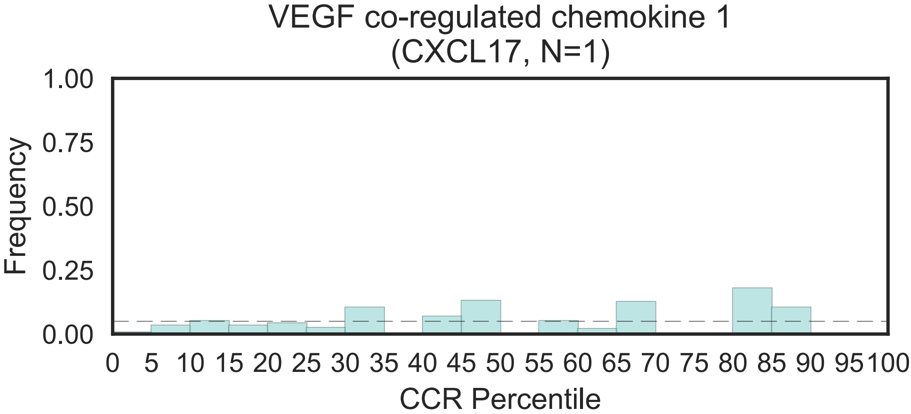

CUE domain
(CUE, N=7)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


CUT domain
(CUT, N=13)
Fisher's OR: 12.1; Bonferroni p-val: 3.35e-09
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

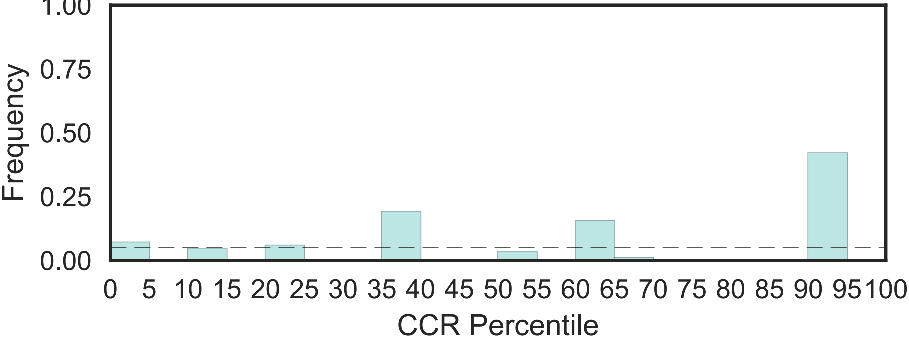

CUT1-like DNA-binding domain of SATB
(CUTL, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

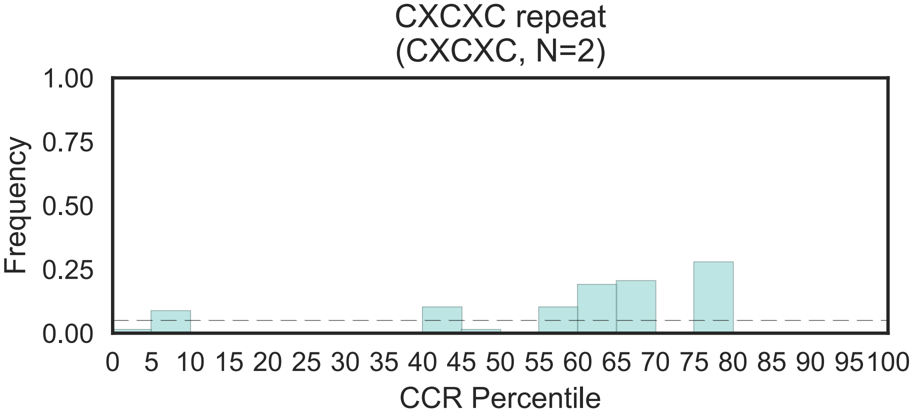

Putative cell wall binding repeat
(CW_binding_1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

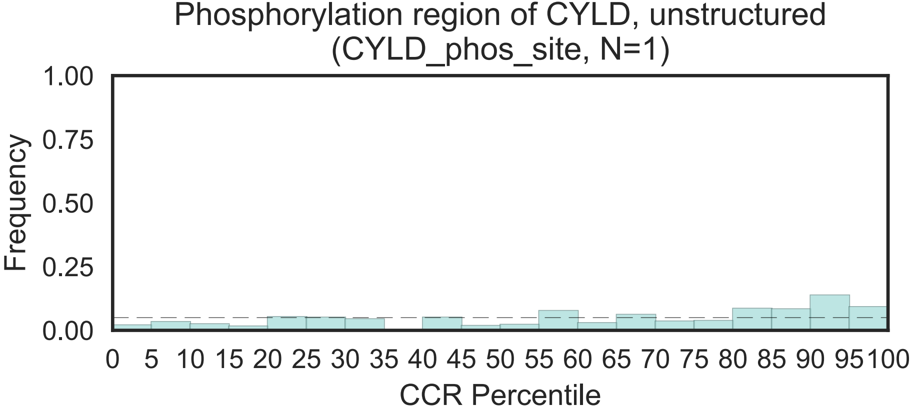

CHCH-CHCH-like Cx9C, IMS import disulfide relay-system,
(CX9C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

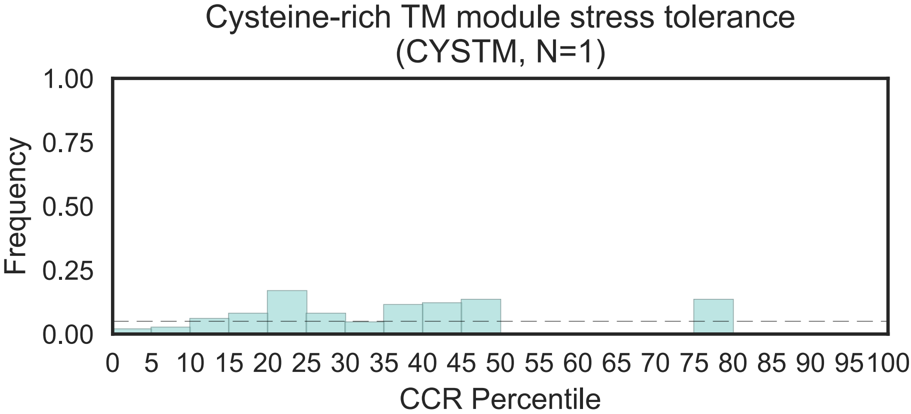

VEGF co-regulated chemokine 1
(CXCL17, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

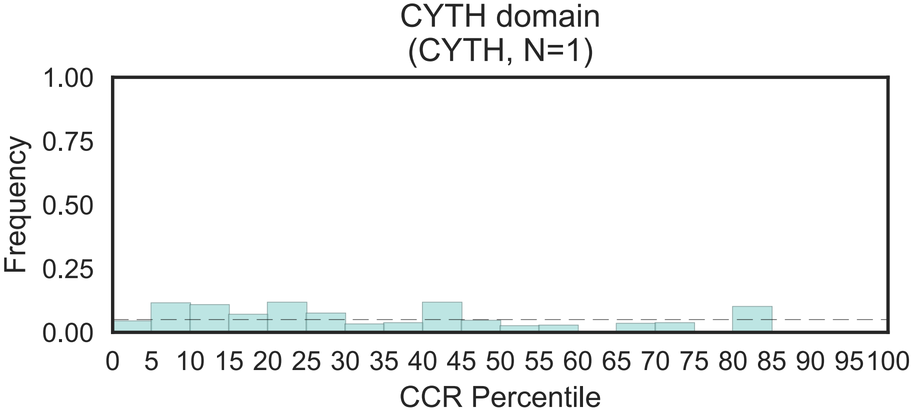
CXCR4 Chemokine receptor N terminal (CXCR4_N, N=1)

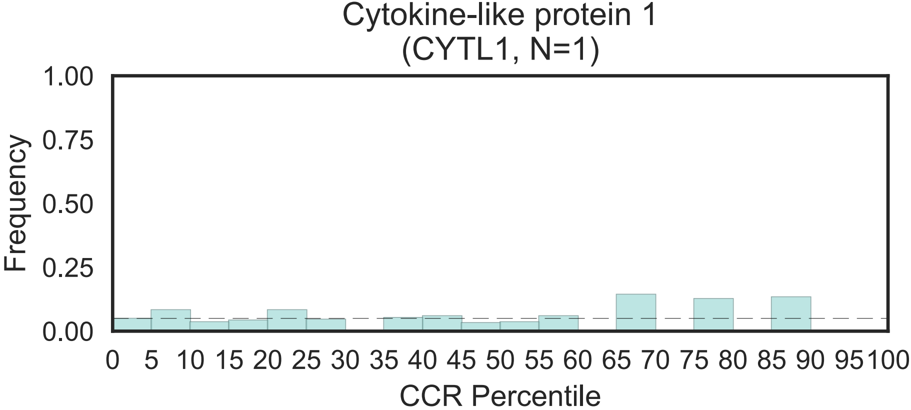


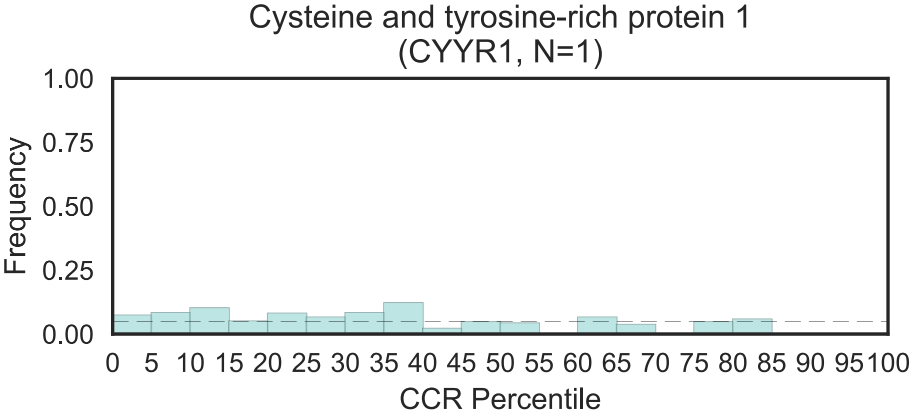

CXCXC repeat
(CXCXC, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Phosphorylation region of CYLD, unstructured
(CYLD_phos_site, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

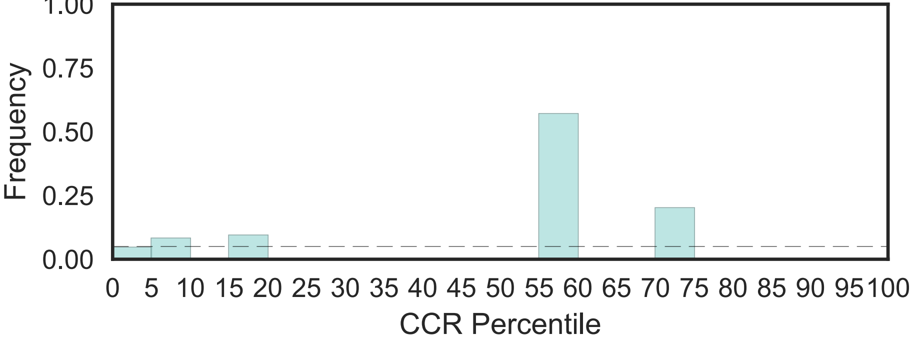

Cysteine-rich TM module stress tolerance
(CYSTM, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

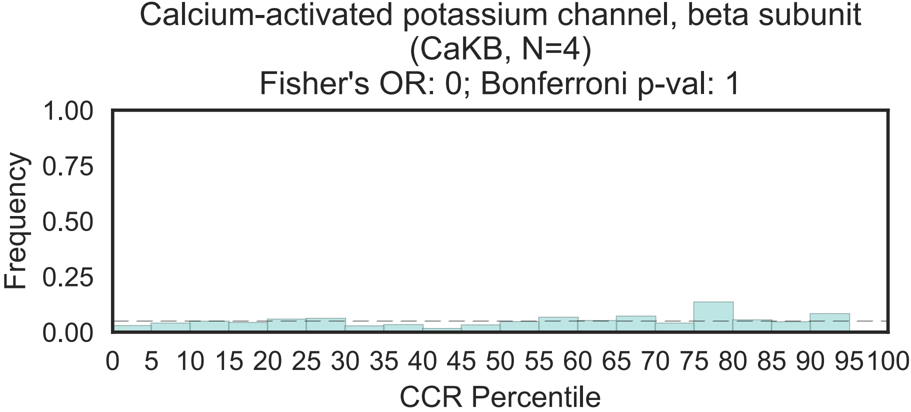

CYTH domain
(CYTH, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Cytokine-like protein 1
(CYTL1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

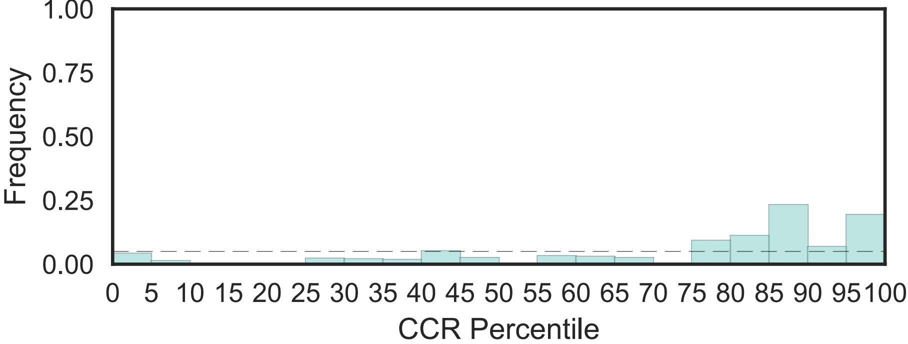

Cysteine and tyrosine-rich protein 1
(CYYR1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

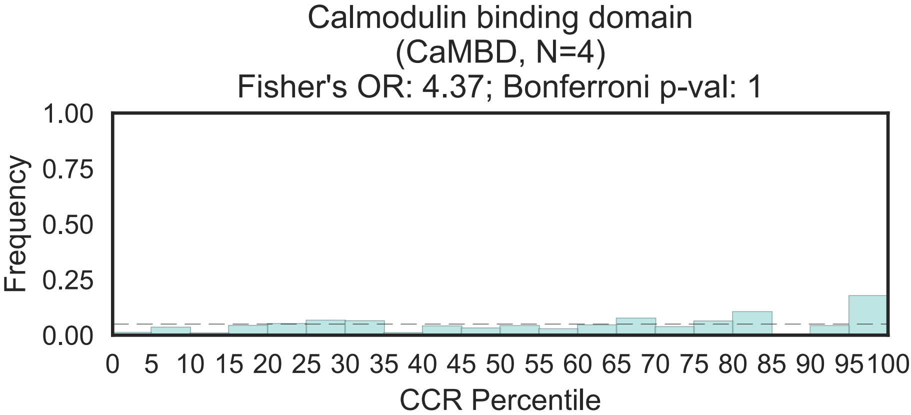
Cysteine rich repeat
(C_tripleX, N=1)

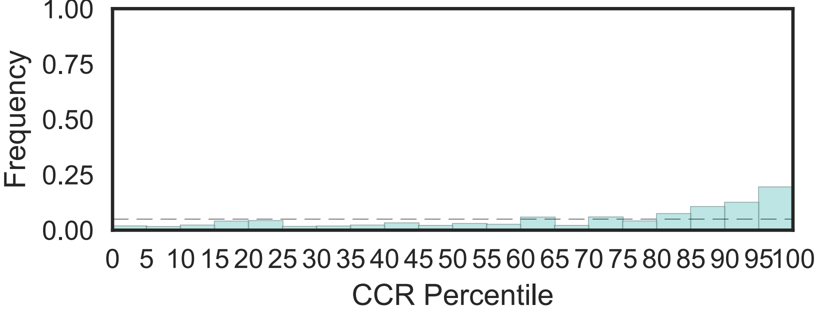


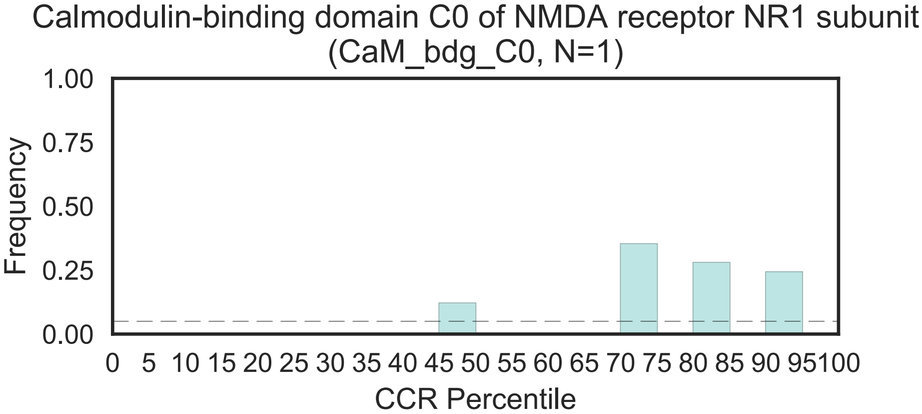

Calcium-activated potassium channel, beta subunit
(CaKB, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

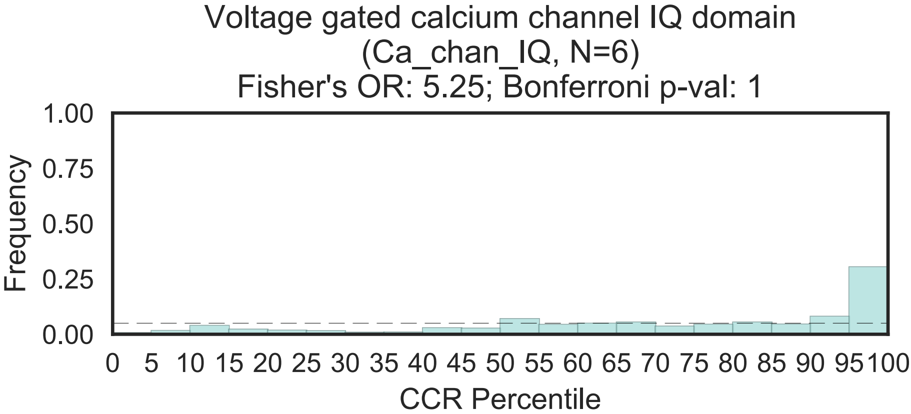
Calcium/calmodulin-dependent protein kinase II inhibitor (CaM-KIIN, N=2)

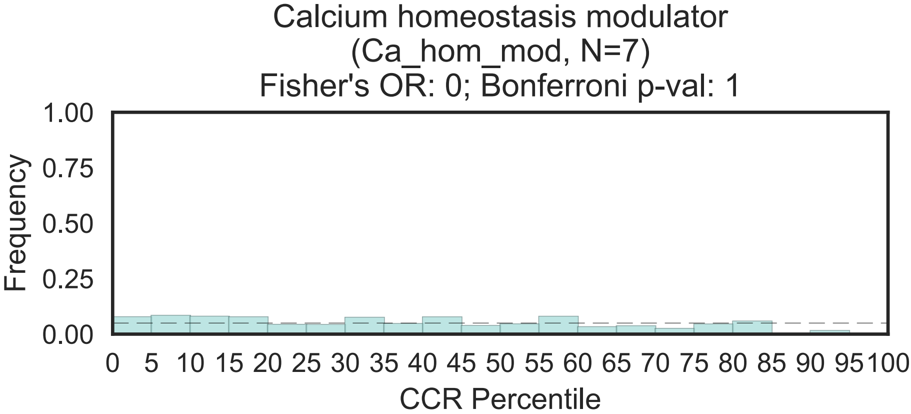


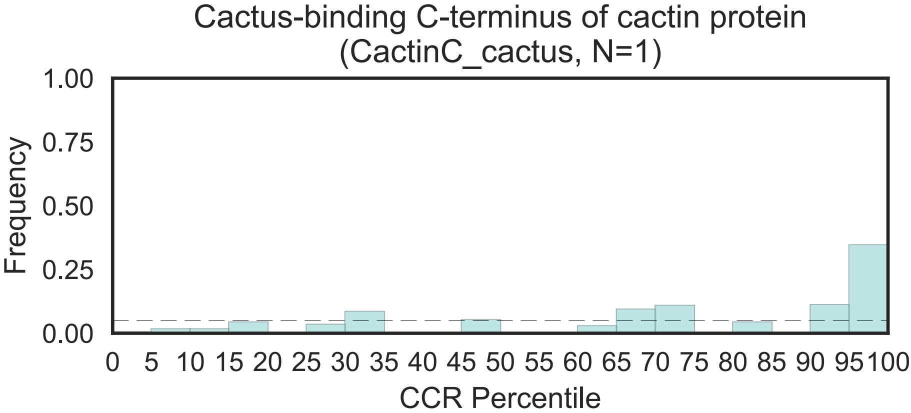

Calmodulin binding domain
(CaMBD, N=4)
Fisher's OR: 4.37; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

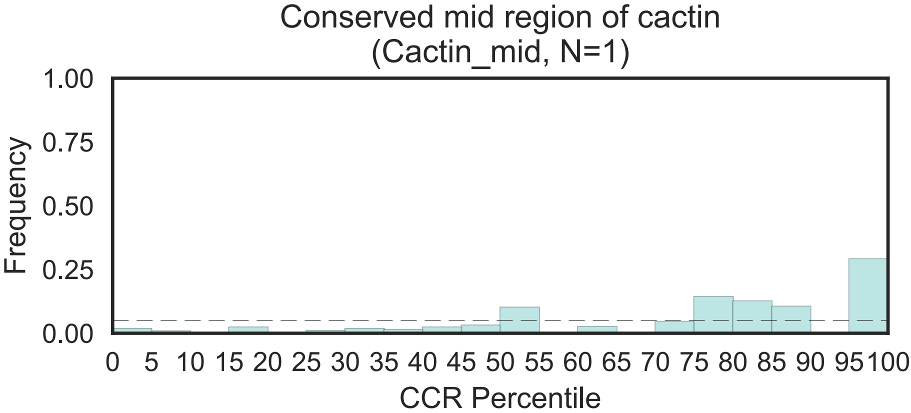

Calcium/calmodulin dependent protein kinase II association domain
(CaMKII_AD, N=4)
Fisher's OR: 3.43; Bonferroni p-val: 1

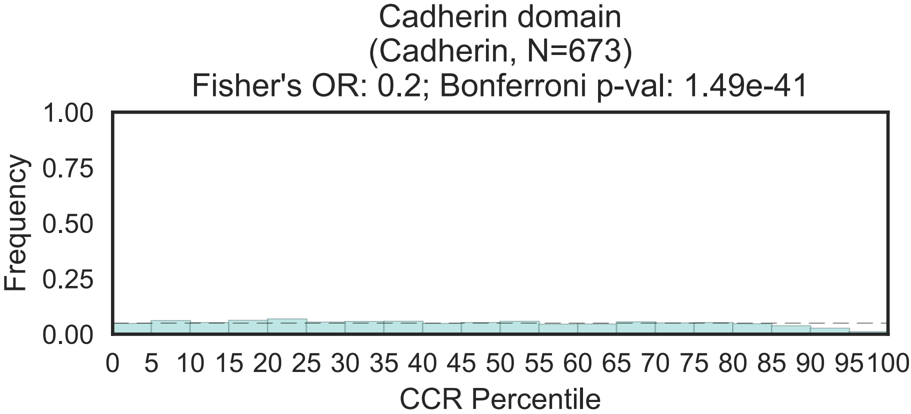

Calmodulin-binding domain C0 of NMDA receptor NR1 subunit
(CaM_bdg_C0, N=1)


Voltage gated calcium channel IQ domain
(Ca_chan_IQ, N=6)
Fisher's OR: 5.25; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

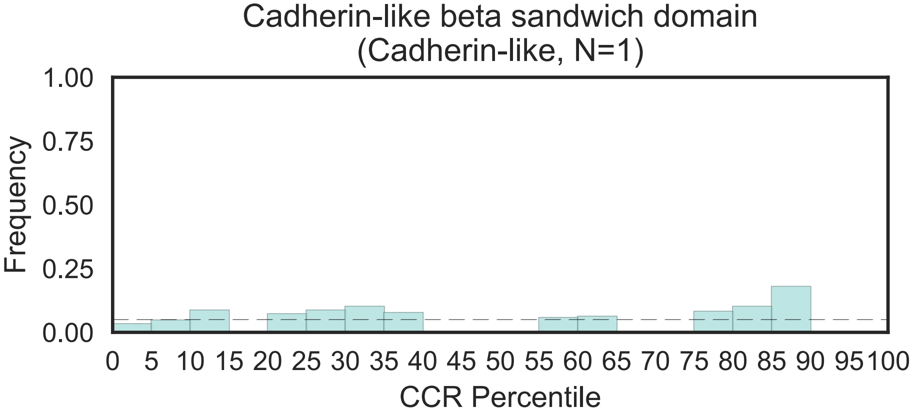

Calcium homeostasis modulator
(Ca_hom_mod, N=7)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

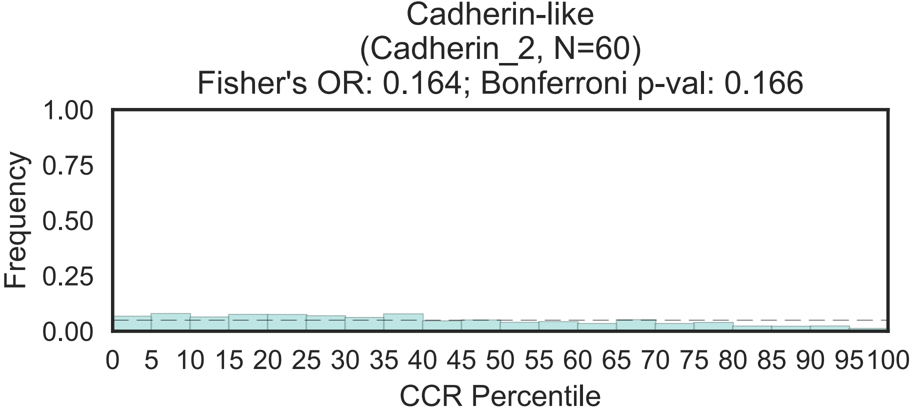

Cactus-binding C-terminus of cactin protein
(CactinC_cactus, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Conserved mid region of cactin
(Cactin_mid, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

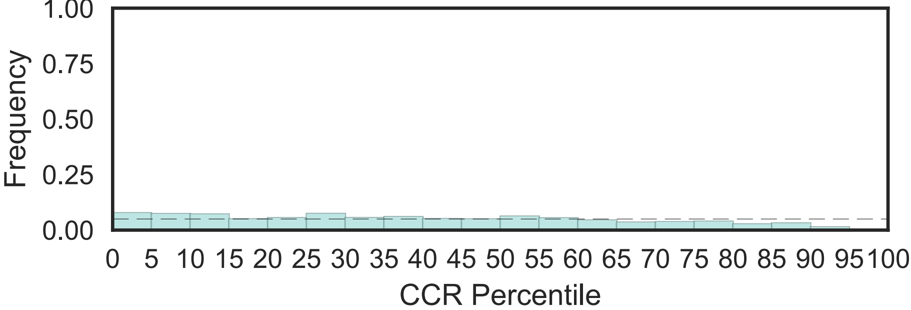


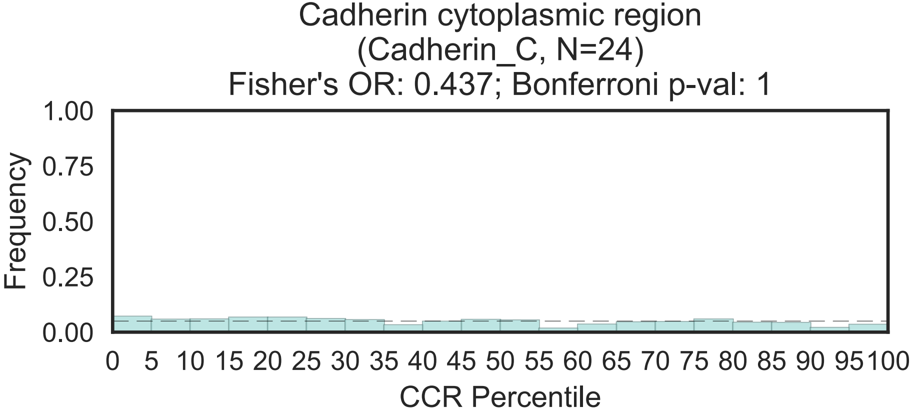
Cadherin domain
(Cadherin, N=673)
Fisher's OR: 0.2; Bonferroni p-val: 1.49e-41

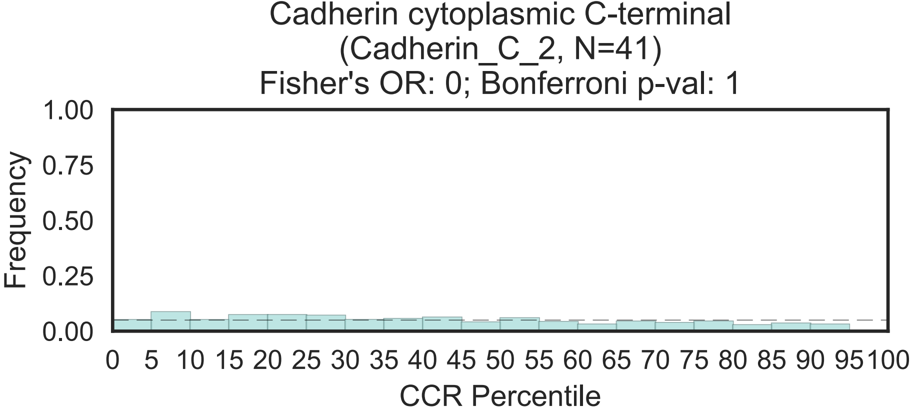

Cadherin-like beta sandwich domain
(Cadherin-like, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

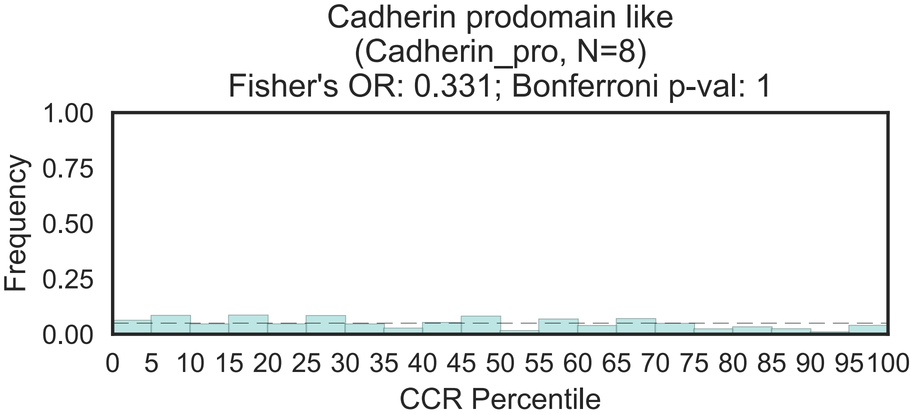

Cadherin-like
(Cadherin_2, N=60)
Fisher's OR: 0.164; Bonferroni p-val: 0.166
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Cadherin-like
(Cadherin_3, N=63)
Fisher's OR: 0.0455; Bonferroni p-val: 9.65e-05

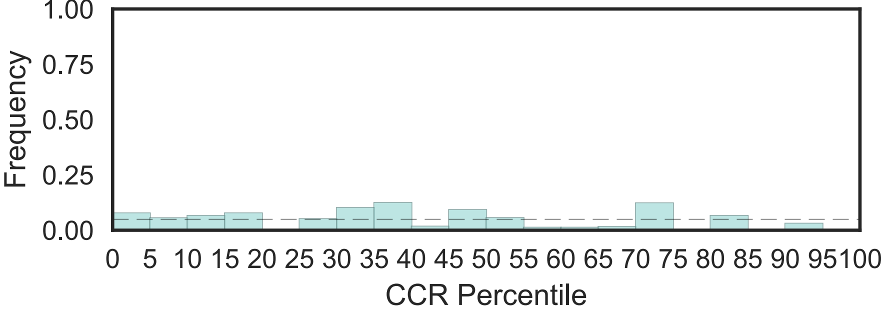


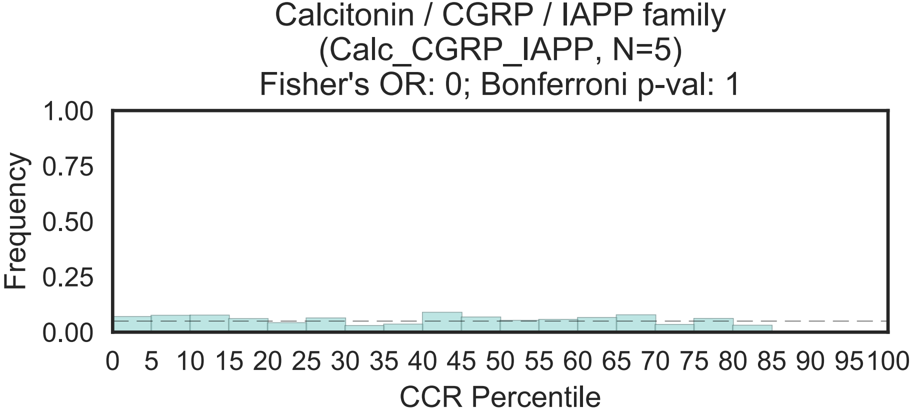

Cadherin cytoplasmic region
(Cadherin_C, N=24)
Fisher's OR: 0.437; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

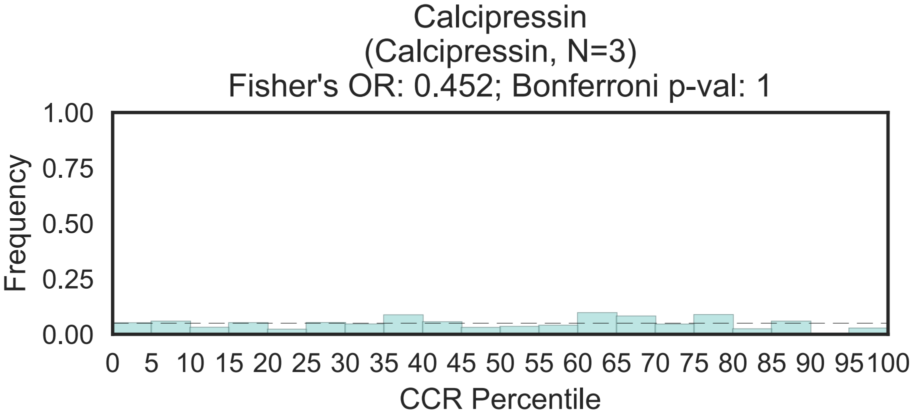

Cadherin cytoplasmic C-terminal
(Cadherin_C_2, N=41)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

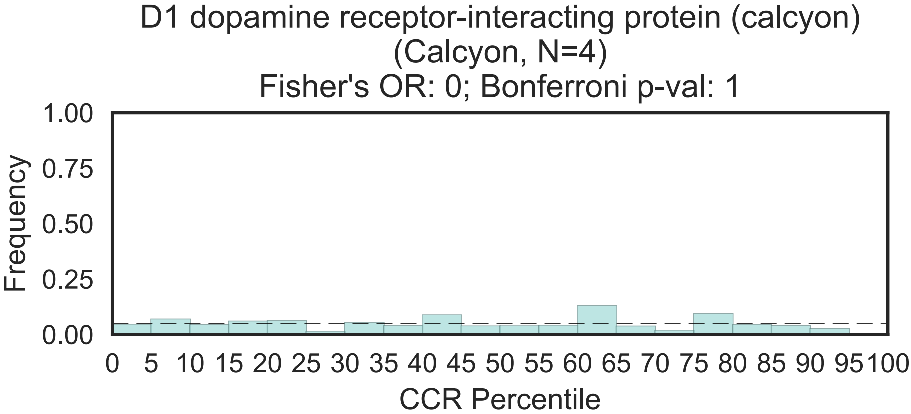

Cadherin prodomain like
(Cadherin_pro, N=8)
Fisher's OR: 0.331; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

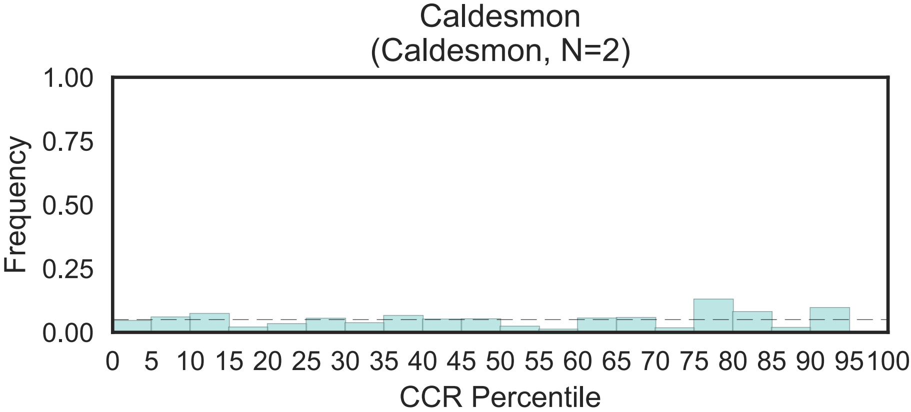
Cadherin C-terminal cytoplasmic tail, catenin-binding region (Cadherin_tail, N=36)
Fisher's OR: 0; Bonferroni p-val: 0.000188

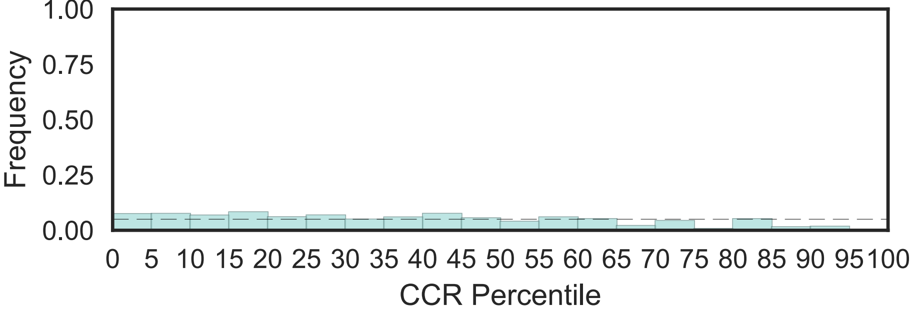



Calcitonin / CGRP / IAPP family
(Calc_CGRP_IAPP, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Calcipressin
(Calcipressin, N=3)
Fisher's OR: 0.452; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

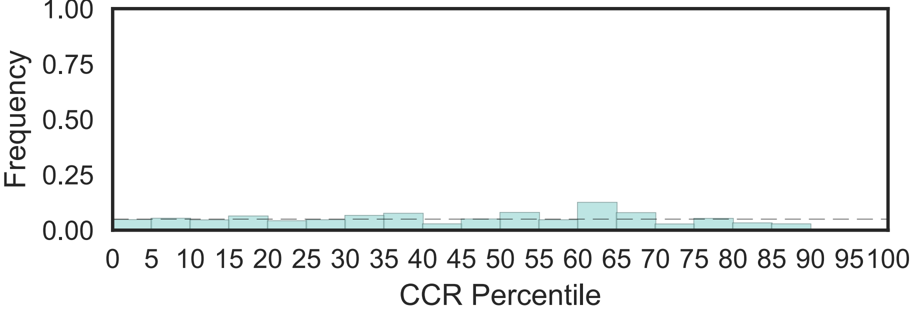

D1 dopamine receptor-interacting protein (calcyon)
(Calcyon, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

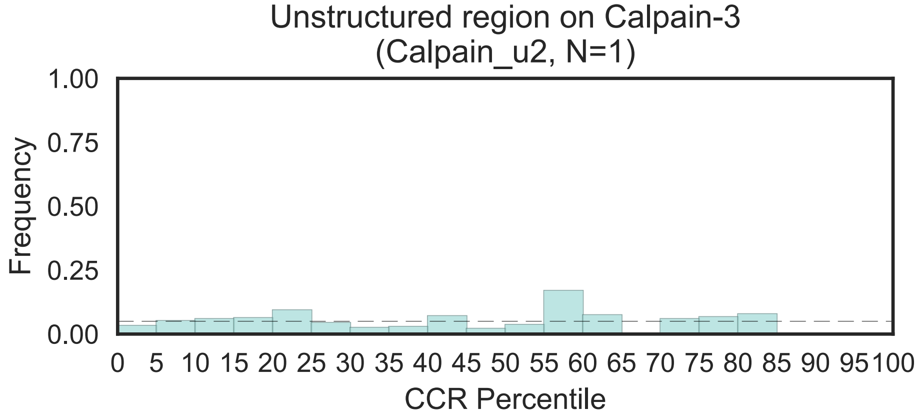

Caldesmon
(Caldesmon, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

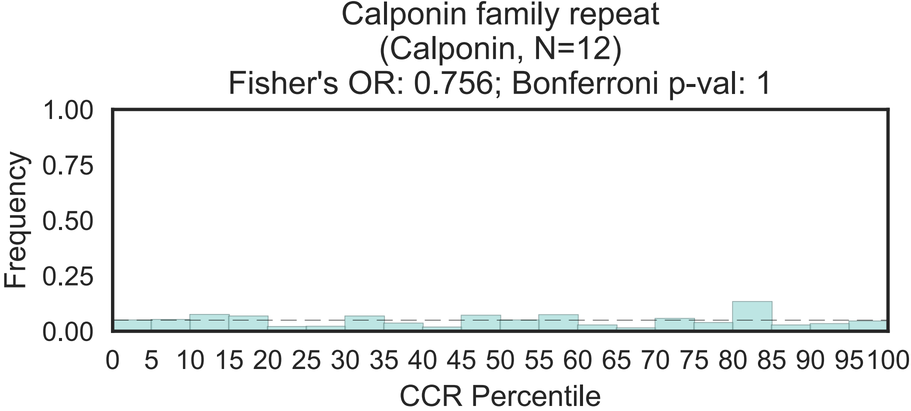


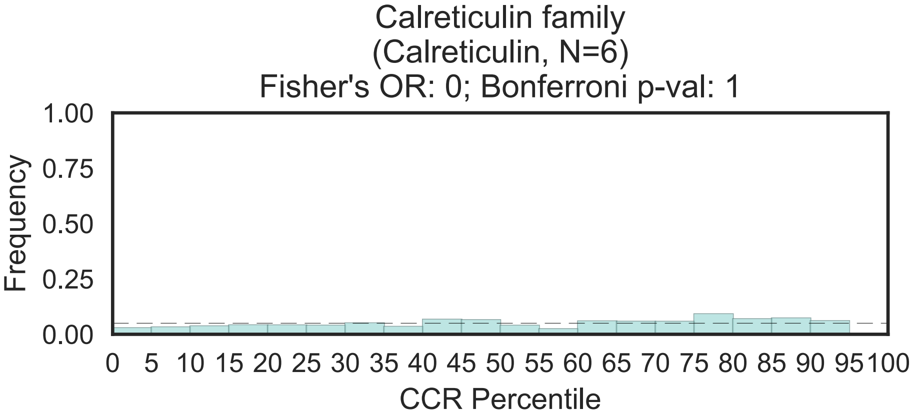
Calpain large subunit, domain III
(Calpain_III, N=13)
Fisher's OR: 0; Bonferroni p-val: 1

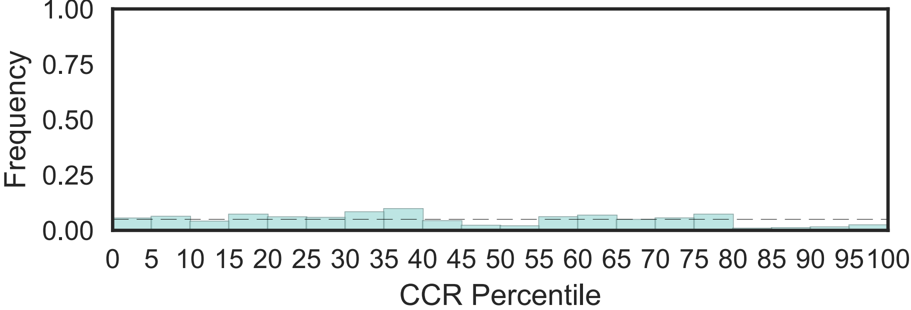
Calpain inhibitor
(Calpain_inhib, N=5)
Fisher's OR: 0; Bonferroni p-val: 1



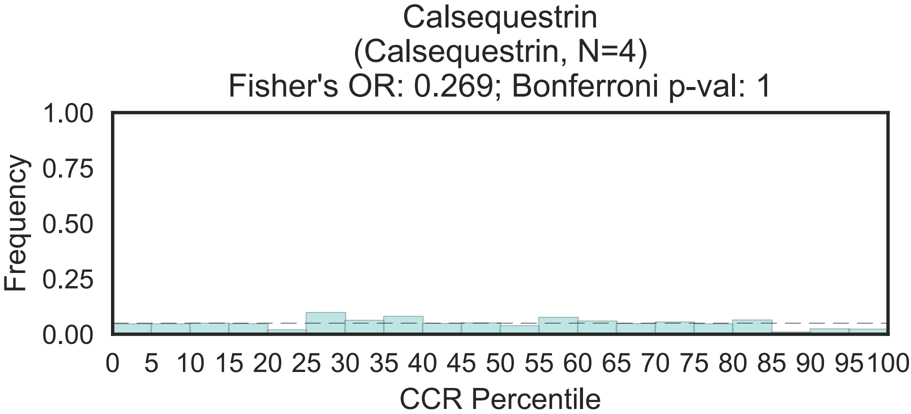

Unstructured region on Calpain-3
(Calpain_u2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Calponin family repeat
(Calponin, N=12)
Fisher's OR: 0.756; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

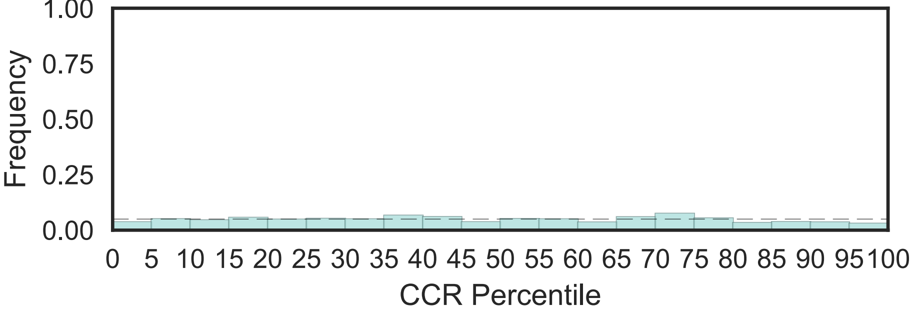

Calreticulin family
(Calreticulin, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

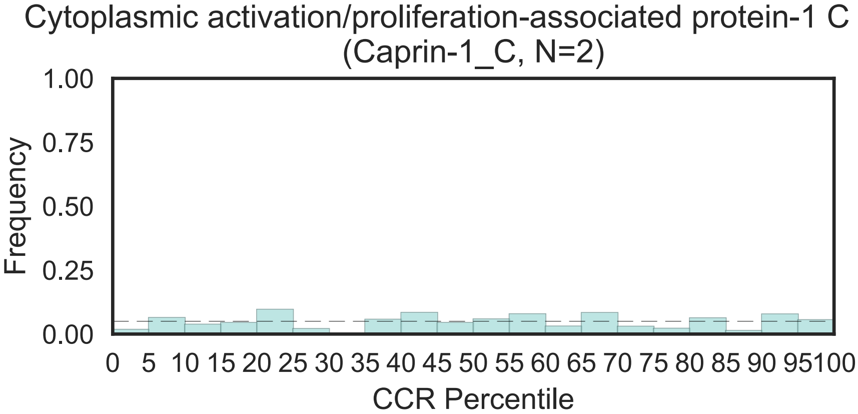


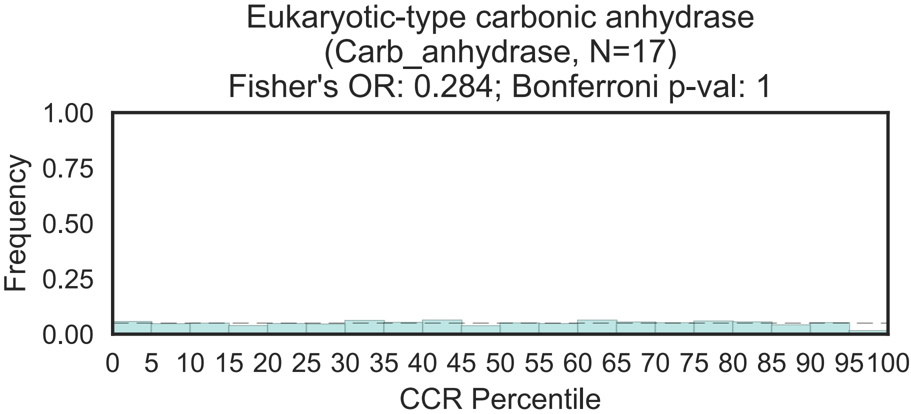
Calcineurin-binding protein (Calsarcin)
(Calsarcin, N=3)
Fisher's OR: 0.299; Bonferroni p-val: 1

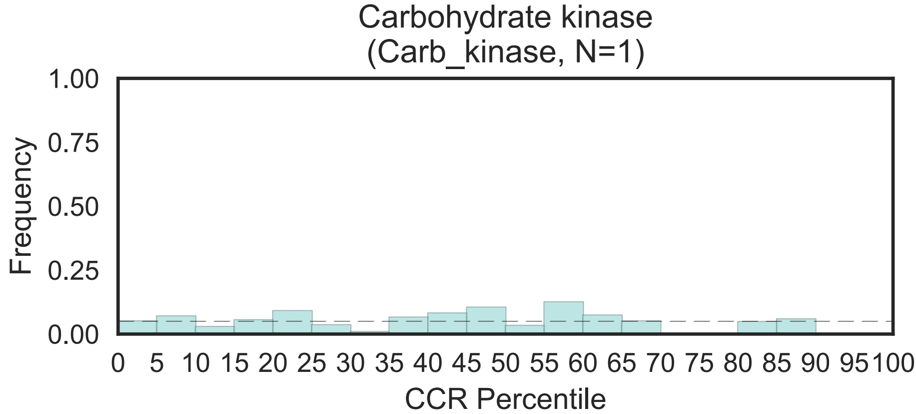

Calsequestrin
(Calsequestrin, N=4)
Fisher's OR: 0.269; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

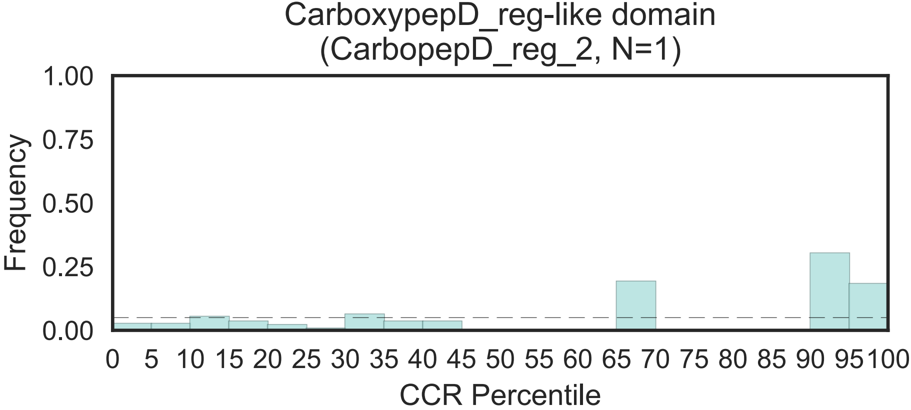
Calx-beta domain
(Calx-beta, N=56)
Fisher's OR: 0.448; Bonferroni p-val: 1

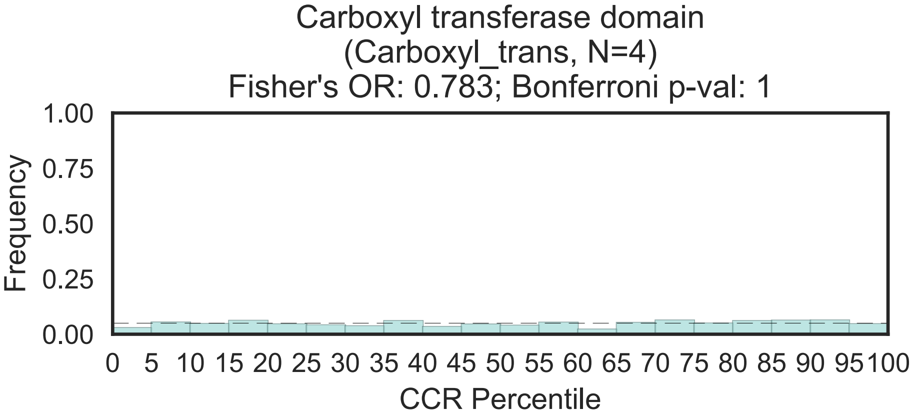


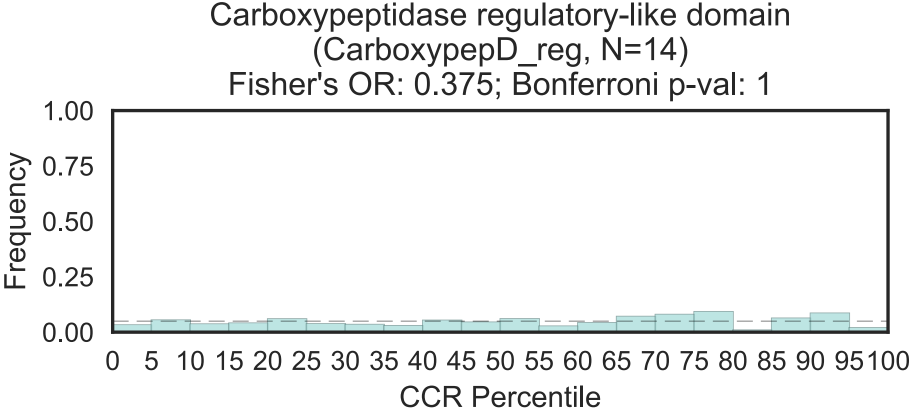

Cytoplasmic activation/proliferation-associated protein-1 C term
(Caprin-1_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

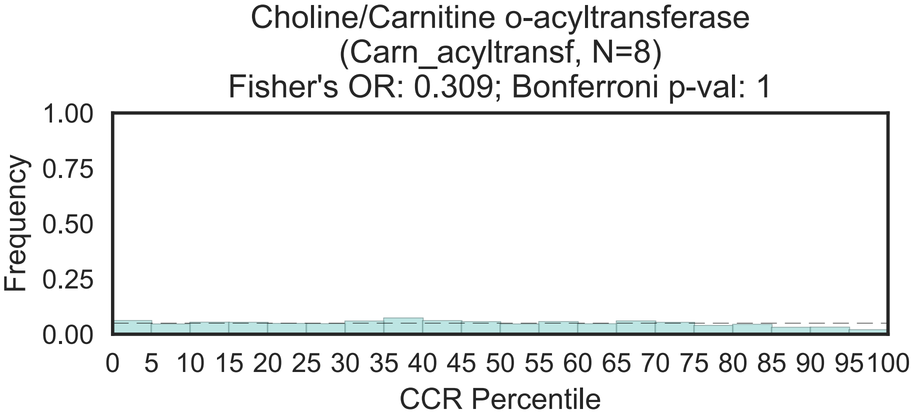

Eukaryotic-type carbonic anhydrase
(Carb_anhydrase, N=17)
Fisher's OR: 0.284; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

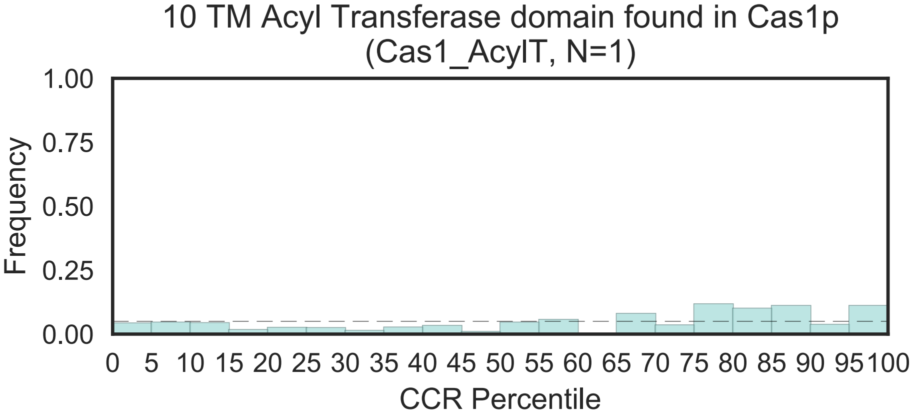

Carbohydrate kinase
(Carb_kinase, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

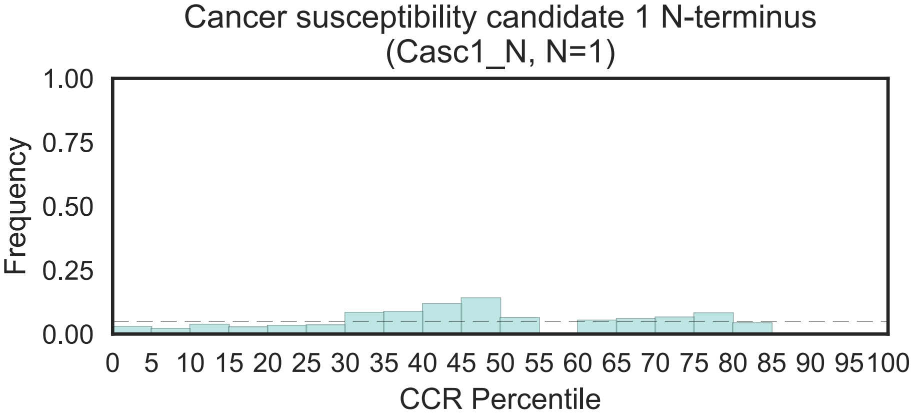

CarboxypepD_reg-like domain
(CarbopepD_reg_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

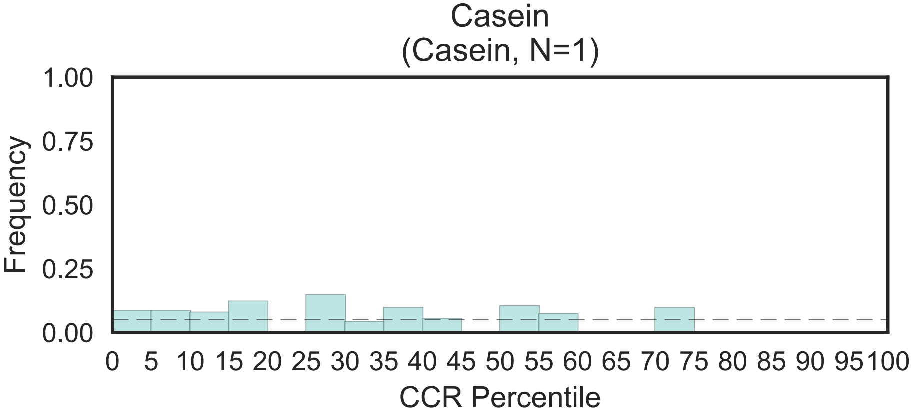

Carboxyl transferase domain
(Carboxyl_trans, N=4)
Fisher's OR: 0.783; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

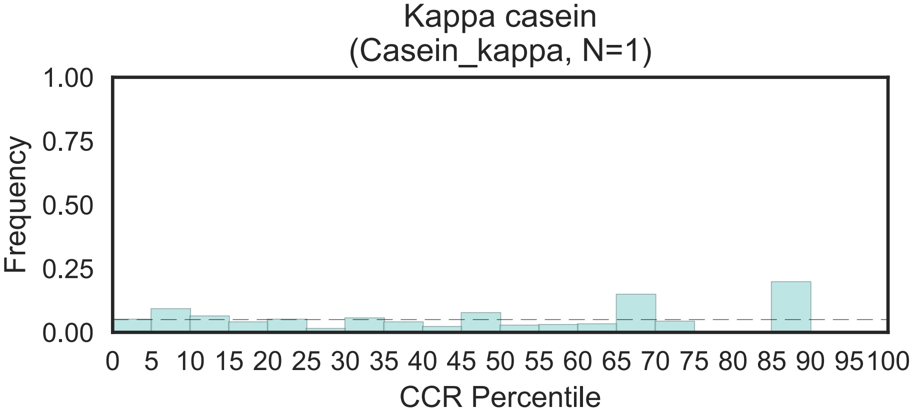

Carboxypeptidase regulatory-like domain
(CarboxypepD_reg, N=14)
Fisher's OR: 0.375; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

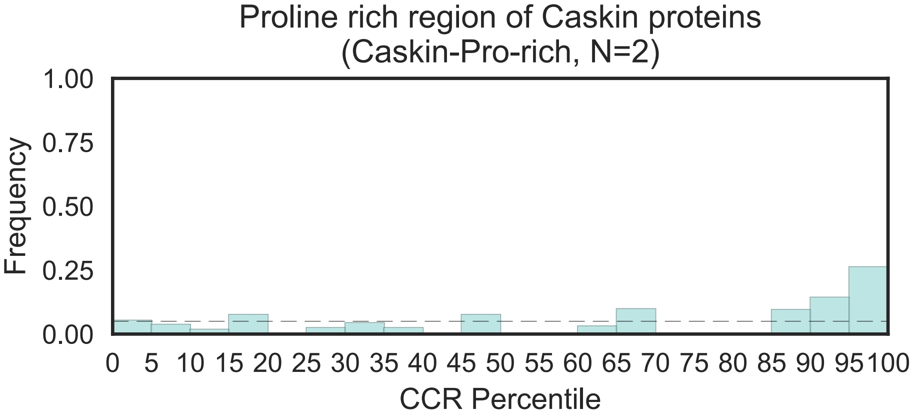

Choline/Carnitine o-acyltransferase
(Carn_acyltransf, N=8)
Fisher's OR: 0.309; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

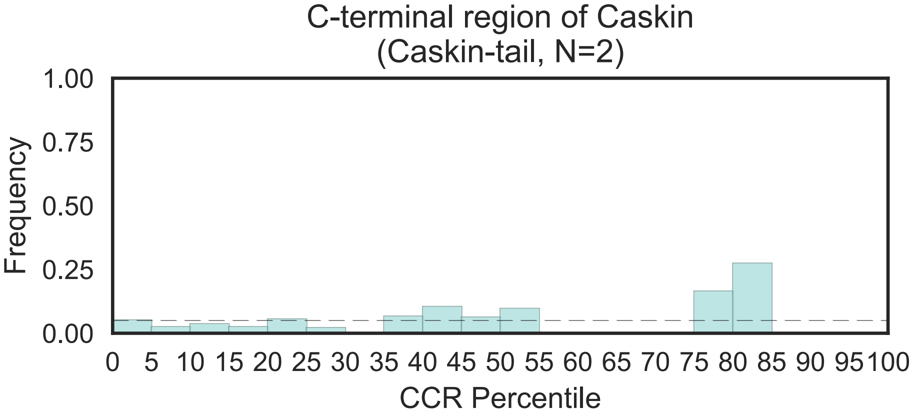

10 TM Acyl Transferase domain found in Cas1p
(Cas1_AcylT, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

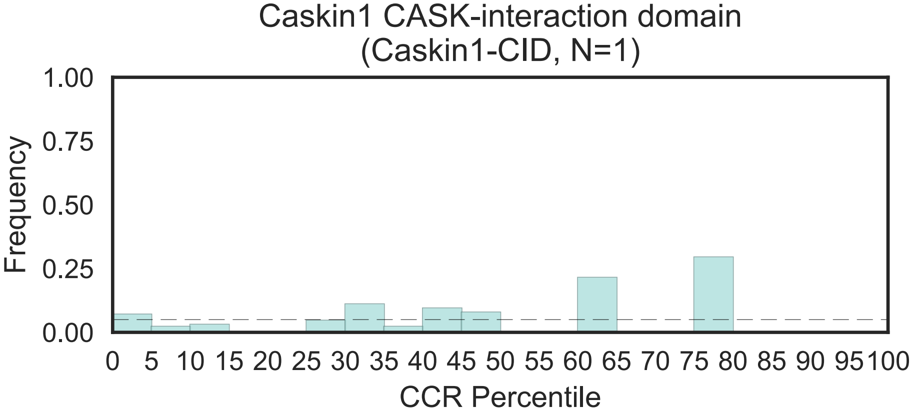

Cancer susceptibility candidate 1 N-terminus
(Casc1_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

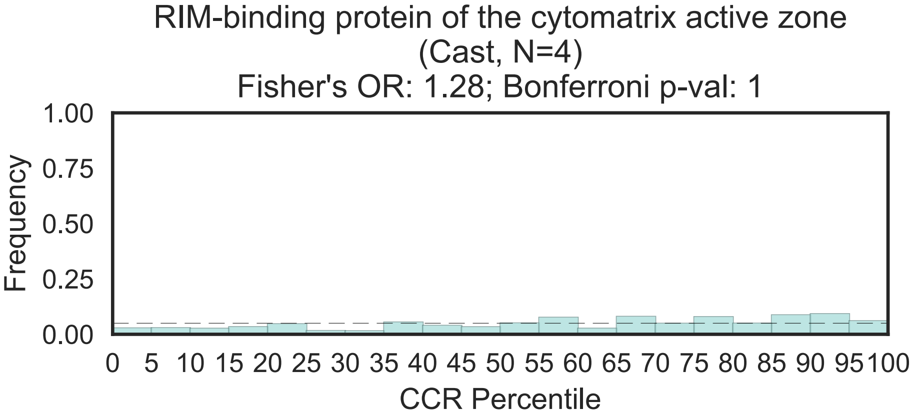

Casein
(Casein, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

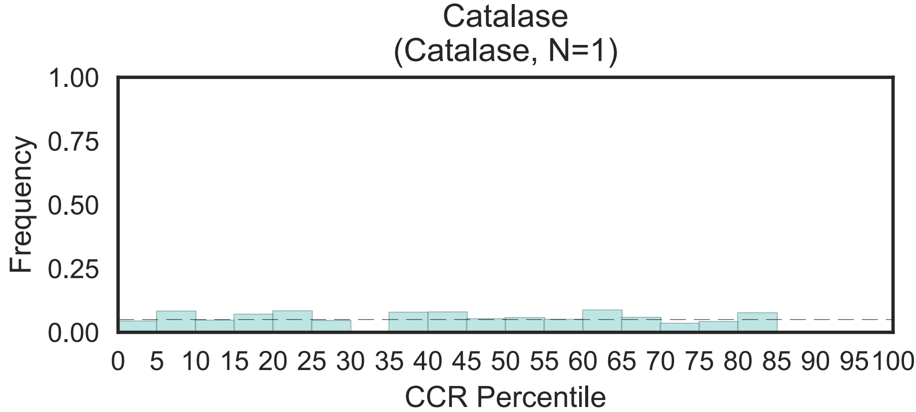

Kappa casein
(Casein_kappa, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

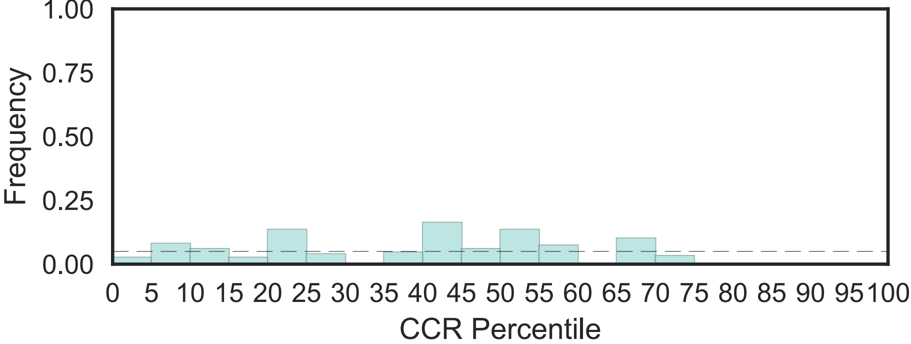

Proline rich region of Caskin proteins
(Caskin-Pro-rich, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


C-terminal region of Caskin
(Caskin-tail, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

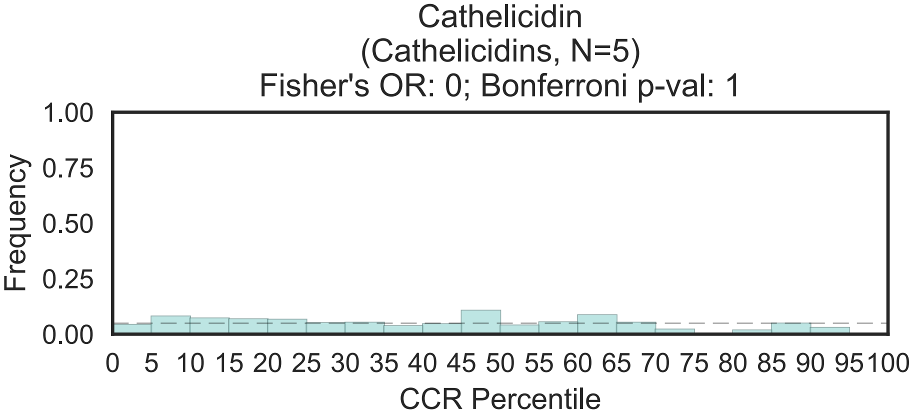

Caskin1 CASK-interaction domain
(Caskin1-CID, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

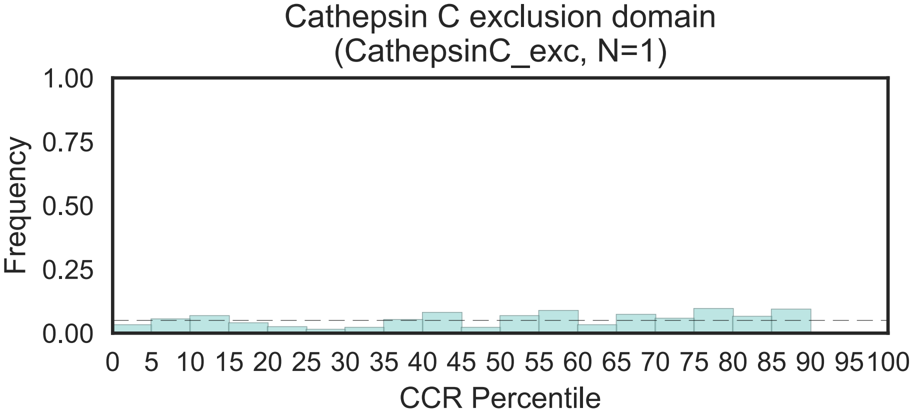

RIM-binding protein of the cytomatrix active zone
(Cast, N=4)
Fisher's OR: 1.28; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

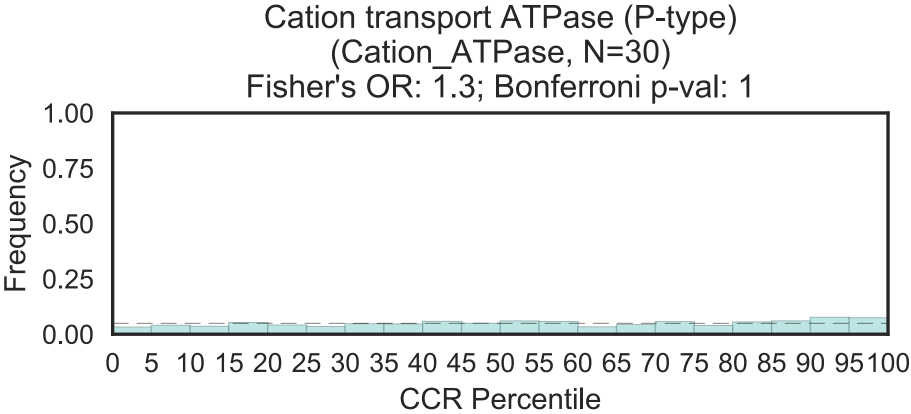

Catalase
(Catalase, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

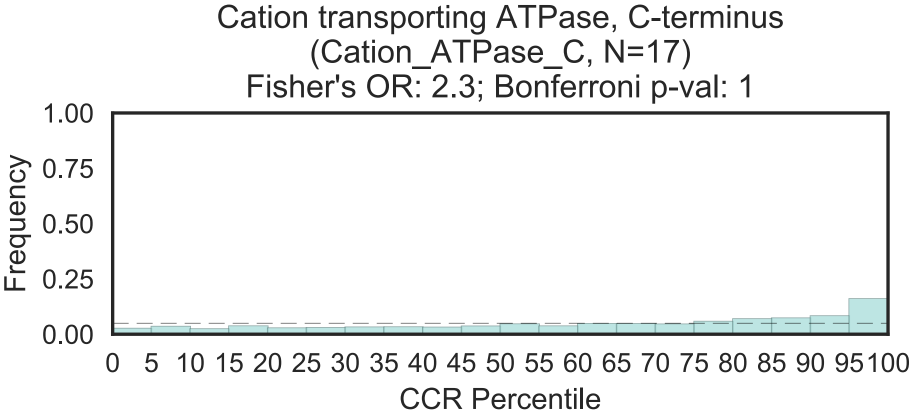


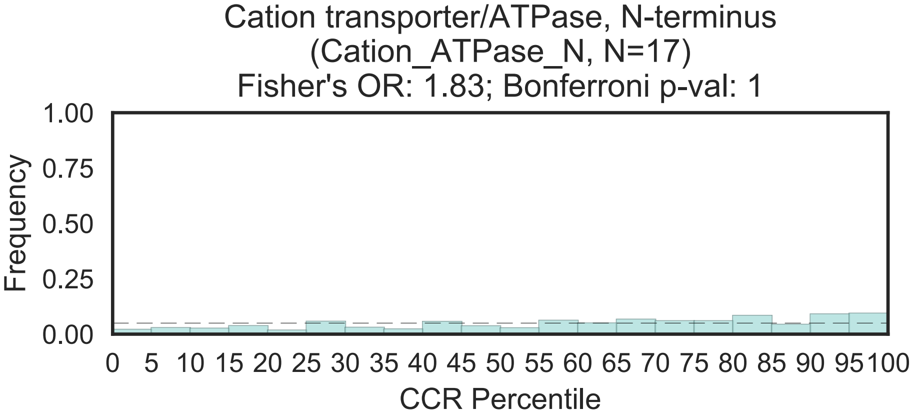
Catalase-related immune-responsive
(Catalase-rel, N=1)

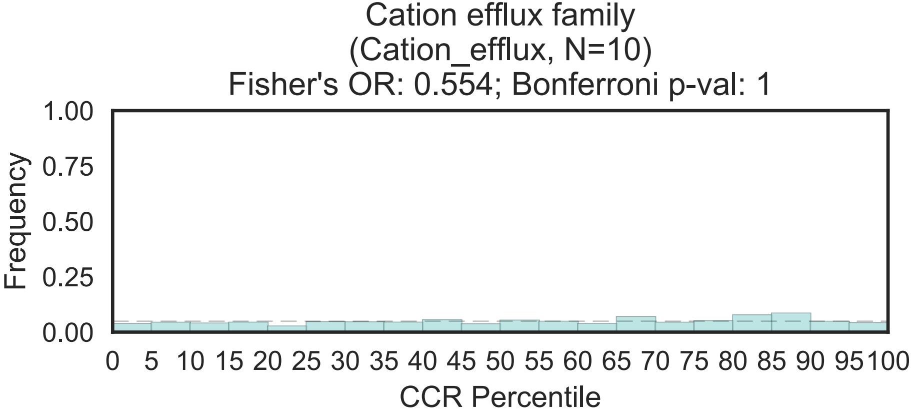

Cathelicidin
(Cathelicidins, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

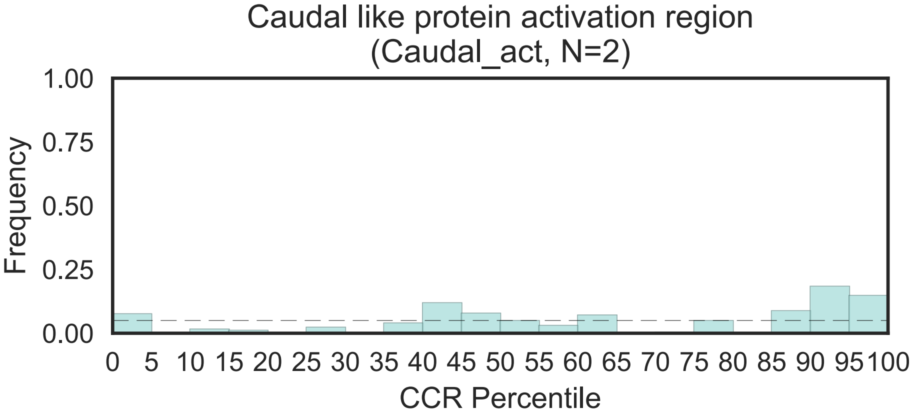

Cathepsin C exclusion domain
(CathepsinC_exc, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

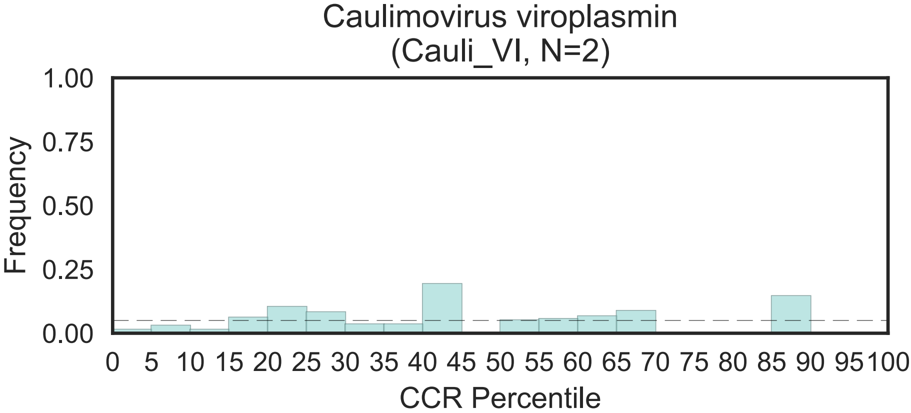

Cation transport ATPase (P-type)
(Cation_ATPase, N=30)
Fisher's OR: 1.3; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

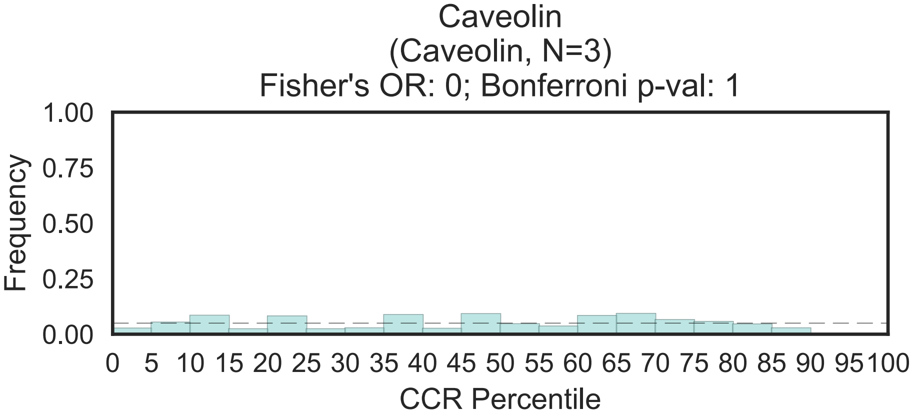

Cation transporting ATPase, C-terminus
(Cation_ATPase_C, N=17)
Fisher's OR: 2.3; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

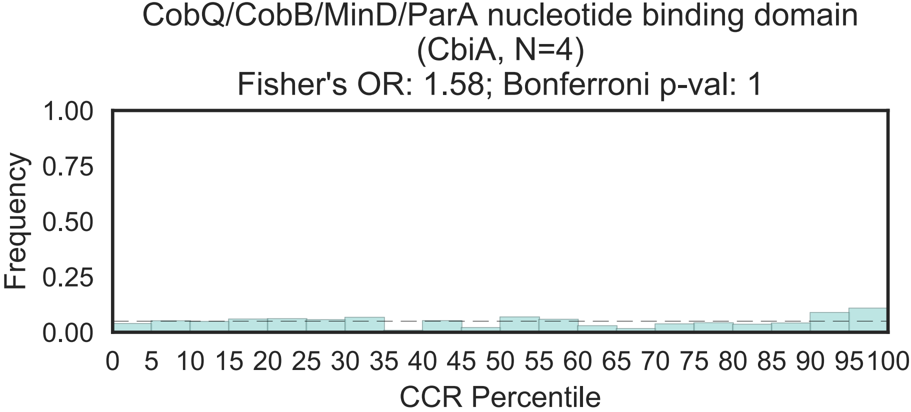

Cation transporter/ATPase, N-terminus
(Cation_ATPase_N, N=17)
Fisher's OR: 1.83; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

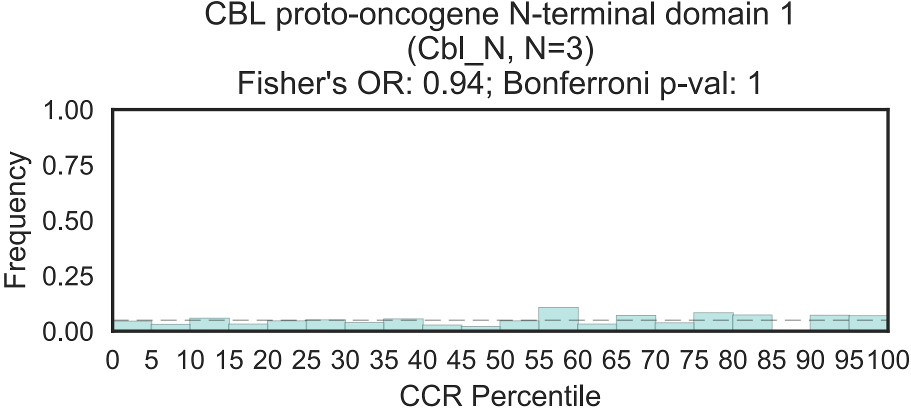

Cation efflux family
(Cation_efflux, N=10)
Fisher's OR: 0.554; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

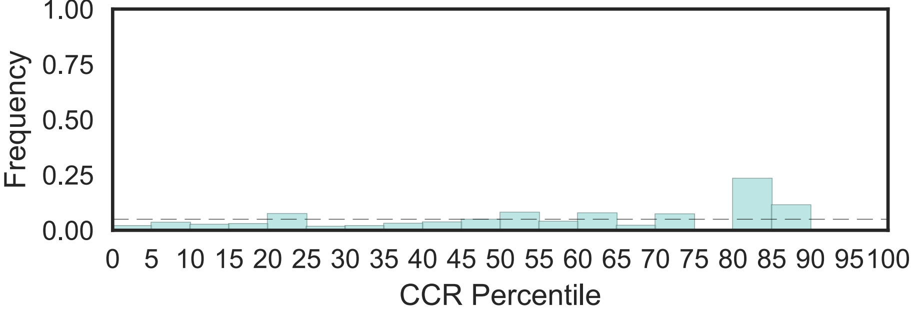

Caudal like protein activation region
(Caudal_act, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Caulimovirus viroplasmin
(Cauli_VI, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

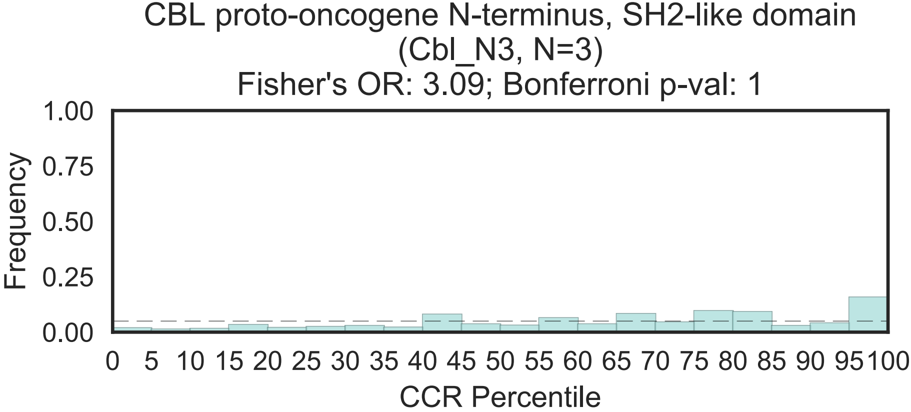

Caveolin
(Caveolin, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

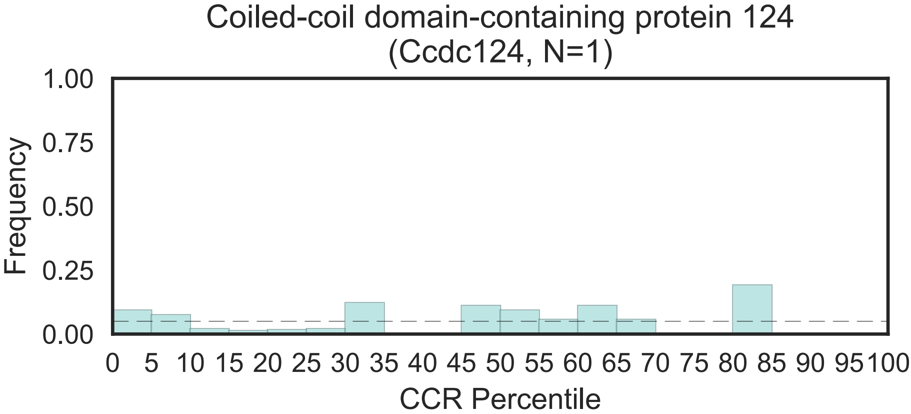

CobQ/CobB/MinD/ParA nucleotide binding domain
(CbiA, N=4)
Fisher's OR: 1.58; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

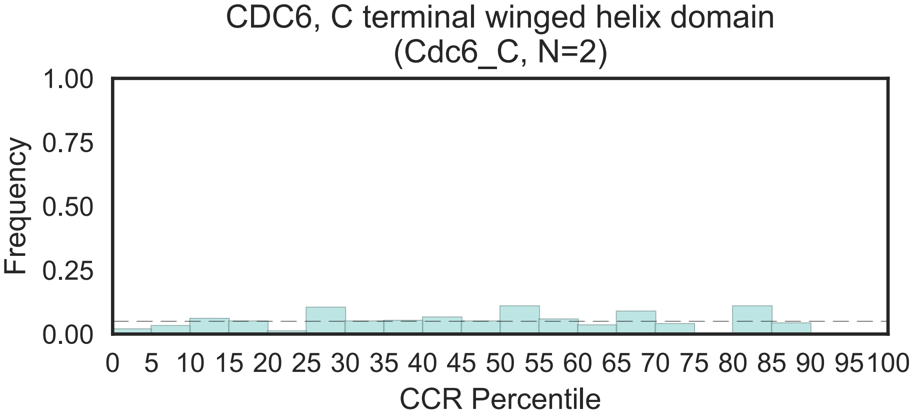

CBL proto-oncogene N-terminal domain 1
(Cbl_N, N=3)
Fisher's OR: 0.94; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

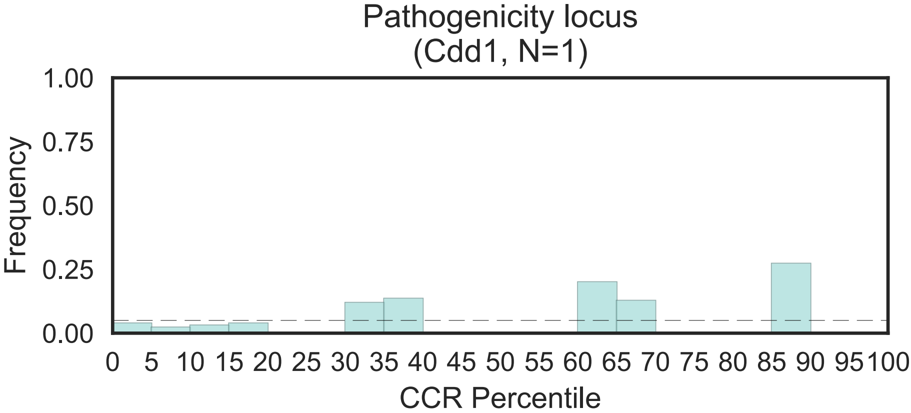


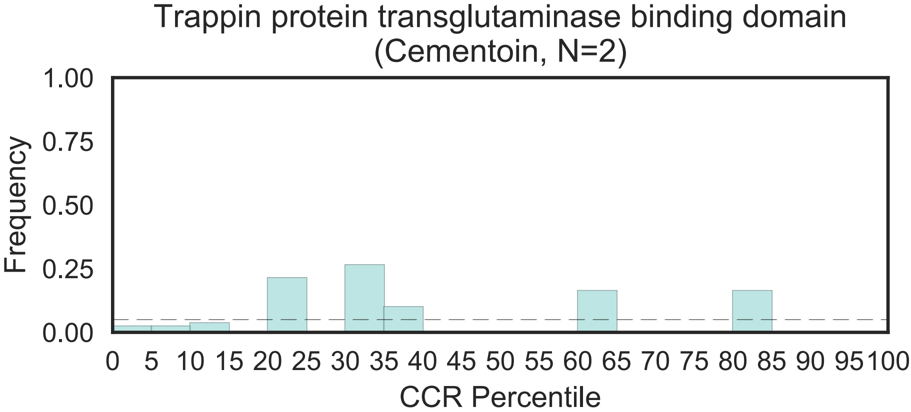
CBL proto-oncogene N-terminus, EF hand-like domain
(Cbl_N2, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

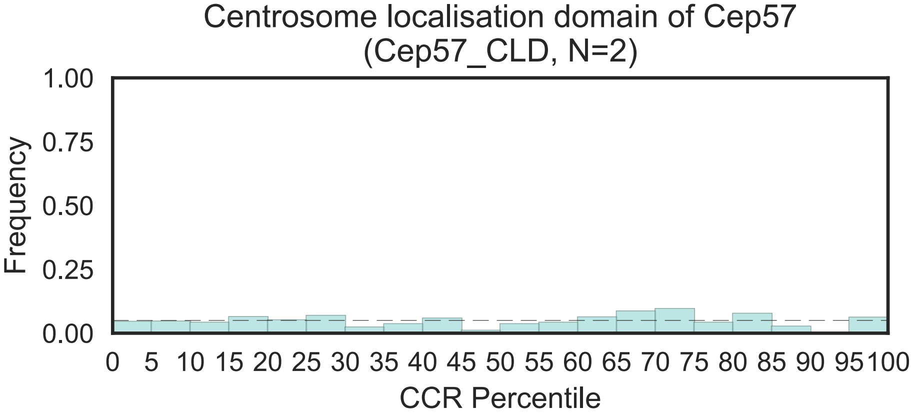

CBL proto-oncogene N-terminus, SH2-like domain
(Cbl_N3, N=3)
Fisher's OR: 3.09; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

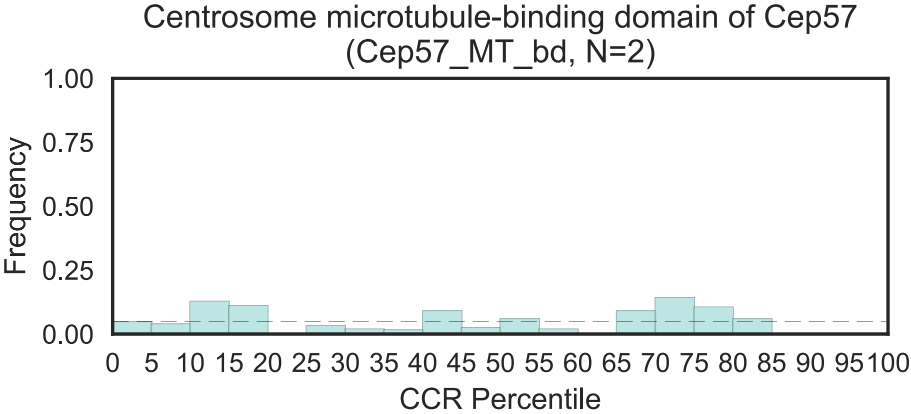

Coiled-coil domain-containing protein 124
(Ccdc124, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

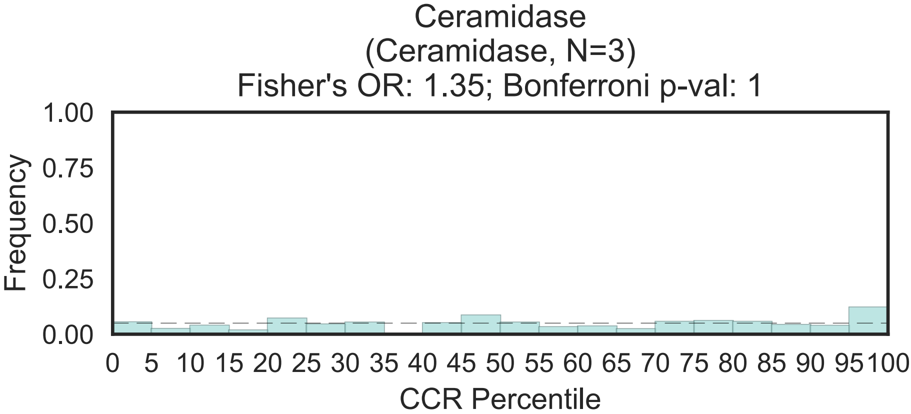

CDC6, C terminal winged helix domain
(Cdc6_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

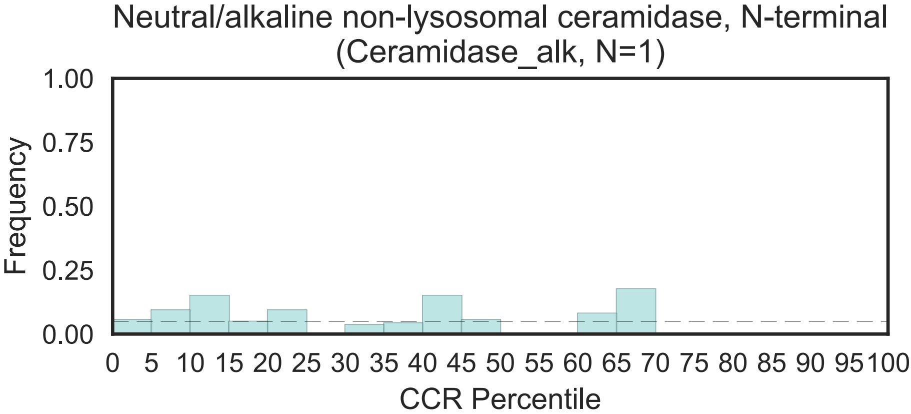

Pathogenicity locus
(Cdd1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

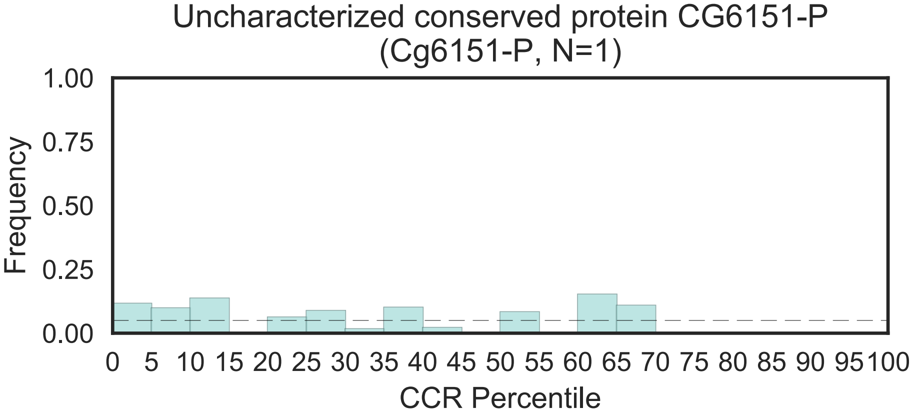

Trappin protein transglutaminase binding domain
(Cementoin, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

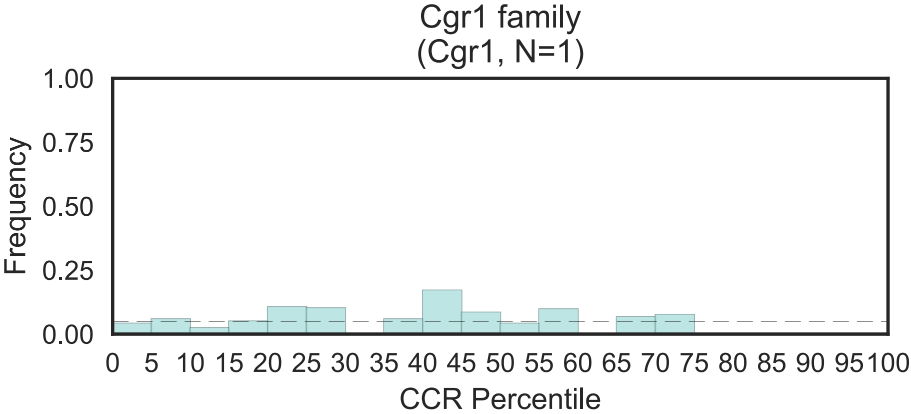

Centrosome localisation domain of Cep57
(Cep57_CLD, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

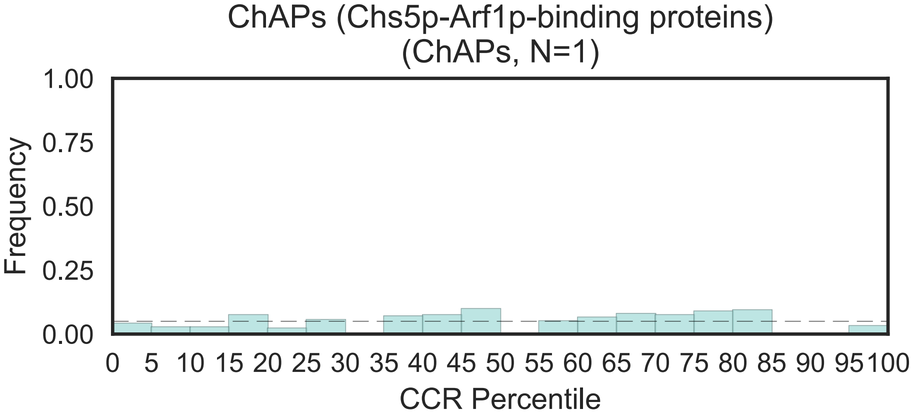

Centrosome microtubule-binding domain of Cep57
(Cep57_MT_bd, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

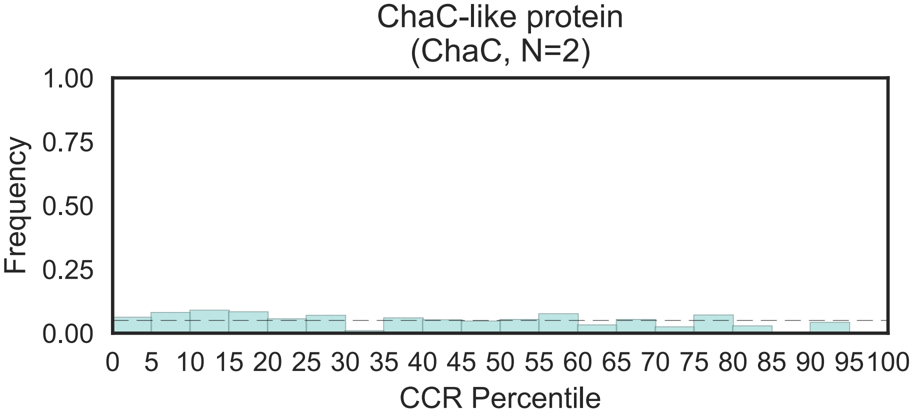

Ceramidase
(Ceramidase, N=3)
Fisher's OR: 1.35; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

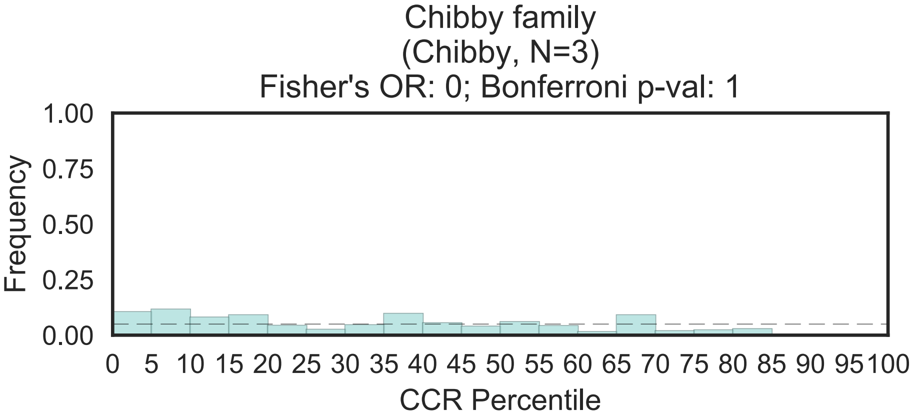

Neutral/alkaline non-lysosomal ceramidase, N-terminal
(Ceramidase_alk, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Uncharacterized conserved protein CG6151-P
(Cg6151-P, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

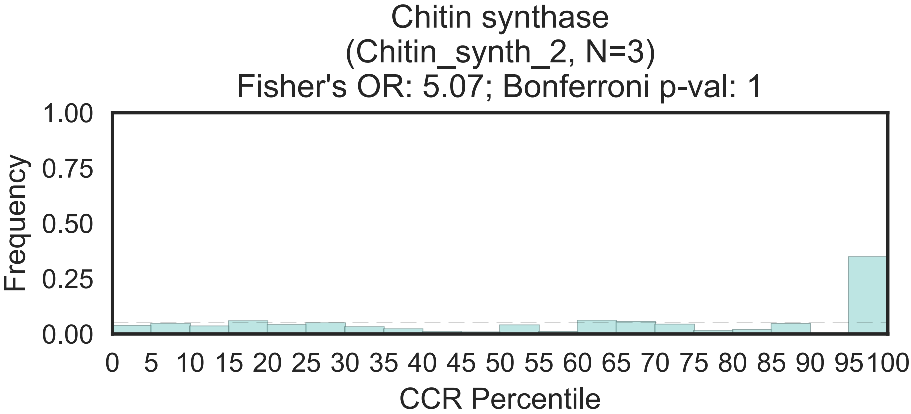

Cgr1 family
(Cgr1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

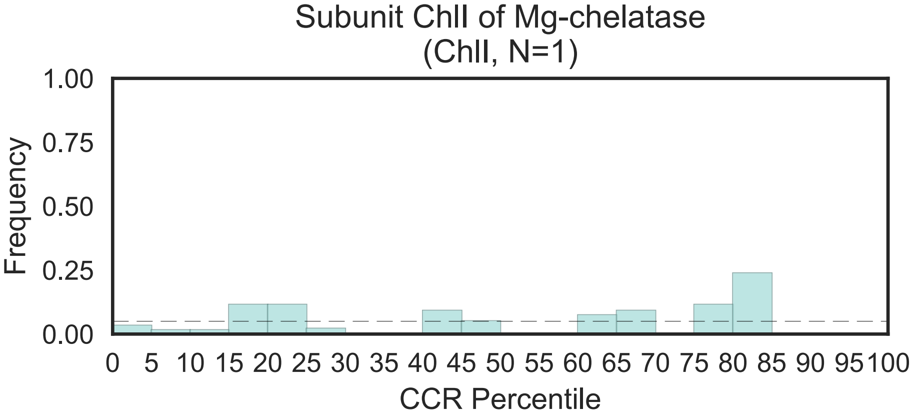

ChAPs (Chs5p-Arf1p-binding proteins)
(ChAPs, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

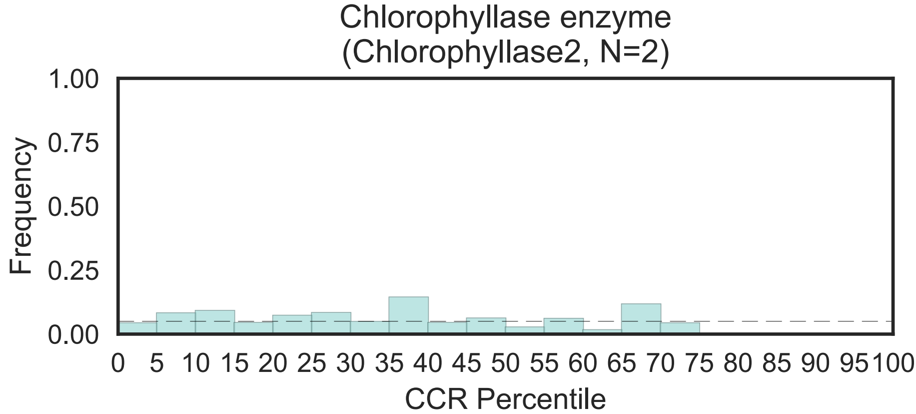

ChaC-like protein
(ChaC, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

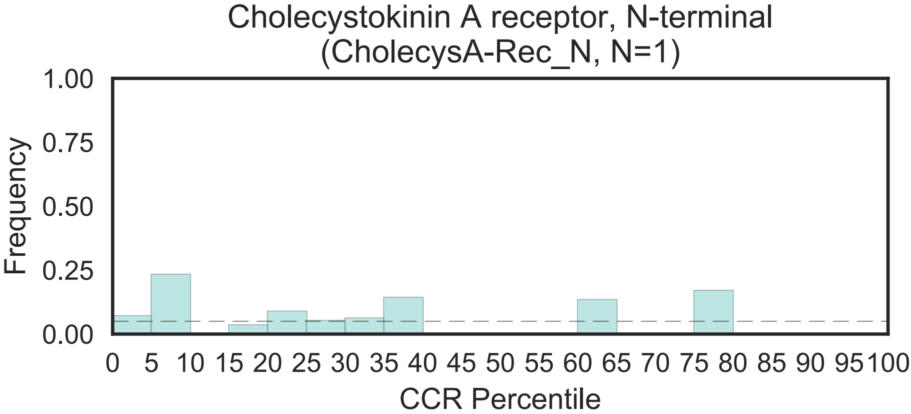


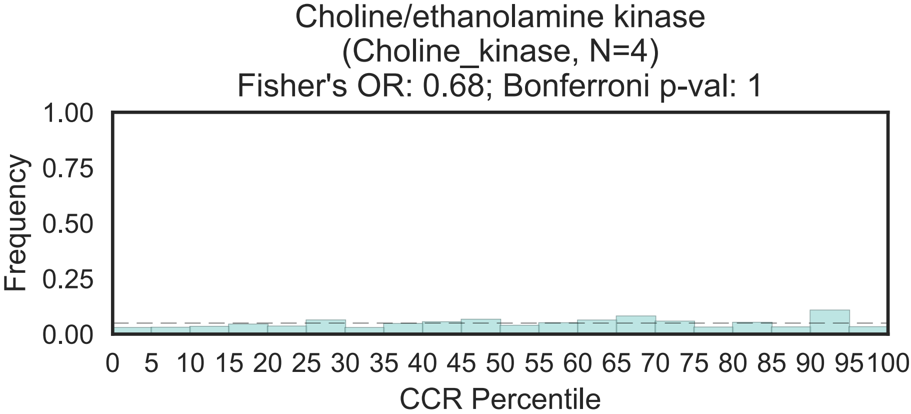
Chibby family
(Chibby, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

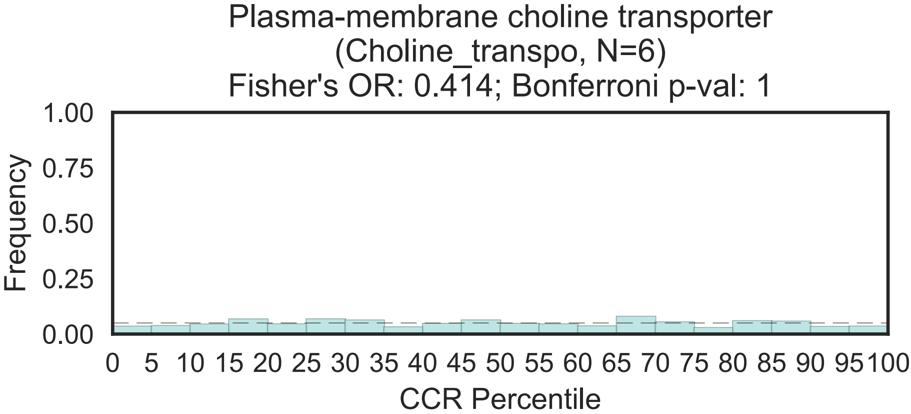

Chitin synthase
(Chitin_synth_2, N=3)
Fisher's OR: 5.07; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

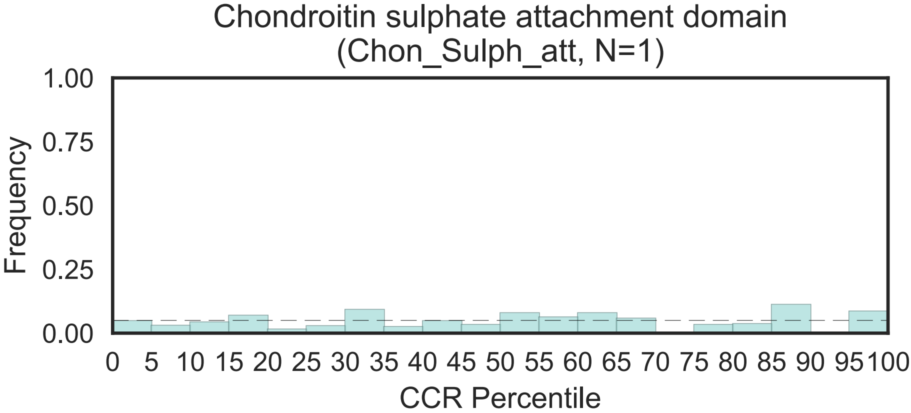

Subunit ChlI of Mg-chelatase
(ChlI, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

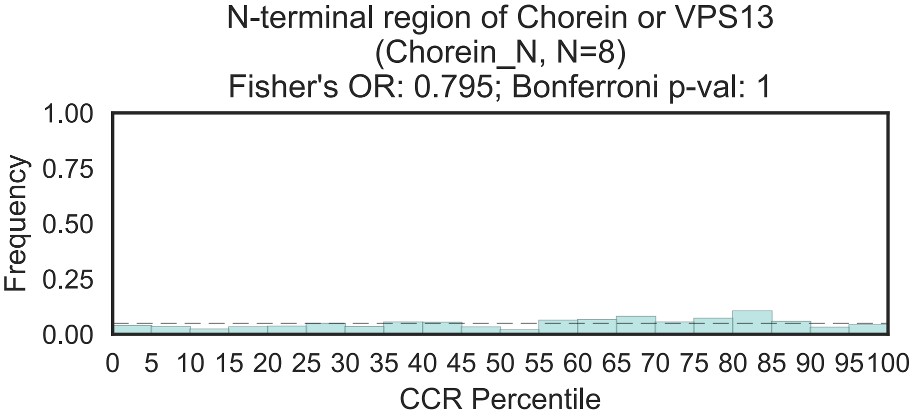

Chlorophyllase enzyme
(Chlorophyllase2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

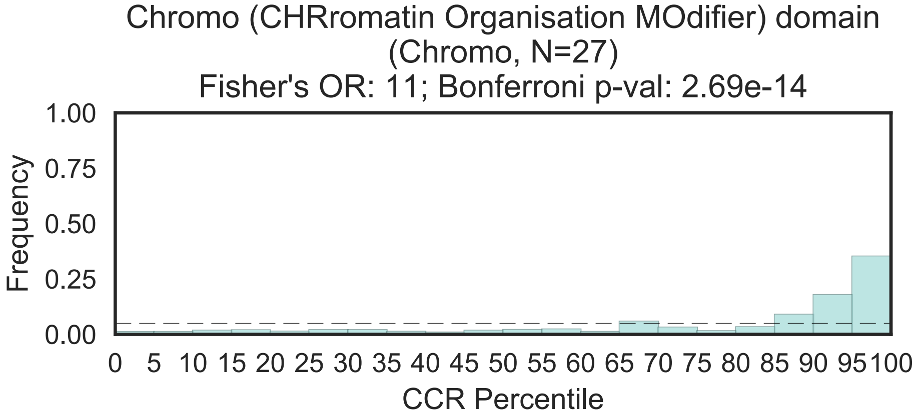

Cholecystokinin A receptor, N-terminal
(CholecysA-Rec_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

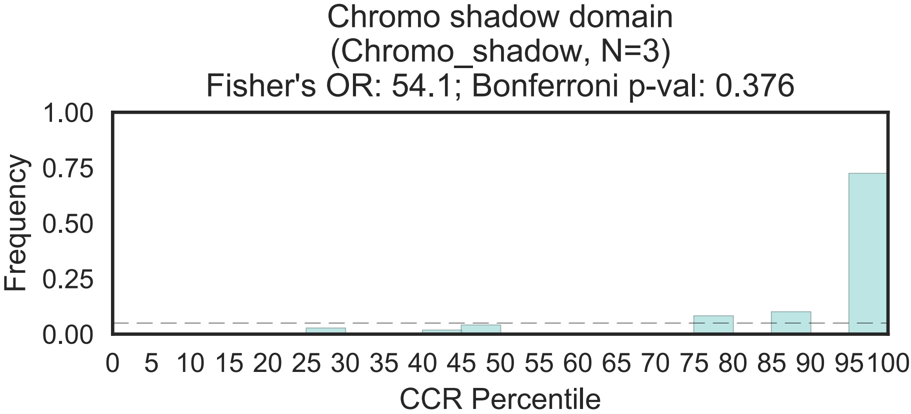

Choline/ethanolamine kinase
(Choline_kinase, N=4)
Fisher's OR: 0.68; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

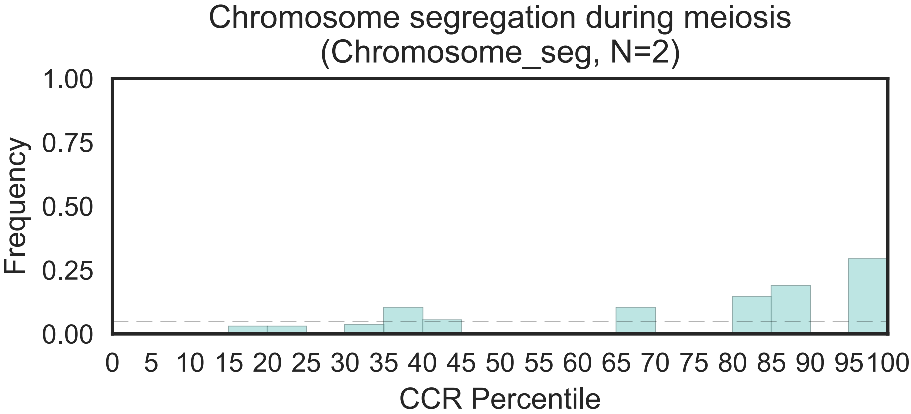

Plasma-membrane choline transporter
(Choline_transpo, N=6)
Fisher's OR: 0.414; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

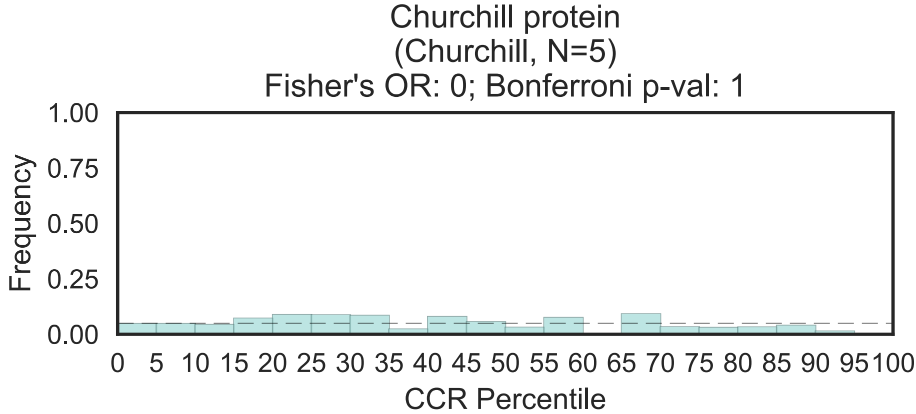

Chondroitin sulphate attachment domain
(Chon_Sulph_att, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

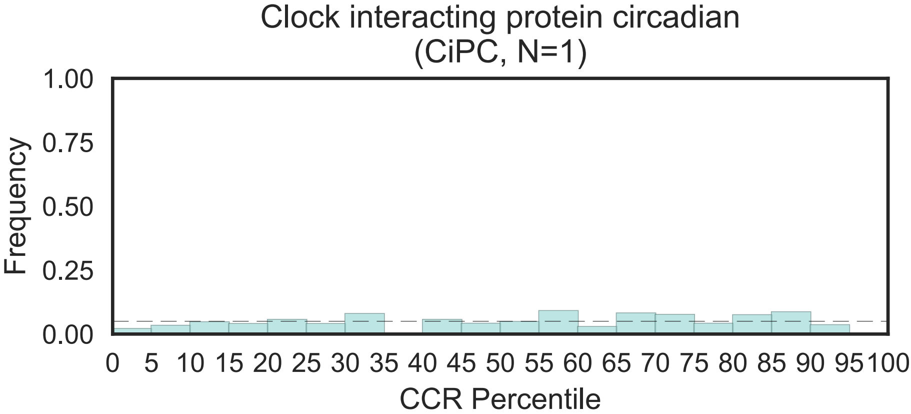

N-terminal region of Chorein or VPS13
(Chorein_N, N=8)
Fisher's OR: 0.795; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

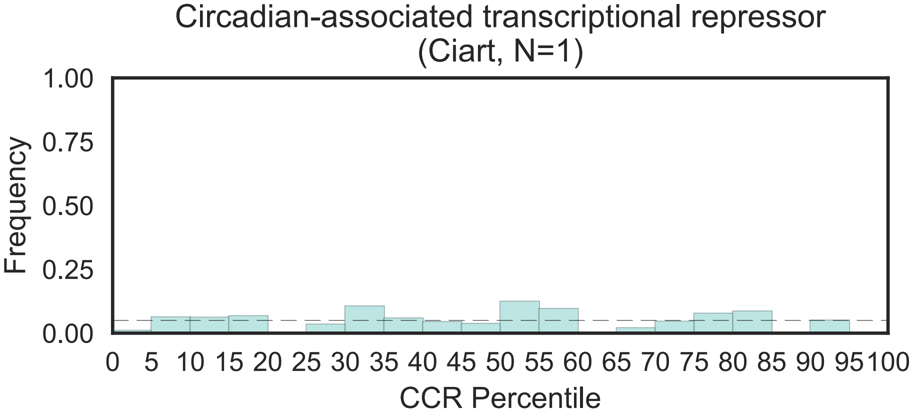

Chromo (CHRromatin Organisation MOdifier) domain
(Chromo, N=27)
Fisher's OR: 11; Bonferroni p-val: 2.69e-14
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

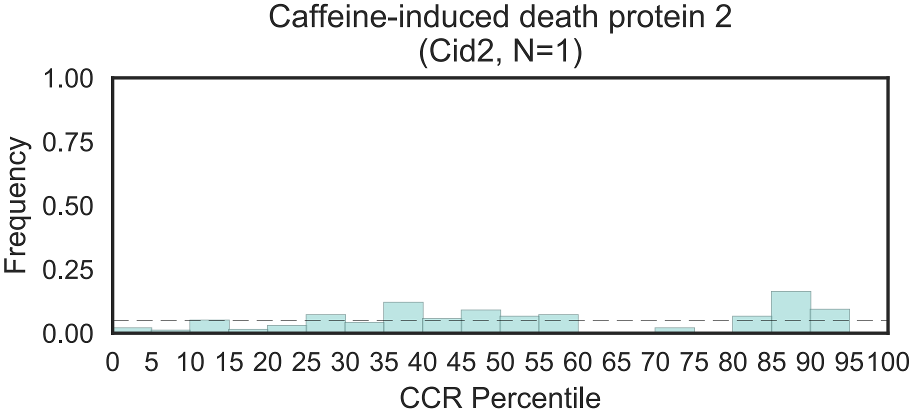

Chromo shadow domain
(Chromo_shadow, N=3)
Fisher's OR: 54.1; Bonferroni p-val: 0.376
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

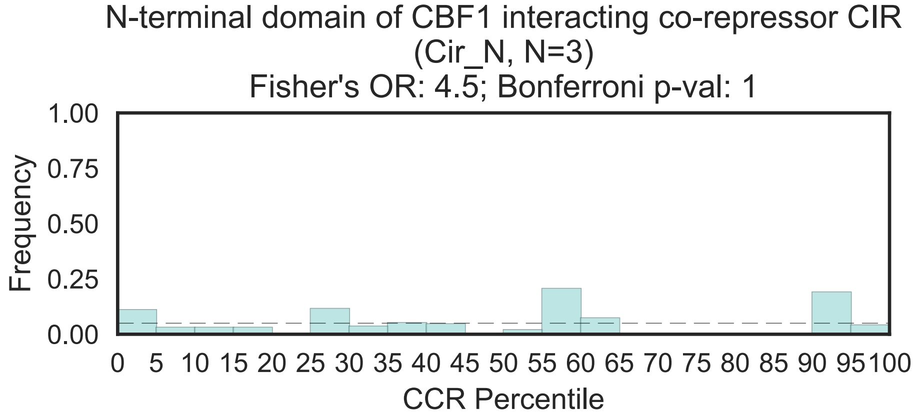

Chromosome segregation during meiosis
(Chromosome_seg, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

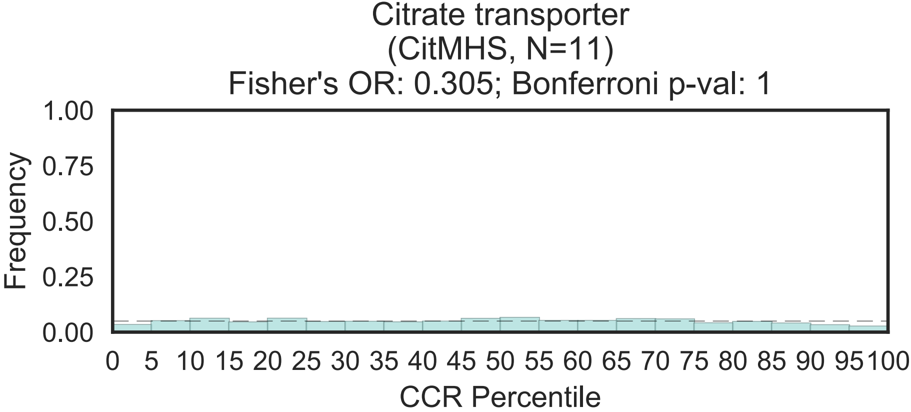

Churchill protein
(Churchill, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

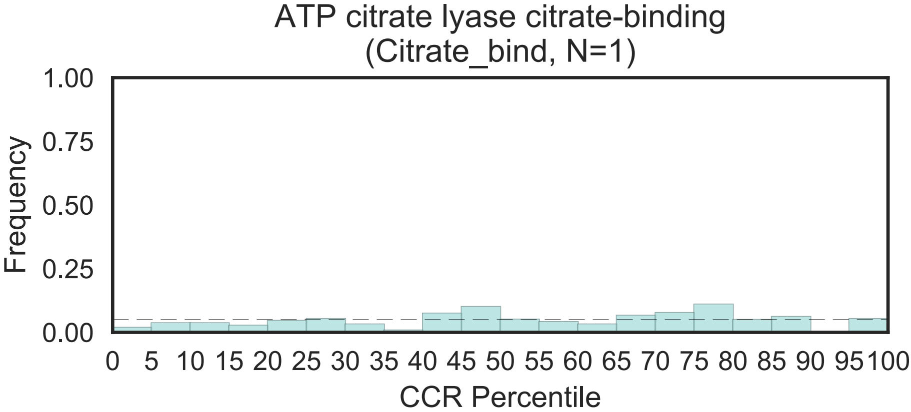

Clock interacting protein circadian
(CiPC, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

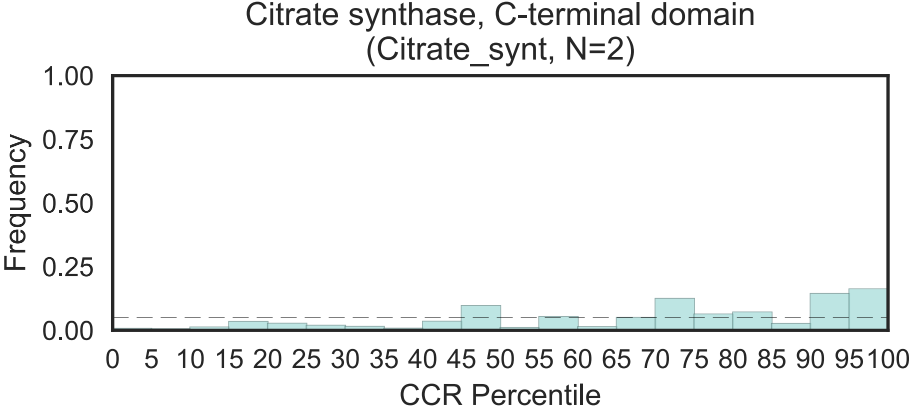

Circadian-associated transcriptional repressor
(Ciart, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

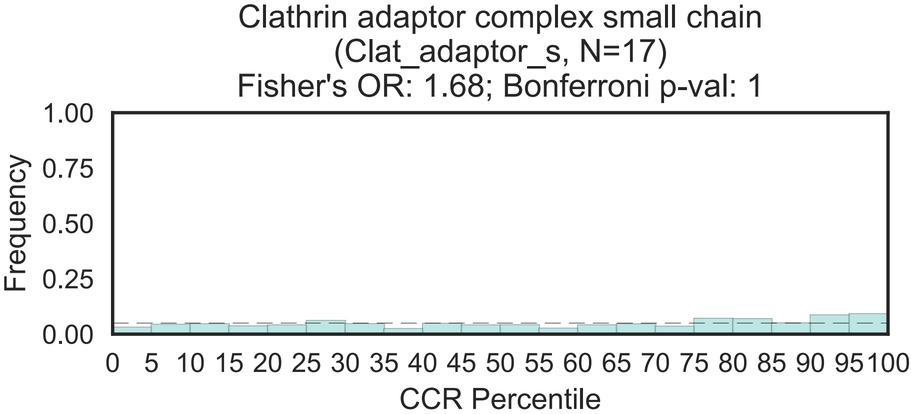

Caffeine-induced death protein 2
(Cid2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

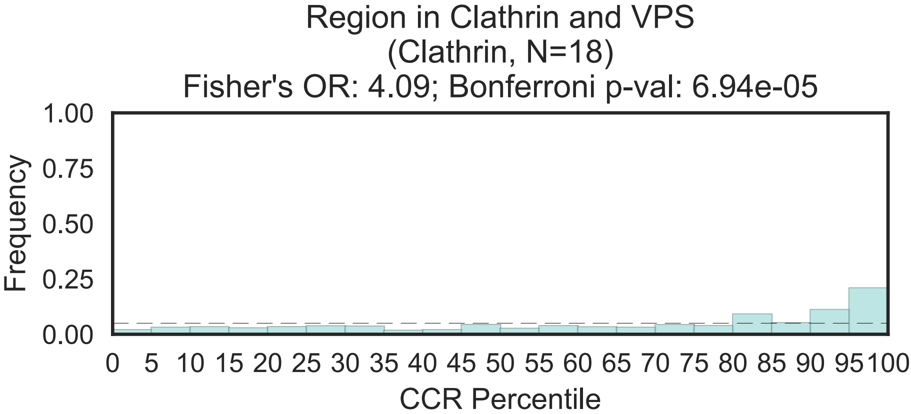

N-terminal domain of CBF1 interacting co-repressor CIR
(Cir_N, N=3)
Fisher's OR: 4.5; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

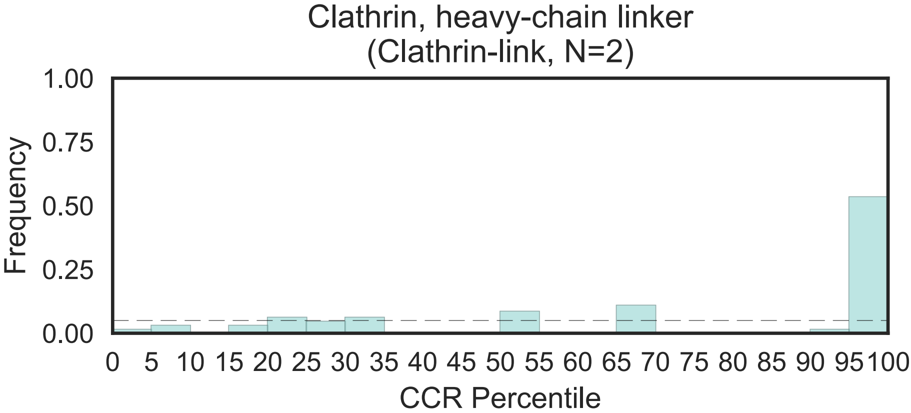

Citrate transporter
(CitMHS, N=11)
Fisher's OR: 0.305; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

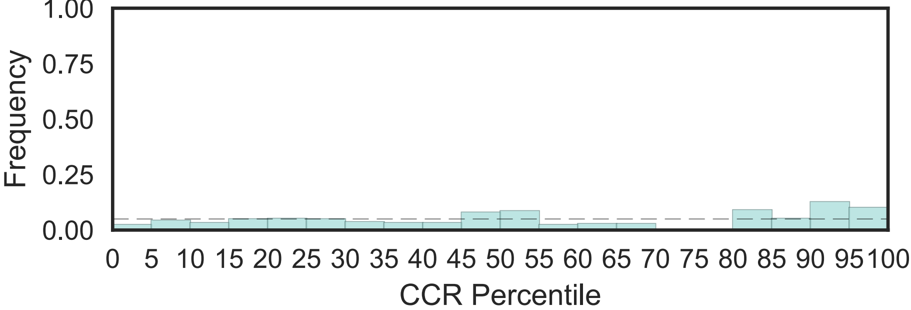

ATP citrate lyase citrate-binding
(Citrate_bind, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Citrate synthase, C-terminal domain
(Citrate_synt, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

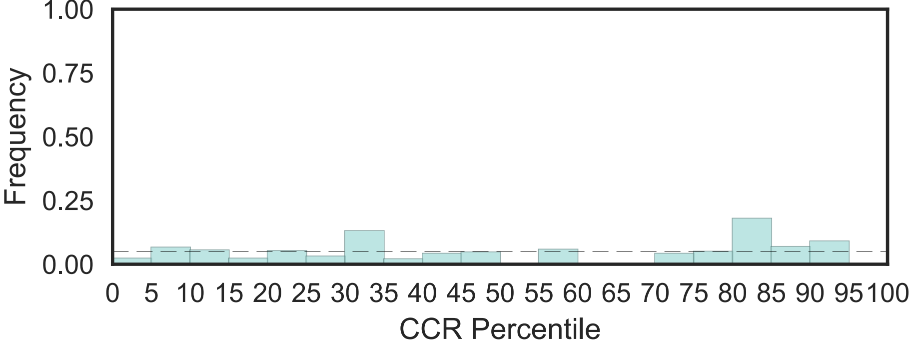

Clathrin adaptor complex small chain
(Clat_adaptor_s, N=17)
Fisher's OR: 1.68; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Region in Clathrin and VPS
(Clathrin, N=18)
Fisher's OR: 4.09; Bonferroni p-val: 6.94e-05
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

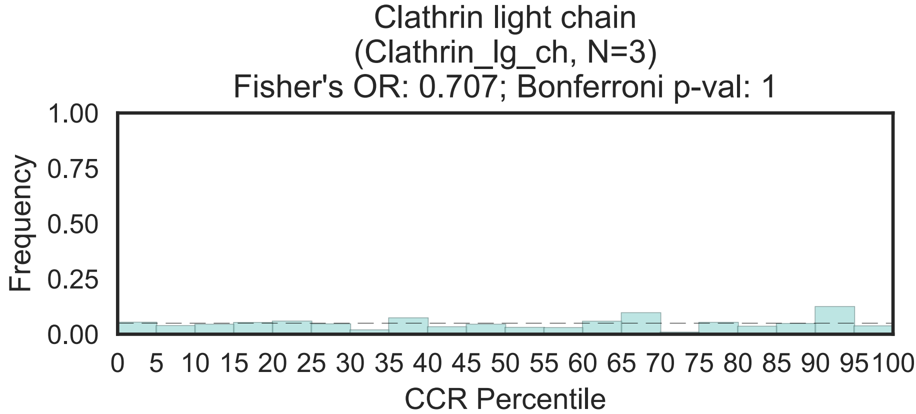

Clathrin, heavy-chain linker
(Clathrin-link, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

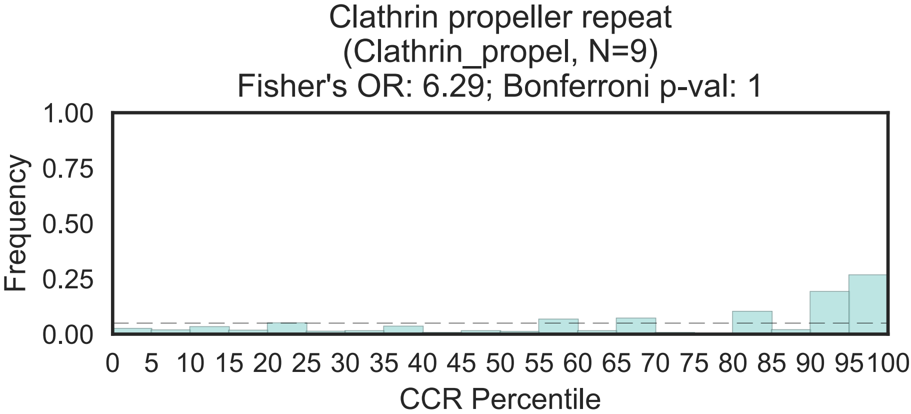


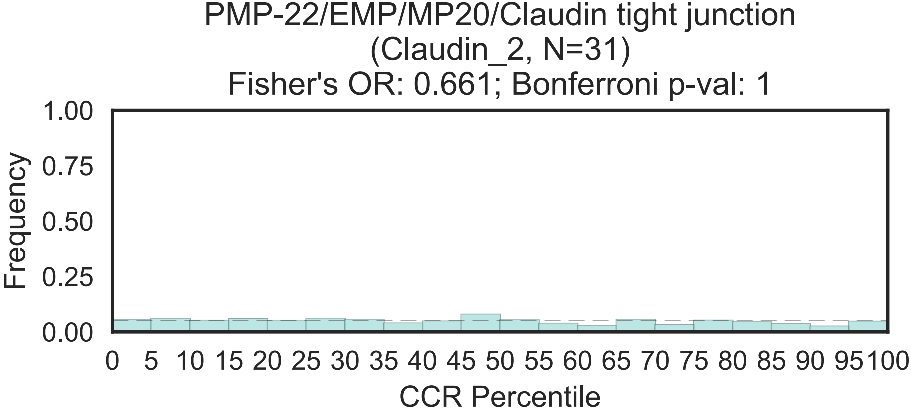
Clathrin-H-link
(Clathrin_H_link, N=3)
Fisher's OR: 1.64; Bonferroni p-val: 1

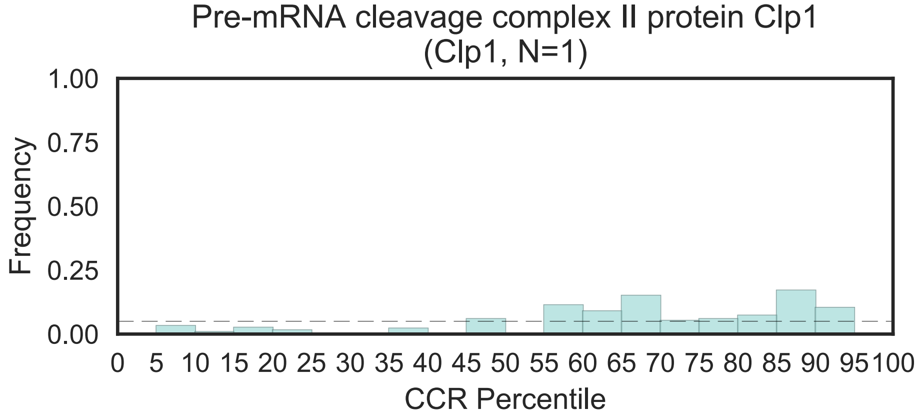


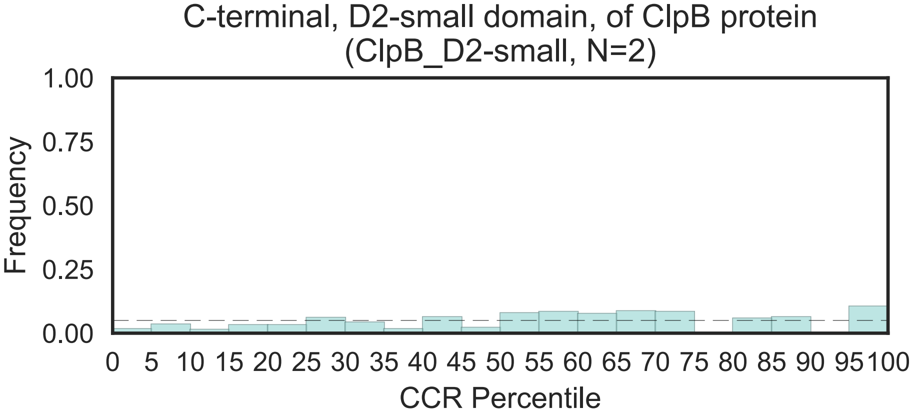
Clathrin-binding box of Aftiphilin, vesicle trafficking
(Clathrin_bdg, N=2)

Clathrin light chain
(Clathrin_lg_ch, N=3)
Fisher's OR: 0.707; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

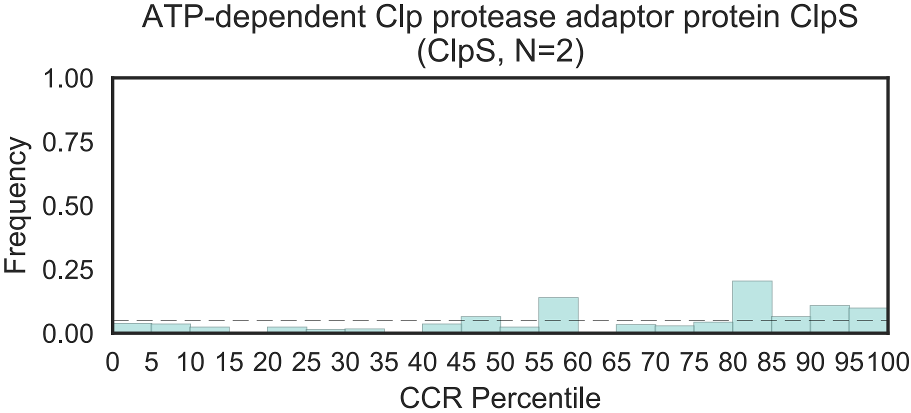

Clathrin propeller repeat
(Clathrin_propel, N=9)
Fisher's OR: 6.29; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

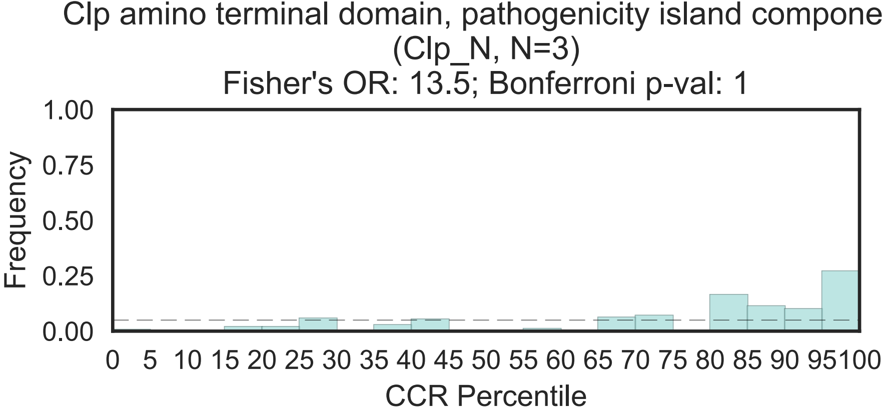

PMP-22/EMP/MP20/Claudin tight junction
(Claudin_2, N=31)
Fisher's OR: 0.661; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Pre-mRNA cleavage complex II protein Clp1
(Clp1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

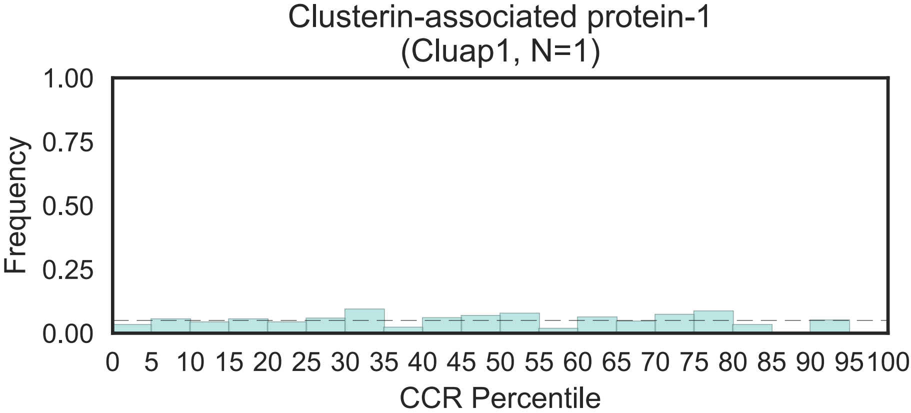


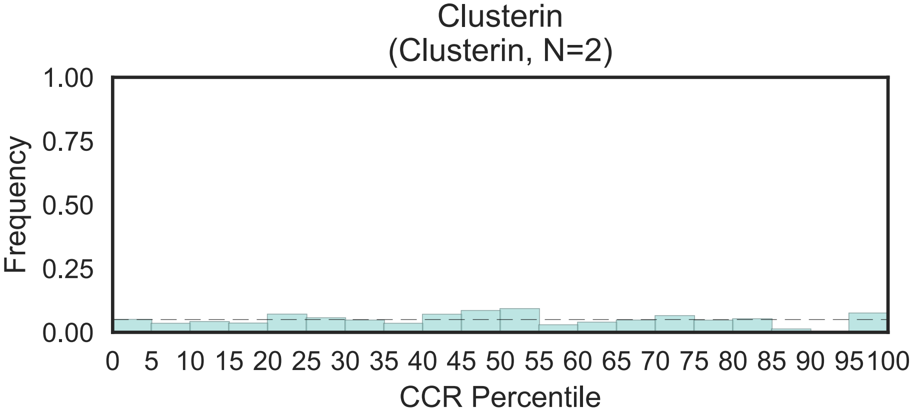
C-terminal, D2-small domain, of ClpB protein
(ClpB_D2-small, N=2)

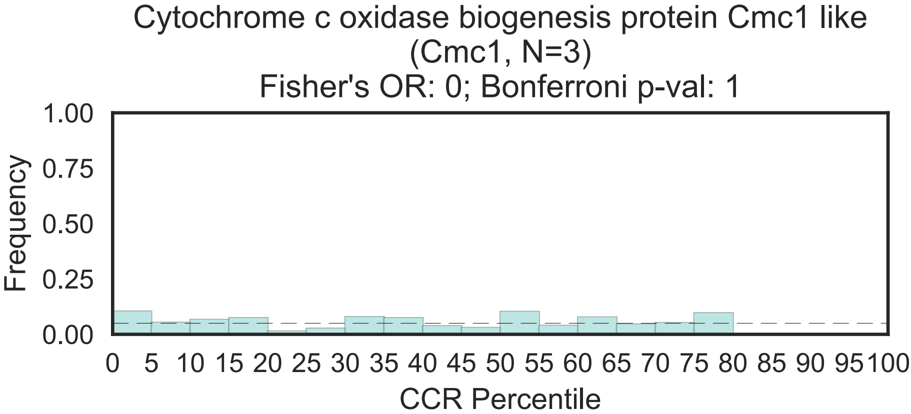

ATP-dependent Clp protease adaptor protein ClpS
(ClpS, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



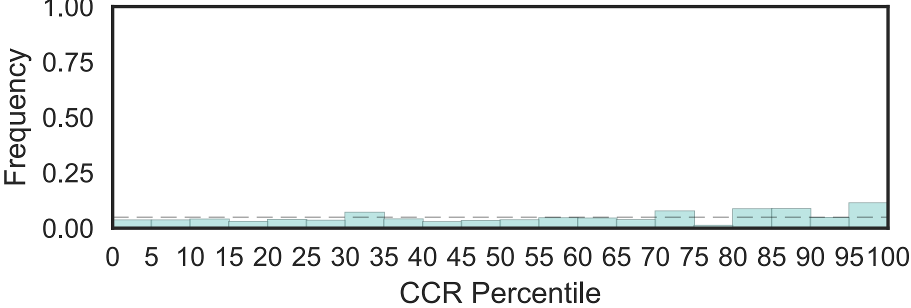
Clp amino terminal domain, pathogenicity island component
(Clp_N, N=3)
Fisher's OR: 13.5; Bonferroni p-val: 1

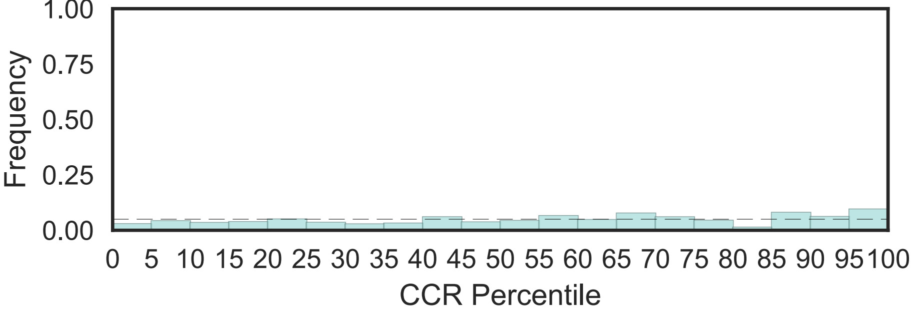

Clusterin-associated protein-1
(Cluap1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Clusterin
(Clusterin, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

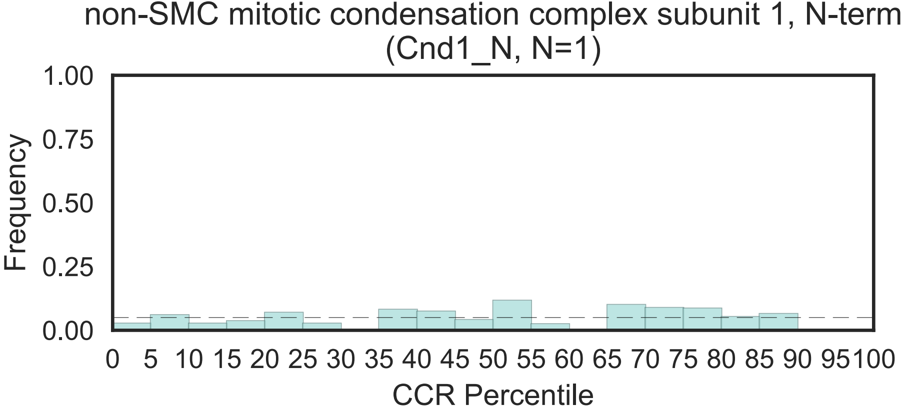

Cytochrome c oxidase biogenesis protein Cmc1 like
(Cmc1, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

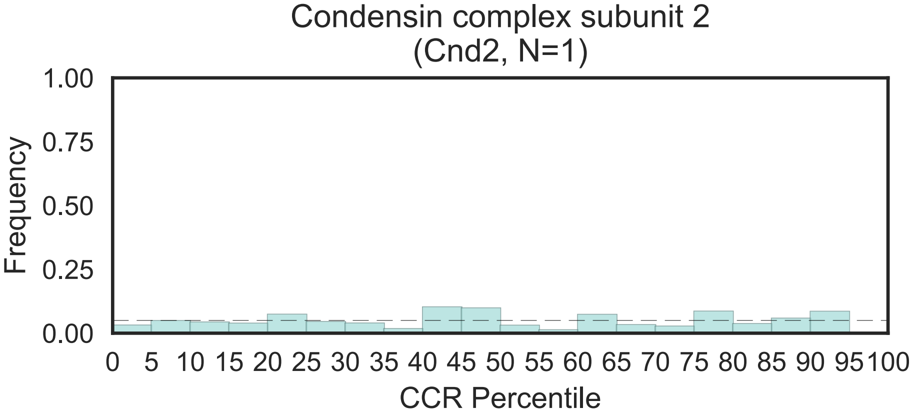
C-myb, C-terminal
(Cmyb_C, N=3)
Fisher's OR: 2.24; Bonferroni p-val: 1

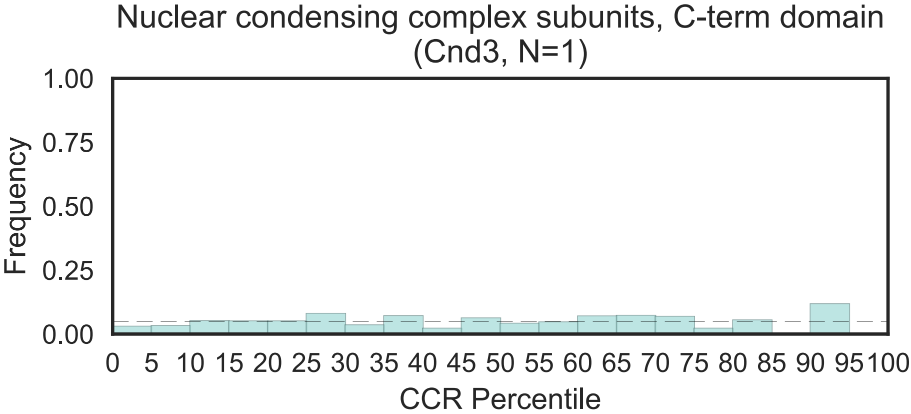


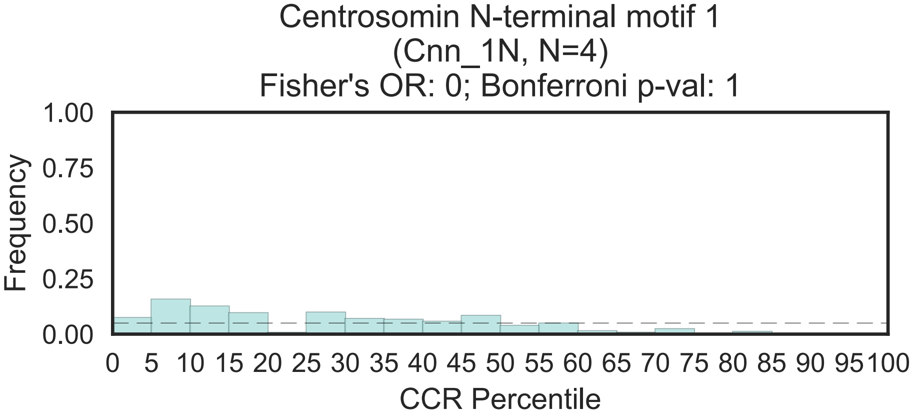


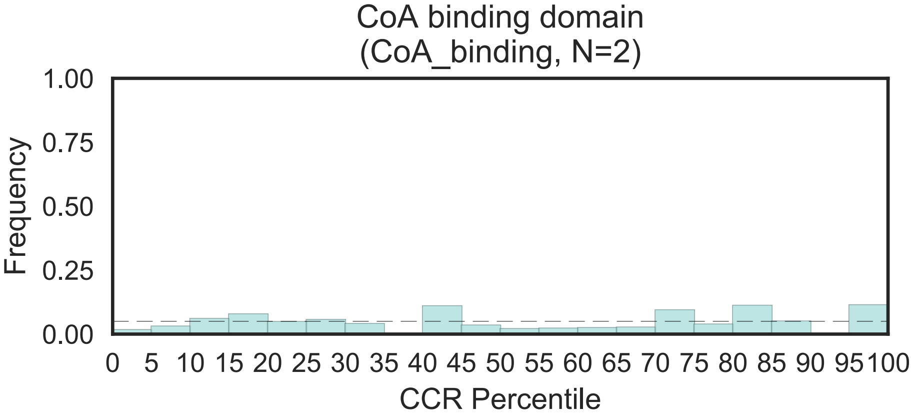
non-SMC mitotic condensation complex subunit 1
(Cnd1, N=12)
Fisher's OR: 1.78; Bonferroni p-val: 1

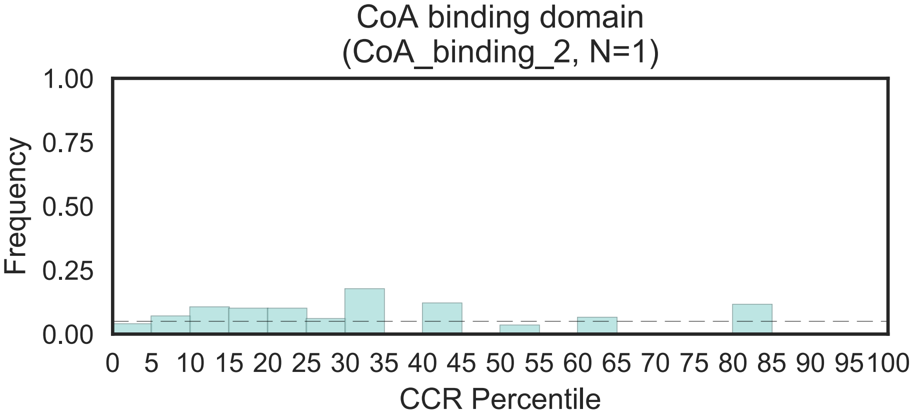

non-SMC mitotic condensation complex subunit 1, N-term
(Cnd1_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Condensin complex subunit 2
(Cnd2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

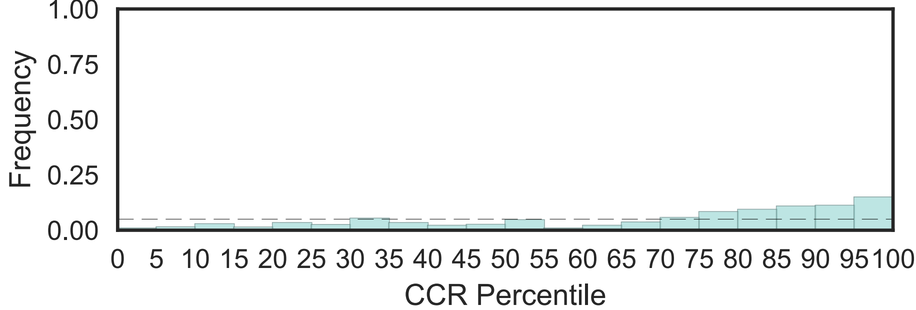

Nuclear condensing complex subunits, C-term domain
(Cnd3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

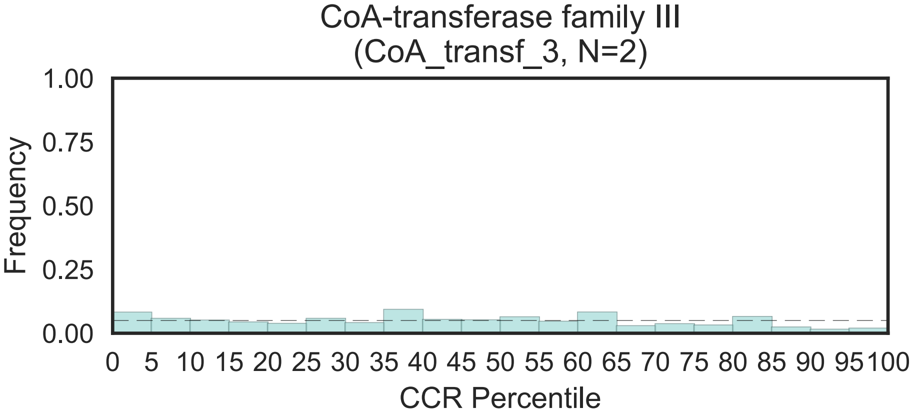

Centrosomin N-terminal motif 1
(Cnn_1N, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

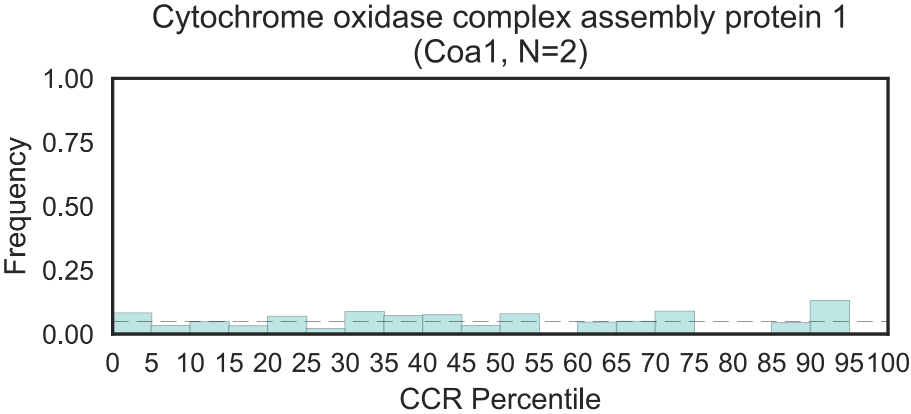

CoA binding domain
(CoA_binding, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

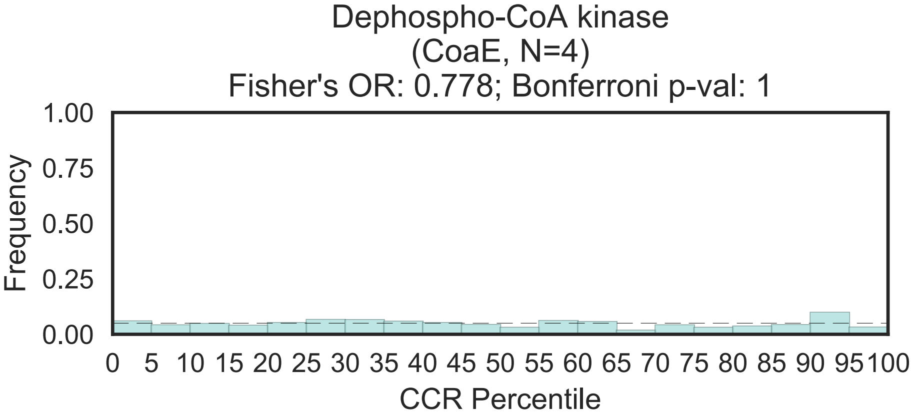

CoA binding domain
(CoA_binding_2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

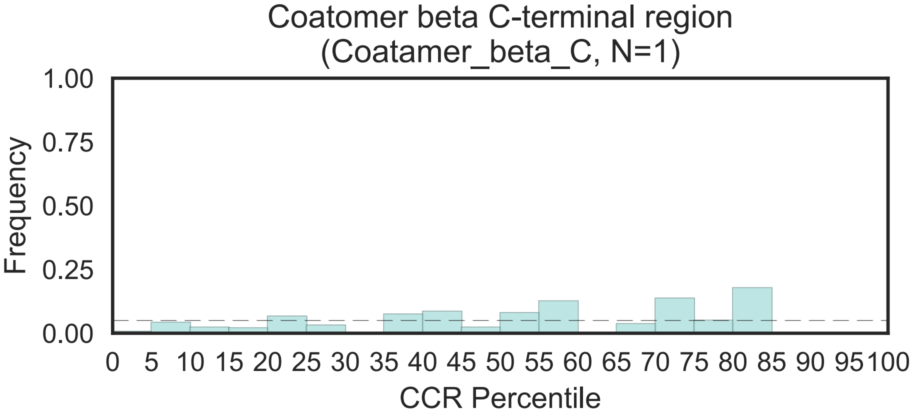
Coenzyme A transferase
(CoA_trans, N=4)
Fisher's OR: 4.24; Bonferroni p-val: 1

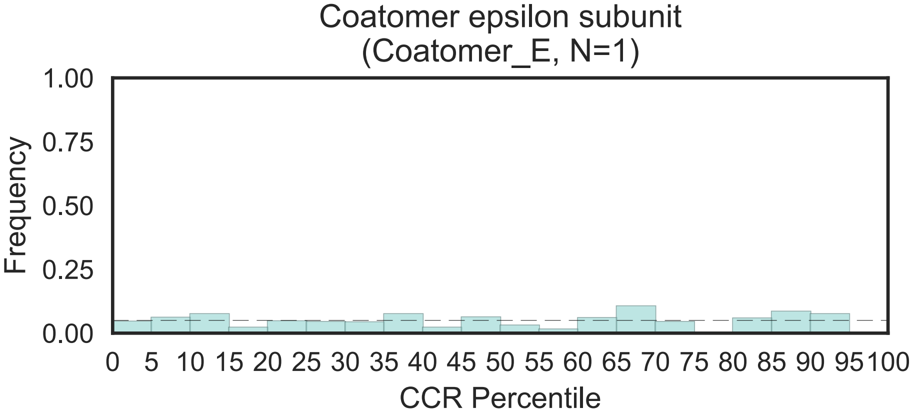


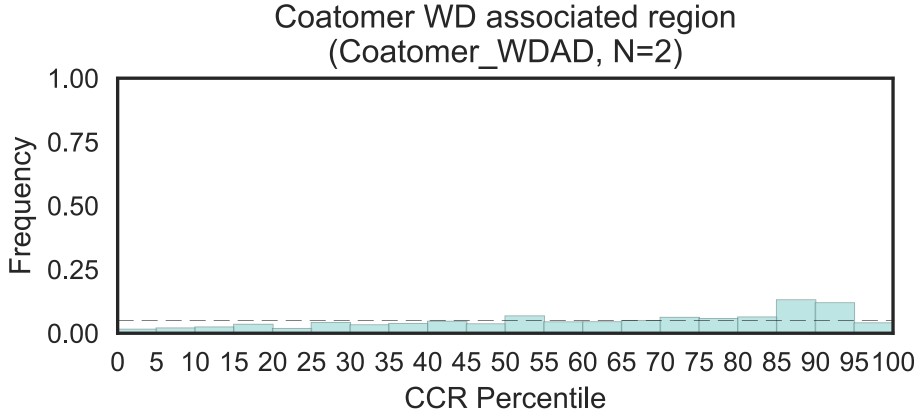

CoA-transferase family III
(CoA_transf_3, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

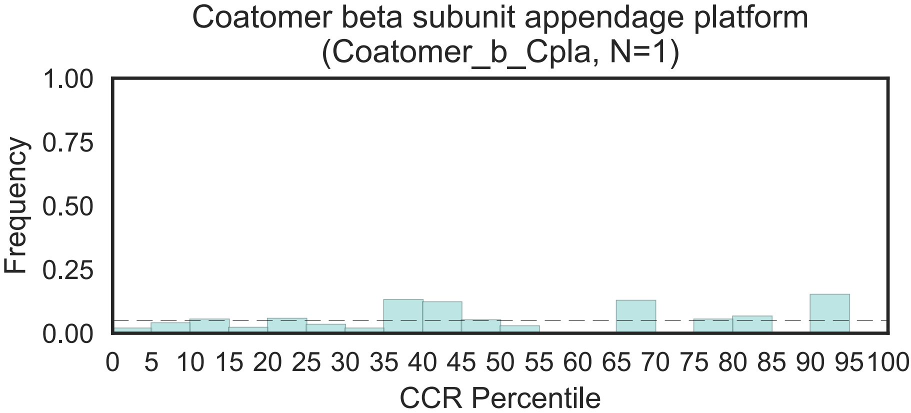

Cytochrome oxidase complex assembly protein 1
(Coa1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

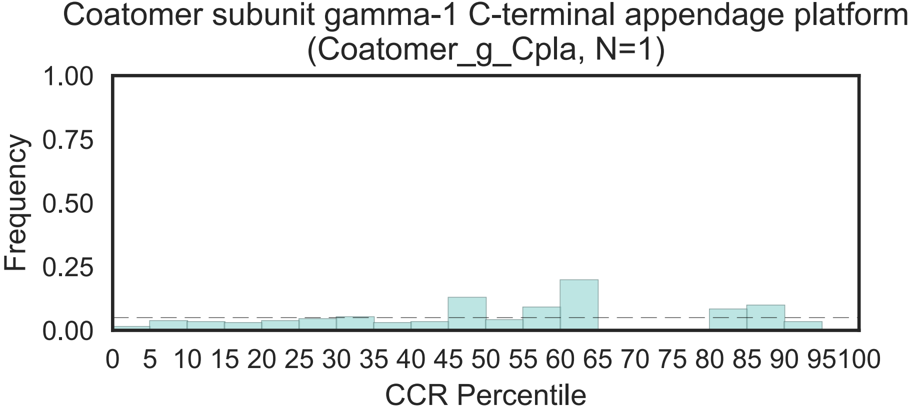

Dephospho-CoA kinase
(CoaE, N=4)
Fisher's OR: 0.778; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

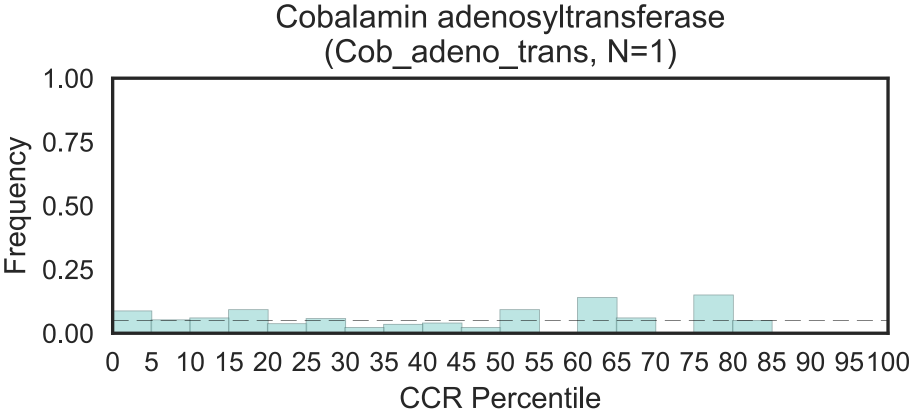

Coatomer beta C-terminal region
(Coatamer_beta_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

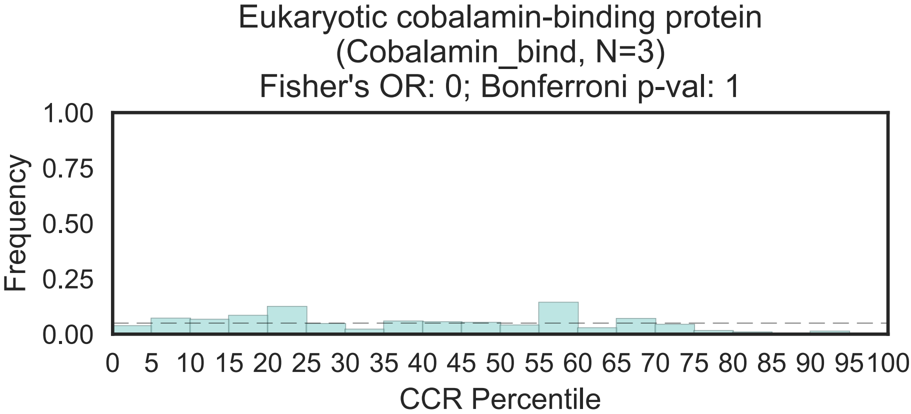

Coatomer epsilon subunit
(Coatomer_E, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Coatomer WD associated region
(Coatomer_WDAD, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

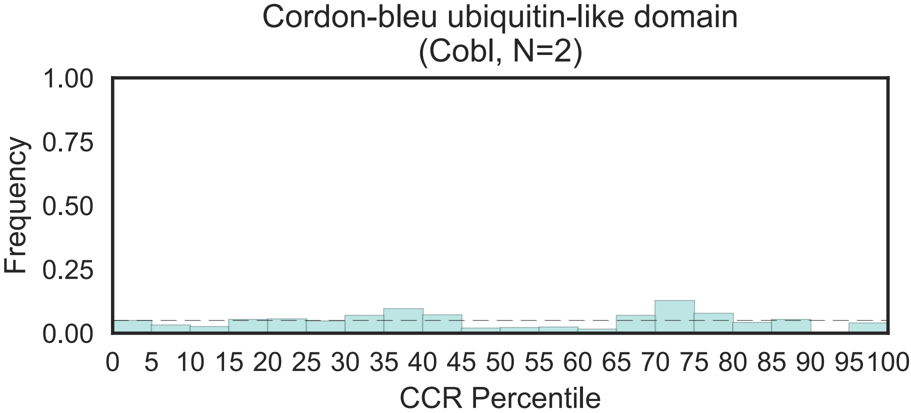

Coatomer beta subunit appendage platform
(Coatomer_b_Cpla, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

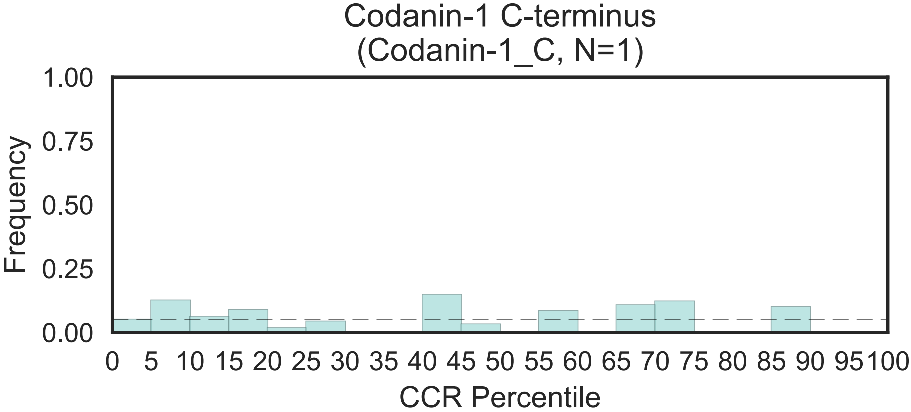

Coatomer subunit gamma-1 C-terminal appendage platform
(Coatomer_g_Cpla, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

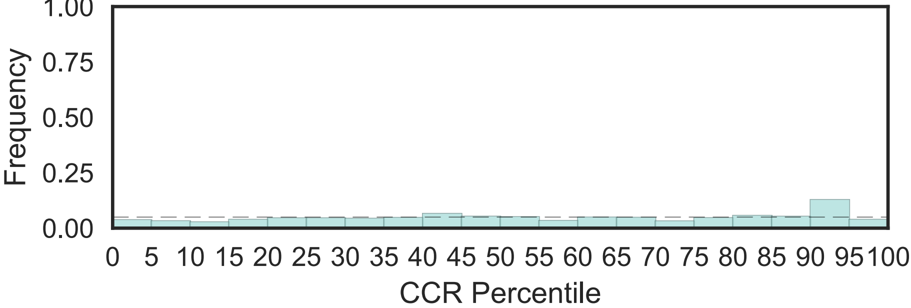

Cobalamin adenosyltransferase
(Cob_adeno_trans, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



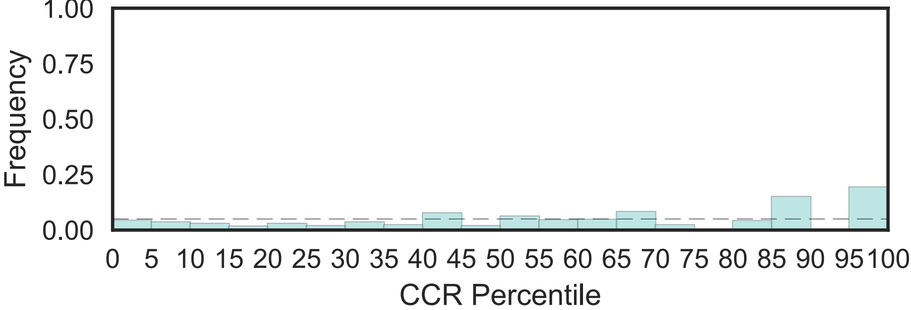
Eukaryotic cobalamin-binding protein
(Cobalamin_bind, N=3)
Fisher's OR: 0; Bonferroni p-val: 1


Cordon-bleu ubiquitin-like domain
(Cobl, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

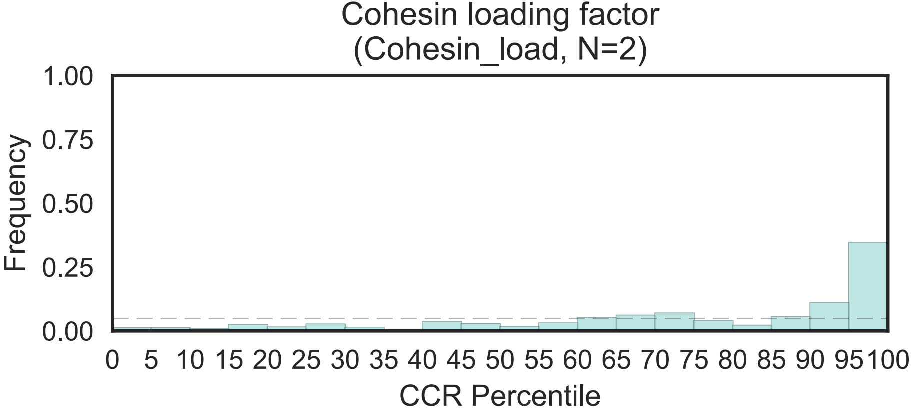

Codanin-1 C-terminus
(Codanin-1_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



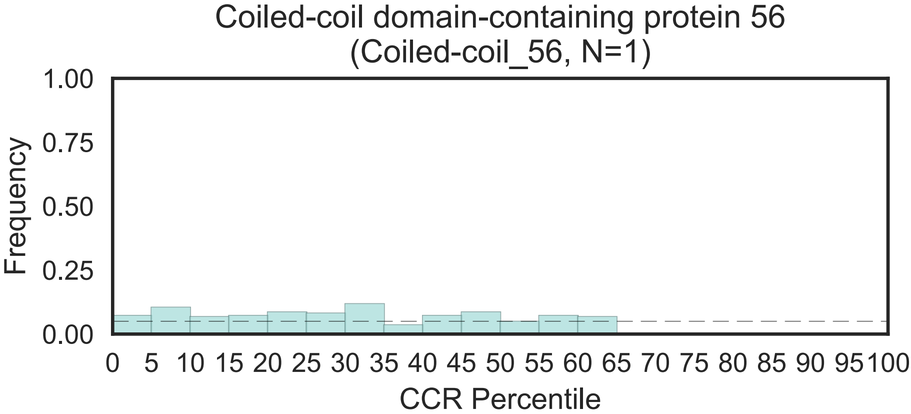
Cofilin/tropomyosin-type actin-binding protein
(Cofilin_ADF, N=13)
Fisher's OR: 0.707; Bonferroni p-val: 1

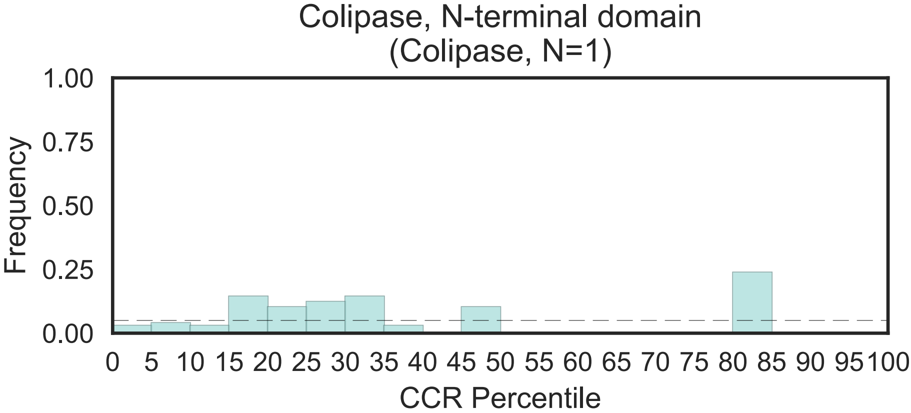


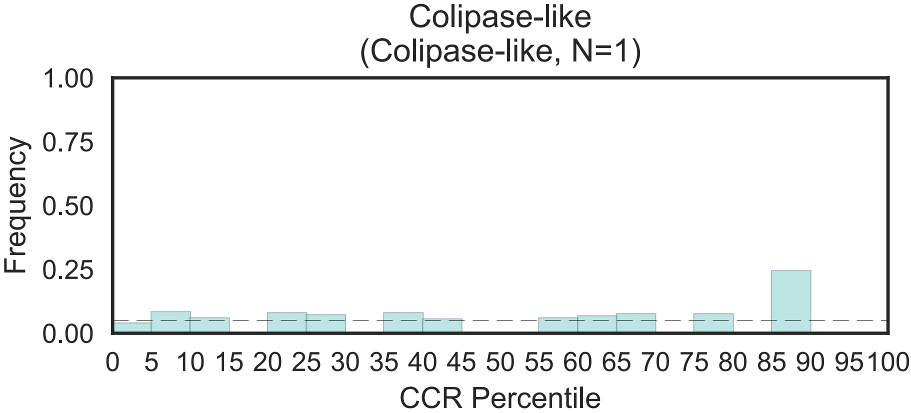
HEAT repeat associated with sister chromatid cohesion
(Cohesin_HEAT, N=7)
Fisher's OR: 3.86; Bonferroni p-val: 1

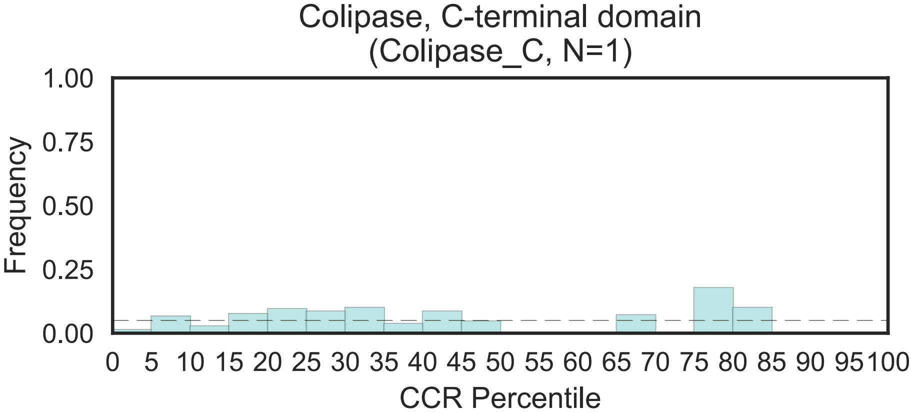


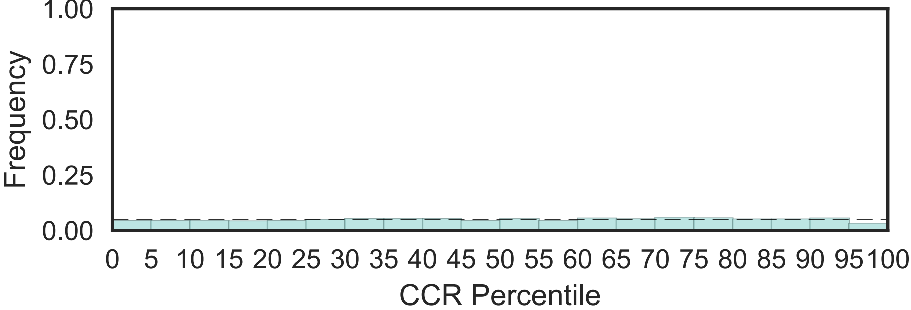
Cohesin loading factor
(Cohesin_load, N=2)


Coiled-coil domain-containing protein 56
(Coiled-coil_56, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

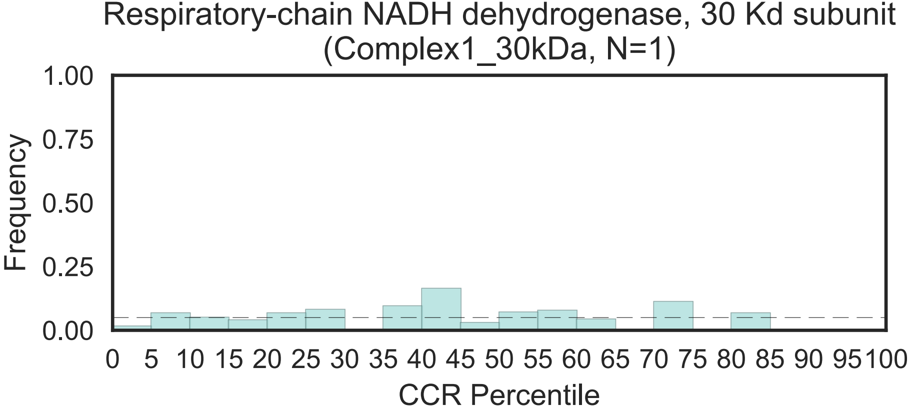

Colipase, N-terminal domain
(Colipase, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Colipase-like
(Colipase-like, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

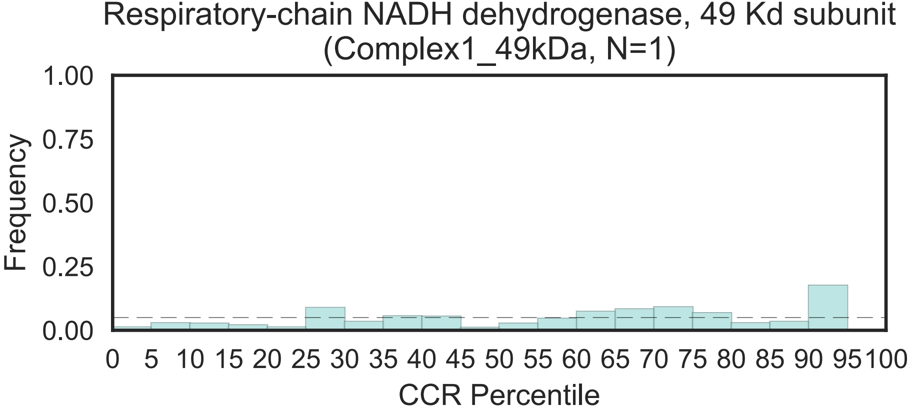

Colipase, C-terminal domain
(Colipase_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

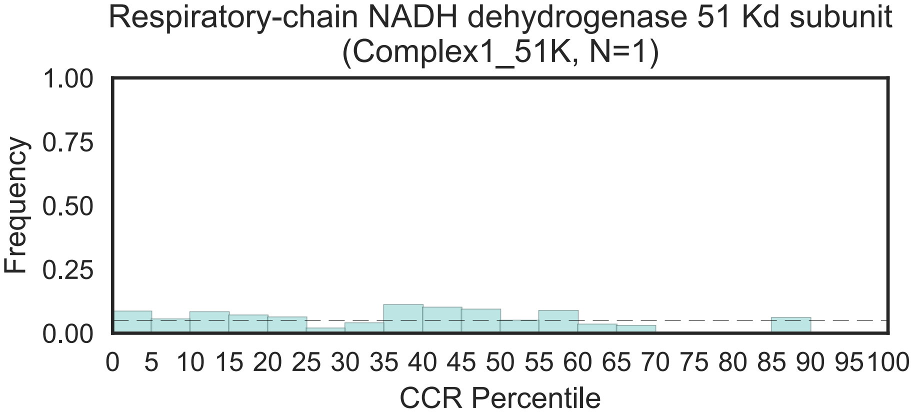


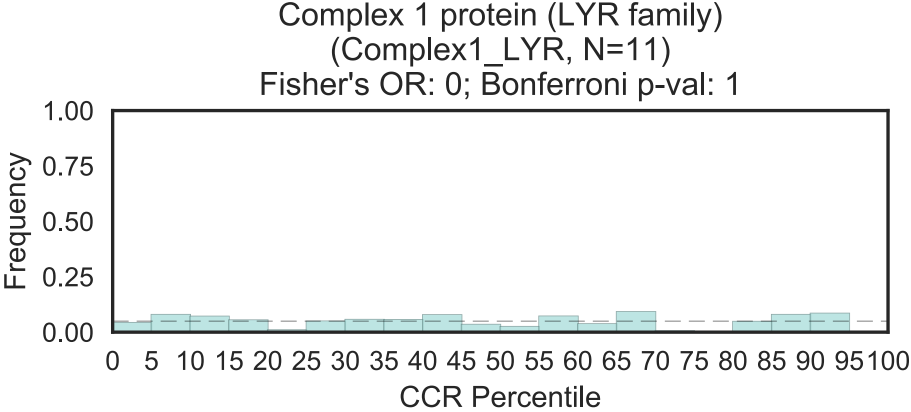
Collagen triple helix repeat (20 copies)
(Collagen, N=291)
Fisher's OR: 0.52; Bonferroni p-val: 0.279

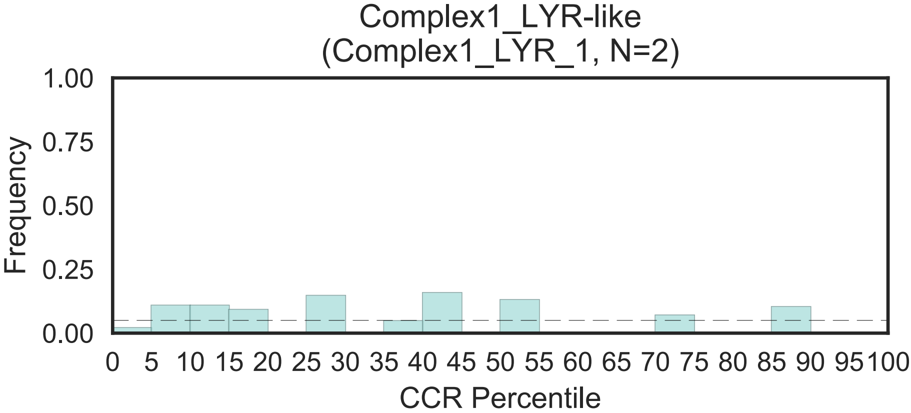


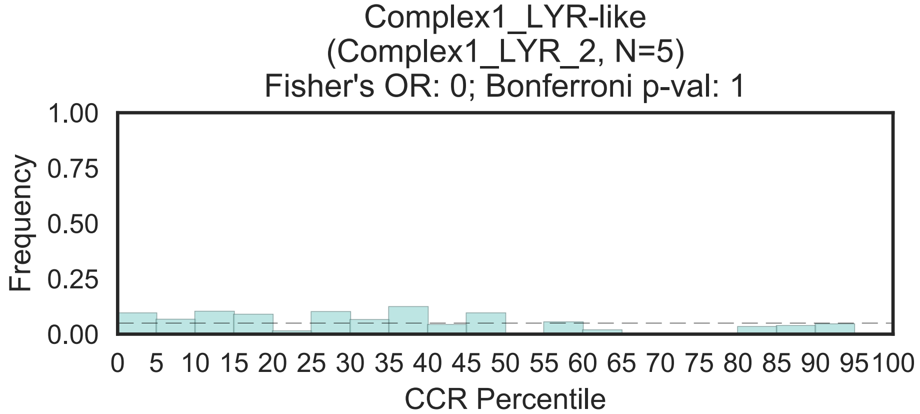
Respiratory-chain NADH dehydrogenase, 30 Kd subunit (Complex1_30kDa, N=1)

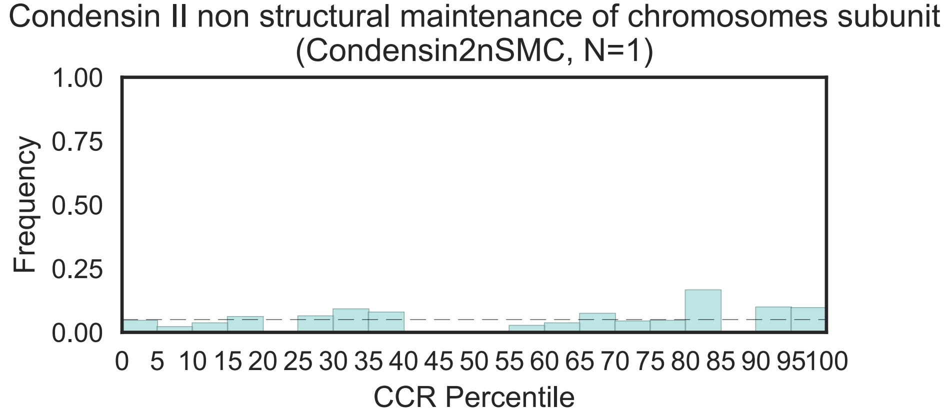

Respiratory-chain NADH dehydrogenase, 49 Kd subunit
(Complex1_49kDa, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

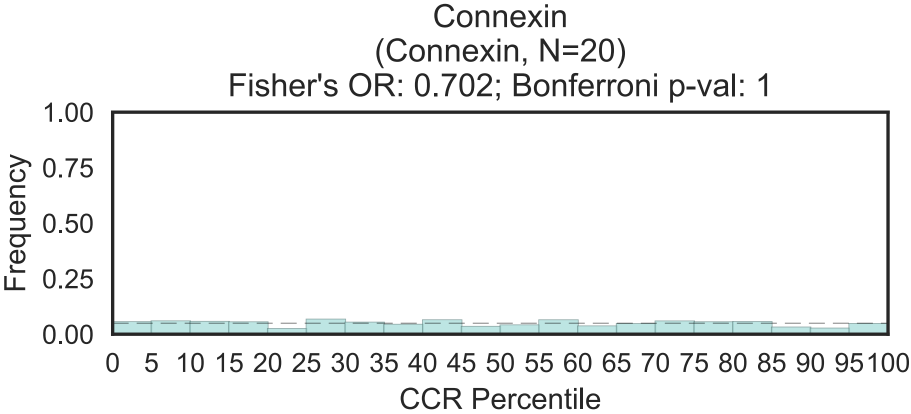

Respiratory-chain NADH dehydrogenase 51 Kd subunit
(Complex1_51K, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

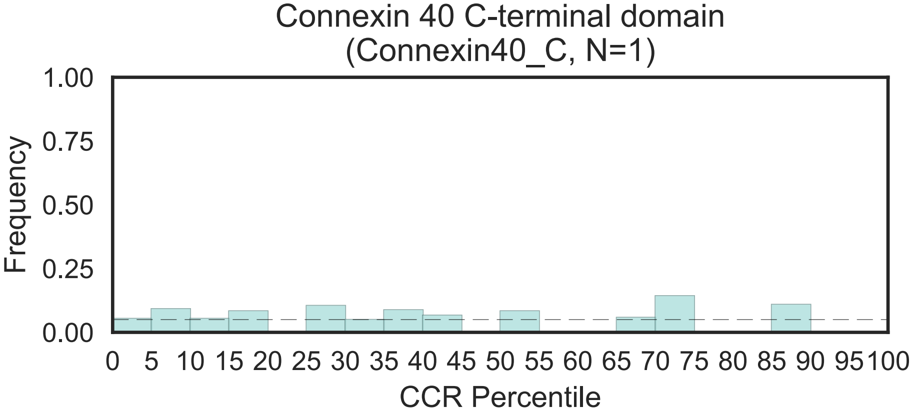

Complex 1 protein (LYR family)
(Complex1_LYR, N=11)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

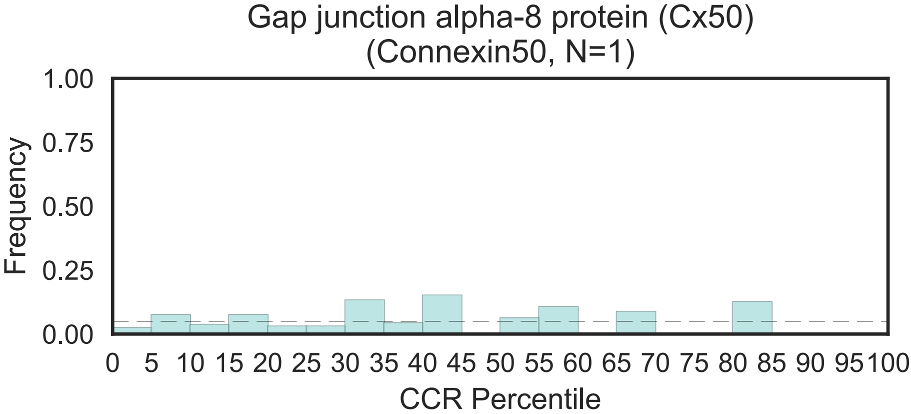

Complex1_LYR-like
(Complex1_LYR_1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

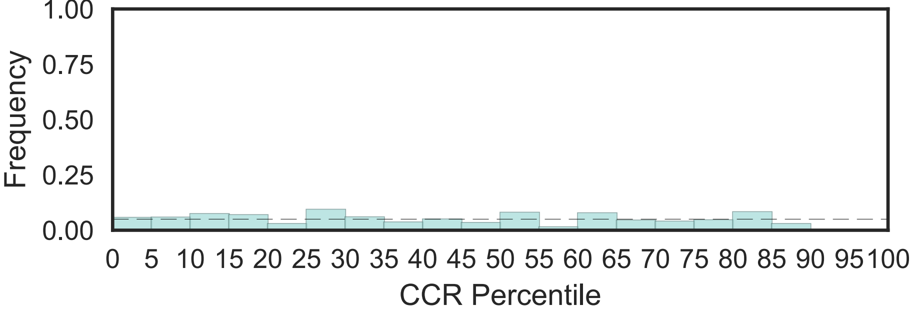

Complex1_LYR-like
(Complex1_LYR_2, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Condensin II non structural maintenance of chromosomes subunit
(Condensin2nSMC, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

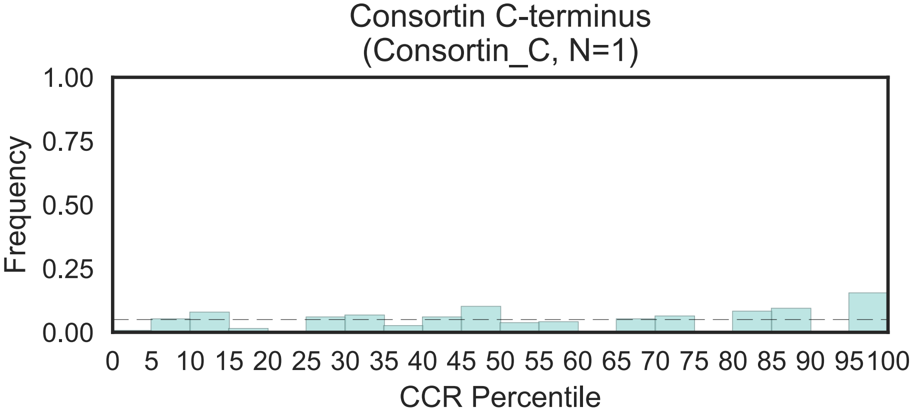

Connexin
(Connexin, N=20)
Fisher's OR: 0.702; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

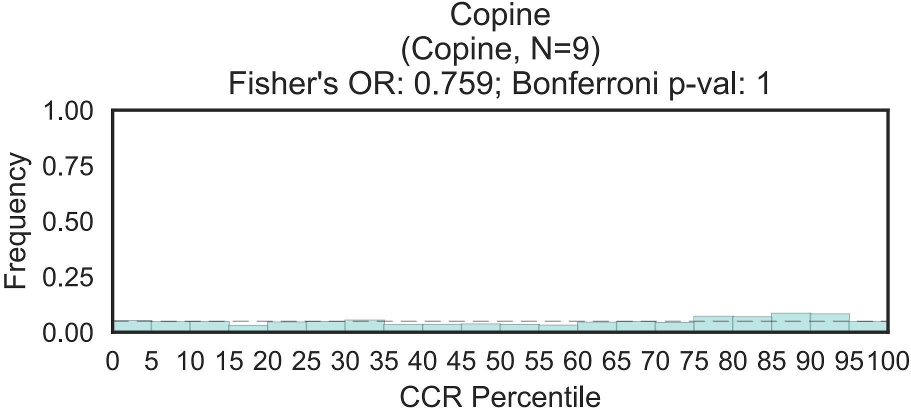

Connexin 40 C-terminal domain
(Connexin40_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

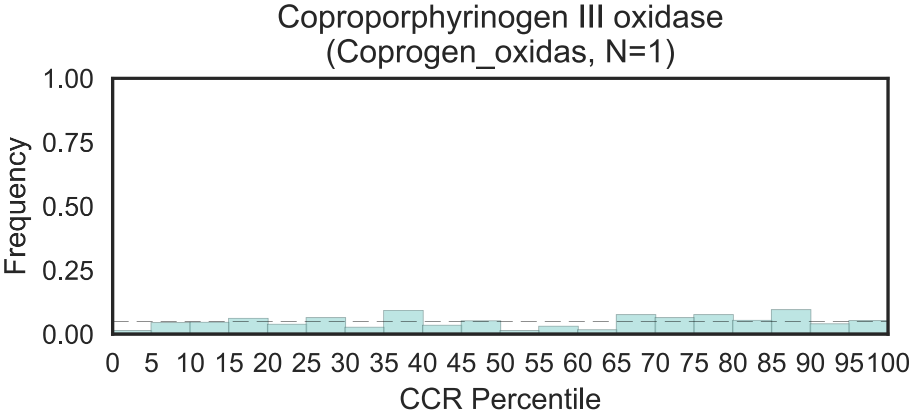

Gap junction alpha-8 protein (Cx50)
(Connexin50, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

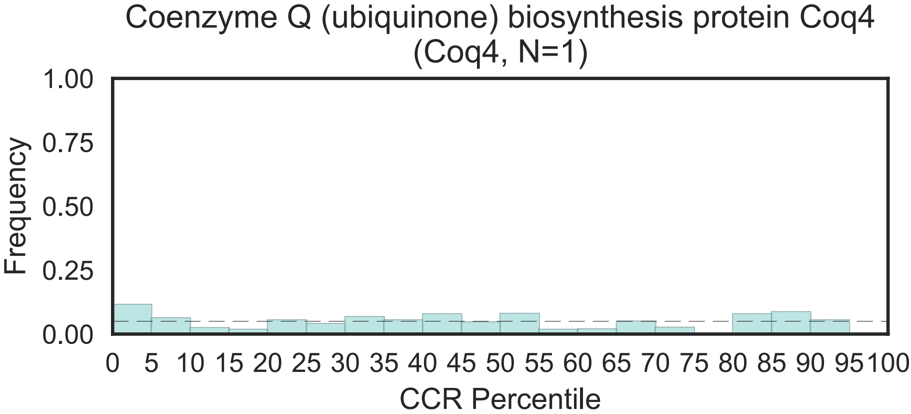


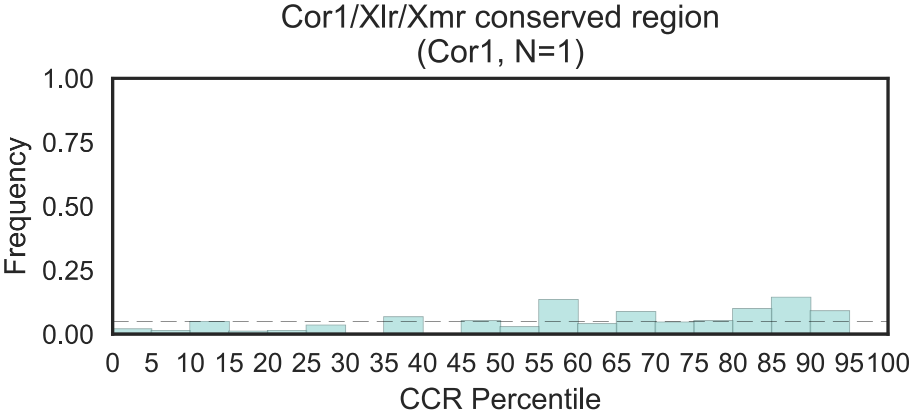
Conserved hypothetical protein 95
(Cons_hypoth95, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

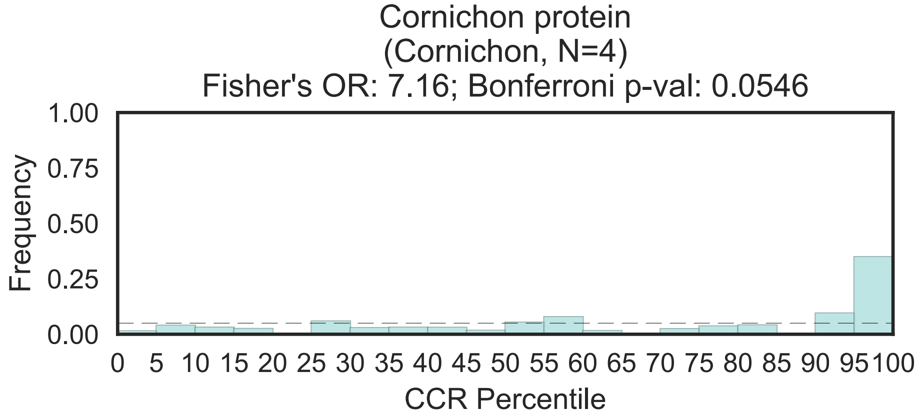

Consortin C-terminus
(Consortin_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

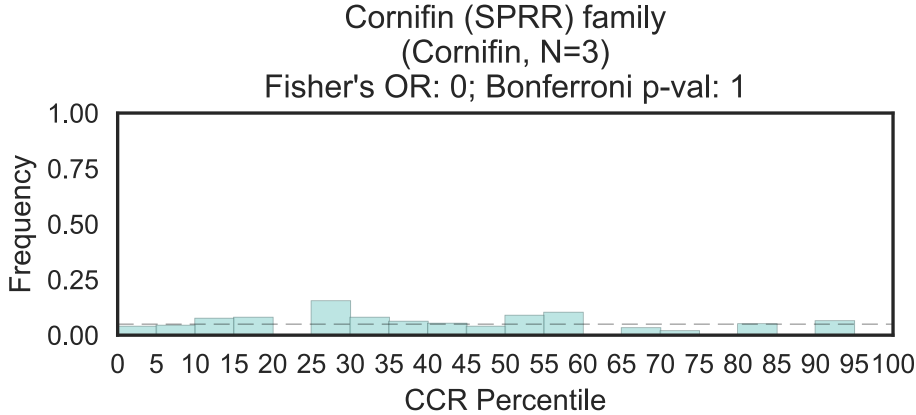

Copine
(Copine, N=9)
Fisher's OR: 0.759; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

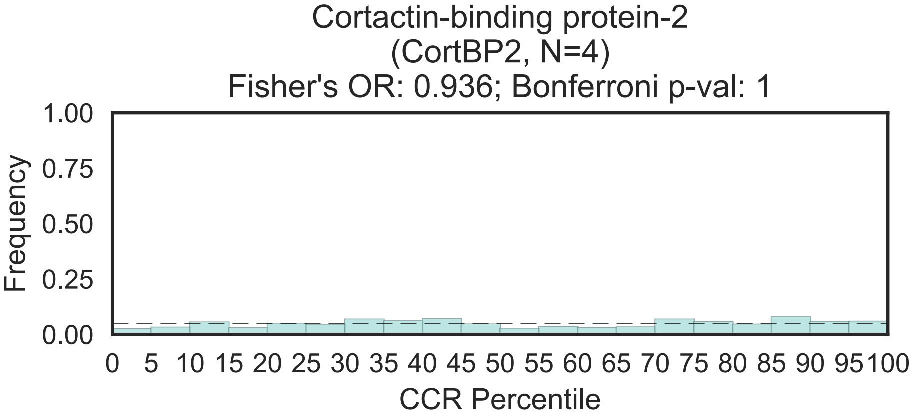

Coproporphyrinogen III oxidase
(Coprogen_oxidas, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

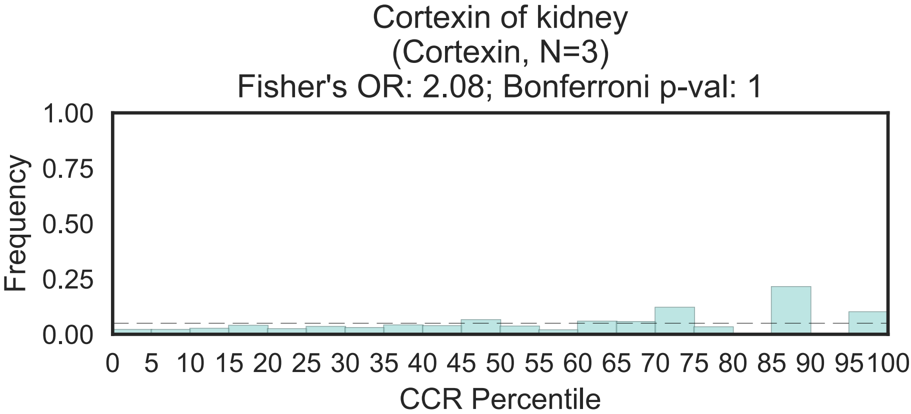

Coenzyme Q (ubiquinone) biosynthesis protein Coq4
(Coq4, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

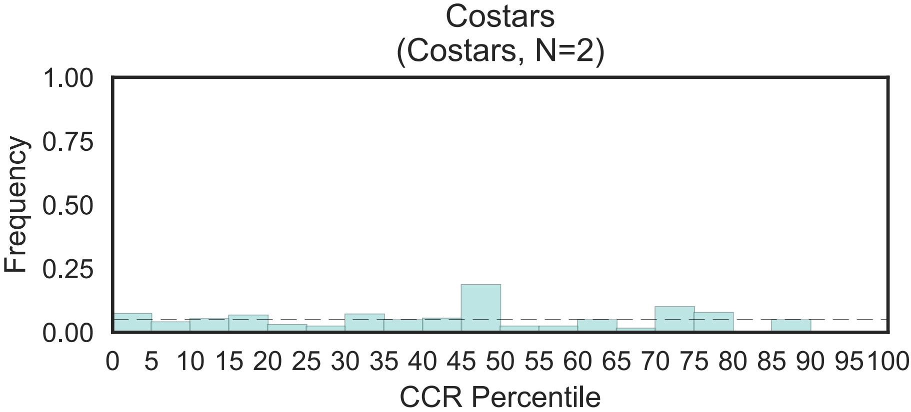

Cor1/Xlr/Xmr conserved region
(Cor1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

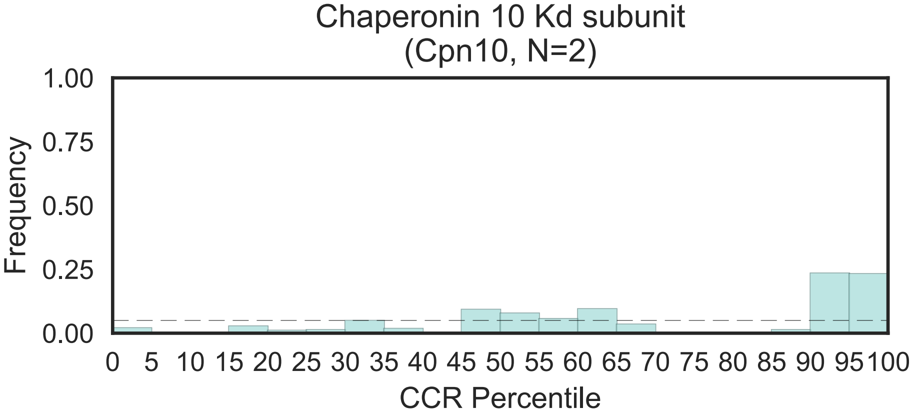

Cornichon protein
(Cornichon, N=4)
Fisher's OR: 7.16; Bonferroni p-val: 0.0546
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

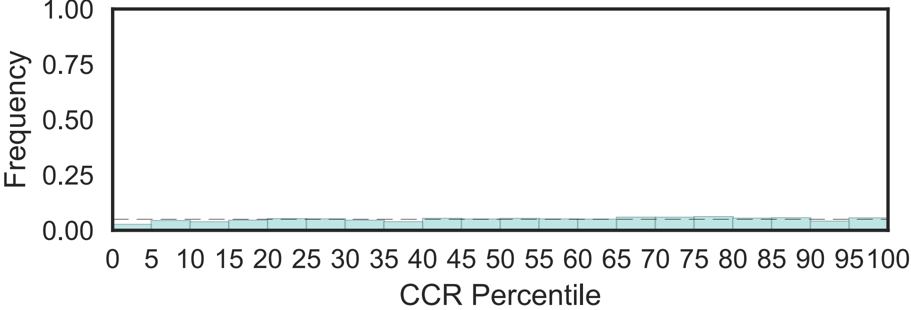

Cornifin (SPRR) family
(Cornifin, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Cortactin-binding protein-2
(CortBP2, N=4)
Fisher's OR: 0.936; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

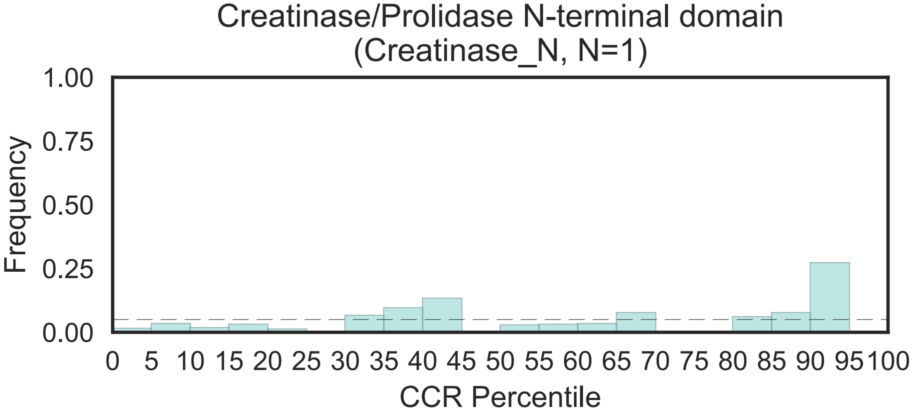

Cortexin of kidney
(Cortexin, N=3)
Fisher's OR: 2.08; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

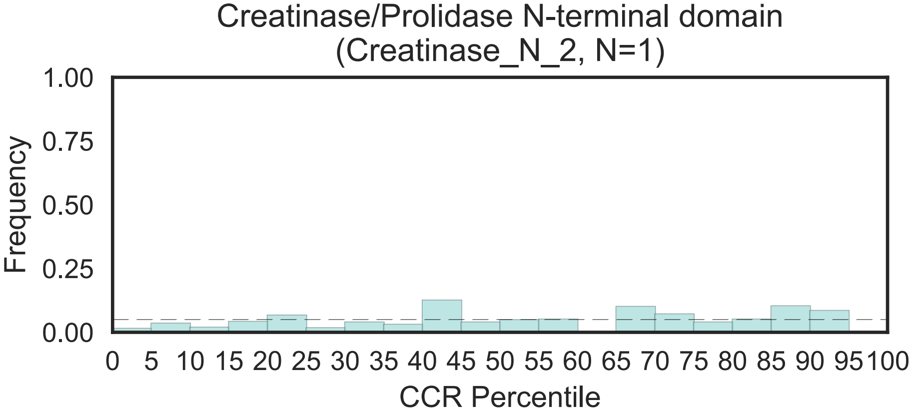

Costars
(Costars, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

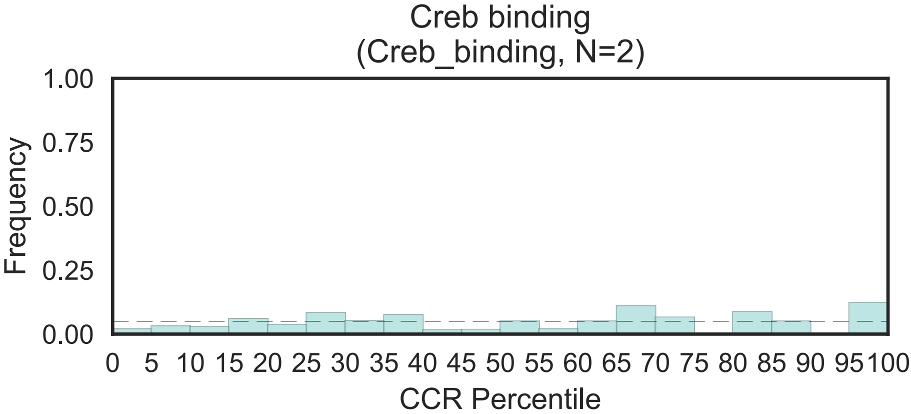

Chaperonin 10 Kd subunit
(Cpn10, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

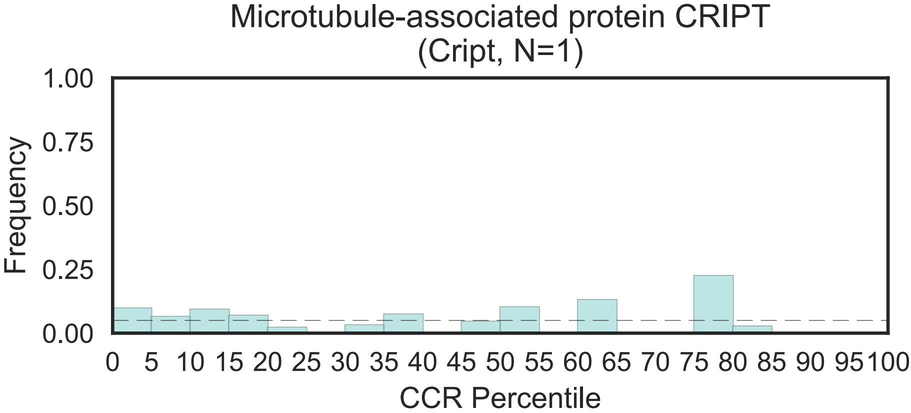


TCP-1/cpn60 chaperonin family
(Cpn60_TCP1, N=17)
Fisher's OR: 0.894; Bonferroni p-val: 1

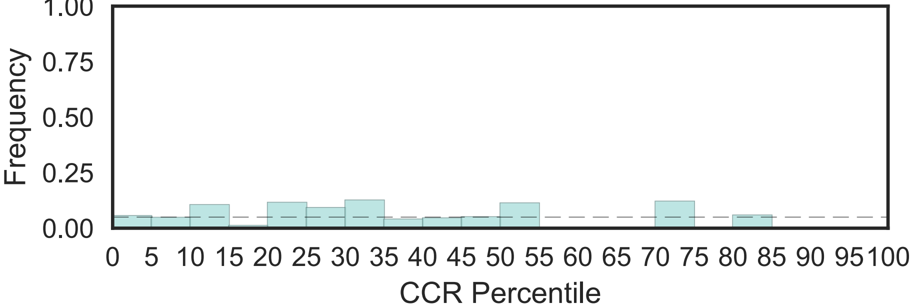

Creatinase/Prolidase N-terminal domain
(Creatinase_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

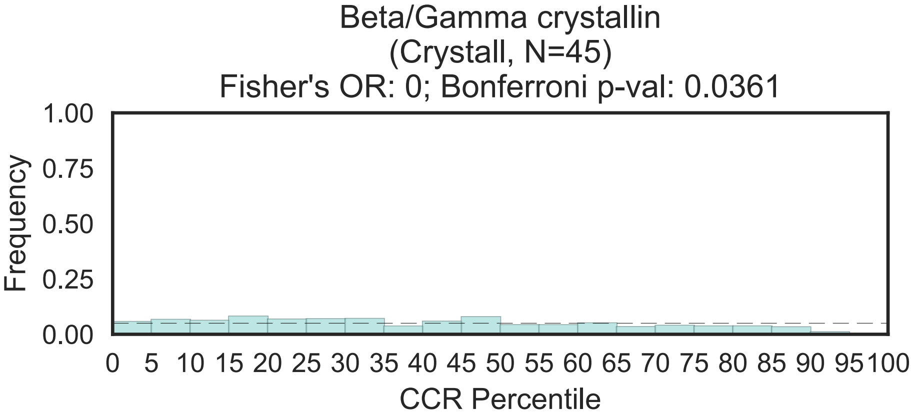

Creatinase/Prolidase N-terminal domain
(Creatinase_N_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

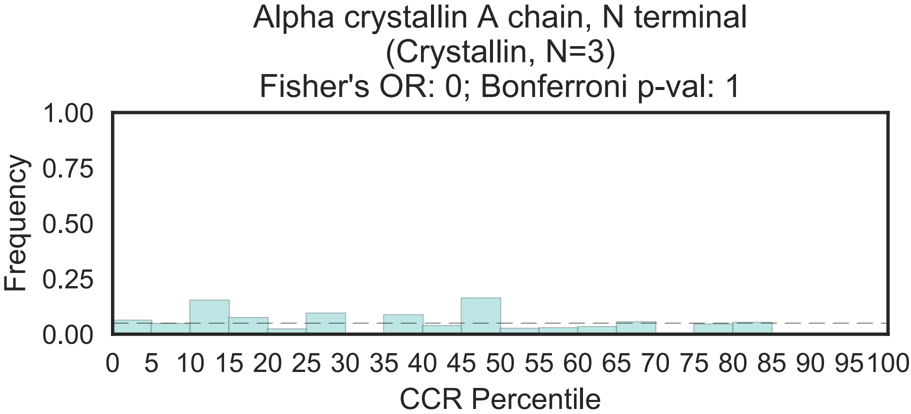

Creb binding
(Creb_binding, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

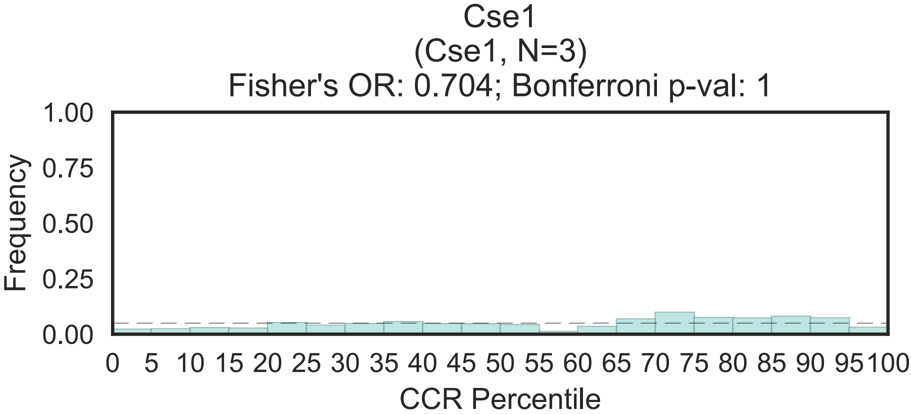

Microtubule-associated protein CRIPT
(Cript, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

Crisp
(Crisp, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

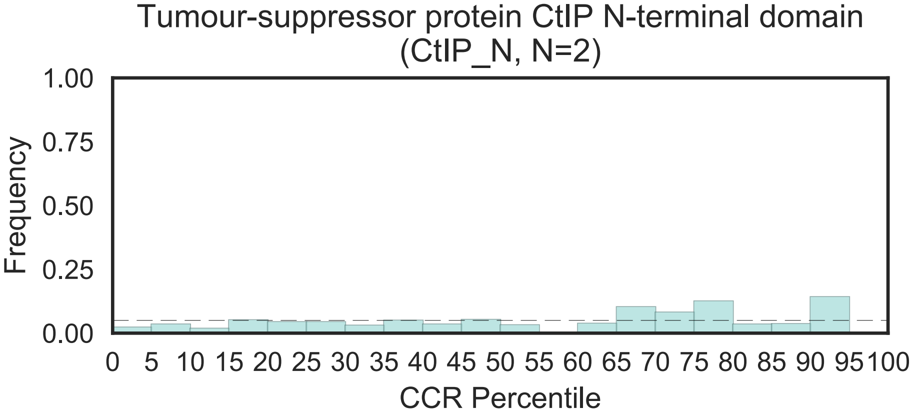


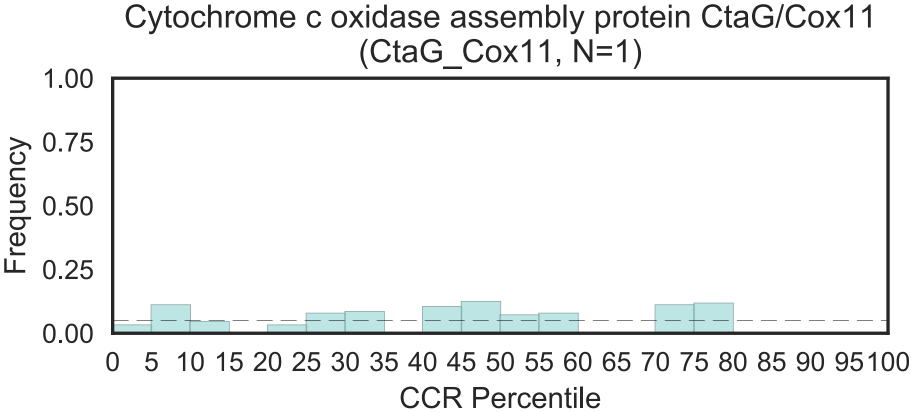

Beta/Gamma crystallin
(Crystall, N=45)
Fisher's OR: 0; Bonferroni p-val: 0.0361
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

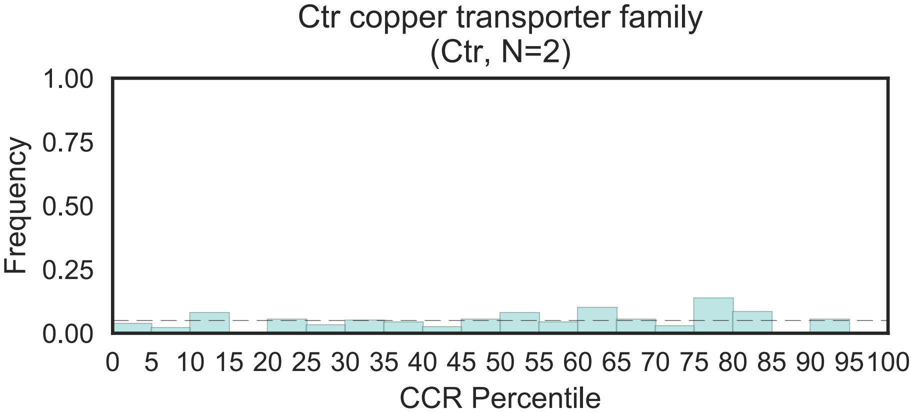

Alpha crystallin A chain, N terminal
(Crystallin, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

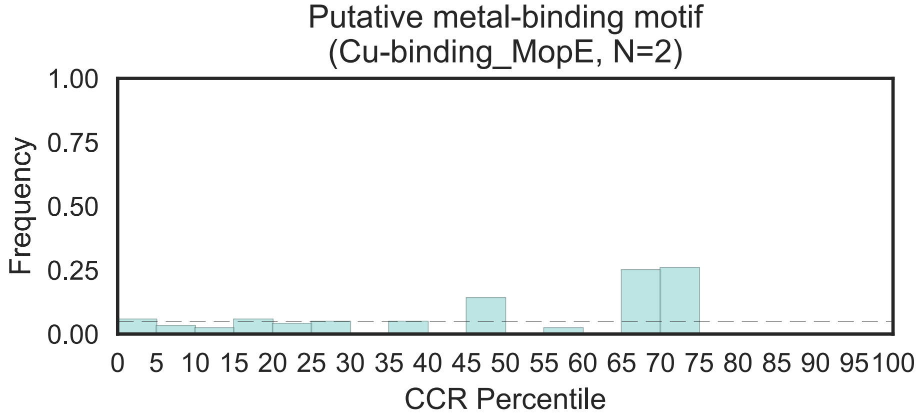


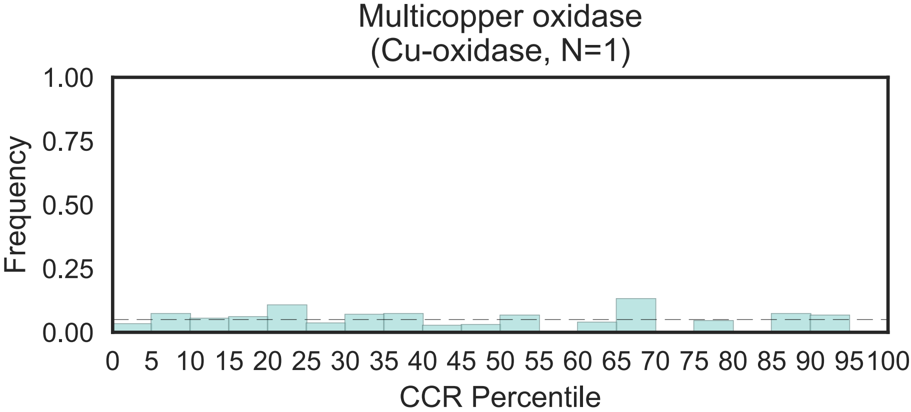
Cse1
(Cse1, N=3)
Fisher's OR: 0.704; Bonferroni p-val: 1


Tumour-suppressor protein CtIP N-terminal domain
(CtIP_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

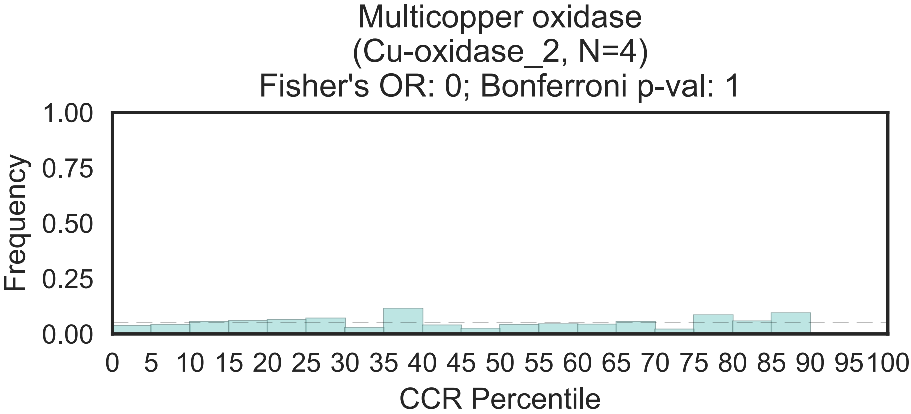

Cytochrome c oxidase assembly protein CtaG/Cox11
(CtaG_Cox11, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

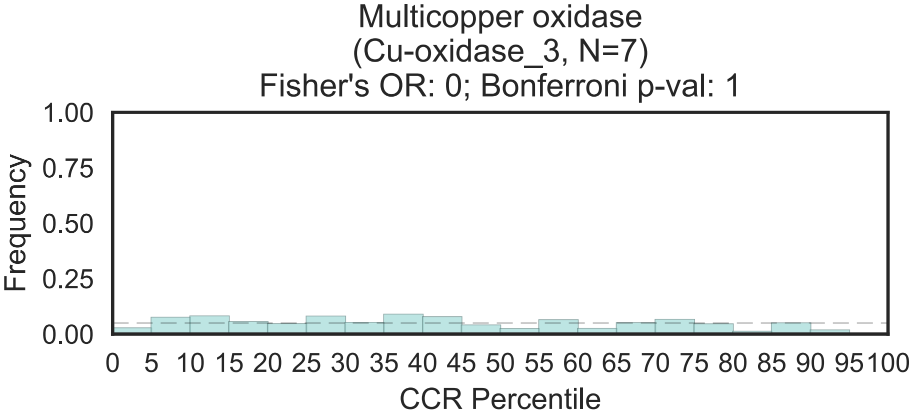

Ctr copper transporter family
(Ctr, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

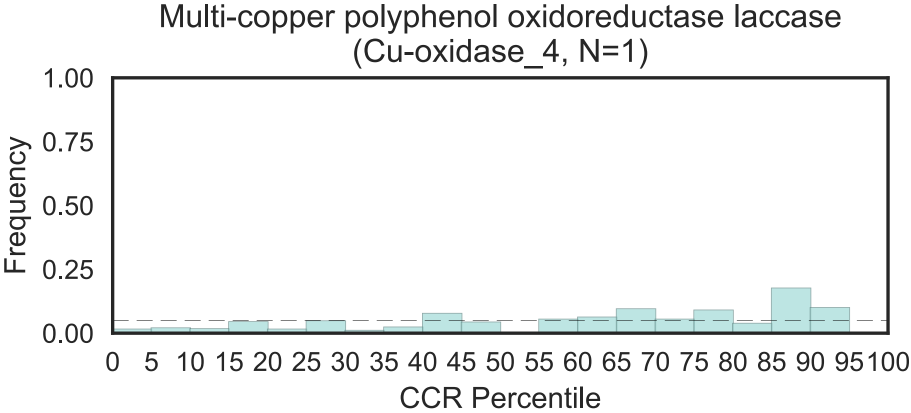

Putative metal-binding motif
(Cu-binding_MopE, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

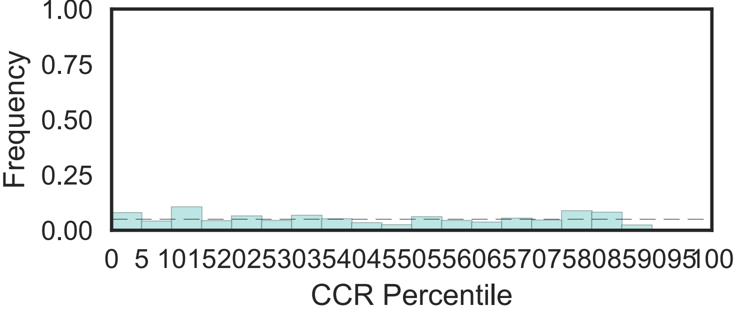


Multicopper oxidase
(Cu-oxidase, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Multicopper oxidase
(Cu-oxidase_2, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

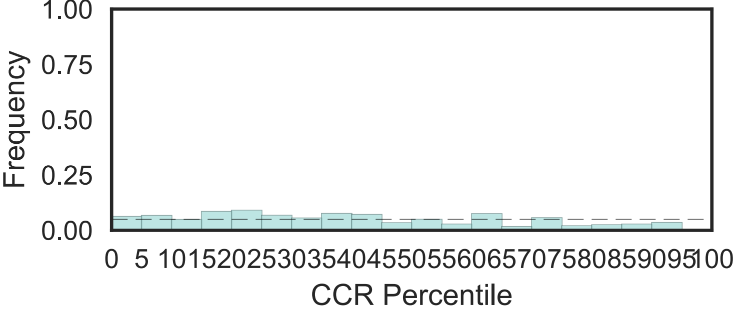

Multicopper oxidase
(Cu-oxidase_3, N=7)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

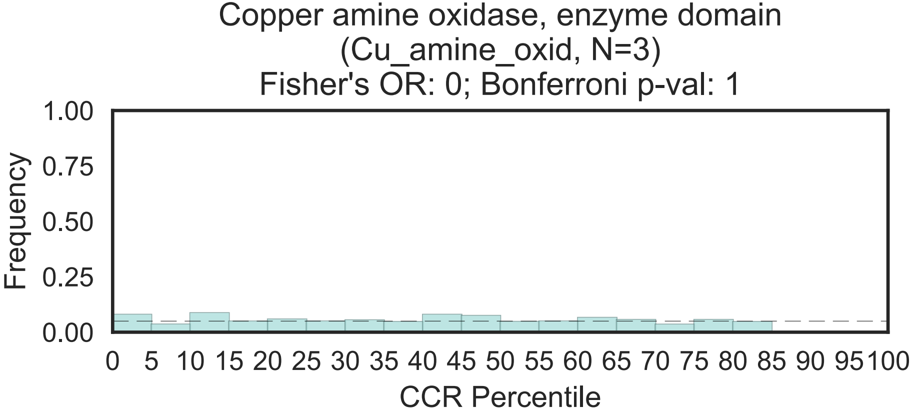

Multi-copper polyphenol oxidoreductase laccase
(Cu-oxidase_4, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

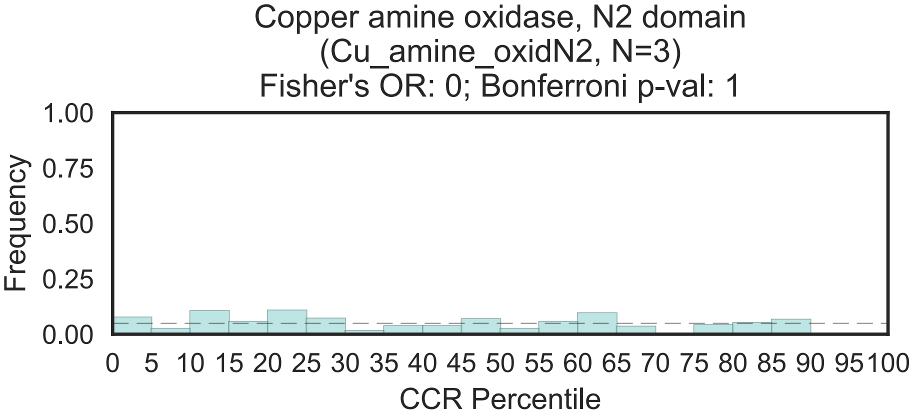


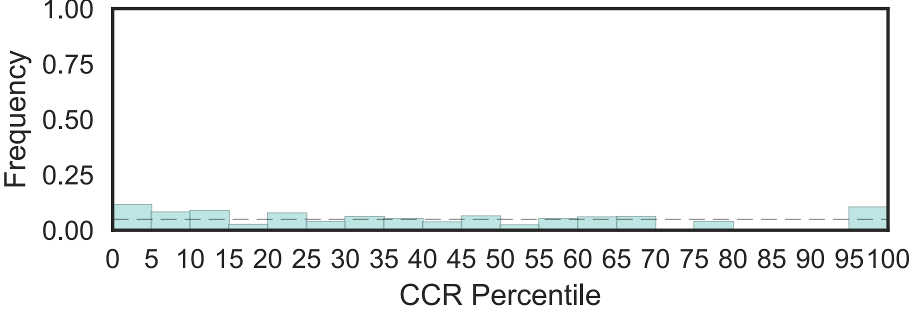
Copper type II ascorbate-dependent monooxygenase, C-terminal domain
(Cu2_monoox_C, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

Copper type II ascorbate-dependent monooxygenase, N-terminal domain
(Cu2_monooxygen, N=3)
Fisher's OR: 0; Bonferroni p-val: 1



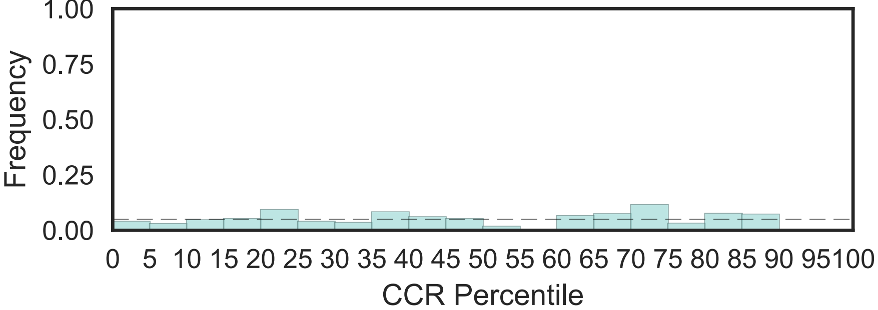

Copper amine oxidase, enzyme domain
(Cu_amine_oxid, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

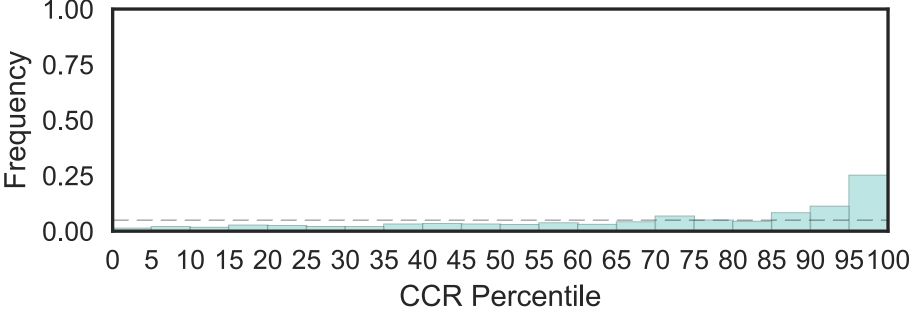

Copper amine oxidase, N2 domain
(Cu_amine_oxidN2, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



Copper amine oxidase, N3 domain
(Cu_amine_oxidN3, N=3)
Fisher's OR: 1.09; Bonferroni p-val: 1

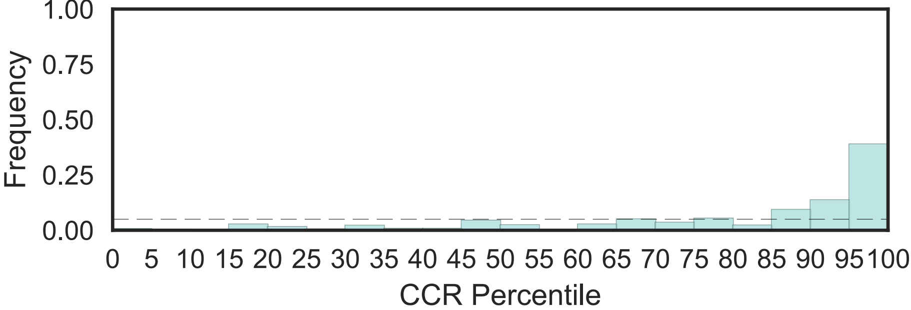
Mouse development and cellular proliferation protein Cullin-7 (Cul7, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

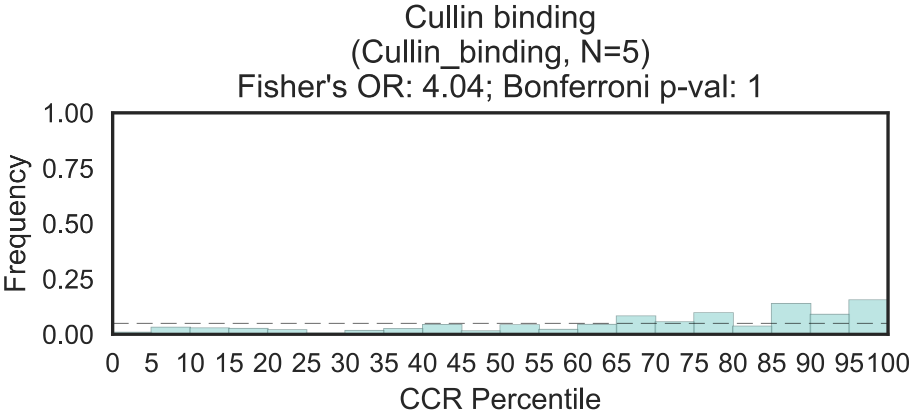


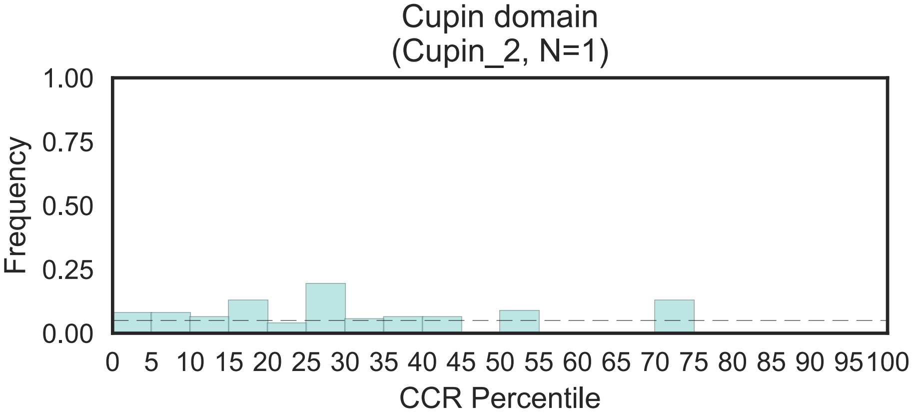


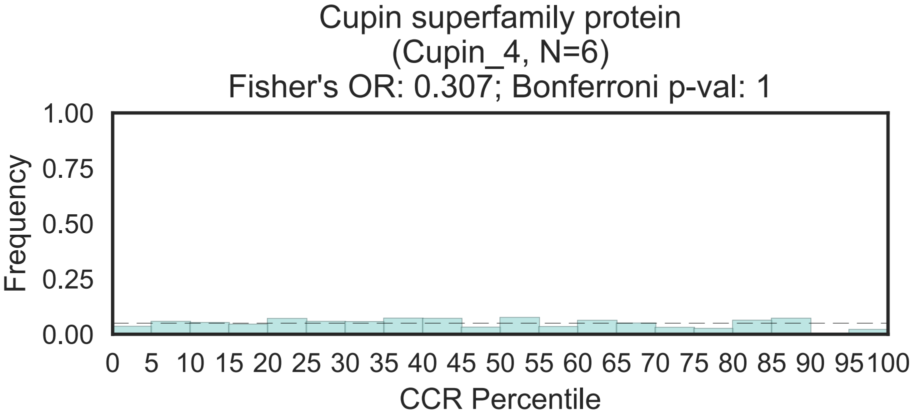
Cullin family
(Cullin, N=9)
Fisher's OR: 5.97; Bonferroni p-val: 7.52e-21

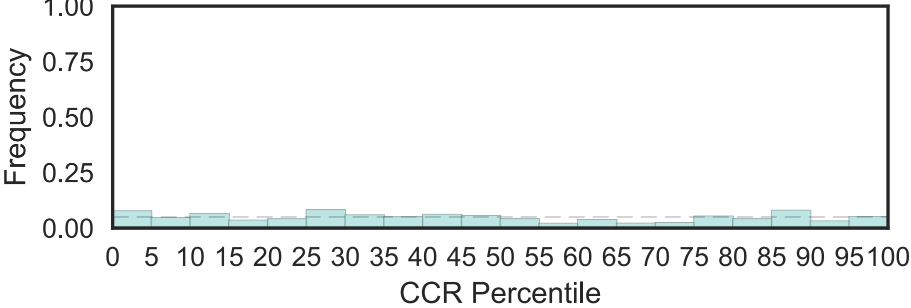
Cullin protein neddylation domain (Cullin_Nedd8, N=5) Fisher's OR: 13.5; Bonferroni p-val: 0.0636



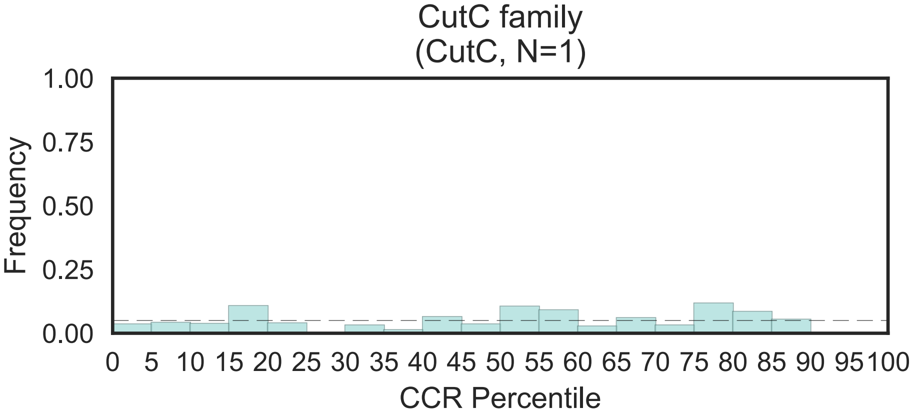

Cullin binding
(Cullin_binding, N=5)
Fisher's OR: 4.04; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

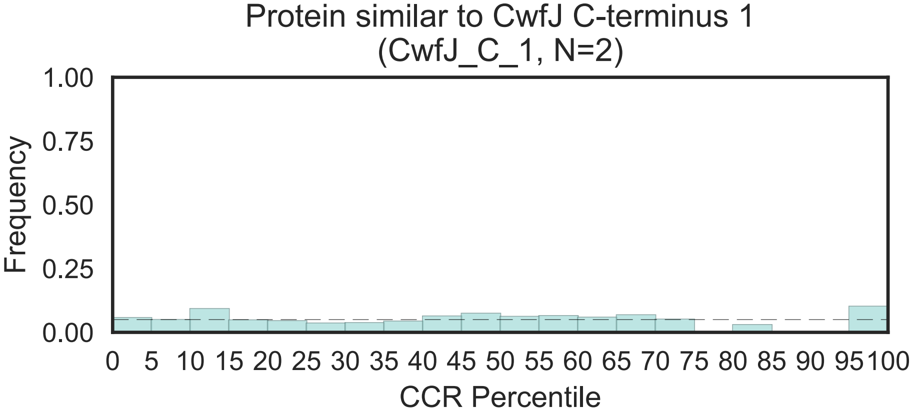

Cupin domain
(Cupin_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

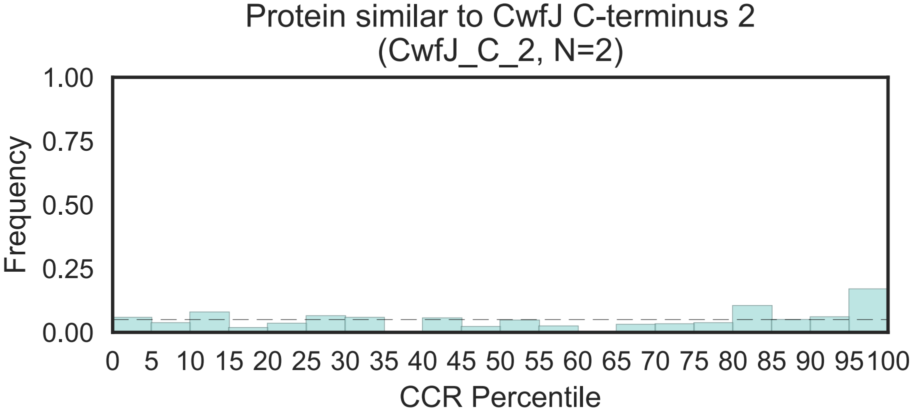

Cupin superfamily protein
(Cupin_4, N=6)
Fisher's OR: 0.307; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

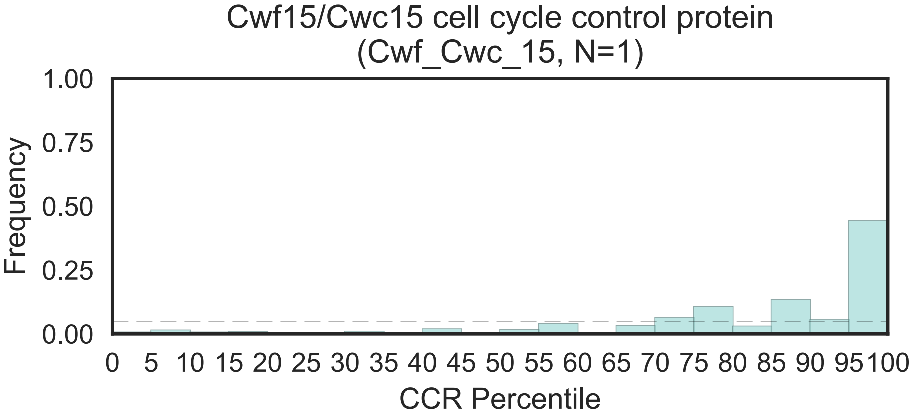


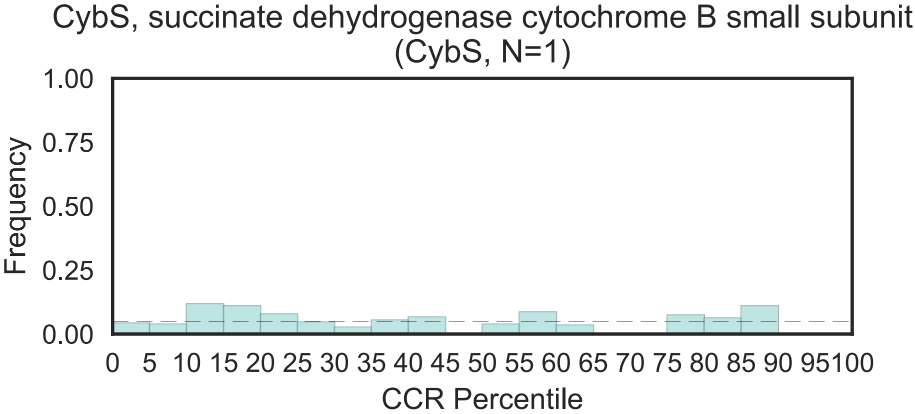
Cupin-like domain
(Cupin_8, N=13)
Fisher's OR: 1.22; Bonferroni p-val: 1

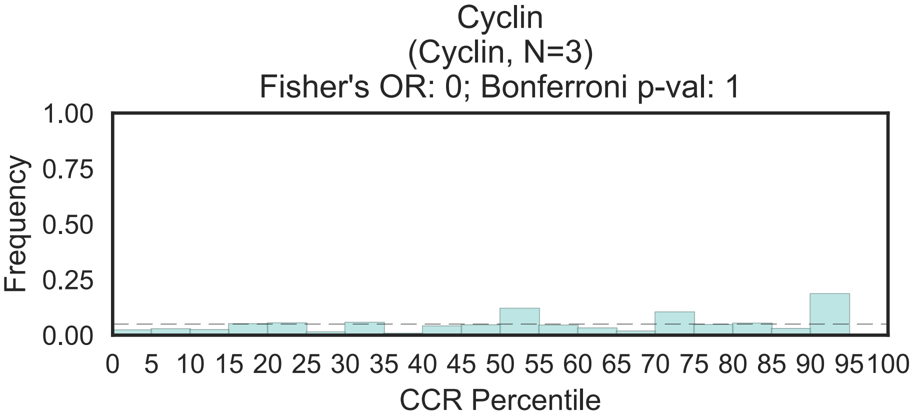

CutC family
(CutC, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

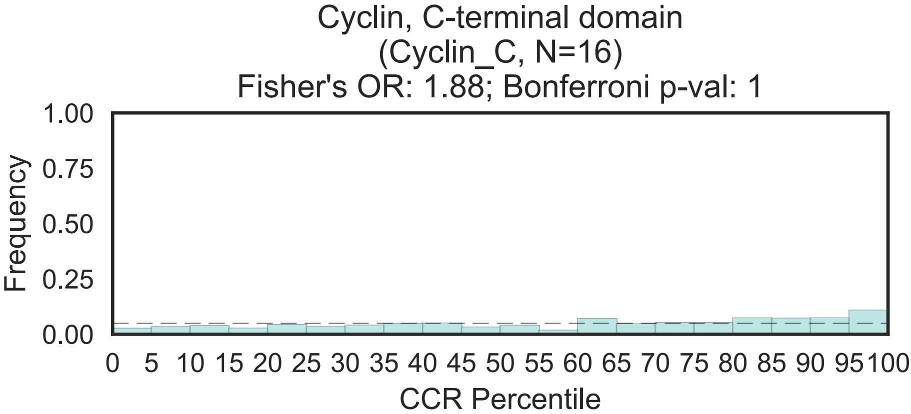

Protein similar to CwfJ C-terminus 1
(CwfJ_C_1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Protein similar to CwfJ C-terminus 2
(CwfJ_C_2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

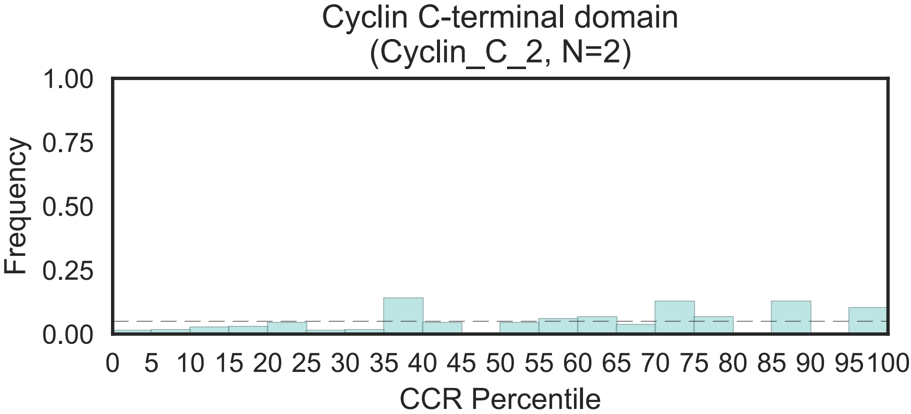

Cwf15/Cwc15 cell cycle control protein
(Cwf_Cwc_15, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

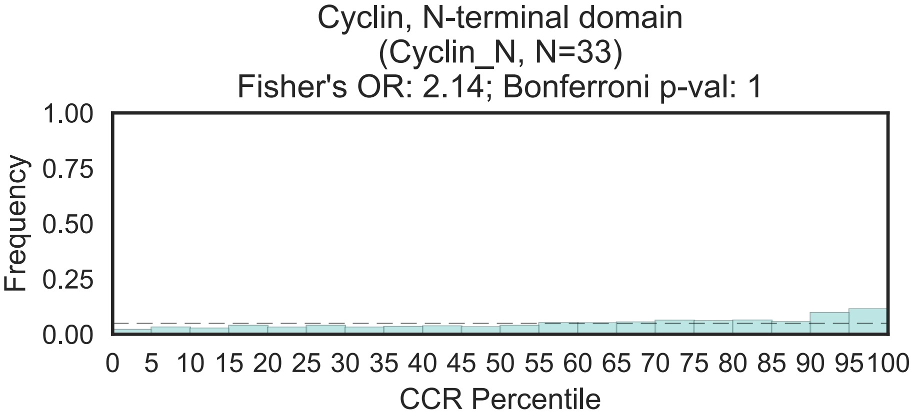

CybS, succinate dehydrogenase cytochrome B small subunit
(CybS, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

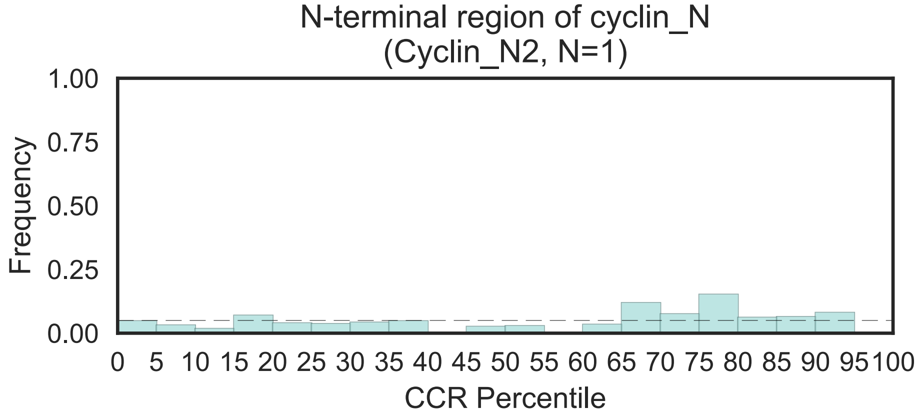

Cyclin
(Cyclin, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

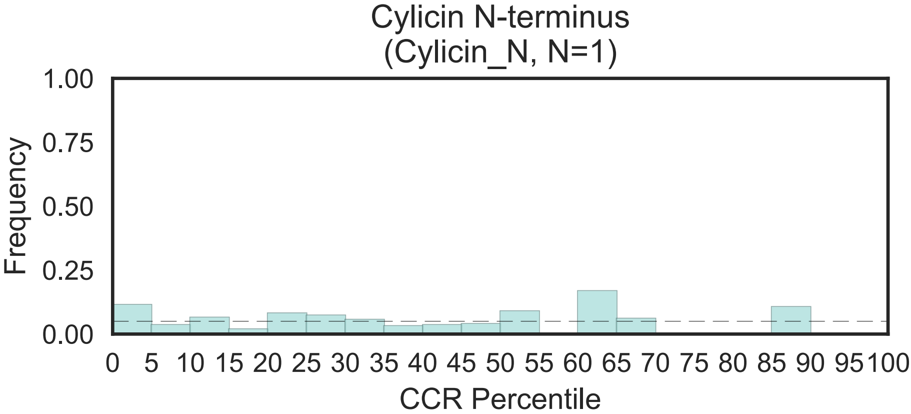


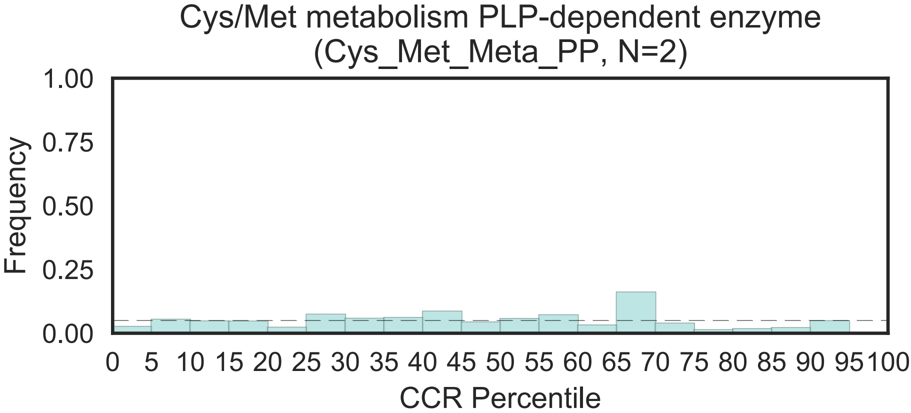
Cyclin, C-terminal domain
(Cyclin_C, N=16)
Fisher's OR: 1.88; Bonferroni p-val: 1

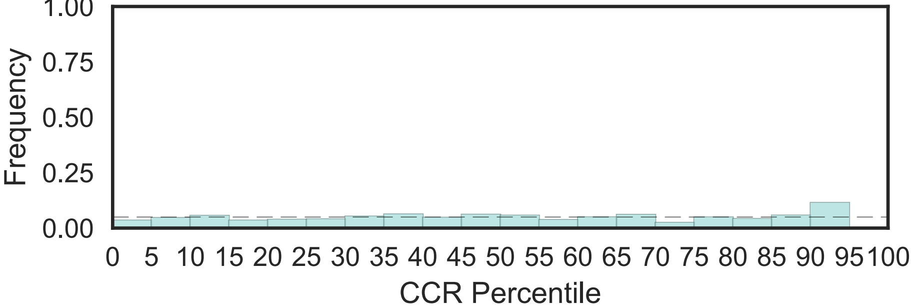

Cyclin C-terminal domain
(Cyclin_C_2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Cyclin, N-terminal domain
(Cyclin_N, N=33)
Fisher's OR: 2.14; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

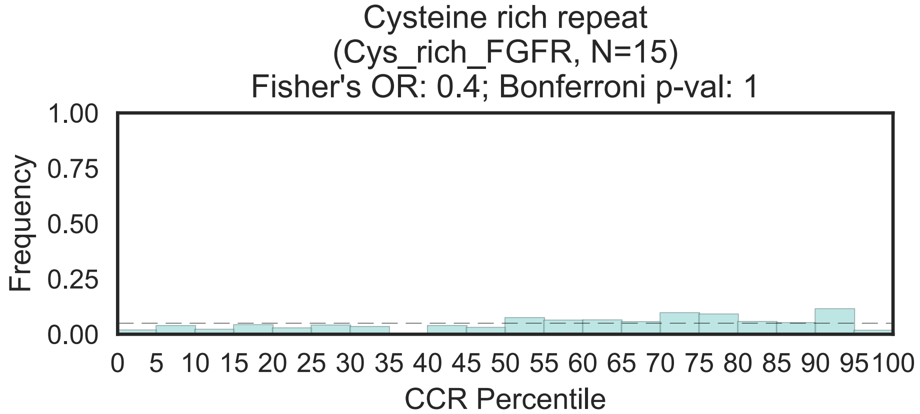

N-terminal region of cyclin_N
(Cyclin_N2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

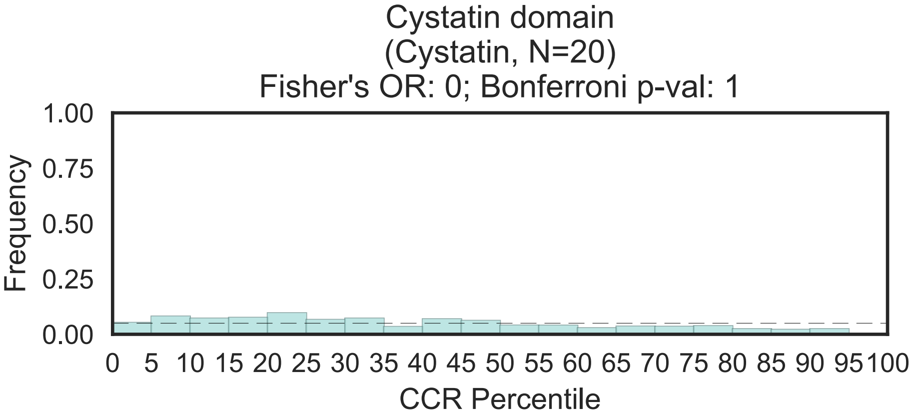

Cylicin N-terminus
(Cylicin_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

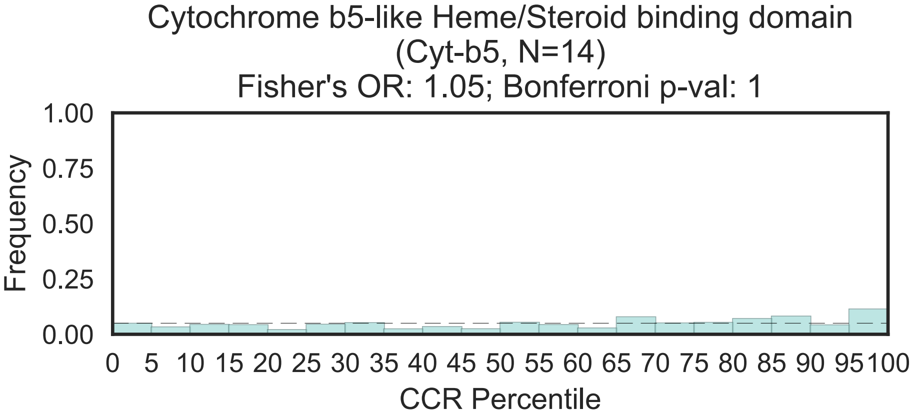

Cys/Met metabolism PLP-dependent enzyme
(Cys_Met_Meta_PP, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



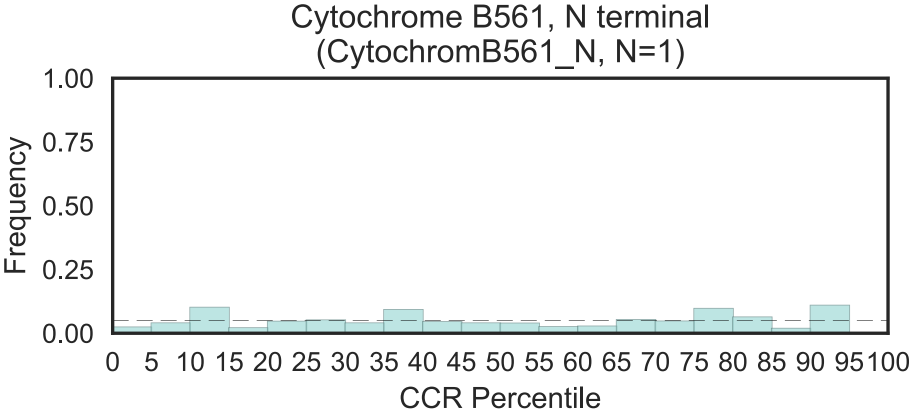
Cystine-knot domain
(Cys_knot, N=20)
Fisher's OR: 0; Bonferroni p-val: 1

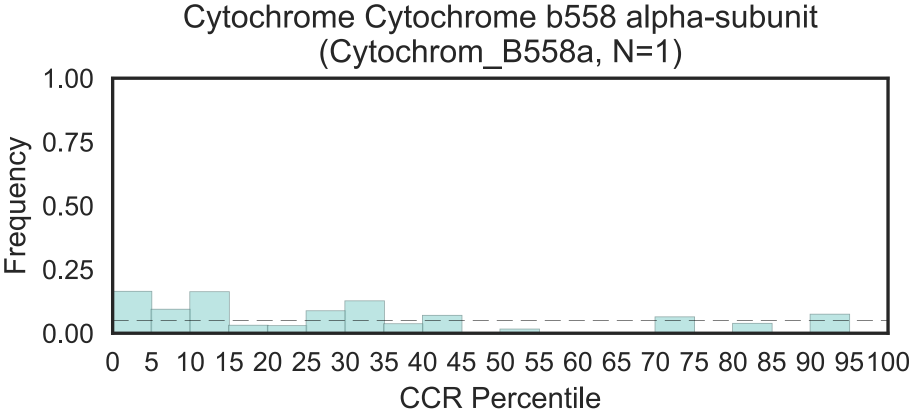
Cysteine rich repeat
(Cys_rich_FGFR, N=15)
Fisher's OR: 0.4; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

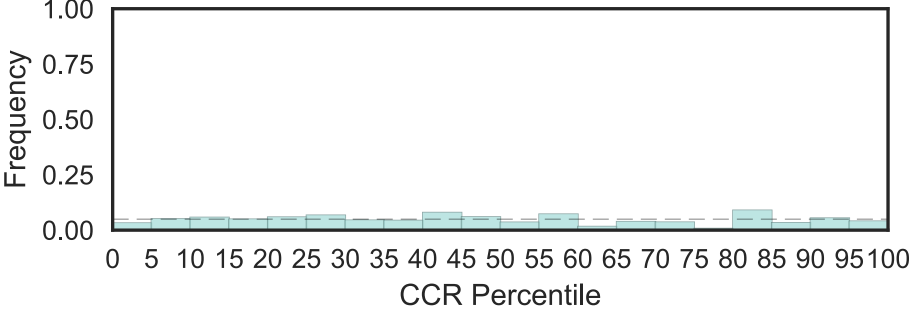

Cystatin domain
(Cystatin, N=20)
Fisher's OR: 0; Bonferroni p-val: 1



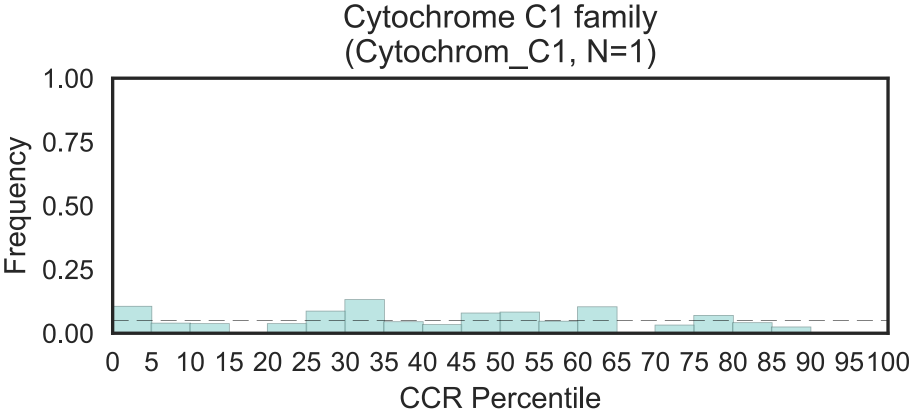
Cytochrome b5-like Heme/Steroid binding domain
(Cyt-b5, N=14)
Fisher's OR: 1.05; Bonferroni p-val: 1

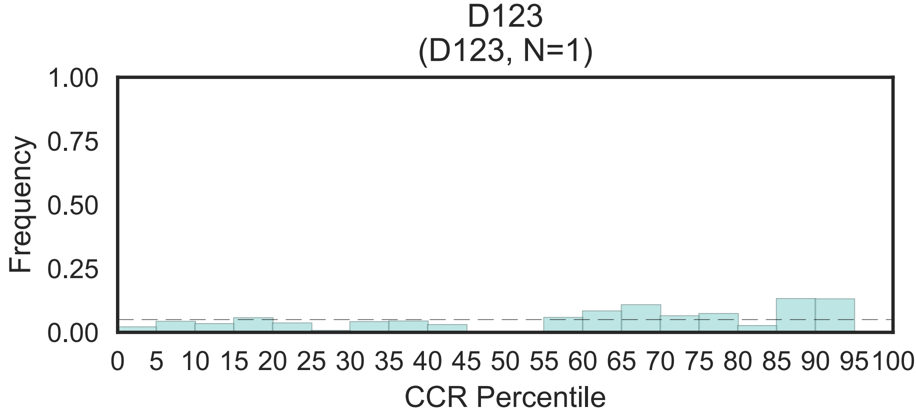

Cytochrome B561, N terminal
(CytochromB561_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

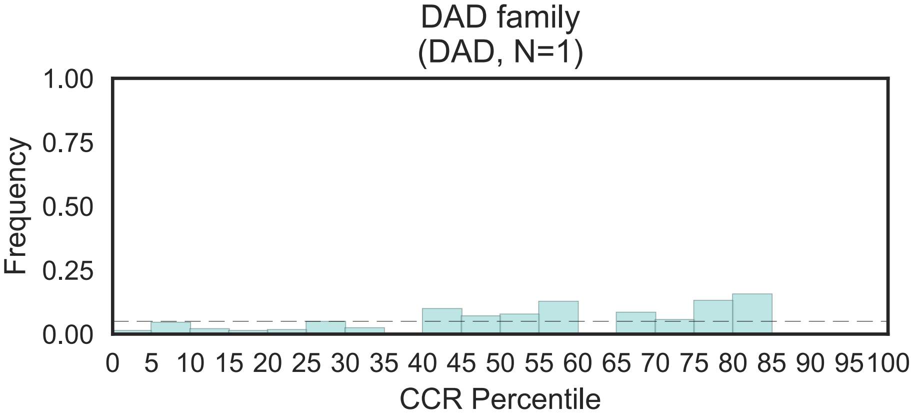

Cytochrome Cytochrome b558 alpha-subunit
(Cytochrom_B558a, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



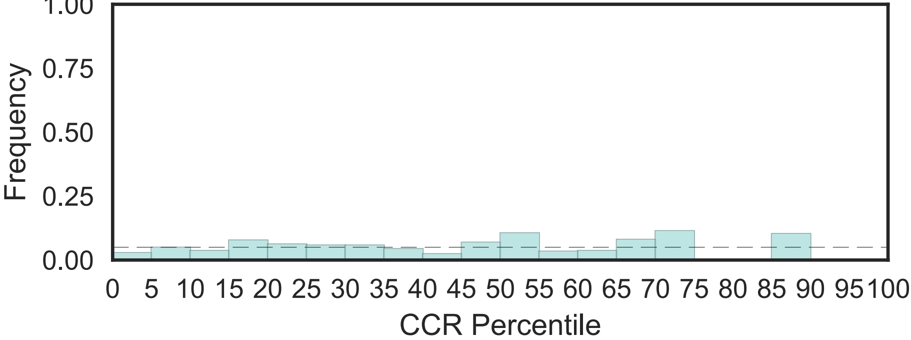
Eukaryotic cytochrome b561
(Cytochrom_B561, N=6)
Fisher's OR: 0.714; Bonferroni p-val: 1

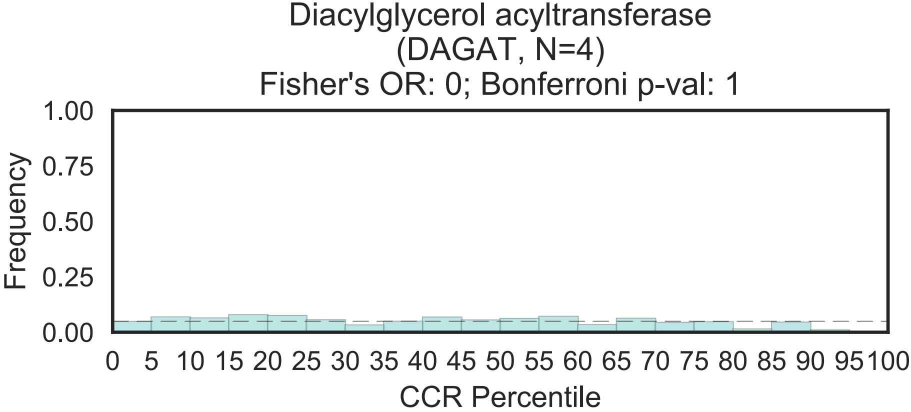

Cytochrome C1 family
(Cytochrom_C1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

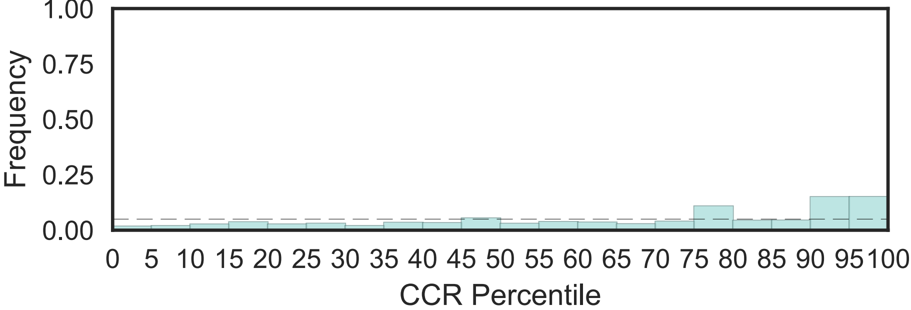

D123
(D123, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

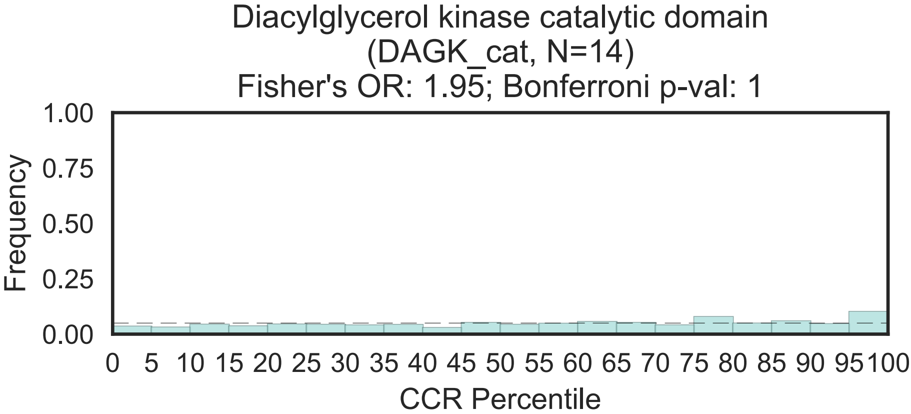

DAD family
(DAD, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

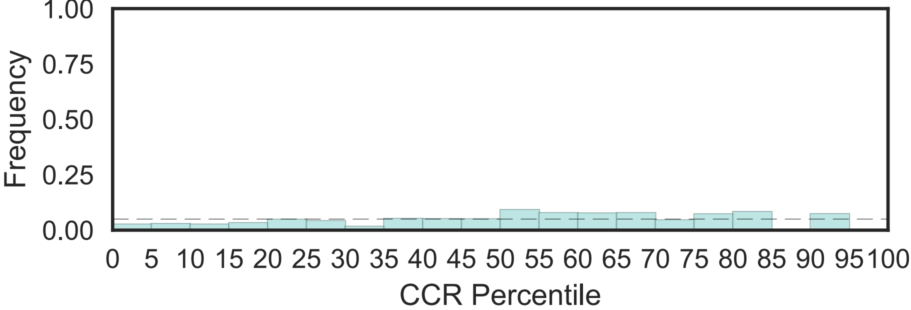
Dystroglycan (Dystrophin-associated glycoprotein 1) (DAG1, N=1)



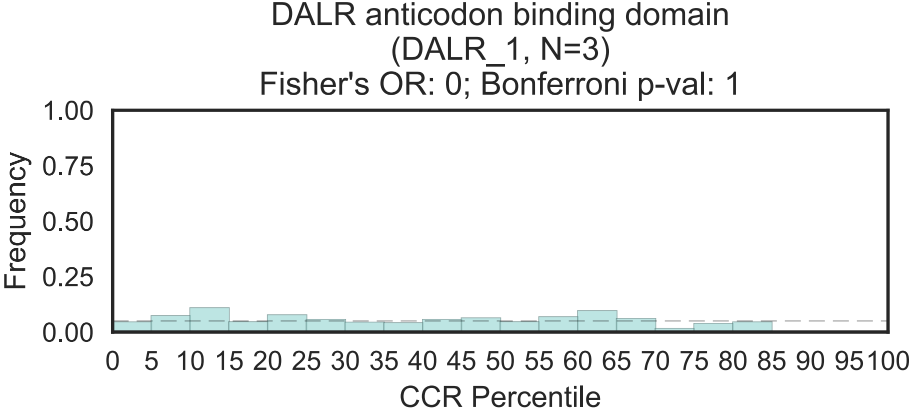

Diacylglycerol acyltransferase
(DAGAT, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

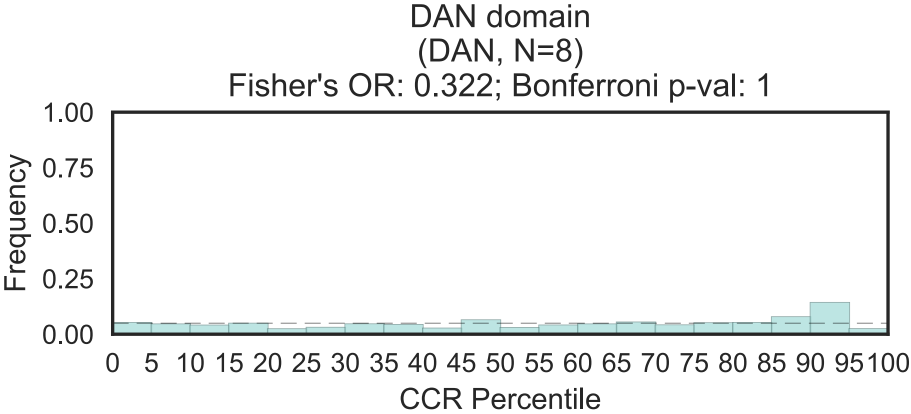

Diacylglycerol kinase accessory domain
(DAGK_acc, N=9)
Fisher's OR: 2.86; Bonferroni p-val: 1

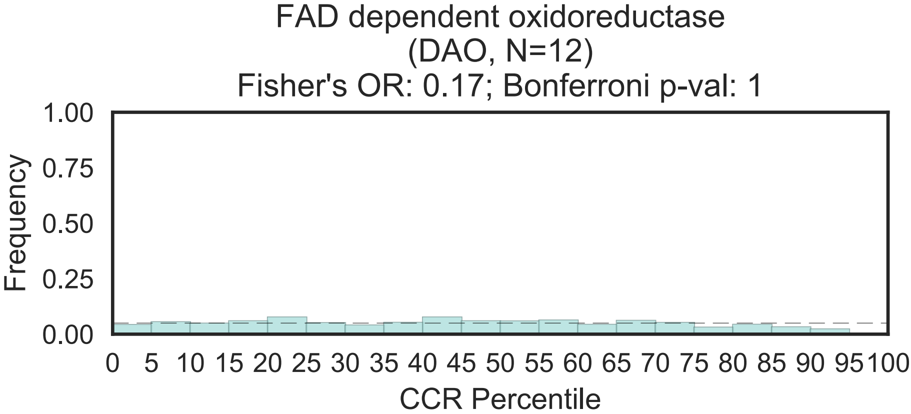

Diacylglycerol kinase catalytic domain
(DAGK_cat, N=14)
Fisher's OR: 1.95; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

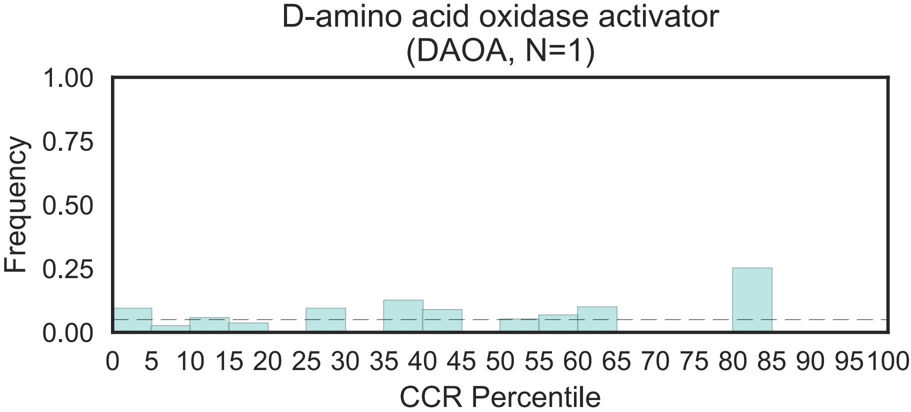


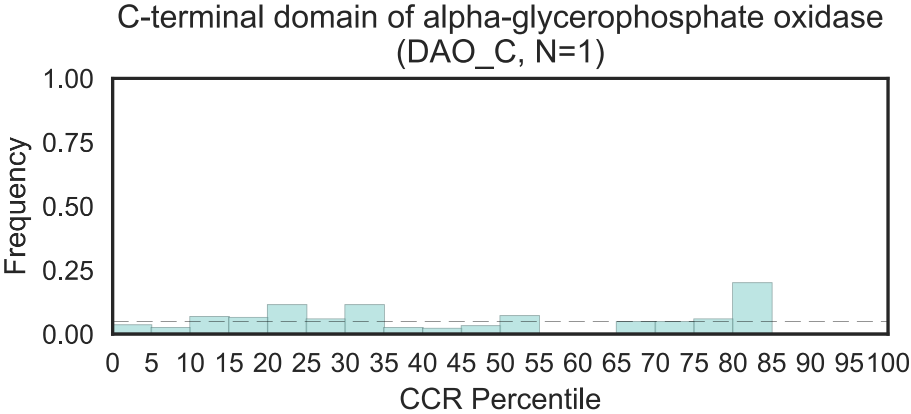
Diacylglycerol kinase N-terminus
(DAG_kinase_N, N=5)
Fisher's OR: 0; Bonferroni p-val: 1

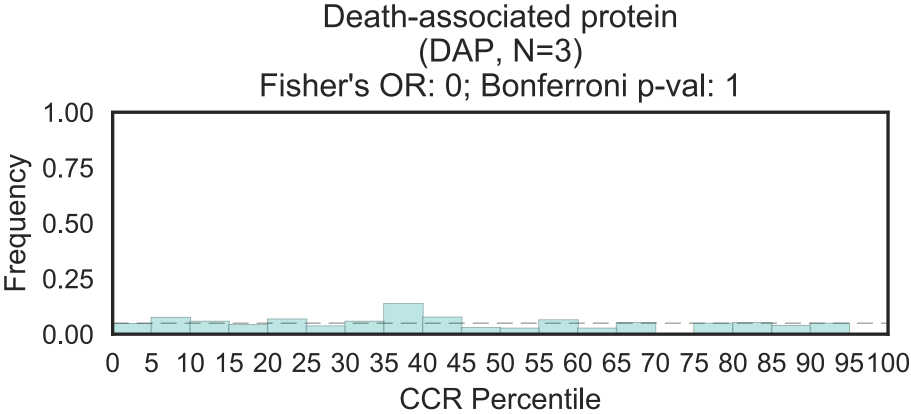

DALR anticodon binding domain
(DALR_1, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

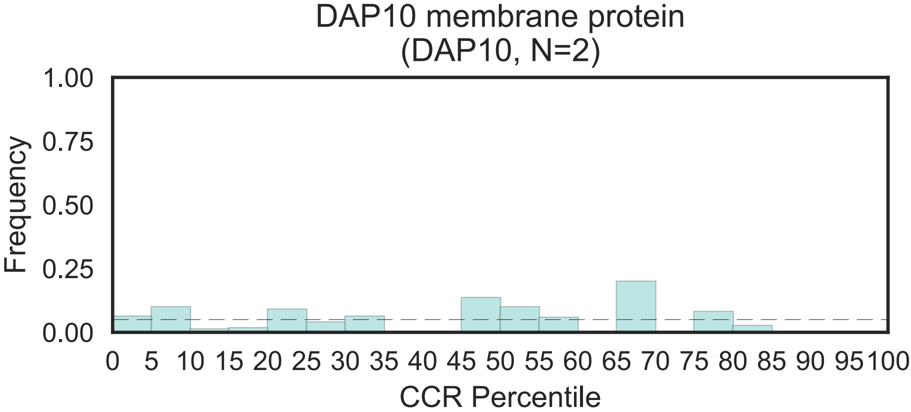

DAN domain
(DAN, N=8)
Fisher's OR: 0.322; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

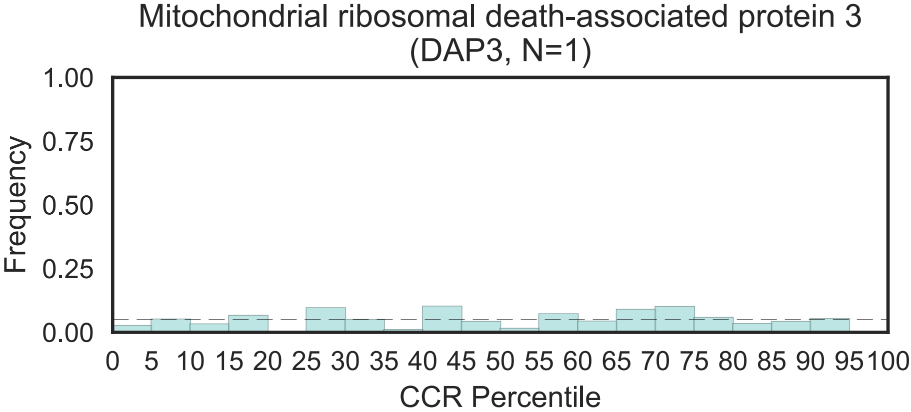

FAD dependent oxidoreductase
(DAO, N=12)
Fisher's OR: 0.17; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

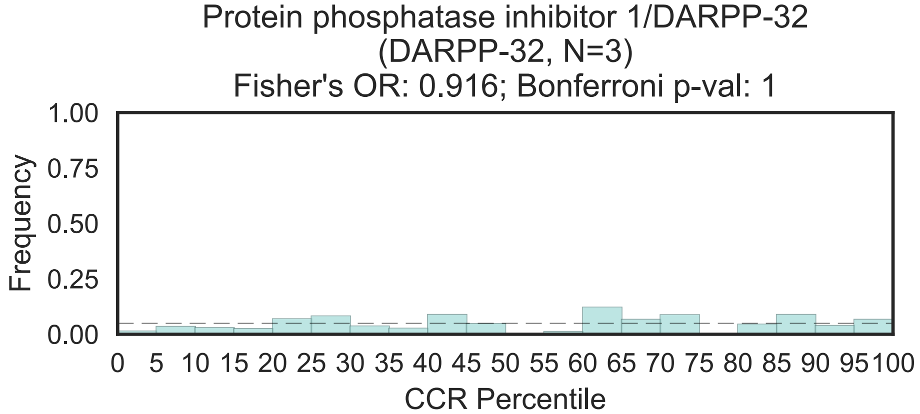

D-amino acid oxidase activator
(DAOA, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


C-terminal domain of alpha-glycerophosphate oxidase
(DAO_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

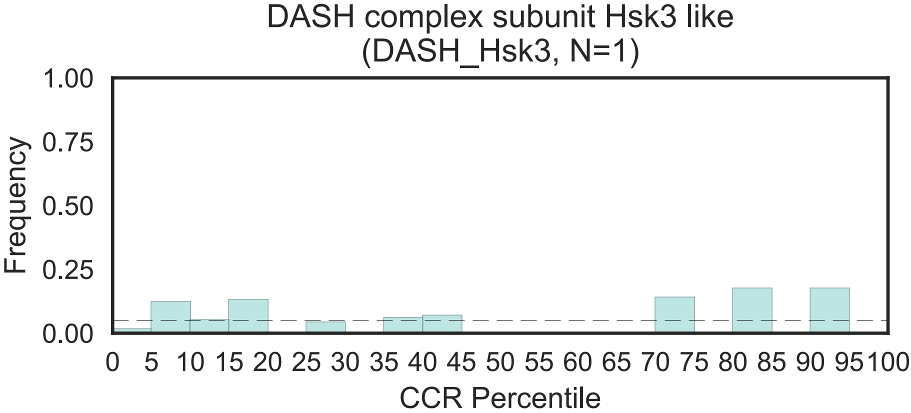

Death-associated protein
(DAP, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

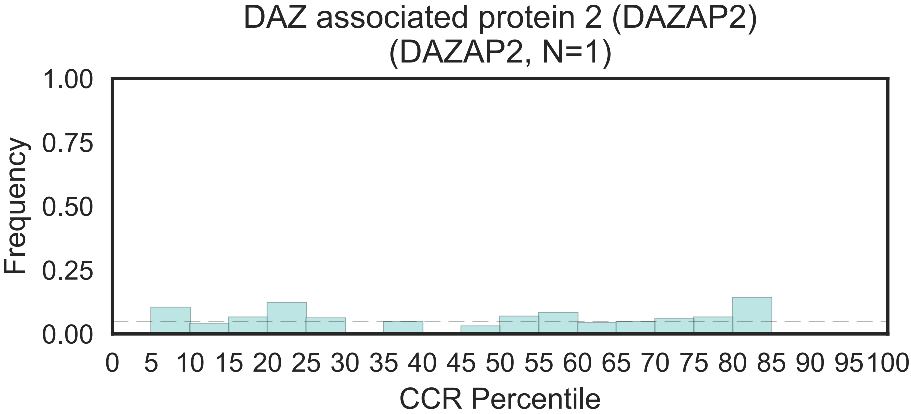

DAP10 membrane protein
(DAP10, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

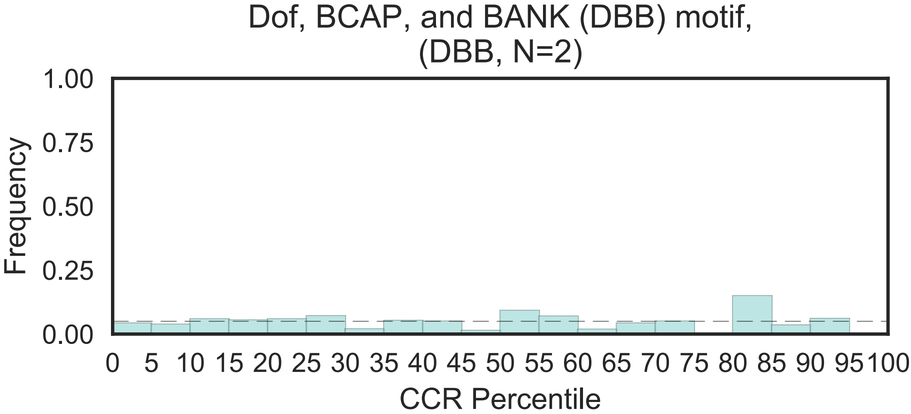

Mitochondrial ribosomal death-associated protein 3
(DAP3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

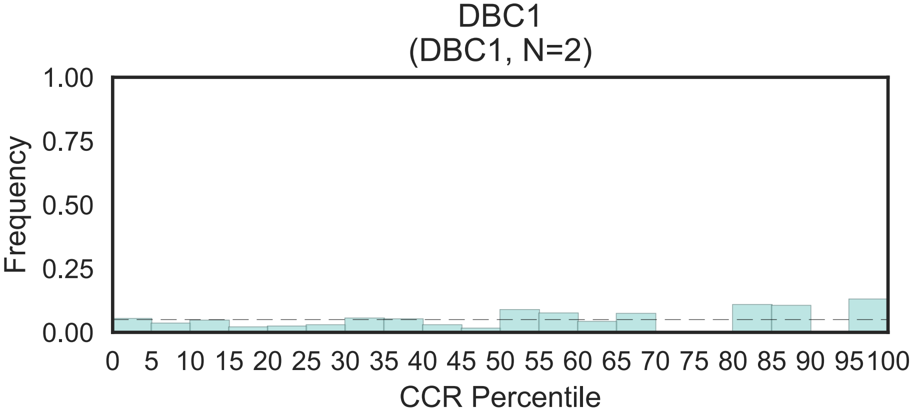


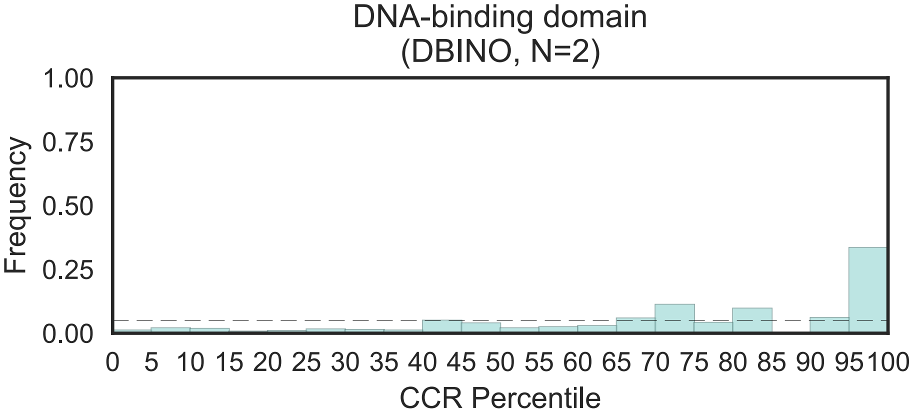
Protein phosphatase inhibitor 1/DARPP-32
(DARPP-32, N=3)
Fisher's OR: 0.916; Bonferroni p-val: 1

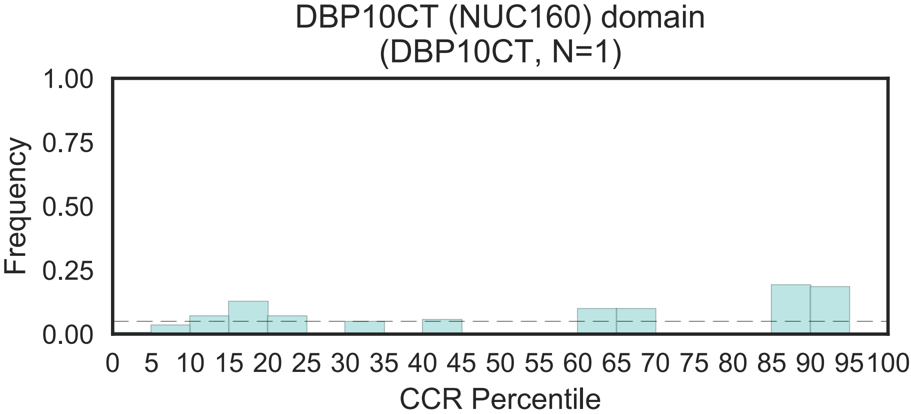

DASH complex subunit Hsk3 like
(DASH_Hsk3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

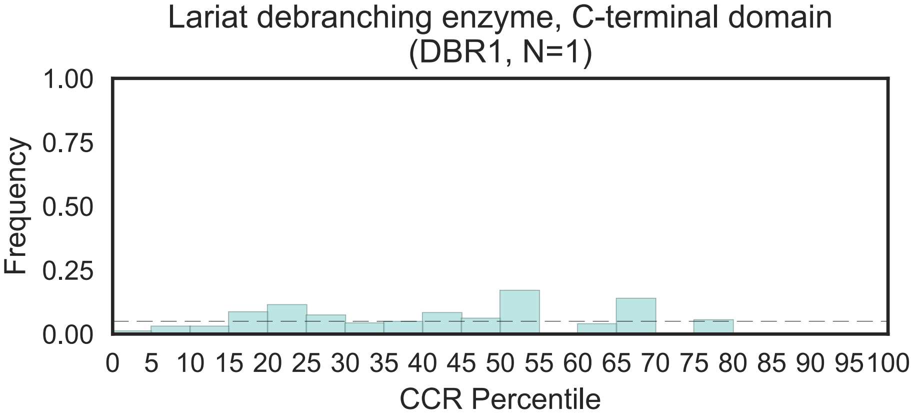

DAZ associated protein 2 (DAZAP2)
(DAZAP2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

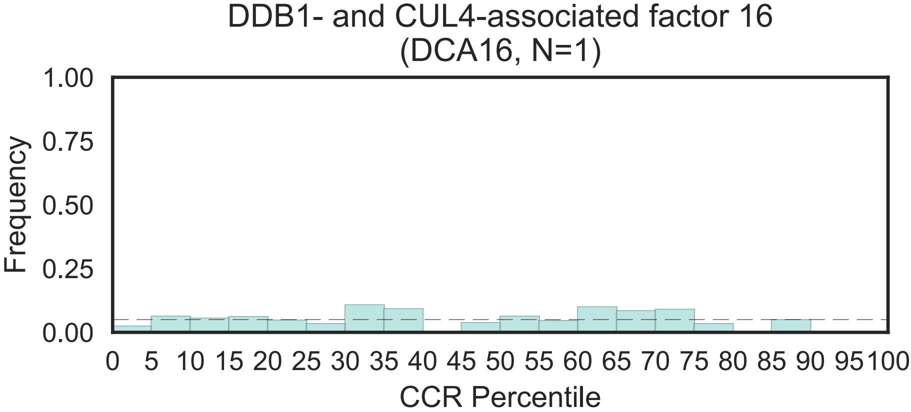

Dof, BCAP, and BANK (DBB) motif,
(DBB, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

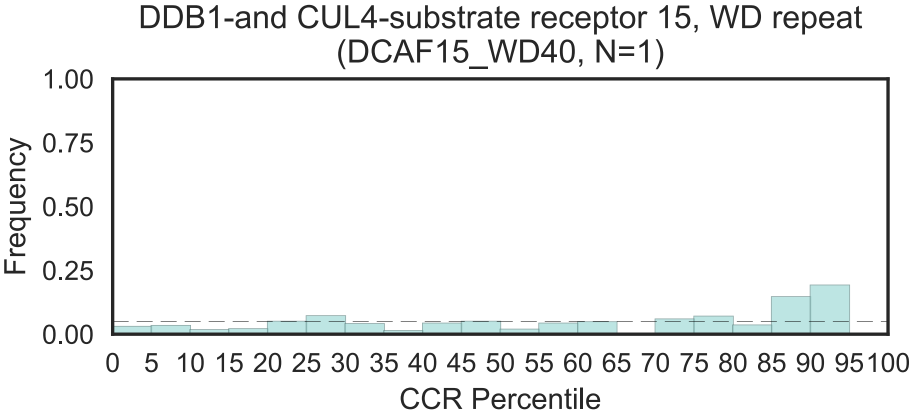

DBC1
(DBC1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

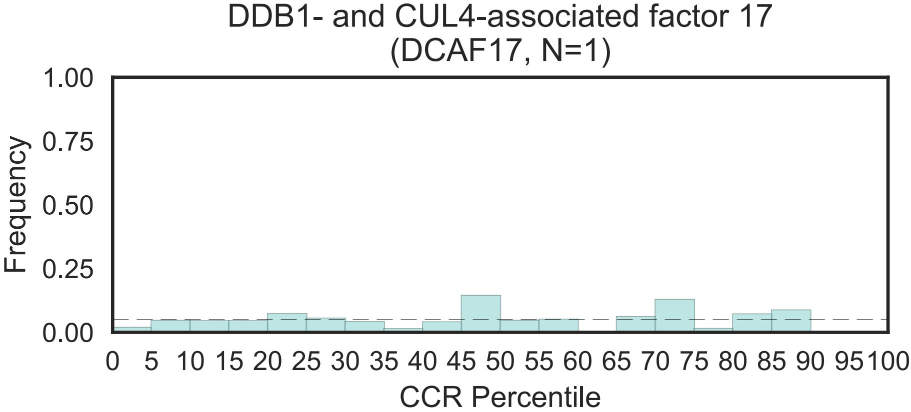

DNA-binding domain
(DBINO, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

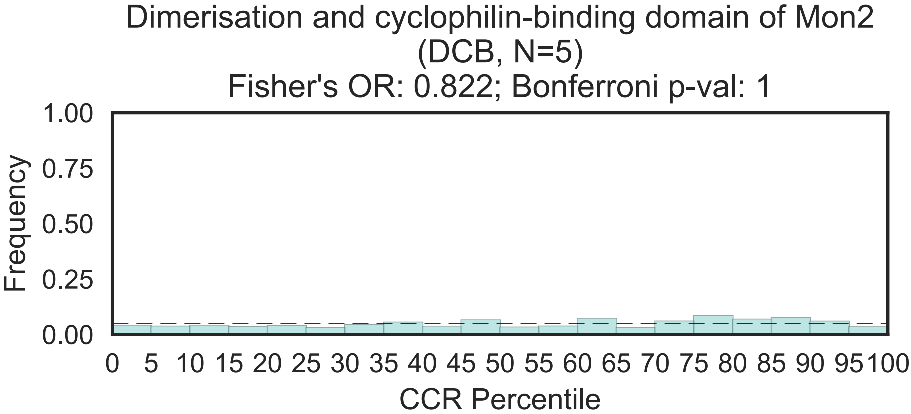

DBP10CT (NUC160) domain
(DBP10CT, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

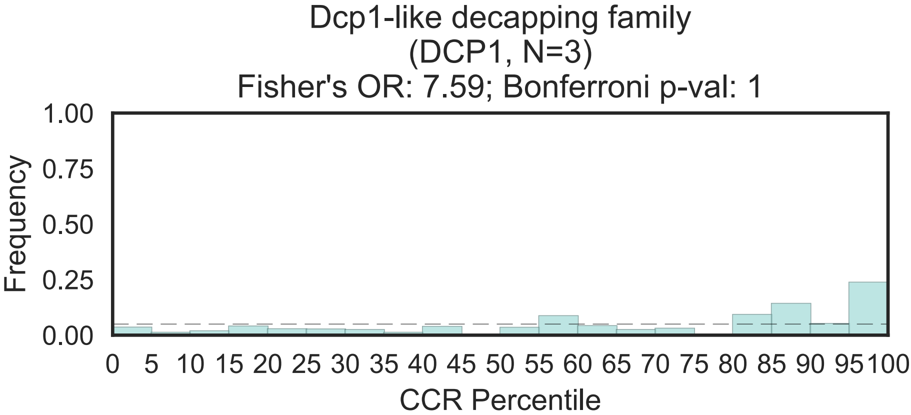

Lariat debranching enzyme, C-terminal domain
(DBR1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

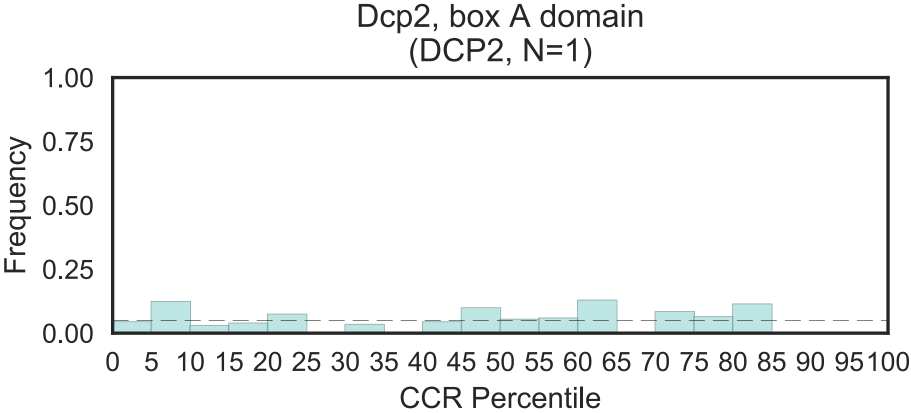

DDB1- and CUL4-associated factor 16
(DCA16, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

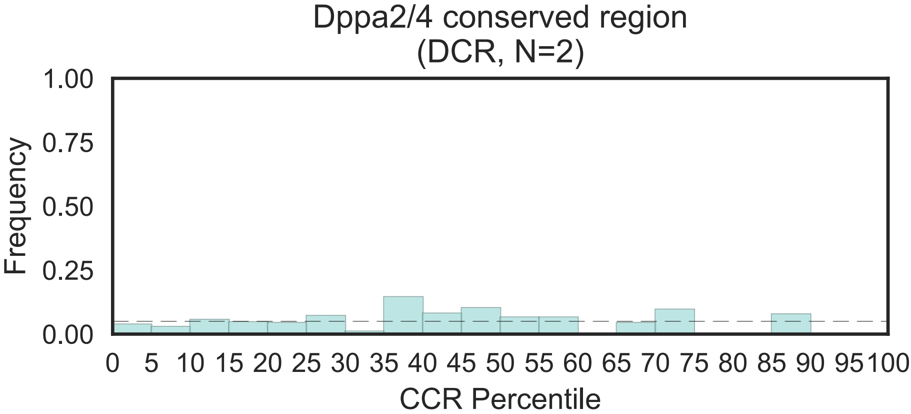

DDB1-and CUL4-substrate receptor 15, WD repeat
(DCAF15_WD40, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

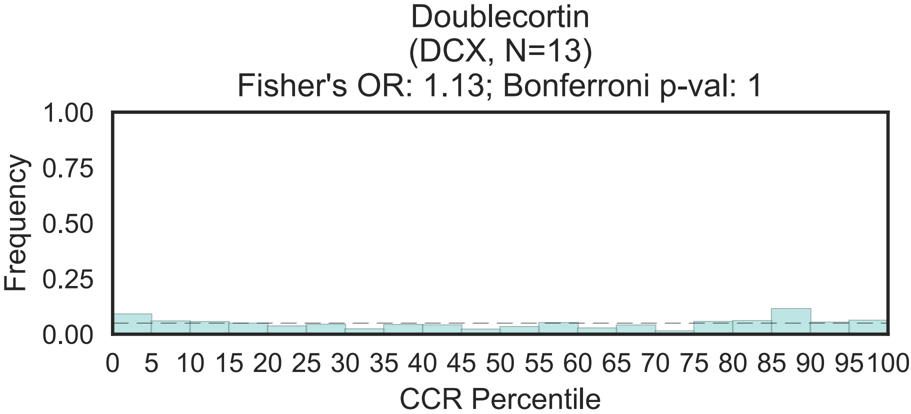

DDB1- and CUL4-associated factor 17
(DCAF17, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Dimerisation and cyclophilin-binding domain of Mon2
(DCB, N=5)
Fisher's OR: 0.822; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Dcp1-like decapping family
(DCP1, N=3)
Fisher's OR: 7.59; Bonferroni p-val: 1

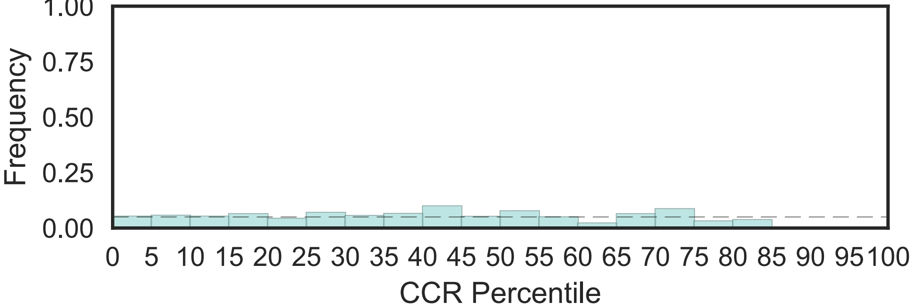

Dcp2, box A domain
(DCP2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Dppa2/4 conserved region
(DCR, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

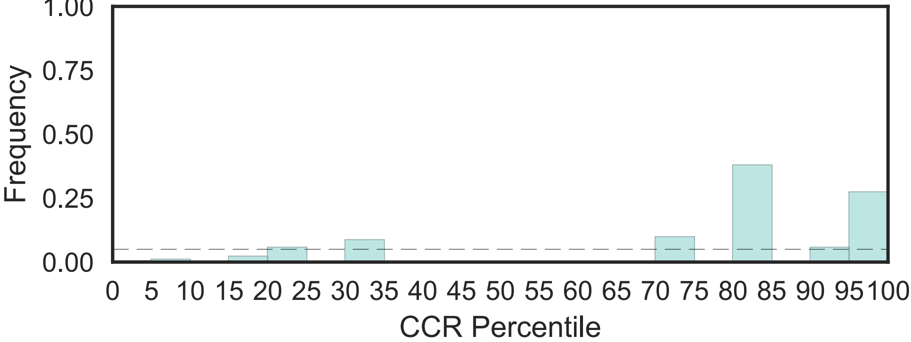


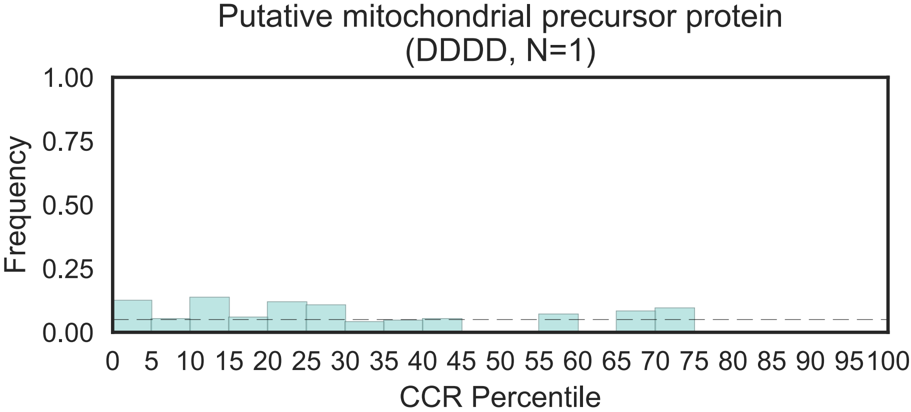
Doublecortin
(DCX, N=13)
Fisher's OR: 1.13; Bonferroni p-val: 1

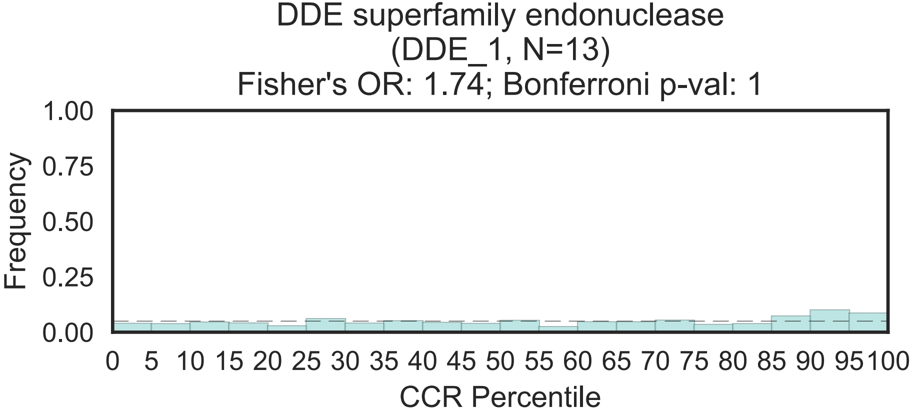
DC-STAMP-like protein
(DC_STAMP, N=4)
Fisher's OR: 0; Bonferroni p-val: 1



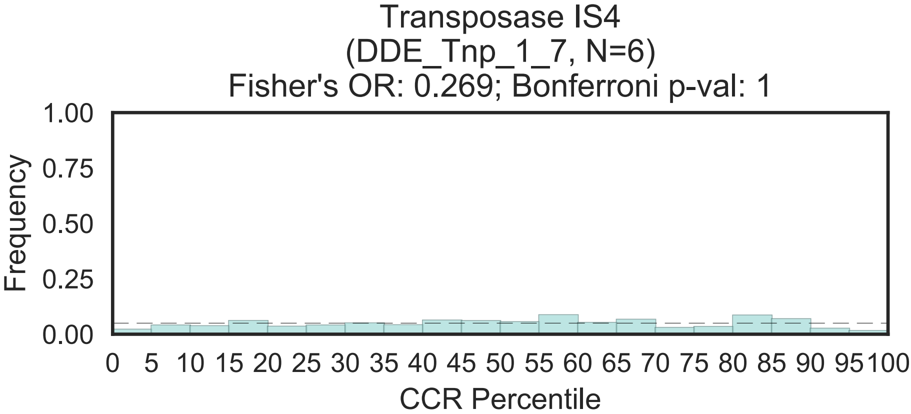
Det1 complexing ubiquitin ligase (DDA1, N=1)

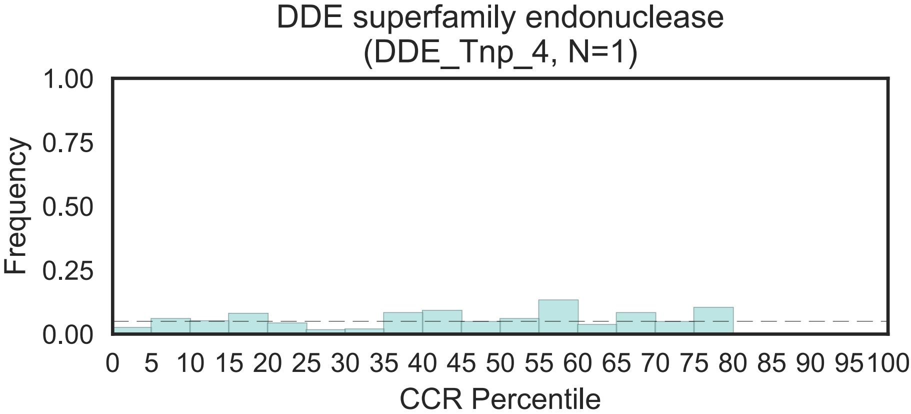


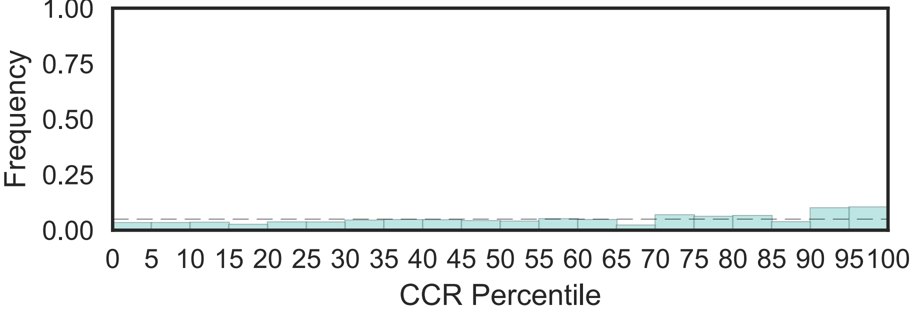

Putative mitochondrial precursor protein
(DDDD, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile



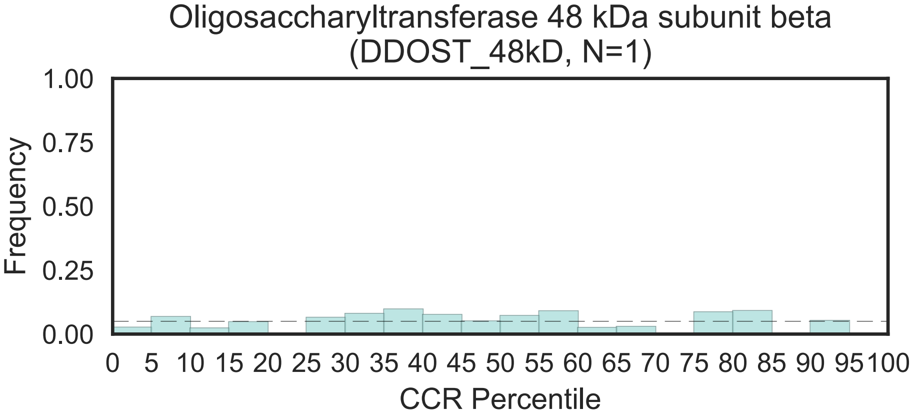
DDE superfamily endonuclease
(DDE_1, N=13)
Fisher's OR: 1.74; Bonferroni p-val: 1

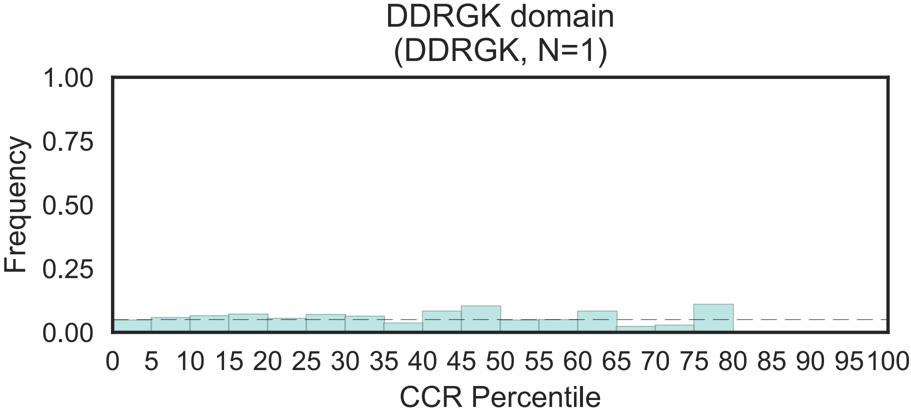

Transposase IS4
(DDE_Tnp_1_7, N=6)
Fisher's OR: 0.269; Bonferroni p-val: 1

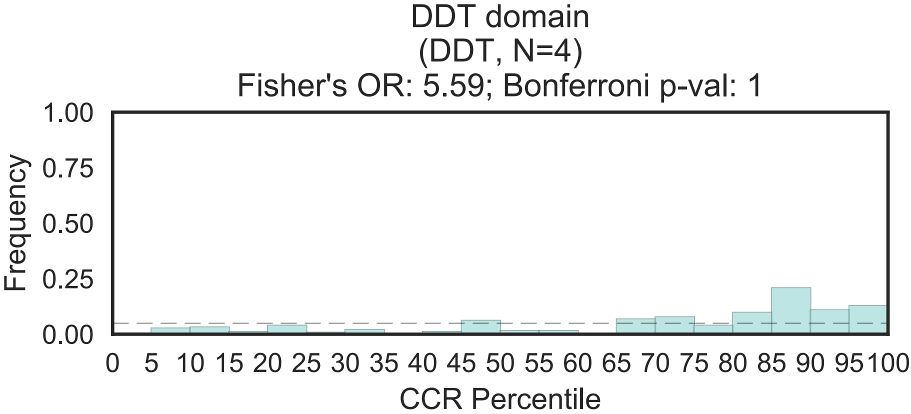

DDE superfamily endonuclease
(DDE_Tnp_4, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

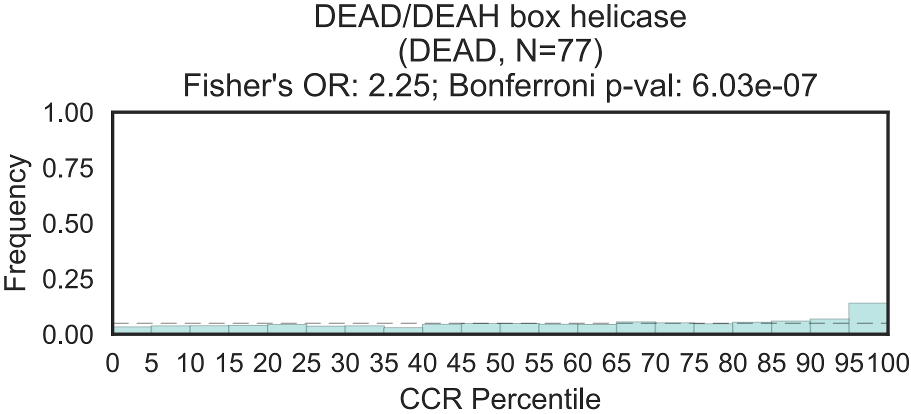


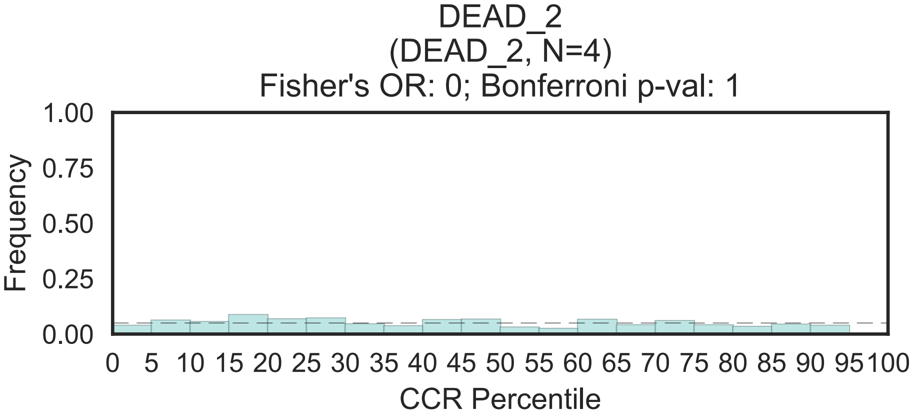
DDHD domain
(DDHD, N=6)
Fisher's OR: 1.65; Bonferroni p-val: 1

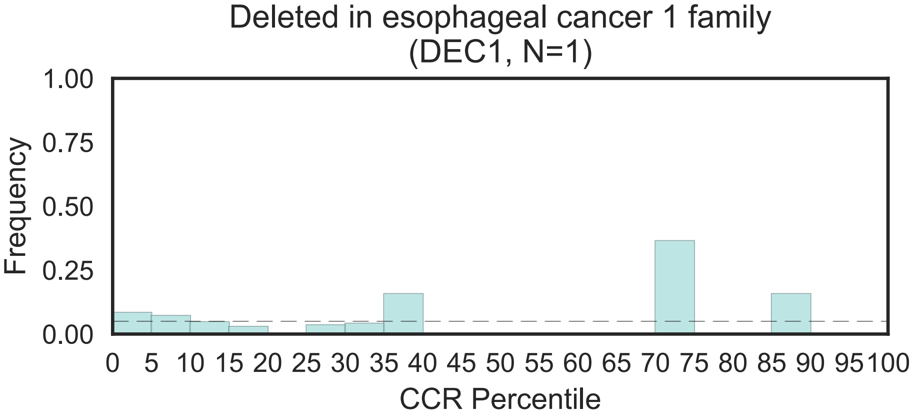

Oligosaccharyltransferase 48 kDa subunit beta
(DDOST_48kD, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

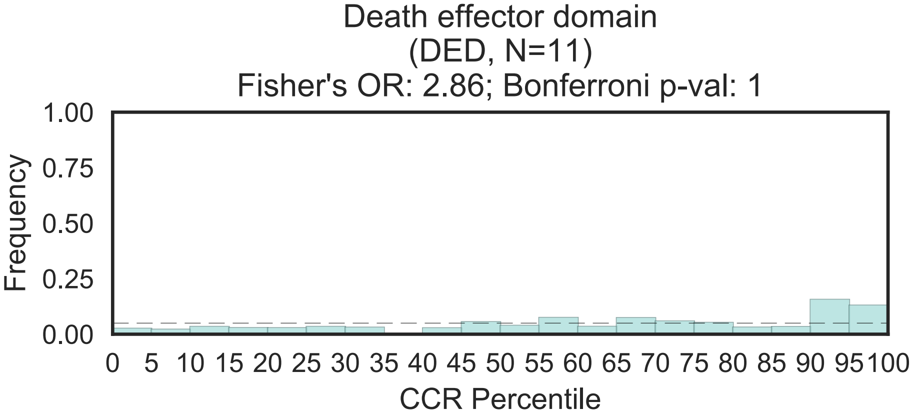

DDRGK domain
(DDRGK, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

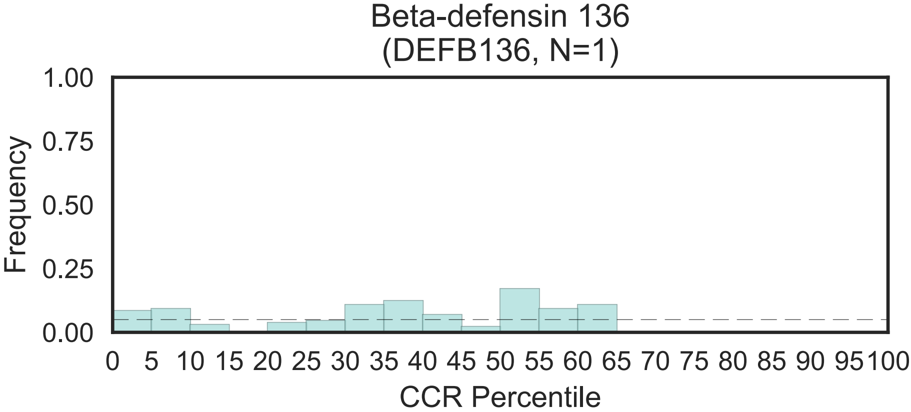

DDT domain
(DDT, N=4)
Fisher's OR: 5.59; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

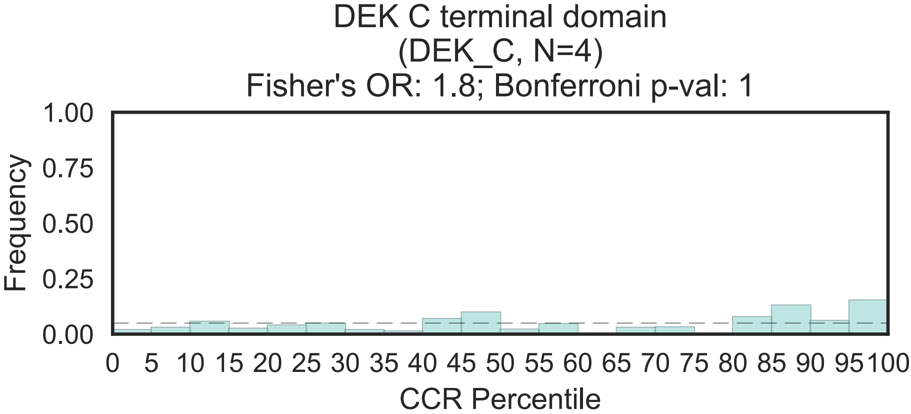

DEAD/DEAH box helicase
(DEAD, N=77)
Fisher's OR: 2.25; Bonferroni p-val: 6.03e-07
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


DEAD_2
(DEAD_2, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

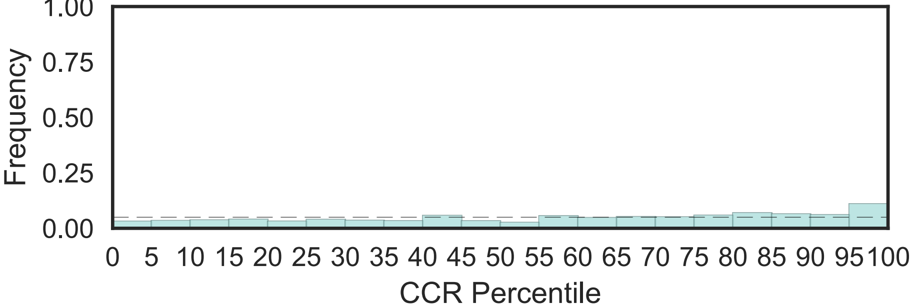

Deleted in esophageal cancer 1 family
(DEC1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

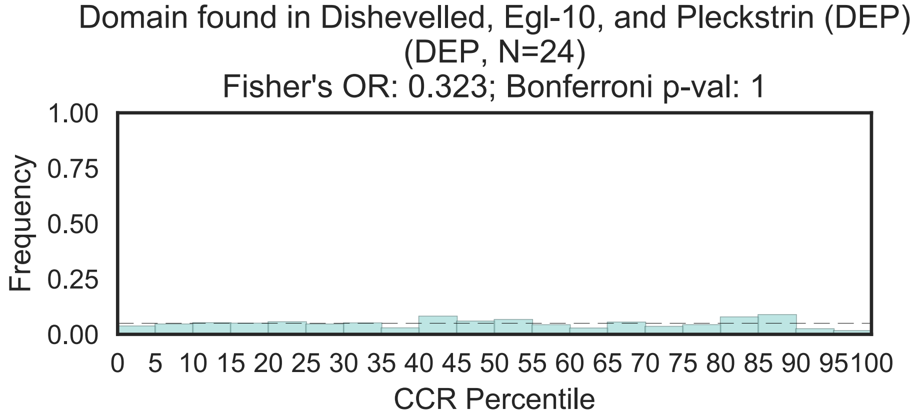

Death effector domain
(DED, N=11)
Fisher's OR: 2.86; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

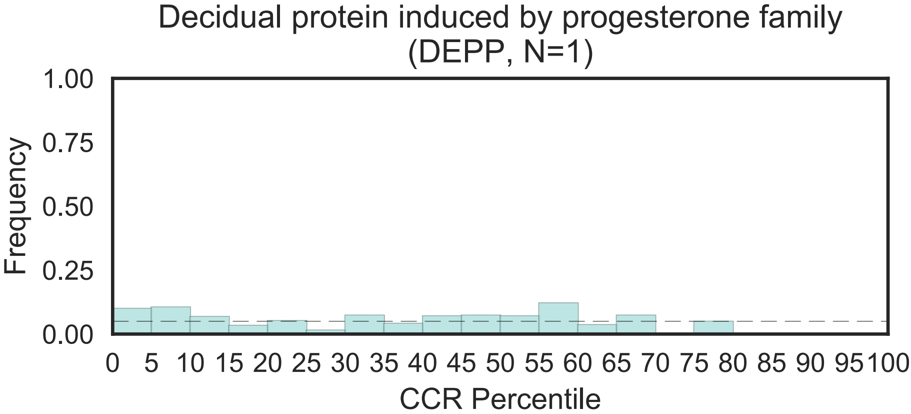

Beta-defensin 136
(DEFB136, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

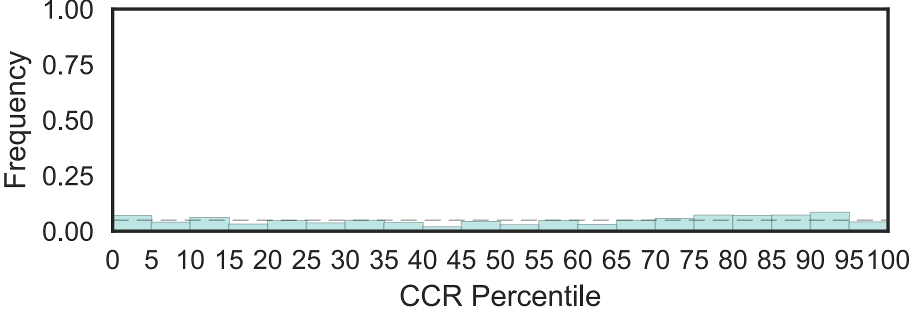

DEK C terminal domain
(DEK_C, N=4)
Fisher's OR: 1.8; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

DENN (AEX-3) domain
(DENN, N=17)
Fisher's OR: 1.69; Bonferroni p-val: 1

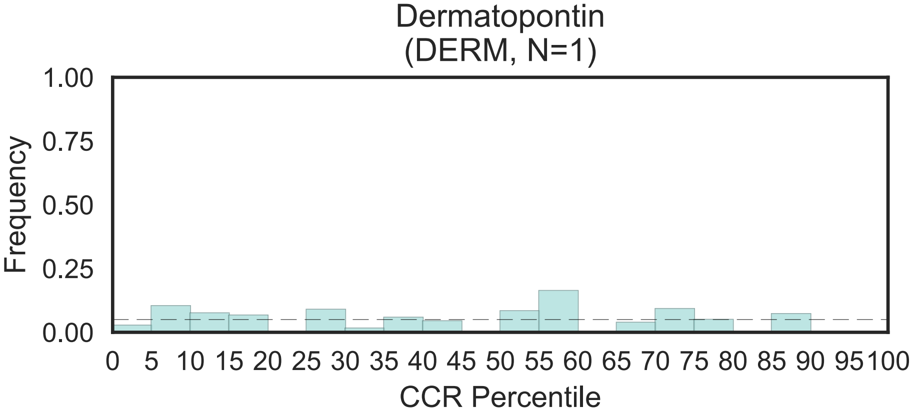


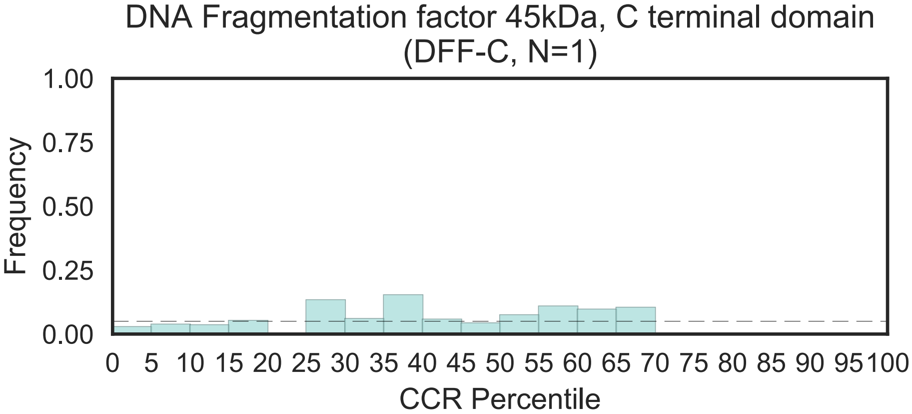

Domain found in Dishevelled, Egl-10, and Pleckstrin (DEP)
(DEP, N=24)
Fisher's OR: 0.323; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

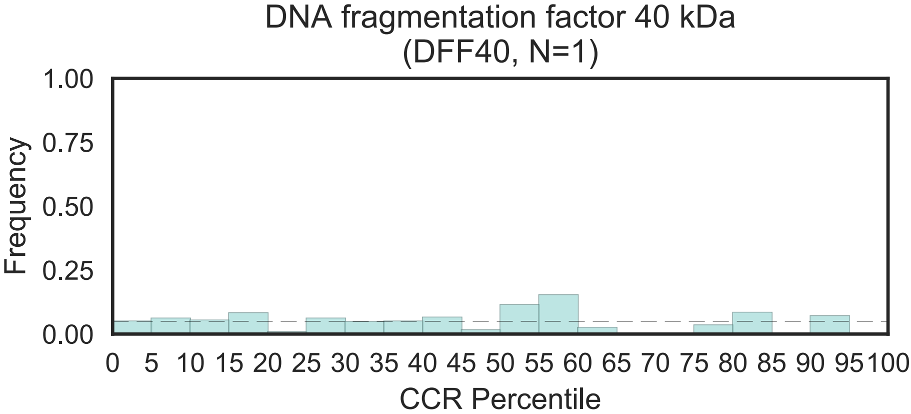

Decidual protein induced by progesterone family
(DEPP, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

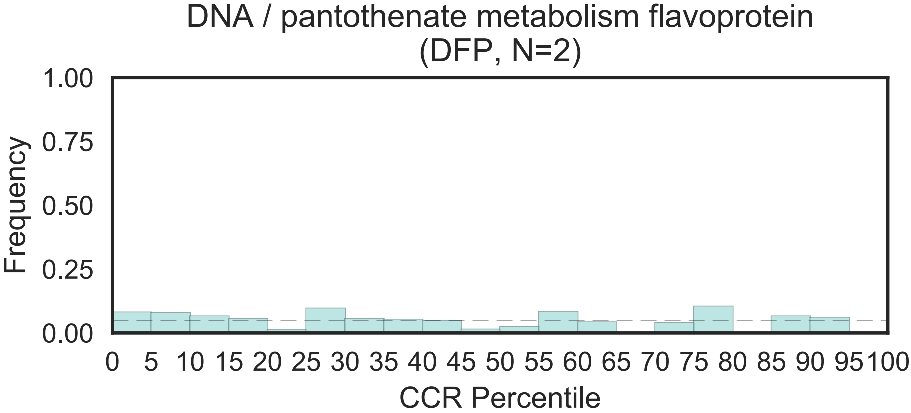


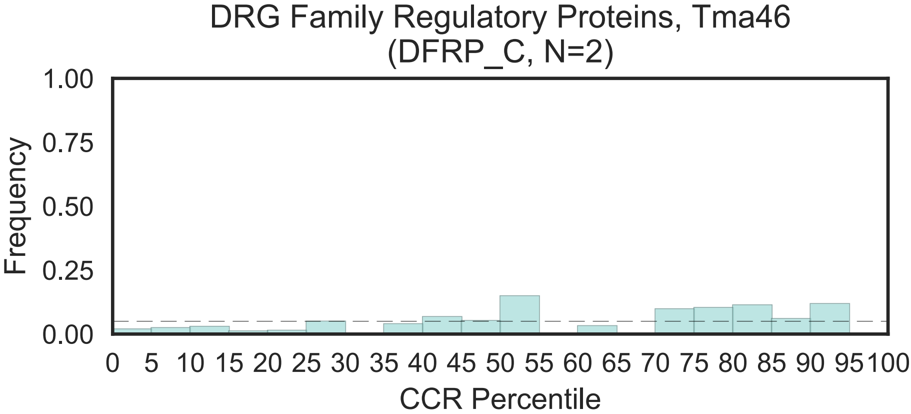
Der1-like family
(DER1, N=3)
Fisher's OR: 0.522; Bonferroni p-val: 1

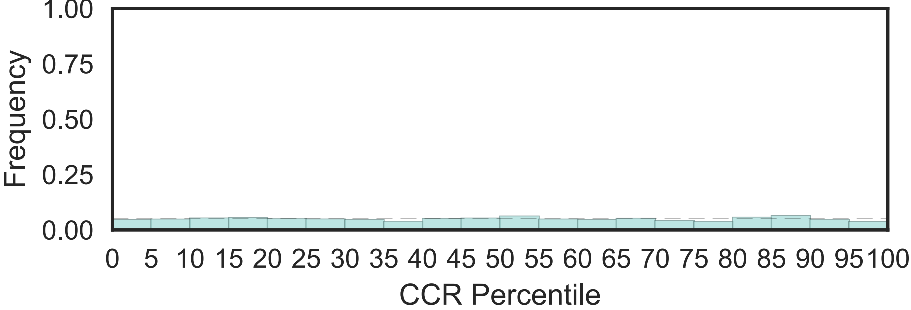

Dermatopontin
(DERM, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


DNA Fragmentation factor 45kDa, C terminal domain
(DFF-C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

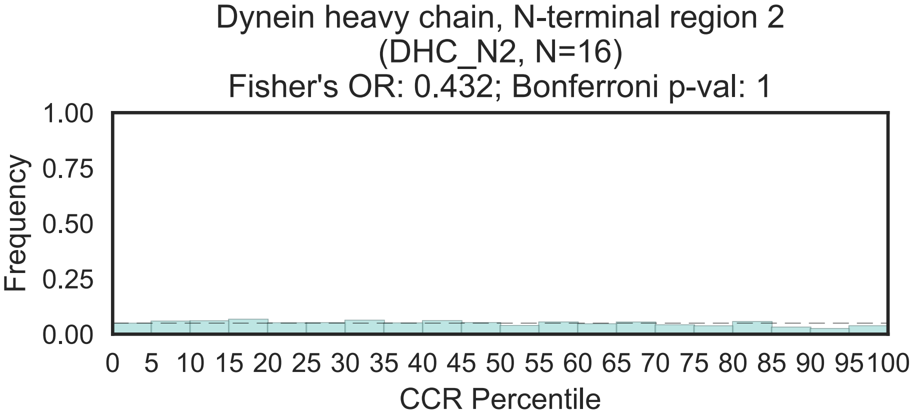

DNA fragmentation factor 40 kDa
(DFF40, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

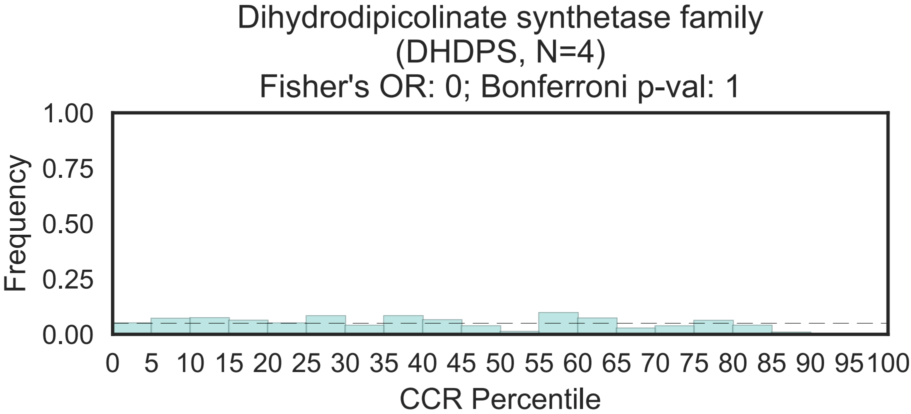

DNA / pantothenate metabolism flavoprotein
(DFP, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

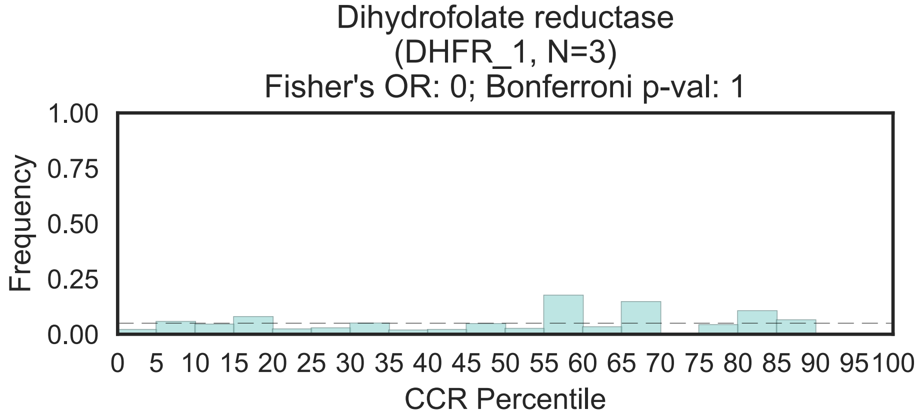

DRG Family Regulatory Proteins, Tma46
(DFRP_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

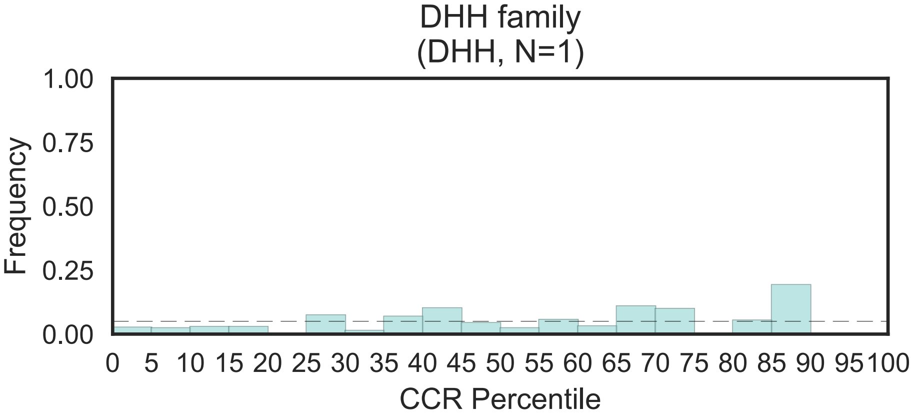


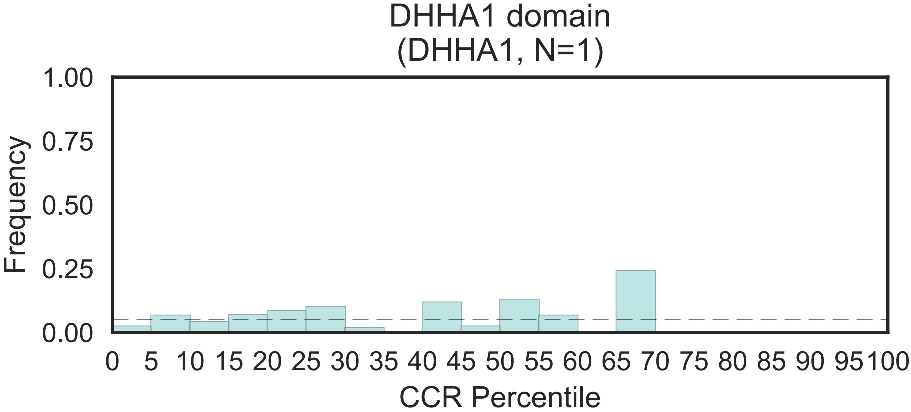
Dynein heavy chain, N-terminal region 1
(DHC_N1, N=11)
Fisher's OR: 0.515; Bonferroni p-val: 1

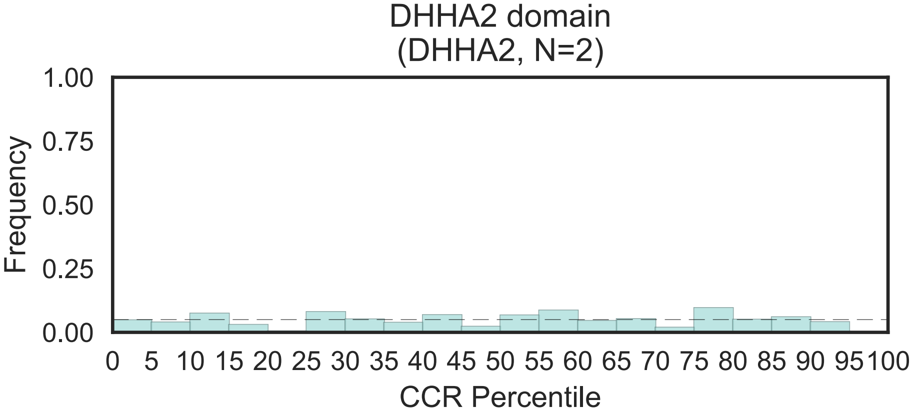

Dynein heavy chain, N-terminal region 2
(DHC_N2, N=16)
Fisher's OR: 0.432; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

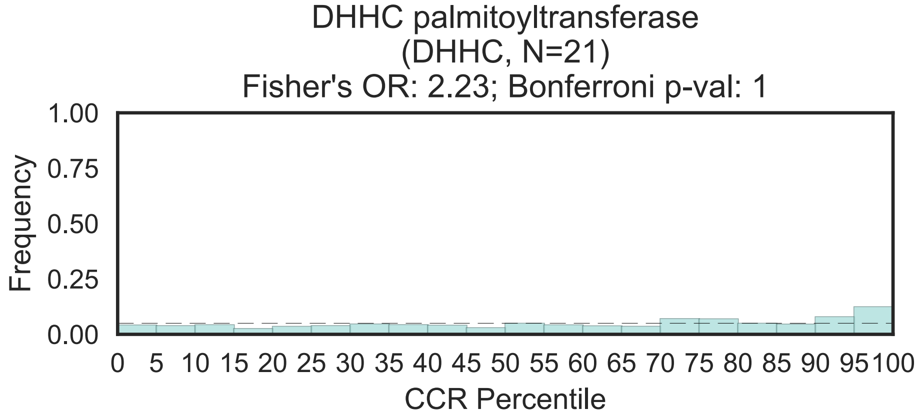

Dihydrodipicolinate synthetase family
(DHDPS, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

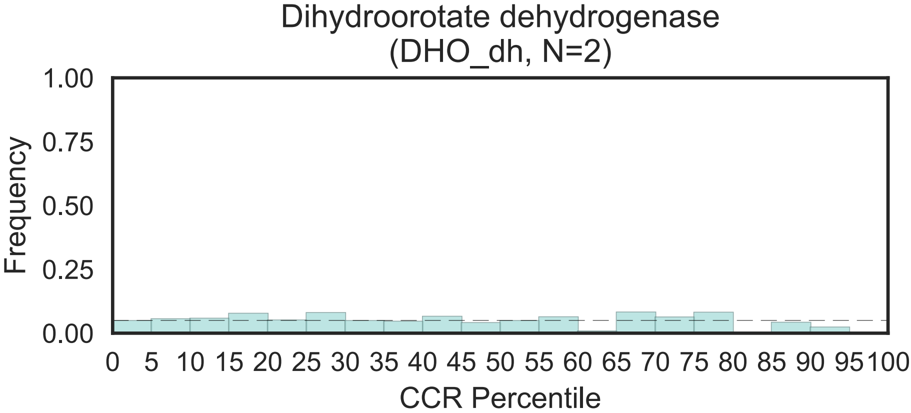

Dihydrofolate reductase
(DHFR_1, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

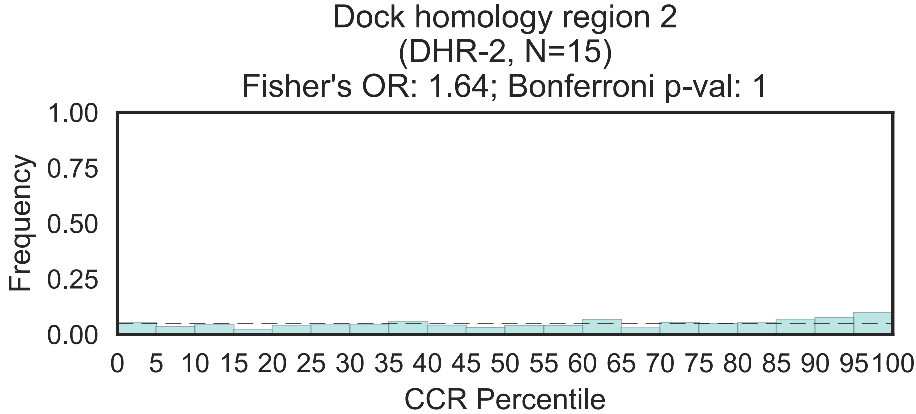

DHH family
(DHH, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


DHHA1 domain
(DHHA1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

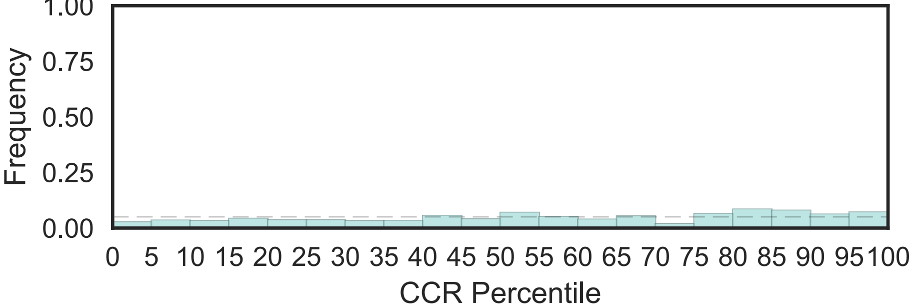

DHHA2 domain
(DHHA2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

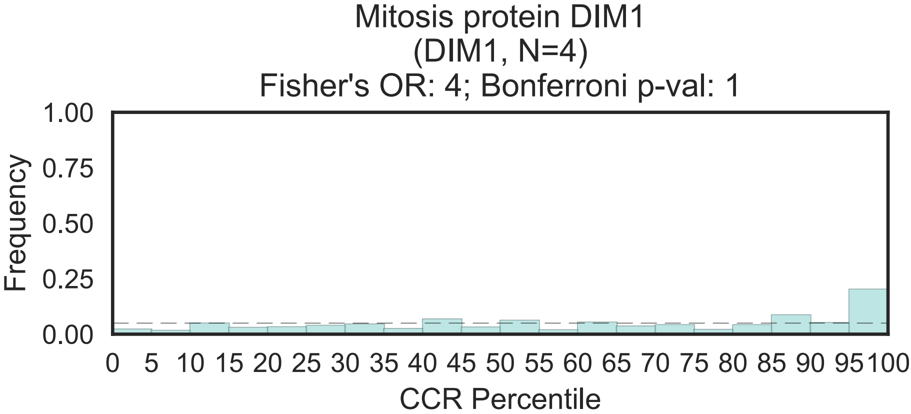

DHHC palmitoyltransferase
(DHHC, N=21)
Fisher's OR: 2.23; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Dihydroorotate dehydrogenase
(DHO_dh, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

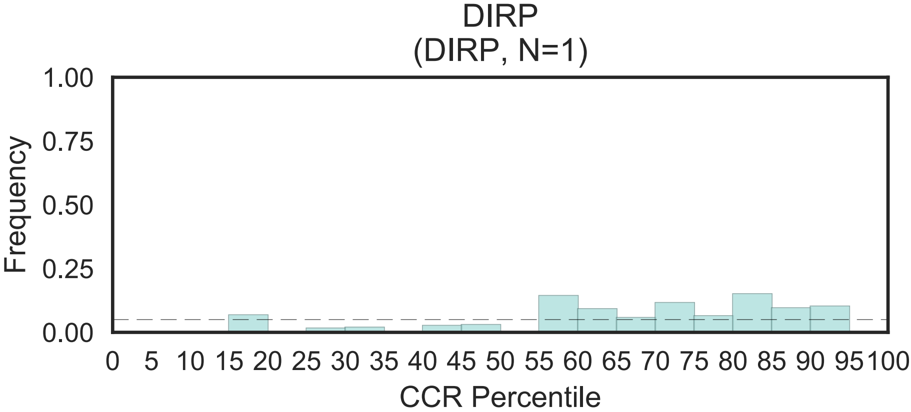

Dock homology region 2
(DHR-2, N=15)
Fisher's OR: 1.64; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

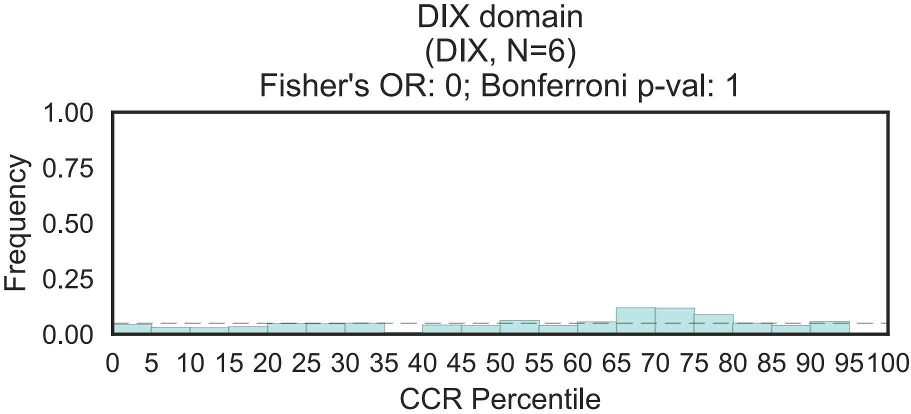
DIL domain
(DIL, N=6)
Fisher's OR: 2.21; Bonferroni p-val: 1

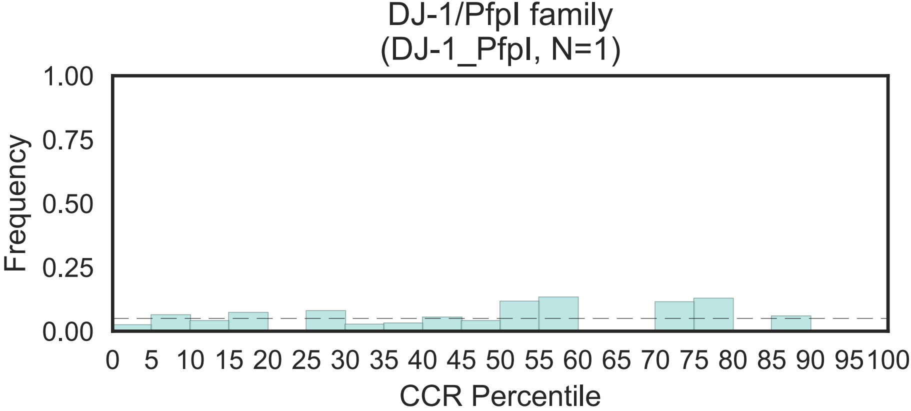


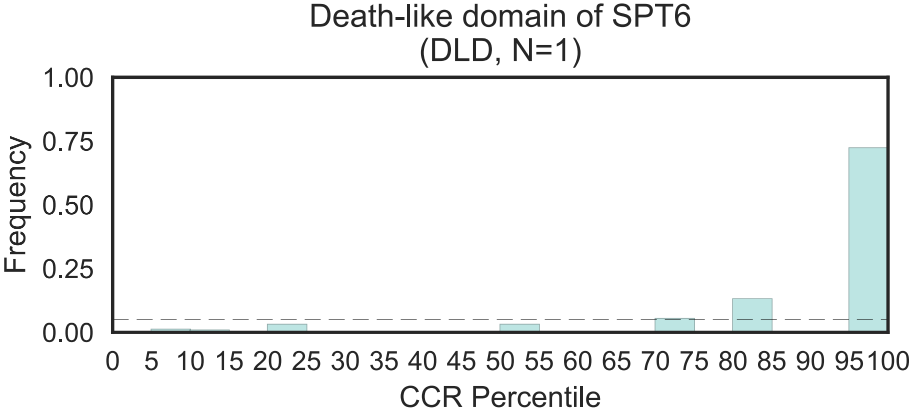


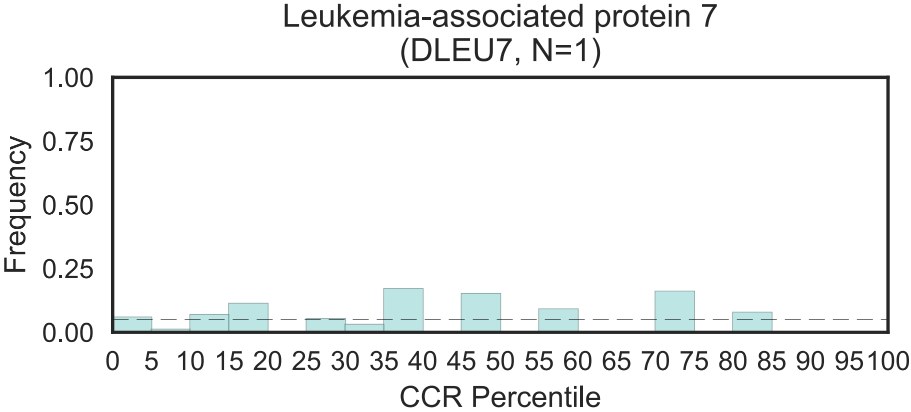
Mitosis protein DIM1
(DIM1, N=4)
Fisher's OR: 4; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

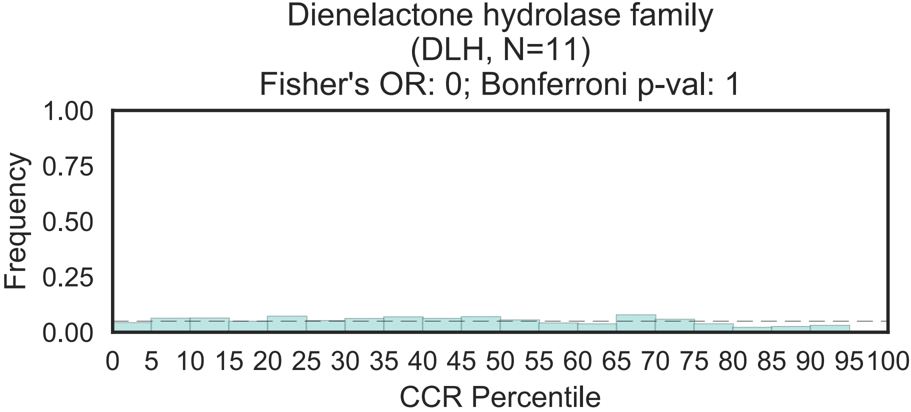

DIRP
(DIRP, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

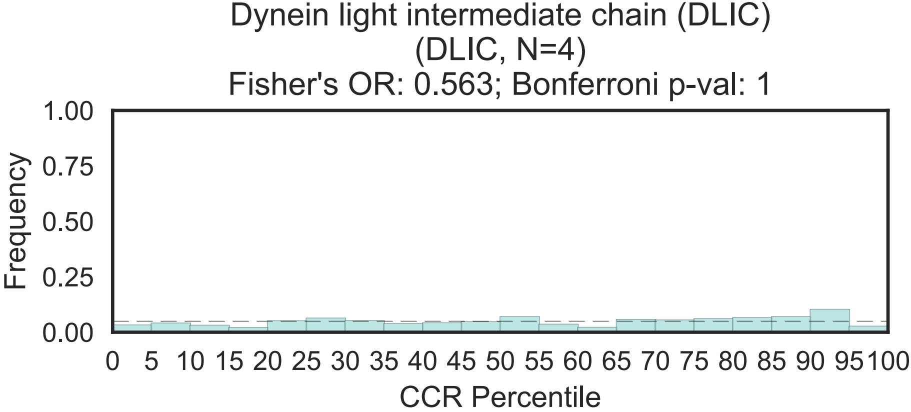

DIX domain
(DIX, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

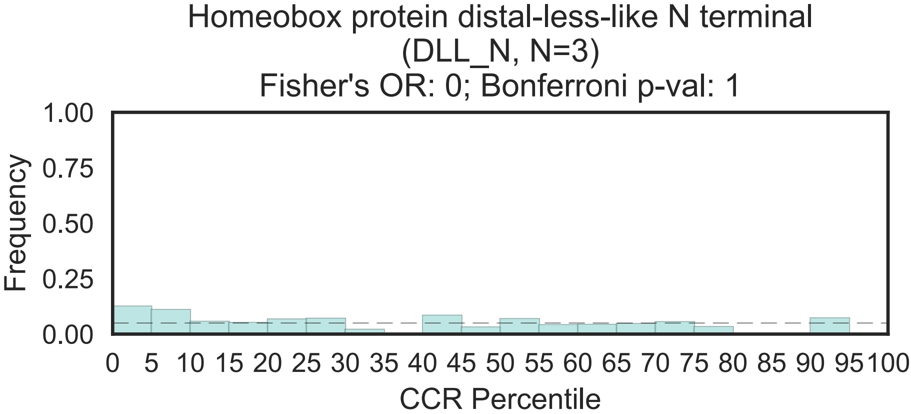

DJ-1/PfpI family
(DJ-1_PfpI, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

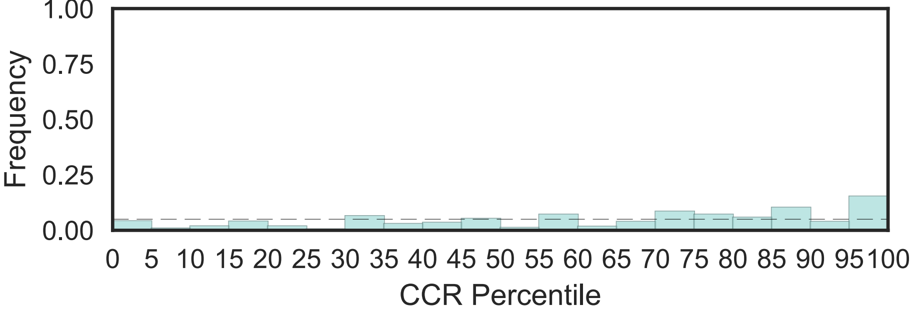

Death-like domain of SPT6
(DLD, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

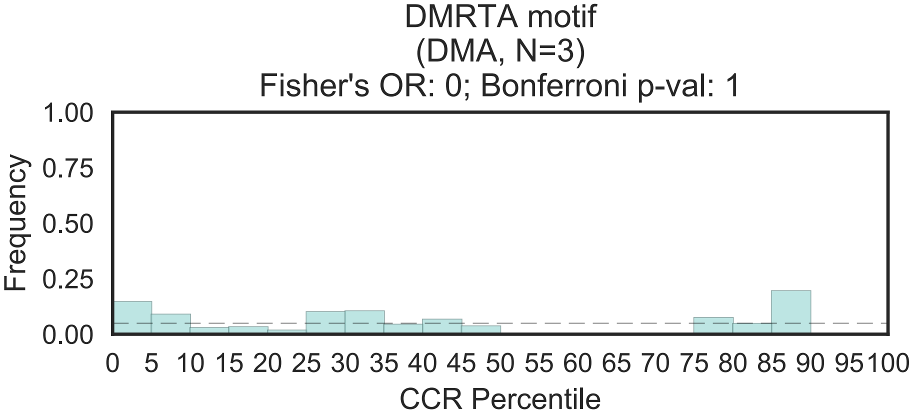

Leukemia-associated protein 7
(DLEU7, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

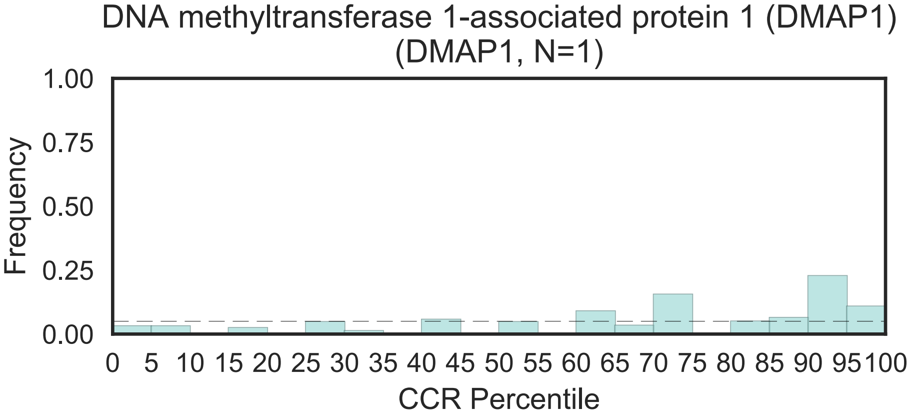

Dienelactone hydrolase family
(DLH, N=11)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

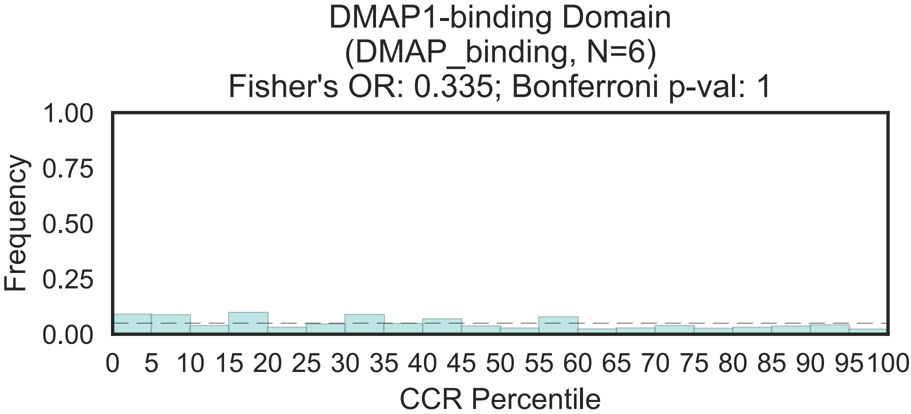

Dynein light intermediate chain (DLIC)
(DLIC, N=4)
Fisher's OR: 0.563; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

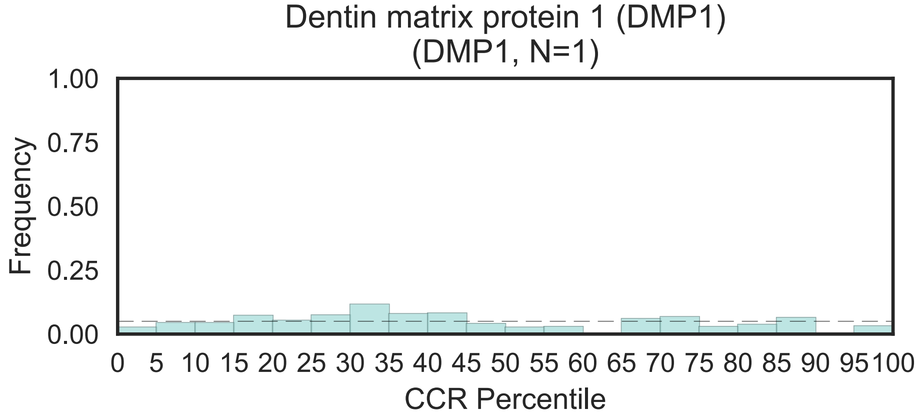

Homeobox protein distal-less-like N terminal
(DLL_N, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

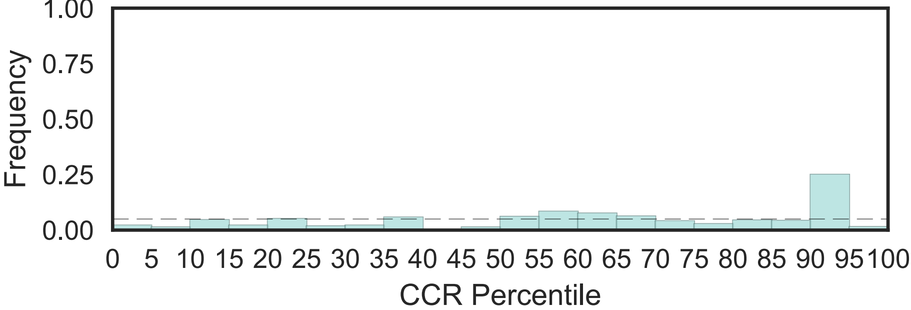

DM DNA binding domain
(DM, N=7)
Fisher's OR: 3.54; Bonferroni p-val: 1


DMRTA motif
(DMA, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

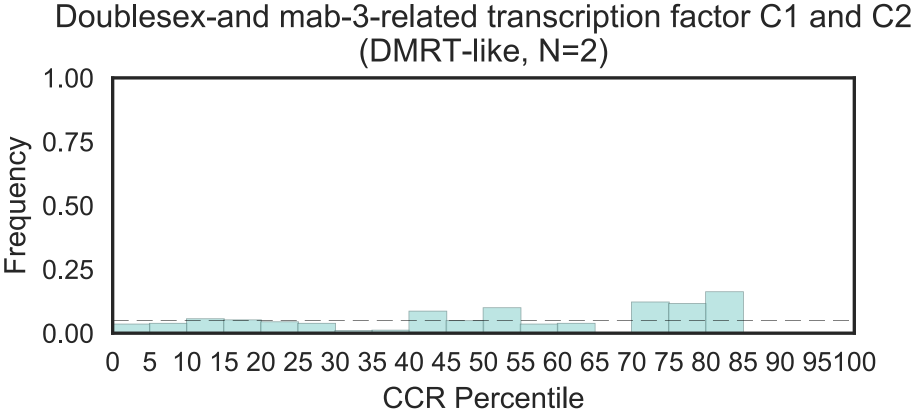

DNA methyltransferase 1-associated protein 1 (DMAP1)
(DMAP1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

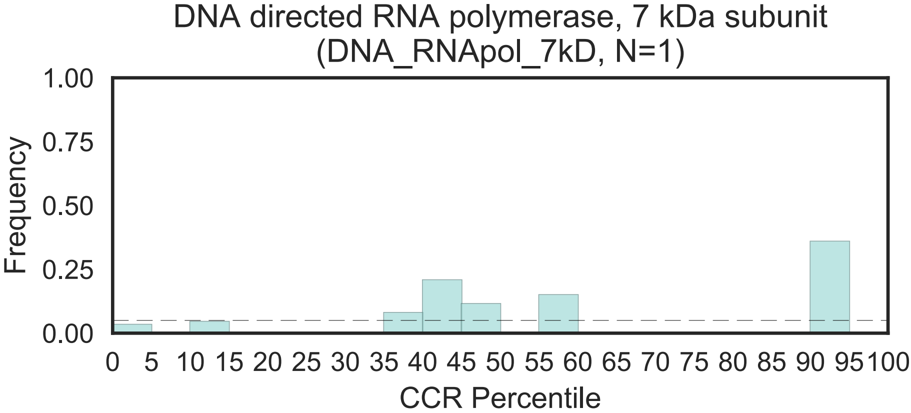

DMAP1-binding Domain
(DMAP_binding, N=6)
Fisher's OR: 0.335; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

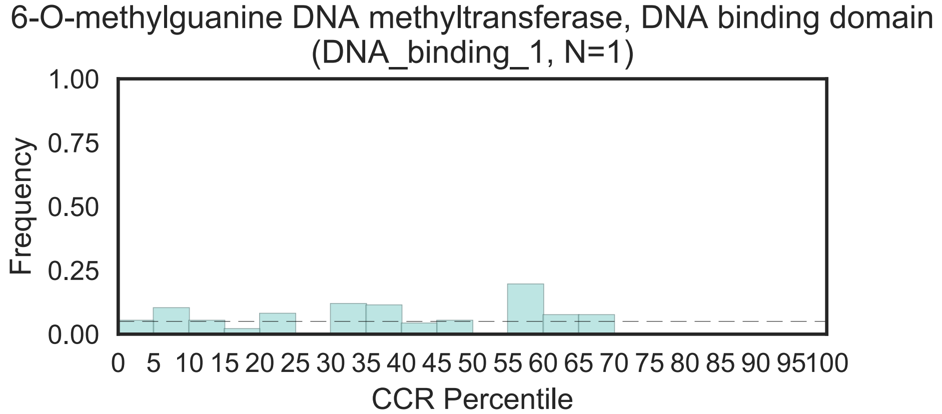

Dentin matrix protein 1 (DMP1)
(DMP1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

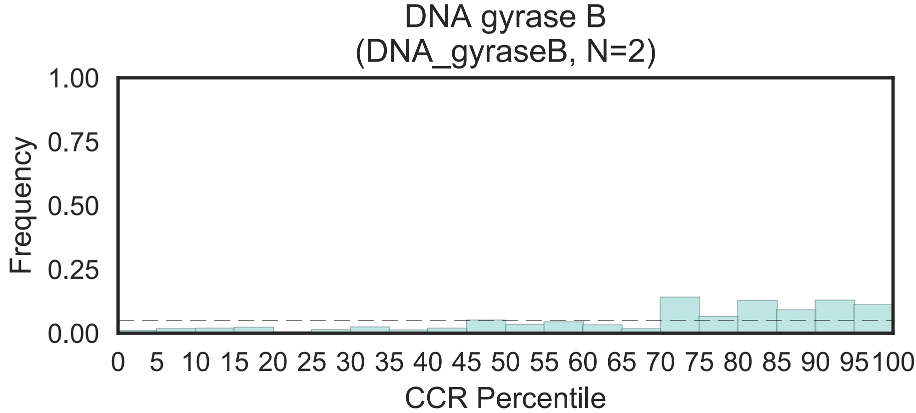


DMPK coiled coil domain like
(DMPK_coil, N=4)
Fisher's OR: 1.69; Bonferroni p-val: 1

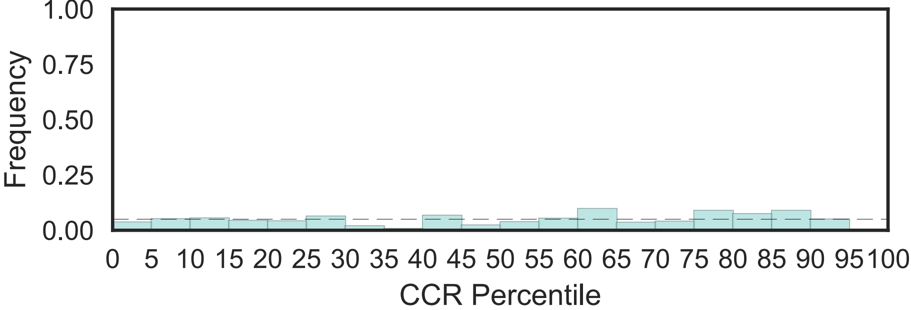

Doublesex-and mab-3-related transcription factor C1 and C2
(DMRT-like, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

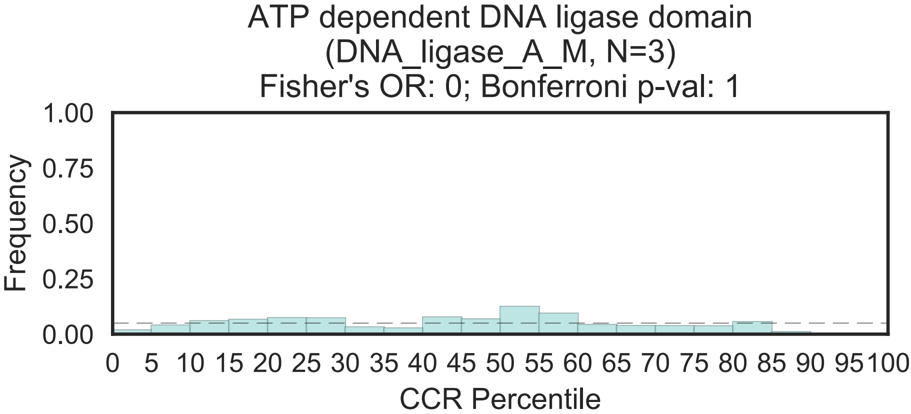

DNA directed RNA polymerase, 7 kDa subunit
(DNA_RNApol_7kD, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

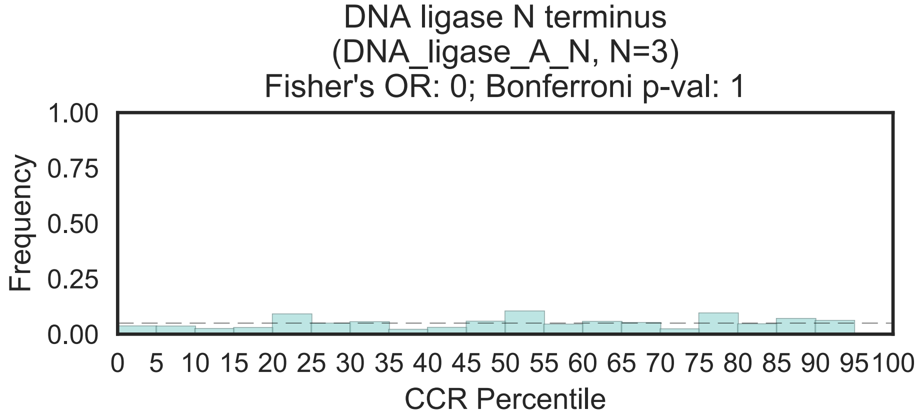

6-O-methylguanine DNA methyltransferase, DNA binding domain
(DNA_binding_1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

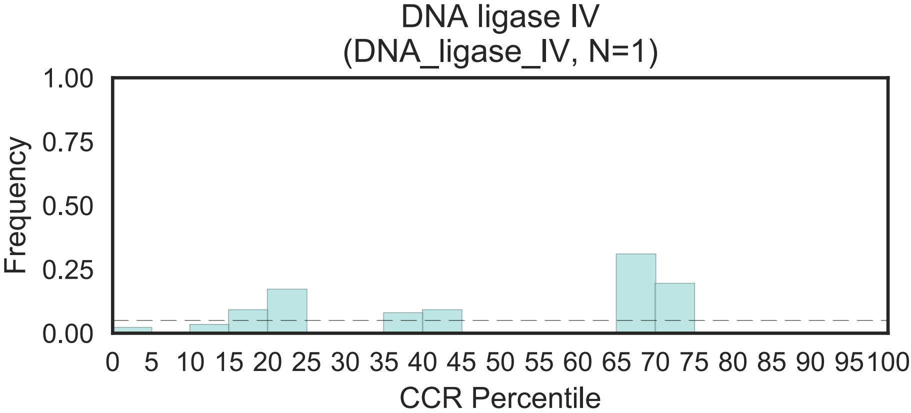

DNA gyrase B
(DNA_gyraseB, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

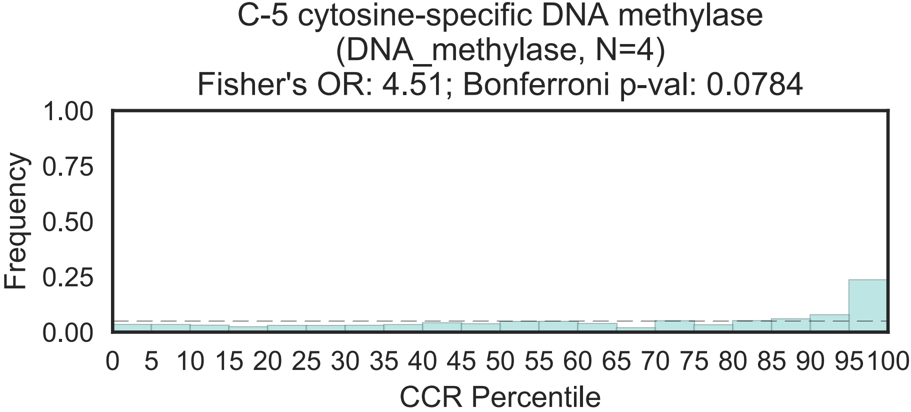
ATP dependent DNA ligase C terminal region (DNA_ligase_A_C, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

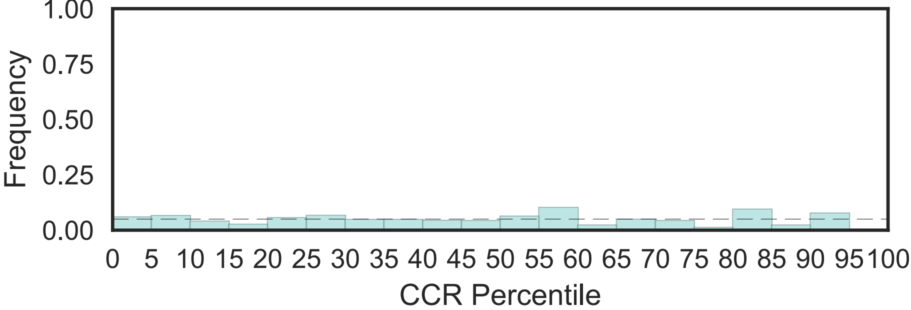



ATP dependent DNA ligase domain
(DNA_ligase_A_M, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

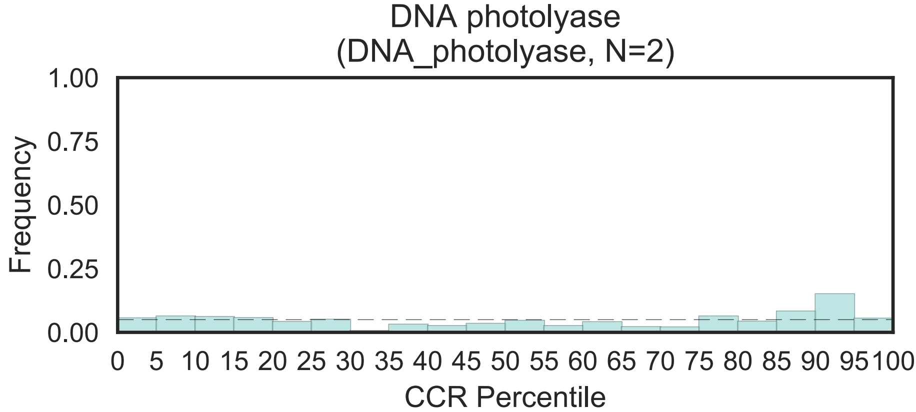

DNA ligase N terminus
(DNA_ligase_A_N, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

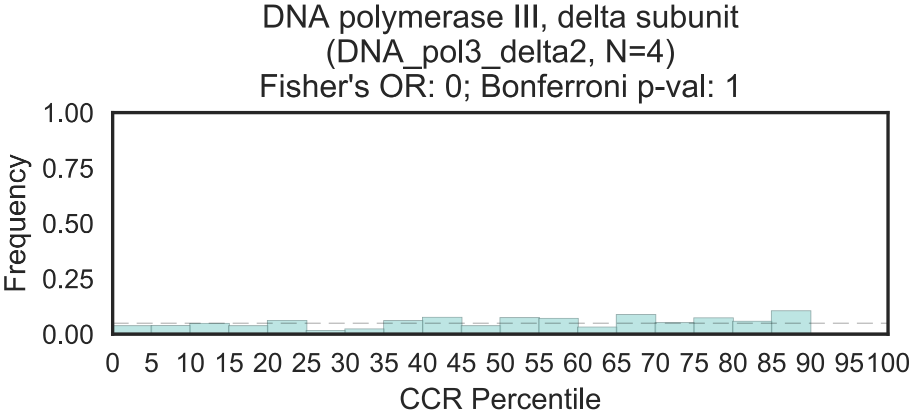

DNA ligase IV
(DNA_ligase_IV, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

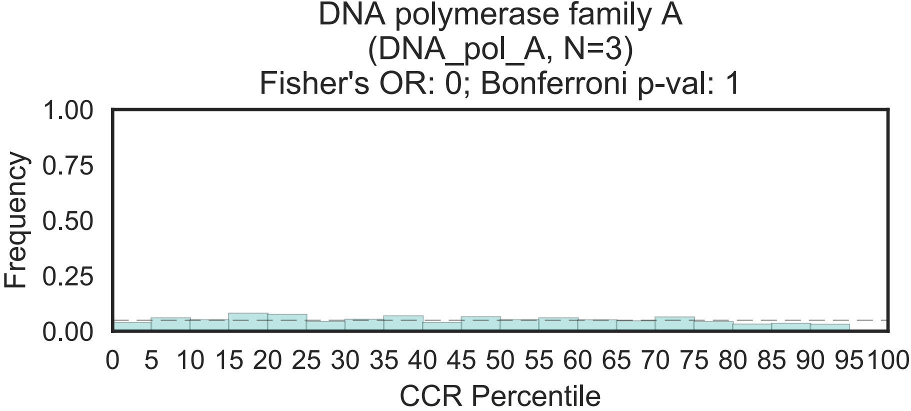

C-5 cytosine-specific DNA methylase
(DNA_methylase, N=4)
Fisher's OR: 4.51; Bonferroni p-val: 0.0784
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

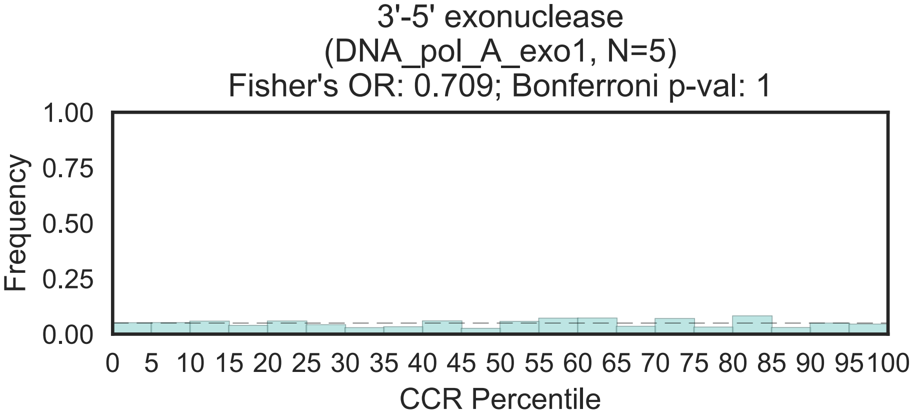


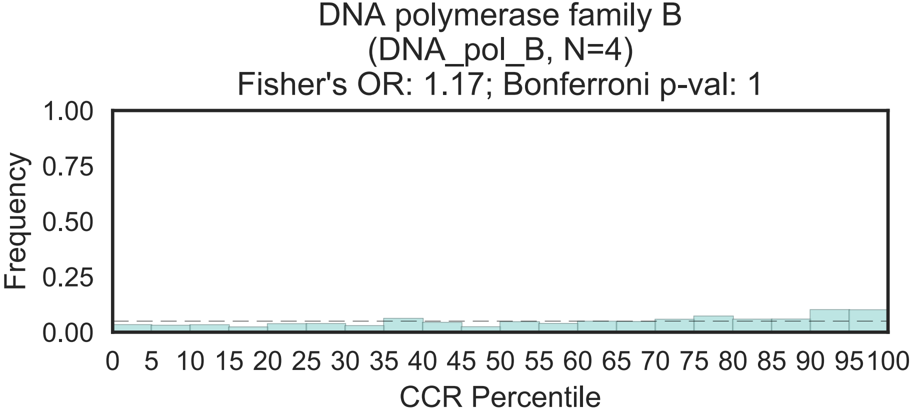
DNA mismatch repair protein, C-terminal domain
(DNA_mis_repair, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

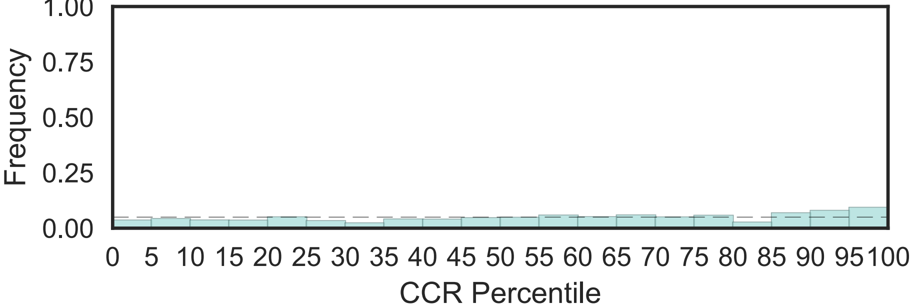

DNA photolyase
(DNA_photolyase, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


DNA polymerase III, delta subunit
(DNA_pol3_delta2, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

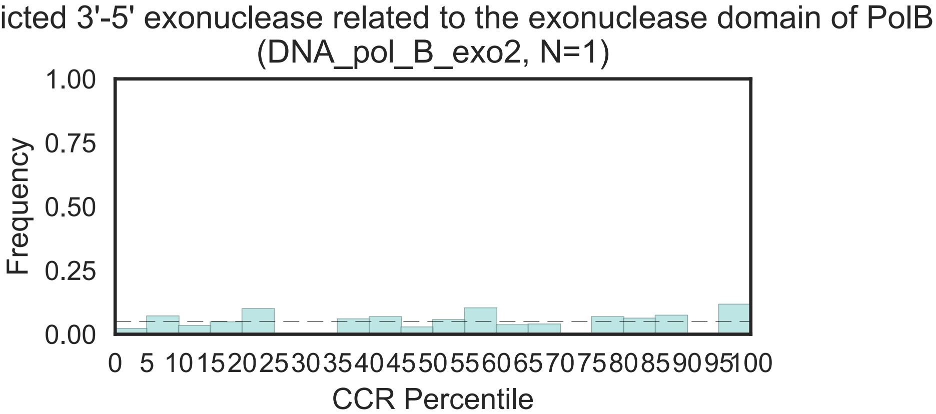

DNA polymerase family A
(DNA_pol_A, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

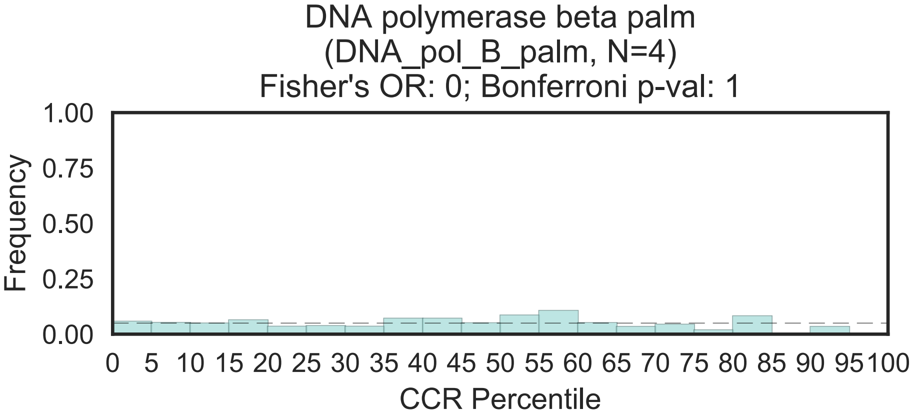

3'-5' exonuclease
(DNA_pol_A_exo1, N=5)
Fisher's OR: 0.709; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


DNA polymerase family B
(DNA_pol_B, N=4)
Fisher's OR: 1.17; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

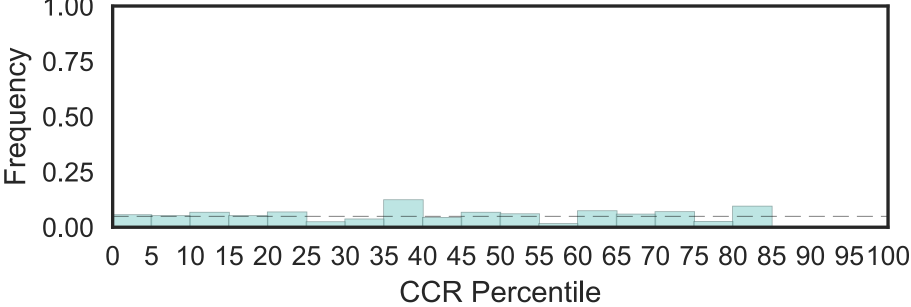


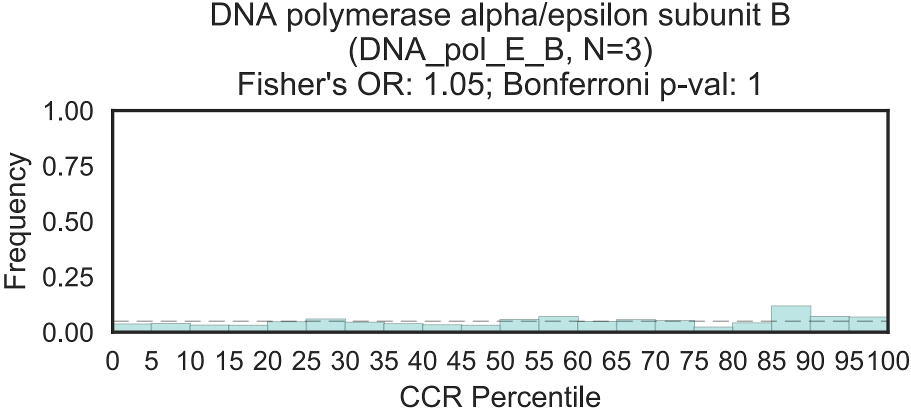
DNA polymerase family B, exonuclease domain
(DNA_pol_B_exo1, N=4)
Fisher's OR: 1.9; Bonferroni p-val: 1

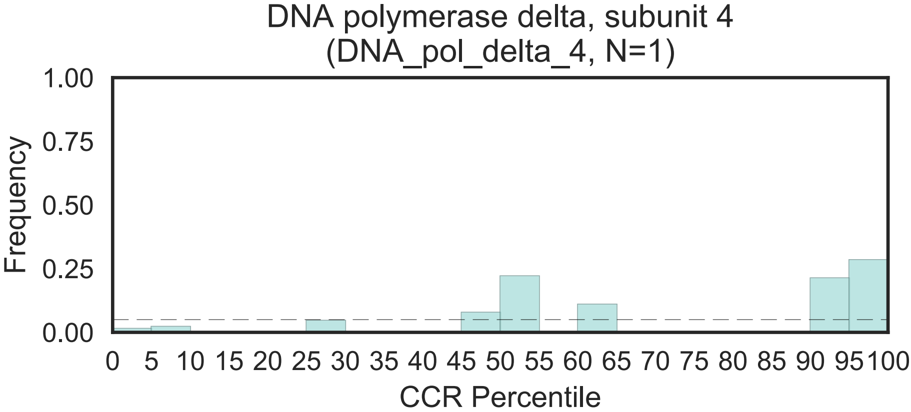

Predicted 3'-5' exonuclease related to the exonuclease domain of PolB
(DNA_pol_B_exo2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

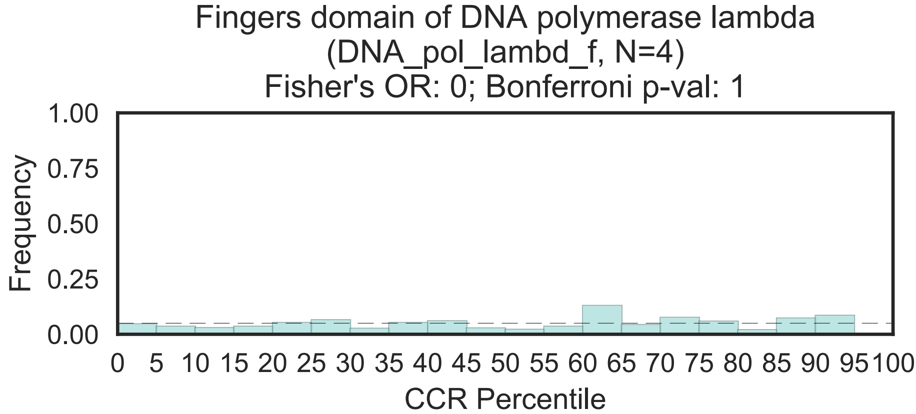

DNA polymerase beta palm
(DNA_pol_B_palm, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

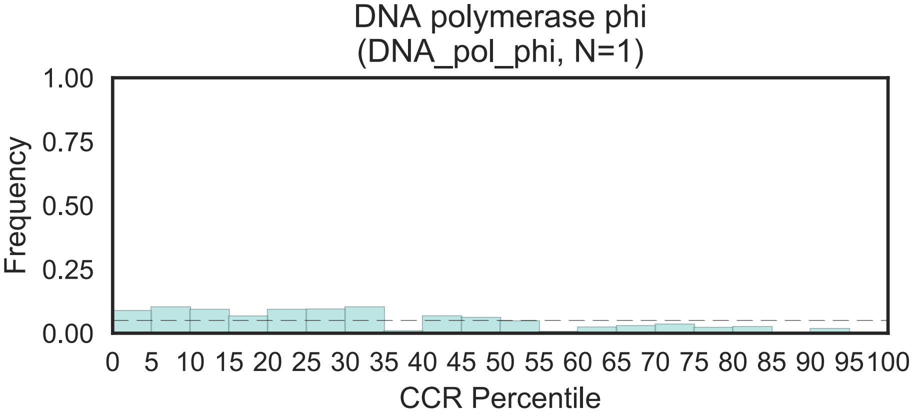
DNA polymerase beta thumb
(DNA_pol_B_thumb, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

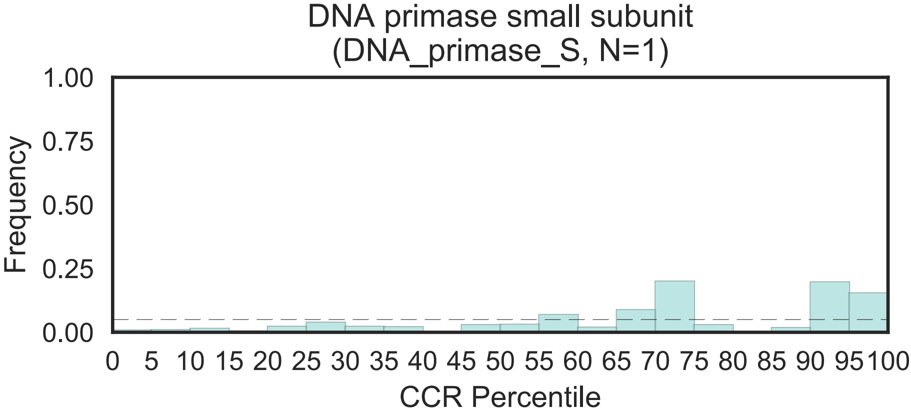


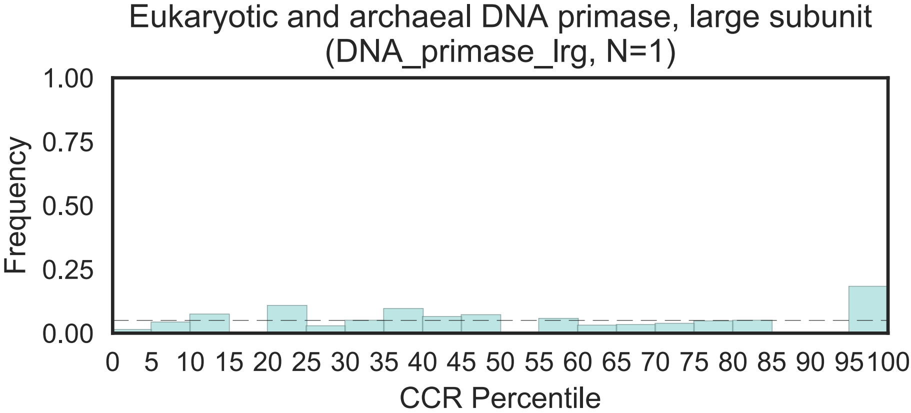

DNA polymerase alpha/epsilon subunit B
(DNA_pol_E_B, N=3)
Fisher's OR: 1.05; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

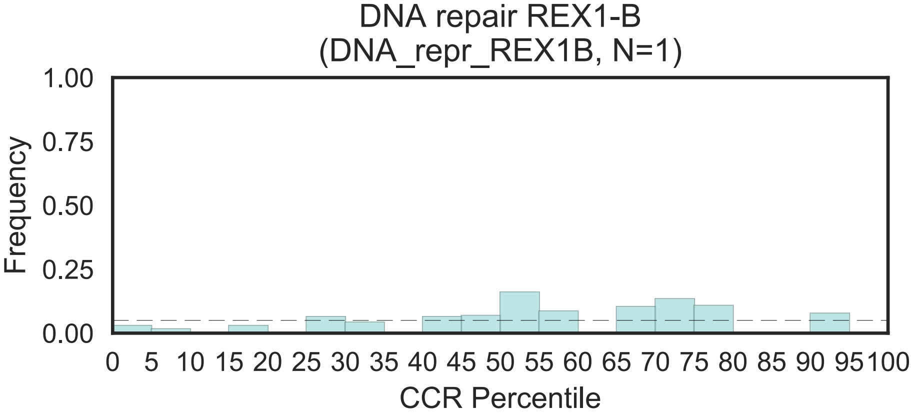

DNA polymerase delta, subunit 4
(DNA_pol_delta_4, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

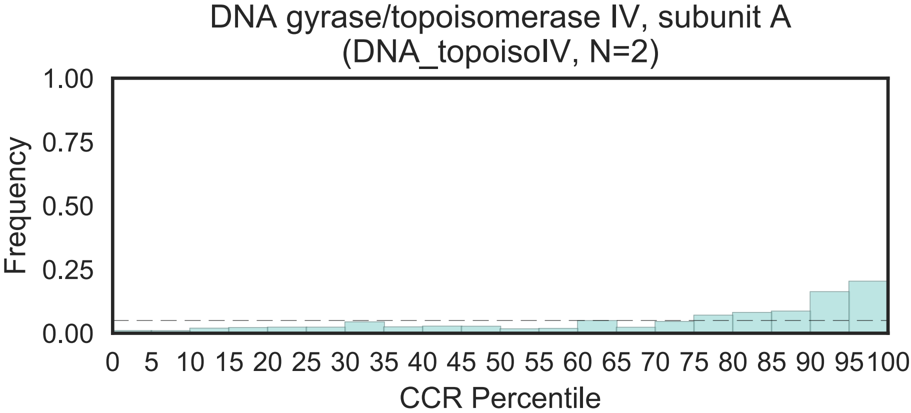

Fingers domain of DNA polymerase lambda
(DNA_pol_lambd_f, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

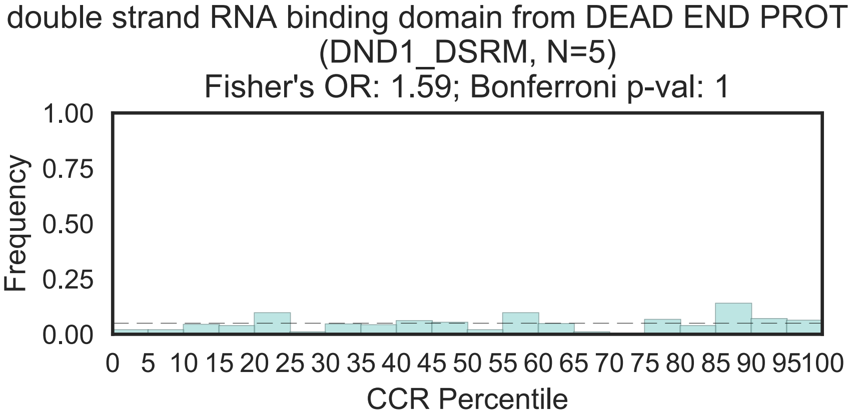

DNA polymerase phi
(DNA_pol_phi, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


DNA primase small subunit
(DNA_primase_S, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Eukaryotic and archaeal DNA primase, large subunit
(DNA_primase_lrg, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

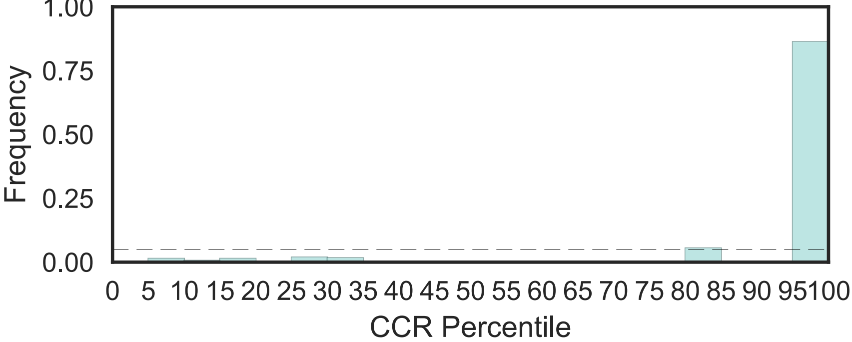

DNA repair REX1-B
(DNA_repr_REX1B, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

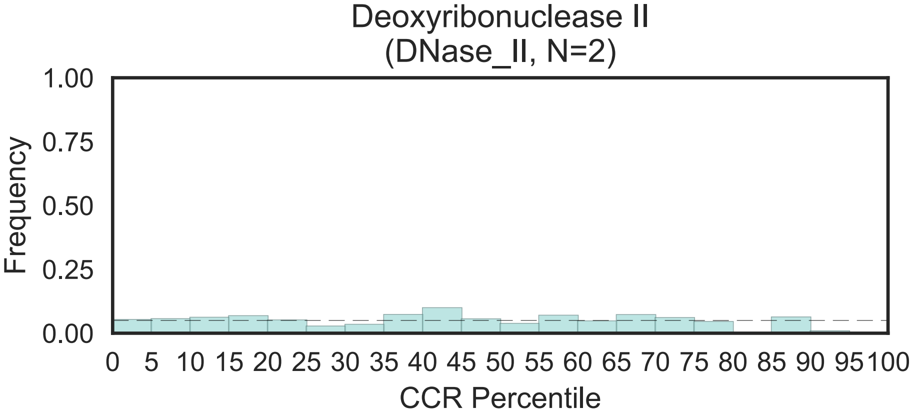

DNA gyrase/topoisomerase IV, subunit A
(DNA_topoisoIV, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

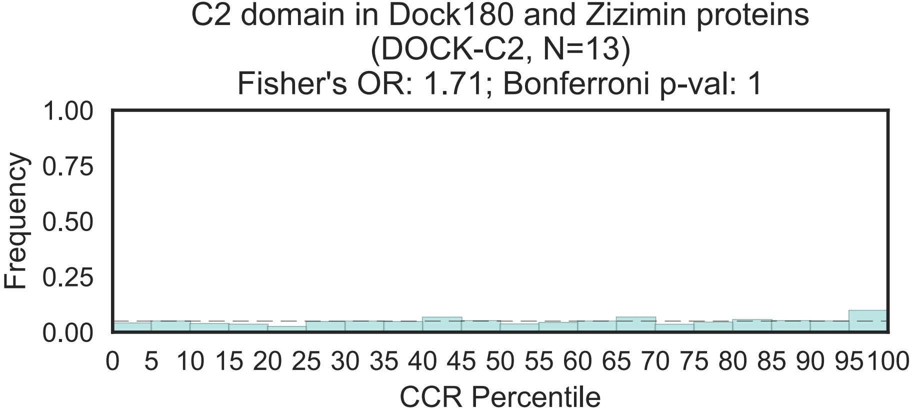


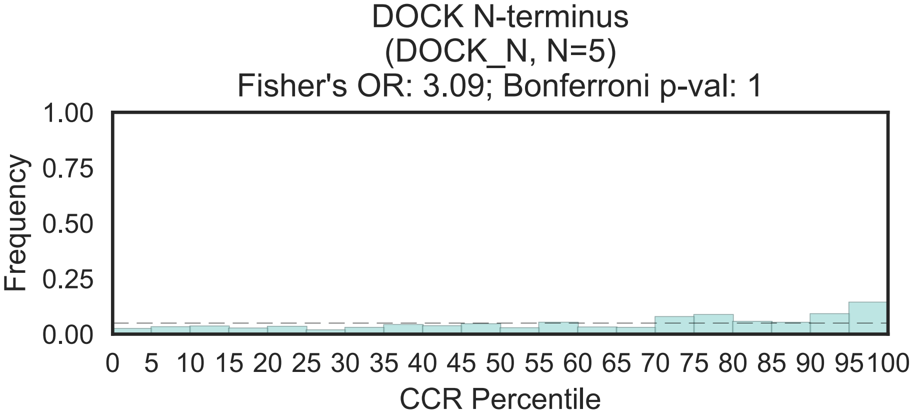
double strand RNA binding domain from DEAD END PROTEIN 1
(DND1_DSRM, N=5)
Fisher's OR: 1.59; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

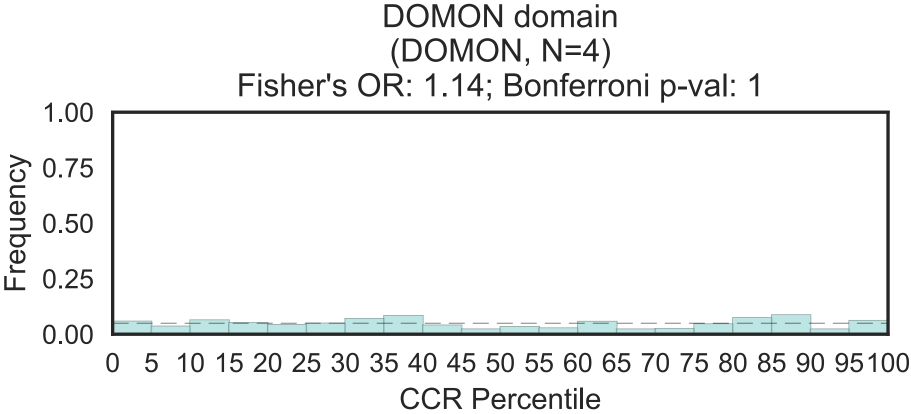
Cytosine specific DNA methyltransferase replication foci domain (DNMT1-RFD, N=1)

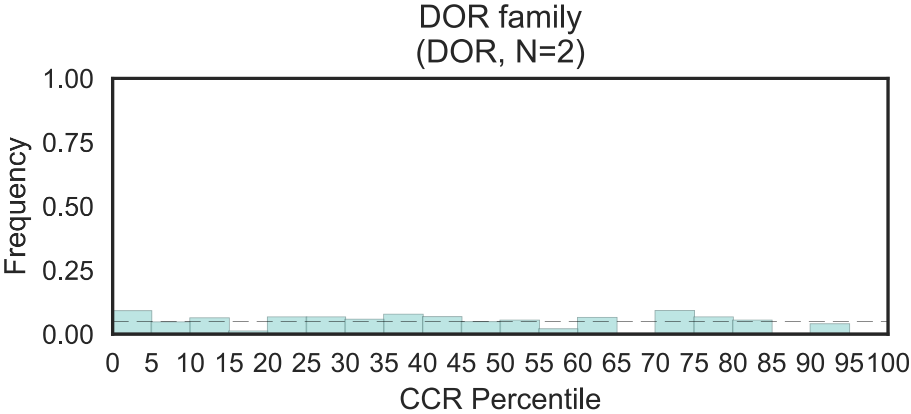


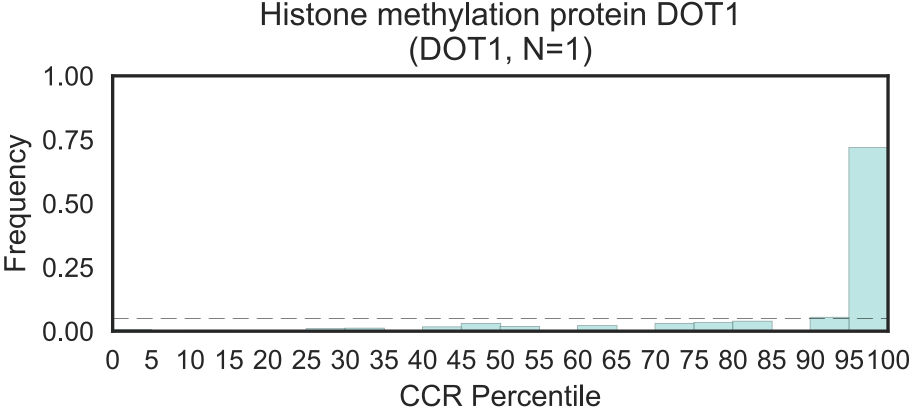

Deoxyribonuclease II
(DNase_II, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

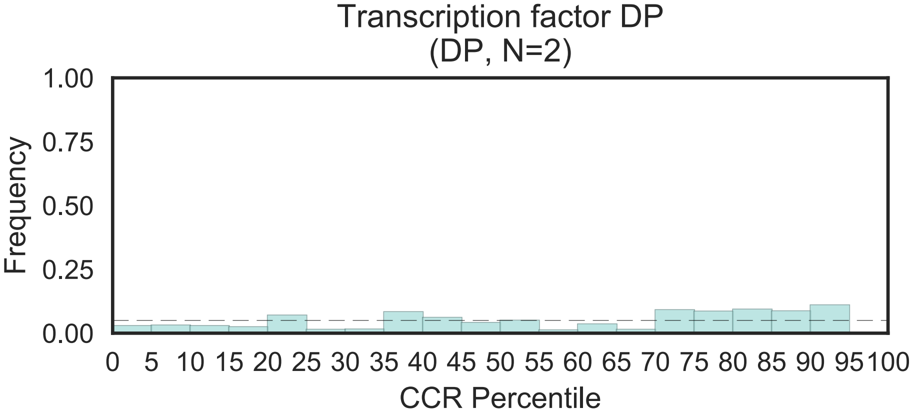

C2 domain in Dock180 and Zizimin proteins
(DOCK-C2, N=13)
Fisher's OR: 1.71; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

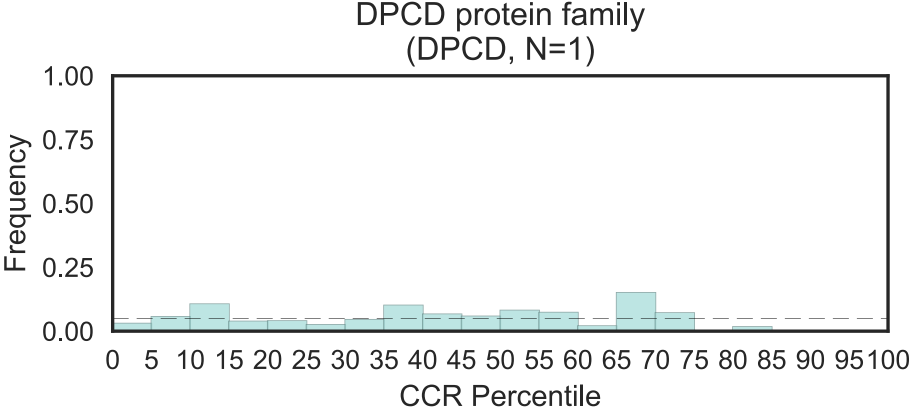

DOCK N-terminus
(DOCK_N, N=5)
Fisher's OR: 3.09; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


DOMON domain
(DOMON, N=4)
Fisher's OR: 1.14; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

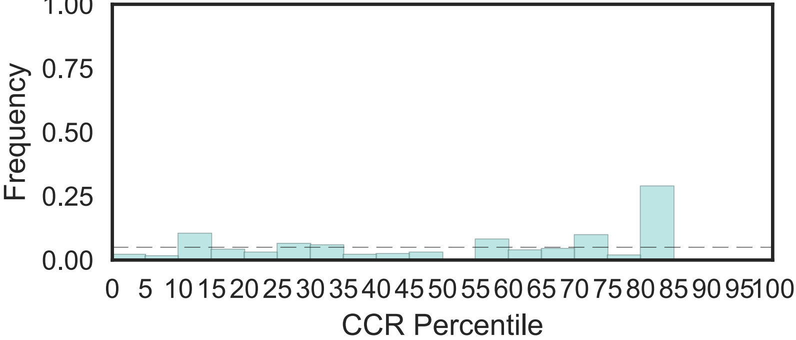

DOR family
(DOR, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

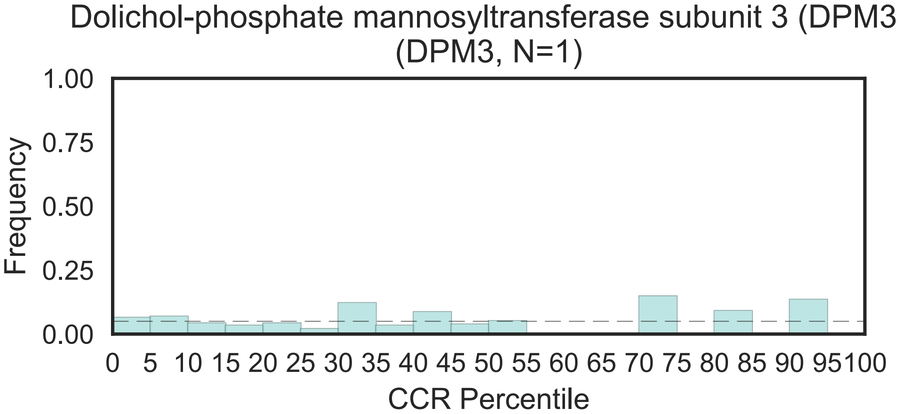

Histone methylation protein DOT1
(DOT1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

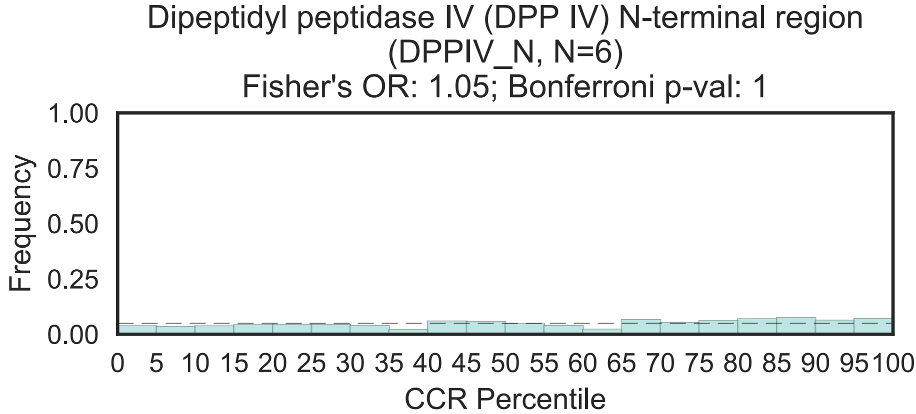

Transcription factor DP
(DP, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

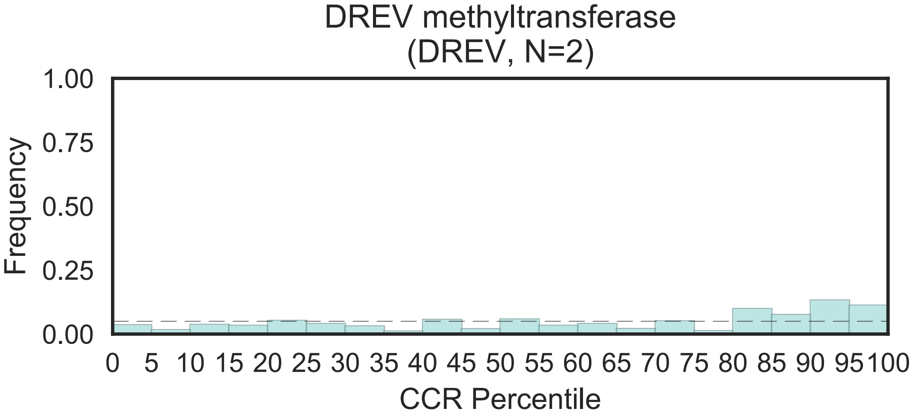

DPCD protein family
(DPCD, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

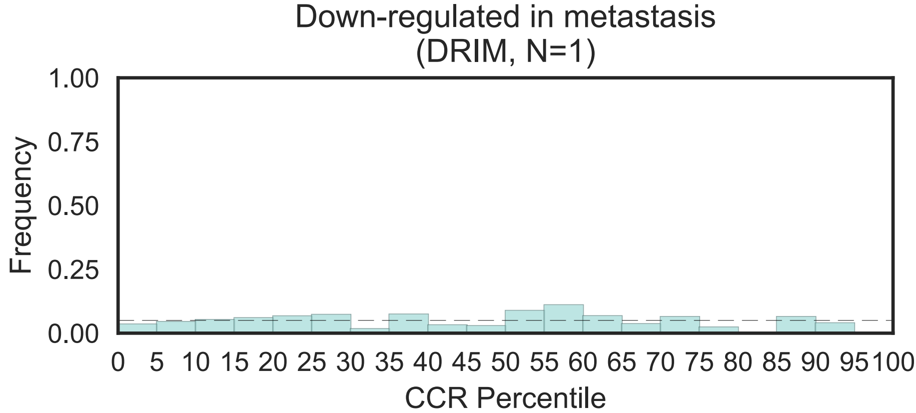
Dolichol phosphate-mannose biosynthesis regulatory protein (DPM2) (DPM2, N=1)

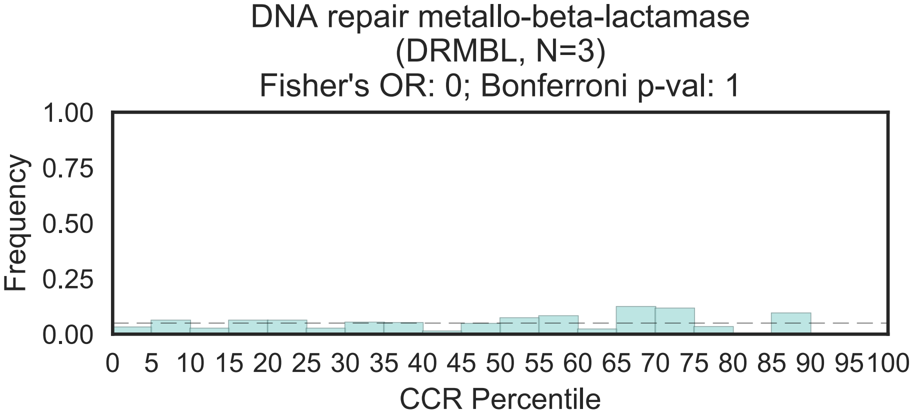


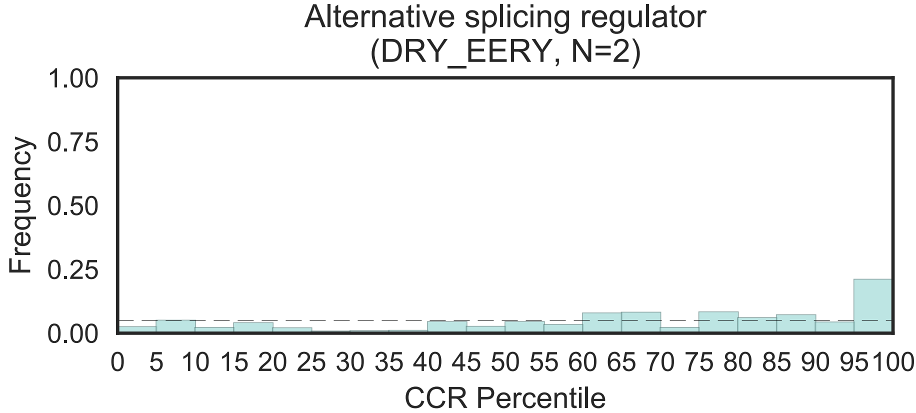

Dolichol-phosphate mannosyltransferase subunit 3 (DPM3)
(DPM3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

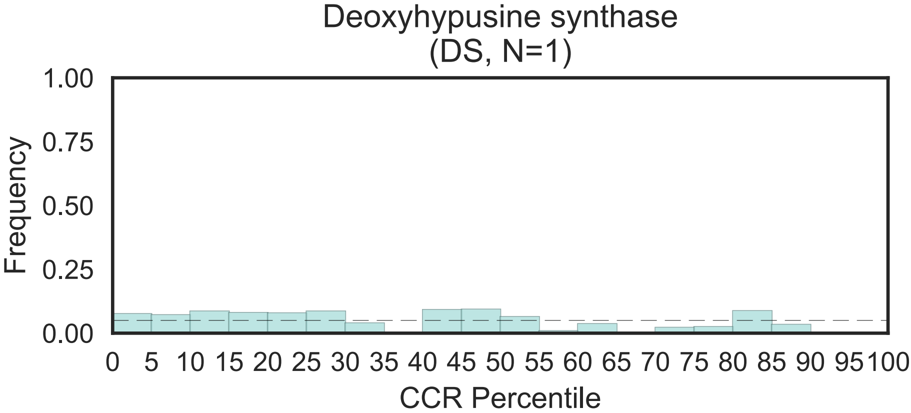

Dipeptidyl peptidase IV (DPP IV) N-terminal region
(DPPIV_N, N=6)
Fisher's OR: 1.05; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

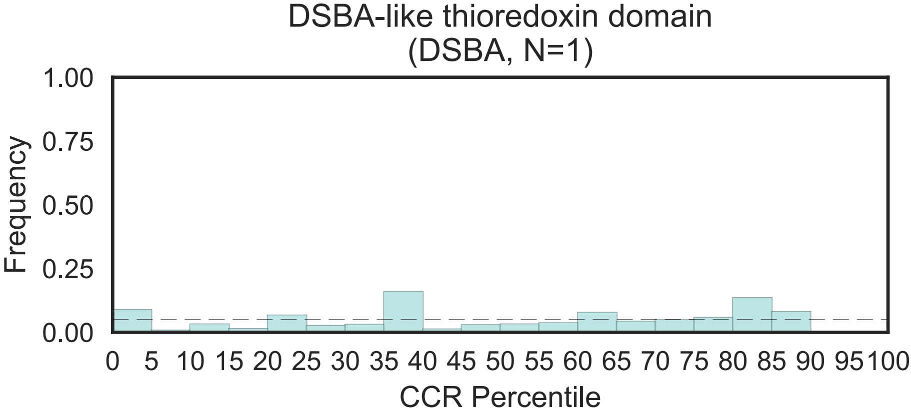

DREV methyltransferase
(DREV, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

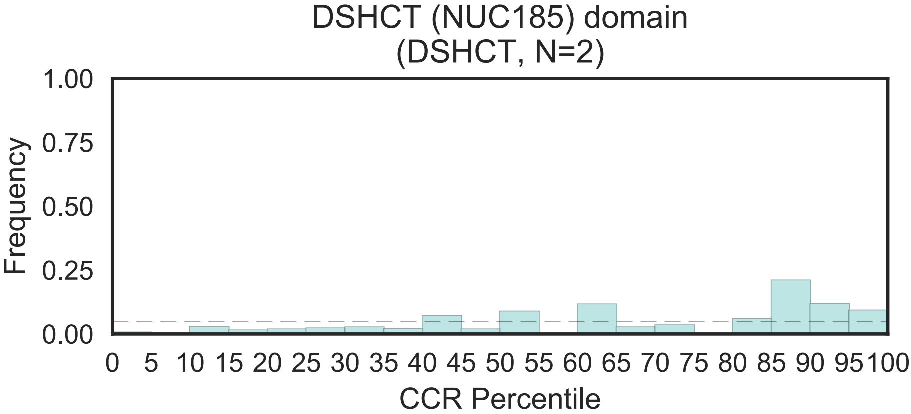

Down-regulated in metastasis
(DRIM, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

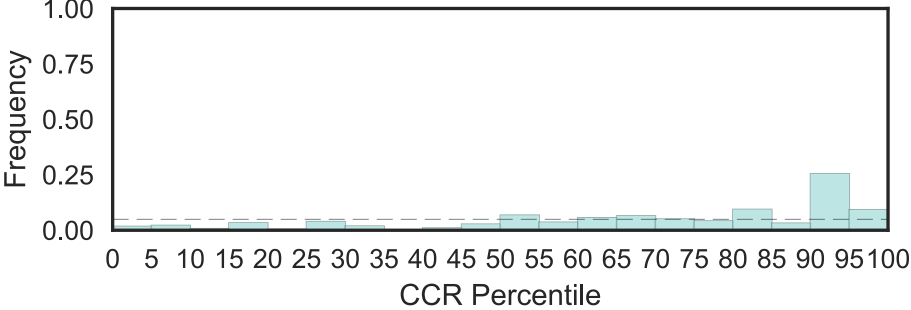

DNA repair metallo-beta-lactamase
(DRMBL, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Alternative splicing regulator
(DRY_EERY, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

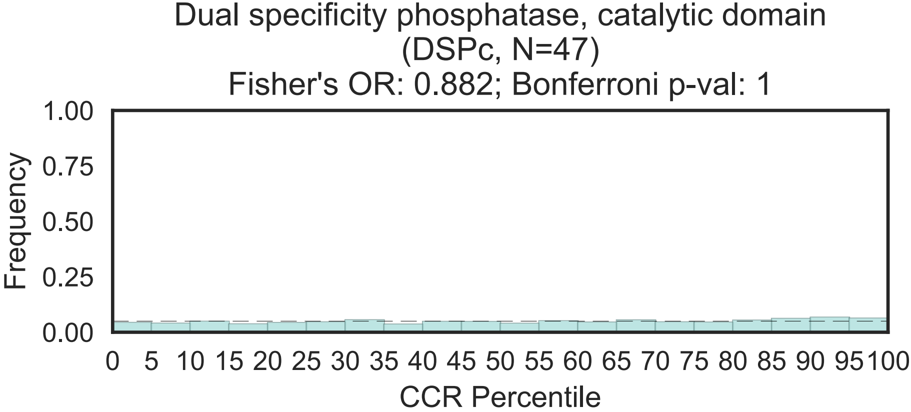

Deoxyhypusine synthase
(DS, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

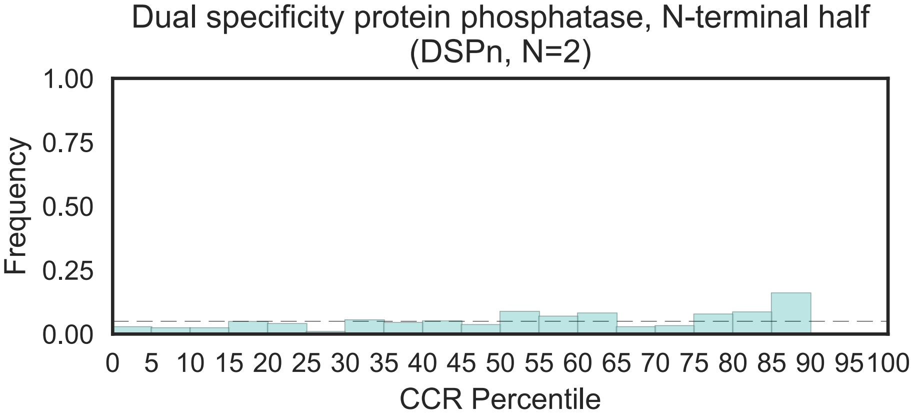

DSBA-like thioredoxin domain
(DSBA, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

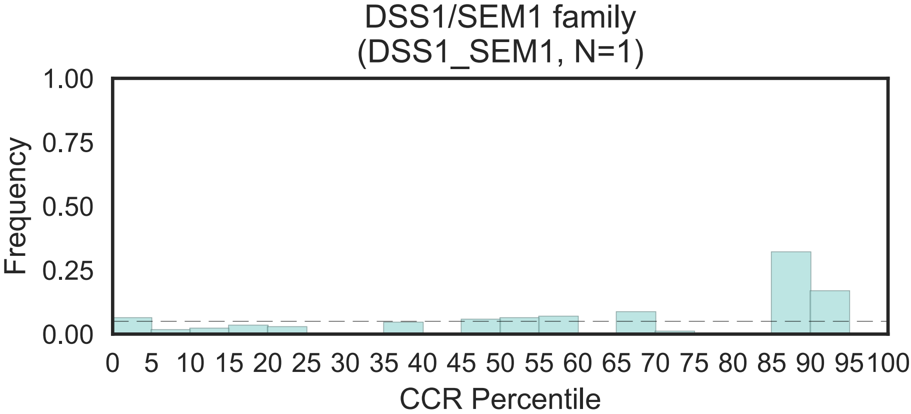

DSHCT (NUC185) domain
(DSHCT, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

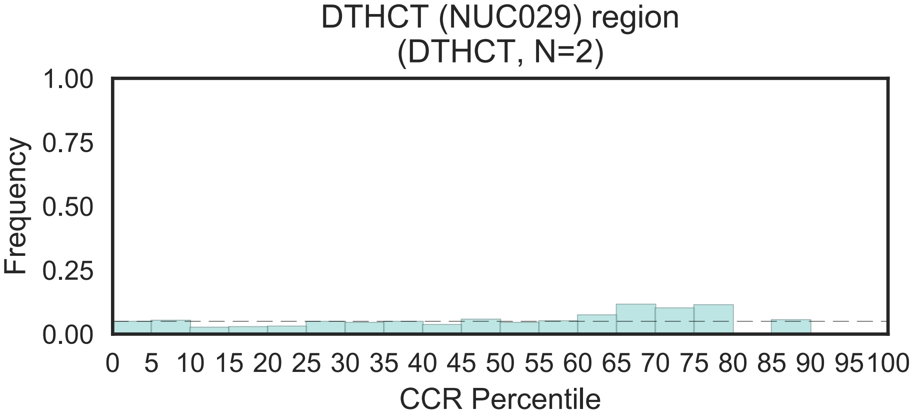


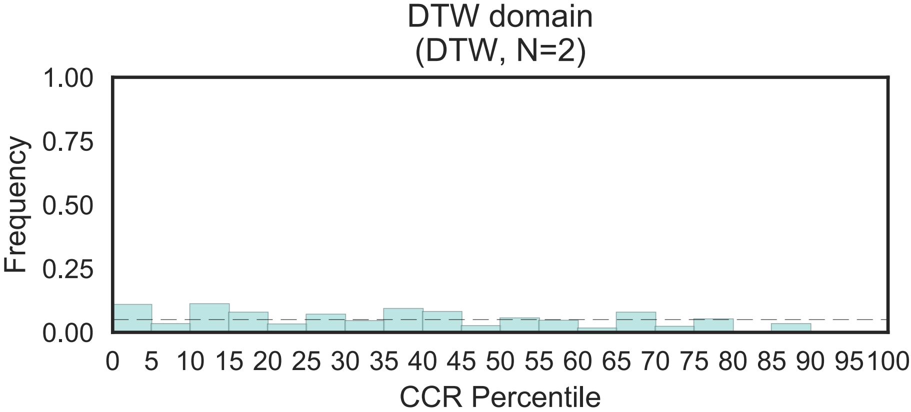
Delta serrate ligand
(DSL, N=4)
Fisher's OR: 1.77; Bonferroni p-val: 1

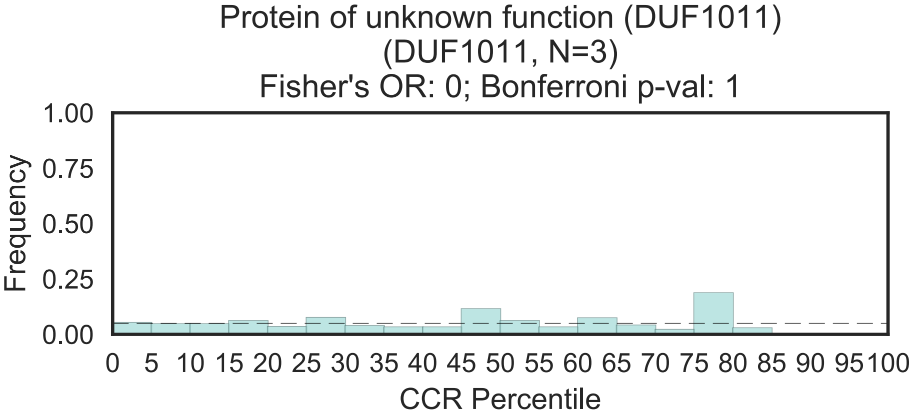

Dual specificity phosphatase, catalytic domain (DSPc, N=47)
Fisher's OR: 0.882; Bonferroni p-val: 1

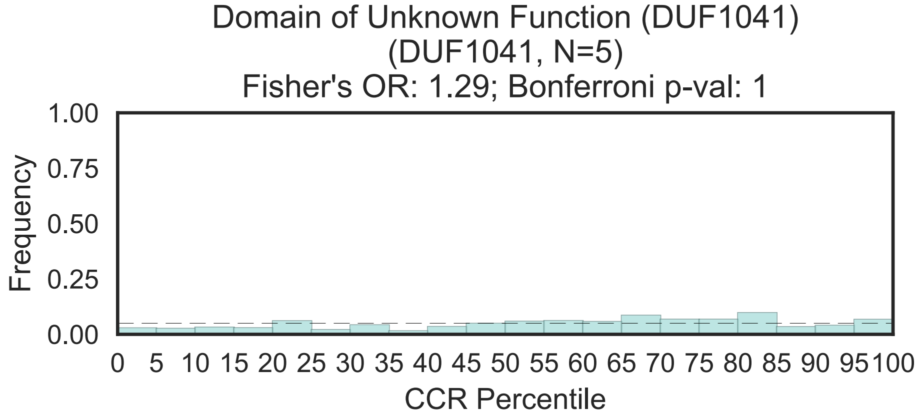

Dual specificity protein phosphatase, N-terminal half
(DSPn, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

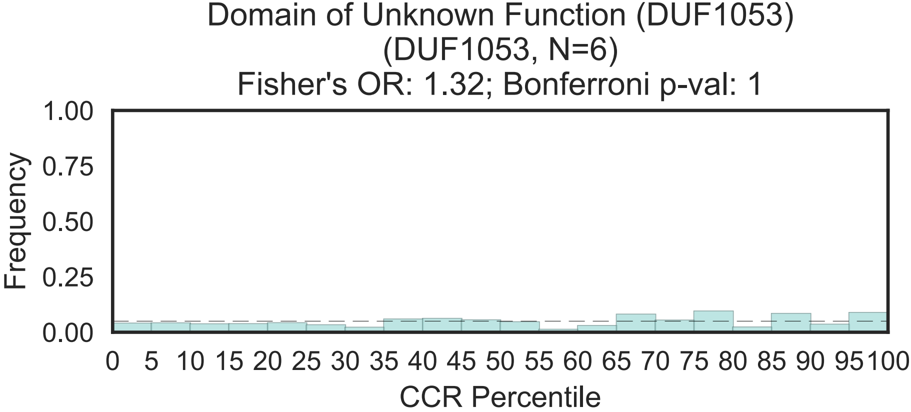

DSS1/SEM1 family
(DSS1_SEM1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


DTHCT (NUC029) region
(DTHCT, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

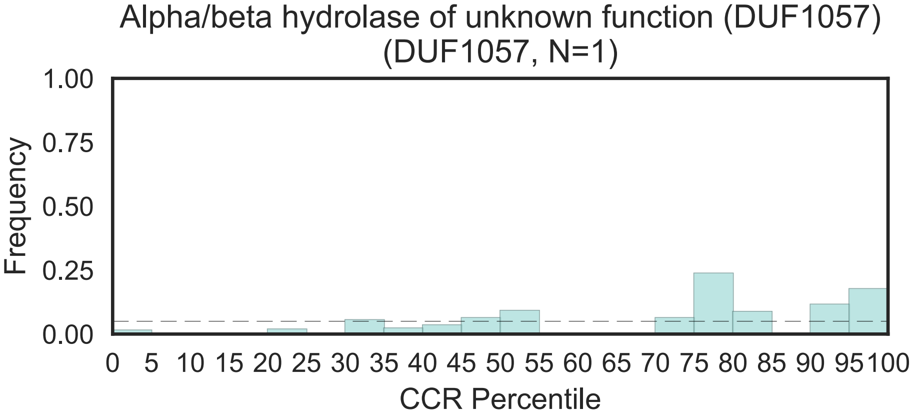

DTW domain
(DTW, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

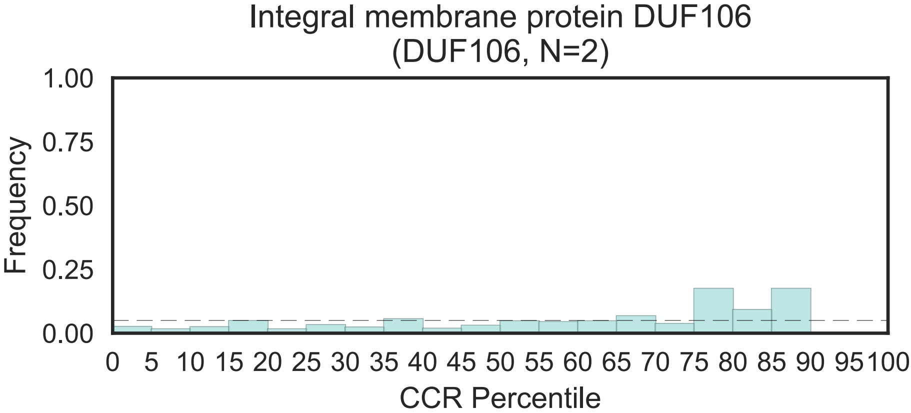

Protein of unknown function (DUF1011)
(DUF1011, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

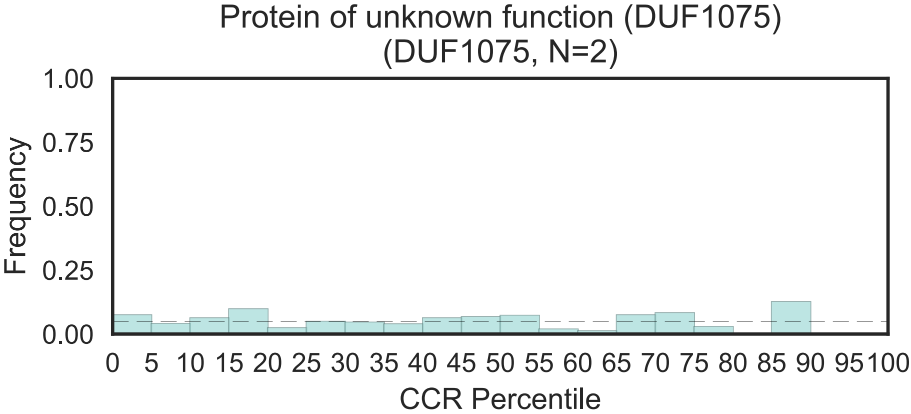

Domain of Unknown Function (DUF1041)
(DUF1041, N=5)
Fisher's OR: 1.29; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

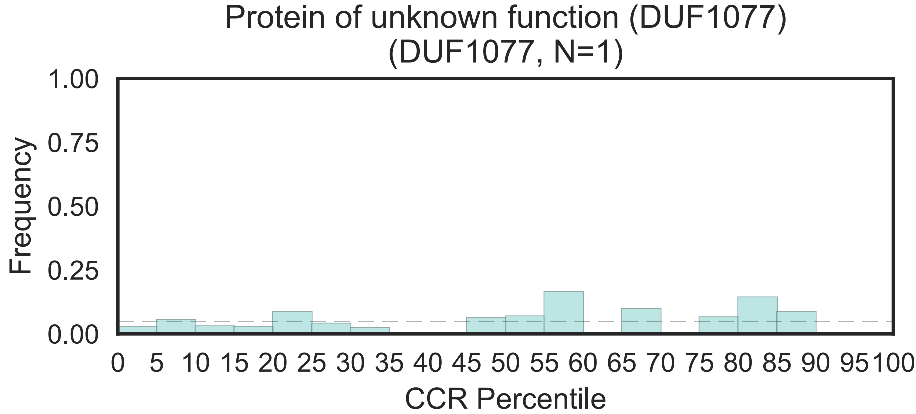


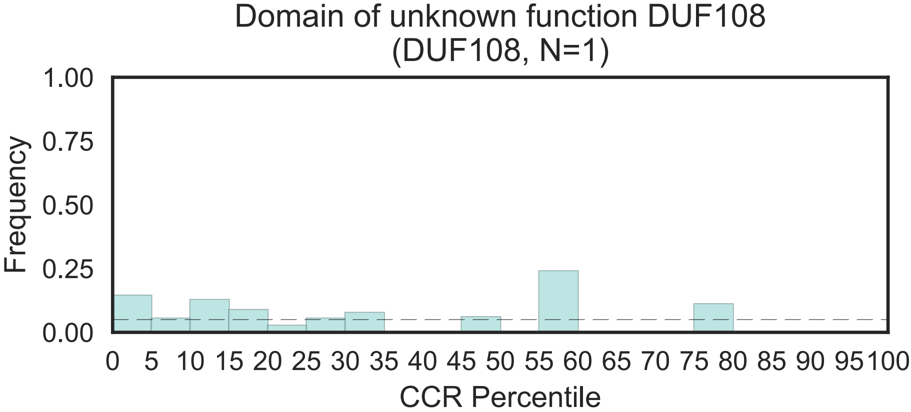
Domain of Unknown Function (DUF1053)
(DUF1053, N=6)
Fisher's OR: 1.32; Bonferroni p-val: 1

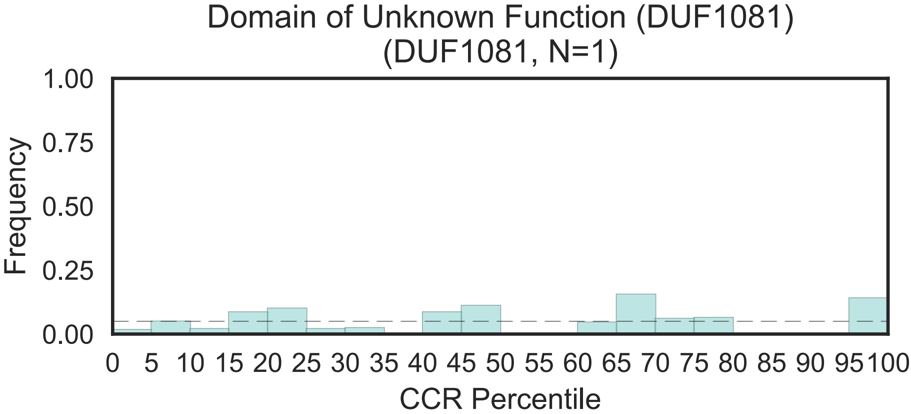

Alpha/beta hydrolase of unknown function (DUF1057)
(DUF1057, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

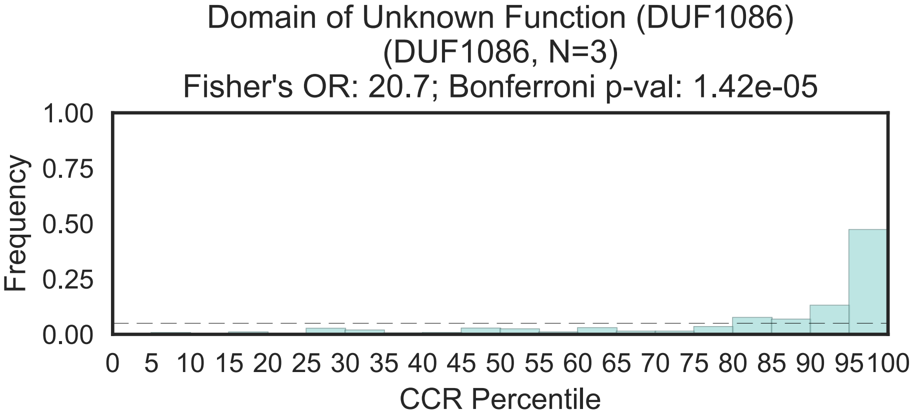

Integral membrane protein DUF106
(DUF106, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

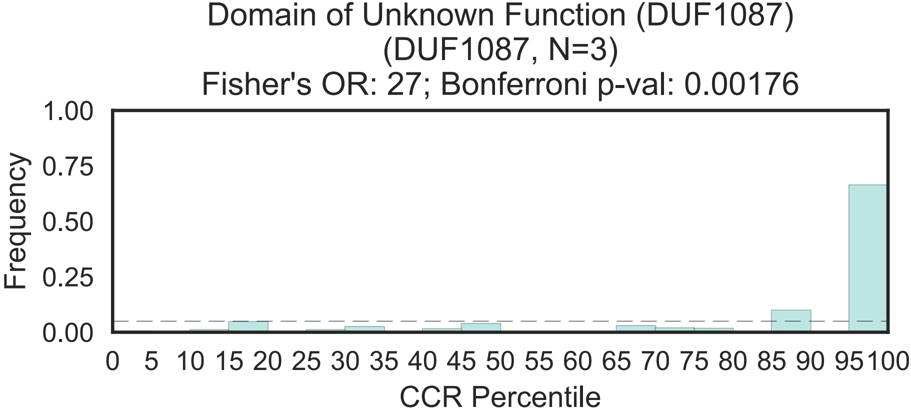

Protein of unknown function (DUF1075)
(DUF1075, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

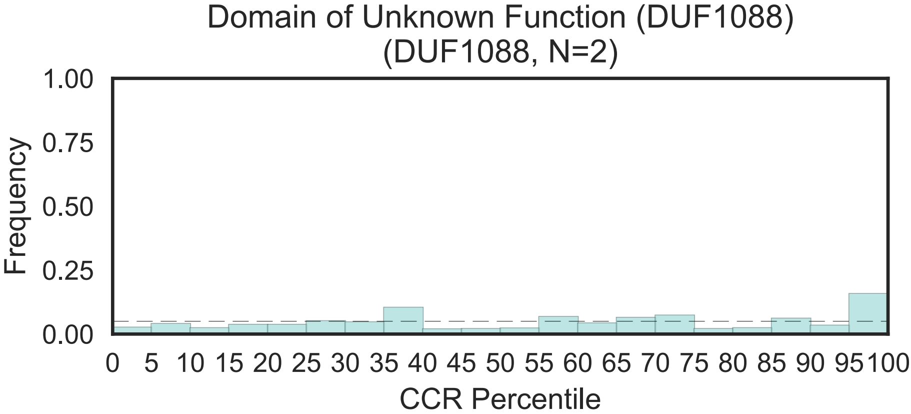

Protein of unknown function (DUF1077)
(DUF1077, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

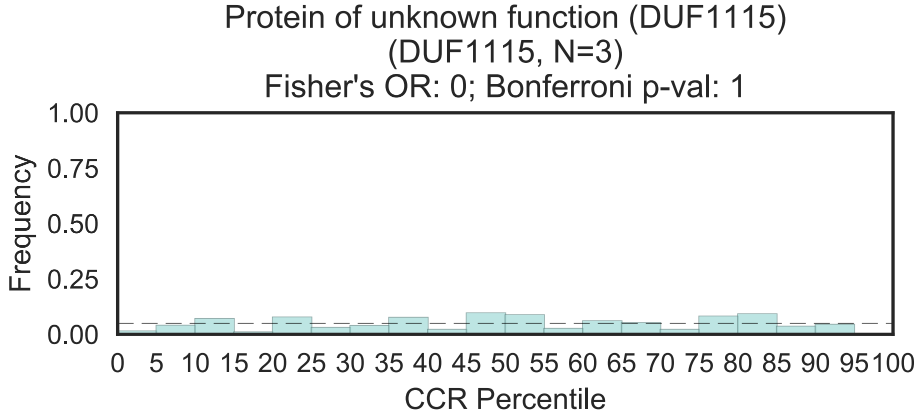

Domain of unknown function DUF108
(DUF108, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

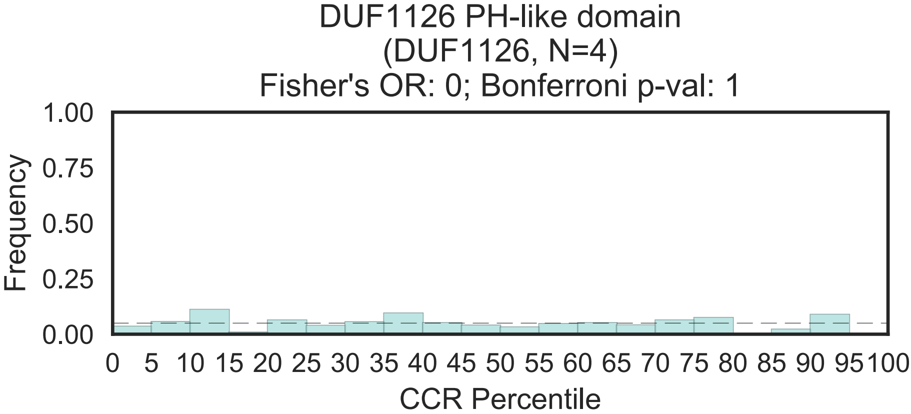

Domain of Unknown Function (DUF1081)
(DUF1081, N=1)


Domain of Unknown Function (DUF1086)
(DUF1086, N=3)
Fisher's OR: 20.7; Bonferroni p-val: 1.42e-05
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

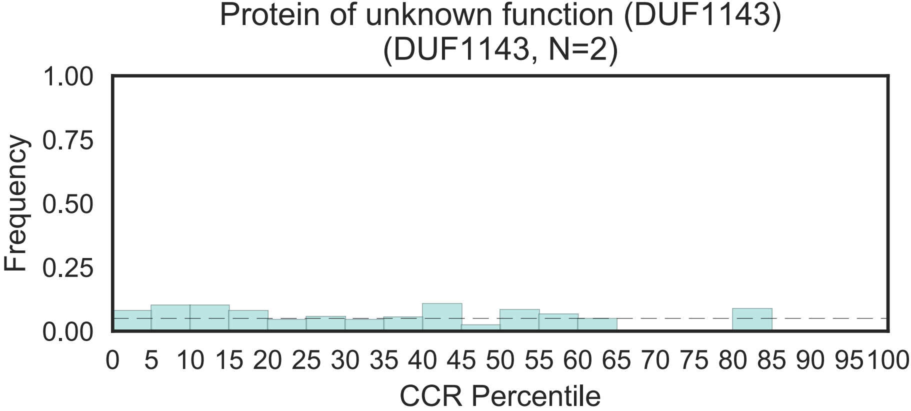

Domain of Unknown Function (DUF1087)
(DUF1087, N=3)
Fisher's OR: 27; Bonferroni p-val: 0.00176

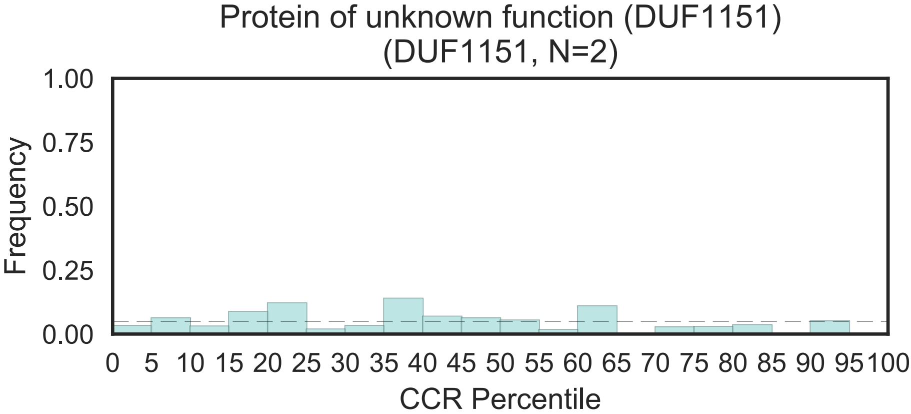

Domain of Unknown Function (DUF1088)
(DUF1088, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

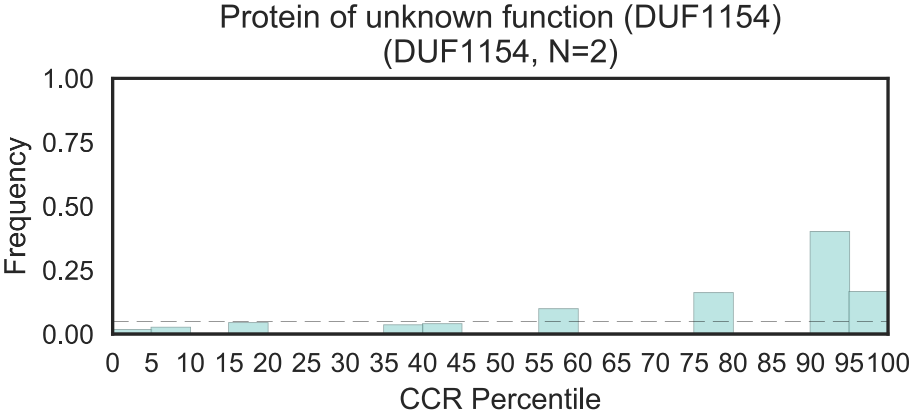

Protein of unknown function (DUF1115)
(DUF1115, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

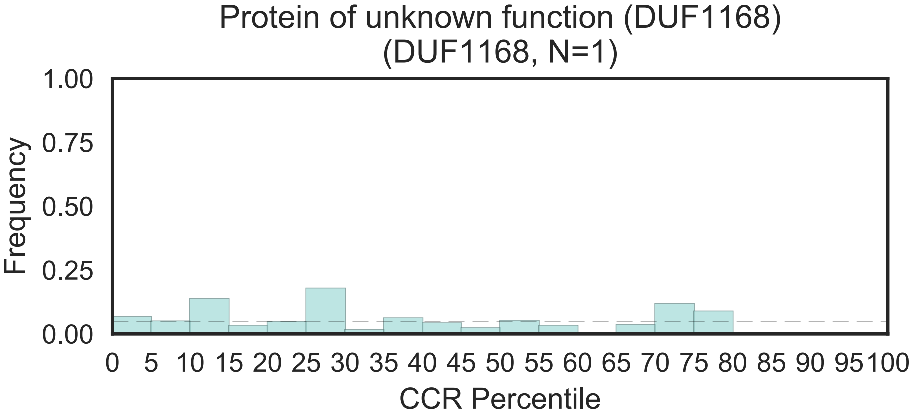


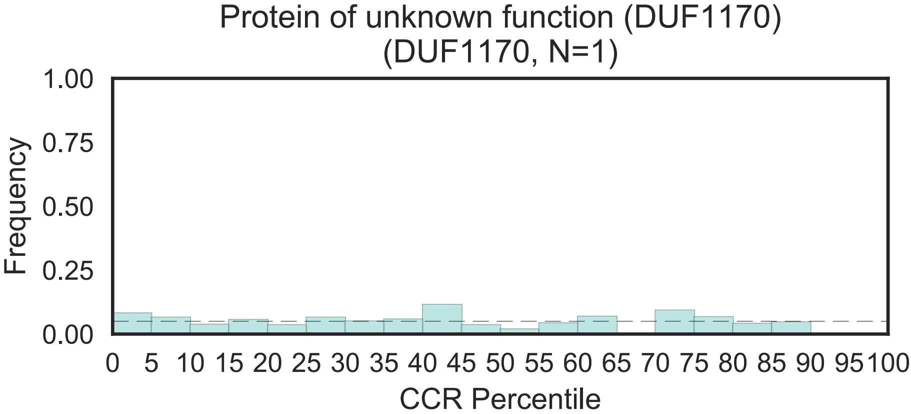
DUF1126 PH-like domain
(DUF1126, N=4)
Fisher's OR: 0; Bonferroni p-val: 1


Protein of unknown function (DUF1143)
(DUF1143, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

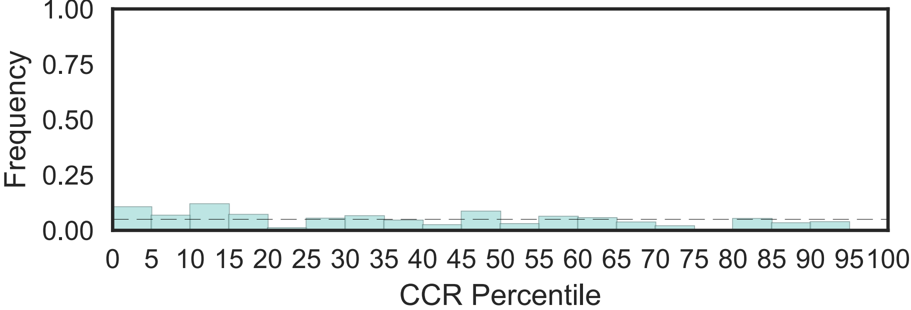

Protein of unknown function (DUF1151)
(DUF1151, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

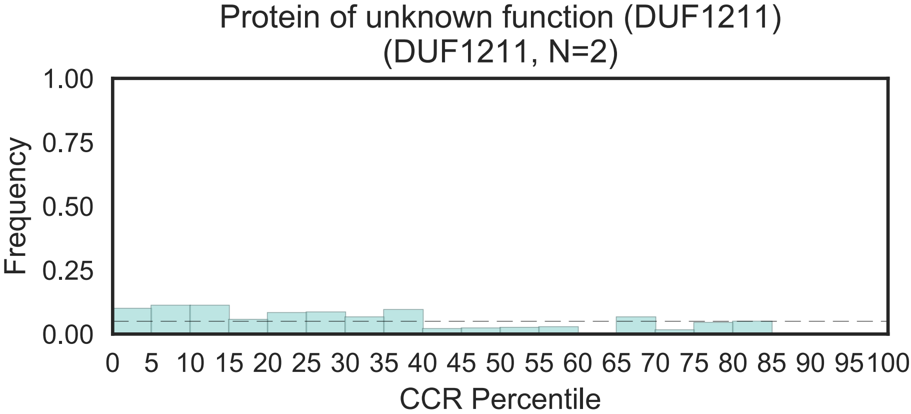

Protein of unknown function (DUF1154)
(DUF1154, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

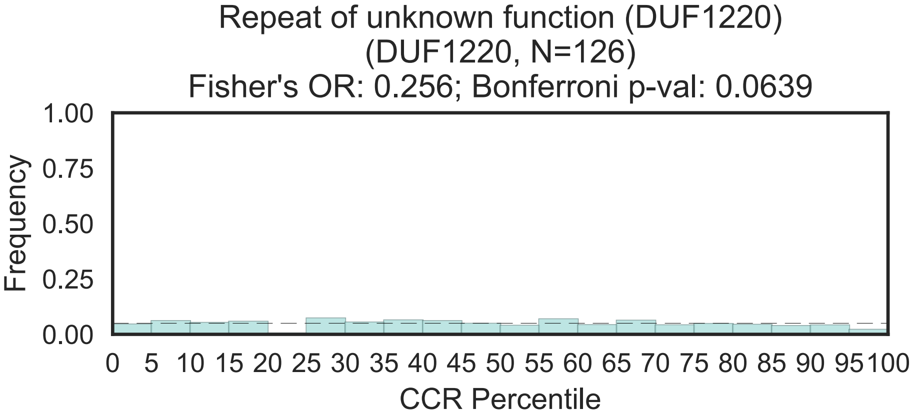

Protein of unknown function (DUF1168)
(DUF1168, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

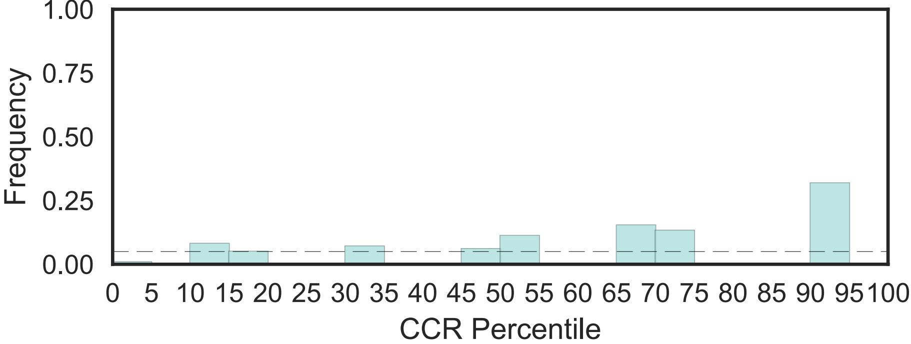

Protein of unknown function (DUF1170)
(DUF1170, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Protein of unknown function (DUF1180)
(DUF1180, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

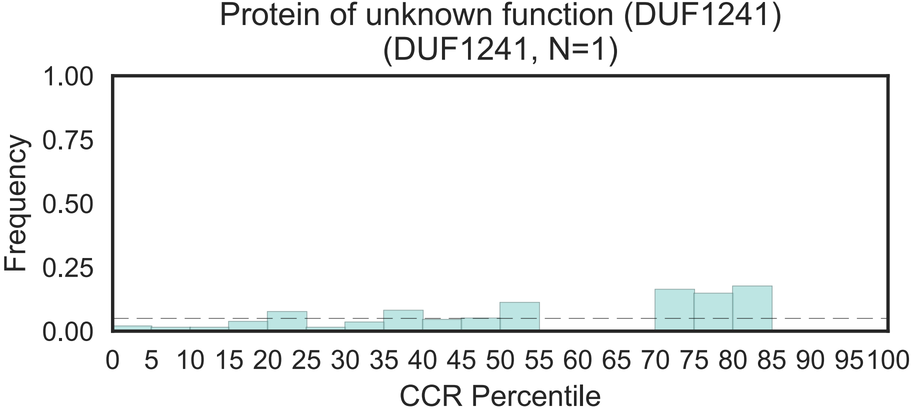


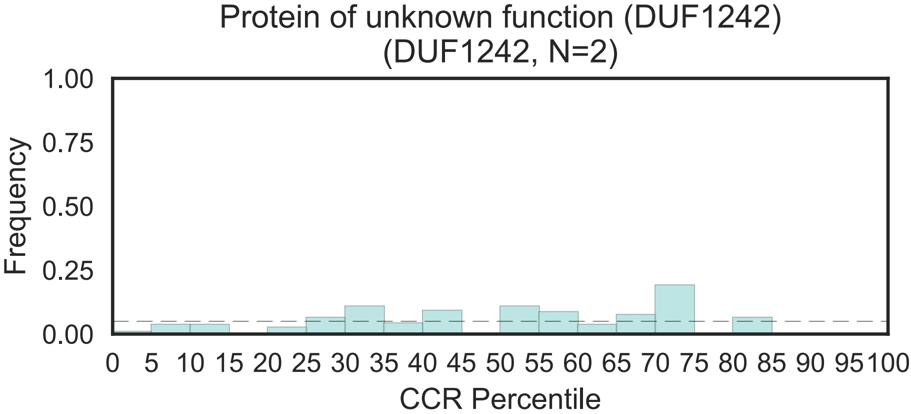

Protein of unknown function (DUF1211)
(DUF1211, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Repeat of unknown function (DUF1220)
(DUF1220, N=126)
Fisher's OR: 0.256; Bonferroni p-val: 0.0639
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

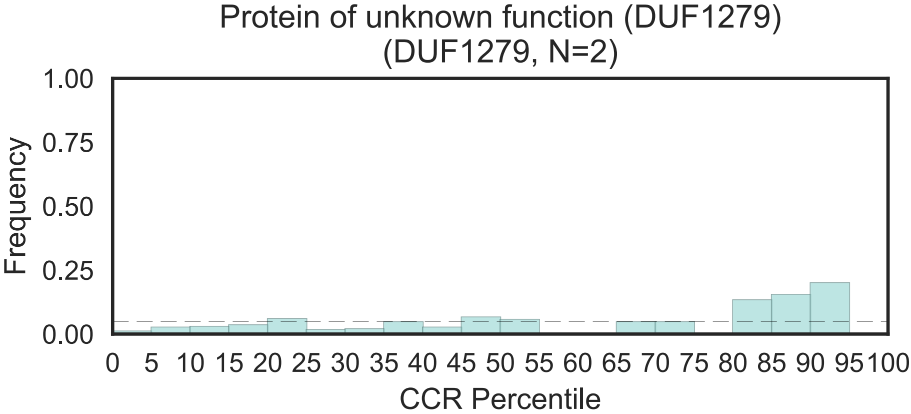


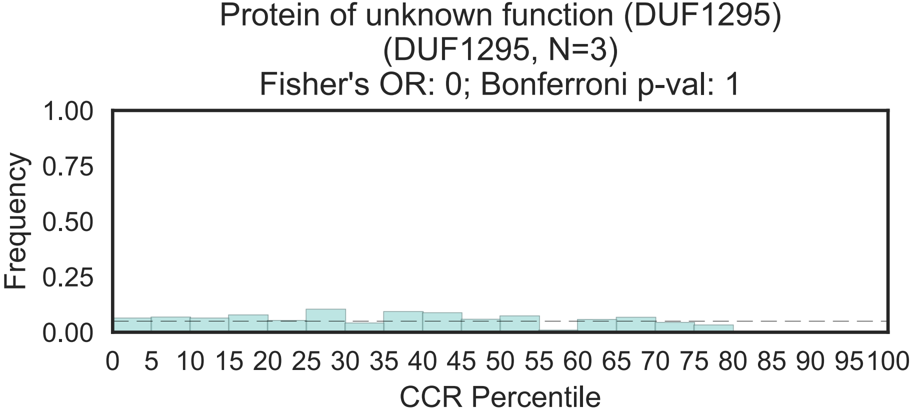
Protein of unknown function (DUF1232)
(DUF1232, N=1)

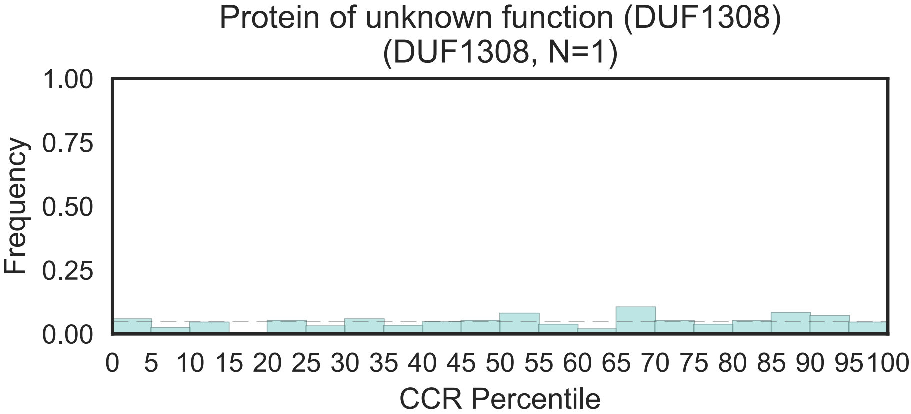

Protein of unknown function (DUF1241)
(DUF1241, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

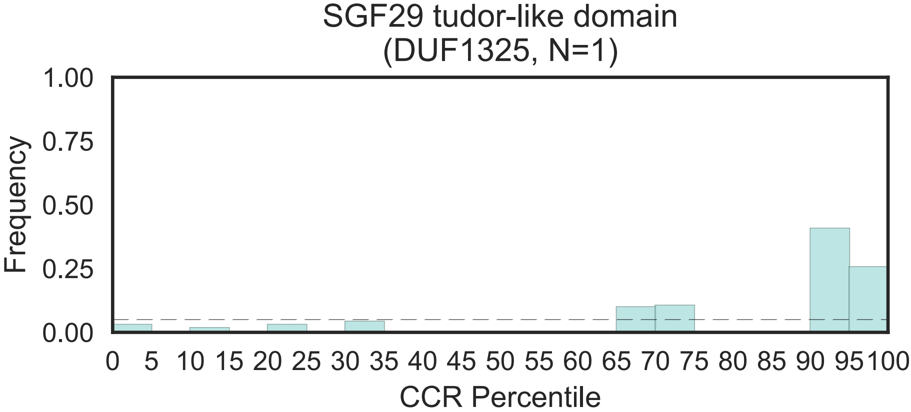


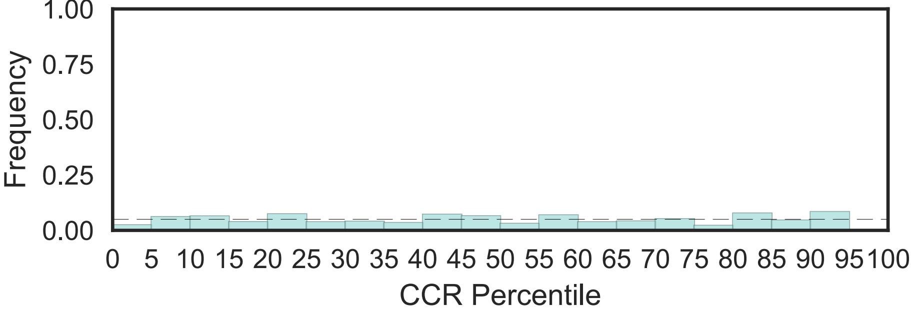
Protein of unknown function (DUF1242)
(DUF1242, N=2)


Protein of unknown function (DUF1279)
(DUF1279, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

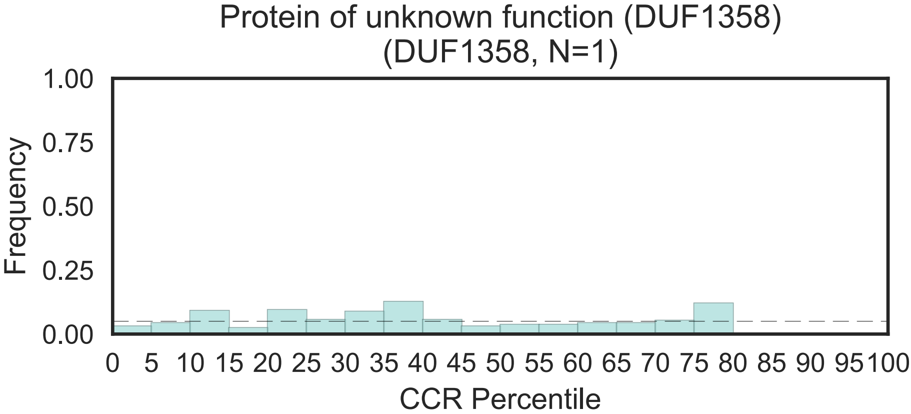

Protein of unknown function (DUF1295)
(DUF1295, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

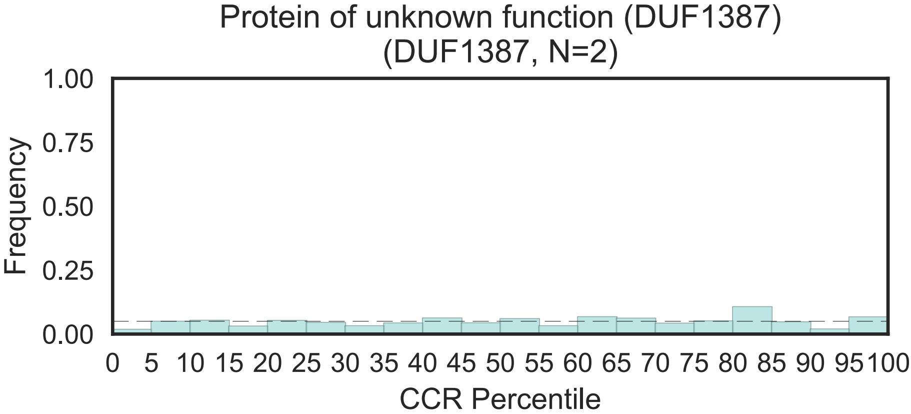

Protein of unknown function (DUF1308)
(DUF1308, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

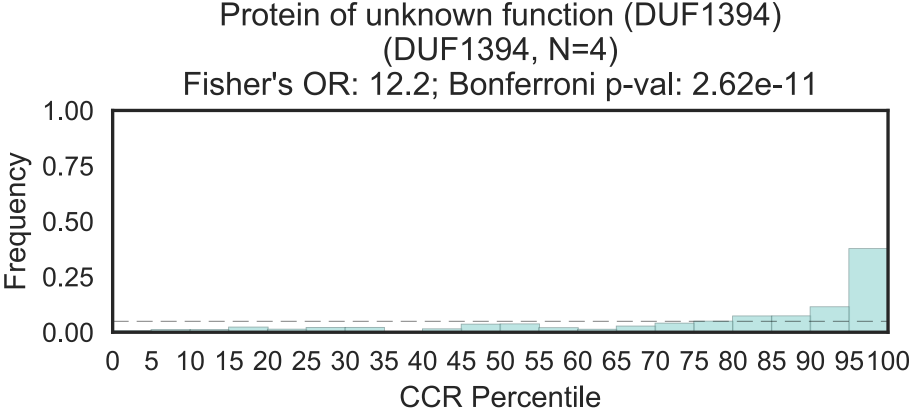

SGF29 tudor-like domain
(DUF1325, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



Protein of unknown function (DUF1356)
(DUF1356, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

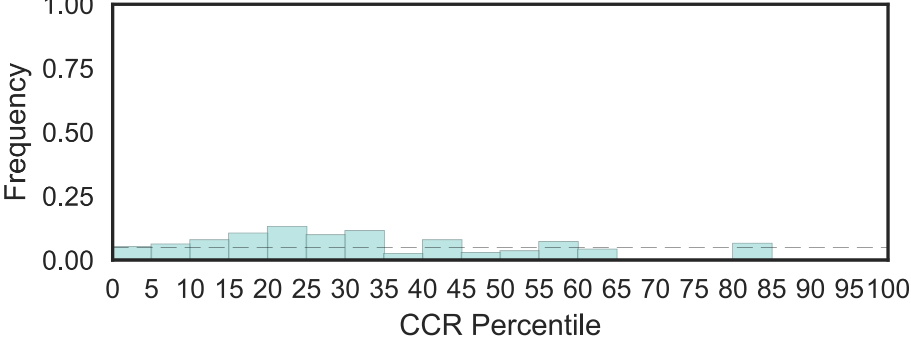

Protein of unknown function (DUF1358)
(DUF1358, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

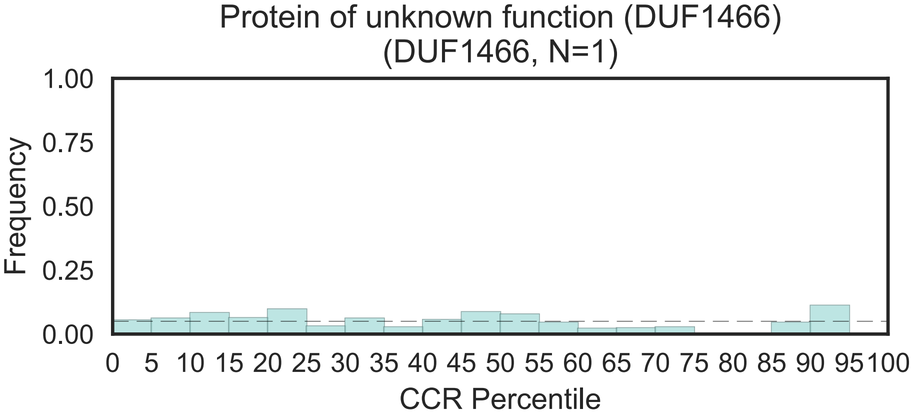

Protein of unknown function (DUF1387)
(DUF1387, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

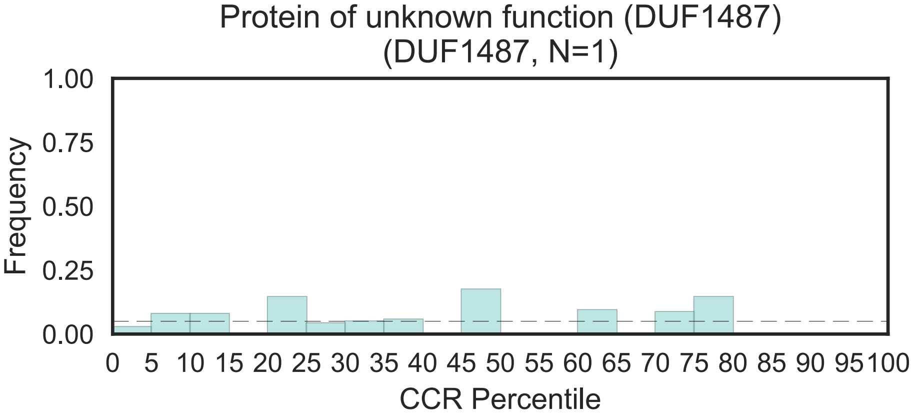


Protein of unknown function (DUF1394)
(DUF1394, N=4)
Fisher's OR: 12.2; Bonferroni p-val: 2.62e-11

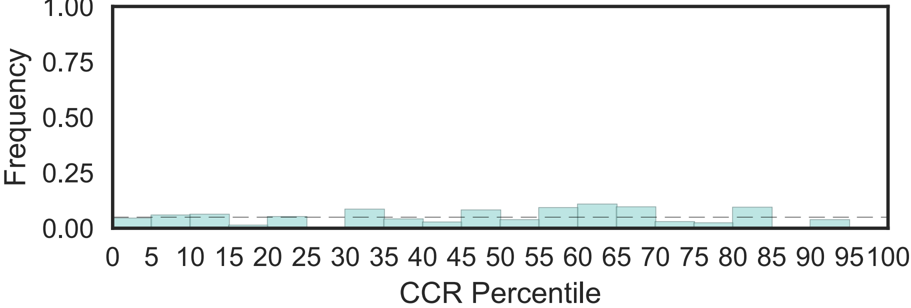
Protein of unknown function (DUF1445) (DUF1445, N=1)

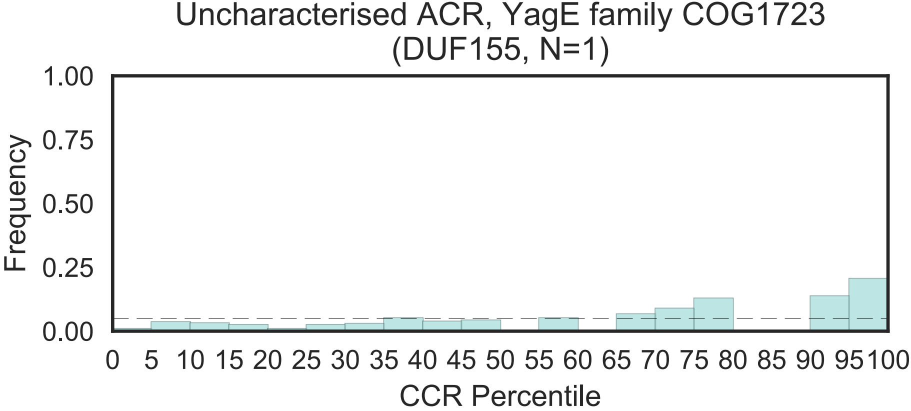


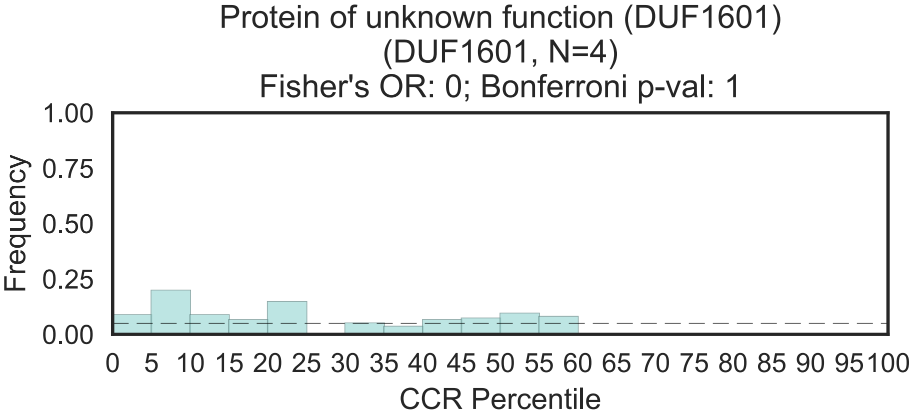

Protein of unknown function (DUF1466)
(DUF1466, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

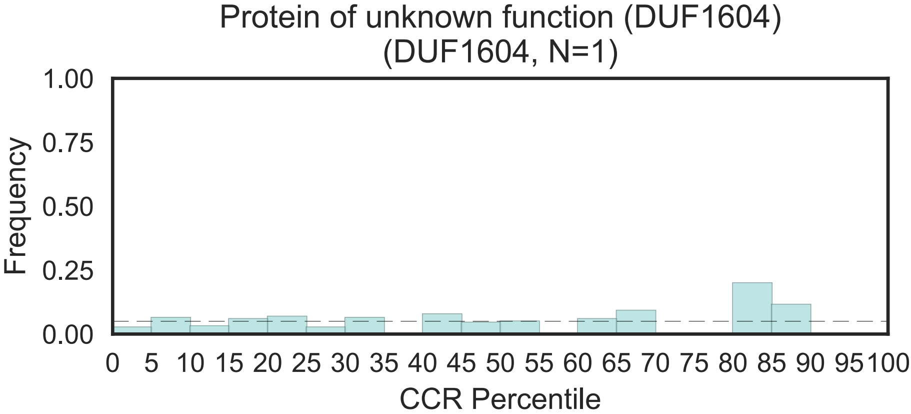

Protein of unknown function (DUF1487)
(DUF1487, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Domain of unknown function (DUF1518)
(DUF1518, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

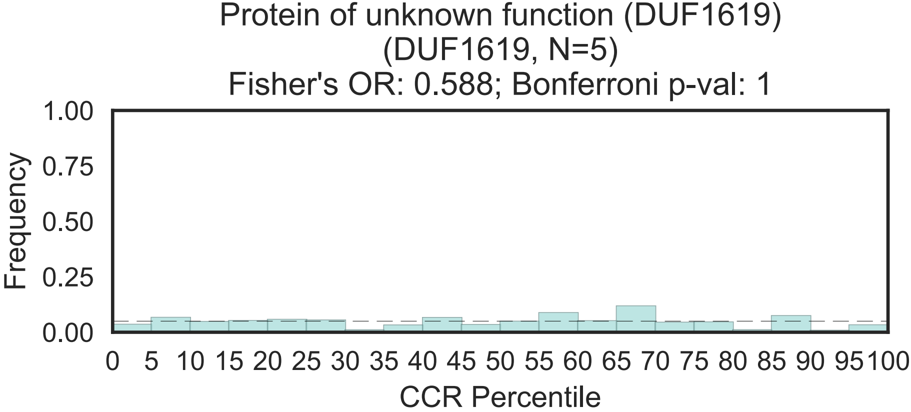



Uncharacterised ACR, YagE family COG1723
(DUF155, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

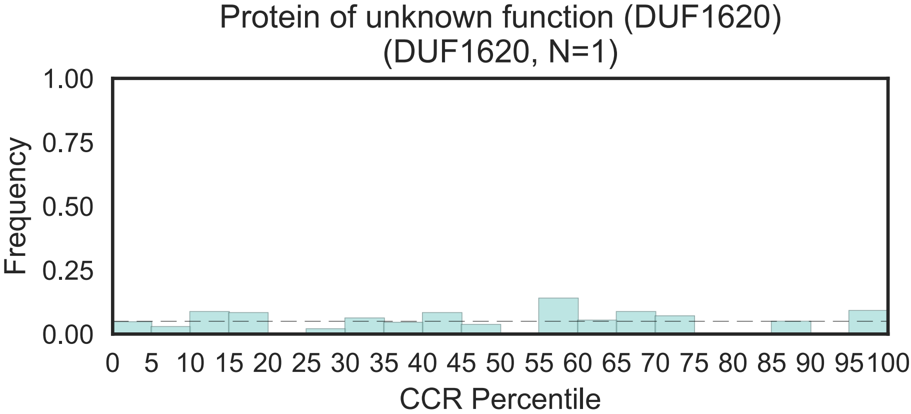

Protein of unknown function (DUF1601)
(DUF1601, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

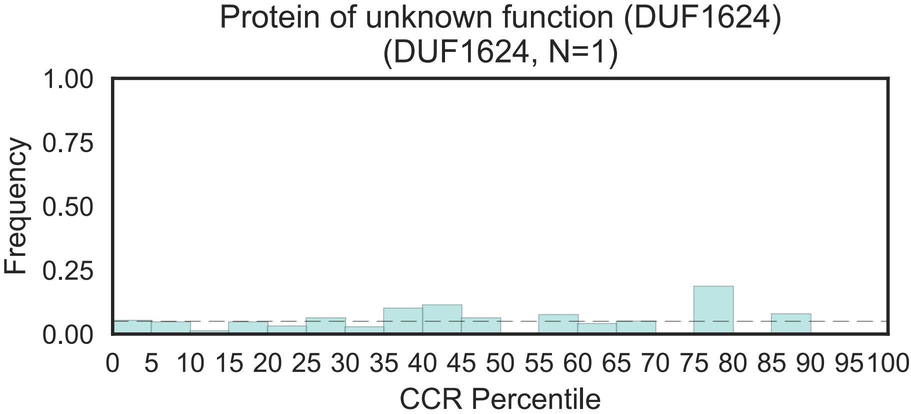


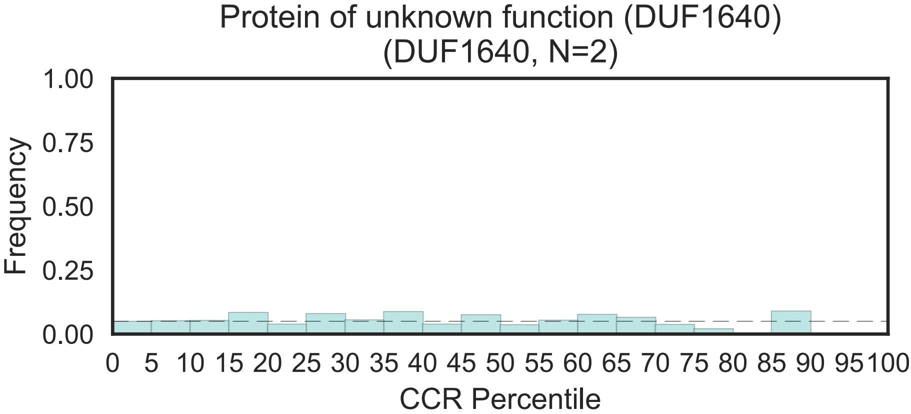
Protein of unknown function (DUF1604)
(DUF1604, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

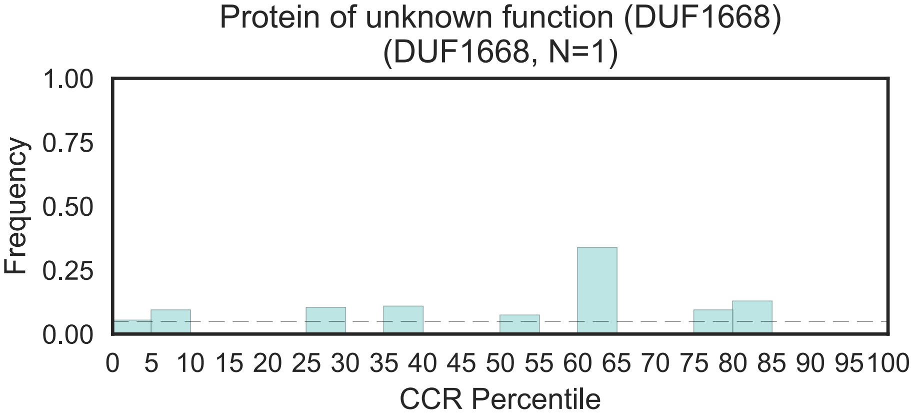


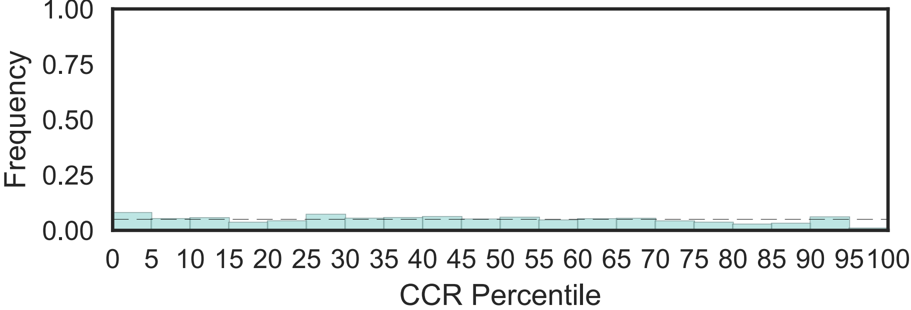
Protein of unknown function (DUF1619)
(DUF1619, N=5)
Fisher's OR: 0.588; Bonferroni p-val: 1


Protein of unknown function (DUF1620)
(DUF1620, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

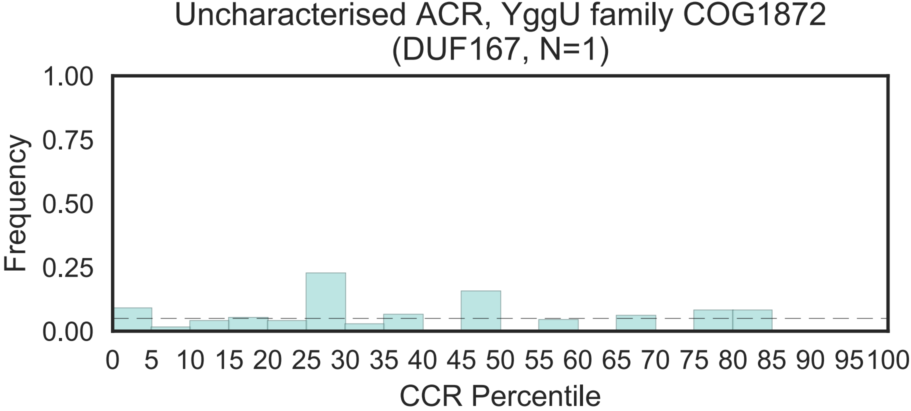

Protein of unknown function (DUF1624)
(DUF1624, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

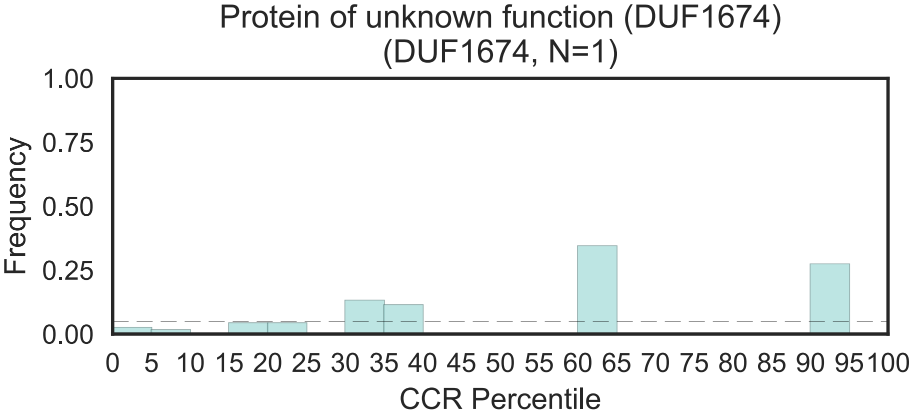

Protein of unknown function (DUF1640)
(DUF1640, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

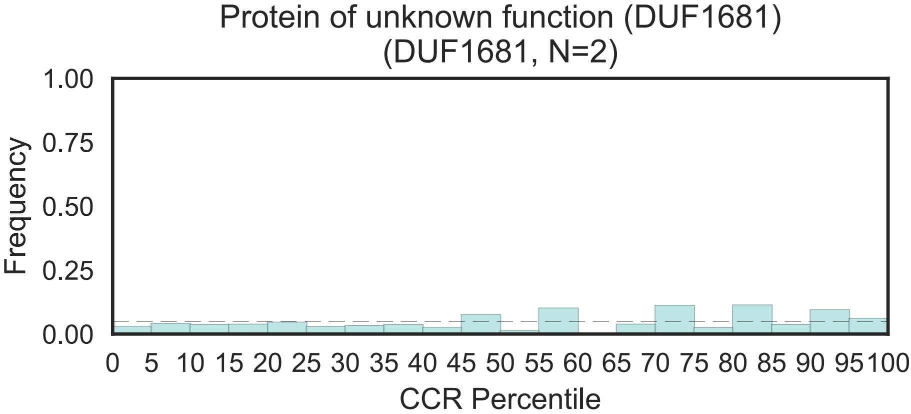

Protein of unknown function (DUF1668)
(DUF1668, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

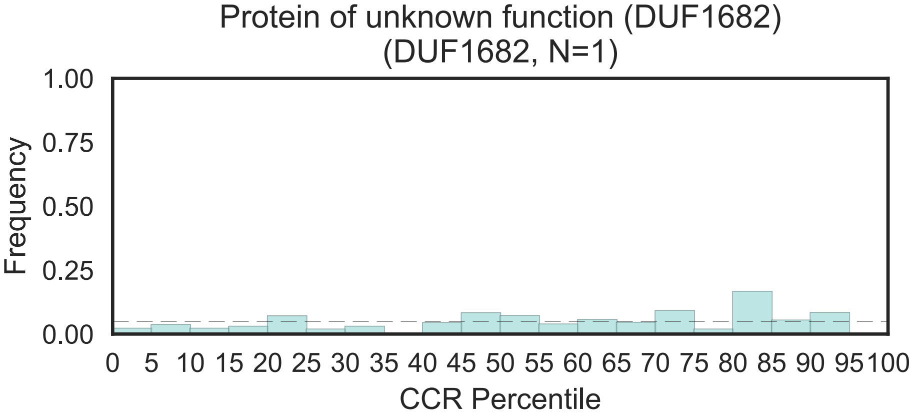


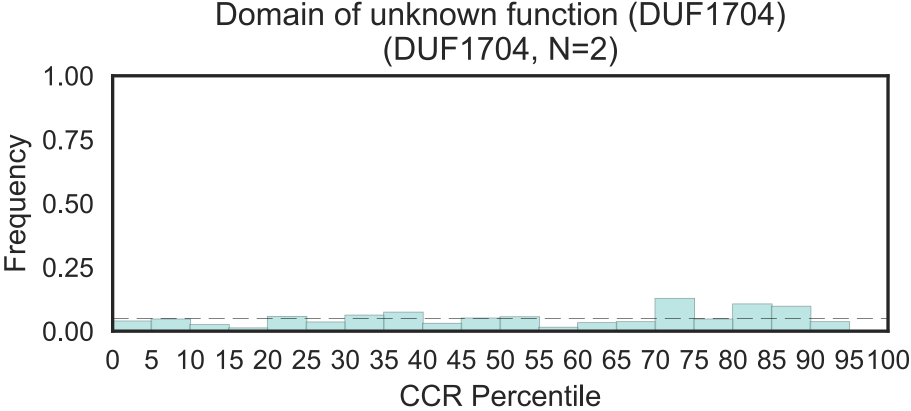
Protein of unknown function (DUF1669)
(DUF1669, N=9)
Fisher's OR: 0.119; Bonferroni p-val: 1

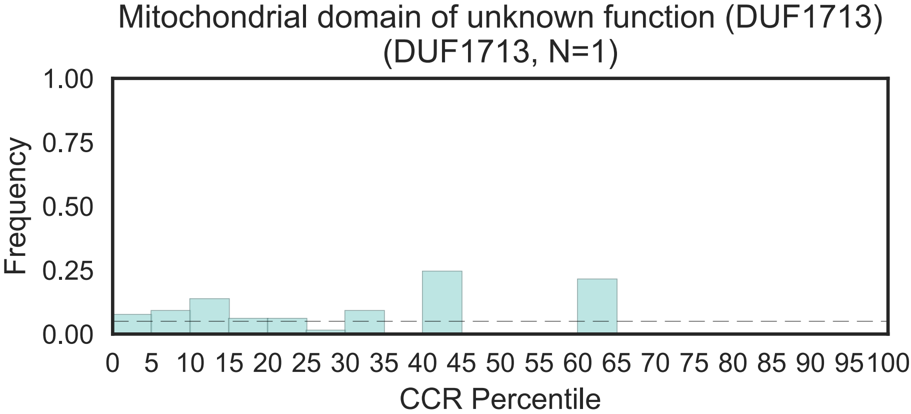

Uncharacterised ACR, YggU family COG1872
(DUF167, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

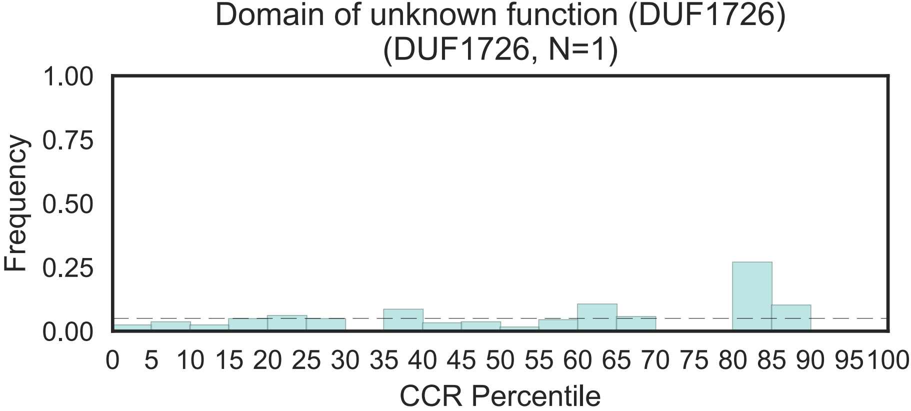

Protein of unknown function (DUF1674)
(DUF1674, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

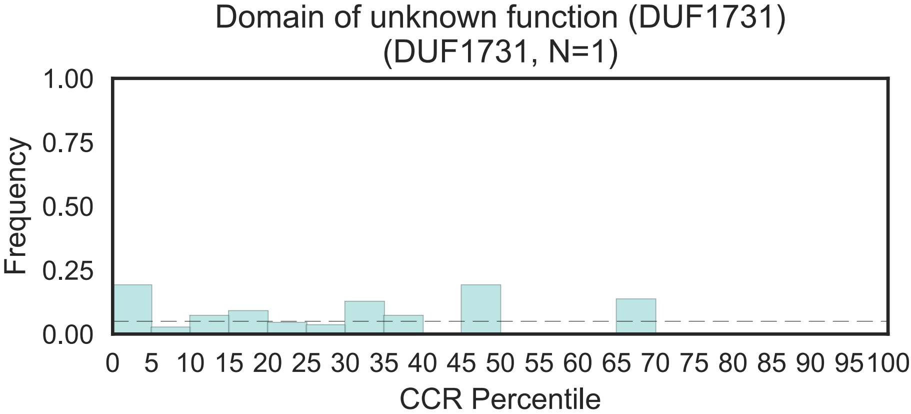

Protein of unknown function (DUF1681)
(DUF1681, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

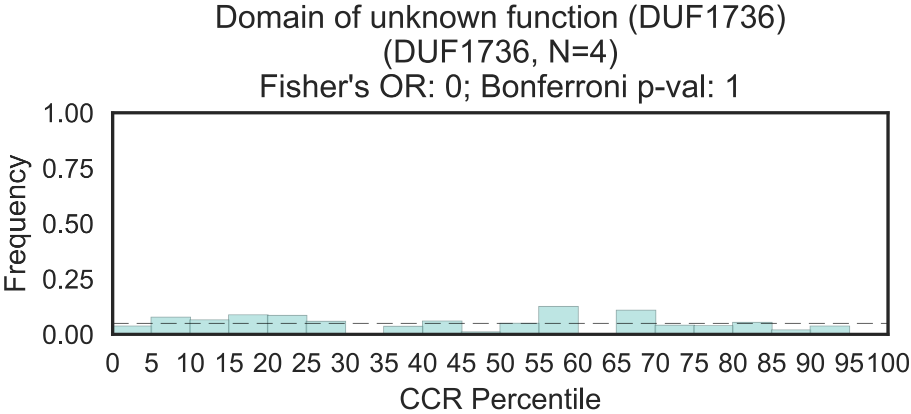

Protein of unknown function (DUF1682)
(DUF1682, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

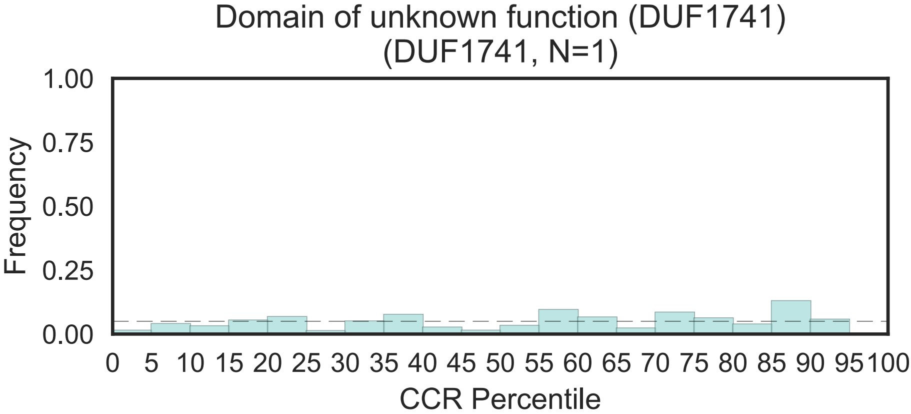

Domain of unknown function (DUF1704)
(DUF1704, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

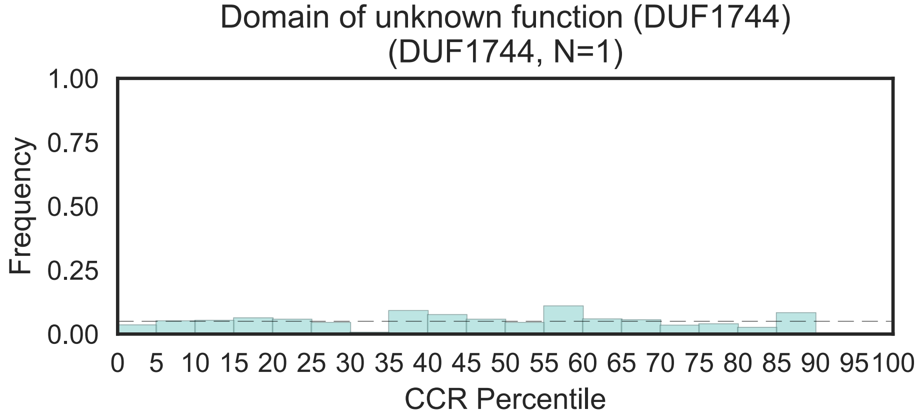

Mitochondrial domain of unknown function (DUF1713)
(DUF1713, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF1726)
(DUF1726, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF1731)
(DUF1731, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF1736)
(DUF1736, N=4)
Fisher's OR: 0; Bonferroni p-val: 1


Domain of unknown function (DUF1741)
(DUF1741, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF1744)
(DUF1744, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
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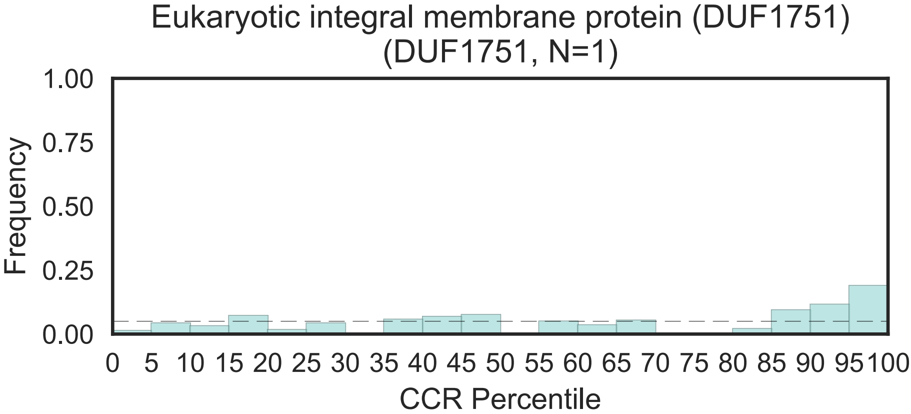
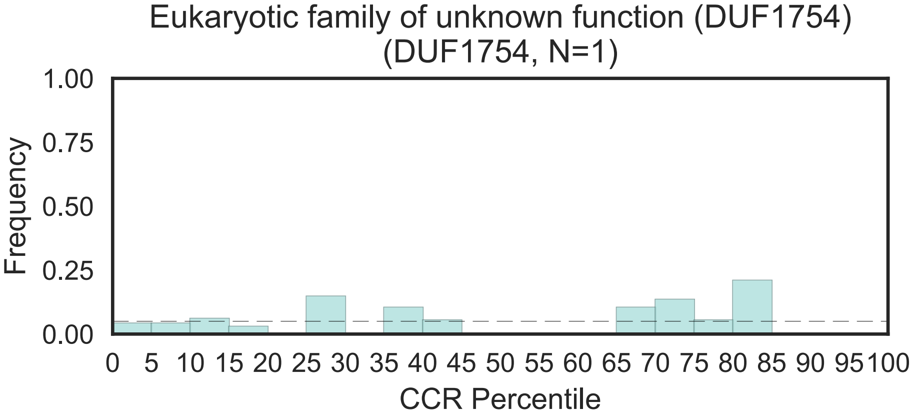
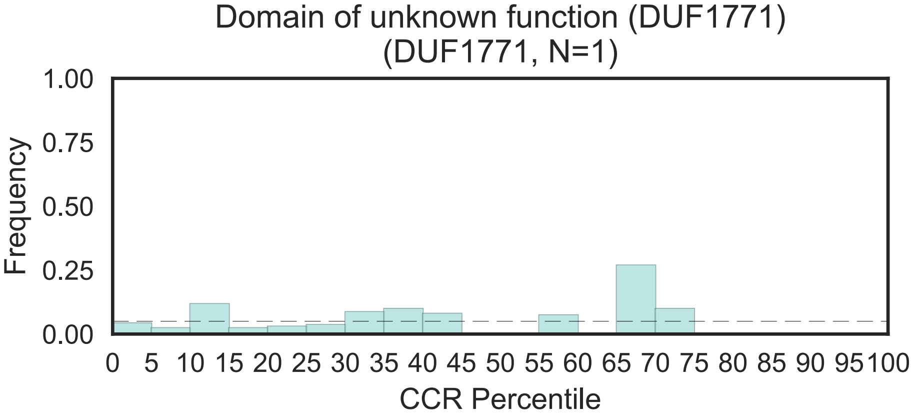
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Eukaryotic integral membrane protein (DUF1751)
(DUF1751, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Eukaryotic family of unknown function (DUF1754)
(DUF1754, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF1771)
(DUF1771, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
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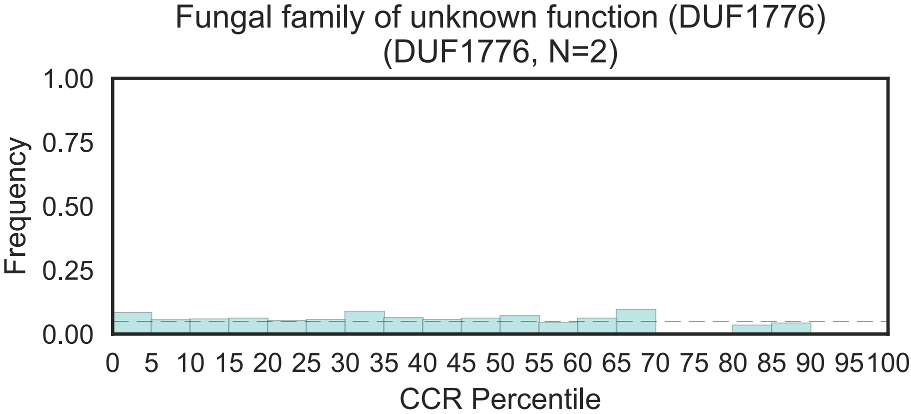
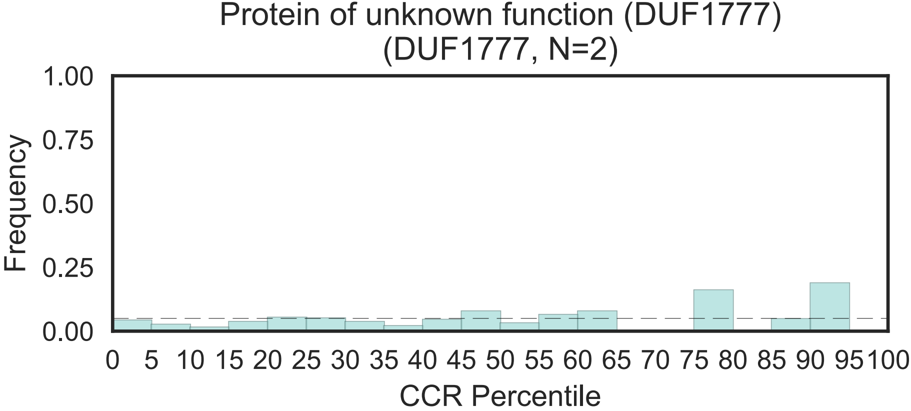
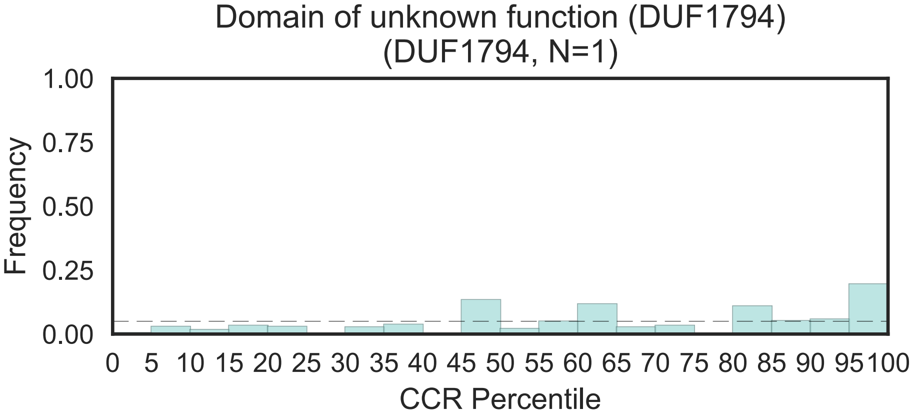
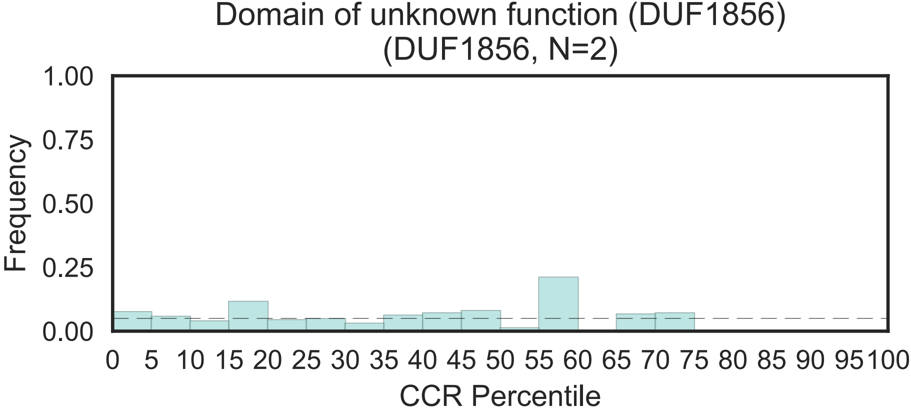
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

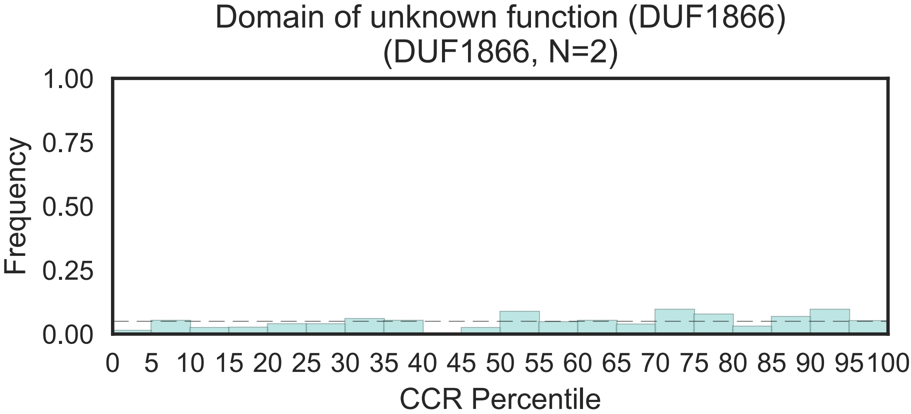


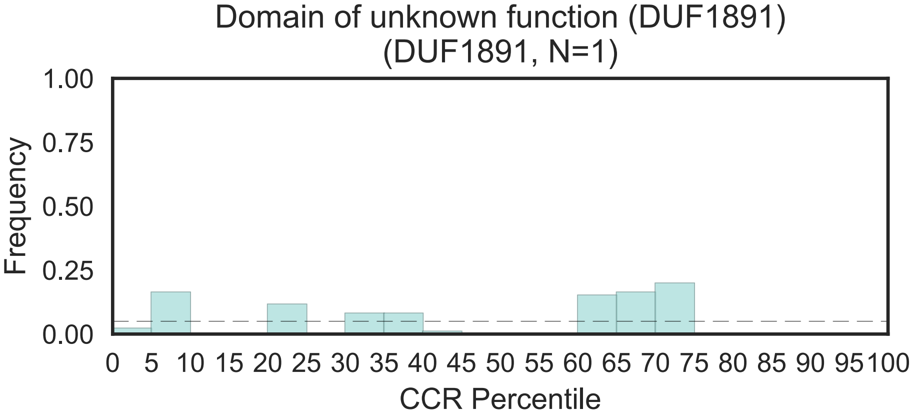
Fungal family of unknown function (DUF1776)
(DUF1776, N=2)

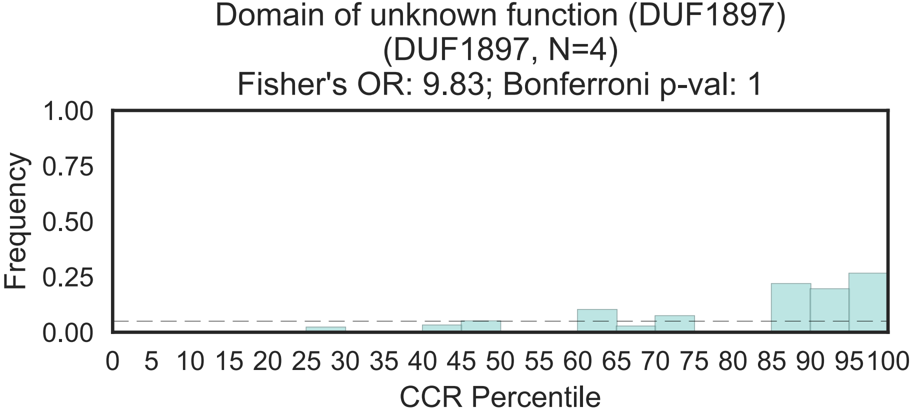

Protein of unknown function (DUF1777)
(DUF1777, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

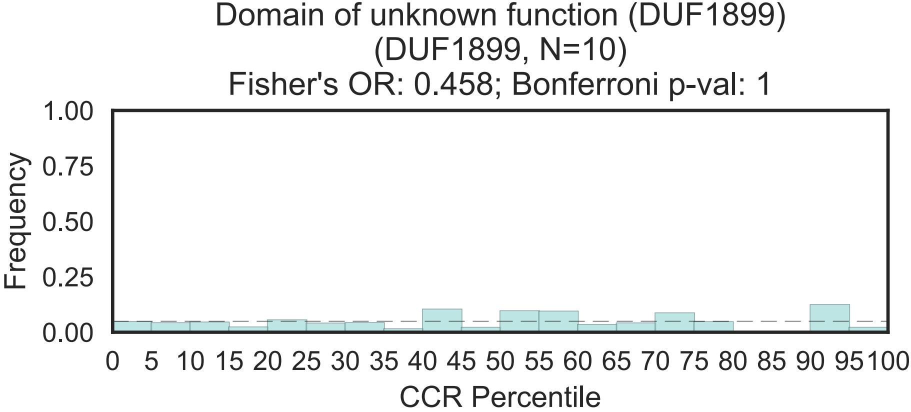

Domain of unknown function (DUF1794)
(DUF1794, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

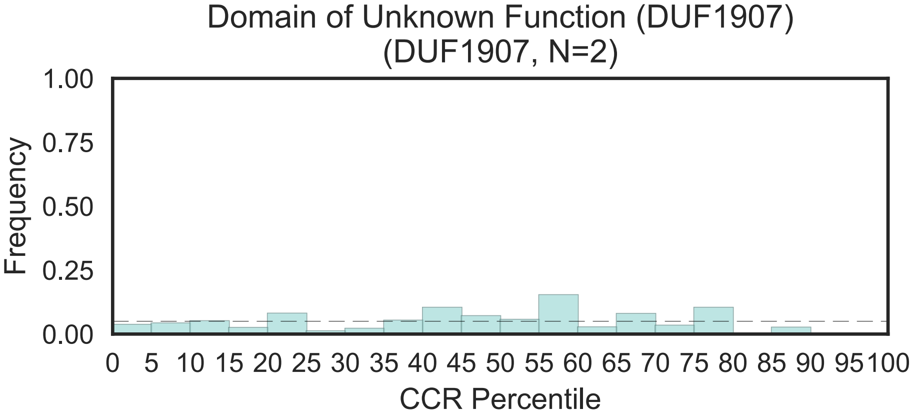

Domain of unknown function (DUF1856)
(DUF1856, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

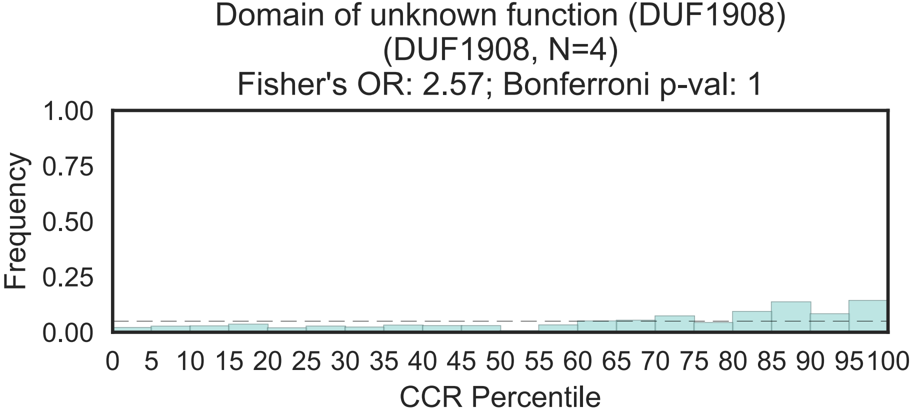

Domain of unknown function (DUF1866)
(DUF1866, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

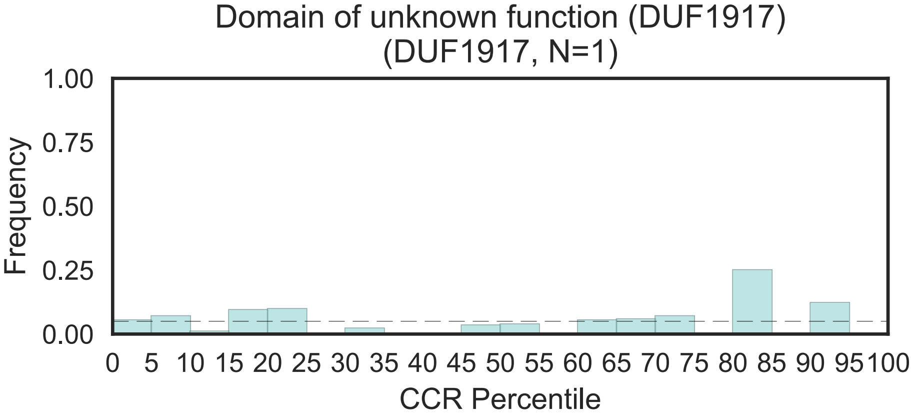

Domain of unknown function (DUF1891)
(DUF1891, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

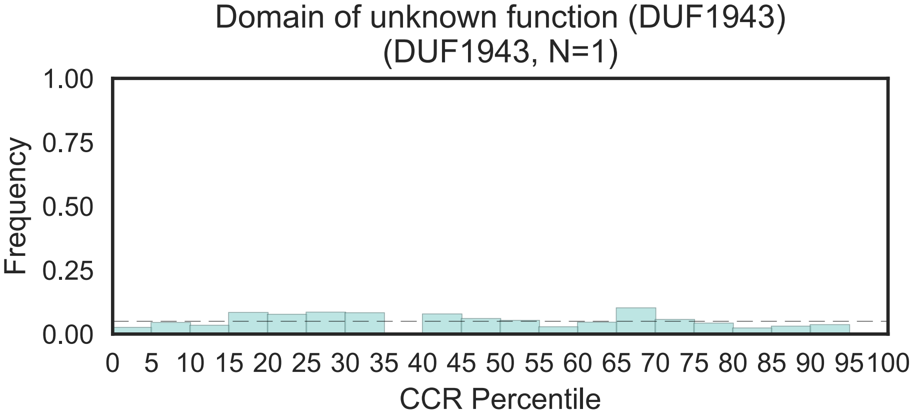

Domain of unknown function (DUF1897)
(DUF1897, N=4)
Fisher's OR: 9.83; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF1899)
(DUF1899, N=10)
Fisher's OR: 0.458; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

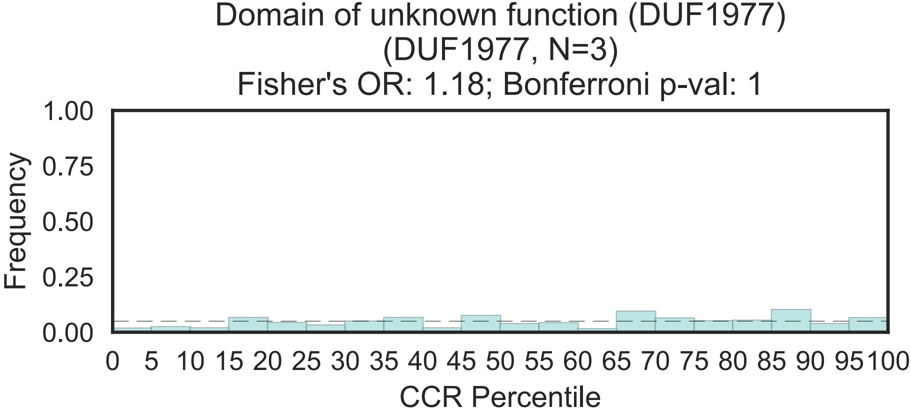

Domain of Unknown Function (DUF1907)
(DUF1907, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF1908)
(DUF1908, N=4)
Fisher's OR: 2.57; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

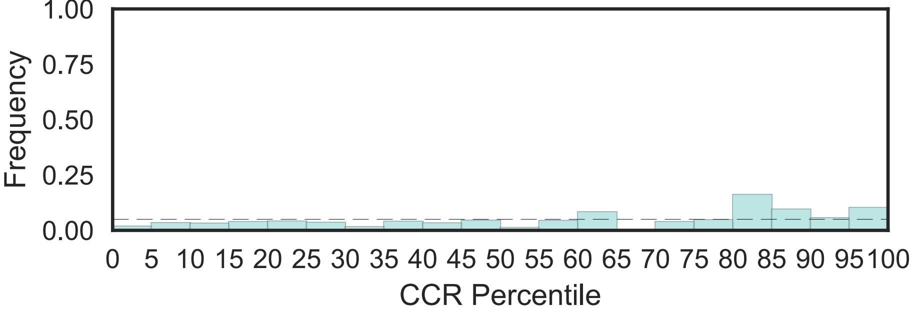

Domain of unknown function (DUF1917)
(DUF1917, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



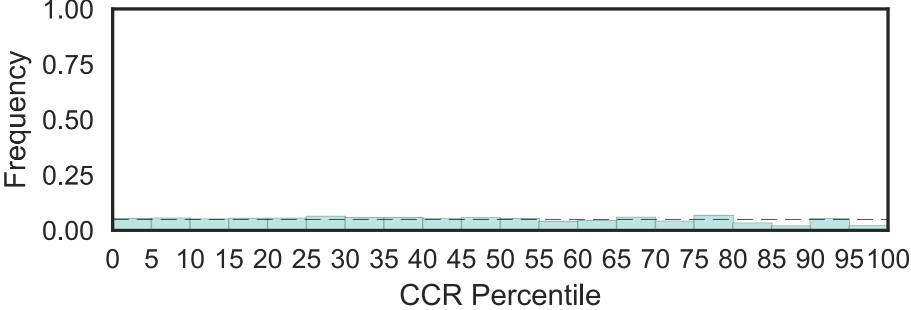
Domain of unknown function (DUF1943)
(DUF1943, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

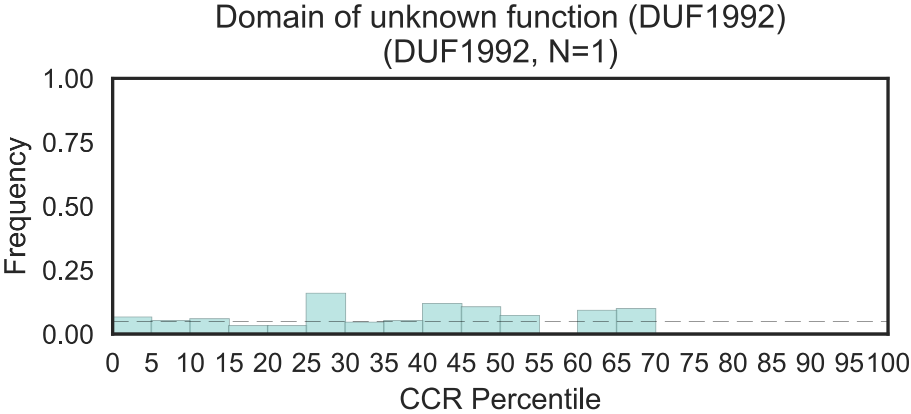


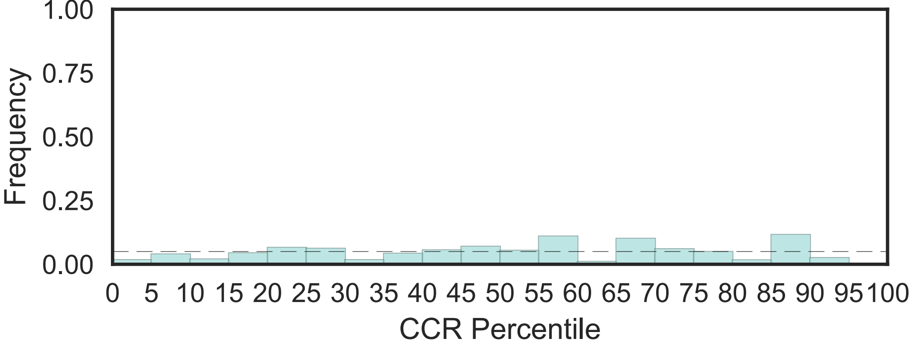
Domain of unknown function (DUF1977)
(DUF1977, N=3)
Fisher's OR: 1.18; Bonferroni p-val: 1



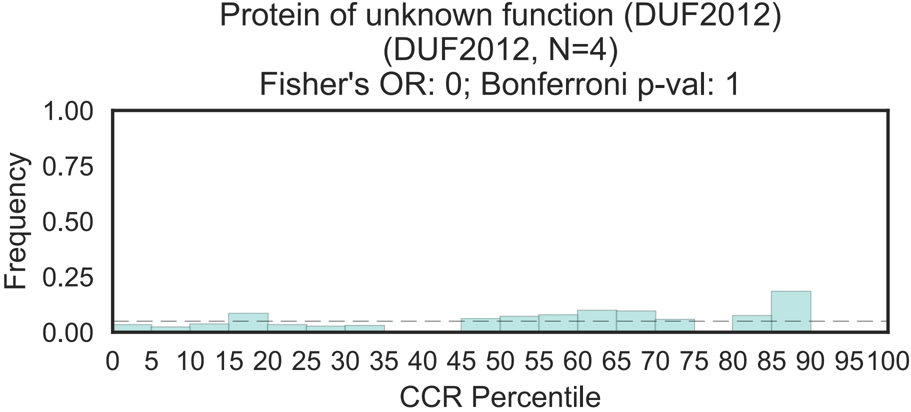
Domain of unknown function (DUF1981)
(DUF1981, N=4)
Fisher's OR: 2.35; Bonferroni p-val: 1

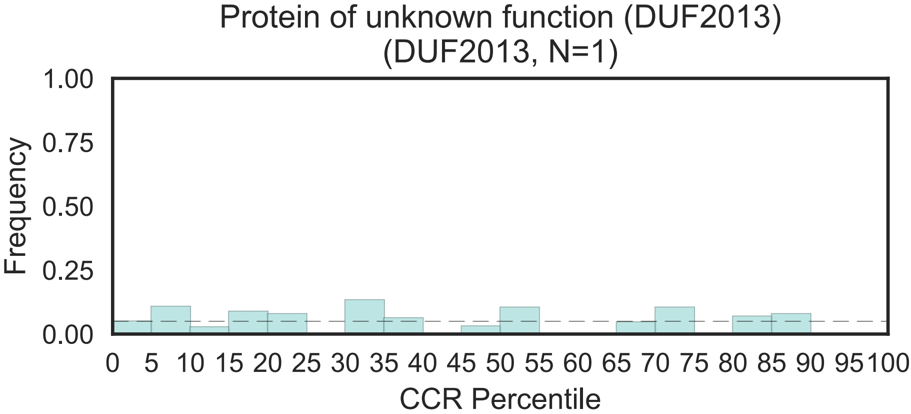

Domain of unknown function (DUF1986)
(DUF1986, N=36)
Fisher's OR: 0.373; Bonferroni p-val: 1

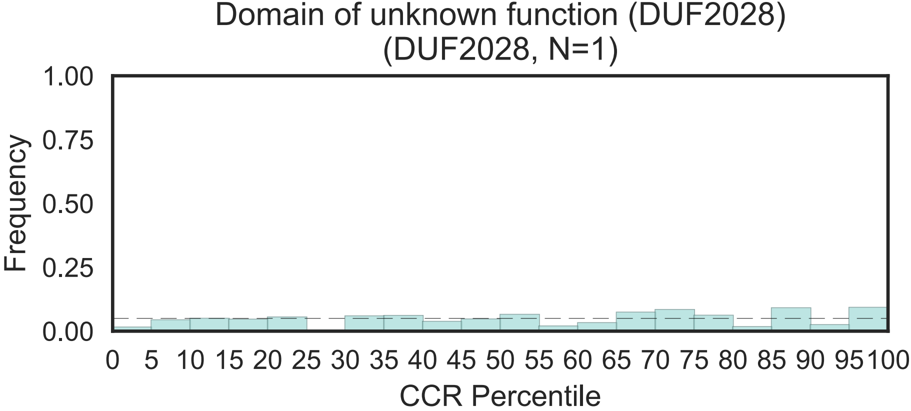

Domain of unknown function (DUF1992)
(DUF1992, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

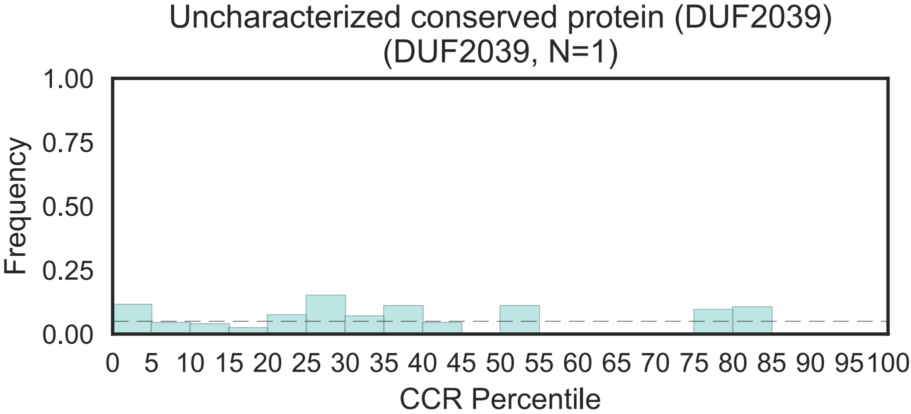


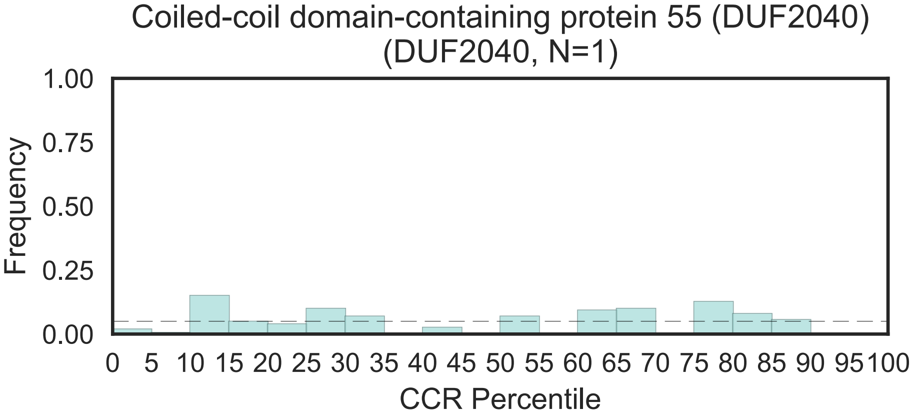
Eukaryotic protein of unknown function (DUF2003)
(DUF2003, N=1)

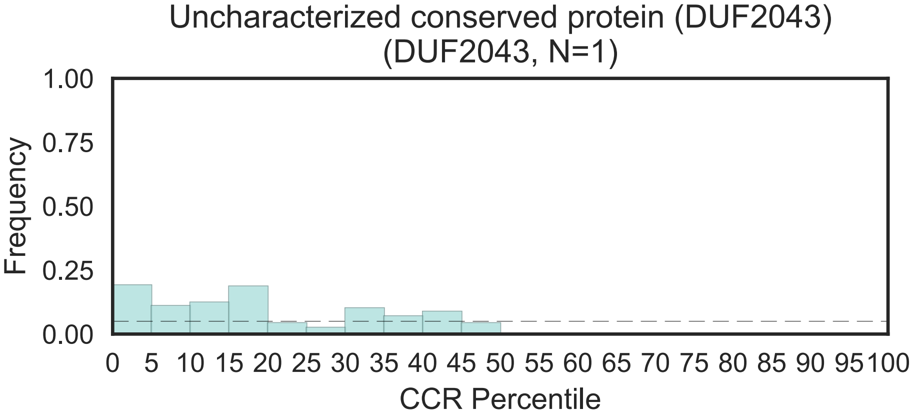

Protein of unknown function (DUF2012)
(DUF2012, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

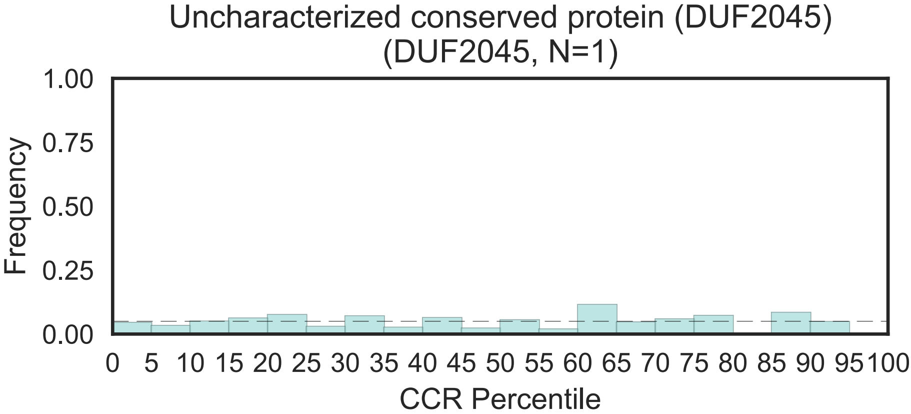

Protein of unknown function (DUF2013)
(DUF2013, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

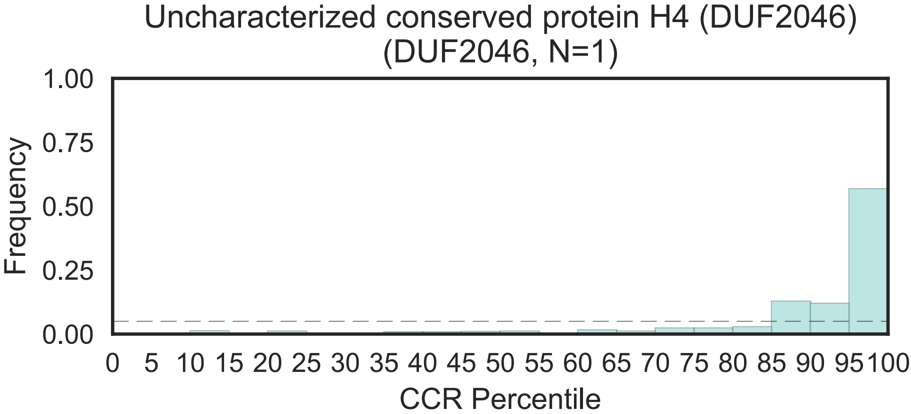

Domain of unknown function (DUF2028)
(DUF2028, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

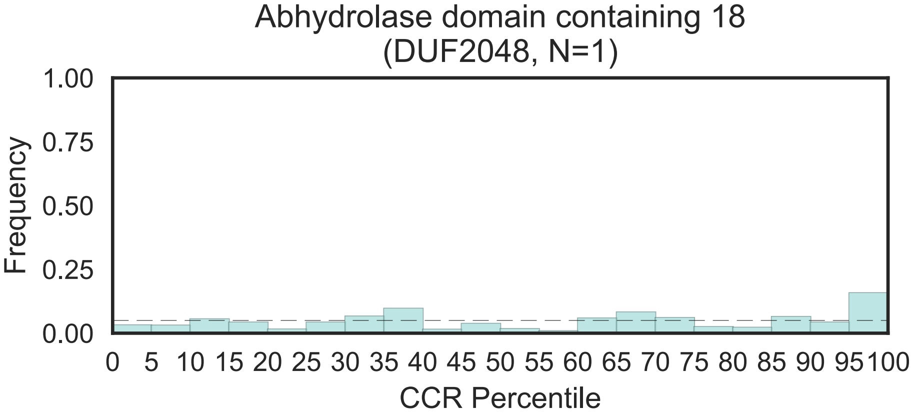

Uncharacterized conserved protein (DUF2039)
(DUF2039, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Coiled-coil domain-containing protein 55 (DUF2040)
(DUF2040, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

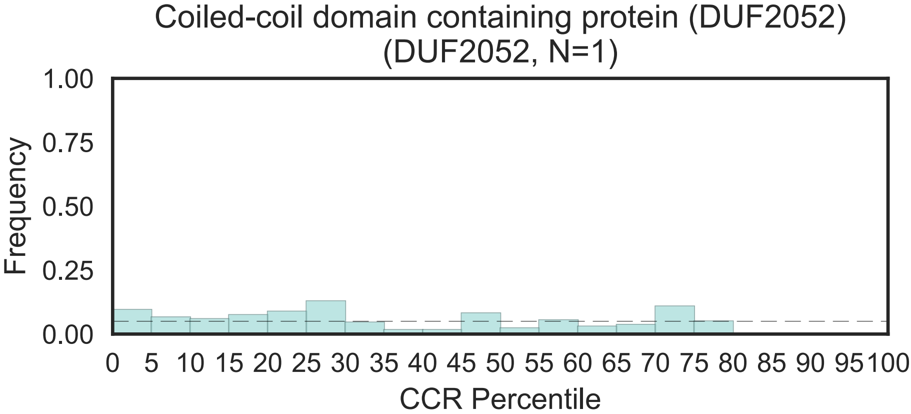

Uncharacterized conserved protein (DUF2043)
(DUF2043, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

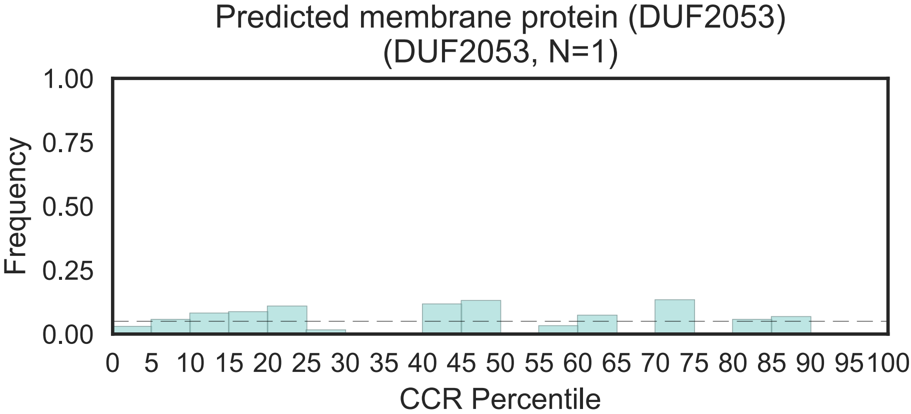

Uncharacterized conserved protein (DUF2045)
(DUF2045, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

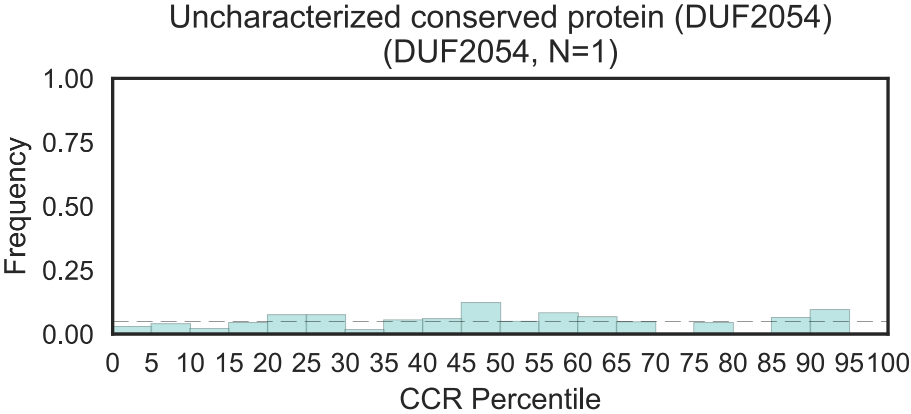

Uncharacterized conserved protein H4 (DUF2046)
(DUF2046, N=1)

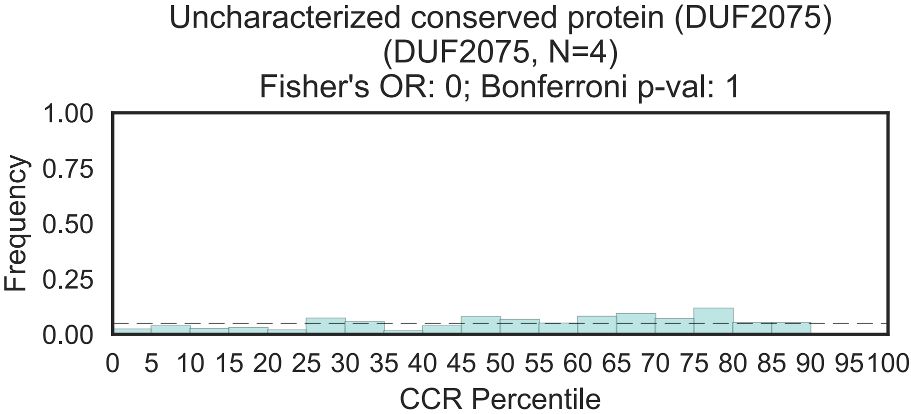


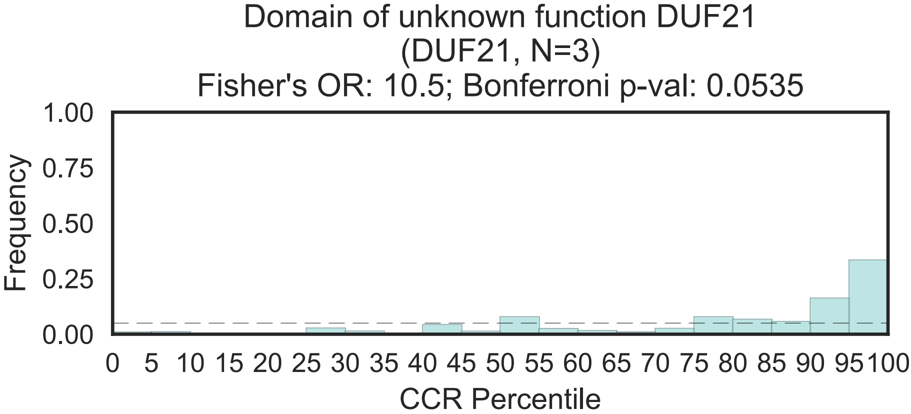
Abhydrolase domain containing 18
(DUF2048, N=1)

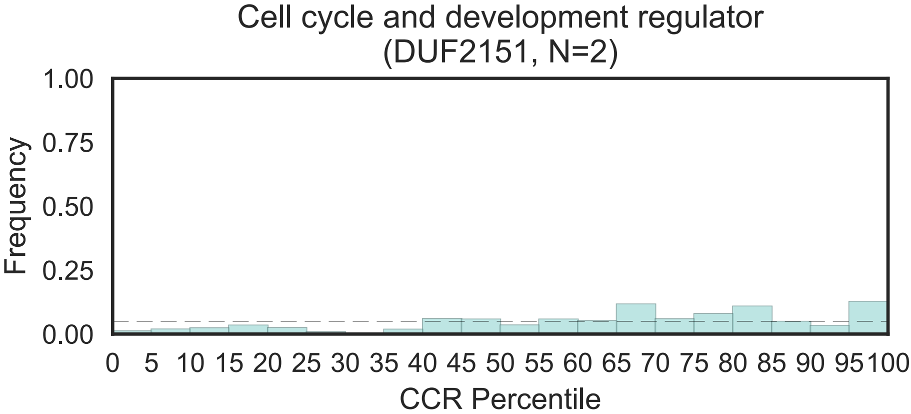

Coiled-coil domain containing protein (DUF2052)
(DUF2052, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

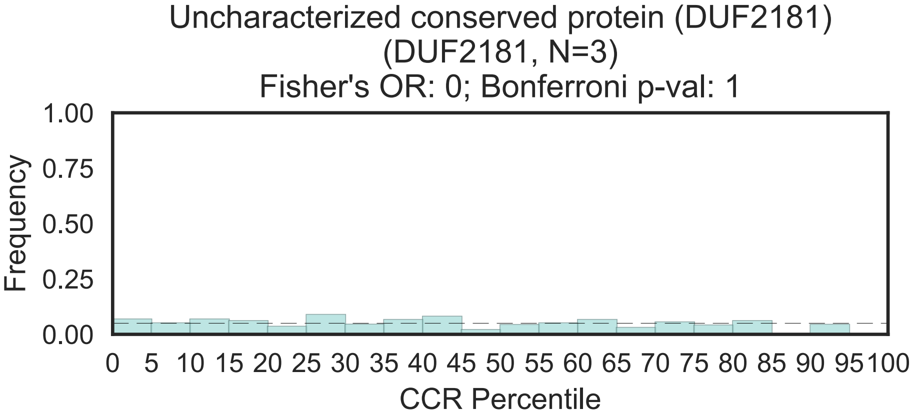

Predicted membrane protein (DUF2053)
(DUF2053, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

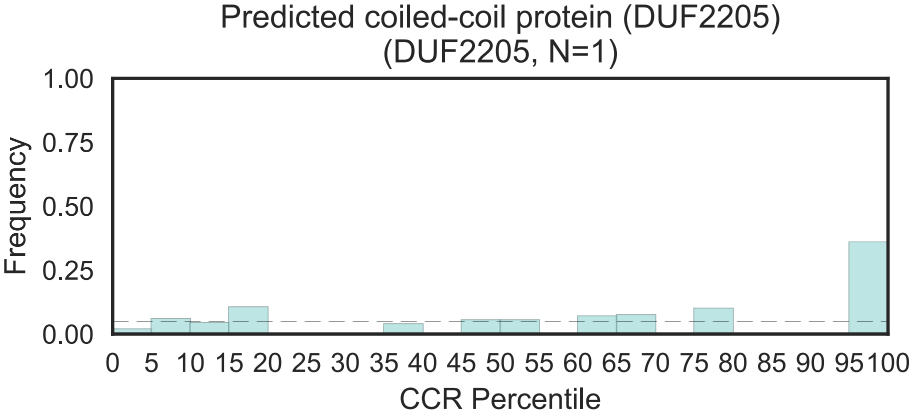

Uncharacterized conserved protein (DUF2054)
(DUF2054, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Uncharacterized conserved protein (DUF2075)
(DUF2075, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

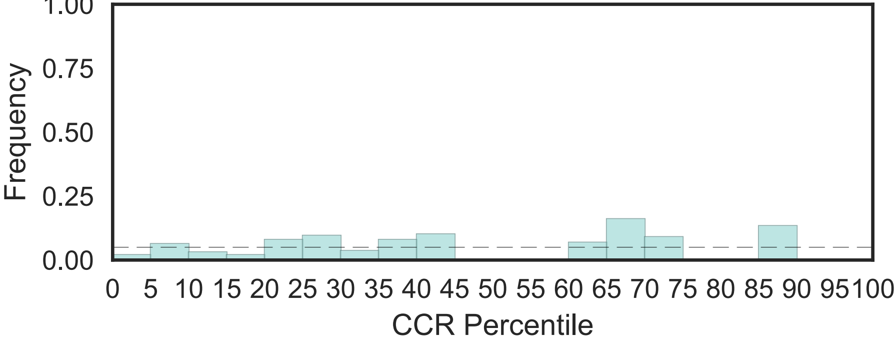

Domain of unknown function DUF21
(DUF21, N=3)
Fisher's OR: 10.5; Bonferroni p-val: 0.0535
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

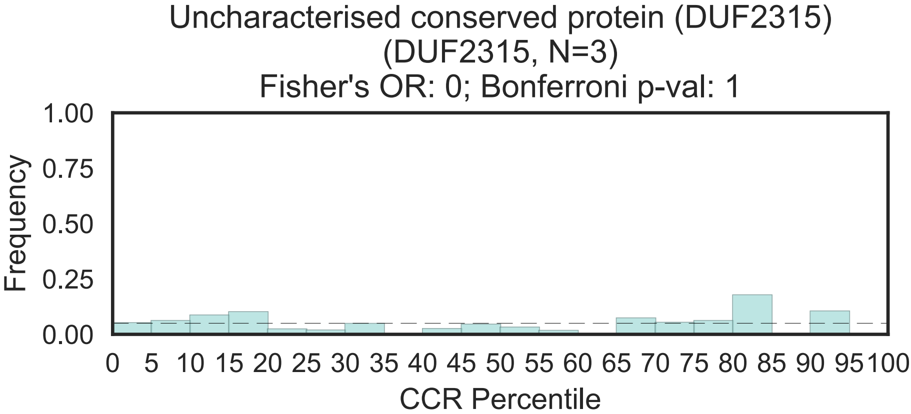

Cell cycle and development regulator
(DUF2151, N=2)

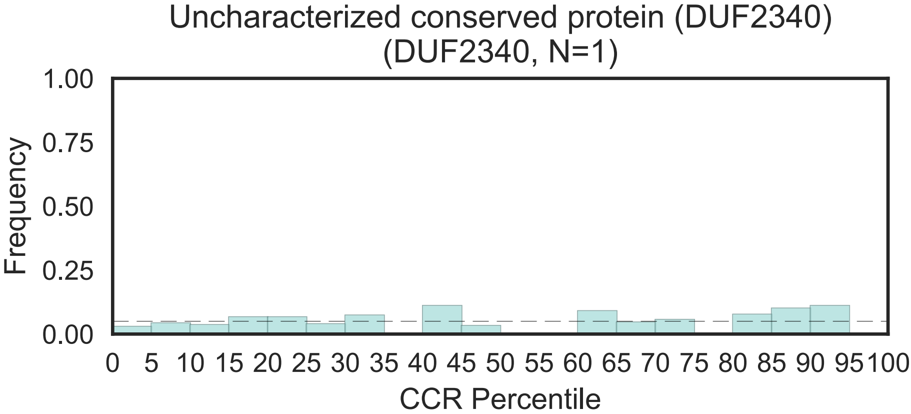

Uncharacterized conserved protein (DUF2181)
(DUF2181, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

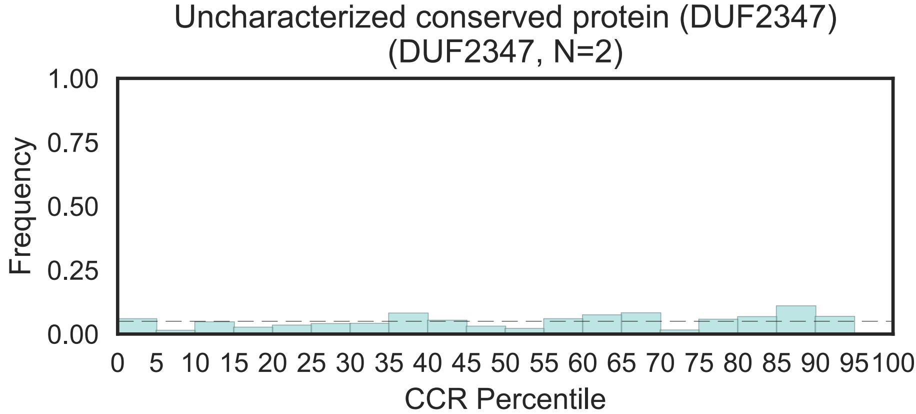

Predicted coiled-coil protein (DUF2205)
(DUF2205, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

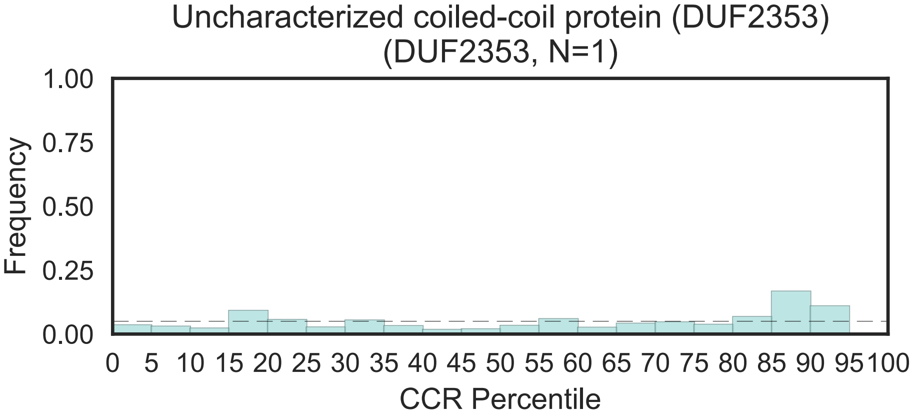
Uncharacterized protein conserved in bacteria (DUF2225) (DUF2225, N=1)

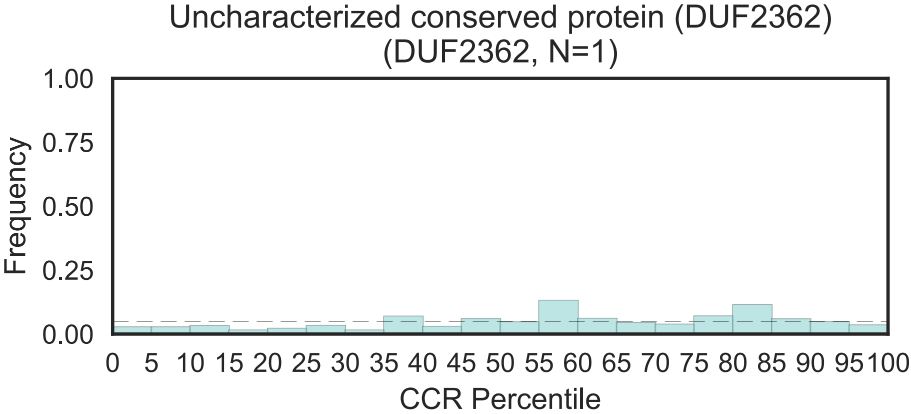


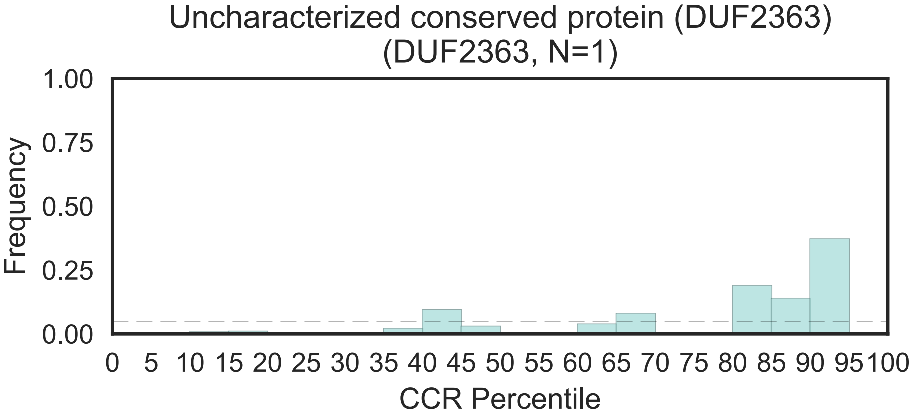

Uncharacterised conserved protein (DUF2315)
(DUF2315, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

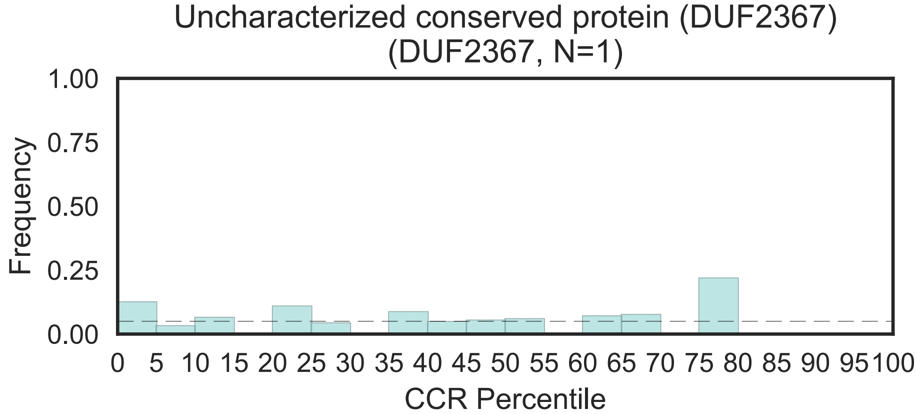

Uncharacterized conserved protein (DUF2340)
(DUF2340, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Uncharacterized conserved protein (DUF2347)
(DUF2347, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Uncharacterized coiled-coil protein (DUF2353)
(DUF2353, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Uncharacterized conserved protein (DUF2362)
(DUF2362, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Uncharacterized conserved protein (DUF2363)
(DUF2363, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Uncharacterized conserved protein (DUF2367)
(DUF2367, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
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55
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75
80
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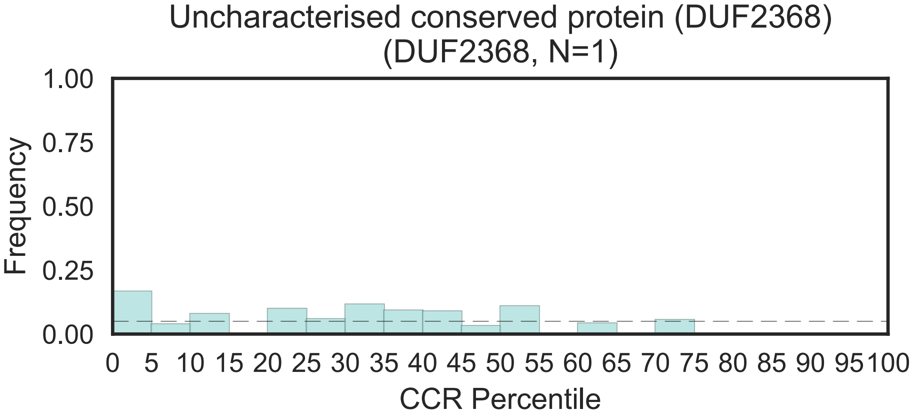
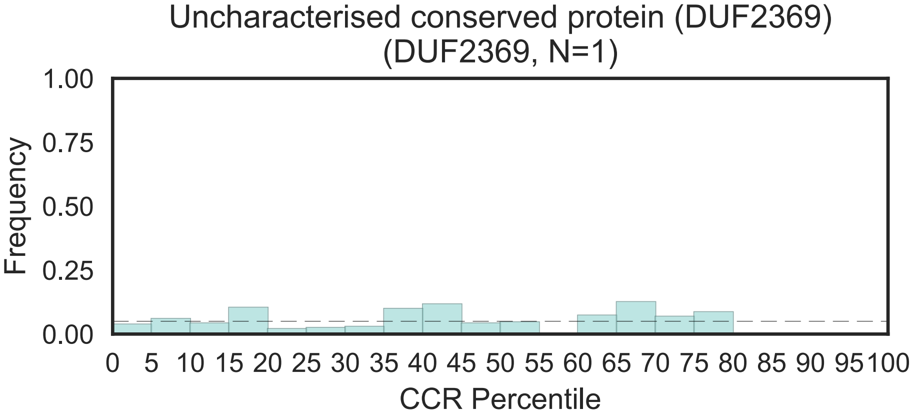
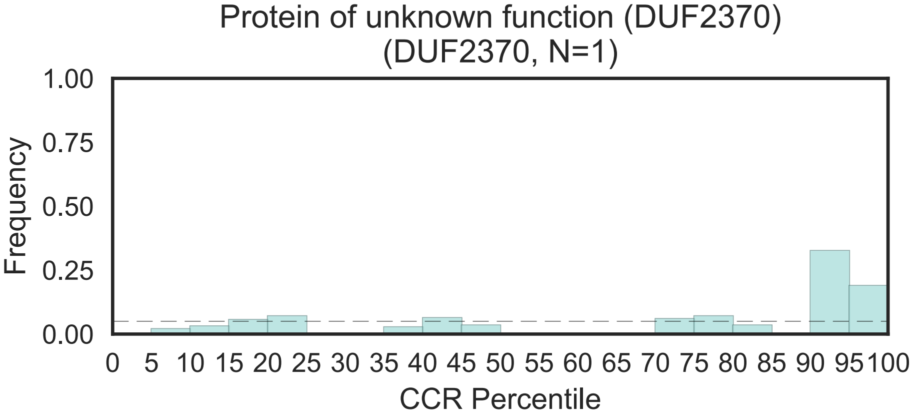
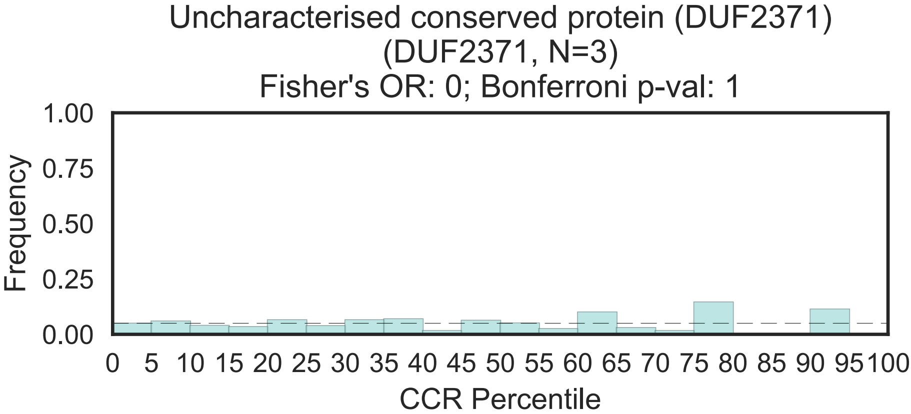
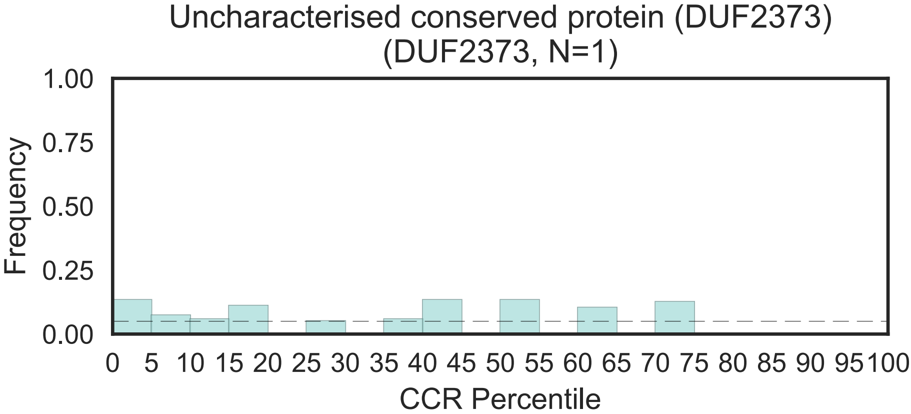
90
95
100
CCR Percentile

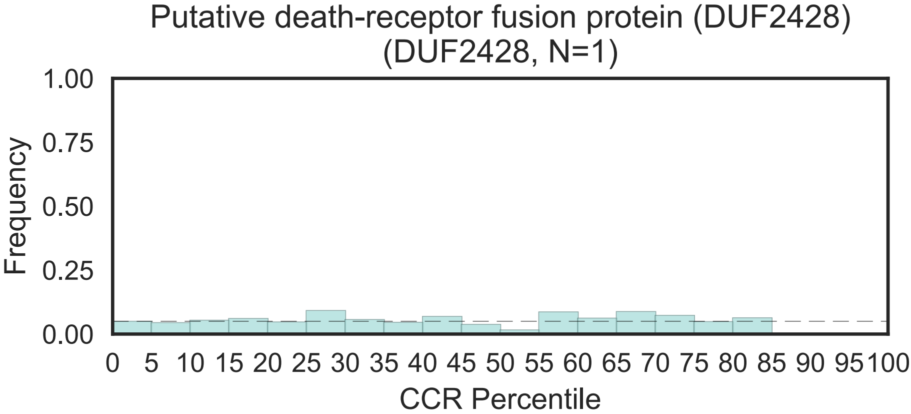

Uncharacterised conserved protein (DUF2368)
(DUF2368, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

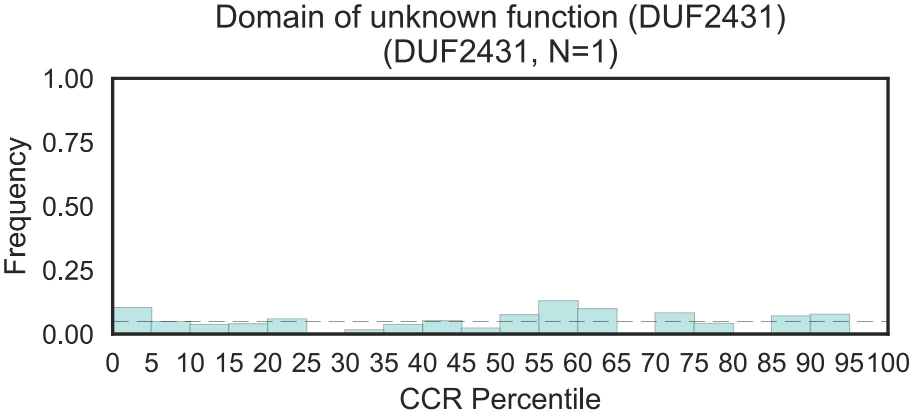

Uncharacterised conserved protein (DUF2369)
(DUF2369, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

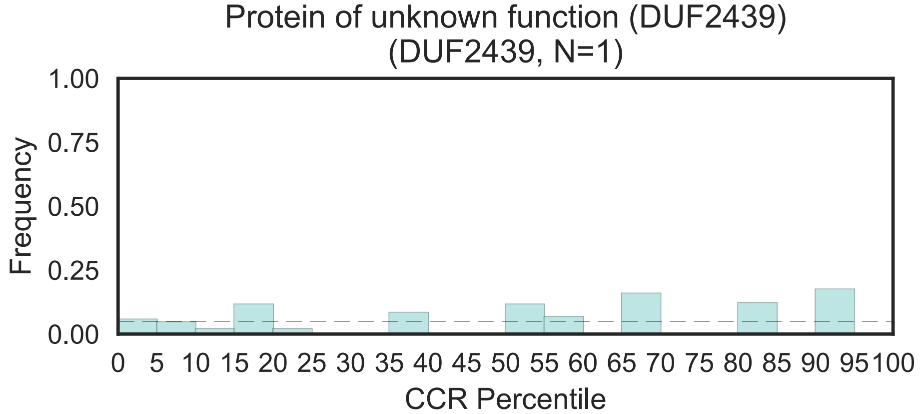

Protein of unknown function (DUF2370)
(DUF2370, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

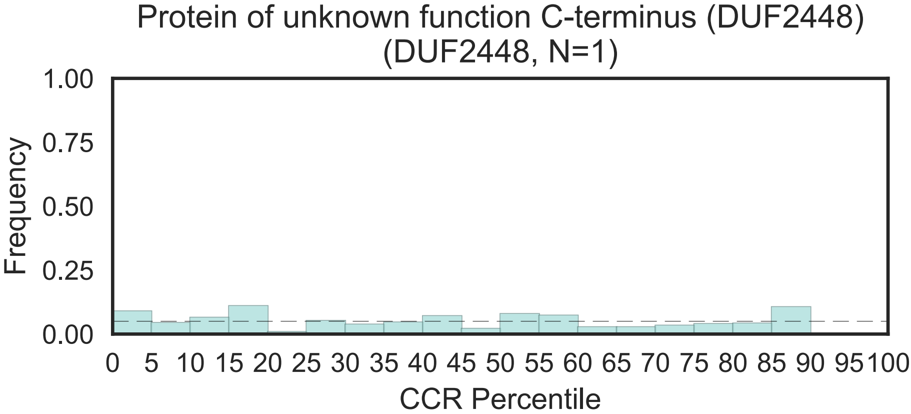

Uncharacterised conserved protein (DUF2371)
(DUF2371, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

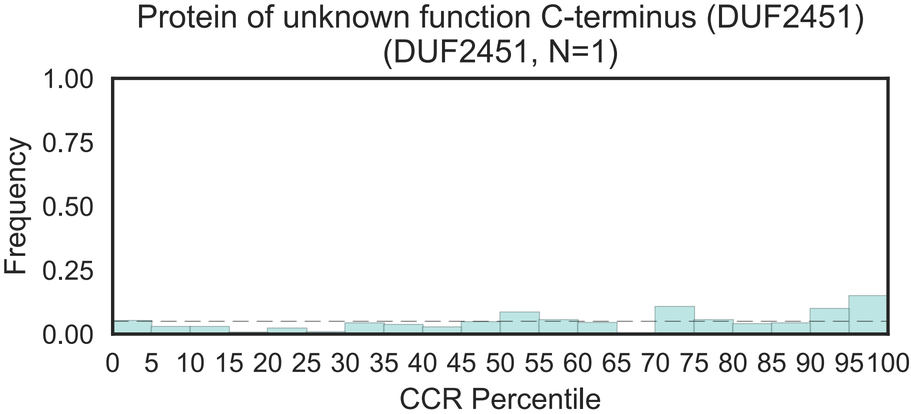

Uncharacterised conserved protein (DUF2373)
(DUF2373, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

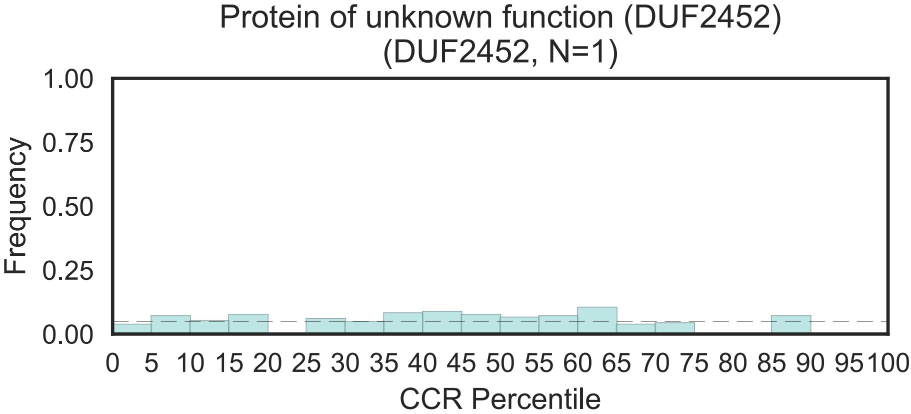

Putative death-receptor fusion protein (DUF2428)
(DUF2428, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

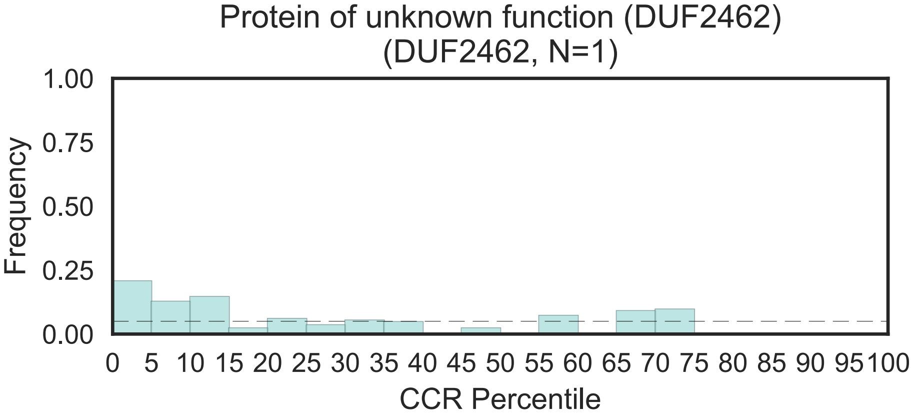

Domain of unknown function (DUF2431)
(DUF2431, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

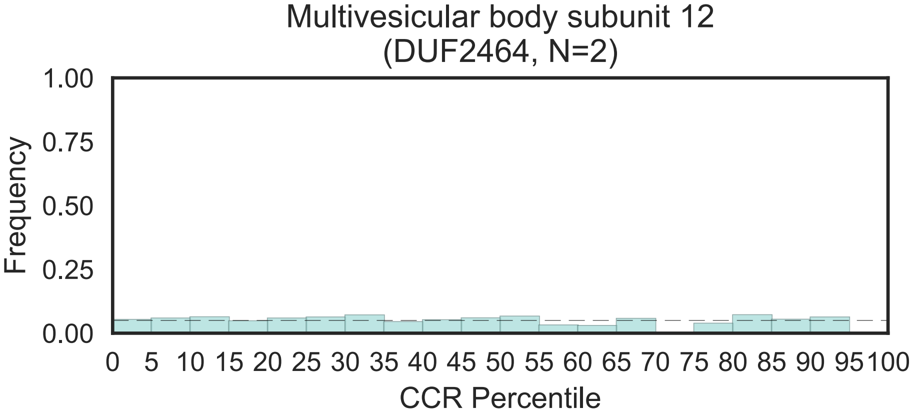

Protein of unknown function (DUF2439)
(DUF2439, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

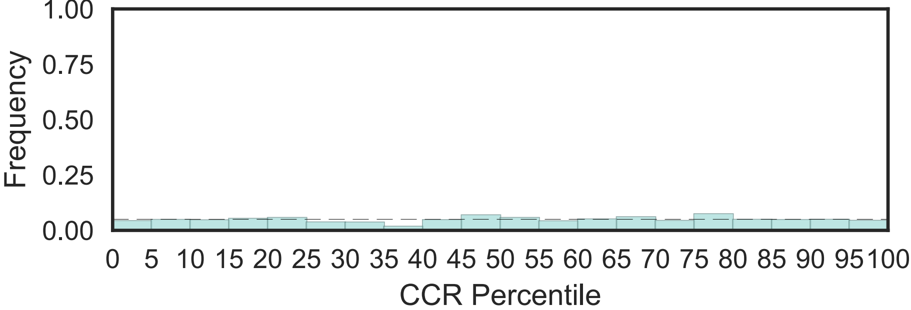

Protein of unknown function C-terminus (DUF2448)
(DUF2448, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Protein of unknown function C-terminus (DUF2451)
(DUF2451, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

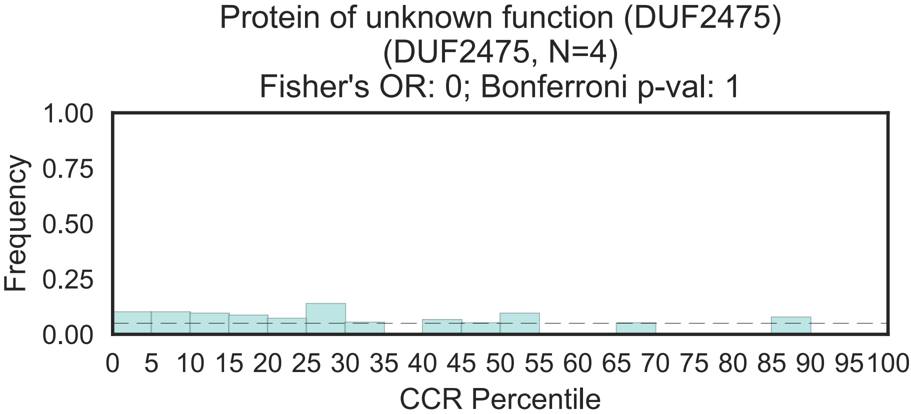

Protein of unknown function (DUF2452)
(DUF2452, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

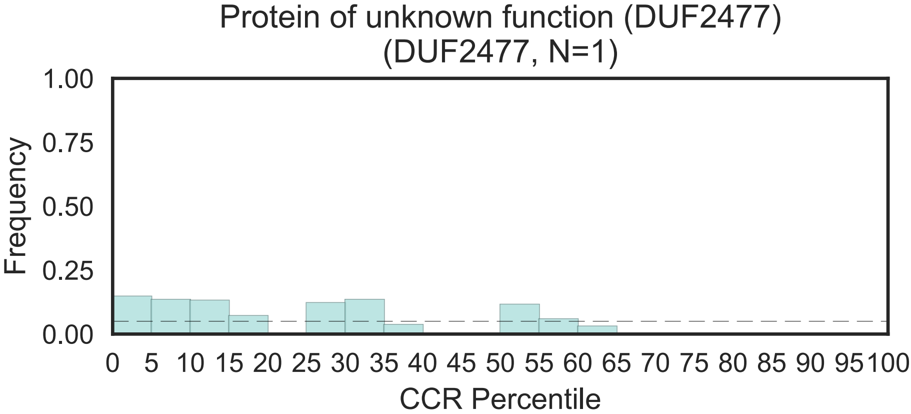

Protein of unknown function (DUF2462)
(DUF2462, N=1)

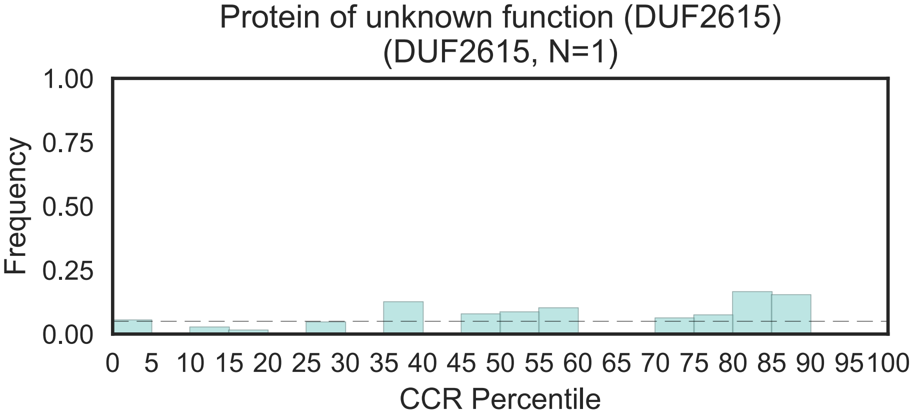

Multivesicular body subunit 12
(DUF2464, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

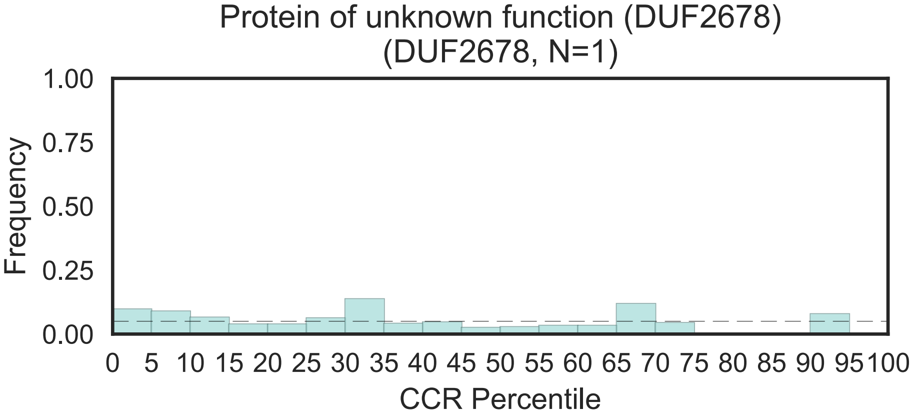


Protein of unknown function (DUF2465)
(DUF2465, N=3)
Fisher's OR: 0.629; Bonferroni p-val: 1

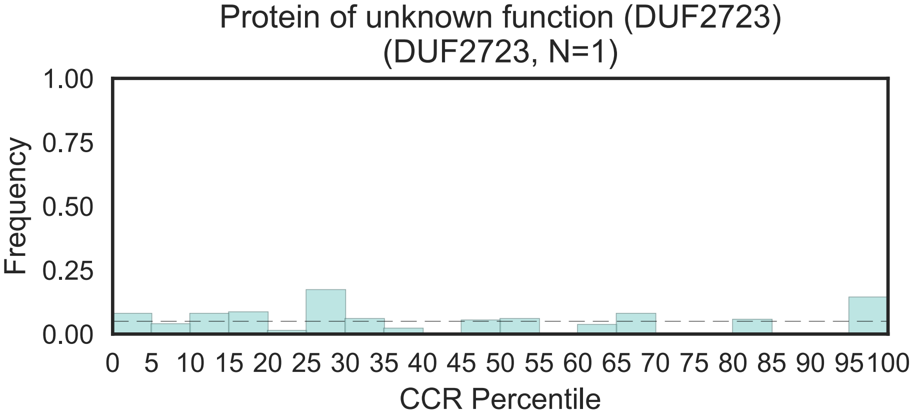

Protein of unknown function (DUF2475)
(DUF2475, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

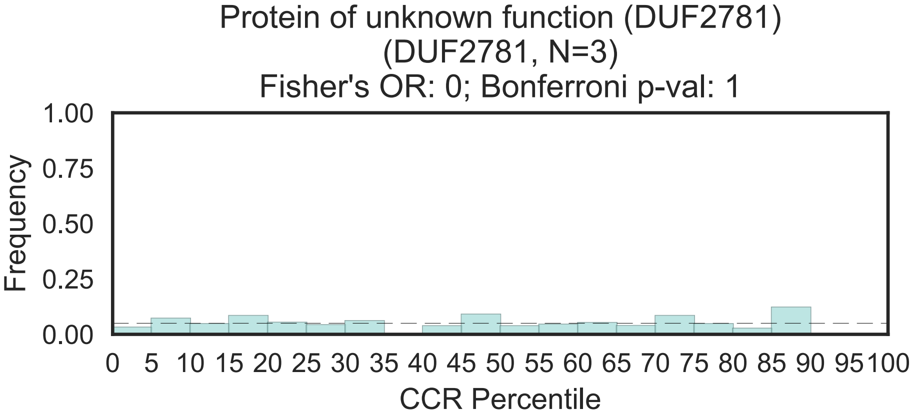

Protein of unknown function (DUF2477)
(DUF2477, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

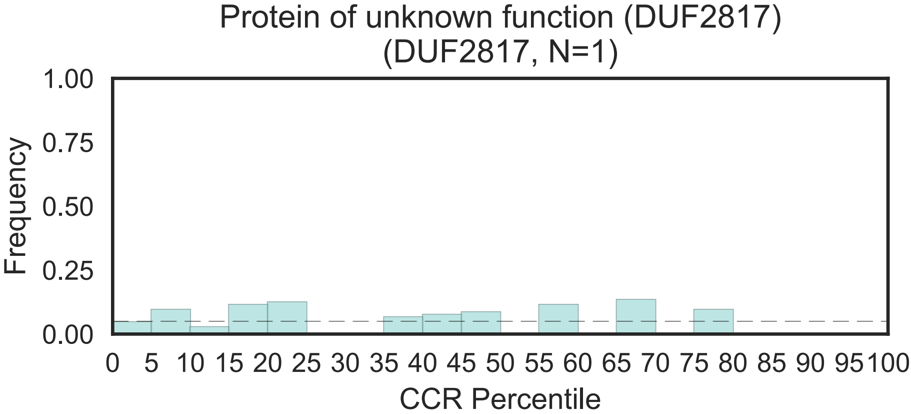

Protein of unknown function (DUF2615)
(DUF2615, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



Protein of unknown function (DUF2678)
(DUF2678, N=1)


Protein of unknown function (DUF2723)
(DUF2723, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Protein of unknown function (DUF2781)
(DUF2781, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Protein of unknown function (DUF2817)
(DUF2817, N=1)
Frequency
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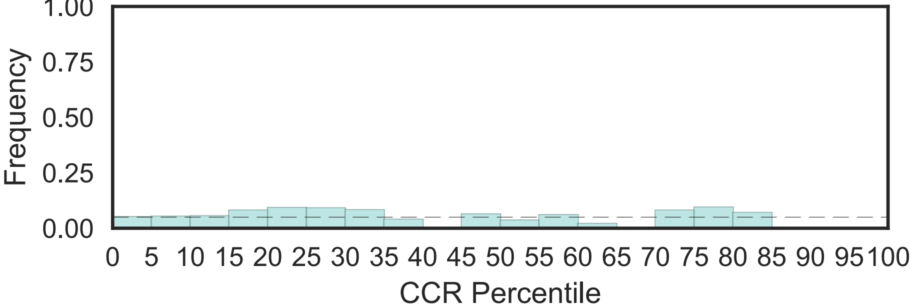
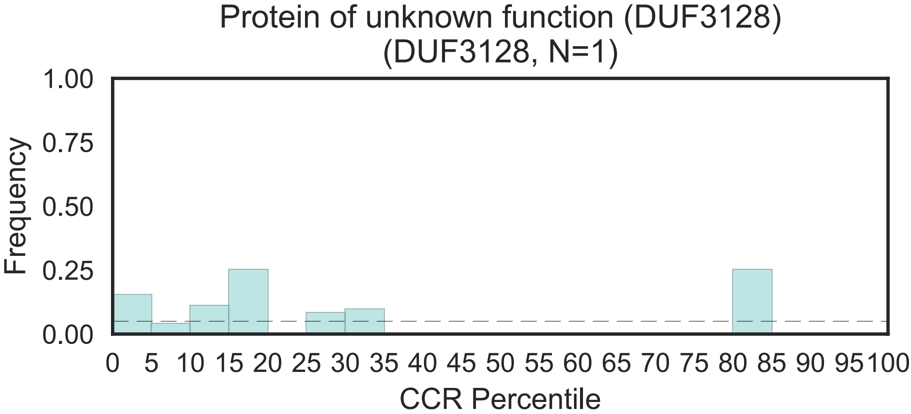
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile



Protein of unknown function (DUF2870)
(DUF2870, N=3)
Fisher's OR: 0; Bonferroni p-val: 1


Protein of unknown function (DUF3128)
(DUF3128, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
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20
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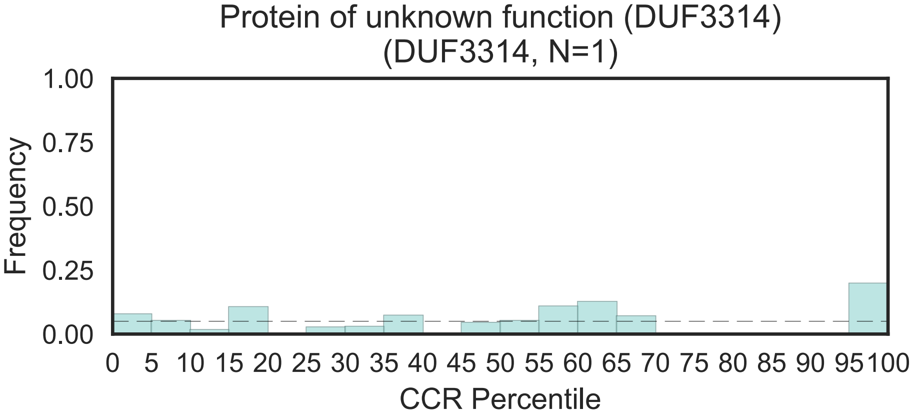
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Protein of unknown function (DUF3314)
(DUF3314, N=1)
Frequency
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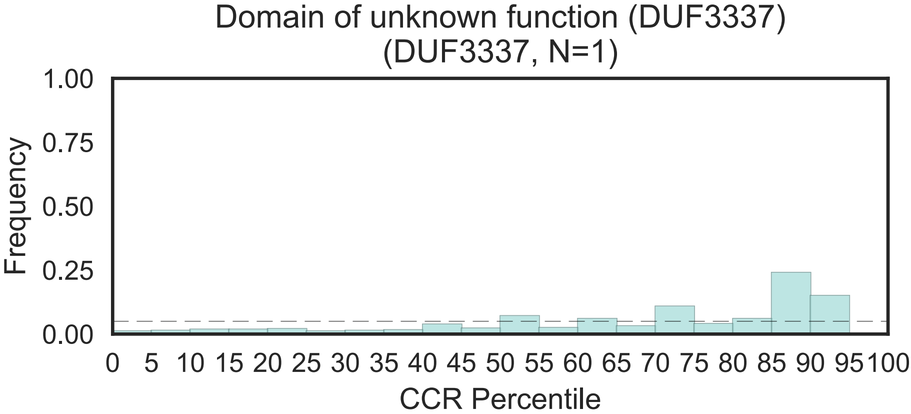
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


Domain of unknown function (DUF3337)
(DUF3337, N=1)
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0.75
0.50
0.25
0.00
Frequency
0
5
10
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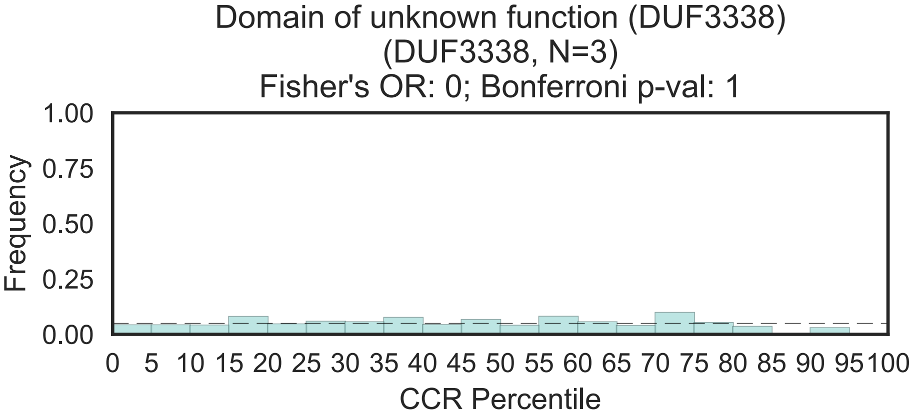
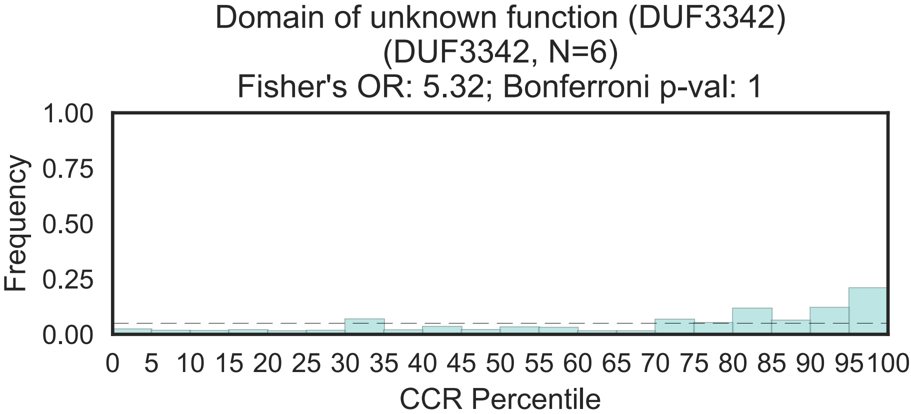
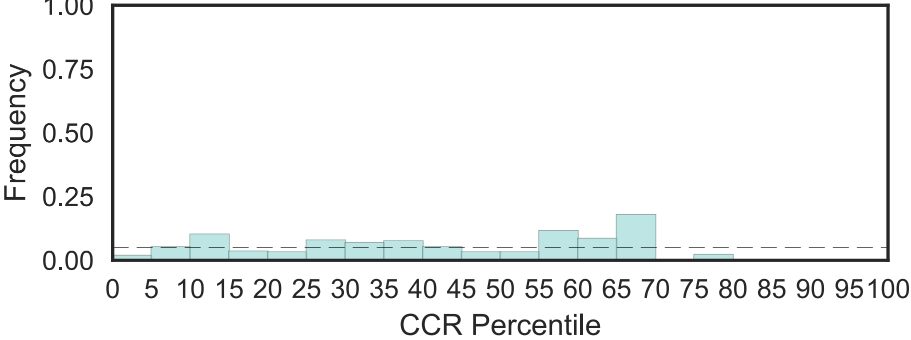
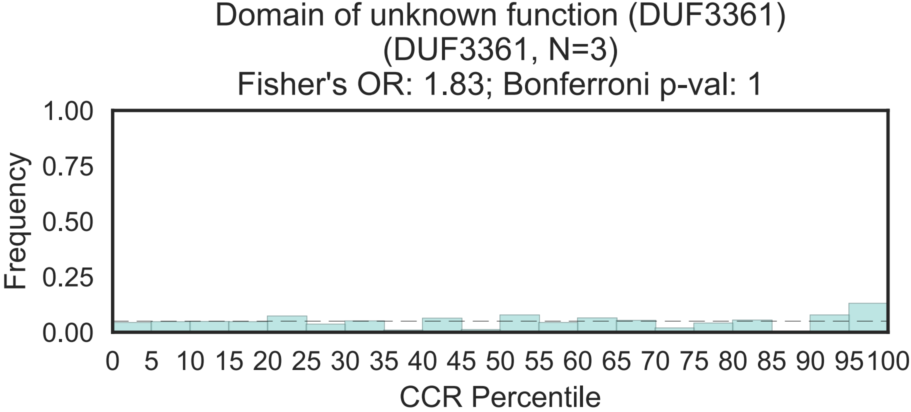
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

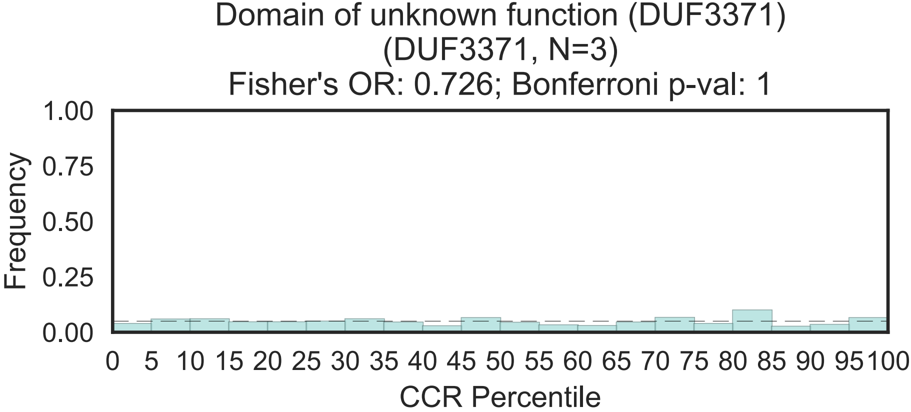

Domain of unknown function (DUF3338)
(DUF3338, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

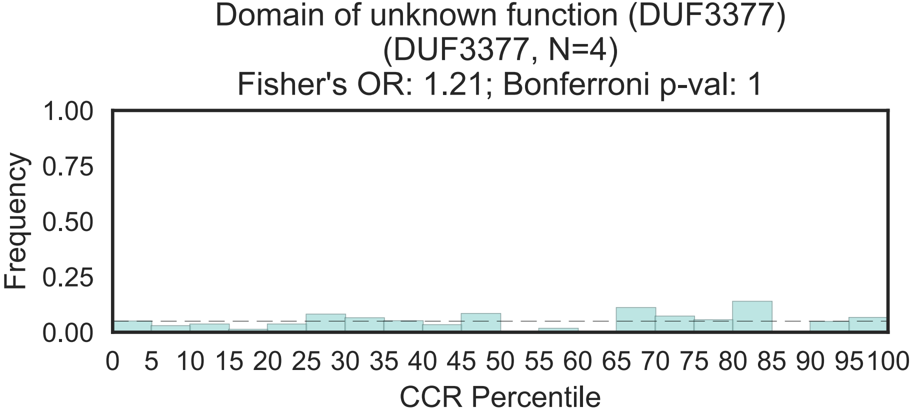

Domain of unknown function (DUF3342)
(DUF3342, N=6)
Fisher's OR: 5.32; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

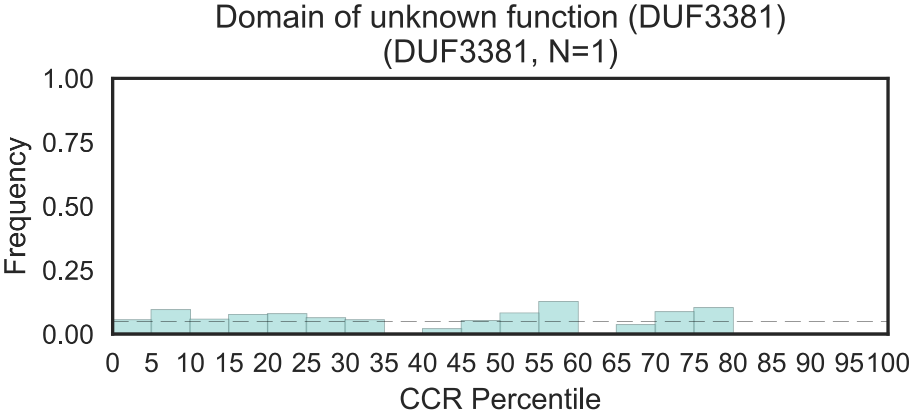
Domain of unknown function (DUF3350)
(DUF3350, N=2)




Domain of unknown function (DUF3361)
(DUF3361, N=3)
Fisher's OR: 1.83; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF3371)
(DUF3371, N=3)
Fisher's OR: 0.726; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF3377)
(DUF3377, N=4)
Fisher's OR: 1.21; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF3381)
(DUF3381, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
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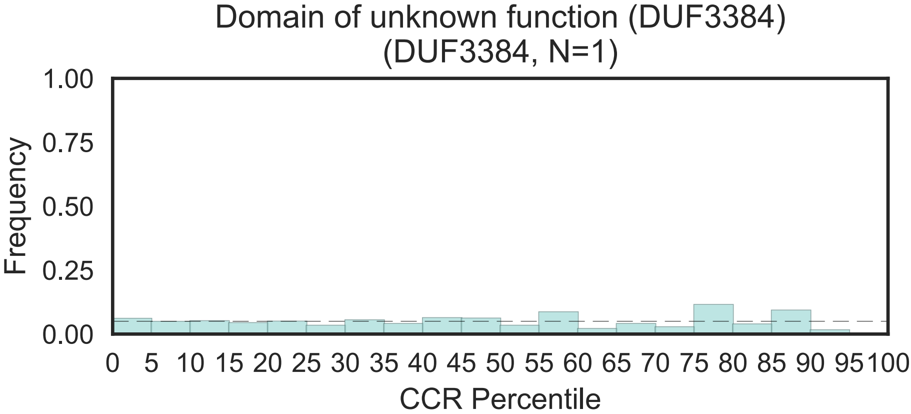
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



Domain of unknown function (DUF3384)
(DUF3384, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
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20
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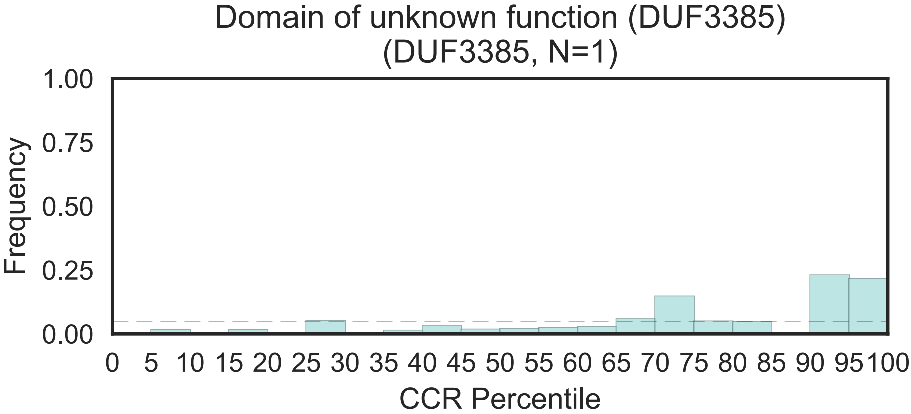
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF3385)
(DUF3385, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
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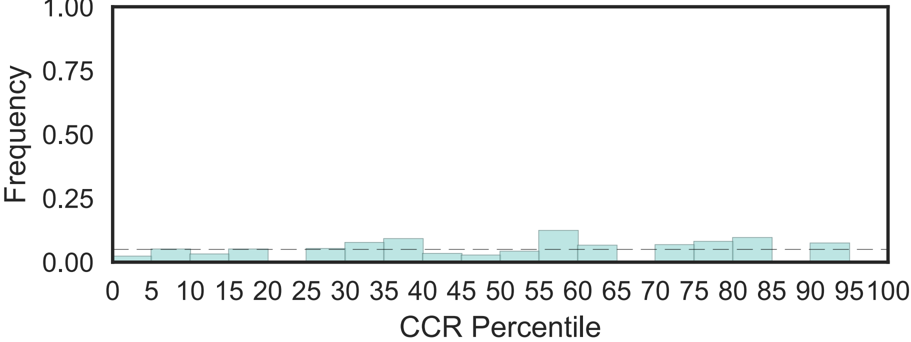
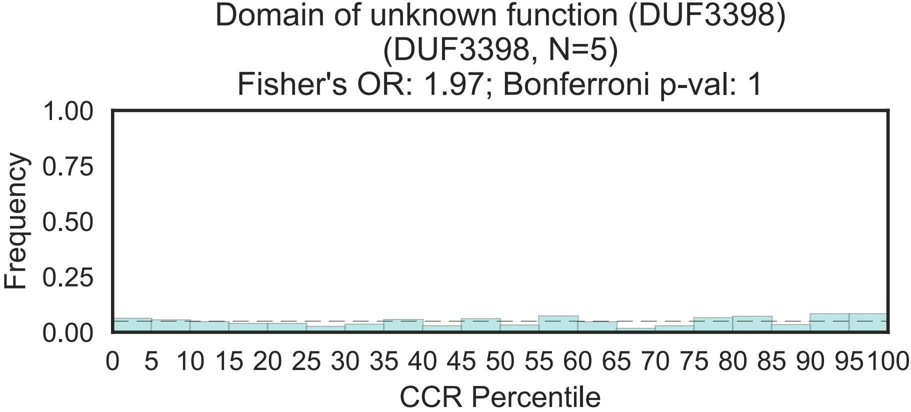
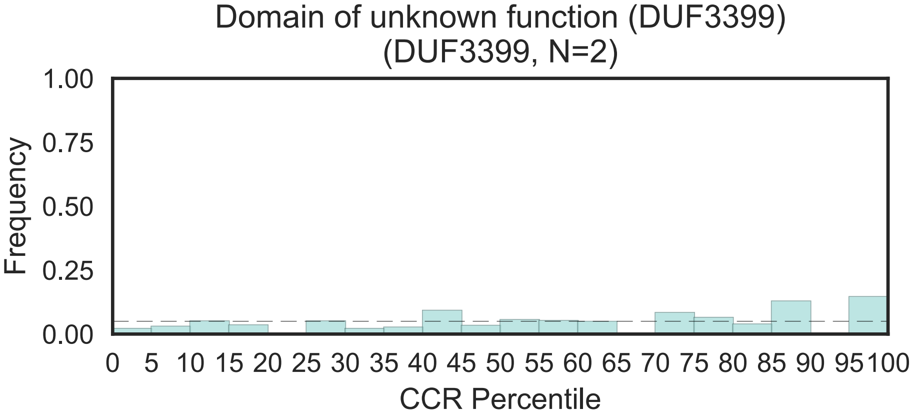
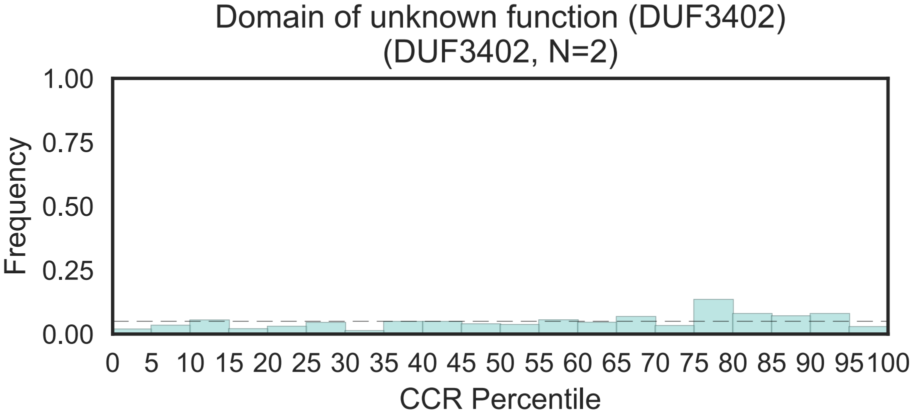
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

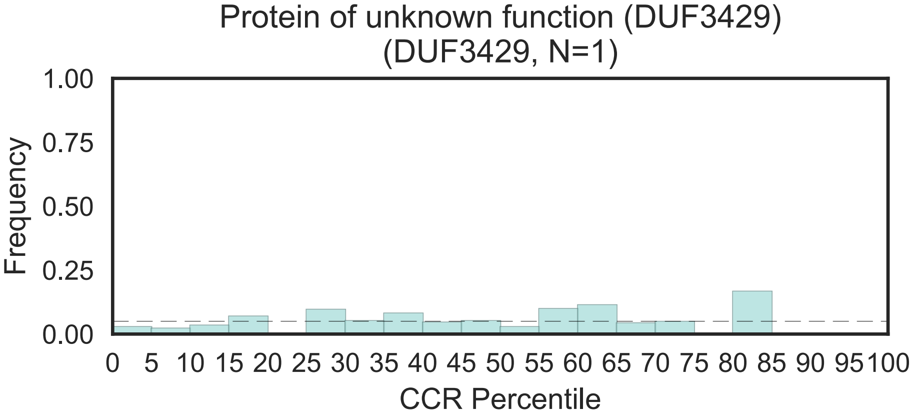

Domain of unknown function (DUF3395)
(DUF3395, N=1)

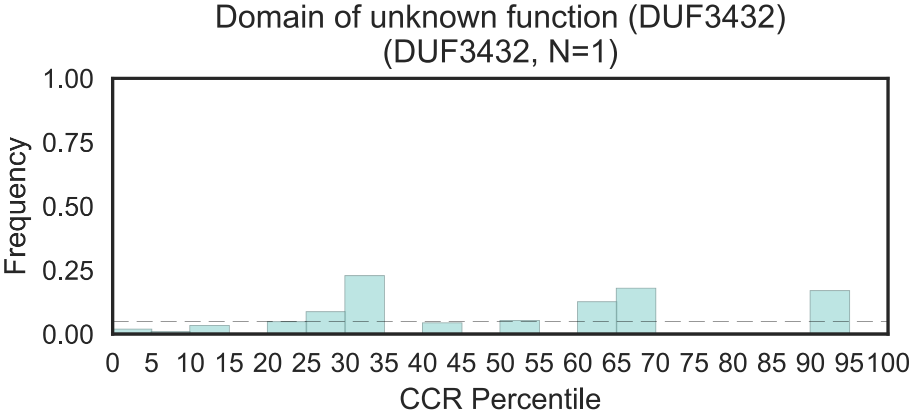

Domain of unknown function (DUF3398)
(DUF3398, N=5)
Fisher's OR: 1.97; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

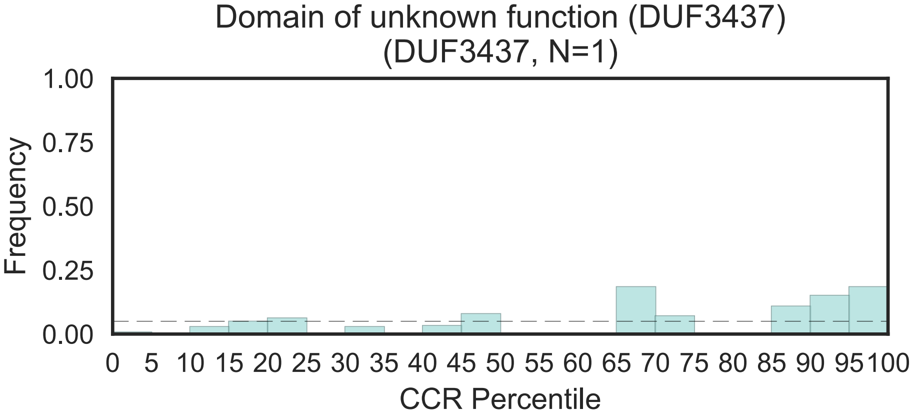


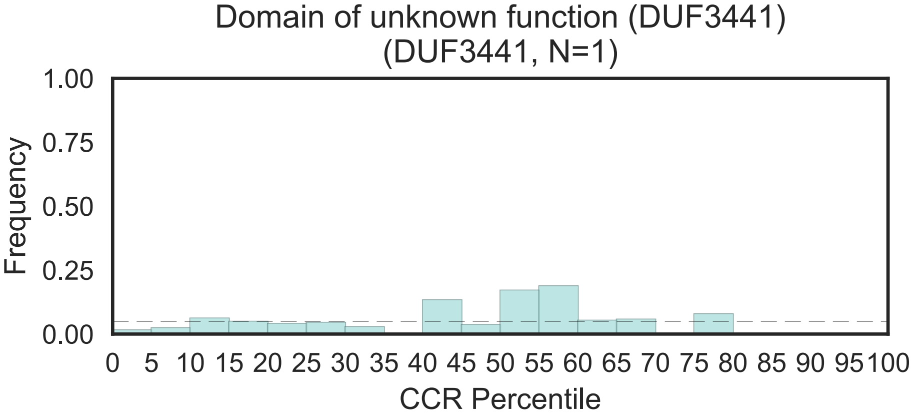
Domain of unknown function (DUF3399)
(DUF3399, N=2)

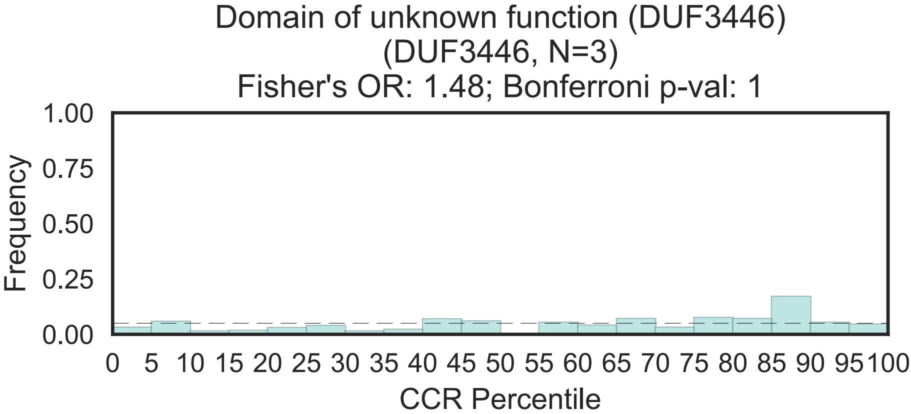

Domain of unknown function (DUF3402)
(DUF3402, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Protein of unknown function (DUF3429)
(DUF3429, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

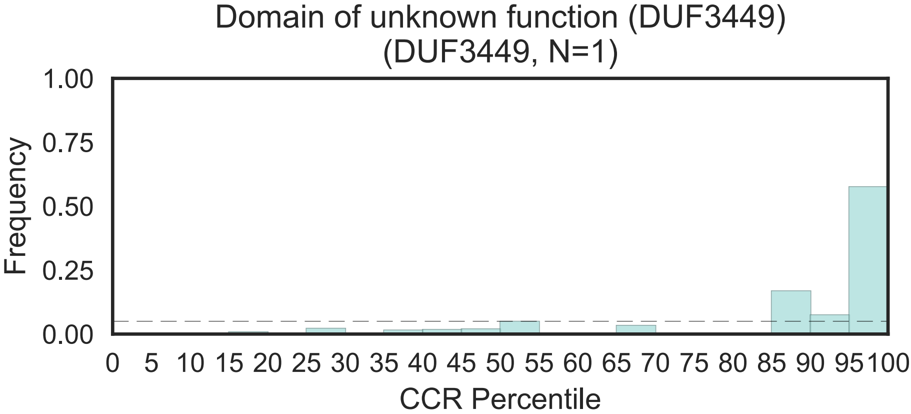

Domain of unknown function (DUF3432)
(DUF3432, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

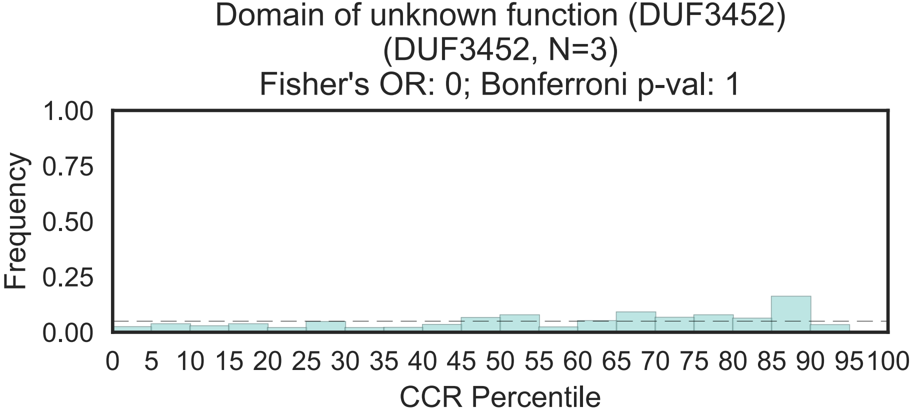

Domain of unknown function (DUF3437)
(DUF3437, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

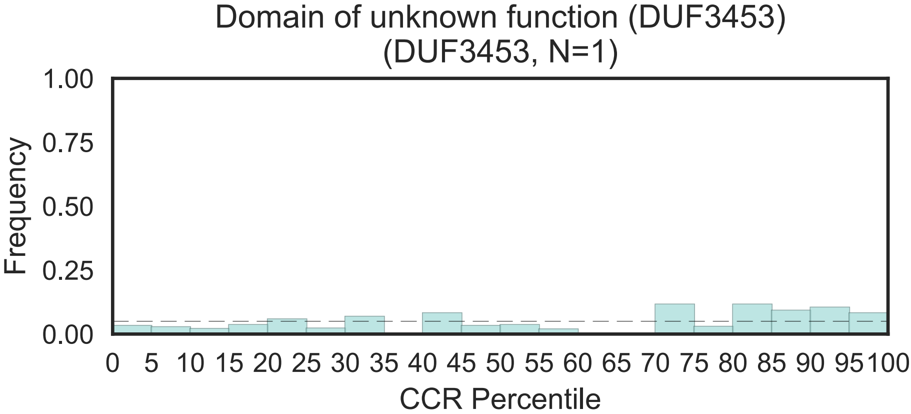

Domain of unknown function (DUF3441)
(DUF3441, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



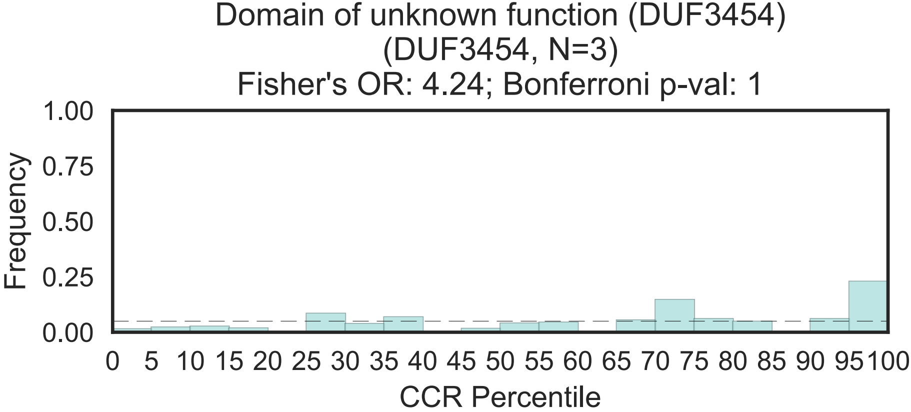
Domain of unknown function (DUF3446)
(DUF3446, N=3)
Fisher's OR: 1.48; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

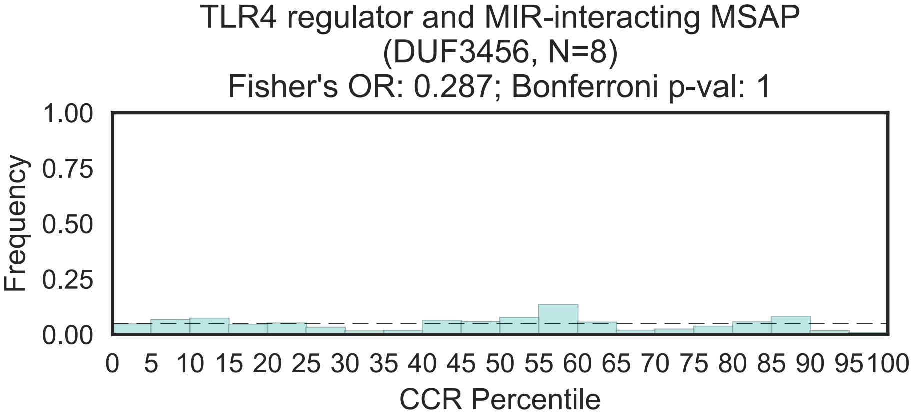

Domain of unknown function (DUF3449)
(DUF3449, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

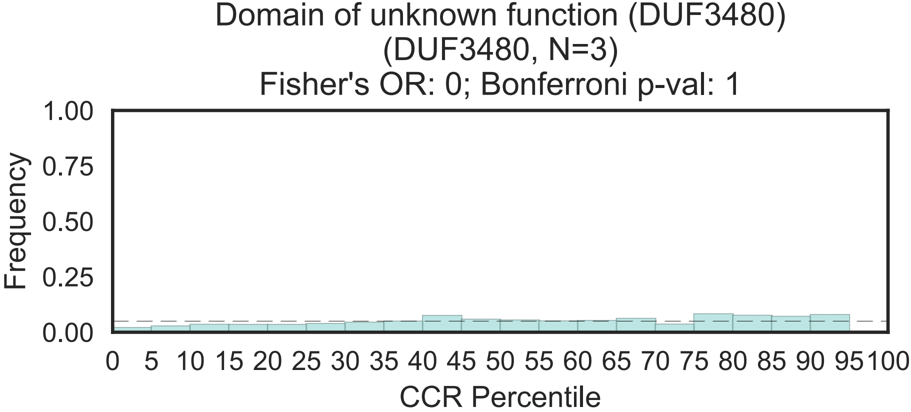

Domain of unknown function (DUF3452)
(DUF3452, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

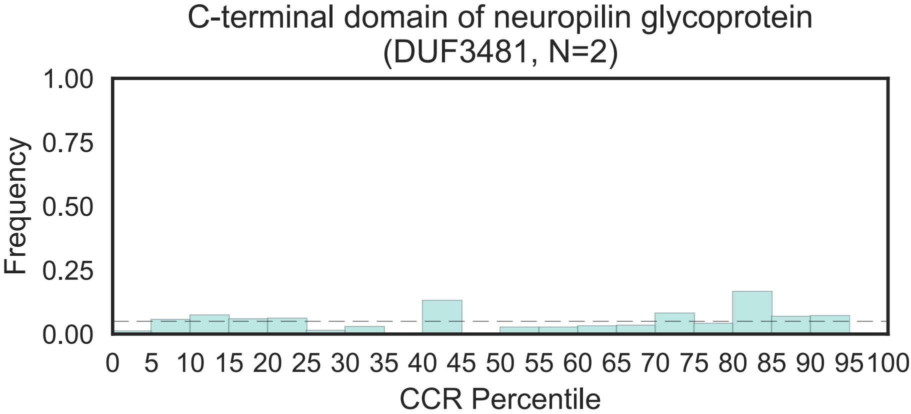


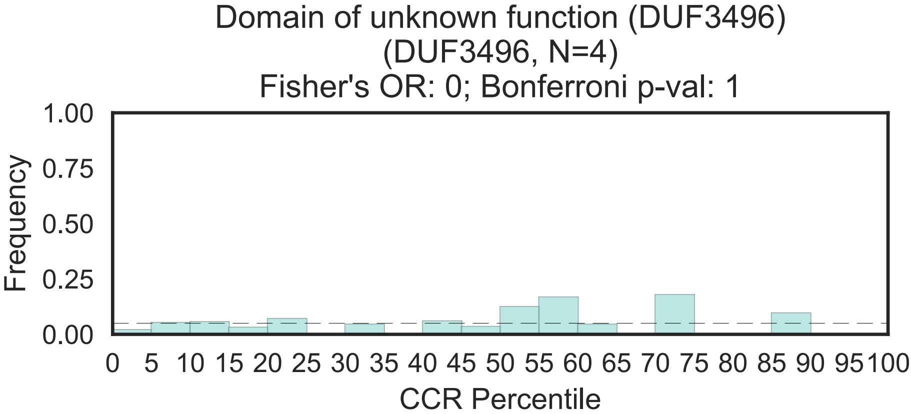
Domain of unknown function (DUF3453)
(DUF3453, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

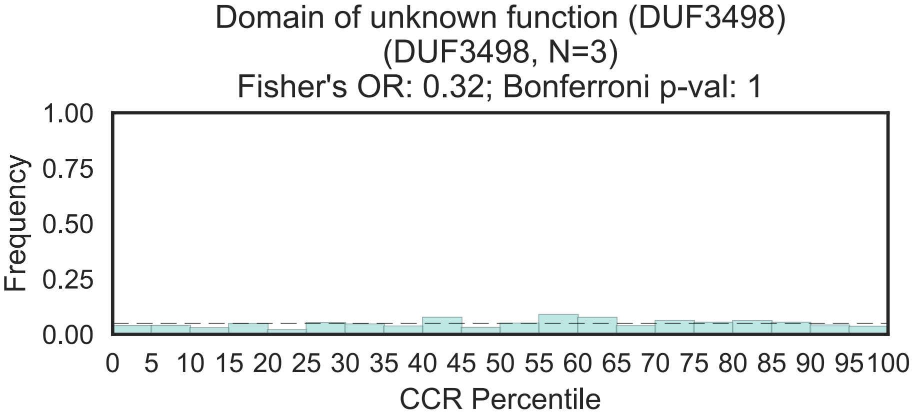

Domain of unknown function (DUF3454)
(DUF3454, N=3)
Fisher's OR: 4.24; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

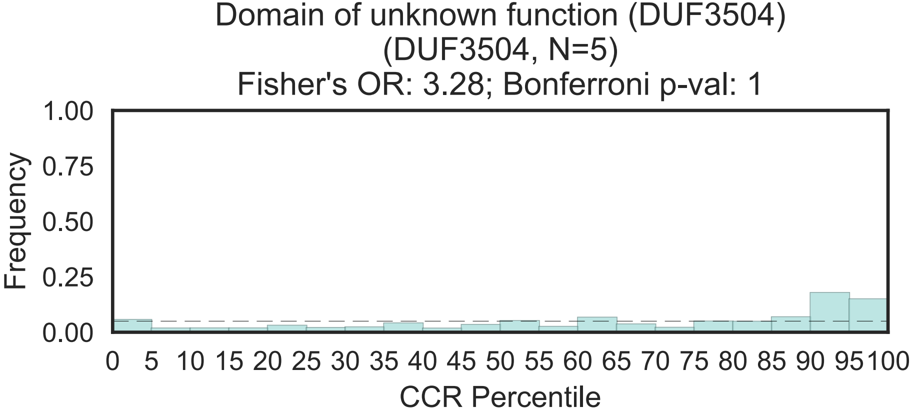

TLR4 regulator and MIR-interacting MSAP
(DUF3456, N=8)
Fisher's OR: 0.287; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

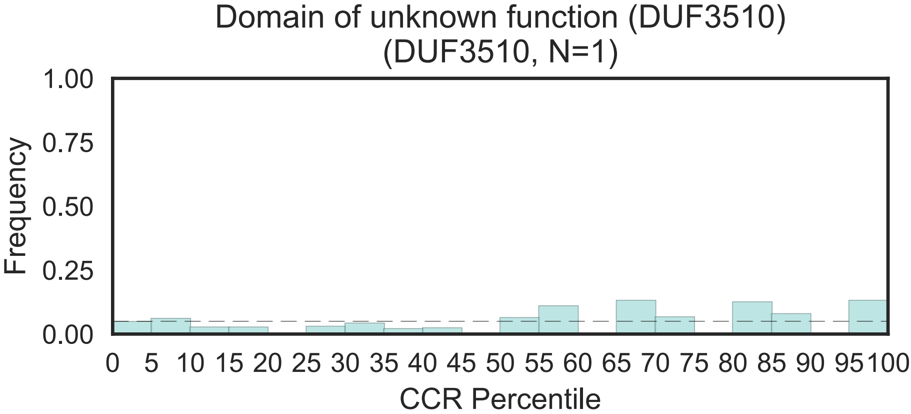

Domain of unknown function (DUF3480)
(DUF3480, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

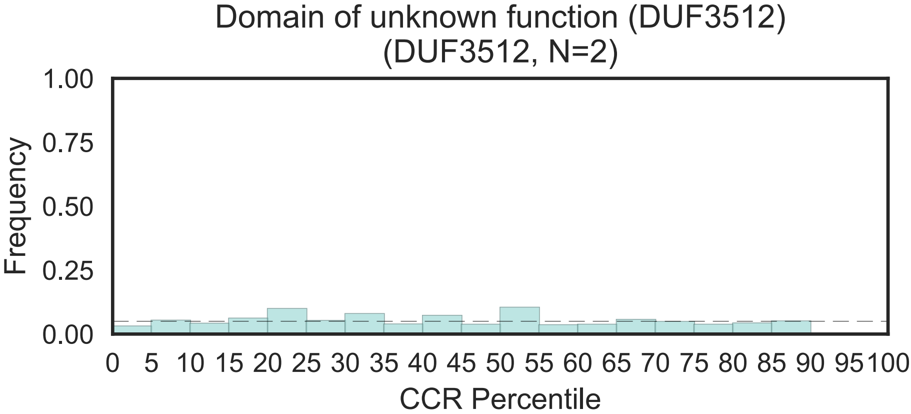

C-terminal domain of neuropilin glycoprotein
(DUF3481, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

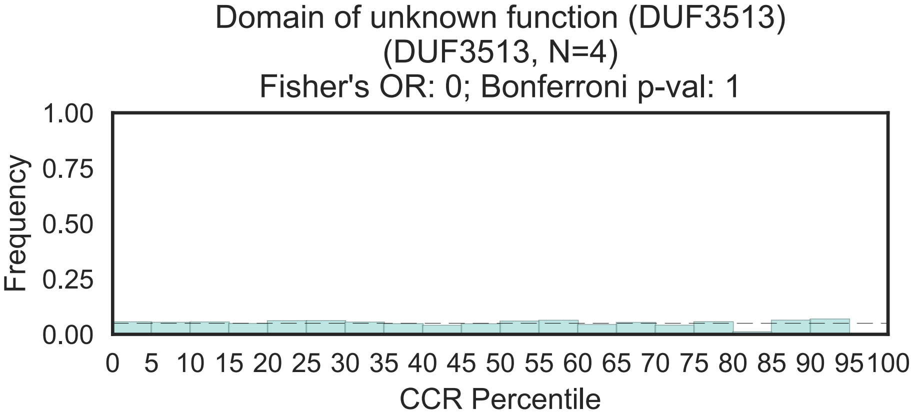

Domain of unknown function (DUF3496)
(DUF3496, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

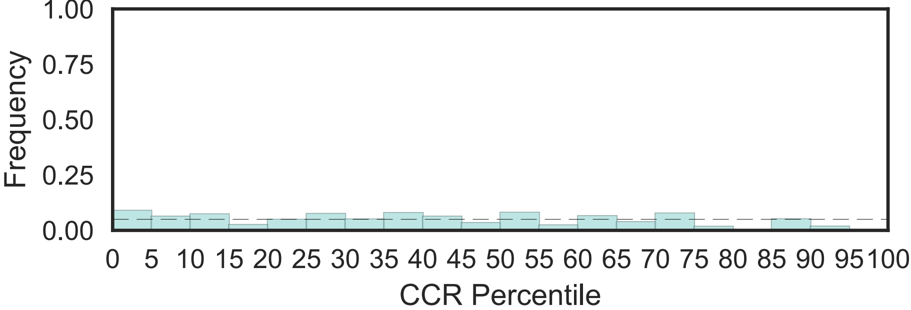

Domain of unknown function (DUF3498)
(DUF3498, N=3)
Fisher's OR: 0.32; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF3504)
(DUF3504, N=5)
Fisher's OR: 3.28; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

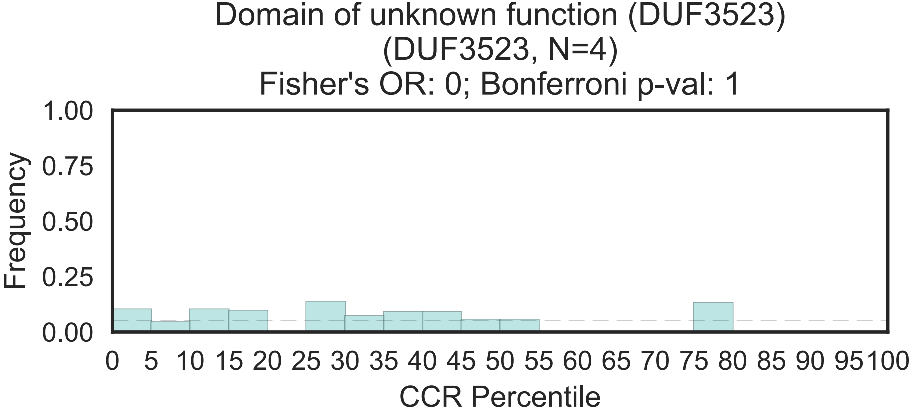

Domain of unknown function (DUF3510)
(DUF3510, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

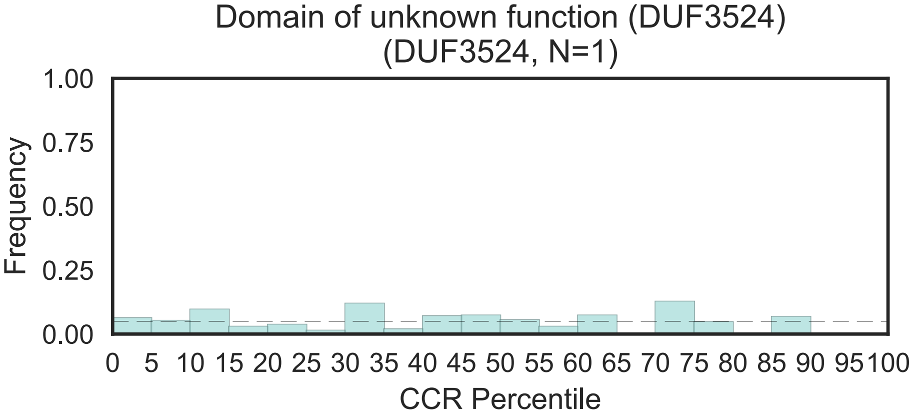

Domain of unknown function (DUF3512)
(DUF3512, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF3513)
(DUF3513, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



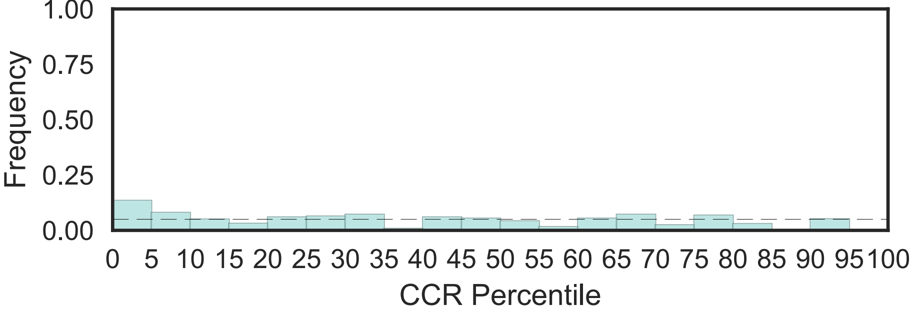
Protein of unknown function (DUF3522)
(DUF3522, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

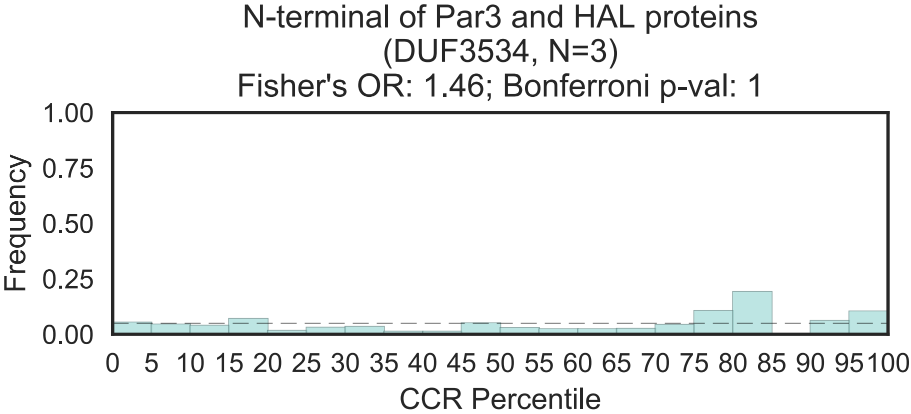

Domain of unknown function (DUF3523)
(DUF3523, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

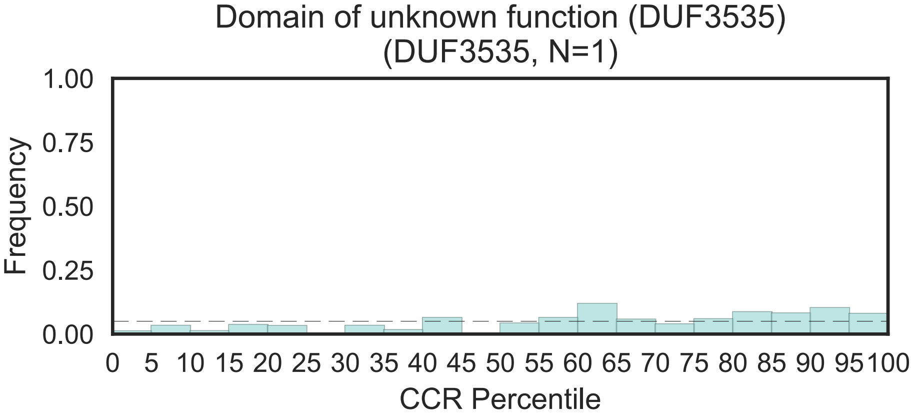


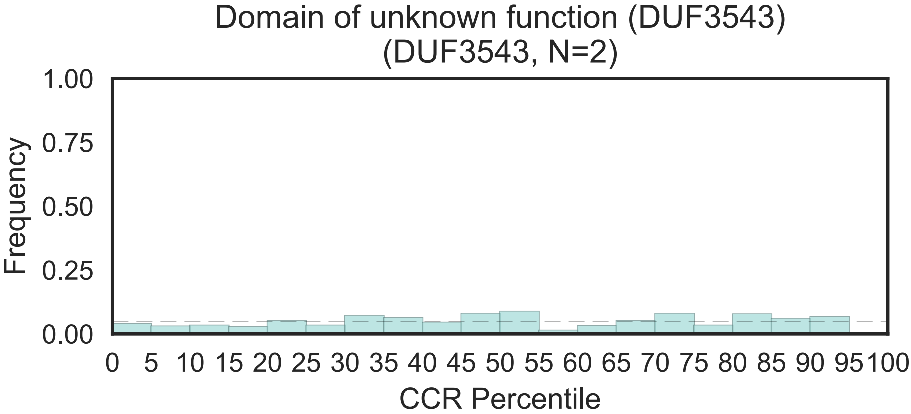
Domain of unknown function (DUF3524)
(DUF3524, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

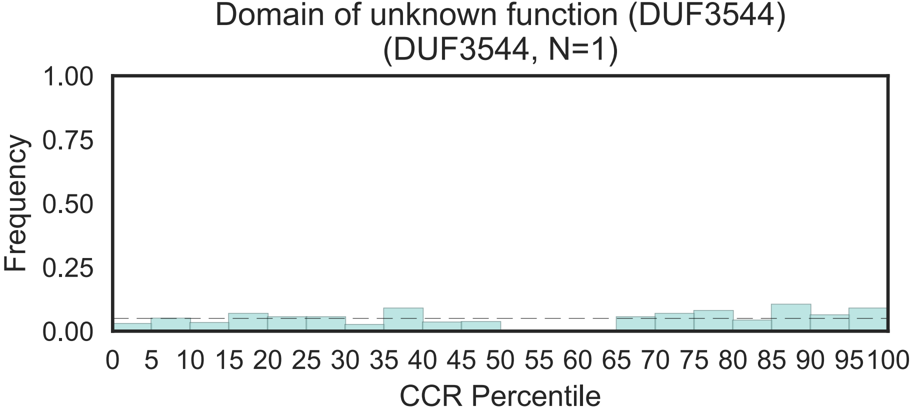
Protein of unknown function (DUF3528)
(DUF3528, N=4)
Fisher's OR: 0; Bonferroni p-val: 1



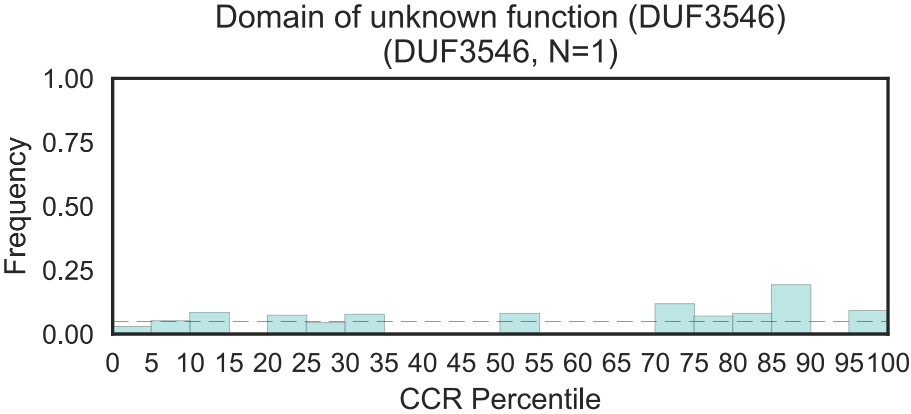

N-terminal of Par3 and HAL proteins
(DUF3534, N=3)
Fisher's OR: 1.46; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

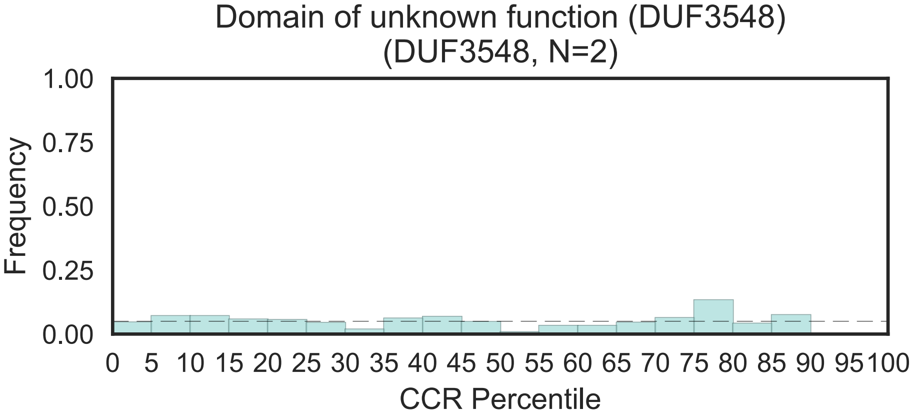

Domain of unknown function (DUF3535)
(DUF3535, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

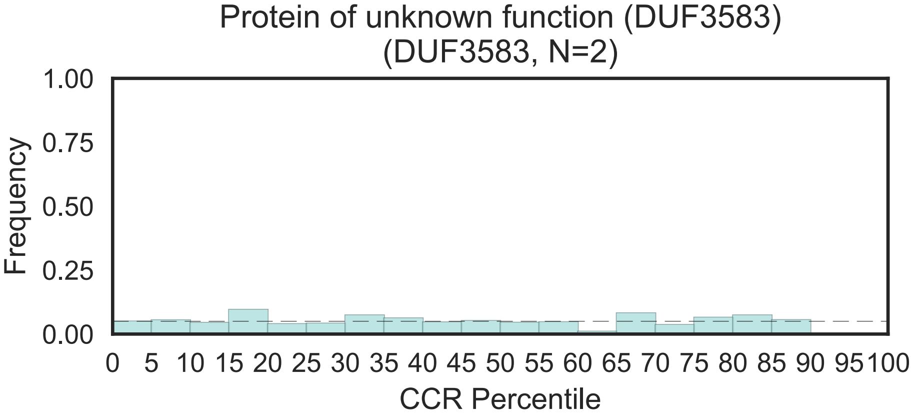

Domain of unknown function (DUF3543)
(DUF3543, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

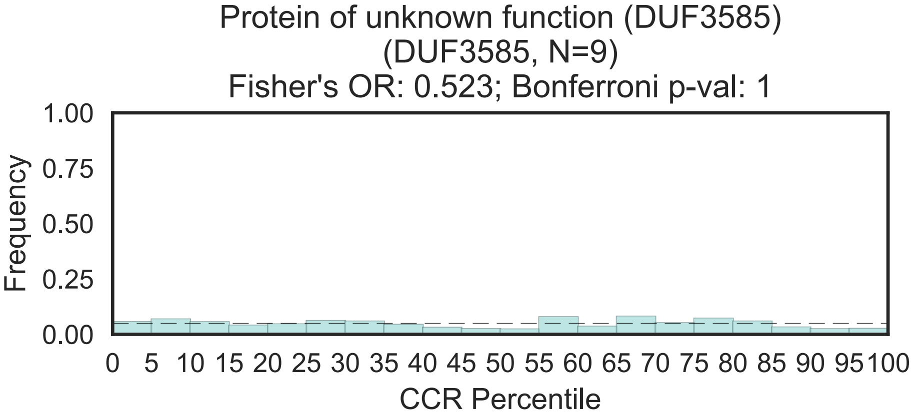


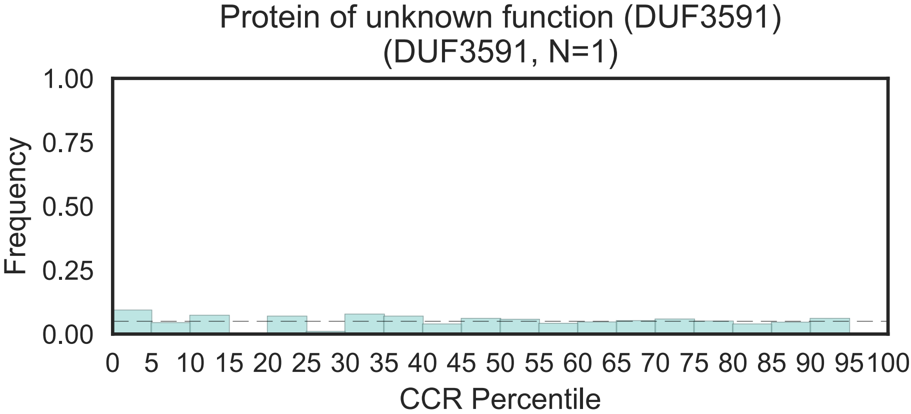
Domain of unknown function (DUF3544)
(DUF3544, N=1)

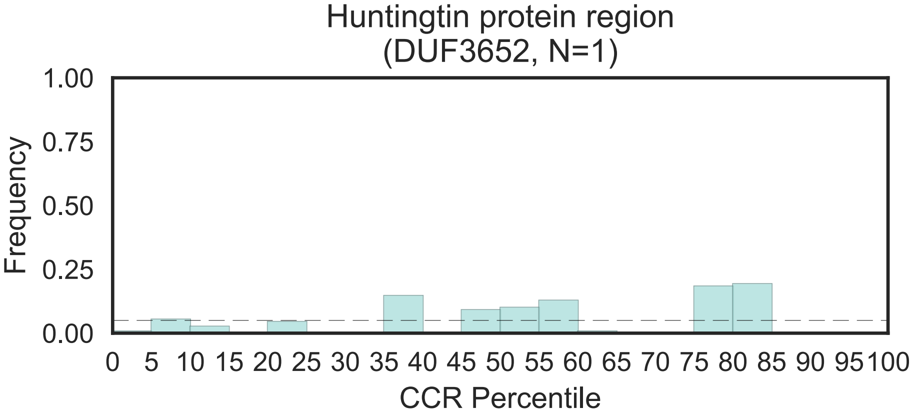

Domain of unknown function (DUF3546)
(DUF3546, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

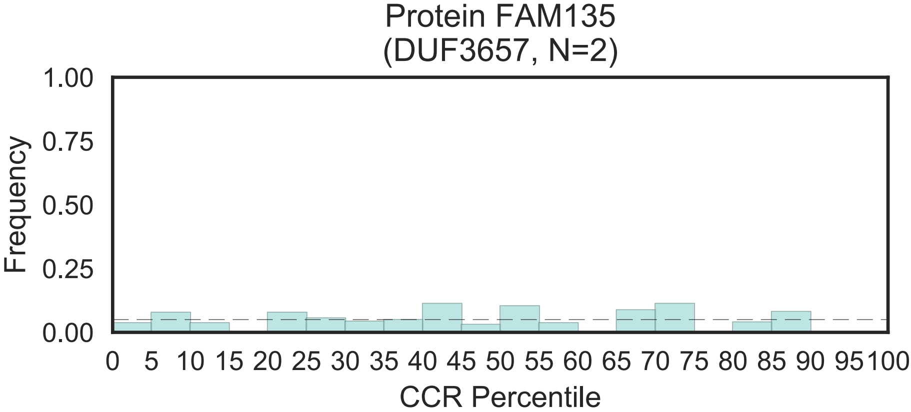

Domain of unknown function (DUF3548)
(DUF3548, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

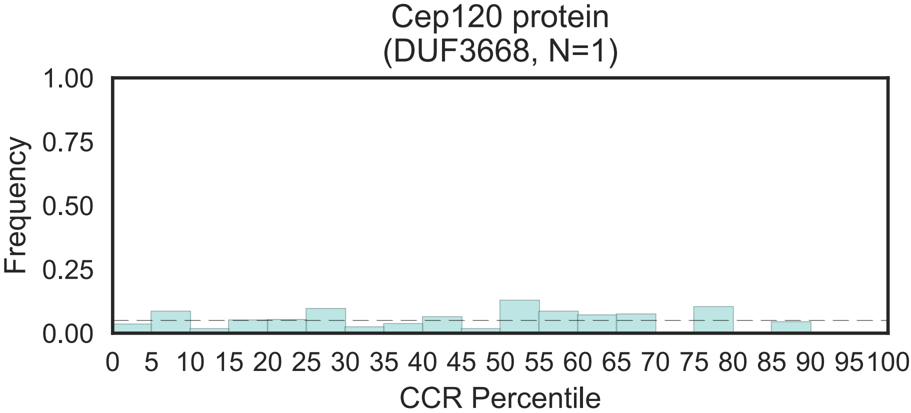
Protein of unknown function (DUF3583)
(DUF3583, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

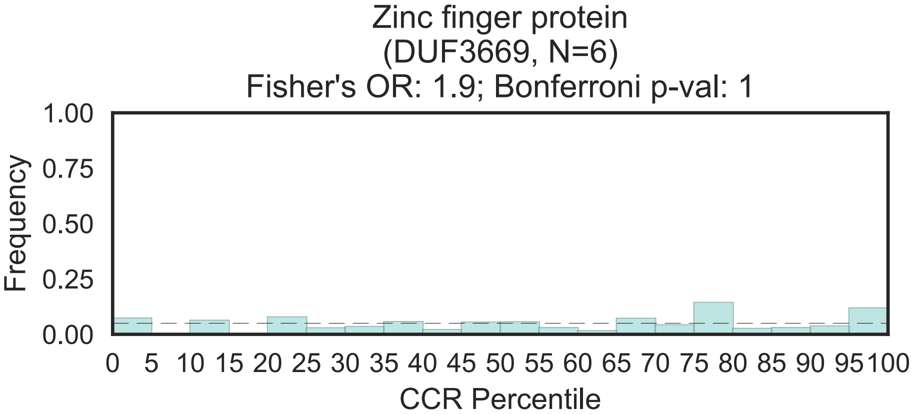

Protein of unknown function (DUF3585)
(DUF3585, N=9)
Fisher's OR: 0.523; Bonferroni p-val: 1

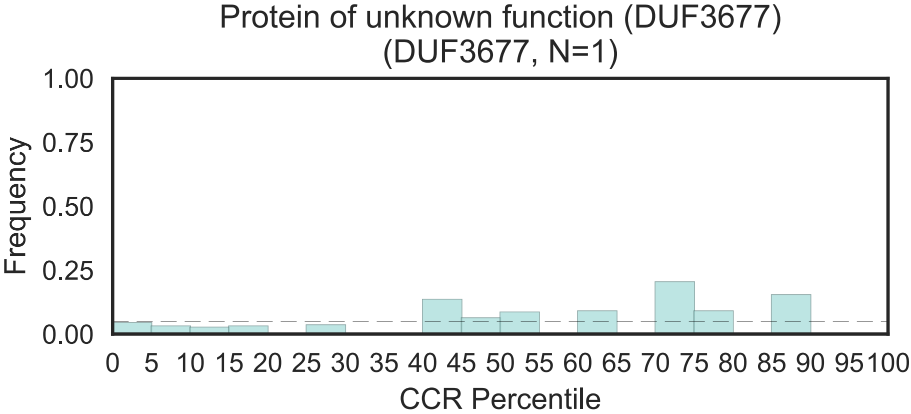

Protein of unknown function (DUF3591)
(DUF3591, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

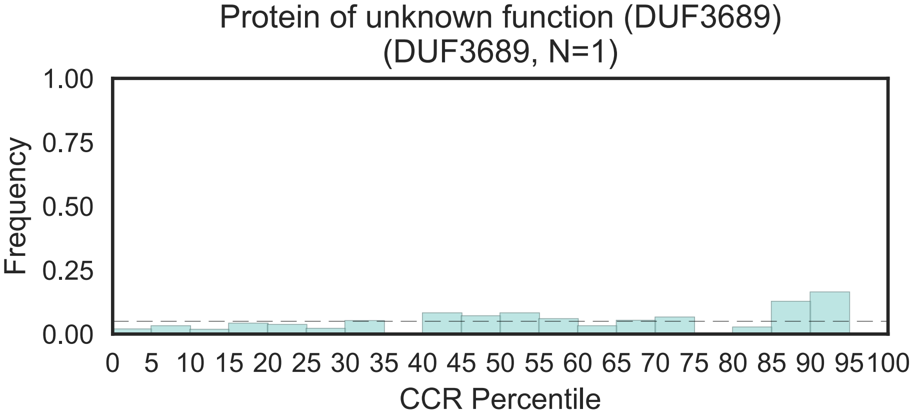

Huntingtin protein region
(DUF3652, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

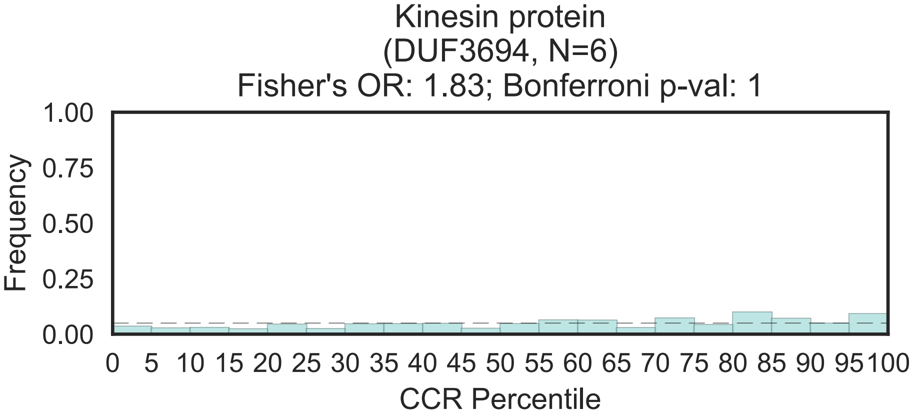

Protein FAM135
(DUF3657, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Cep120 protein
(DUF3668, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

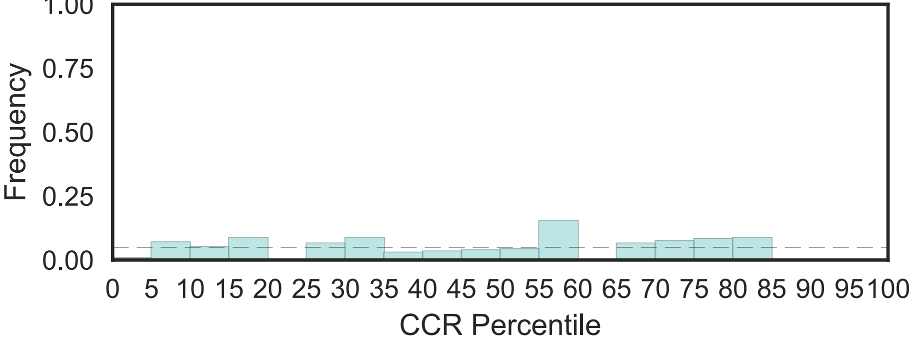

Zinc finger protein
(DUF3669, N=6)
Fisher's OR: 1.9; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

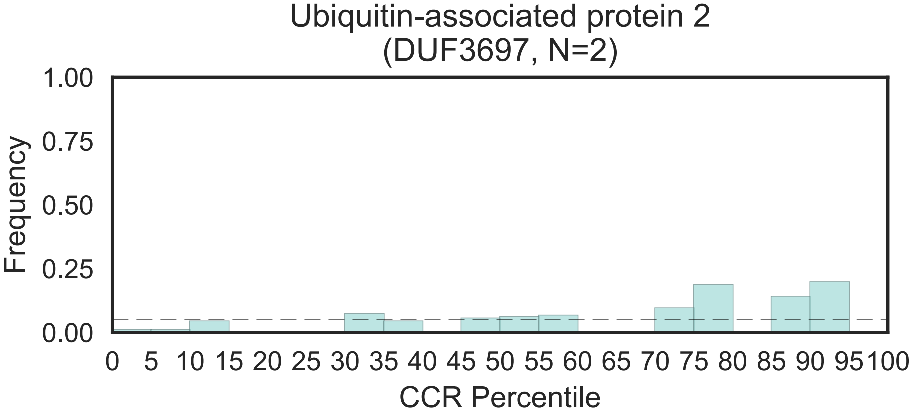

Protein of unknown function (DUF3677)
(DUF3677, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

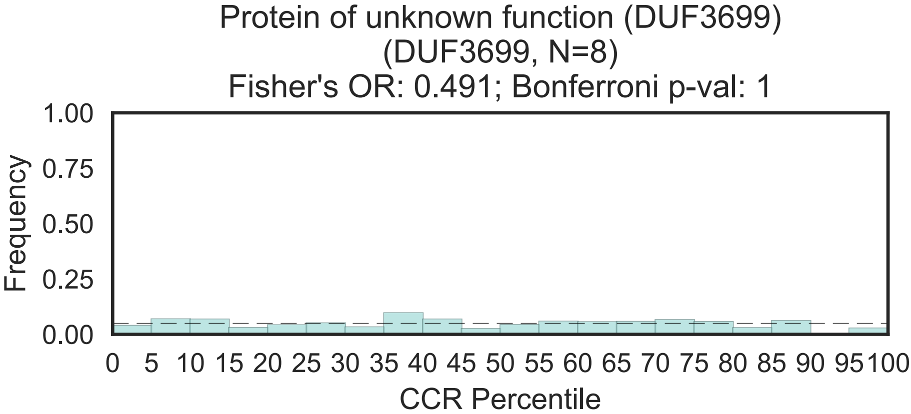

Protein of unknown function (DUF3689)
(DUF3689, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Kinesin protein
(DUF3694, N=6)
Fisher's OR: 1.83; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

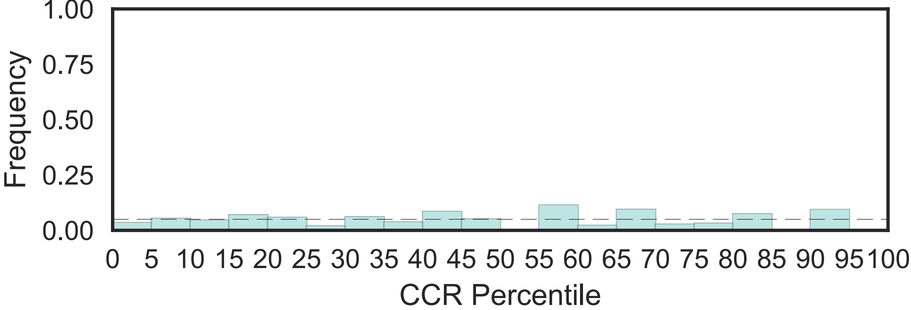
Protein of unknown function (DUF3695) (DUF3695, N=1)



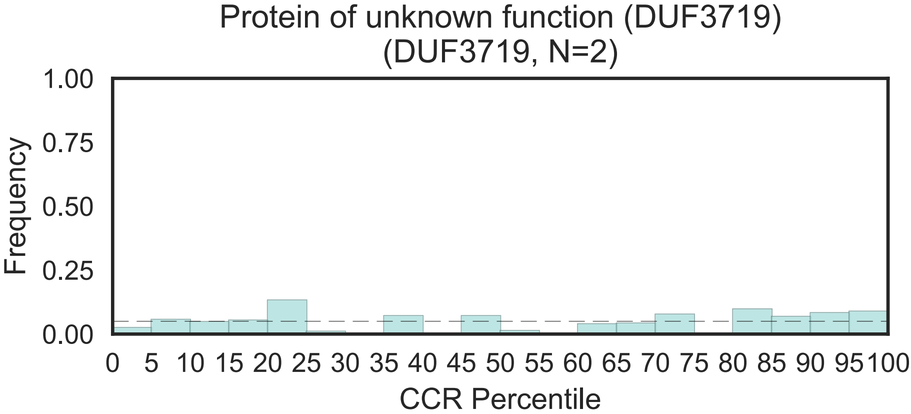

Ubiquitin-associated protein 2
(DUF3697, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

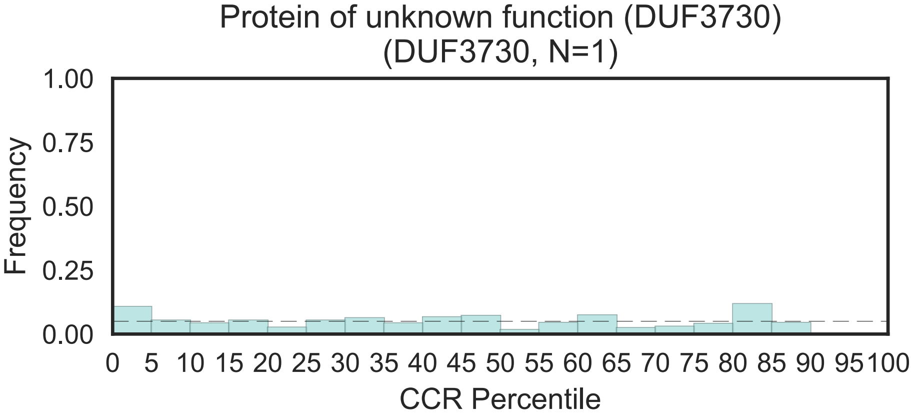


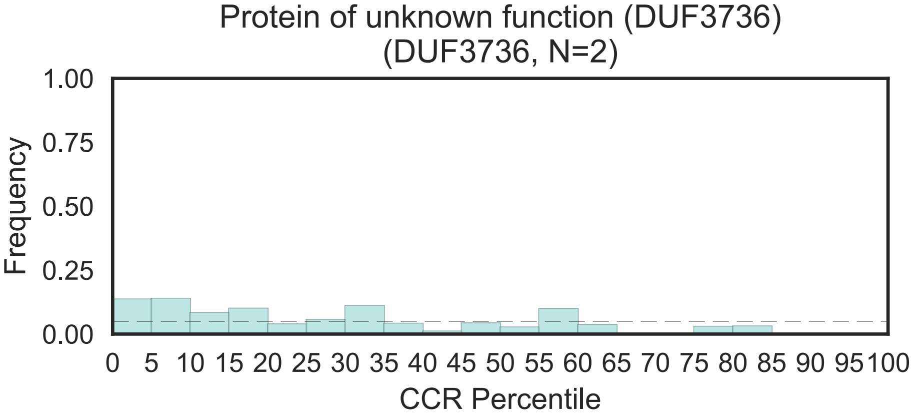
Protein of unknown function (DUF3699)
(DUF3699, N=8)
Fisher's OR: 0.491; Bonferroni p-val: 1

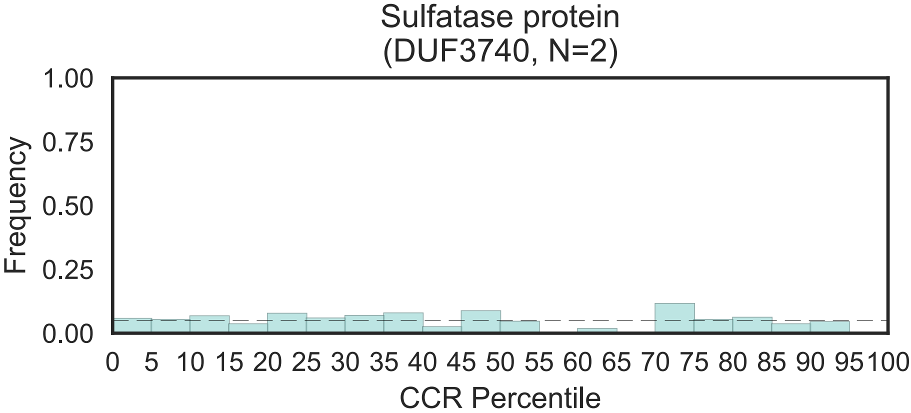


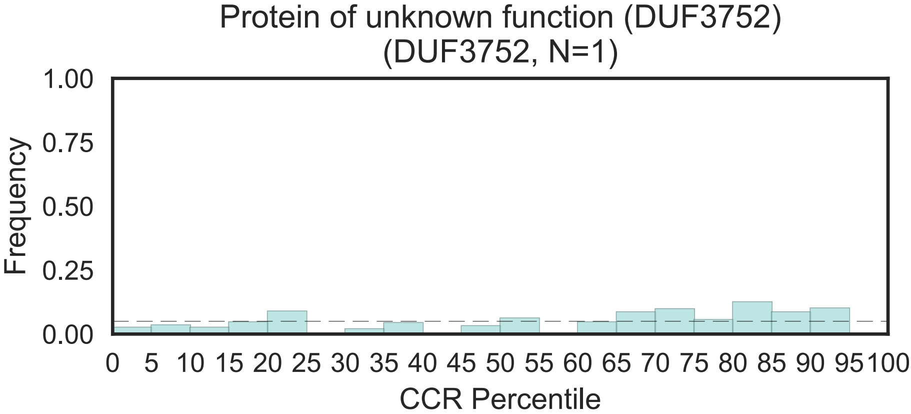
Protein of unknown function (DUF3715)
(DUF3715, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

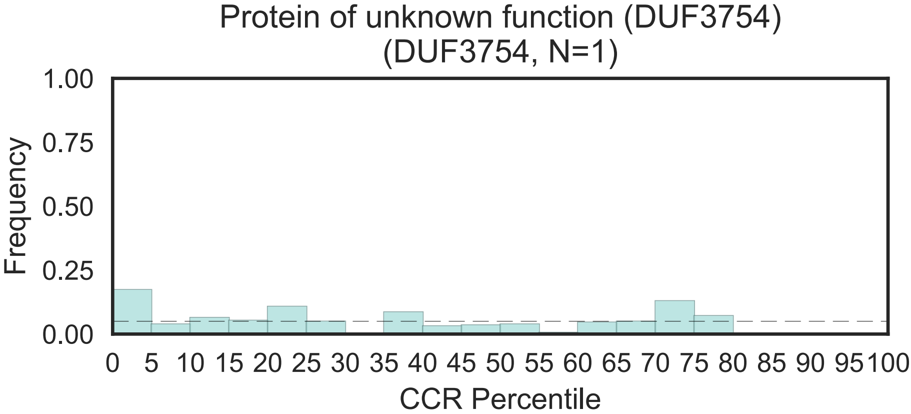

Protein of unknown function (DUF3719)
(DUF3719, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

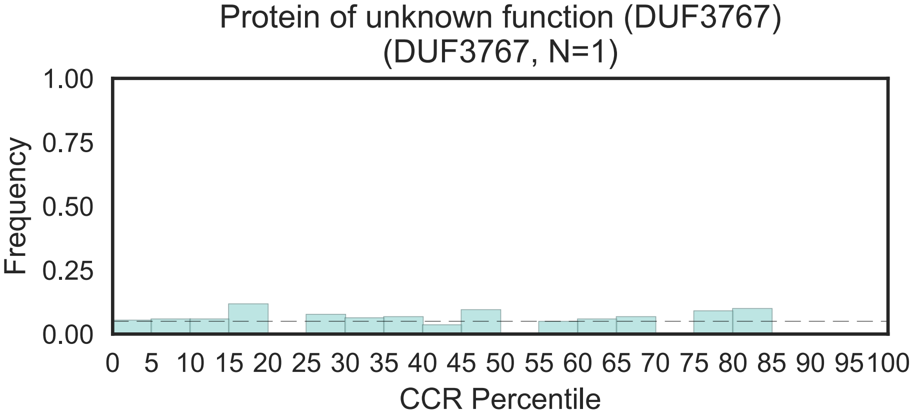

Protein of unknown function (DUF3730)
(DUF3730, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Protein of unknown function (DUF3736)
(DUF3736, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

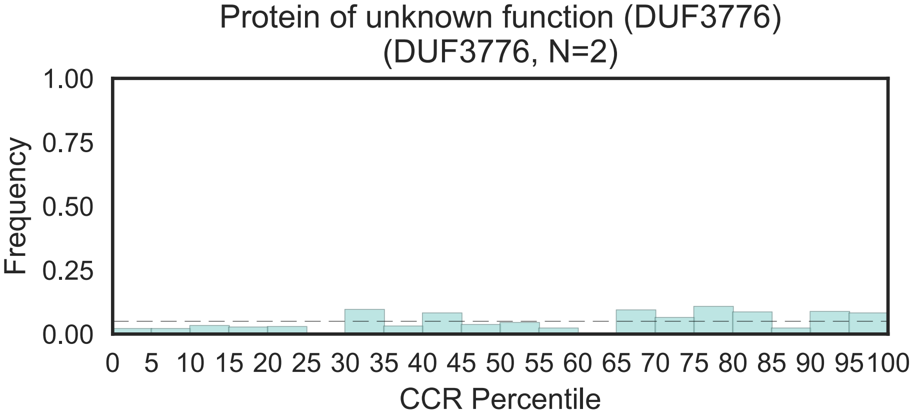

Sulfatase protein
(DUF3740, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

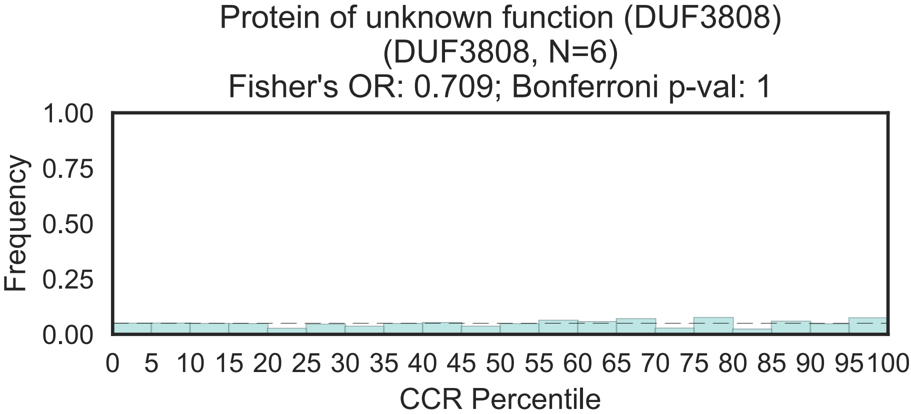

Protein of unknown function (DUF3752)
(DUF3752, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

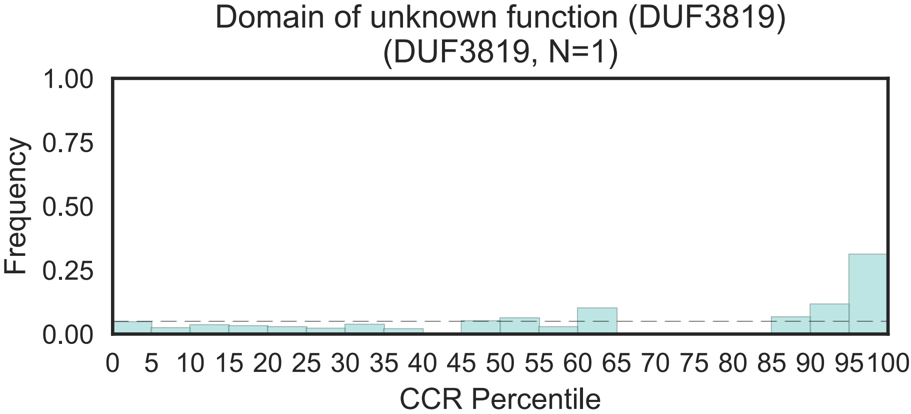

Protein of unknown function (DUF3754)
(DUF3754, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

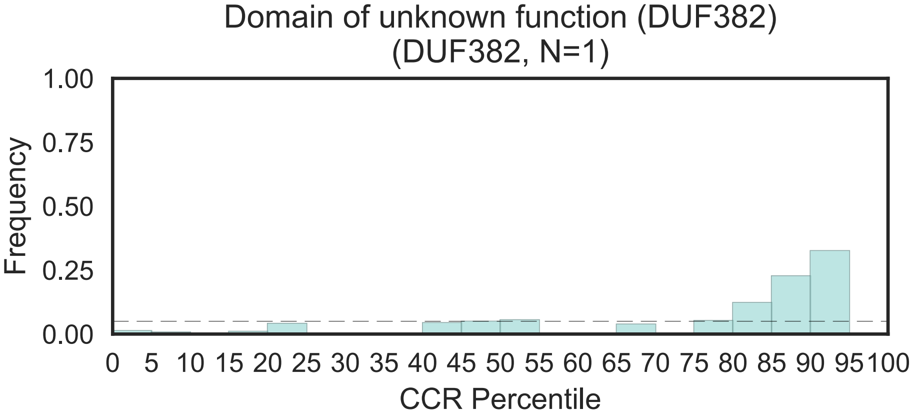


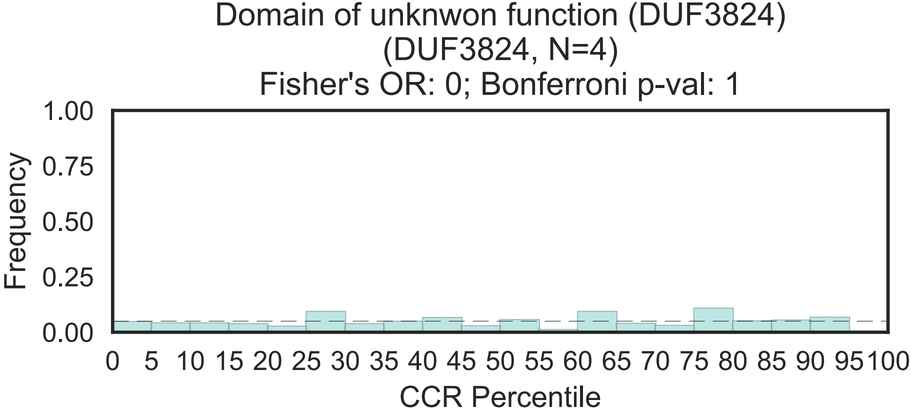
Protein of unknown function (DUF3767)
(DUF3767, N=1)

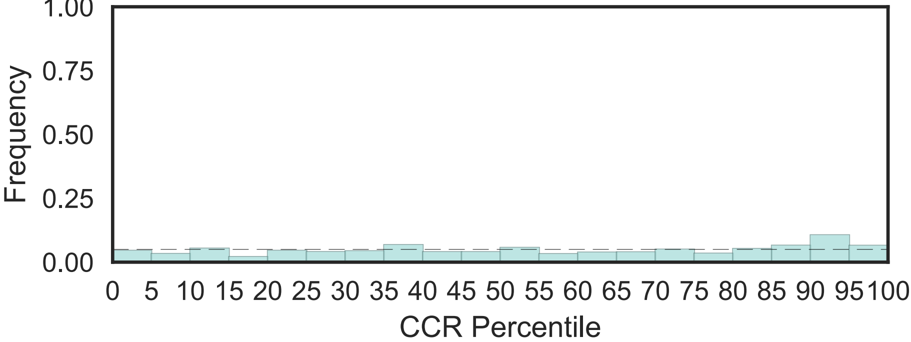

Protein of unknown function (DUF3776)
(DUF3776, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Protein of unknown function (DUF3808)
(DUF3808, N=6)
Fisher's OR: 0.709; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

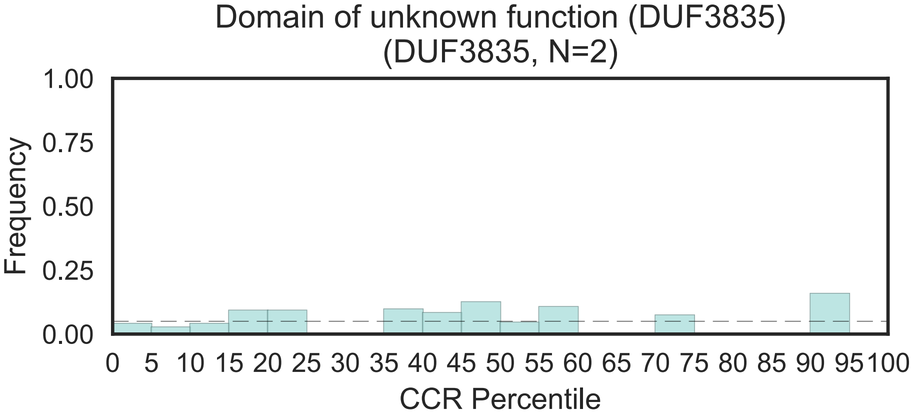

Domain of unknown function (DUF3819)
(DUF3819, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

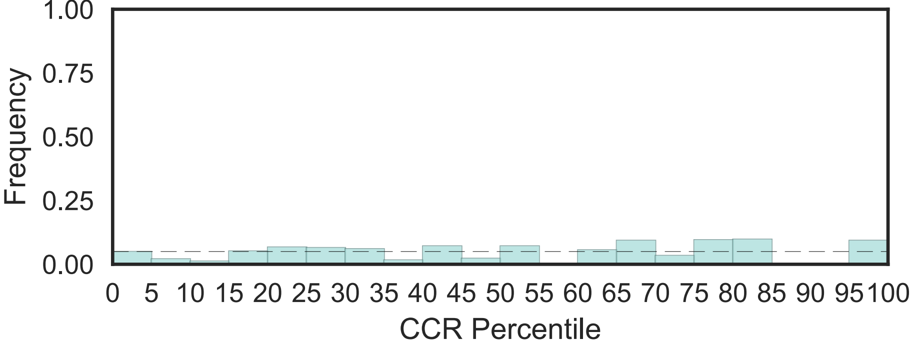

Domain of unknown function (DUF382)
(DUF382, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

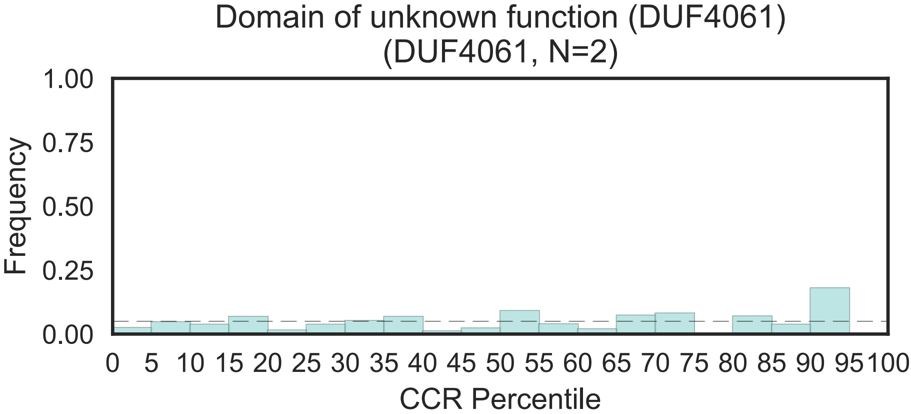

Domain of unknwon function (DUF3824)
(DUF3824, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

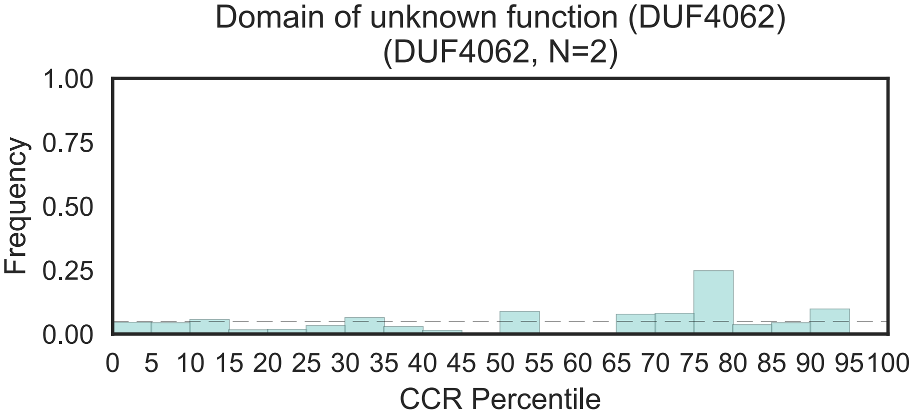


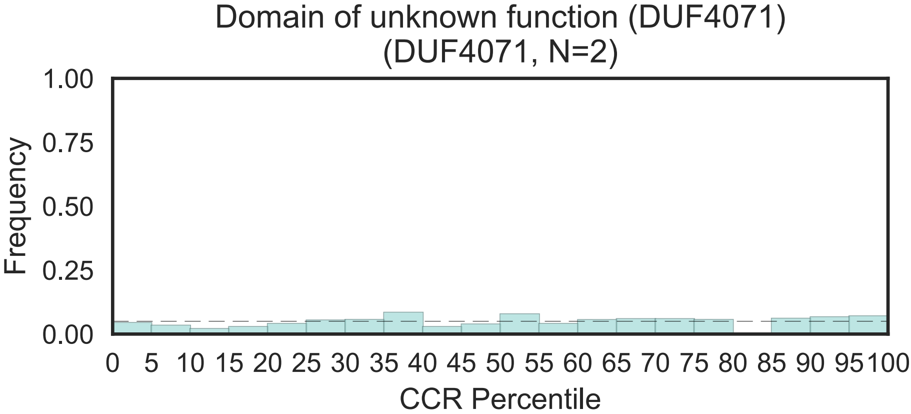
Domain of unknown function (DUF3827)
(DUF3827, N=2)

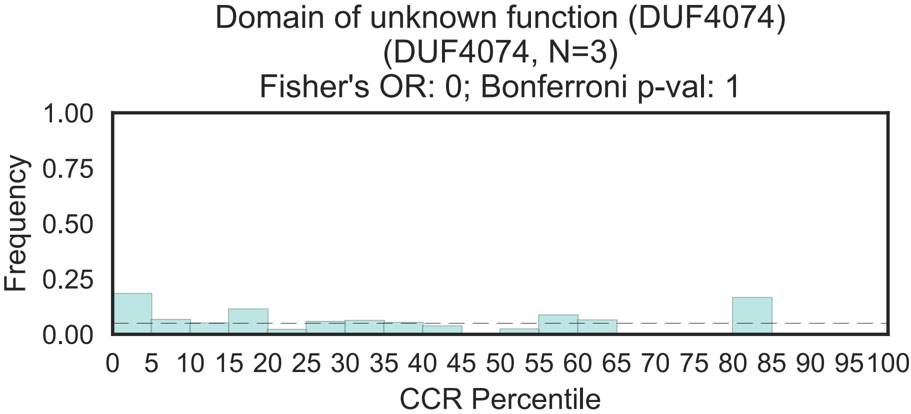

Domain of unknown function (DUF3835)
(DUF3835, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

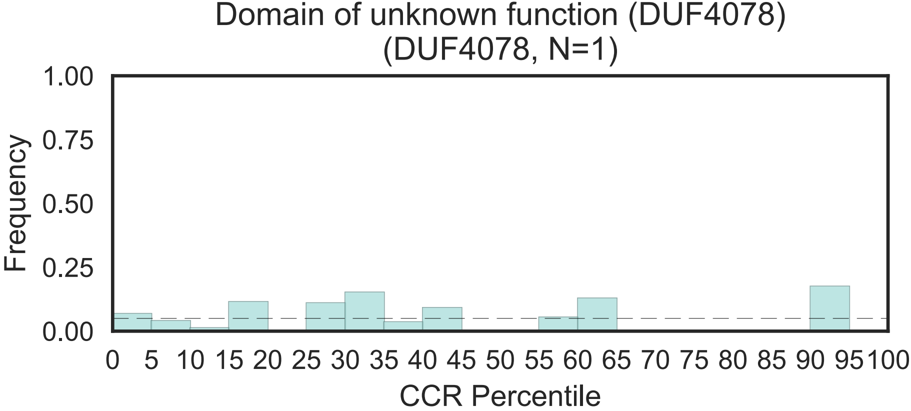

Domain of unknown function (DUF4042)
(DUF4042, N=1)

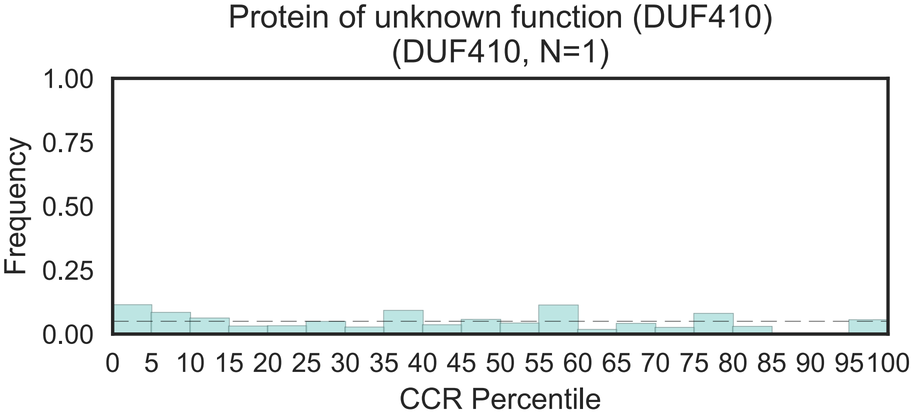

Domain of unknown function (DUF4061)
(DUF4061, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

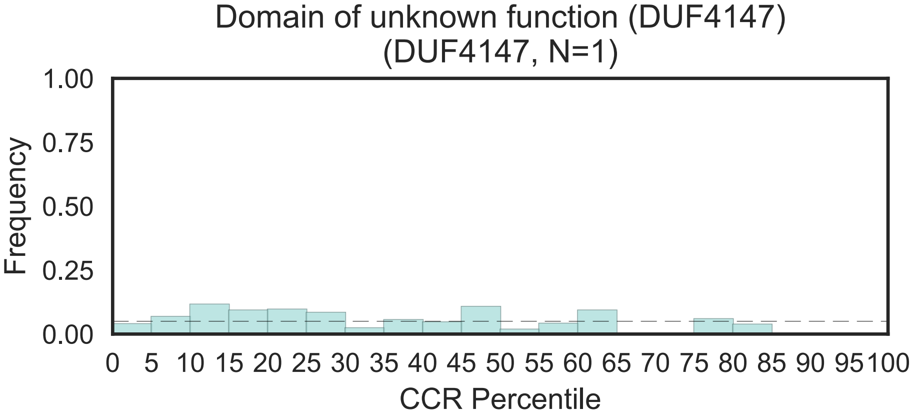

Domain of unknown function (DUF4062)
(DUF4062, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

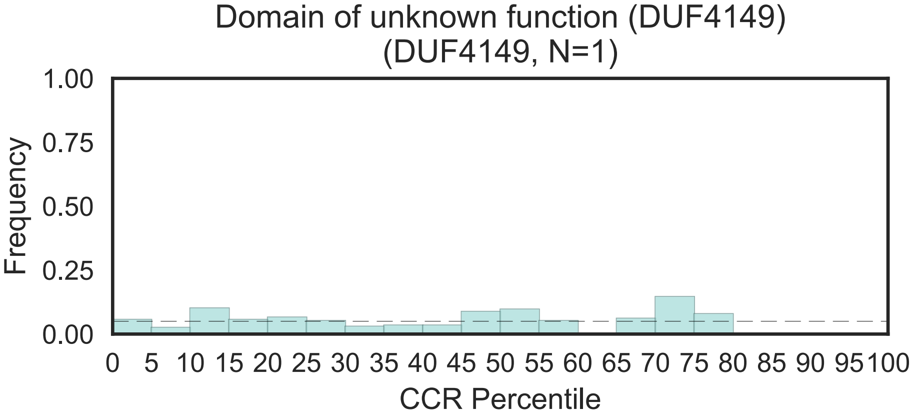

Domain of unknown function (DUF4071)
(DUF4071, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

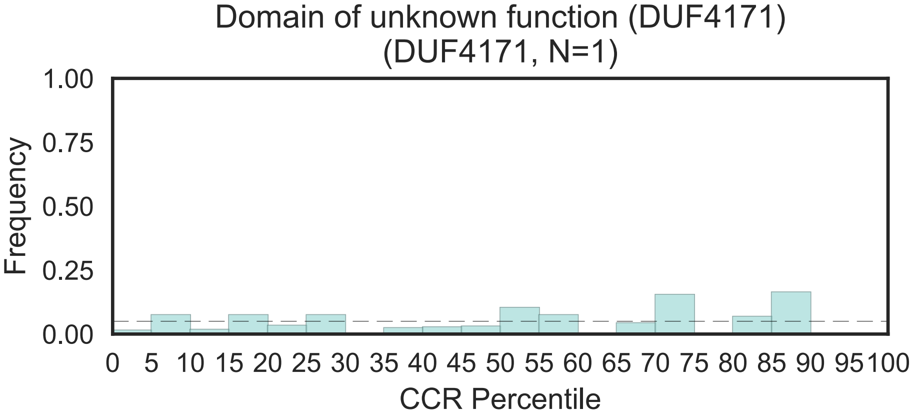

Domain of unknown function (DUF4074)
(DUF4074, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

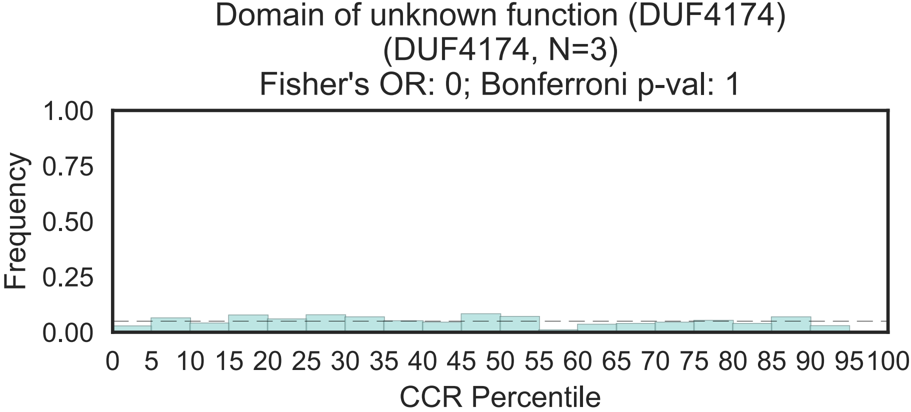

Domain of unknown function (DUF4078)
(DUF4078, N=1)

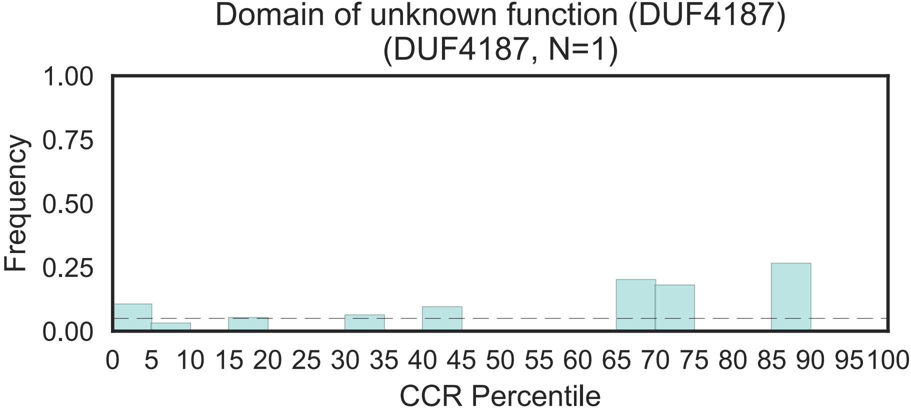

Protein of unknown function (DUF410)
(DUF410, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

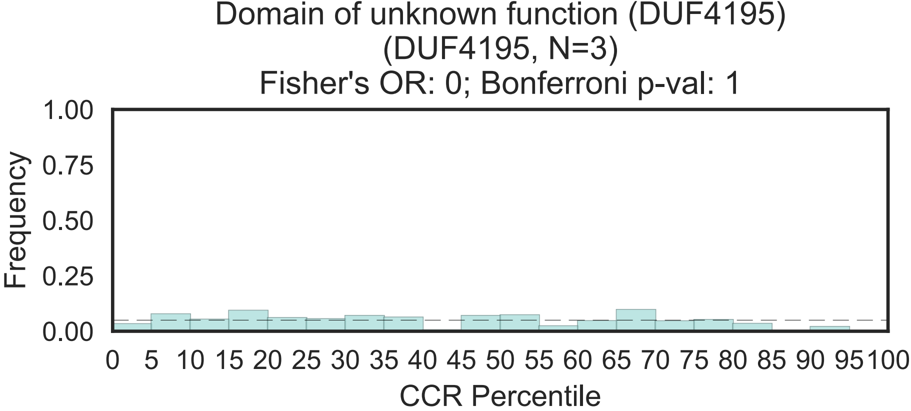

Domain of unknown function (DUF4147)
(DUF4147, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

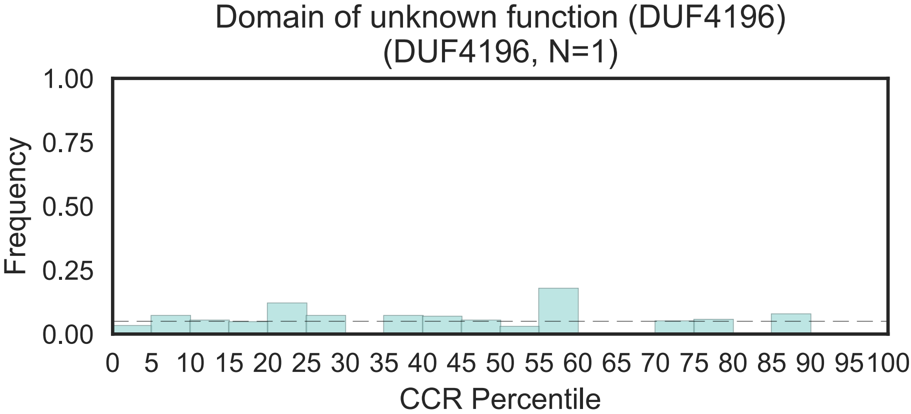

Domain of unknown function (DUF4149)
(DUF4149, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

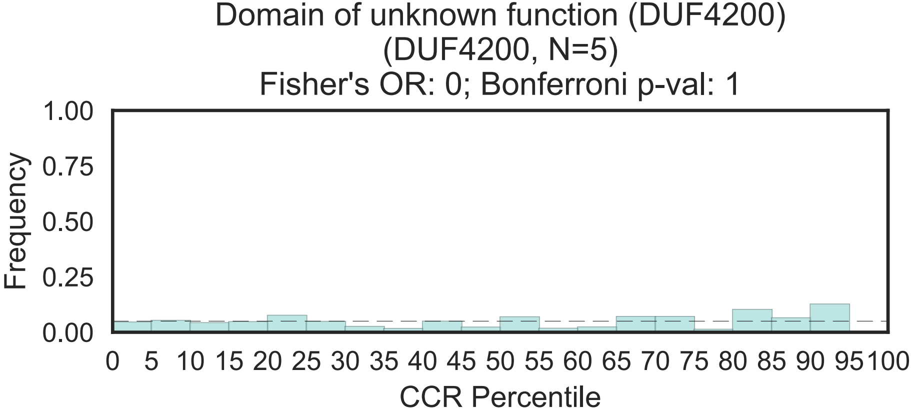

Domain of unknown function (DUF4171)
(DUF4171, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

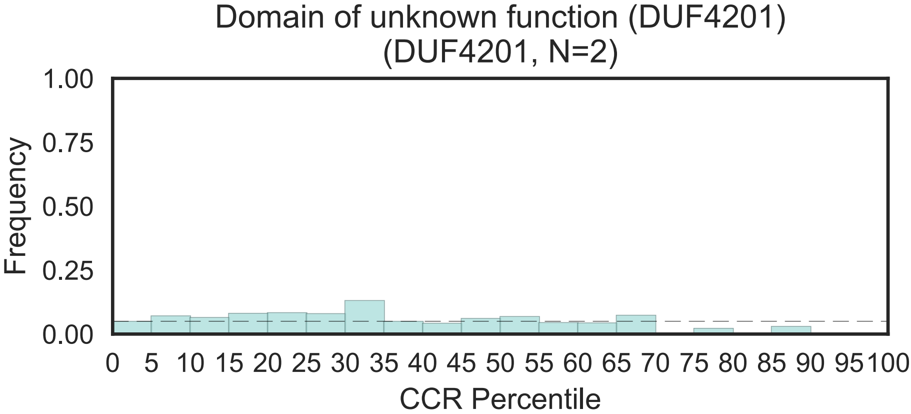

Domain of unknown function (DUF4174)
(DUF4174, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

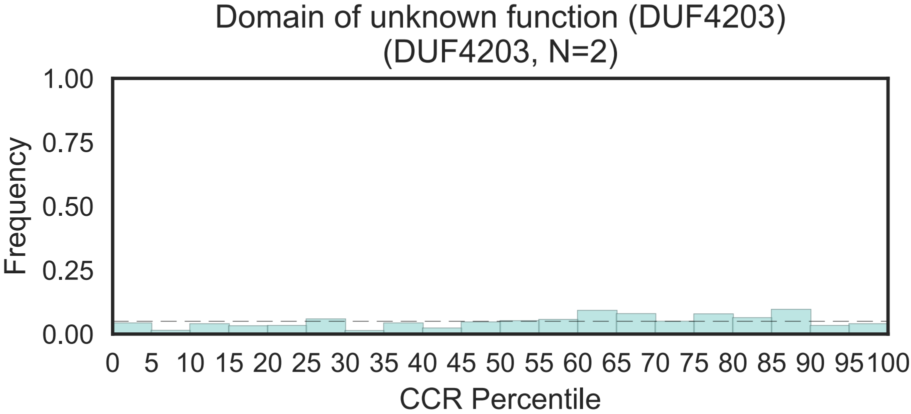

Domain of unknown function (DUF4187)
(DUF4187, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

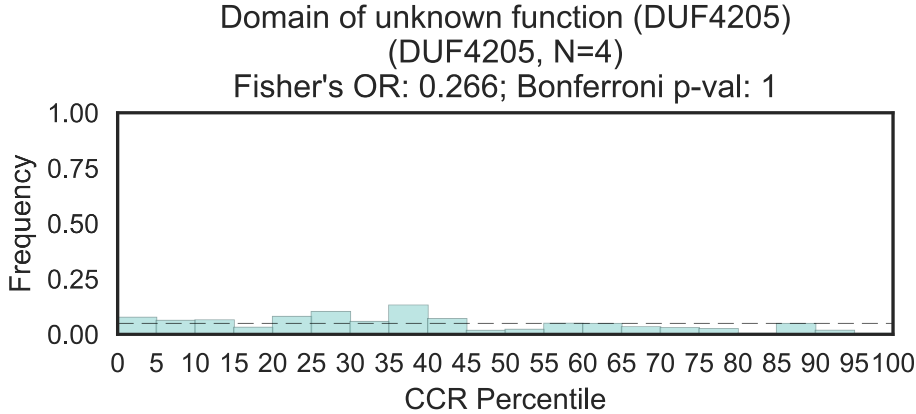

Domain of unknown function (DUF4195)
(DUF4195, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

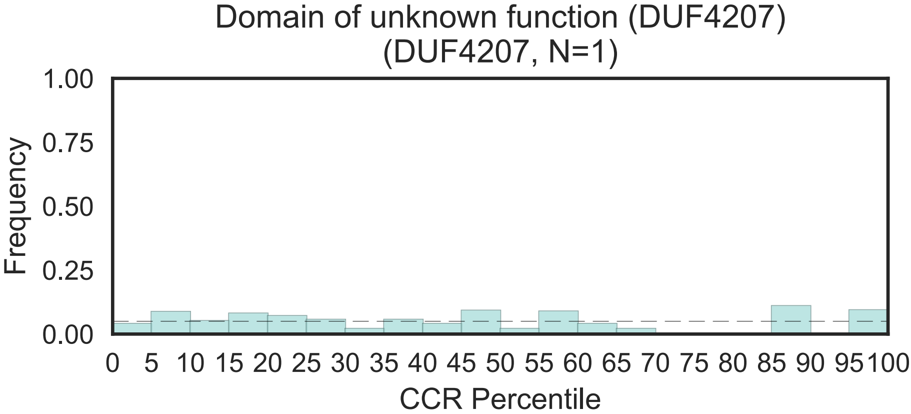

Domain of unknown function (DUF4196)
(DUF4196, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

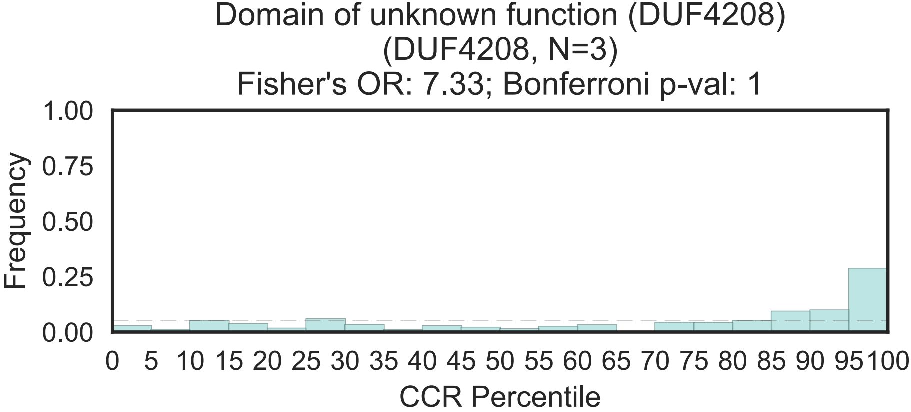

Domain of unknown function (DUF4200)
(DUF4200, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

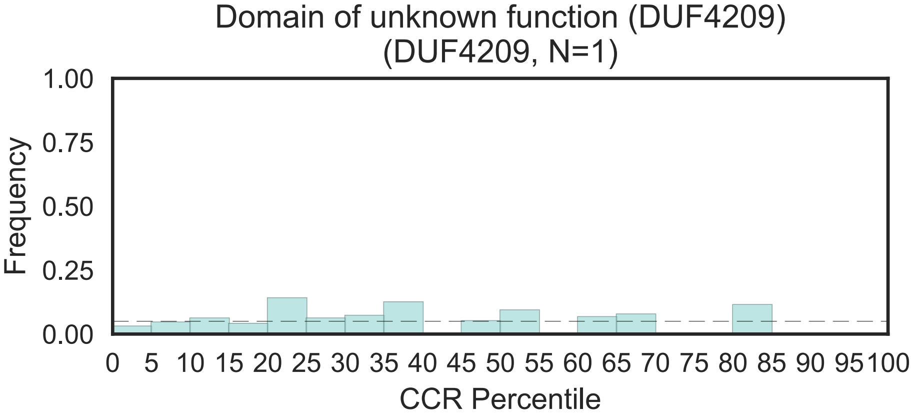

Domain of unknown function (DUF4201)
(DUF4201, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

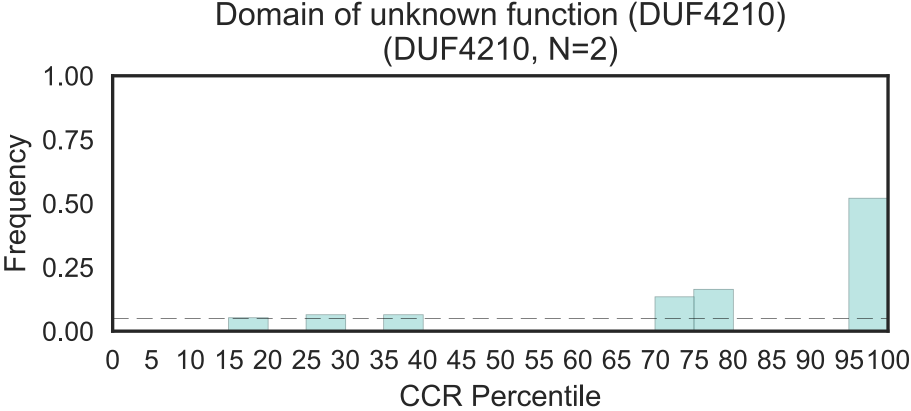

Domain of unknown function (DUF4203)
(DUF4203, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

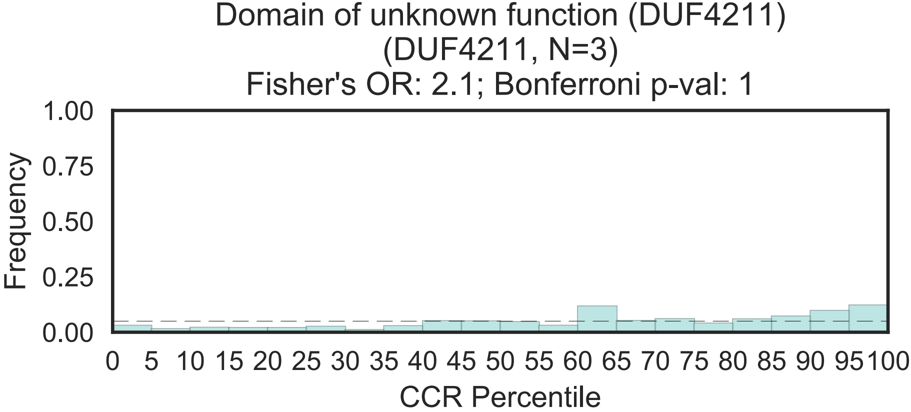

Domain of unknown function (DUF4205)
(DUF4205, N=4)
Fisher's OR: 0.266; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

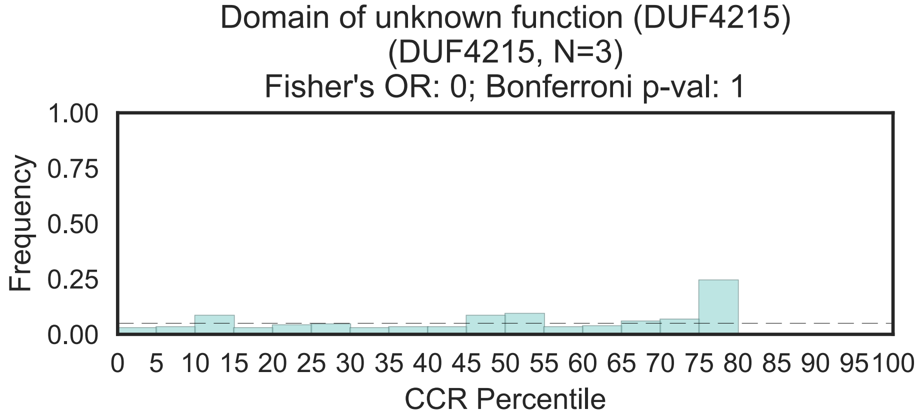

Domain of unknown function (DUF4207)
(DUF4207, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

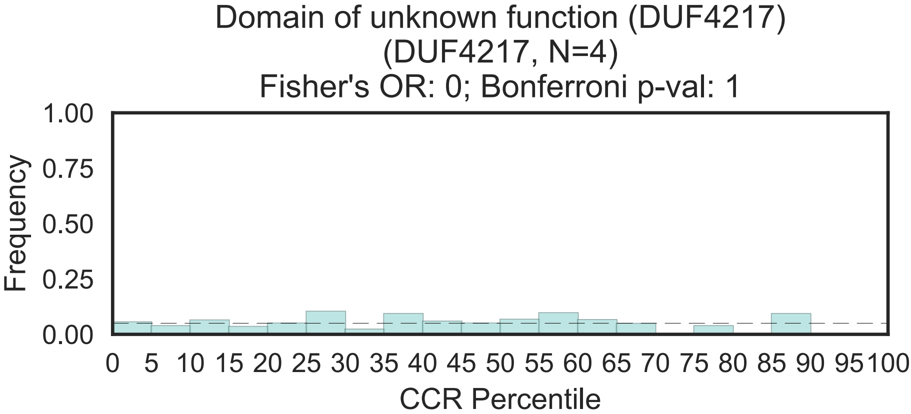

Domain of unknown function (DUF4208)
(DUF4208, N=3)
Fisher's OR: 7.33; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

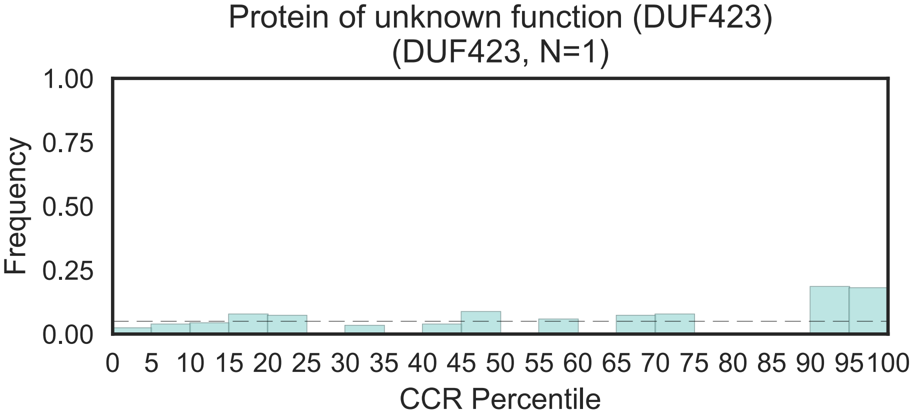
Domain of unknown function (DUF4209)
(DUF4209, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

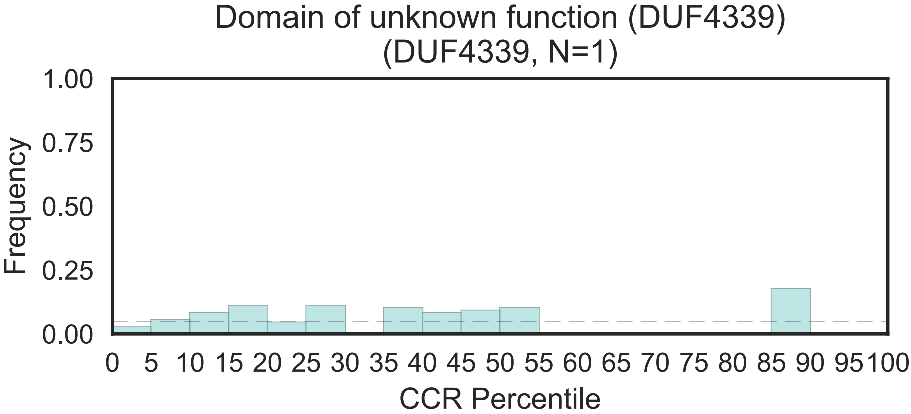

Domain of unknown function (DUF4210)
(DUF4210, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

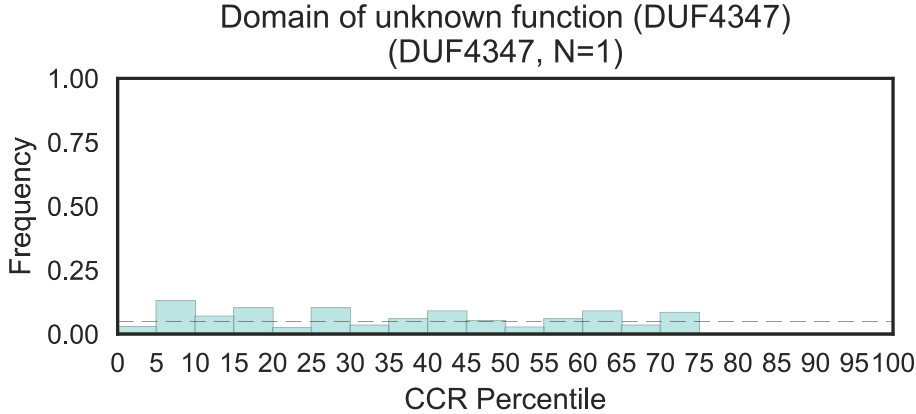

Domain of unknown function (DUF4211)
(DUF4211, N=3)
Fisher's OR: 2.1; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

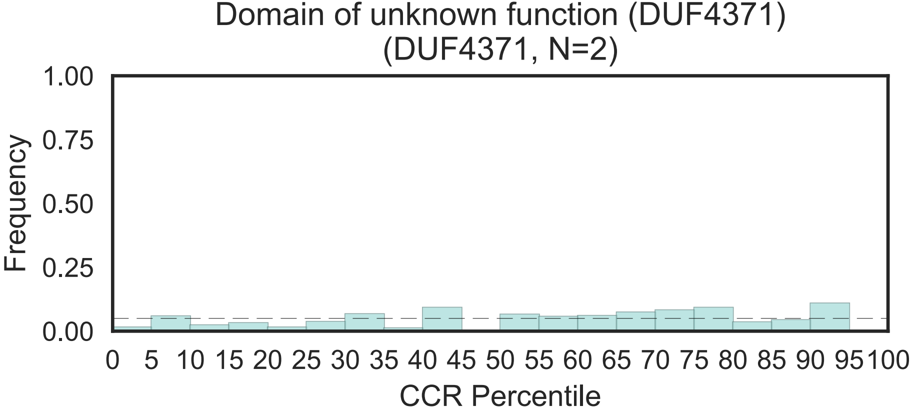

Domain of unknown function (DUF4215)
(DUF4215, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

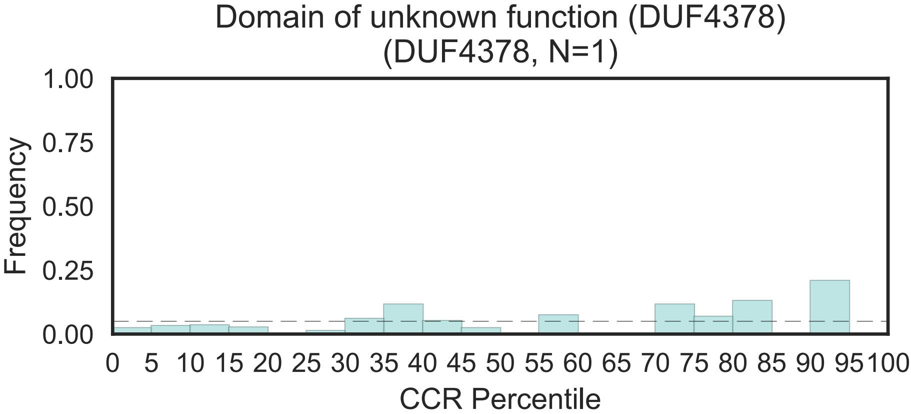

Domain of unknown function (DUF4217)
(DUF4217, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

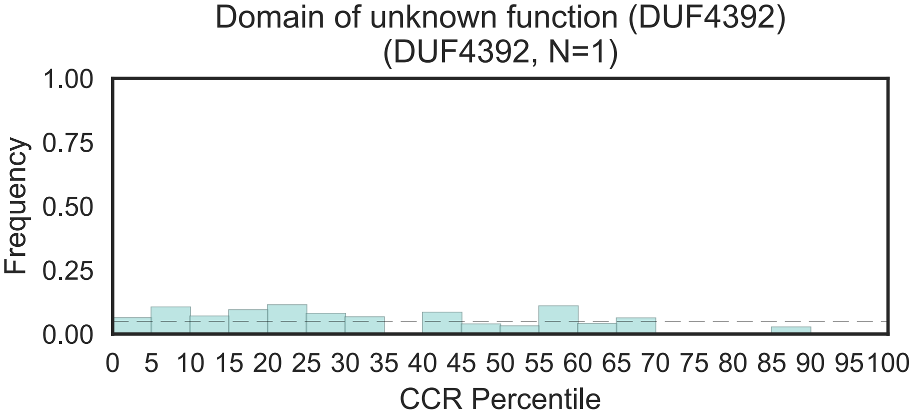

Protein of unknown function (DUF423)
(DUF423, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

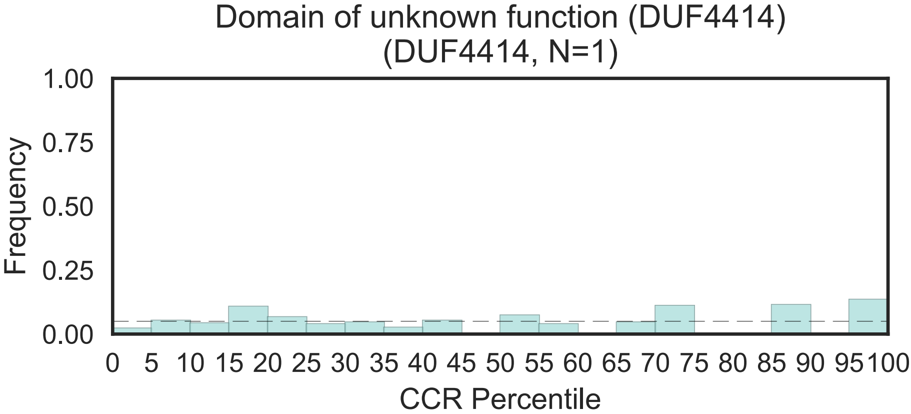

Domain of unknown function (DUF4339)
(DUF4339, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

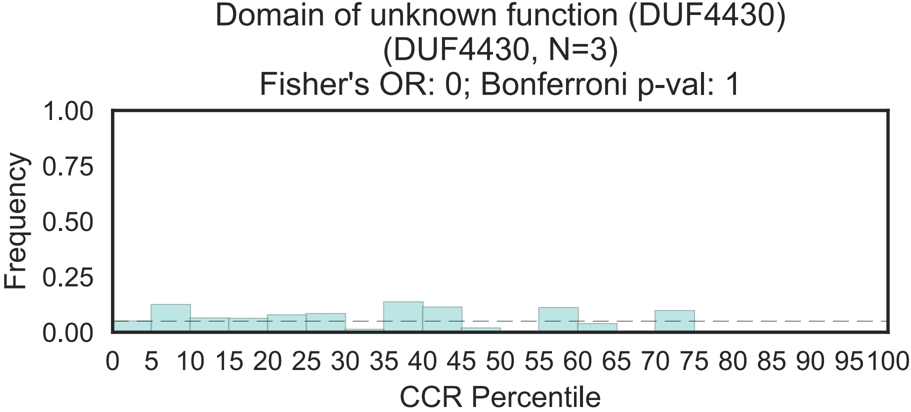

Domain of unknown function (DUF4347)
(DUF4347, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

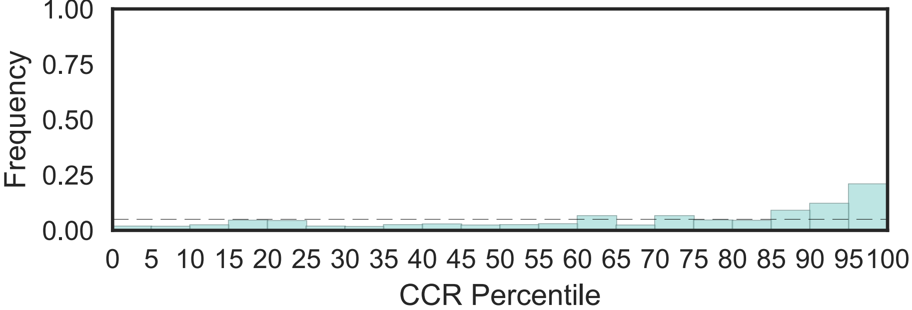

Domain of unknown function (DUF4371)
(DUF4371, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4378)
(DUF4378, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

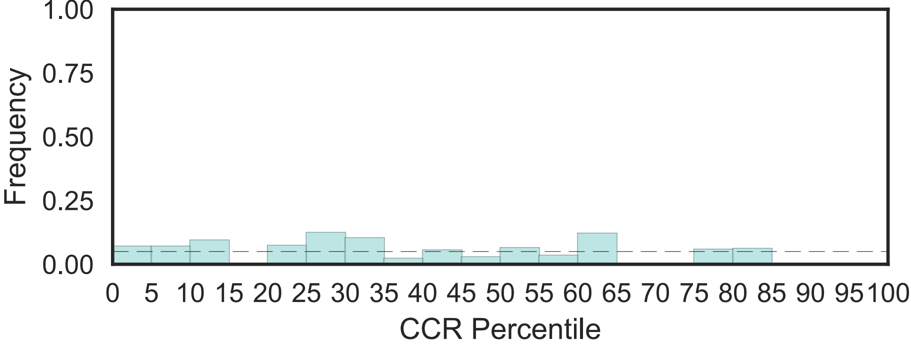

Domain of unknown function (DUF4392)
(DUF4392, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4414)
(DUF4414, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

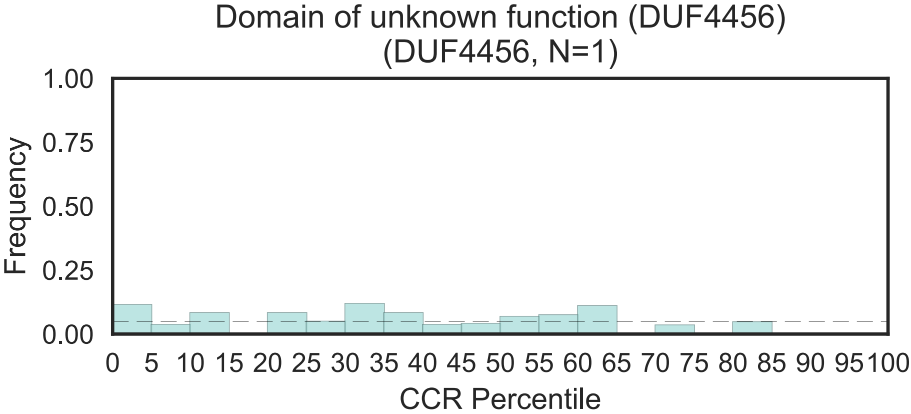

Domain of unknown function (DUF4430)
(DUF4430, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

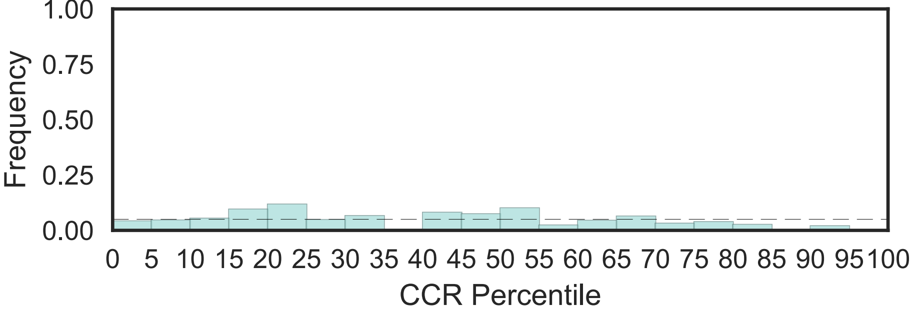


Domain of unknown function (DUF4440)
(DUF4440, N=4)
Fisher's OR: 3.73; Bonferroni p-val: 1

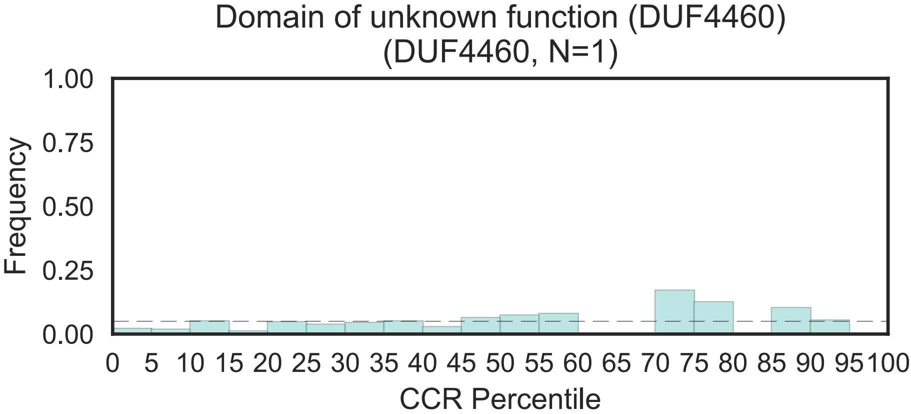


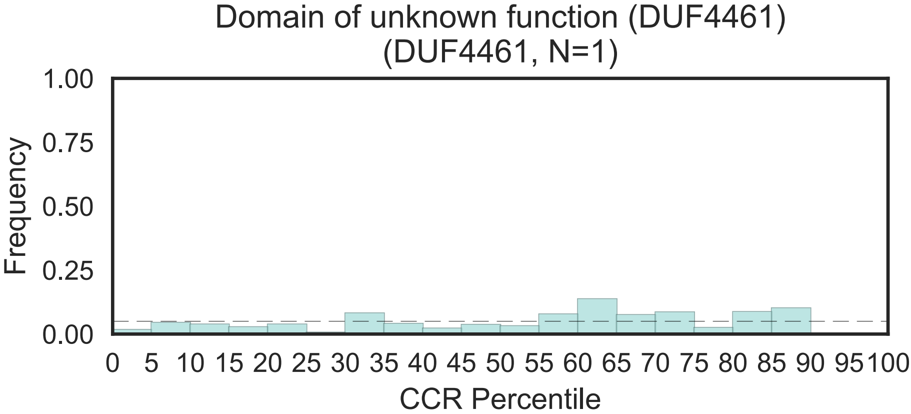
Domain of unknown function (DUF4455)
(DUF4455, N=1)

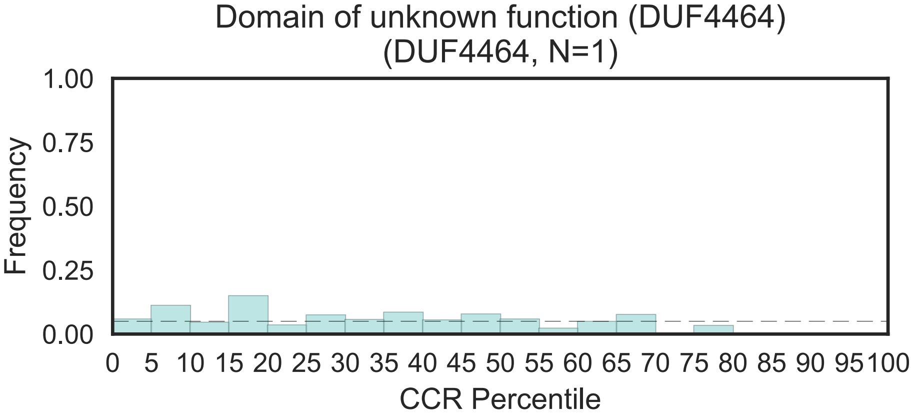

Domain of unknown function (DUF4456)
(DUF4456, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

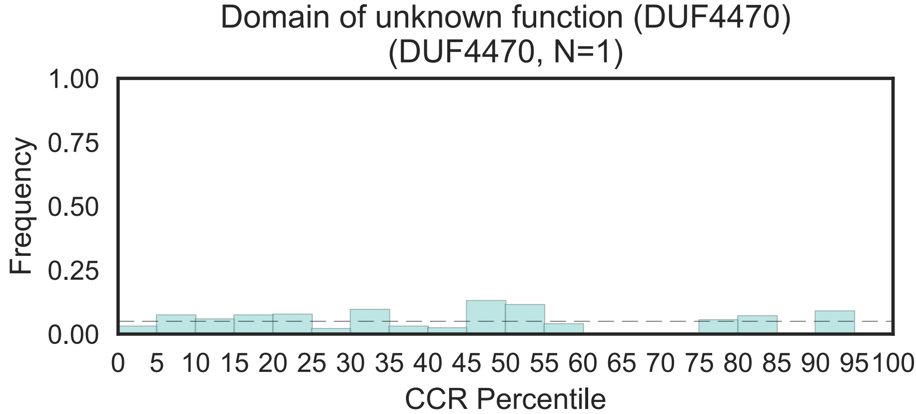


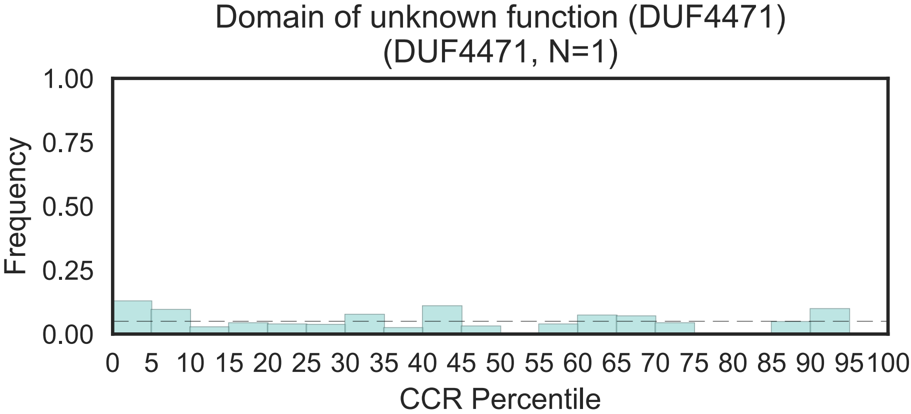
Domain of unknown function (DUF4457)
(DUF4457, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

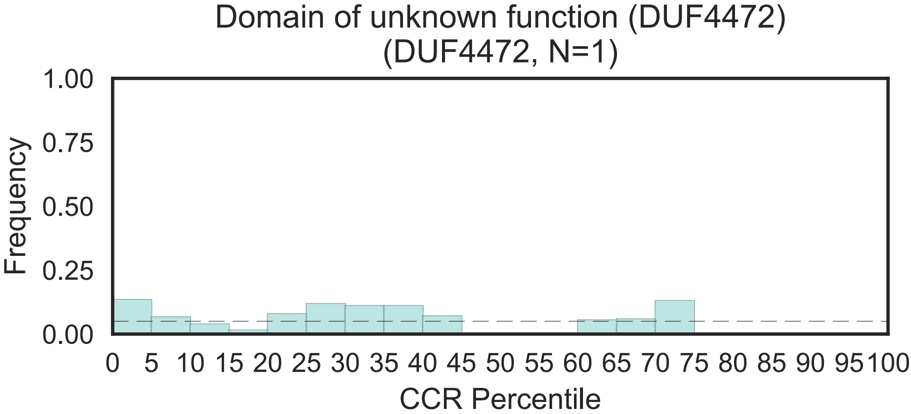

Domain of unknown function (DUF4460)
(DUF4460, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

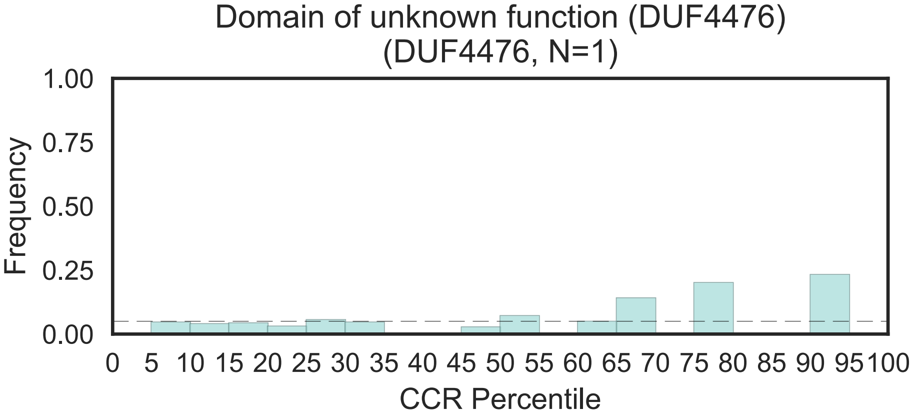

Domain of unknown function (DUF4461)
(DUF4461, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

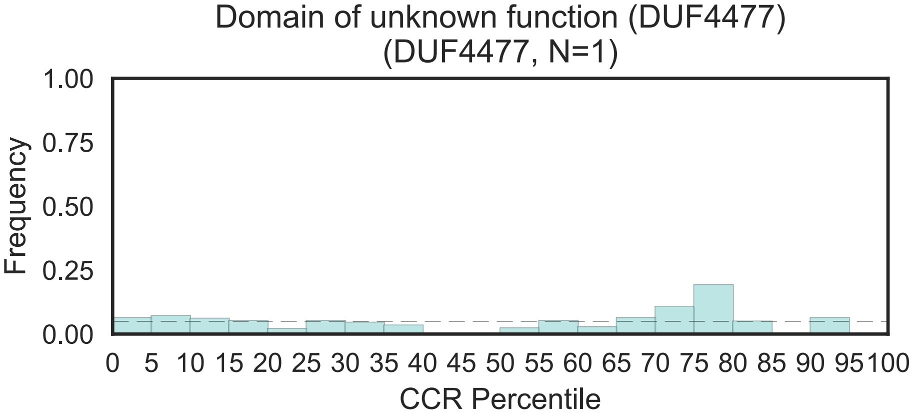

Domain of unknown function (DUF4464)
(DUF4464, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

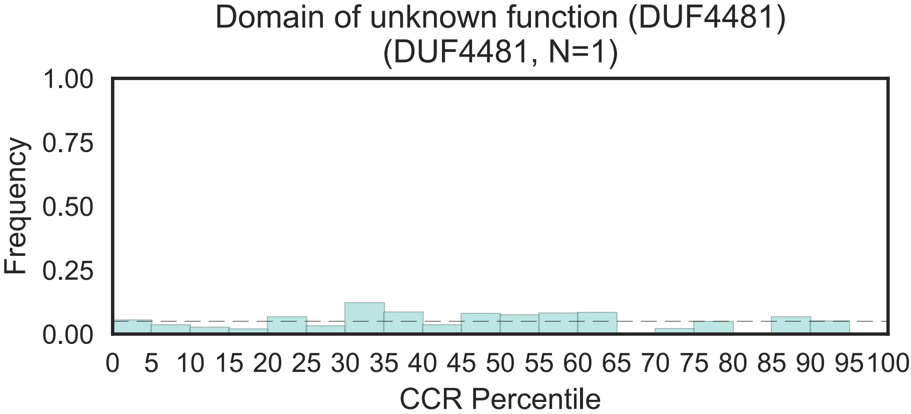

Domain of unknown function (DUF4470)
(DUF4470, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

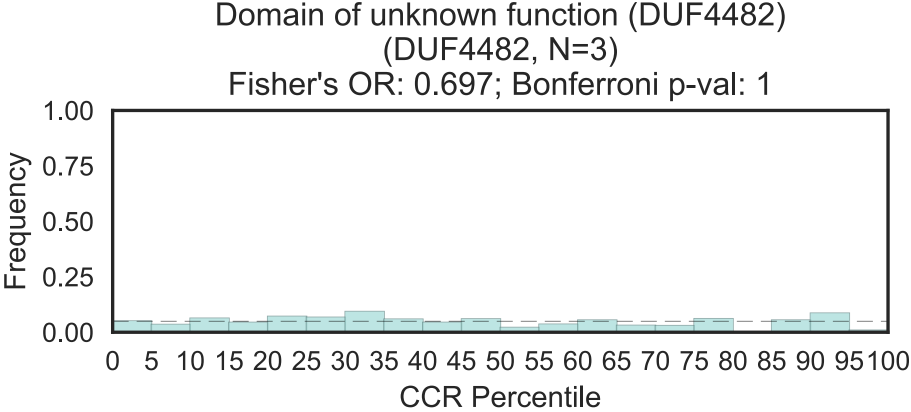

Domain of unknown function (DUF4471)
(DUF4471, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

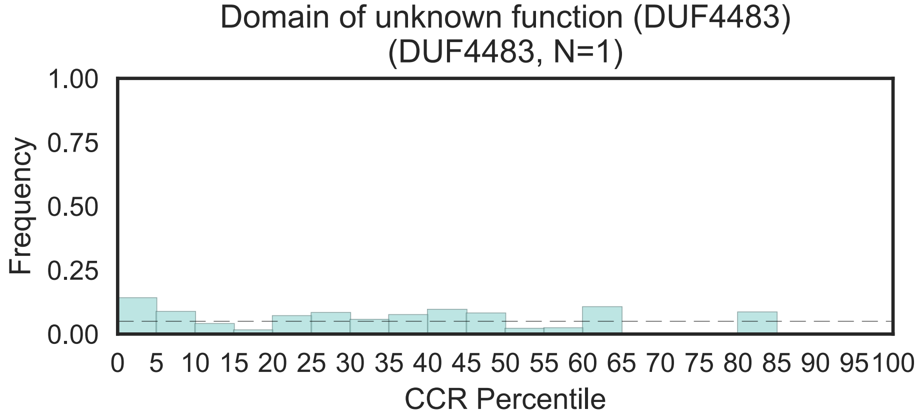

Domain of unknown function (DUF4472)
(DUF4472, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

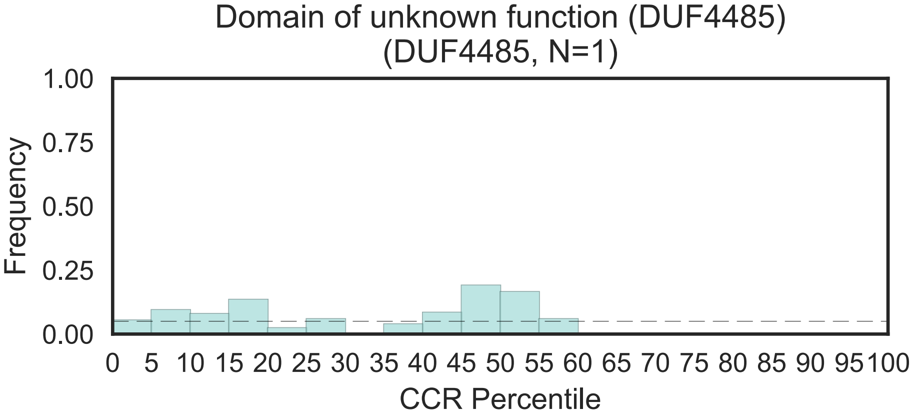

Domain of unknown function (DUF4476)
(DUF4476, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

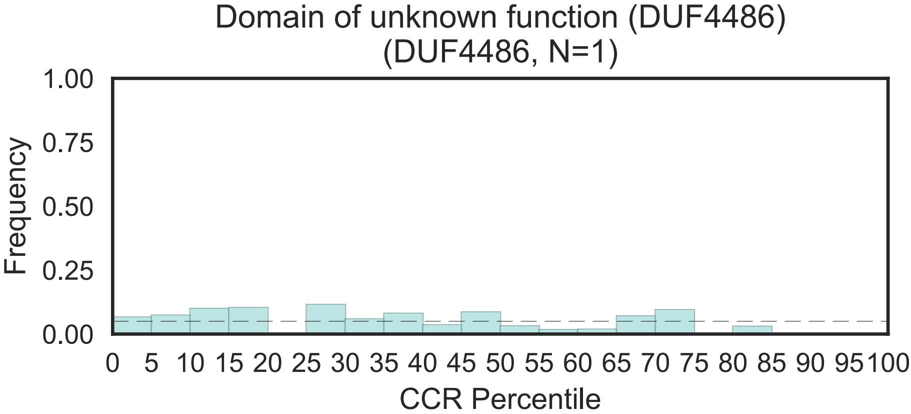

Domain of unknown function (DUF4477)
(DUF4477, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

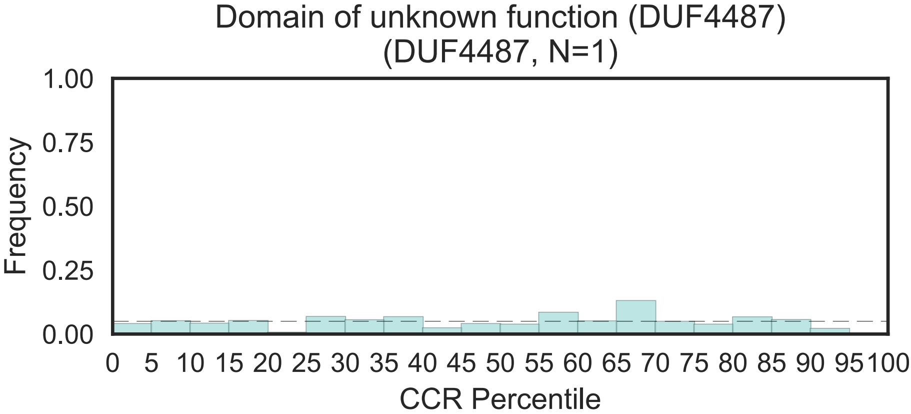

Domain of unknown function (DUF4481)
(DUF4481, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4482)
(DUF4482, N=3)
Fisher's OR: 0.697; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4483)
(DUF4483, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4485)
(DUF4485, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4486)
(DUF4486, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4487)
(DUF4487, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
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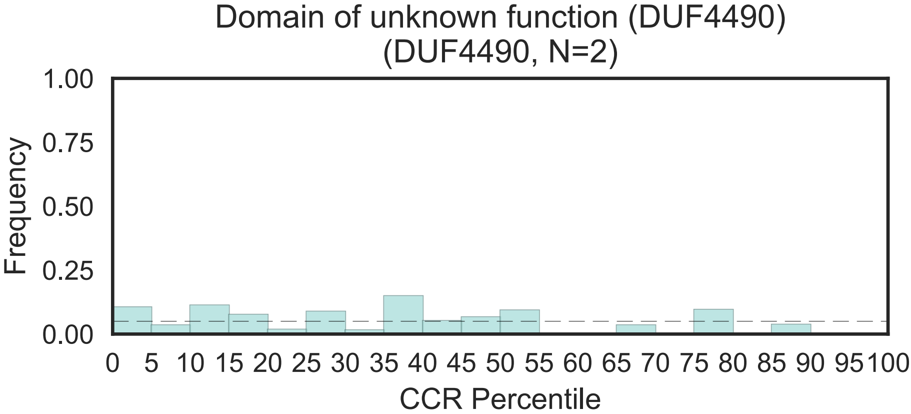
90
95
100
CCR Percentile


Domain of unknown function (DUF4490)
(DUF4490, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
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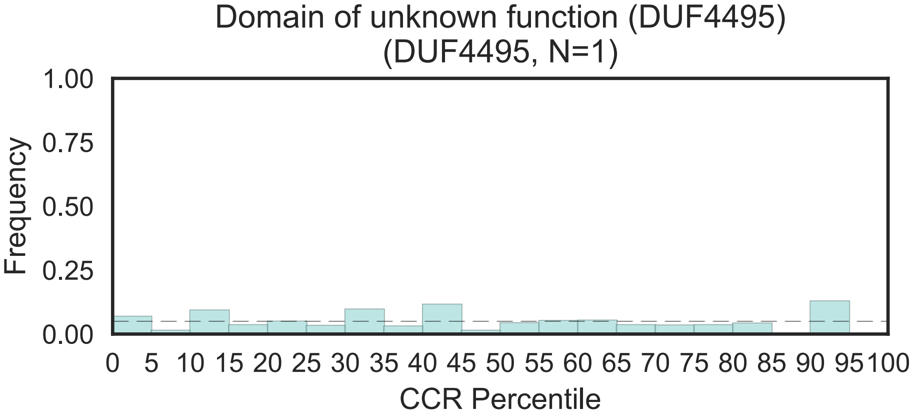
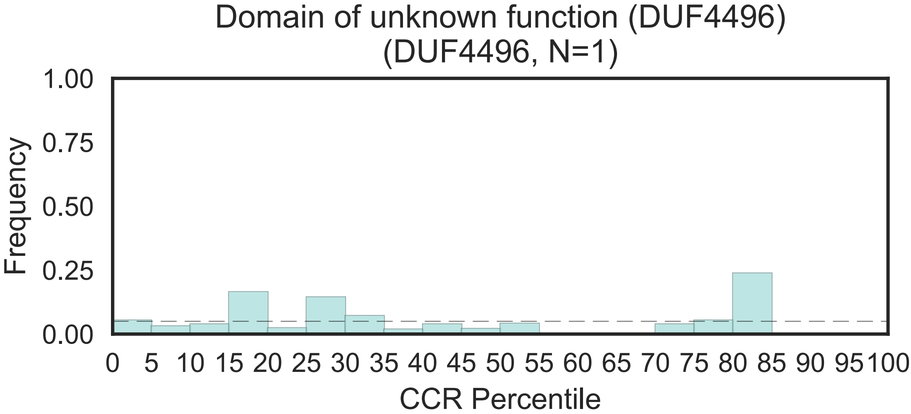
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4495)
(DUF4495, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4496)
(DUF4496, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
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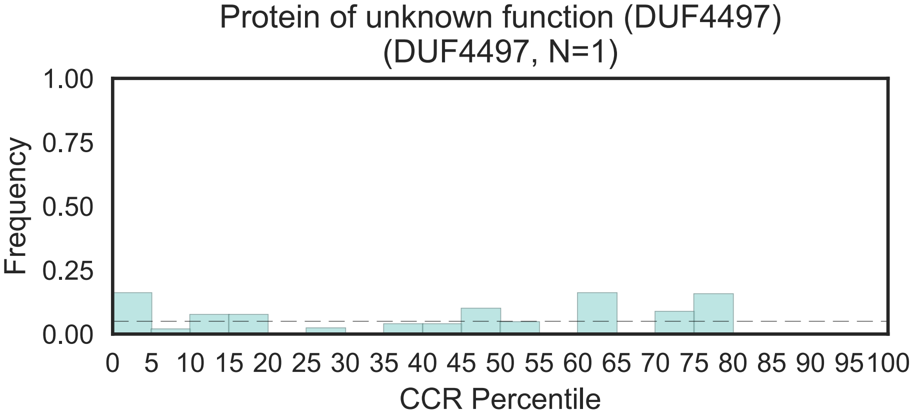
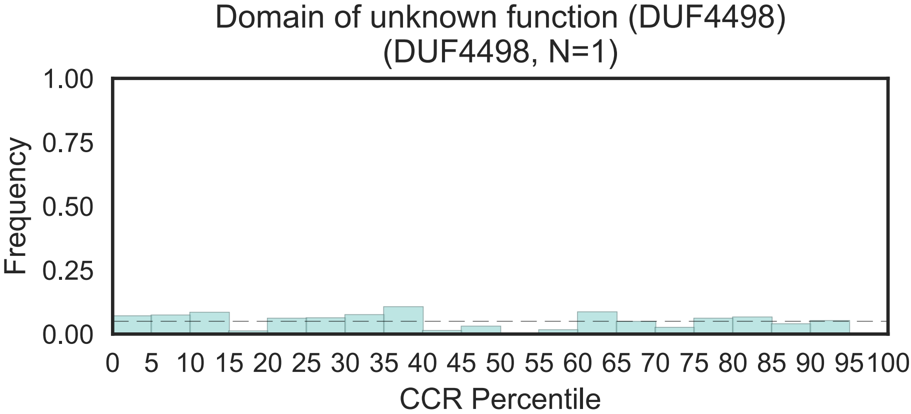
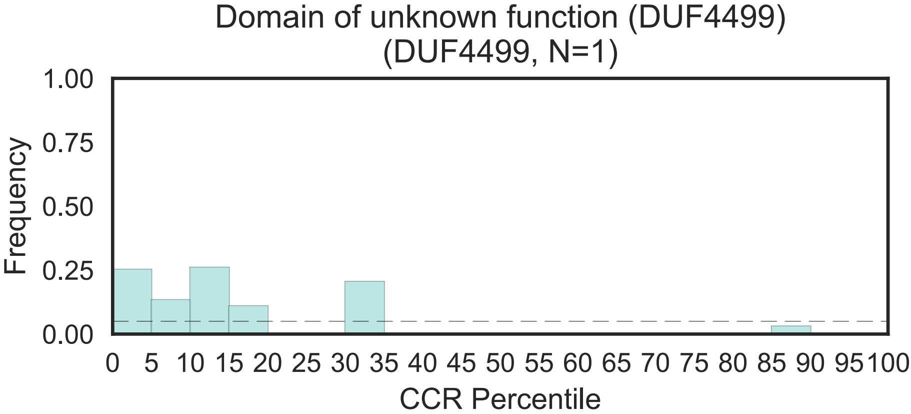
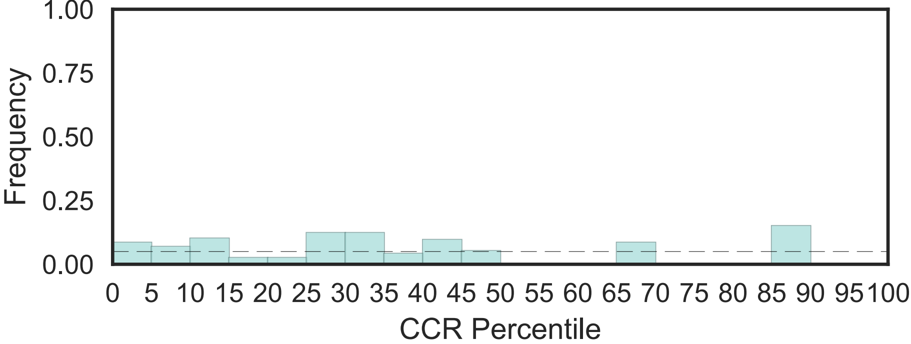
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

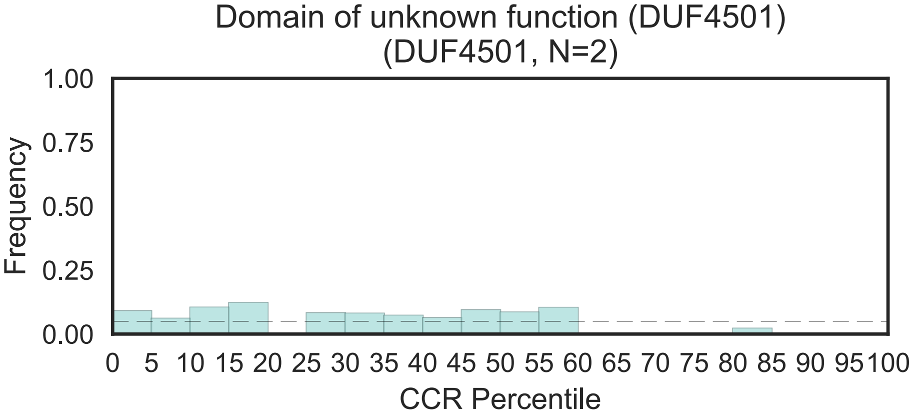

Protein of unknown function (DUF4497)
(DUF4497, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

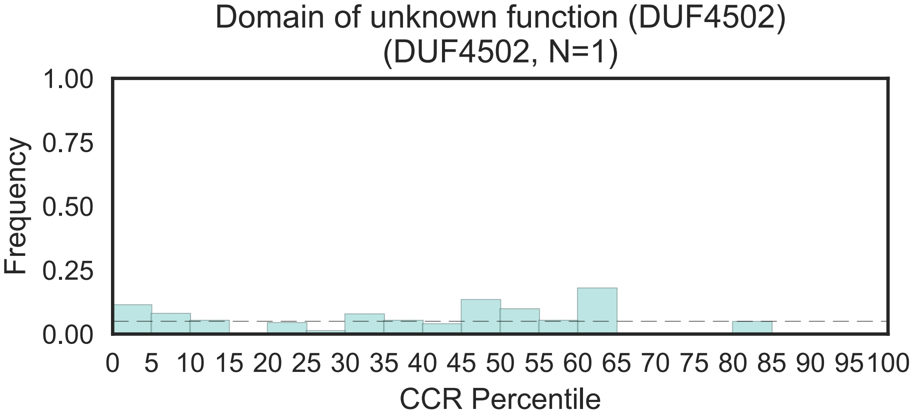

Domain of unknown function (DUF4498)
(DUF4498, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4499)
(DUF4499, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

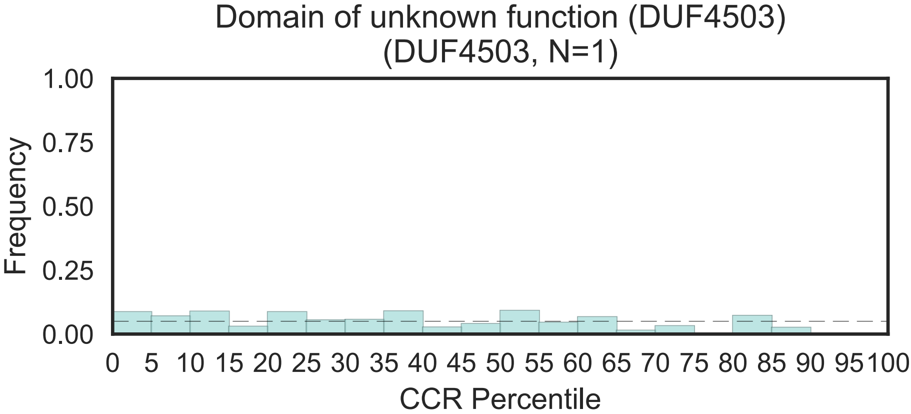
Domain of unknown function (DUF4500)
(DUF4500, N=1)

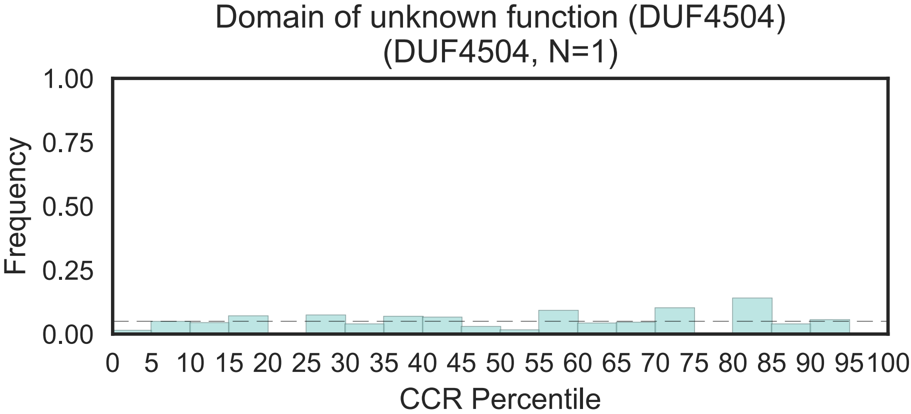


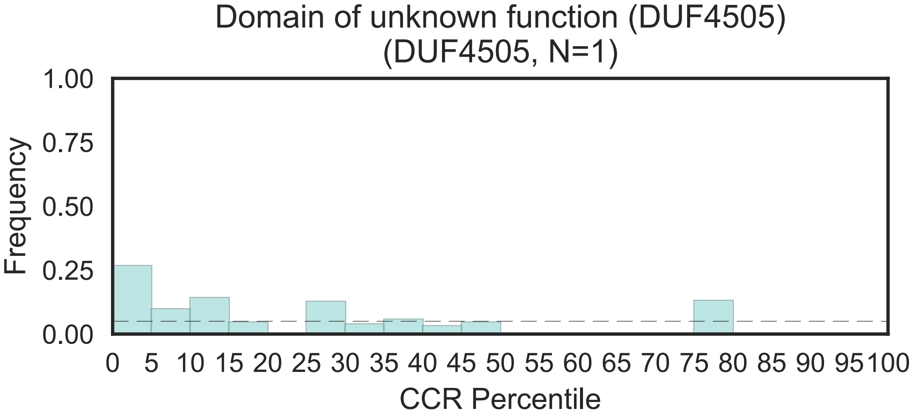

Domain of unknown function (DUF4501)
(DUF4501, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

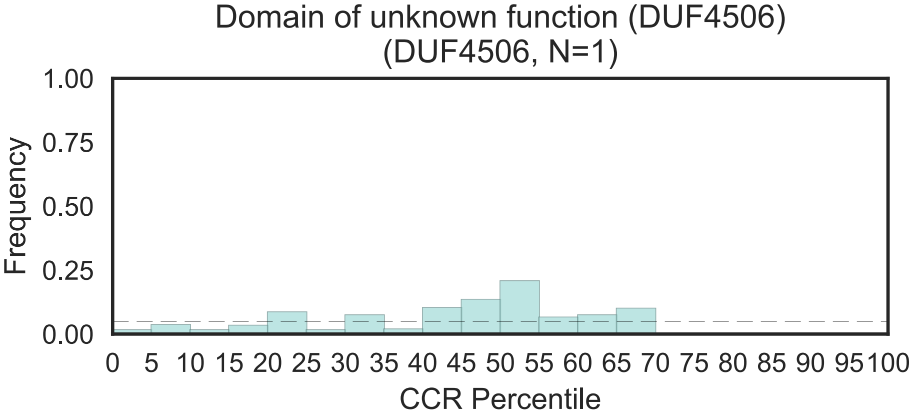


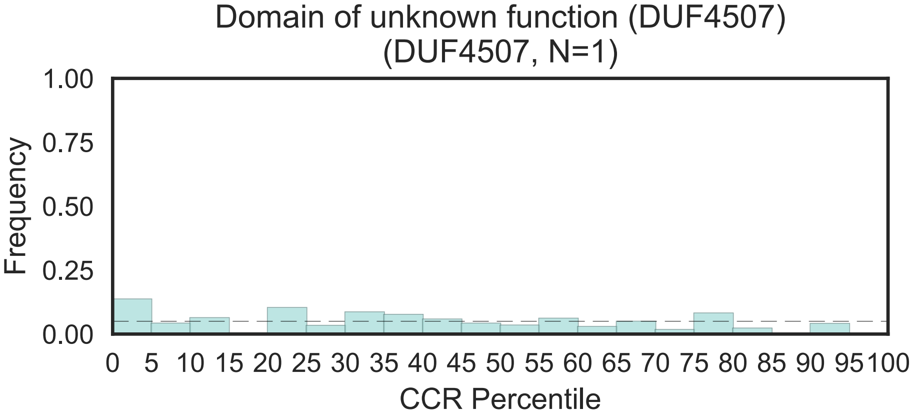
Domain of unknown function (DUF4502)
(DUF4502, N=1)

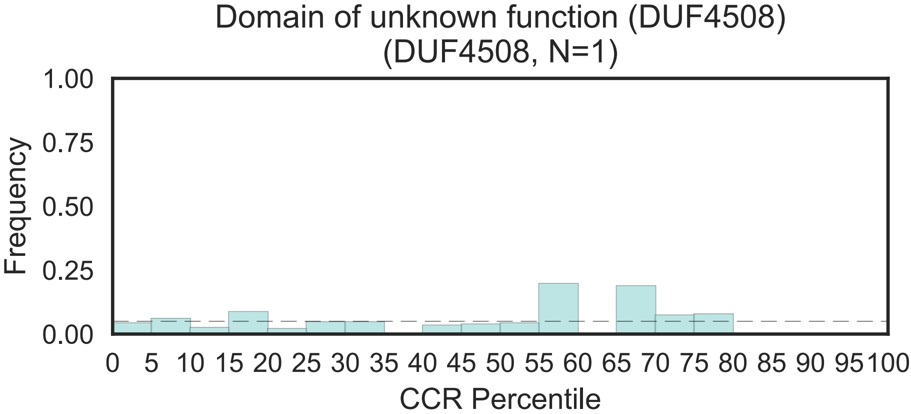

Domain of unknown function (DUF4503)
(DUF4503, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

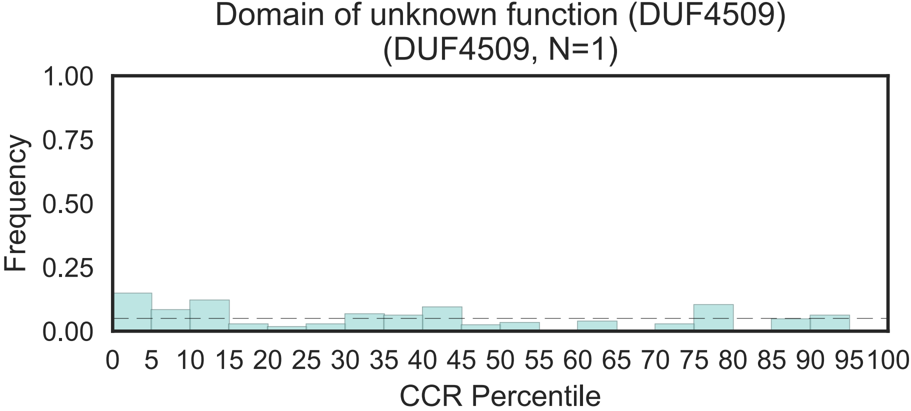

Domain of unknown function (DUF4504)
(DUF4504, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

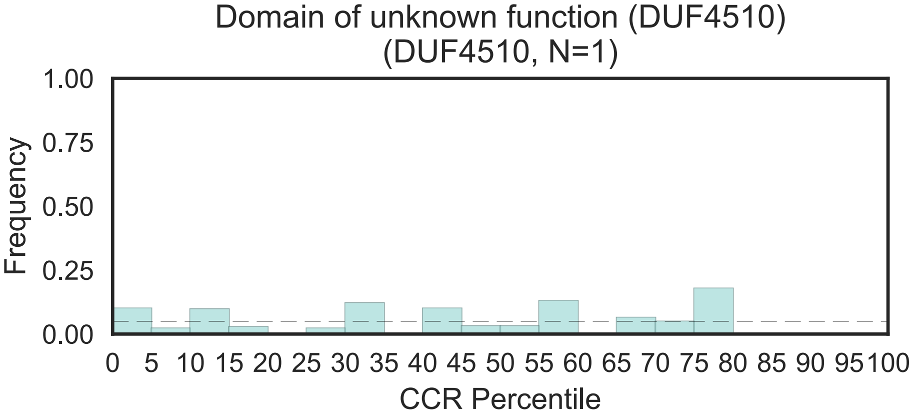

Domain of unknown function (DUF4505)
(DUF4505, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4506)
(DUF4506, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

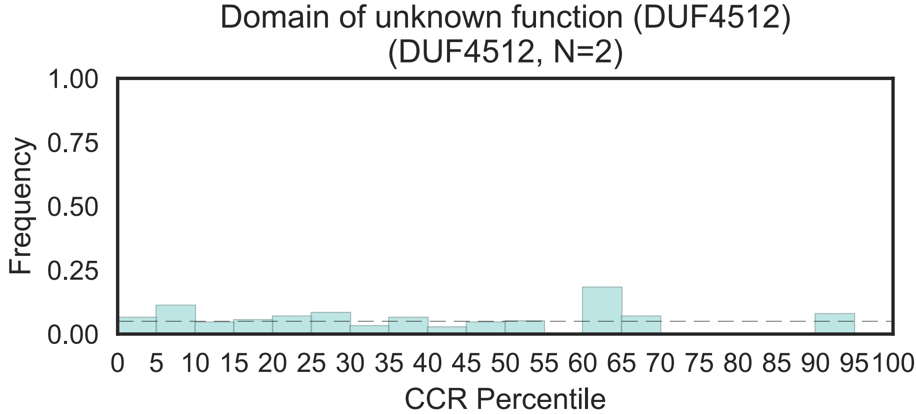

Domain of unknown function (DUF4507)
(DUF4507, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

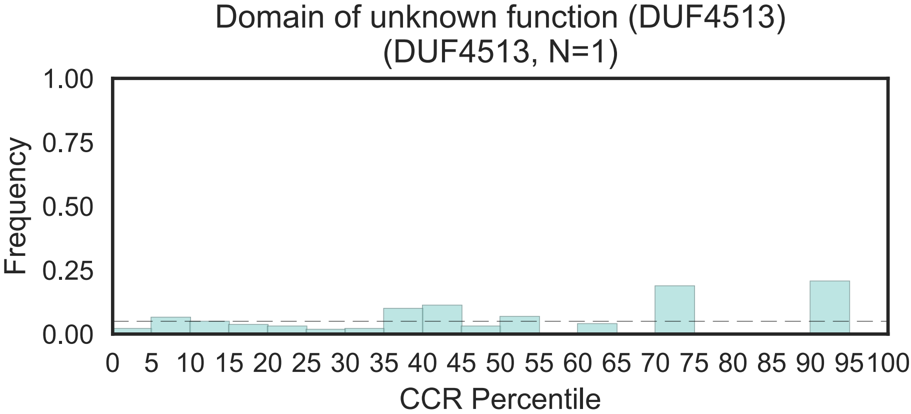

Domain of unknown function (DUF4508)
(DUF4508, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

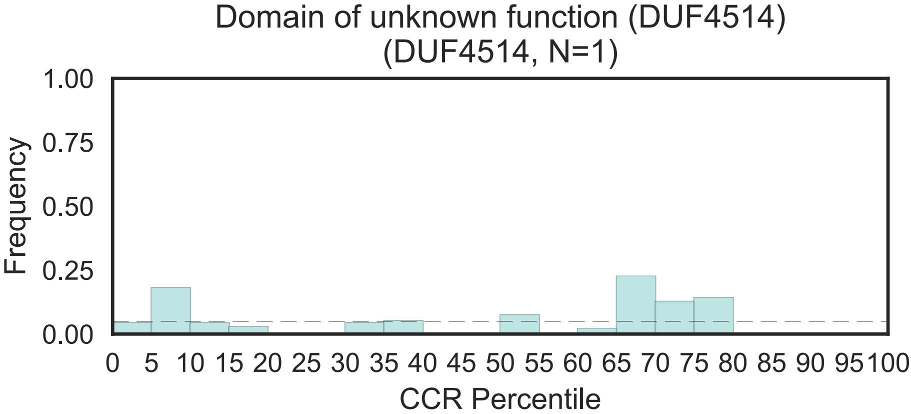

Domain of unknown function (DUF4509)
(DUF4509, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

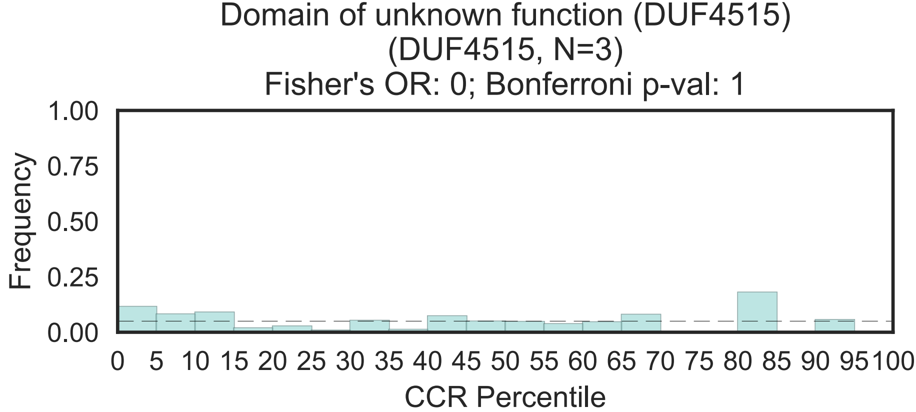


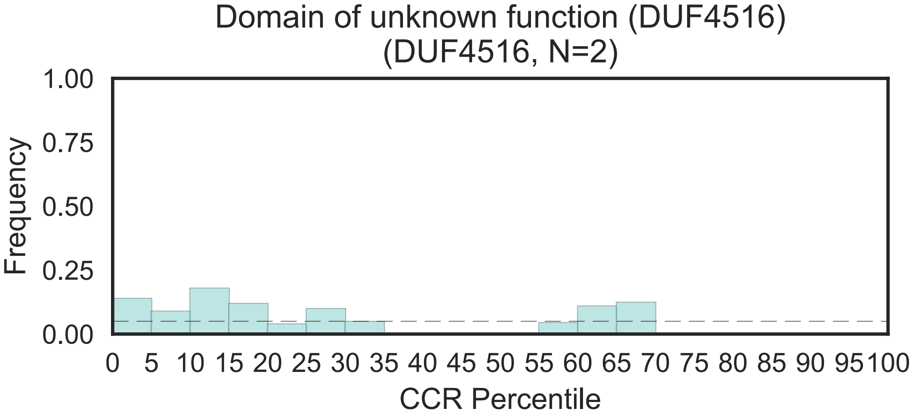
Domain of unknown function (DUF4510)
(DUF4510, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4512)
(DUF4512, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

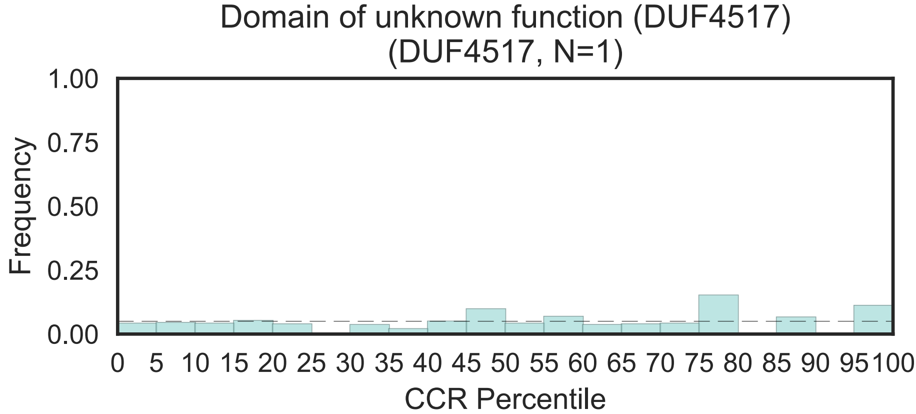

Domain of unknown function (DUF4513)
(DUF4513, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

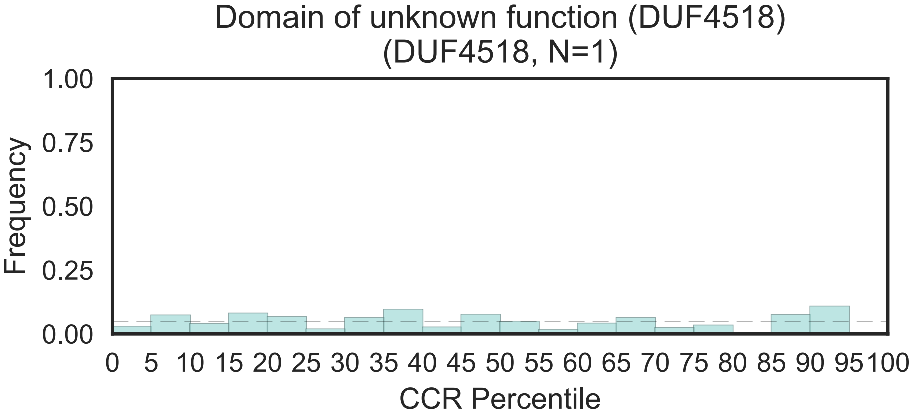

Domain of unknown function (DUF4514)
(DUF4514, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

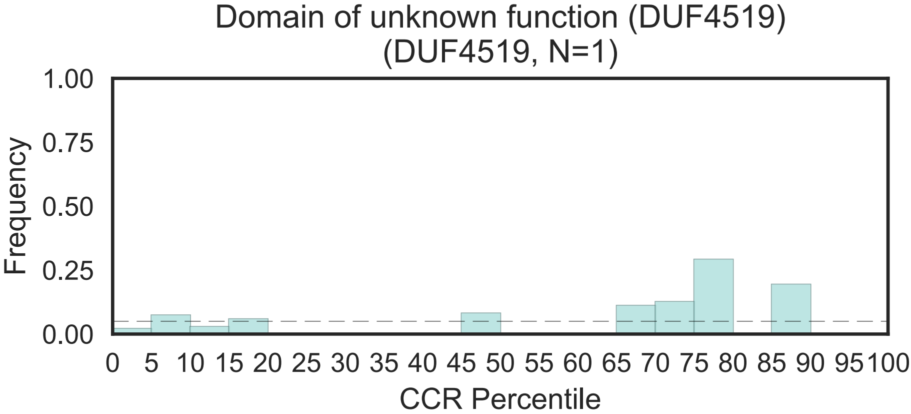

Domain of unknown function (DUF4515)
(DUF4515, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

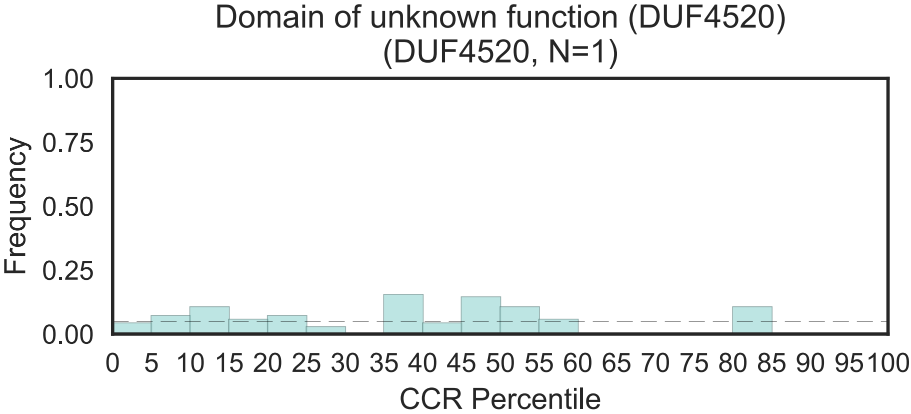


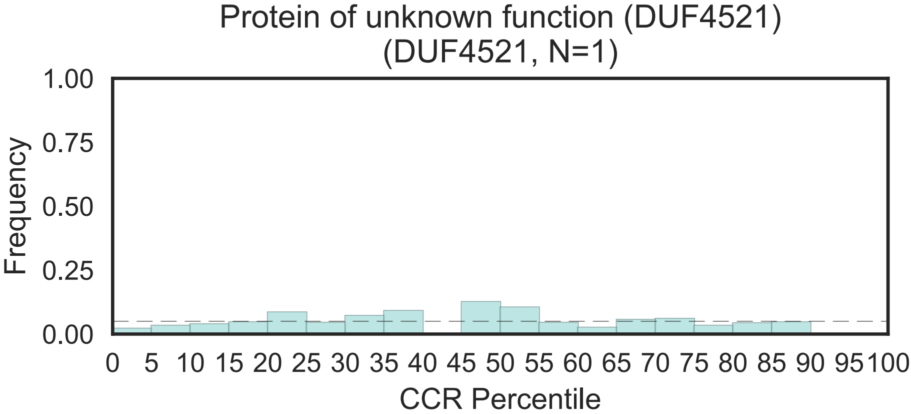
Domain of unknown function (DUF4516)
(DUF4516, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4517)
(DUF4517, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

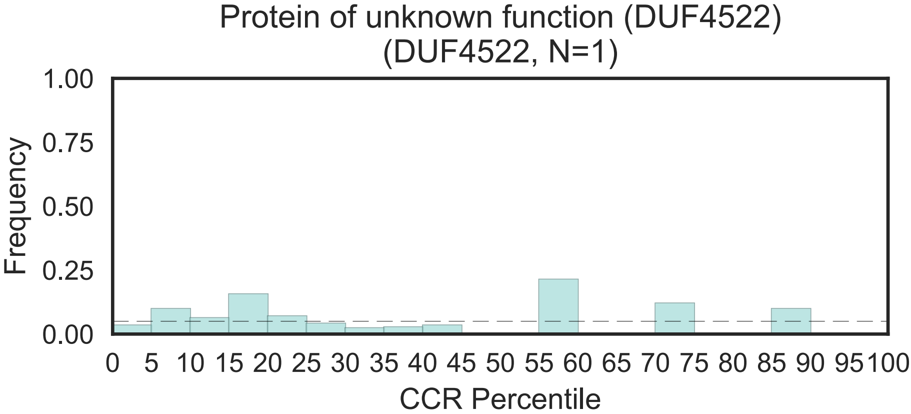

Domain of unknown function (DUF4518)
(DUF4518, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

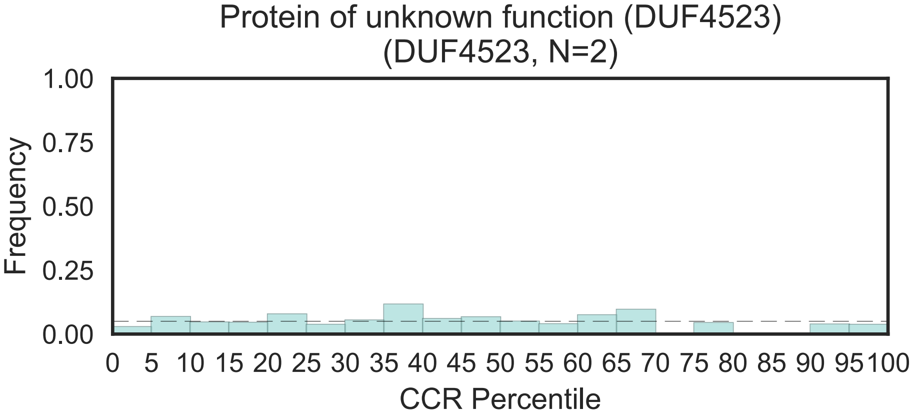

Domain of unknown function (DUF4519)
(DUF4519, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

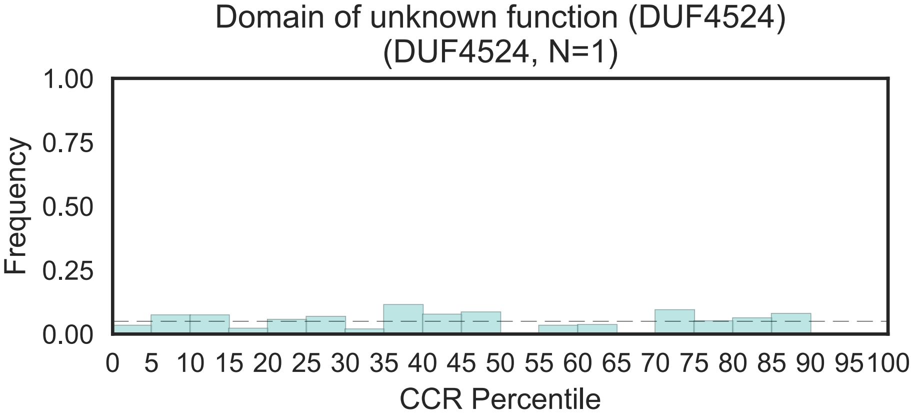

Domain of unknown function (DUF4520)
(DUF4520, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

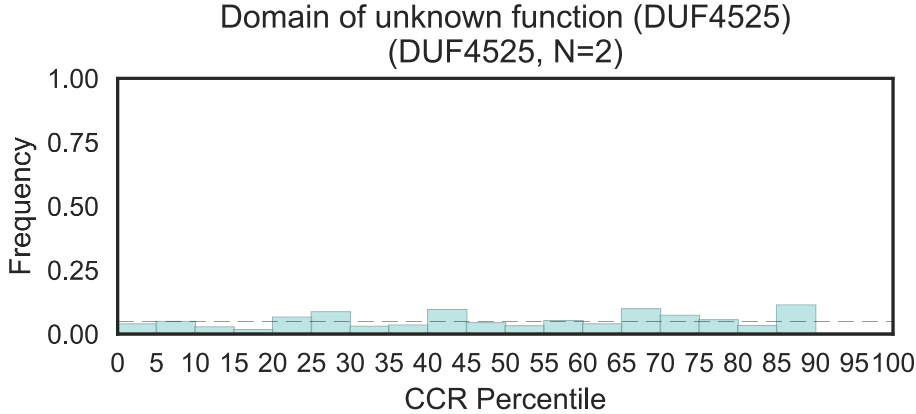


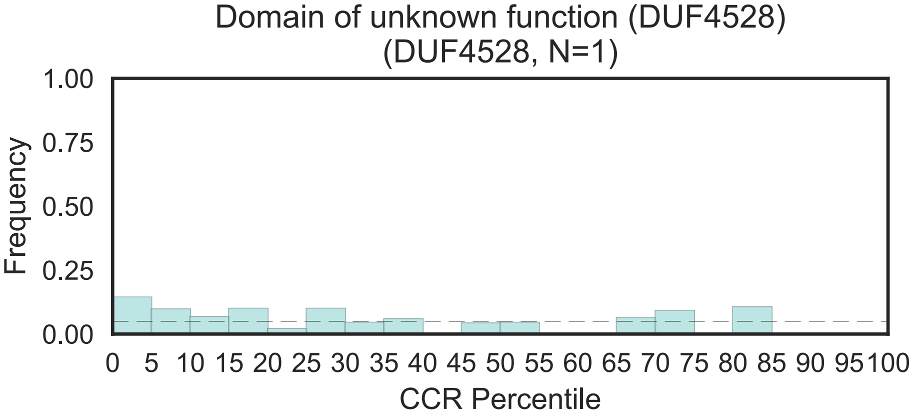
Protein of unknown function (DUF4521)
(DUF4521, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

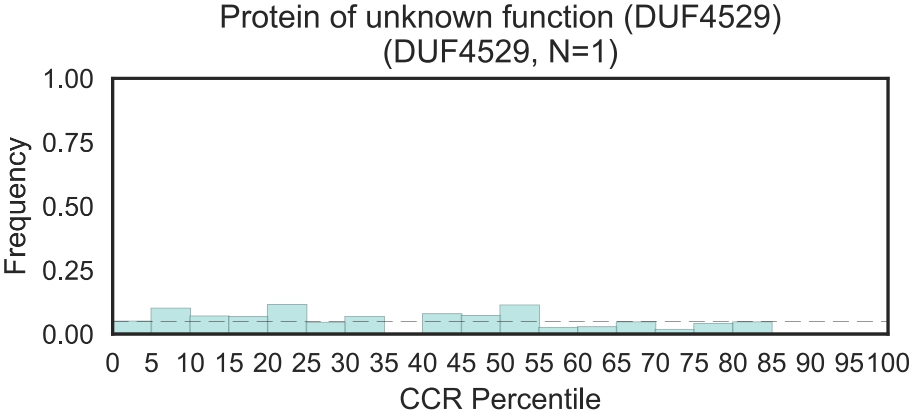

Protein of unknown function (DUF4522)
(DUF4522, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

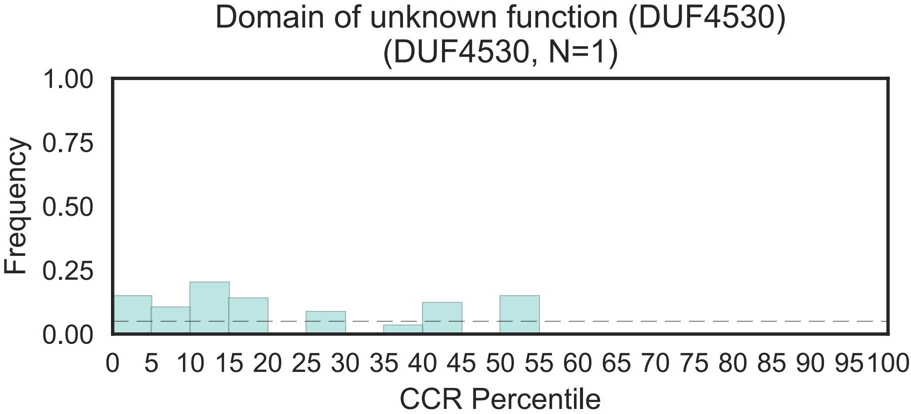

Protein of unknown function (DUF4523)
(DUF4523, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4524)
(DUF4524, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4525)
(DUF4525, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4528)
(DUF4528, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Protein of unknown function (DUF4529)
(DUF4529, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4530)
(DUF4530, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
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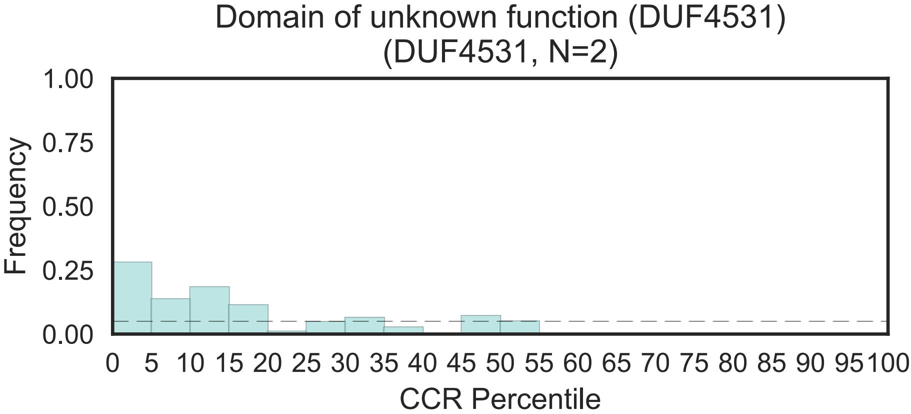
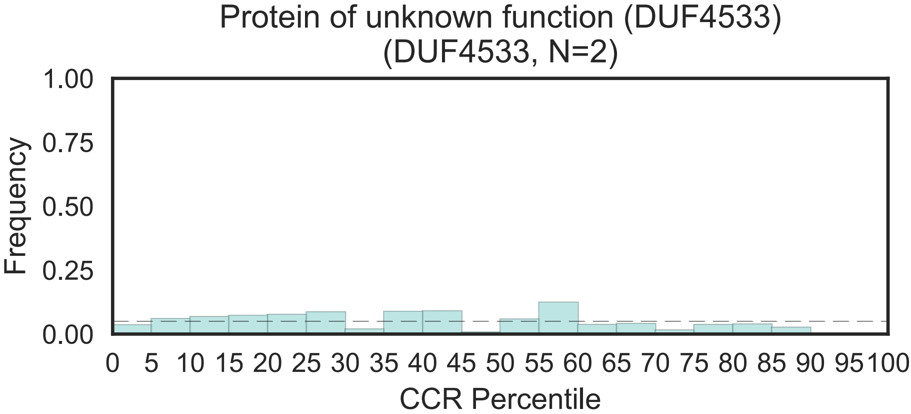
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4531)
(DUF4531, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Protein of unknown function (DUF4533)
(DUF4533, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
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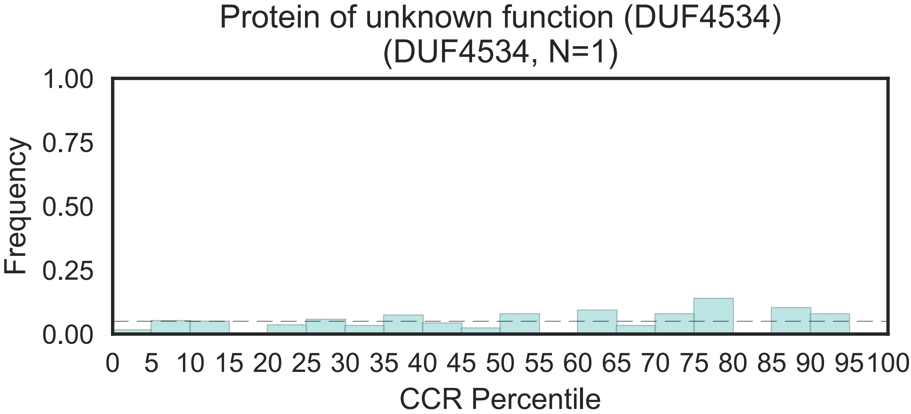
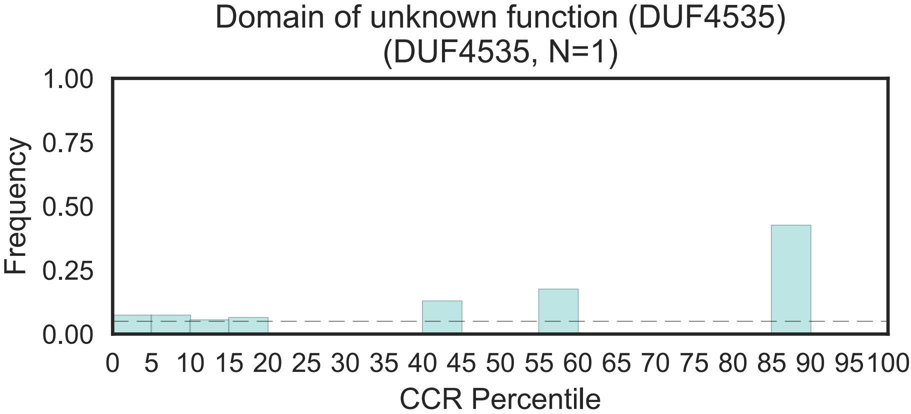
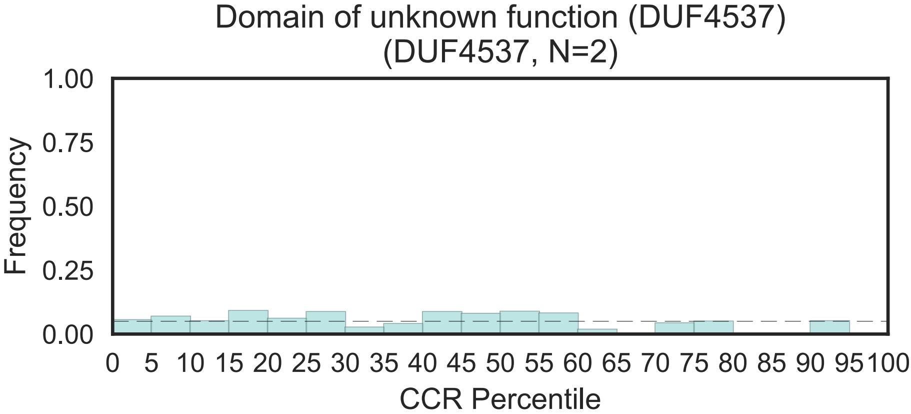
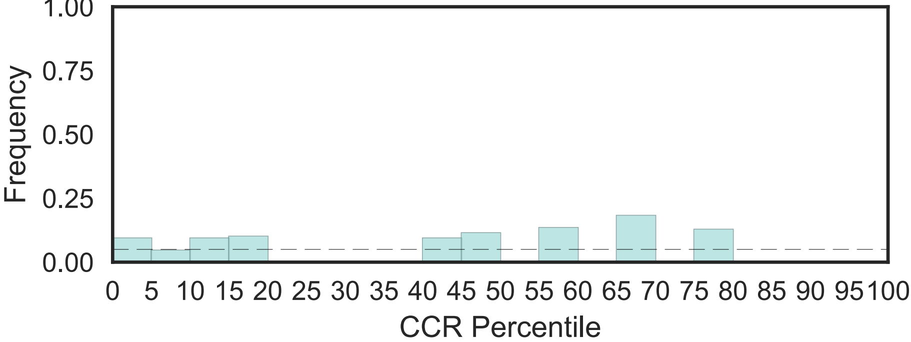
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

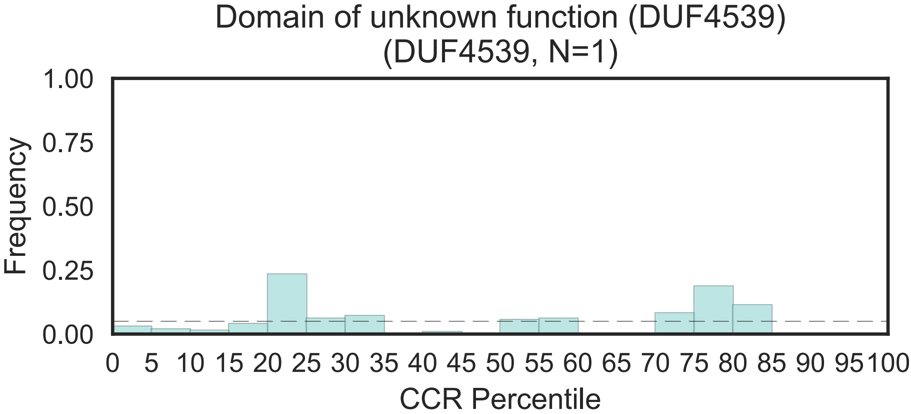

Protein of unknown function (DUF4534)
(DUF4534, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4535)
(DUF4535, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4537)
(DUF4537, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



Domain of unknown function (DUF4538)
(DUF4538, N=1)


Domain of unknown function (DUF4539)
(DUF4539, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
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20
25
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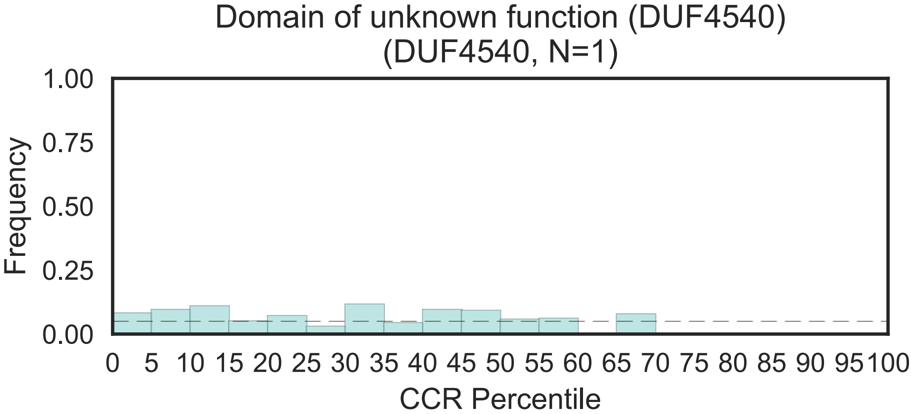
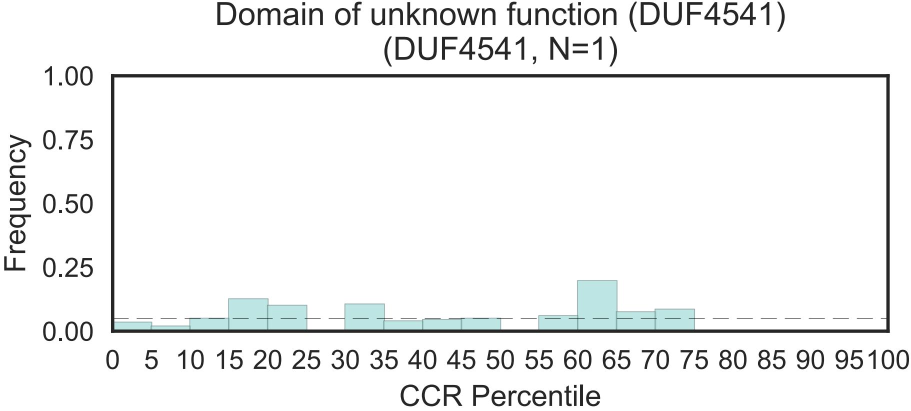
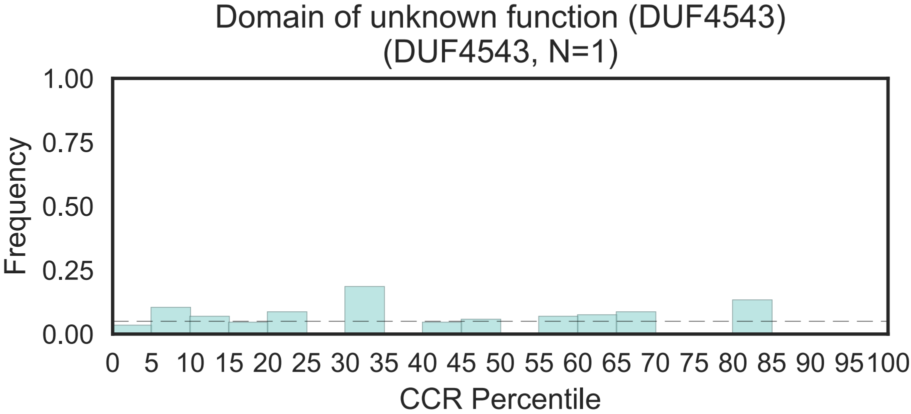
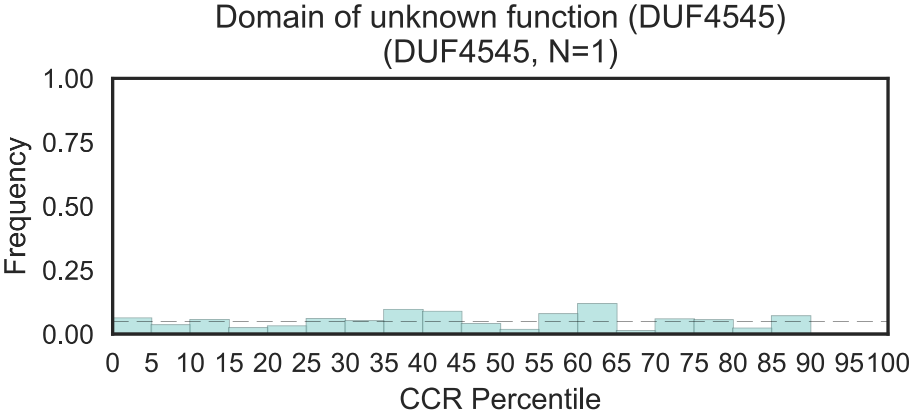
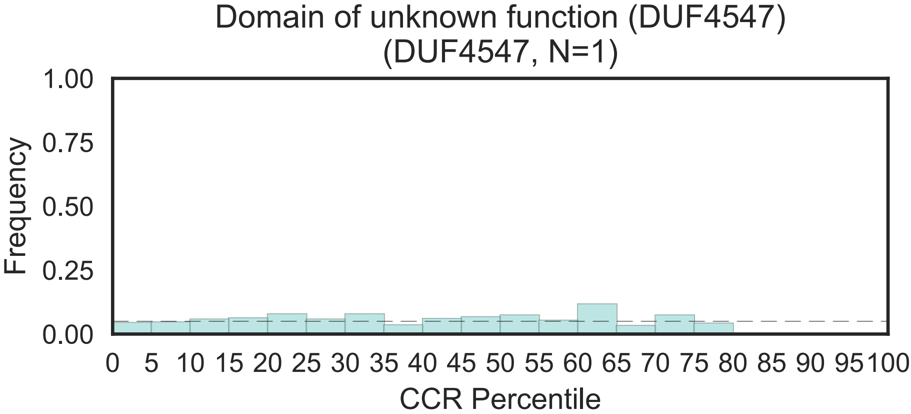
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

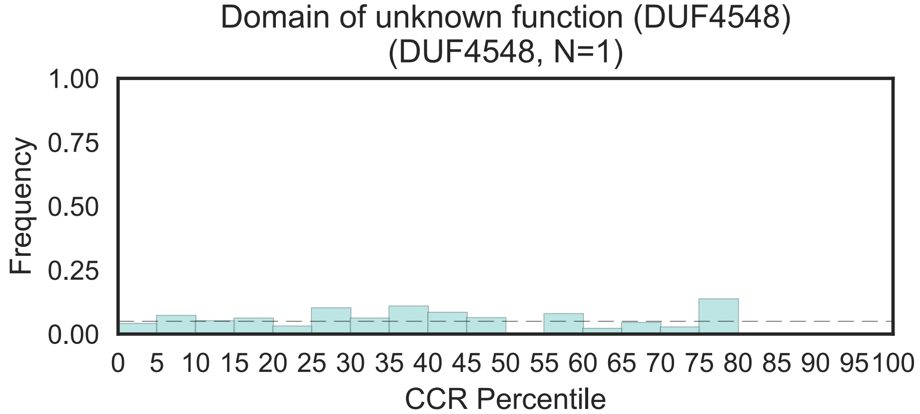

Domain of unknown function (DUF4540)
(DUF4540, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4541)
(DUF4541, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

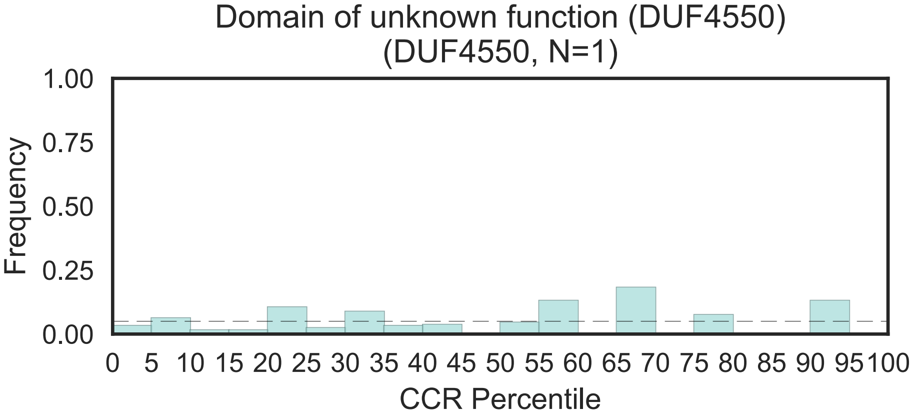

Domain of unknown function (DUF4543)
(DUF4543, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4545)
(DUF4545, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

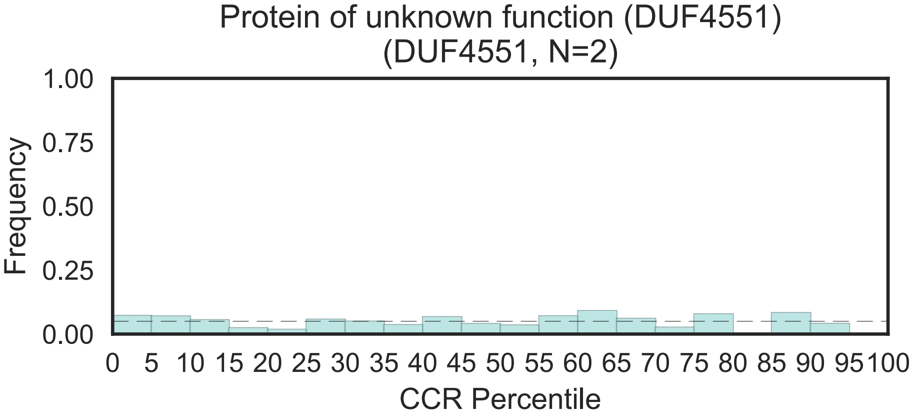

Domain of unknown function (DUF4547)
(DUF4547, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

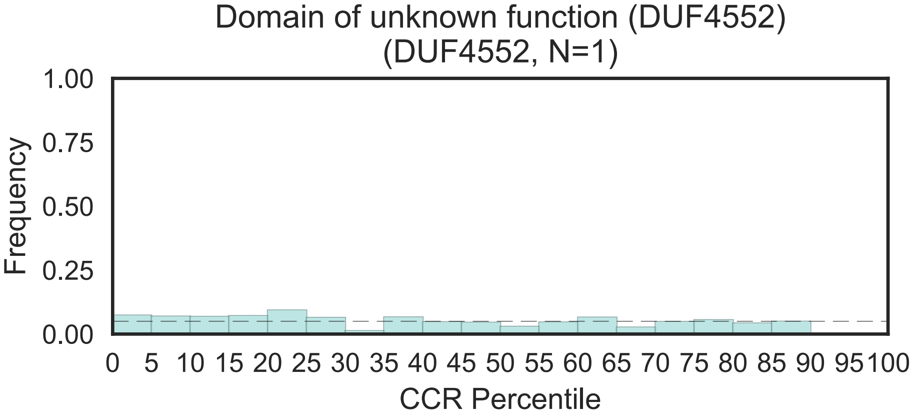


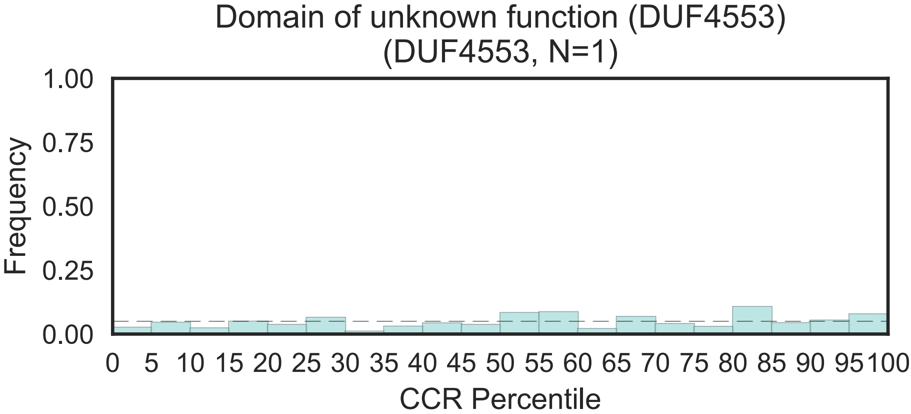
Domain of unknown function (DUF4548)
(DUF4548, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

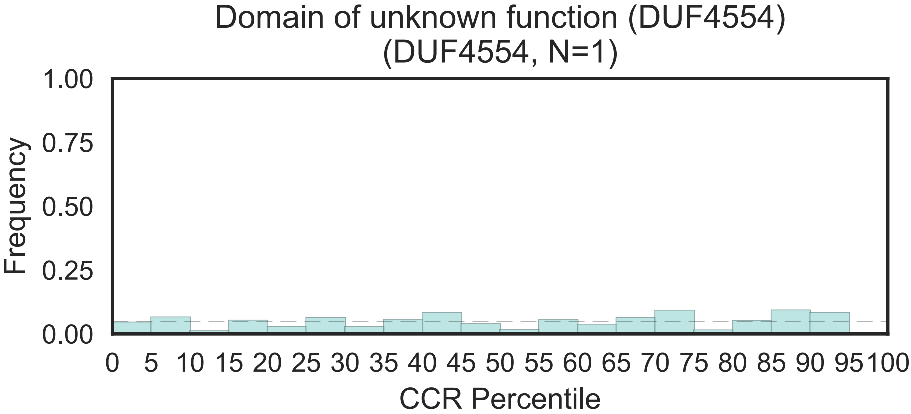


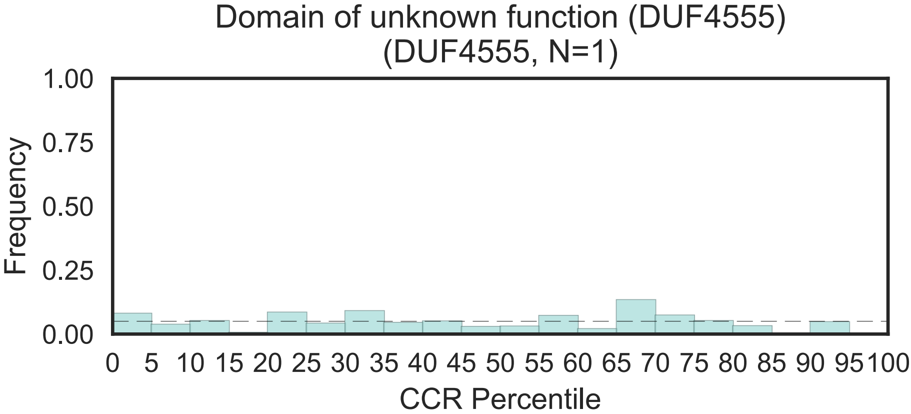
Domain of unknown function (DUF4550)
(DUF4550, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

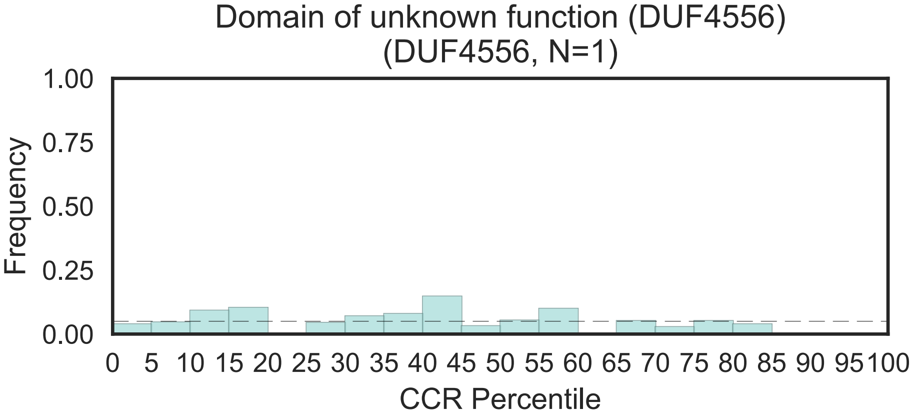

Protein of unknown function (DUF4551)
(DUF4551, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

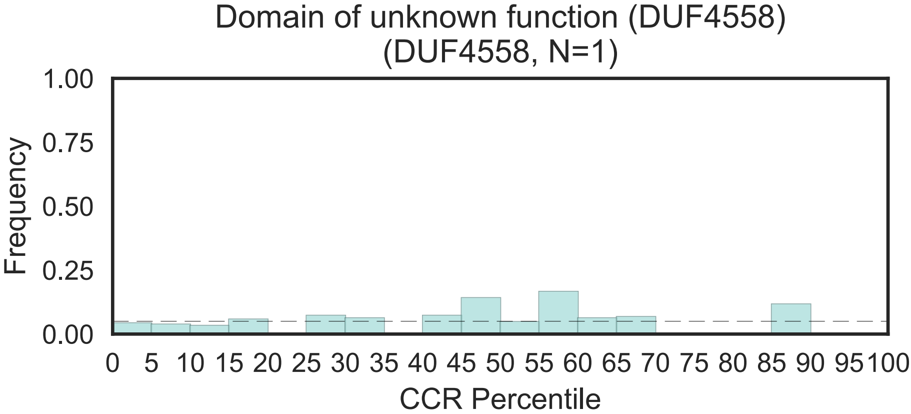

Domain of unknown function (DUF4552)
(DUF4552, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

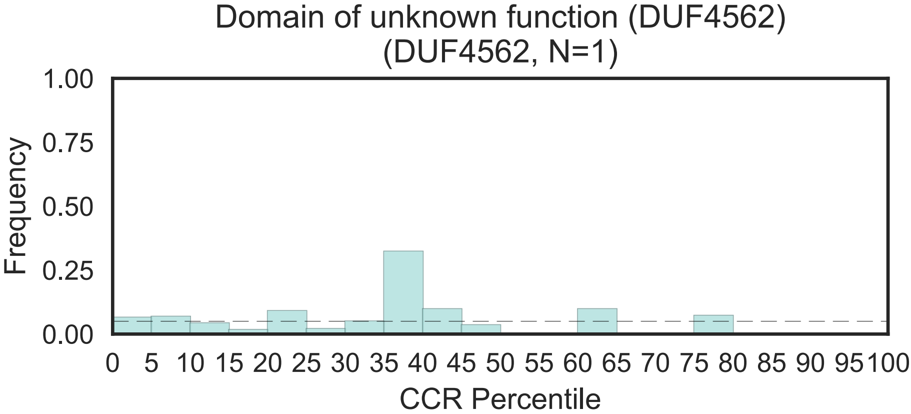

Domain of unknown function (DUF4553)
(DUF4553, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

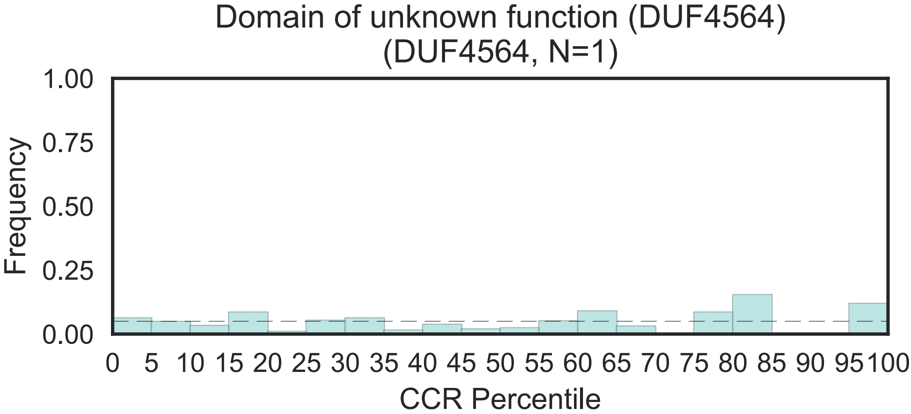

Domain of unknown function (DUF4554)
(DUF4554, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4555)
(DUF4555, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

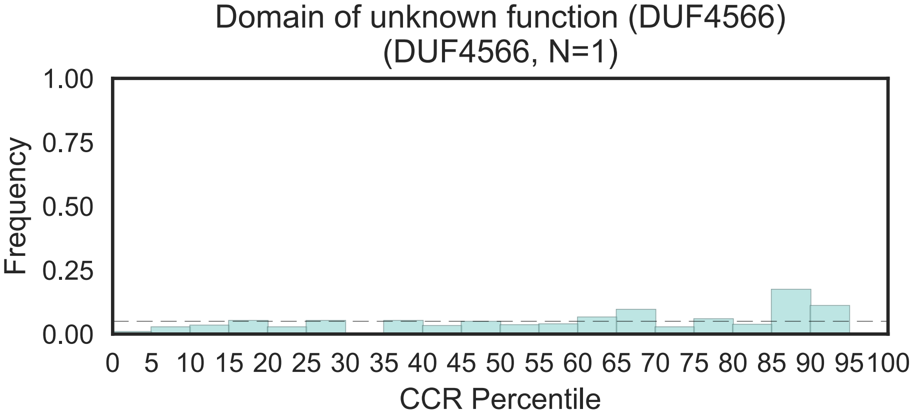

Domain of unknown function (DUF4556)
(DUF4556, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

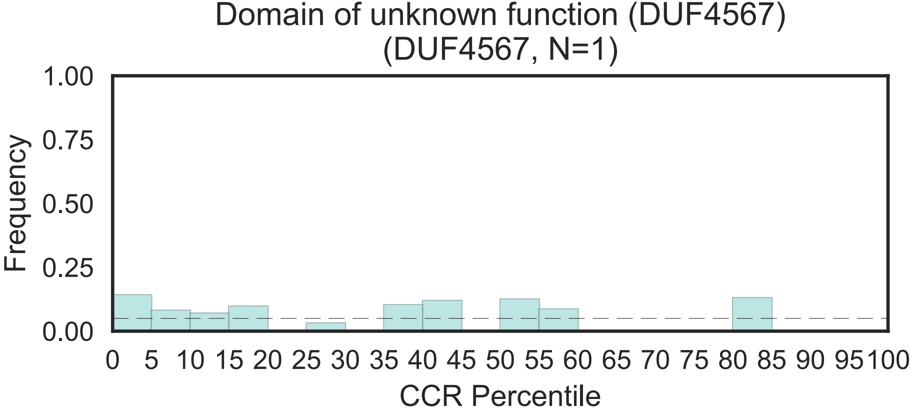

Domain of unknown function (DUF4558)
(DUF4558, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

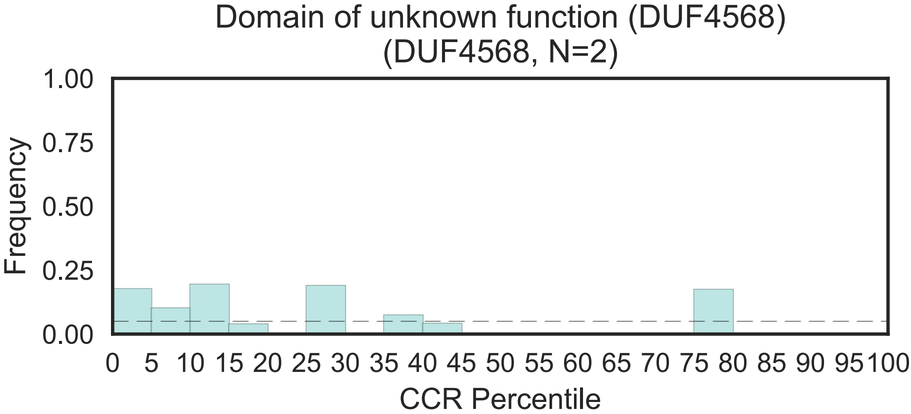

Domain of unknown function (DUF4562)
(DUF4562, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

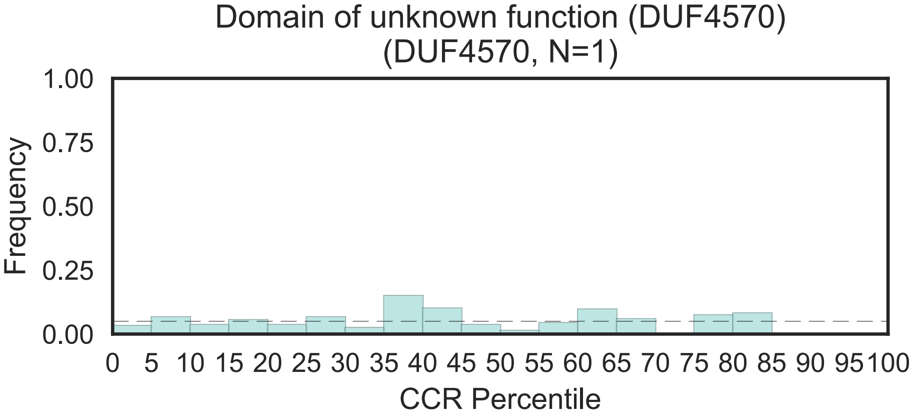


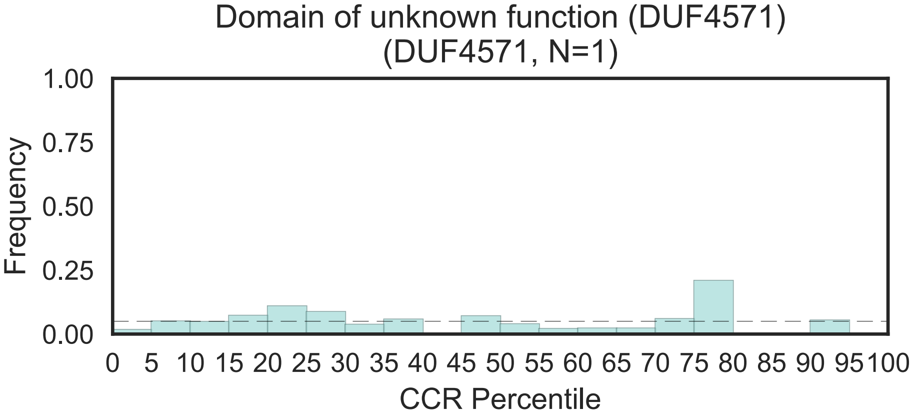
Domain of unknown function (DUF4564)
(DUF4564, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

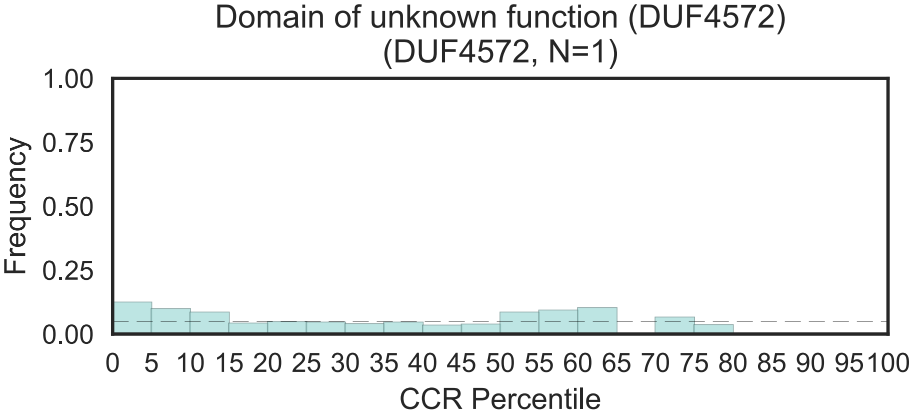

Domain of unknown function (DUF4566)
(DUF4566, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

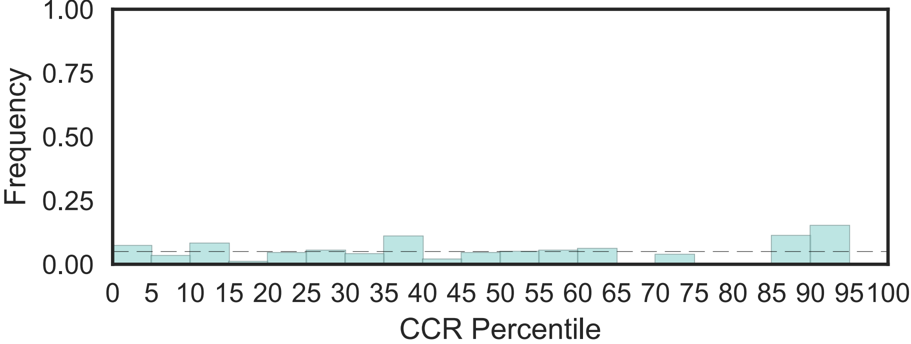

Domain of unknown function (DUF4567)
(DUF4567, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4568)
(DUF4568, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

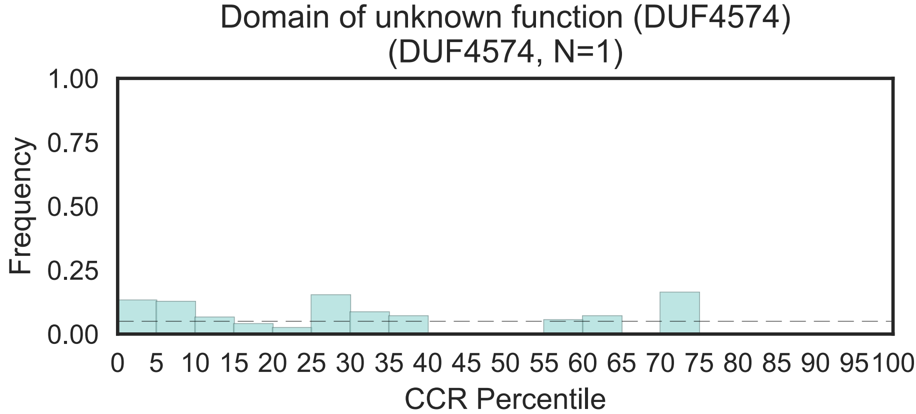

Domain of unknown function (DUF4570)
(DUF4570, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

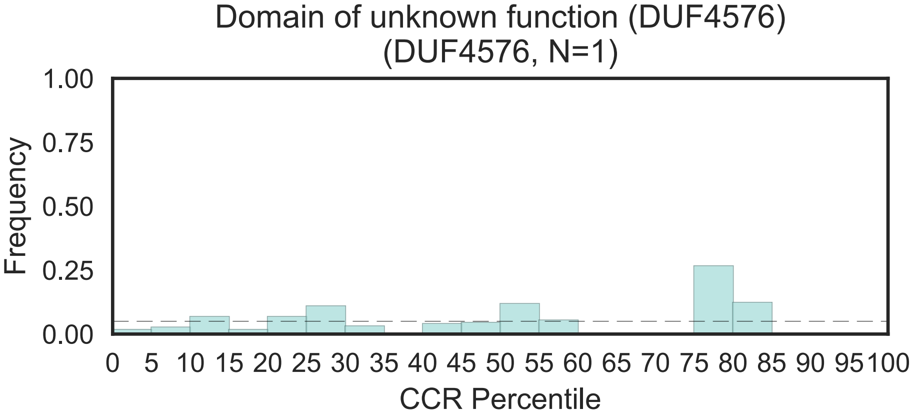

Domain of unknown function (DUF4571)
(DUF4571, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

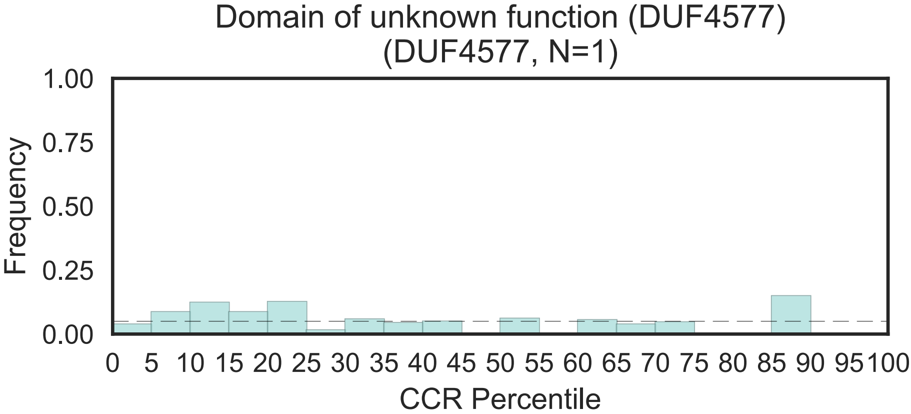

Domain of unknown function (DUF4572)
(DUF4572, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

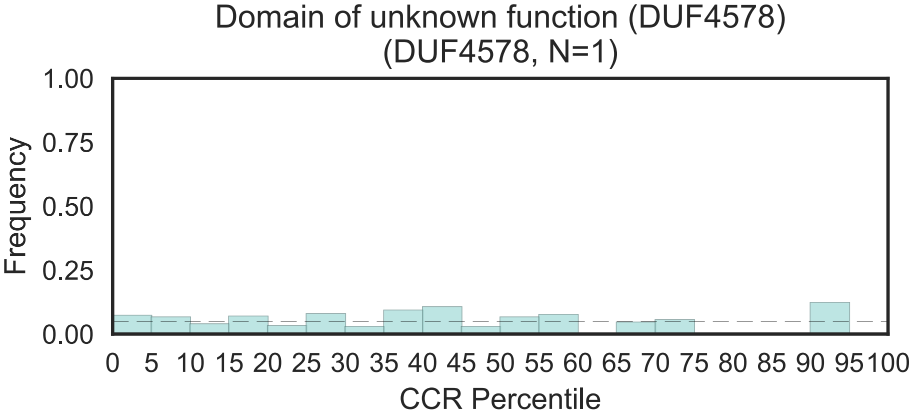


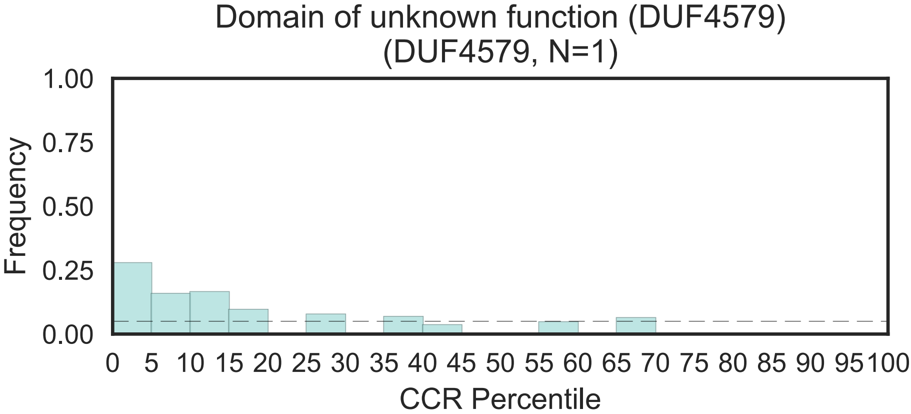
Domain of unknown function (DUF4573)
(DUF4573, N=1)

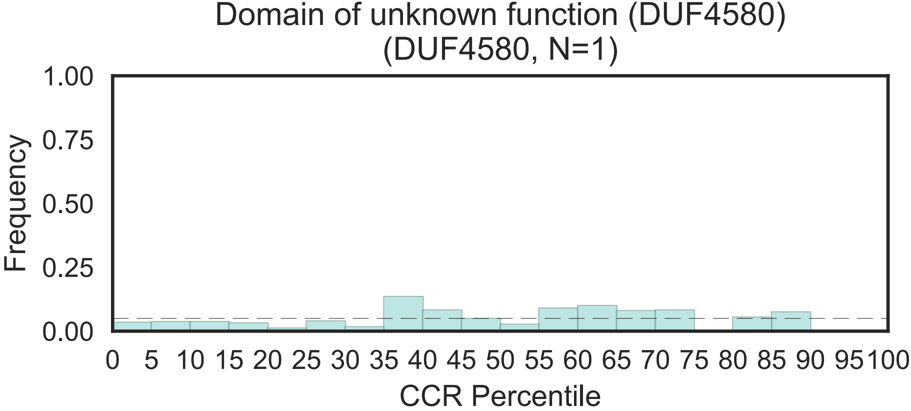

Domain of unknown function (DUF4574)
(DUF4574, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

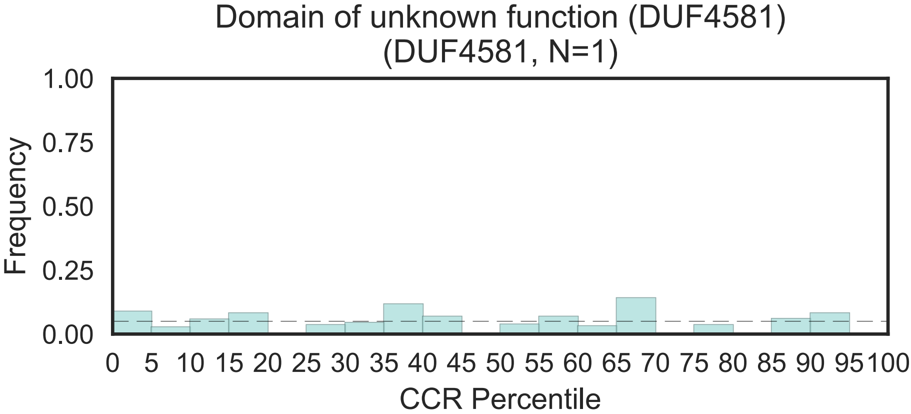

Domain of unknown function (DUF4576)
(DUF4576, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

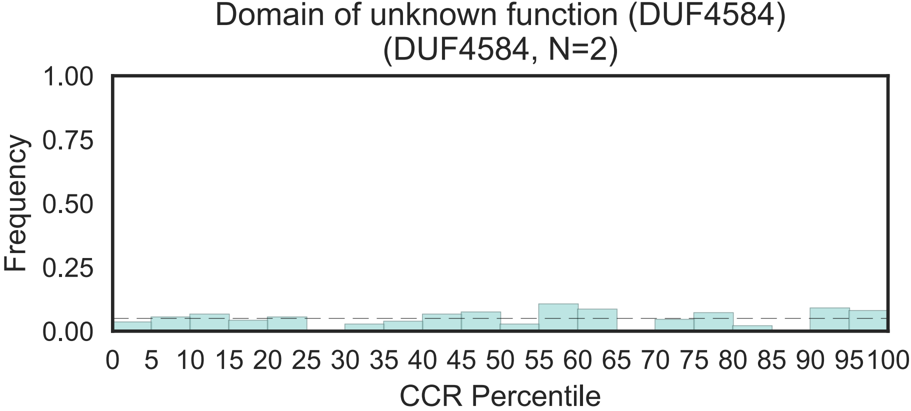

Domain of unknown function (DUF4577)
(DUF4577, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

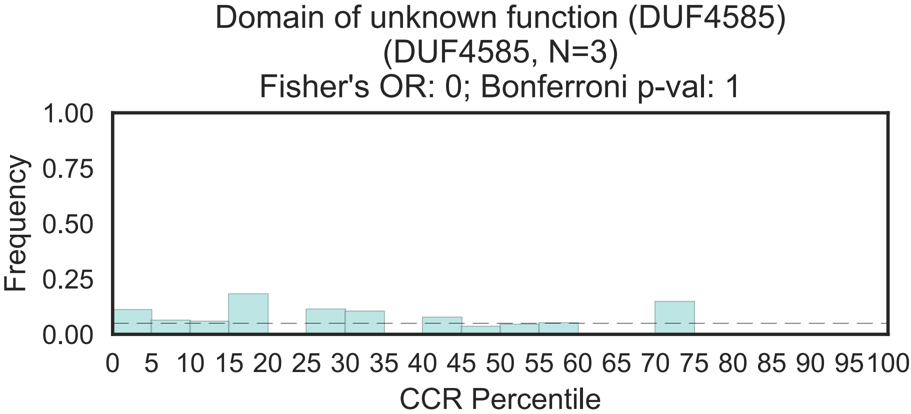

Domain of unknown function (DUF4578)
(DUF4578, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

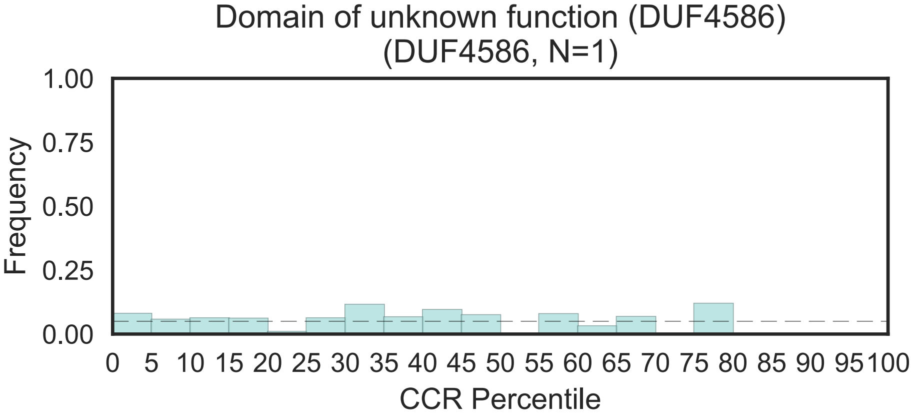

Domain of unknown function (DUF4579)
(DUF4579, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4580)
(DUF4580, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

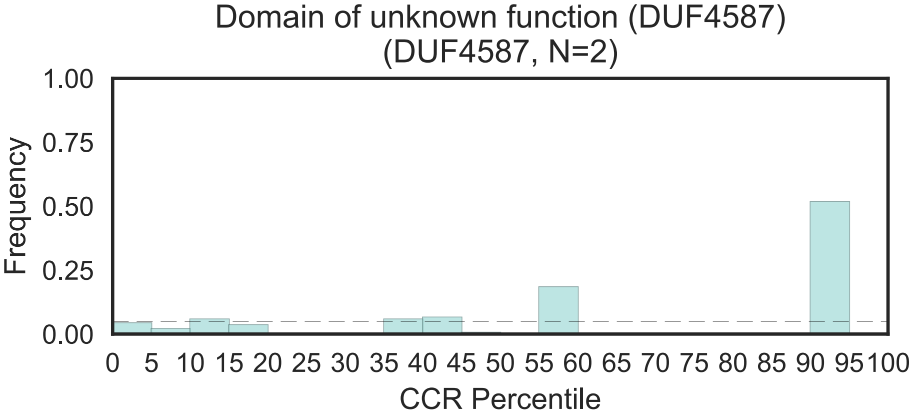

Domain of unknown function (DUF4581)
(DUF4581, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

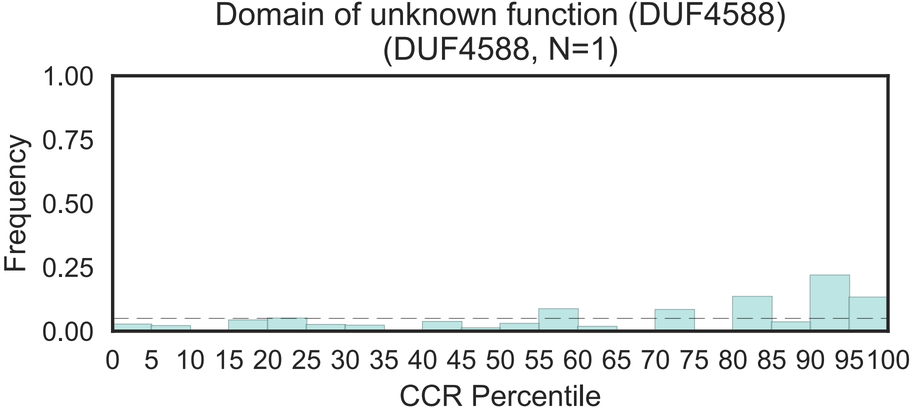

Domain of unknown function (DUF4584)
(DUF4584, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

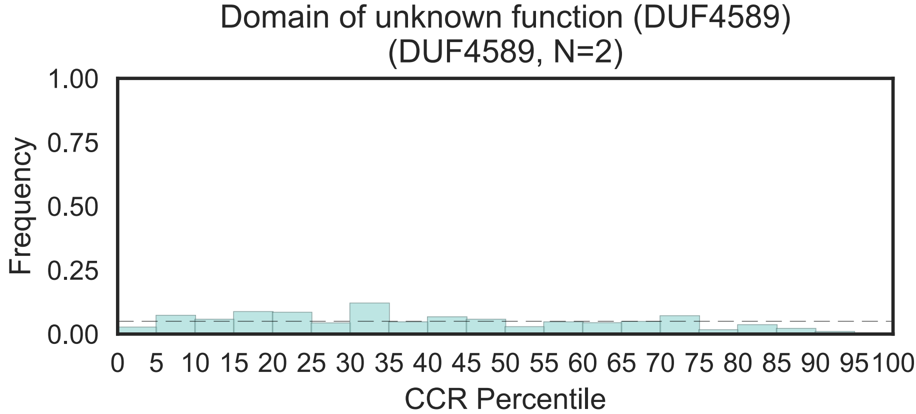

Domain of unknown function (DUF4585)
(DUF4585, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

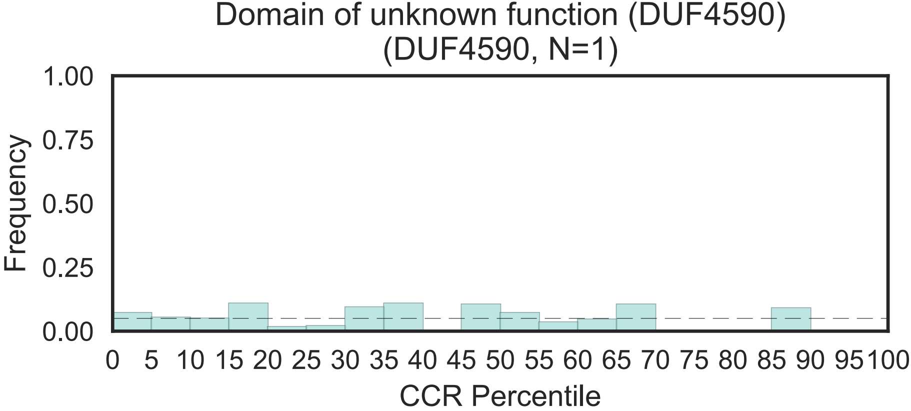


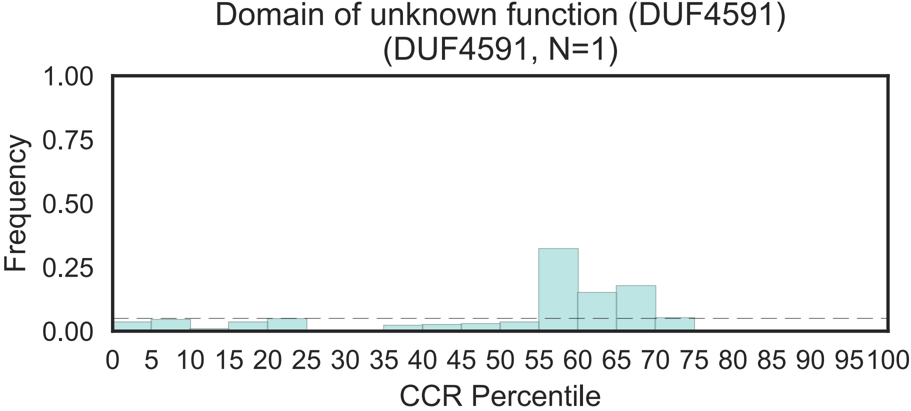
Domain of unknown function (DUF4586)
(DUF4586, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4587)
(DUF4587, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4588)
(DUF4588, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4589)
(DUF4589, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4590)
(DUF4590, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4591)
(DUF4591, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
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55
60
65
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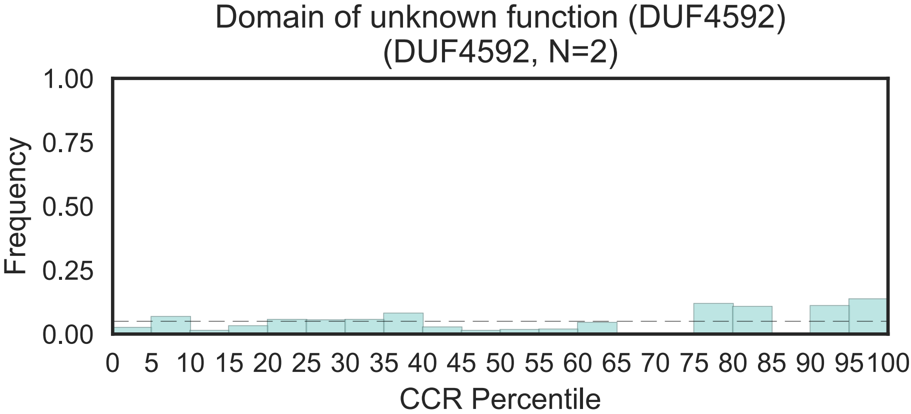
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4592)
(DUF4592, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
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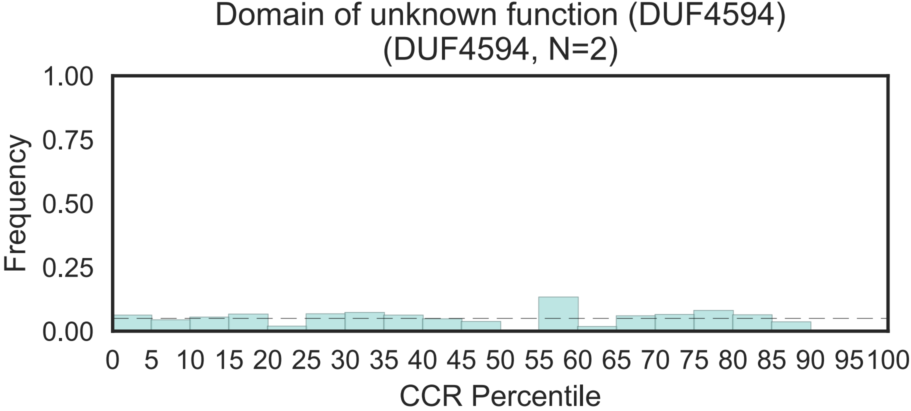
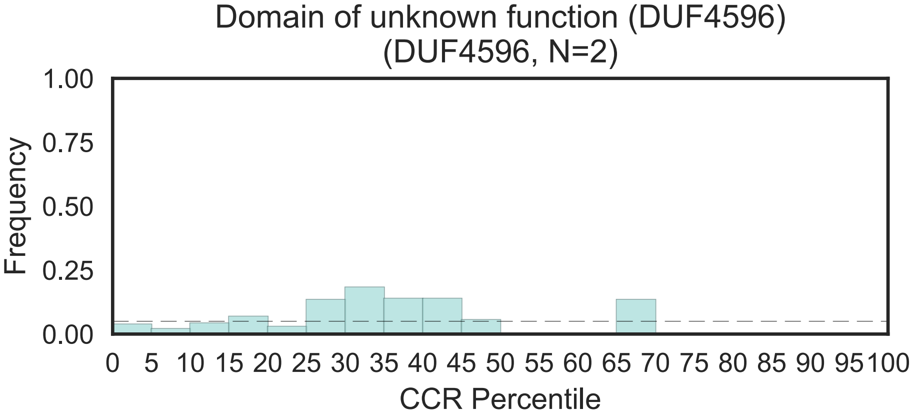
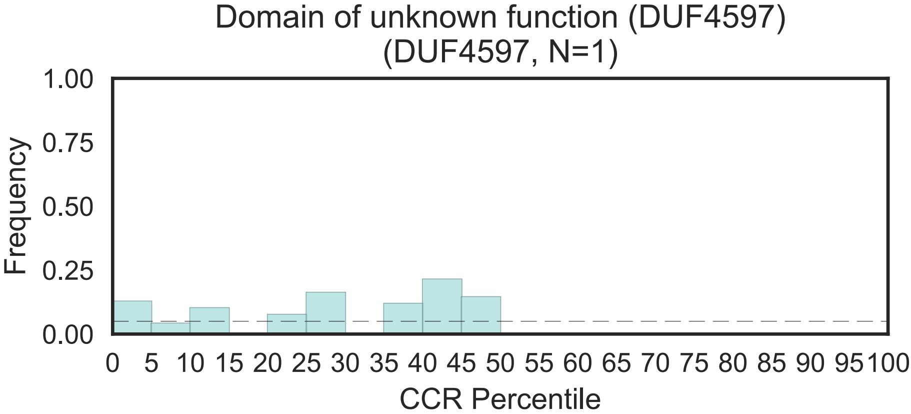
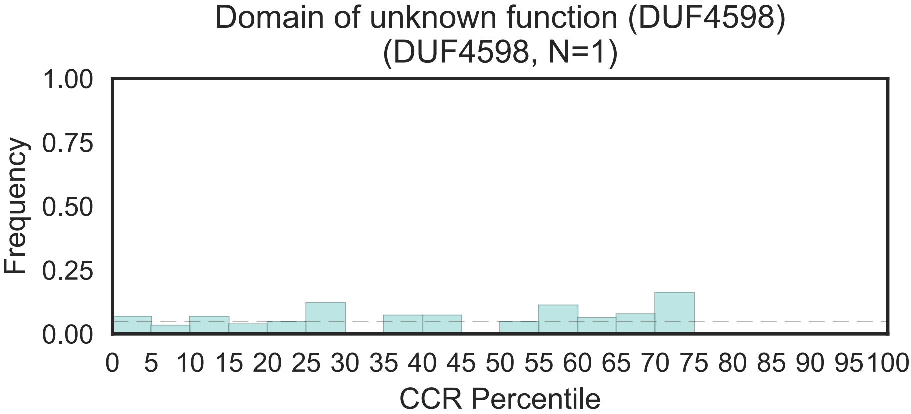
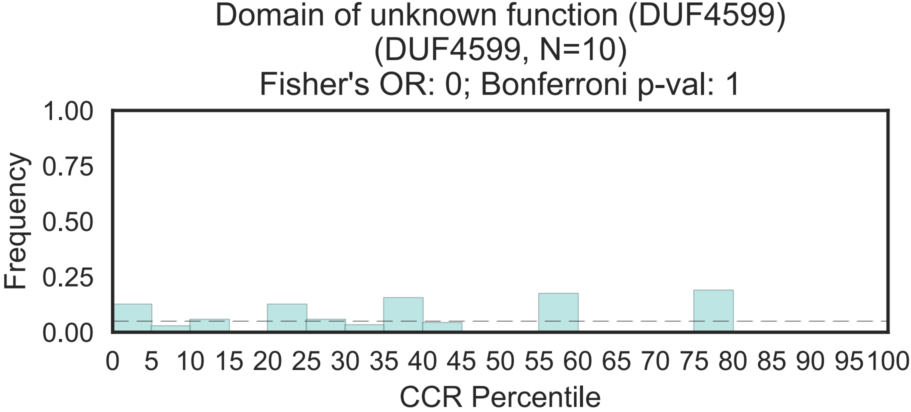
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4594)
(DUF4594, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

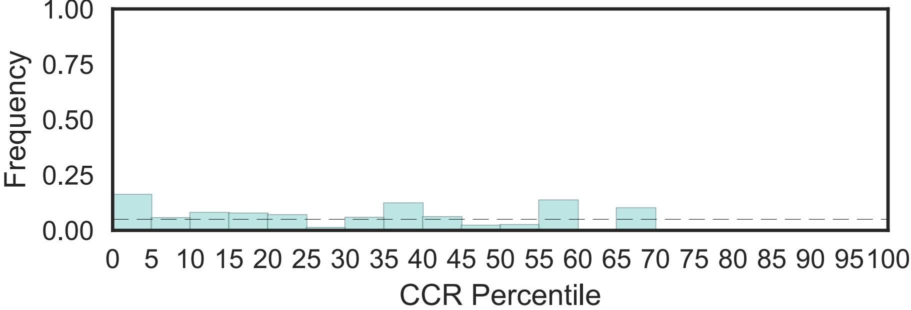

Domain of unknown function (DUF4596)
(DUF4596, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4597)
(DUF4597, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

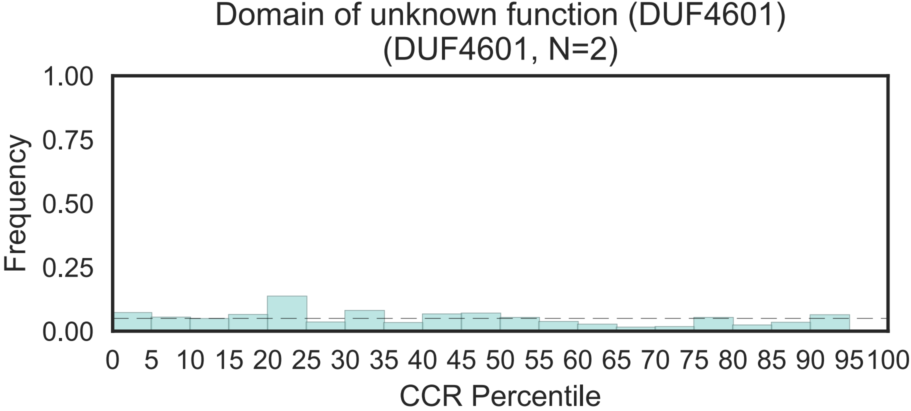

Domain of unknown function (DUF4598)
(DUF4598, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

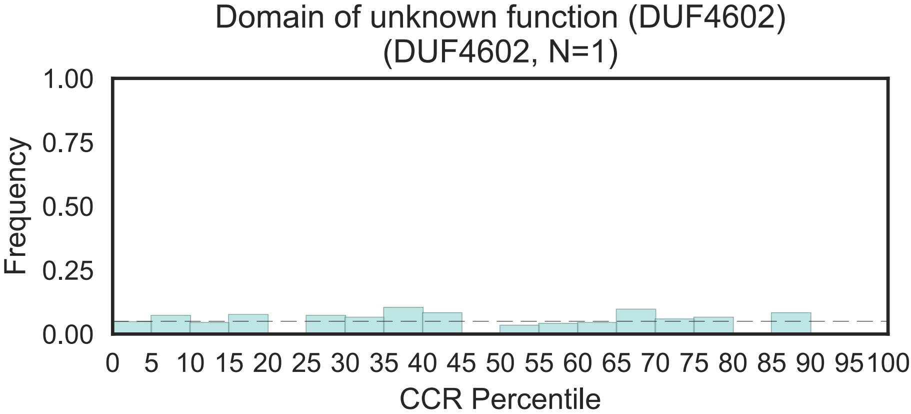


Domain of unknown function (DUF4599)
(DUF4599, N=10)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

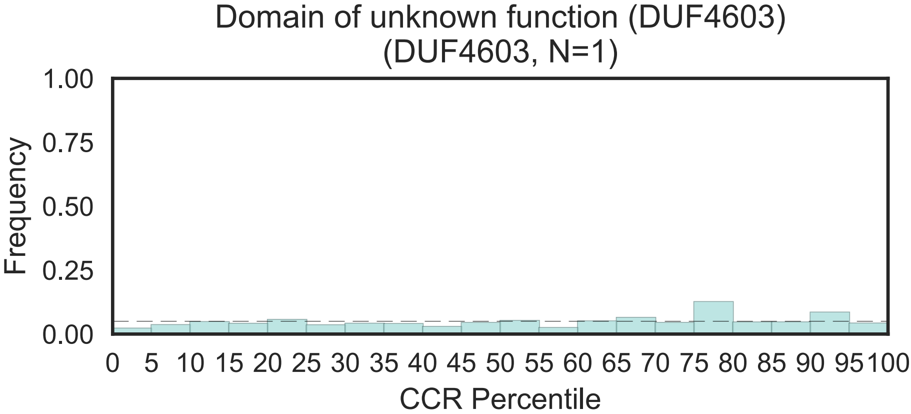


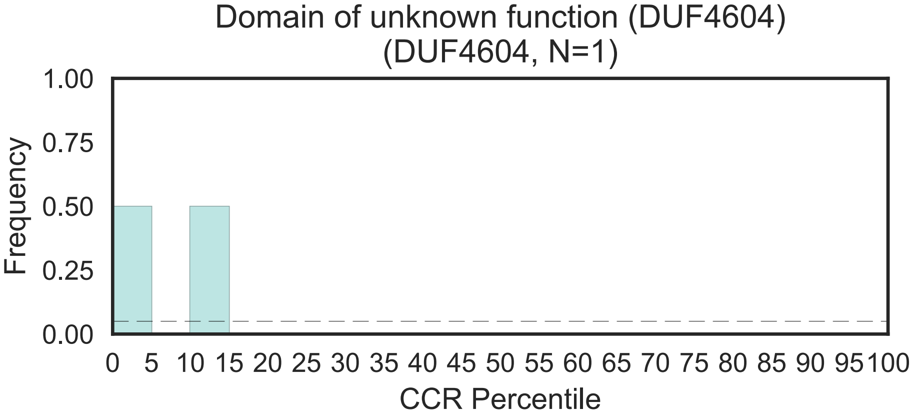
Domain of unknown function (DUF4600)
(DUF4600, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

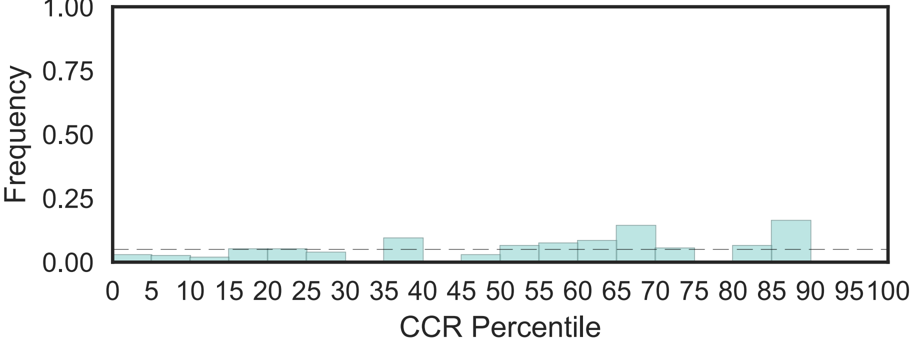

Domain of unknown function (DUF4601)
(DUF4601, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



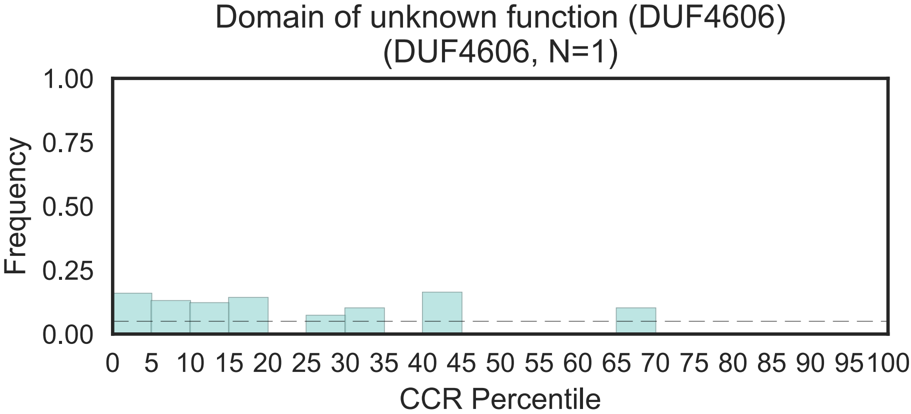
Domain of unknown function (DUF4602)
(DUF4602, N=1)

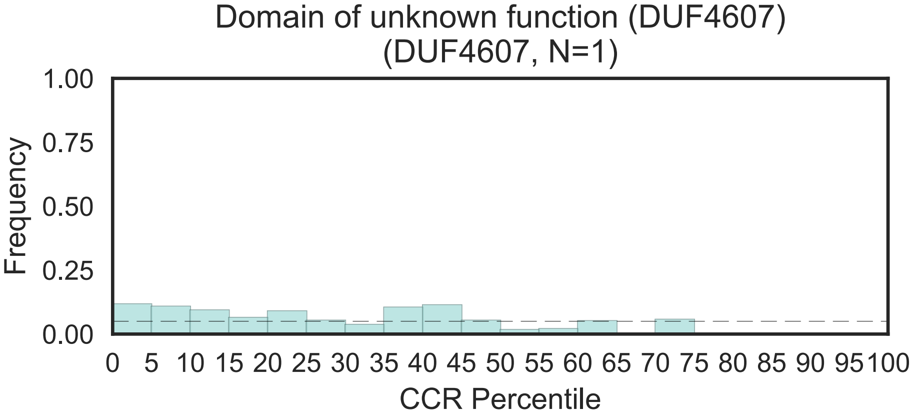

Domain of unknown function (DUF4603)
(DUF4603, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

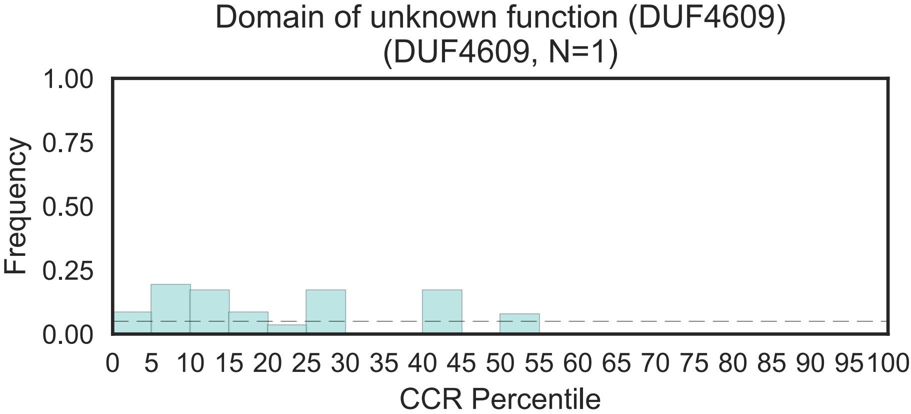

Domain of unknown function (DUF4604)
(DUF4604, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



Domain of unknown function (DUF4605)
(DUF4605, N=2)


Domain of unknown function (DUF4606)
(DUF4606, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4607)
(DUF4607, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4609)
(DUF4609, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
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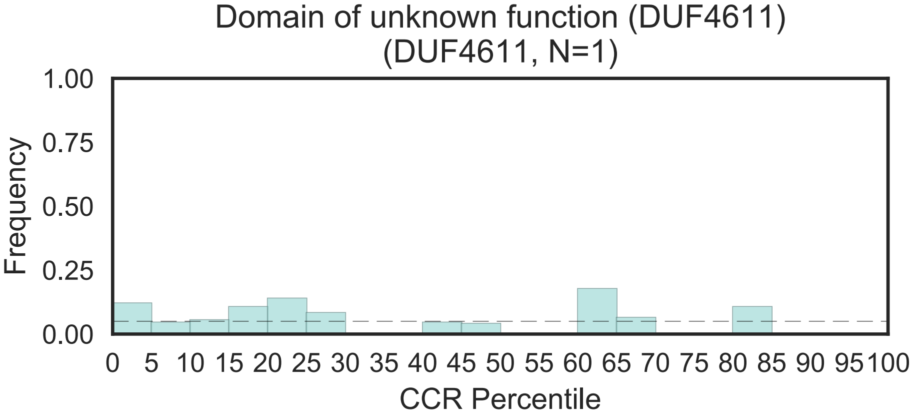
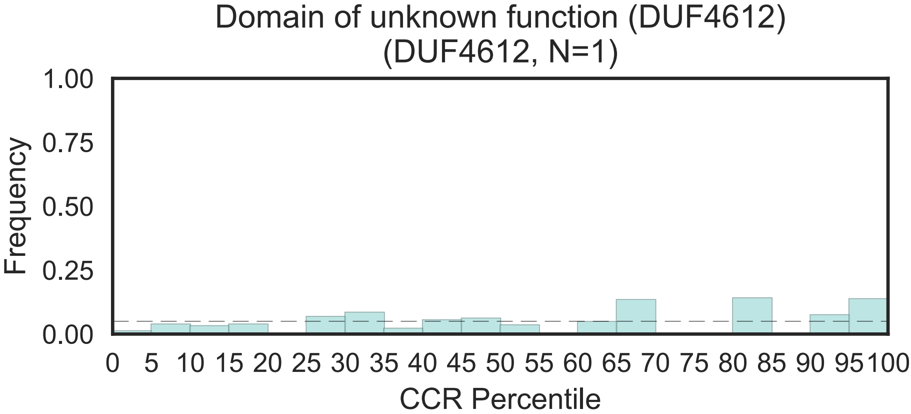
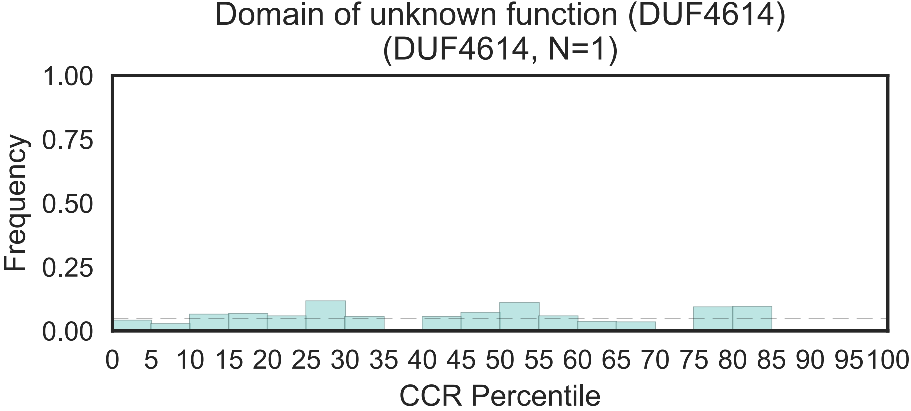
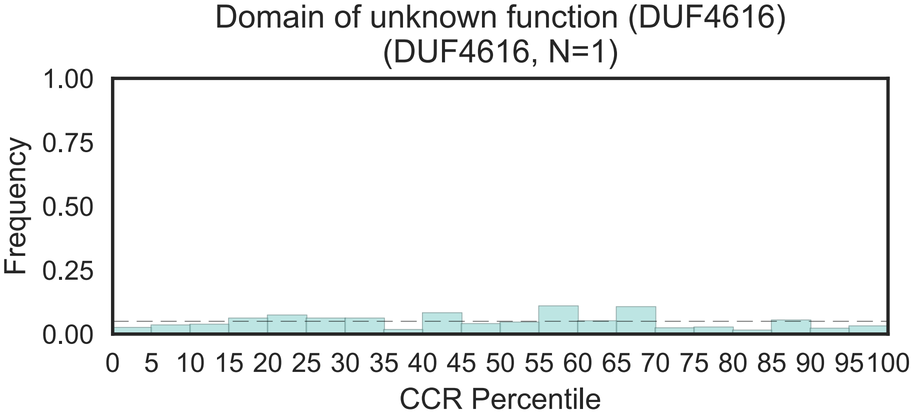
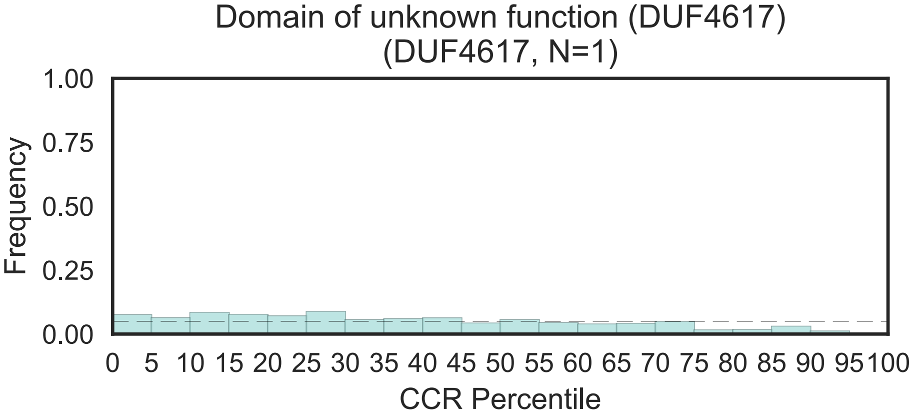
75
80
85
90
95
100
CCR Percentile

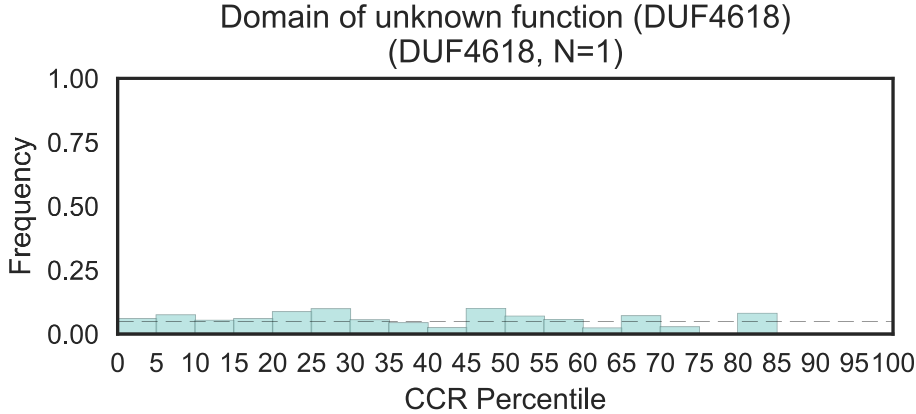

Domain of unknown function (DUF4611)
(DUF4611, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

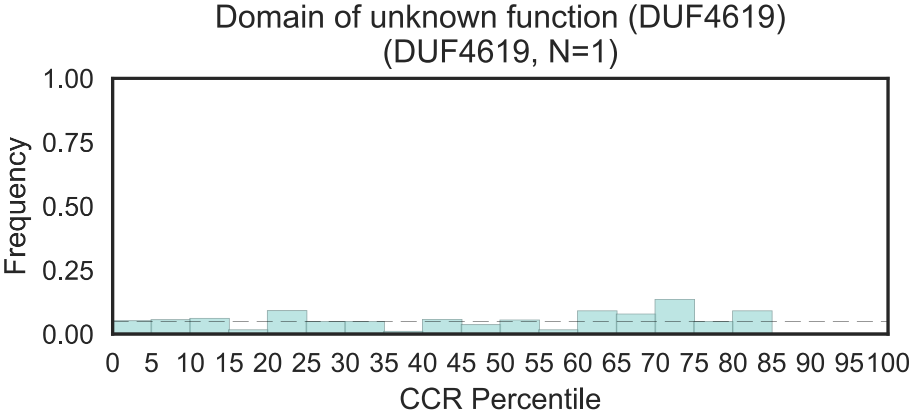

Domain of unknown function (DUF4612)
(DUF4612, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4614)
(DUF4614, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4616)
(DUF4616, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4617)
(DUF4617, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4618)
(DUF4618, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



Domain of unknown function (DUF4619)
(DUF4619, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
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20
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35
40
45
50
55
60
65
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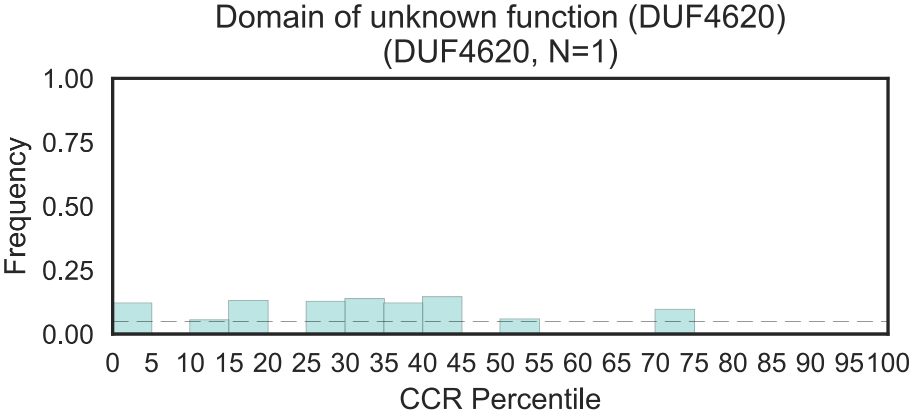
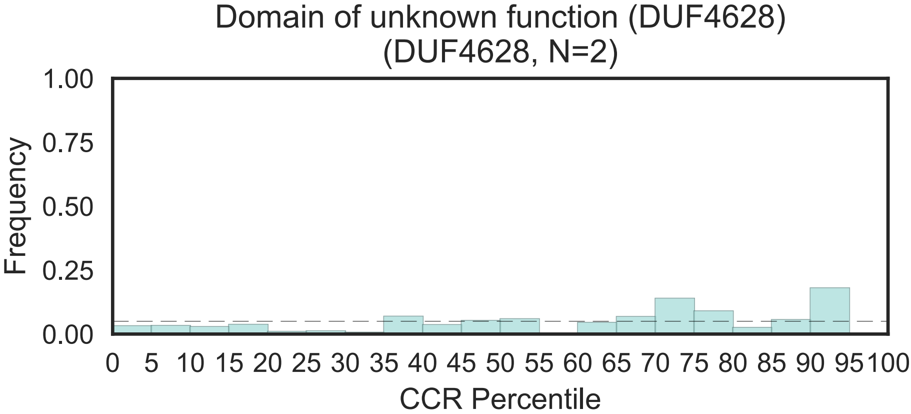
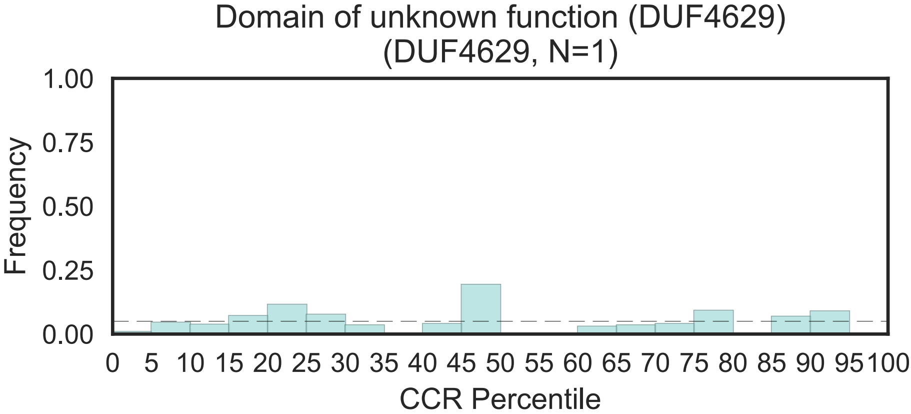
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4620)
(DUF4620, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4628)
(DUF4628, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4629)
(DUF4629, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
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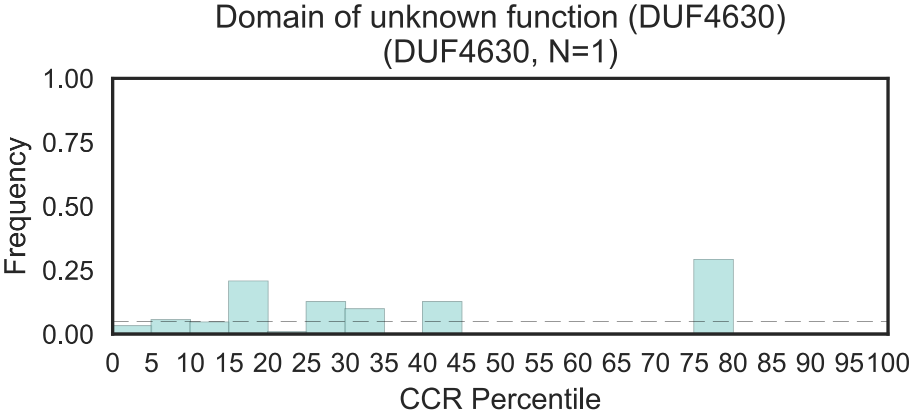
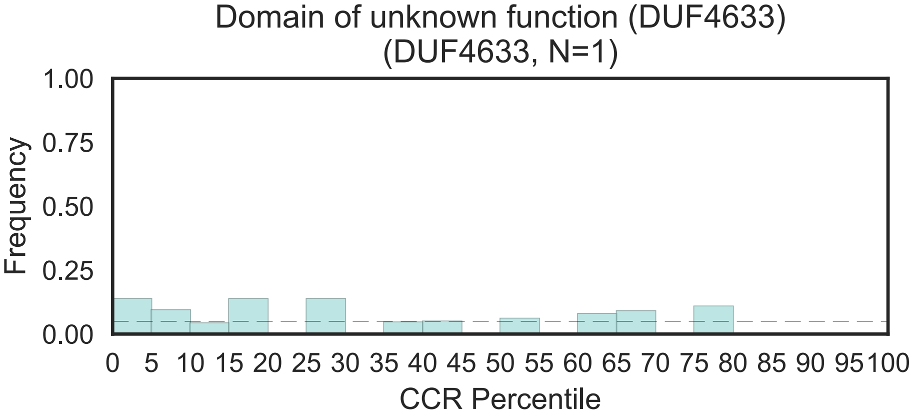
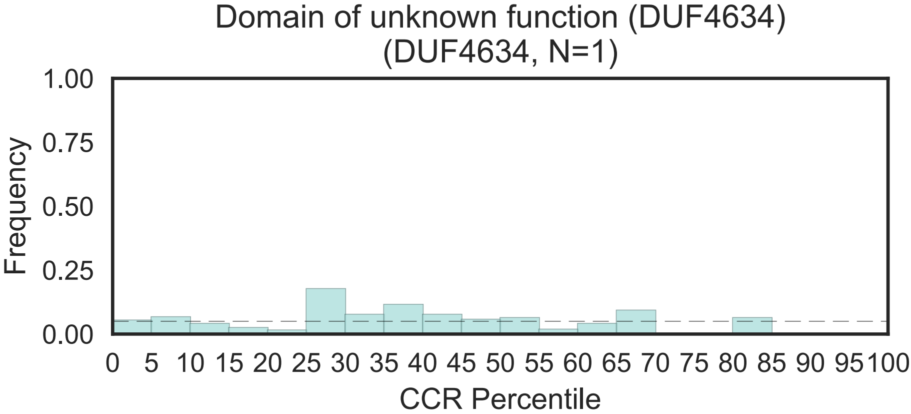
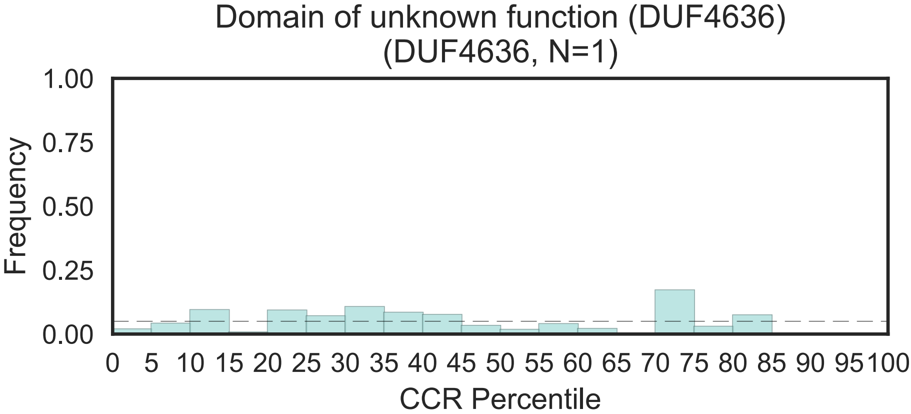
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

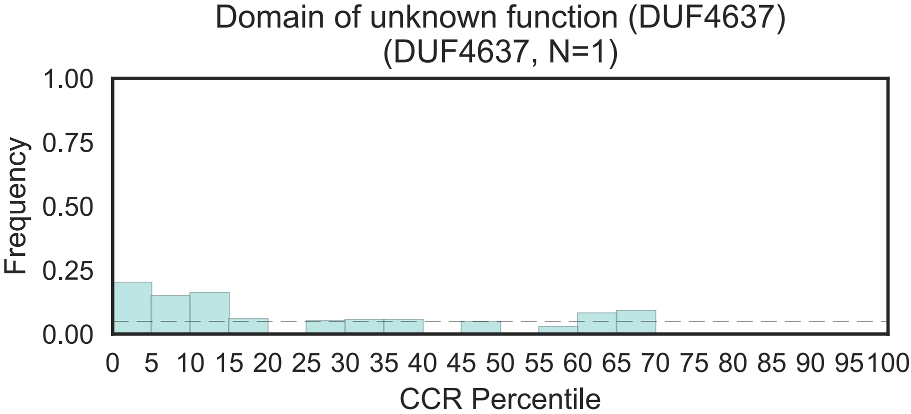

Domain of unknown function (DUF4630)
(DUF4630, N=1)


Domain of unknown function (DUF4633)
(DUF4633, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4634)
(DUF4634, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



Domain of unknown function (DUF4636)
(DUF4636, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4637)
(DUF4637, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
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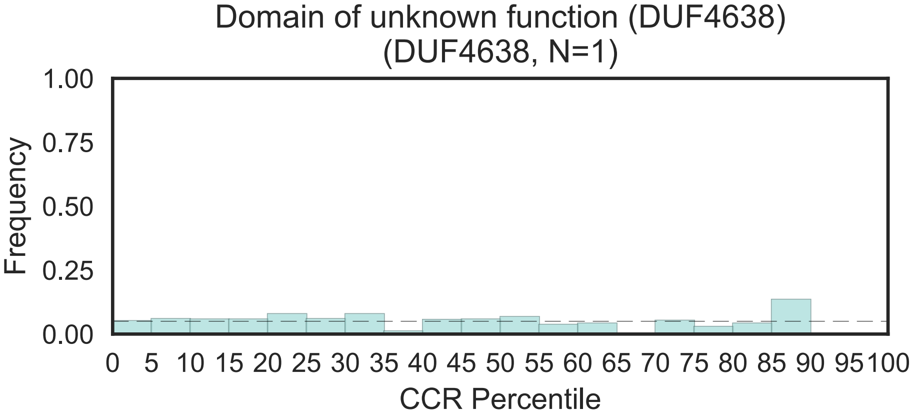
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4638)
(DUF4638, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
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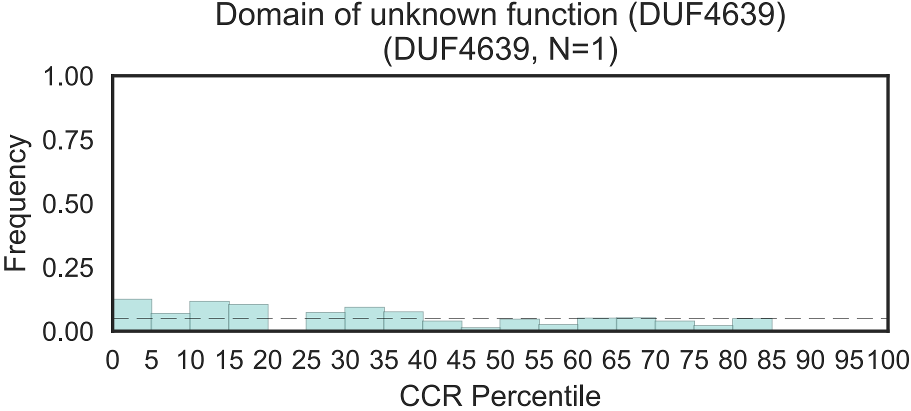
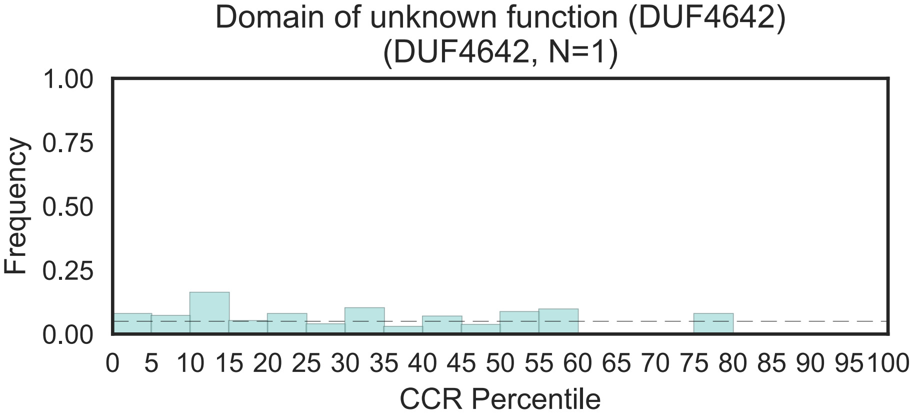
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4639)
(DUF4639, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


Domain of unknown function (DUF4642)
(DUF4642, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
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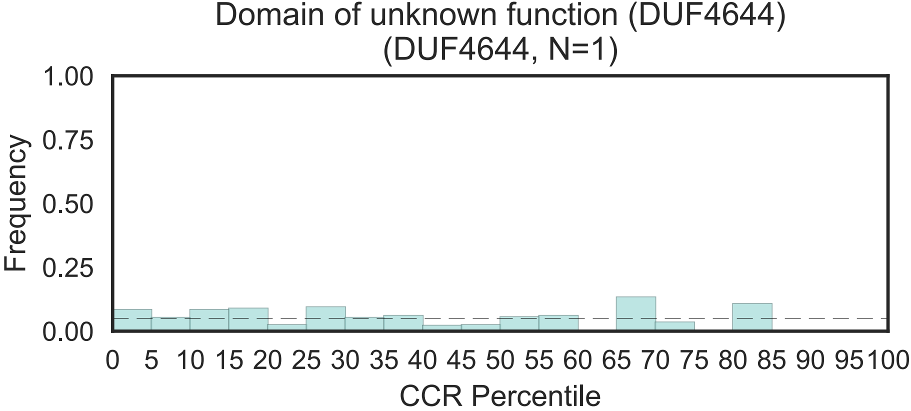
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4644)
(DUF4644, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
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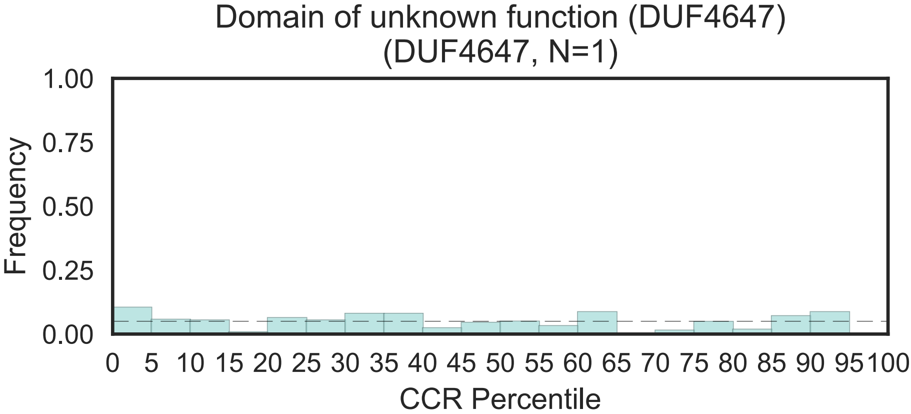
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4647)
(DUF4647, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
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20
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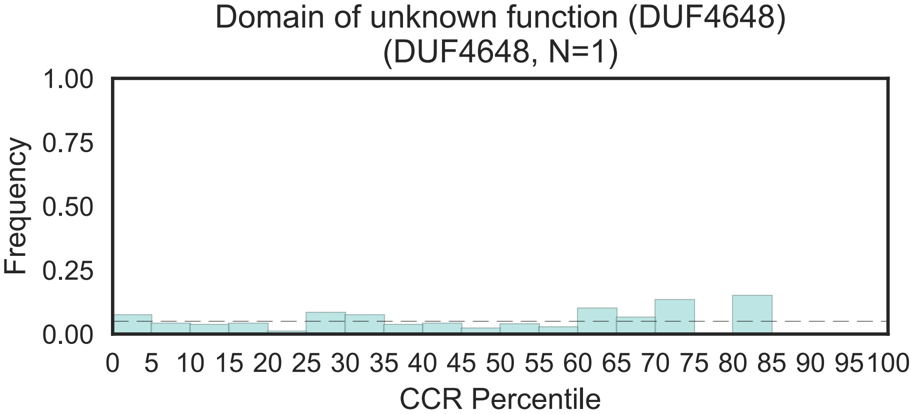
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4648)
(DUF4648, N=1)
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0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
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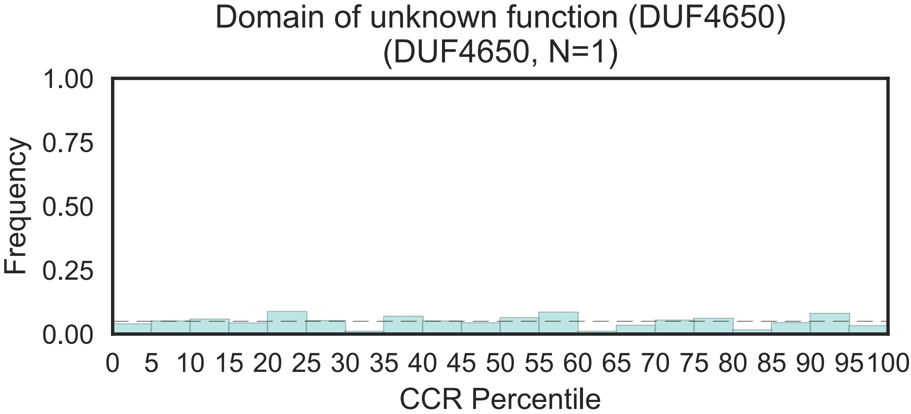
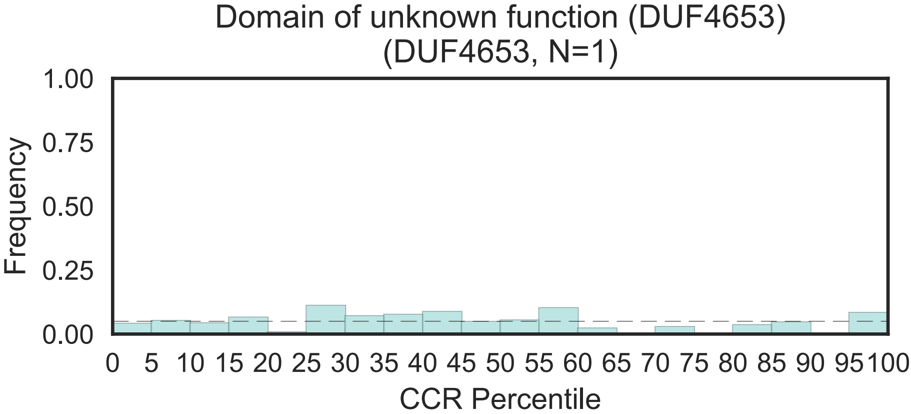
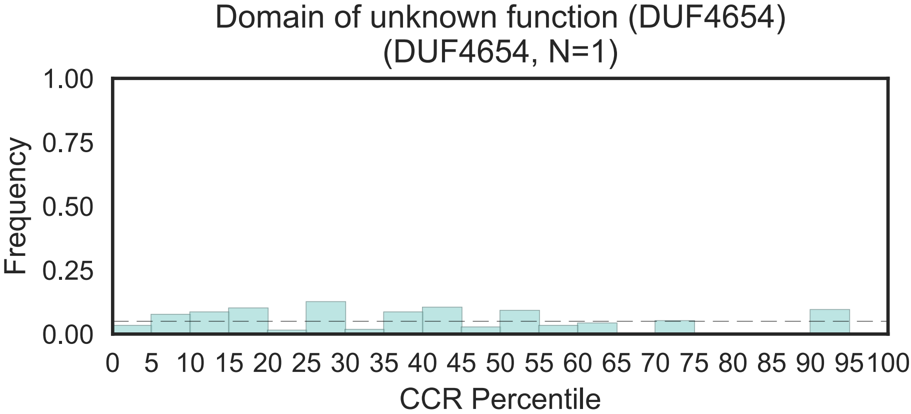
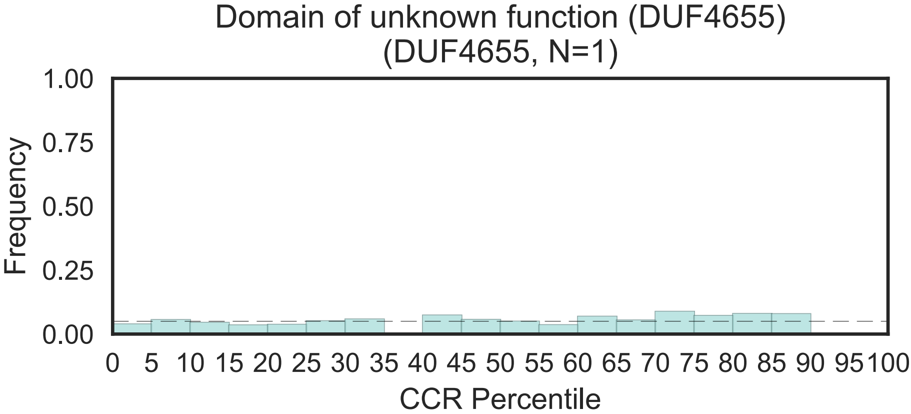
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4650)
(DUF4650, N=1)

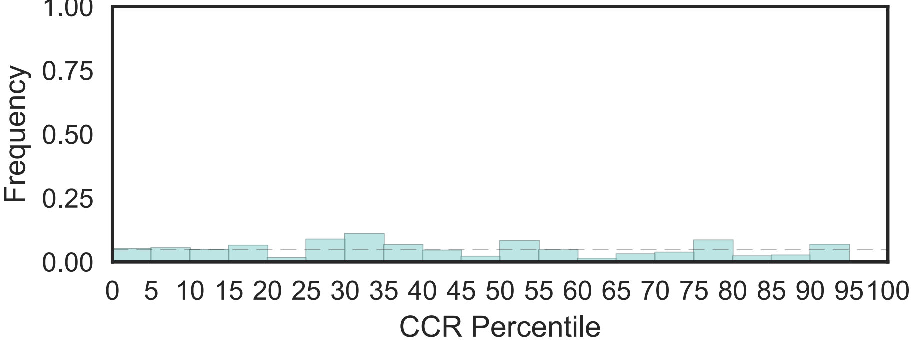

Domain of unknown function (DUF4653)
(DUF4653, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

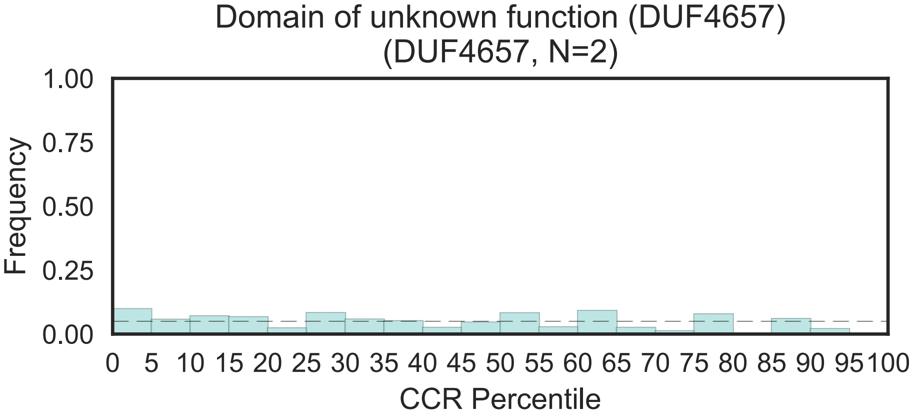

Domain of unknown function (DUF4654)
(DUF4654, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



Domain of unknown function (DUF4655)
(DUF4655, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Domain of unknown function (DUF4656) (DUF4656, N=1)




Domain of unknown function (DUF4657)
(DUF4657, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
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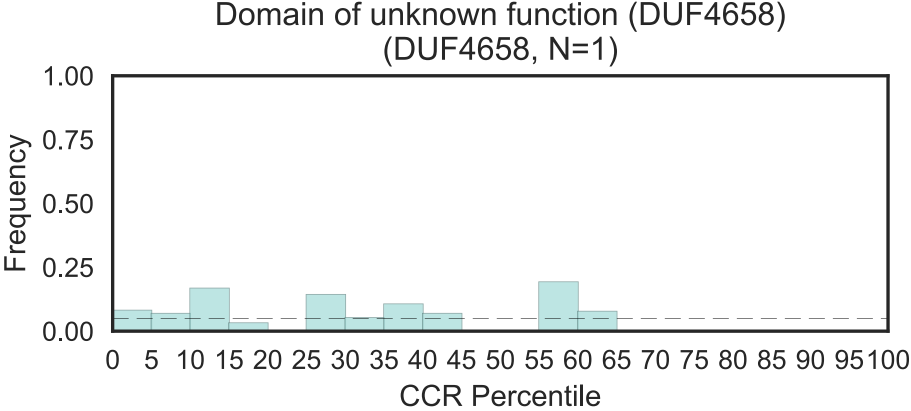
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4658)
(DUF4658, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
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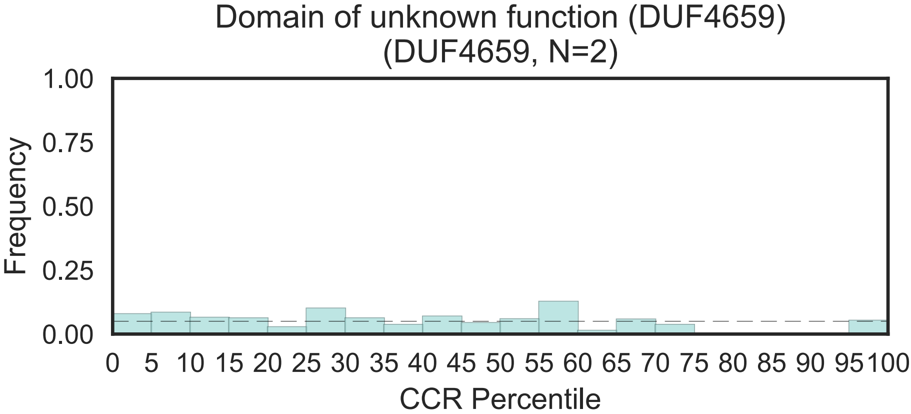
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4659)
(DUF4659, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
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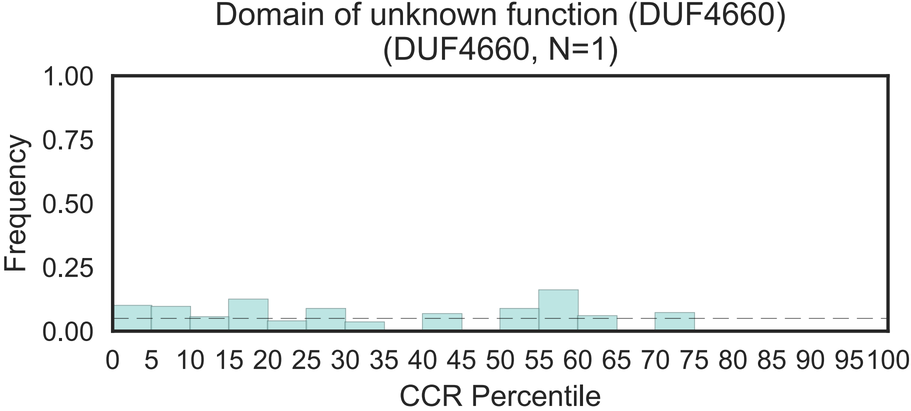
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4660)
(DUF4660, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
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20
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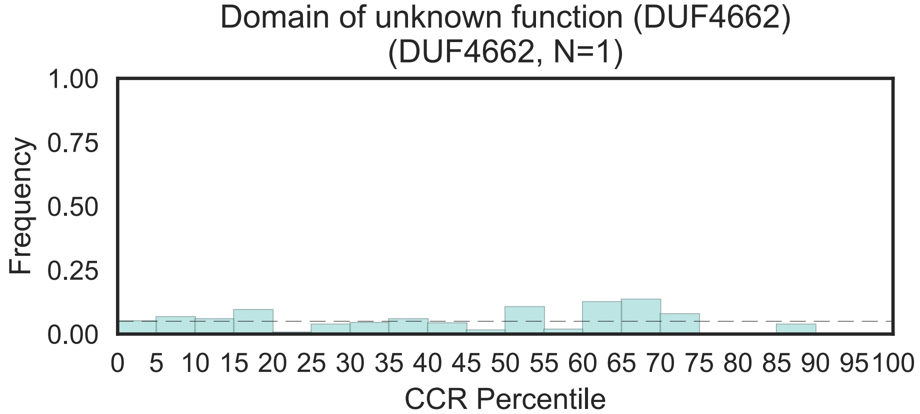
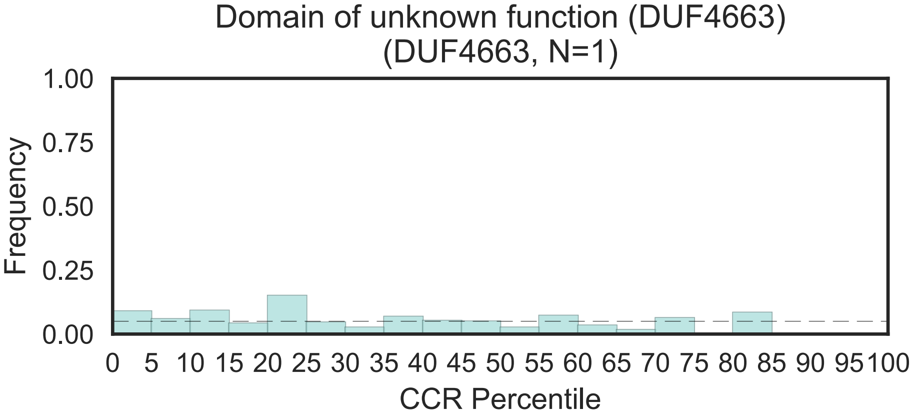
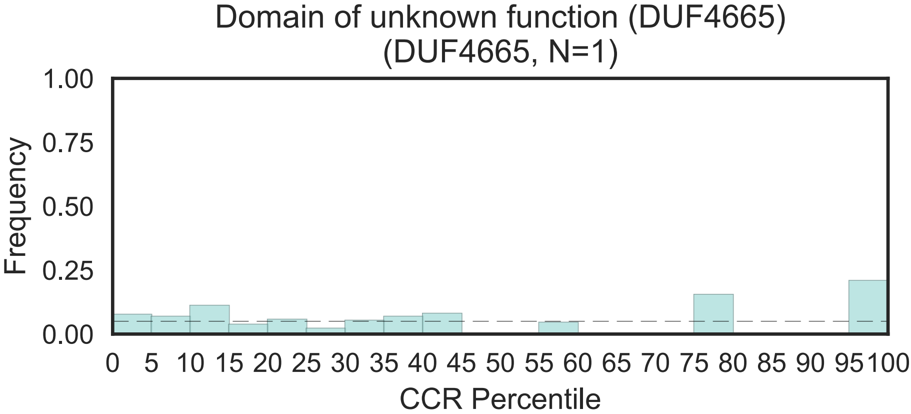
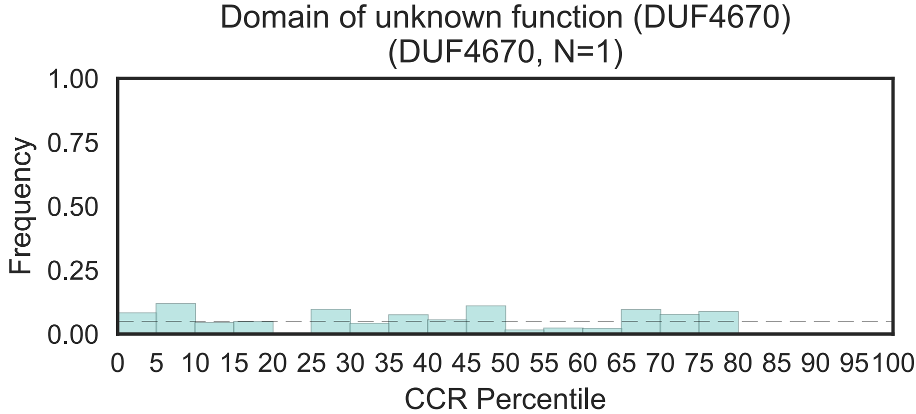
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

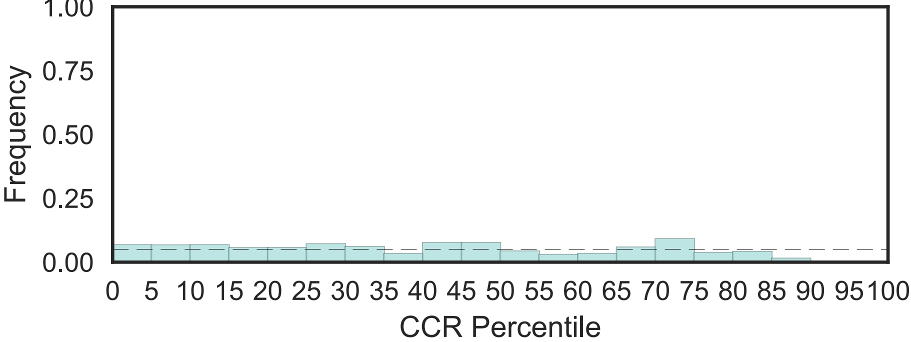

Domain of unknown function (DUF4662)
(DUF4662, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

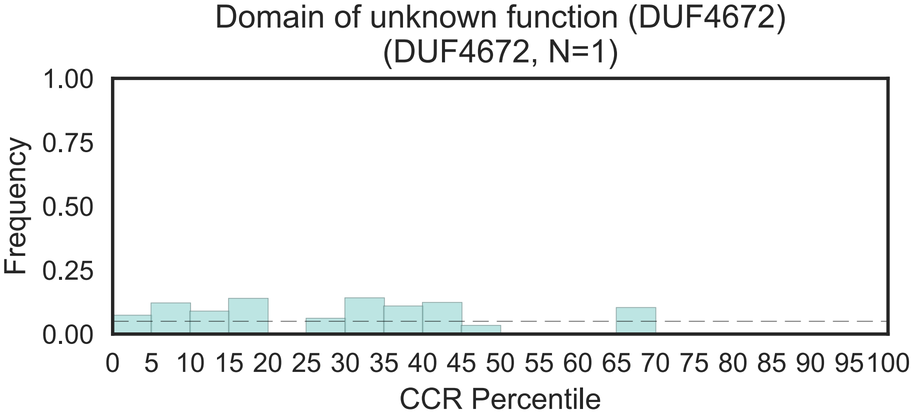

Domain of unknown function (DUF4663)
(DUF4663, N=1)

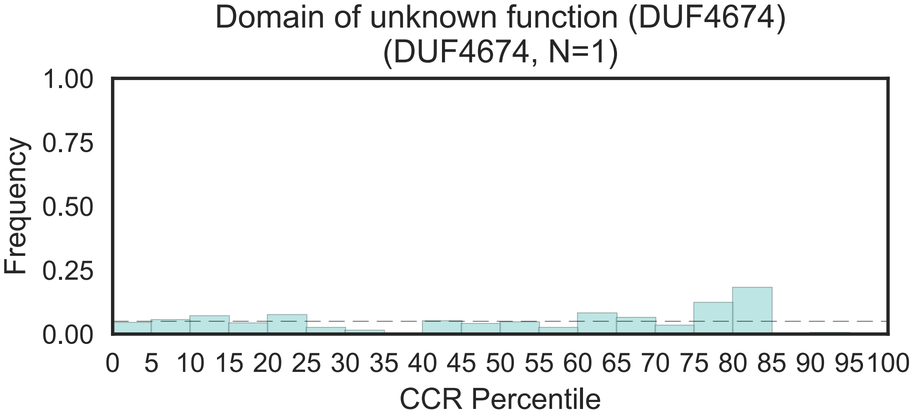

Domain of unknown function (DUF4665)
(DUF4665, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

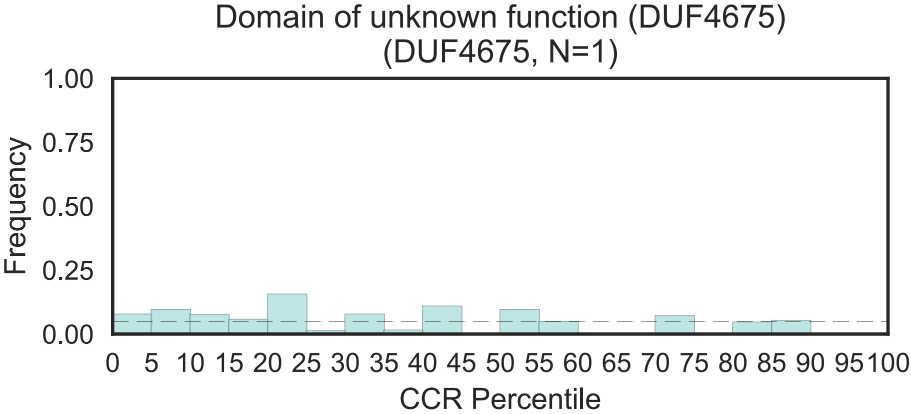

Domain of unknown function (DUF4670)
(DUF4670, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

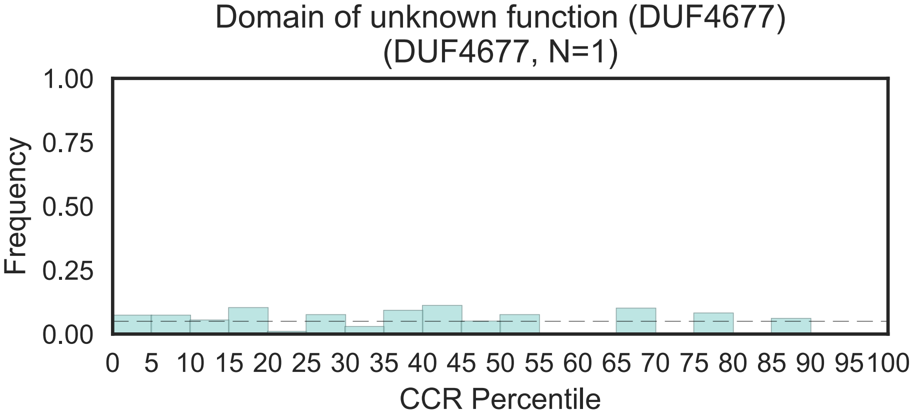
Domain of unknown function (DUF4671)
(DUF4671, N=1)




Domain of unknown function (DUF4672)
(DUF4672, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4674)
(DUF4674, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4675)
(DUF4675, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4677)
(DUF4677, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
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20
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35
40
45
50
55
60
65
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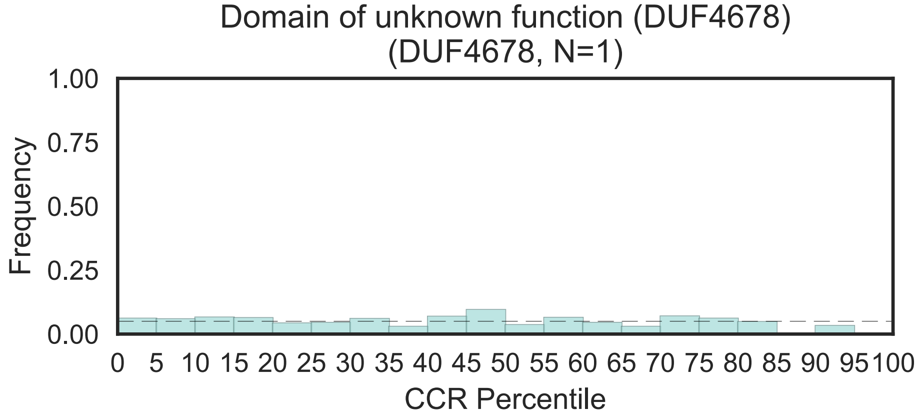
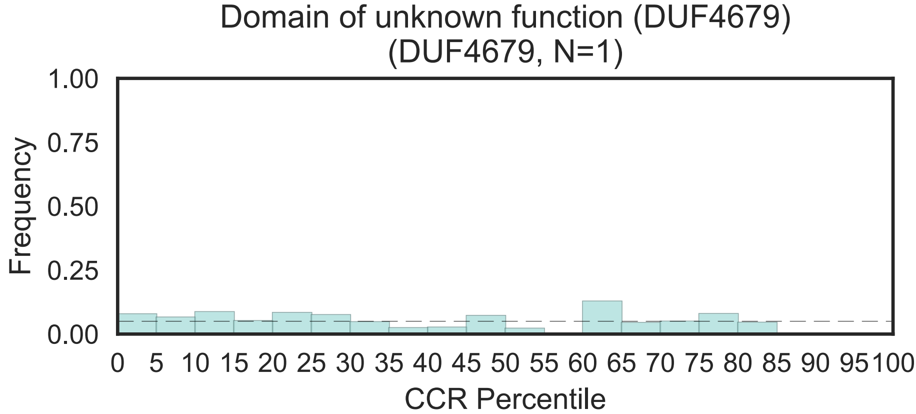
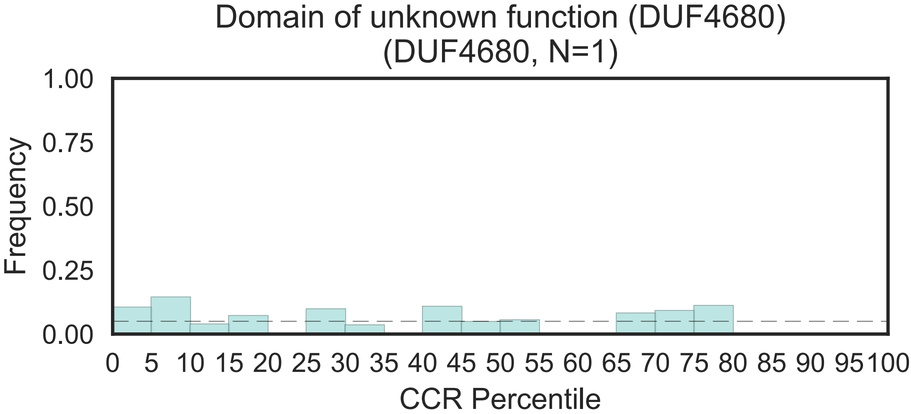
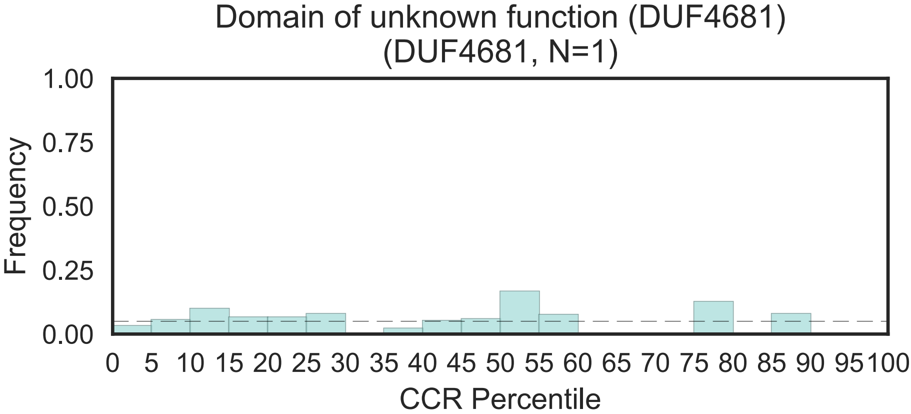
75
80
85
90
95
100
CCR Percentile

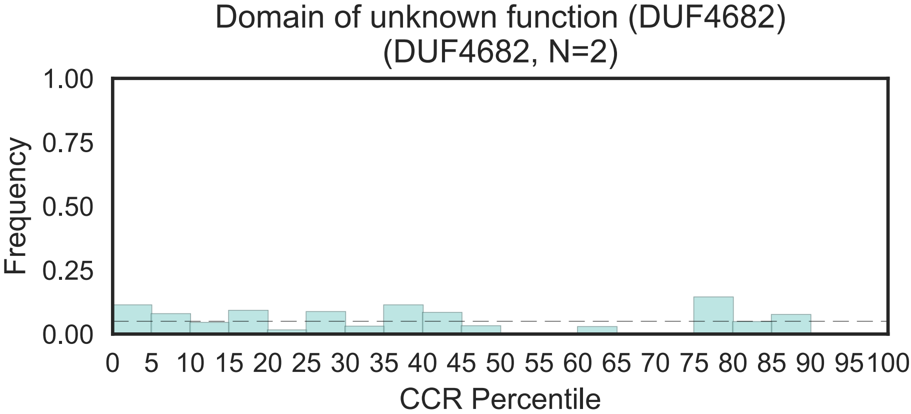

Domain of unknown function (DUF4678)
(DUF4678, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



Domain of unknown function (DUF4679)
(DUF4679, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4680)
(DUF4680, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4681)
(DUF4681, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4682)
(DUF4682, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
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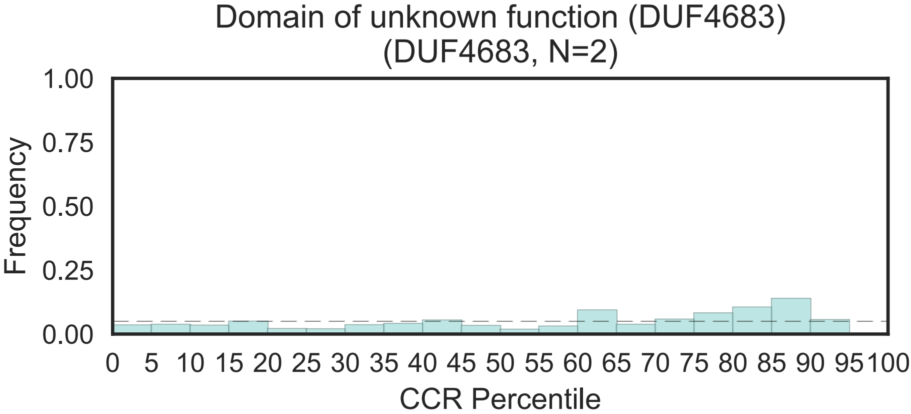
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4683)
(DUF4683, N=2)
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0.75
0.50
0.25
0.00
Frequency
0
5
10
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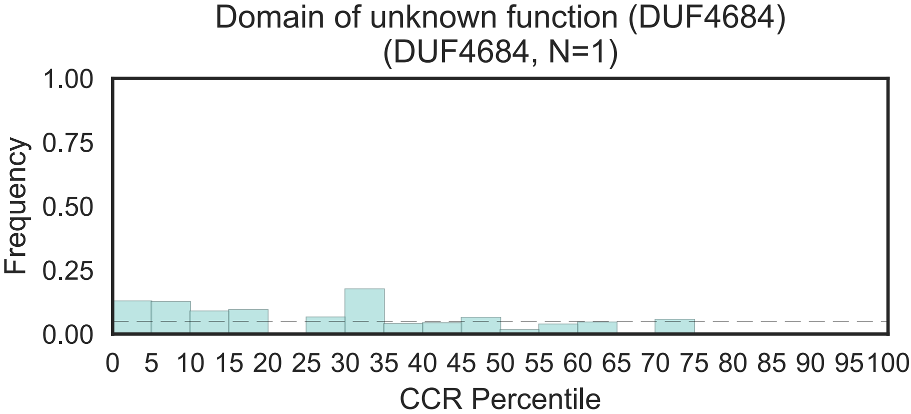
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4684)
(DUF4684, N=1)
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0.75
0.50
0.25
0.00
Frequency
0
5
10
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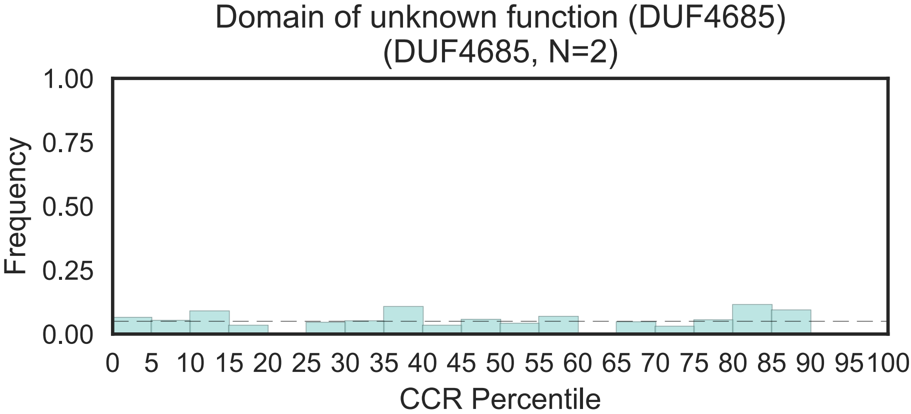
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4685)
(DUF4685, N=2)
Frequency
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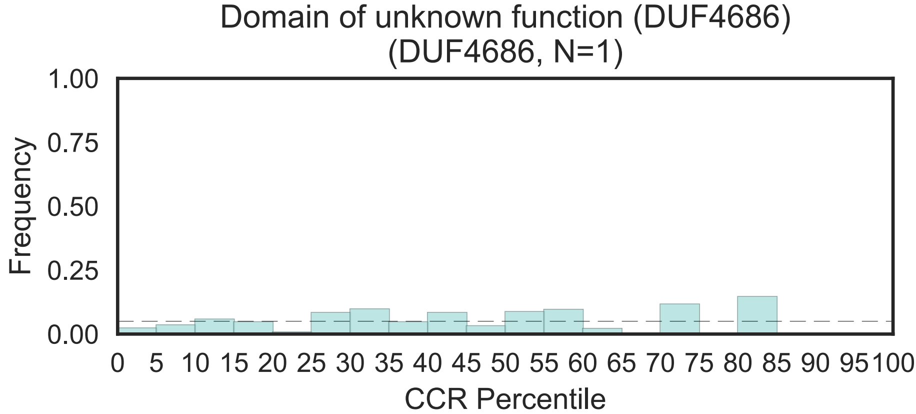
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


Domain of unknown function (DUF4686)
(DUF4686, N=1)
Frequency
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0.25
0.00
0
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20
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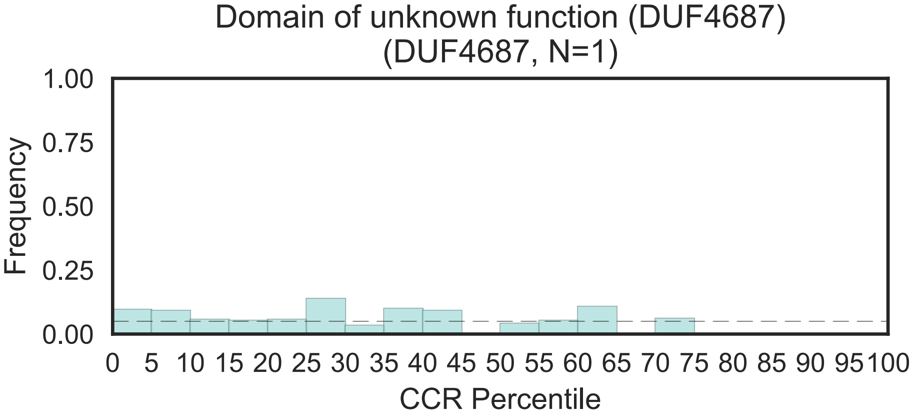
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4687)
(DUF4687, N=1)
Frequency
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0.00
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50
55
60
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75
80
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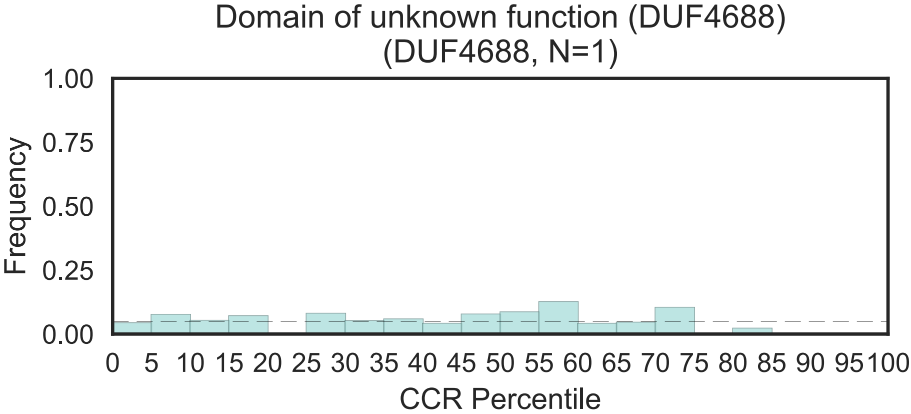
95
100
CCR Percentile


Domain of unknown function (DUF4688)
(DUF4688, N=1)
Frequency
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0.25
0.00
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50
55
60
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75
80
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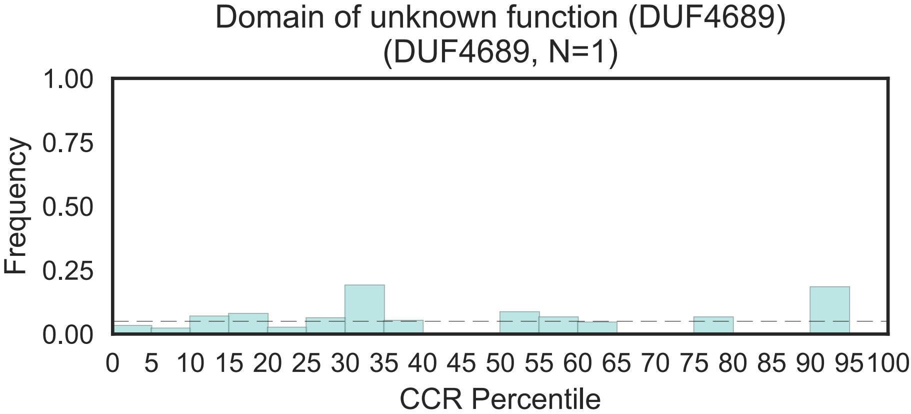
95
100
CCR Percentile


Domain of unknown function (DUF4689)
(DUF4689, N=1)
Frequency
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0.00
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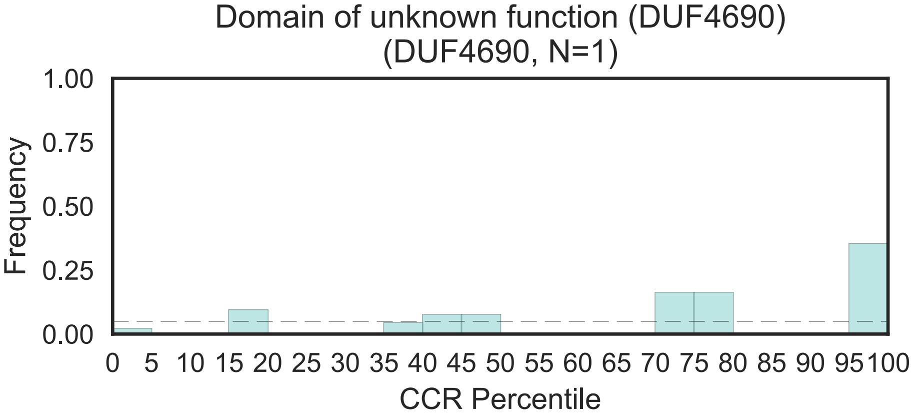
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4690)
(DUF4690, N=1)
Frequency
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0.00
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40
45
50
55
60
65
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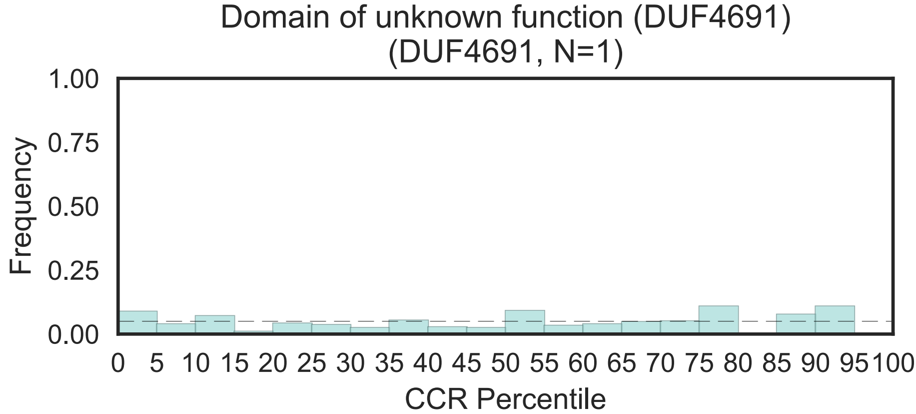
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4691)
(DUF4691, N=1)
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0.75
0.50
0.25
0.00
Frequency
0
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40
45
50
55
60
65
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75
80
85
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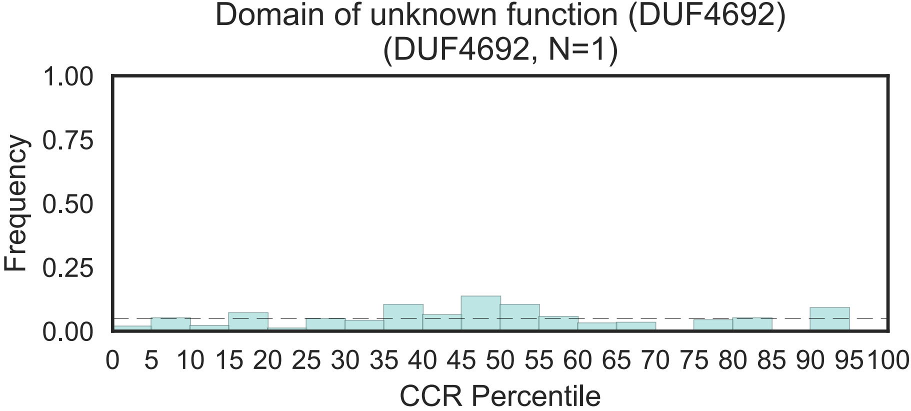
95
100
CCR Percentile


Domain of unknown function (DUF4692)
(DUF4692, N=1)
Frequency
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0.50
0.25
0.00
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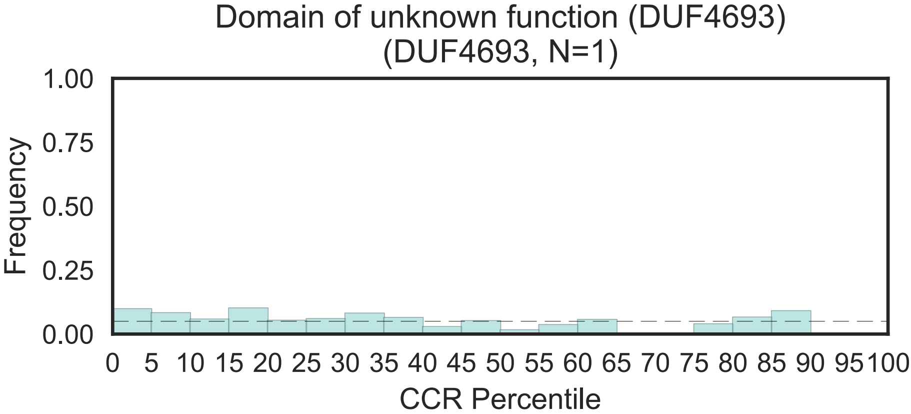
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4693)
(DUF4693, N=1)
Frequency
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0.50
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0.00
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50
55
60
65
70
75
80
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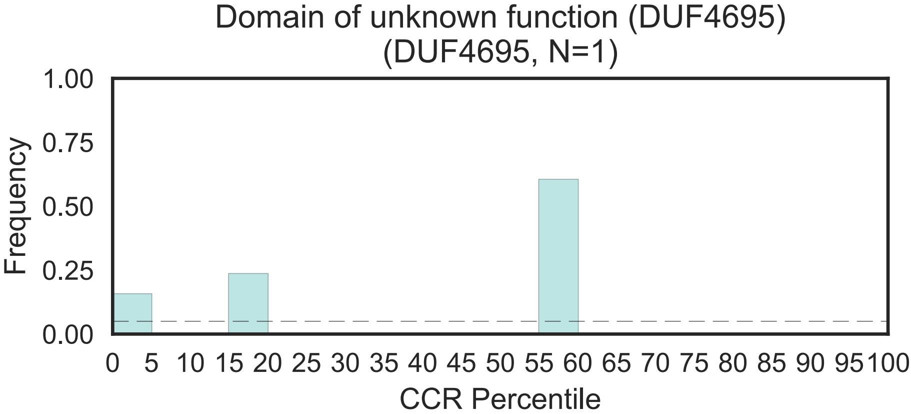
90
95
100
CCR Percentile


Domain of unknown function (DUF4695)
(DUF4695, N=1)
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0.75
0.50
0.25
0.00
Frequency
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50
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60
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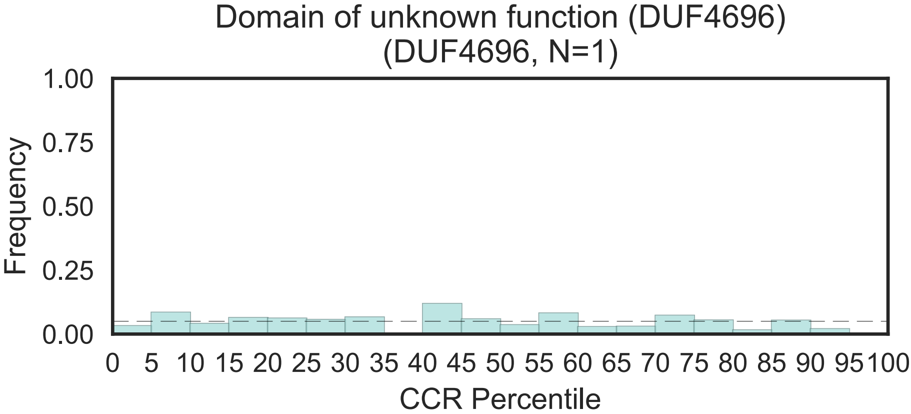
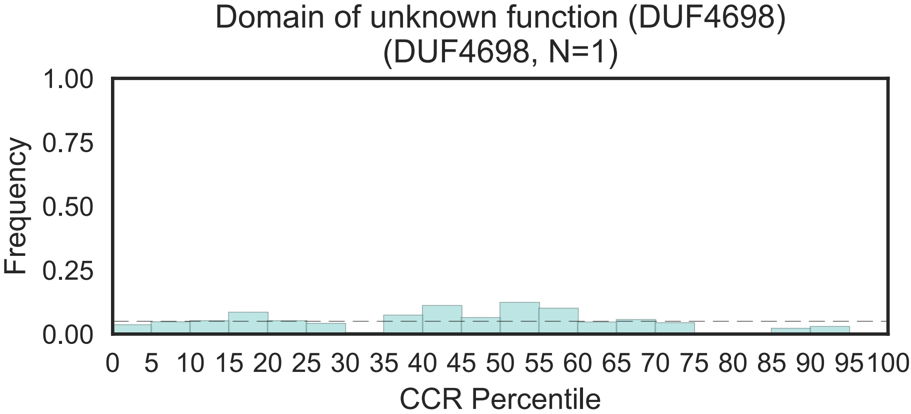
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4696)
(DUF4696, N=1)


Domain of unknown function (DUF4698)
(DUF4698, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
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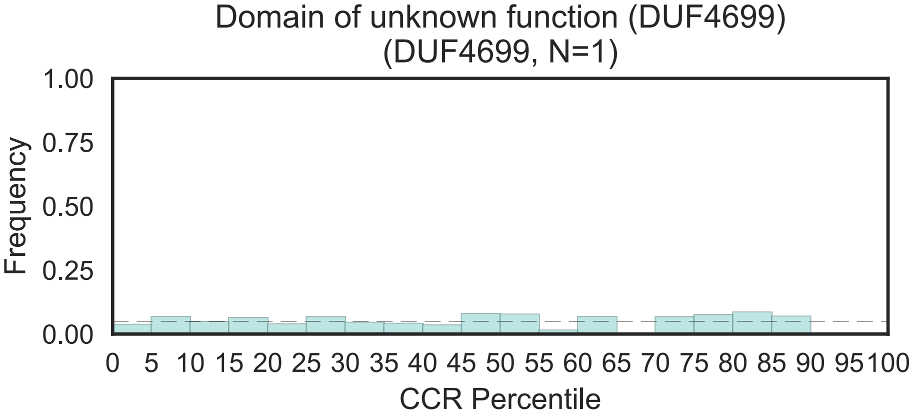
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4699)
(DUF4699, N=1)
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0.75
0.50
0.25
0.00
Frequency
0
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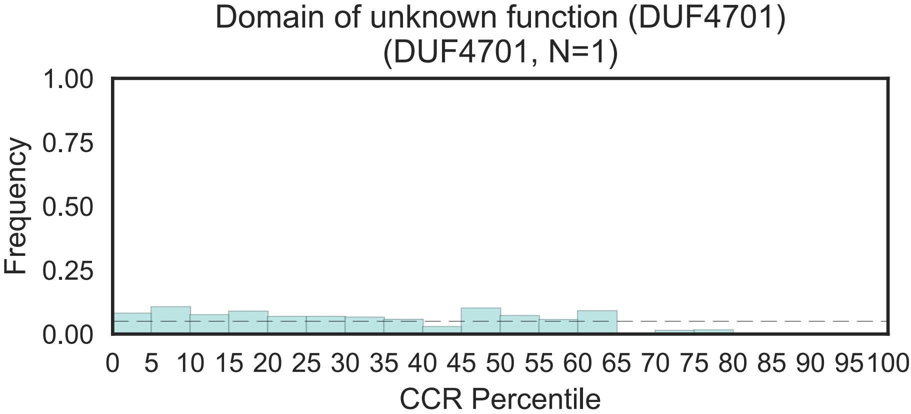
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4701)
(DUF4701, N=1)
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0.50
0.25
0.00
Frequency
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5
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35
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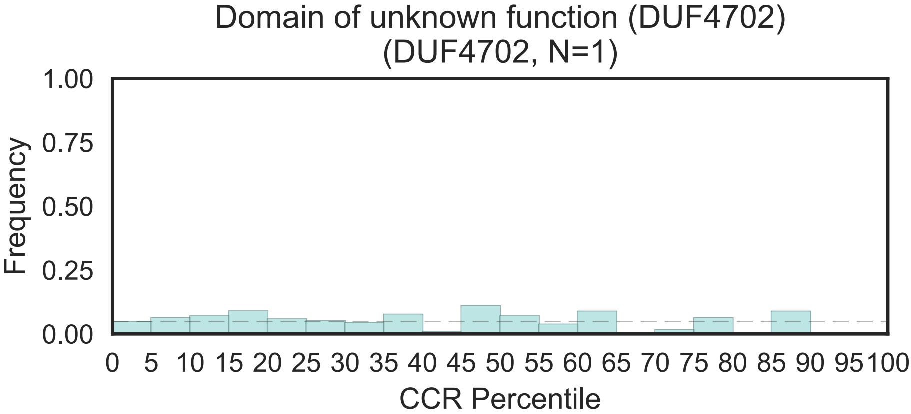
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4702)
(DUF4702, N=1)
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0.00
Frequency
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5
10
15
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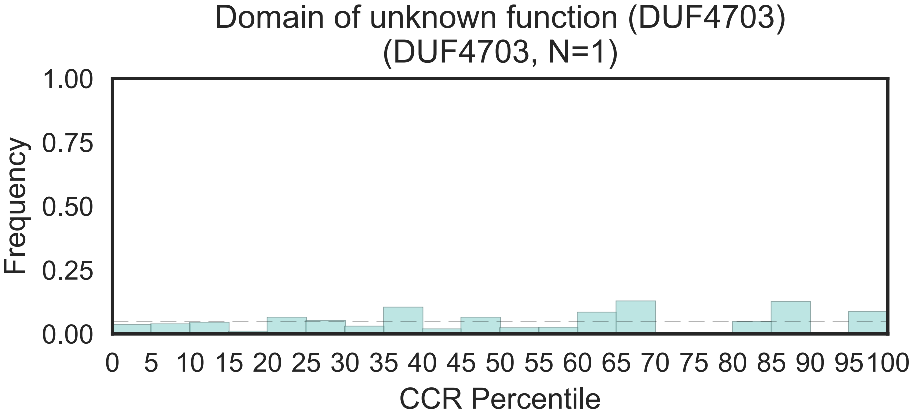
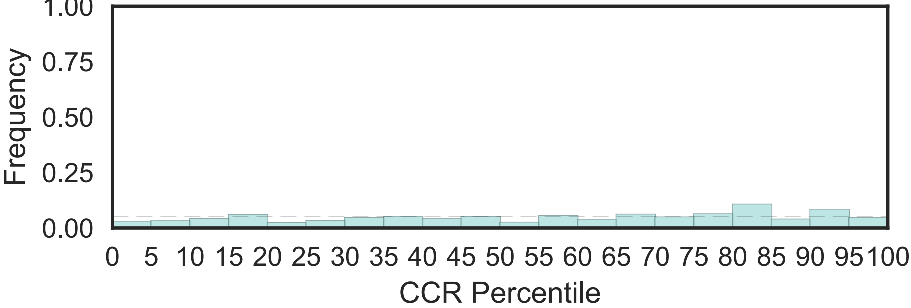
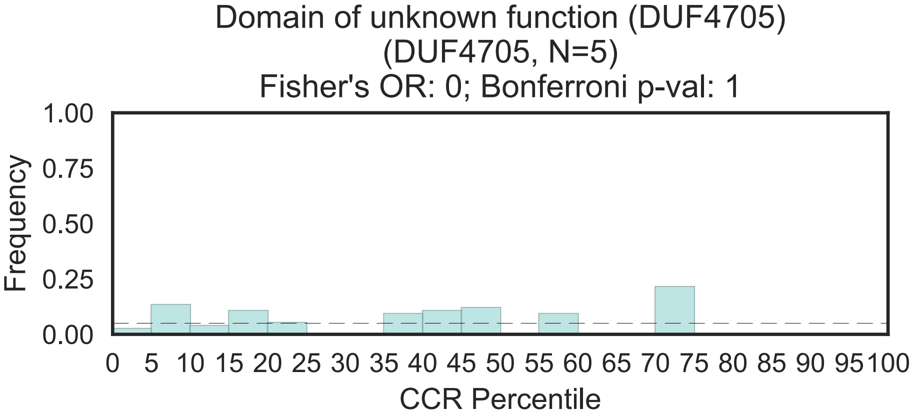
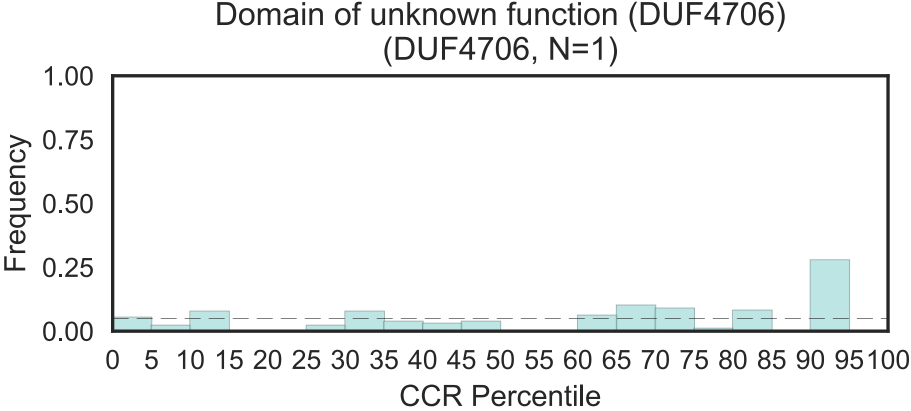
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

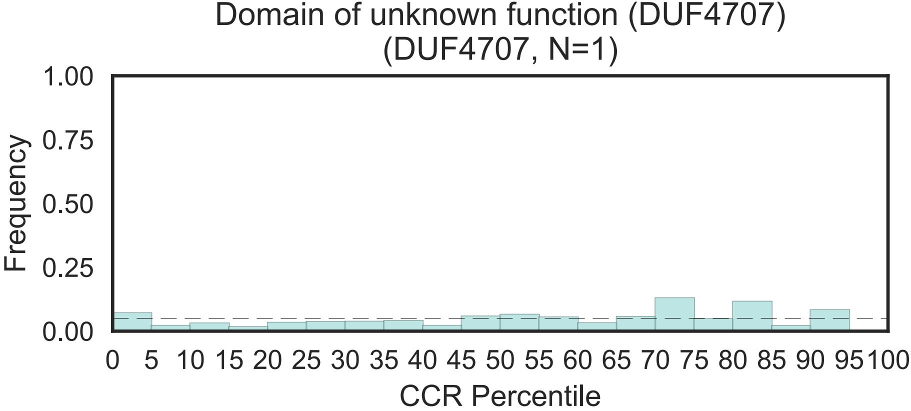

Domain of unknown function (DUF4703)
(DUF4703, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

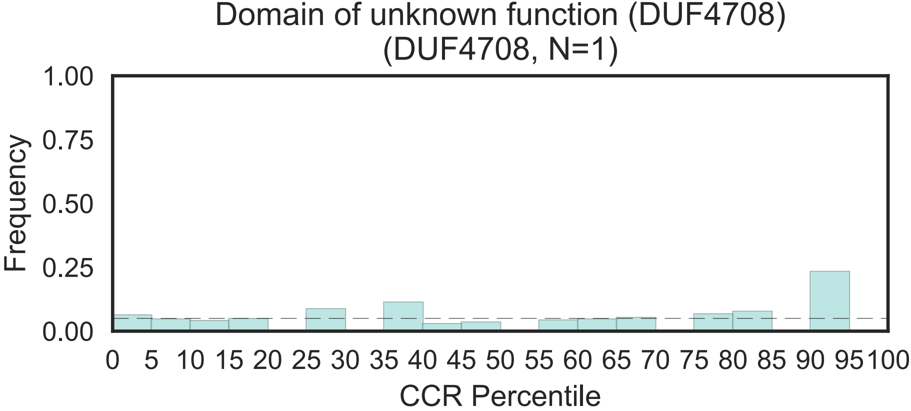
Domain of unknown function (DUF4704)
(DUF4704, N=5)
Fisher's OR: 0.835; Bonferroni p-val: 1

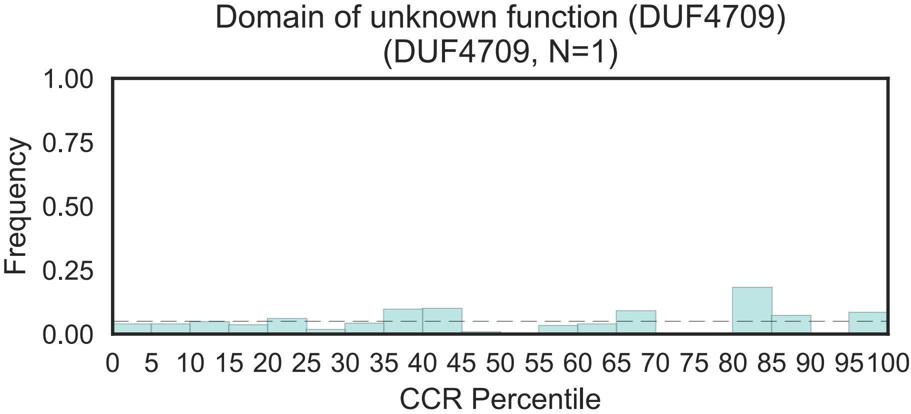


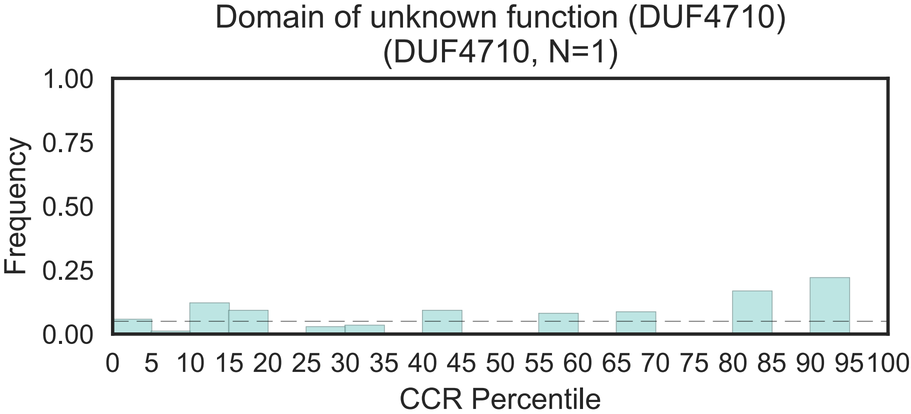

Domain of unknown function (DUF4705)
(DUF4705, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

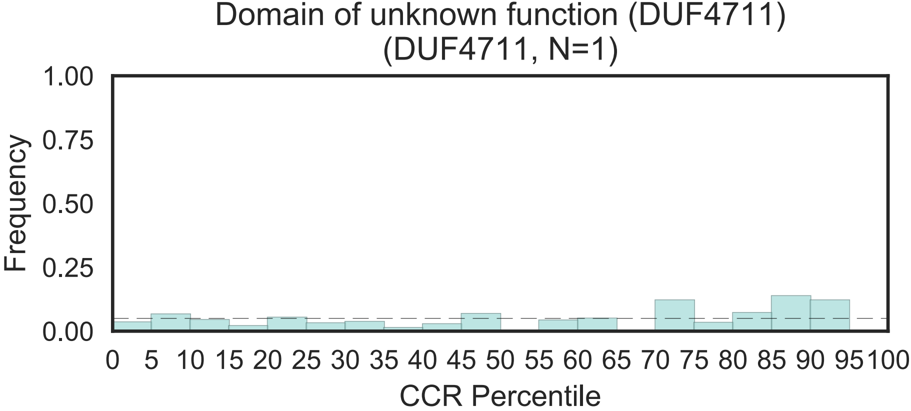

Domain of unknown function (DUF4706)
(DUF4706, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

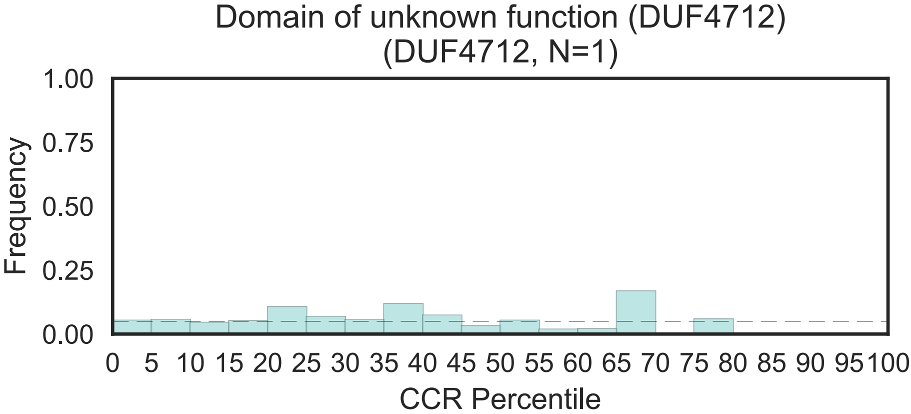

Domain of unknown function (DUF4707)
(DUF4707, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

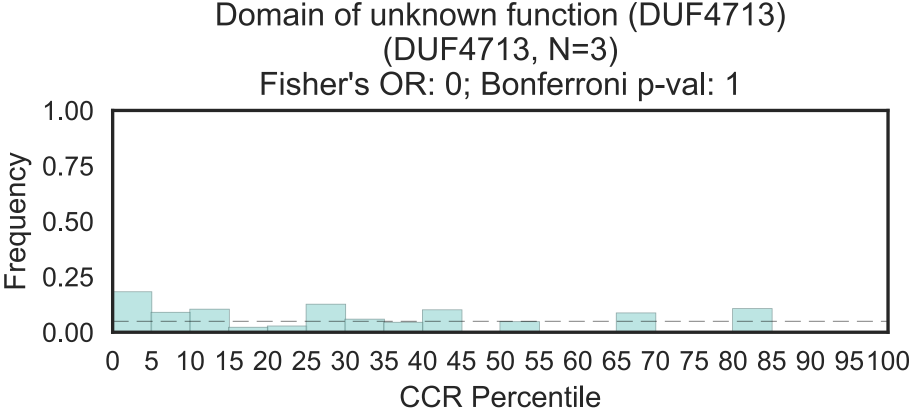

Domain of unknown function (DUF4708)
(DUF4708, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

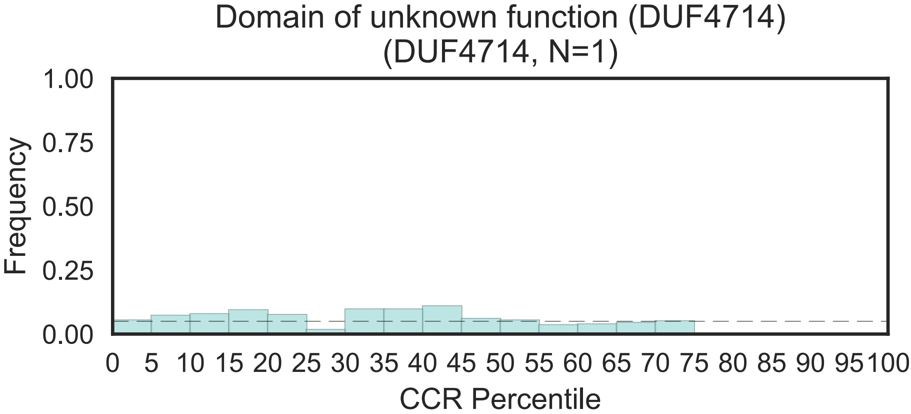

Domain of unknown function (DUF4709)
(DUF4709, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

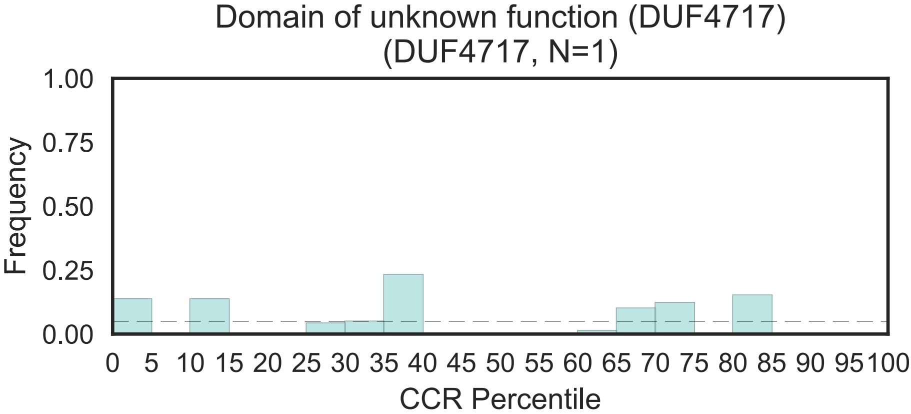

Domain of unknown function (DUF4710)
(DUF4710, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

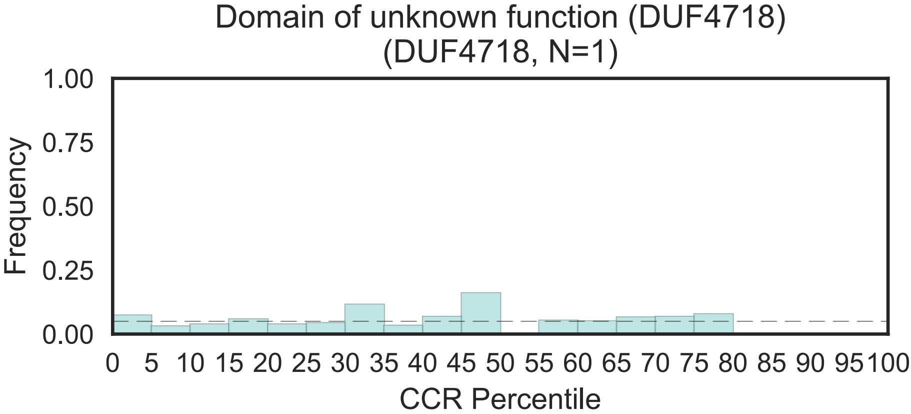

Domain of unknown function (DUF4711)
(DUF4711, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

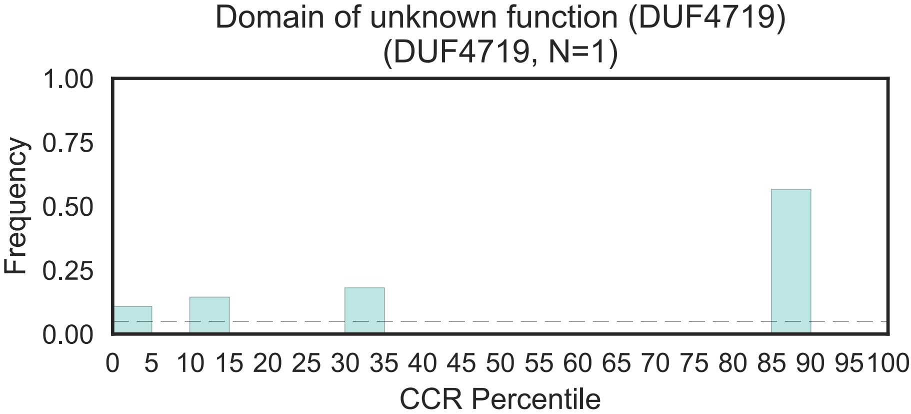

Domain of unknown function (DUF4712)
(DUF4712, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

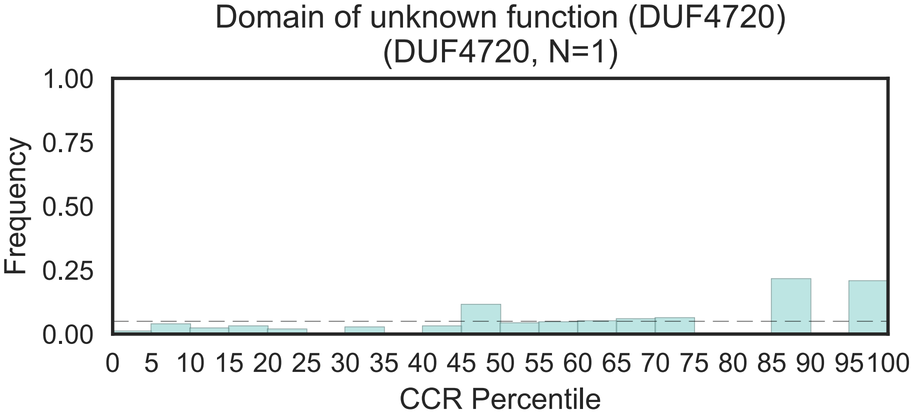

Domain of unknown function (DUF4713)
(DUF4713, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

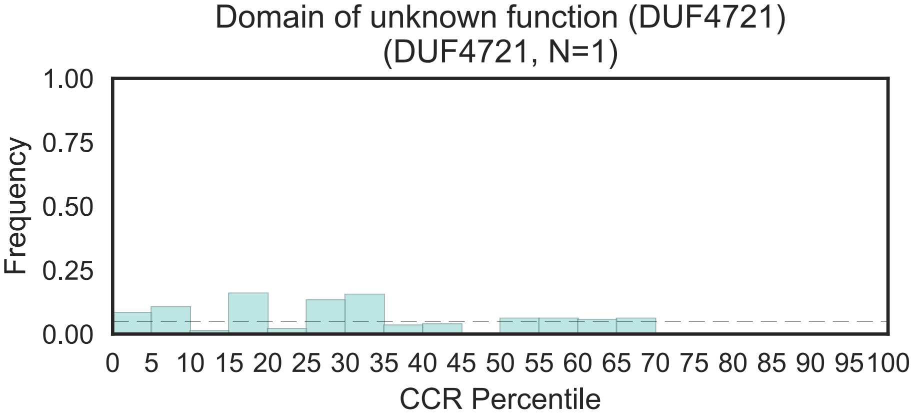

Domain of unknown function (DUF4714)
(DUF4714, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

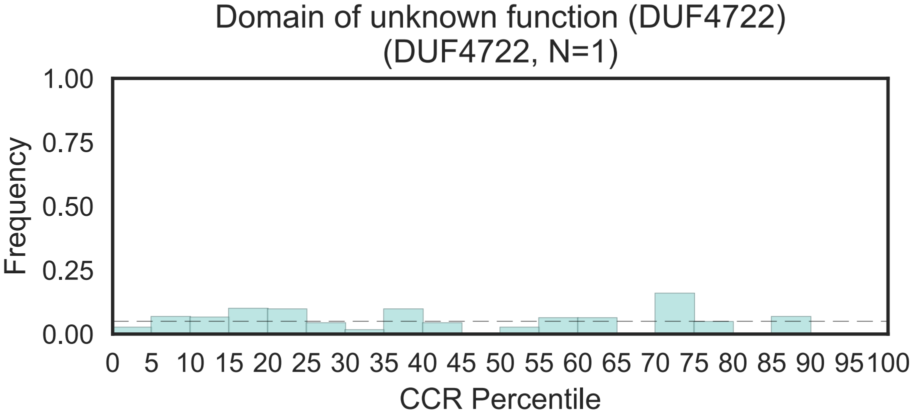

Domain of unknown function (DUF4717)
(DUF4717, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

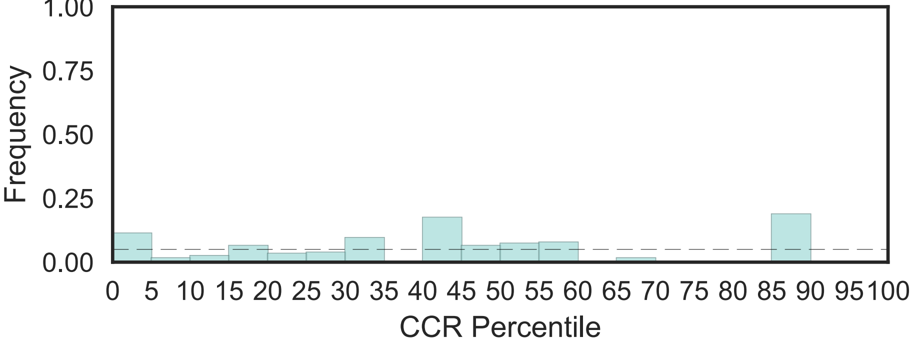
Domain of unknown function (DUF4718)
(DUF4718, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4719)
(DUF4719, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

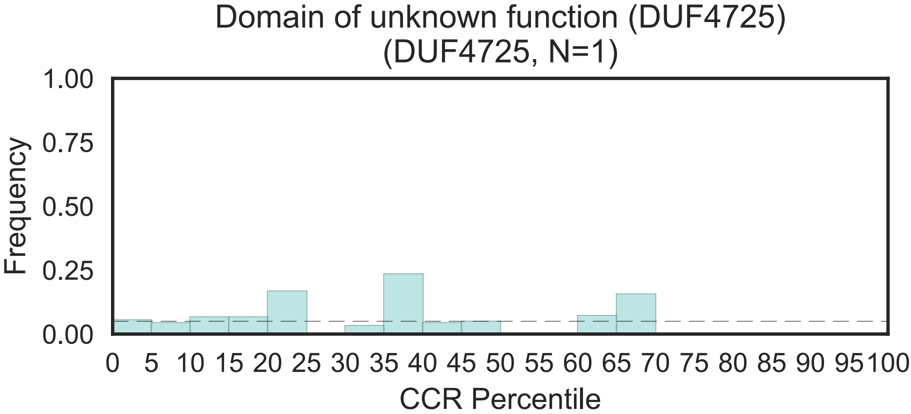

Domain of unknown function (DUF4720)
(DUF4720, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

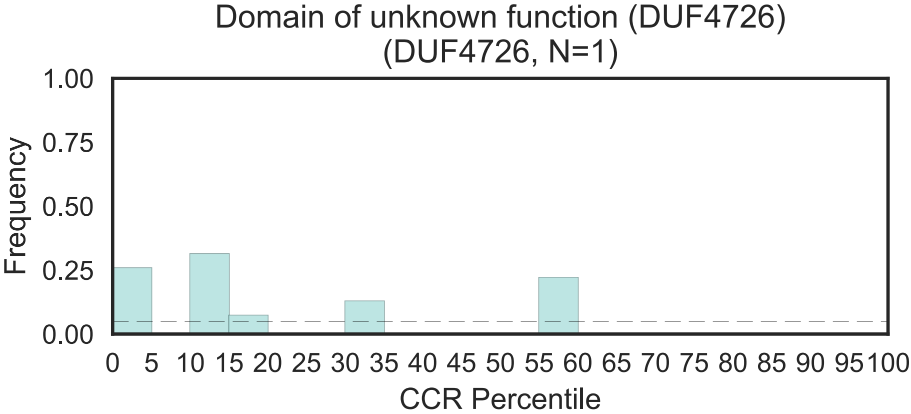

Domain of unknown function (DUF4721)
(DUF4721, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

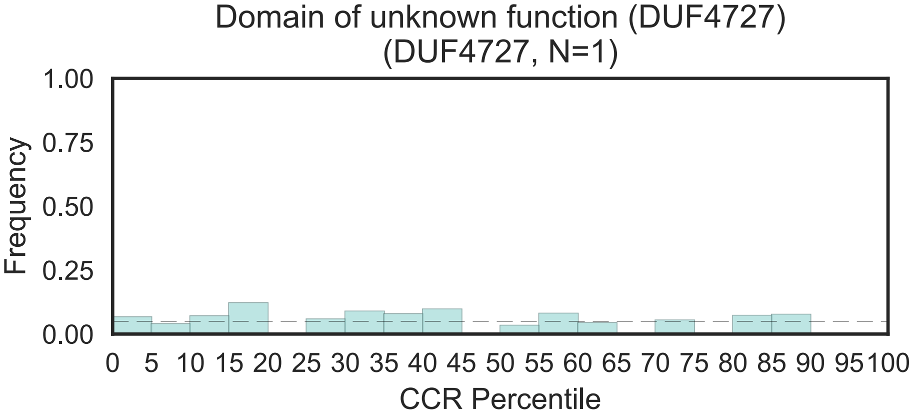

Domain of unknown function (DUF4722)
(DUF4722, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

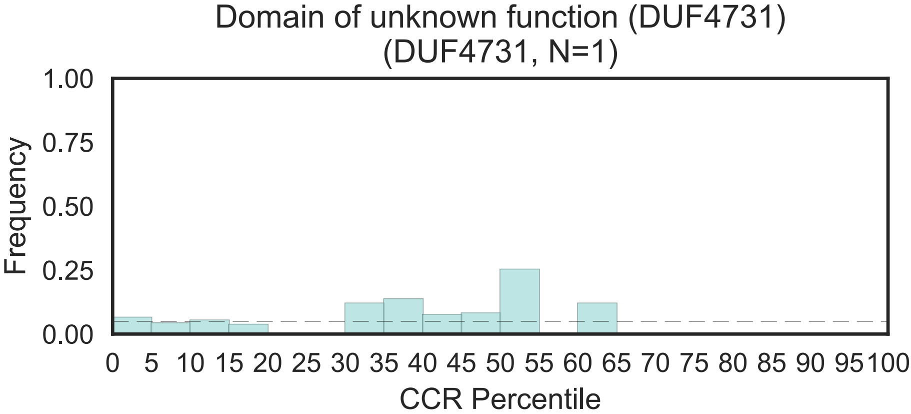


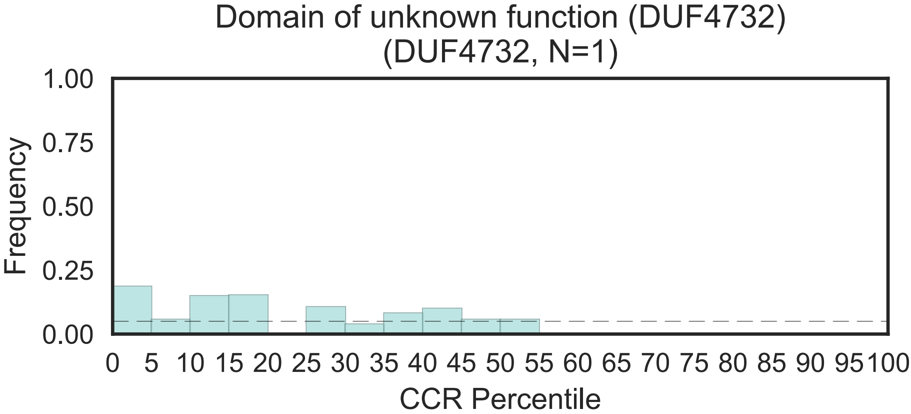
Domain of unknown function (DUF4723)
(DUF4723, N=1)

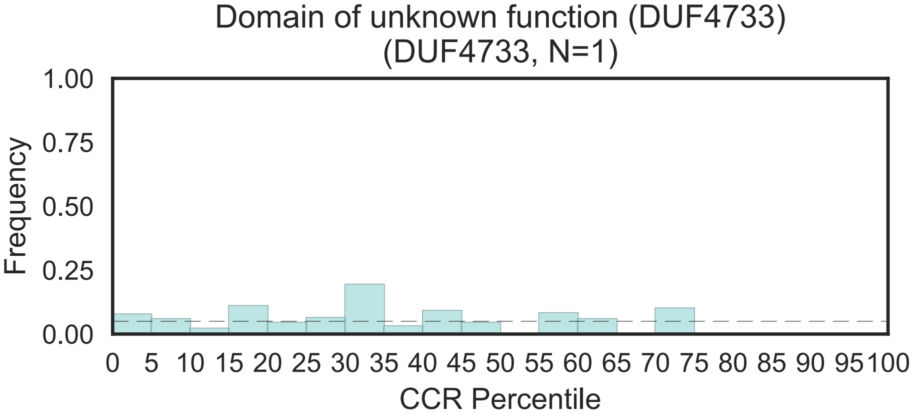

Domain of unknown function (DUF4725)
(DUF4725, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

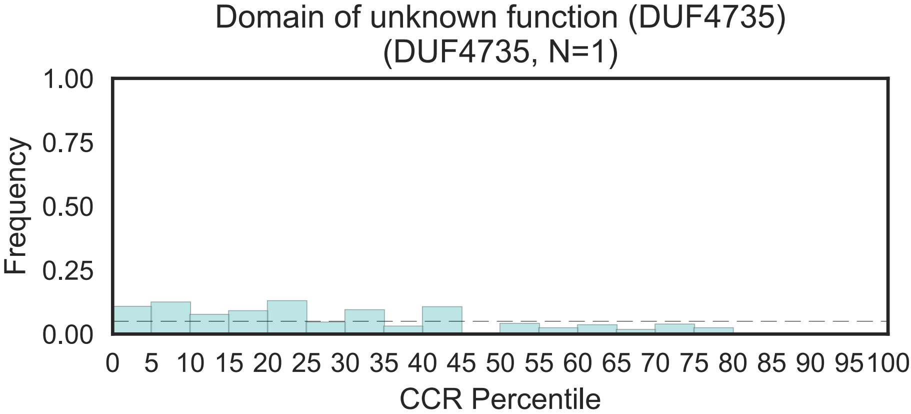

Domain of unknown function (DUF4726)
(DUF4726, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

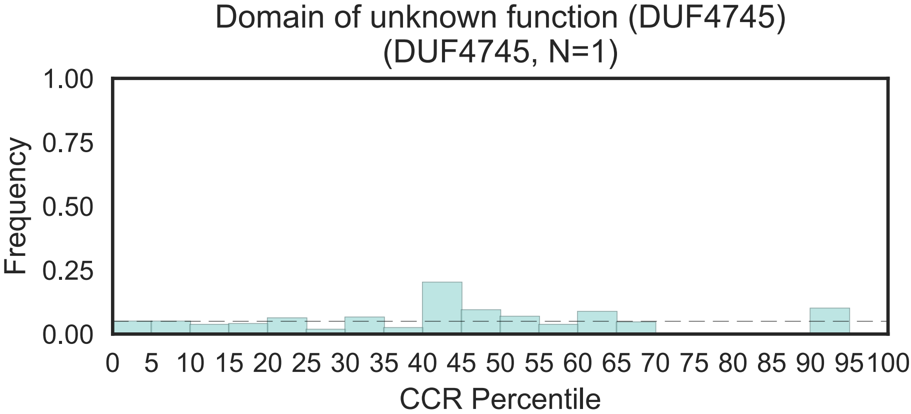

Domain of unknown function (DUF4727)
(DUF4727, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

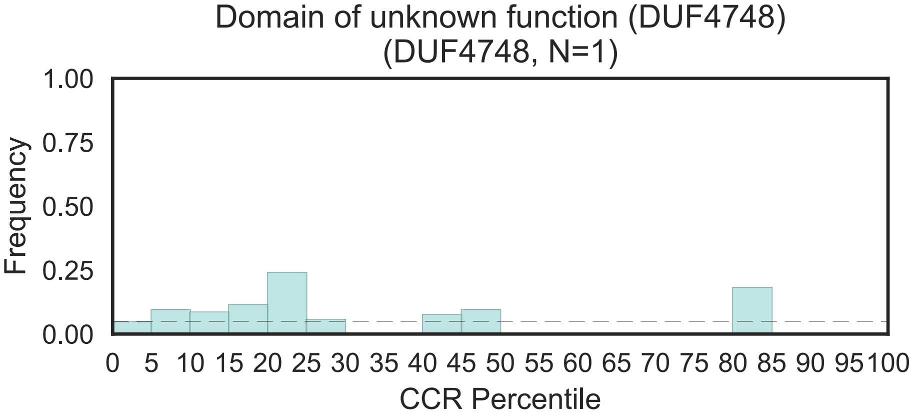

Domain of unknown function (DUF4731)
(DUF4731, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

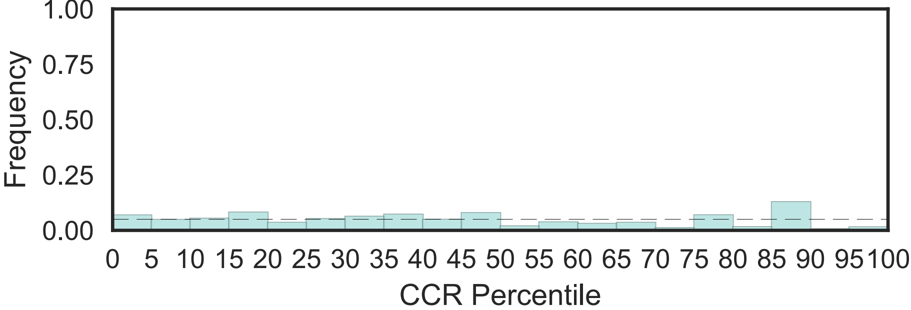

Domain of unknown function (DUF4732)
(DUF4732, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4733)
(DUF4733, N=1)

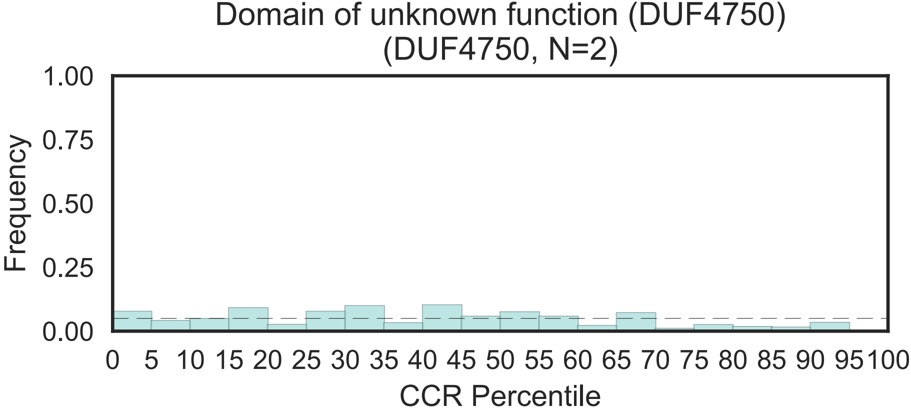

Domain of unknown function (DUF4735)
(DUF4735, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

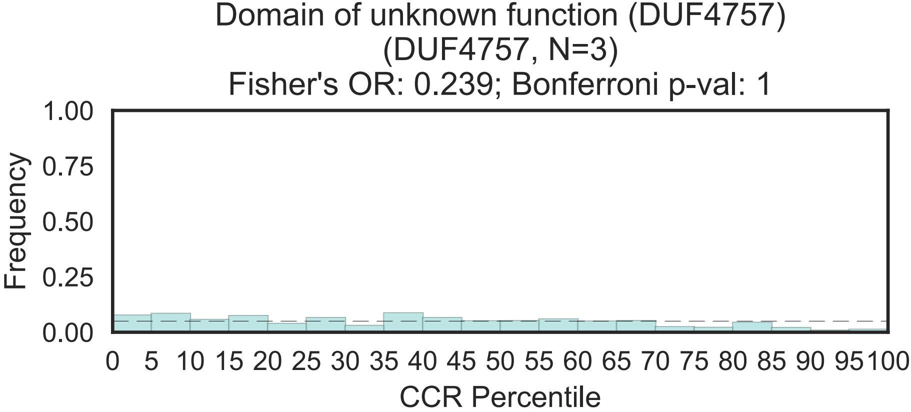

Domain of unknown function (DUF4745)
(DUF4745, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

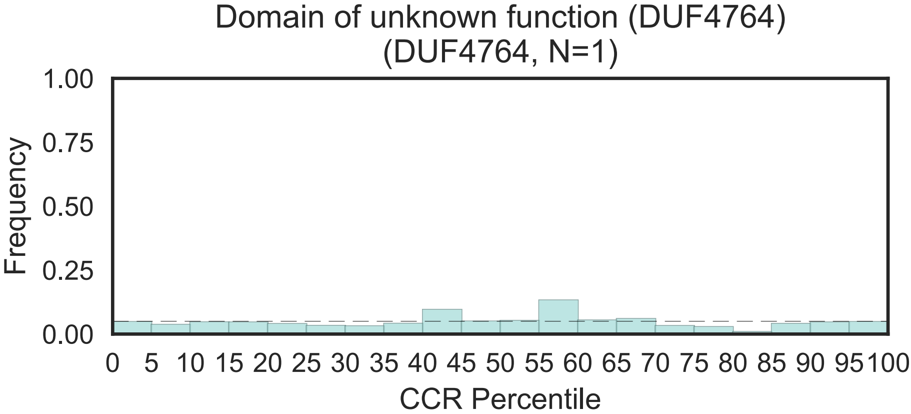

Domain of unknown function (DUF4748)
(DUF4748, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

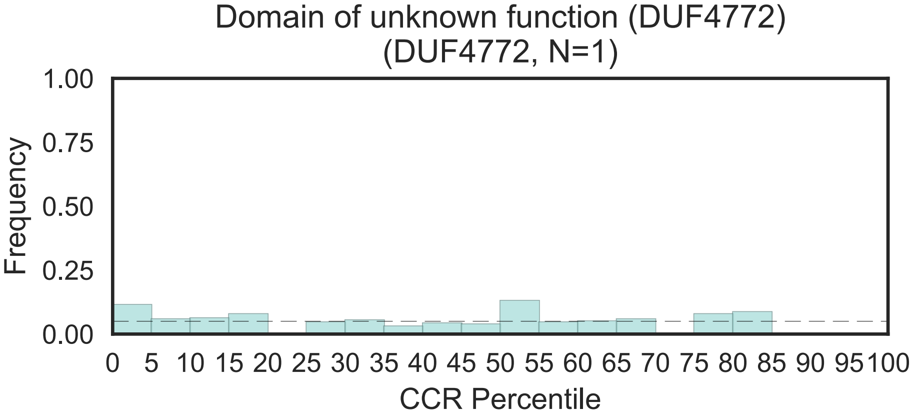


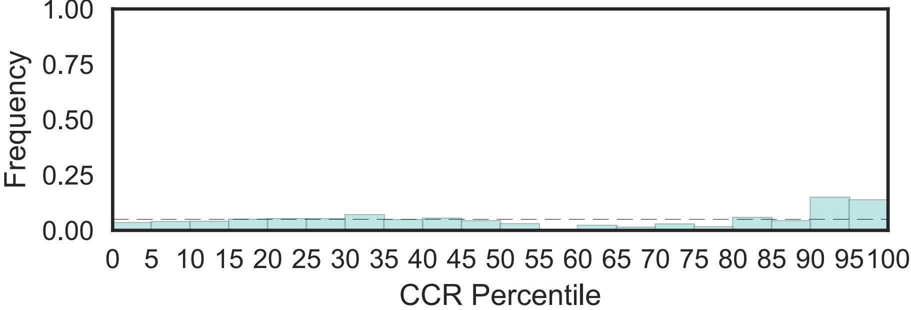
Domain of unknown function (DUF4749)
(DUF4749, N=8)
Fisher's OR: 0.308; Bonferroni p-val: 1


Domain of unknown function (DUF4750)
(DUF4750, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

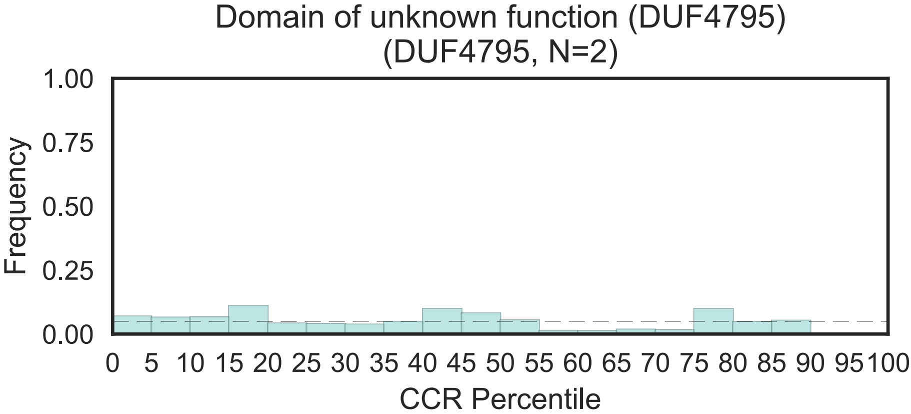

Domain of unknown function (DUF4757)
(DUF4757, N=3)
Fisher's OR: 0.239; Bonferroni p-val: 1


Domain of unknown function (DUF4764)
(DUF4764, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

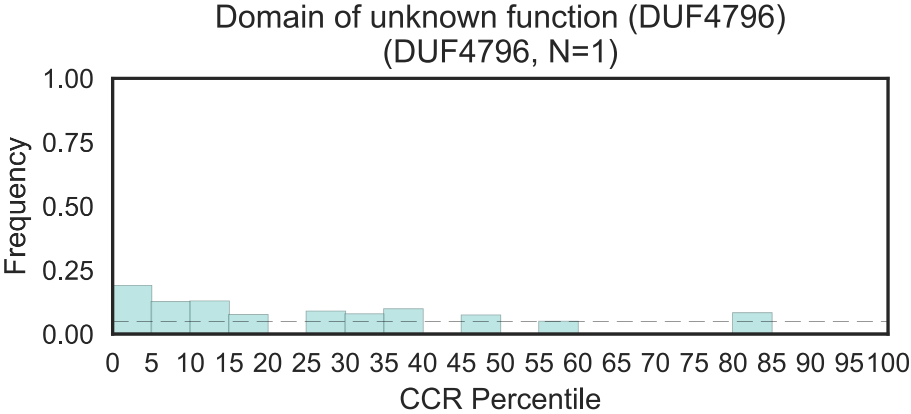

Domain of unknown function (DUF4772)
(DUF4772, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

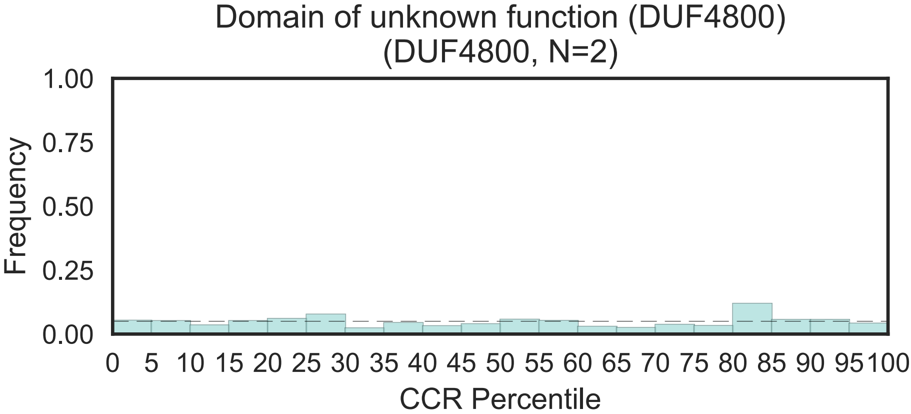


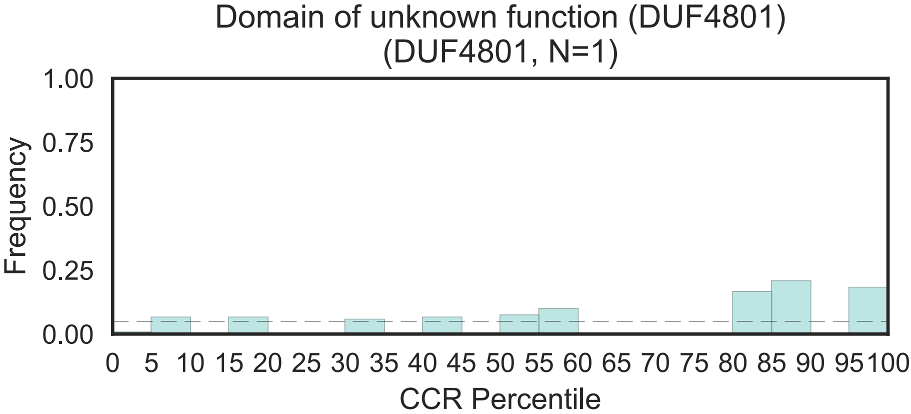
Domain of unknown function (DUF4782)
(DUF4782, N=3)
Fisher's OR: 2.11; Bonferroni p-val: 1

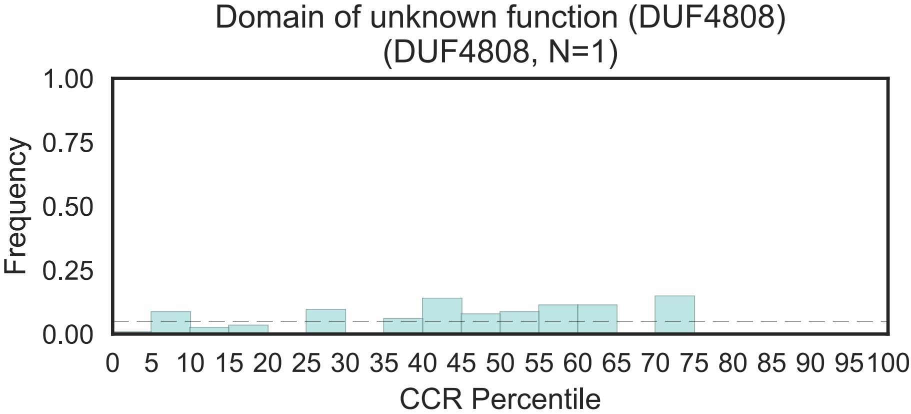


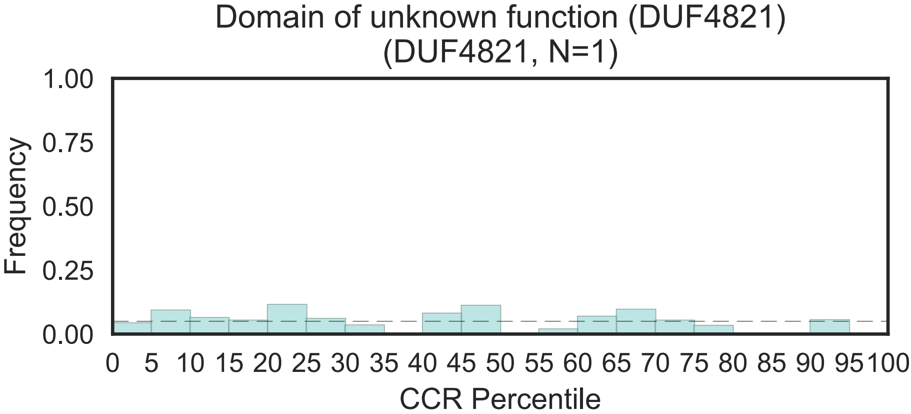
Domain of unknown function (DUF4795)
(DUF4795, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

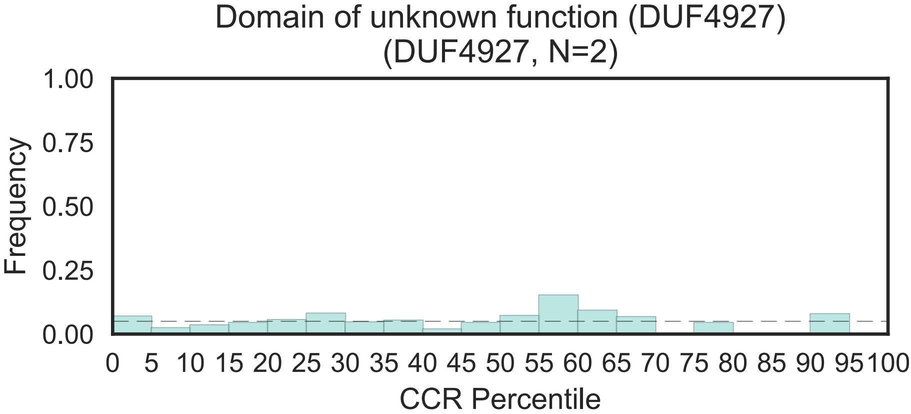

Domain of unknown function (DUF4796)
(DUF4796, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

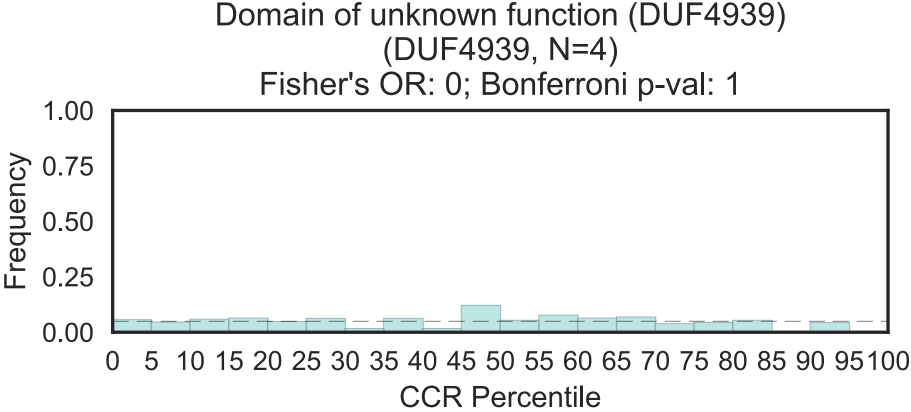

Domain of unknown function (DUF4800)
(DUF4800, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF4801)
(DUF4801, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

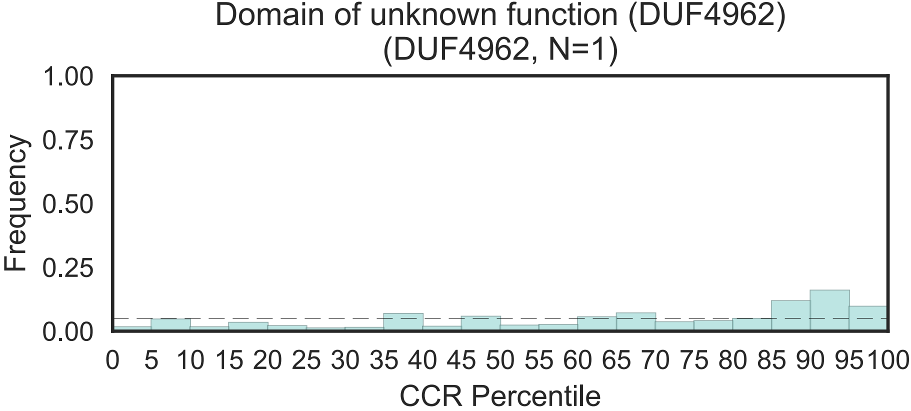

Domain of unknown function (DUF4808)
(DUF4808, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

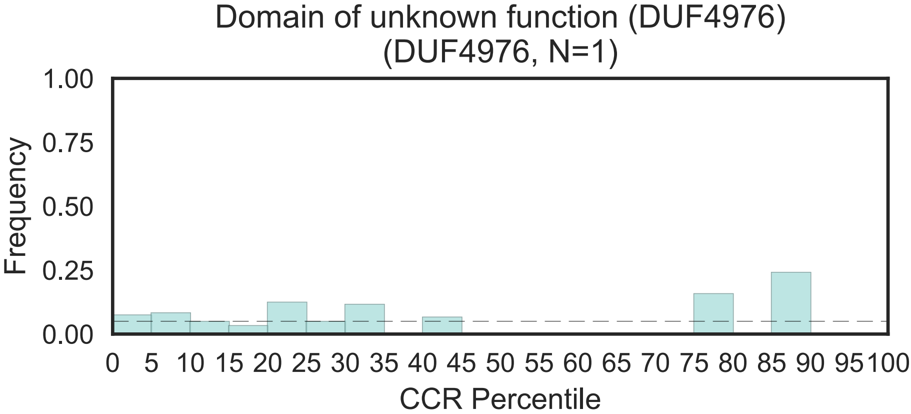

Domain of unknown function (DUF4821)
(DUF4821, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

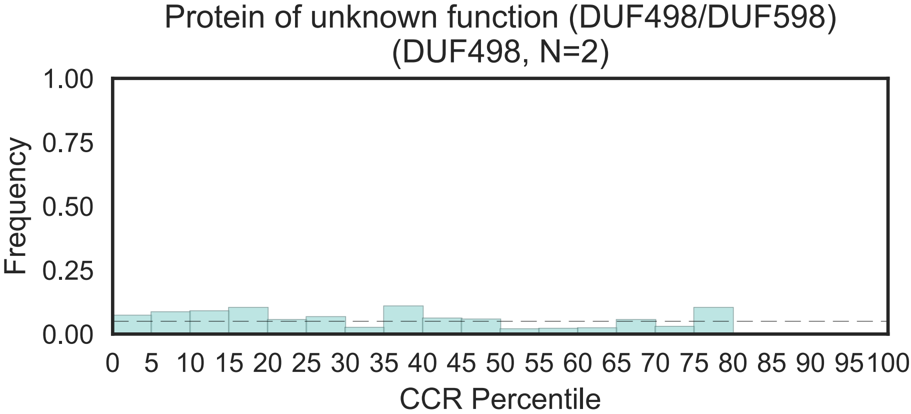

Domain of unknown function (DUF4927)
(DUF4927, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

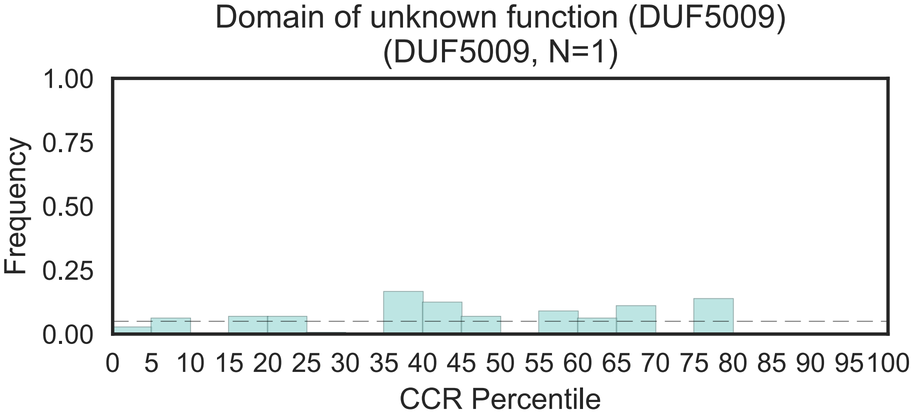


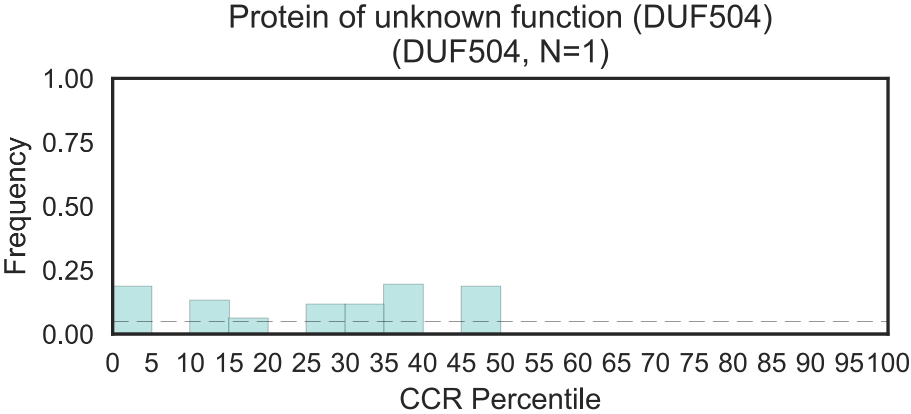
Domain of unknown function (DUF4939)
(DUF4939, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

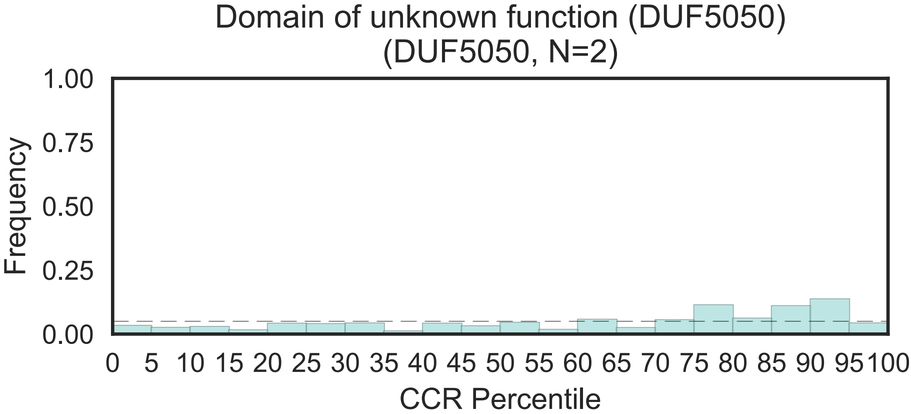

Domain of unknown function (DUF4962)
(DUF4962, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

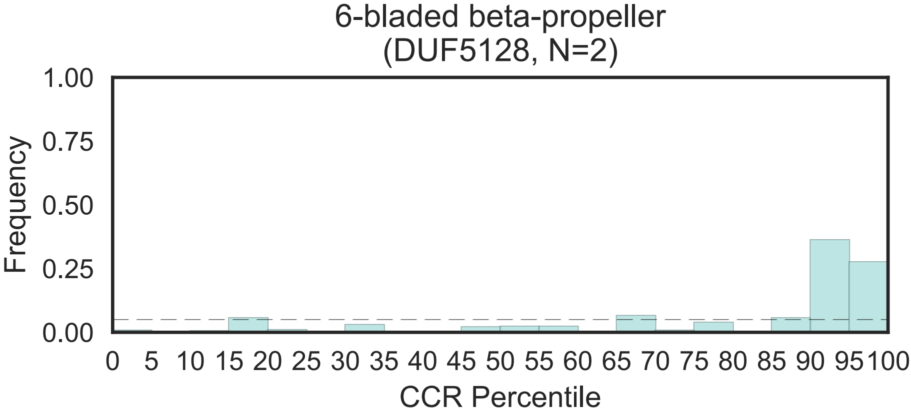

Domain of unknown function (DUF4976)
(DUF4976, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

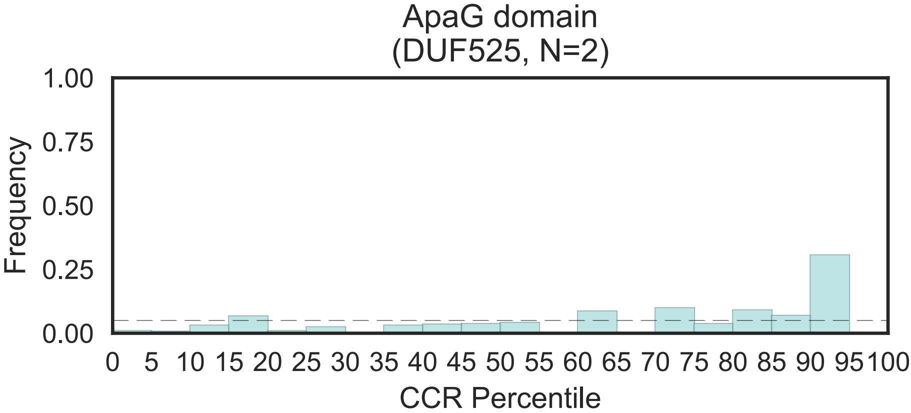

Protein of unknown function (DUF498/DUF598)
(DUF498, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

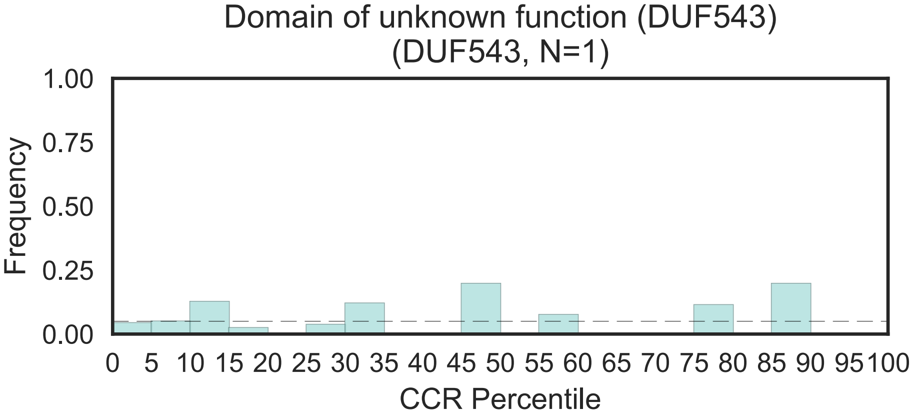

Domain of unknown function (DUF5009)
(DUF5009, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Protein of unknown function (DUF504)
(DUF504, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

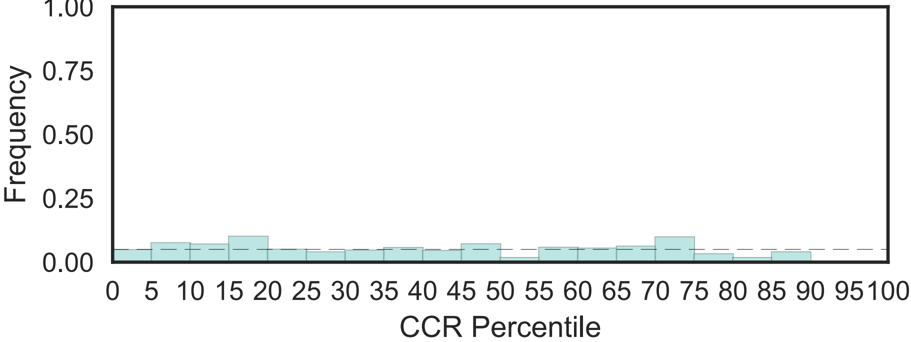

Domain of unknown function (DUF5050)
(DUF5050, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

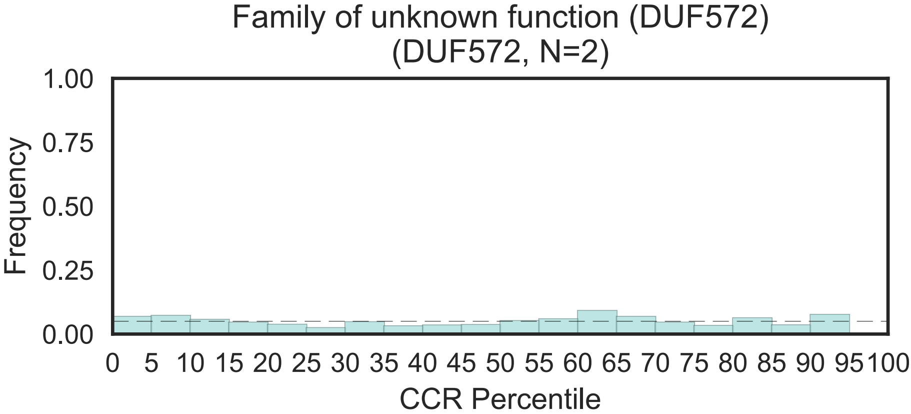

6-bladed beta-propeller
(DUF5128, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

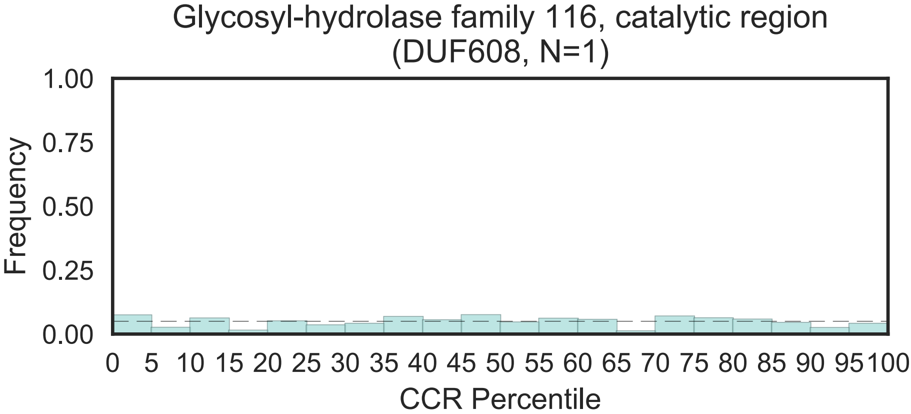

ApaG domain
(DUF525, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Domain of unknown function (DUF543)
(DUF543, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

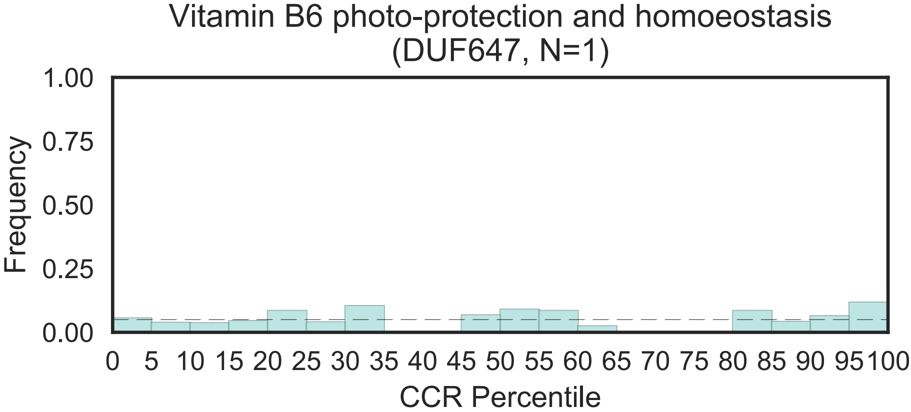
Protein of unknown function (DUF563) (DUF563, N=2)

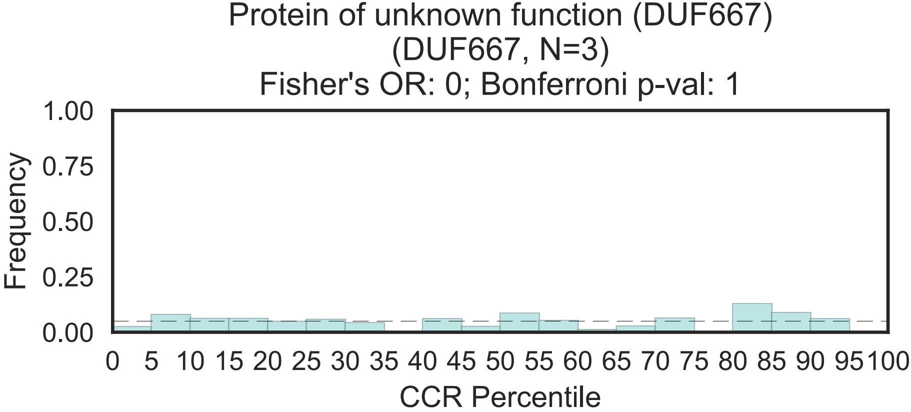


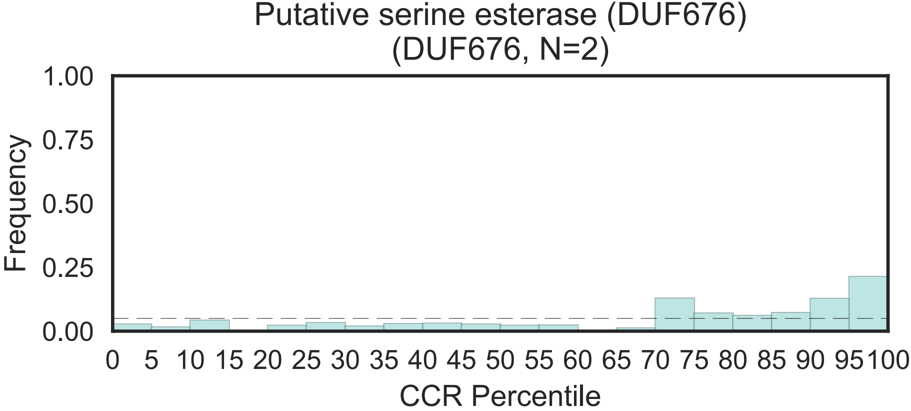

Family of unknown function (DUF572)
(DUF572, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

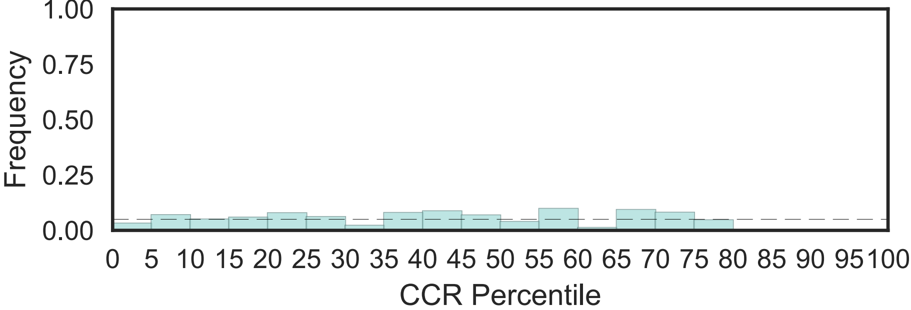


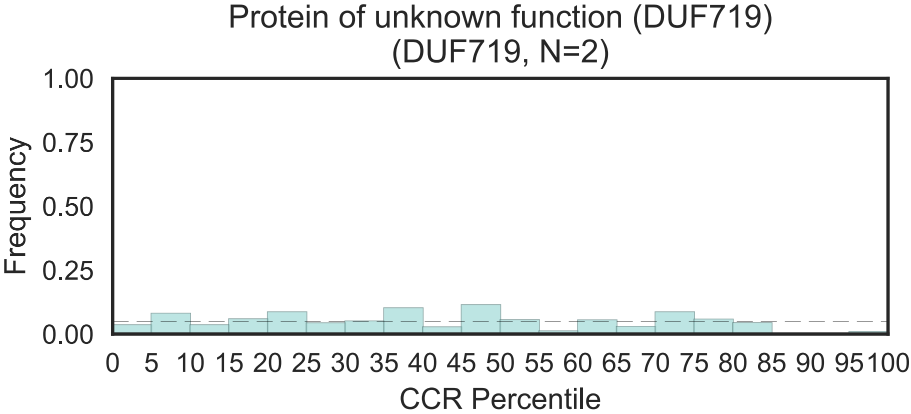
Glycosyl-hydrolase family 116, catalytic region
(DUF608, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

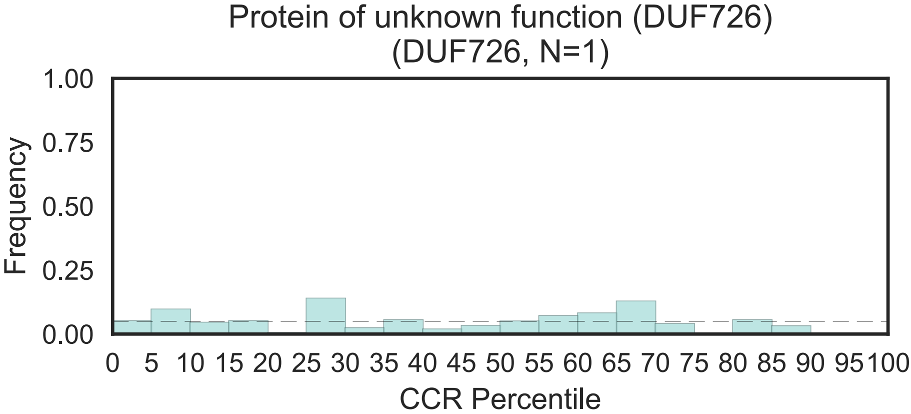

Vitamin B6 photo-protection and homoeostasis
(DUF647, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Protein of unknown function (DUF667)
(DUF667, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

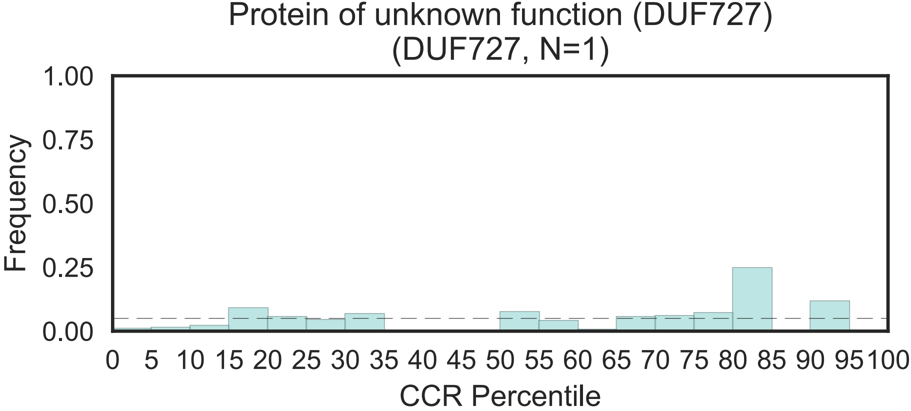

Putative serine esterase (DUF676)
(DUF676, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

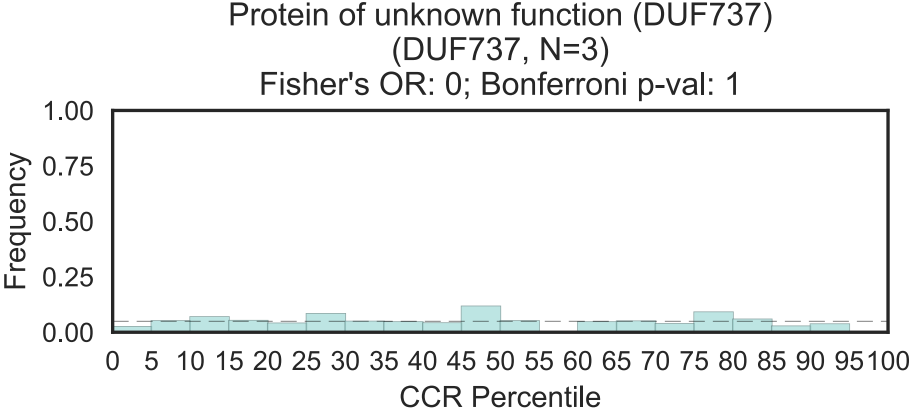

Family of unknown function (DUF716)
(DUF716, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

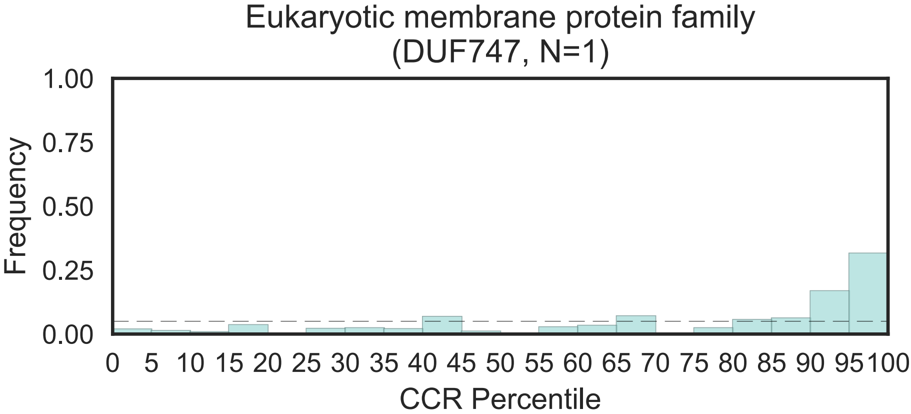

Protein of unknown function (DUF719)
(DUF719, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

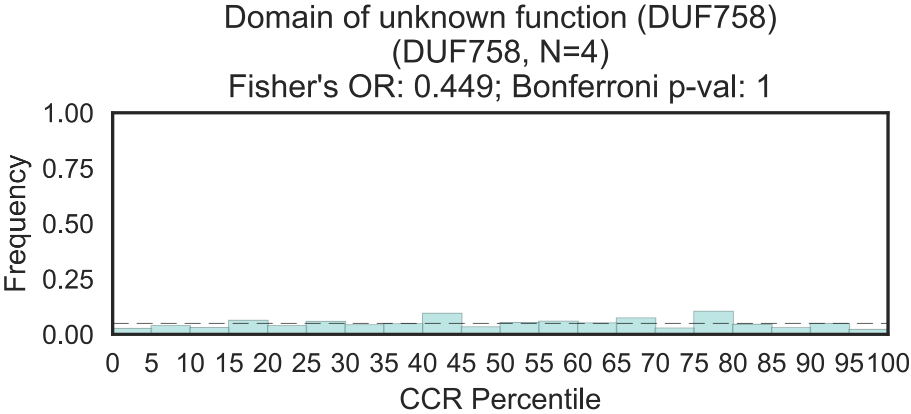


Protein of unknown function (DUF726)
(DUF726, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

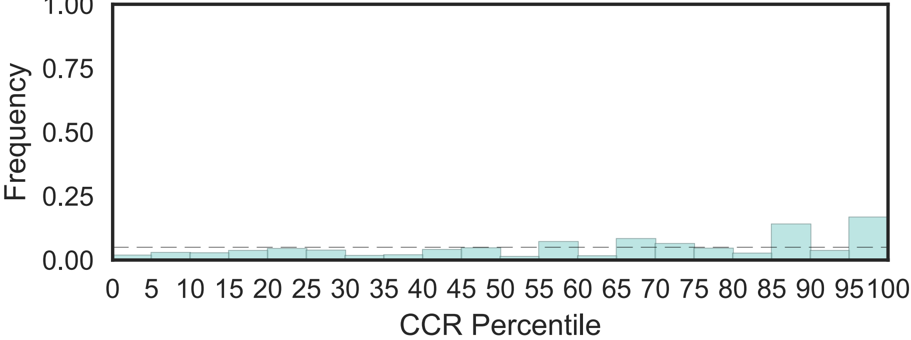

Protein of unknown function (DUF727)
(DUF727, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

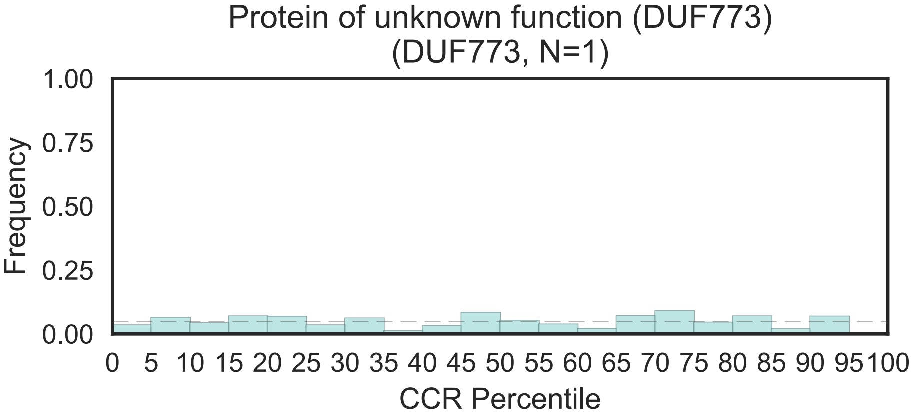

Protein of unknown function (DUF737)
(DUF737, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

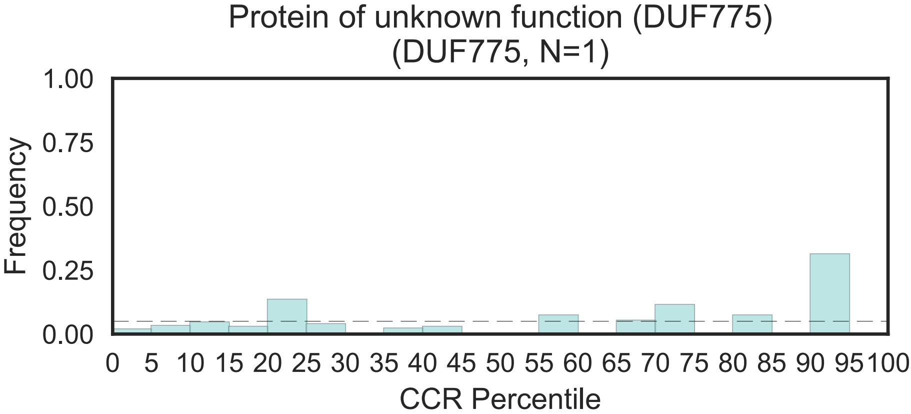

Eukaryotic membrane protein family
(DUF747, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

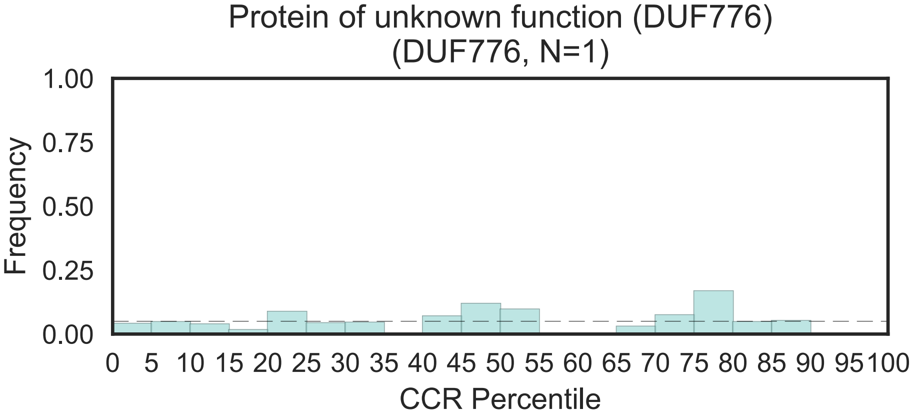

Domain of unknown function (DUF758)
(DUF758, N=4)
Fisher's OR: 0.449; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

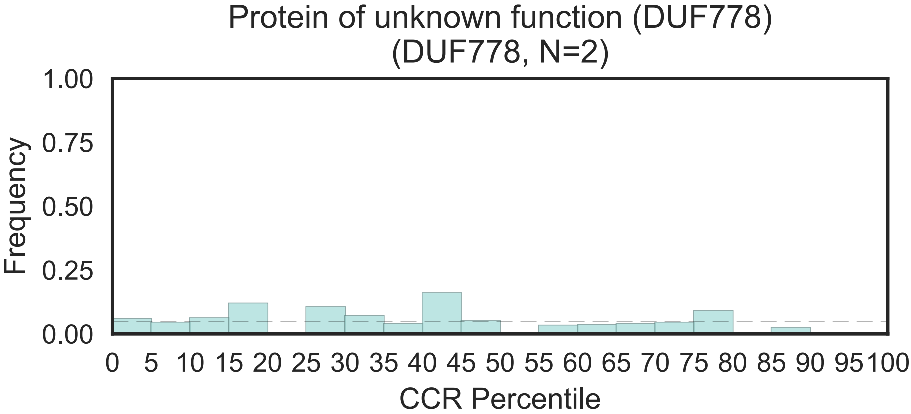
Protein of unknown function (DUF766) (DUF766, N=1)

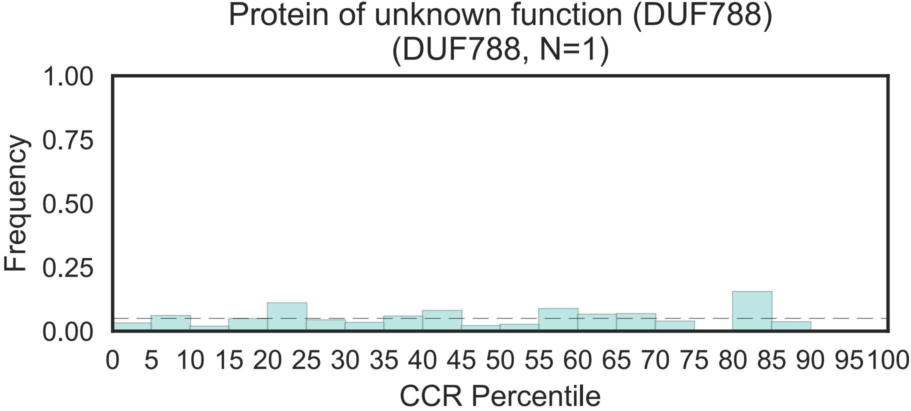



Protein of unknown function (DUF773)
(DUF773, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

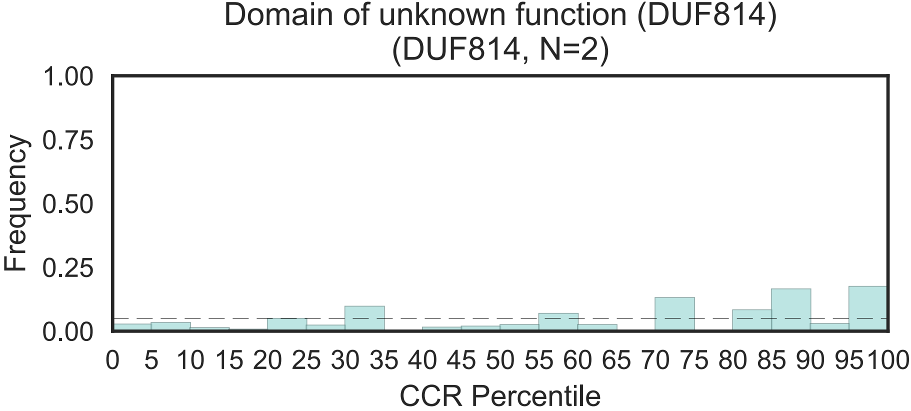

Protein of unknown function (DUF775)
(DUF775, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

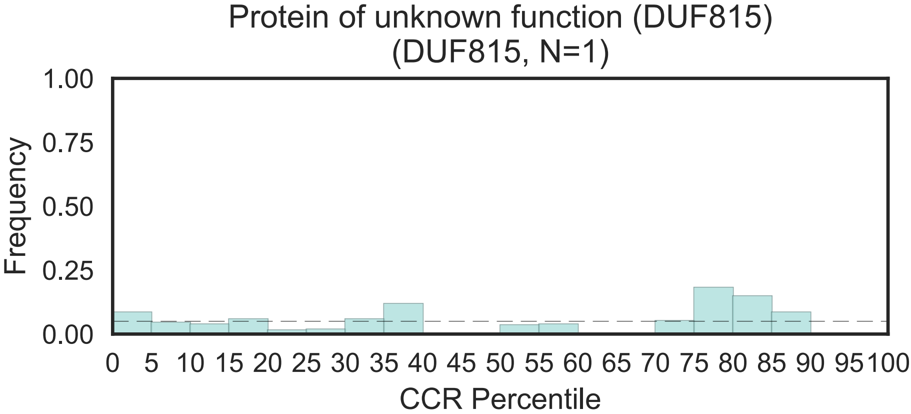

Protein of unknown function (DUF776)
(DUF776, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

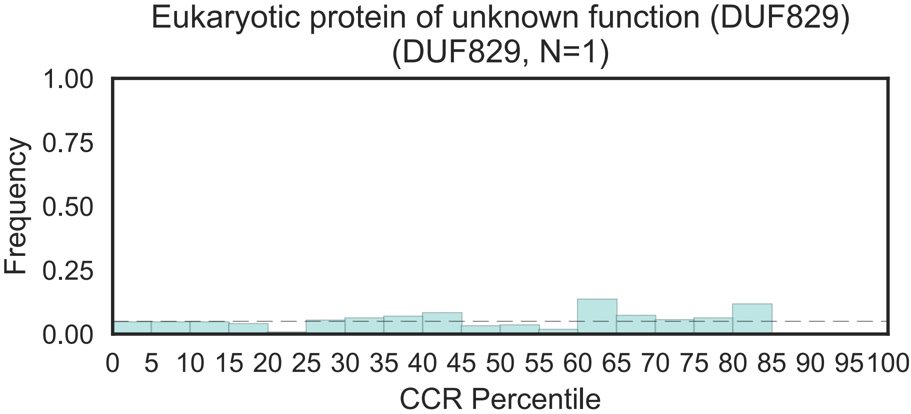

Protein of unknown function (DUF778)
(DUF778, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

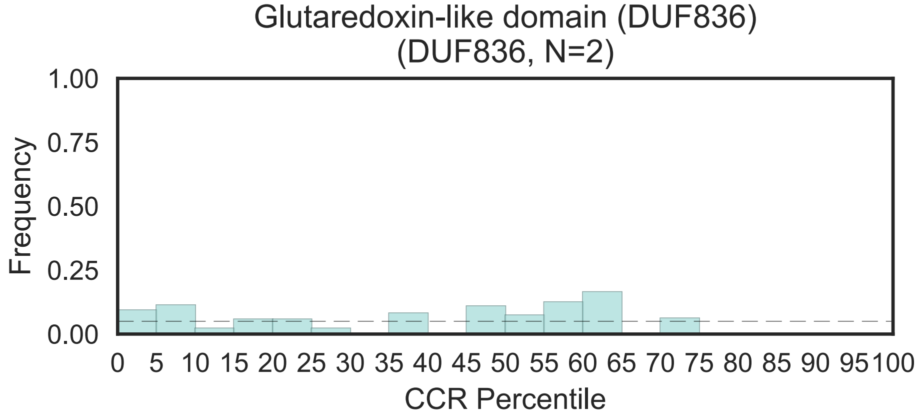


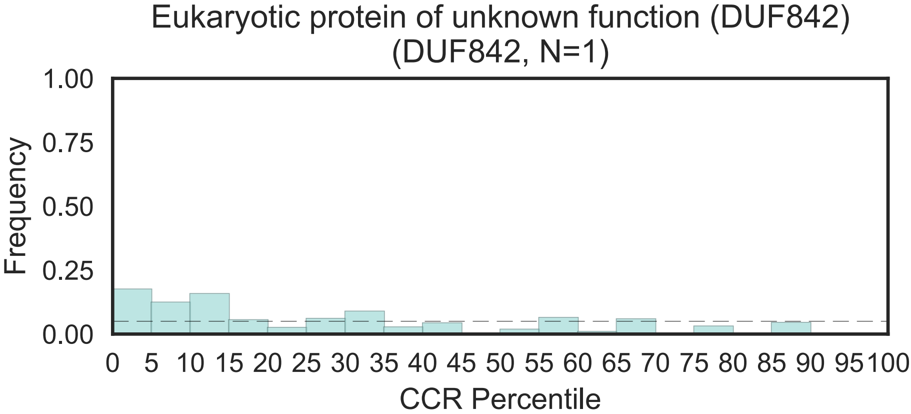
Protein of unknown function (DUF788)
(DUF788, N=1)

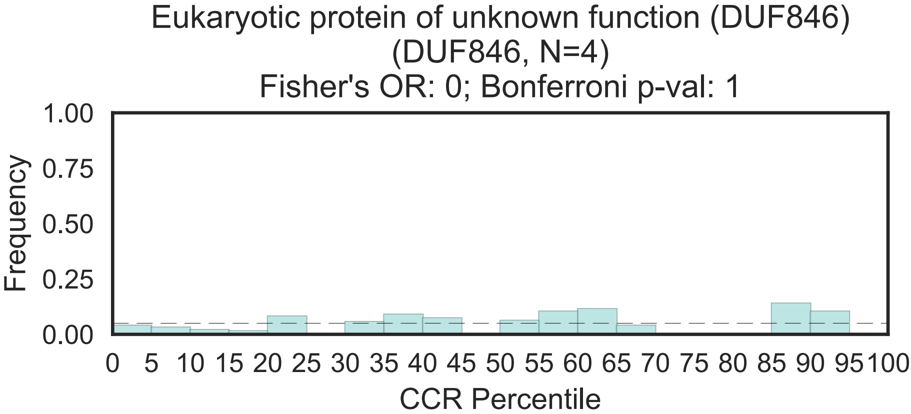

Domain of unknown function (DUF814)
(DUF814, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

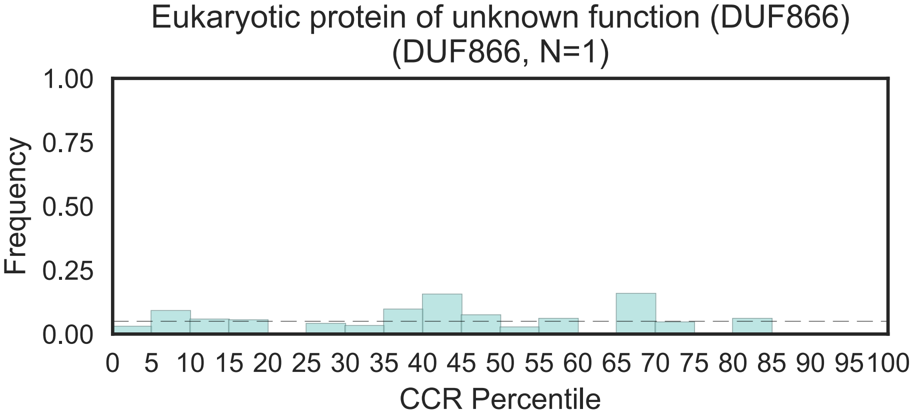

Protein of unknown function (DUF815)
(DUF815, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

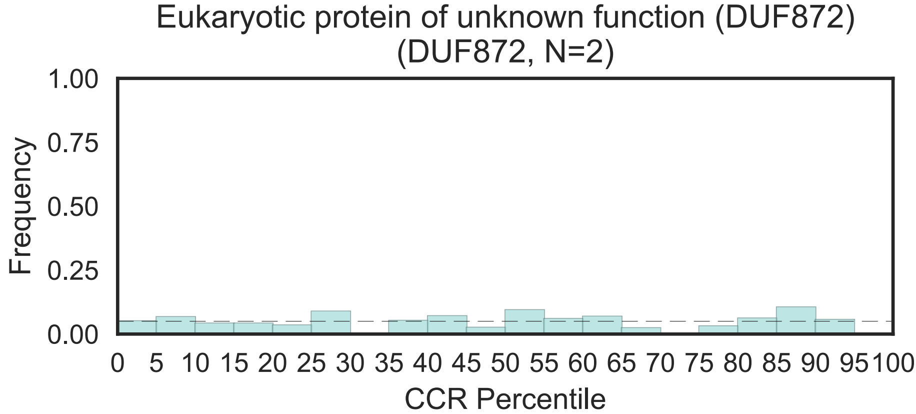

Eukaryotic protein of unknown function (DUF829)
(DUF829, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

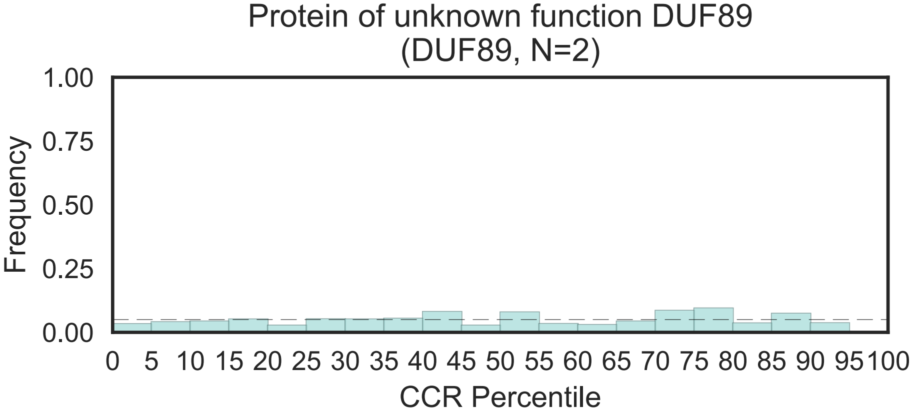

Glutaredoxin-like domain (DUF836)
(DUF836, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

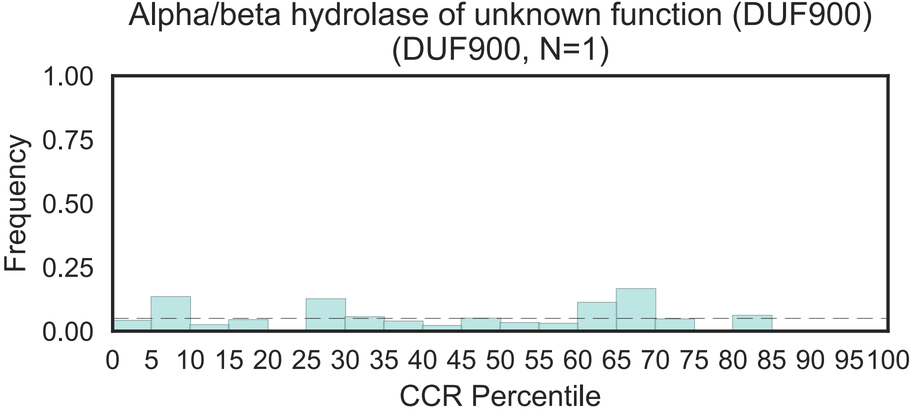

Eukaryotic protein of unknown function (DUF842)
(DUF842, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

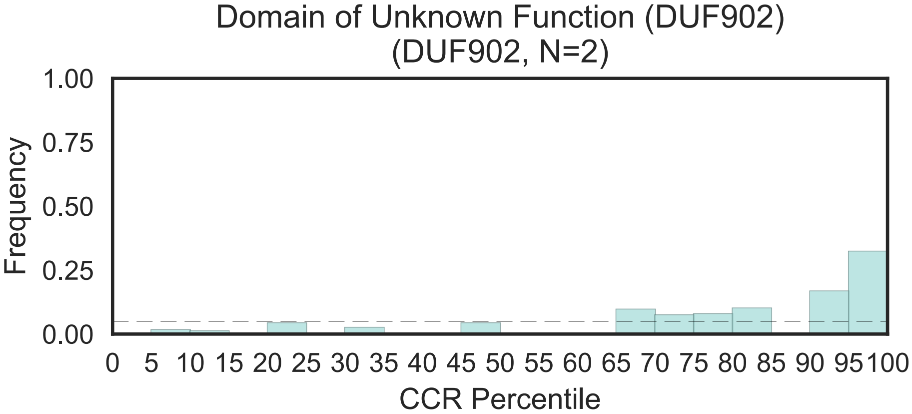

Eukaryotic protein of unknown function (DUF846)
(DUF846, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

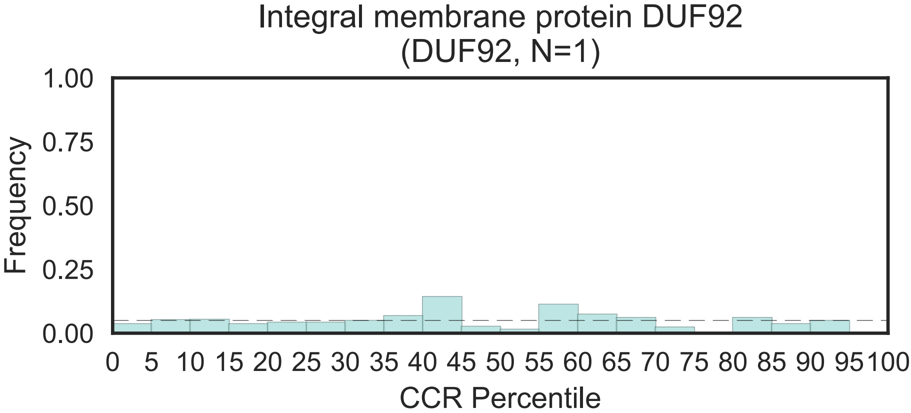

Eukaryotic protein of unknown function (DUF866)
(DUF866, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

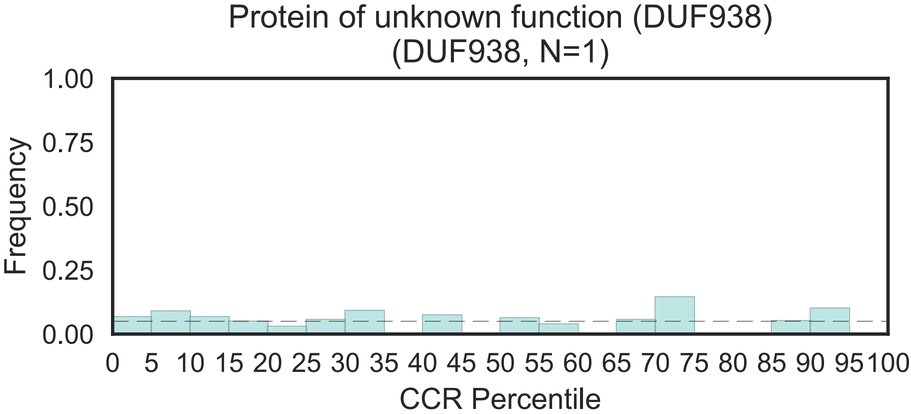

Eukaryotic protein of unknown function (DUF872)
(DUF872, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

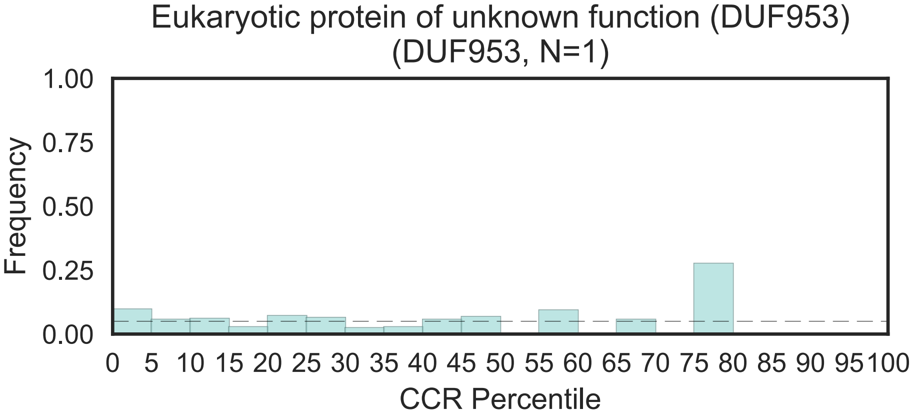

Protein of unknown function DUF89
(DUF89, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

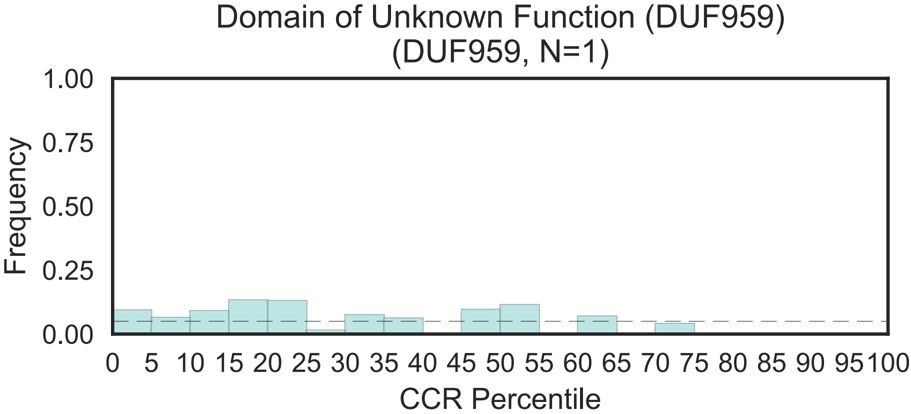

Alpha/beta hydrolase of unknown function (DUF900)
(DUF900, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

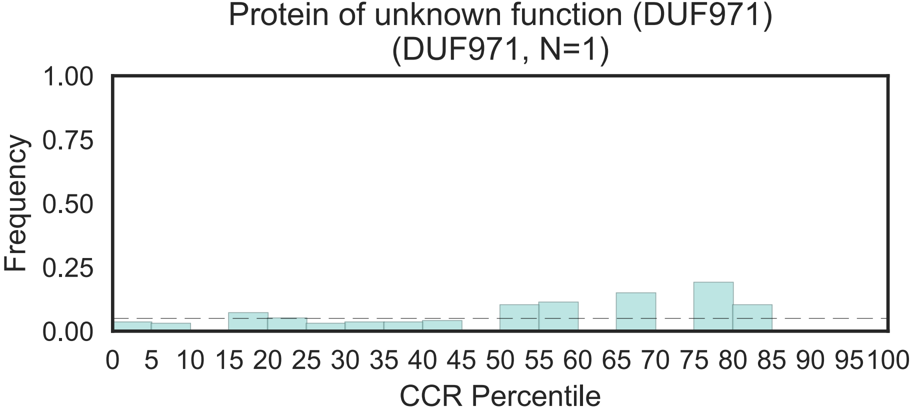

Domain of Unknown Function (DUF902)
(DUF902, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

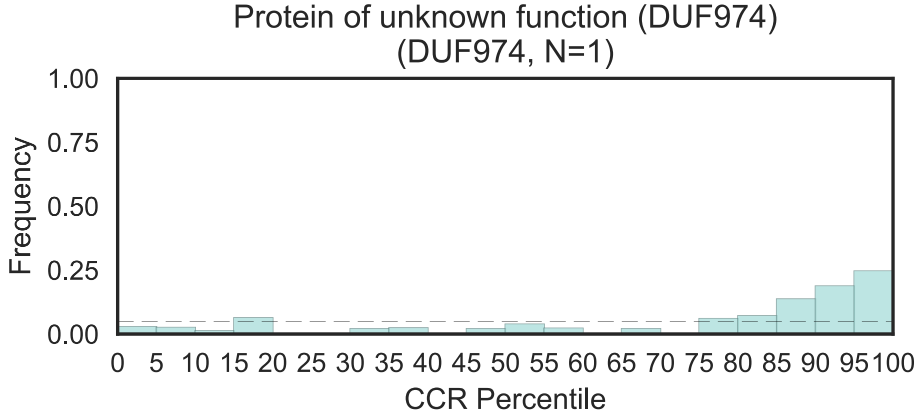

Integral membrane protein DUF92
(DUF92, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

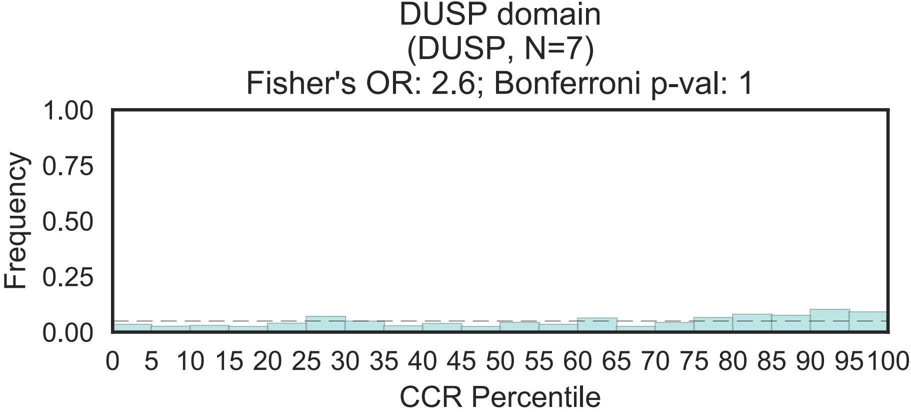

Protein of unknown function (DUF938)
(DUF938, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

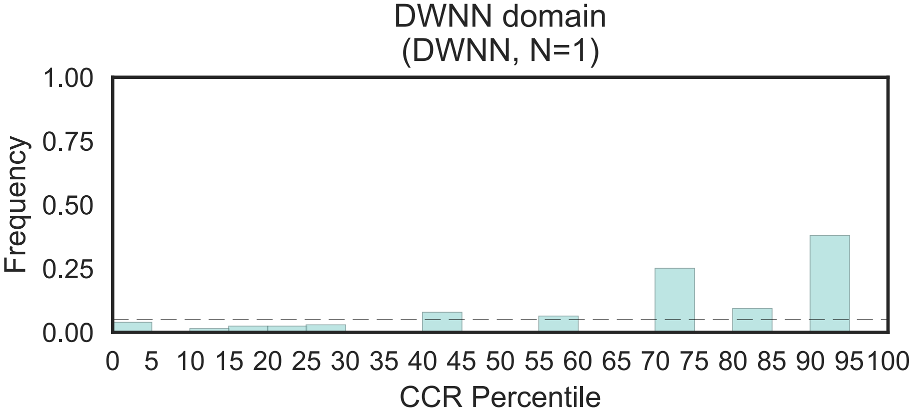

Eukaryotic protein of unknown function (DUF953)
(DUF953, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

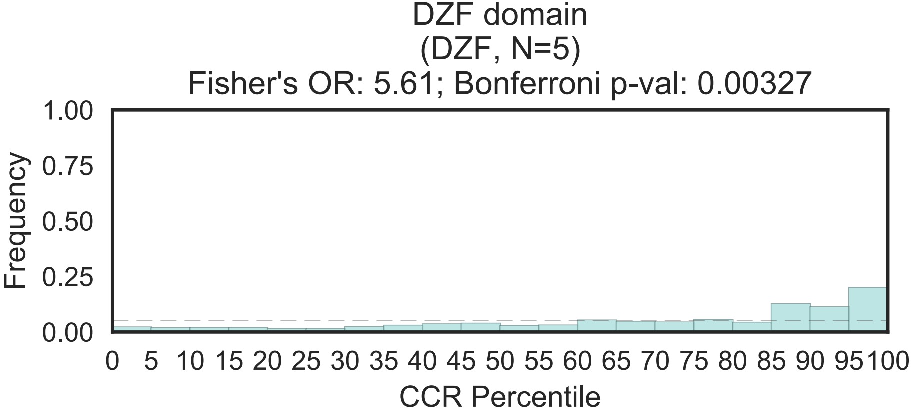

Domain of Unknown Function (DUF959)
(DUF959, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

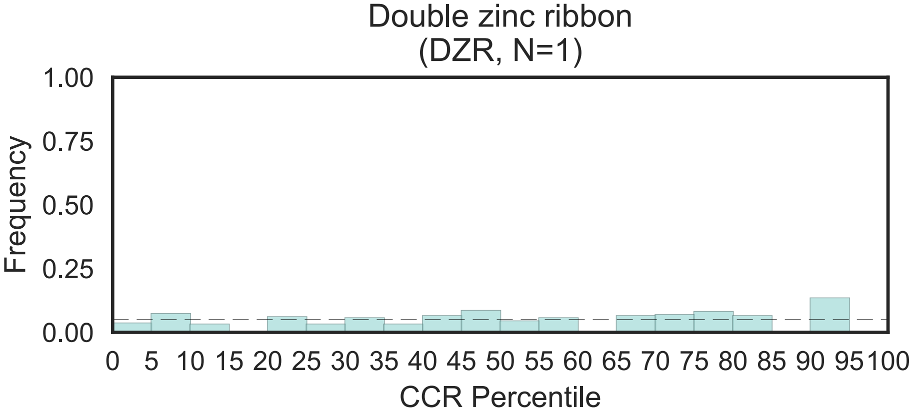

Protein of unknown function (DUF971)
(DUF971, N=1)

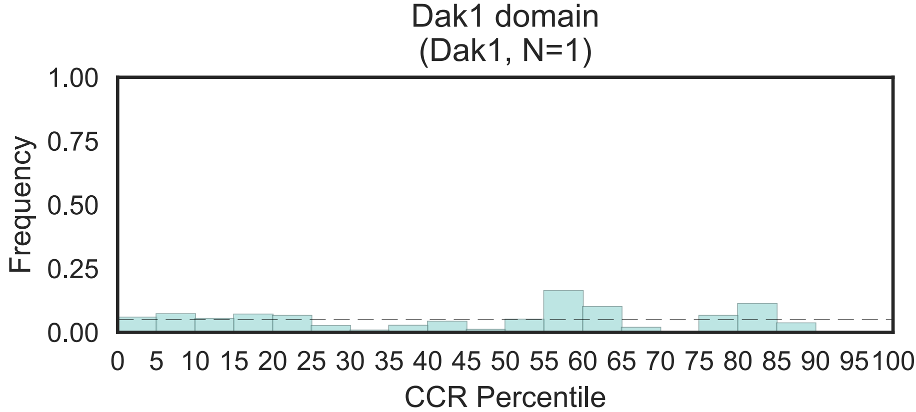

Protein of unknown function (DUF974)
(DUF974, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

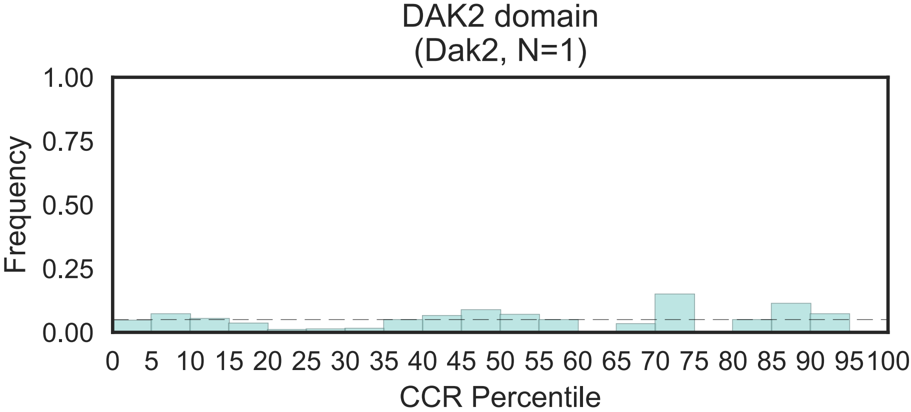

DUSP domain
(DUSP, N=7)
Fisher's OR: 2.6; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

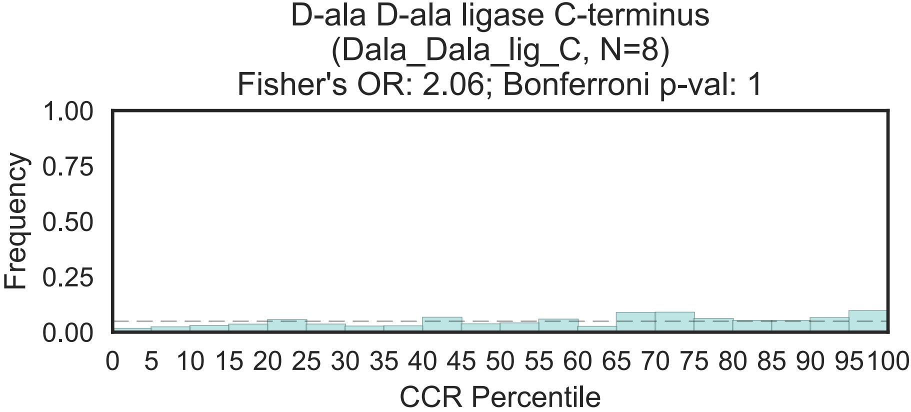

DWNN domain
(DWNN, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

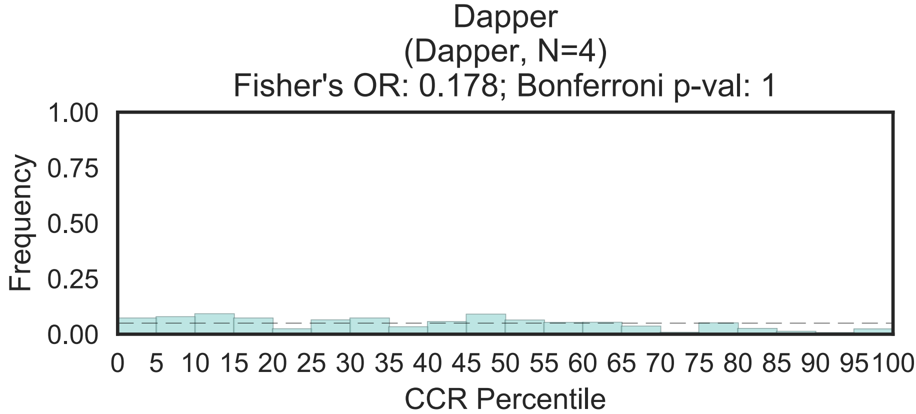

DZF domain
(DZF, N=5)
Fisher's OR: 5.61; Bonferroni p-val: 0.00327
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

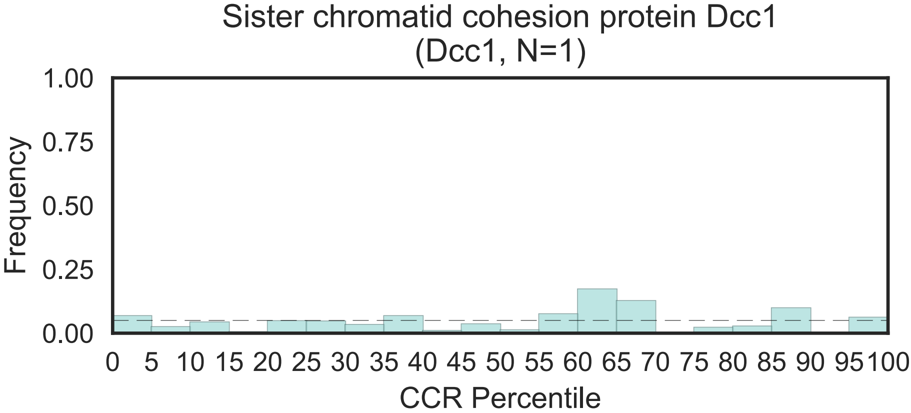

Double zinc ribbon
(DZR, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

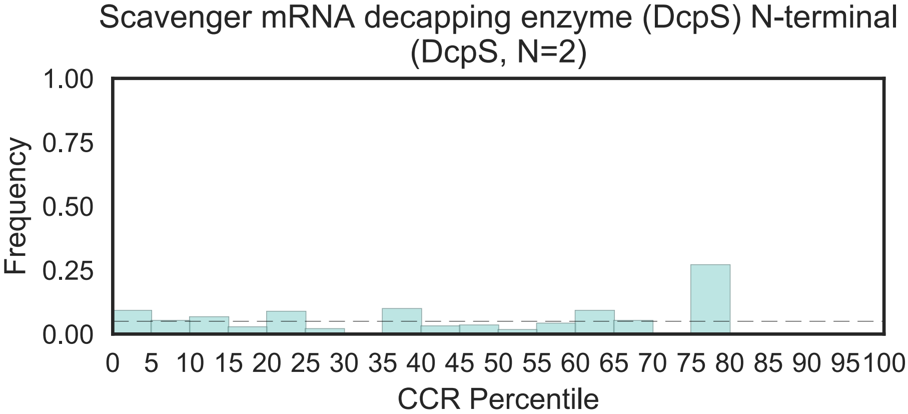

Dak1 domain
(Dak1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


DAK2 domain
(Dak2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

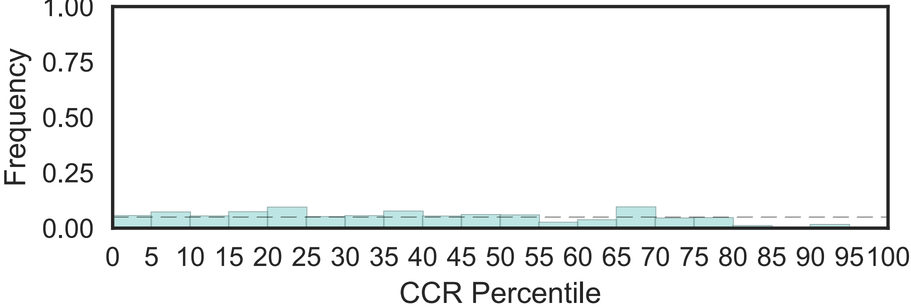

D-ala D-ala ligase C-terminus
(Dala_Dala_lig_C, N=8)
Fisher's OR: 2.06; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

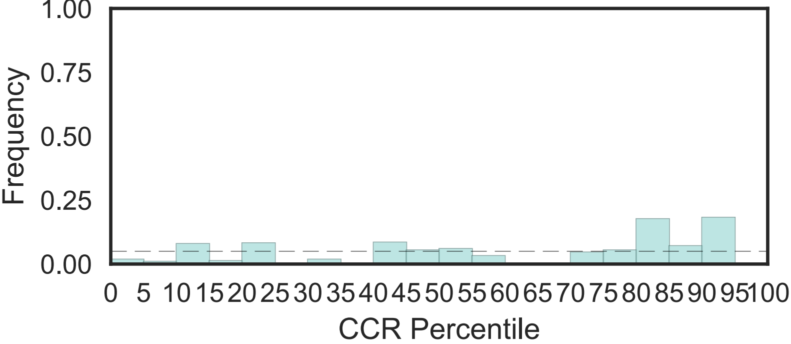

Dapper
(Dapper, N=4)
Fisher's OR: 0.178; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Sister chromatid cohesion protein Dcc1
(Dcc1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

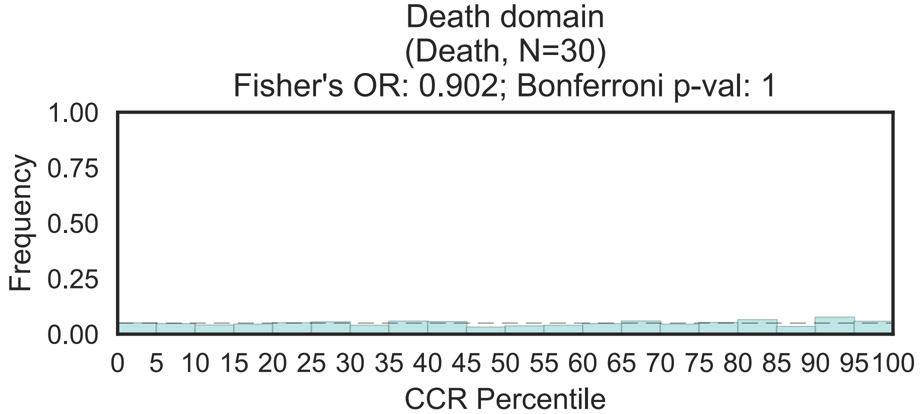

Scavenger mRNA decapping enzyme (DcpS) N-terminal
(DcpS, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

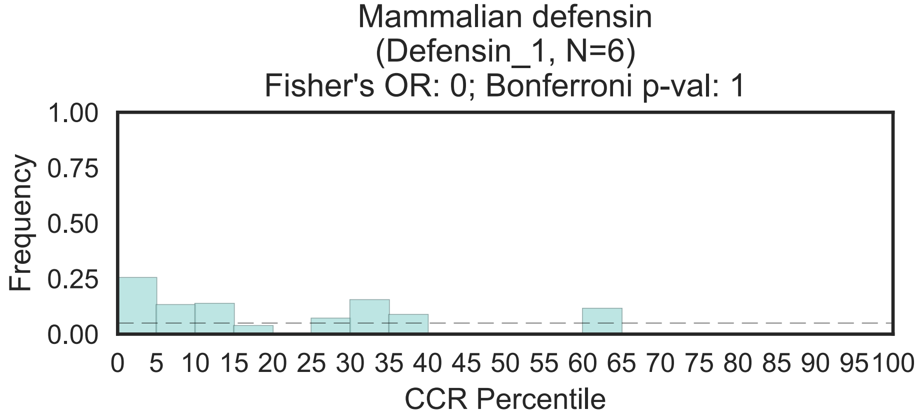
Scavenger mRNA decapping enzyme C-term binding (DcpS_C, N=7) Fisher's OR: 0; Bonferroni p-val: 1

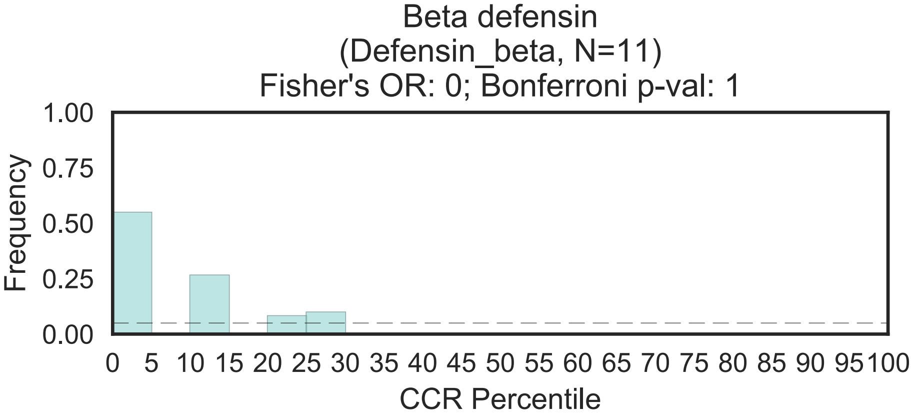




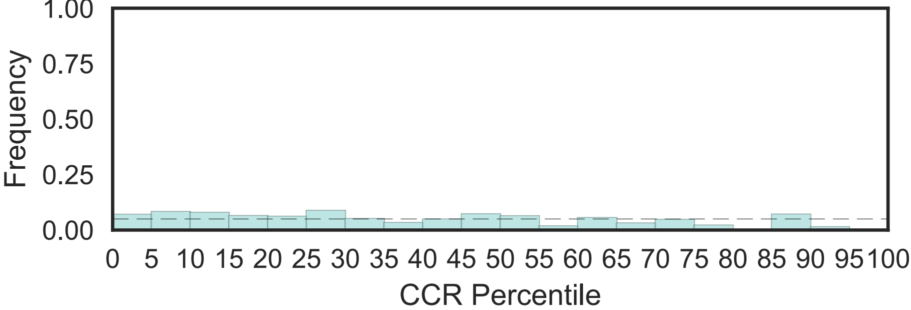
Tripartite ATP-independent periplasmic transporter, DctM component (DctM, N=1)

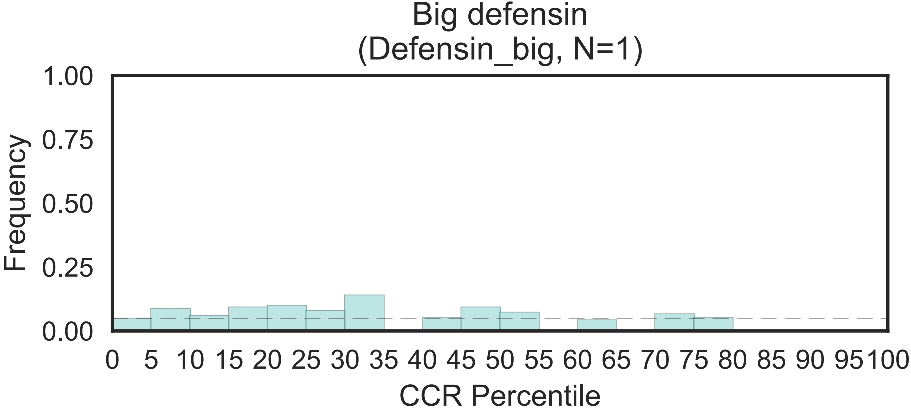

Death domain
(Death, N=30)
Fisher's OR: 0.902; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

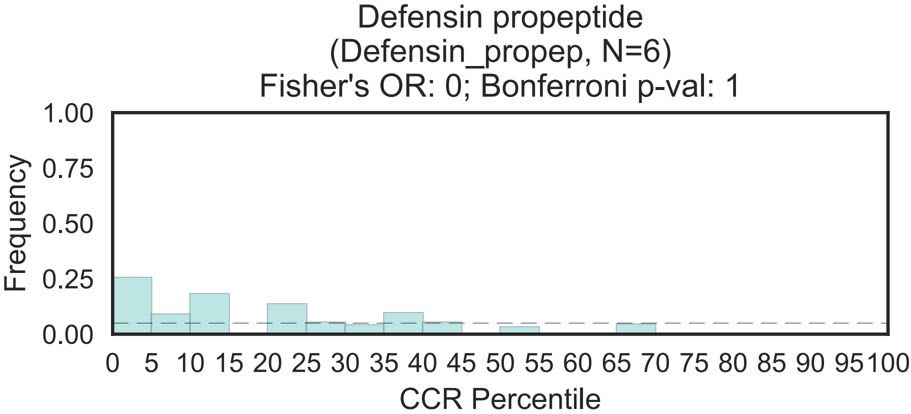

Mammalian defensin
(Defensin_1, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

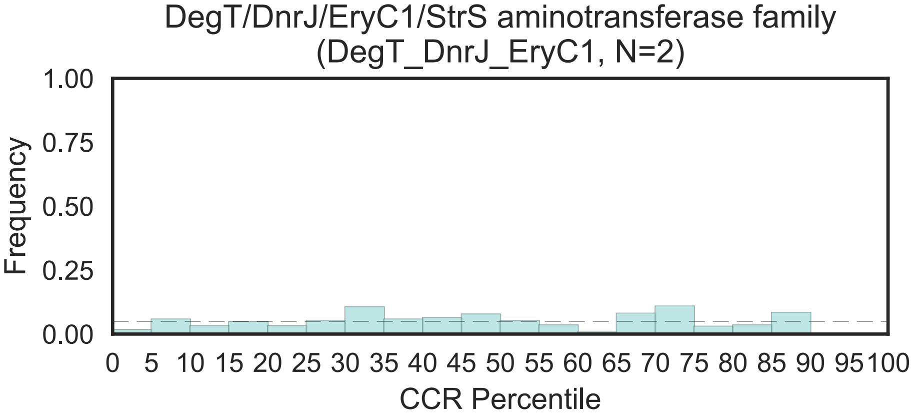

Beta defensin
(Defensin_beta, N=11)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

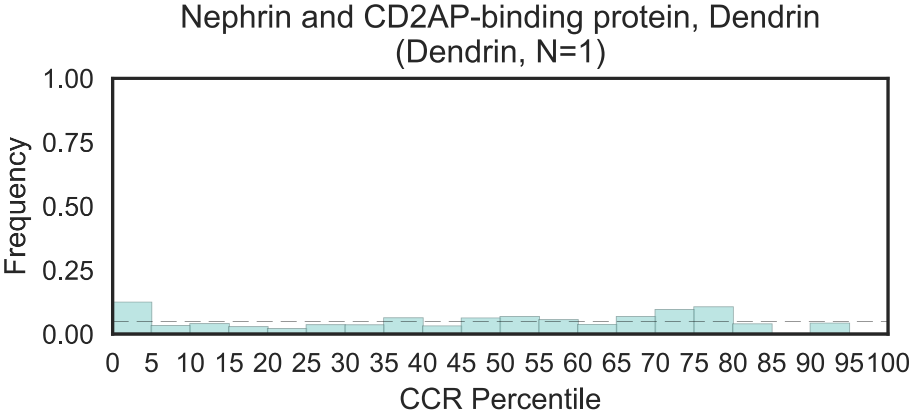
Beta defensin
(Defensin_beta_2, N=30)
Fisher's OR: 0; Bonferroni p-val: 1

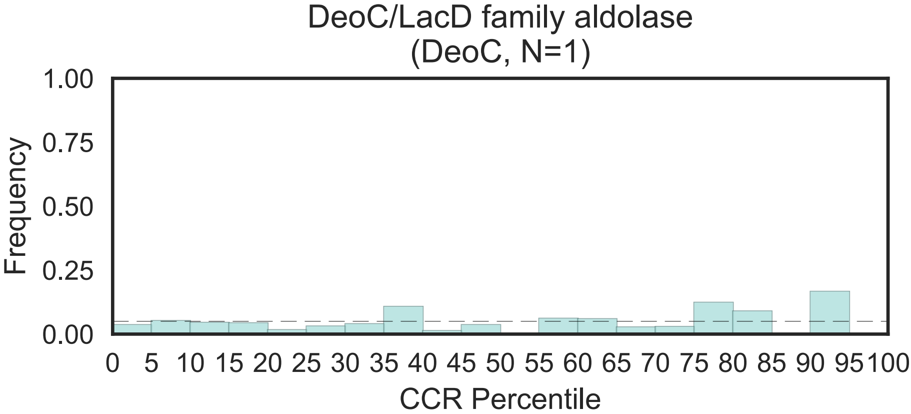


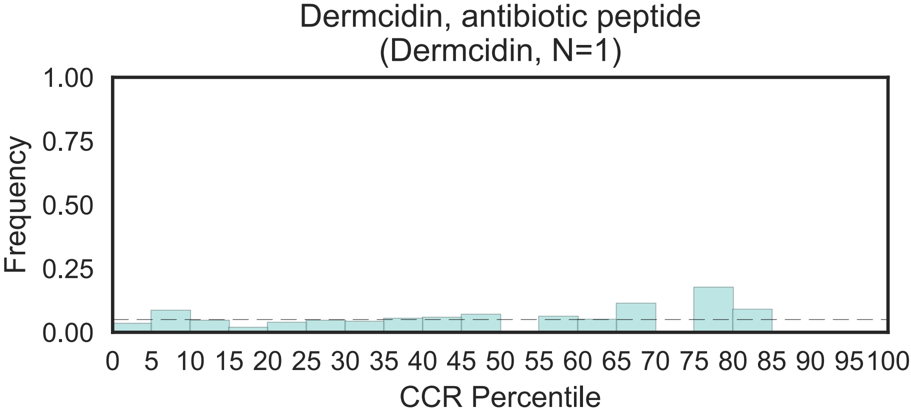

Big defensin
(Defensin_big, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

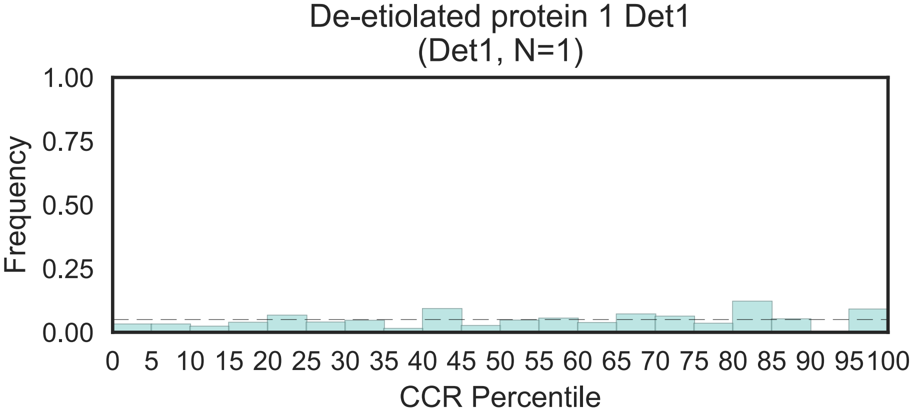

Defensin propeptide
(Defensin_propep, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

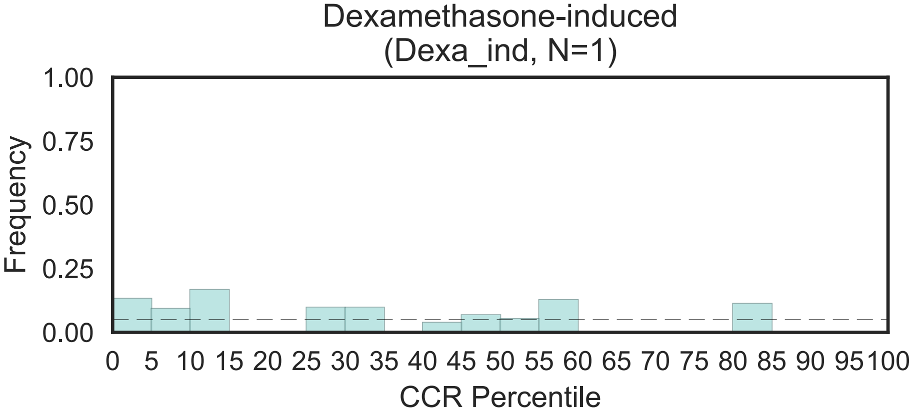

DegT/DnrJ/EryC1/StrS aminotransferase family
(DegT_DnrJ_EryC1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

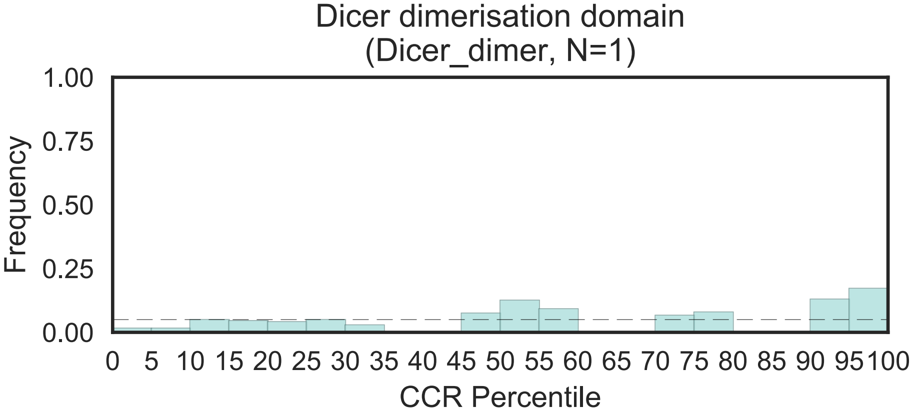

Nephrin and CD2AP-binding protein, Dendrin
(Dendrin, N=1)

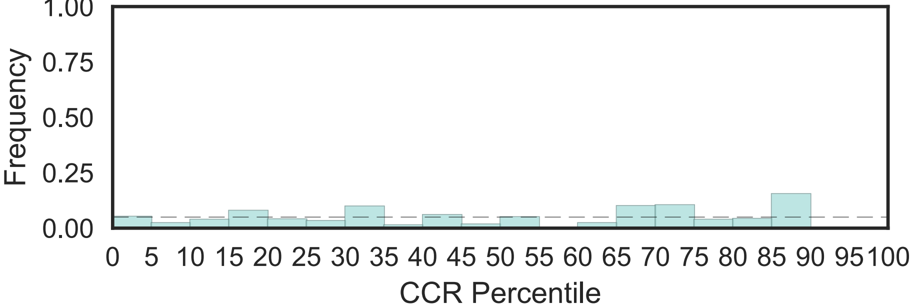

DeoC/LacD family aldolase
(DeoC, N=1)


Dermcidin, antibiotic peptide
(Dermcidin, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

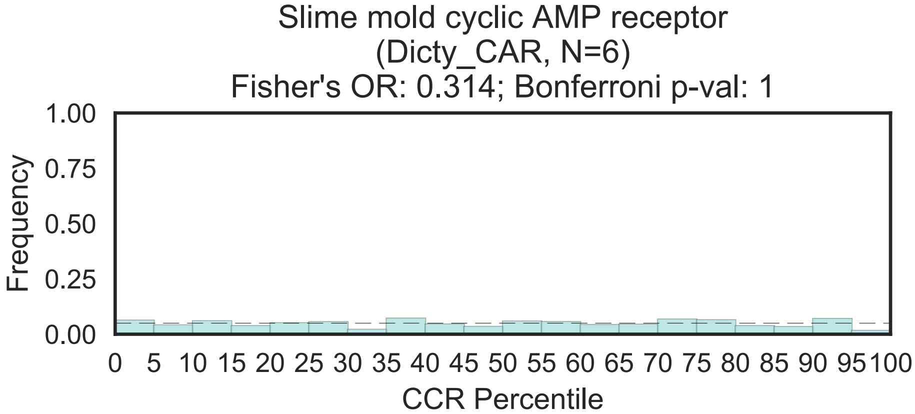

De-etiolated protein 1 Det1
(Det1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Dexamethasone-induced
(Dexa_ind, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

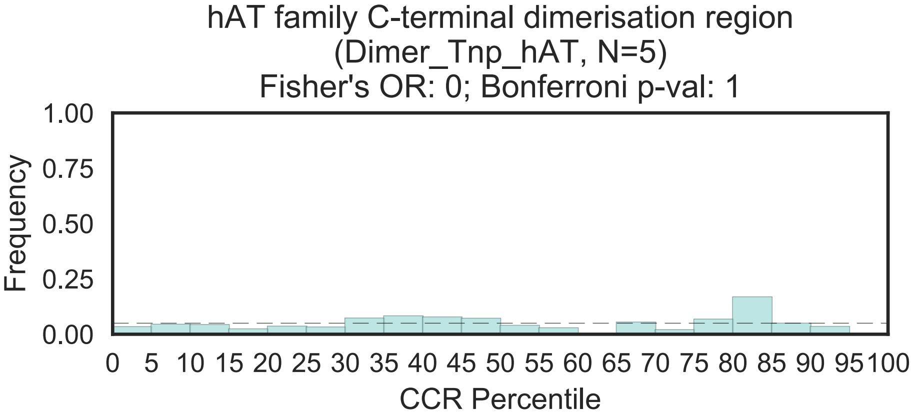

Dicer dimerisation domain
(Dicer_dimer, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

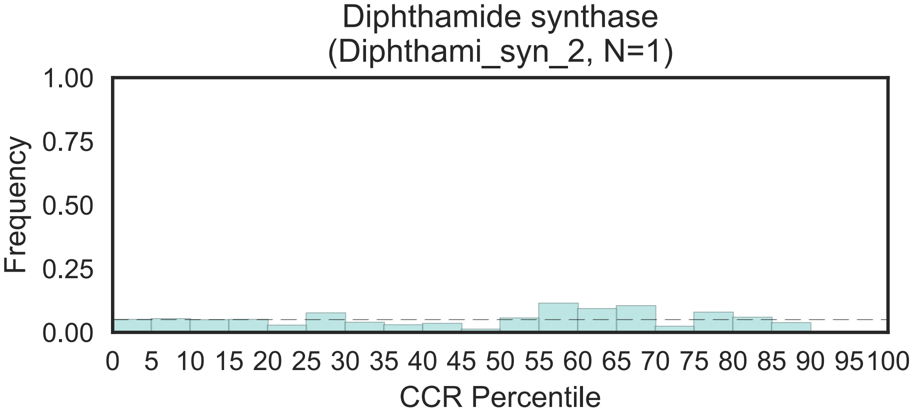


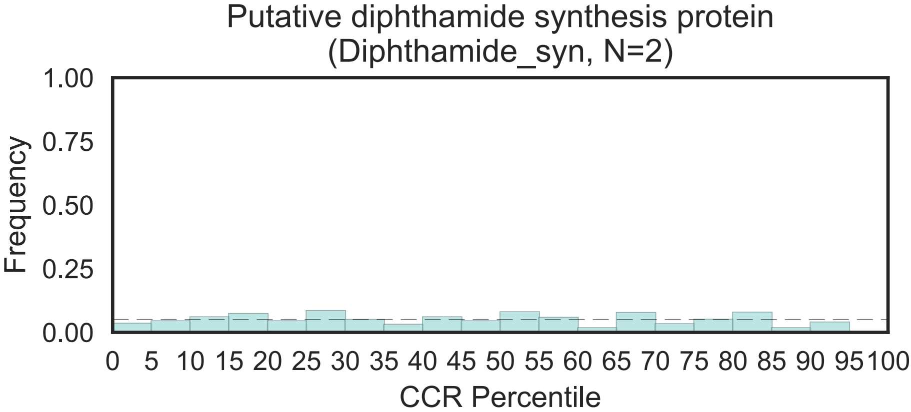
Dickkopf N-terminal cysteine-rich region
(Dickkopf_N, N=4)
Fisher's OR: 0; Bonferroni p-val: 1



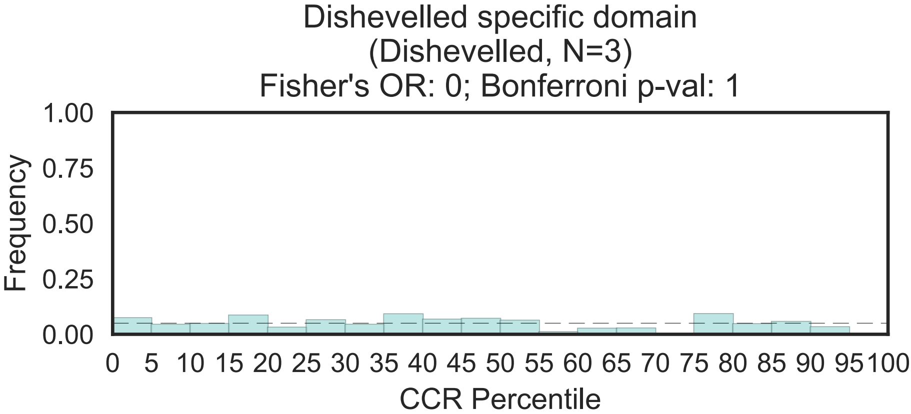
Slime mold cyclic AMP receptor
(Dicty_CAR, N=6)
Fisher's OR: 0.314; Bonferroni p-val: 1

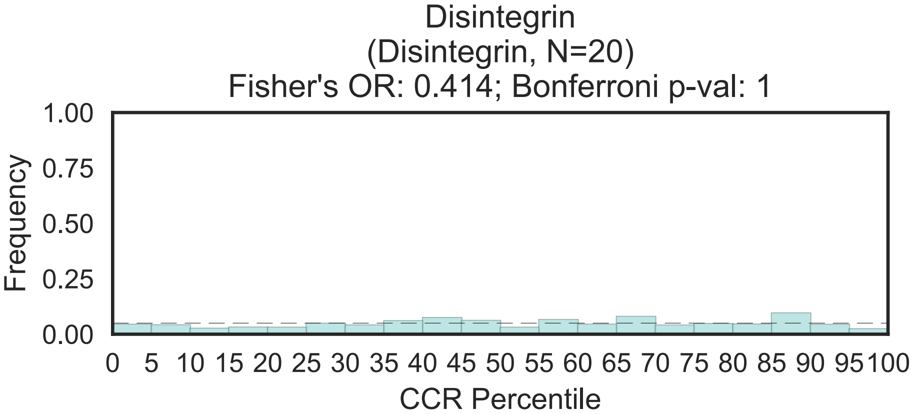

hAT family C-terminal dimerisation region
(Dimer_Tnp_hAT, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

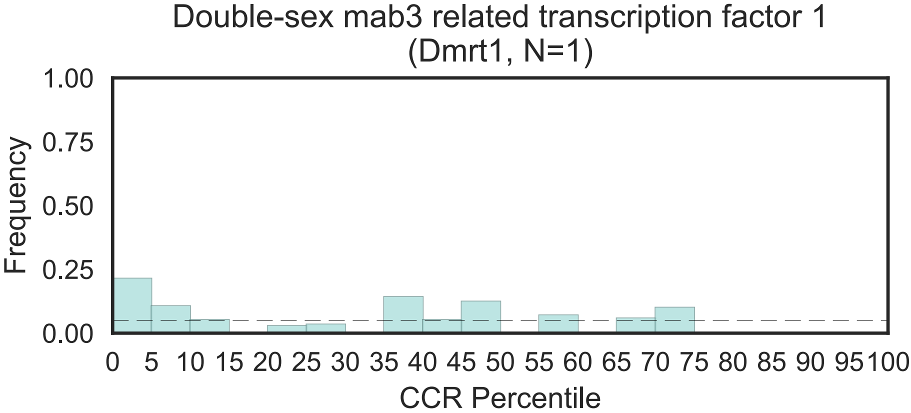

Diphthamide synthase
(Diphthami_syn_2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

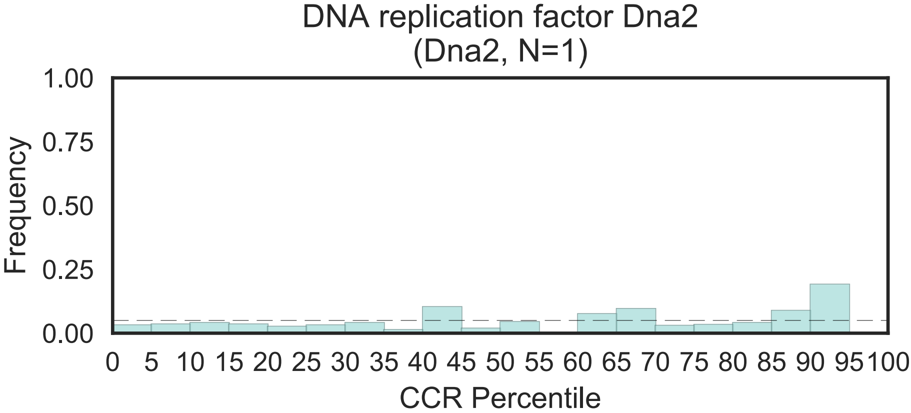


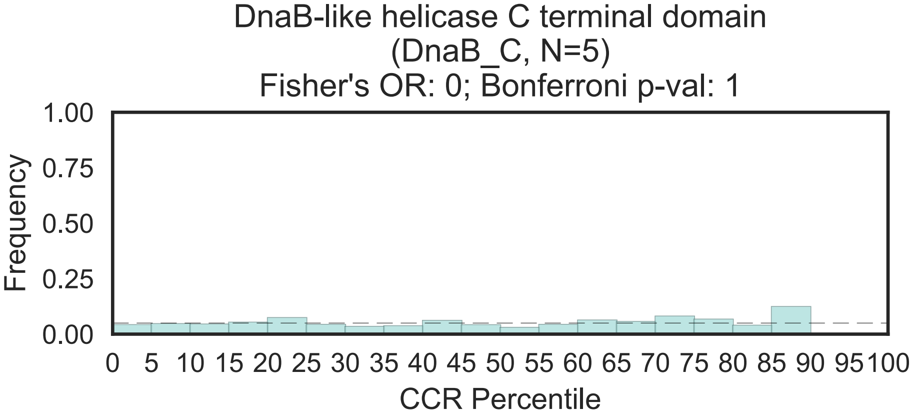
Putative diphthamide synthesis protein
(Diphthamide_syn, N=2)

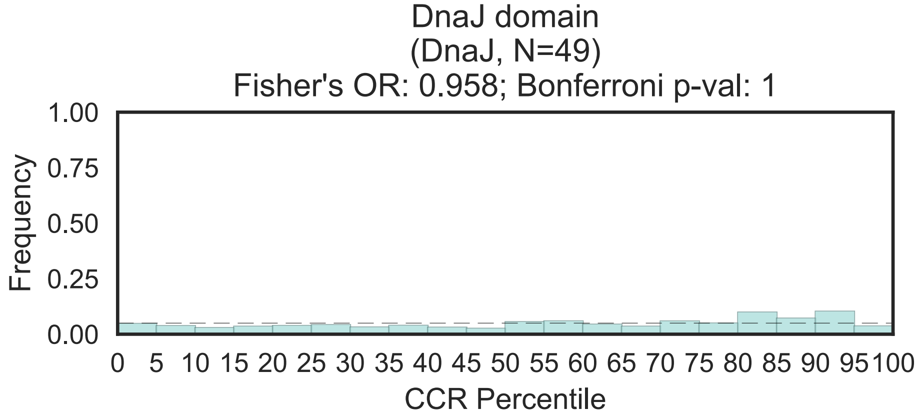

Dishevelled specific domain
(Dishevelled, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

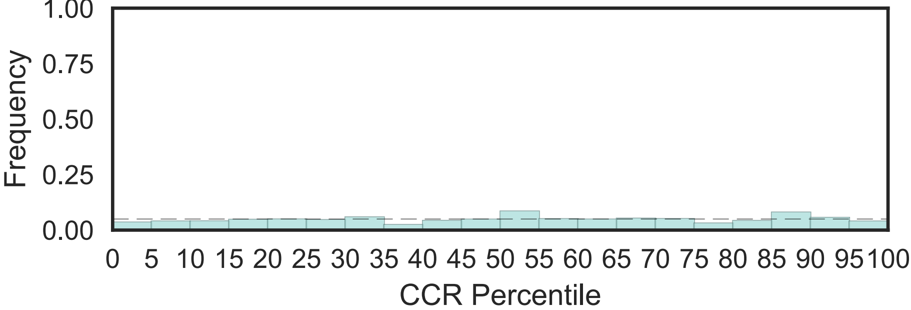

Disintegrin
(Disintegrin, N=20)
Fisher's OR: 0.414; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Double-sex mab3 related transcription factor 1
(Dmrt1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

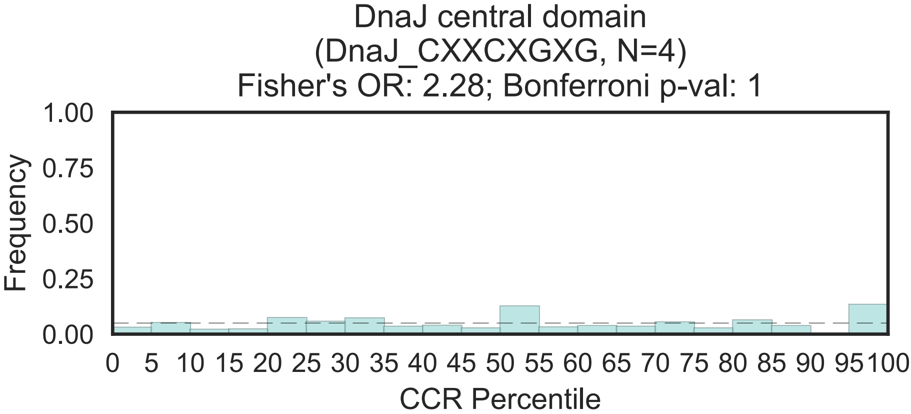

DNA replication factor Dna2
(Dna2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

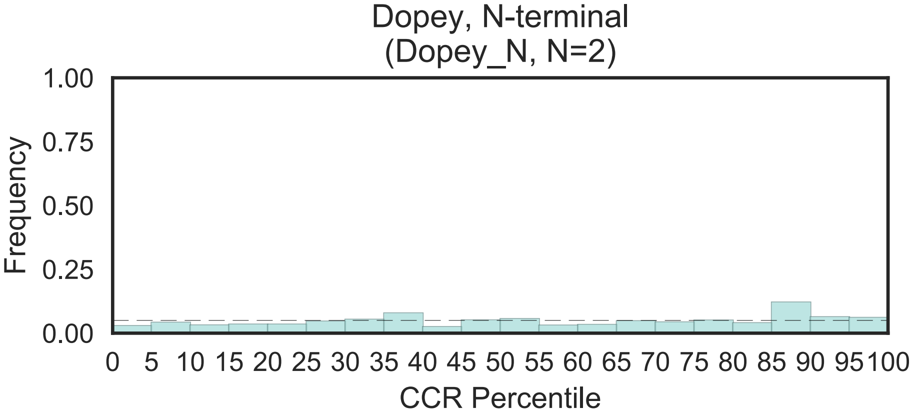

DnaB-like helicase C terminal domain
(DnaB_C, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

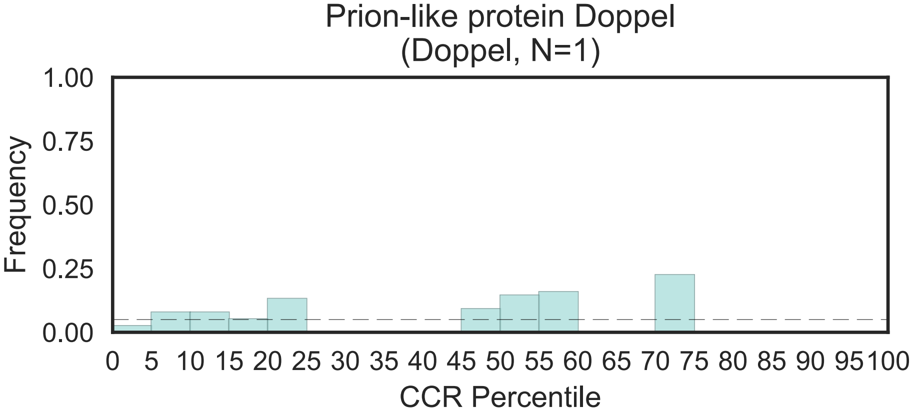

DnaJ domain
(DnaJ, N=49)
Fisher's OR: 0.958; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

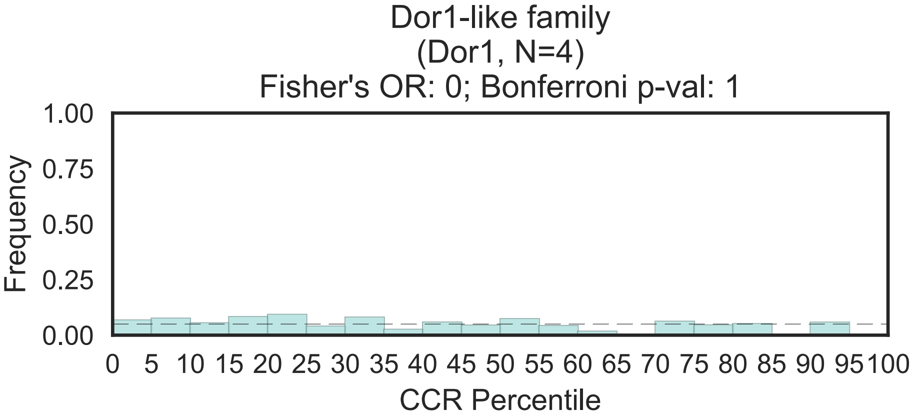


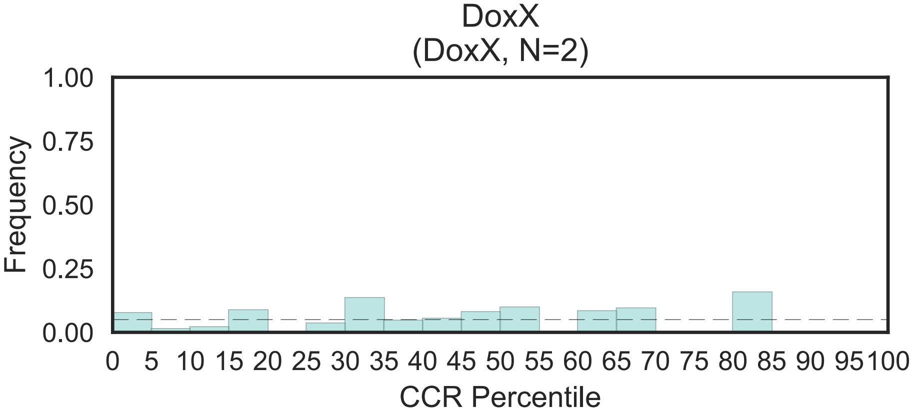
DnaJ C terminal domain
(DnaJ_C, N=10)
Fisher's OR: 0.779; Bonferroni p-val: 1

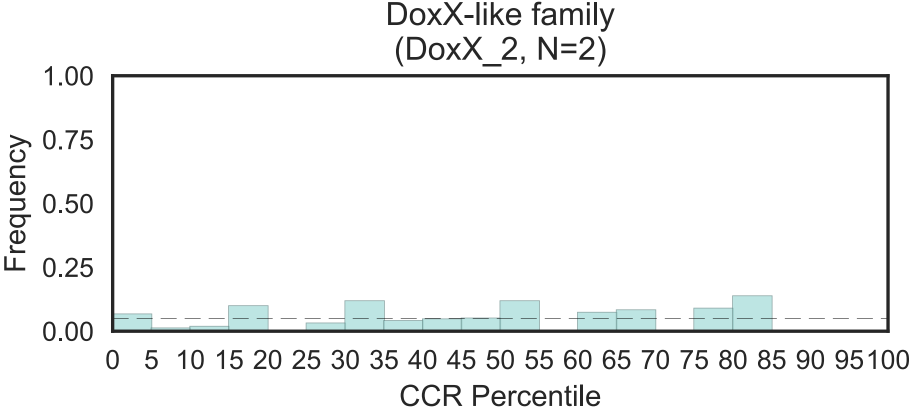

DnaJ central domain
(DnaJ_CXXCXGXG, N=4)
Fisher's OR: 2.28; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

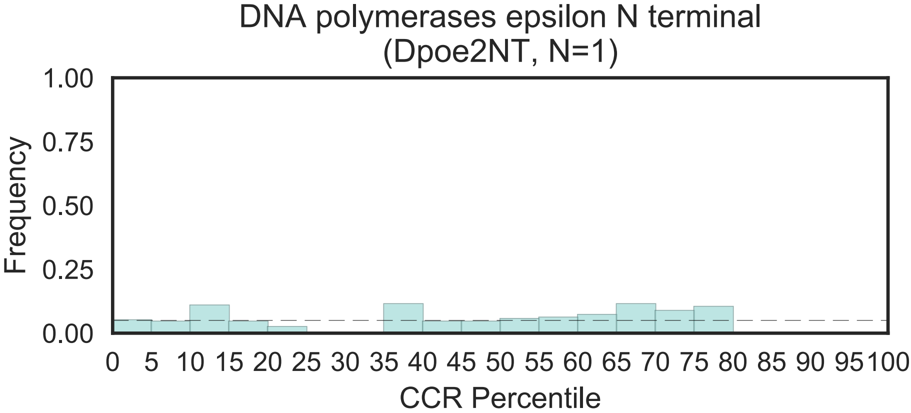

Dopey, N-terminal
(Dopey_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

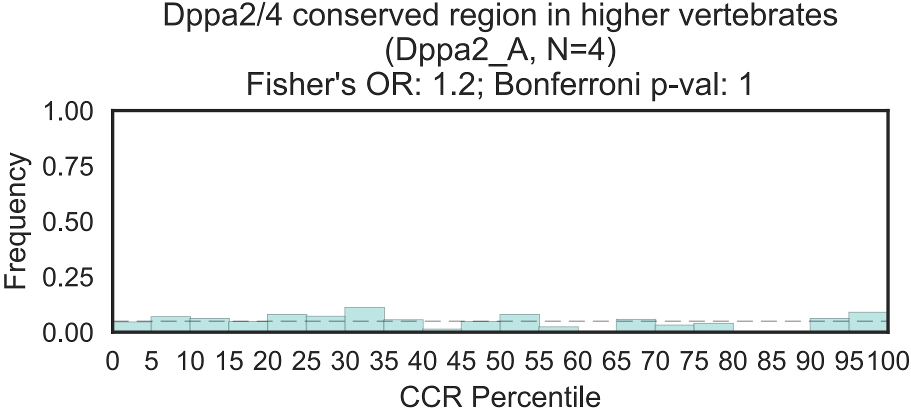

Prion-like protein Doppel
(Doppel, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

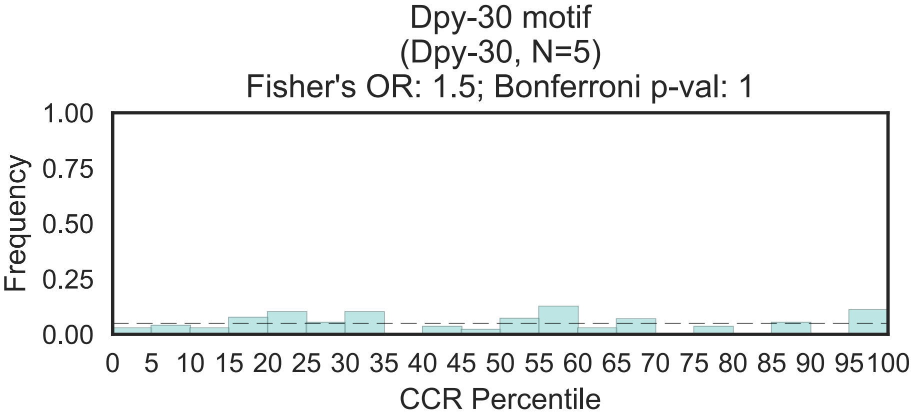

Dor1-like family
(Dor1, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

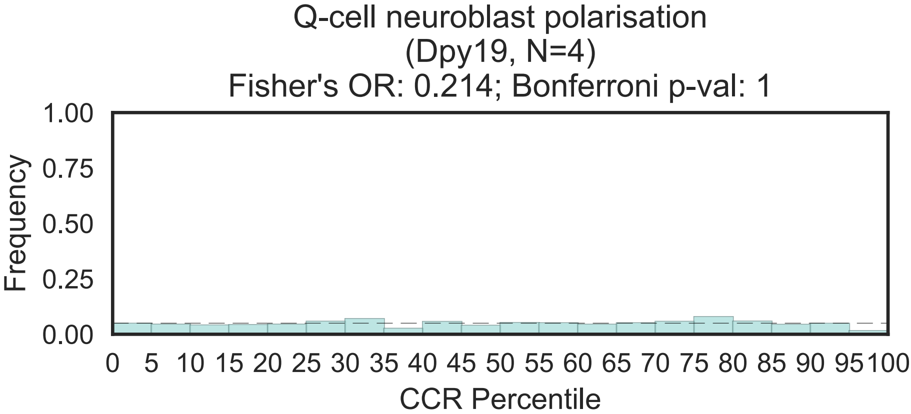

DoxX
(DoxX, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

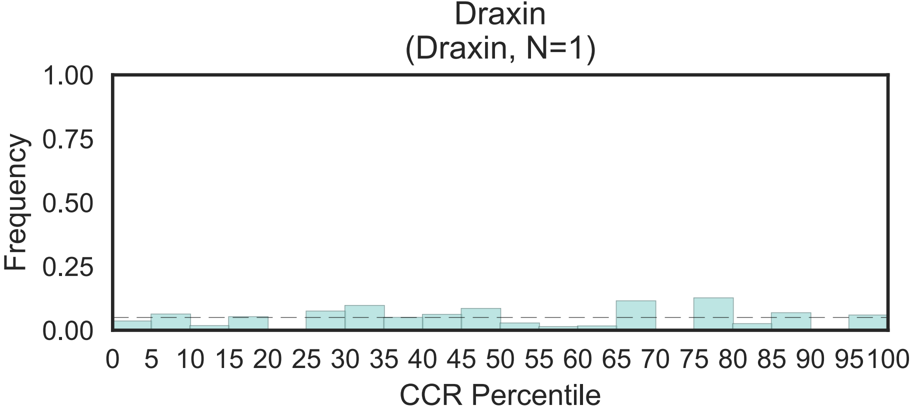

DoxX-like family
(DoxX_2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

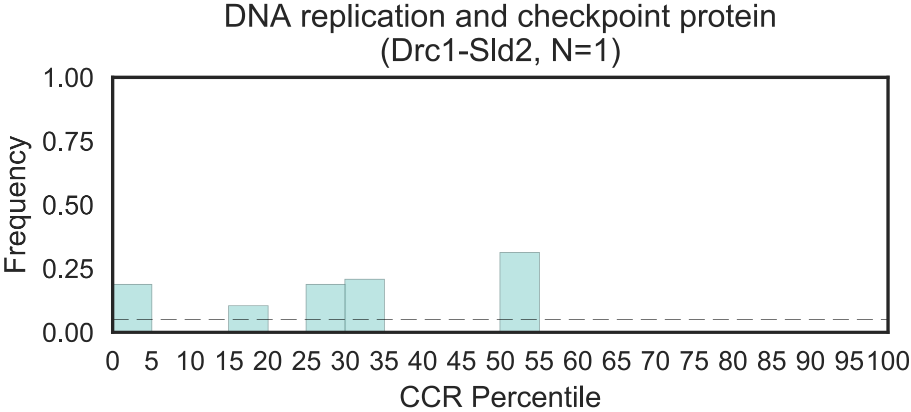

DNA polymerases epsilon N terminal
(Dpoe2NT, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

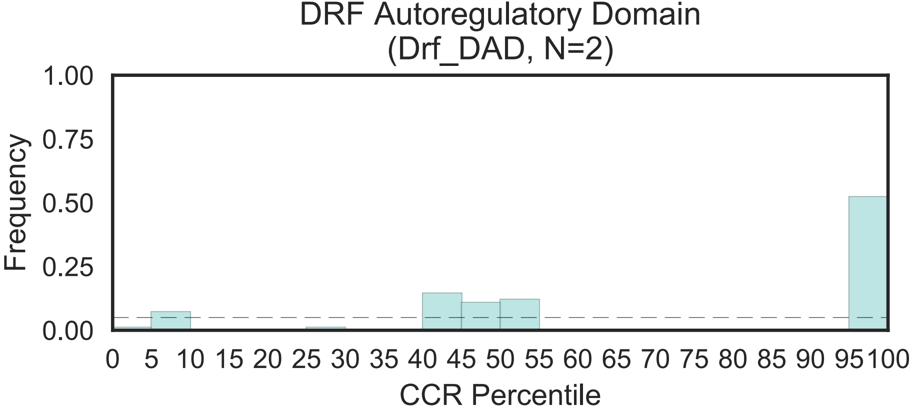

Dppa2/4 conserved region in higher vertebrates
(Dppa2_A, N=4)
Fisher's OR: 1.2; Bonferroni p-val: 1


Dpy-30 motif
(Dpy-30, N=5)
Fisher's OR: 1.5; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

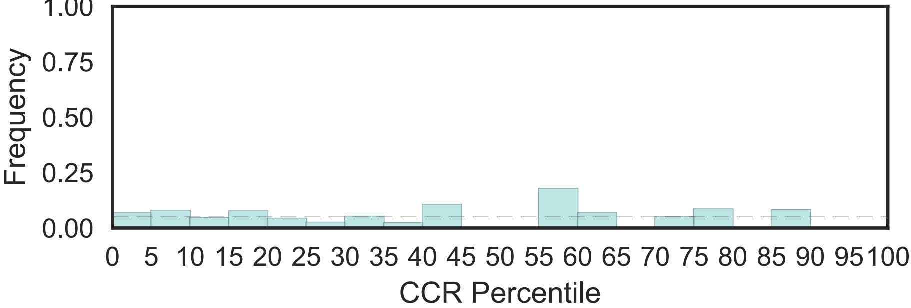

Q-cell neuroblast polarisation
(Dpy19, N=4)
Fisher's OR: 0.214; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

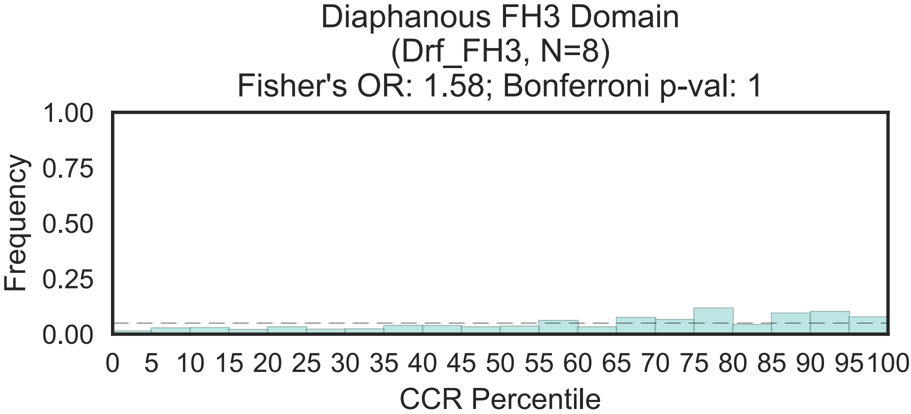

Draxin
(Draxin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

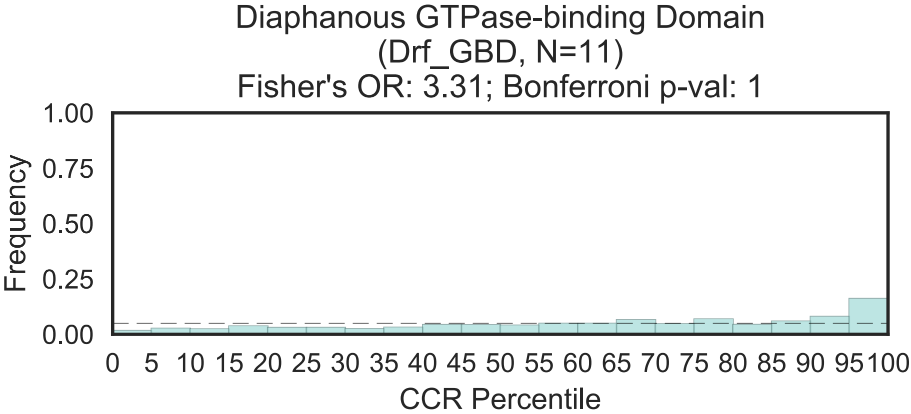

DNA replication and checkpoint protein
(Drc1-Sld2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


DRF Autoregulatory Domain
(Drf_DAD, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

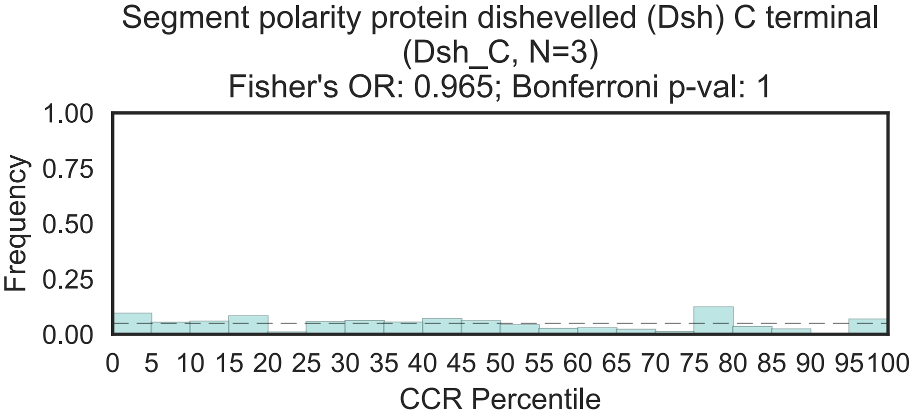
Formin Homology Region 1
(Drf_FH1, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

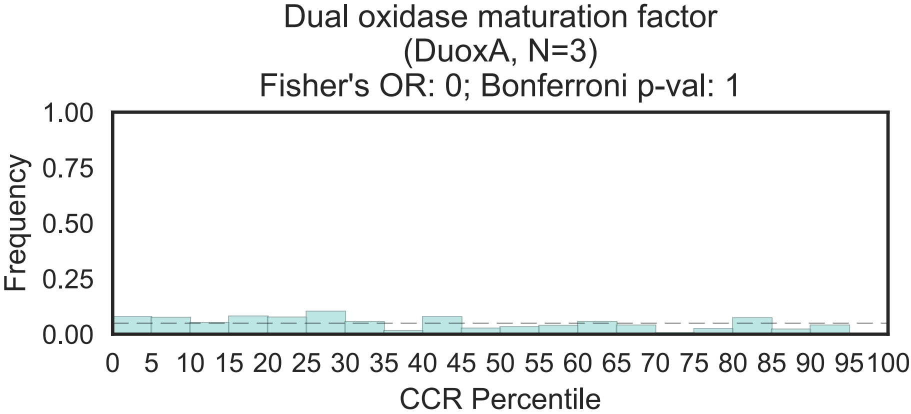



Diaphanous FH3 Domain
(Drf_FH3, N=8)
Fisher's OR: 1.58; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

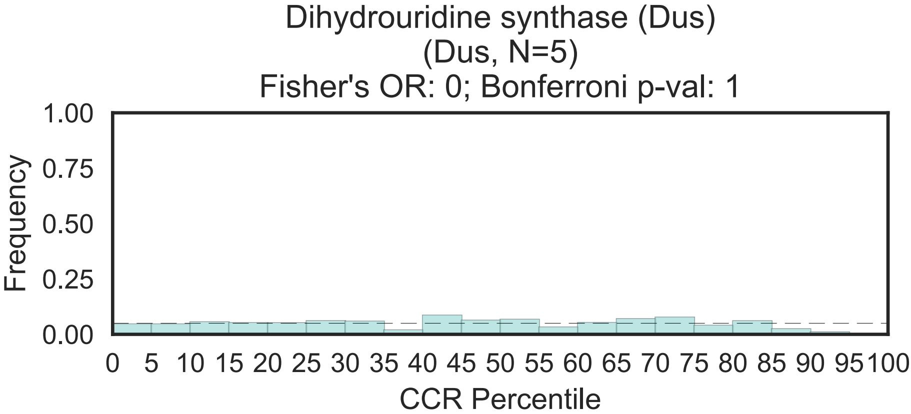


Diaphanous GTPase-binding Domain
(Drf_GBD, N=11)
Fisher's OR: 3.31; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

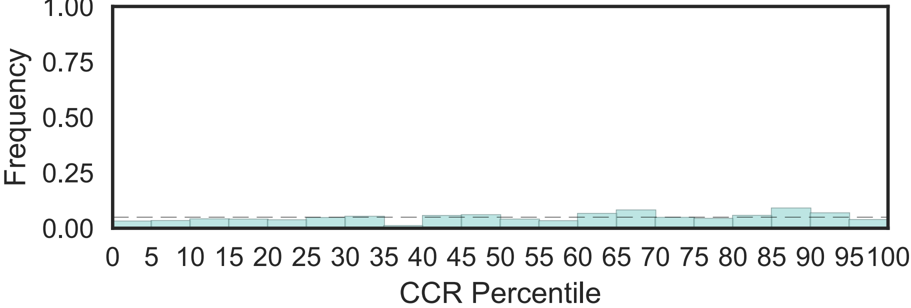

Segment polarity protein dishevelled (Dsh) C terminal
(Dsh_C, N=3)
Fisher's OR: 0.965; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

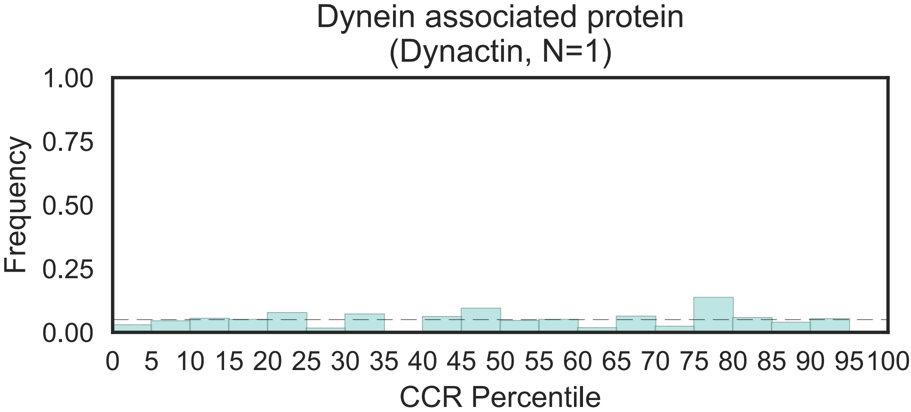


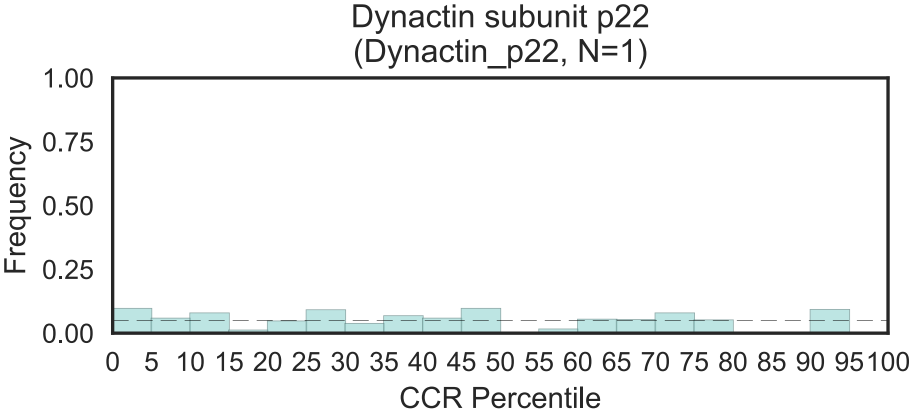
Dual oxidase maturation factor
(DuoxA, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

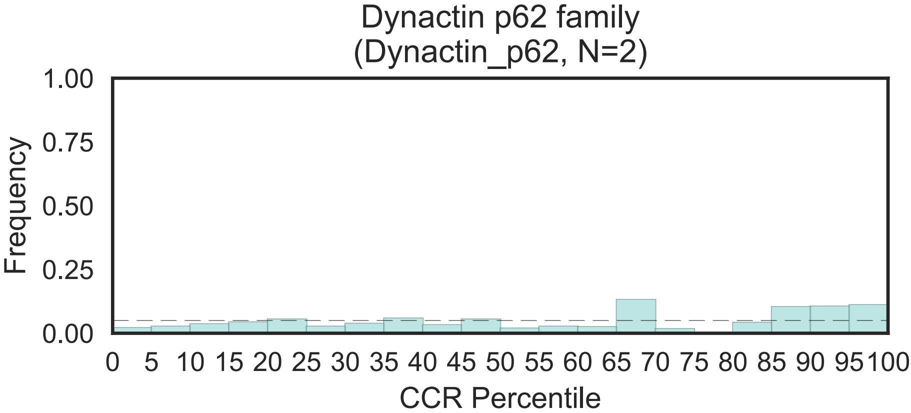


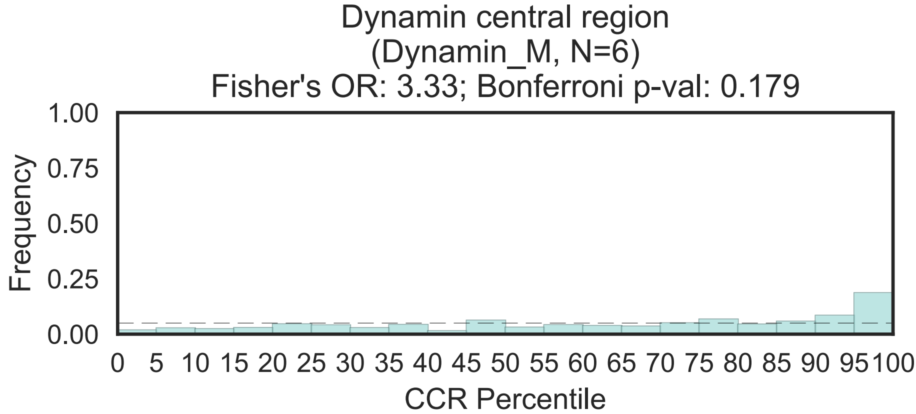
Dihydrouridine synthase (Dus)
(Dus, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

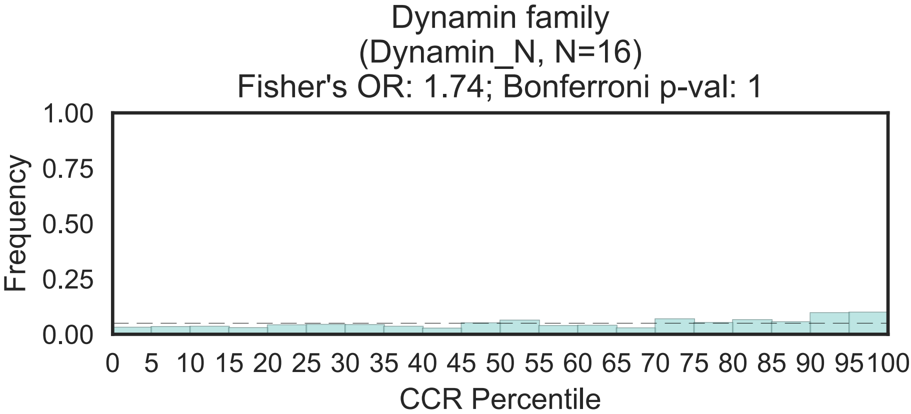

Dyggve-Melchior-Clausen syndrome protein
(Dymeclin, N=3)
Fisher's OR: 0.654; Bonferroni p-val: 1

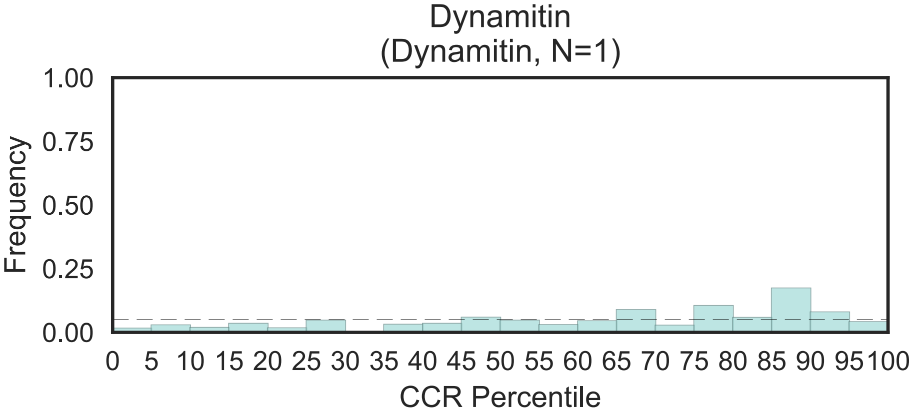

Dynein associated protein
(Dynactin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

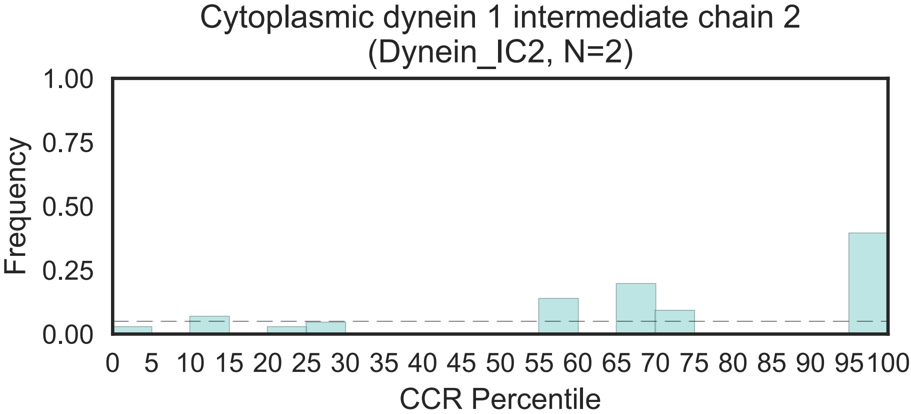

Dynactin subunit p22
(Dynactin_p22, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

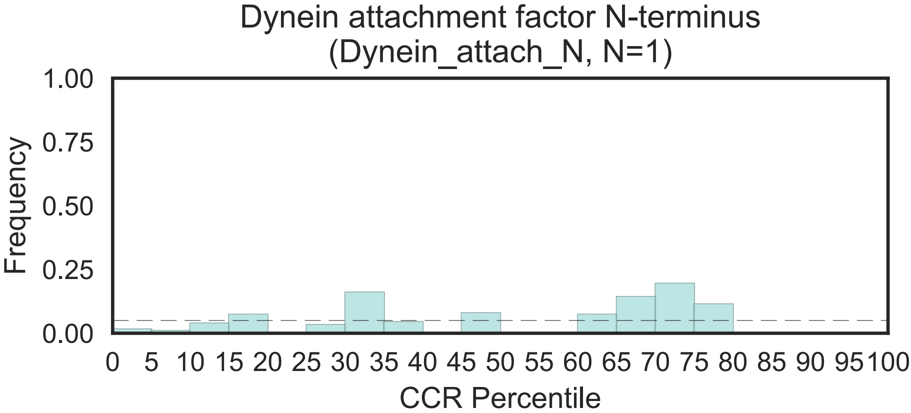

Dynactin p62 family
(Dynactin_p62, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

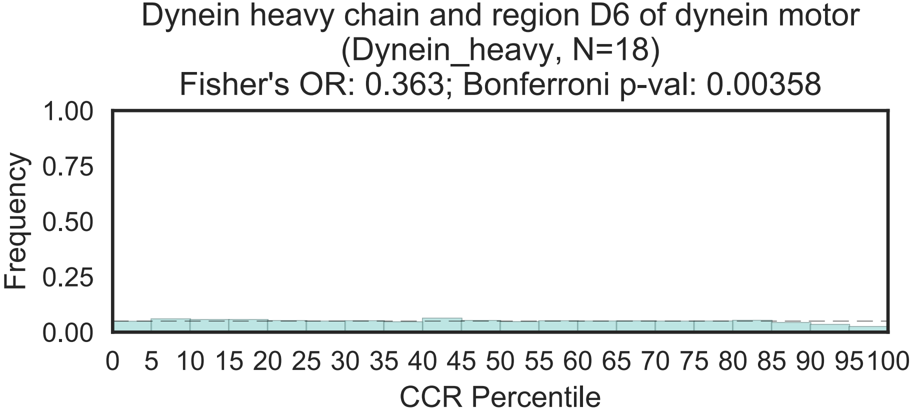

Dynamin central region
(Dynamin_M, N=6)
Fisher's OR: 3.33; Bonferroni p-val: 0.179
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

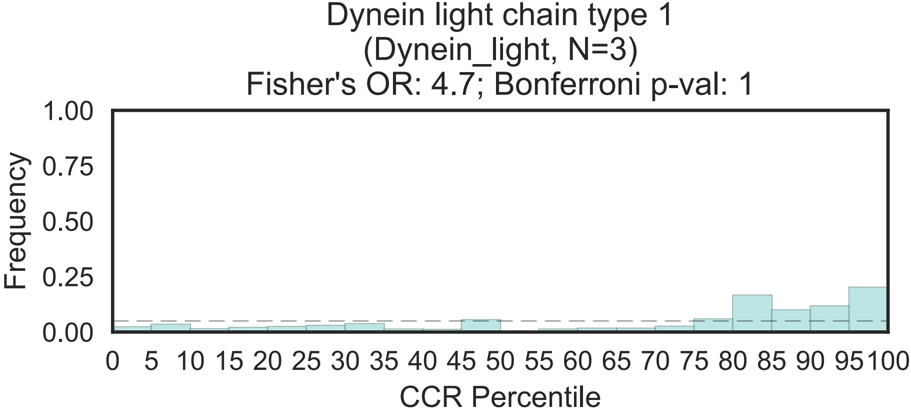

Dynamin family
(Dynamin_N, N=16)
Fisher's OR: 1.74; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

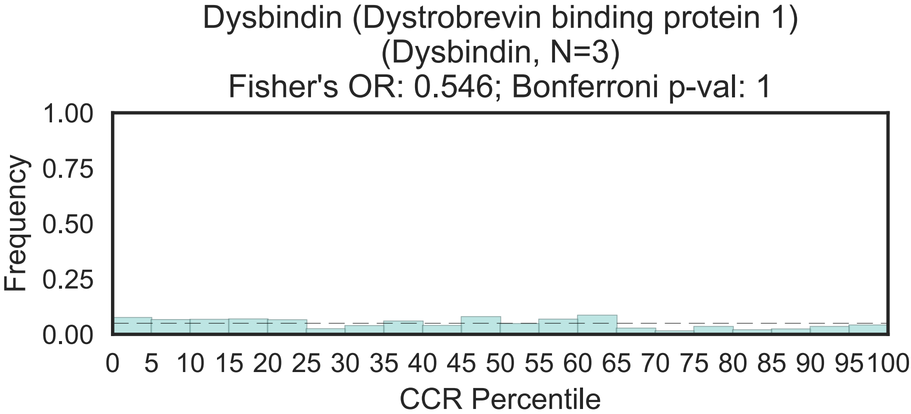

Dynamitin
(Dynamitin, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


Cytoplasmic dynein 1 intermediate chain 2
(Dynein_IC2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

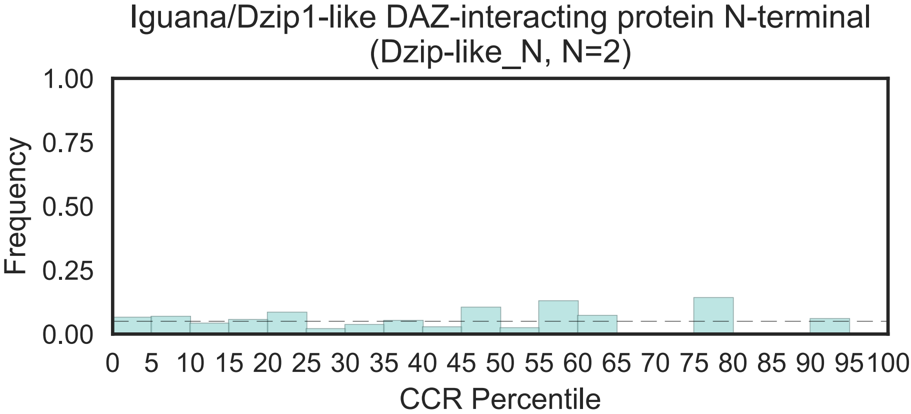

Dynein attachment factor N-terminus
(Dynein_attach_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

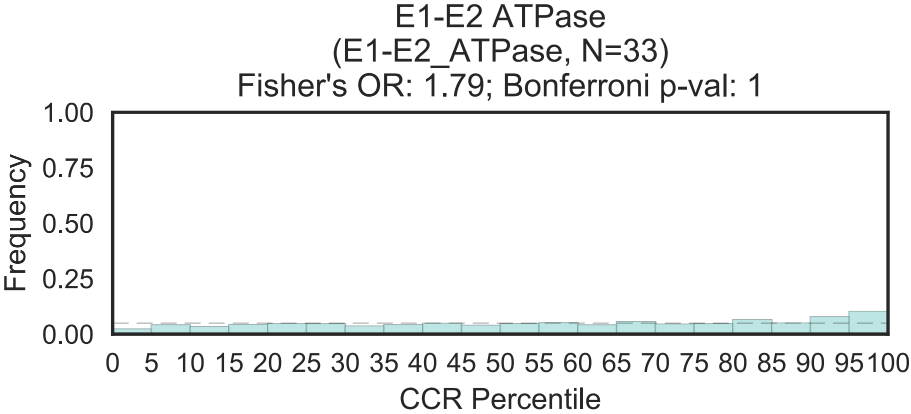

Dynein heavy chain and region D6 of dynein motor
(Dynein_heavy, N=18)
Fisher's OR: 0.363; Bonferroni p-val: 0.00358
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

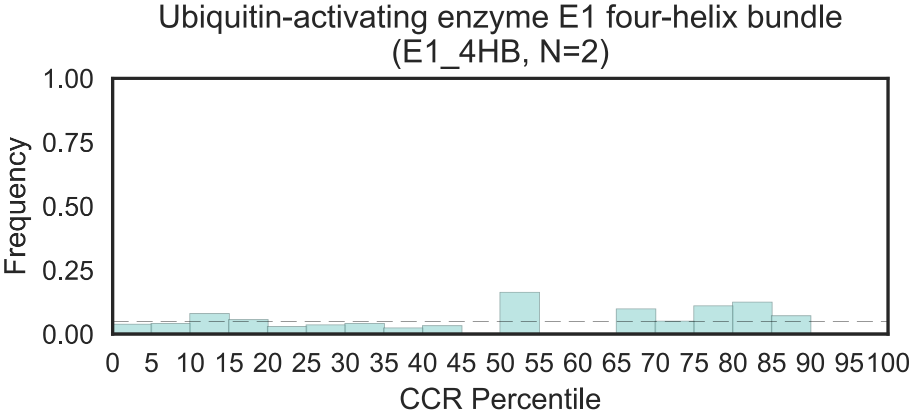

Dynein light chain type 1
(Dynein_light, N=3)
Fisher's OR: 4.7; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



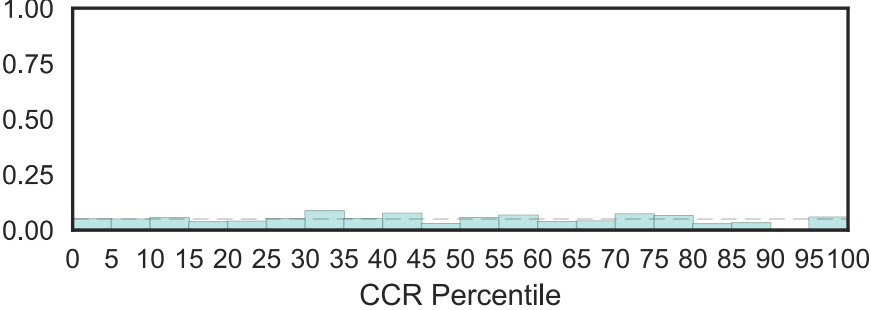
Dysbindin (Dystrobrevin binding protein 1)
(Dysbindin, N=3)
Fisher's OR: 0.546; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

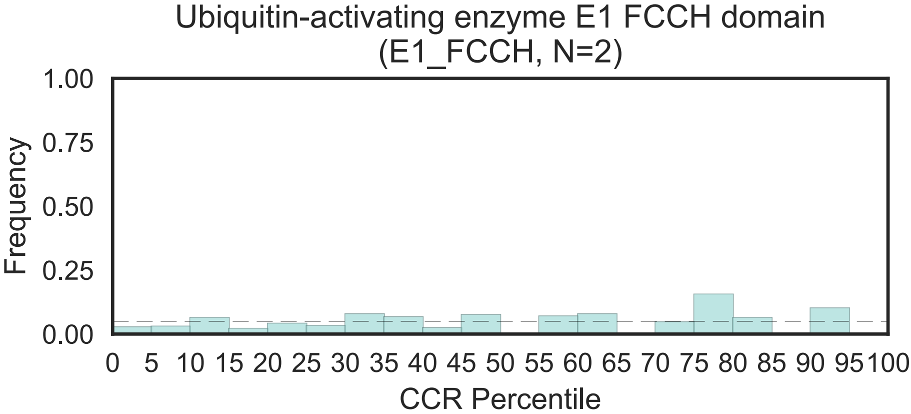

Iguana/Dzip1-like DAZ-interacting protein N-terminal
(Dzip-like_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

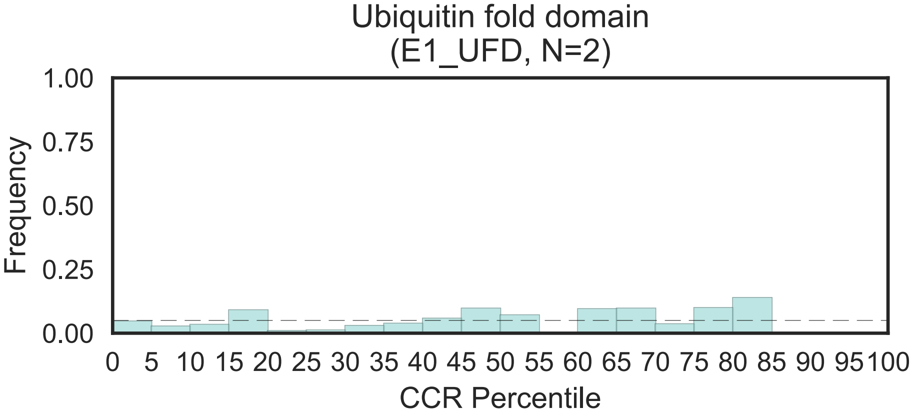

E1-E2 ATPase
(E1-E2_ATPase, N=33)
Fisher's OR: 1.79; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ubiquitin-activating enzyme E1 four-helix bundle
(E1_4HB, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

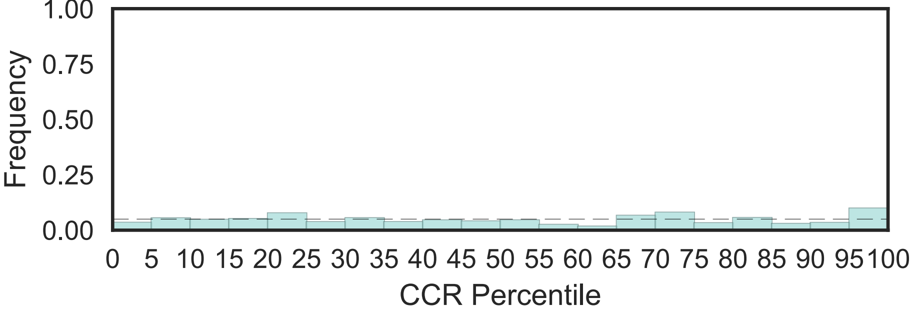
ML domain
(E1_DerP2_DerF2, N=4)
Fisher's OR: 0.498; Bonferroni p-val: 1

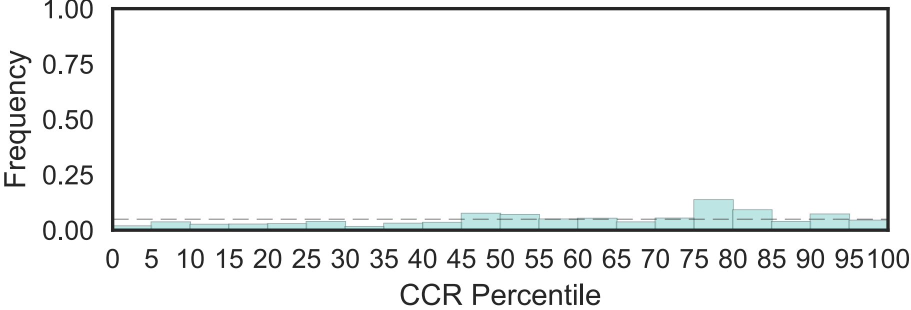


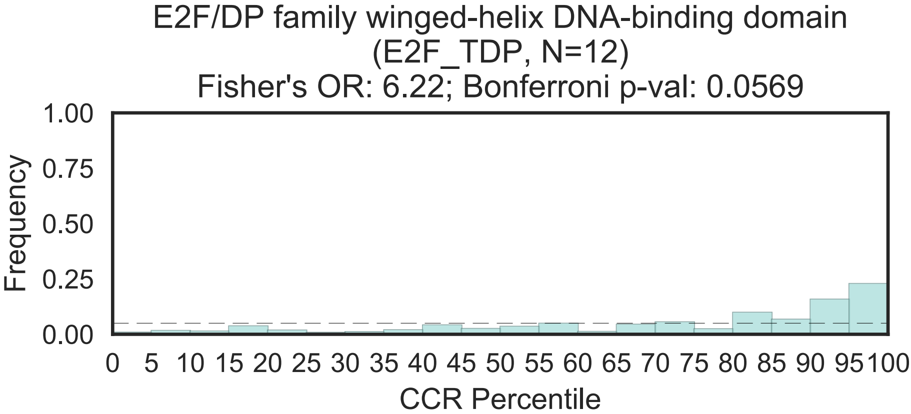

Ubiquitin-activating enzyme E1 FCCH domain
(E1_FCCH, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

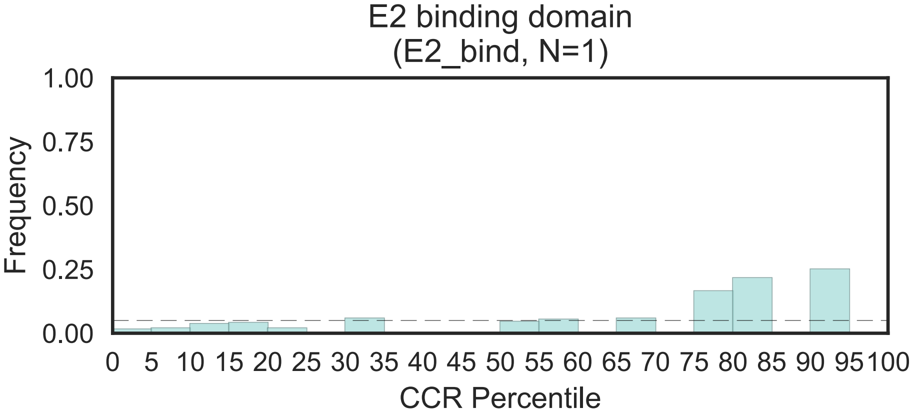

Ubiquitin fold domain
(E1_UFD, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Dehydrogenase E1 component (E1_dh, N=8) Fisher's OR: 1.29; Bonferroni p-val: 1

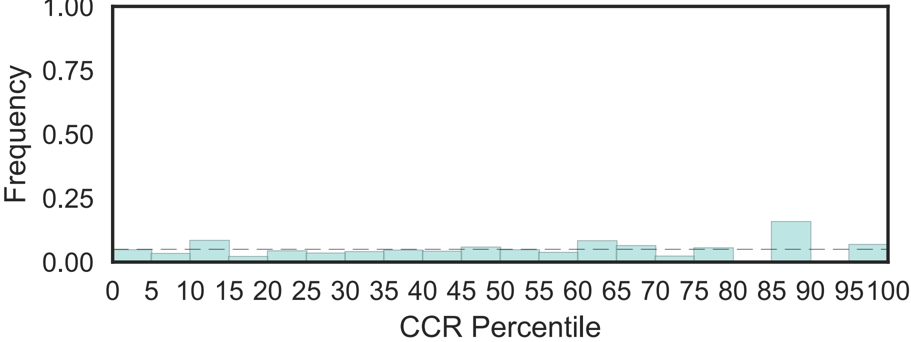


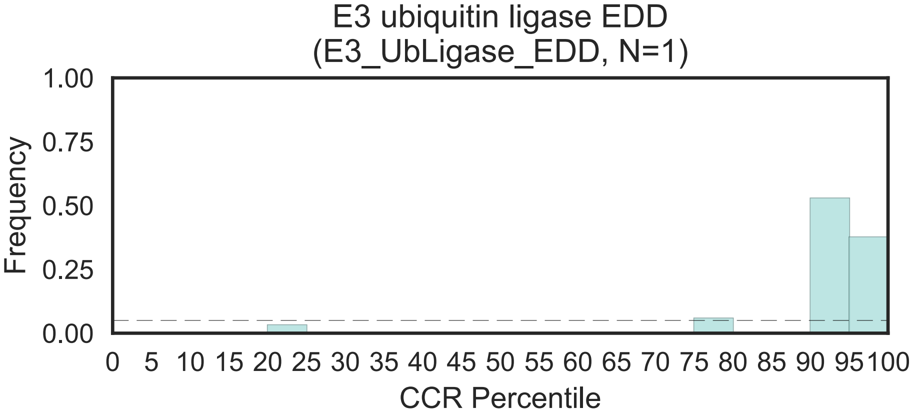

E2F transcription factor CC-MB domain
(E2F_CC-MB, N=6)
Fisher's OR: 0.594; Bonferroni p-val: 1

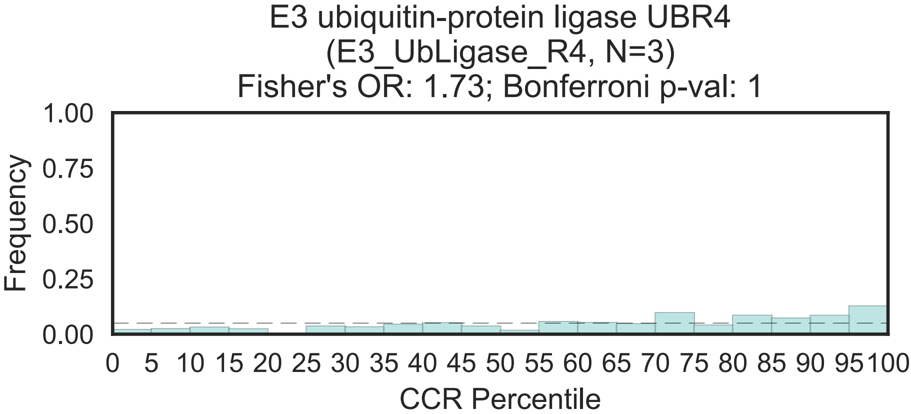

E2F/DP family winged-helix DNA-binding domain
(E2F_TDP, N=12)
Fisher's OR: 6.22; Bonferroni p-val: 0.0569
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

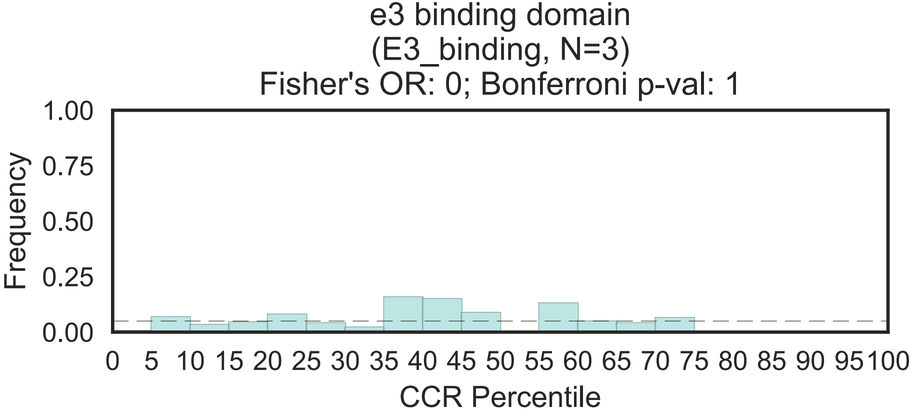

E2 binding domain
(E2_bind, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

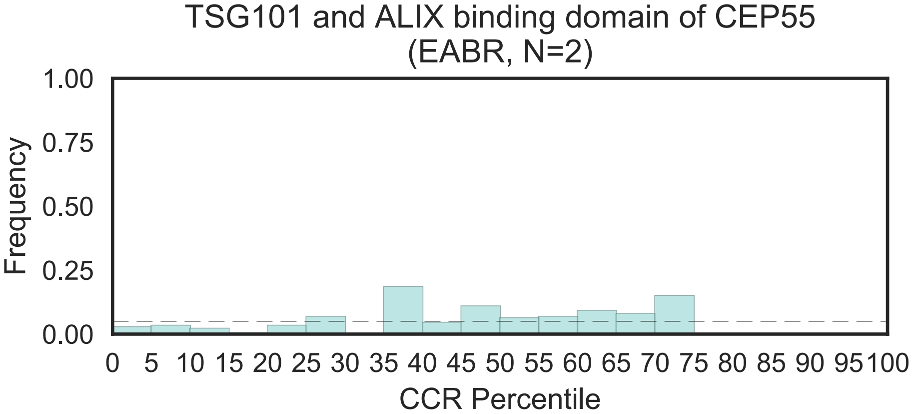
E3 UFM1-protein ligase 1
(E3_UFM1_ligase, N=1)

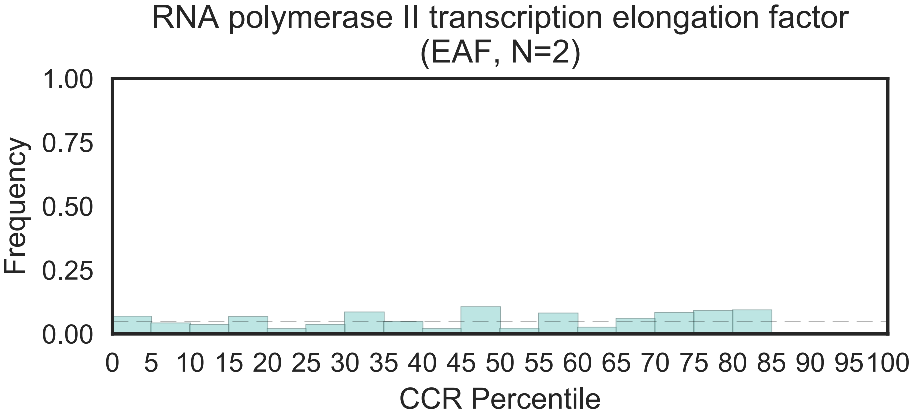


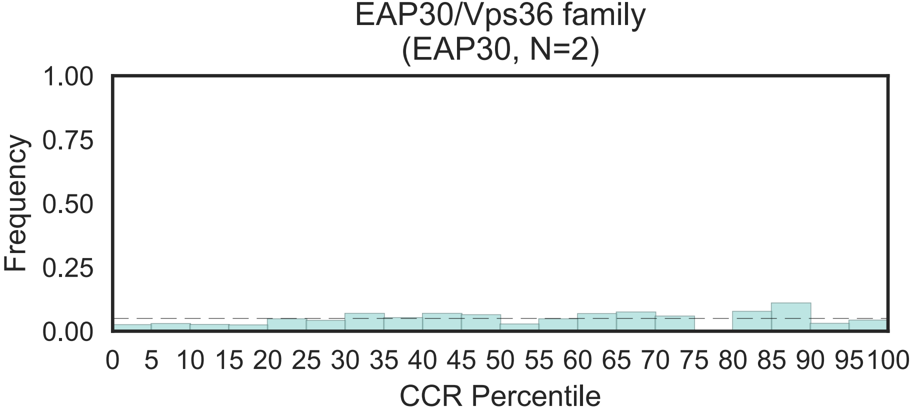

E3 ubiquitin ligase EDD
(E3_UbLigase_EDD, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

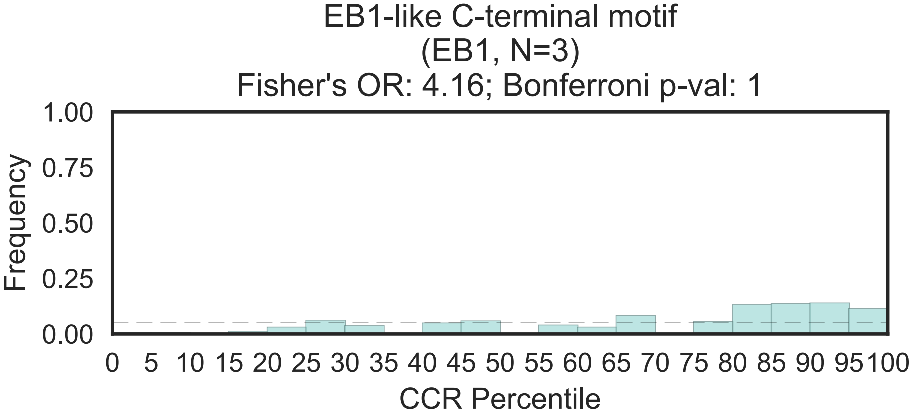

E3 ubiquitin-protein ligase UBR4
(E3_UbLigase_R4, N=3)
Fisher's OR: 1.73; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

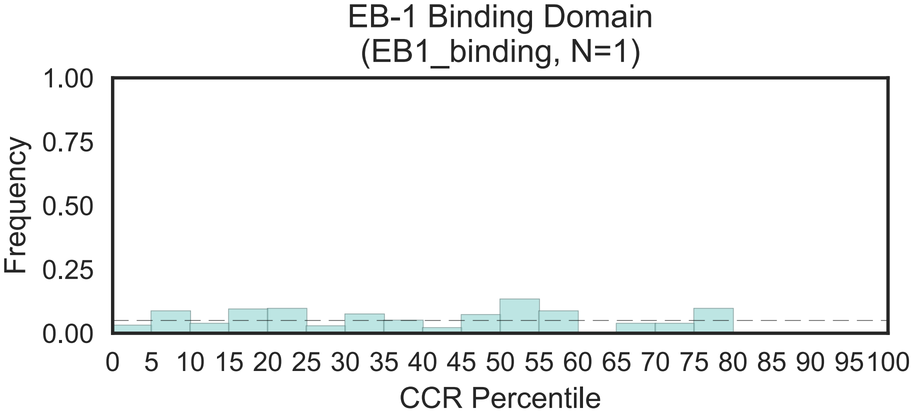

e3 binding domain
(E3_binding, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

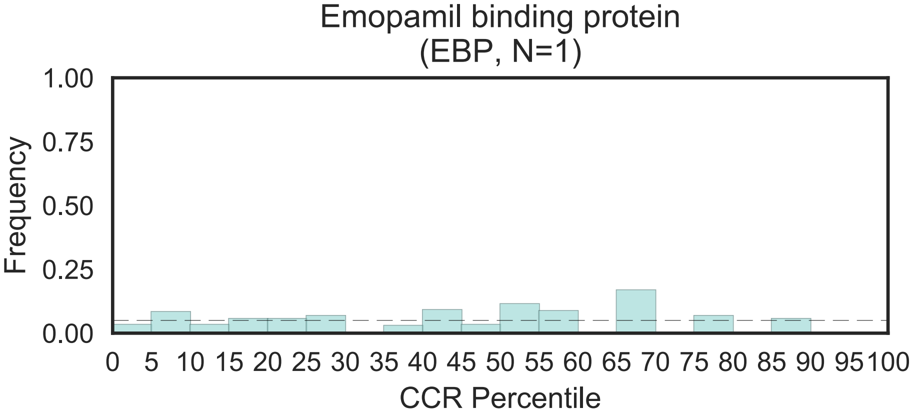

TSG101 and ALIX binding domain of CEP55
(EABR, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

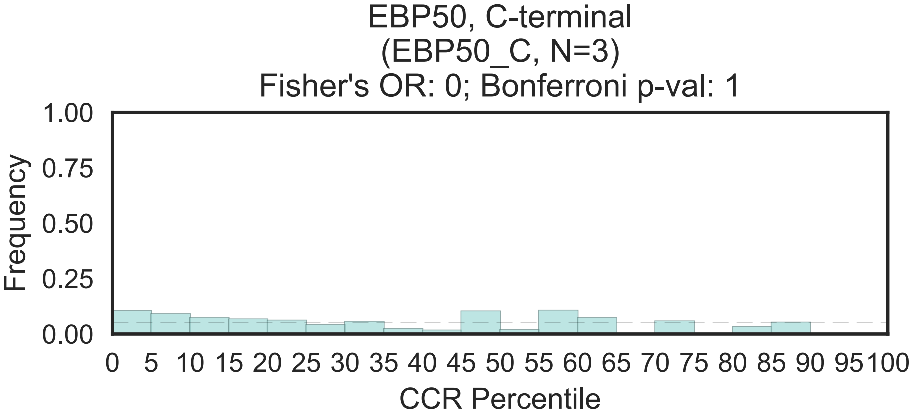

RNA polymerase II transcription elongation factor
(EAF, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

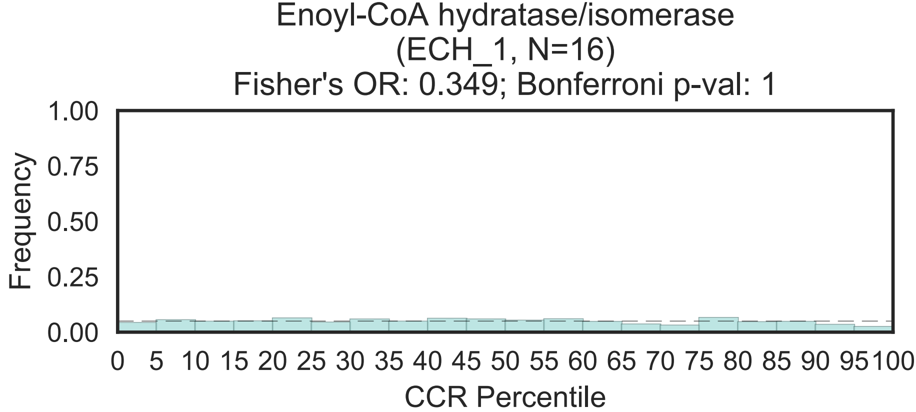

EAP30/Vps36 family
(EAP30, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

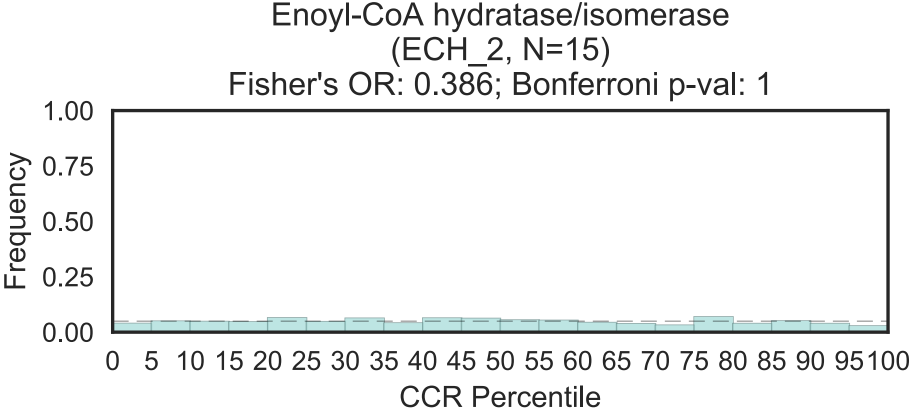

EB1-like C-terminal motif
(EB1, N=3)
Fisher's OR: 4.16; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

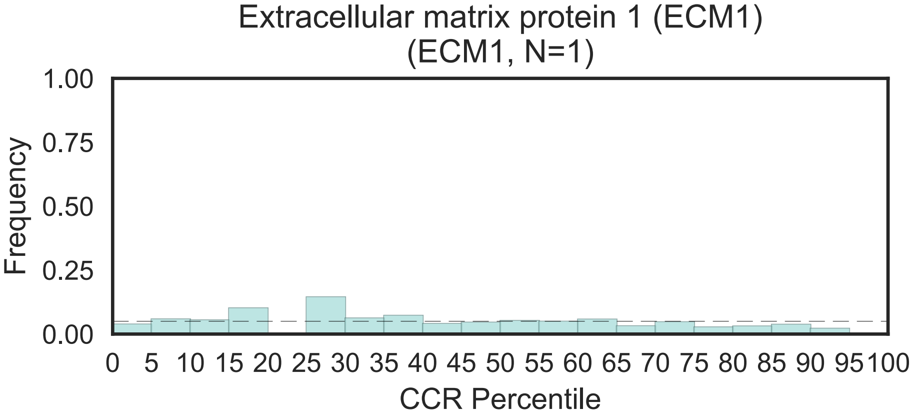

EB-1 Binding Domain
(EB1_binding, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

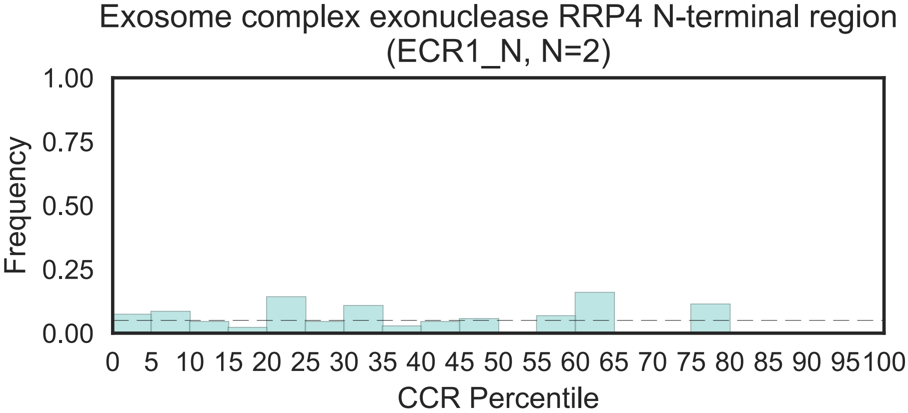

Emopamil binding protein
(EBP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

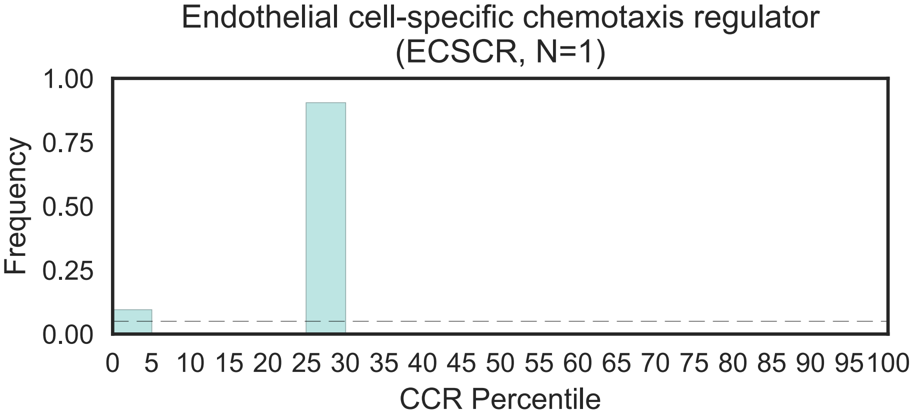

EBP50, C-terminal
(EBP50_C, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

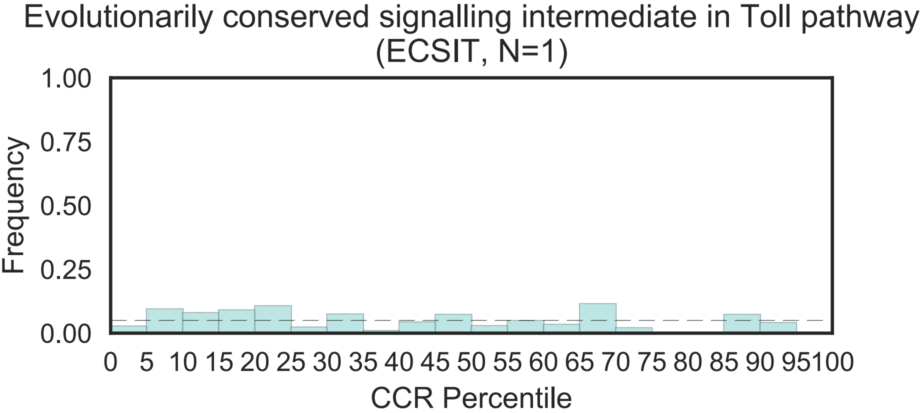

Enoyl-CoA hydratase/isomerase
(ECH_1, N=16)
Fisher's OR: 0.349; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

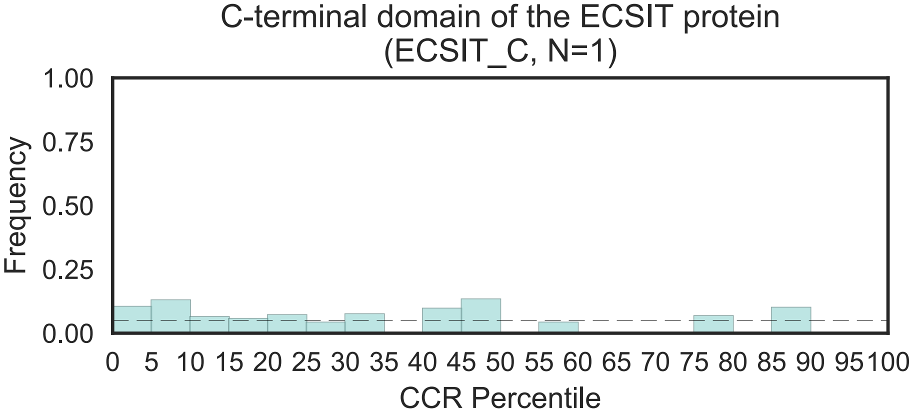

Enoyl-CoA hydratase/isomerase
(ECH_2, N=15)
Fisher's OR: 0.386; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

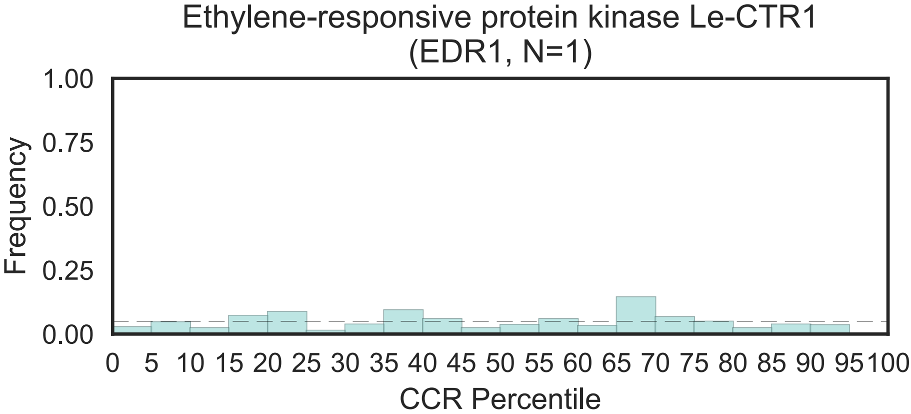

Extracellular matrix protein 1 (ECM1)
(ECM1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

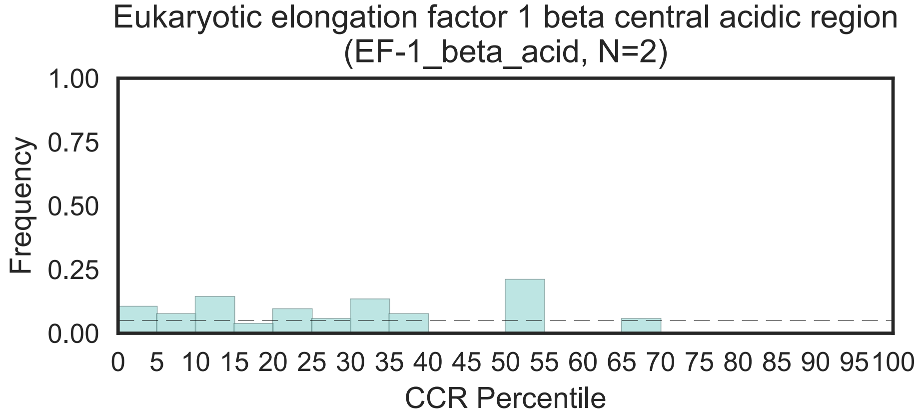

Exosome complex exonuclease RRP4 N-terminal region
(ECR1_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

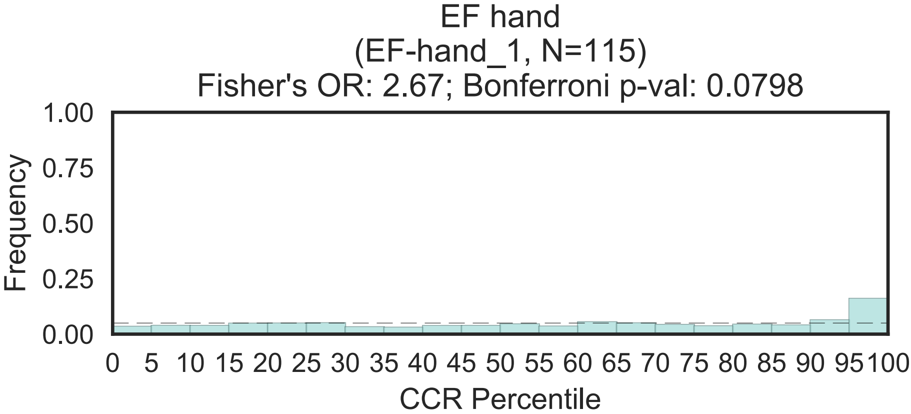

Endothelial cell-specific chemotaxis regulator
(ECSCR, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

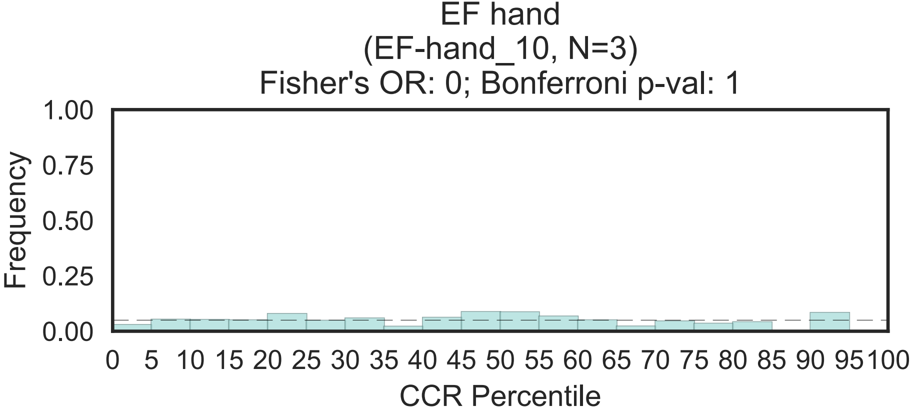

Evolutionarily conserved signalling intermediate in Toll pathway
(ECSIT, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

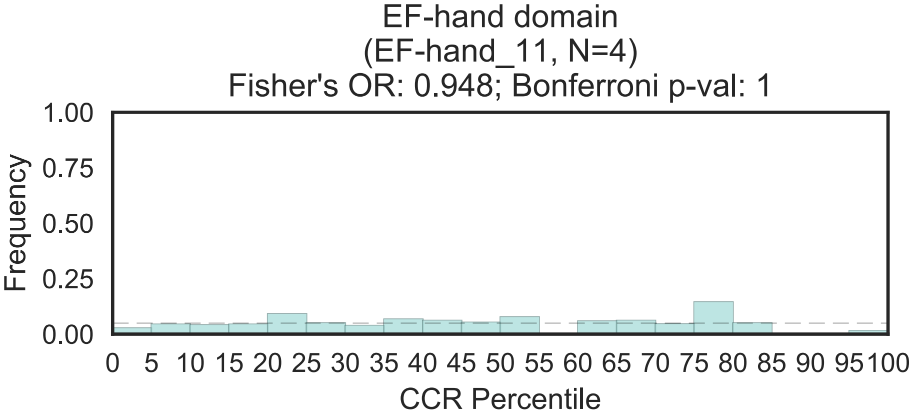

C-terminal domain of the ECSIT protein
(ECSIT_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

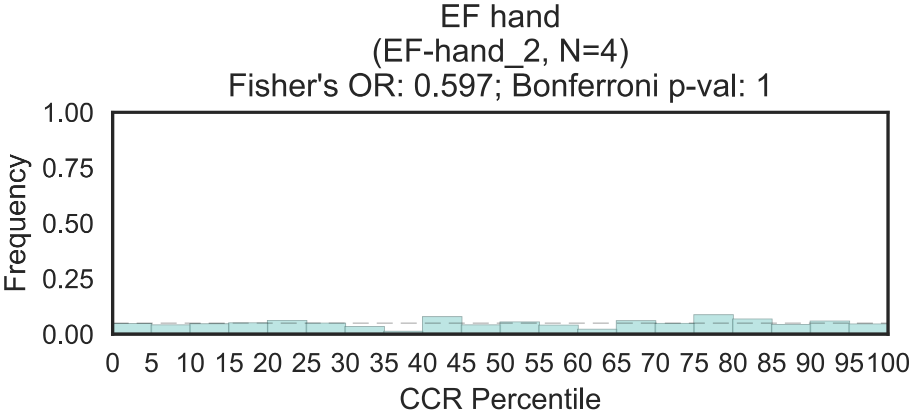

Ethylene-responsive protein kinase Le-CTR1
(EDR1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

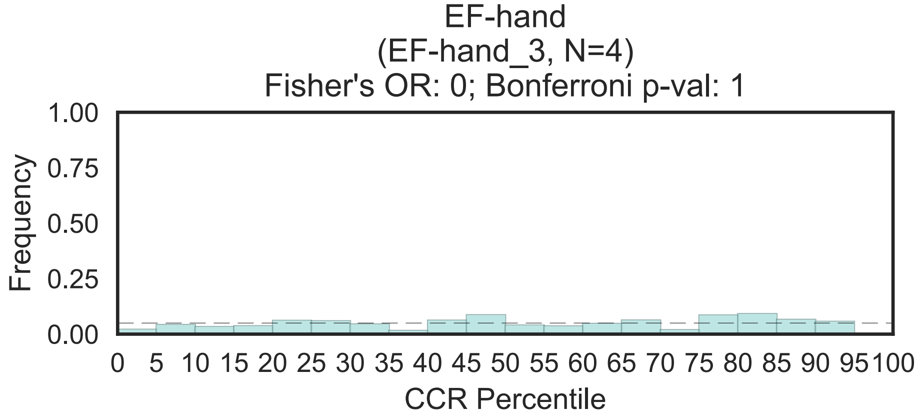

Eukaryotic elongation factor 1 beta central acidic region
(EF-1_beta_acid, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


EF hand
(EF-hand_1, N=115)
Fisher's OR: 2.67; Bonferroni p-val: 0.0798
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

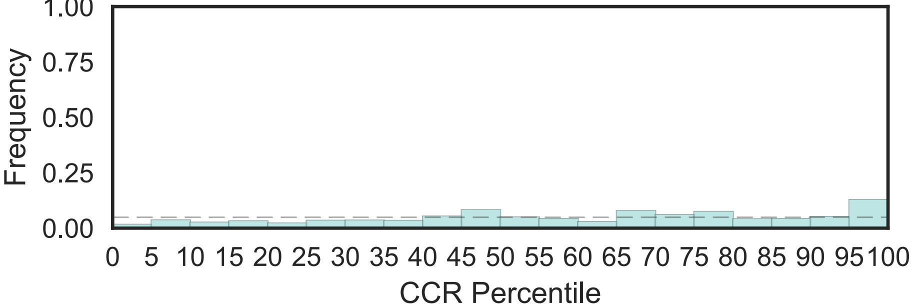

EF hand
(EF-hand_10, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

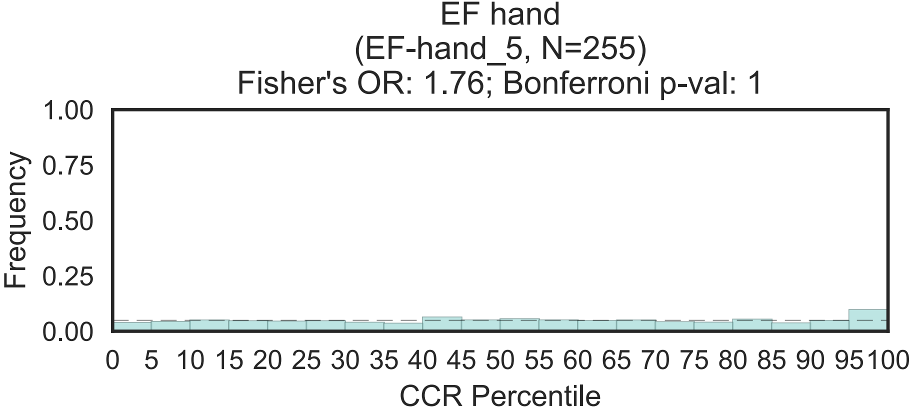

EF-hand domain
(EF-hand_11, N=4)
Fisher's OR: 0.948; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


EF hand
(EF-hand_2, N=4)
Fisher's OR: 0.597; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

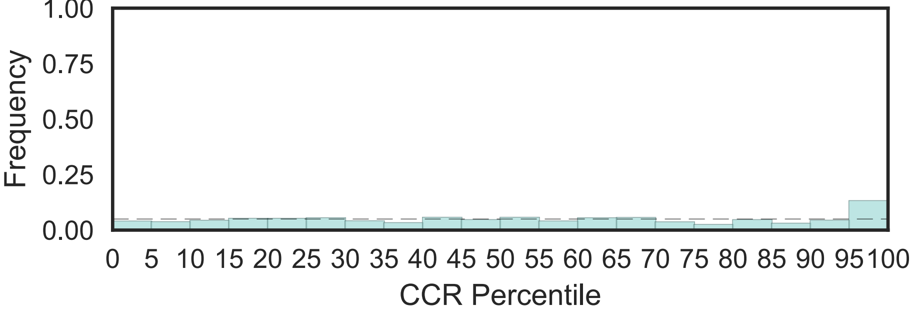

EF-hand
(EF-hand_3, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

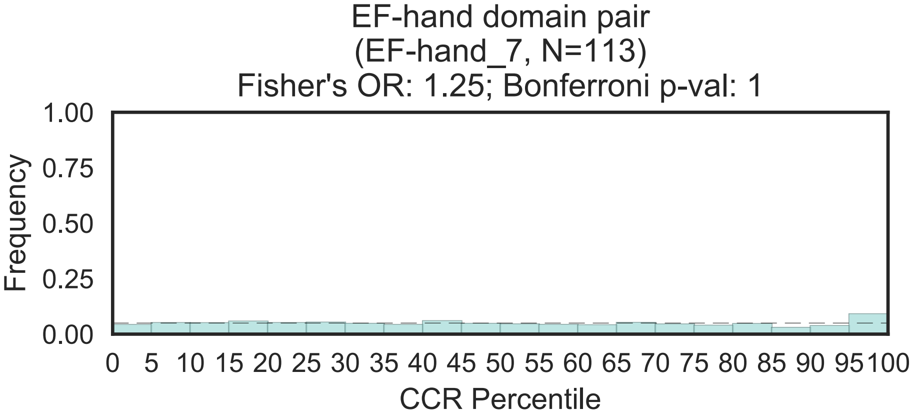
Cytoskeletal-regulatory complex EF hand (EF-hand_4, N=18) Fisher's OR: 1.57; Bonferroni p-val: 1

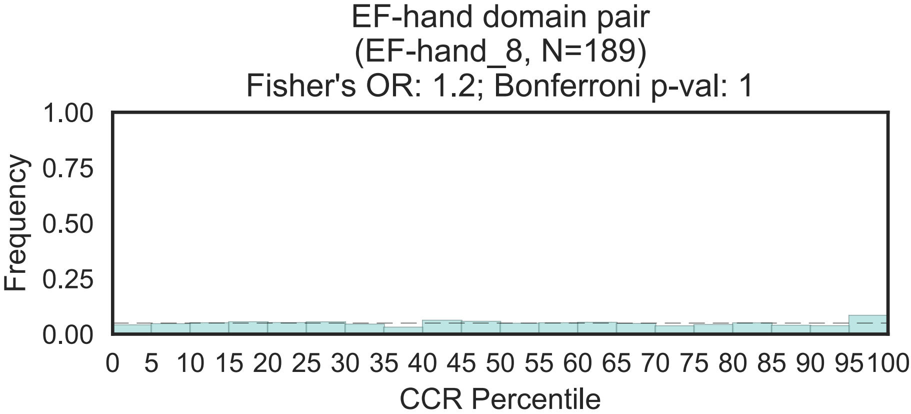


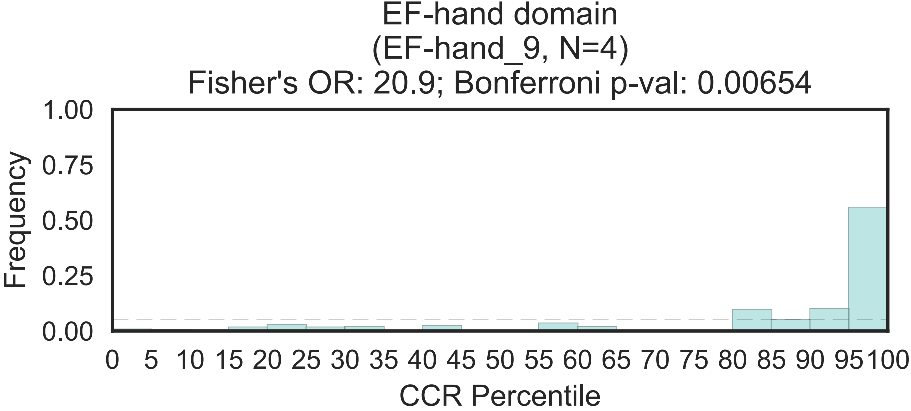

EF hand
(EF-hand_5, N=255)
Fisher's OR: 1.76; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

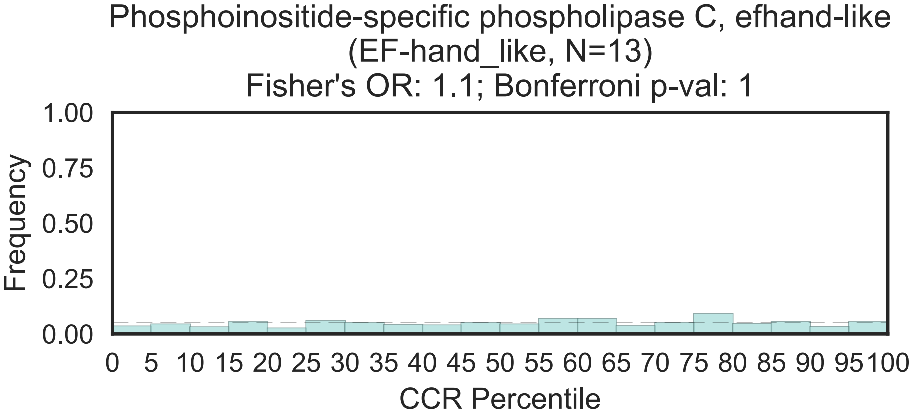
EF-hand domain
(EF-hand_6, N=86)
Fisher's OR: 2.48; Bonferroni p-val: 1

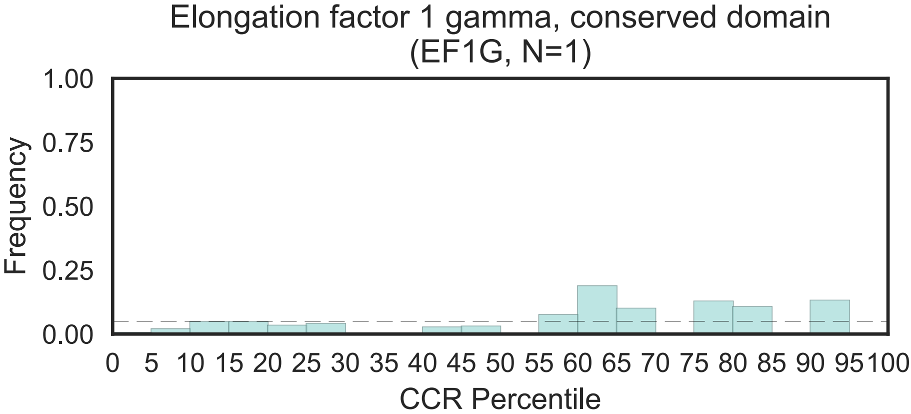


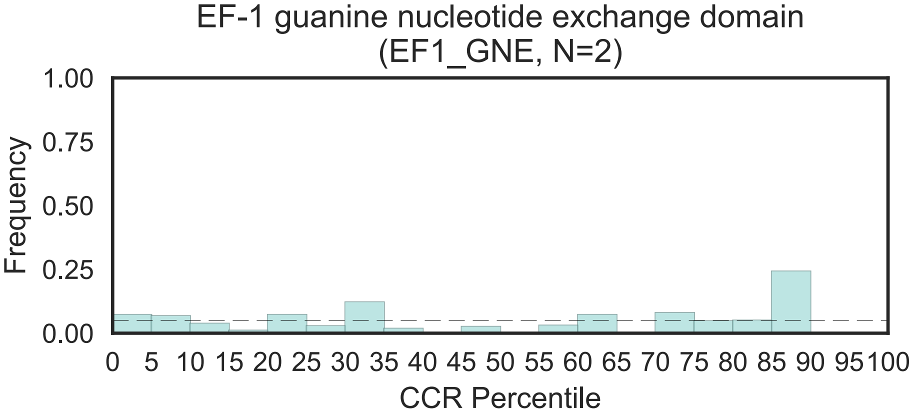

EF-hand domain pair
(EF-hand_7, N=113)
Fisher's OR: 1.25; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

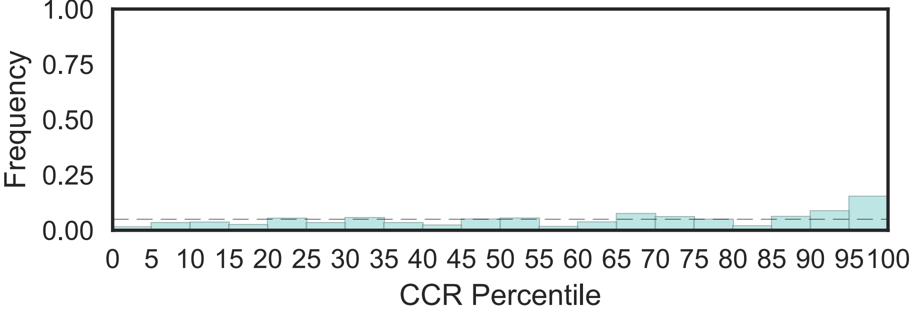

EF-hand domain pair
(EF-hand_8, N=189)
Fisher's OR: 1.2; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


EF-hand domain
(EF-hand_9, N=4)
Fisher's OR: 20.9; Bonferroni p-val: 0.00654
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

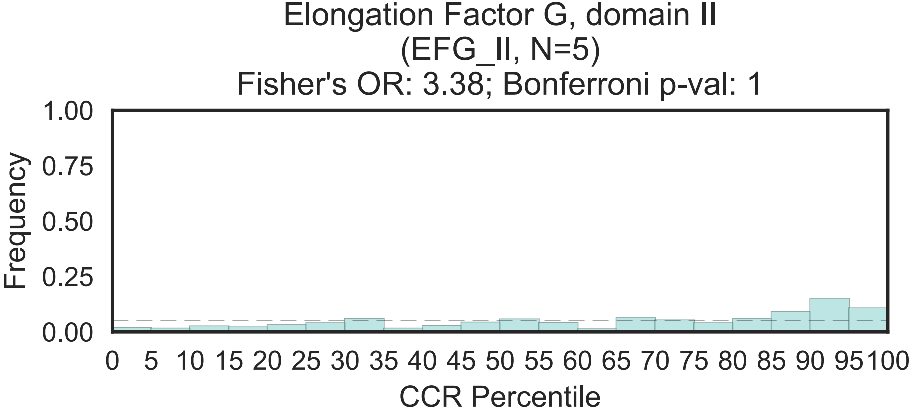

Phosphoinositide-specific phospholipase C, efhand-like
(EF-hand_like, N=13)
Fisher's OR: 1.1; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

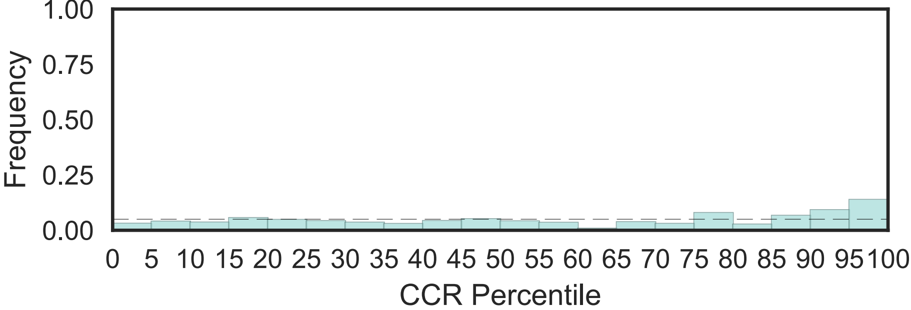

Elongation factor 1 gamma, conserved domain
(EF1G, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


EF-1 guanine nucleotide exchange domain
(EF1_GNE, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



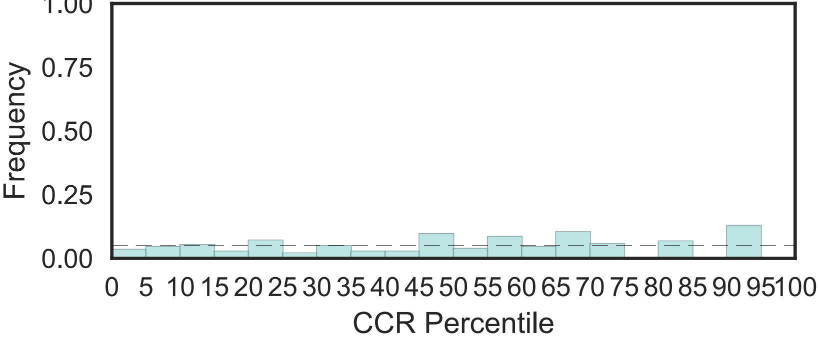
Elongation factor G C-terminus
(EFG_C, N=6)
Fisher's OR: 2.83; Bonferroni p-val: 1

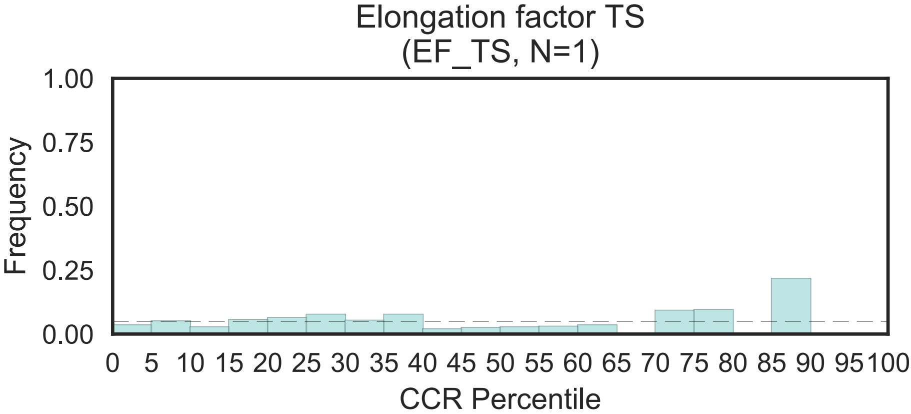

Elongation Factor G, domain II
(EFG_II, N=5)
Fisher's OR: 3.38; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



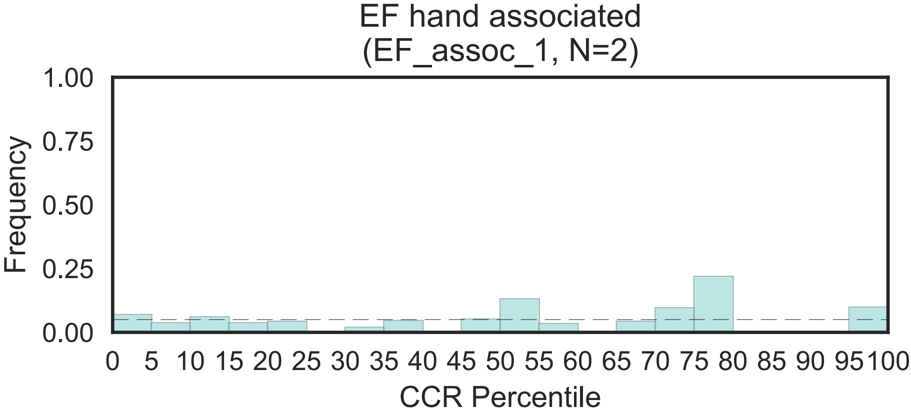
Elongation factor G, domain IV
(EFG_IV, N=5)
Fisher's OR: 3.07; Bonferroni p-val: 1

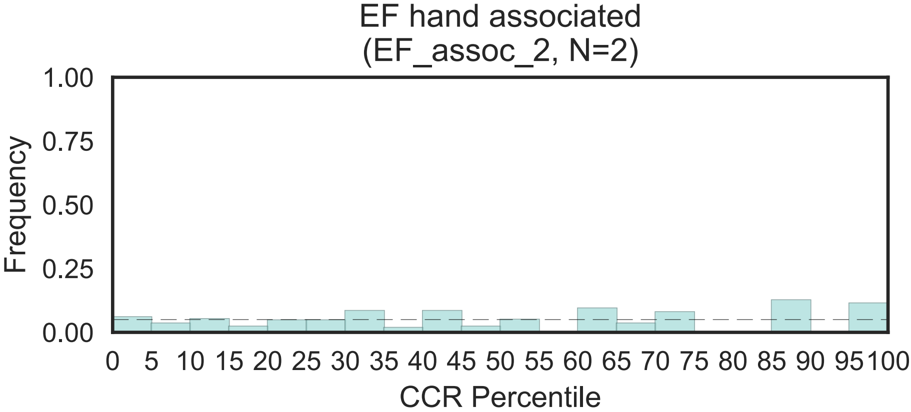
116 kDa U5 small nuclear ribonucleoprotein component N-terminus (EFTUD2, N=1)

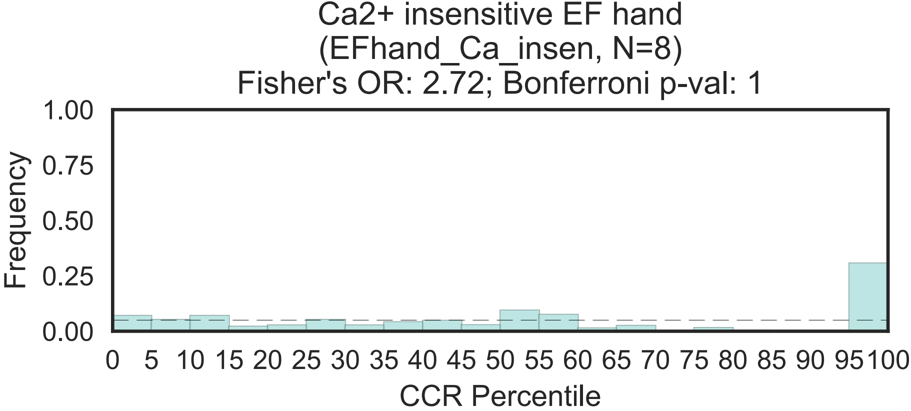


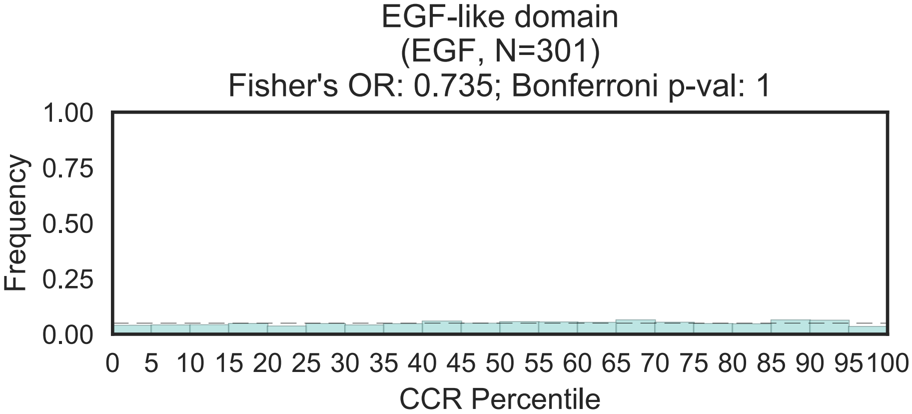


Elongation factor TS
(EF_TS, N=1)


EF hand associated
(EF_assoc_1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

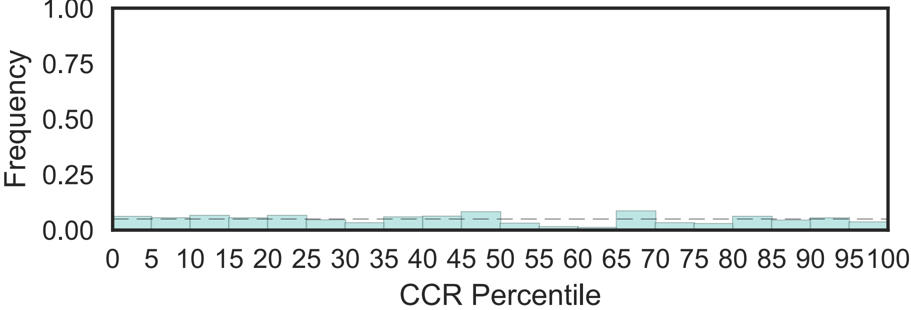

EF hand associated
(EF_assoc_2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

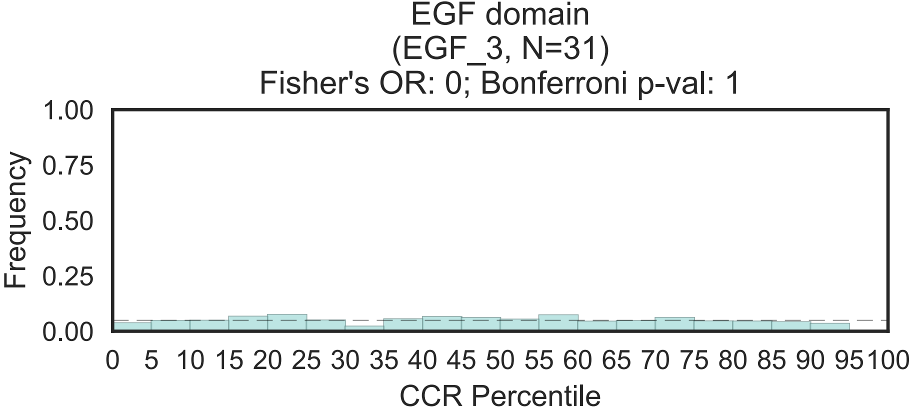

Ca2+ insensitive EF hand
(EFhand_Ca_insen, N=8)
Fisher's OR: 2.72; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



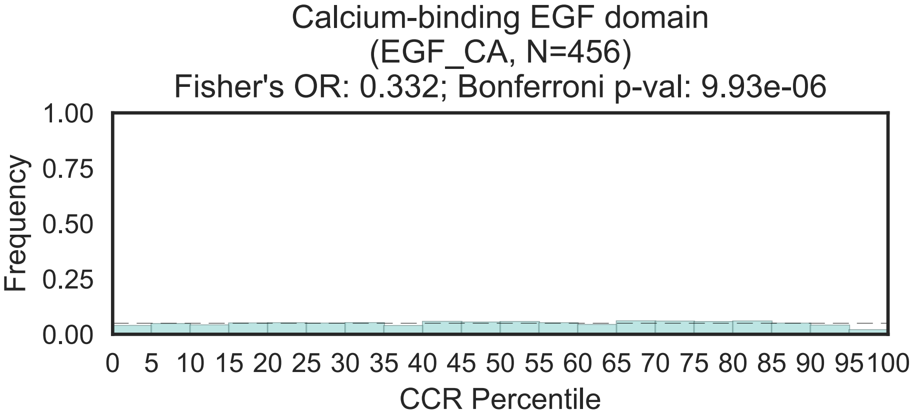
EGF-like domain
(EGF, N=301)
Fisher's OR: 0.735; Bonferroni p-val: 1

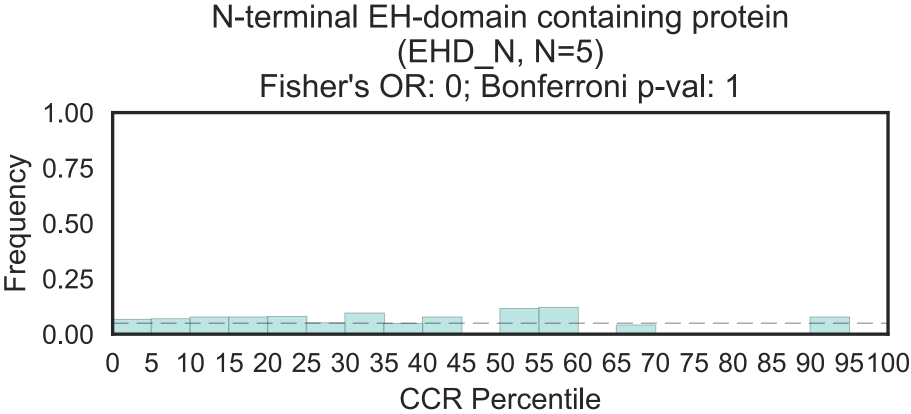
EGF-like domain
(EGF_2, N=31)
Fisher's OR: 0.597; Bonferroni p-val: 1

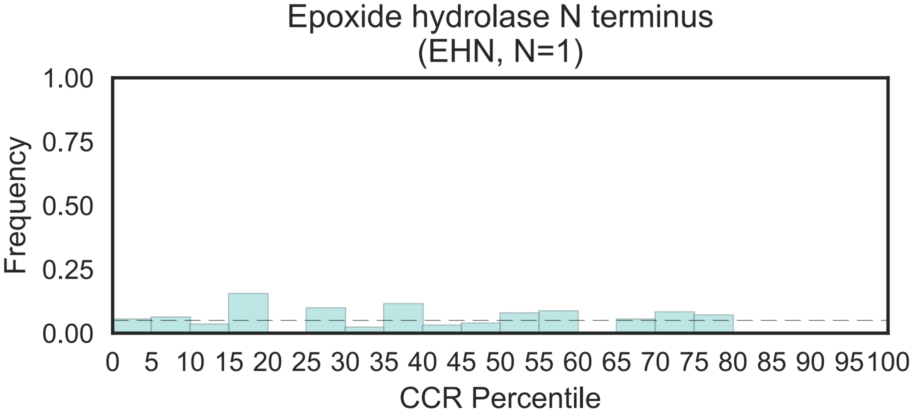




EGF domain
(EGF_3, N=31)
Fisher's OR: 0; Bonferroni p-val: 1

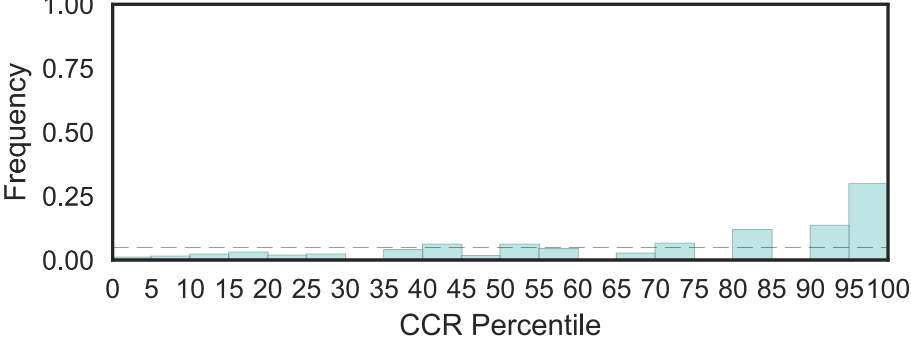

Calcium-binding EGF domain
(EGF_CA, N=456)
Fisher's OR: 0.332; Bonferroni p-val: 9.93e-06
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

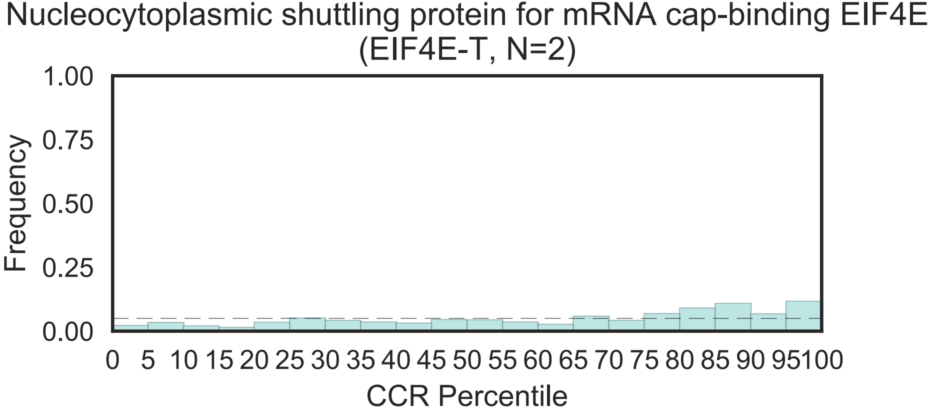

N-terminal EH-domain containing protein
(EHD_N, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

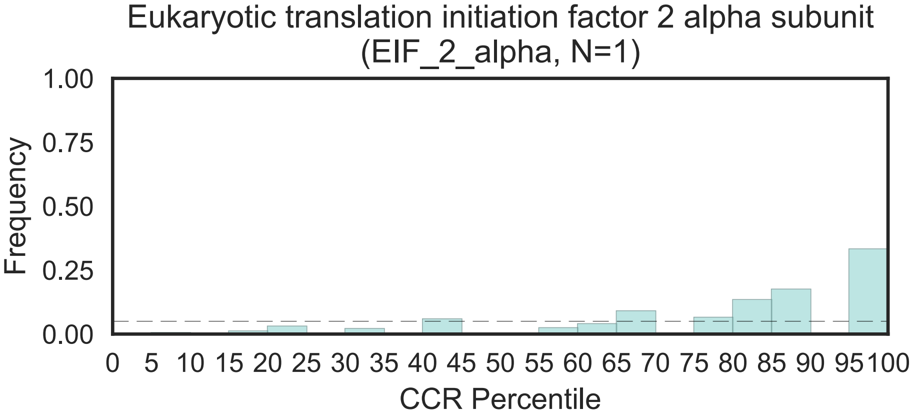


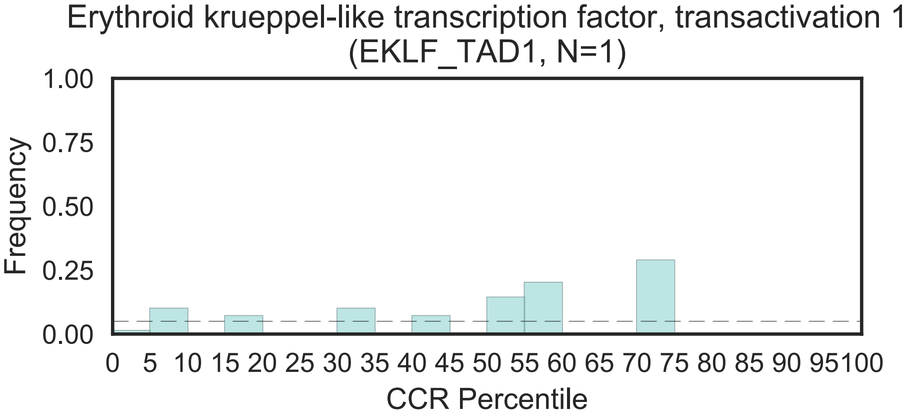
Epoxide hydrolase N terminus
(EHN, N=1)

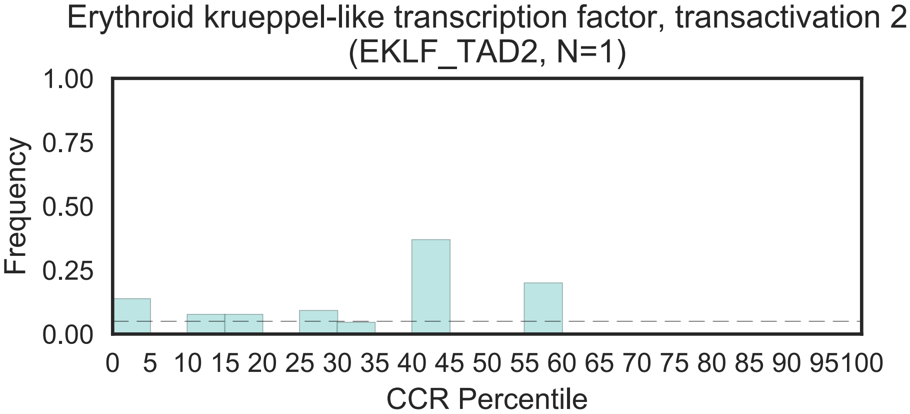
Etoposide-induced protein 2.4 (EI24)
(EI24, N=1)

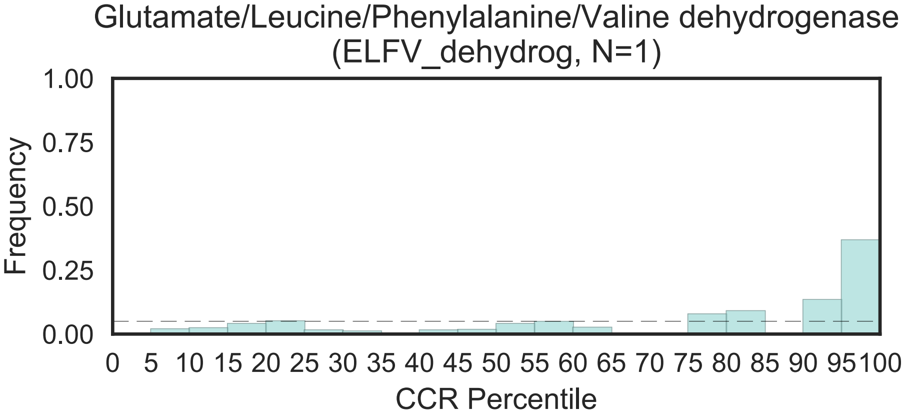


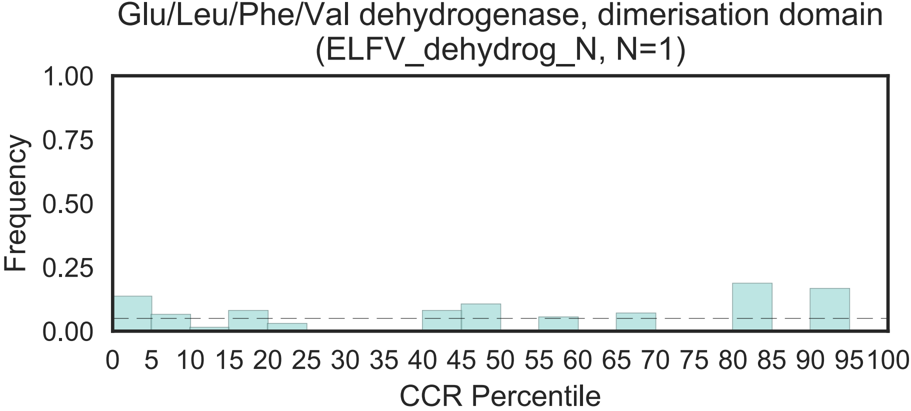

Nucleocytoplasmic shuttling protein for mRNA cap-binding EIF4E
(EIF4E-T, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

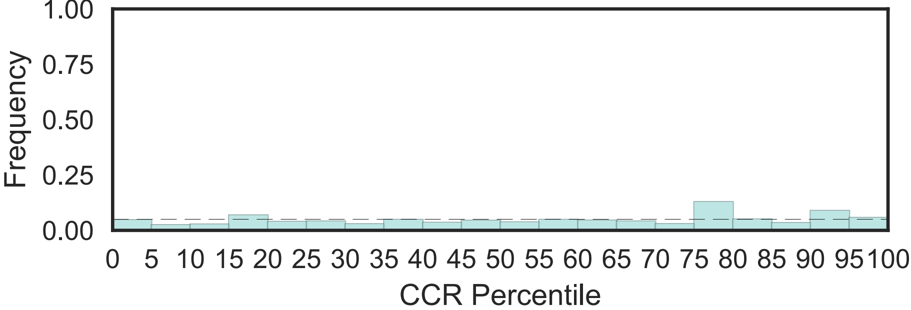

Eukaryotic translation initiation factor 2 alpha subunit
(EIF_2_alpha, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

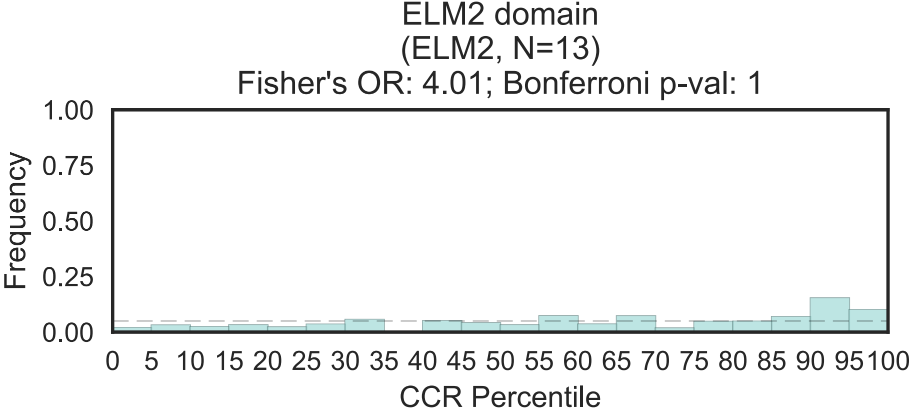

Erythroid krueppel-like transcription factor, transactivation 1
(EKLF_TAD1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95100
CCR Percentile


Erythroid krueppel-like transcription factor, transactivation 2
(EKLF_TAD2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

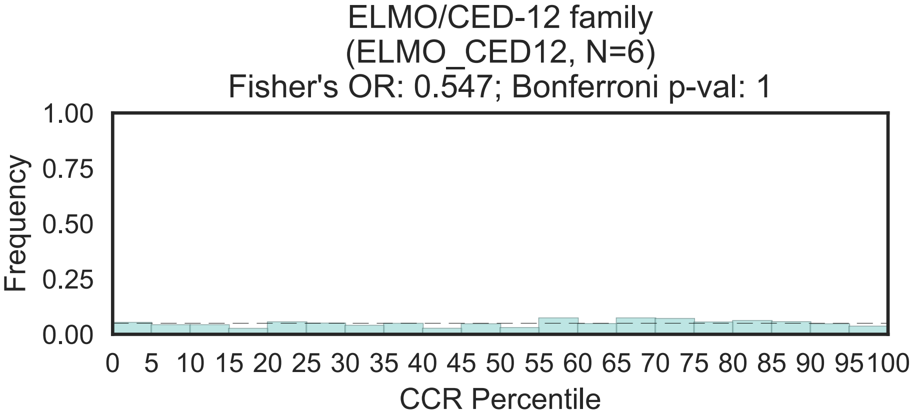

Glutamate/Leucine/Phenylalanine/Valine dehydrogenase
(ELFV_dehydrog, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

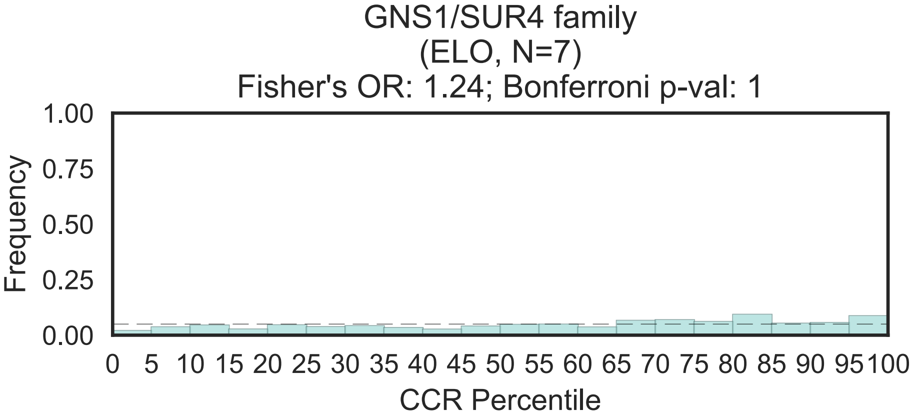

Glu/Leu/Phe/Val dehydrogenase, dimerisation domain
(ELFV_dehydrog_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


RNA polymerase II elongation factor ELL
(ELL, N=3)
Fisher's OR: 1.02; Bonferroni p-val: 1

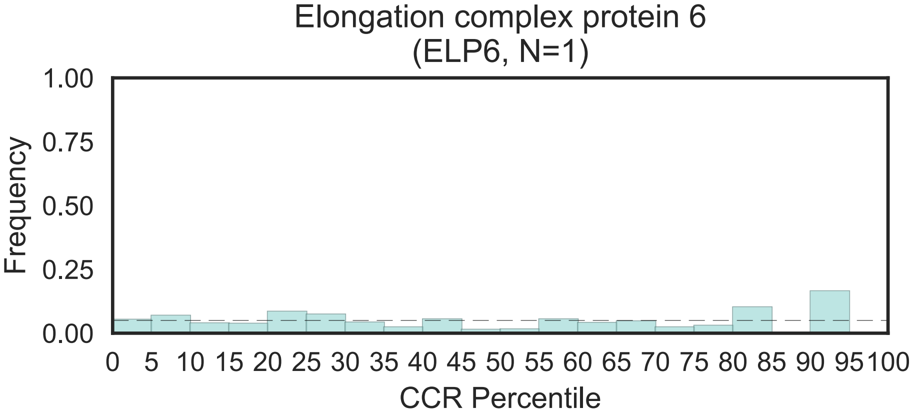


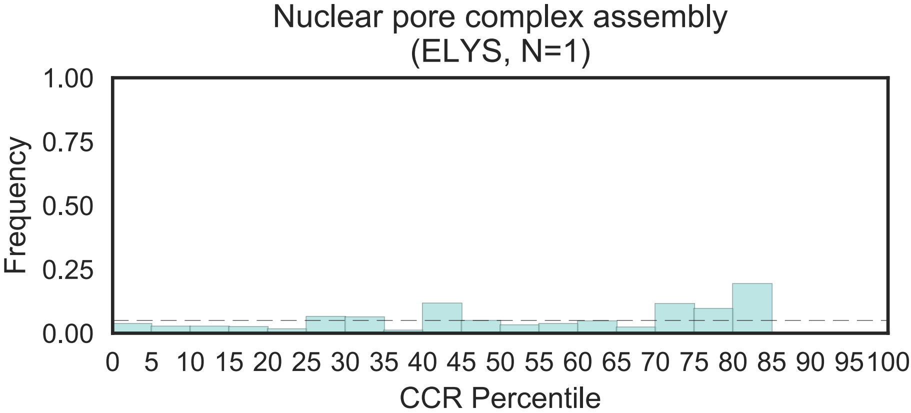
ELM2 domain
(ELM2, N=13)
Fisher's OR: 4.01; Bonferroni p-val: 1

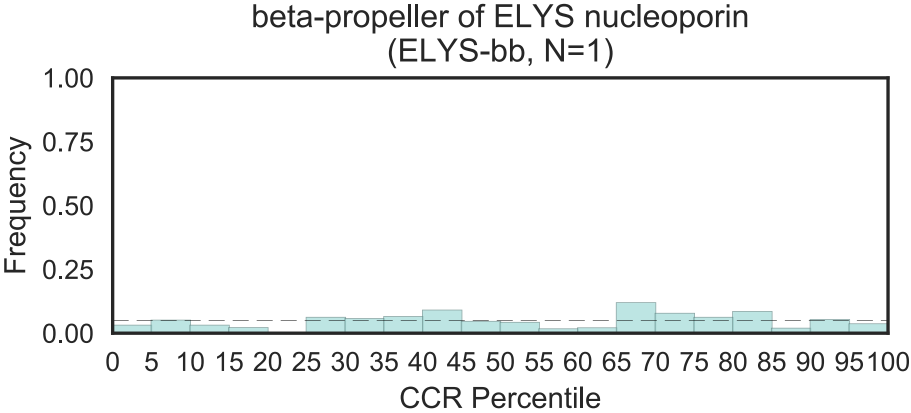

ELMO/CED-12 family
(ELMO_CED12, N=6)
Fisher's OR: 0.547; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

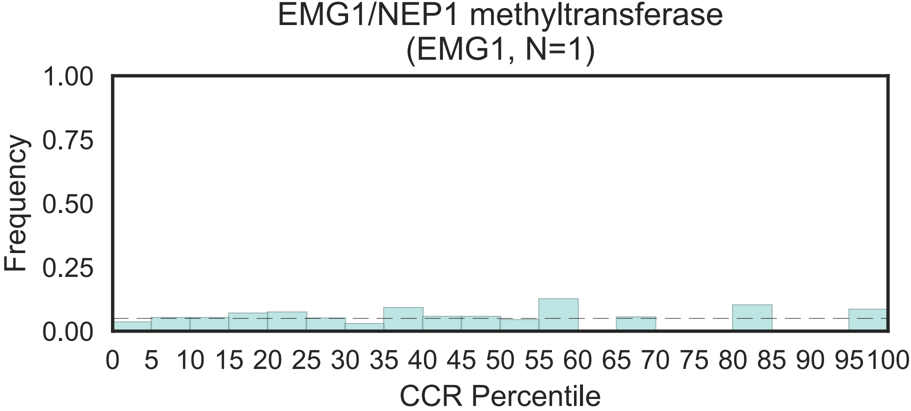


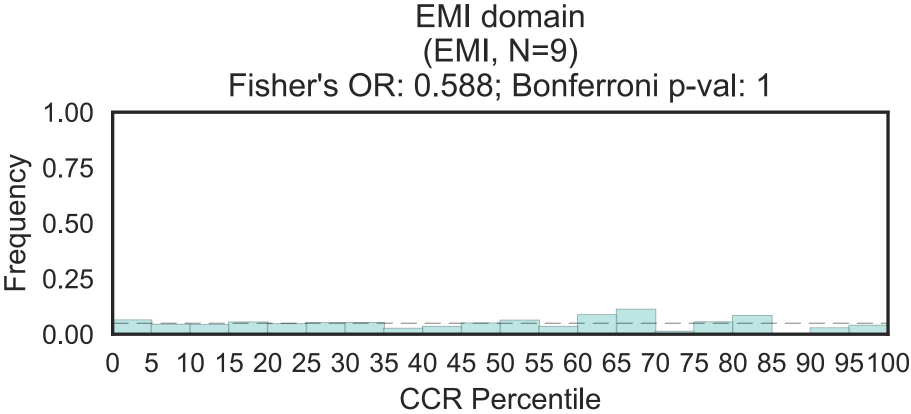
GNS1/SUR4 family
(ELO, N=7)
Fisher's OR: 1.24; Bonferroni p-val: 1

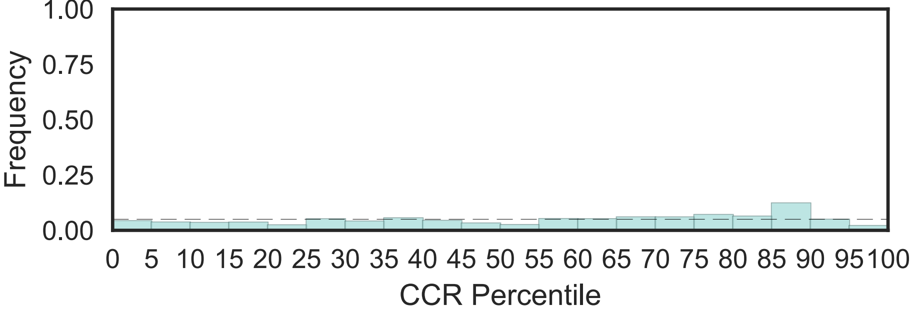

Elongation complex protein 6
(ELP6, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


Nuclear pore complex assembly
(ELYS, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

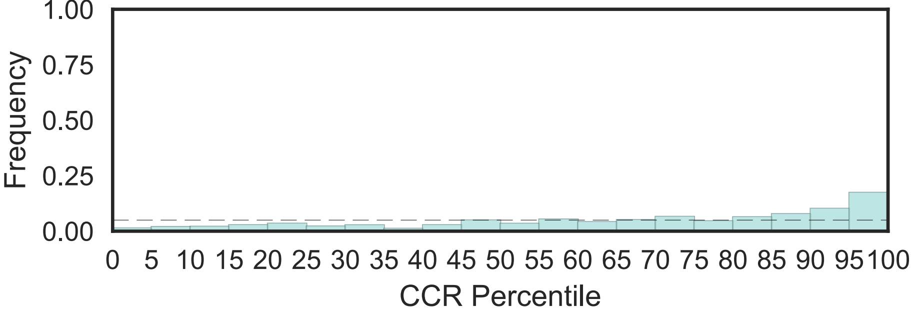

beta-propeller of ELYS nucleoporin
(ELYS-bb, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


EMG1/NEP1 methyltransferase
(EMG1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

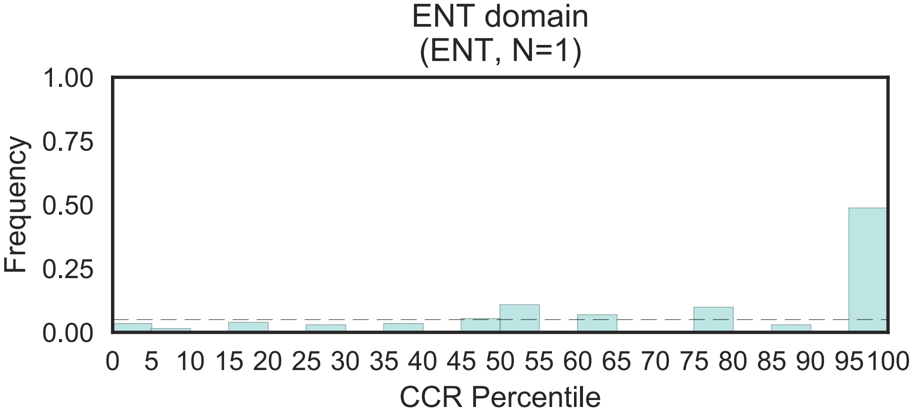

EMI domain
(EMI, N=9)
Fisher's OR: 0.588; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

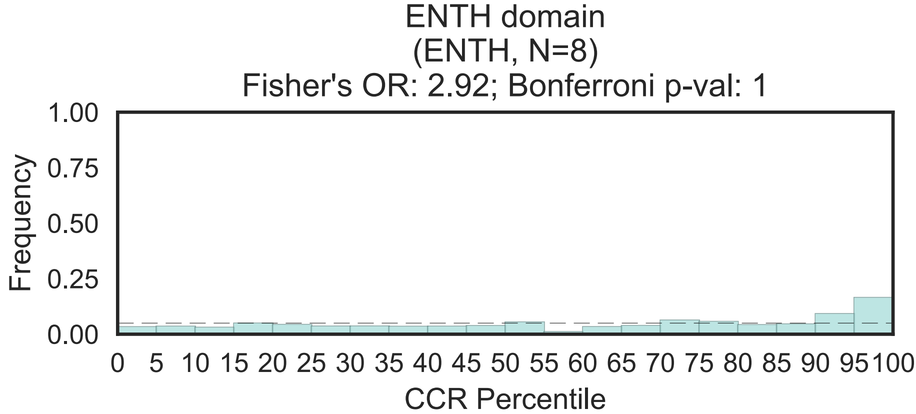


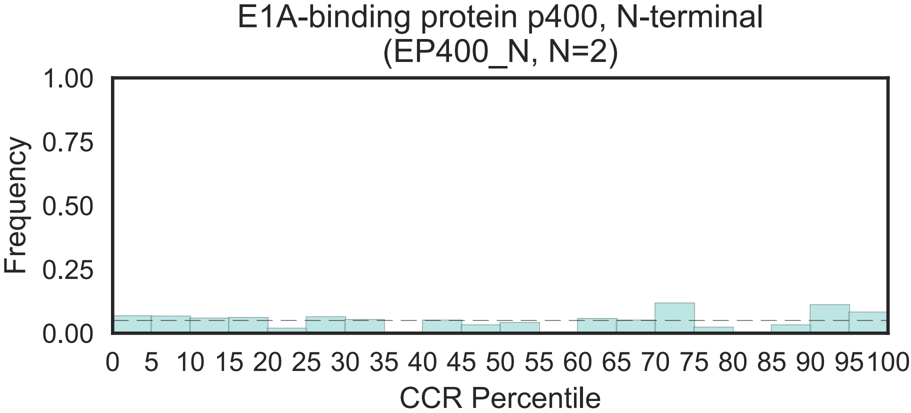
emp24/gp25L/p24 family/GOLD
(EMP24_GP25L, N=12)
Fisher's OR: 0.597; Bonferroni p-val: 1

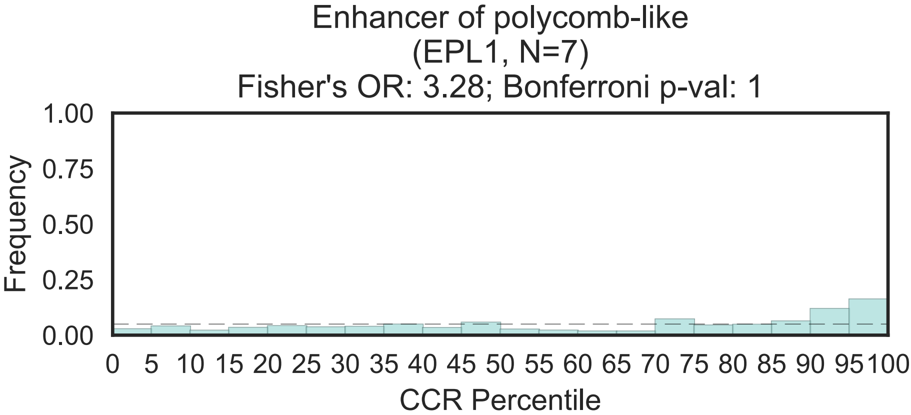


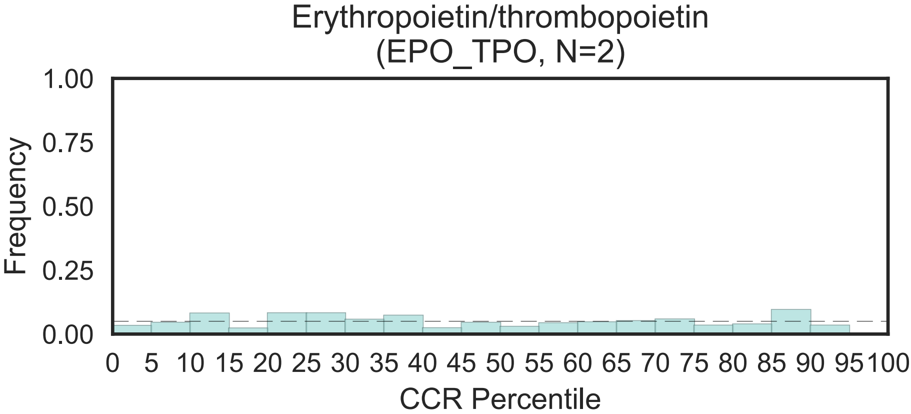
Endomembrane protein 70
(EMP70, N=4)
Fisher's OR: 3.89; Bonferroni p-val: 0.00739

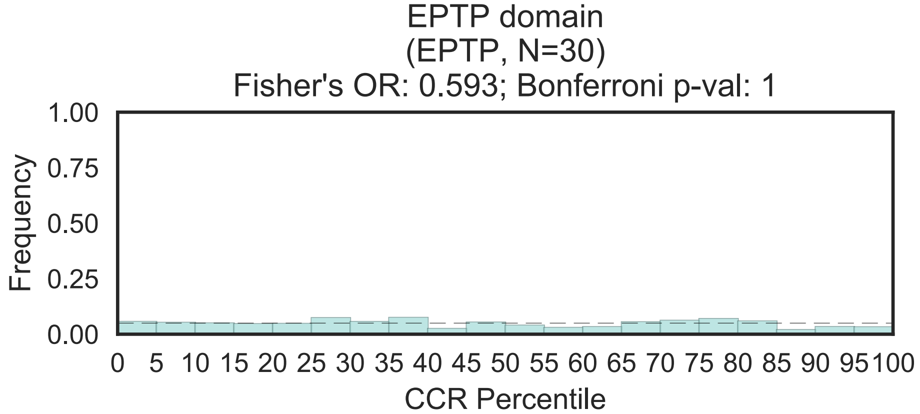

ENT domain
(ENT, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

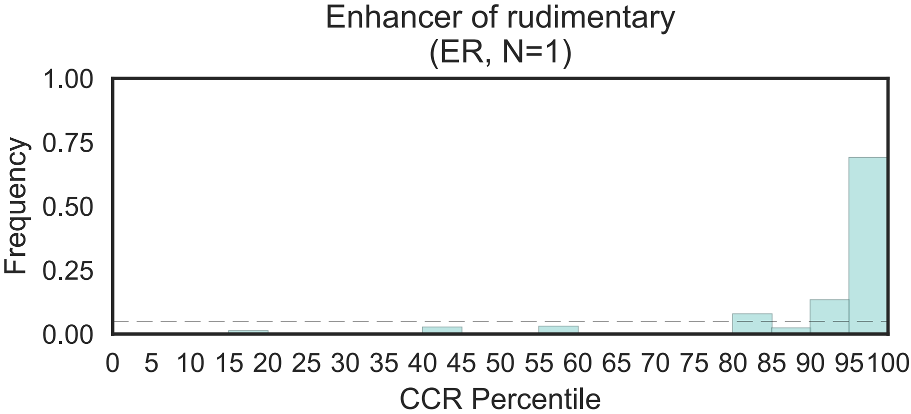

ENTH domain
(ENTH, N=8)
Fisher's OR: 2.92; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

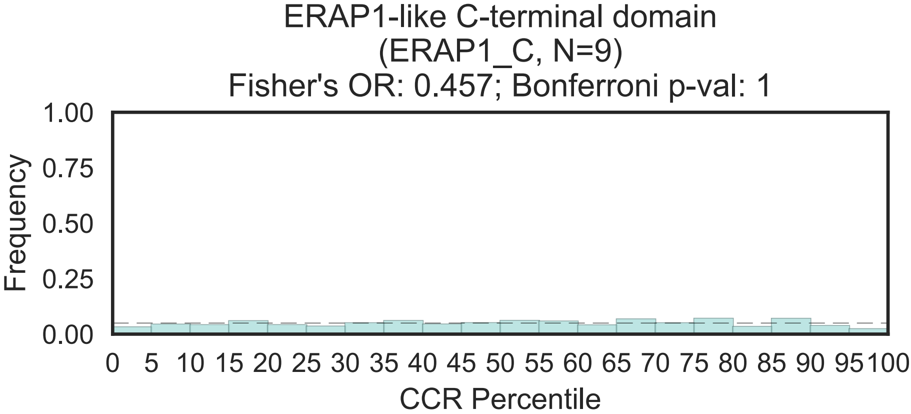

E1A-binding protein p400, N-terminal
(EP400_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Enhancer of polycomb-like
(EPL1, N=7)
Fisher's OR: 3.28; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

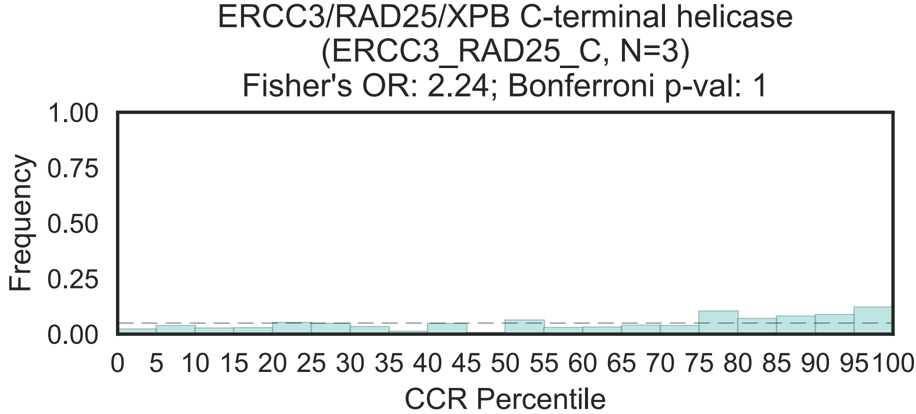

Erythropoietin/thrombopoietin
(EPO_TPO, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


EPTP domain
(EPTP, N=30)
Fisher's OR: 0.593; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

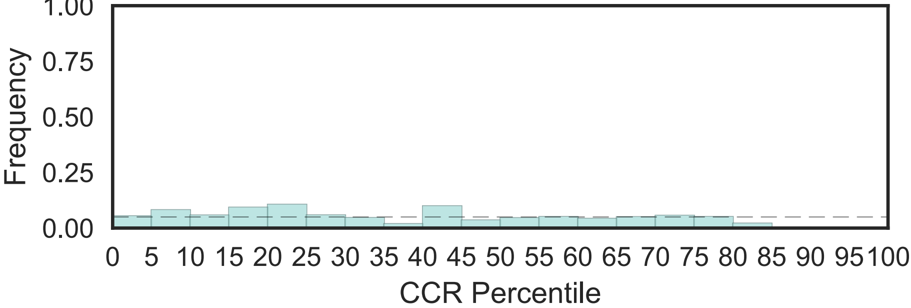

Enhancer of rudimentary
(ER, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

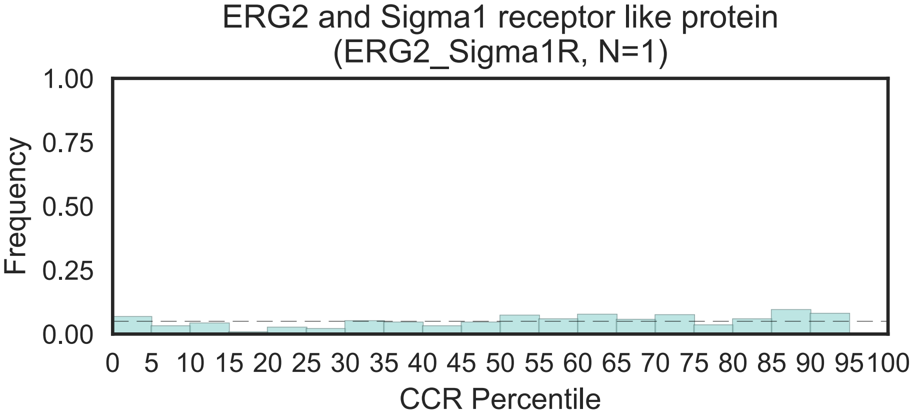


ERAP1-like C-terminal domain
(ERAP1_C, N=9)
Fisher's OR: 0.457; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

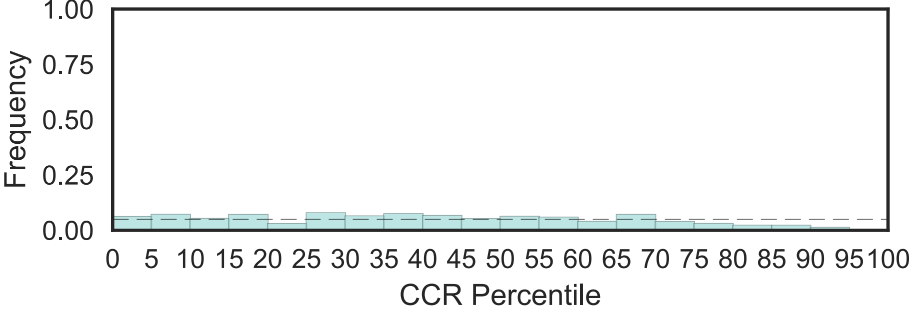

ERCC3/RAD25/XPB C-terminal helicase
(ERCC3_RAD25_C, N=3)
Fisher's OR: 2.24; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

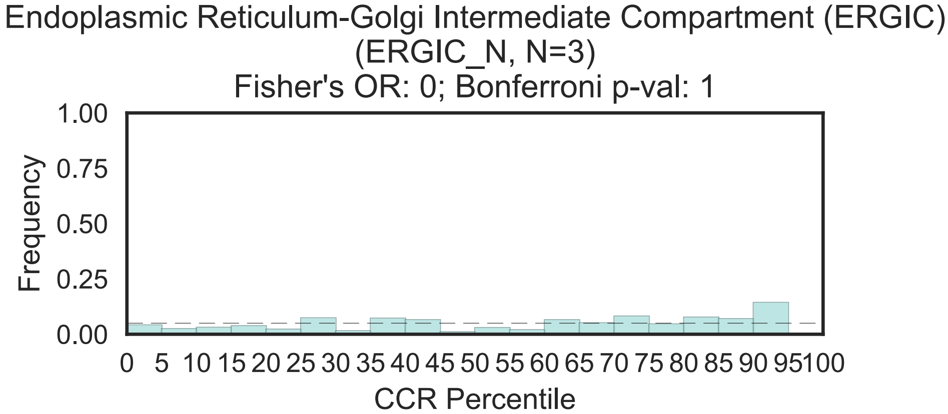
ERCC4 domain
(ERCC4, N=5)
Fisher's OR: 0; Bonferroni p-val: 1

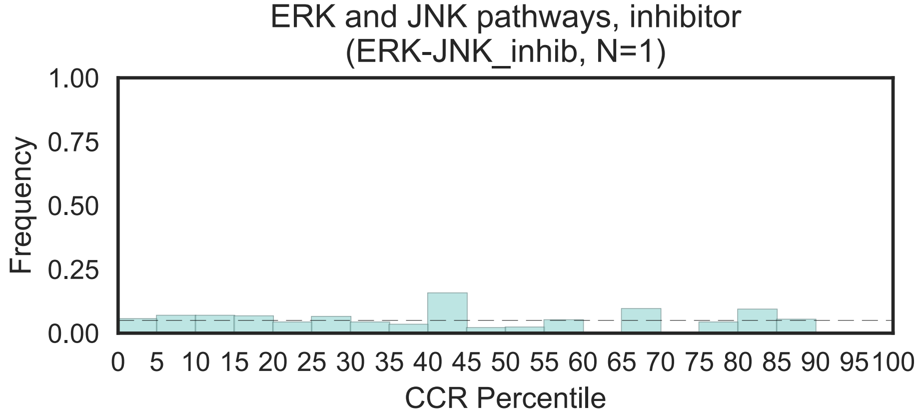


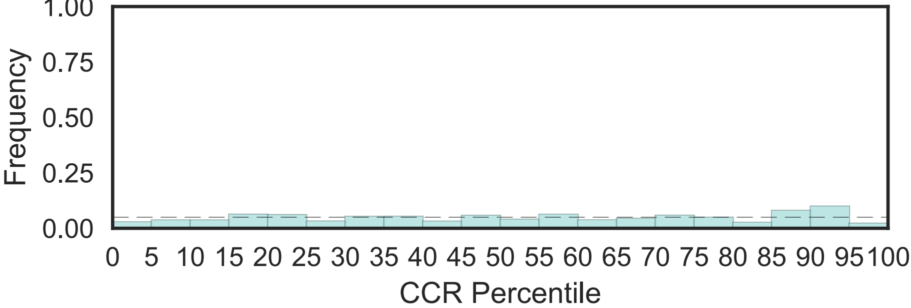


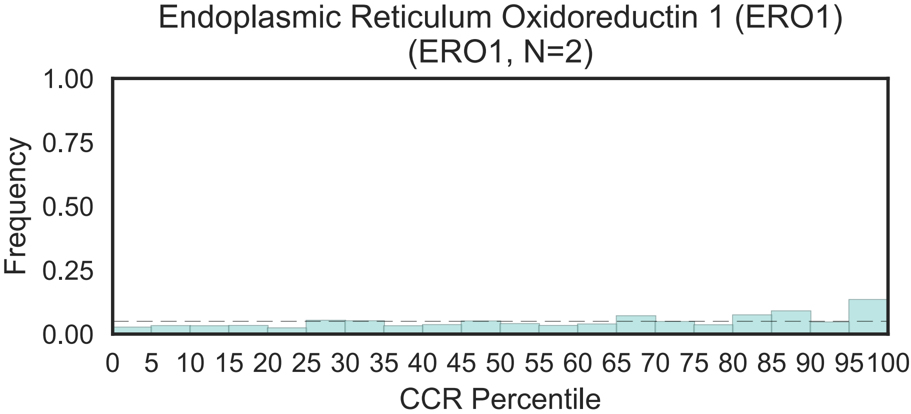
ERG2 and Sigma1 receptor like protein
(ERG2_Sigma1R, N=1)


Ergosterol biosynthesis ERG4/ERG24 family
(ERG4_ERG24, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

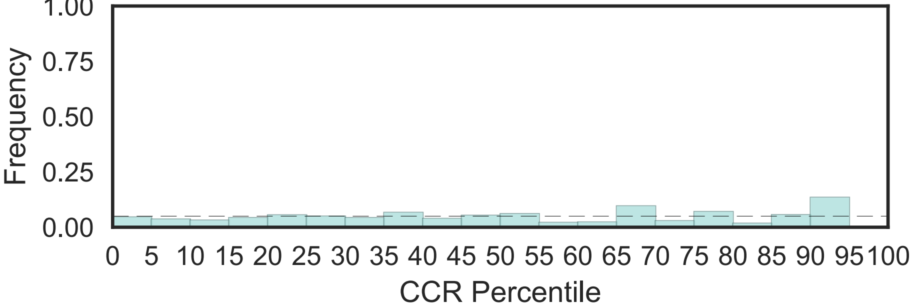

Endoplasmic Reticulum-Golgi Intermediate Compartment (ERGIC)
(ERGIC_N, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

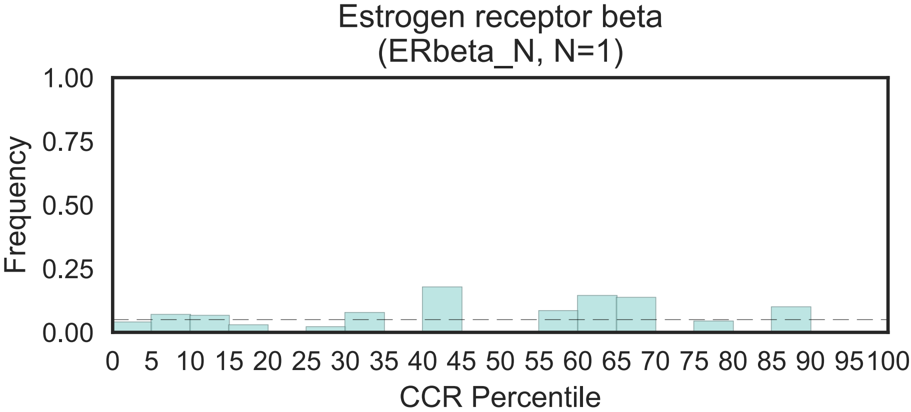

ERK and JNK pathways, inhibitor
(ERK-JNK_inhib, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

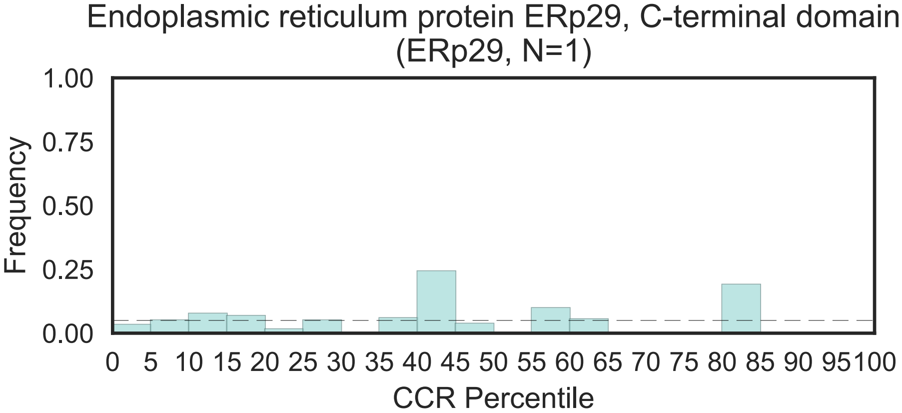

Ezrin/radixin/moesin family
(ERM, N=3)
Fisher's OR: 0.331; Bonferroni p-val: 1

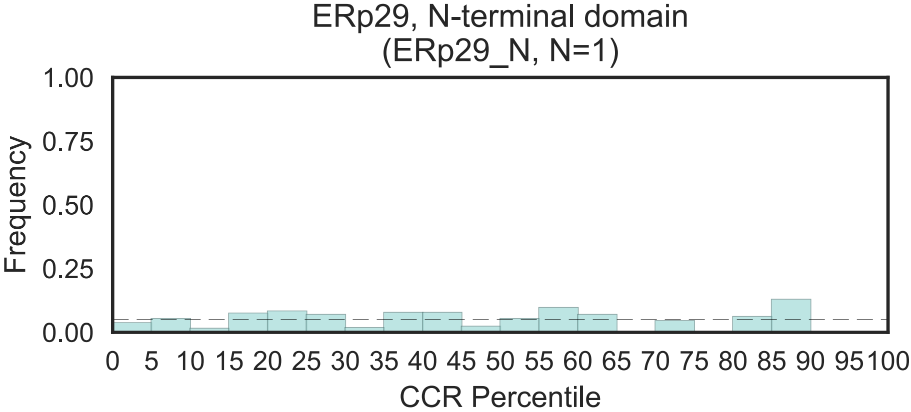

Endoplasmic Reticulum Oxidoreductin 1 (ERO1)
(ERO1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

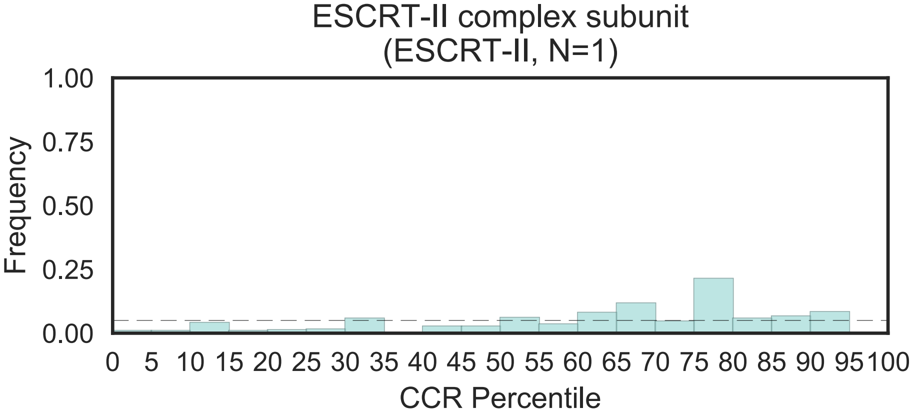
ER lumen protein retaining receptor
(ER_lumen_recept, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

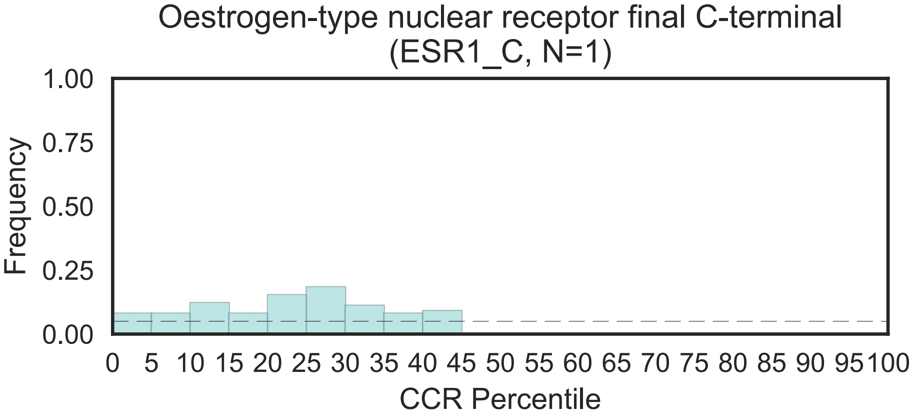


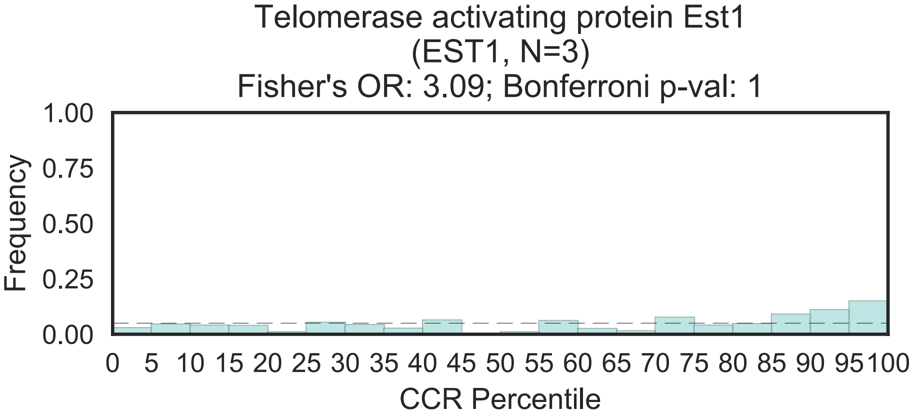

Estrogen receptor beta
(ERbeta_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

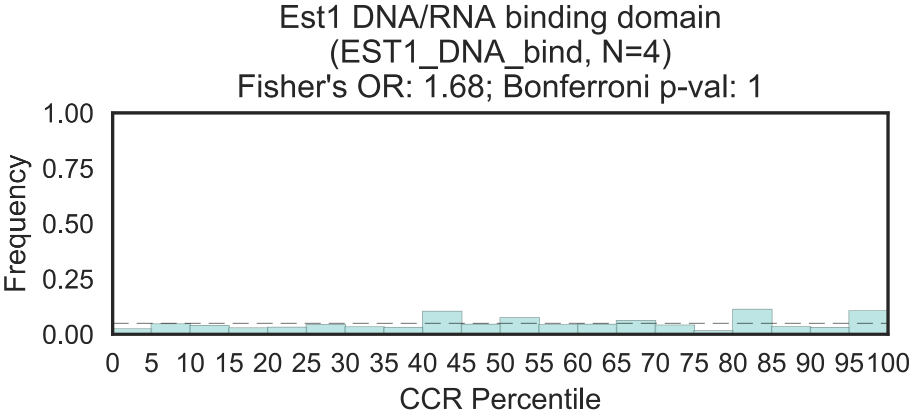

Endoplasmic reticulum protein ERp29, C-terminal domain
(ERp29, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


ERp29, N-terminal domain
(ERp29_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

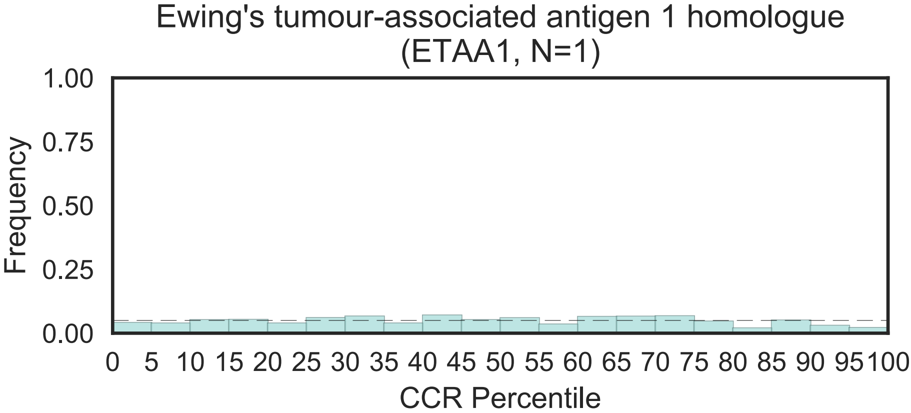

ESCRT-II complex subunit
(ESCRT-II, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

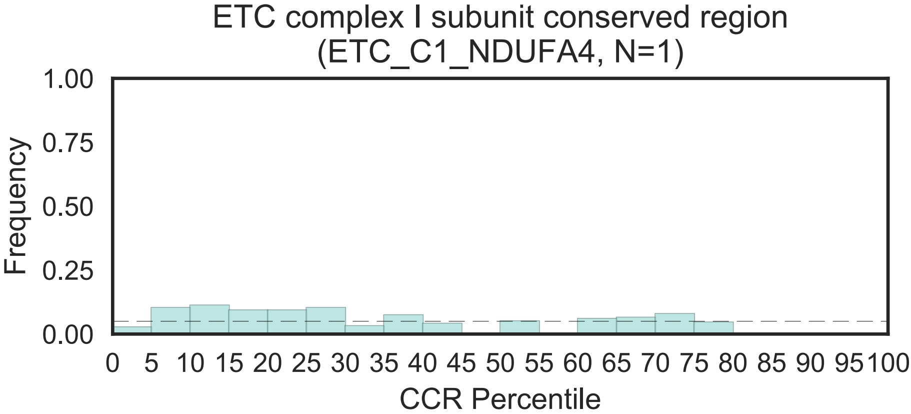

Oestrogen-type nuclear receptor final C-terminal
(ESR1_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

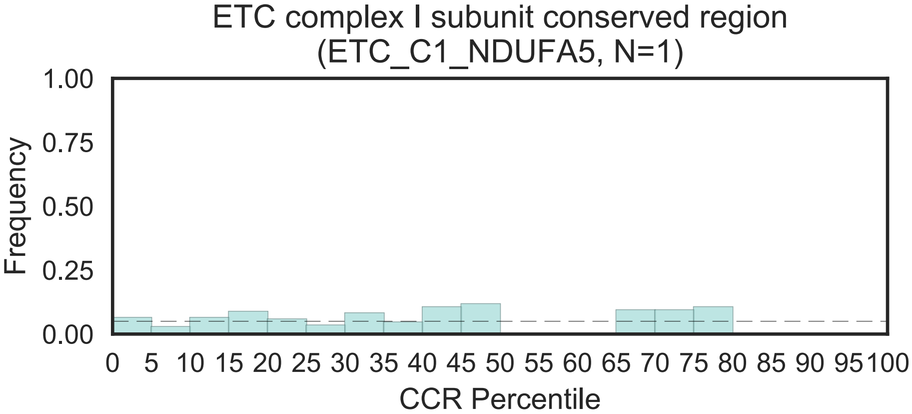

Telomerase activating protein Est1
(EST1, N=3)
Fisher's OR: 3.09; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



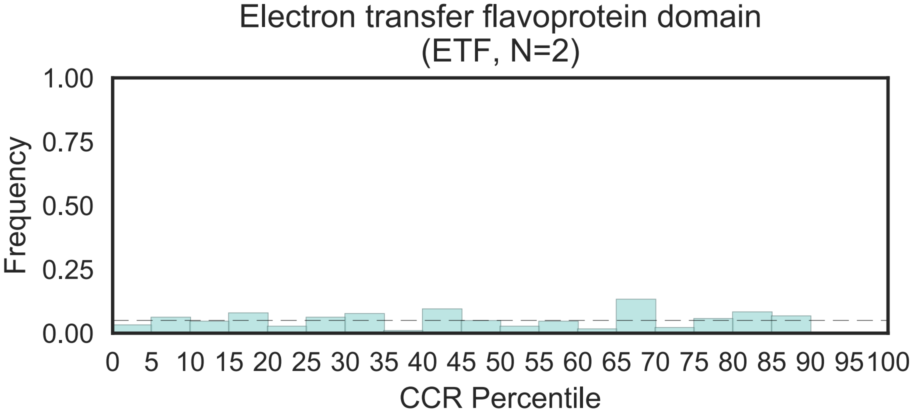
Est1 DNA/RNA binding domain
(EST1_DNA_bind, N=4)
Fisher's OR: 1.68; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

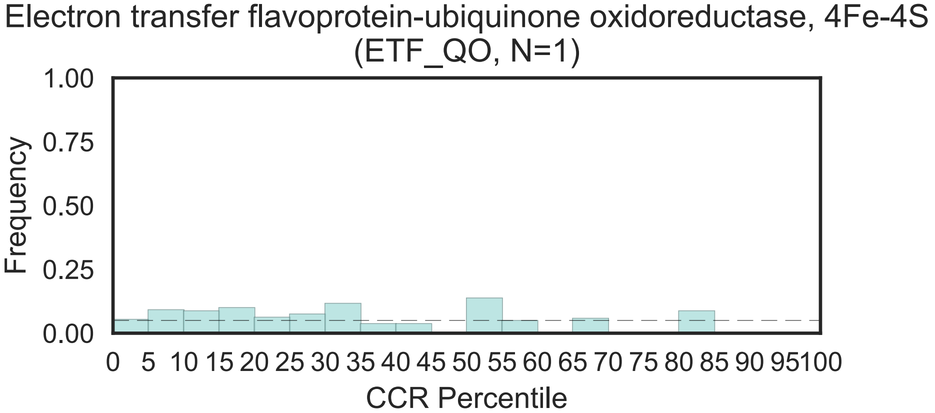

Ewing's tumour-associated antigen 1 homologue
(ETAA1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

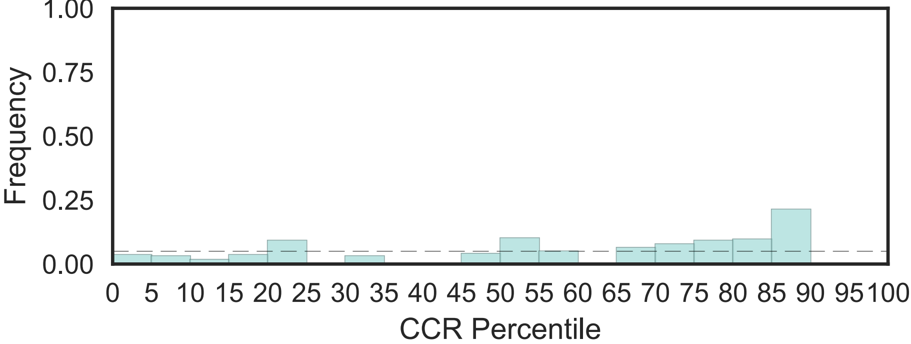

ETC complex I subunit conserved region
(ETC_C1_NDUFA4, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



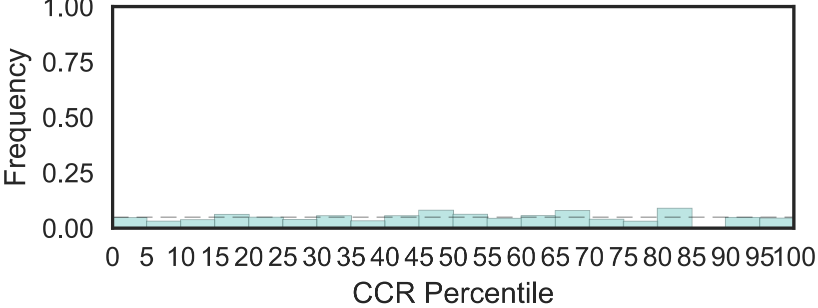
ETC complex I subunit conserved region
(ETC_C1_NDUFA5, N=1)


Electron transfer flavoprotein domain
(ETF, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

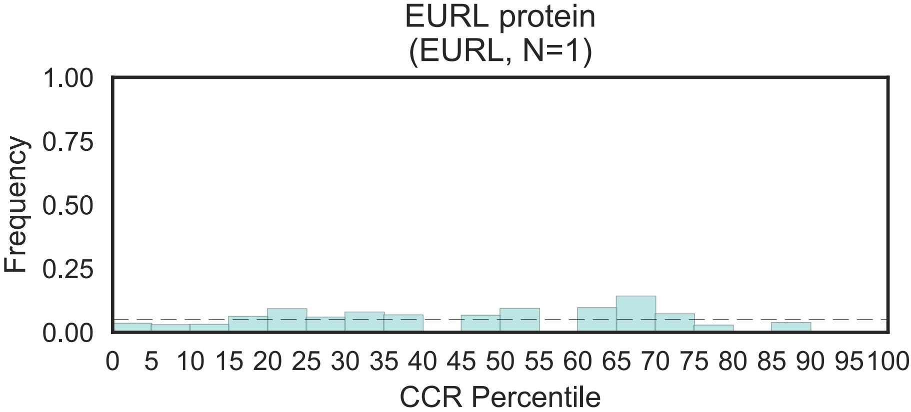

Electron transfer flavoprotein-ubiquinone oxidoreductase, 4Fe-4S
(ETF_QO, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

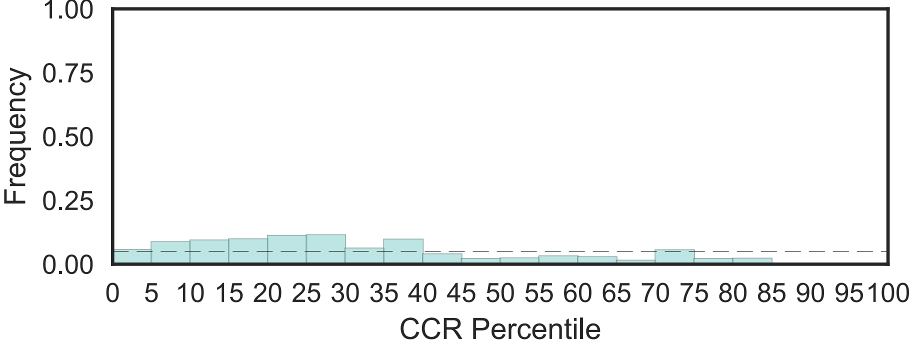


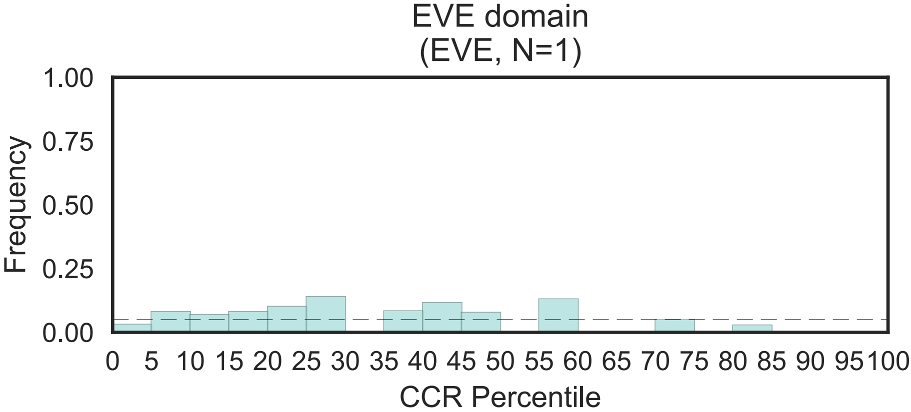
Electron transfer flavoprotein FAD-binding domain
(ETF_alpha, N=1)

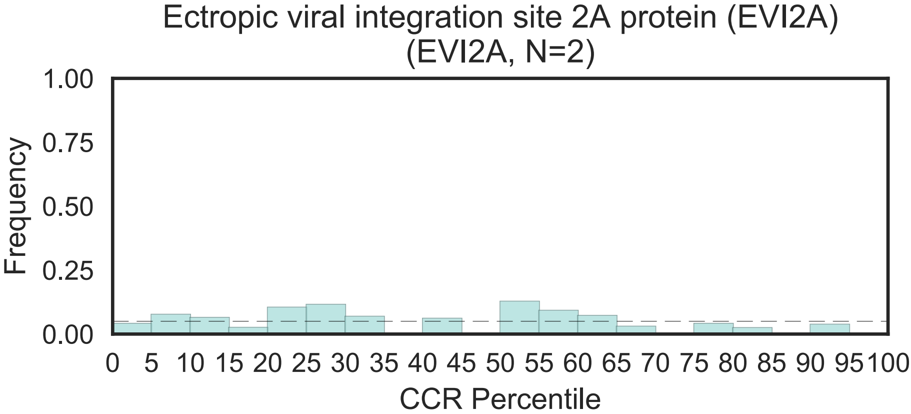


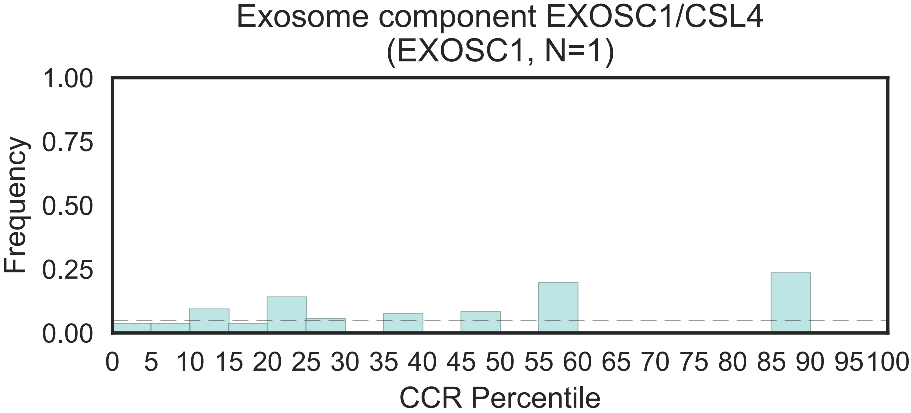
PEA3 subfamily ETS-domain transcription factor N terminal domain
(ETS_PEA3_N, N=6)
Fisher's OR: 1.09; Bonferroni p-val: 1

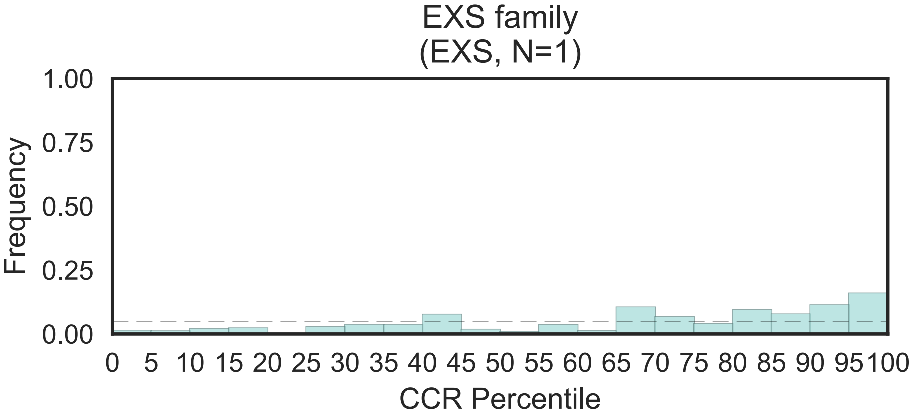

EURL protein
(EURL, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

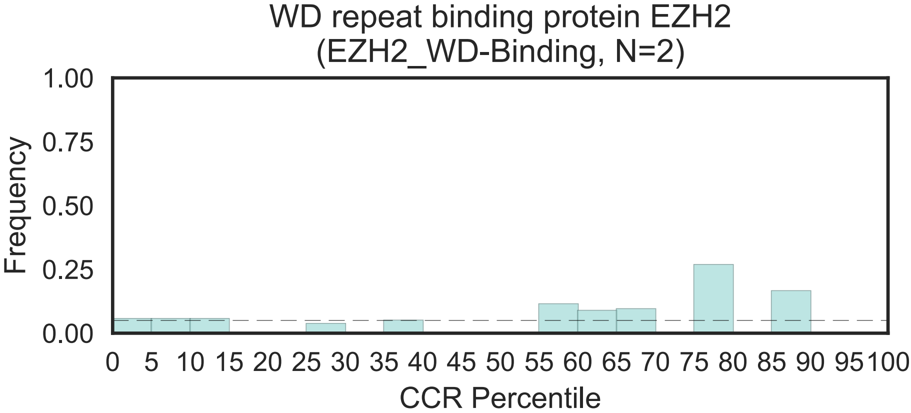

Ellis van Creveld protein 2 like protein
(EVC2_like, N=1)

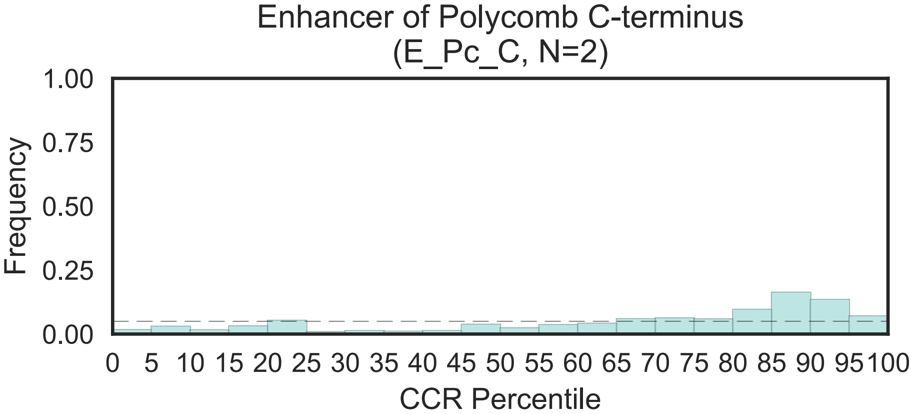

EVE domain
(EVE, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

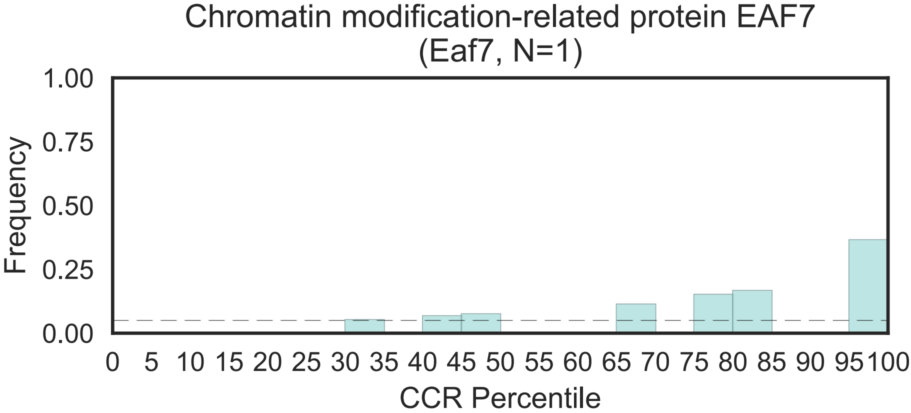

Ectropic viral integration site 2A protein (EVI2A)
(EVI2A, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

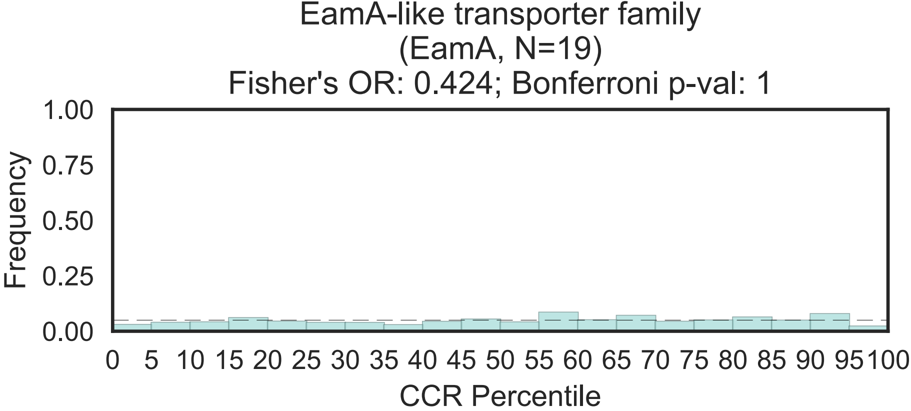

Exosome component EXOSC1/CSL4
(EXOSC1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


EXS family
(EXS, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

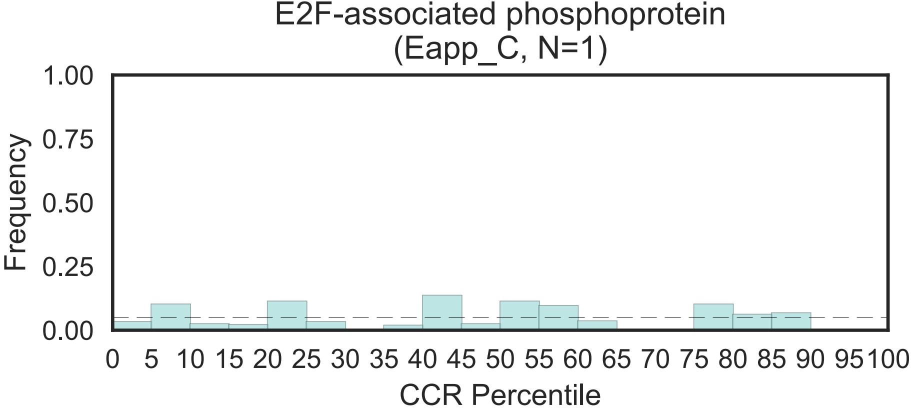

WD repeat binding protein EZH2
(EZH2_WD-Binding, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

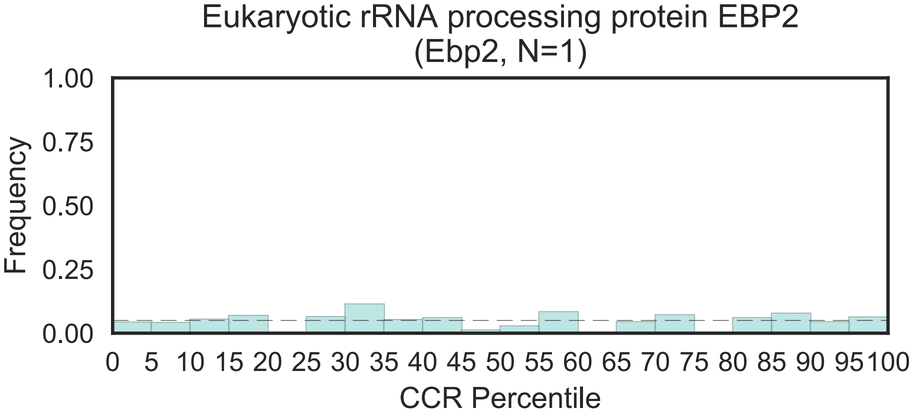

Enhancer of Polycomb C-terminus
(E_Pc_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

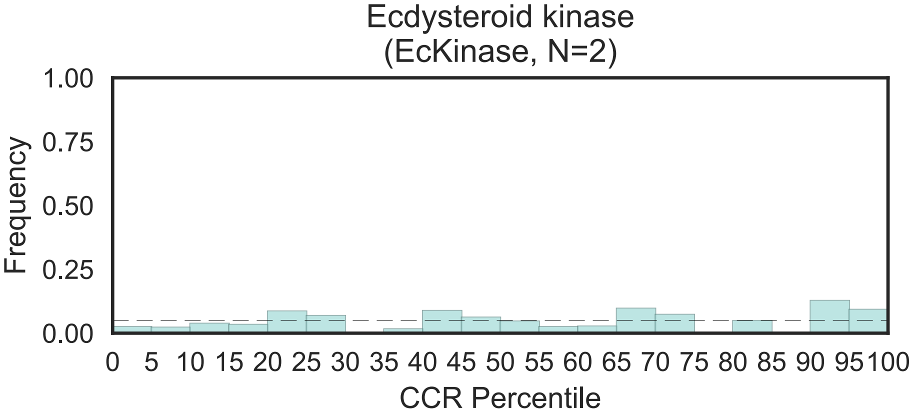

Chromatin modification-related protein EAF7
(Eaf7, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

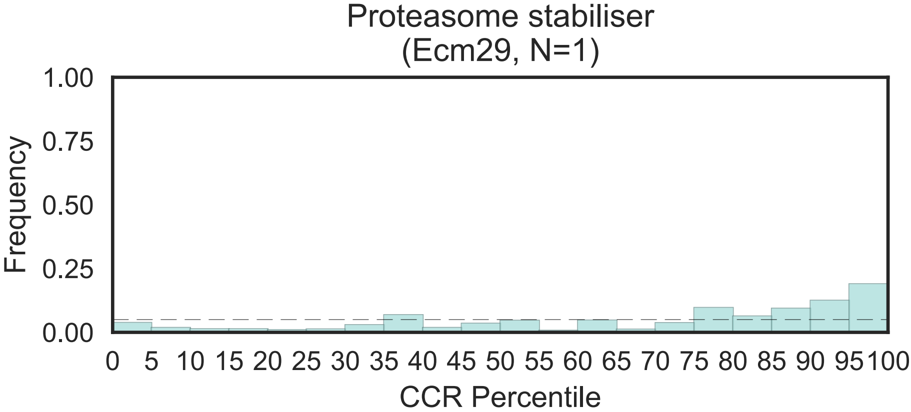


EamA-like transporter family
(EamA, N=19)
Fisher's OR: 0.424; Bonferroni p-val: 1

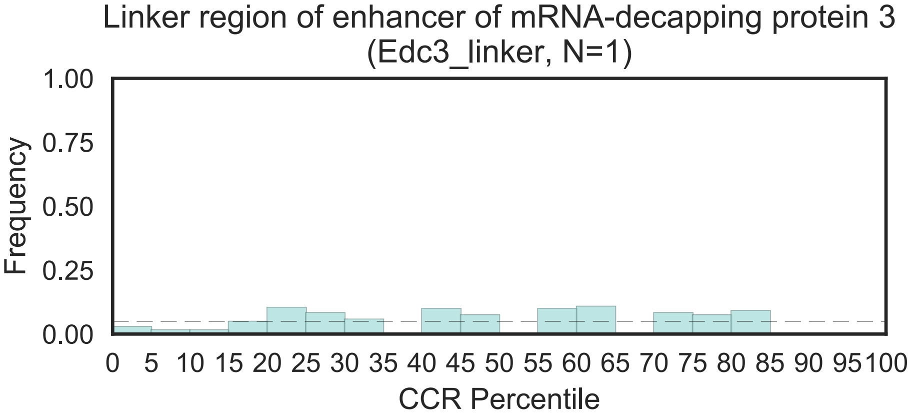

E2F-associated phosphoprotein
(Eapp_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Eukaryotic rRNA processing protein EBP2
(Ebp2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

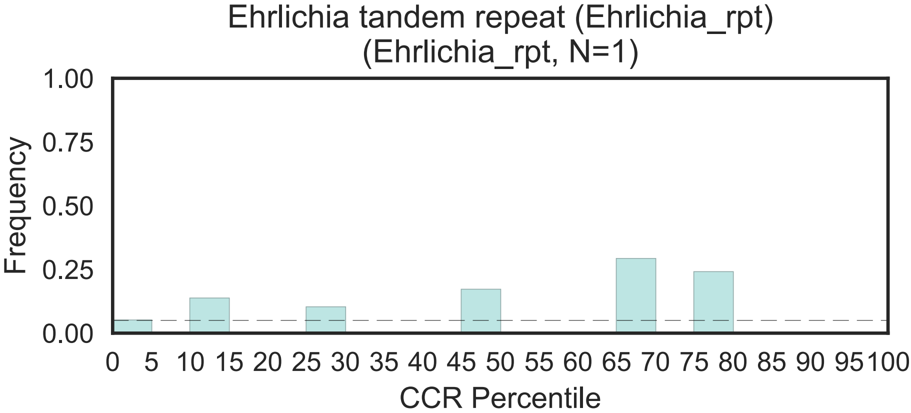

Ecdysteroid kinase
(EcKinase, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

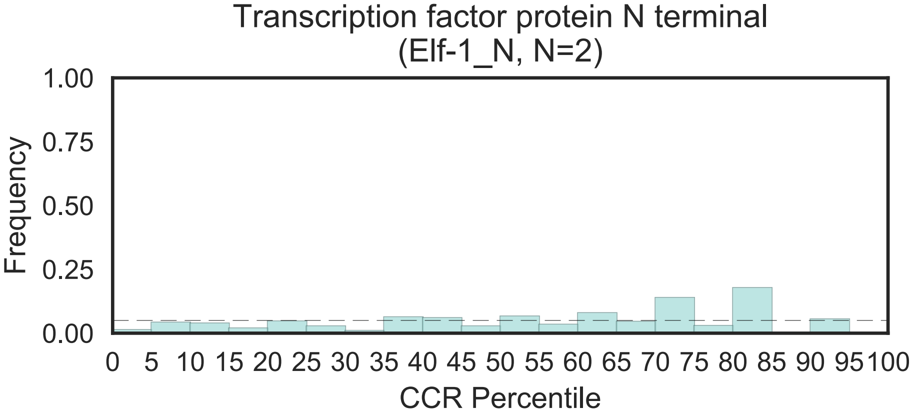


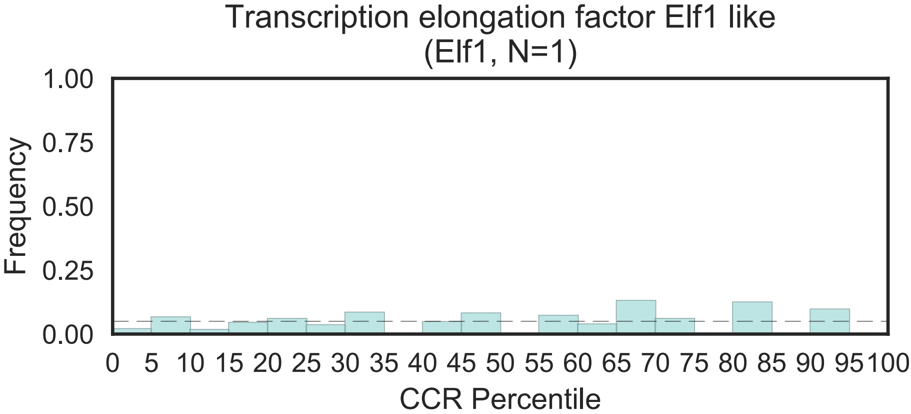
Proteasome stabiliser
(Ecm29, N=1)

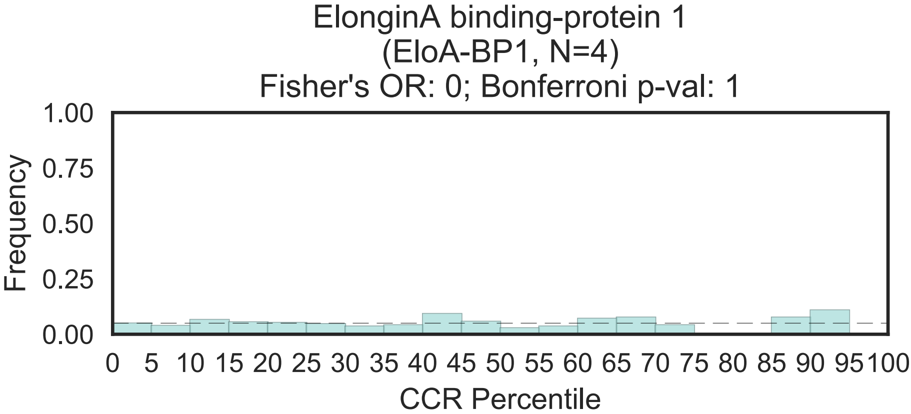


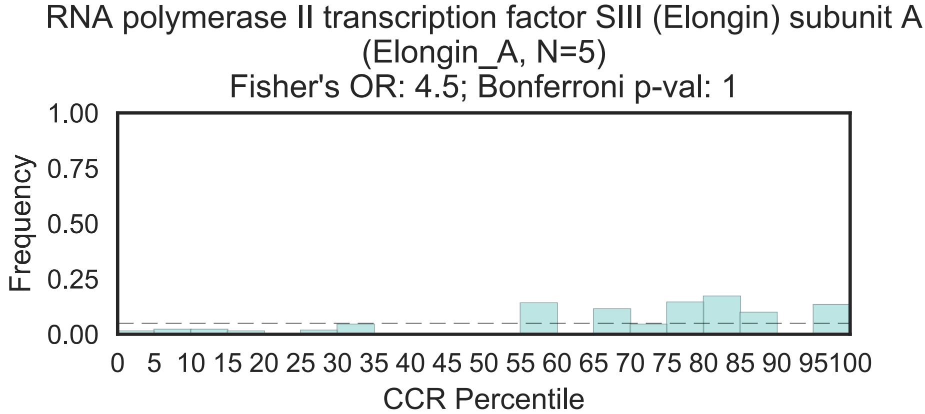
Linker region of enhancer of mRNA-decapping protein 3
(Edc3_linker, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

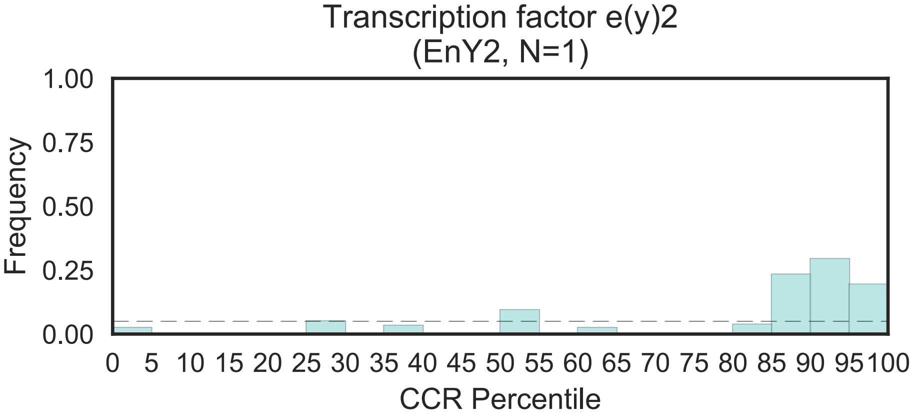

Ehrlichia tandem repeat (Ehrlichia_rpt)
(Ehrlichia_rpt, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

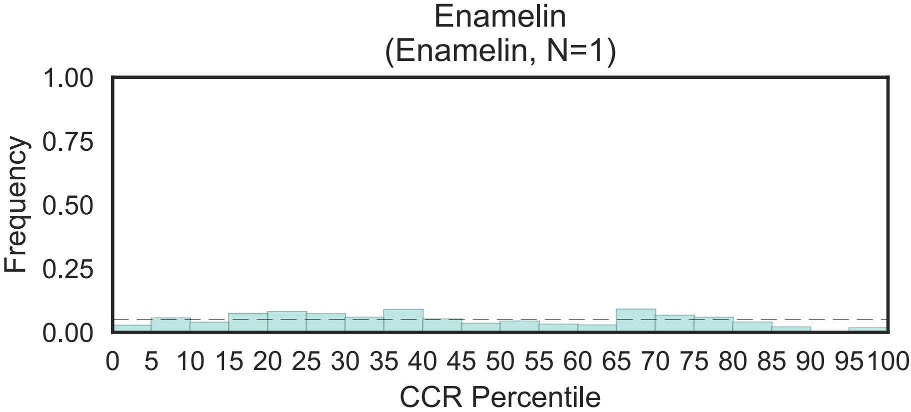

Transcription factor protein N terminal
(Elf-1_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

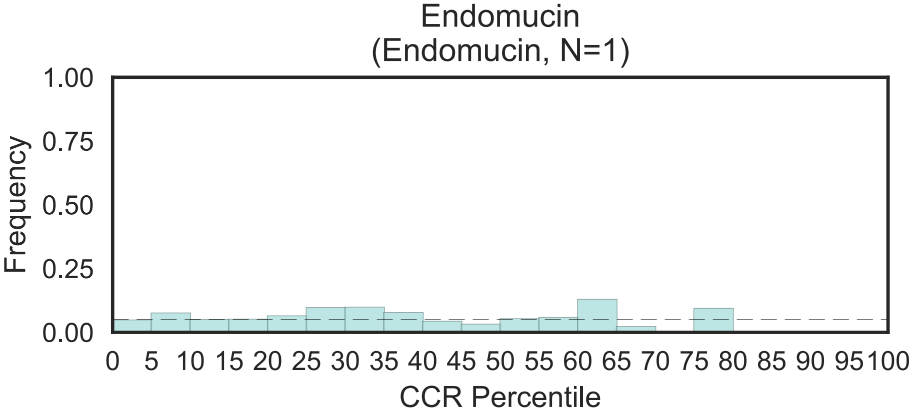

Transcription elongation factor Elf1 like
(Elf1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

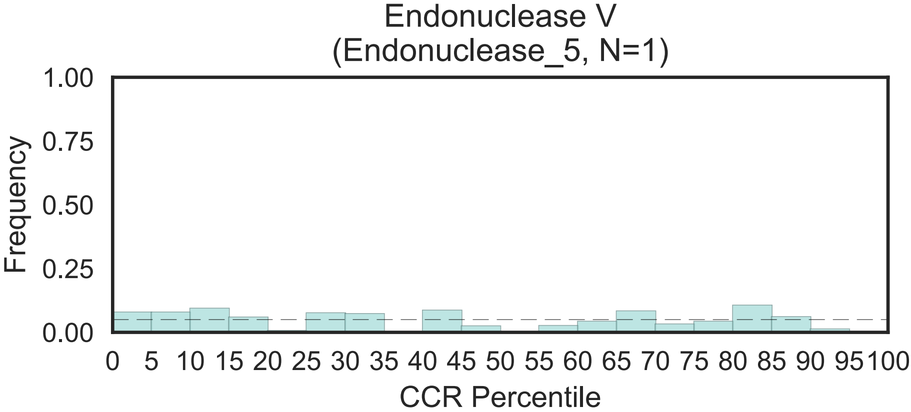

ElonginA binding-protein 1
(EloA-BP1, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

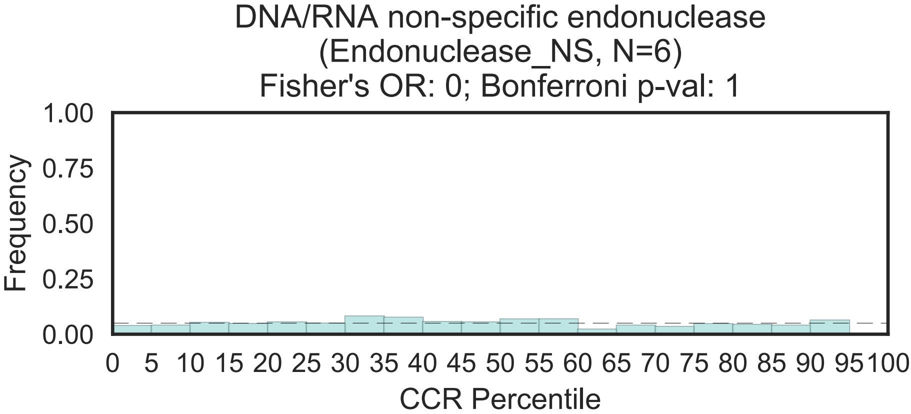

RNA polymerase II transcription factor SIII (Elongin) subunit A
(Elongin_A, N=5)
Fisher's OR: 4.5; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

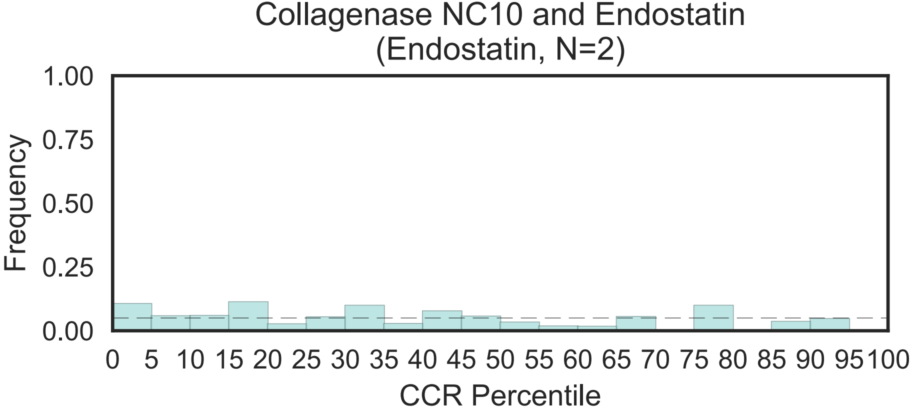

Transcription factor e(y)2
(EnY2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

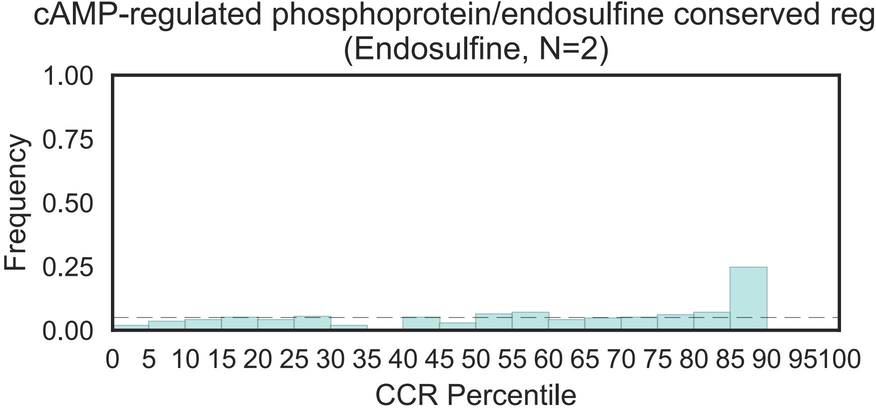

Enamelin
(Enamelin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

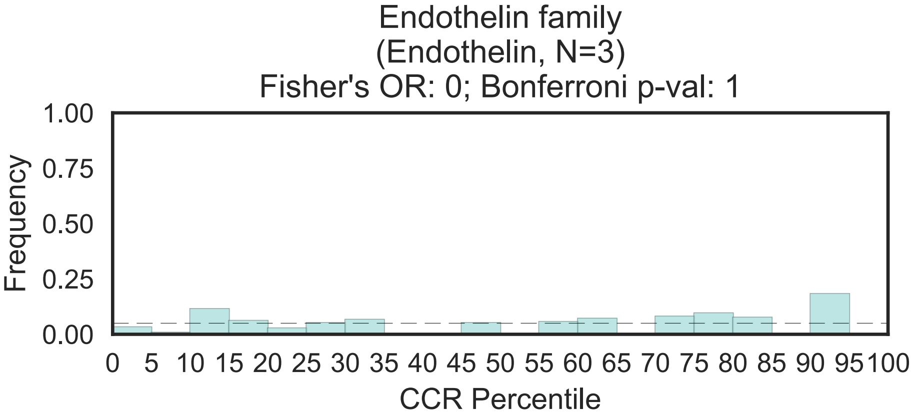

Endomucin
(Endomucin, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

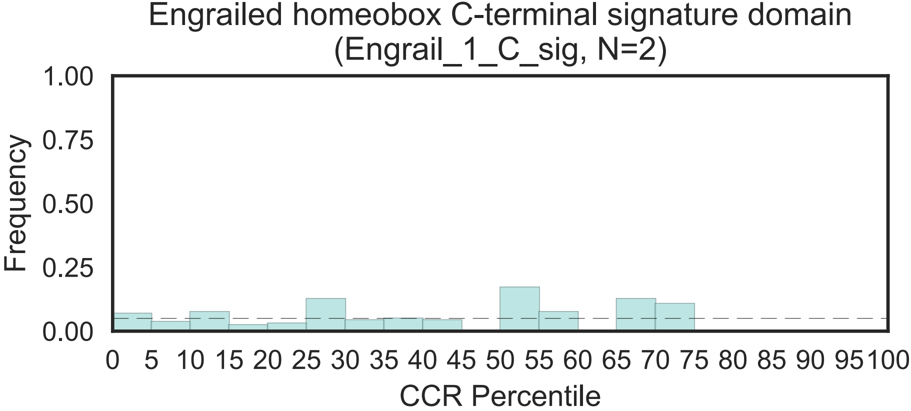

Endonuclease V
(Endonuclease_5, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


DNA/RNA non-specific endonuclease
(Endonuclease_NS, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

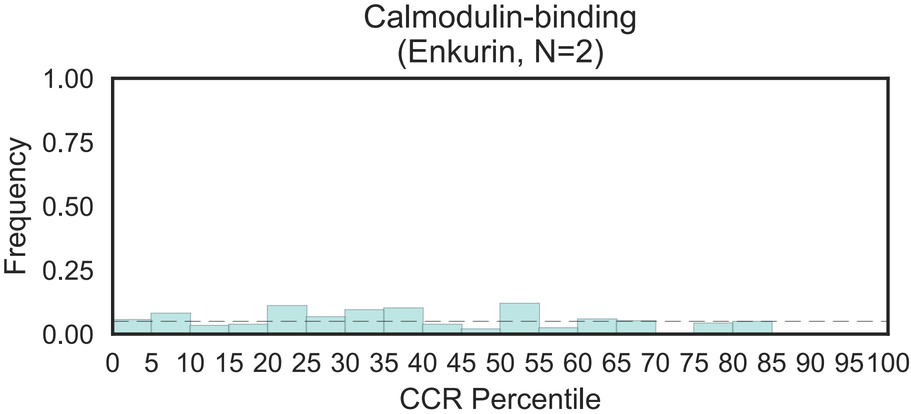

Collagenase NC10 and Endostatin
(Endostatin, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

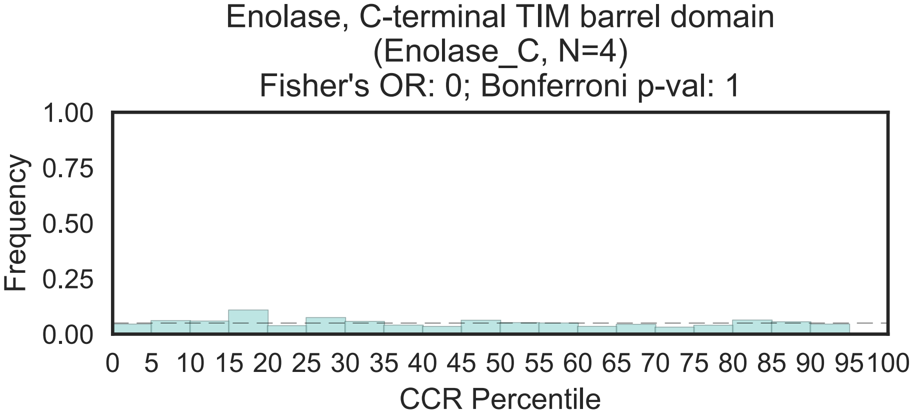

cAMP-regulated phosphoprotein/endosulfine conserved region
(Endosulfine, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

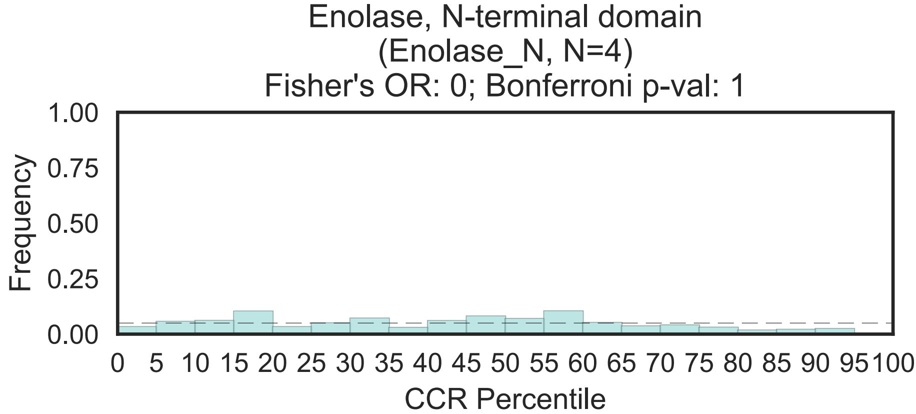

Endothelin family
(Endothelin, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

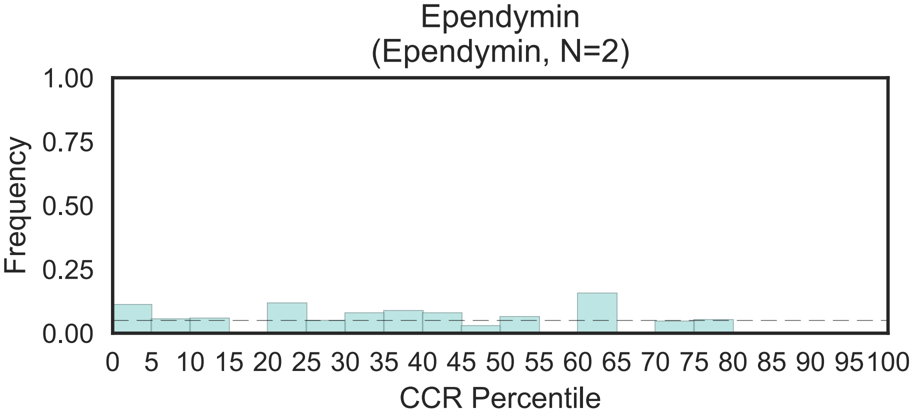


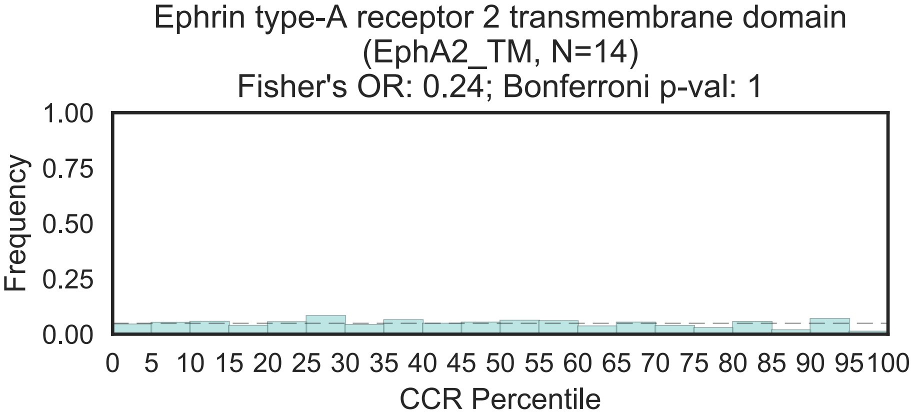
Engrailed homeobox C-terminal signature domain
(Engrail_1_C_sig, N=2)

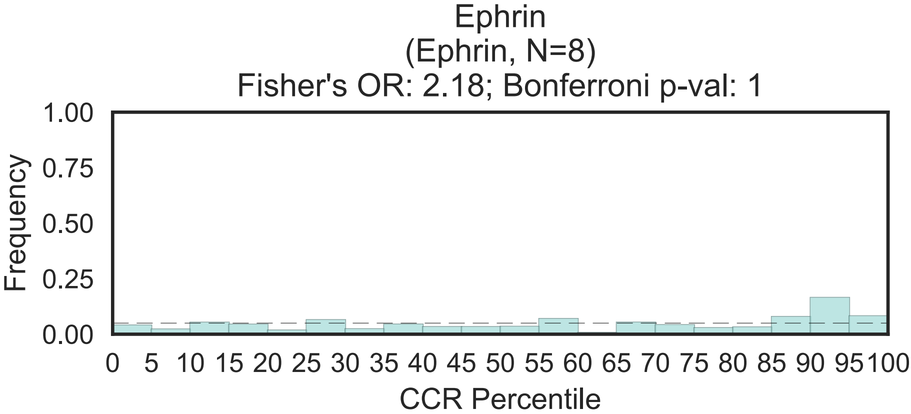

Calmodulin-binding
(Enkurin, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

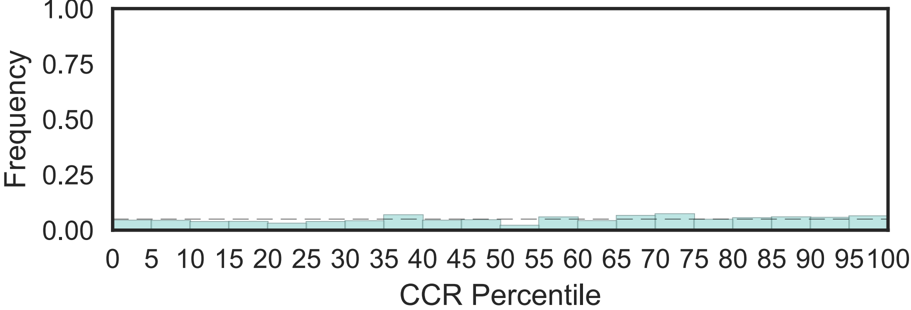

Enolase, C-terminal TIM barrel domain
(Enolase_C, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Enolase, N-terminal domain
(Enolase_N, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

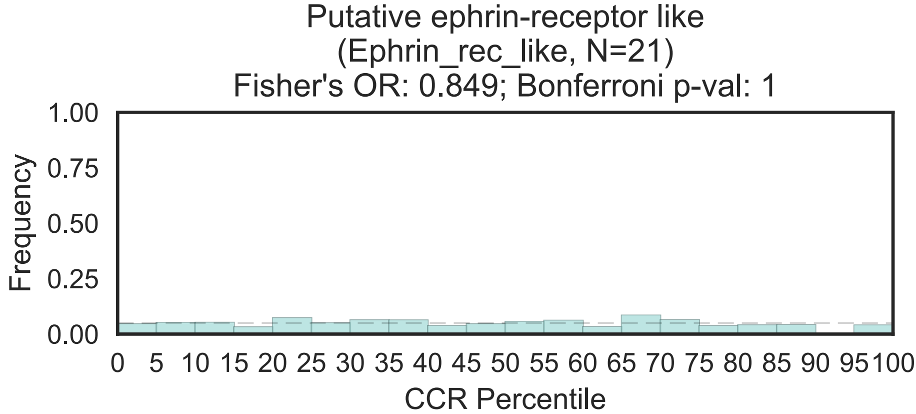

Ependymin
(Ependymin, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

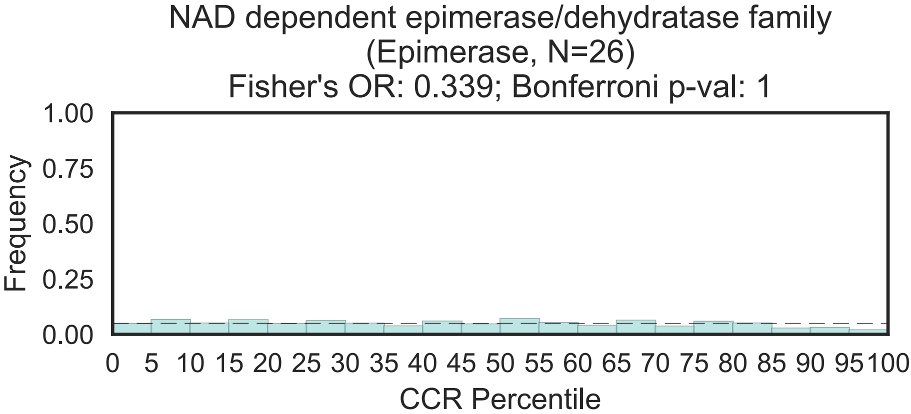

Ephrin type-A receptor 2 transmembrane domain
(EphA2_TM, N=14)
Fisher's OR: 0.24; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

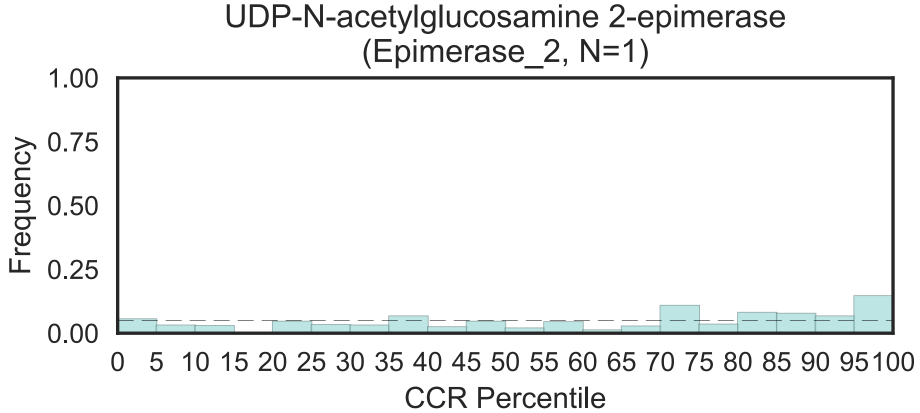

Ephrin
(Ephrin, N=8)
Fisher's OR: 2.18; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

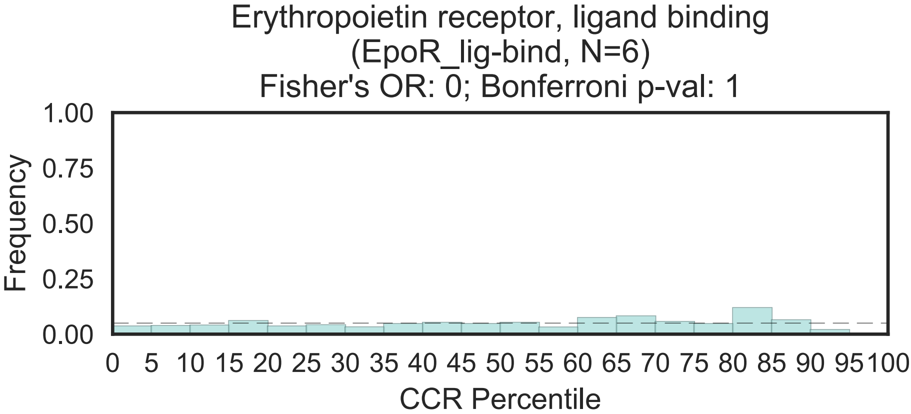


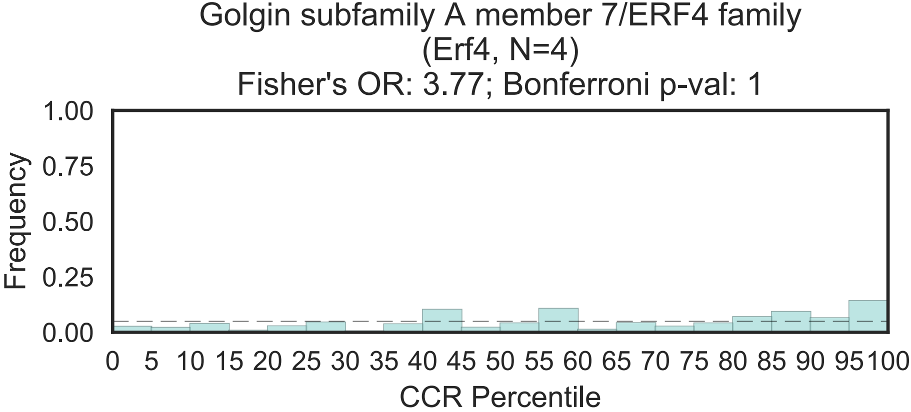
Ephrin receptor ligand binding domain
(Ephrin_lbd, N=14)
Fisher's OR: 0.859; Bonferroni p-val: 1

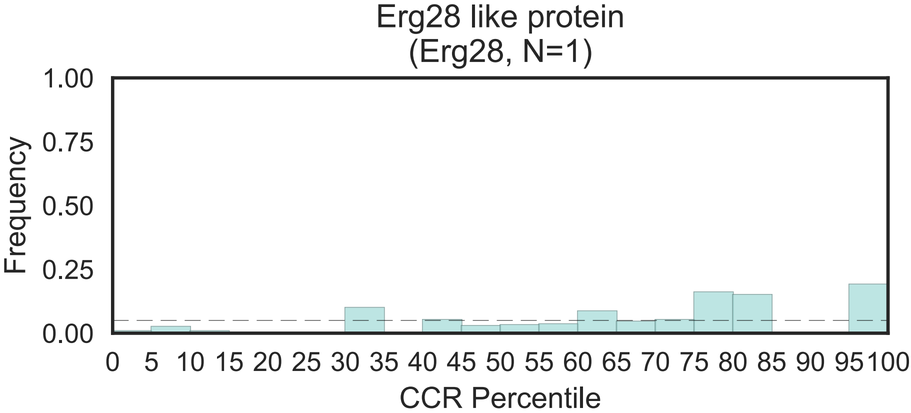

Putative ephrin-receptor like
(Ephrin_rec_like, N=21)
Fisher's OR: 0.849; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

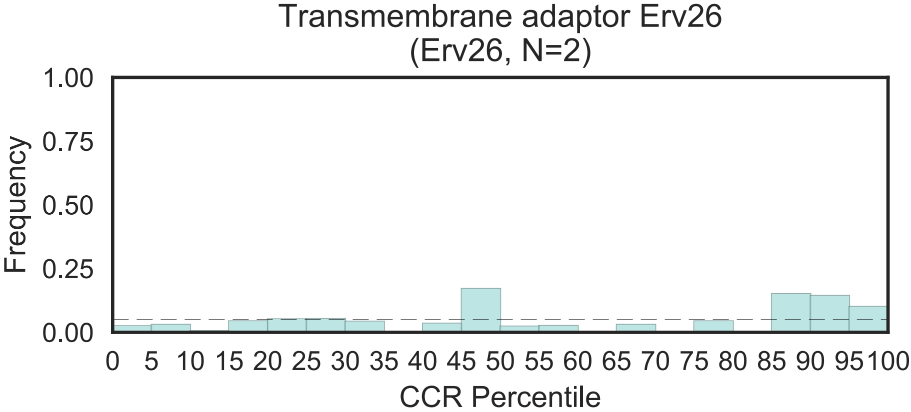

NAD dependent epimerase/dehydratase family
(Epimerase, N=26)
Fisher's OR: 0.339; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

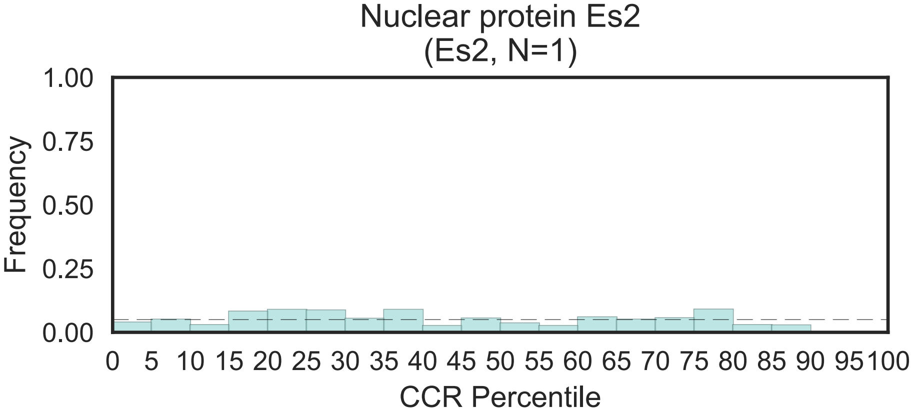

UDP-N-acetylglucosamine 2-epimerase
(Epimerase_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

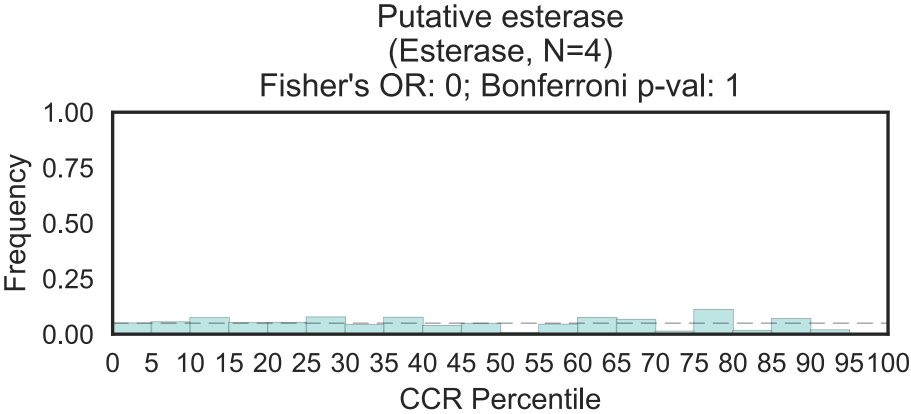

Erythropoietin receptor, ligand binding
(EpoR_lig-bind, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

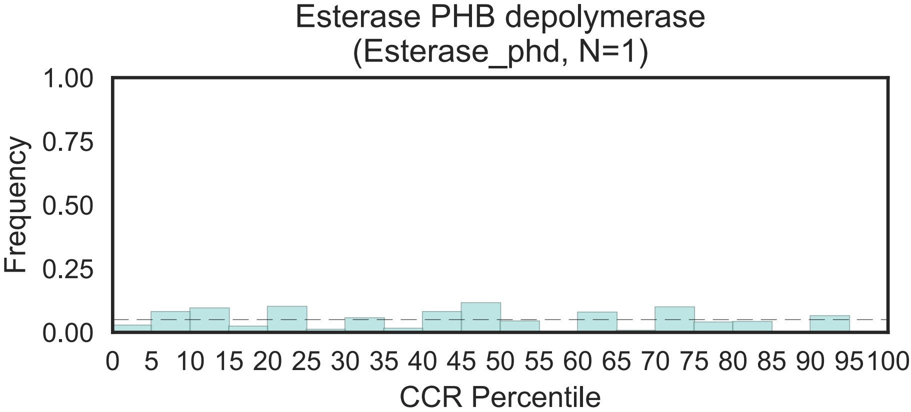

Golgin subfamily A member 7/ERF4 family
(Erf4, N=4)
Fisher's OR: 3.77; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

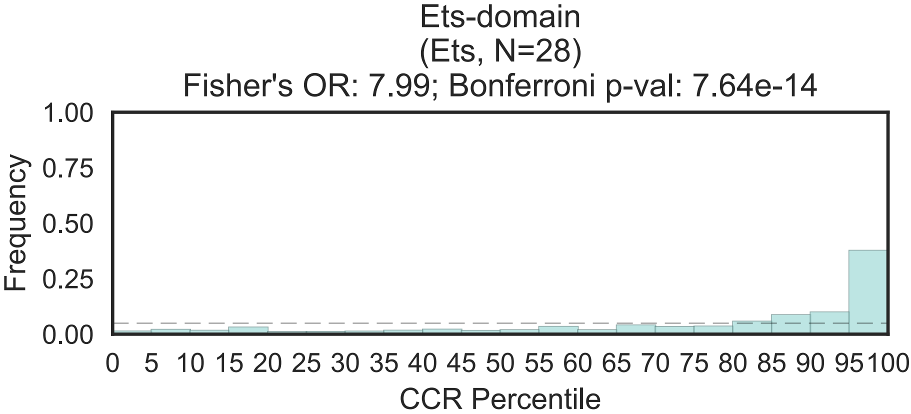

Erg28 like protein
(Erg28, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

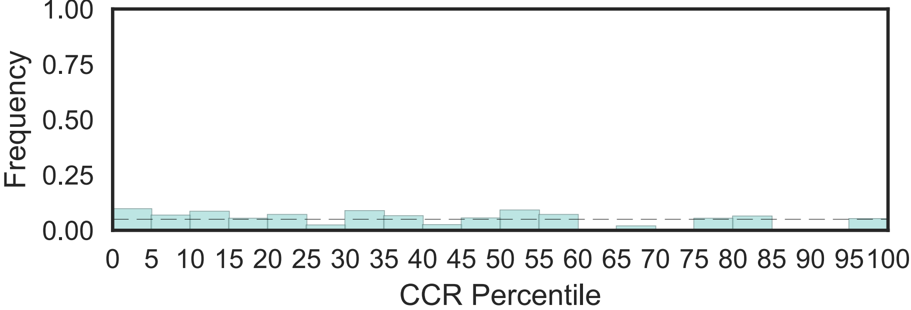

Transmembrane adaptor Erv26
(Erv26, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Nuclear protein Es2
(Es2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

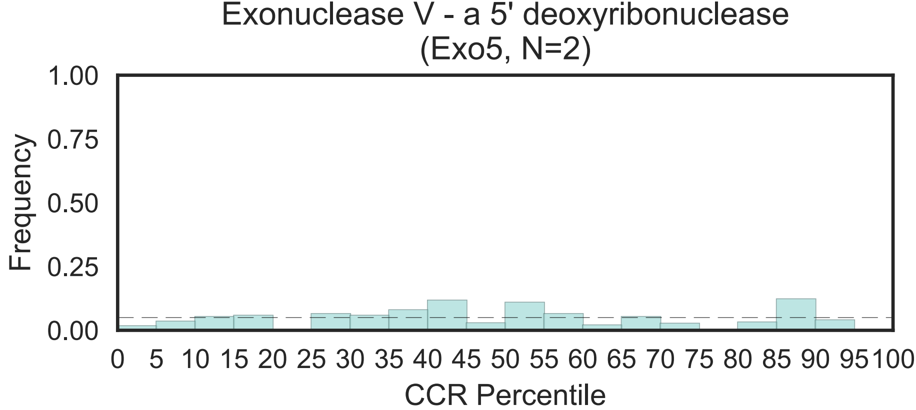
Putative esterase
(Esterase, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

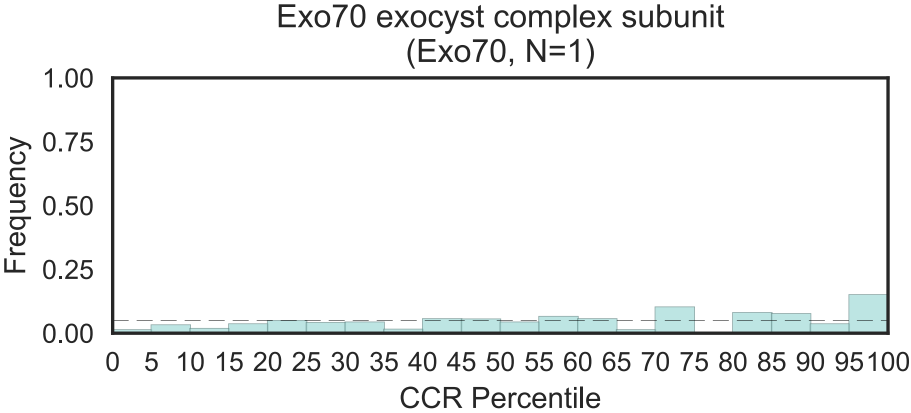

Esterase PHB depolymerase
(Esterase_phd, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

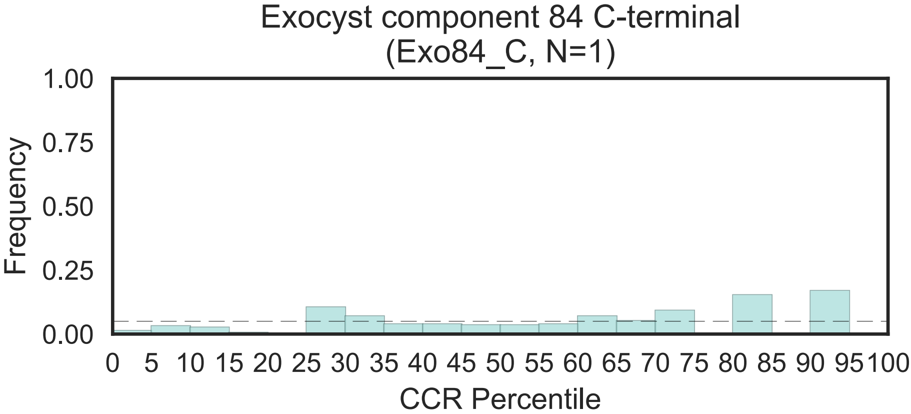

Ets-domain
(Ets, N=28)
Fisher's OR: 7.99; Bonferroni p-val: 7.64e-14
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

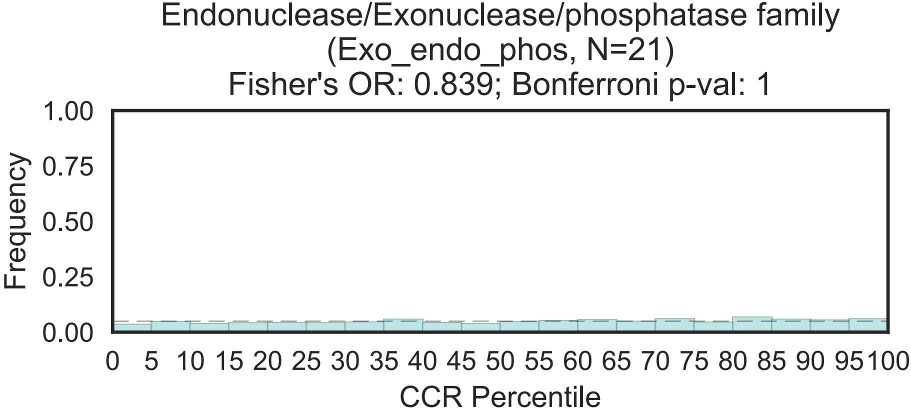


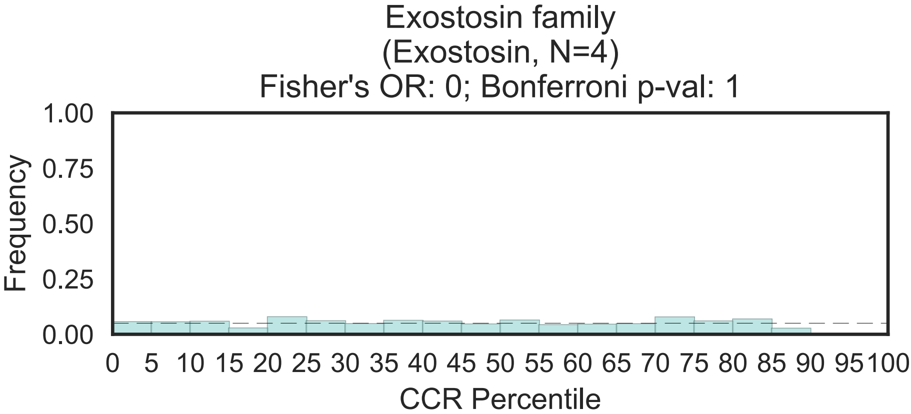
Erv1 / Alr family
(Evr1_Alr, N=3)
Fisher's OR: 0.751; Bonferroni p-val: 1

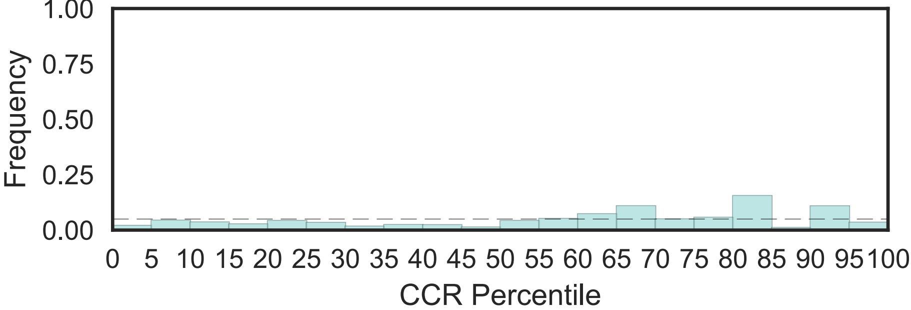

Exonuclease V - a 5' deoxyribonuclease
(Exo5, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Exo70 exocyst complex subunit
(Exo70, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

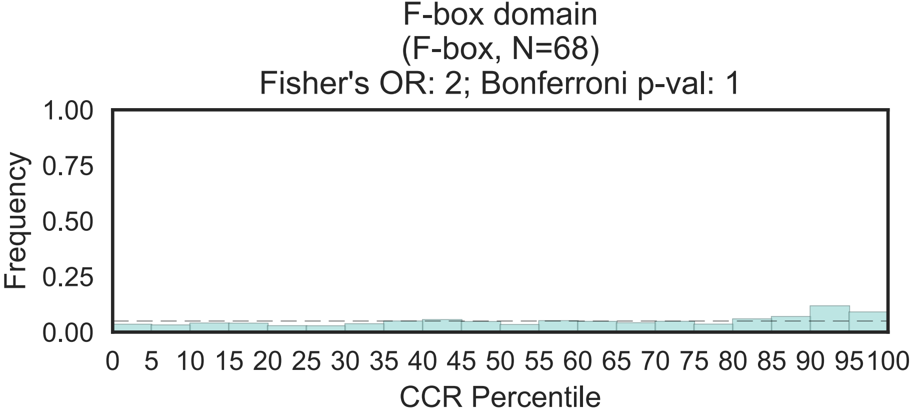

Exocyst component 84 C-terminal
(Exo84_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

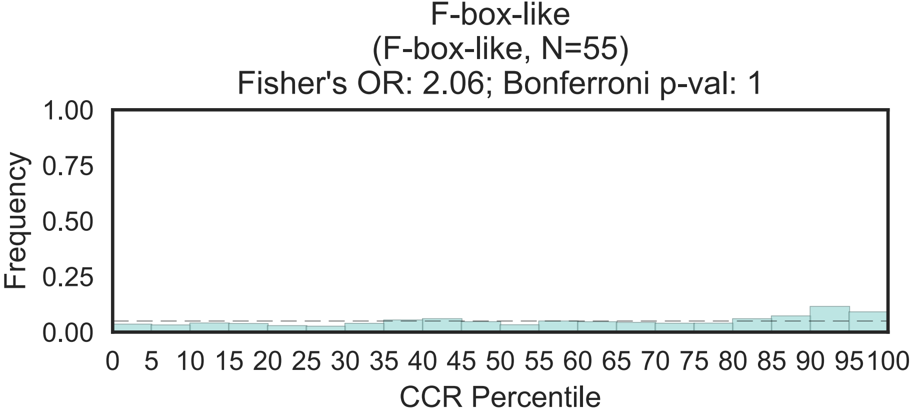

Endonuclease/Exonuclease/phosphatase family
(Exo_endo_phos, N=21)
Fisher's OR: 0.839; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

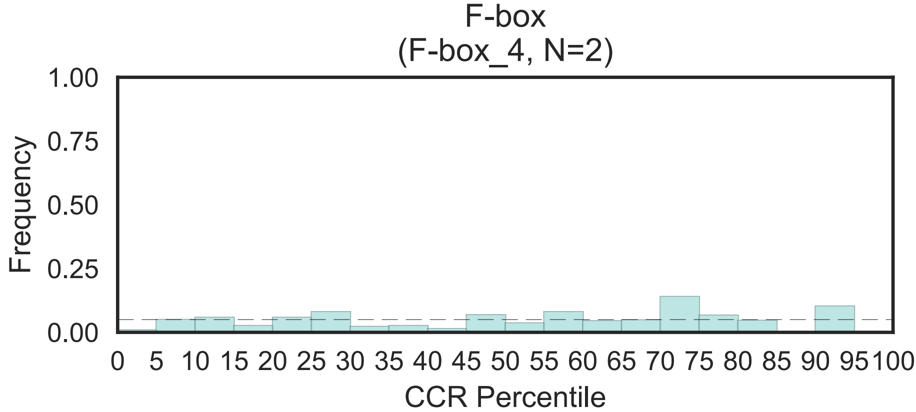

Exostosin family
(Exostosin, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

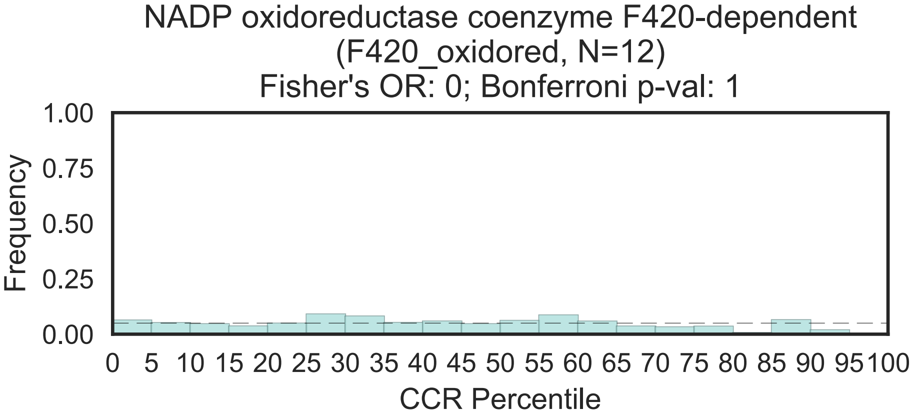


F-actin capping protein alpha subunit
(F-actin_cap_A, N=3)
Fisher's OR: 0.449; Bonferroni p-val: 1

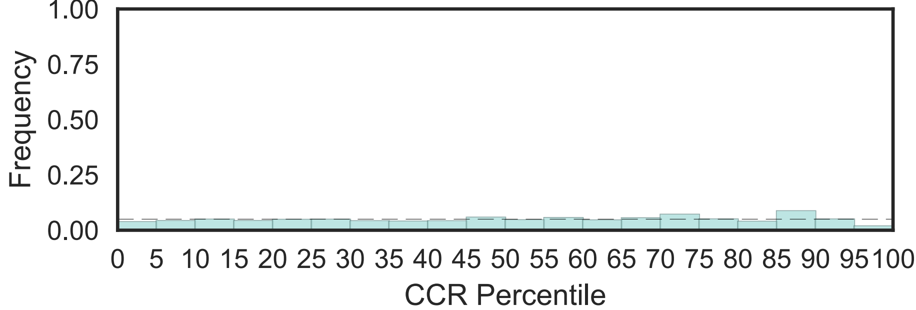

F-box domain
(F-box, N=68)
Fisher's OR: 2; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

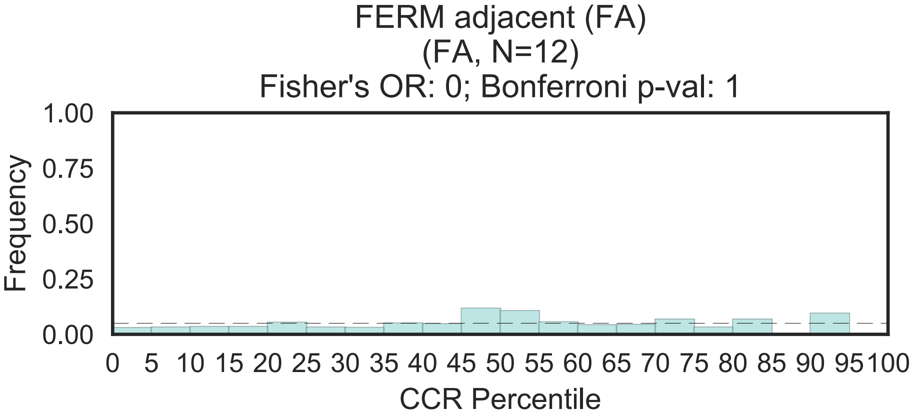

F-box-like
(F-box-like, N=55)
Fisher's OR: 2.06; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


F-box
(F-box_4, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

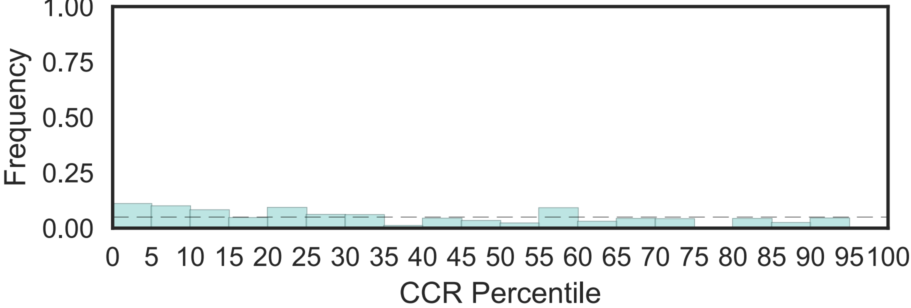

NADP oxidoreductase coenzyme F420-dependent
(F420_oxidored, N=12)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

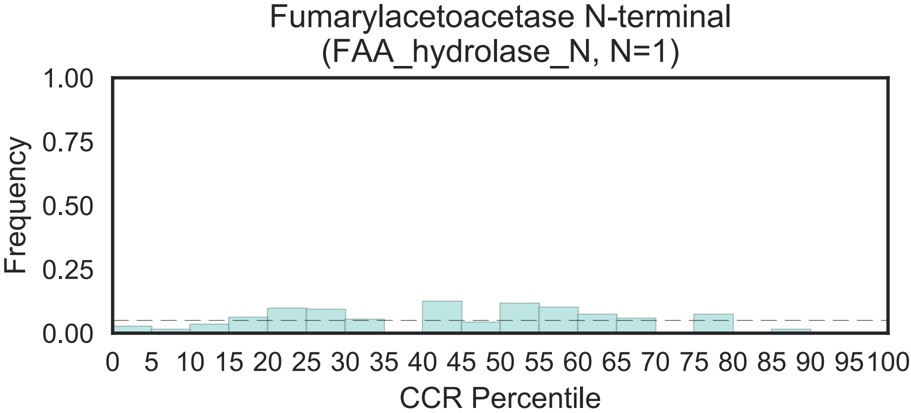
F5/8 type C domain
(F5_F8_type_C, N=27)
Fisher's OR: 0.26; Bonferroni p-val: 1

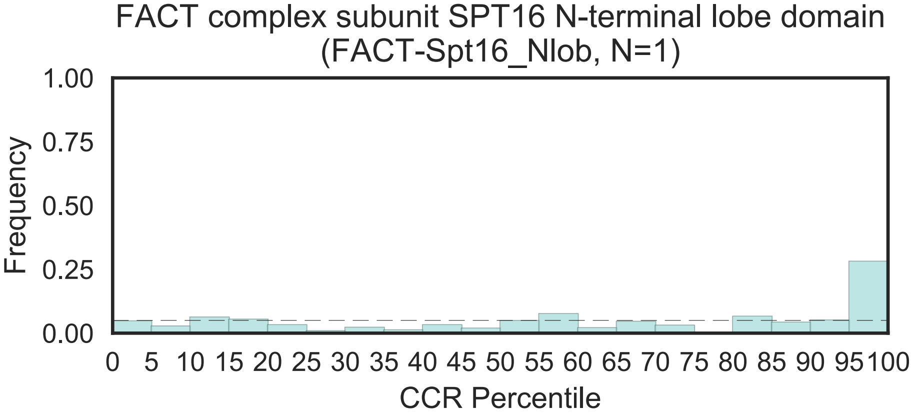



FERM adjacent (FA)
(FA, N=12)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

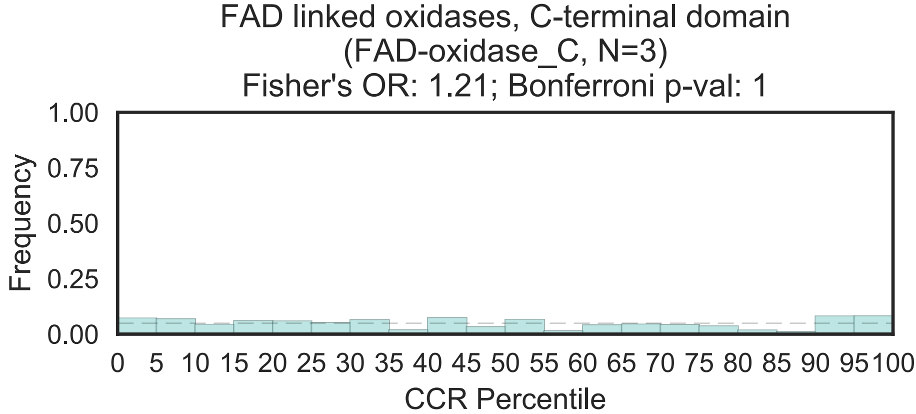
Fumarylacetoacetate (FAA) hydrolase family
(FAA_hydrolase, N=5)
Fisher's OR: 0; Bonferroni p-val: 1



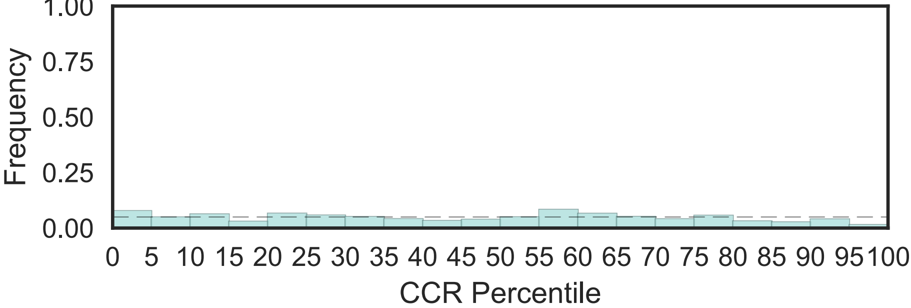

Fumarylacetoacetase N-terminal
(FAA_hydrolase_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

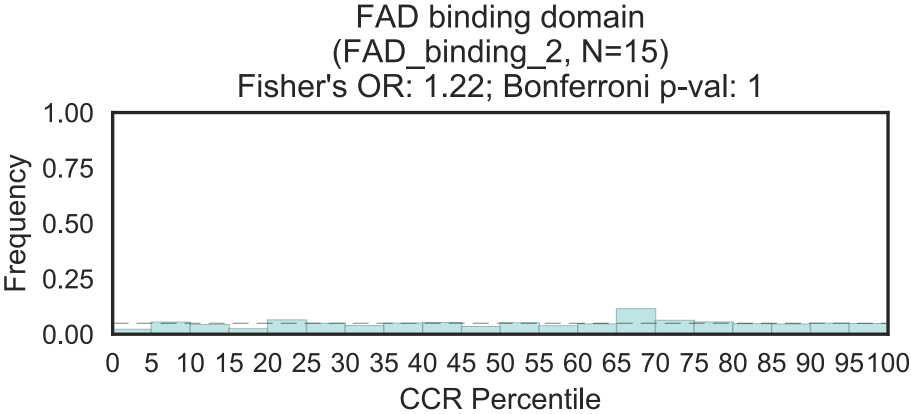


FACT complex subunit SPT16 N-terminal lobe domain (FACT-Spt16_Nlob, N=1)

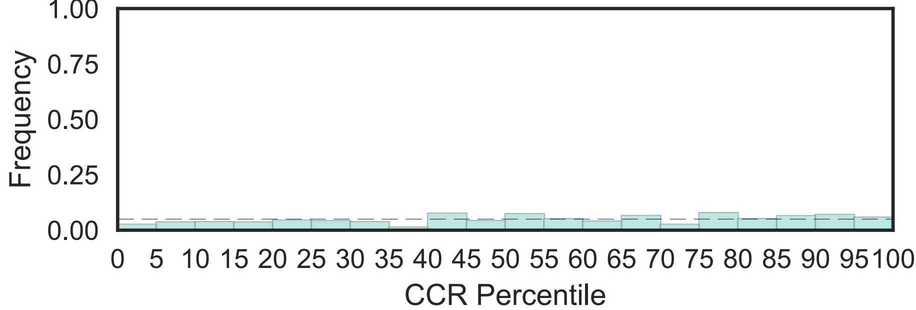

FAD linked oxidases, C-terminal domain
(FAD-oxidase_C, N=3)
Fisher's OR: 1.21; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

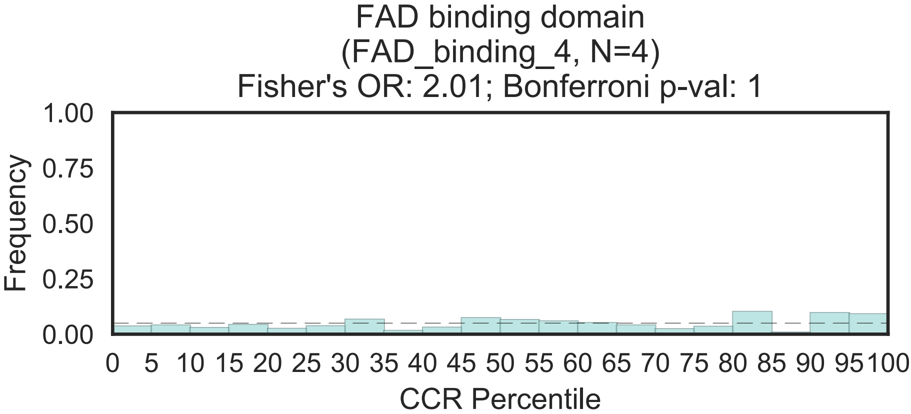
FAD binding domain
(FAD_binding_1, N=6)
Fisher's OR: 0.237; Bonferroni p-val: 1

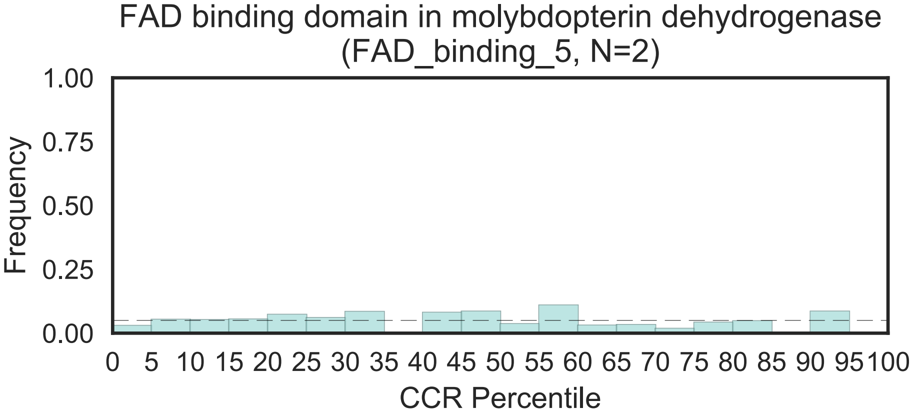


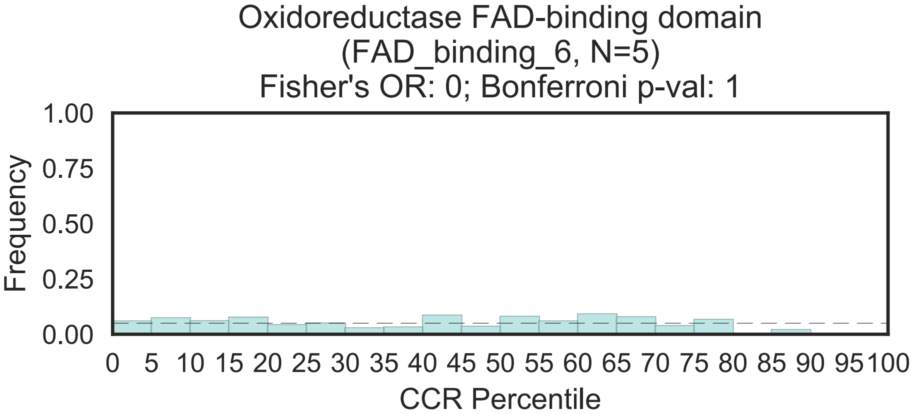

FAD binding domain
(FAD_binding_2, N=15)
Fisher's OR: 1.22; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

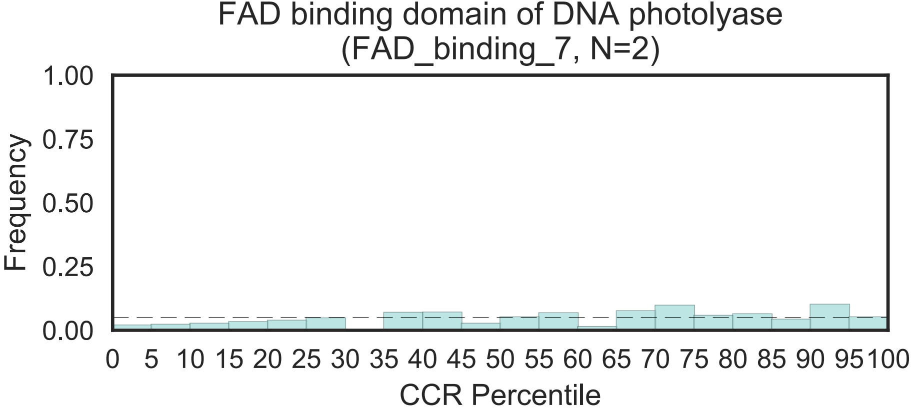
FAD binding domain
(FAD_binding_3, N=12)
Fisher's OR: 1.3; Bonferroni p-val: 1



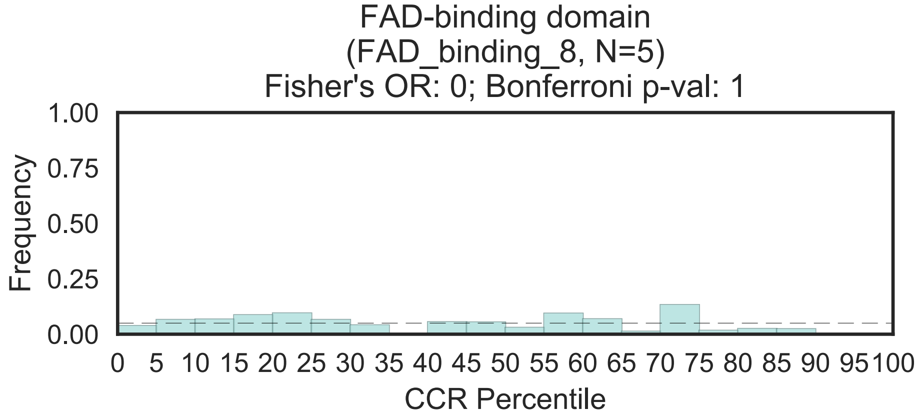

FAD binding domain
(FAD_binding_4, N=4)
Fisher's OR: 2.01; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

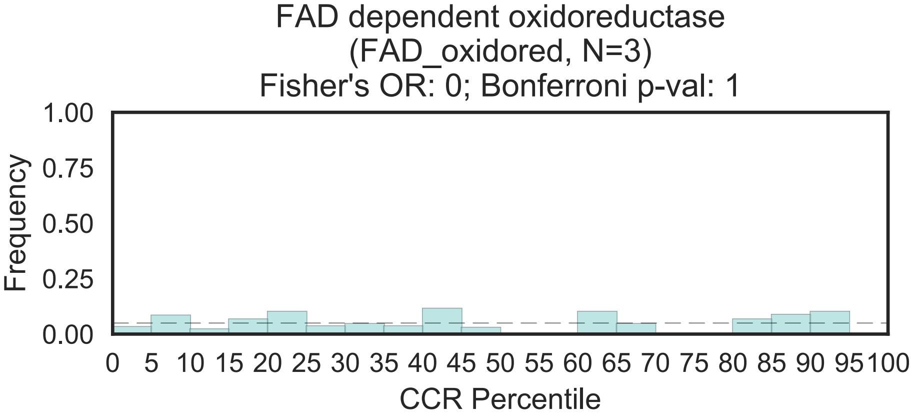

FAD binding domain in molybdopterin dehydrogenase
(FAD_binding_5, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

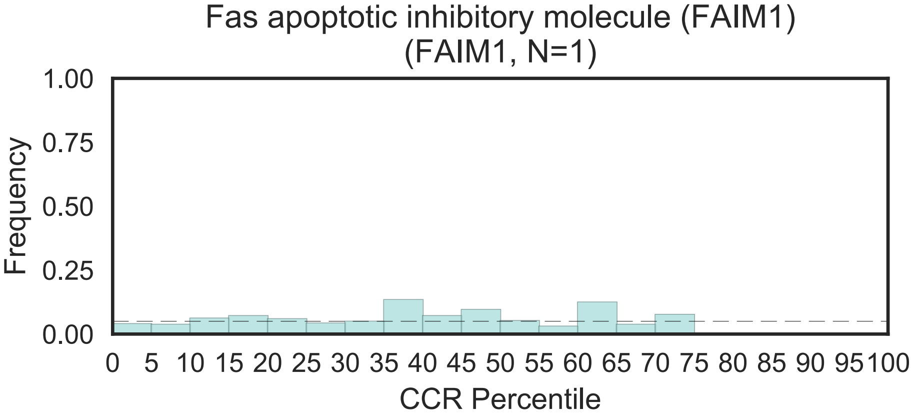

Oxidoreductase FAD-binding domain
(FAD_binding_6, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

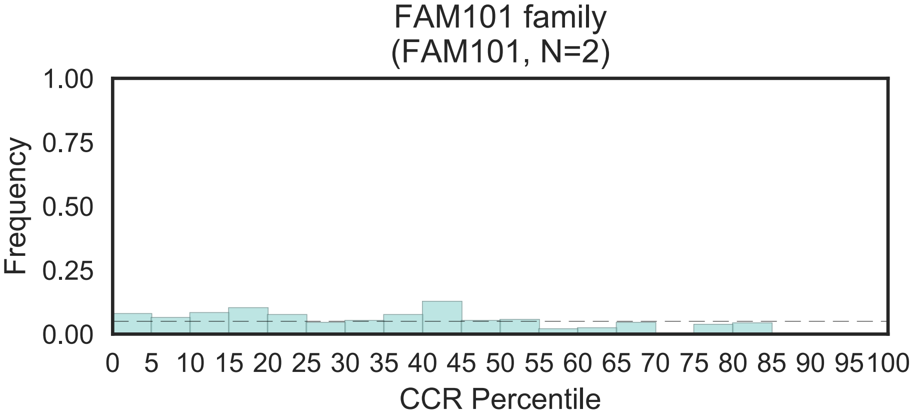


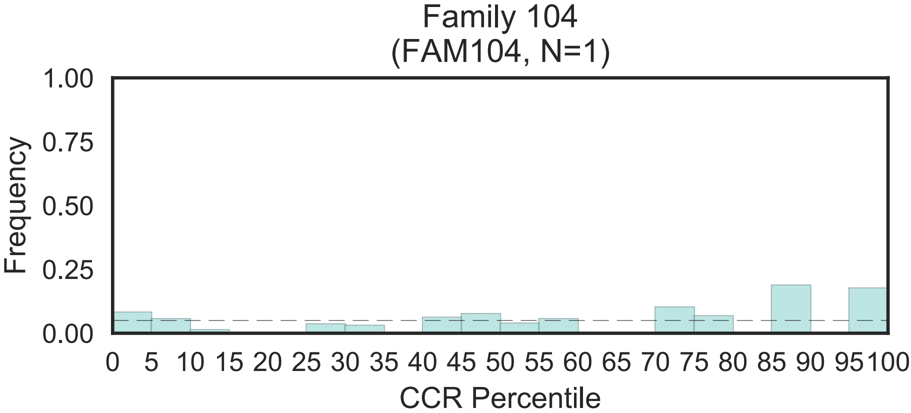
FAD binding domain of DNA photolyase
(FAD_binding_7, N=2)


FAD-binding domain
(FAD_binding_8, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

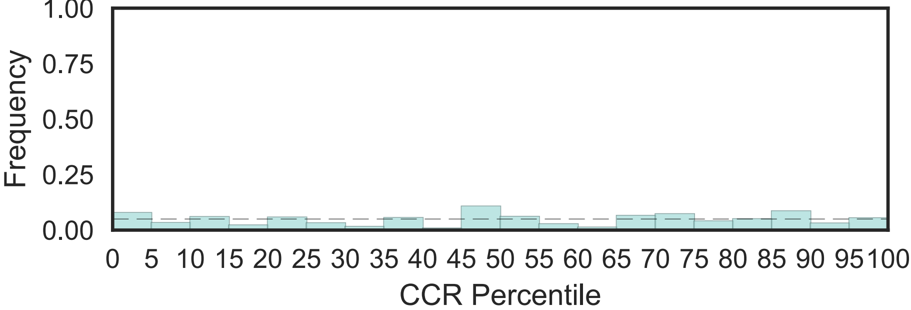

FAD dependent oxidoreductase
(FAD_oxidored, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

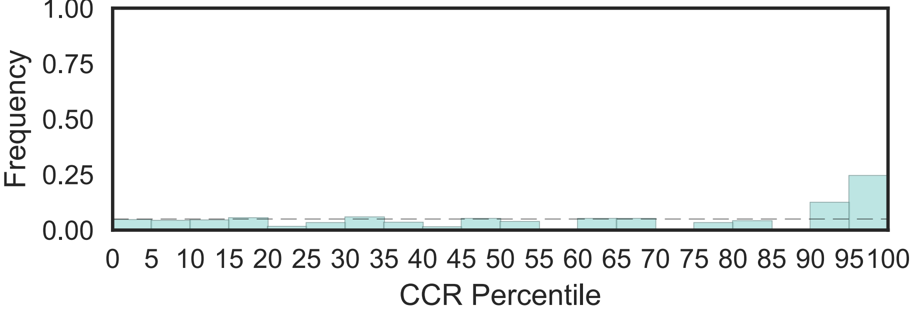

Fas apoptotic inhibitory molecule (FAIM1)
(FAIM1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


FAM101 family
(FAM101, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Family 104
(FAM104, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

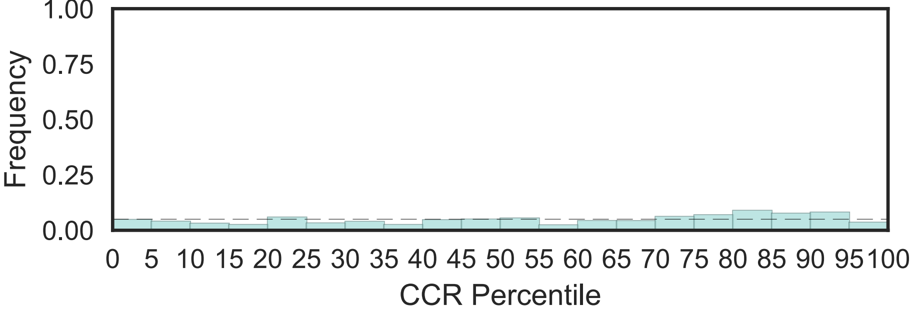
Centrosome-associated C terminus
(FAM110_C, N=4)
Fisher's OR: 0.901; Bonferroni p-val: 1

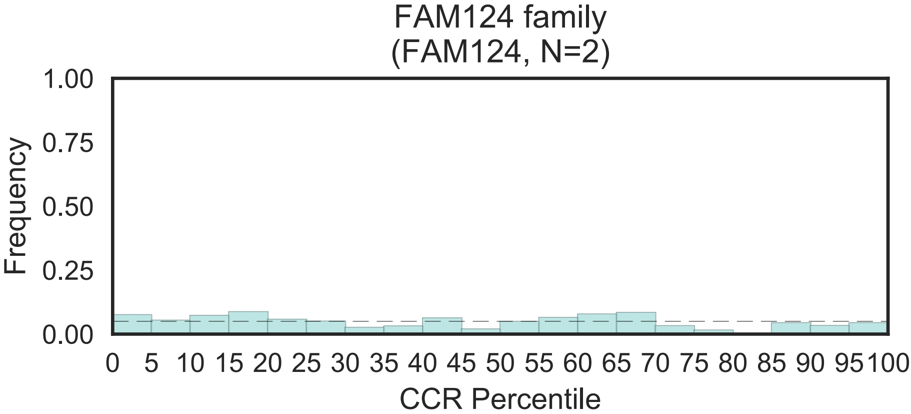


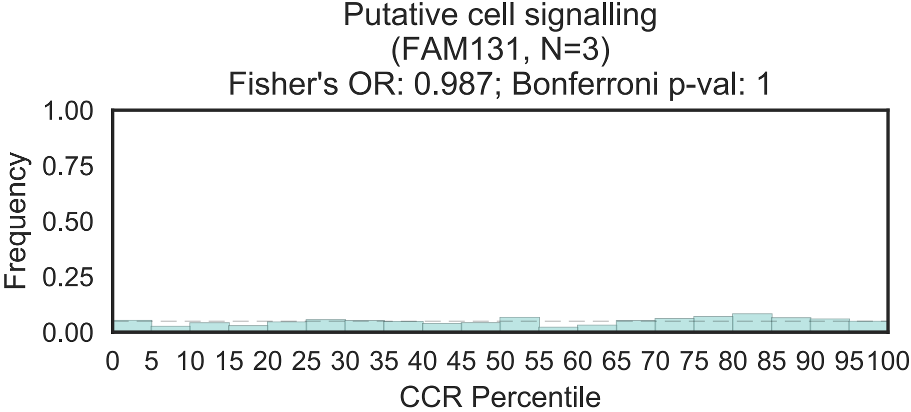


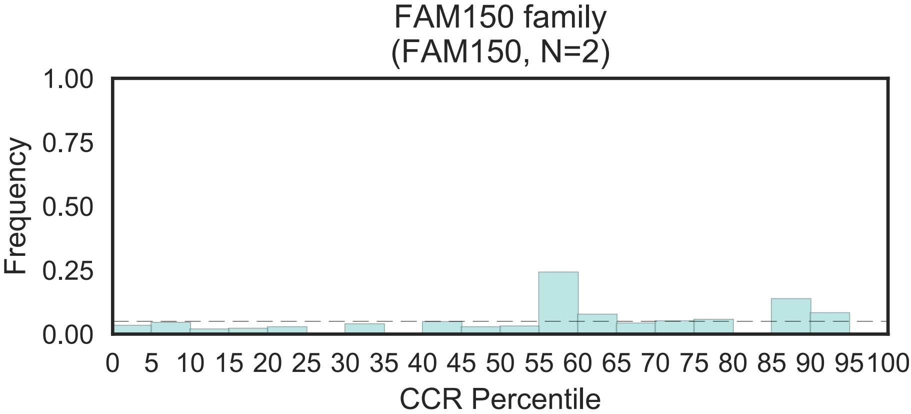
Centrosome-associated N terminus
(FAM110_N, N=4)
Fisher's OR: 3.49; Bonferroni p-val: 1

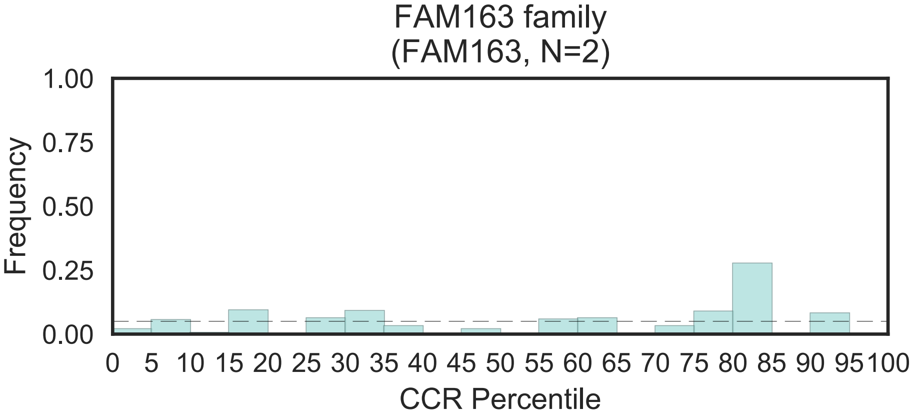
Protein Family FAM117
(FAM117, N=3)
Fisher's OR: 0.655; Bonferroni p-val: 1

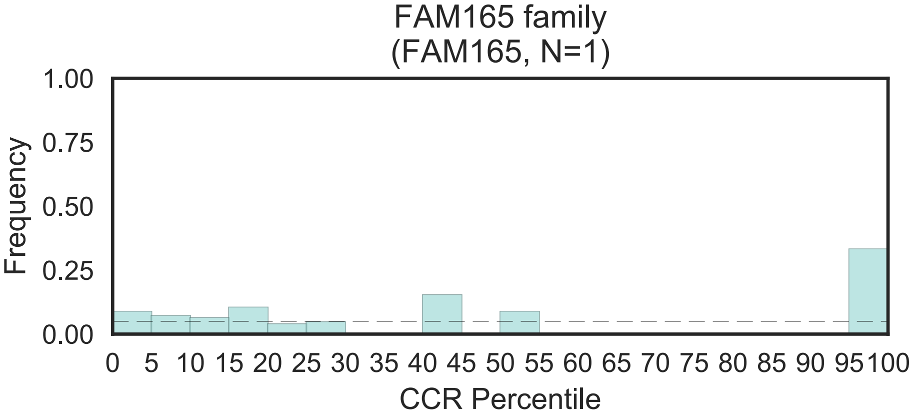


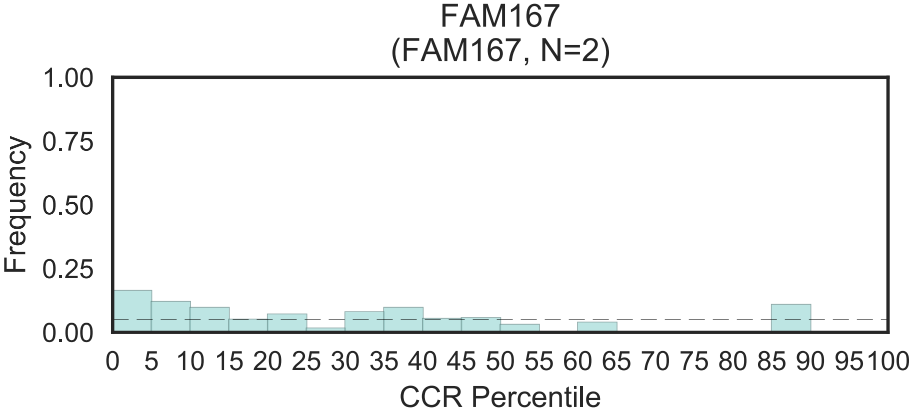

FAM124 family
(FAM124, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

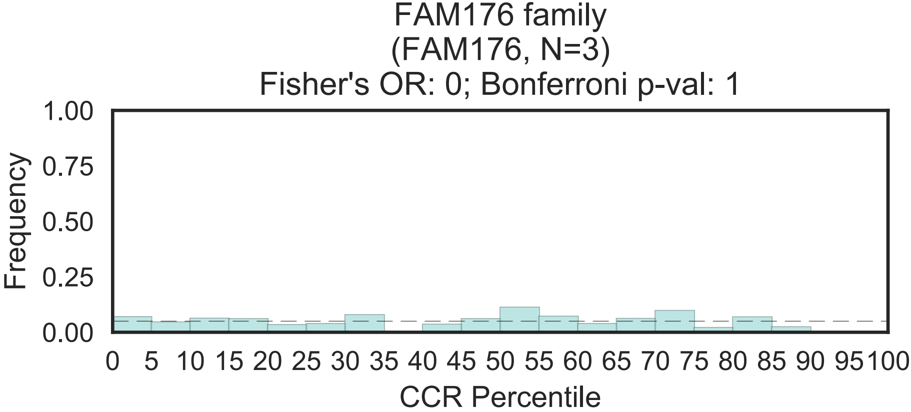

Putative cell signalling
(FAM131, N=3)
Fisher's OR: 0.987; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

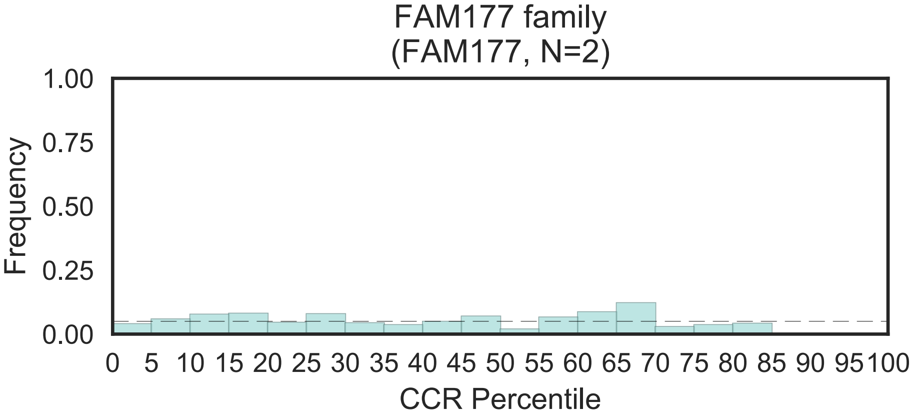

FAM150 family
(FAM150, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

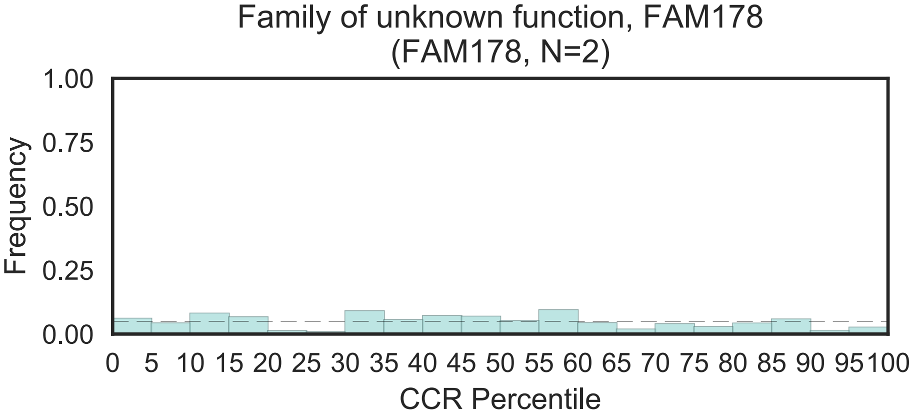

FAM163 family
(FAM163, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

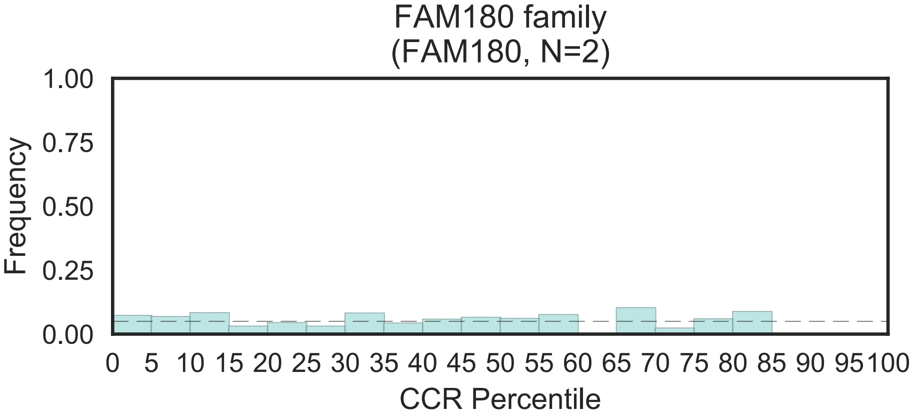

FAM165 family
(FAM165, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

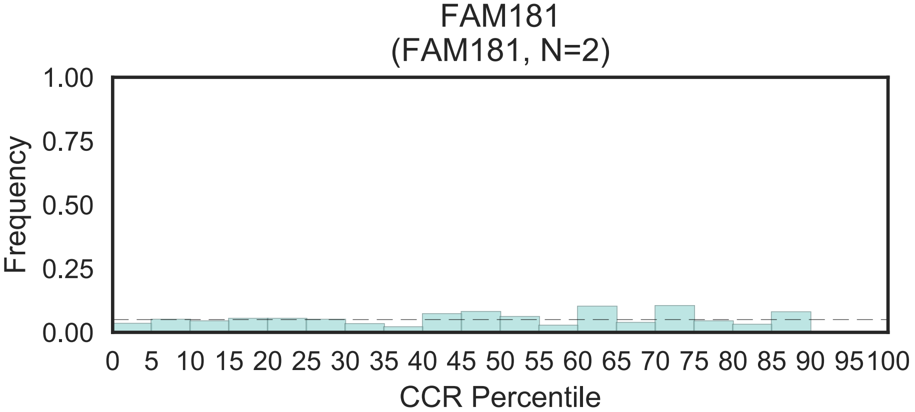

FAM167
(FAM167, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

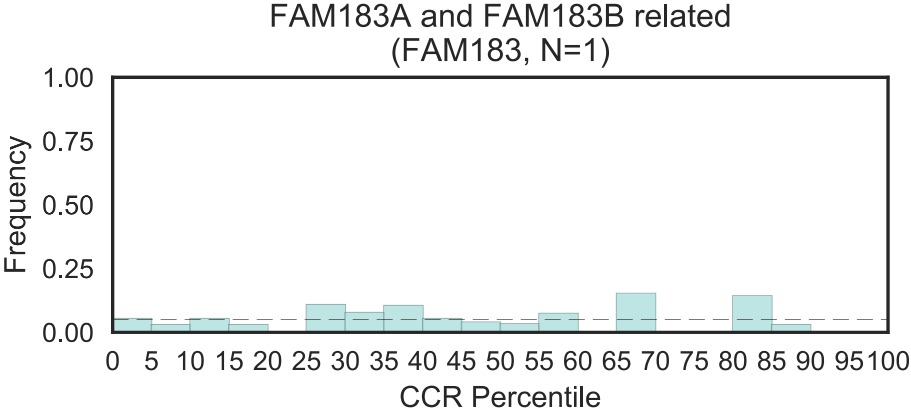

FAM176 family
(FAM176, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

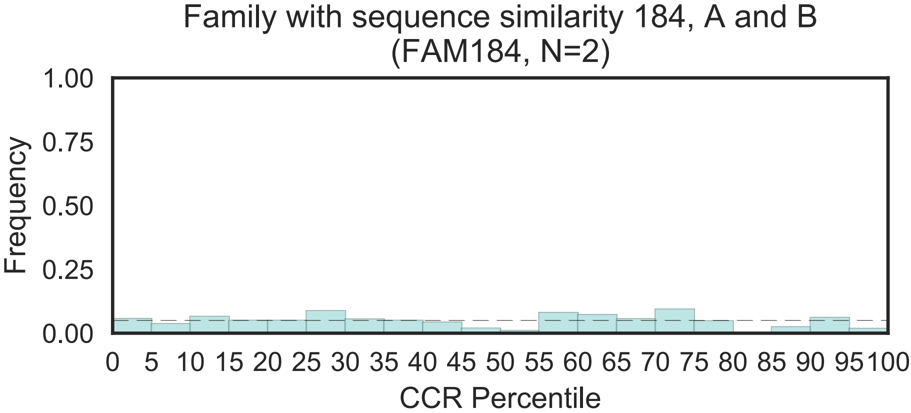

FAM177 family
(FAM177, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

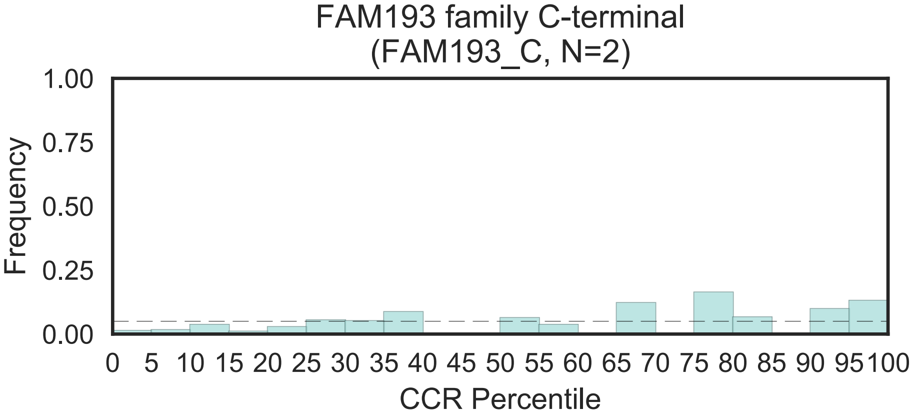

Family of unknown function, FAM178
(FAM178, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

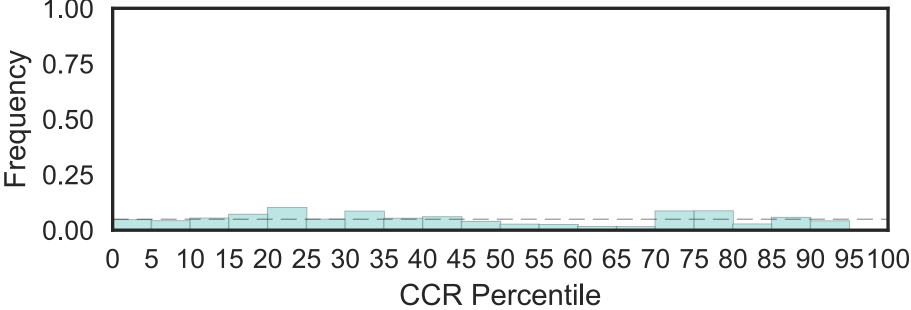

FAM180 family
(FAM180, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


FAM181
(FAM181, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

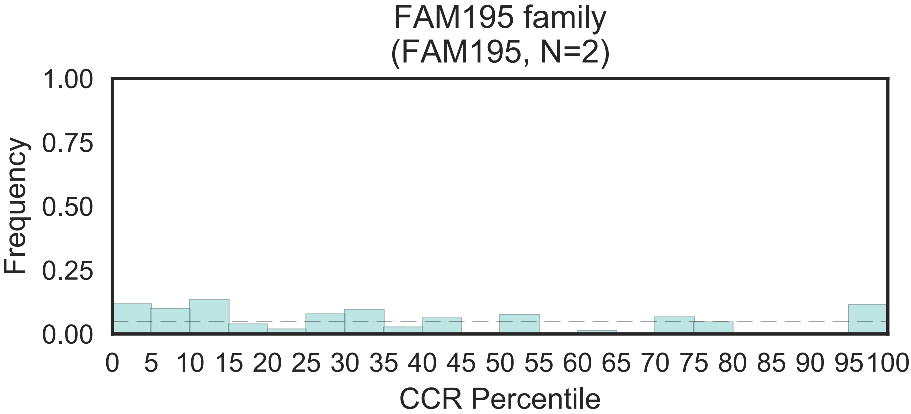

FAM183A and FAM183B related
(FAM183, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

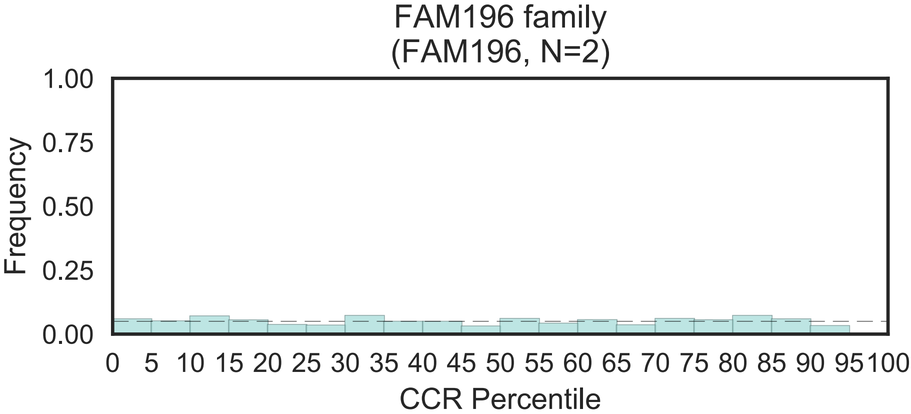

Family with sequence similarity 184, A and B
(FAM184, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

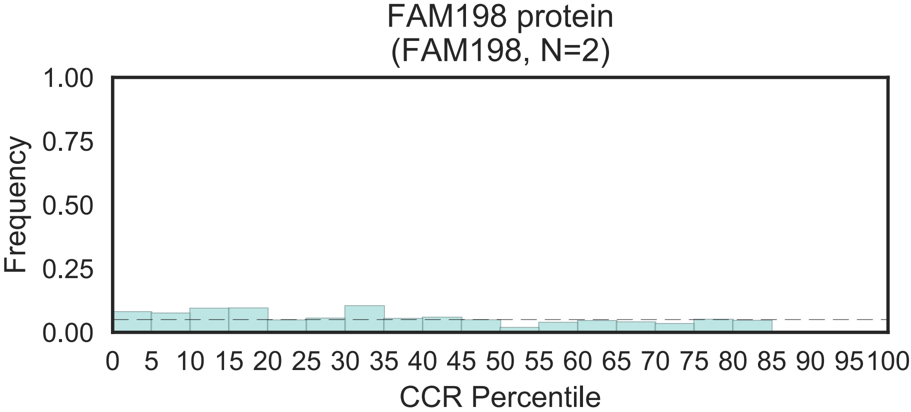

FAM193 family C-terminal
(FAM193_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

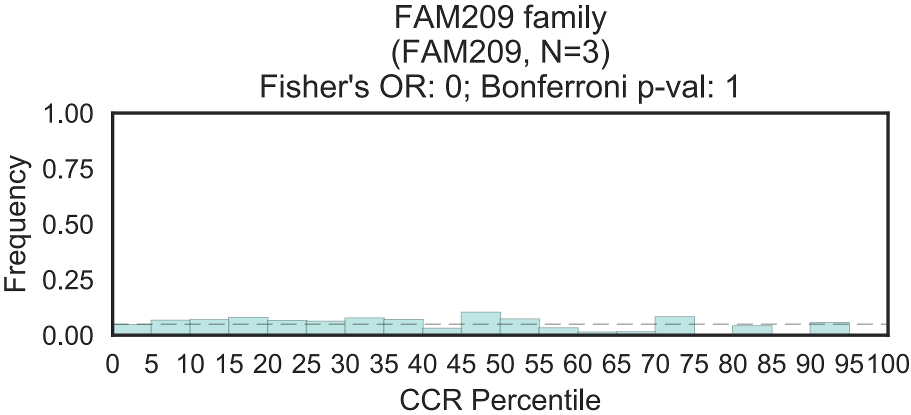


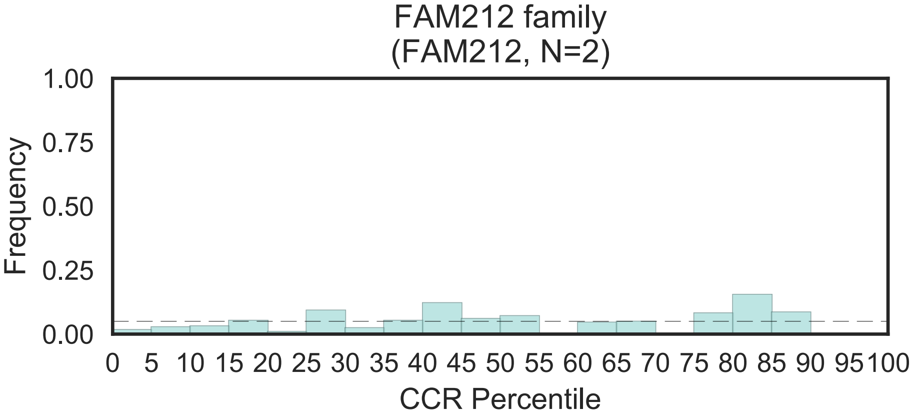
FAM194 protein
(FAM194, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

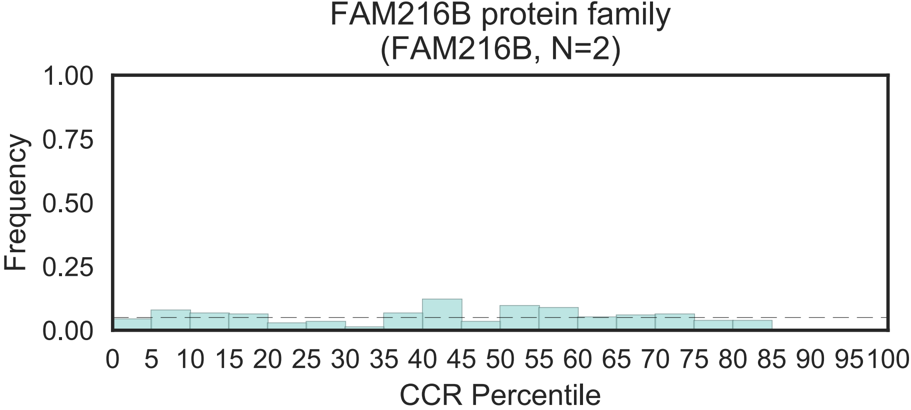

FAM195 family
(FAM195, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

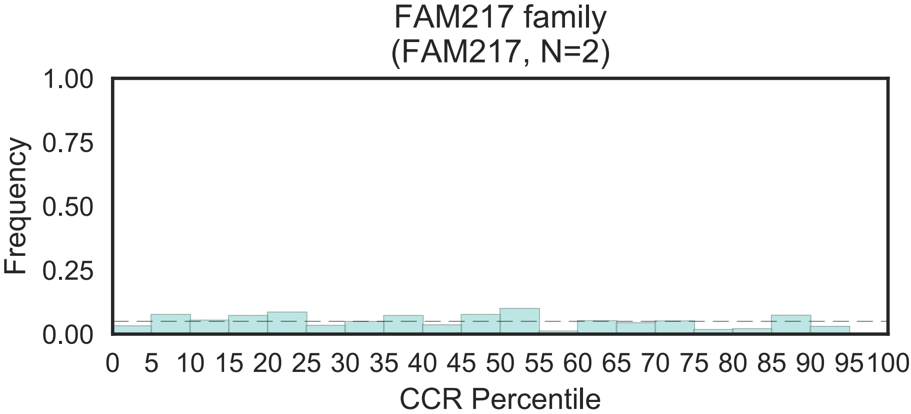

FAM196 family
(FAM196, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

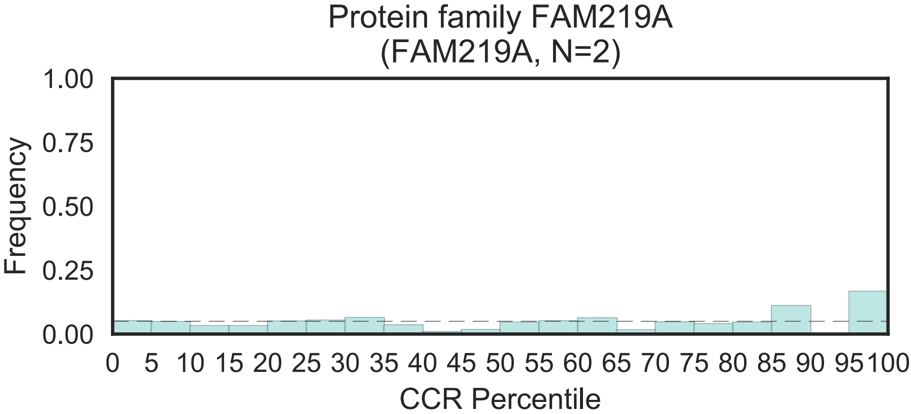

FAM198 protein
(FAM198, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

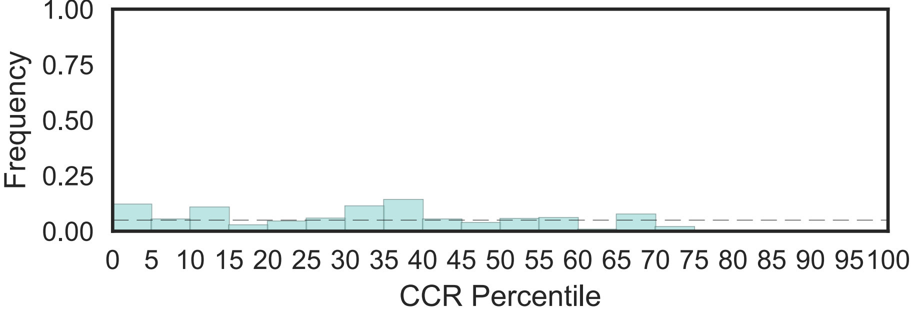

FAM209 family
(FAM209, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

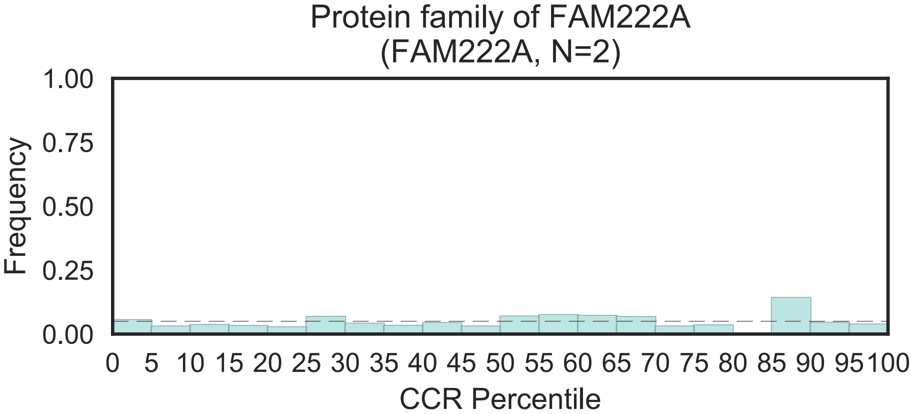

FAM212 family
(FAM212, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

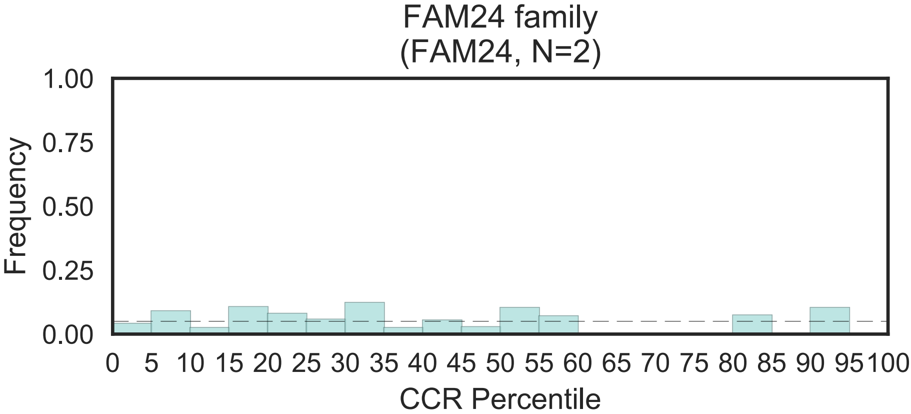

FAM216B protein family
(FAM216B, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

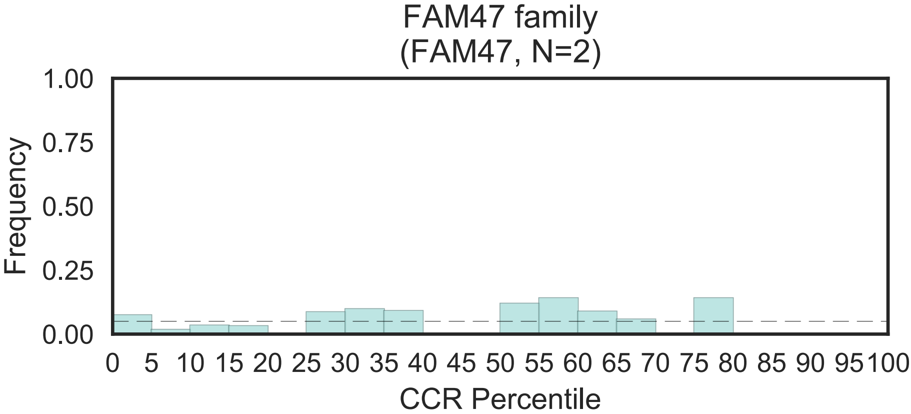

FAM217 family
(FAM217, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

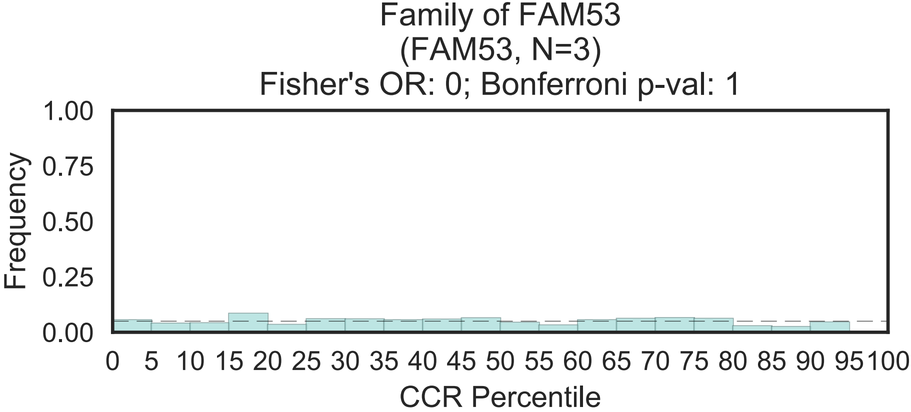

Protein family FAM219A
(FAM219A, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

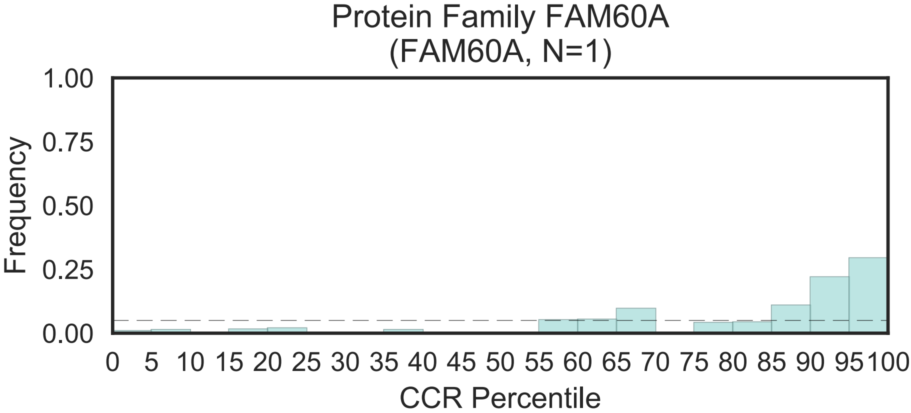

Protein FAM221A/B
(FAM221, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

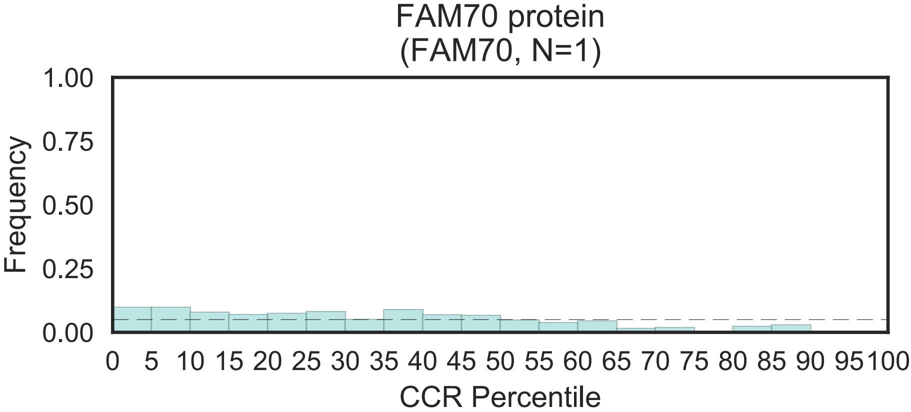

Protein family of FAM222A
(FAM222A, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

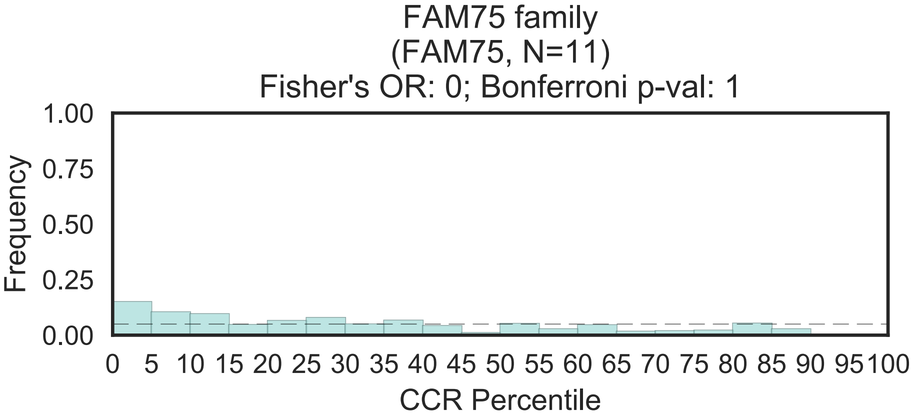

FAM24 family
(FAM24, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

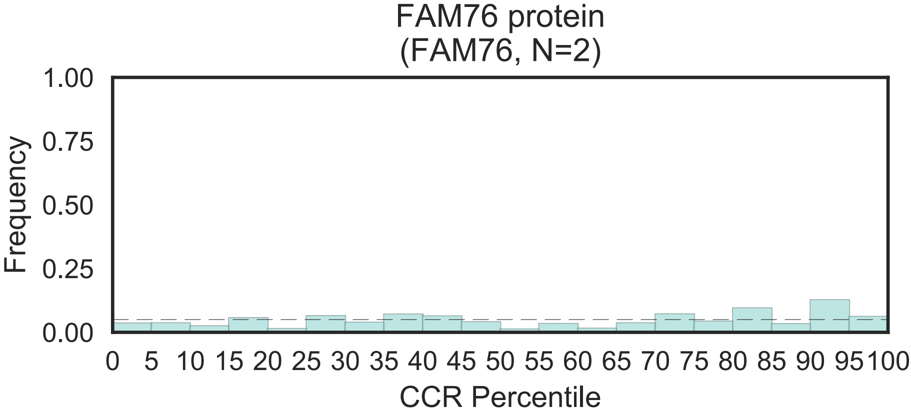

FAM47 family
(FAM47, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

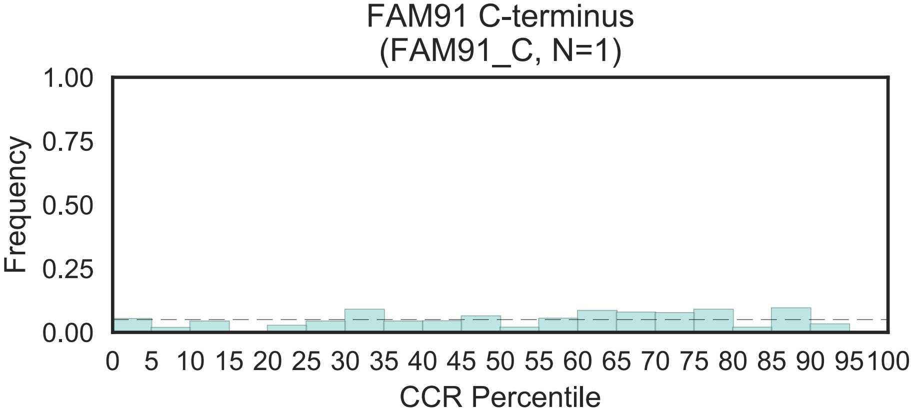

Family of FAM53
(FAM53, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

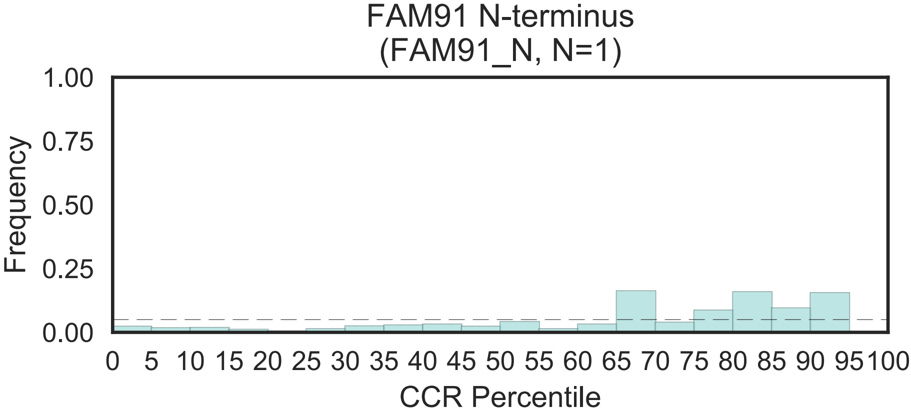

Protein Family FAM60A
(FAM60A, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

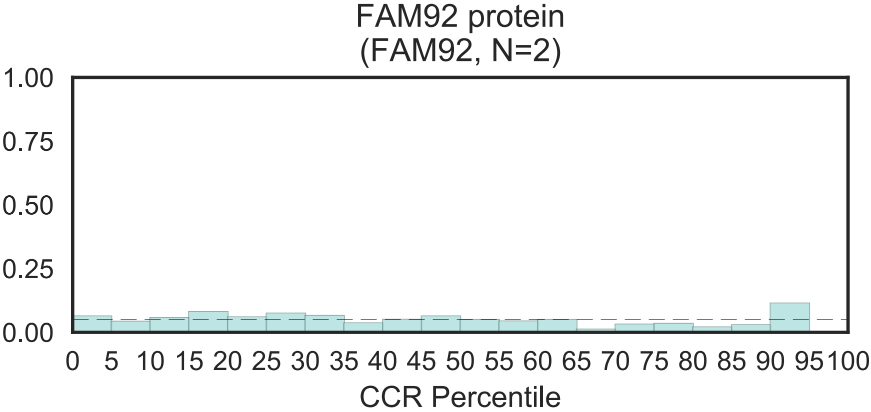

FAM70 protein
(FAM70, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

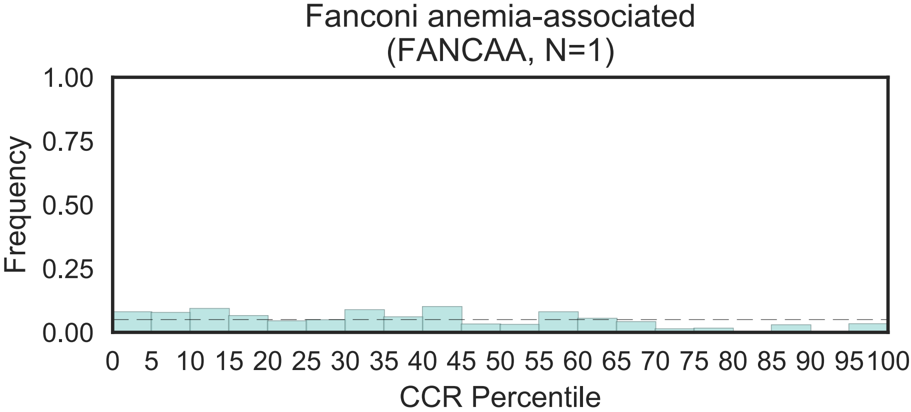

FAM75 family
(FAM75, N=11)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

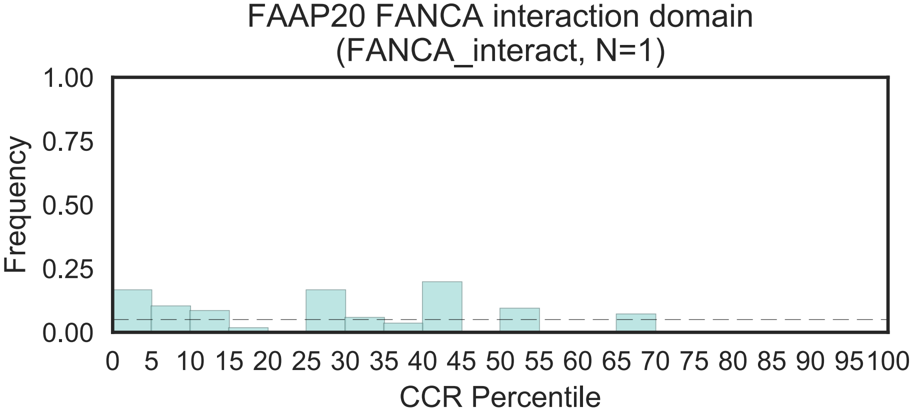

FAM76 protein
(FAM76, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

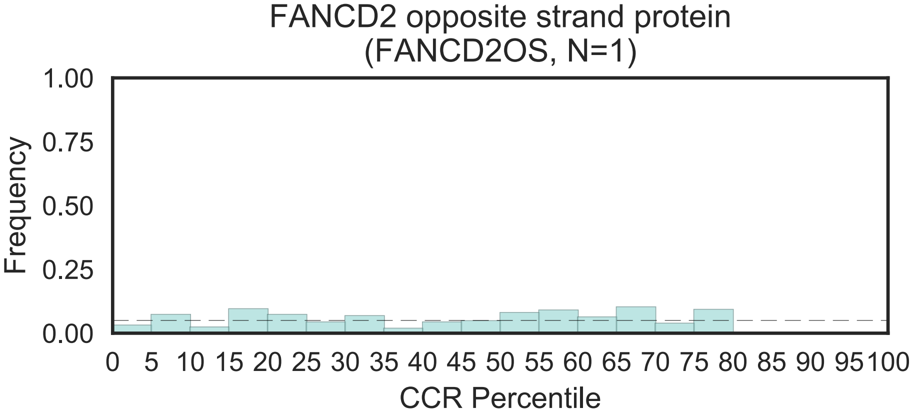

FAM91 C-terminus
(FAM91_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

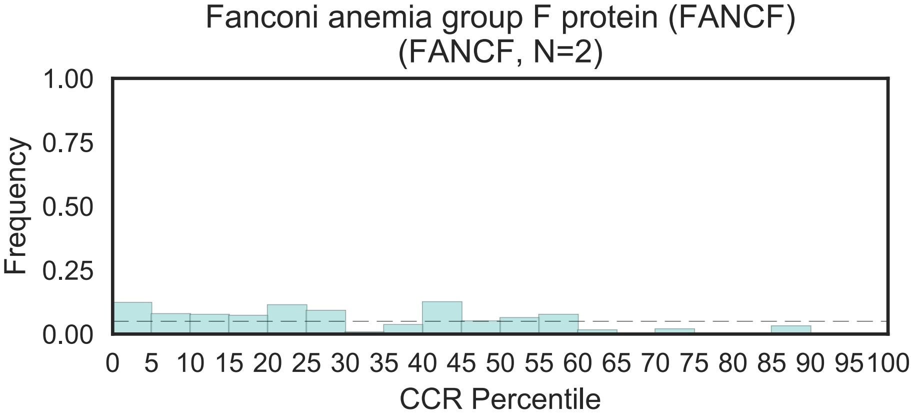

FAM91 N-terminus
(FAM91_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

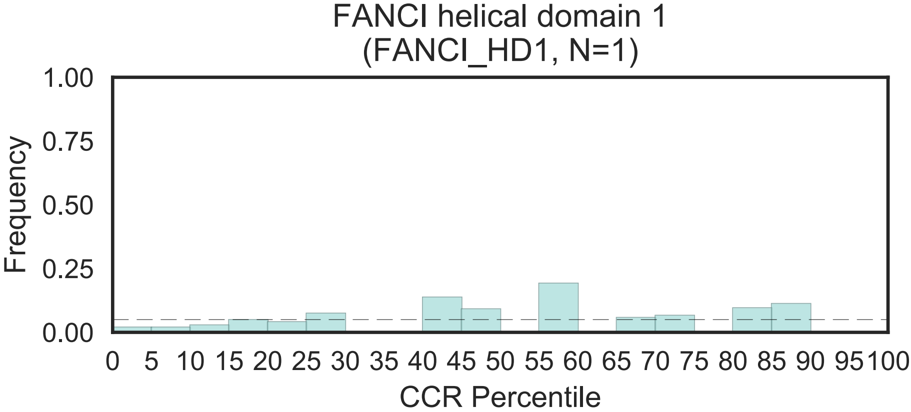

FAM92 protein
(FAM92, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

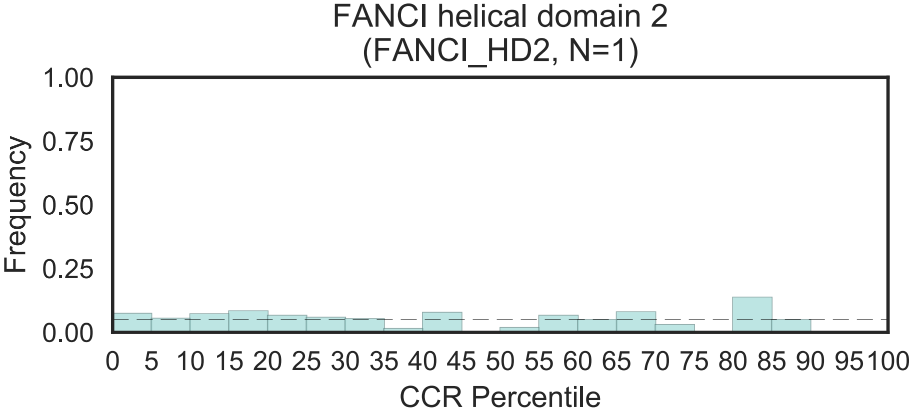

Fanconi anemia-associated
(FANCAA, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

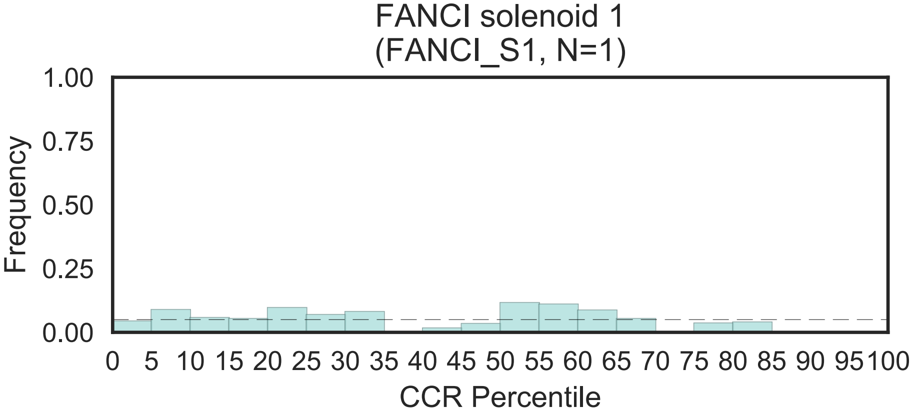

FAAP20 FANCA interaction domain
(FANCA_interact, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

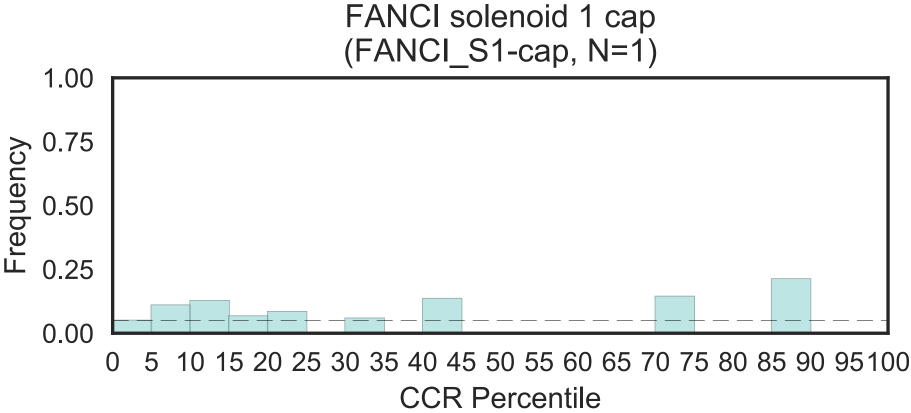

FANCD2 opposite strand protein
(FANCD2OS, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

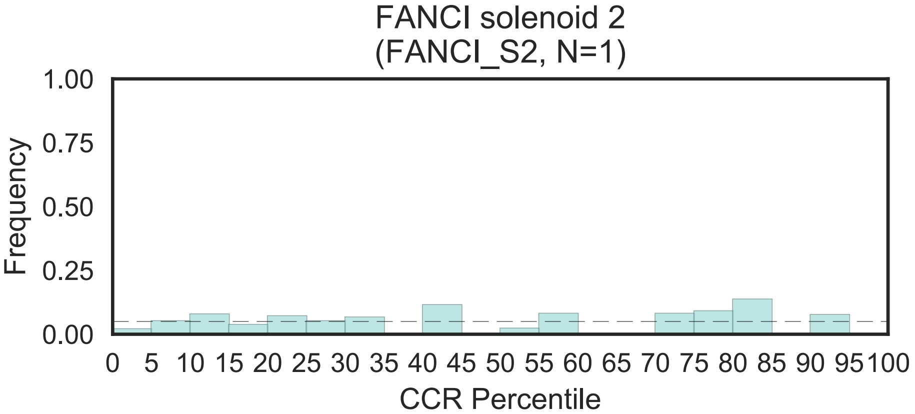

Fanconi anemia group F protein (FANCF)
(FANCF, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

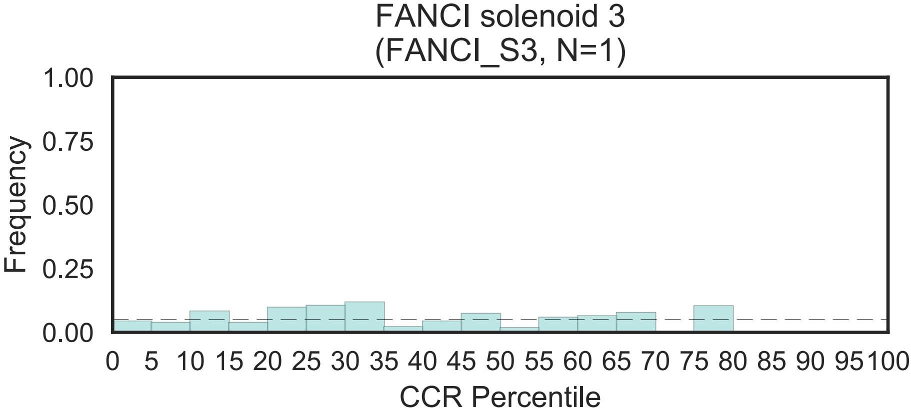

FANCI helical domain 1
(FANCI_HD1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

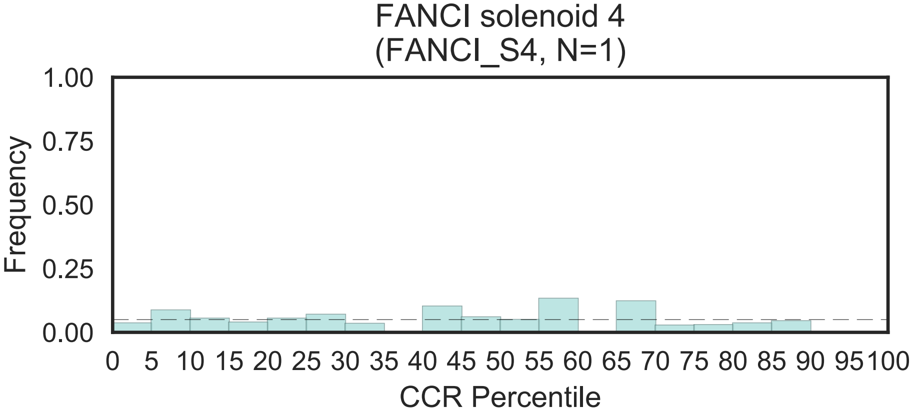

FANCI helical domain 2
(FANCI_HD2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

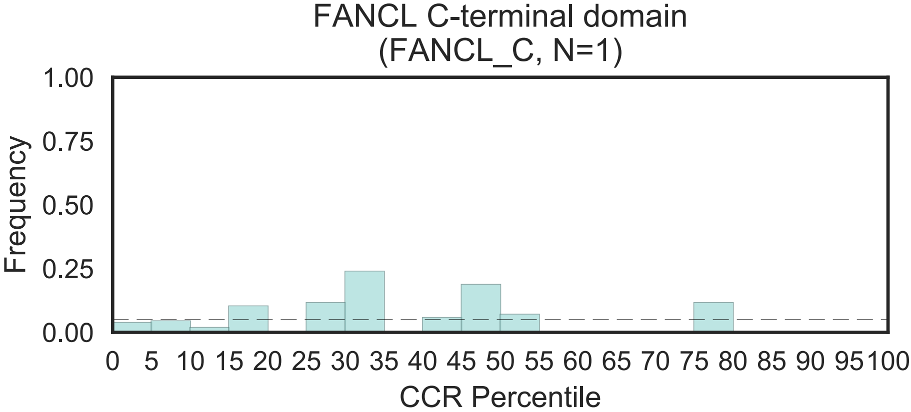

FANCI solenoid 1
(FANCI_S1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


FANCI solenoid 1 cap
(FANCI_S1-cap, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

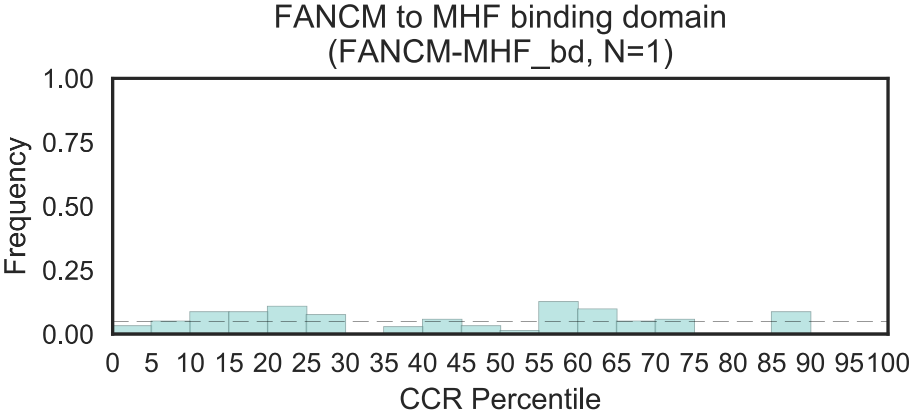

FANCI solenoid 2
(FANCI_S2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

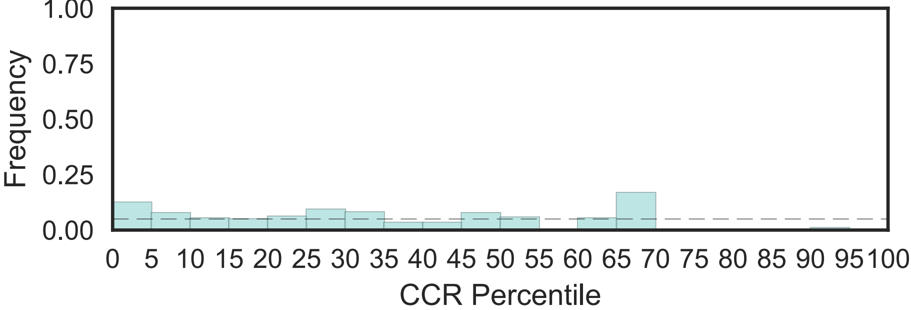

FANCI solenoid 3
(FANCI_S3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


FANCI solenoid 4
(FANCI_S4, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

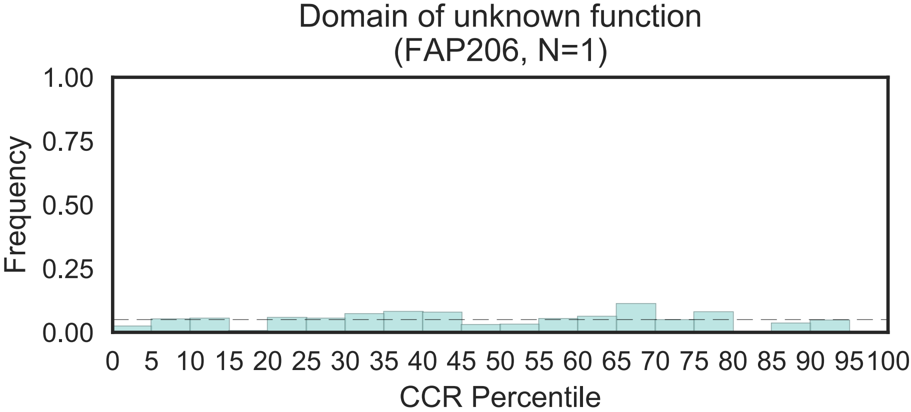


FANCL C-terminal domain
(FANCL_C, N=1)

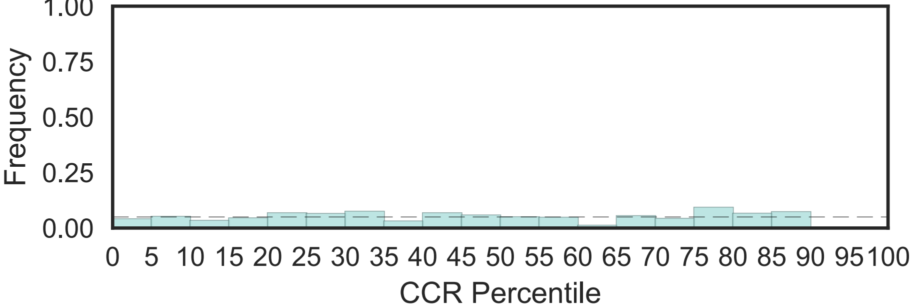

FANCM to MHF binding domain
(FANCM-MHF_bd, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

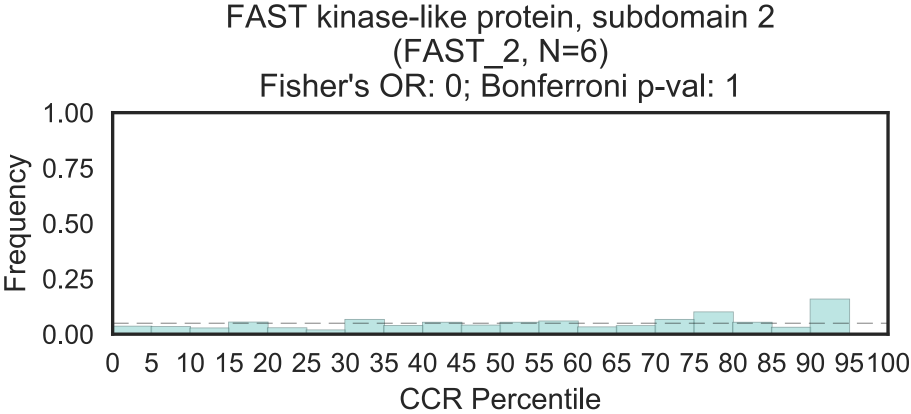


FAD dependent oxidoreductase central domain
(FAO_M, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

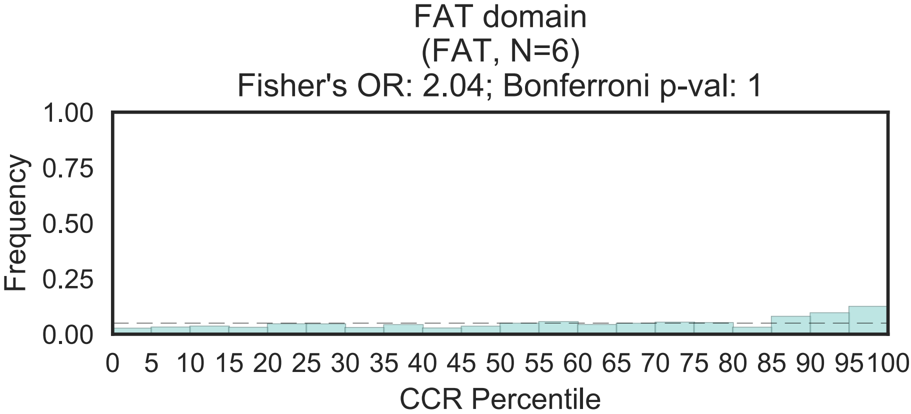

Domain of unknown function
(FAP206, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

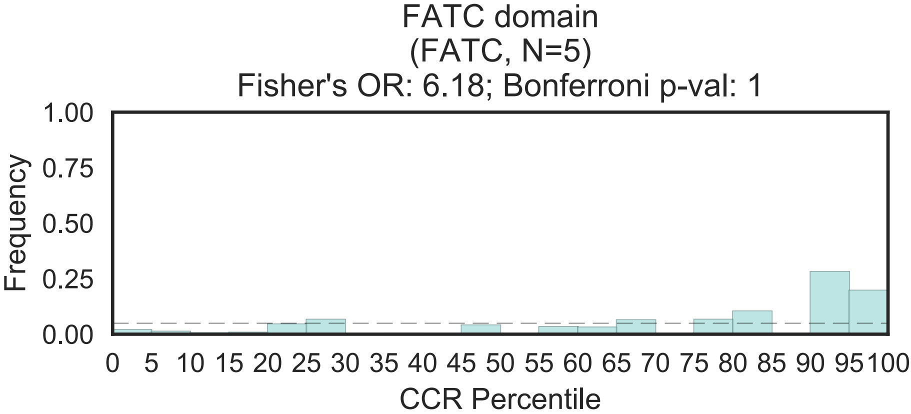
FAST kinase-like protein, subdomain 1
(FAST_1, N=6)
Fisher's OR: 0.676; Bonferroni p-val: 1

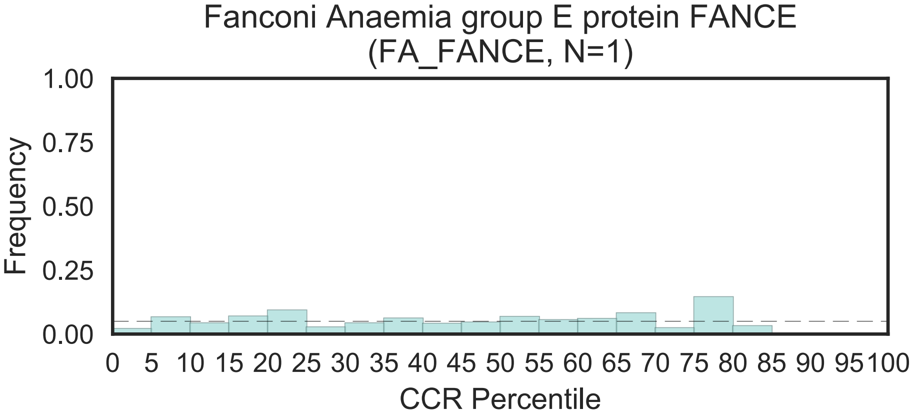


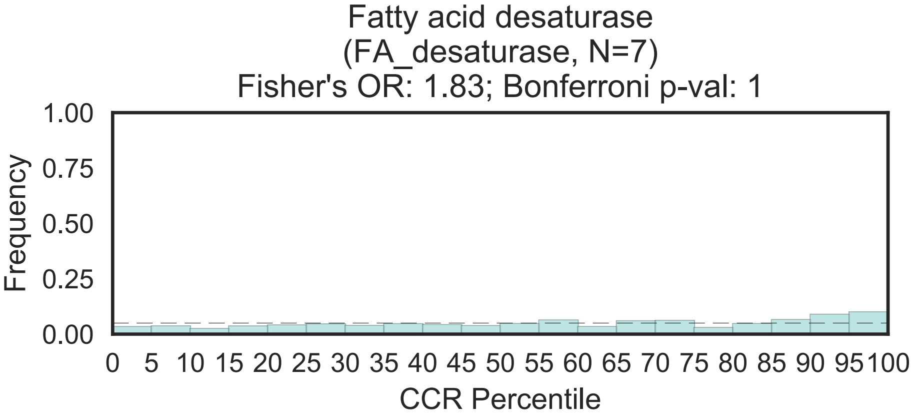


FAST kinase-like protein, subdomain 2
(FAST_2, N=6)
Fisher's OR: 0; Bonferroni p-val: 1

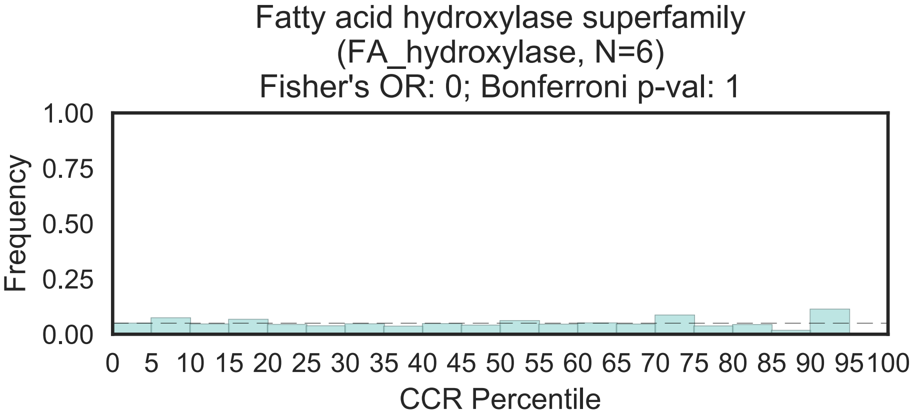

FAT domain
(FAT, N=6)
Fisher's OR: 2.04; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

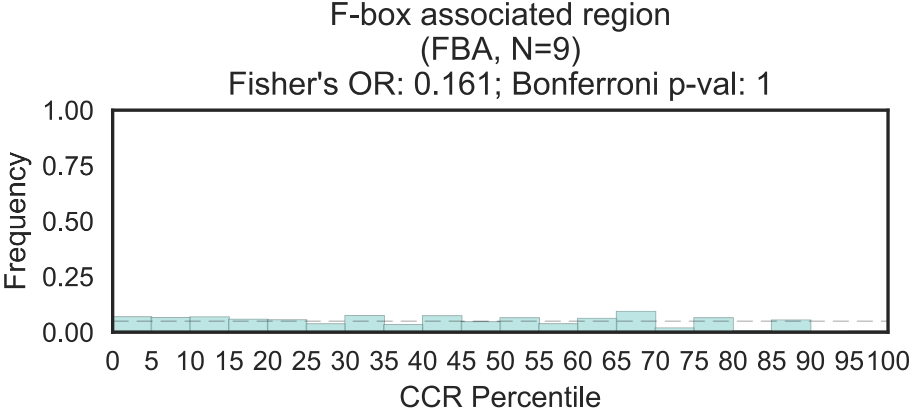

FATC domain
(FATC, N=5)
Fisher's OR: 6.18; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

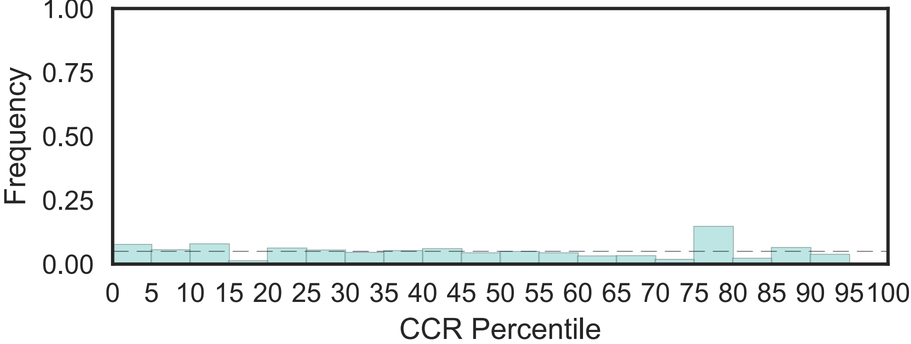

Fanconi Anaemia group E protein FANCE
(FA_FANCE, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

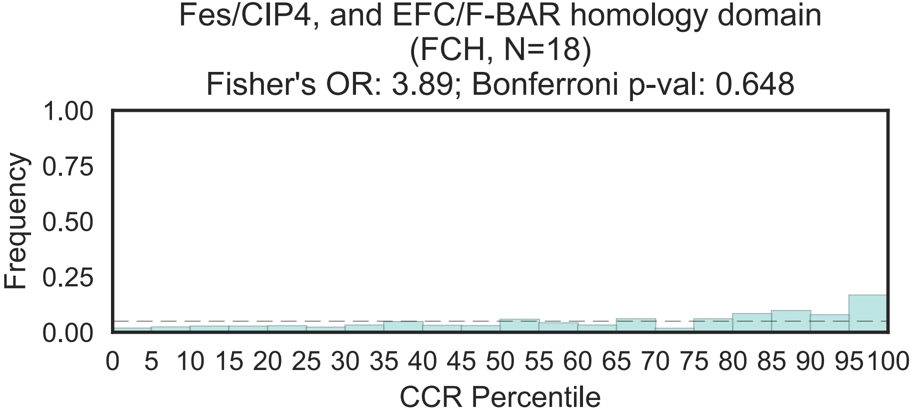


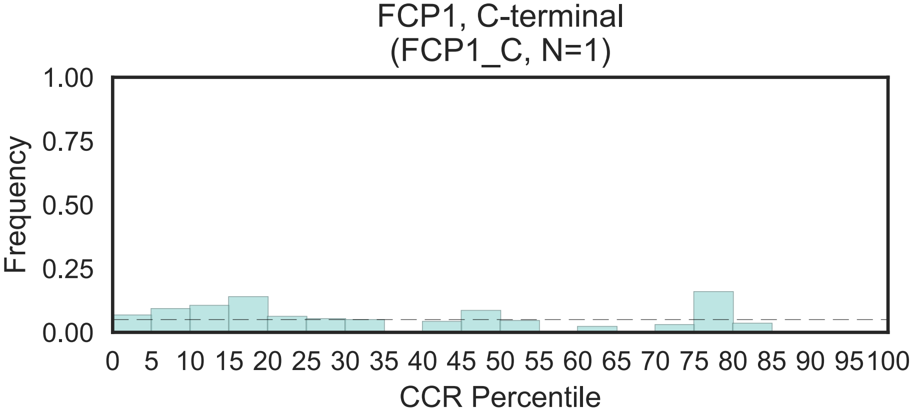
Fatty acid desaturase
(FA_desaturase, N=7)
Fisher's OR: 1.83; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

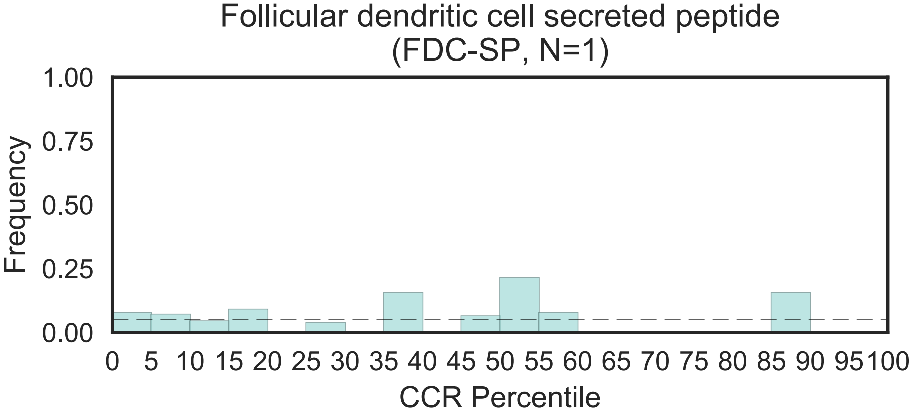

Fatty acid hydroxylase superfamily
(FA_hydroxylase, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

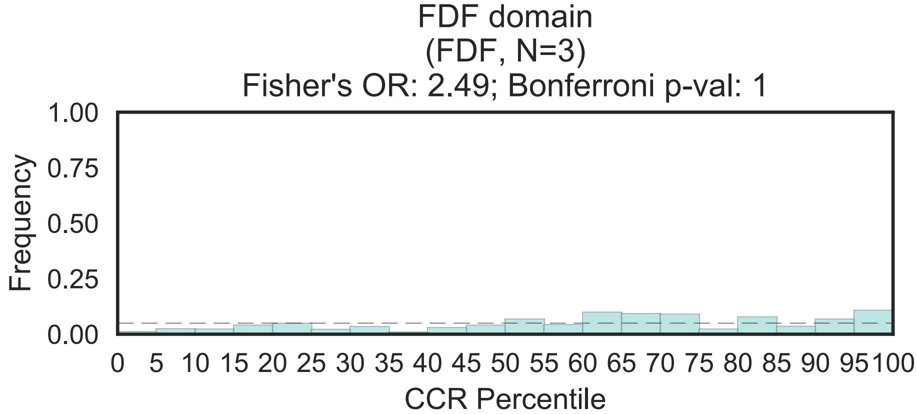

F-box associated region
(FBA, N=9)
Fisher's OR: 0.161; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

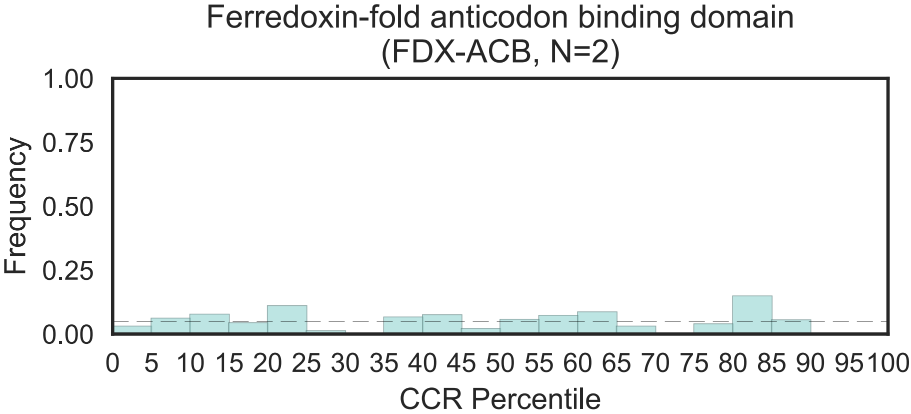

Fructose-1-6-bisphosphatase, N-terminal domain (FBPase, N=2)


Fes/CIP4, and EFC/F-BAR homology domain
(FCH, N=18)
Fisher's OR: 3.89; Bonferroni p-val: 0.648
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


FCP1, C-terminal
(FCP1_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

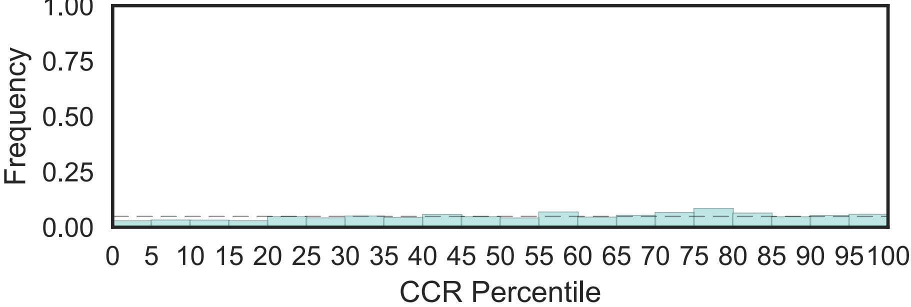

Follicular dendritic cell secreted peptide
(FDC-SP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

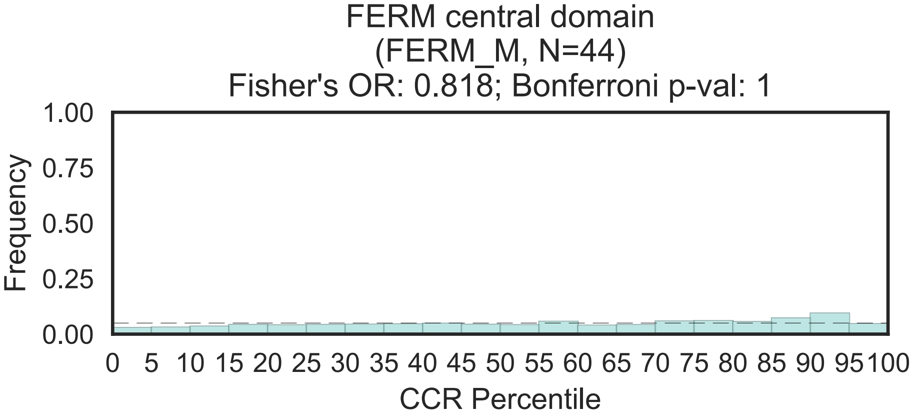

FDF domain
(FDF, N=3)
Fisher's OR: 2.49; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ferredoxin-fold anticodon binding domain
(FDX-ACB, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

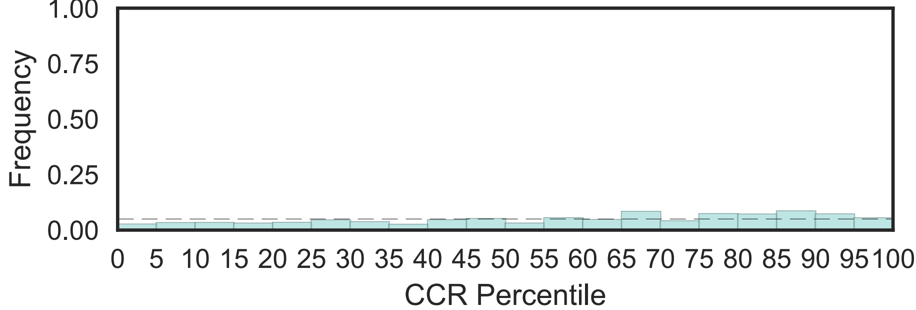
FERM C-terminal PH-like domain (FERM_C, N=25)

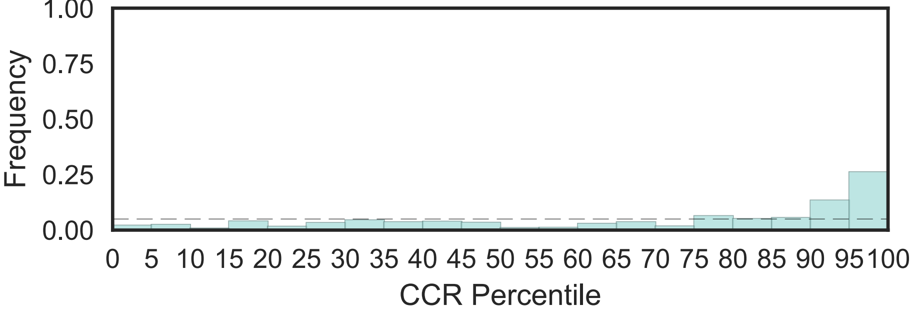
Fisher's OR: 0.92; Bonferroni p-val: 1

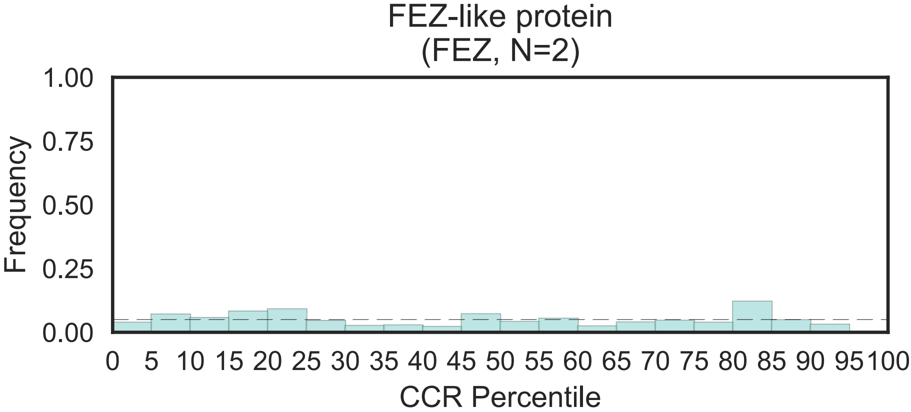


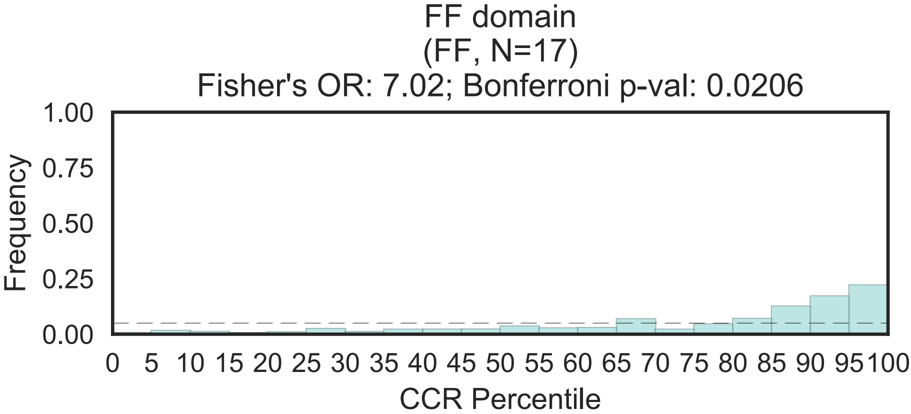

FERM central domain
(FERM_M, N=44)
Fisher's OR: 0.818; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

FERM N-terminal domain
(FERM_N, N=27)
Fisher's OR: 1.32; Bonferroni p-val: 1

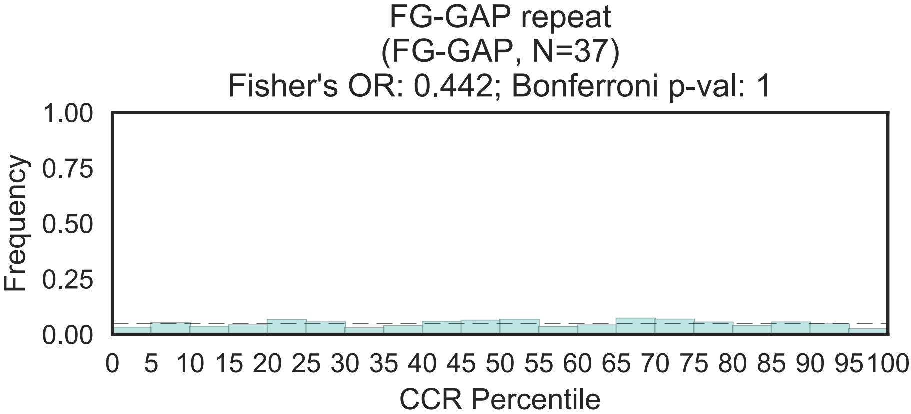


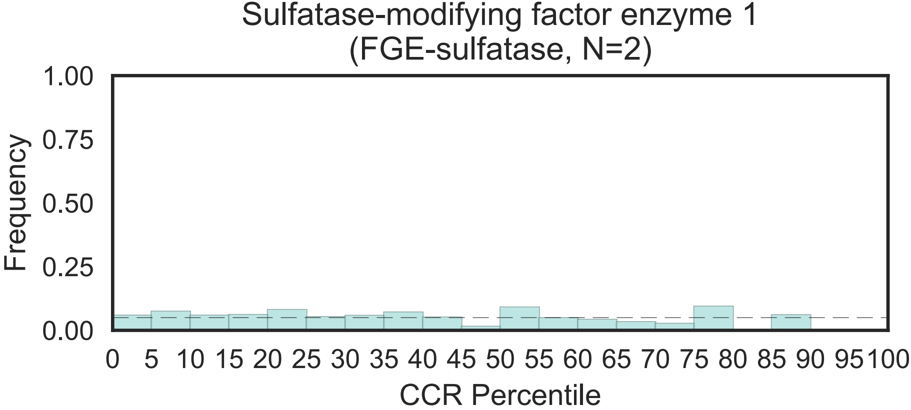

N-terminal or F0 domain of Talin-head FERM
(FERM_f0, N=5)
Fisher's OR: 5.92; Bonferroni p-val: 1

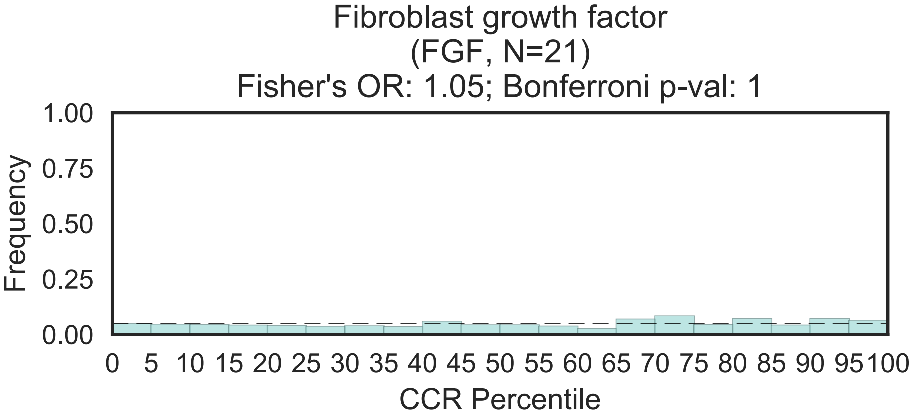

FEZ-like protein
(FEZ, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

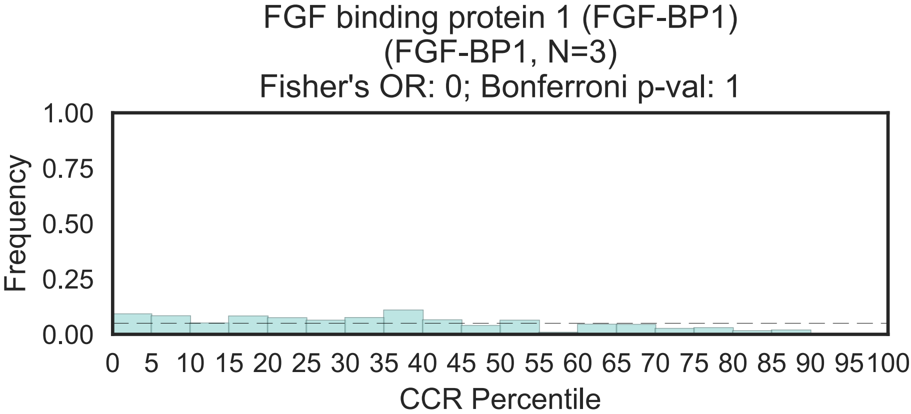


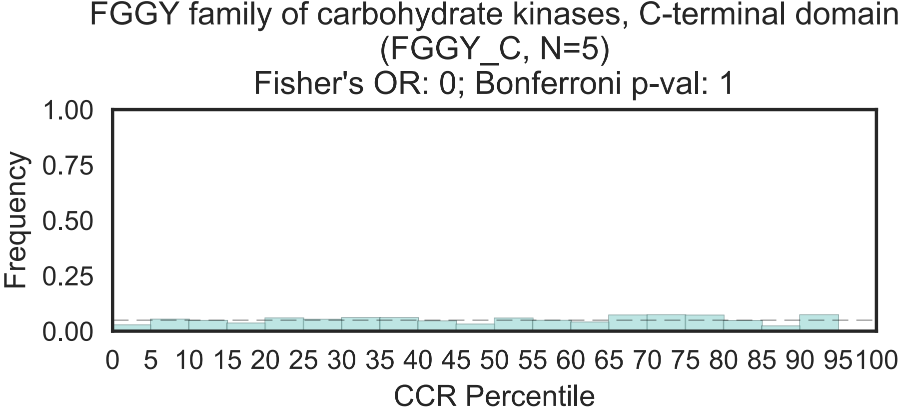
FF domain
(FF, N=17)
Fisher's OR: 7.02; Bonferroni p-val: 0.0206

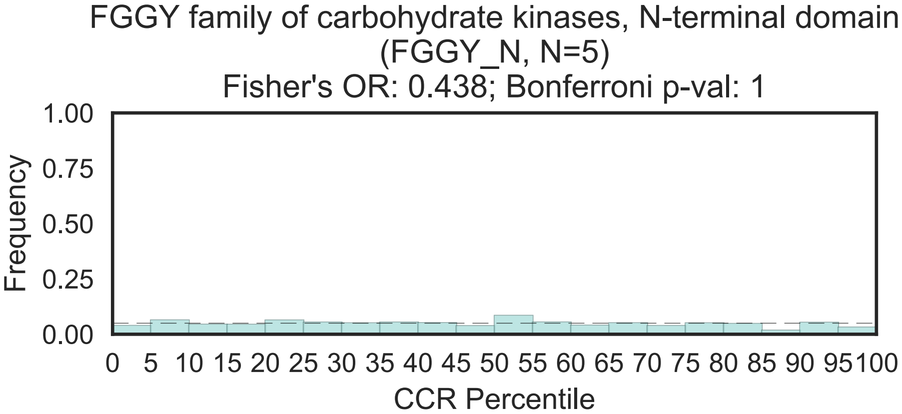

FG-GAP repeat
(FG-GAP, N=37)
Fisher's OR: 0.442; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

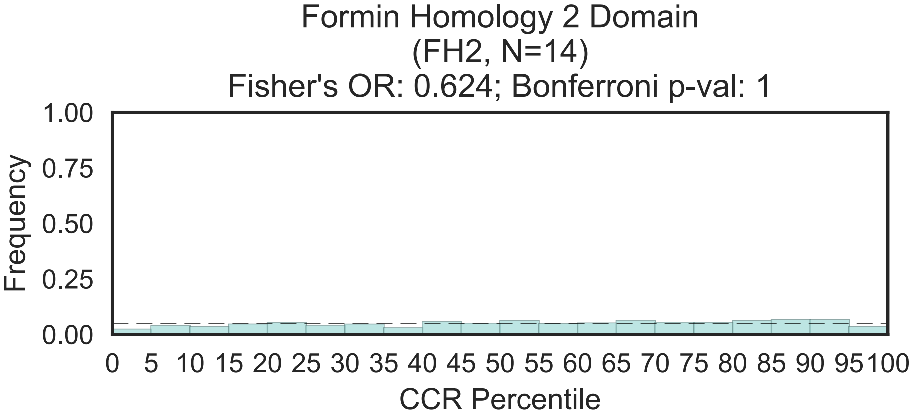

Sulfatase-modifying factor enzyme 1
(FGE-sulfatase, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

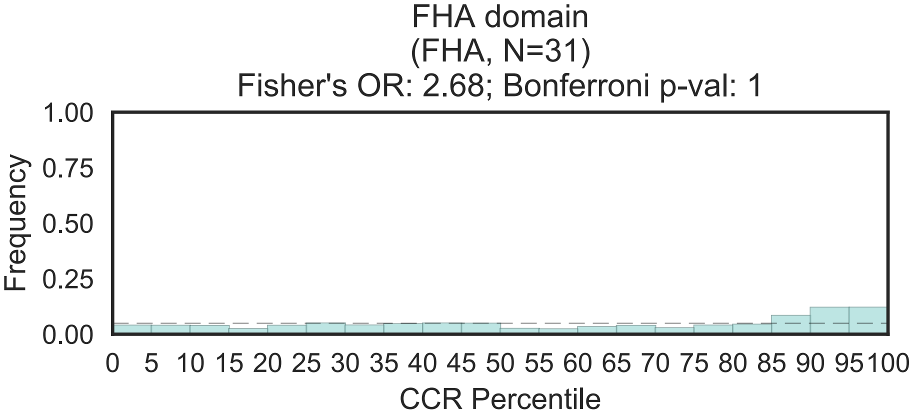

Fibroblast growth factor
(FGF, N=21)
Fisher's OR: 1.05; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

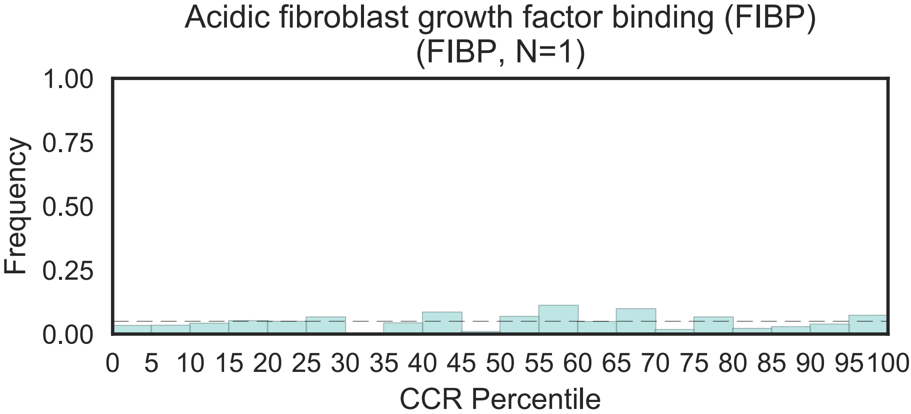

FGF binding protein 1 (FGF-BP1)
(FGF-BP1, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

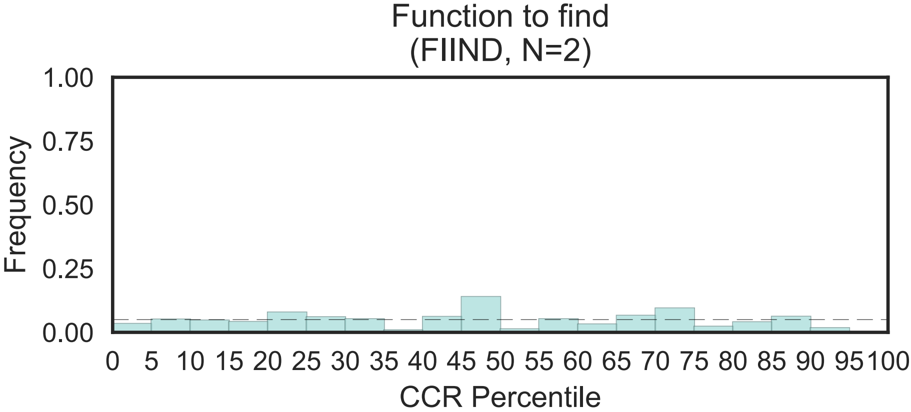

FGGY family of carbohydrate kinases, C-terminal domain
(FGGY_C, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

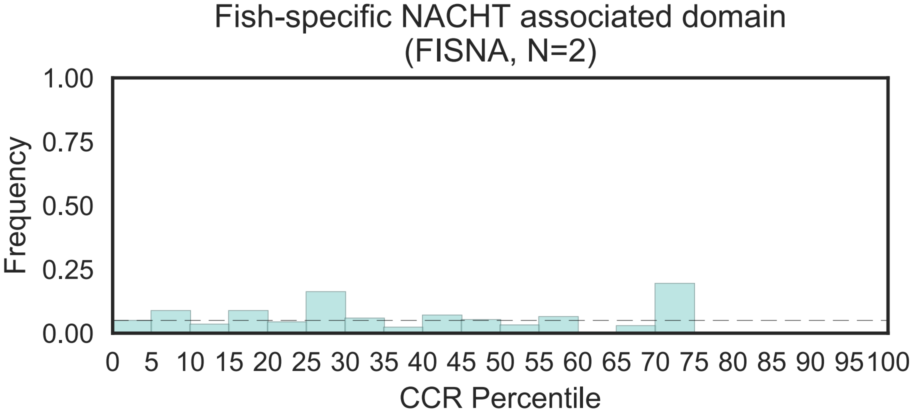

FGGY family of carbohydrate kinases, N-terminal domain
(FGGY_N, N=5)
Fisher's OR: 0.438; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

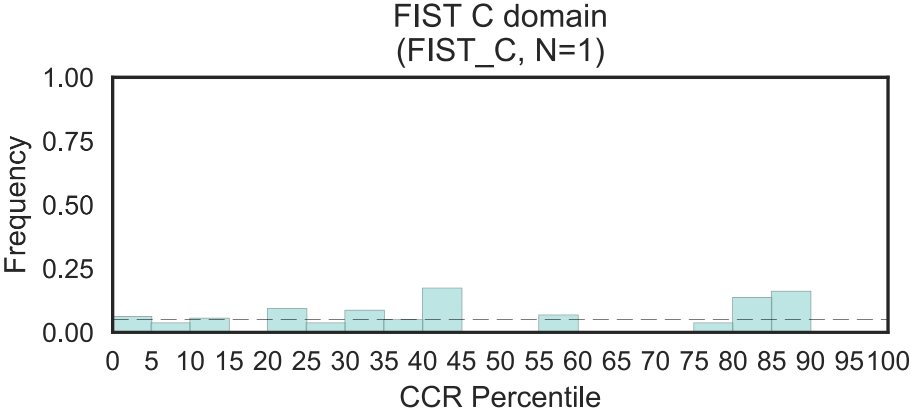

Formin Homology 2 Domain
(FH2, N=14)
Fisher's OR: 0.624; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

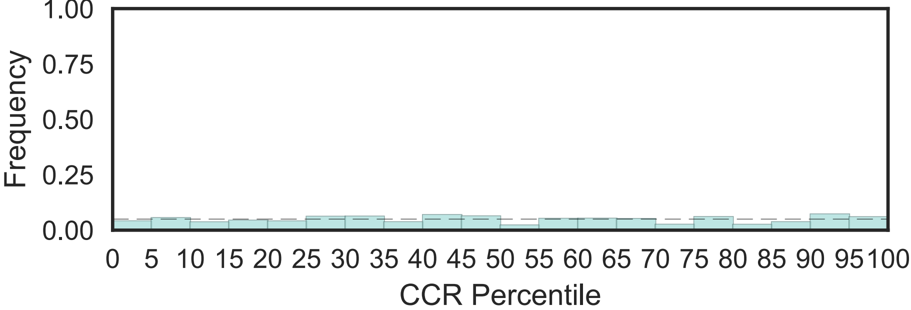

FHA domain
(FHA, N=31)
Fisher's OR: 2.68; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

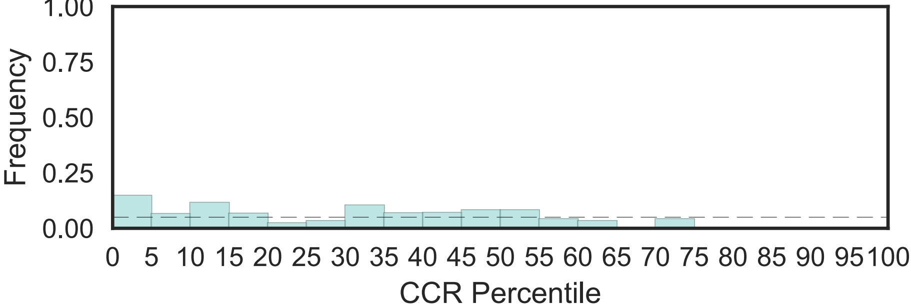

Acidic fibroblast growth factor binding (FIBP)
(FIBP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

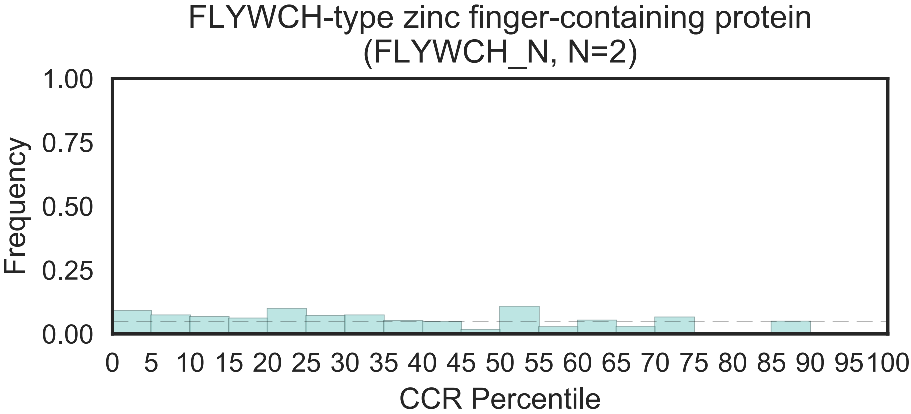

Function to find
(FIIND, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

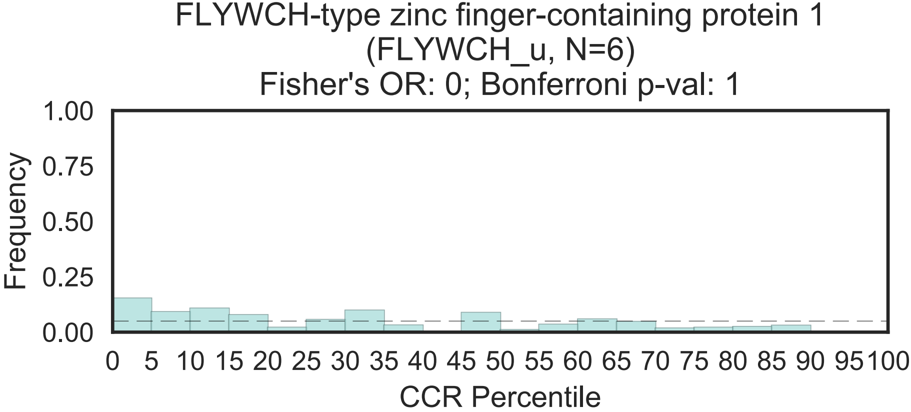

Fish-specific NACHT associated domain
(FISNA, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

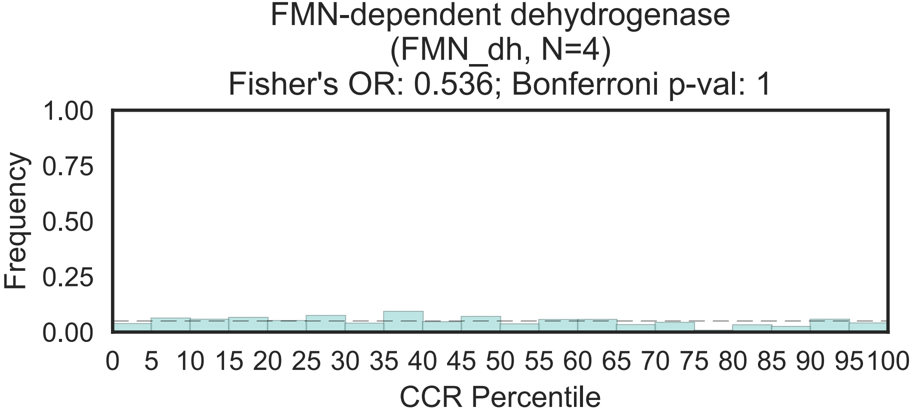

FIST C domain
(FIST_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

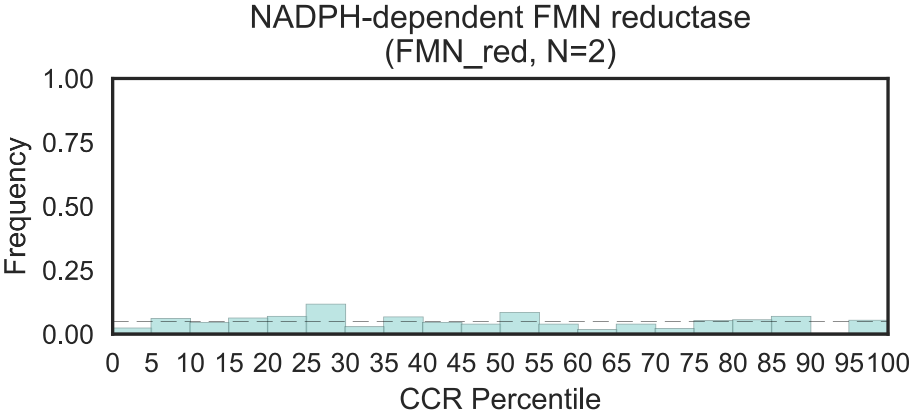

FKBP-type peptidyl-prolyl cis-trans isomerase
(FKBP_C, N=25)
Fisher's OR: 0.995; Bonferroni p-val: 1

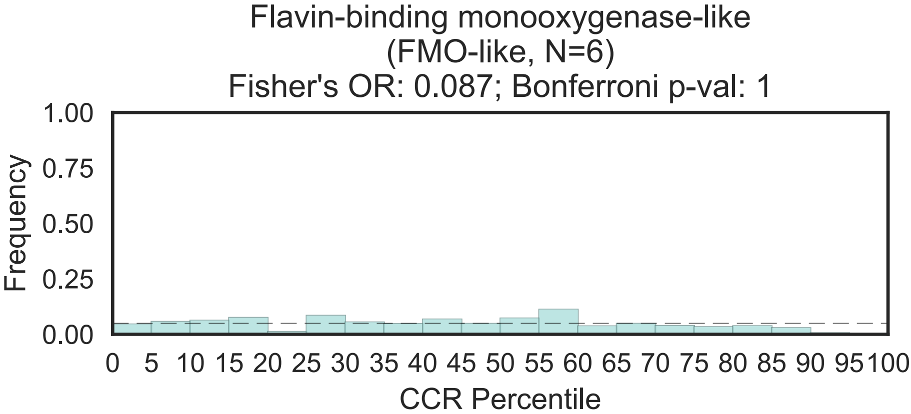

FLYWCH zinc finger domain
(FLYWCH, N=5)
Fisher's OR: 0; Bonferroni p-val: 1

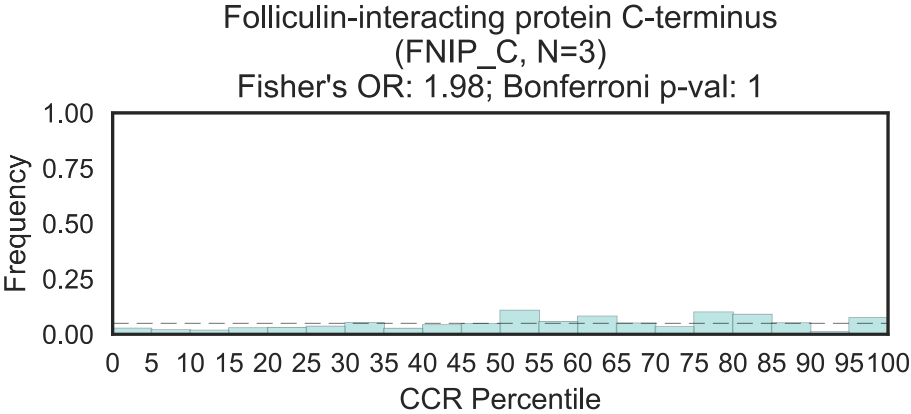

FLYWCH-type zinc finger-containing protein
(FLYWCH_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

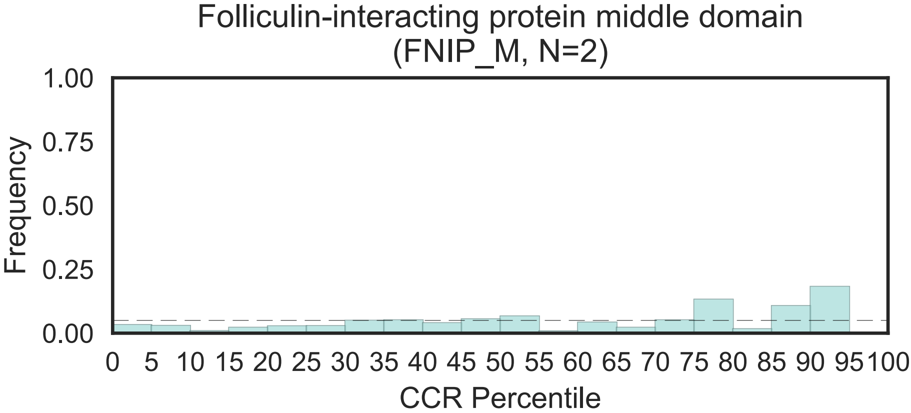

FLYWCH-type zinc finger-containing protein 1
(FLYWCH_u, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


FMN-dependent dehydrogenase
(FMN_dh, N=4)
Fisher's OR: 0.536; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

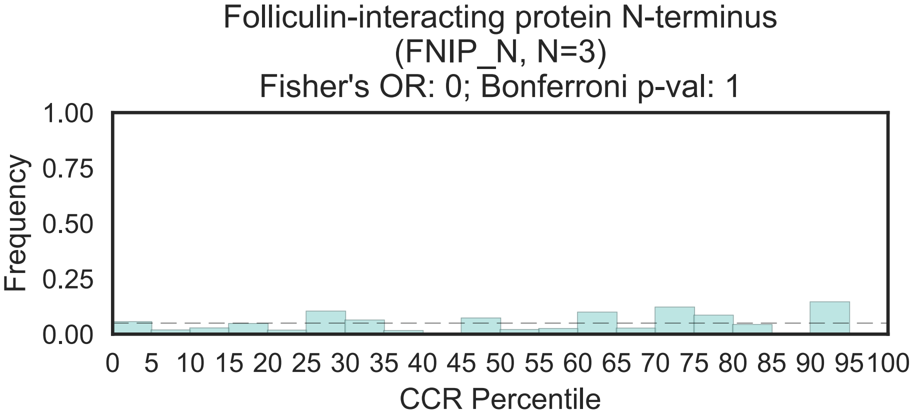

NADPH-dependent FMN reductase
(FMN_red, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Flavin-binding monooxygenase-like
(FMO-like, N=6)
Fisher's OR: 0.087; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

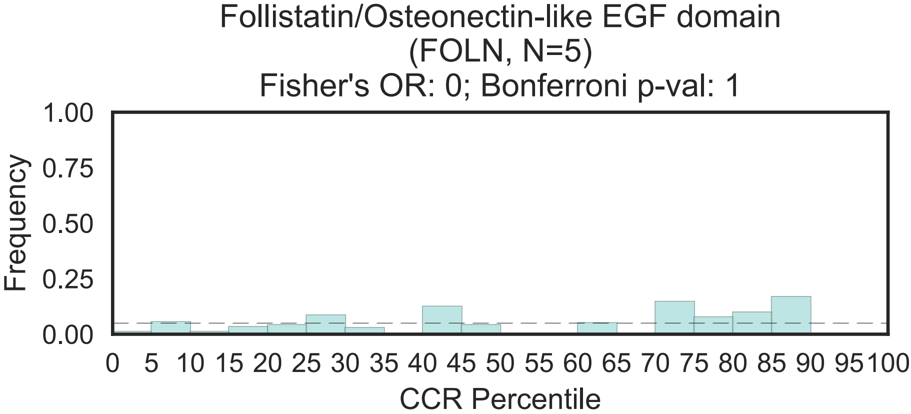

Folliculin-interacting protein C-terminus
(FNIP_C, N=3)
Fisher's OR: 1.98; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

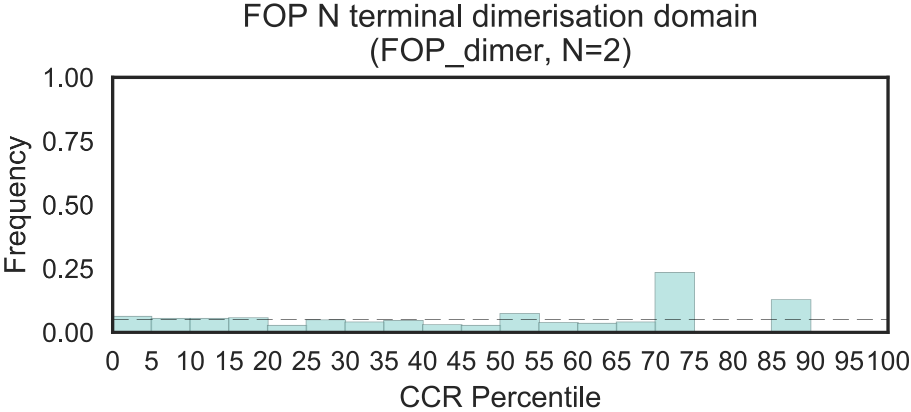


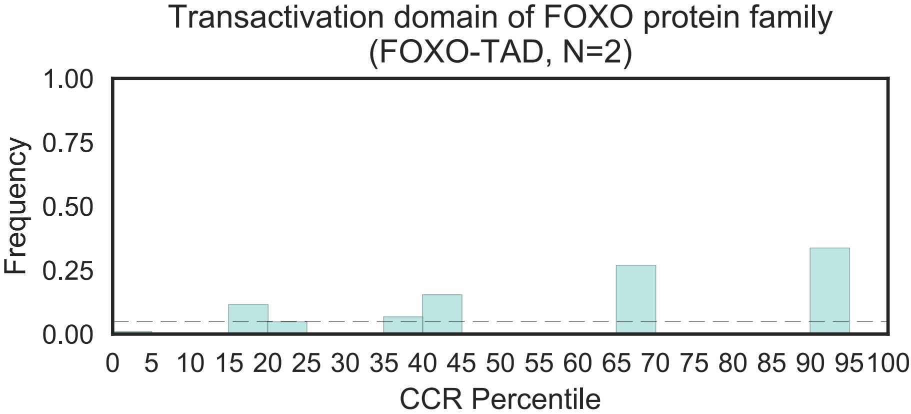
Folliculin-interacting protein middle domain
(FNIP_M, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

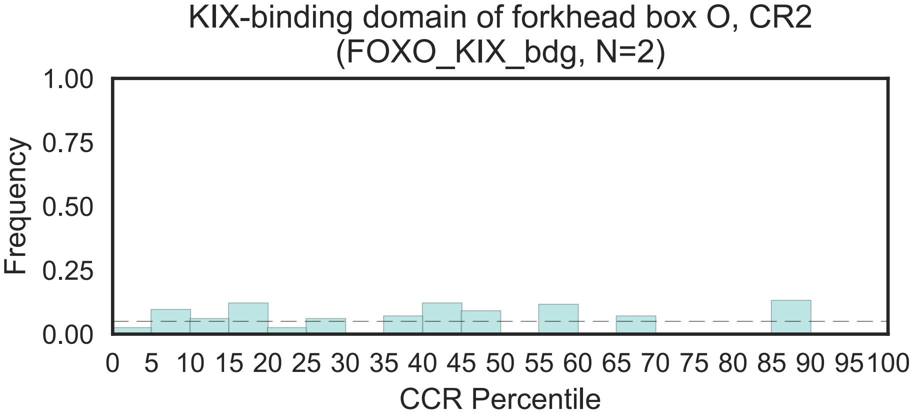


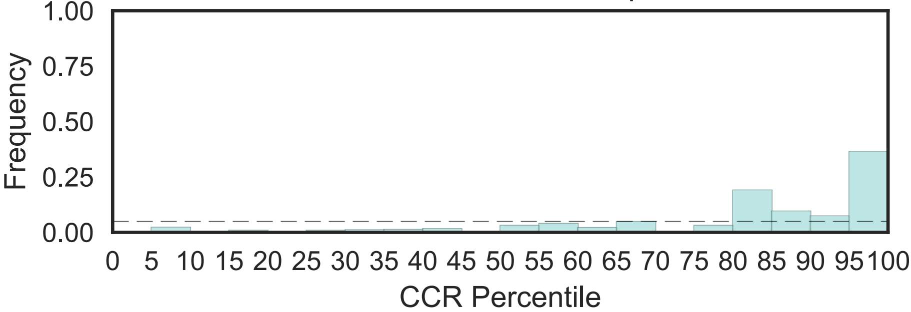
Folliculin-interacting protein N-terminus
(FNIP_N, N=3)
Fisher's OR: 0; Bonferroni p-val: 1


Follistatin/Osteonectin-like EGF domain
(FOLN, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

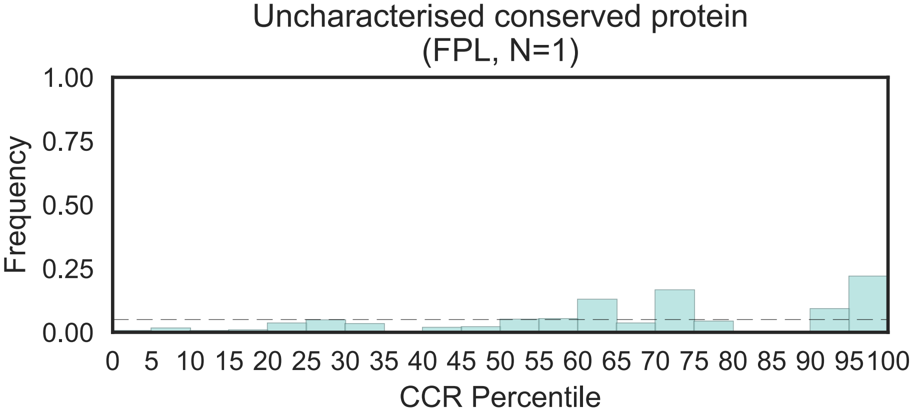

FOP N terminal dimerisation domain
(FOP_dimer, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

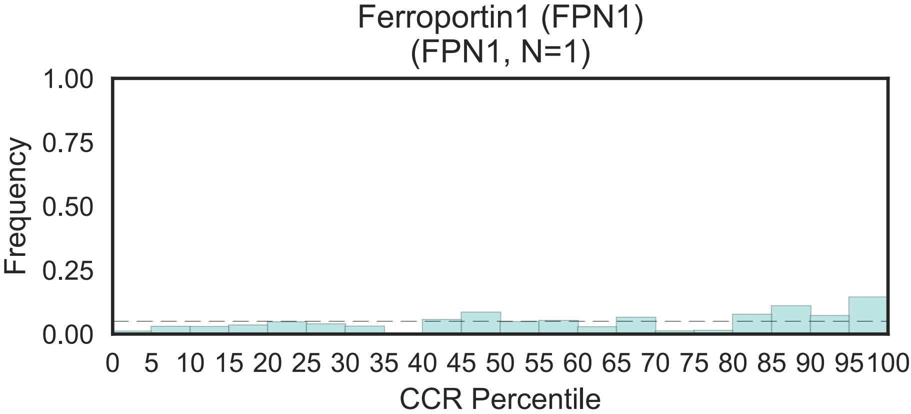

Transactivation domain of FOXO protein family
(FOXO-TAD, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

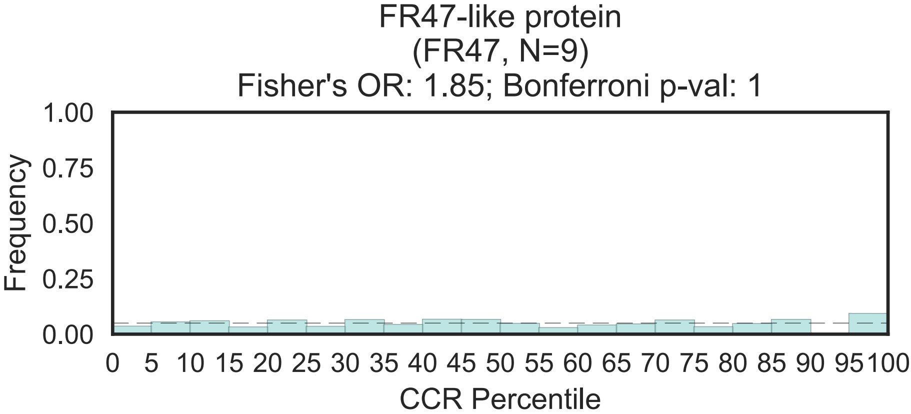

KIX-binding domain of forkhead box O, CR2
(FOXO_KIX_bdg, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



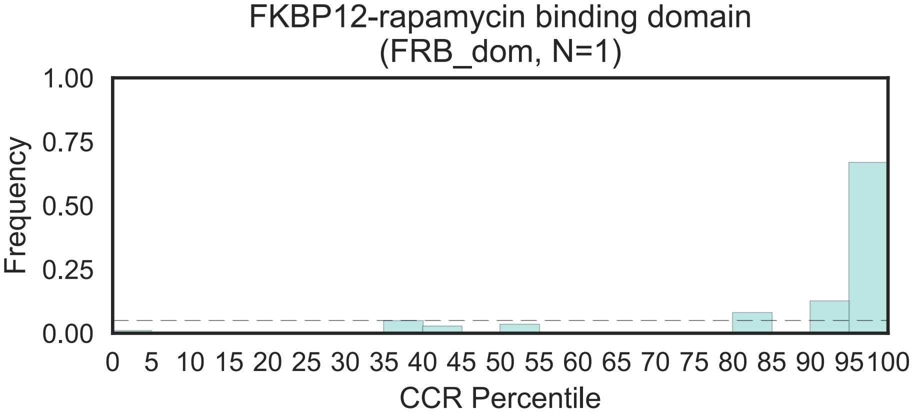
FOXP coiled-coil domain
(FOXP-CC, N=3)
Fisher's OR: 17.4; Bonferroni p-val: 0.117

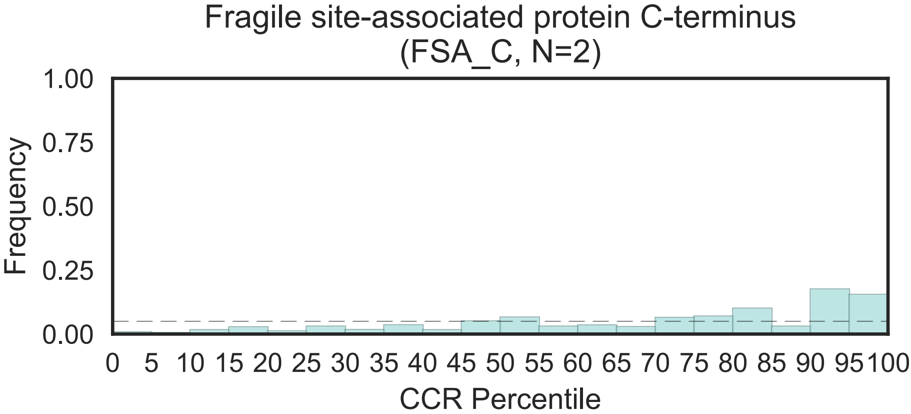

Uncharacterised conserved protein
(FPL, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

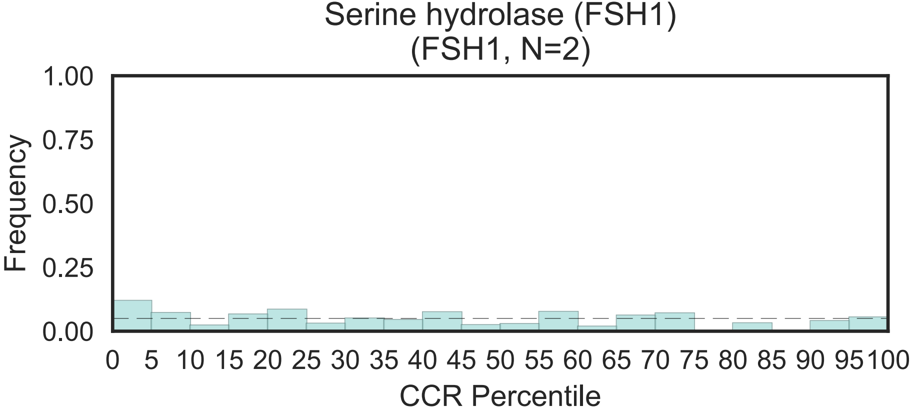

Ferroportin1 (FPN1)
(FPN1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

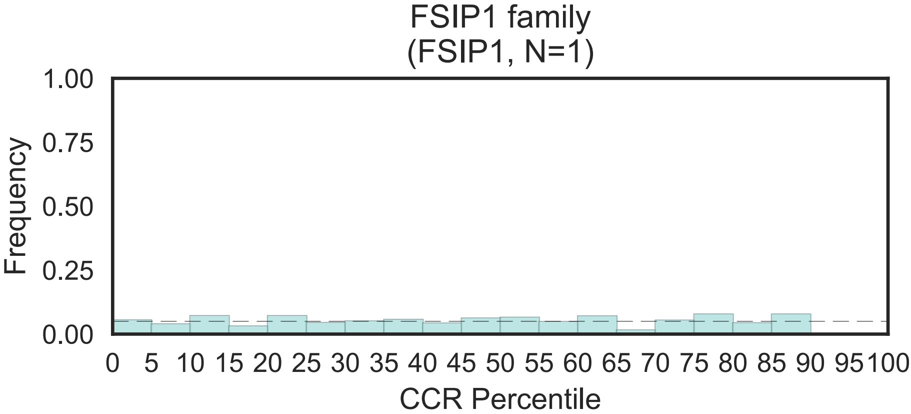


FR47-like protein
(FR47, N=9)
Fisher's OR: 1.85; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

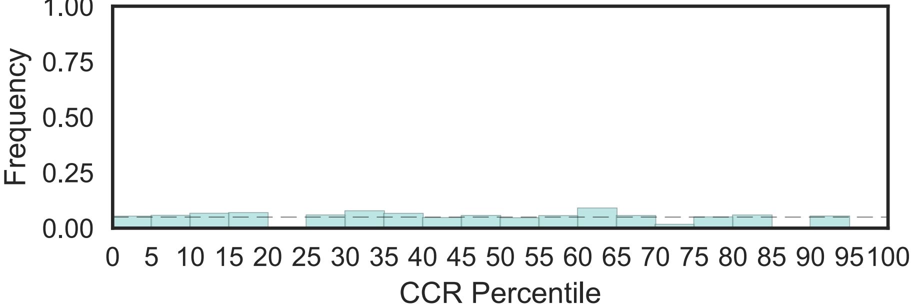

FKBP12-rapamycin binding domain
(FRB_dom, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

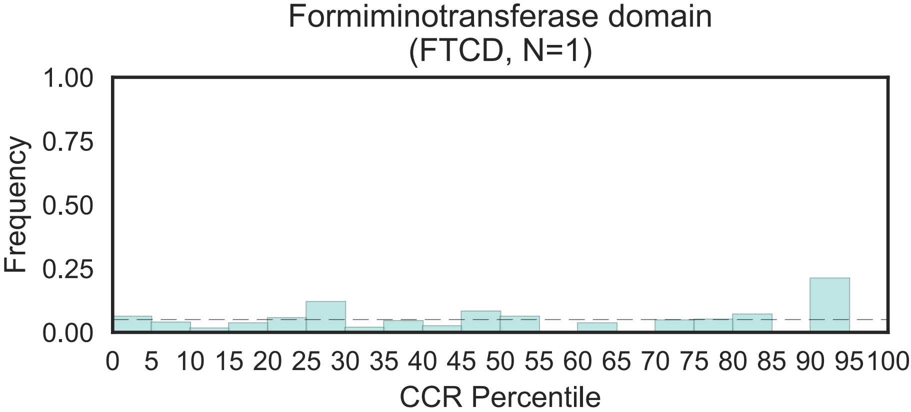

Fragile site-associated protein C-terminus
(FSA_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

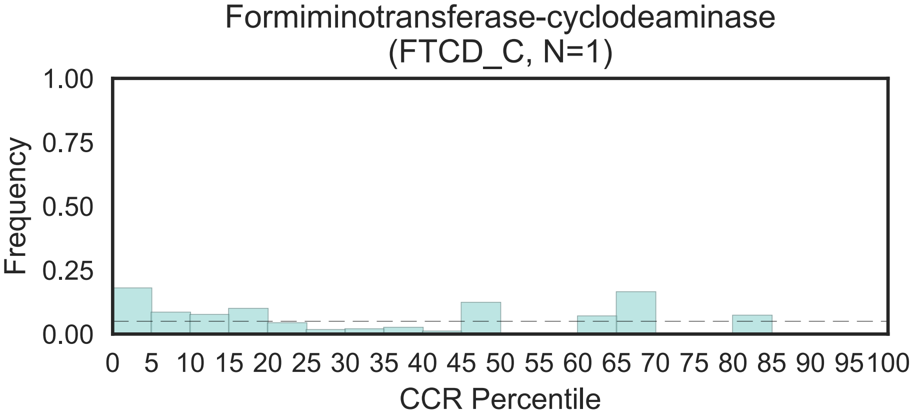

Serine hydrolase (FSH1)
(FSH1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

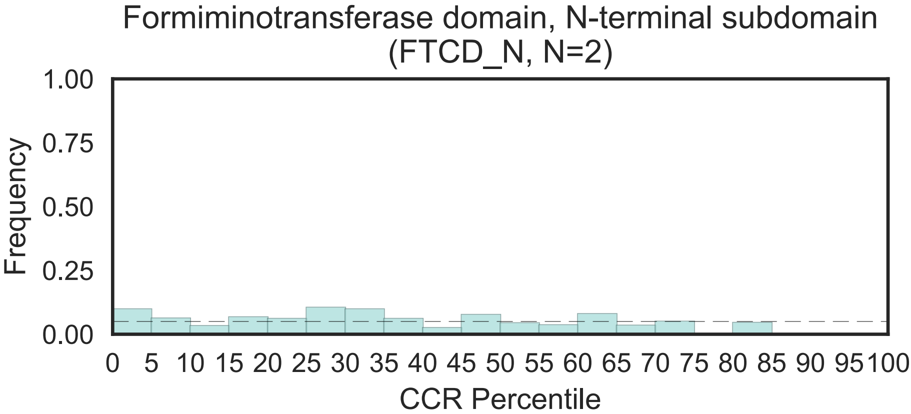

FSIP1 family
(FSIP1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

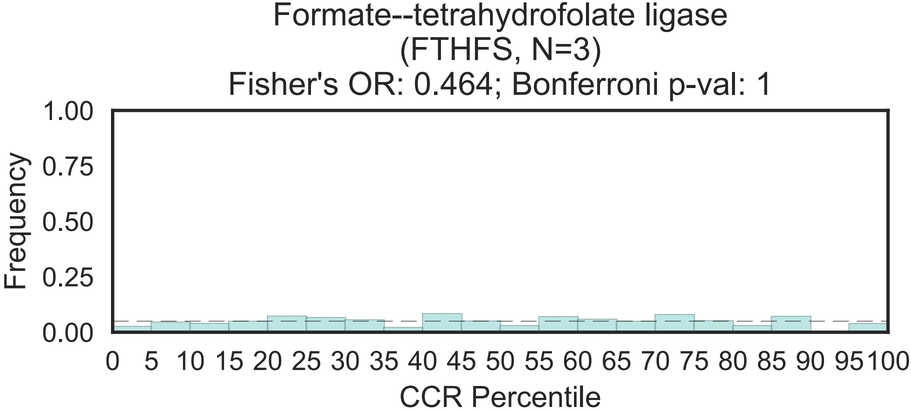
Fibrous sheath-interacting protein 2
(FSIP2, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

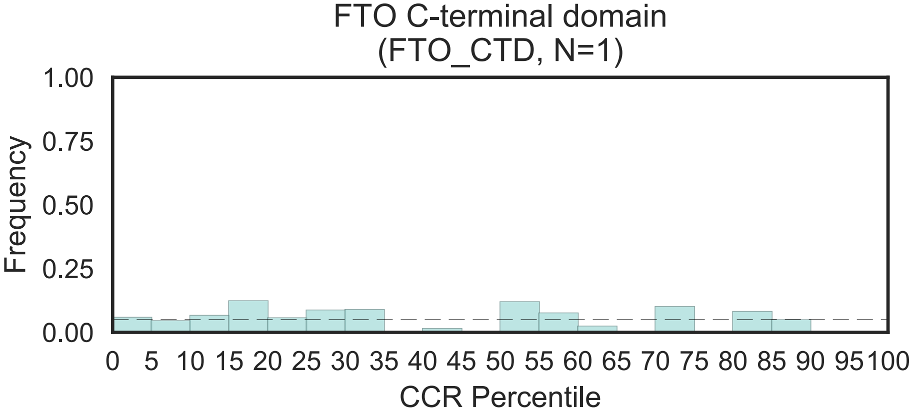


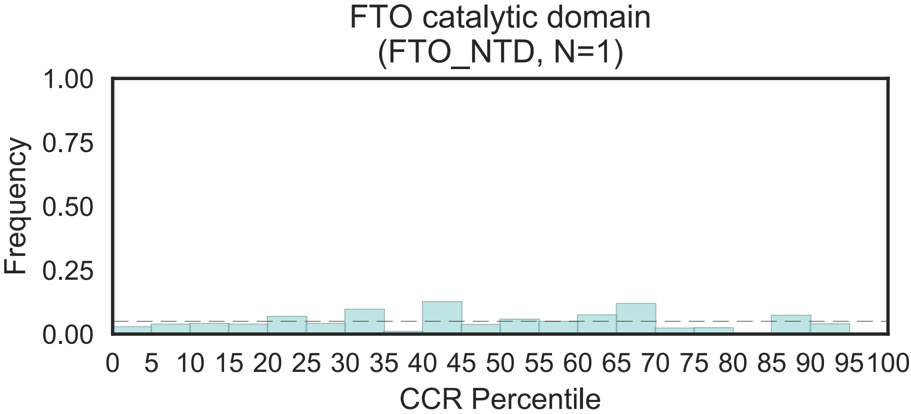

Formiminotransferase domain
(FTCD, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

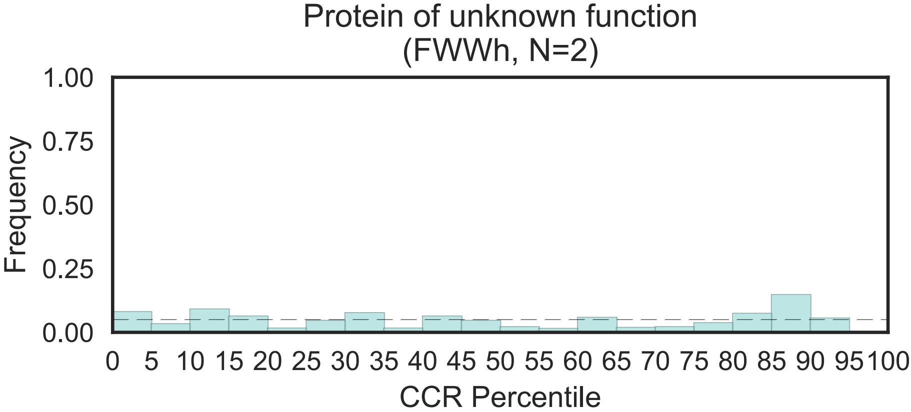

Formiminotransferase-cyclodeaminase
(FTCD_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

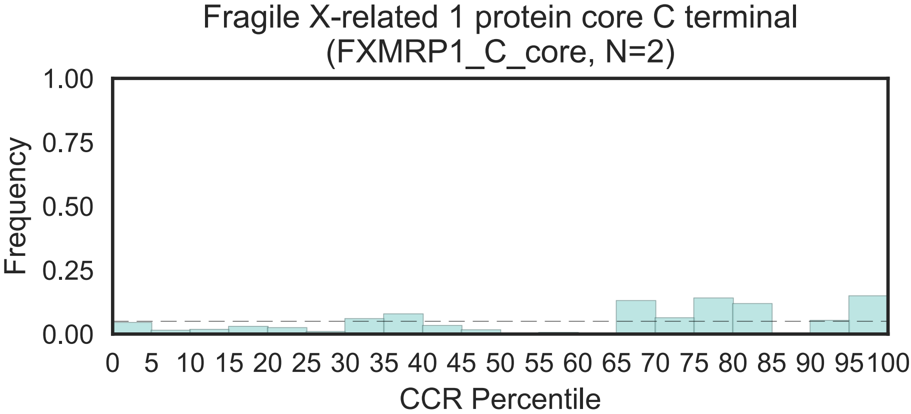

Formiminotransferase domain, N-terminal subdomain
(FTCD_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

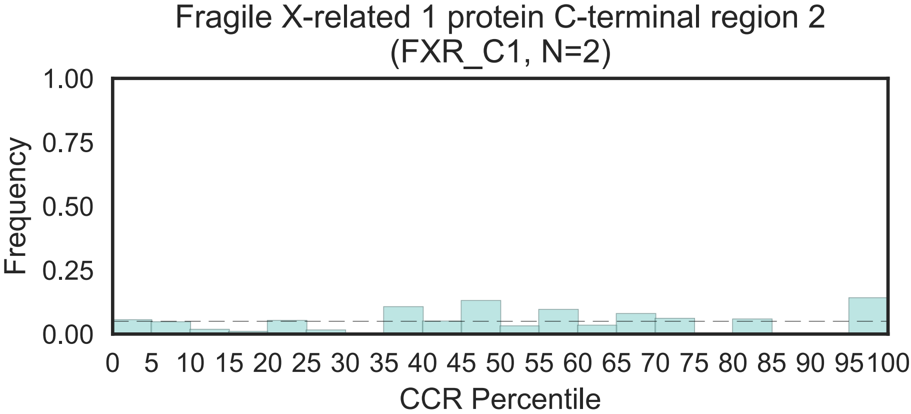

Formate--tetrahydrofolate ligase
(FTHFS, N=3)
Fisher's OR: 0.464; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

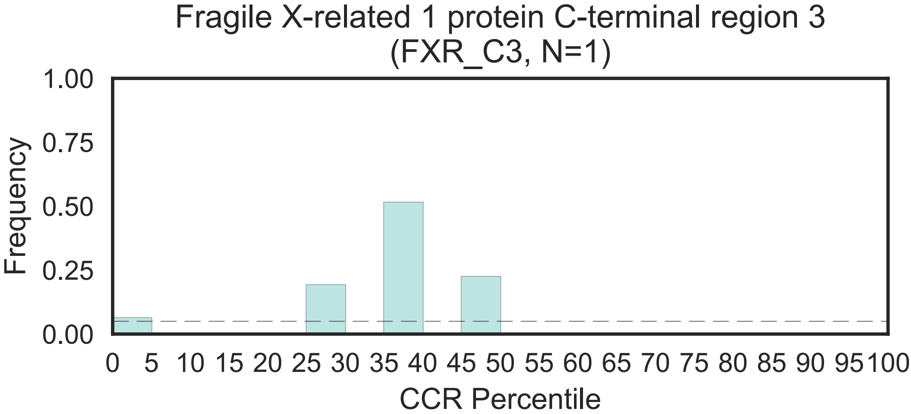

FTO C-terminal domain
(FTO_CTD, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

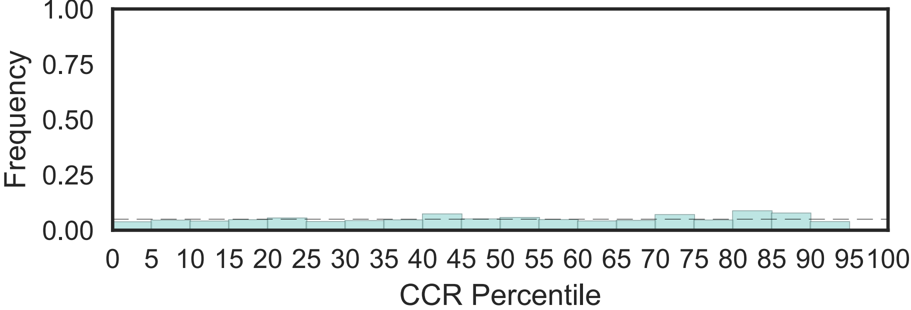

FTO catalytic domain
(FTO_NTD, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Protein of unknown function
(FWWh, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

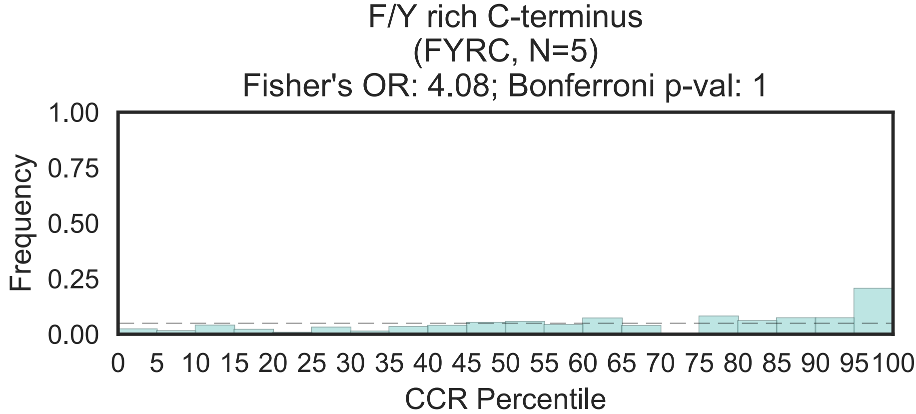

Fragile X-related 1 protein core C terminal
(FXMRP1_C_core, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

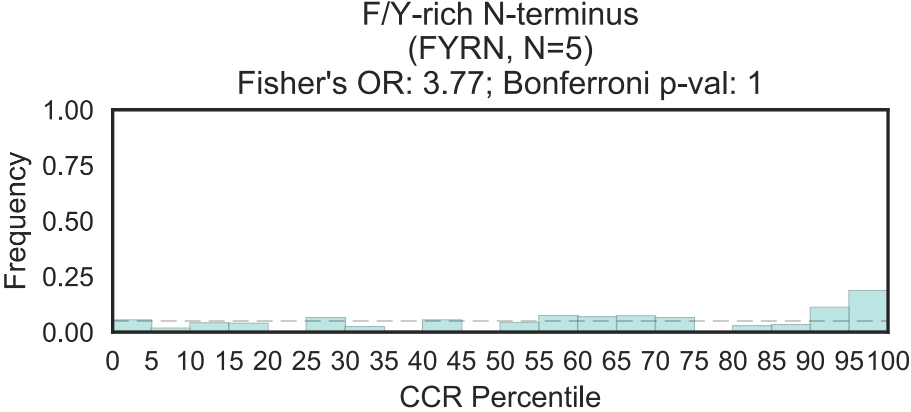

Fragile X-related 1 protein C-terminal region 2
(FXR_C1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

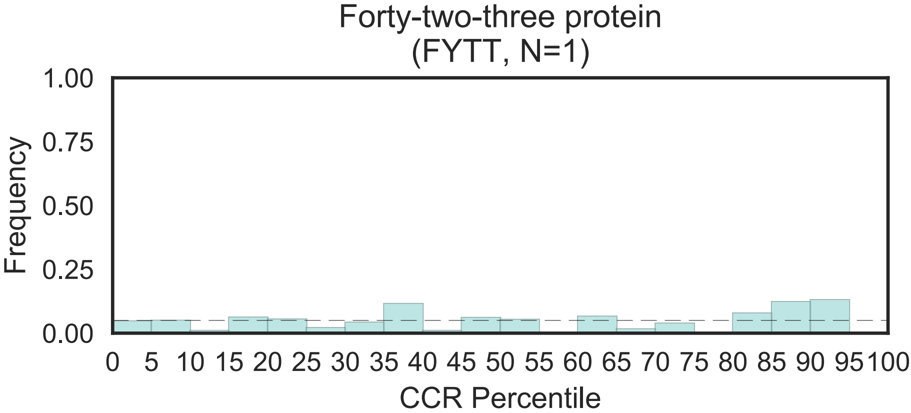

Fragile X-related 1 protein C-terminal region 3
(FXR_C3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

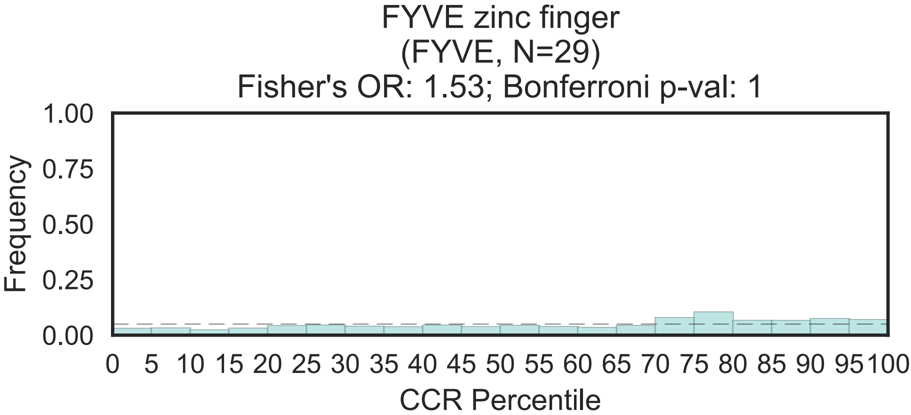


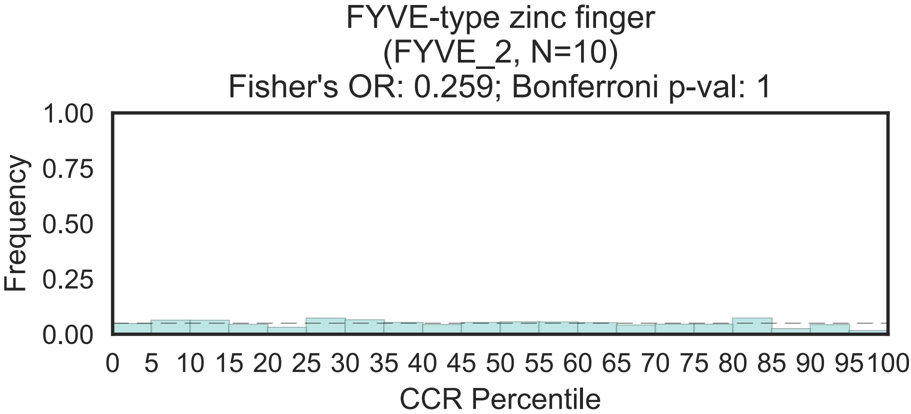
Coagulation Factor Xa inhibitory site
(FXa_inhibition, N=71)
Fisher's OR: 0.113; Bonferroni p-val: 1

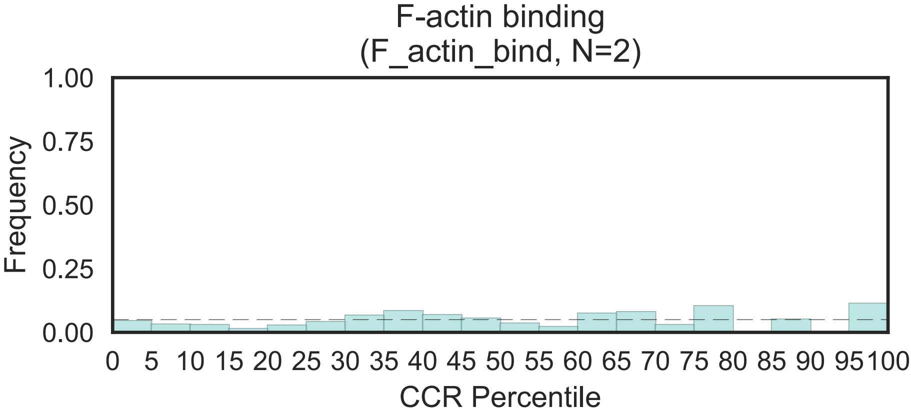

F/Y rich C-terminus
(FYRC, N=5)
Fisher's OR: 4.08; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

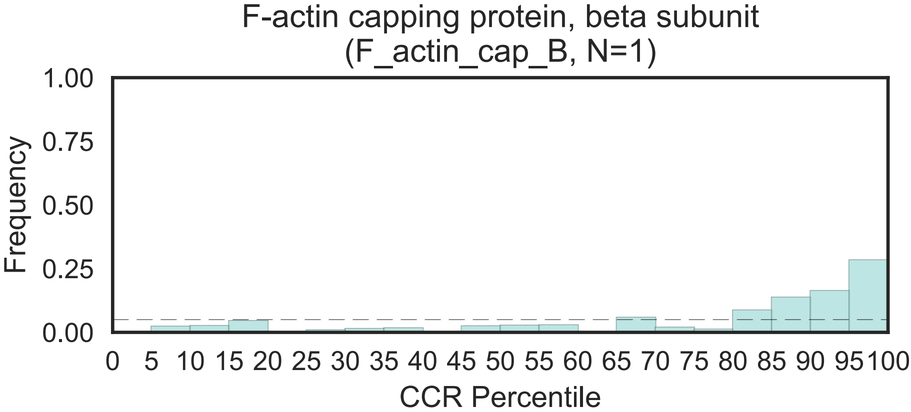

F/Y-rich N-terminus
(FYRN, N=5)
Fisher's OR: 3.77; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

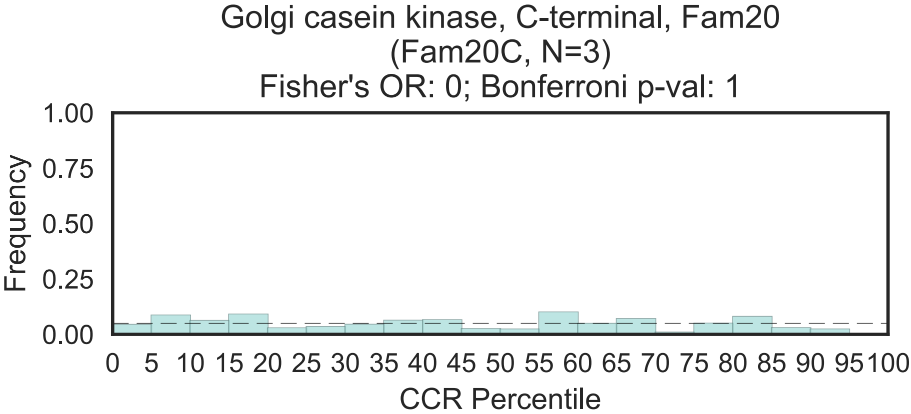

Forty-two-three protein
(FYTT, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

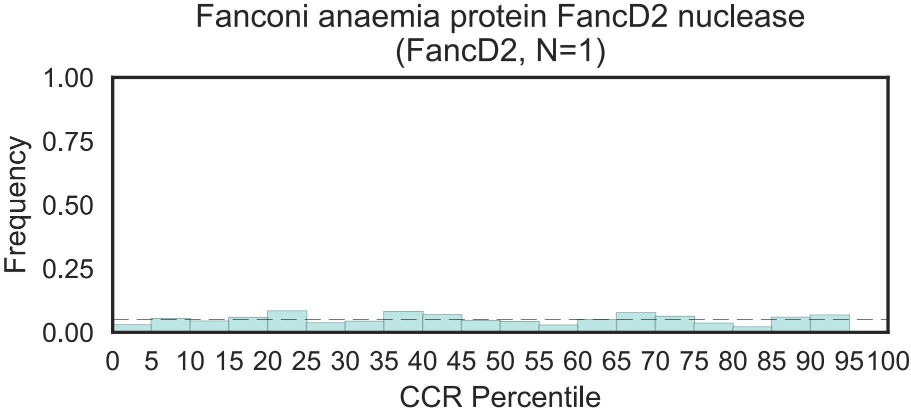

FYVE zinc finger
(FYVE, N=29)
Fisher's OR: 1.53; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

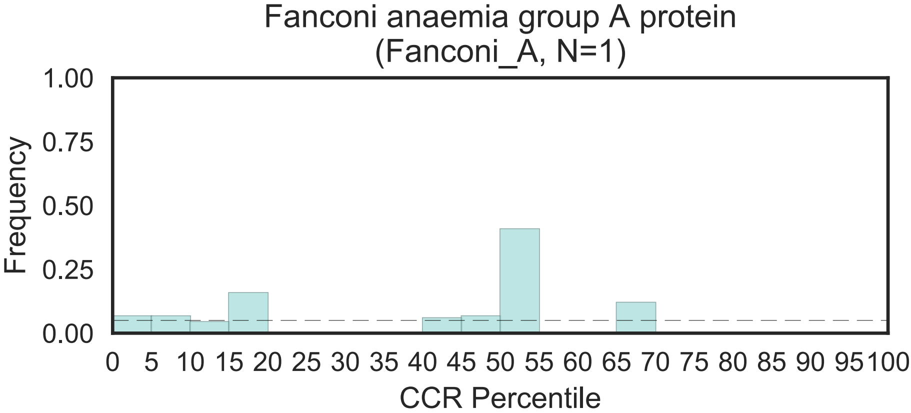

FYVE-type zinc finger
(FYVE_2, N=10)
Fisher's OR: 0.259; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

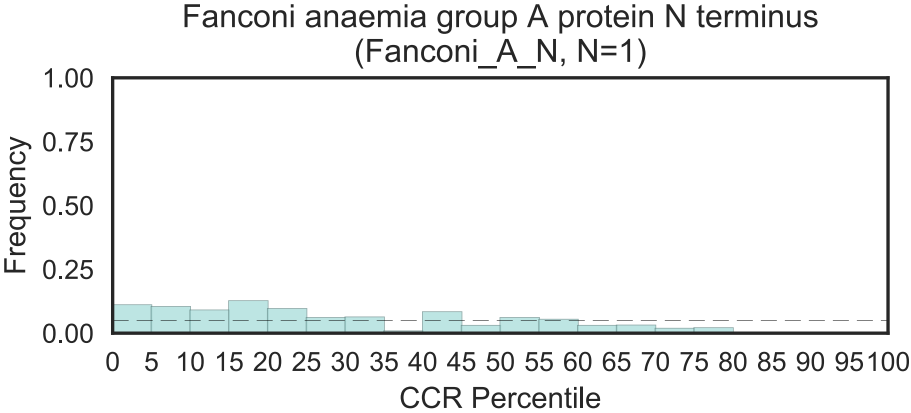

F-actin binding
(F_actin_bind, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

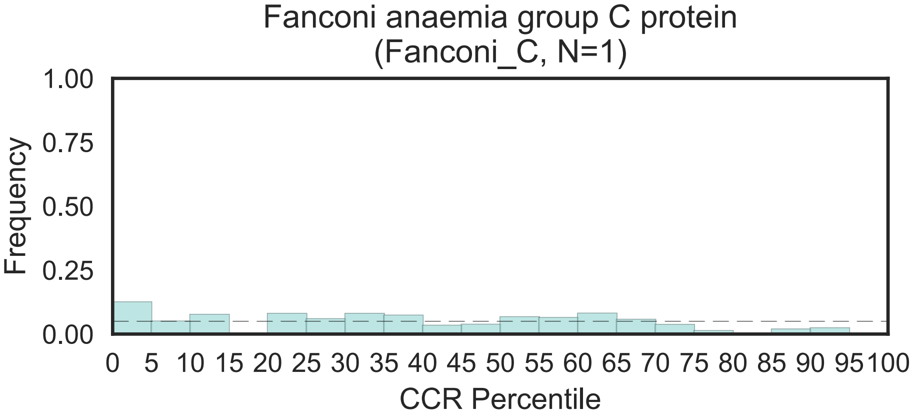

F-actin capping protein, beta subunit
(F_actin_cap_B, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

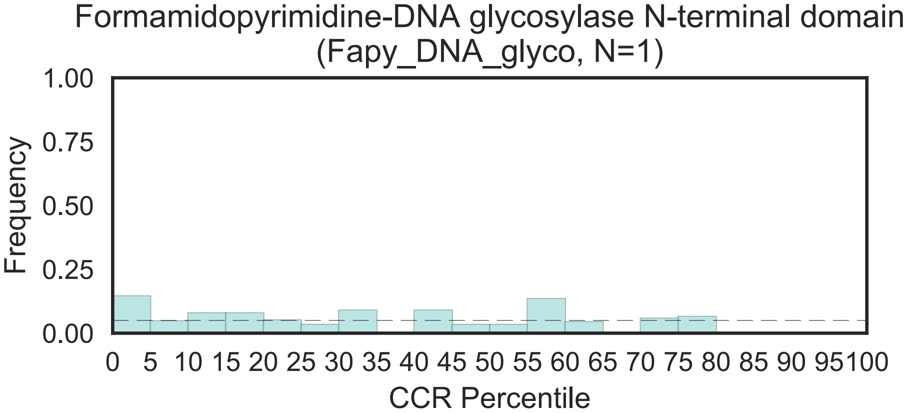

Golgi casein kinase, C-terminal, Fam20
(Fam20C, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

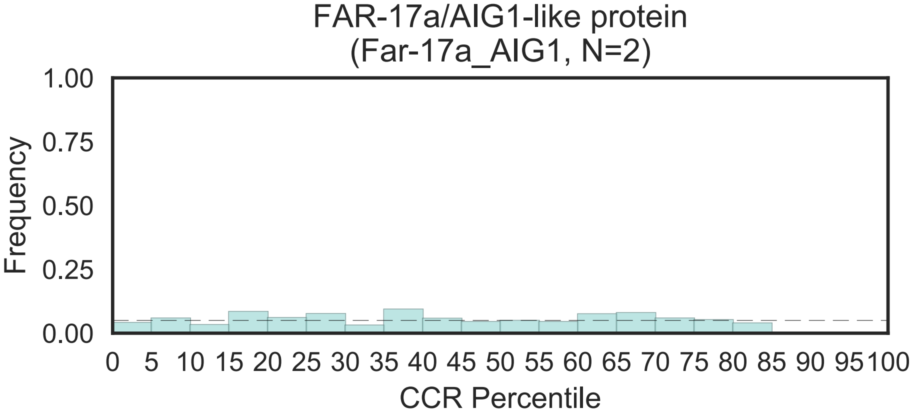

Fanconi anaemia protein FancD2 nuclease
(FancD2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

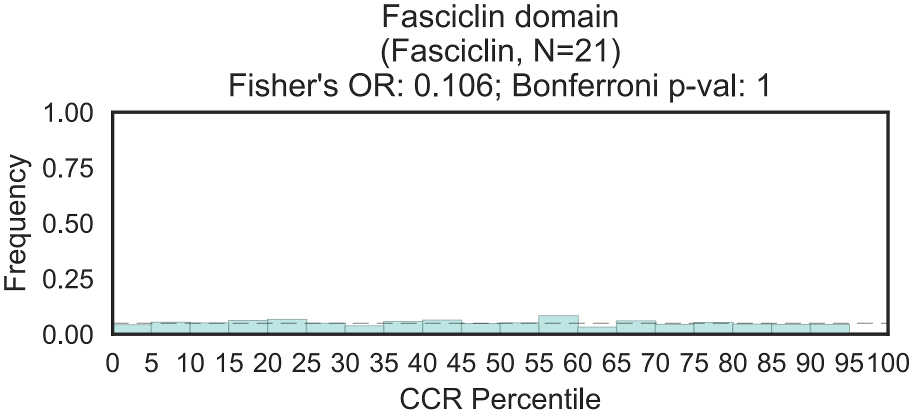

Fanconi anaemia group A protein
(Fanconi_A, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

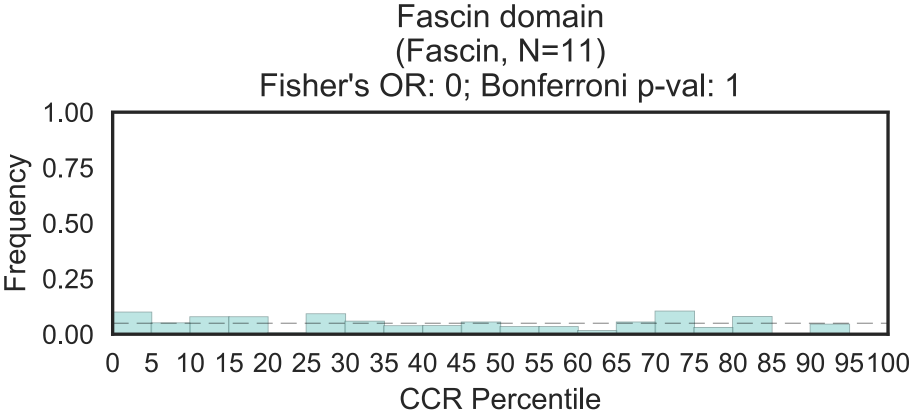

Fanconi anaemia group A protein N terminus
(Fanconi_A_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

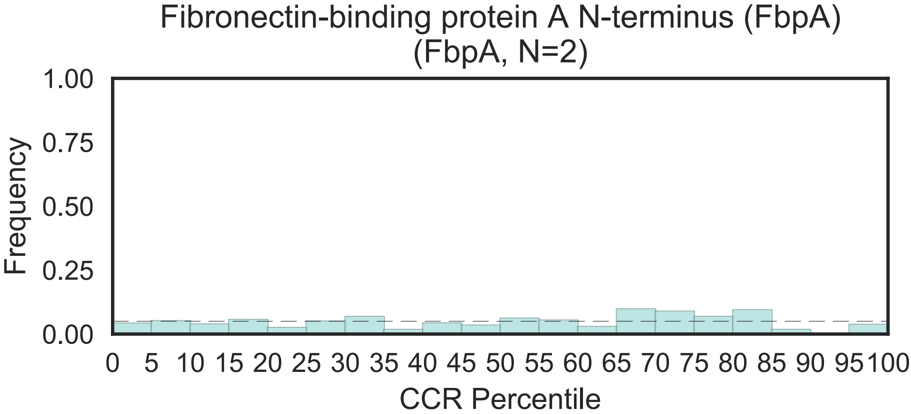

Fanconi anaemia group C protein
(Fanconi_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Formamidopyrimidine-DNA glycosylase N-terminal domain
(Fapy_DNA_glyco, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

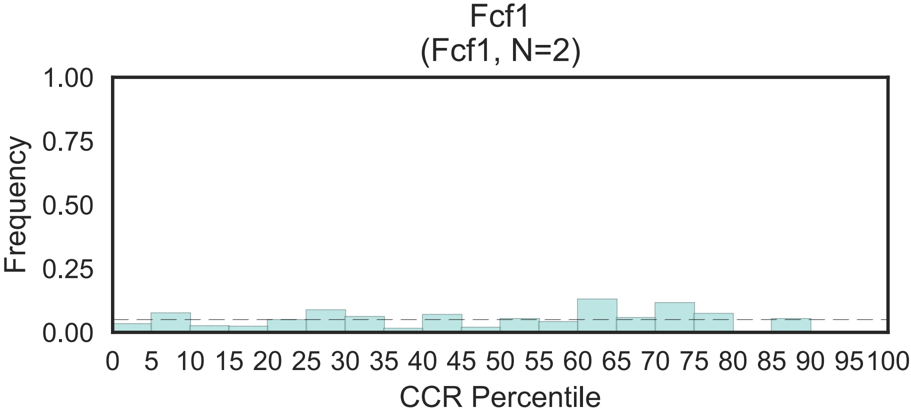

FAR-17a/AIG1-like protein
(Far-17a_AIG1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

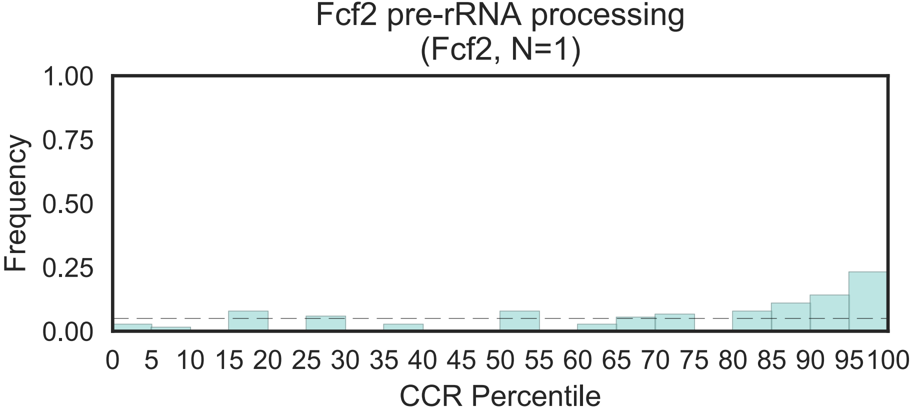

Fasciclin domain
(Fasciclin, N=21)
Fisher's OR: 0.106; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

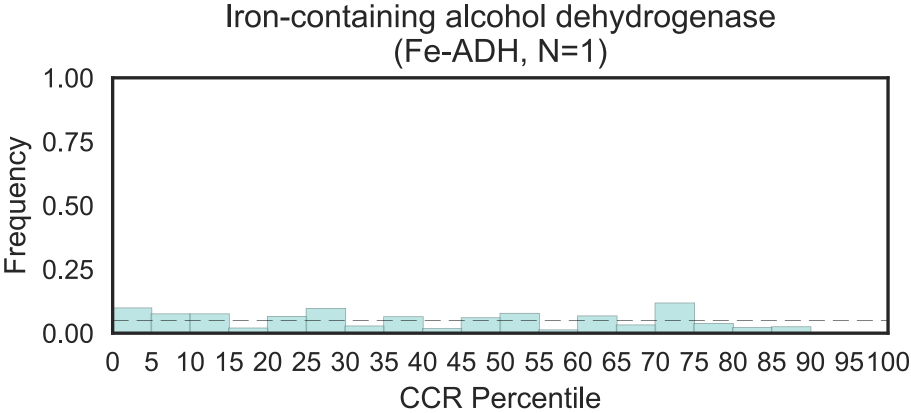

Fascin domain
(Fascin, N=11)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

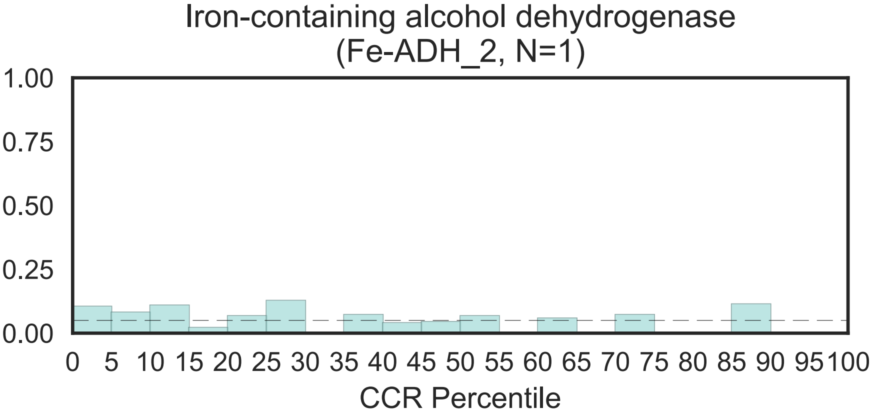


Fibronectin-binding protein A N-terminus (FbpA)
(FbpA, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

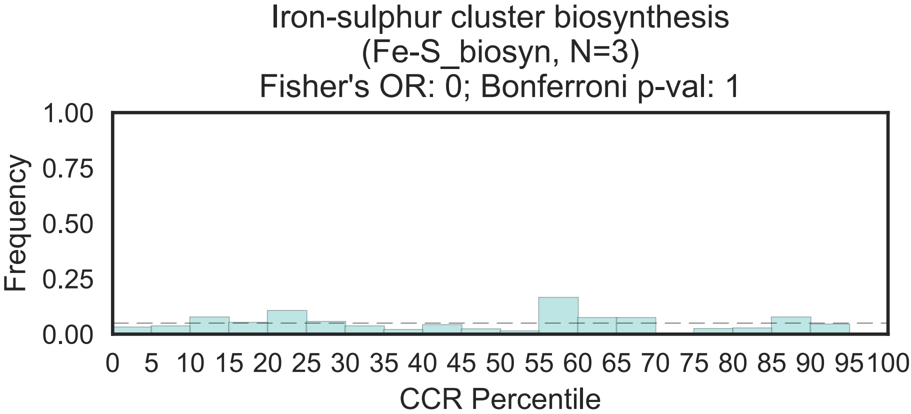
Fcf1
(Fcf1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

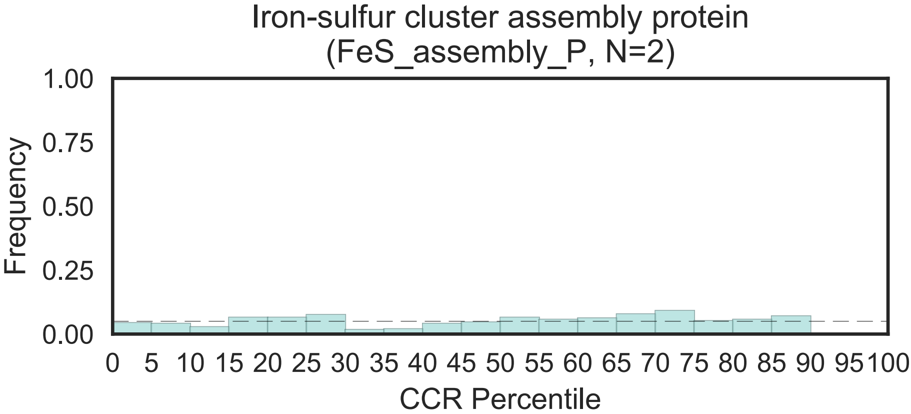

Fcf2 pre-rRNA processing
(Fcf2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

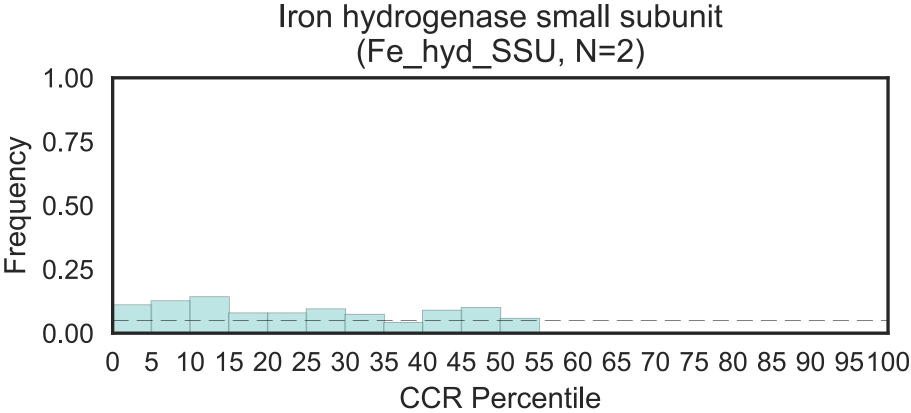

Iron-containing alcohol dehydrogenase
(Fe-ADH, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



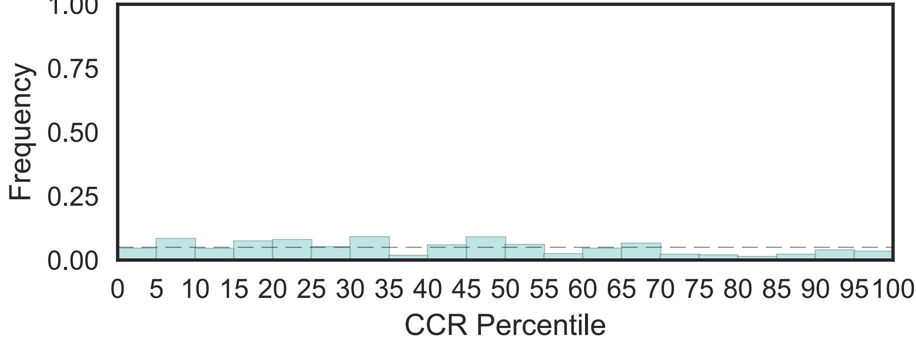
Iron-containing alcohol dehydrogenase
(Fe-ADH_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

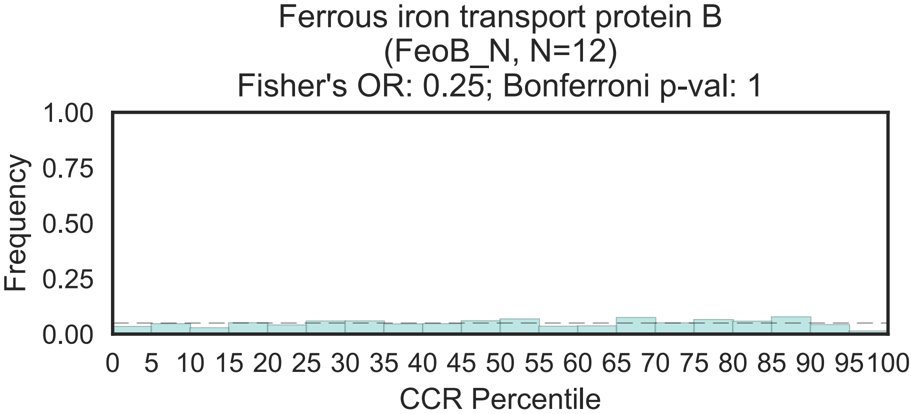

Iron-sulphur cluster biosynthesis
(Fe-S_biosyn, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

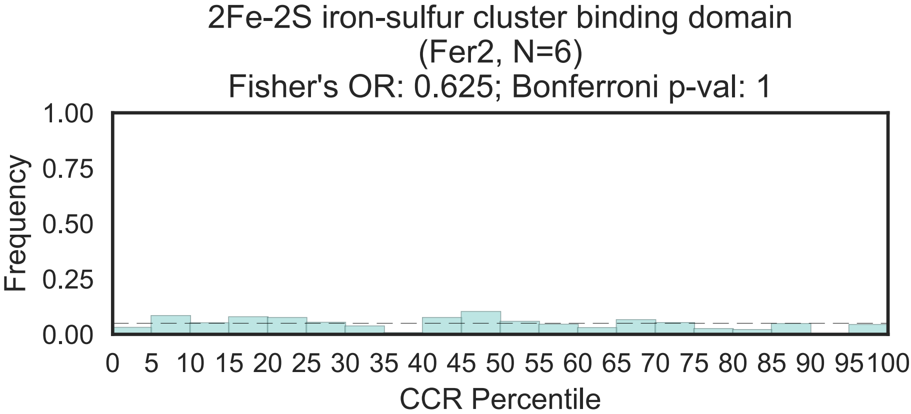

Iron-sulfur cluster assembly protein
(FeS_assembly_P, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

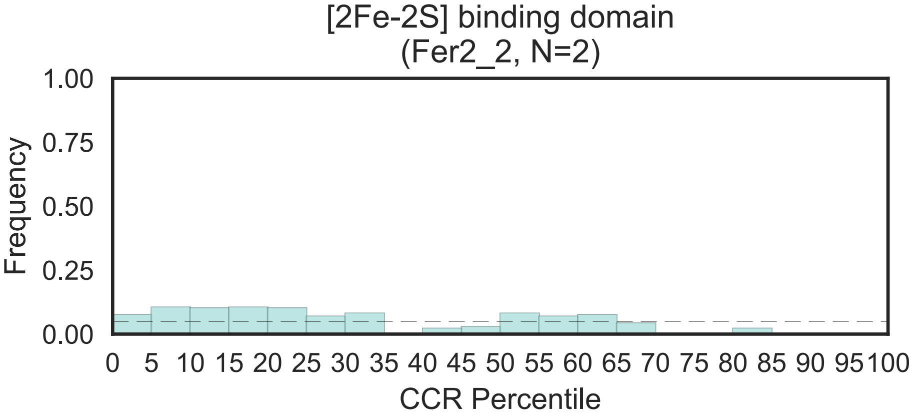

Iron hydrogenase small subunit
(Fe_hyd_SSU, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

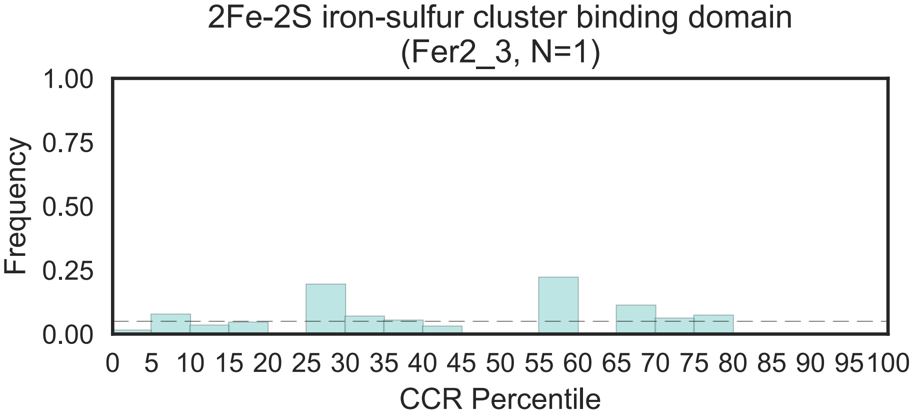
Iron only hydrogenase large subunit, C-terminal domain (Fe_hyd_lg_C, N=2)

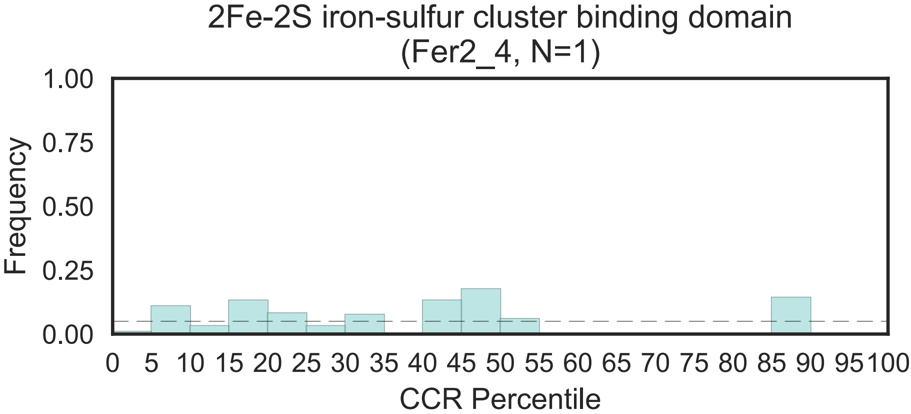


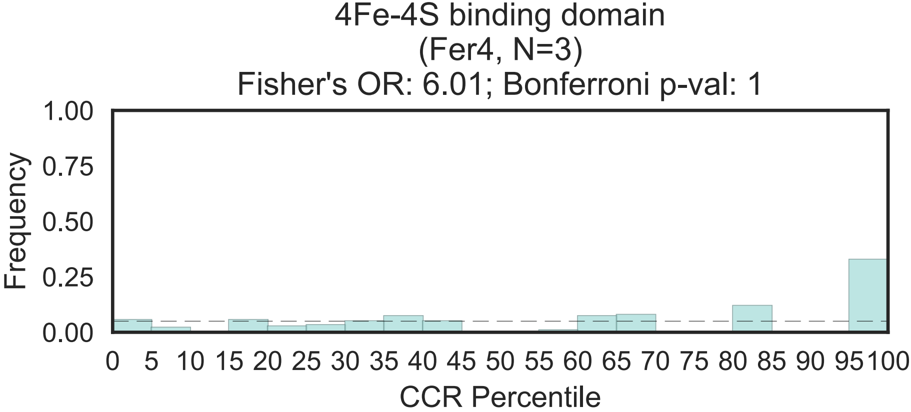

Ferrous iron transport protein B
(FeoB_N, N=12)
Fisher's OR: 0.25; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

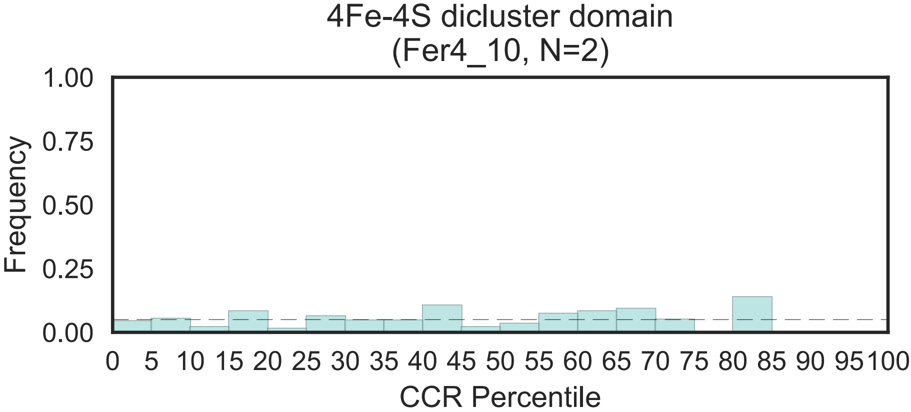

2Fe-2S iron-sulfur cluster binding domain
(Fer2, N=6)
Fisher's OR: 0.625; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

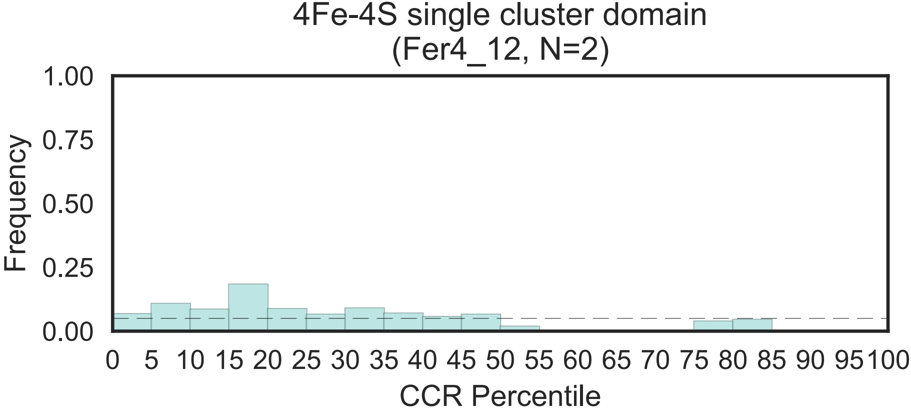

[2Fe-2S] binding domain
(Fer2_2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

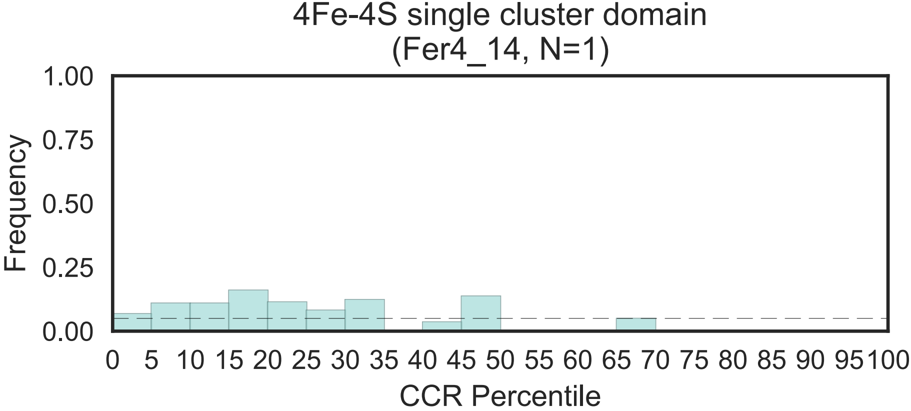

2Fe-2S iron-sulfur cluster binding domain
(Fer2_3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

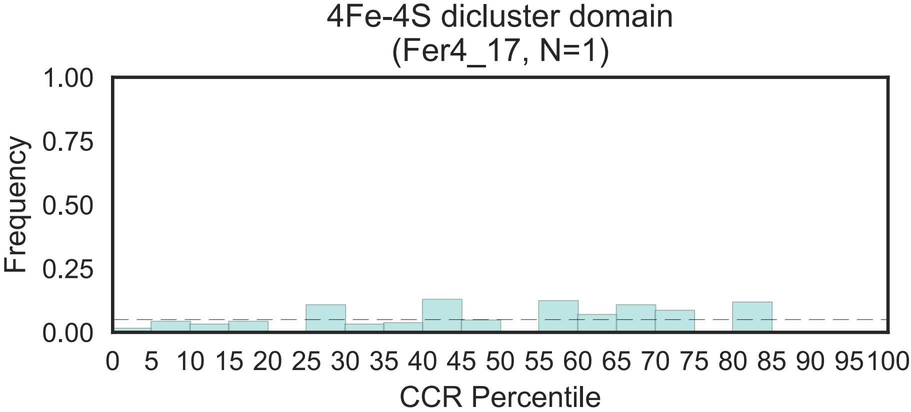

2Fe-2S iron-sulfur cluster binding domain
(Fer2_4, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

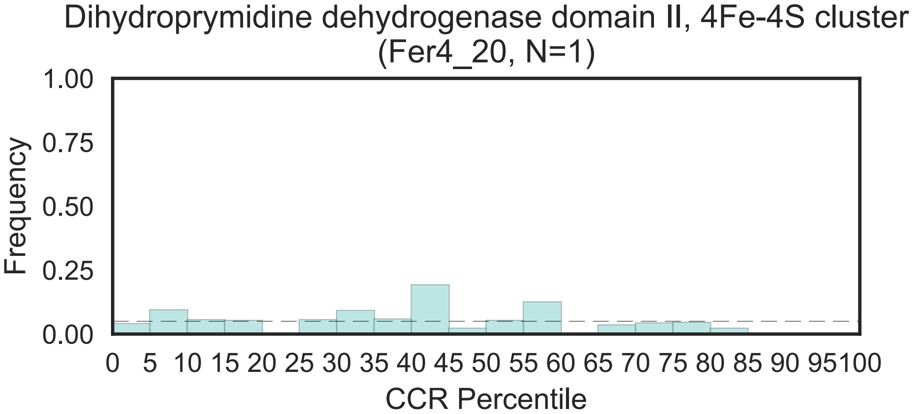

4Fe-4S binding domain
(Fer4, N=3)
Fisher's OR: 6.01; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

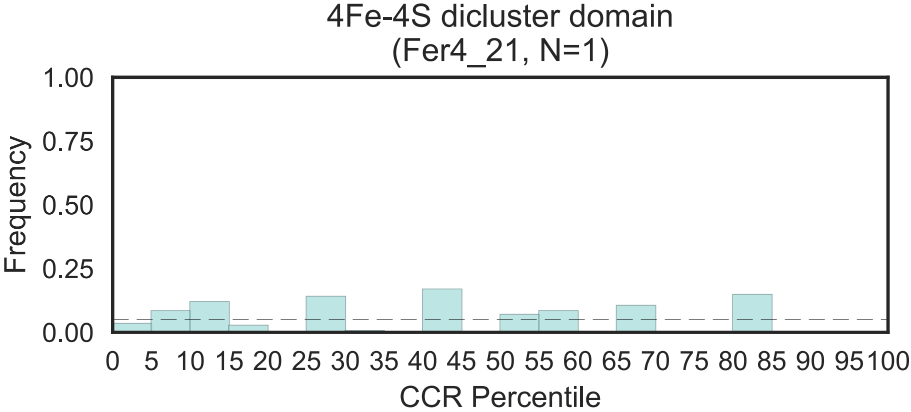

4Fe-4S dicluster domain
(Fer4_10, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

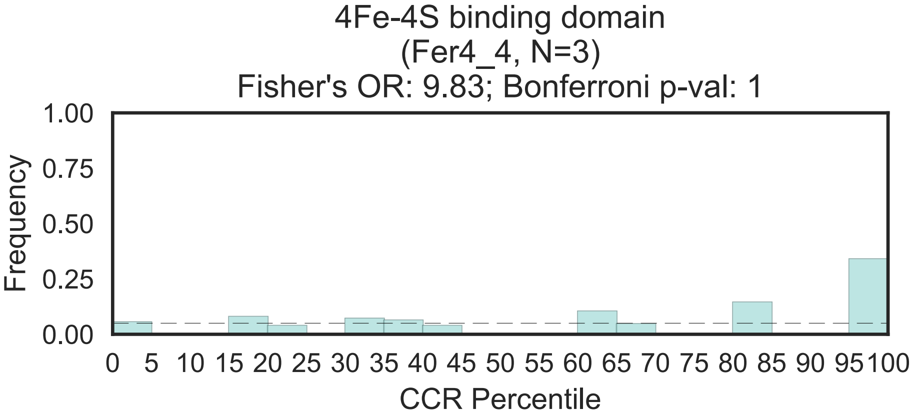

4Fe-4S single cluster domain
(Fer4_12, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

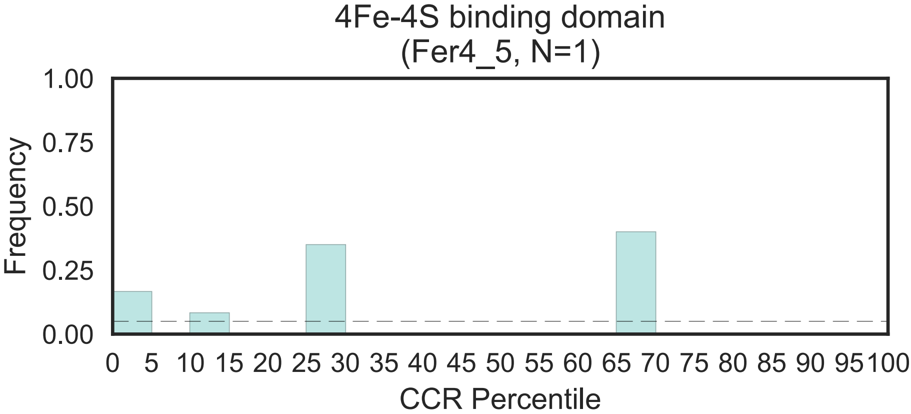

4Fe-4S single cluster domain
(Fer4_14, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

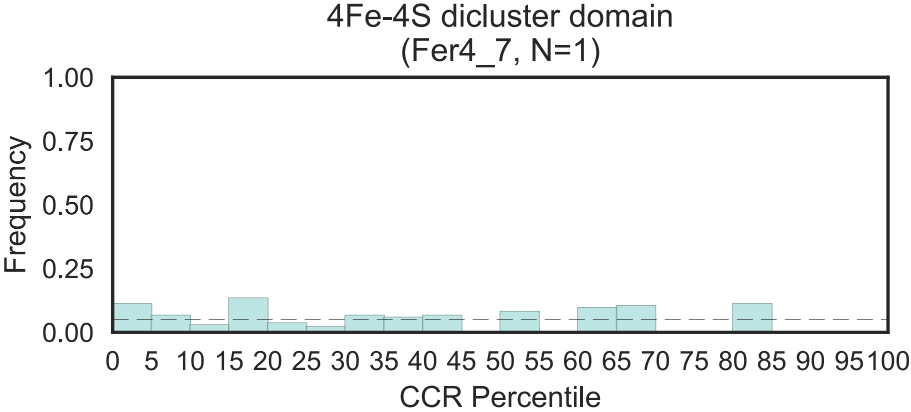

4Fe-4S dicluster domain
(Fer4_17, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

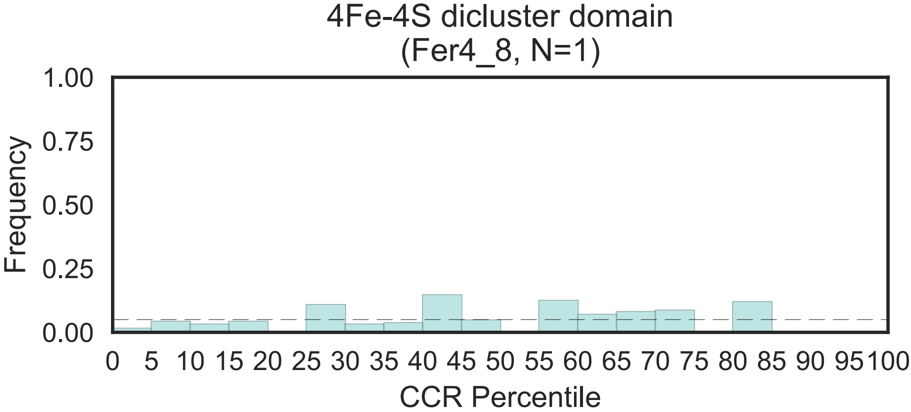

Dihydroprymidine dehydrogenase domain II, 4Fe-4S cluster
(Fer4_20, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

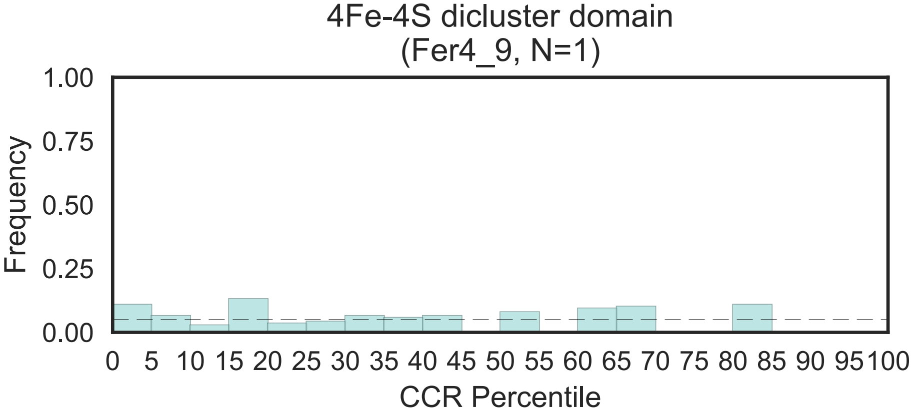

4Fe-4S dicluster domain
(Fer4_21, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

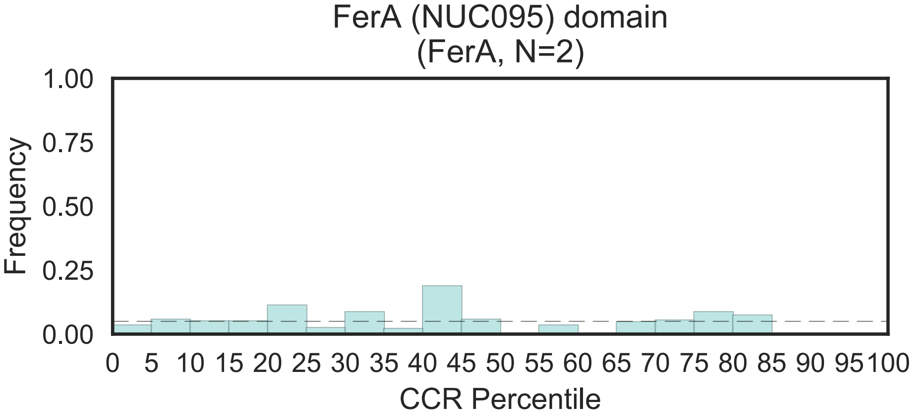

4Fe-4S binding domain
(Fer4_4, N=3)
Fisher's OR: 9.83; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

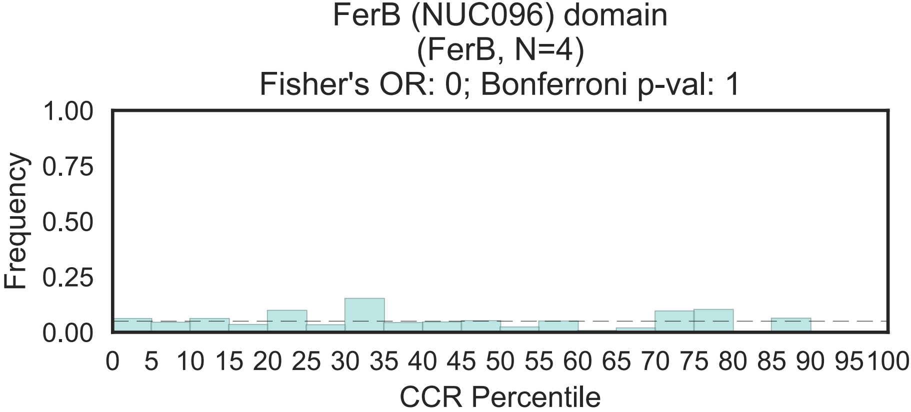

4Fe-4S binding domain
(Fer4_5, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

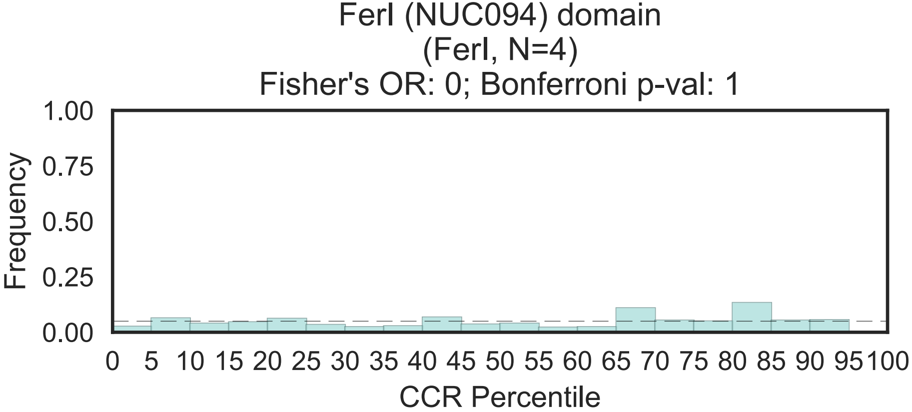

4Fe-4S dicluster domain
(Fer4_7, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

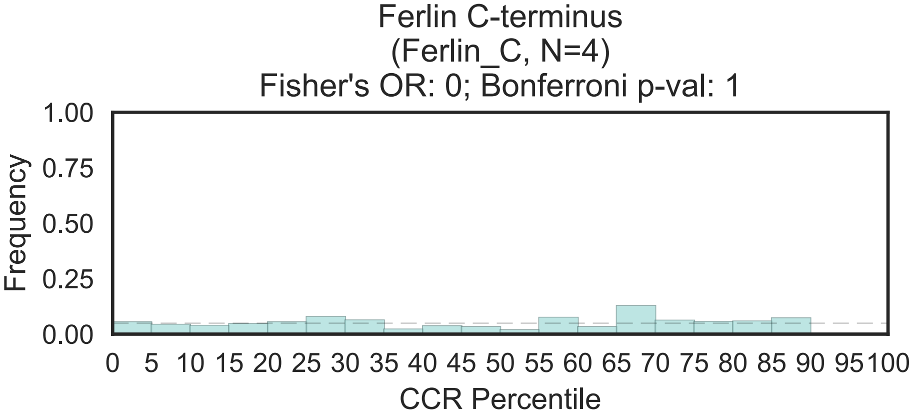

4Fe-4S dicluster domain
(Fer4_8, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

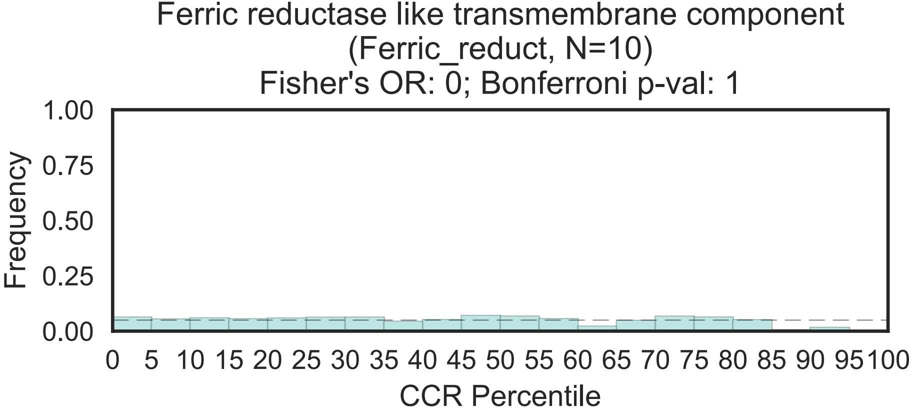

4Fe-4S dicluster domain
(Fer4_9, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

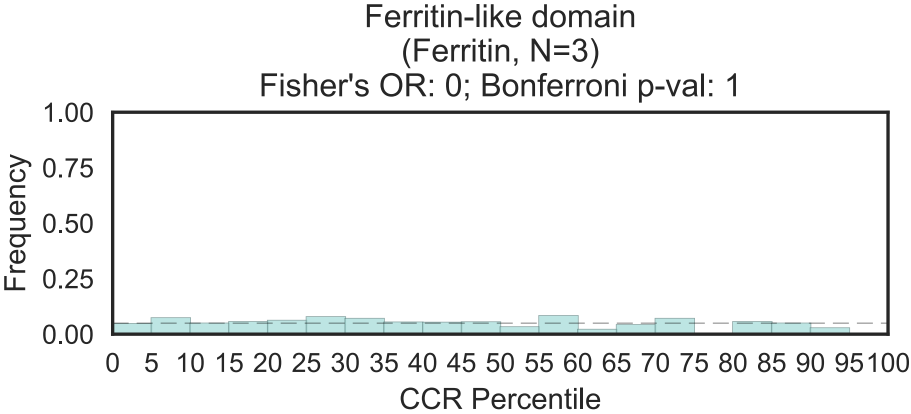

FerA (NUC095) domain
(FerA, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


FerB (NUC096) domain
(FerB, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

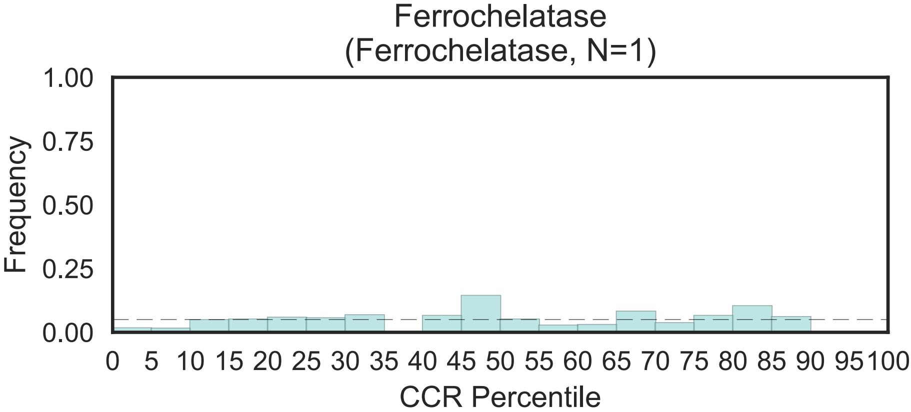

FerI (NUC094) domain
(FerI, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ferlin C-terminus
(Ferlin_C, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

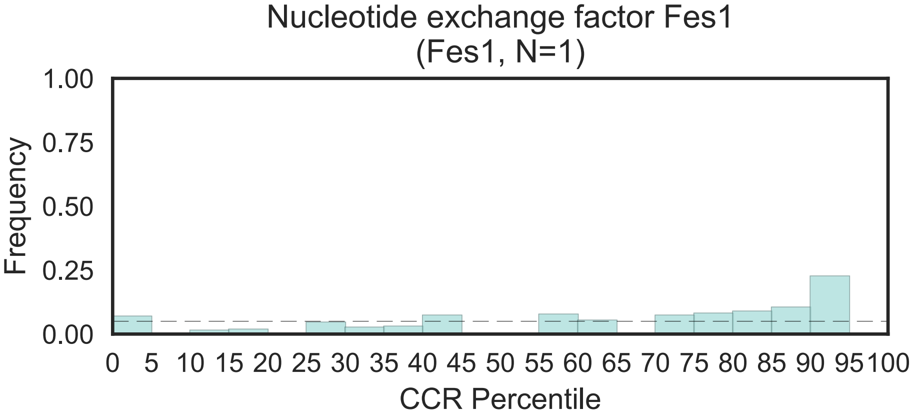

Ferric reductase like transmembrane component
(Ferric_reduct, N=10)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

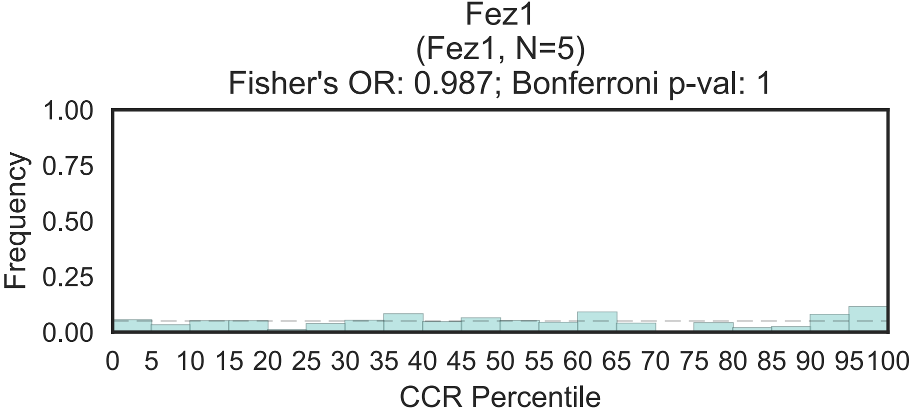


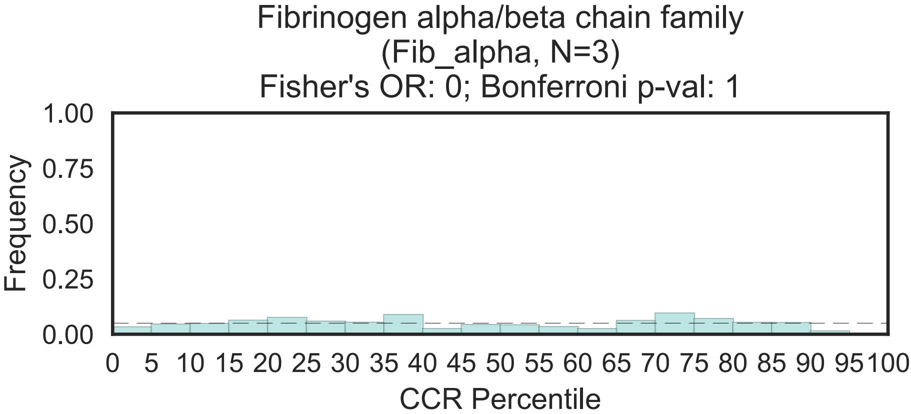
Ferritin-like domain
(Ferritin, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

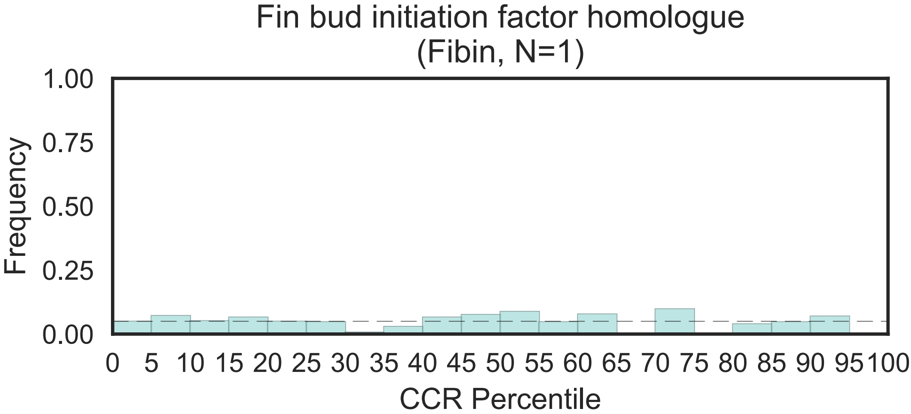


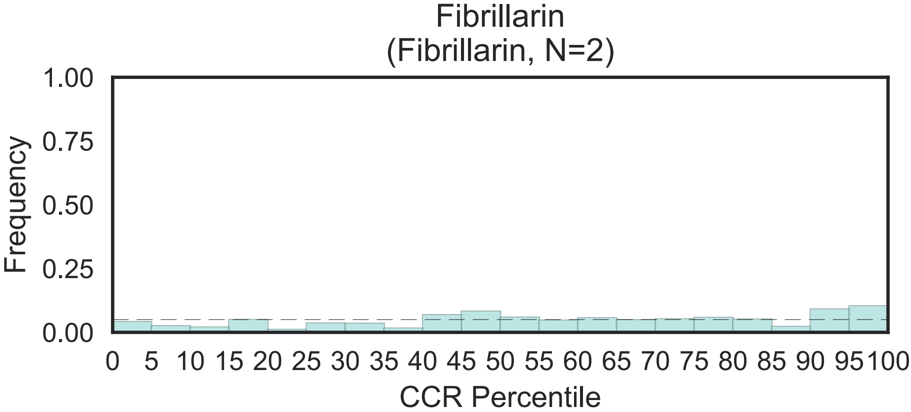
Ferrochelatase
(Ferrochelatase, N=1)


Nucleotide exchange factor Fes1
(Fes1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

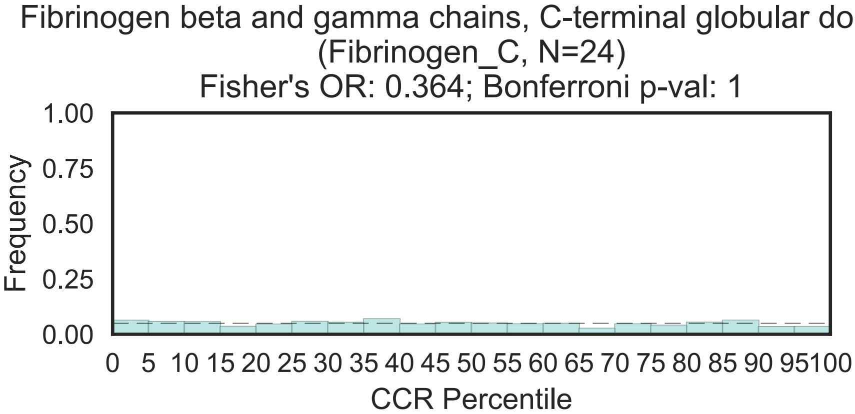

Fez1
(Fez1, N=5)
Fisher's OR: 0.987; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

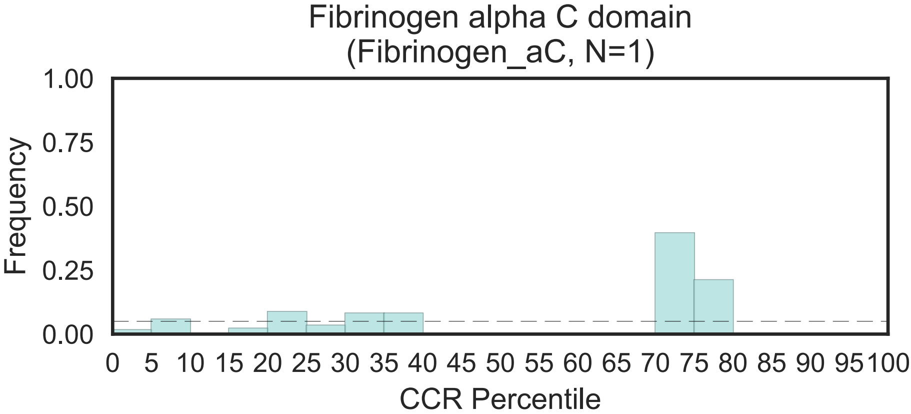

Fibrinogen alpha/beta chain family
(Fib_alpha, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

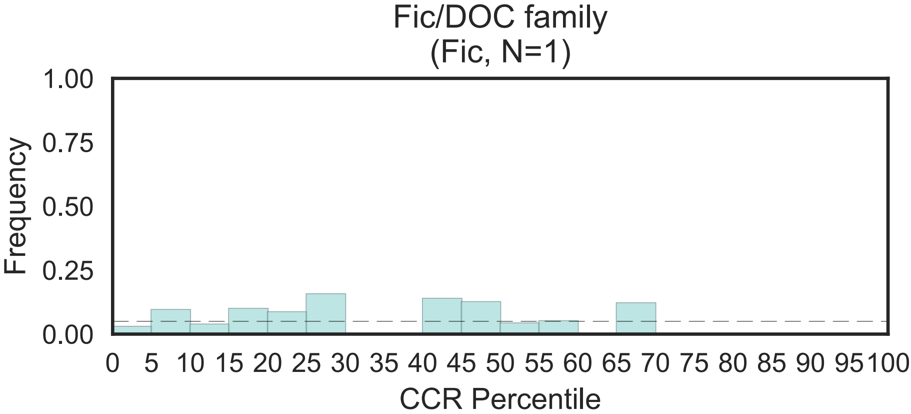

Fin bud initiation factor homologue
(Fibin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

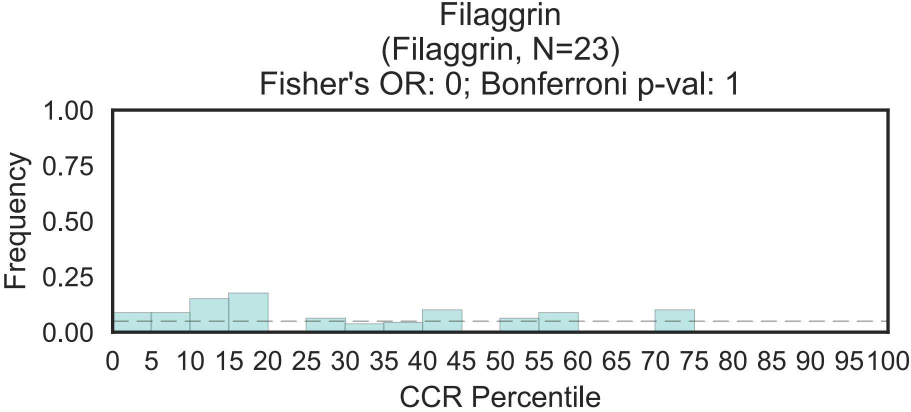


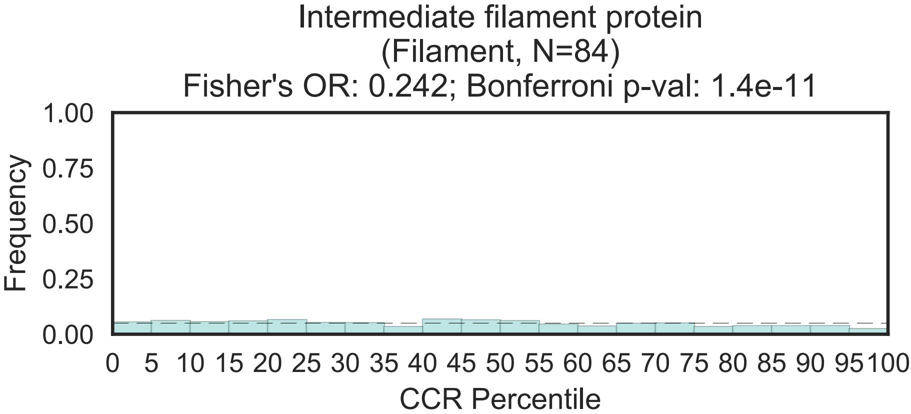
Fibrillarin
(Fibrillarin, N=2)

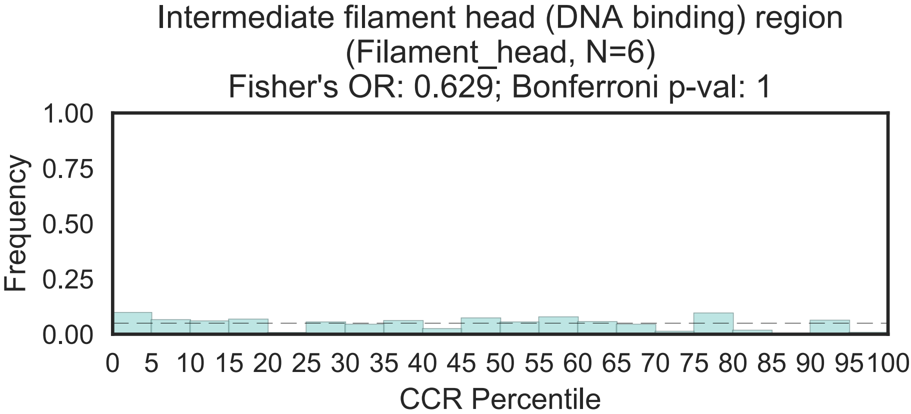

Fibrinogen beta and gamma chains, C-terminal globular domain
(Fibrinogen_C, N=24)
Fisher's OR: 0.364; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

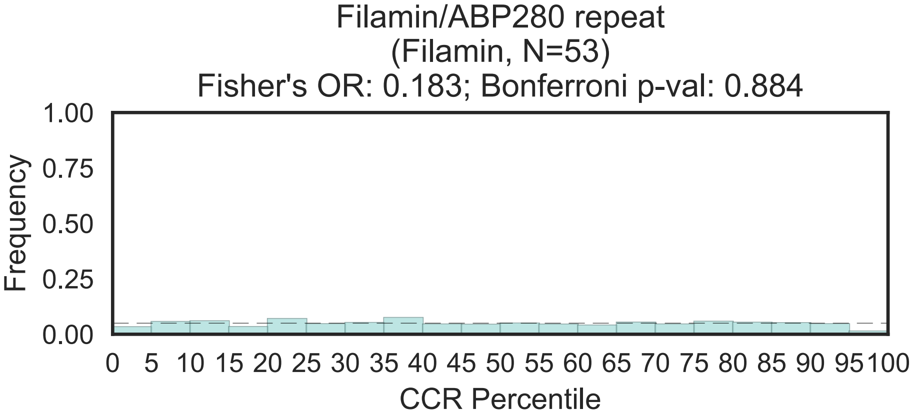

Fibrinogen alpha C domain
(Fibrinogen_aC, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

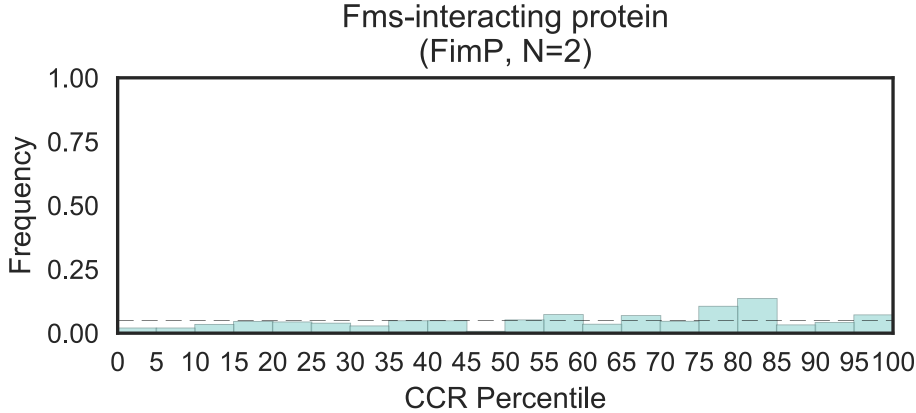

Fic/DOC family
(Fic, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

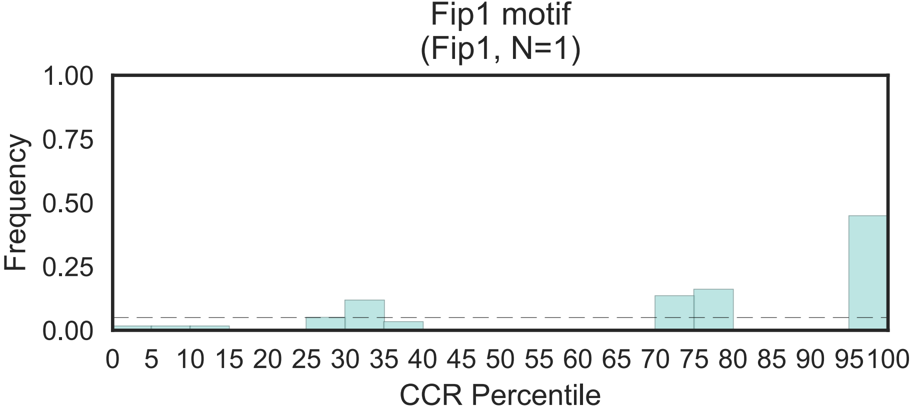

Filaggrin
(Filaggrin, N=23)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

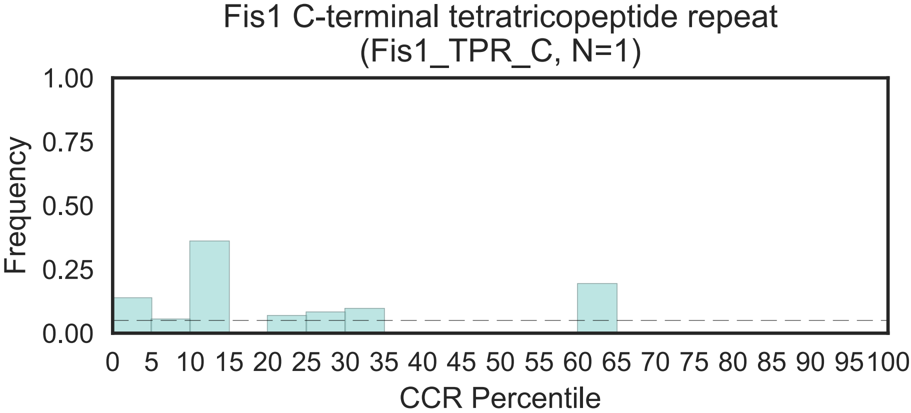

Intermediate filament protein
(Filament, N=84)
Fisher's OR: 0.242; Bonferroni p-val: 1.4e-11
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

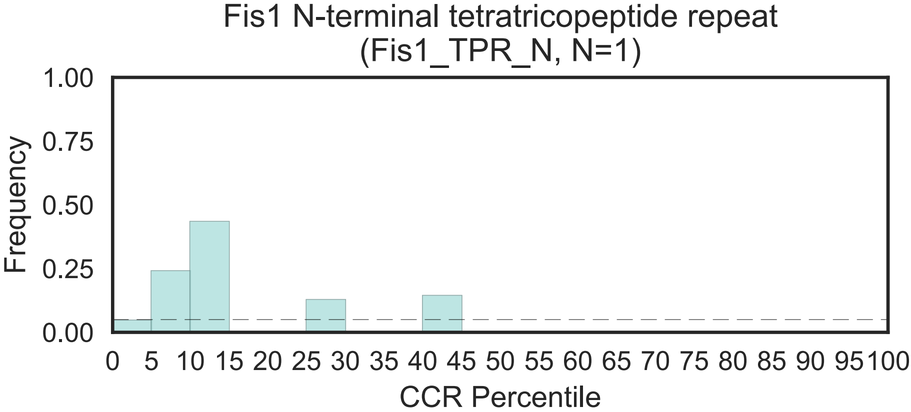

Intermediate filament head (DNA binding) region
(Filament_head, N=6)
Fisher's OR: 0.629; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

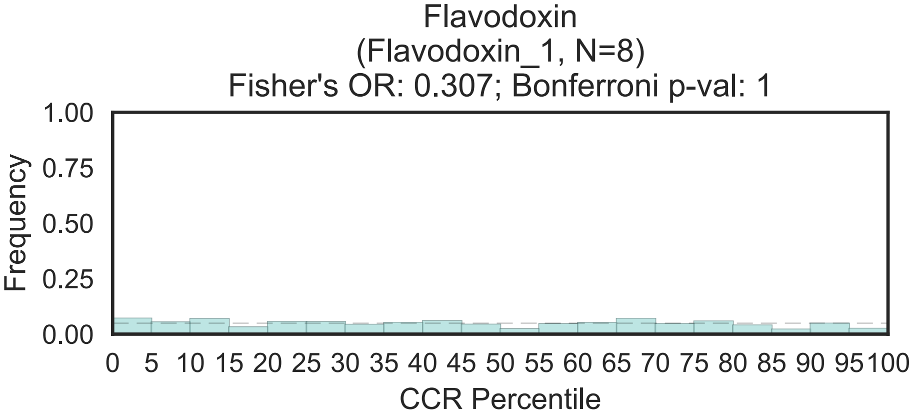

Filamin/ABP280 repeat
(Filamin, N=53)
Fisher's OR: 0.183; Bonferroni p-val: 0.884
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

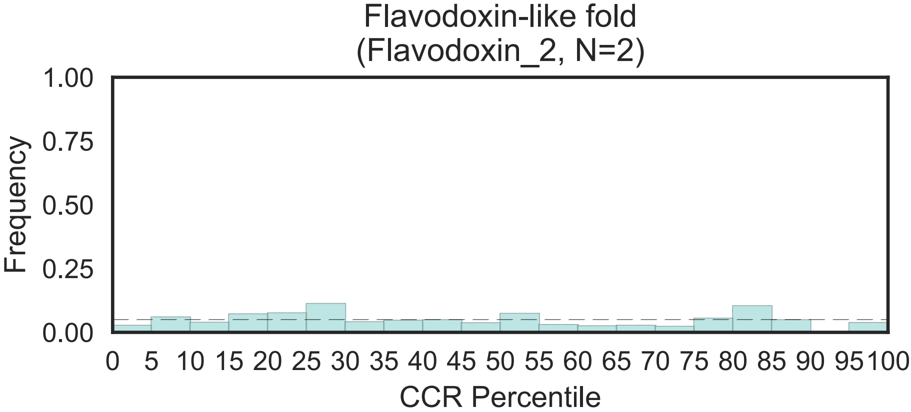

Fms-interacting protein
(FimP, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

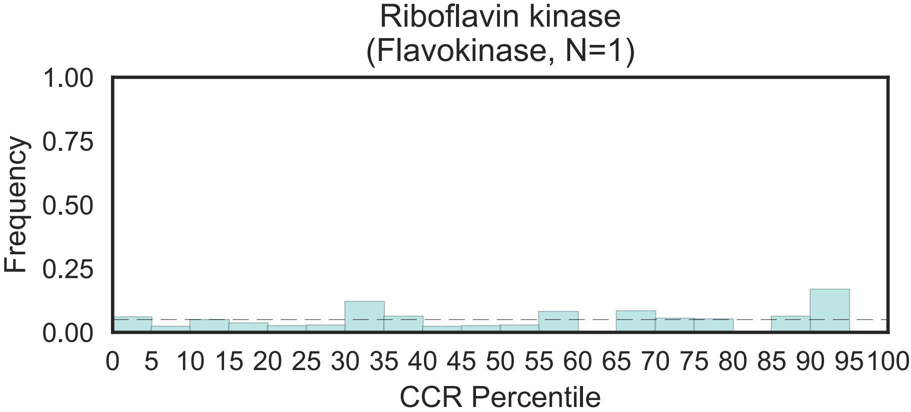

Fip1 motif
(Fip1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

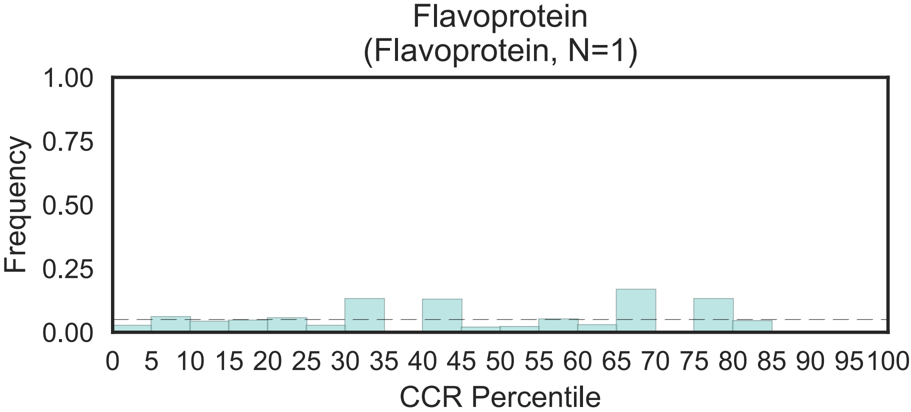

Fis1 C-terminal tetratricopeptide repeat
(Fis1_TPR_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

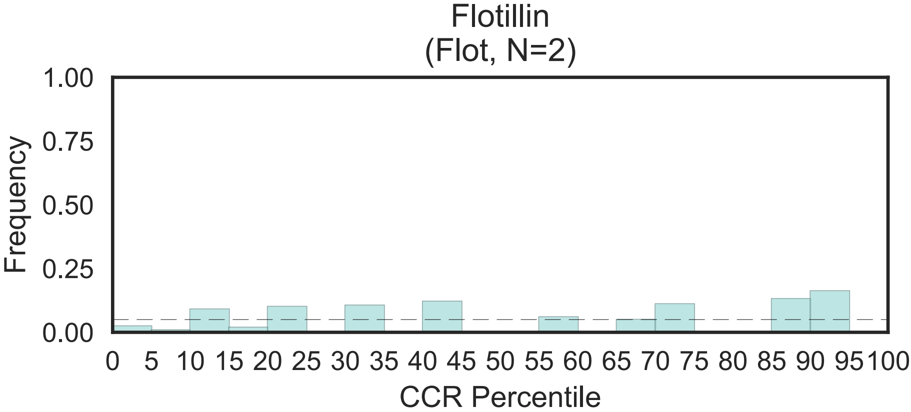

Fis1 N-terminal tetratricopeptide repeat
(Fis1_TPR_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

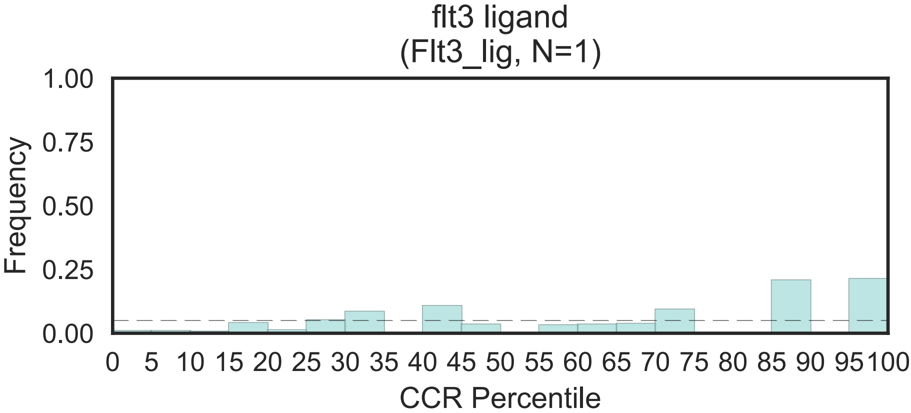

Flavodoxin
(Flavodoxin_1, N=8)
Fisher's OR: 0.307; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

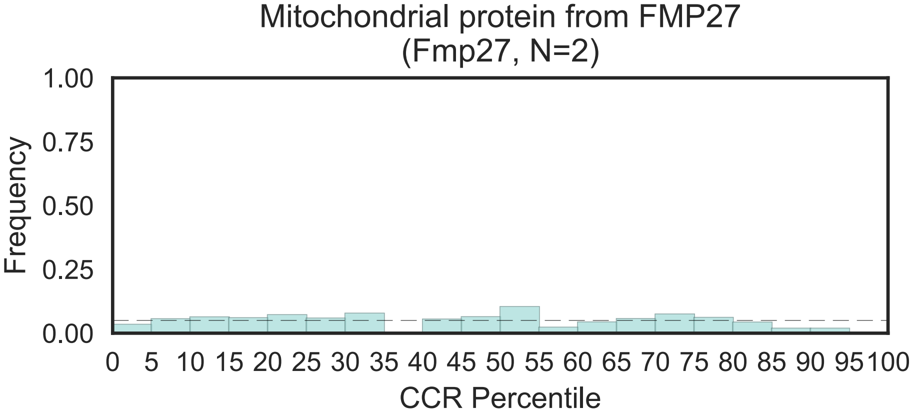

Flavodoxin-like fold
(Flavodoxin_2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

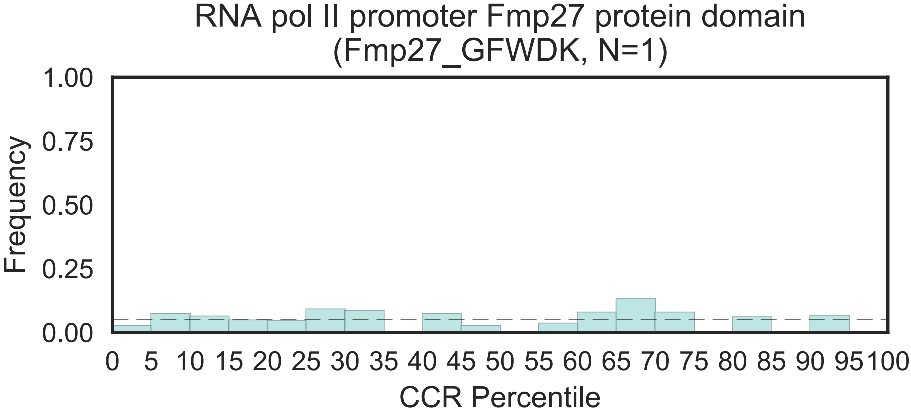

Riboflavin kinase
(Flavokinase, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

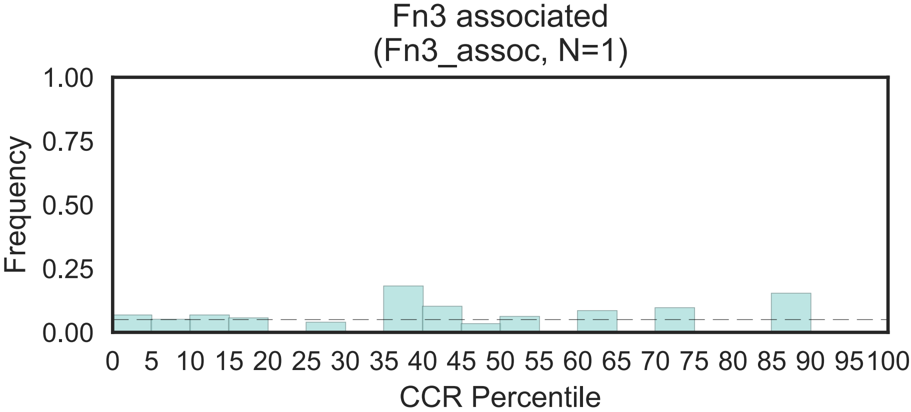

Flavoprotein
(Flavoprotein, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

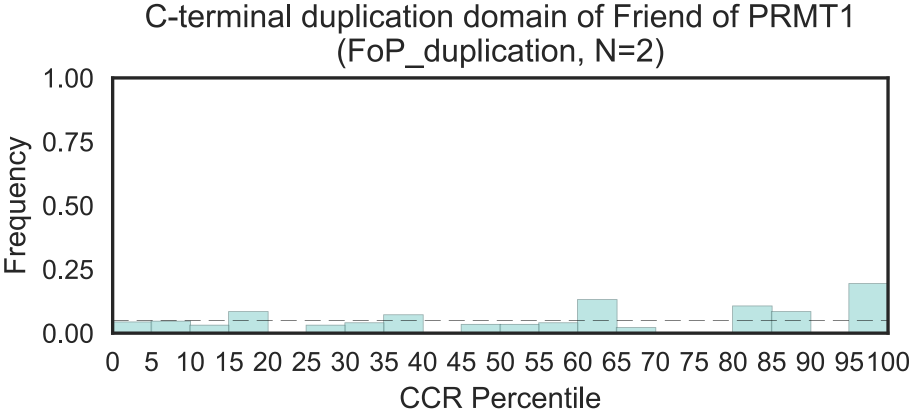

Flotillin
(Flot, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

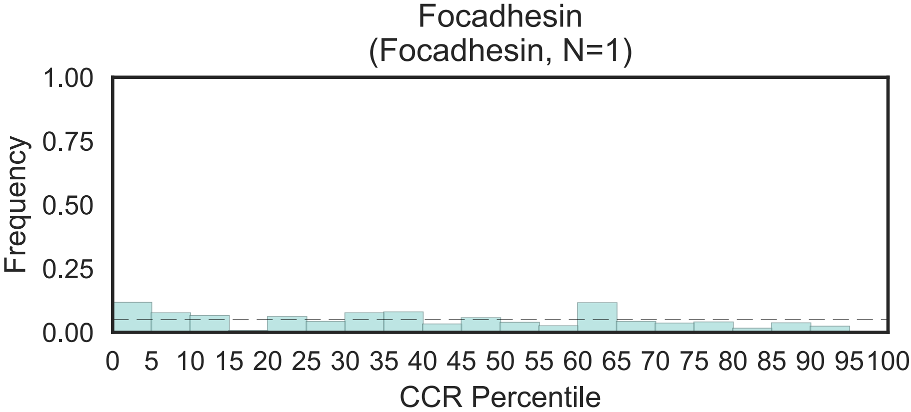

flt3 ligand
(Flt3_lig, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

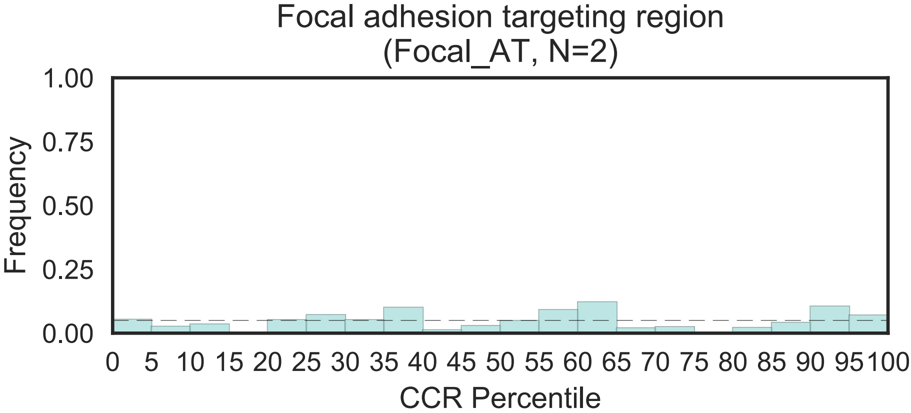

Mitochondrial protein from FMP27
(Fmp27, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

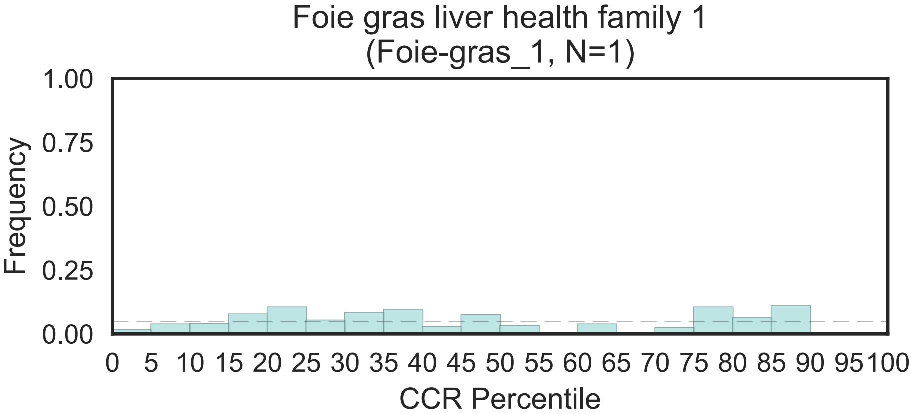

RNA pol II promoter Fmp27 protein domain
(Fmp27_GFWDK, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

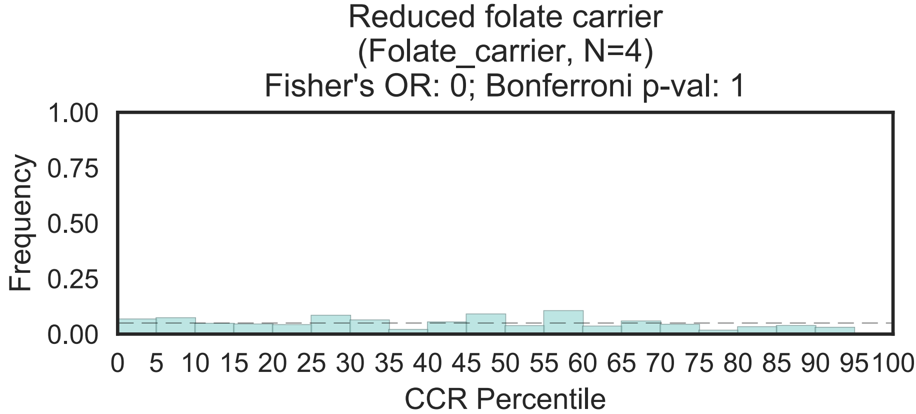

Fn3 associated
(Fn3_assoc, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

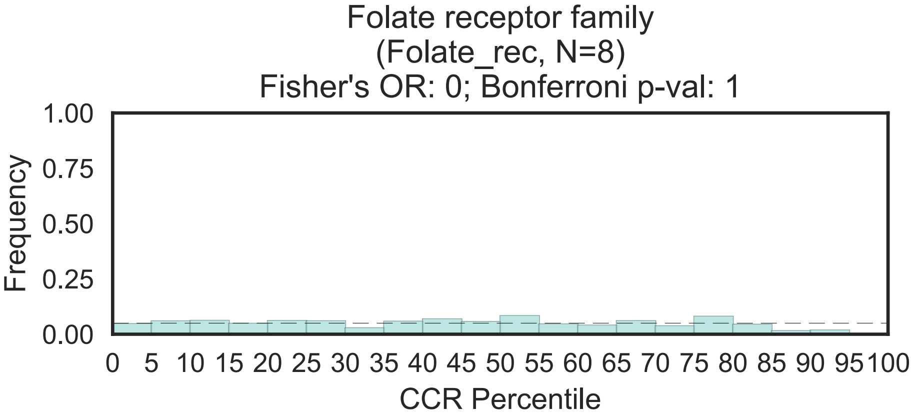

C-terminal duplication domain of Friend of PRMT1
(FoP_duplication, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

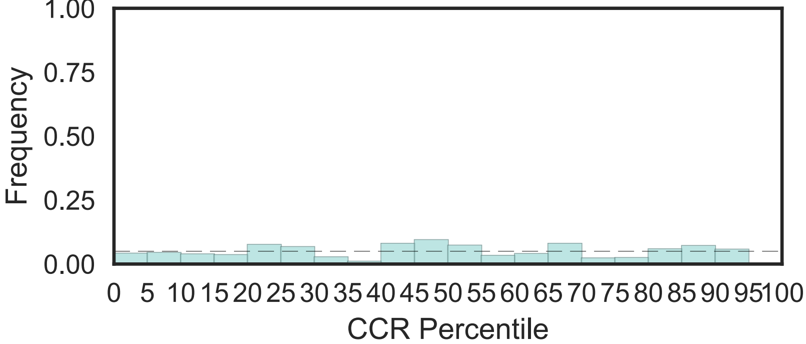

Focadhesin
(Focadhesin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Focal adhesion targeting region
(Focal_AT, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

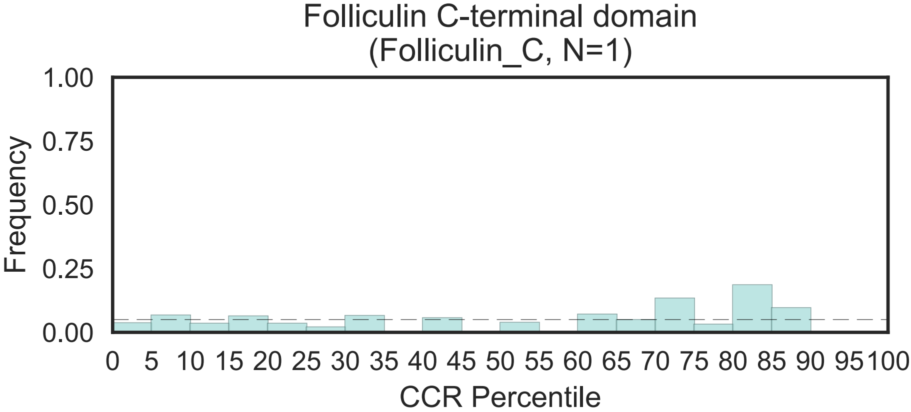

Foie gras liver health family 1
(Foie-gras_1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

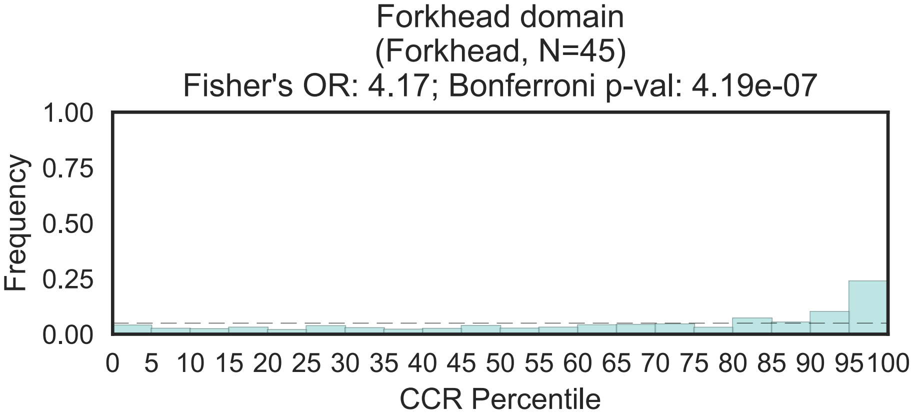

Reduced folate carrier
(Folate_carrier, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

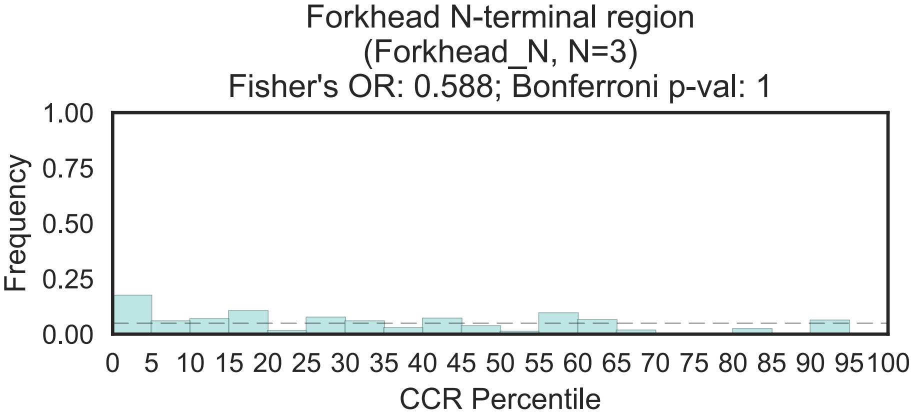

Folate receptor family
(Folate_rec, N=8)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

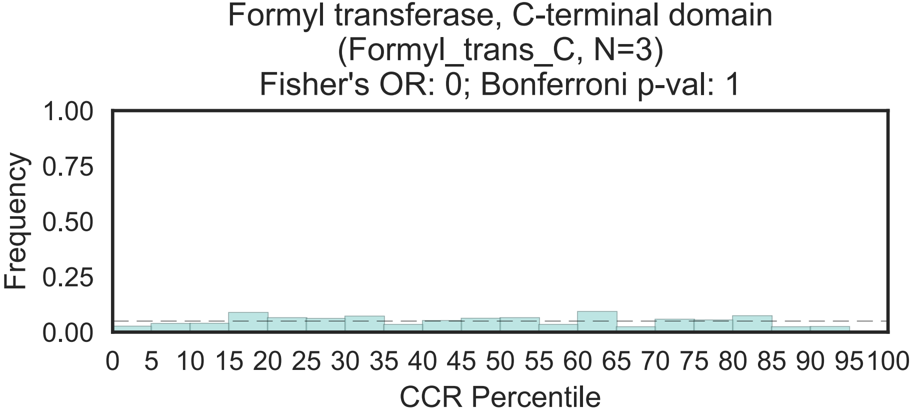


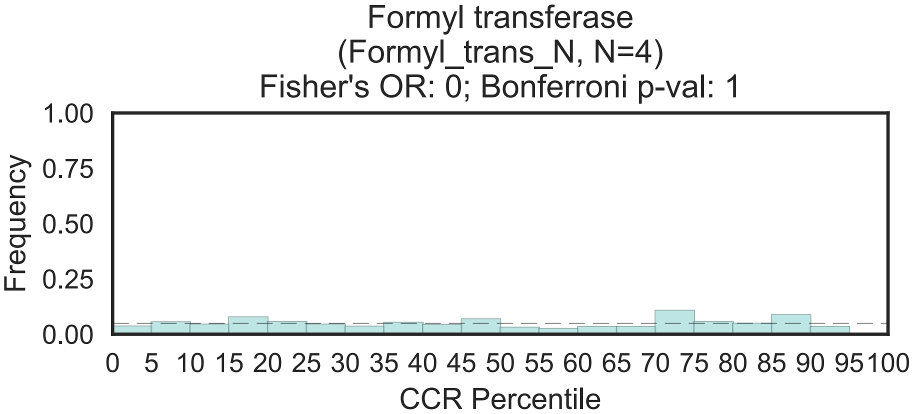
Vesicle coat protein involved in Golgi to plasma membrane transport (Folliculin, N=2)

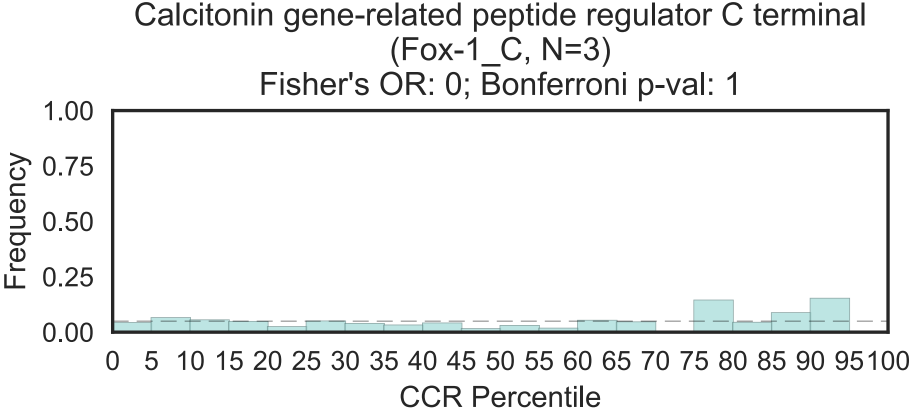

Folliculin C-terminal domain
(Folliculin_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

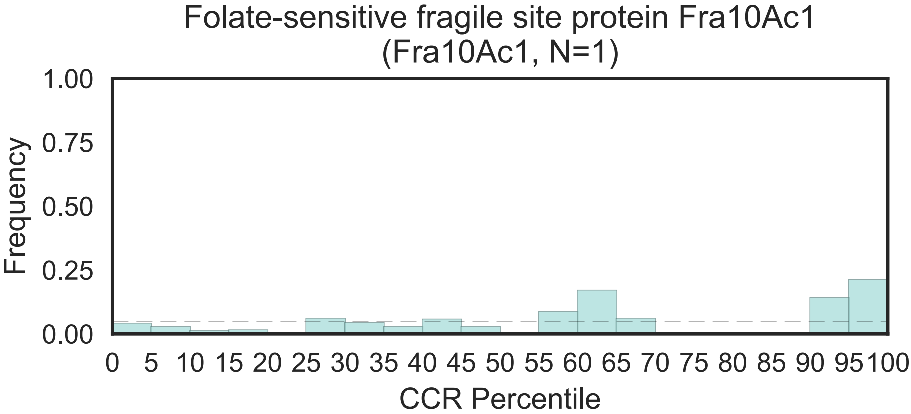

Forkhead domain
(Forkhead, N=45)
Fisher's OR: 4.17; Bonferroni p-val: 4.19e-07
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Forkhead N-terminal region
(Forkhead_N, N=3)
Fisher's OR: 0.588; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

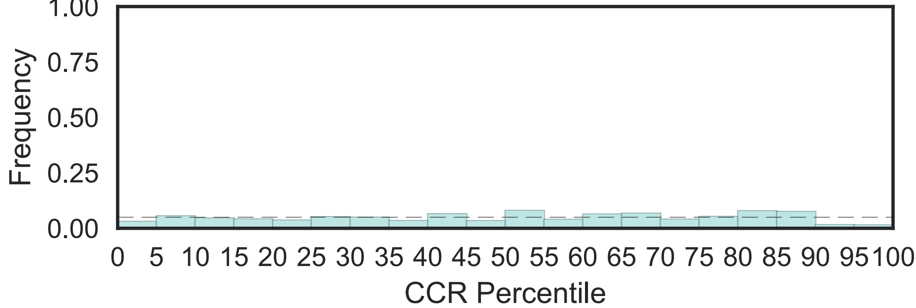

Formyl transferase, C-terminal domain
(Formyl_trans_C, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

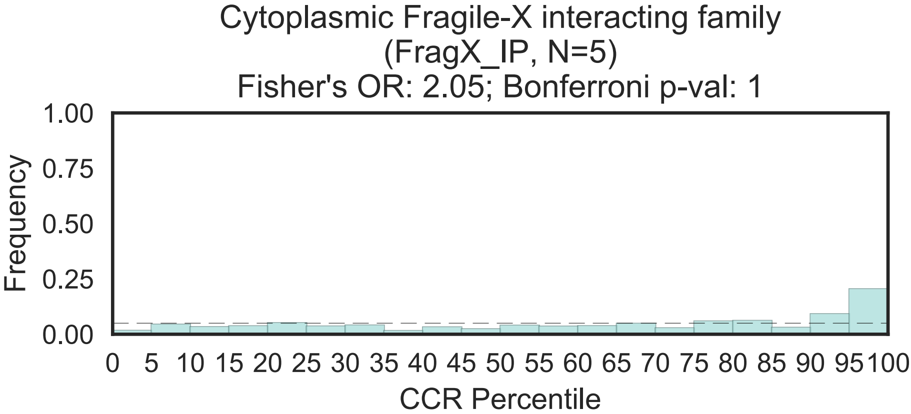

Formyl transferase
(Formyl_trans_N, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

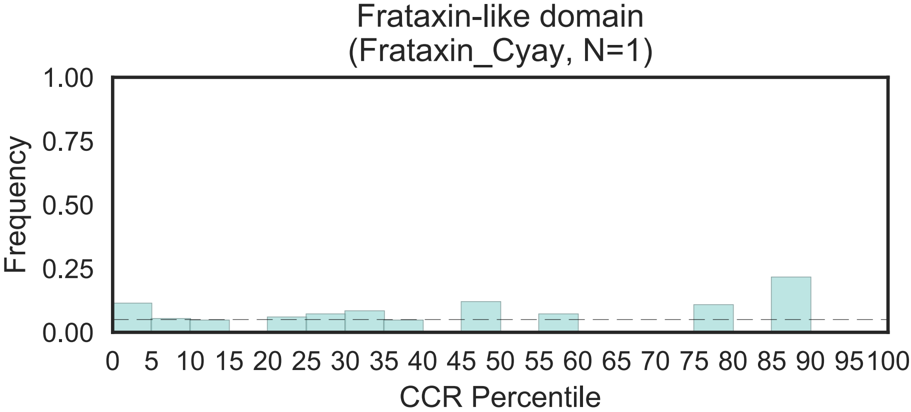

Calcitonin gene-related peptide regulator C terminal
(Fox-1_C, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

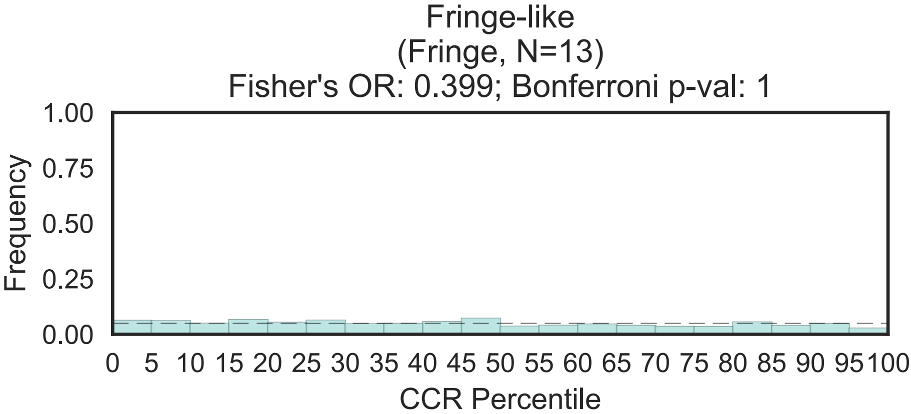

Folate-sensitive fragile site protein Fra10Ac1
(Fra10Ac1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

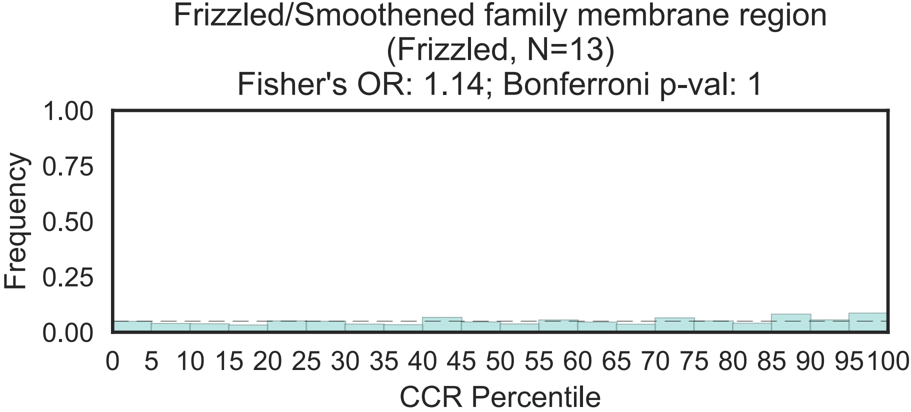
Frag1/DRAM/Sfk1 family
(Frag1, N=6)
Fisher's OR: 0.206; Bonferroni p-val: 1

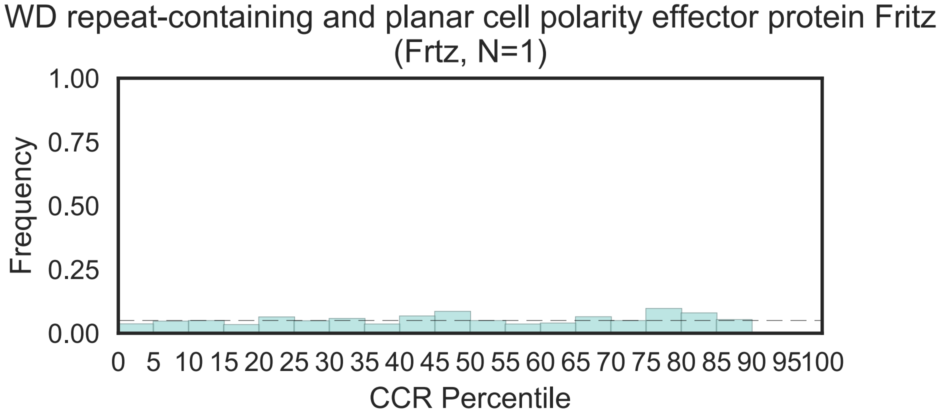


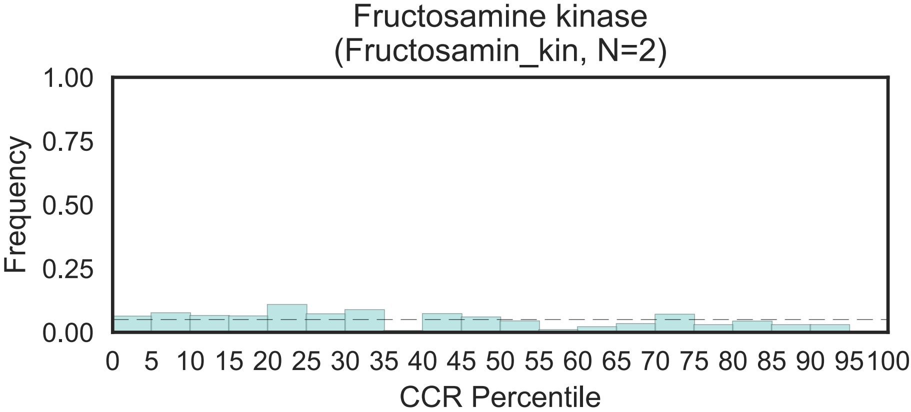

Cytoplasmic Fragile-X interacting family
(FragX_IP, N=5)
Fisher's OR: 2.05; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

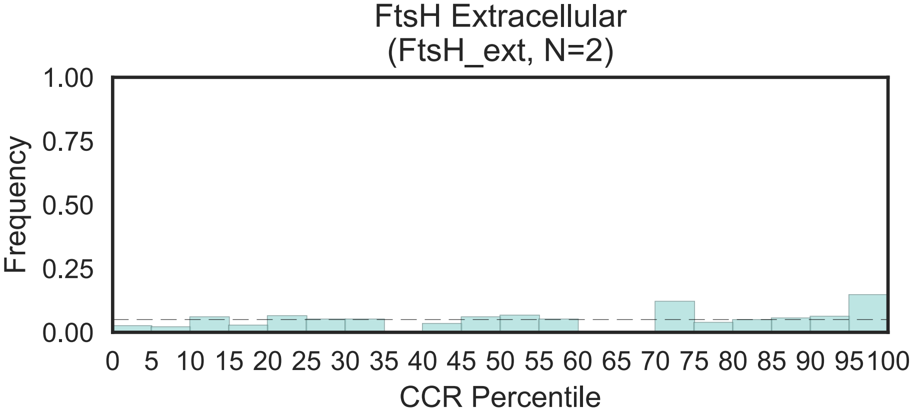

Frataxin-like domain
(Frataxin_Cyay, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

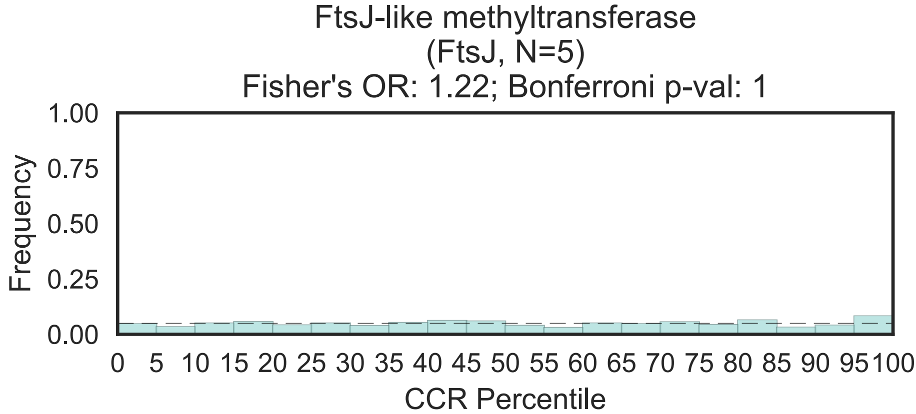

Fringe-like
(Fringe, N=13)
Fisher's OR: 0.399; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

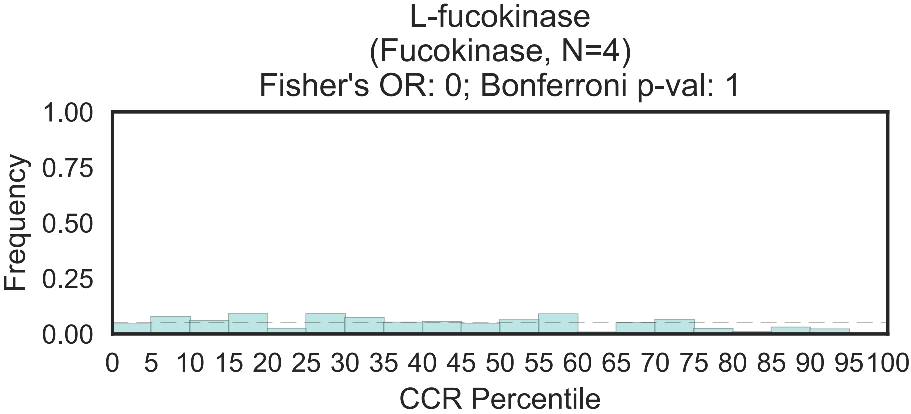

Frizzled/Smoothened family membrane region
(Frizzled, N=13)
Fisher's OR: 1.14; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

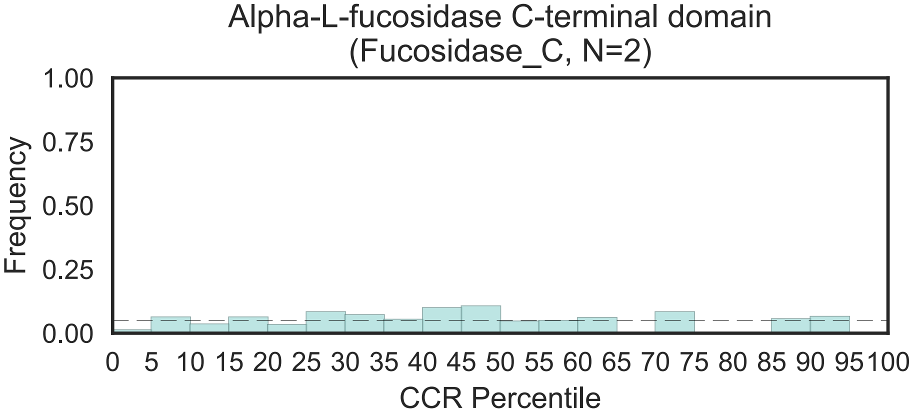

WD repeat-containing and planar cell polarity effector protein Fritz
(Frtz, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

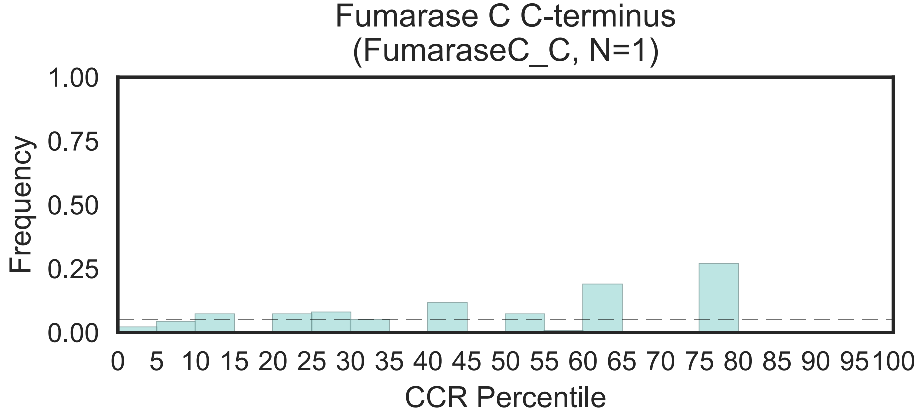

Fructosamine kinase
(Fructosamin_kin, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

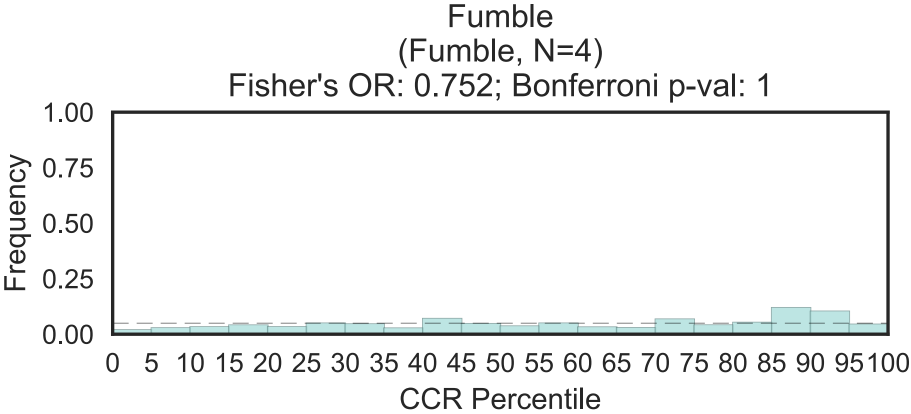

FtsH Extracellular
(FtsH_ext, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

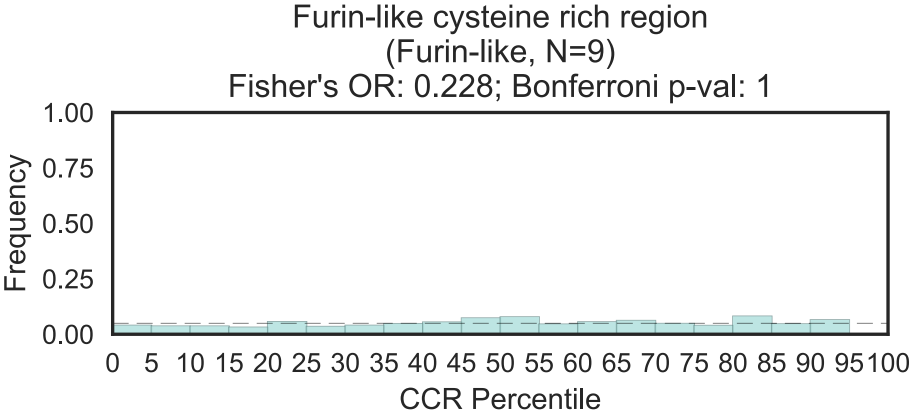

FtsJ-like methyltransferase
(FtsJ, N=5)
Fisher's OR: 1.22; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

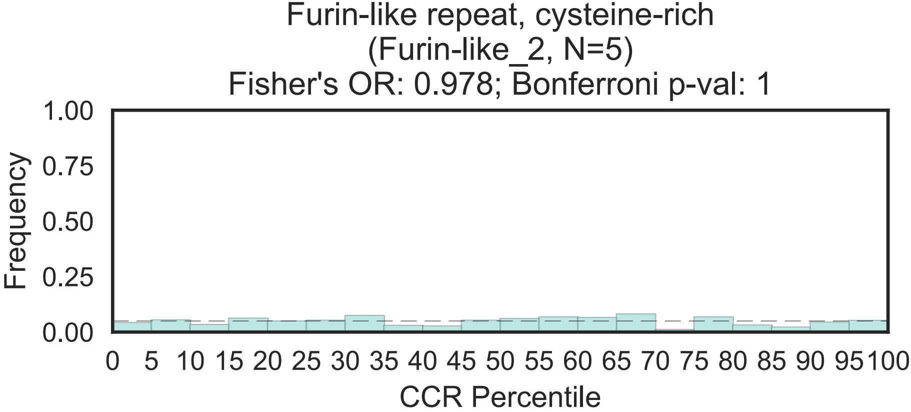

L-fucokinase
(Fucokinase, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

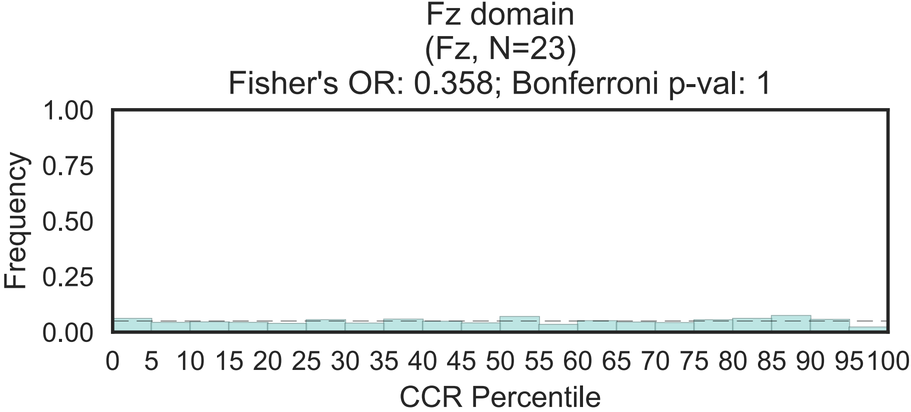

Alpha-L-fucosidase C-terminal domain
(Fucosidase_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

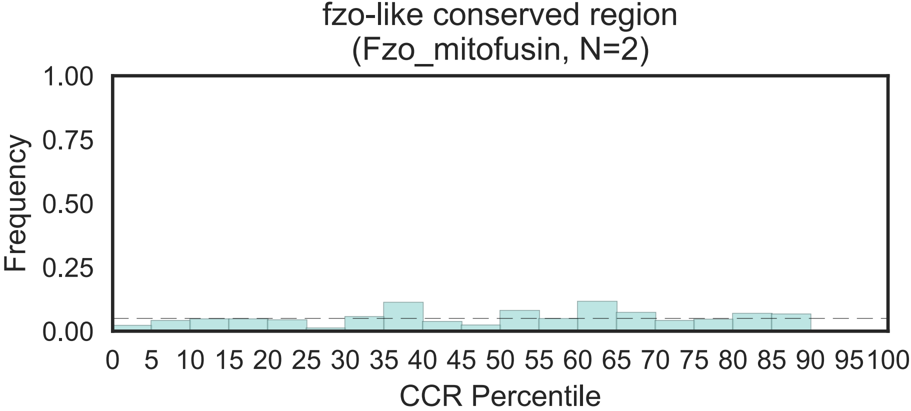

Fumarase C C-terminus
(FumaraseC_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

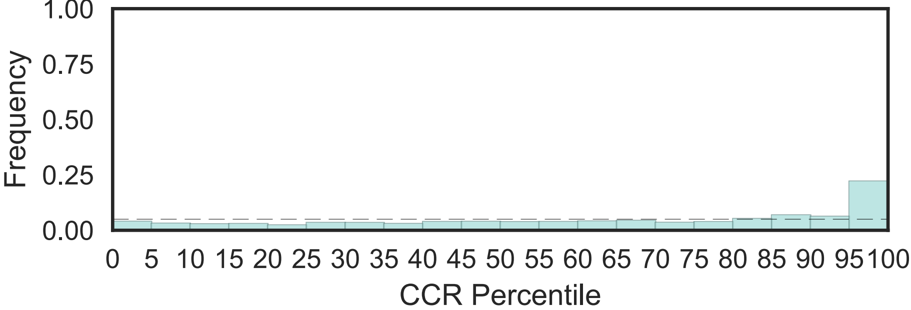

Fumble
(Fumble, N=4)
Fisher's OR: 0.752; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Furin-like cysteine rich region
(Furin-like, N=9)
Fisher's OR: 0.228; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

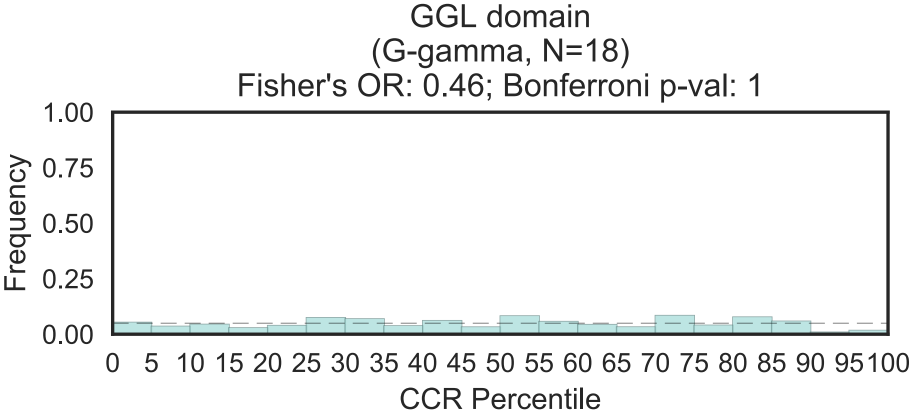

Furin-like repeat, cysteine-rich
(Furin-like_2, N=5)
Fisher's OR: 0.978; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

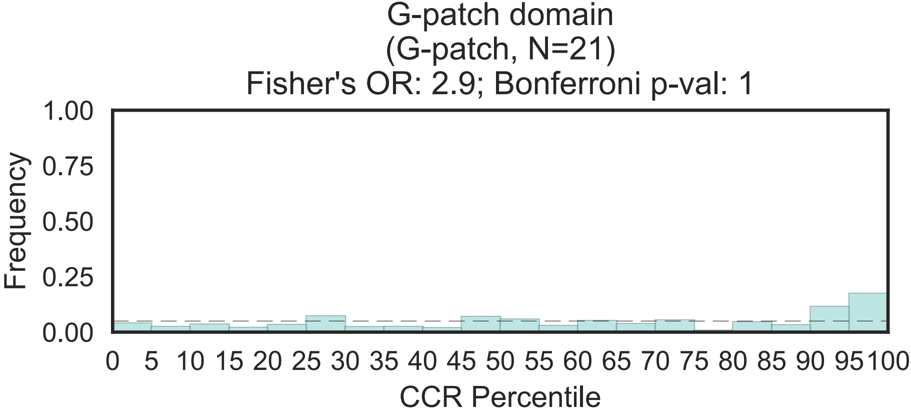

Fz domain
(Fz, N=23)
Fisher's OR: 0.358; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


fzo-like conserved region
(Fzo_mitofusin, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

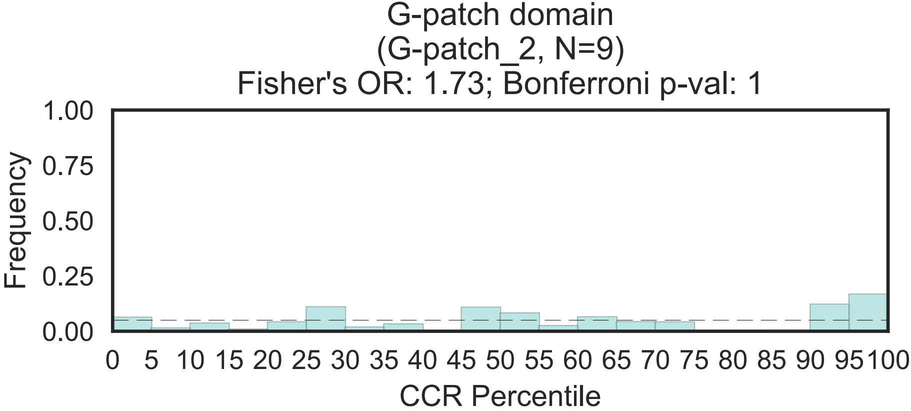


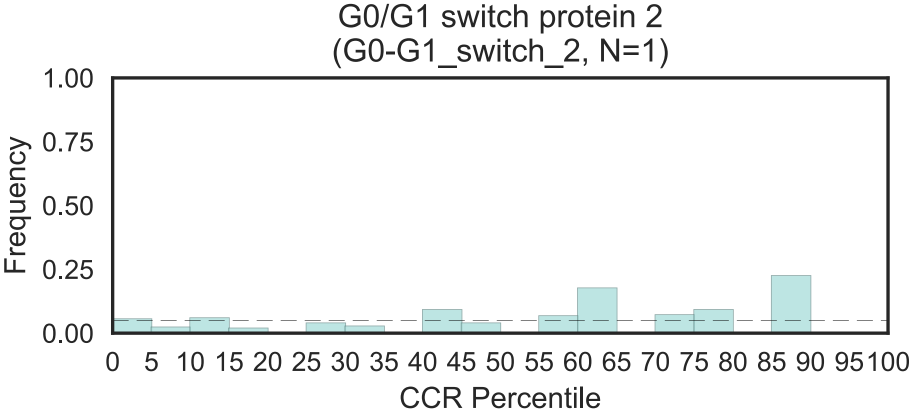
G-protein alpha subunit
(G-alpha, N=17)
Fisher's OR: 3.05; Bonferroni p-val: 1.12e-07

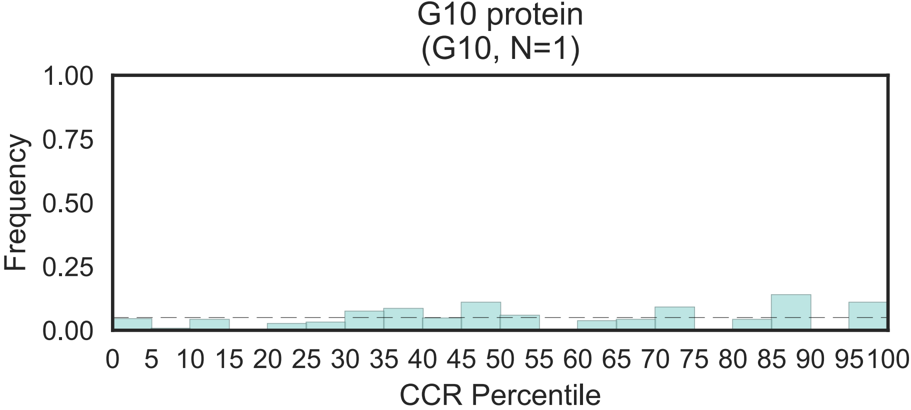

GGL domain
(G-gamma, N=18)
Fisher's OR: 0.46; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

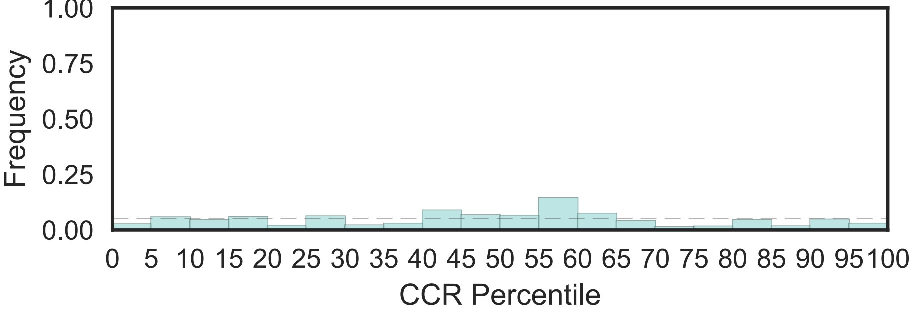


G-patch domain
(G-patch, N=21)
Fisher's OR: 2.9; Bonferroni p-val: 1

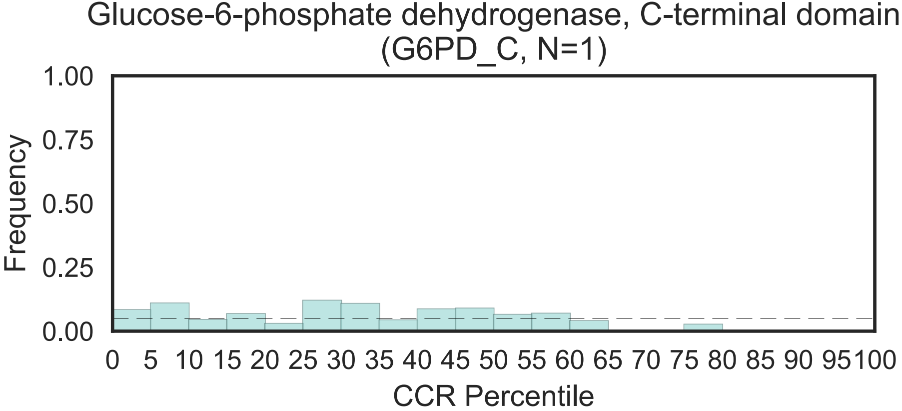

G-patch domain
(G-patch_2, N=9)
Fisher's OR: 1.73; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

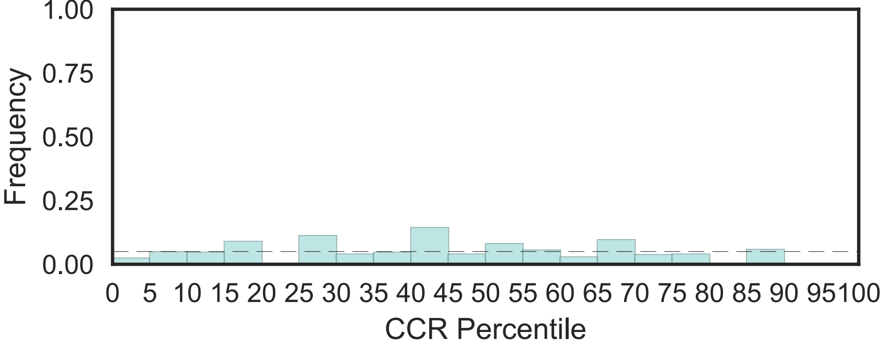

G0/G1 switch protein 2
(G0-G1_switch_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


G10 protein
(G10, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

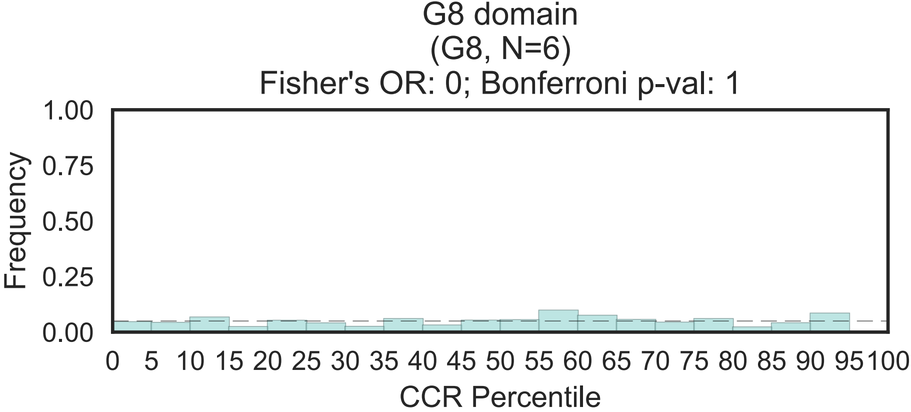


G2F domain
(G2F, N=3)
Fisher's OR: 0.498; Bonferroni p-val: 1

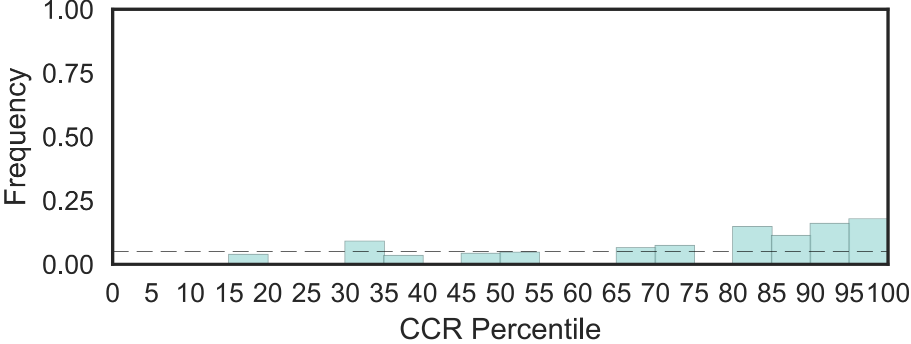

Glucose-6-phosphate dehydrogenase, C-terminal domain
(G6PD_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

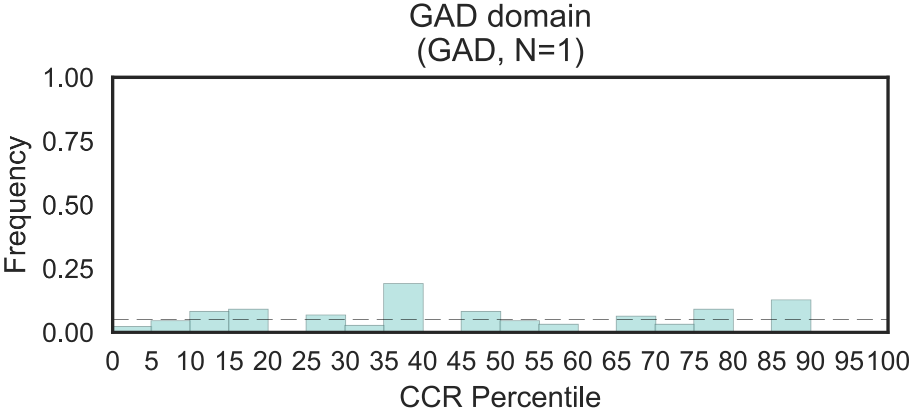


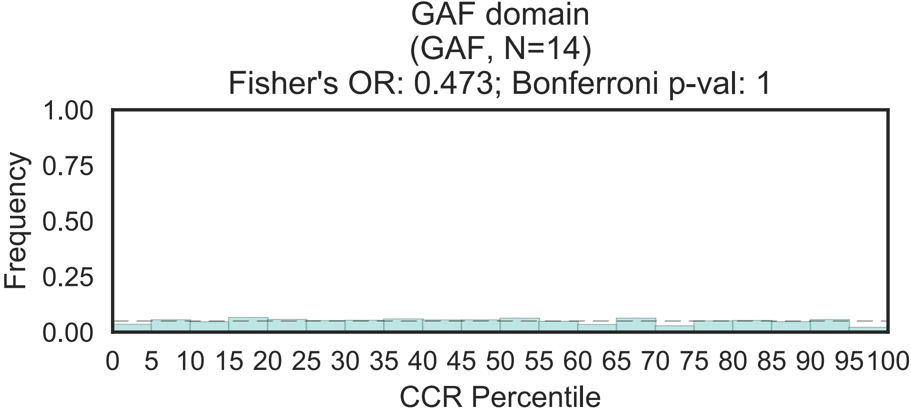
Glucose-6-phosphate dehydrogenase, NAD binding domain
(G6PD_N, N=1)

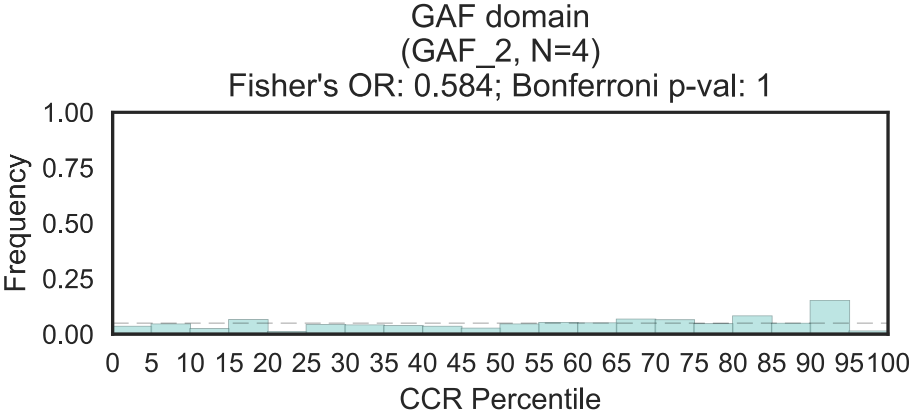

G8 domain
(G8, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

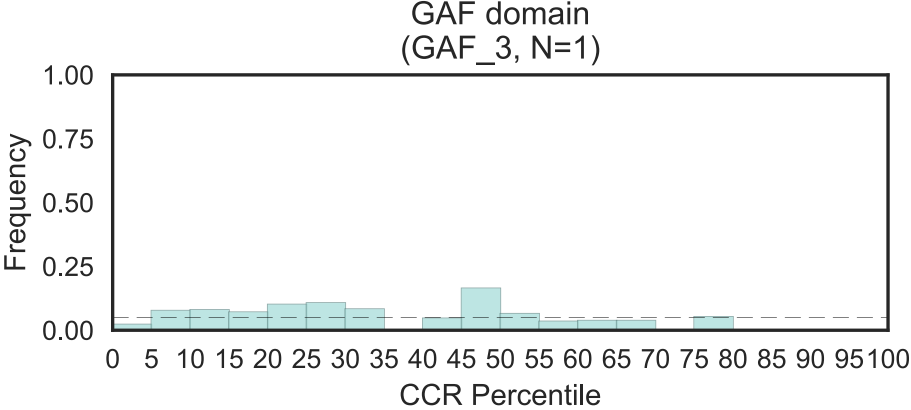
GA-binding protein alpha chain (GABP-alpha, N=1)

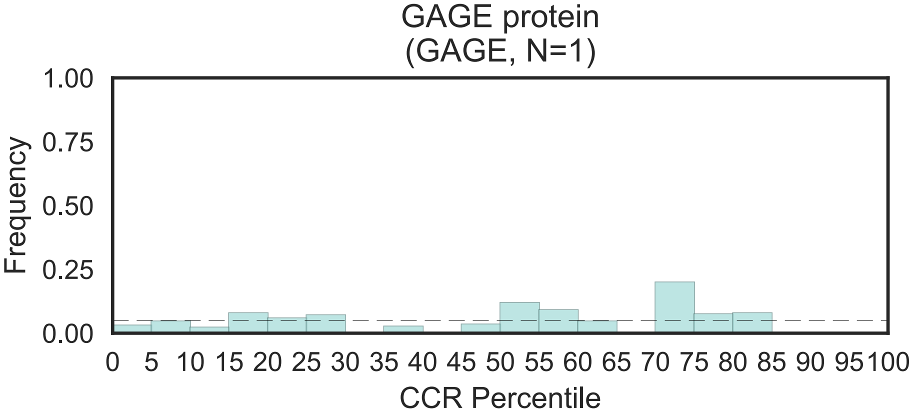


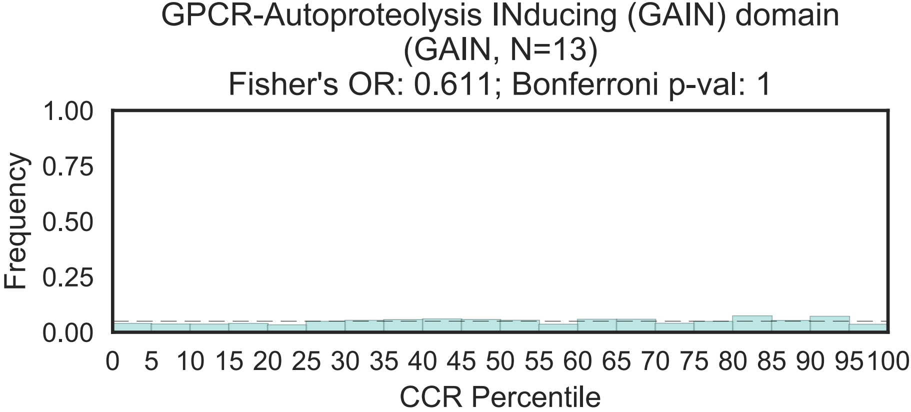

GAD domain
(GAD, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


GAF domain
(GAF, N=14)
Fisher's OR: 0.473; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


GAF domain
(GAF_2, N=4)
Fisher's OR: 0.584; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

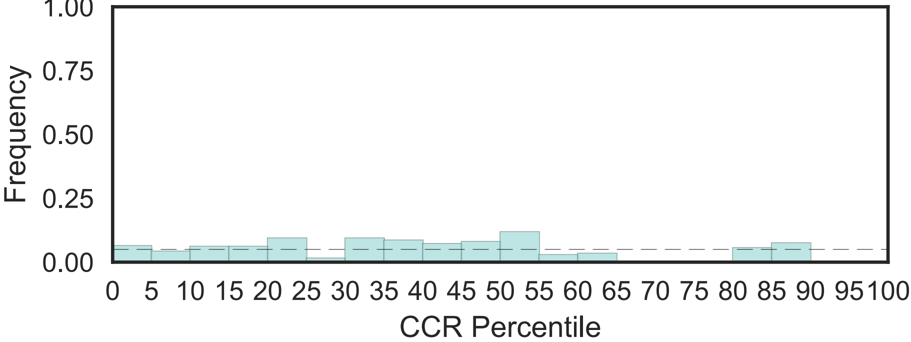

GAF domain
(GAF_3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

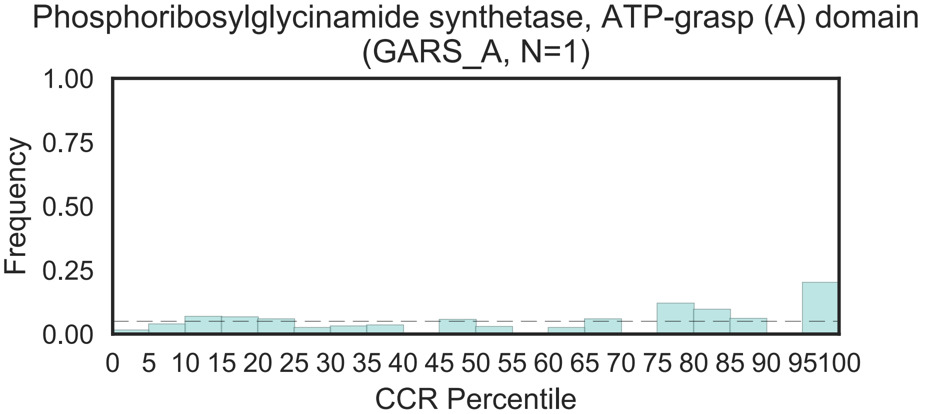

GAGE protein
(GAGE, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

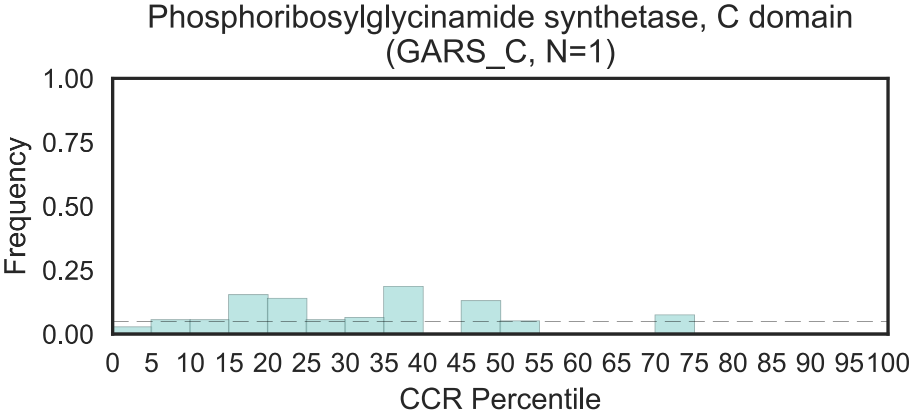


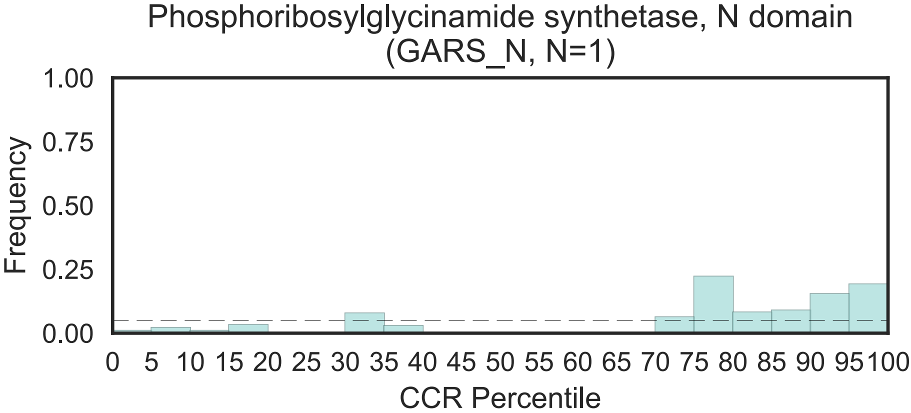
GPCR-Autoproteolysis INducing (GAIN) domain
(GAIN, N=13)
Fisher's OR: 0.611; Bonferroni p-val: 1

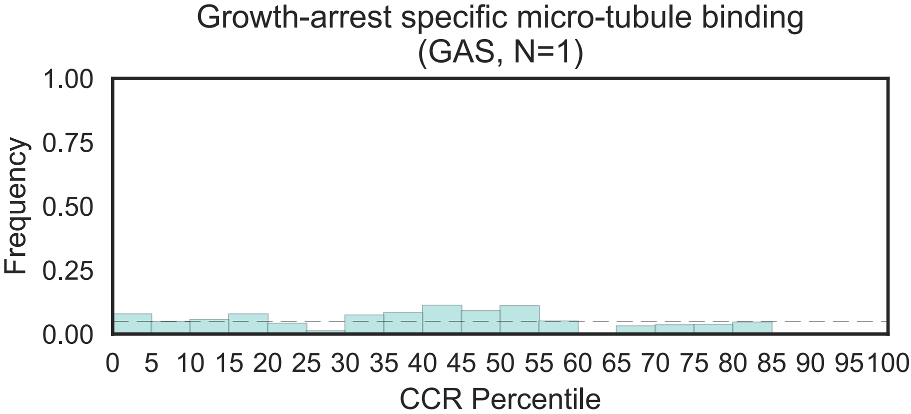
GRB2-binding adapter (GAPT)
(GAPT, N=1)



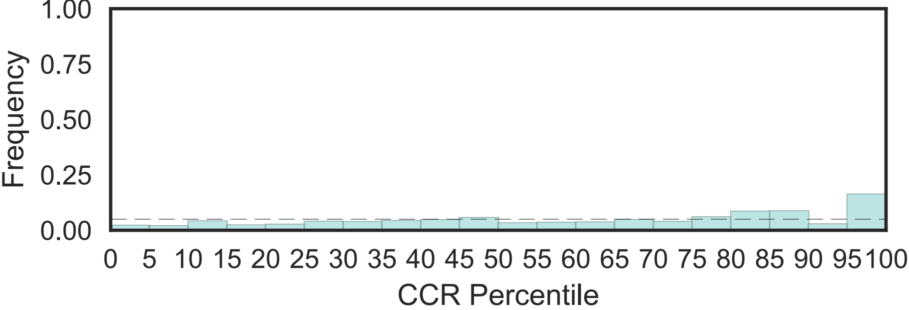

Phosphoribosylglycinamide synthetase, ATP-grasp (A) domain
(GARS_A, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

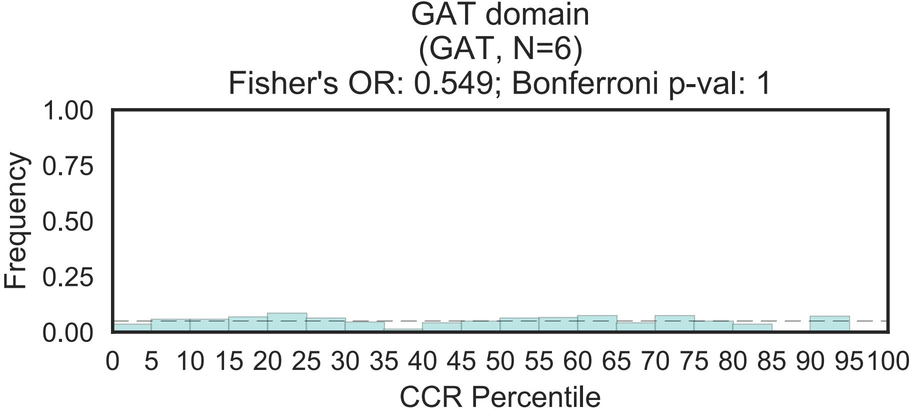

Phosphoribosylglycinamide synthetase, C domain
(GARS_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

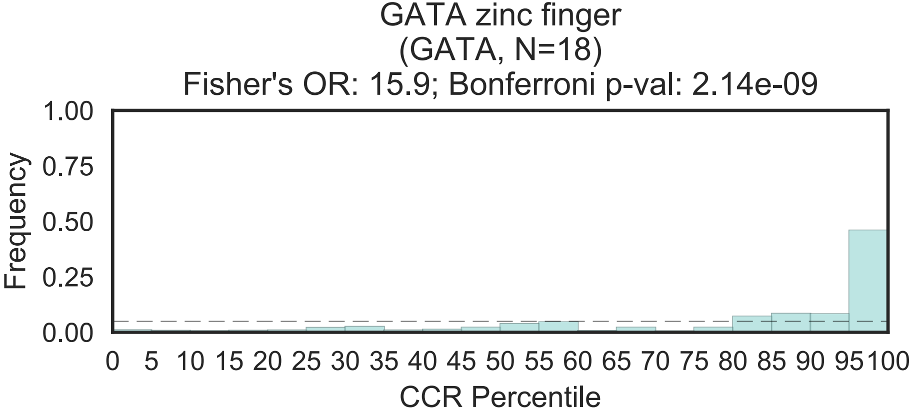

Phosphoribosylglycinamide synthetase, N domain
(GARS_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

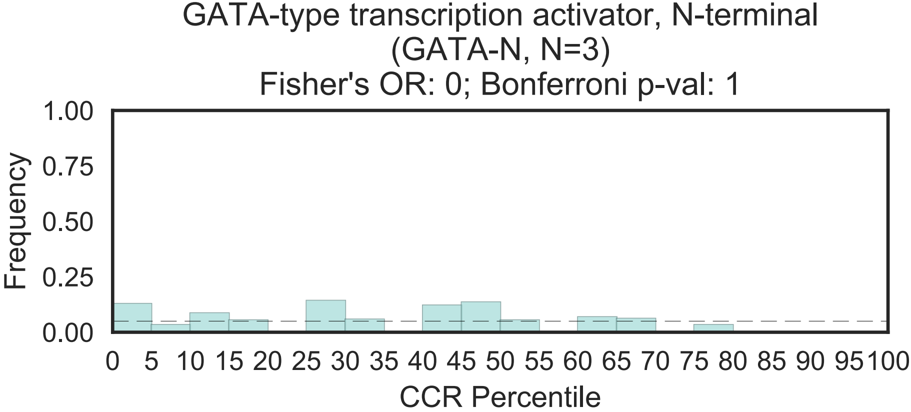

Growth-arrest specific micro-tubule binding
(GAS, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

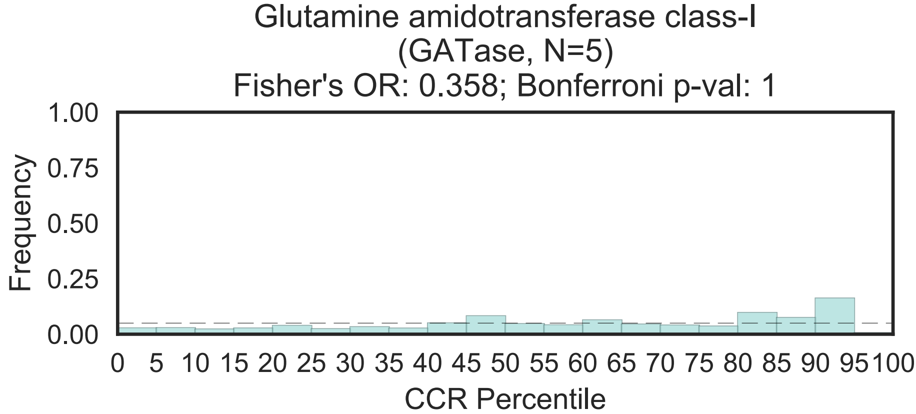
Growth-Arrest-Specific Protein 2 Domain
(GAS2, N=6)
Fisher's OR: 3.05; Bonferroni p-val: 1

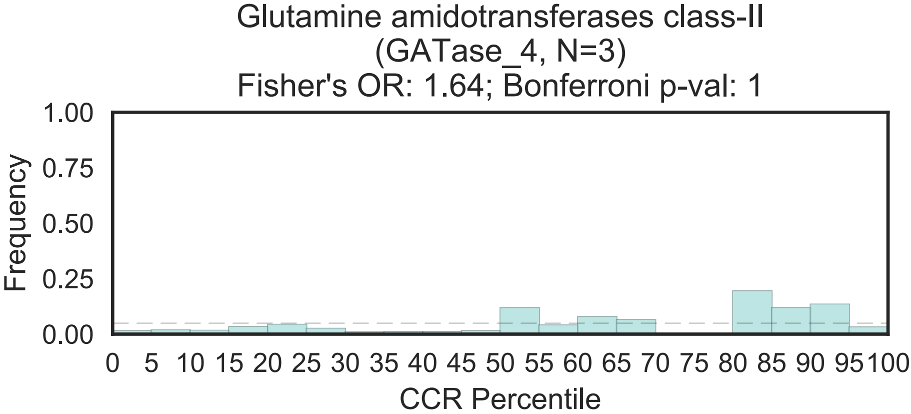


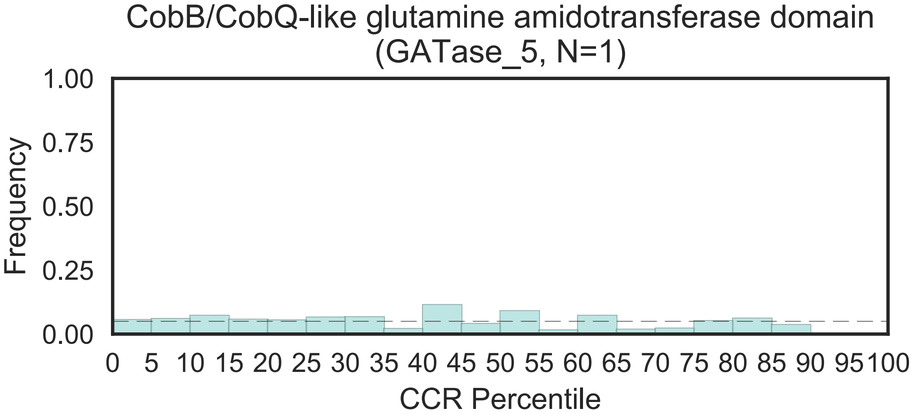

GAT domain
(GAT, N=6)
Fisher's OR: 0.549; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

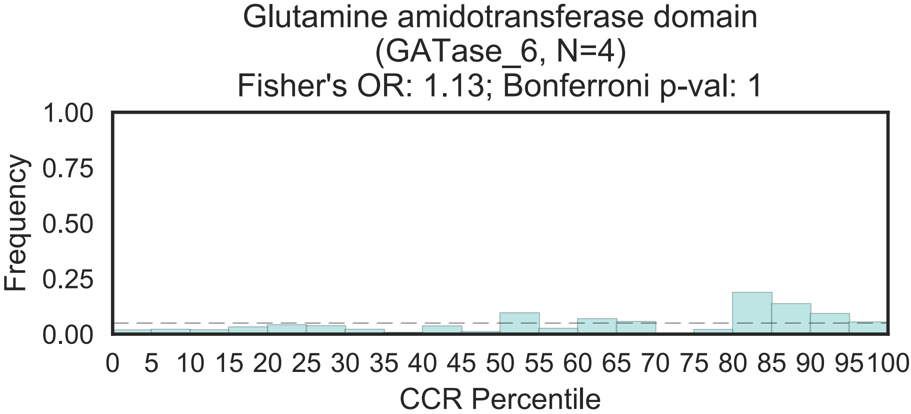

GATA zinc finger
(GATA, N=18)
Fisher's OR: 15.9; Bonferroni p-val: 2.14e-09
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

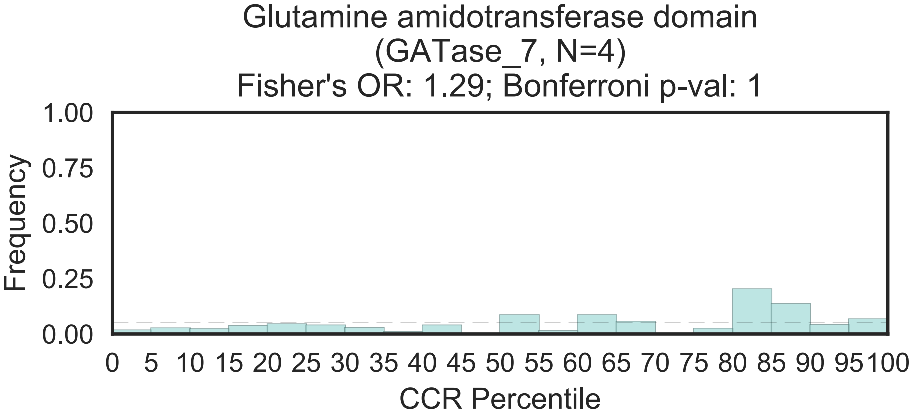

GATA-type transcription activator, N-terminal
(GATA-N, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Glutamine amidotransferase class-I
(GATase, N=5)
Fisher's OR: 0.358; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

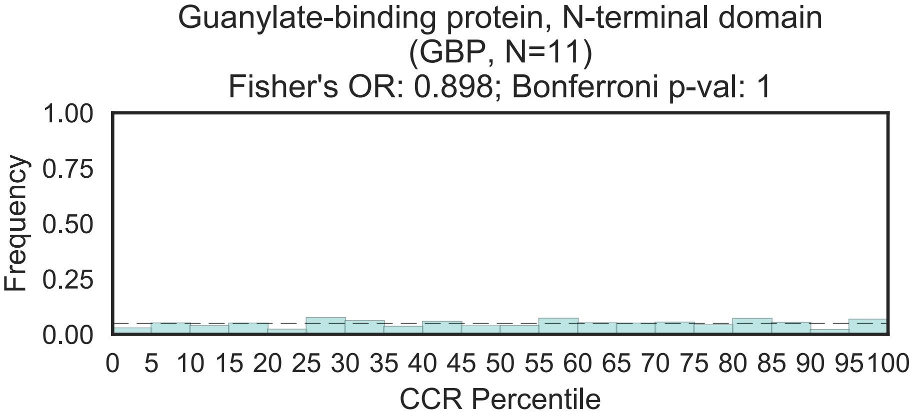

Glutamine amidotransferases class-II
(GATase_4, N=3)
Fisher's OR: 1.64; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

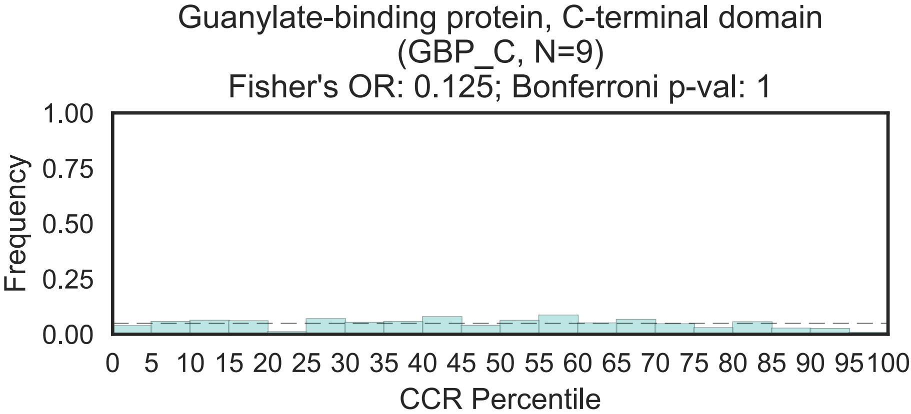

CobB/CobQ-like glutamine amidotransferase domain
(GATase_5, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Glutamine amidotransferase domain
(GATase_6, N=4)
Fisher's OR: 1.13; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

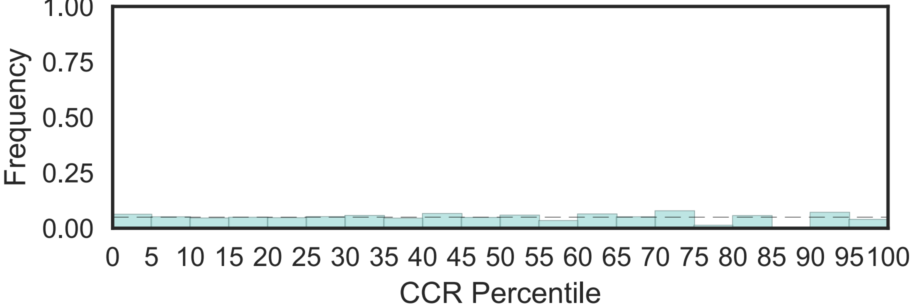


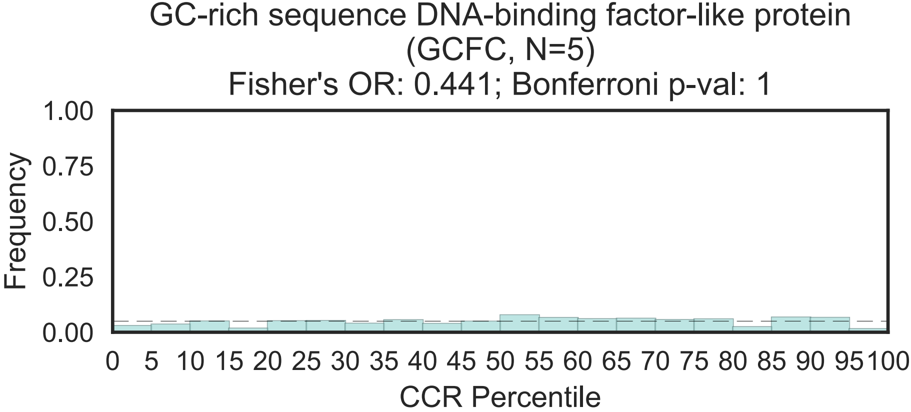
Glutamine amidotransferase domain
(GATase_7, N=4)
Fisher's OR: 1.29; Bonferroni p-val: 1

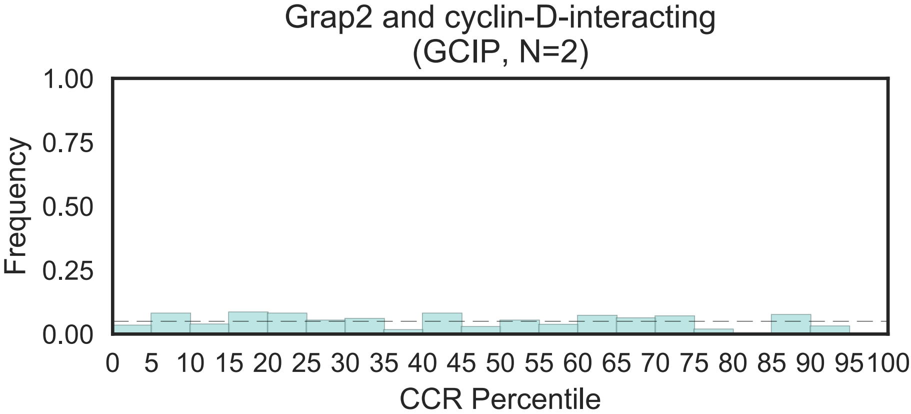

Guanylate-binding protein, N-terminal domain
(GBP, N=11)
Fisher's OR: 0.898; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

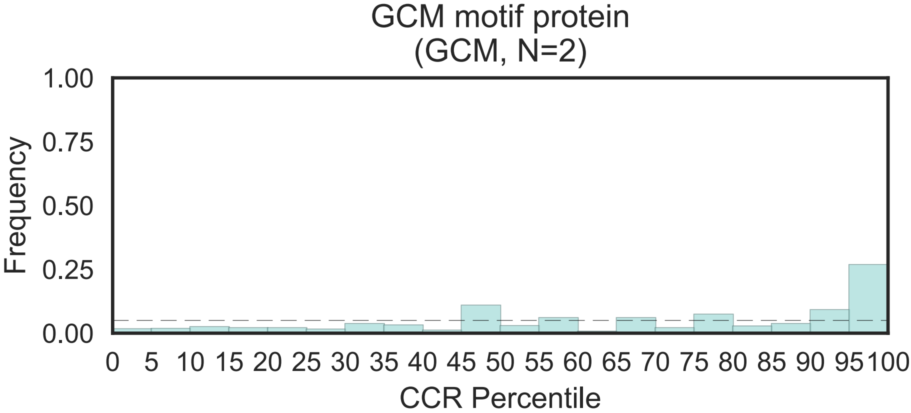

Guanylate-binding protein, C-terminal domain
(GBP_C, N=9)
Fisher's OR: 0.125; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

tRNA methyltransferase complex GCD14 subunit
(GCD14, N=3)
Fisher's OR: 0.476; Bonferroni p-val: 1

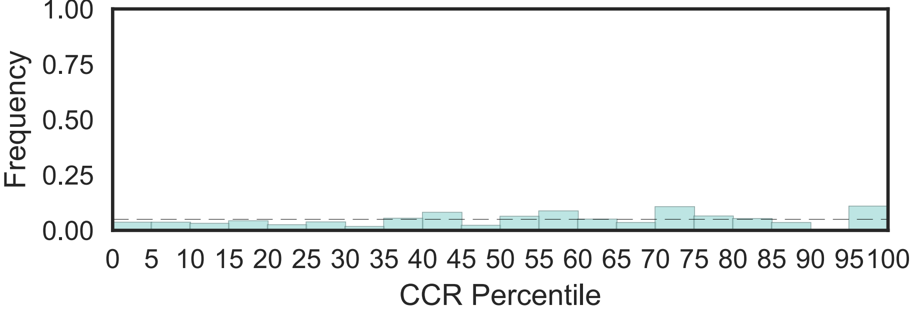


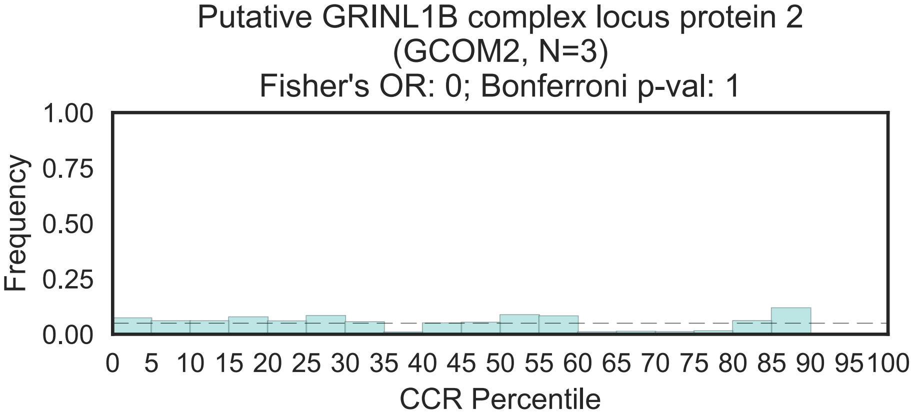

GC-rich sequence DNA-binding factor-like protein
(GCFC, N=5)
Fisher's OR: 0.441; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

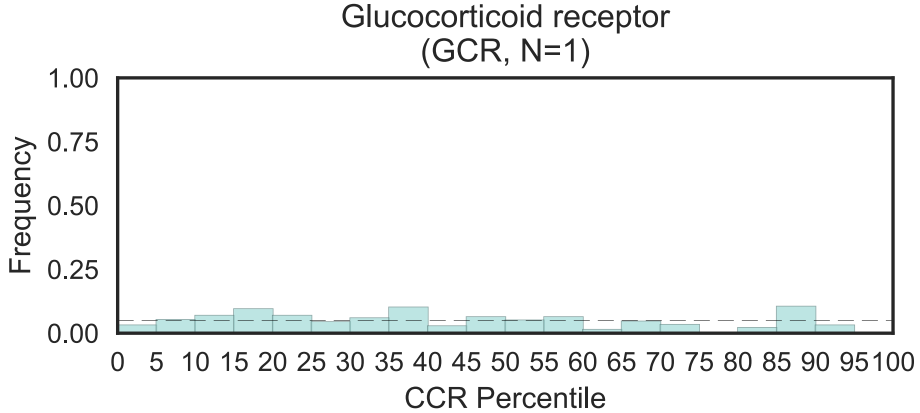

Grap2 and cyclin-D-interacting
(GCIP, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


GCM motif protein
(GCM, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

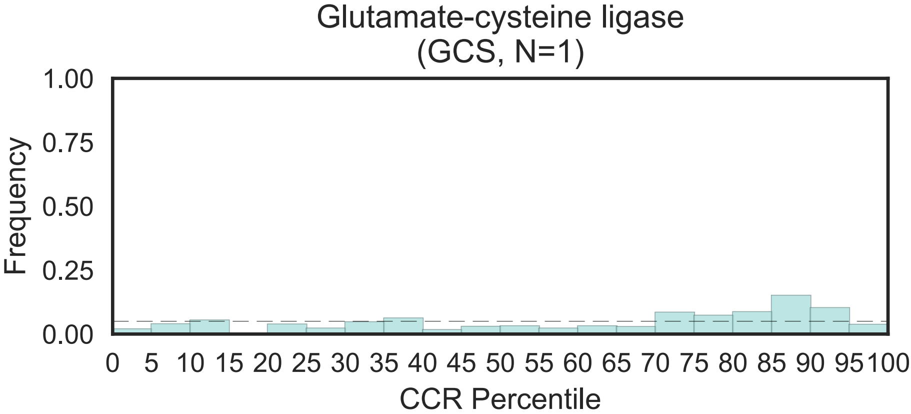
GCN5-like protein 1 (GCN5L1)
(GCN5L1, N=3)
Fisher's OR: 2.02; Bonferroni p-val: 1

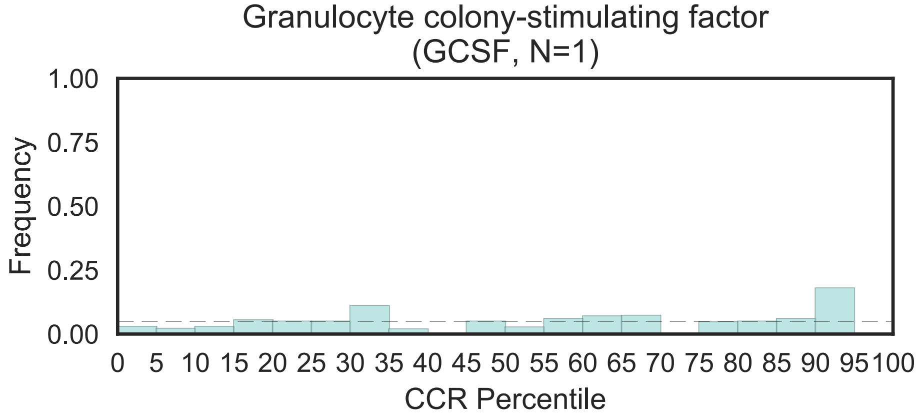


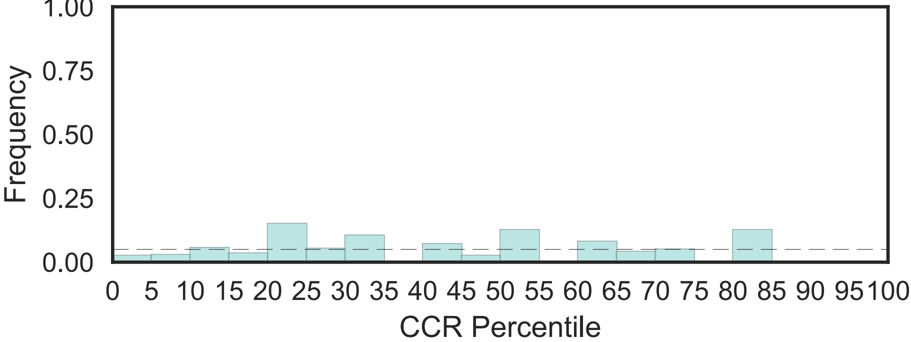

Putative GRINL1B complex locus protein 2
(GCOM2, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



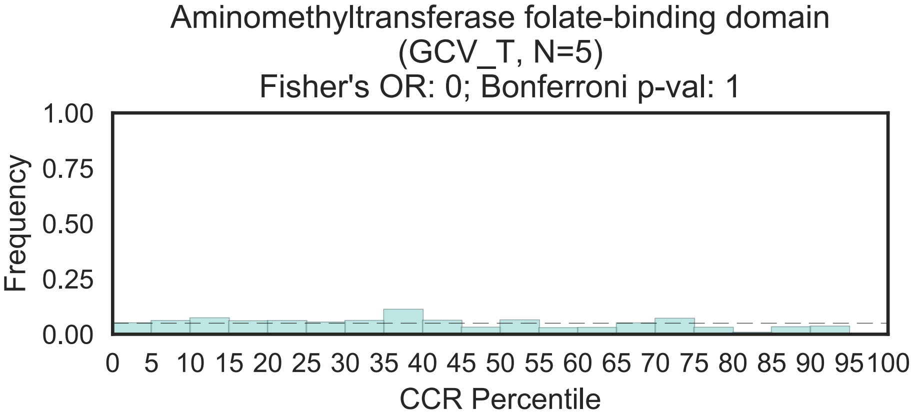
Glucocorticoid receptor
(GCR, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

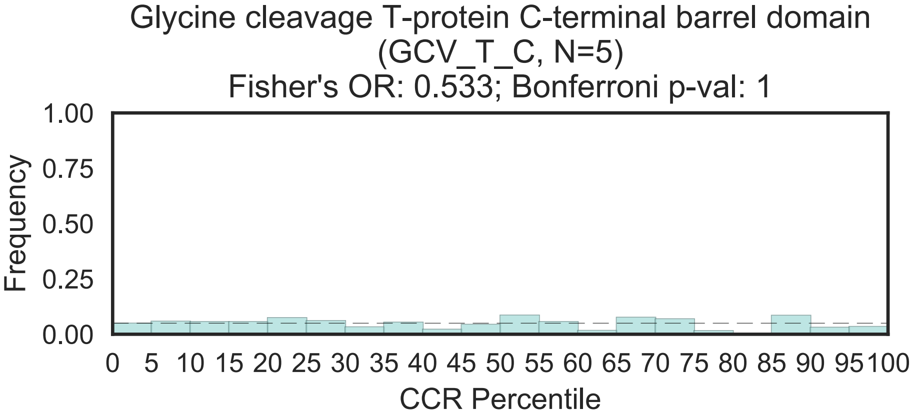

Glutamate-cysteine ligase
(GCS, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

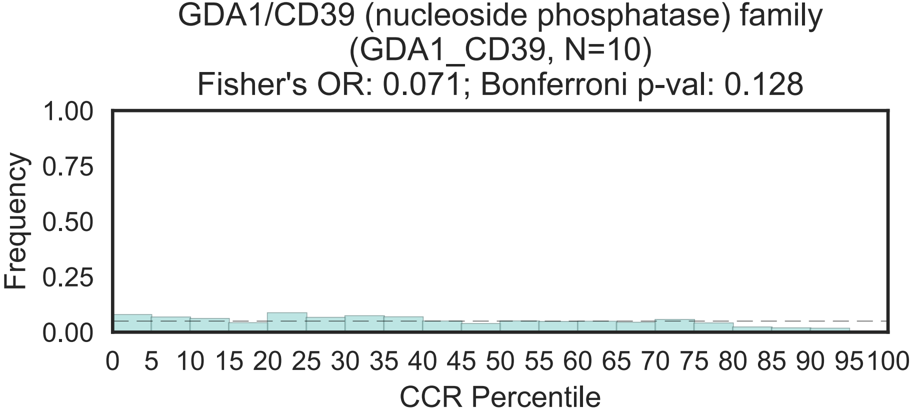

Granulocyte colony-stimulating factor
(GCSF, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

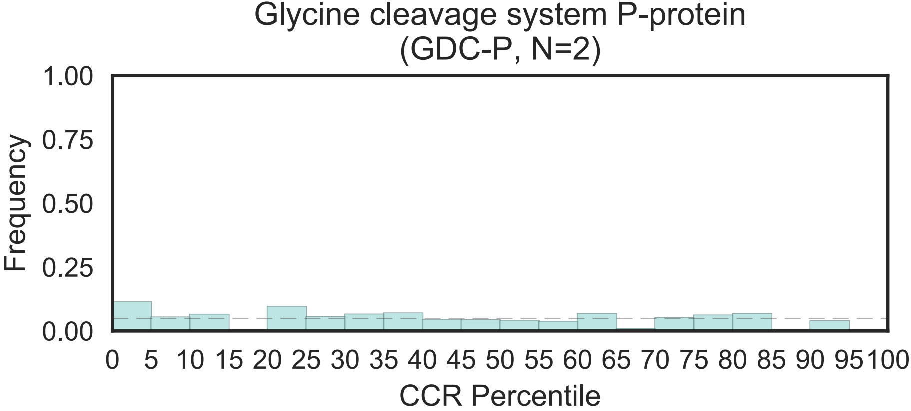


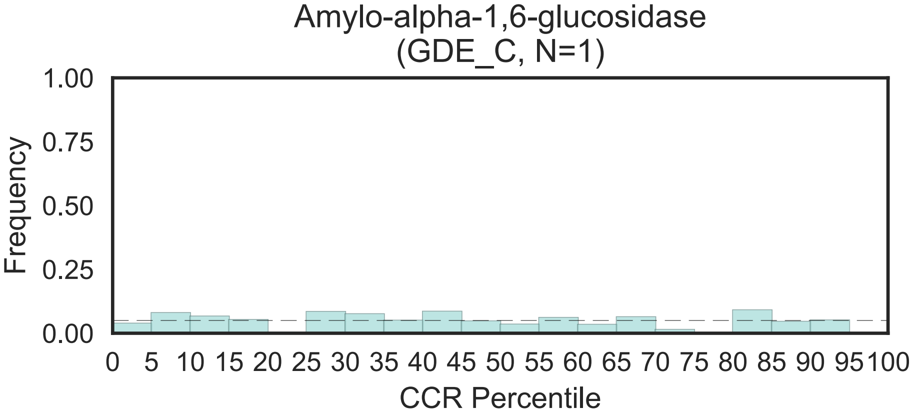
Glycine cleavage H-protein
(GCV_H, N=2)

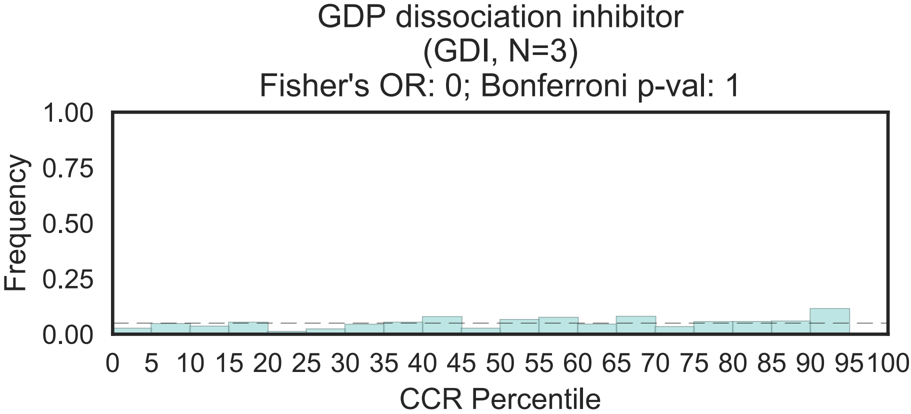

Aminomethyltransferase folate-binding domain
(GCV_T, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

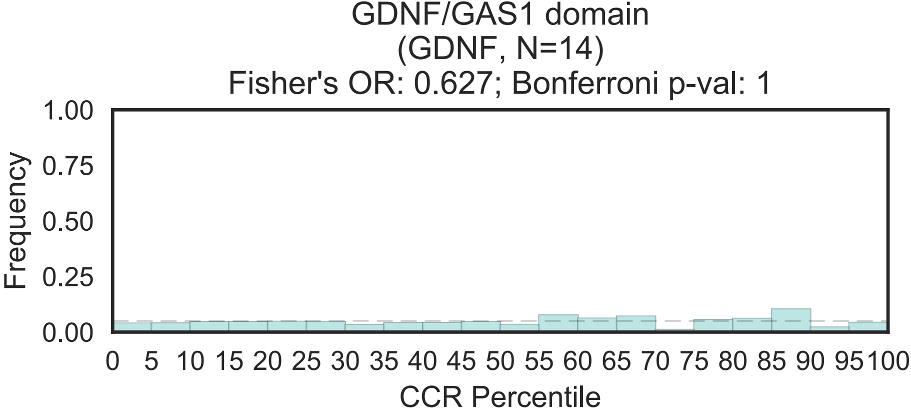

Glycine cleavage T-protein C-terminal barrel domain
(GCV_T_C, N=5)
Fisher's OR: 0.533; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

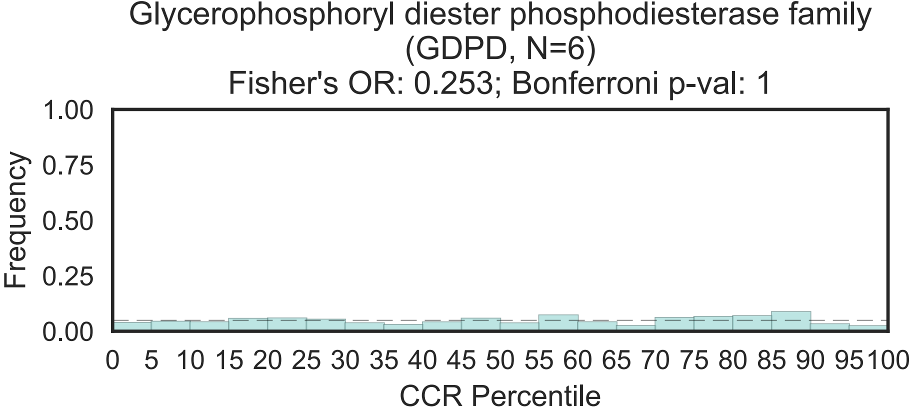

GDA1/CD39 (nucleoside phosphatase) family
(GDA1_CD39, N=10)
Fisher's OR: 0.071; Bonferroni p-val: 0.128
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Glycine cleavage system P-protein
(GDC-P, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

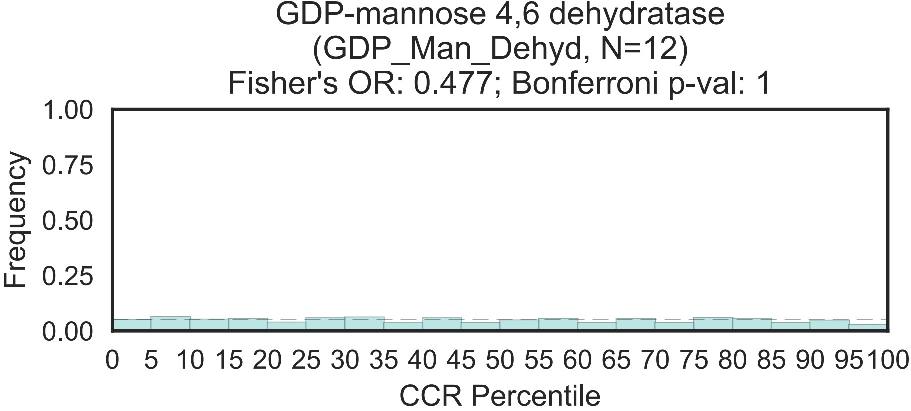

Amylo-alpha-1,6-glucosidase
(GDE_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

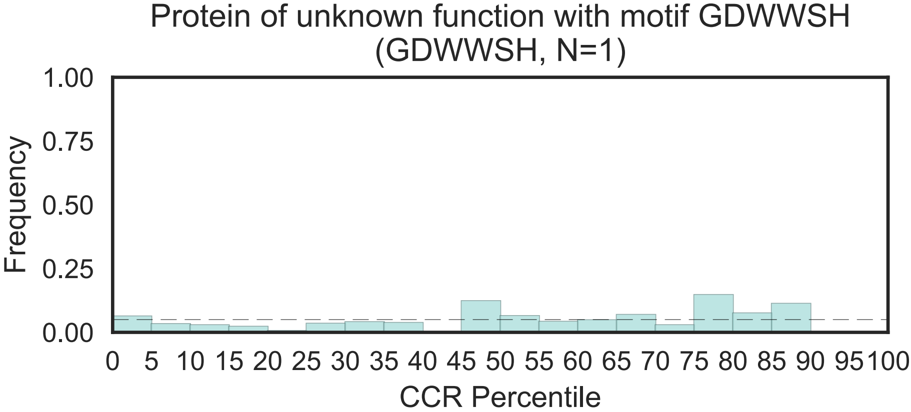

GDP dissociation inhibitor
(GDI, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

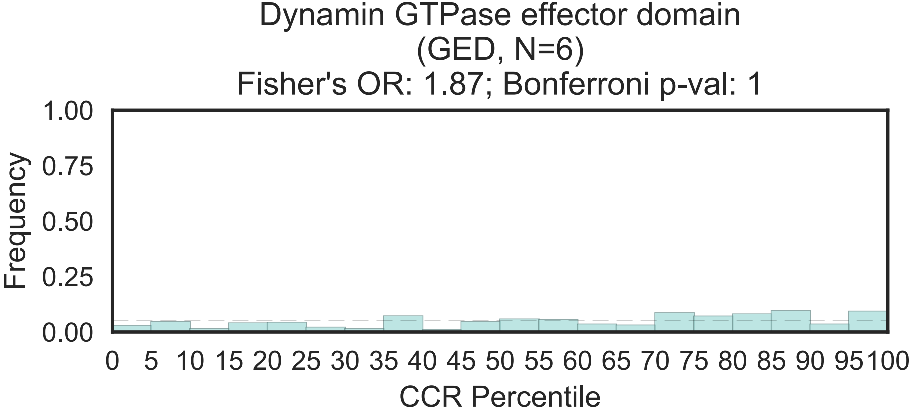

GDNF/GAS1 domain
(GDNF, N=14)
Fisher's OR: 0.627; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

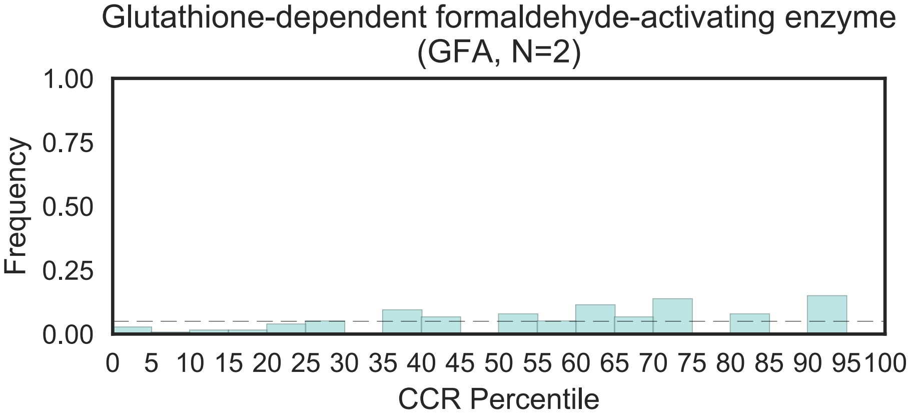


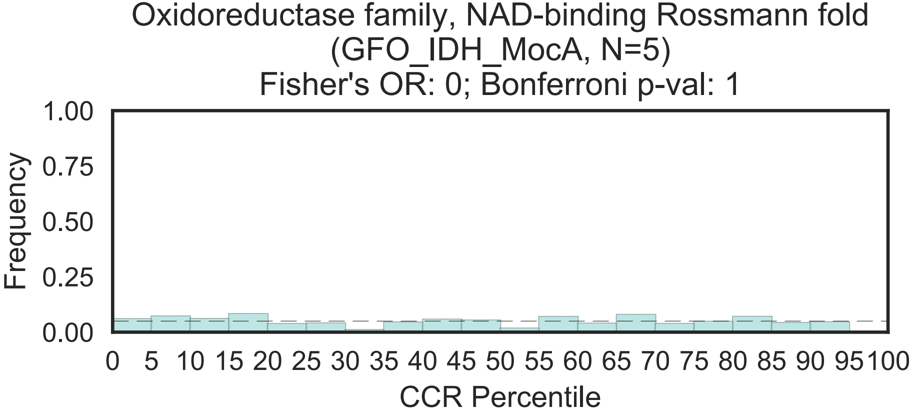
Glycerophosphoryl diester phosphodiesterase family
(GDPD, N=6)
Fisher's OR: 0.253; Bonferroni p-val: 1

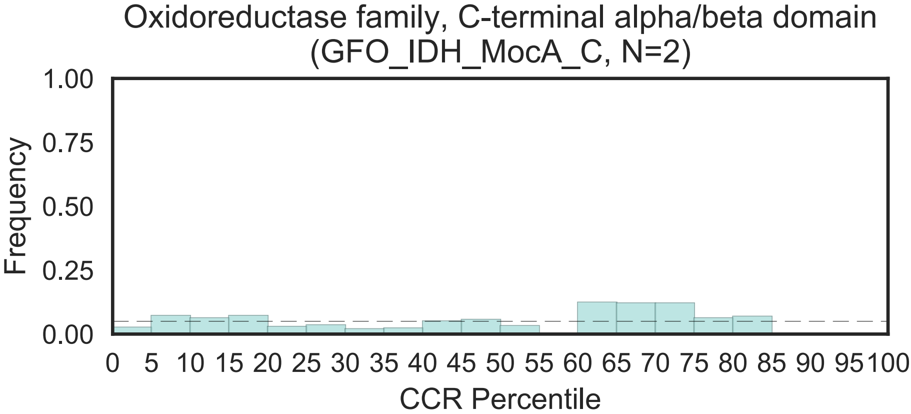

GDP-mannose 4,6 dehydratase
(GDP_Man_Dehyd, N=12)
Fisher's OR: 0.477; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

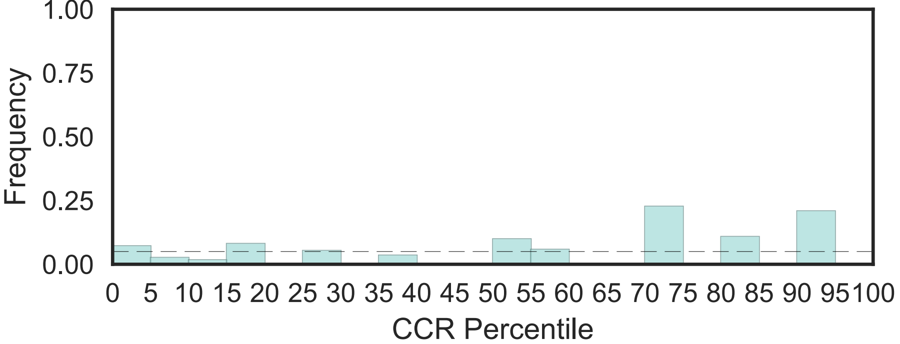

Protein of unknown function with motif GDWWSH
(GDWWSH, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Dynamin GTPase effector domain
(GED, N=6)
Fisher's OR: 1.87; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Glutathione-dependent formaldehyde-activating enzyme
(GFA, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

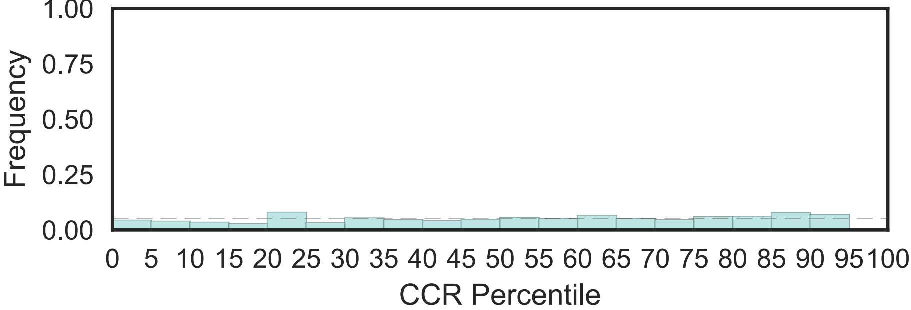

Oxidoreductase family, NAD-binding Rossmann fold
(GFO_IDH_MocA, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

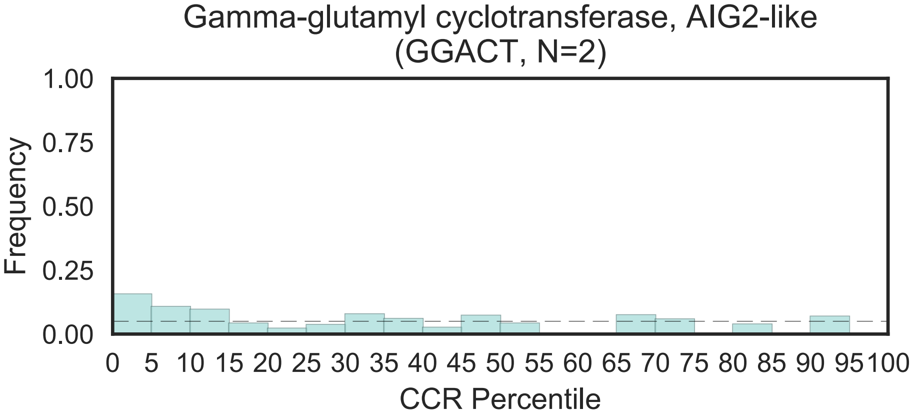

Oxidoreductase family, C-terminal alpha/beta domain
(GFO_IDH_MocA_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



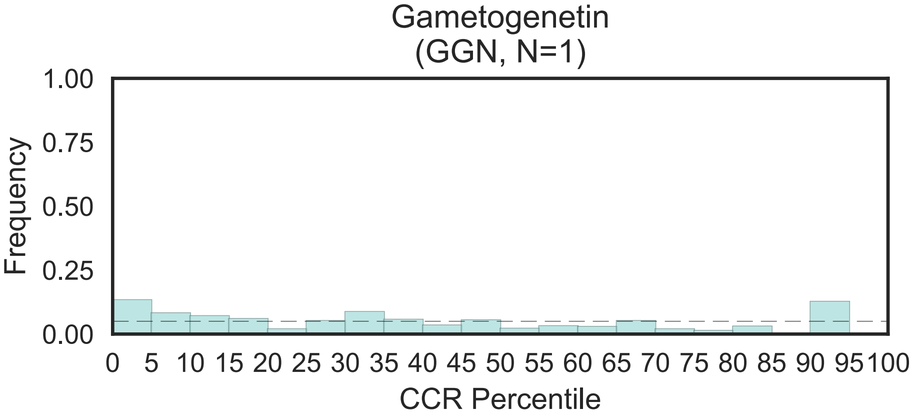
GTP cyclohydrolase I feedback regulatory protein (GFRP) (GFRP, N=1)

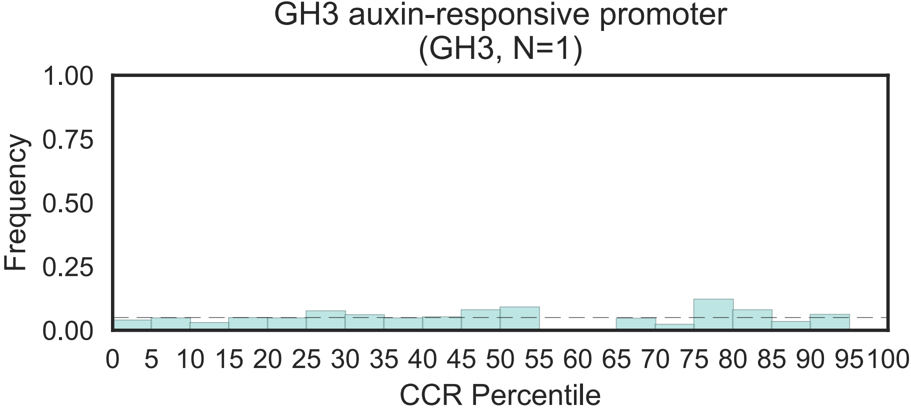
Growth factor receptor domain IV
(GF_recep_IV, N=6)
Fisher's OR: 0.342; Bonferroni p-val: 1

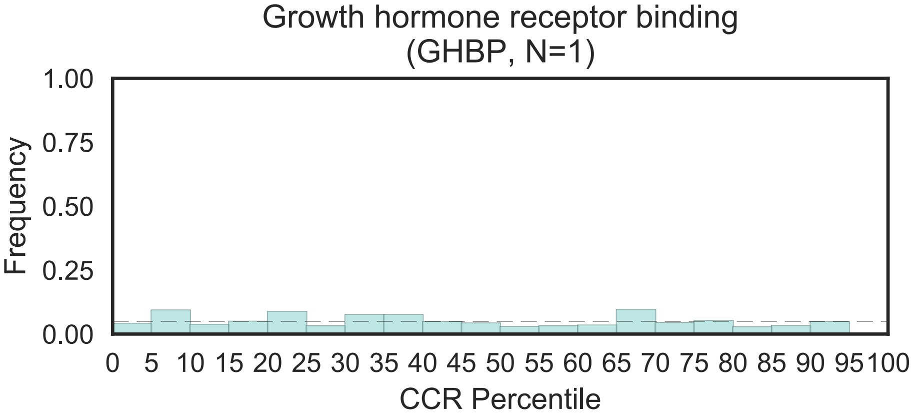


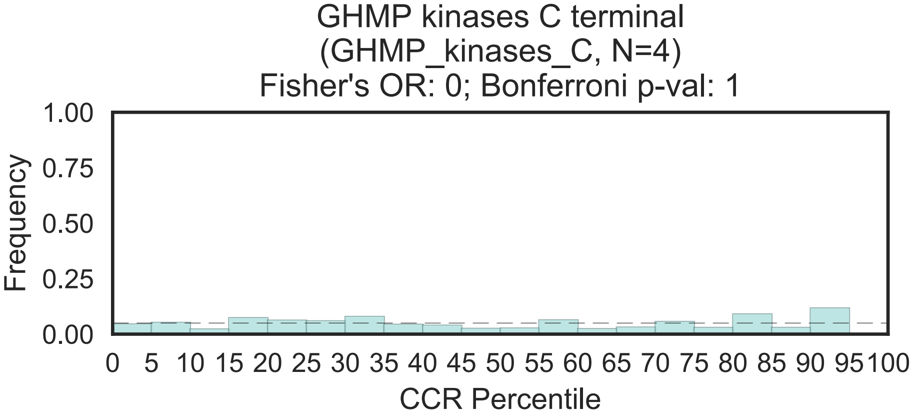


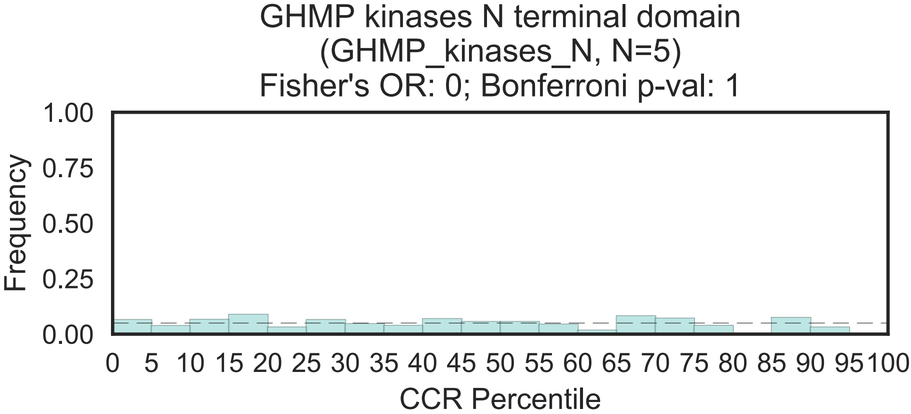
Gamma-glutamyl cyclotransferase, AIG2-like (GGACT, N=2)


Gametogenetin
(GGN, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

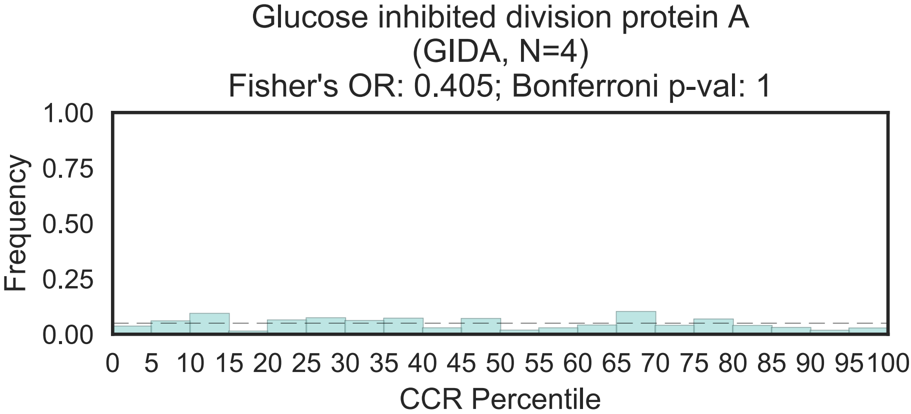

GH3 auxin-responsive promoter
(GH3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Growth hormone receptor binding
(GHBP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

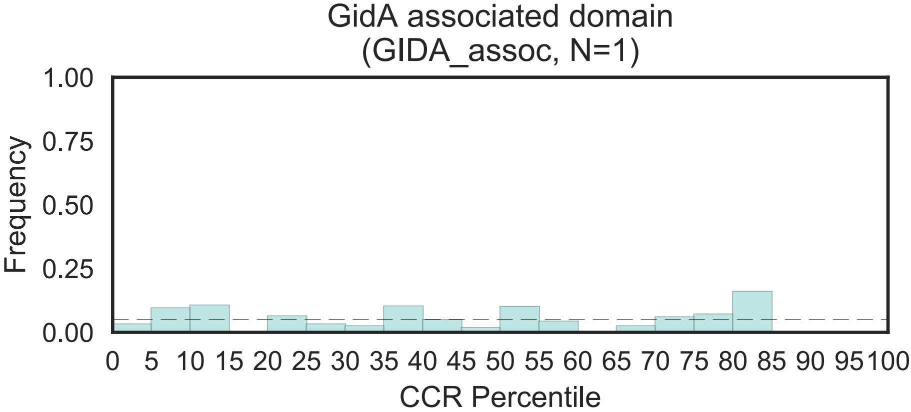

GHMP kinases C terminal
(GHMP_kinases_C, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

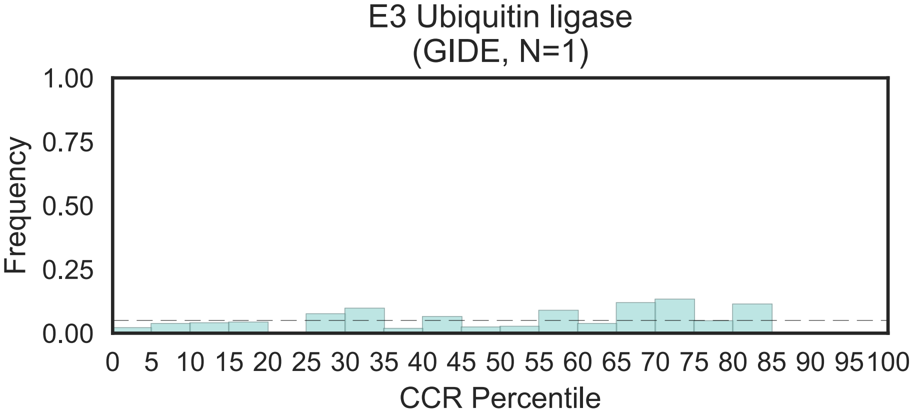


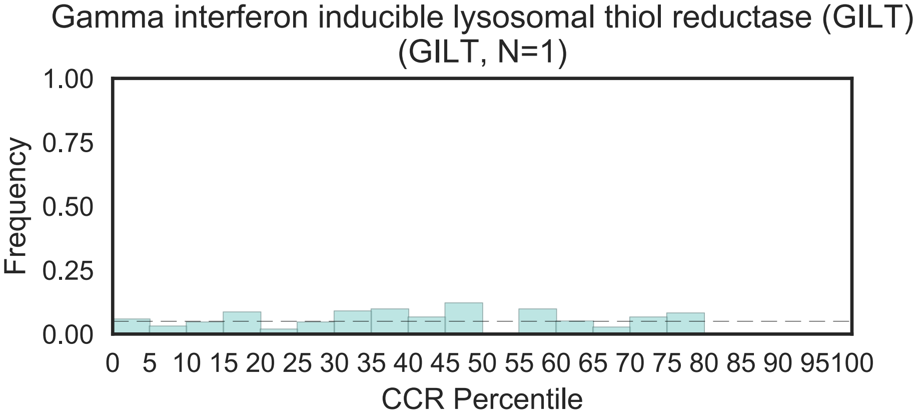
GHMP kinases N terminal domain
(GHMP_kinases_N, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

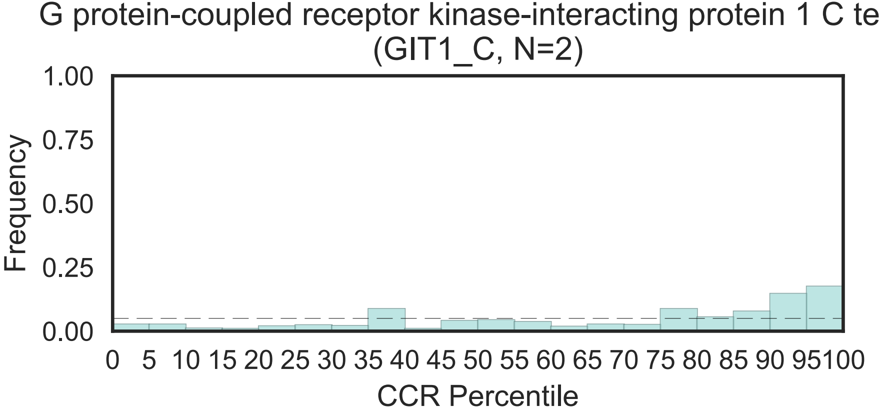


Glucose inhibited division protein A
(GIDA, N=4)
Fisher's OR: 0.405; Bonferroni p-val: 1

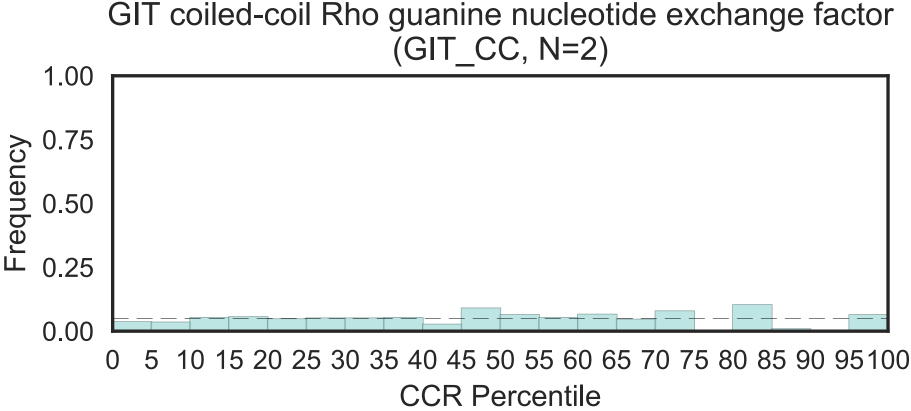

GidA associated domain
(GIDA_assoc, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

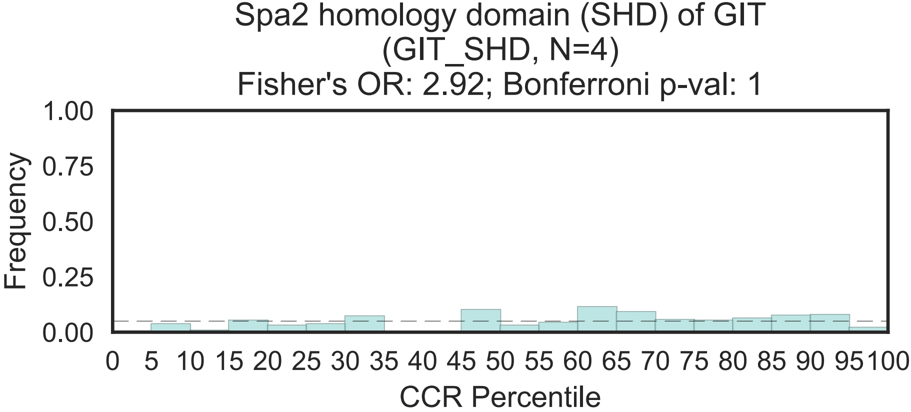

E3 Ubiquitin ligase
(GIDE, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

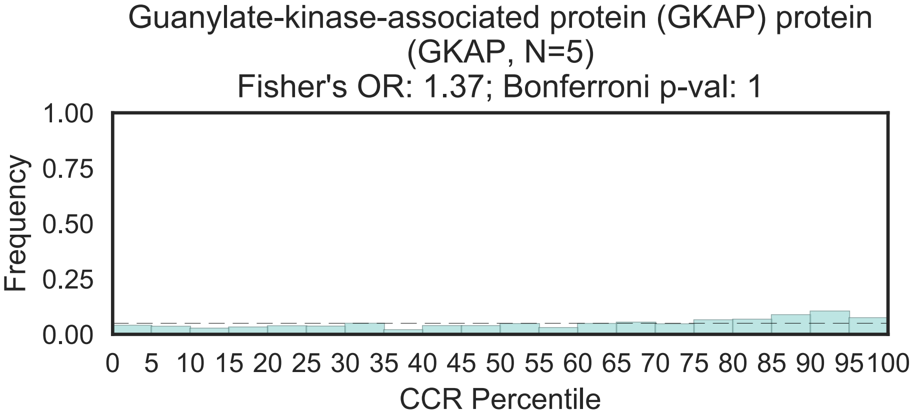

Gamma interferon inducible lysosomal thiol reductase (GILT)
(GILT, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

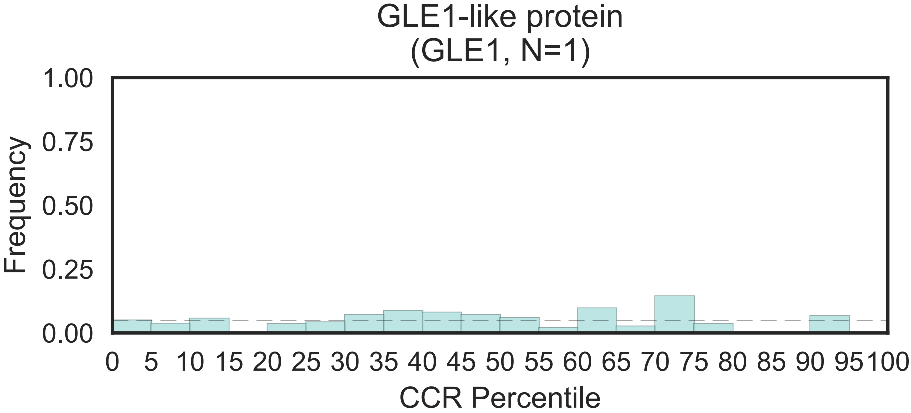


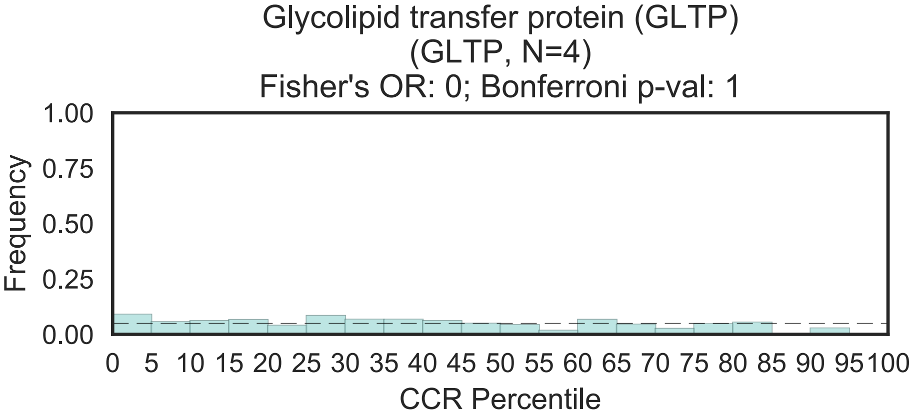
G protein-coupled receptor kinase-interacting protein 1 C term
(GIT1_C, N=2)


GIT coiled-coil Rho guanine nucleotide exchange factor
(GIT_CC, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

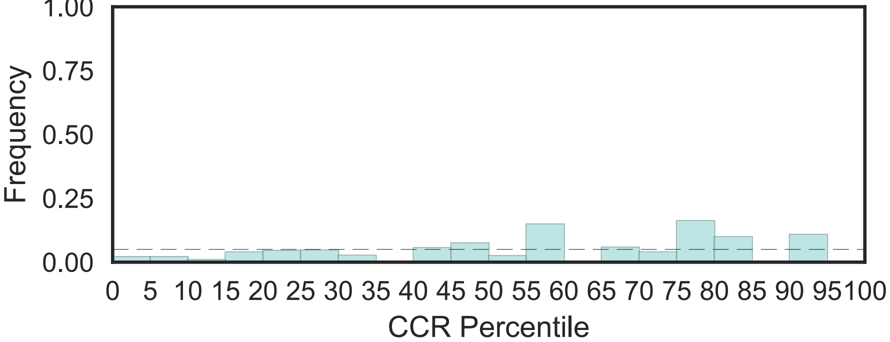

Spa2 homology domain (SHD) of GIT
(GIT_SHD, N=4)
Fisher's OR: 2.92; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

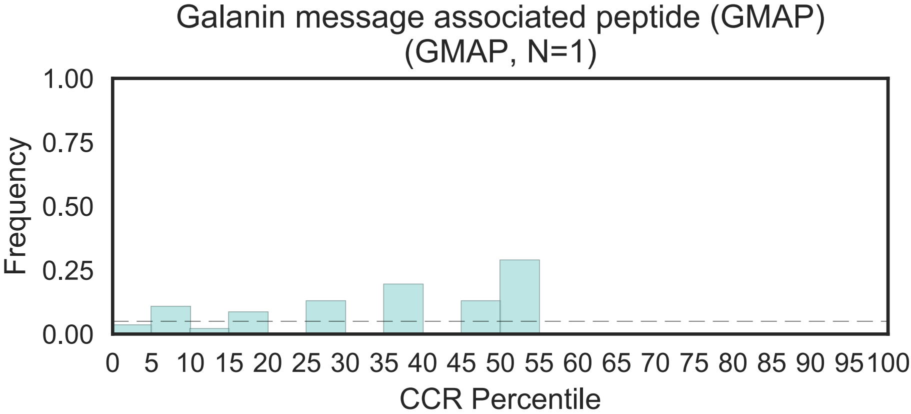

Guanylate-kinase-associated protein (GKAP) protein
(GKAP, N=5)
Fisher's OR: 1.37; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

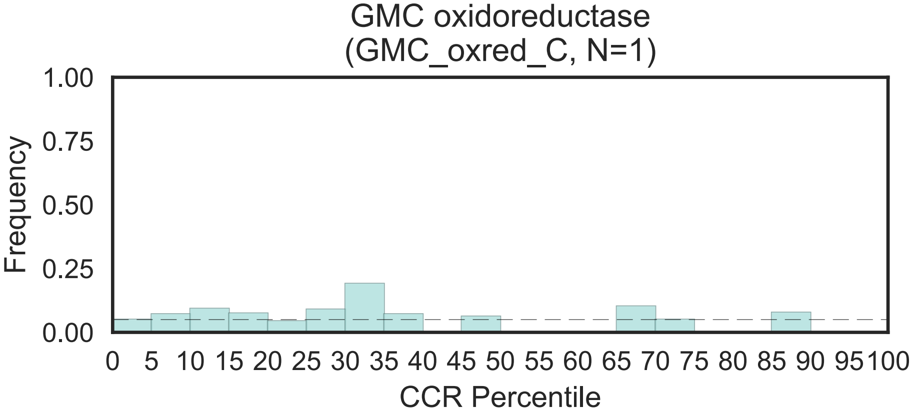

GLE1-like protein
(GLE1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

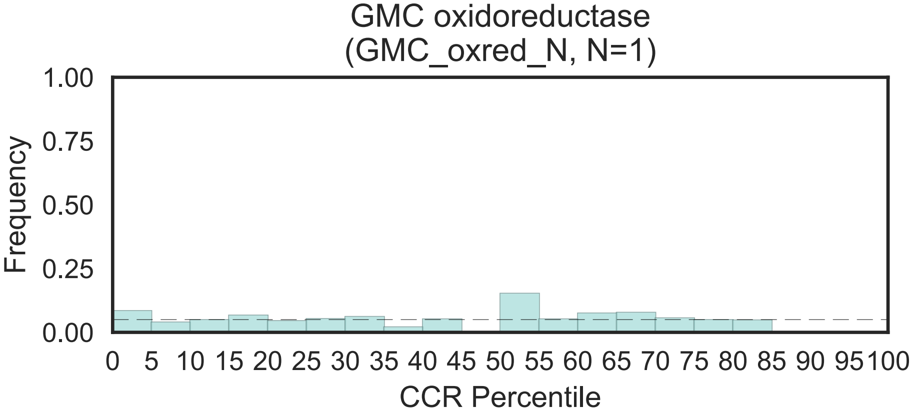

Glycolipid transfer protein (GLTP)
(GLTP, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

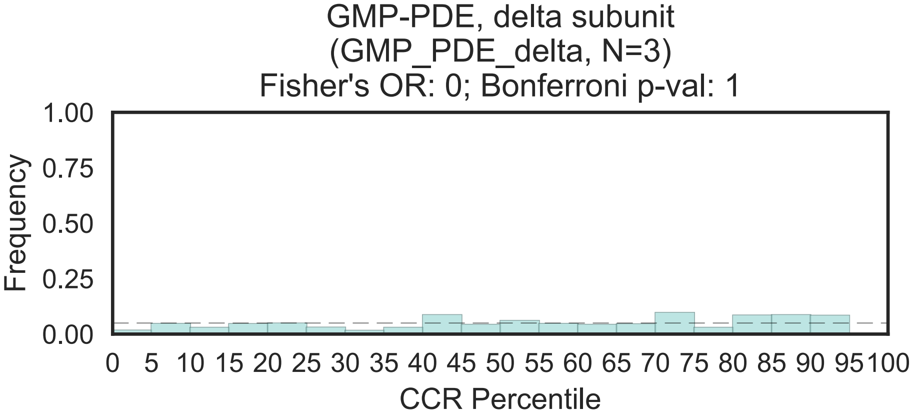
Conserved region of unknown function on GLTSCR protein (GLTSCR1, N=2)

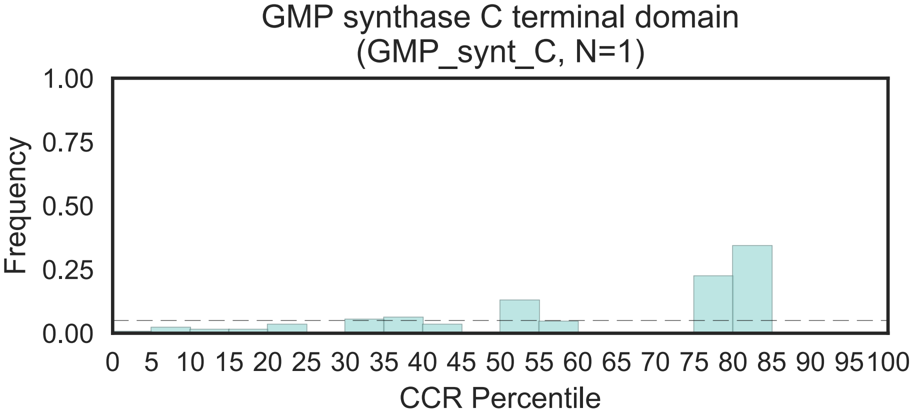


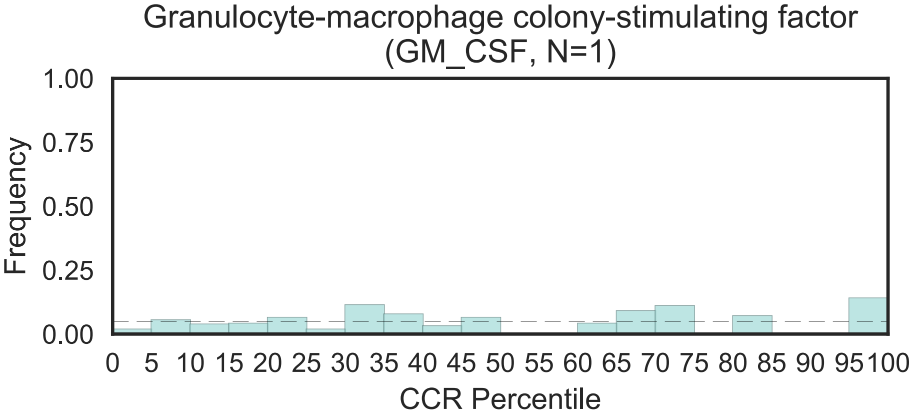

Galanin message associated peptide (GMAP)
(GMAP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

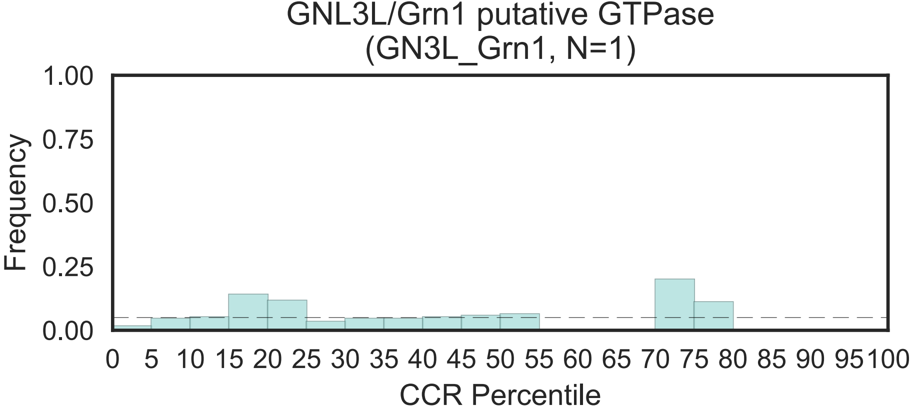

GMC oxidoreductase
(GMC_oxred_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

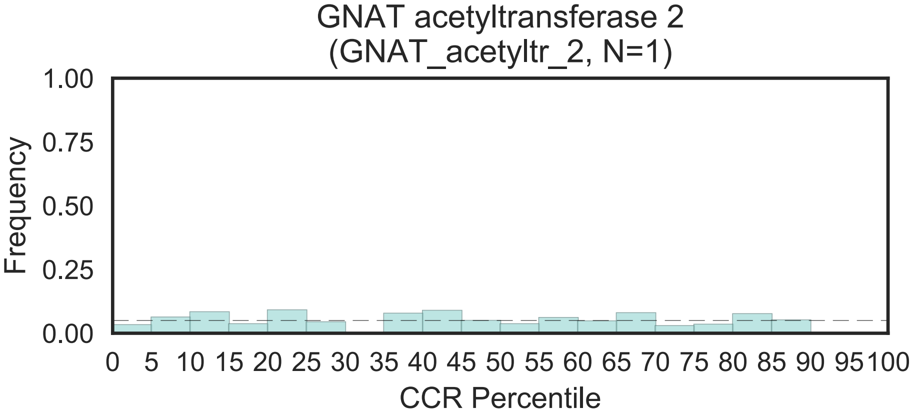

GMC oxidoreductase
(GMC_oxred_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

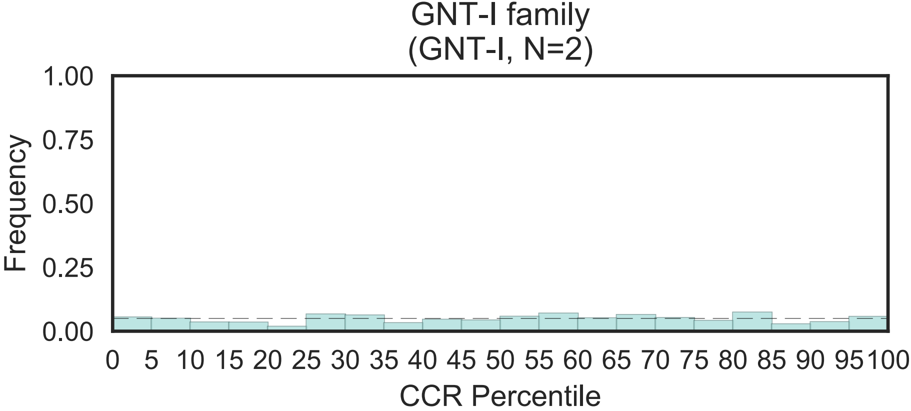

GMP-PDE, delta subunit
(GMP_PDE_delta, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

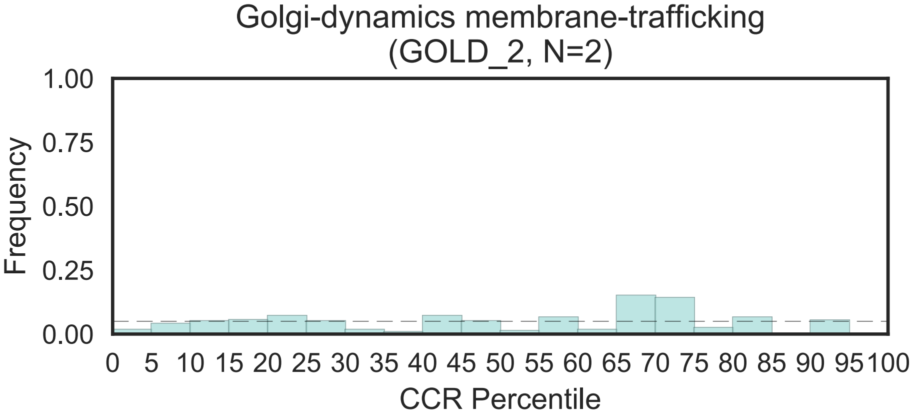

GMP synthase C terminal domain
(GMP_synt_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Granulocyte-macrophage colony-stimulating factor
(GM_CSF, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

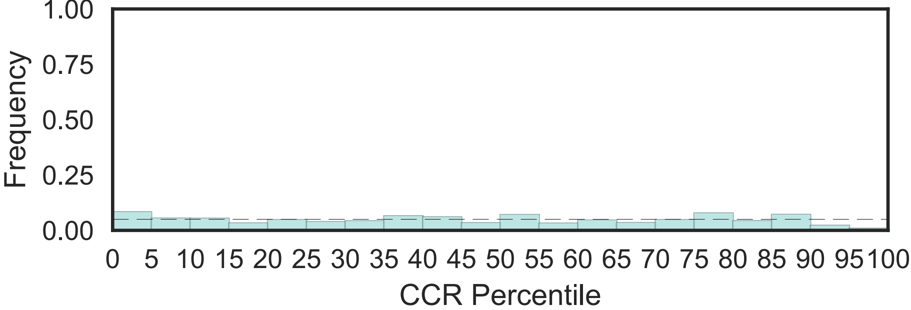

GNL3L/Grn1 putative GTPase
(GN3L_Grn1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

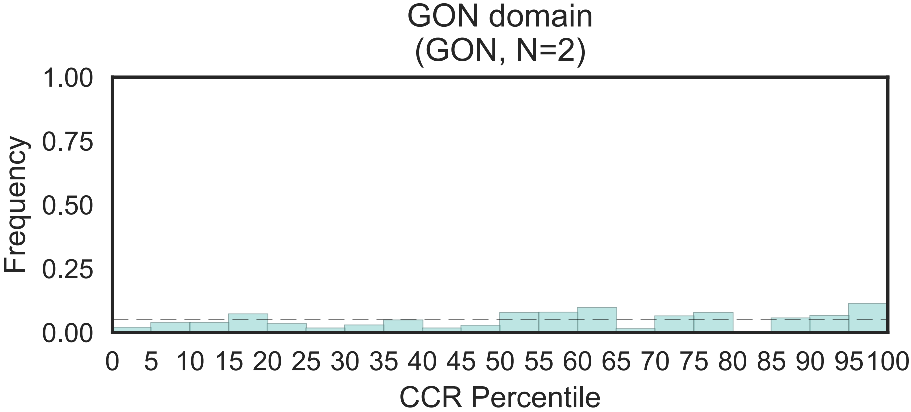

GNAT acetyltransferase 2
(GNAT_acetyltr_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

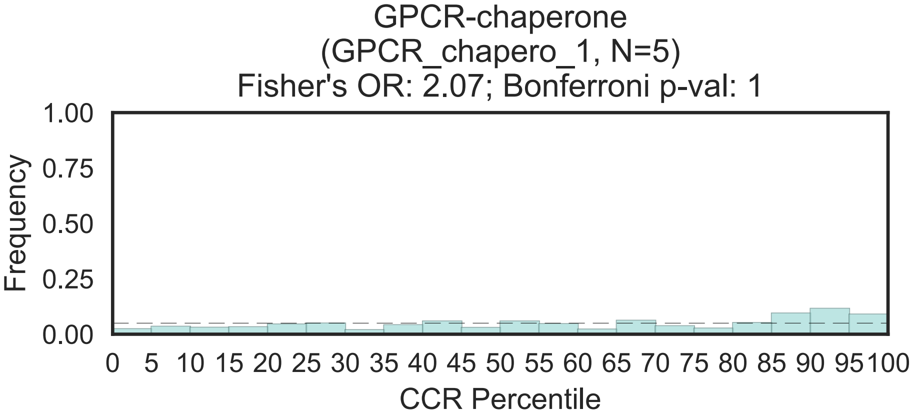

GNT-I family
(GNT-I, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

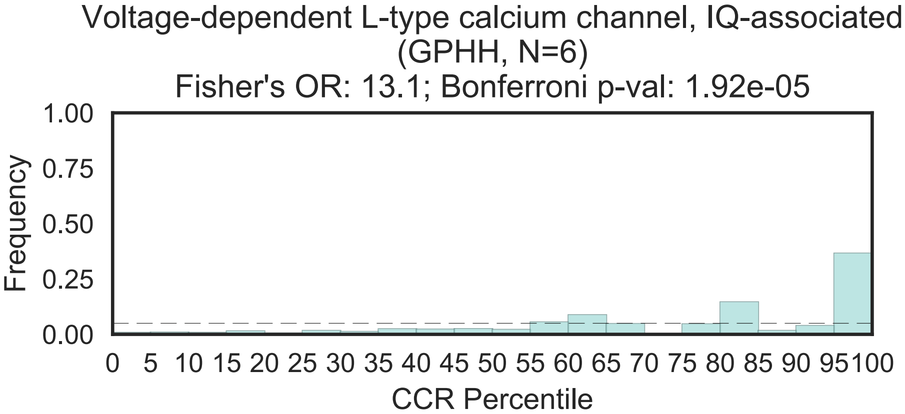

Golgi-dynamics membrane-trafficking
(GOLD_2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Putative golgin subfamily A member 2-like protein 5
(GOLGA2L5, N=36)
Fisher's OR: 0.246; Bonferroni p-val: 1

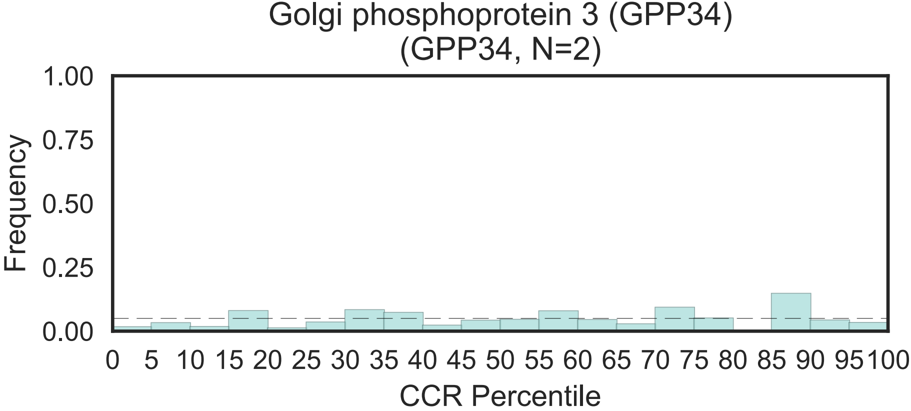


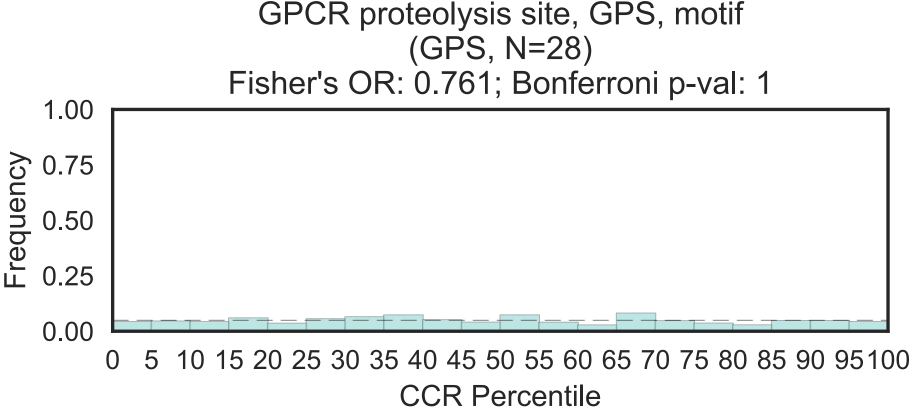

GON domain
(GON, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

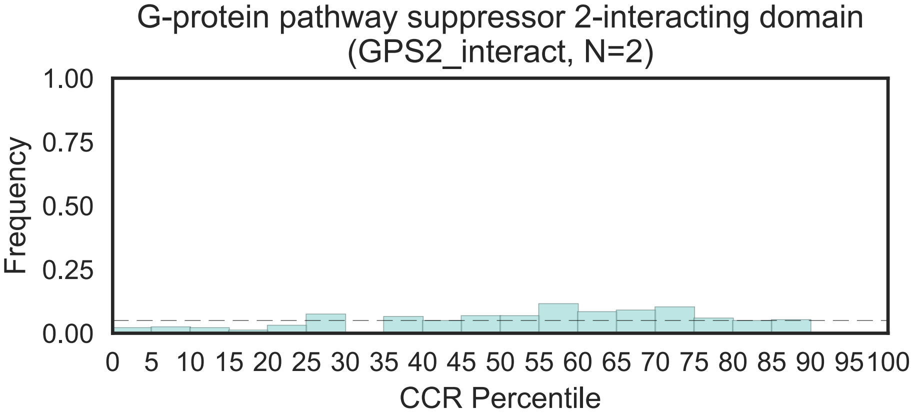

GPCR-chaperone
(GPCR_chapero_1, N=5)
Fisher's OR: 2.07; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

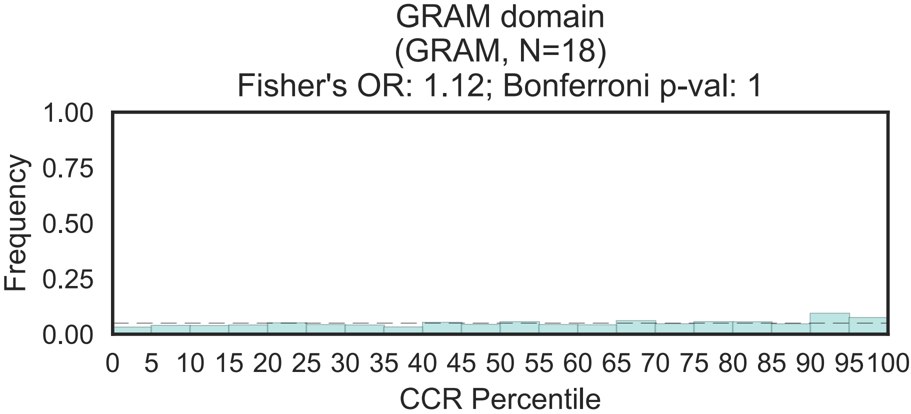


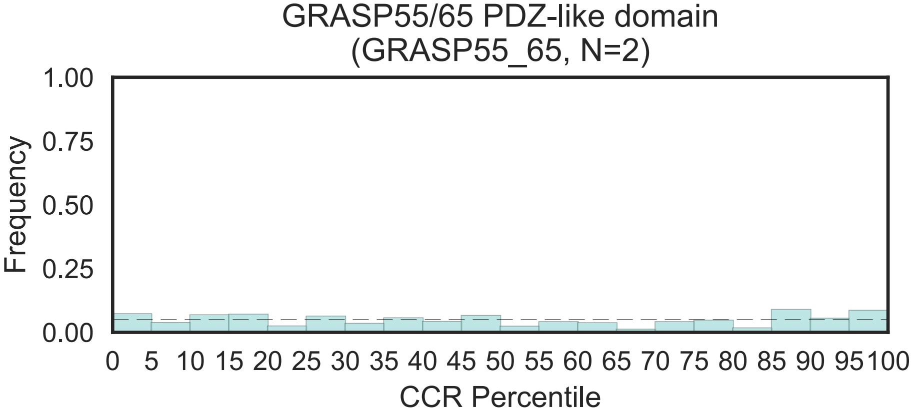
Voltage-dependent L-type calcium channel, IQ-associated
(GPHH, N=6)
Fisher's OR: 13.1; Bonferroni p-val: 1.92e-05

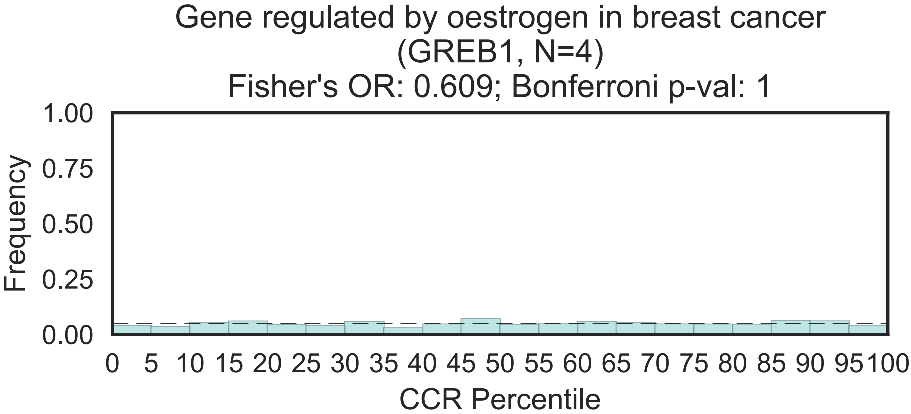

Golgi phosphoprotein 3 (GPP34)
(GPP34, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


GPCR proteolysis site, GPS, motif
(GPS, N=28)
Fisher's OR: 0.761; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


G-protein pathway suppressor 2-interacting domain
(GPS2_interact, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

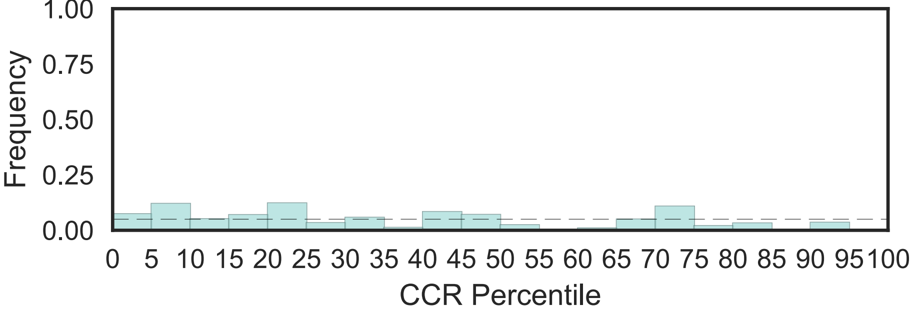

GRAM domain
(GRAM, N=18)
Fisher's OR: 1.12; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

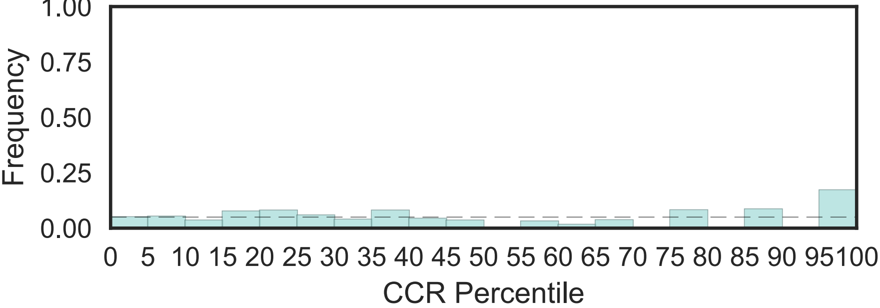

GRASP55/65 PDZ-like domain
(GRASP55_65, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



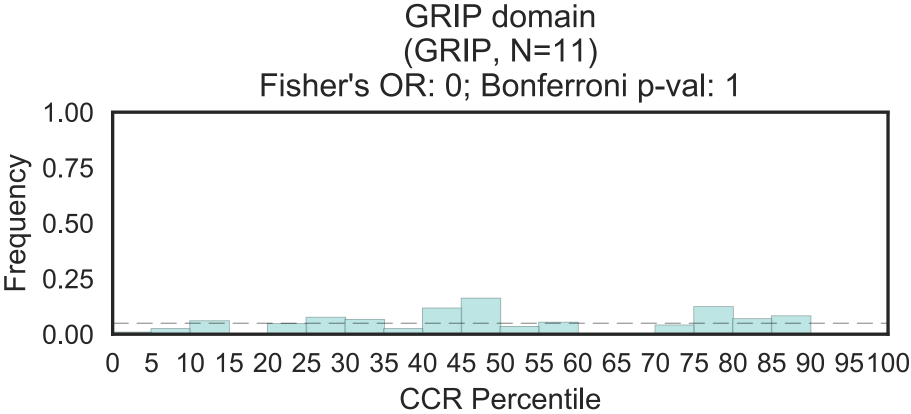
Gene regulated by oestrogen in breast cancer
(GREB1, N=4)
Fisher's OR: 0.609; Bonferroni p-val: 1

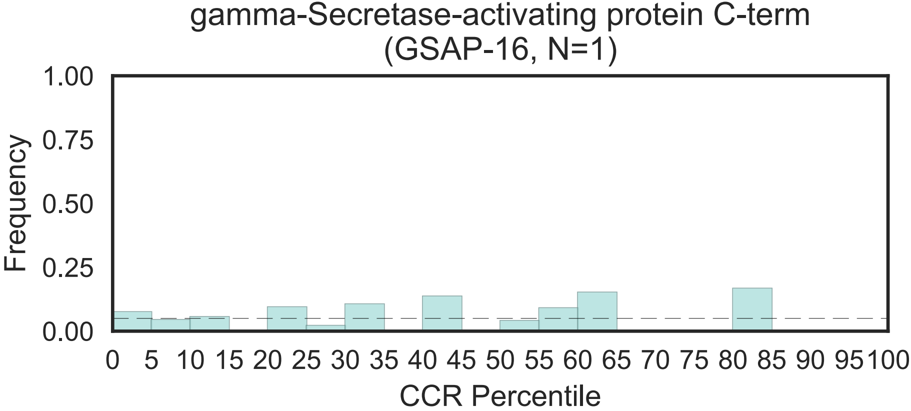
GRIM-19 protein
(GRIM-19, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

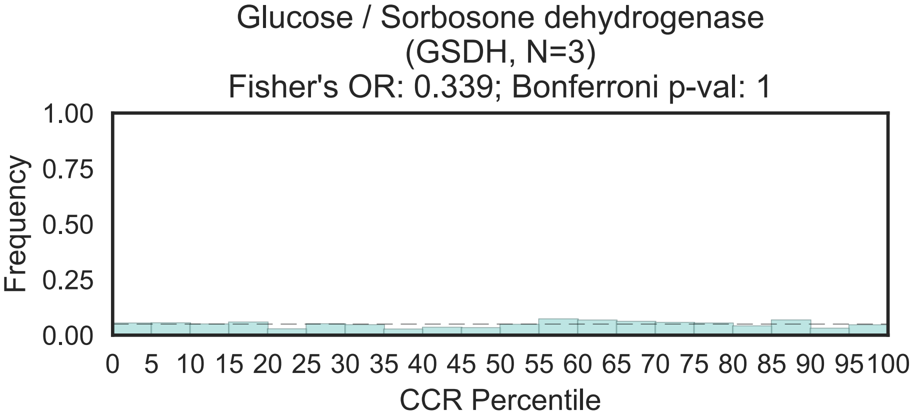


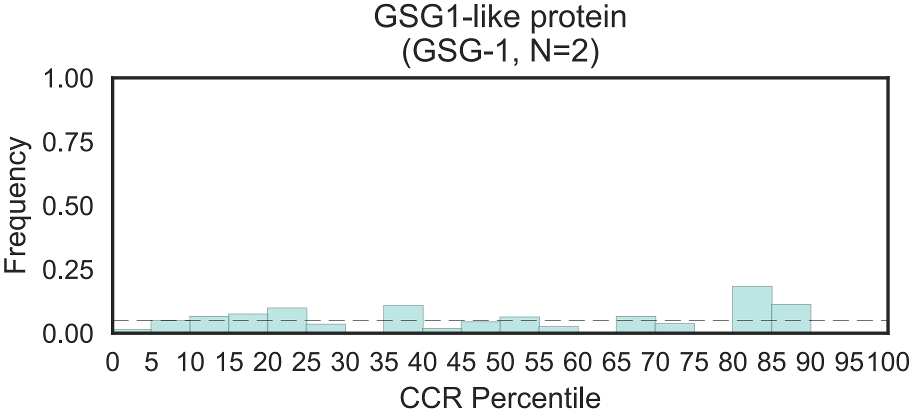


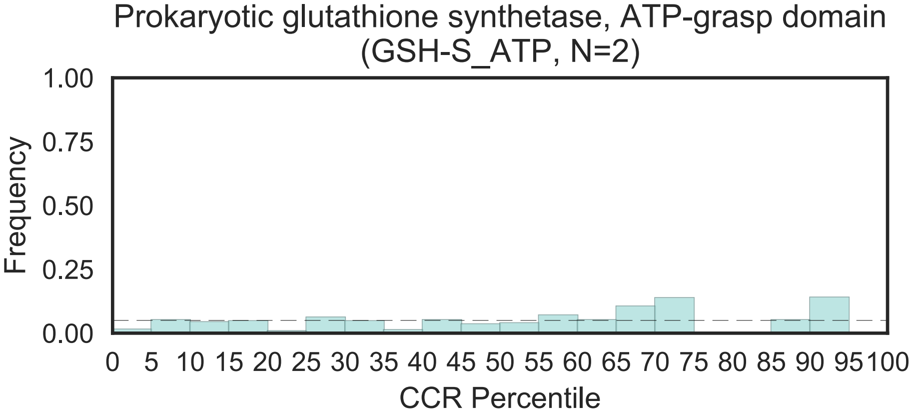
G protein-regulated inducer of neurite outgrowth C-terminus (GRIN_C, N=3)
Fisher's OR: 2.06; Bonferroni p-val: 1


GRIP domain
(GRIP, N=11)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

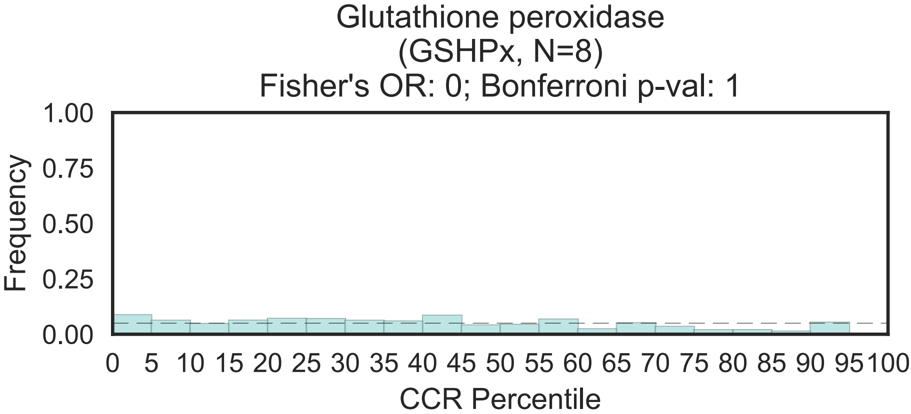

gamma-Secretase-activating protein C-term
(GSAP-16, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

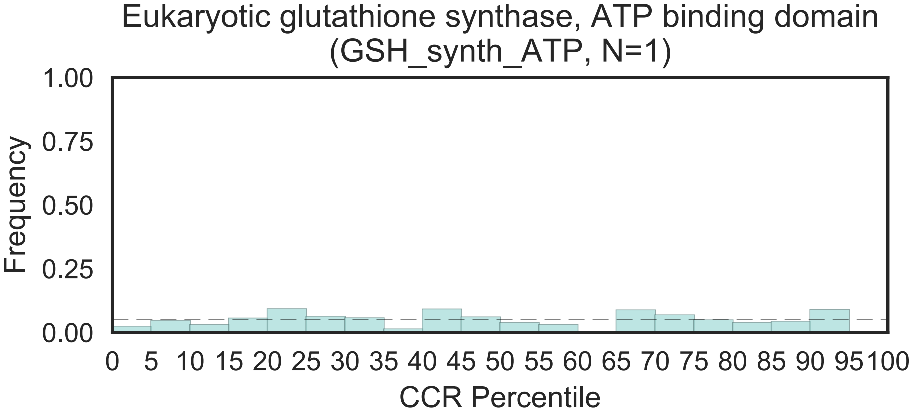

Glucose / Sorbosone dehydrogenase
(GSDH, N=3)
Fisher's OR: 0.339; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

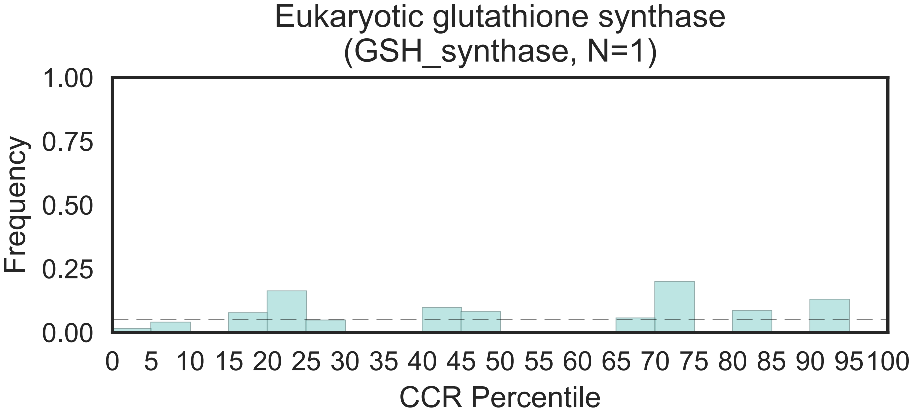

GSG1-like protein
(GSG-1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

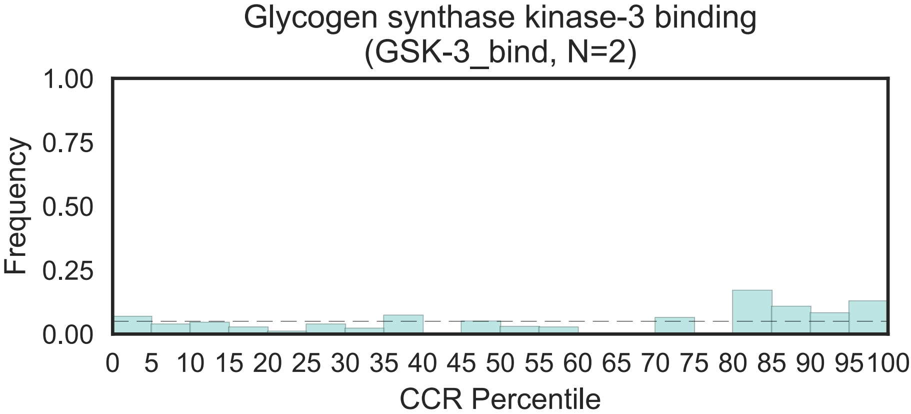


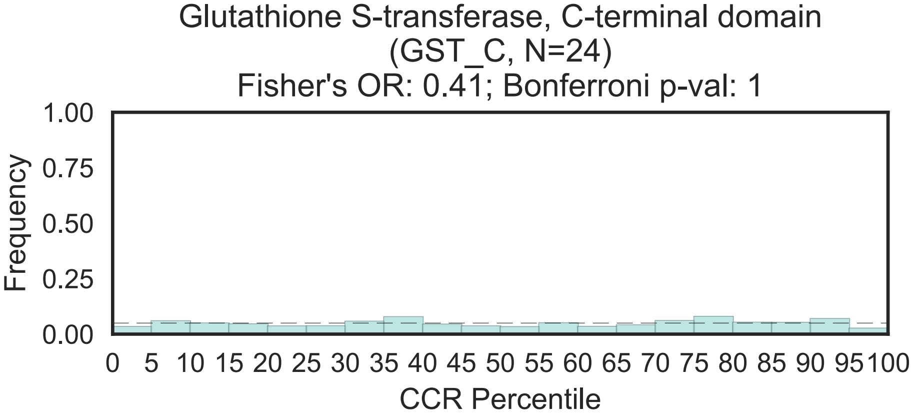
Prokaryotic glutathione synthetase, ATP-grasp domain (GSH-S_ATP, N=2)

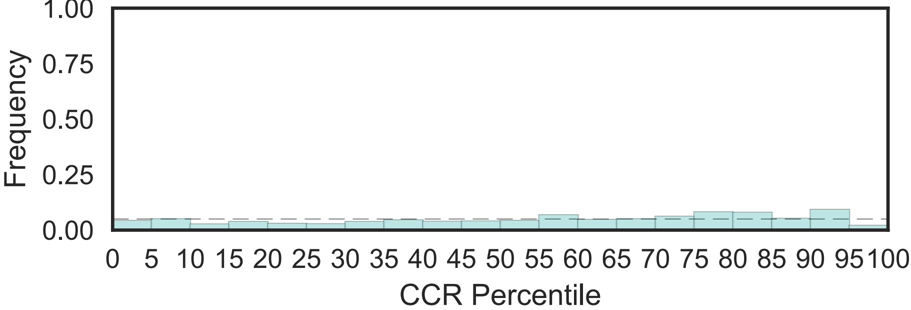

Glutathione peroxidase
(GSHPx, N=8)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Eukaryotic glutathione synthase, ATP binding domain
(GSH_synth_ATP, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

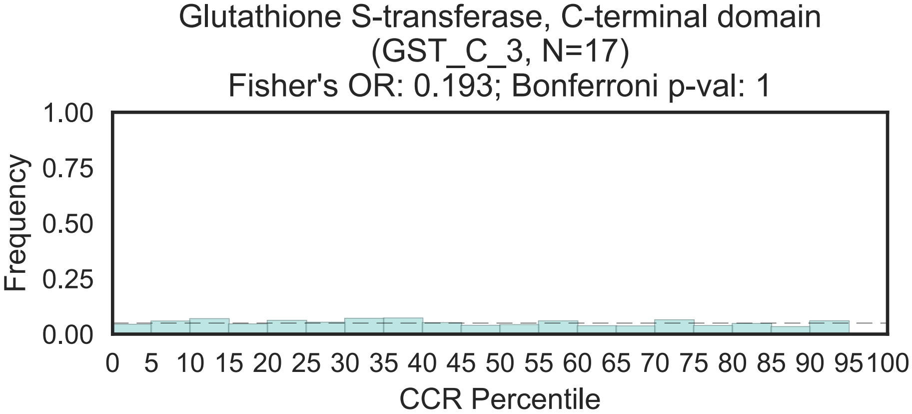

Eukaryotic glutathione synthase
(GSH_synthase, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

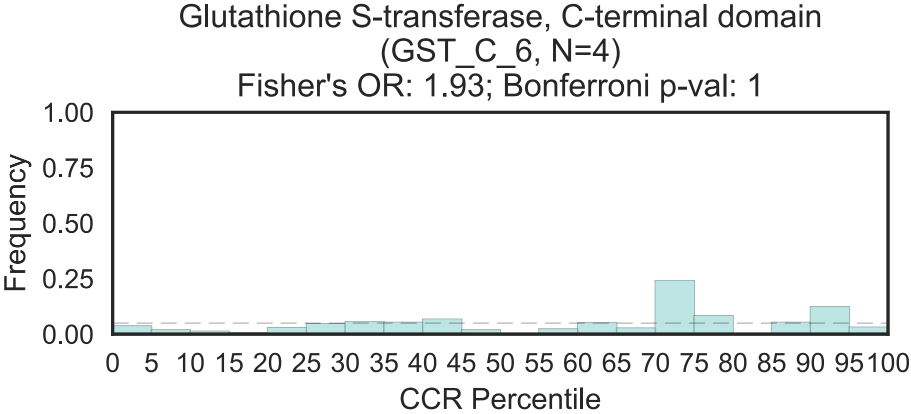

Glycogen synthase kinase-3 binding
(GSK-3_bind, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

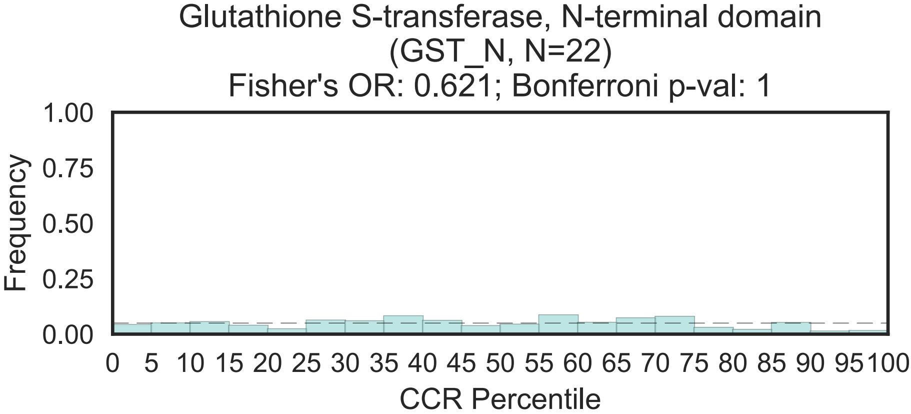

Glutathione S-transferase, C-terminal domain
(GST_C, N=24)
Fisher's OR: 0.41; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

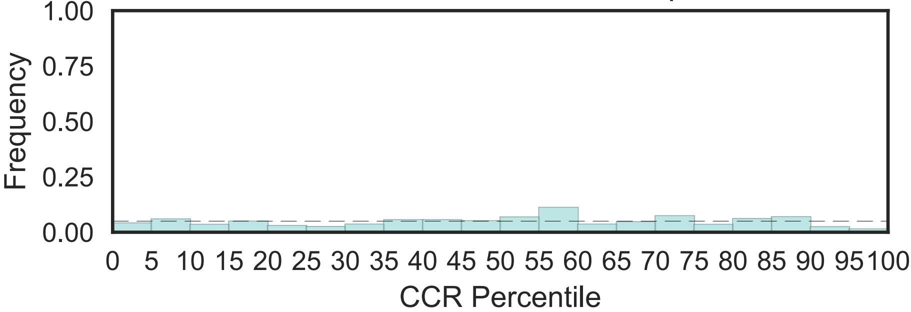


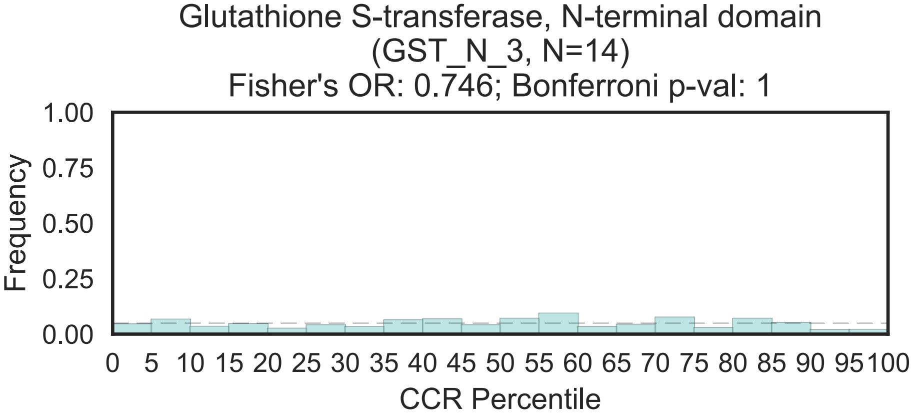
Glutathione S-transferase, C-terminal domain
(GST_C_2, N=14)
Fisher's OR: 0.801; Bonferroni p-val: 1

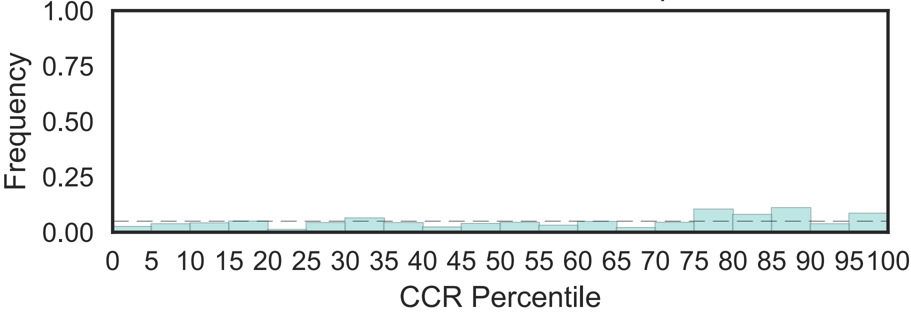

Glutathione S-transferase, C-terminal domain
(GST_C_3, N=17)
Fisher's OR: 0.193; Bonferroni p-val: 1

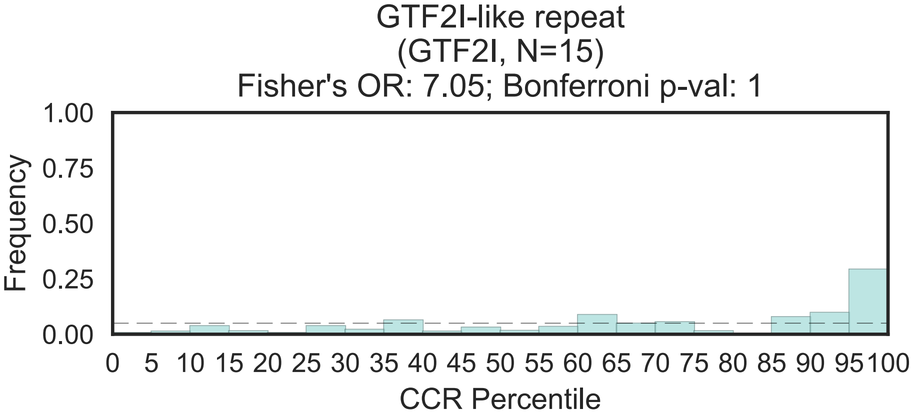

Glutathione S-transferase, C-terminal domain
(GST_C_6, N=4)
Fisher's OR: 1.93; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

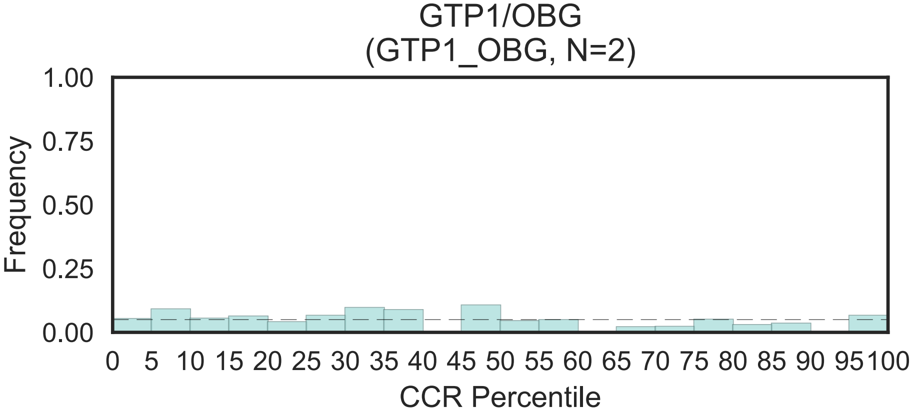

Glutathione S-transferase, N-terminal domain
(GST_N, N=22)
Fisher's OR: 0.621; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

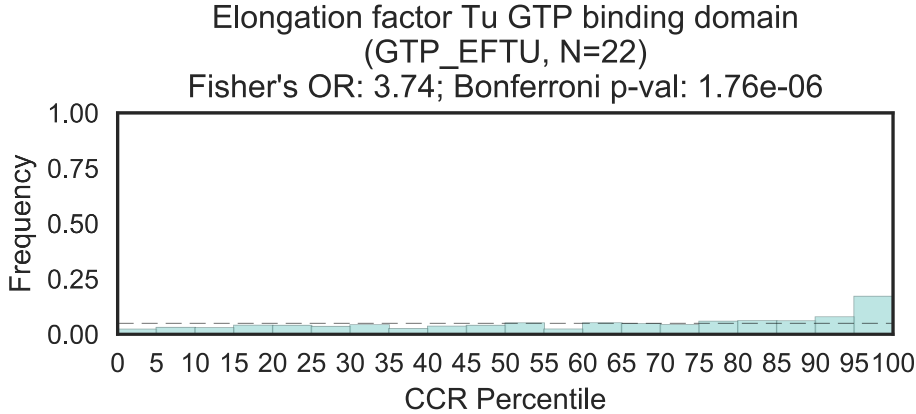

Glutathione S-transferase, N-terminal domain
(GST_N_2, N=10)
Fisher's OR: 0.651; Bonferroni p-val: 1

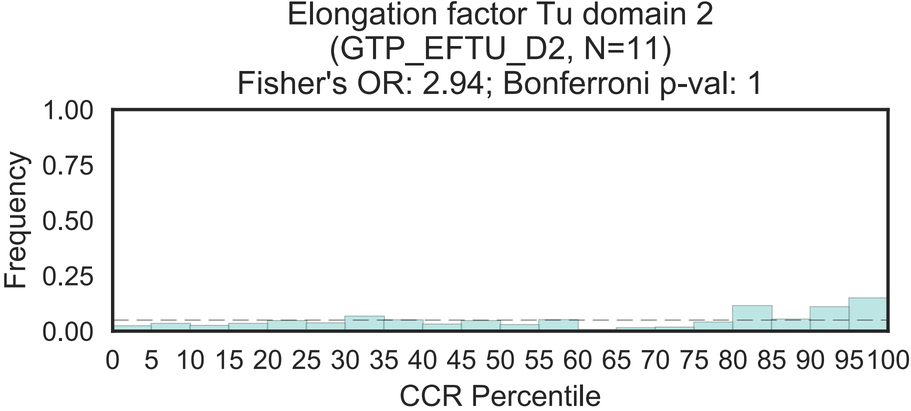

Glutathione S-transferase, N-terminal domain
(GST_N_3, N=14)
Fisher's OR: 0.746; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

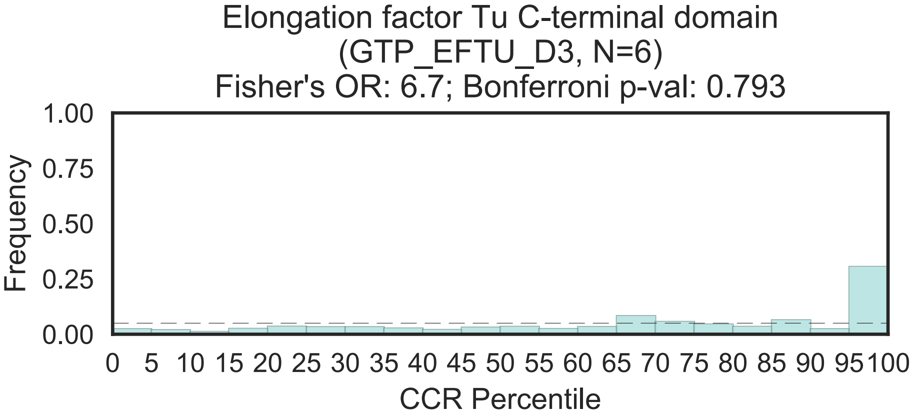

Glutathione S-transferase N-terminal domain
(GST_N_4, N=4)
Fisher's OR: 2.43; Bonferroni p-val: 1

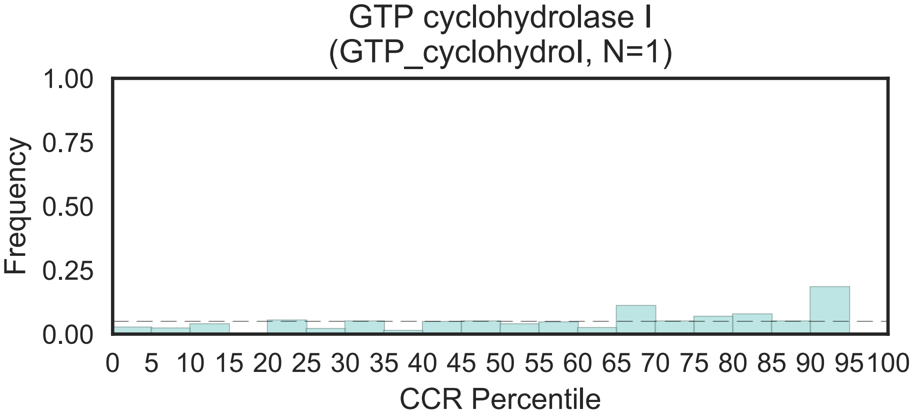

GTF2I-like repeat
(GTF2I, N=15)
Fisher's OR: 7.05; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

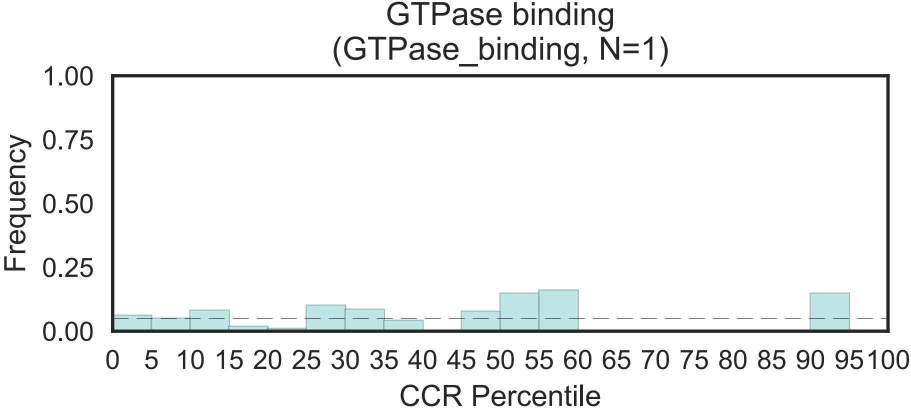

GTP1/OBG
(GTP1_OBG, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

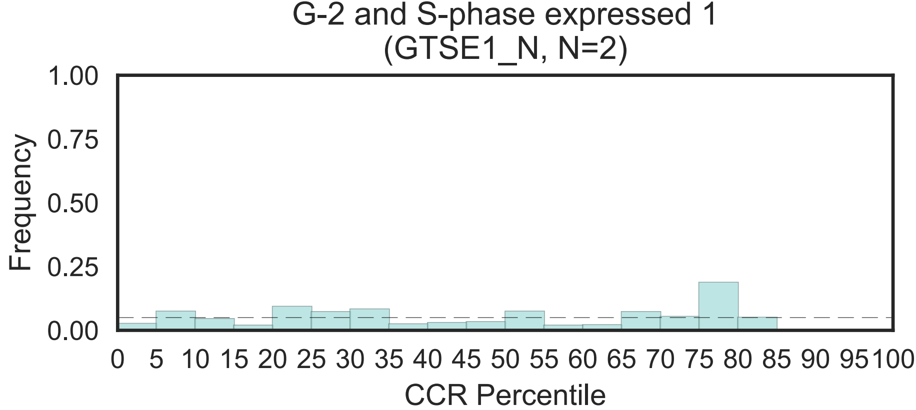

Elongation factor Tu GTP binding domain
(GTP_EFTU, N=22)
Fisher's OR: 3.74; Bonferroni p-val: 1.76e-06
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

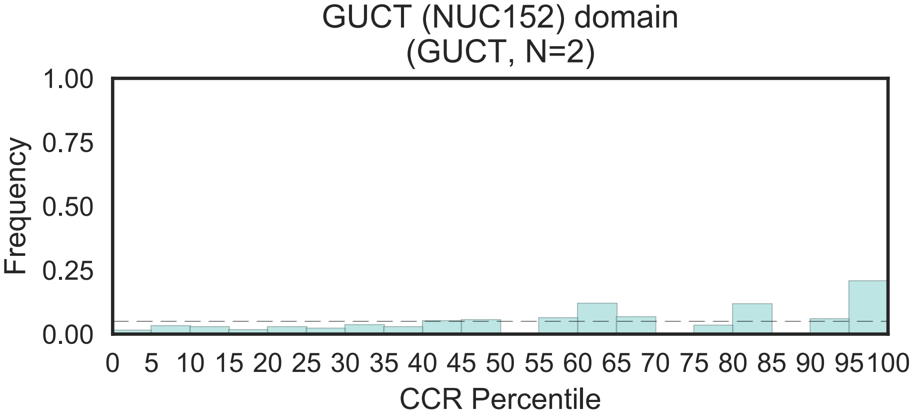

Elongation factor Tu domain 2
(GTP_EFTU_D2, N=11)
Fisher's OR: 2.94; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

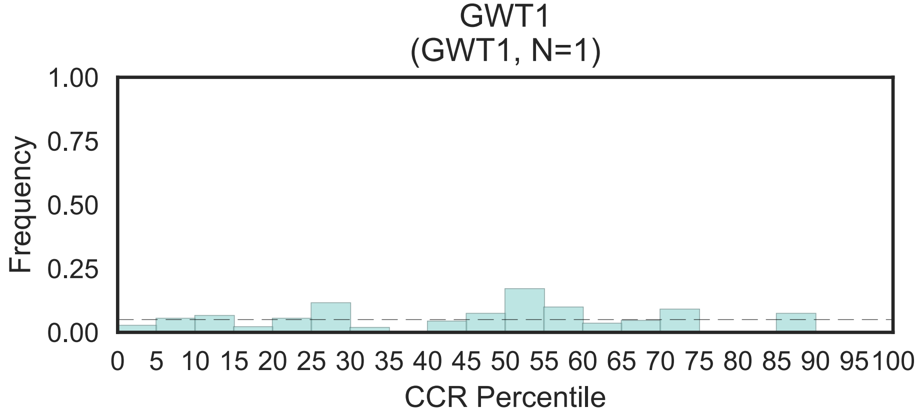

Elongation factor Tu C-terminal domain
(GTP_EFTU_D3, N=6)
Fisher's OR: 6.7; Bonferroni p-val: 0.793

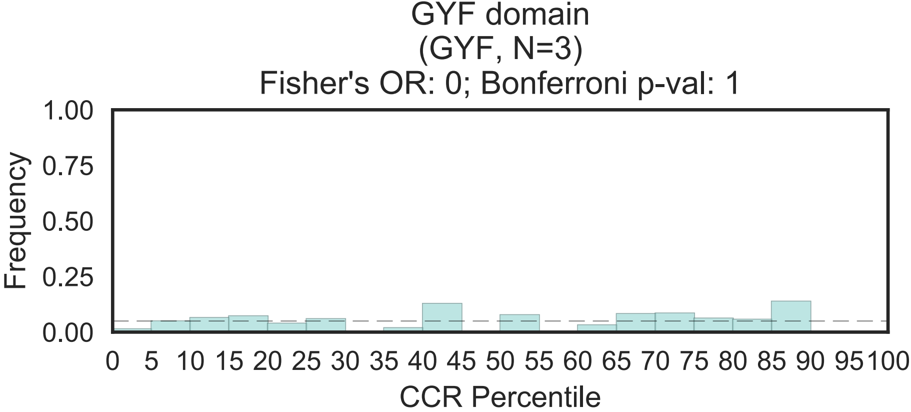

GTP cyclohydrolase I
(GTP_cyclohydroI, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

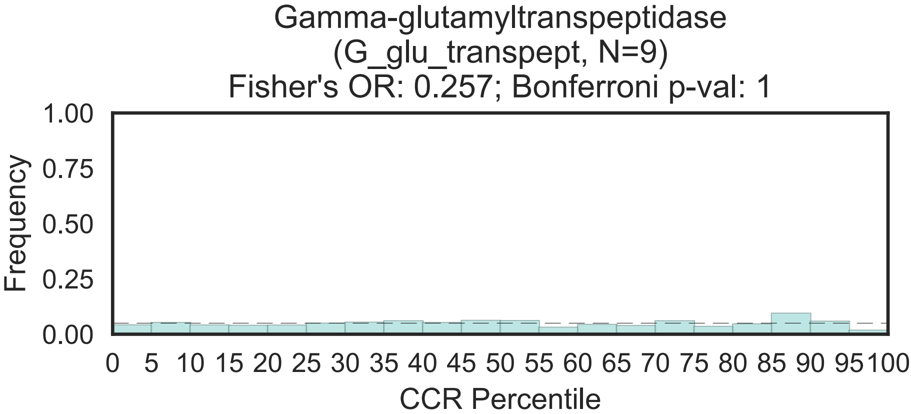

GTPase binding
(GTPase_binding, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


G-2 and S-phase expressed 1
(GTSE1_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

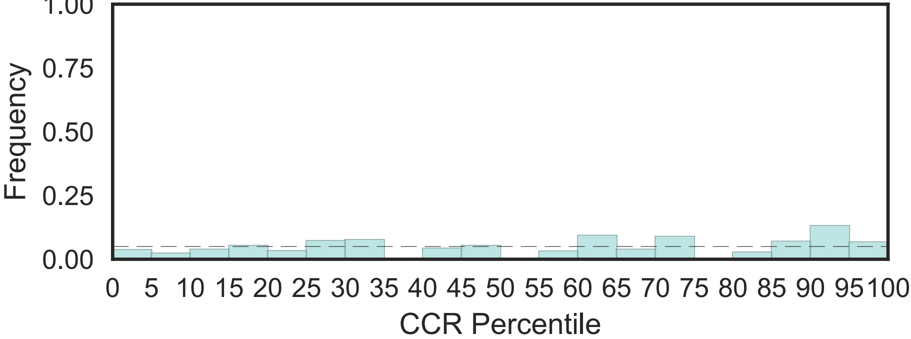

GUCT (NUC152) domain
(GUCT, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

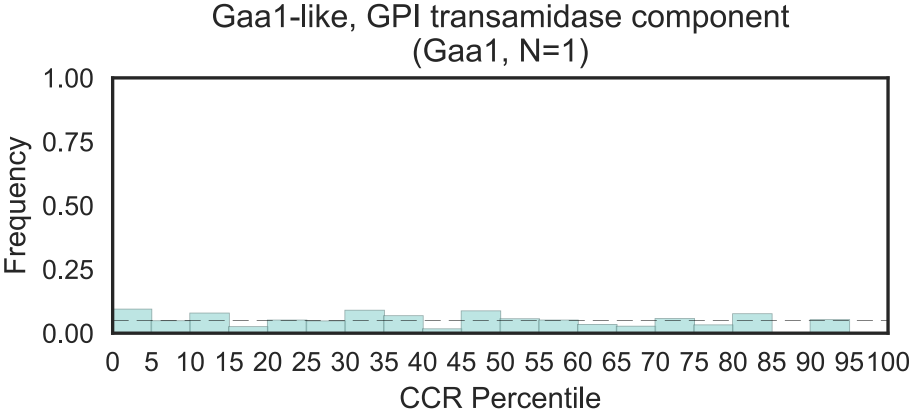

GWT1
(GWT1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

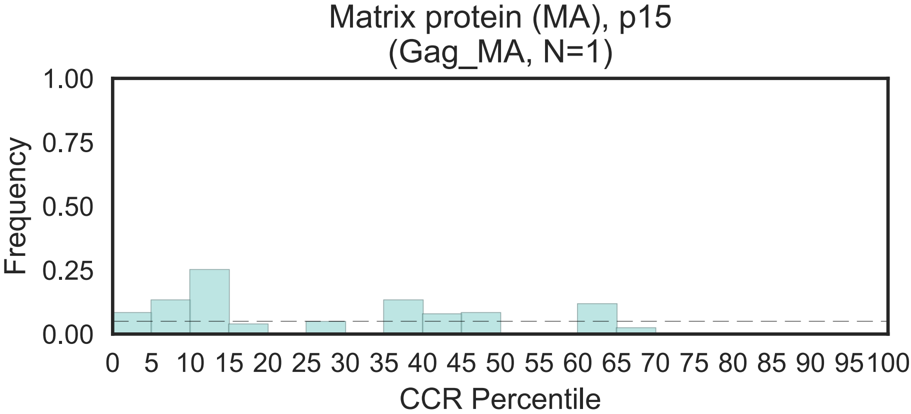

GYF domain
(GYF, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Gamma-glutamyltranspeptidase
(G_glu_transpept, N=9)
Fisher's OR: 0.257; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

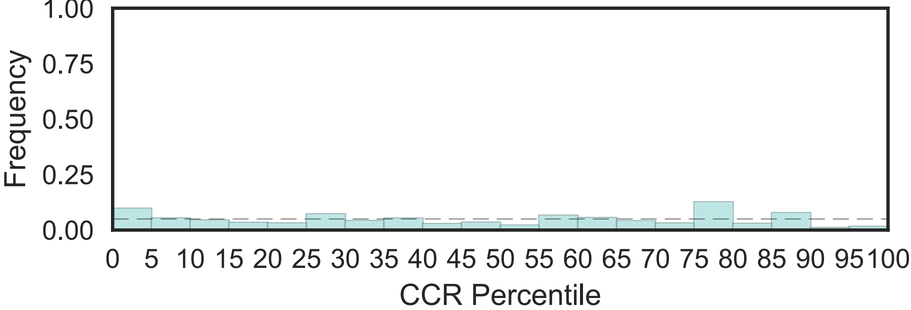
G-protein pathway suppressor
(G_path_suppress, N=1)

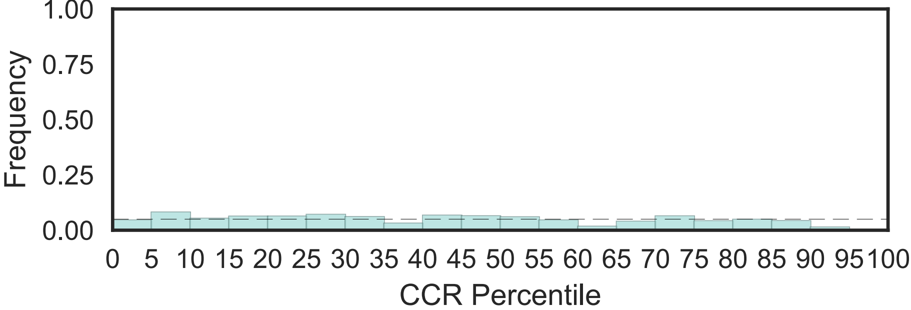



Gaa1-like, GPI transamidase component
(Gaa1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

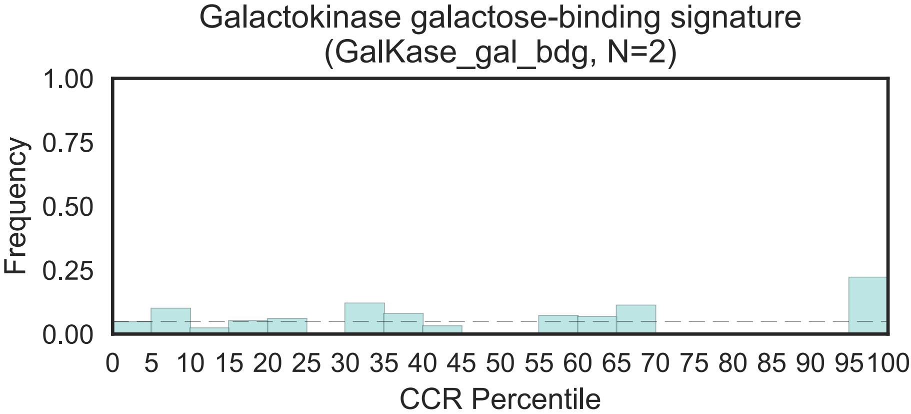

Matrix protein (MA), p15
(Gag_MA, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

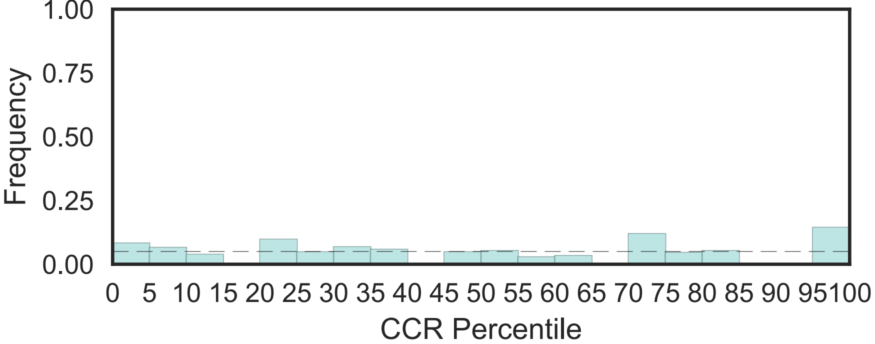
Galactose-3-O-sulfotransferase
(Gal-3-0_sulfotr, N=8)
Fisher's OR: 0.291; Bonferroni p-val: 1

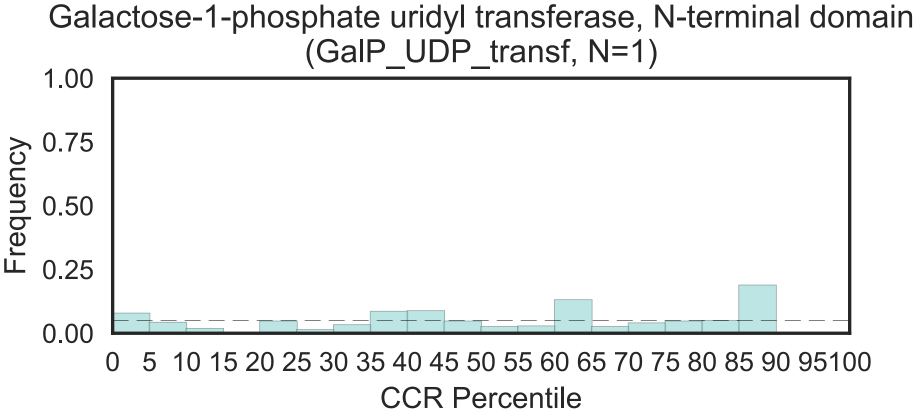


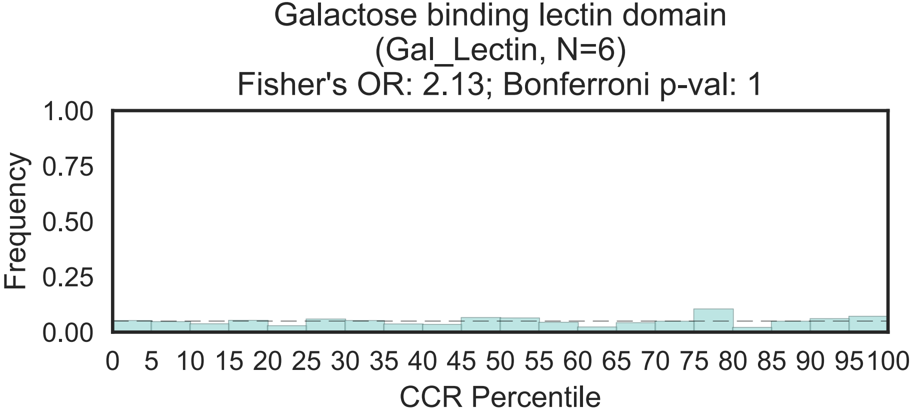


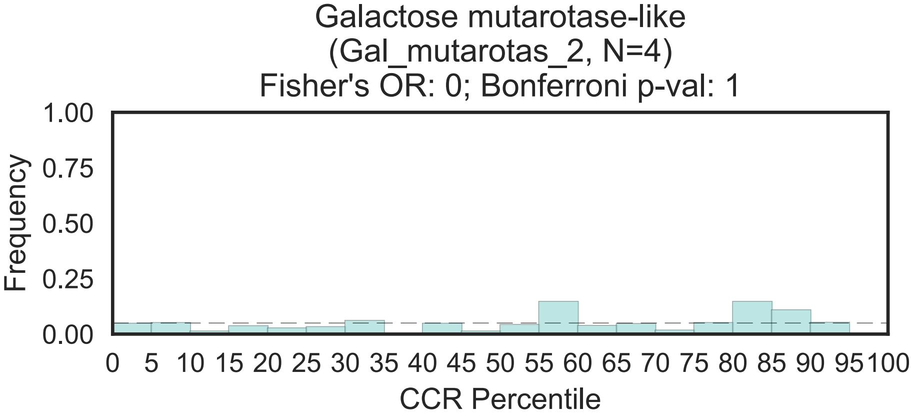
Galactoside-binding lectin
(Gal-bind_lectin, N=22)
Fisher's OR: 0; Bonferroni p-val: 1

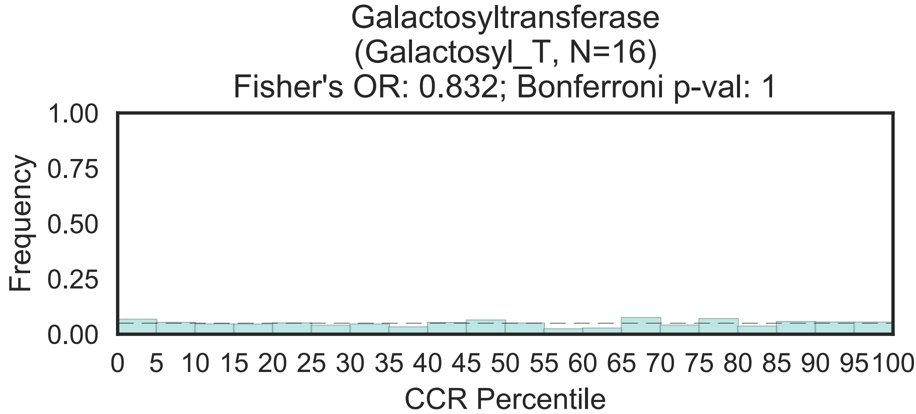

Galactokinase galactose-binding signature
(GalKase_gal_bdg, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

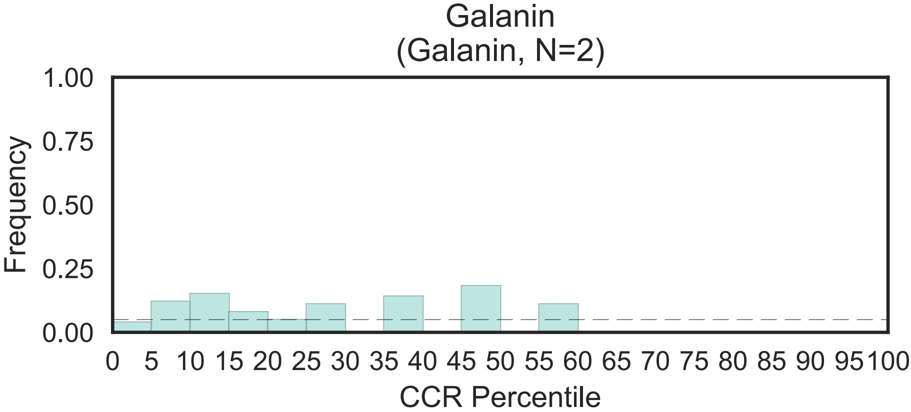

Galactose-1-phosphate uridyl transferase, C-terminal domain
(GalP_UDP_tr_C, N=1)

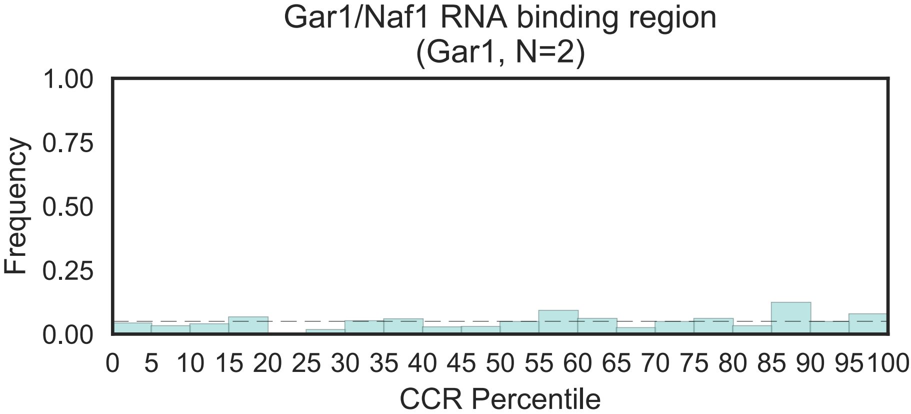

Galactose-1-phosphate uridyl transferase, N-terminal domain
(GalP_UDP_transf, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

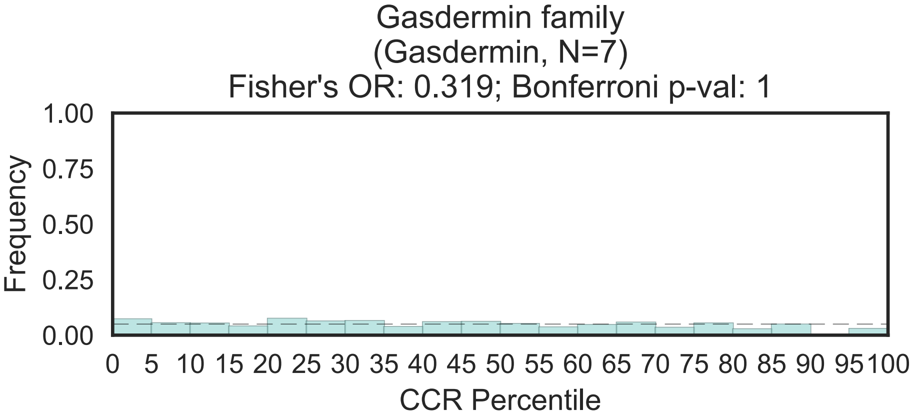

Galactose binding lectin domain
(Gal_Lectin, N=6)
Fisher's OR: 2.13; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

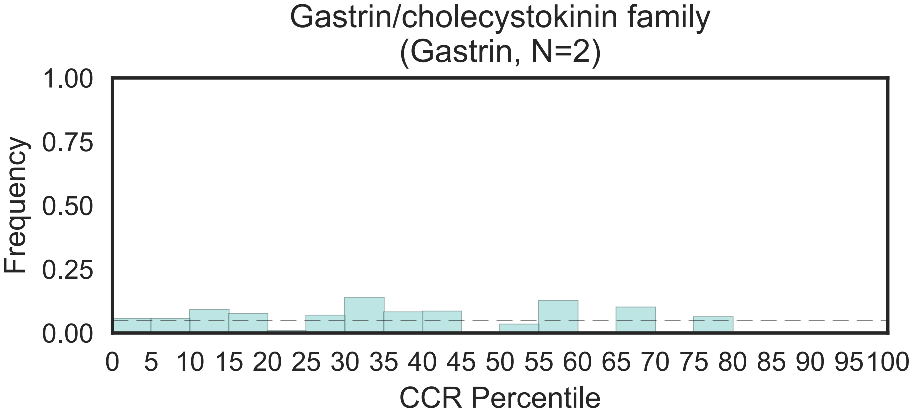

Galactose mutarotase-like
(Gal_mutarotas_2, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

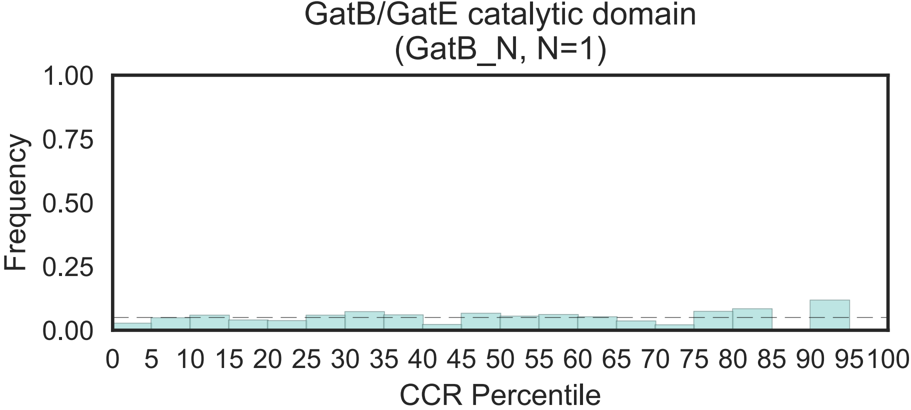

Galactosyltransferase
(Galactosyl_T, N=16)
Fisher's OR: 0.832; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

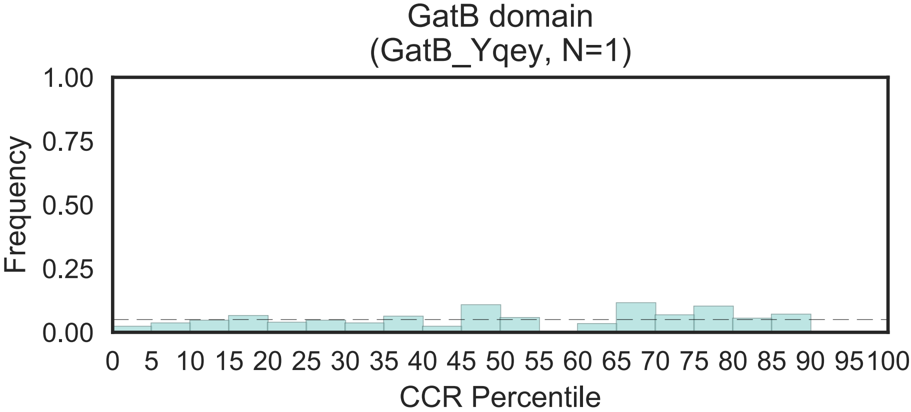

Galanin
(Galanin, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

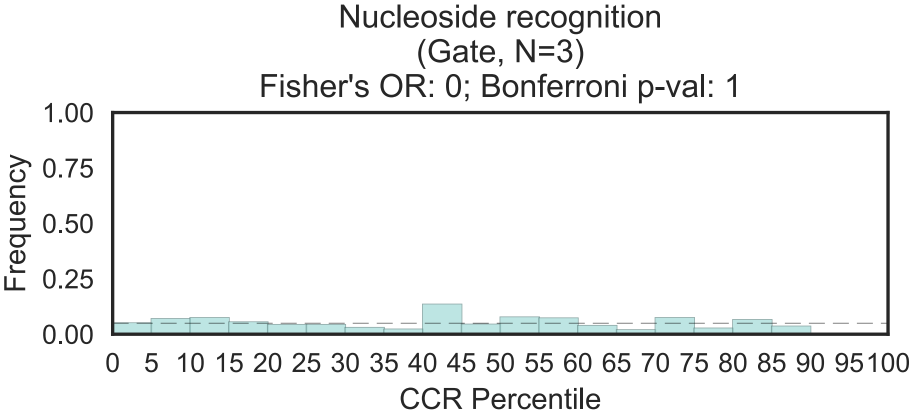

Gar1/Naf1 RNA binding region
(Gar1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

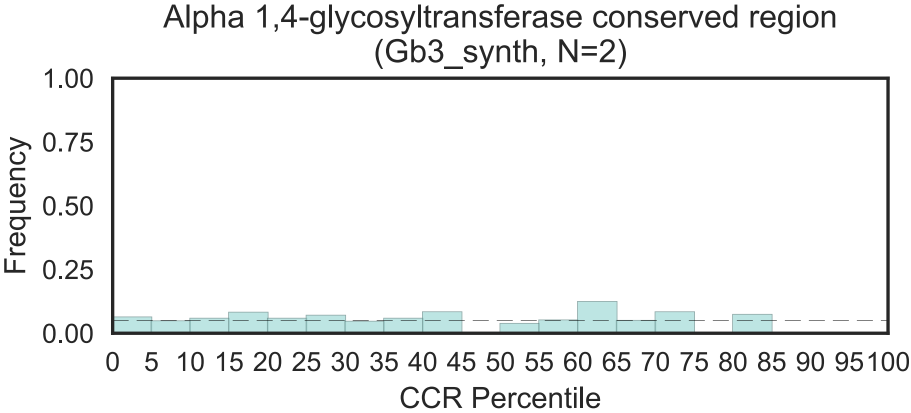

Gasdermin family
(Gasdermin, N=7)
Fisher's OR: 0.319; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

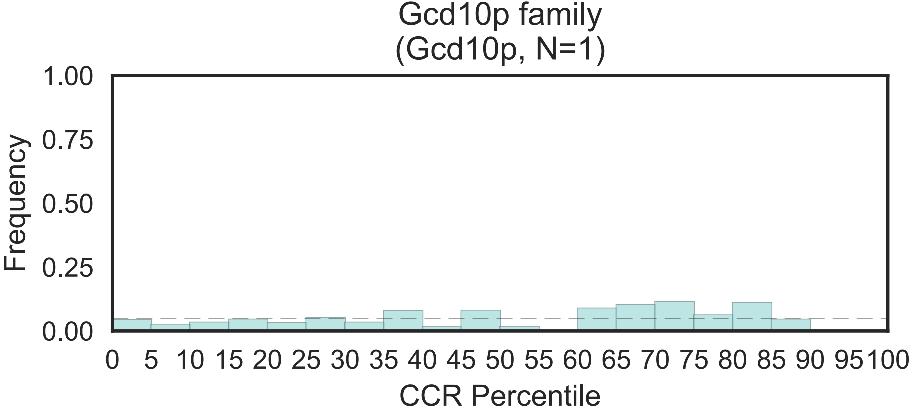

Gastrin/cholecystokinin family
(Gastrin, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

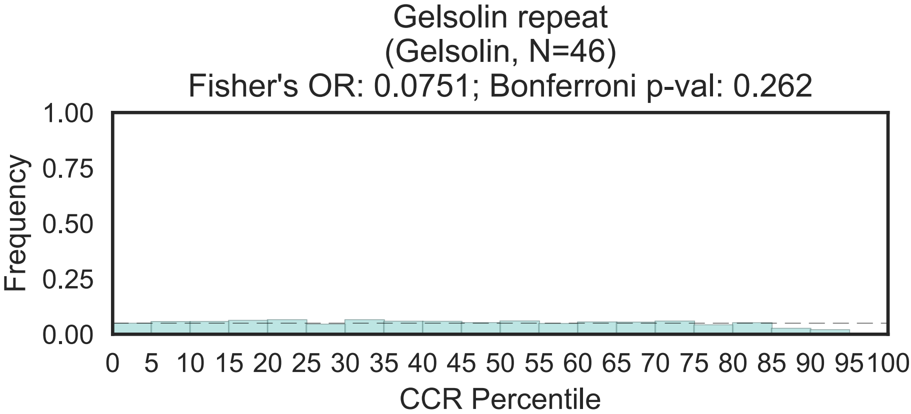

GatB/GatE catalytic domain
(GatB_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

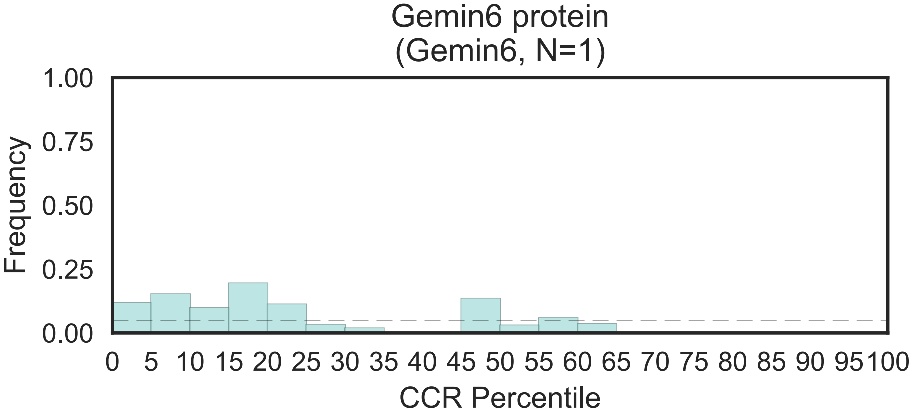

GatB domain
(GatB_Yqey, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

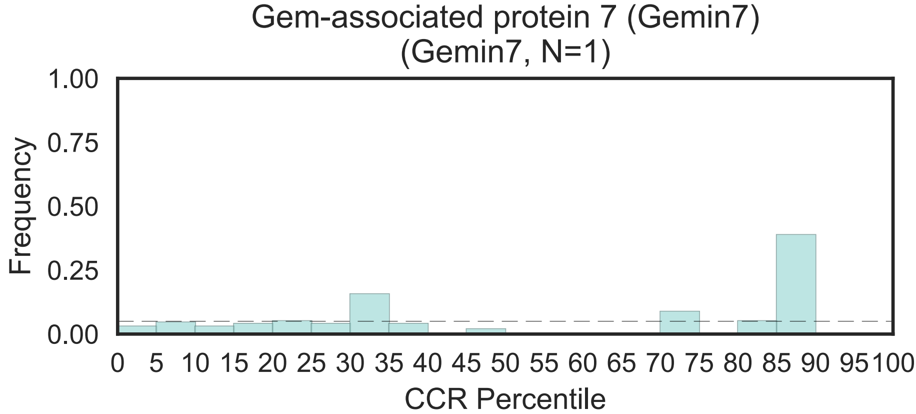

Nucleoside recognition
(Gate, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

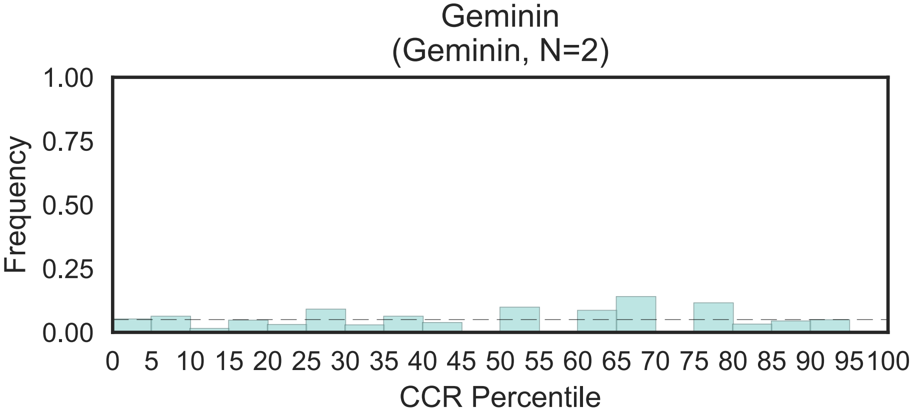

Alpha 1,4-glycosyltransferase conserved region
(Gb3_synth, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

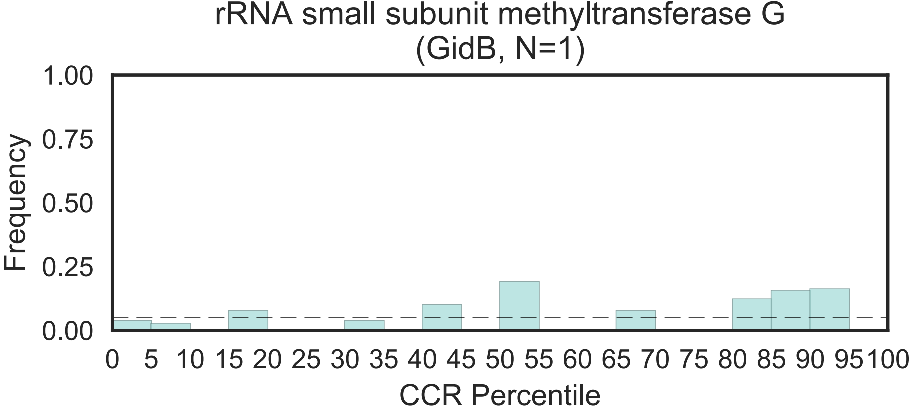

Gcd10p family
(Gcd10p, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

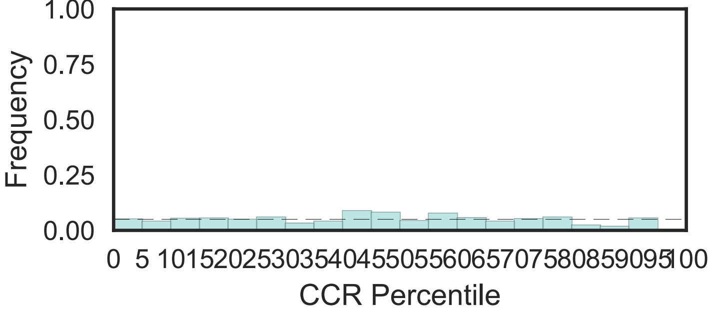

Gelsolin repeat
(Gelsolin, N=46)
Fisher's OR: 0.0751; Bonferroni p-val: 0.262
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Gemin6 protein
(Gemin6, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

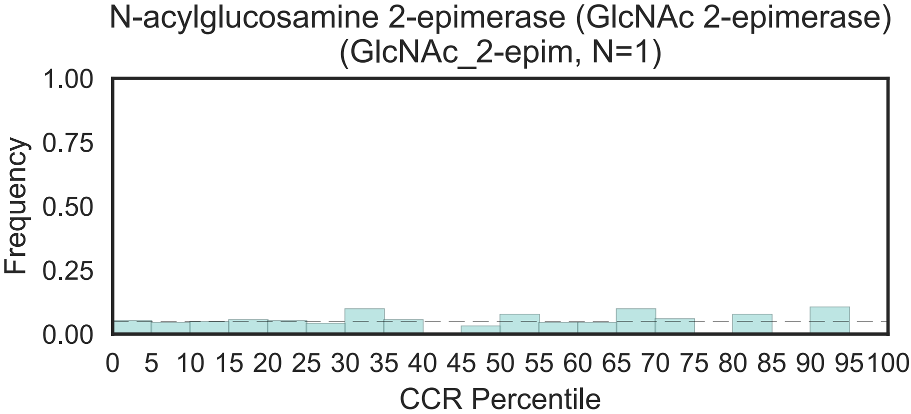

Gem-associated protein 7 (Gemin7)
(Gemin7, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

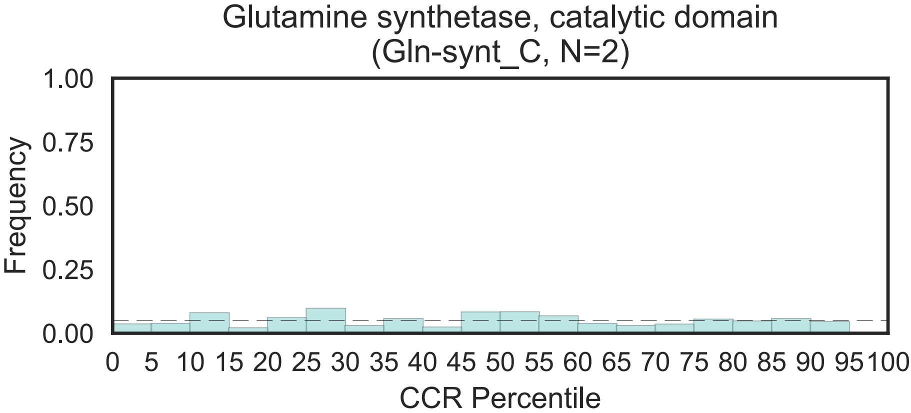

Geminin
(Geminin, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

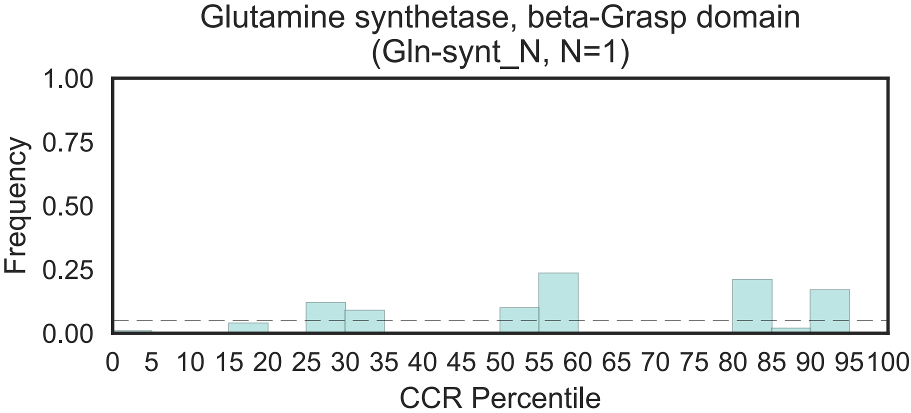

rRNA small subunit methyltransferase G
(GidB, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

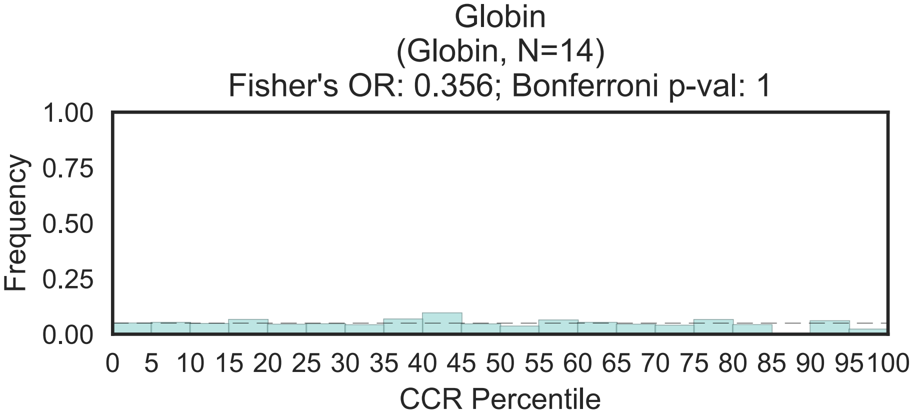


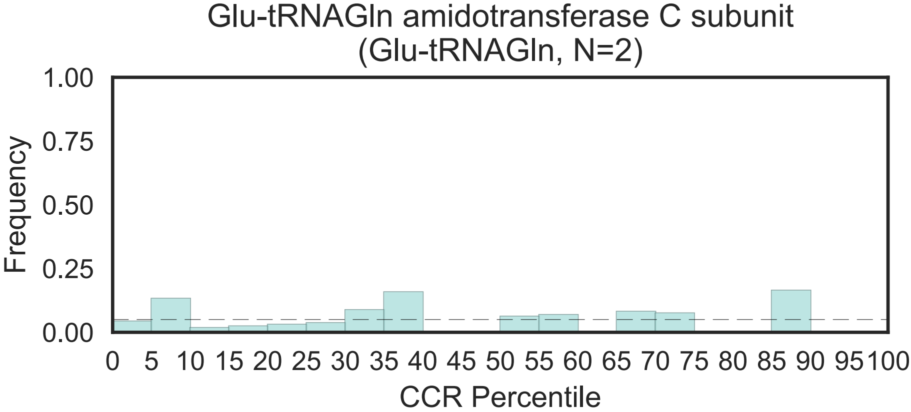
Vitamin K-dependent carboxylation/gamma-carboxyglutamic (GLA) domain
(Gla, N=9)
Fisher's OR: 0; Bonferroni p-val: 1

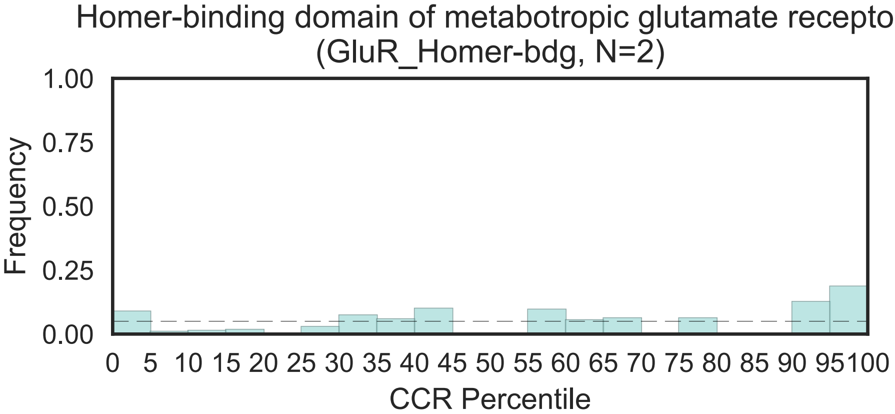

N-acylglucosamine 2-epimerase (GlcNAc 2-epimerase)
(GlcNAc_2-epim, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Glutamine synthetase, catalytic domain
(Gln-synt_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

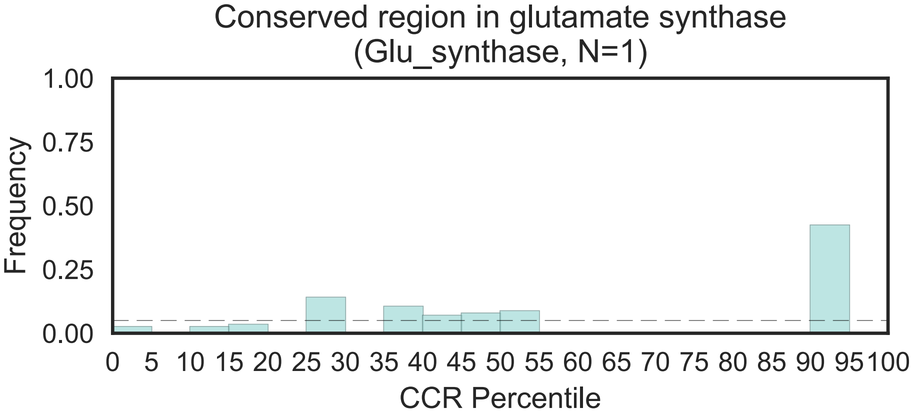

Glutamine synthetase, beta-Grasp domain
(Gln-synt_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

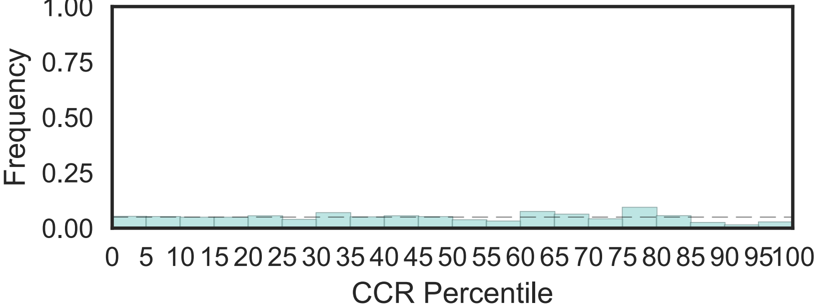

Globin
(Globin, N=14)
Fisher's OR: 0.356; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

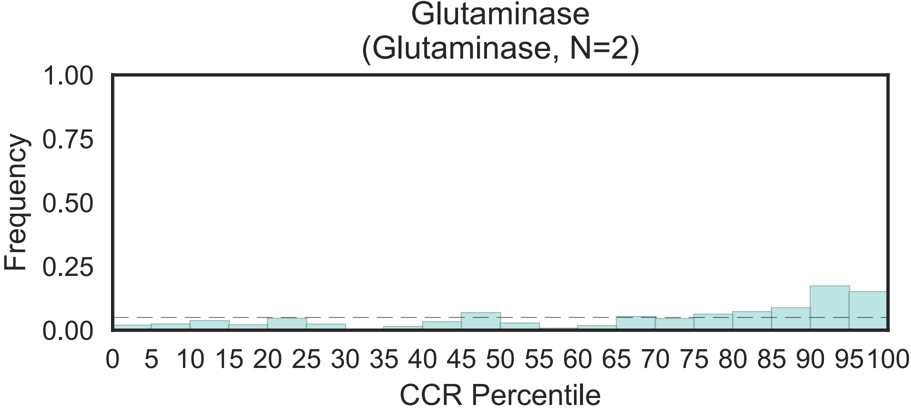

Glu-tRNAGln amidotransferase C subunit
(Glu-tRNAGln, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

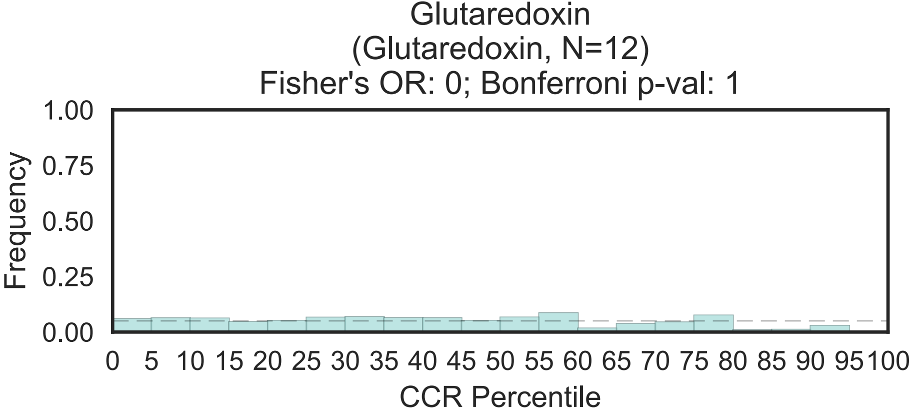


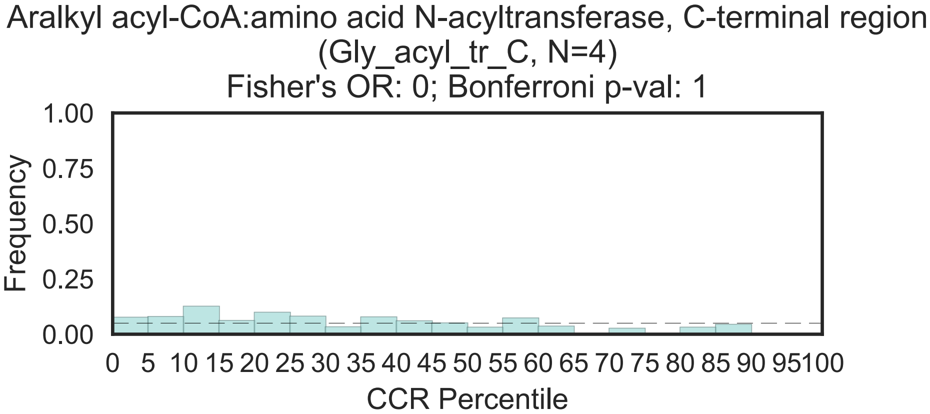
Homer-binding domain of metabotropic glutamate receptor
(GluR_Homer-bdg, N=2)

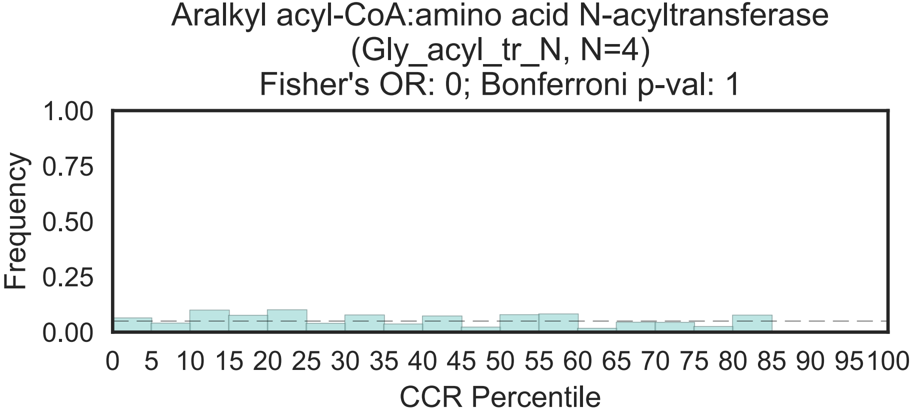

Conserved region in glutamate synthase
(Glu_synthase, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

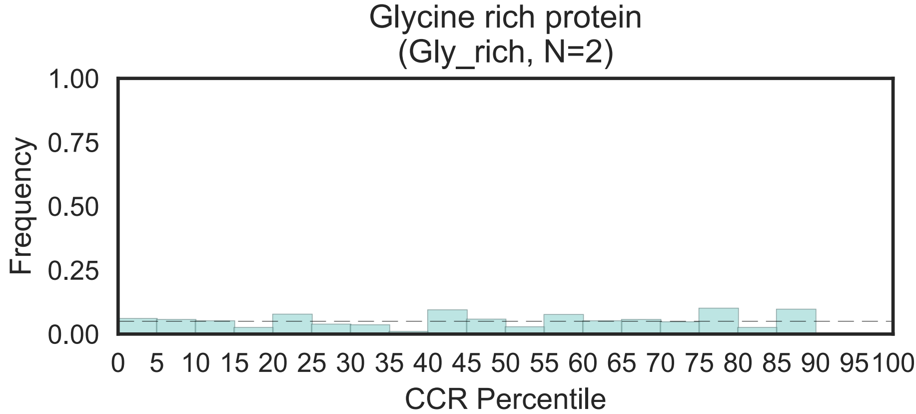

Glucosamine-6-phosphate isomerases/6-phosphogluconolactonase (Glucosamine_iso, N=4)
Fisher's OR: 0.342; Bonferroni p-val: 1

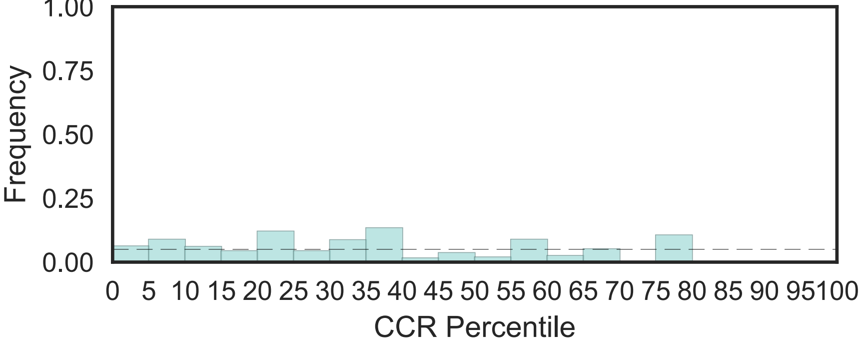

Glutaminase
(Glutaminase, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Glutaredoxin
(Glutaredoxin, N=12)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

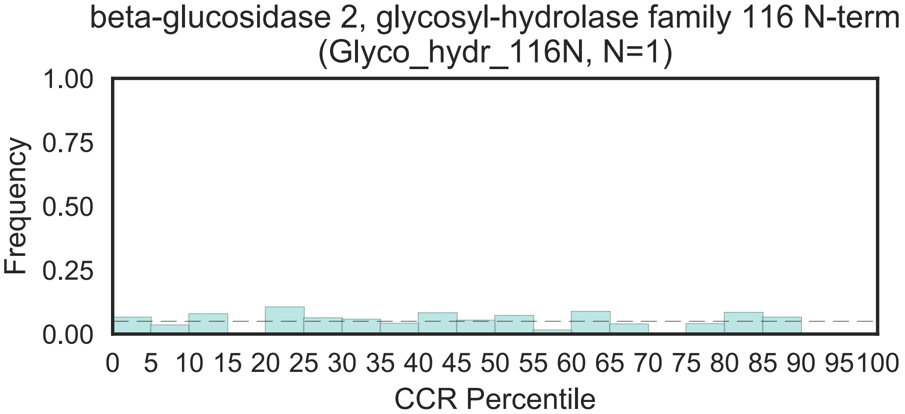

Aralkyl acyl-CoA:amino acid N-acyltransferase, C-terminal region
(Gly_acyl_tr_C, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

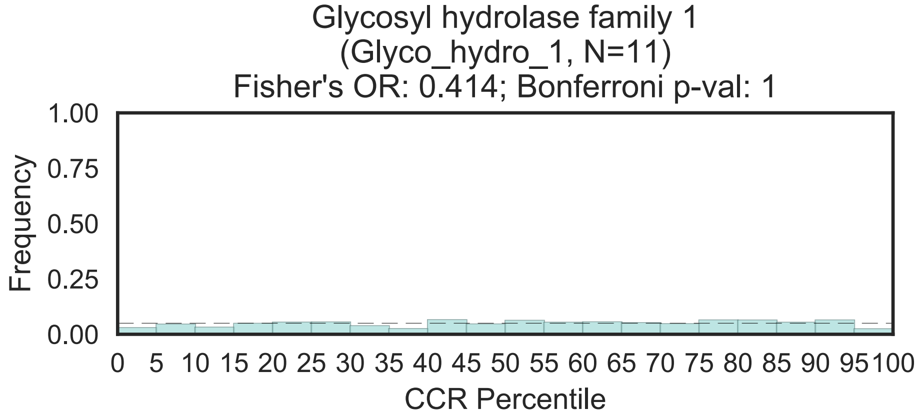

Aralkyl acyl-CoA:amino acid N-acyltransferase
(Gly_acyl_tr_N, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

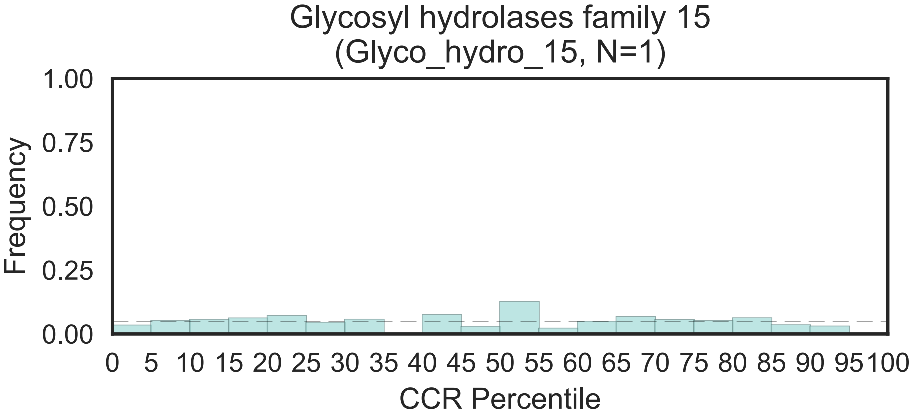

Glycine rich protein
(Gly_rich, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

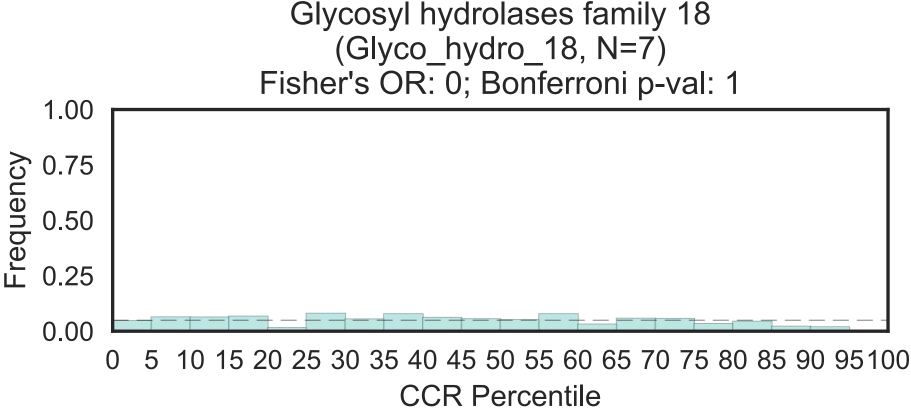


Glycosyltransferase sugar-binding region containing DXD motif
(Gly_transf_sug, N=2)

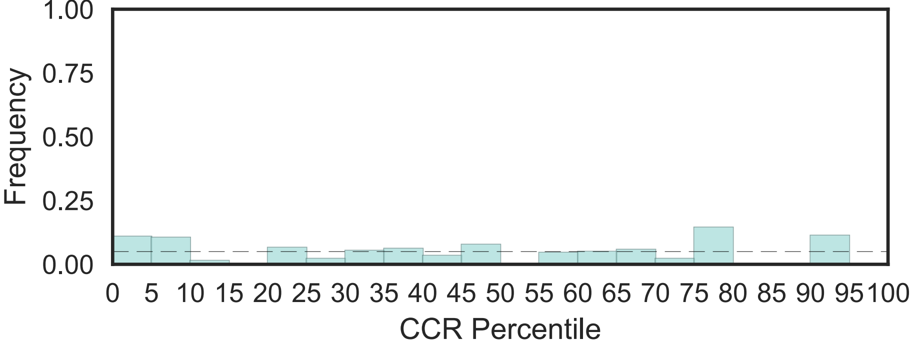

beta-glucosidase 2, glycosyl-hydrolase family 116 N-term
(Glyco_hydr_116N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

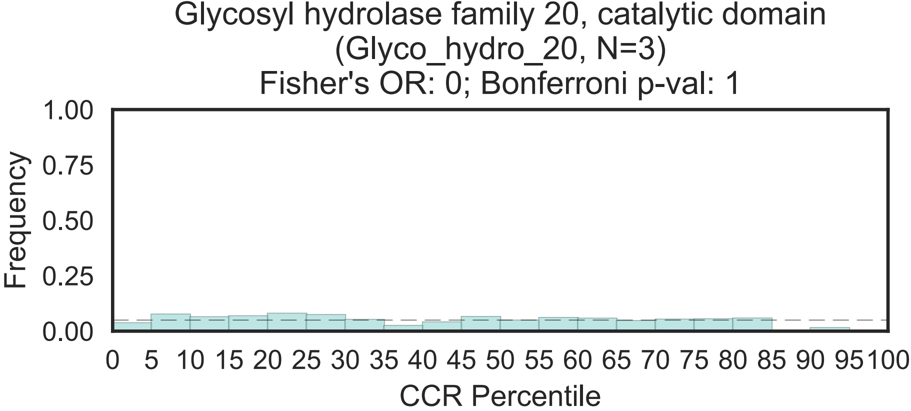

Glycosyl hydrolase family 1
(Glyco_hydro_1, N=11)
Fisher's OR: 0.414; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

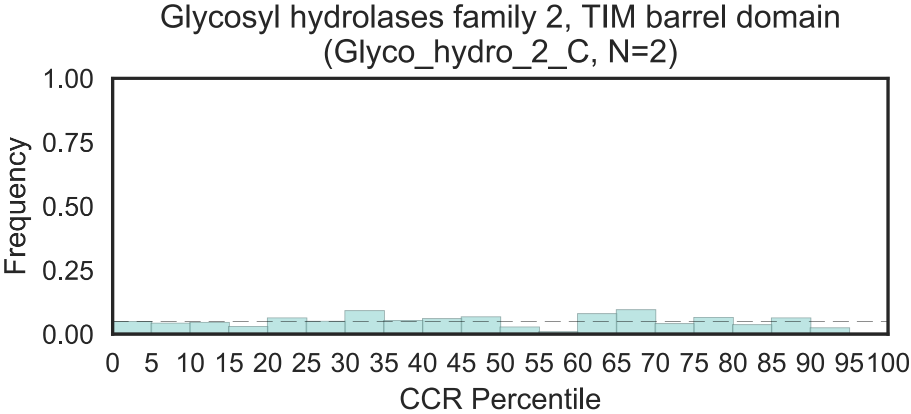

Glycosyl hydrolases family 15
(Glyco_hydro_15, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Glycosyl hydrolases family 18
(Glyco_hydro_18, N=7)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

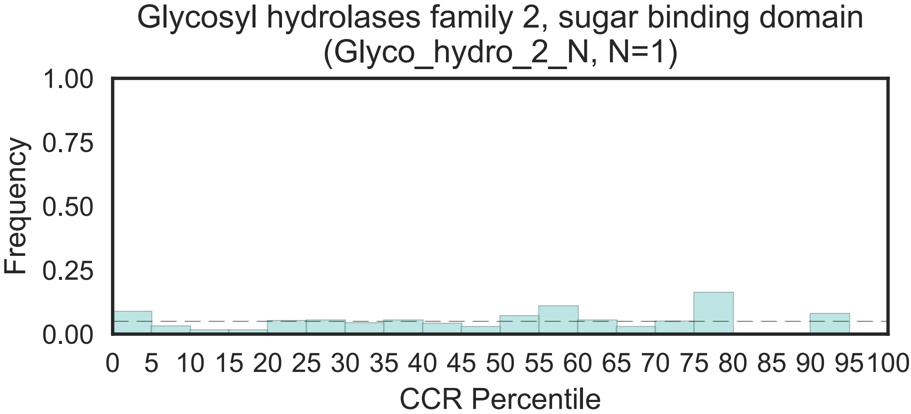
Glycosyl hydrolases family 2 (Glyco_hydro_2, N=1)

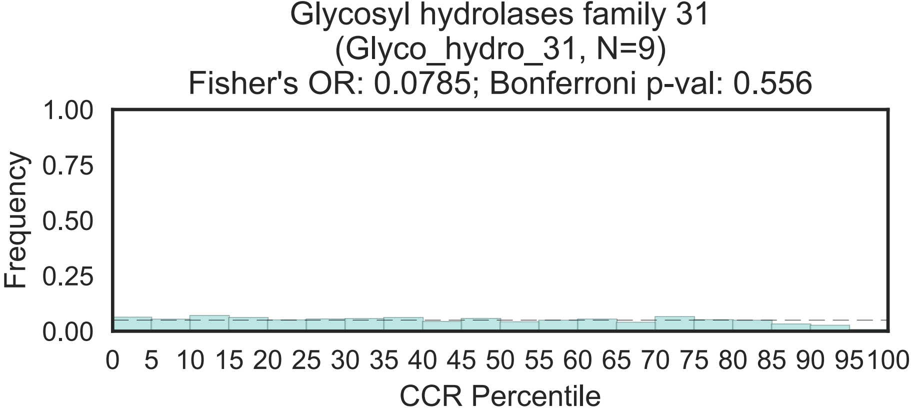


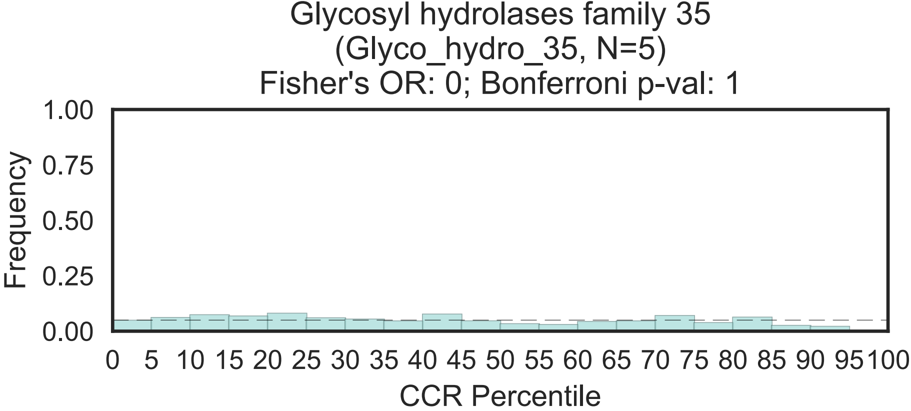

Glycosyl hydrolase family 20, catalytic domain
(Glyco_hydro_20, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

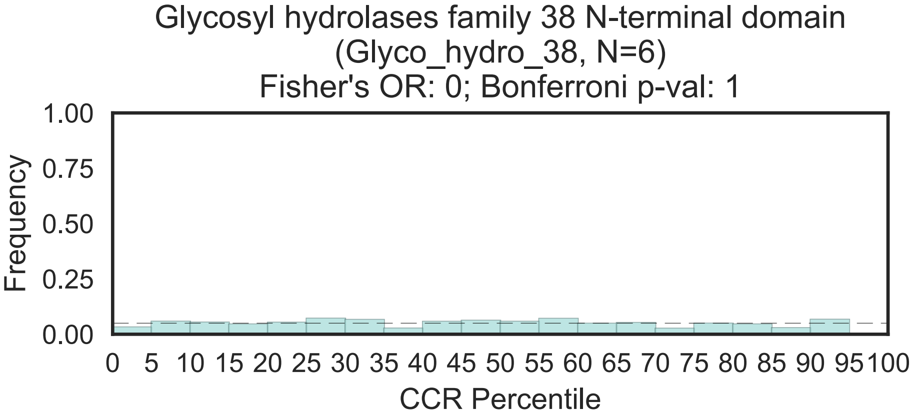


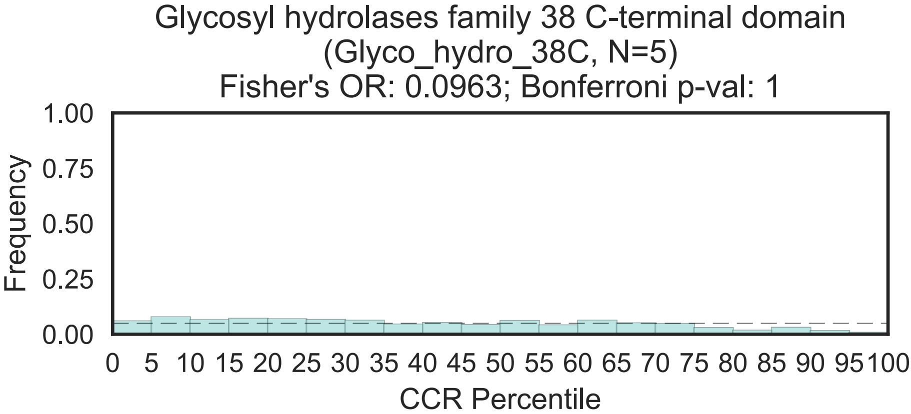
Glycosyl hydrolases family 2, TIM barrel domain
(Glyco_hydro_2_C, N=2)

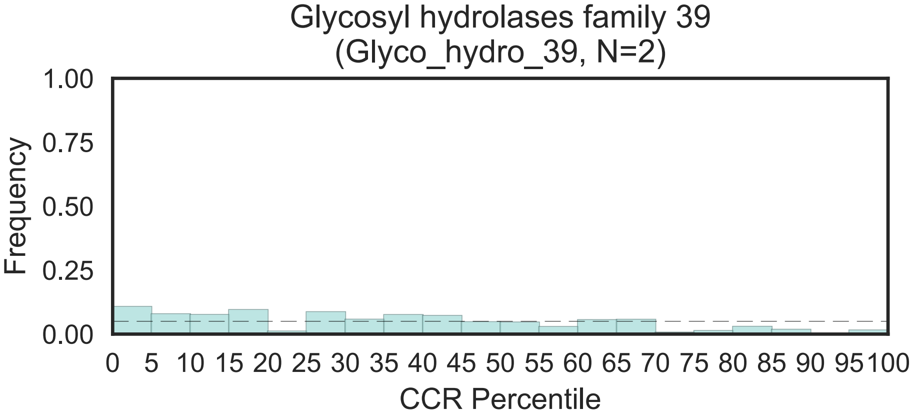

Glycosyl hydrolases family 2, sugar binding domain
(Glyco_hydro_2_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

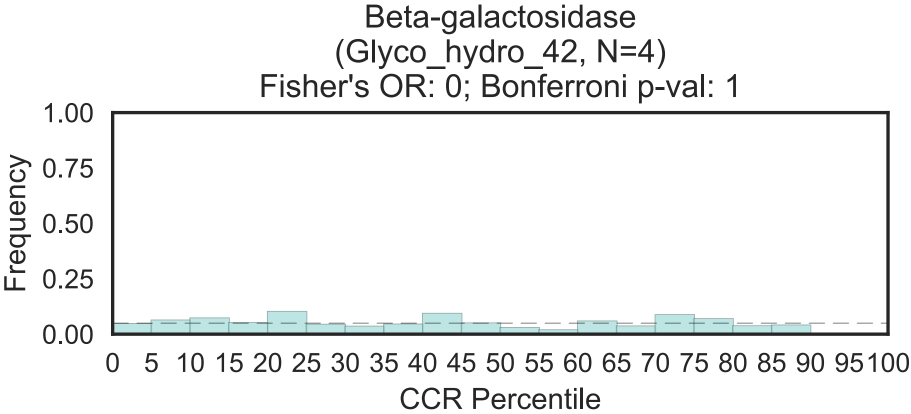

Glycosyl hydrolases family 31
(Glyco_hydro_31, N=9)
Fisher's OR: 0.0785; Bonferroni p-val: 0.556
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

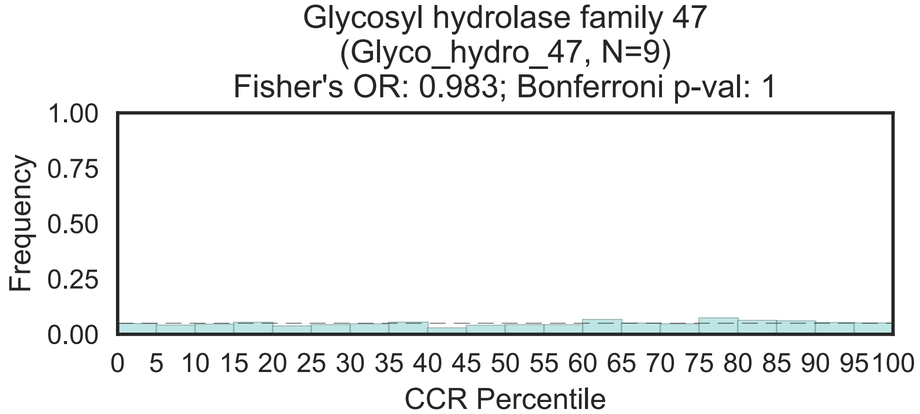

Glycosyl hydrolases family 35
(Glyco_hydro_35, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Glycosyl hydrolases family 38 N-terminal domain
(Glyco_hydro_38, N=6)
Fisher's OR: 0; Bonferroni p-val: 1

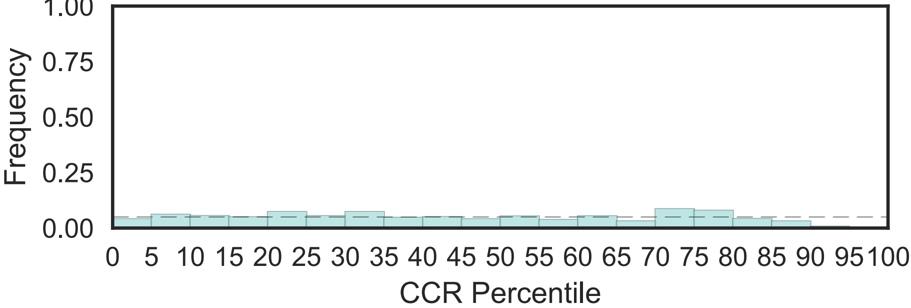

Glycosyl hydrolases family 38 C-terminal domain
(Glyco_hydro_38C, N=5)
Fisher's OR: 0.0963; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

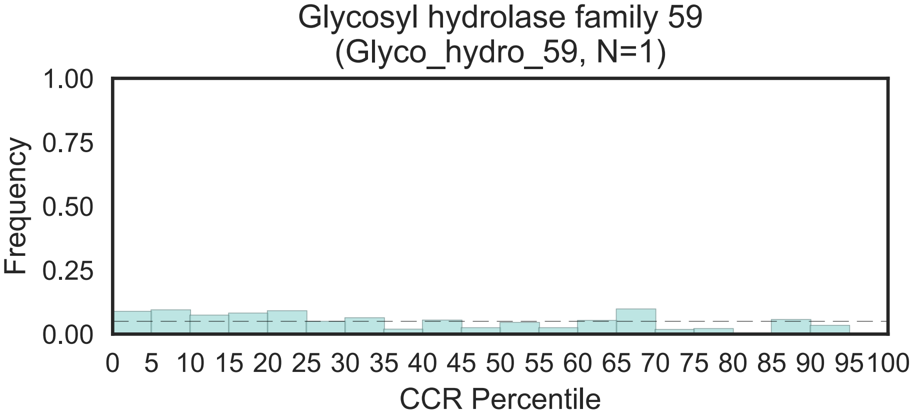

Glycosyl hydrolases family 39
(Glyco_hydro_39, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

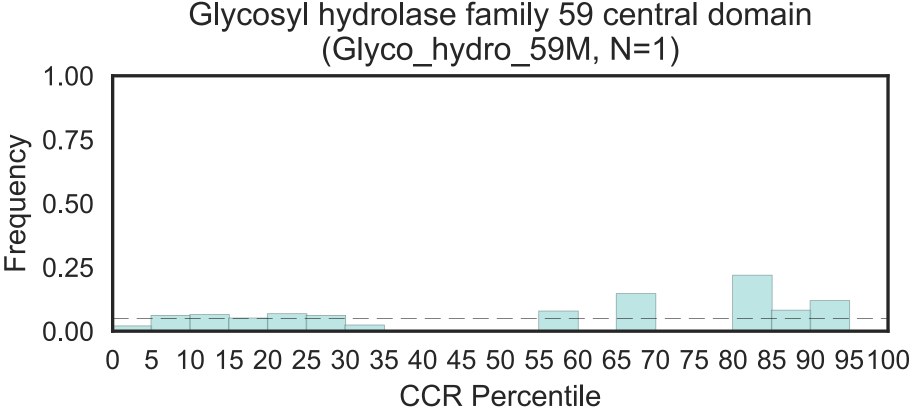

Beta-galactosidase
(Glyco_hydro_42, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

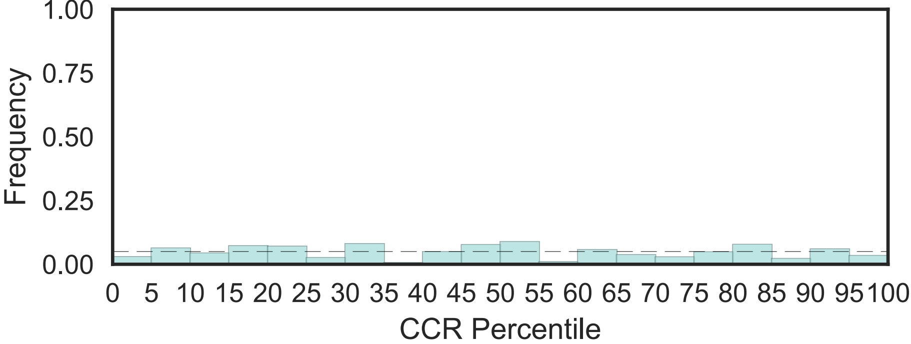

Glycosyl hydrolase family 47
(Glyco_hydro_47, N=9)
Fisher's OR: 0.983; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Hyaluronidase
(Glyco_hydro_56, N=5)
Fisher's OR: 0; Bonferroni p-val: 1

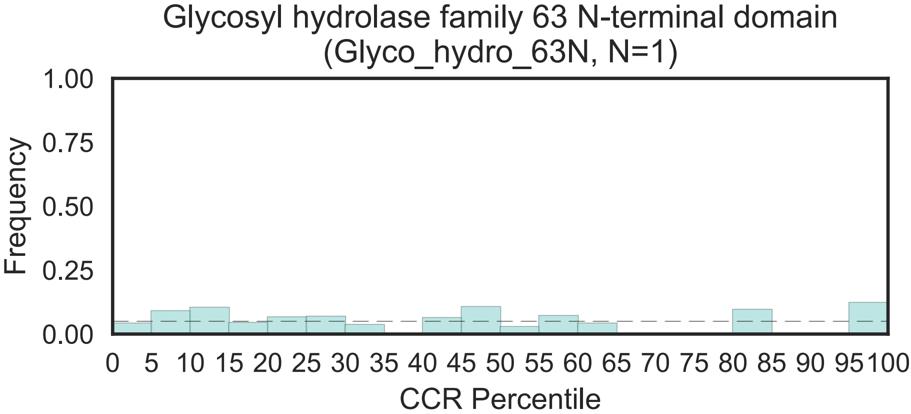



Glycosyl hydrolase family 59
(Glyco_hydro_59, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

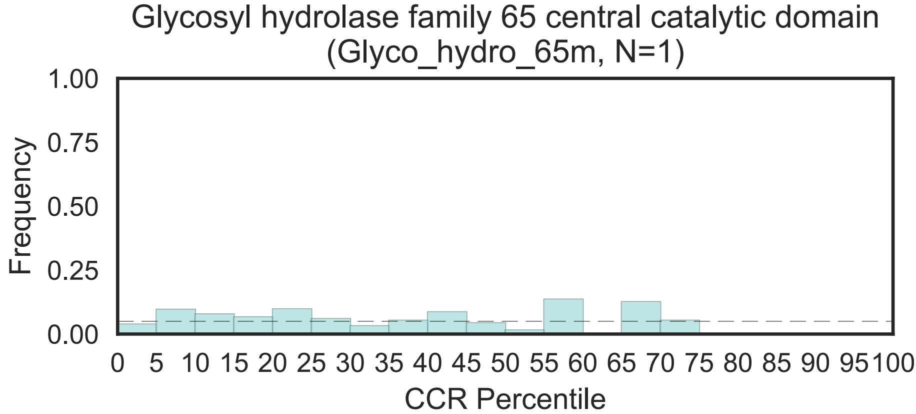

Glycosyl hydrolase family 59 central domain
(Glyco_hydro_59M, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

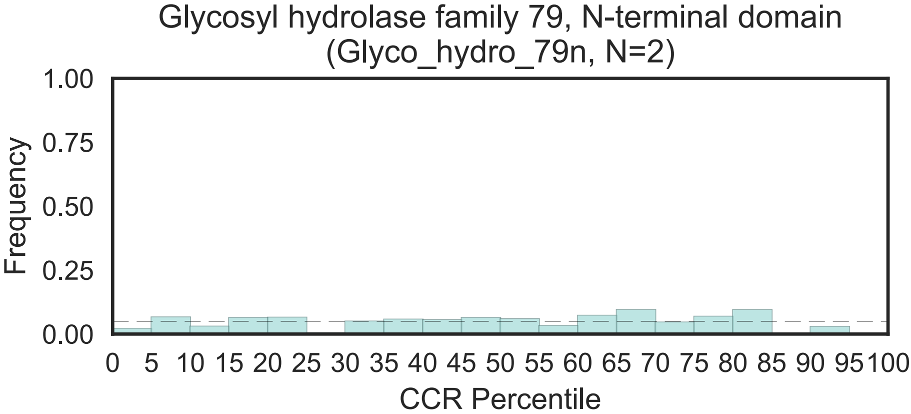


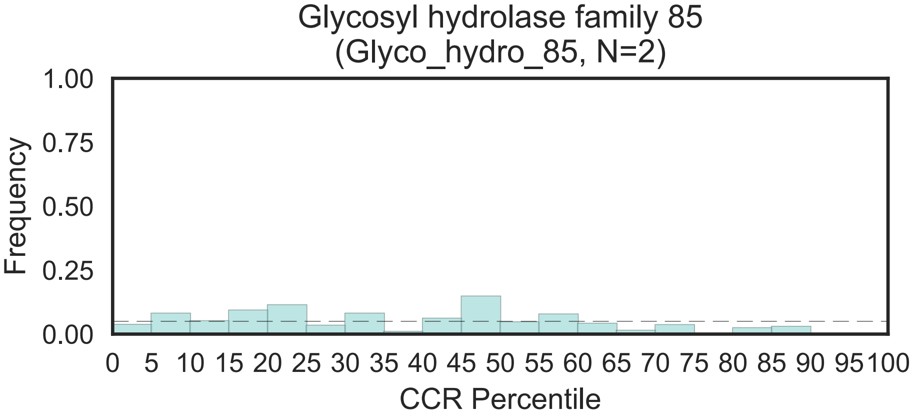
Glycosyl hydrolase family 63 C-terminal domain
(Glyco_hydro_63, N=1)

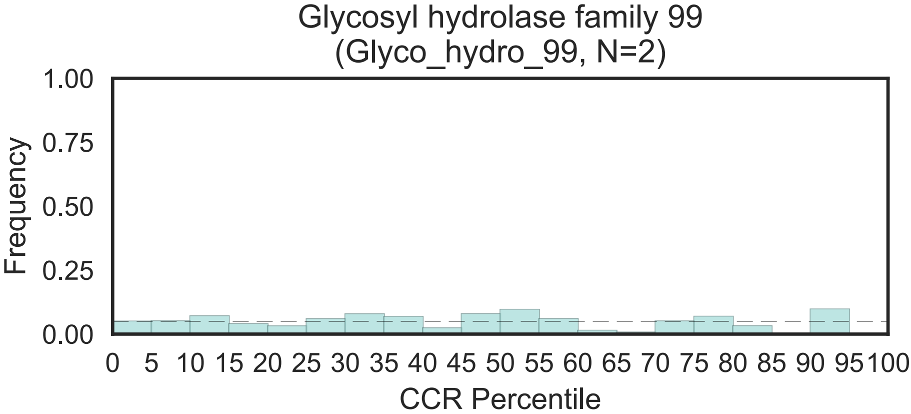


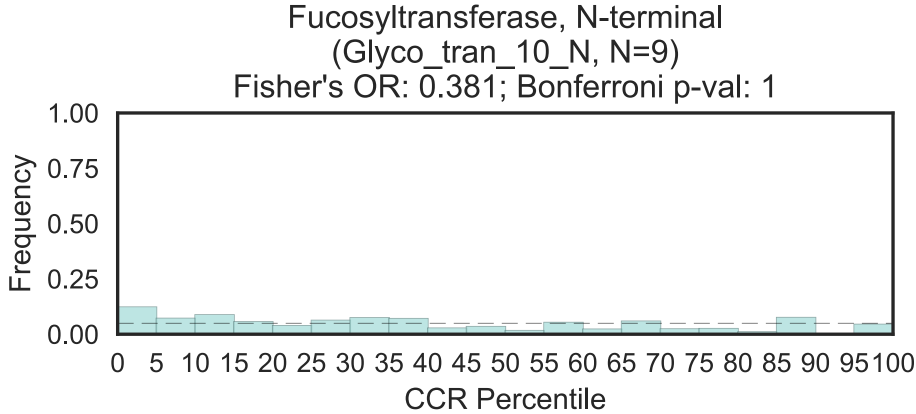
Glycosyl hydrolase family 63 N-terminal domain (Glyco_hydro_63N, N=1)

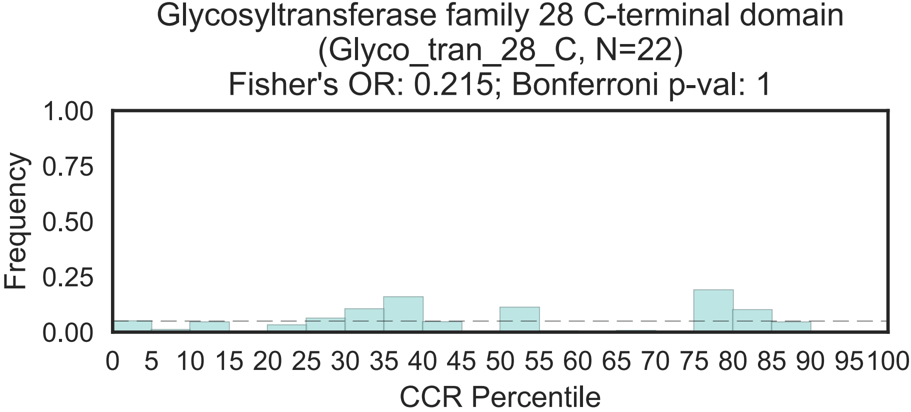

Glycosyl hydrolase family 65 central catalytic domain
(Glyco_hydro_65m, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Glycosyl hydrolase family 79, N-terminal domain
(Glyco_hydro_79n, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

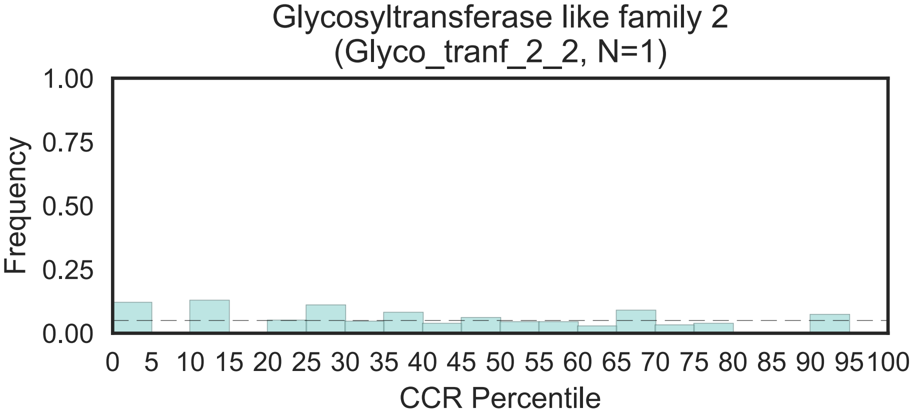

Glycosyl hydrolase family 85
(Glyco_hydro_85, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

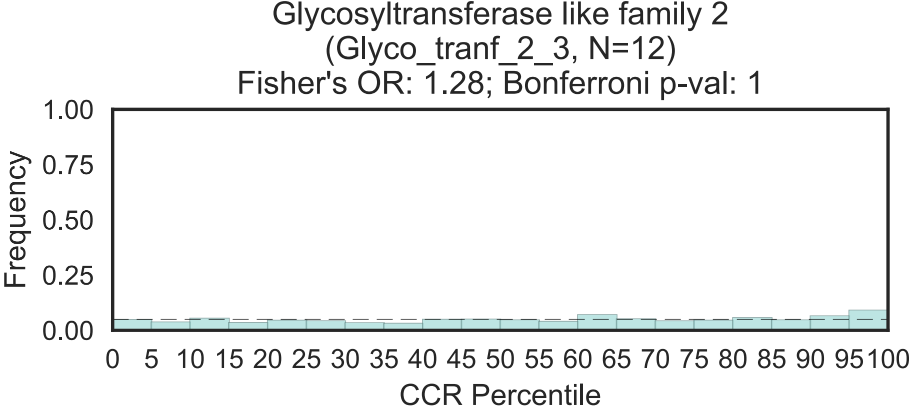

Glycosyl hydrolase family 99
(Glyco_hydro_99, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

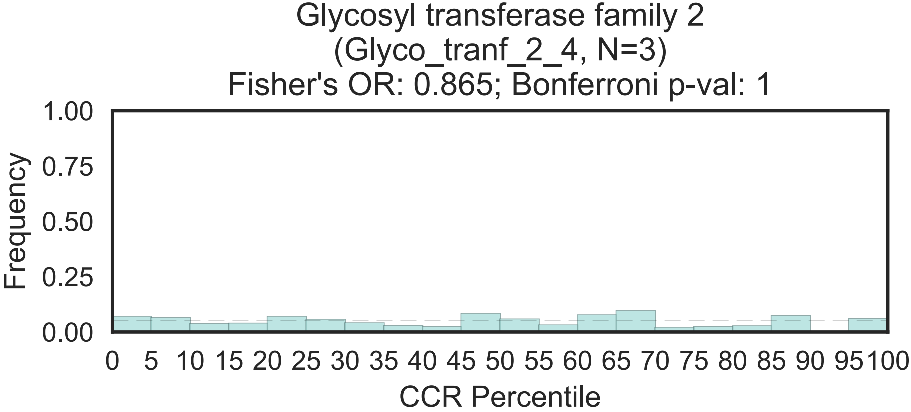

Fucosyltransferase, N-terminal
(Glyco_tran_10_N, N=9)
Fisher's OR: 0.381; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

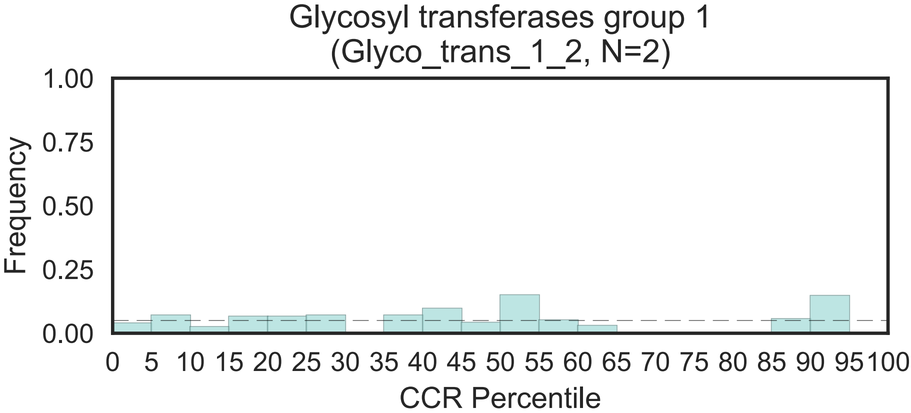


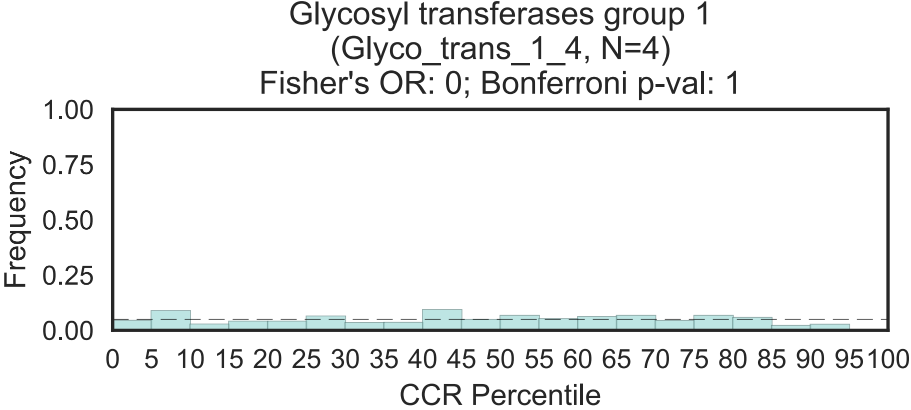
Glycosyltransferase family 28 C-terminal domain
(Glyco_tran_28_C, N=22)
Fisher's OR: 0.215; Bonferroni p-val: 1

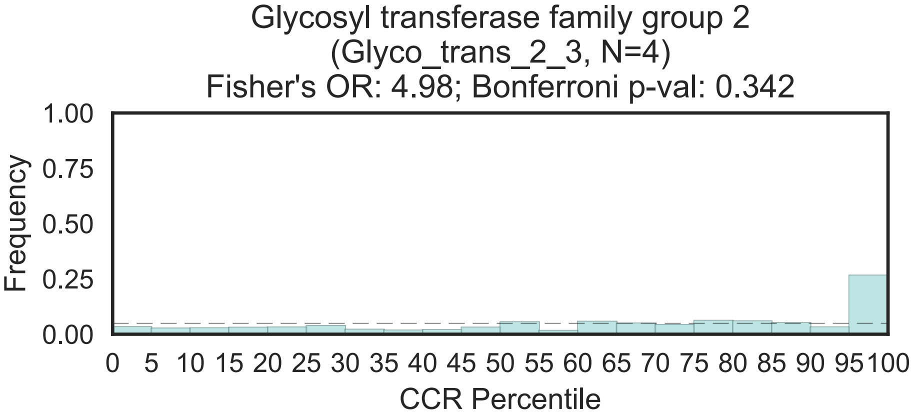

Glycosyltransferase like family 2
(Glyco_tranf_2_2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

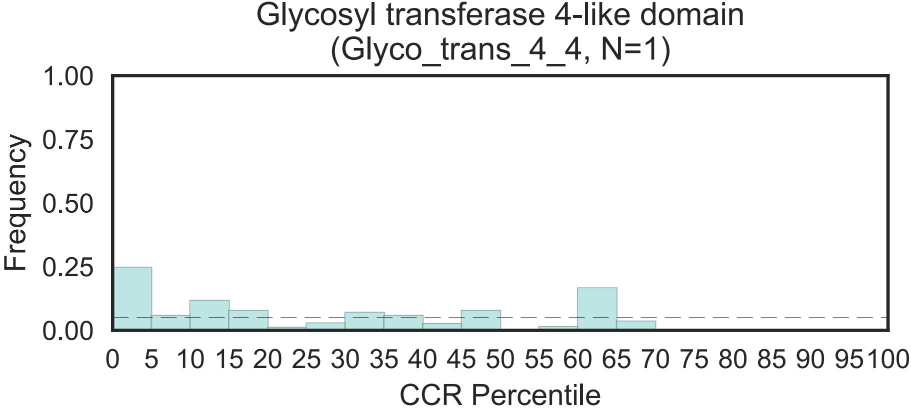

Glycosyltransferase like family 2
(Glyco_tranf_2_3, N=12)
Fisher's OR: 1.28; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

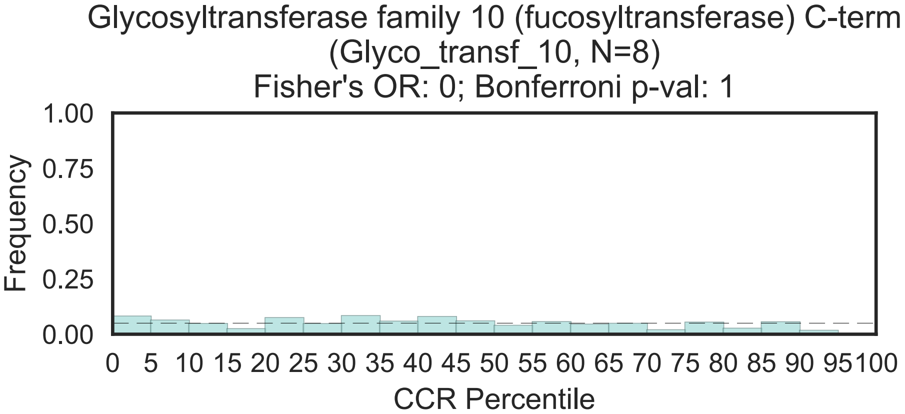

Glycosyl transferase family 2
(Glyco_tranf_2_4, N=3)
Fisher's OR: 0.865; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

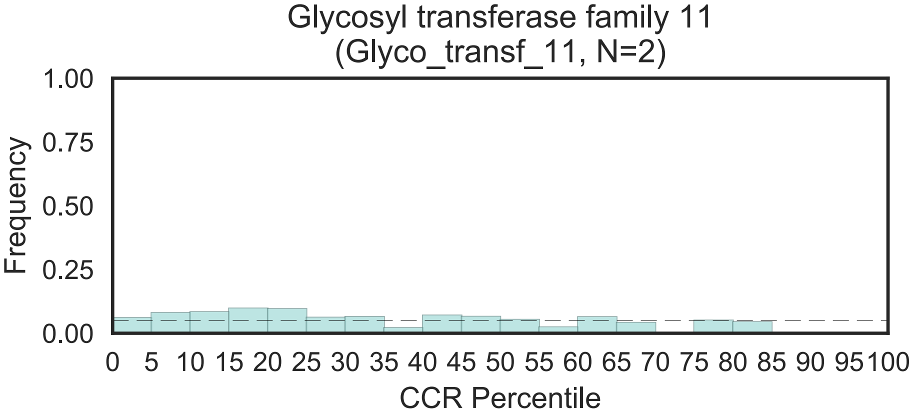

Glycosyl transferases group 1
(Glyco_trans_1_2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

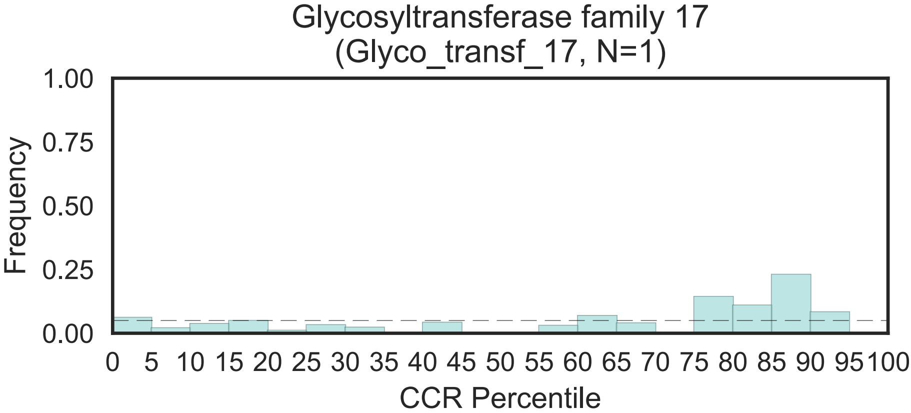

Glycosyl transferases group 1
(Glyco_trans_1_4, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Glycosyl transferase family group 2
(Glyco_trans_2_3, N=4)
Fisher's OR: 4.98; Bonferroni p-val: 0.342
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

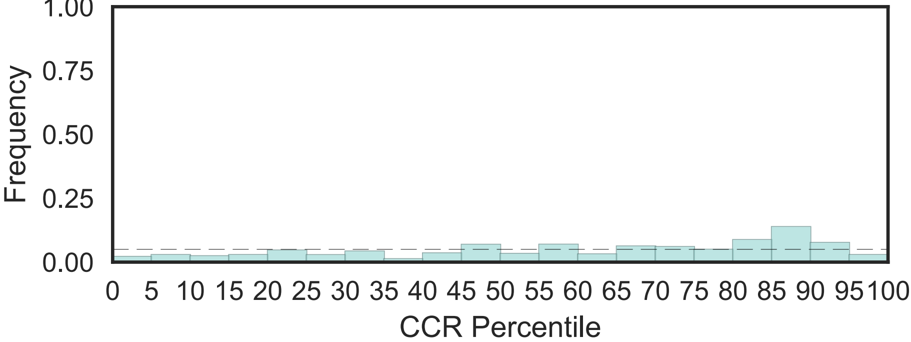

Glycosyl transferase 4-like domain
(Glyco_trans_4_4, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

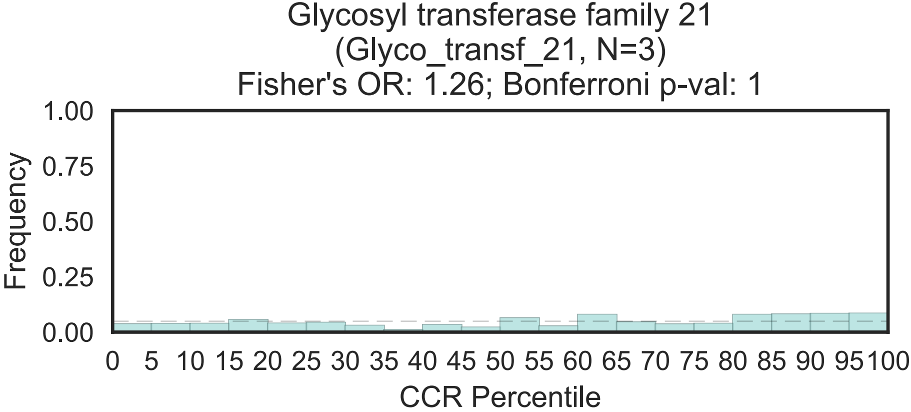

Glycosyltransferase family 10 (fucosyltransferase) C-term
(Glyco_transf_10, N=8)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

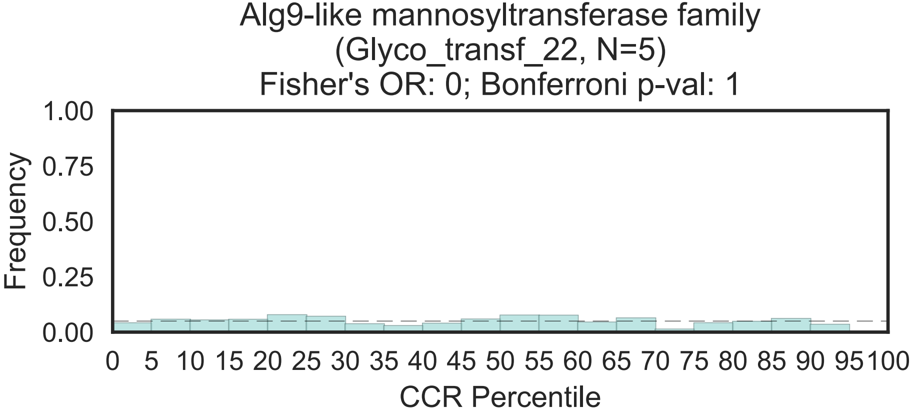

Glycosyl transferase family 11
(Glyco_transf_11, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

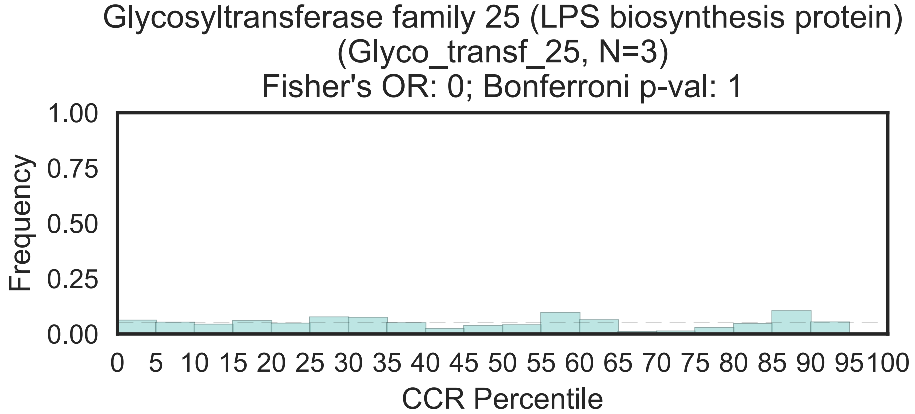

Glycosyltransferase family 17
(Glyco_transf_17, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

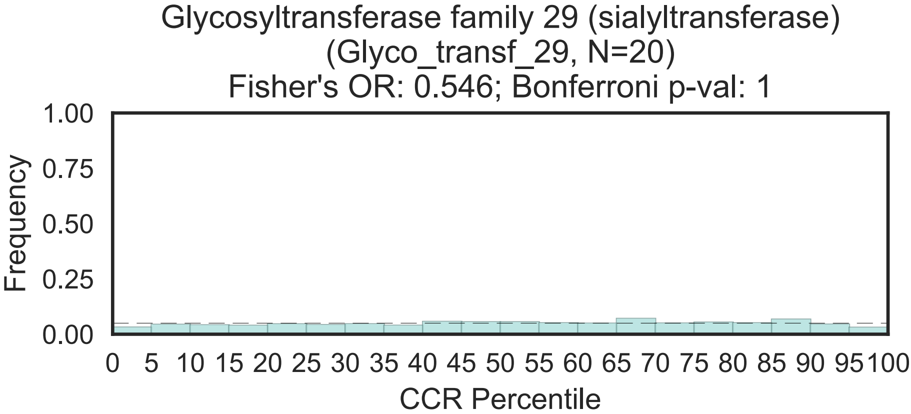
Glycosyltransferase family 18 (Glyco_transf_18, N=2)

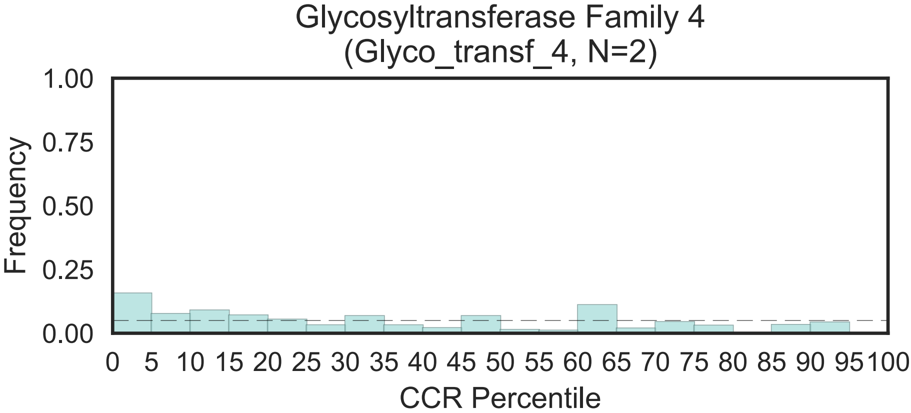


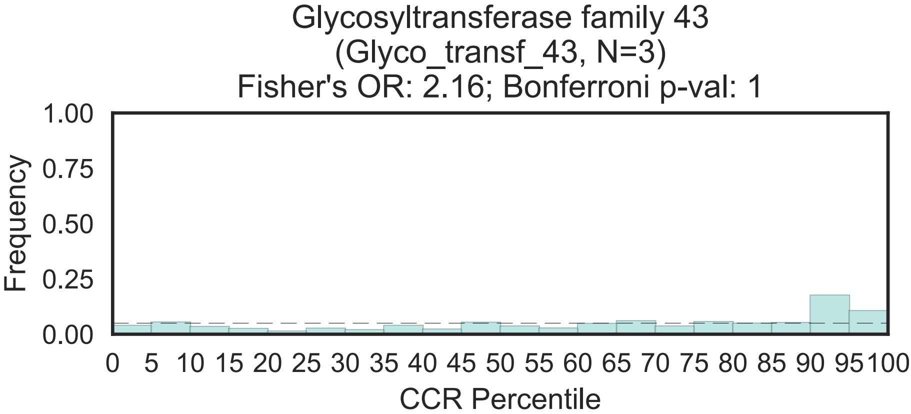

Glycosyl transferase family 21
(Glyco_transf_21, N=3)
Fisher's OR: 1.26; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

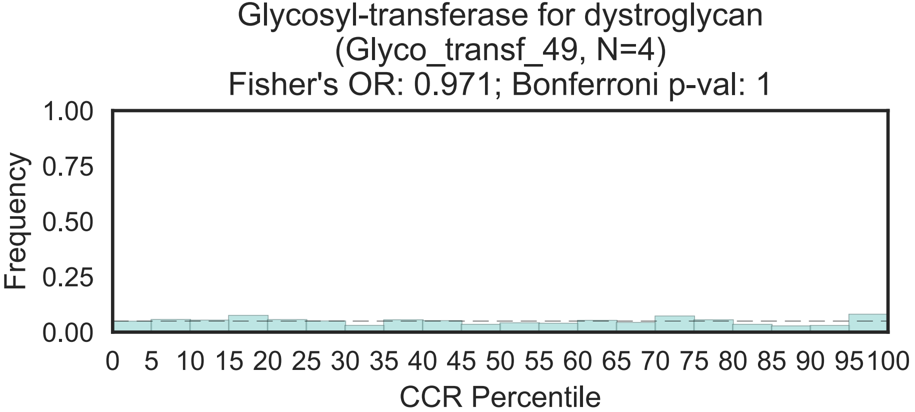

Alg9-like mannosyltransferase family
(Glyco_transf_22, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

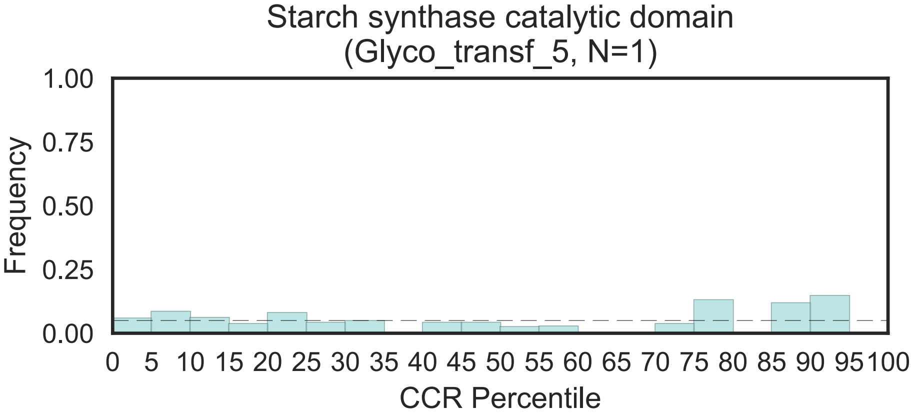

Glycosyltransferase family 25 (LPS biosynthesis protein)
(Glyco_transf_25, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

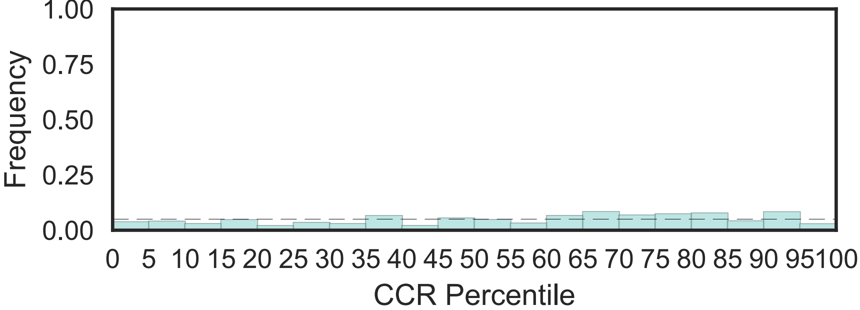

Glycosyltransferase family 29 (sialyltransferase)
(Glyco_transf_29, N=20)
Fisher's OR: 0.546; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Glycosyltransferase Family 4
(Glyco_transf_4, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

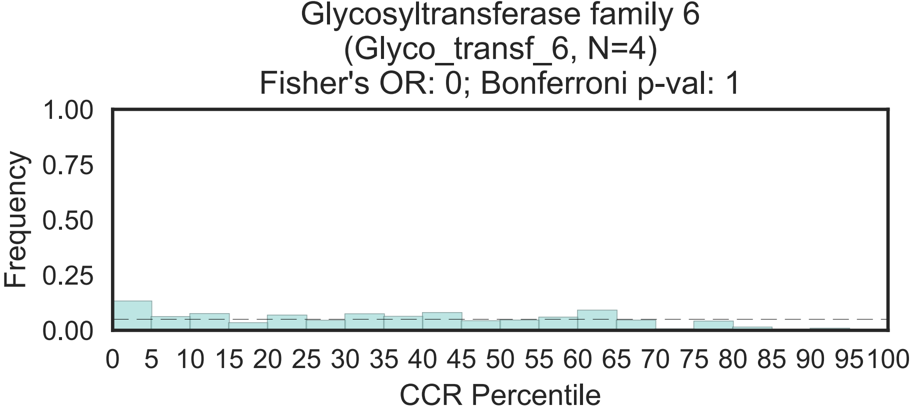

Glycosyltransferase family 43
(Glyco_transf_43, N=3)
Fisher's OR: 2.16; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Glycosyl-transferase for dystroglycan
(Glyco_transf_49, N=4)
Fisher's OR: 0.971; Bonferroni p-val: 1

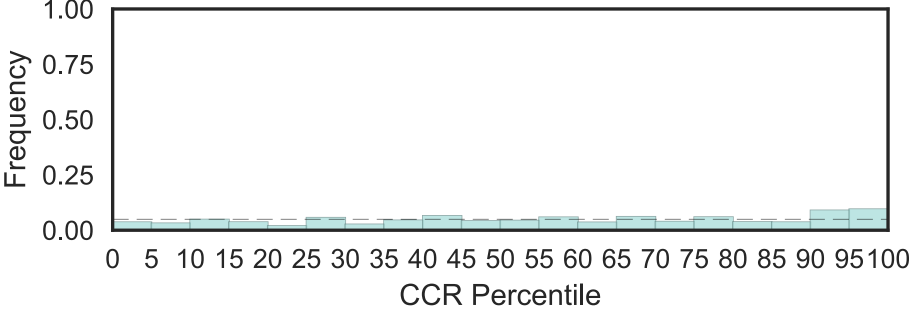

Starch synthase catalytic domain
(Glyco_transf_5, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

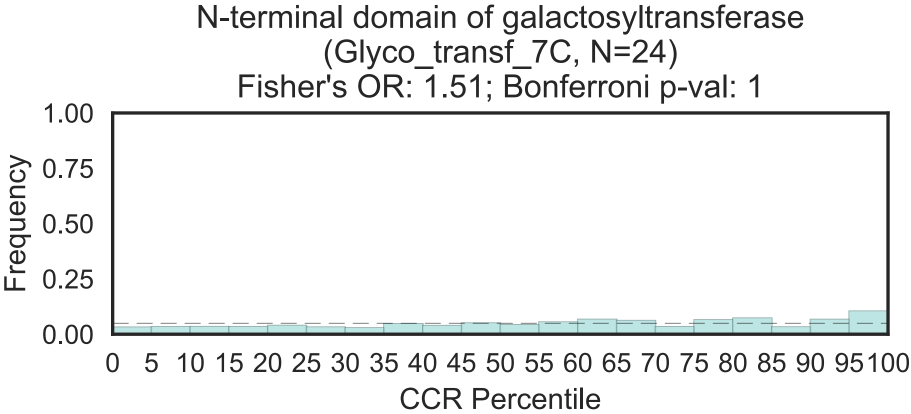


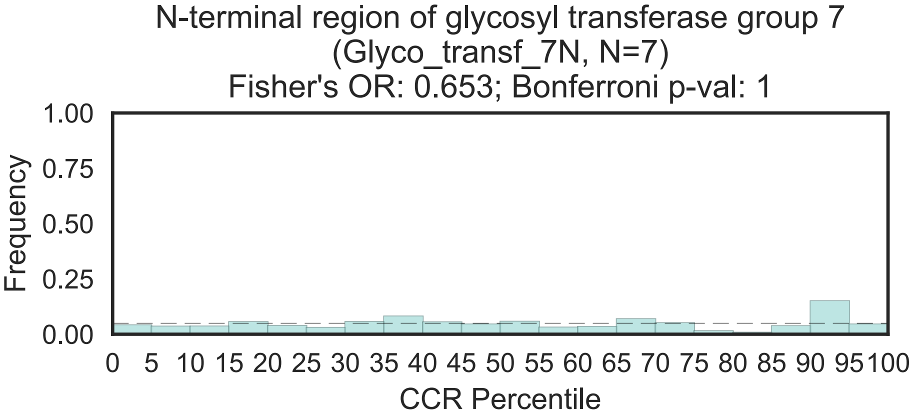
N-Acetylglucosaminyltransferase-IV (GnT-IV) conserved region
(Glyco_transf_54, N=5)
Fisher's OR: 0.671; Bonferroni p-val: 1

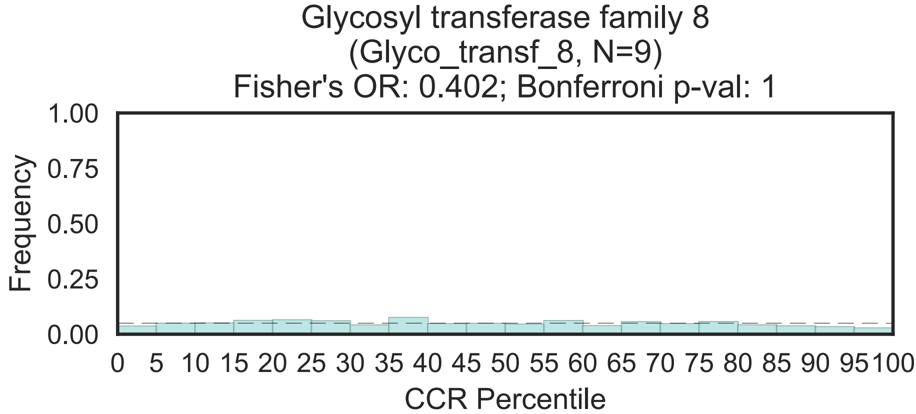

Glycosyltransferase family 6
(Glyco_transf_6, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

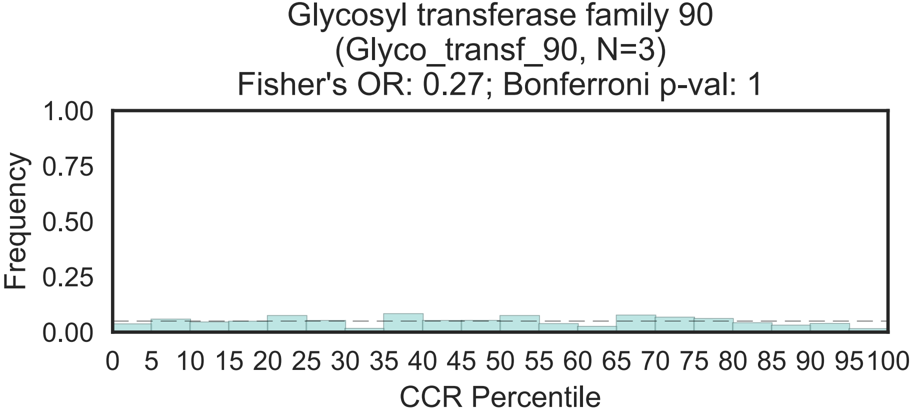
Glycosyl transferase family 64 domain
(Glyco_transf_64, N=5)
Fisher's OR: 1.74; Bonferroni p-val: 1

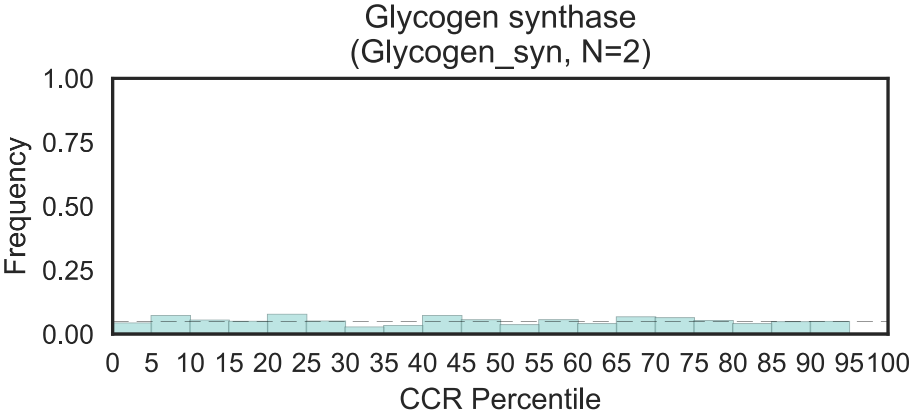


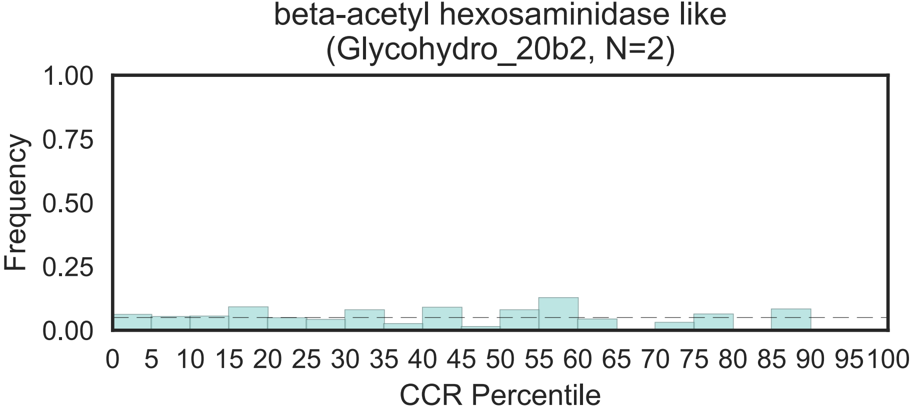

N-terminal domain of galactosyltransferase
(Glyco_transf_7C, N=24)
Fisher's OR: 1.51; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

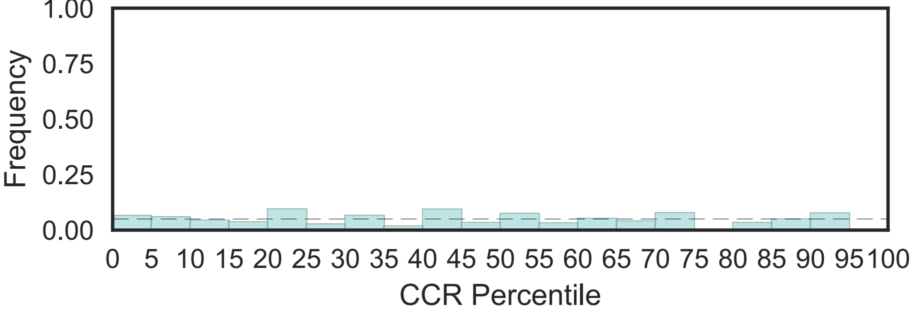

N-terminal region of glycosyl transferase group 7
(Glyco_transf_7N, N=7)
Fisher's OR: 0.653; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Glycosyl transferase family 8
(Glyco_transf_8, N=9)
Fisher's OR: 0.402; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

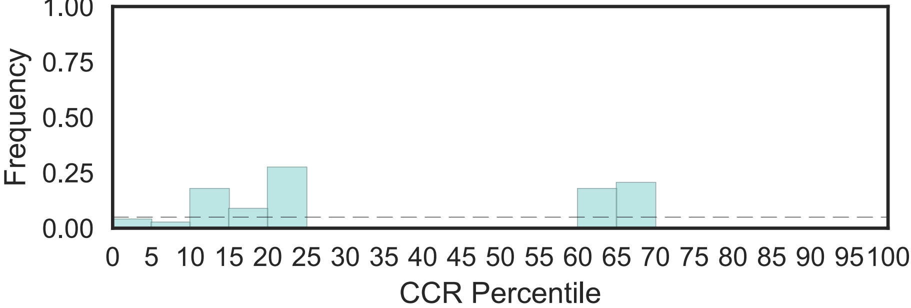

Glycosyl transferase family 90
(Glyco_transf_90, N=3)
Fisher's OR: 0.27; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

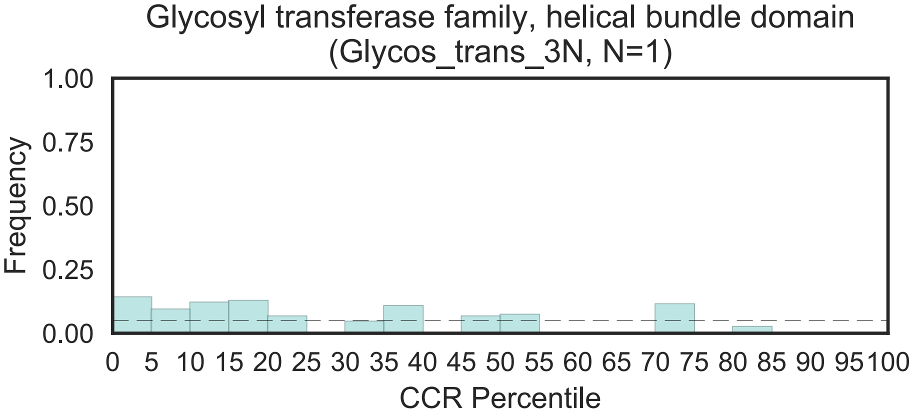

Glycogen synthase
(Glycogen_syn, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

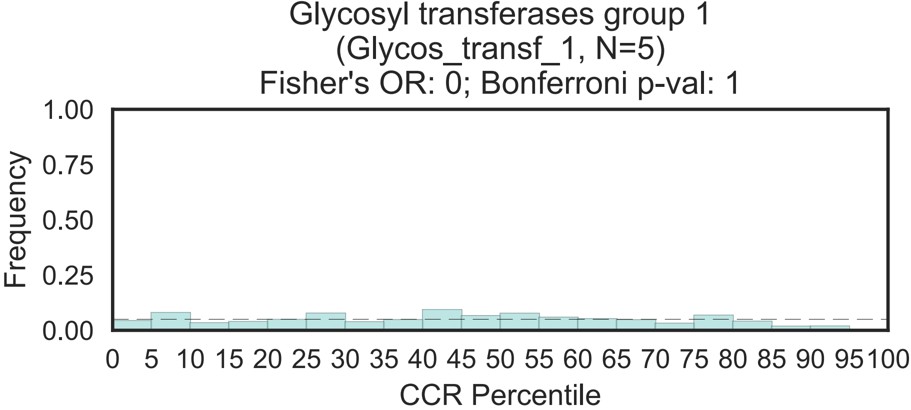

beta-acetyl hexosaminidase like
(Glycohydro_20b2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

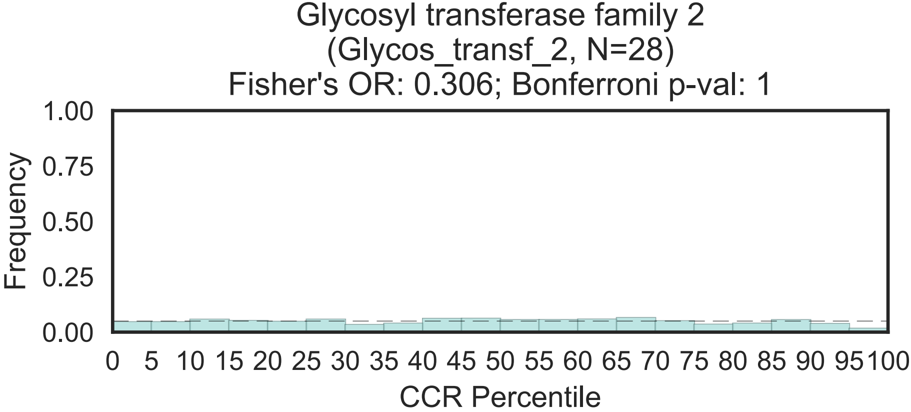

Fructose-bisphosphate aldolase class-I
(Glycolytic, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

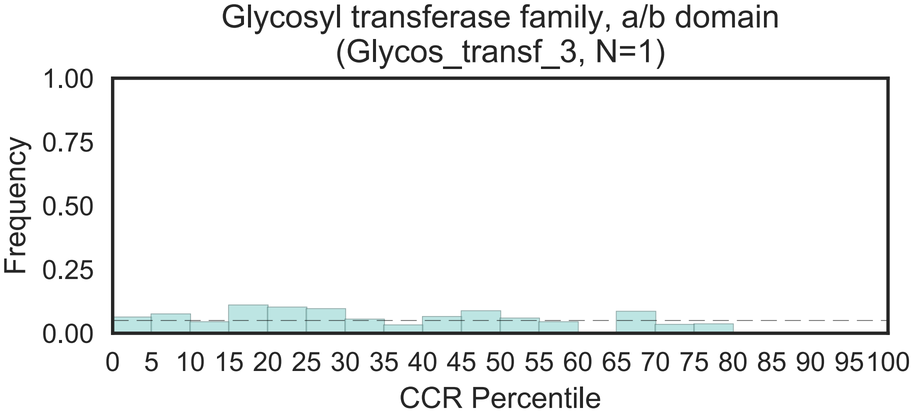
Glycophorin A
(Glycophorin_A, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

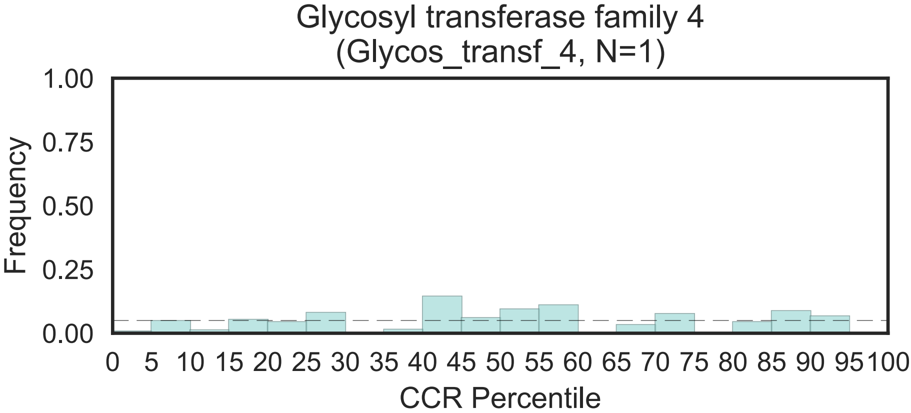



Glycosyl transferase family, helical bundle domain
(Glycos_trans_3N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

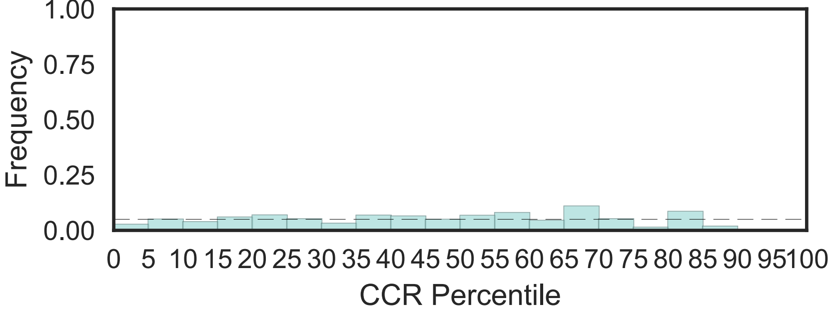

Glycosyl transferases group 1
(Glycos_transf_1, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

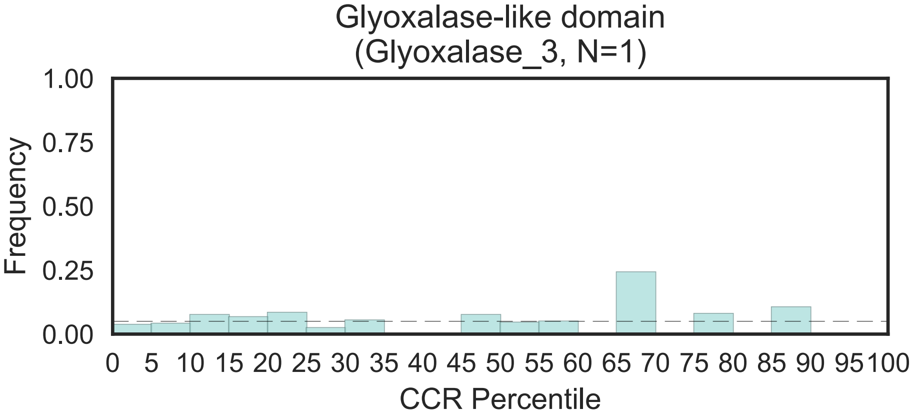

Glycosyl transferase family 2
(Glycos_transf_2, N=28)
Fisher's OR: 0.306; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

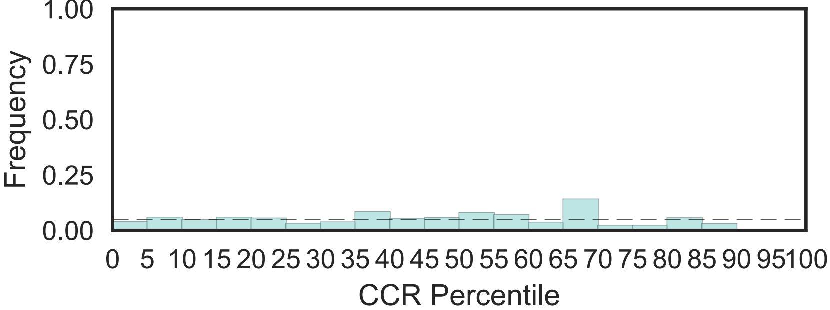

Glycosyl transferase family, a/b domain
(Glycos_transf_3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

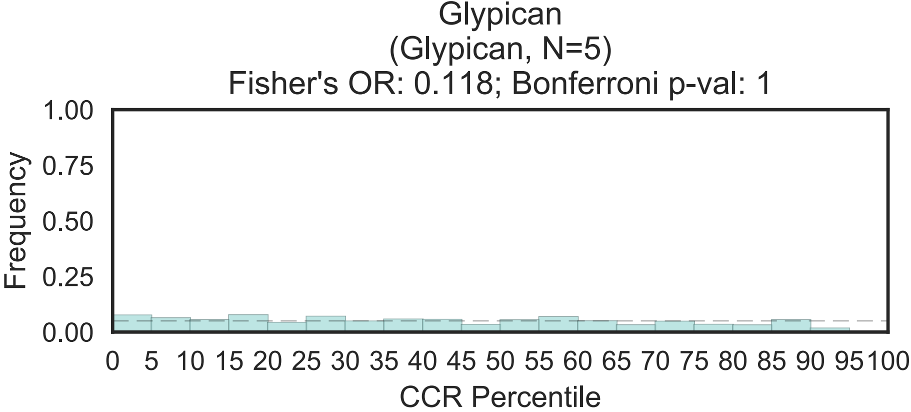

Glycosyl transferase family 4
(Glycos_transf_4, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily
(Glyoxalase, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

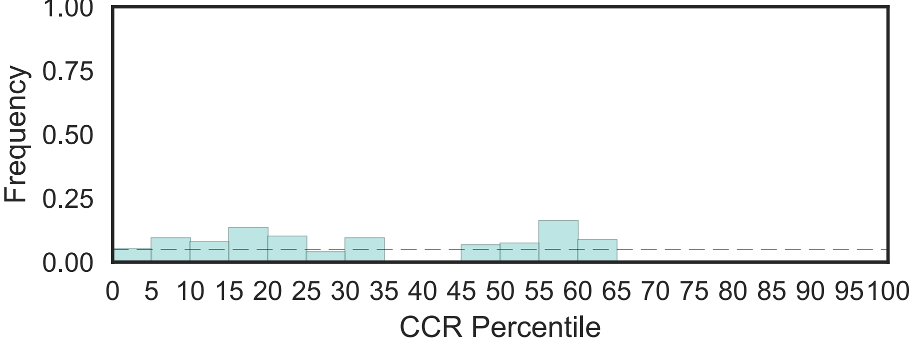


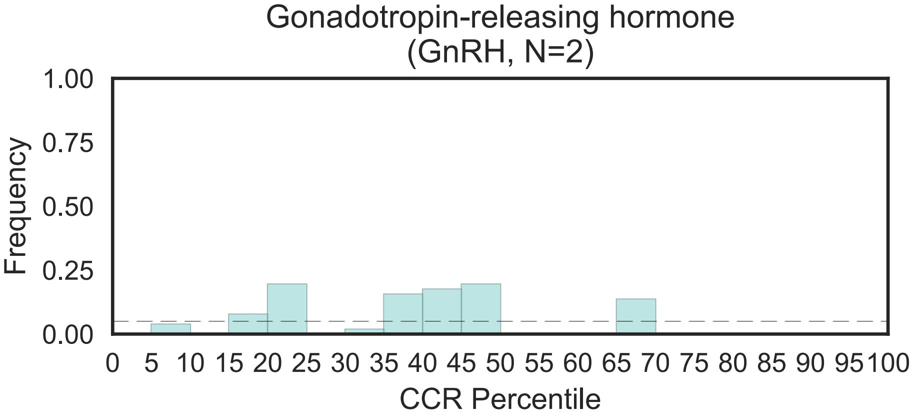

Glyoxalase-like domain
(Glyoxalase_3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

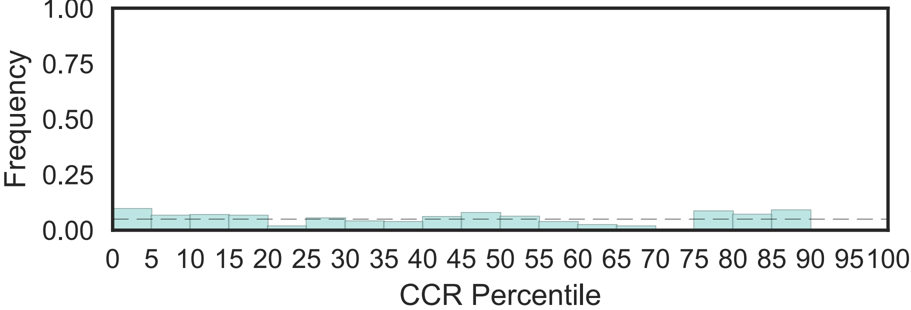

Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily
(Glyoxalase_4, N=3)
Fisher's OR: 0; Bonferroni p-val: 1


Glypican
(Glypican, N=5)
Fisher's OR: 0.118; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

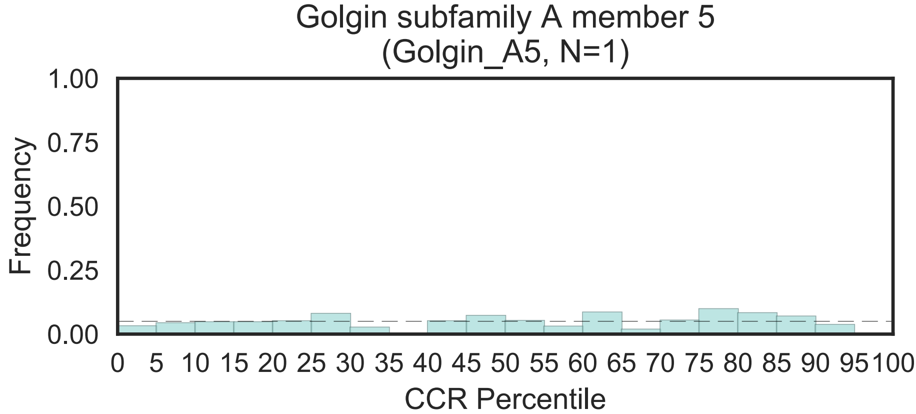
Gonadotropin hormone receptor transmembrane region
(GnHR_trans, N=1)

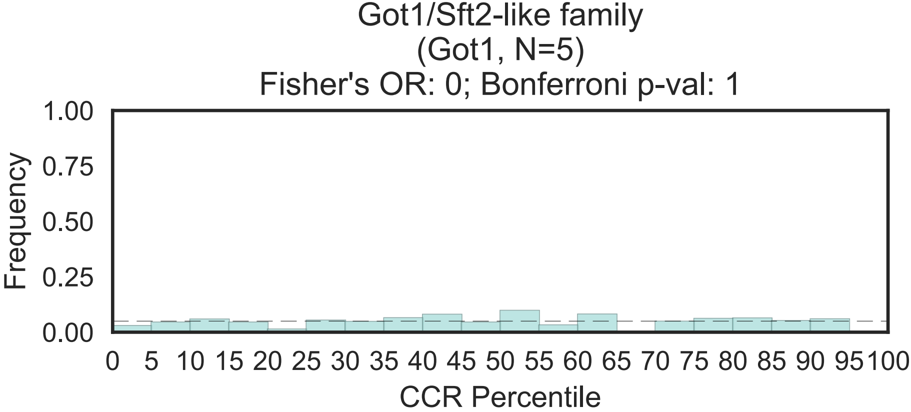


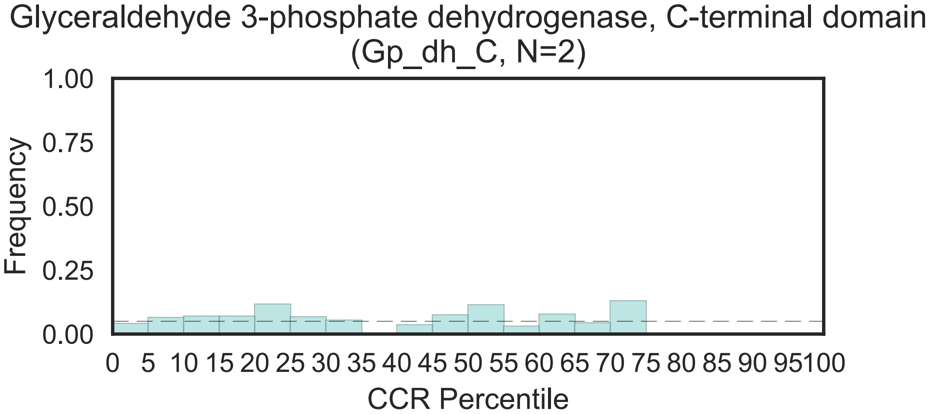

Gonadotropin-releasing hormone
(GnRH, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

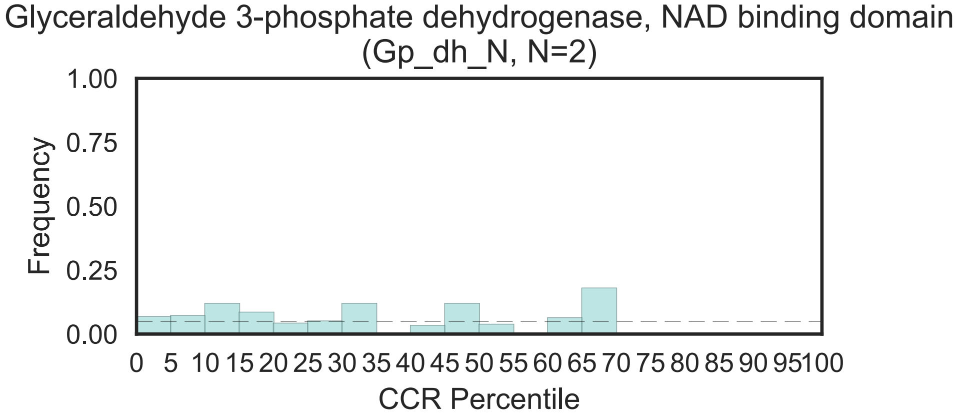


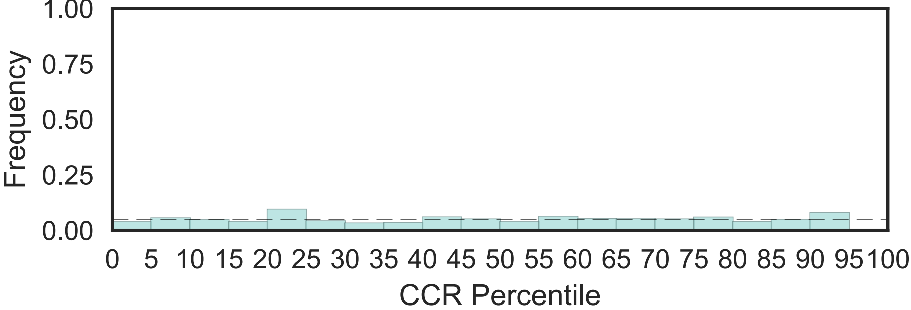
GoLoco motif
(GoLoco, N=16)
Fisher's OR: 0; Bonferroni p-val: 1


Golgin subfamily A member 5
(Golgin_A5, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

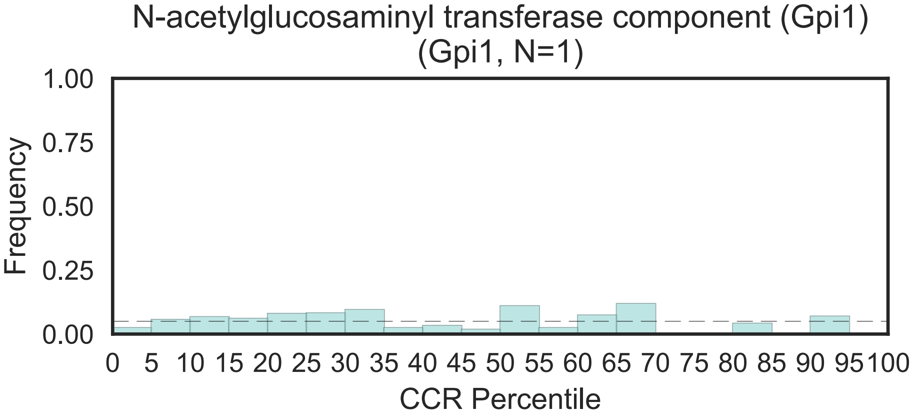

Got1/Sft2-like family
(Got1, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

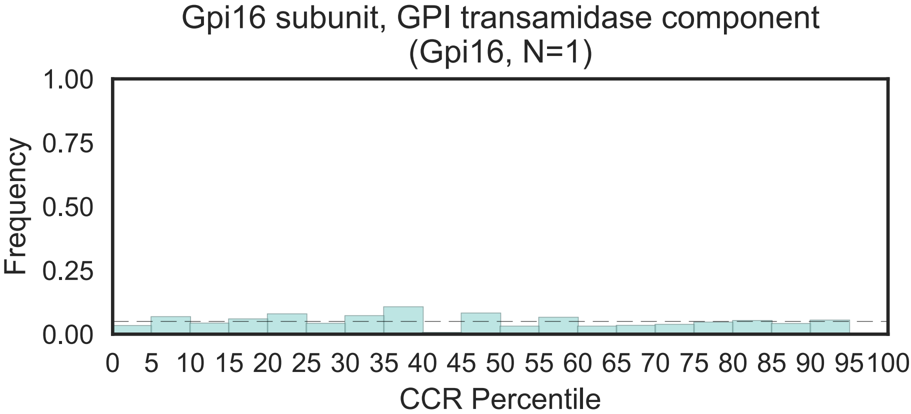

Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain
(Gp_dh_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

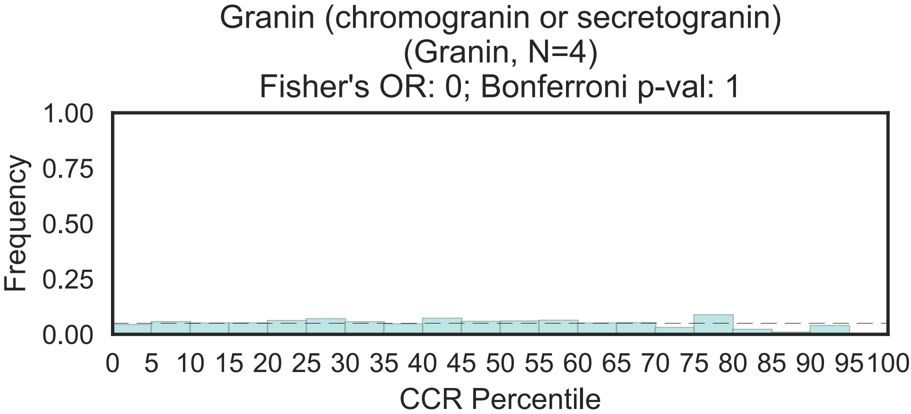

Glyceraldehyde 3-phosphate dehydrogenase, NAD binding domain
(Gp_dh_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

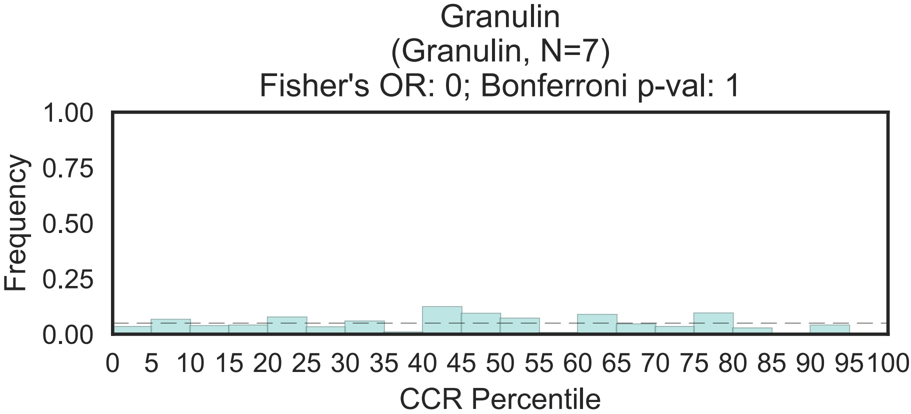


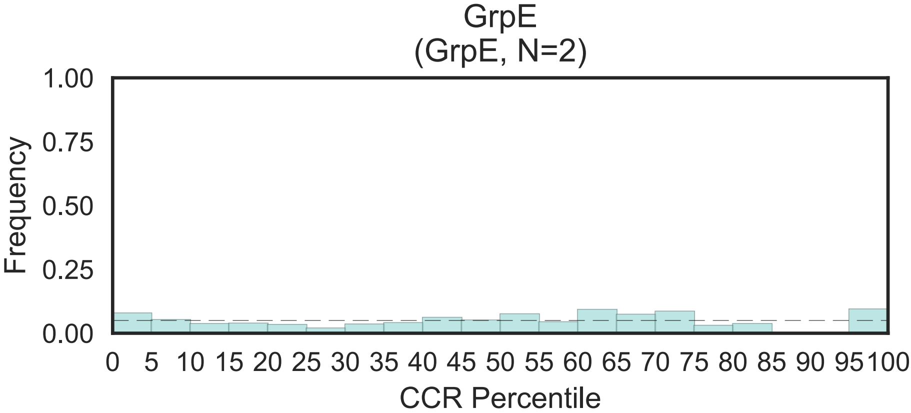
Rhodopsin-like GPCR transmembrane domain
(GpcrRhopsn4, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

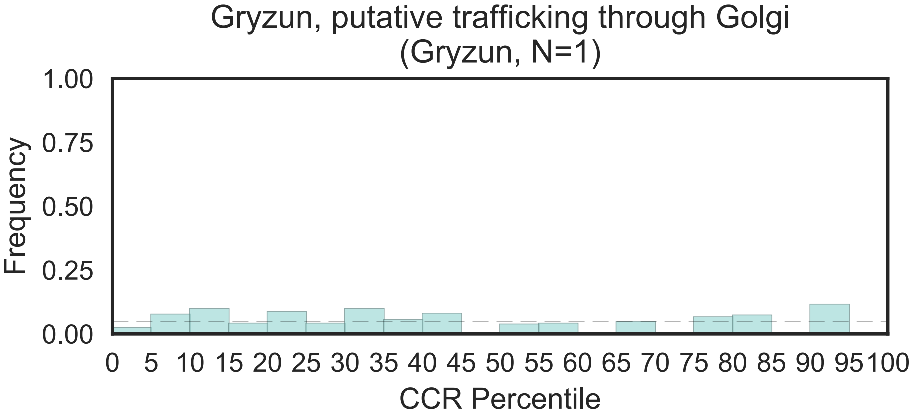

N-acetylglucosaminyl transferase component (Gpi1)
(Gpi1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

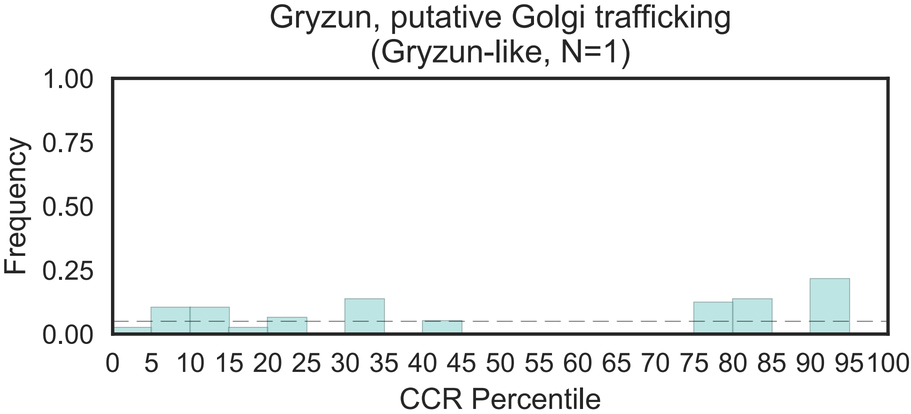

Gpi16 subunit, GPI transamidase component
(Gpi16, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

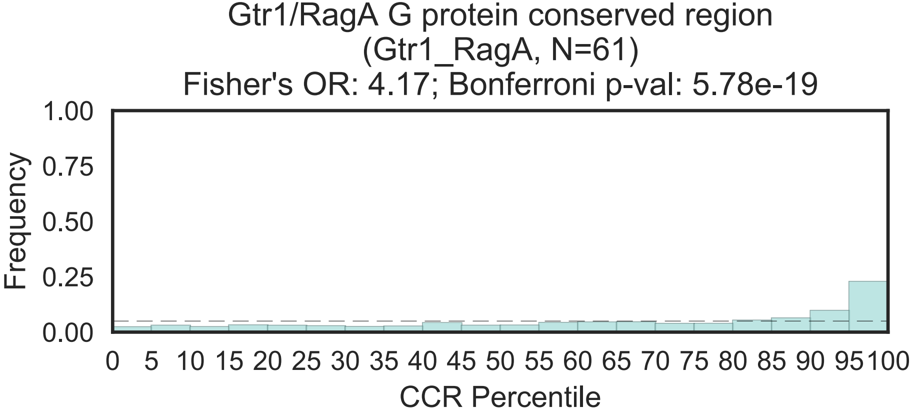

Granin (chromogranin or secretogranin)
(Granin, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

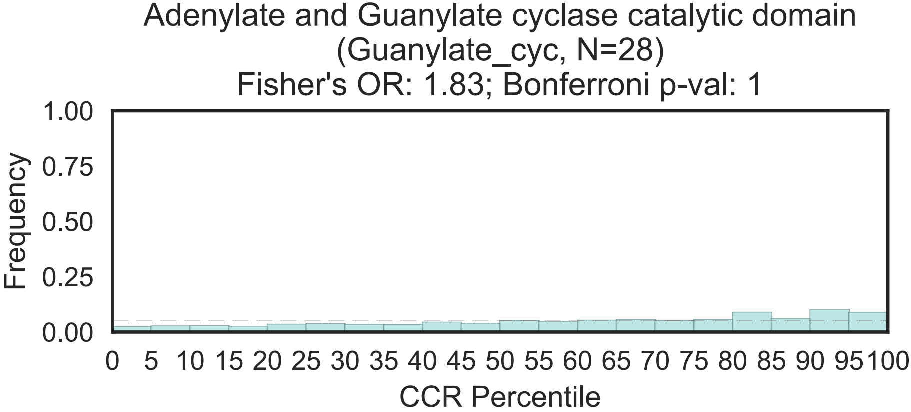

Granulin
(Granulin, N=7)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

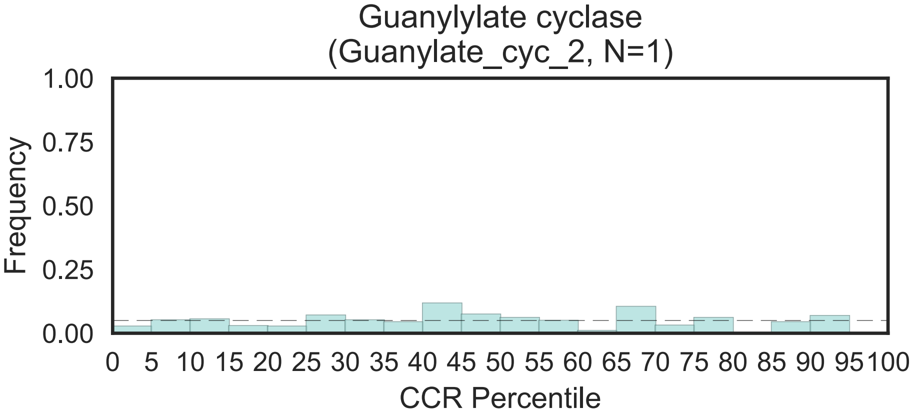

GrpE
(GrpE, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

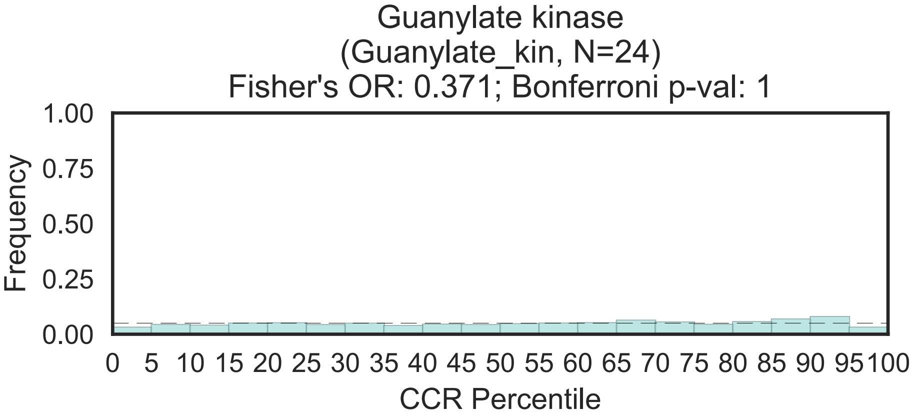

Gryzun, putative trafficking through Golgi
(Gryzun, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

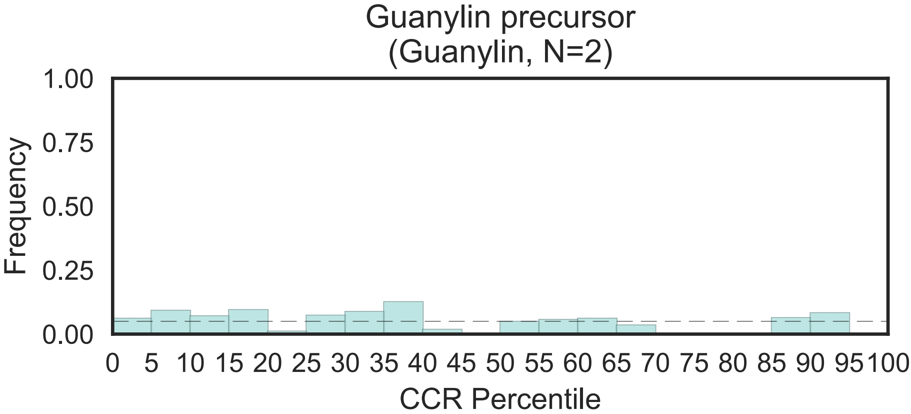

Gryzun, putative Golgi trafficking
(Gryzun-like, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

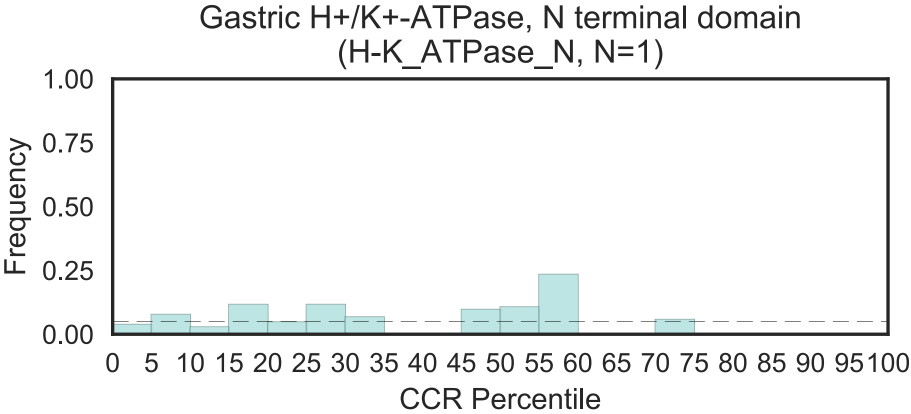

Gtr1/RagA G protein conserved region
(Gtr1_RagA, N=61)
Fisher's OR: 4.17; Bonferroni p-val: 5.78e-19
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

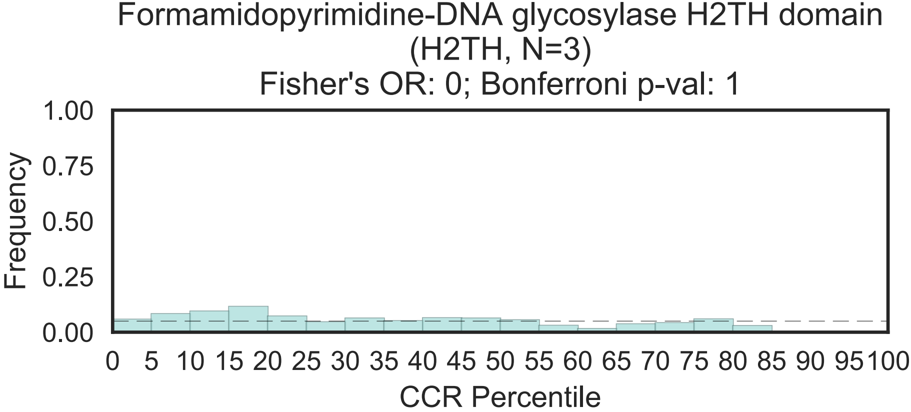

Adenylate and Guanylate cyclase catalytic domain
(Guanylate_cyc, N=28)
Fisher's OR: 1.83; Bonferroni p-val: 1

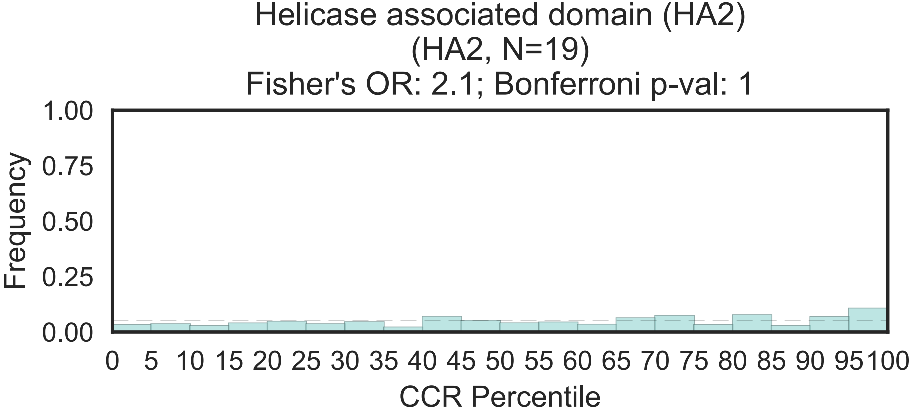

Guanylylate cyclase
(Guanylate_cyc_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

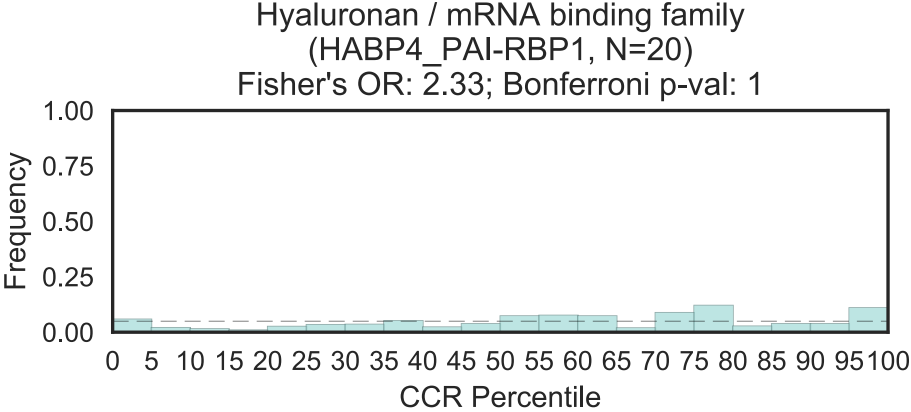

Guanylate kinase
(Guanylate_kin, N=24)
Fisher's OR: 0.371; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

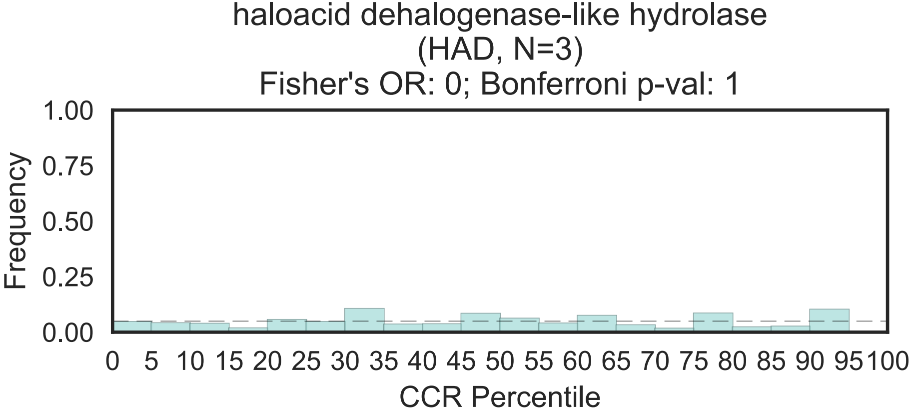

Guanylin precursor
(Guanylin, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Gastric H+/K+-ATPase, N terminal domain
(H-K_ATPase_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

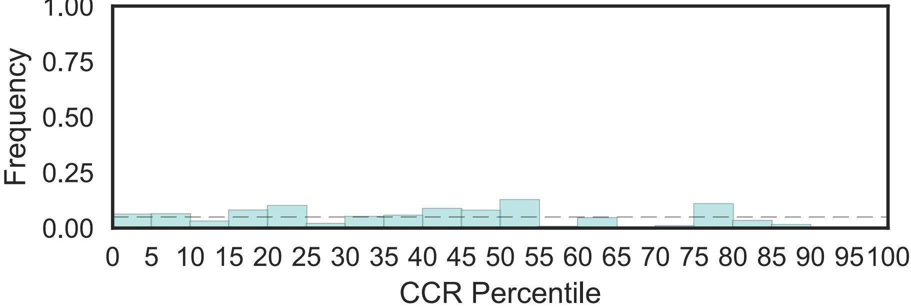

Formamidopyrimidine-DNA glycosylase H2TH domain
(H2TH, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

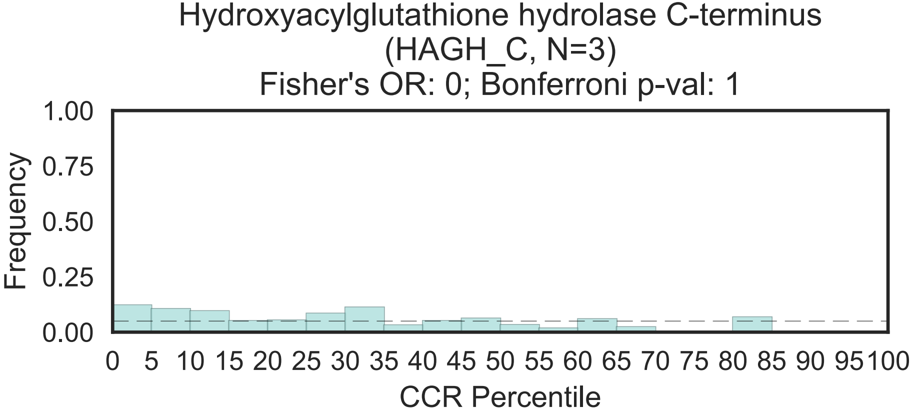

Helicase associated domain (HA2)
(HA2, N=19)
Fisher's OR: 2.1; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

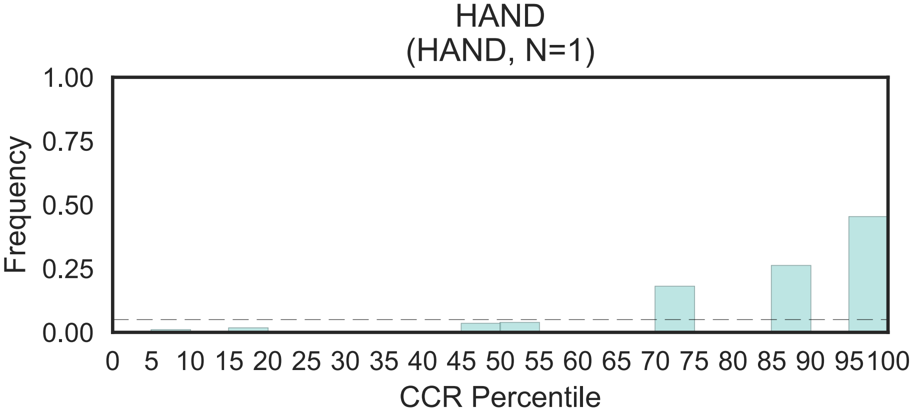

Hyaluronan / mRNA binding family
(HABP4_PAI-RBP1, N=20)
Fisher's OR: 2.33; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

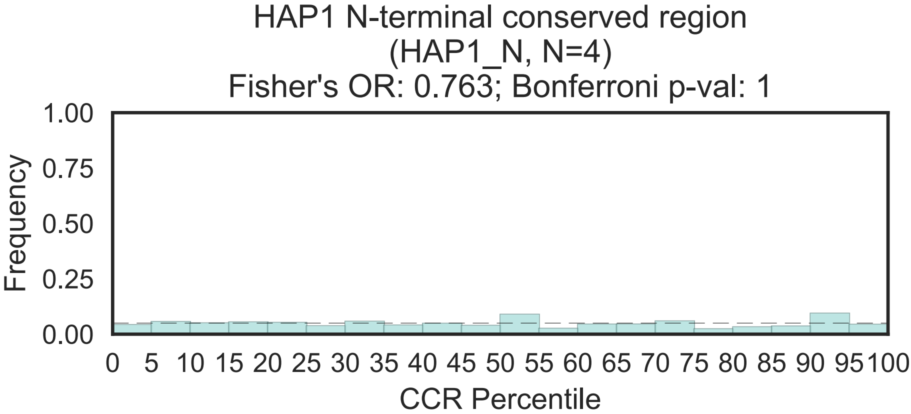

haloacid dehalogenase-like hydrolase
(HAD, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

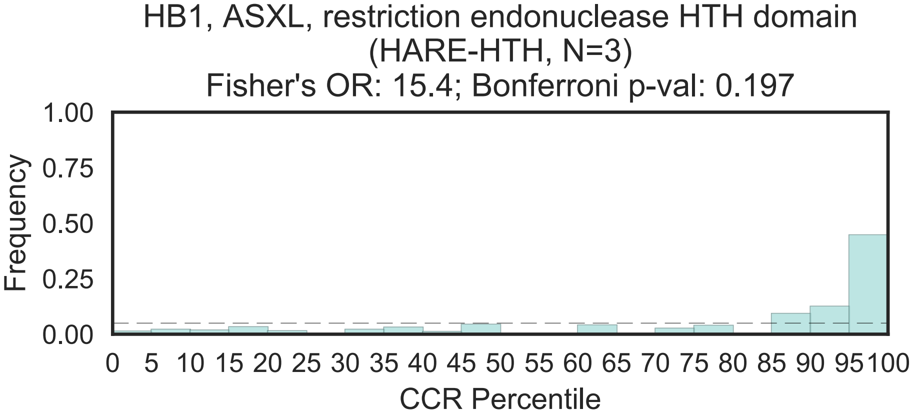
Haloacid dehalogenase-like hydrolase
(HAD_2, N=8)
Fisher's OR: 0; Bonferroni p-val: 1

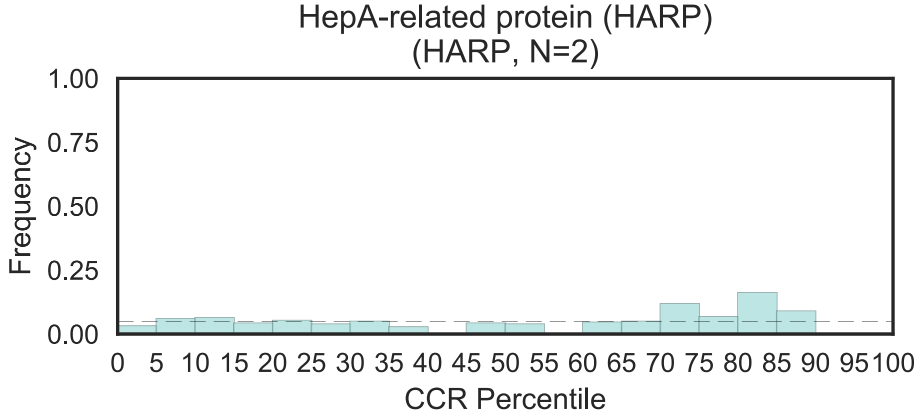


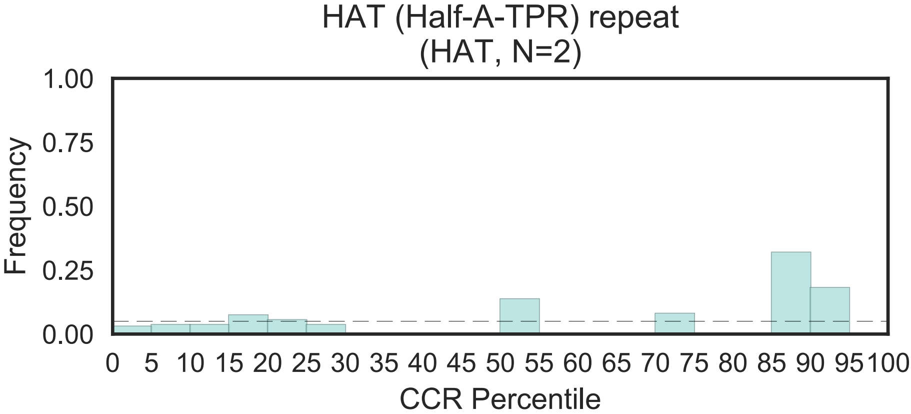

Hydroxyacylglutathione hydrolase C-terminus
(HAGH_C, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


HAND
(HAND, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

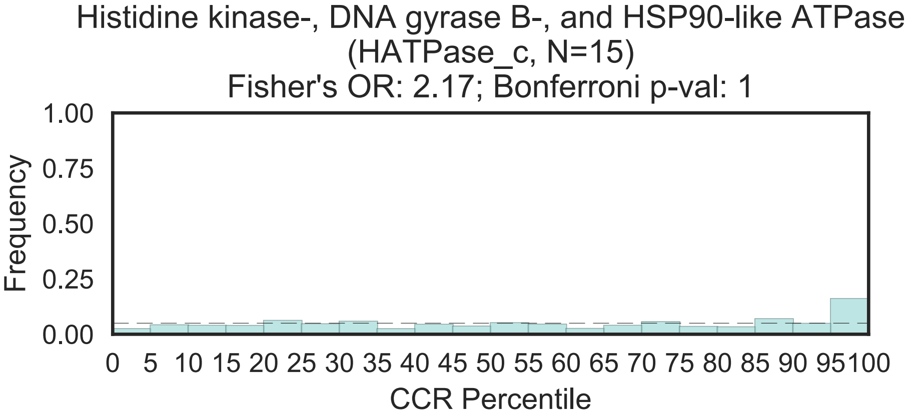

HAP1 N-terminal conserved region
(HAP1_N, N=4)
Fisher's OR: 0.763; Bonferroni p-val: 1

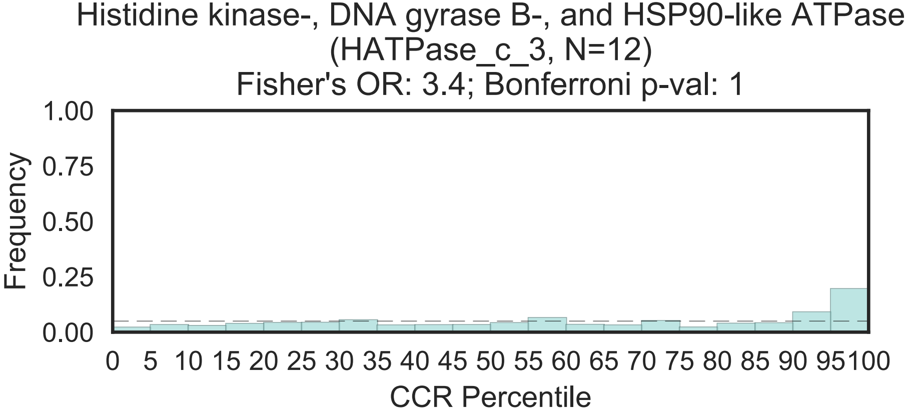

HB1, ASXL, restriction endonuclease HTH domain
(HARE-HTH, N=3)
Fisher's OR: 15.4; Bonferroni p-val: 0.197
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


HepA-related protein (HARP)
(HARP, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

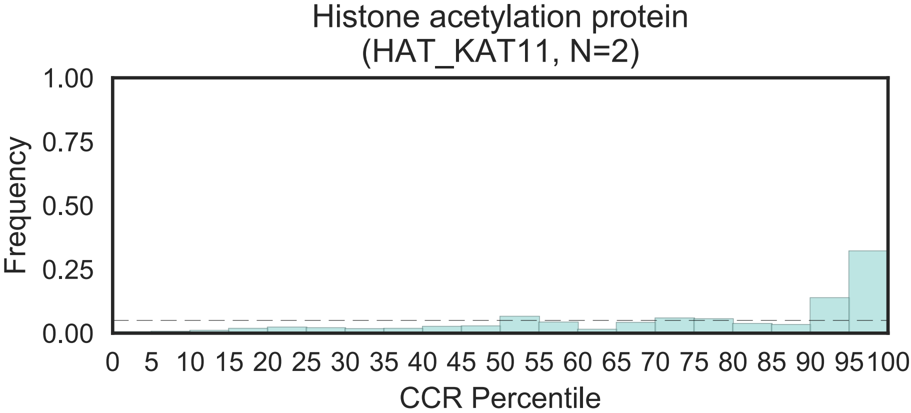


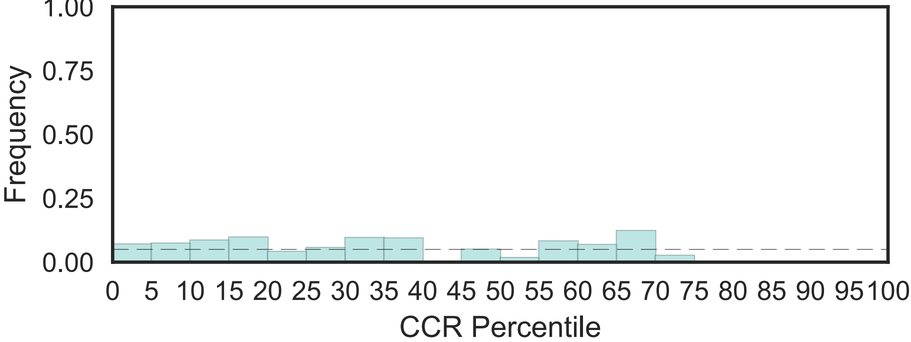
HAT (Half-A-TPR) repeat
(HAT, N=2)


Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase
(HATPase_c, N=15)
Fisher's OR: 2.17; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

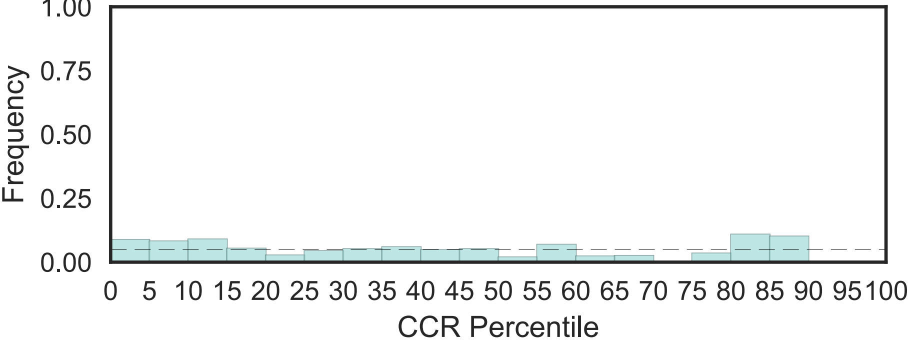


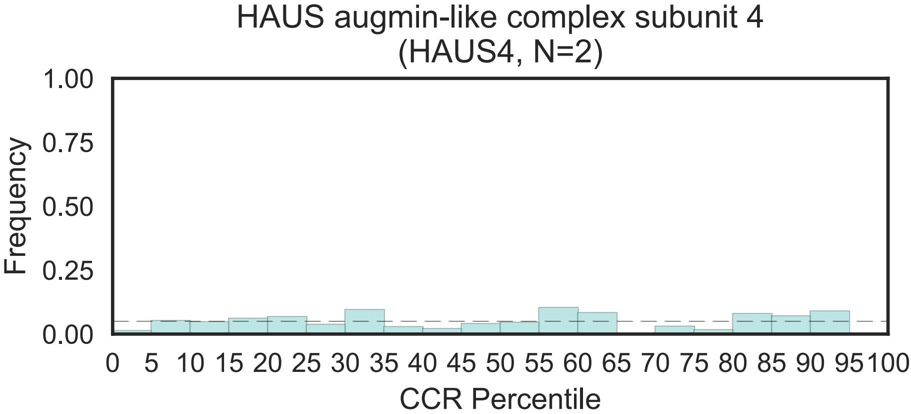
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase
(HATPase_c_3, N=12)
Fisher's OR: 3.4; Bonferroni p-val: 1

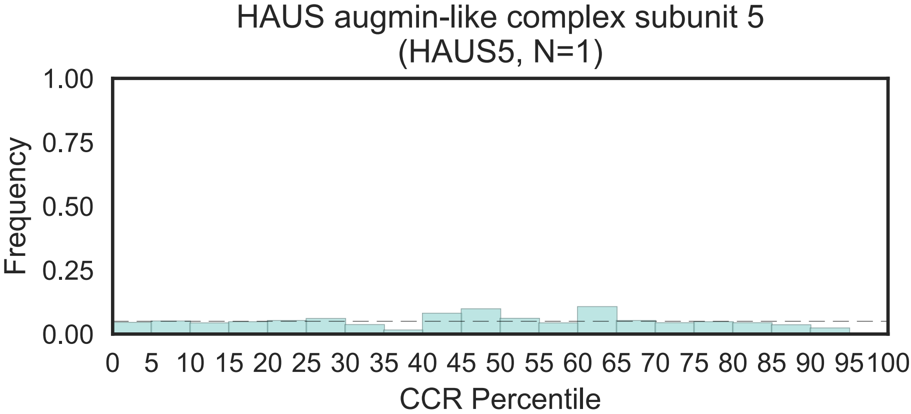

Histone acetylation protein
(HAT_KAT11, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

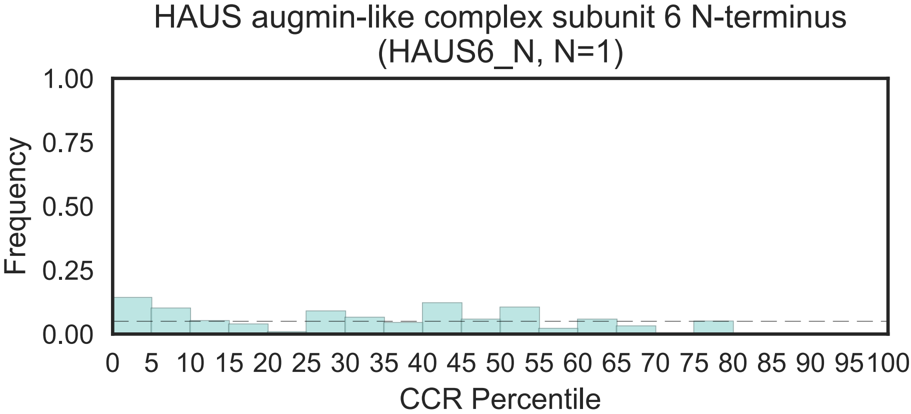


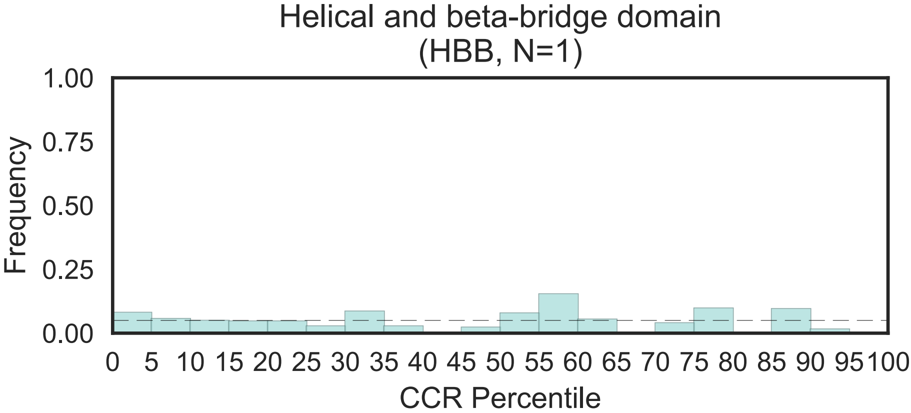
HAUS augmin-like complex subunit 3
(HAUS-augmin3, N=1)

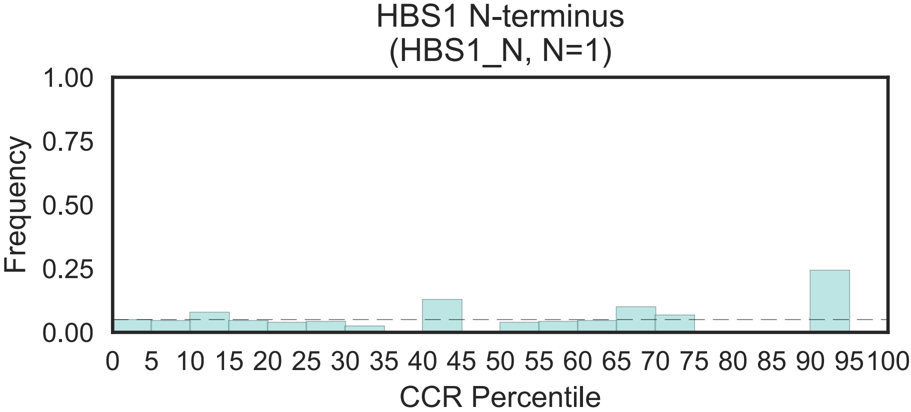

HAUS augmin-like complex subunit 2
(HAUS2, N=1)

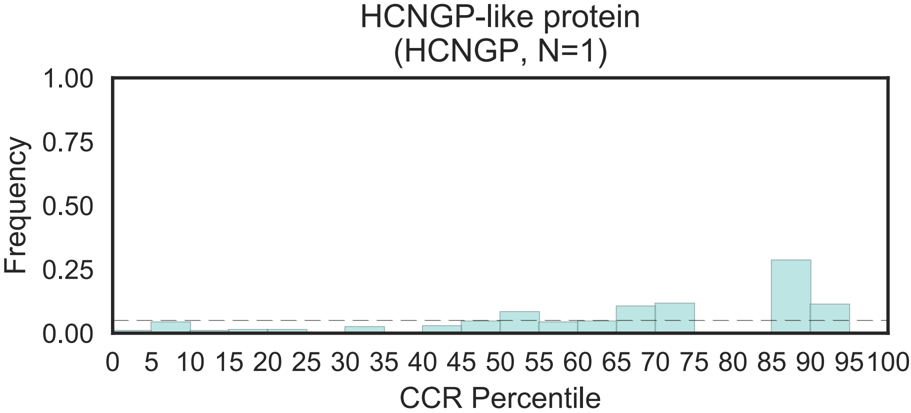

HAUS augmin-like complex subunit 4
(HAUS4, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


HAUS augmin-like complex subunit 5
(HAUS5, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

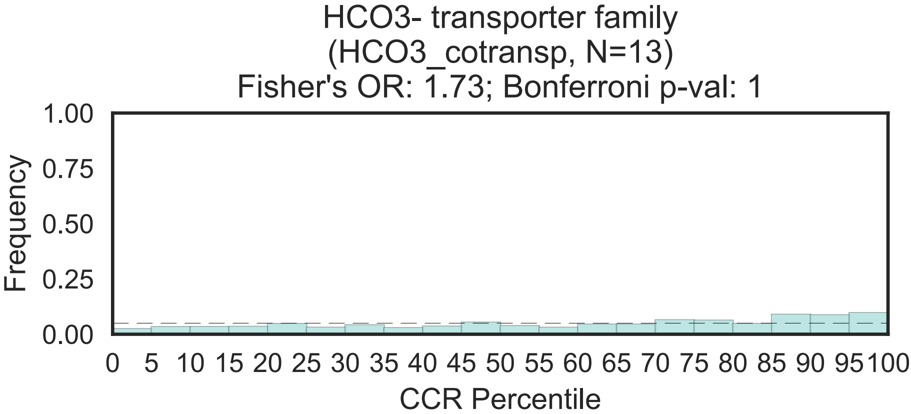

HAUS augmin-like complex subunit 6 N-terminus
(HAUS6_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

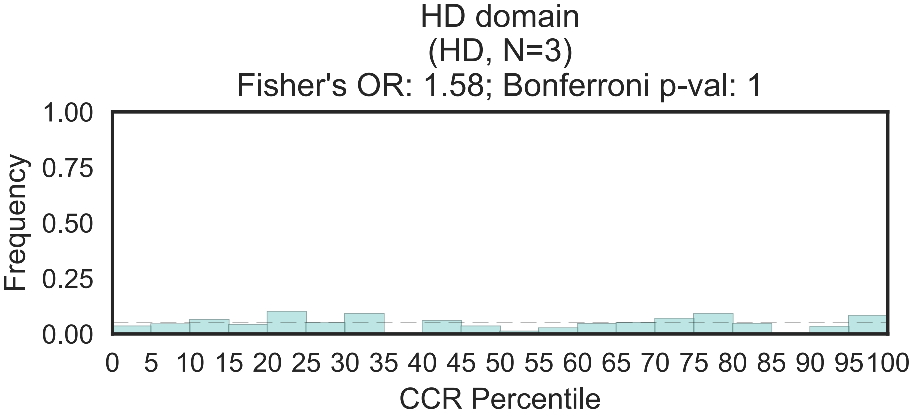

Helical and beta-bridge domain
(HBB, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

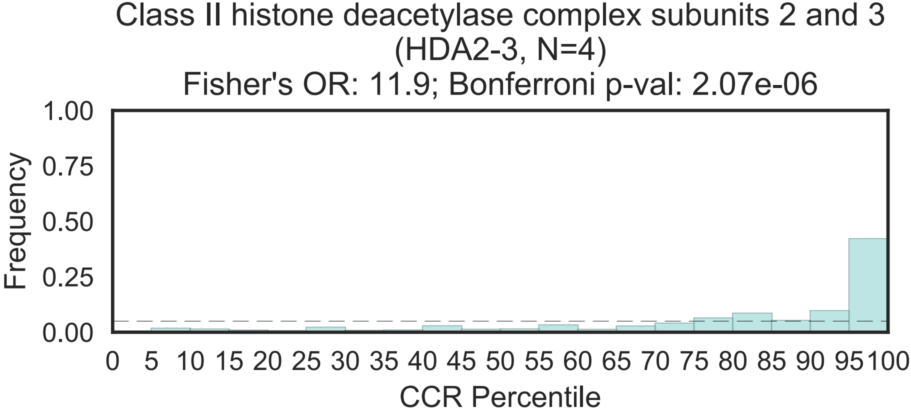

HBS1 N-terminus
(HBS1_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

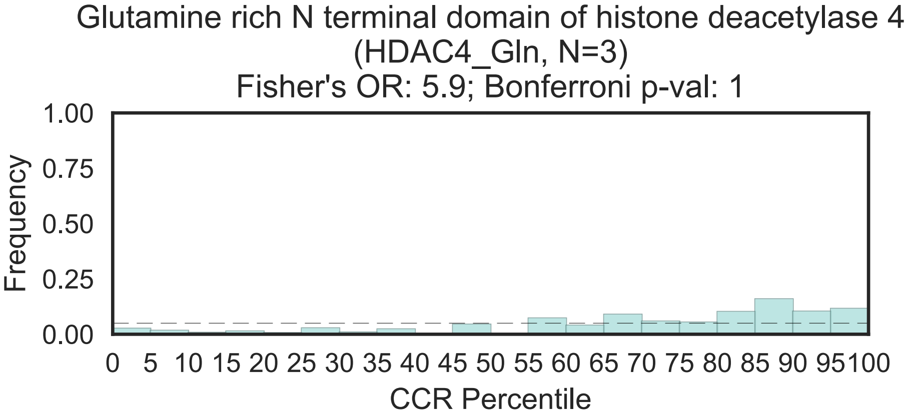


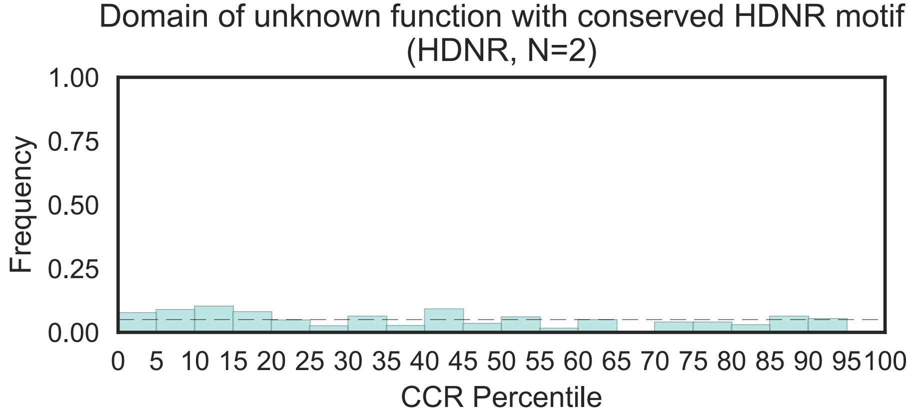
HCNGP-like protein
(HCNGP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

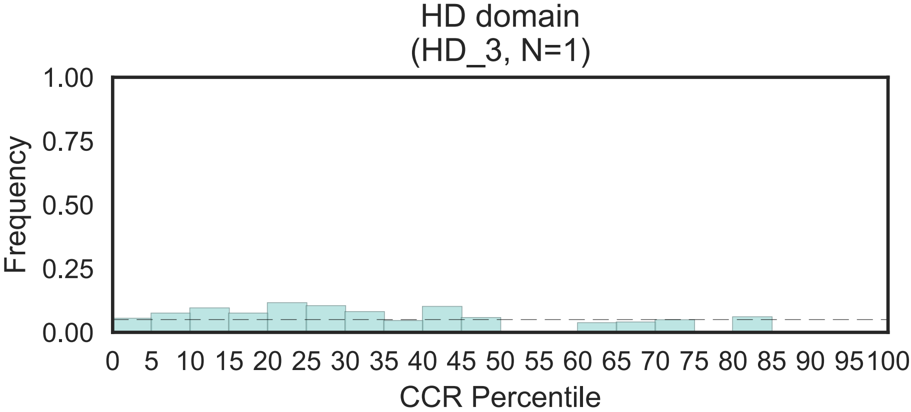

HCO3- transporter family
(HCO3_cotransp, N=13)
Fisher's OR: 1.73; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

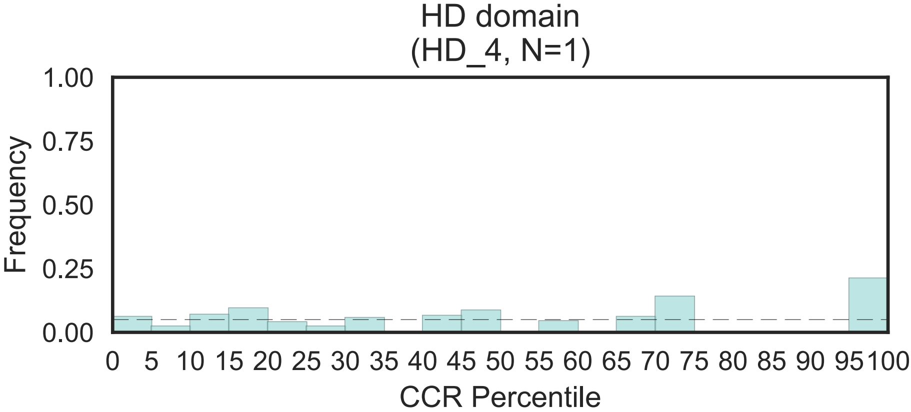

HD domain
(HD, N=3)
Fisher's OR: 1.58; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

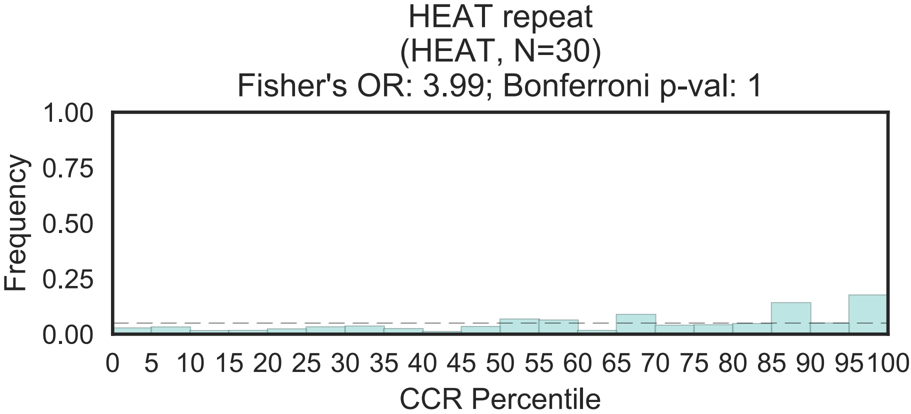

Class II histone deacetylase complex subunits 2 and 3
(HDA2-3, N=4)
Fisher's OR: 11.9; Bonferroni p-val: 2.07e-06
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

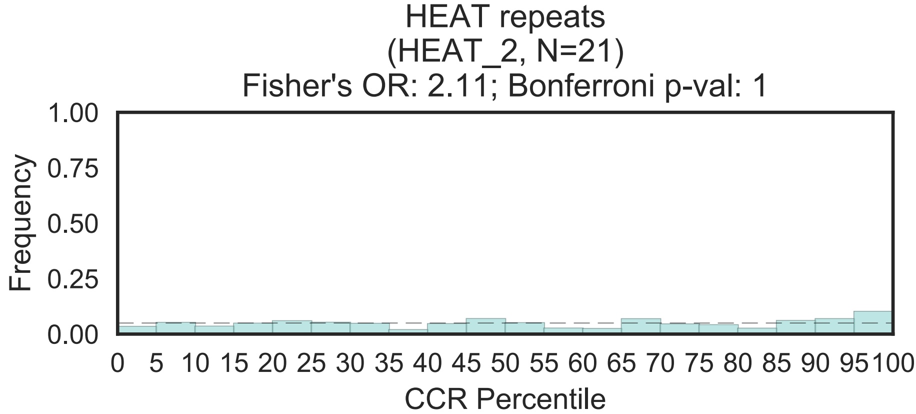

Glutamine rich N terminal domain of histone deacetylase 4
(HDAC4_Gln, N=3)
Fisher's OR: 5.9; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

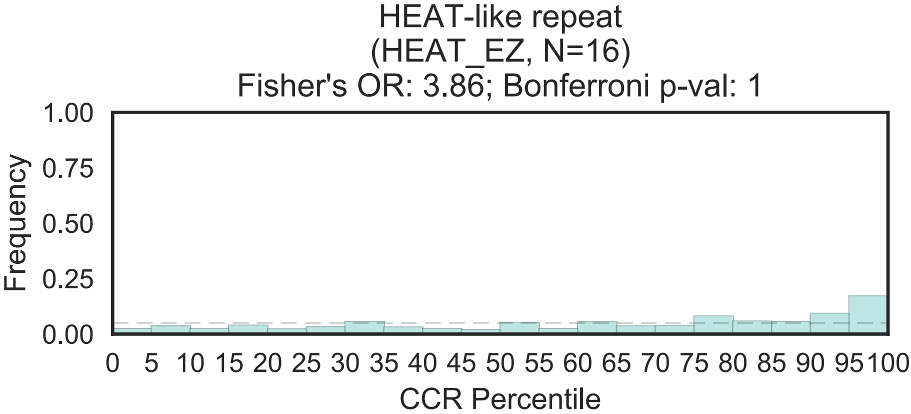

Domain of unknown function with conserved HDNR motif
(HDNR, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

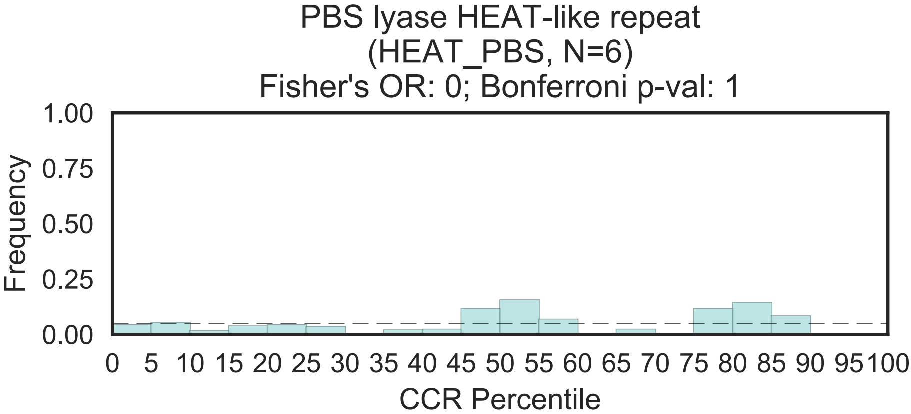

HD domain
(HD_3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


HD domain
(HD_4, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

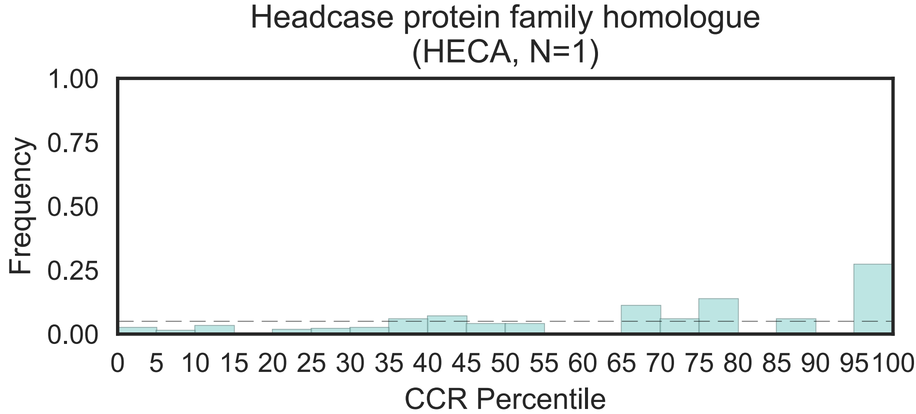

HEAT repeat
(HEAT, N=30)
Fisher's OR: 3.99; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

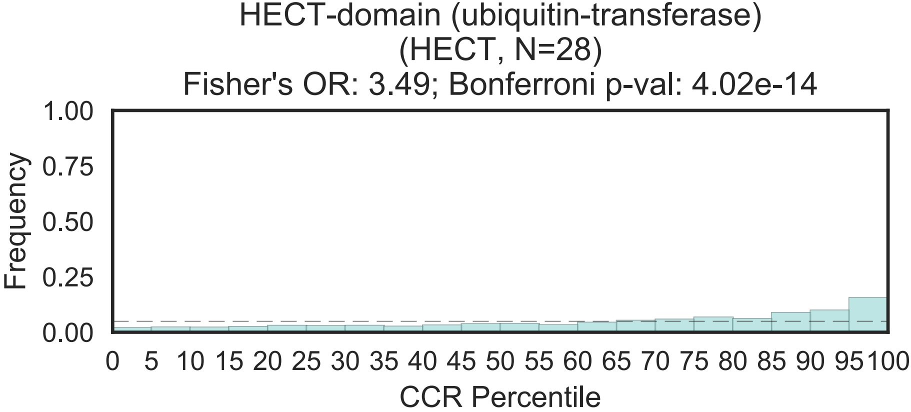

HEAT repeats
(HEAT_2, N=21)
Fisher's OR: 2.11; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

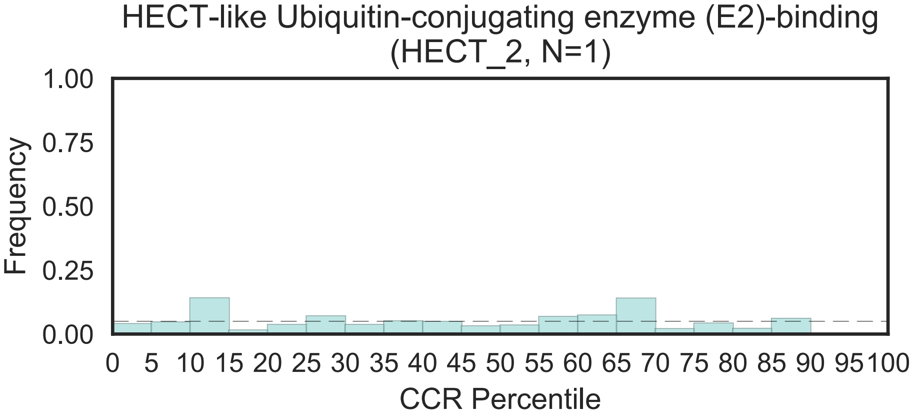

HEAT-like repeat
(HEAT_EZ, N=16)
Fisher's OR: 3.86; Bonferroni p-val: 1

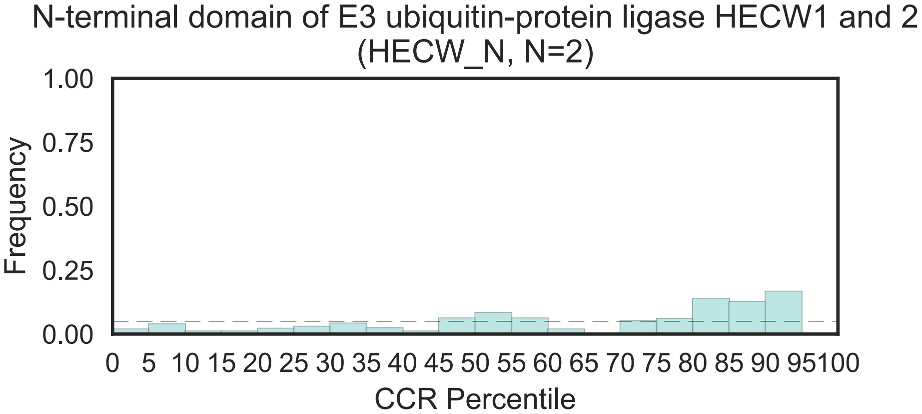


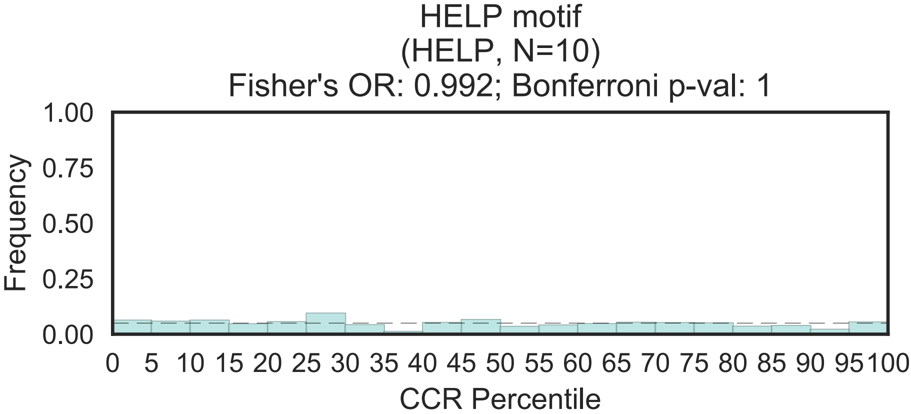
PBS lyase HEAT-like repeat
(HEAT_PBS, N=6)
Fisher's OR: 0; Bonferroni p-val: 1

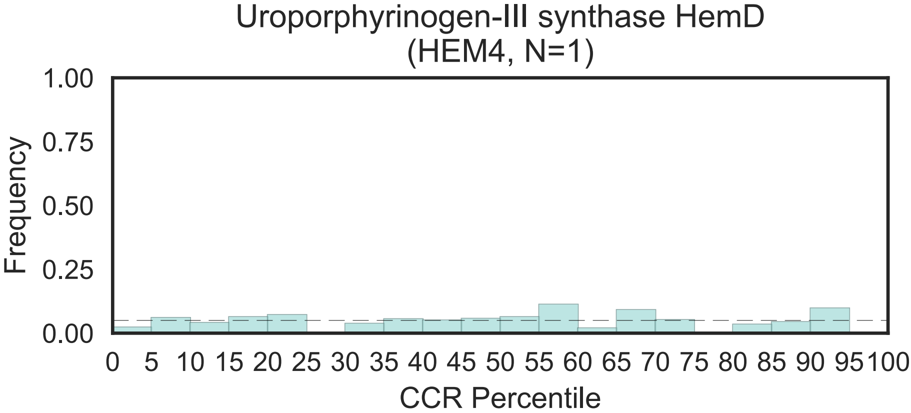

Headcase protein family homologue
(HECA, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


HECT-domain (ubiquitin-transferase)
(HECT, N=28)
Fisher's OR: 3.49; Bonferroni p-val: 4.02e-14
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

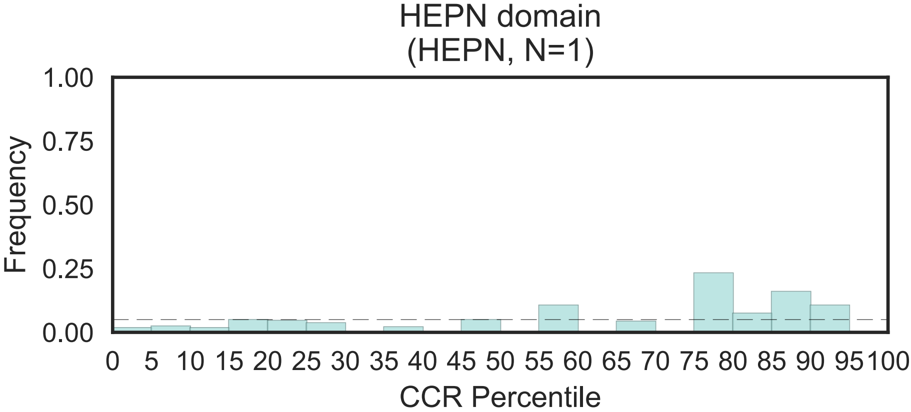

HECT-like Ubiquitin-conjugating enzyme (E2)-binding
(HECT_2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

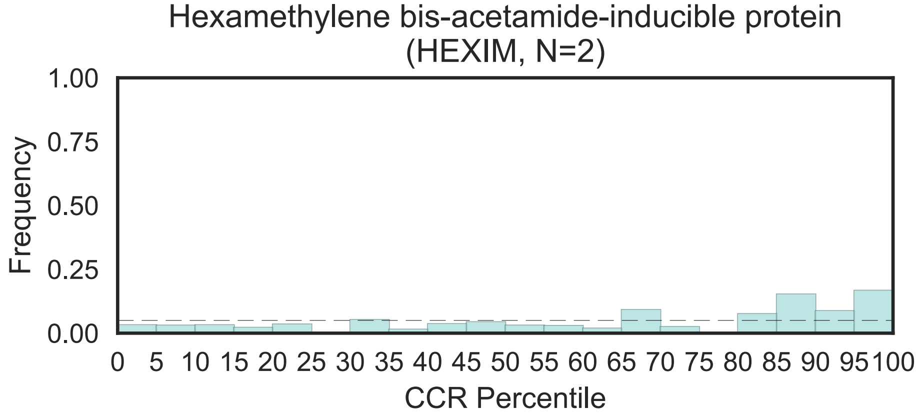

N-terminal domain of E3 ubiquitin-protein ligase HECW1 and 2
(HECW_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

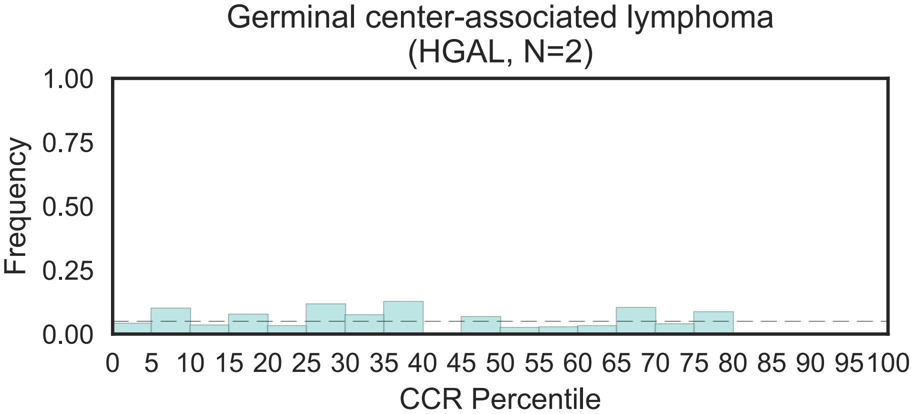

HELP motif
(HELP, N=10)
Fisher's OR: 0.992; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

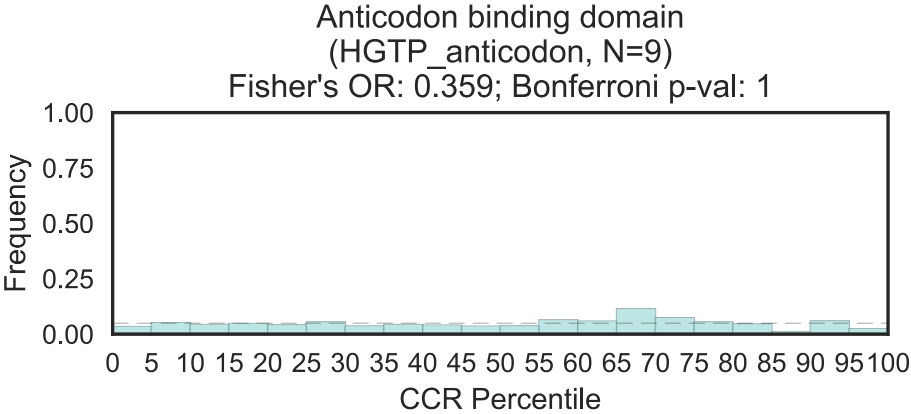


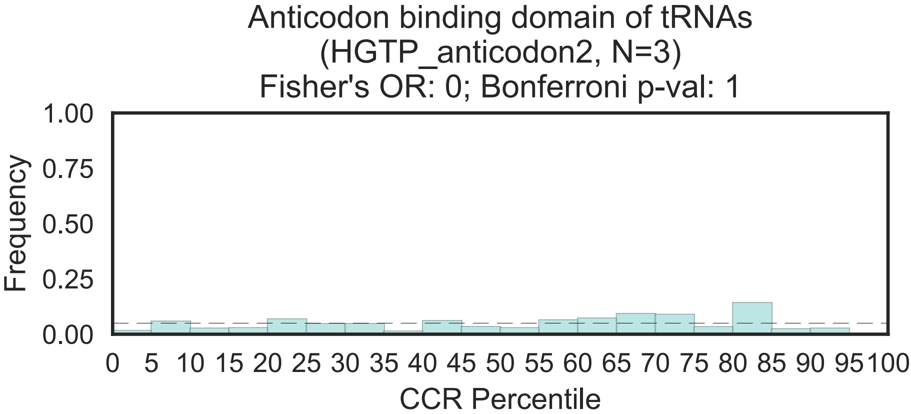
Uroporphyrinogen-III synthase HemD
(HEM4, N=1)

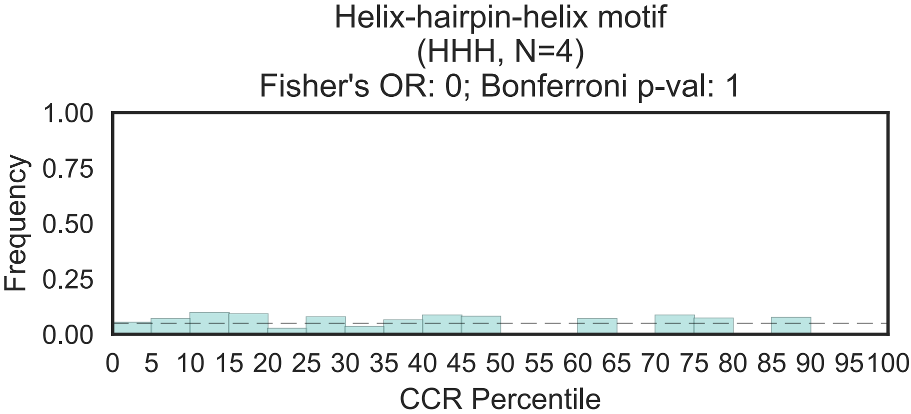

HEPN domain
(HEPN, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

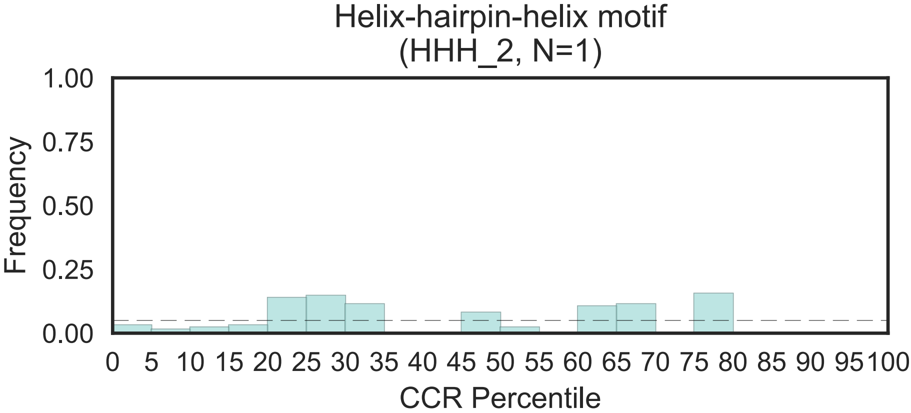

Hexamethylene bis-acetamide-inducible protein
(HEXIM, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

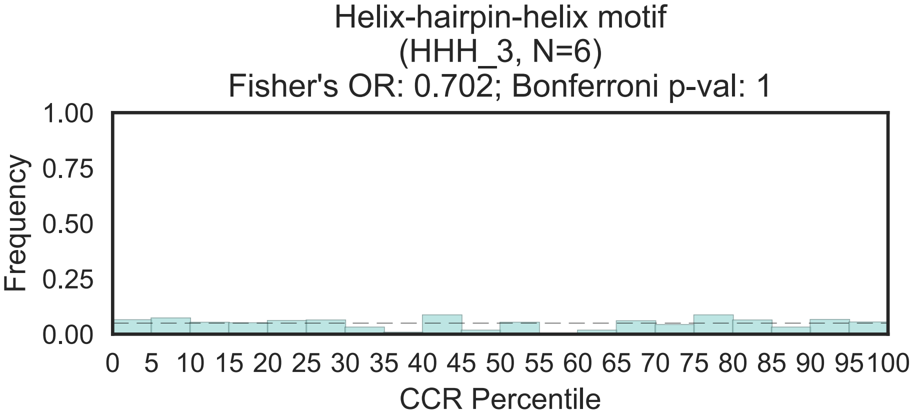

Germinal center-associated lymphoma
(HGAL, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

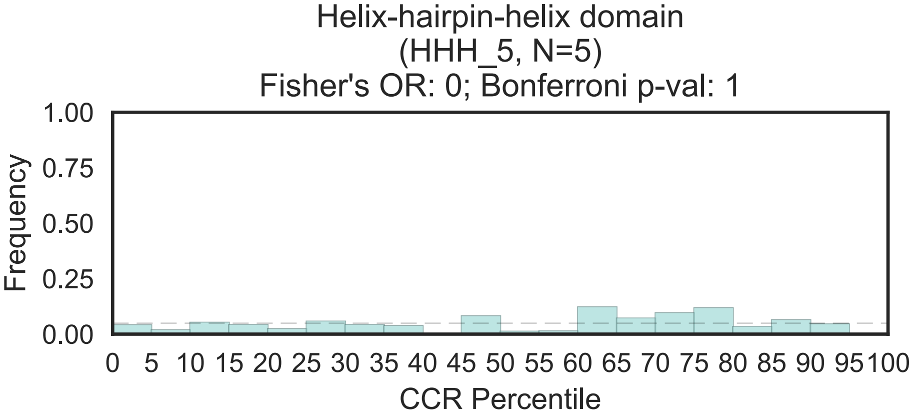

Anticodon binding domain
(HGTP_anticodon, N=9)
Fisher's OR: 0.359; Bonferroni p-val: 1

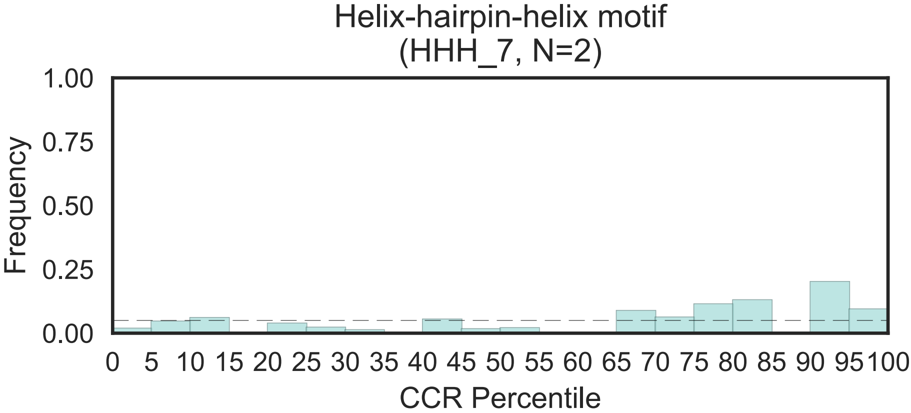

Anticodon binding domain of tRNAs
(HGTP_anticodon2, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

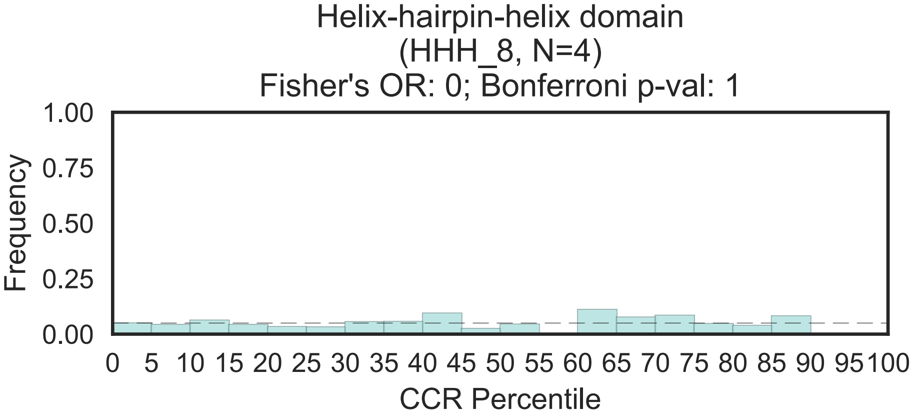

Helix-hairpin-helix motif
(HHH, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

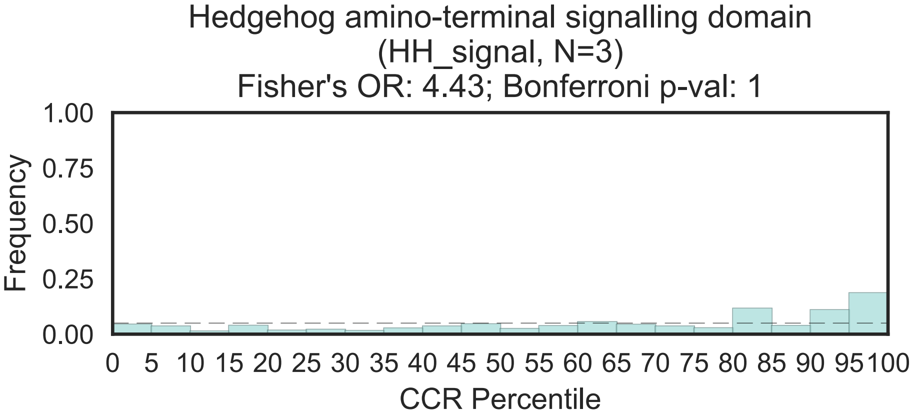

Helix-hairpin-helix motif
(HHH_2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Helix-hairpin-helix motif
(HHH_3, N=6)
Fisher's OR: 0.702; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

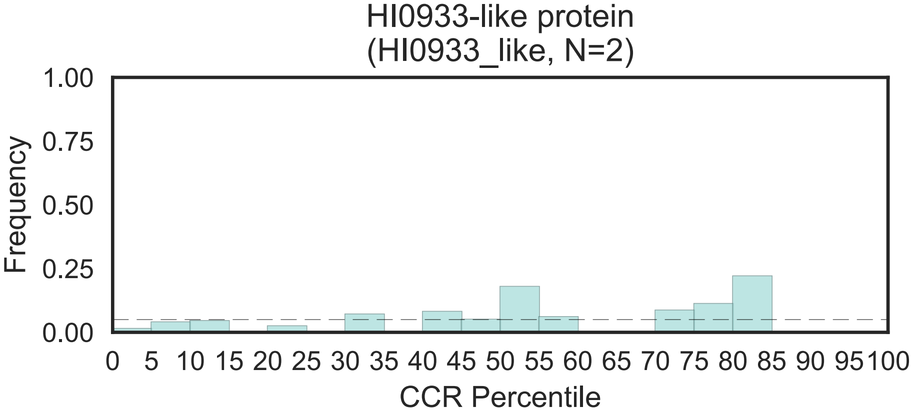

Helix-hairpin-helix domain
(HHH_5, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

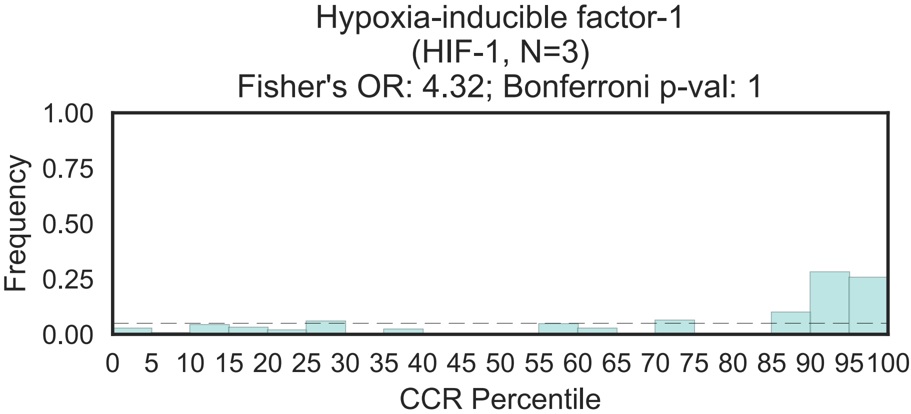

Helix-hairpin-helix motif
(HHH_7, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

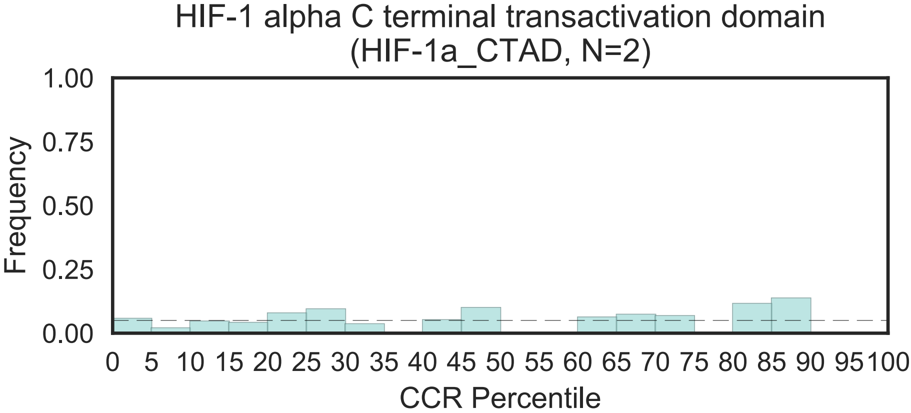

Helix-hairpin-helix domain
(HHH_8, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

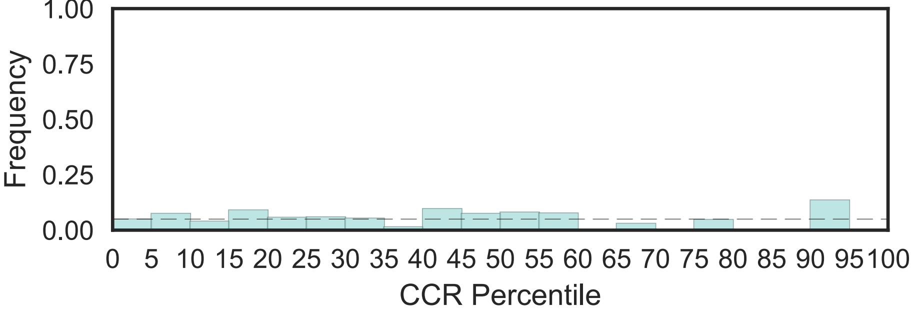


Hedgehog amino-terminal signalling domain
(HH_signal, N=3)
Fisher's OR: 4.43; Bonferroni p-val: 1

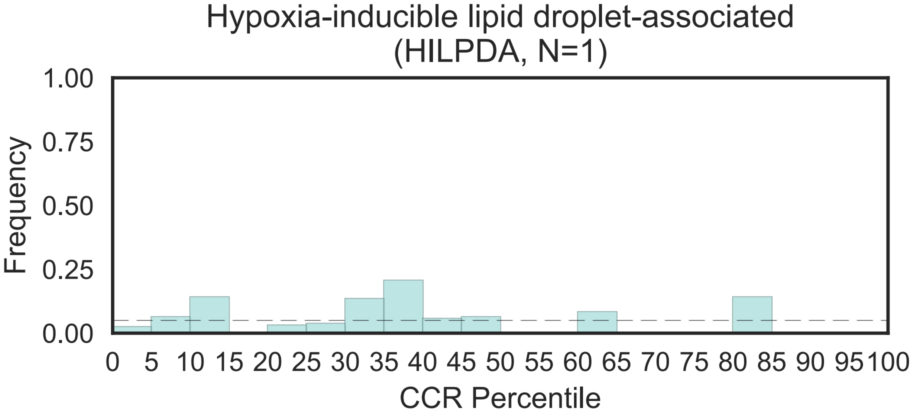

HI0933-like protein
(HI0933_like, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

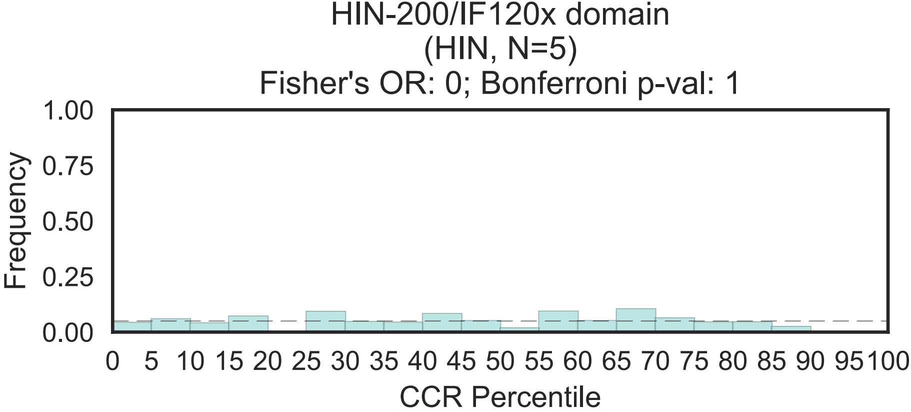

Hypoxia-inducible factor-1
(HIF-1, N=3)
Fisher's OR: 4.32; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

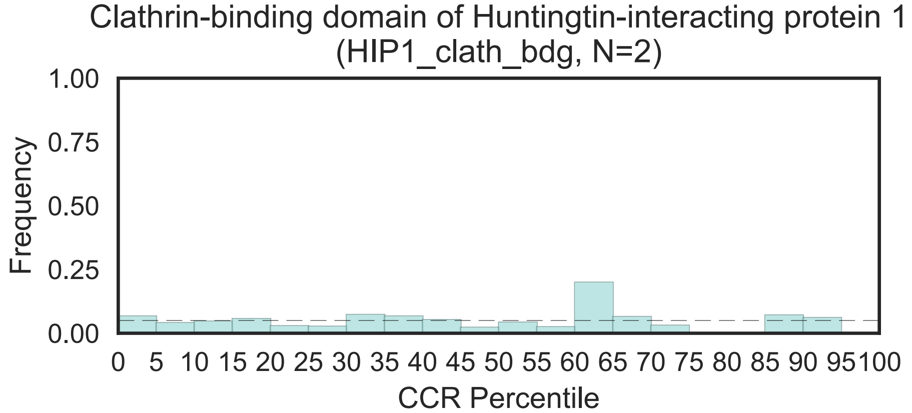

HIF-1 alpha C terminal transactivation domain
(HIF-1a_CTAD, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

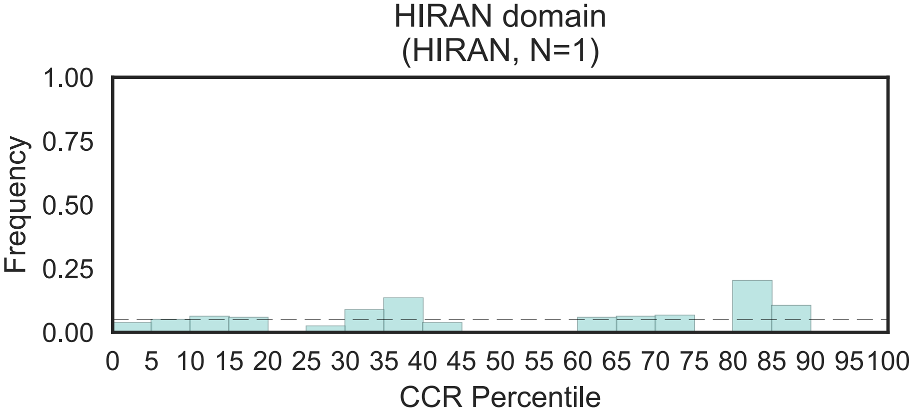


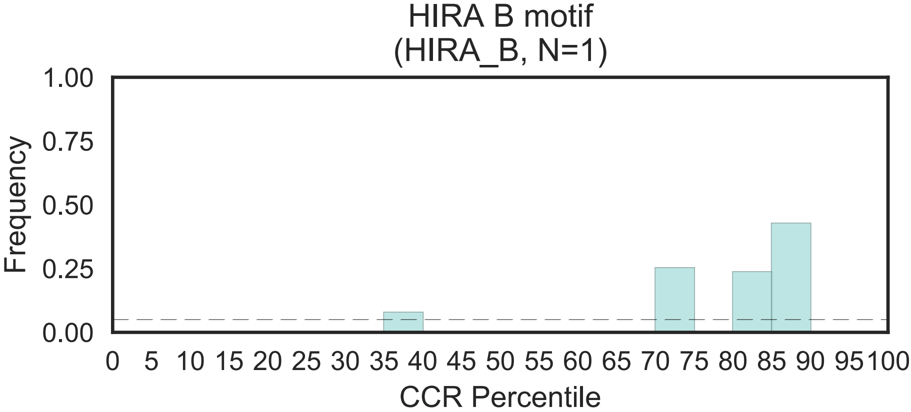
Hypoxia induced protein conserved region
(HIG_1_N, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

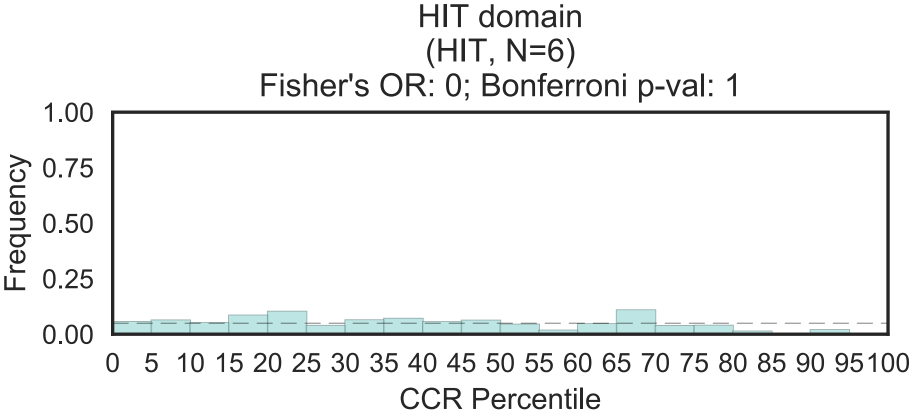

Hypoxia-inducible lipid droplet-associated
(HILPDA, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

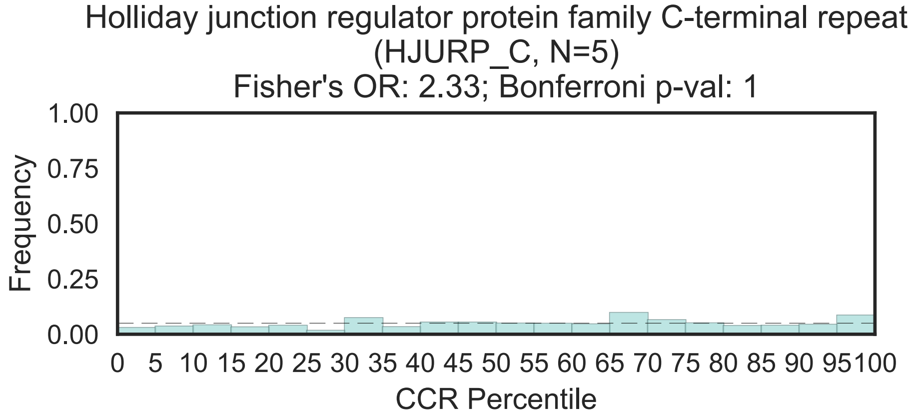

HIN-200/IF120x domain
(HIN, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

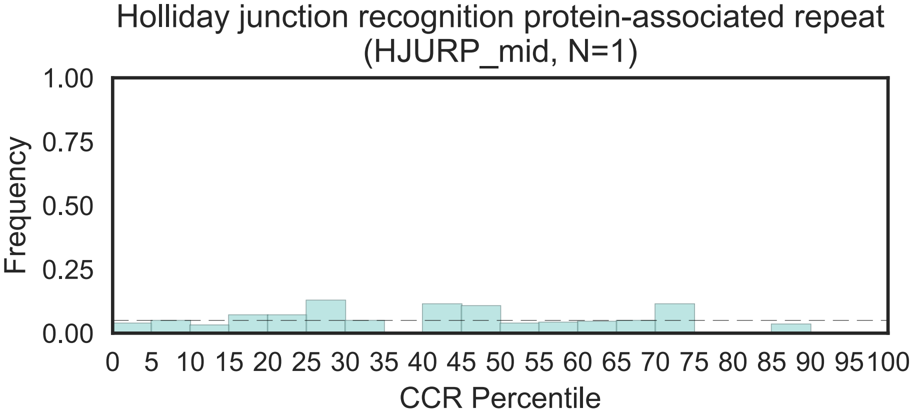

Clathrin-binding domain of Huntingtin-interacting protein 1
(HIP1_clath_bdg, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

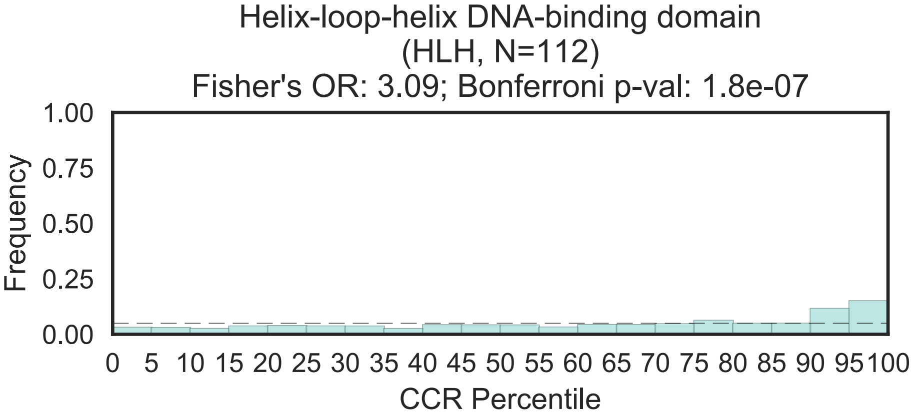

HIRAN domain
(HIRAN, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

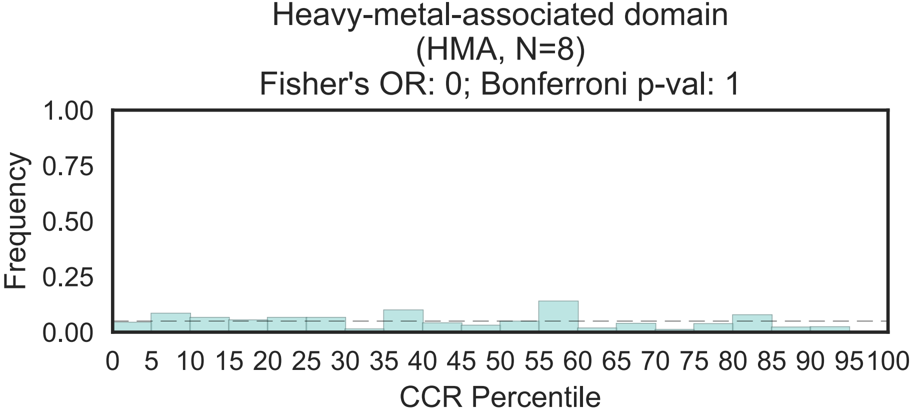

HIRA B motif
(HIRA_B, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

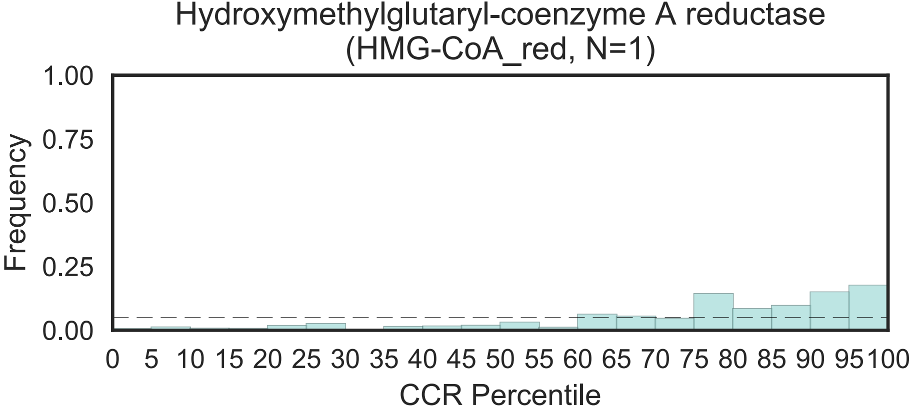

HIT domain
(HIT, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

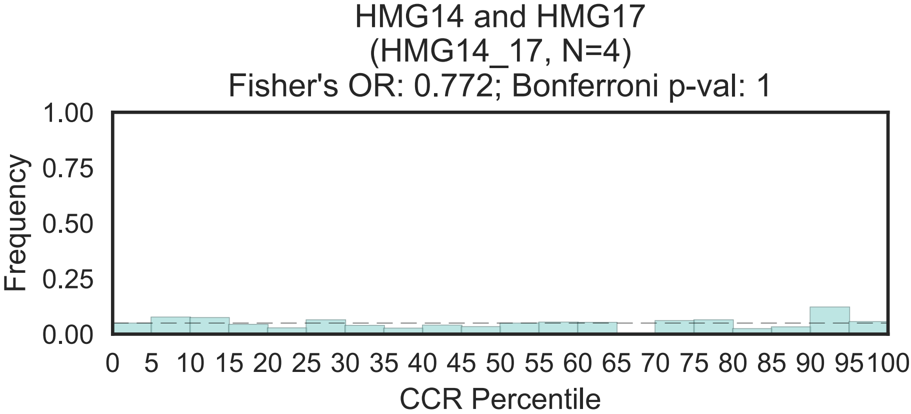

Holliday junction regulator protein family C-terminal repeat
(HJURP_C, N=5)
Fisher's OR: 2.33; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

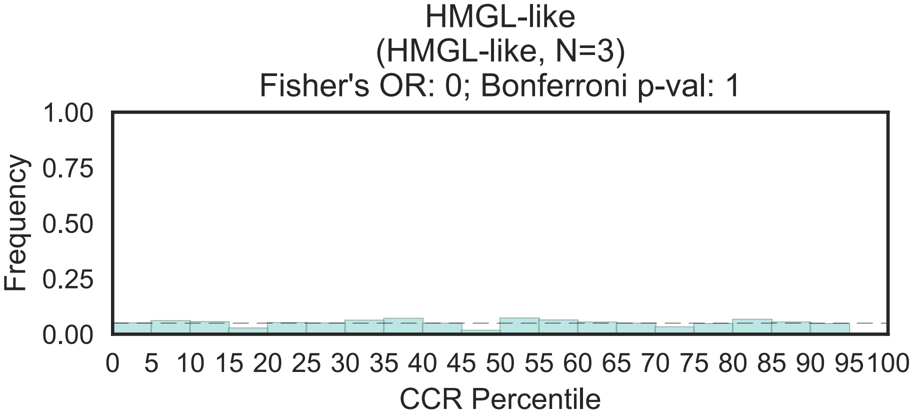

Holliday junction recognition protein-associated repeat
(HJURP_mid, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

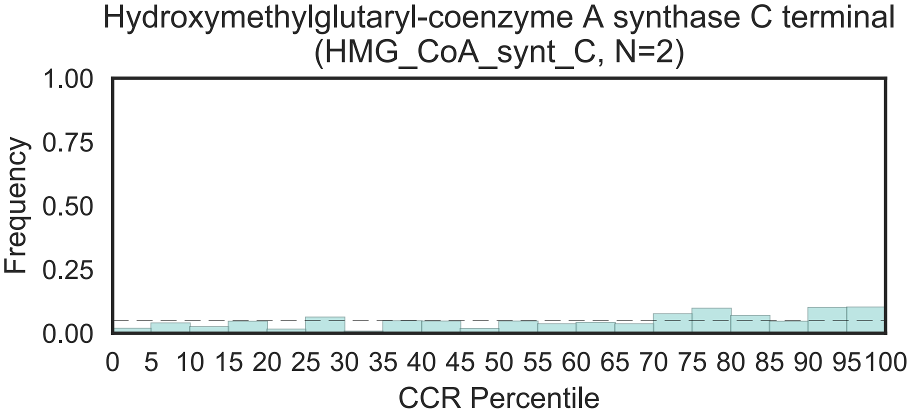

Helix-loop-helix DNA-binding domain
(HLH, N=112)
Fisher's OR: 3.09; Bonferroni p-val: 1.8e-07
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

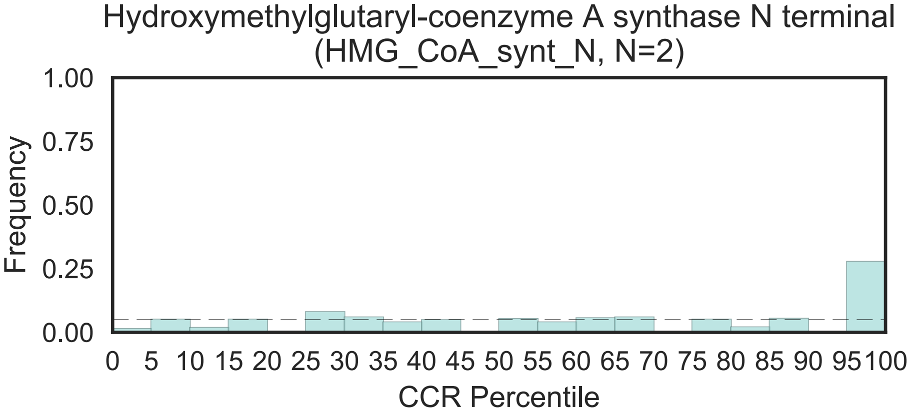

Heavy-metal-associated domain
(HMA, N=8)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

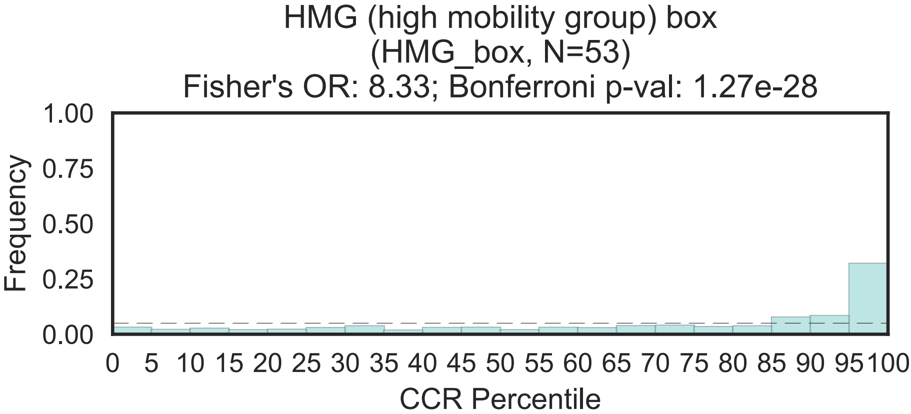

Hydroxymethylglutaryl-coenzyme A reductase
(HMG-CoA_red, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

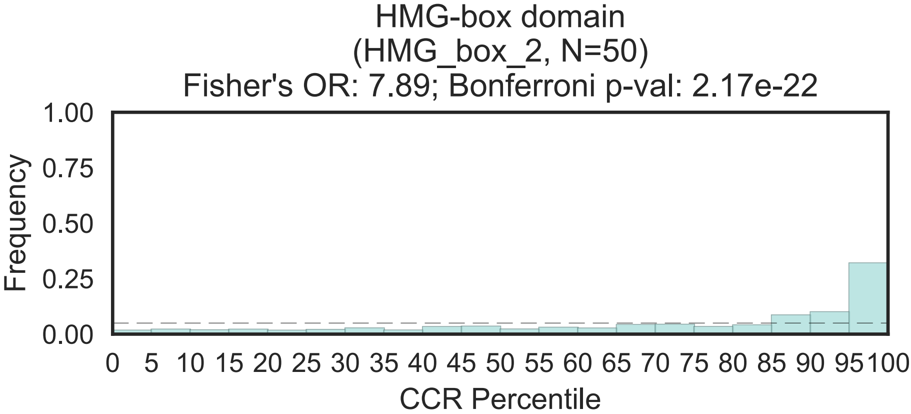

HMG14 and HMG17
(HMG14_17, N=4)
Fisher's OR: 0.772; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


HMGL-like
(HMGL-like, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

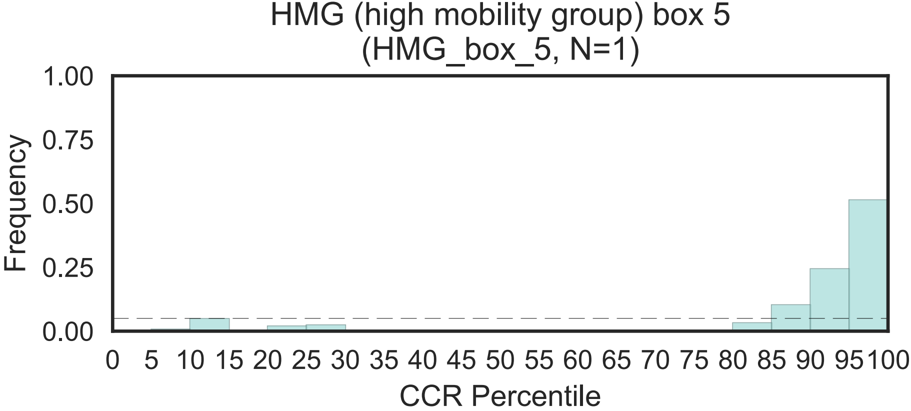

Hydroxymethylglutaryl-coenzyme A synthase C terminal
(HMG_CoA_synt_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

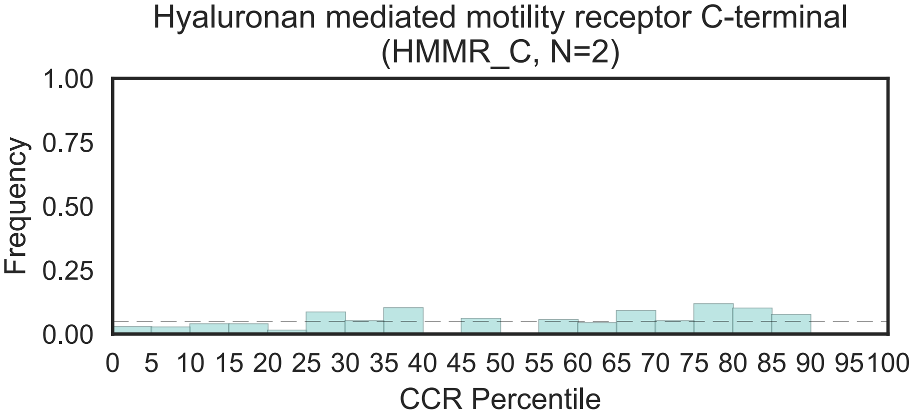

Hydroxymethylglutaryl-coenzyme A synthase N terminal
(HMG_CoA_synt_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

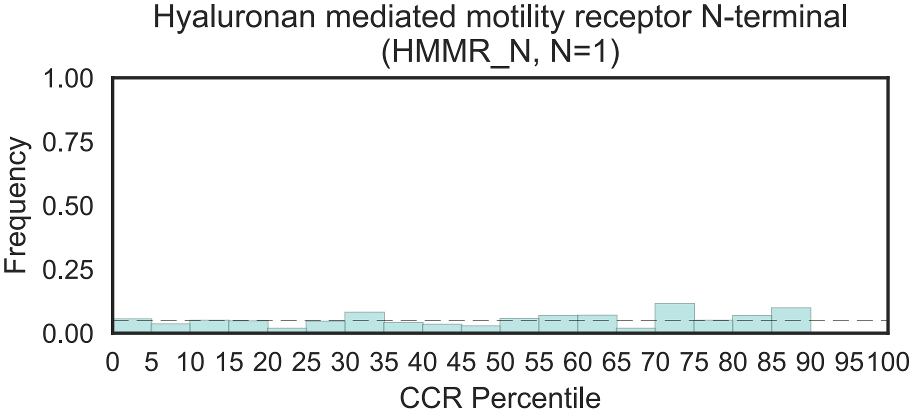

HMG (high mobility group) box
(HMG_box, N=53)
Fisher's OR: 8.33; Bonferroni p-val: 1.27e-28
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

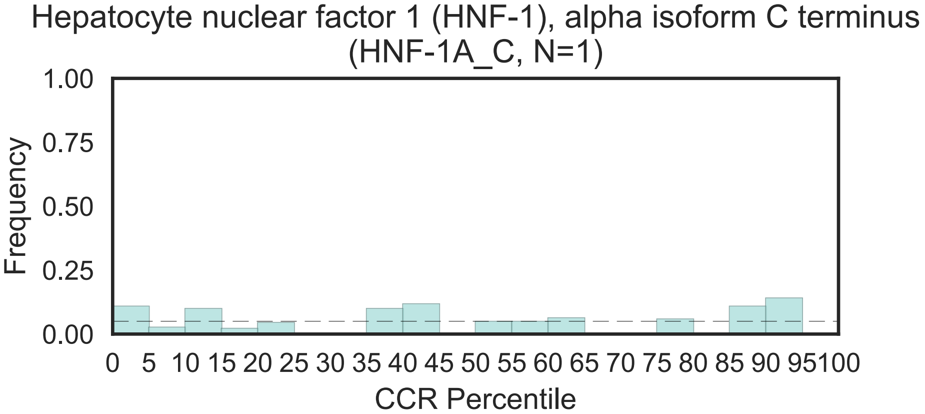


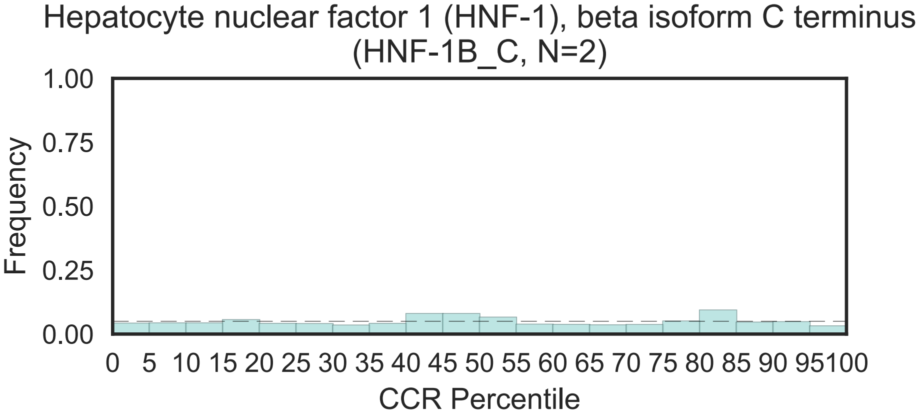
HMG-box domain
(HMG_box_2, N=50)
Fisher's OR: 7.89; Bonferroni p-val: 2.17e-22


HMG (high mobility group) box 5
(HMG_box_5, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

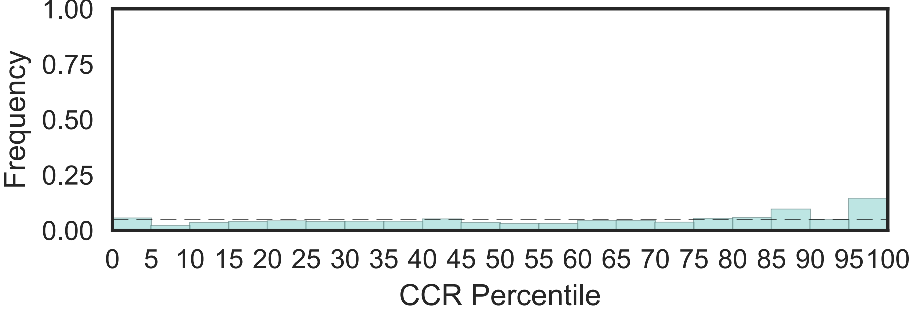

Hyaluronan mediated motility receptor C-terminal
(HMMR_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

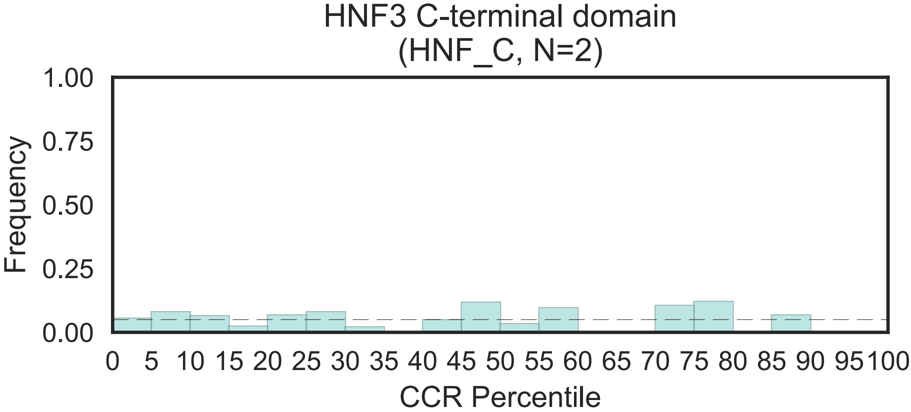

Hyaluronan mediated motility receptor N-terminal
(HMMR_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

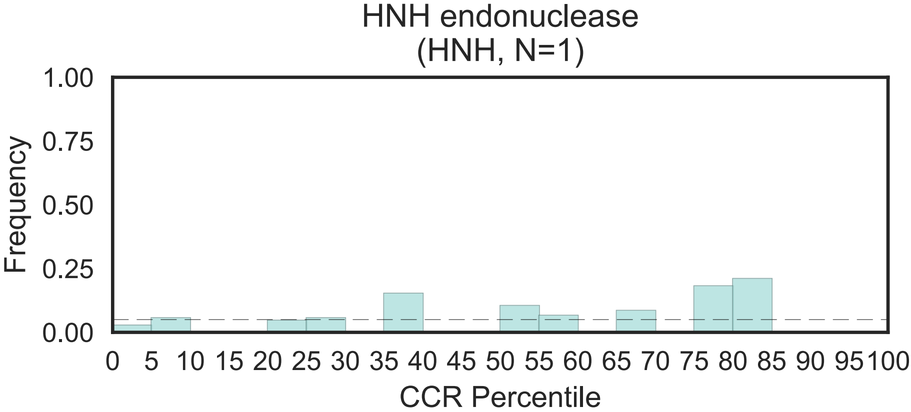

Hepatocyte nuclear factor 1 (HNF-1), alpha isoform C terminus
(HNF-1A_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

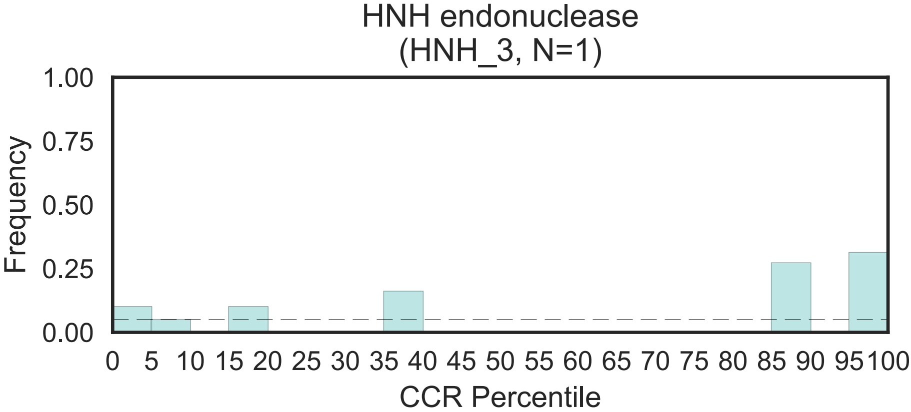

Hepatocyte nuclear factor 1 (HNF-1), beta isoform C terminus
(HNF-1B_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

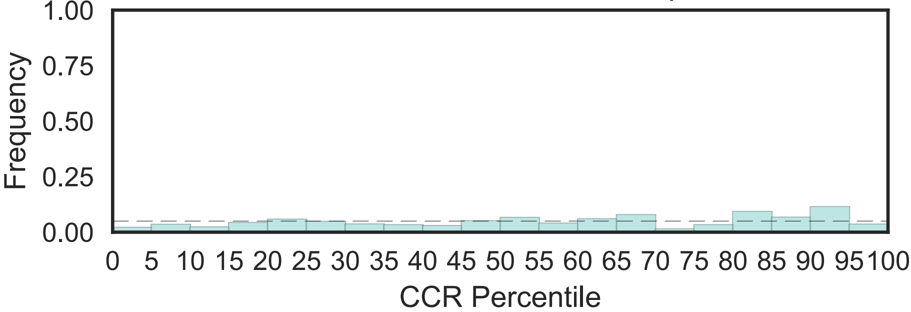
Hepatocyte nuclear factor 1 (HNF-1), N terminus
(HNF-1_N, N=3)
Fisher's OR: 1.93; Bonferroni p-val: 1

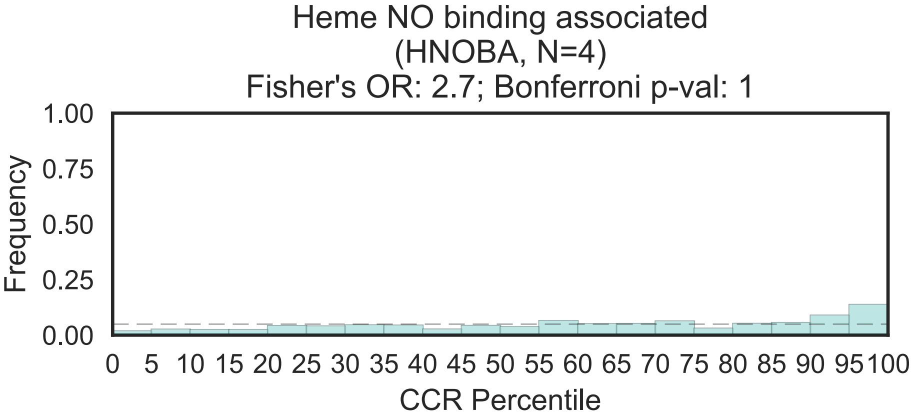


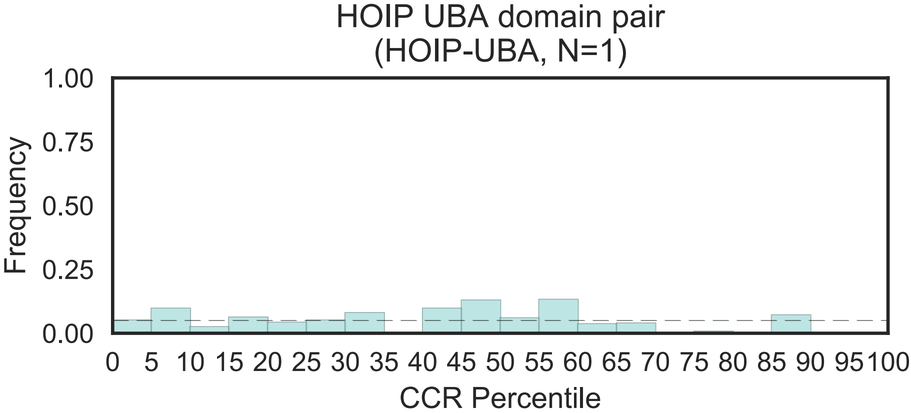

HNF3 C-terminal domain
(HNF_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

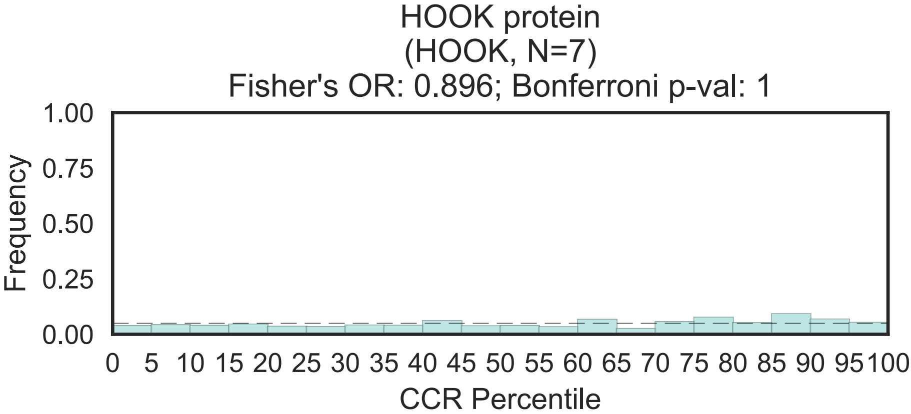

HNH endonuclease
(HNH, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

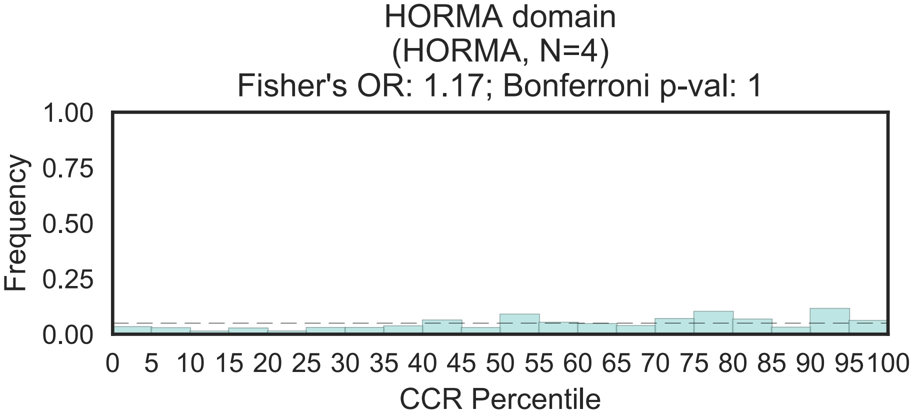

HNH endonuclease
(HNH_3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Haem-NO-binding
(HNOB, N=3)
Fisher's OR: 0.801; Bonferroni p-val: 1

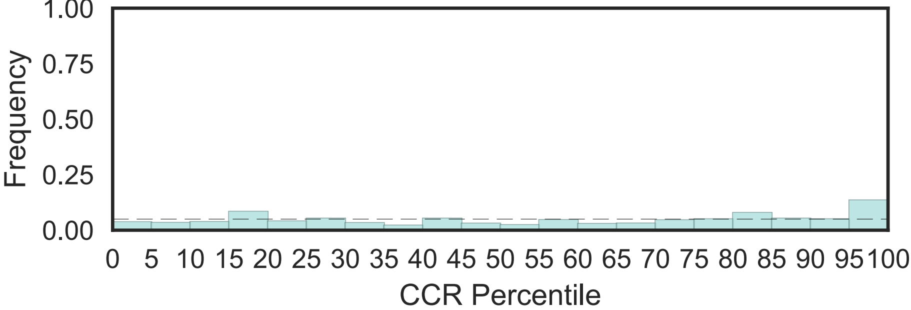

Heme NO binding associated
(HNOBA, N=4)
Fisher's OR: 2.7; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

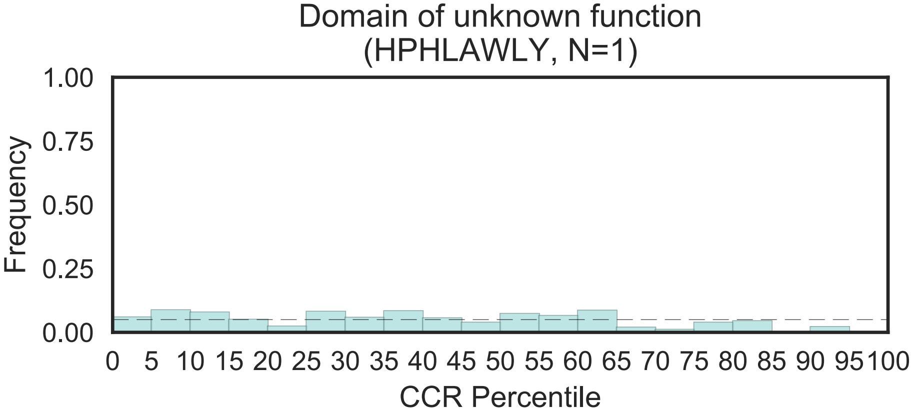

HOIP UBA domain pair
(HOIP-UBA, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

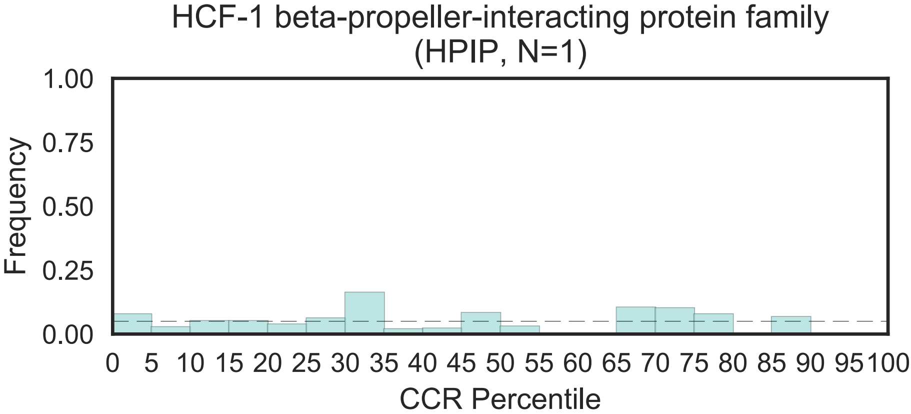

HOOK protein
(HOOK, N=7)
Fisher's OR: 0.896; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

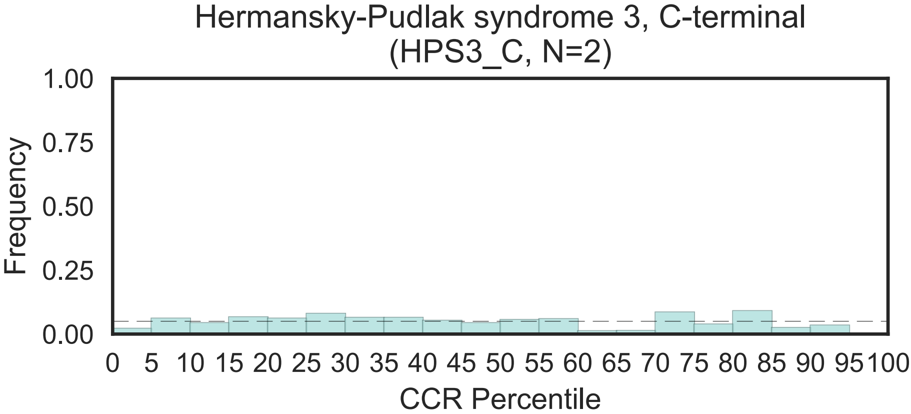

HORMA domain
(HORMA, N=4)
Fisher's OR: 1.17; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

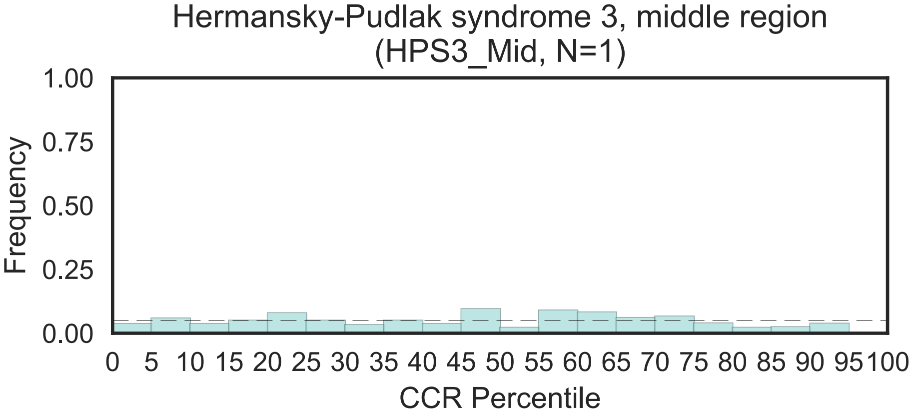
Homeo-prospero domain
(HPD, N=3)
Fisher's OR: 2.46; Bonferroni p-val: 1

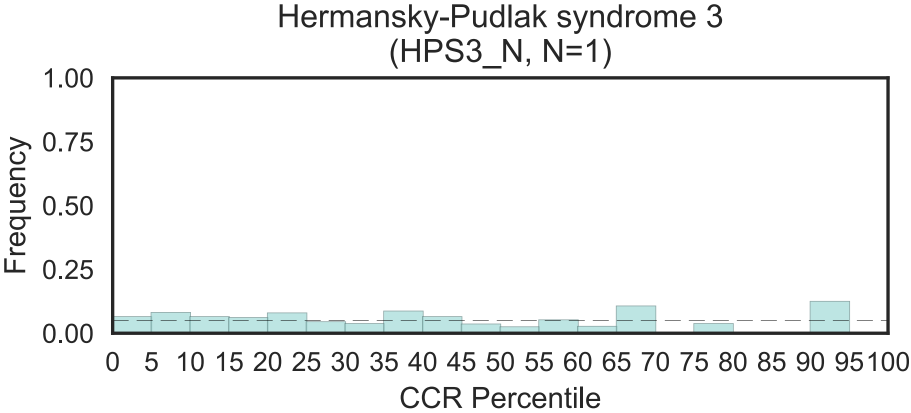


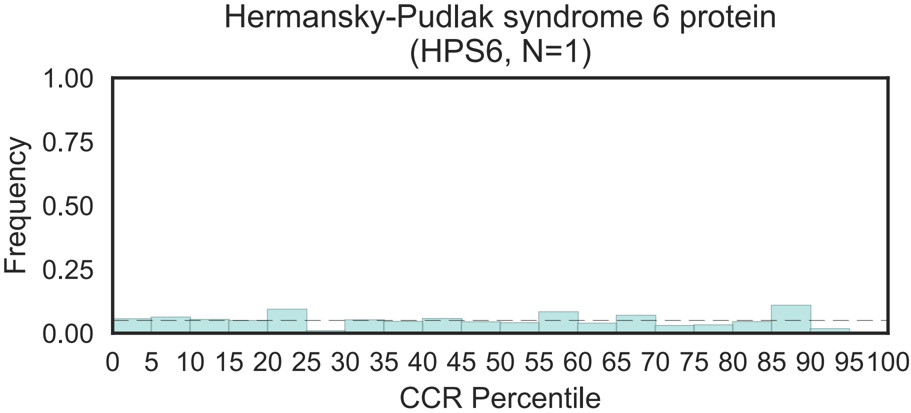

Domain of unknown function
(HPHLAWLY, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

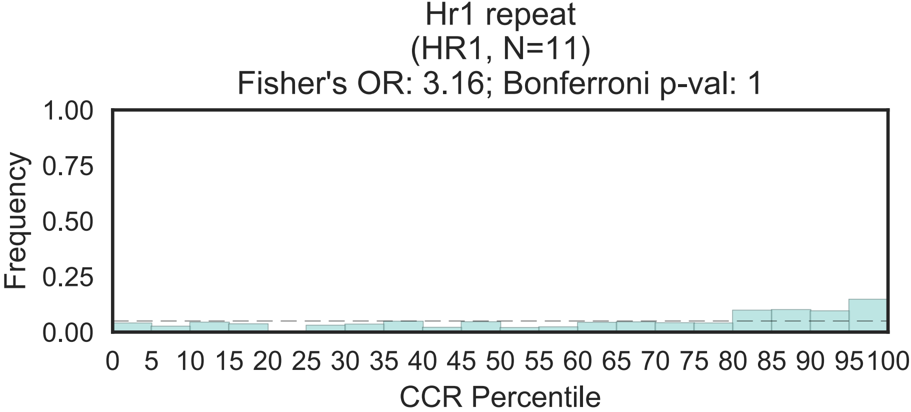

HCF-1 beta-propeller-interacting protein family
(HPIP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

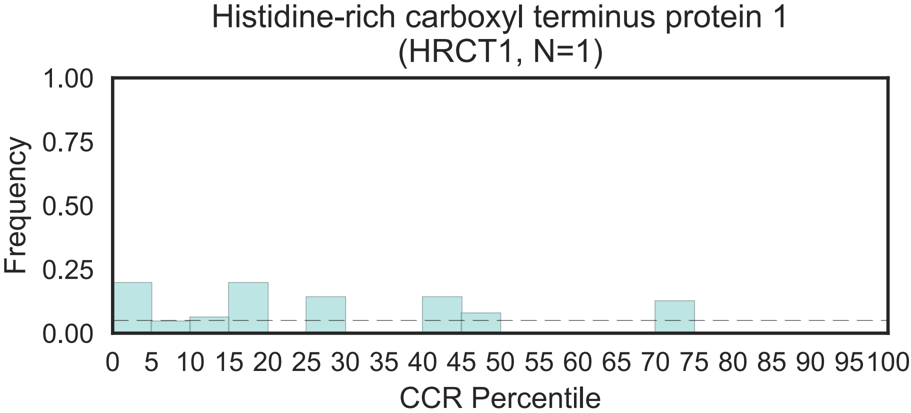

Hermansky-Pudlak syndrome 3, C-terminal
(HPS3_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

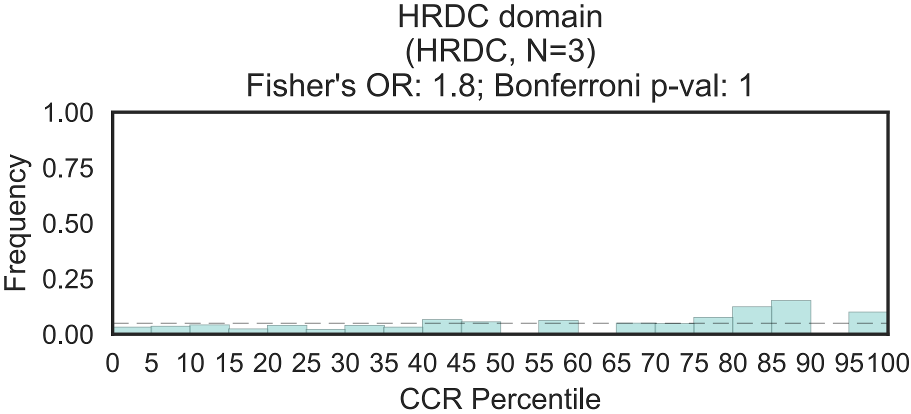

Hermansky-Pudlak syndrome 3, middle region
(HPS3_Mid, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

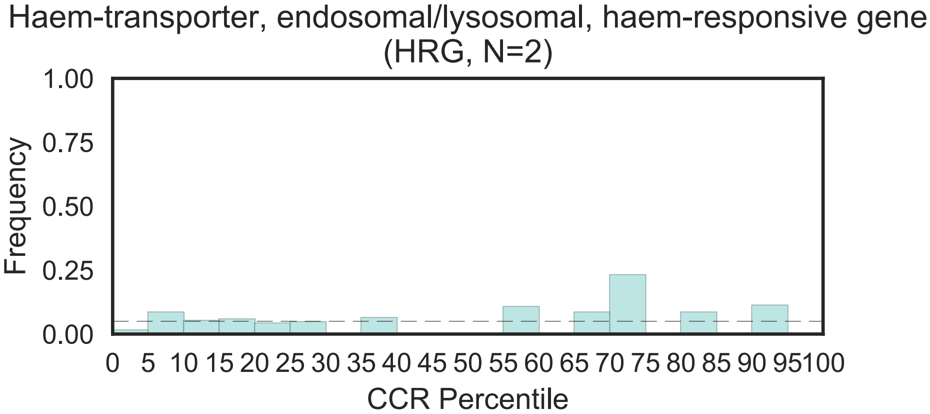

Hermansky-Pudlak syndrome 3
(HPS3_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

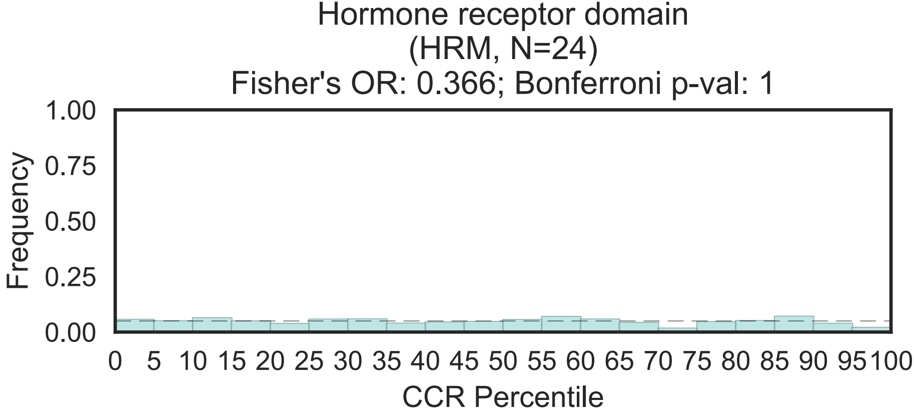

Hermansky-Pudlak syndrome 6 protein
(HPS6, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

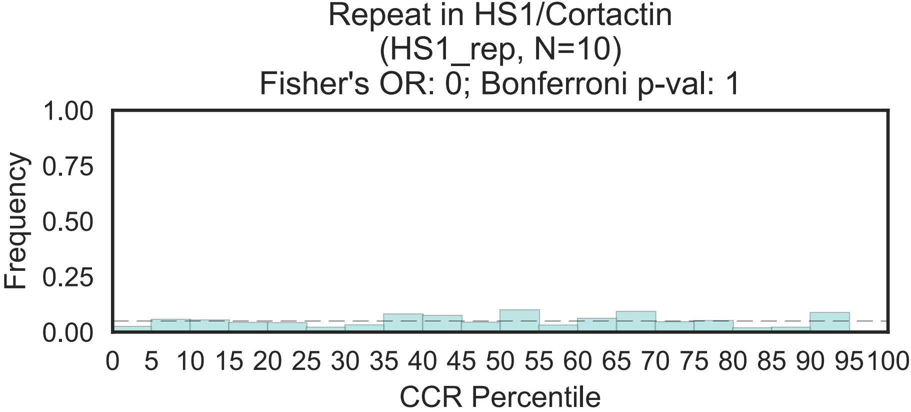

Hr1 repeat
(HR1, N=11)
Fisher's OR: 3.16; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

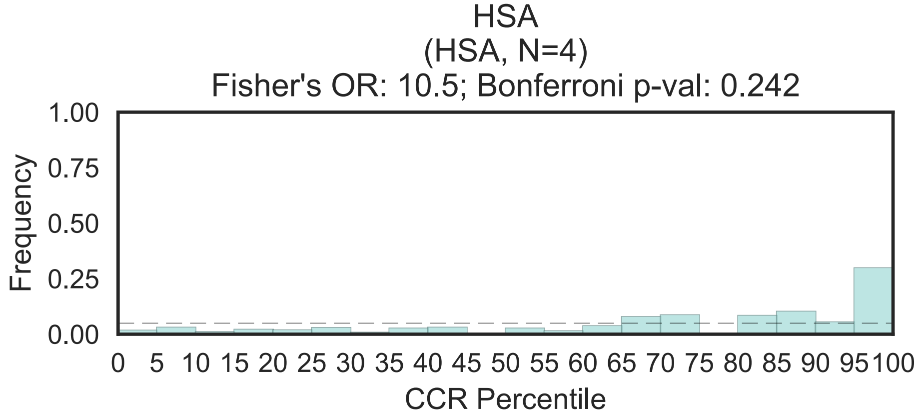

Histidine-rich carboxyl terminus protein 1
(HRCT1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

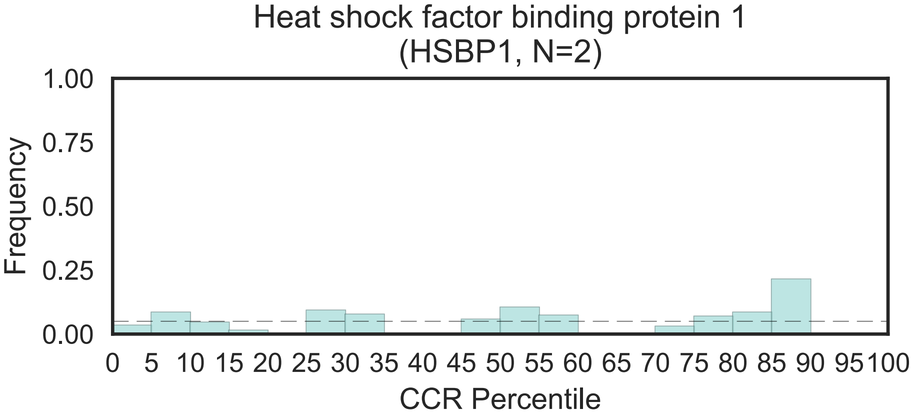

HRDC domain
(HRDC, N=3)
Fisher's OR: 1.8; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

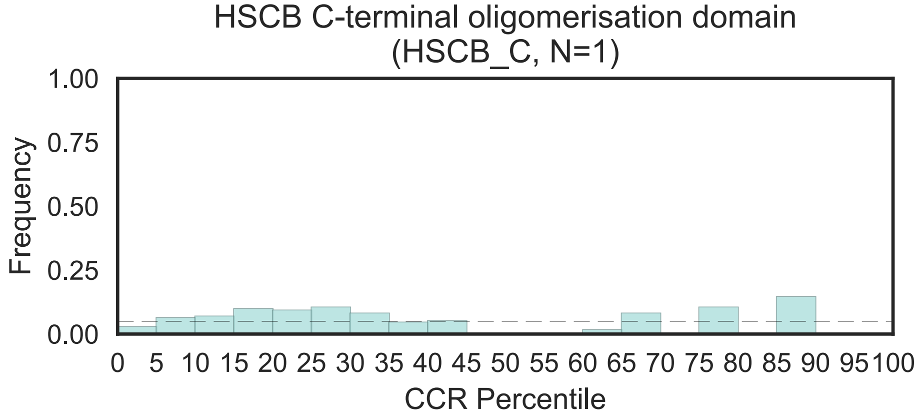

Haem-transporter, endosomal/lysosomal, haem-responsive gene
(HRG, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

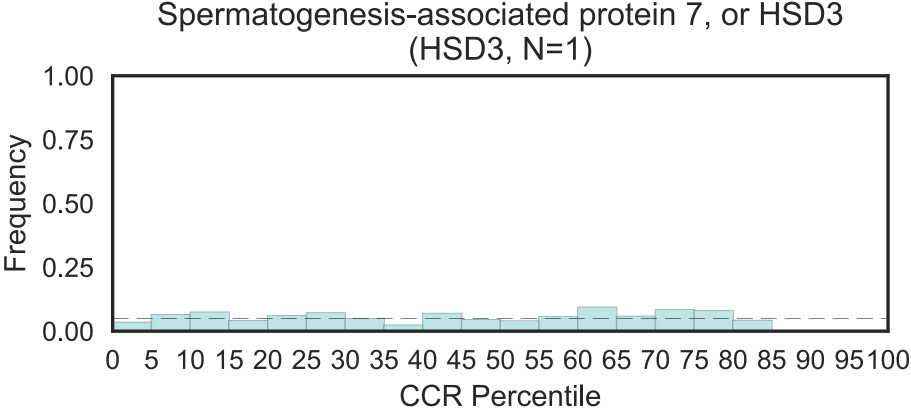

Hormone receptor domain
(HRM, N=24)
Fisher's OR: 0.366; Bonferroni p-val: 1

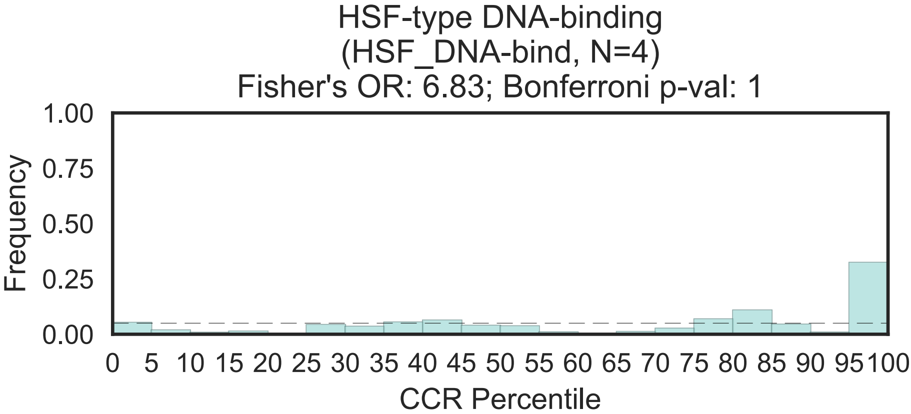

Repeat in HS1/Cortactin
(HS1_rep, N=10)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


HSA
(HSA, N=4)
Fisher's OR: 10.5; Bonferroni p-val: 0.242
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

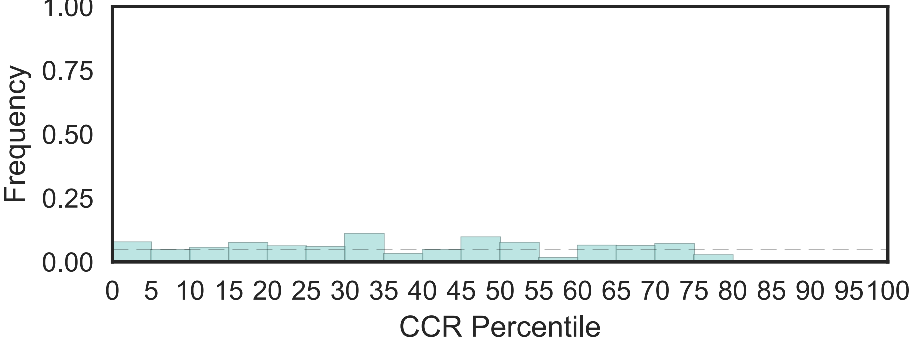

Heat shock factor binding protein 1
(HSBP1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

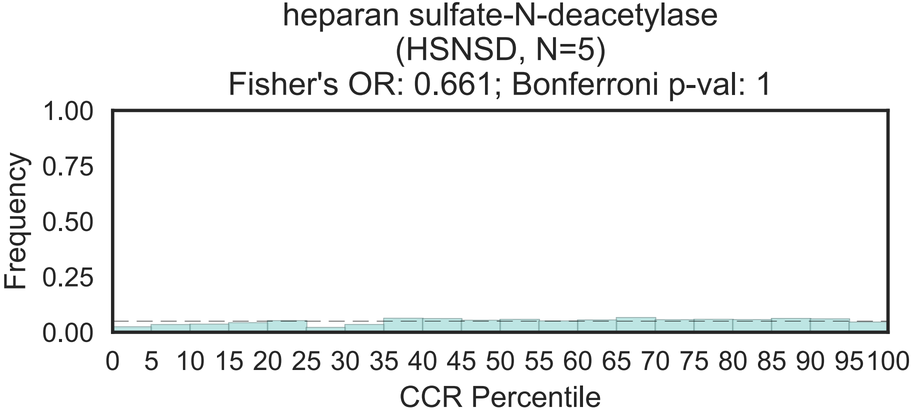

HSCB C-terminal oligomerisation domain
(HSCB_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

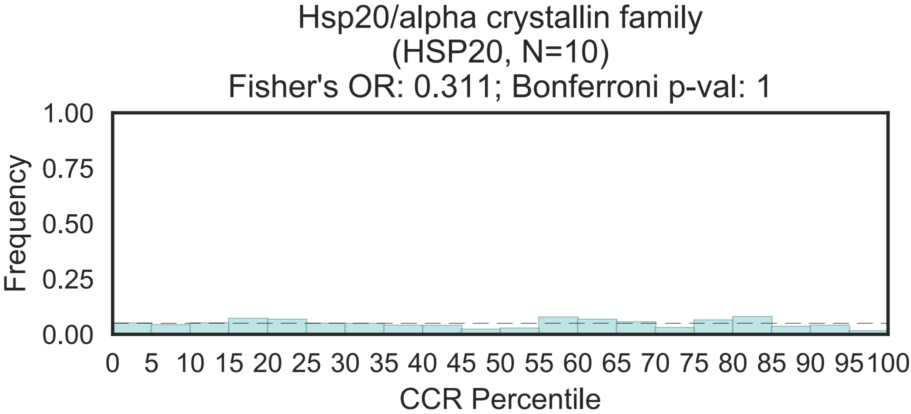

Spermatogenesis-associated protein 7, or HSD3
(HSD3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

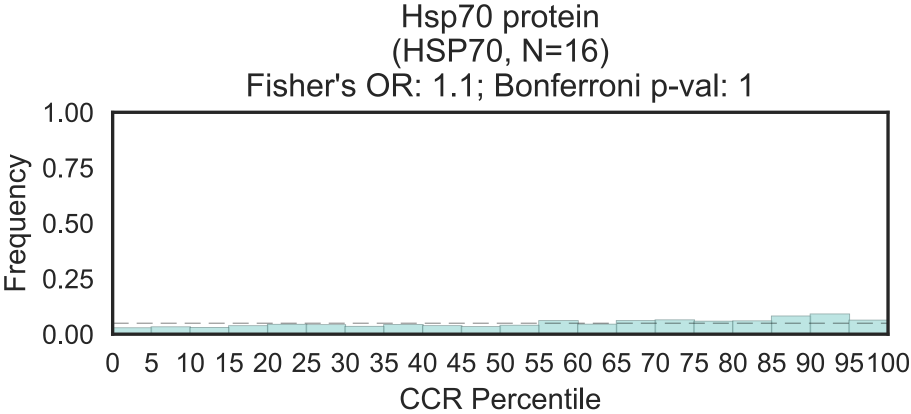

HSF-type DNA-binding
(HSF_DNA-bind, N=4)
Fisher's OR: 6.83; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

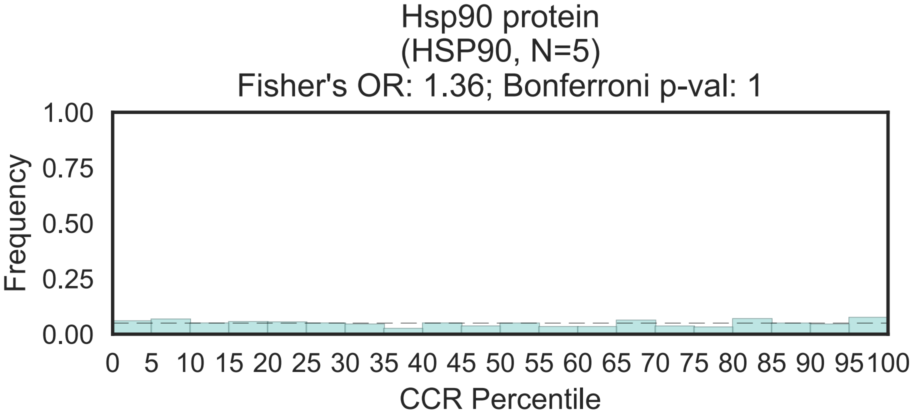
Hormone-sensitive lipase (HSL) N-terminus (HSL_N, N=1)



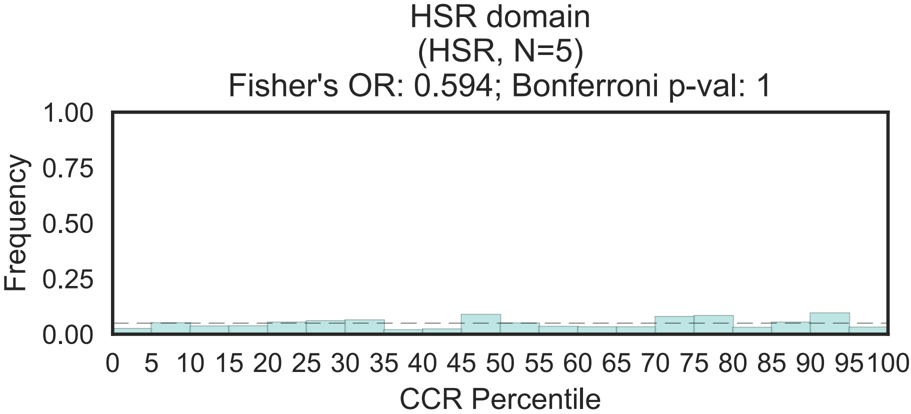

heparan sulfate-N-deacetylase
(HSNSD, N=5)
Fisher's OR: 0.661; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

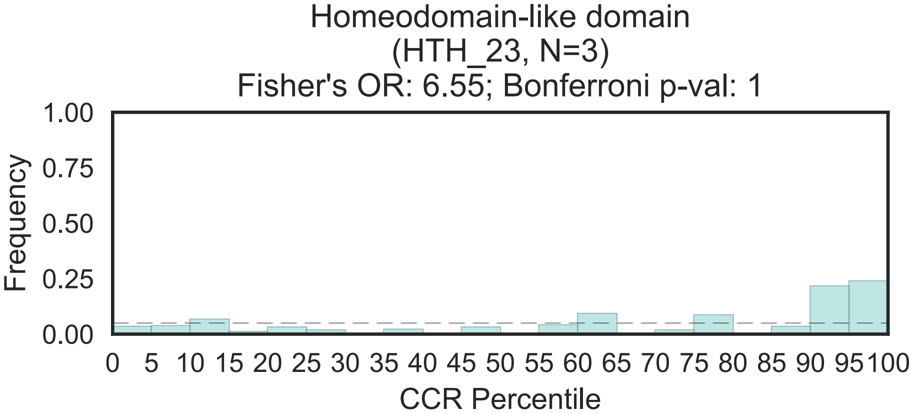

Hsp20/alpha crystallin family
(HSP20, N=10)
Fisher's OR: 0.311; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

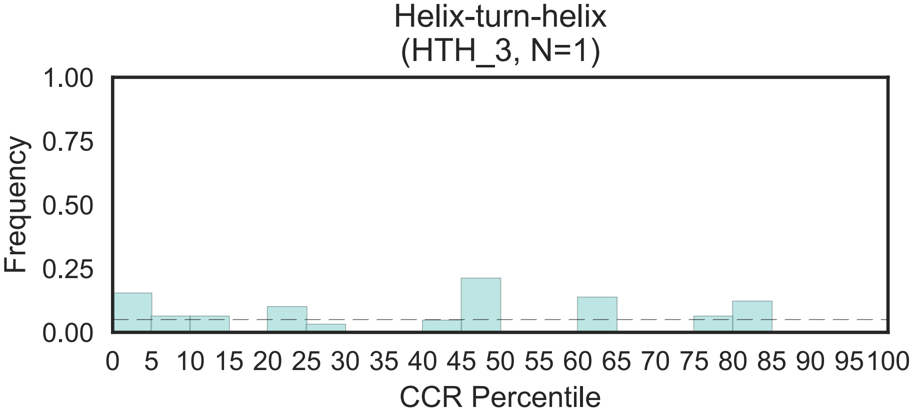

Hsp70 protein
(HSP70, N=16)
Fisher's OR: 1.1; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

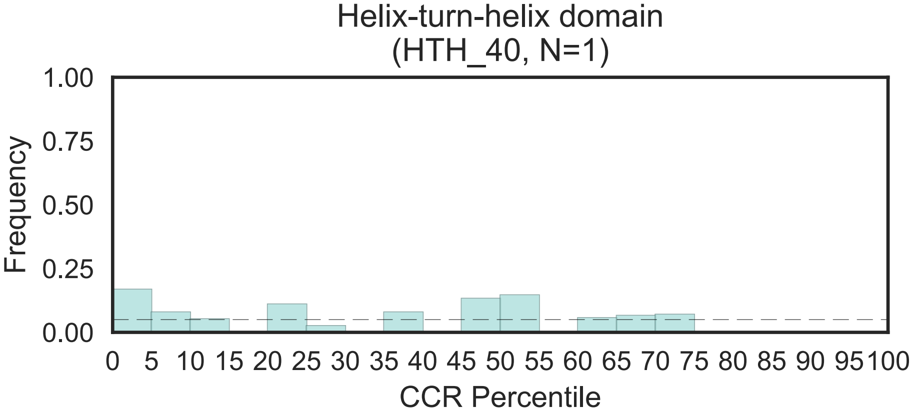


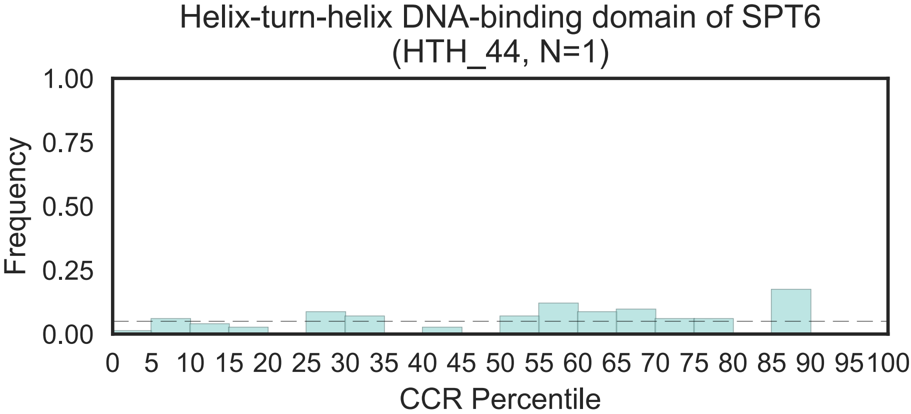
Hsp90 protein
(HSP90, N=5)
Fisher's OR: 1.36; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


HSR domain
(HSR, N=5)
Fisher's OR: 0.594; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

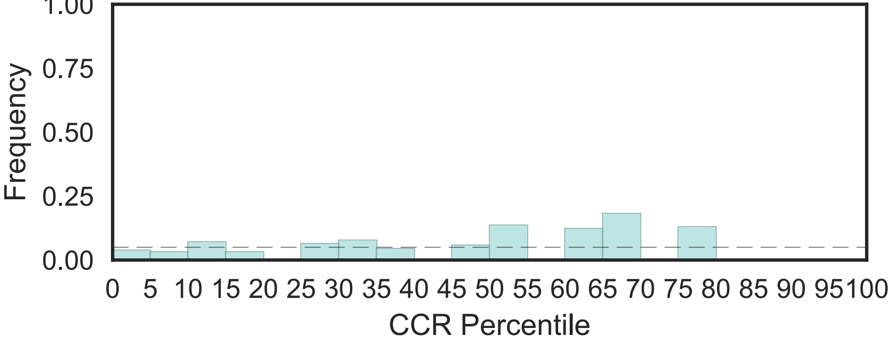

Homeodomain-like domain
(HTH_23, N=3)
Fisher's OR: 6.55; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

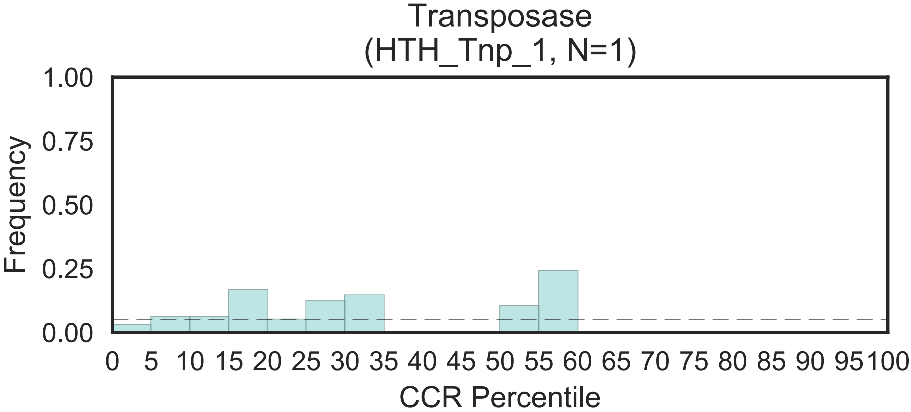

Helix-turn-helix
(HTH_3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

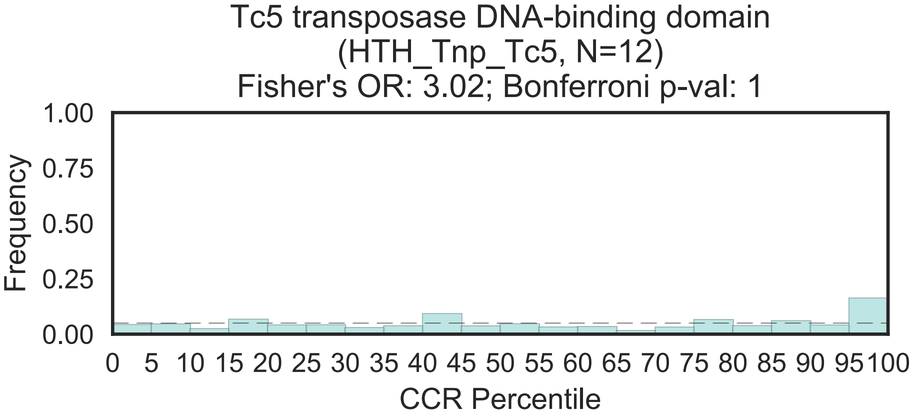

Helix-turn-helix domain
(HTH_40, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Helix-turn-helix DNA-binding domain of SPT6
(HTH_44, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

RNA polymerase III subunit RPC82 helix-turn-helix domain (HTH_9, N=1)

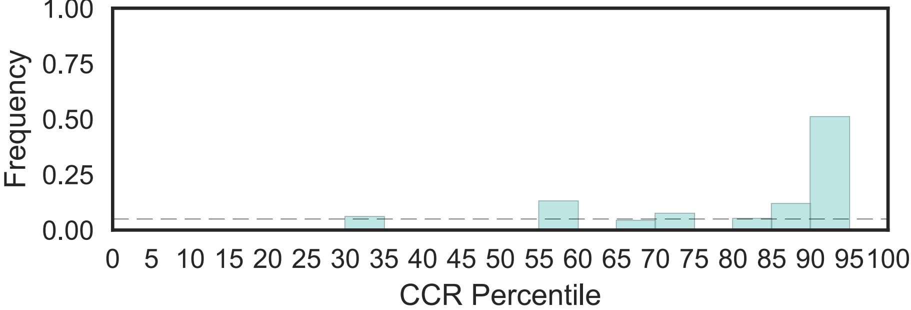


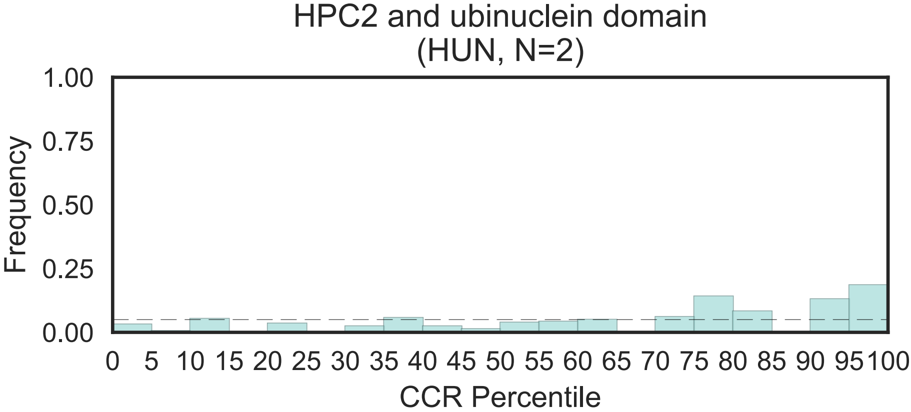

Transposase
(HTH_Tnp_1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

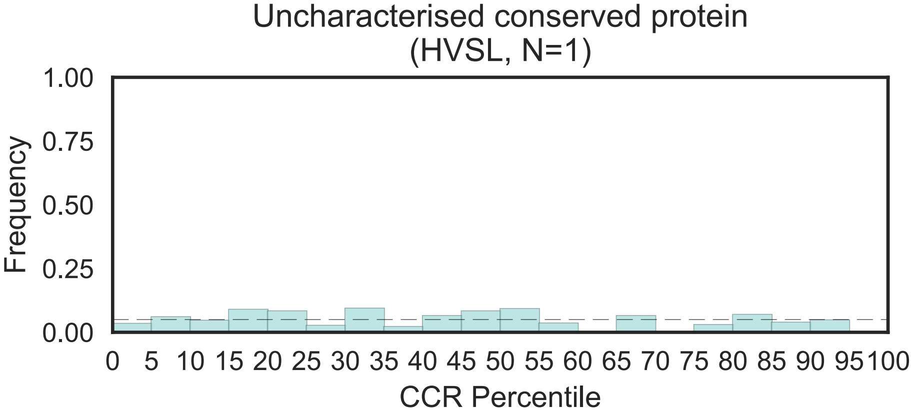


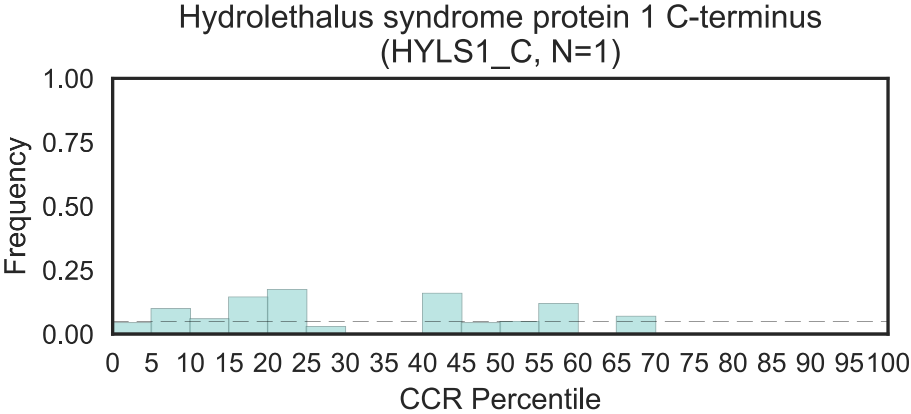
Tc5 transposase DNA-binding domain
(HTH_Tnp_Tc5, N=12)
Fisher's OR: 3.02; Bonferroni p-val: 1

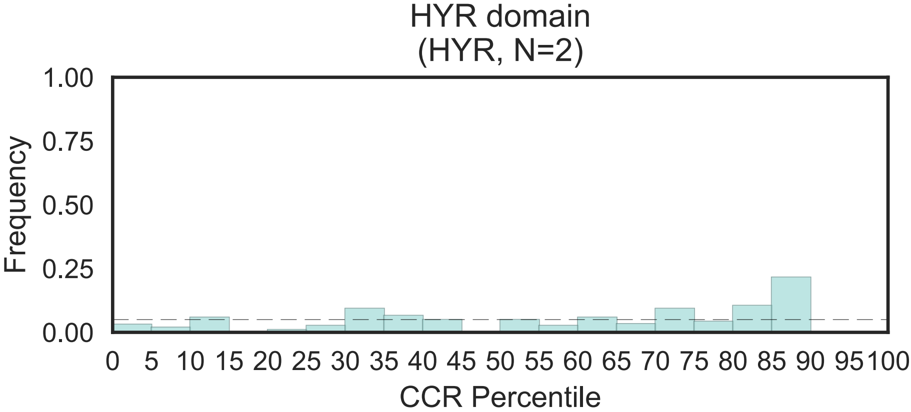
helix-turn-helix, Psq domain
(HTH_psq, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

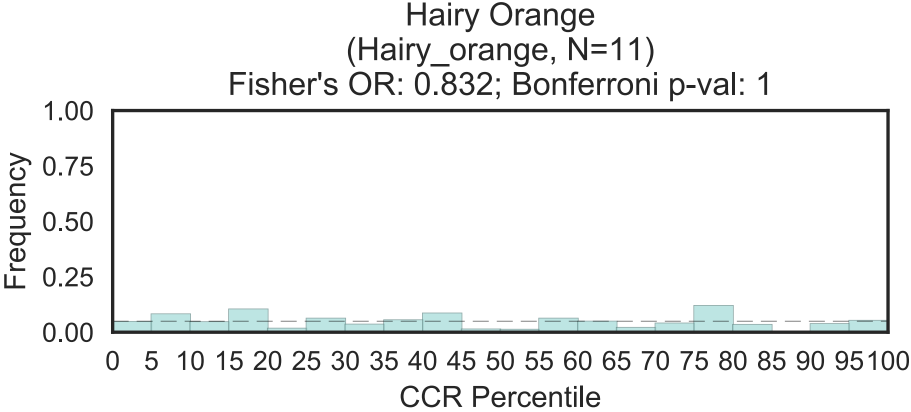


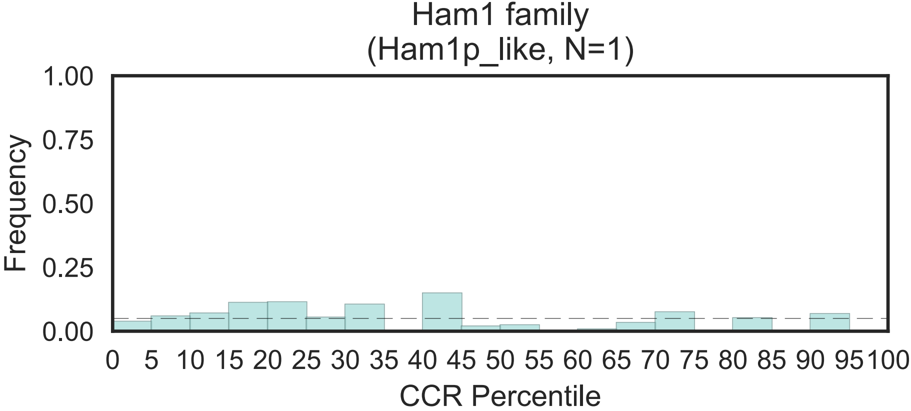

HPC2 and ubinuclein domain
(HUN, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

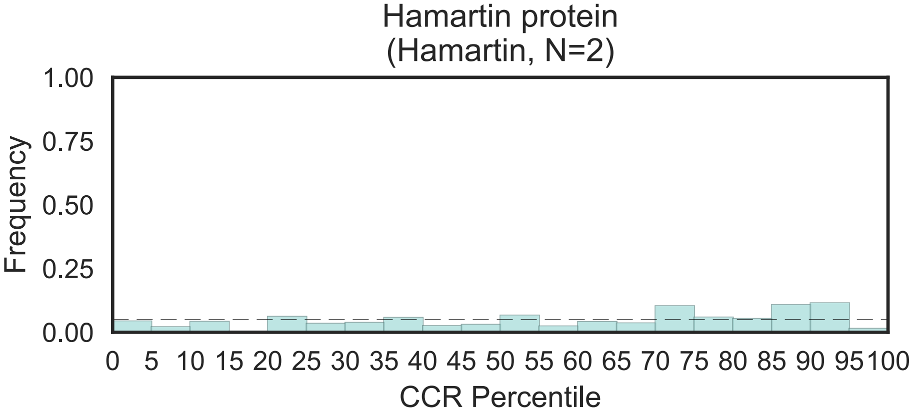

Uncharacterised conserved protein
(HVSL, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

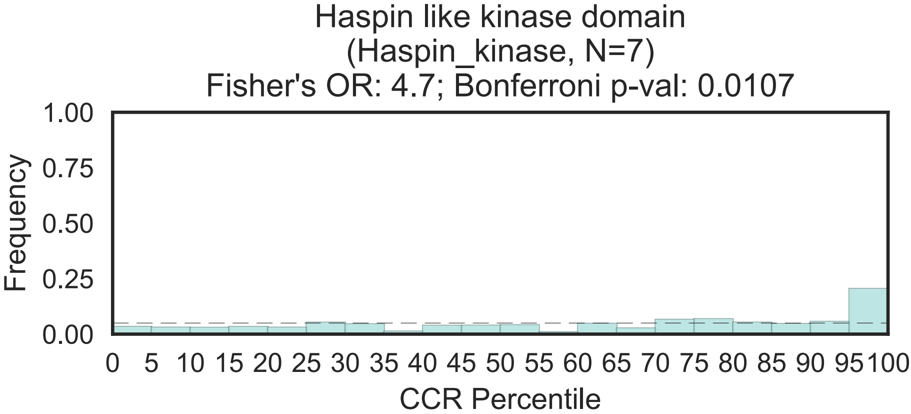

Hydrolethalus syndrome protein 1 C-terminus
(HYLS1_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

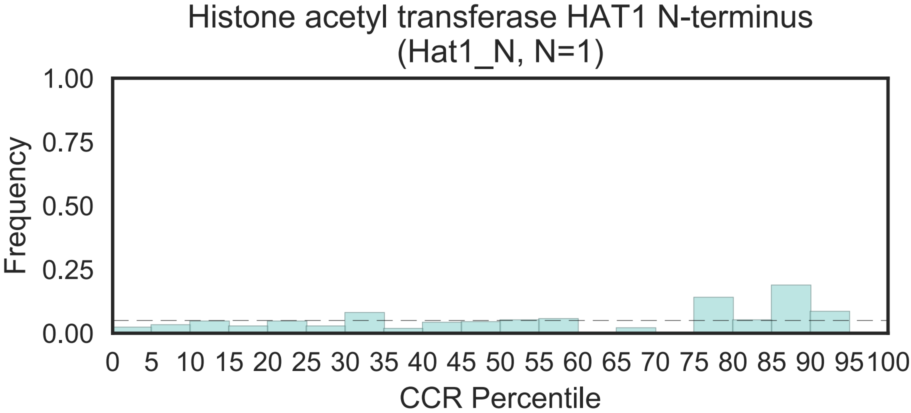

HYR domain
(HYR, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

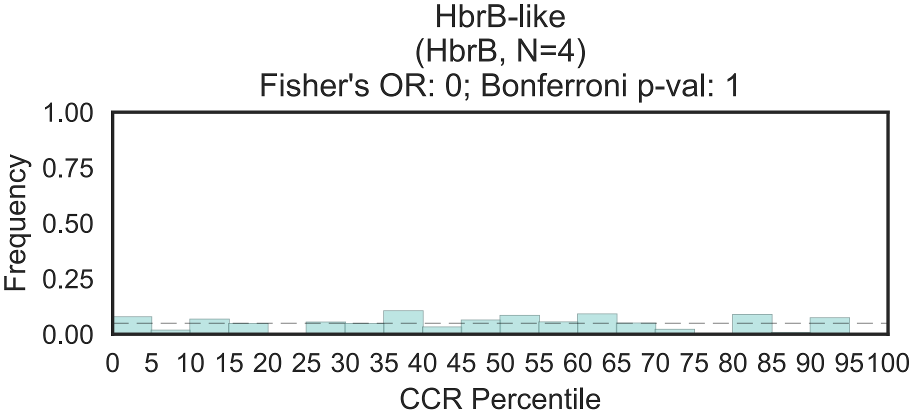

Hairy Orange
(Hairy_orange, N=11)
Fisher's OR: 0.832; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

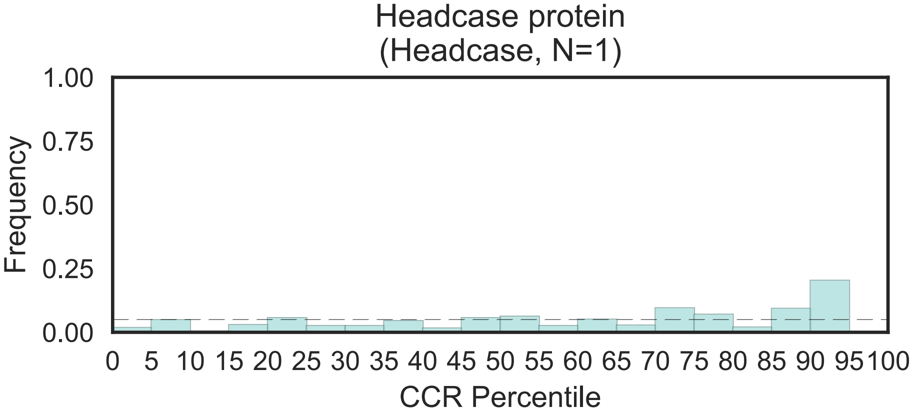

Ham1 family
(Ham1p_like, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

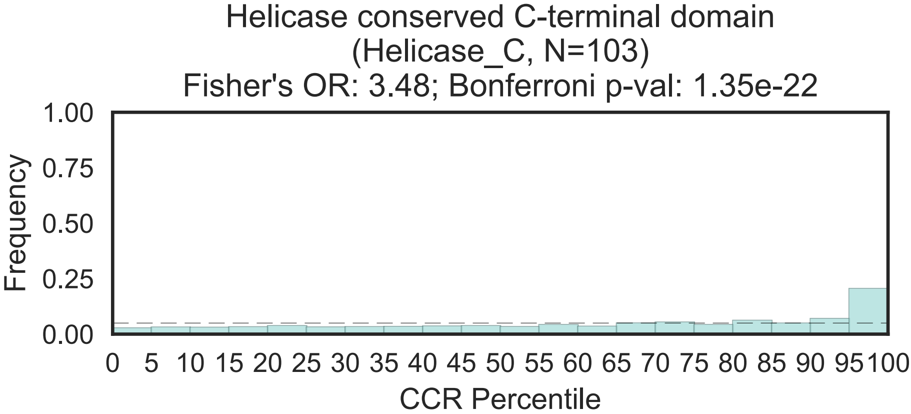

Hamartin protein
(Hamartin, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

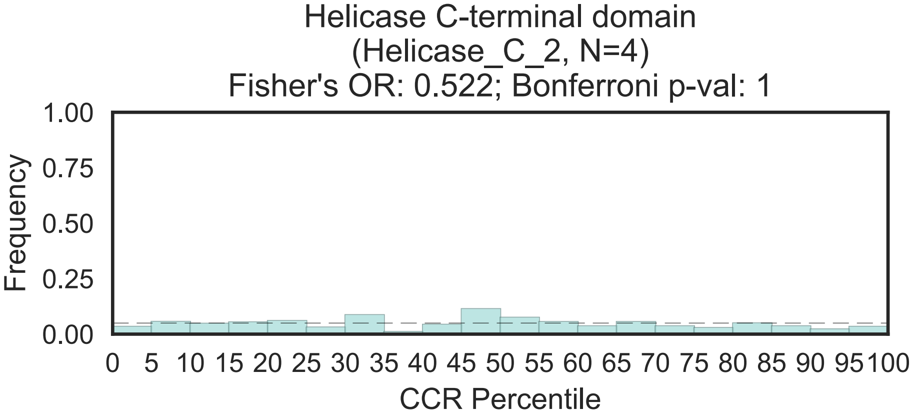

Haspin like kinase domain
(Haspin_kinase, N=7)
Fisher's OR: 4.7; Bonferroni p-val: 0.0107
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

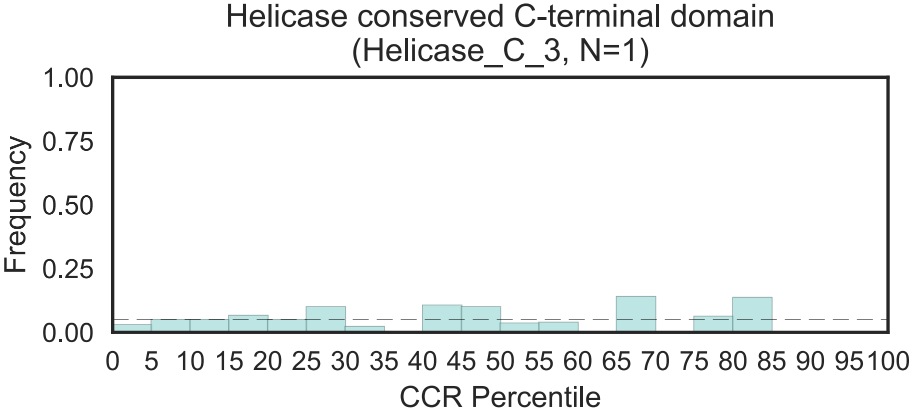

Histone acetyl transferase HAT1 N-terminus
(Hat1_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

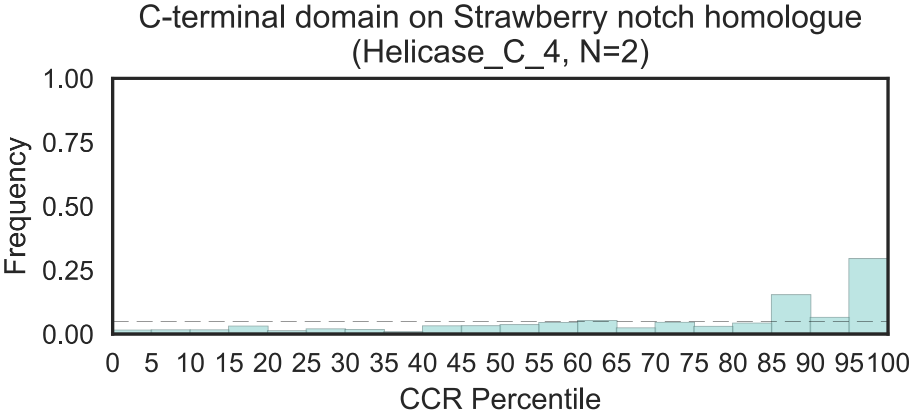

HbrB-like
(HbrB, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

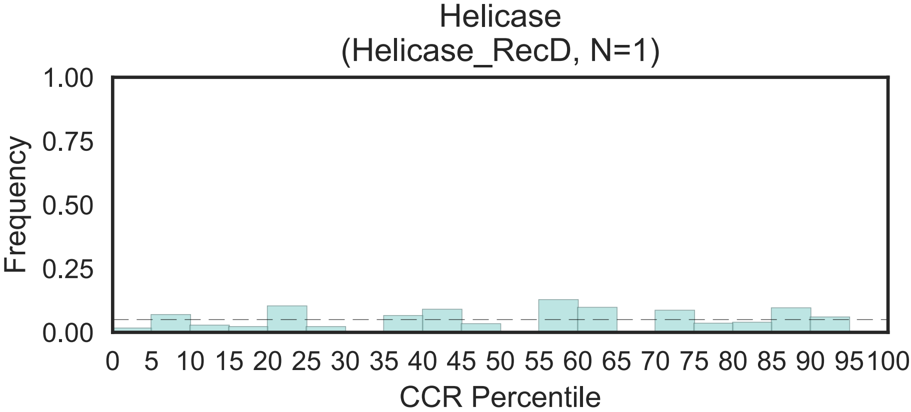

Headcase protein
(Headcase, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

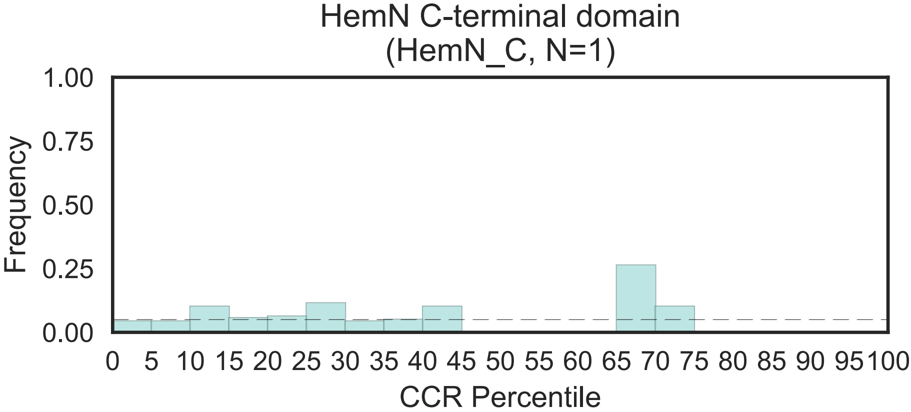

Helicase conserved C-terminal domain
(Helicase_C, N=103)
Fisher's OR: 3.48; Bonferroni p-val: 1.35e-22
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

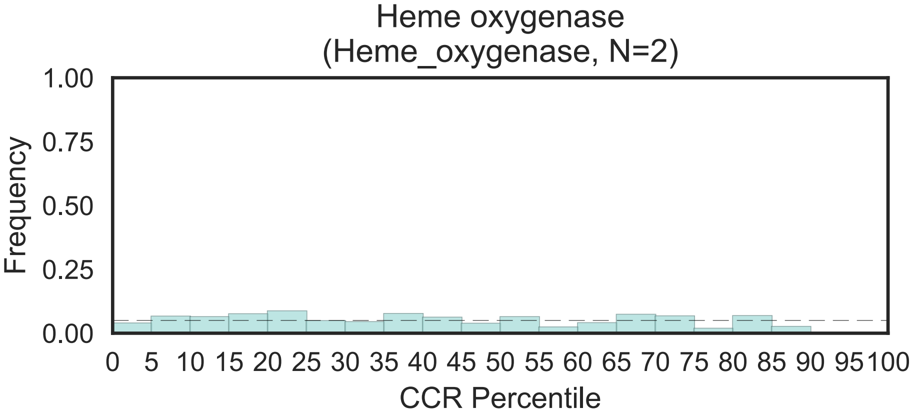

Helicase C-terminal domain
(Helicase_C_2, N=4)
Fisher's OR: 0.522; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

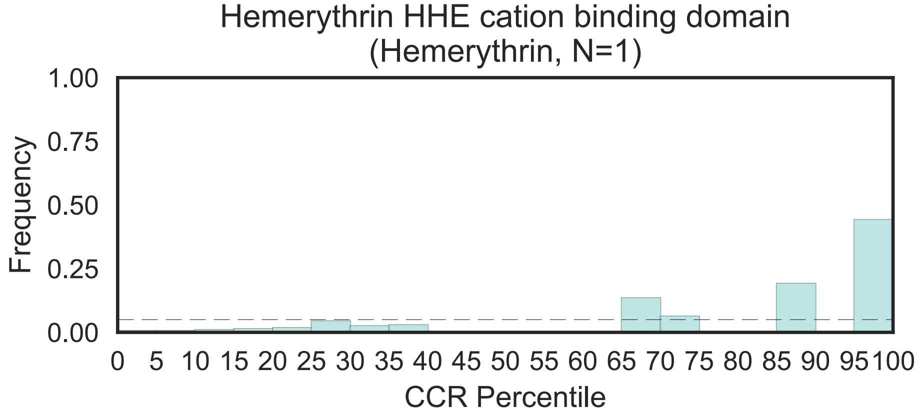

Helicase conserved C-terminal domain
(Helicase_C_3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

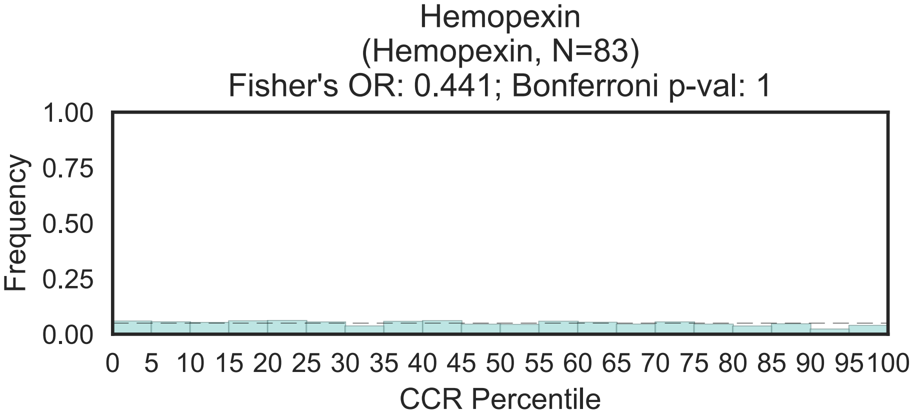

C-terminal domain on Strawberry notch homologue
(Helicase_C_4, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

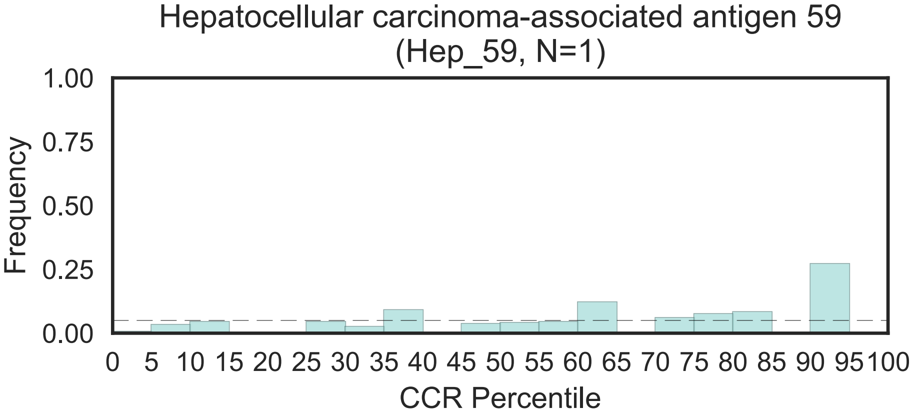

Helicase
(Helicase_RecD, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

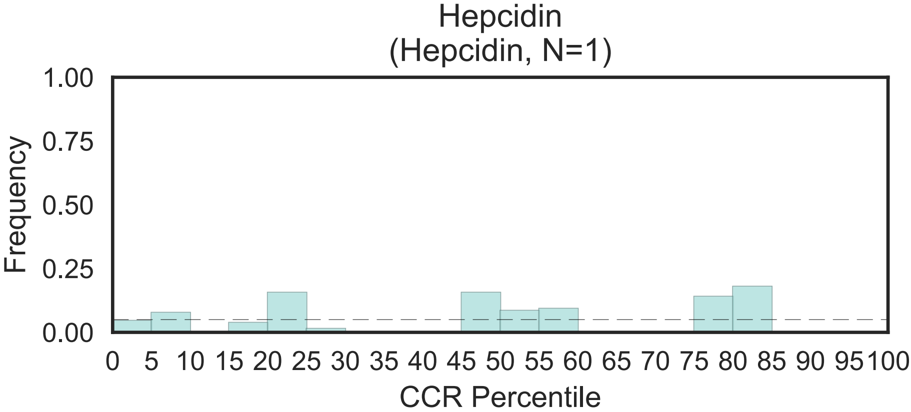

HemN C-terminal domain
(HemN_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

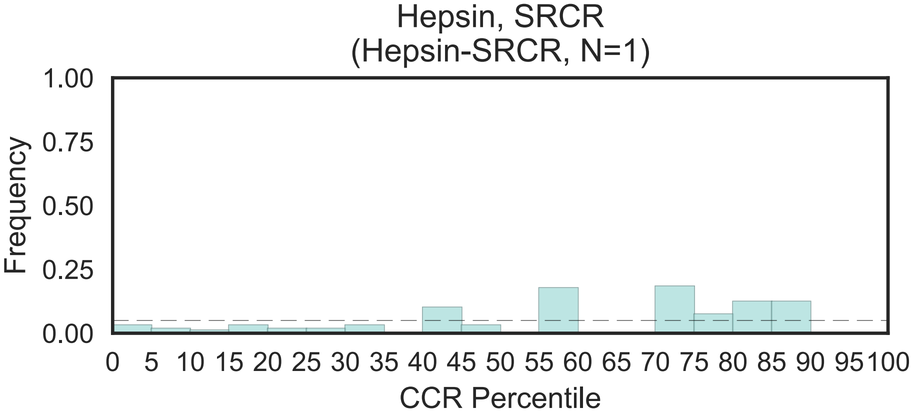

Heme oxygenase
(Heme_oxygenase, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

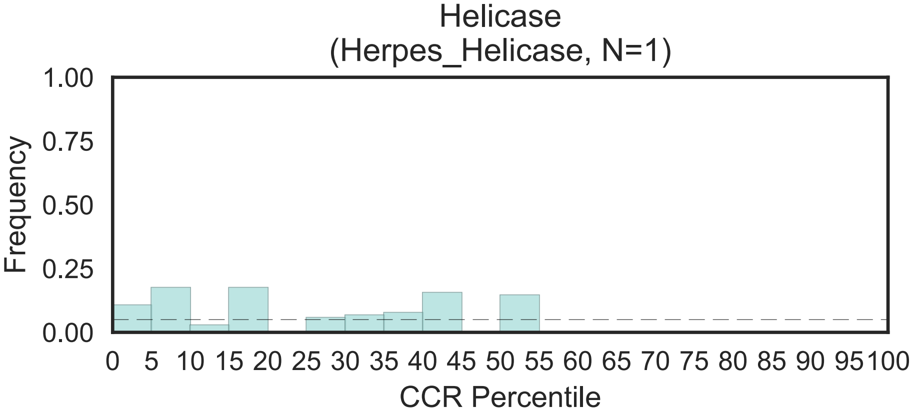

Hemerythrin HHE cation binding domain
(Hemerythrin, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

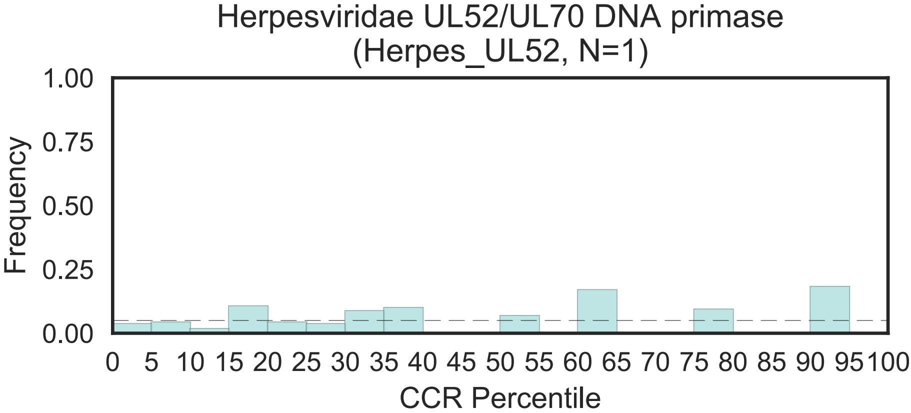

Hemopexin
(Hemopexin, N=83)
Fisher's OR: 0.441; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Hepatocellular carcinoma-associated antigen 59
(Hep_59, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

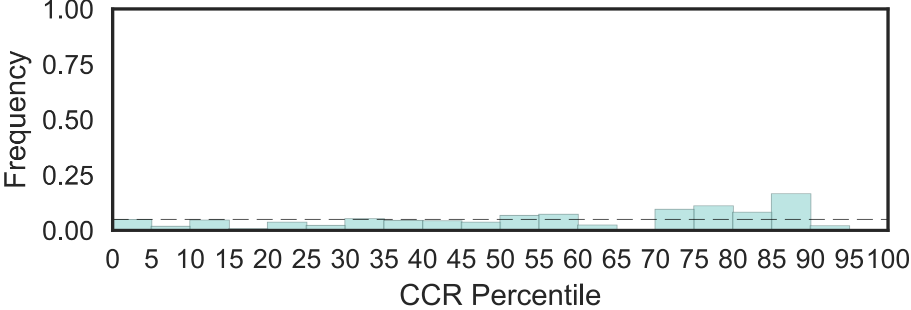

Hepcidin
(Hepcidin, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

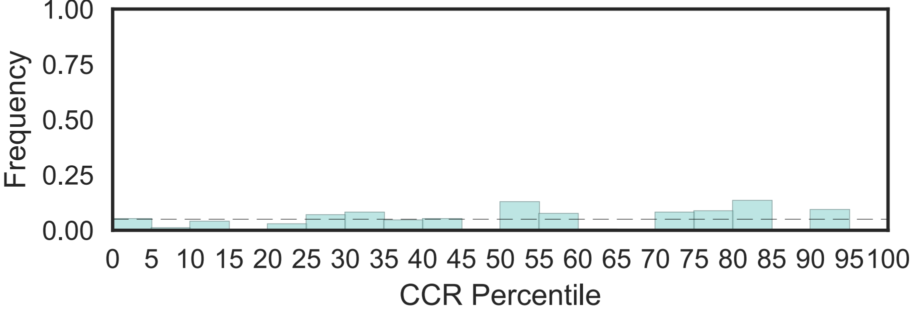

Hepsin, SRCR
(Hepsin-SRCR, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Helicase
(Herpes_Helicase, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

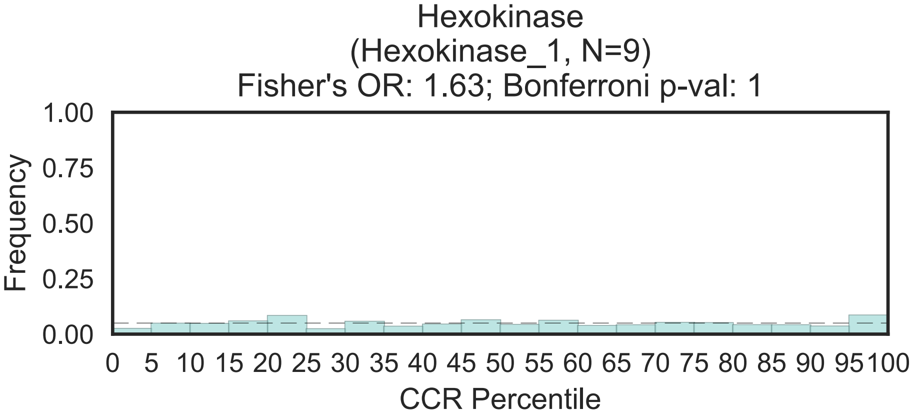

Herpesviridae UL52/UL70 DNA primase
(Herpes_UL52, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

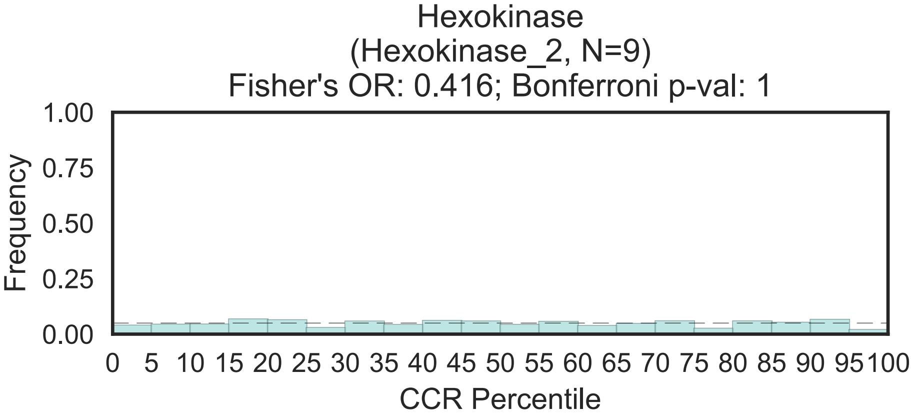
Bacterial transferase hexapeptide (six repeats)
(Hexapep, N=5)
Fisher's OR: 0; Bonferroni p-val: 1

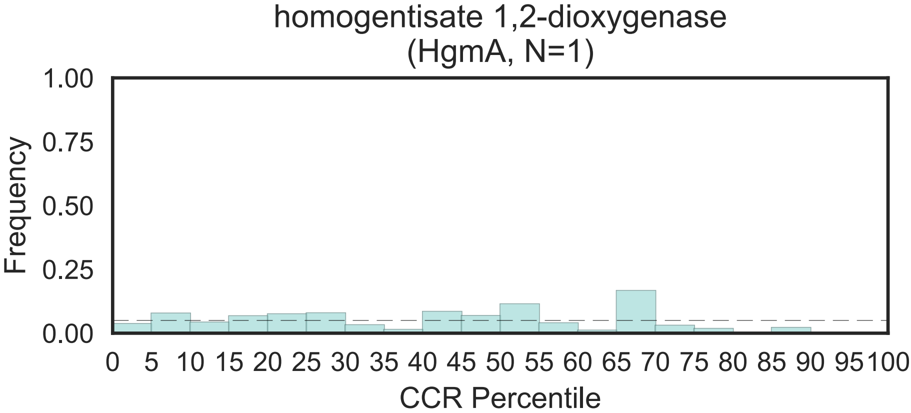


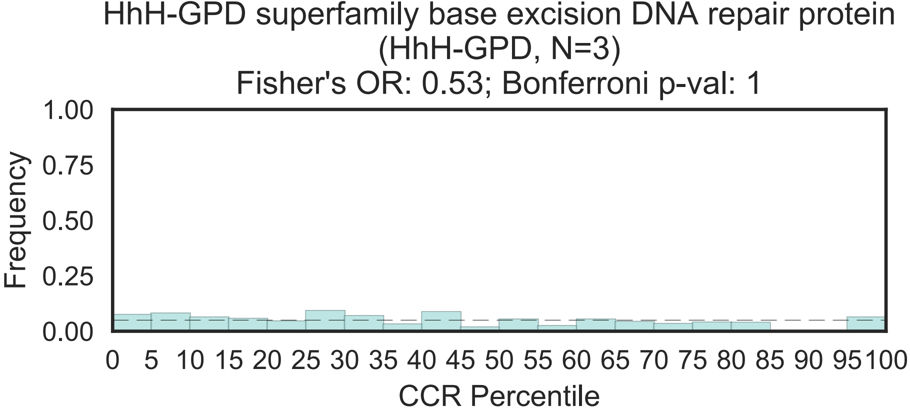


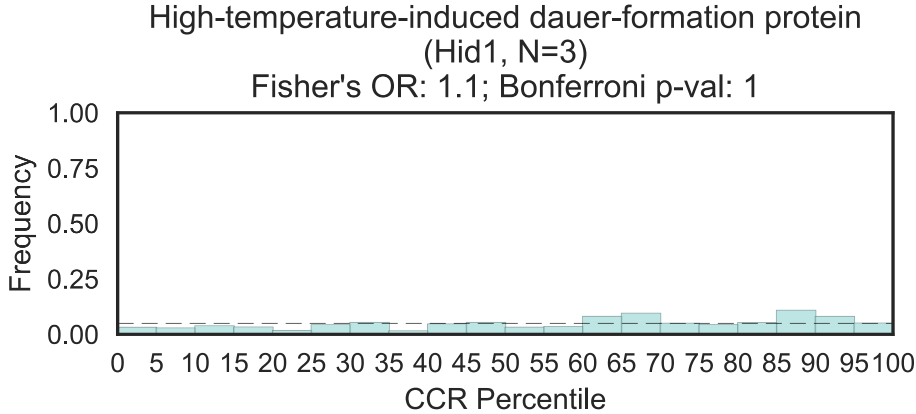
Hexapeptide repeat of succinyl-transferase
(Hexapep_2, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

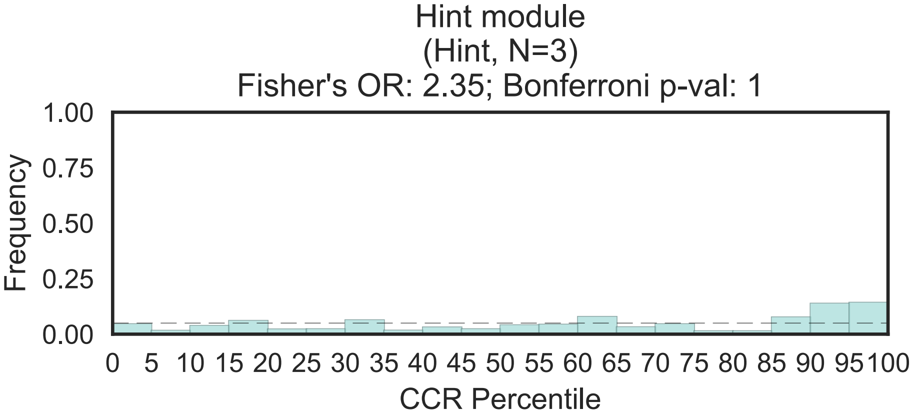

Hexokinase
(Hexokinase_1, N=9)
Fisher's OR: 1.63; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

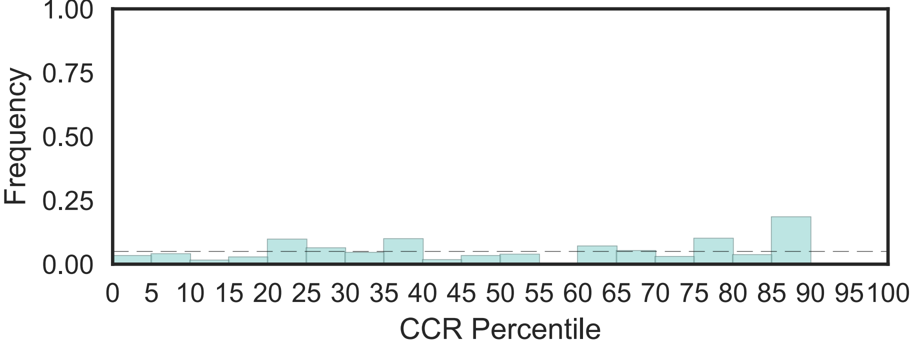

Hexokinase
(Hexokinase_2, N=9)
Fisher's OR: 0.416; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


homogentisate 1,2-dioxygenase
(HgmA, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

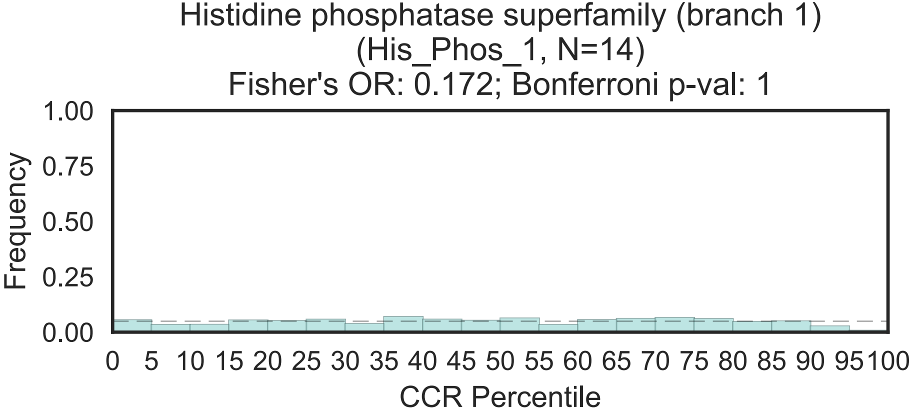

HhH-GPD superfamily base excision DNA repair protein
(HhH-GPD, N=3)
Fisher's OR: 0.53; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


High-temperature-induced dauer-formation protein
(Hid1, N=3)
Fisher's OR: 1.1; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

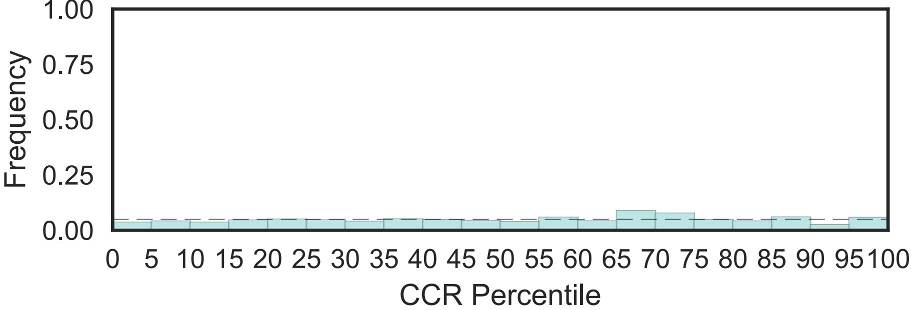

Hint module
(Hint, N=3)
Fisher's OR: 2.35; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



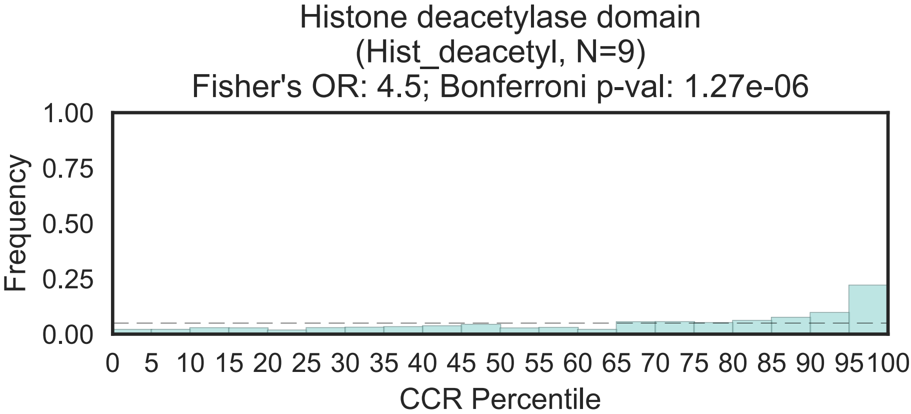
TUP1-like enhancer of split
(Hira, N=1)



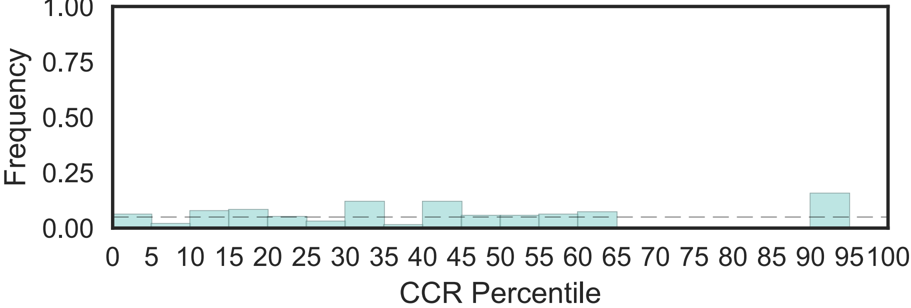
Histidine phosphatase superfamily (branch 1)
(His_Phos_1, N=14)
Fisher's OR: 0.172; Bonferroni p-val: 1

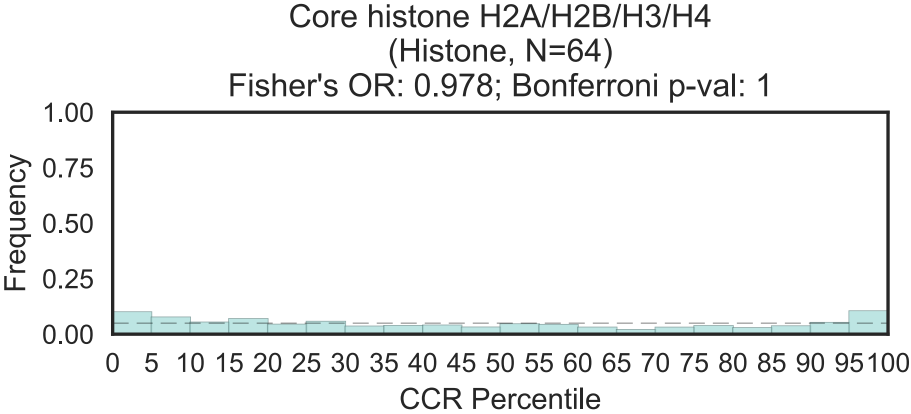


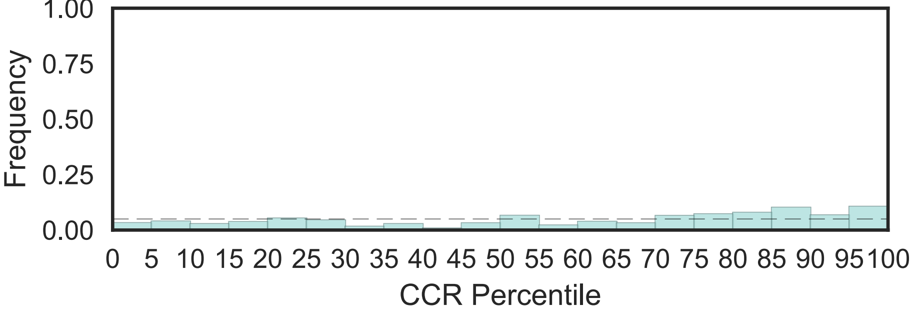
Histidine phosphatase superfamily (branch 2)
(His_Phos_2, N=9)
Fisher's OR: 0.865; Bonferroni p-val: 1


Histone deacetylase domain
(Hist_deacetyl, N=9)
Fisher's OR: 4.5; Bonferroni p-val: 1.27e-06
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

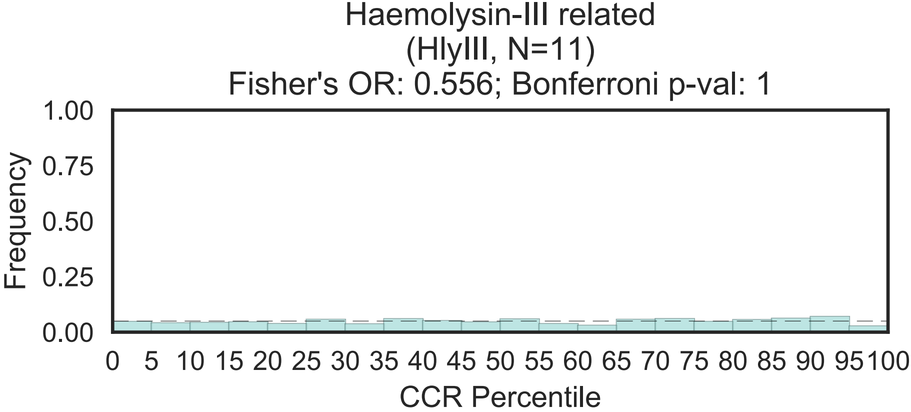
Histidine-rich Calcium-binding repeat region
(Hist_rich_Ca-bd, N=6)
Fisher's OR: 0; Bonferroni p-val: 1



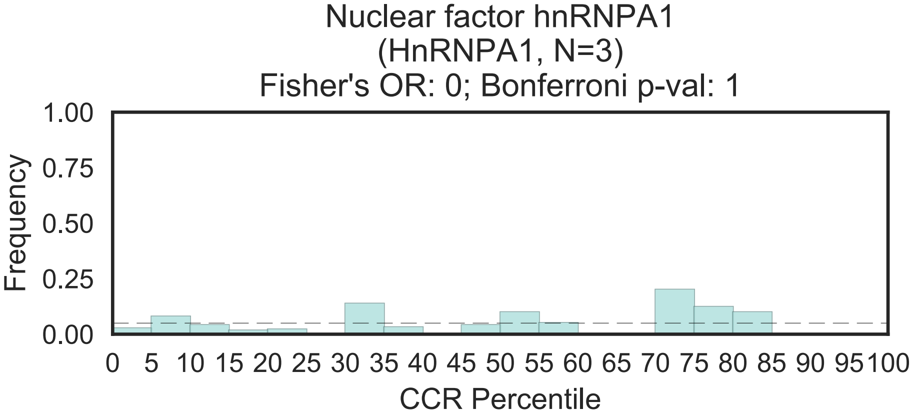

Core histone H2A/H2B/H3/H4
(Histone, N=64)
Fisher's OR: 0.978; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

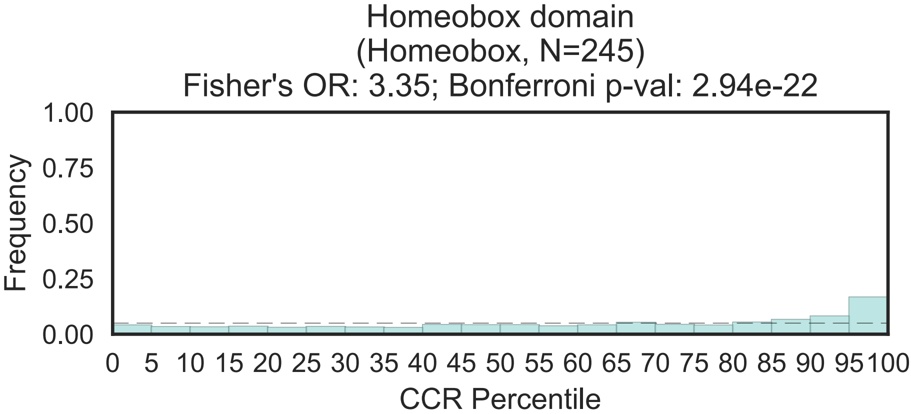


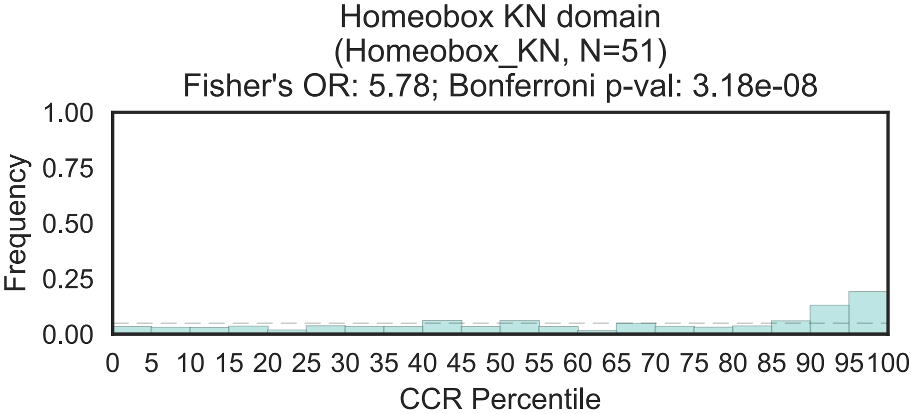
C-terminus of histone H2A
(Histone_H2A_C, N=22)
Fisher's OR: 1.05; Bonferroni p-val: 1

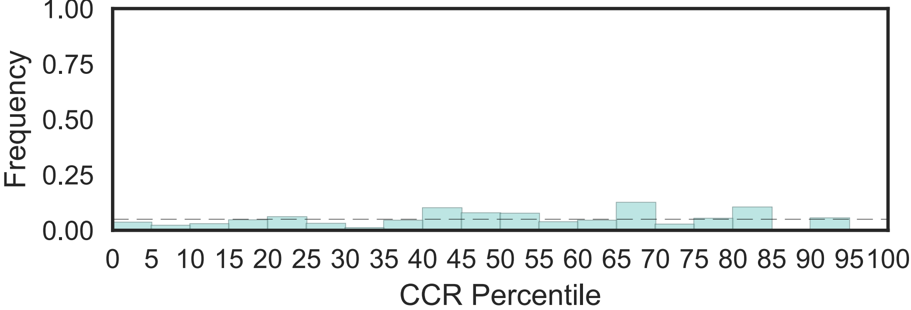


Haemolysin-III related
(HlyIII, N=11)
Fisher's OR: 0.556; Bonferroni p-val: 1

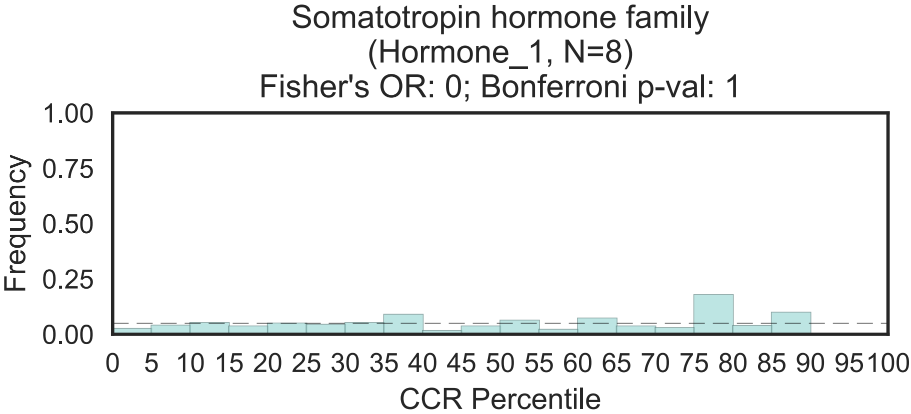

Nuclear factor hnRNPA1
(HnRNPA1, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

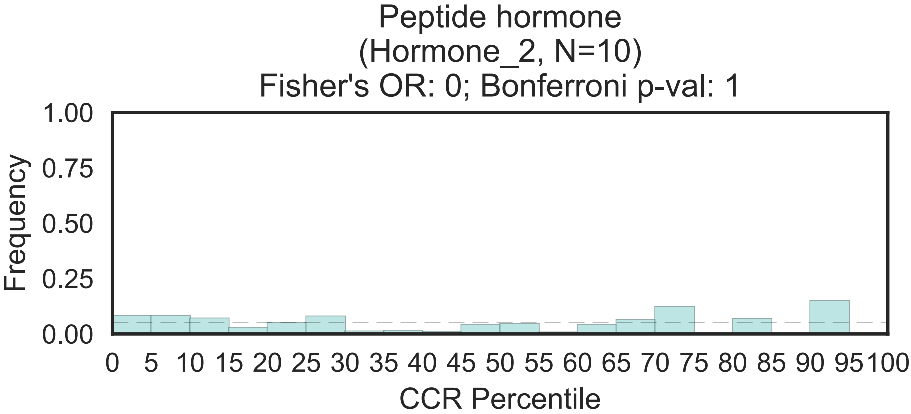

Homeobox domain
(Homeobox, N=245)
Fisher's OR: 3.35; Bonferroni p-val: 2.94e-22
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

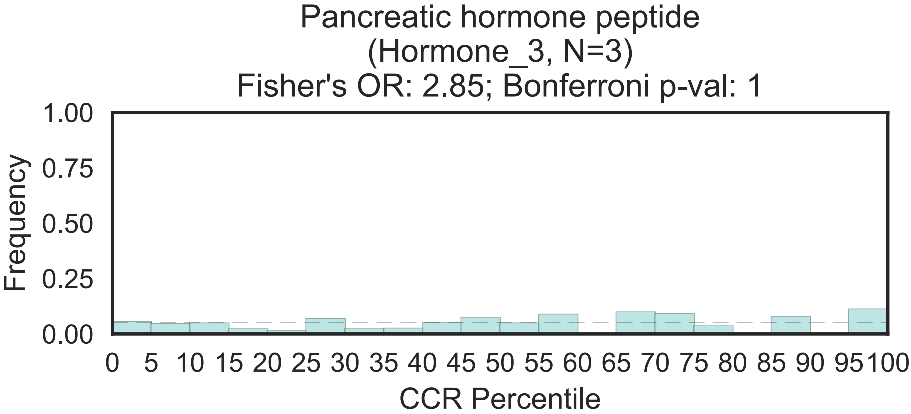

Homeobox KN domain
(Homeobox_KN, N=51)
Fisher's OR: 5.78; Bonferroni p-val: 3.18e-08
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



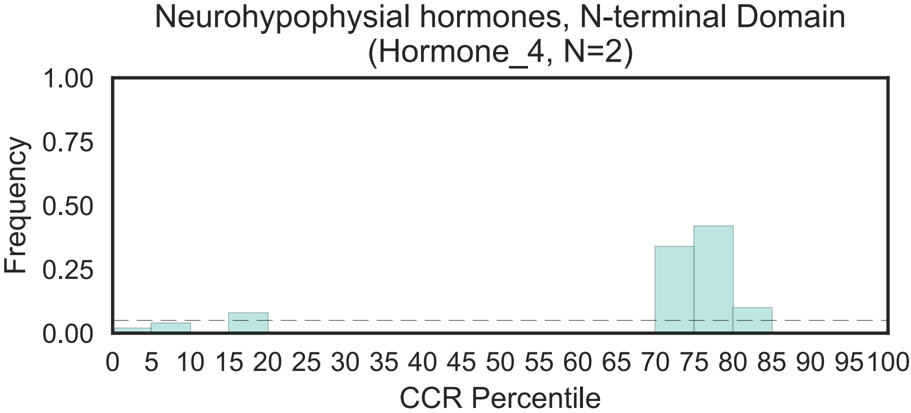
Homeodomain leucine-zipper encoding, Homez
(Homez, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

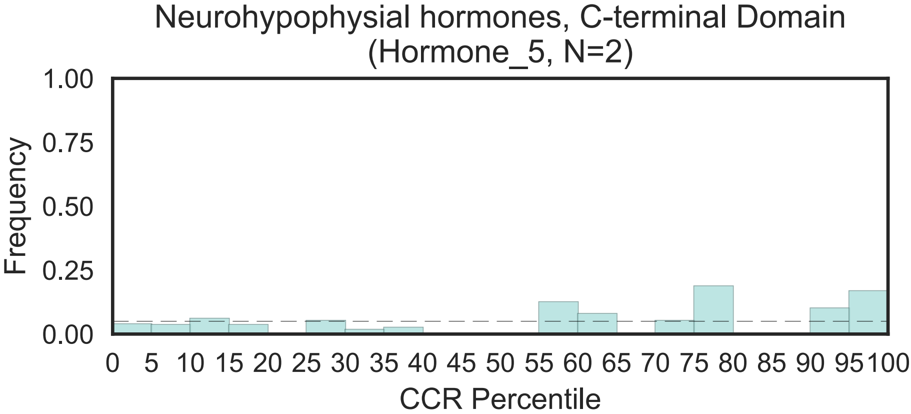

Somatotropin hormone family
(Hormone_1, N=8)
Fisher's OR: 0; Bonferroni p-val: 1

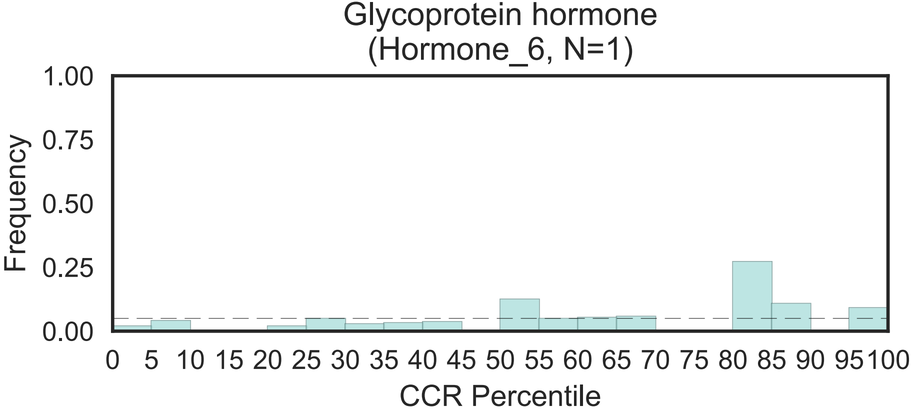

Peptide hormone
(Hormone_2, N=10)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

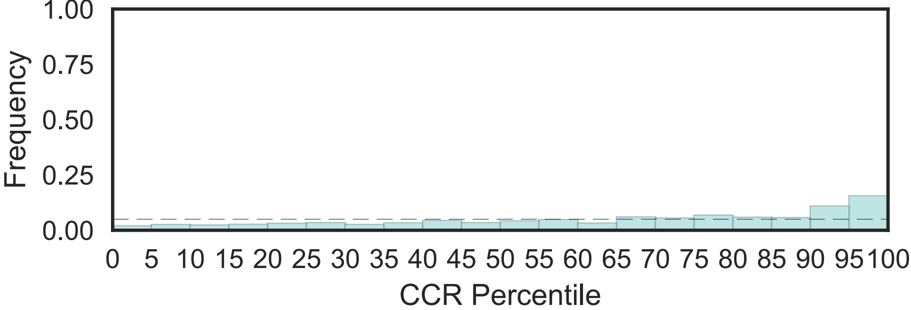


Pancreatic hormone peptide
(Hormone_3, N=3)
Fisher's OR: 2.85; Bonferroni p-val: 1

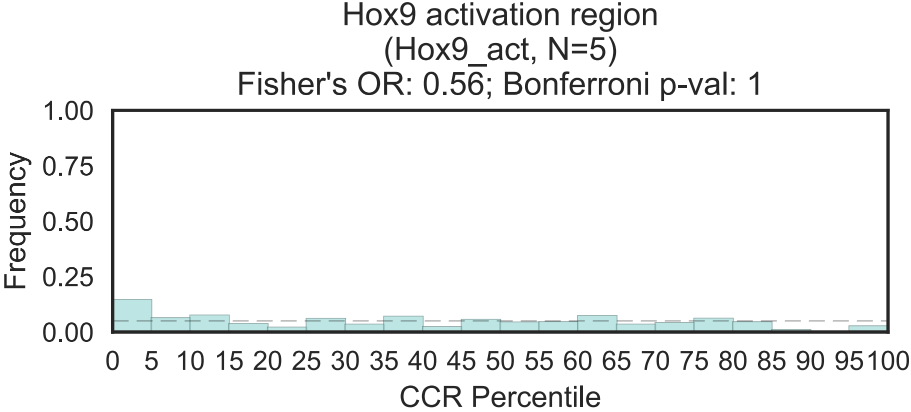

Neurohypophysial hormones, N-terminal Domain
(Hormone_4, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

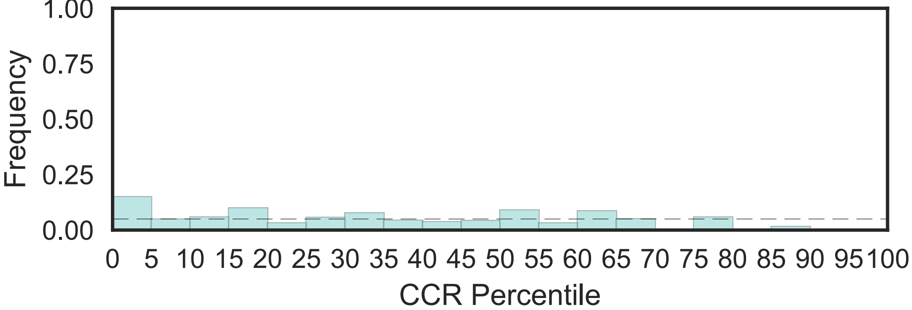

Neurohypophysial hormones, C-terminal Domain
(Hormone_5, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Glycoprotein hormone
(Hormone_6, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

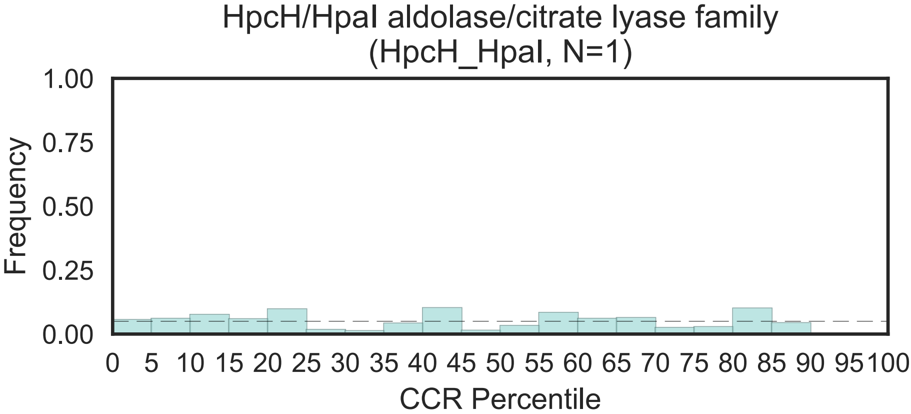


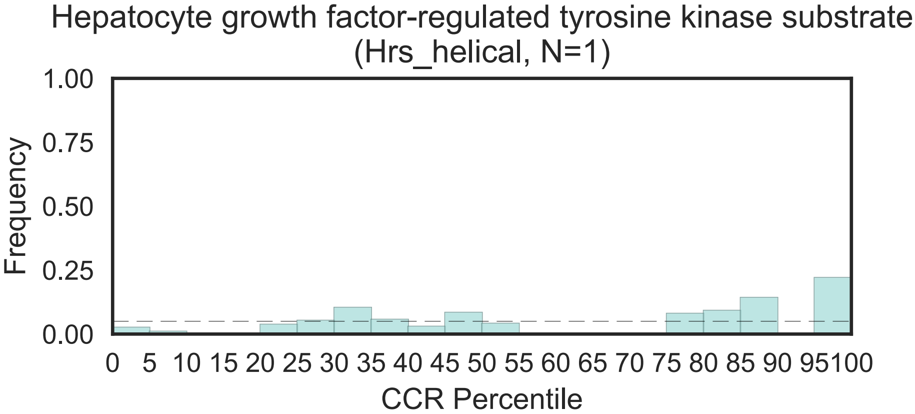
Ligand-binding domain of nuclear hormone receptor
(Hormone_recep, N=47)
Fisher's OR: 3.29; Bonferroni p-val: 3.05e-12

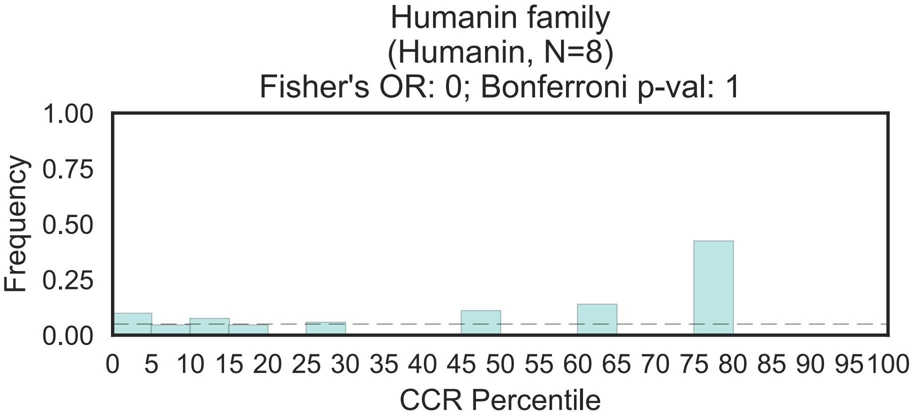

Hox9 activation region
(Hox9_act, N=5)
Fisher's OR: 0.56; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

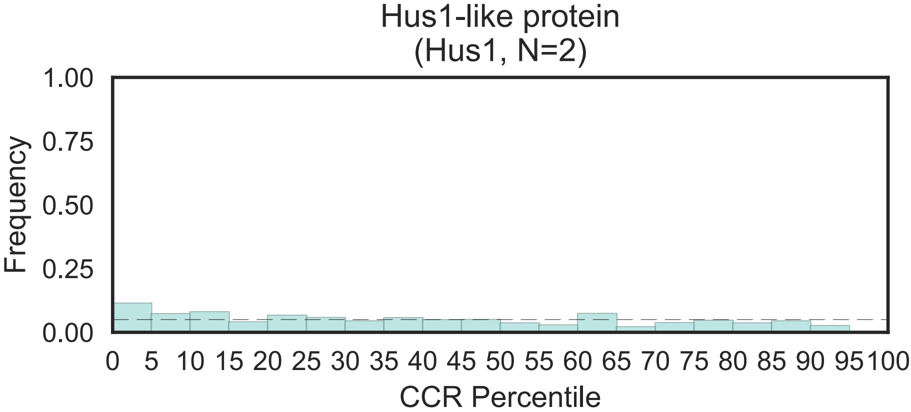


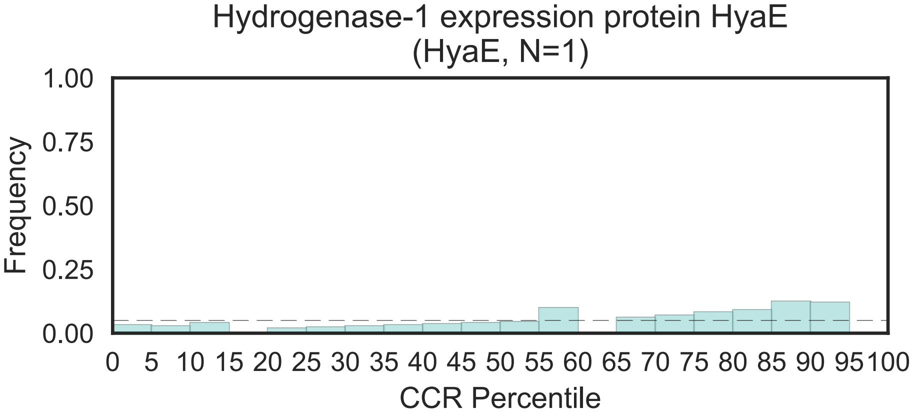
Hox protein A13 N terminal
(HoxA13_N, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

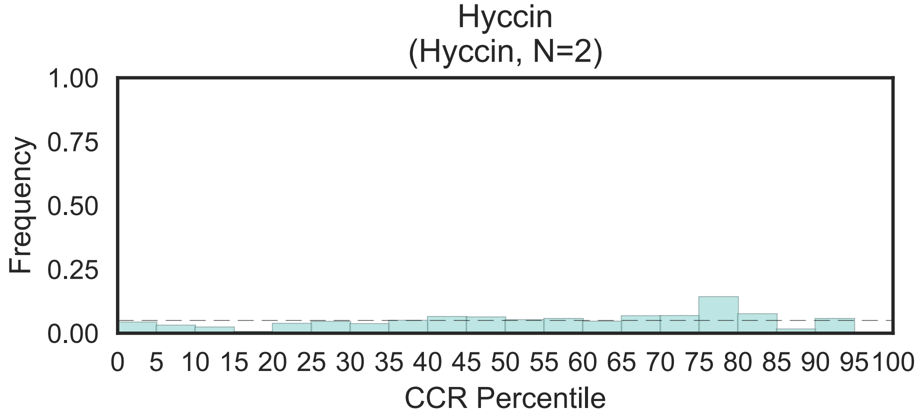

HpcH/HpaI aldolase/citrate lyase family
(HpcH_HpaI, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

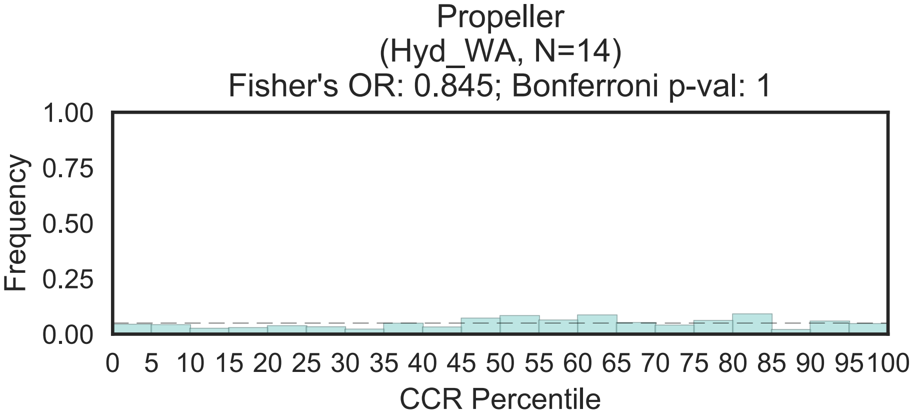

Hepatocyte growth factor-regulated tyrosine kinase substrate
(Hrs_helical, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

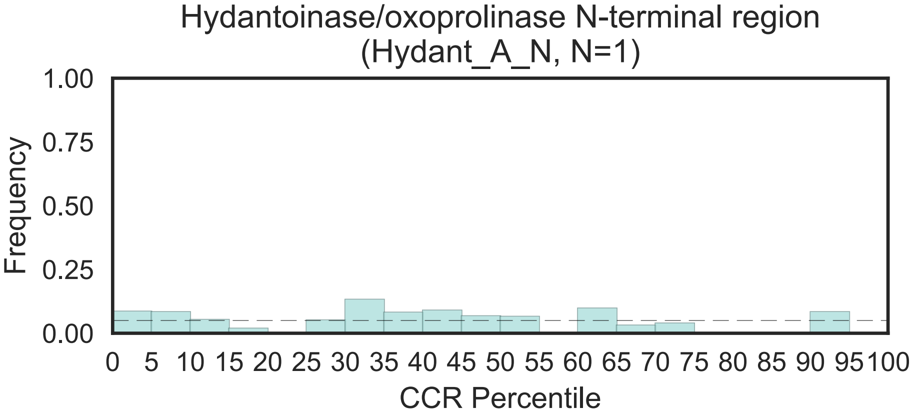

Humanin family
(Humanin, N=8)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

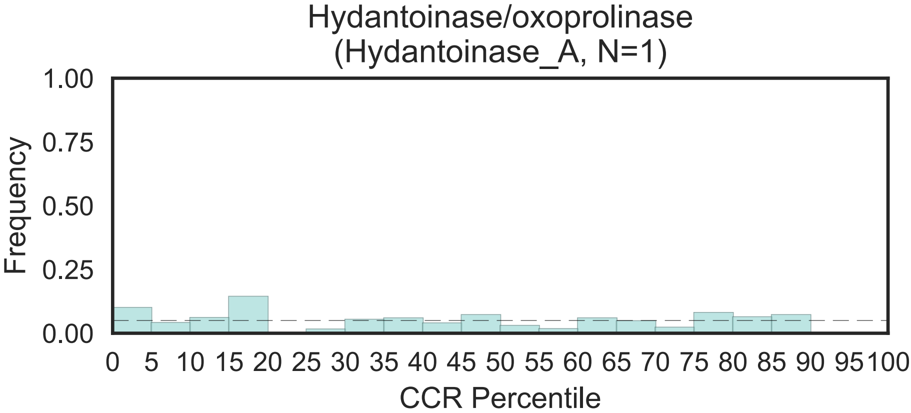

Hus1-like protein
(Hus1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

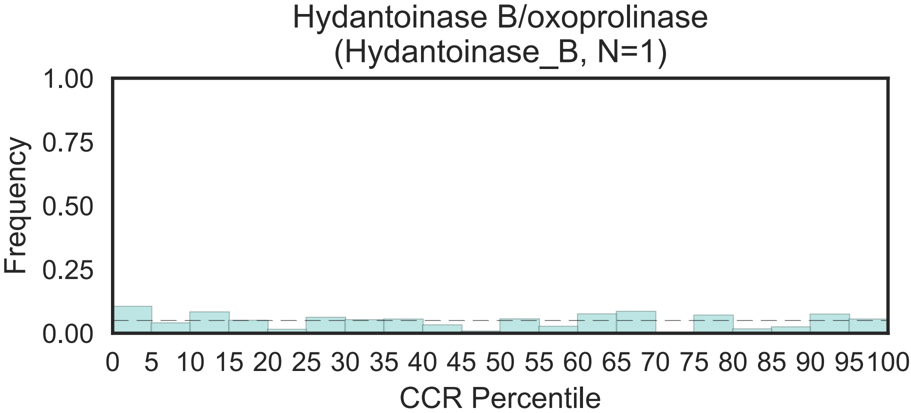

Hydrogenase-1 expression protein HyaE
(HyaE, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

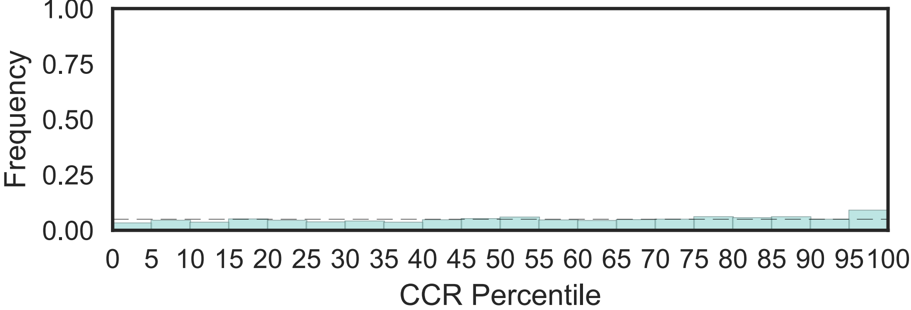

Hyccin
(Hyccin, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Propeller
(Hyd_WA, N=14)
Fisher's OR: 0.845; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

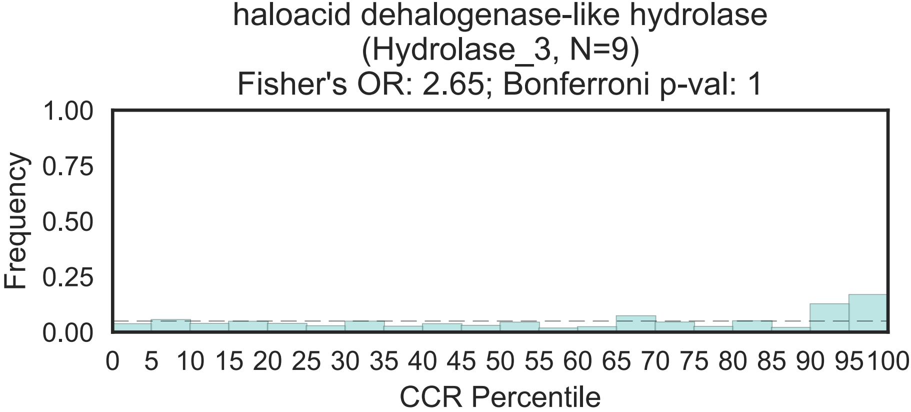

Hydantoinase/oxoprolinase N-terminal region
(Hydant_A_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

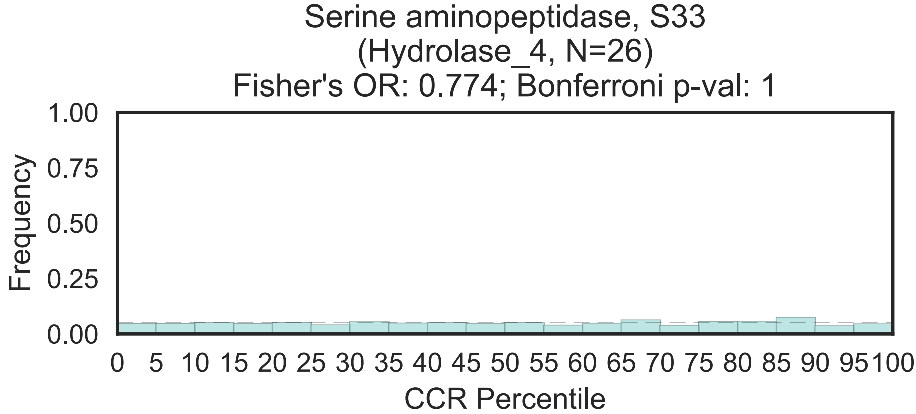

Hydantoinase/oxoprolinase
(Hydantoinase_A, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

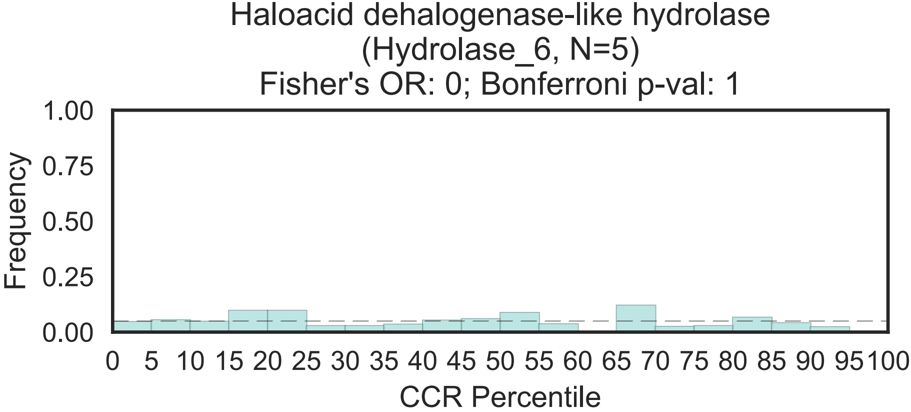

Hydantoinase B/oxoprolinase
(Hydantoinase_B, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

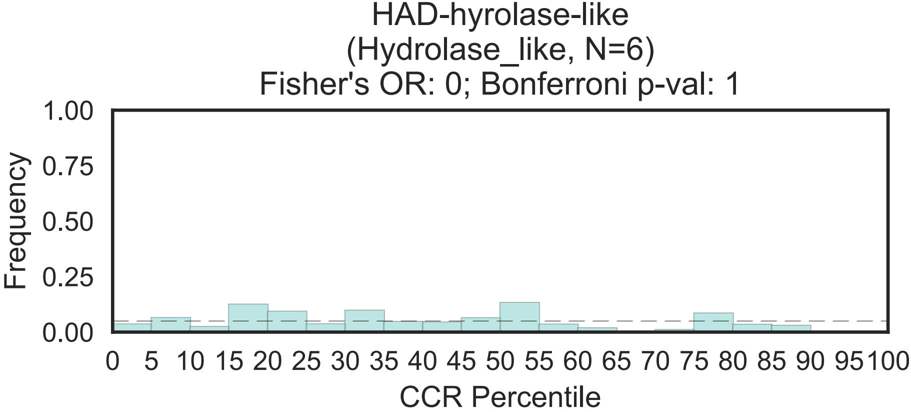


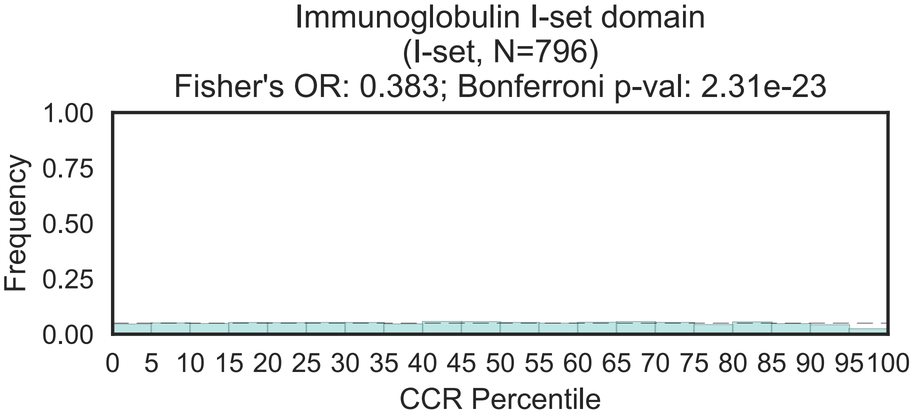
haloacid dehalogenase-like hydrolase
(Hydrolase, N=39)
Fisher's OR: 1.23; Bonferroni p-val: 1

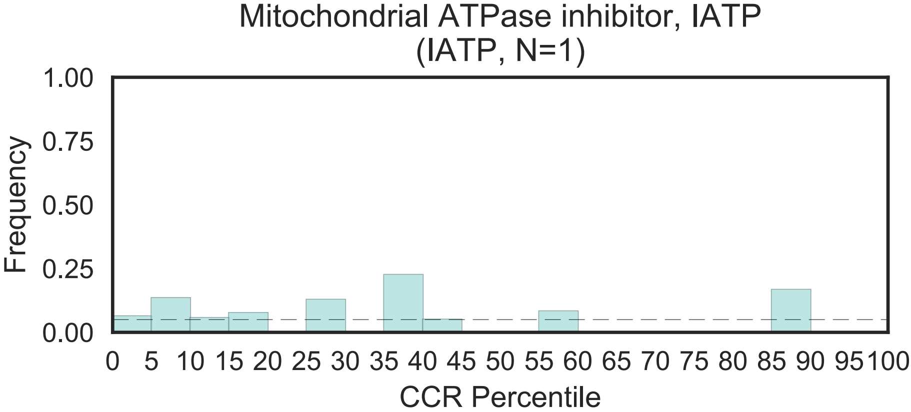

haloacid dehalogenase-like hydrolase
(Hydrolase_3, N=9)
Fisher's OR: 2.65; Bonferroni p-val: 1

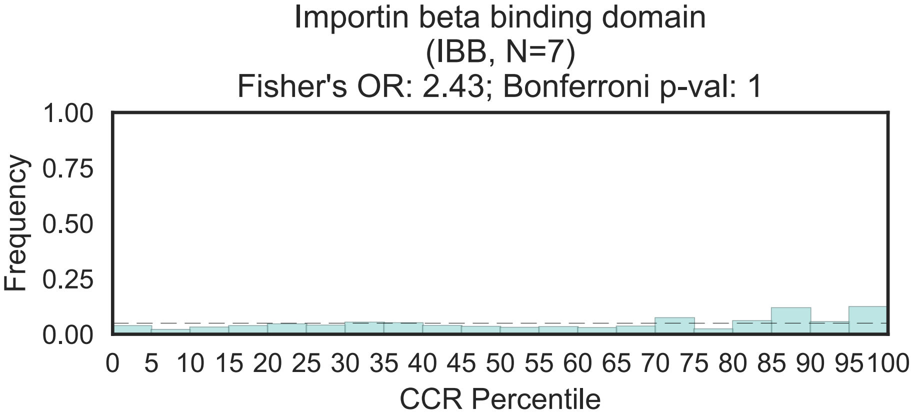

Serine aminopeptidase, S33
(Hydrolase_4, N=26)
Fisher's OR: 0.774; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

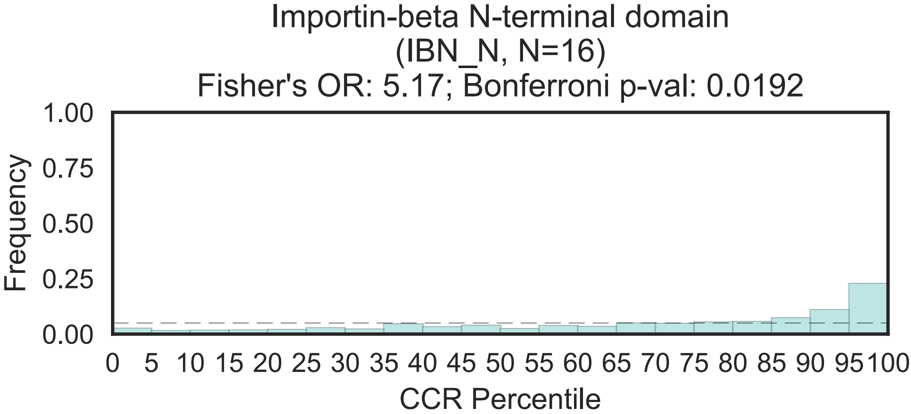

Haloacid dehalogenase-like hydrolase
(Hydrolase_6, N=5)
Fisher's OR: 0; Bonferroni p-val: 1

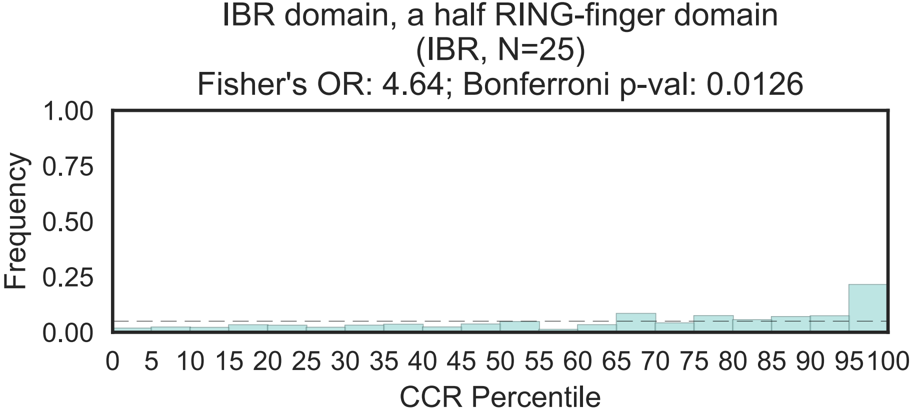

HAD-hyrolase-like
(Hydrolase_like, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

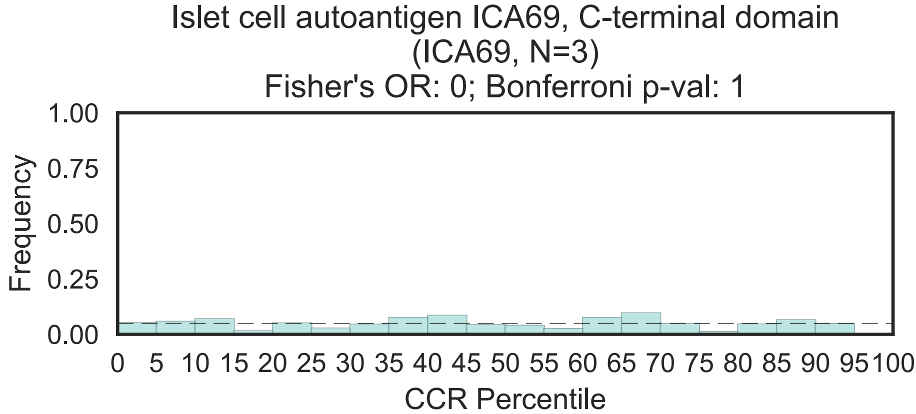

Immunoglobulin I-set domain
(I-set, N=796)
Fisher's OR: 0.383; Bonferroni p-val: 2.31e-23
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

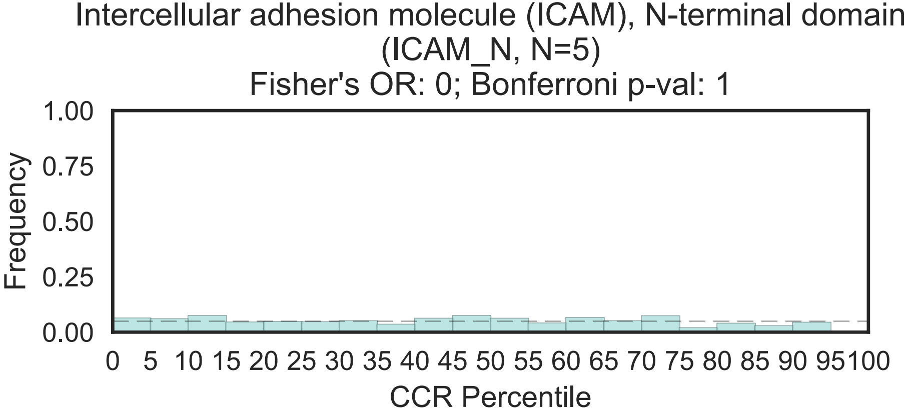

Mitochondrial ATPase inhibitor, IATP
(IATP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Importin beta binding domain
(IBB, N=7)
Fisher's OR: 2.43; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

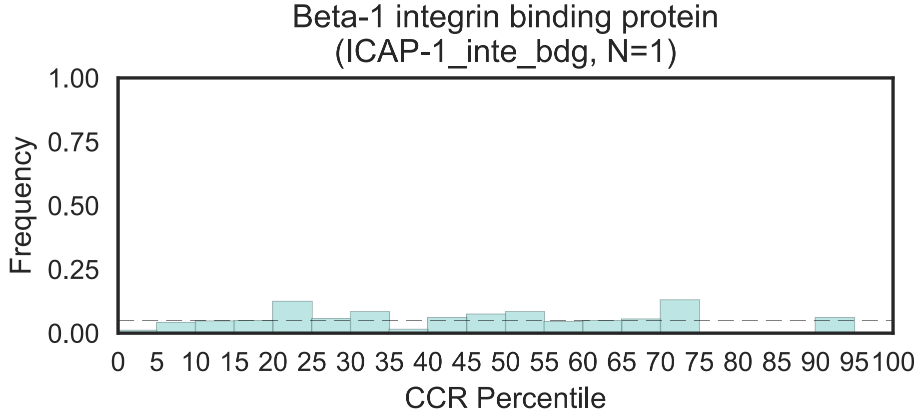

Importin-beta N-terminal domain
(IBN_N, N=16)
Fisher's OR: 5.17; Bonferroni p-val: 0.0192
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

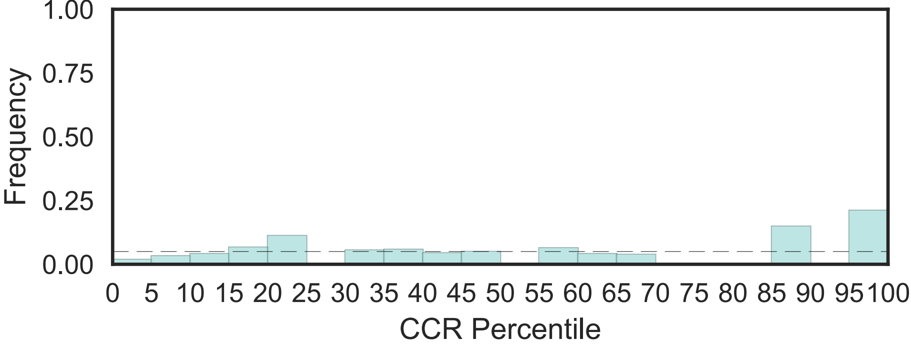

IBR domain, a half RING-finger domain
(IBR, N=25)
Fisher's OR: 4.64; Bonferroni p-val: 0.0126
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Islet cell autoantigen ICA69, C-terminal domain
(ICA69, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

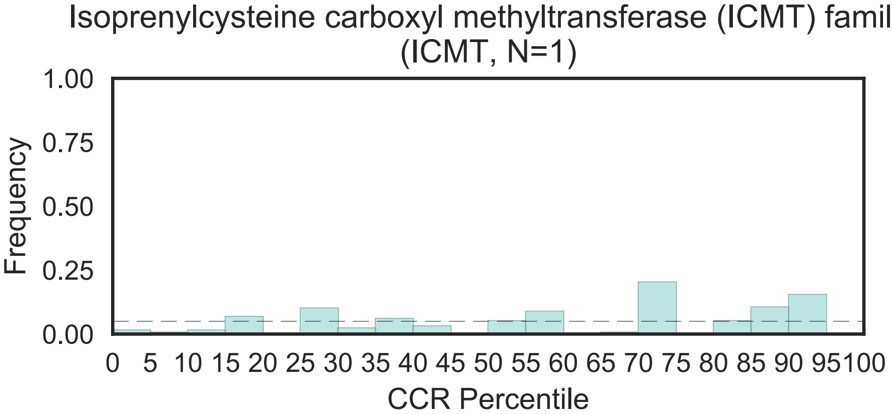


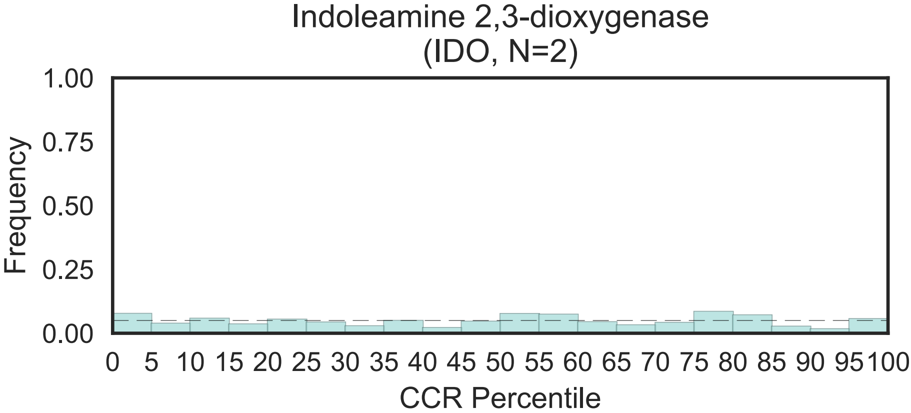
Intercellular adhesion molecule (ICAM), N-terminal domain
(ICAM_N, N=5)
Fisher's OR: 0; Bonferroni p-val: 1

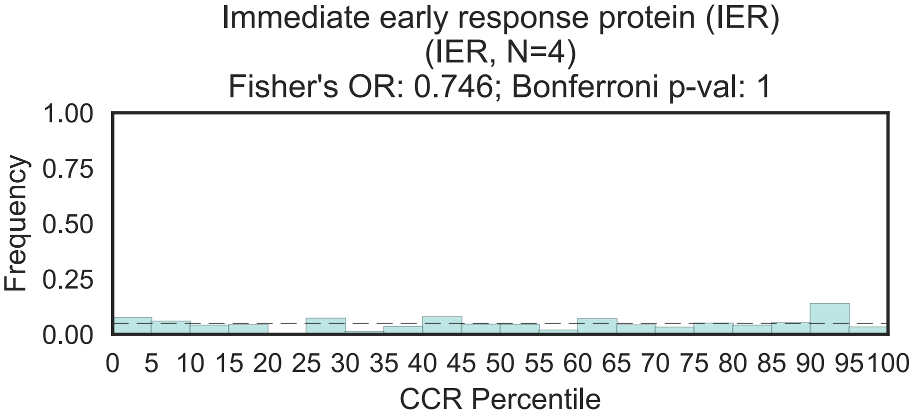

Beta-1 integrin binding protein
(ICAP-1_inte_bdg, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

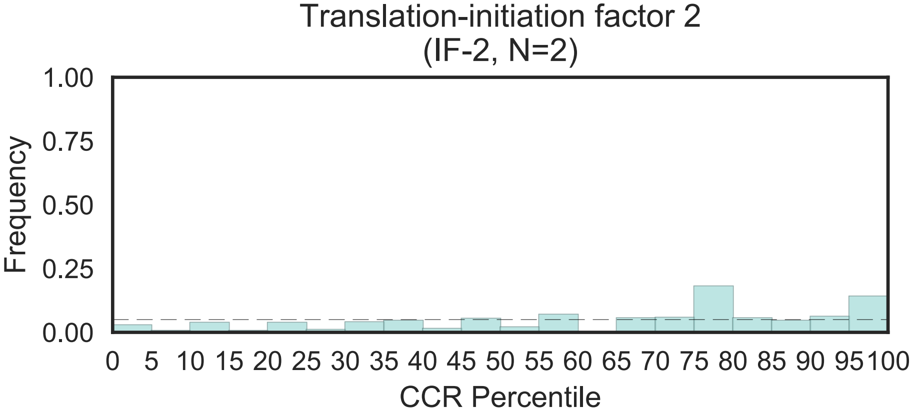


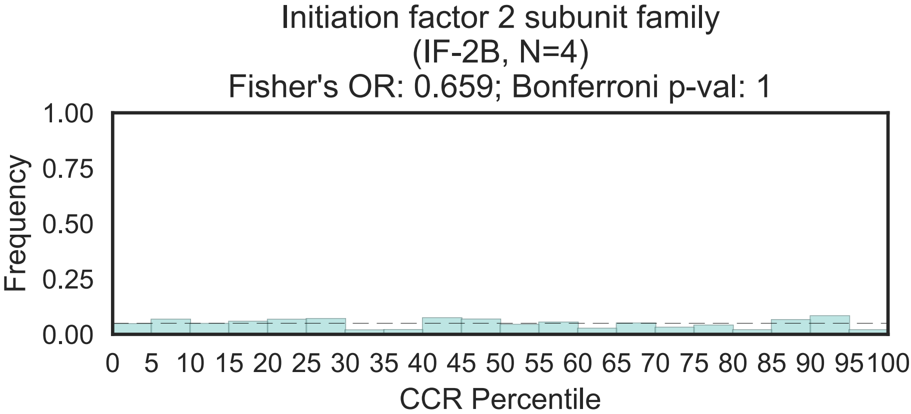
Beta-catenin-interacting protein ICAT
(ICAT, N=2)

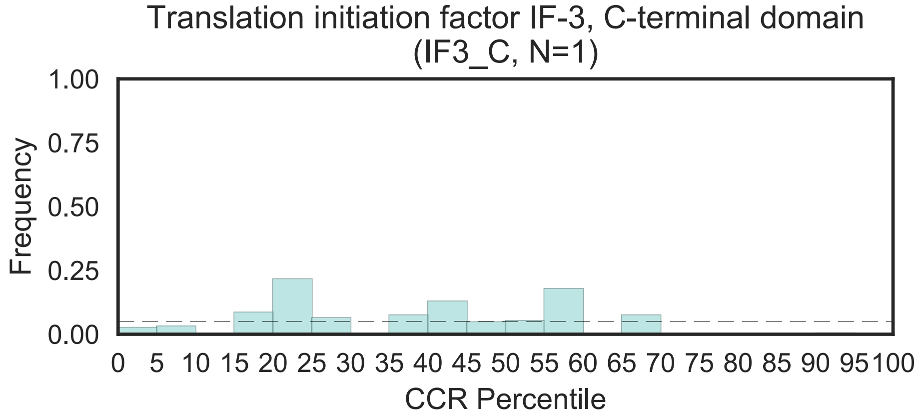

Isoprenylcysteine carboxyl methyltransferase (ICMT) family
(ICMT, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

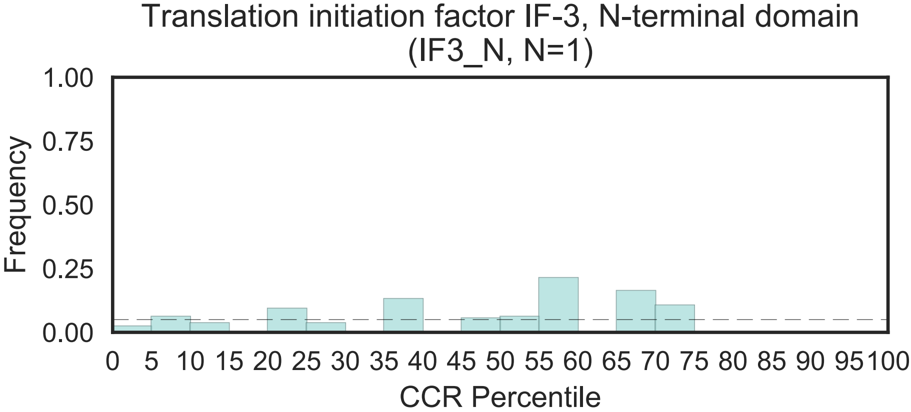

Indoleamine 2,3-dioxygenase
(IDO, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Immediate early response protein (IER)
(IER, N=4)
Fisher's OR: 0.746; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

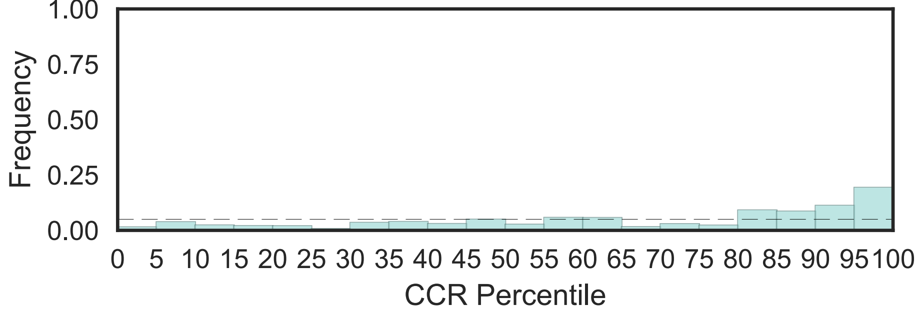

Translation-initiation factor 2
(IF-2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

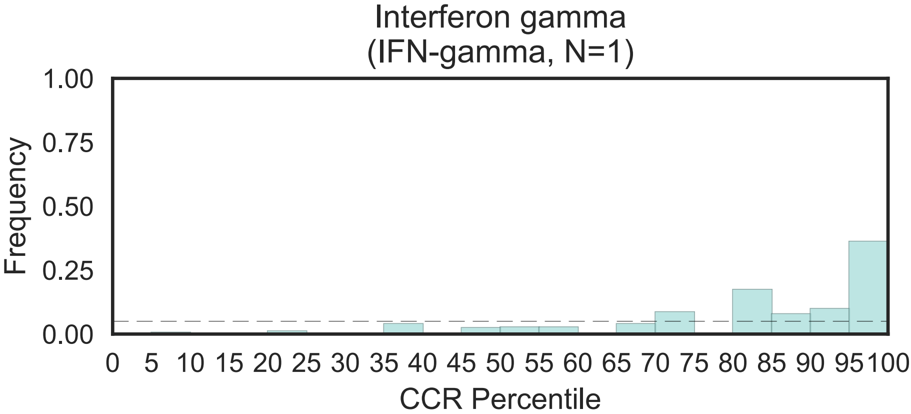

Initiation factor 2 subunit family
(IF-2B, N=4)
Fisher's OR: 0.659; Bonferroni p-val: 1

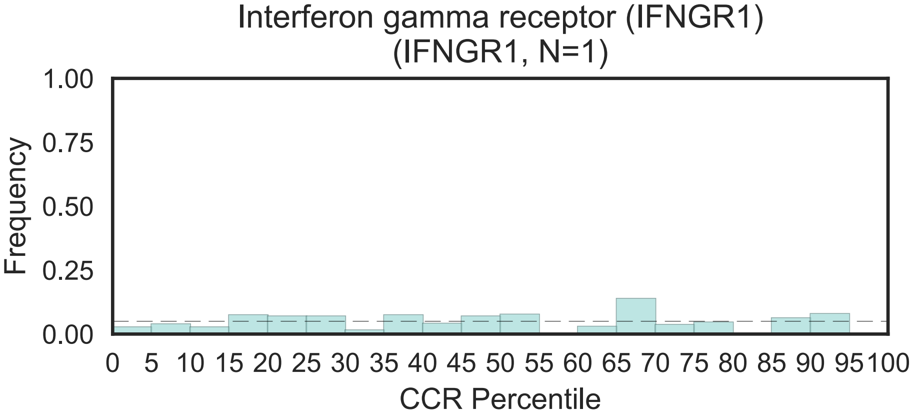

Translation initiation factor IF-3, C-terminal domain
(IF3_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

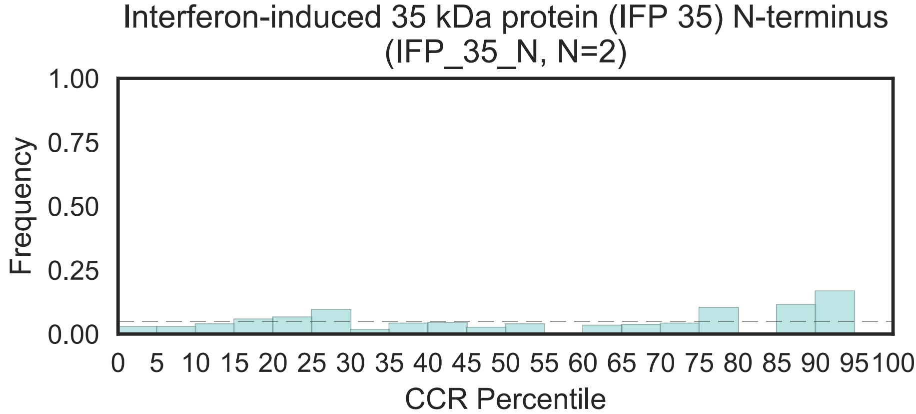

Translation initiation factor IF-3, N-terminal domain
(IF3_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

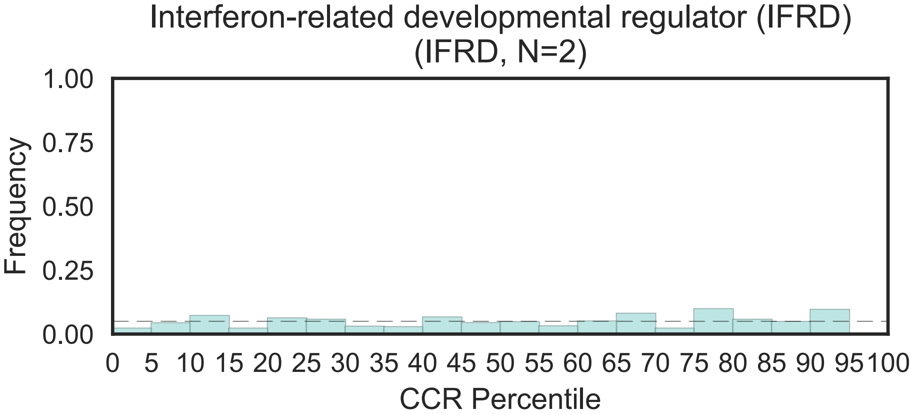
Eukaryotic initiation factor 4E
(IF4E, N=4)
Fisher's OR: 4.41; Bonferroni p-val: 1

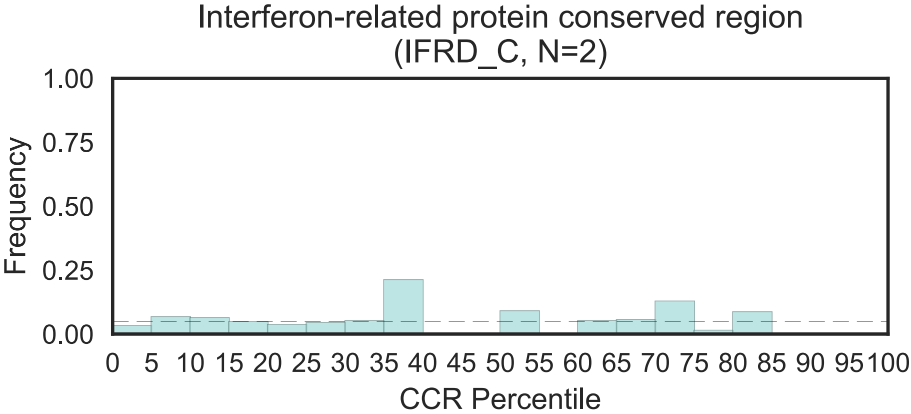


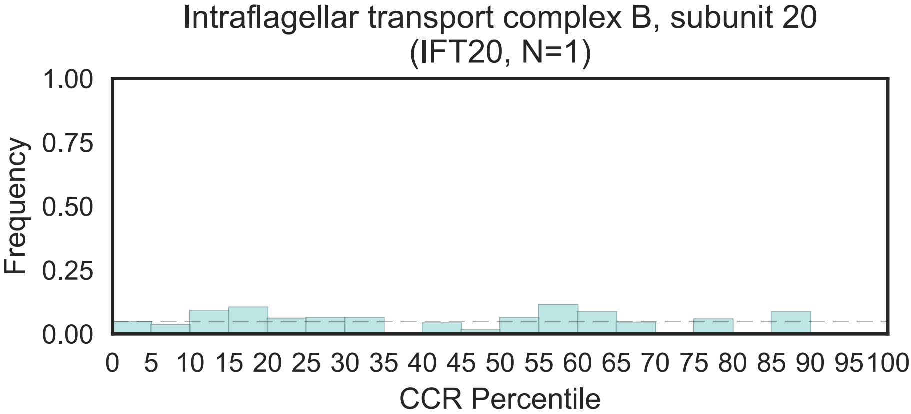

Interferon gamma
(IFN-gamma, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

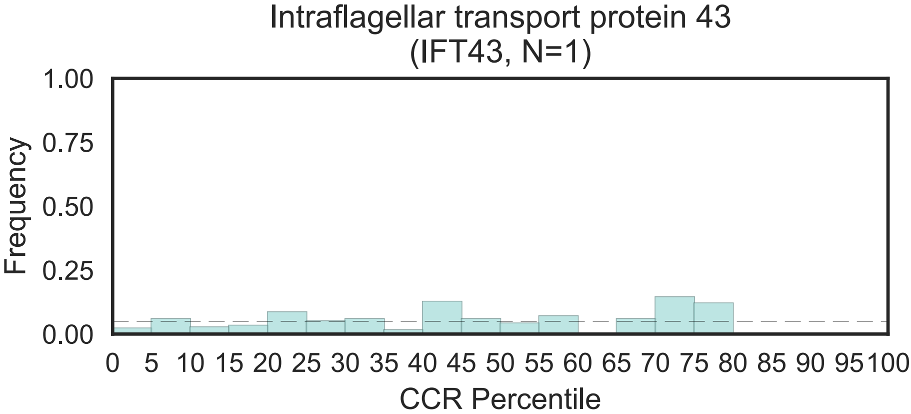

Interferon gamma receptor (IFNGR1)
(IFNGR1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

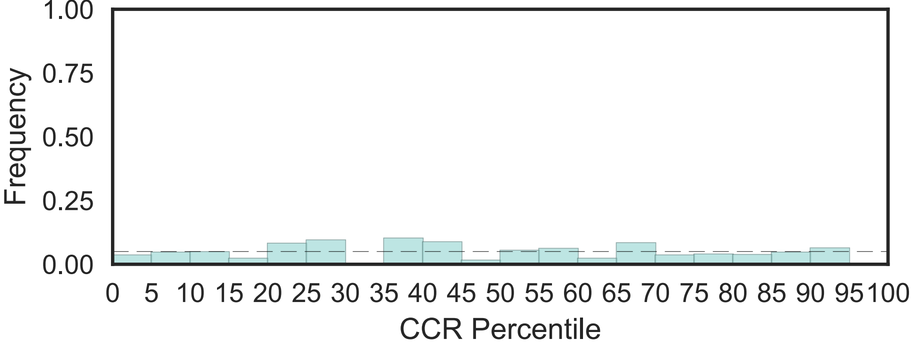

Interferon-induced 35 kDa protein (IFP 35) N-terminus
(IFP_35_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Interferon-related developmental regulator (IFRD)
(IFRD, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

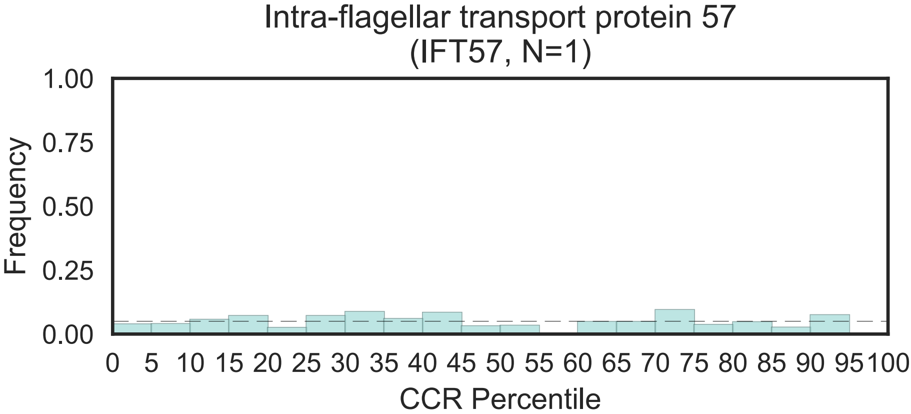

Interferon-related protein conserved region
(IFRD_C, N=2)

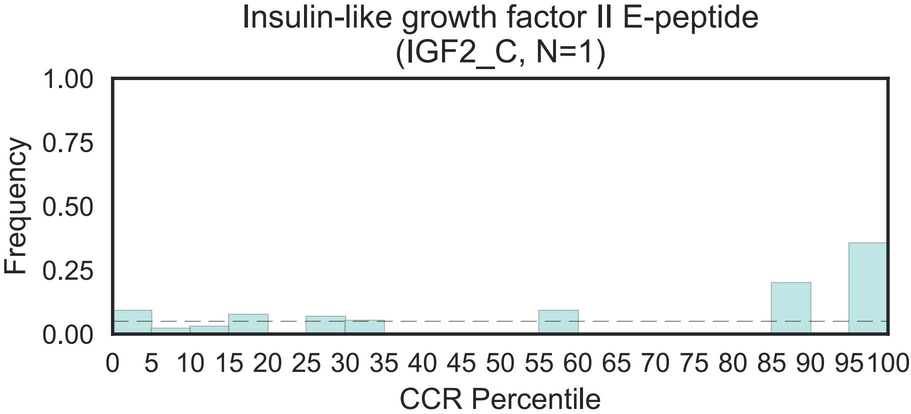

Intraflagellar transport complex B, subunit 20
(IFT20, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

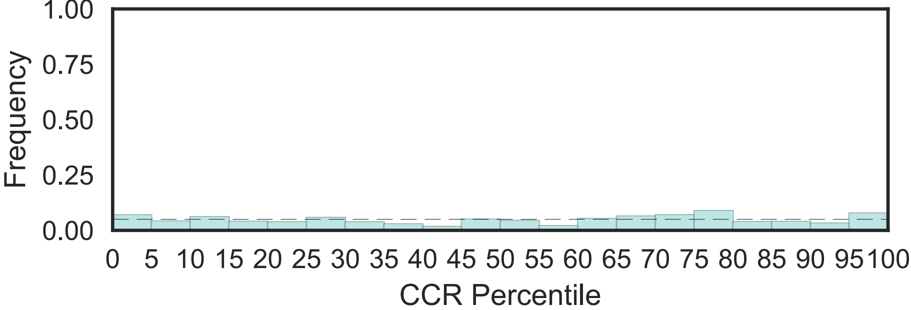

Intraflagellar transport protein 43
(IFT43, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



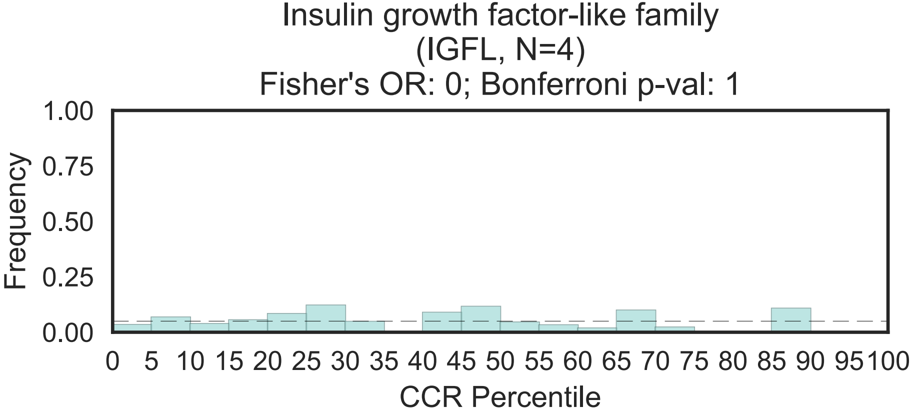
Intraflagellar transport complex B protein 46 C terminal
(IFT46_B_C, N=2)

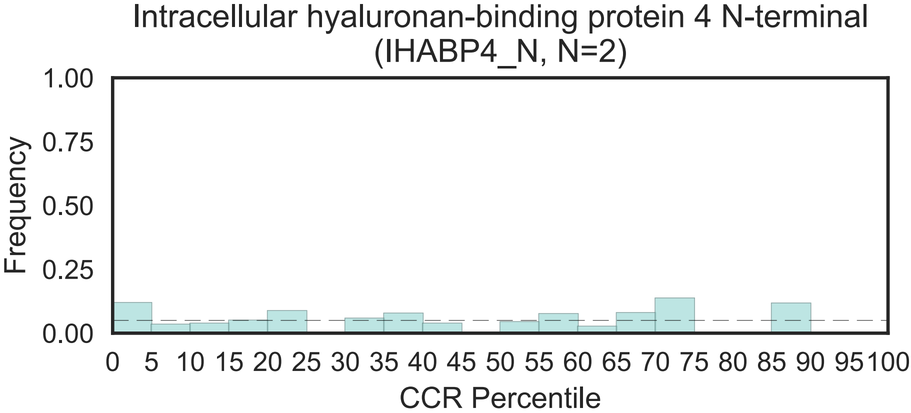

Intra-flagellar transport protein 57
(IFT57, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

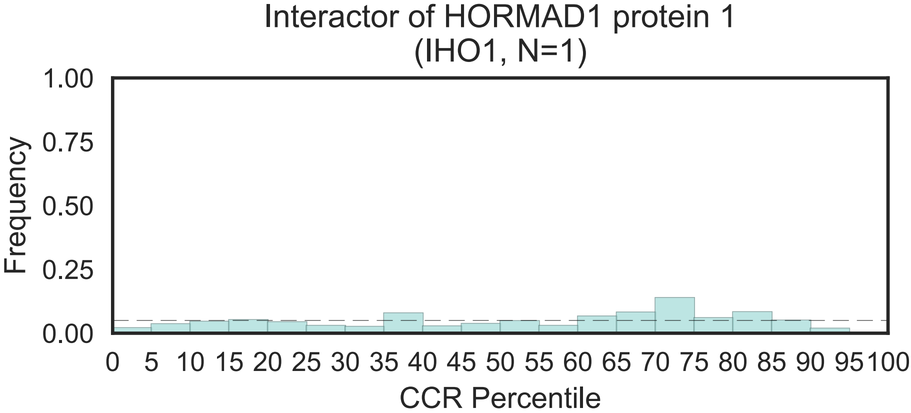

Insulin-like growth factor II E-peptide
(IGF2_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

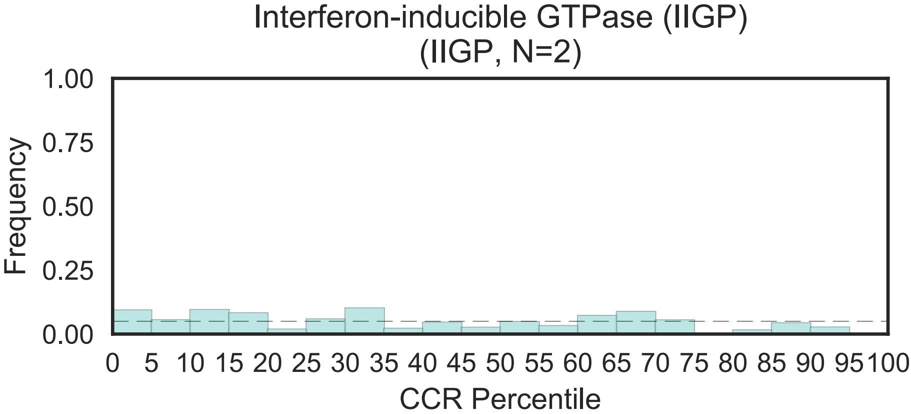


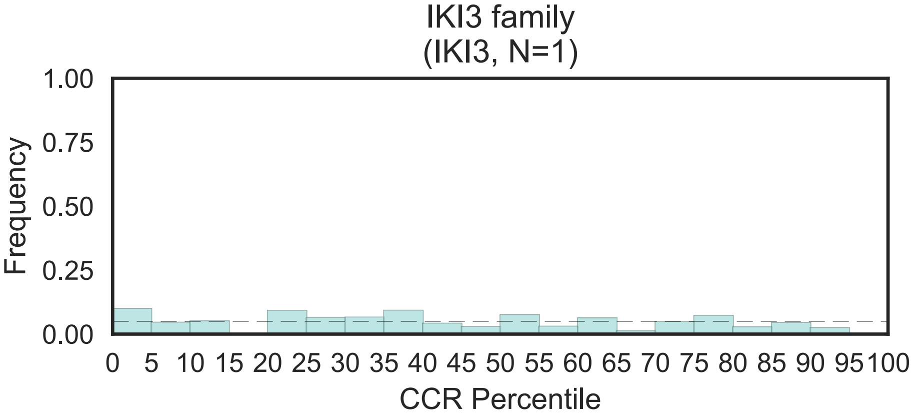
Insulin-like growth factor binding protein
(IGFBP, N=19)
Fisher's OR: 0.498; Bonferroni p-val: 1

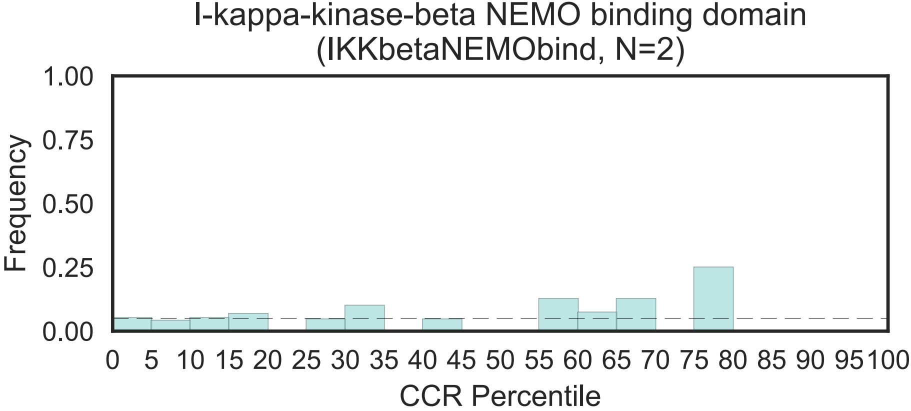

Insulin growth factor-like family
(IGFL, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

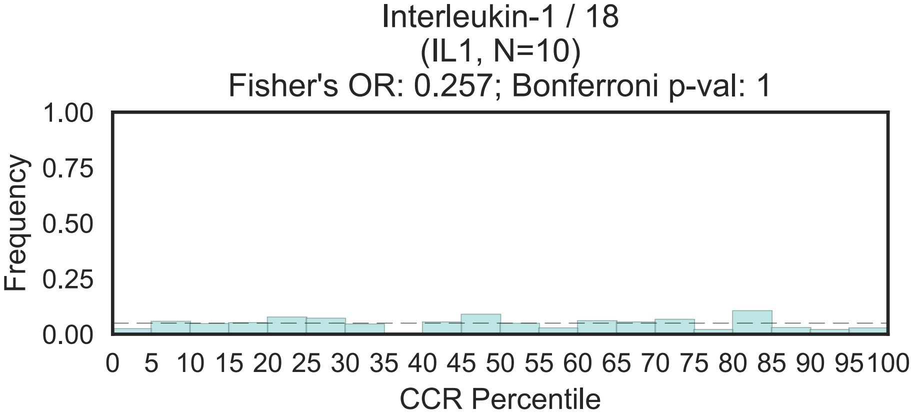

Intracellular hyaluronan-binding protein 4 N-terminal
(IHABP4_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

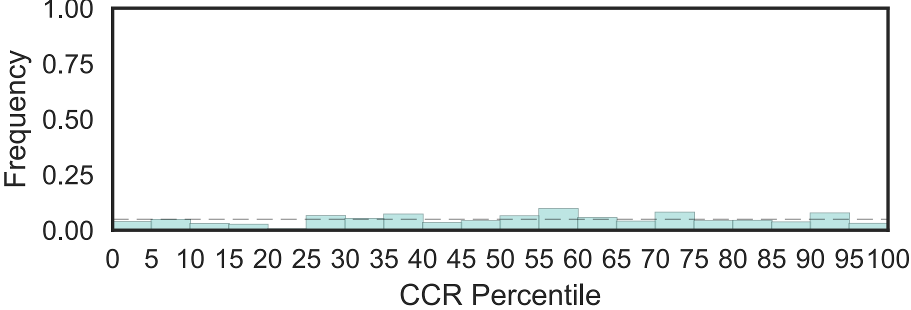

Interactor of HORMAD1 protein 1
(IHO1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Interferon-inducible GTPase (IIGP)
(IIGP, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

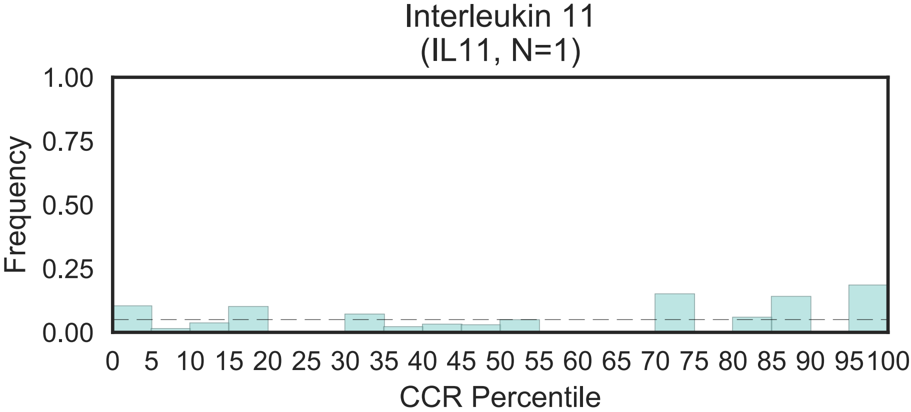

IKI3 family
(IKI3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

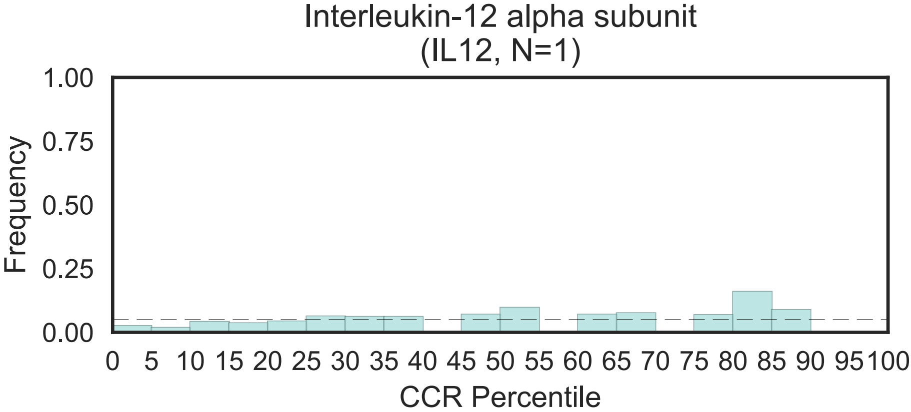

I-kappa-kinase-beta NEMO binding domain
(IKKbetaNEMObind, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

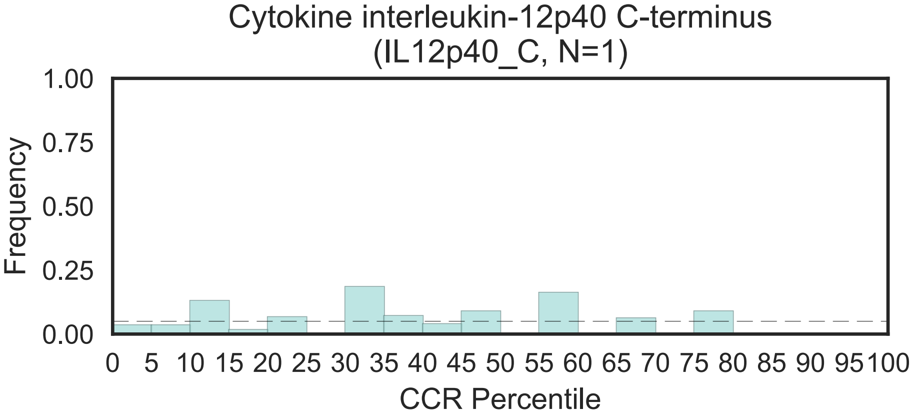

Interleukin-1 / 18
(IL1, N=10)
Fisher's OR: 0.257; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



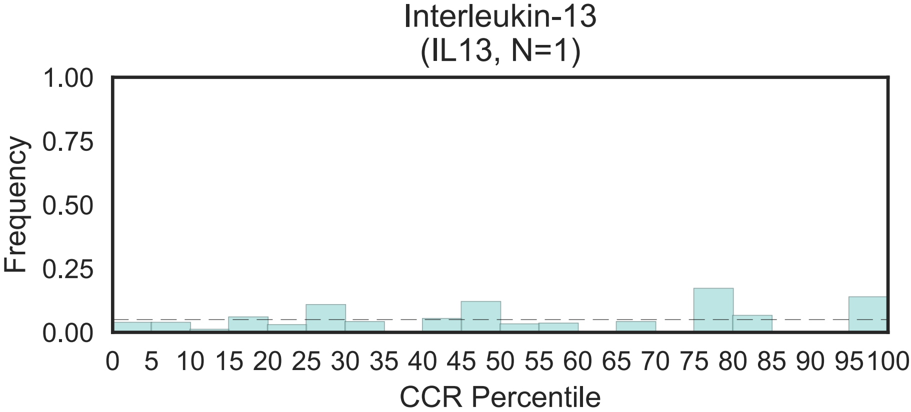
Interleukin 10
(IL10, N=4)
Fisher's OR: 0.512; Bonferroni p-val: 1

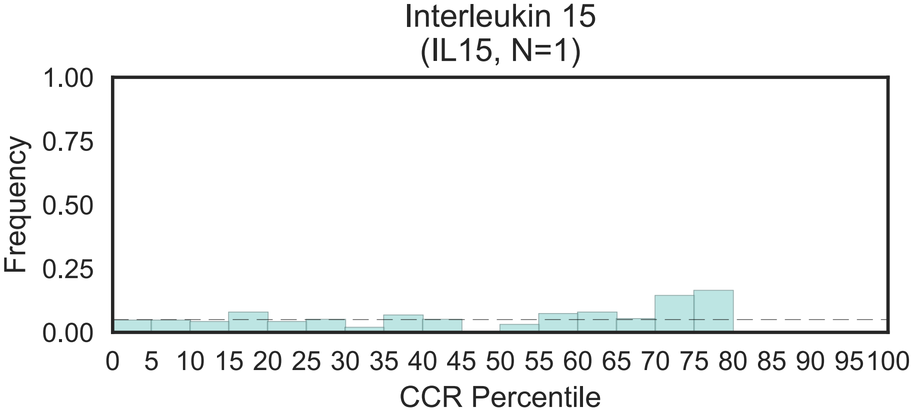

Interleukin 11
(IL11, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

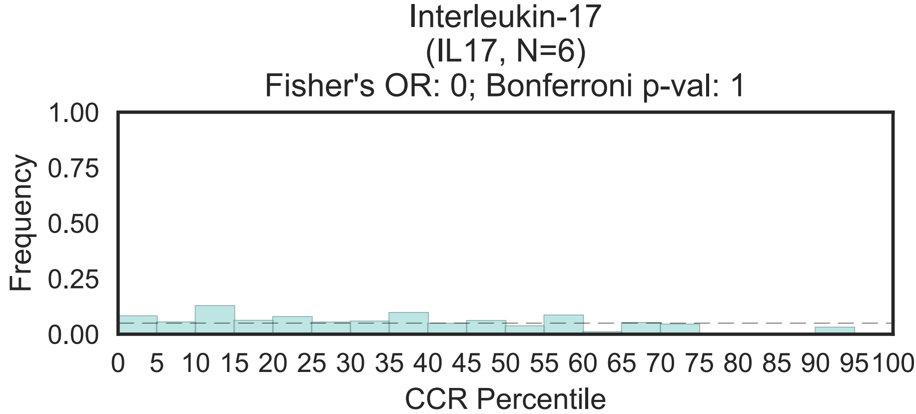

Interleukin-12 alpha subunit
(IL12, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

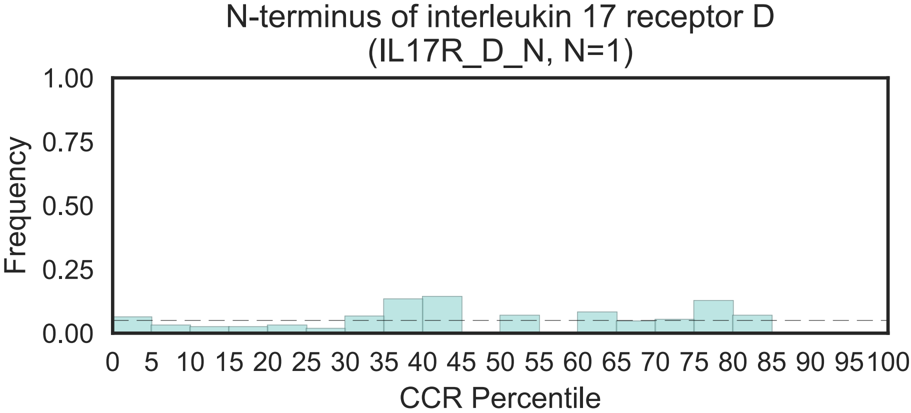


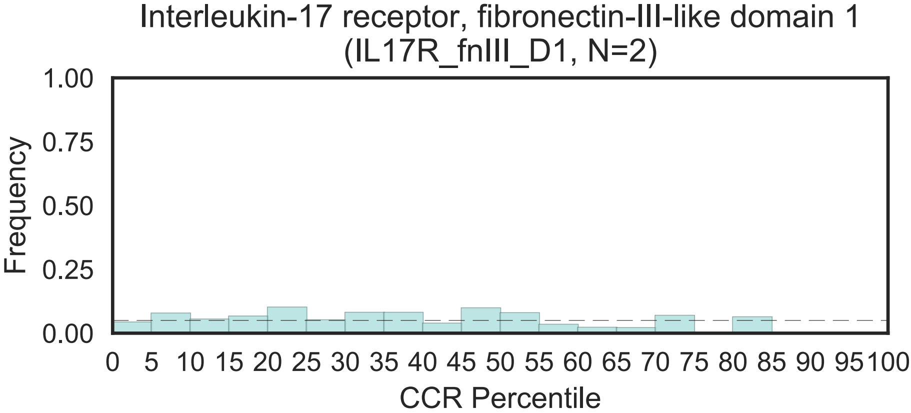
Cytokine interleukin-12p40 C-terminus
(IL12p40_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Interleukin-13
(IL13, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

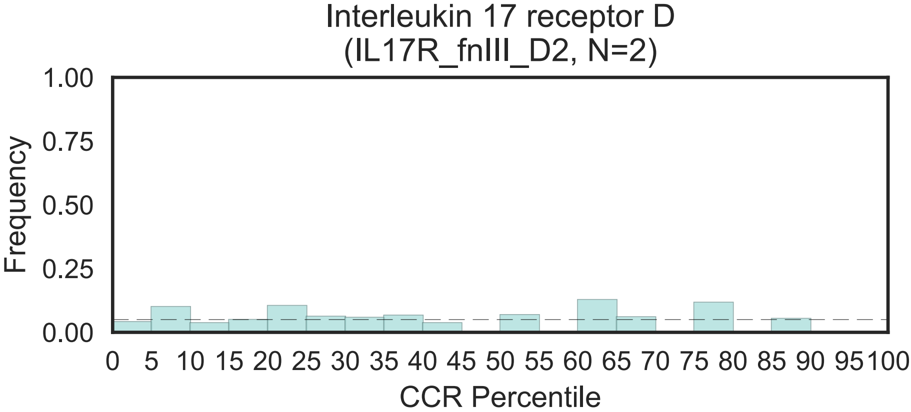

Interleukin 15
(IL15, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

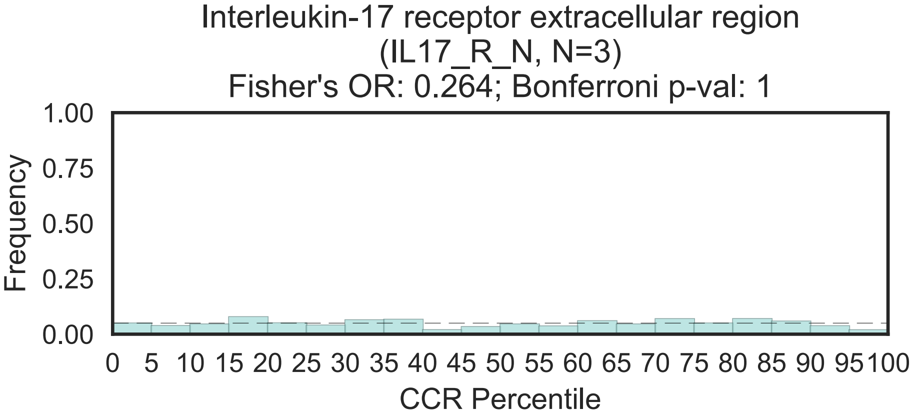

Interleukin-17
(IL17, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

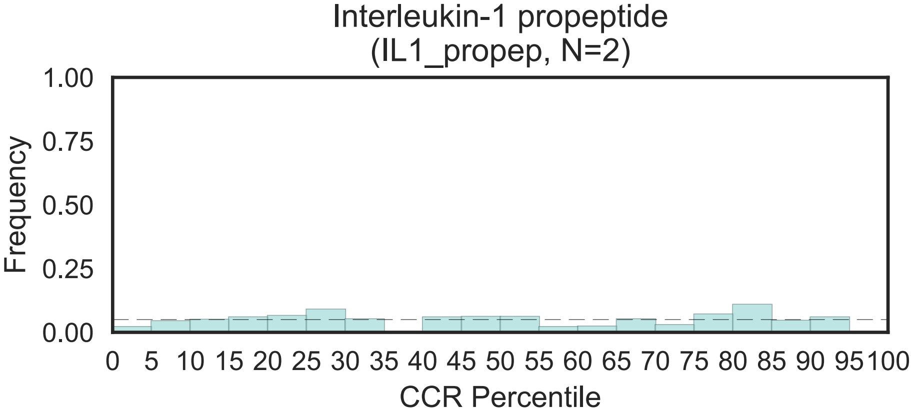

N-terminus of interleukin 17 receptor D
(IL17R_D_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

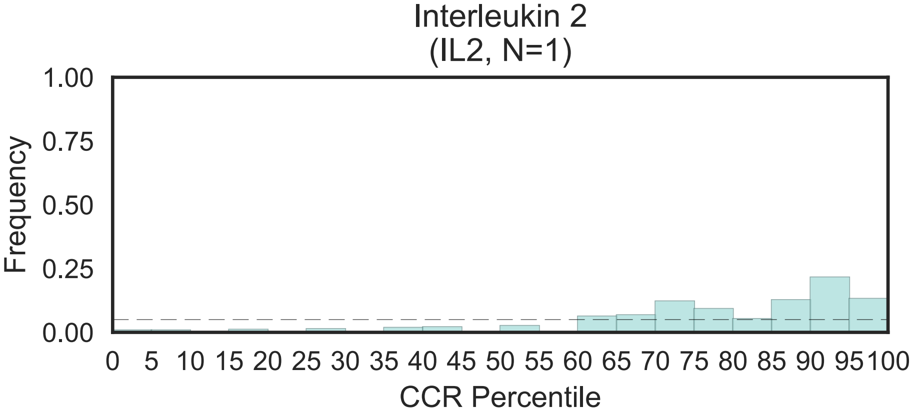


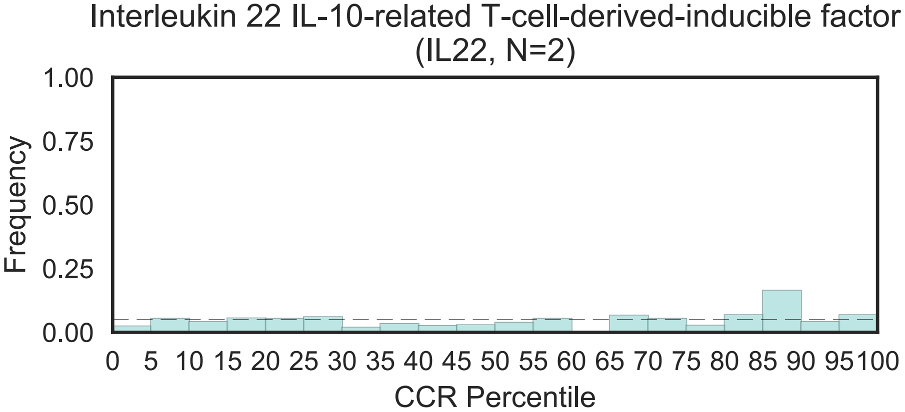
Interleukin-17 receptor, fibronectin-III-like domain 1
(IL17R_fnIII_D1, N=2)

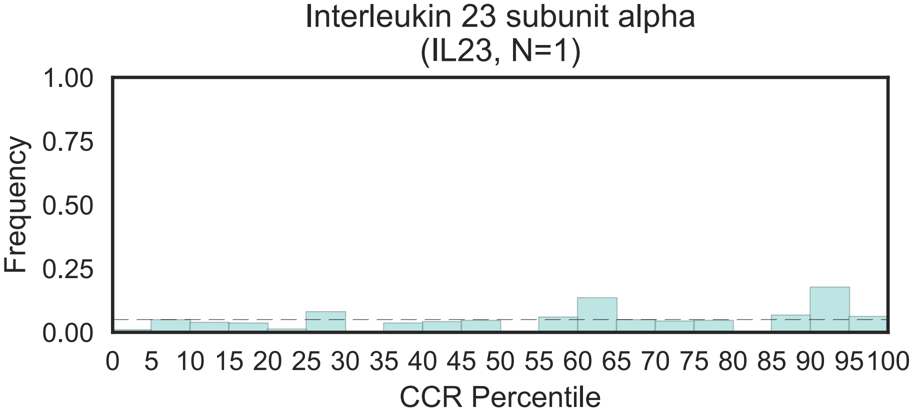

Interleukin 17 receptor D
(IL17R_fnIII_D2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

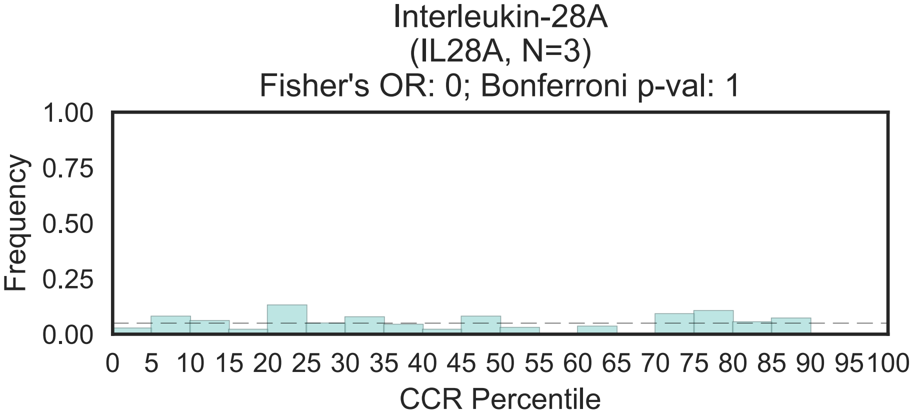

Interleukin-17 receptor extracellular region
(IL17_R_N, N=3)
Fisher's OR: 0.264; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

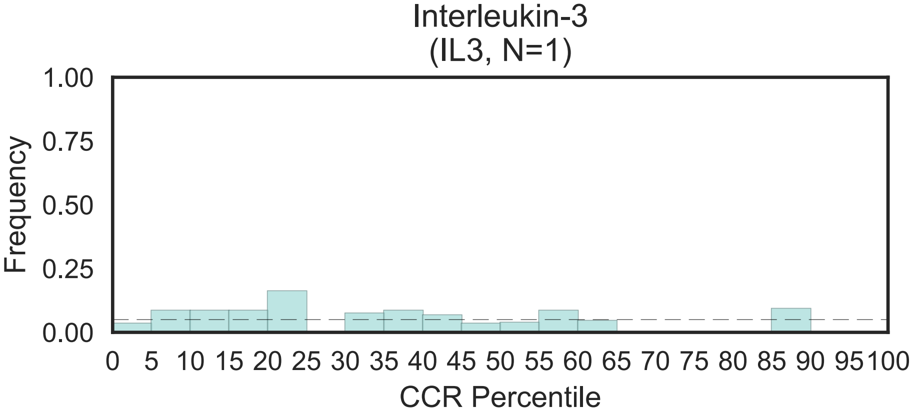

Interleukin-1 propeptide
(IL1_propep, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

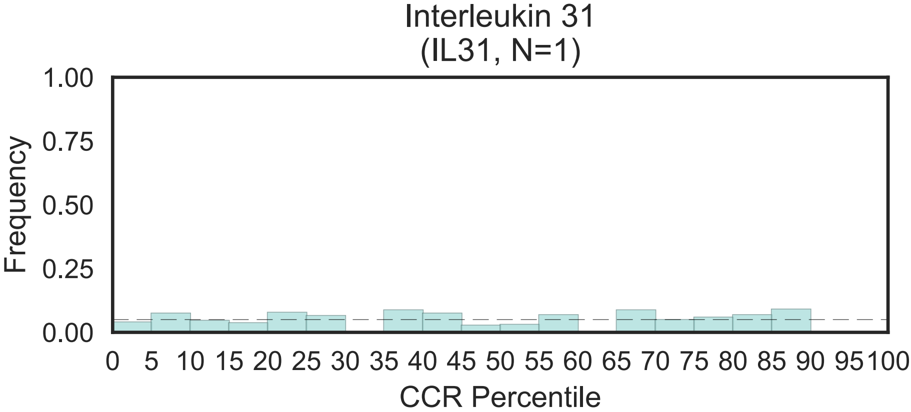

Interleukin 2
(IL2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

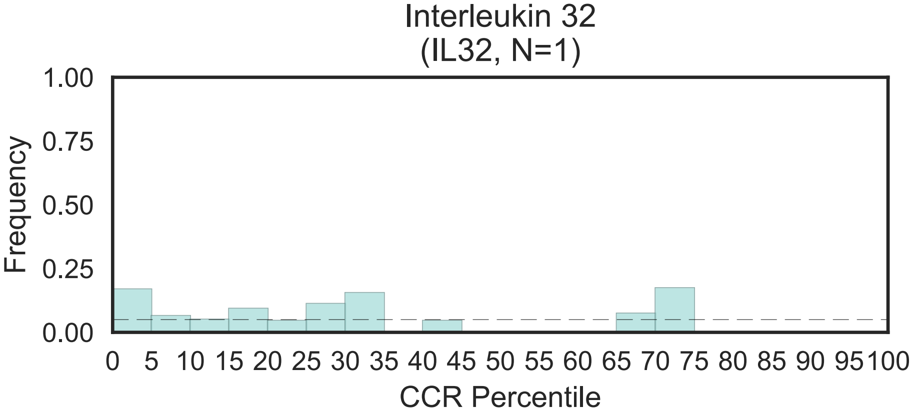

Interleukin 22 IL-10-related T-cell-derived-inducible factor
(IL22, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

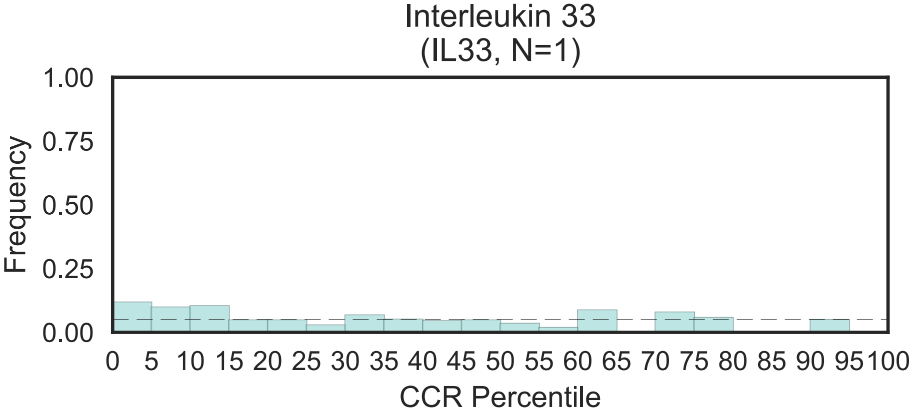

Interleukin 23 subunit alpha
(IL23, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

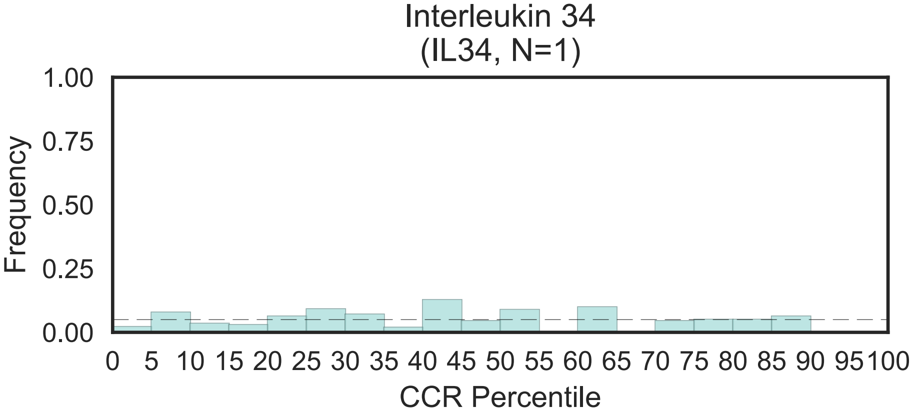

Interleukin-28A
(IL28A, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

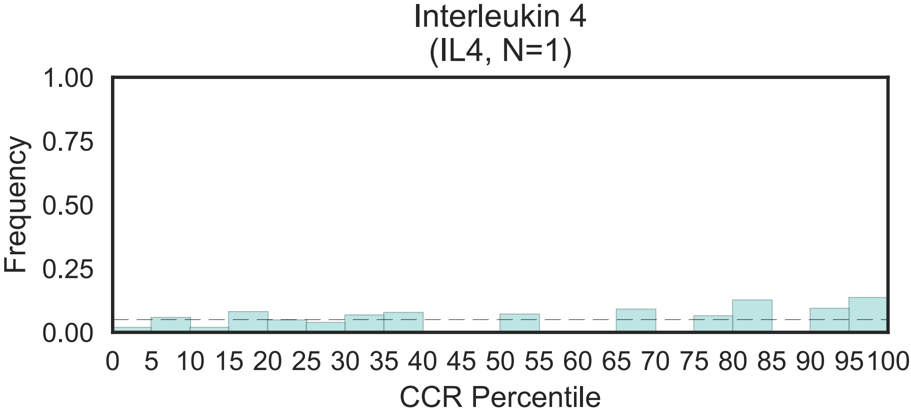

Interleukin-3
(IL3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Interleukin 31
(IL31, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

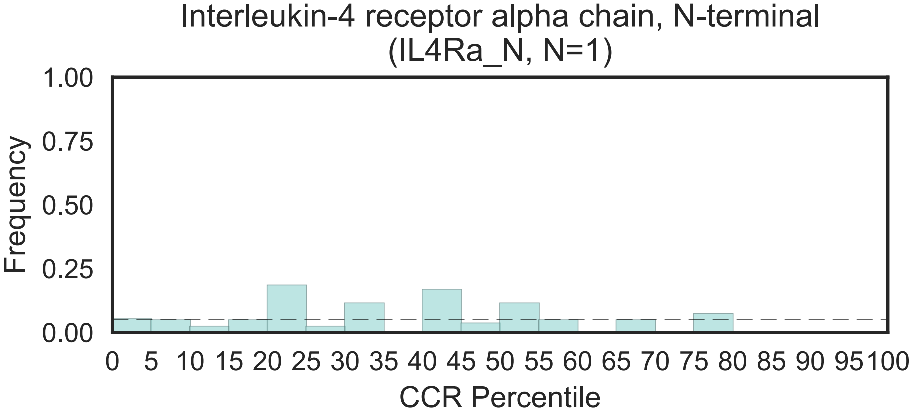

Interleukin 32
(IL32, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Interleukin 33
(IL33, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

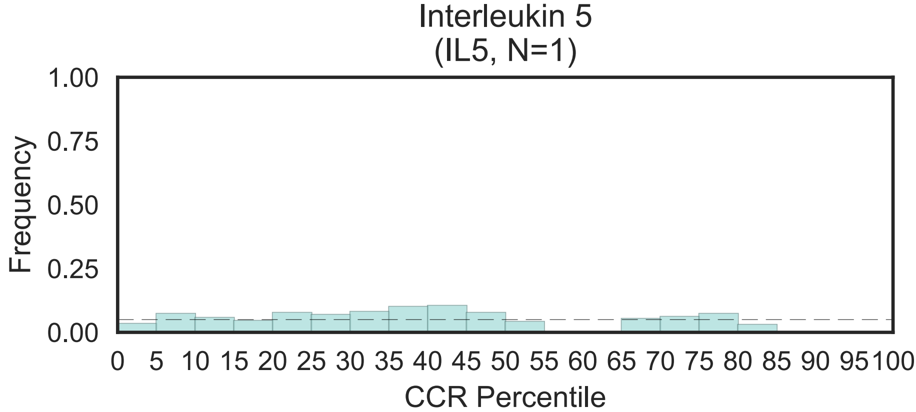

Interleukin 34
(IL34, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

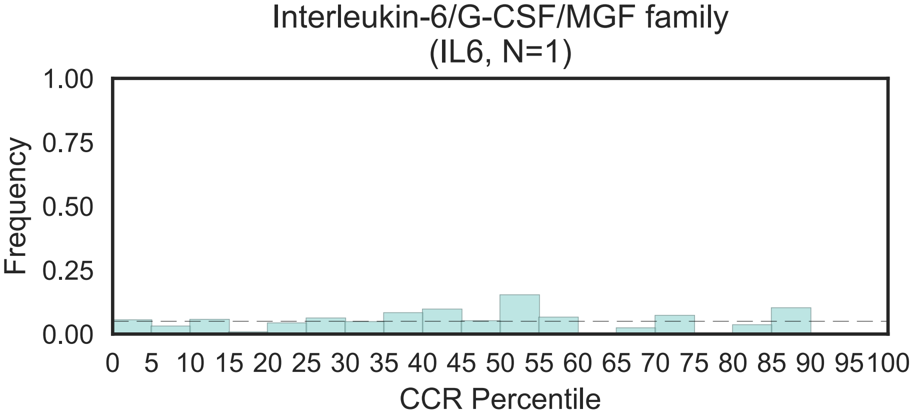


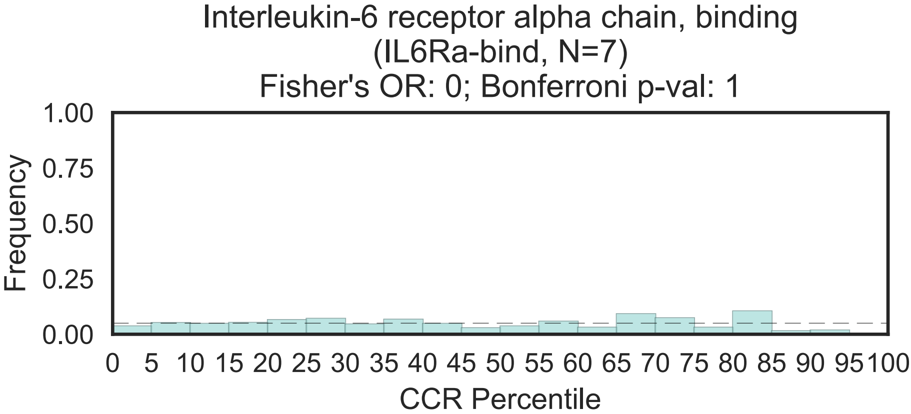
Interleukin 4
(IL4, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

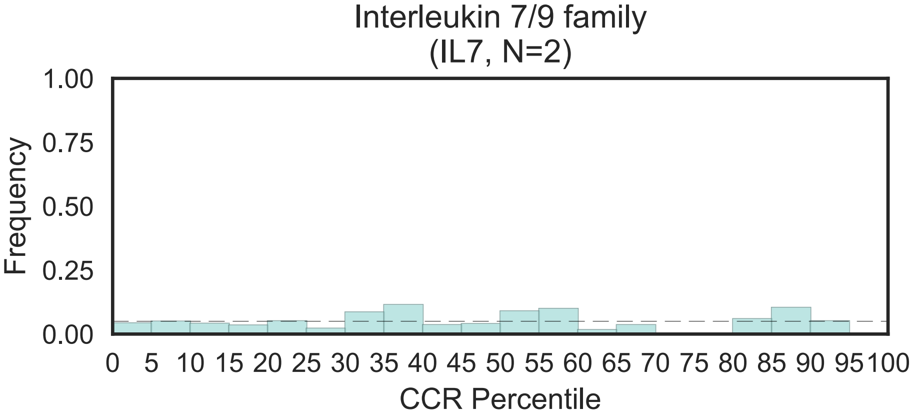


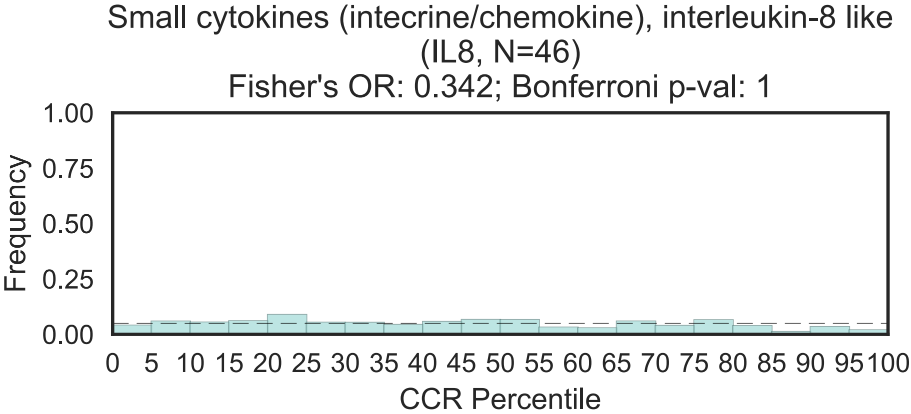
Interleukin-4 receptor alpha chain, N-terminal (IL4Ra_N, N=1)

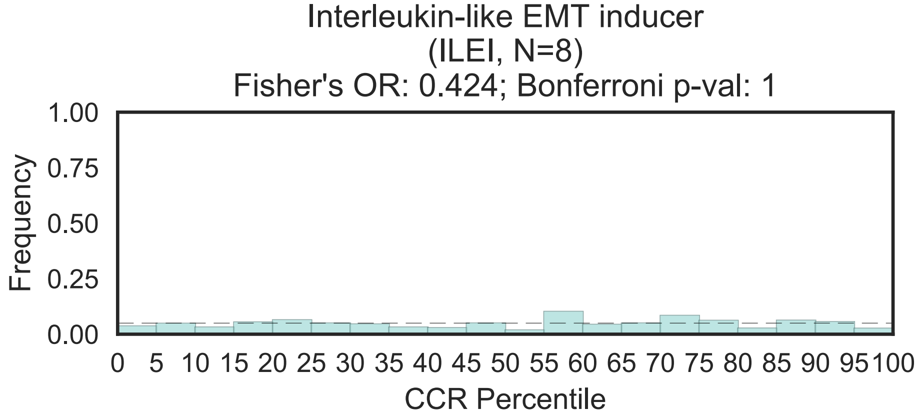

Interleukin 5
(IL5, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

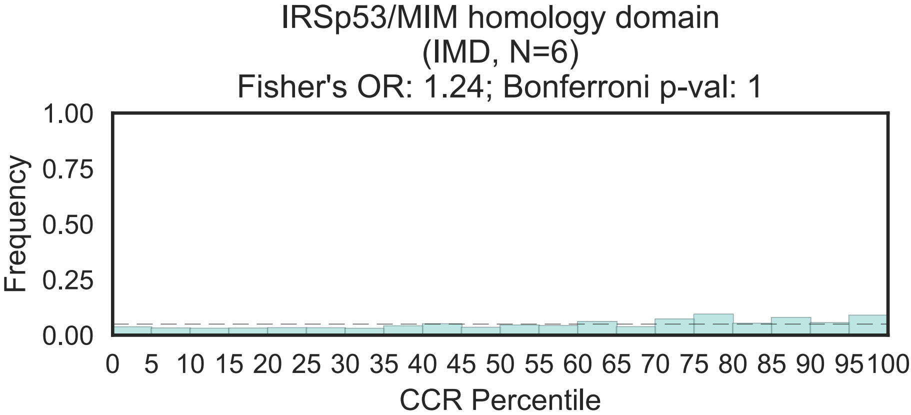

Interleukin-6/G-CSF/MGF family
(IL6, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

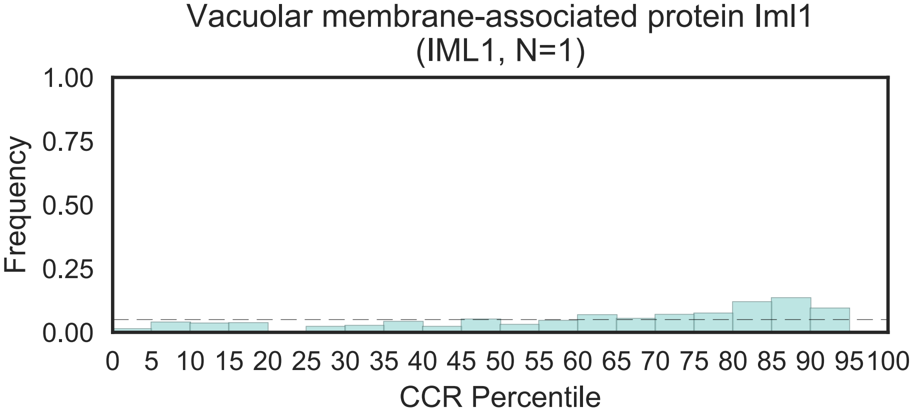

Interleukin-6 receptor alpha chain, binding
(IL6Ra-bind, N=7)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

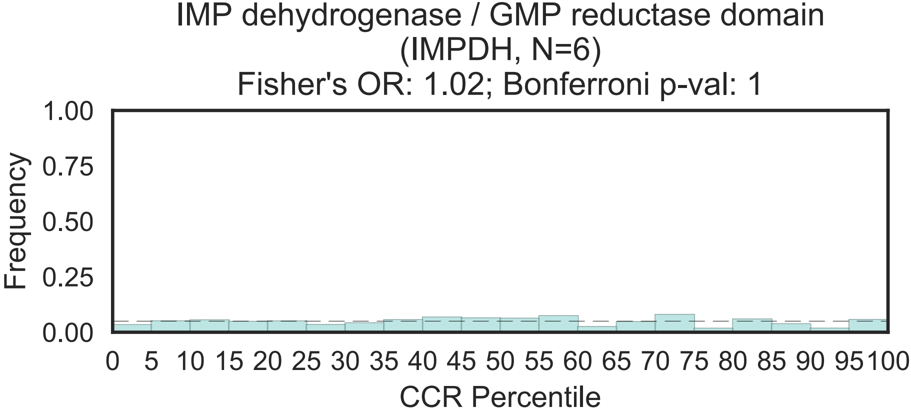

Interleukin 7/9 family
(IL7, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Small cytokines (intecrine/chemokine), interleukin-8 like
(IL8, N=46)
Fisher's OR: 0.342; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

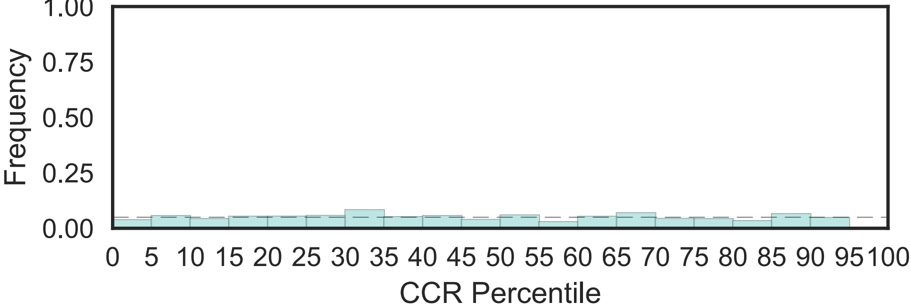

Interleukin-like EMT inducer
(ILEI, N=8)
Fisher's OR: 0.424; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

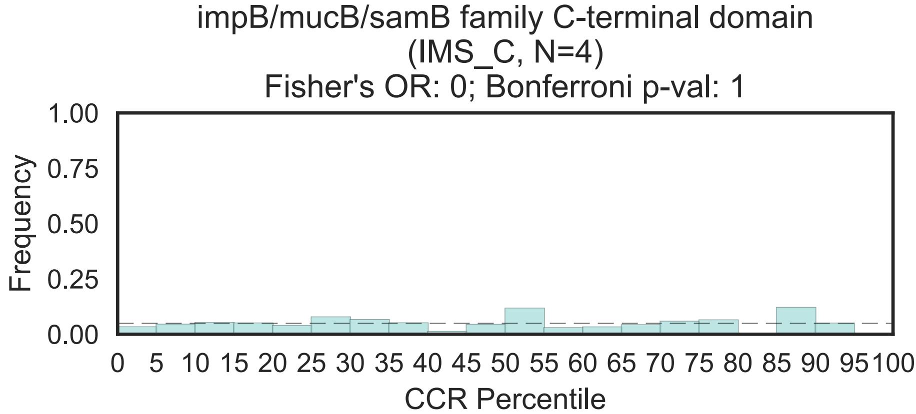

IRSp53/MIM homology domain
(IMD, N=6)
Fisher's OR: 1.24; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Vacuolar membrane-associated protein Iml1
(IML1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

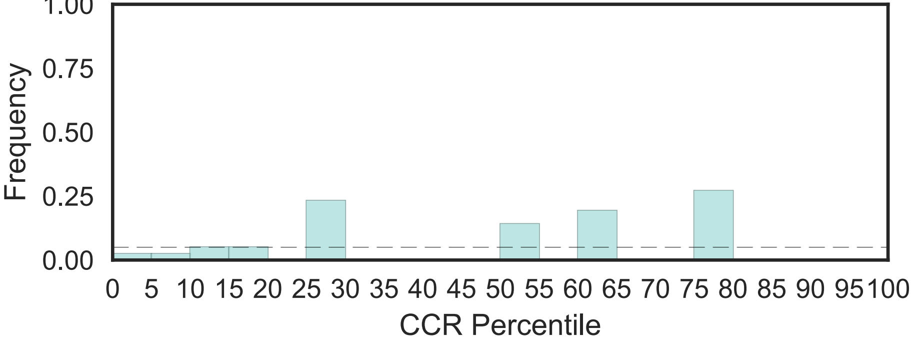

IMP dehydrogenase / GMP reductase domain
(IMPDH, N=6)
Fisher's OR: 1.02; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

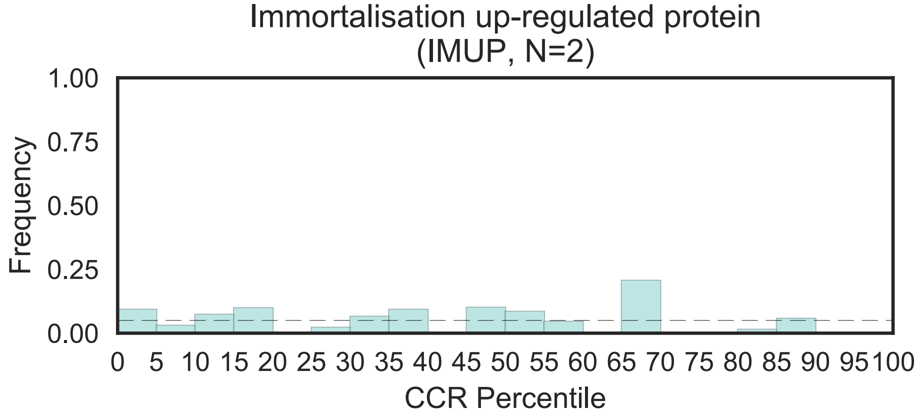
impB/mucB/samB family
(IMS, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

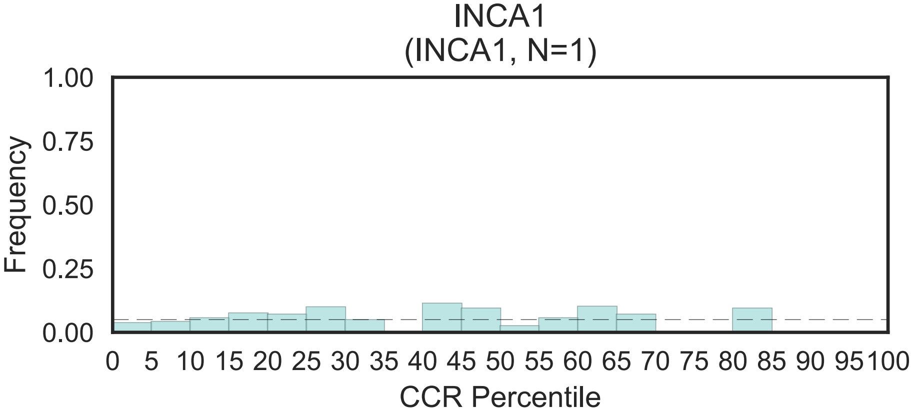


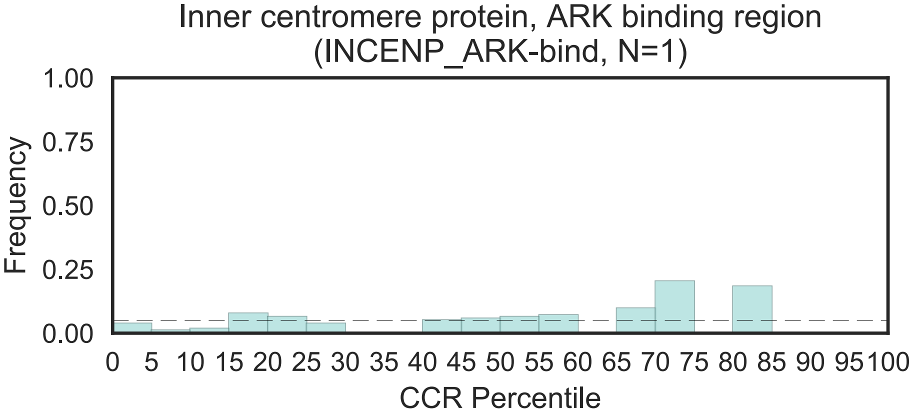

impB/mucB/samB family C-terminal domain
(IMS_C, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

IMS family HHH motif
(IMS_HHH, N=1)

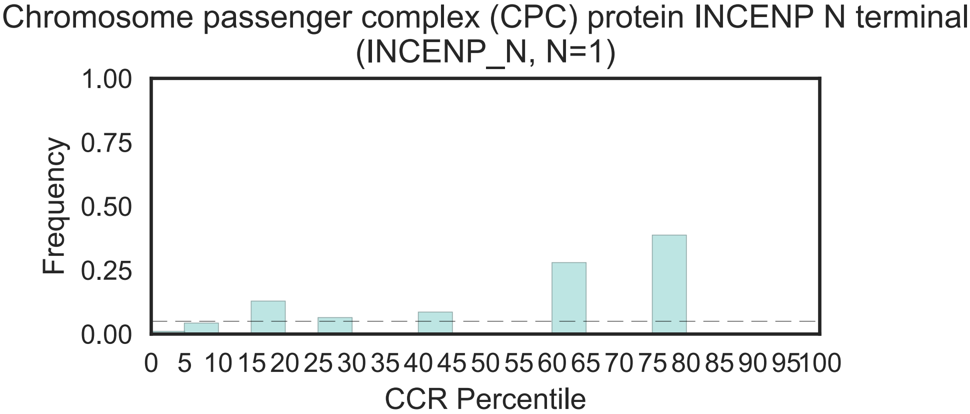


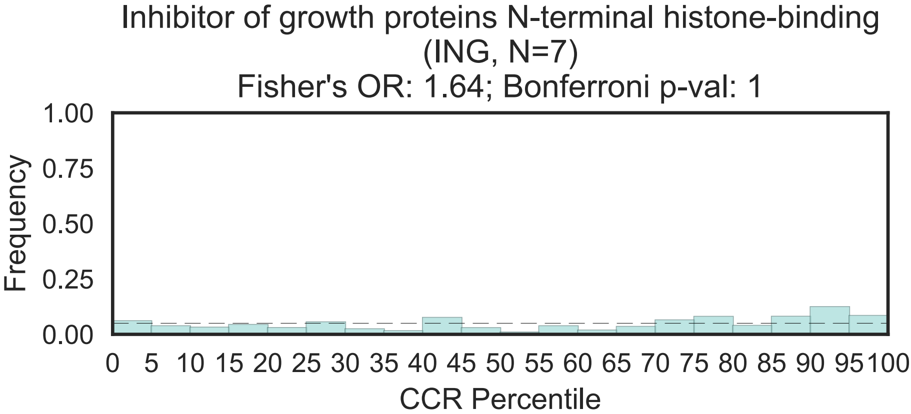

Immortalisation up-regulated protein
(IMUP, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


INCA1
(INCA1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

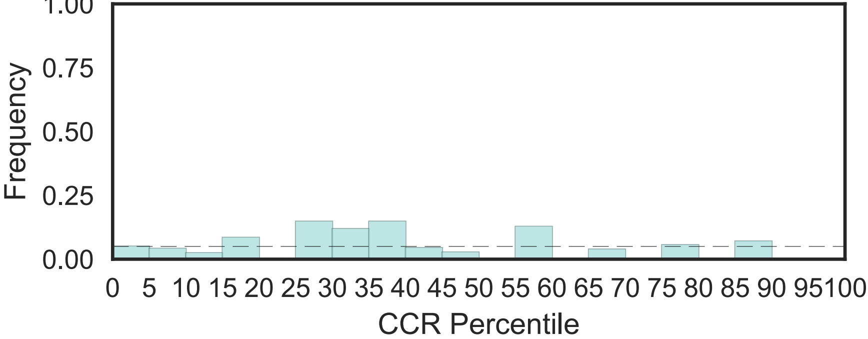


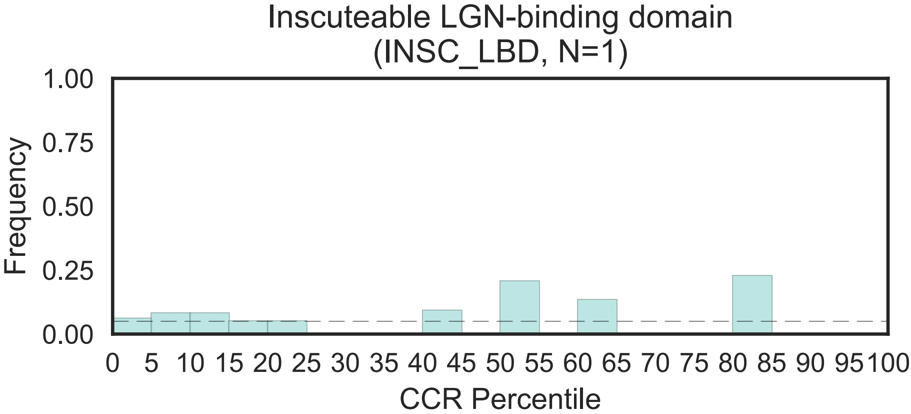
Inner centromere protein, ARK binding region
(INCENP_ARK-bind, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

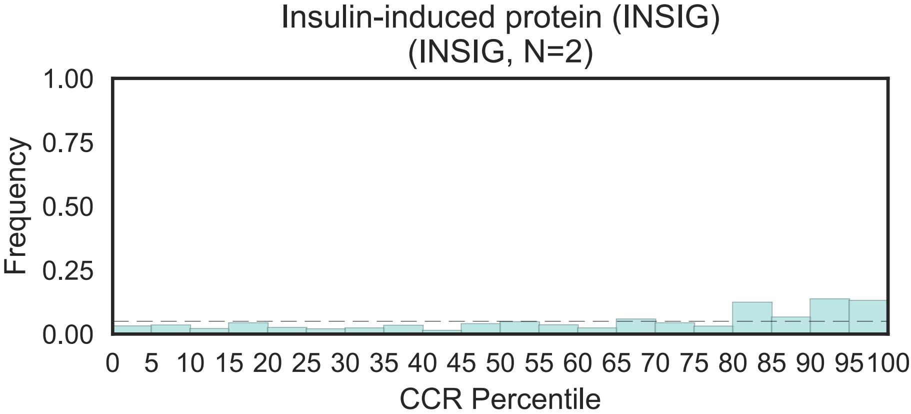

Chromosome passenger complex (CPC) protein INCENP N terminal
(INCENP_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

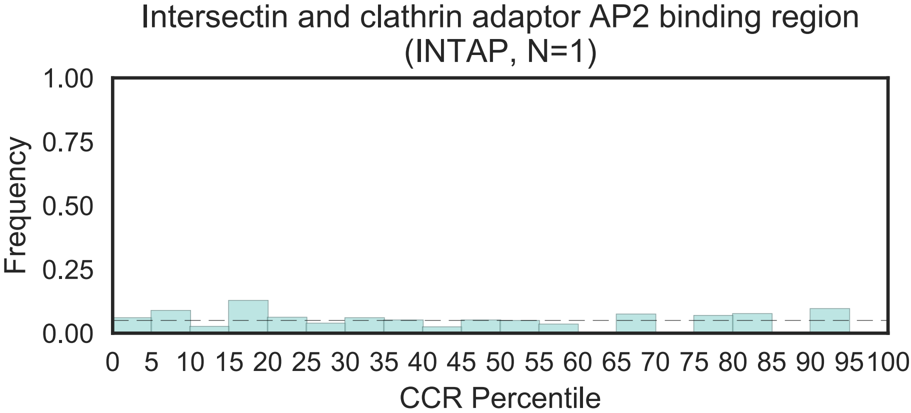

Inhibitor of growth proteins N-terminal histone-binding
(ING, N=7)
Fisher's OR: 1.64; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

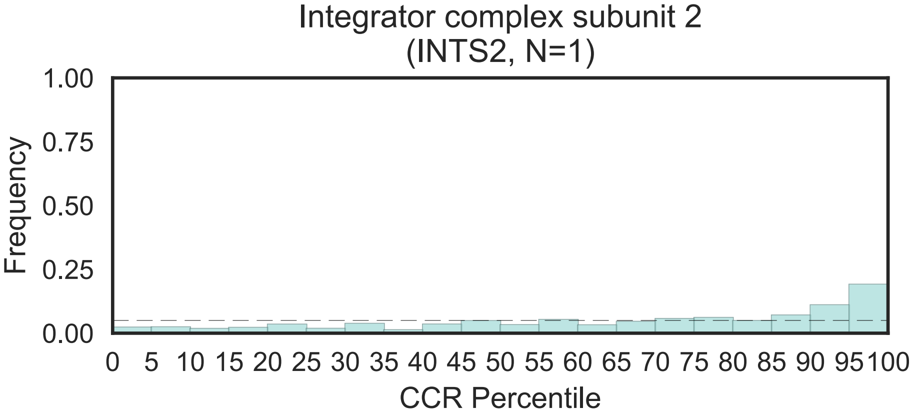
Type II inositol 1,4,5-trisphosphate 5-phosphatase PH domain (INPP5B_PH, N=1)

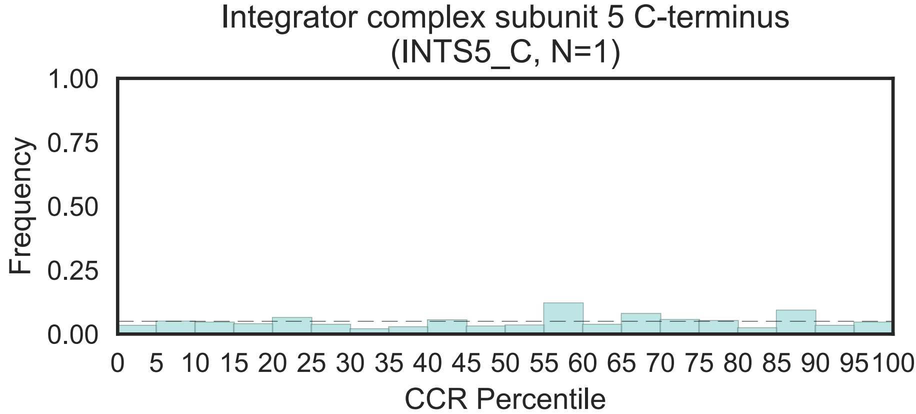


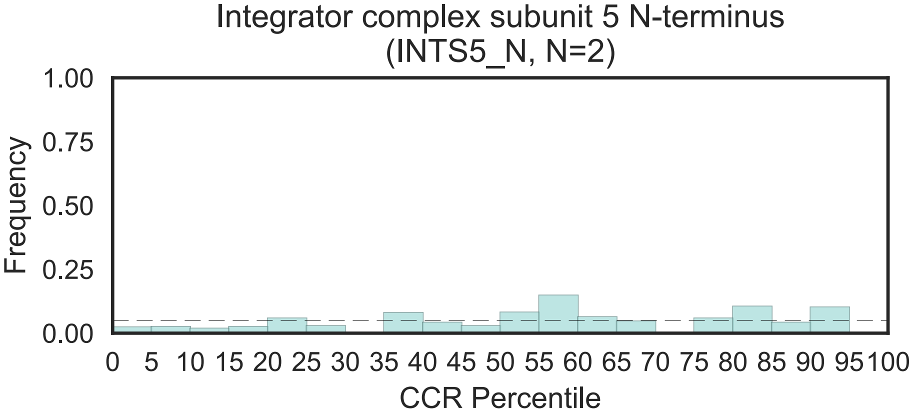

Inscuteable LGN-binding domain
(INSC_LBD, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

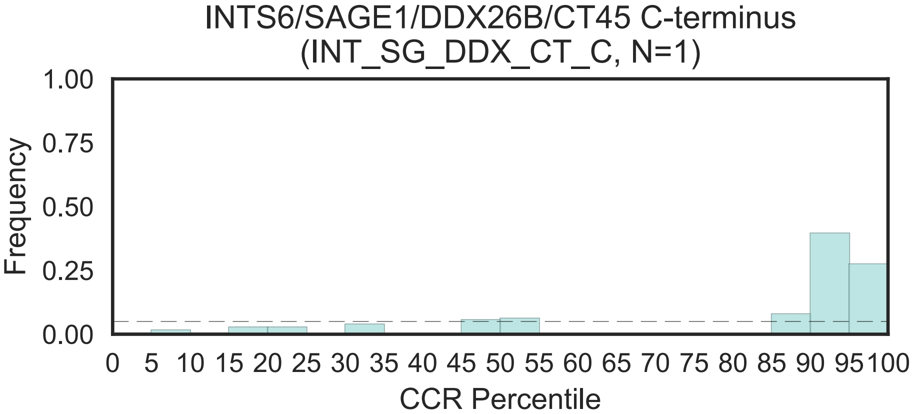

Insulin-induced protein (INSIG)
(INSIG, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

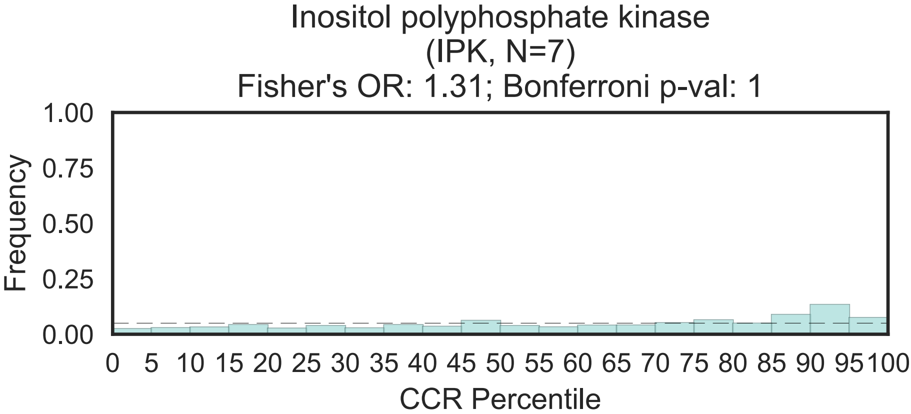

Intersectin and clathrin adaptor AP2 binding region
(INTAP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Integrator complex subunit 2
(INTS2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

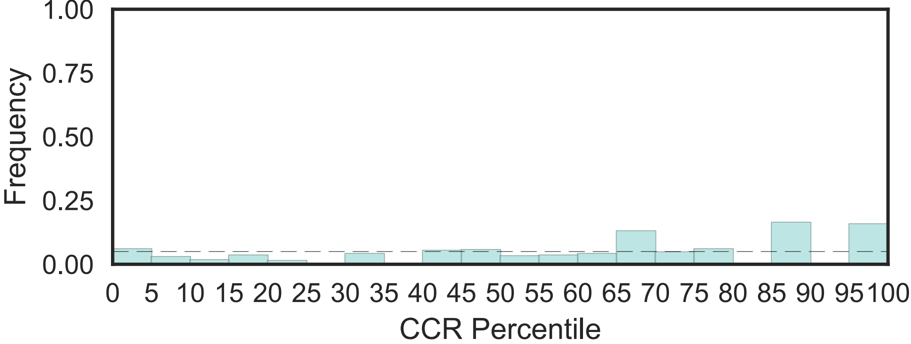

Integrator complex subunit 5 C-terminus
(INTS5_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

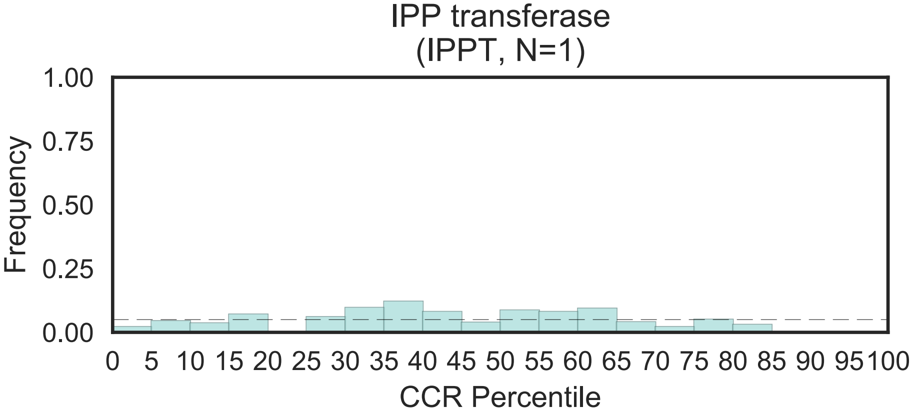

Integrator complex subunit 5 N-terminus
(INTS5_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

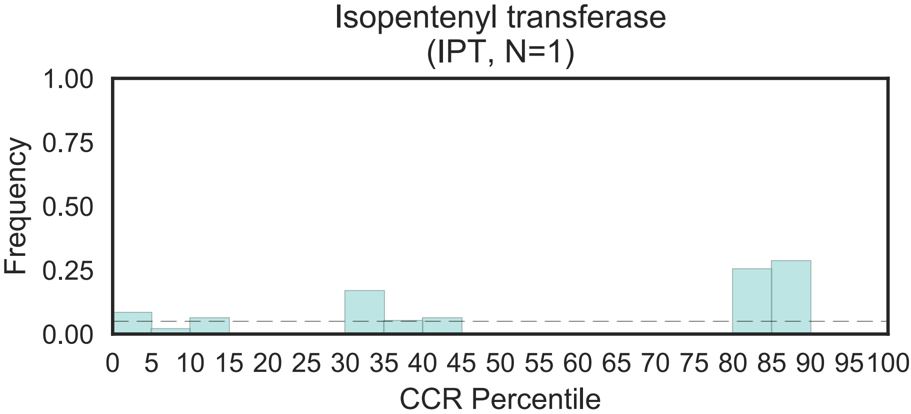

INTS6/SAGE1/DDX26B/CT45 C-terminus
(INT_SG_DDX_CT_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

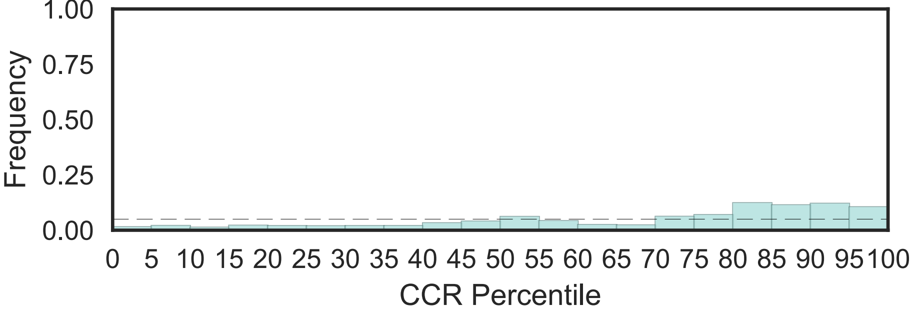

Inositol polyphosphate kinase
(IPK, N=7)
Fisher's OR: 1.31; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Protein phosphatase inhibitor 2 (IPP-2)
(IPP-2, N=1)

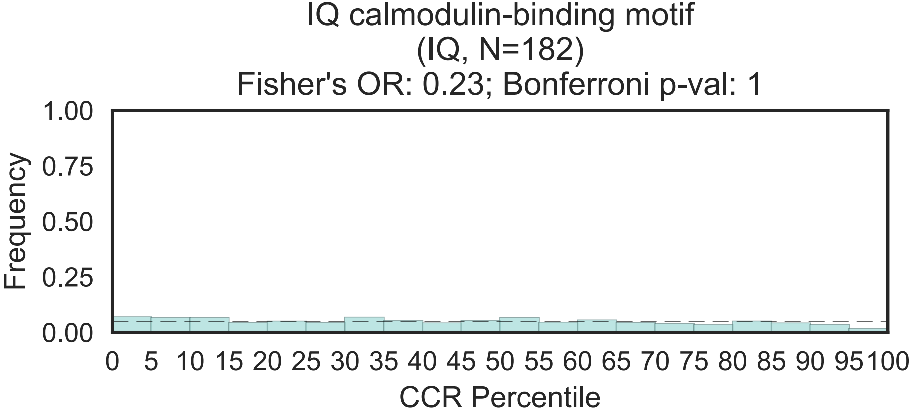


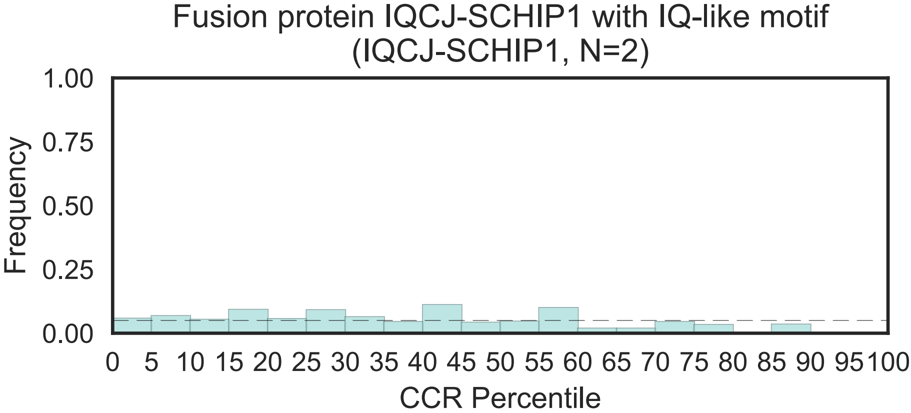

IPP transferase
(IPPT, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

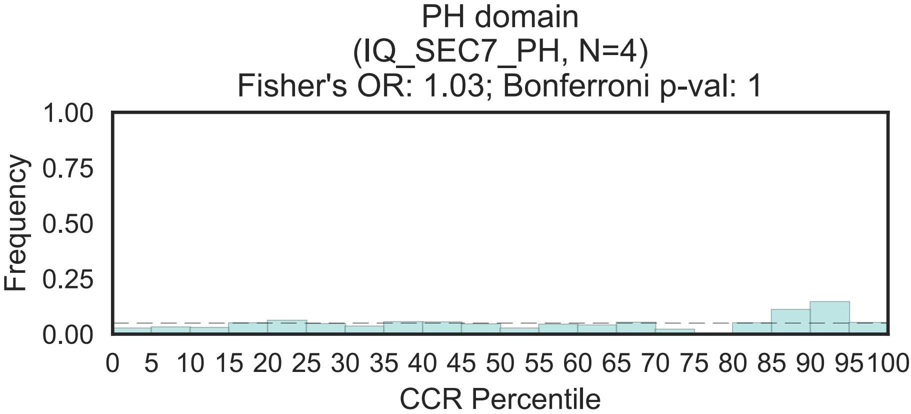

Isopentenyl transferase
(IPT, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

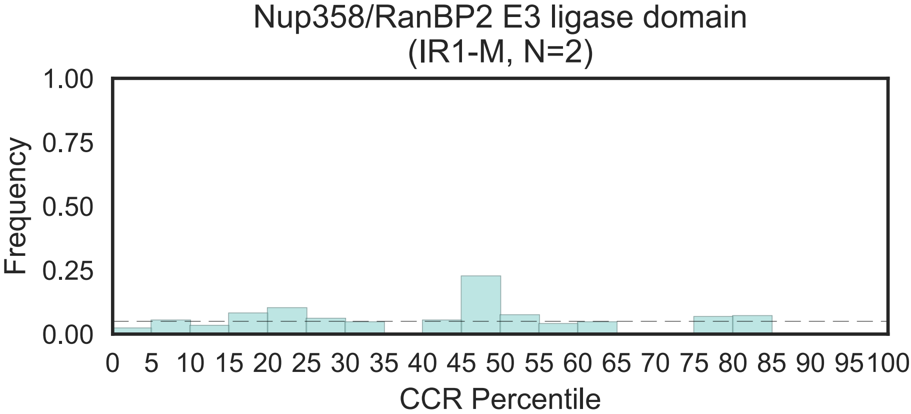


Phosphatidylinositol transfer protein
(IP_trans, N=5)
Fisher's OR: 2.49; Bonferroni p-val: 1

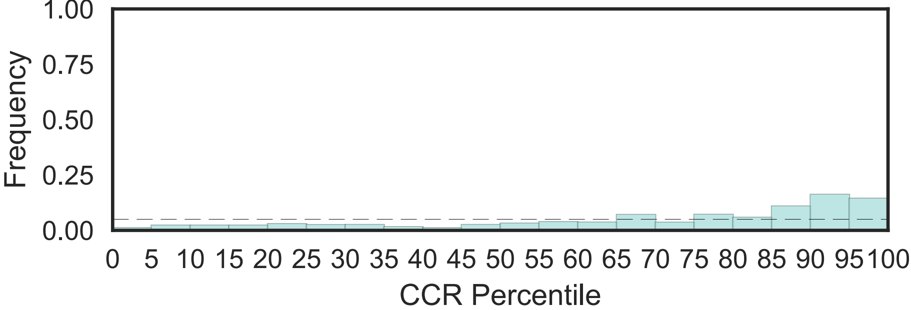

IQ calmodulin-binding motif
(IQ, N=182)
Fisher's OR: 0.23; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Fusion protein IQCJ-SCHIP1 with IQ-like motif
(IQCJ-SCHIP1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

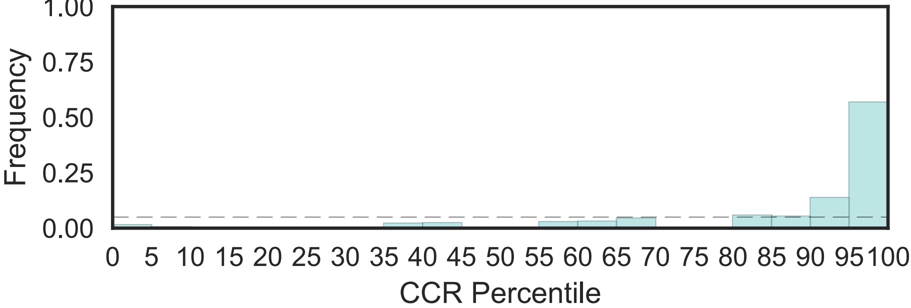

PH domain
(IQ_SEC7_PH, N=4)
Fisher's OR: 1.03; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

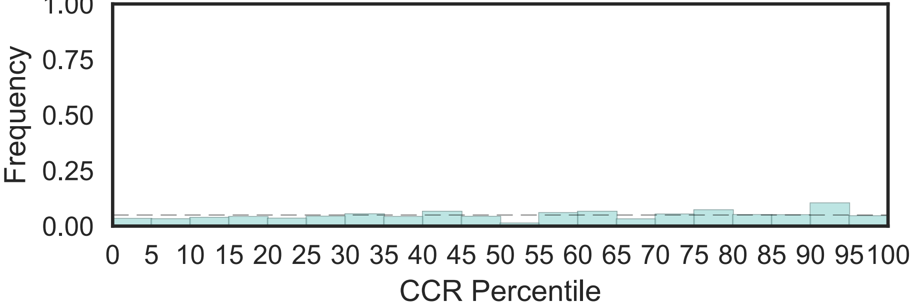

Nup358/RanBP2 E3 ligase domain
(IR1-M, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Interferon regulatory factor transcription factor
(IRF, N=9)
Fisher's OR: 3.49; Bonferroni p-val: 1



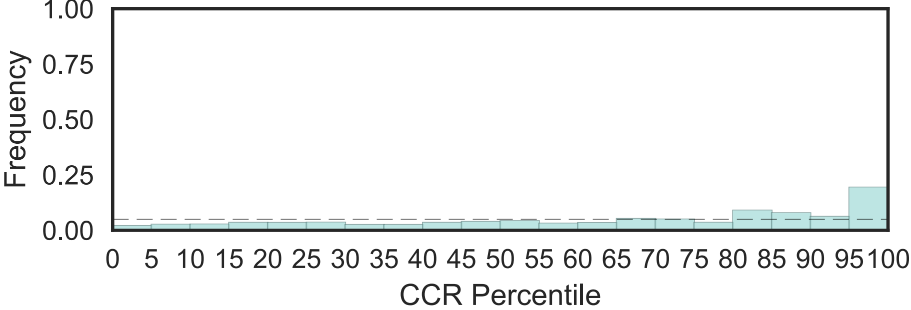
Interferon regulatory factor 2-binding protein zinc finger (IRF-2BP1_2, N=3)
Fisher's OR: 14.4; Bonferroni p-val: 1

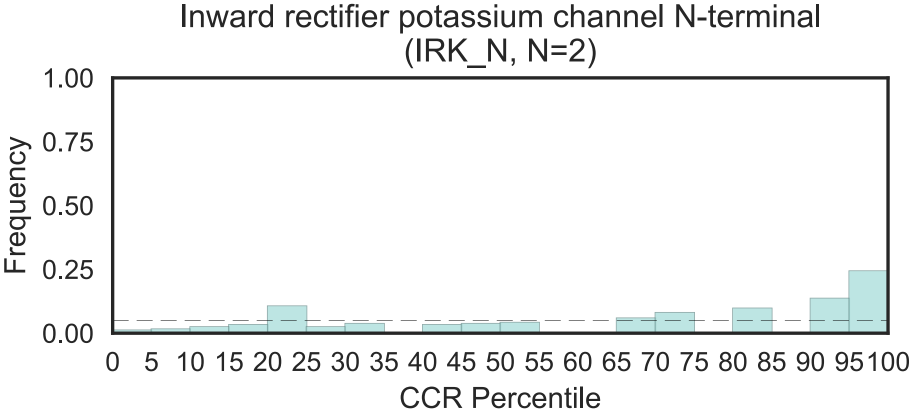


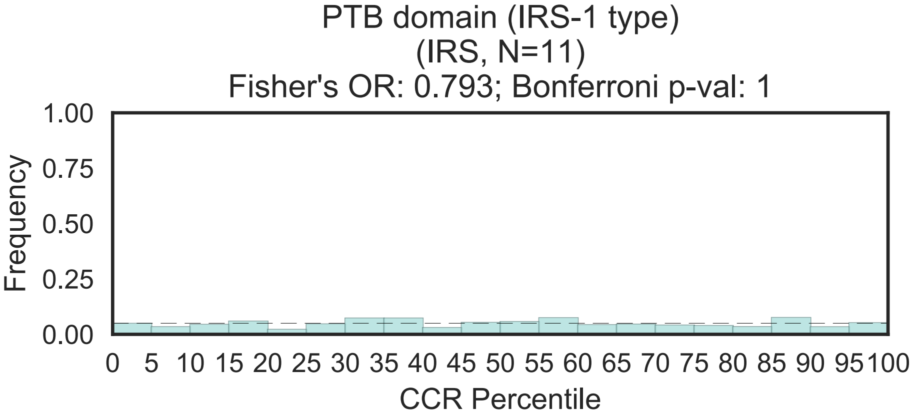


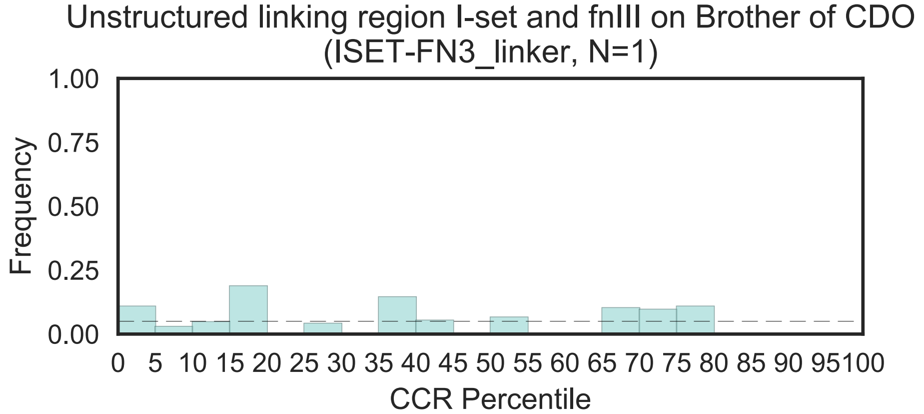
Interferon-regulatory factor 3
(IRF-3, N=8)
Fisher's OR: 0.978; Bonferroni p-val: 1

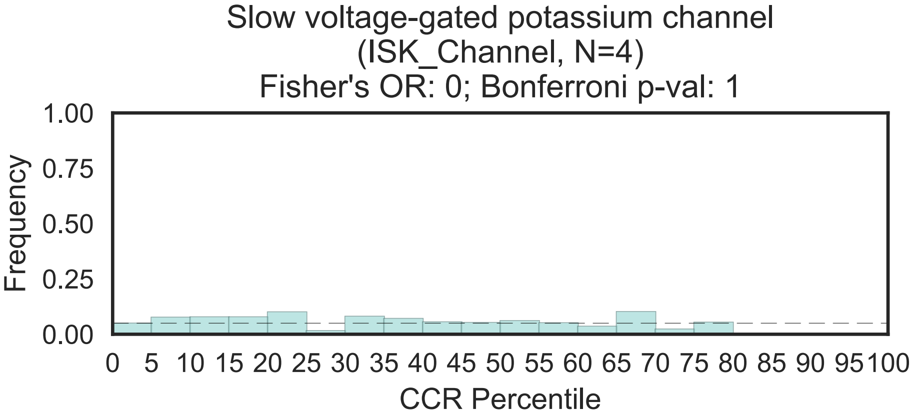
Inward rectifier potassium channel
(IRK, N=16)
Fisher's OR: 3.61; Bonferroni p-val: 4.52e-08

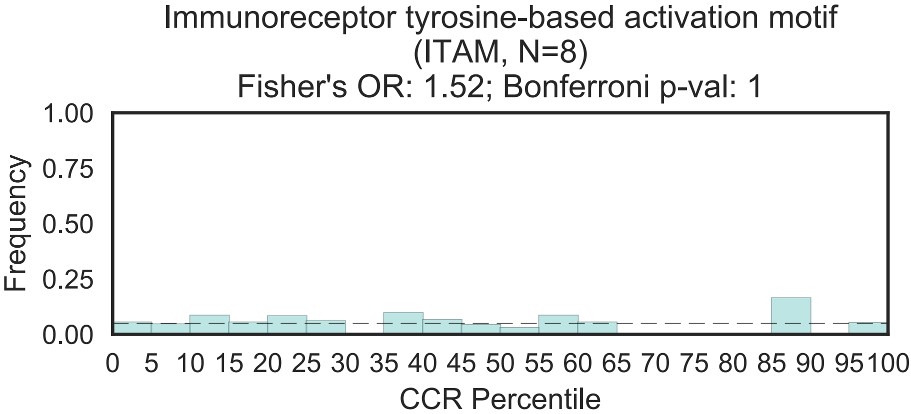



Inward rectifier potassium channel N-terminal
(IRK_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

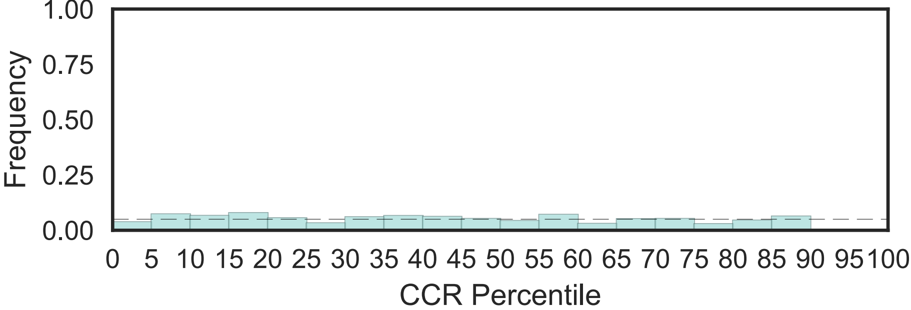

PTB domain (IRS-1 type)
(IRS, N=11)
Fisher's OR: 0.793; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

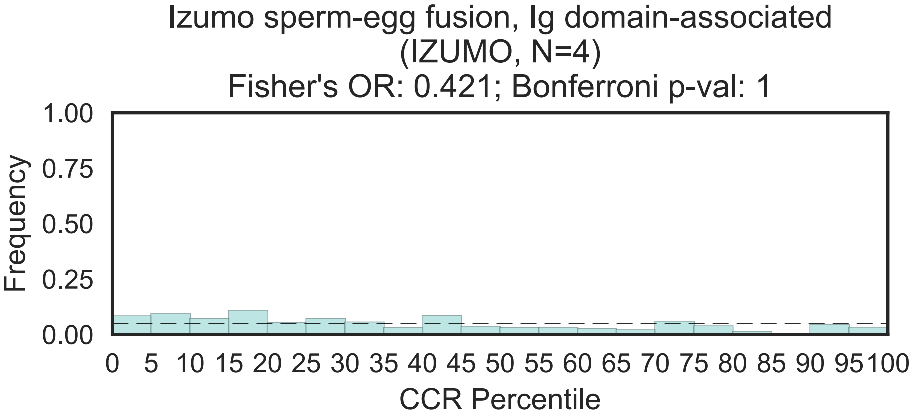

Unstructured linking region I-set and fnIII on Brother of CDO
(ISET-FN3_linker, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

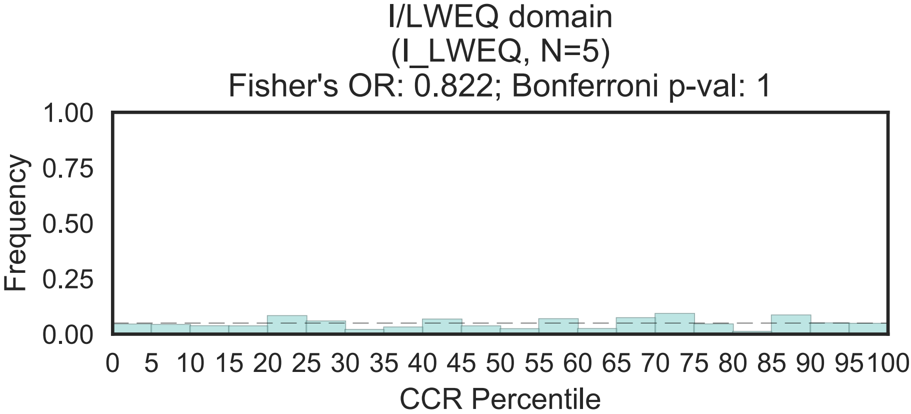

Slow voltage-gated potassium channel
(ISK_Channel, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

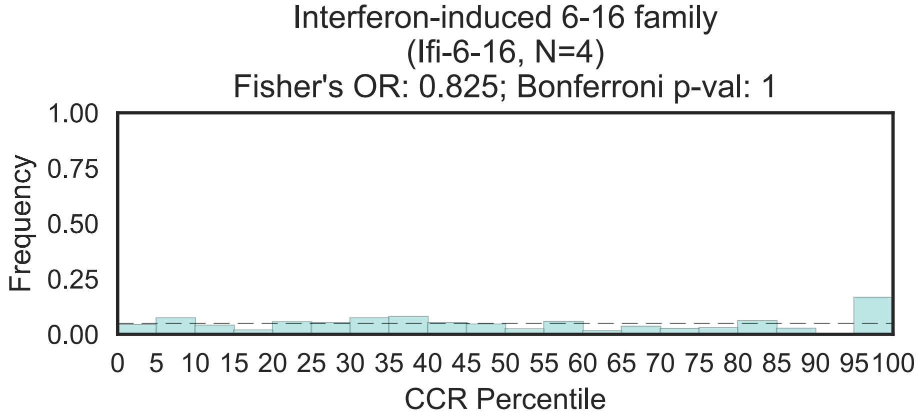

Immunoreceptor tyrosine-based activation motif
(ITAM, N=8)
Fisher's OR: 1.52; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

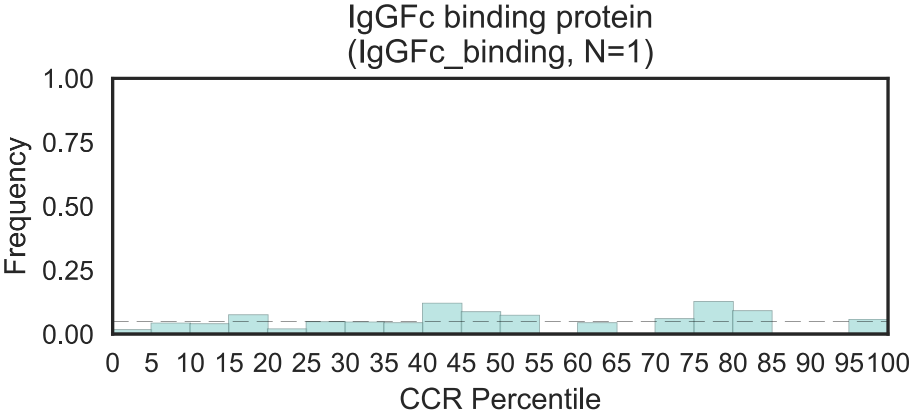
Inter-alpha-trypsin inhibitor heavy chain C-terminus
(ITI_HC_C, N=5)
Fisher's OR: 0; Bonferroni p-val: 1

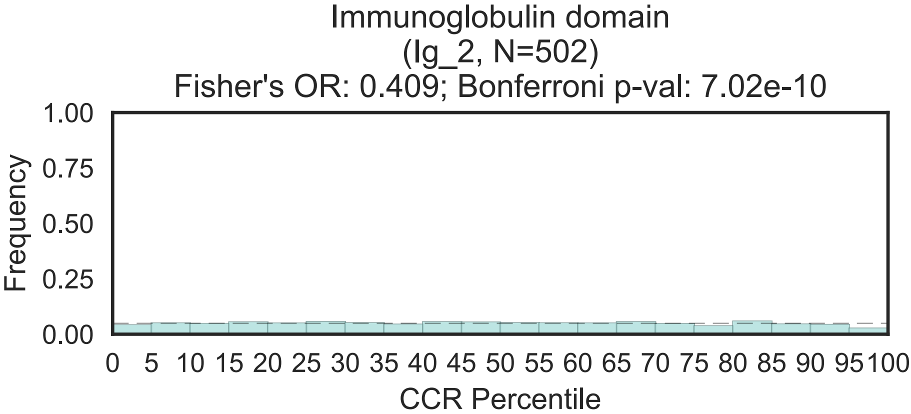


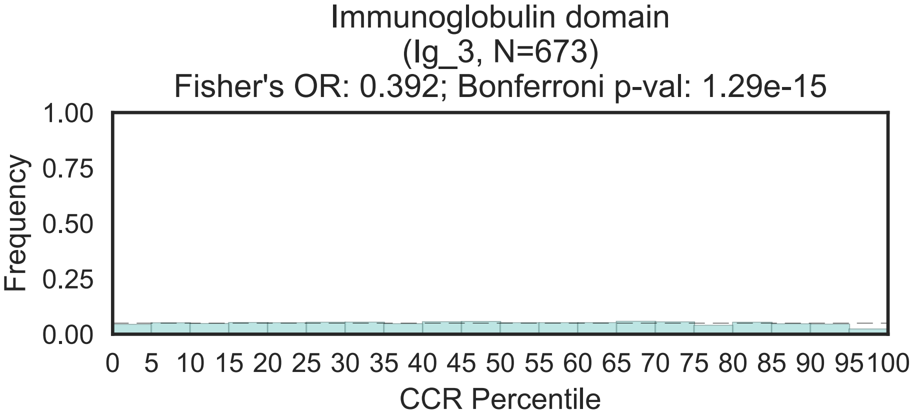

Izumo sperm-egg fusion, Ig domain-associated
(IZUMO, N=4)
Fisher's OR: 0.421; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


I/LWEQ domain
(I_LWEQ, N=5)
Fisher's OR: 0.822; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

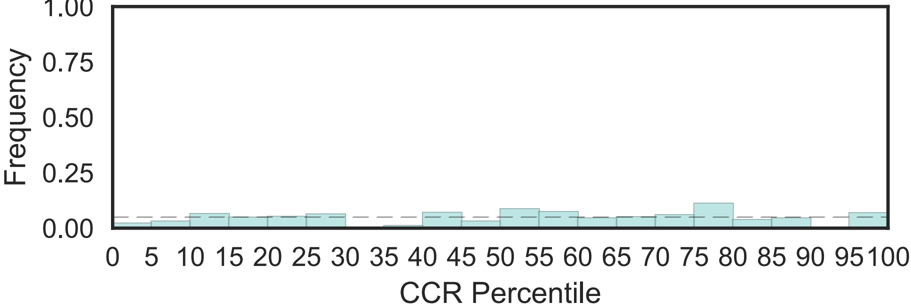

Interferon-induced 6-16 family
(Ifi-6-16, N=4)
Fisher's OR: 0.825; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


IgGFc binding protein
(IgGFc_binding, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Immunoglobulin domain
(Ig_2, N=502)
Fisher's OR: 0.409; Bonferroni p-val: 7.02e-10
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

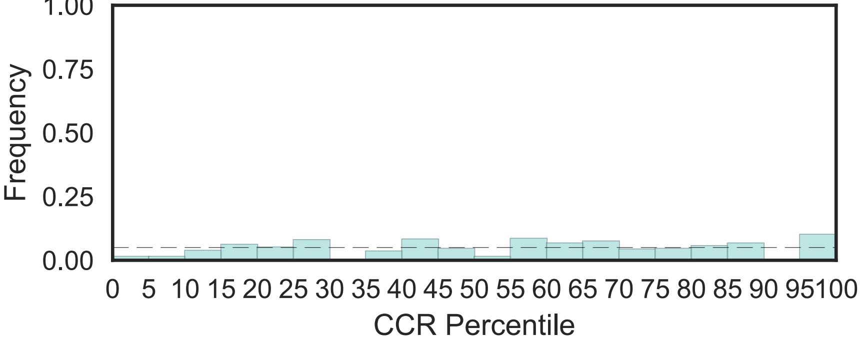


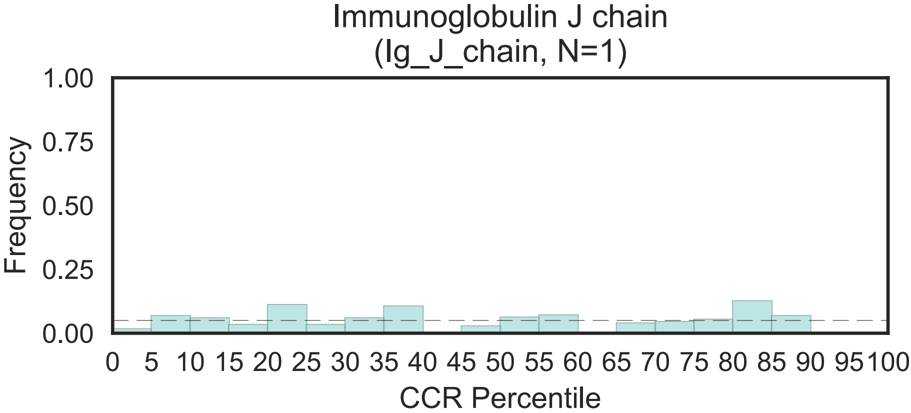
Immunoglobulin domain
(Ig_3, N=673)
Fisher's OR: 0.392; Bonferroni p-val: 1.29e-15

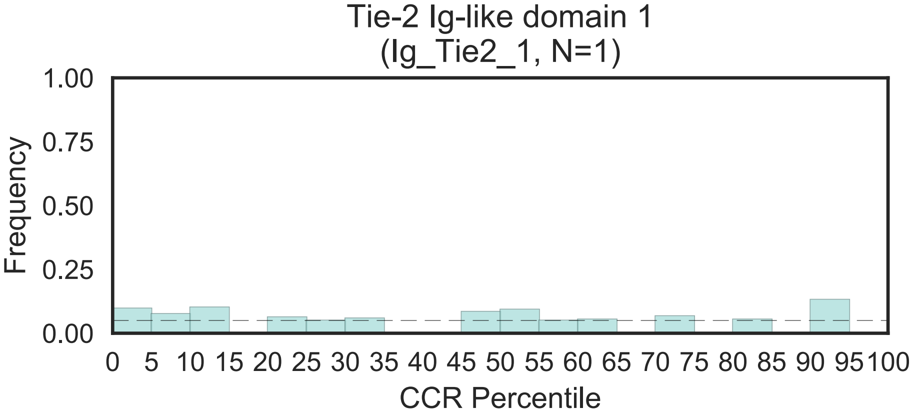


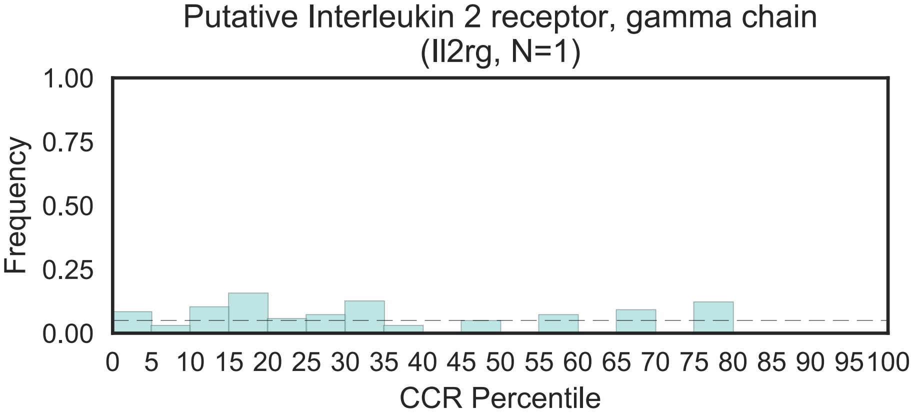
T-cell surface glycoprotein CD3 delta chain
(Ig_4, N=3)
Fisher's OR: 1.3; Bonferroni p-val: 1

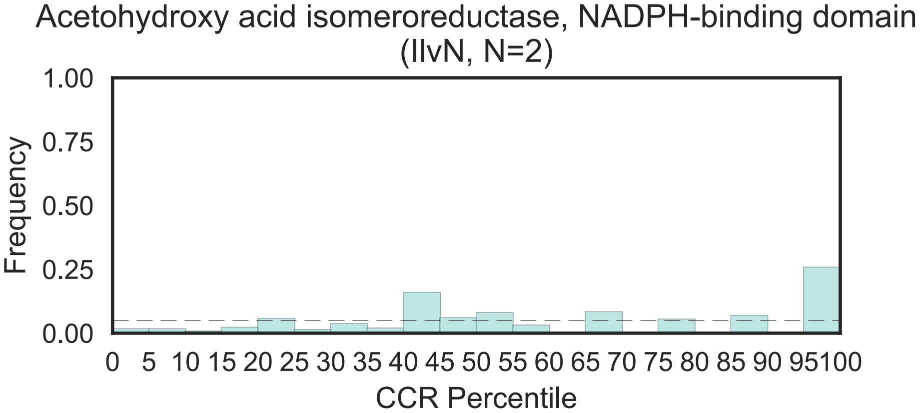
Ig-like domain on T-cell surface glycoprotein CD3 epsilon chain (Ig_5, N=2)

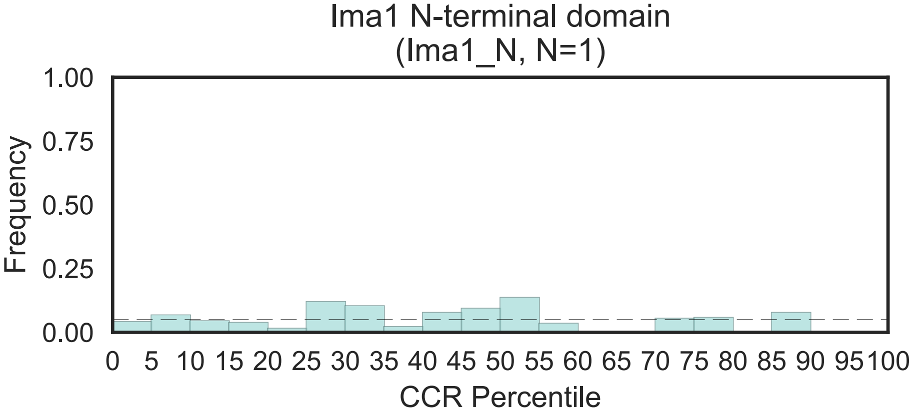


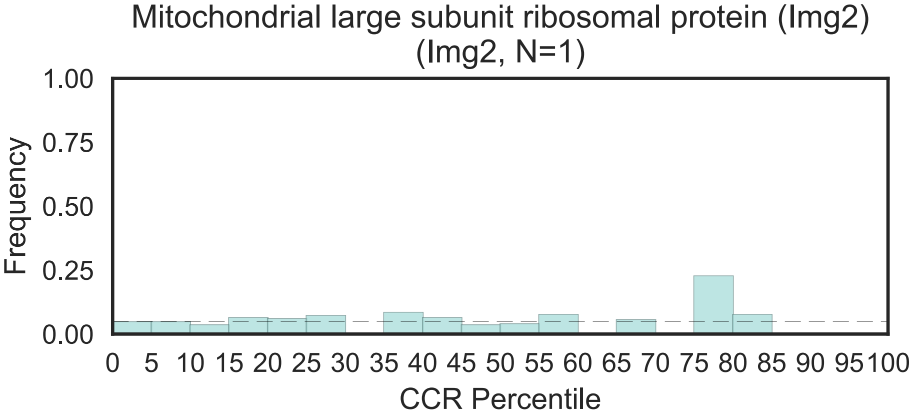

Immunoglobulin J chain
(Ig_J_chain, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

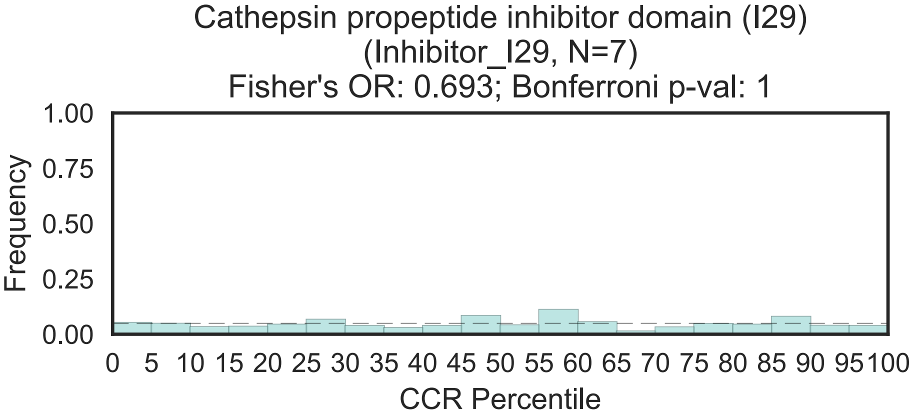

Tie-2 Ig-like domain 1
(Ig_Tie2_1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

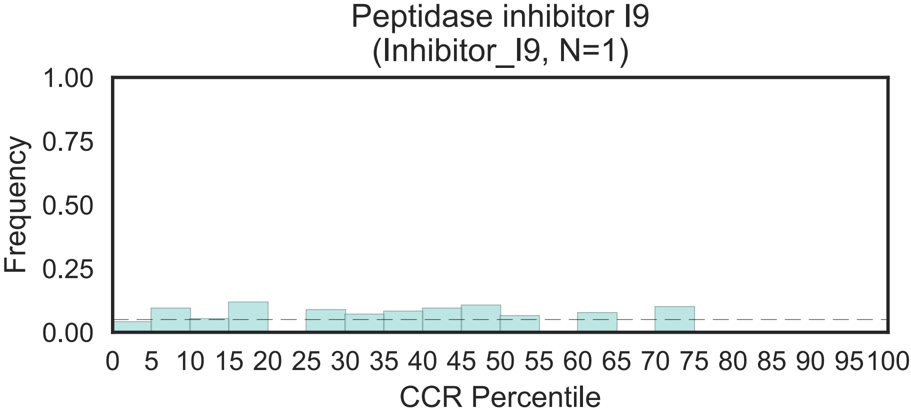

Putative Interleukin 2 receptor, gamma chain
(Il2rg, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

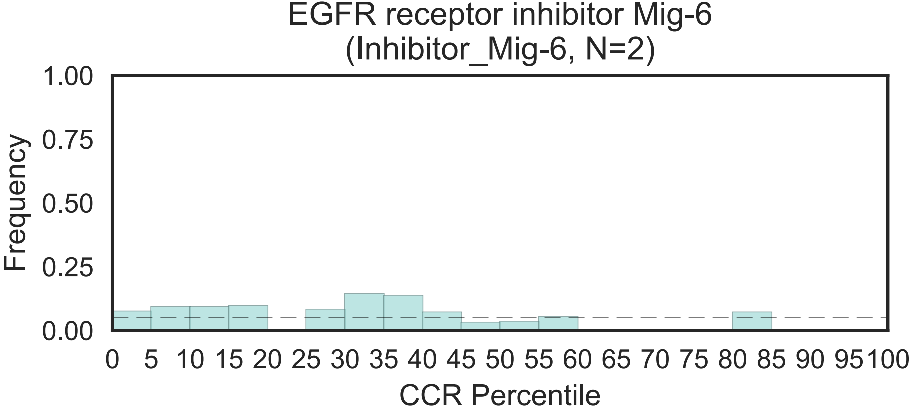

Acetohydroxy acid isomeroreductase, NADPH-binding domain
(IlvN, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

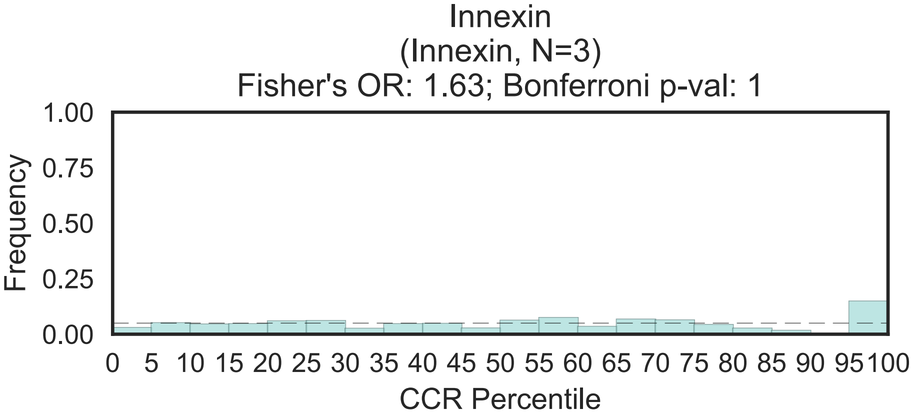

Ima1 N-terminal domain
(Ima1_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

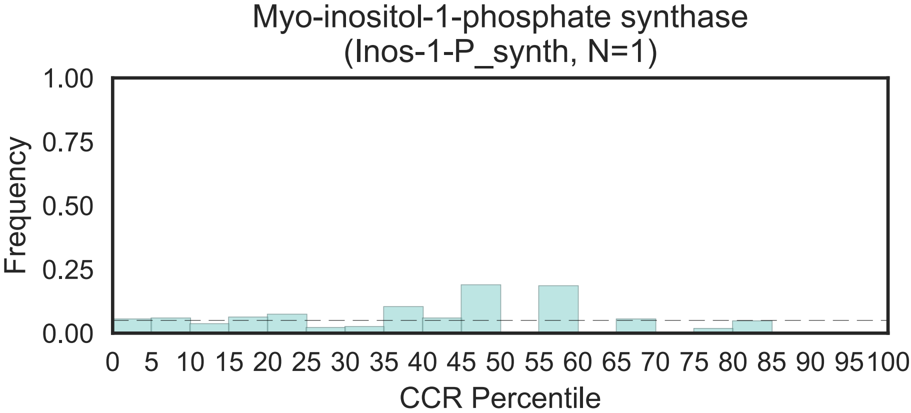

Mitochondrial large subunit ribosomal protein (Img2)
(Img2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

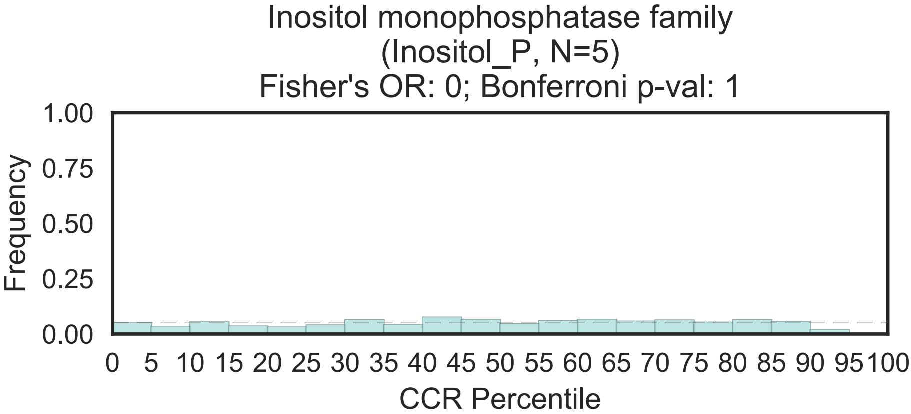

Cathepsin propeptide inhibitor domain (I29)
(Inhibitor_I29, N=7)
Fisher's OR: 0.693; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

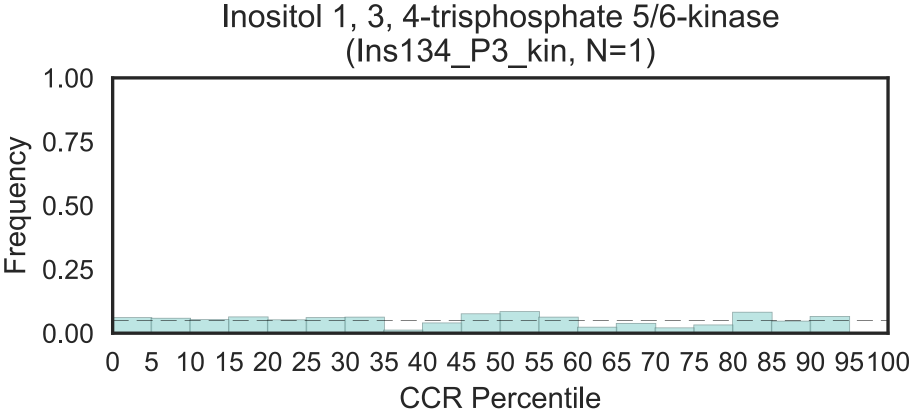

Peptidase inhibitor I9
(Inhibitor_I9, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

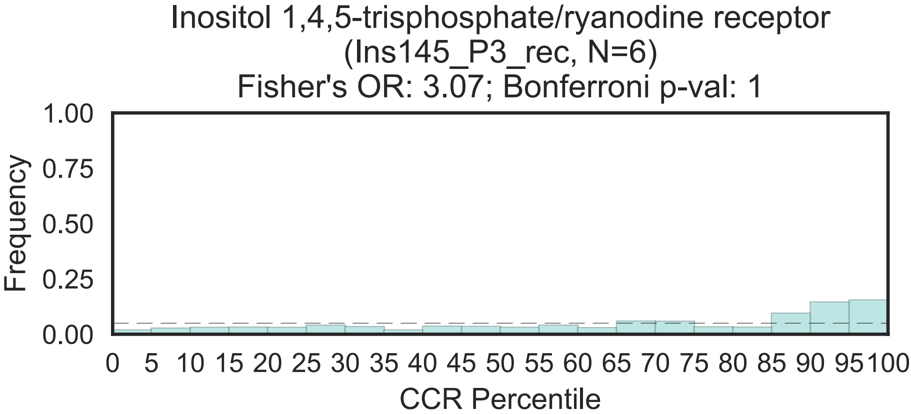

EGFR receptor inhibitor Mig-6
(Inhibitor_Mig-6, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Innexin
(Innexin, N=3)
Fisher's OR: 1.63; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

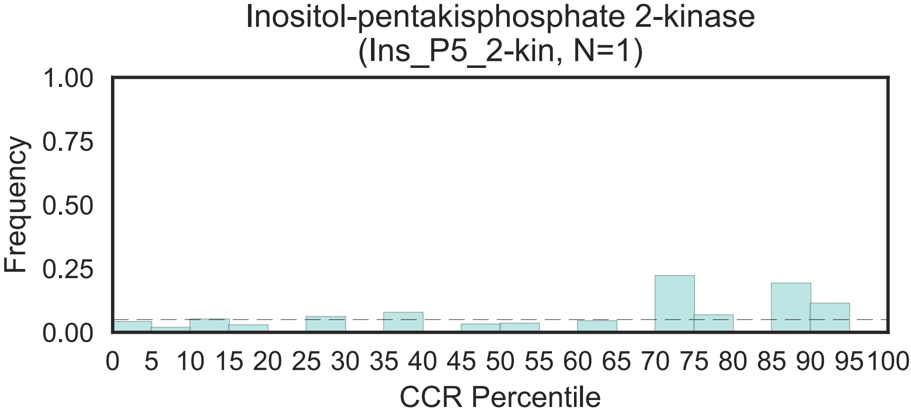

Myo-inositol-1-phosphate synthase
(Inos-1-P_synth, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Inosititol monophosphatase family
(Inositol_P, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

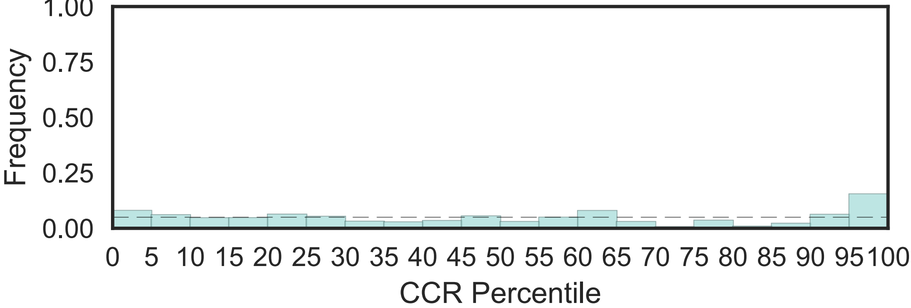

Inositol 1, 3, 4-trisphosphate 5/6-kinase
(Ins134_P3_kin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

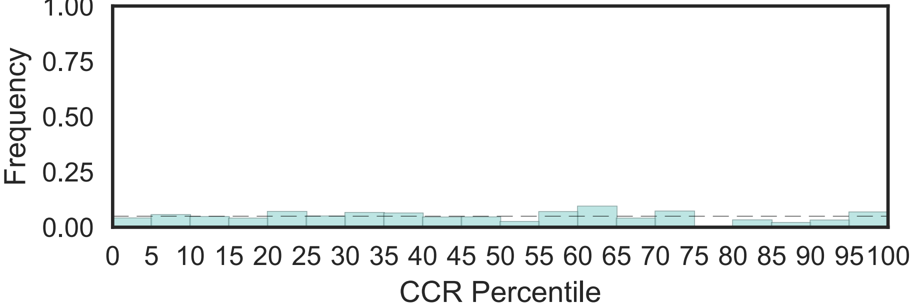


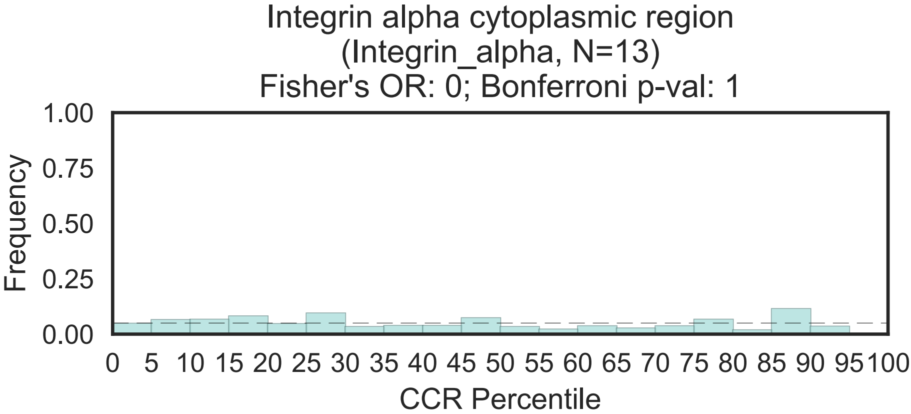
Inositol 1,4,5-trisphosphate/ryanodine receptor
(Ins145_P3_rec, N=6)
Fisher's OR: 3.07; Bonferroni p-val: 1

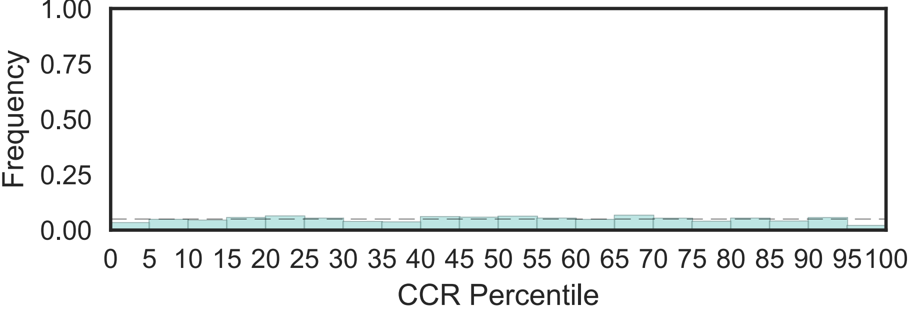

Inositol-pentakisphosphate 2-kinase
(Ins_P5_2-kin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Insulin/IGF/Relaxin family
(Insulin, N=10)
Fisher's OR: 1.36; Bonferroni p-val: 1

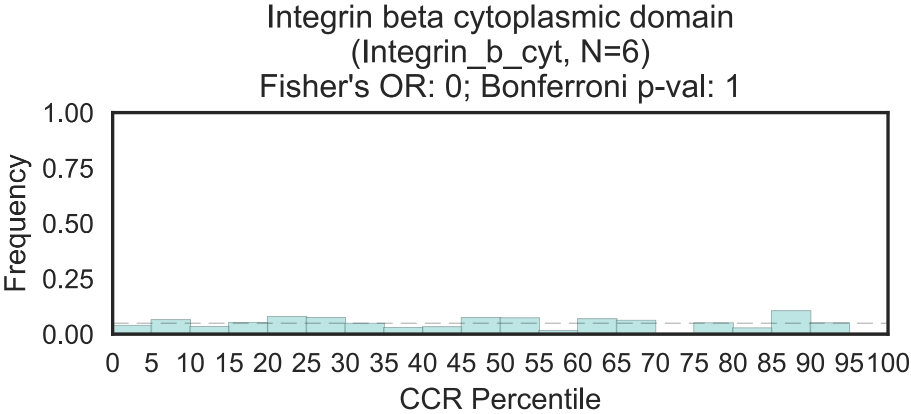


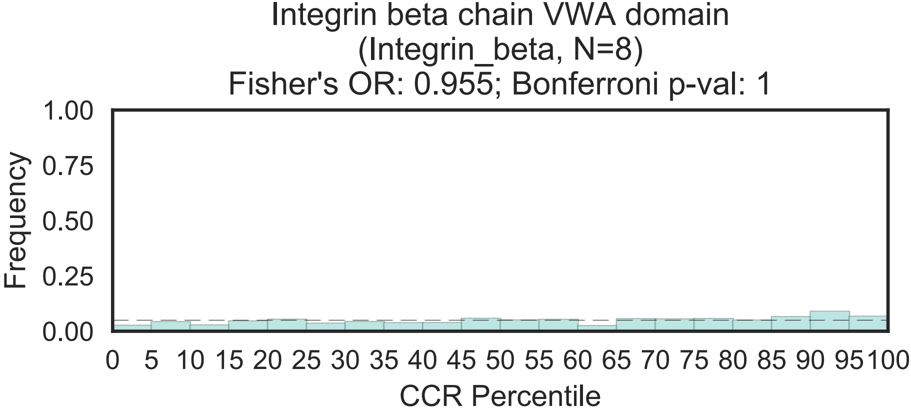

Integrin beta tail domain
(Integrin_B_tail, N=6)
Fisher's OR: 1.05; Bonferroni p-val: 1


Integrin alpha cytoplasmic region
(Integrin_alpha, N=13)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

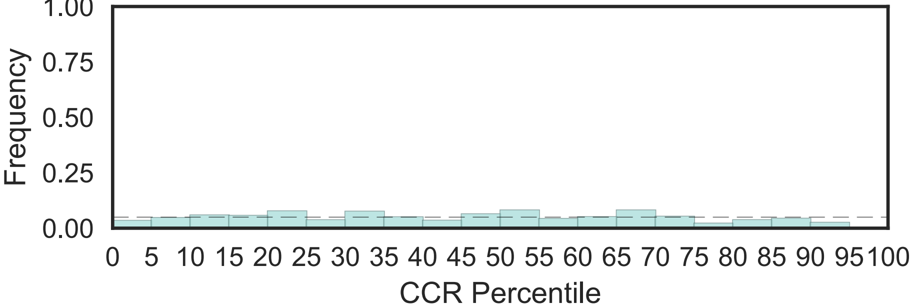


Integrin alpha
(Integrin_alpha2, N=18)
Fisher's OR: 0.269; Bonferroni p-val: 0.156

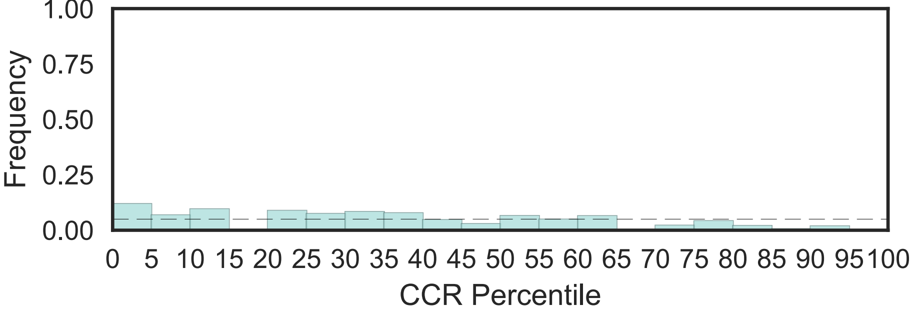

Integrin beta cytoplasmic domain
(Integrin_b_cyt, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

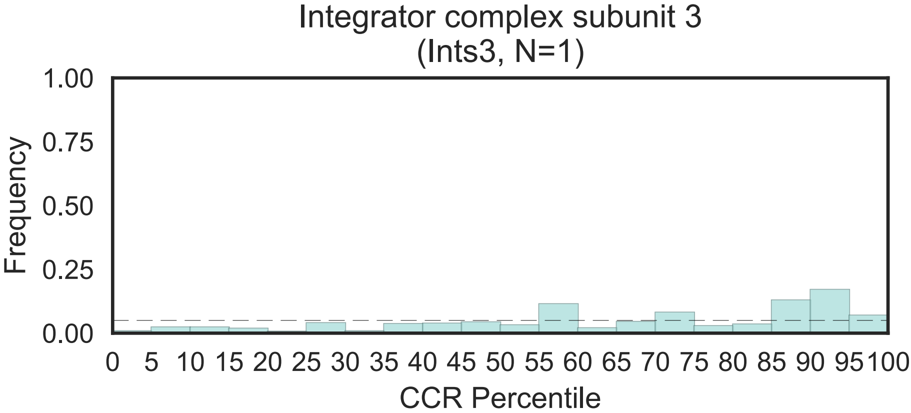

Integrin beta chain VWA domain
(Integrin_beta, N=8)
Fisher's OR: 0.955; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

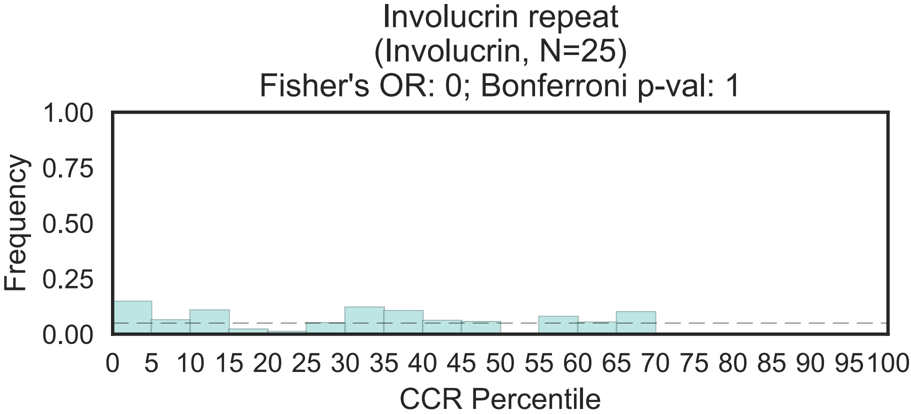
Interferon-alpha/beta receptor, fibronectin type III (Interfer-bind, N=15)
Fisher's OR: 0; Bonferroni p-val: 1

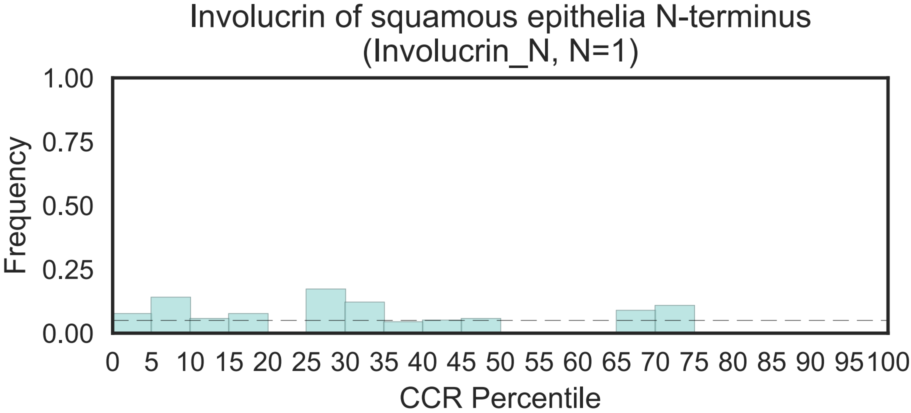


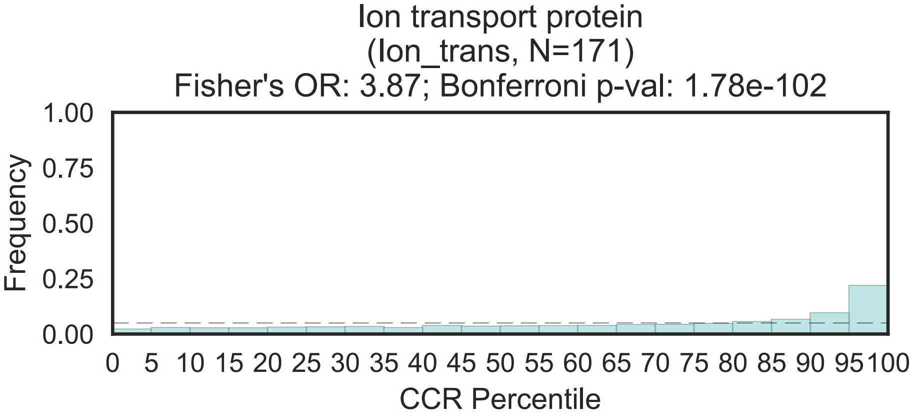
Interferon alpha/beta domain
(Interferon, N=17)
Fisher's OR: 0; Bonferroni p-val: 1

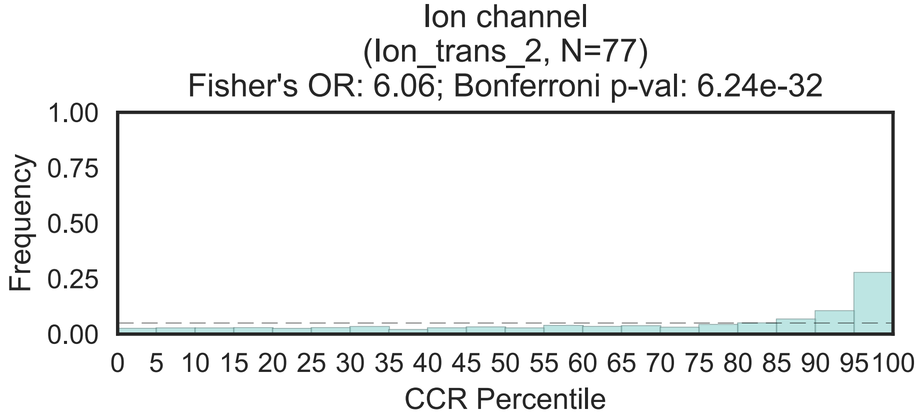


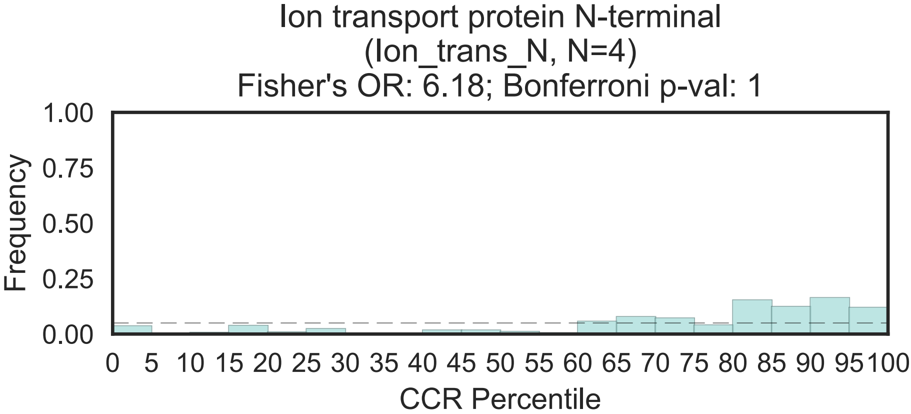

Integrator complex subunit 3
(Ints3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

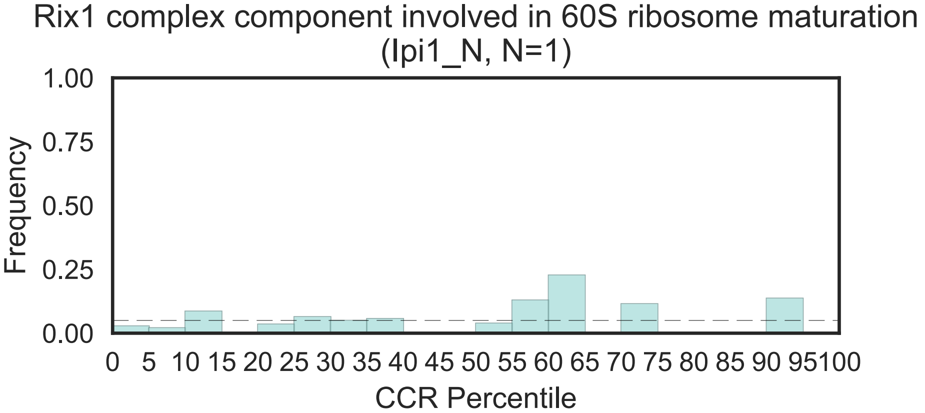

Involucrin repeat
(Involucrin, N=25)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Involucrin of squamous epithelia N-terminus
(Involucrin_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ion transport protein
(Ion_trans, N=171)
Fisher's OR: 3.87; Bonferroni p-val: 1.78e-102
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

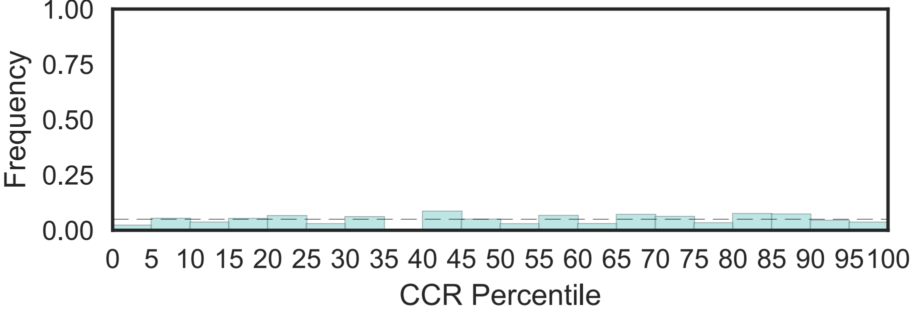

Ion channel
(Ion_trans_2, N=77)
Fisher's OR: 6.06; Bonferroni p-val: 6.24e-32
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

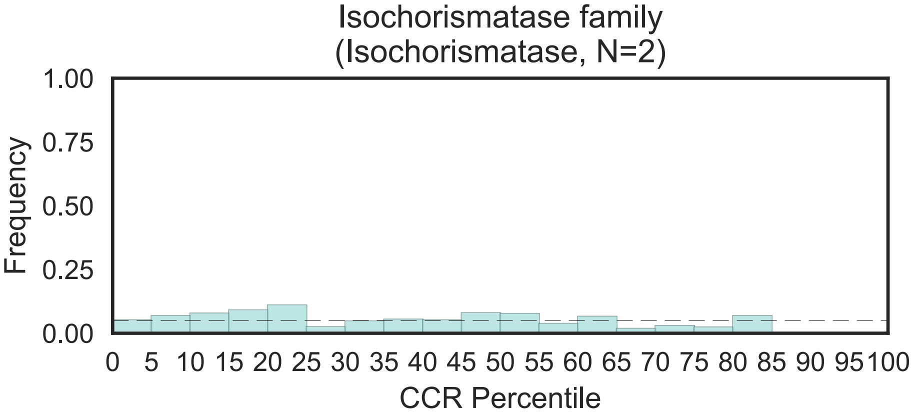

Ion transport protein N-terminal
(Ion_trans_N, N=4)
Fisher's OR: 6.18; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

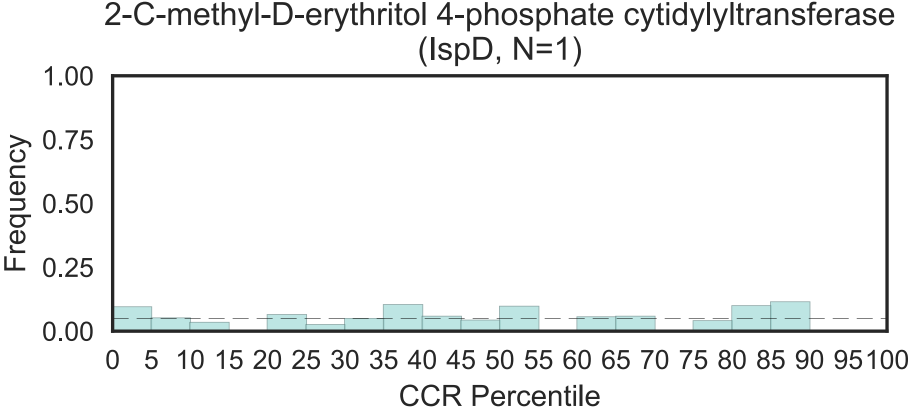


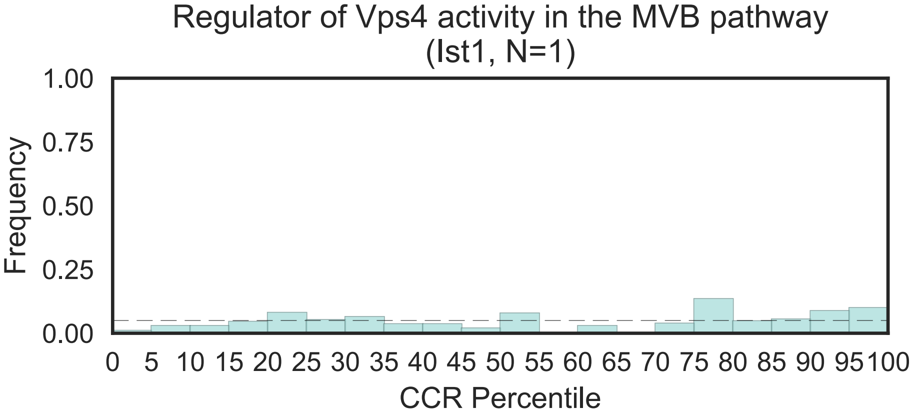
Rix1 complex component involved in 60S ribosome maturation
(Ipi1_N, N=1)

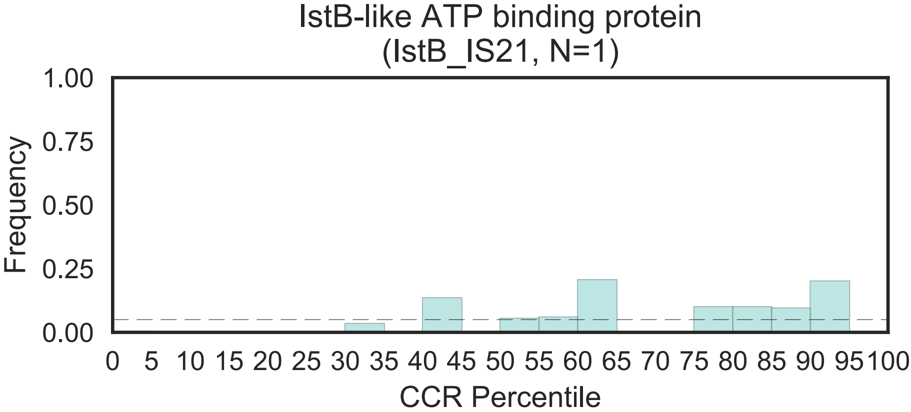
Isocitrate/isopropylmalate dehydrogenase
(Iso_dh, N=4)
Fisher's OR: 0.611; Bonferroni p-val: 1

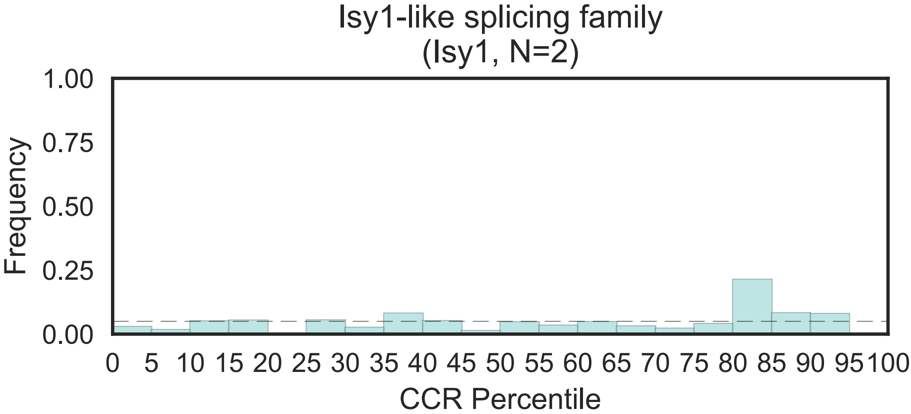


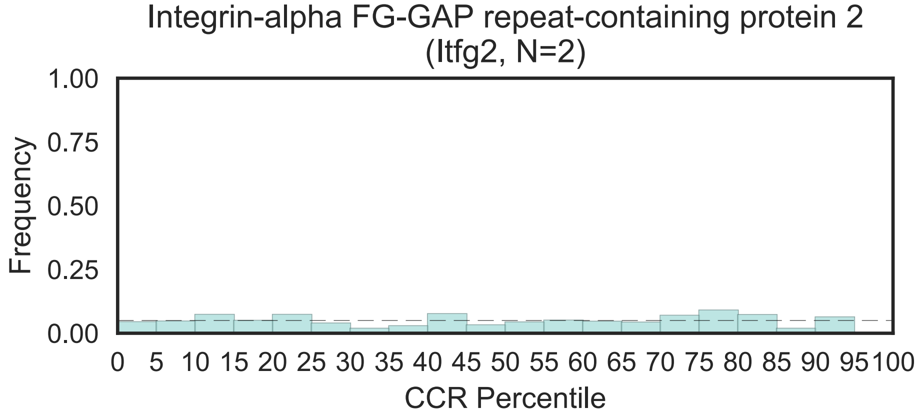

Isochorismatase family
(Isochorismatase, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

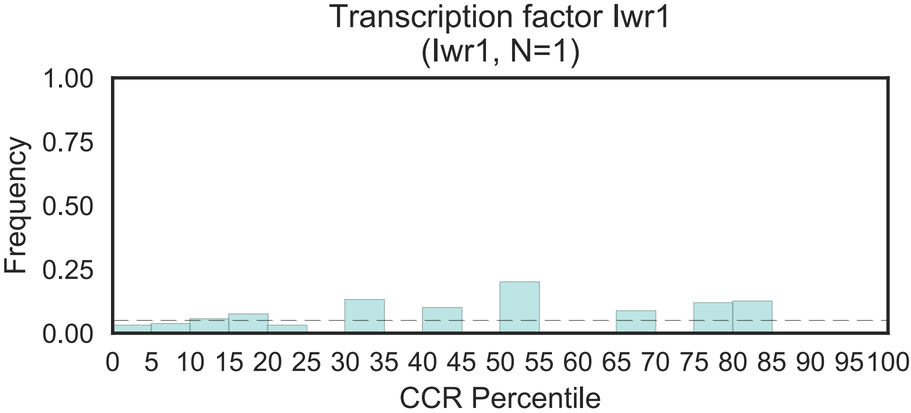

2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase
(IspD, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

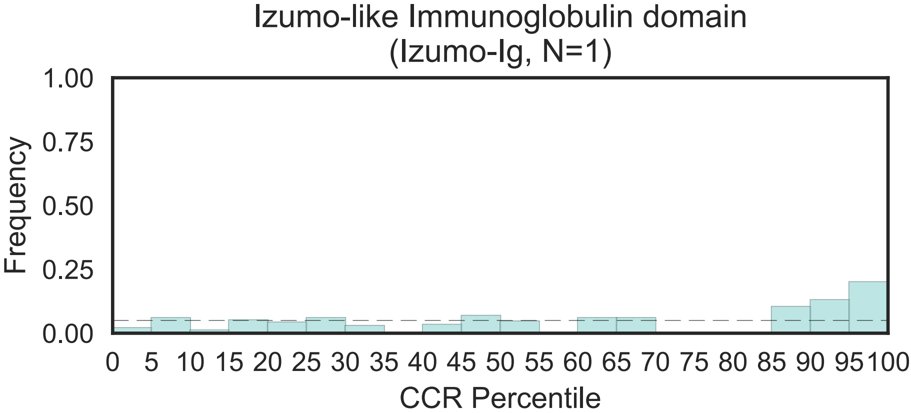

Regulator of Vps4 activity in the MVB pathway
(Ist1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


IstB-like ATP binding protein
(IstB_IS21, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Isy1-like splicing family
(Isy1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Integrin-alpha FG-GAP repeat-containing protein 2
(Itfg2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Transcription factor Iwr1
(Iwr1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


Izumo-like Immunoglobulin domain
(Izumo-Ig, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
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70
75
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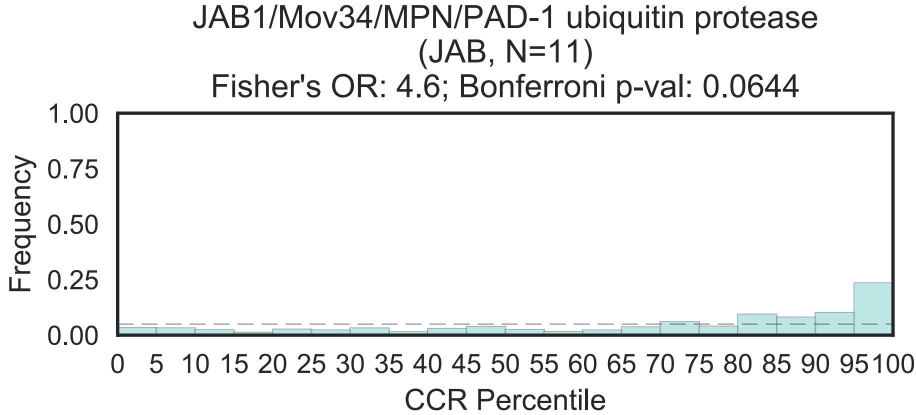
90
95
100
CCR Percentile


JAB1/Mov34/MPN/PAD-1 ubiquitin protease
(JAB, N=11)
Fisher's OR: 4.6; Bonferroni p-val: 0.0644
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
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75
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85
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95
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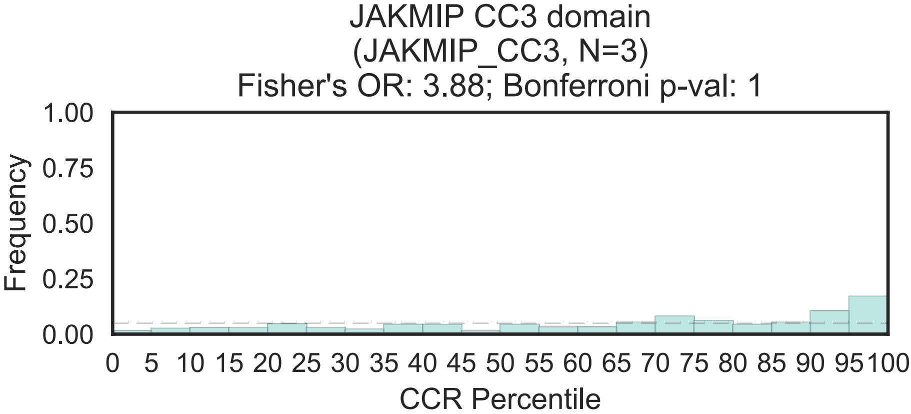
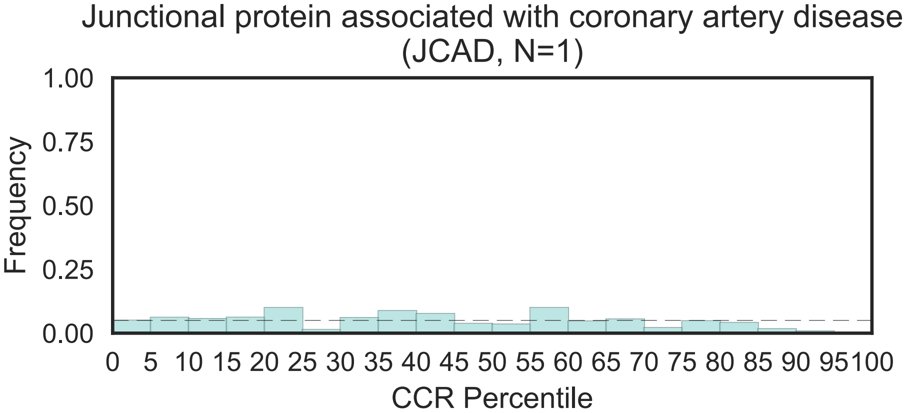
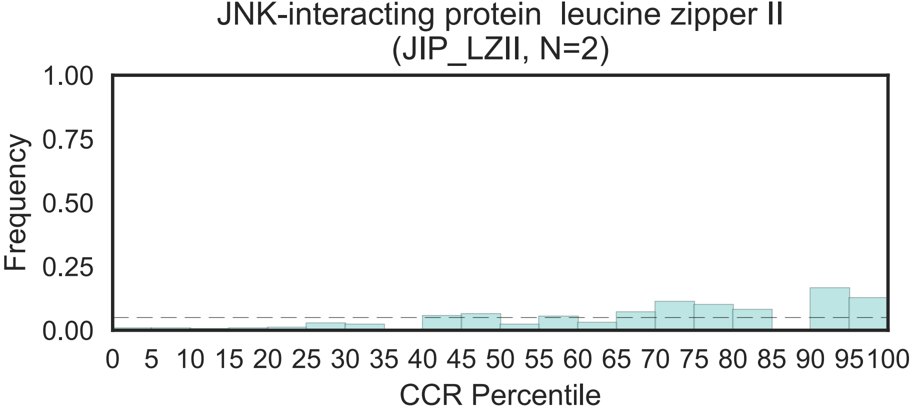
CCR Percentile


JAKMIP CC3 domain
(JAKMIP_CC3, N=3)
Fisher's OR: 3.88; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Junctional protein associated with coronary artery disease
(JCAD, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


JNK-interacting protein leucine zipper II
(JIP_LZII, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
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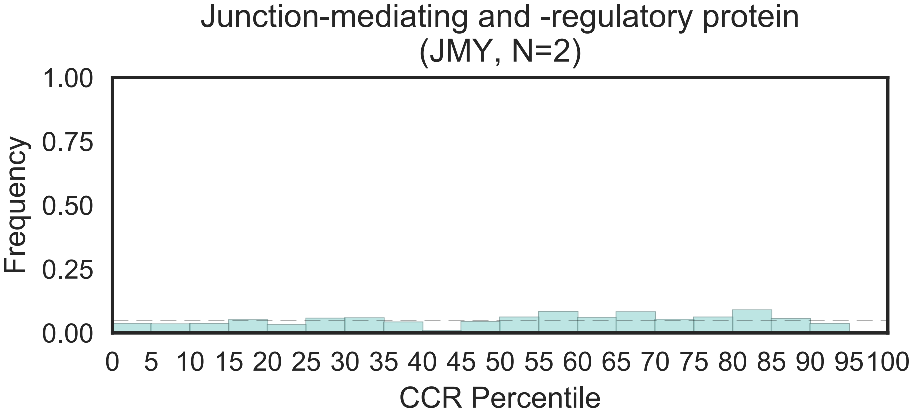
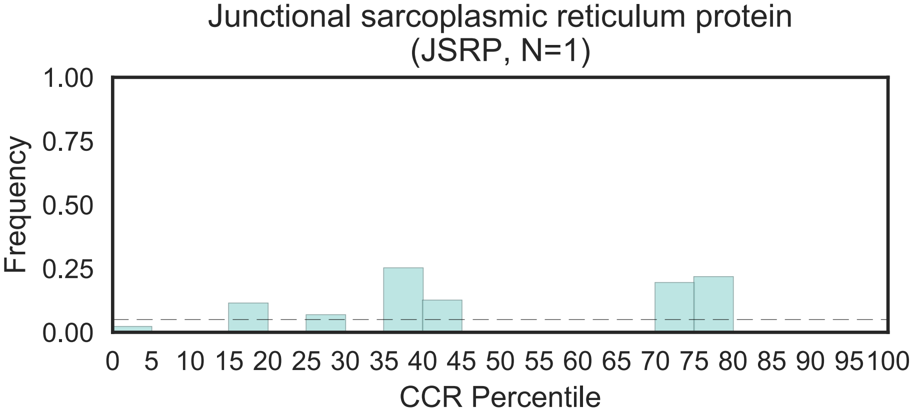
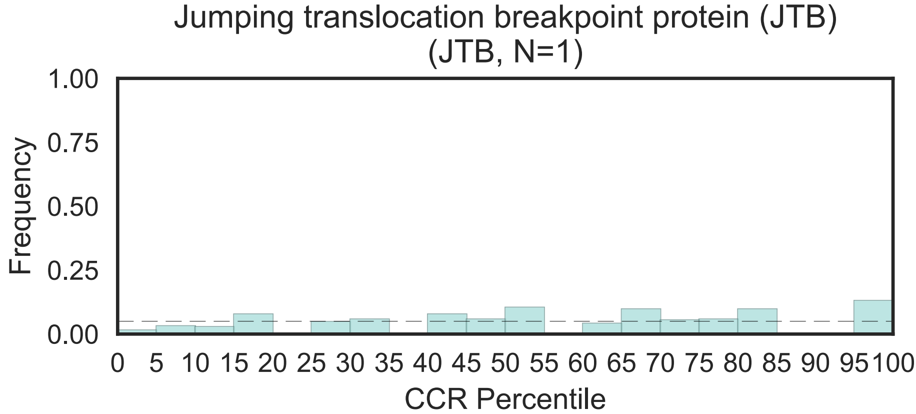
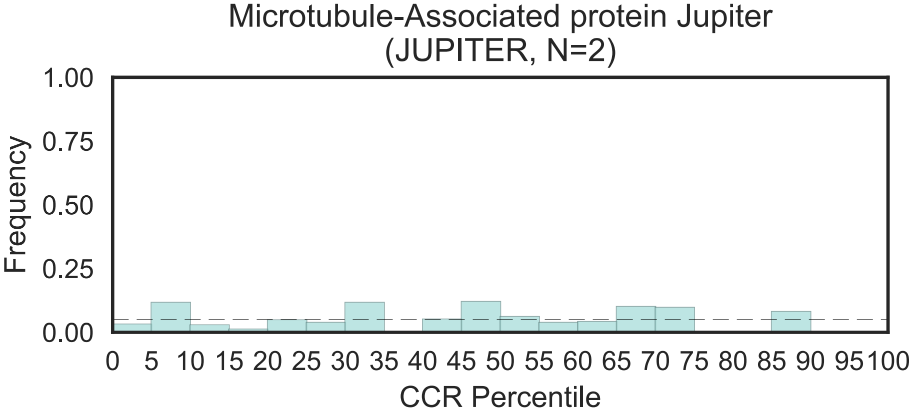
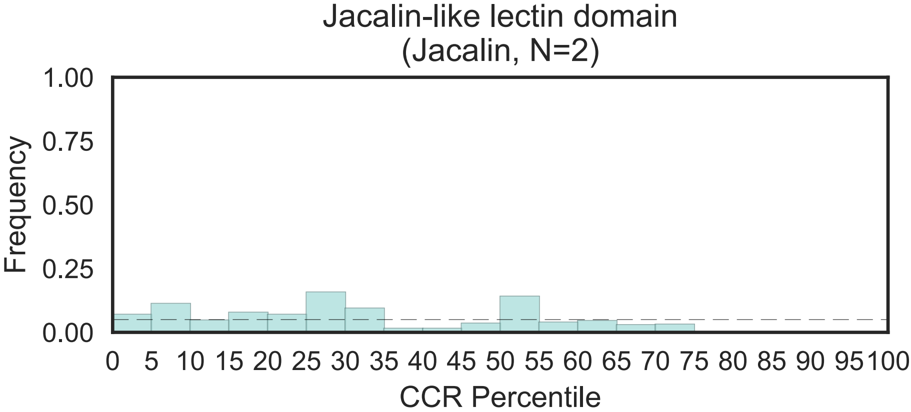
75
80
85
90
95
100
CCR Percentile

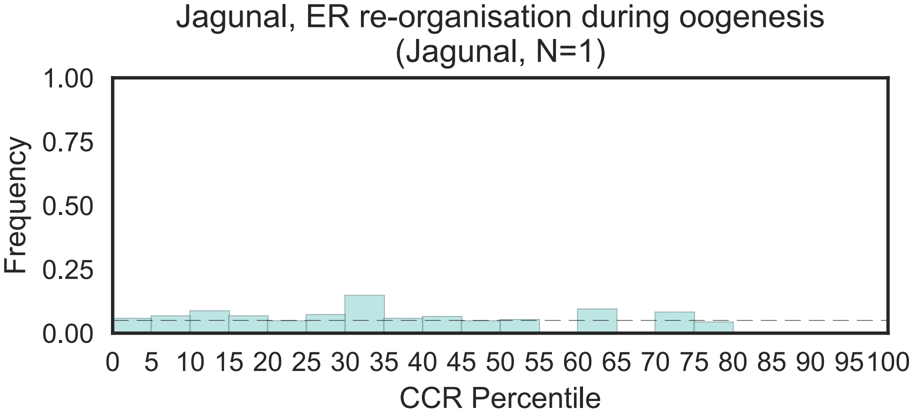

Junction-mediating and -regulatory protein
(JMY, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

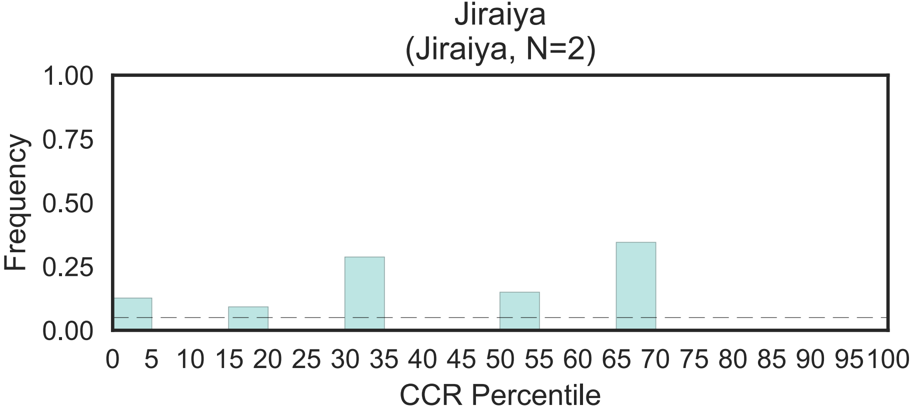

Junctional sarcoplasmic reticulum protein
(JSRP, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

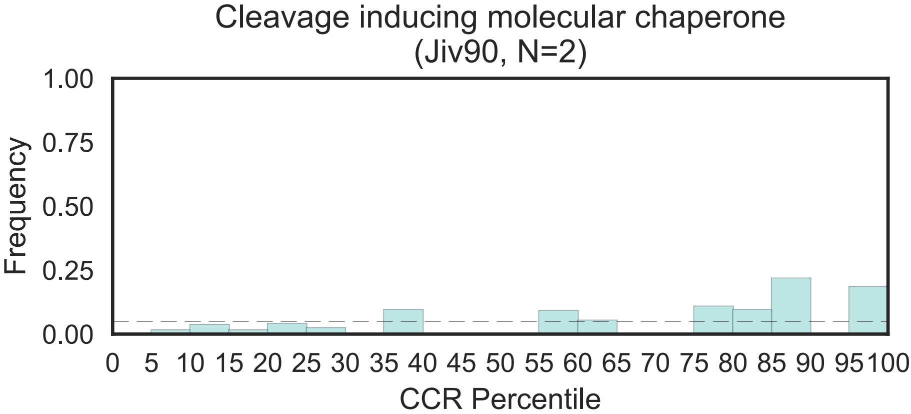

Jumping translocation breakpoint protein (JTB)
(JTB, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Microtubule-Associated protein Jupiter
(JUPITER, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

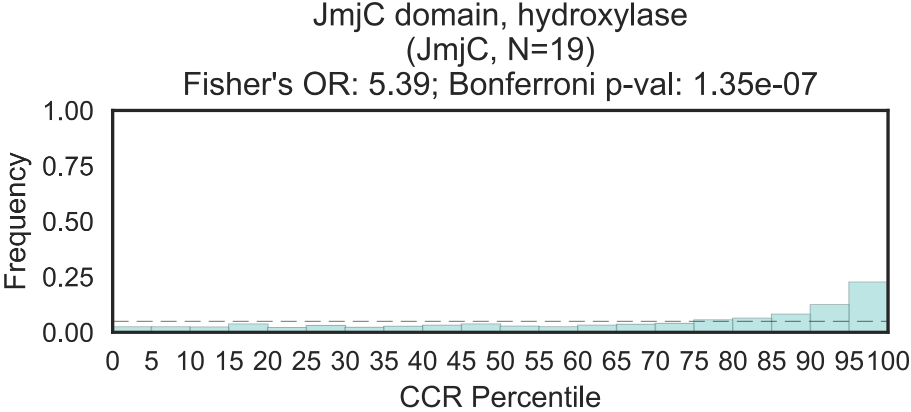

Jacalin-like lectin domain
(Jacalin, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

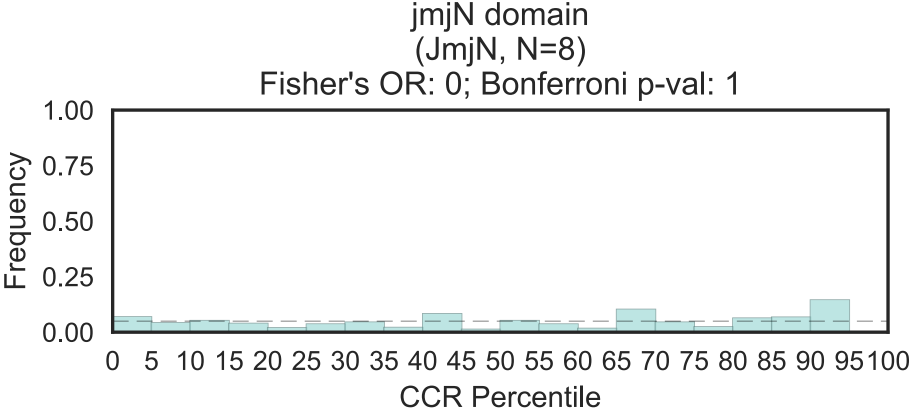

Jagunal, ER re-organisation during oogenesis
(Jagunal, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

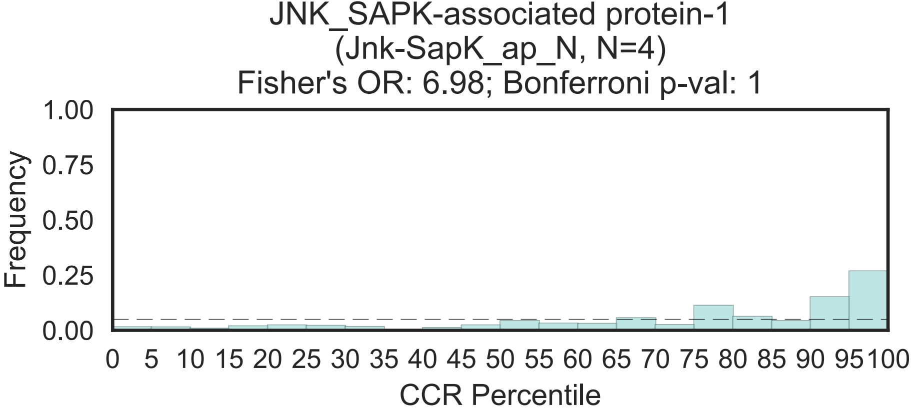

Jiraiya
(Jiraiya, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

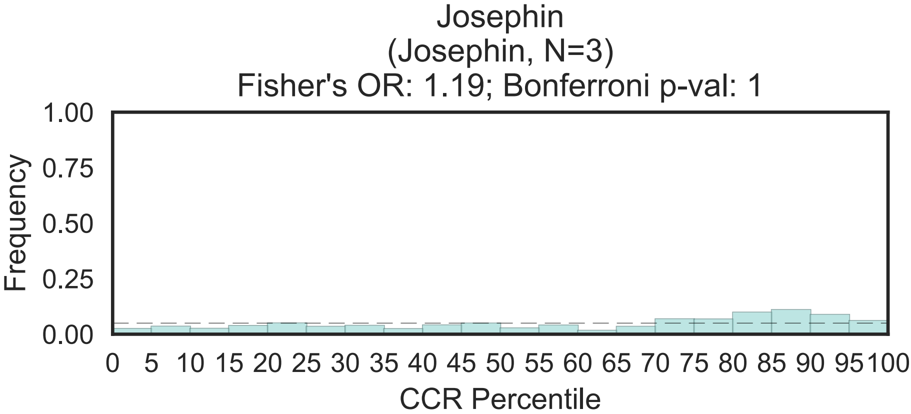


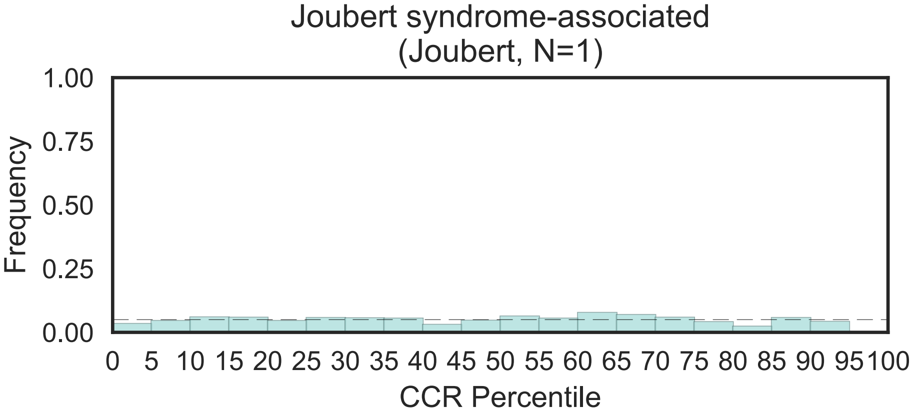
Cleavage inducing molecular chaperone
(Jiv90, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

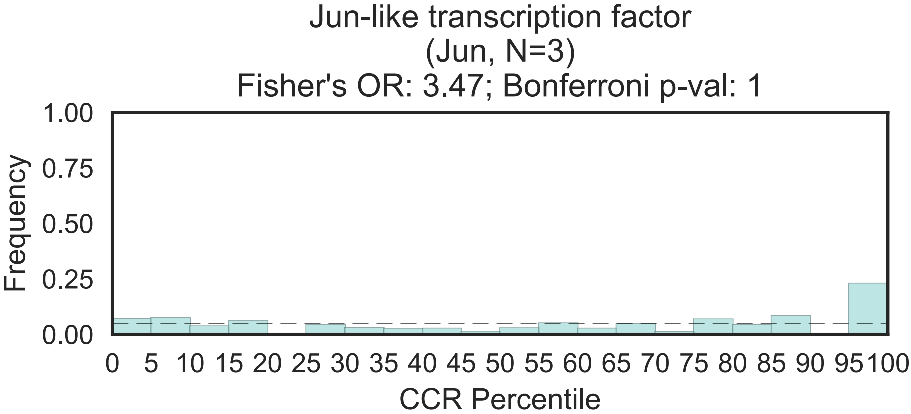

JmjC domain, hydroxylase
(JmjC, N=19)
Fisher's OR: 5.39; Bonferroni p-val: 1.35e-07
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

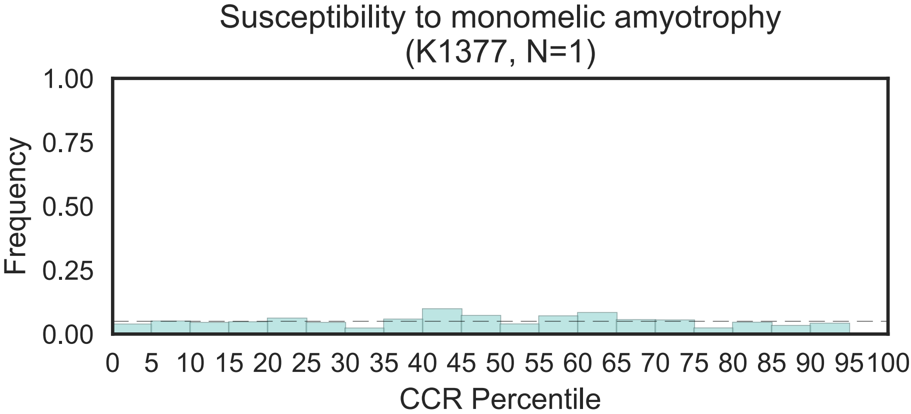

jmjN domain
(JmjN, N=8)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


JNK_SAPK-associated protein-1
(Jnk-SapK_ap_N, N=4)
Fisher's OR: 6.98; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

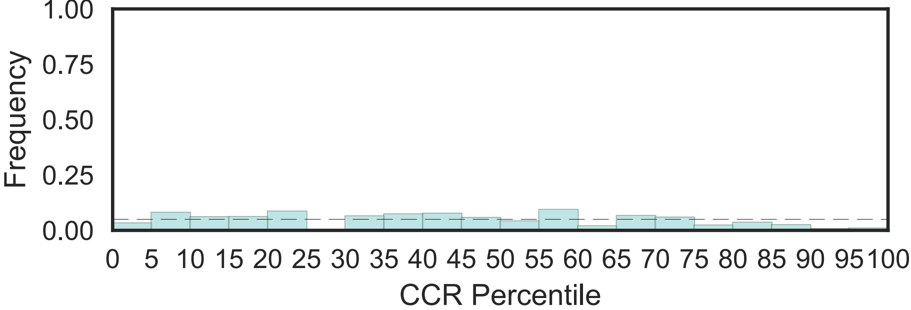

Josephin
(Josephin, N=3)
Fisher's OR: 1.19; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

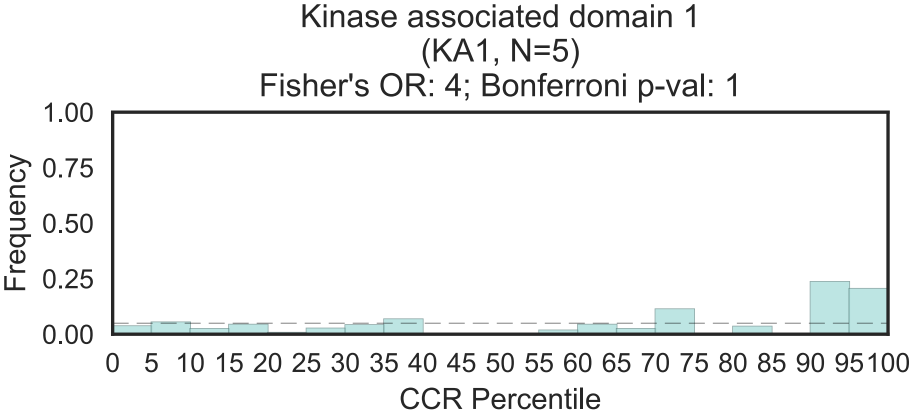

Joubert syndrome-associated
(Joubert, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

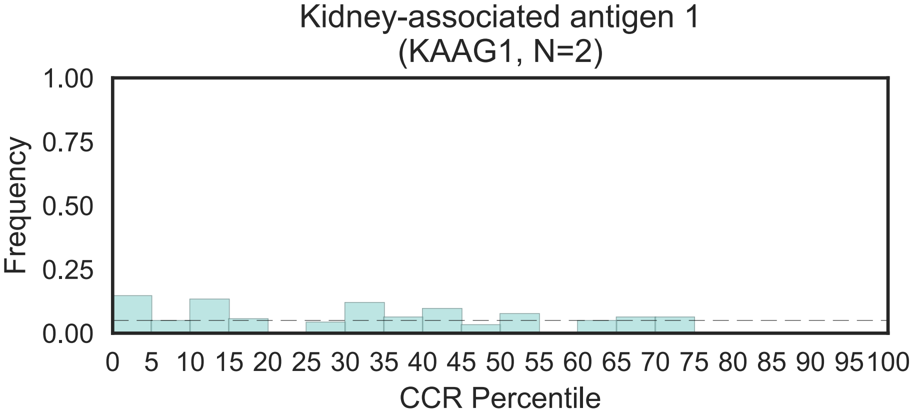

Jun-like transcription factor
(Jun, N=3)
Fisher's OR: 3.47; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

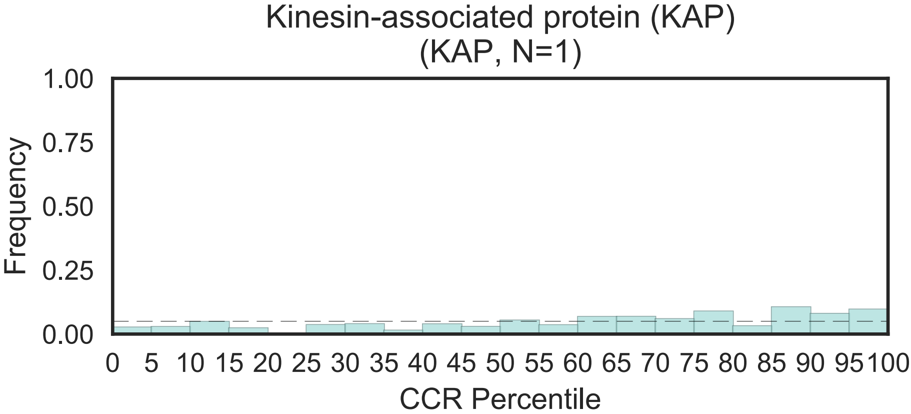

Susceptibility to monomelic amyotrophy
(K1377, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

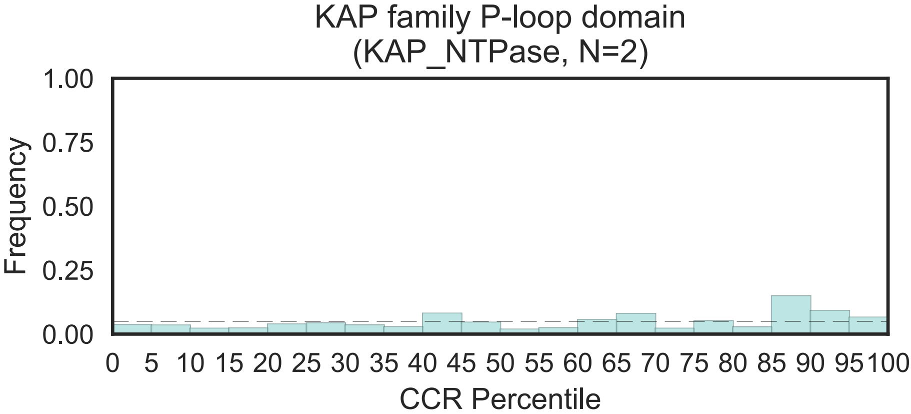
K167R (NUC007) repeat
(K167R, N=16)
Fisher's OR: 0.144; Bonferroni p-val: 1

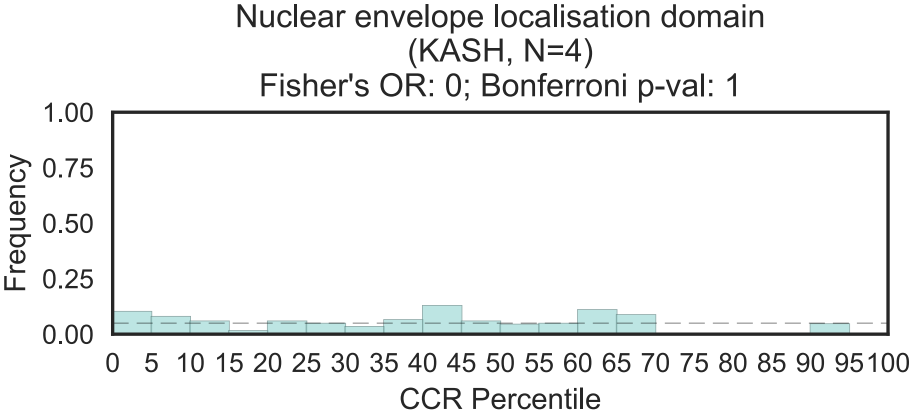


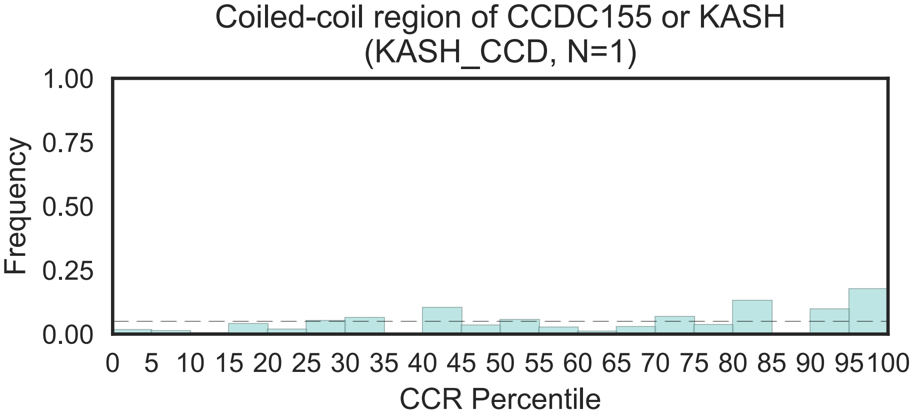

Kinase associated domain 1
(KA1, N=5)
Fisher's OR: 4; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

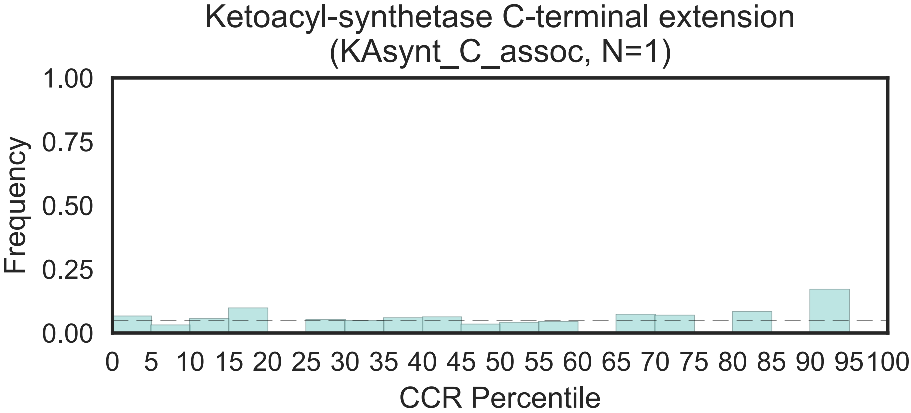

Kidney-associated antigen 1
(KAAG1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

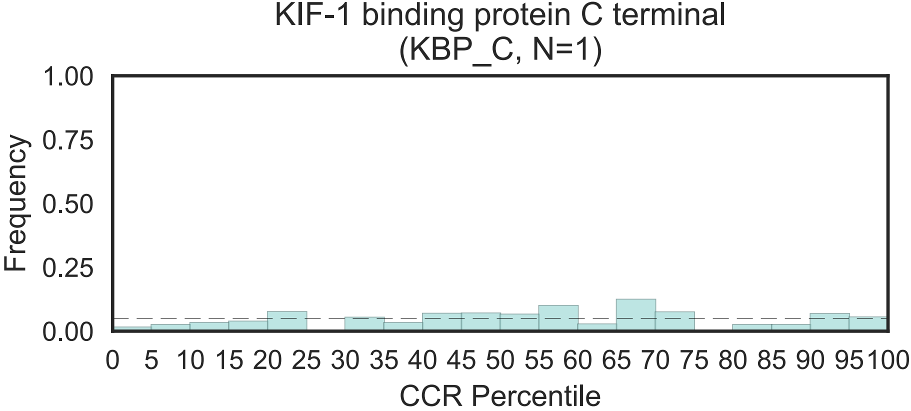

Kinesin-associated protein (KAP)
(KAP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

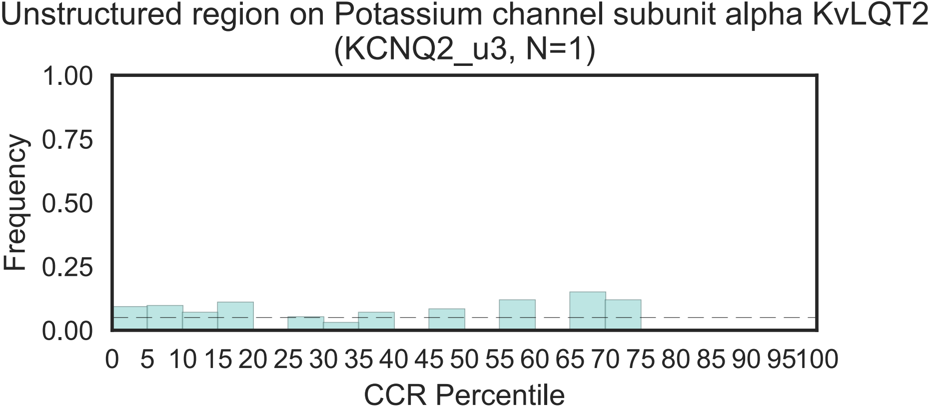

KAP family P-loop domain
(KAP_NTPase, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

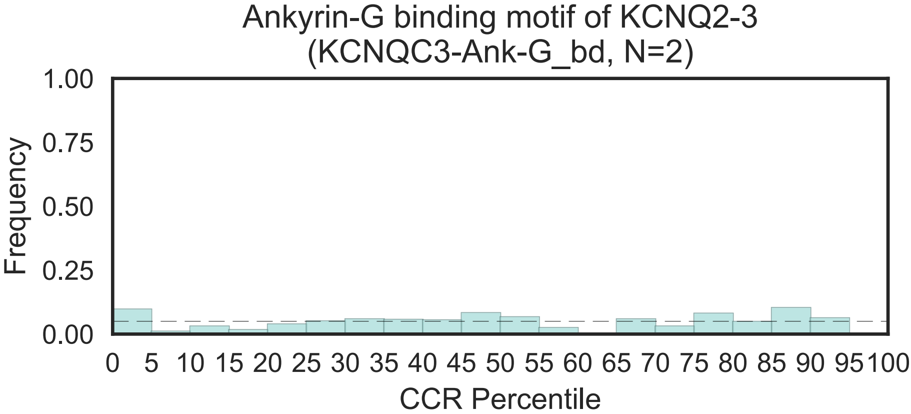

Nuclear envelope localisation domain
(KASH, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

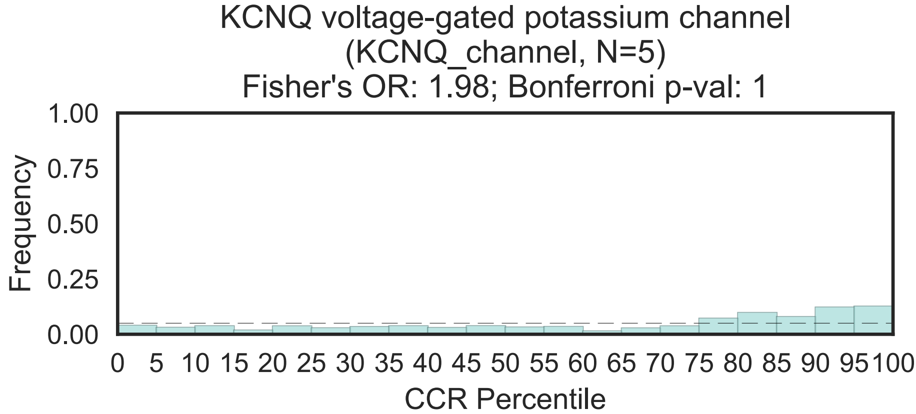

Coiled-coil region of CCDC155 or KASH
(KASH_CCD, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

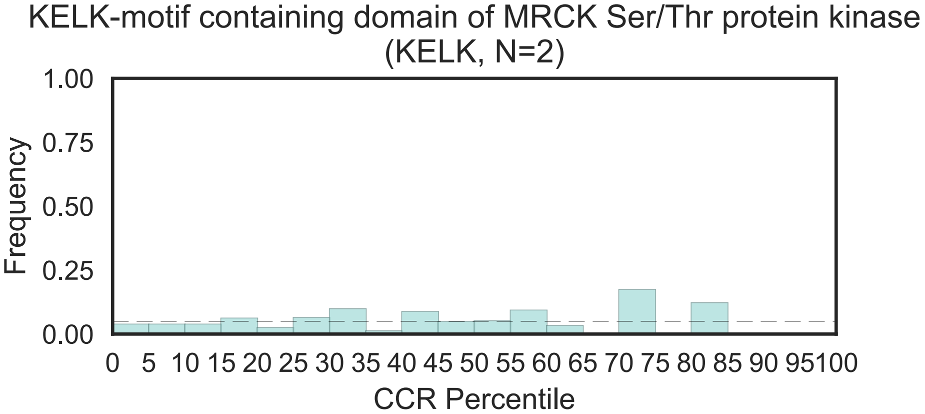

Ketoacyl-synthetase C-terminal extension
(KAsynt_C_assoc, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

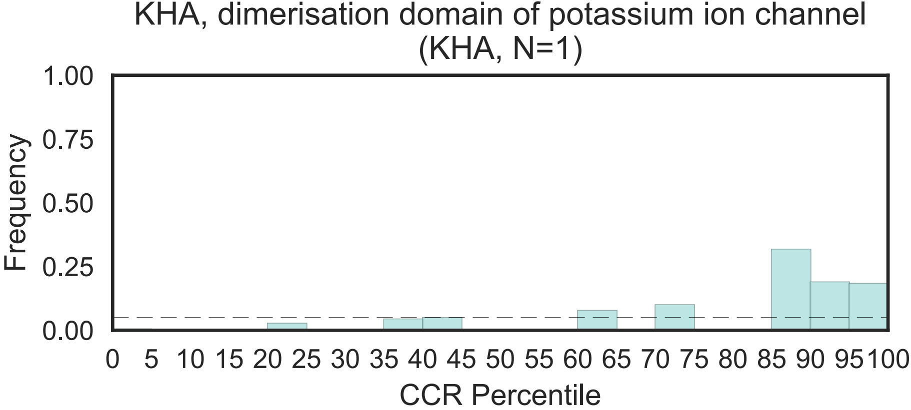

KIF-1 binding protein C terminal
(KBP_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

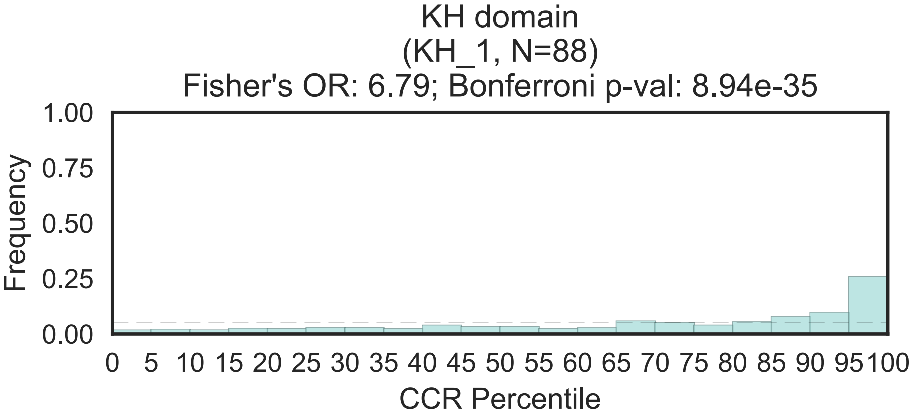

Unstructured region on Potassium channel subunit alpha KvLQT2
(KCNQ2_u3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

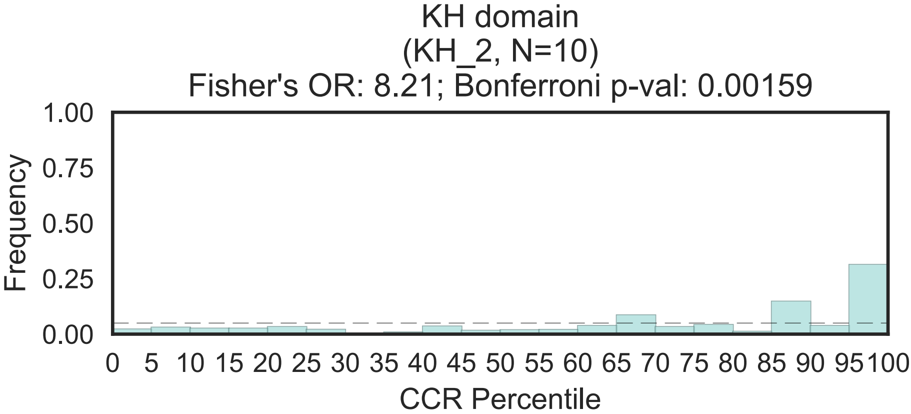

Ankyrin-G binding motif of KCNQ2-3
(KCNQC3-Ank-G_bd, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

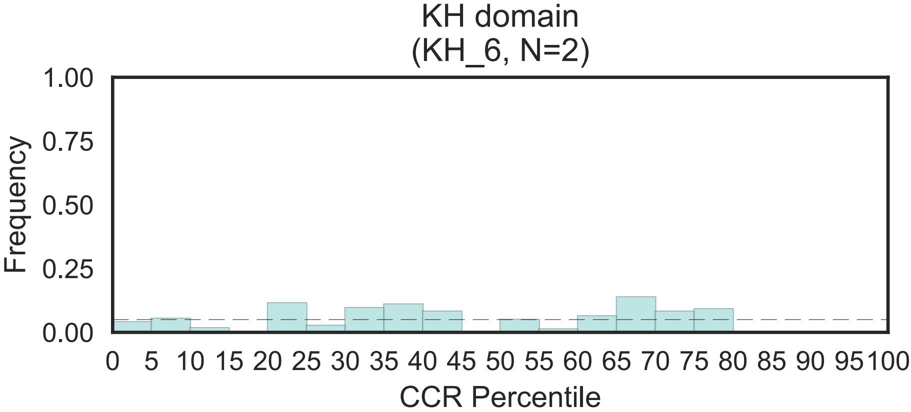

KCNQ voltage-gated potassium channel
(KCNQ_channel, N=5)
Fisher's OR: 1.98; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

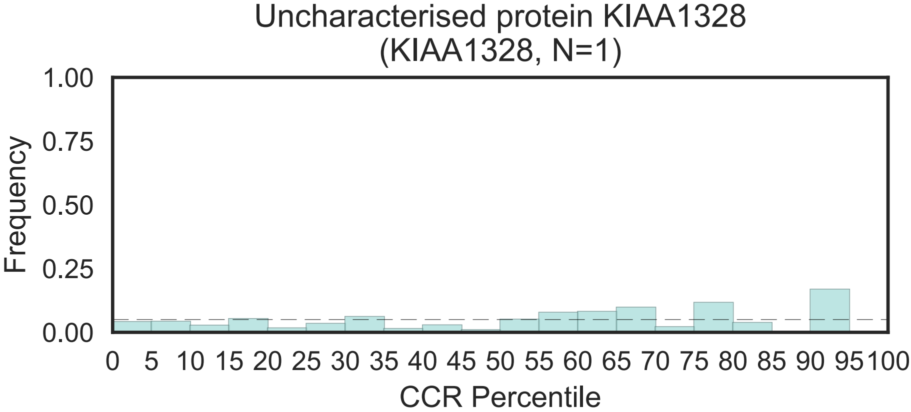

KELK-motif containing domain of MRCK Ser/Thr protein kinase
(KELK, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95100
CCR Percentile

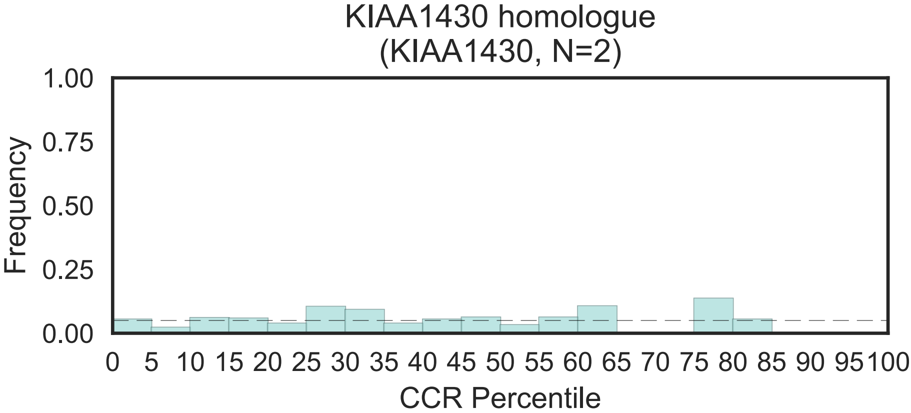

KHA, dimerisation domain of potassium ion channel
(KHA, N=1)

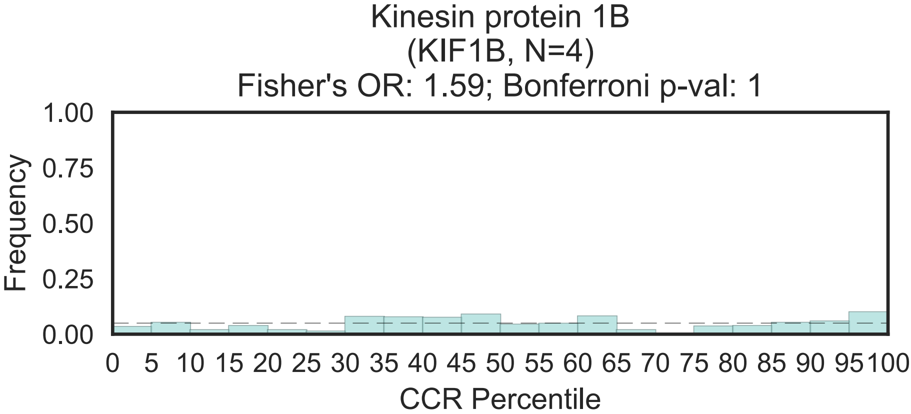

KH domain
(KH_1, N=88)
Fisher's OR: 6.79; Bonferroni p-val: 8.94e-35
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

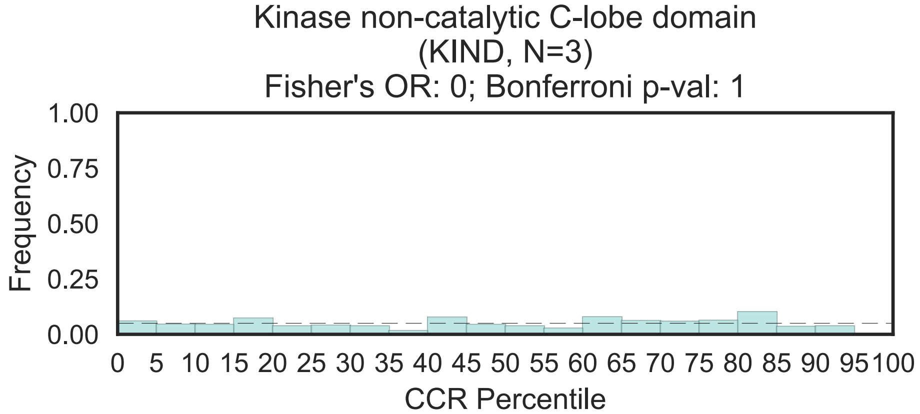

KH domain
(KH_2, N=10)
Fisher's OR: 8.21; Bonferroni p-val: 0.00159
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


KH domain
(KH_6, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

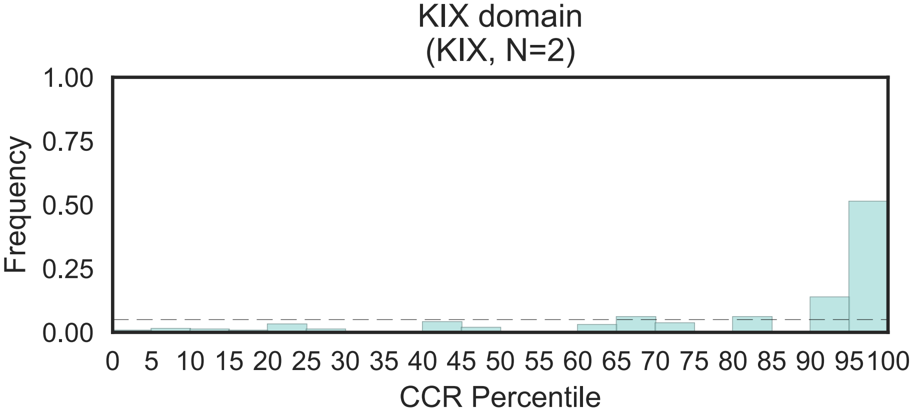

Uncharacterised protein KIAA1328
(KIAA1328, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

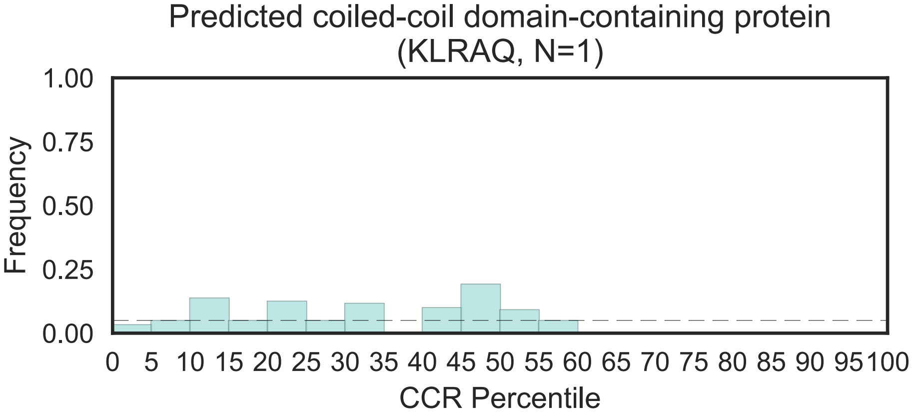

KIAA1430 homologue
(KIAA1430, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

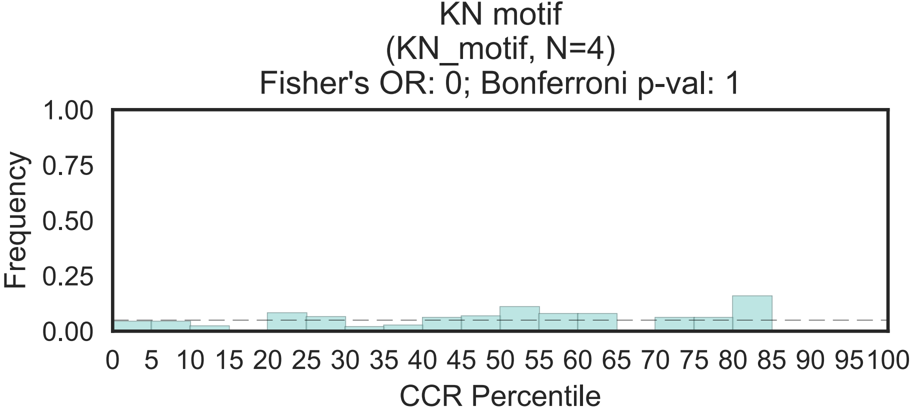

Kinesin protein 1B
(KIF1B, N=4)
Fisher's OR: 1.59; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

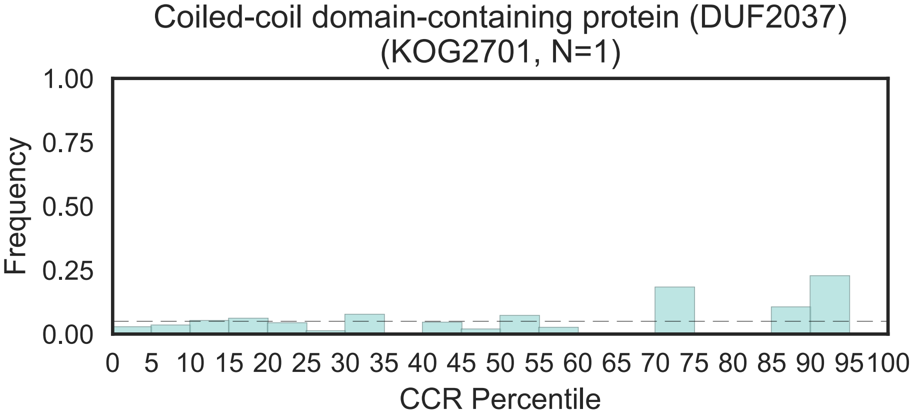


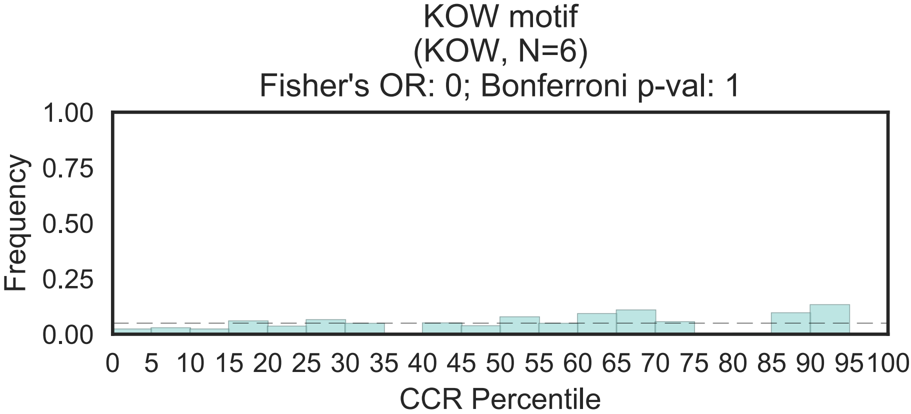
Kinase non-catalytic C-lobe domain
(KIND, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

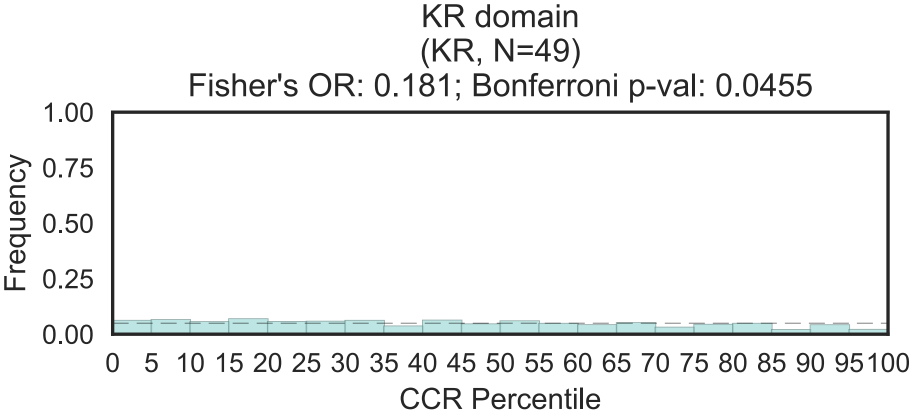

KIX domain
(KIX, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

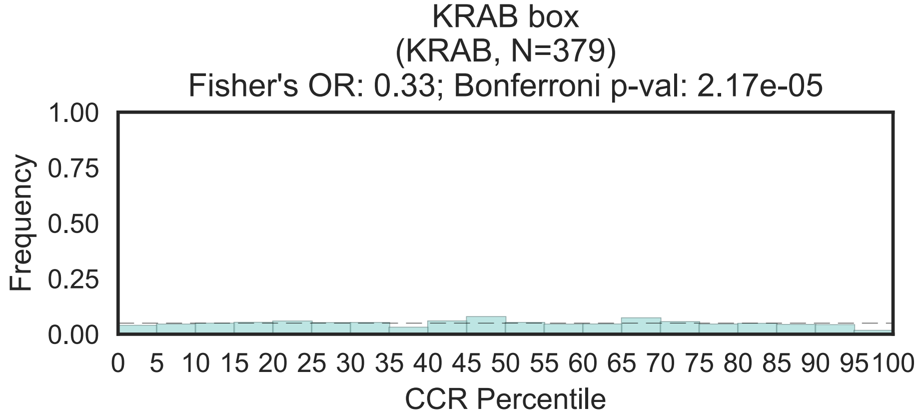

Predicted coiled-coil domain-containing protein
(KLRAQ, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

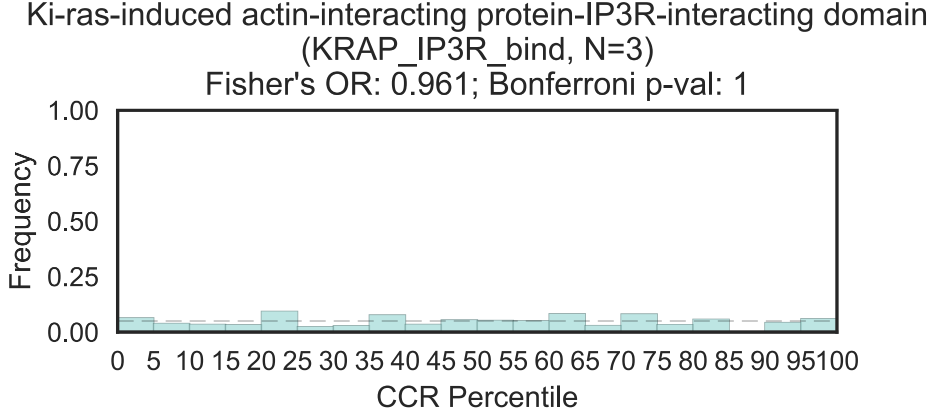

KN motif
(KN_motif, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

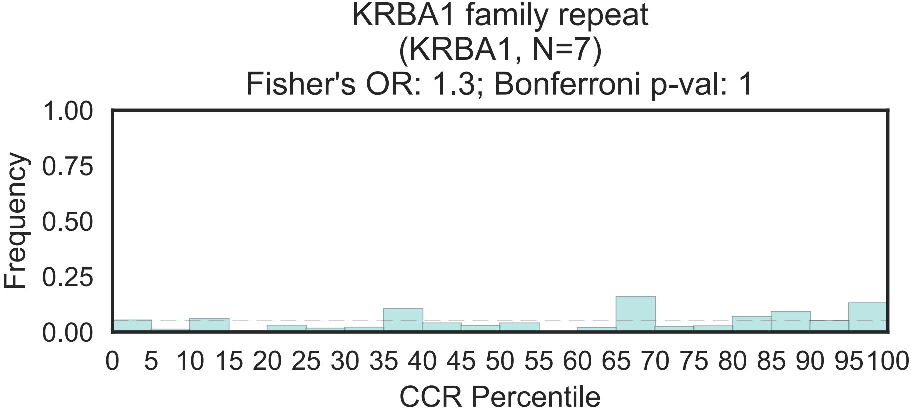

Coiled-coil domain-containing protein (DUF2037)
(KOG2701, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

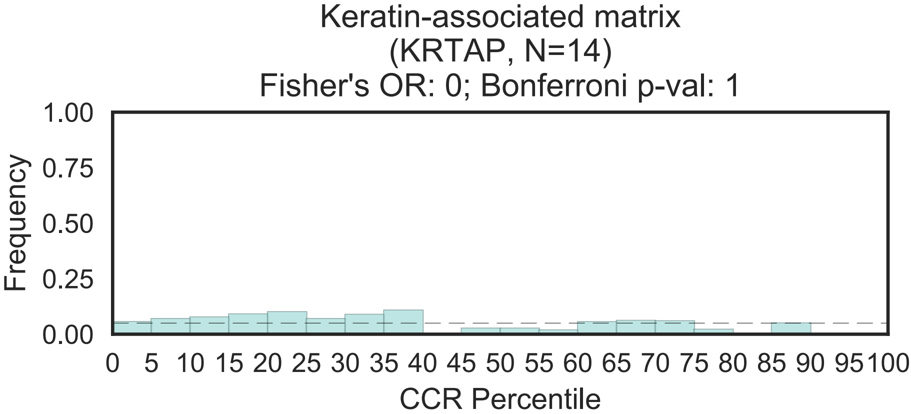

KOW motif
(KOW, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

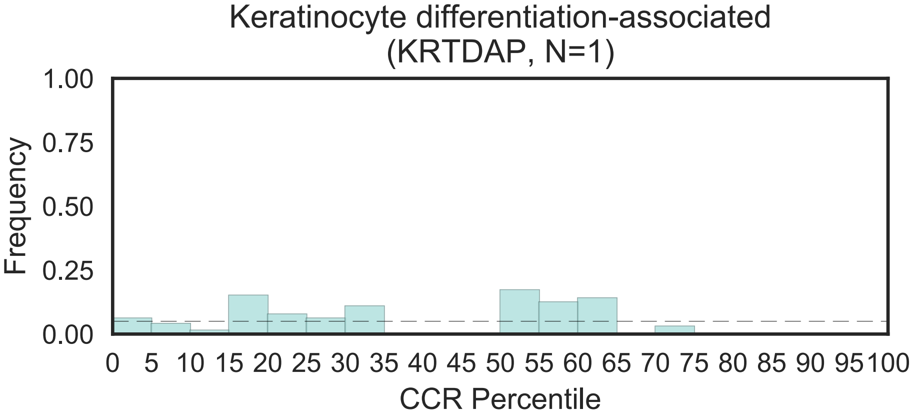

KR domain
(KR, N=49)
Fisher's OR: 0.181; Bonferroni p-val: 0.0455
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

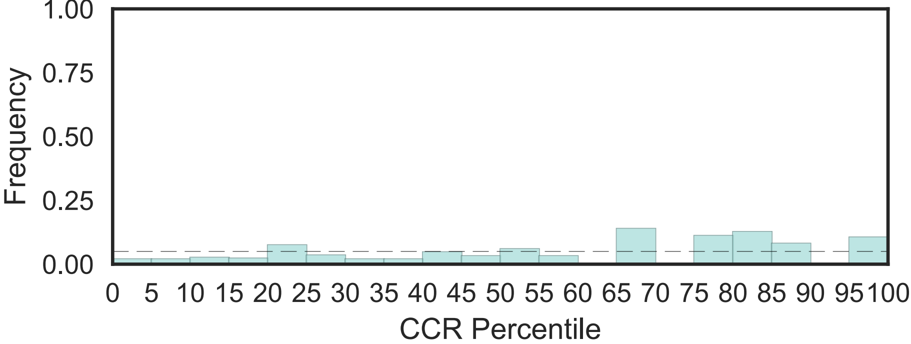

KRAB box
(KRAB, N=379)
Fisher's OR: 0.33; Bonferroni p-val: 2.17e-05
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ki-ras-induced actin-interacting protein-IP3R-interacting domain
(KRAP_IP3R_bind, N=3)
Fisher's OR: 0.961; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

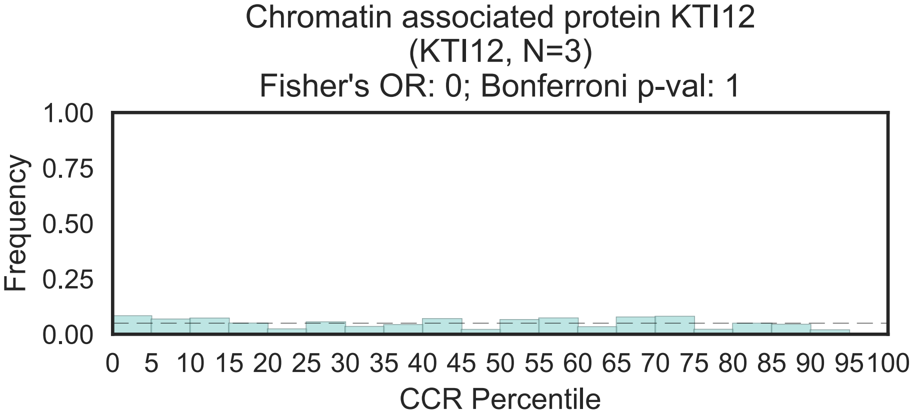

KRBA1 family repeat
(KRBA1, N=7)
Fisher's OR: 1.3; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

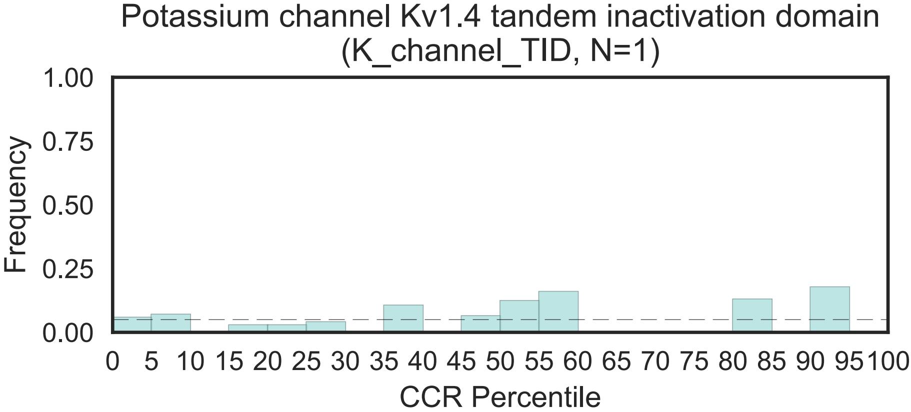

Keratin-associated matrix
(KRTAP, N=14)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

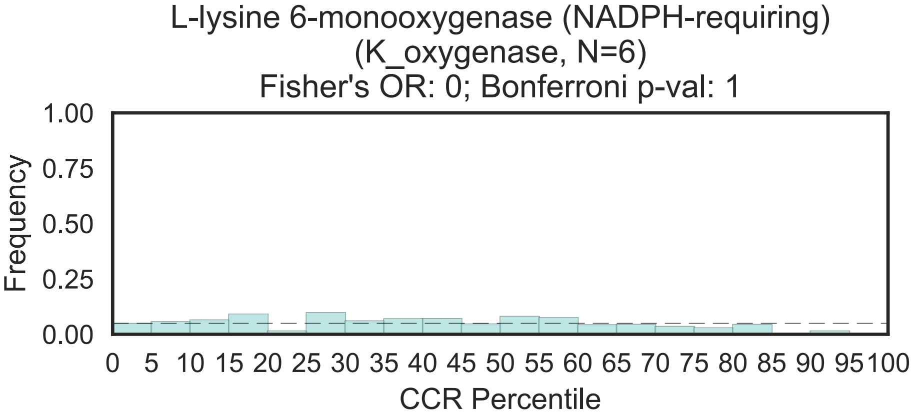

Keratinocyte differentiation-associated
(KRTDAP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

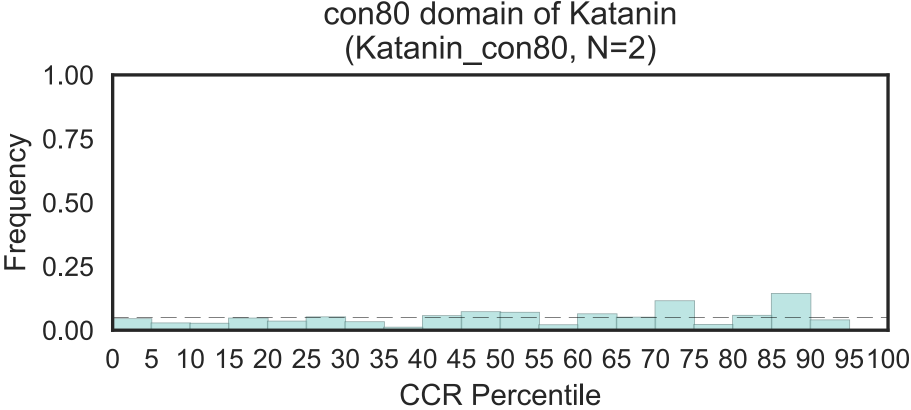


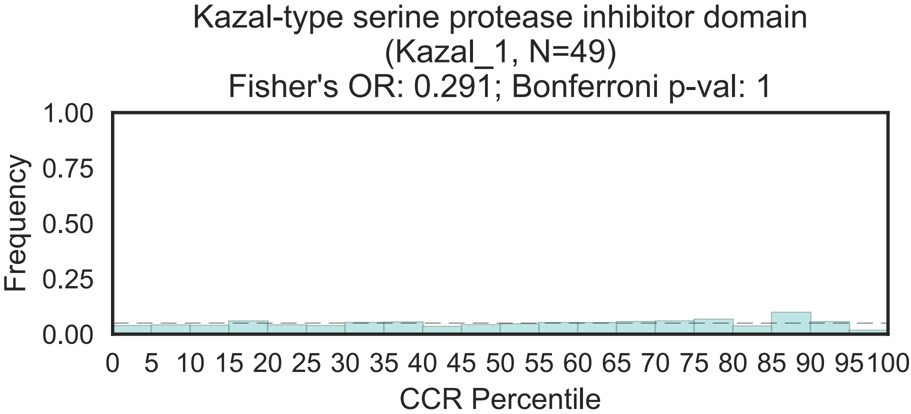
SAM like domain present in kinase suppressor RAS 1 (KSR1-SAM, N=1)

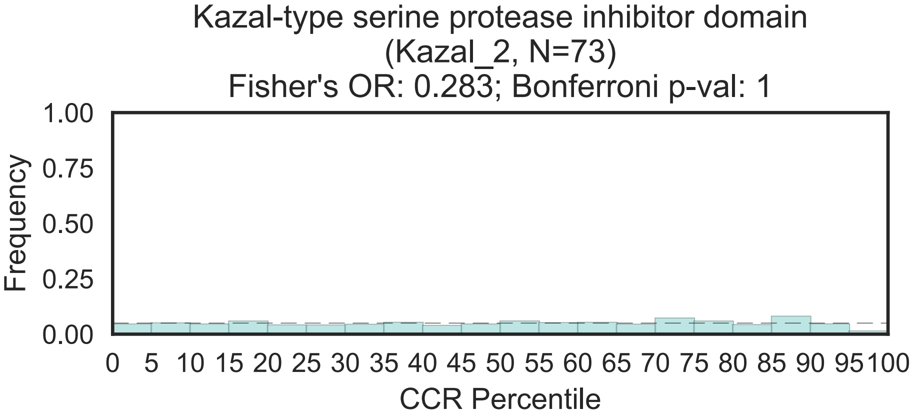

Chromatin associated protein KTI12
(KTI12, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Potassium channel Kv1.4 tandem inactivation domain
(K_channel_TID, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

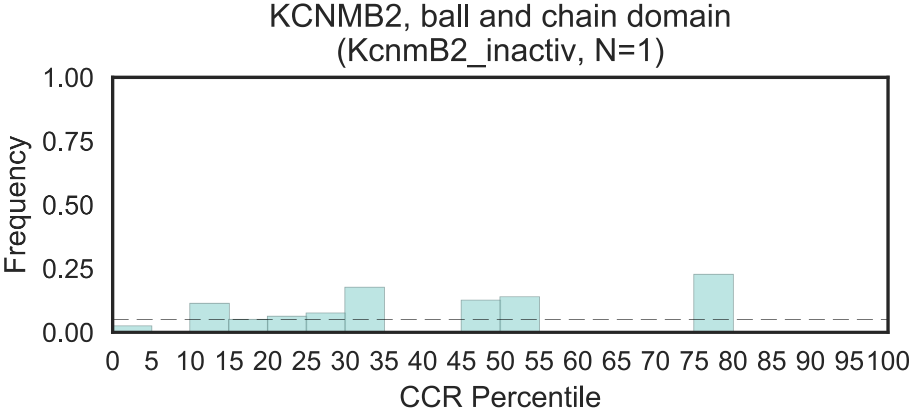

L-lysine 6-monooxygenase (NADPH-requiring)
(K_oxygenase, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

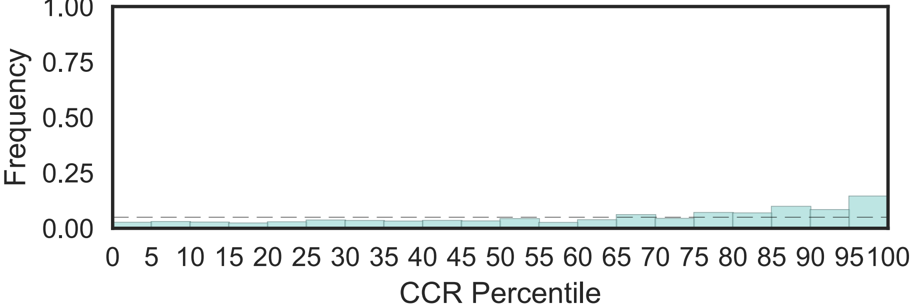

con80 domain of Katanin
(Katanin_con80, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Kazal-type serine protease inhibitor domain
(Kazal_1, N=49)
Fisher's OR: 0.291; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

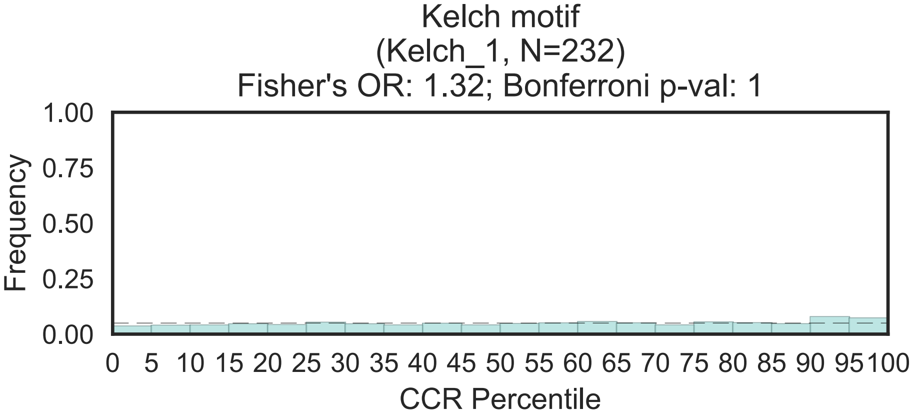


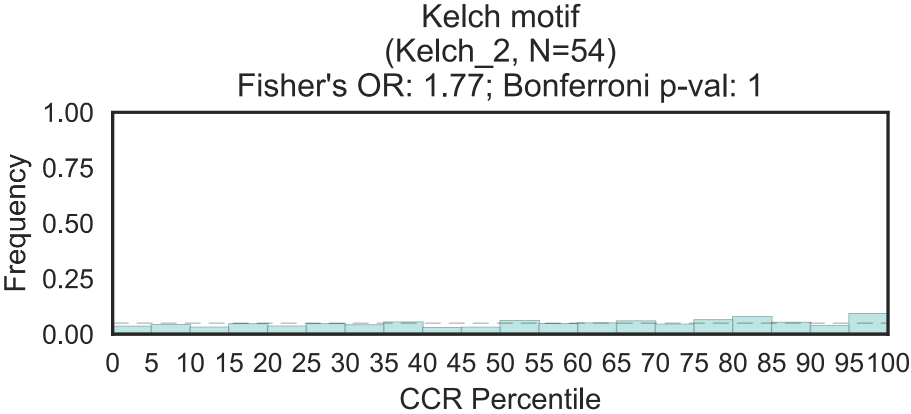
Kazal-type serine protease inhibitor domain
(Kazal_2, N=73)
Fisher's OR: 0.283; Bonferroni p-val: 1

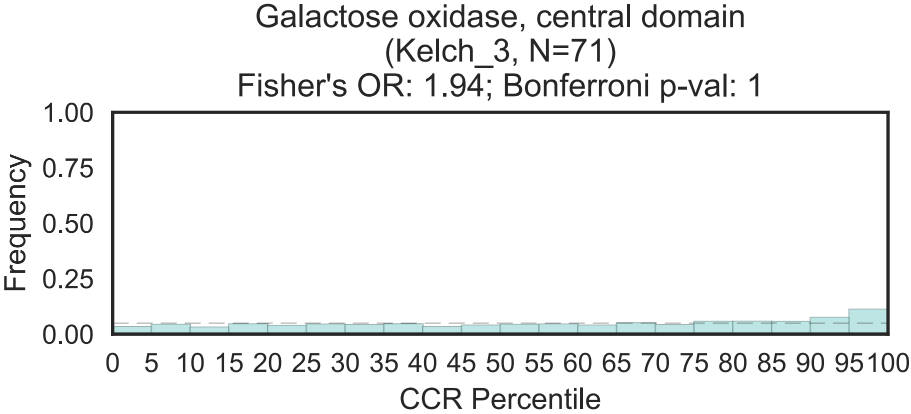

KCNMB2, ball and chain domain
(KcnmB2_inactiv, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

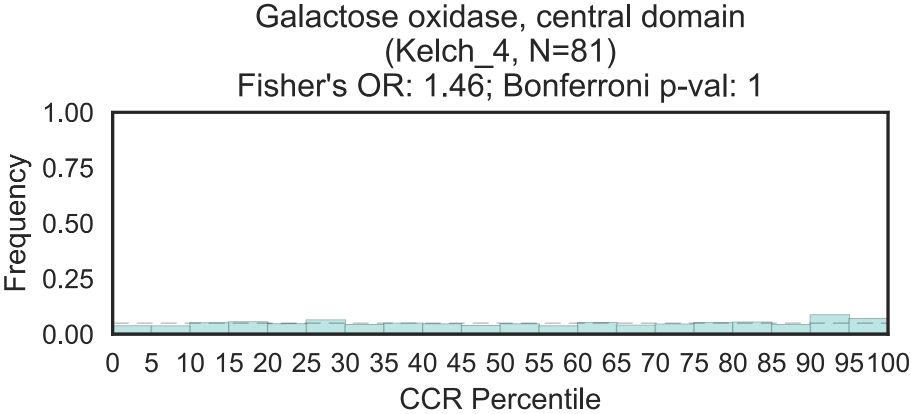


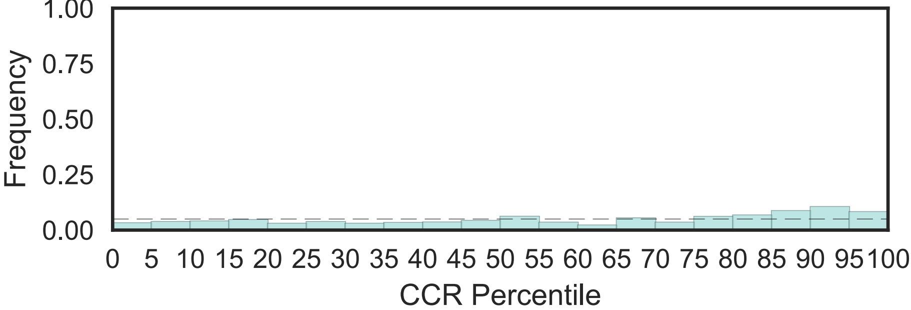
Lipopolysaccharide kinase (Kdo/WaaP) family
(Kdo, N=45)
Fisher's OR: 2.82; Bonferroni p-val: 0.00285


Kelch motif
(Kelch_1, N=232)
Fisher's OR: 1.32; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

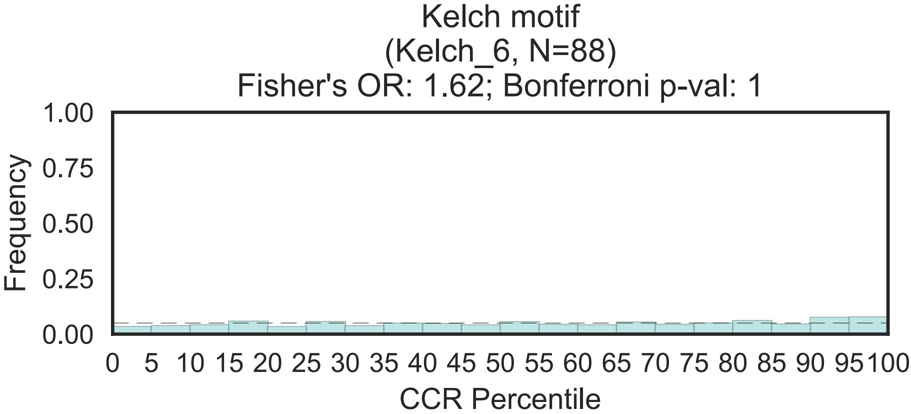

Kelch motif
(Kelch_2, N=54)
Fisher's OR: 1.77; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

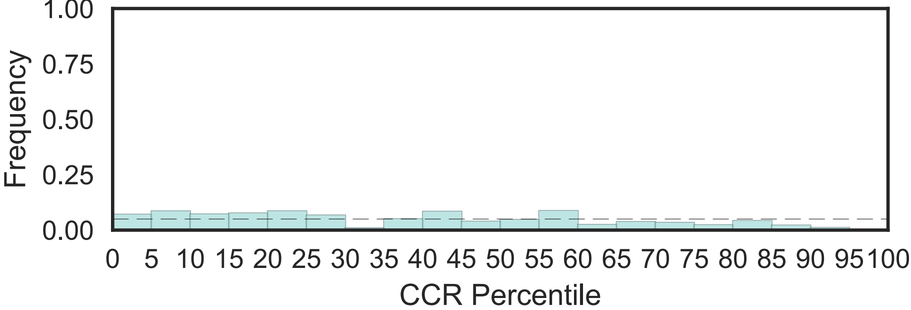

Galactose oxidase, central domain
(Kelch_3, N=71)
Fisher's OR: 1.94; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Galactose oxidase, central domain
(Kelch_4, N=81)
Fisher's OR: 1.46; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

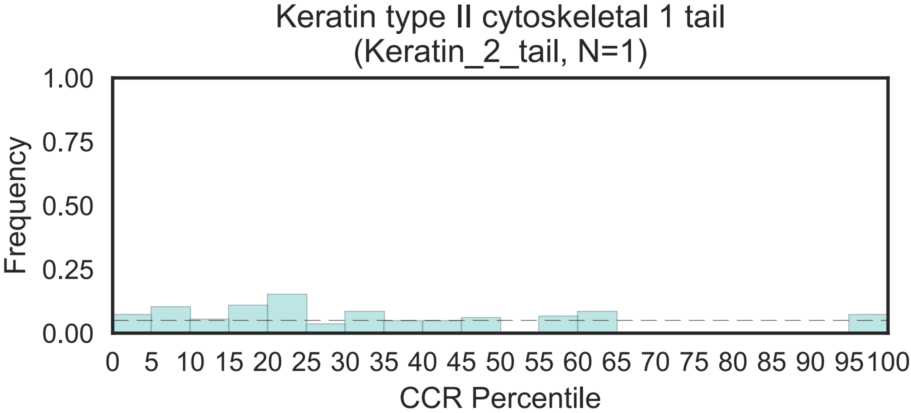


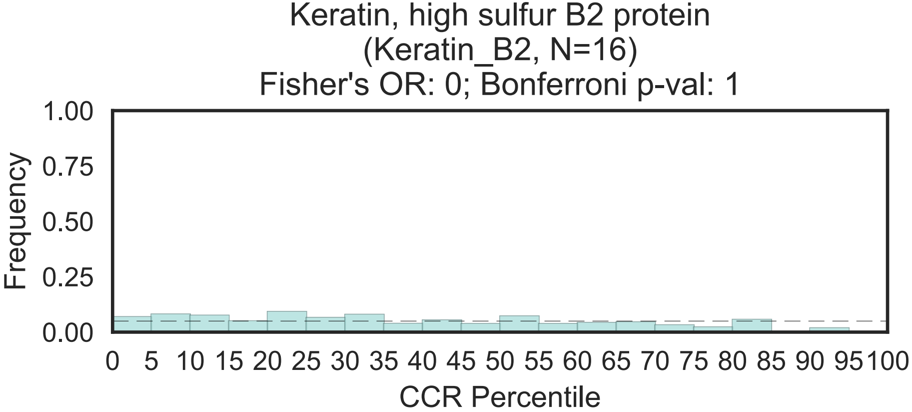
Kelch motif
(Kelch_5, N=29)
Fisher's OR: 2.05; Bonferroni p-val: 1

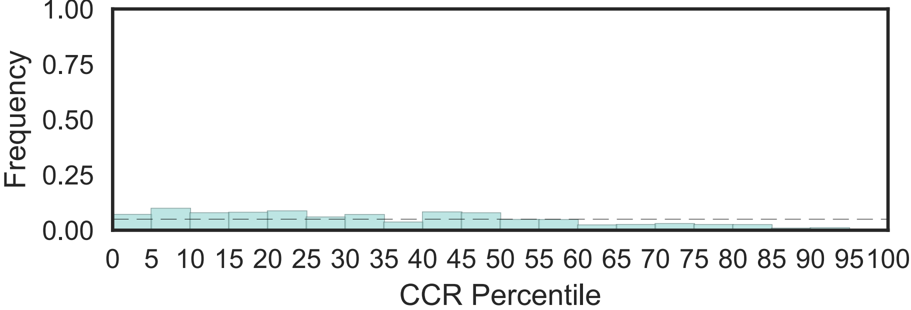

Kelch motif
(Kelch_6, N=88)
Fisher's OR: 1.62; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



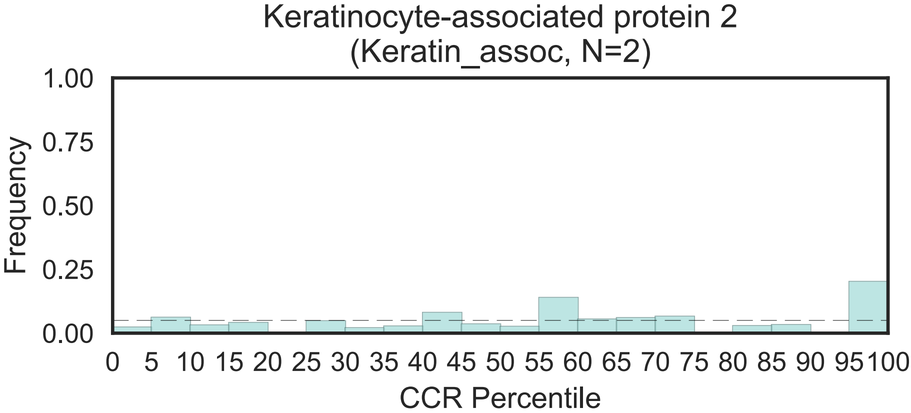
Keratin type II head
(Keratin_2_head, N=26)
Fisher's OR: 0.108; Bonferroni p-val: 1

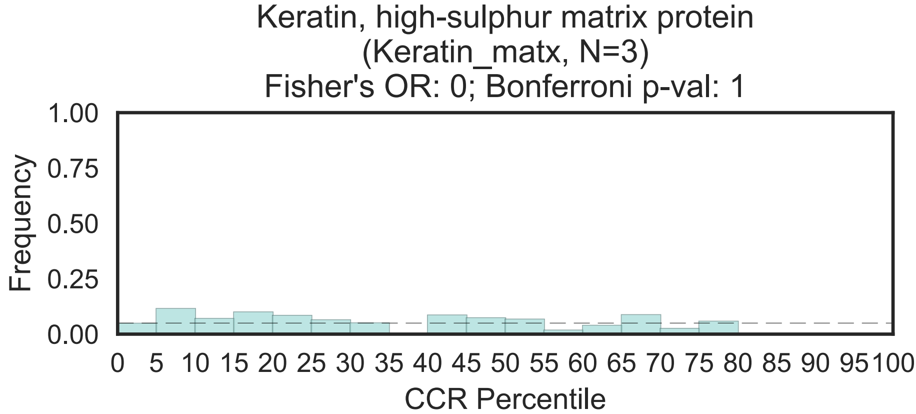

Keratin type II cytoskeletal 1 tail
(Keratin_2_tail, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

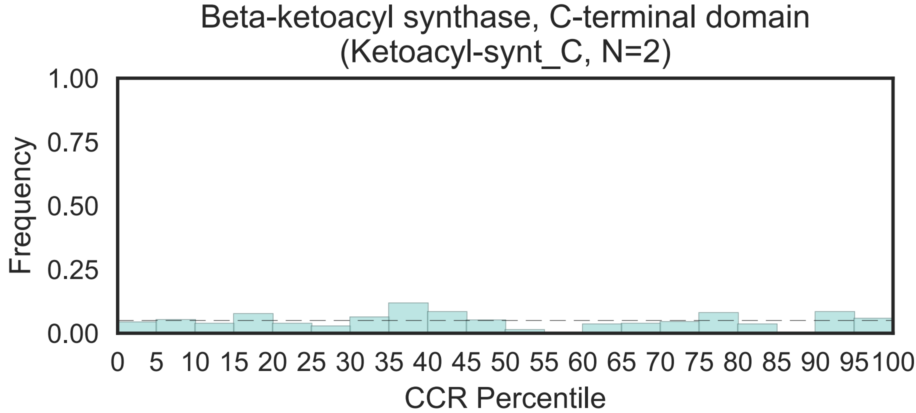

Keratin, high sulfur B2 protein
(Keratin_B2, N=16)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



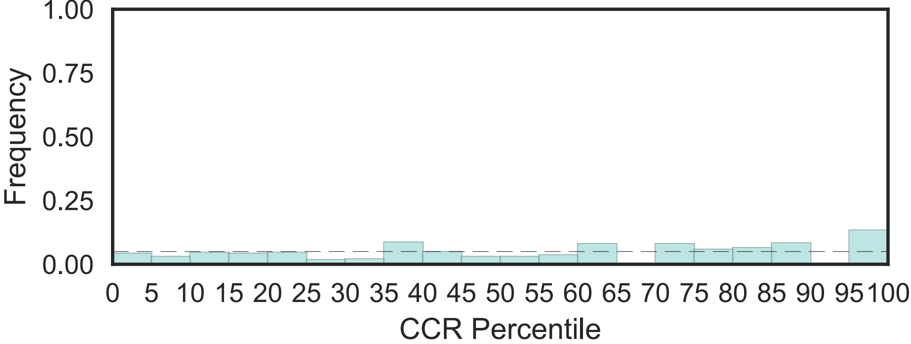
Keratin, high sulfur B2 protein
(Keratin_B2_2, N=118)
Fisher's OR: 0; Bonferroni p-val: 0.354

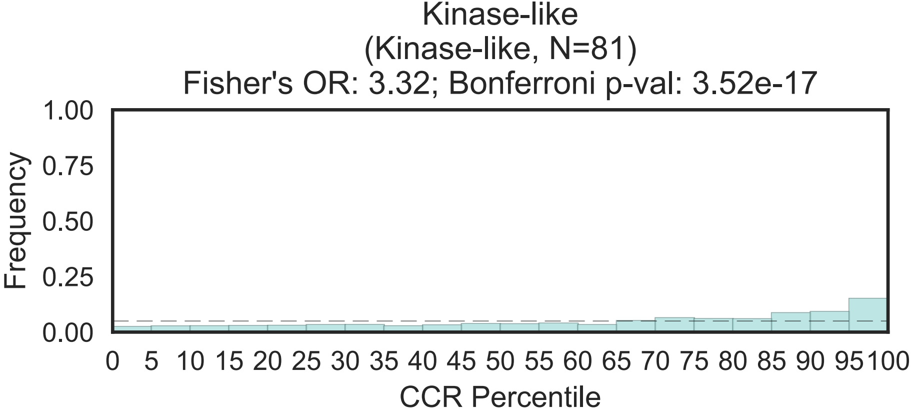

Keratinocyte-associated protein 2
(Keratin_assoc, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

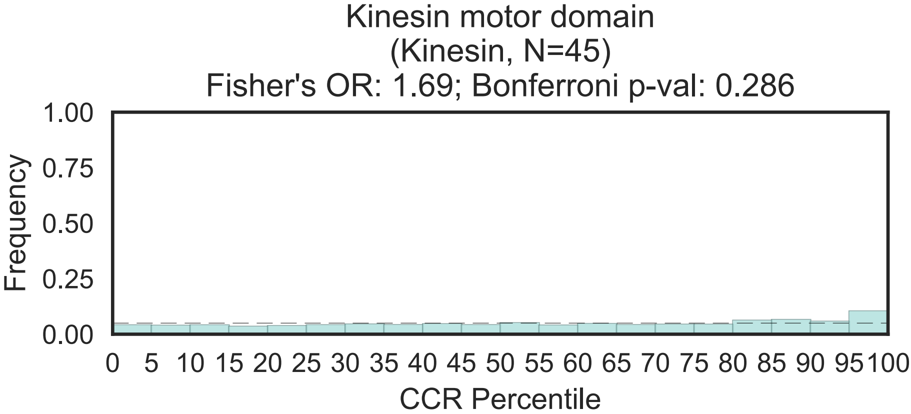

Keratin, high-sulphur matrix protein
(Keratin_matx, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

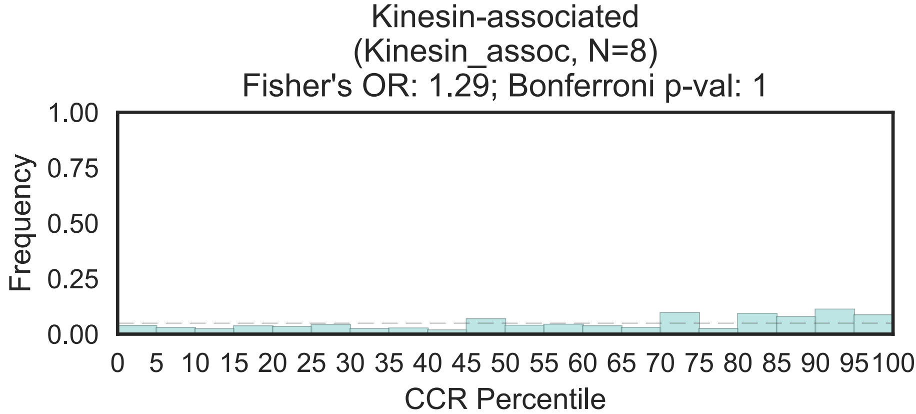

Beta-ketoacyl synthase, C-terminal domain
(Ketoacyl-synt_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

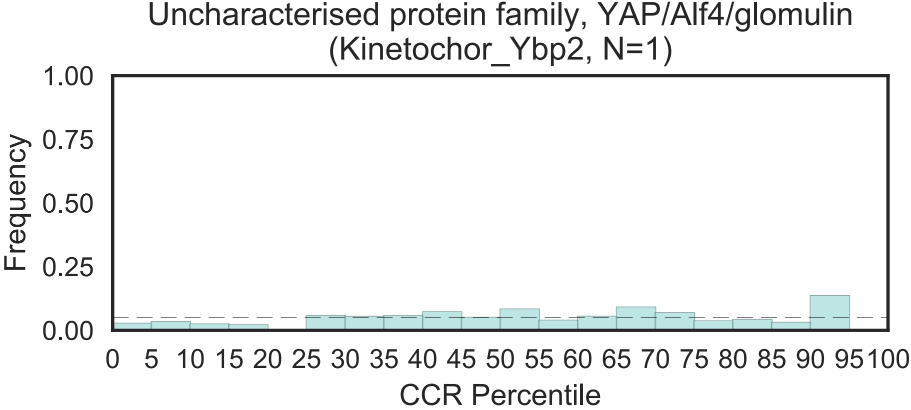
Domain of Kin17 curved DNA-binding protein
(Kin17_mid, N=1)

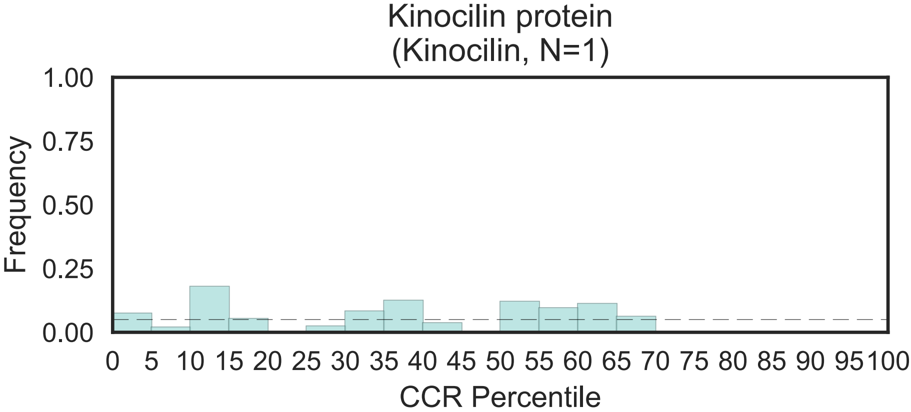


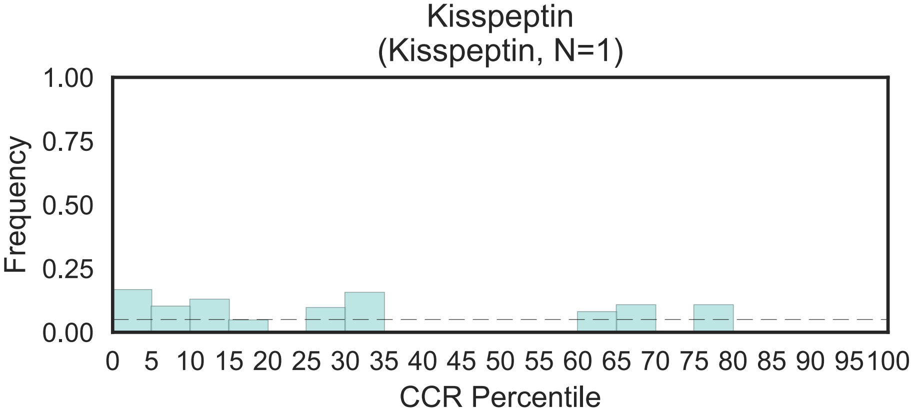

Kinase-like
(Kinase-like, N=81)
Fisher's OR: 3.32; Bonferroni p-val: 3.52e-17
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

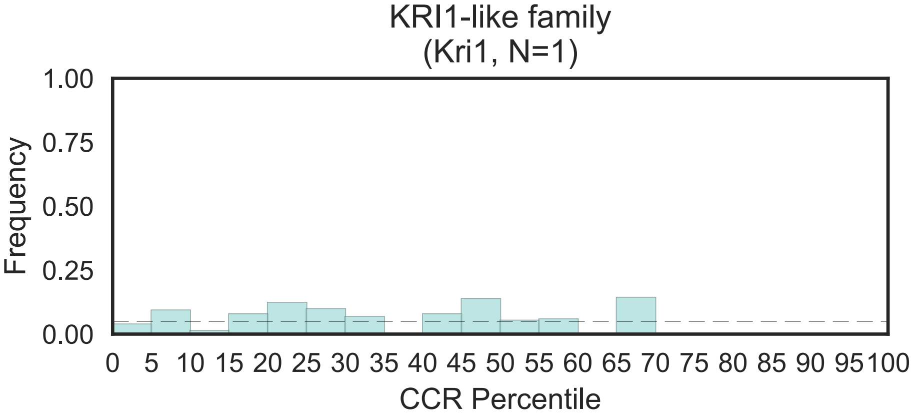

Kinesin motor domain
(Kinesin, N=45)
Fisher's OR: 1.69; Bonferroni p-val: 0.286
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

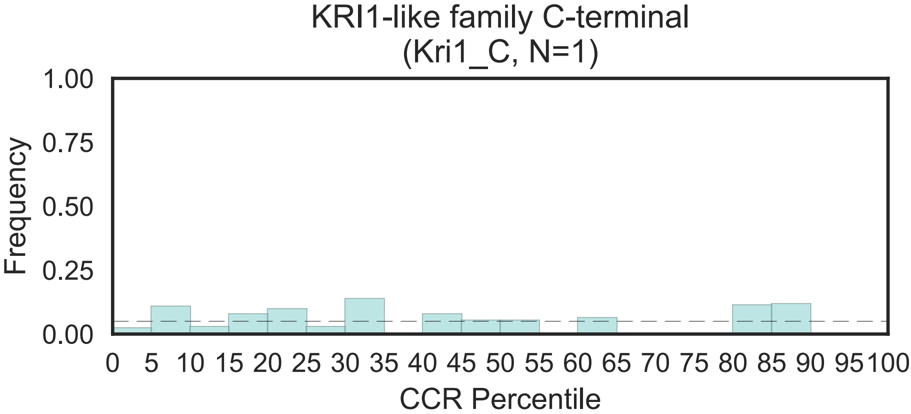

Kinesin-associated
(Kinesin_assoc, N=8)
Fisher's OR: 1.29; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

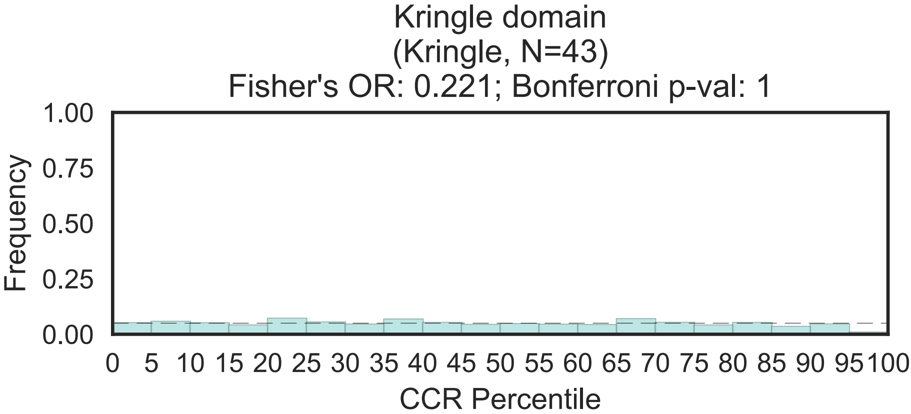

Uncharacterised protein family, YAP/Alf4/glomulin
(Kinetochor_Ybp2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

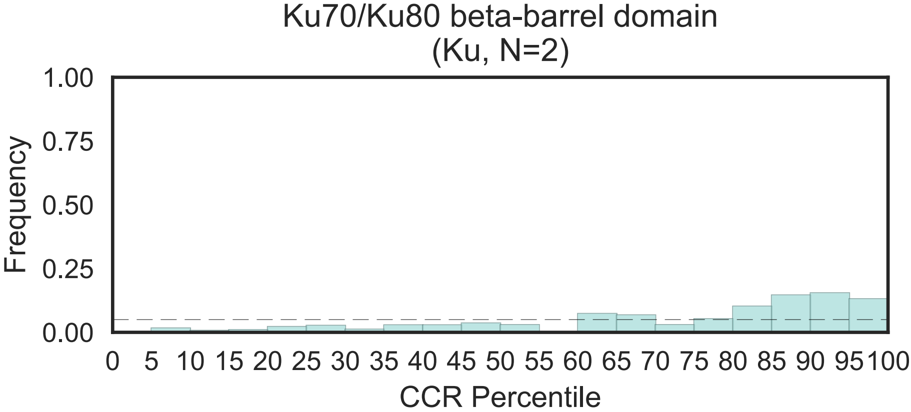

Kinocilin protein
(Kinocilin, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

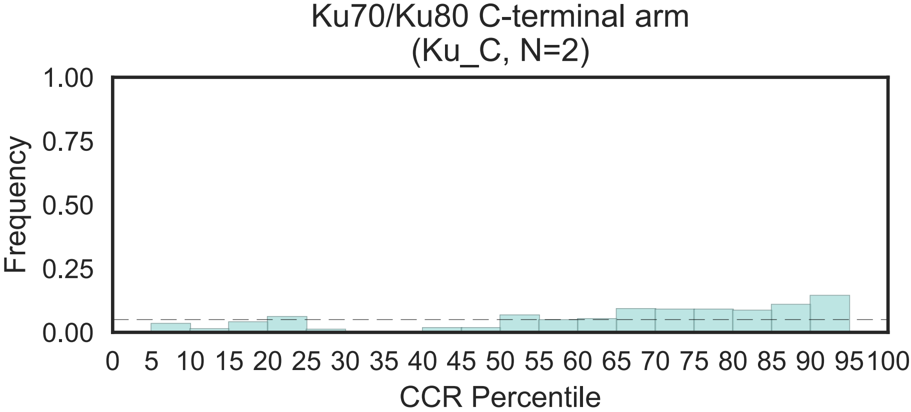

Kisspeptin
(Kisspeptin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

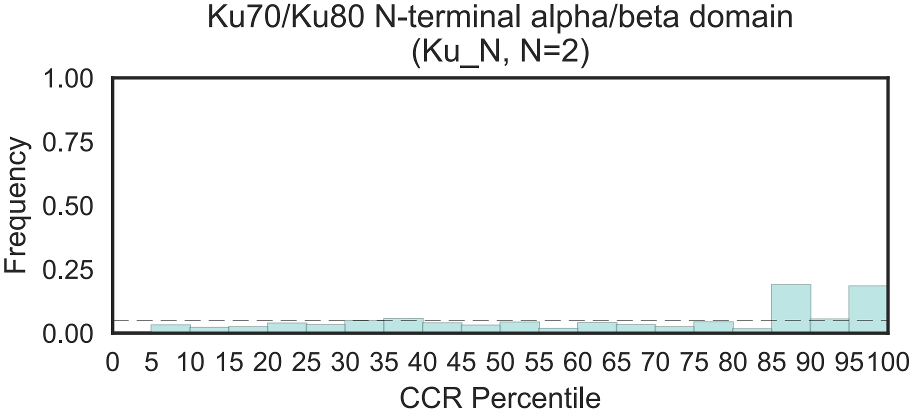

KRI1-like family
(Kri1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


KRI1-like family C-terminal
(Kri1_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

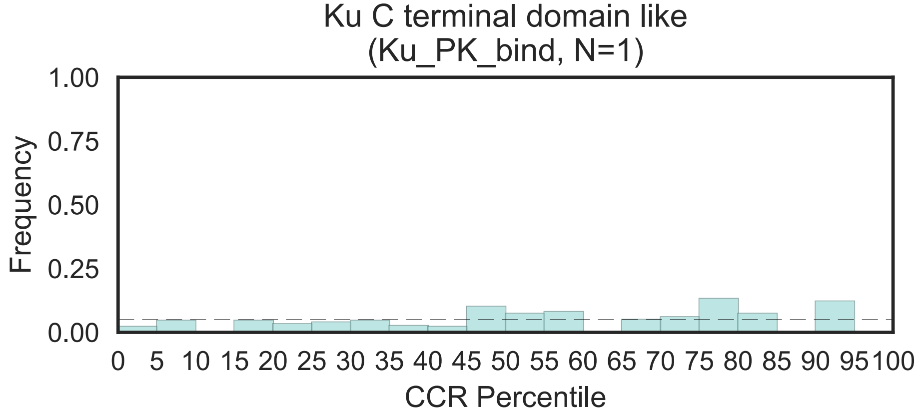

Kringle domain
(Kringle, N=43)
Fisher's OR: 0.221; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

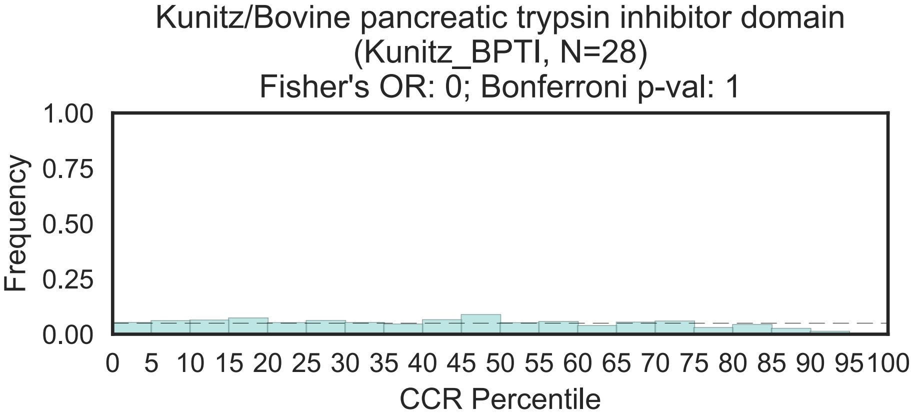

Ku70/Ku80 beta-barrel domain
(Ku, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

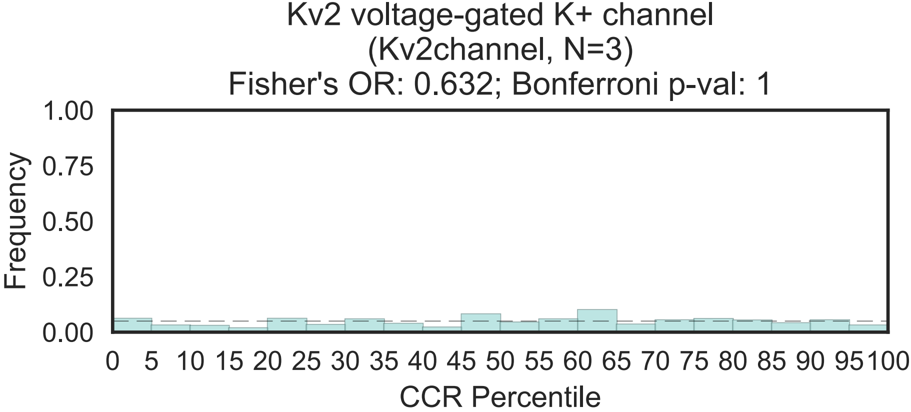

Ku70/Ku80 C-terminal arm
(Ku_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



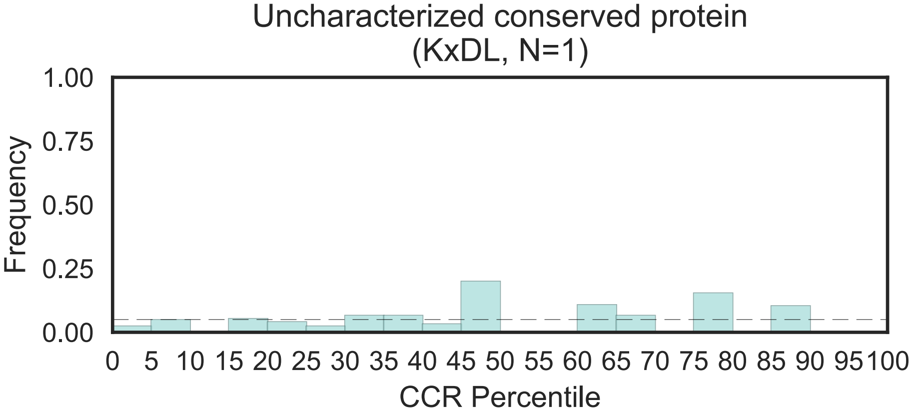
Ku70/Ku80 N-terminal alpha/beta domain
(Ku_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ku C terminal domain like
(Ku_PK_bind, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

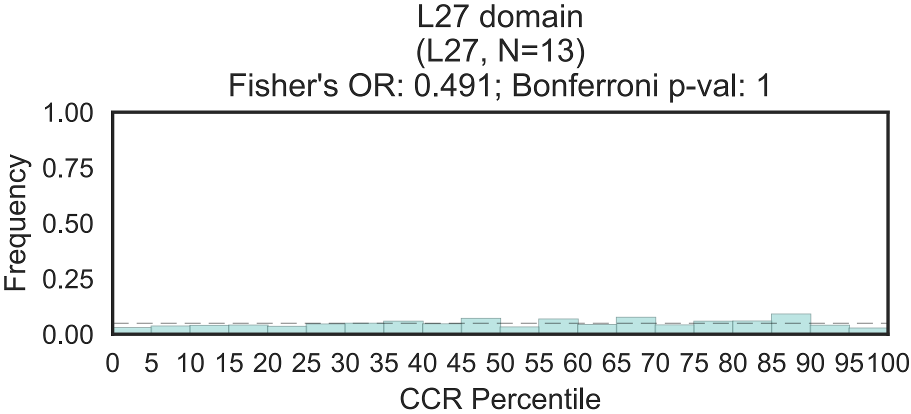

Kunitz/Bovine pancreatic trypsin inhibitor domain
(Kunitz_BPTI, N=28)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

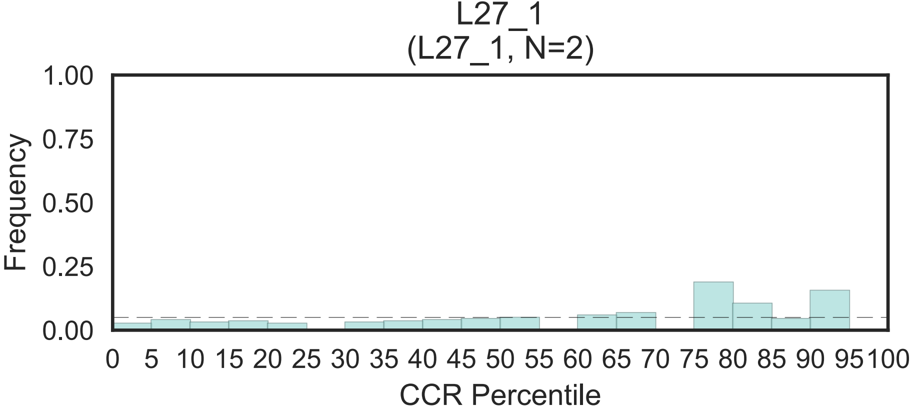


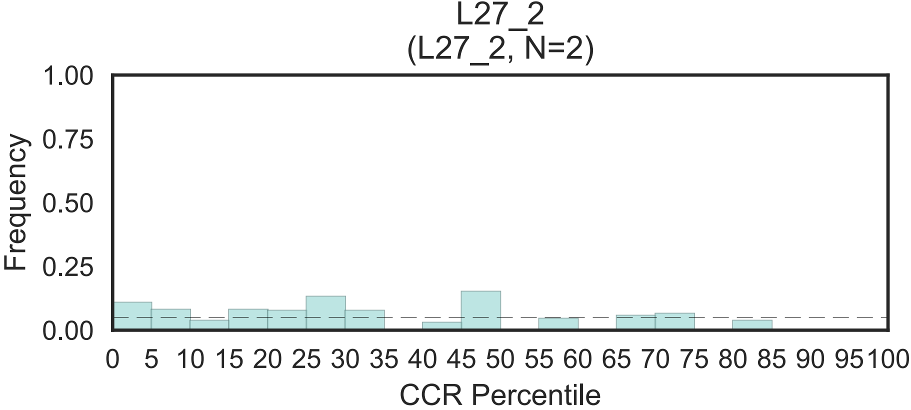
Kv2 voltage-gated K+ channel
(Kv2channel, N=3)
Fisher's OR: 0.632; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

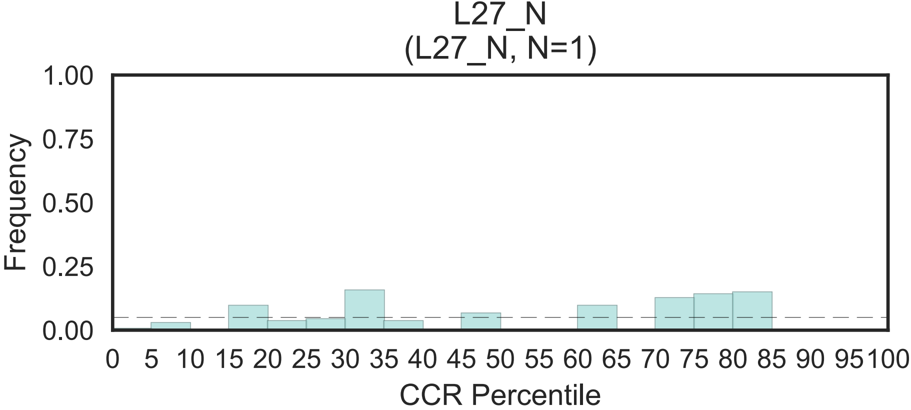


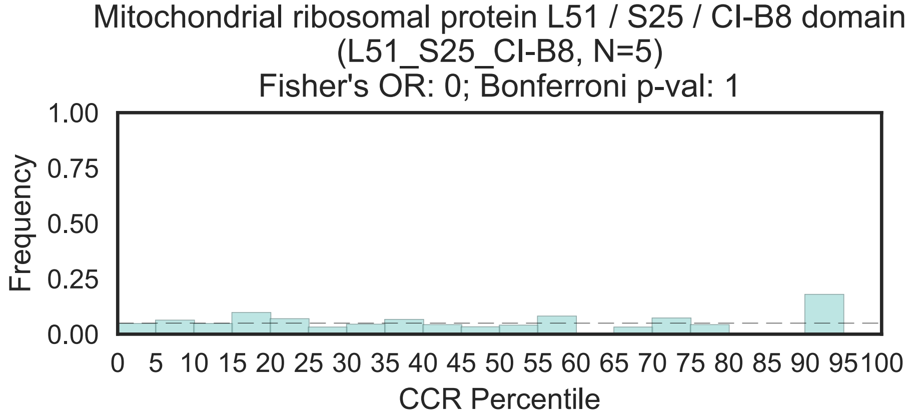
Uncharacterized conserved protein
(KxDL, N=1)


L27 domain
(L27, N=13)
Fisher's OR: 0.491; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

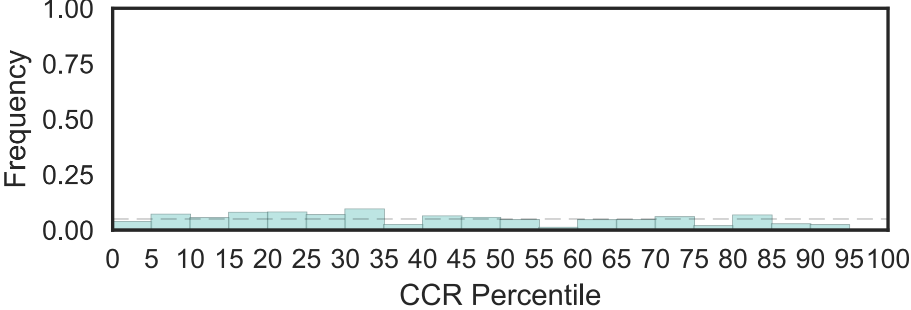

L27_1
(L27_1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

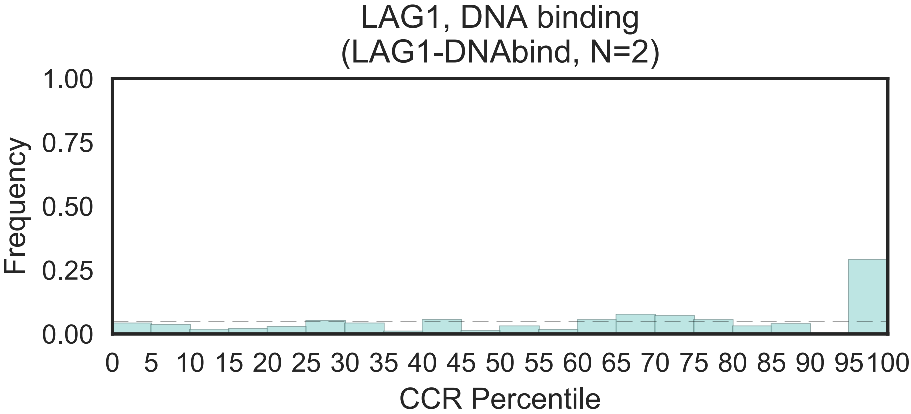

L27_2
(L27_2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

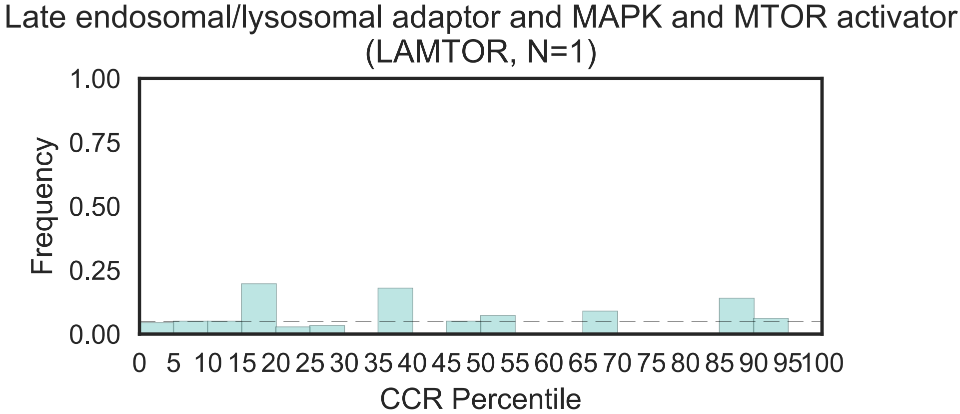

L27_N
(L27_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

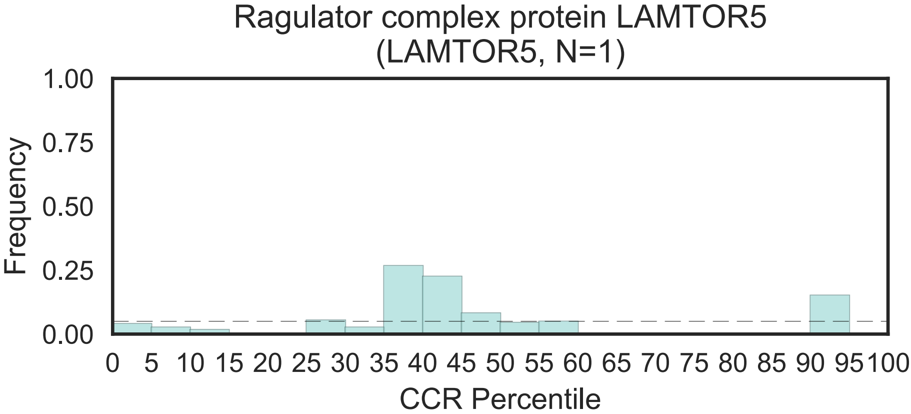

Mitochondrial ribosomal protein L51 / S25 / CI-B8 domain
(L51_S25_CI-B8, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

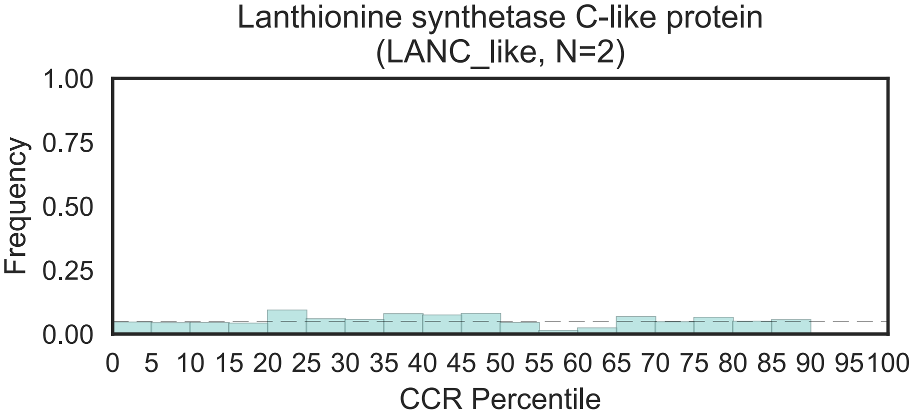
L6 membrane protein
(L6_membrane, N=6)
Fisher's OR: 0; Bonferroni p-val: 1

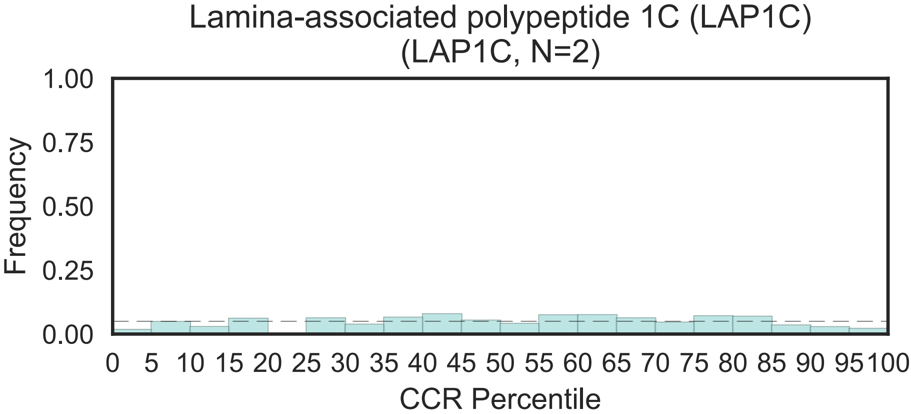


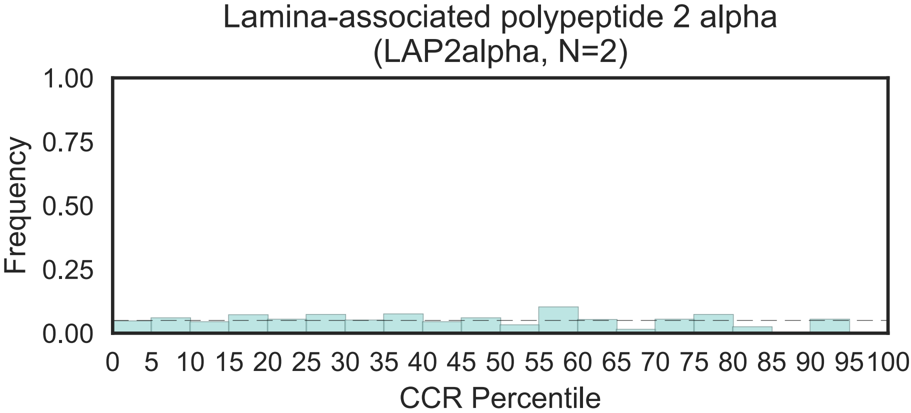

LAG1, DNA binding
(LAG1-DNAbind, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

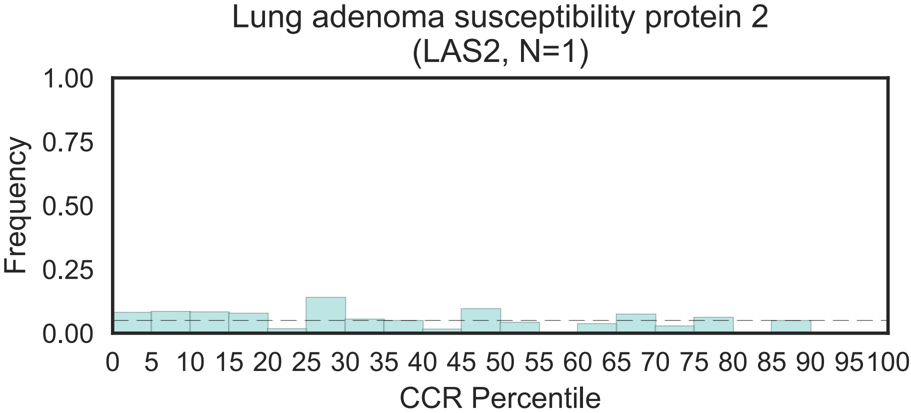

Late endosomal/lysosomal adaptor and MAPK and MTOR activator
(LAMTOR, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

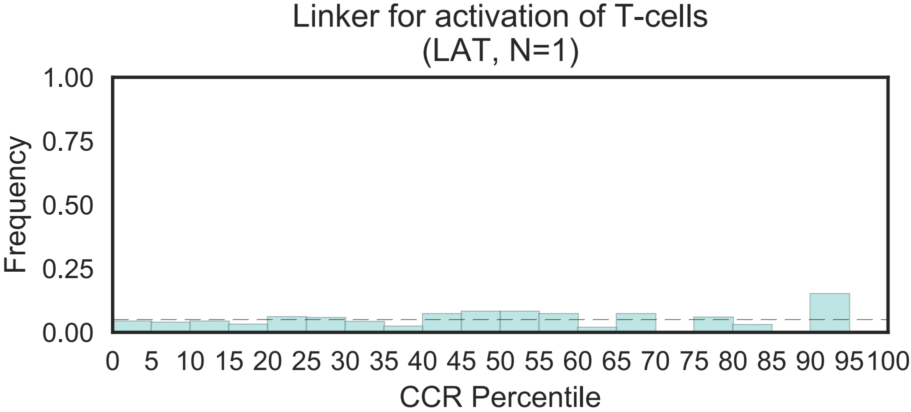

Ragulator complex protein LAMTOR5
(LAMTOR5, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

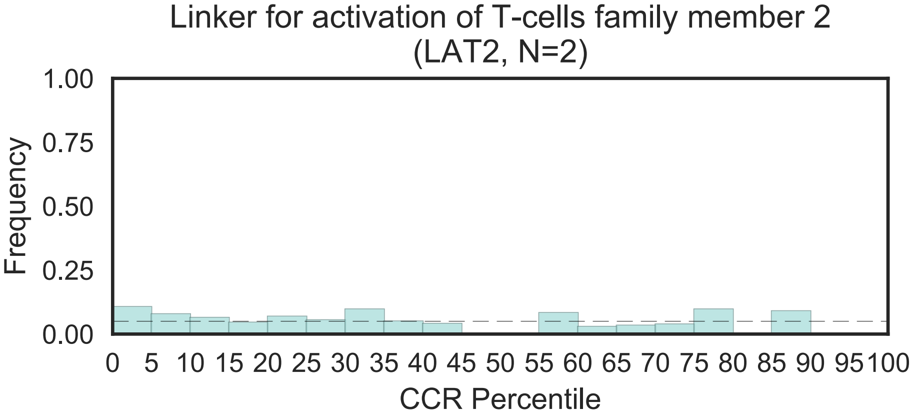

Lanthionine synthetase C-like protein
(LANC_like, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

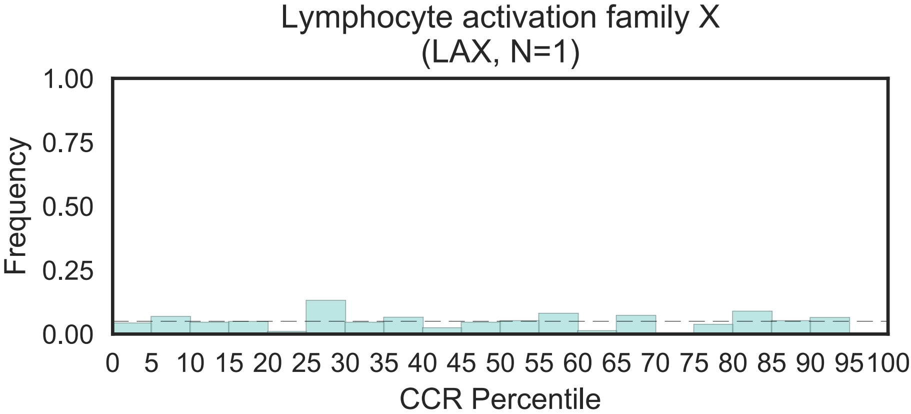

Lamina-associated polypeptide 1C (LAP1C)
(LAP1C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

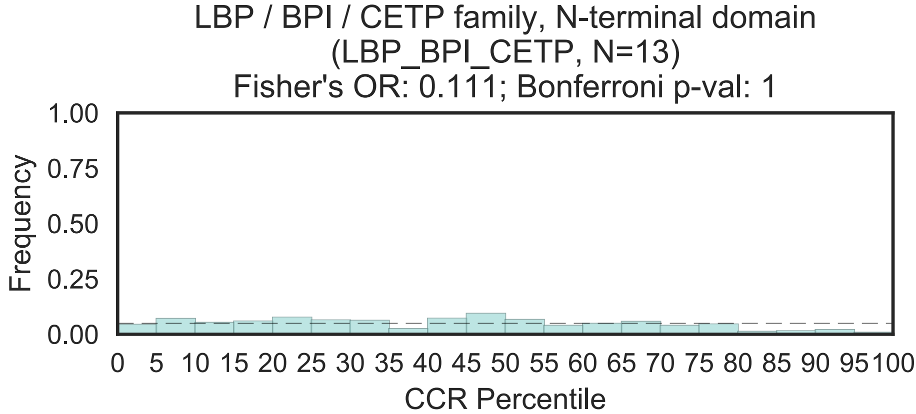

Lamina-associated polypeptide 2 alpha
(LAP2alpha, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

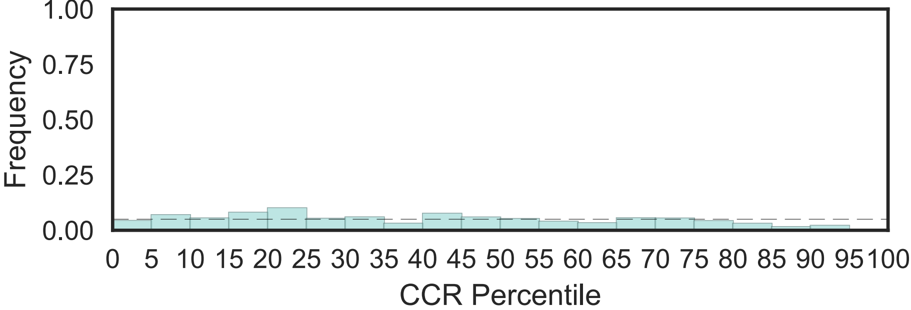

Lung adenoma susceptibility protein 2
(LAS2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Linker for activation of T-cells
(LAT, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

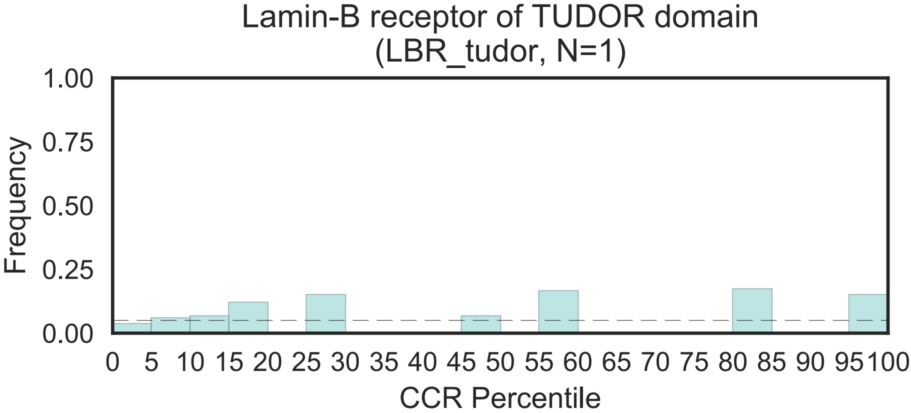

Linker for activation of T-cells family member 2
(LAT2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

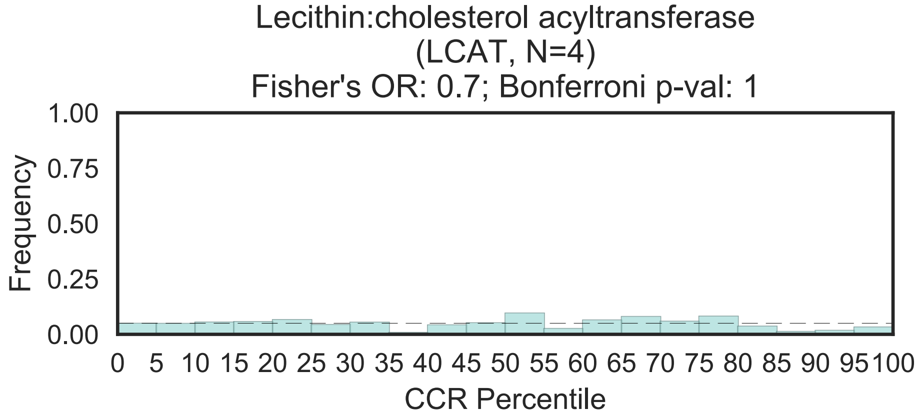

Lymphocyte activation family X
(LAX, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

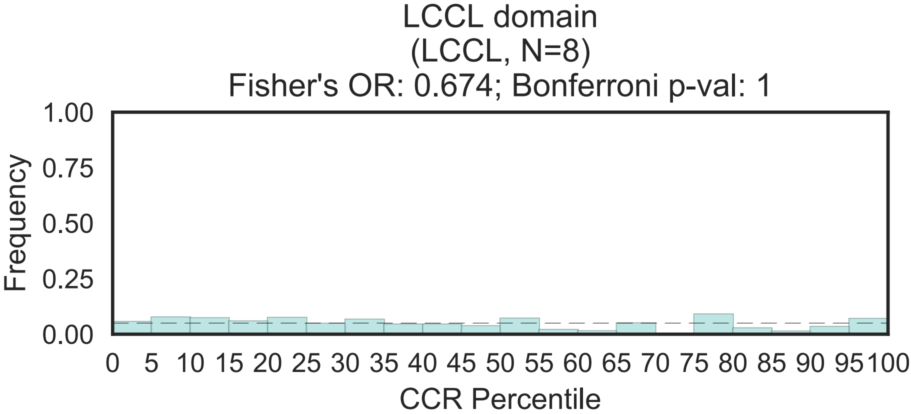

LBP / BPI / CETP family, N-terminal domain
(LBP_BPI_CETP, N=13)
Fisher's OR: 0.111; Bonferroni p-val: 1



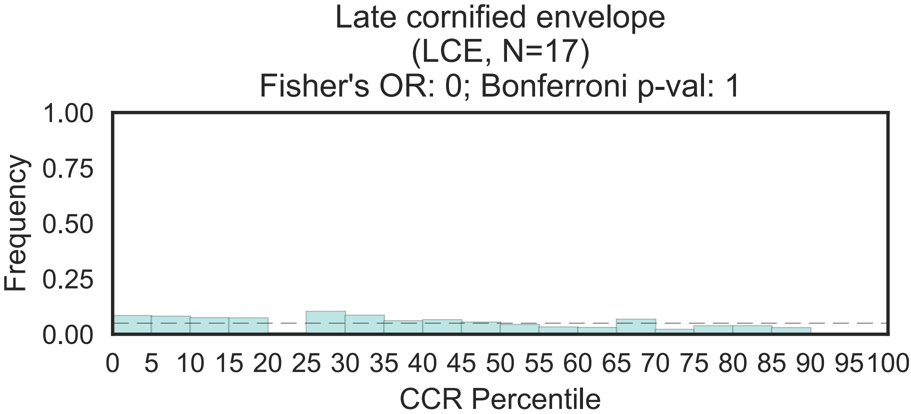
LBP / BPI / CETP family, C-terminal domain
(LBP_BPI_CETP_C, N=10)
Fisher's OR: 0; Bonferroni p-val: 1

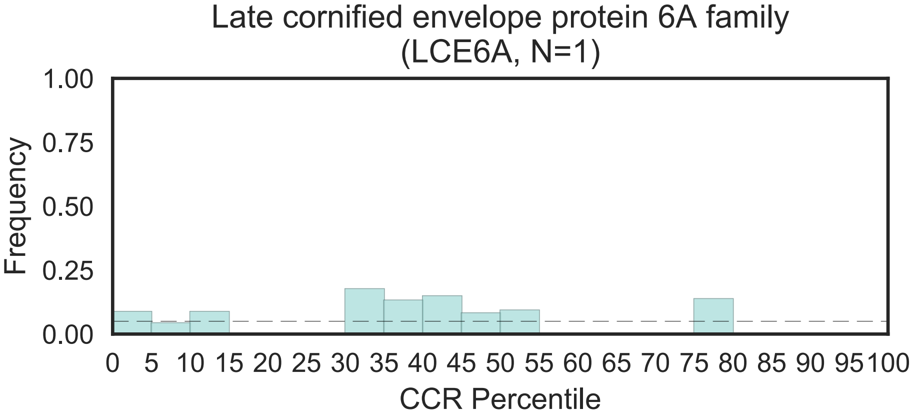

Lamin-B receptor of TUDOR domain
(LBR_tudor, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

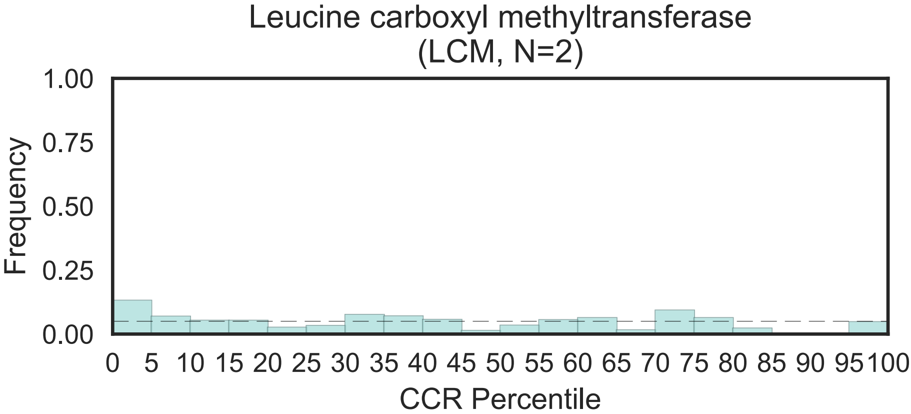

Lecithin:cholesterol acyltransferase
(LCAT, N=4)
Fisher's OR: 0.7; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

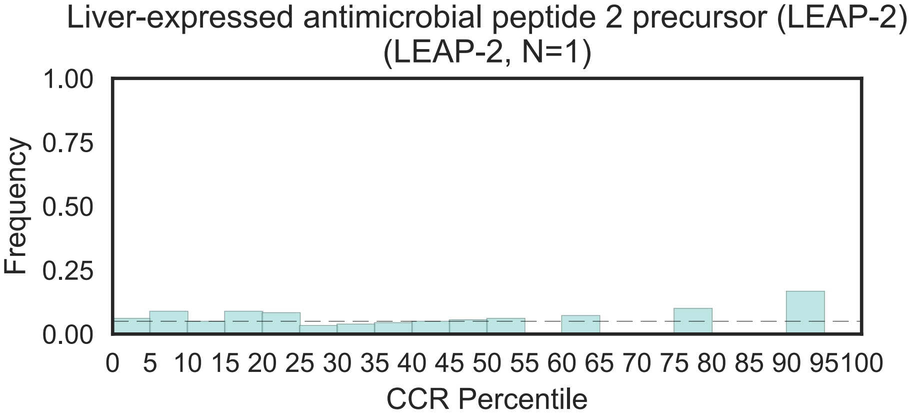


LCCL domain
(LCCL, N=8)
Fisher's OR: 0.674; Bonferroni p-val: 1

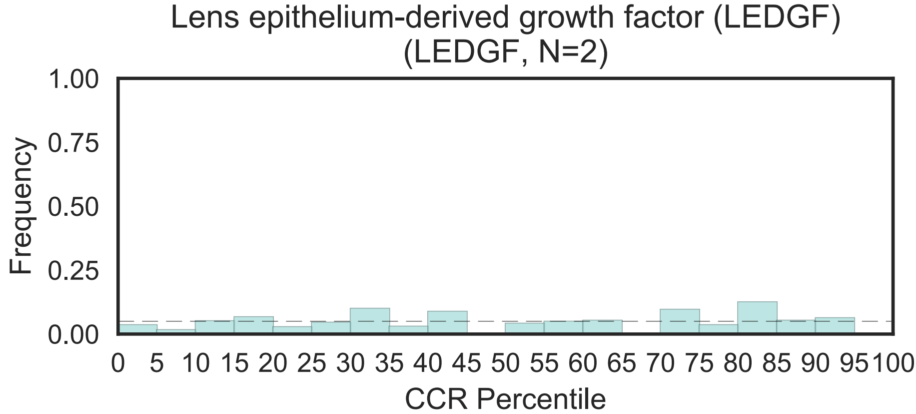

Late cornified envelope
(LCE, N=17)
Fisher's OR: 0; Bonferroni p-val: 1

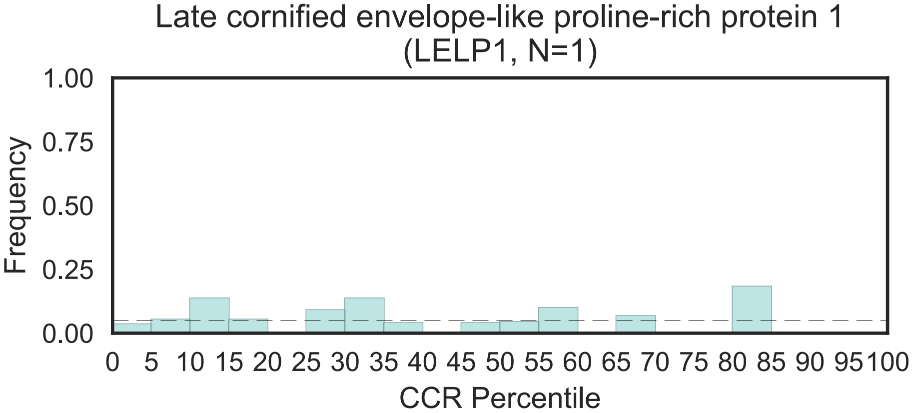

Late cornified envelope protein 6A family
(LCE6A, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Leucine carboxyl methyltransferase
(LCM, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

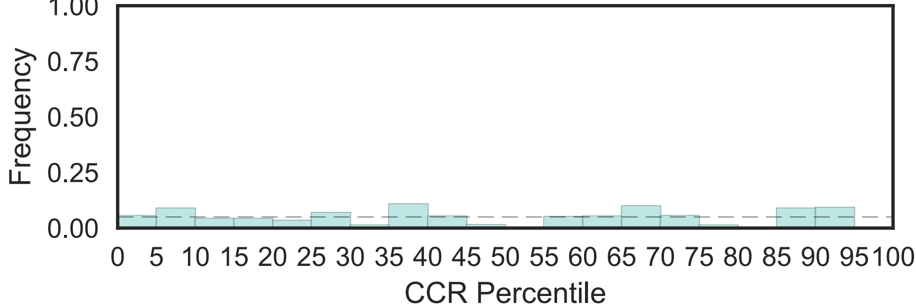


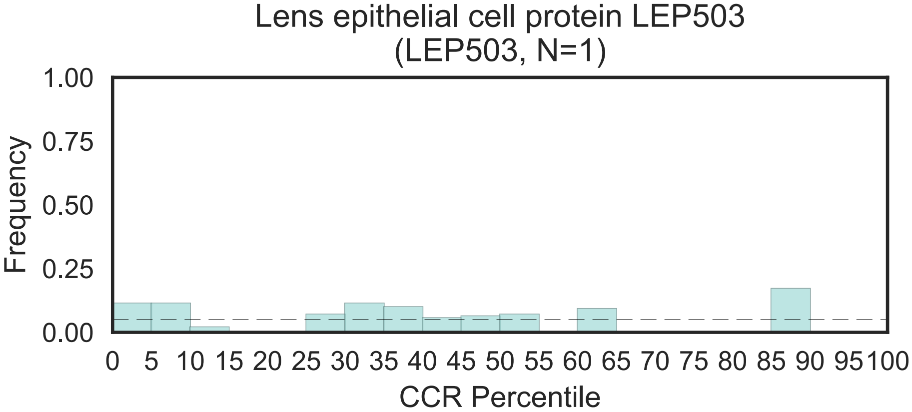
Liver-expressed antimicrobial peptide 2 precursor (LEAP-2) (LEAP-2, N=1)

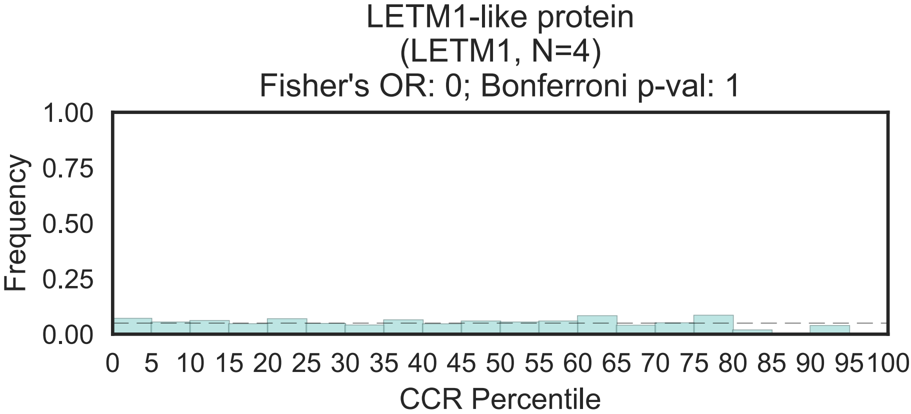

Lens epithelium-derived growth factor (LEDGF)
(LEDGF, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

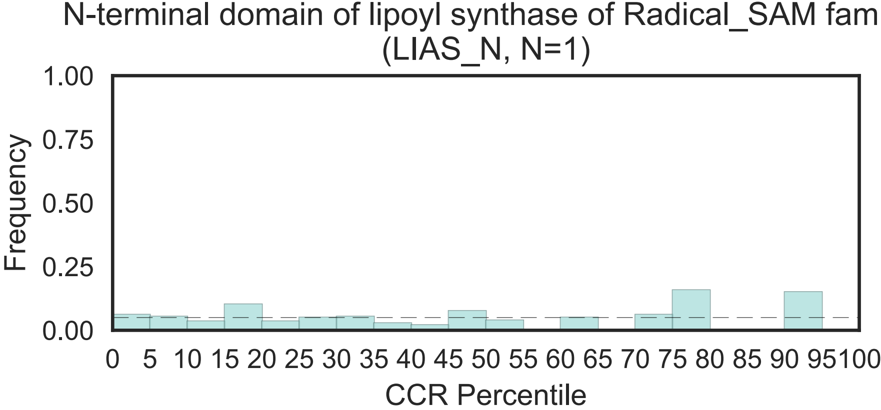

Late cornified envelope-like proline-rich protein 1
(LELP1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

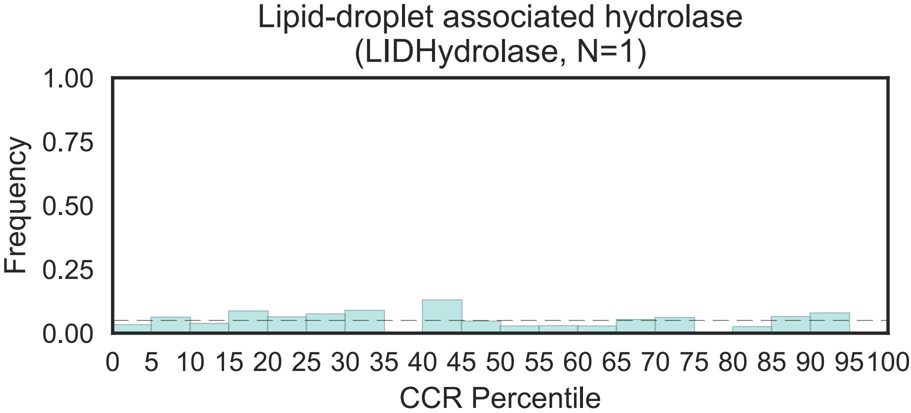
LEM domain
(LEM, N=6)
Fisher's OR: 0; Bonferroni p-val: 1

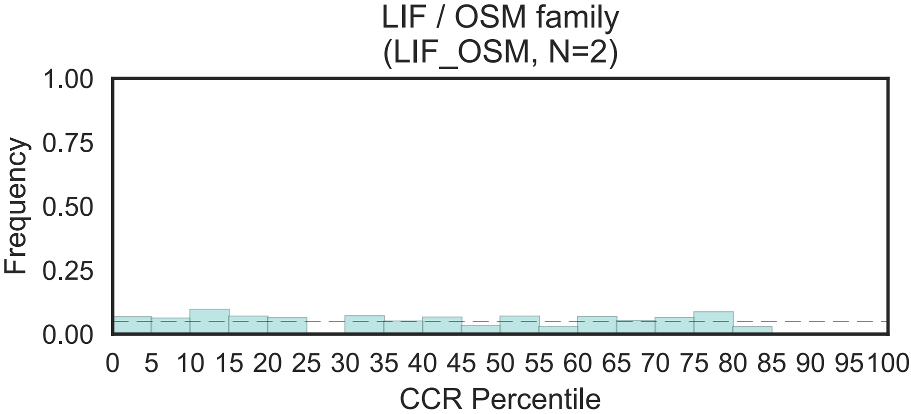


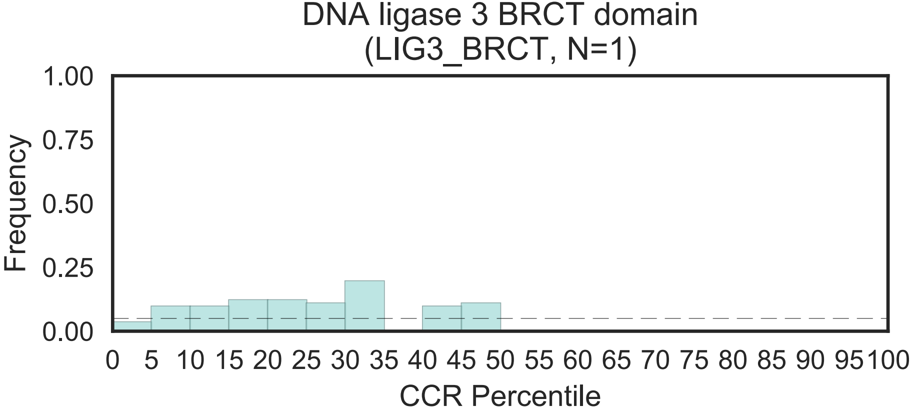

Lens epithelial cell protein LEP503
(LEP503, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

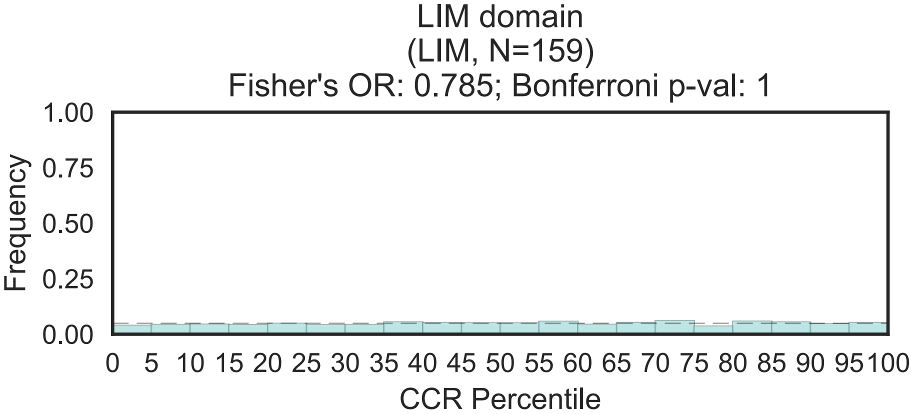

LETM1-like protein
(LETM1, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

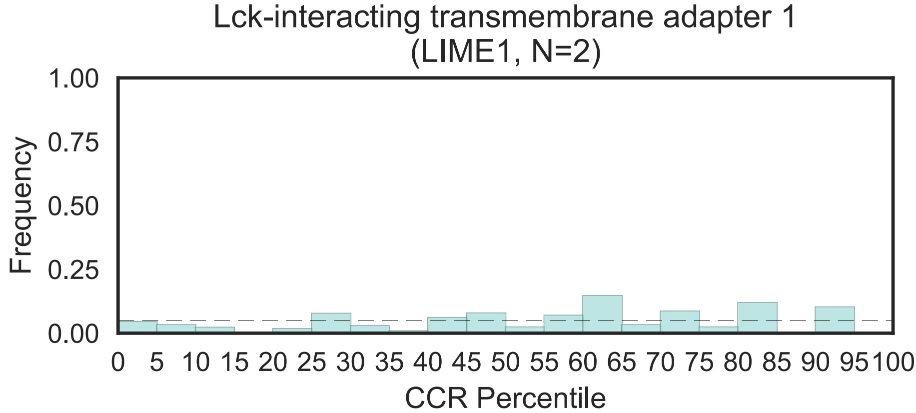

N-terminal domain of lipoyl synthase of Radical_SAM family
(LIAS_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

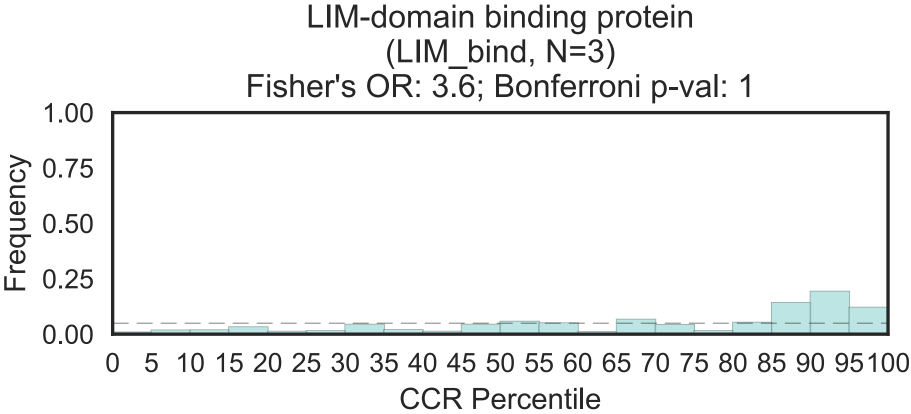

Lipid-droplet associated hydrolase
(LIDHydrolase, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

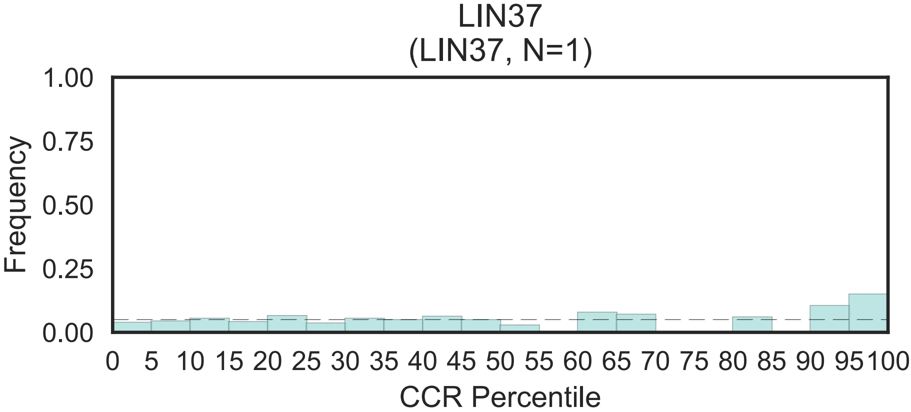

LIF / OSM family
(LIF_OSM, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

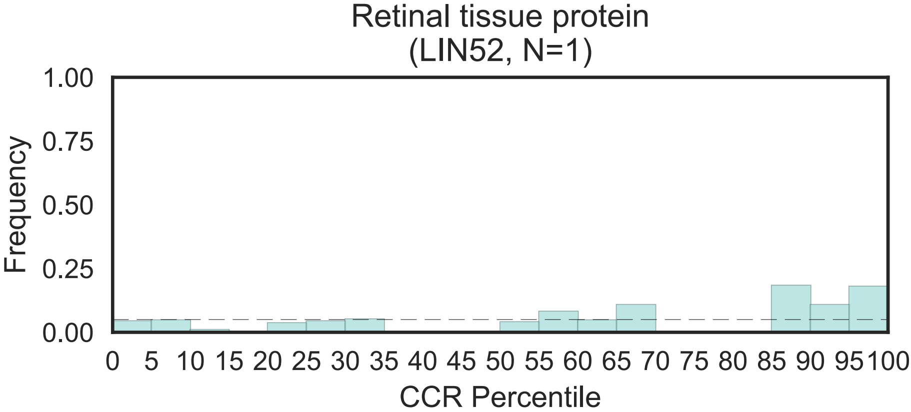

DNA ligase 3 BRCT domain
(LIG3_BRCT, N=1)

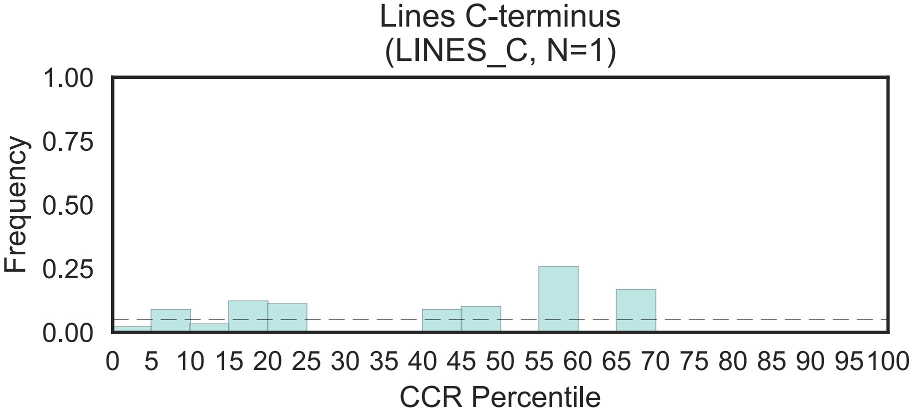

LIM domain
(LIM, N=159)
Fisher's OR: 0.785; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

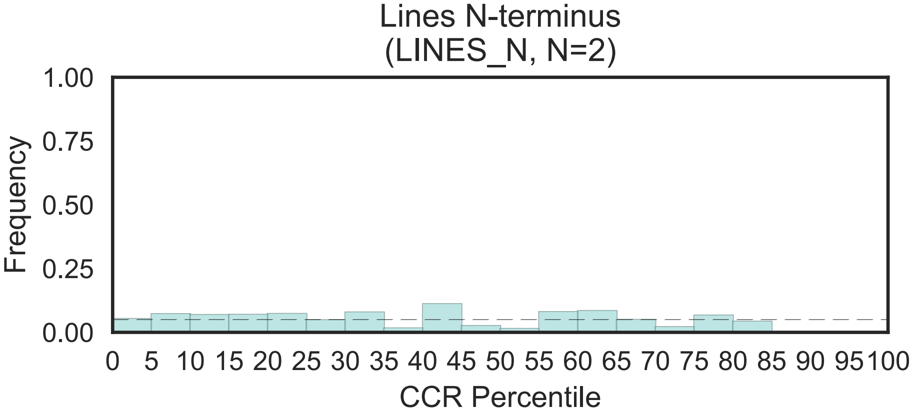

Lck-interacting transmembrane adapter 1
(LIME1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

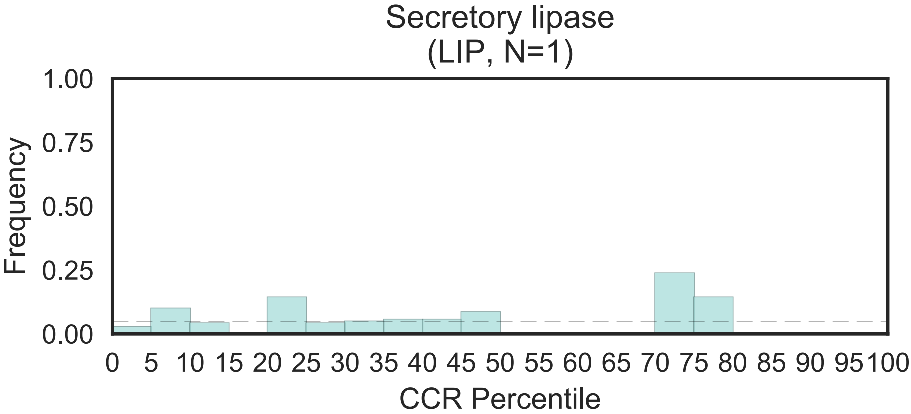

LIM-domain binding protein
(LIM_bind, N=3)
Fisher's OR: 3.6; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

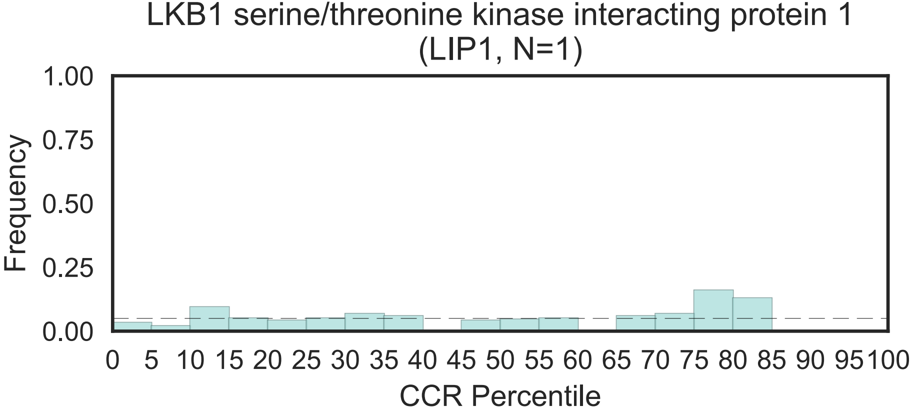

LIN37
(LIN37, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

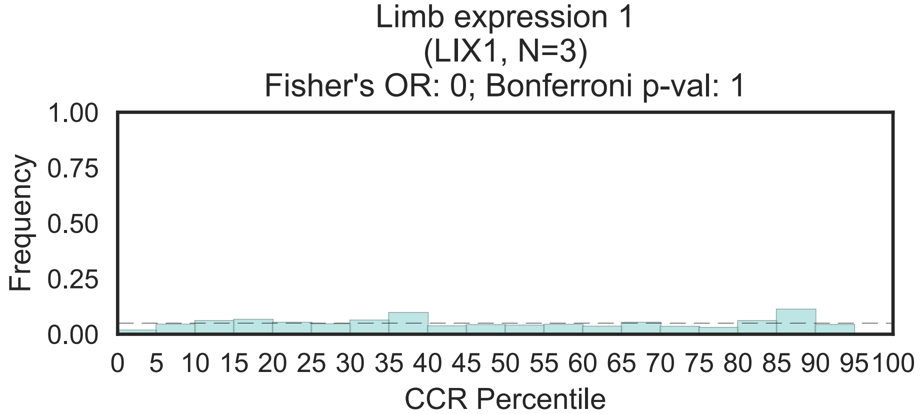

Retinal tissue protein
(LIN52, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

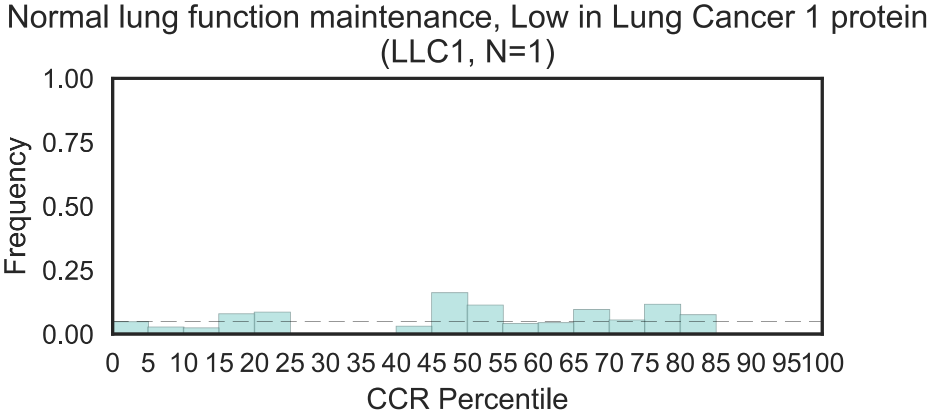

Lines C-terminus
(LINES_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

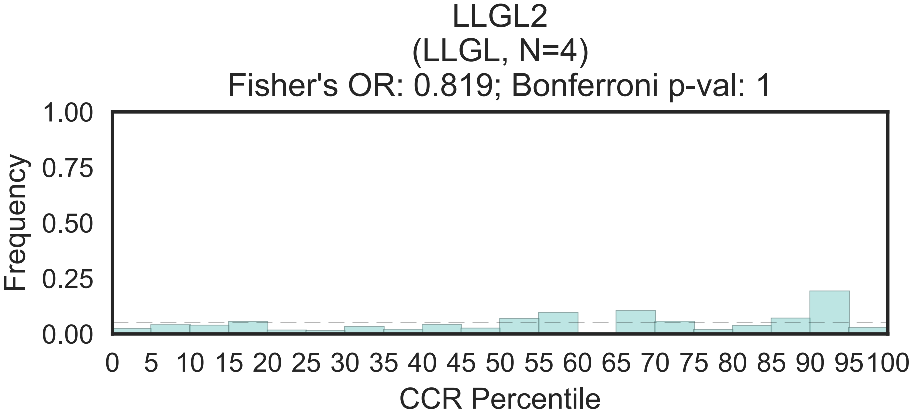

Lines N-terminus
(LINES_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Secretory lipase
(LIP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

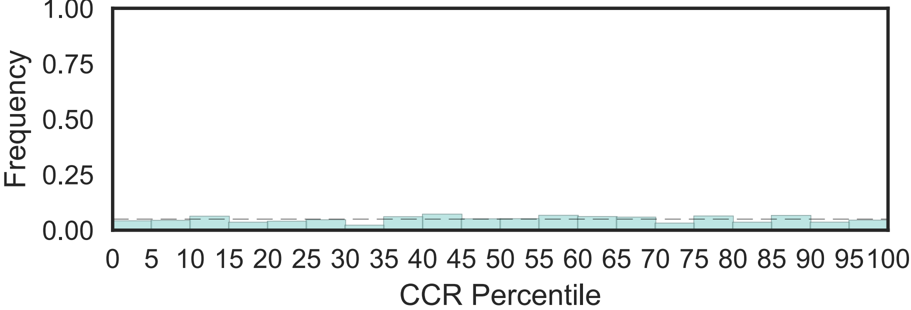

LKB1 serine/threonine kinase interacting protein 1
(LIP1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

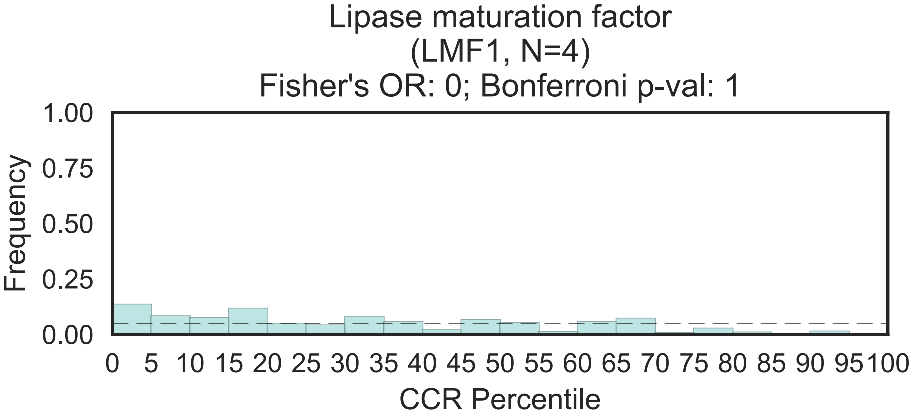

Limb expression 1
(LIX1, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

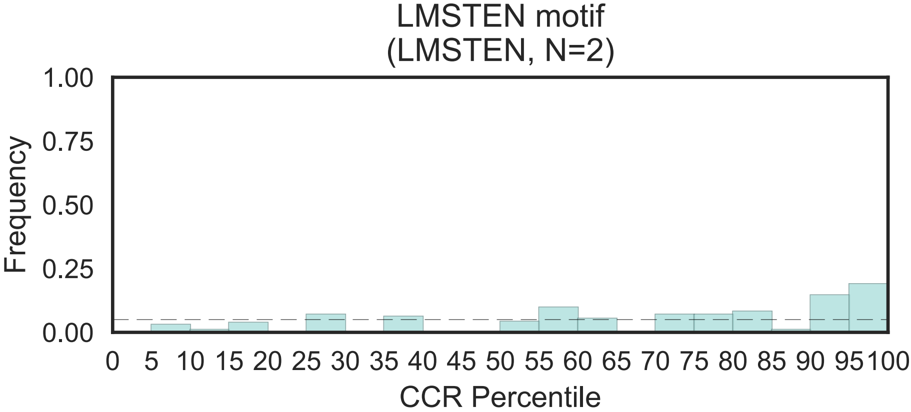

Normal lung function maintenance, Low in Lung Cancer 1 protein
(LLC1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

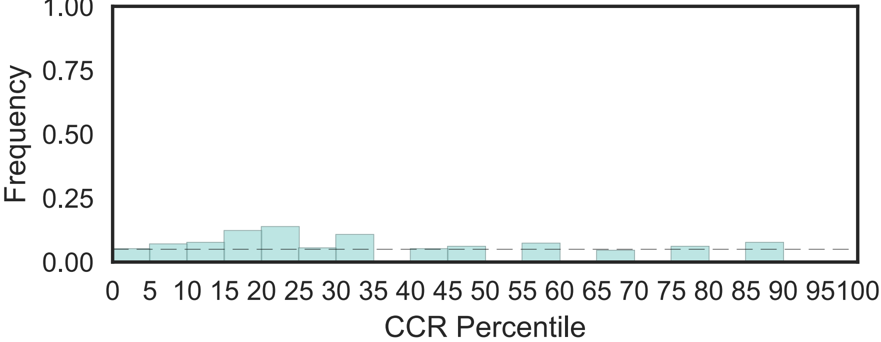

LLGL2
(LLGL, N=4)
Fisher's OR: 0.819; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

LMBR1-like membrane protein
(LMBR1, N=6)
Fisher's OR: 0.668; Bonferroni p-val: 1

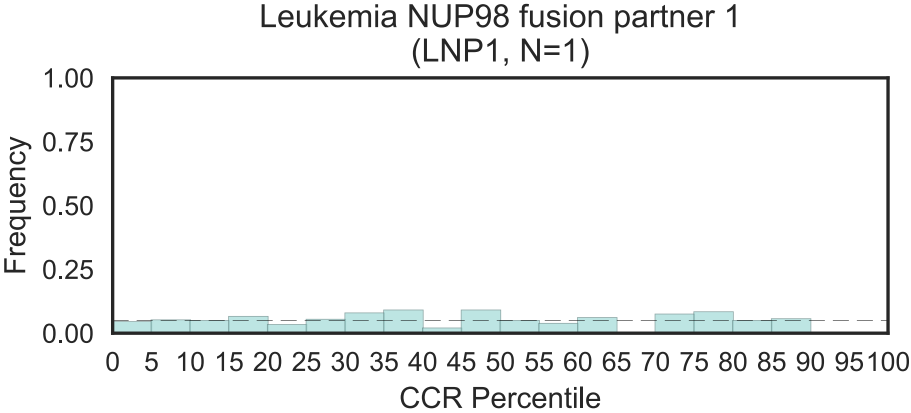


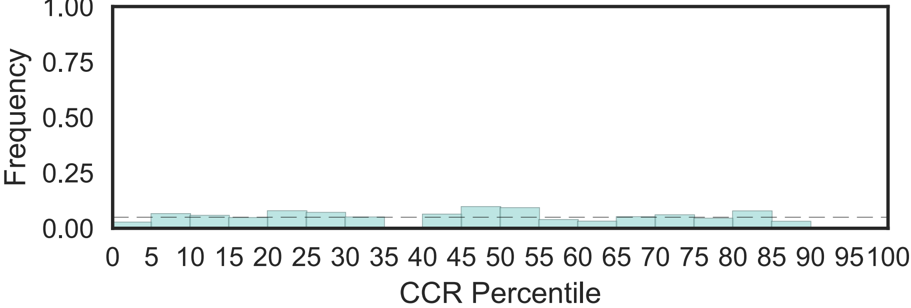

Lipase maturation factor
(LMF1, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


LMSTEN motif
(LMSTEN, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

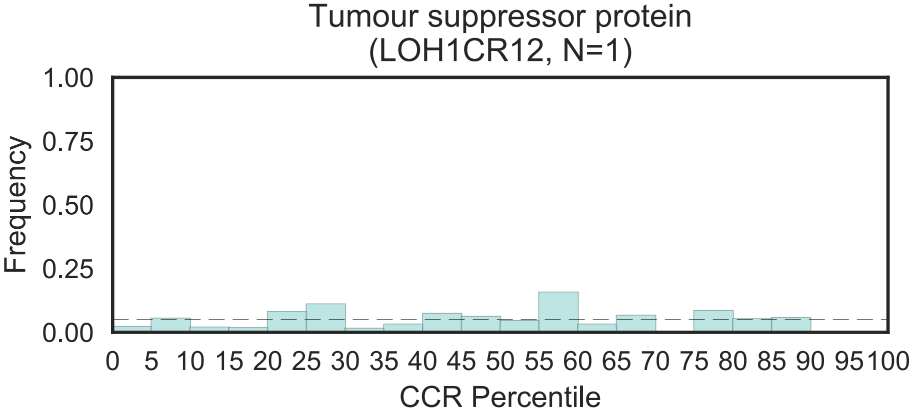


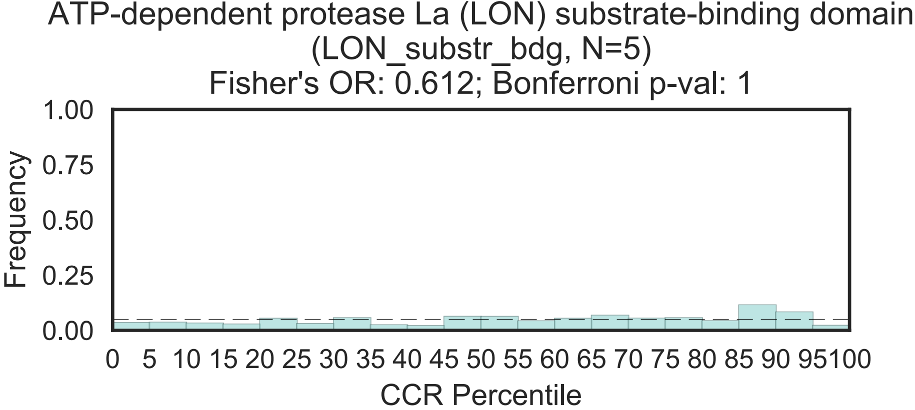
Low molecular weight phosphotyrosine protein phosphatase (LMWPc, N=1)

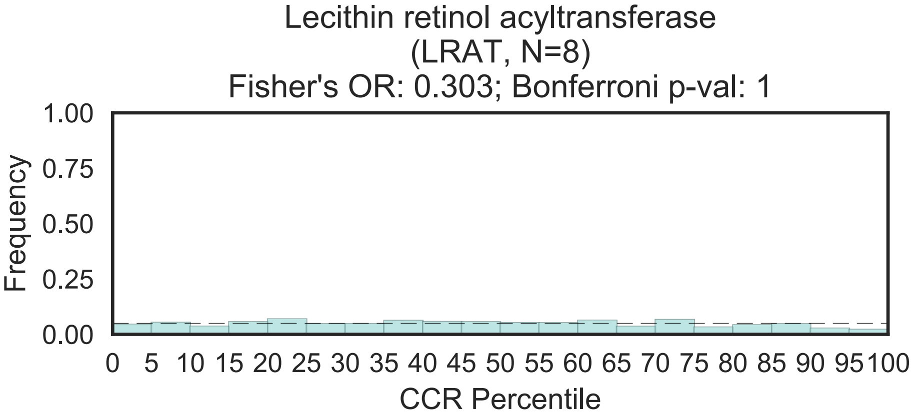

Leukemia NUP98 fusion partner 1
(LNP1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

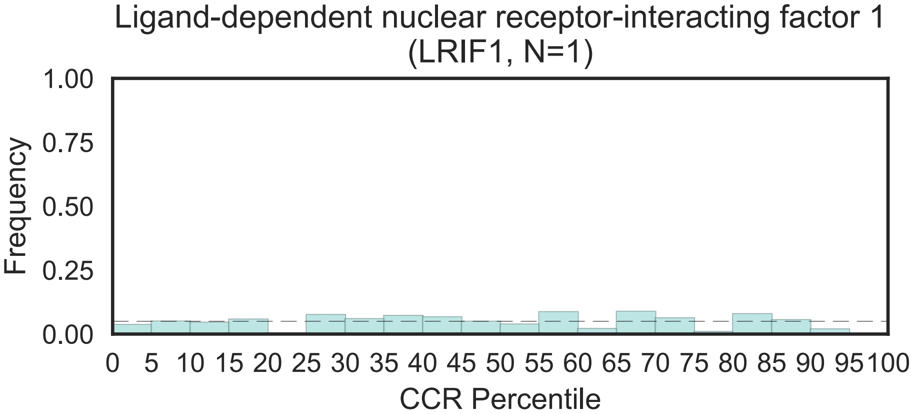


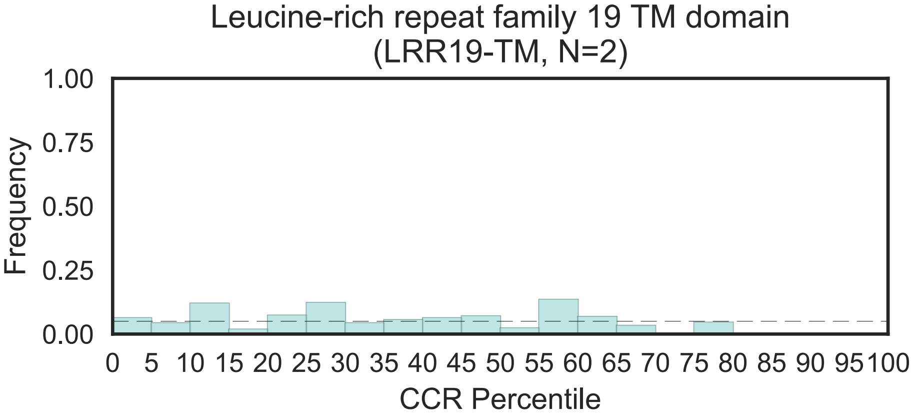
LNS2 (Lipin/Ned1/Smp2)
(LNS2, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

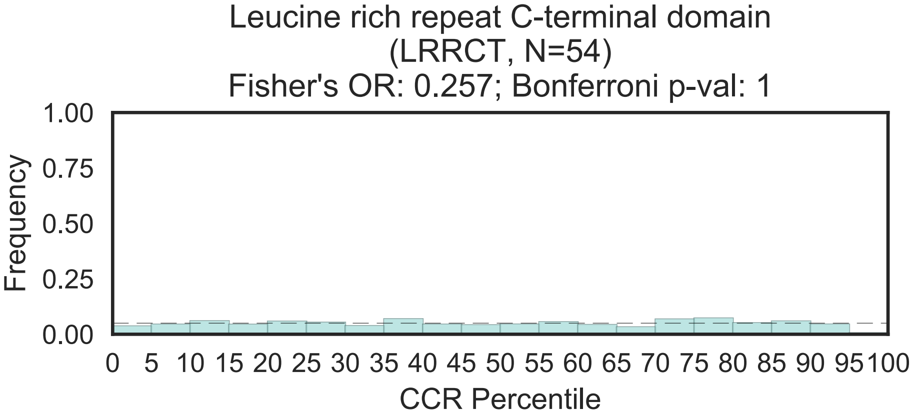

Tumour suppressor protein
(LOH1CR12, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

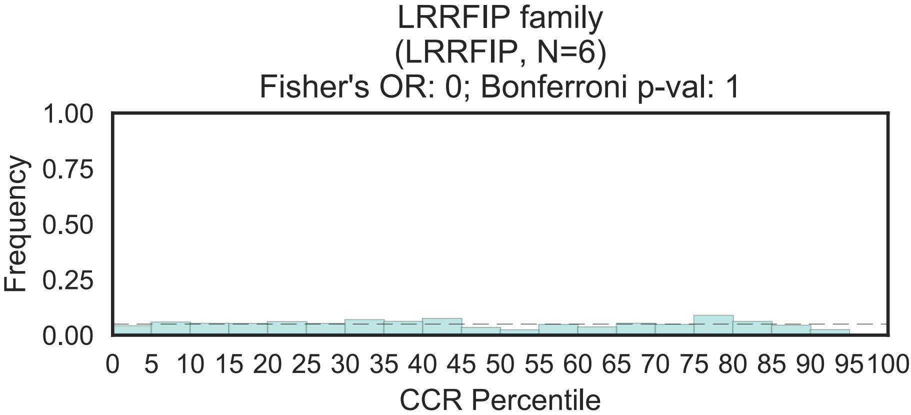

ATP-dependent protease La (LON) substrate-binding domain
(LON_substr_bdg, N=5)
Fisher's OR: 0.612; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

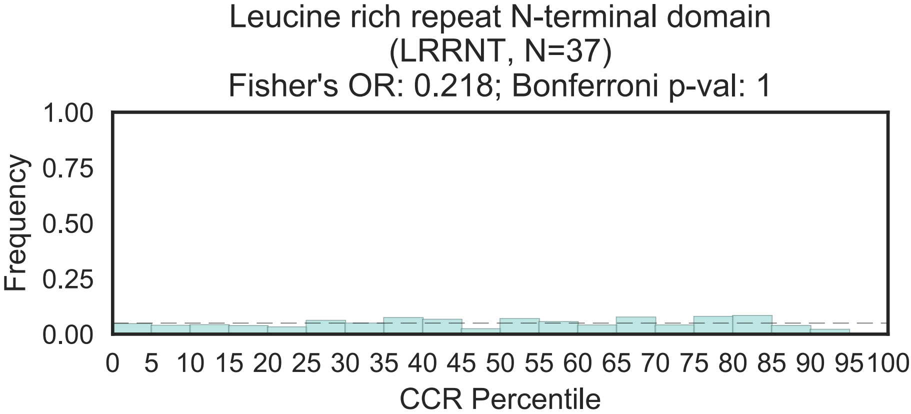

Lecithin retinol acyltransferase
(LRAT, N=8)
Fisher's OR: 0.303; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

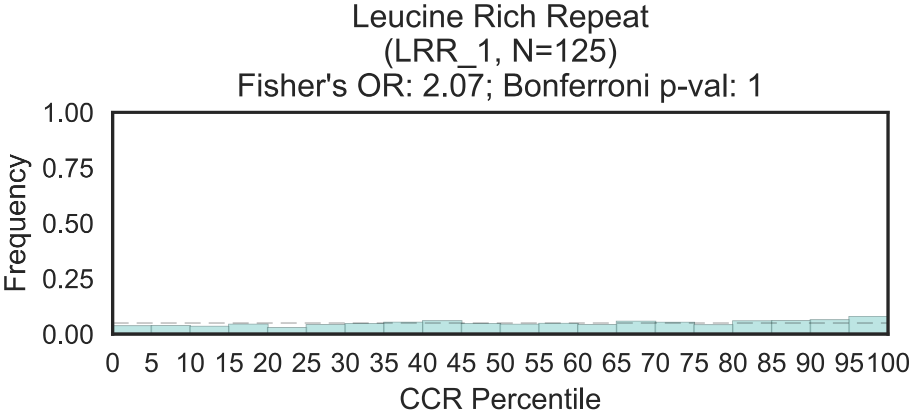

Ligand-dependent nuclear receptor-interacting factor 1
(LRIF1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

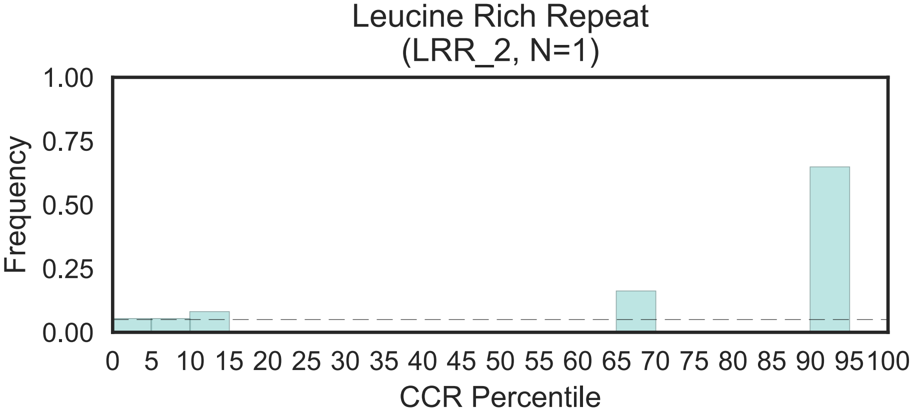

Leucine-rich repeat family 19 TM domain
(LRR19-TM, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

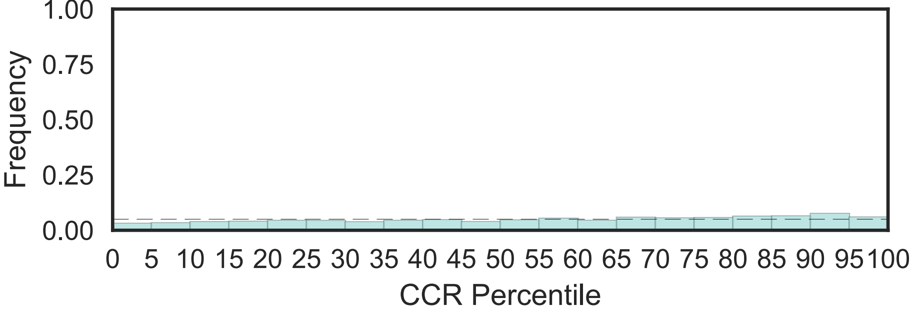

Leucine rich repeat C-terminal domain
(LRRCT, N=54)
Fisher's OR: 0.257; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


LRRFIP family
(LRRFIP, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

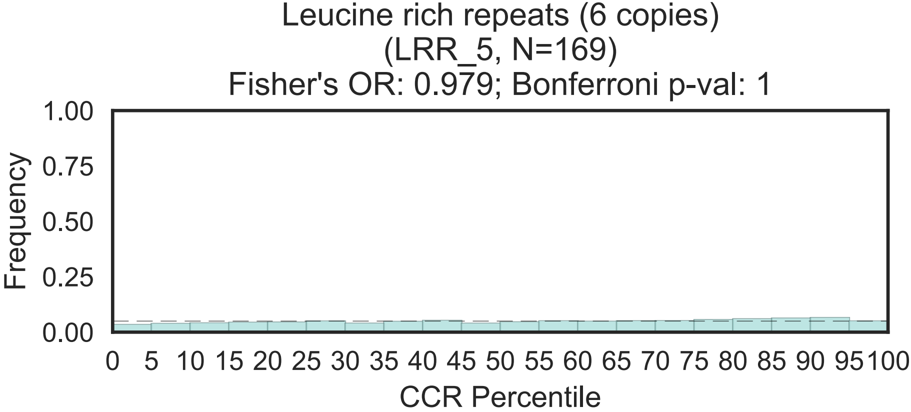

Leucine rich repeat N-terminal domain
(LRRNT, N=37)
Fisher's OR: 0.218; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

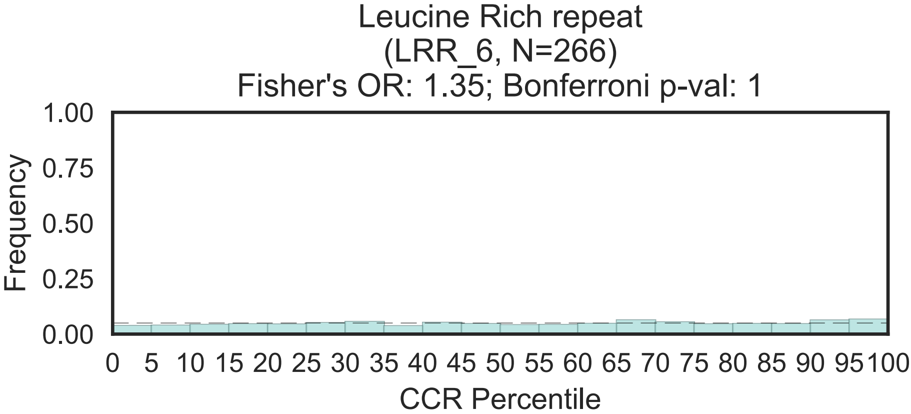

Leucine Rich Repeat
(LRR_1, N=125)
Fisher's OR: 2.07; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

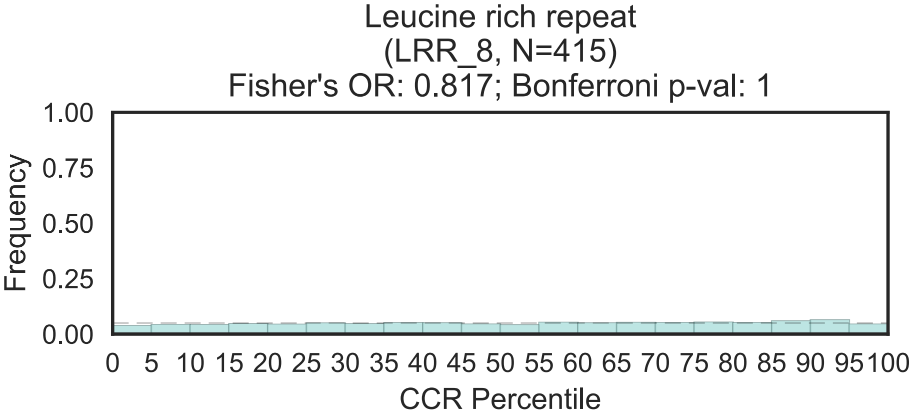

Leucine Rich Repeat
(LRR_2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

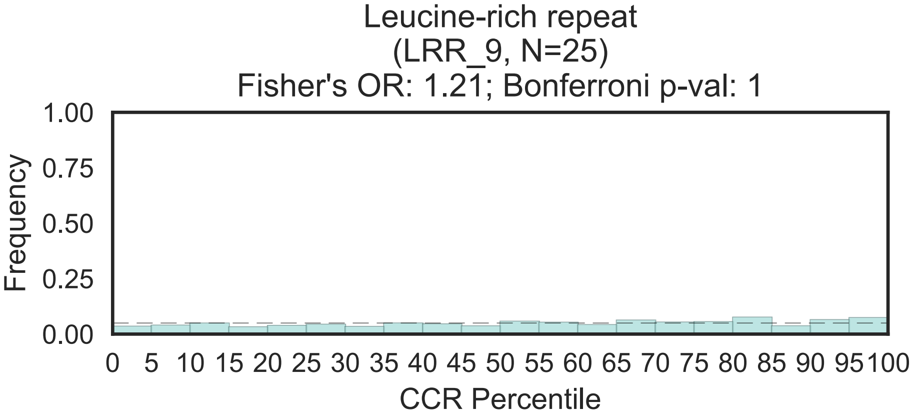


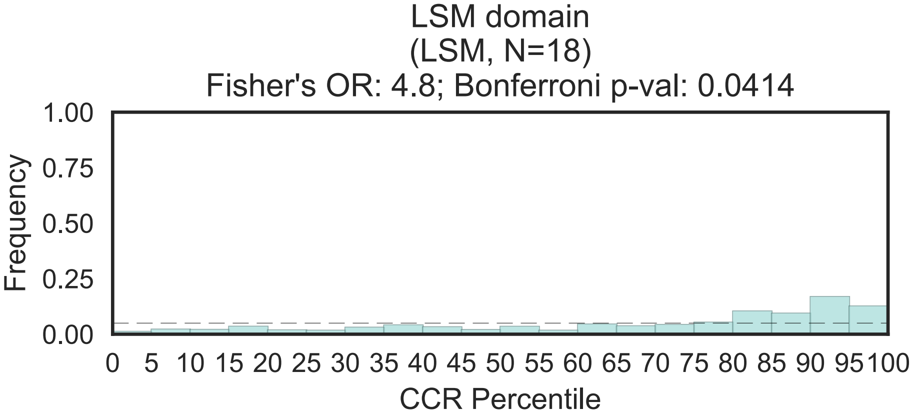
Leucine Rich repeats (2 copies)
(LRR_4, N=71)
Fisher's OR: 1.27; Bonferroni p-val: 1

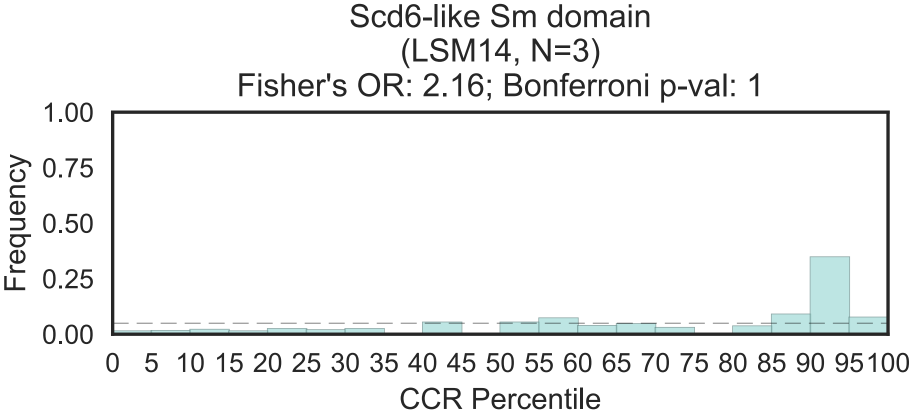

Leucine rich repeats (6 copies)
(LRR_5, N=169)
Fisher's OR: 0.979; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

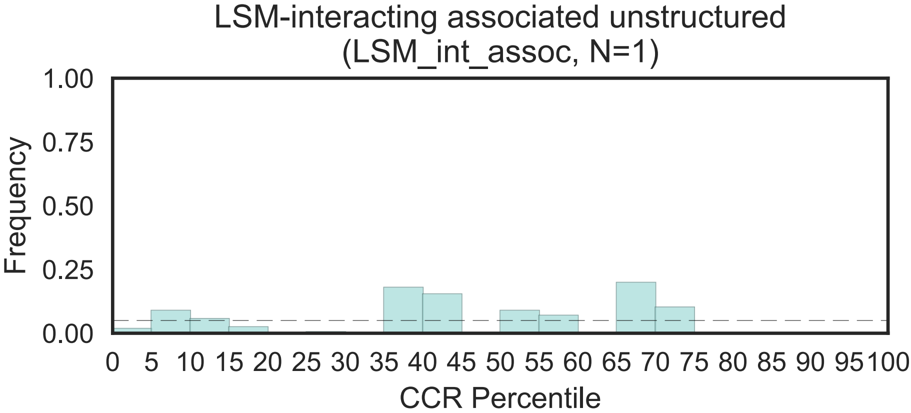

Leucine Rich repeat
(LRR_6, N=266)
Fisher's OR: 1.35; Bonferroni p-val: 1

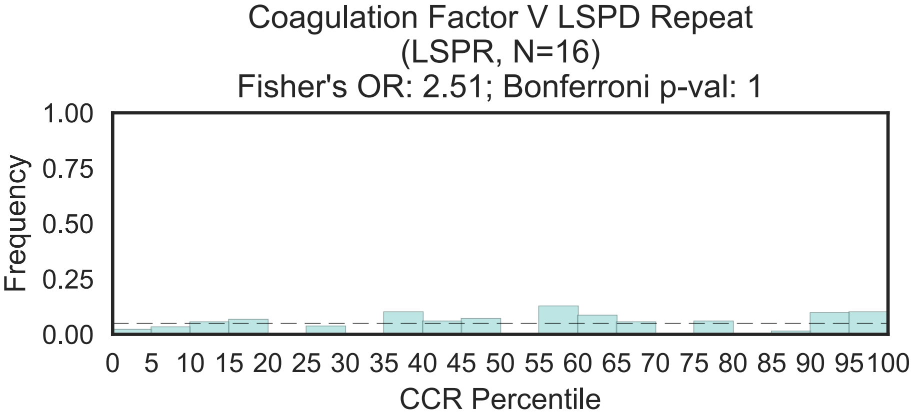

Leucine rich repeat
(LRR_8, N=415)
Fisher's OR: 0.817; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

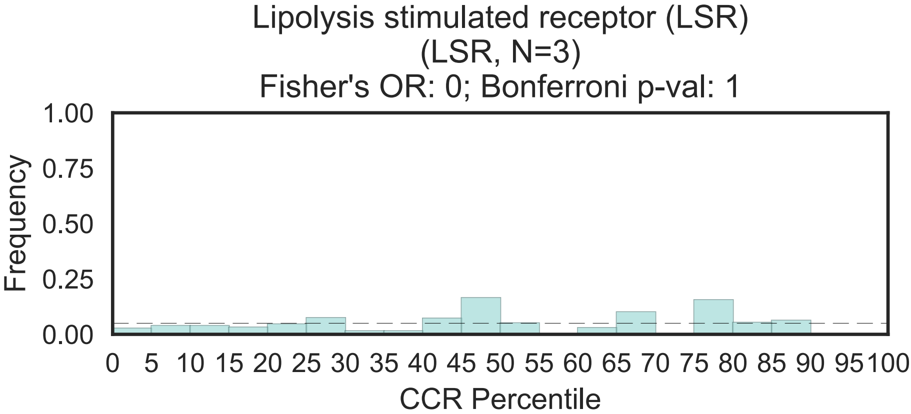

Leucine-rich repeat
(LRR_9, N=25)
Fisher's OR: 1.21; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

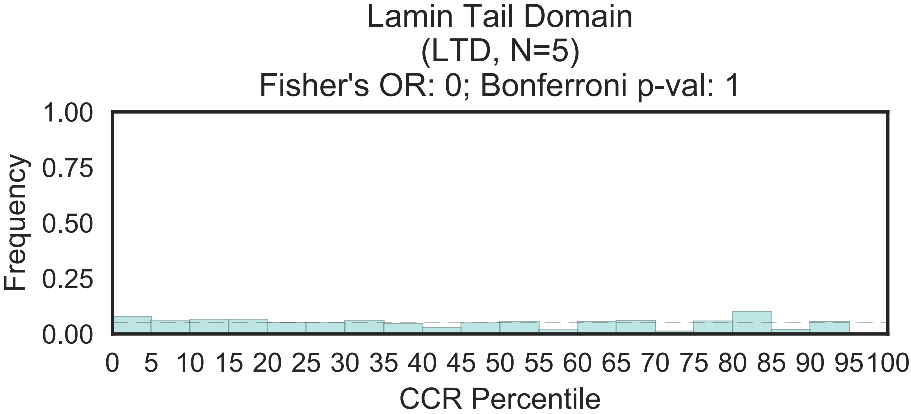

LSM domain
(LSM, N=18)
Fisher's OR: 4.8; Bonferroni p-val: 0.0414
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

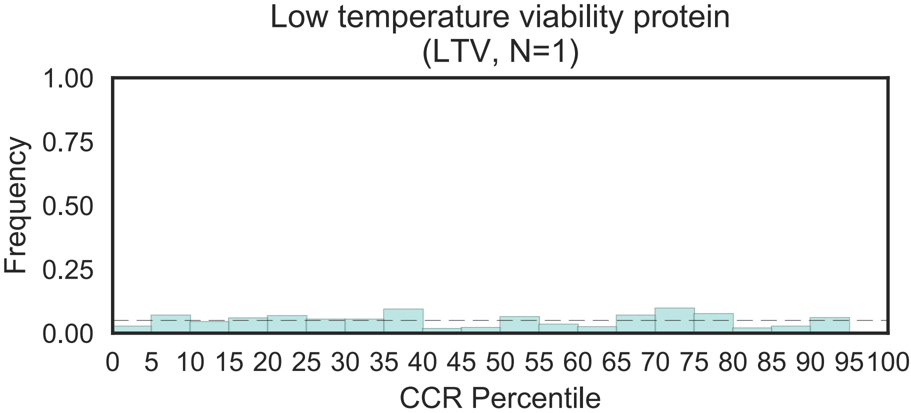

Scd6-like Sm domain
(LSM14, N=3)
Fisher's OR: 2.16; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

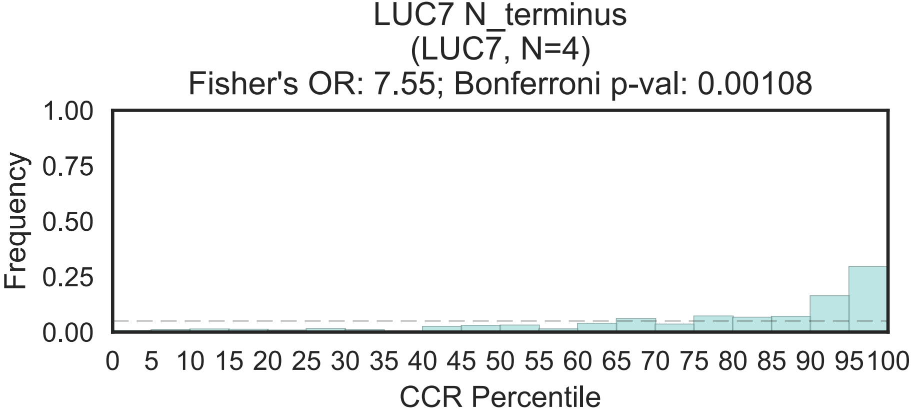

LSM-interacting associated unstructured
(LSM_int_assoc, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

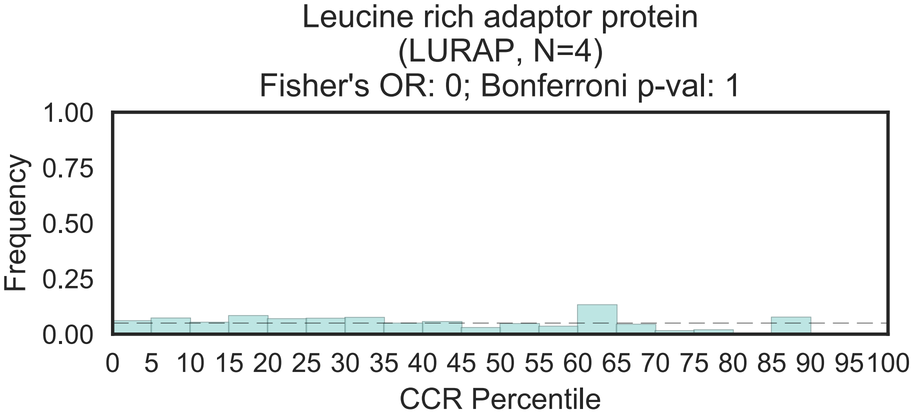

Coagulation Factor V LSPD Repeat
(LSPR, N=16)
Fisher's OR: 2.51; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

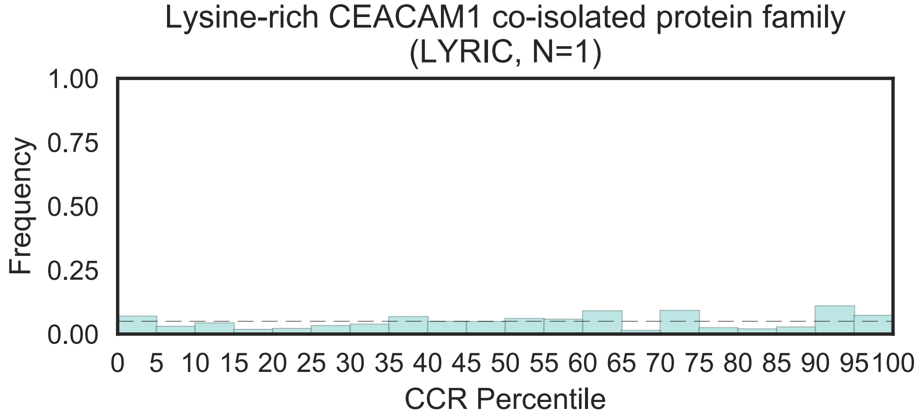

Lipolysis stimulated receptor (LSR)
(LSR, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Lamin Tail Domain
(LTD, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

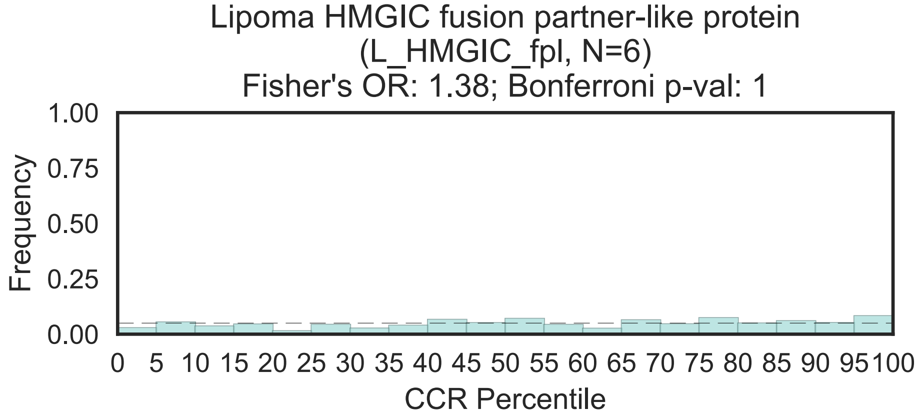

Low temperature viability protein
(LTV, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

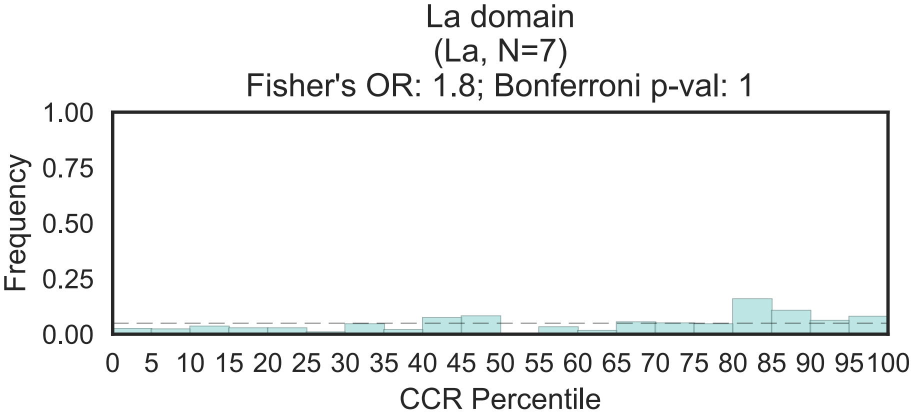

LUC7 N_terminus
(LUC7, N=4)
Fisher's OR: 7.55; Bonferroni p-val: 0.00108
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

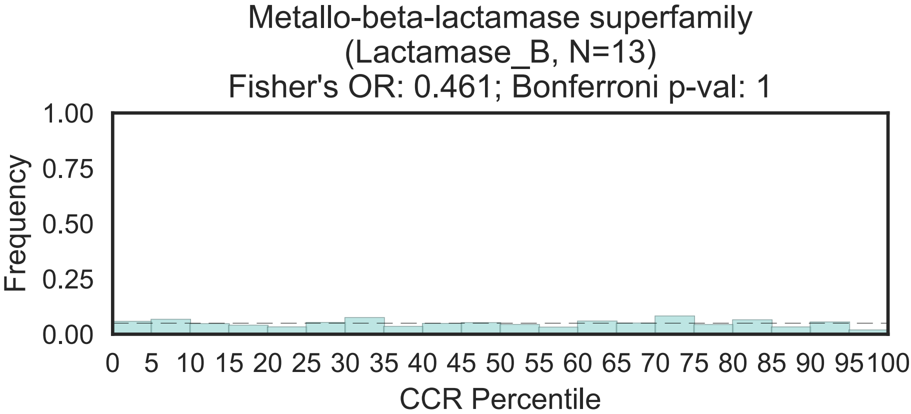

Leucine rich adaptor protein
(LURAP, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

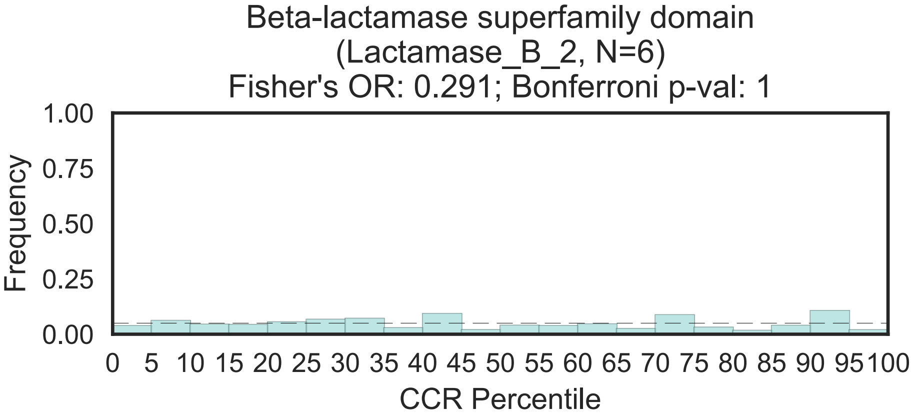


Lysine-rich CEACAM1 co-isolated protein family
(LYRIC, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

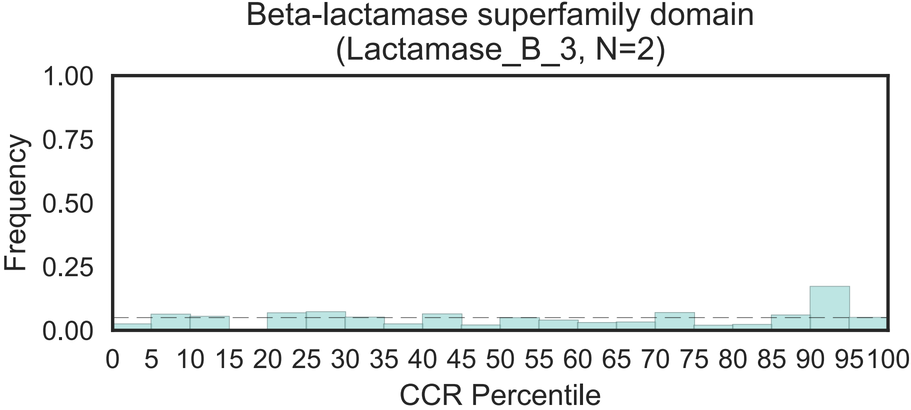

Lipoma HMGIC fusion partner-like protein
(L_HMGIC_fpl, N=6)
Fisher's OR: 1.38; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

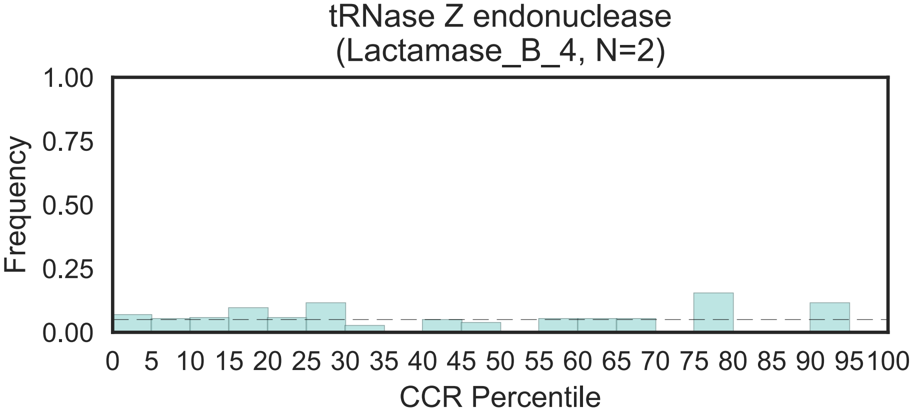

La domain
(La, N=7)
Fisher's OR: 1.8; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

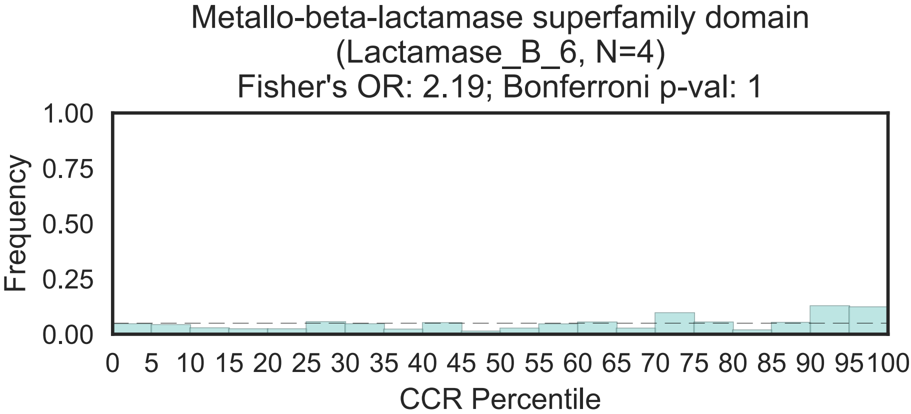
Metallo-beta-lactamase superfamily
(Lactamase_B, N=13)
Fisher's OR: 0.461; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



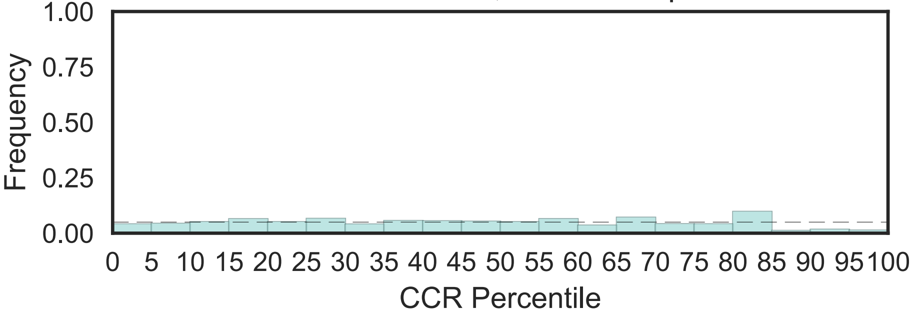
Beta-lactamase superfamily domain
(Lactamase_B_2, N=6)
Fisher's OR: 0.291; Bonferroni p-val: 1


Beta-lactamase superfamily domain
(Lactamase_B_3, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

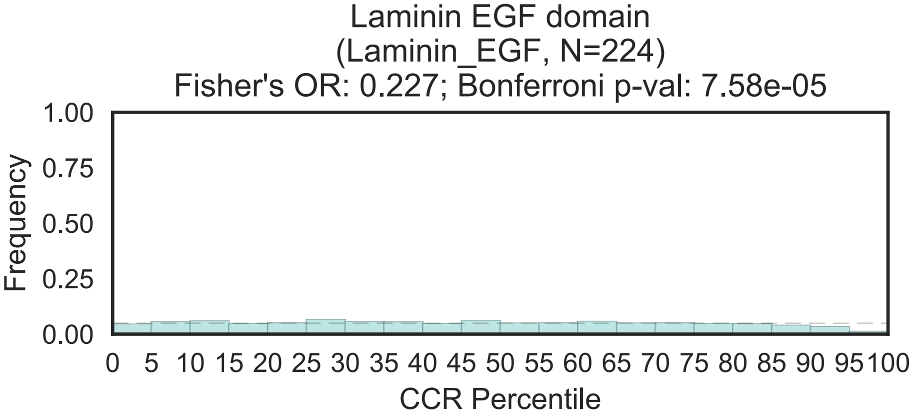

tRNase Z endonuclease
(Lactamase_B_4, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

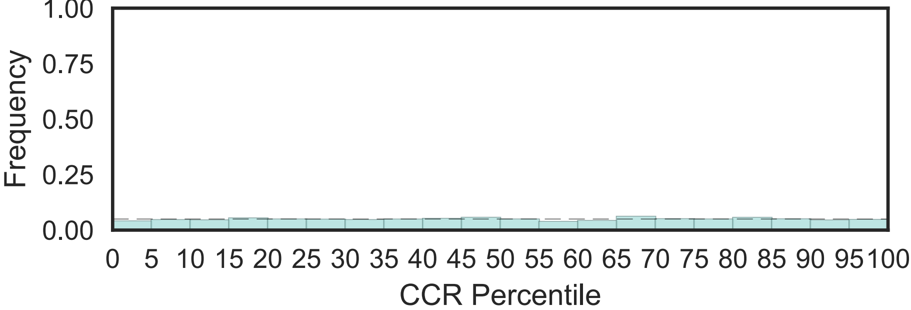


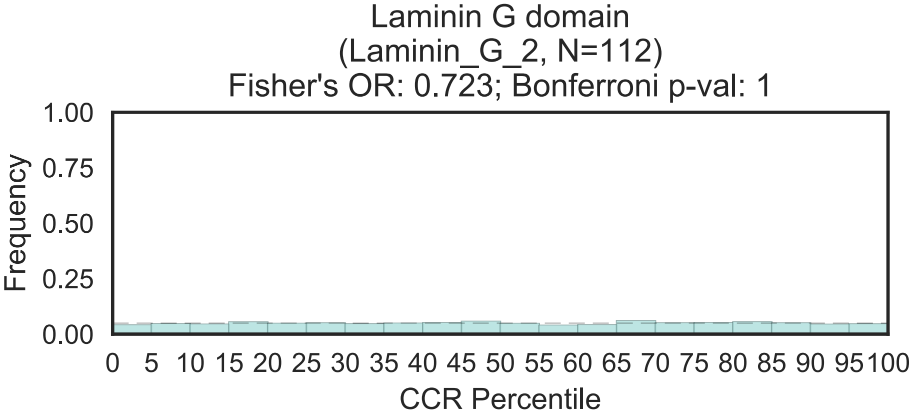
Metallo-beta-lactamase superfamily domain
(Lactamase_B_6, N=4)
Fisher's OR: 2.19; Bonferroni p-val: 1

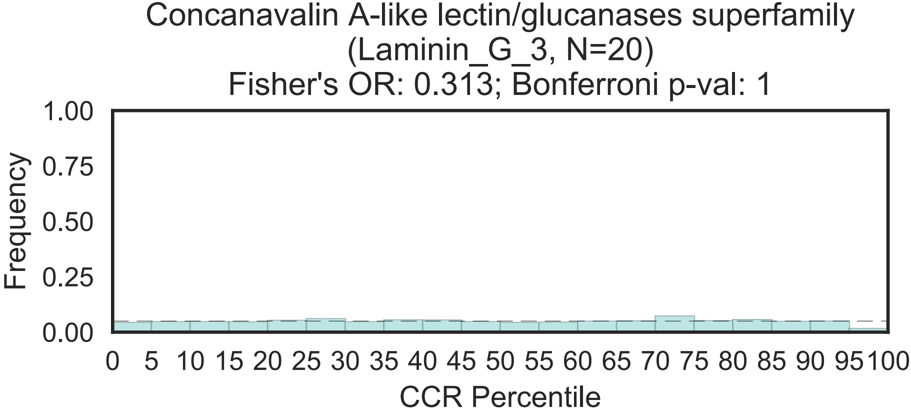


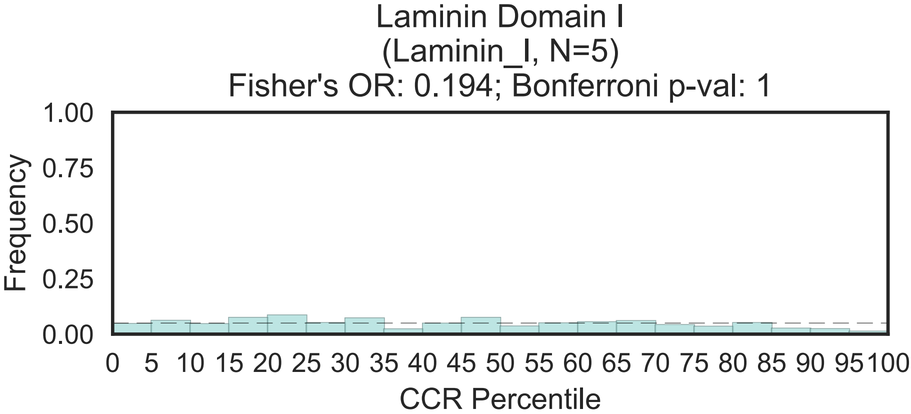
Laminin B (Domain IV)
(Laminin_B, N=12)
Fisher's OR: 0.164; Bonferroni p-val: 1

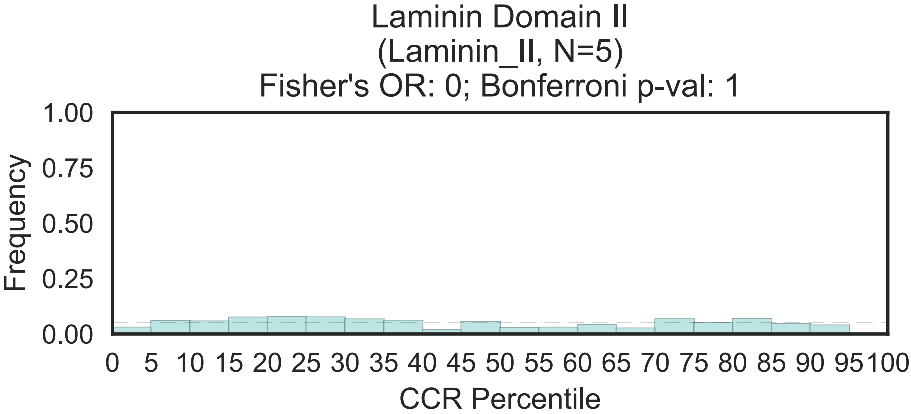

Laminin EGF domain
(Laminin_EGF, N=224)
Fisher's OR: 0.227; Bonferroni p-val: 7.58e-05
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

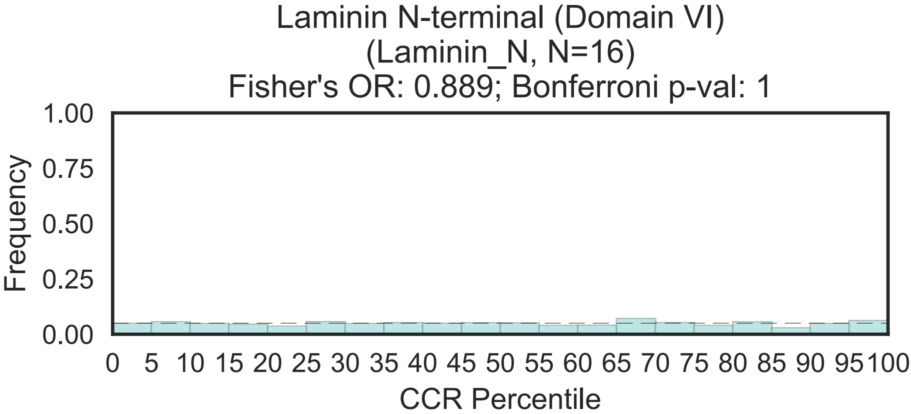

Laminin G domain
(Laminin_G_1, N=104)
Fisher's OR: 0.735; Bonferroni p-val: 1


Laminin G domain
(Laminin_G_2, N=112)
Fisher's OR: 0.723; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

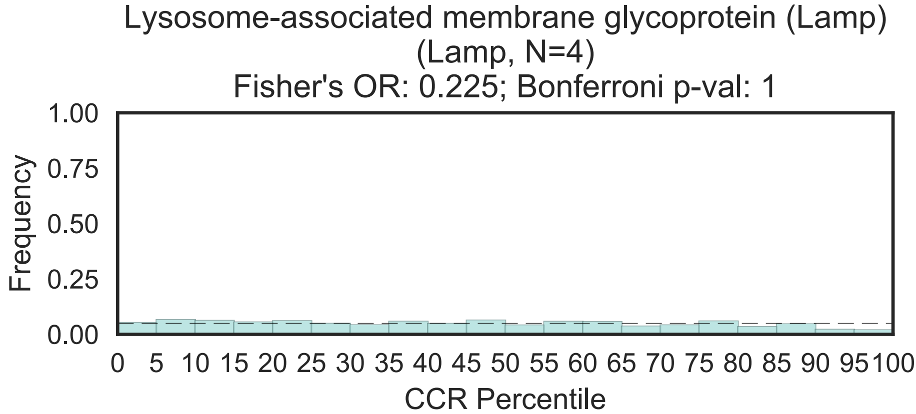

Concanavalin A-like lectin/glucanases superfamily
(Laminin_G_3, N=20)
Fisher's OR: 0.313; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

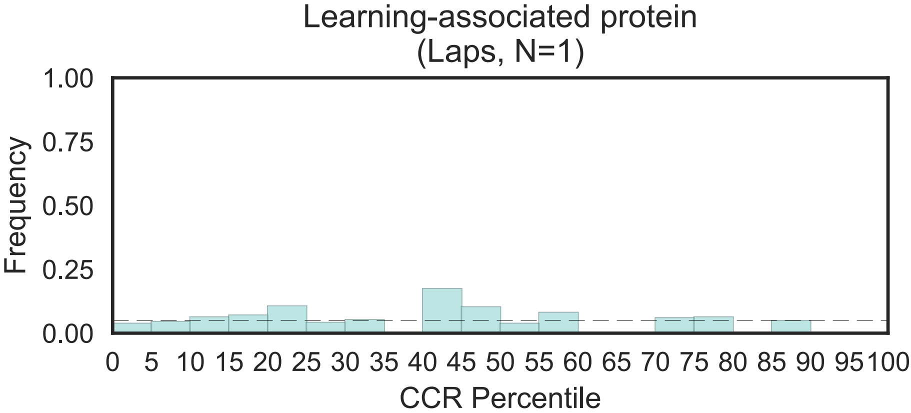

Laminin Domain I
(Laminin_I, N=5)
Fisher's OR: 0.194; Bonferroni p-val: 1

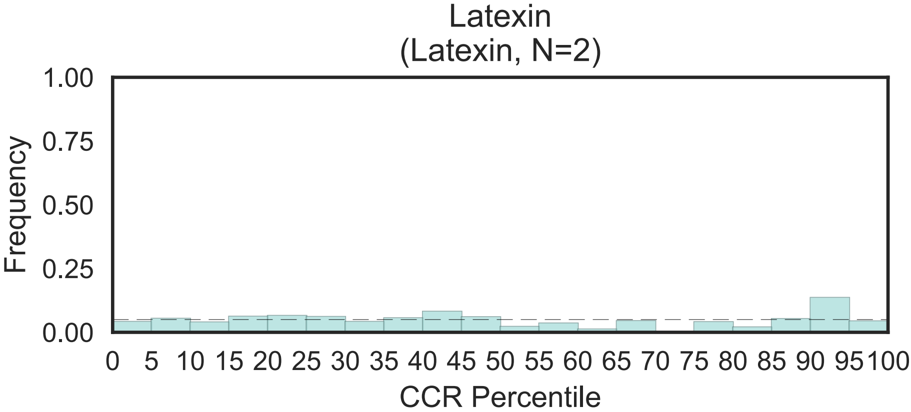

Laminin Domain II
(Laminin_II, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



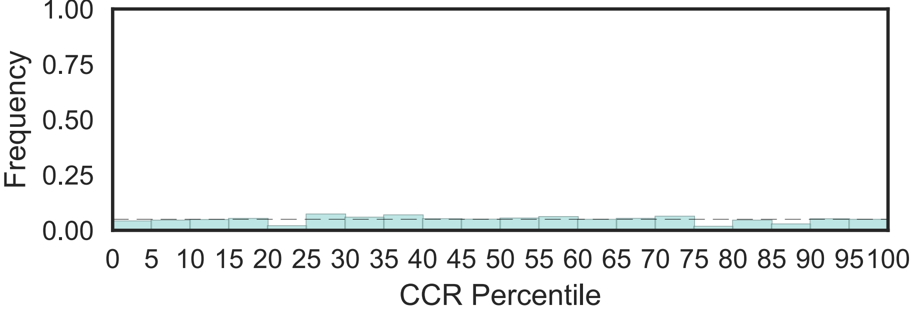
Laminin N-terminal (Domain VI)
(Laminin_N, N=16)
Fisher's OR: 0.889; Bonferroni p-val: 1

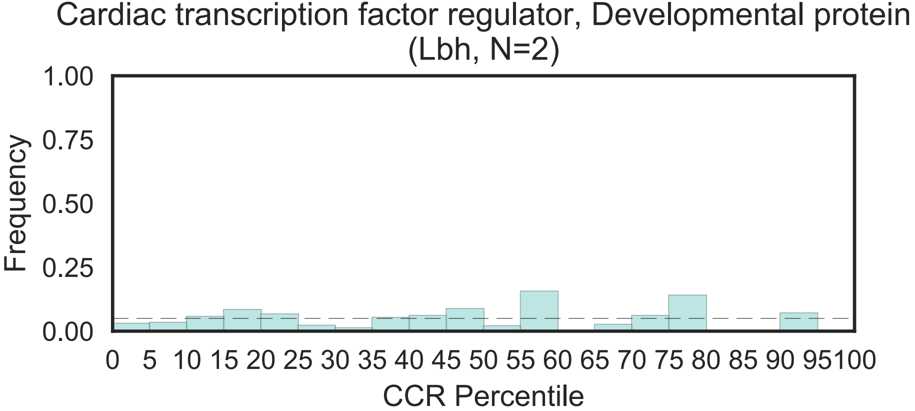

Lysosome-associated membrane glycoprotein (Lamp)
(Lamp, N=4)
Fisher's OR: 0.225; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Learning-associated protein
(Laps, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

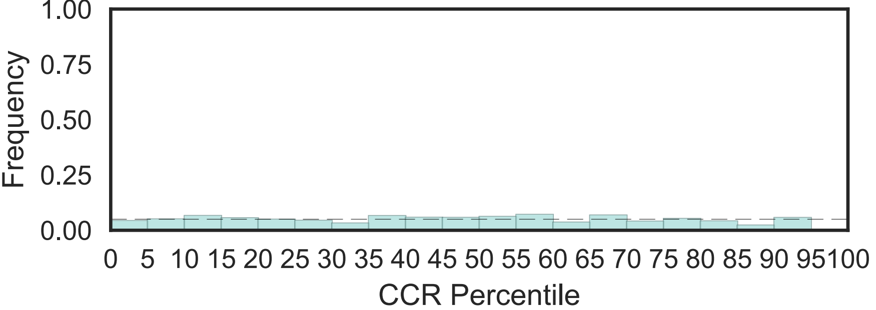

Latexin
(Latexin, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

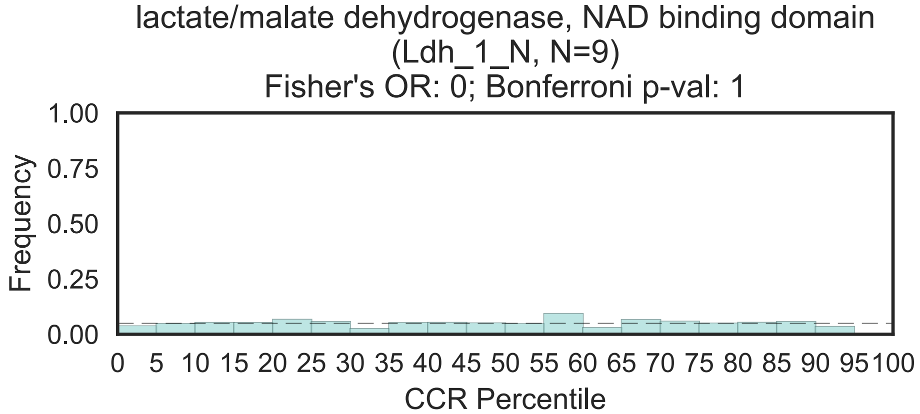
Latrophilin Cytoplasmic C-terminal region (Latrophilin, N=4) Fisher's OR: 0.699; Bonferroni p-val: 1

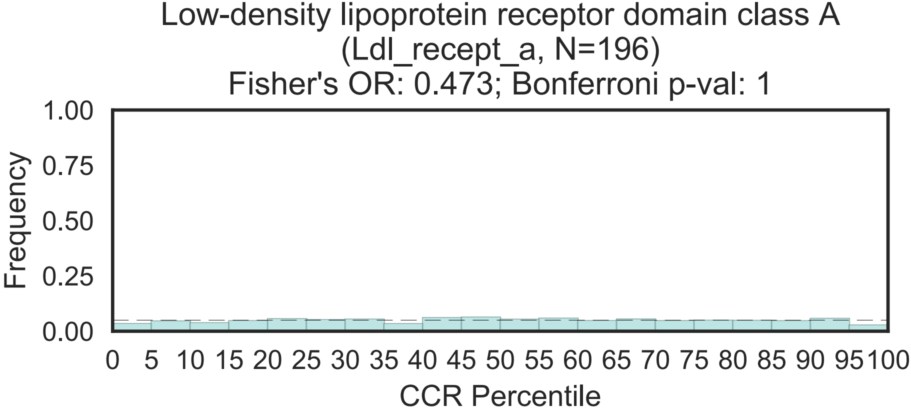


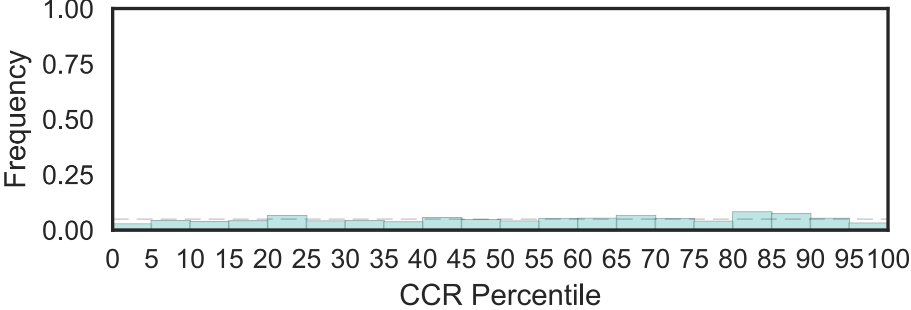

Cardiac transcription factor regulator, Developmental protein
(Lbh, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95100
CCR Percentile

lactate/malate dehydrogenase, alpha/beta C-terminal domain
(Ldh_1_C, N=8)
Fisher's OR: 0; Bonferroni p-val: 1

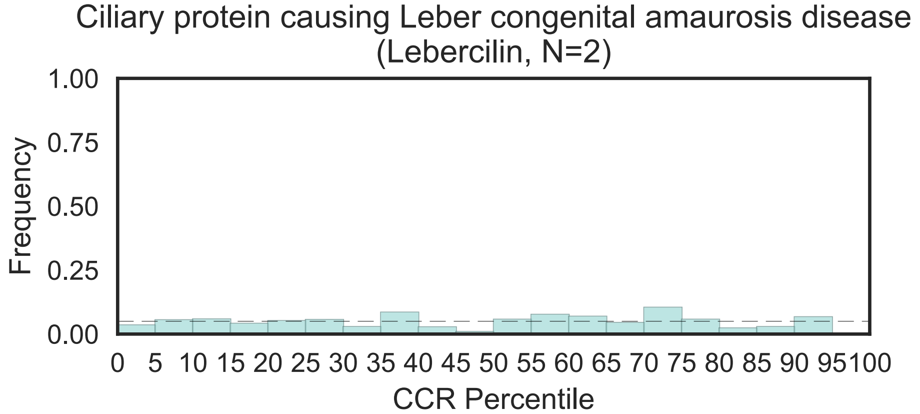



lactate/malate dehydrogenase, NAD binding domain
(Ldh_1_N, N=9)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

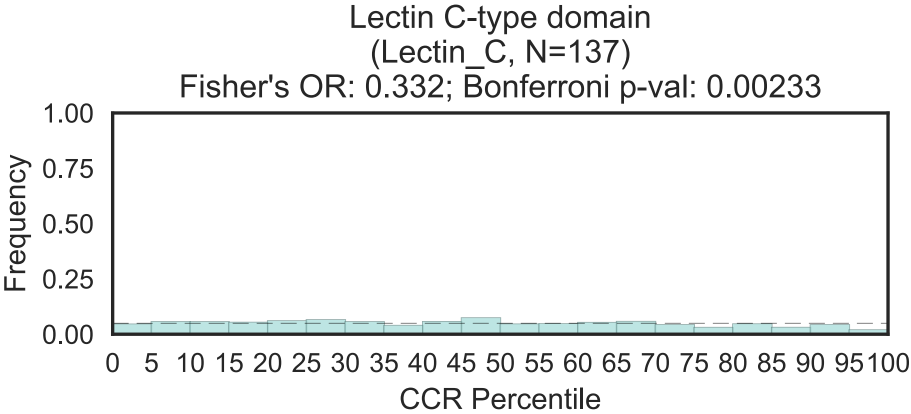

Low-density lipoprotein receptor domain class A
(Ldl_recept_a, N=196)
Fisher's OR: 0.473; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

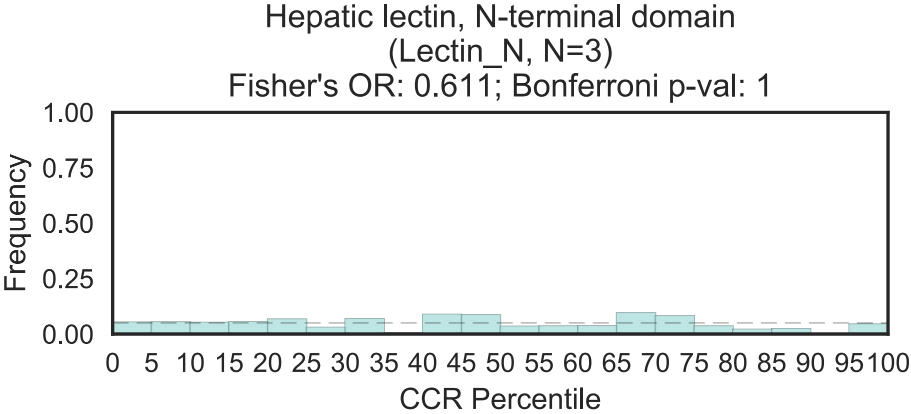


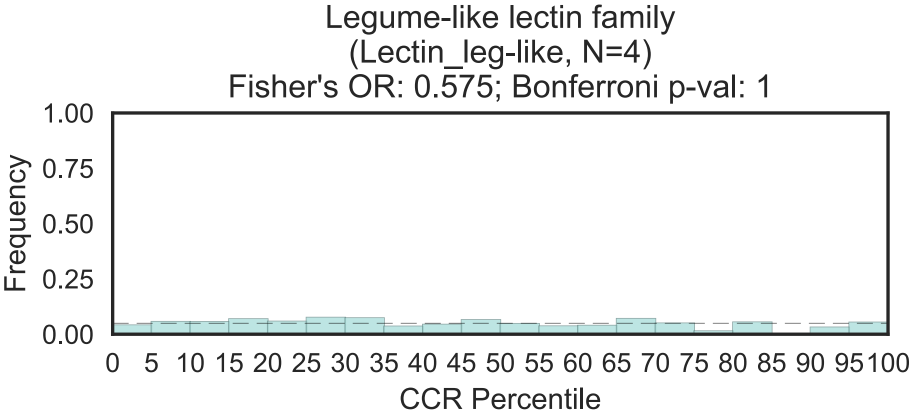
Low-density lipoprotein receptor repeat class B
(Ldl_recept_b, N=113)
Fisher's OR: 0.686; Bonferroni p-val: 1

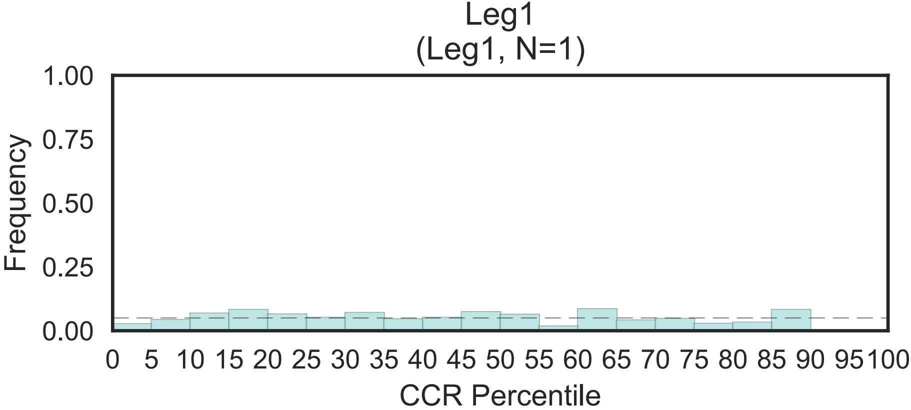


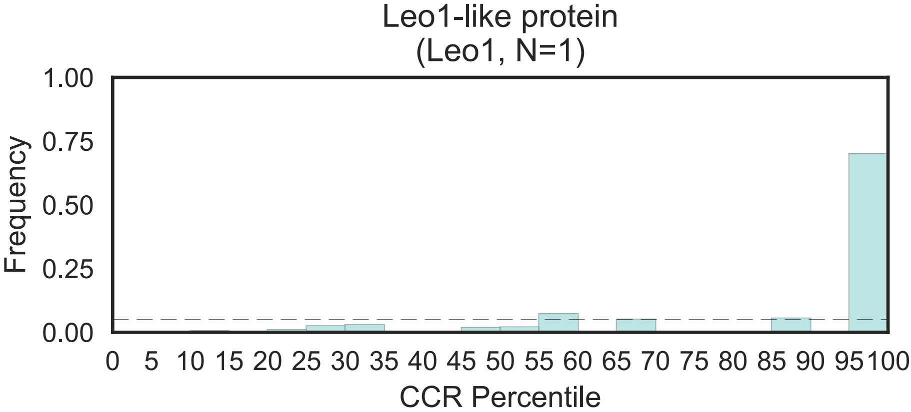
Ciliary protein causing Leber congenital amaurosis disease
(Lebercilin, N=2)


Lectin C-type domain
(Lectin_C, N=137)
Fisher's OR: 0.332; Bonferroni p-val: 0.00233

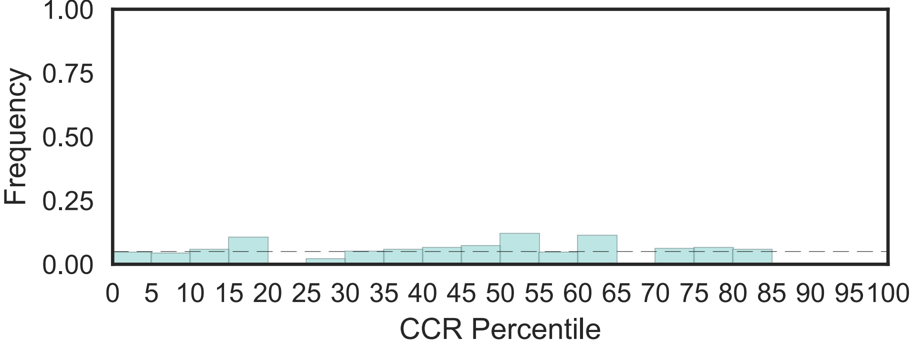

Hepatic lectin, N-terminal domain
(Lectin_N, N=3)
Fisher's OR: 0.611; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Legume-like lectin family
(Lectin_leg-like, N=4)
Fisher's OR: 0.575; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

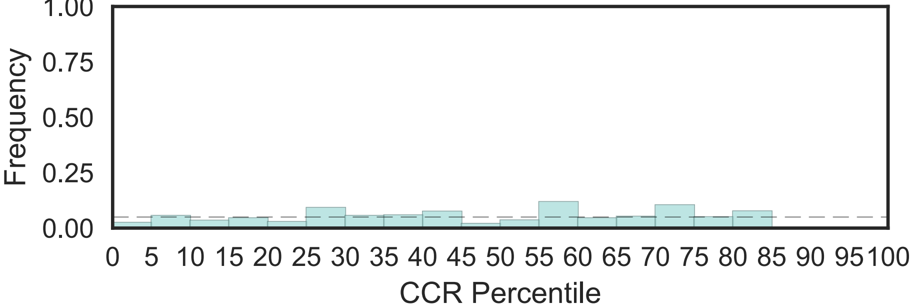

Leg1
(Leg1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

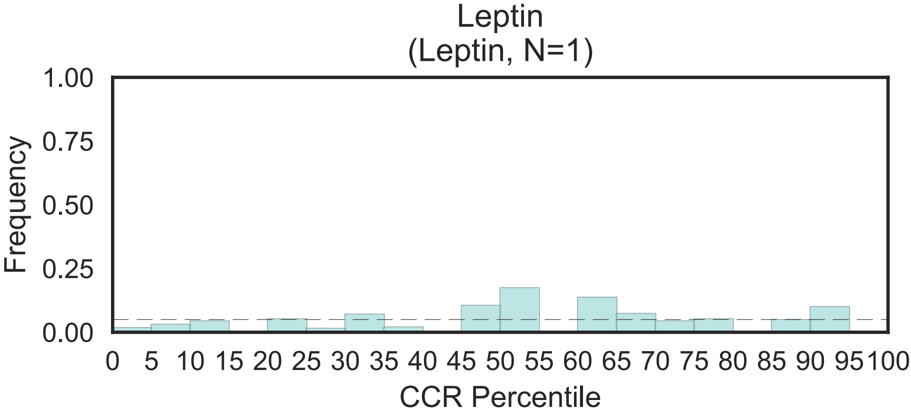

Leo1-like protein
(Leo1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

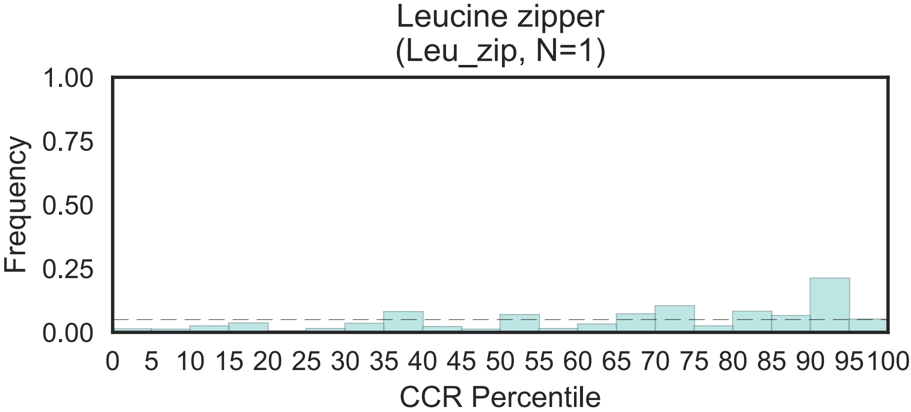
GTP-binding protein LepA C-terminus (LepA_C, N=1)

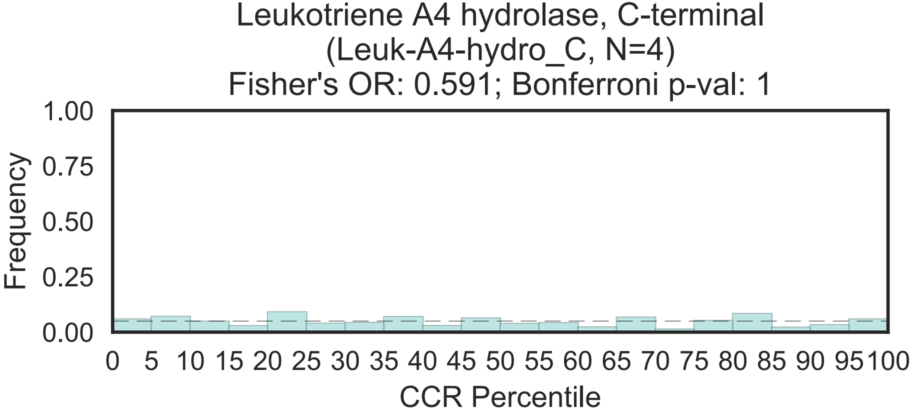


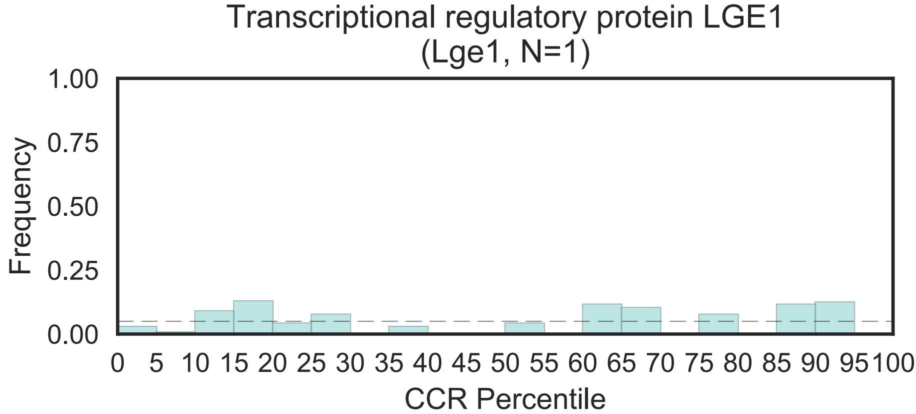
Ig-like C2-type domain
(Lep_receptor_Ig, N=4)
Fisher's OR: 0; Bonferroni p-val: 1



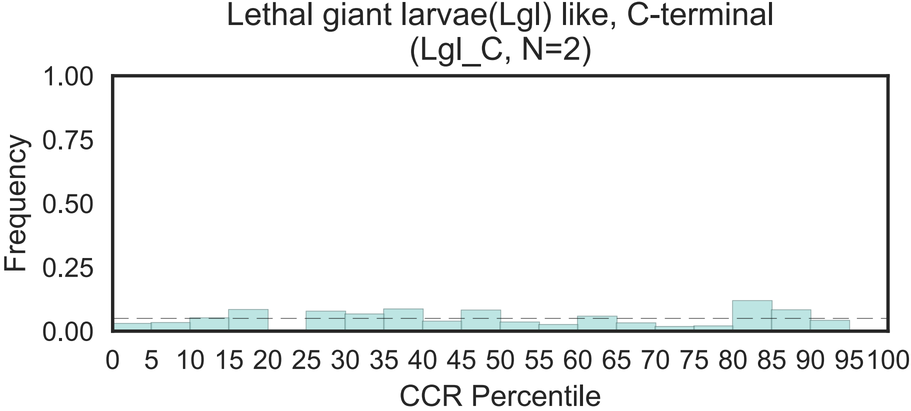

Leptin
(Leptin, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

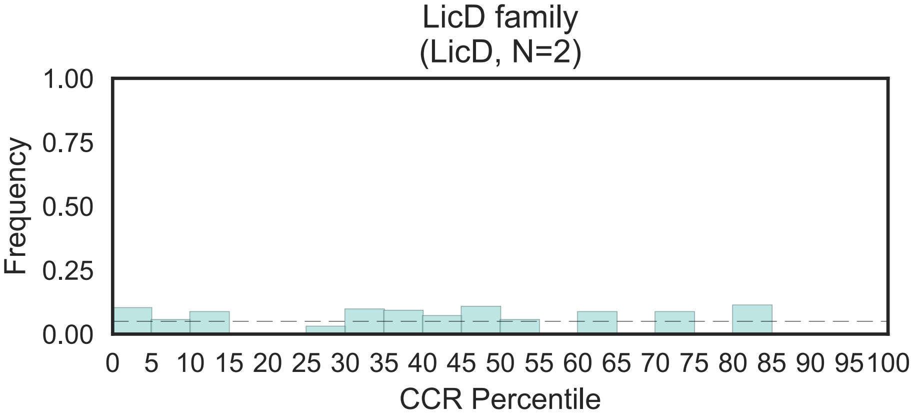

Leucine zipper
(Leu_zip, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

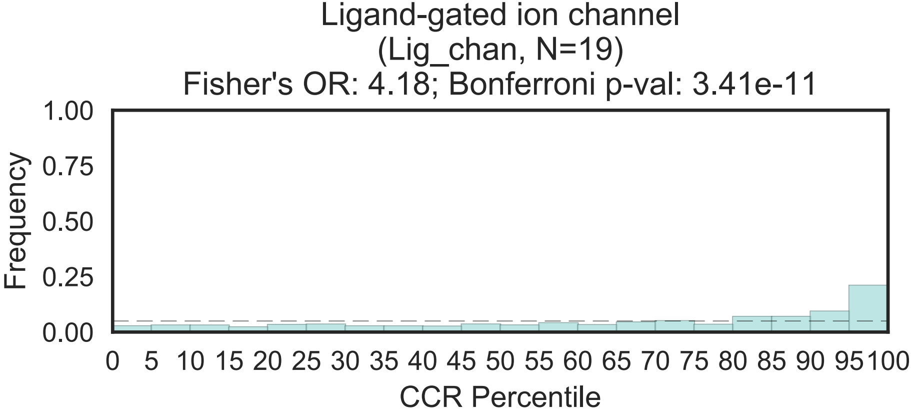

Leukotriene A4 hydrolase, C-terminal
(Leuk-A4-hydro_C, N=4)
Fisher's OR: 0.591; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

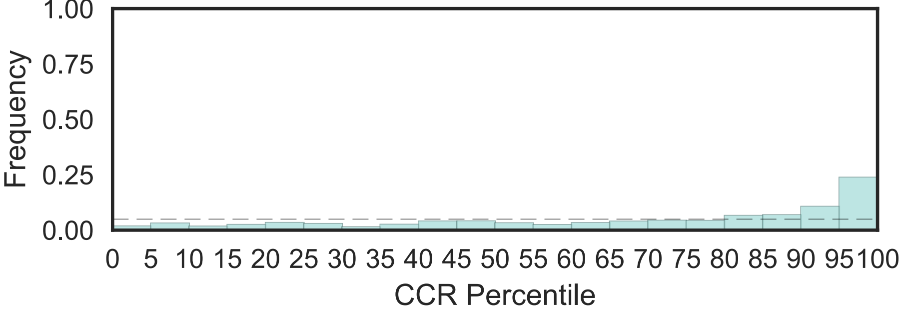


Transcriptional regulatory protein LGE1
(Lge1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

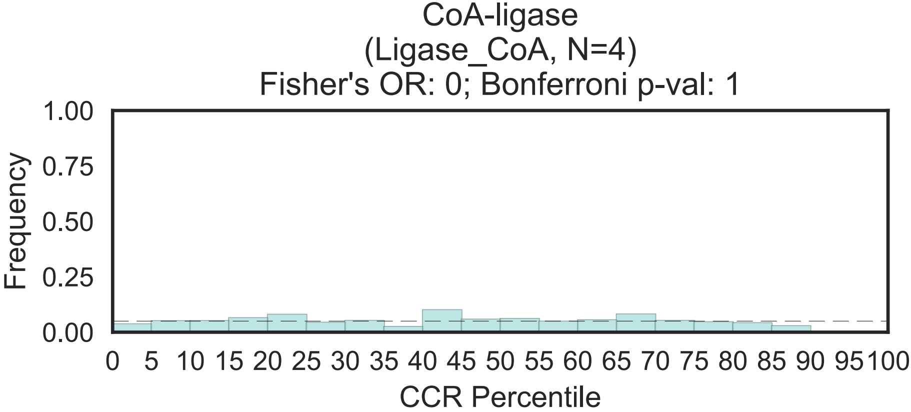

Lethal giant larvae(Lgl) like, C-terminal
(Lgl_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

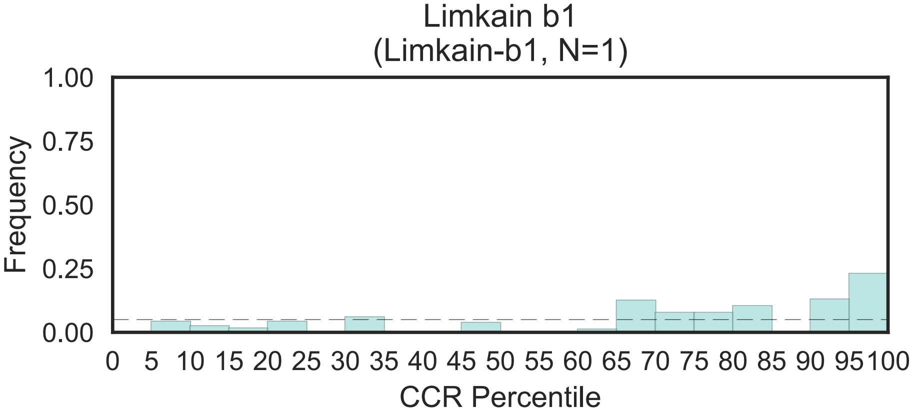

LicD family
(LicD, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ligand-gated ion channel
(Lig_chan, N=19)
Fisher's OR: 4.18; Bonferroni p-val: 3.41e-11
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

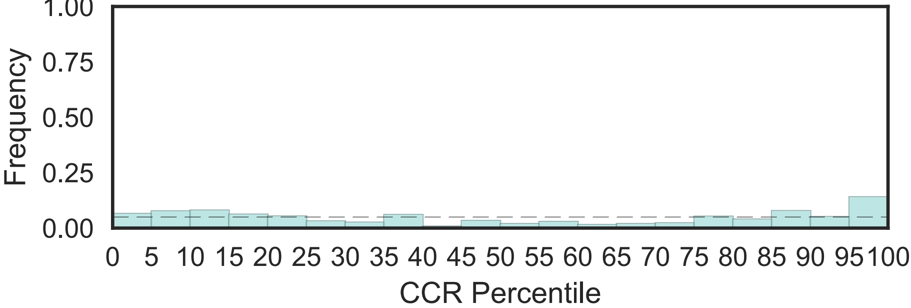


Ligated ion channel L-glutamate- and glycine-binding site
(Lig_chan-Glu_bd, N=17)
Fisher's OR: 4.6; Bonferroni p-val: 0.000148

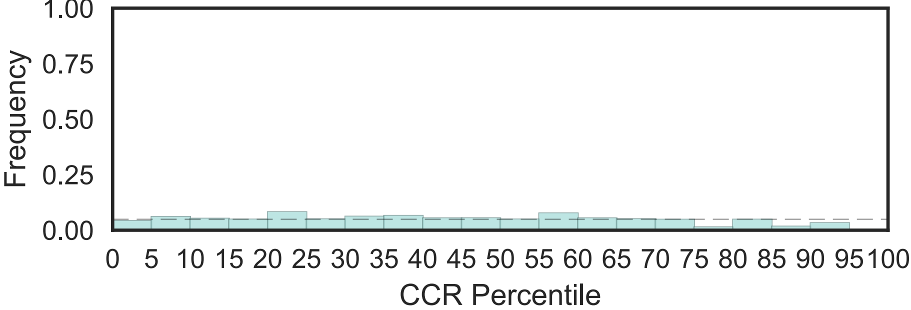

CoA-ligase
(Ligase_CoA, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

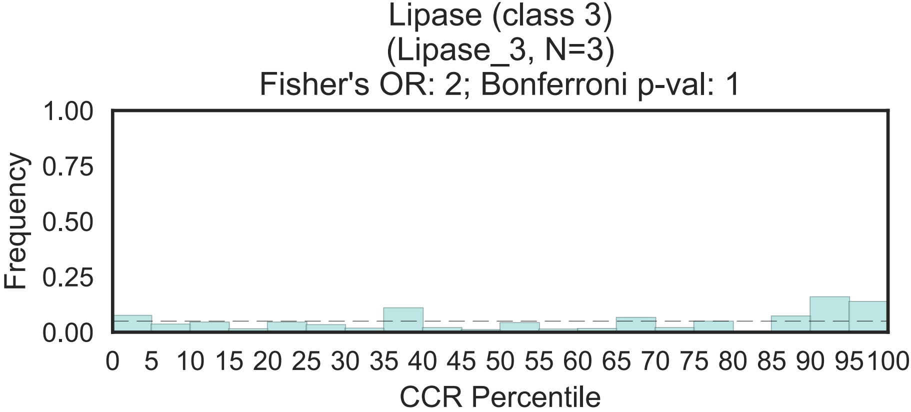

Limkain b1
(Limkain-b1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

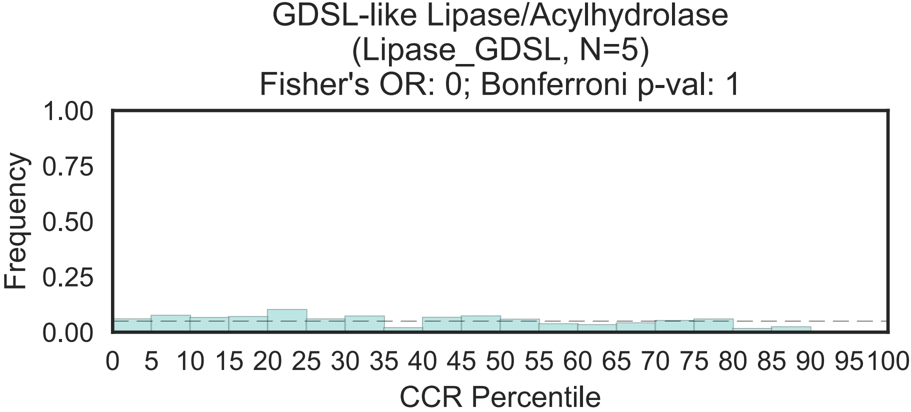
linker histone H1 and H5 family
(Linker_histone, N=13)
Fisher's OR: 1.72; Bonferroni p-val: 1

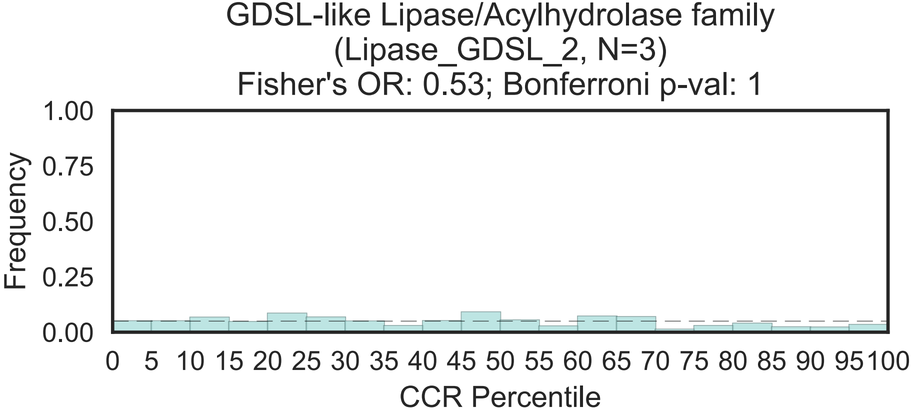


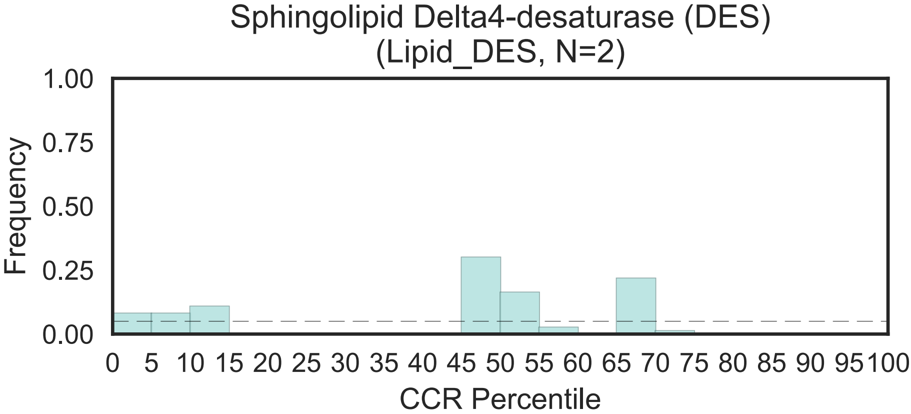
Lipase
(Lipase, N=10)
Fisher's OR: 0.0782; Bonferroni p-val: 0.565

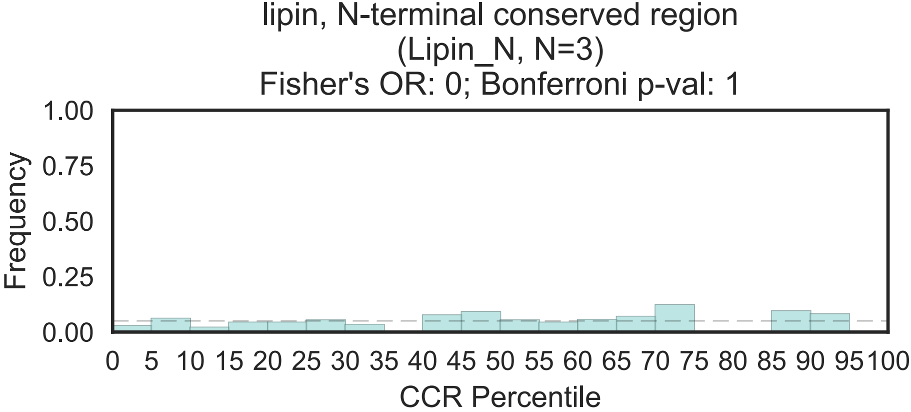



Lipase (class 3)
(Lipase_3, N=3)
Fisher's OR: 2; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

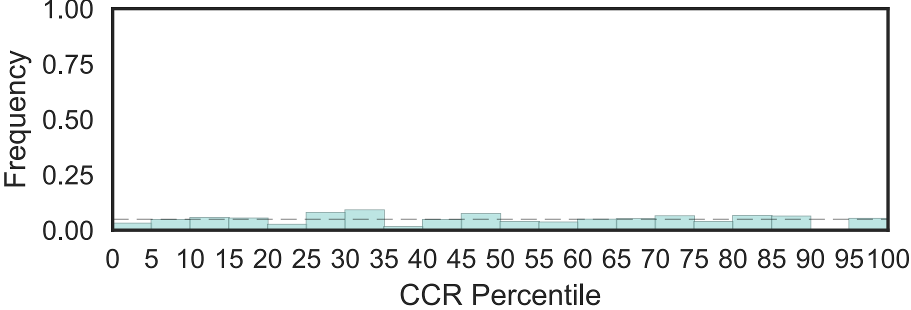

GDSL-like Lipase/Acylhydrolase
(Lipase_GDSL, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

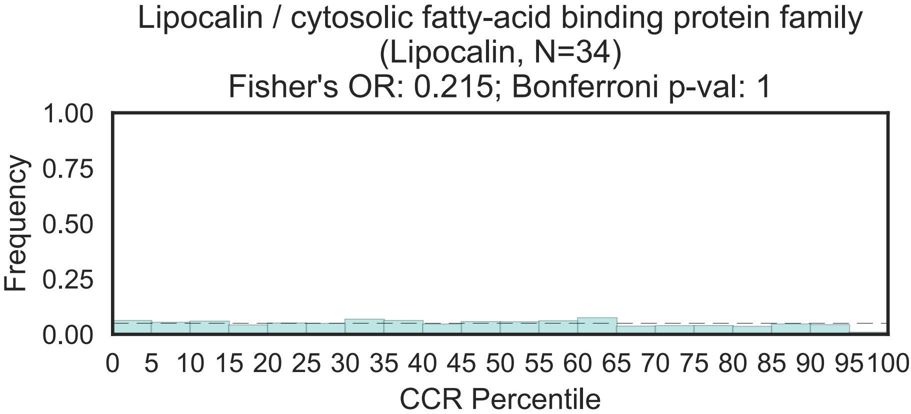

GDSL-like Lipase/Acylhydrolase family
(Lipase_GDSL_2, N=3)
Fisher's OR: 0.53; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

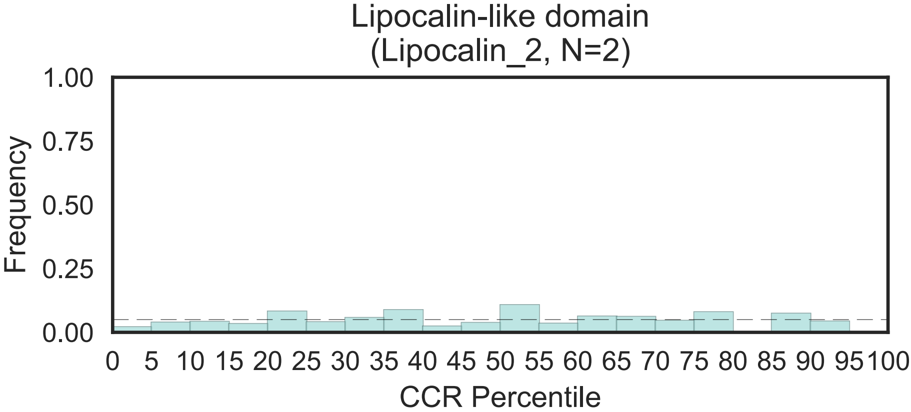

Sphingolipid Delta4-desaturase (DES)
(Lipid_DES, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

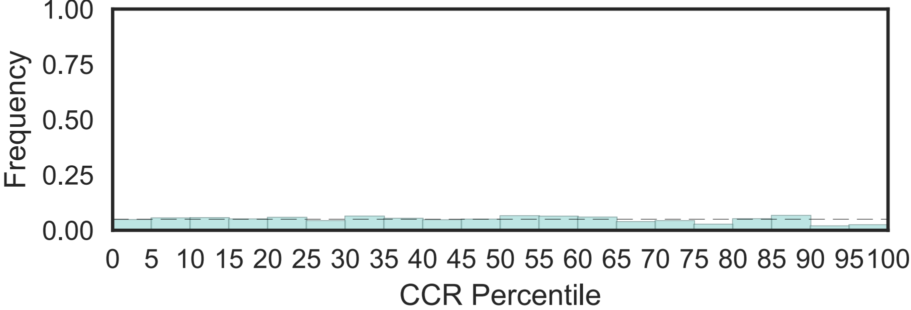


lipin, N-terminal conserved region
(Lipin_N, N=3)
Fisher's OR: 0; Bonferroni p-val: 1


Lipin/Ned1/Smp2 multi-domain protein middle domain (Lipin_mid, N=3)
Fisher's OR: 0.94; Bonferroni p-val: 1

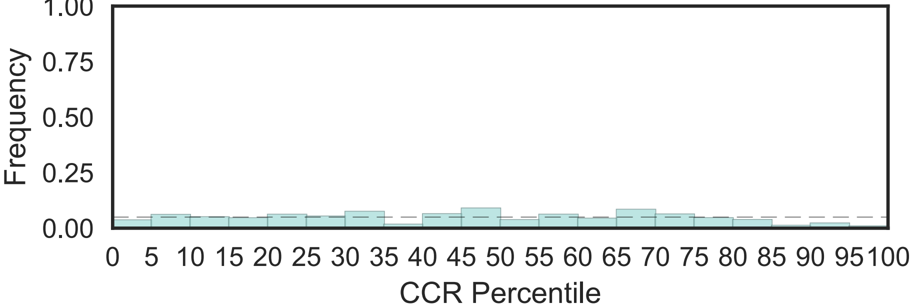

Lipocalin / cytosolic fatty-acid binding protein family
(Lipocalin, N=34)
Fisher's OR: 0.215; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

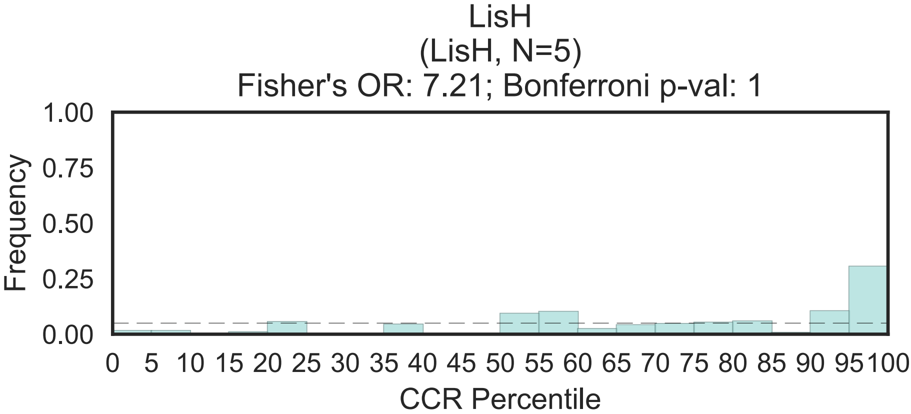

Lipocalin-like domain
(Lipocalin_2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

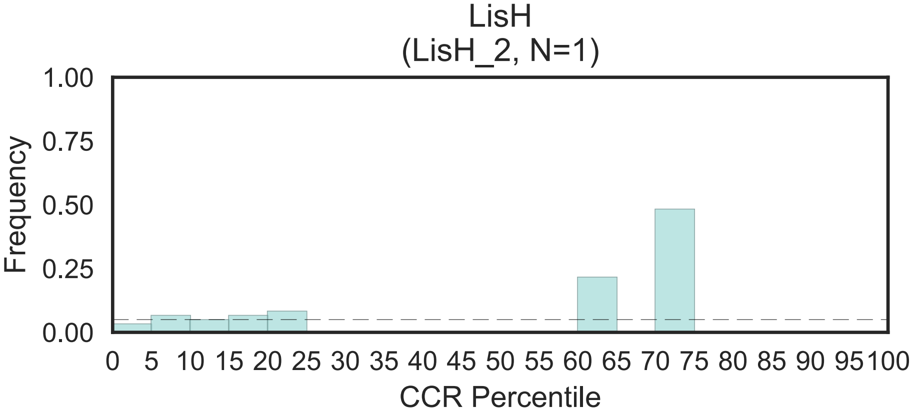


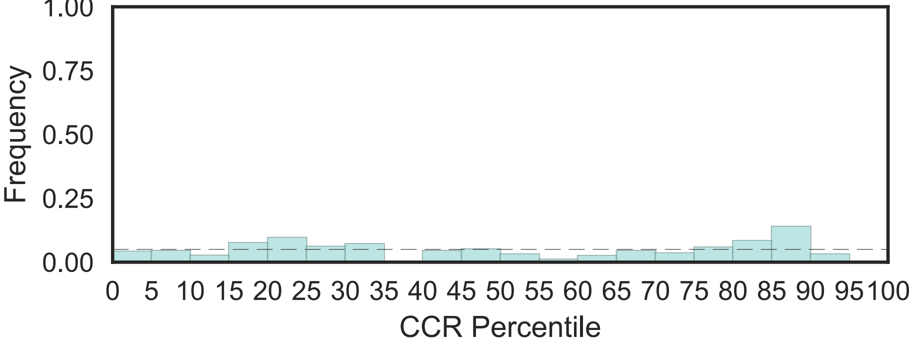
Lipocalin / cytosolic fatty-acid binding protein family
(Lipocalin_7, N=11)
Fisher's OR: 0.398; Bonferroni p-val: 1

Lipoxygenase
(Lipoxygenase, N=7)
Fisher's OR: 0.214; Bonferroni p-val: 1

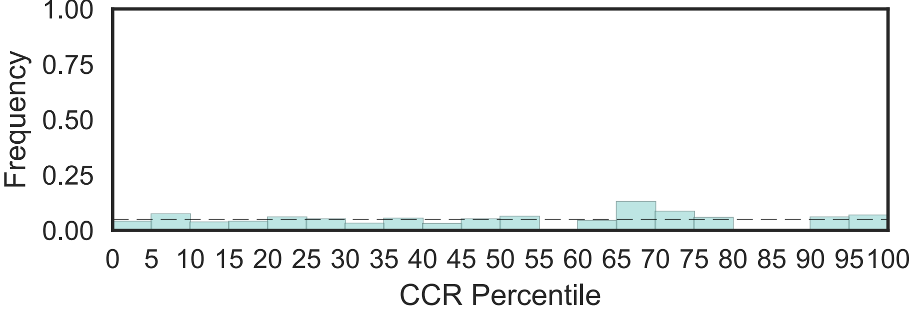



LisH
(LisH, N=5)
Fisher's OR: 7.21; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

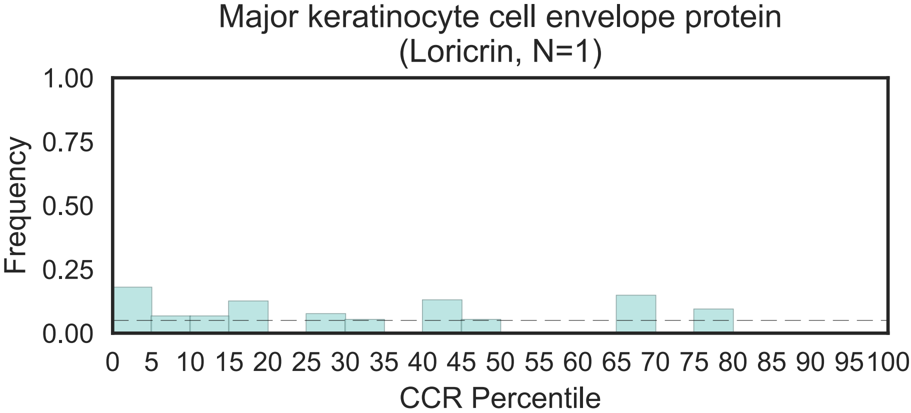

LisH
(LisH_2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

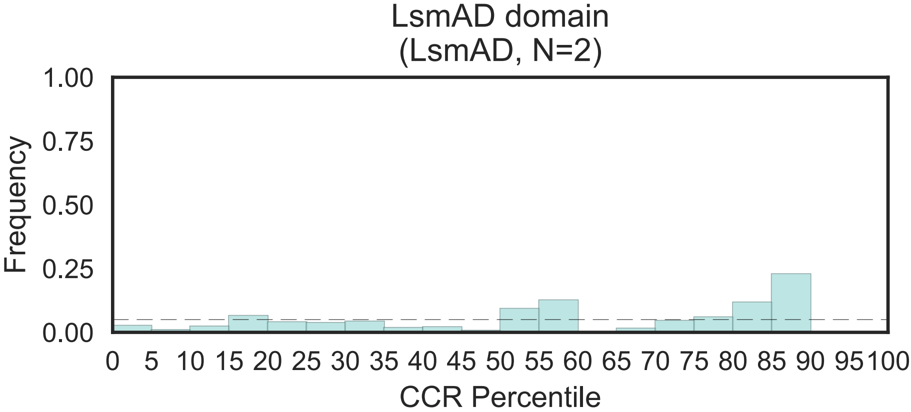


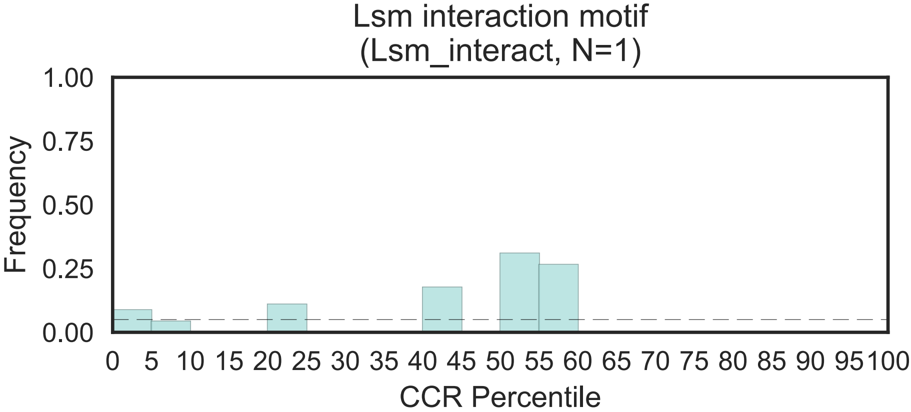
Lon protease (S16) C-terminal proteolytic domain
(Lon_C, N=2)

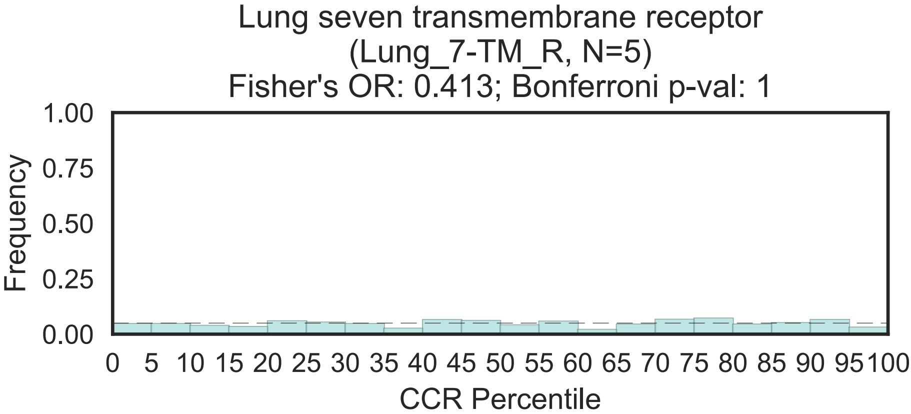


Regulated-SNARE-like domain
(Longin, N=3)
Fisher's OR: 1.29; Bonferroni p-val: 1

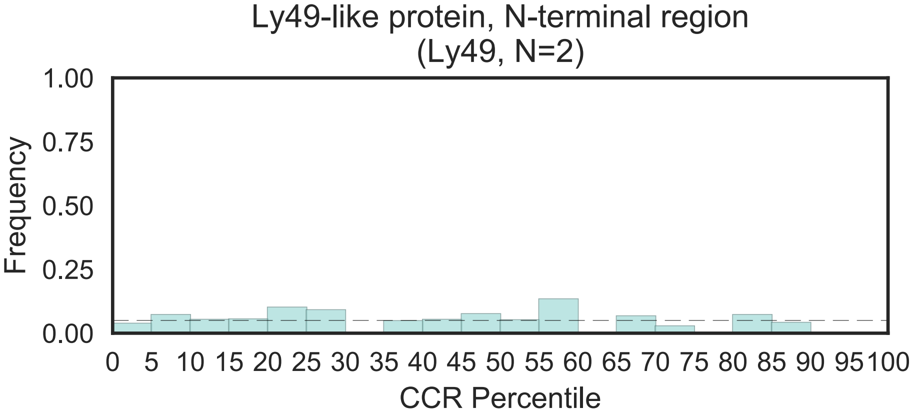

Major keratinocyte cell envelope protein
(Loricrin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

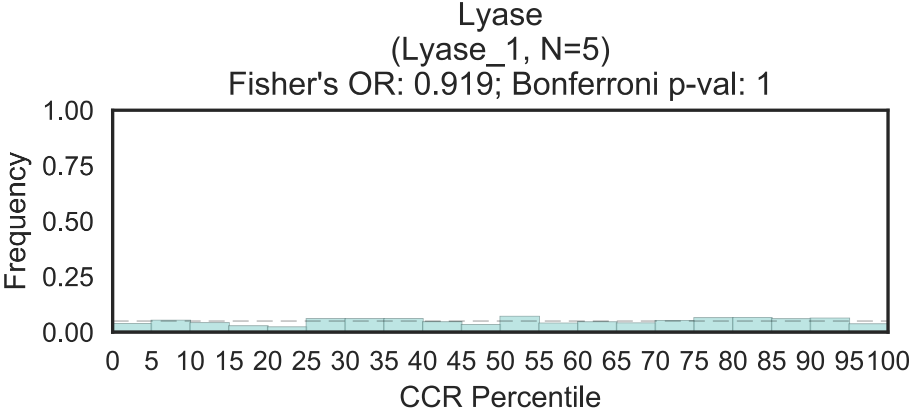

LsmAD domain
(LsmAD, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

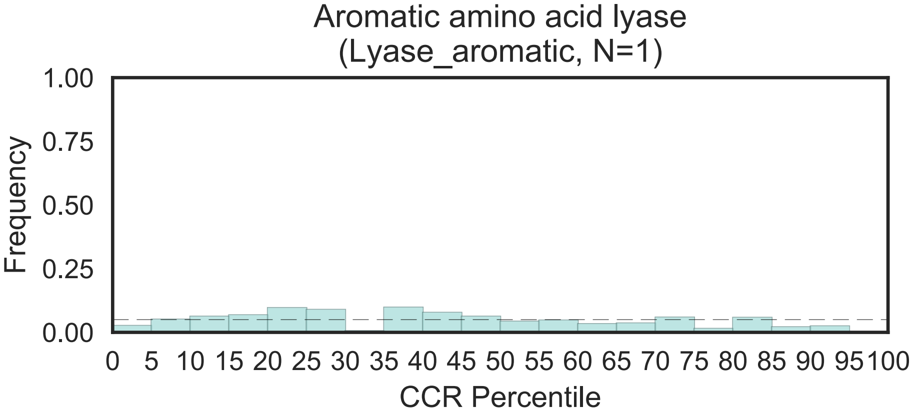

Lsm interaction motif
(Lsm_interact, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



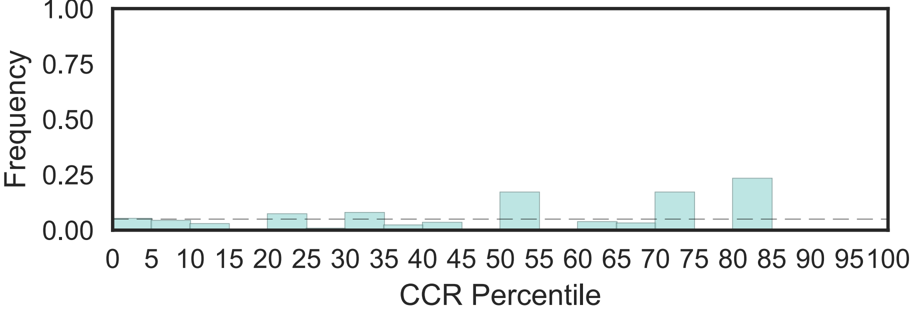
Lung seven transmembrane receptor
(Lung_7-TM_R, N=5)
Fisher's OR: 0.413; Bonferroni p-val: 1


Ly49-like protein, N-terminal region
(Ly49, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

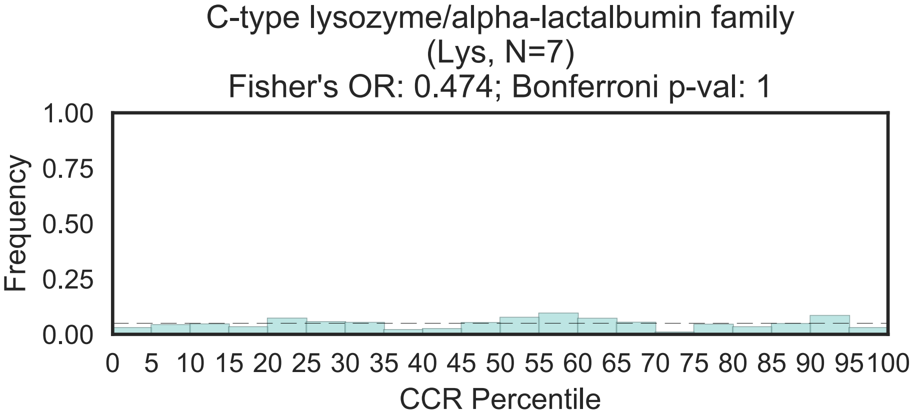

Lyase
(Lyase_1, N=5)
Fisher's OR: 0.919; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

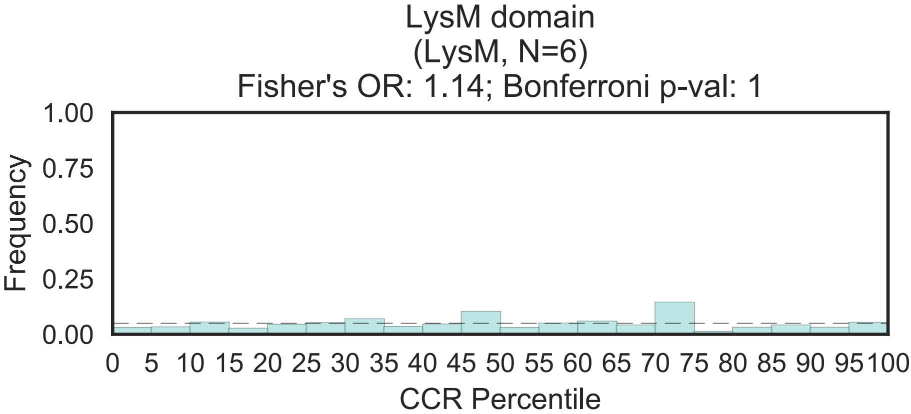


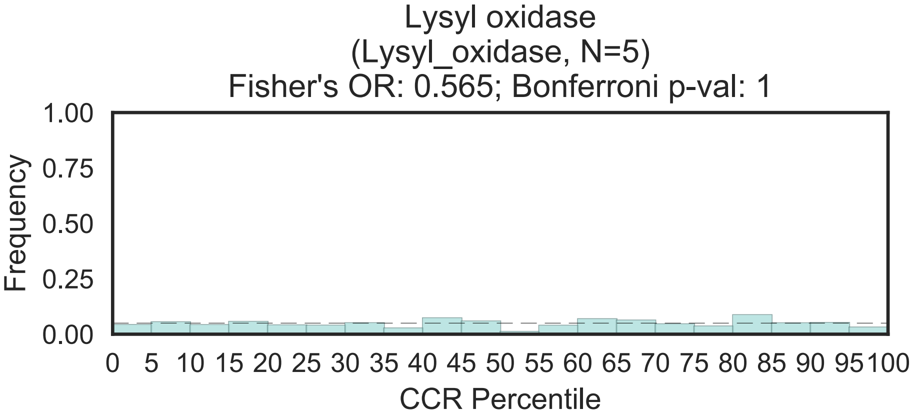
Aromatic amino acid lyase
(Lyase_aromatic, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

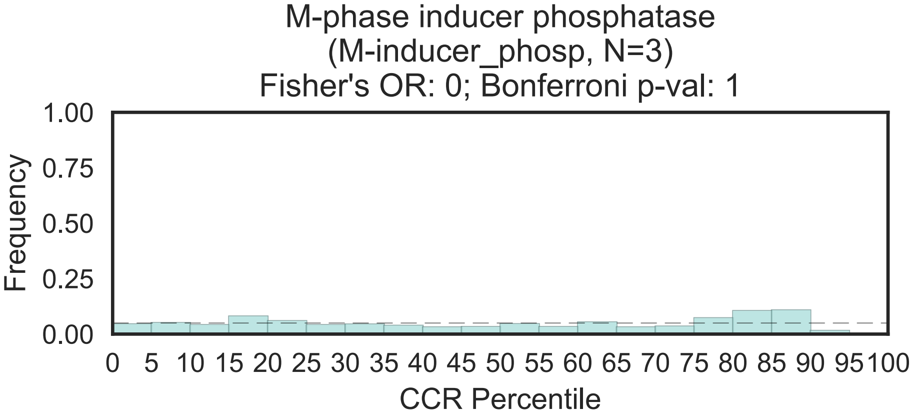


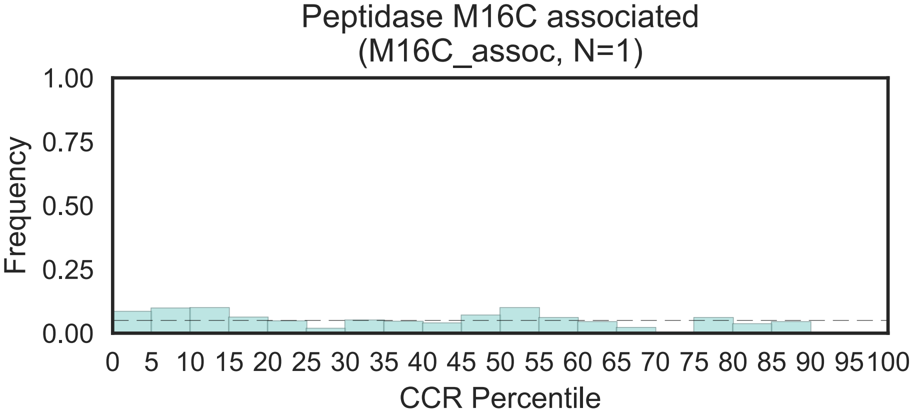
Lycopene cyclase protein
(Lycopene_cycl, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

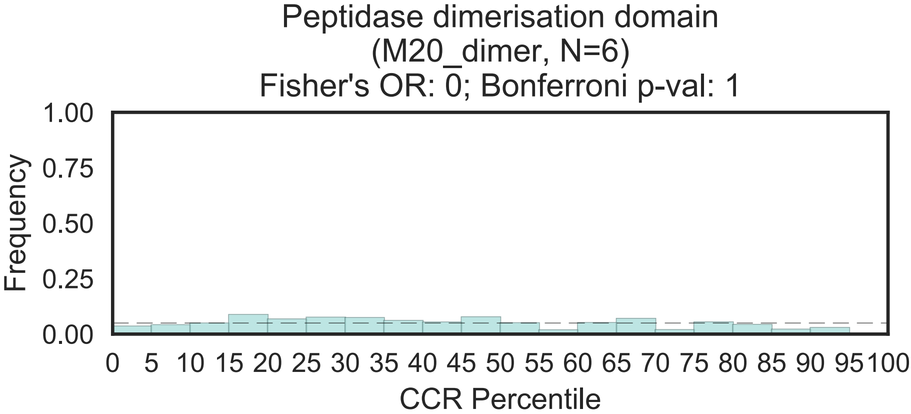

C-type lysozyme/alpha-lactalbumin family
(Lys, N=7)
Fisher's OR: 0.474; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

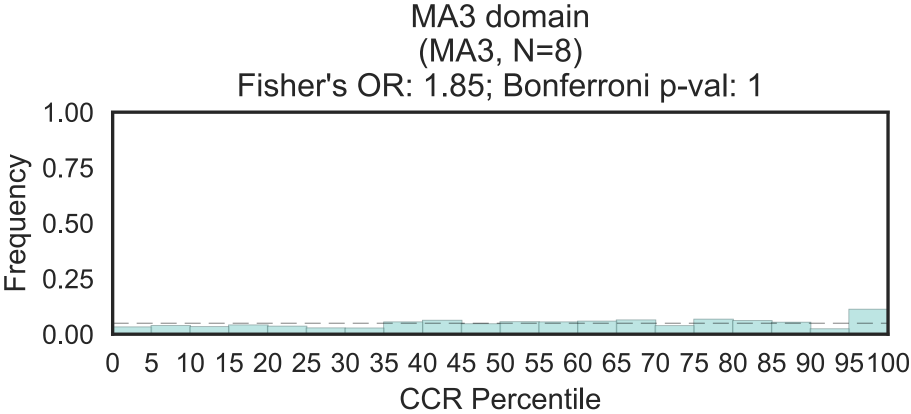

LysM domain
(LysM, N=6)
Fisher's OR: 1.14; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

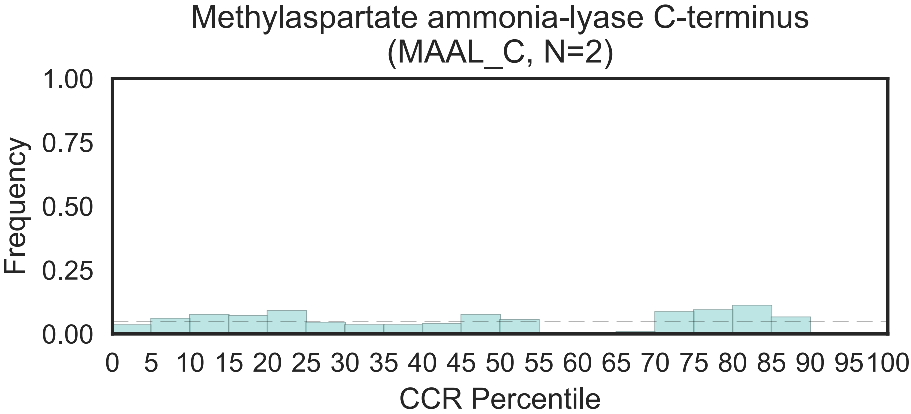

Lysyl oxidase
(Lysyl_oxidase, N=5)
Fisher's OR: 0.565; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

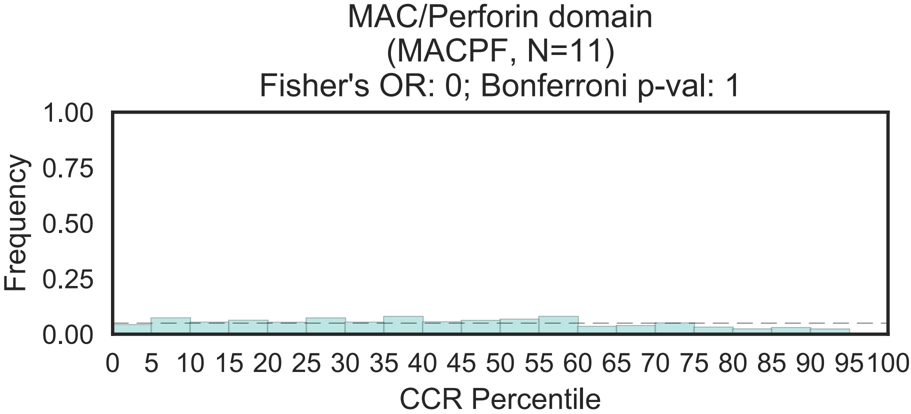

M-phase inducer phosphatase
(M-inducer_phosp, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

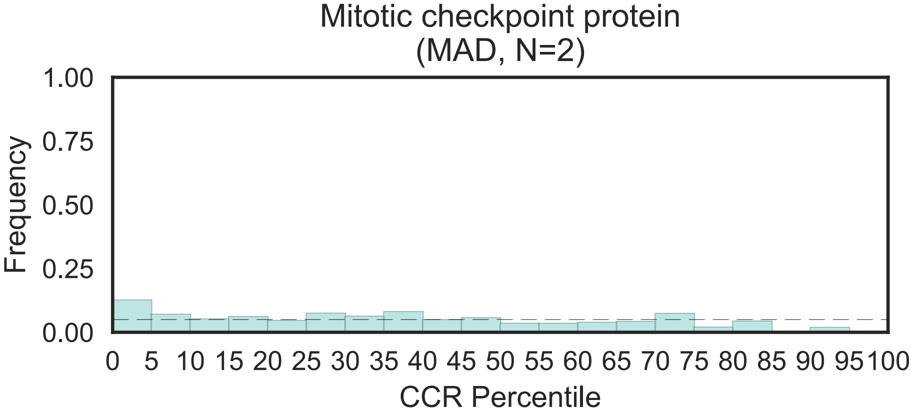

Peptidase M16C associated
(M16C_assoc, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

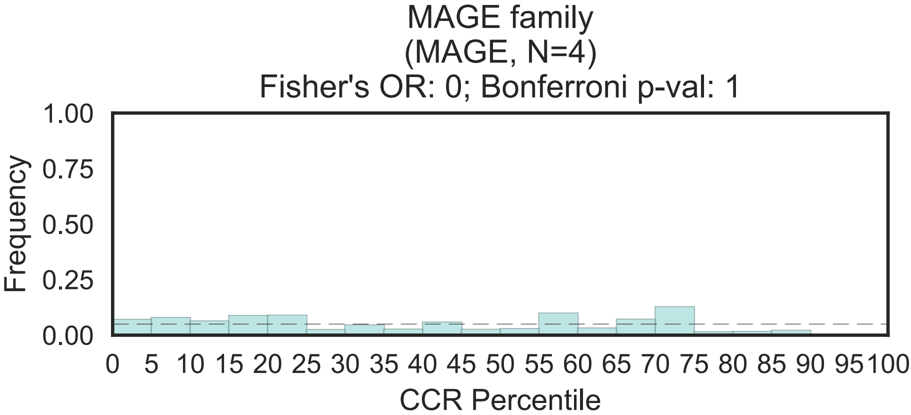

Peptidase dimerisation domain
(M20_dimer, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

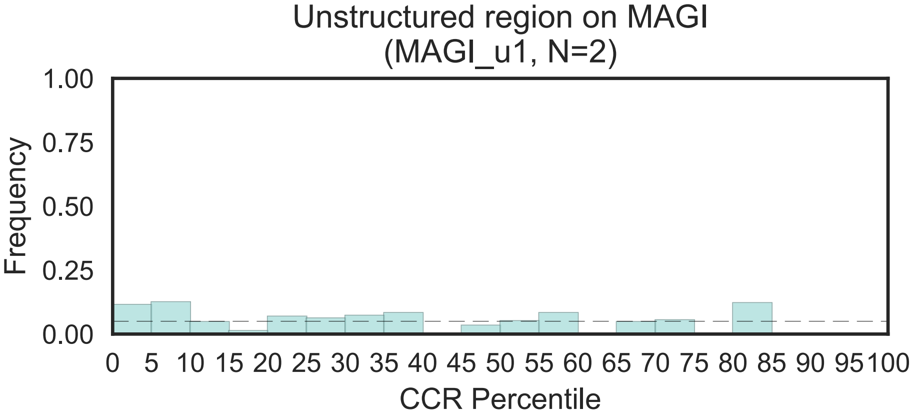

MA3 domain
(MA3, N=8)
Fisher's OR: 1.85; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

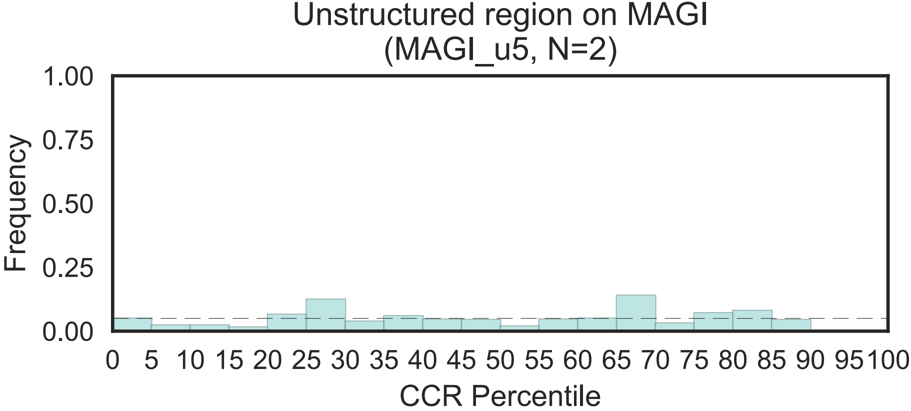

Methylaspartate ammonia-lyase C-terminus
(MAAL_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

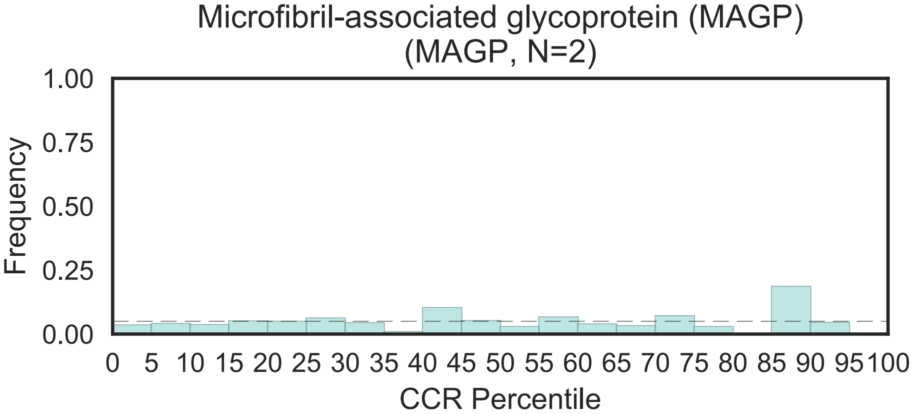

MAC/Perforin domain
(MACPF, N=11)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

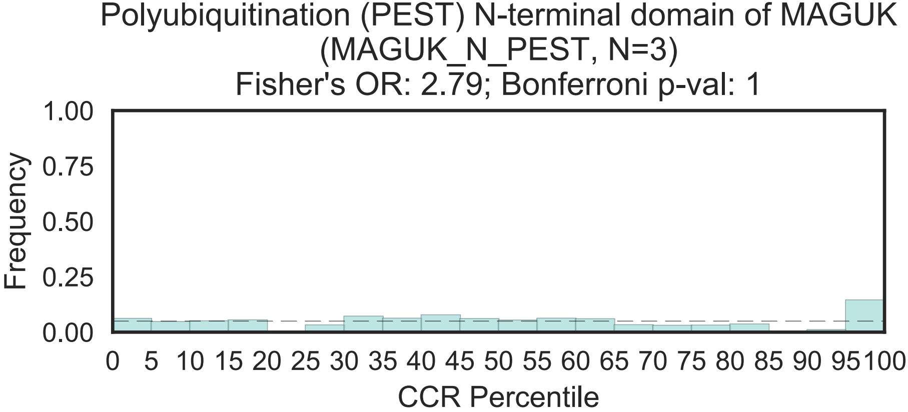

Mitotic checkpoint protein
(MAD, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

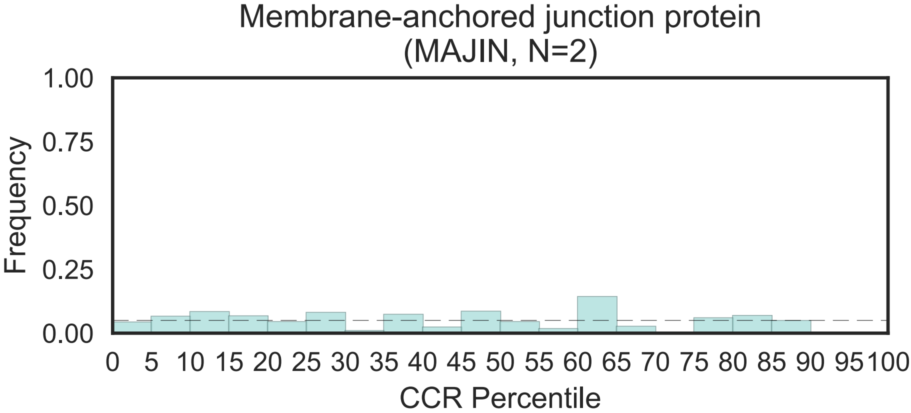

MAGE family
(MAGE, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

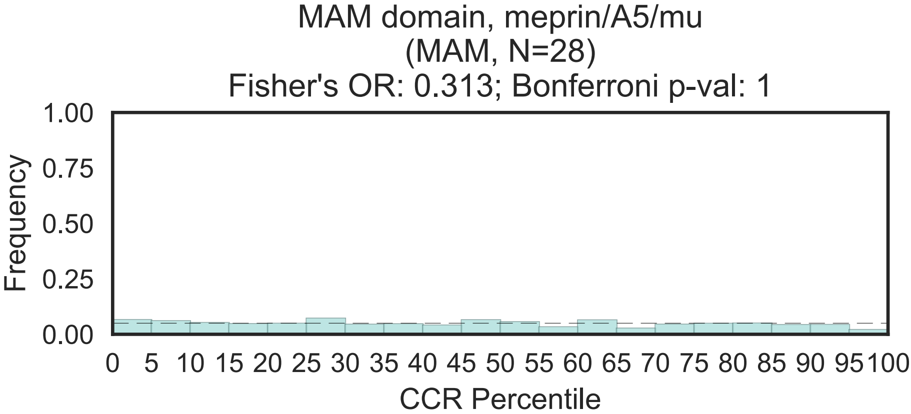

Unstructured region on MAGI
(MAGI_u1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

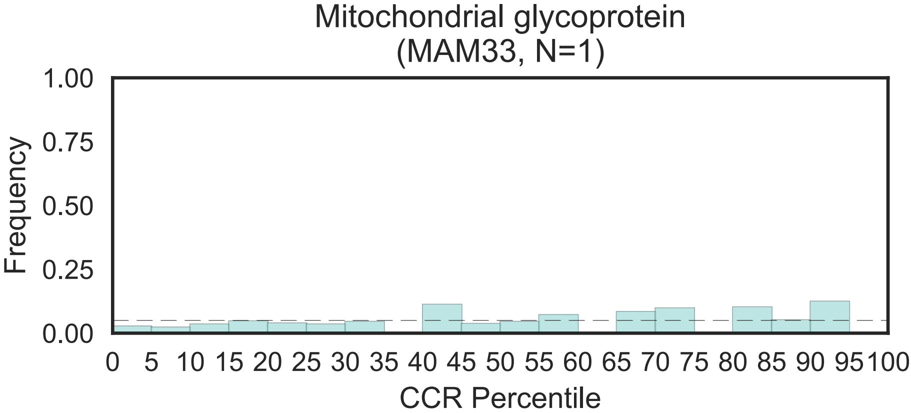

Unstructured region on MAGI
(MAGI_u5, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

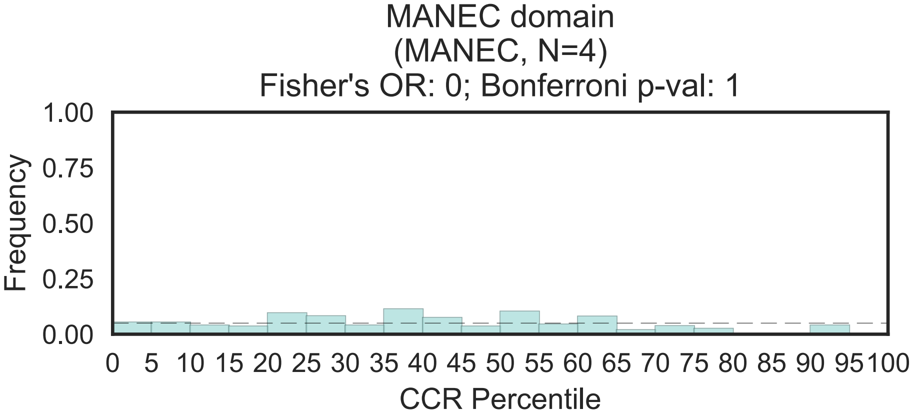

Microfibril-associated glycoprotein (MAGP)
(MAGP, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

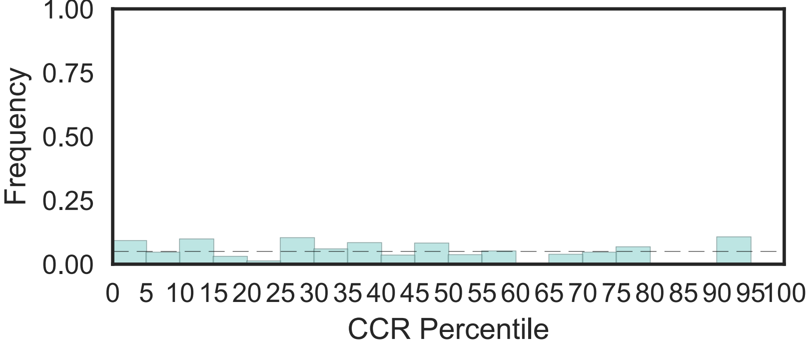

Polyubiquitination (PEST) N-terminal domain of MAGUK
(MAGUK_N_PEST, N=3)
Fisher's OR: 2.79; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Membrane-anchored junction protein
(MAJIN, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

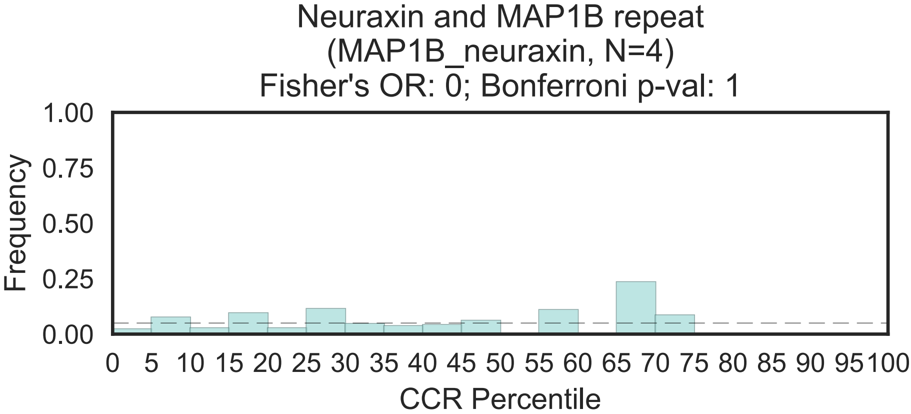

MAM domain, meprin/A5/mu
(MAM, N=28)
Fisher's OR: 0.313; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

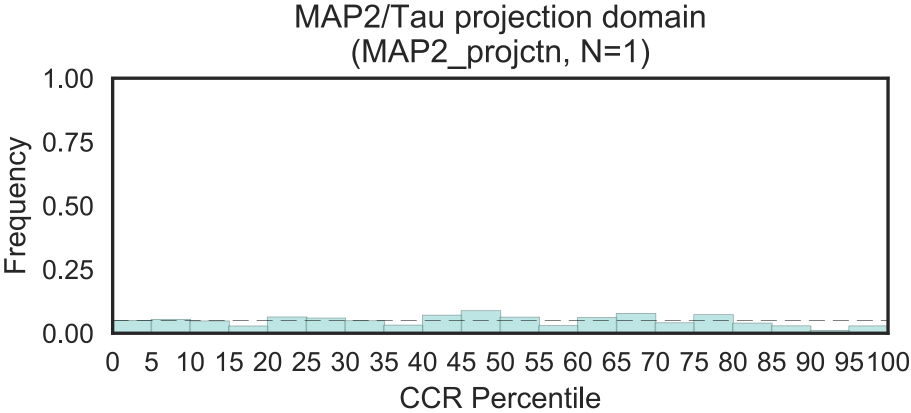

Mitochondrial glycoprotein
(MAM33, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

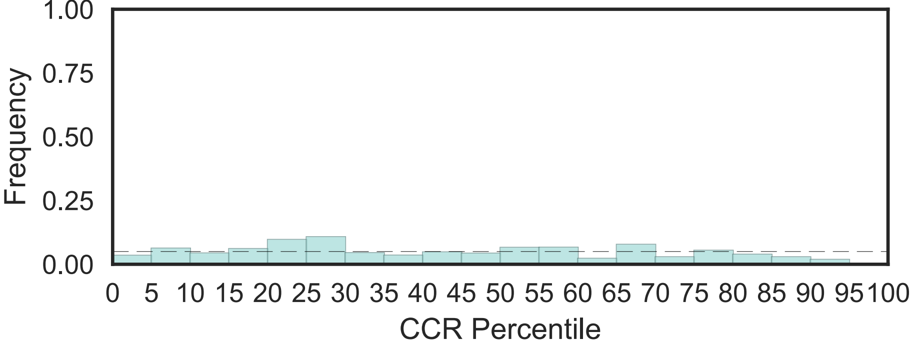

MANEC domain
(MANEC, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



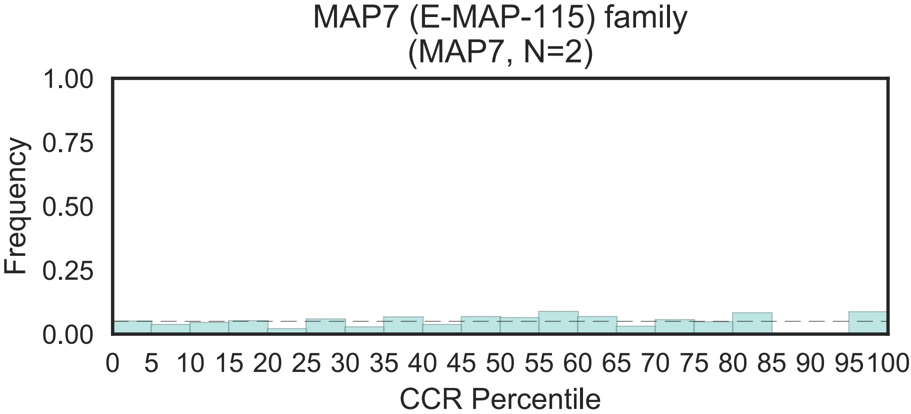
Membrane-associated protein 117 kDa, PDZK1-interacting protein 1 (MAP17, N=2)

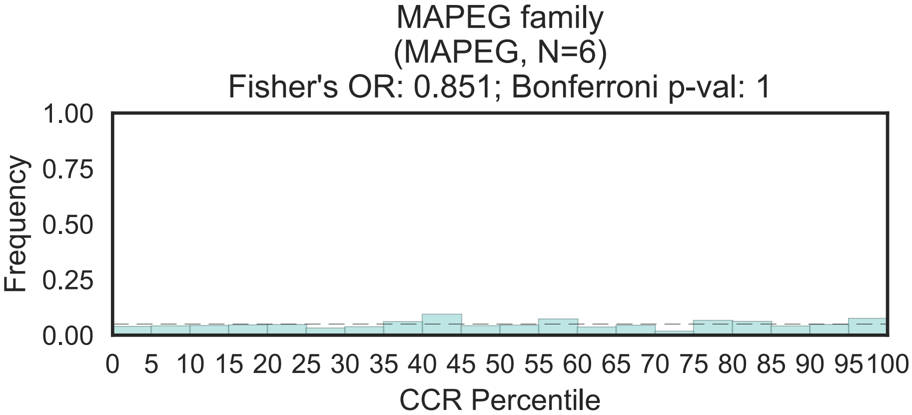

Neuraxin and MAP1B repeat
(MAP1B_neuraxin, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

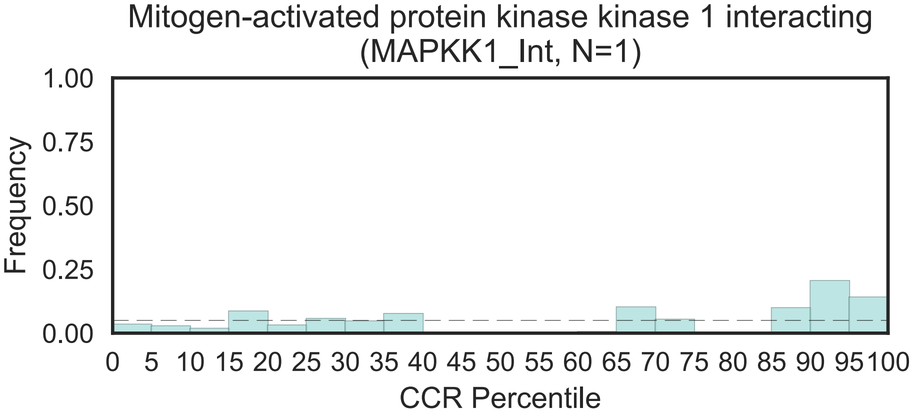

MAP2/Tau projection domain
(MAP2_projctn, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

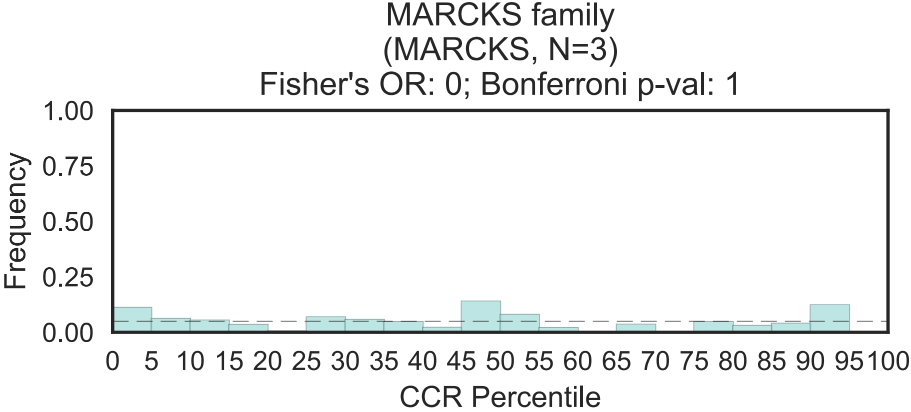


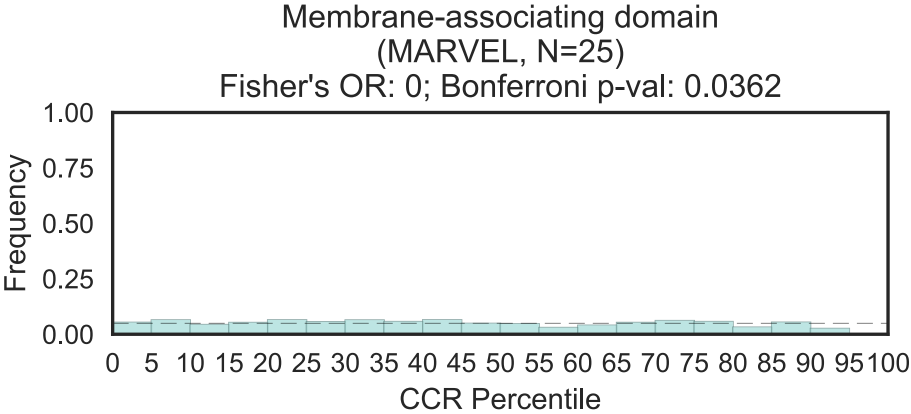
Microtubule associated protein (MAP65/ASE1 family)
(MAP65_ASE1, N=2)

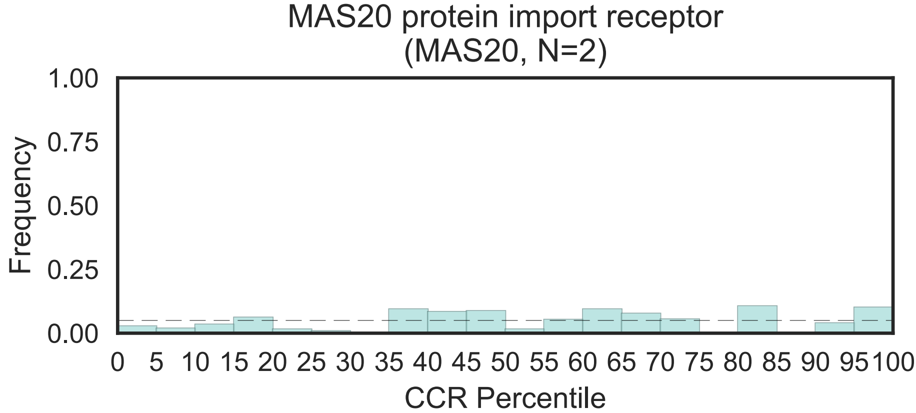

MAP7 (E-MAP-115) family
(MAP7, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

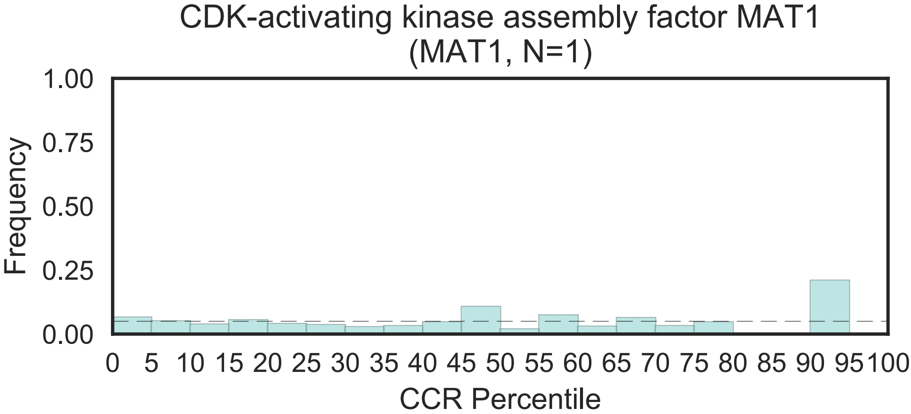

MAPEG family
(MAPEG, N=6)
Fisher's OR: 0.851; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

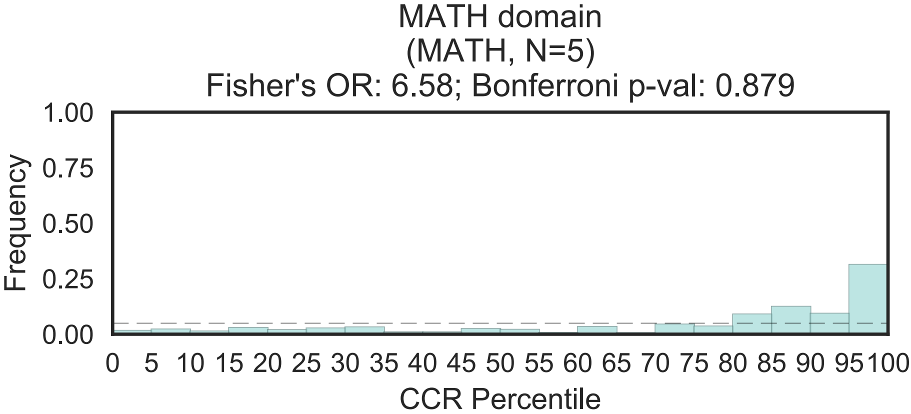

Mitogen-activated protein kinase kinase 1 interacting
(MAPKK1_Int, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

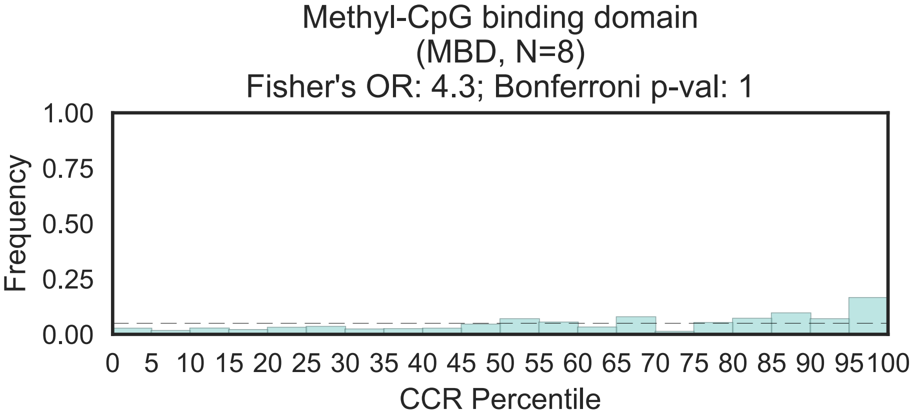

MARCKS family
(MARCKS, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

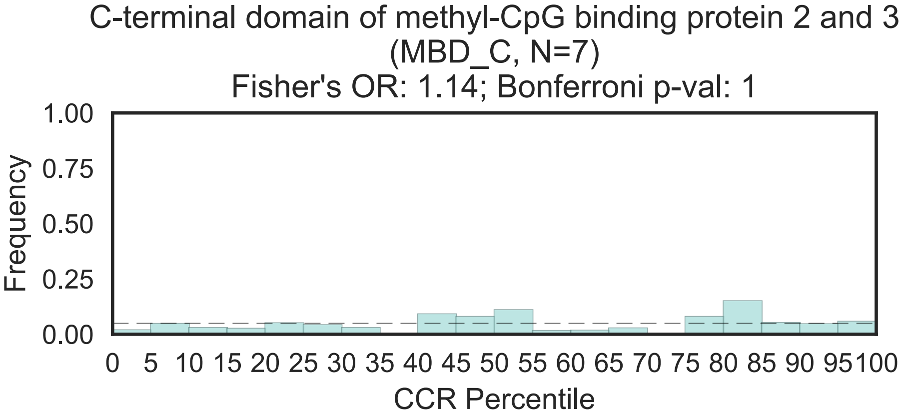

Membrane-associating domain
(MARVEL, N=25)
Fisher's OR: 0; Bonferroni p-val: 0.0362
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

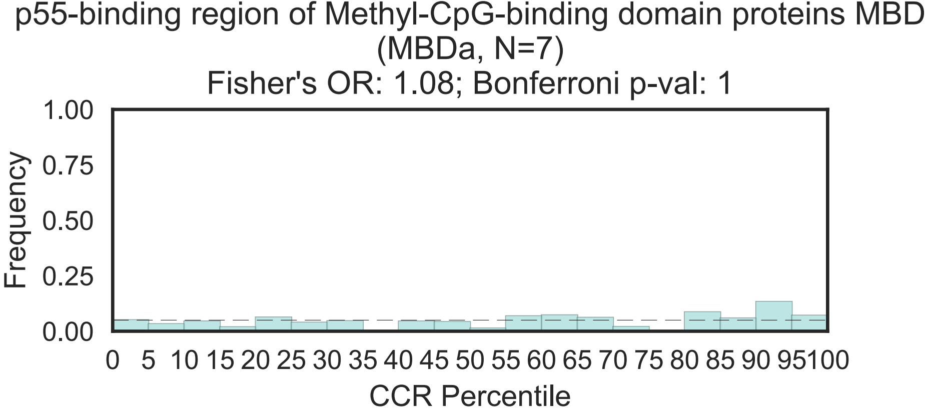

MAS20 protein import receptor
(MAS20, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

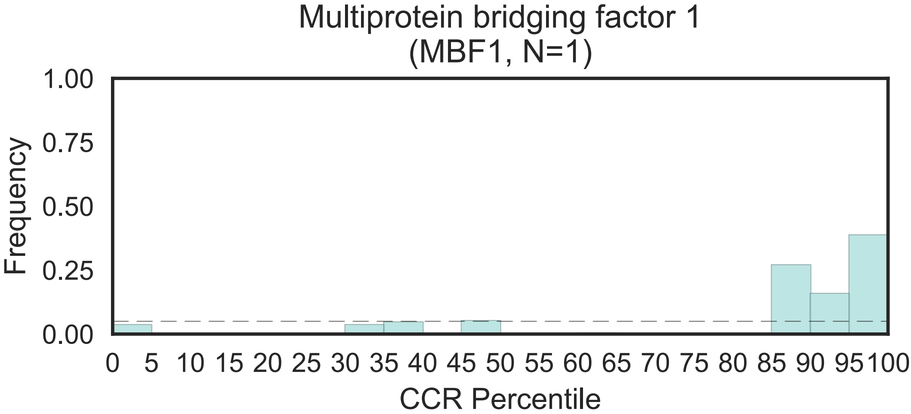

CDK-activating kinase assembly factor MAT1
(MAT1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

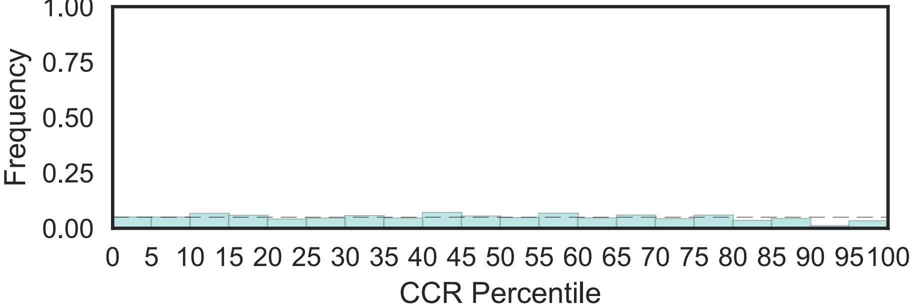

MATH domain
(MATH, N=5)
Fisher's OR: 6.58; Bonferroni p-val: 0.879
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Methyl-CpG binding domain
(MBD, N=8)
Fisher's OR: 4.3; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

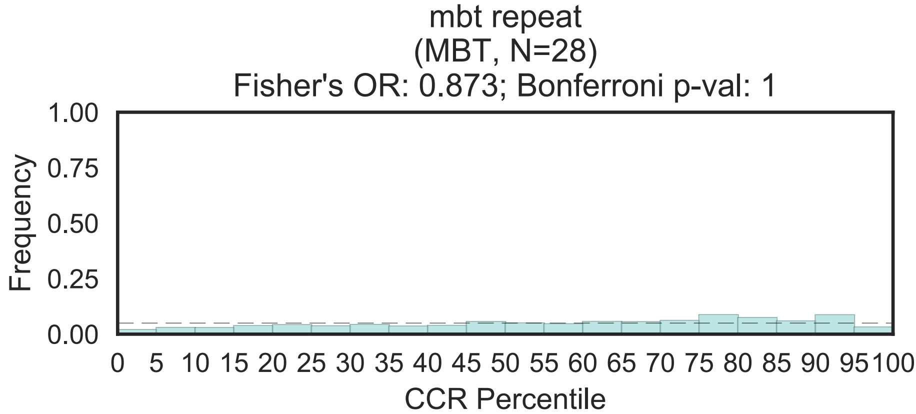

C-terminal domain of methyl-CpG binding protein 2 and 3
(MBD_C, N=7)
Fisher's OR: 1.14; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

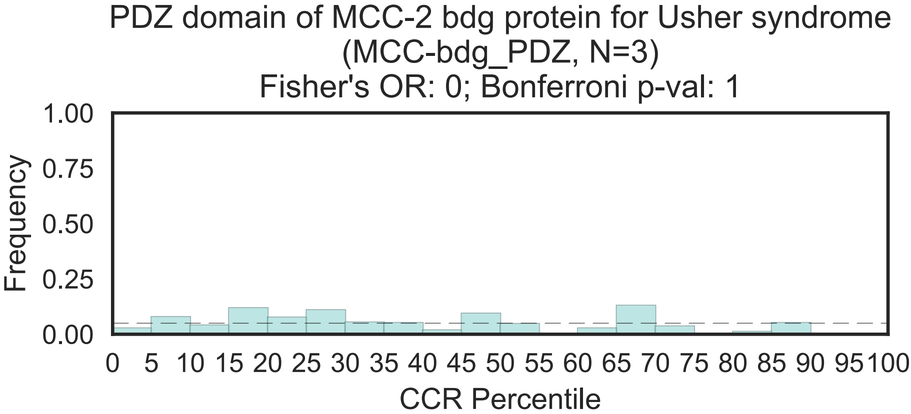

p55-binding region of Methyl-CpG-binding domain proteins MBD
(MBDa, N=7)
Fisher's OR: 1.08; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

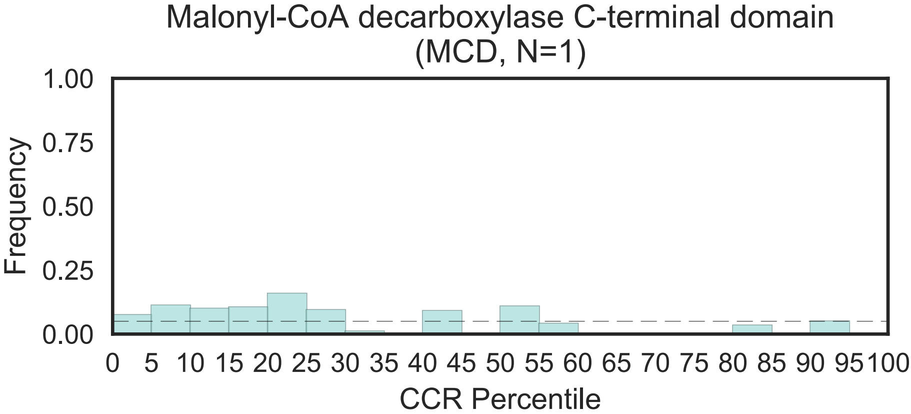

Multiprotein bridging factor 1
(MBF1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



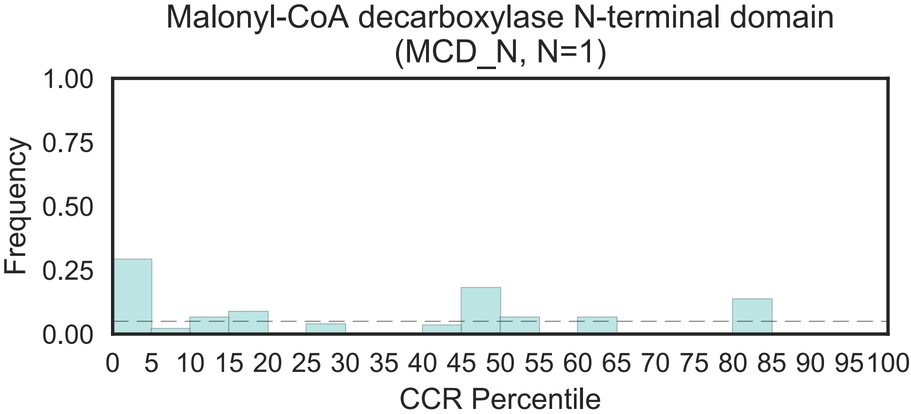
MBOAT, membrane-bound O-acyltransferase family
(MBOAT, N=11)
Fisher's OR: 0.621; Bonferroni p-val: 1

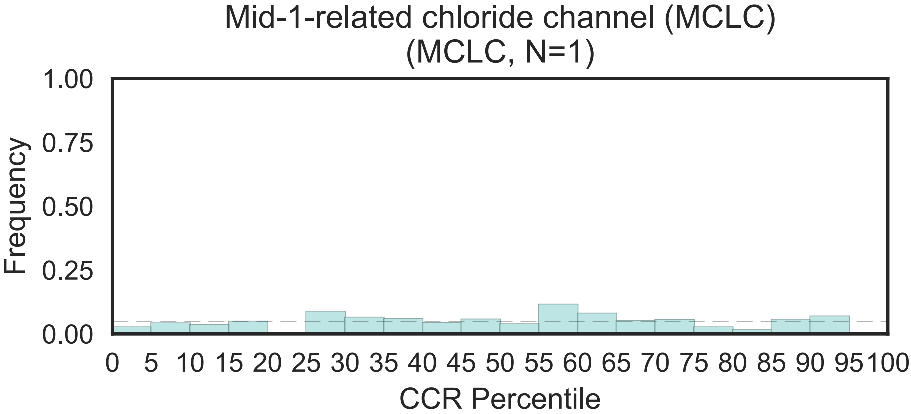

mbt repeat
(MBT, N=28)
Fisher's OR: 0.873; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

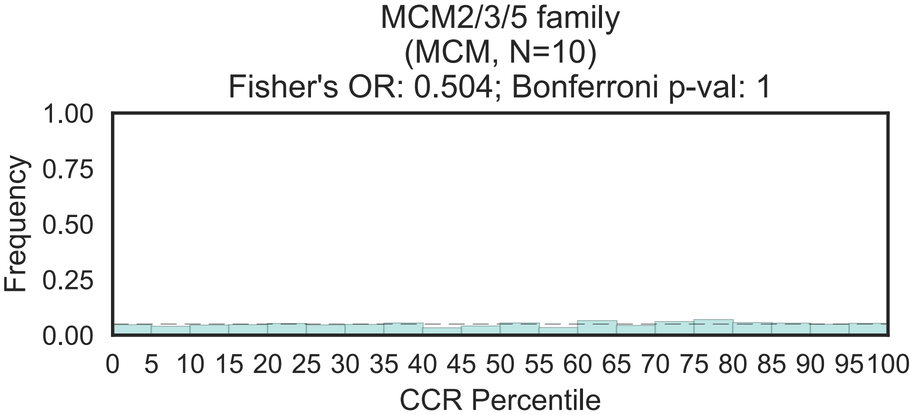

PDZ domain of MCC-2 bdg protein for Usher syndrome
(MCC-bdg_PDZ, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

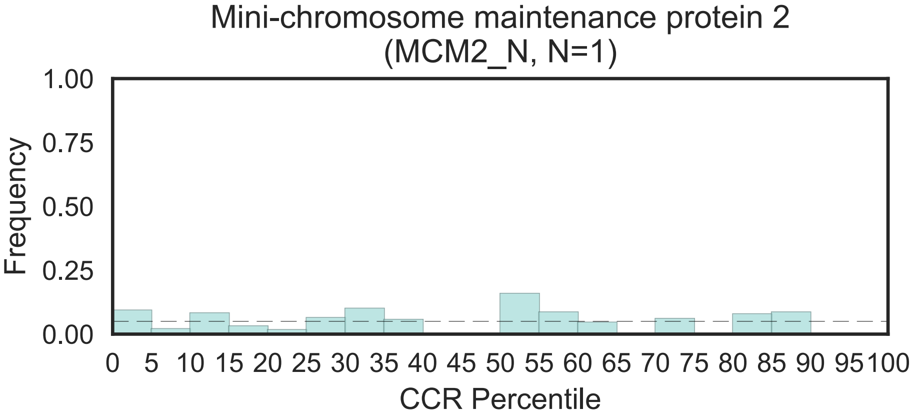


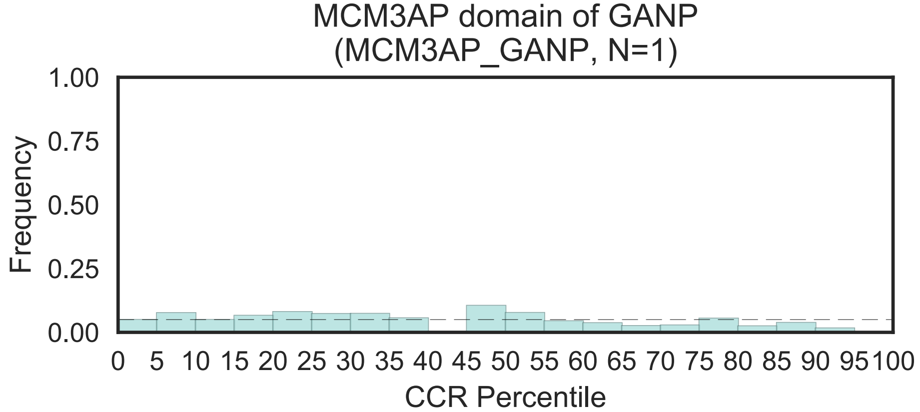
Malonyl-CoA decarboxylase C-terminal domain
(MCD, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

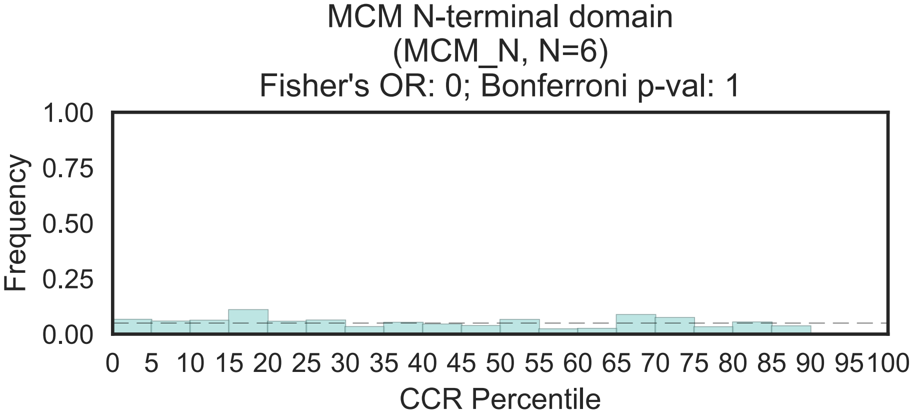

Malonyl-CoA decarboxylase N-terminal domain
(MCD_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

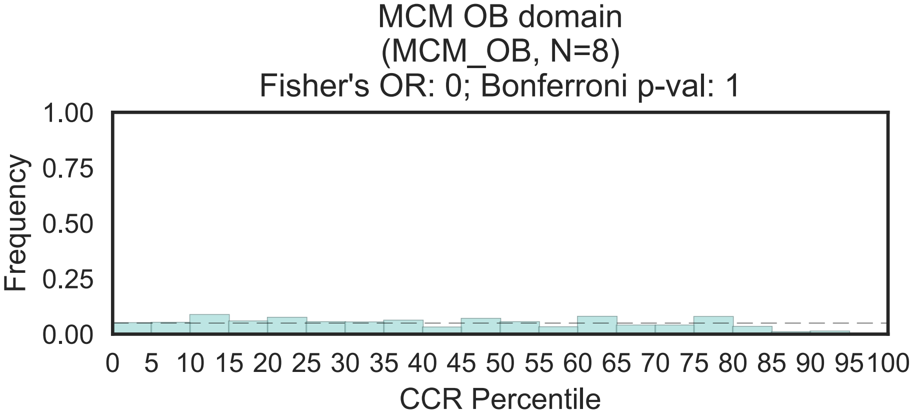

Mid-1-related chloride channel (MCLC)
(MCLC, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

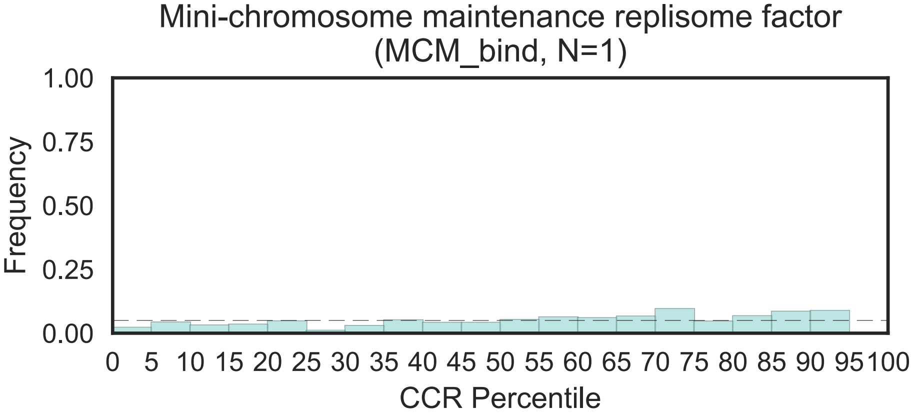

MCM2/3/5 family
(MCM, N=10)
Fisher's OR: 0.504; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

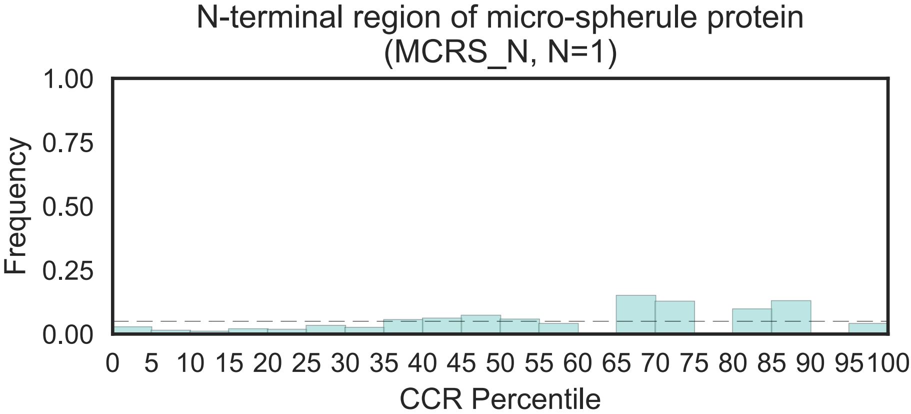

Mini-chromosome maintenance protein 2
(MCM2_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

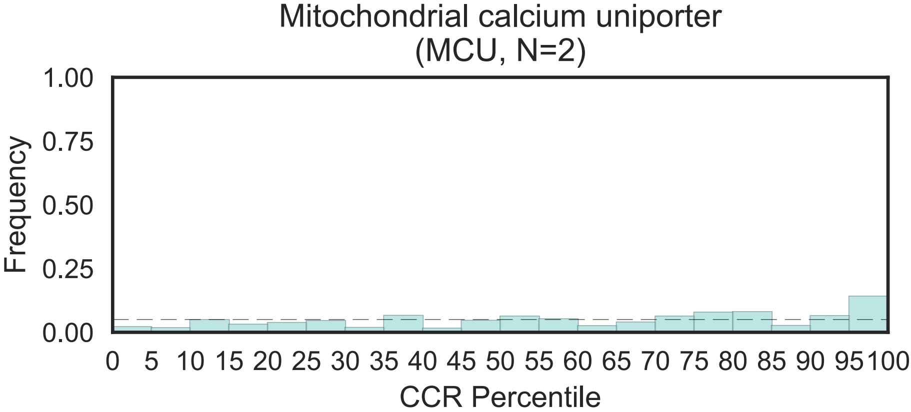

MCM3AP domain of GANP
(MCM3AP_GANP, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

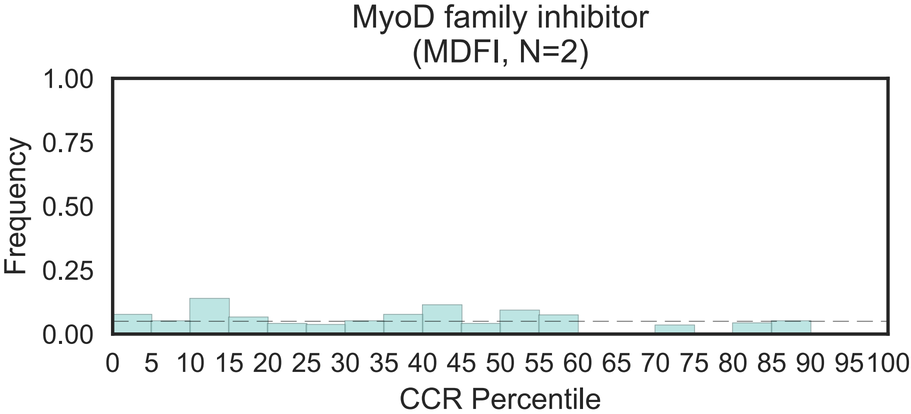

MCM N-terminal domain
(MCM_N, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


MCM OB domain
(MCM_OB, N=8)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

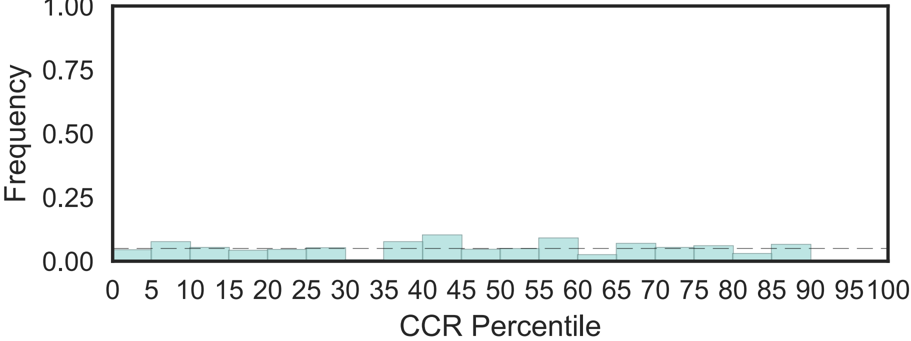

Mini-chromosome maintenance replisome factor
(MCM_bind, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

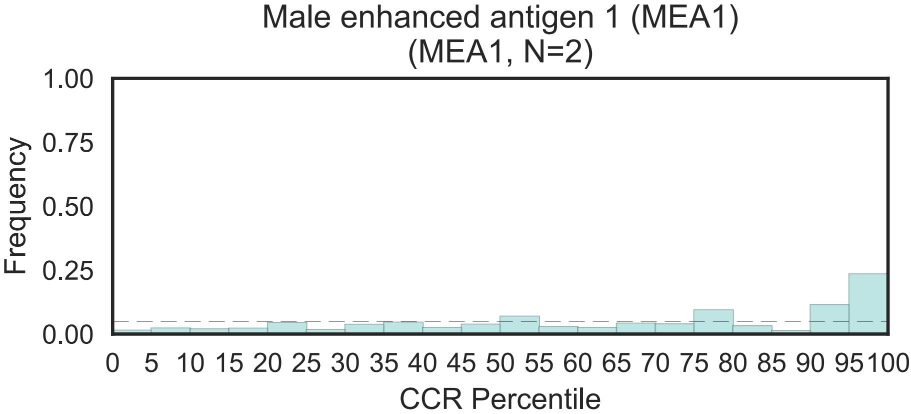

N-terminal region of micro-spherule protein
(MCRS_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

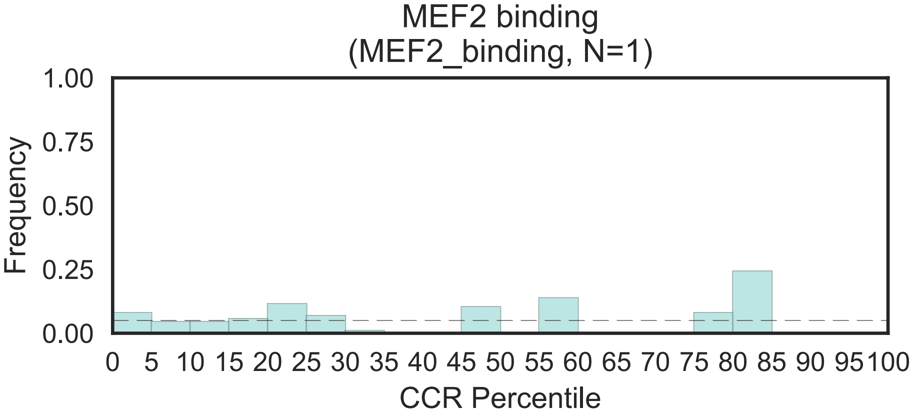

Mitochondrial calcium uniporter
(MCU, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

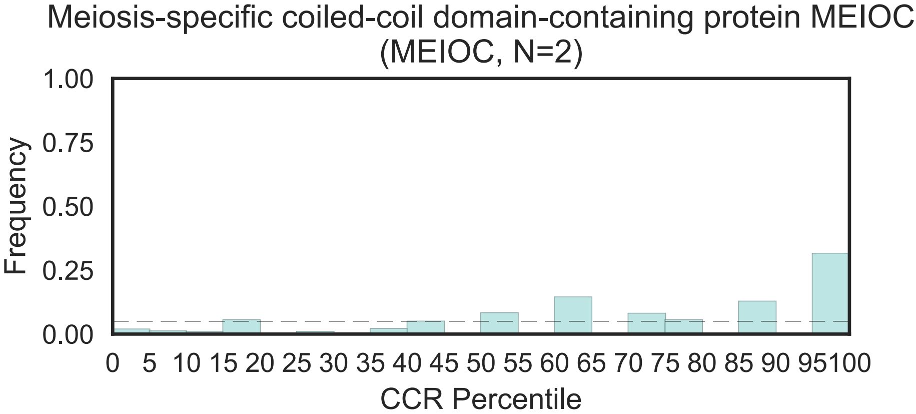

MyoD family inhibitor
(MDFI, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

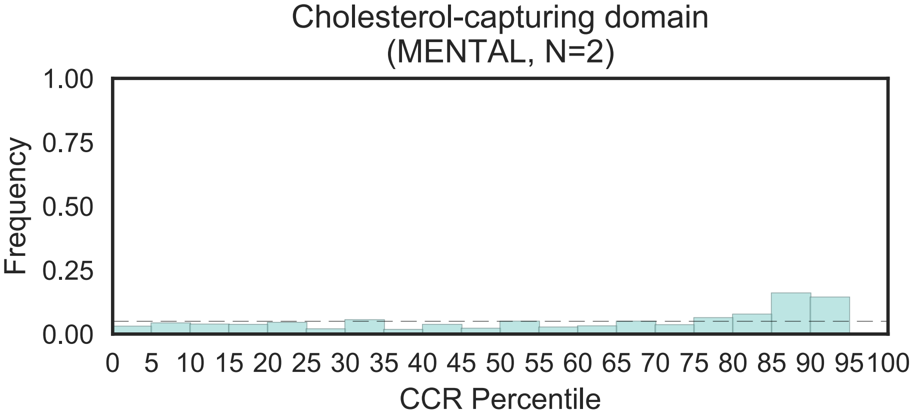
Nuclear protein MDM1 (MDM1, N=1)

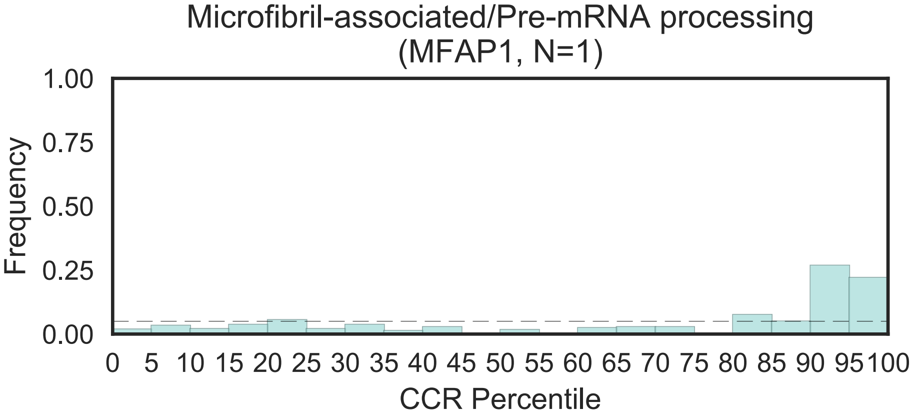


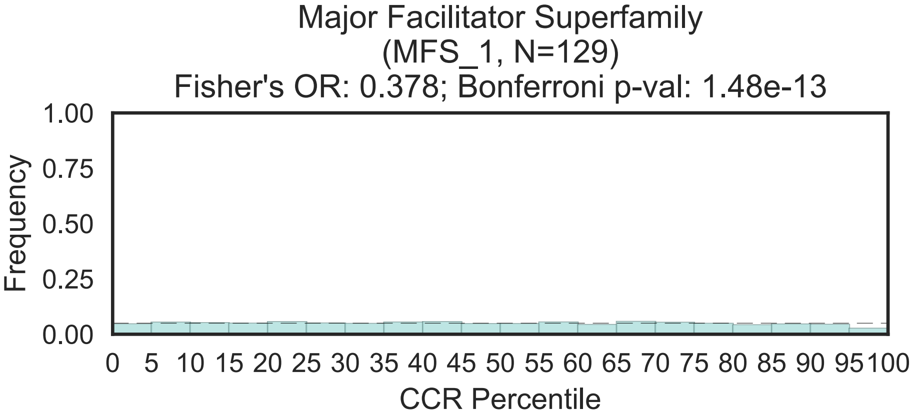

Male enhanced antigen 1 (MEA1)
(MEA1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

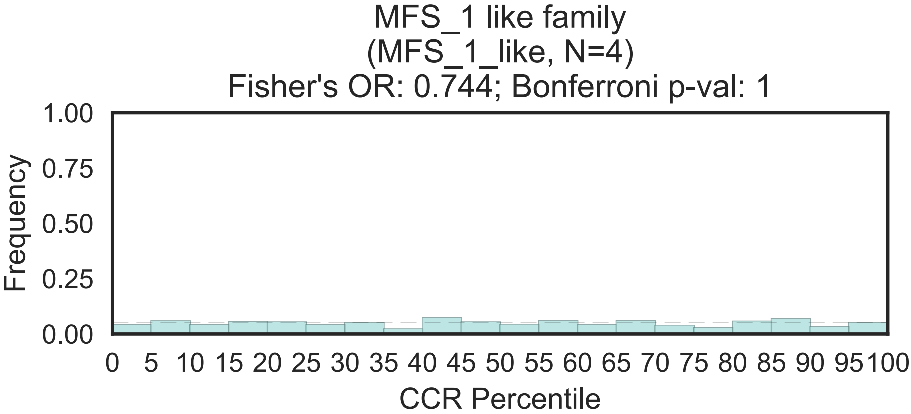

MEF2 binding
(MEF2_binding, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

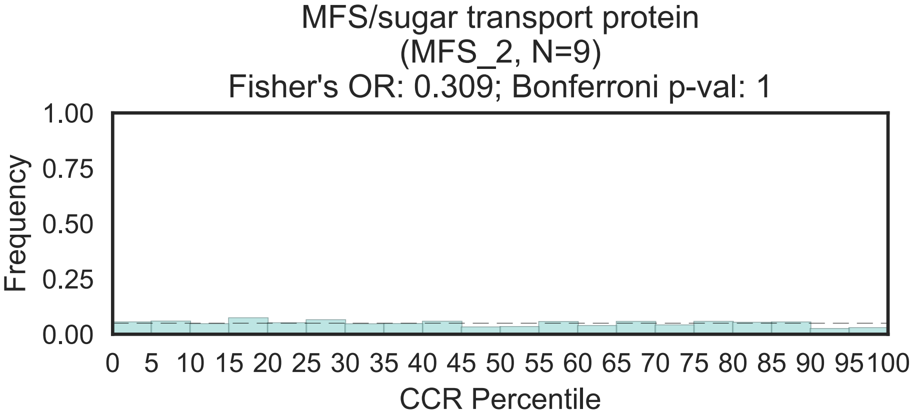

Meiosis-specific coiled-coil domain-containing protein MEIOC
(MEIOC, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

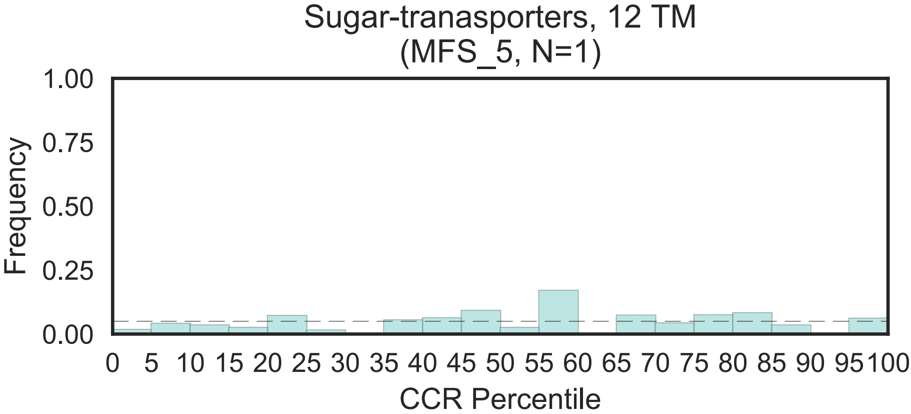

Cholesterol-capturing domain
(MENTAL, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

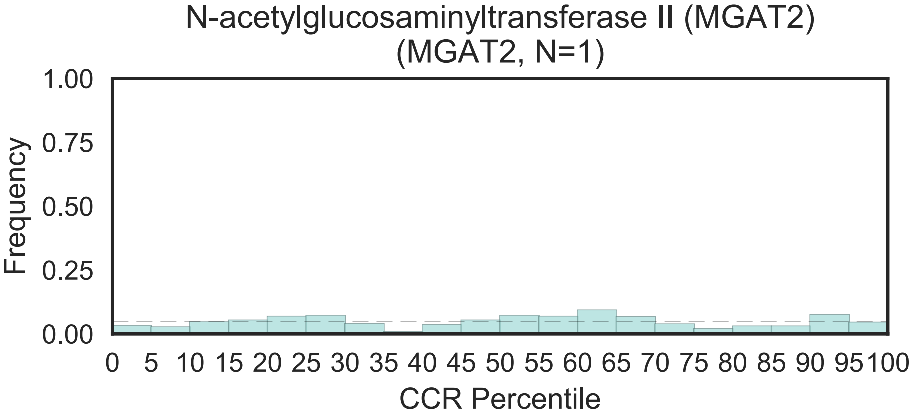

Microfibril-associated/Pre-mRNA processing
(MFAP1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

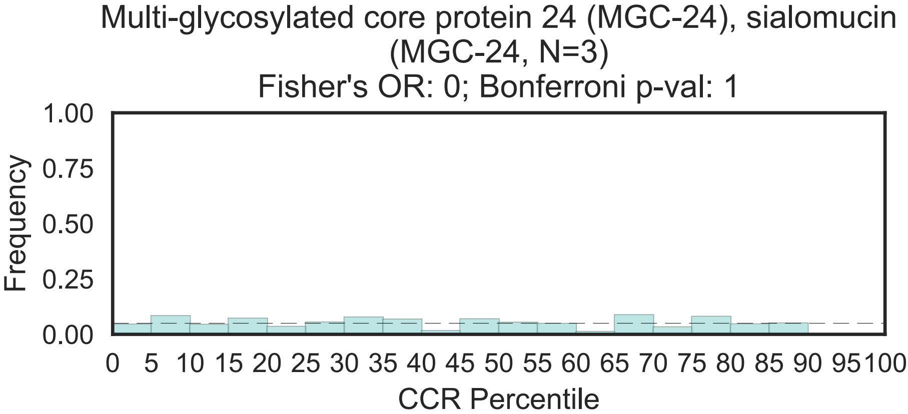

Major Facilitator Superfamily
(MFS_1, N=129)
Fisher's OR: 0.378; Bonferroni p-val: 1.48e-13
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

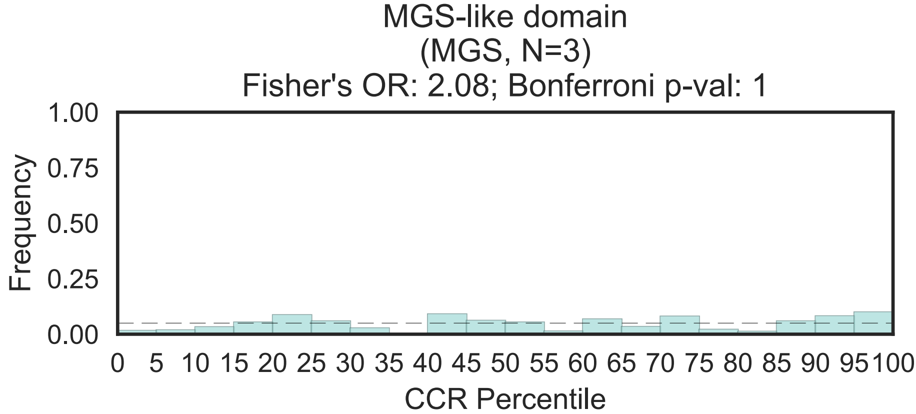

MFS_1 like family
(MFS_1_like, N=4)
Fisher's OR: 0.744; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


MFS/sugar transport protein
(MFS_2, N=9)
Fisher's OR: 0.309; Bonferroni p-val: 1

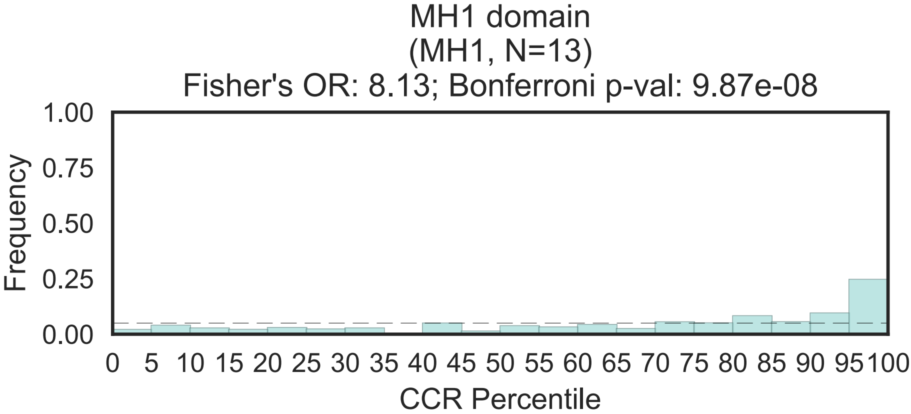

Sugar-tranasporters, 12 TM
(MFS_5, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


N-acetylglucosaminyltransferase II (MGAT2)
(MGAT2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

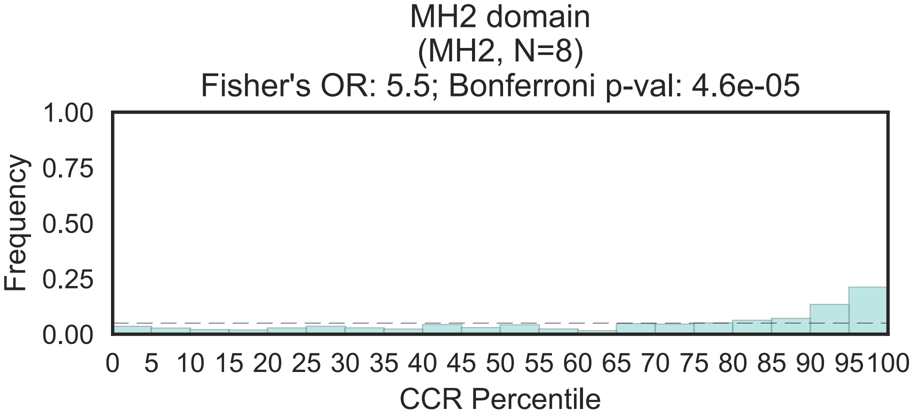

Multi-glycosylated core protein 24 (MGC-24), sialomucin
(MGC-24, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



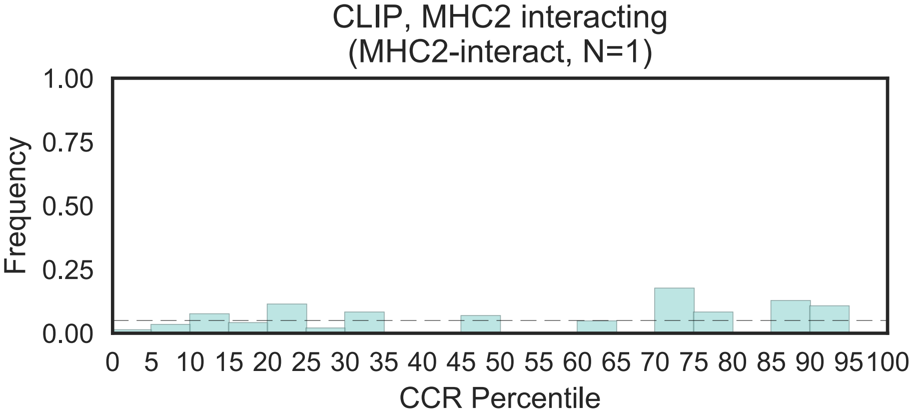
MGS-like domain
(MGS, N=3)
Fisher's OR: 2.08; Bonferroni p-val: 1

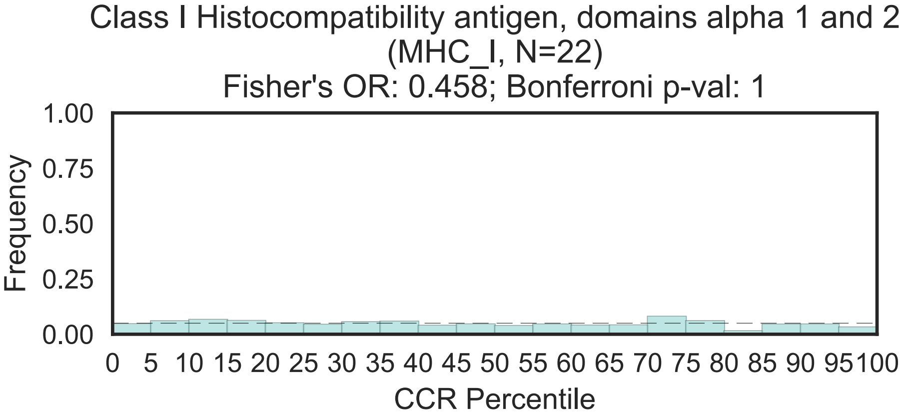


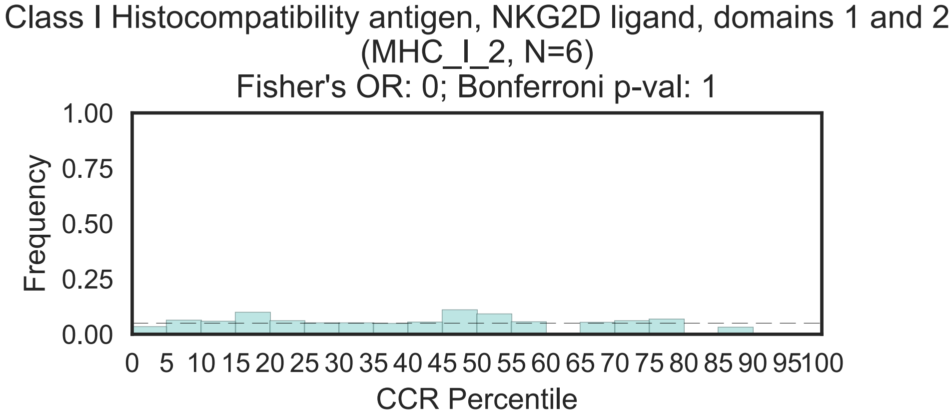
MH1 domain
(MH1, N=13)
Fisher's OR: 8.13; Bonferroni p-val: 9.87e-08



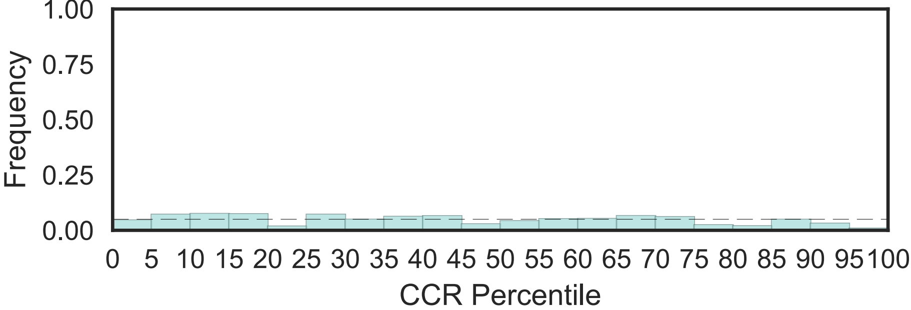
MH2 domain
(MH2, N=8)
Fisher's OR: 5.5; Bonferroni p-val: 4.6e-05

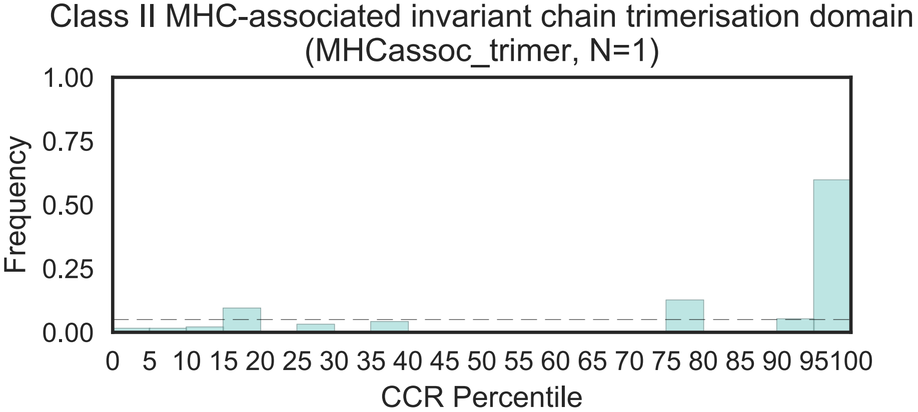

CLIP, MHC2 interacting
(MHC2-interact, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

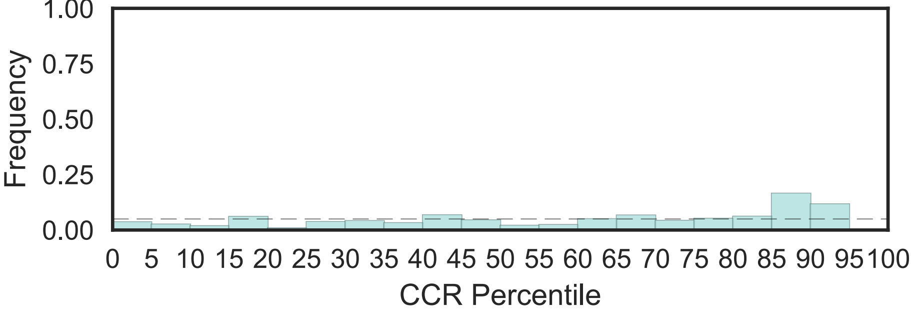
Class I Histocompatibility antigen, domains alpha 1 and 2
(MHC_I, N=22)
Fisher's OR: 0.458; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Class I Histocompatibility antigen, NKG2D ligand, domains 1 and 2
(MHC_I_2, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

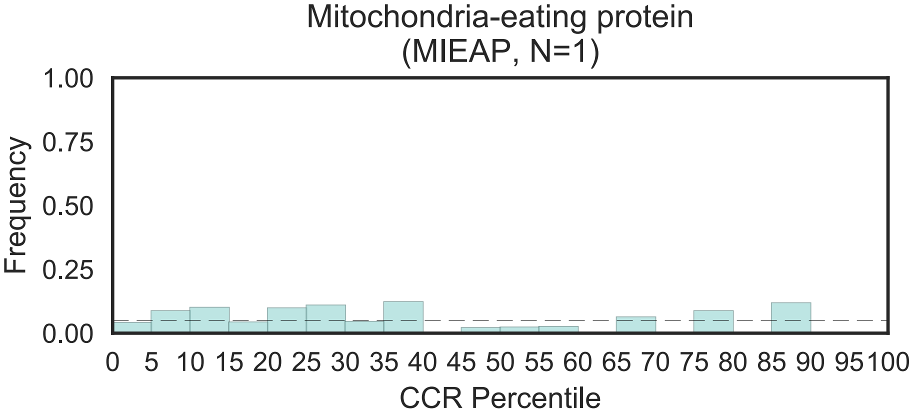
MHC-I family domain
(MHC_I_3, N=8)
Fisher's OR: 0.189; Bonferroni p-val: 1

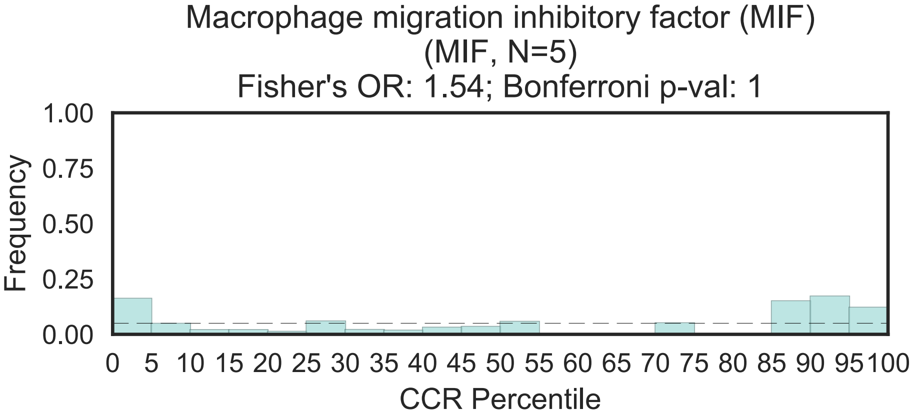


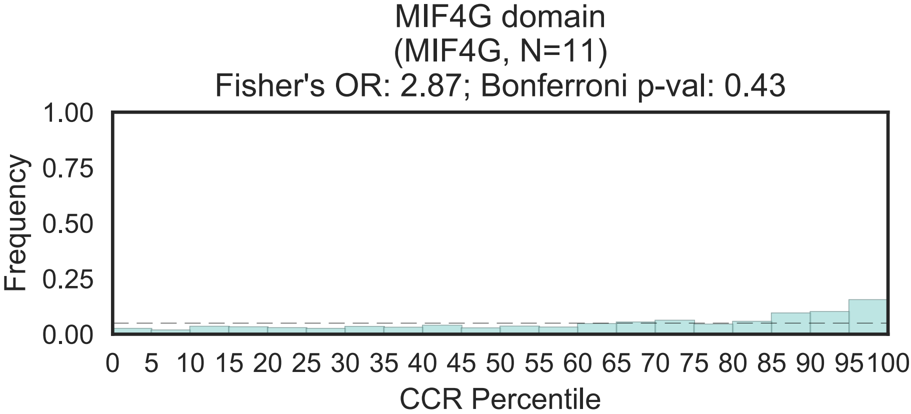

Class II MHC-associated invariant chain trimerisation domain
(MHCassoc_trimer, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

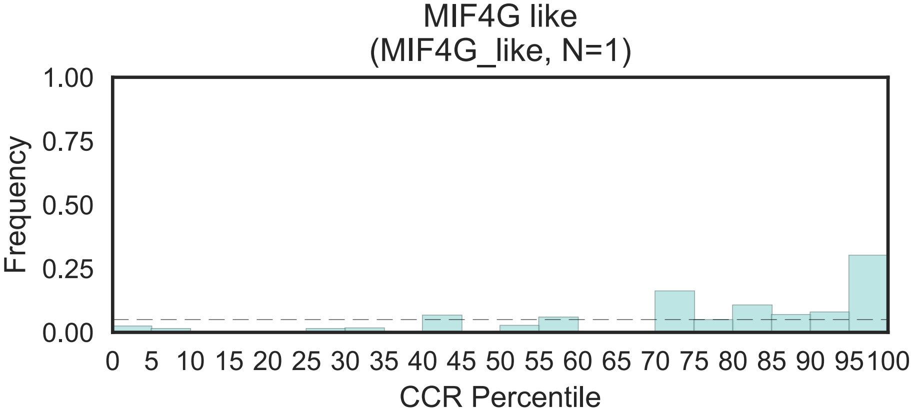


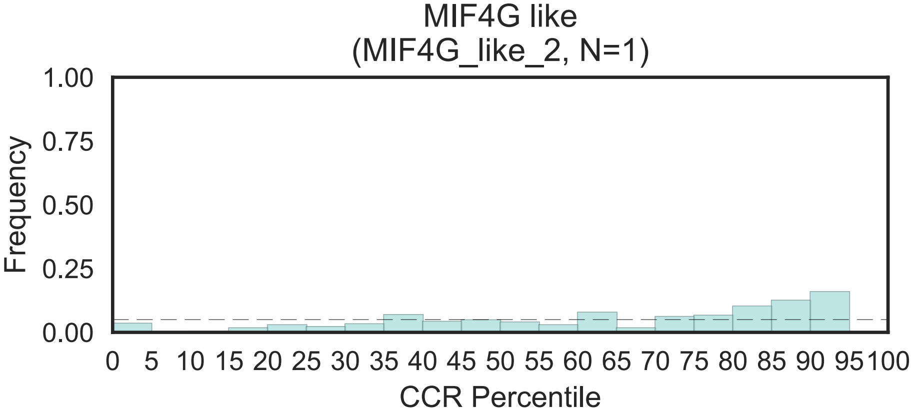
Mib_herc2
(MIB_HERC2, N=6)
Fisher's OR: 0; Bonferroni p-val: 1

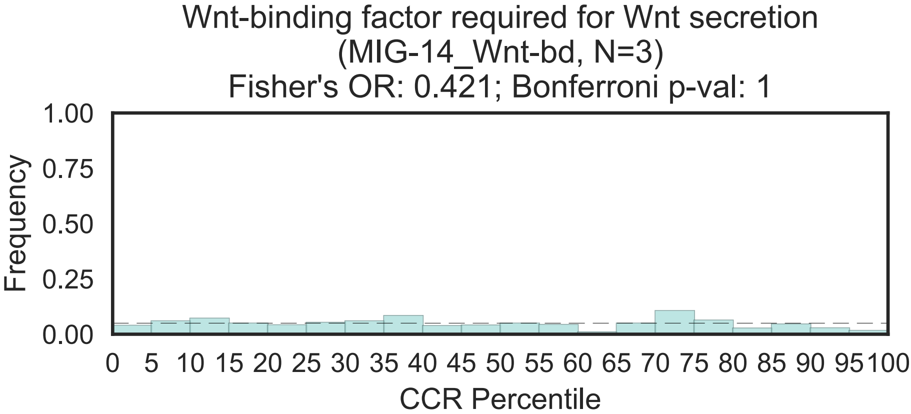

Mitochondria-eating protein
(MIEAP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Macrophage migration inhibitory factor (MIF)
(MIF, N=5)
Fisher's OR: 1.54; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

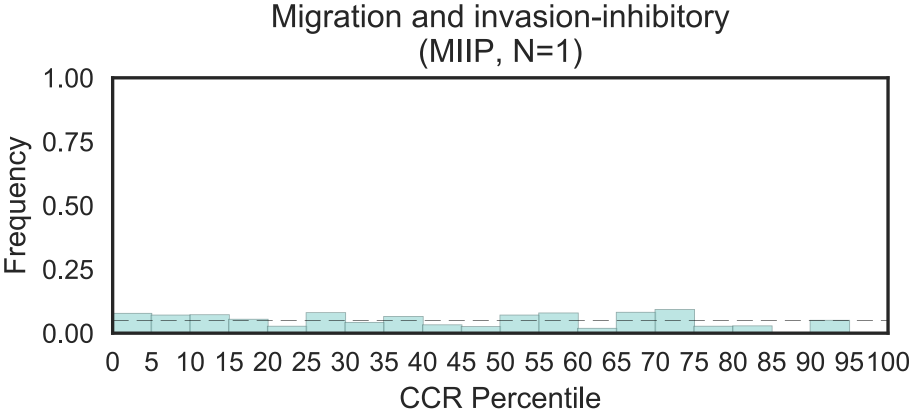

MIF4G domain
(MIF4G, N=11)
Fisher's OR: 2.87; Bonferroni p-val: 0.43
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

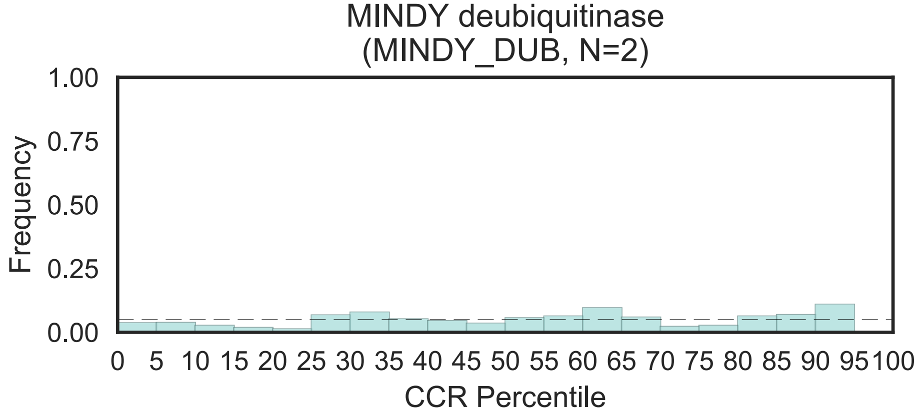

MIF4G like
(MIF4G_like, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

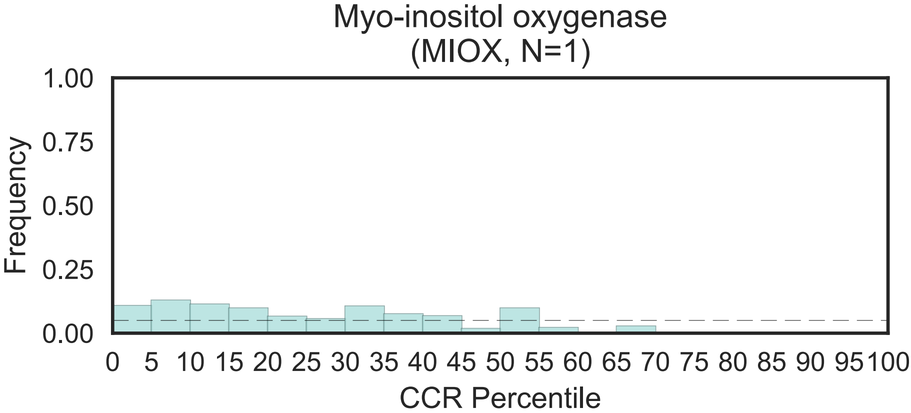

MIF4G like
(MIF4G_like_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

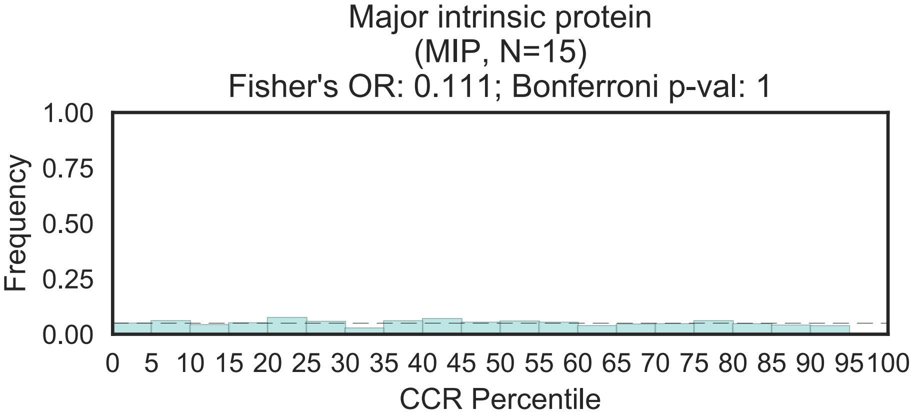


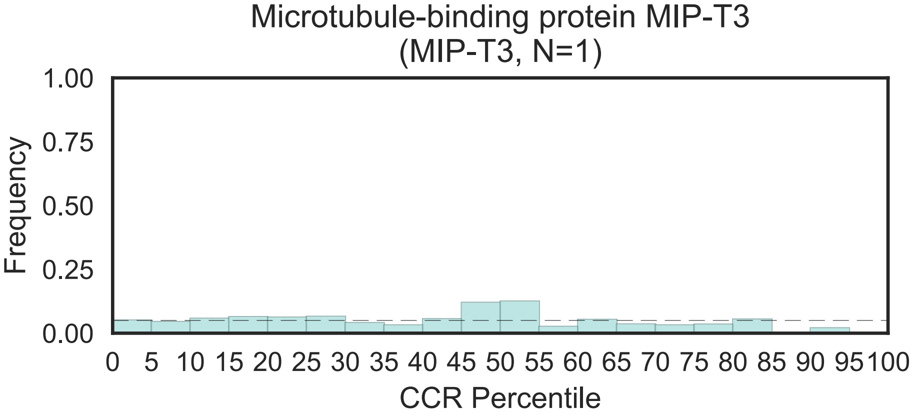
Wnt-binding factor required for Wnt secretion
(MIG-14_Wnt-bd, N=3)
Fisher's OR: 0.421; Bonferroni p-val: 1

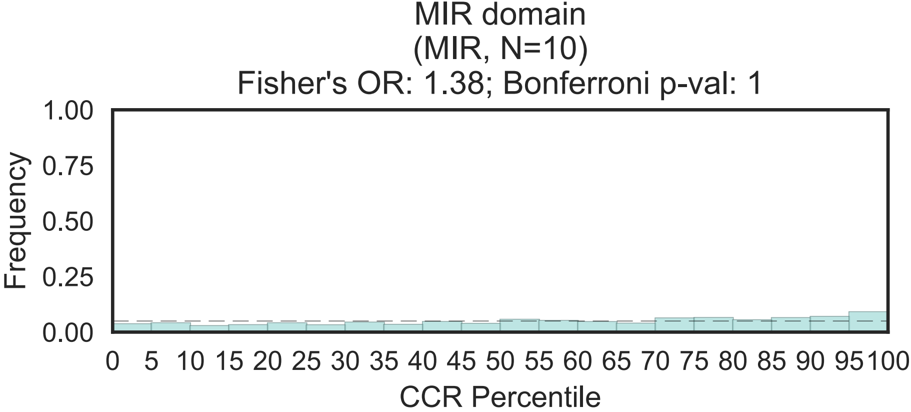

Migration and invasion-inhibitory
(MIIP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

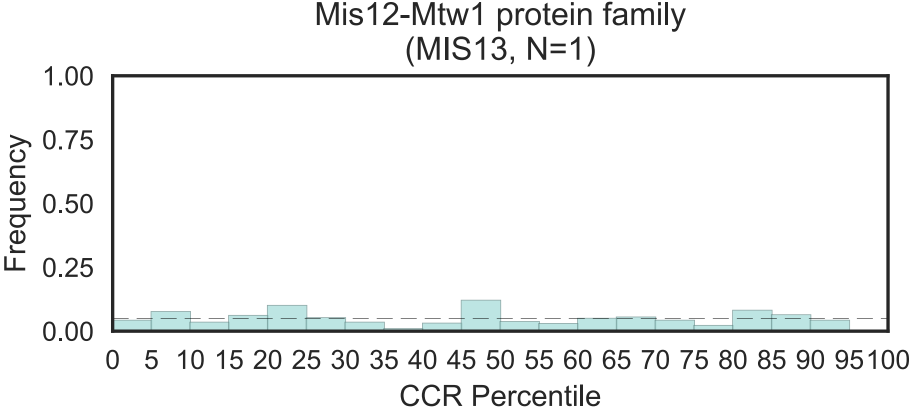

MINDY deubiquitinase
(MINDY_DUB, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

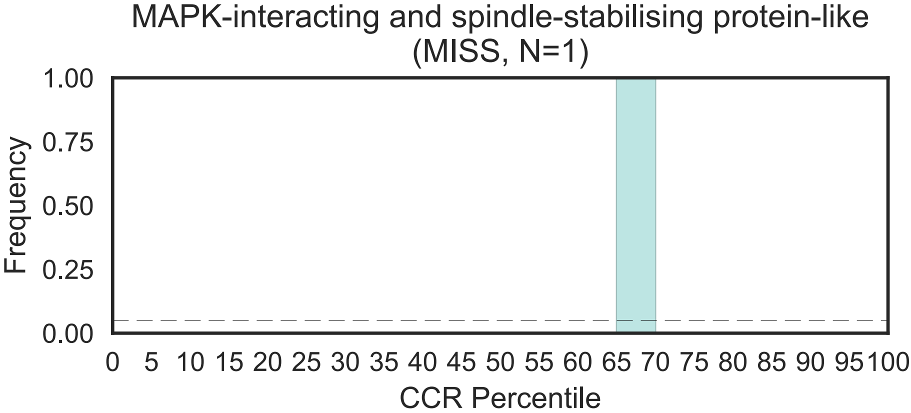

Myo-inositol oxygenase
(MIOX, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

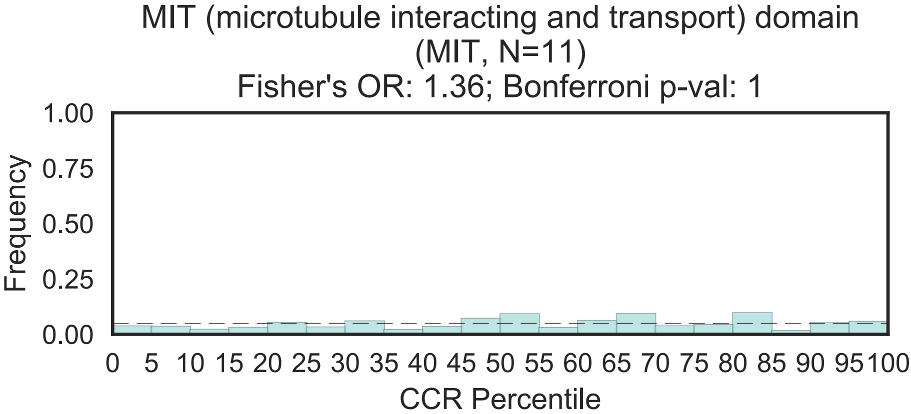

Major intrinsic protein
(MIP, N=15)
Fisher's OR: 0.111; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

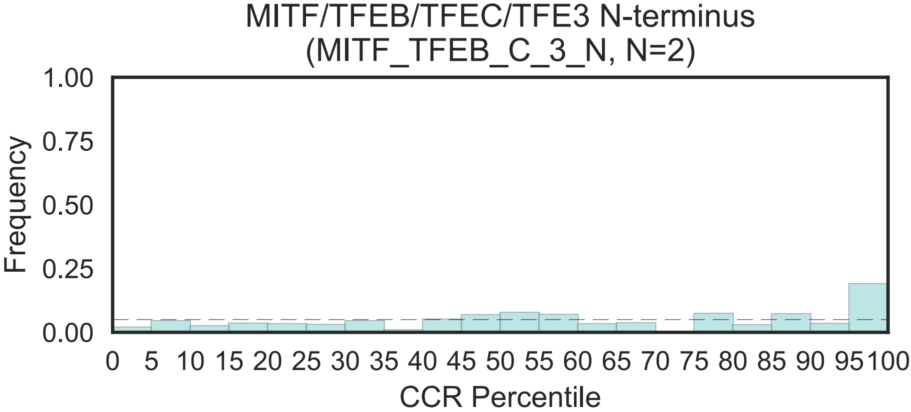

Microtubule-binding protein MIP-T3
(MIP-T3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

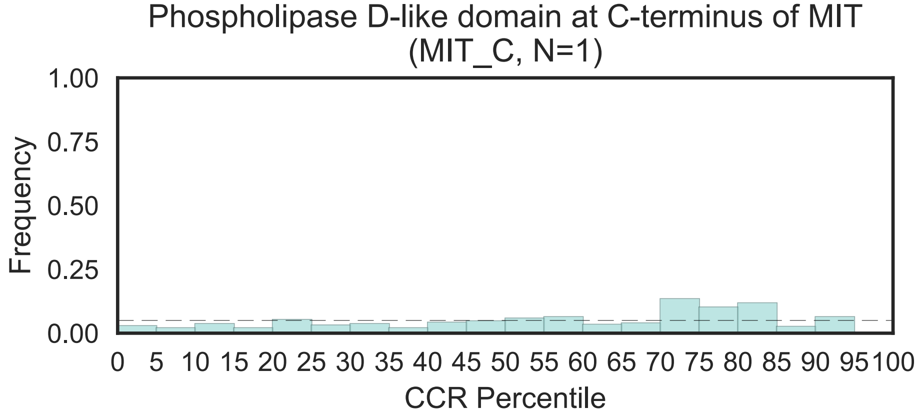

MIR domain
(MIR, N=10)
Fisher's OR: 1.38; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Mis12-Mtw1 protein family
(MIS13, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

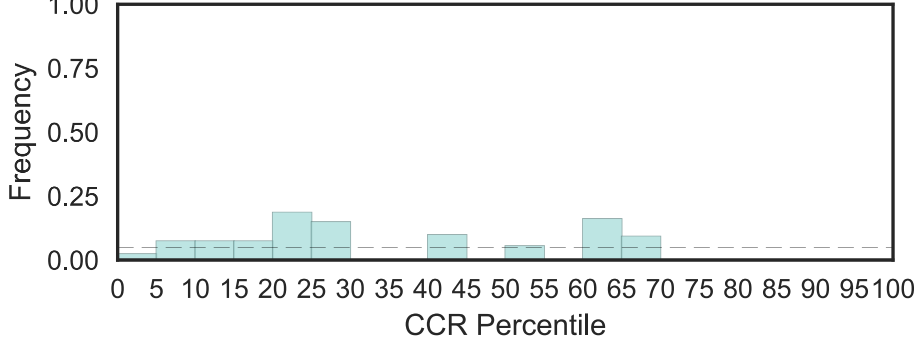

MAPK-interacting and spindle-stabilising protein-like
(MISS, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

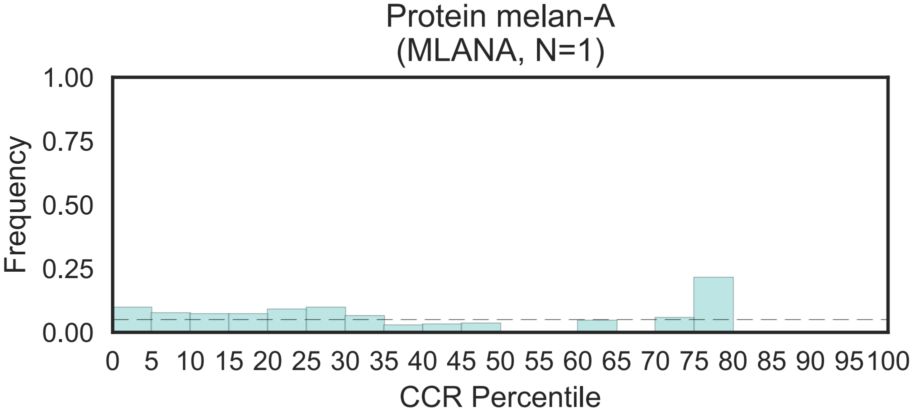

MIT (microtubule interacting and transport) domain
(MIT, N=11)
Fisher's OR: 1.36; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

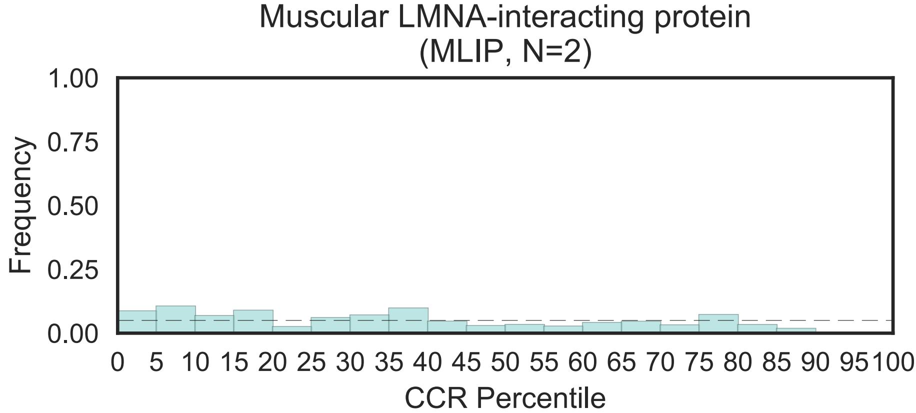

MITF/TFEB/TFEC/TFE3 N-terminus
(MITF_TFEB_C_3_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

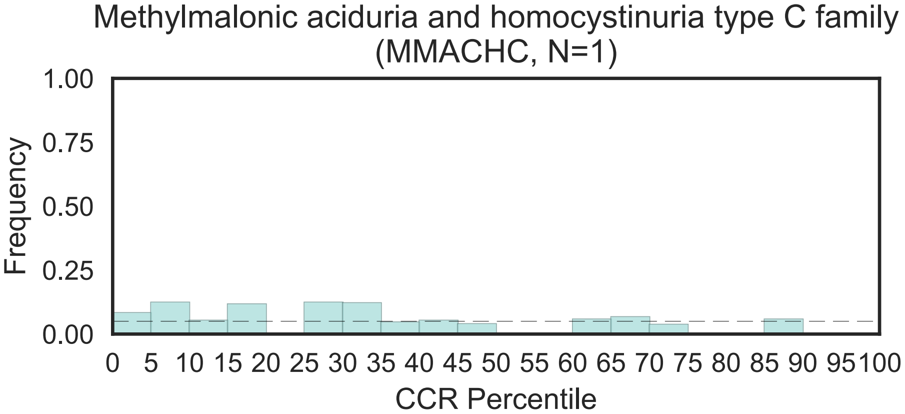

Phospholipase D-like domain at C-terminus of MIT
(MIT_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

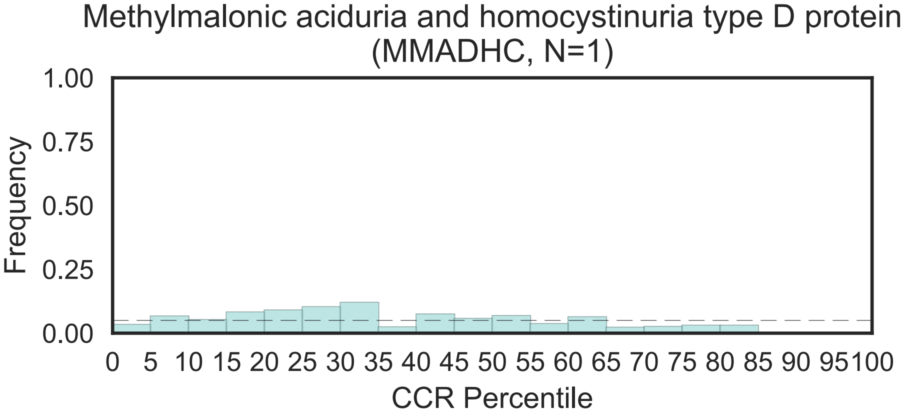
E3 ubiquitin-protein ligase makorin-1, C-terminal (MKRN1_C, N=2)

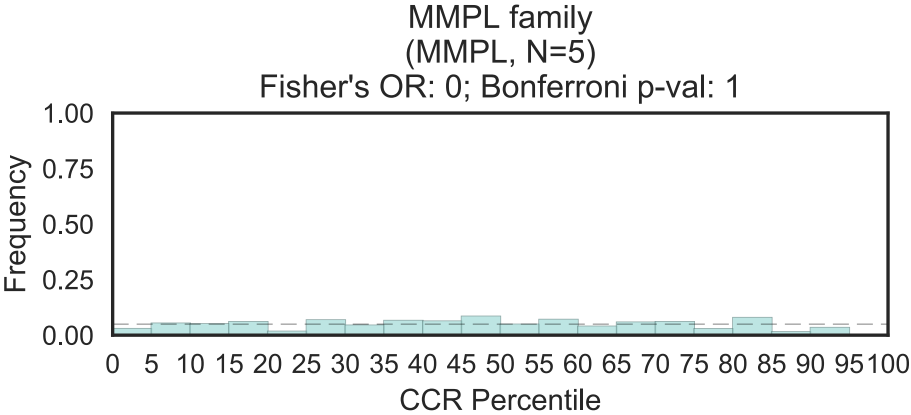


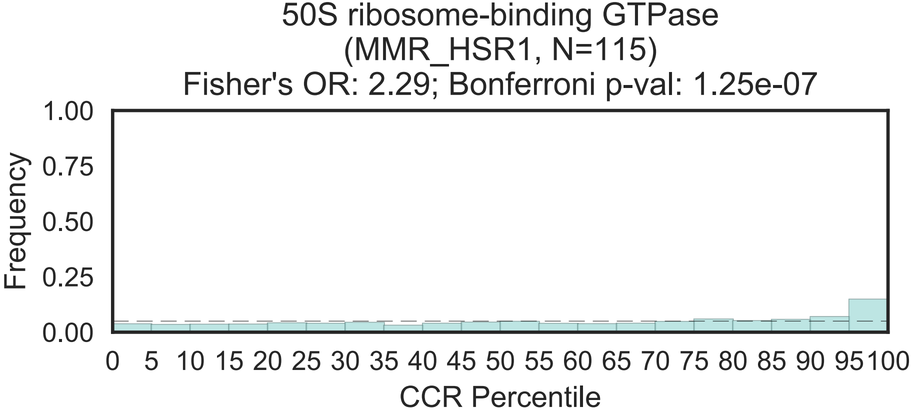

Protein melan-A
(MLANA, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

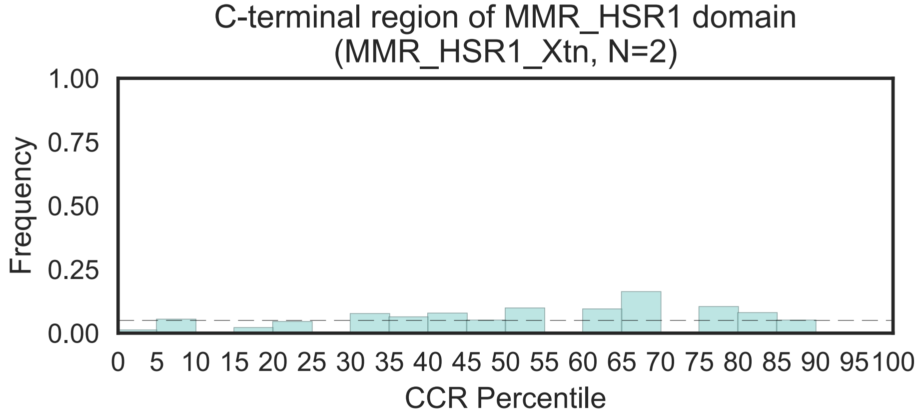

Muscular LMNA-interacting protein
(MLIP, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

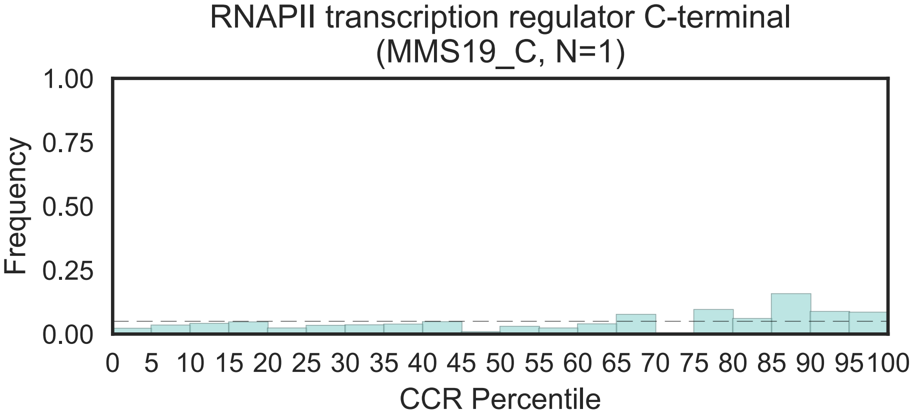

Methylmalonic aciduria and homocystinuria type C family
(MMACHC, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Methylmalonic aciduria and homocystinuria type D protein
(MMADHC, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

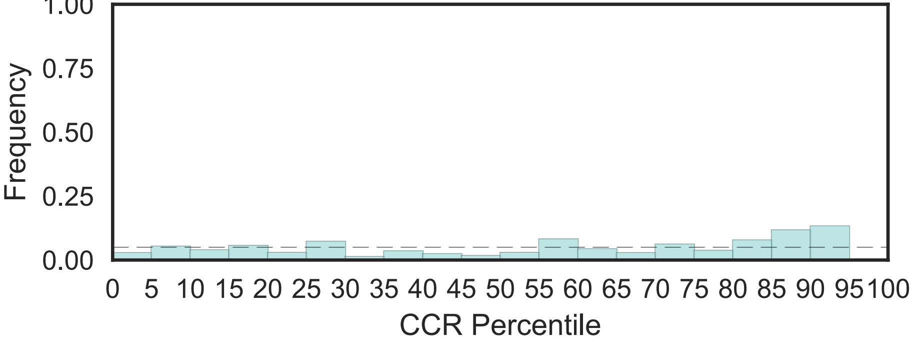

MMPL family
(MMPL, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

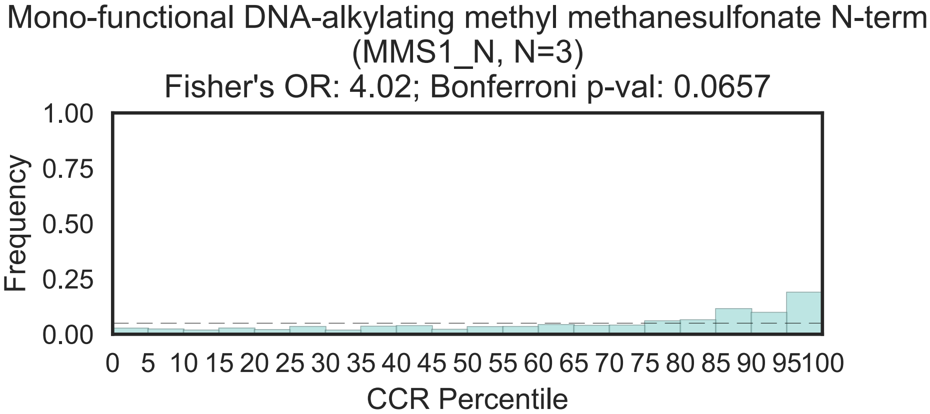

50S ribosome-binding GTPase
(MMR_HSR1, N=115)
Fisher's OR: 2.29; Bonferroni p-val: 1.25e-07
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

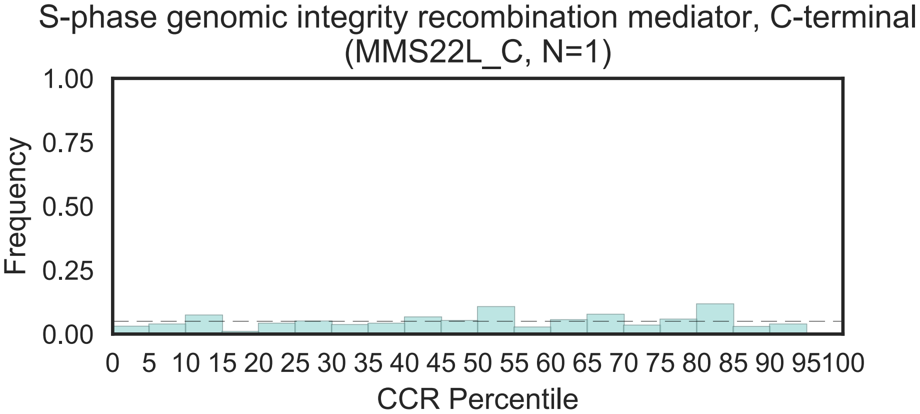

C-terminal region of MMR_HSR1 domain
(MMR_HSR1_Xtn, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


RNAPII transcription regulator C-terminal
(MMS19_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

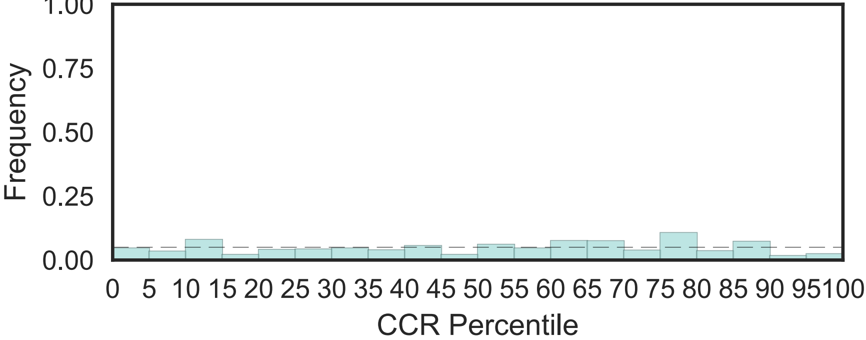
Dos2-interacting transcription regulator of RNA-Pol-II (MMS19_N, N=1)

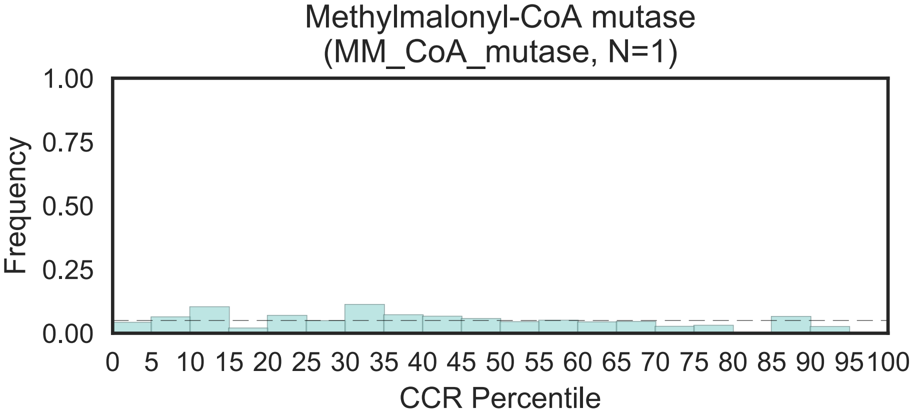


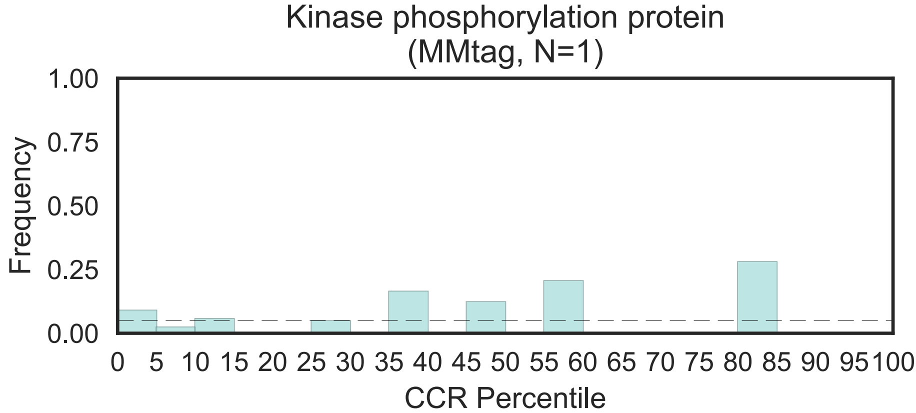

Mono-functional DNA-alkylating methyl methanesulfonate N-term
(MMS1_N, N=3)
Fisher's OR: 4.02; Bonferroni p-val: 0.0657
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

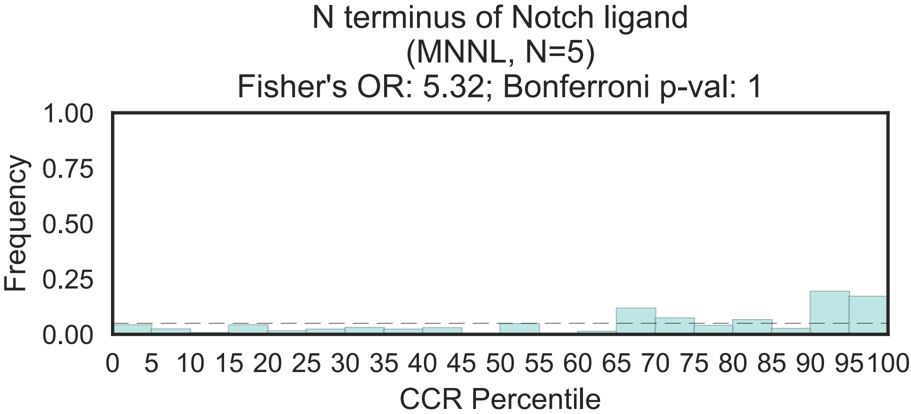

S-phase genomic integrity recombination mediator, C-terminal
(MMS22L_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

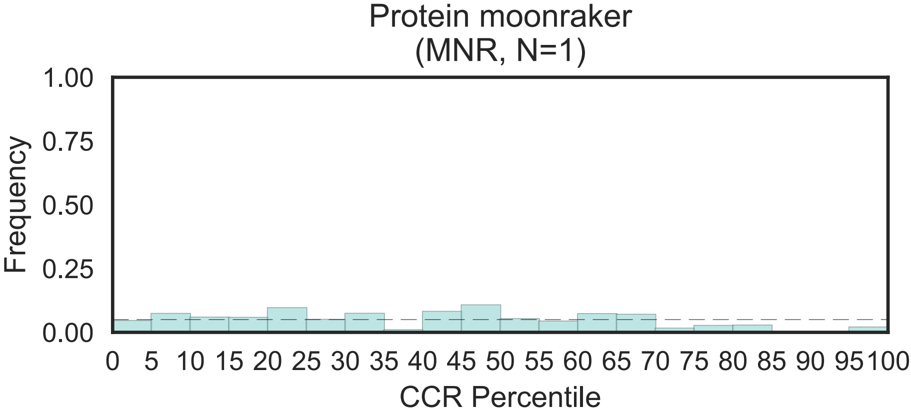
S-phase genomic integrity recombination mediator, N-terminal (MMS22L_N, N=1)

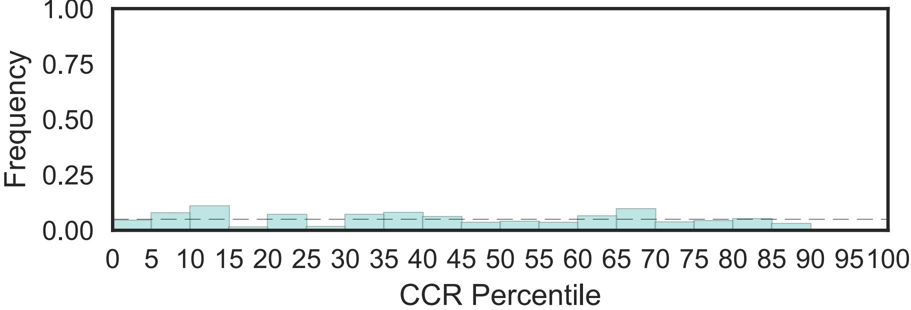


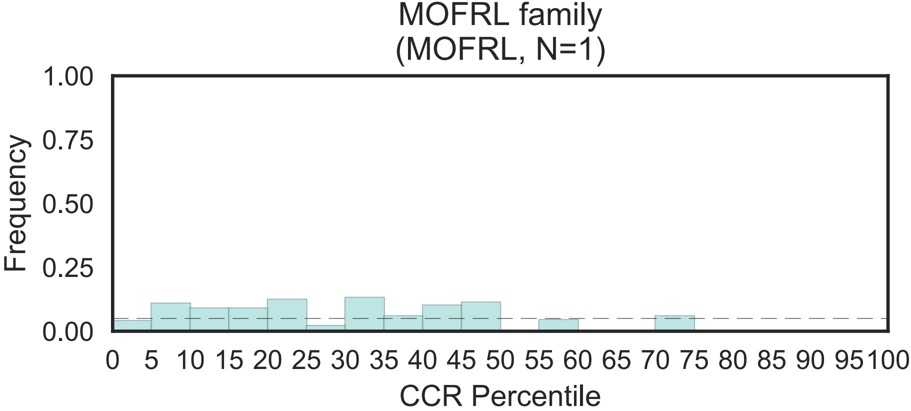

Methylmalonyl-CoA mutase
(MM_CoA_mutase, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

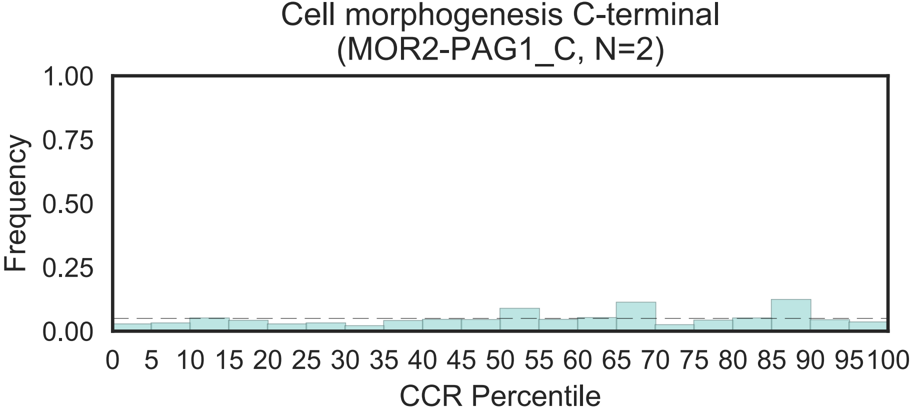

Kinase phosphorylation protein
(MMtag, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

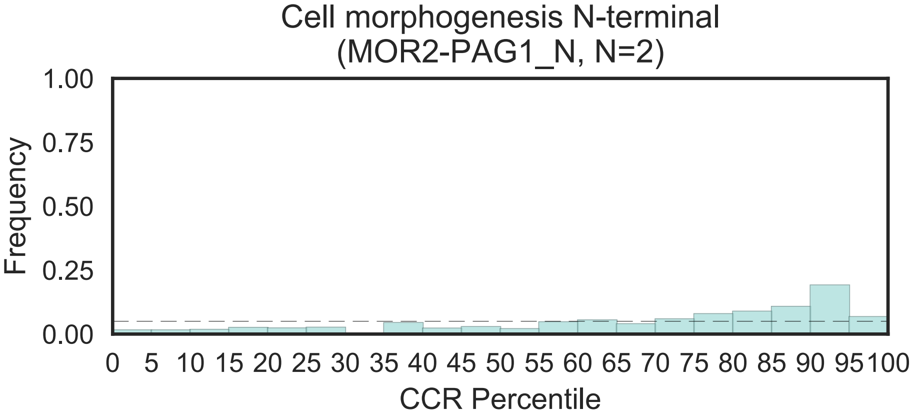

N terminus of Notch ligand
(MNNL, N=5)
Fisher's OR: 5.32; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

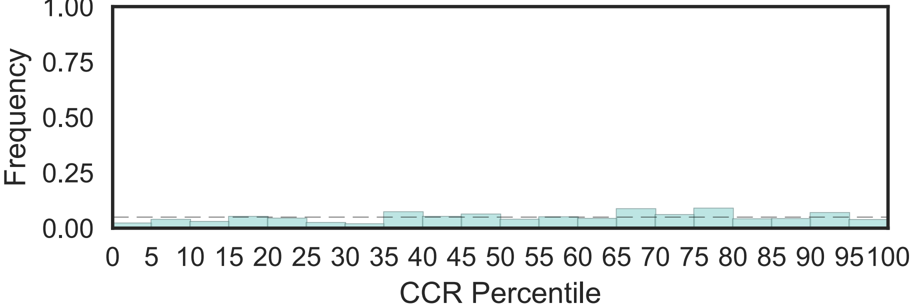

Protein moonraker
(MNR, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


KH-like RNA-binding domain
(MOEP19, N=5)
Fisher's OR: 0; Bonferroni p-val: 1

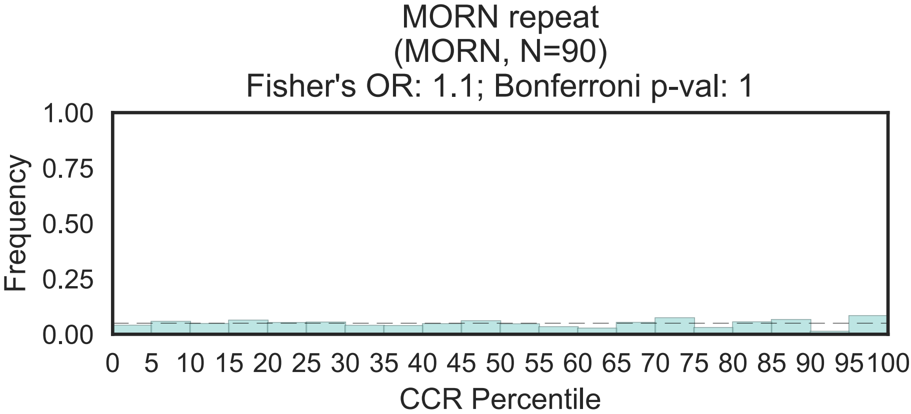

MOFRL family
(MOFRL, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Cell morphogenesis C-terminal
(MOR2-PAG1_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

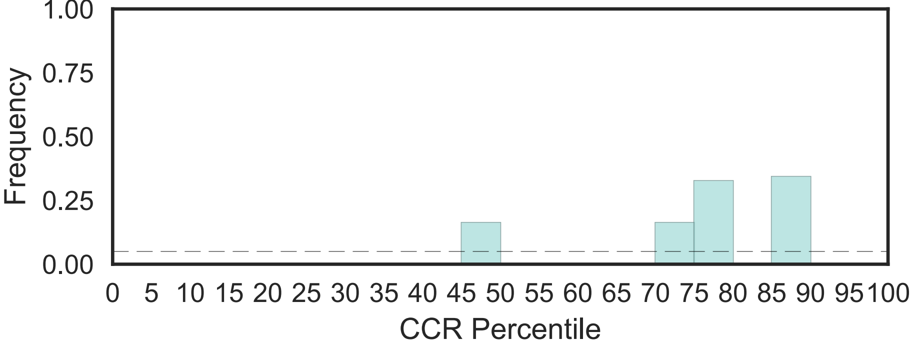

Cell morphogenesis N-terminal
(MOR2-PAG1_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

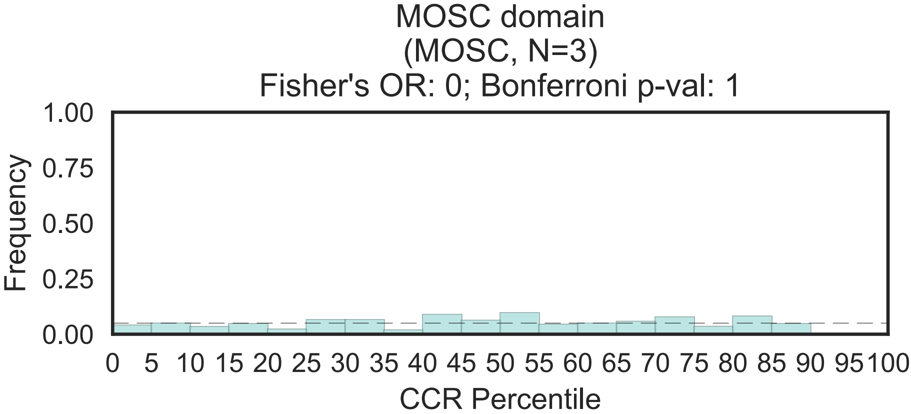


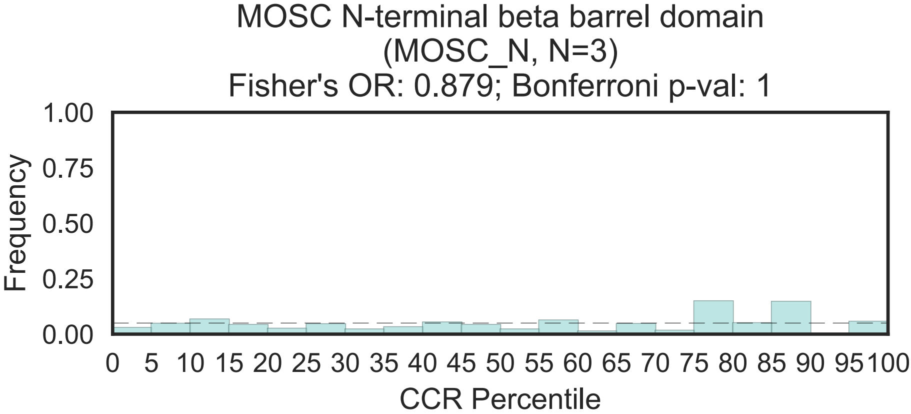
Cell morphogenesis central region
(MOR2-PAG1_mid, N=8)
Fisher's OR: 1.15; Bonferroni p-val: 1

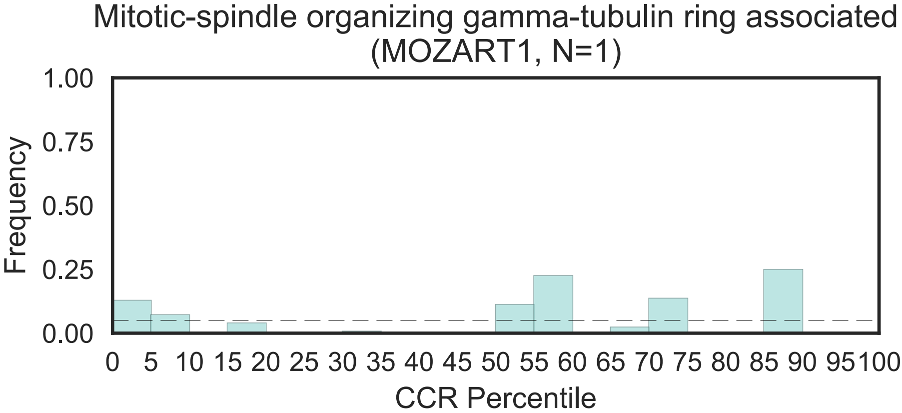

MORN repeat
(MORN, N=90)
Fisher's OR: 1.1; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

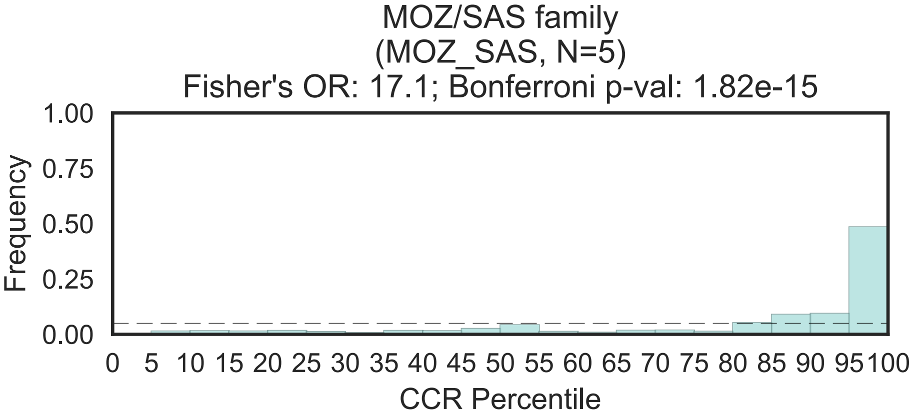
MORN repeat variant (MORN_2, N=2)

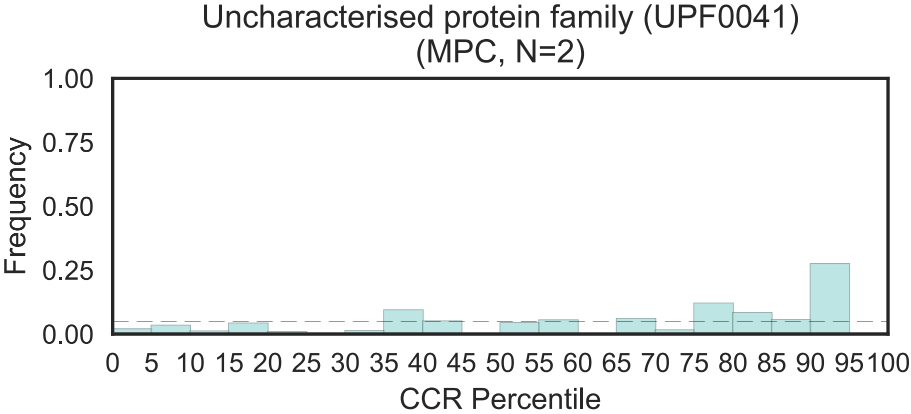


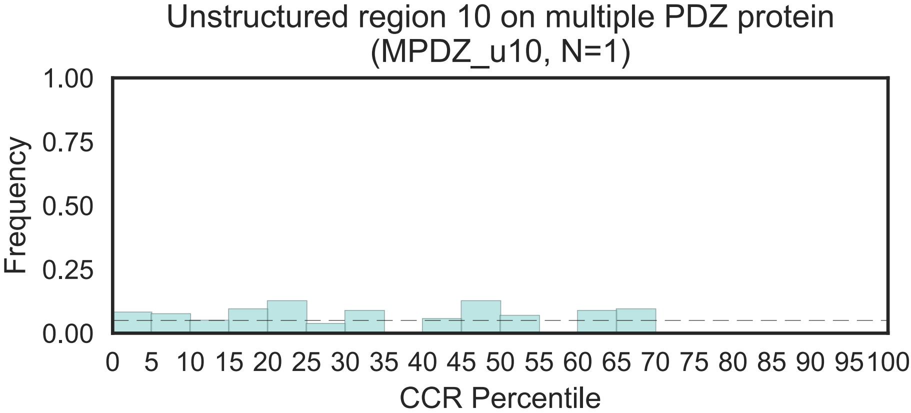

MOSC domain
(MOSC, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


MOSC N-terminal beta barrel domain
(MOSC_N, N=3)
Fisher's OR: 0.879; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Mitotic-spindle organizing gamma-tubulin ring associated
(MOZART1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

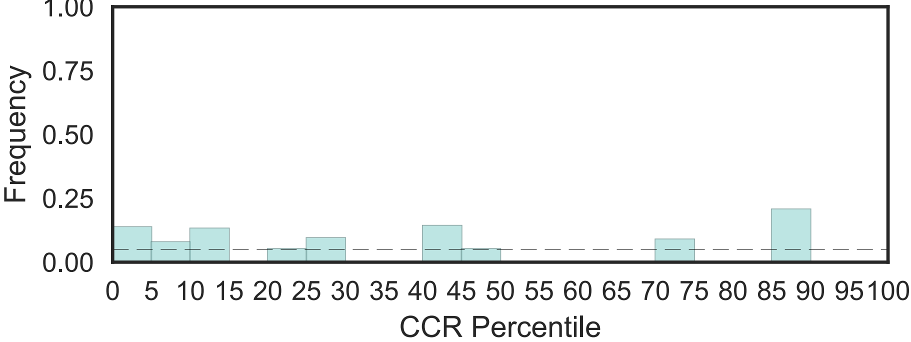

MOZ/SAS family
(MOZ_SAS, N=5)
Fisher's OR: 17.1; Bonferroni p-val: 1.82e-15
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

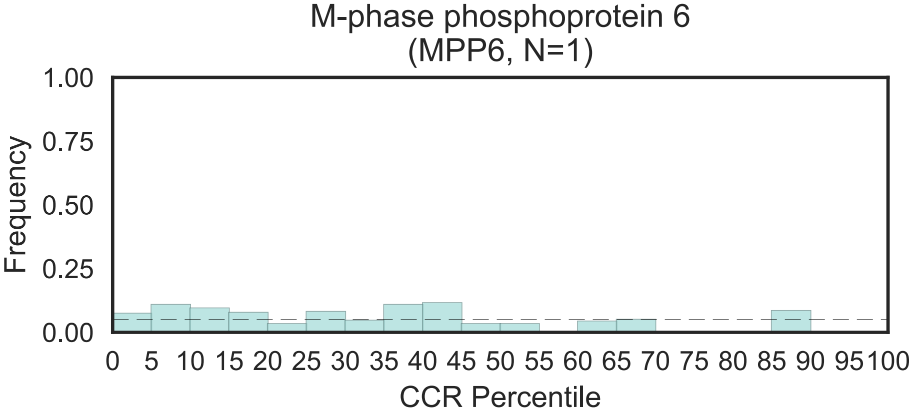

Uncharacterised protein family (UPF0041)
(MPC, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

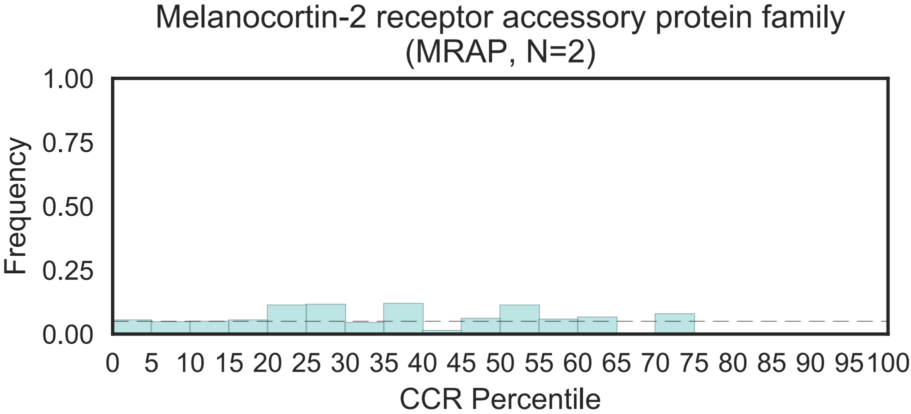


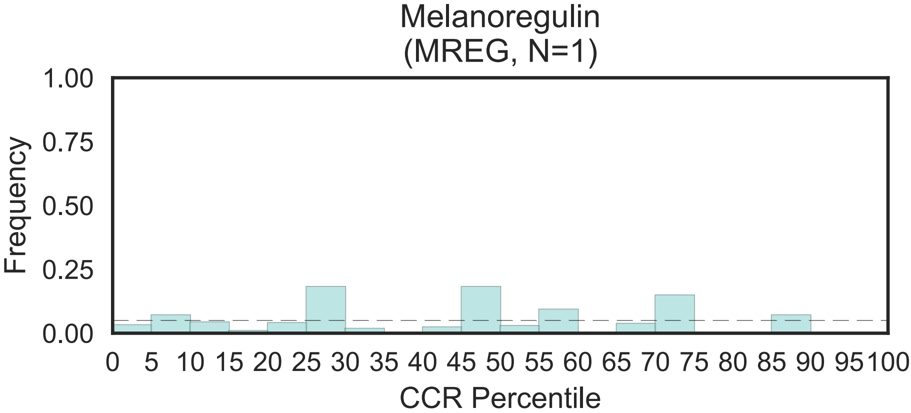
Unstructured region 10 on multiple PDZ protein
(MPDZ_u10, N=1)

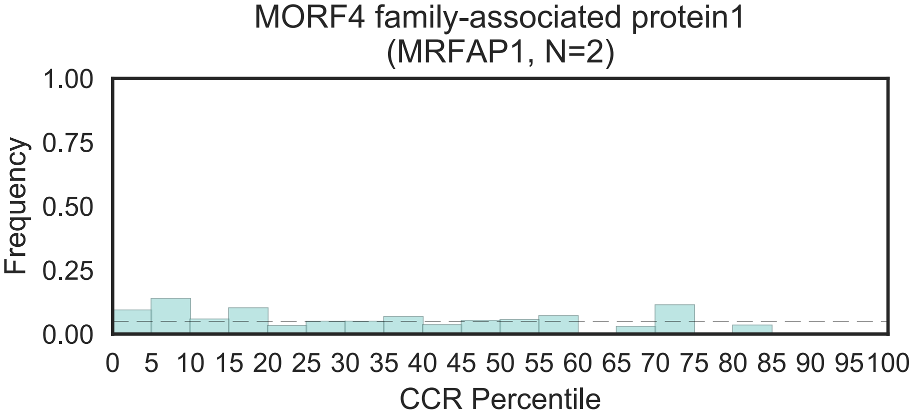
M-phase-specific PLK1-interacting protein (MPLKIP, N=1)

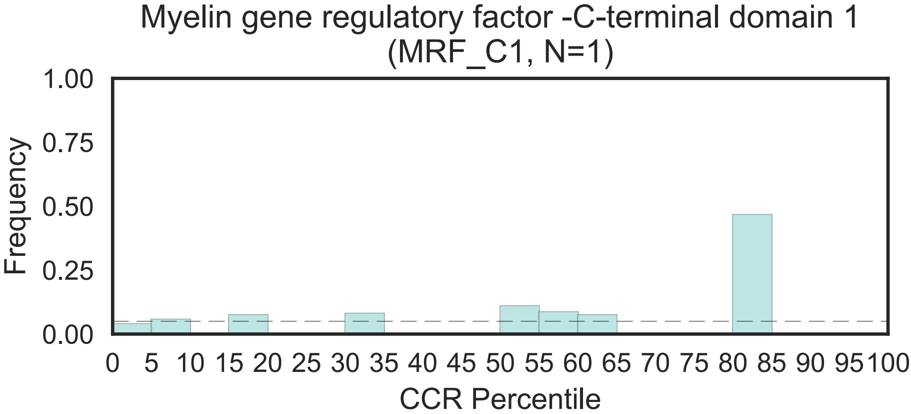


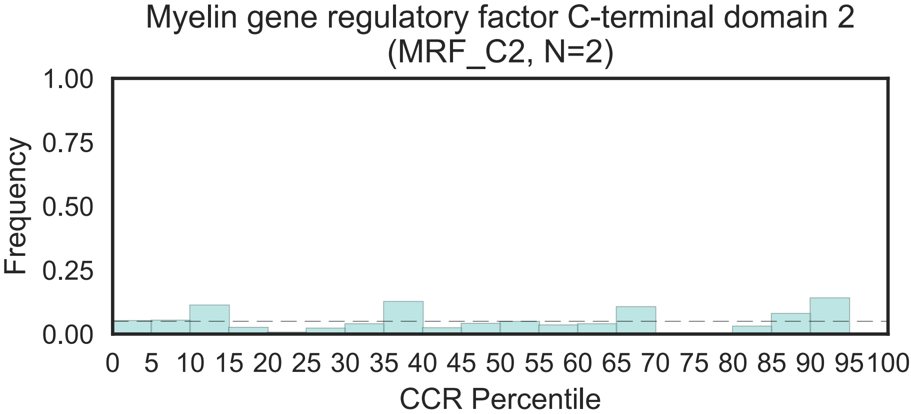

M-phase phosphoprotein 6
(MPP6, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

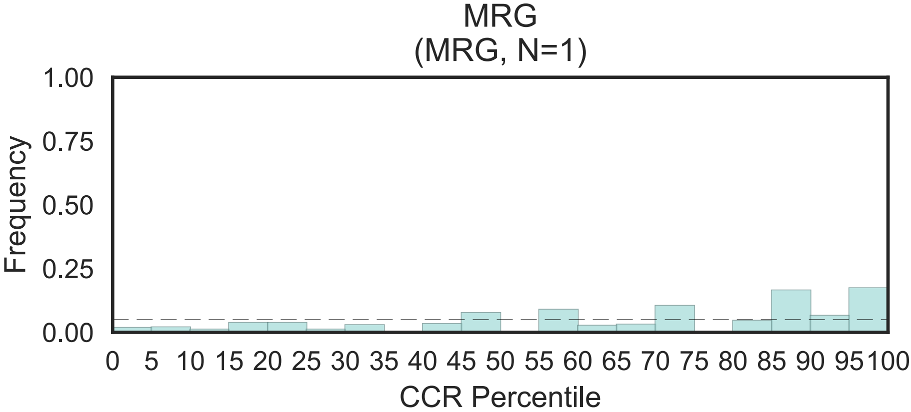

Melanocortin-2 receptor accessory protein family
(MRAP, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

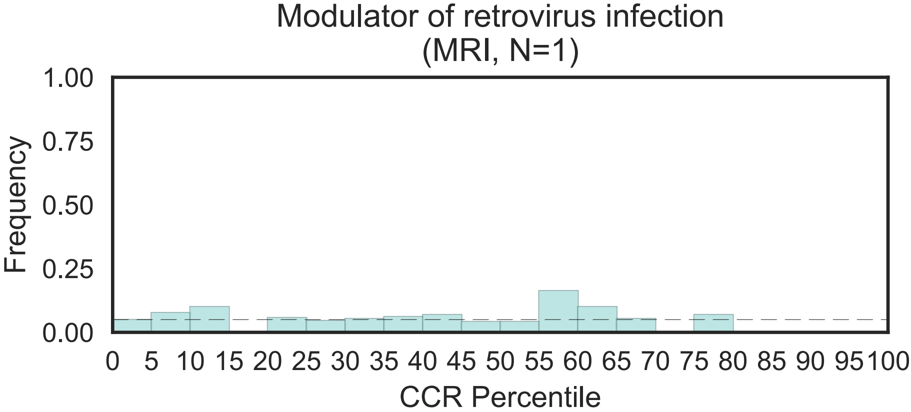

Melanoregulin
(MREG, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

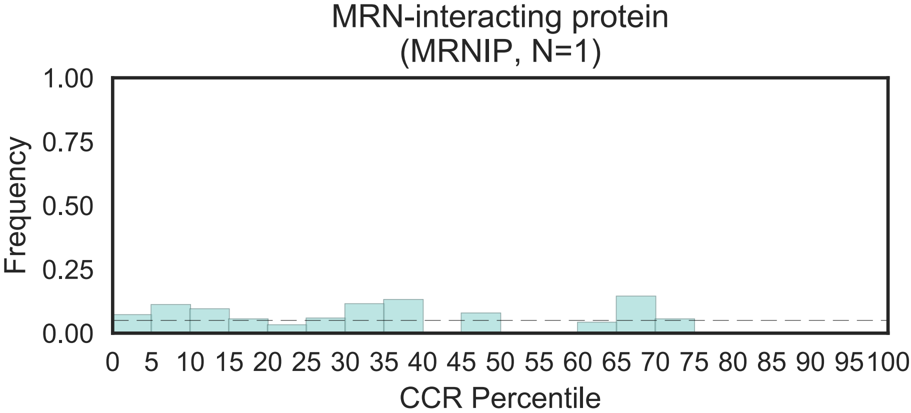

MORF4 family-associated protein1
(MRFAP1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

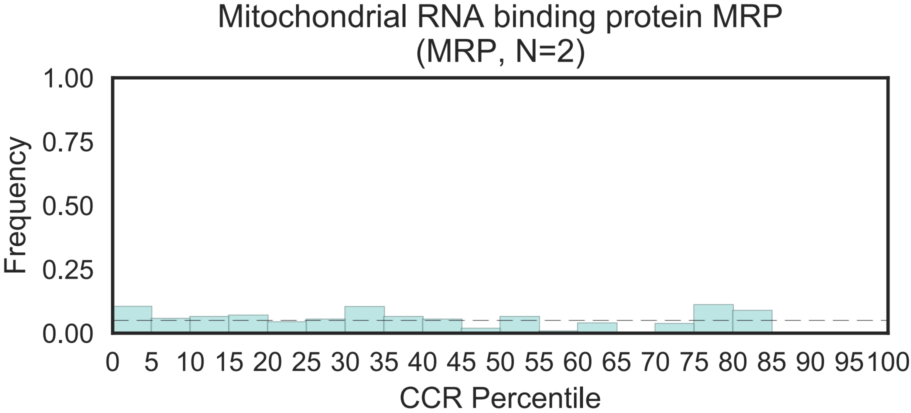

Myelin gene regulatory factor -C-terminal domain 1
(MRF_C1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

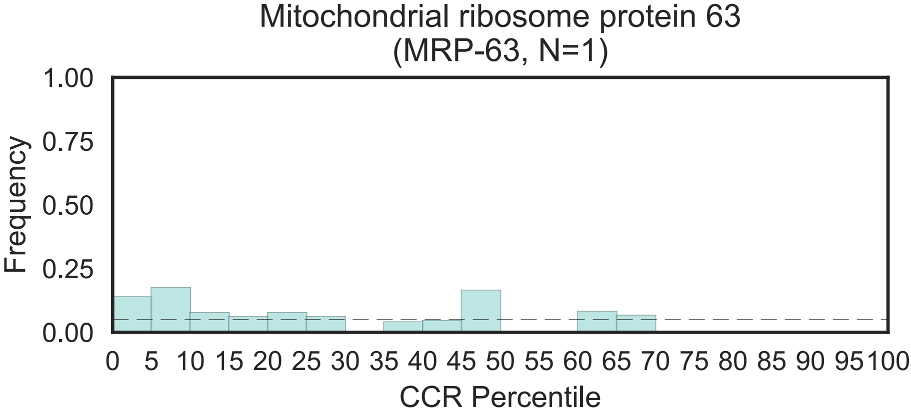

Myelin gene regulatory factor C-terminal domain 2
(MRF_C2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

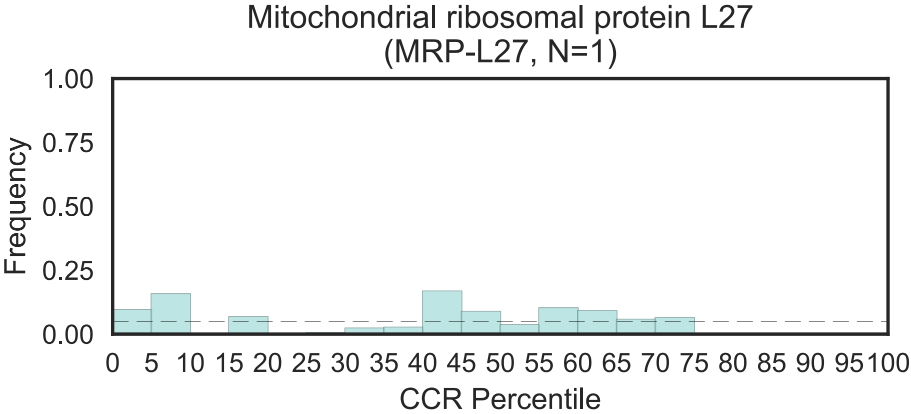

MRG
(MRG, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Modulator of retrovirus infection
(MRI, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

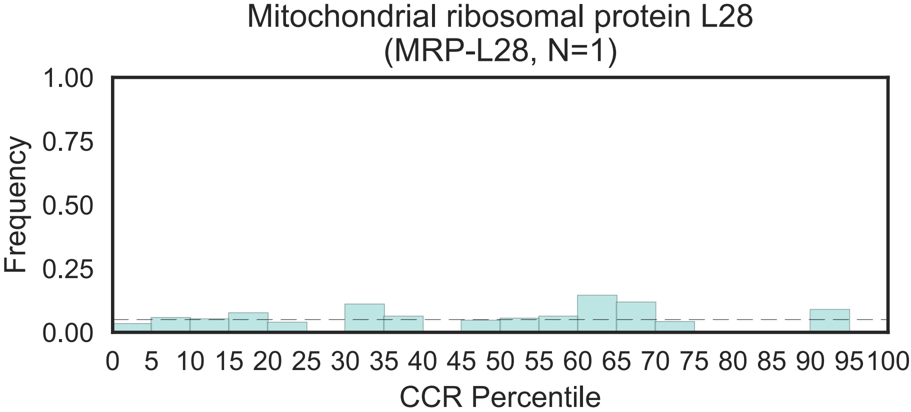

MRN-interacting protein
(MRNIP, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

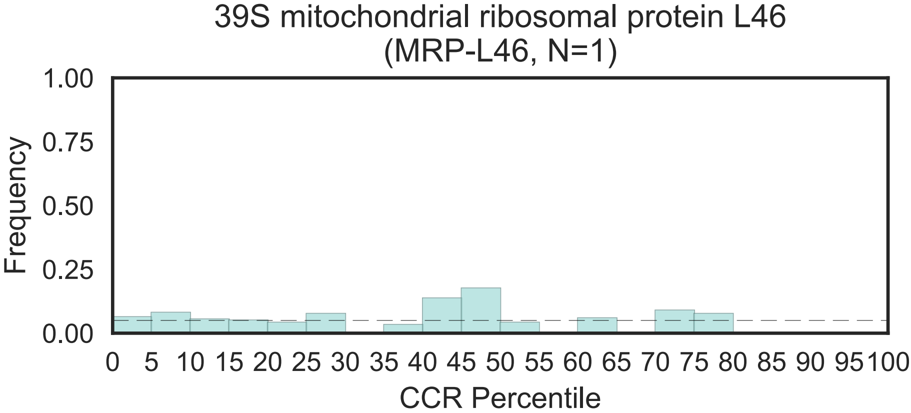

Mitochondrial RNA binding protein MRP
(MRP, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

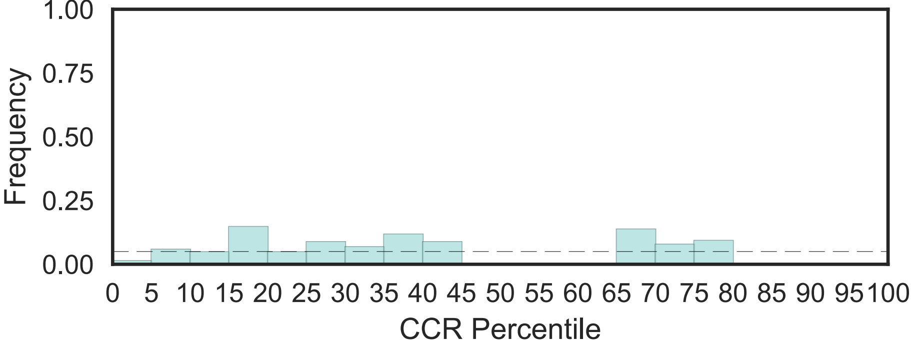

Mitochondrial ribosome protein 63
(MRP-63, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile



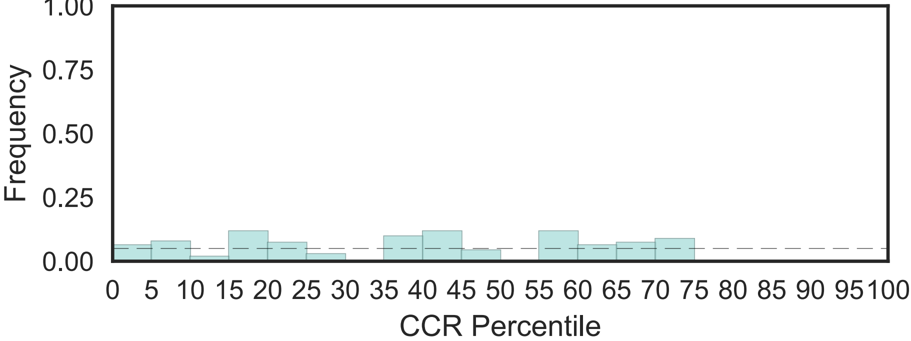
Mitochondrial ribosomal protein L27
(MRP-L27, N=1)

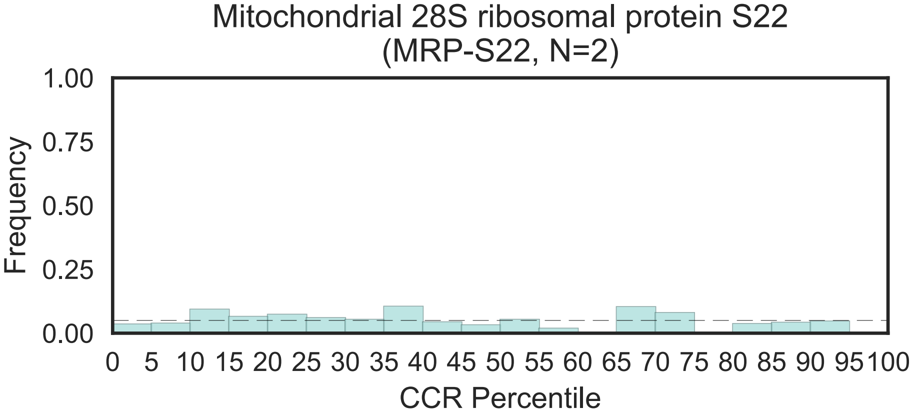

Mitochondrial ribosomal protein L28
(MRP-L28, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

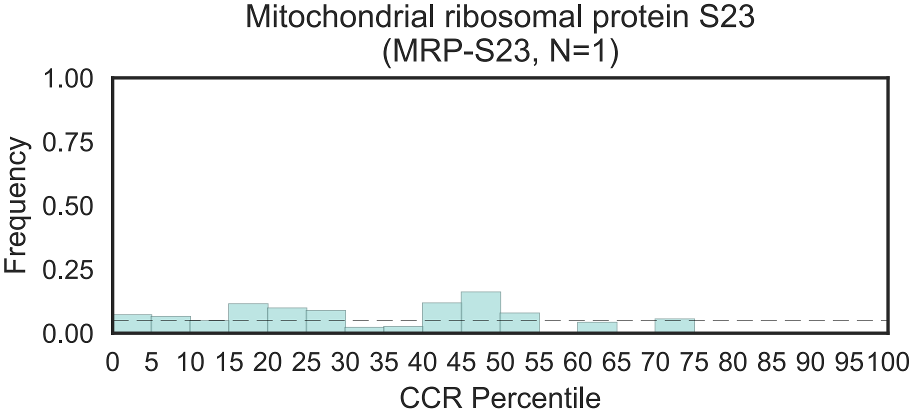

39S mitochondrial ribosomal protein L46
(MRP-L46, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

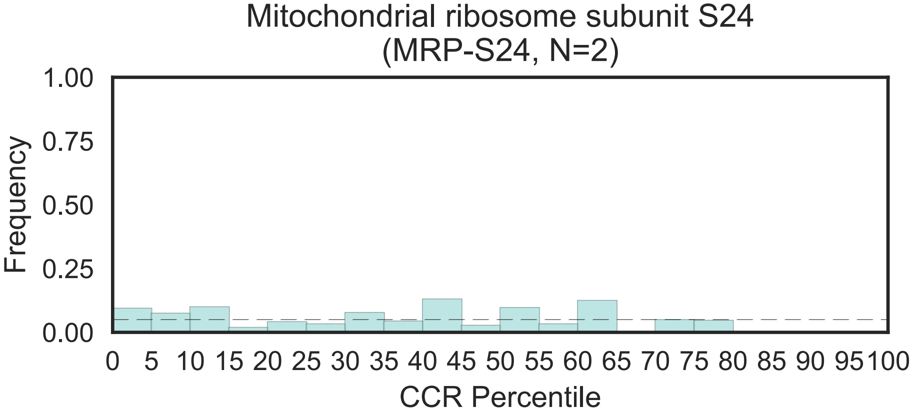

Mitochondrial 39-S ribosomal protein L47 (MRP-L47) (MRP-L47, N=1)

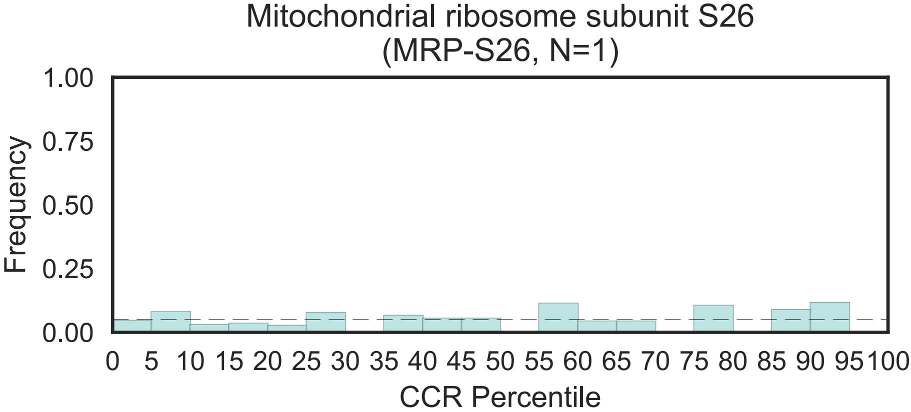
Mitochondrial ribosomal subunit
(MRP-L51, N=1)

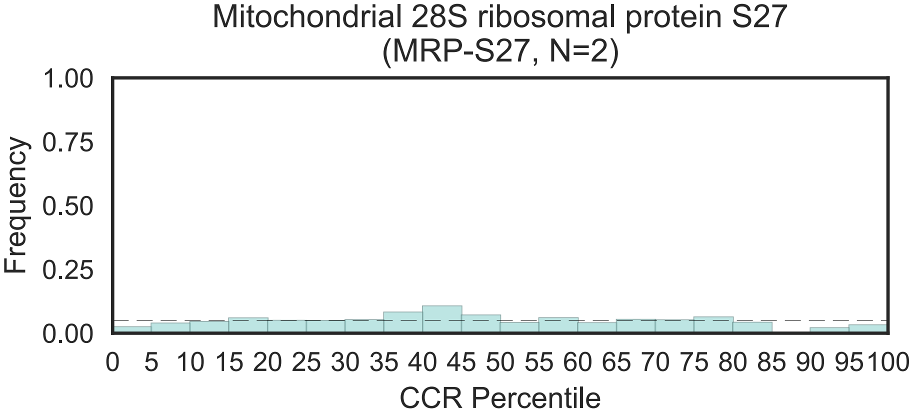


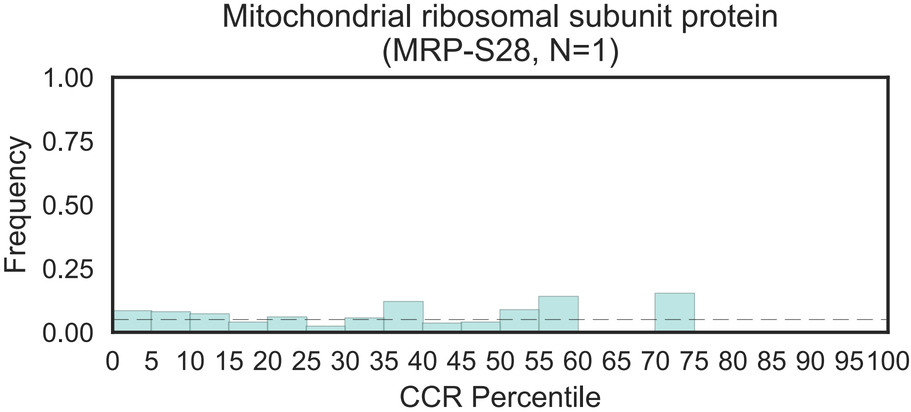

Mitochondrial 28S ribosomal protein S22
(MRP-S22, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Mitochondrial ribosomal protein S23
(MRP-S23, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

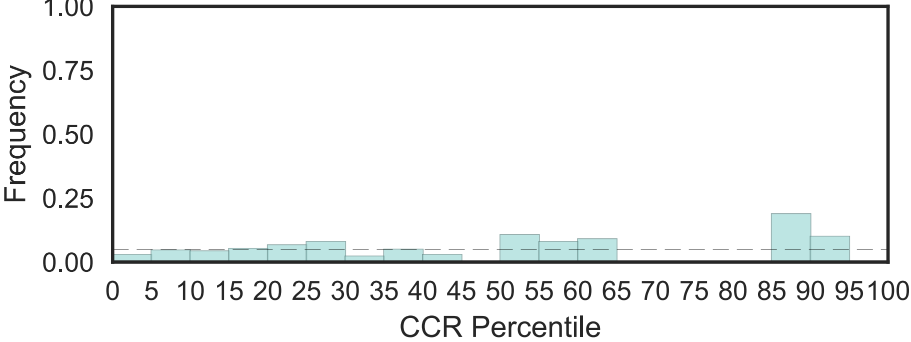

Mitochondrial ribosome subunit S24
(MRP-S24, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

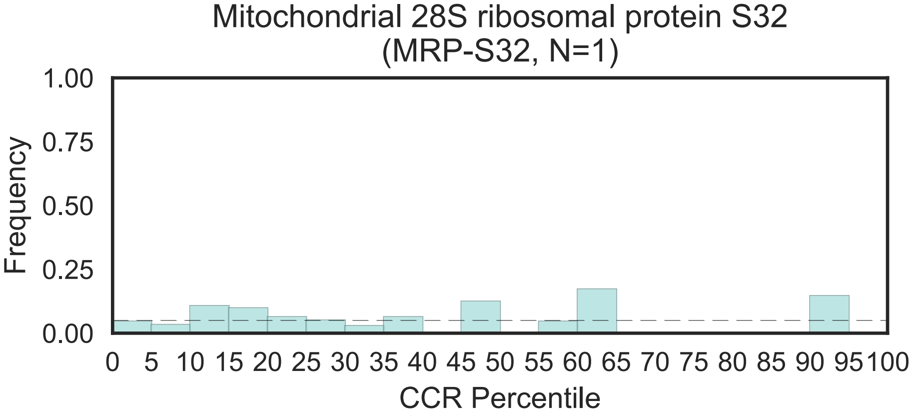

Mitochondrial ribosome subunit S26
(MRP-S26, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

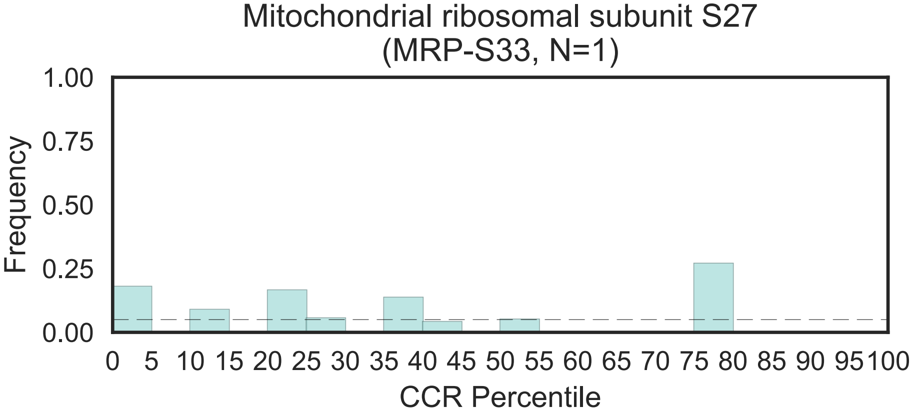

Mitochondrial 28S ribosomal protein S27
(MRP-S27, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

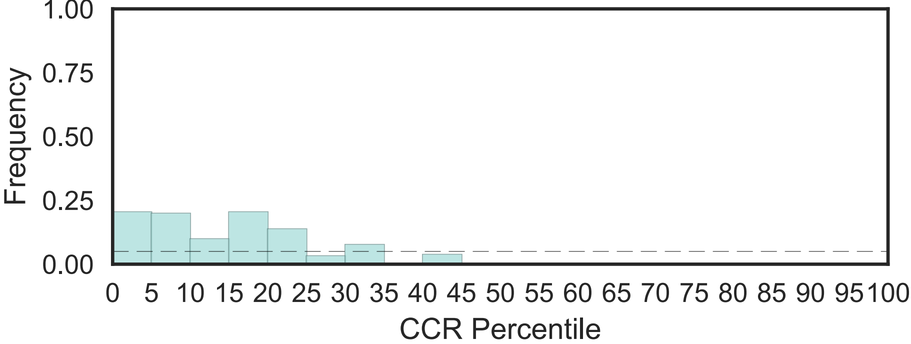

Mitochondrial ribosomal subunit protein
(MRP-S28, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Mitochondrial 28S ribosomal protein S31
(MRP-S31, N=1)

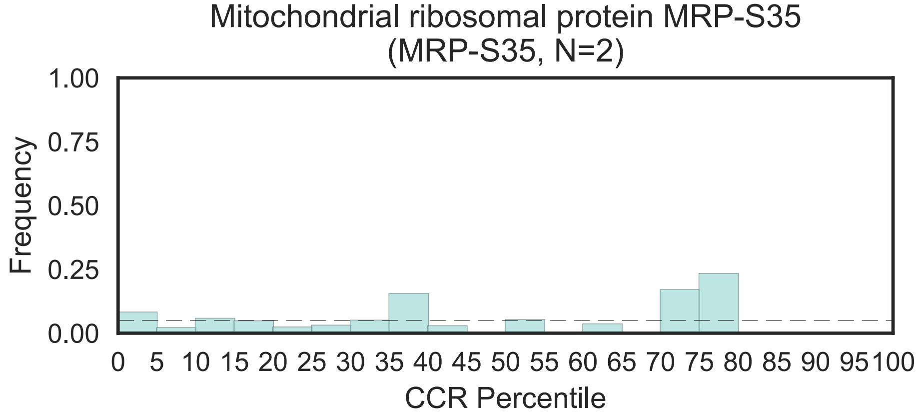


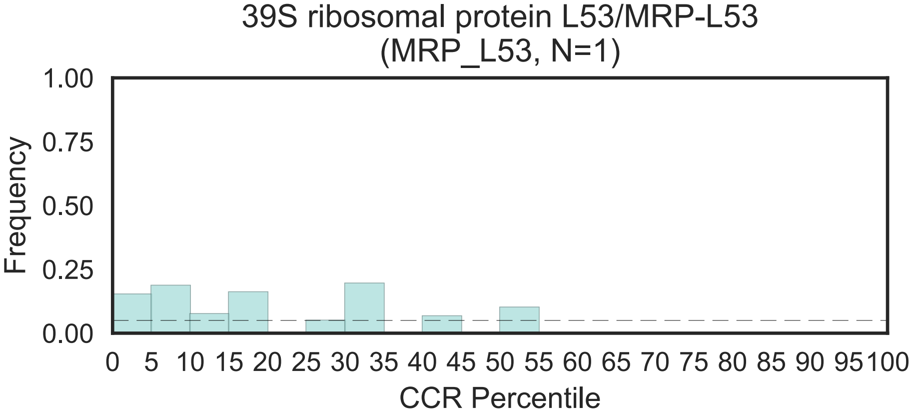

Mitochondrial 28S ribosomal protein S32
(MRP-S32, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

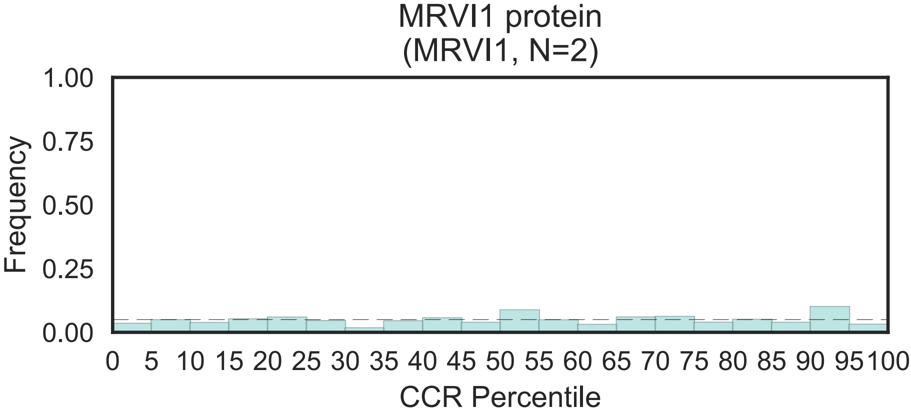

Mitochondrial ribosomal subunit S27
(MRP-S33, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

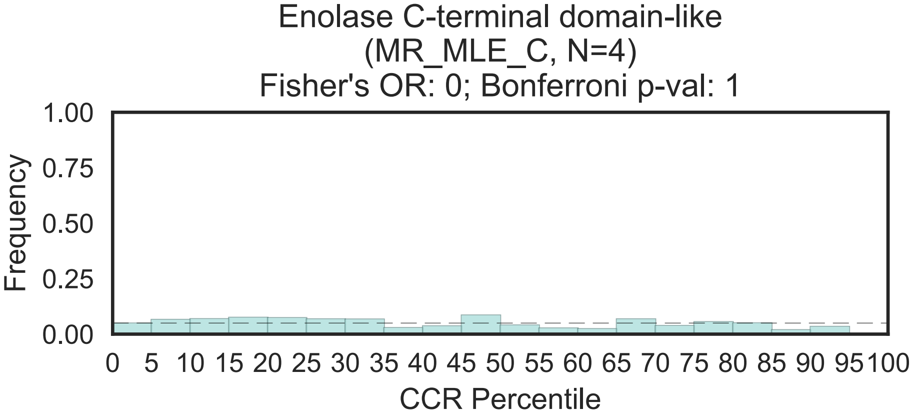


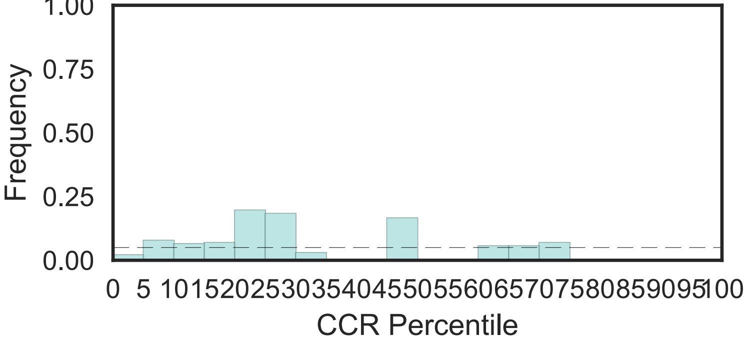
Mitochondrial 28S ribosomal protein S34
(MRP-S34, N=1)


Mitochondrial ribosomal protein MRP-S35
(MRP-S35, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

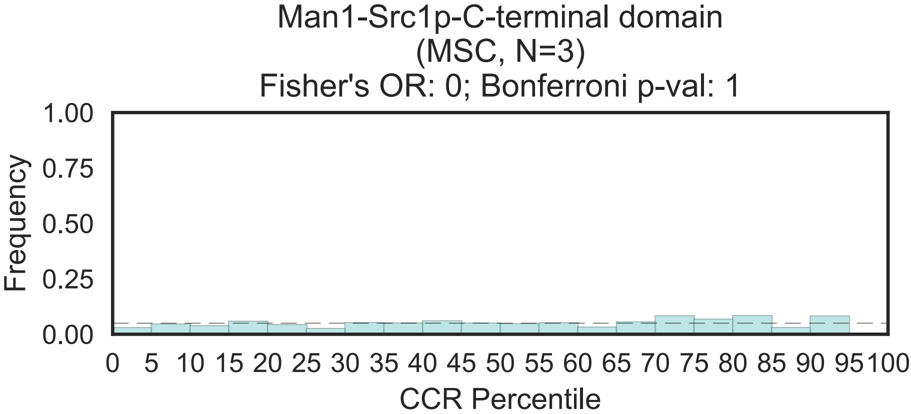

39S ribosomal protein L53/MRP-L53
(MRP_L53, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

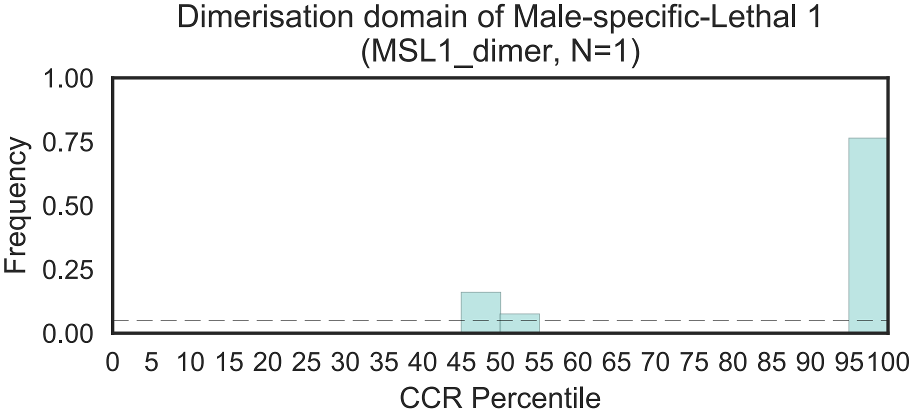

MRVI1 protein
(MRVI1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

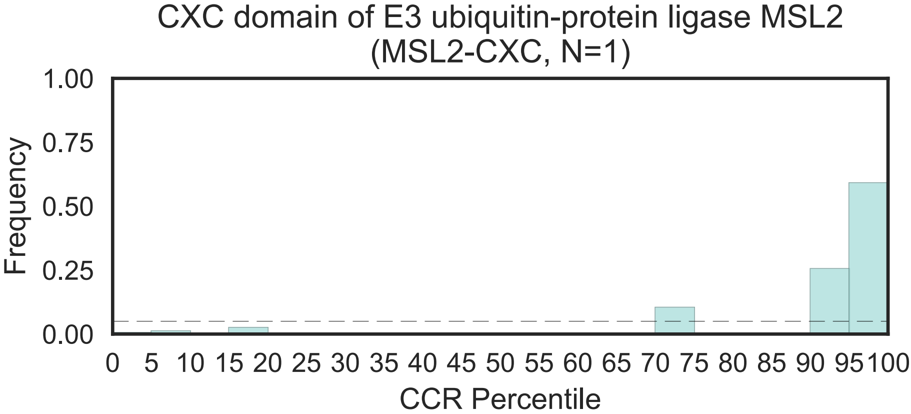

Enolase C-terminal domain-like
(MR_MLE_C, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

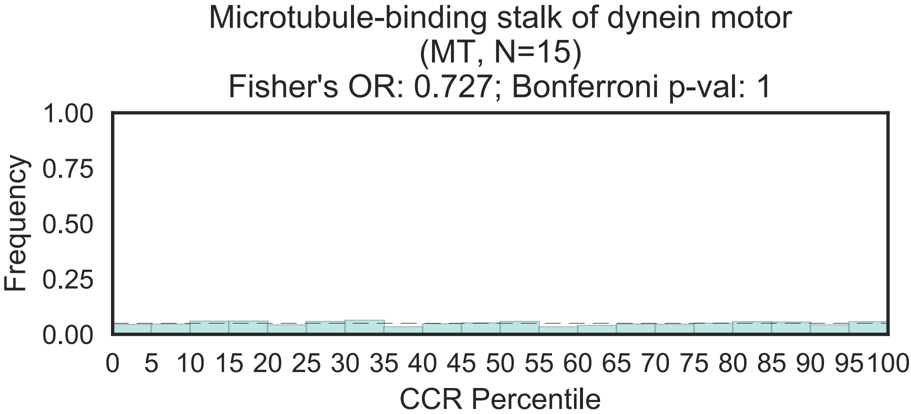


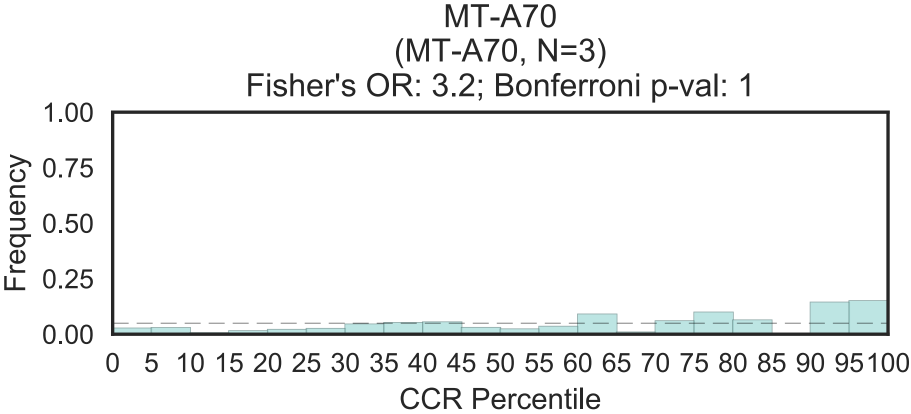
Mandelate racemase / muconate lactonizing enzyme, N-terminal domain (MR_MLE_N, N=1)

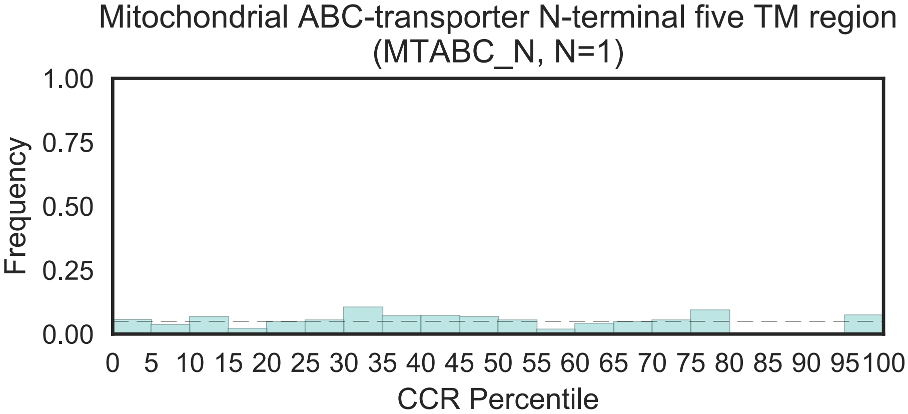

Man1-Src1p-C-terminal domain
(MSC, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

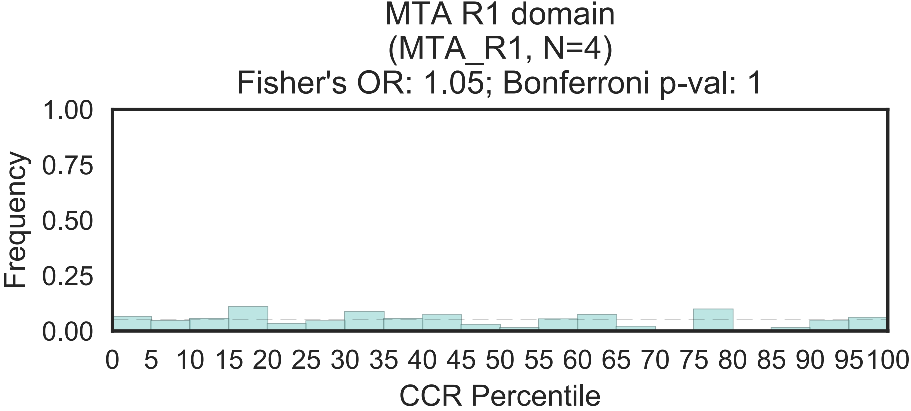

Dimerisation domain of Male-specific-Lethal 1
(MSL1_dimer, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

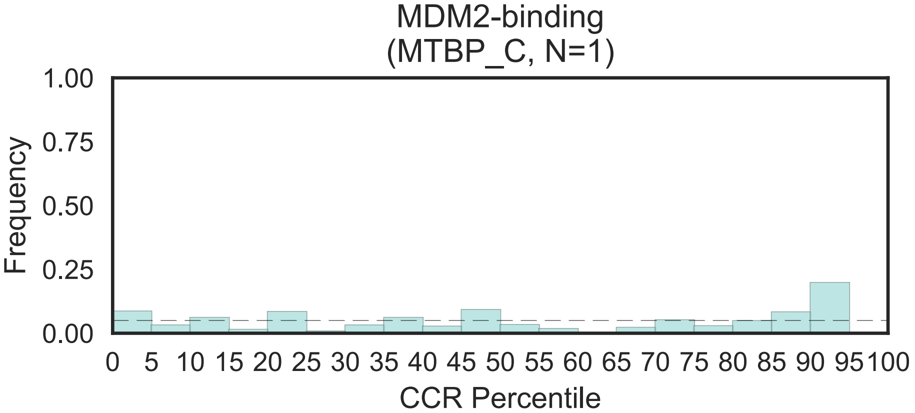

CXC domain of E3 ubiquitin-protein ligase MSL2
(MSL2-CXC, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

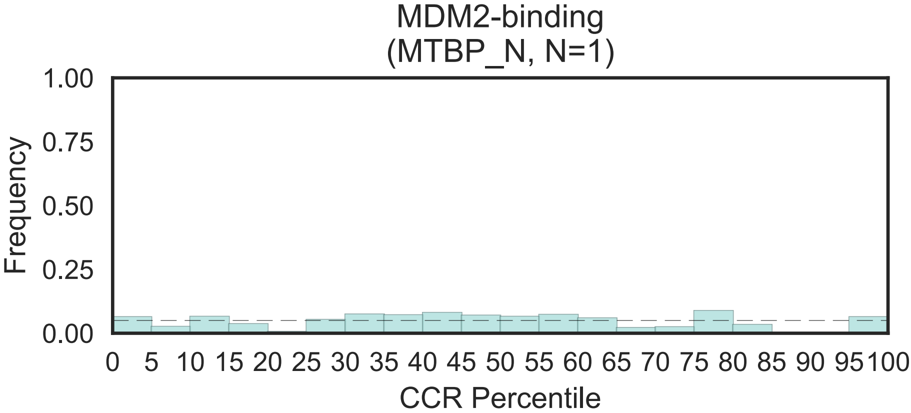

Microtubule-binding stalk of dynein motor
(MT, N=15)
Fisher's OR: 0.727; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

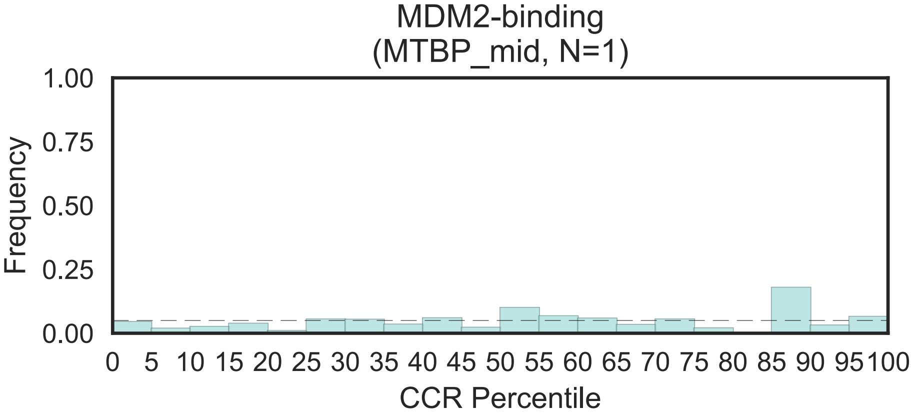

MT-A70
(MT-A70, N=3)
Fisher's OR: 3.2; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

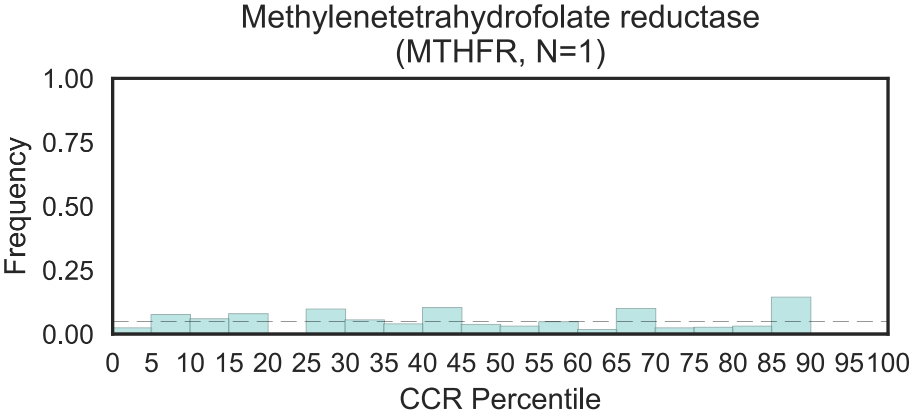

Mitochondrial ABC-transporter N-terminal five TM region
(MTABC_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

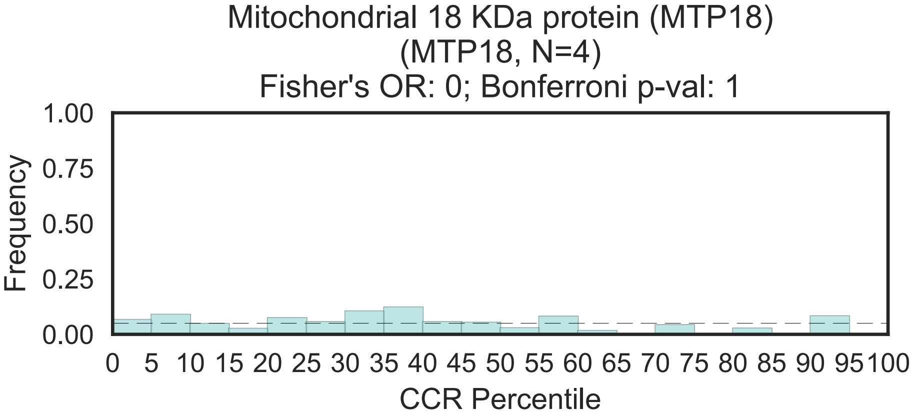

MTA R1 domain
(MTA_R1, N=4)
Fisher's OR: 1.05; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

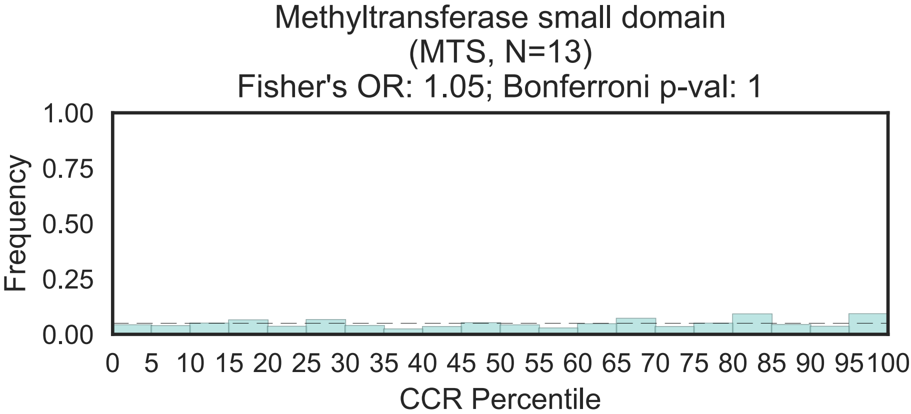

MDM2-binding
(MTBP_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

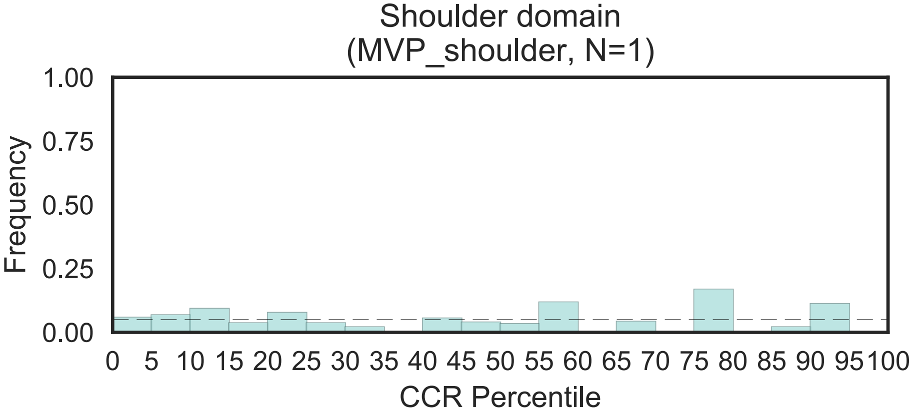

MDM2-binding
(MTBP_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

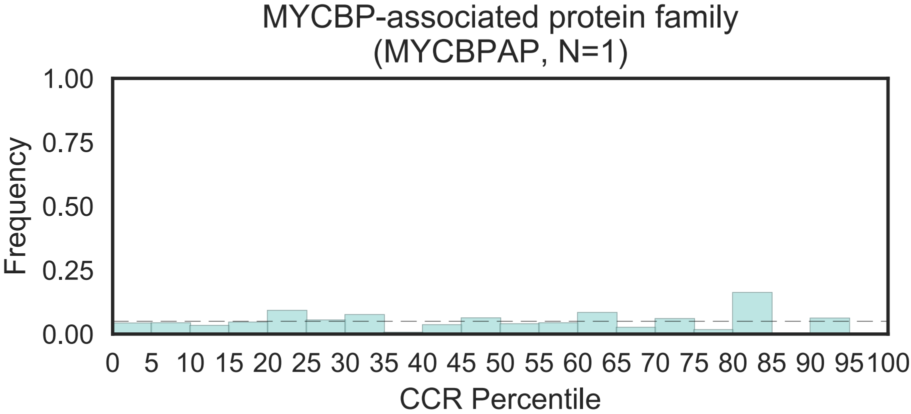

MDM2-binding
(MTBP_mid, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

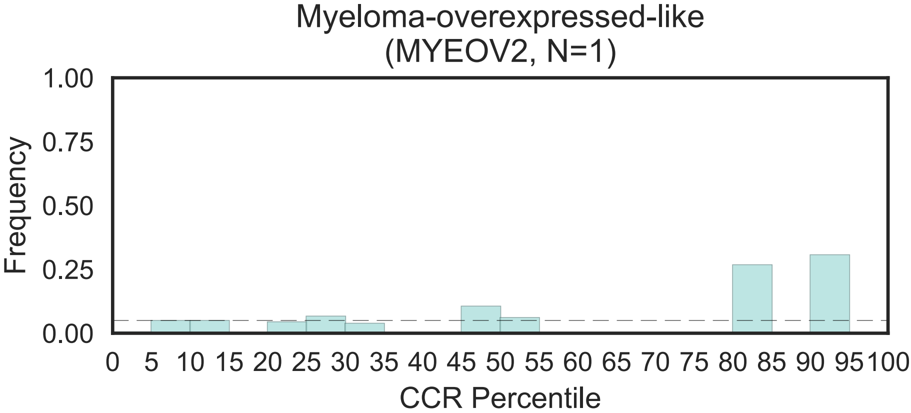

Methylenetetrahydrofolate reductase
(MTHFR, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

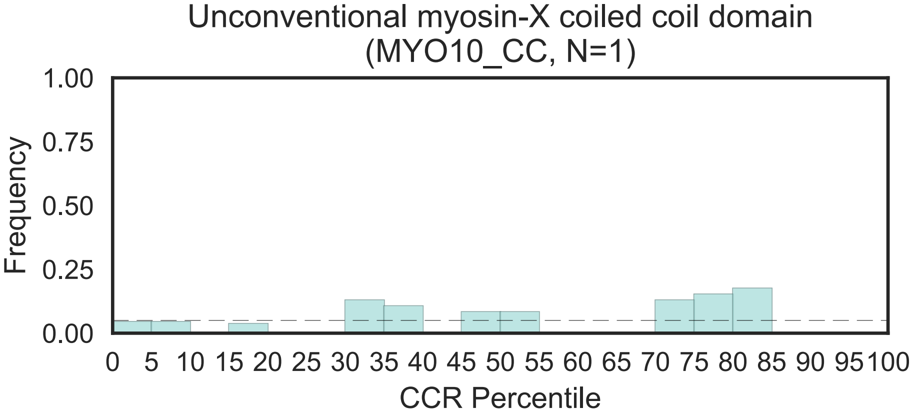

Mitochondrial 18 KDa protein (MTP18)
(MTP18, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

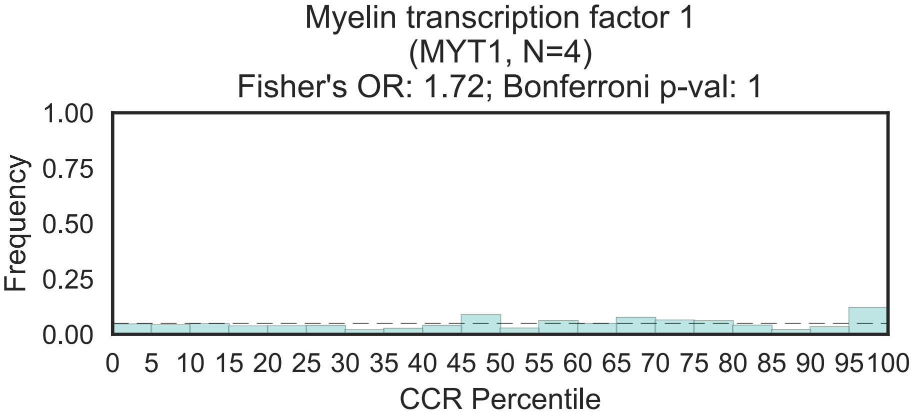

Methyltransferase small domain
(MTS, N=13)
Fisher's OR: 1.05; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

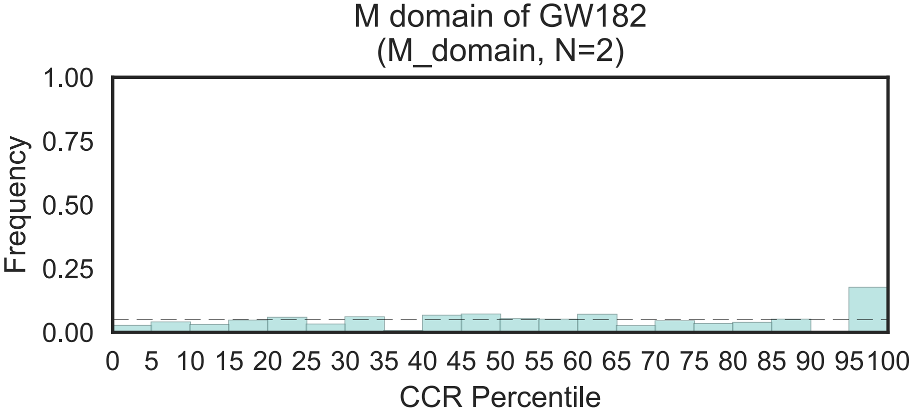

Shoulder domain
(MVP_shoulder, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

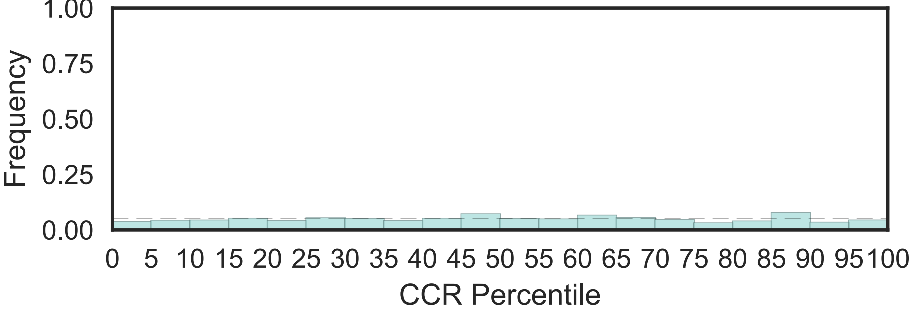

MYCBP-associated protein family
(MYCBPAP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Myeloma-overexpressed-like
(MYEOV2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

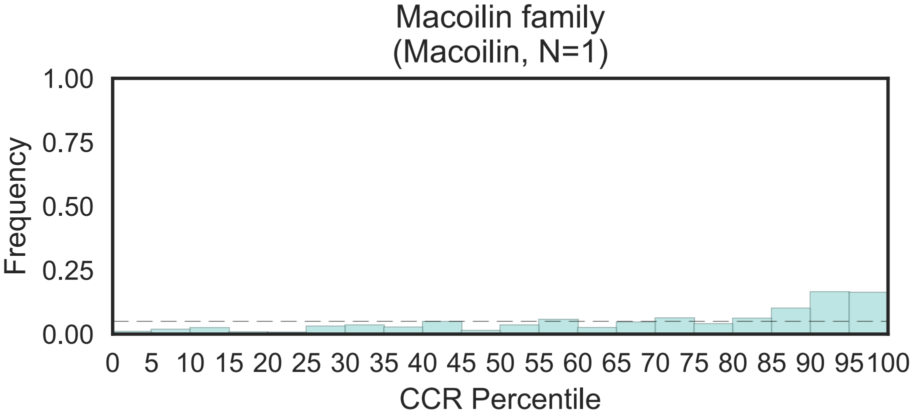

Unconventional myosin-X coiled coil domain
(MYO10_CC, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Myelin transcription factor 1
(MYT1, N=4)
Fisher's OR: 1.72; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

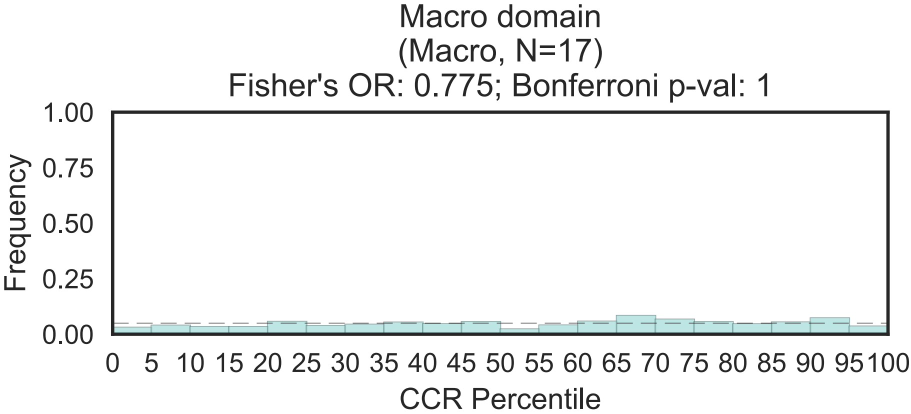

M domain of GW182
(M_domain, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

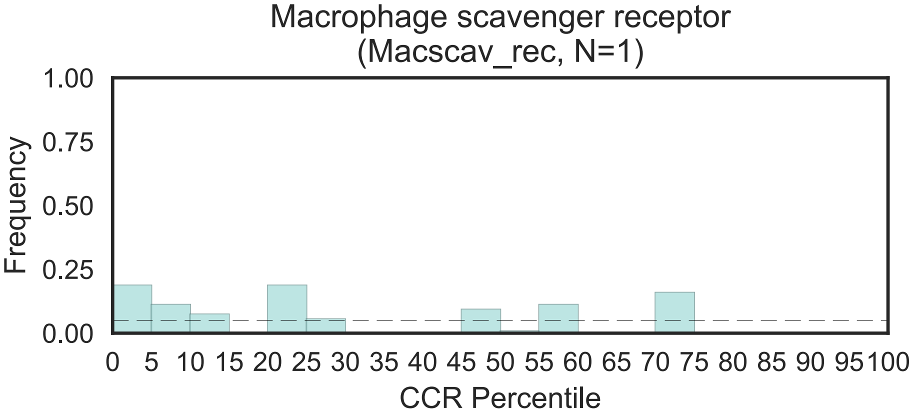


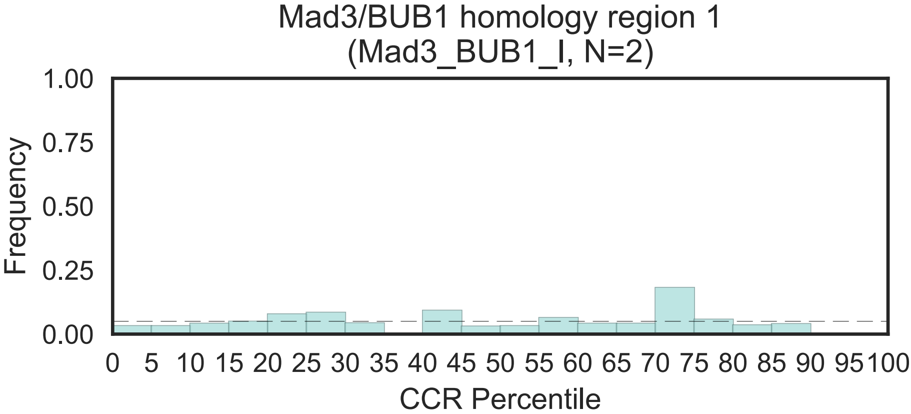
Mab-21 protein
(Mab-21, N=12)
Fisher's OR: 0.737; Bonferroni p-val: 1

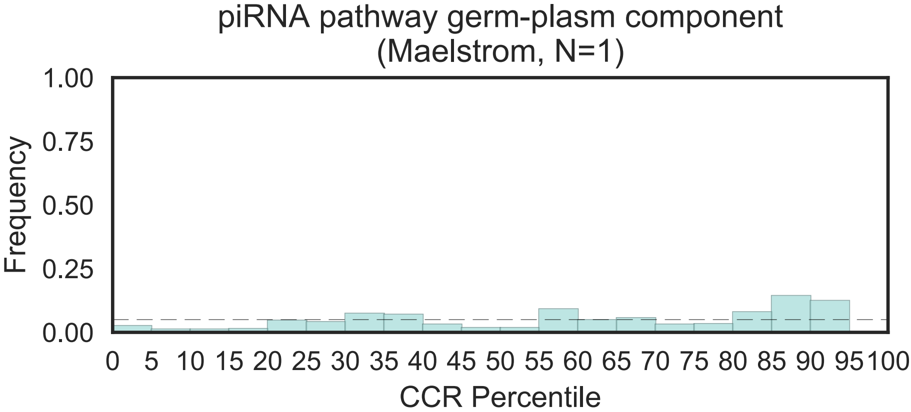


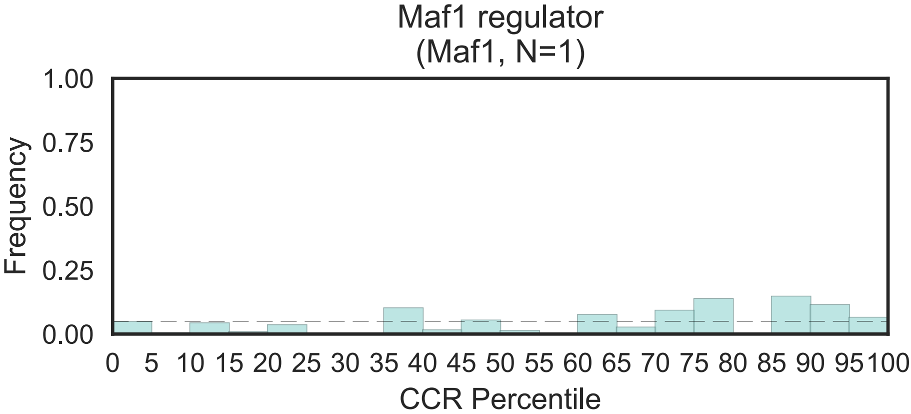
Macoilin family
(Macoilin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

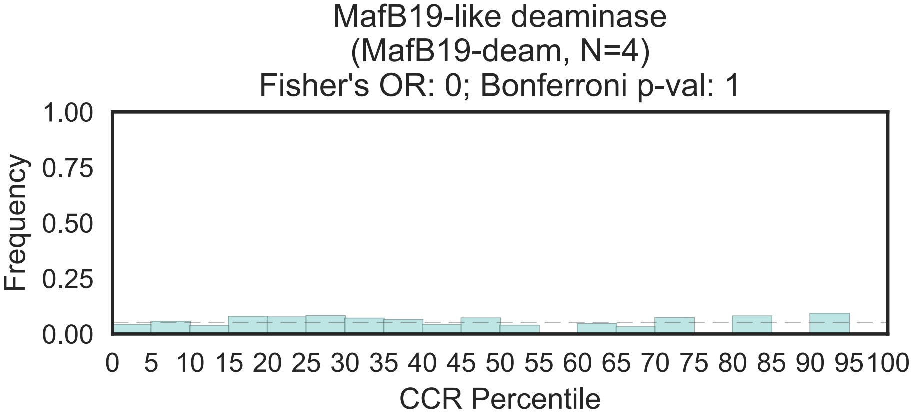

Macro domain
(Macro, N=17)
Fisher's OR: 0.775; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

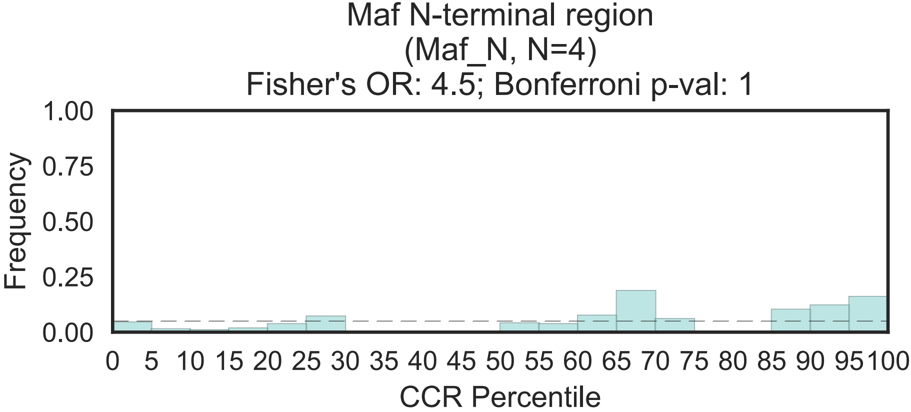

Macrophage scavenger receptor
(Macscav_rec, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

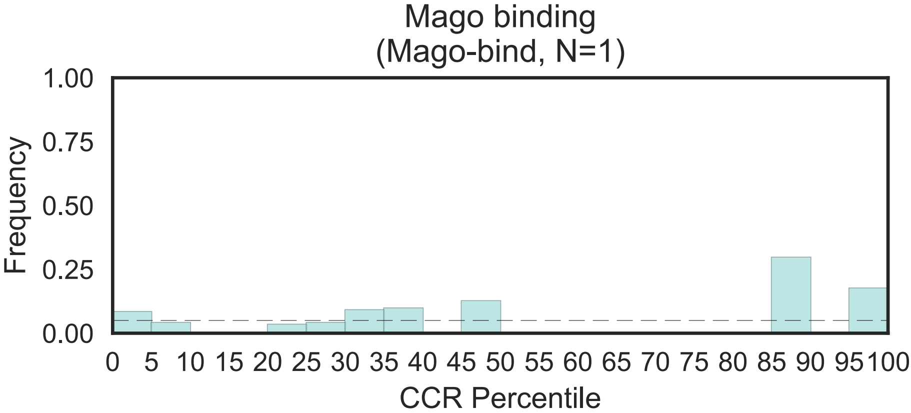

Mad3/BUB1 homology region 1
(Mad3_BUB1_I, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

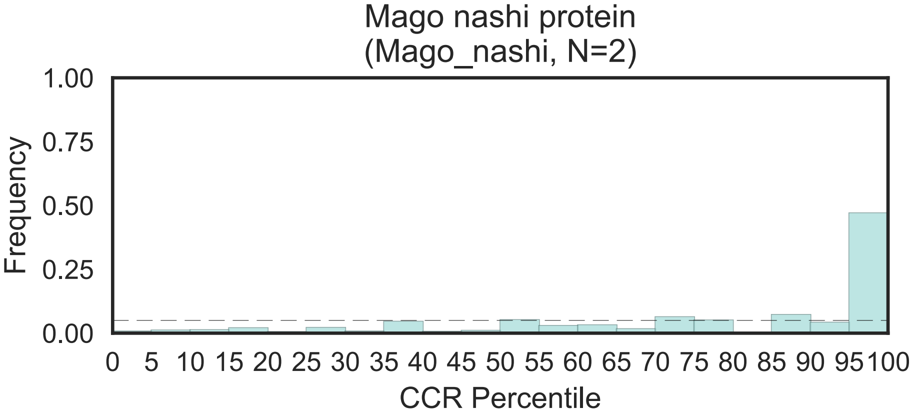

piRNA pathway germ-plasm component
(Maelstrom, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

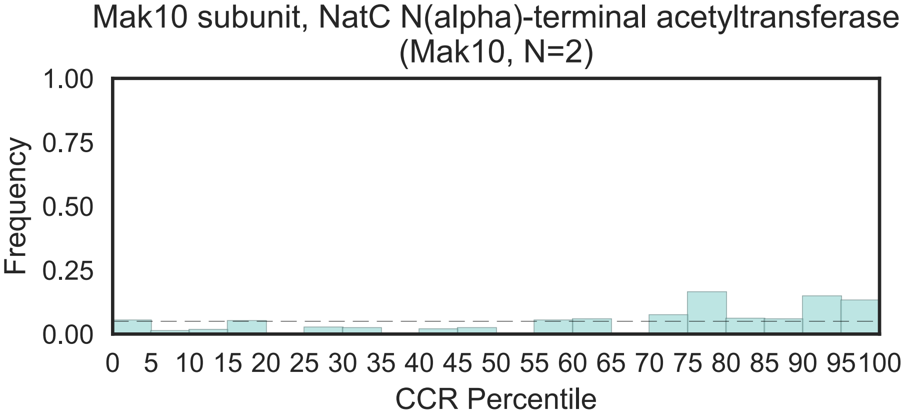

Maf1 regulator
(Maf1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

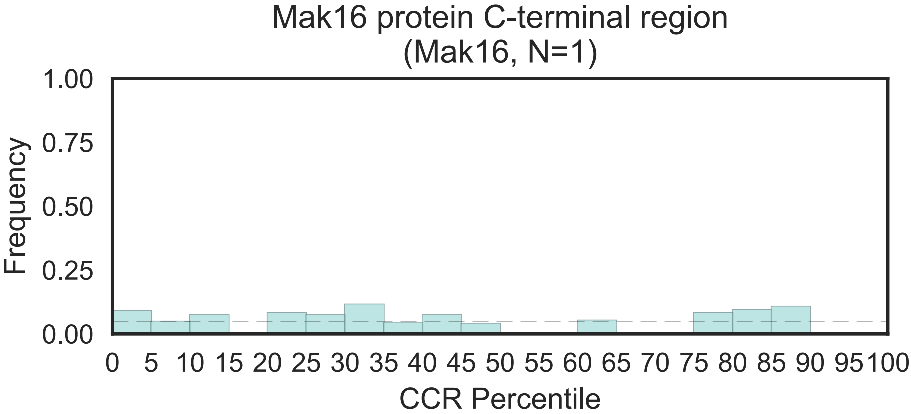

MafB19-like deaminase
(MafB19-deam, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

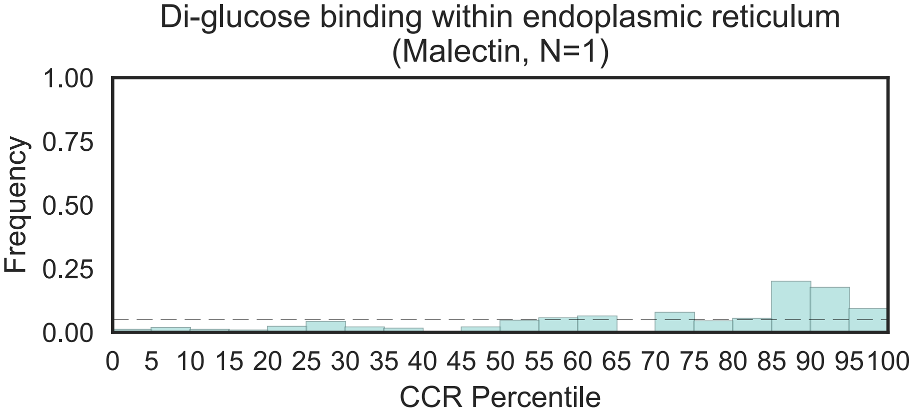

Maf N-terminal region
(Maf_N, N=4)
Fisher's OR: 4.5; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Mago binding
(Mago-bind, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

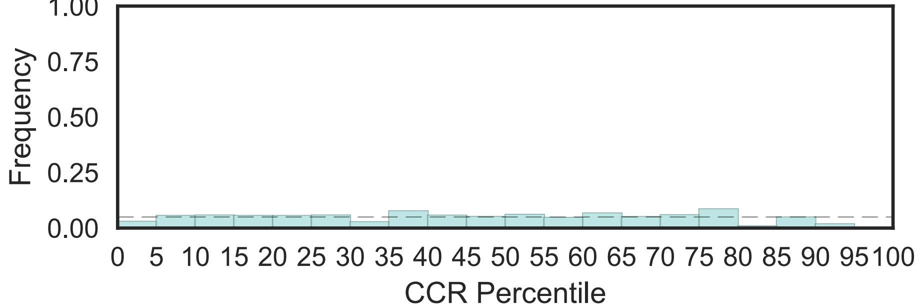

Mago nashi protein
(Mago_nashi, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

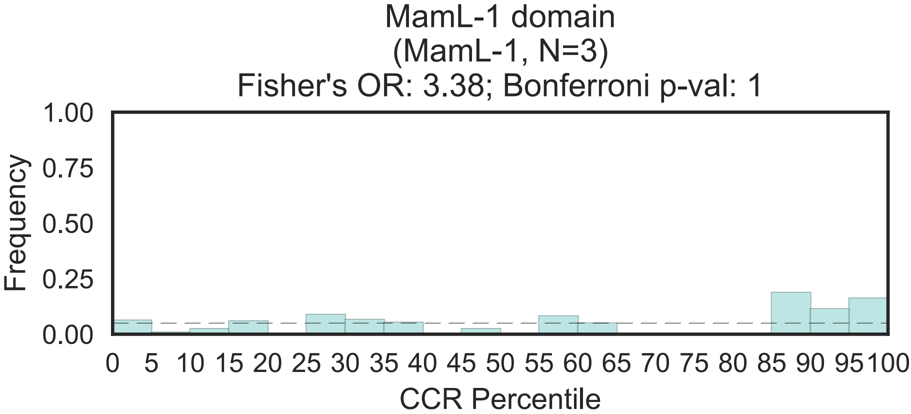

Mak10 subunit, NatC N(alpha)-terminal acetyltransferase
(Mak10, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

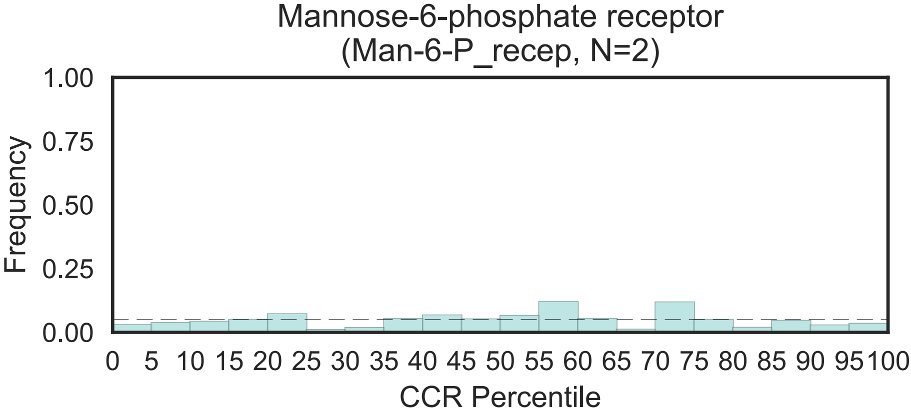

Mak16 protein C-terminal region
(Mak16, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

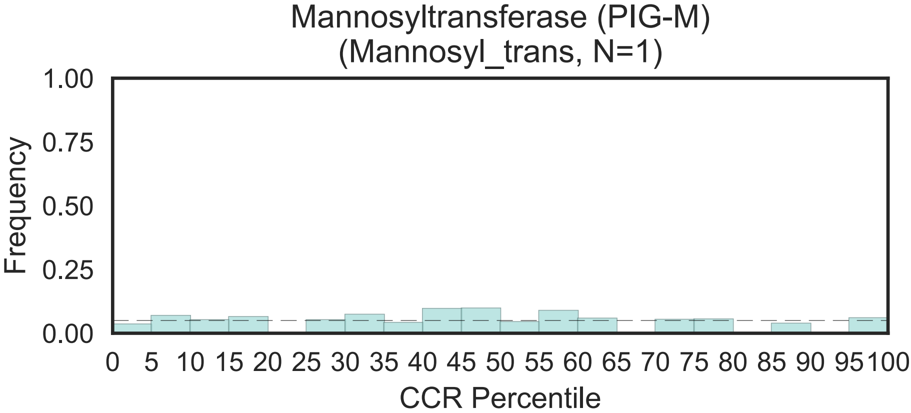

Di-glucose binding within endoplasmic reticulum
(Malectin, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

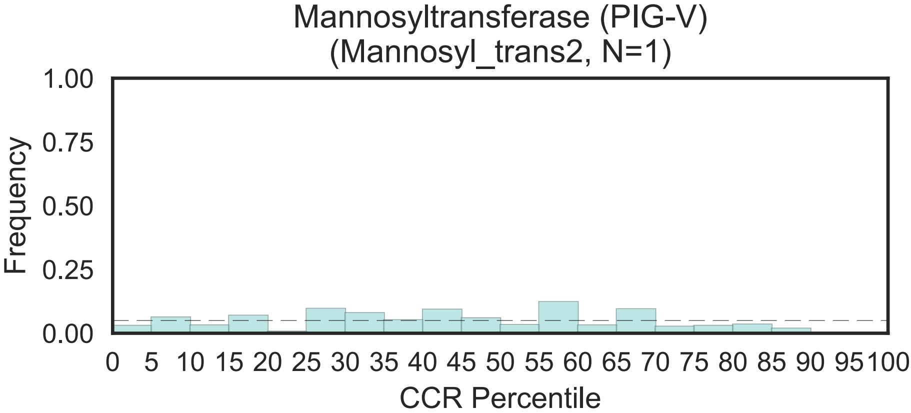
Malic enzyme, NAD binding domain (Malic_M, N=3) Fisher's OR: 0; Bonferroni p-val: 1

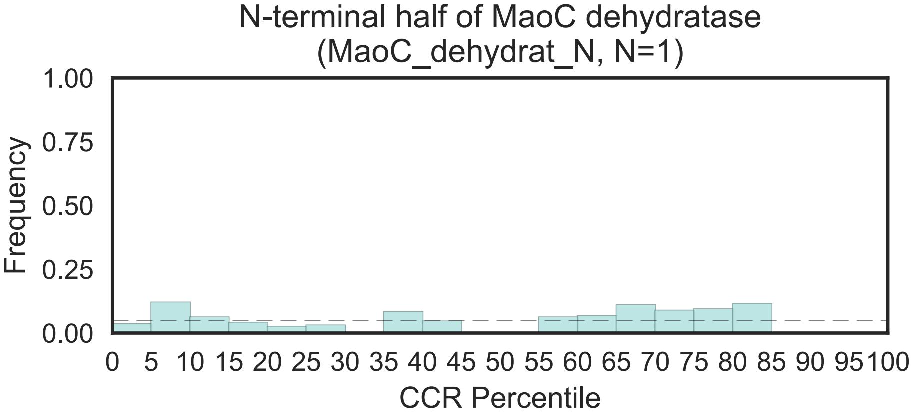


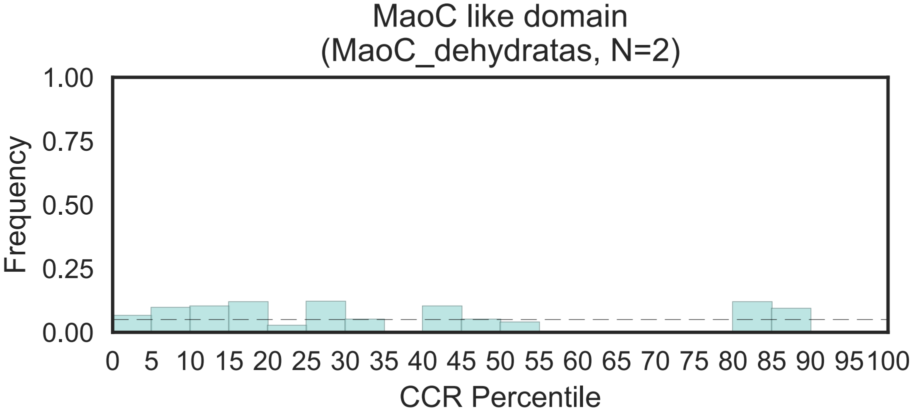

MamL-1 domain
(MamL-1, N=3)
Fisher's OR: 3.38; Bonferroni p-val: 1

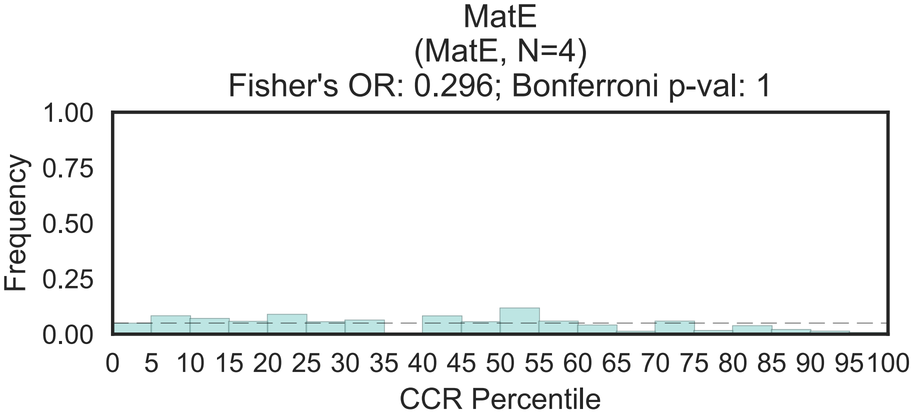

Mannose-6-phosphate receptor
(Man-6-P_recep, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

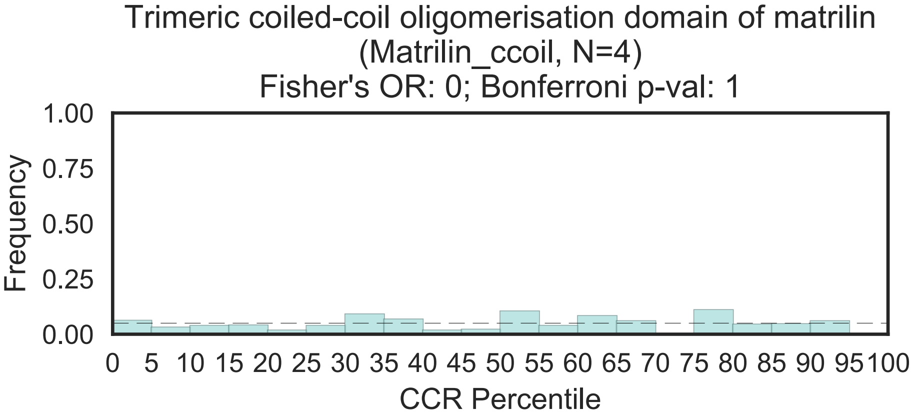

Mannosyltransferase (PIG-M)
(Mannosyl_trans, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

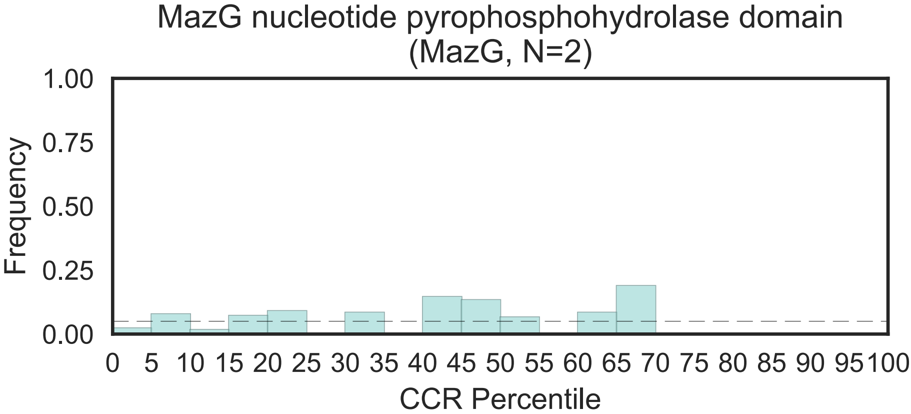

Mannosyltransferase (PIG-V)
(Mannosyl_trans2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

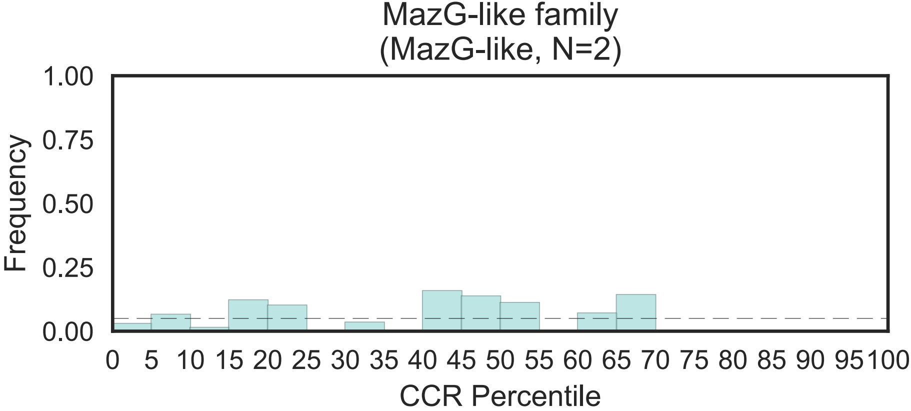

N-terminal half of MaoC dehydratase
(MaoC_dehydrat_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

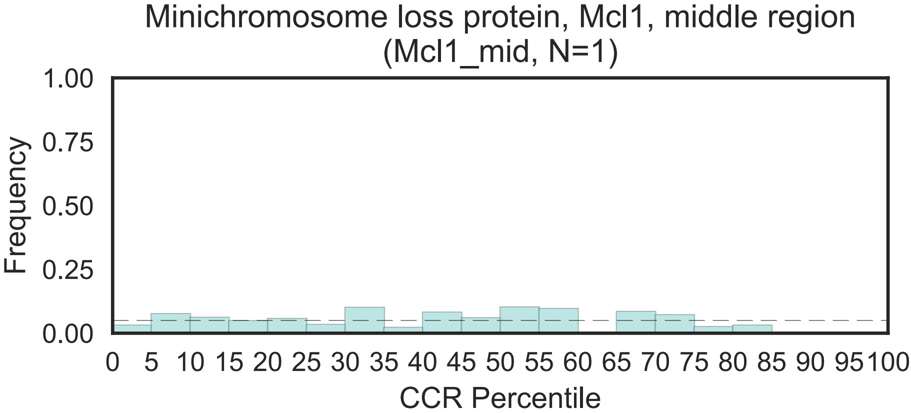

MaoC like domain
(MaoC_dehydratas, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

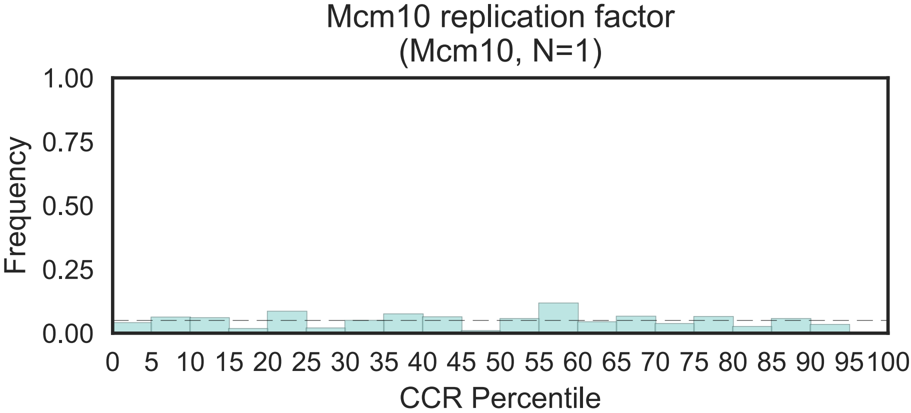

MatE
(MatE, N=4)
Fisher's OR: 0.296; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

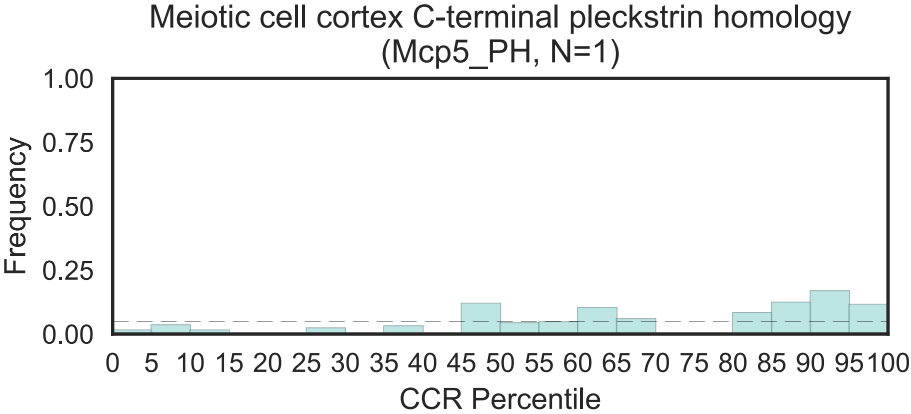

Trimeric coiled-coil oligomerisation domain of matrilin
(Matrilin_ccoil, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


MazG nucleotide pyrophosphohydrolase domain
(MazG, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

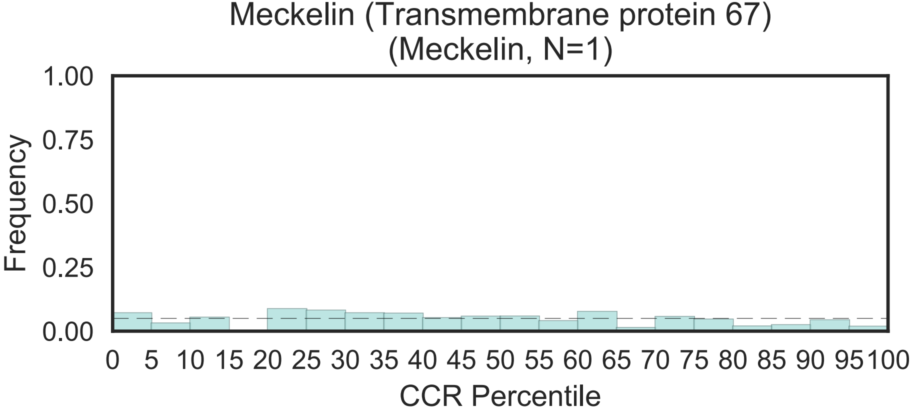

MazG-like family
(MazG-like, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

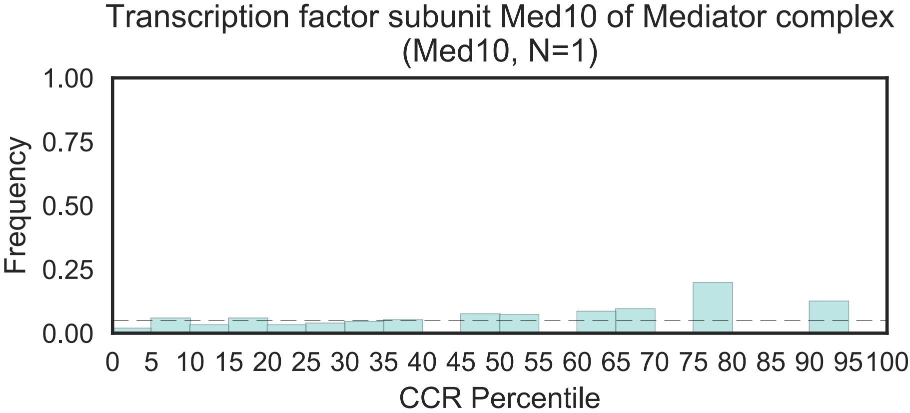

Minichromosome loss protein, Mcl1, middle region
(Mcl1_mid, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

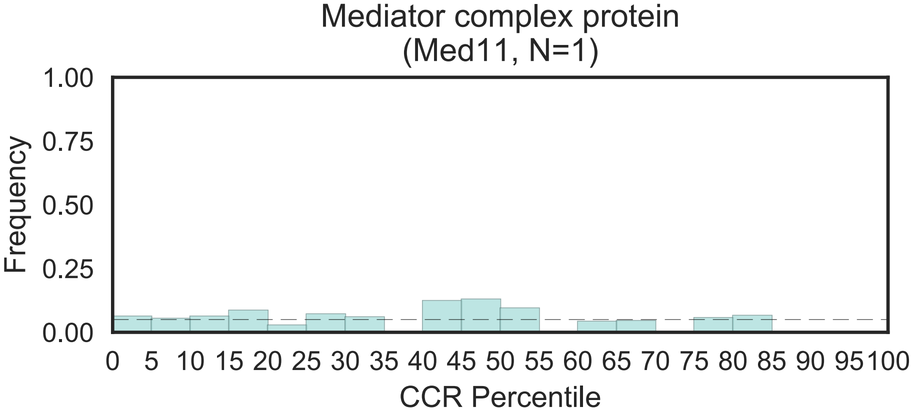

Mcm10 replication factor
(Mcm10, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

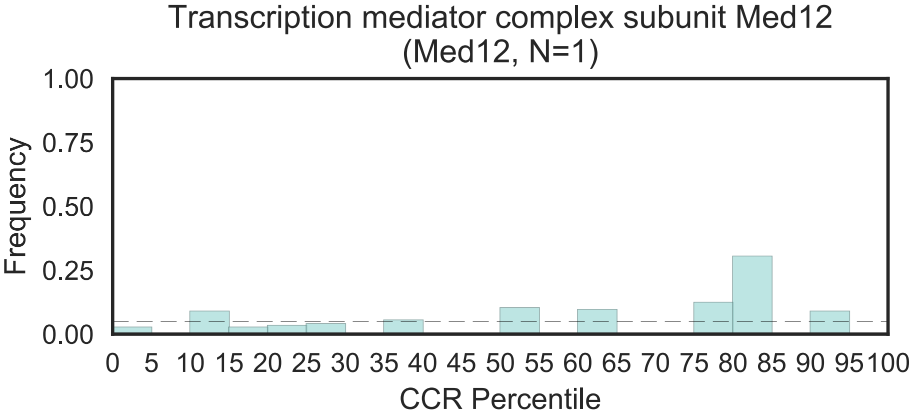


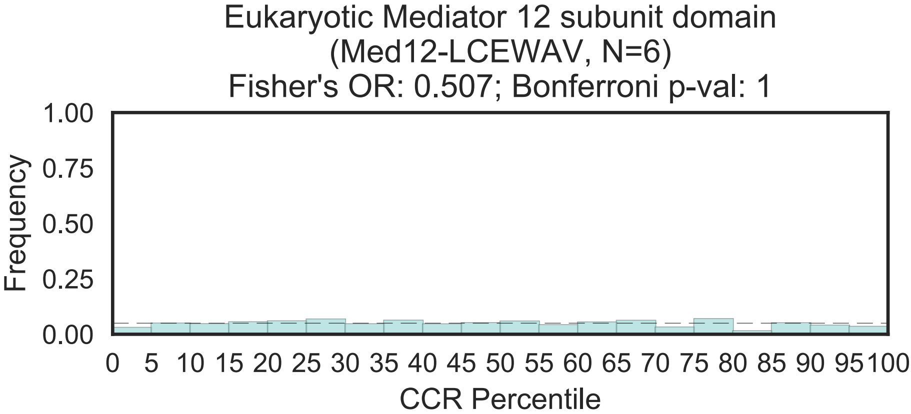
Meiotic cell cortex C-terminal pleckstrin homology (Mcp5_PH, N=1)

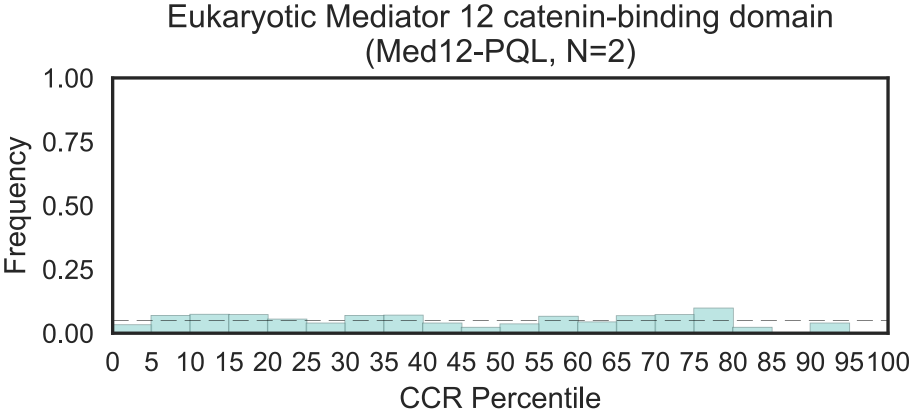

Meckelin (Transmembrane protein 67)
(Meckelin, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

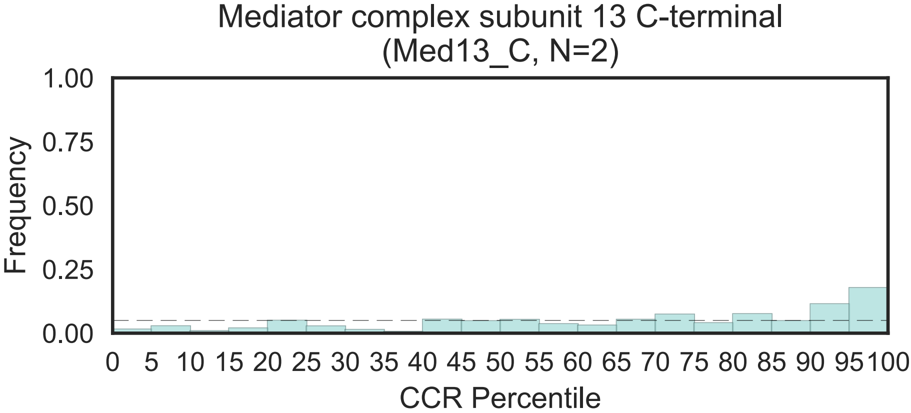

Transcription factor subunit Med10 of Mediator complex
(Med10, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

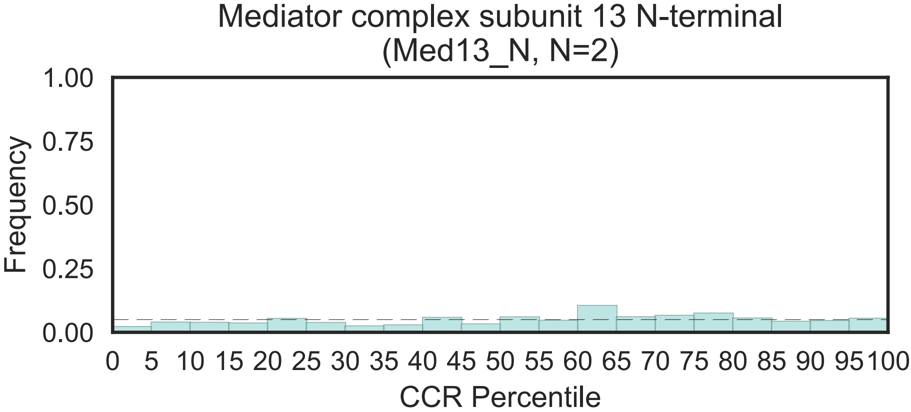

Mediator complex protein
(Med11, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

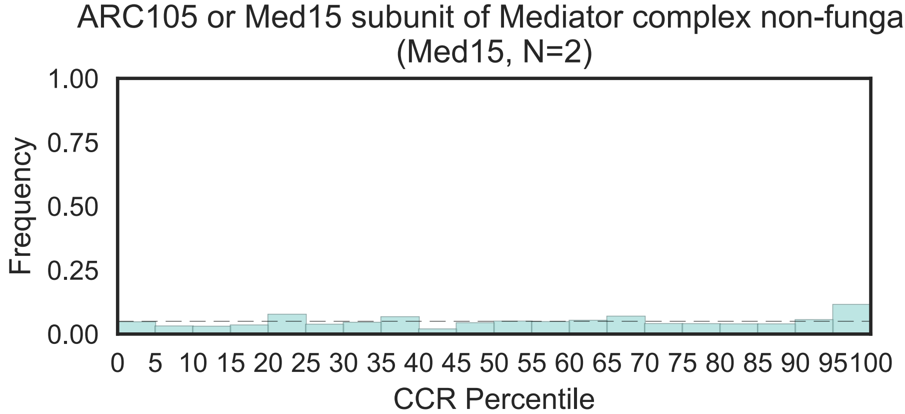

Transcription mediator complex subunit Med12
(Med12, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

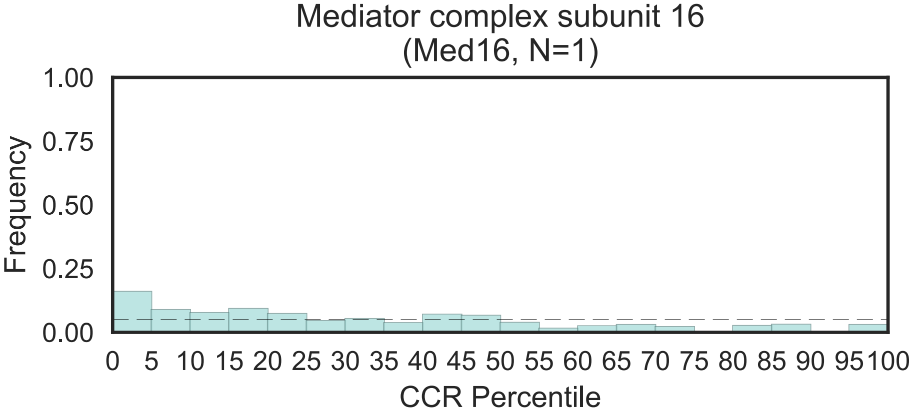

Eukaryotic Mediator 12 subunit domain
(Med12-LCEWAV, N=6)
Fisher's OR: 0.507; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Eukaryotic Mediator 12 catenin-binding domain
(Med12-PQL, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

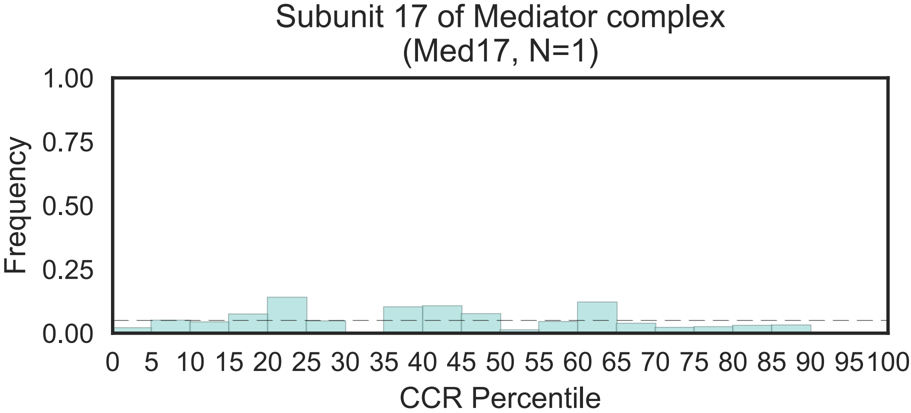

Mediator complex subunit 13 C-terminal
(Med13_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

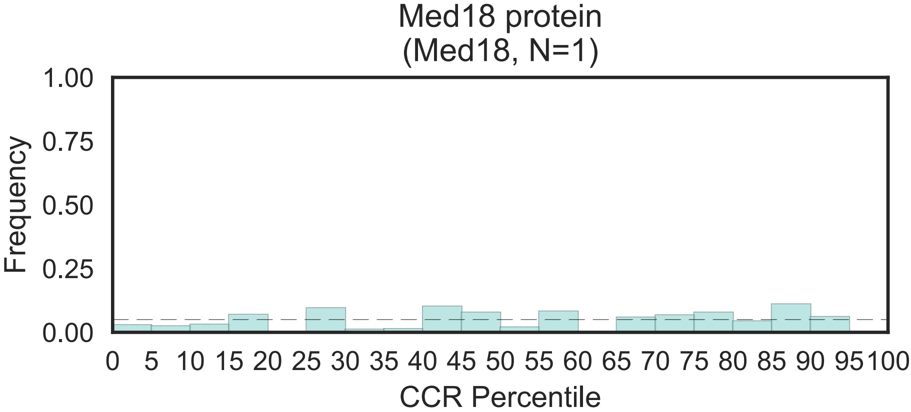

Mediator complex subunit 13 N-terminal
(Med13_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

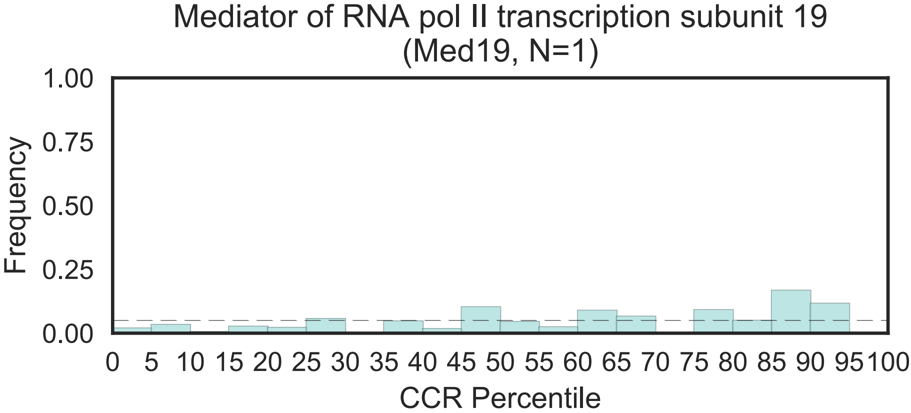

ARC105 or Med15 subunit of Mediator complex non-fungal
(Med15, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

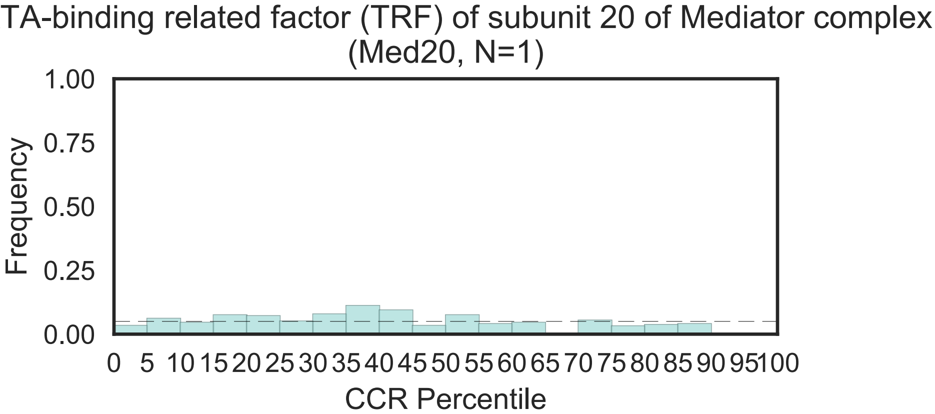


Mediator complex subunit 16
(Med16, N=1)

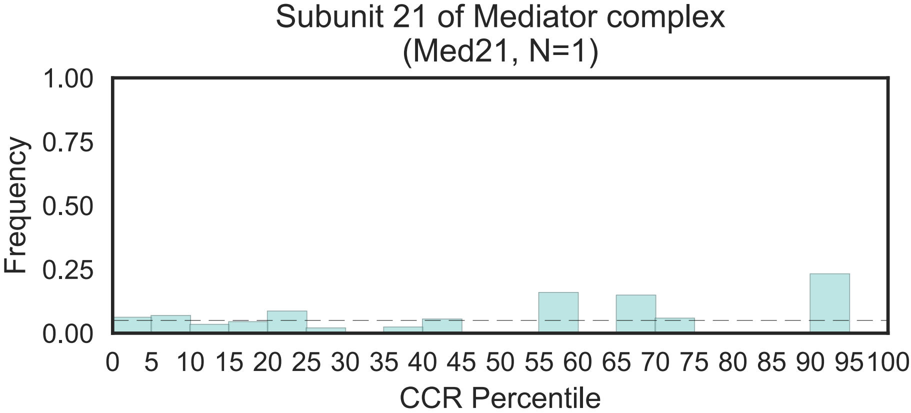

Subunit 17 of Mediator complex
(Med17, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

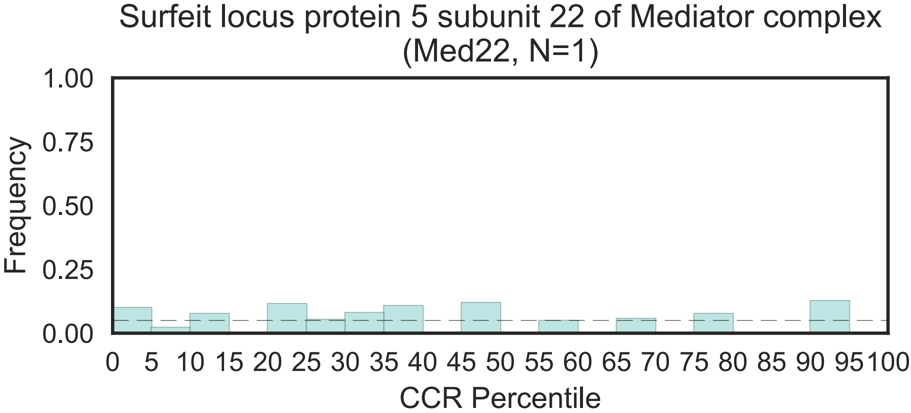

Med18 protein
(Med18, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

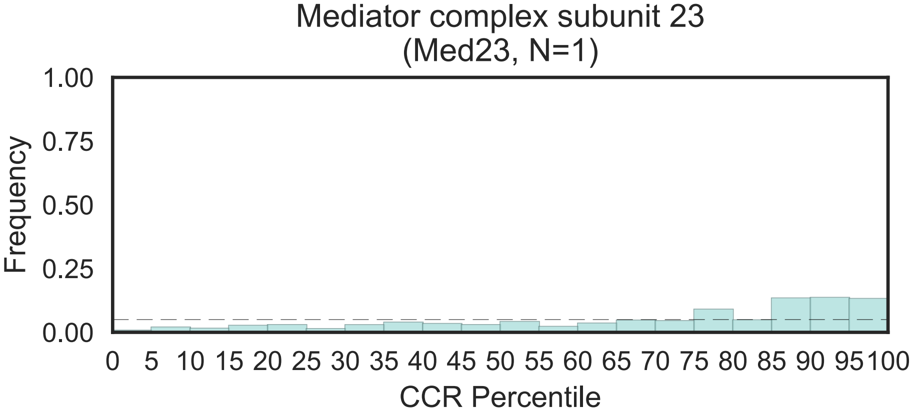

Mediator of RNA pol II transcription subunit 19
(Med19, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

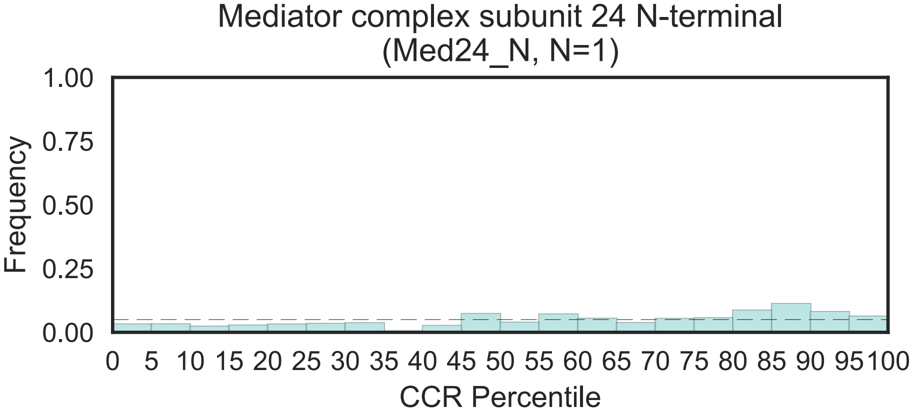


TATA-binding related factor (TRF) of subunit 20 of Mediator complex (Med20, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

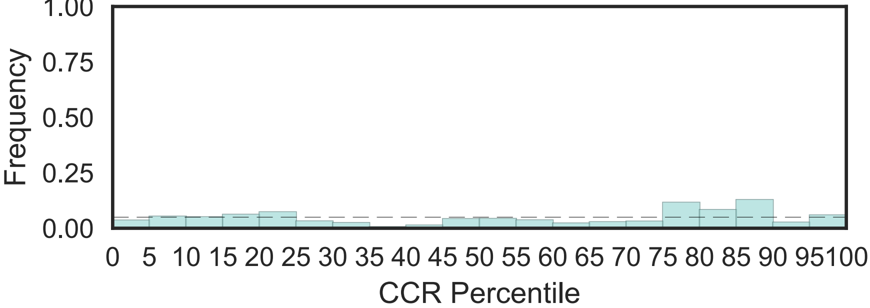

Subunit 21 of Mediator complex
(Med21, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Surfeit locus protein 5 subunit 22 of Mediator complex
(Med22, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

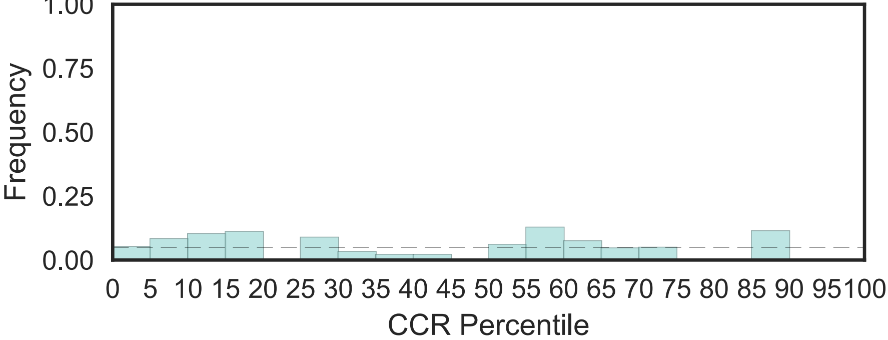

Mediator complex subunit 23
(Med23, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

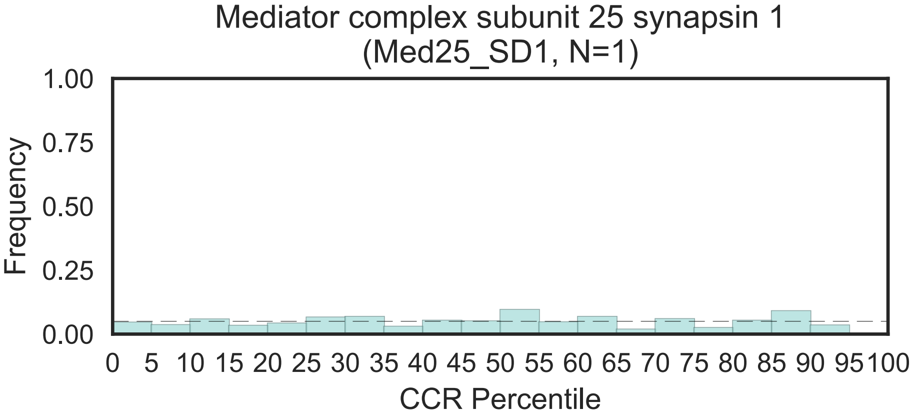

Mediator complex subunit 24 N-terminal
(Med24_N, N=1)

Mediator complex subunit 25 PTOV activation and synapsin 2 (Med25, N=3)
Fisher's OR: 0.667; Bonferroni p-val: 1

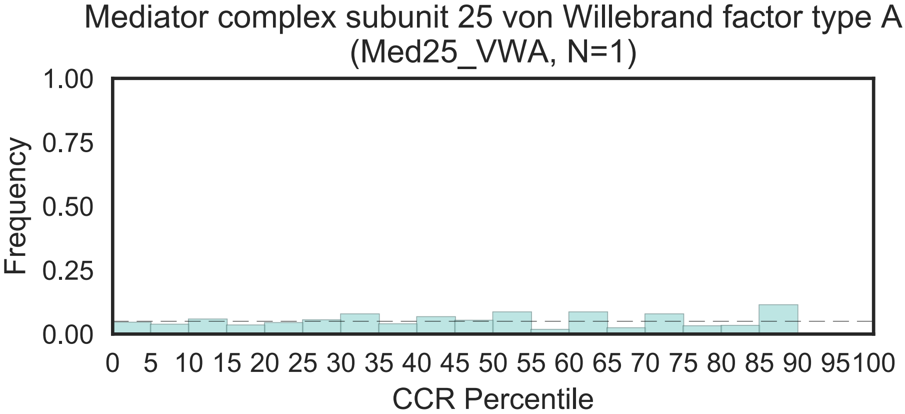


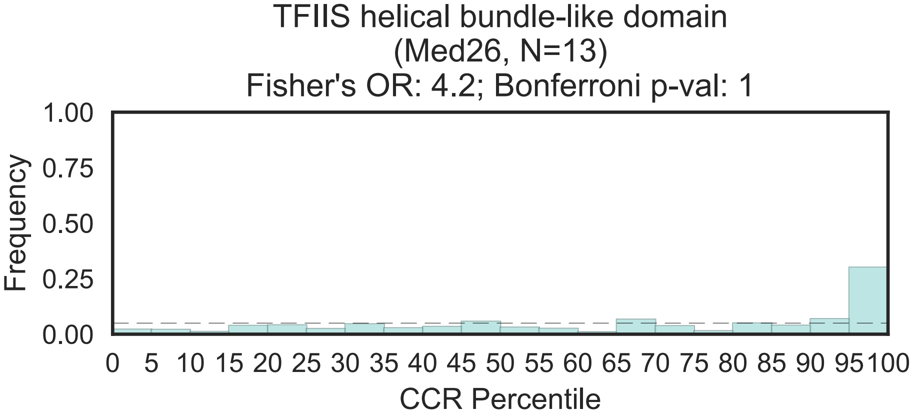
Mediator complex subunit 25 C-terminal NR box-containing (Med25_NR-box, N=1)

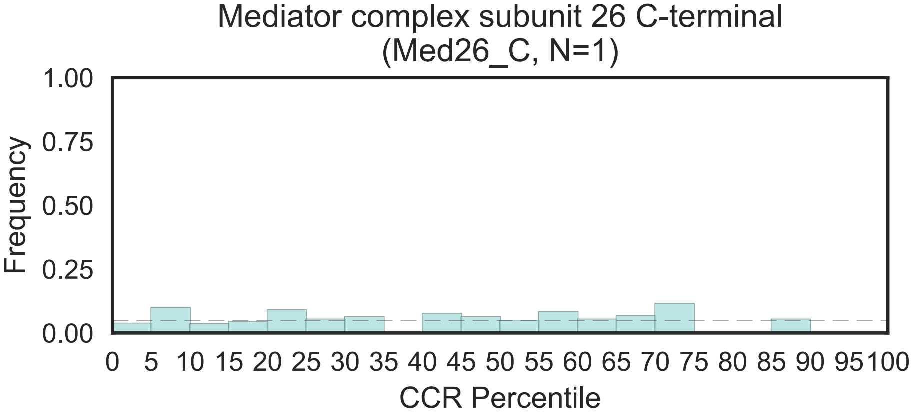


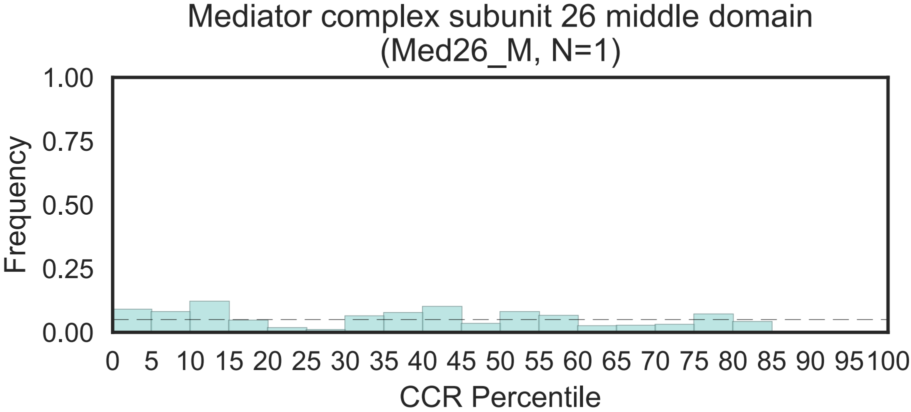


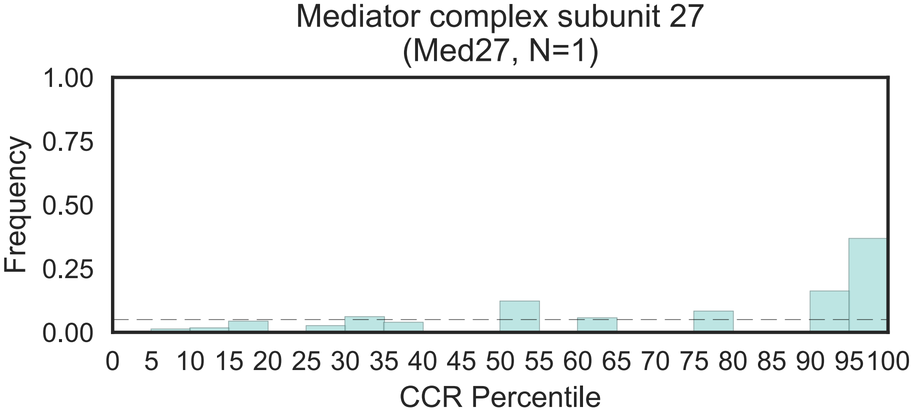
Mediator complex subunit 25 synapsin 1
(Med25_SD1, N=1)

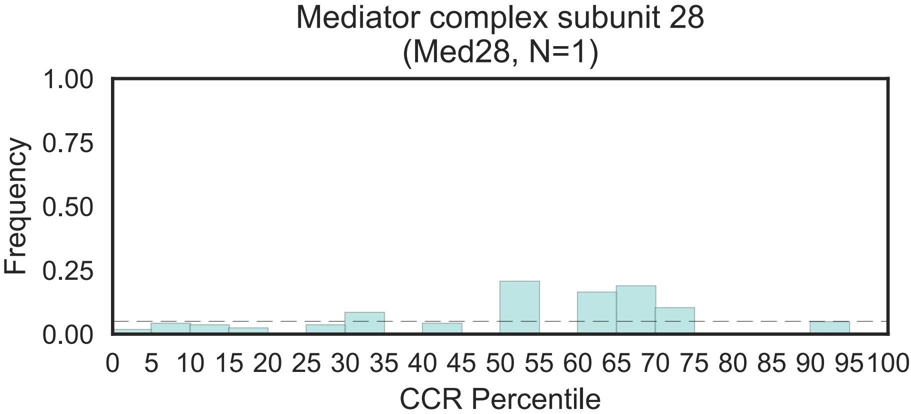

Mediator complex subunit 25 von Willebrand factor type A
(Med25_VWA, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

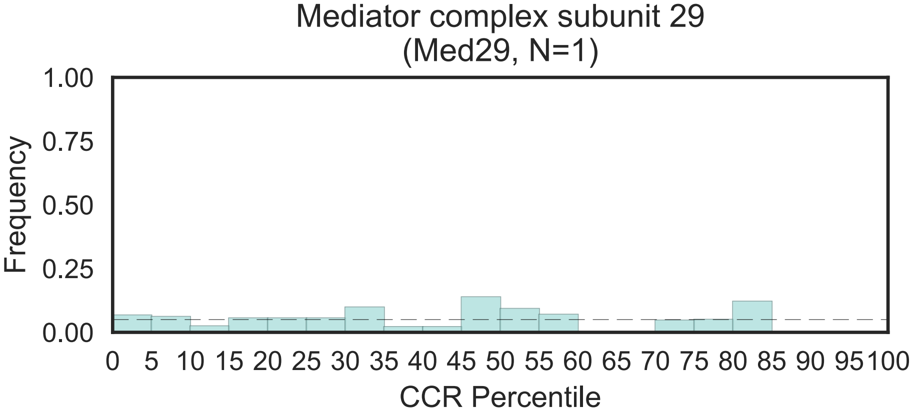

TFIIS helical bundle-like domain
(Med26, N=13)
Fisher's OR: 4.2; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

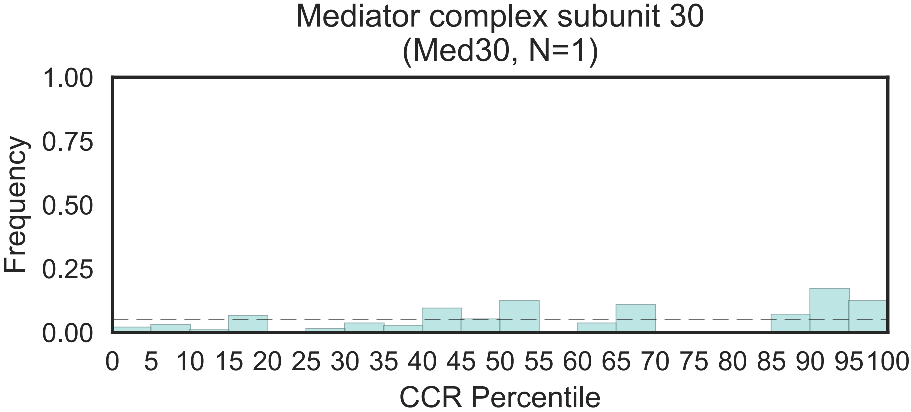

Mediator complex subunit 26 C-terminal
(Med26_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

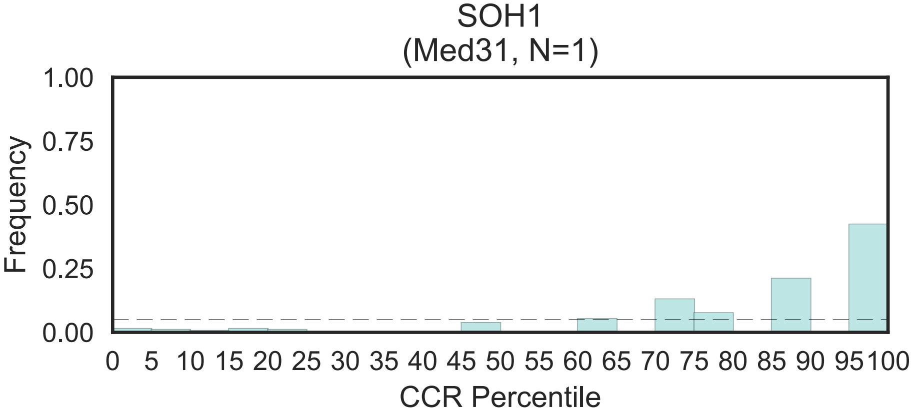

Mediator complex subunit 26 middle domain
(Med26_M, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

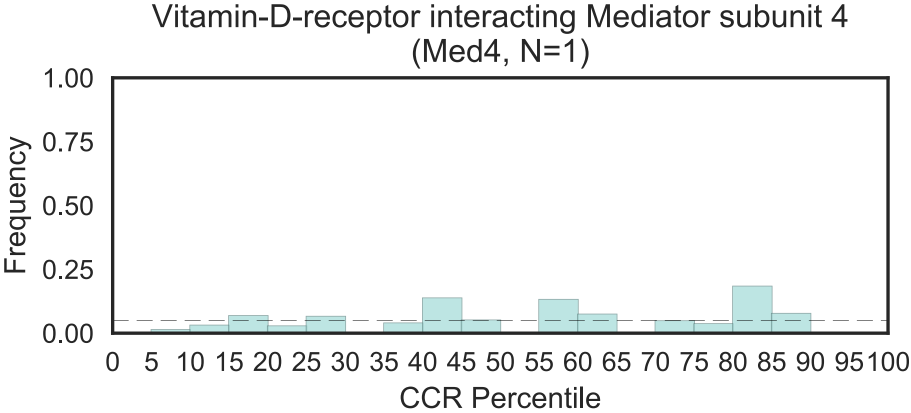

Mediator complex subunit 27
(Med27, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

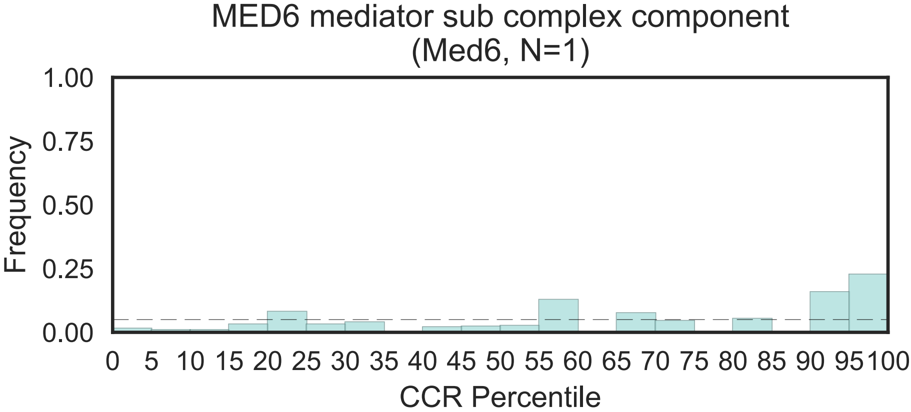

Mediator complex subunit 28
(Med28, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

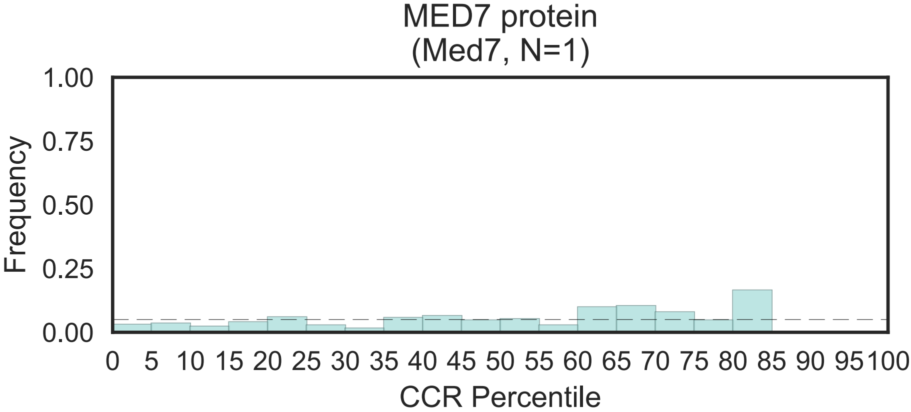

Mediator complex subunit 29
(Med29, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

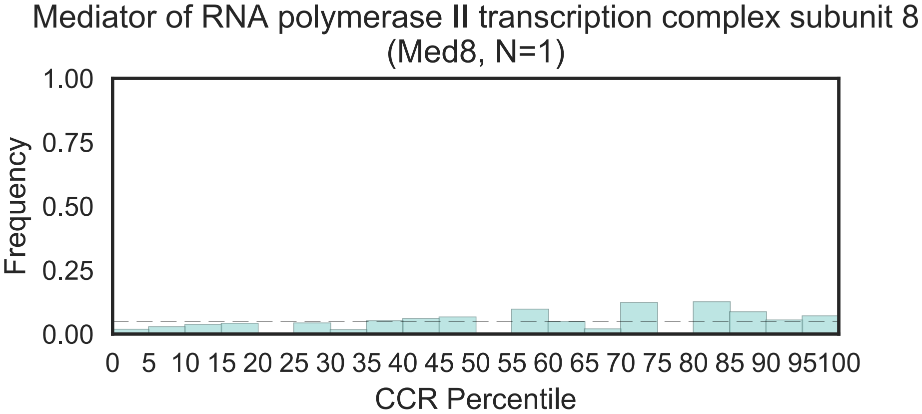

Mediator complex subunit 30
(Med30, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

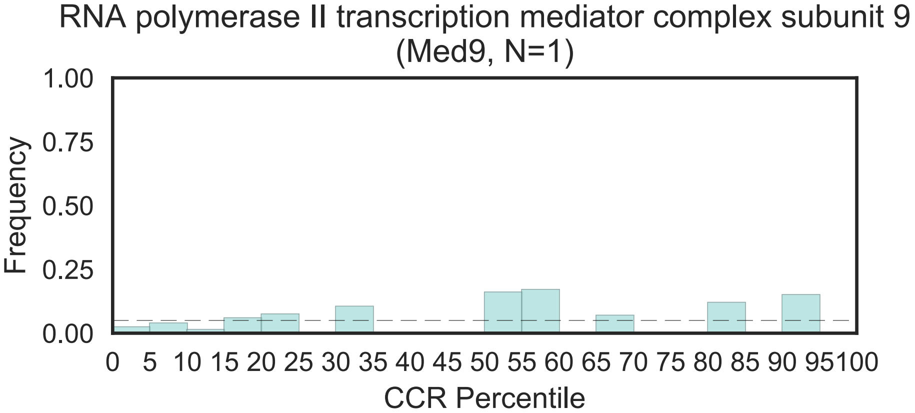

SOH1
(Med31, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

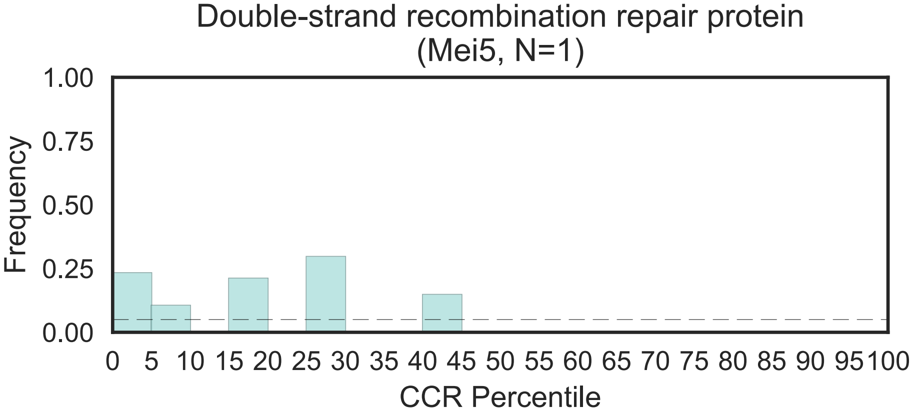

Vitamin-D-receptor interacting Mediator subunit 4
(Med4, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

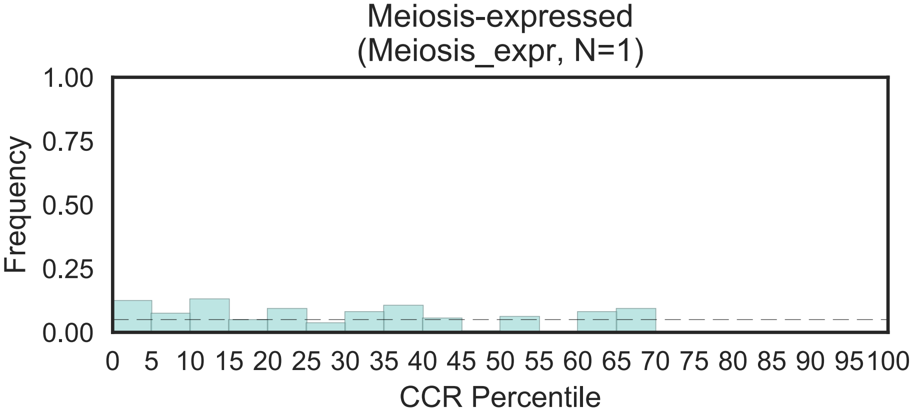

MED6 mediator sub complex component
(Med6, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


MED7 protein
(Med7, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

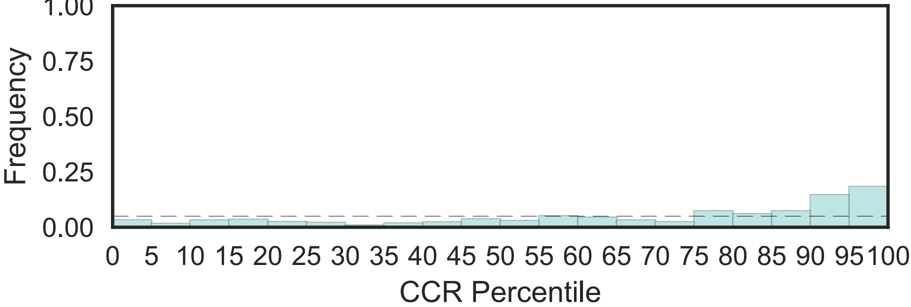

Mediator of RNA polymerase II transcription complex subunit 8
(Med8, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

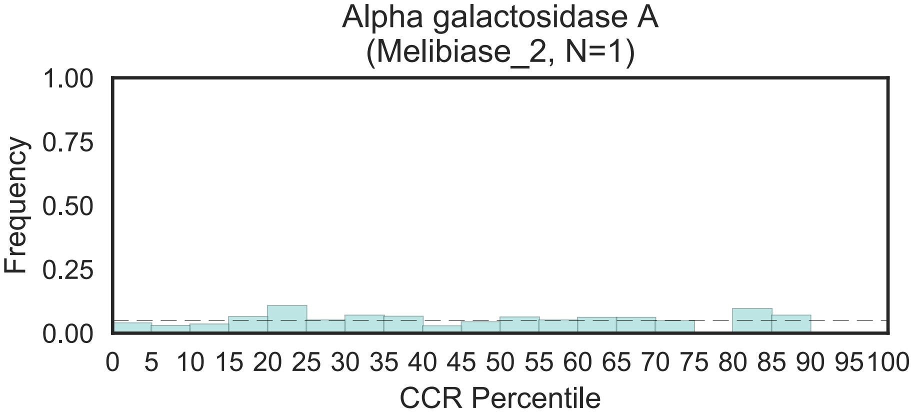

RNA polymerase II transcription mediator complex subunit 9
(Med9, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95100
CCR Percentile

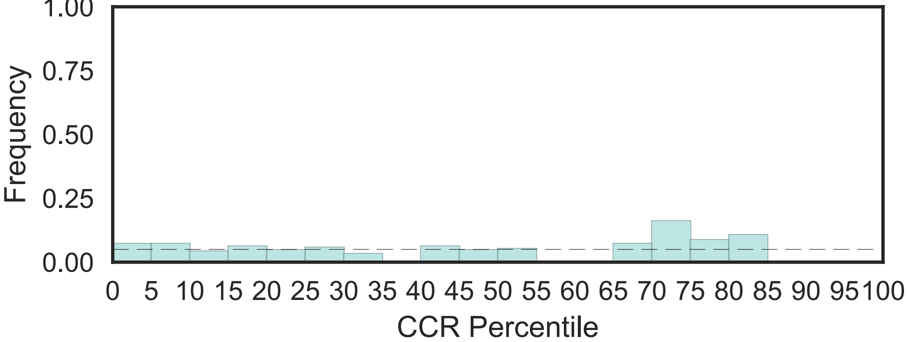

Double-strand recombination repair protein
(Mei5, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Meiosis-expressed
(Meiosis_expr, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

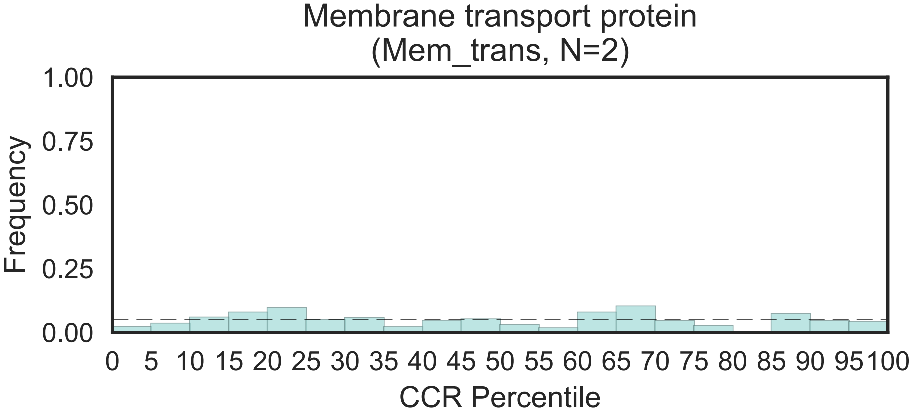
N-terminal of Homeobox Meis and PKNOX1 (Meis_PKNOX_N, N=5) Fisher's OR: 2.62; Bonferroni p-val: 1

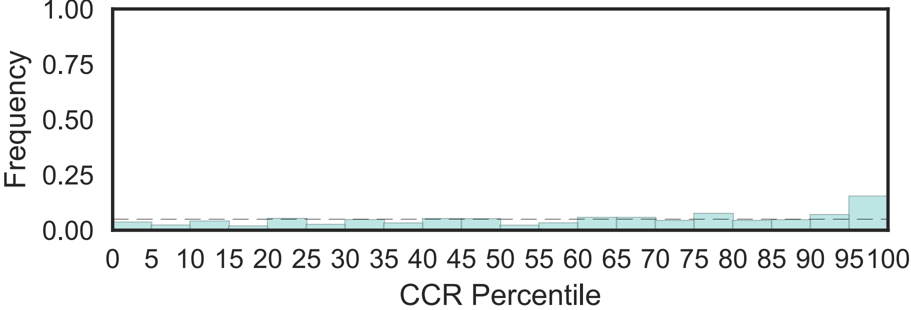



Alpha galactosidase A
(Melibiase_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

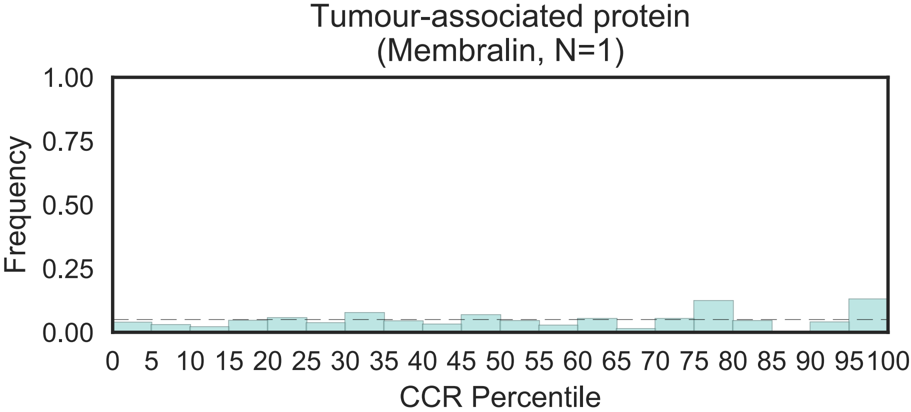


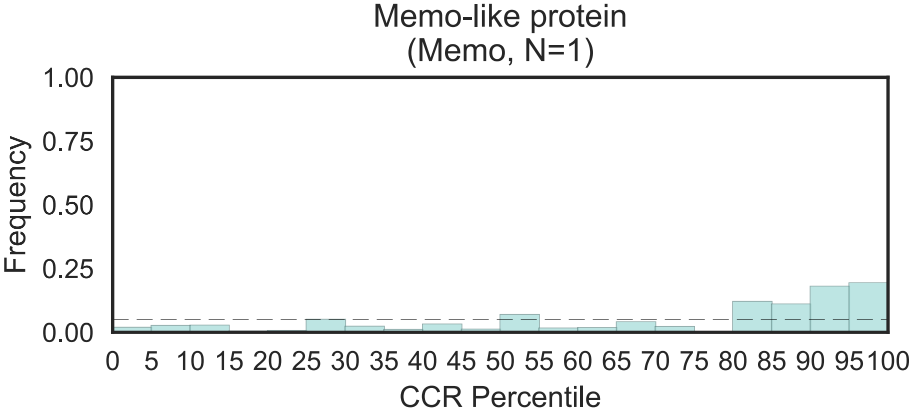
Alpha galactosidase A C-terminal beta sandwich domain (Melibiase_2_C, N=1)

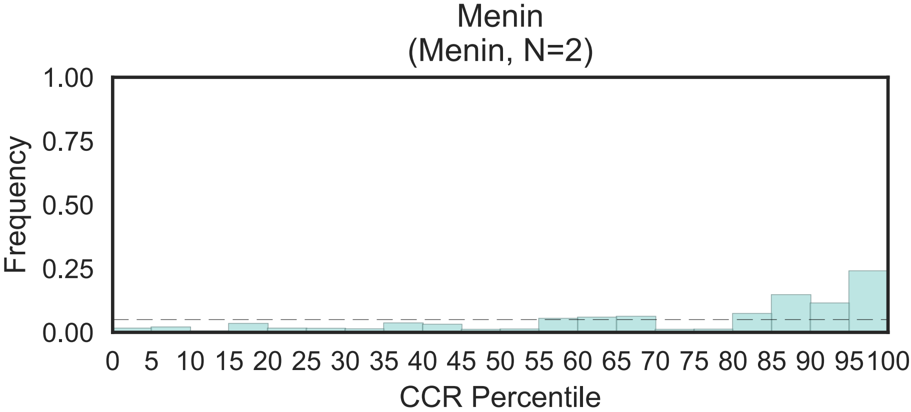

Membrane transport protein
(Mem_trans, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

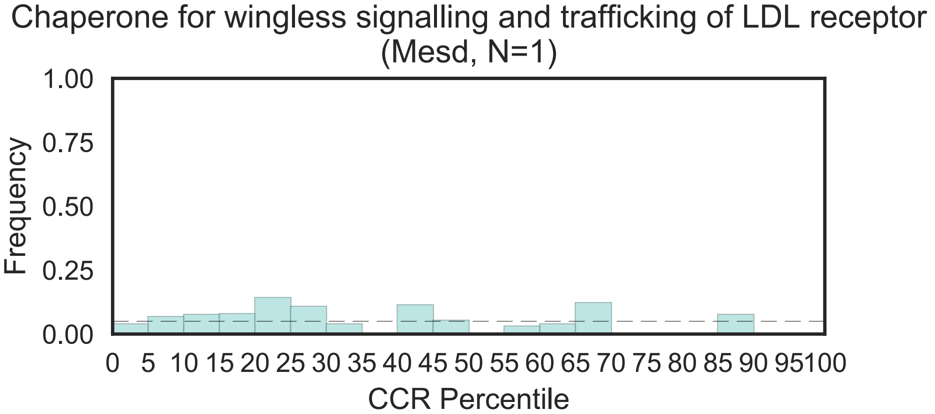


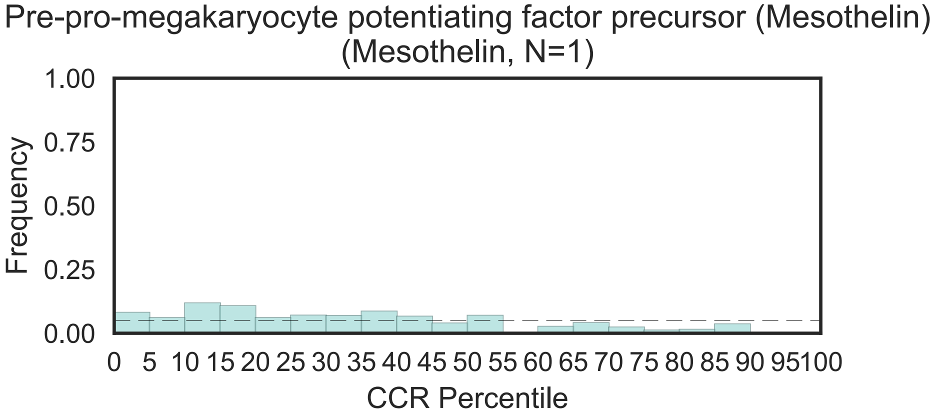
Munc13 (mammalian uncoordinated) homology domain
(Membr_traf_MHD, N=5)
Fisher's OR: 2.54; Bonferroni p-val: 1

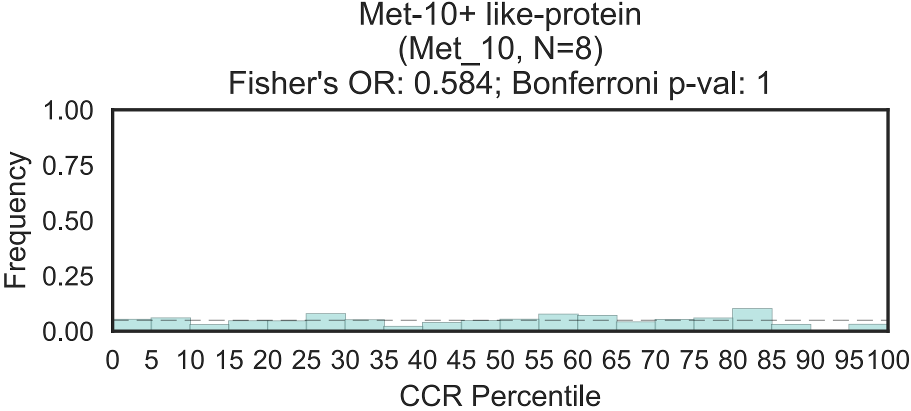

Tumour-associated protein
(Membralin, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

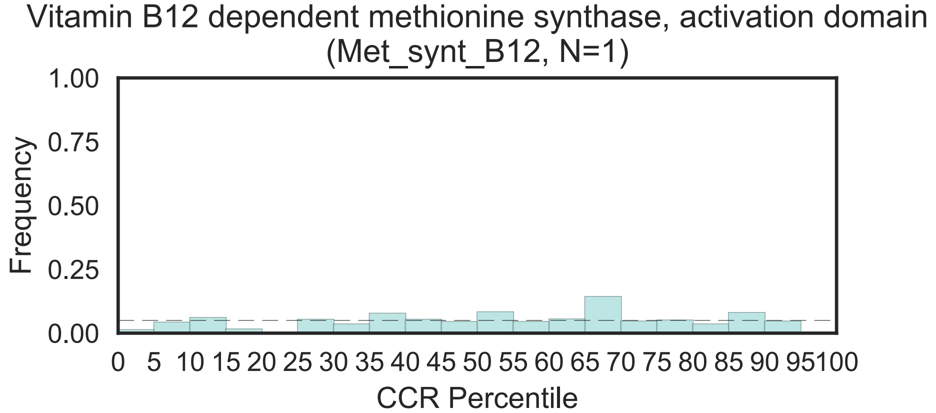

Memo-like protein
(Memo, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

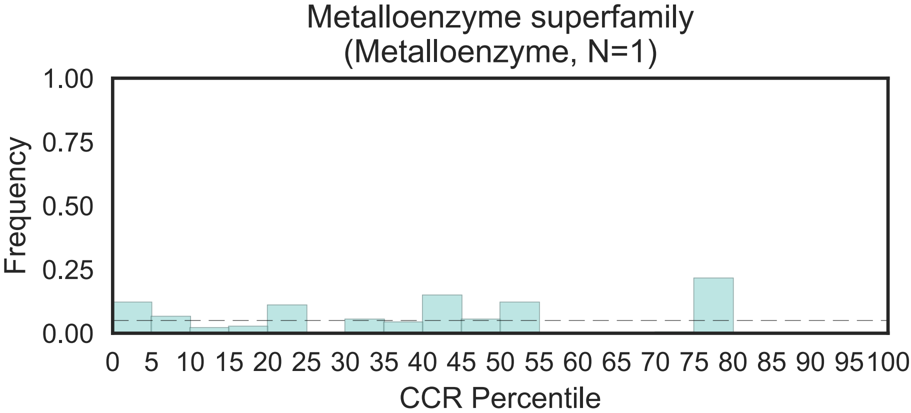

Menin
(Menin, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

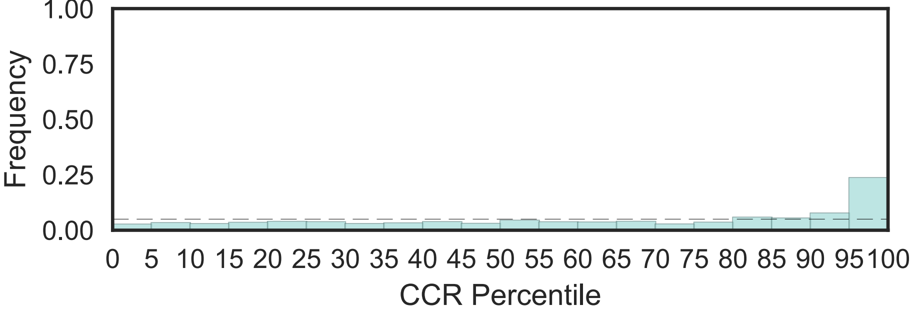

Chaperone for wingless signalling and trafficking of LDL receptor
(Mesd, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Pre-pro-megakaryocyte potentiating factor precursor (Mesothelin)
(Mesothelin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Met-10+ like-protein
(Met_10, N=8)
Fisher's OR: 0.584; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Vitamin B12 dependent methionine synthase, activation domain
(Met_synt_B12, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

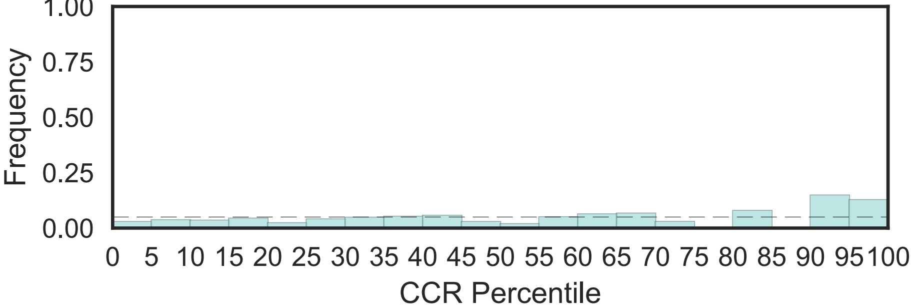

Metalloenzyme superfamily
(Metalloenzyme, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

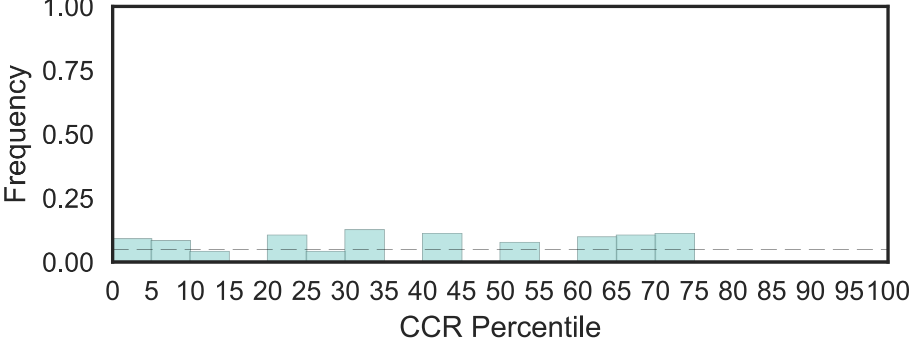


Calcineurin-like phosphoesterase
(Metallophos, N=28)
Fisher's OR: 2.81; Bonferroni p-val: 1.77e-05

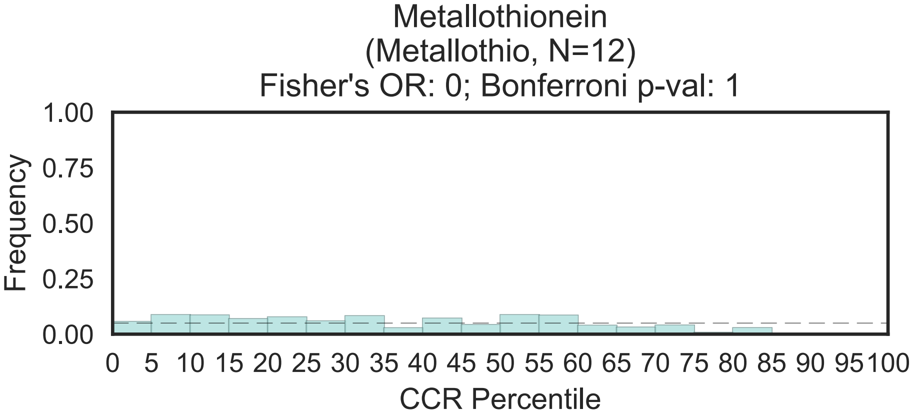
Calcineurin-like phosphoesterase superfamily domain (Metallophos_2, N=3)

Fisher's OR: 2.82; Bonferroni p-val: 1



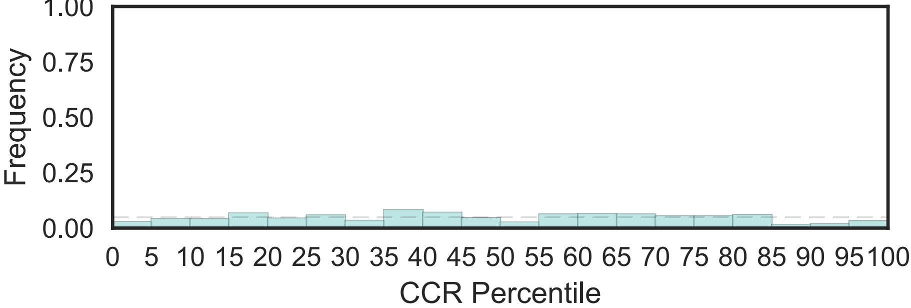


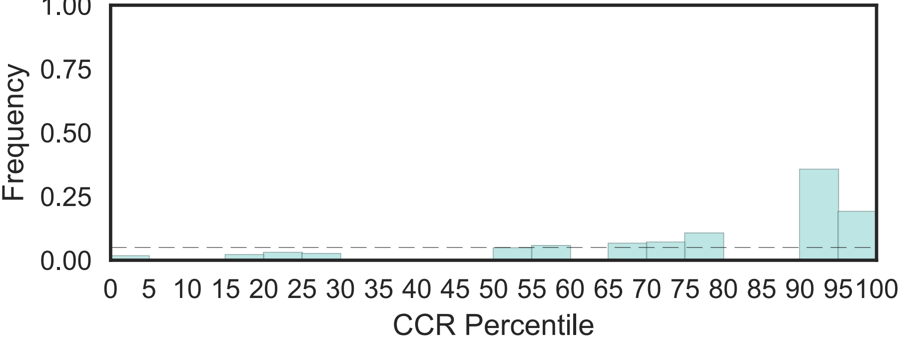
Iron/zinc purple acid phosphatase-like protein C (Metallophos_C, N=1)



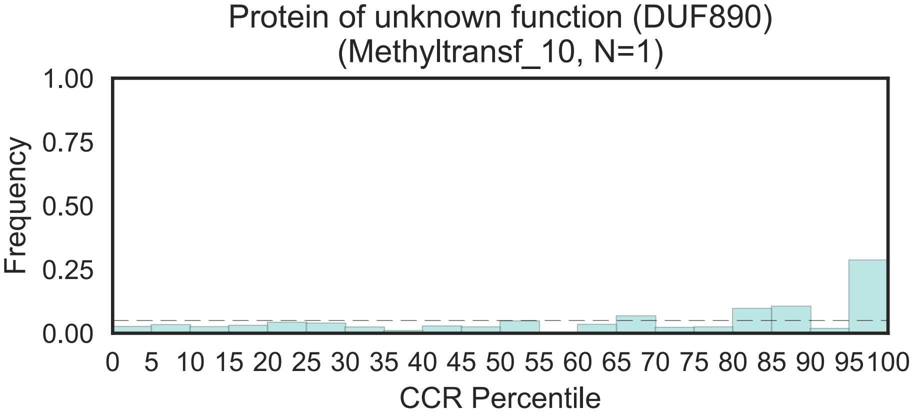
Metallothionein
(Metallothio, N=12)
Fisher's OR: 0; Bonferroni p-val: 1

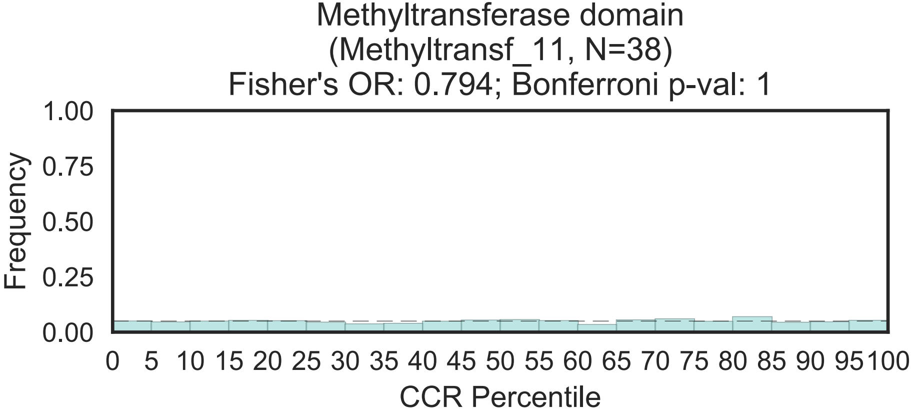
16S rRNA methyltransferase RsmB/F (Methyltr_RsmB-F, N=7) Fisher's OR: 0.515; Bonferroni p-val: 1

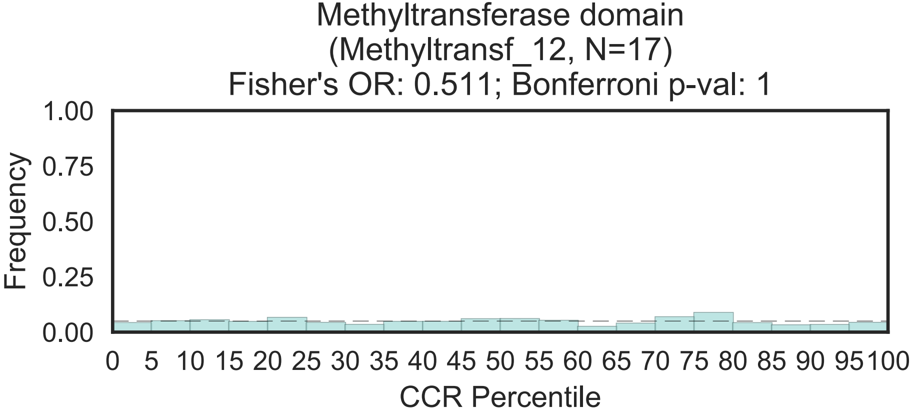


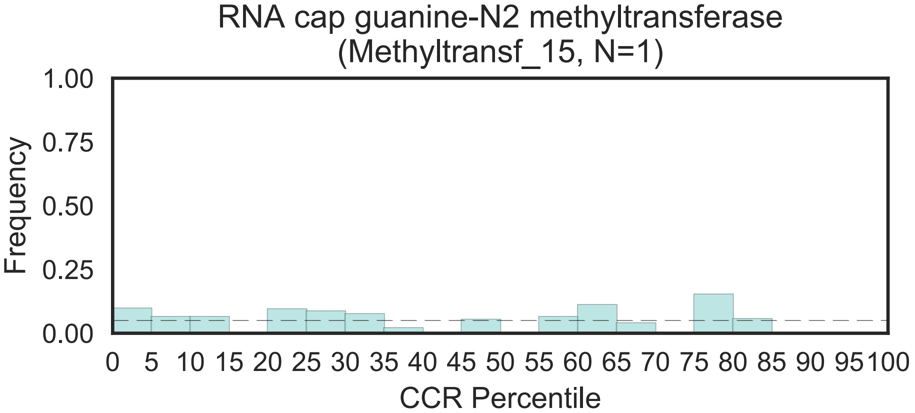


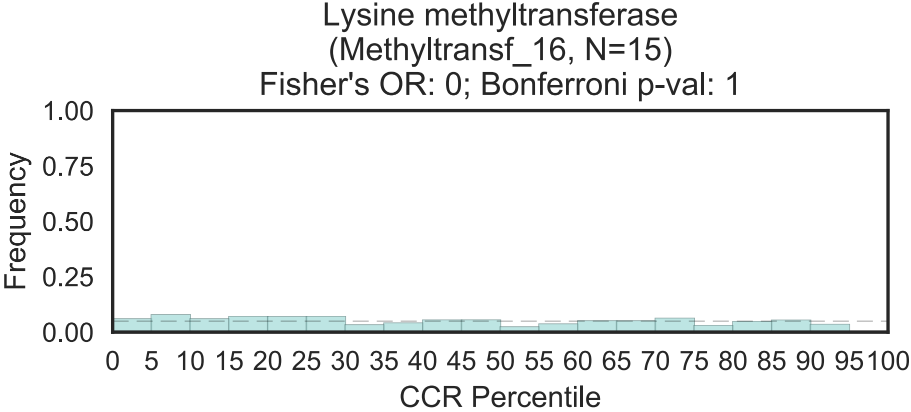
N-terminal domain of 16S rRNA methyltransferase RsmF
(Methyltr_RsmF_N, N=1)

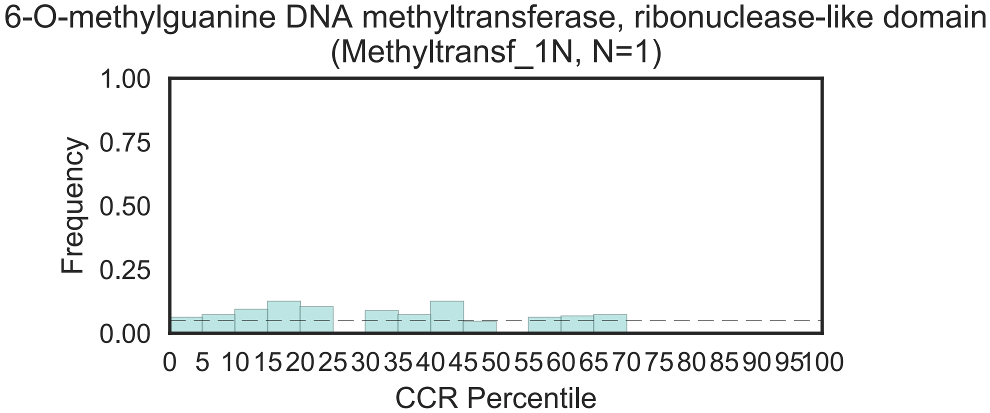

Protein of unknown function (DUF890)
(Methyltransf_10, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

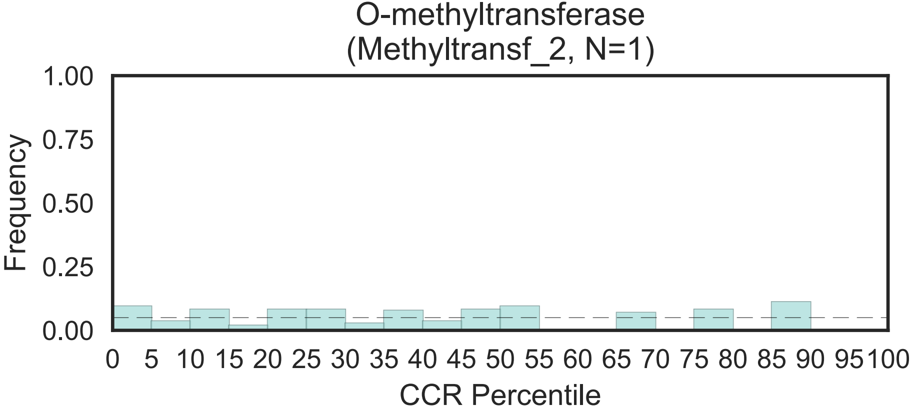

Methyltransferase domain
(Methyltransf_11, N=38)
Fisher's OR: 0.794; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

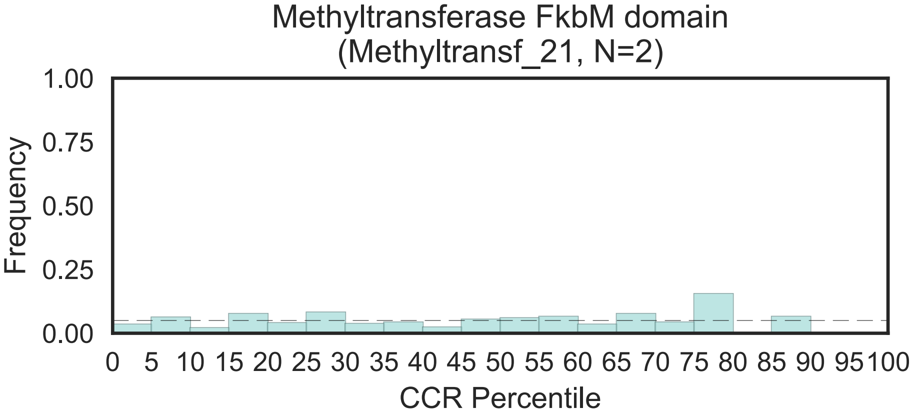

Methyltransferase domain
(Methyltransf_12, N=17)
Fisher's OR: 0.511; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

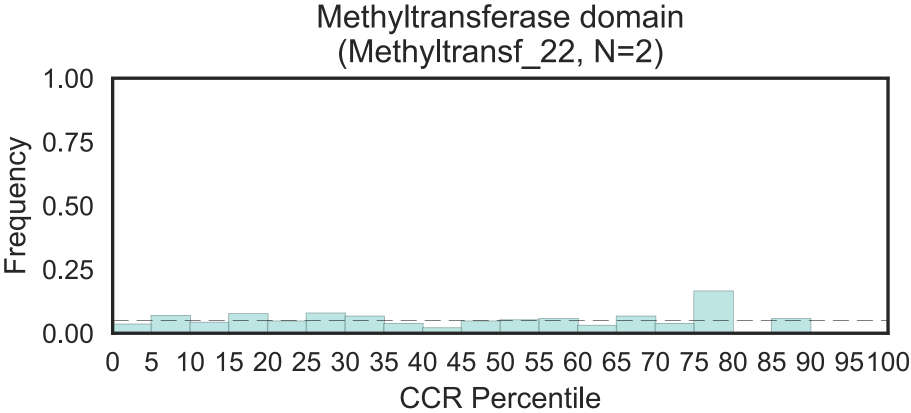

RNA cap guanine-N2 methyltransferase
(Methyltransf_15, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

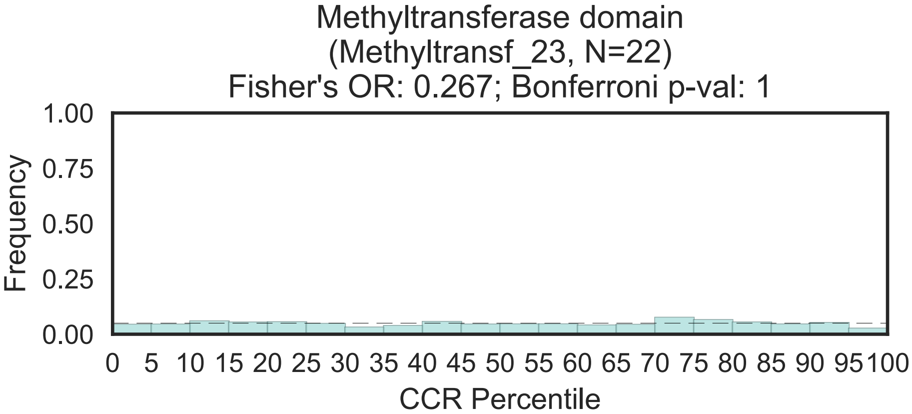

Lysine methyltransferase
(Methyltransf_16, N=15)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


6-O-methylguanine DNA methyltransferase, ribonuclease-like domain
(Methyltransf_1N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

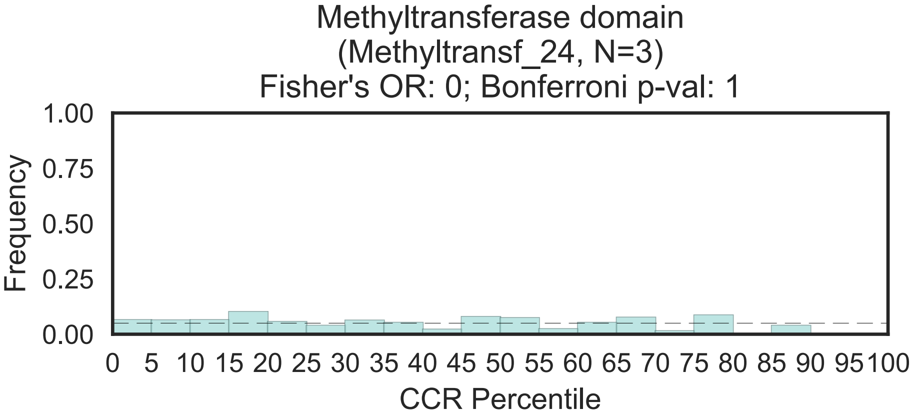

O-methyltransferase
(Methyltransf_2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Methyltransferase FkbM domain
(Methyltransf_21, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

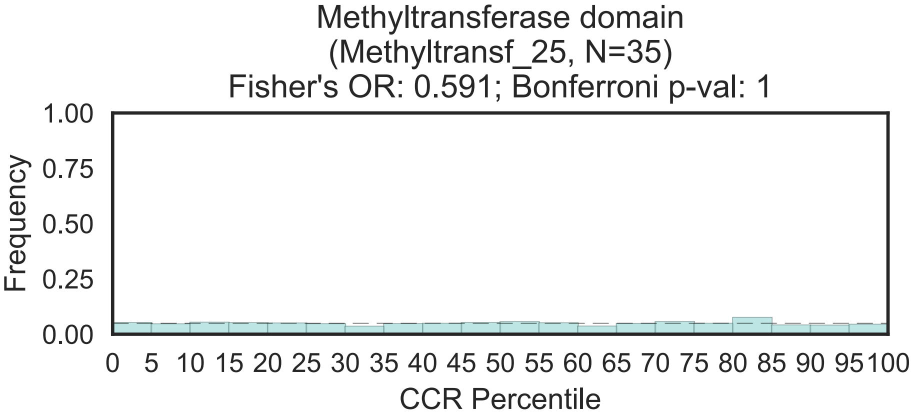

Methyltransferase domain
(Methyltransf_22, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

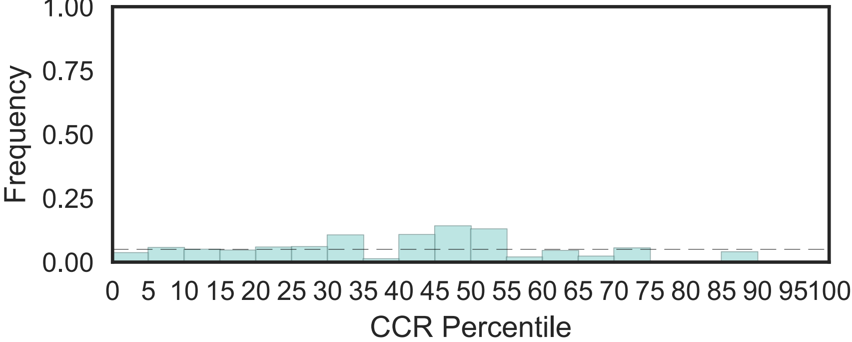


Methyltransferase domain
(Methyltransf_23, N=22)
Fisher's OR: 0.267; Bonferroni p-val: 1

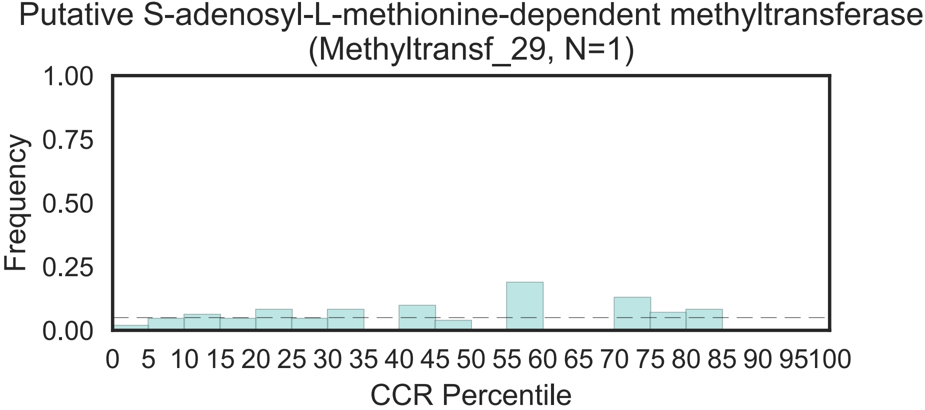


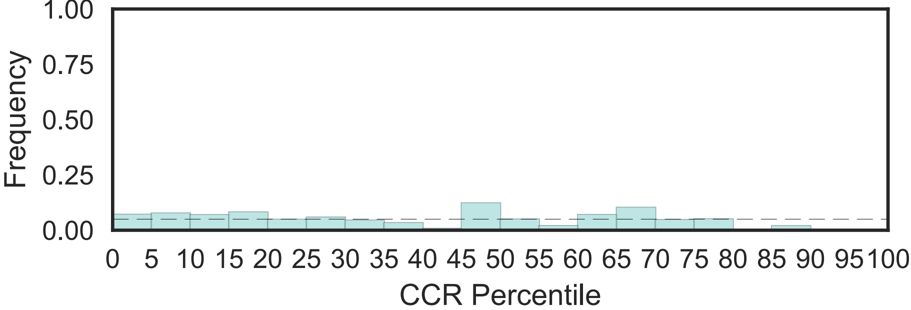
Methyltransferase domain
(Methyltransf_24, N=3)
Fisher's OR: 0; Bonferroni p-val: 1


Methyltransferase domain
(Methyltransf_25, N=35)
Fisher's OR: 0.591; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

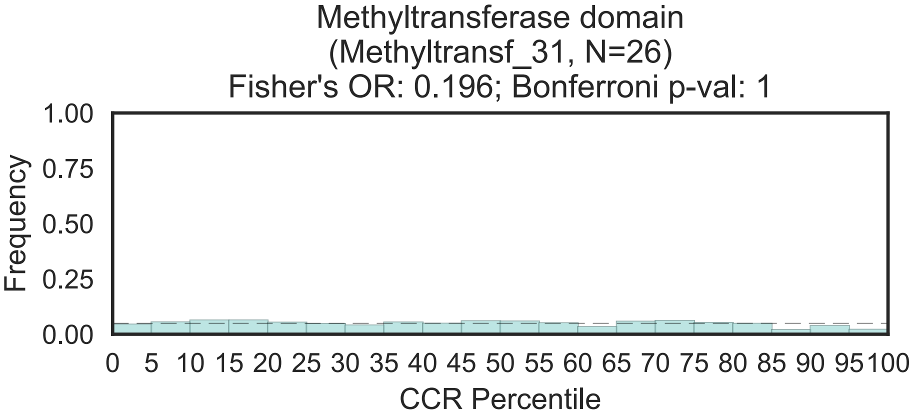


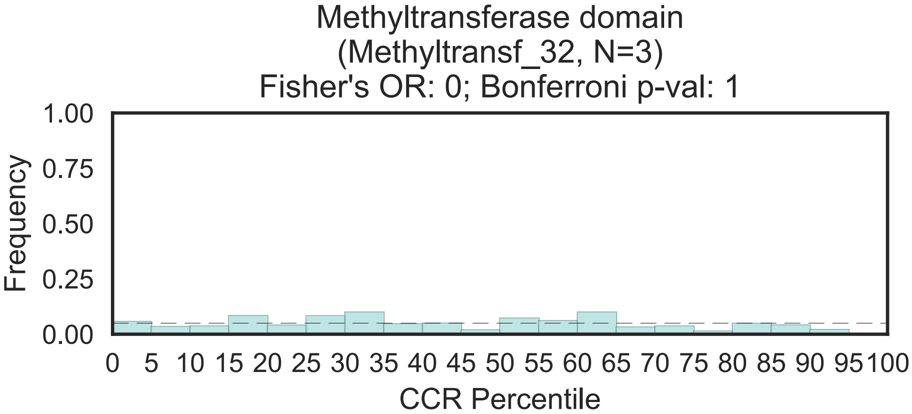
Putative S-adenosyl-L-methionine-dependent methyltransferase (Methyltransf_28, N=1)

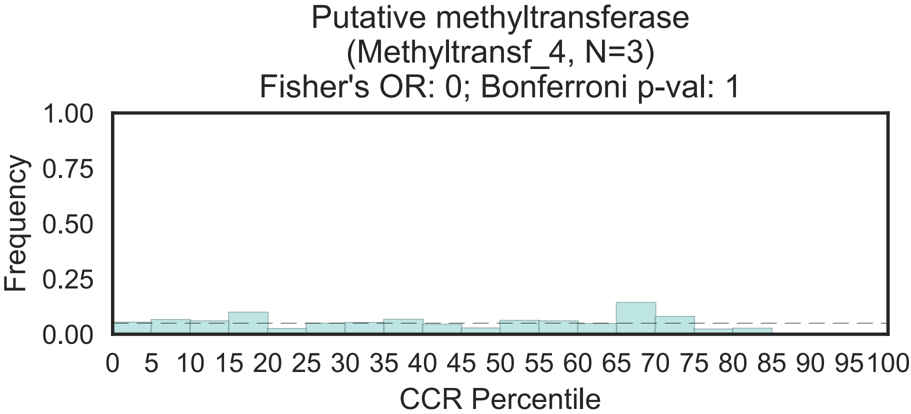

Putative S-adenosyl-L-methionine-dependent methyltransferase
(Methyltransf_29, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

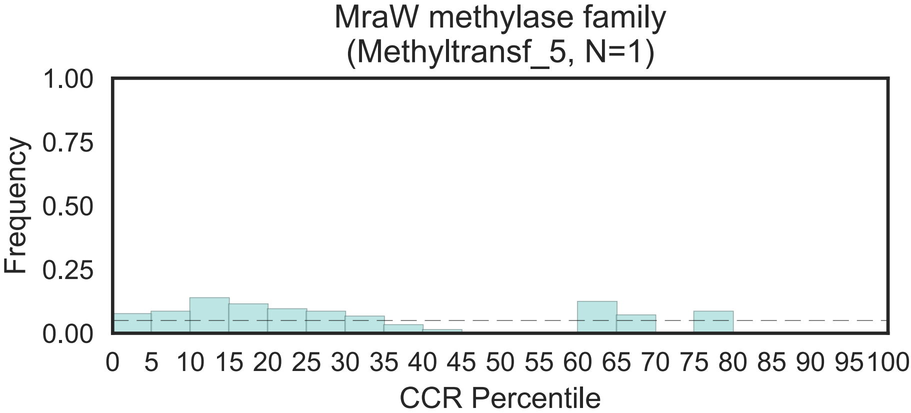


O-methyltransferase
(Methyltransf_3, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

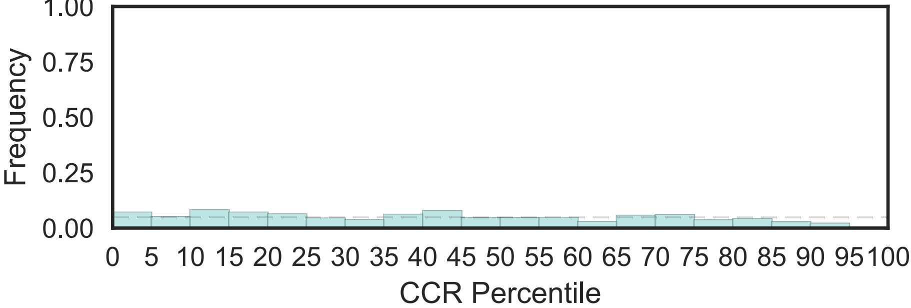

Methyltransferase domain
(Methyltransf_31, N=26)
Fisher's OR: 0.196; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

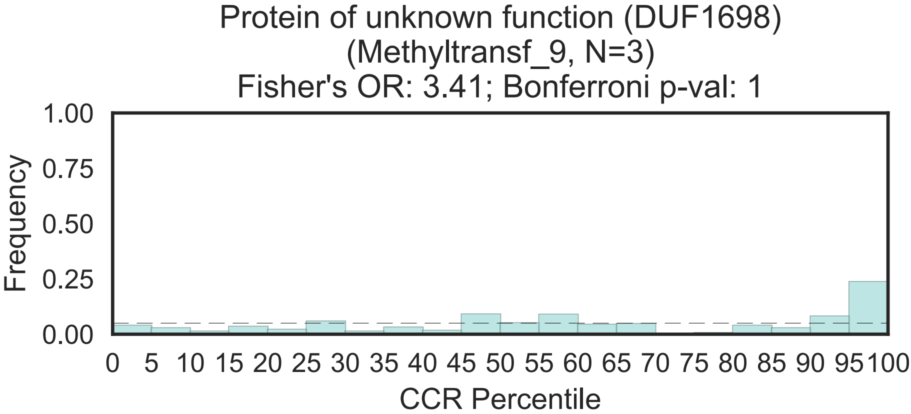

Methyltransferase domain
(Methyltransf_32, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Putative methyltransferase
(Methyltransf_4, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

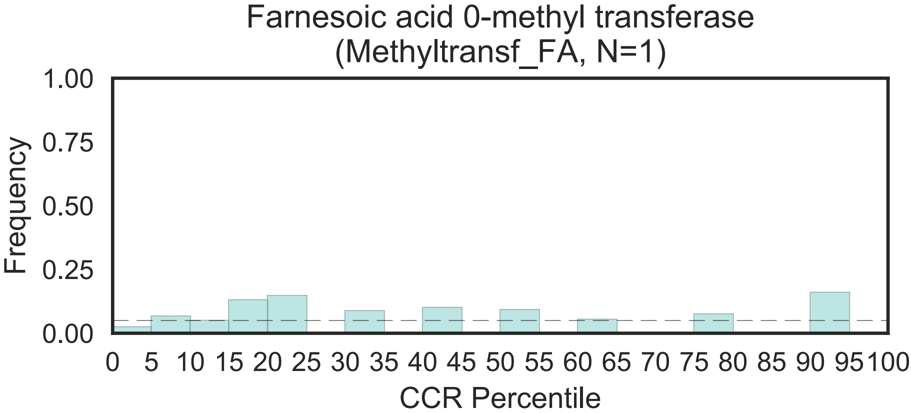

MraW methylase family
(Methyltransf_5, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

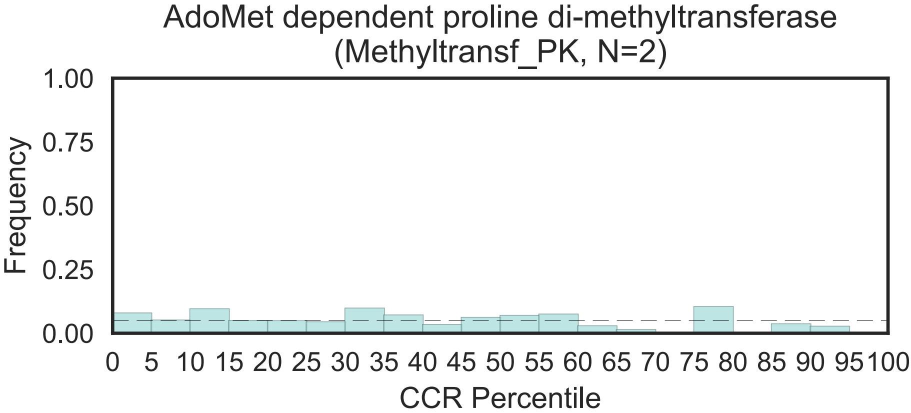
Hypothetical methyltransferase
(Methyltransf_8, N=6)
Fisher's OR: 0; Bonferroni p-val: 1

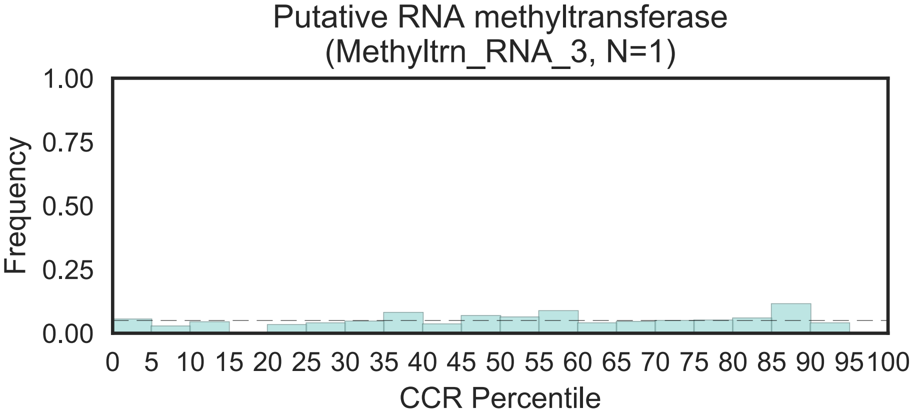


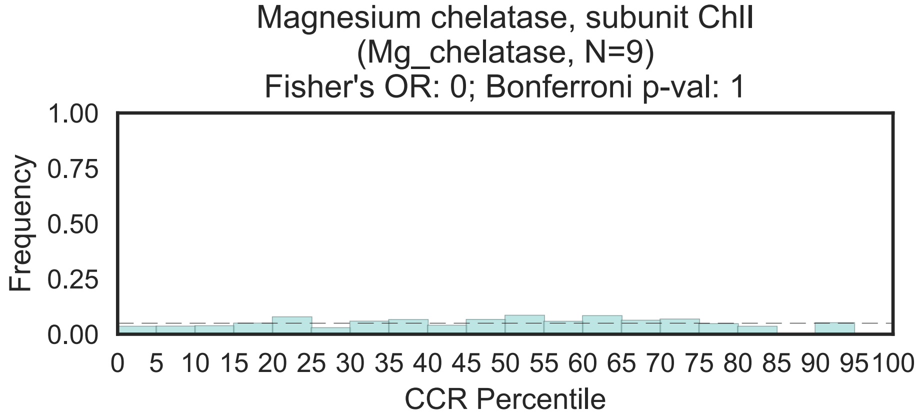


Protein of unknown function (DUF1698)
(Methyltransf_9, N=3)
Fisher's OR: 3.41; Bonferroni p-val: 1

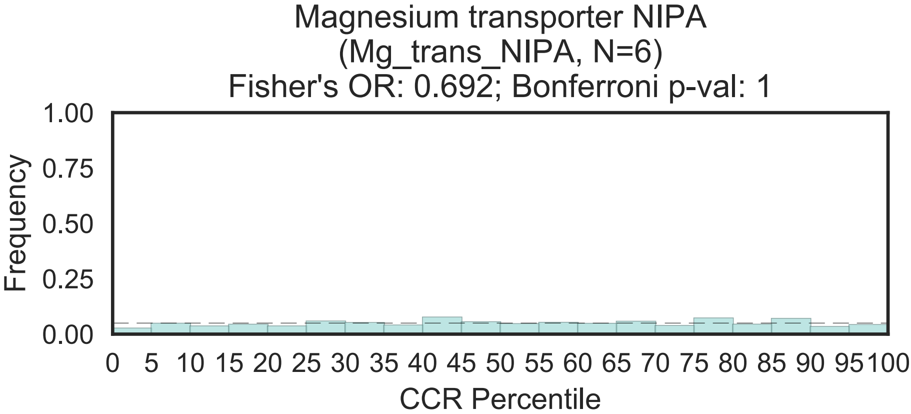

Farnesoic acid 0-methyl transferase
(Methyltransf_FA, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

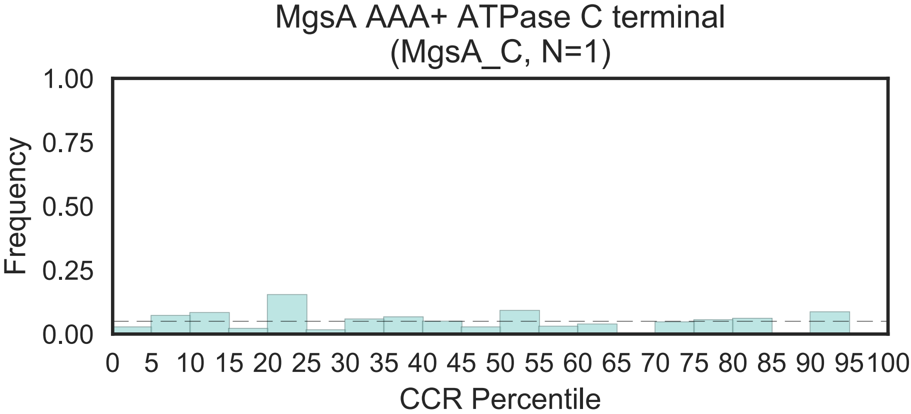

AdoMet dependent proline di-methyltransferase
(Methyltransf_PK, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

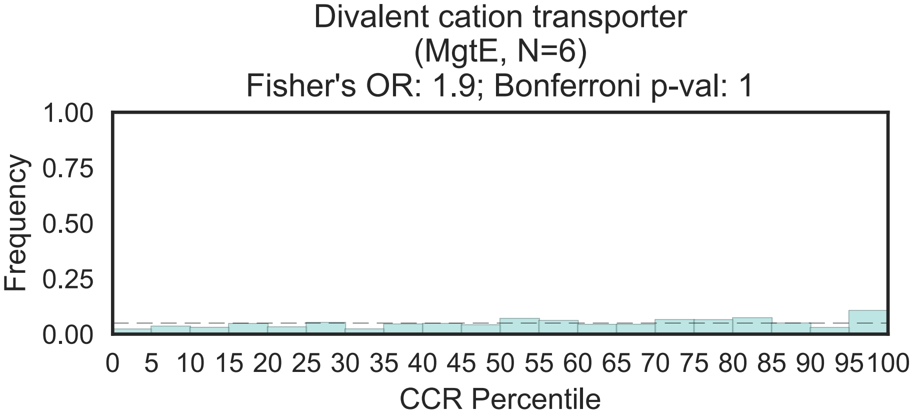

Putative RNA methyltransferase
(Methyltrn_RNA_3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



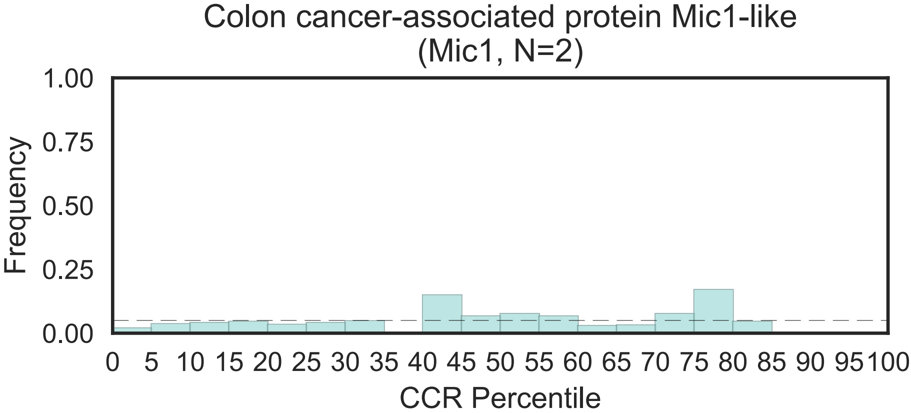
Magnesium chelatase, subunit ChlI
(Mg_chelatase, N=9)
Fisher's OR: 0; Bonferroni p-val: 1

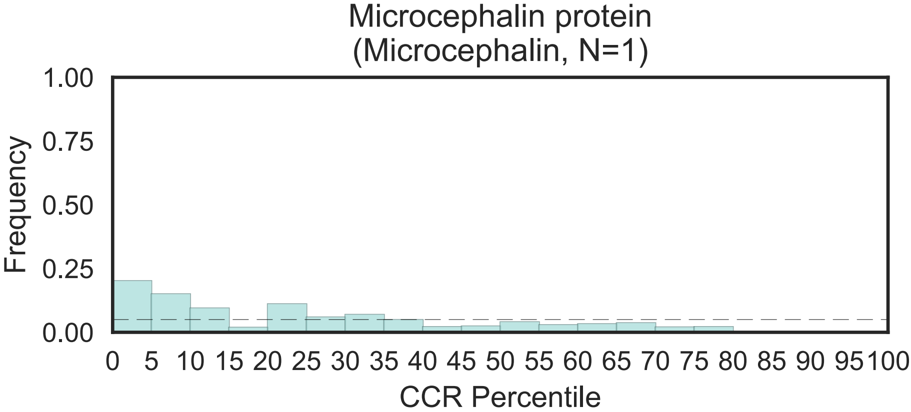

Magnesium transporter NIPA
(Mg_trans_NIPA, N=6)
Fisher's OR: 0.692; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

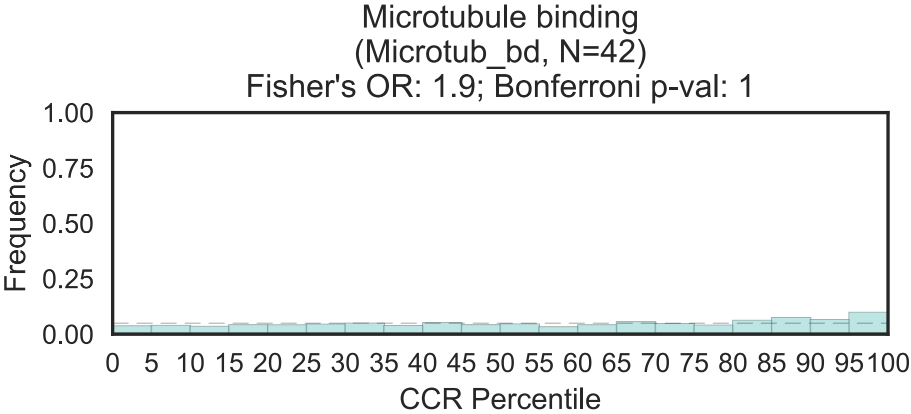

MgsA AAA+ ATPase C terminal
(MgsA_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

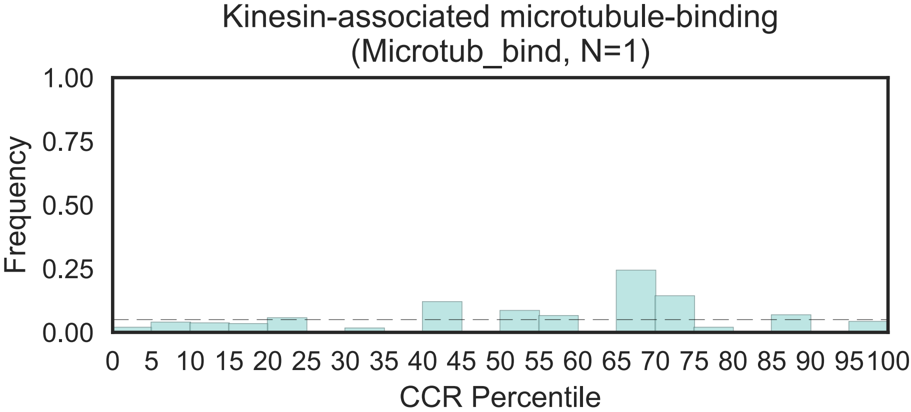


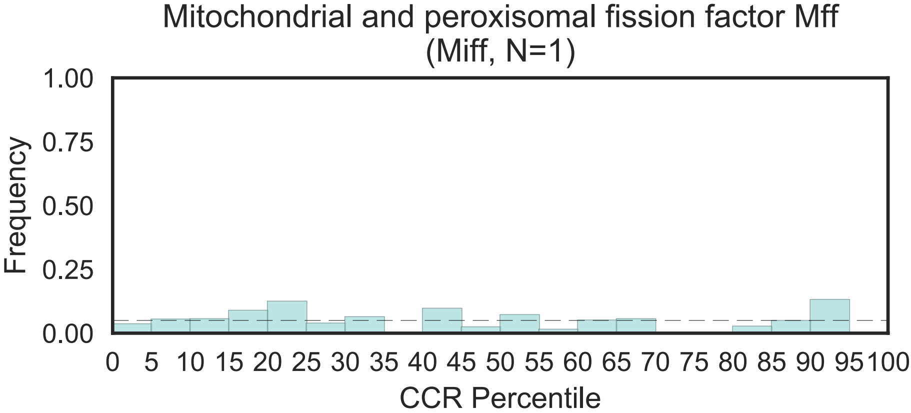
Divalent cation transporter
(MgtE, N=6)
Fisher's OR: 1.9; Bonferroni p-val: 1

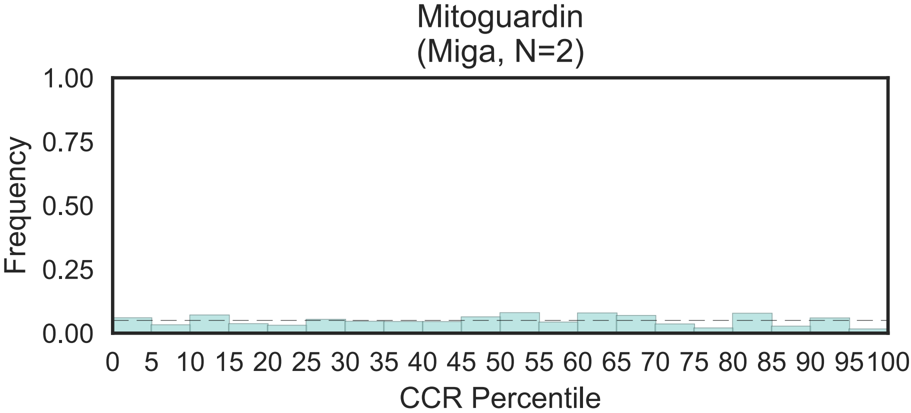

Colon cancer-associated protein Mic1-like
(Mic1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

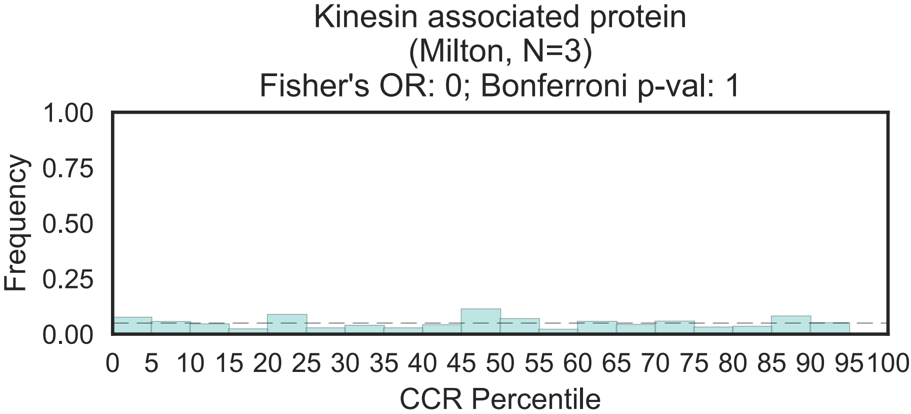

Microcephalin protein
(Microcephalin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

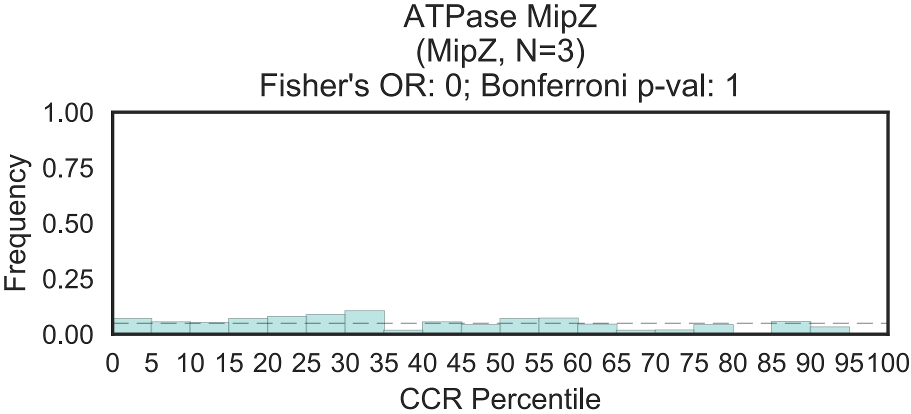

Microtubule binding
(Microtub_bd, N=42)
Fisher's OR: 1.9; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

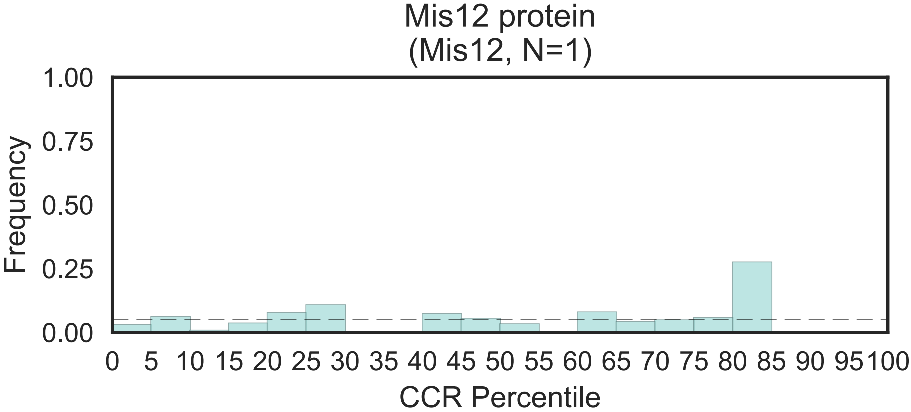

Kinesin-associated microtubule-binding
(Microtub_bind, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

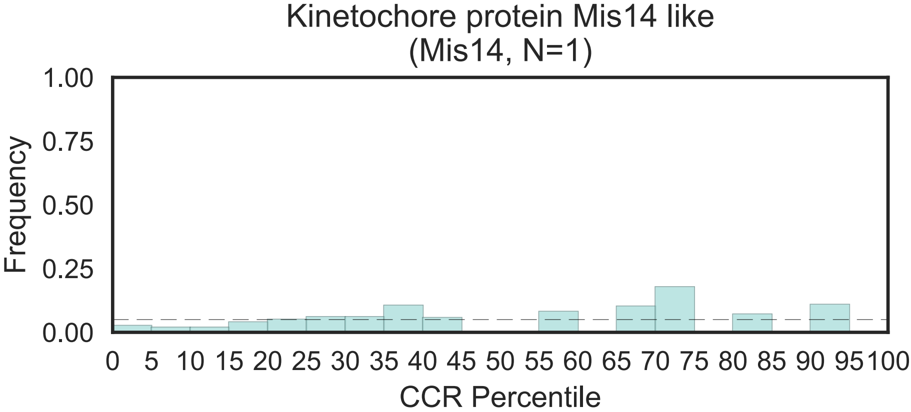

Mitochondrial and peroxisomal fission factor Mff
(Miff, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

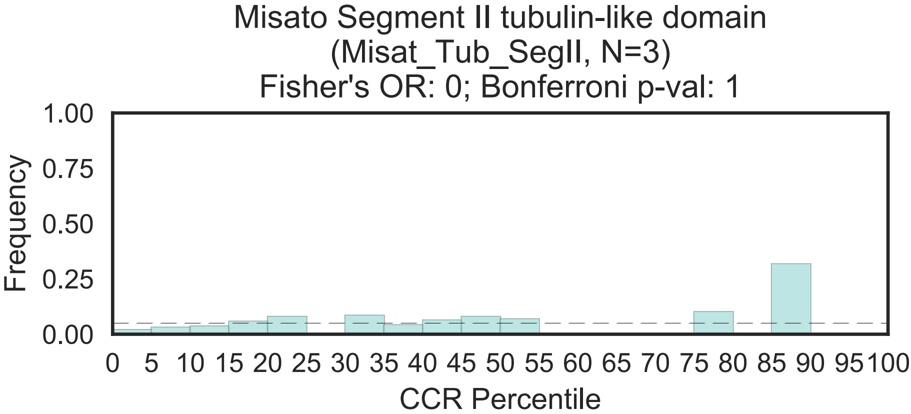

Mitoguardin
(Miga, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

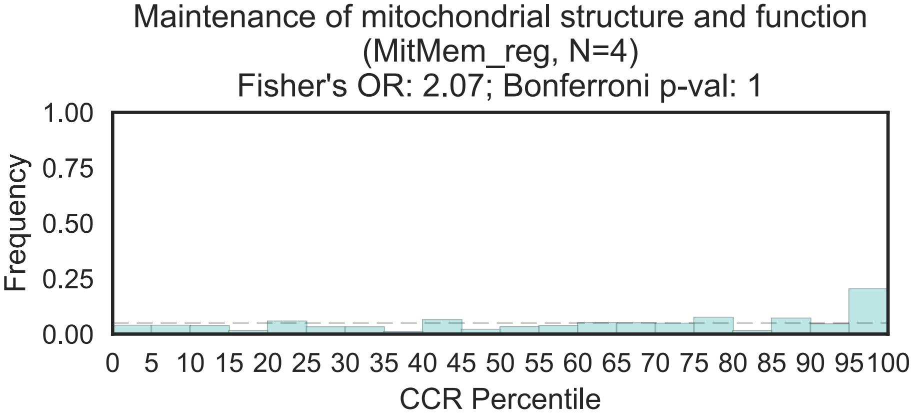

Kinesin associated protein
(Milton, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

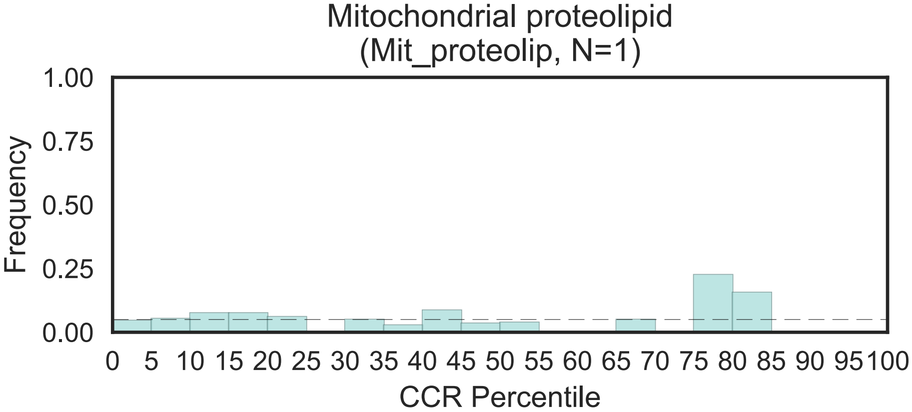

ATPase MipZ
(MipZ, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

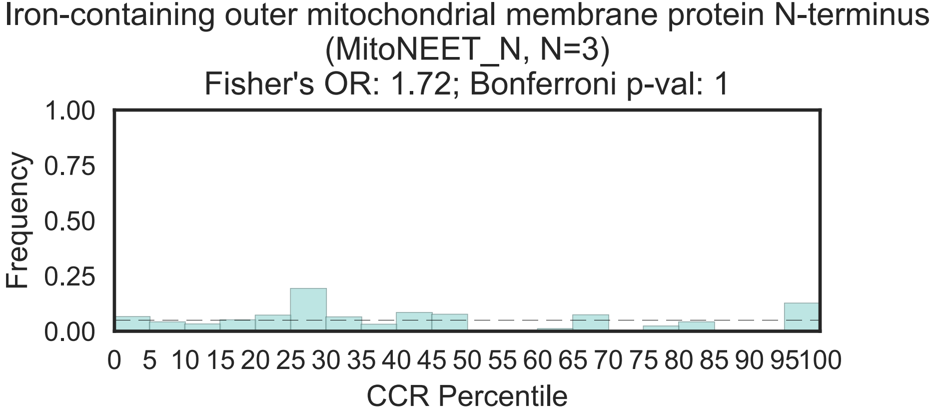

Mis12 protein
(Mis12, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

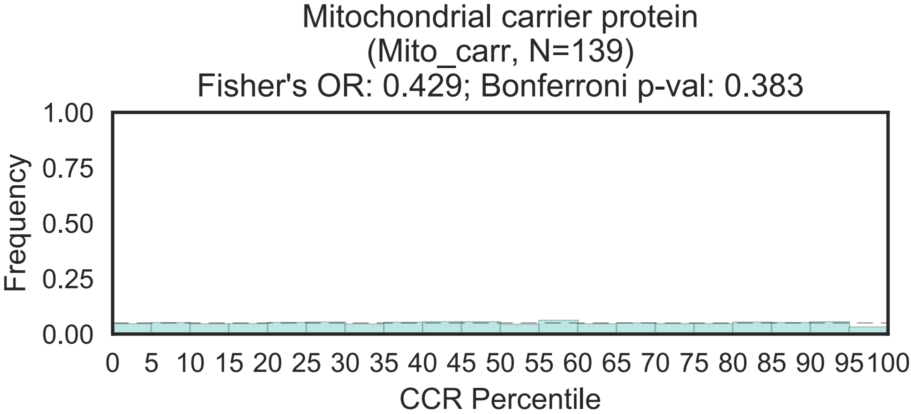

Kinetochore protein Mis14 like
(Mis14, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Misato Segment II tubulin-like domain
(Misat_Tub_SegII, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Maintenance of mitochondrial structure and function
(MitMem_reg, N=4)
Fisher's OR: 2.07; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

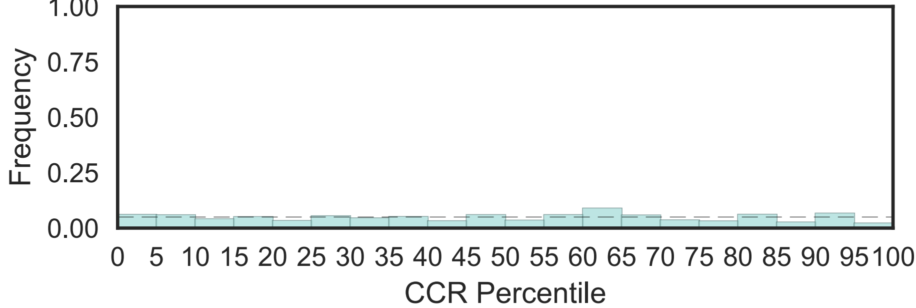

Mitochondrial proteolipid
(Mit_proteolip, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Iron-containing outer mitochondrial membrane protein N-terminus
(MitoNEET_N, N=3)
Fisher's OR: 1.72; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

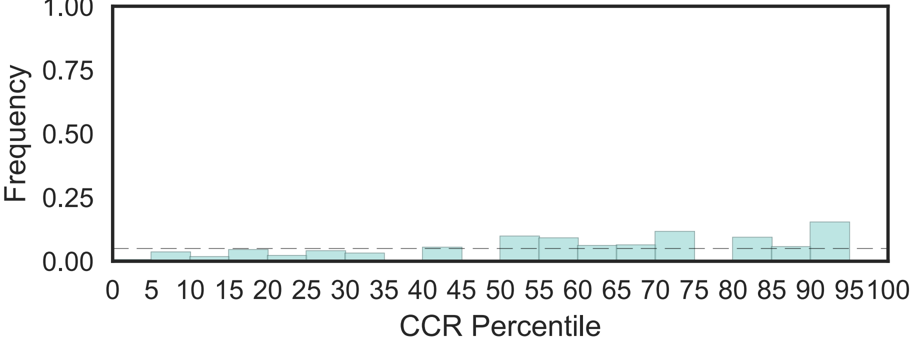


Mitochondrial carrier protein
(Mito_carr, N=139)
Fisher's OR: 0.429; Bonferroni p-val: 0.383

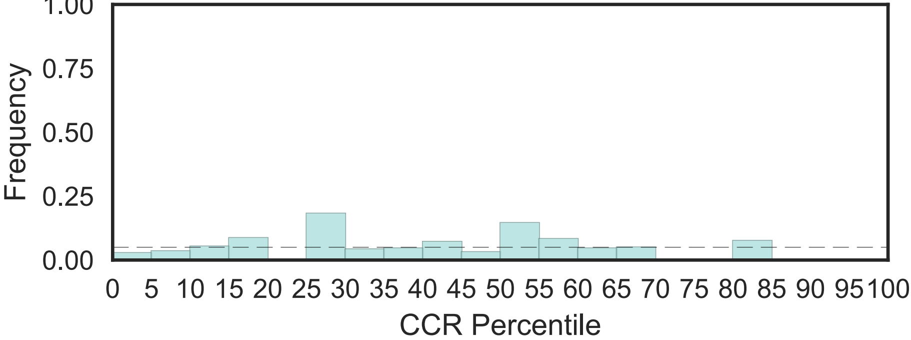
Mitochondrial fission regulator (Mito_fiss_reg, N=3) Fisher's OR: 0.363; Bonferroni p-val: 1

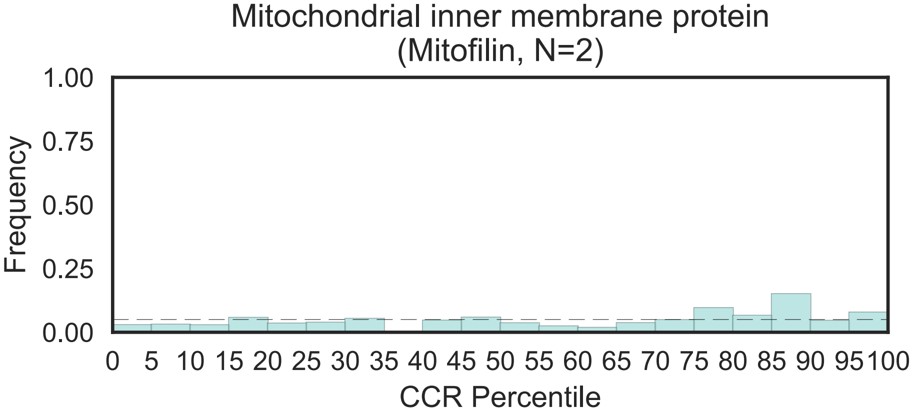


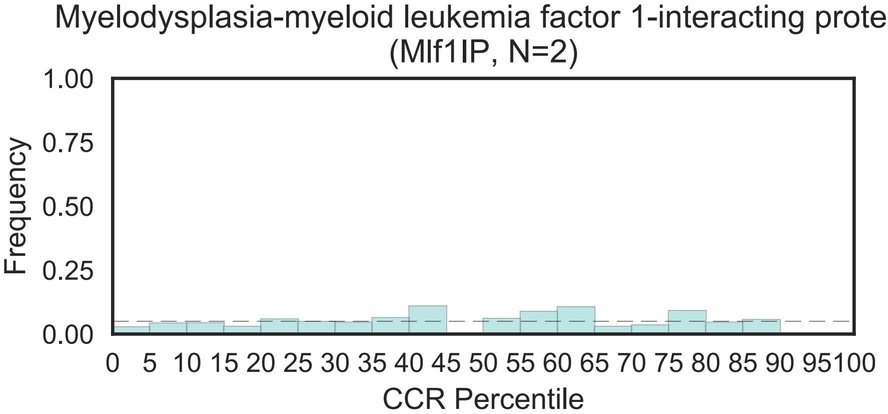
Mitochondrial morphogenesis regulator (Mito_morph_reg, N=1)

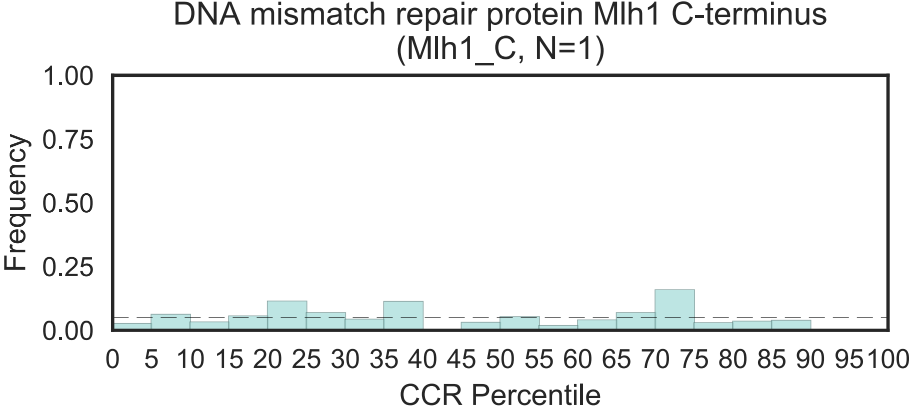


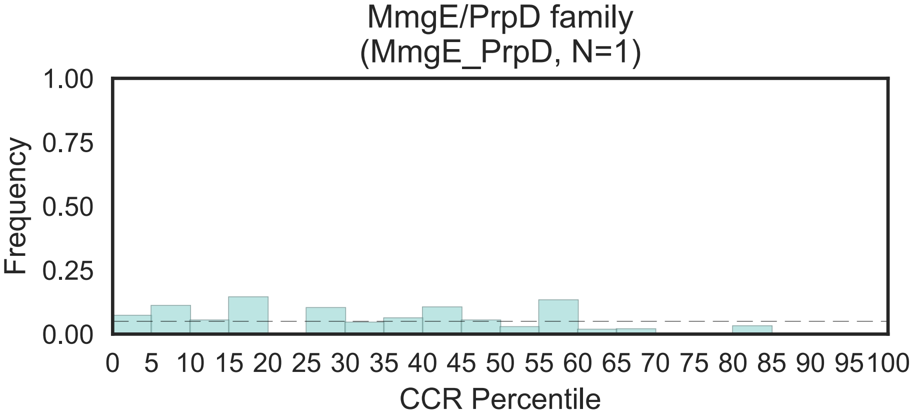
Mitochondrial ribosomal protein L55
(Mitoc_L55, N=1)

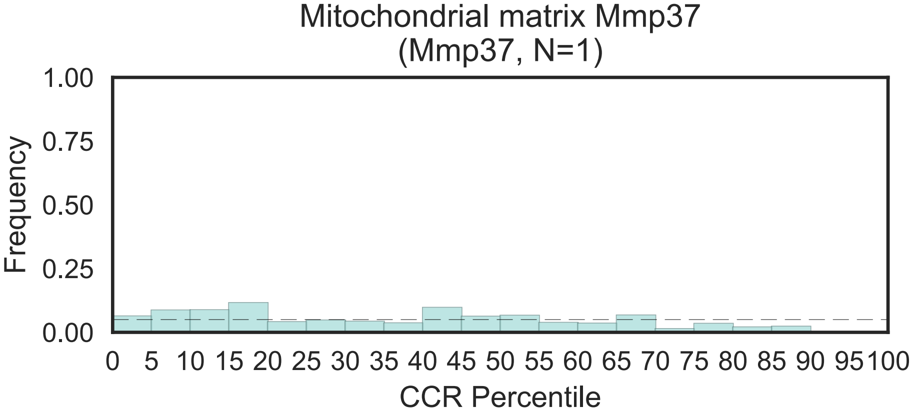


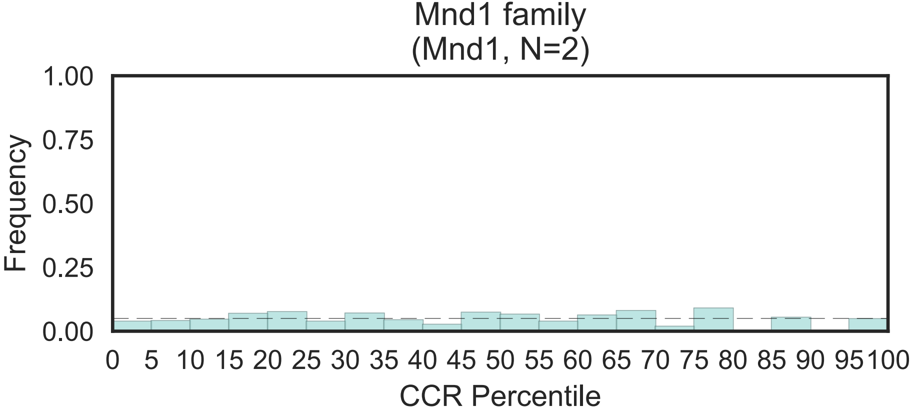

Mitochondrial inner membrane protein
(Mitofilin, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

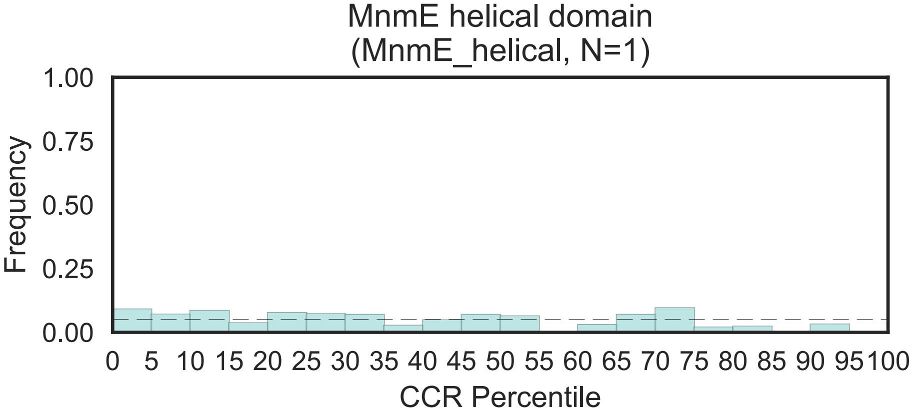

Myelodysplasia-myeloid leukemia factor 1-interacting protein
(Mlf1IP, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

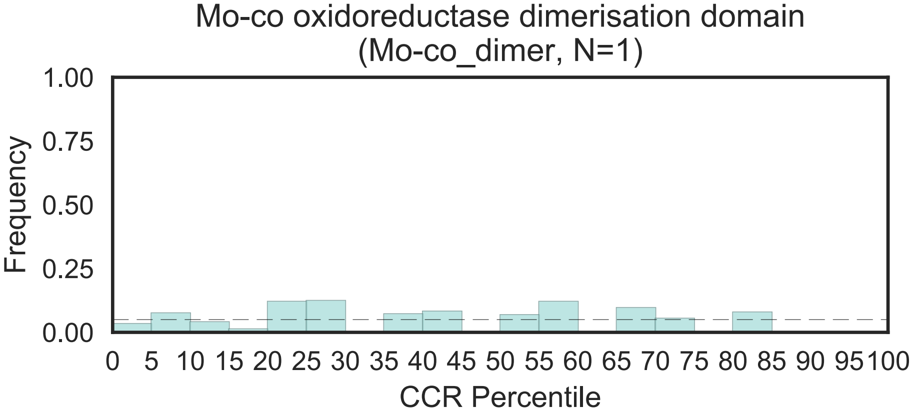

DNA mismatch repair protein Mlh1 C-terminus
(Mlh1_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

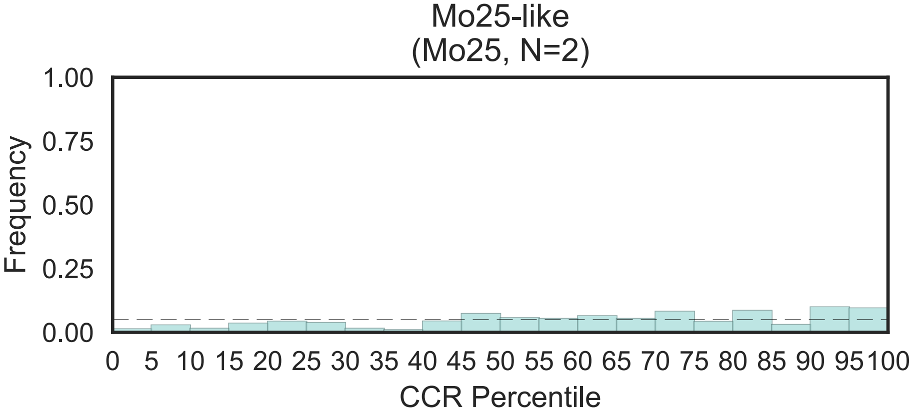

MmgE/PrpD family
(MmgE_PrpD, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

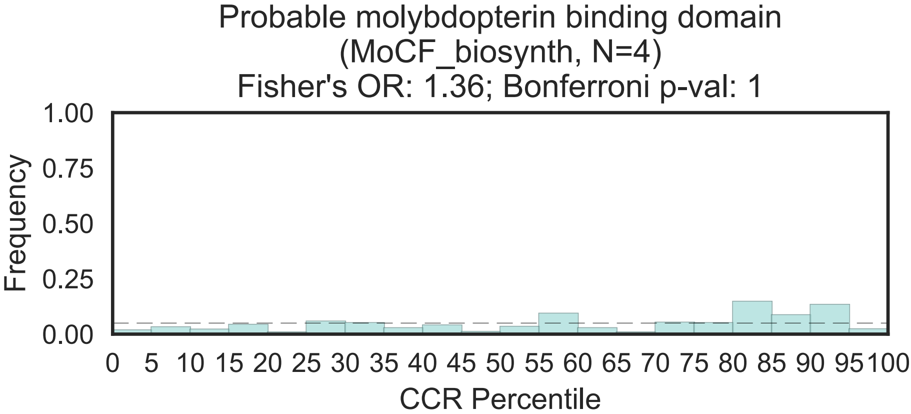

Mitochondrial matrix Mmp37
(Mmp37, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Mnd1 family
(Mnd1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

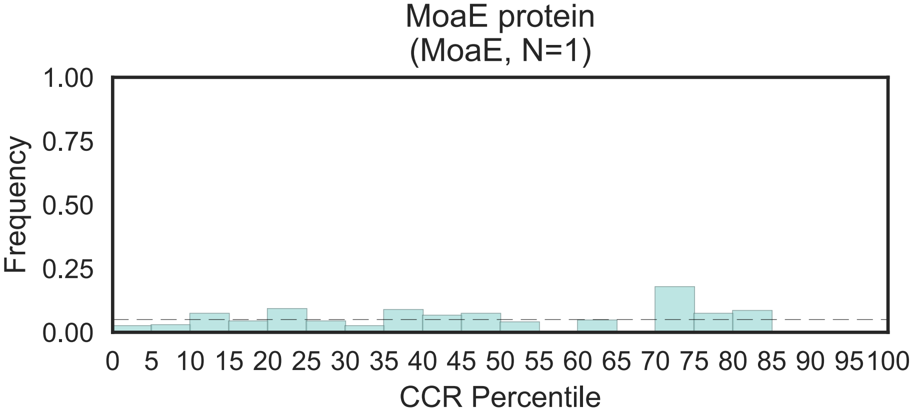

MnmE helical domain
(MnmE_helical, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

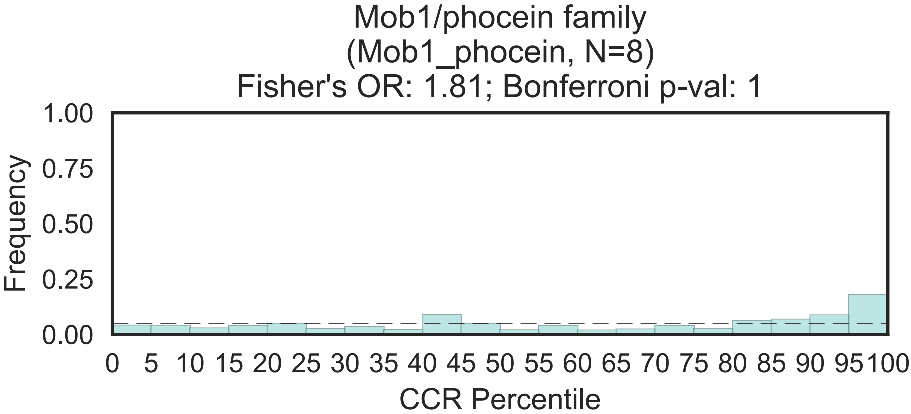

Mo-co oxidoreductase dimerisation domain
(Mo-co_dimer, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

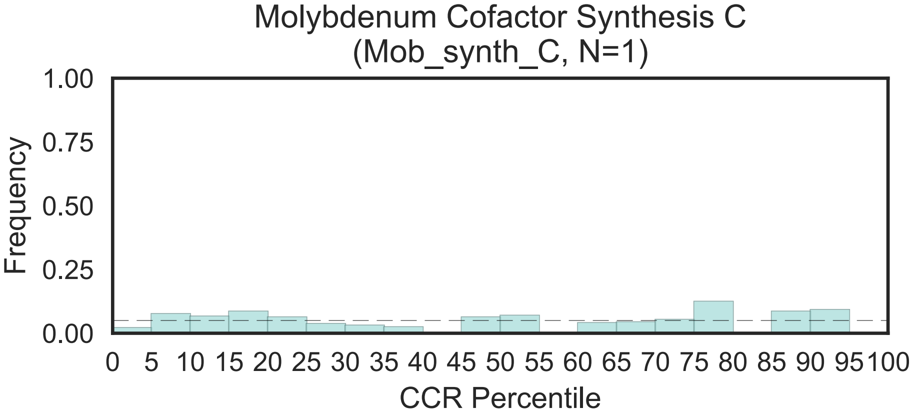

Mo25-like
(Mo25, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

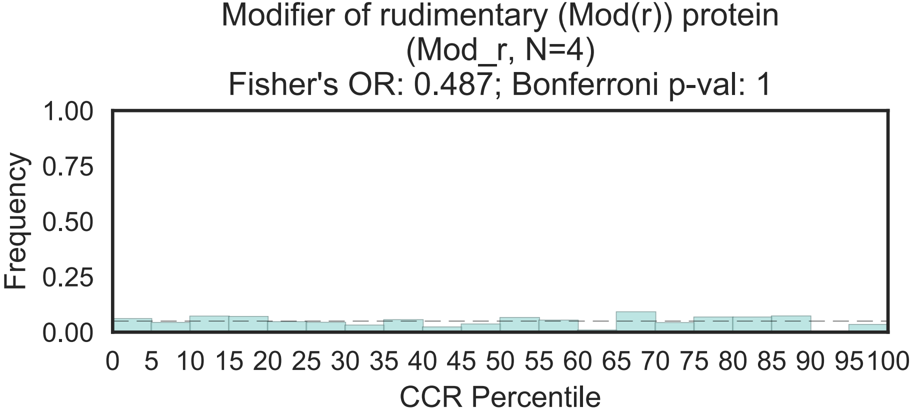


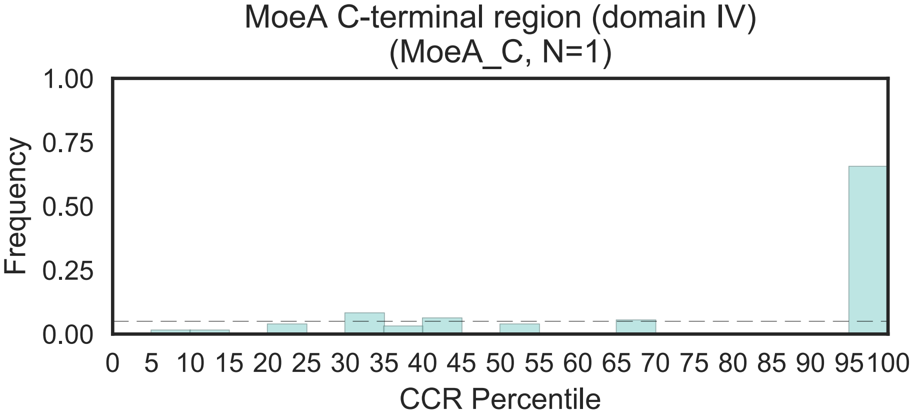
Probable molybdopterin binding domain
(MoCF_biosynth, N=4)
Fisher's OR: 1.36; Bonferroni p-val: 1

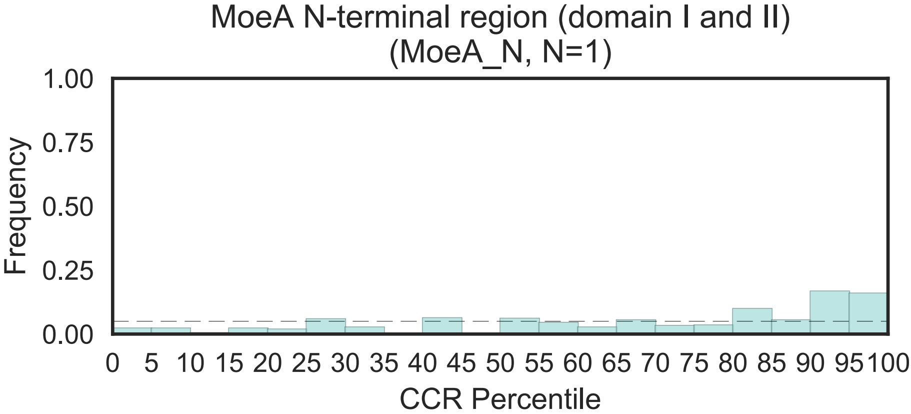

MoaE protein
(MoaE, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Mob1/phocein family
(Mob1_phocein, N=8)
Fisher's OR: 1.81; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

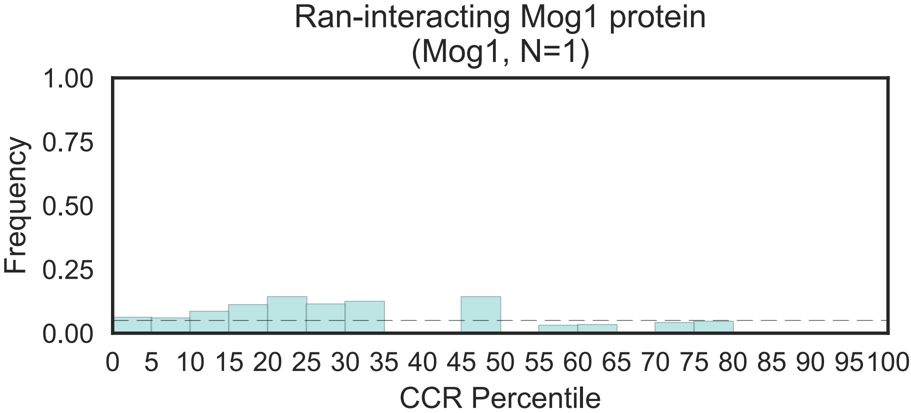

Molybdenum Cofactor Synthesis C
(Mob_synth_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

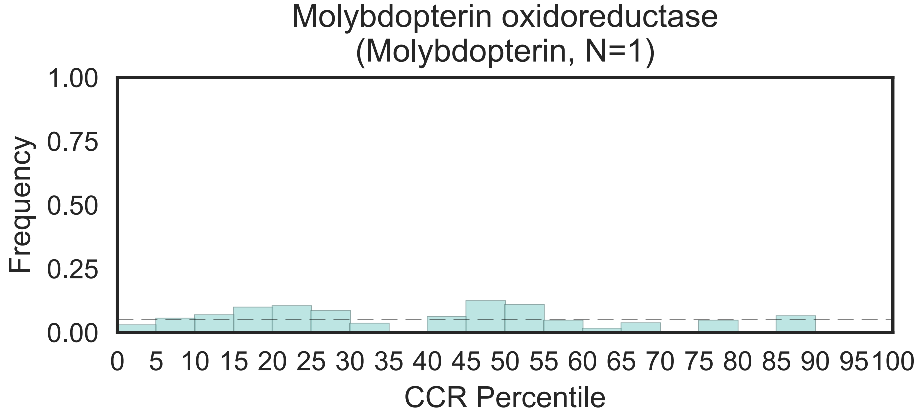

Modifier of rudimentary (Mod(r)) protein
(Mod_r, N=4)
Fisher's OR: 0.487; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

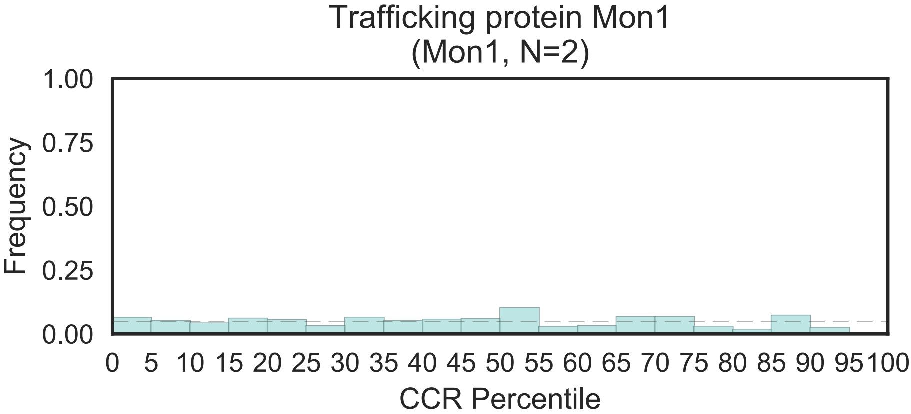

MoeA C-terminal region (domain IV)
(MoeA_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

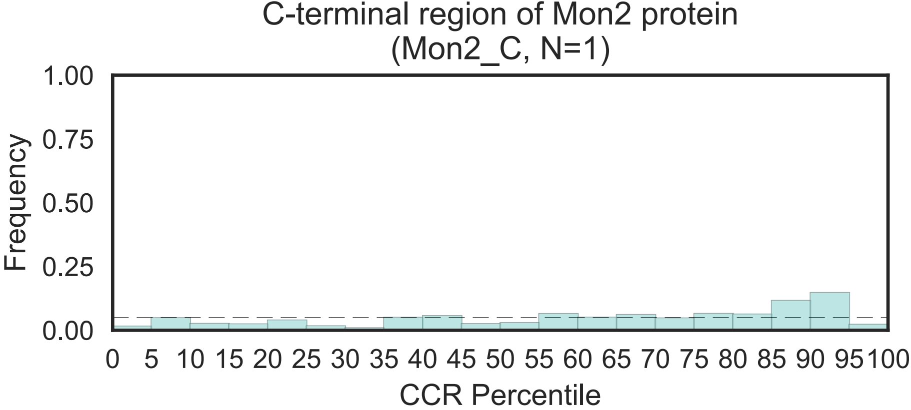


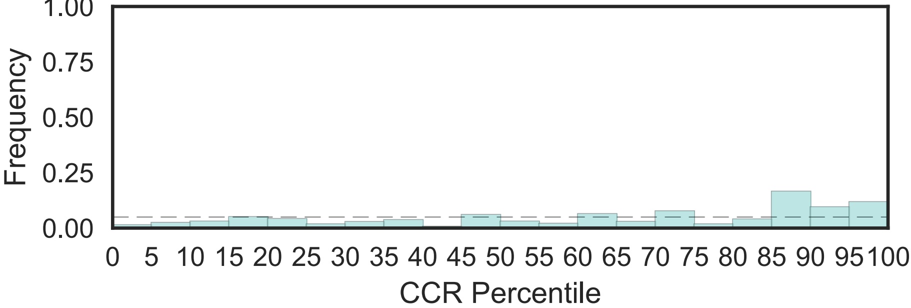
MoeA N-terminal region (domain I and II)
(MoeA_N, N=1)

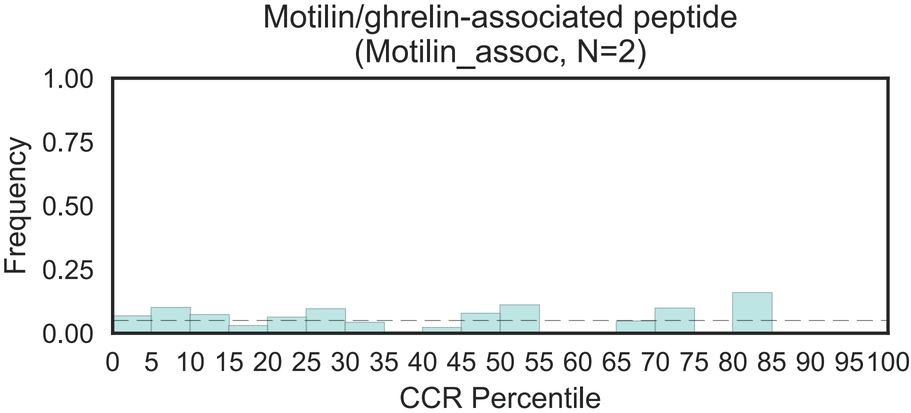

Ran-interacting Mog1 protein
(Mog1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

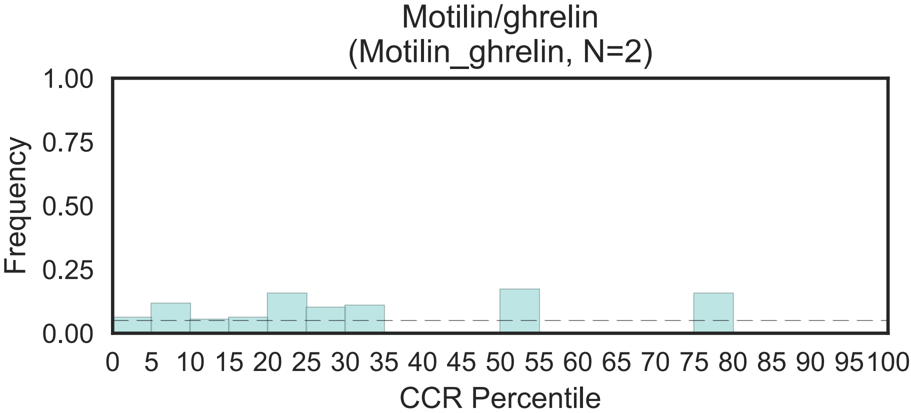

Molybdopterin oxidoreductase
(Molybdopterin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

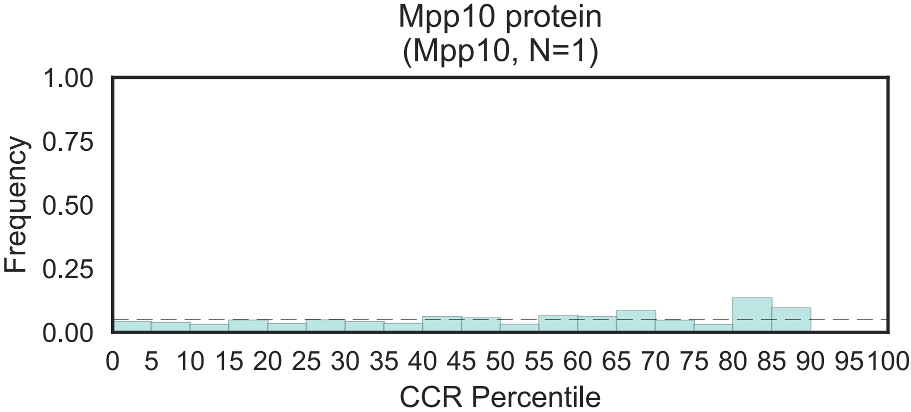

Trafficking protein Mon1
(Mon1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

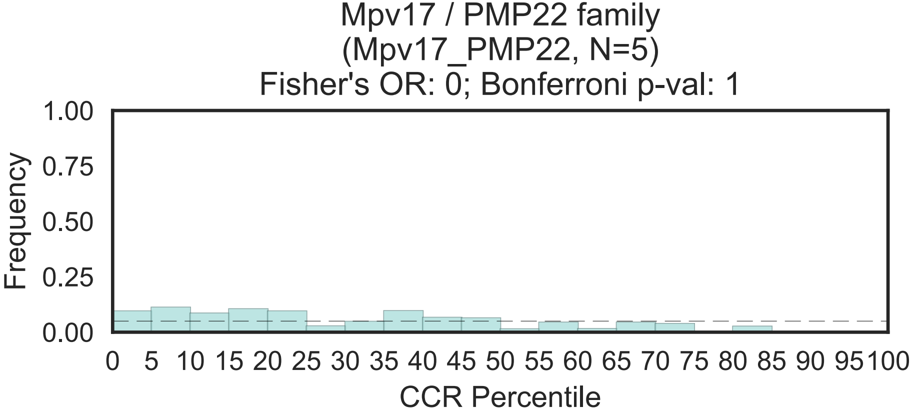

C-terminal region of Mon2 protein
(Mon2_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


MSP (Major sperm protein) domain
(Motile_Sperm, N=4)
Fisher's OR: 3.03; Bonferroni p-val: 1

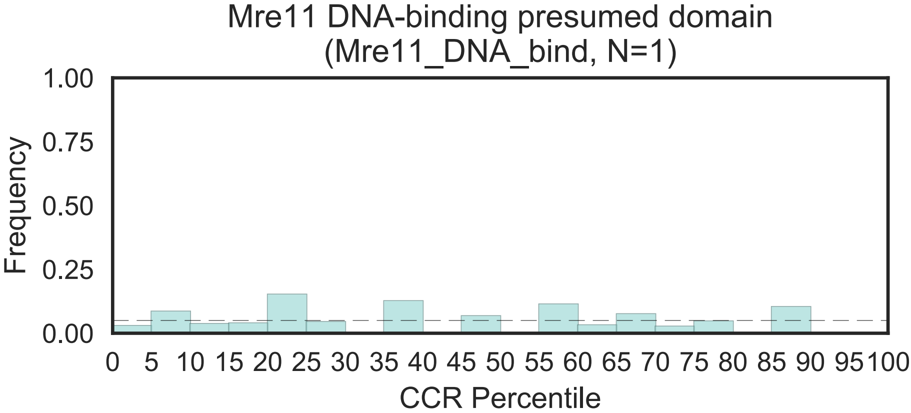

Motilin/ghrelin-associated peptide
(Motilin_assoc, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

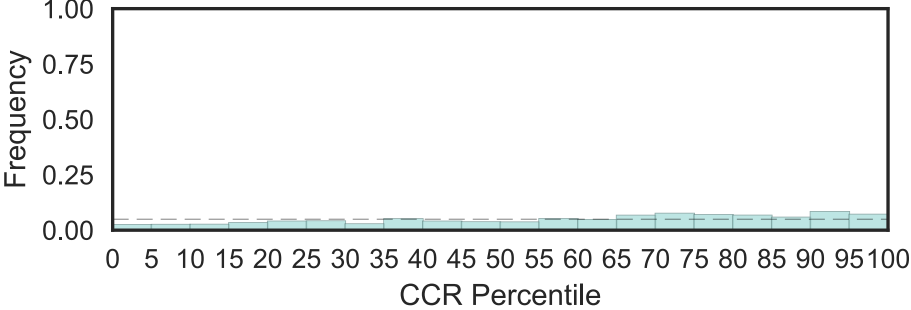

Motilin/ghrelin
(Motilin_ghrelin, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Mpp10 protein
(Mpp10, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

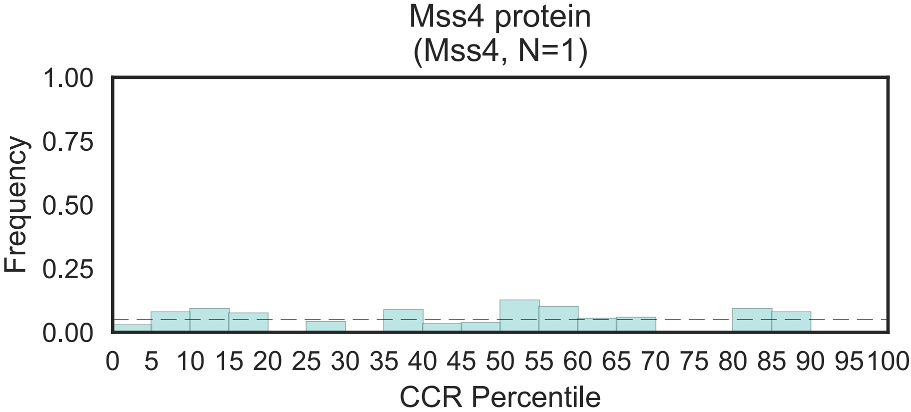


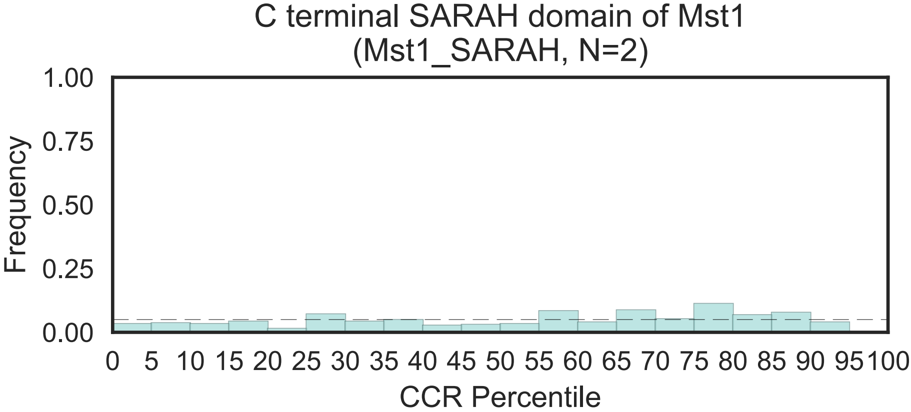
Mpv17 / PMP22 family
(Mpv17_PMP22, N=5)
Fisher's OR: 0; Bonferroni p-val: 1

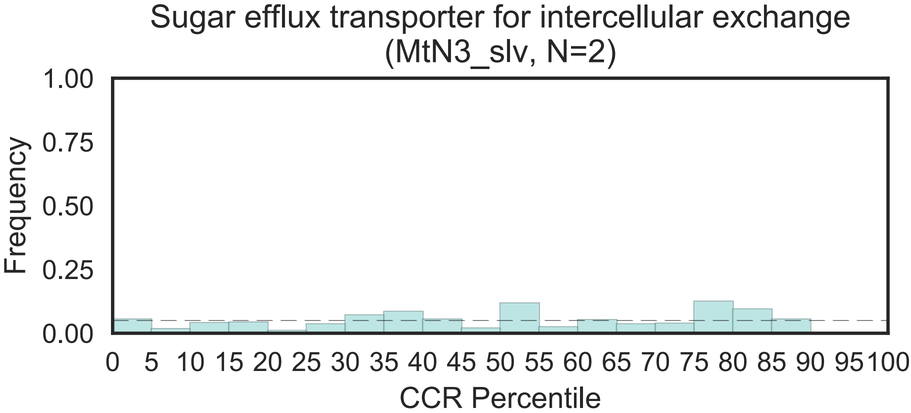

Mre11 DNA-binding presumed domain
(Mre11_DNA_bind, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

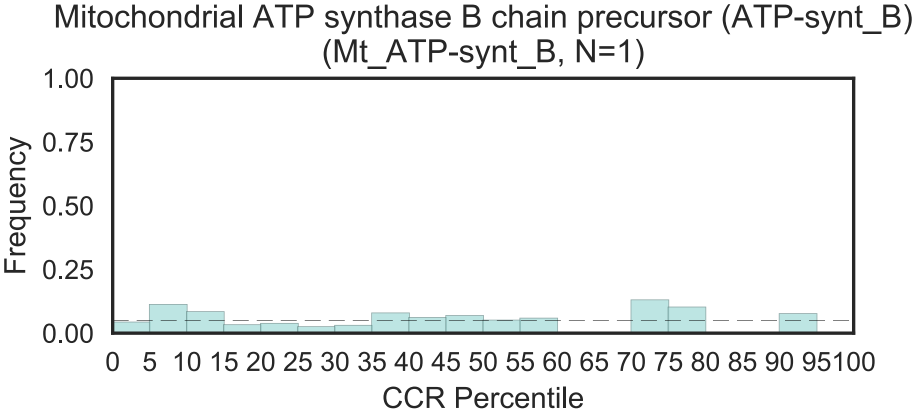


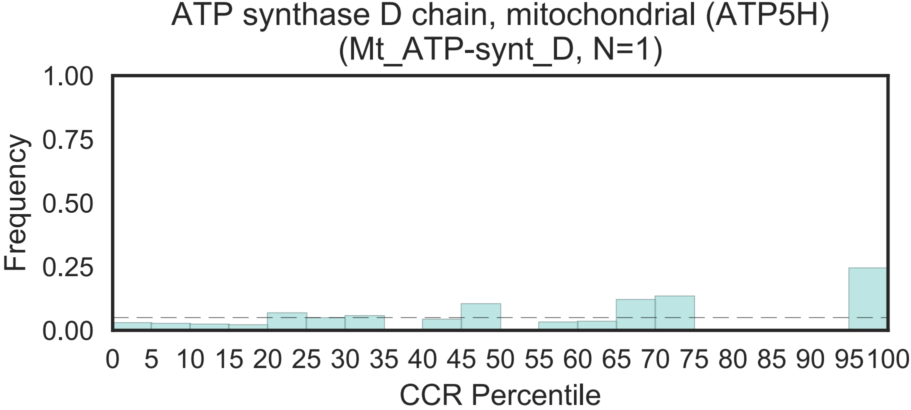
MreB/Mbl protein
(MreB_Mbl, N=14)
Fisher's OR: 1.22; Bonferroni p-val: 1


Mss4 protein
(Mss4, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

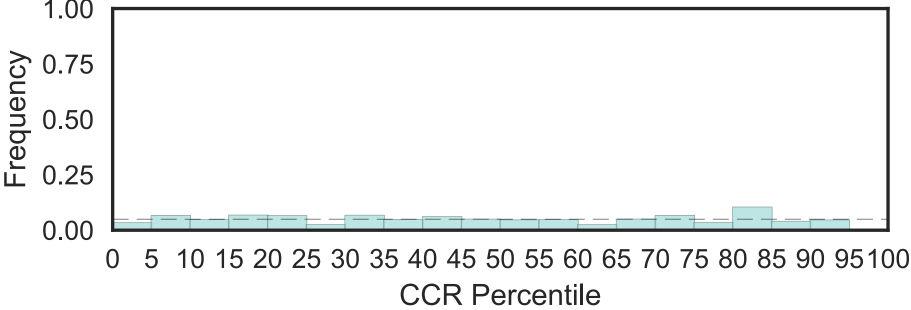

C terminal SARAH domain of Mst1
(Mst1_SARAH, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

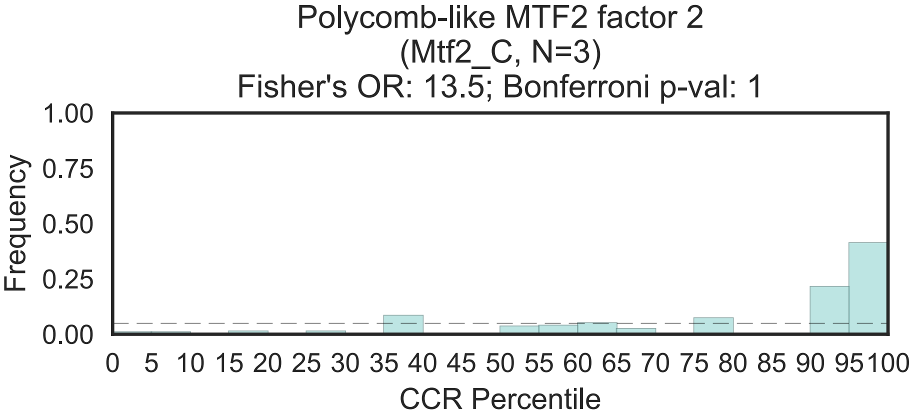

Sugar efflux transporter for intercellular exchange
(MtN3_slv, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

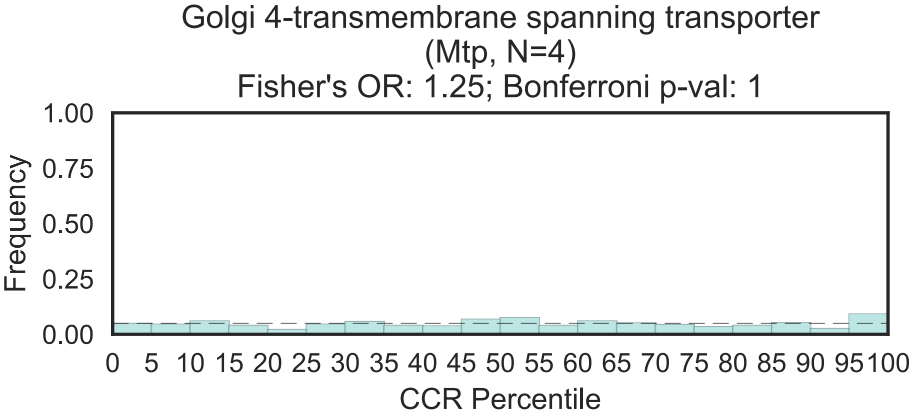

Mitochondrial ATP synthase B chain precursor (ATP-synt_B)
(Mt_ATP-synt_B, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

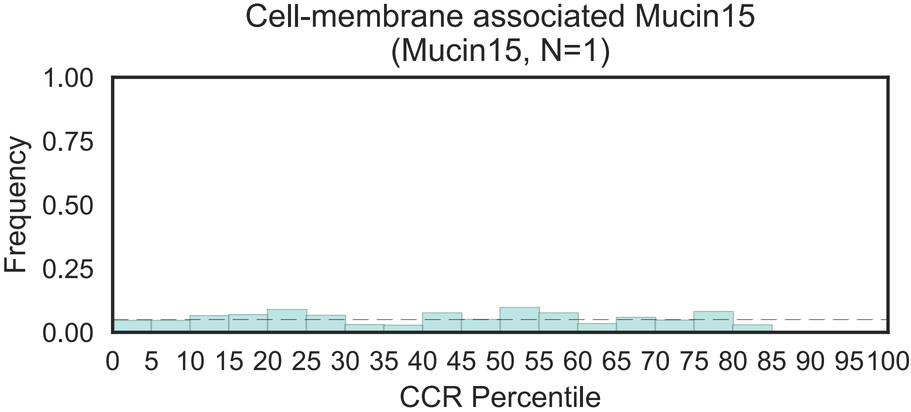

ATP synthase D chain, mitochondrial (ATP5H)
(Mt_ATP-synt_D, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

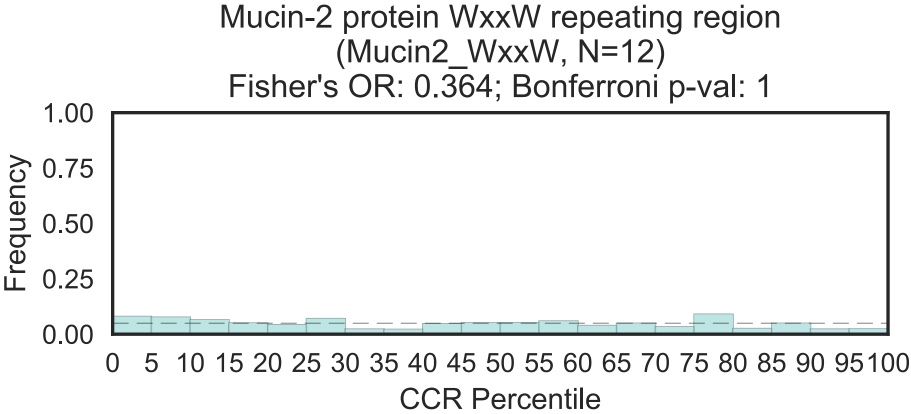
Tricarboxylate carrier
(Mtc, N=5)
Fisher's OR: 0; Bonferroni p-val: 1



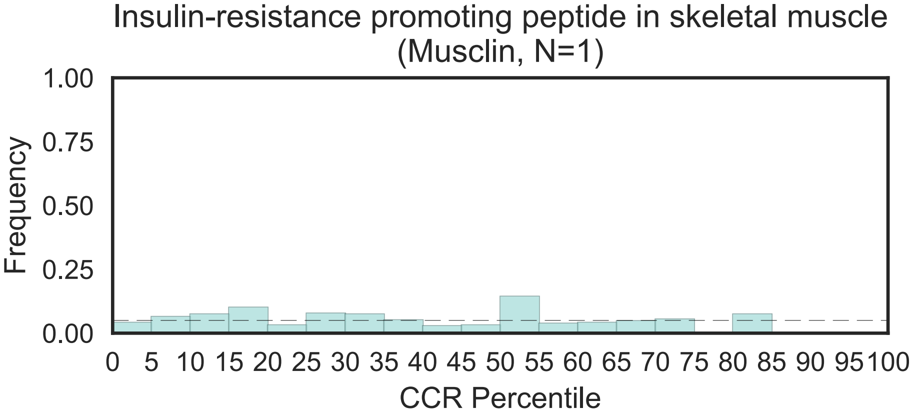

Polycomb-like MTF2 factor 2
(Mtf2_C, N=3)
Fisher's OR: 13.5; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Golgi 4-transmembrane spanning transporter
(Mtp, N=4)
Fisher's OR: 1.25; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

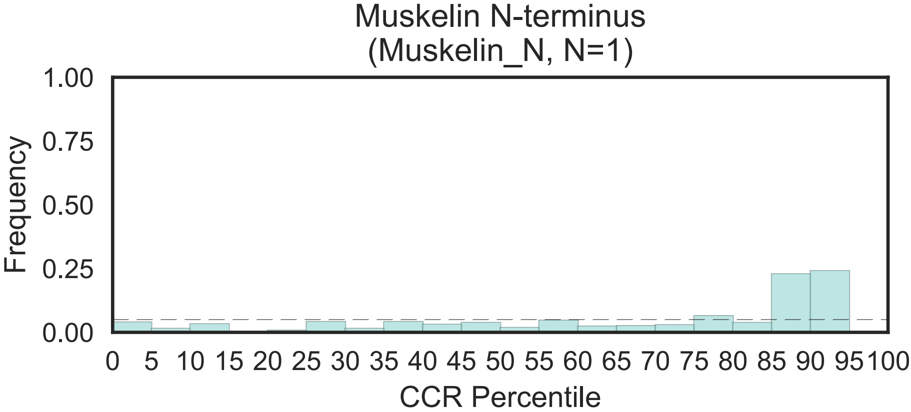

Cell-membrane associated Mucin15
(Mucin15, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

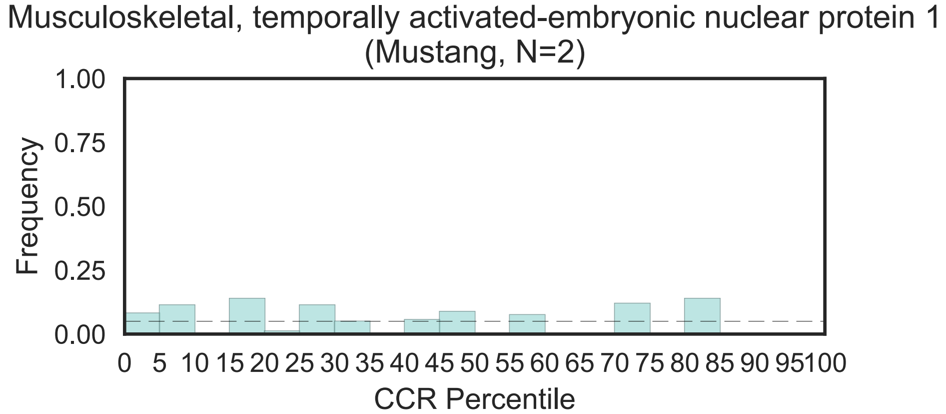


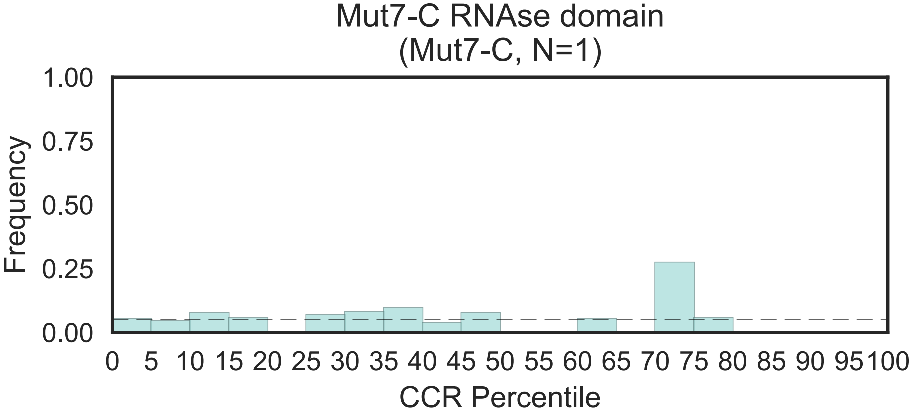
Mucin-2 protein WxxW repeating region
(Mucin2_WxxW, N=12)
Fisher's OR: 0.364; Bonferroni p-val: 1

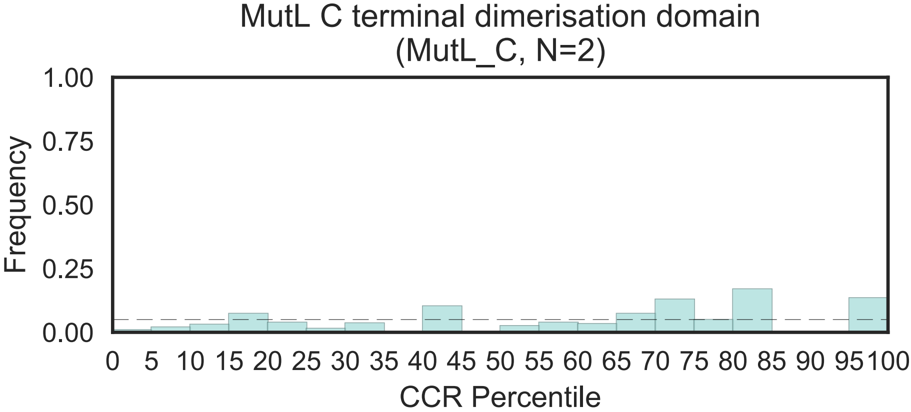


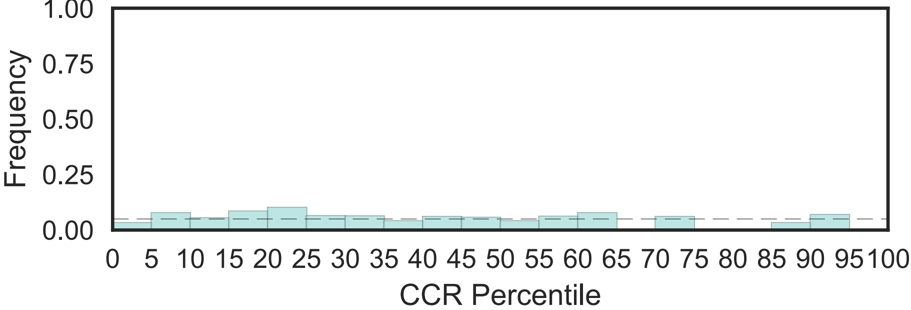
Insulin-resistance promoting peptide in skeletal muscle (Musclin, N=1)

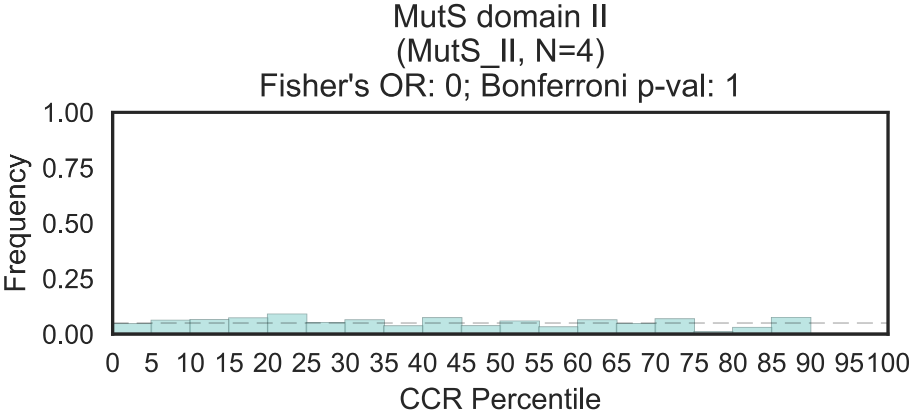

Muskelin N-terminus
(Muskelin_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

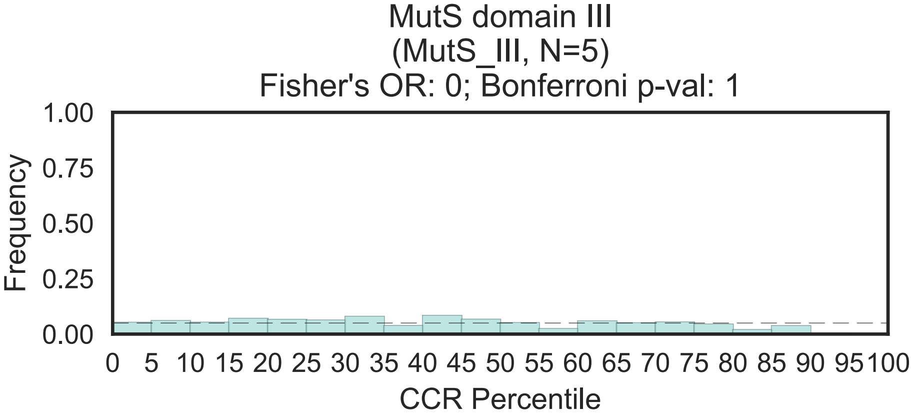

Musculoskeletal, temporally activated-embryonic nuclear protein 1
(Mustang, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

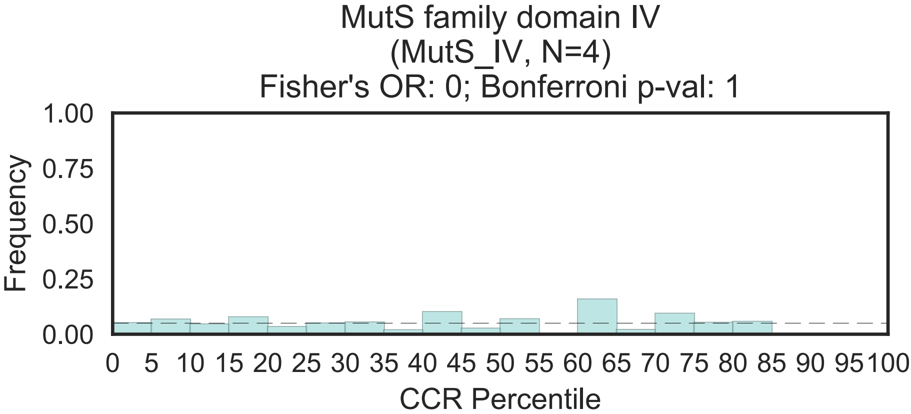

Mut7-C RNAse domain
(Mut7-C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

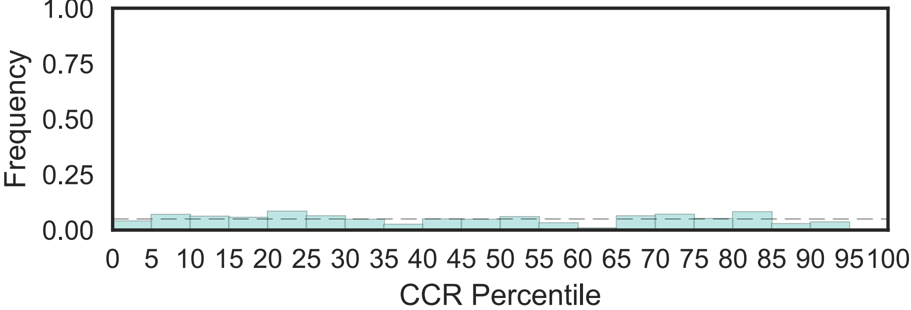

MutL C terminal dimerisation domain
(MutL_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


MutS domain I
(MutS_I, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

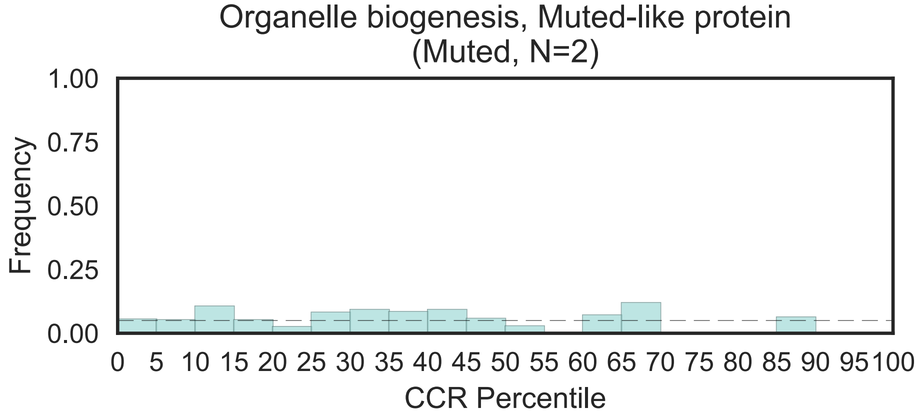

MutS domain II
(MutS_II, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

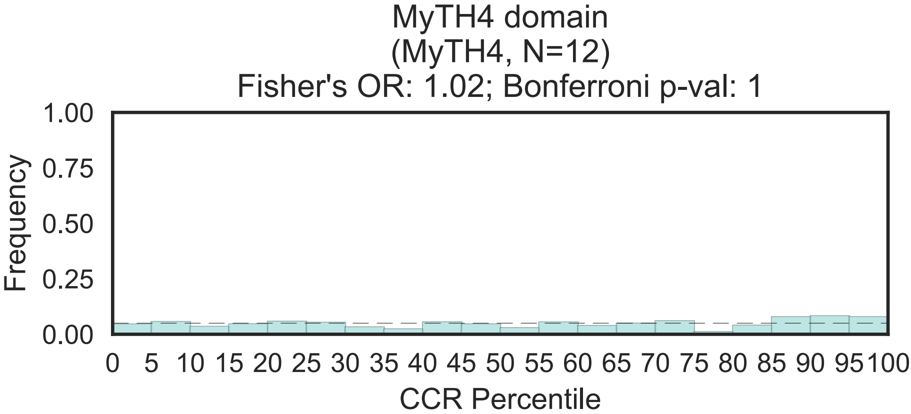

MutS domain III
(MutS_III, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

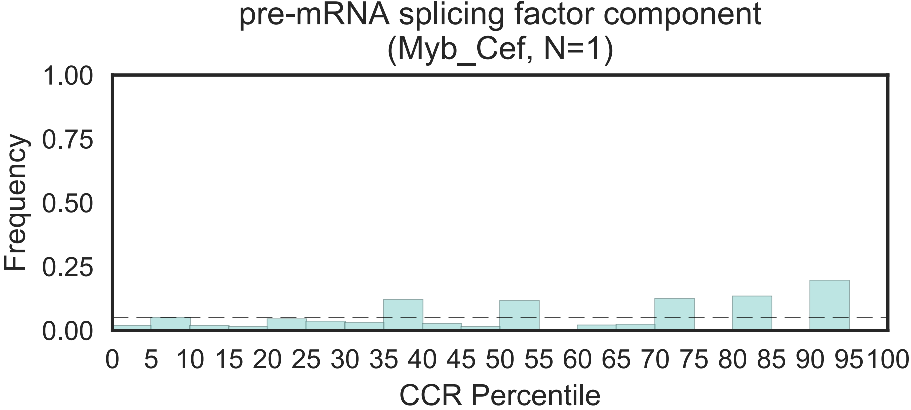

MutS family domain IV
(MutS_IV, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

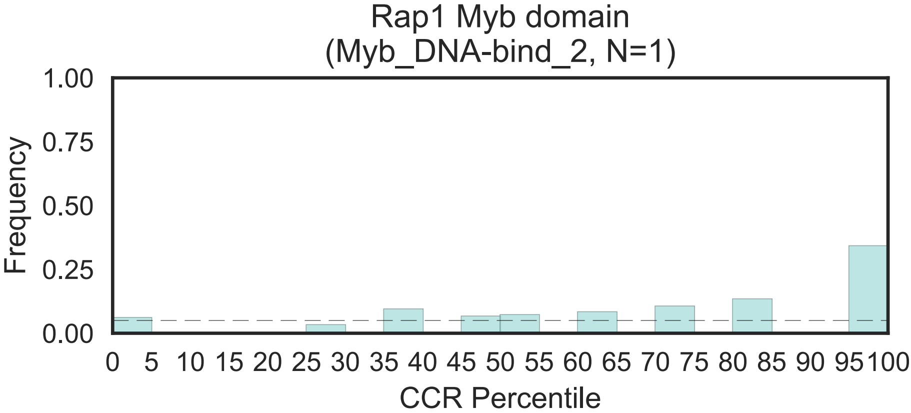


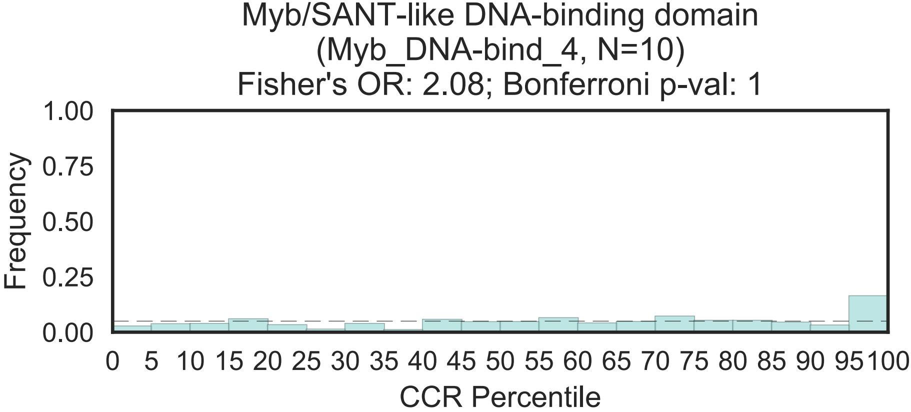
MutS domain V
(MutS_V, N=5)
Fisher's OR: 0; Bonferroni p-val: 1

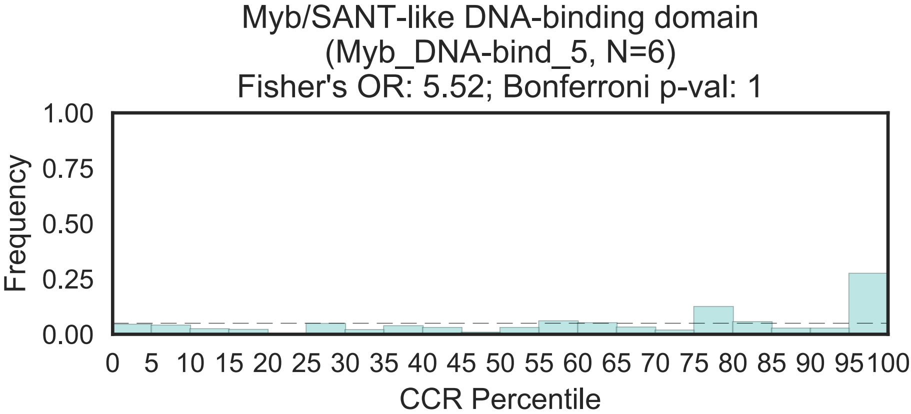

Organelle biogenesis, Muted-like protein
(Muted, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

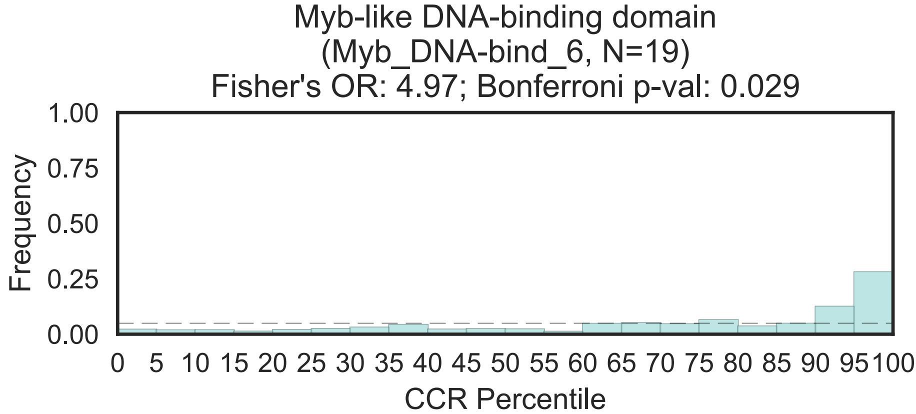

MyTH4 domain
(MyTH4, N=12)
Fisher's OR: 1.02; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

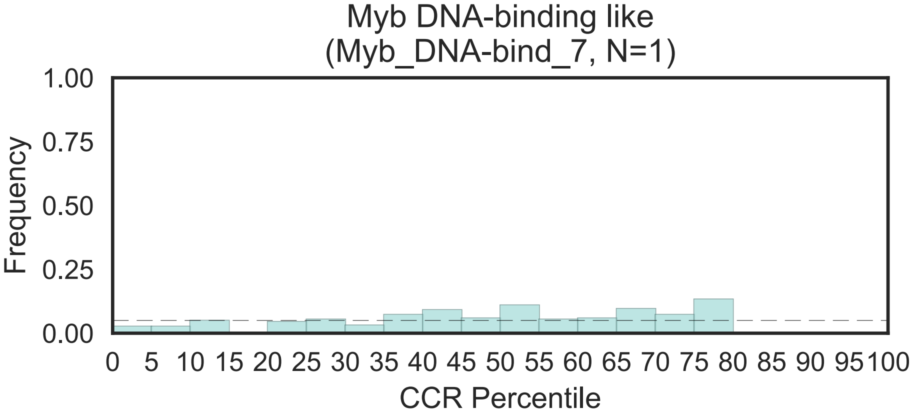

pre-mRNA splicing factor component
(Myb_Cef, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

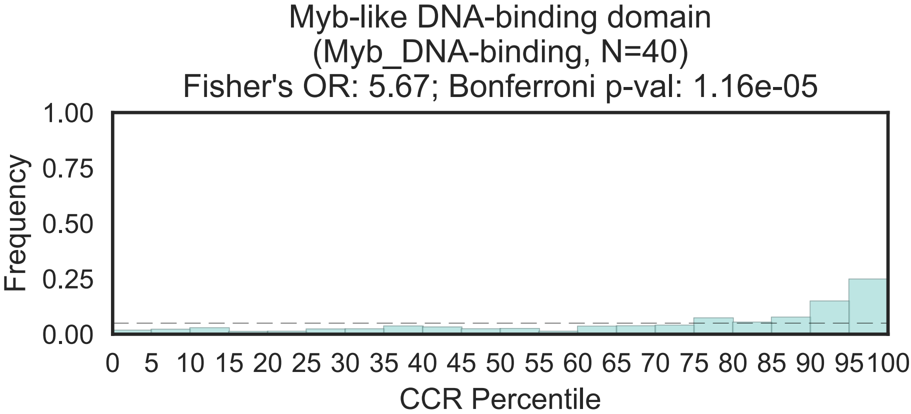

Rap1 Myb domain
(Myb_DNA-bind_2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

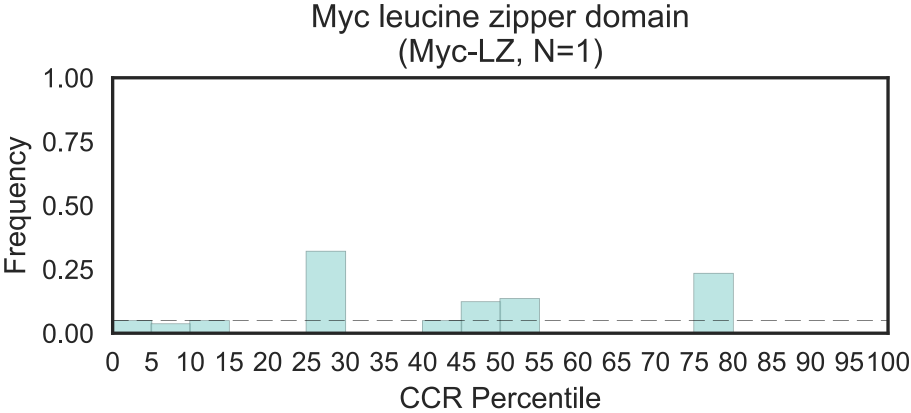

Myb/SANT-like DNA-binding domain
(Myb_DNA-bind_4, N=10)
Fisher's OR: 2.08; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

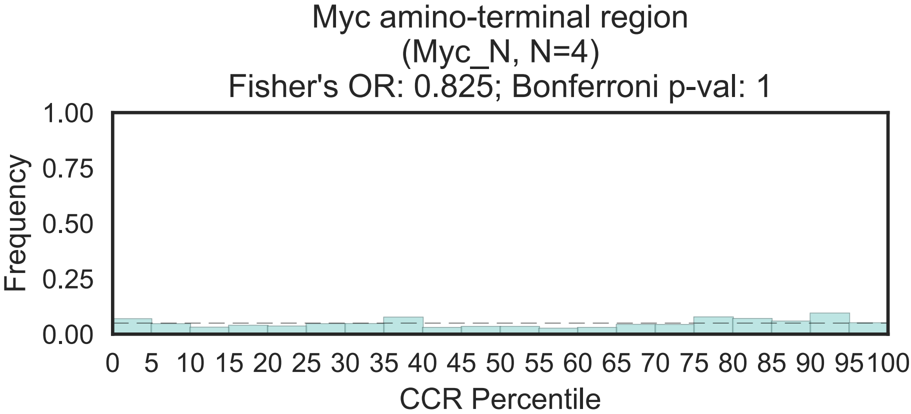

Myb/SANT-like DNA-binding domain
(Myb_DNA-bind_5, N=6)
Fisher's OR: 5.52; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

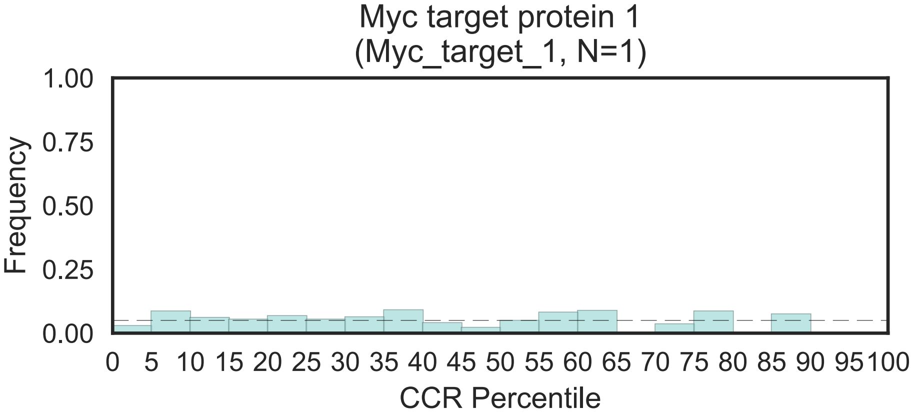

Myb-like DNA-binding domain
(Myb_DNA-bind_6, N=19)
Fisher's OR: 4.97; Bonferroni p-val: 0.029
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

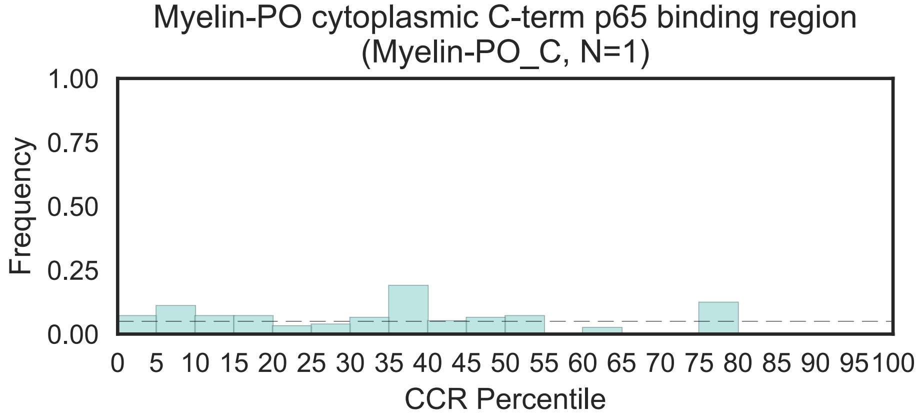

Myb DNA-binding like
(Myb_DNA-bind_7, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

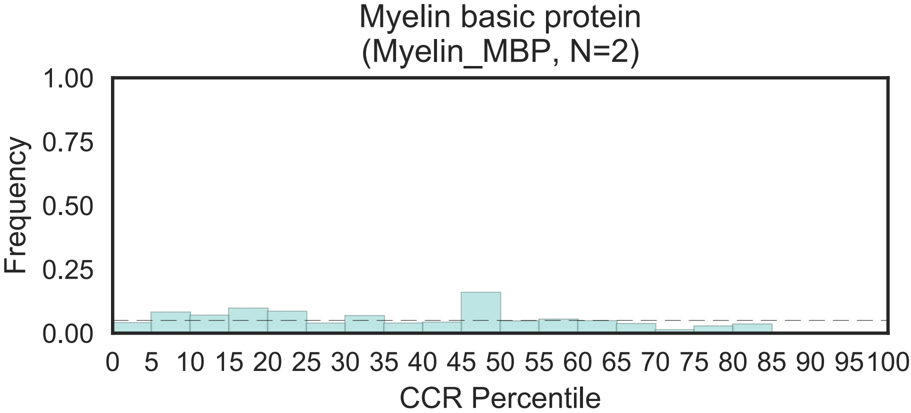

Myb-like DNA-binding domain
(Myb_DNA-binding, N=40)
Fisher's OR: 5.67; Bonferroni p-val: 1.16e-05
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

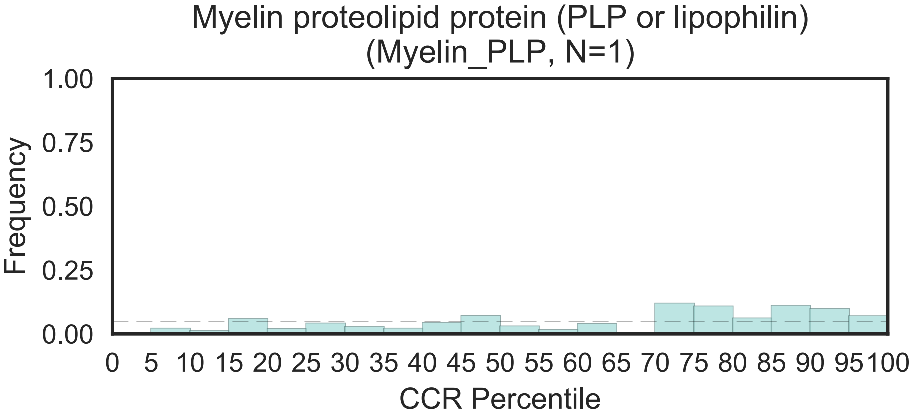

Myc leucine zipper domain
(Myc-LZ, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

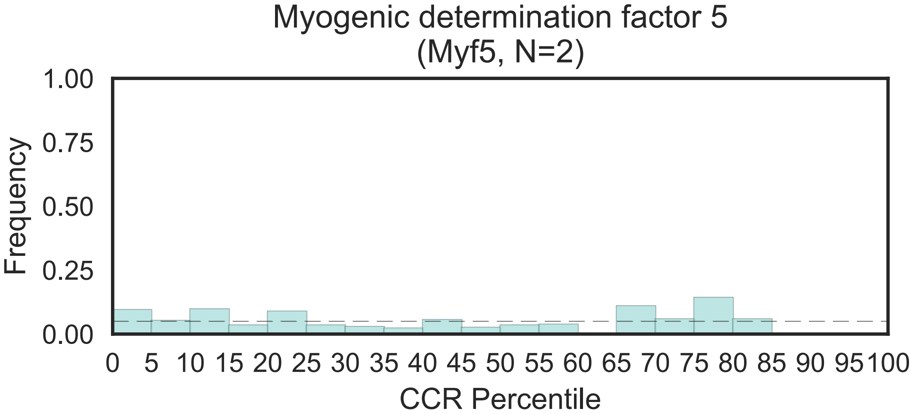

Myc amino-terminal region
(Myc_N, N=4)
Fisher's OR: 0.825; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

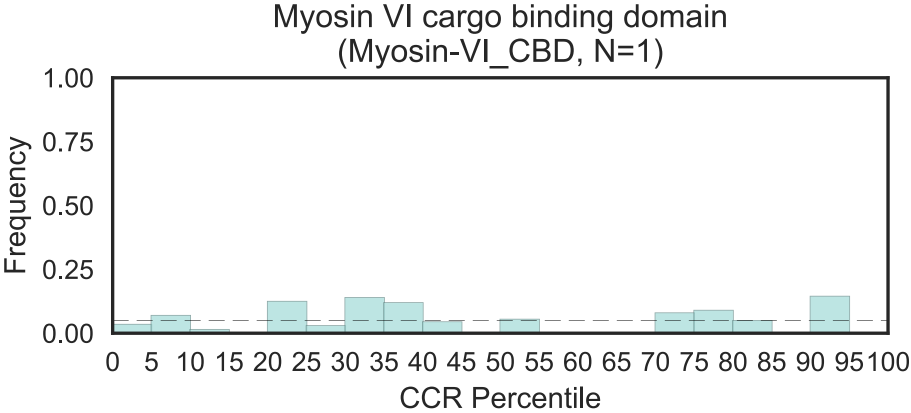

Myc target protein 1
(Myc_target_1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Myelin-PO cytoplasmic C-term p65 binding region
(Myelin-PO_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

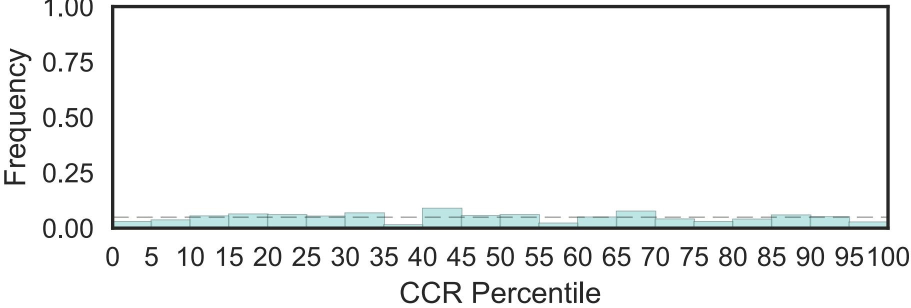

Myelin basic protein
(Myelin_MBP, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Myelin proteolipid protein (PLP or lipophilin)
(Myelin_PLP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

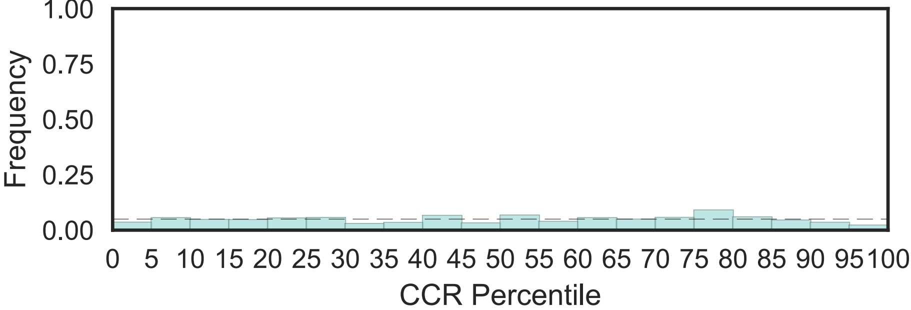

Myogenic determination factor 5
(Myf5, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

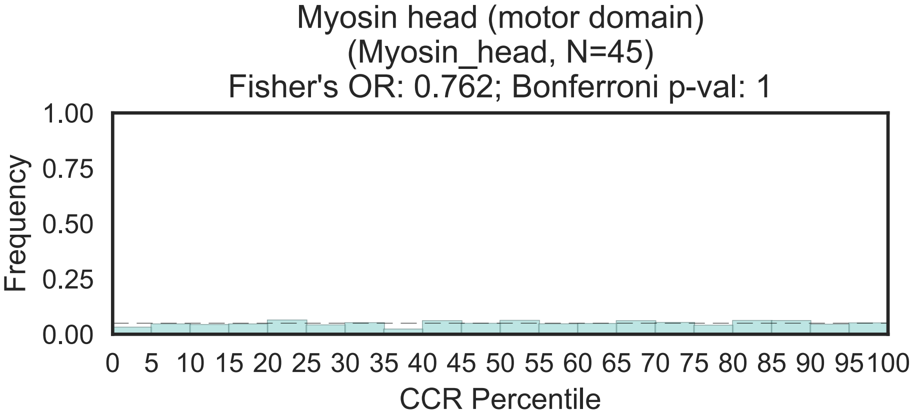

Myosin VI cargo binding domain
(Myosin-VI_CBD, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

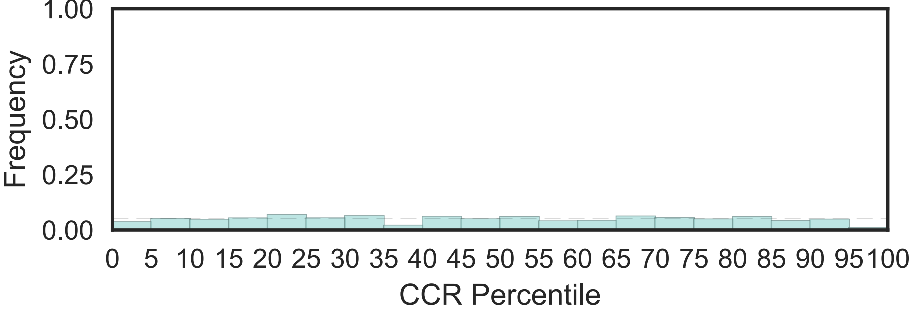
Myosin N-terminal SH3-like domain
(Myosin_N, N=14)
Fisher's OR: 0.498; Bonferroni p-val: 1



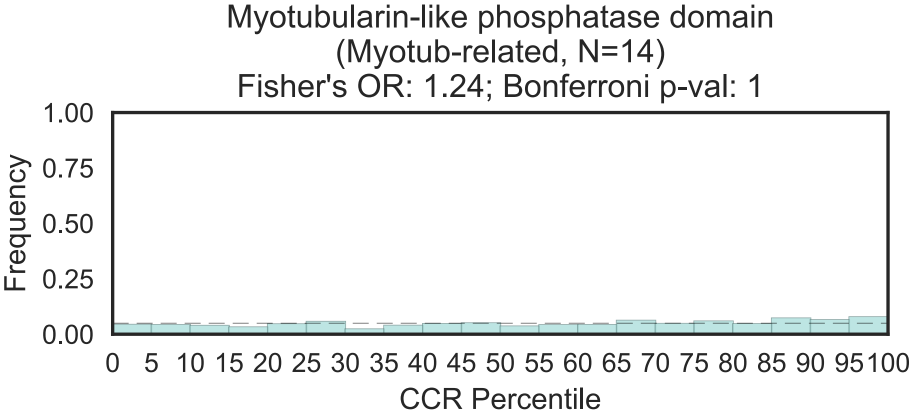
Unconventional myosin tail, actin- and lipid-binding
(Myosin_TH1, N=8)
Fisher's OR: 0.392; Bonferroni p-val: 1

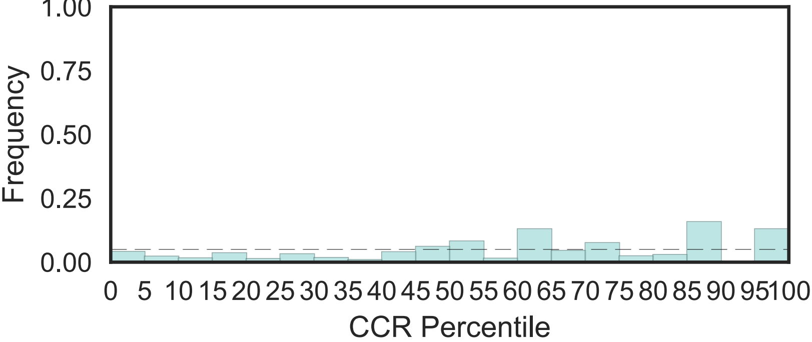


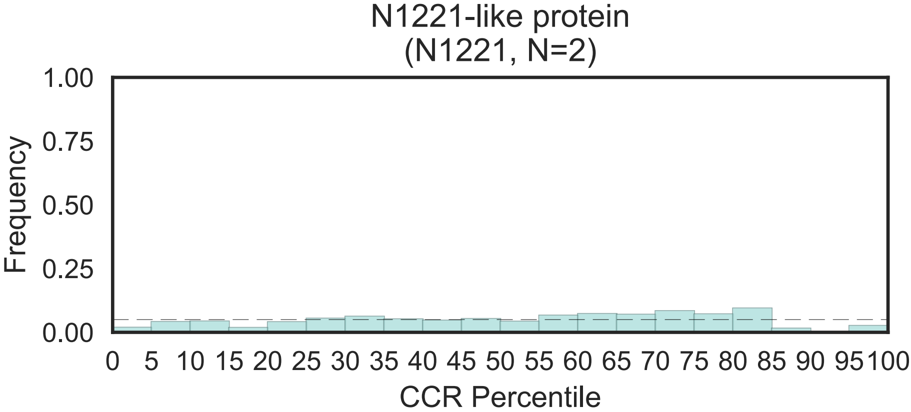

Myosin head (motor domain)
(Myosin_head, N=45)
Fisher's OR: 0.762; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

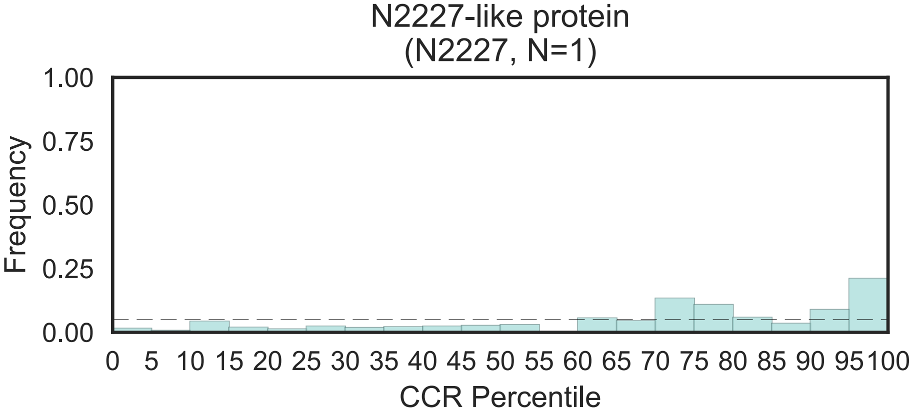


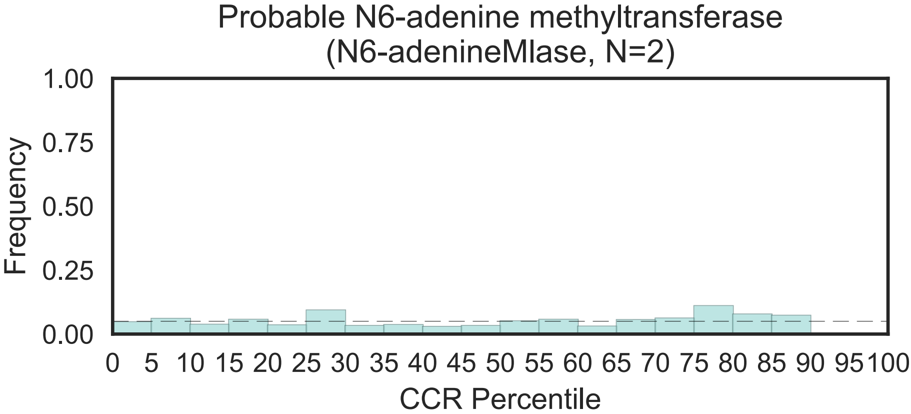
Myosin tail
(Myosin_tail_1, N=20)
Fisher's OR: 0.162; Bonferroni p-val: 7.54e-12

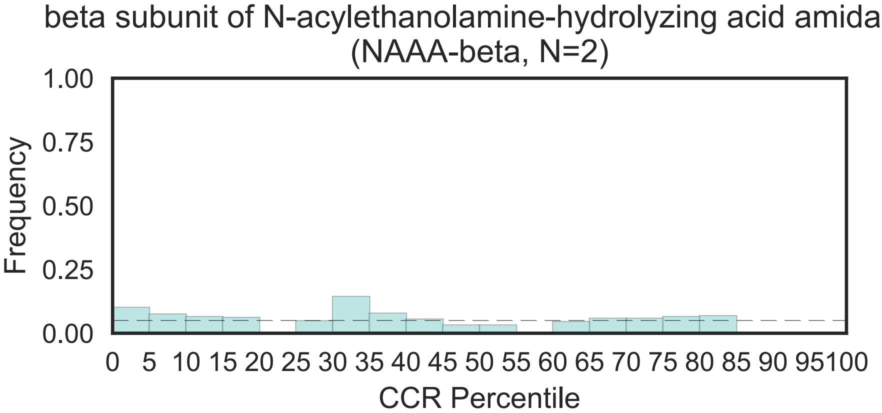

Myotubularin-like phosphatase domain
(Myotub-related, N=14)
Fisher's OR: 1.24; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

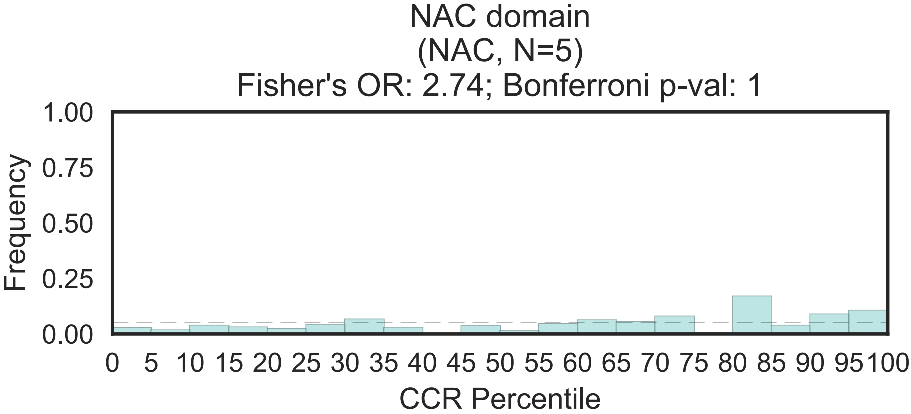

COMPASS (Complex proteins associated with Set1p) component N (N-SET, N=2)

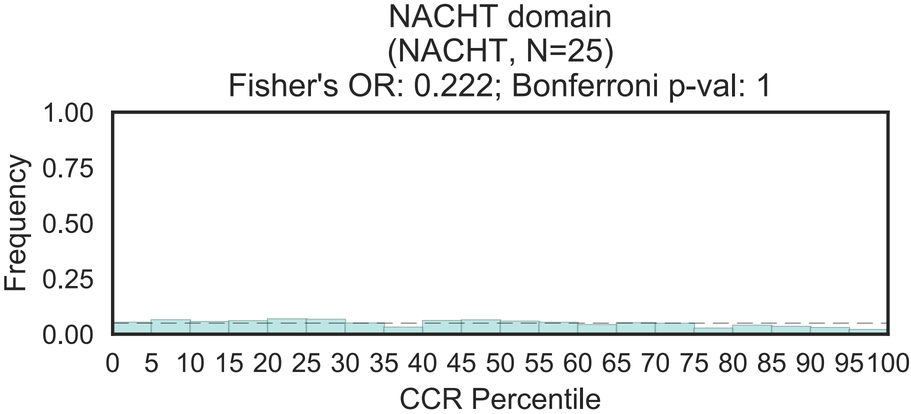

N1221-like protein
(N1221, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

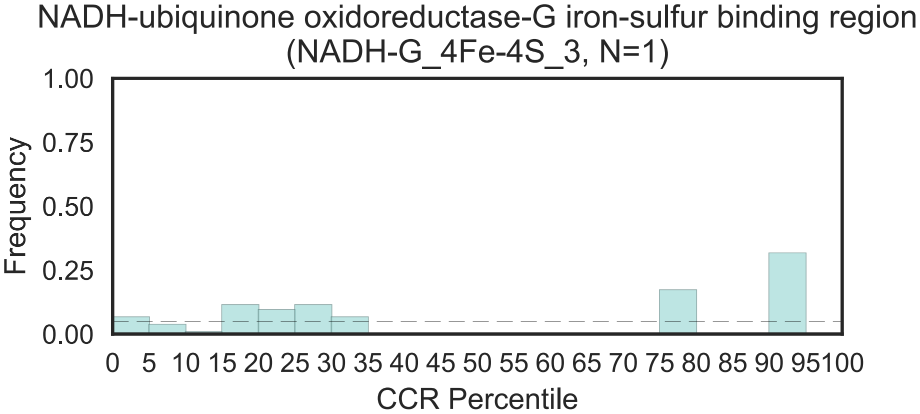

N2227-like protein
(N2227, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

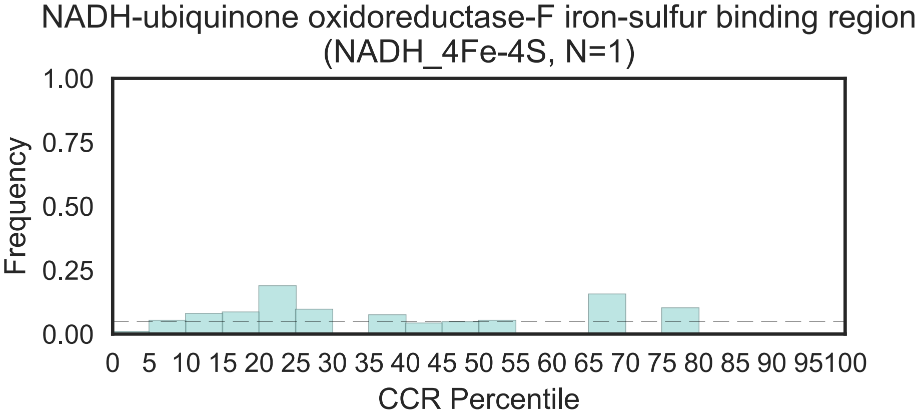

Probable N6-adenine methyltransferase
(N6-adenineMlase, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

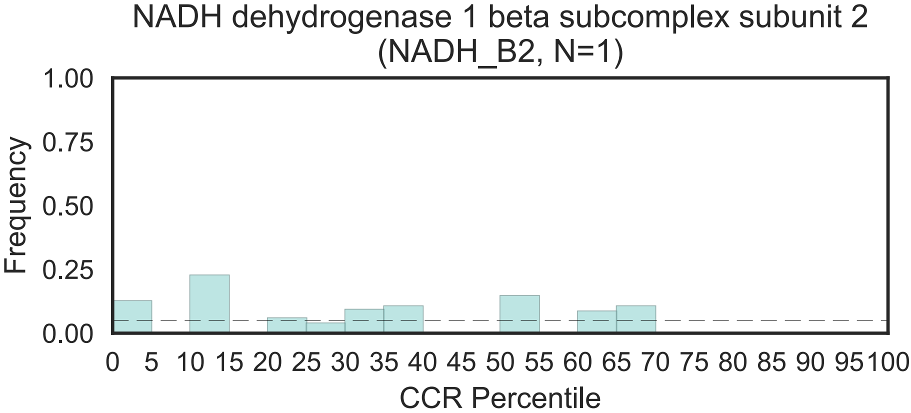

beta subunit of N-acylethanolamine-hydrolyzing acid amidase
(NAAA-beta, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

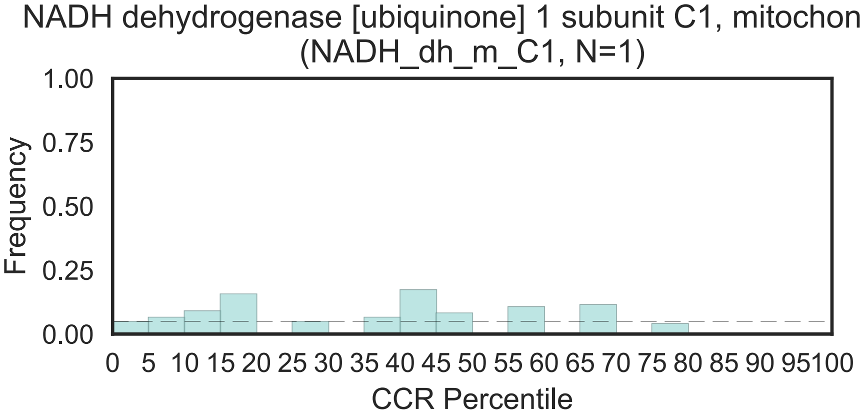

NAC domain
(NAC, N=5)
Fisher's OR: 2.74; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

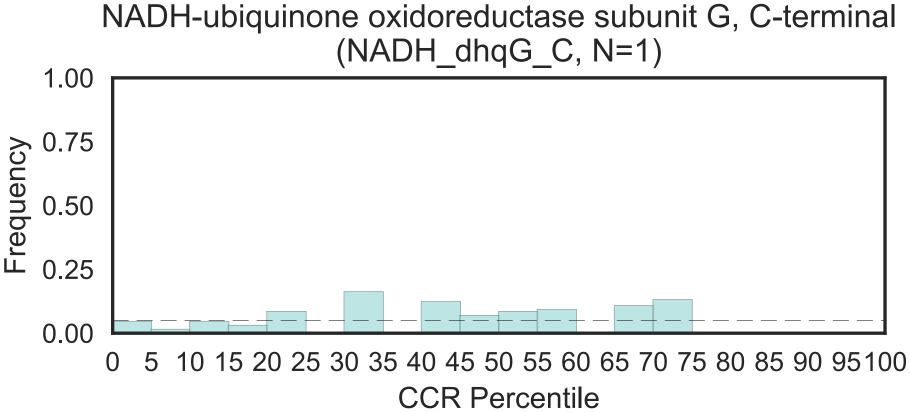

NACHT domain
(NACHT, N=25)
Fisher's OR: 0.222; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

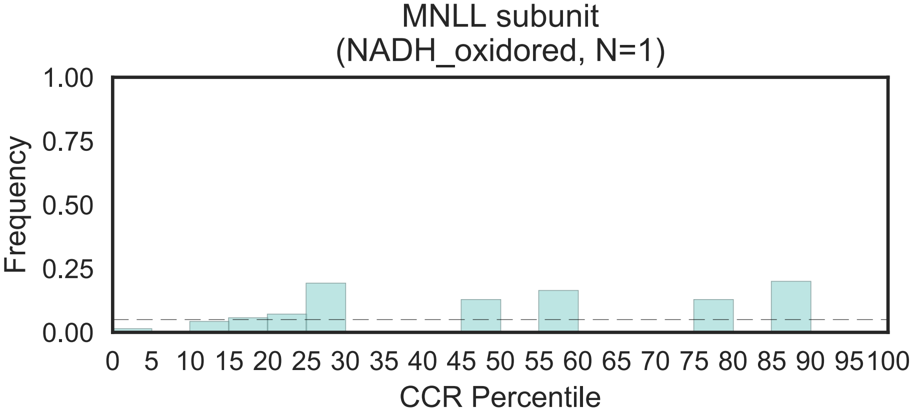

NADH-ubiquinone oxidoreductase-G iron-sulfur binding region
(NADH-G_4Fe-4S_3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

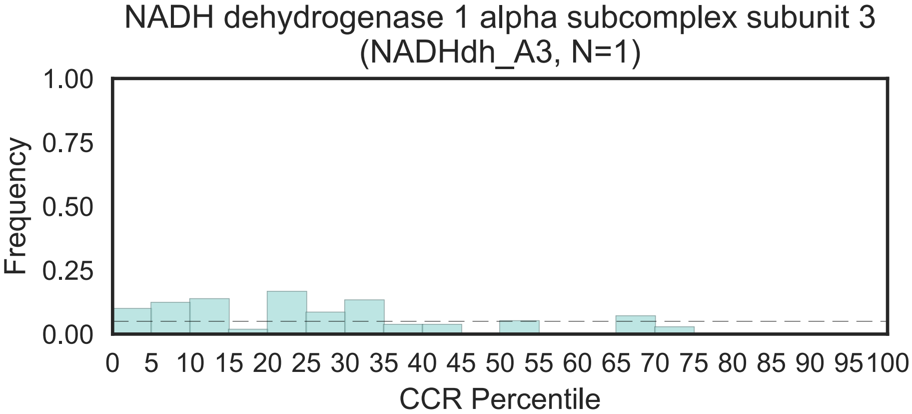

NADH-ubiquinone oxidoreductase-F iron-sulfur binding region
(NADH_4Fe-4S, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


NADH dehydrogenase 1 beta subcomplex subunit 2
(NADH_B2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

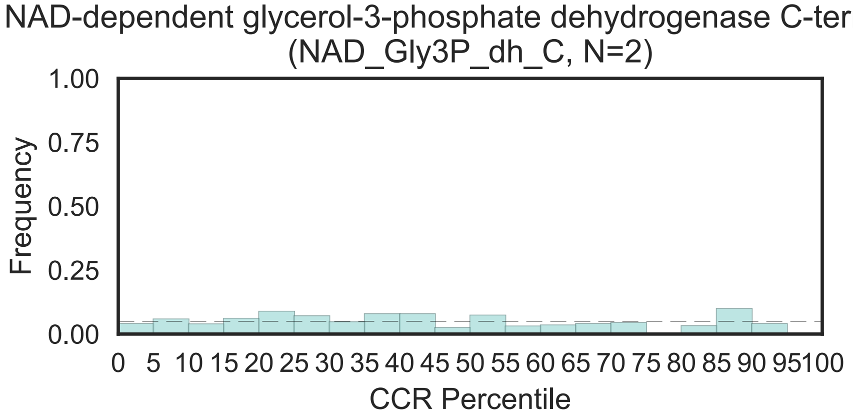

NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial
(NADH_dh_m_C1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

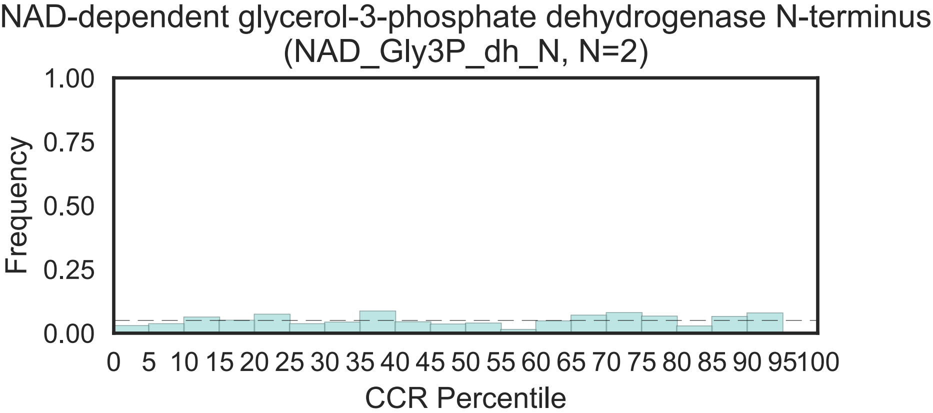

NADH-ubiquinone oxidoreductase subunit G, C-terminal
(NADH_dhqG_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

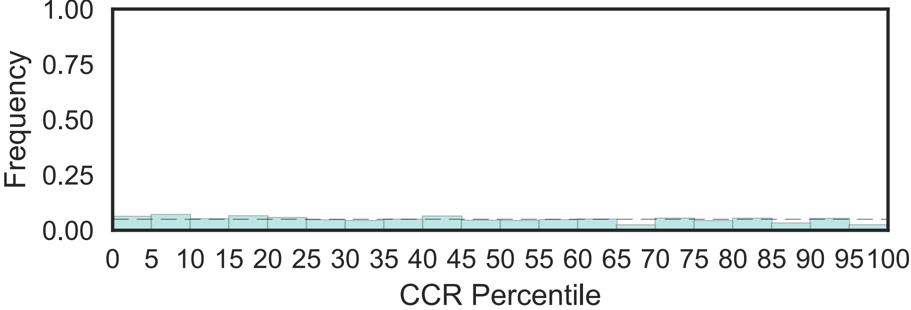

MNLL subunit
(NADH_oxidored, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile



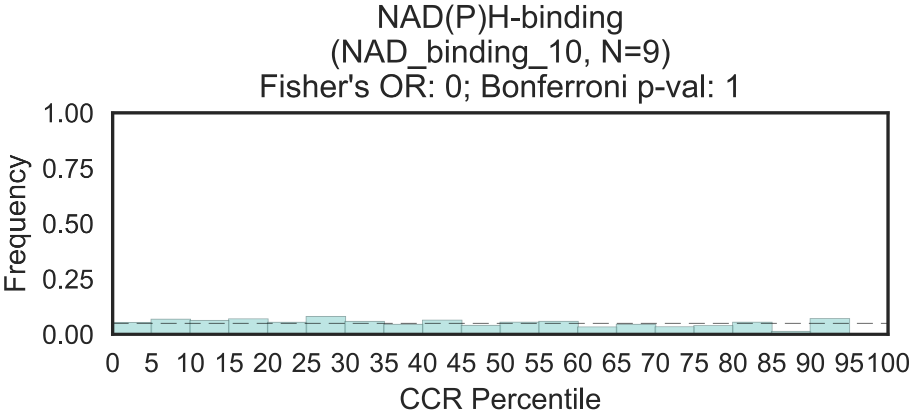
NADH dehydrogenase 1 alpha subcomplex subunit 3 (NADHdh_A3, N=1)

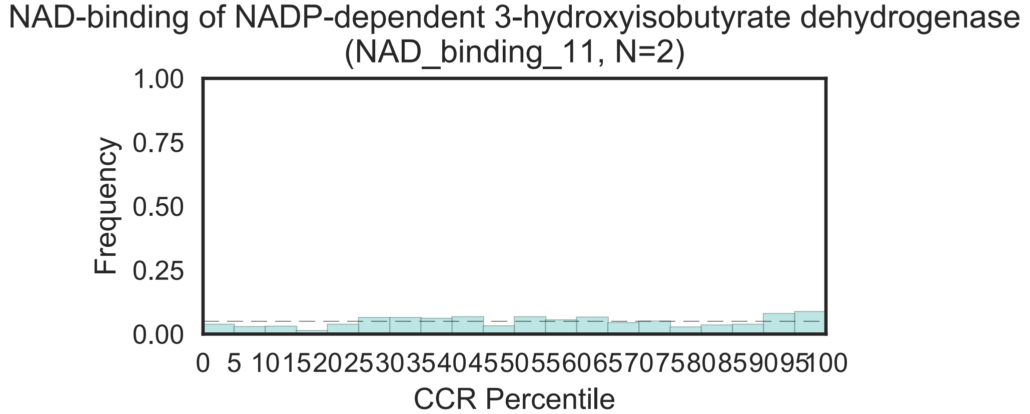

NAD-dependent glycerol-3-phosphate dehydrogenase C-terminus
(NAD_Gly3P_dh_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

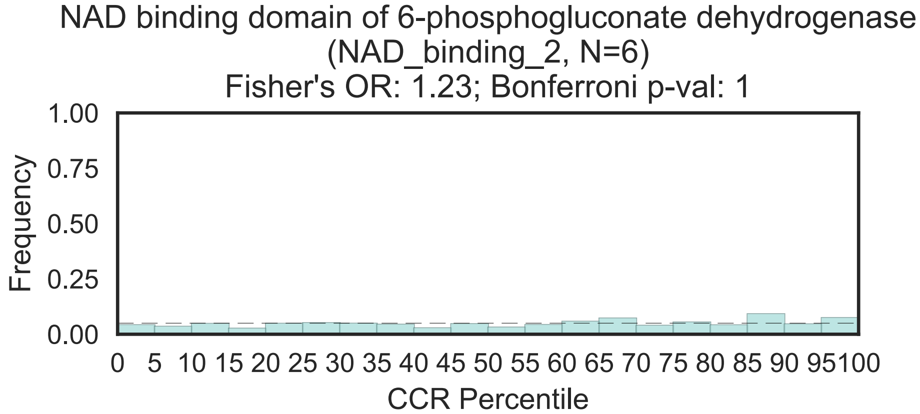

NAD-dependent glycerol-3-phosphate dehydrogenase N-terminus
(NAD_Gly3P_dh_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



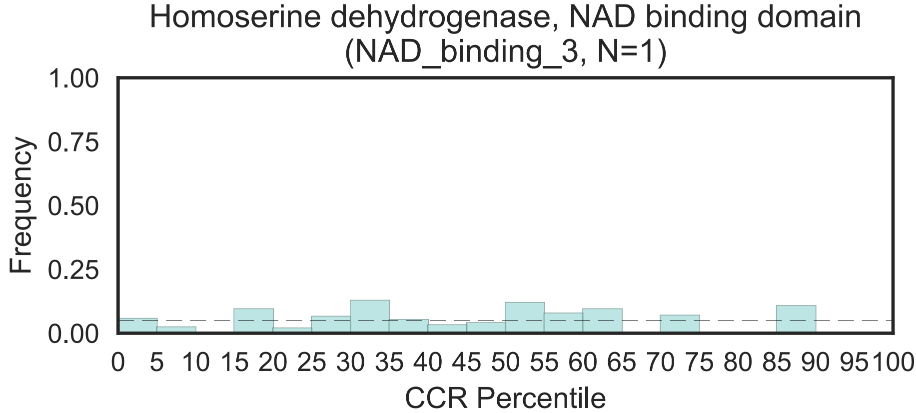
Oxidoreductase NAD-binding domain
(NAD_binding_1, N=12)
Fisher's OR: 0.395; Bonferroni p-val: 1

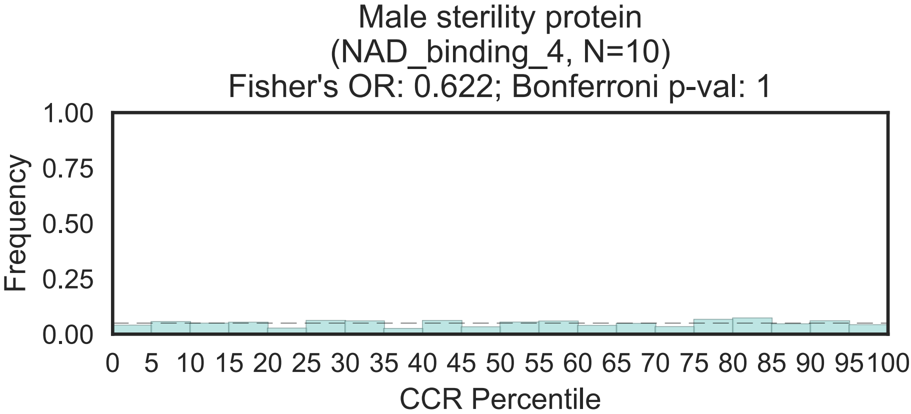

NAD(P)H-binding
(NAD_binding_10, N=9)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

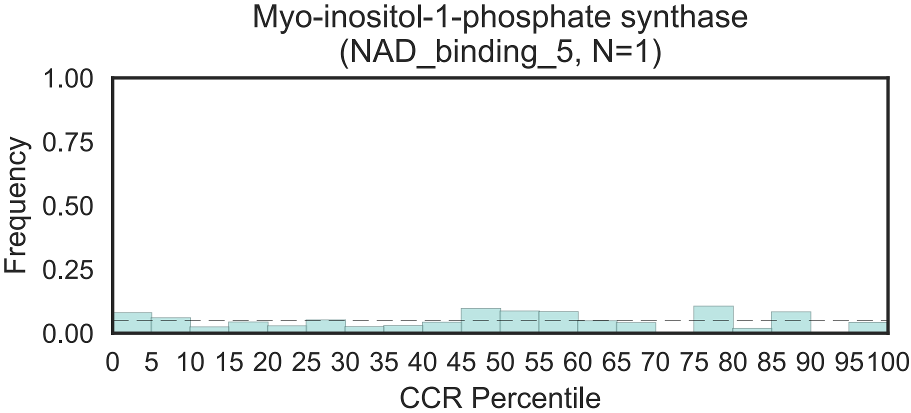

NAD-binding of NADP-dependent 3-hydroxyisobutyrate dehydrogenase
(NAD_binding_11, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

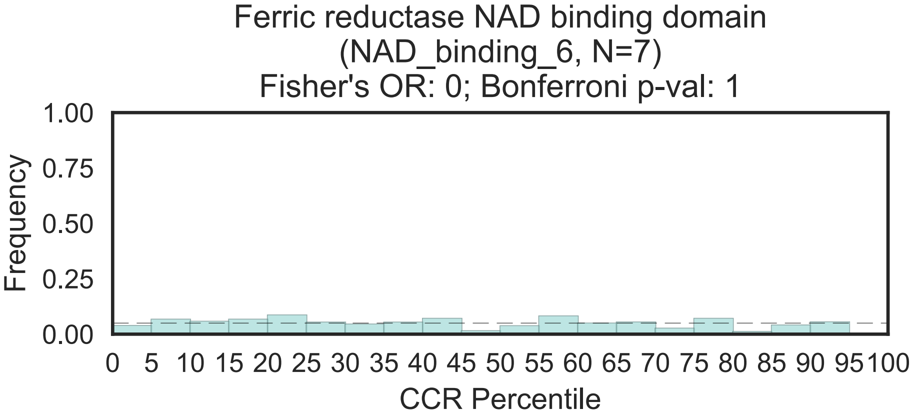


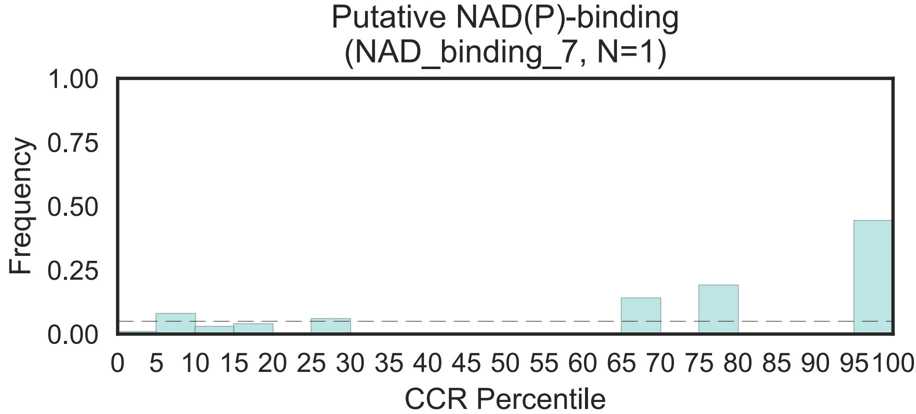
NAD binding domain of 6-phosphogluconate dehydrogenase
(NAD_binding_2, N=6)
Fisher's OR: 1.23; Bonferroni p-val: 1

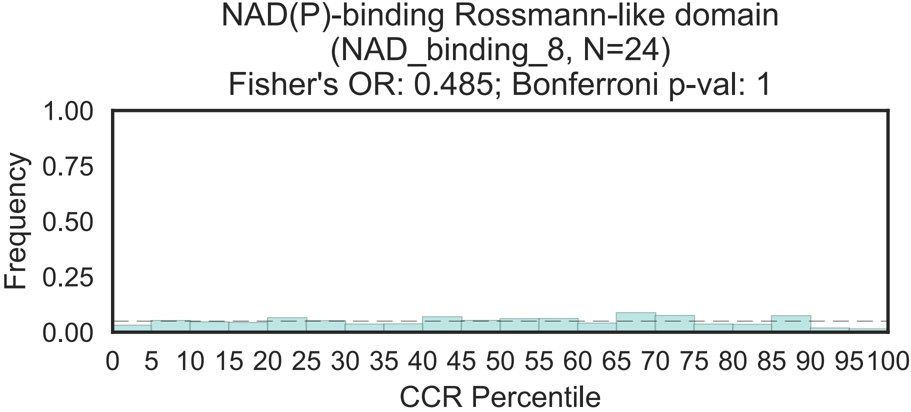

Homoserine dehydrogenase, NAD binding domain
(NAD_binding_3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

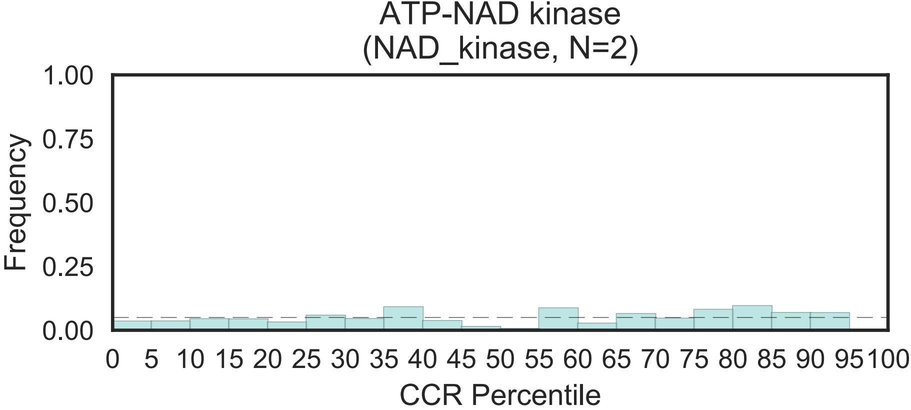

Male sterility protein
(NAD_binding_4, N=10)
Fisher's OR: 0.622; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

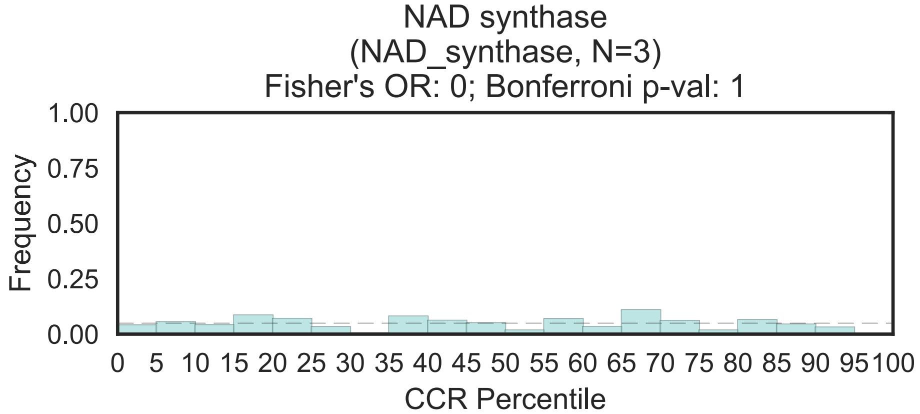

Myo-inositol-1-phosphate synthase
(NAD_binding_5, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

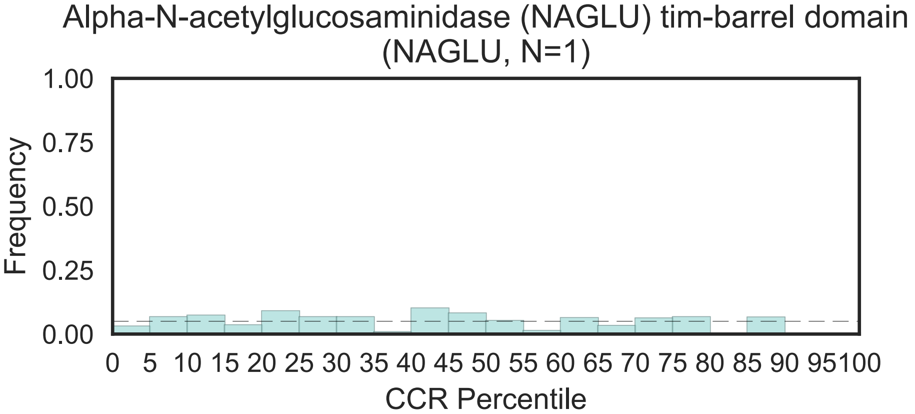

Ferric reductase NAD binding domain
(NAD_binding_6, N=7)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Putative NAD(P)-binding
(NAD_binding_7, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

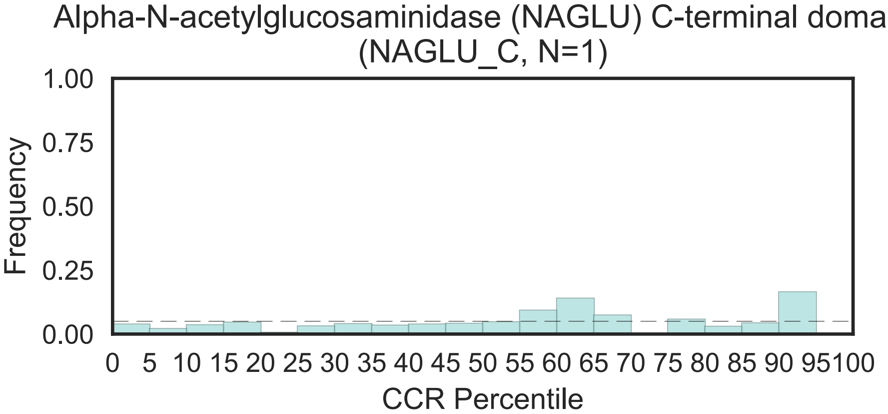

NAD(P)-binding Rossmann-like domain
(NAD_binding_8, N=24)
Fisher's OR: 0.485; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

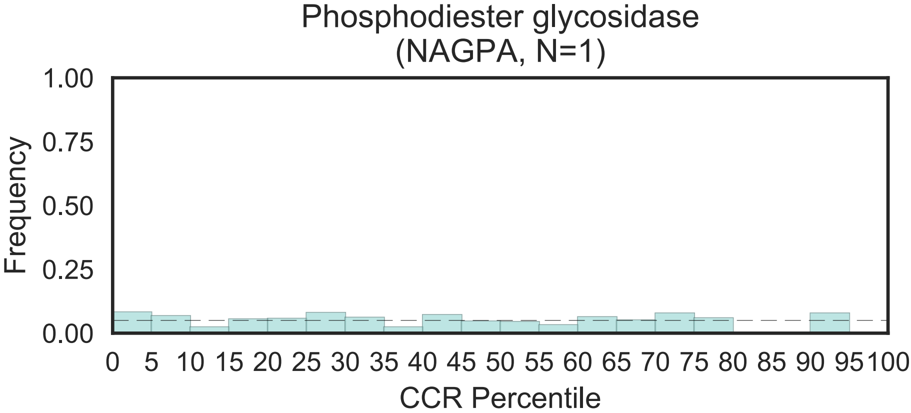

ATP-NAD kinase
(NAD_kinase, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

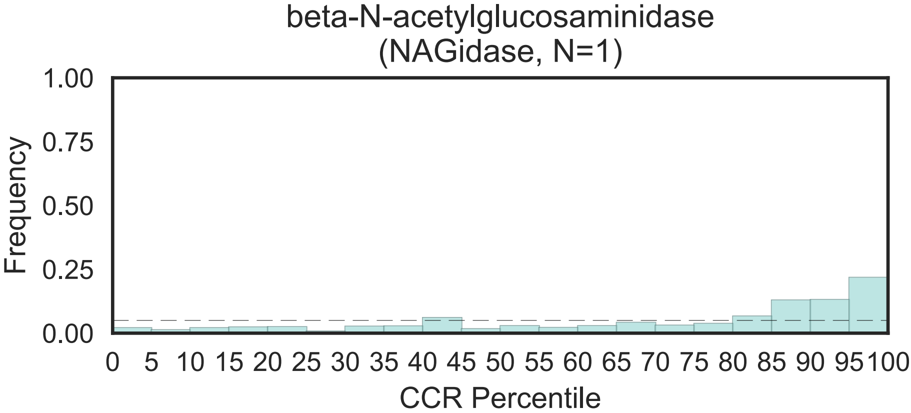

NAD synthase
(NAD_synthase, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

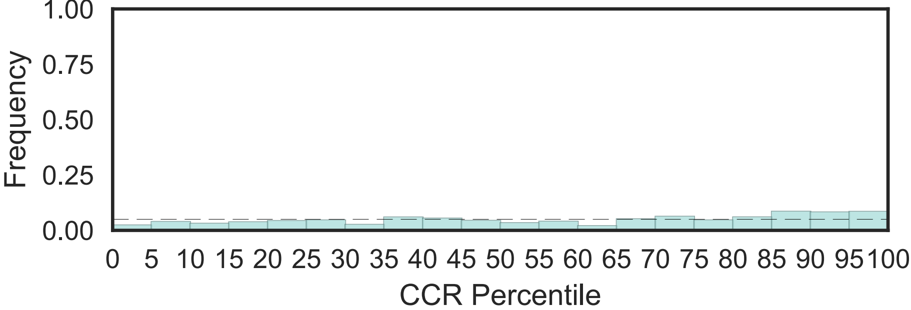


Alpha-N-acetylglucosaminidase (NAGLU) tim-barrel domain (NAGLU, N=1)

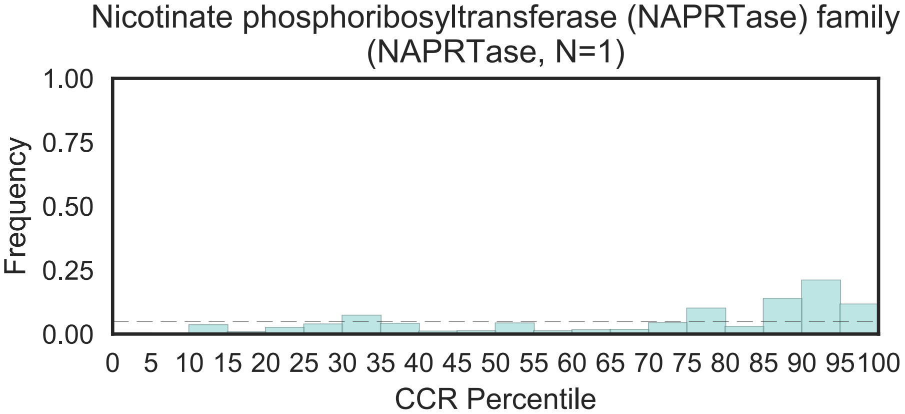

Alpha-N-acetylglucosaminidase (NAGLU) C-terminal domain
(NAGLU_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

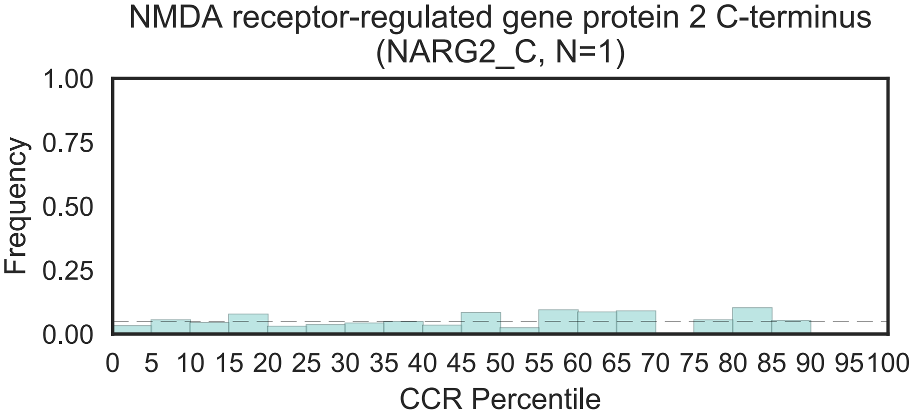

Phosphodiester glycosidase
(NAGPA, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

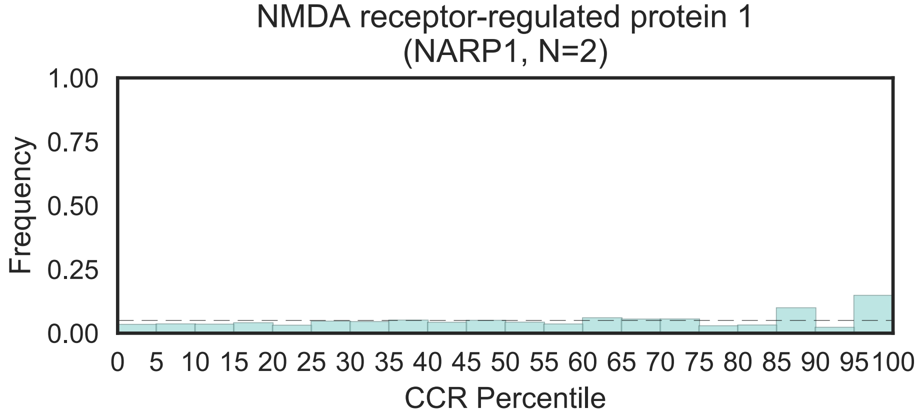

beta-N-acetylglucosaminidase
(NAGidase, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

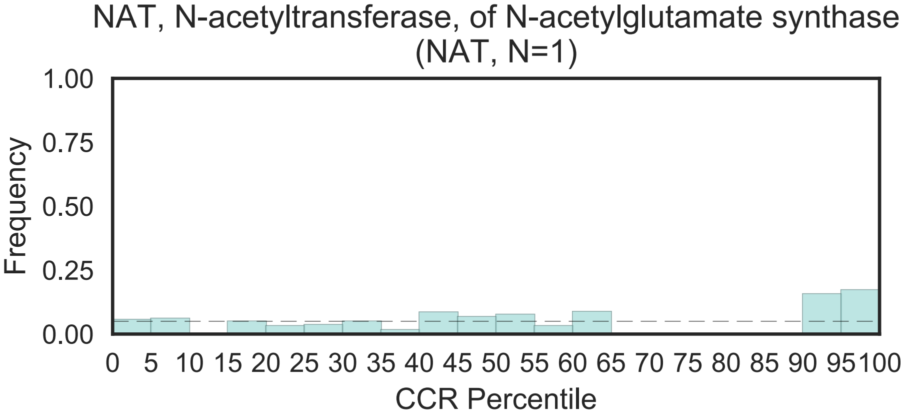


Nucleosome assembly protein (NAP)
(NAP, N=8)
Fisher's OR: 1.69; Bonferroni p-val: 1

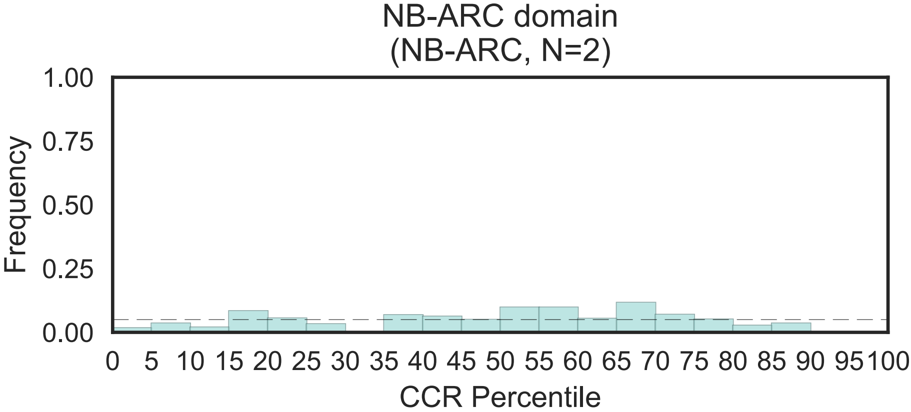

Nicotinate phosphoribosyltransferase (NAPRTase) family
(NAPRTase, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

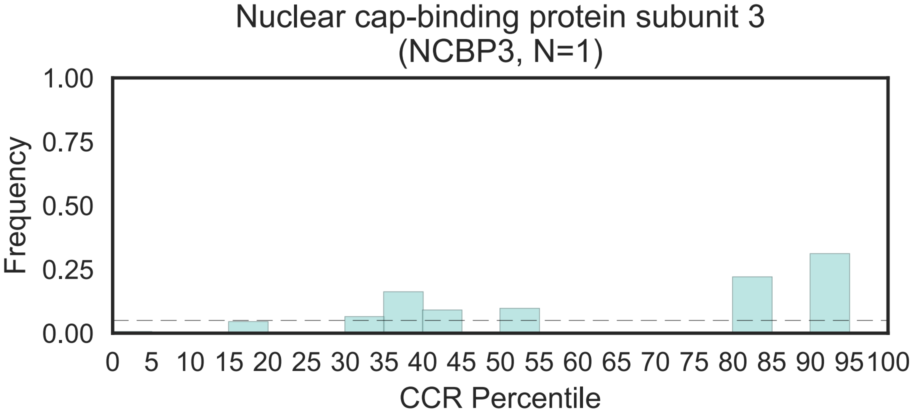

NMDA receptor-regulated gene protein 2 C-terminus
(NARG2_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

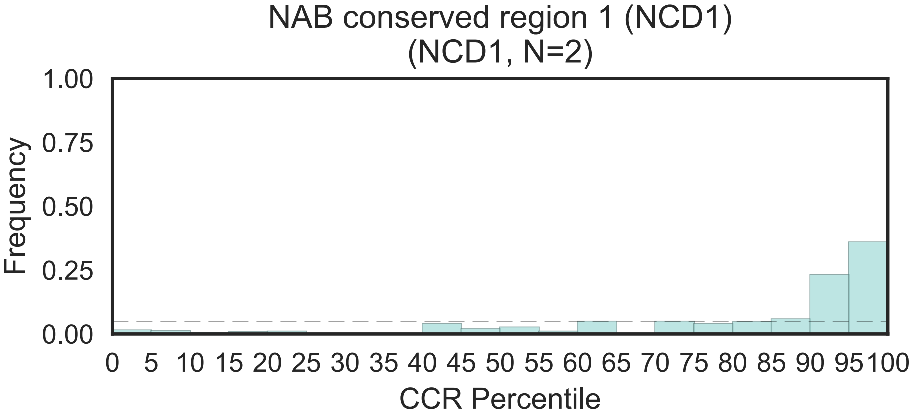

NMDA receptor-regulated protein 1
(NARP1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

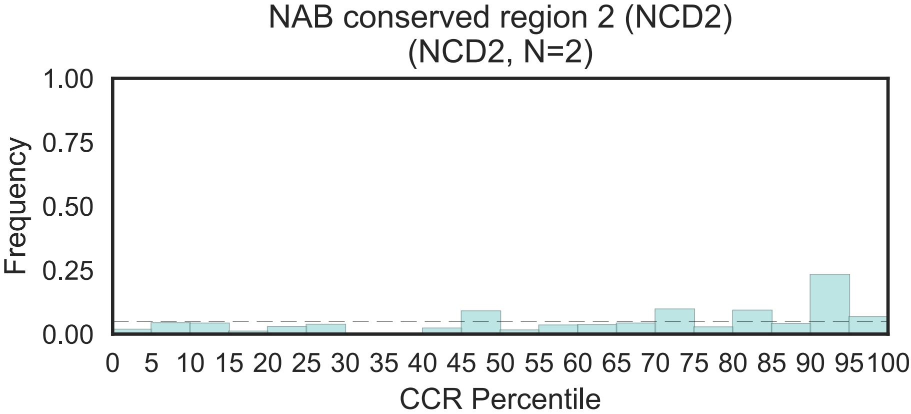


NAT, N-acetyltransferase, of N-acetylglutamate synthase (NAT, N=1)

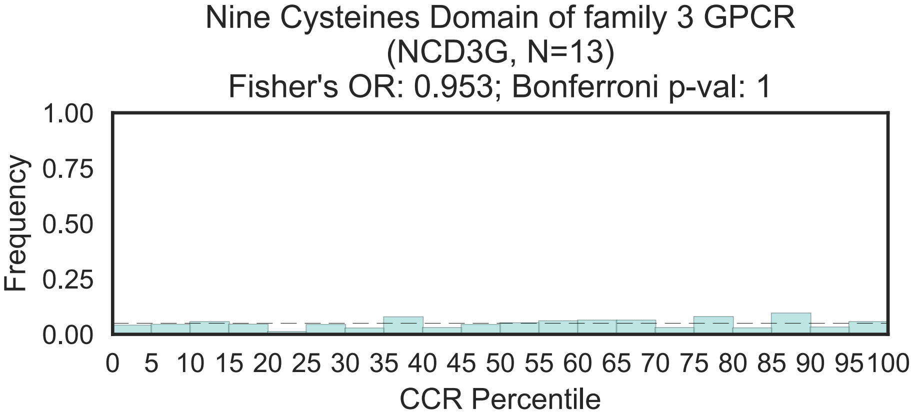

NB-ARC domain
(NB-ARC, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

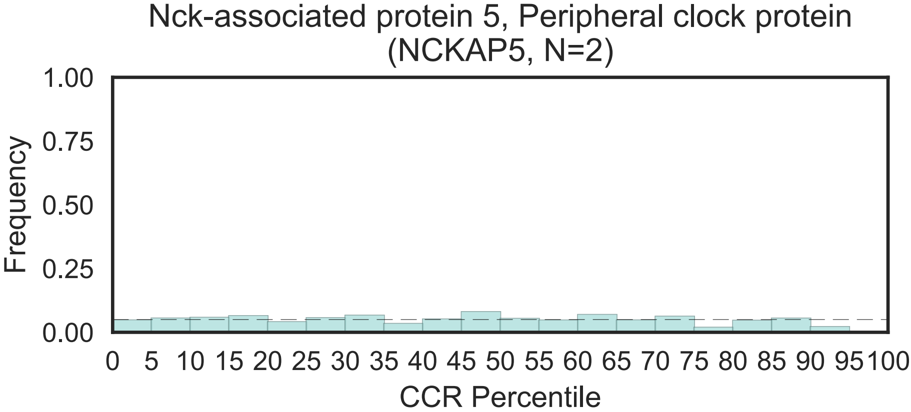

Nuclear cap-binding protein subunit 3
(NCBP3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

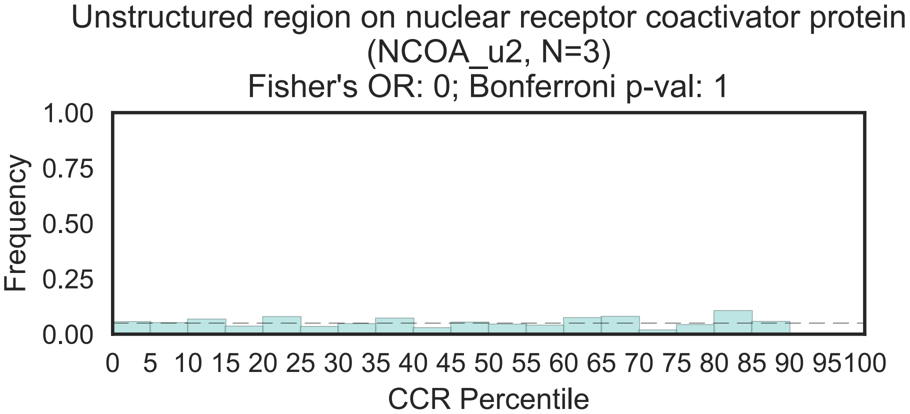

NAB conserved region 1 (NCD1)
(NCD1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



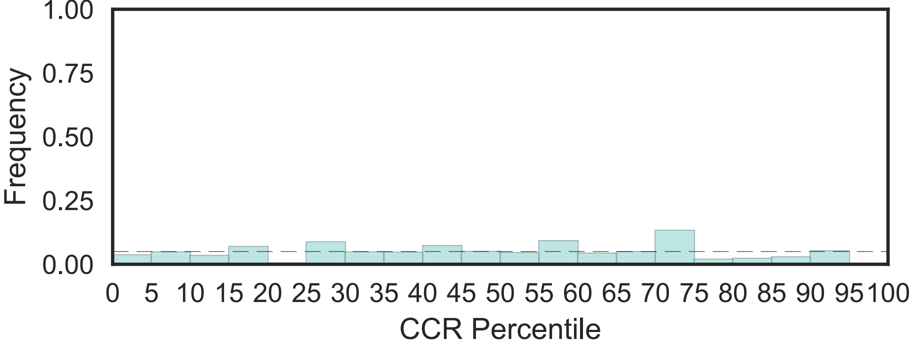
NAB conserved region 2 (NCD2)
(NCD2, N=2)

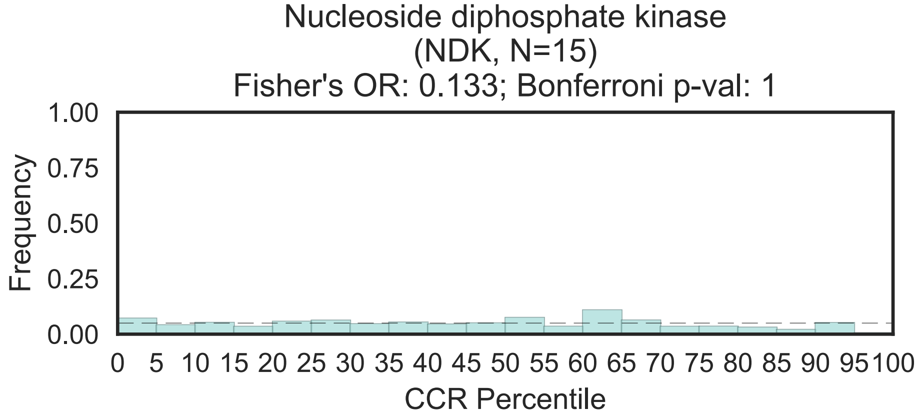

Nine Cysteines Domain of family 3 GPCR
(NCD3G, N=13)
Fisher's OR: 0.953; Bonferroni p-val: 1

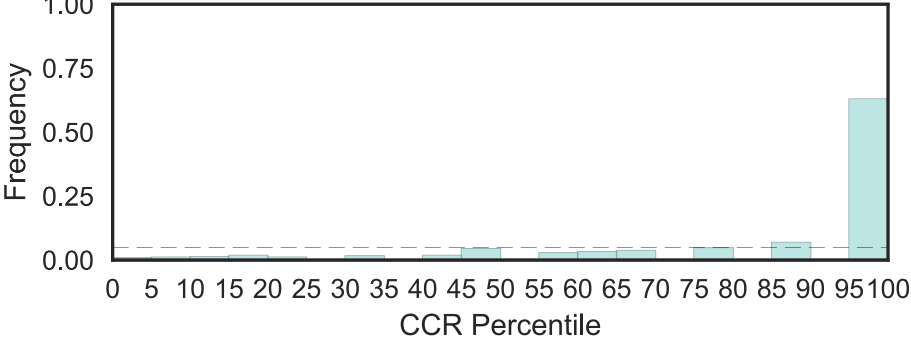

Nck-associated protein 5, Peripheral clock protein
(NCKAP5, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Unstructured region on nuclear receptor coactivator protein
(NCOA_u2, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

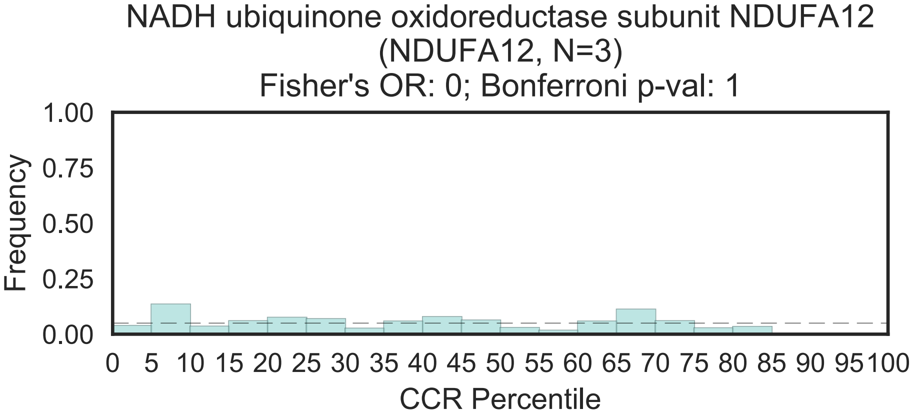
Lysosomal transcription factor, NCU-G1
(NCU-G1, N=1)

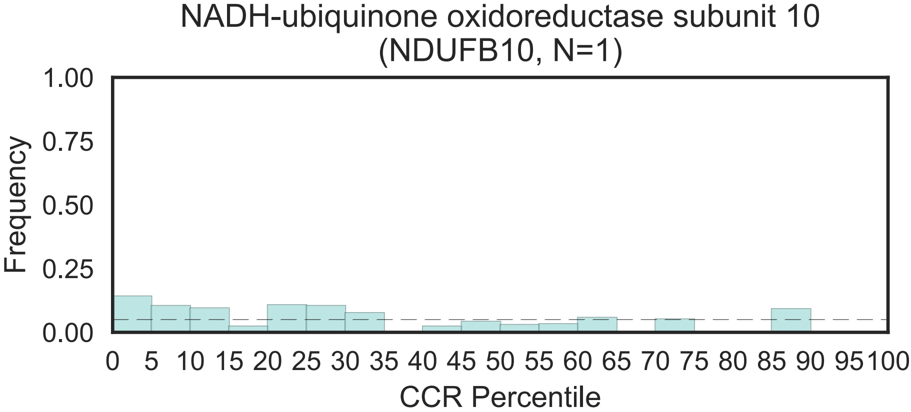


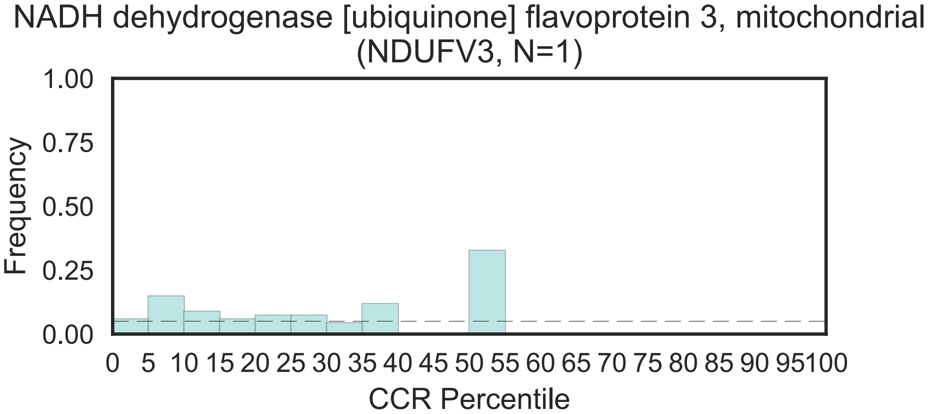

Nucleoside diphosphate kinase
(NDK, N=15)
Fisher's OR: 0.133; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

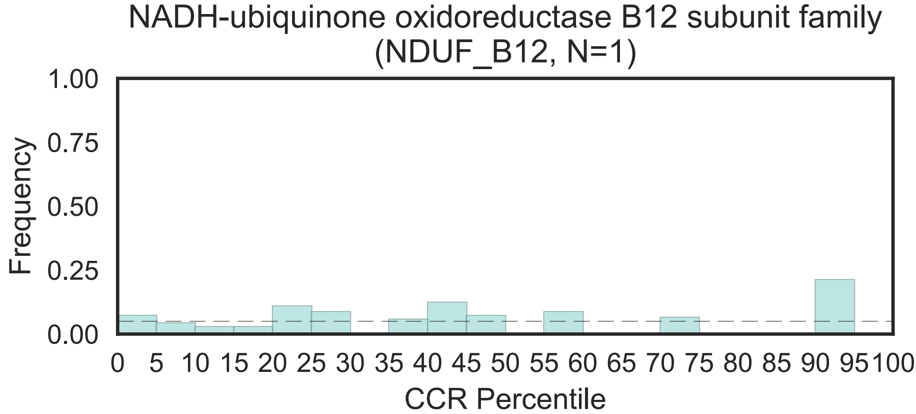


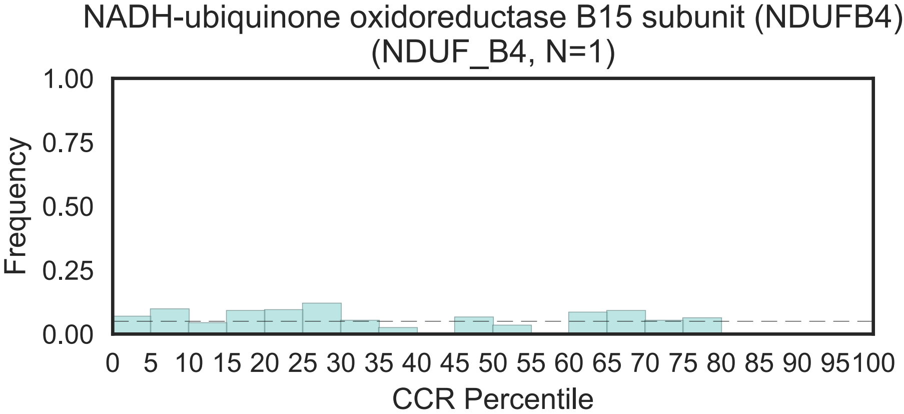
NDT80 / PhoG like DNA-binding family
(NDT80_PhoG, N=1)

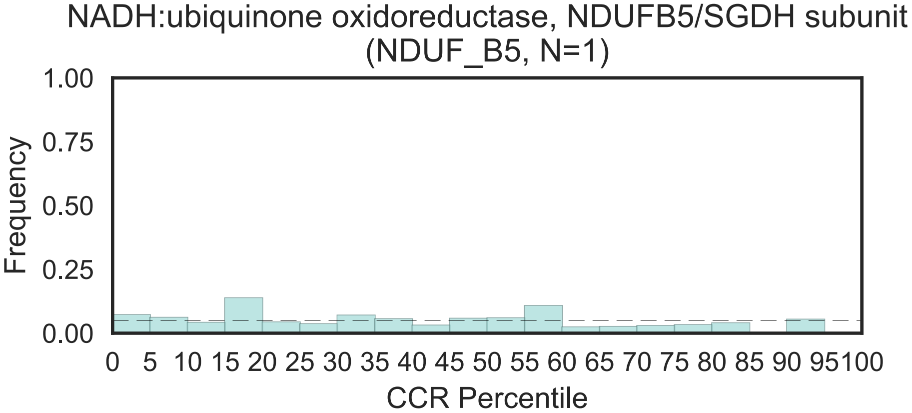

NADH ubiquinone oxidoreductase subunit NDUFA12
(NDUFA12, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

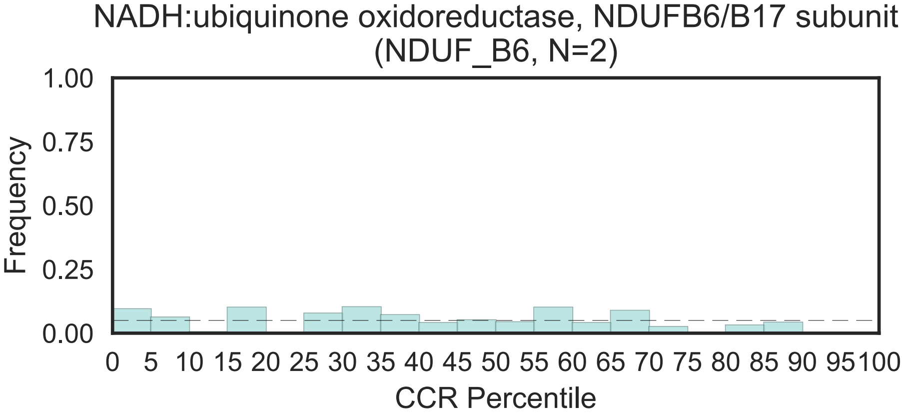

NADH-ubiquinone oxidoreductase subunit 10
(NDUFB10, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

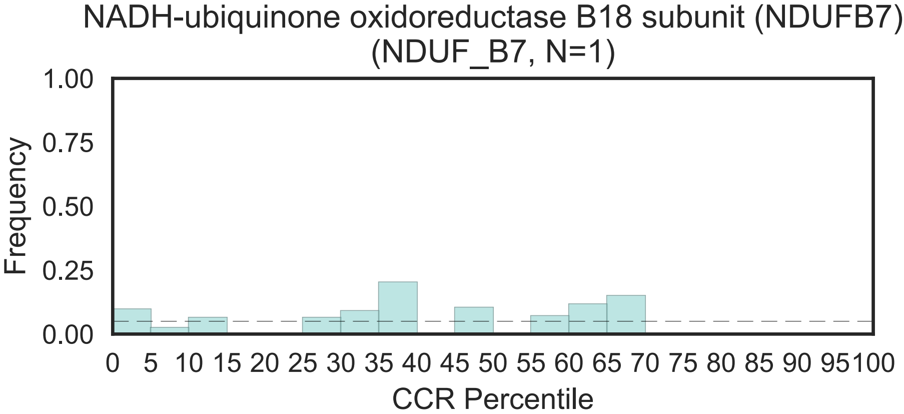

NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial
(NDUFV3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

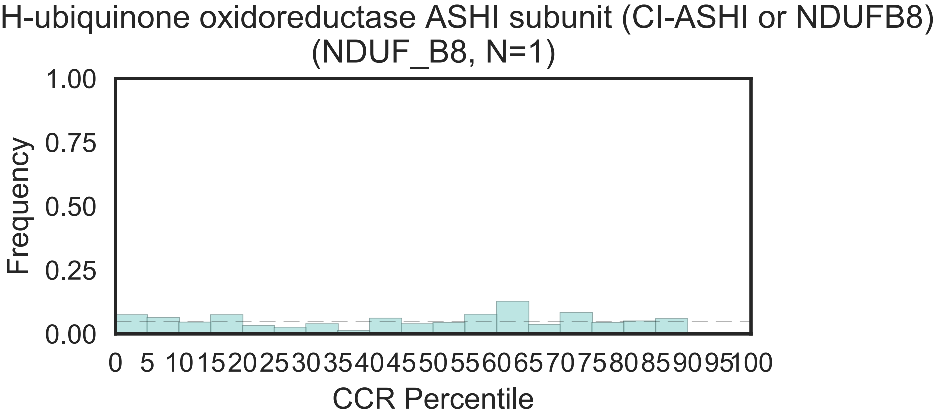

NADH-ubiquinone oxidoreductase B12 subunit family
(NDUF_B12, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


NADH-ubiquinone oxidoreductase B15 subunit (NDUFB4)
(NDUF_B4, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

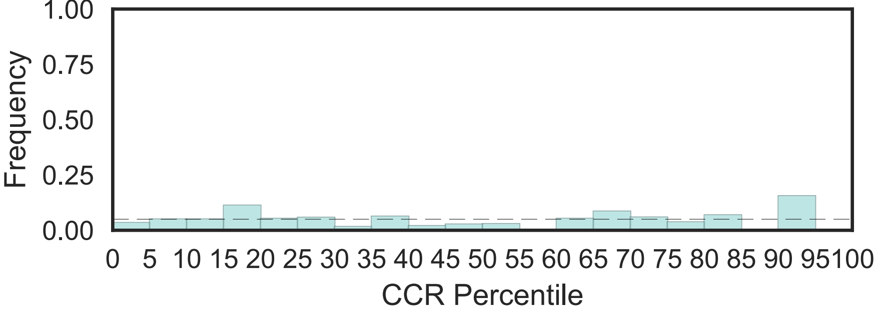

NADH:ubiquinone oxidoreductase, NDUFB5/SGDH subunit
(NDUF_B5, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

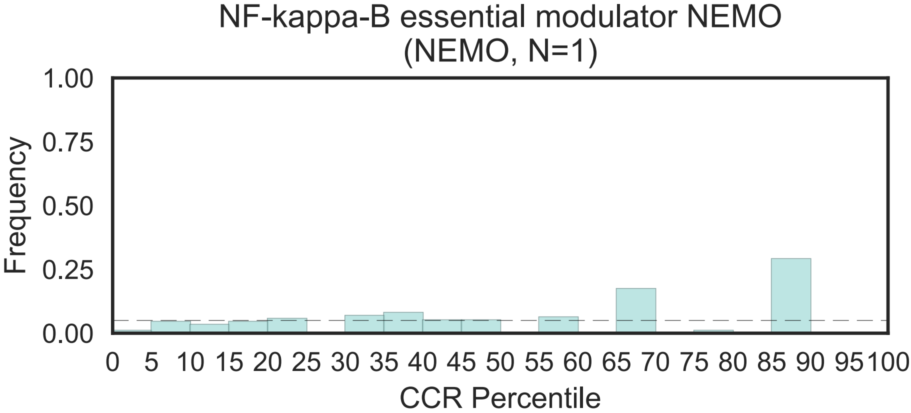

NADH:ubiquinone oxidoreductase, NDUFB6/B17 subunit
(NDUF_B6, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

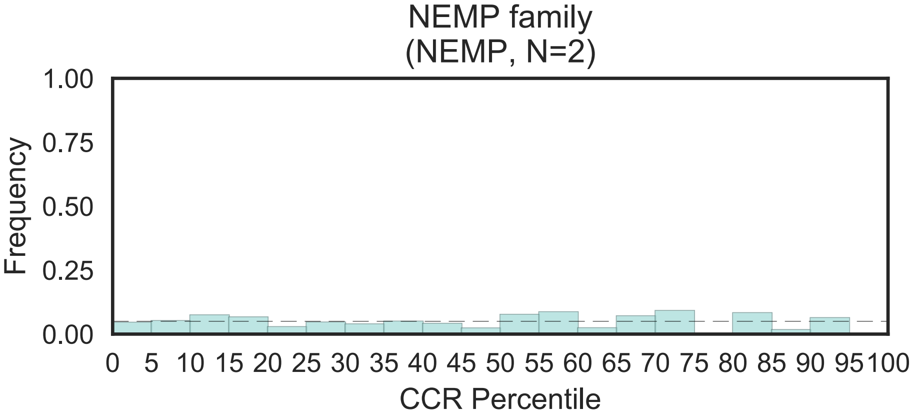

NADH-ubiquinone oxidoreductase B18 subunit (NDUFB7)
(NDUF_B7, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

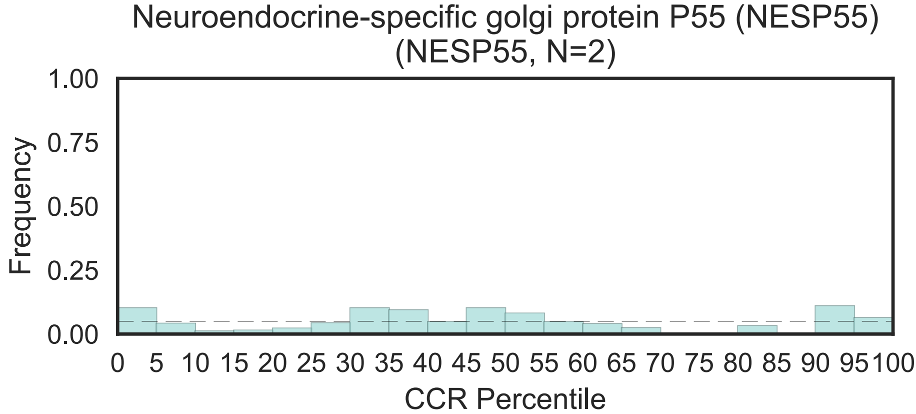

NADH-ubiquinone oxidoreductase ASHI subunit (CI-ASHI or NDUFB8)
(NDUF_B8, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

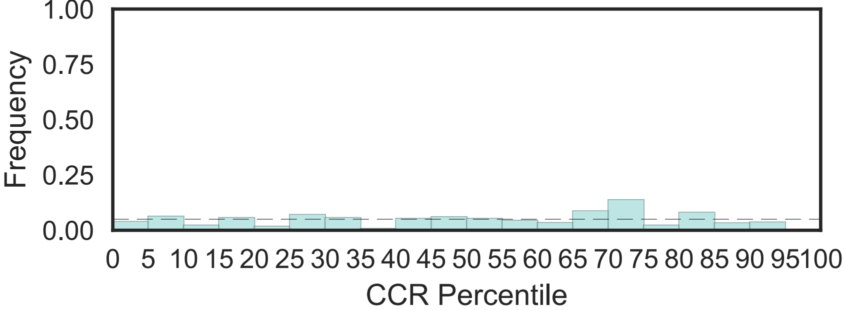
NADH-ubiquinone oxidoreductase subunit b14.5b (NDUFC2)
(NDUF_C2, N=4)
Fisher's OR: 0; Bonferroni p-val: 1



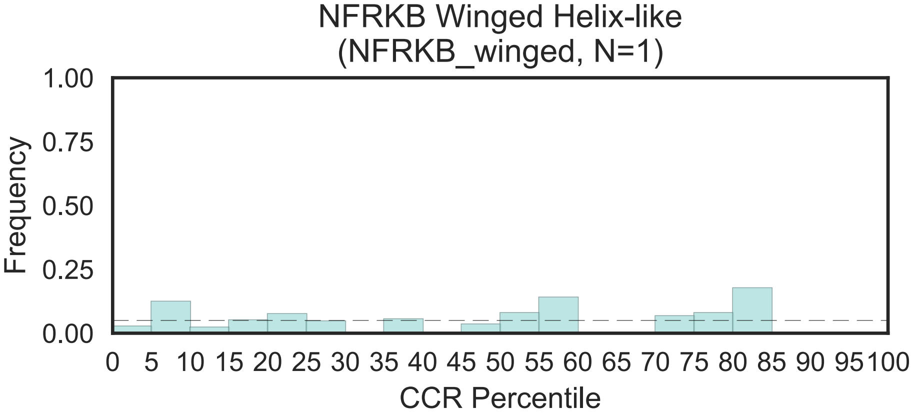

NF-kappa-B essential modulator NEMO
(NEMO, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

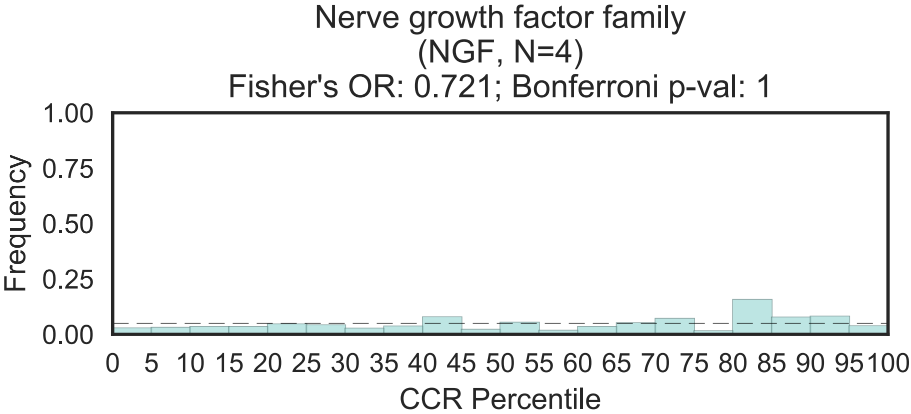

NEMP family
(NEMP, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

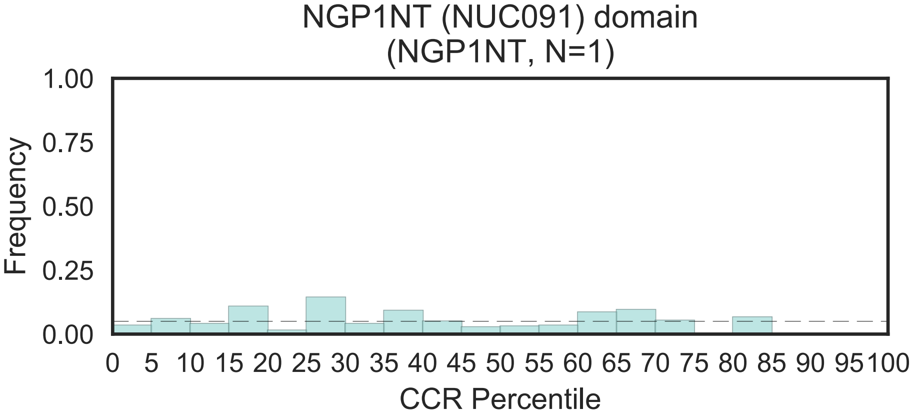

Neuroendocrine-specific golgi protein P55 (NESP55)
(NESP55, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

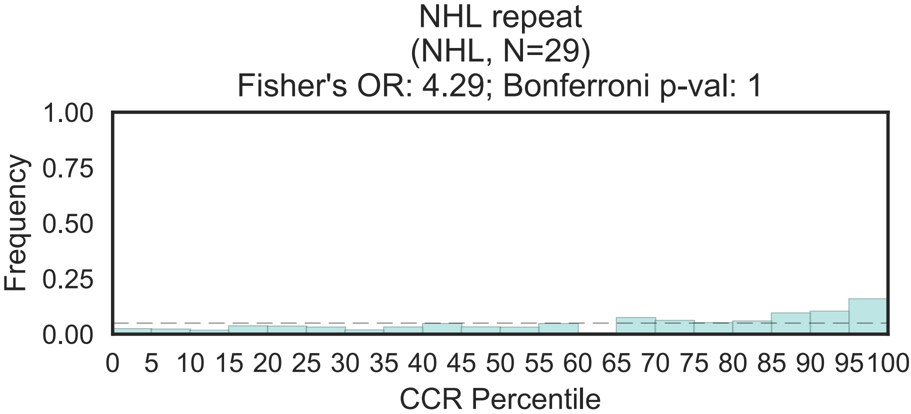


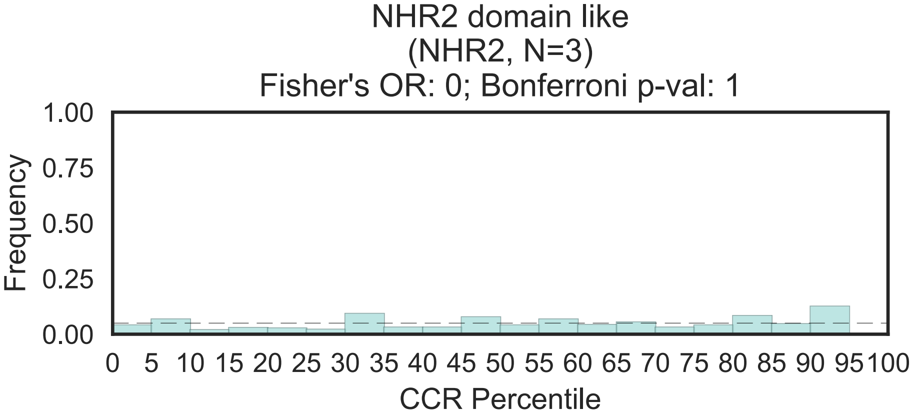
Regulatory region of Na+/H+ exchanger NHE binds to calmodulin
(NEXCaM_BD, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

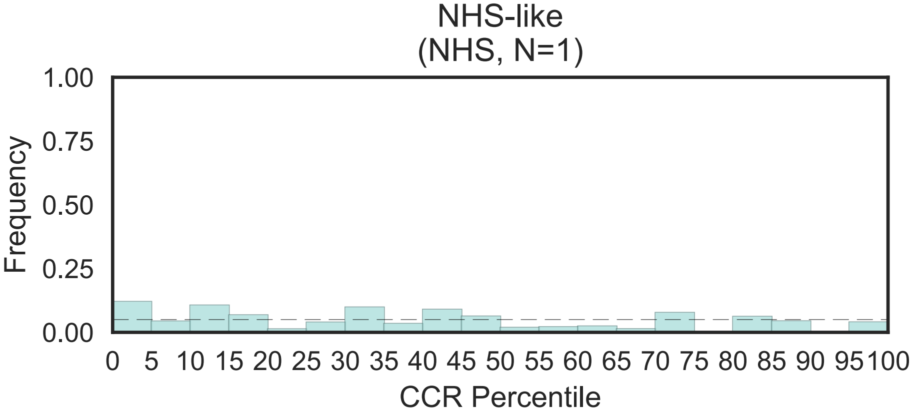

NFRKB Winged Helix-like
(NFRKB_winged, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Nerve growth factor family
(NGF, N=4)
Fisher's OR: 0.721; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

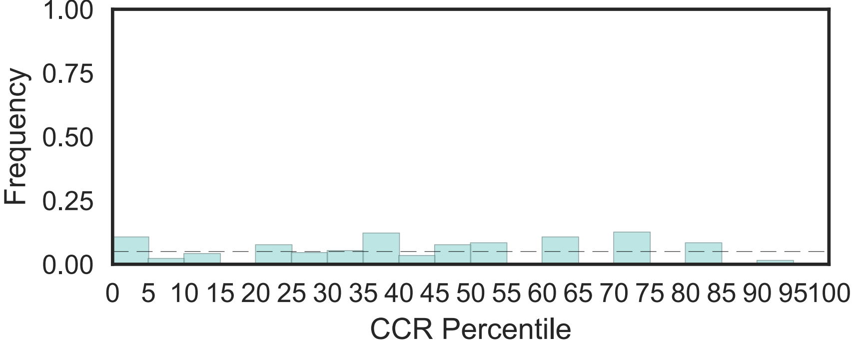

NGP1NT (NUC091) domain
(NGP1NT, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

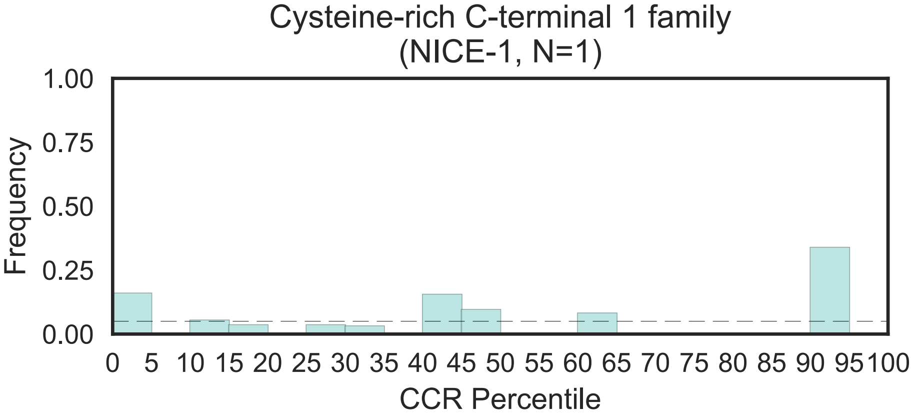

NHL repeat
(NHL, N=29)
Fisher's OR: 4.29; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

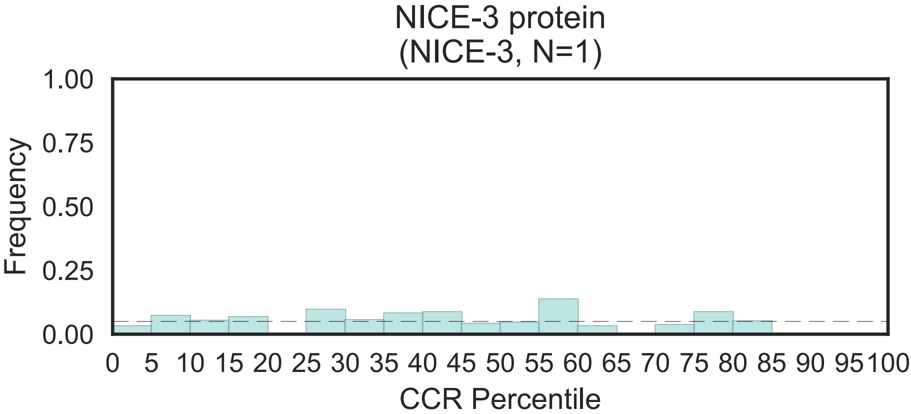

NHR2 domain like
(NHR2, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

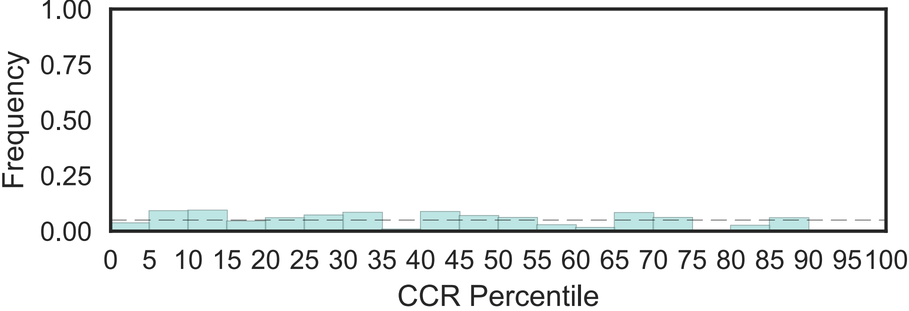

NHS-like
(NHS, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Second BRCT domain on Nijmegen syndrome breakage protein (NIBRIN_BRCT_II, N=1)



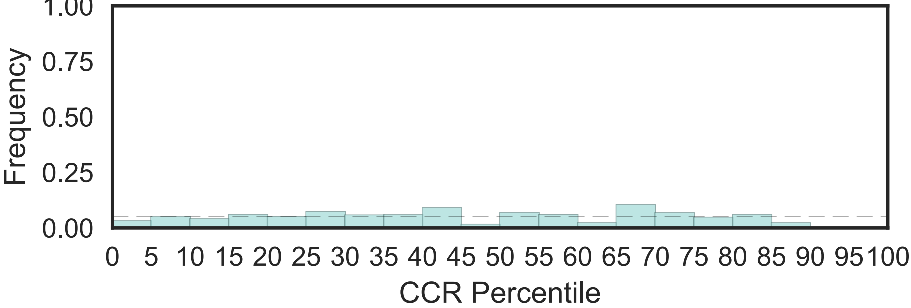

Cysteine-rich C-terminal 1 family
(NICE-1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

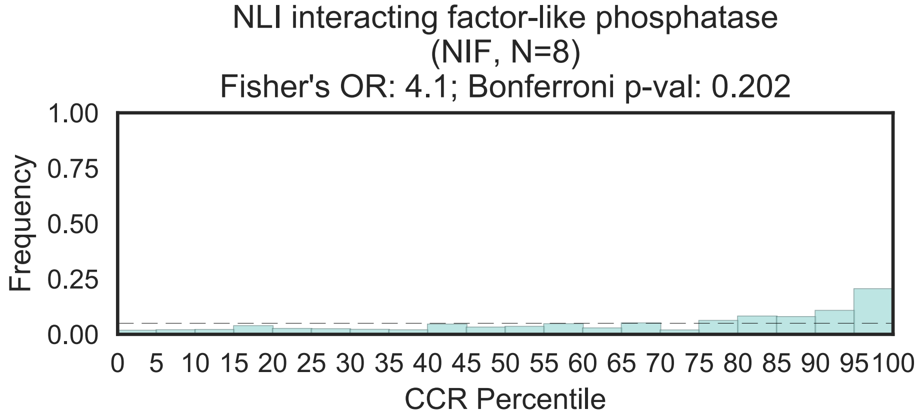

NICE-3 protein
(NICE-3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

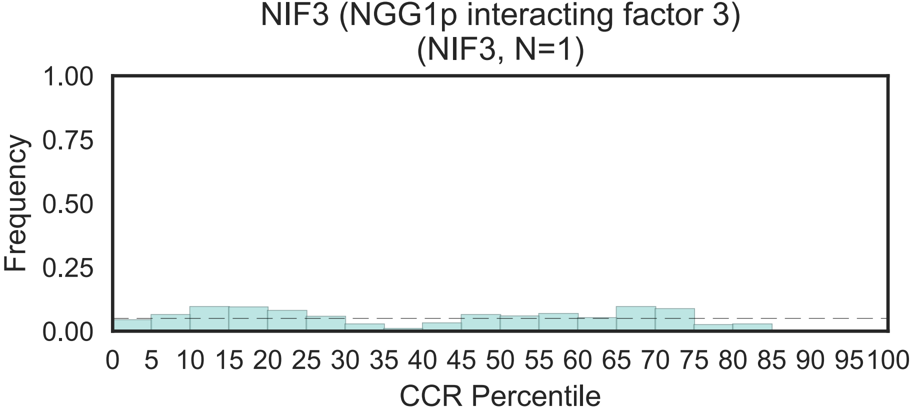


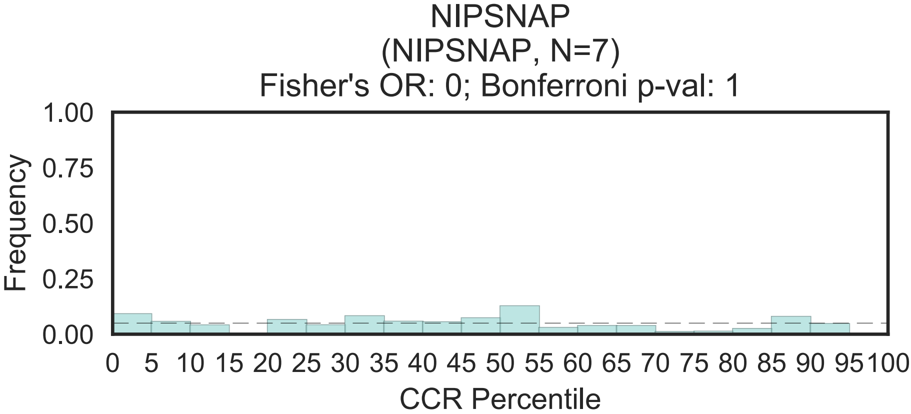
Nmi/IFP 35 domain (NID)
(NID, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

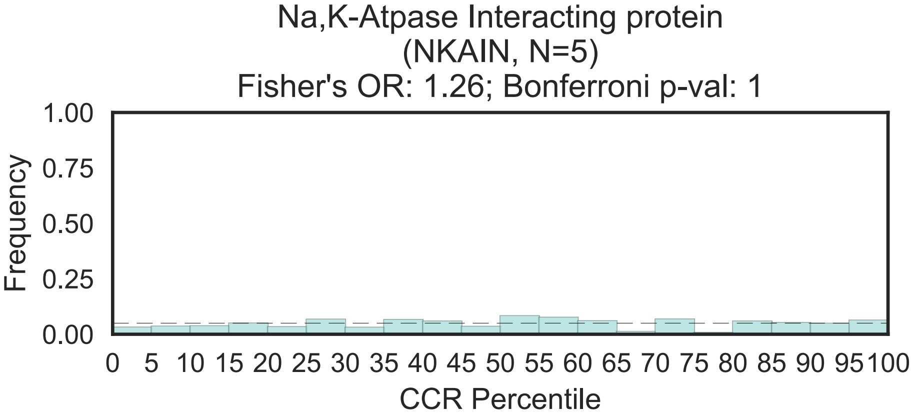
Nidogen-like
(NIDO, N=5)
Fisher's OR: 0; Bonferroni p-val: 1

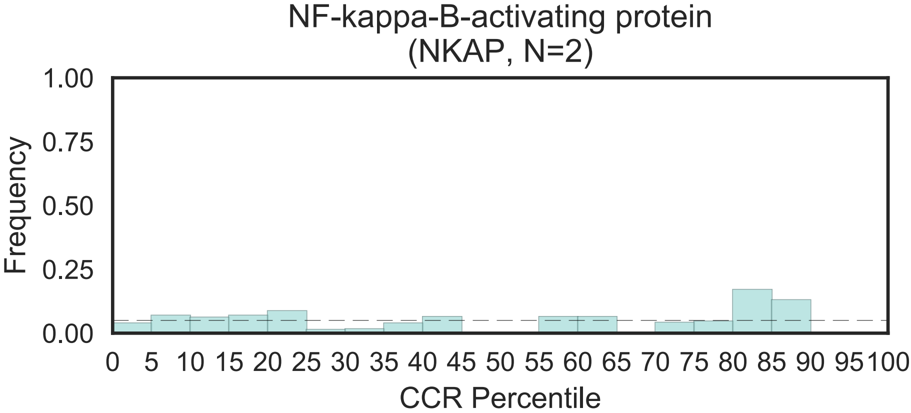


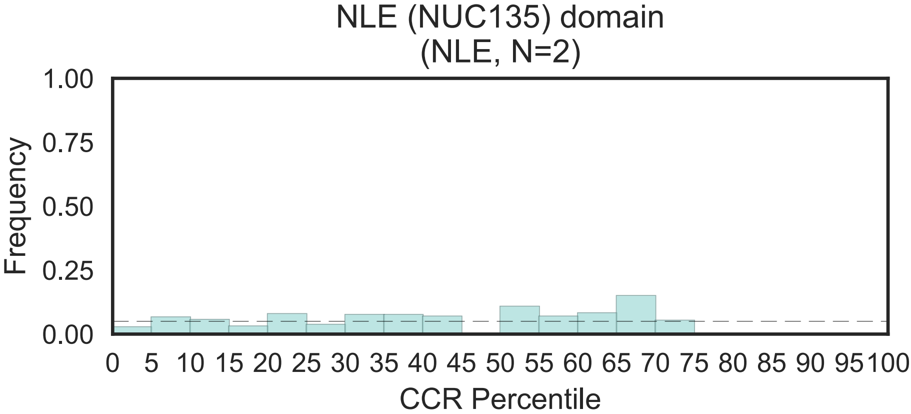

NLI interacting factor-like phosphatase
(NIF, N=8)
Fisher's OR: 4.1; Bonferroni p-val: 0.202
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

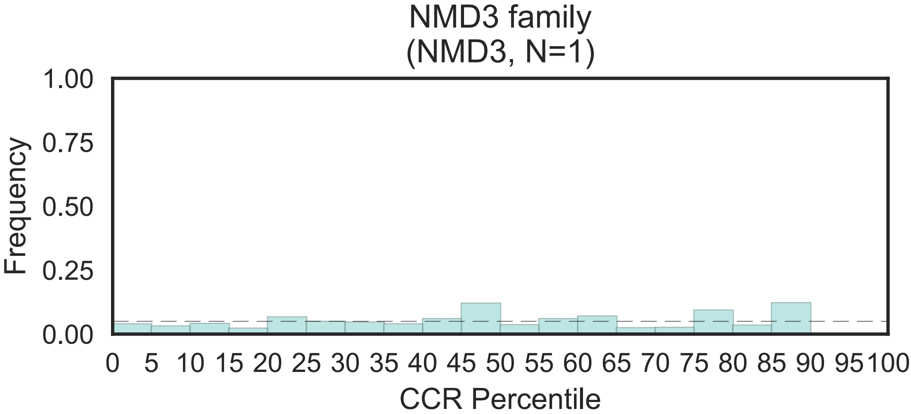

NIF3 (NGG1p interacting factor 3)
(NIF3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

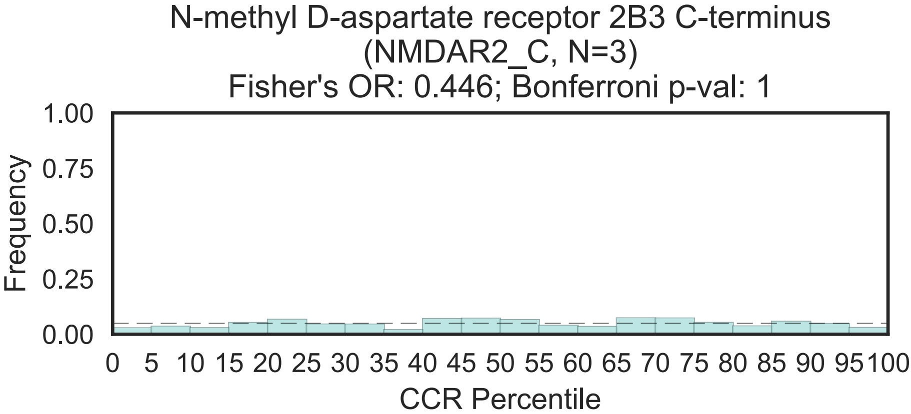

NIPSNAP
(NIPSNAP, N=7)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

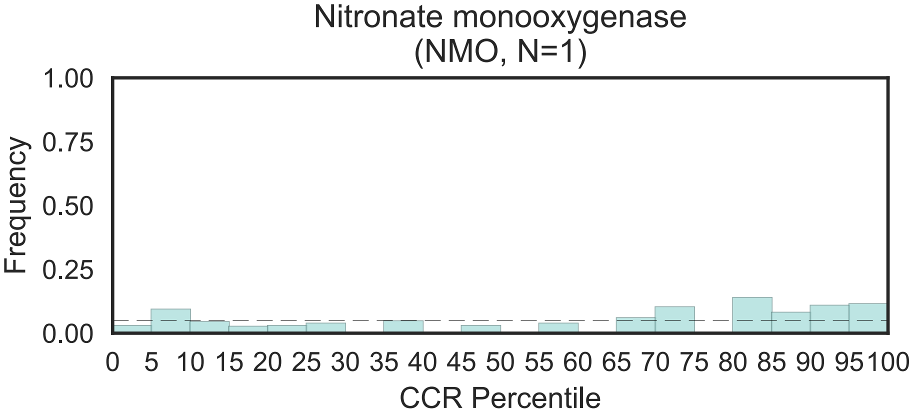

Na,K-Atpase Interacting protein
(NKAIN, N=5)
Fisher's OR: 1.26; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

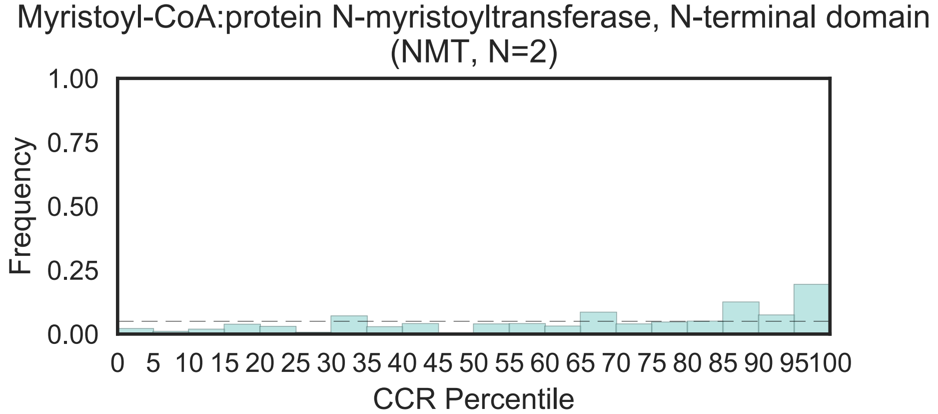

NF-kappa-B-activating protein
(NKAP, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

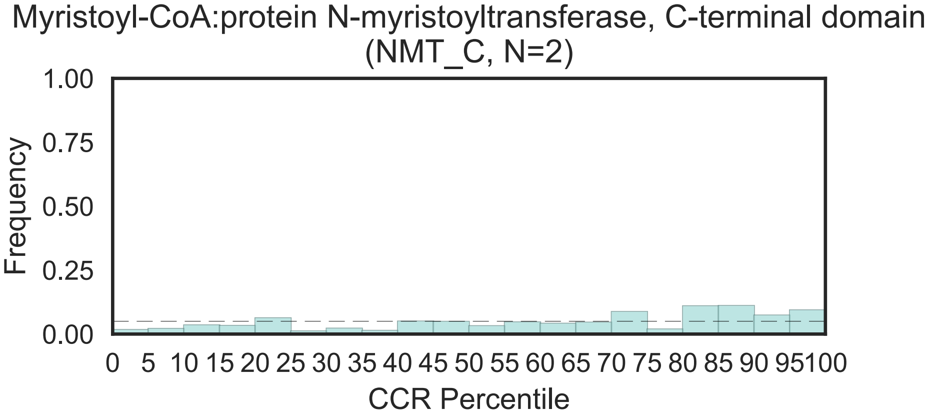

NLE (NUC135) domain
(NLE, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

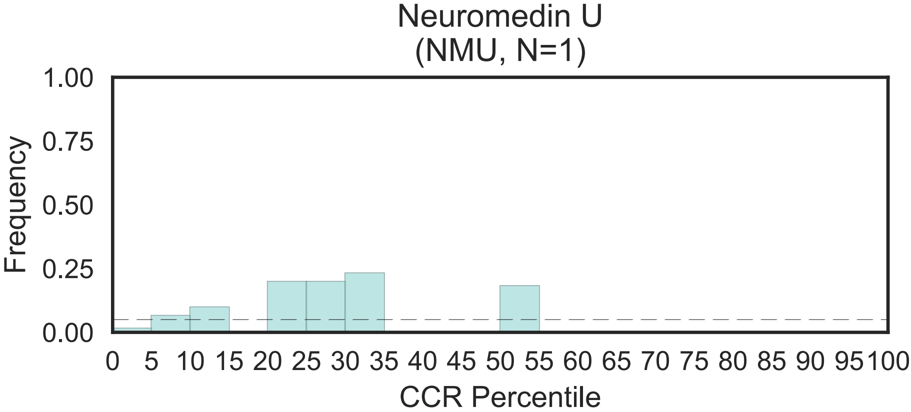

NMD3 family
(NMD3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

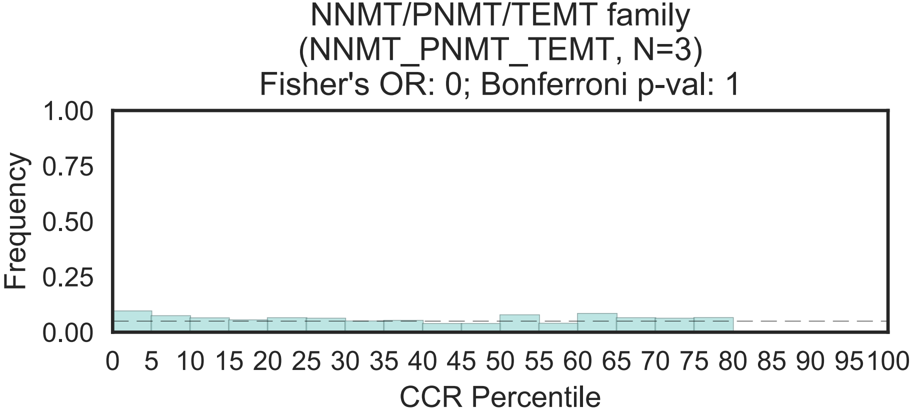

N-methyl D-aspartate receptor 2B3 C-terminus
(NMDAR2_C, N=3)
Fisher's OR: 0.446; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

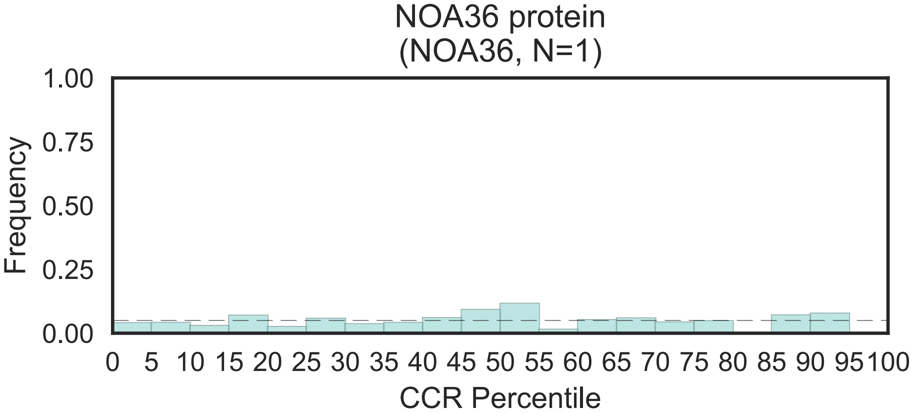

Nitronate monooxygenase
(NMO, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

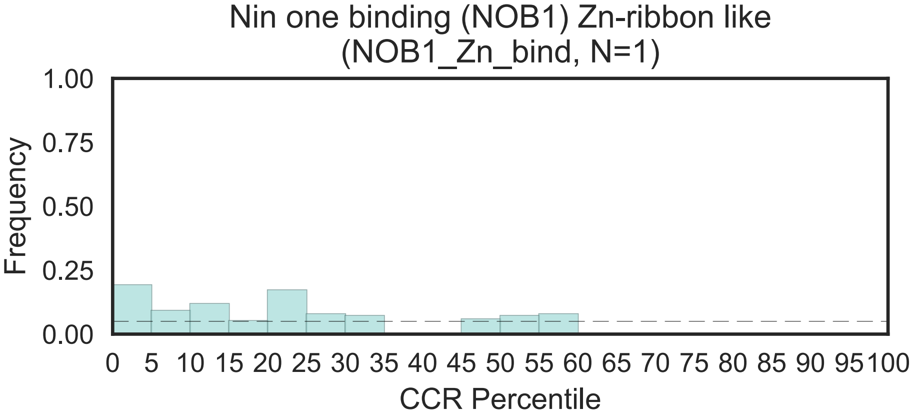

Myristoyl-CoA:protein N-myristoyltransferase, N-terminal domain
(NMT, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

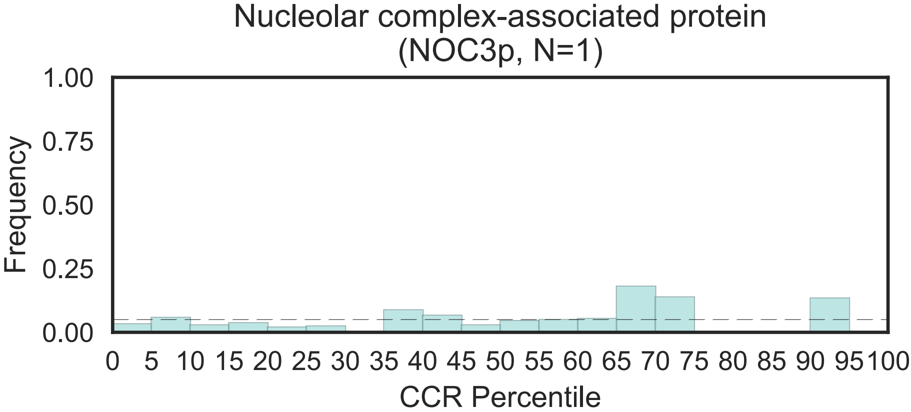

Myristoyl-CoA:protein N-myristoyltransferase, C-terminal domain
(NMT_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Neuromedin U
(NMU, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

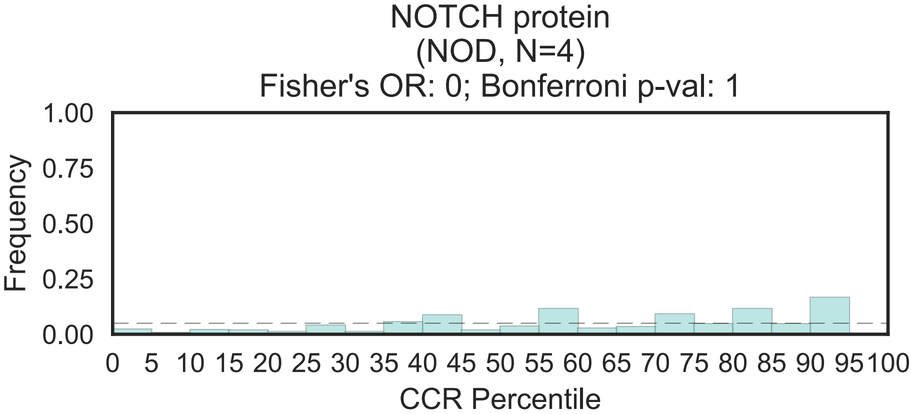

NNMT/PNMT/TEMT family
(NNMT_PNMT_TEMT, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

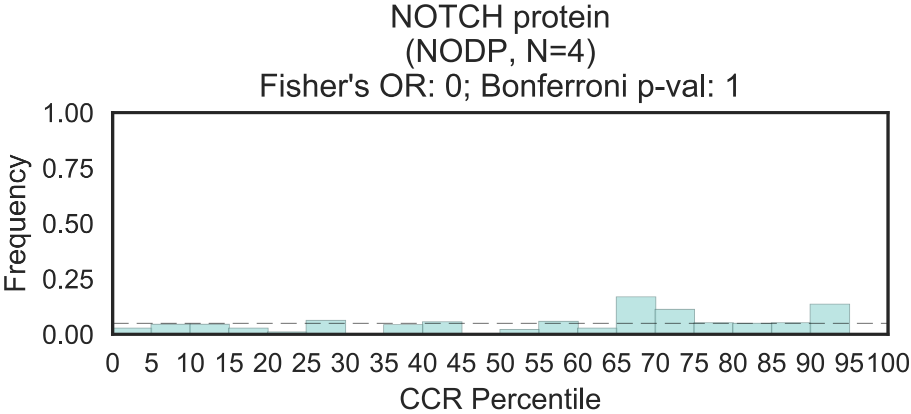

NOA36 protein
(NOA36, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

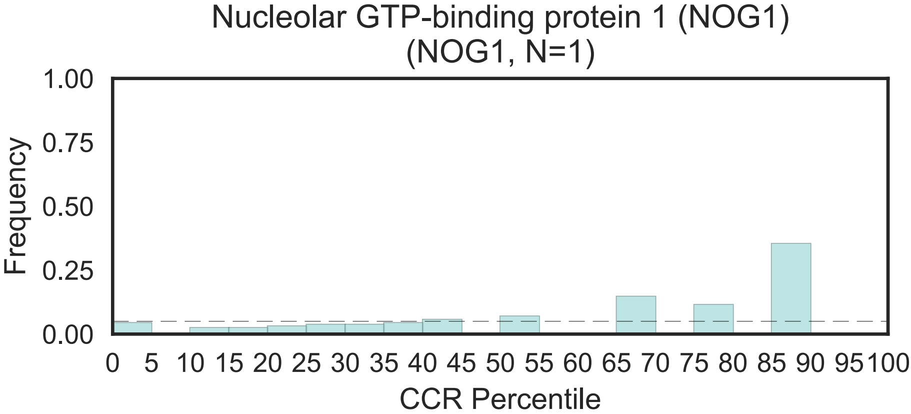

Nin one binding (NOB1) Zn-ribbon like
(NOB1_Zn_bind, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



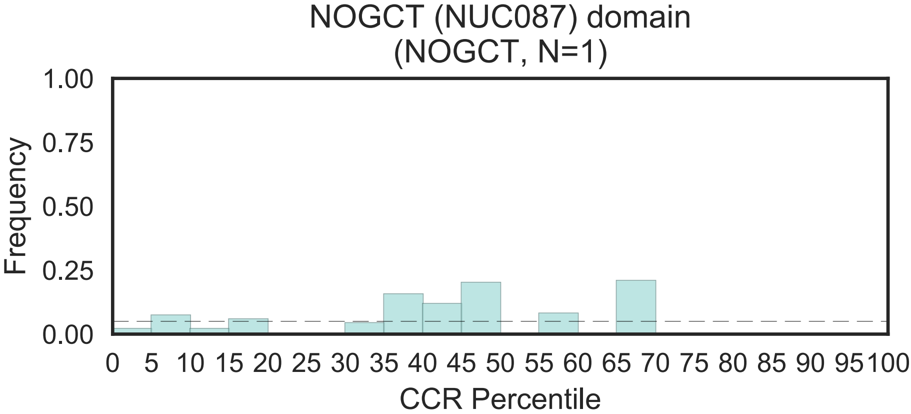
Nucleolar complex-associated protein
(NOC3p, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

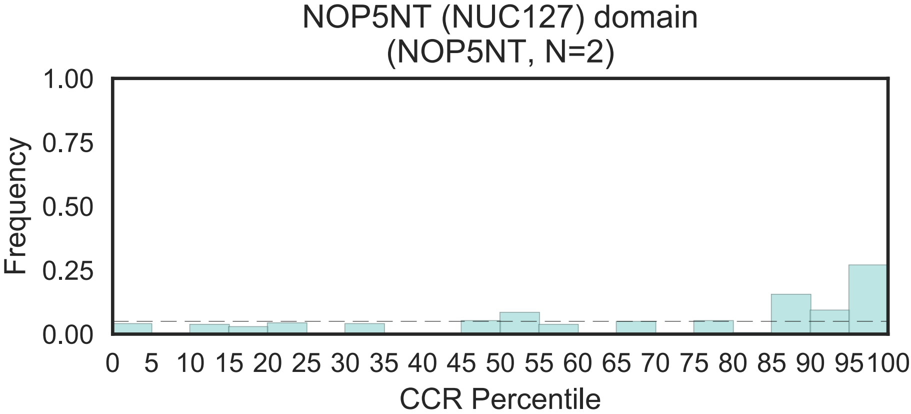

NOTCH protein
(NOD, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

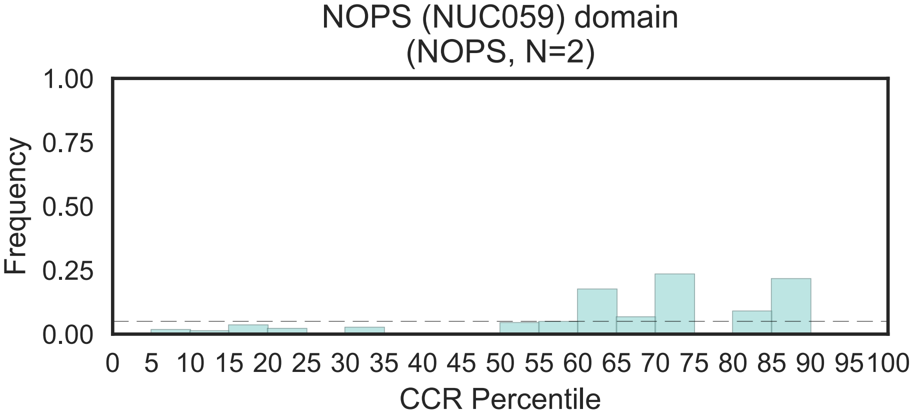

NOTCH protein
(NODP, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

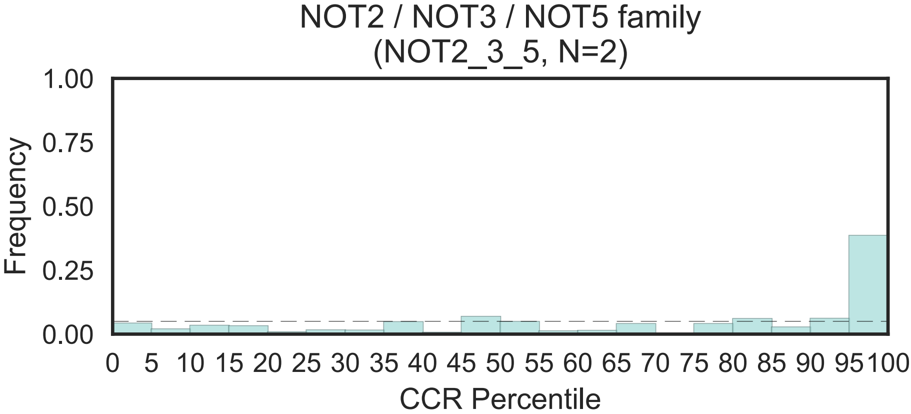


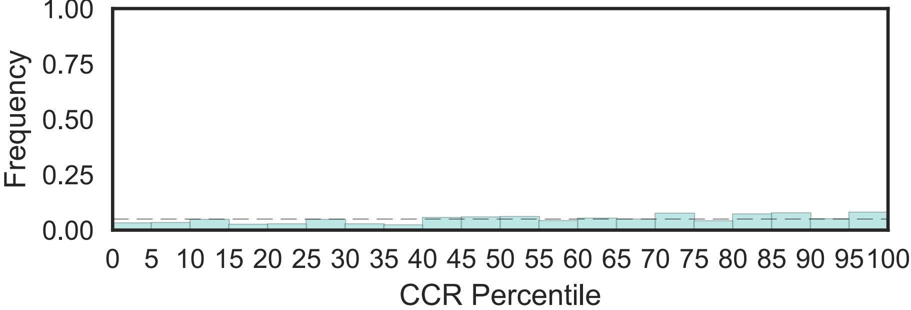
Nucleolar GTP-binding protein 1 (NOG1)
(NOG1, N=1)


NOGCT (NUC087) domain
(NOGCT, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

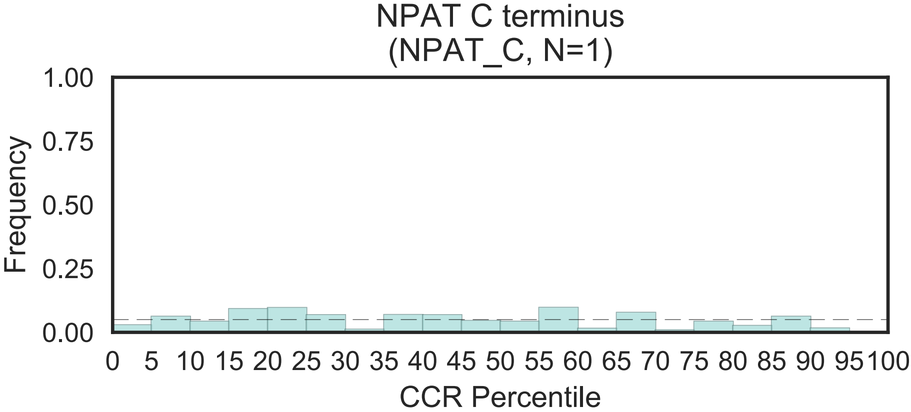

NOP5NT (NUC127) domain
(NOP5NT, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

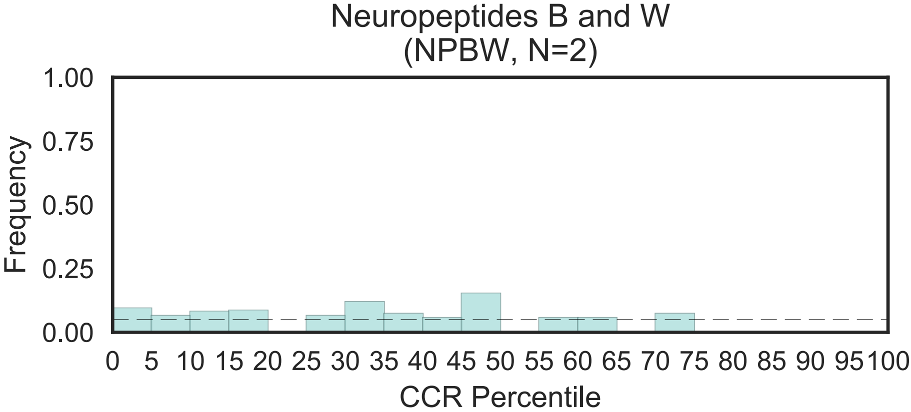

NOPS (NUC059) domain
(NOPS, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

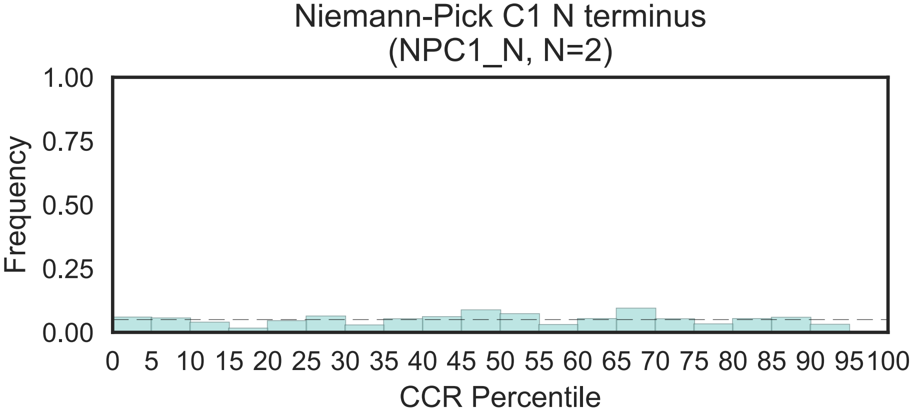

NOT2 / NOT3 / NOT5 family
(NOT2_3_5, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

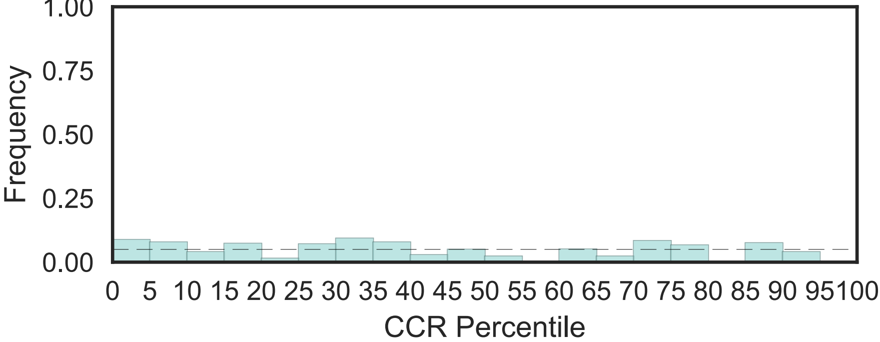


Nitric oxide synthase, oxygenase domain
(NO_synthase, N=3)
Fisher's OR: 1.26; Bonferroni p-val: 1

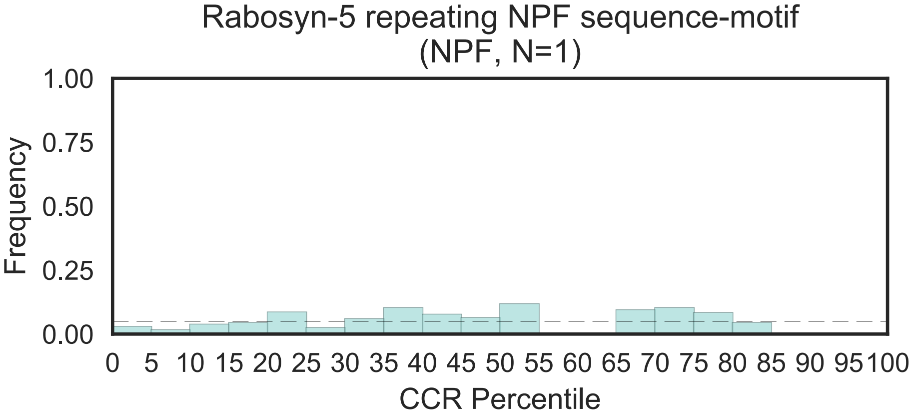

NPAT C terminus
(NPAT_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

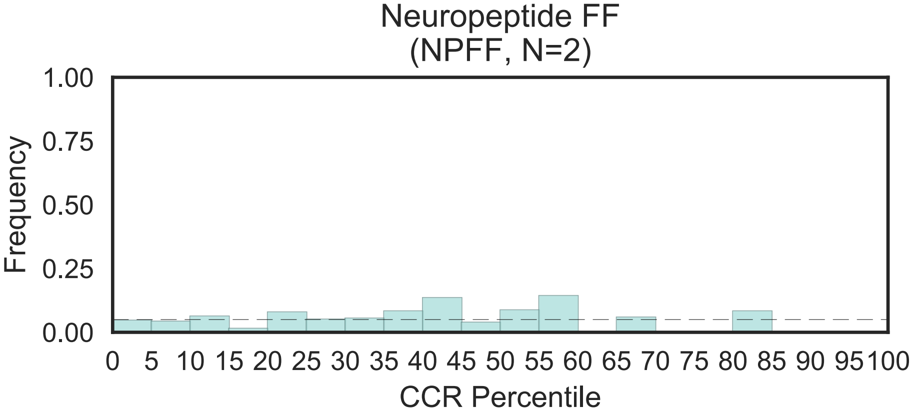

Neuropeptides B and W
(NPBW, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

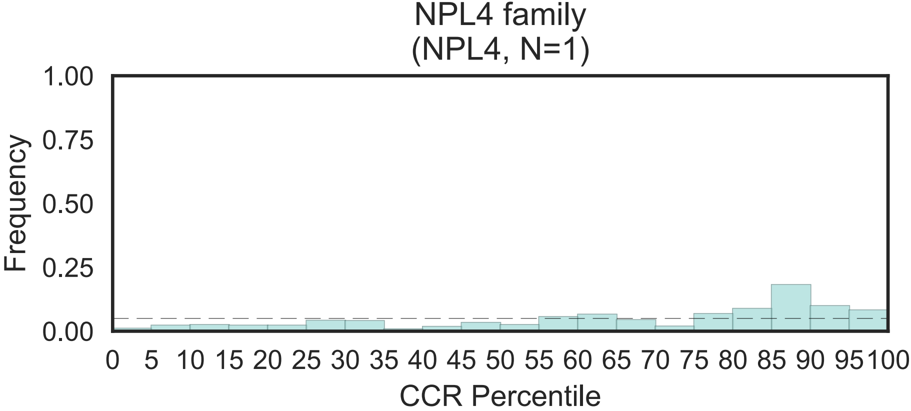

Niemann-Pick C1 N terminus
(NPC1_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

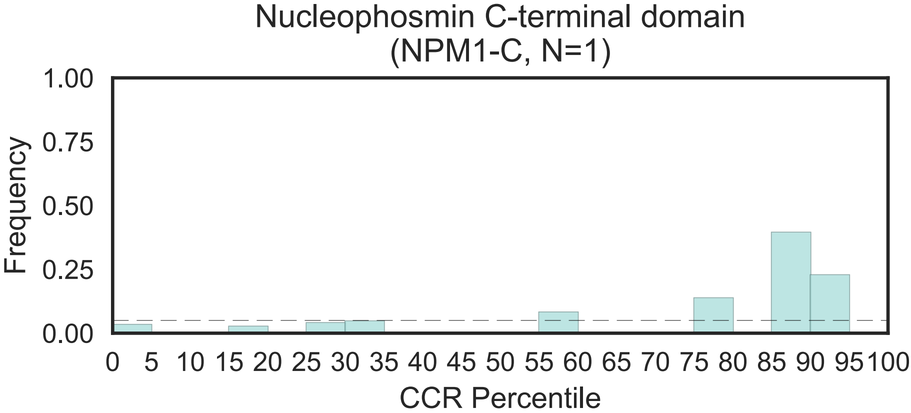


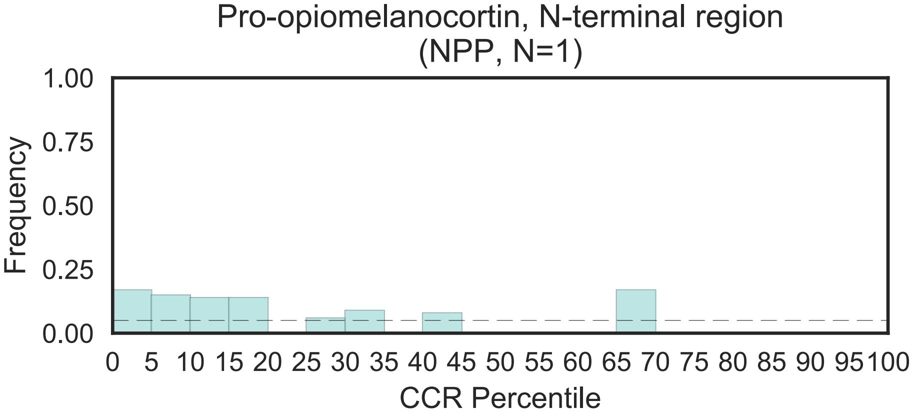
Neural proliferation differentiation control-1 protein (NPDC1)
(NPDC1, N=1)

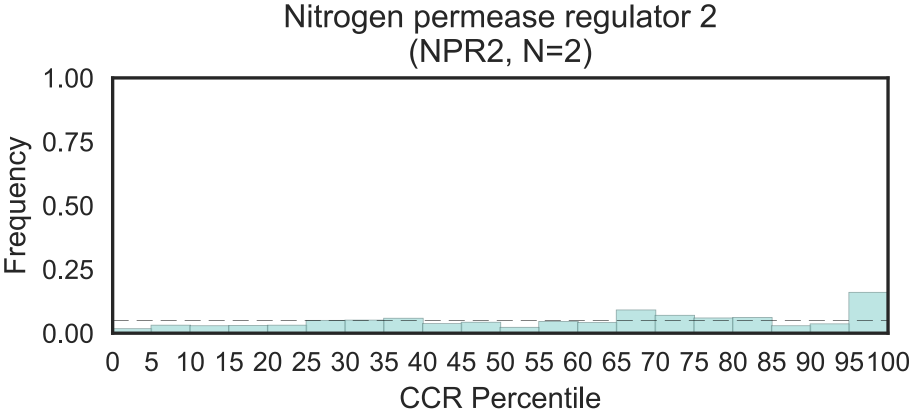

Rabosyn-5 repeating NPF sequence-motif
(NPF, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

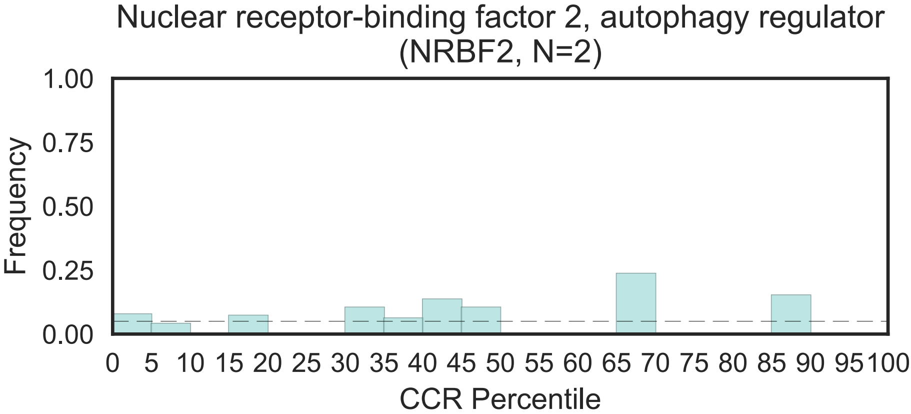

Neuropeptide FF
(NPFF, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

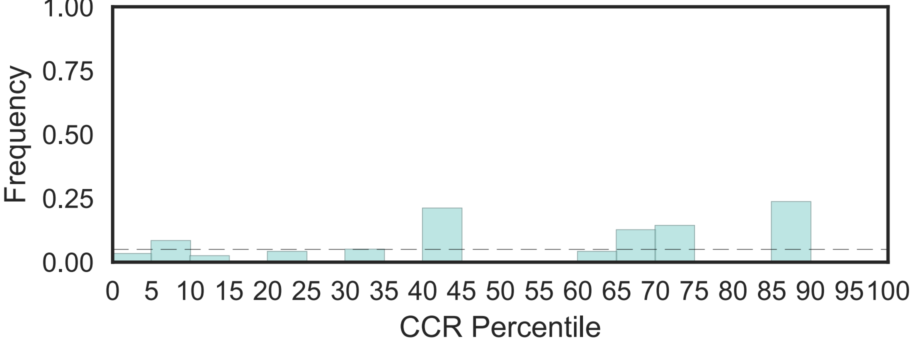

NPL4 family
(NPL4, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

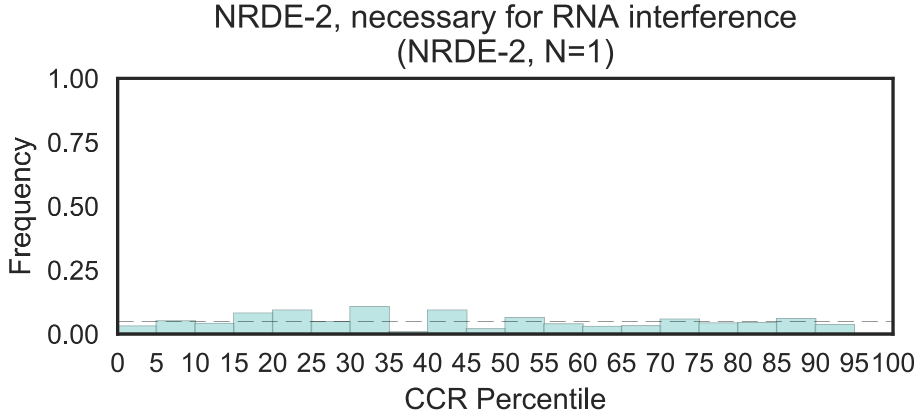

Nucleophosmin C-terminal domain
(NPM1-C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

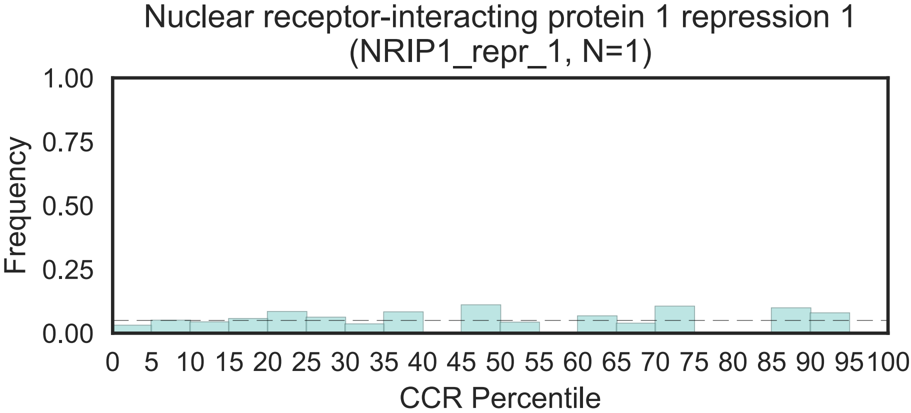

Pro-opiomelanocortin, N-terminal region
(NPP, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

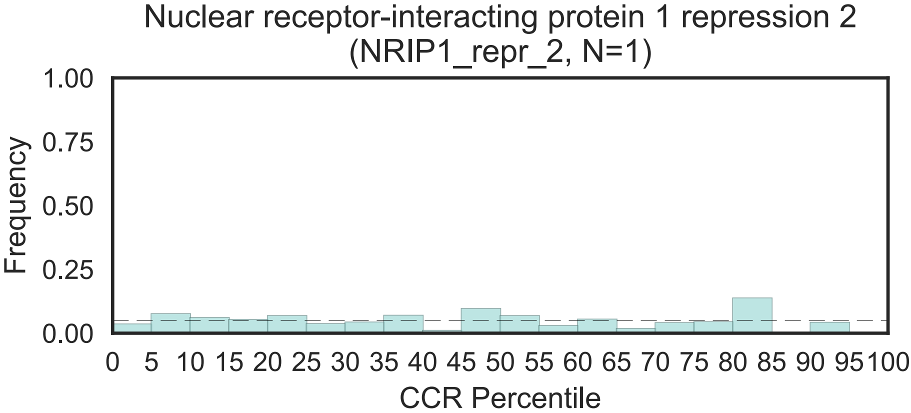

Nitrogen permease regulator 2
(NPR2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

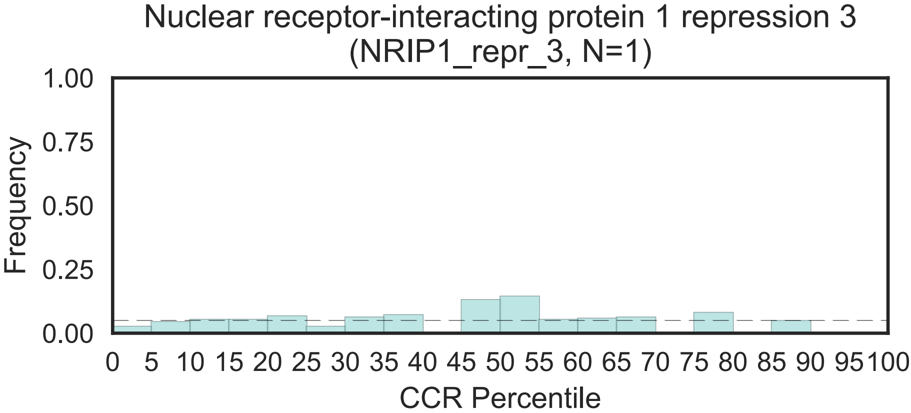

Nuclear receptor-binding factor 2, autophagy regulator
(NRBF2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

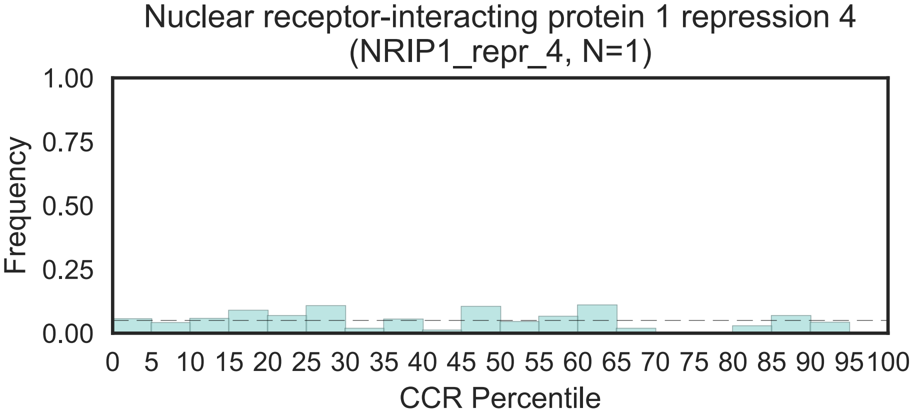

MIT domain of nuclear receptor-binding factor 2
(NRBF2_MIT, N=1)

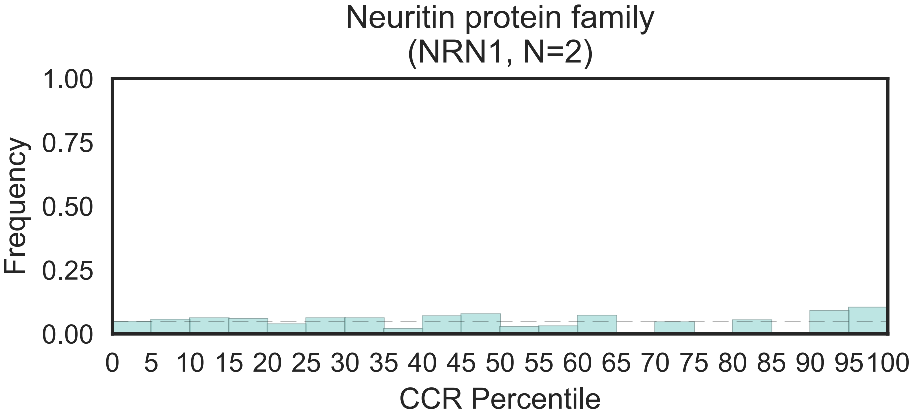

NRDE-2, necessary for RNA interference
(NRDE-2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

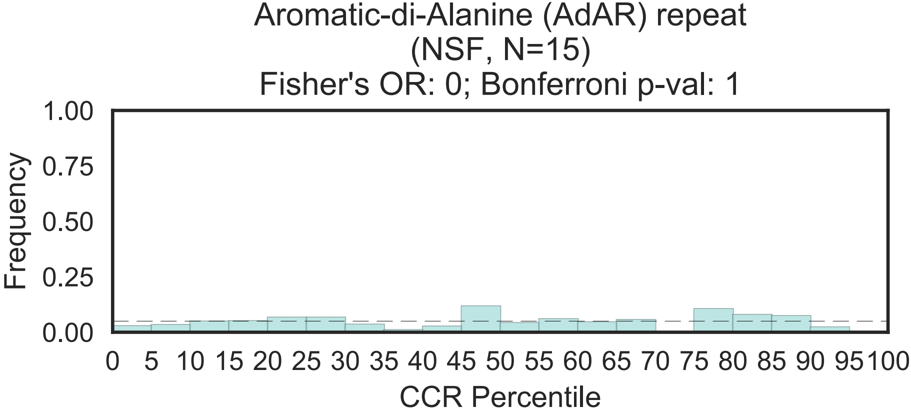

Nuclear receptor-interacting protein 1 repression 1
(NRIP1_repr_1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

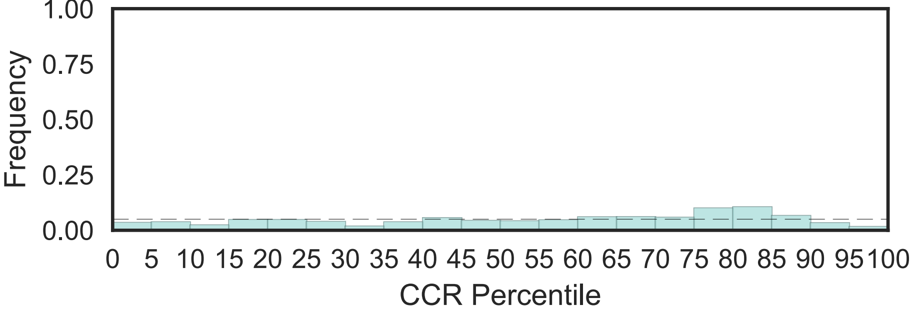

Nuclear receptor-interacting protein 1 repression 2
(NRIP1_repr_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Nuclear receptor-interacting protein 1 repression 3
(NRIP1_repr_3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

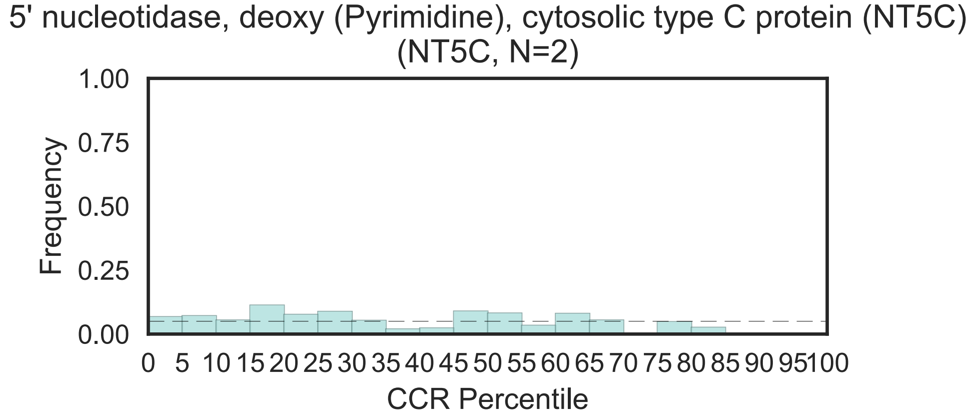

Nuclear receptor-interacting protein 1 repression 4
(NRIP1_repr_4, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

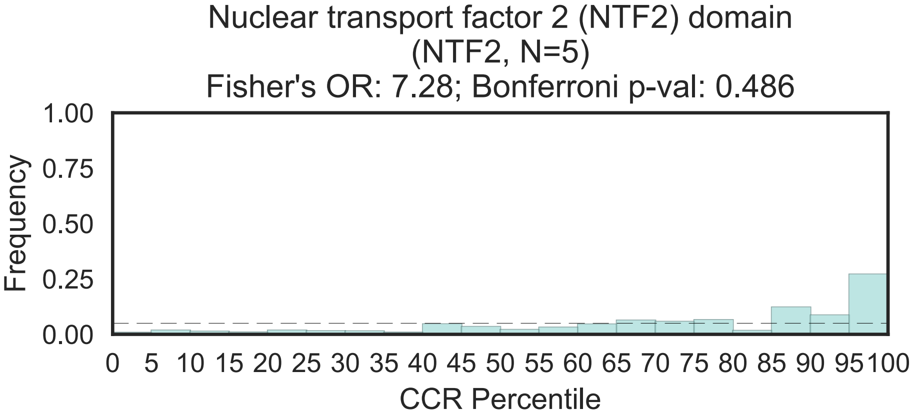

Neuritin protein family
(NRN1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

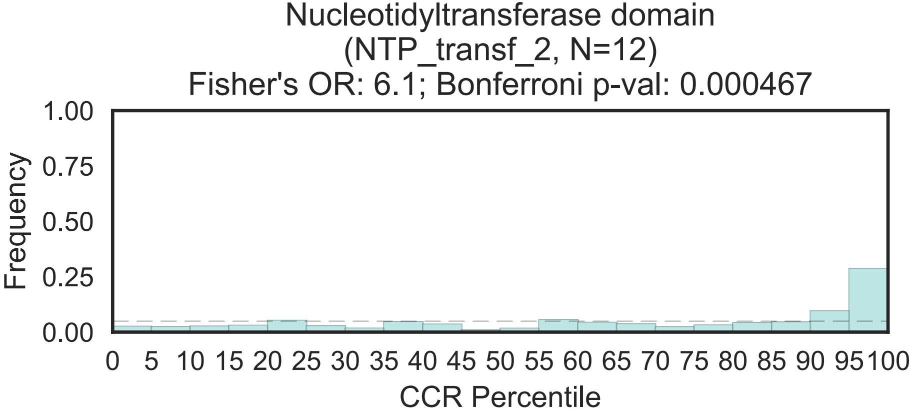

Aromatic-di-Alanine (AdAR) repeat
(NSF, N=15)
Fisher's OR: 0; Bonferroni p-val: 1



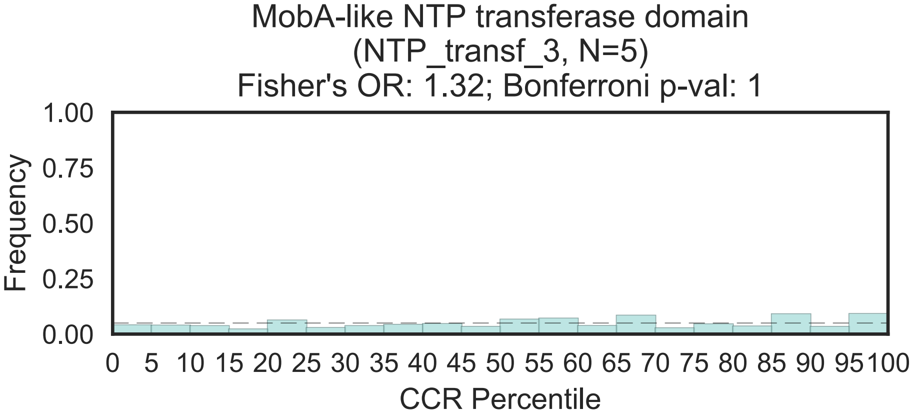
N-terminal C2 in EEIG1 and EHBP1 proteins
(NT-C2, N=4)
Fisher's OR: 0.557; Bonferroni p-val: 1

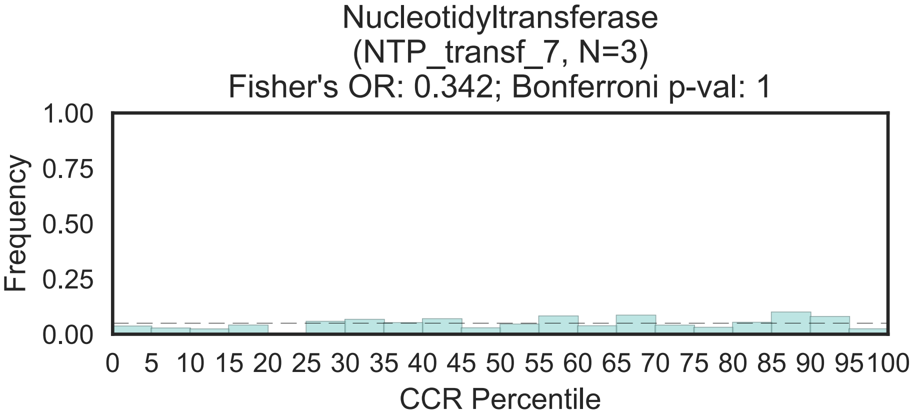

5' nucleotidase, deoxy (Pyrimidine), cytosolic type C protein (NT5C)
(NT5C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

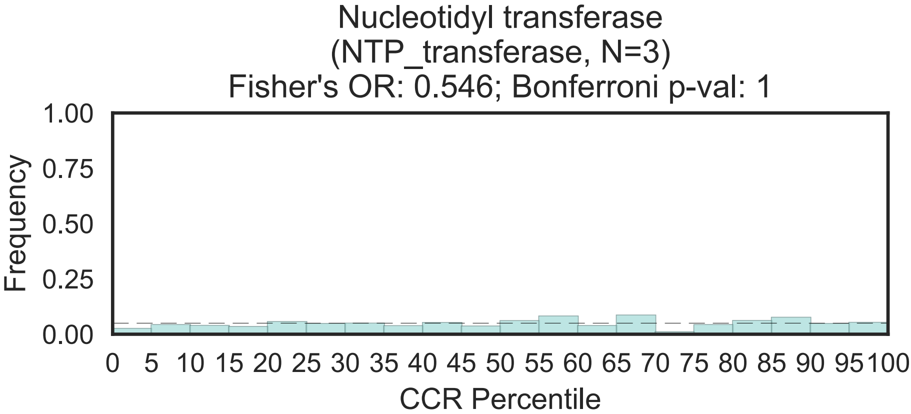

Nuclear transport factor 2 (NTF2) domain
(NTF2, N=5)
Fisher's OR: 7.28; Bonferroni p-val: 0.486
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

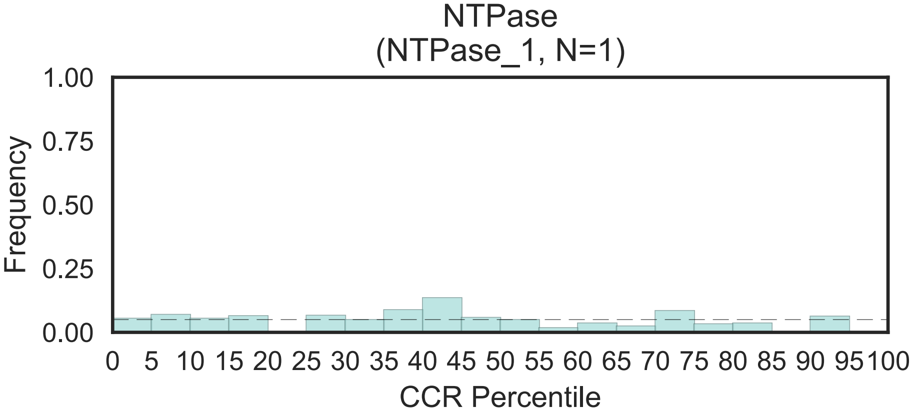


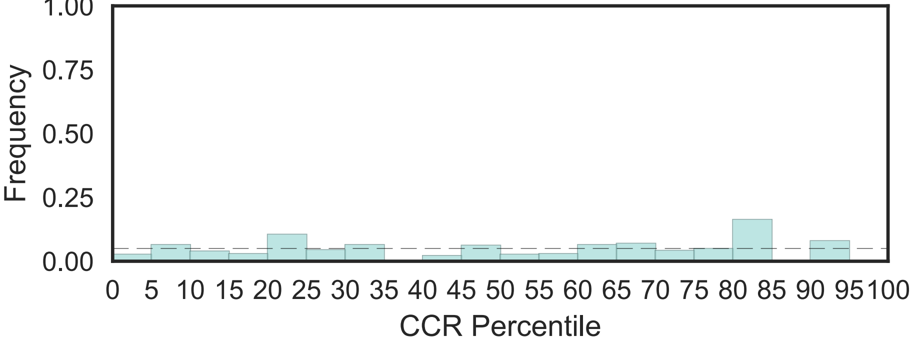
Nucleotidyltransferase domain
(NTP_transf_2, N=12)
Fisher's OR: 6.1; Bonferroni p-val: 0.000467


MobA-like NTP transferase domain
(NTP_transf_3, N=5)
Fisher's OR: 1.32; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

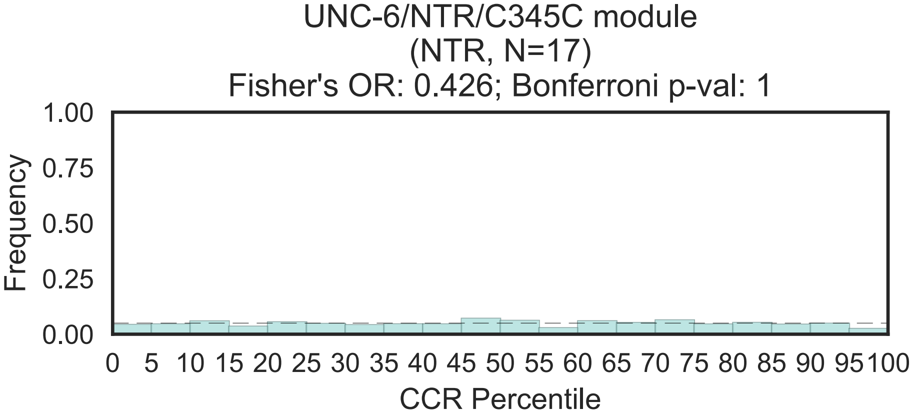

Nucleotidyltransferase
(NTP_transf_7, N=3)
Fisher's OR: 0.342; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

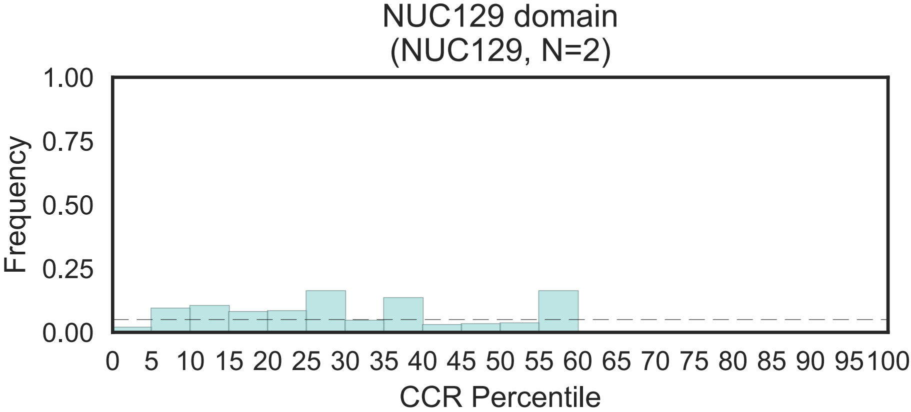

Nucleotidyl transferase
(NTP_transferase, N=3)
Fisher's OR: 0.546; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

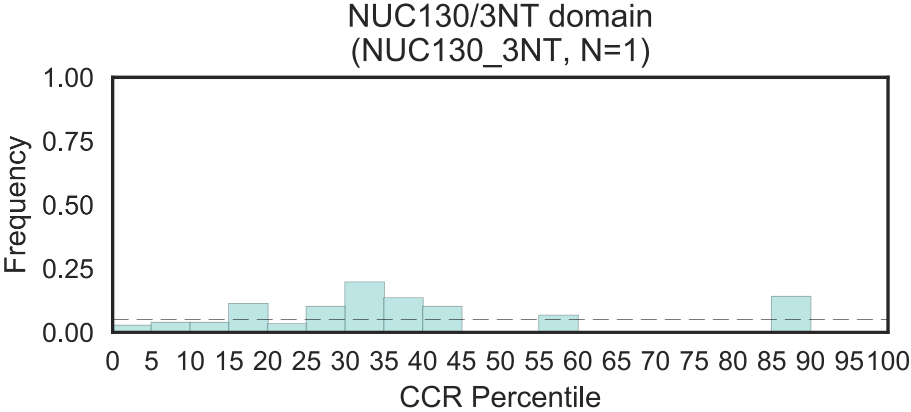

NTPase
(NTPase_1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

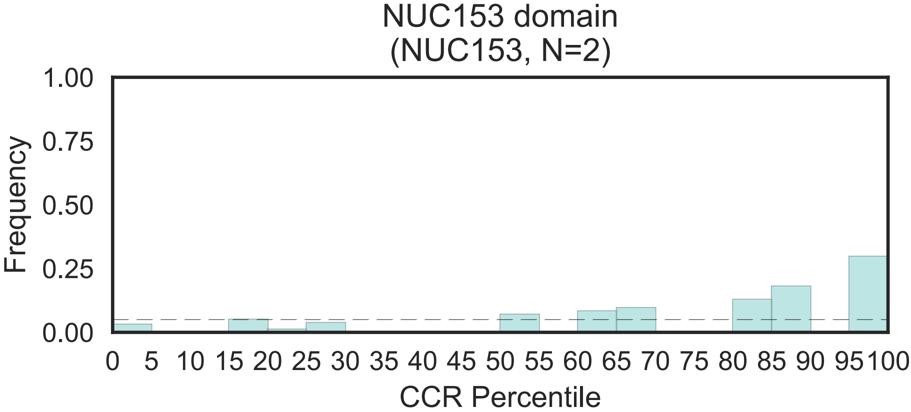


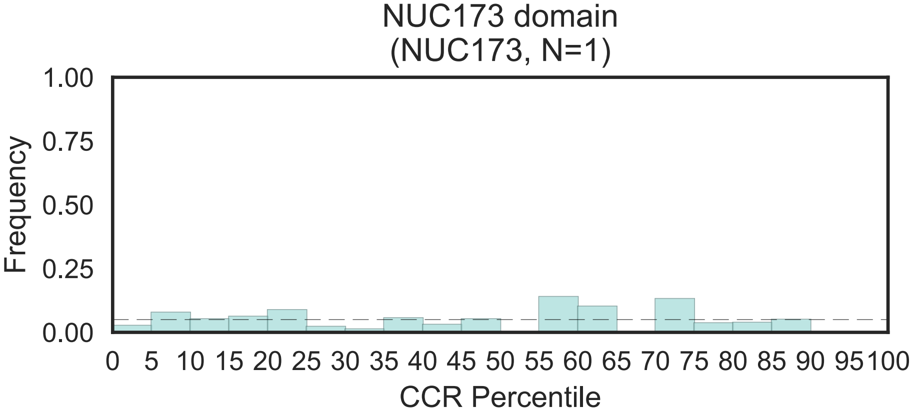
Protein of unknown function DUF84
(NTPase_I-T, N=1)

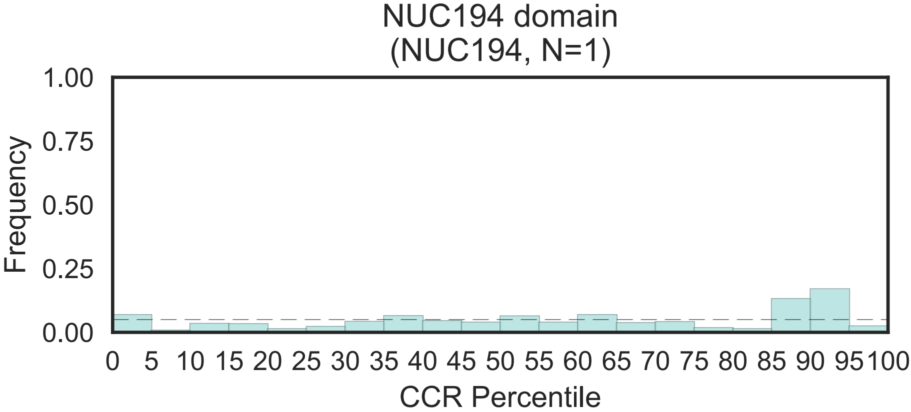

UNC-6/NTR/C345C module
(NTR, N=17)
Fisher's OR: 0.426; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

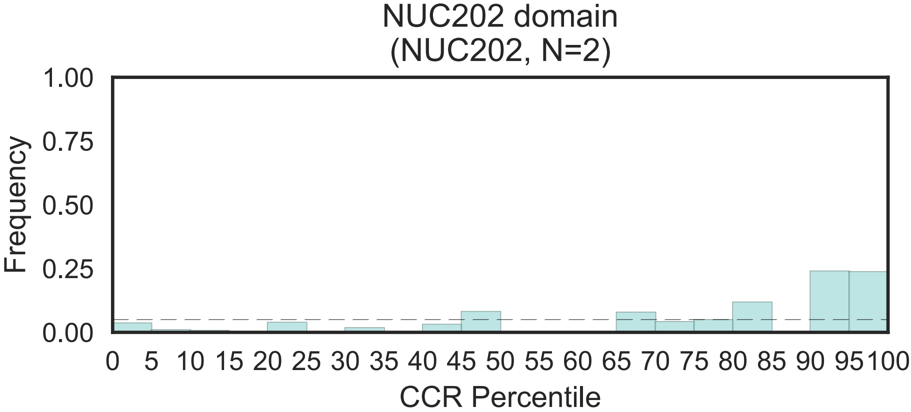

NUC129 domain
(NUC129, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

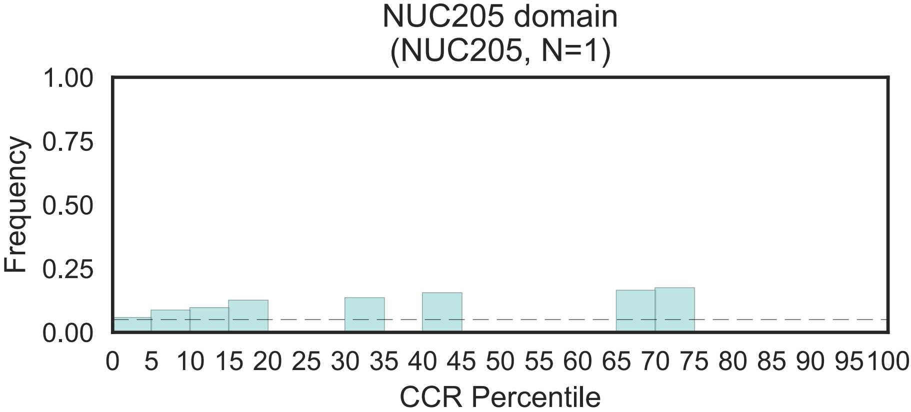

NUC130/3NT domain
(NUC130_3NT, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

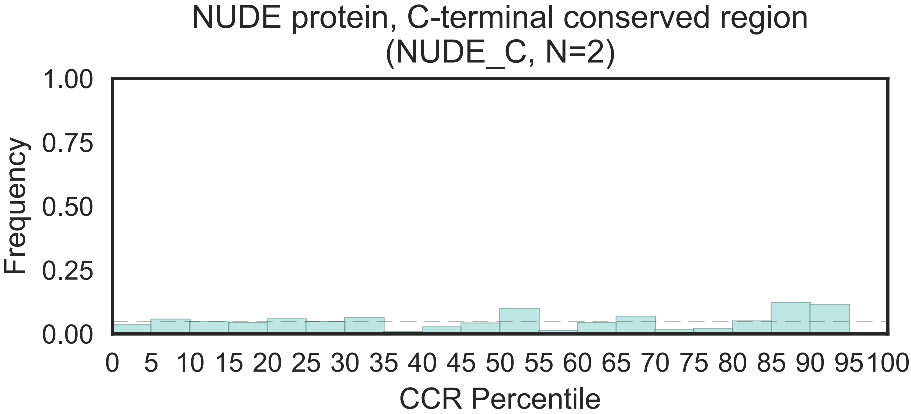

NUC153 domain
(NUC153, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

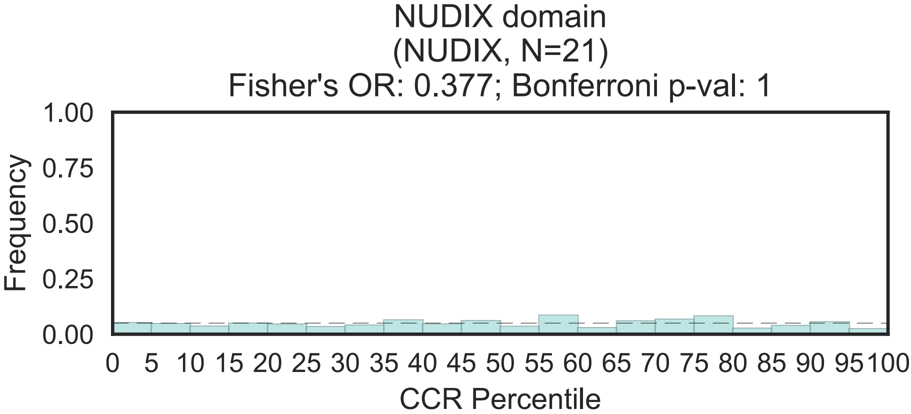

NUC173 domain
(NUC173, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

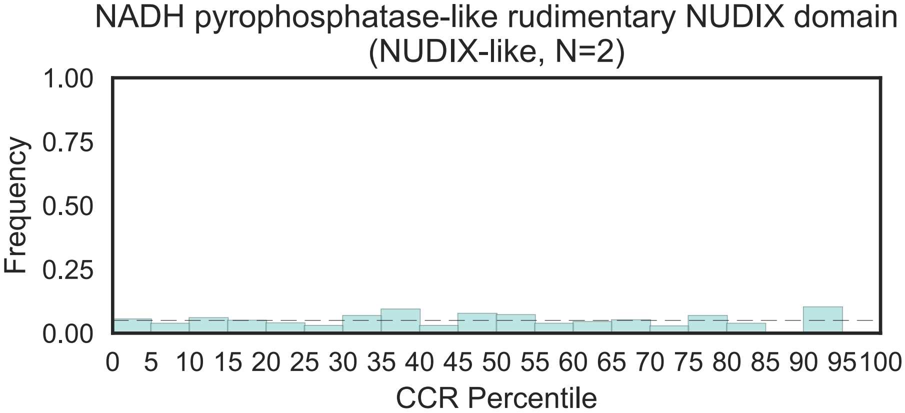

NUC194 domain
(NUC194, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

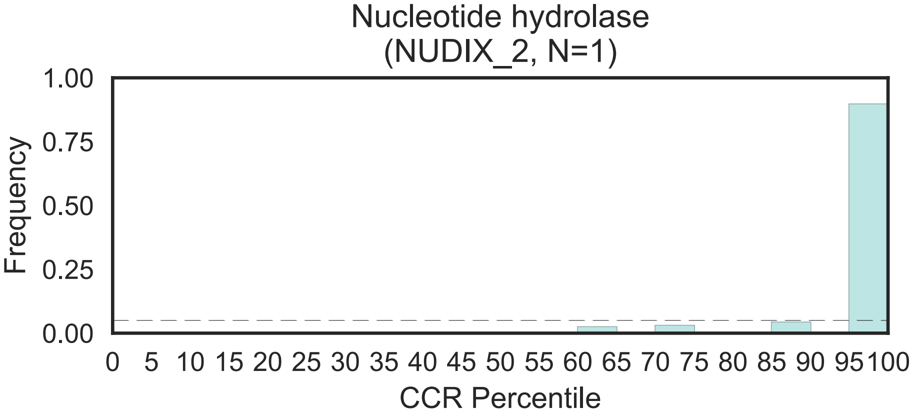

NUC202 domain
(NUC202, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

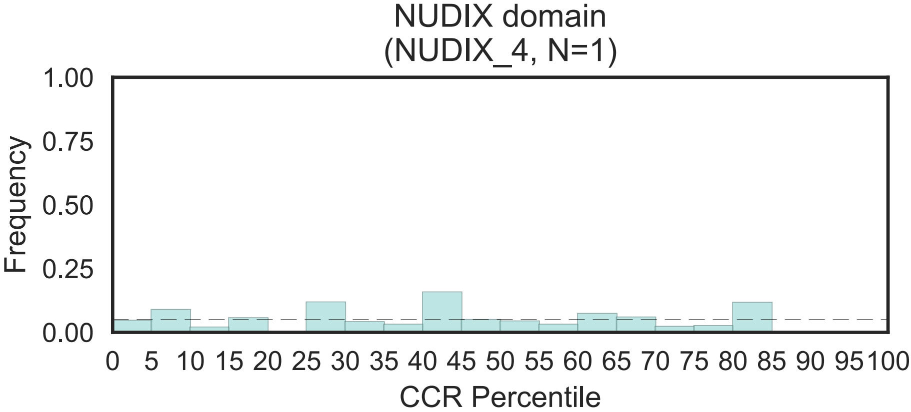

NUC205 domain
(NUC205, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


NUDE protein, C-terminal conserved region
(NUDE_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

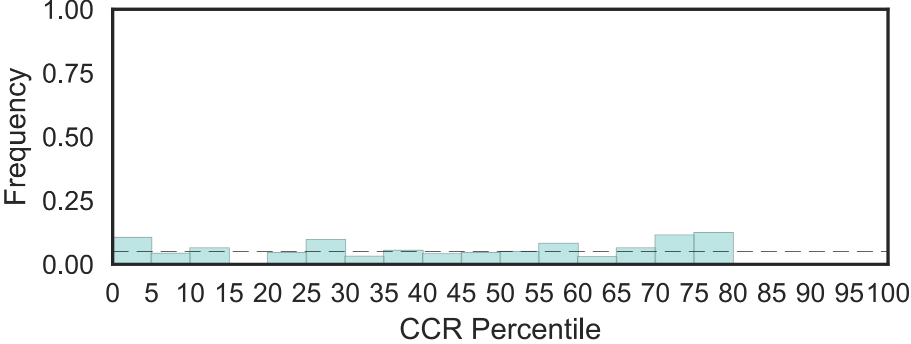

NUDIX domain
(NUDIX, N=21)
Fisher's OR: 0.377; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

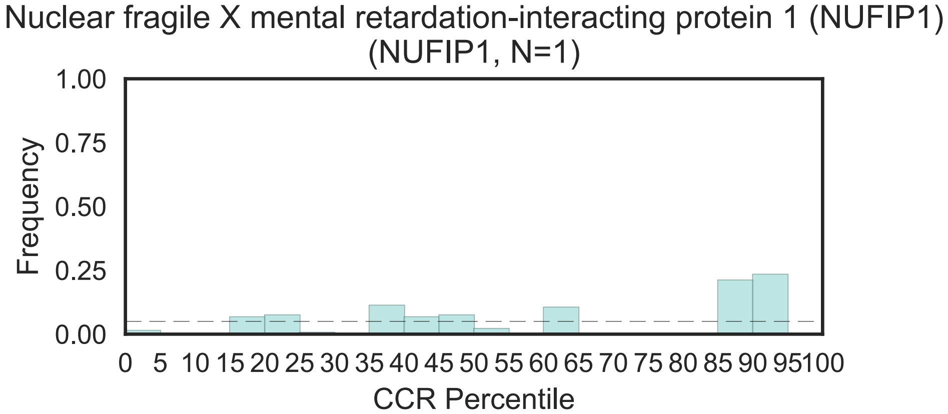

NADH pyrophosphatase-like rudimentary NUDIX domain
(NUDIX-like, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

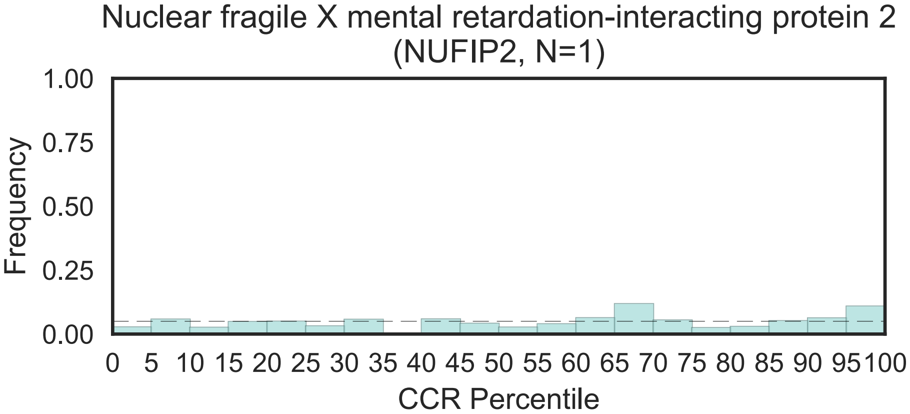

Nucleotide hydrolase
(NUDIX_2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


NUDIX domain
(NUDIX_4, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

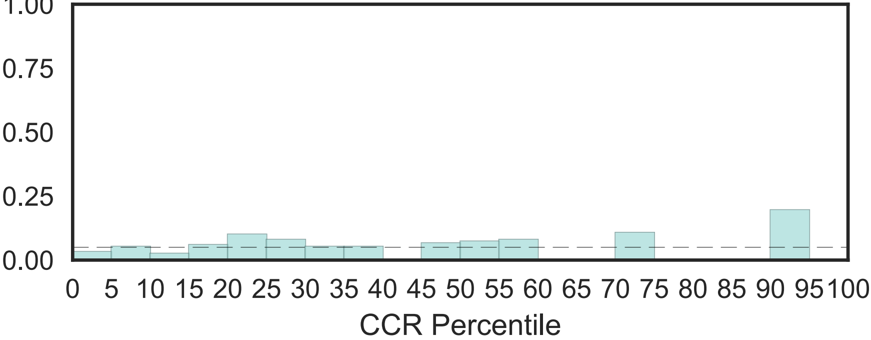
NUDIX, or N-terminal NPxY motif-rich, region of KRIT (NUDIX_5, N=1)

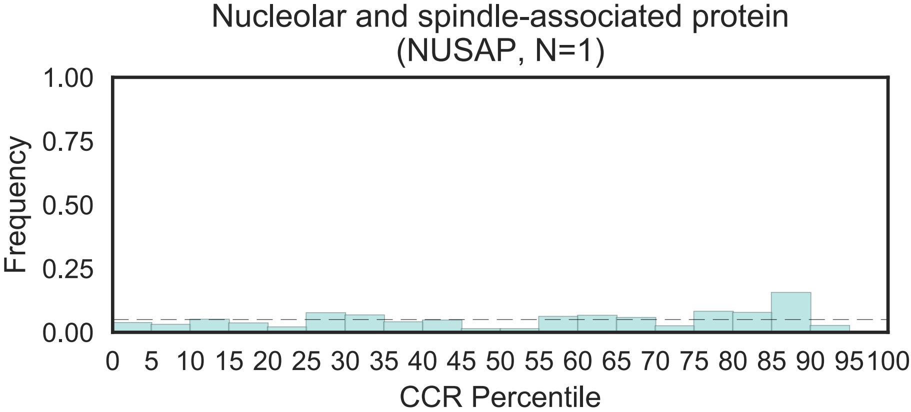


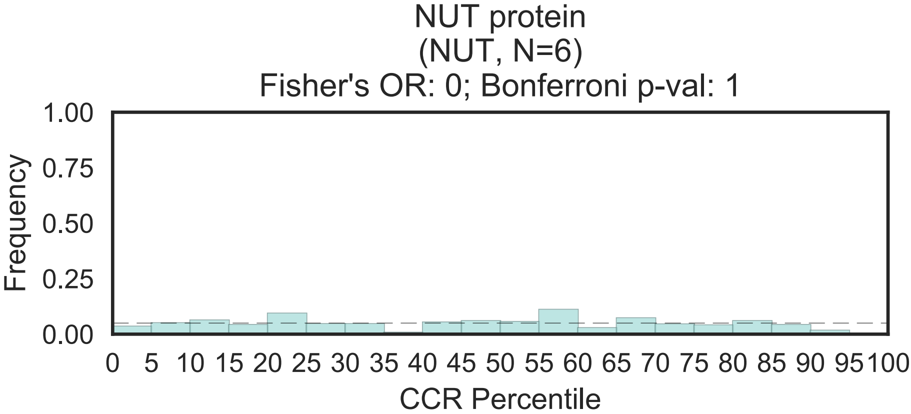

Nuclear fragile X mental retardation-interacting protein 1 (NUFIP1)
(NUFIP1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Nuclear fragile X mental retardation-interacting protein 2
(NUFIP2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

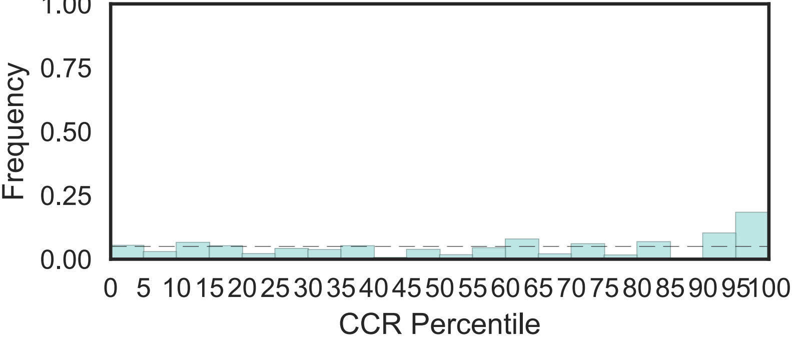
NUP50 (Nucleoporin 50 kDa)
(NUP50, N=1)

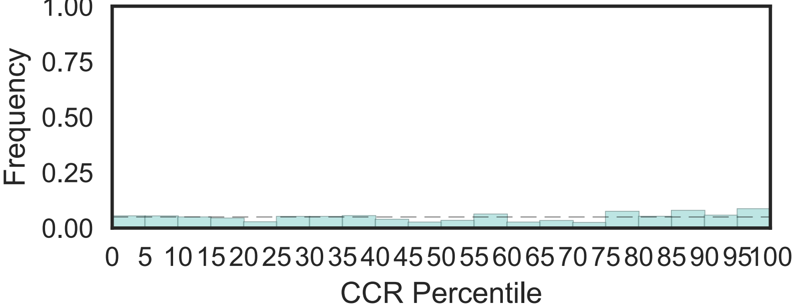



Nucleolar and spindle-associated protein
(NUSAP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

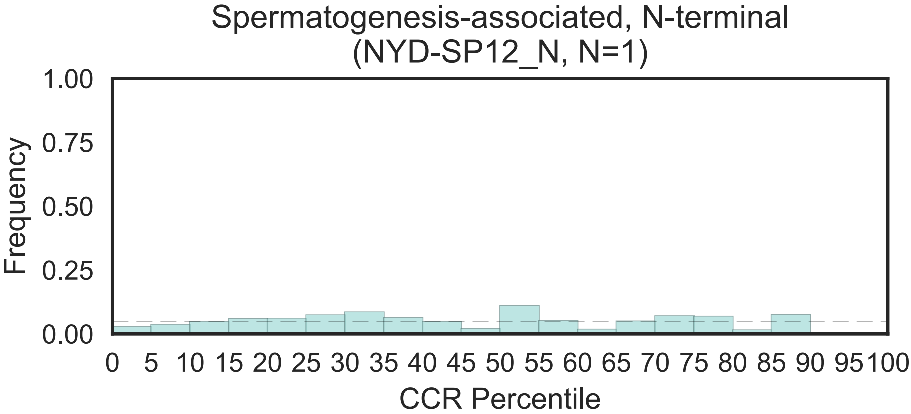

NUT protein
(NUT, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adapter (NYAP_C, N=2)

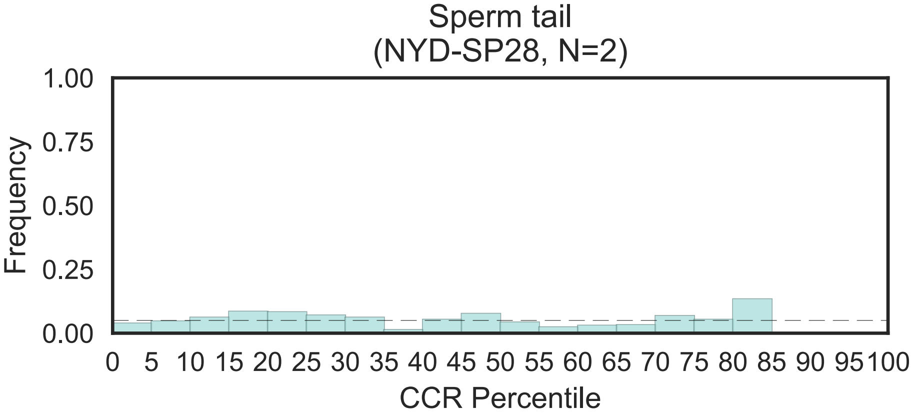


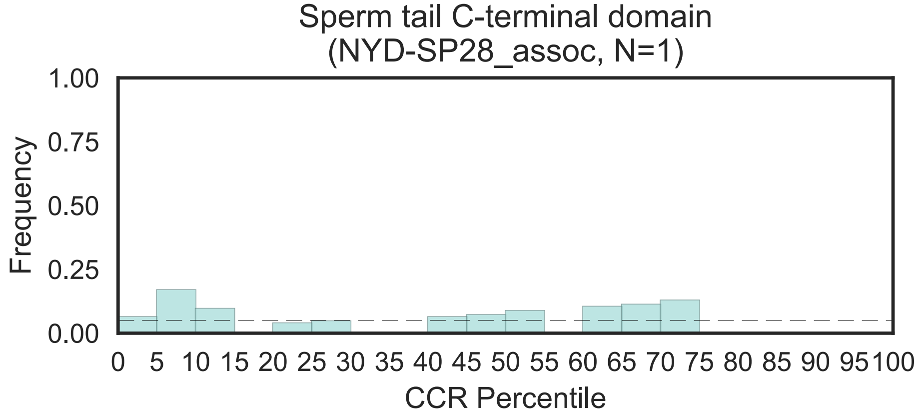


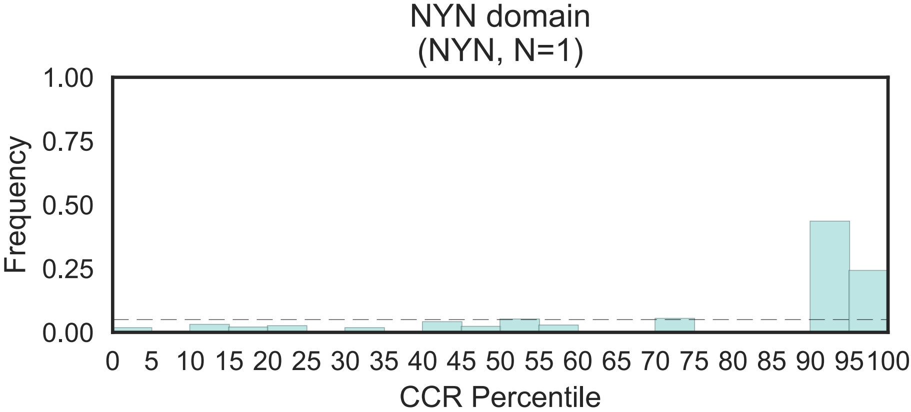
Neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adapter
(NYAP_N, N=3)
Fisher's OR: 1.17; Bonferroni p-val: 1

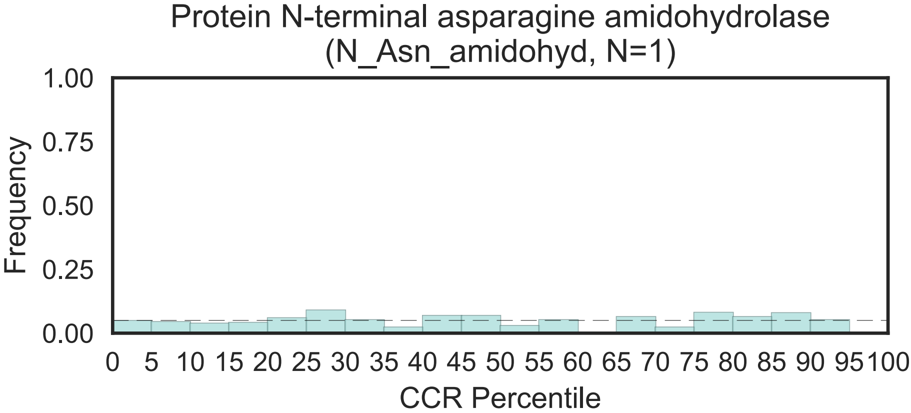


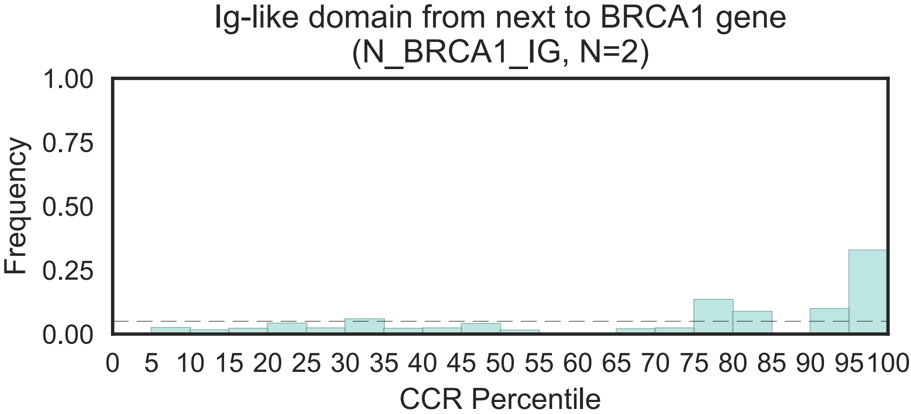
Spermatogenesis-associated, N-terminal
(NYD-SP12_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

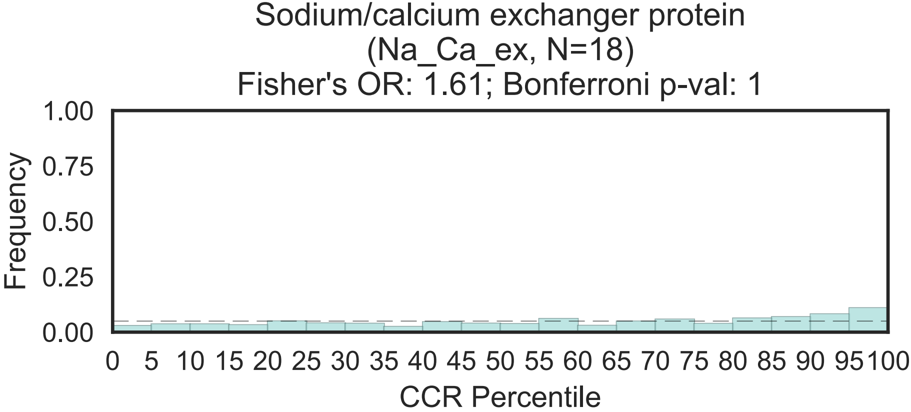

Sperm tail
(NYD-SP28, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

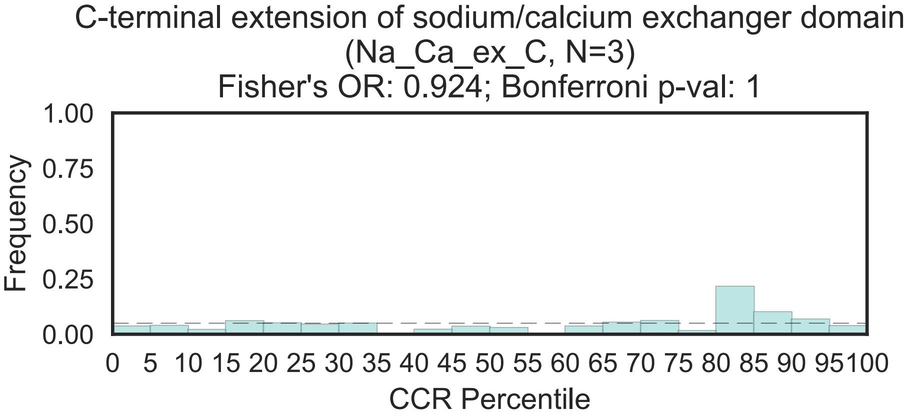

Sperm tail C-terminal domain
(NYD-SP28_assoc, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

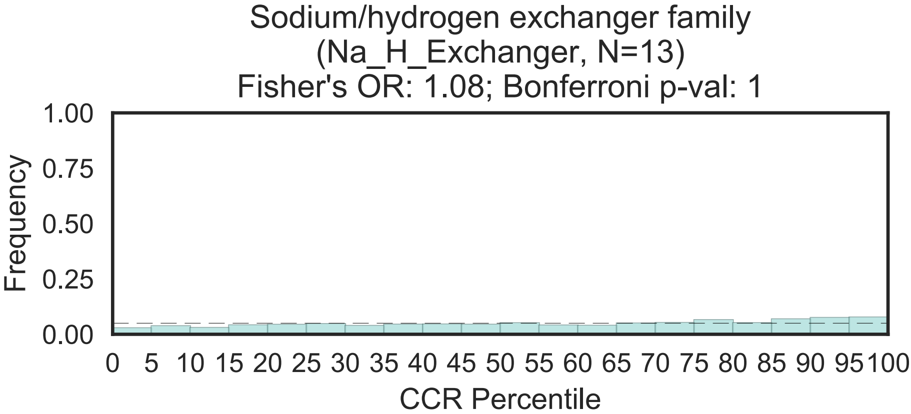

NYN domain
(NYN, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

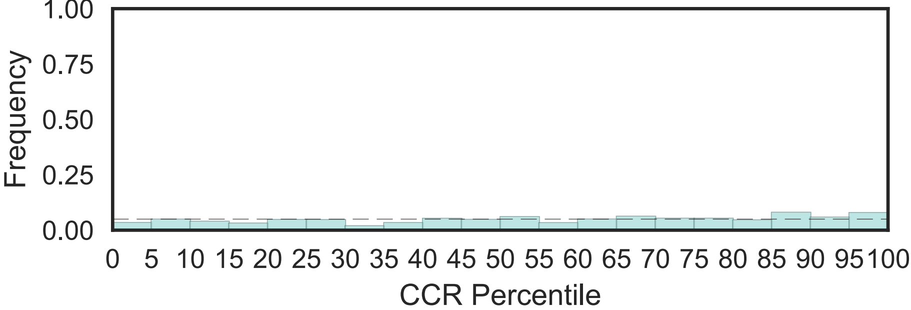

Protein N-terminal asparagine amidohydrolase
(N_Asn_amidohyd, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ig-like domain from next to BRCA1 gene
(N_BRCA1_IG, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

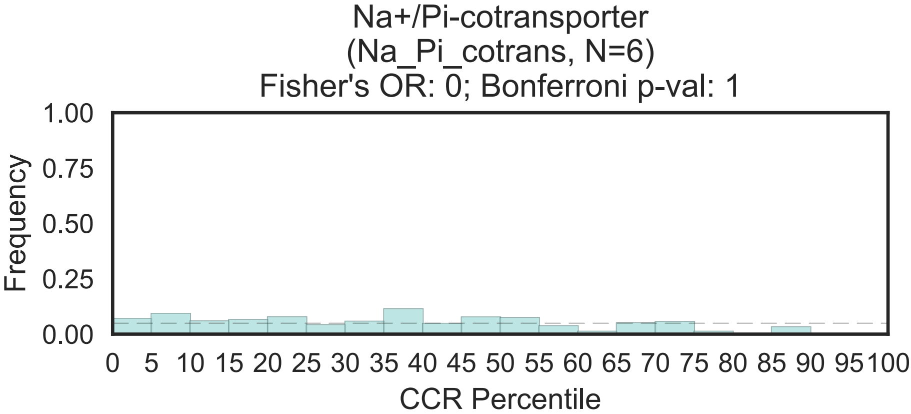

Sodium/calcium exchanger protein
(Na_Ca_ex, N=18)
Fisher's OR: 1.61; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

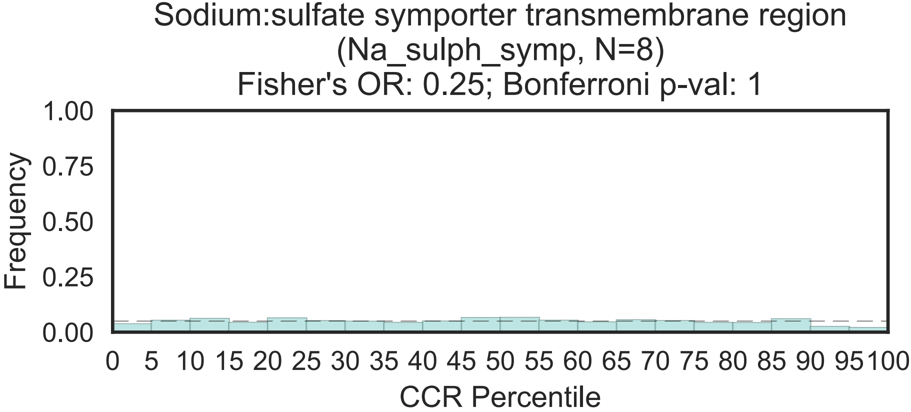

C-terminal extension of sodium/calcium exchanger domain
(Na_Ca_ex_C, N=3)
Fisher's OR: 0.924; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

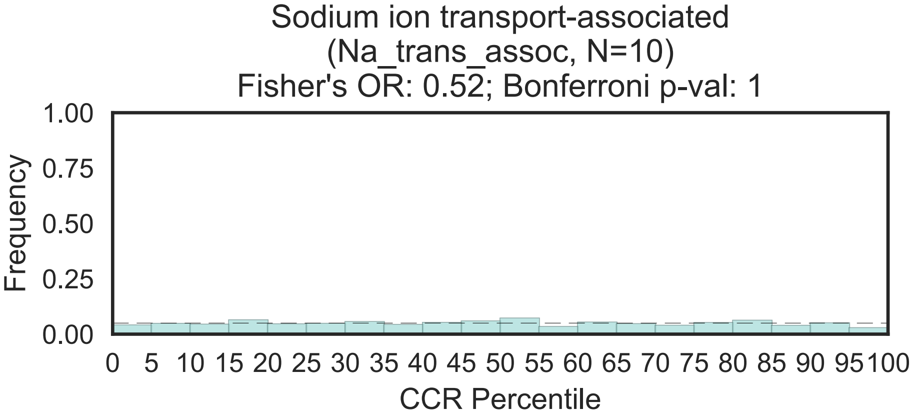

Sodium/hydrogen exchanger family
(Na_H_Exchanger, N=13)
Fisher's OR: 1.08; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



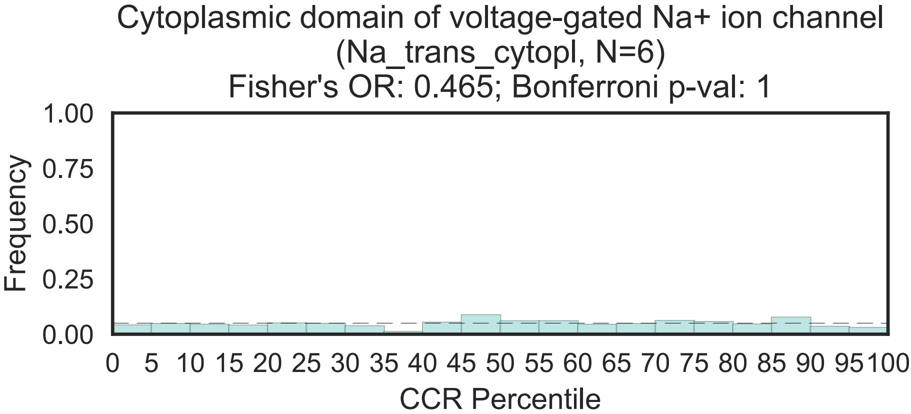
Sodium / potassium ATPase beta chain
(Na_K-ATPase, N=4)
Fisher's OR: 1.17; Bonferroni p-val: 1

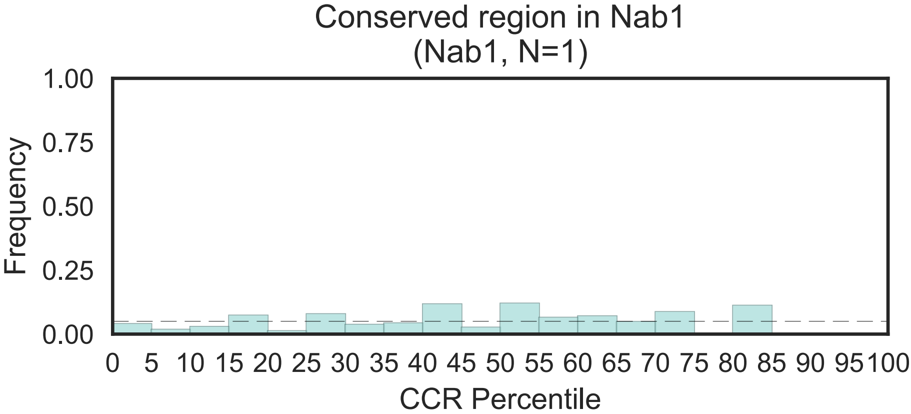

Na+/Pi-cotransporter
(Na_Pi_cotrans, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Sodium:sulfate symporter transmembrane region
(Na_sulph_symp, N=8)
Fisher's OR: 0.25; Bonferroni p-val: 1

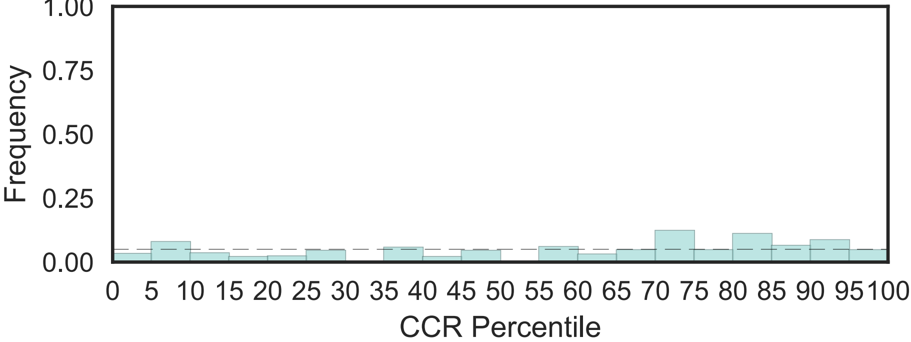


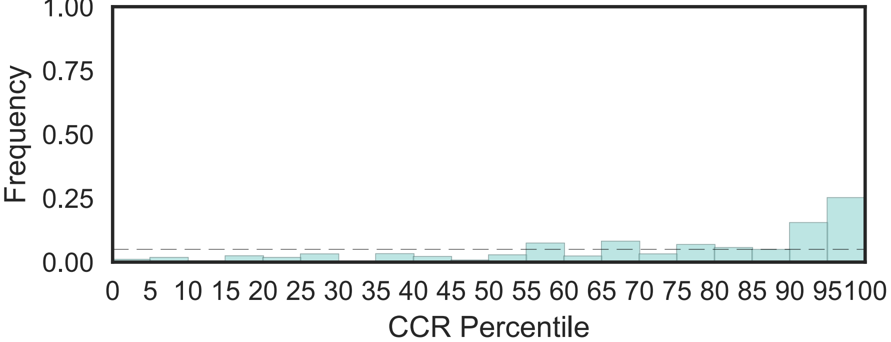
Sodium ion transport-associated
(Na_trans_assoc, N=10)
Fisher's OR: 0.52; Bonferroni p-val: 1


Cytoplasmic domain of voltage-gated Na+ ion channel
(Na_trans_cytopl, N=6)
Fisher's OR: 0.465; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

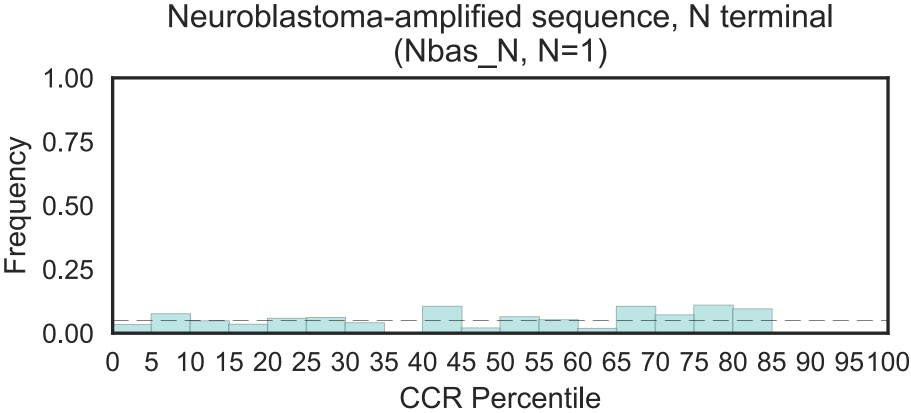

Conserved region in Nab1
(Nab1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

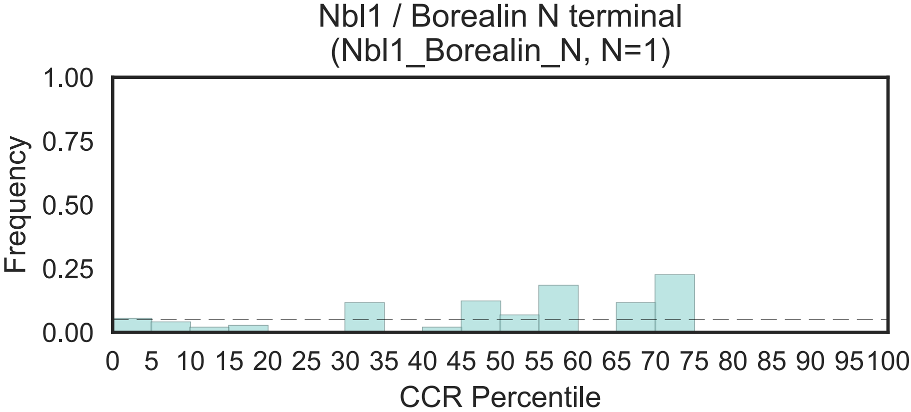
Putative N-acetylmannosamine-6-phosphate epimerase (NanE, N=1)

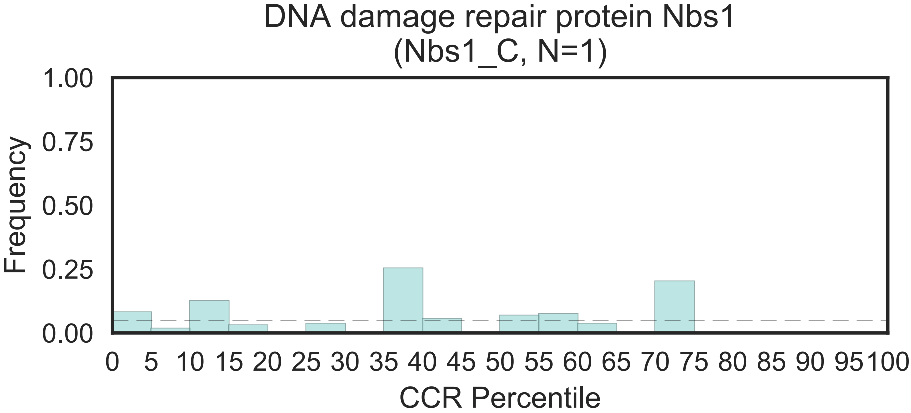


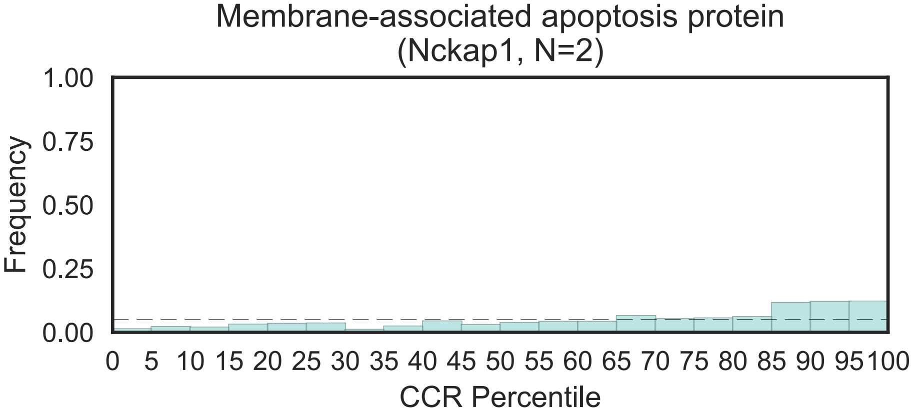


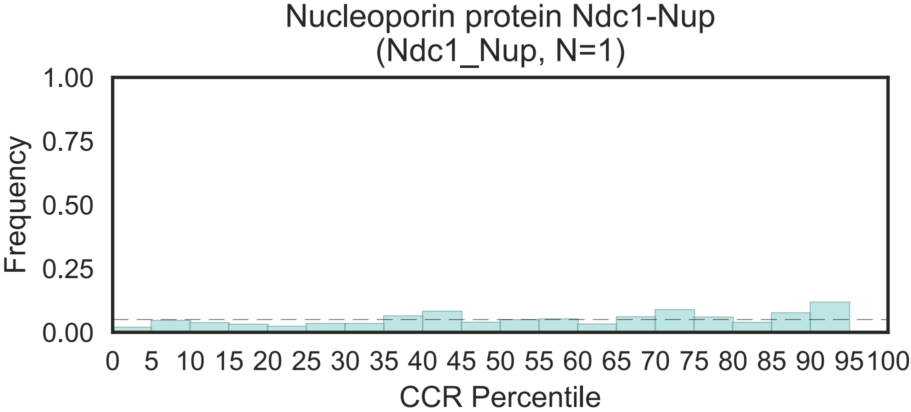
N-acetyltransferase B complex (NatB) non catalytic subunit (NatB_MDM20, N=1)

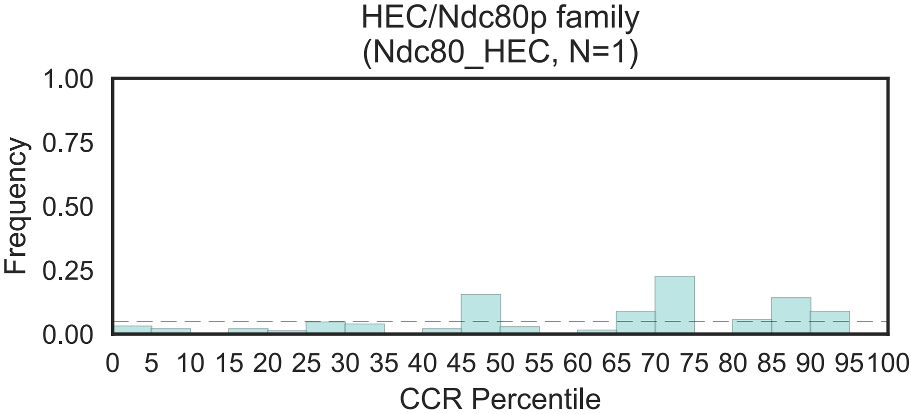

Neuroblastoma-amplified sequence, N terminal
(Nbas_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

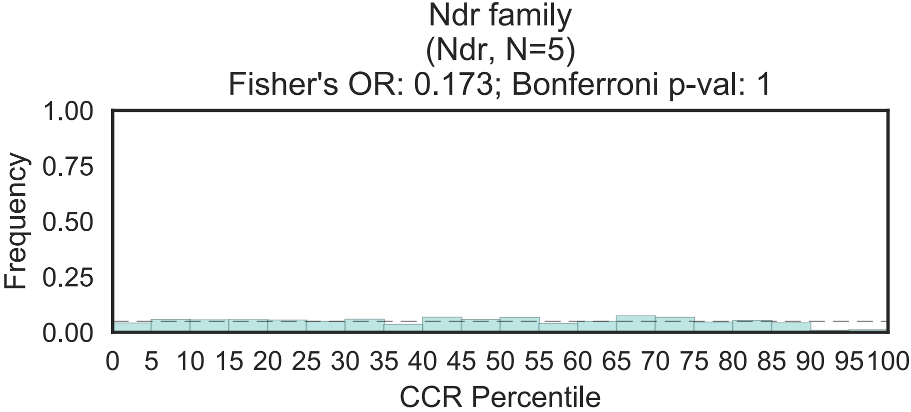

Nbl1 / Borealin N terminal
(Nbl1_Borealin_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

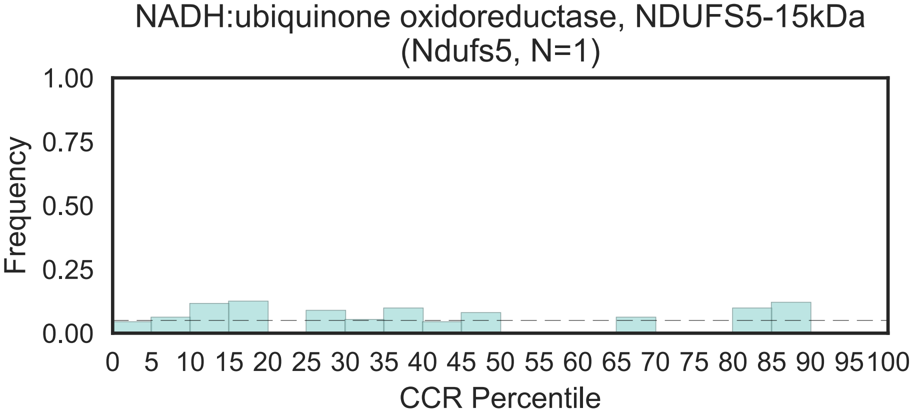

DNA damage repair protein Nbs1
(Nbs1_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

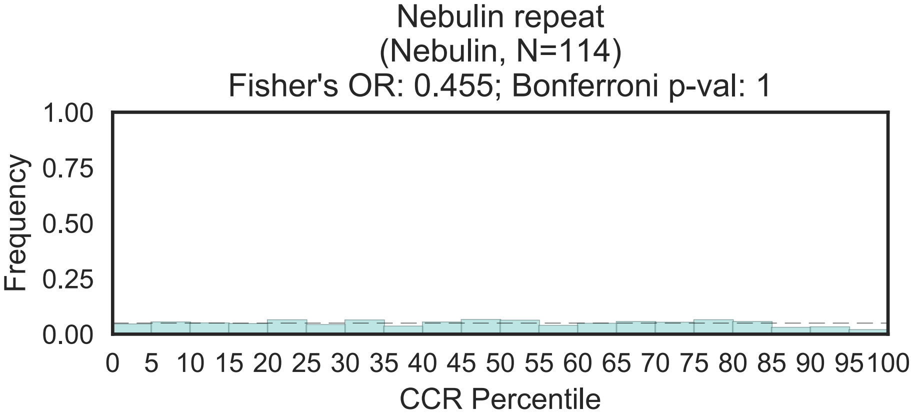

Membrane-associated apoptosis protein
(Nckap1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

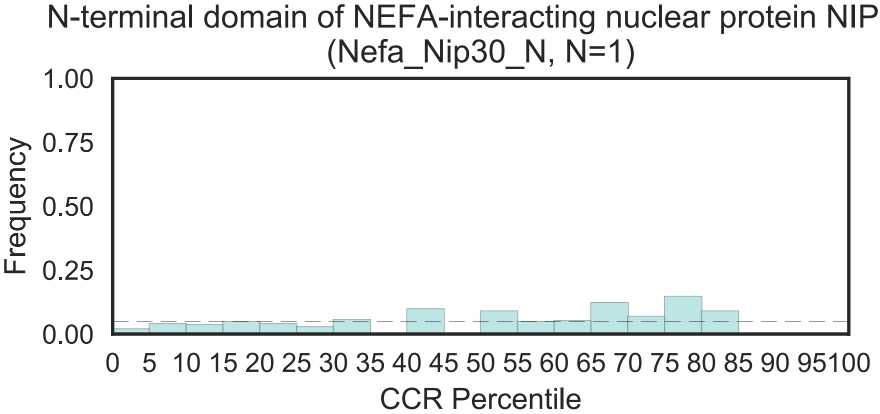

Nucleoporin protein Ndc1-Nup
(Ndc1_Nup, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

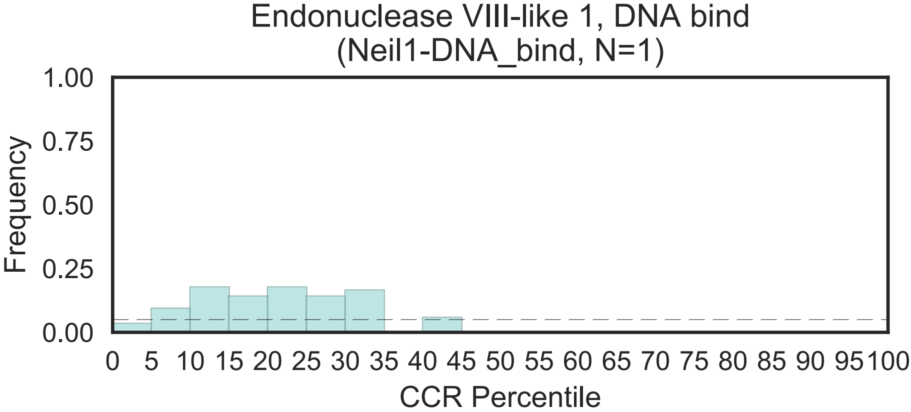

HEC/Ndc80p family
(Ndc80_HEC, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

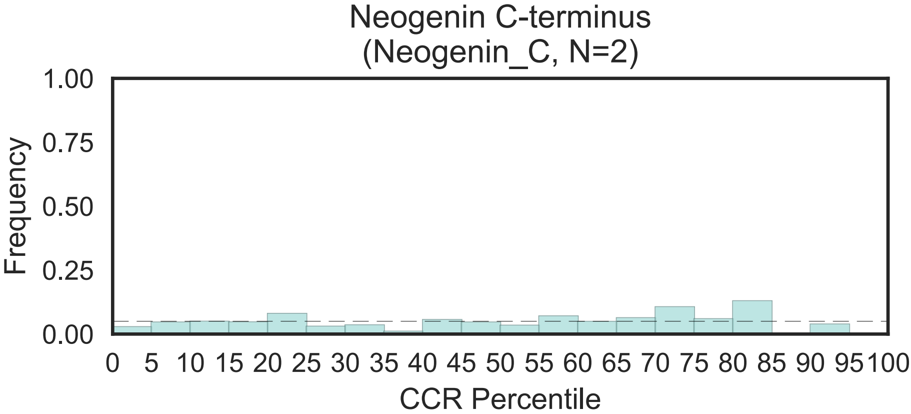

Ndr family
(Ndr, N=5)
Fisher's OR: 0.173; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

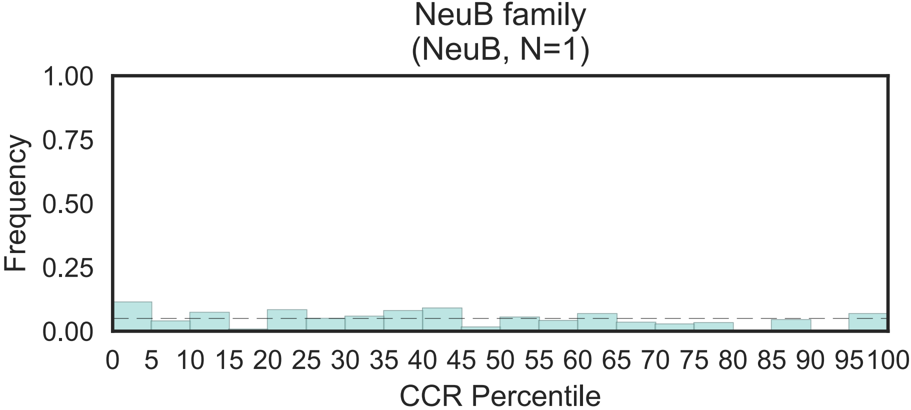

NADH:ubiquinone oxidoreductase, NDUFS5-15kDa
(Ndufs5, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

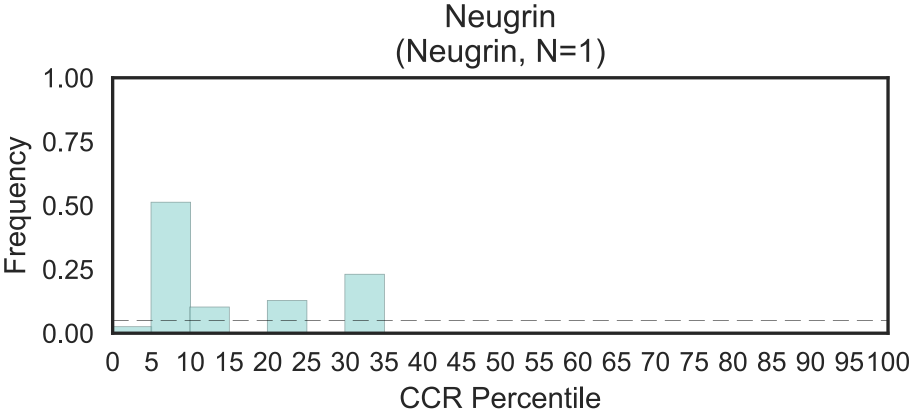

Nebulin repeat
(Nebulin, N=114)
Fisher's OR: 0.455; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

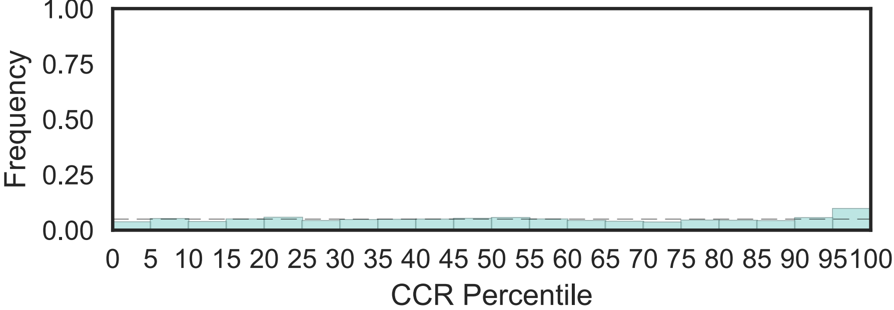
N-terminal domain of NEFA-interacting nuclear protein NIP30
(Nefa_Nip30_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Endonuclease VIII-like 1, DNA bind
(Neil1-DNA_bind, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

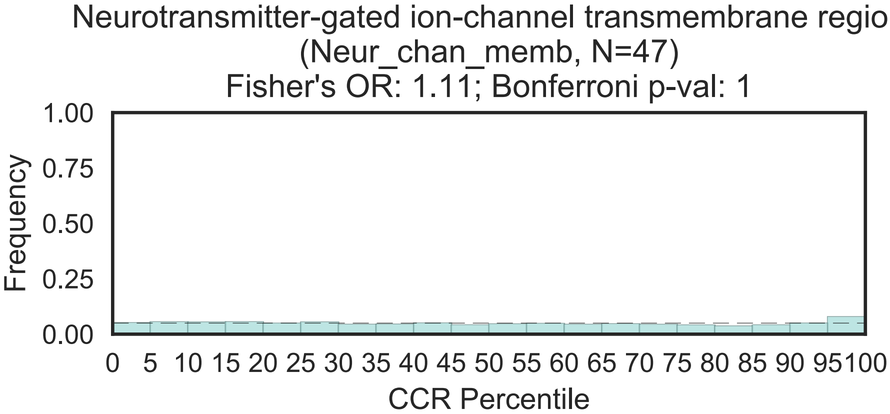

Neogenin C-terminus
(Neogenin_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

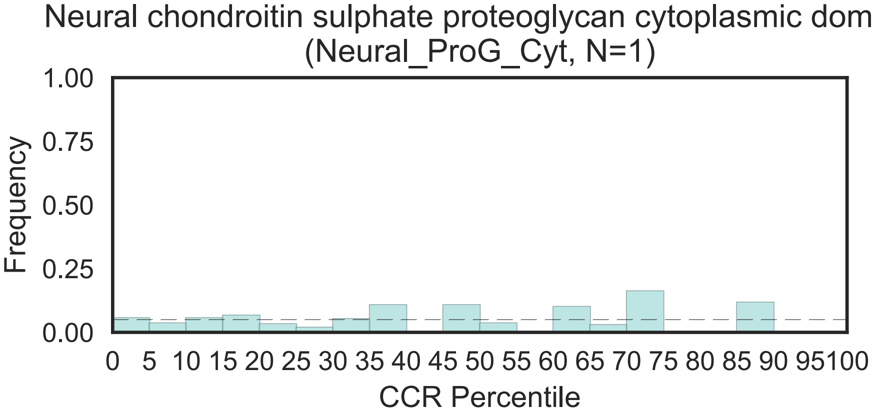

NeuB family
(NeuB, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

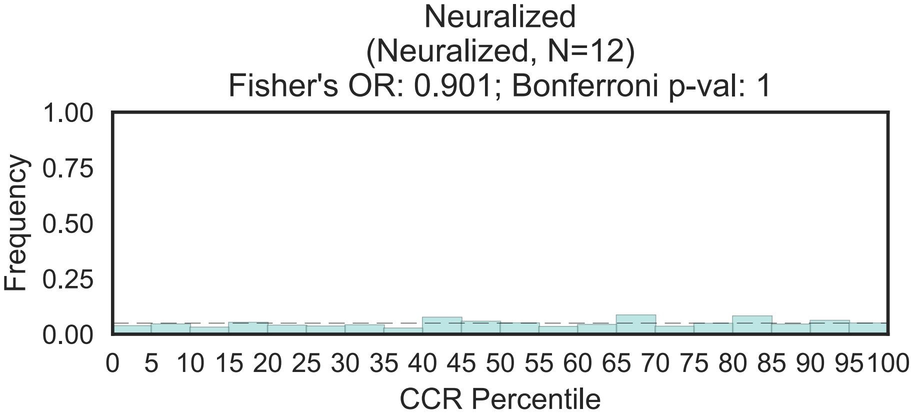

Neugrin
(Neugrin, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

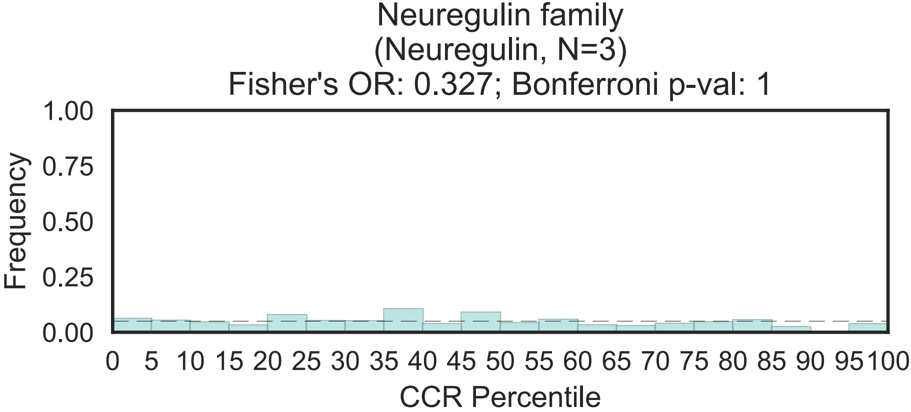


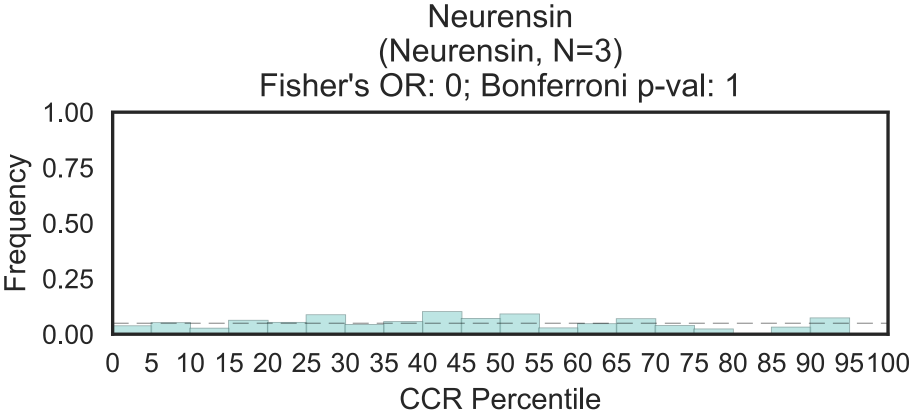
Neurotransmitter-gated ion-channel ligand binding domain
(Neur_chan_LBD, N=43)
Fisher's OR: 1.35; Bonferroni p-val: 1

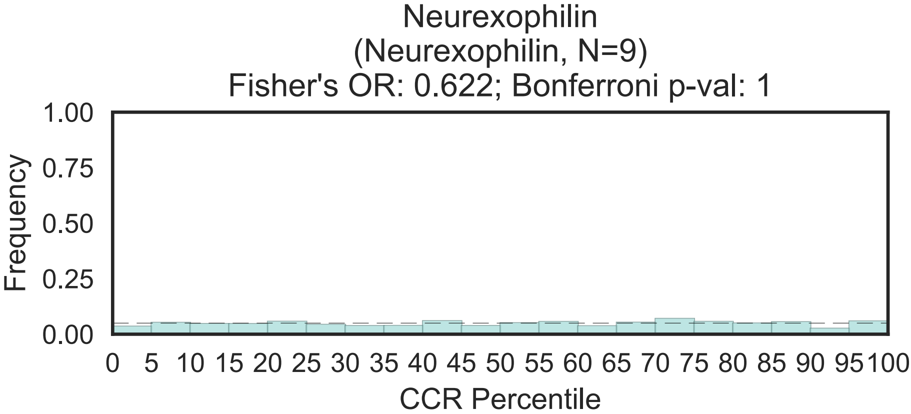

Neurotransmitter-gated ion-channel transmembrane region
(Neur_chan_memb, N=47)
Fisher's OR: 1.11; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

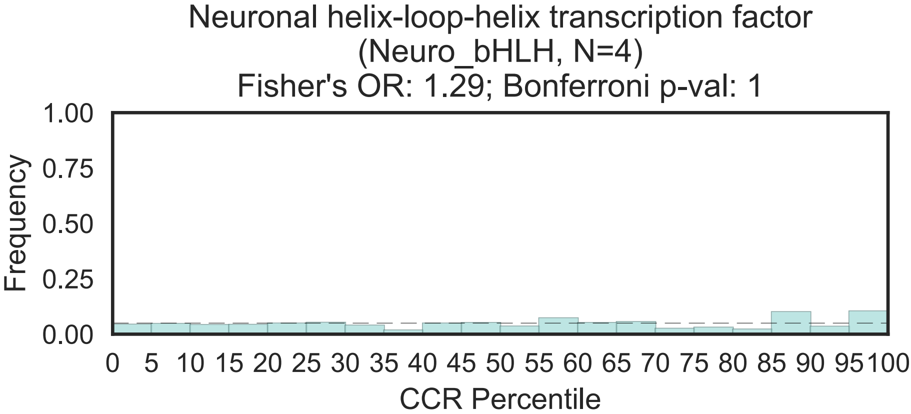

Neural chondroitin sulphate proteoglycan cytoplasmic domain
(Neural_ProG_Cyt, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

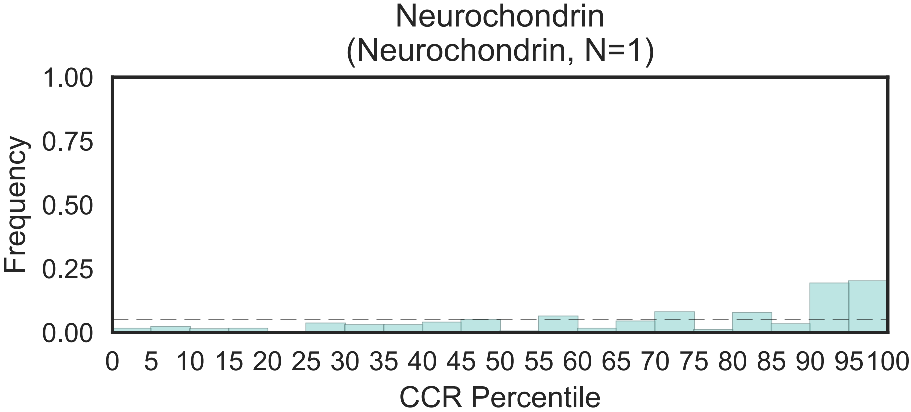

Neuralized
(Neuralized, N=12)
Fisher's OR: 0.901; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Neuregulin family
(Neuregulin, N=3)
Fisher's OR: 0.327; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

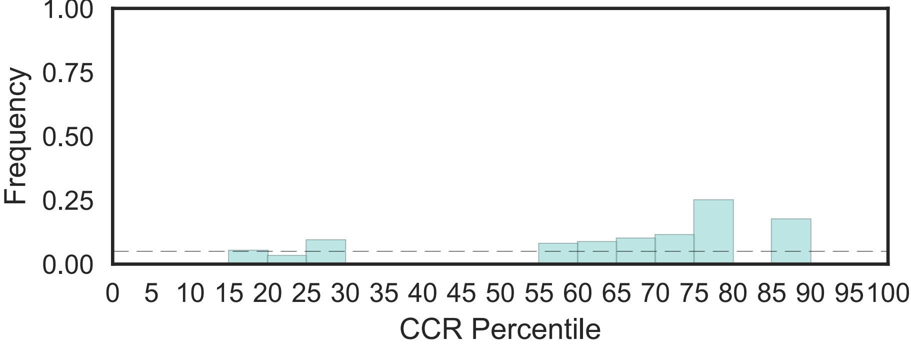

Neurensin
(Neurensin, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

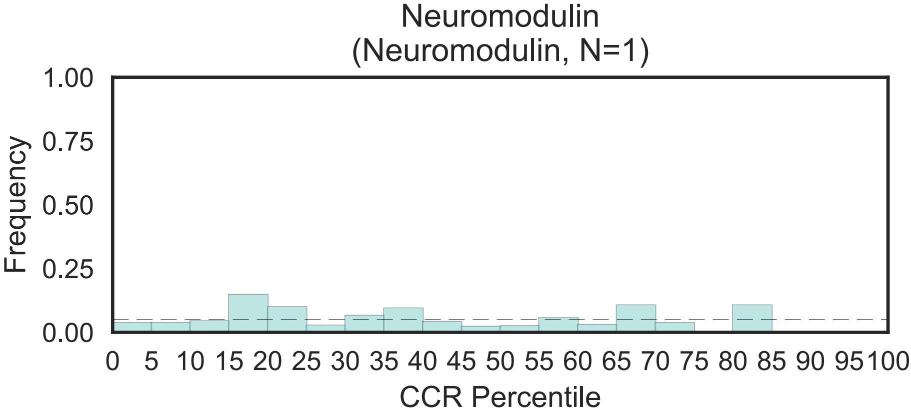

Neurexophilin
(Neurexophilin, N=9)
Fisher's OR: 0.622; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

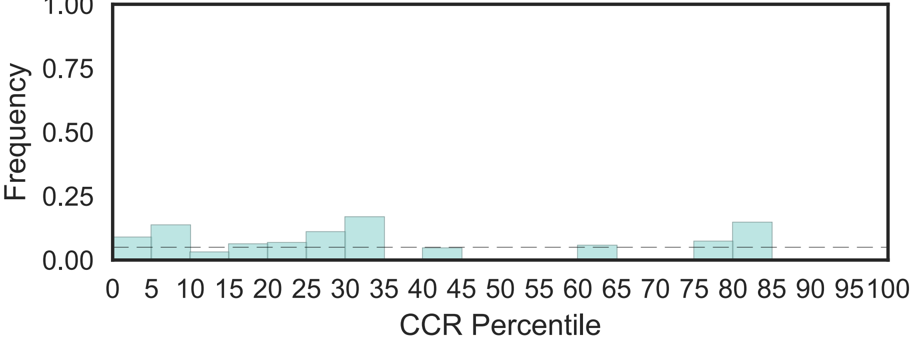

Neuronal helix-loop-helix transcription factor
(Neuro_bHLH, N=4)
Fisher's OR: 1.29; Bonferroni p-val: 1


Neurochondrin
(Neurochondrin, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

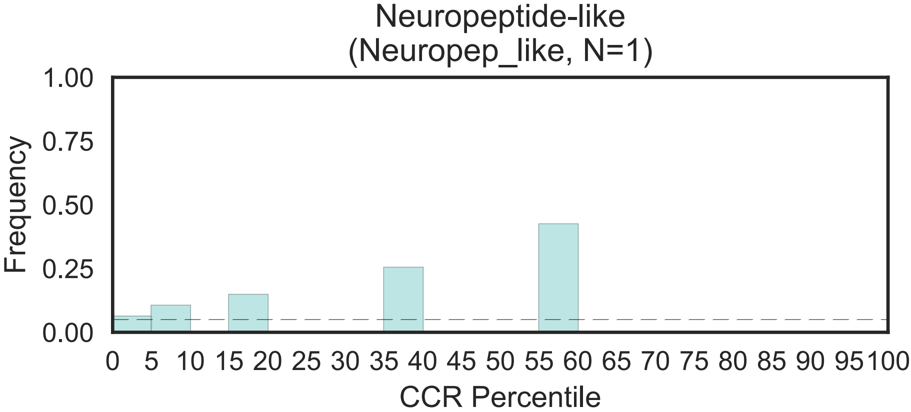
Neurokinin B
(Neurokinin_B, N=1)

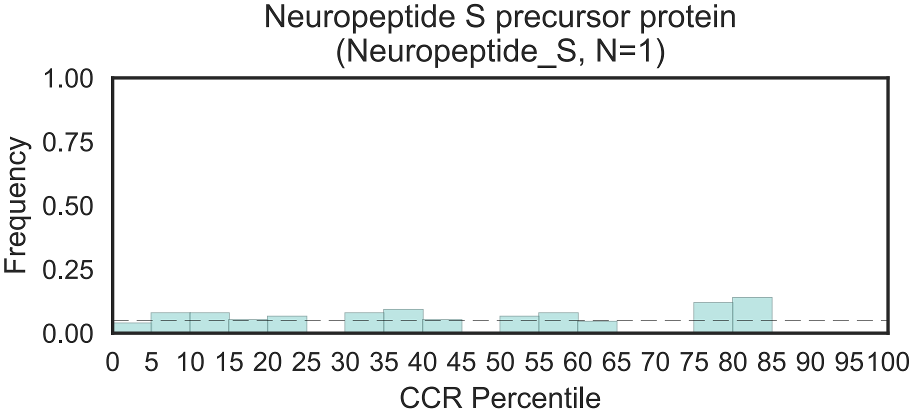


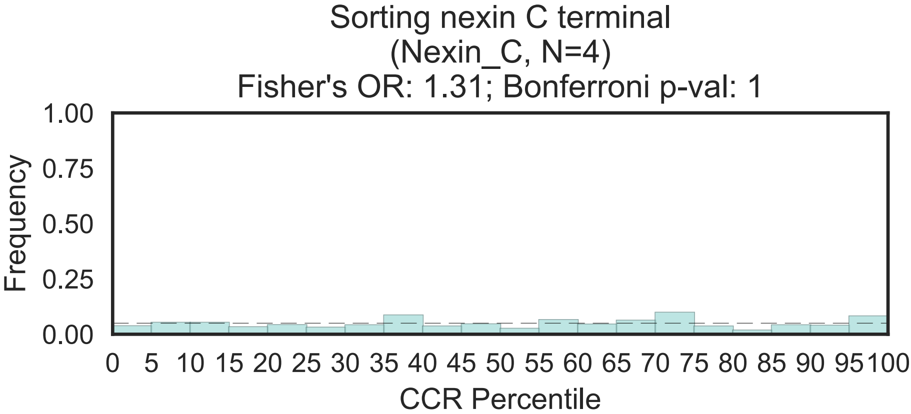

Neuromodulin
(Neuromodulin, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

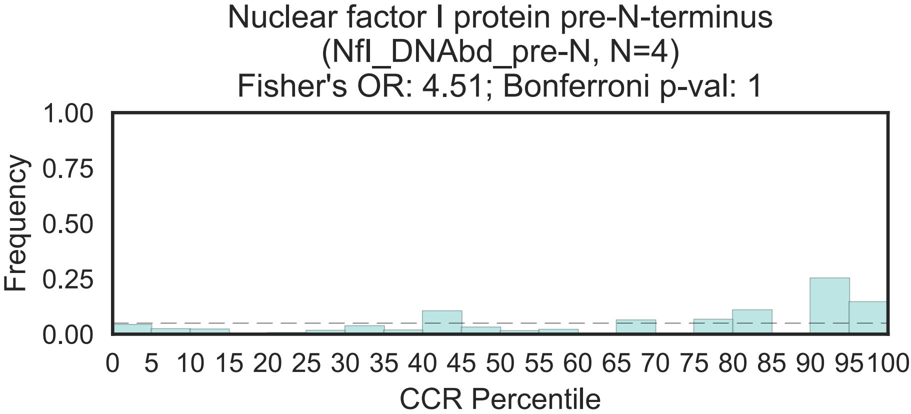


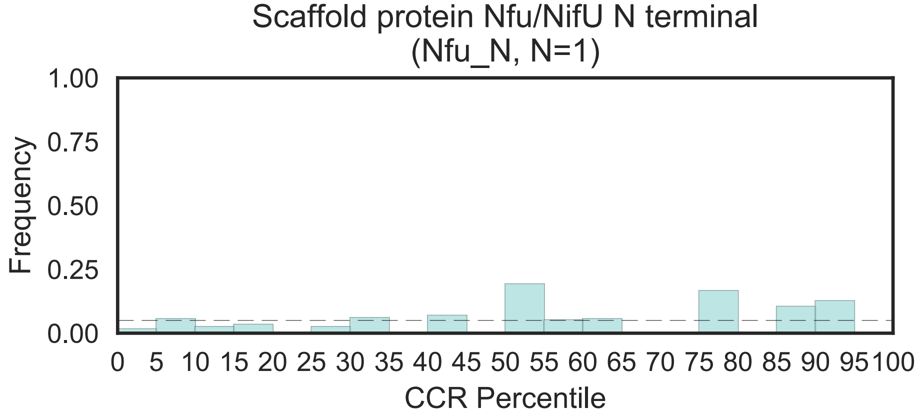
Gap junction protein N-terminal region
(Neuromodulin_N, N=1)

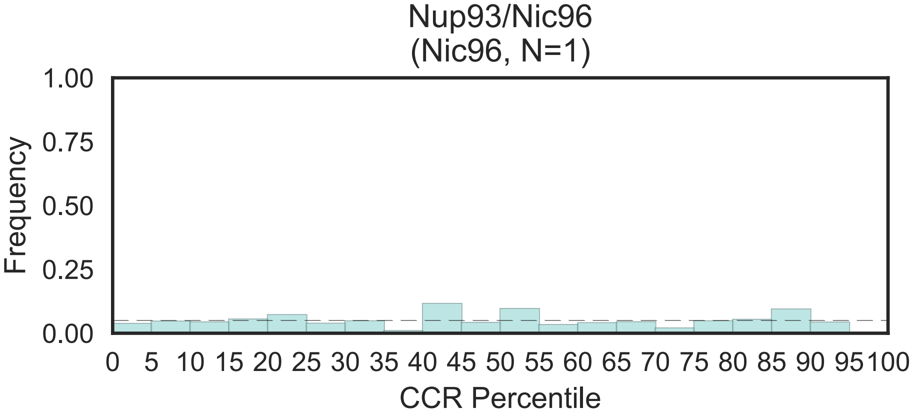

Neuropeptide-like
(Neuropep_like, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

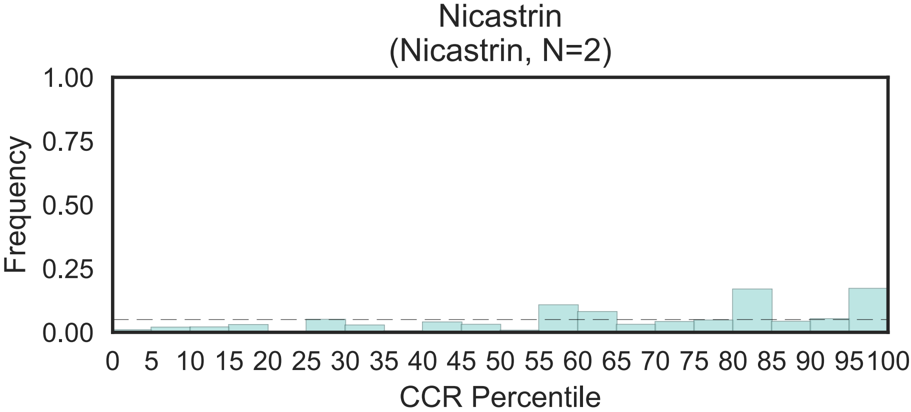

Neuropeptide S precursor protein
(Neuropeptide_S, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

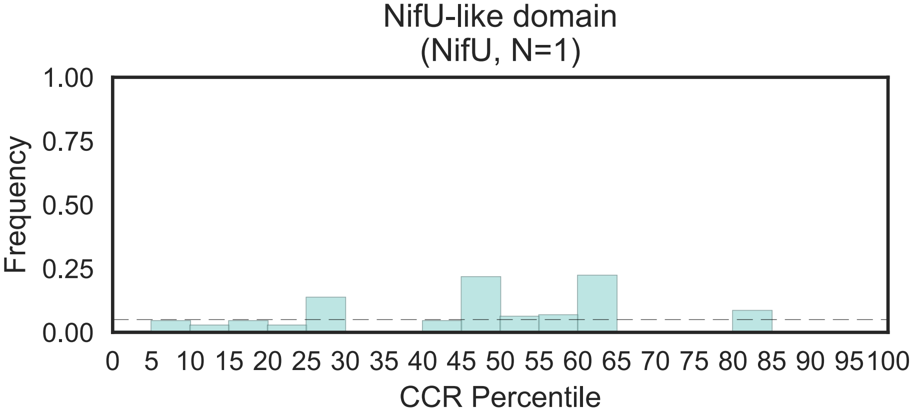

Sorting nexin C terminal
(Nexin_C, N=4)
Fisher's OR: 1.31; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

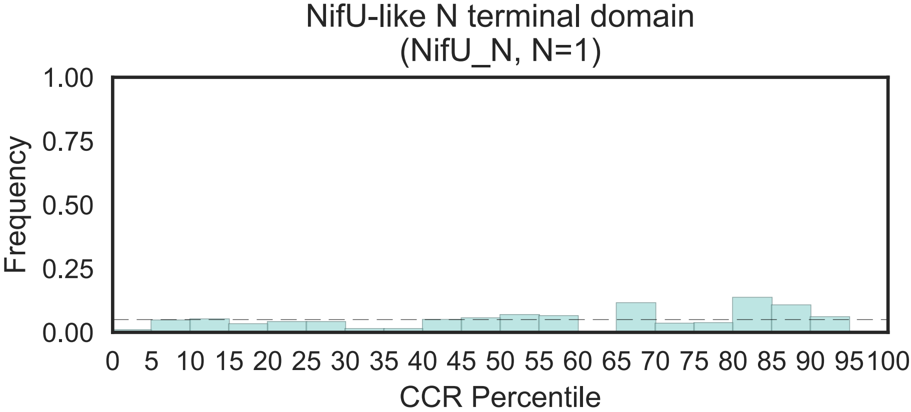

Nuclear factor I protein pre-N-terminus
(NfI_DNAbd_pre-N, N=4)
Fisher's OR: 4.51; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

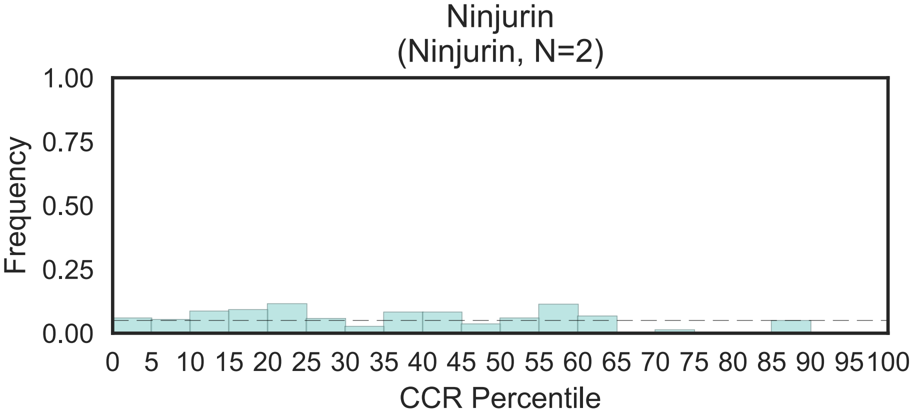

Scaffold protein Nfu/NifU N terminal
(Nfu_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

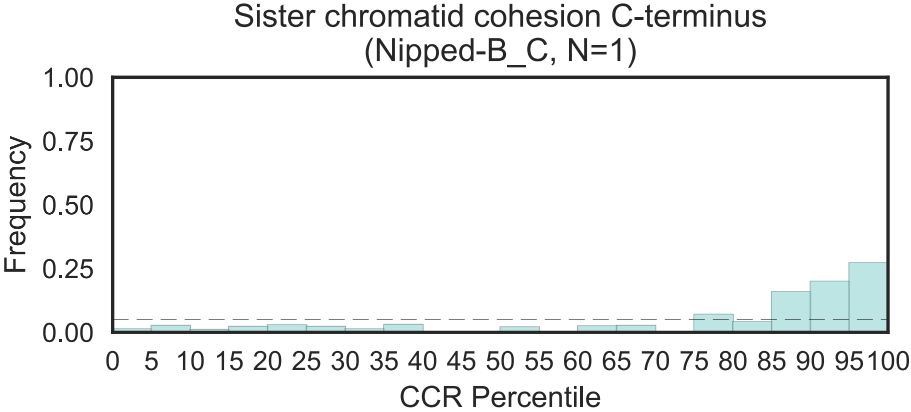

Nup93/Nic96
(Nic96, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

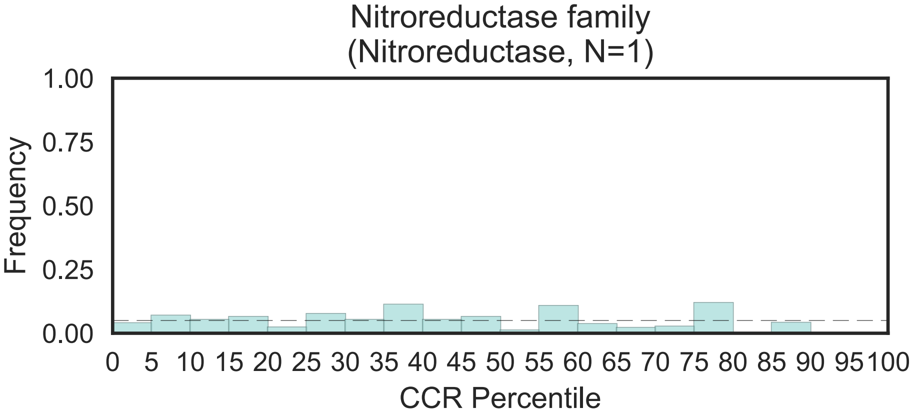

Nicastrin
(Nicastrin, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

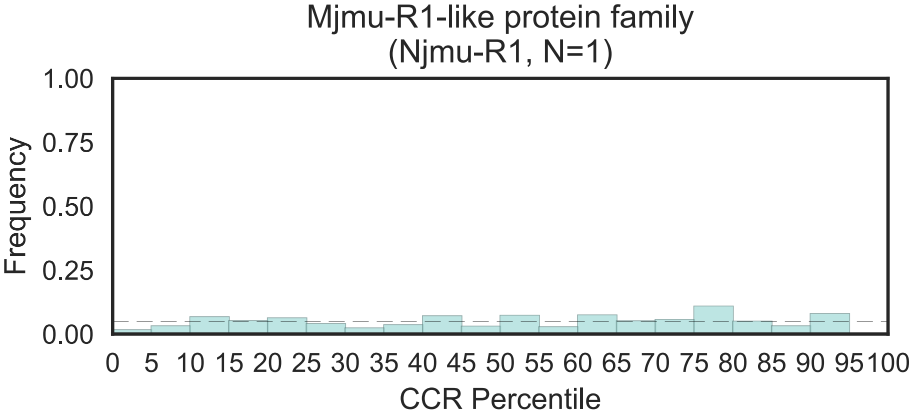

NifU-like domain
(NifU, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

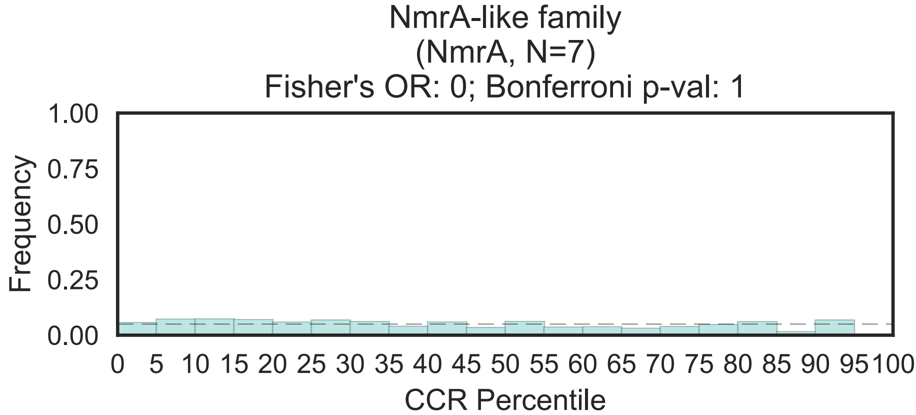

NifU-like N terminal domain
(NifU_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

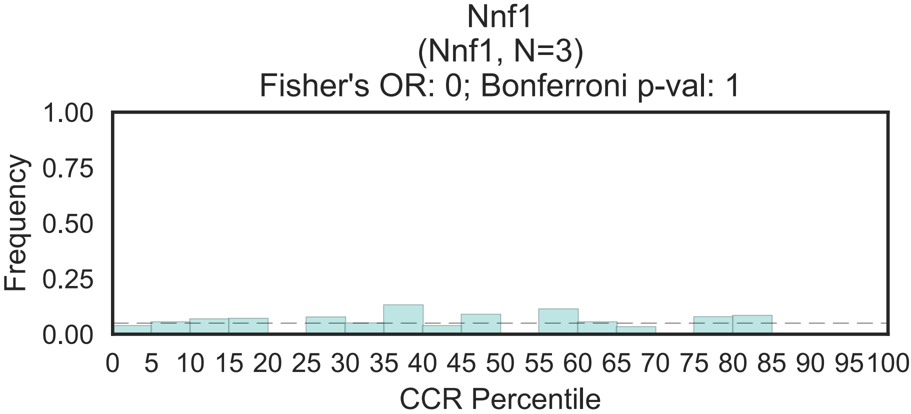

Ninjurin
(Ninjurin, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

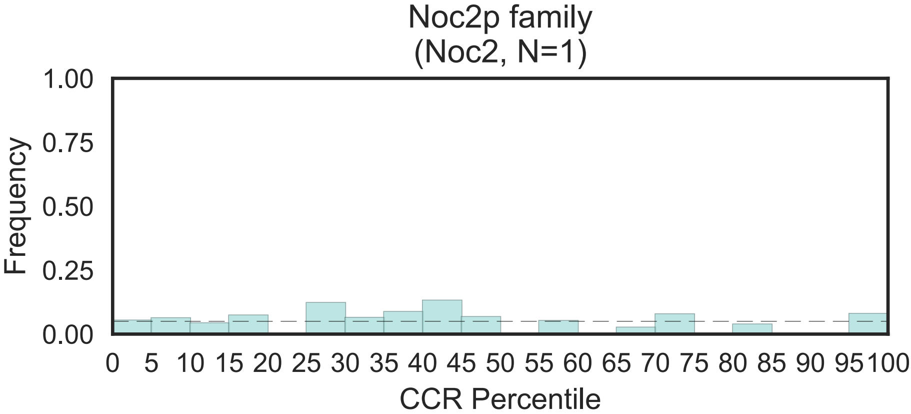

Sister chromatid cohesion C-terminus
(Nipped-B_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

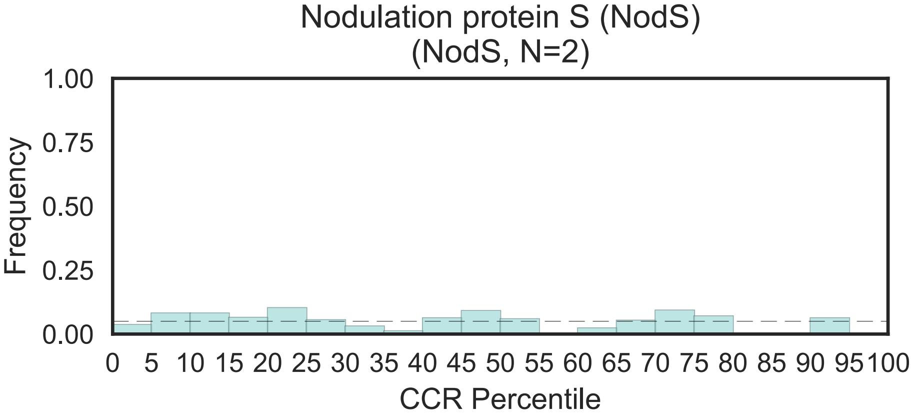

Nitroreductase family
(Nitroreductase, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

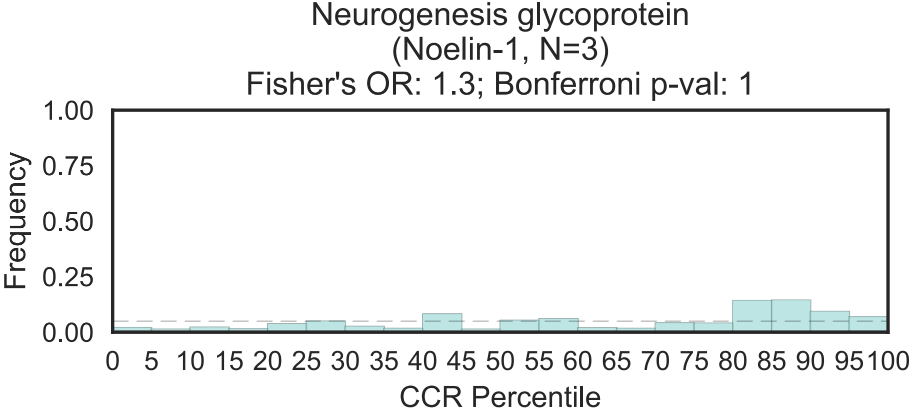

Mjmu-R1-like protein family
(Njmu-R1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

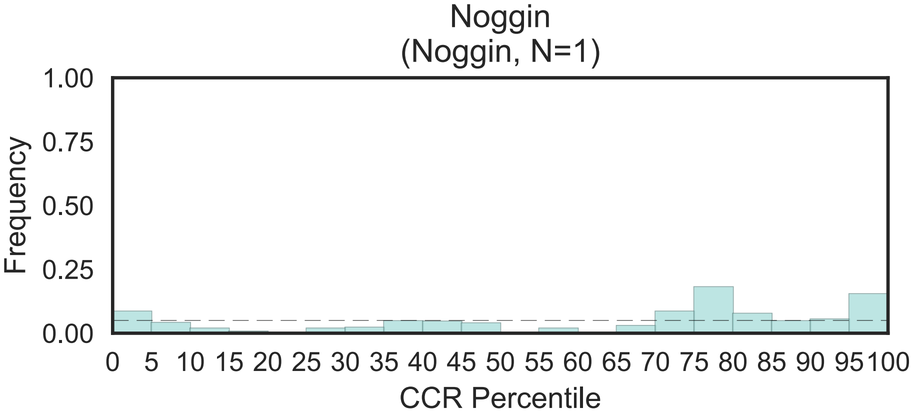

NmrA-like family
(NmrA, N=7)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

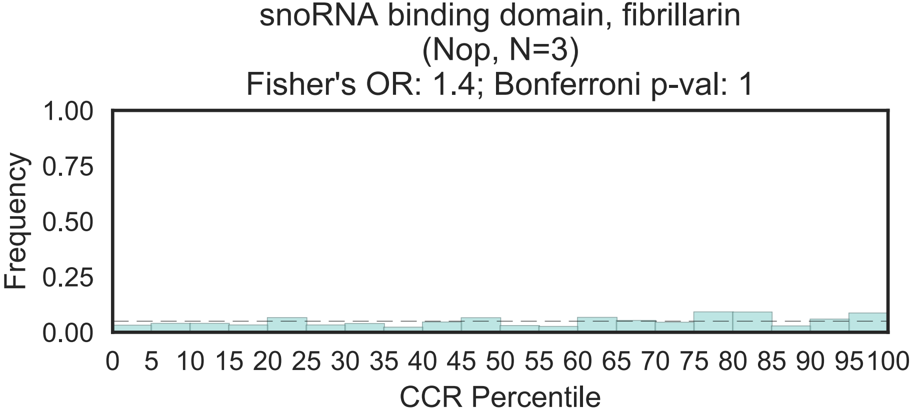

Nnf1
(Nnf1, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

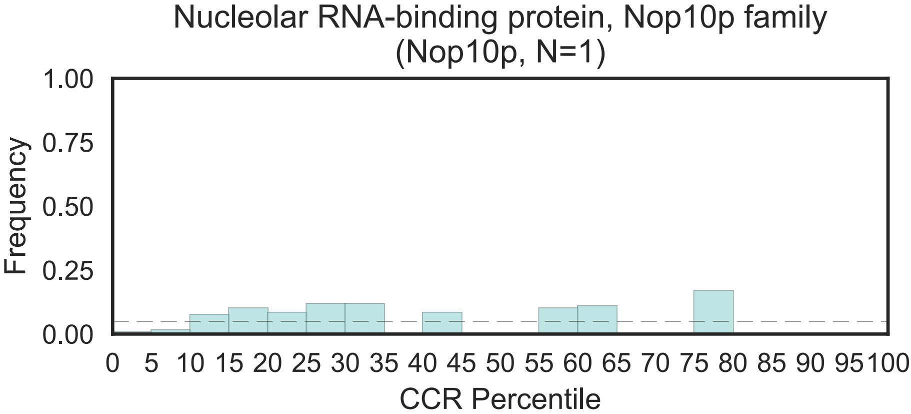

Noc2p family
(Noc2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

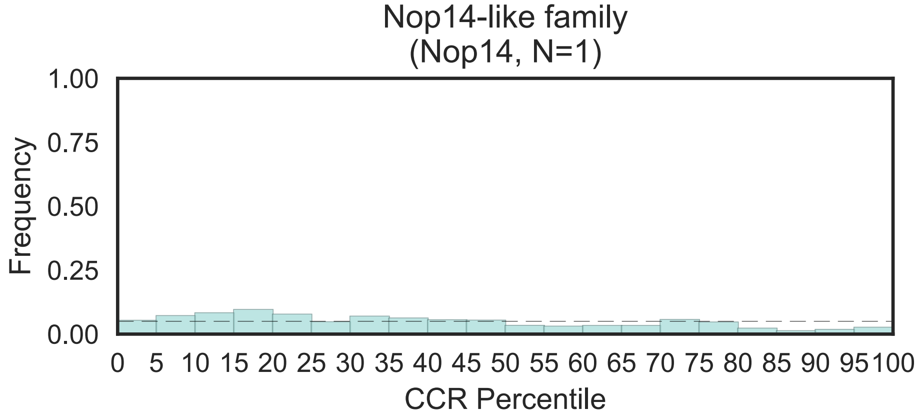

Nodulation protein S (NodS)
(NodS, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


Neurogenesis glycoprotein
(Noelin-1, N=3)
Fisher's OR: 1.3; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

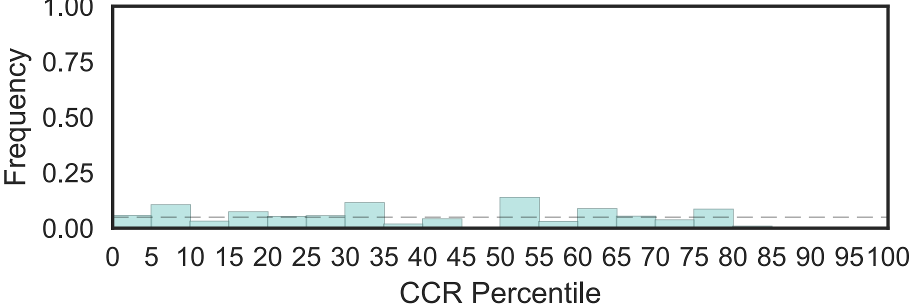

Noggin
(Noggin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

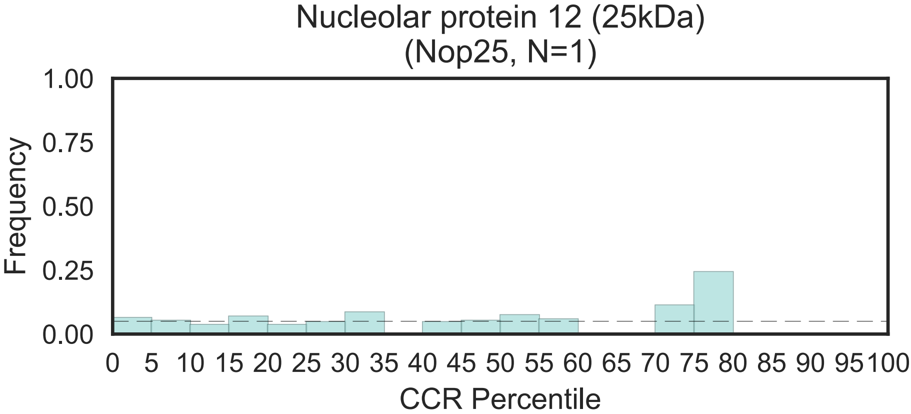

snoRNA binding domain, fibrillarin
(Nop, N=3)
Fisher's OR: 1.4; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

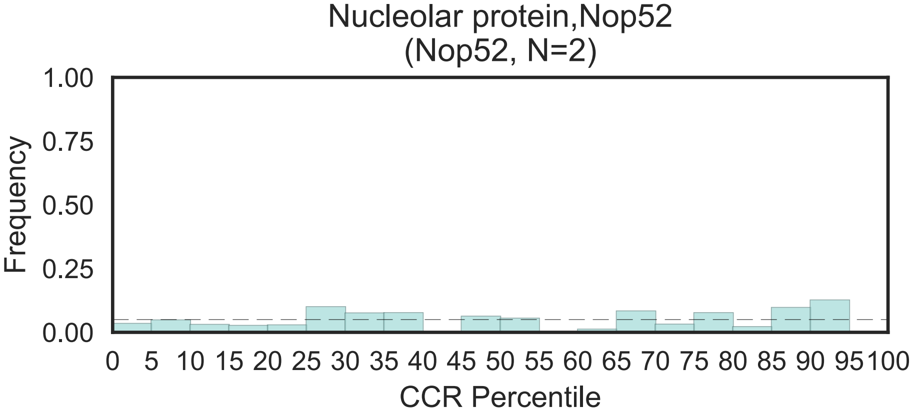

Nucleolar RNA-binding protein, Nop10p family
(Nop10p, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

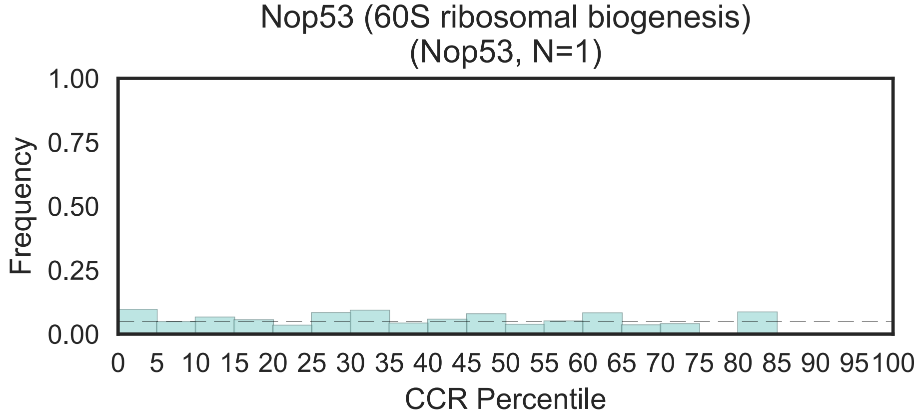

Nop14-like family
(Nop14, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

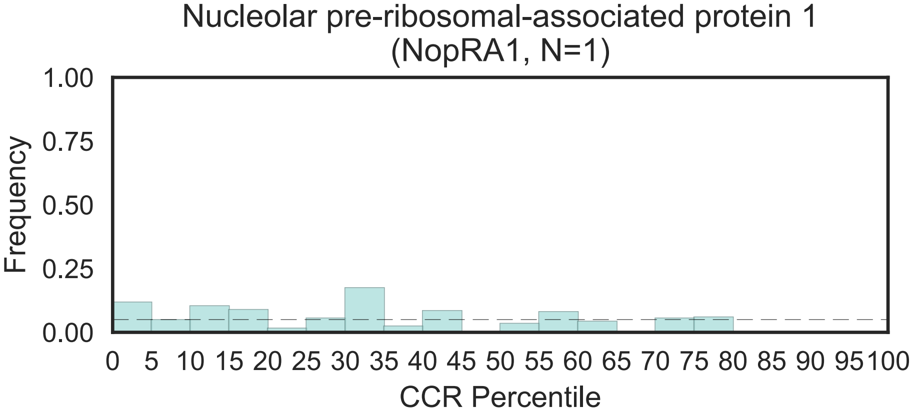
Ribosome biogenesis protein Nop16
(Nop16, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

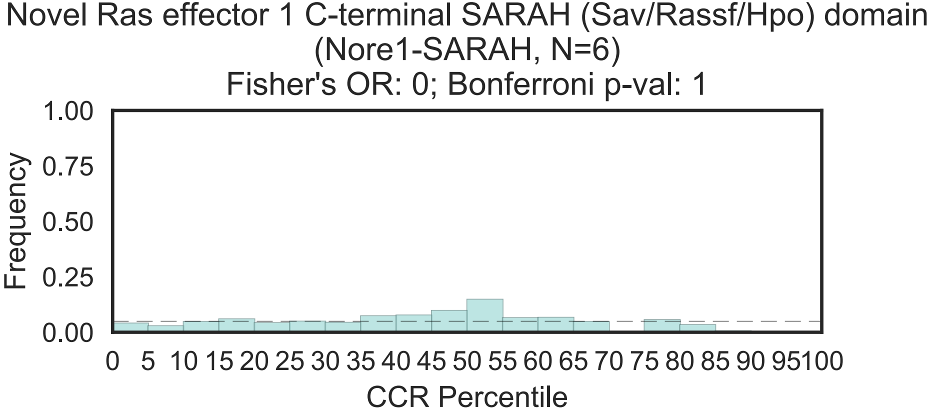


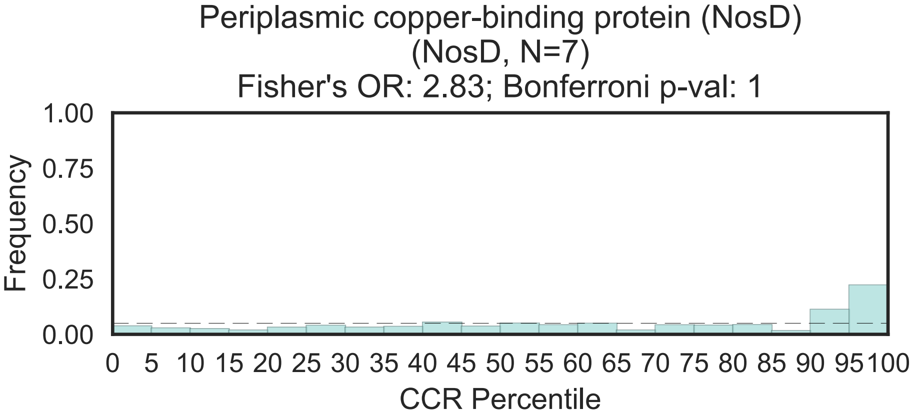

Nucleolar protein 12 (25kDa)
(Nop25, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

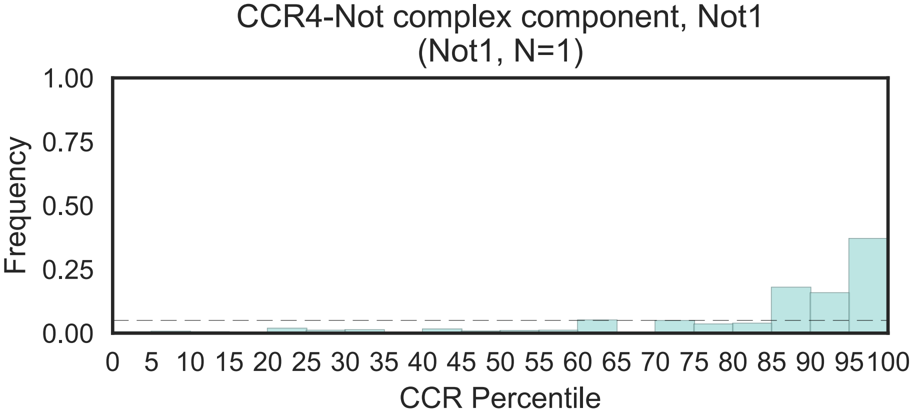

Nucleolar protein,Nop52
(Nop52, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

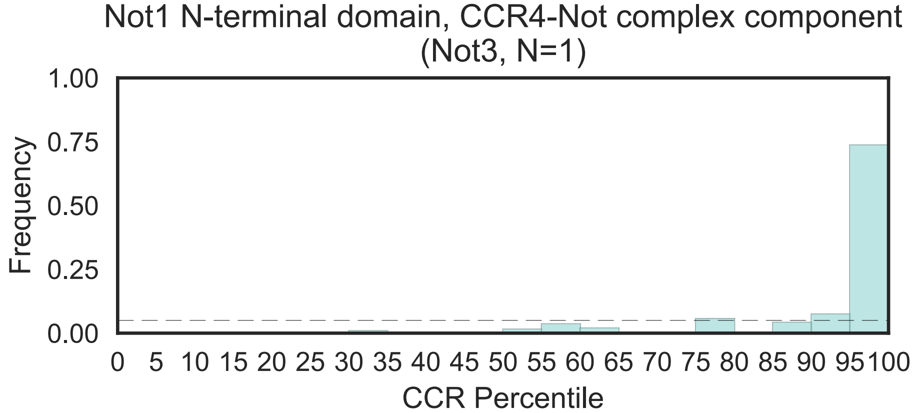

Nop53 (60S ribosomal biogenesis)
(Nop53, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

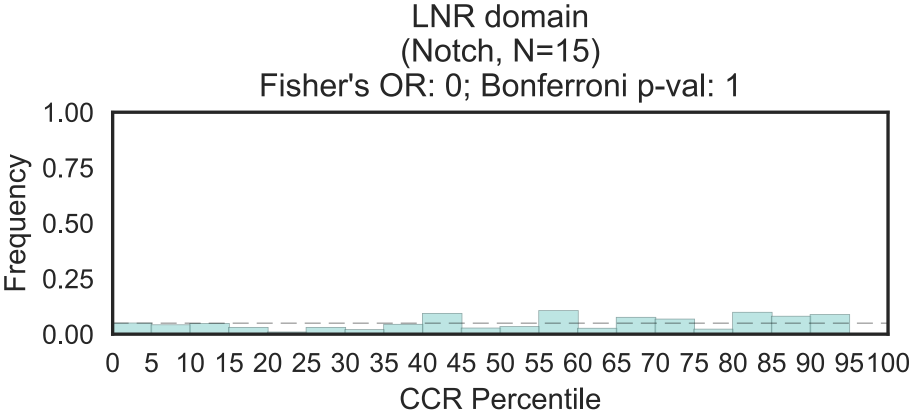

Nucleolar pre-ribosomal-associated protein 1
(NopRA1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

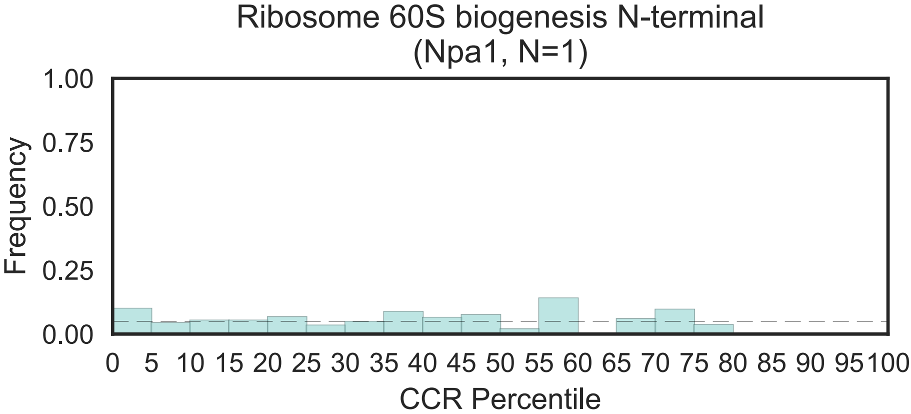

Novel Ras effector 1 C-terminal SARAH (Sav/Rassf/Hpo) domain
(Nore1-SARAH, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

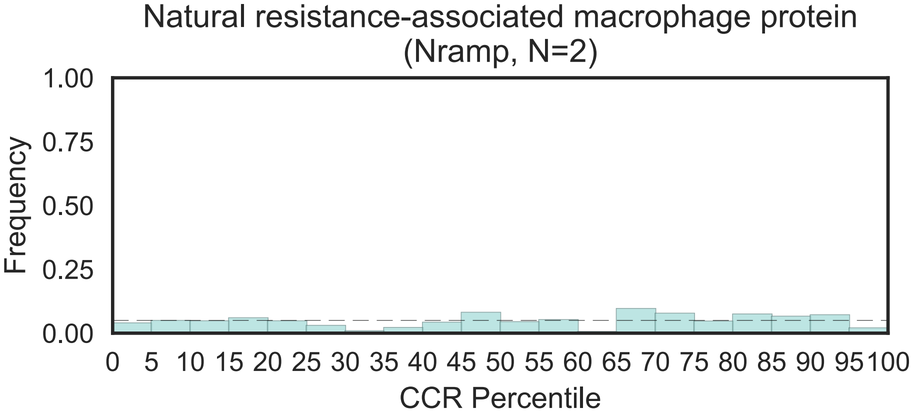

Periplasmic copper-binding protein (NosD)
(NosD, N=7)
Fisher's OR: 2.83; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

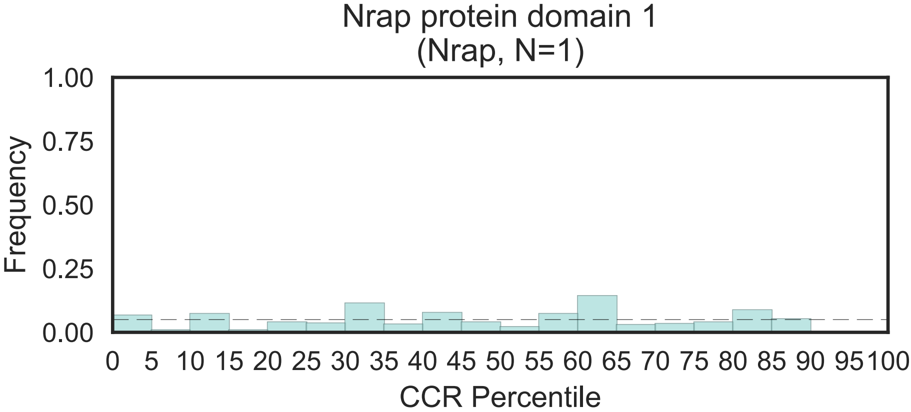

CCR4-Not complex component, Not1
(Not1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

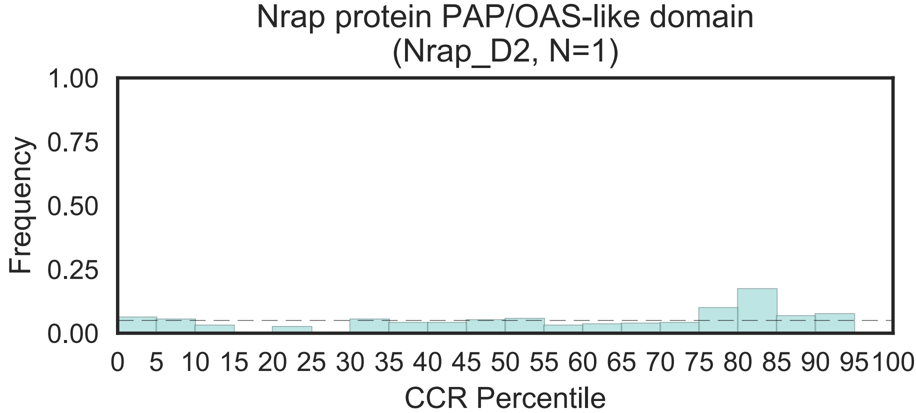

Not1 N-terminal domain, CCR4-Not complex component
(Not3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

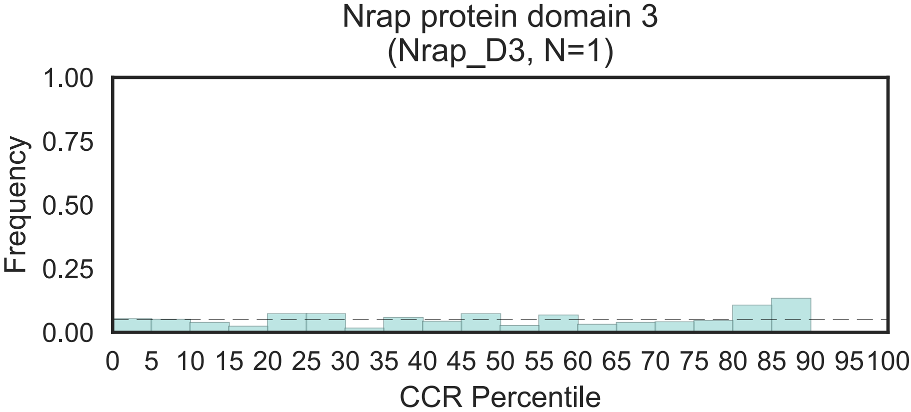

LNR domain
(Notch, N=15)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

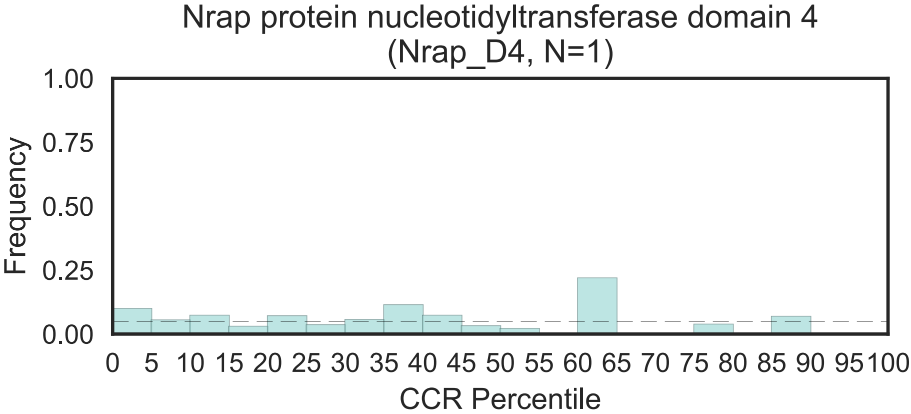

Ribosome 60S biogenesis N-terminal
(Npa1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

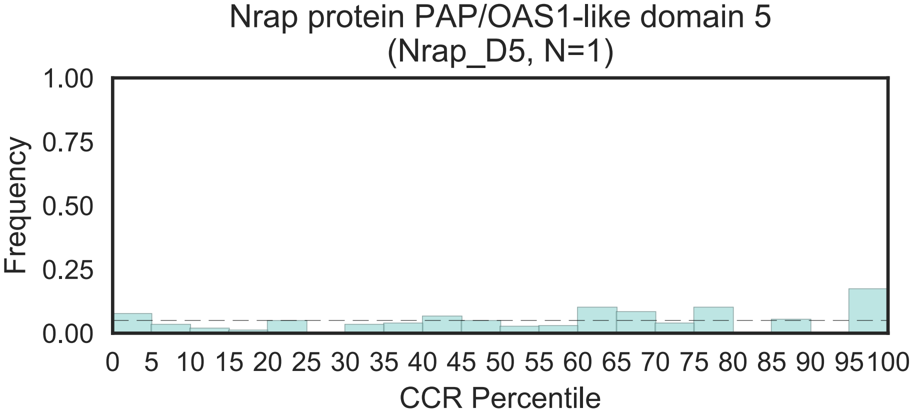

Natural resistance-associated macrophage protein
(Nramp, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

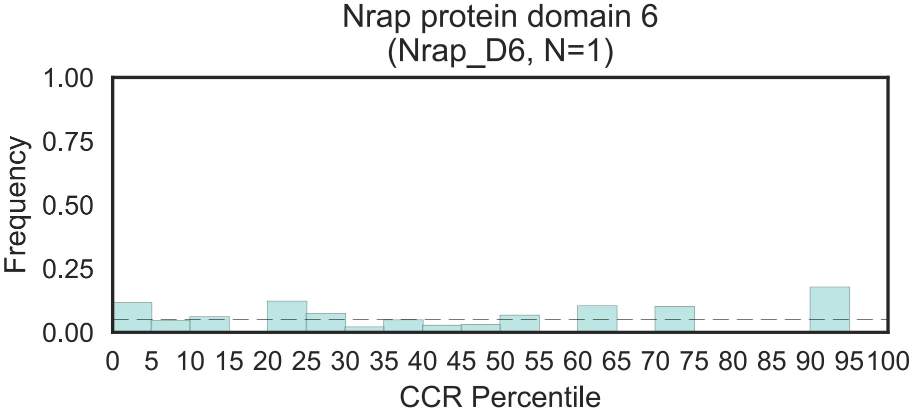

Nrap protein domain 1
(Nrap, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

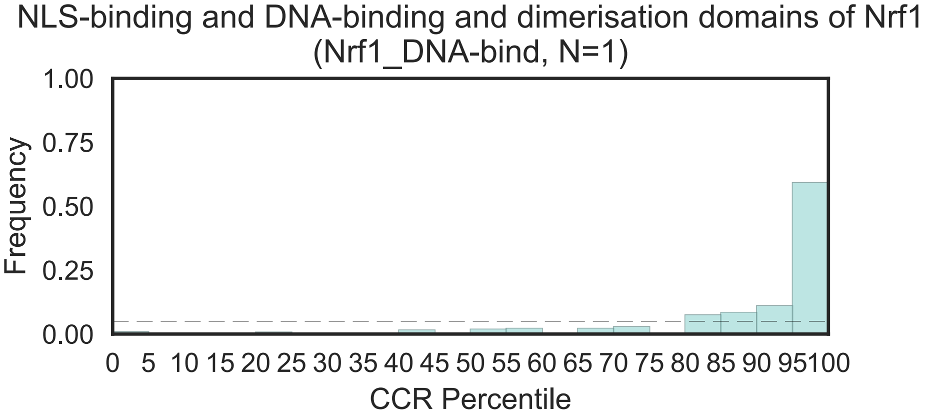

Nrap protein PAP/OAS-like domain
(Nrap_D2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

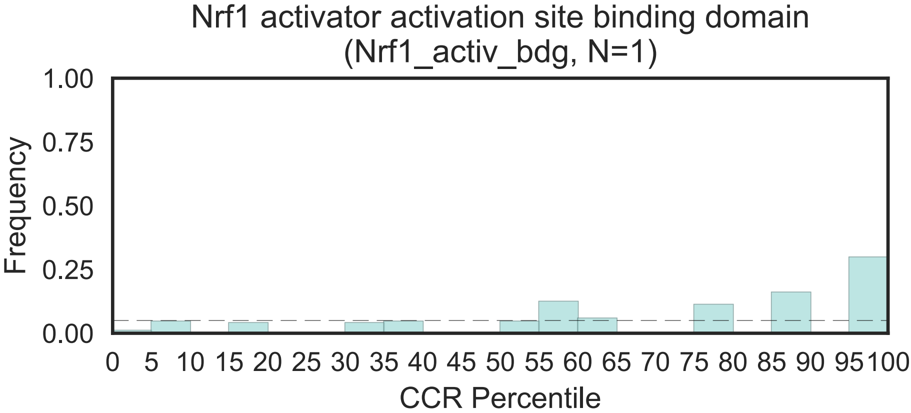

Nrap protein domain 3
(Nrap_D3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

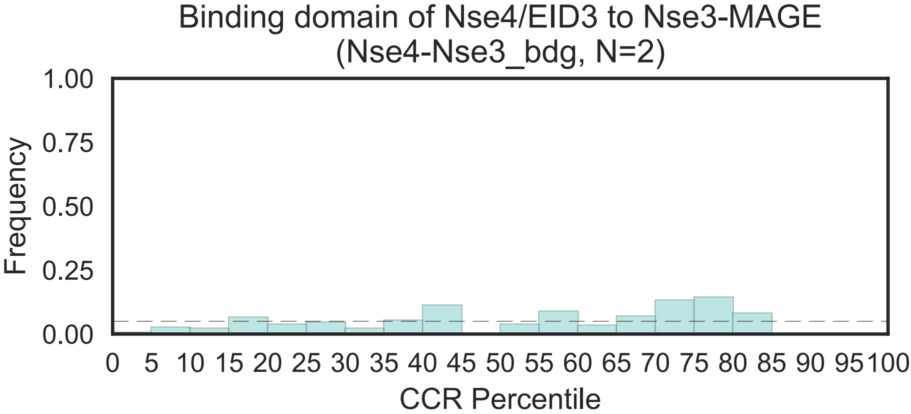

Nrap protein nucleotidyltransferase domain 4
(Nrap_D4, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

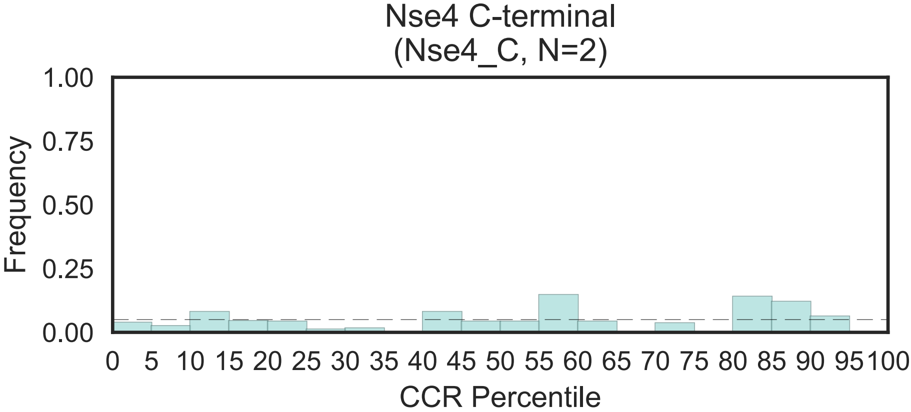

Nrap protein PAP/OAS1-like domain 5
(Nrap_D5, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

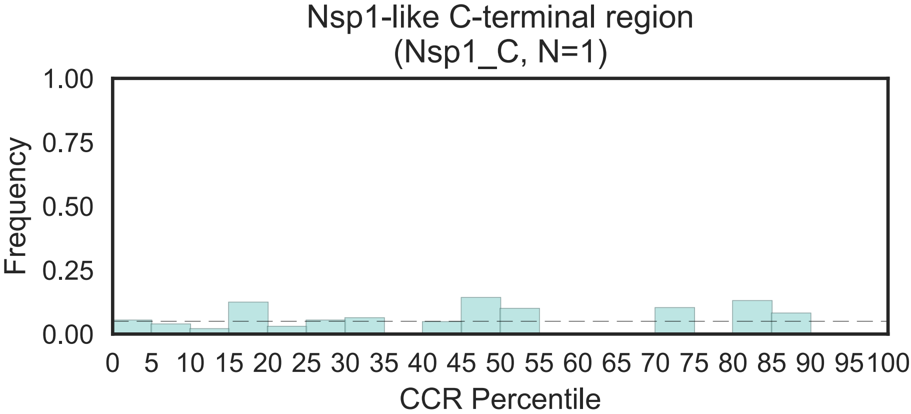

Nrap protein domain 6
(Nrap_D6, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

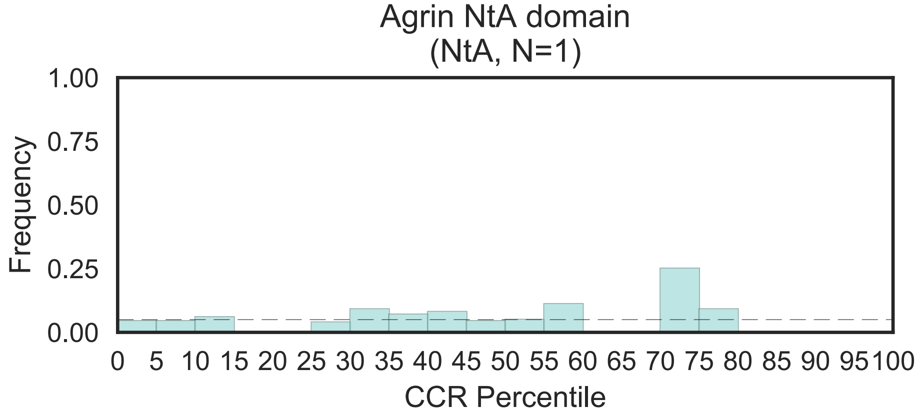

NLS-binding and DNA-binding and dimerisation domains of Nrf1
(Nrf1_DNA-bind, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

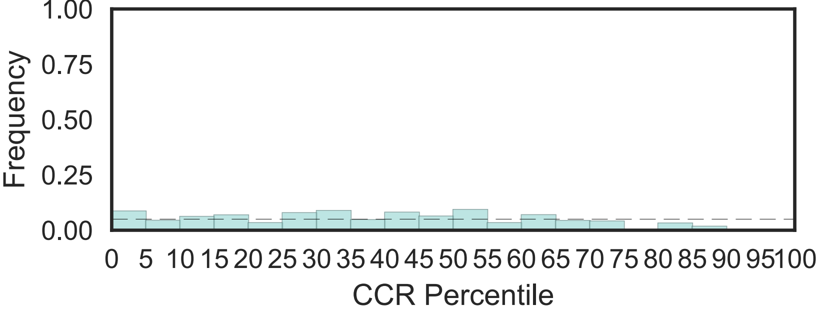

Nrf1 activator activation site binding domain
(Nrf1_activ_bdg, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

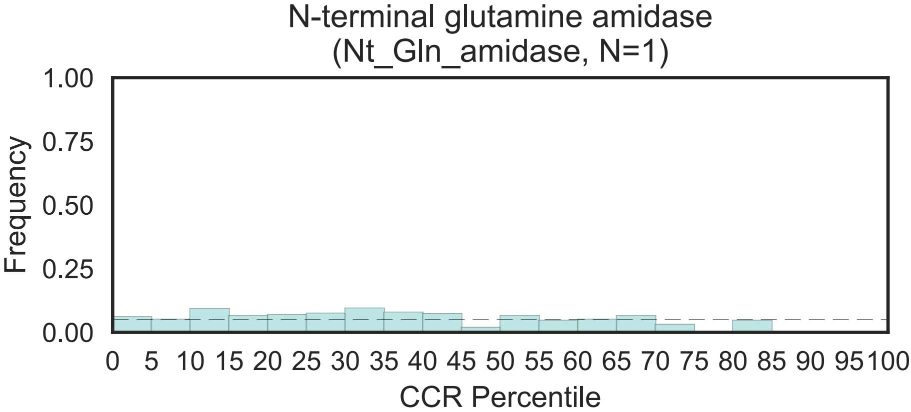

Binding domain of Nse4/EID3 to Nse3-MAGE
(Nse4-Nse3_bdg, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

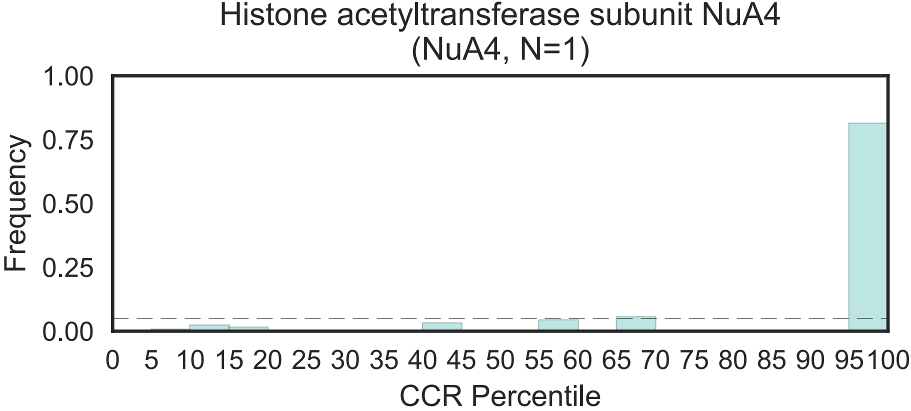

Nse4 C-terminal
(Nse4_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

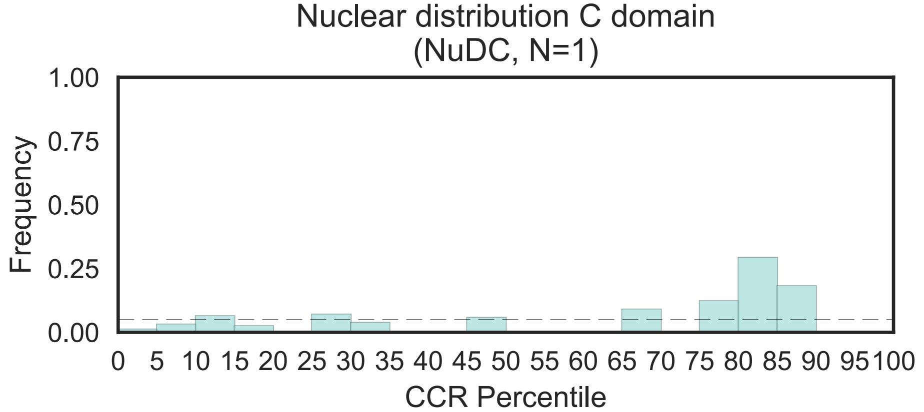

Nsp1-like C-terminal region
(Nsp1_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

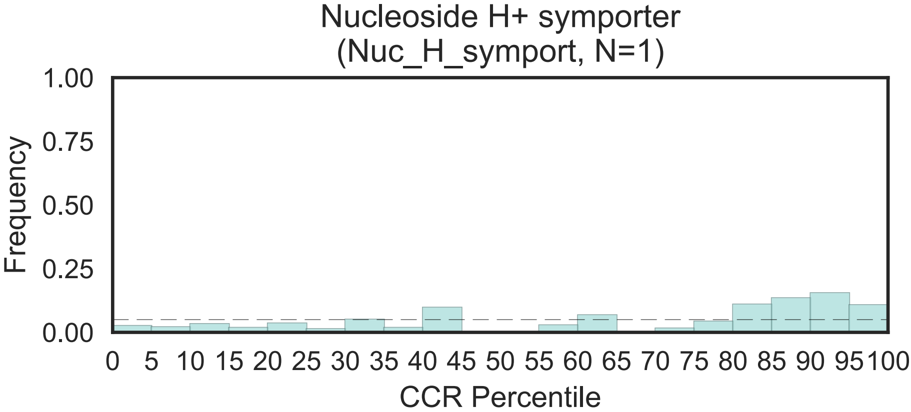

Agrin NtA domain
(NtA, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

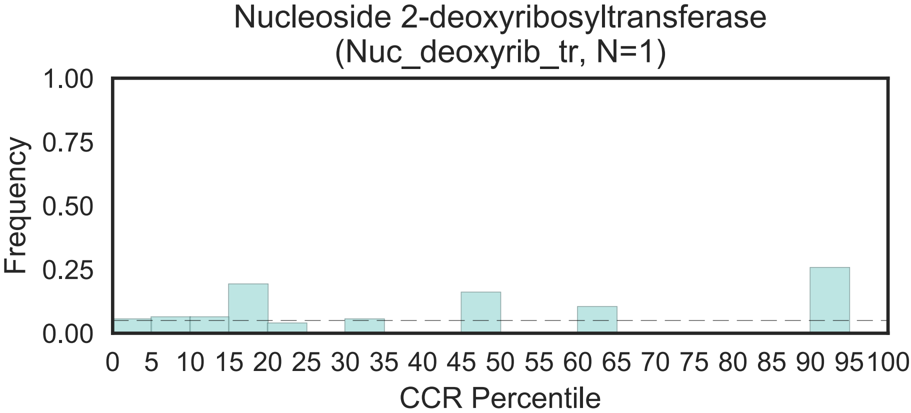

N-terminal barrel of NtMGAM and CtMGAM, maltase-glucoamylase
(NtCtMGAM_N, N=6)
Fisher's OR: 0; Bonferroni p-val: 1

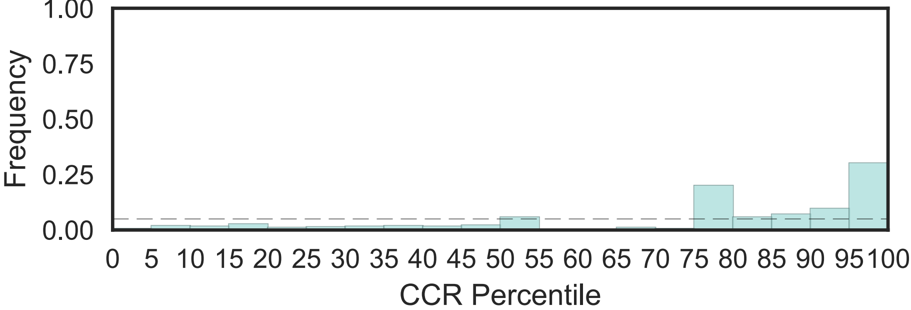

N-terminal glutamine amidase
(Nt_Gln_amidase, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Histone acetyltransferase subunit NuA4
(NuA4, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

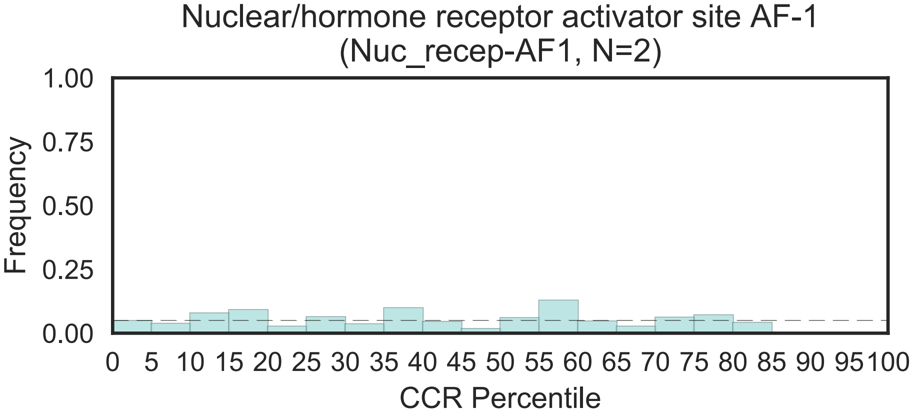

Nuclear distribution C domain
(NuDC, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

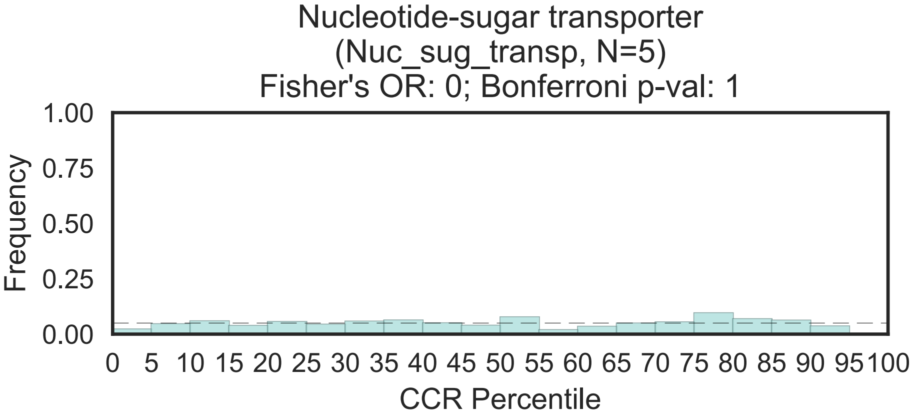

Nucleoside H+ symporter
(Nuc_H_symport, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

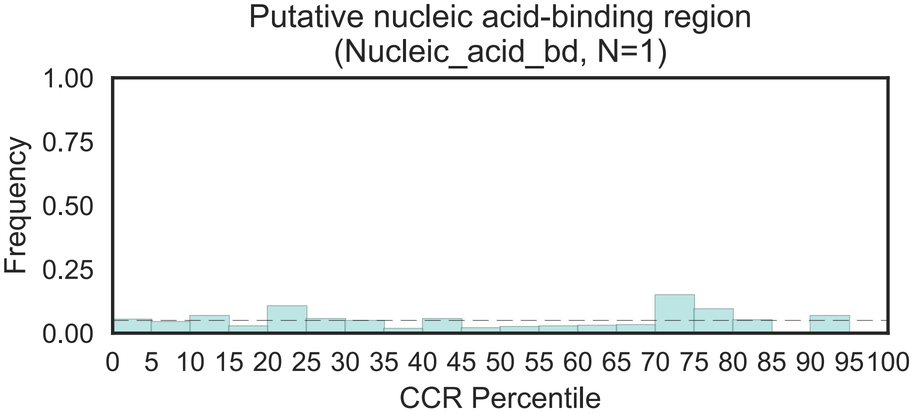

Nucleoside 2-deoxyribosyltransferase
(Nuc_deoxyrib_tr, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

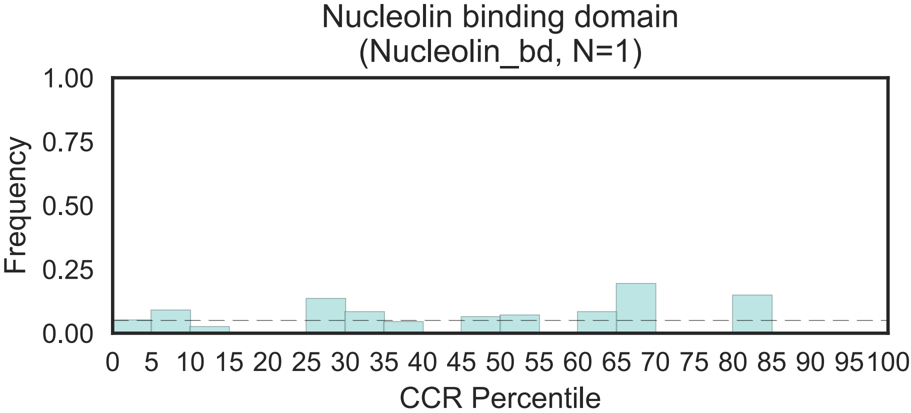


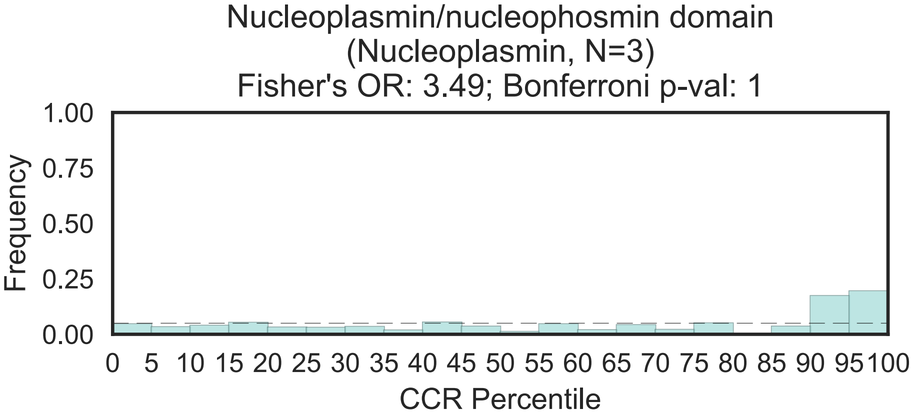
Nuclear receptor coactivator
(Nuc_rec_co-act, N=3)
Fisher's OR: 7.46; Bonferroni p-val: 1

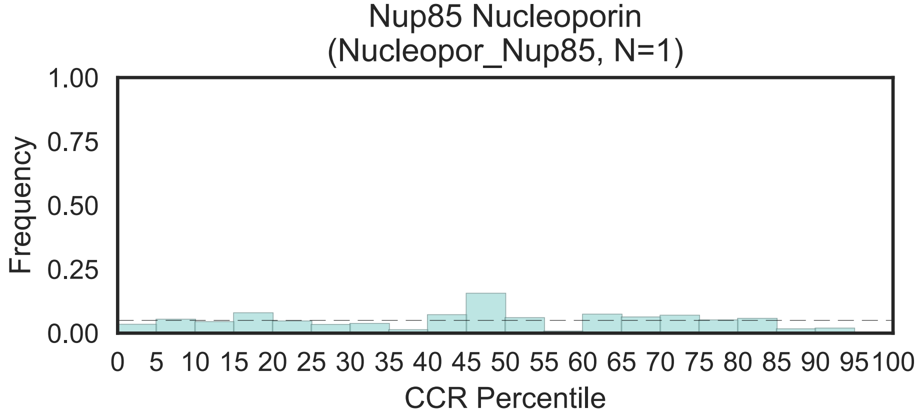

Nuclear/hormone receptor activator site AF-1
(Nuc_recep-AF1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

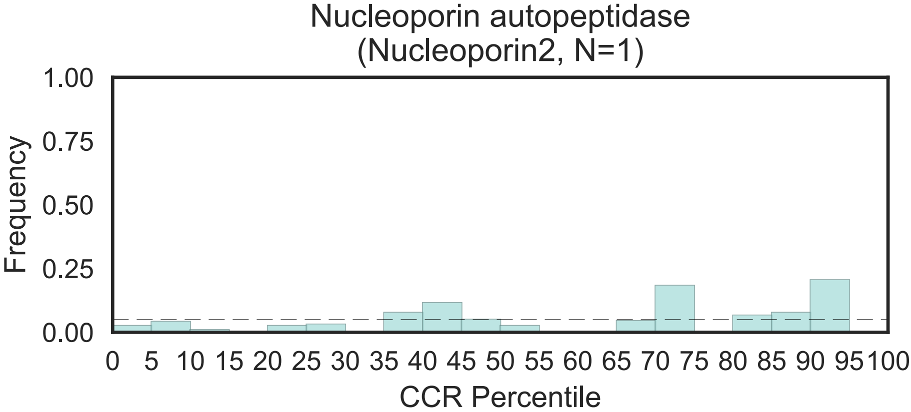

Nucleotide-sugar transporter
(Nuc_sug_transp, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

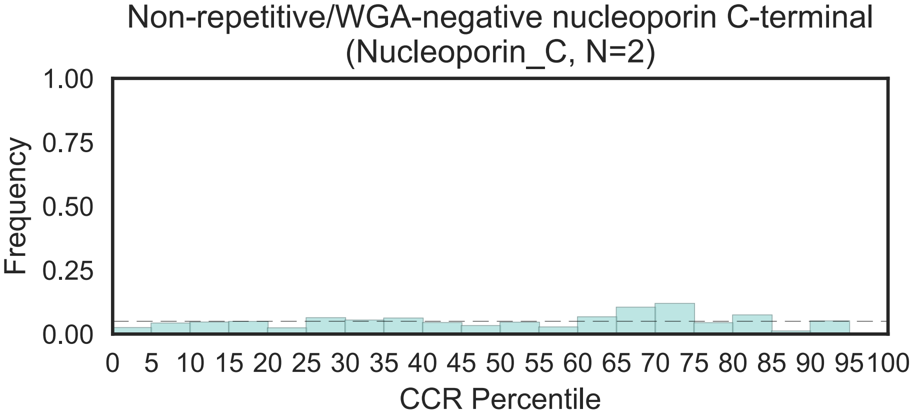

Putative nucleic acid-binding region
(Nucleic_acid_bd, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

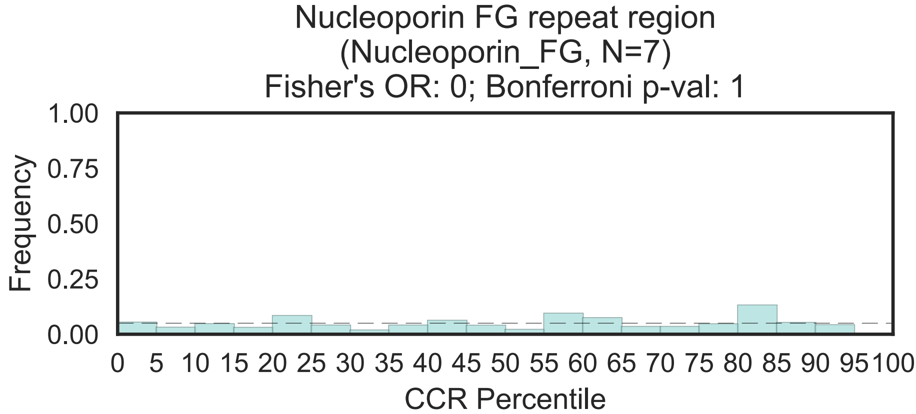

Nucleolin binding domain
(Nucleolin_bd, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

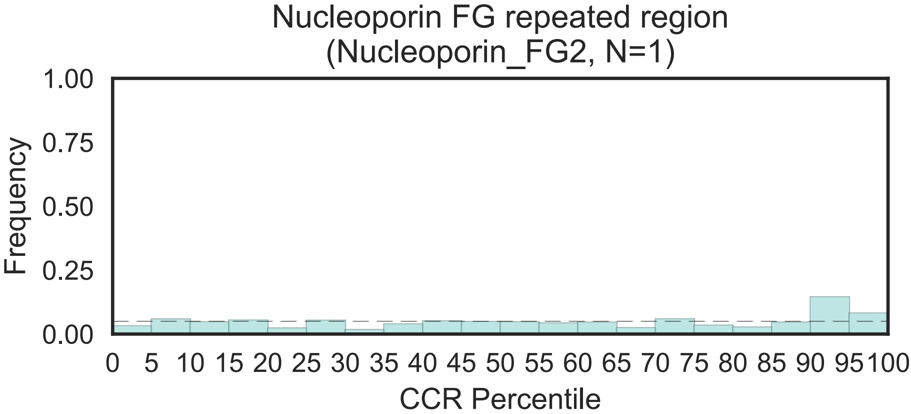

Nucleoplasmin/nucleophosmin domain
(Nucleoplasmin, N=3)
Fisher's OR: 3.49; Bonferroni p-val: 1

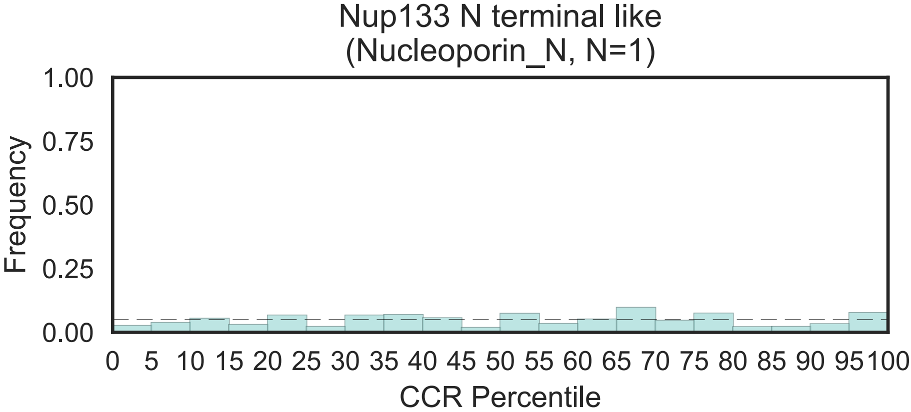

Nup85 Nucleoporin
(Nucleopor_Nup85, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

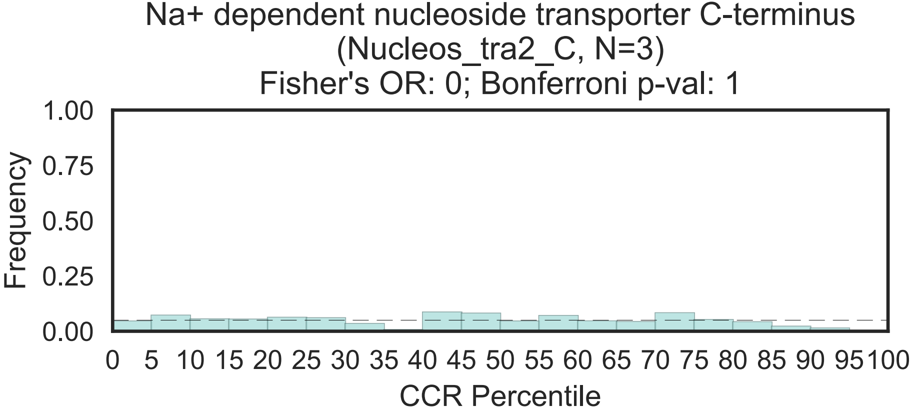

Nucleoporin autopeptidase
(Nucleoporin2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

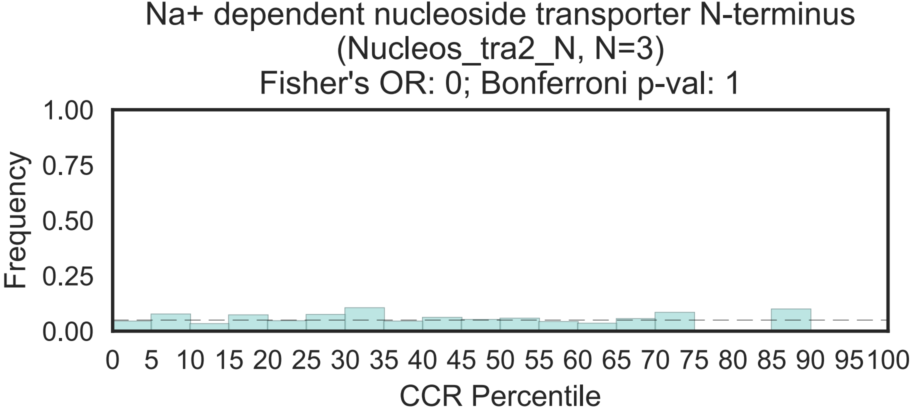

Non-repetitive/WGA-negative nucleoporin C-terminal
(Nucleoporin_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Nucleoporin FG repeat region
(Nucleoporin_FG, N=7)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

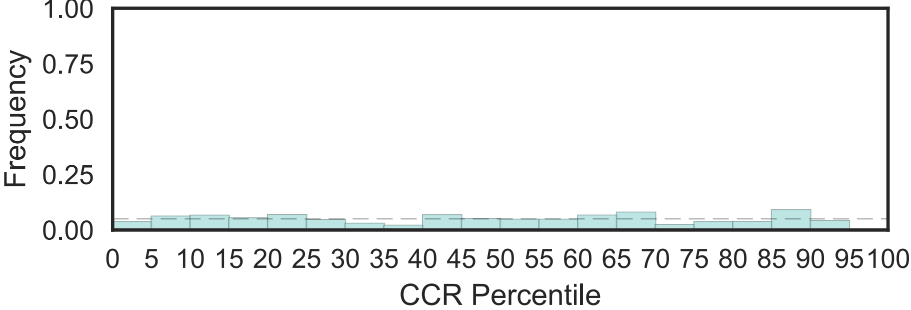

Nucleoporin FG repeated region
(Nucleoporin_FG2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

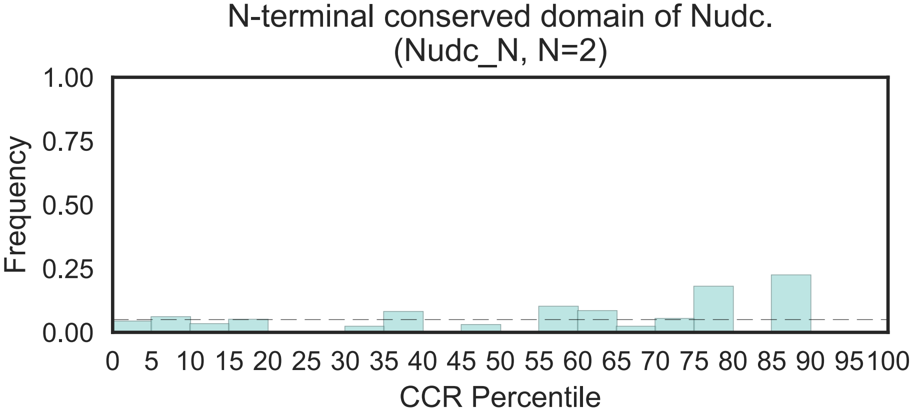

Nup133 N terminal like
(Nucleoporin_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

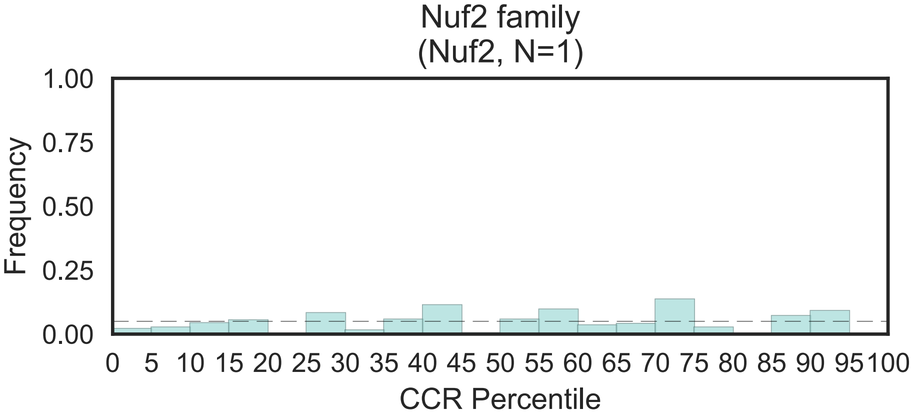

Na+ dependent nucleoside transporter C-terminus
(Nucleos_tra2_C, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

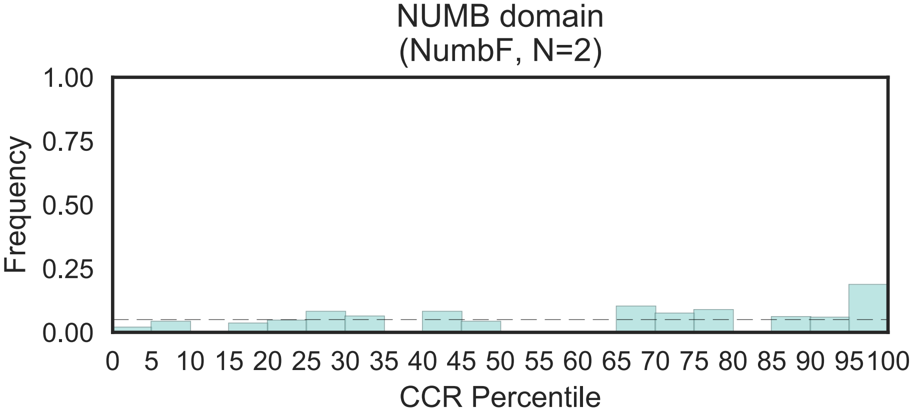

Na+ dependent nucleoside transporter N-terminus
(Nucleos_tra2_N, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

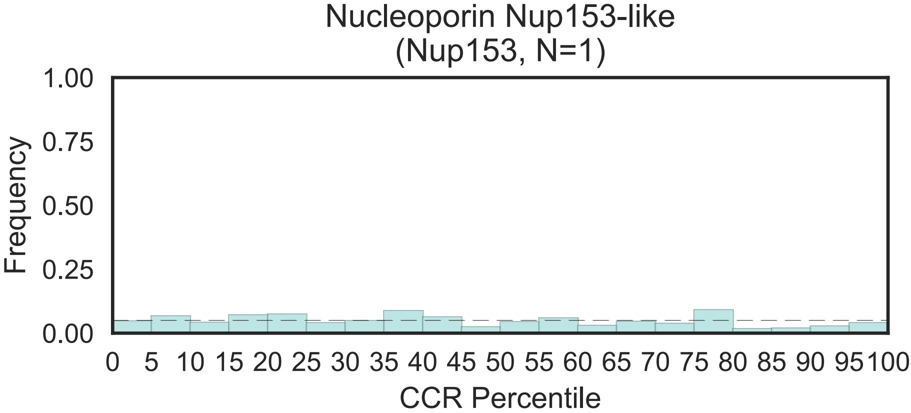
Nucleoside transporter (Nucleoside_tran, N=5) Fisher's OR: 0; Bonferroni p-val: 1

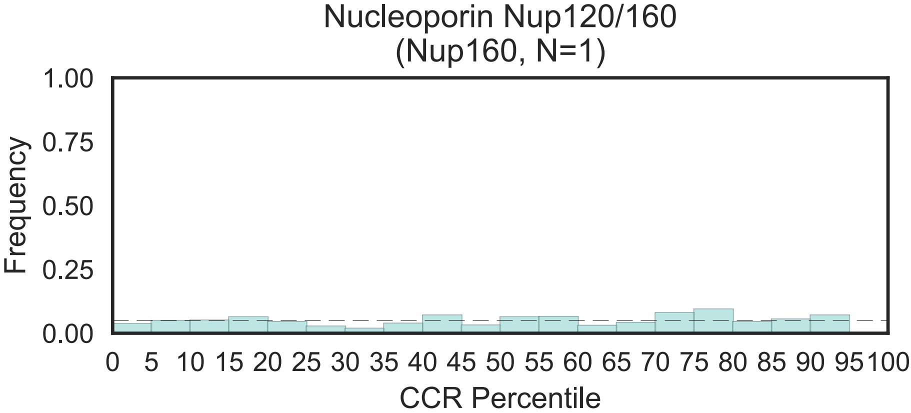


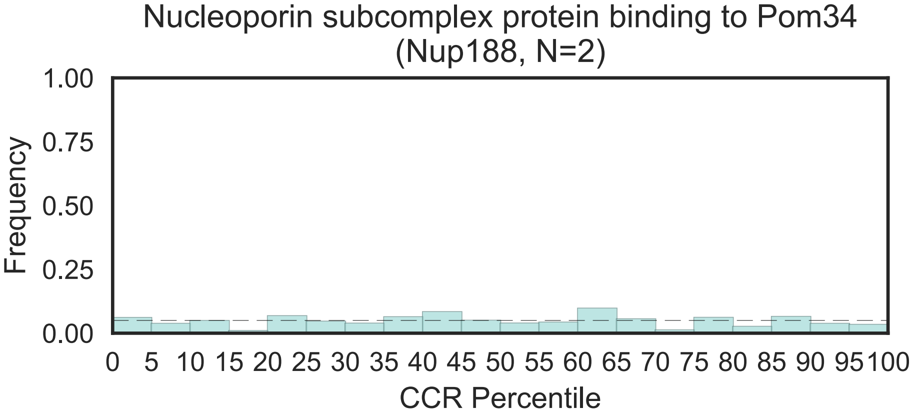

N-terminal conserved domain of Nudc.
(Nudc_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

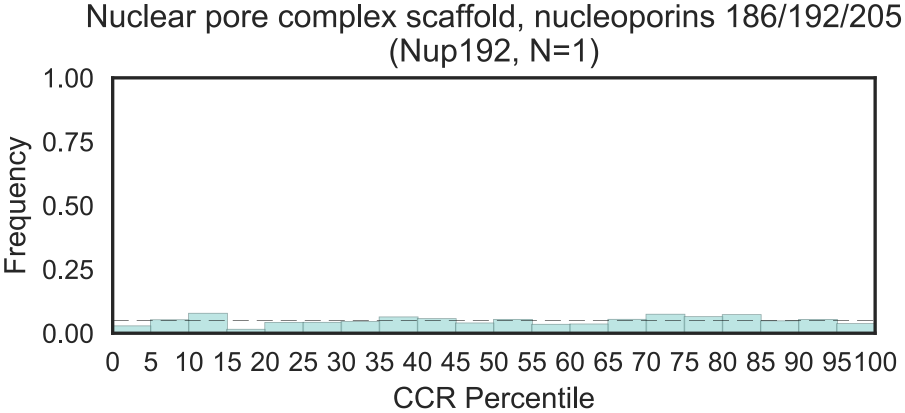

Nuf2 family
(Nuf2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

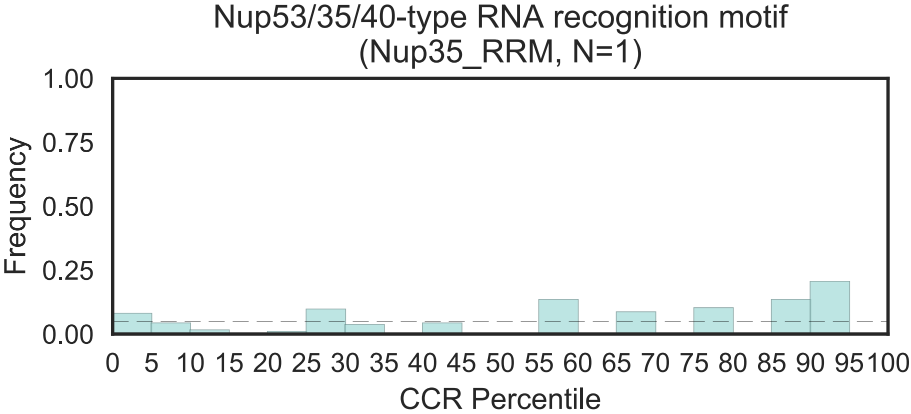

NUMB domain
(NumbF, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

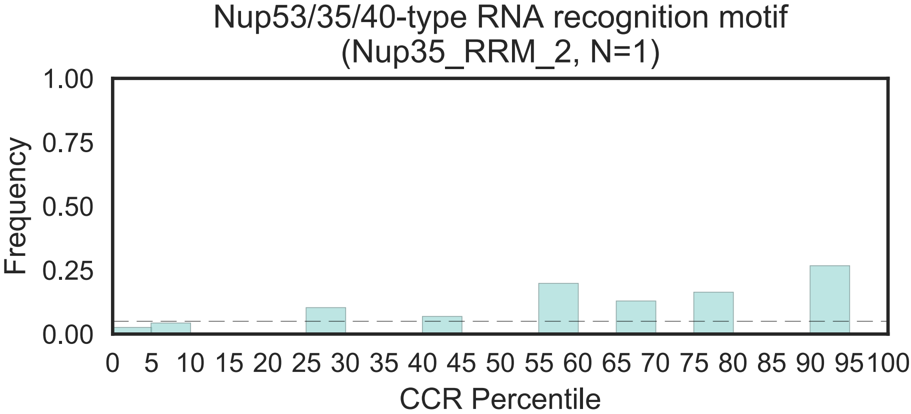

Nucleoporin Nup153-like
(Nup153, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Nucleoporin Nup120/160
(Nup160, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

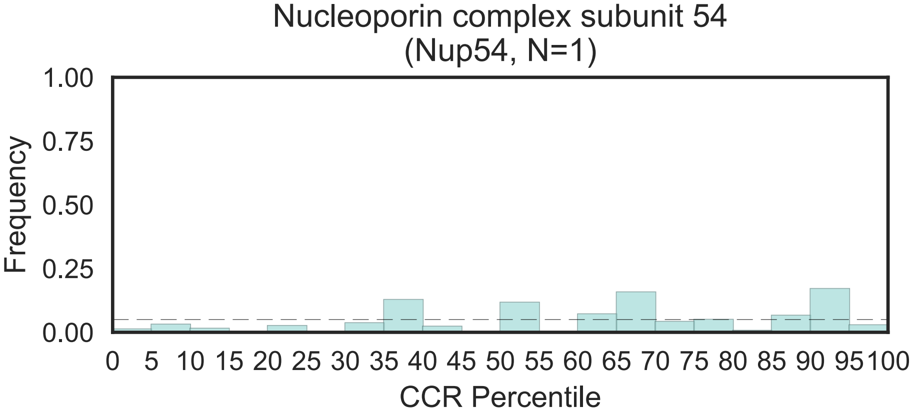

Nucleoporin subcomplex protein binding to Pom34
(Nup188, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

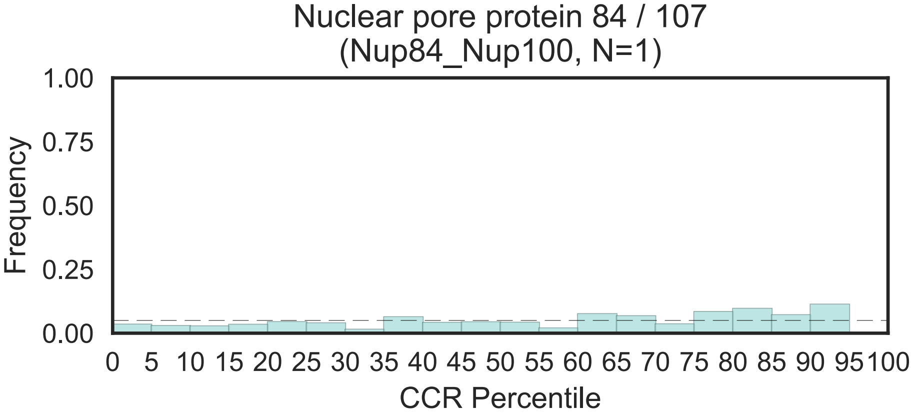

Nuclear pore complex scaffold, nucleoporins 186/192/205
(Nup192, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

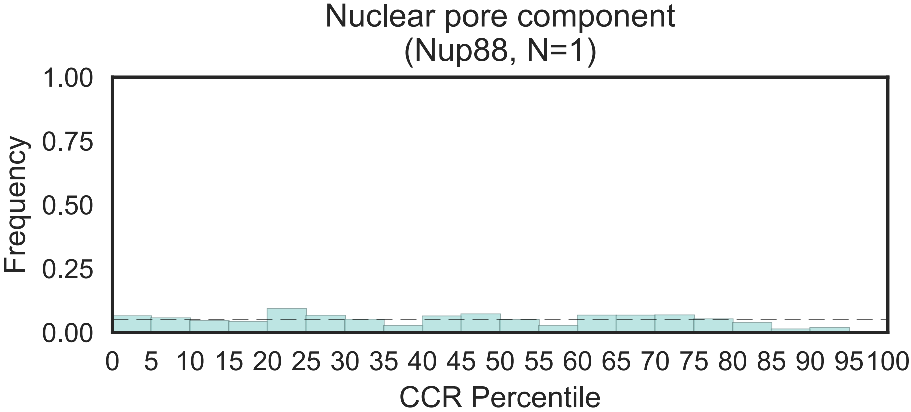

Nup53/35/40-type RNA recognition motif
(Nup35_RRM, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

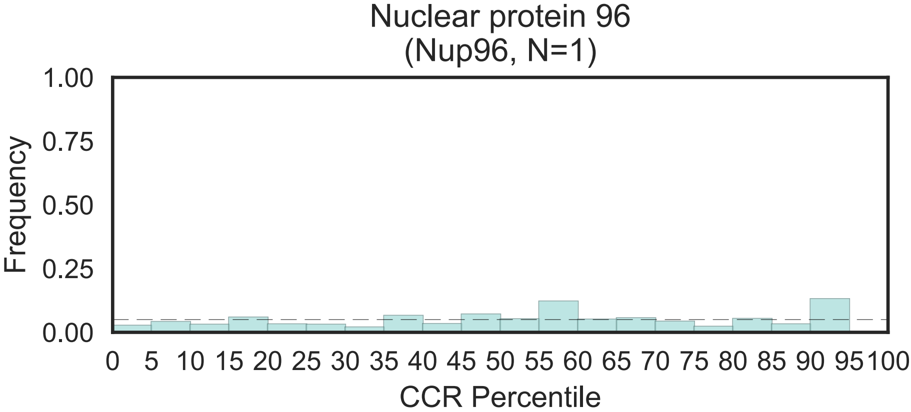


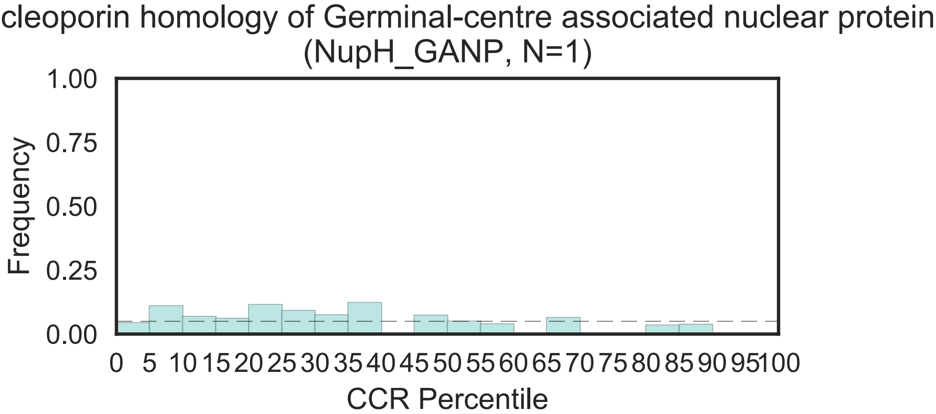
Nup53/35/40-type RNA recognition motif
(Nup35_RRM_2, N=1)

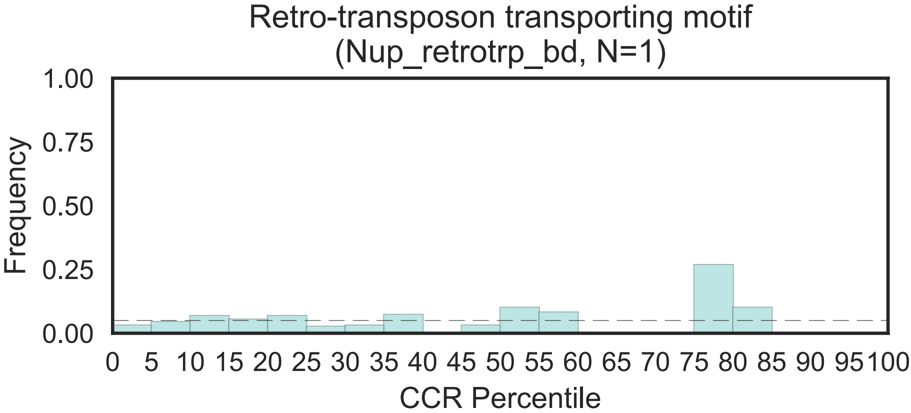

Nucleoporin complex subunit 54
(Nup54, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

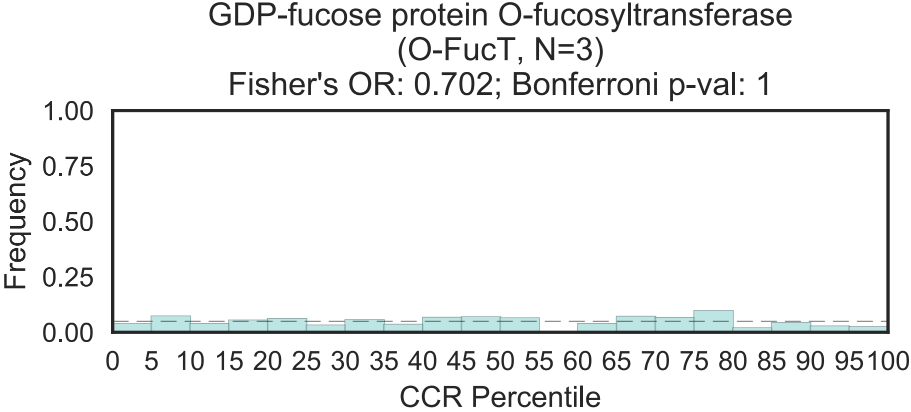

Nuclear pore protein 84 / 107
(Nup84_Nup100, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

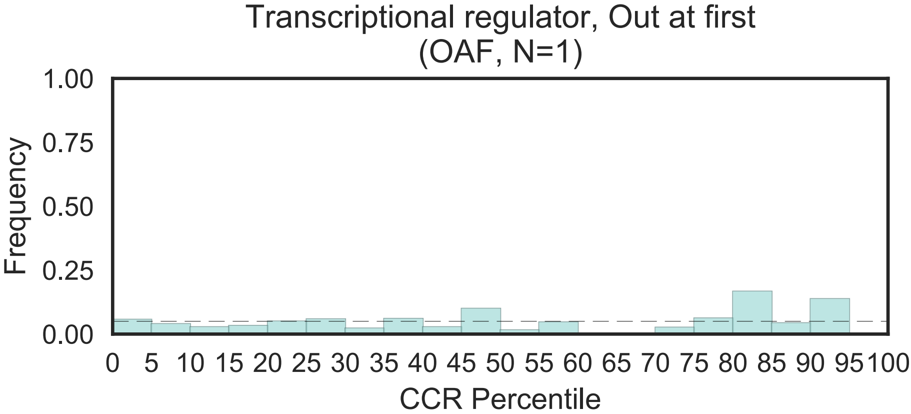

Nuclear pore component
(Nup88, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

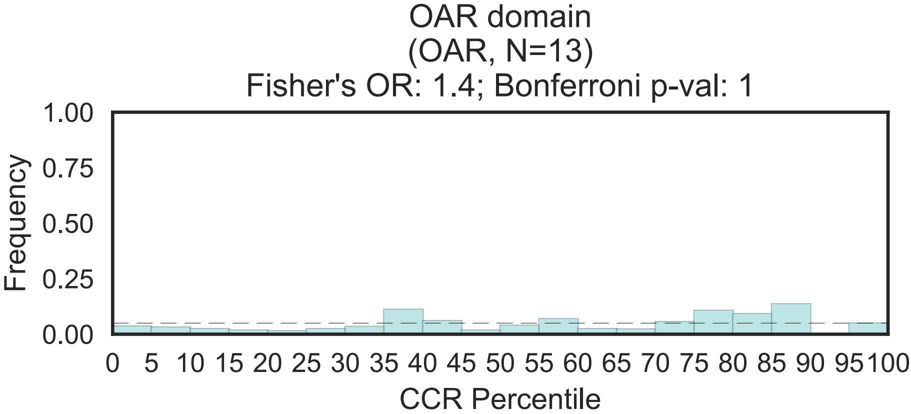

Nuclear protein 96
(Nup96, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

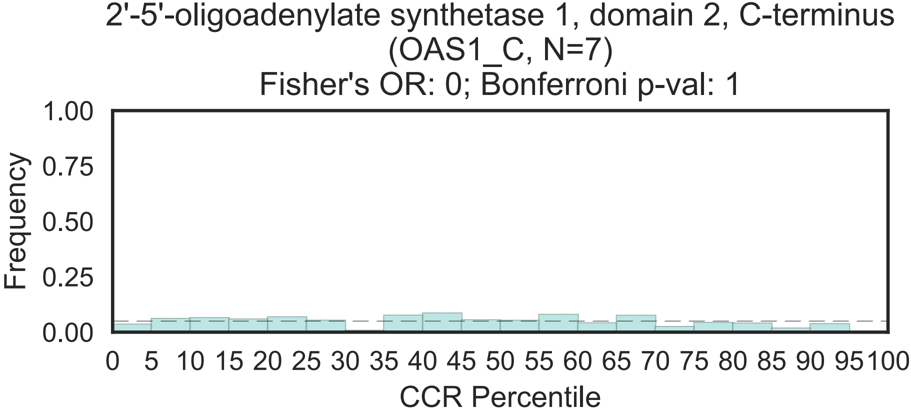

Nucleoporin homology of Germinal-centre associated nuclear protein
(NupH_GANP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

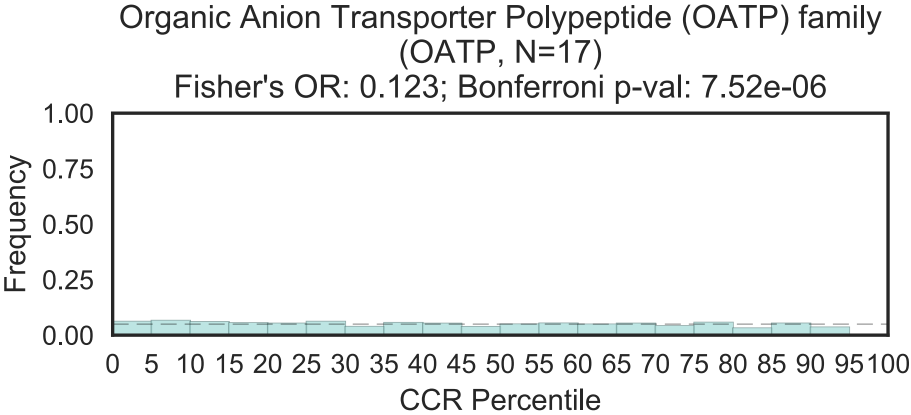

Retro-transposon transporting motif
(Nup_retrotrp_bd, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

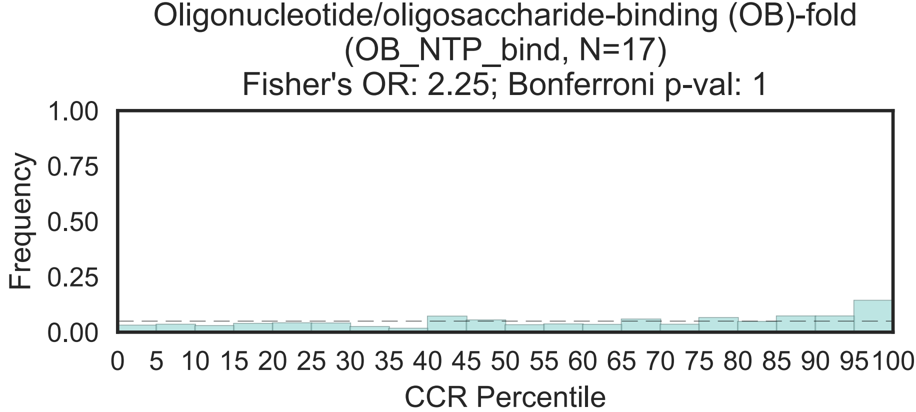

GDP-fucose protein O-fucosyltransferase
(O-FucT, N=3)
Fisher's OR: 0.702; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Transcriptional regulator, Out at first
(OAF, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

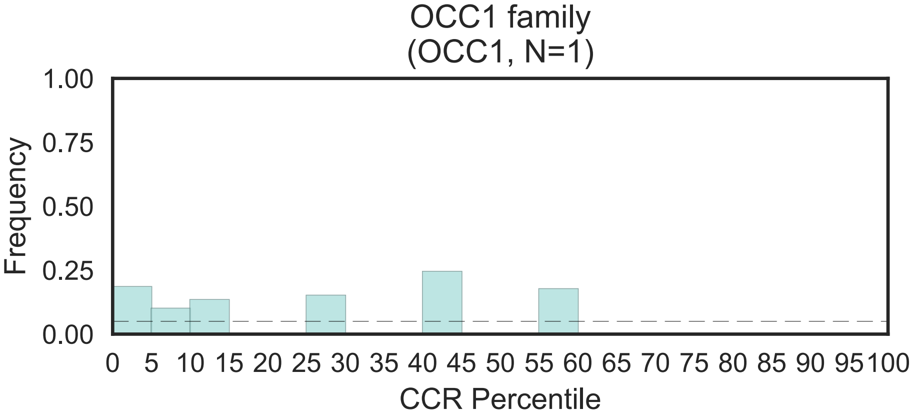

OAR domain
(OAR, N=13)
Fisher's OR: 1.4; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

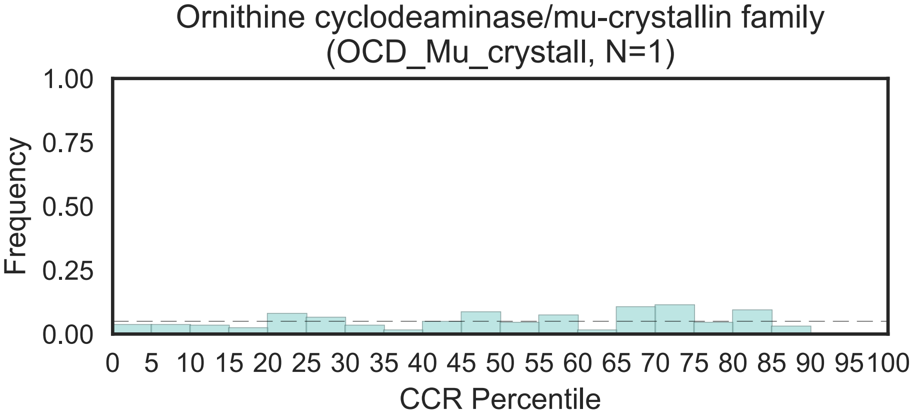

2'-5'-oligoadenylate synthetase 1, domain 2, C-terminus
(OAS1_C, N=7)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Organic Anion Transporter Polypeptide (OATP) family
(OATP, N=17)
Fisher's OR: 0.123; Bonferroni p-val: 7.52e-06
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

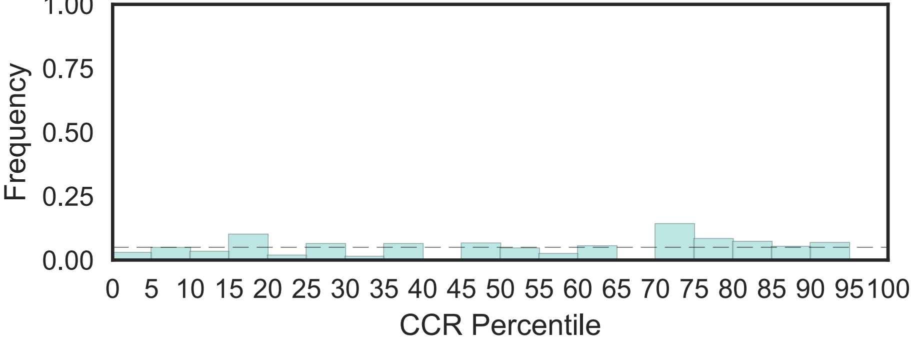


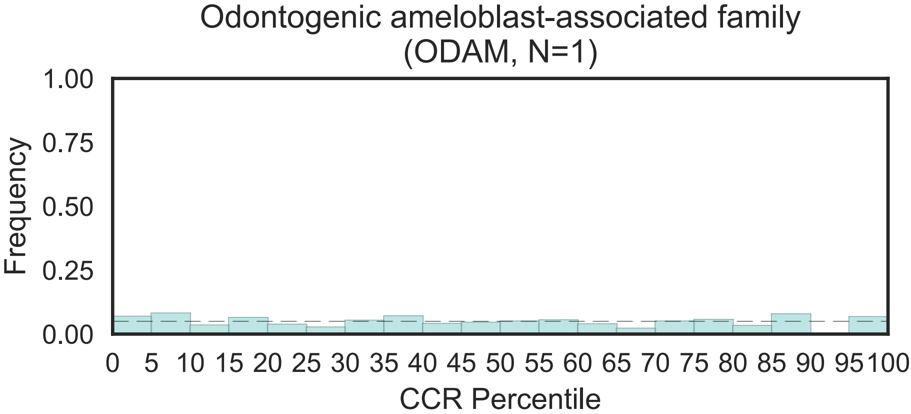
Oligonucleotide/oligosaccharide-binding (OB)-fold (OB_NTP_bind, N=17) Fisher's OR: 2.25; Bonferroni p-val: 1

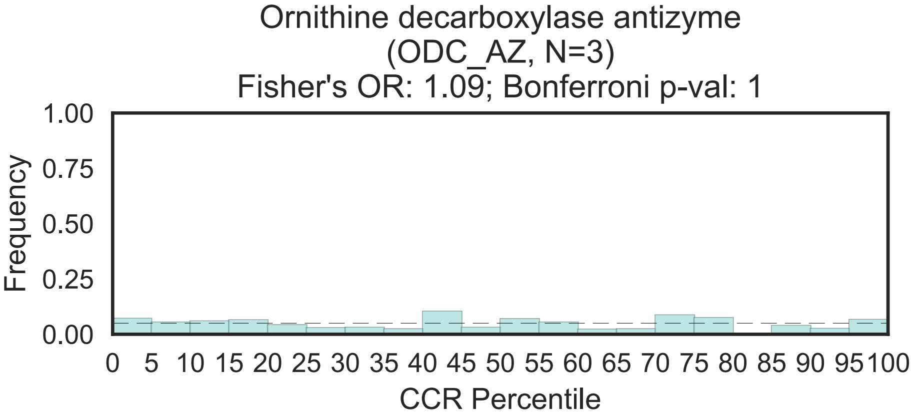

OCC1 family
(OCC1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

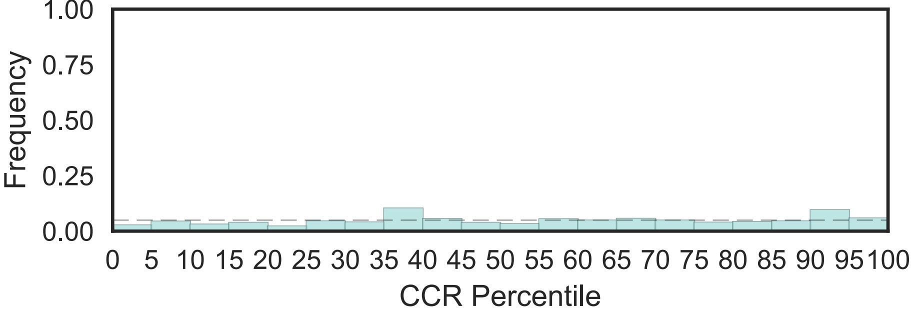

Ornithine cyclodeaminase/mu-crystallin family
(OCD_Mu_crystall, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Ovarian carcinoma immunoreactive antigen (OCIA) (OCIA, N=2)

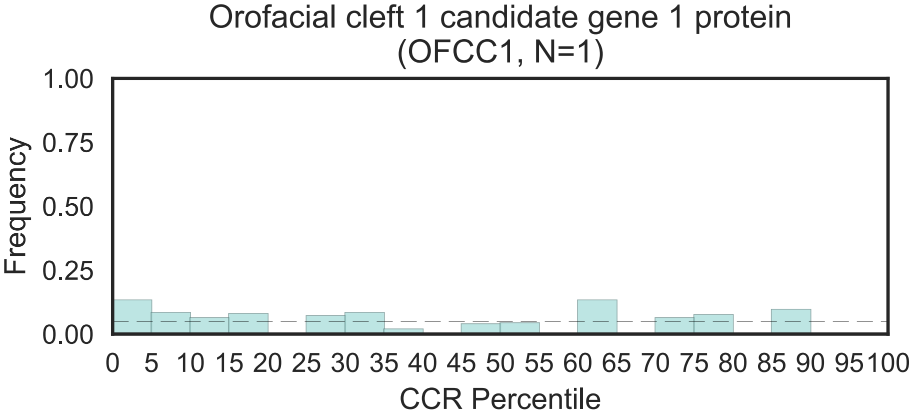


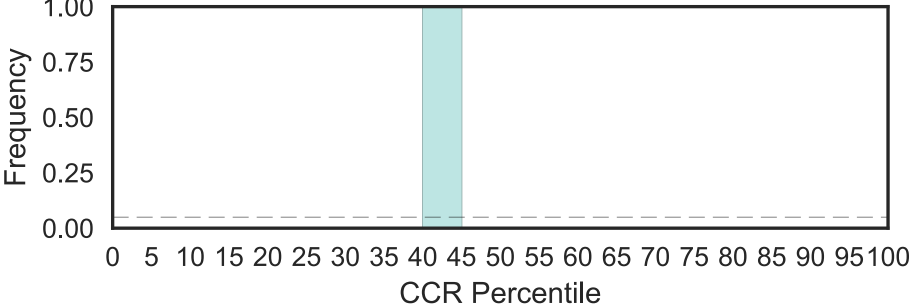

Odontogenic ameloblast-associated family
(ODAM, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ornithine decarboxylase antizyme
(ODC_AZ, N=3)
Fisher's OR: 1.09; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

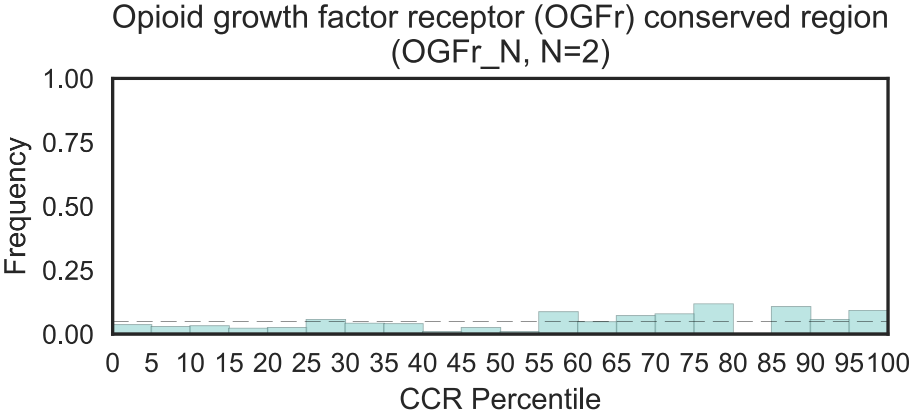


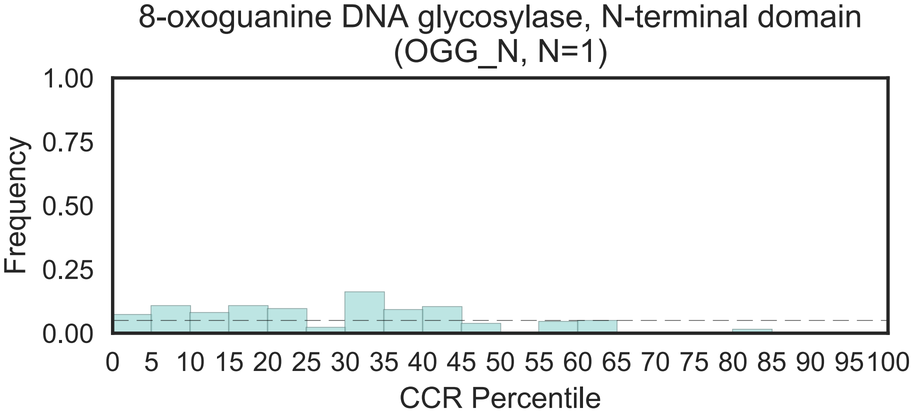
Olfactory receptor 4-like
(ODR4-like, N=3)
Fisher's OR: 0.872; Bonferroni p-val: 1

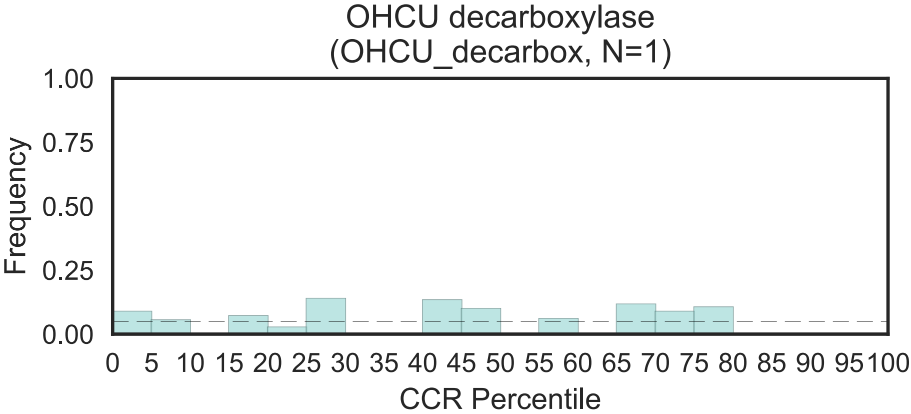

Orofacial cleft 1 candidate gene 1 protein
(OFCC1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



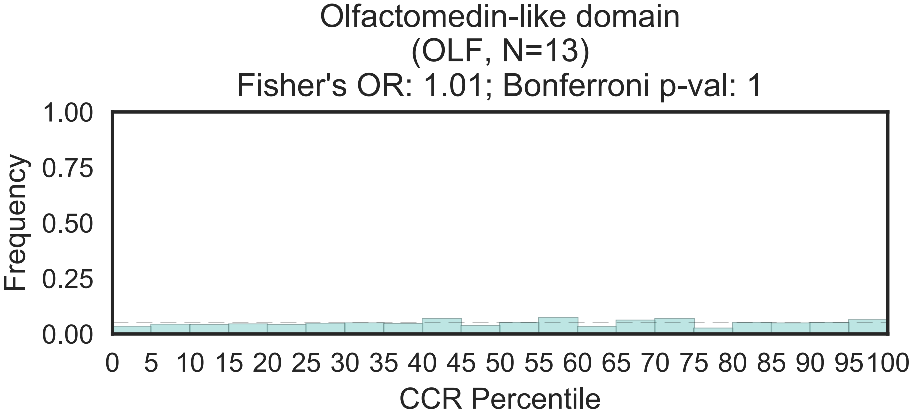
Opioid growth factor receptor repeat
(OGFr_III, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

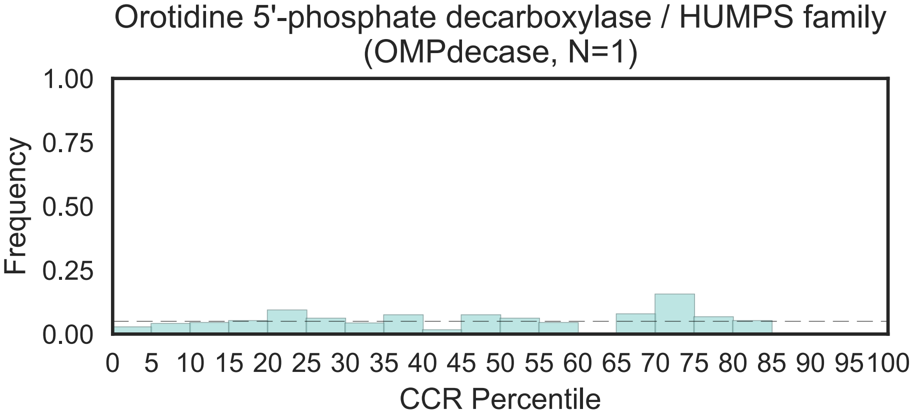

Opioid growth factor receptor (OGFr) conserved region
(OGFr_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

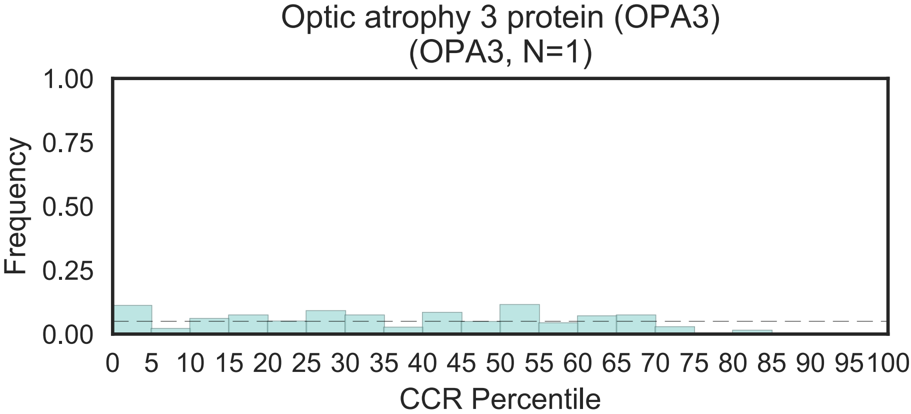

8-oxoguanine DNA glycosylase, N-terminal domain
(OGG_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

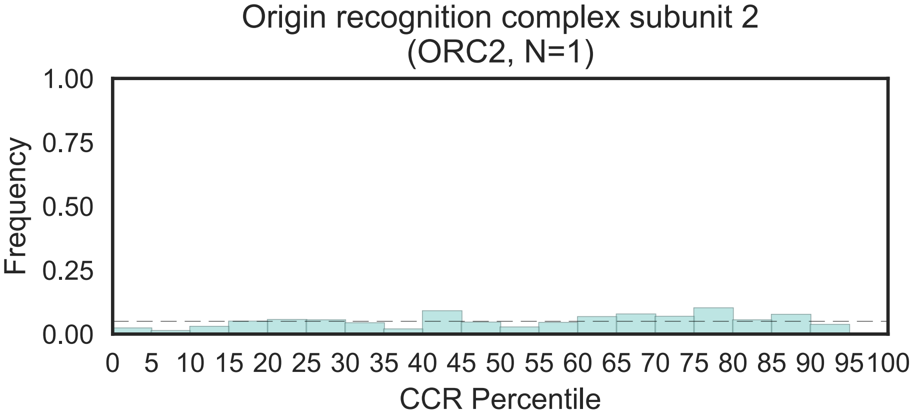


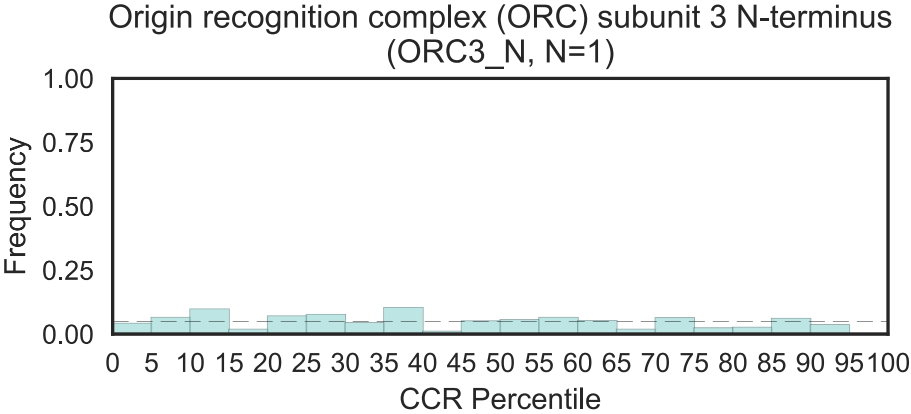
OHCU decarboxylase
(OHCU_decarbox, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Olfactomedin-like domain
(OLF, N=13)
Fisher's OR: 1.01; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

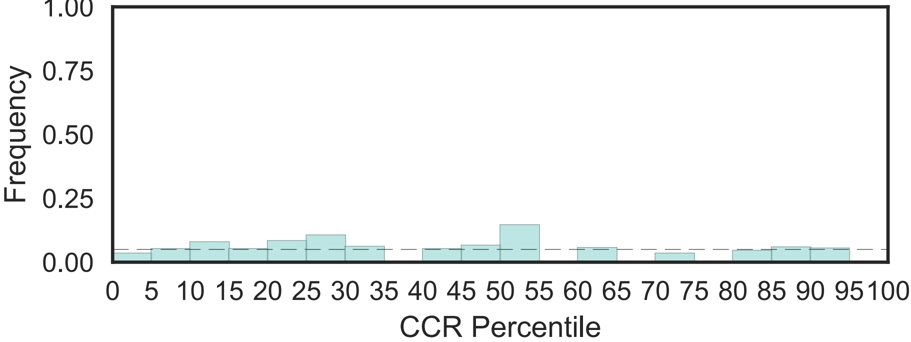

Orotidine 5'-phosphate decarboxylase / HUMPS family
(OMPdecase, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

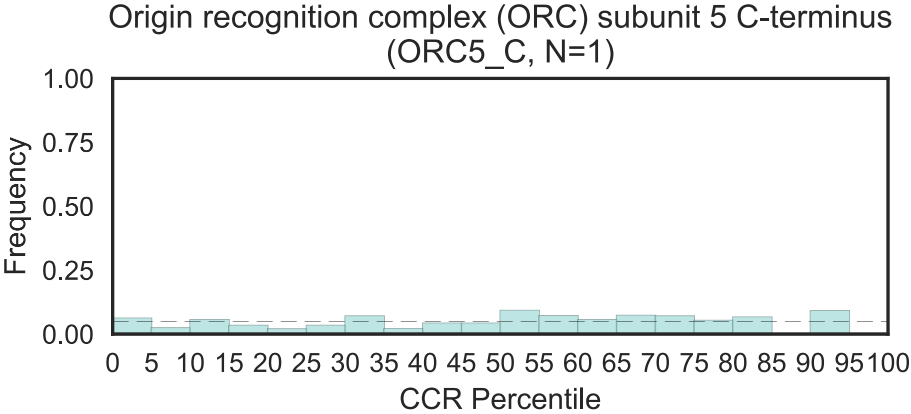

Optic atrophy 3 protein (OPA3)
(OPA3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Origin recognition complex subunit 2
(ORC2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

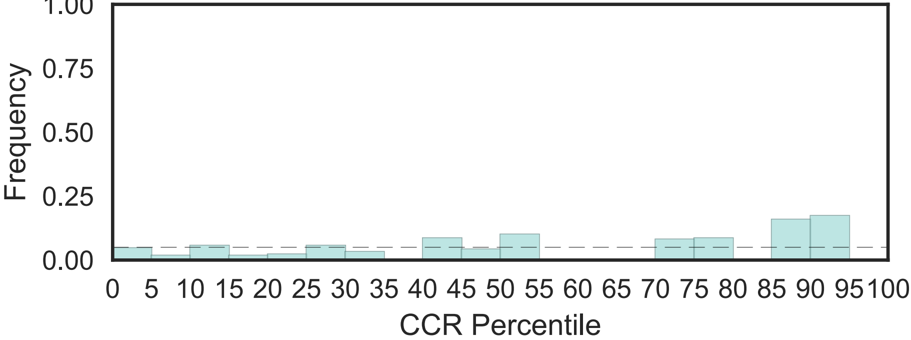


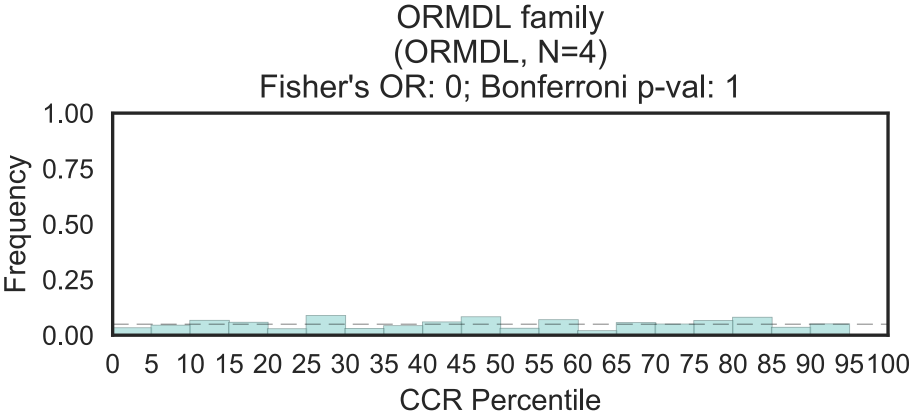
Origin recognition complex (ORC) subunit 3 N-terminus
(ORC3_N, N=1)

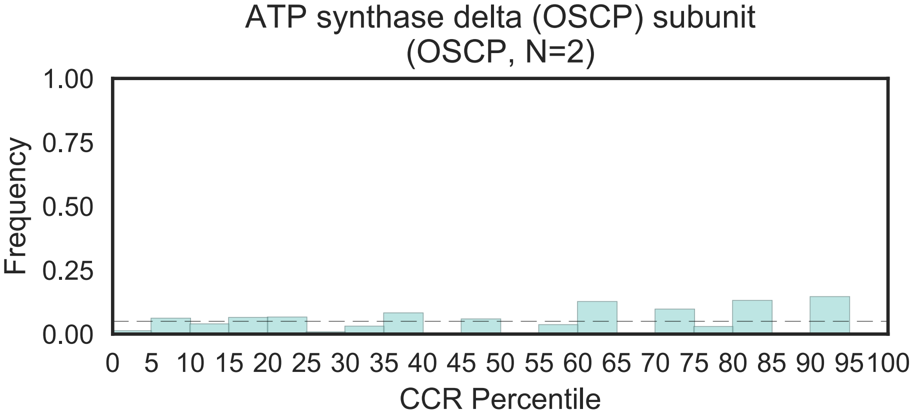

Origin recognition complex (ORC) subunit 4 C-terminus (ORC4_C, N=1)

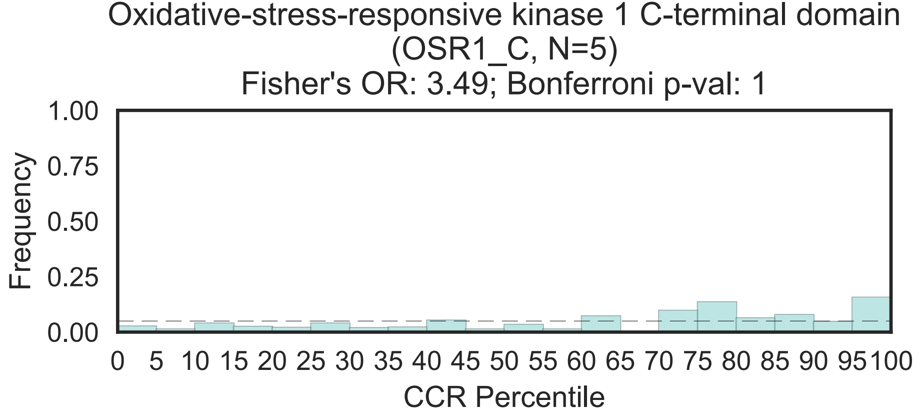

Origin recognition complex (ORC) subunit 5 C-terminus
(ORC5_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

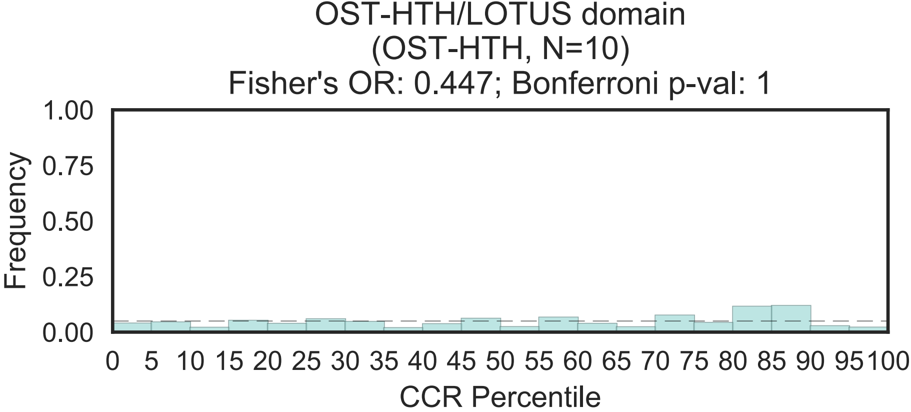
Origin recognition complex subunit 6 (ORC6)
(ORC6, N=1)




ORMDL family
(ORMDL, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

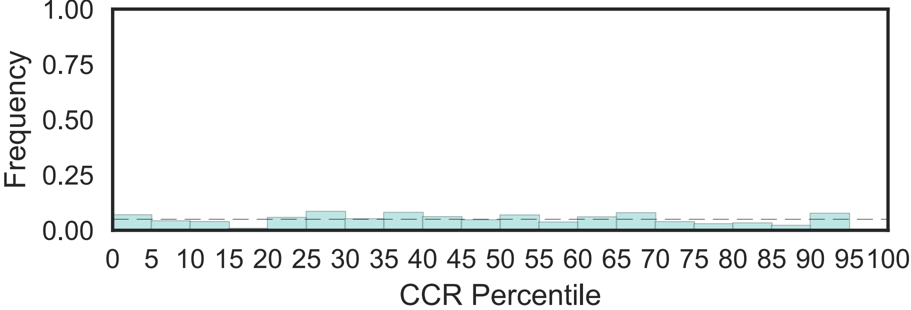

ATP synthase delta (OSCP) subunit
(OSCP, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

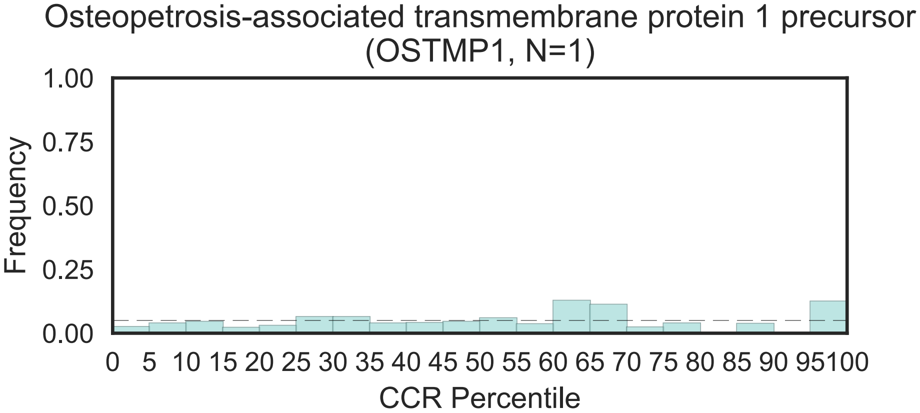

Oxidative-stress-responsive kinase 1 C-terminal domain
(OSR1_C, N=5)
Fisher's OR: 3.49; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

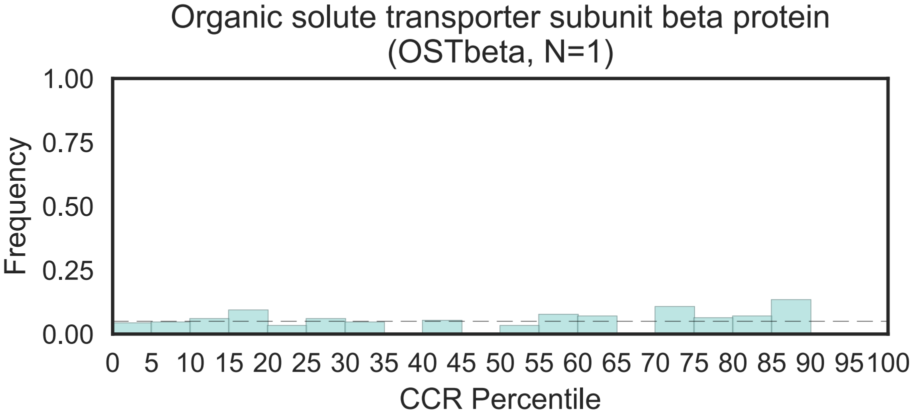


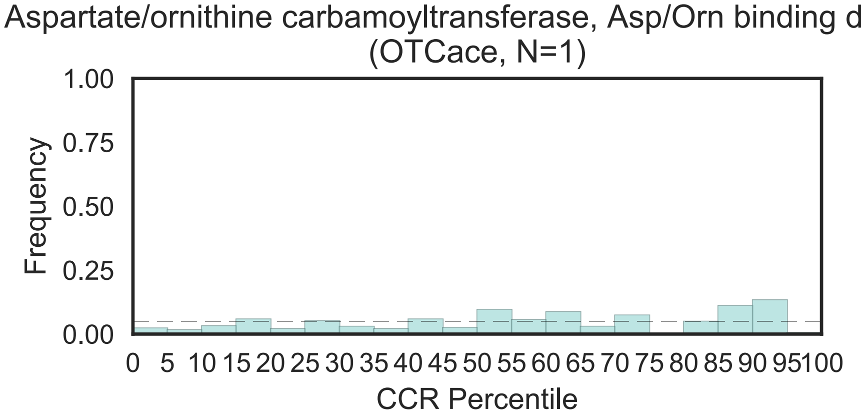
OST-HTH/LOTUS domain
(OST-HTH, N=10)
Fisher's OR: 0.447; Bonferroni p-val: 1

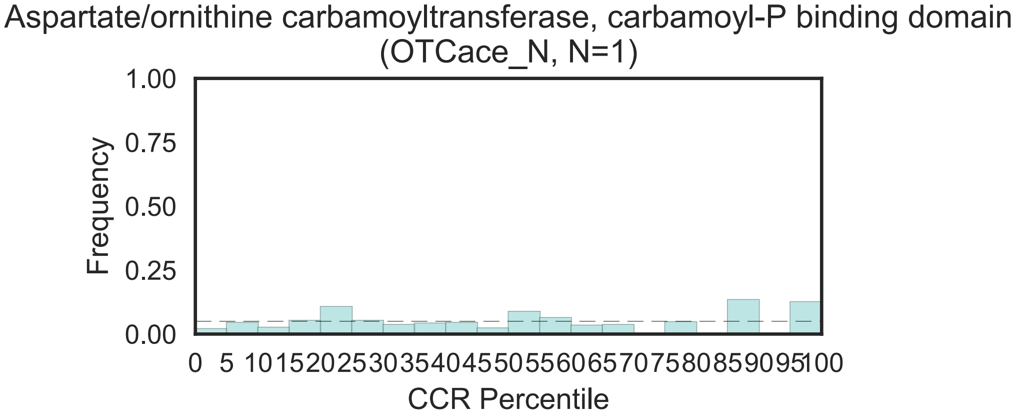
OST3 / OST6 family, transporter family
(OST3_OST6, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

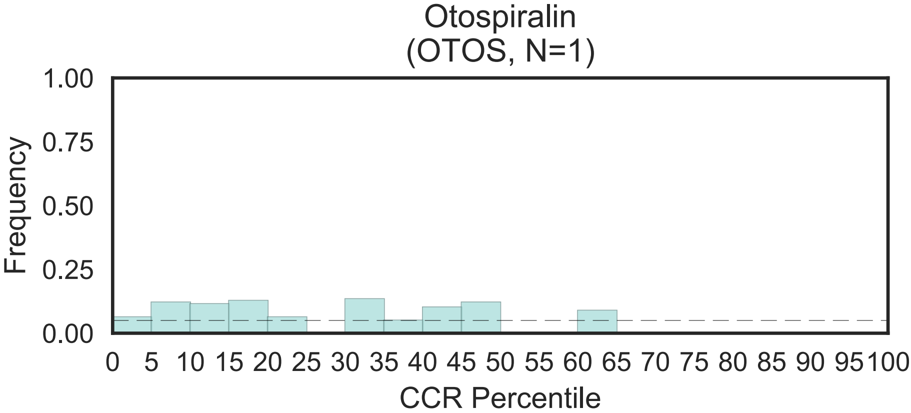


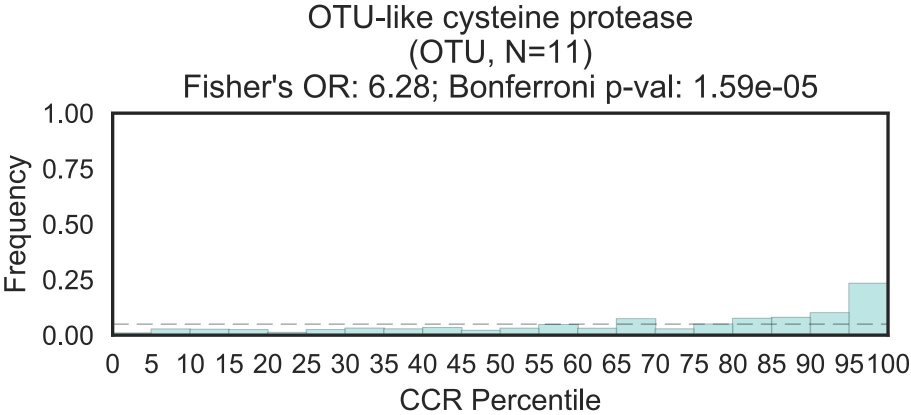

Osteopetrosis-associated transmembrane protein 1 precursor
(OSTMP1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

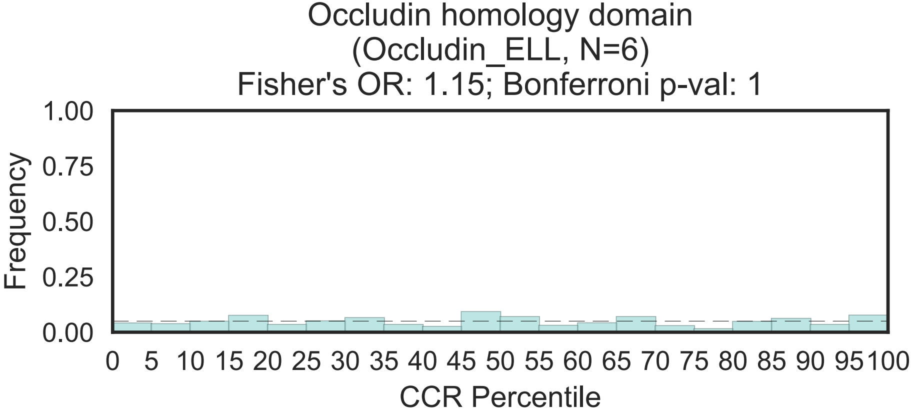

Organic solute transporter subunit beta protein
(OSTbeta, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

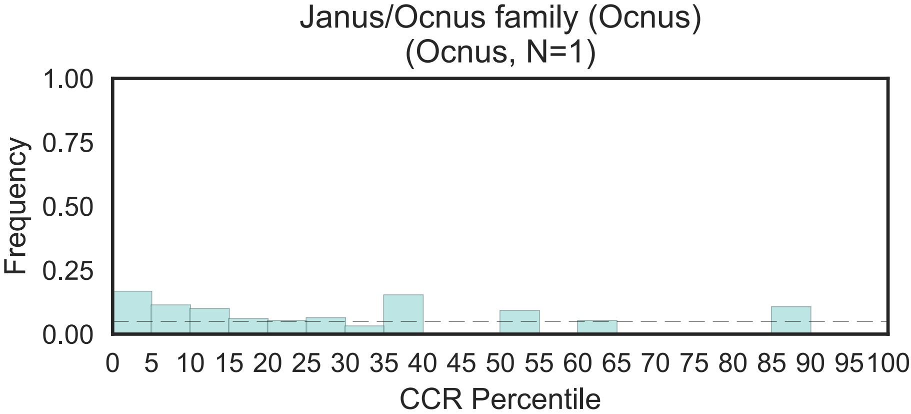

Aspartate/ornithine carbamoyltransferase, Asp/Orn binding domain
(OTCace, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

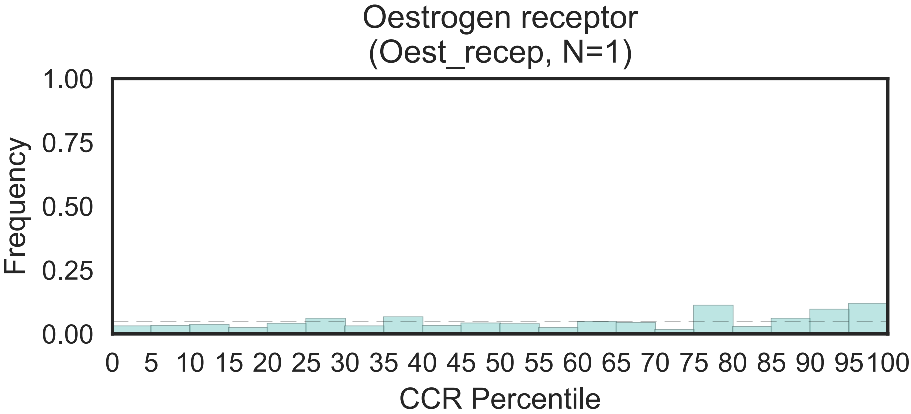

Aspartate/ornithine carbamoyltransferase, carbamoyl-P binding domain
(OTCace_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

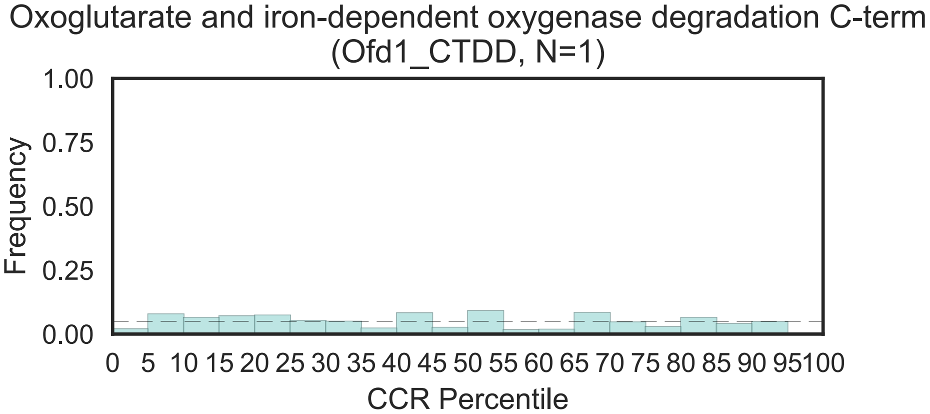

Otospiralin
(OTOS, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

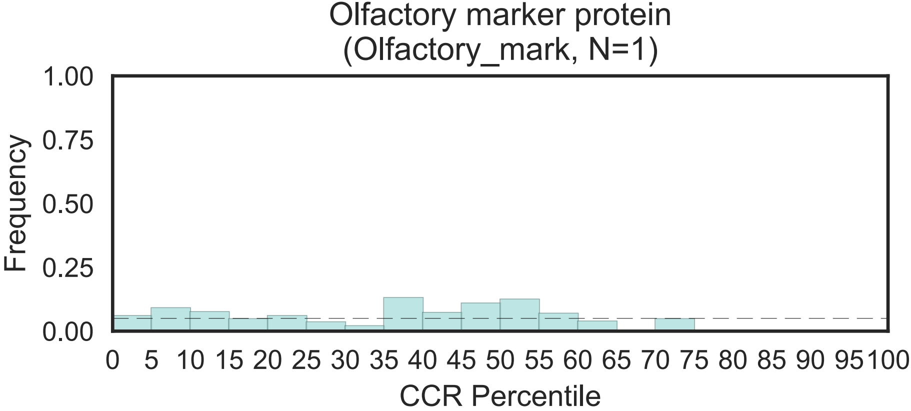

OTU-like cysteine protease
(OTU, N=11)
Fisher's OR: 6.28; Bonferroni p-val: 1.59e-05
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

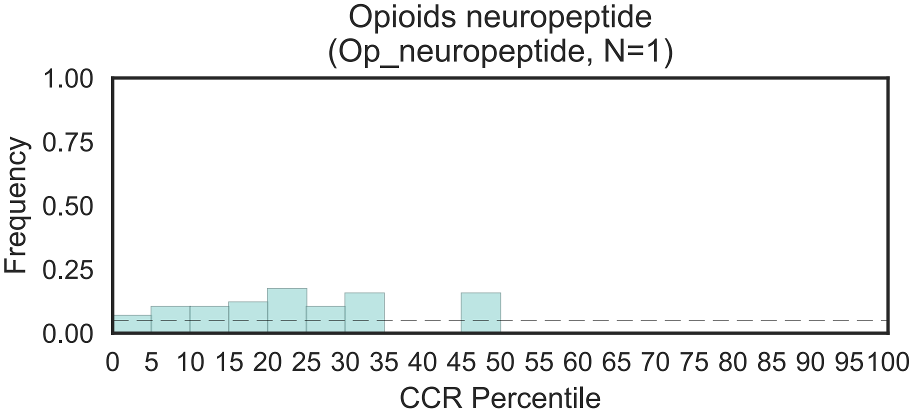

Occludin homology domain
(Occludin_ELL, N=6)
Fisher's OR: 1.15; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

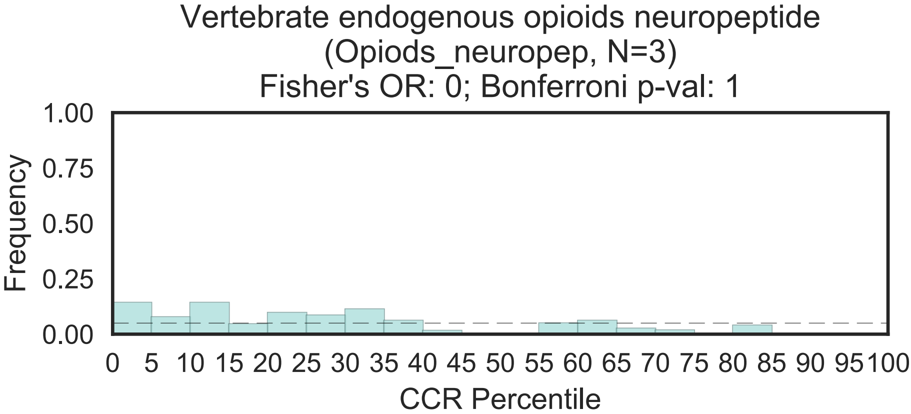

Janus/Ocnus family (Ocnus)
(Ocnus, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

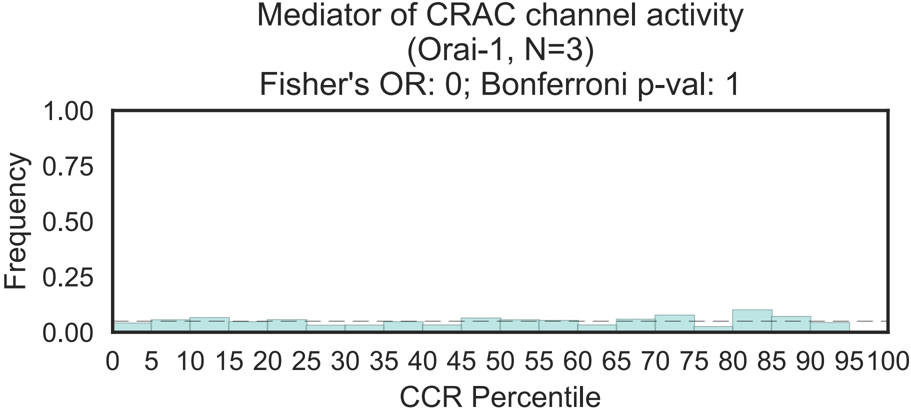

Oestrogen receptor
(Oest_recep, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

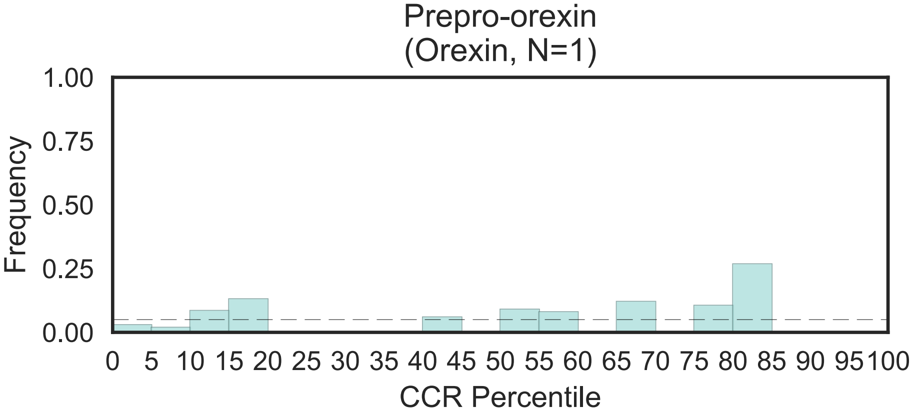

Oxoglutarate and iron-dependent oxygenase degradation C-term
(Ofd1_CTDD, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

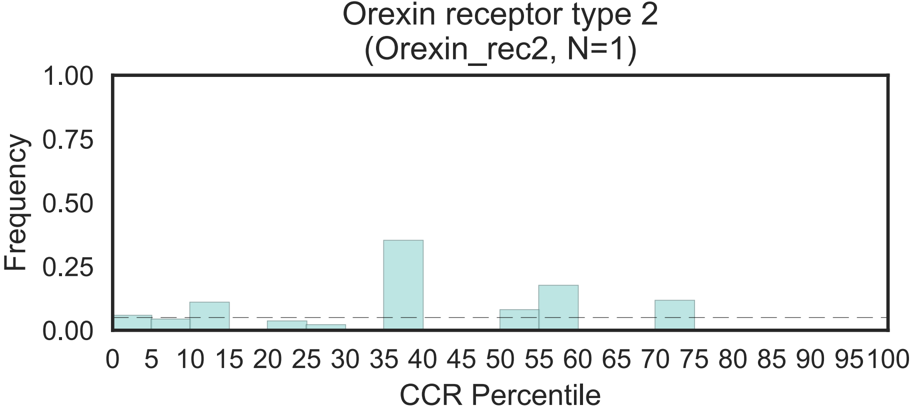

Olfactory marker protein
(Olfactory_mark, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

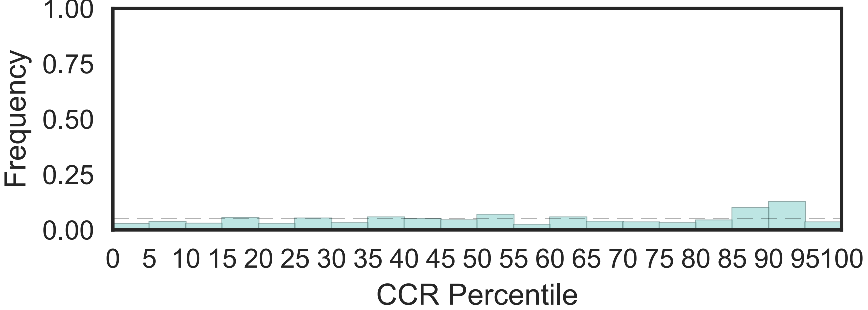

Opioids neuropeptide
(Op_neuropeptide, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

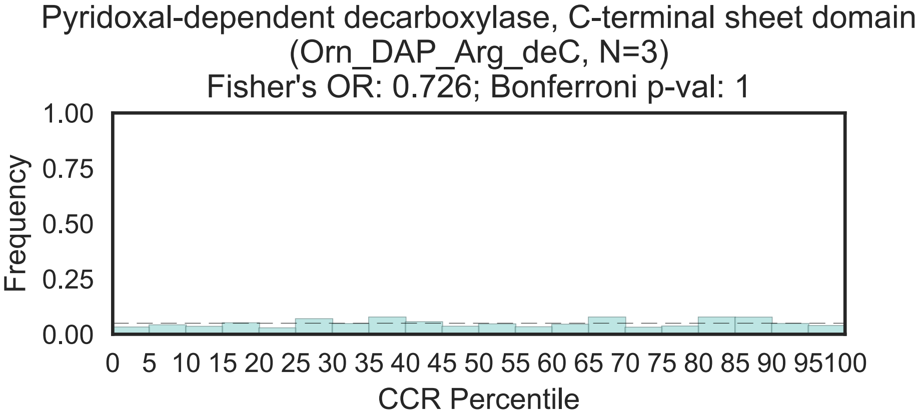

Vertebrate endogenous opioids neuropeptide
(Opiods_neuropep, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

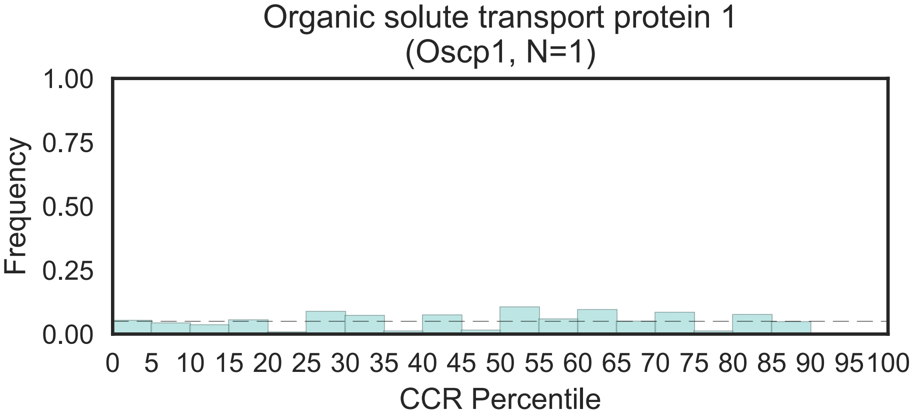

Mediator of CRAC channel activity
(Orai-1, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

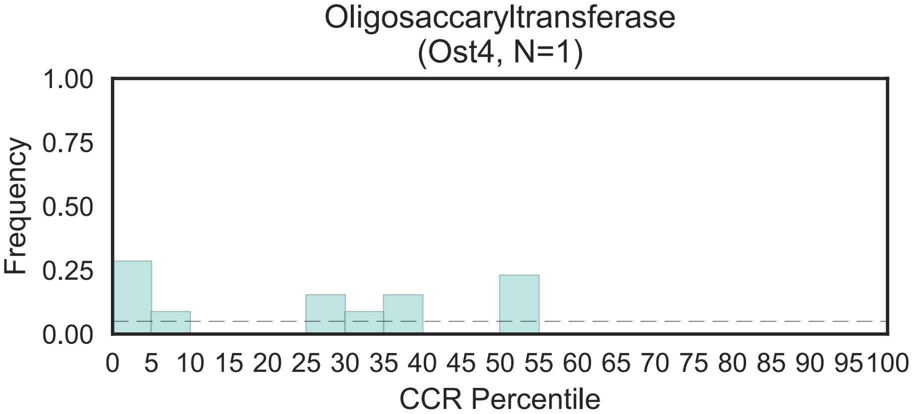

Prepro-orexin
(Orexin, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Orexin receptor type 2
(Orexin_rec2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

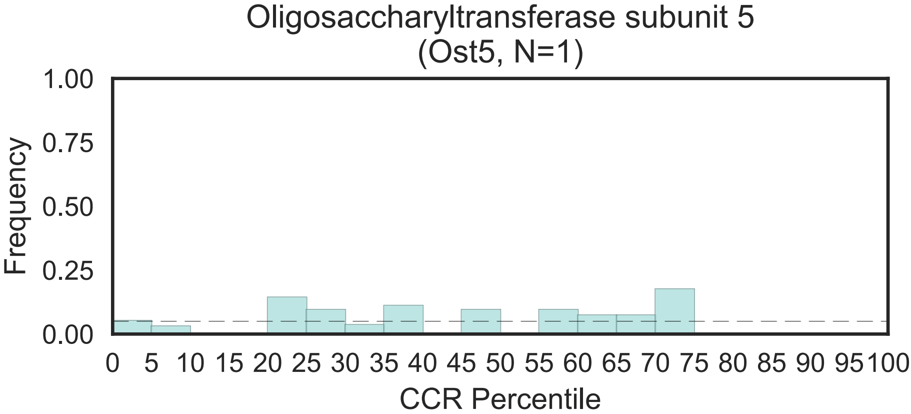

Pyridoxal-dependent decarboxylase, pyridoxal binding domain
(Orn_Arg_deC_N, N=3)
Fisher's OR: 0.449; Bonferroni p-val: 1

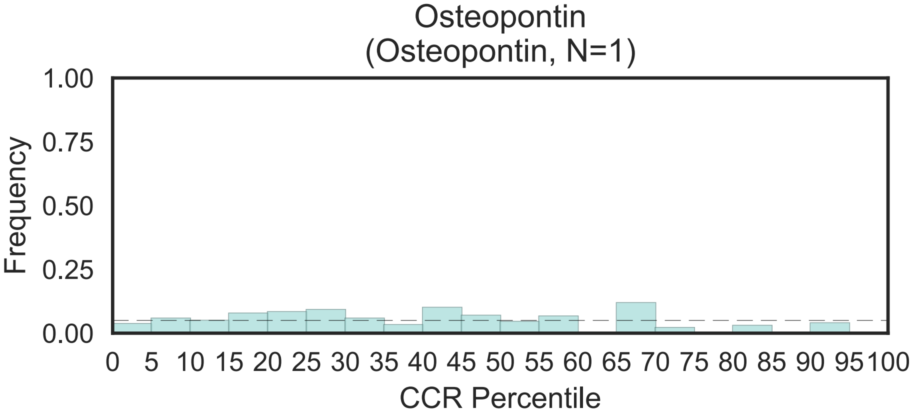

Pyridoxal-dependent decarboxylase, C-terminal sheet domain
(Orn_DAP_Arg_deC, N=3)
Fisher's OR: 0.726; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95100
CCR Percentile

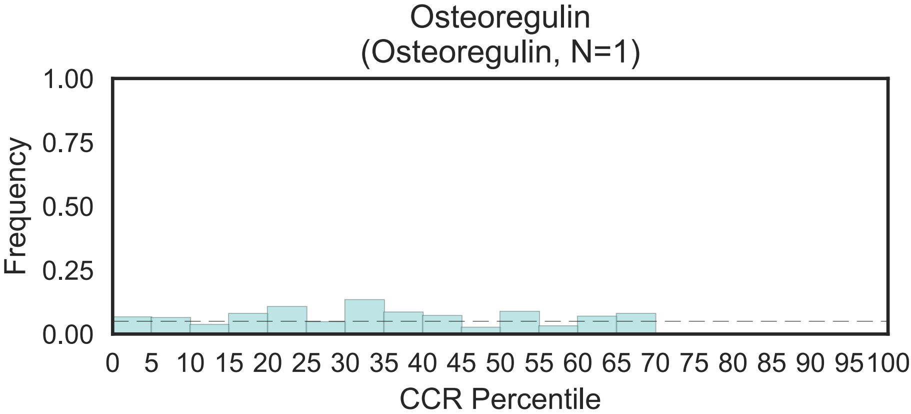

Organic solute transport protein 1
(Oscp1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



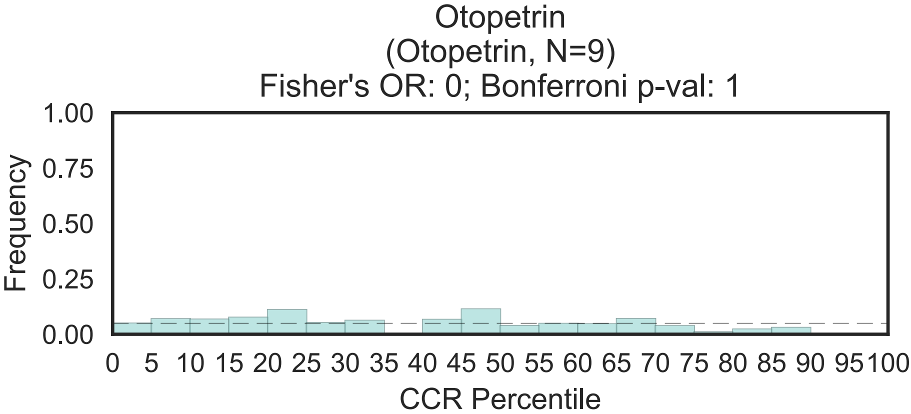
Oligosaccaryltransferase
(Ost4, N=1)

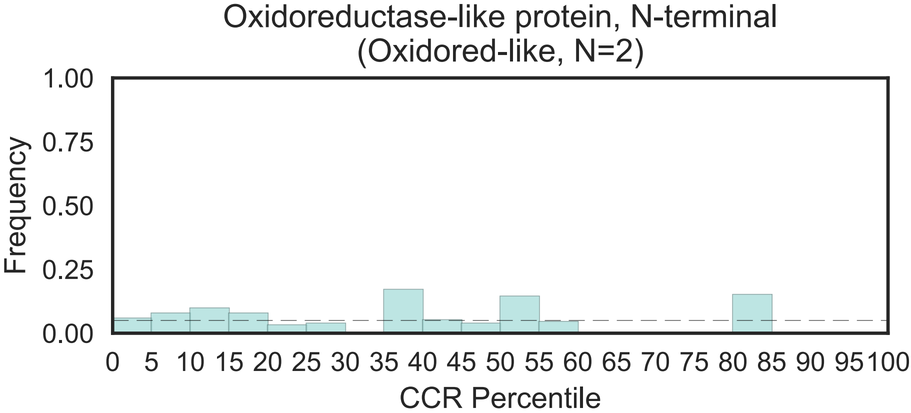

Oligosaccharyltransferase subunit 5
(Ost5, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

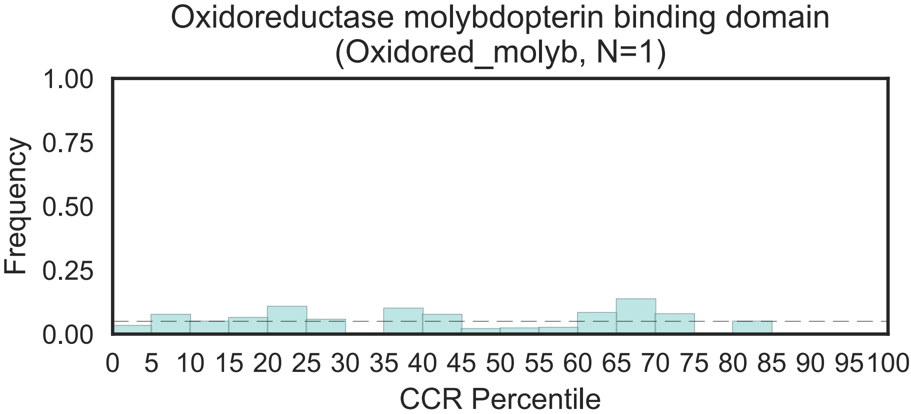

Osteopontin
(Osteopontin, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

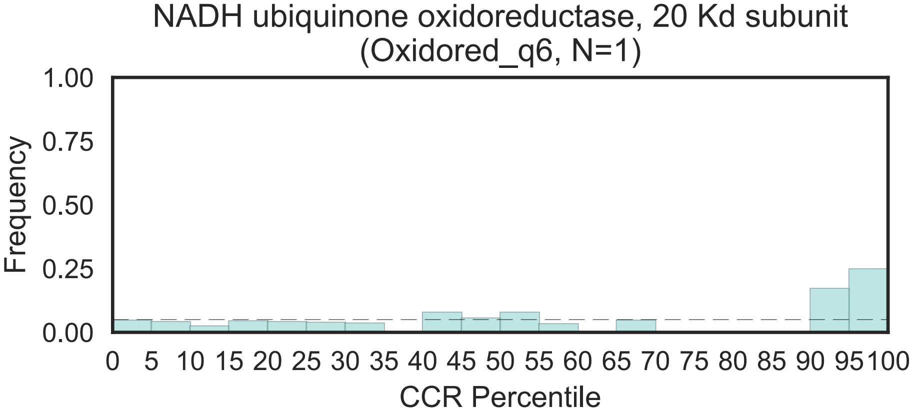


Osteoregulin
(Osteoregulin, N=1)

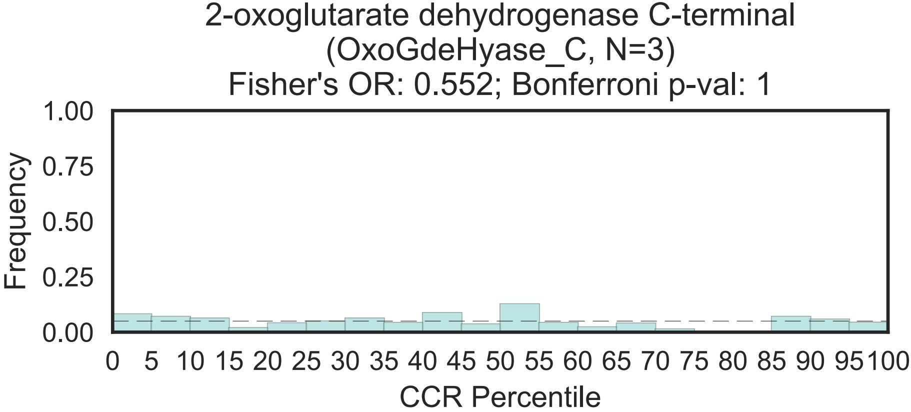

Otopetrin
(Otopetrin, N=9)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

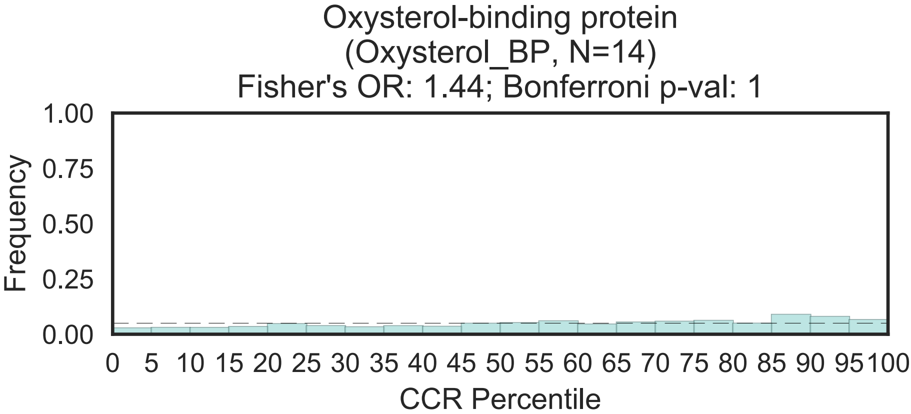

Oxidoreductase-like protein, N-terminal
(Oxidored-like, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

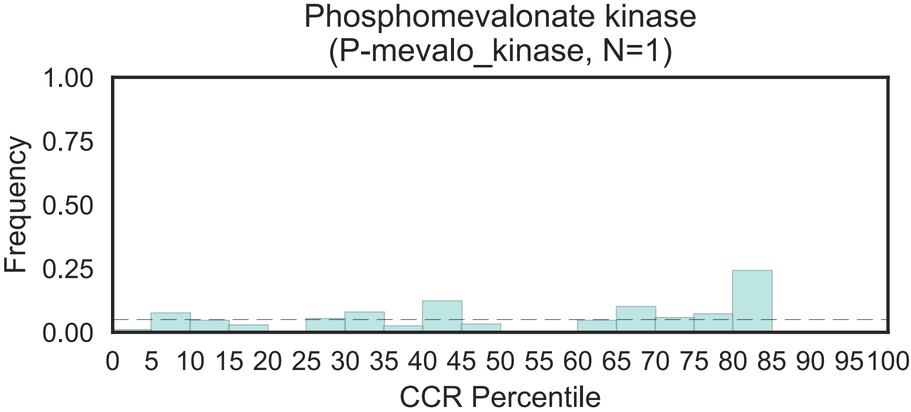

Oxidoreductase molybdopterin binding domain
(Oxidored_molyb, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

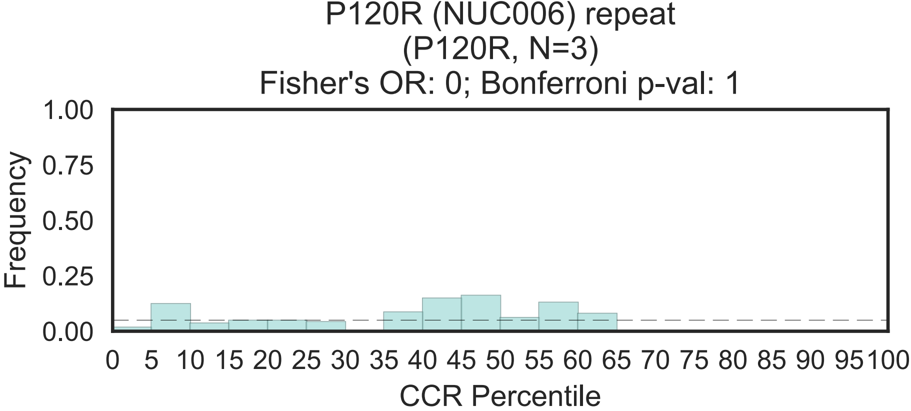


NADH ubiquinone oxidoreductase, 20 Kd subunit
(Oxidored_q6, N=1)

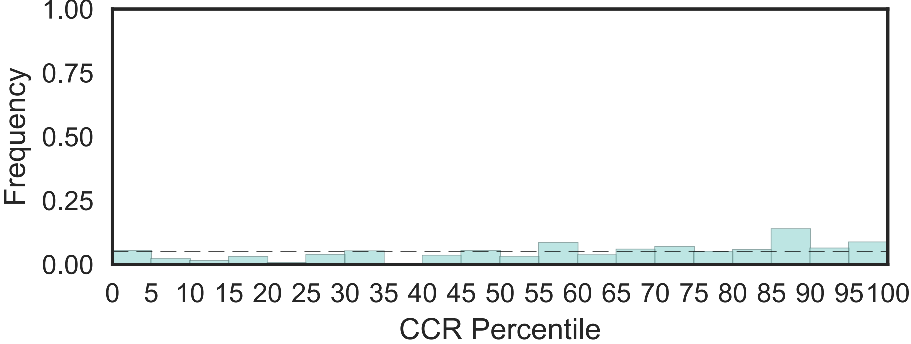

2-oxoglutarate dehydrogenase C-terminal
(OxoGdeHyase_C, N=3)
Fisher's OR: 0.552; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

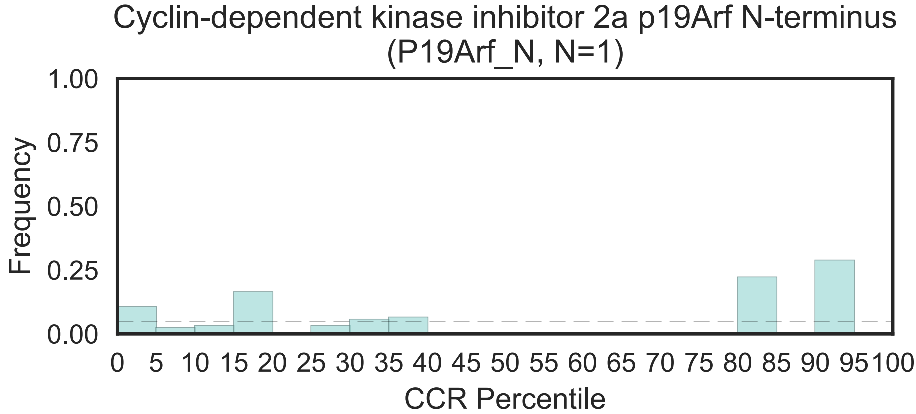

Oxysterol-binding protein
(Oxysterol_BP, N=14)
Fisher's OR: 1.44; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

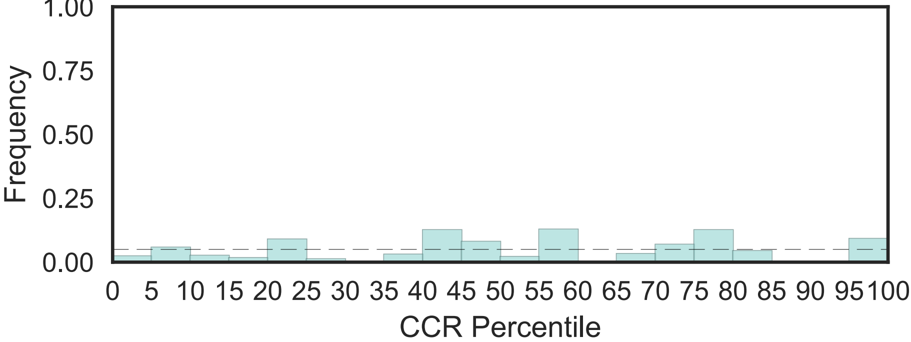

Phosphomevalonate kinase
(P-mevalo_kinase, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


P120R (NUC006) repeat
(P120R, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

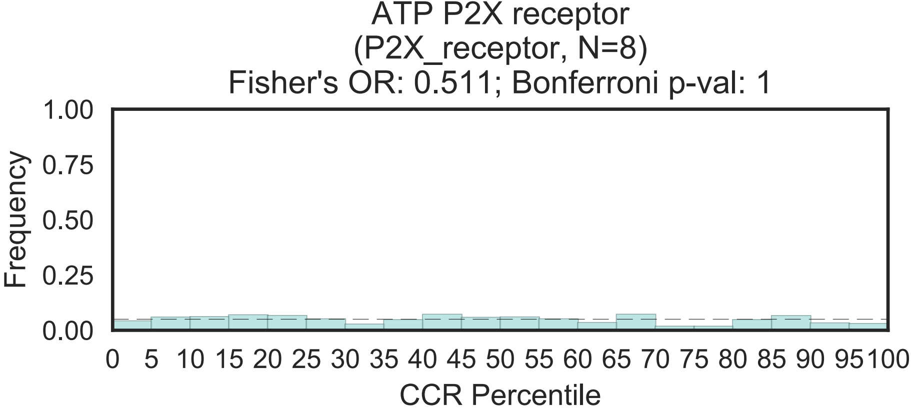
ARP2/3 complex 16 kDa subunit (p16-Arc)
(P16-Arc, N=2)

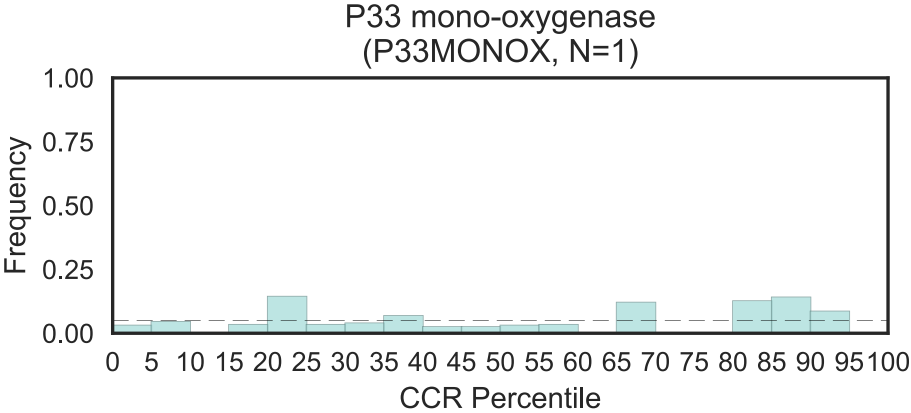



Cyclin-dependent kinase inhibitor 2a p19Arf N-terminus
(P19Arf_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

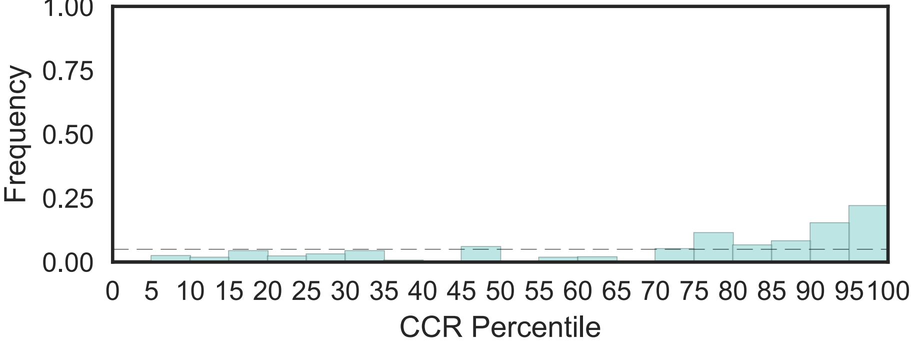


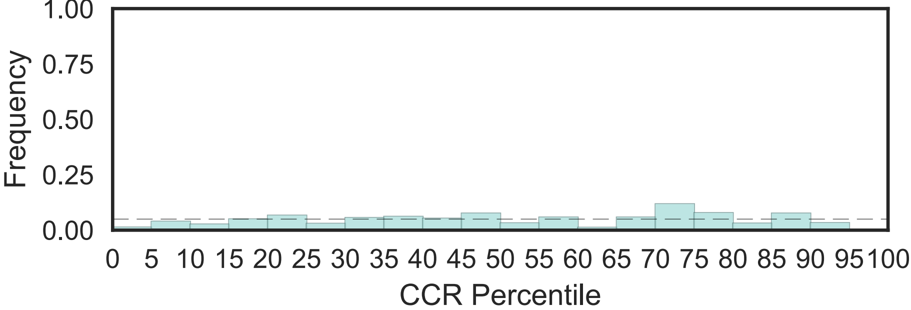
ARP2/3 complex ARPC3 (21 kDa) subunit
(P21-Arc, N=1)


ATP P2X receptor
(P2X_receptor, N=8)
Fisher's OR: 0.511; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

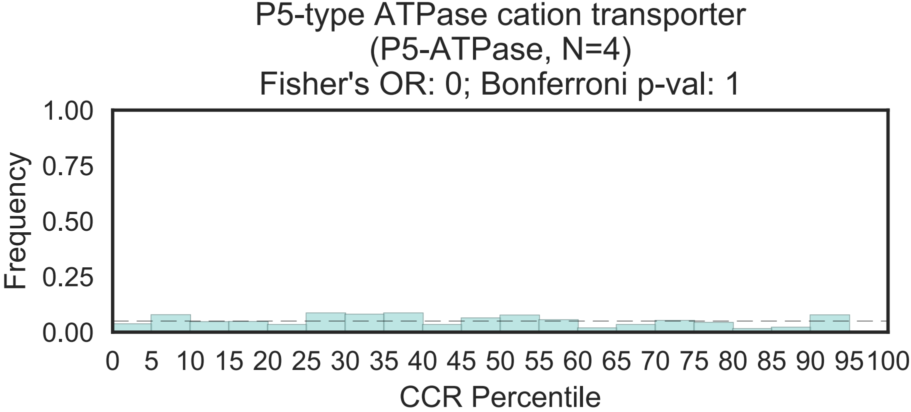

P33 mono-oxygenase
(P33MONOX, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Arp2/3 complex, 34 kD subunit p34-Arc (P34-Arc, N=1)

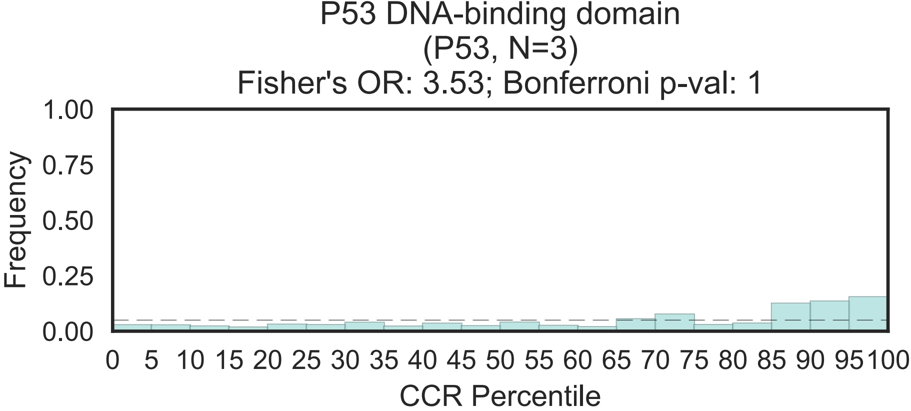


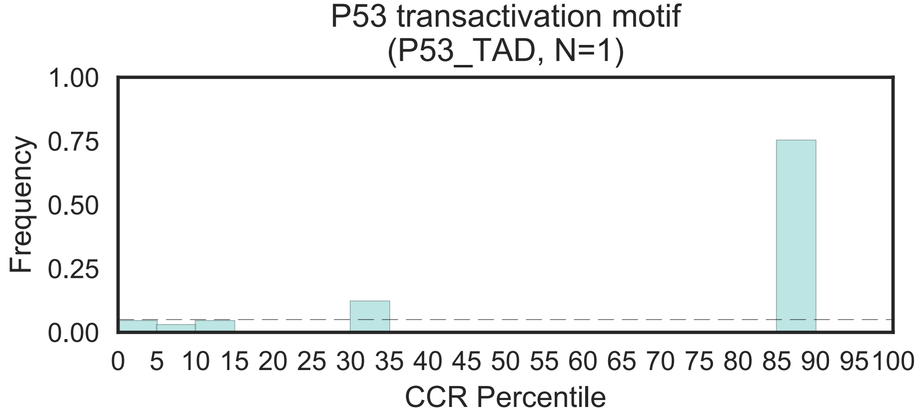


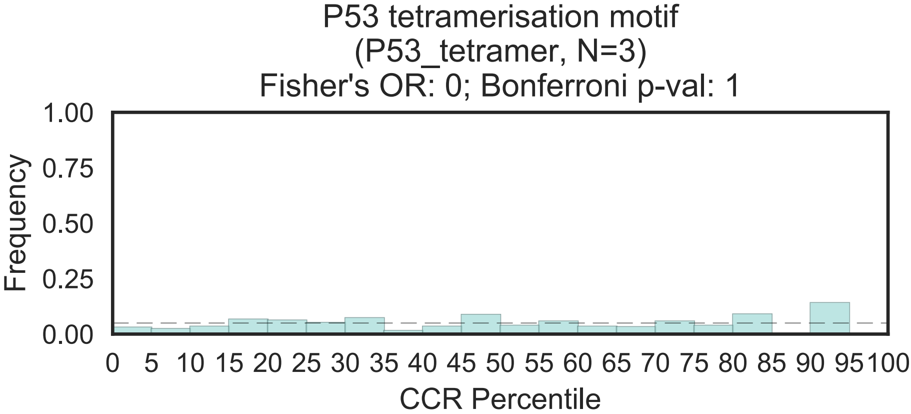
Prolyl 4-Hydroxylase alpha-subunit, N-terminal region
(P4Ha_N, N=3)
Fisher's OR: 0; Bonferroni p-val: 1



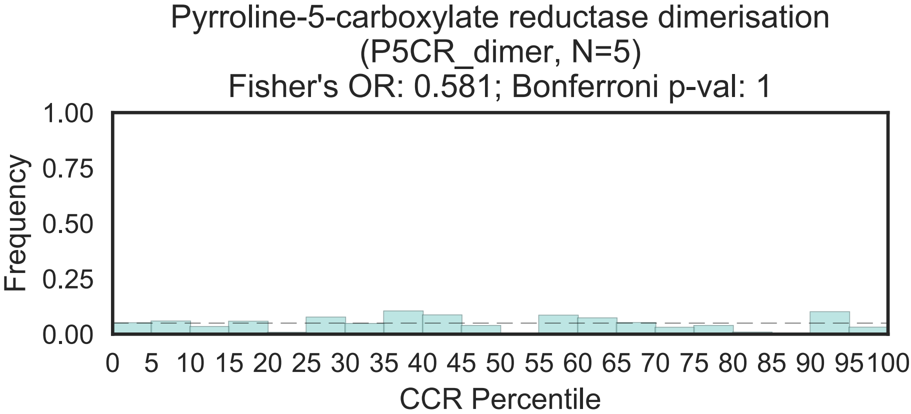
P5-type ATPase cation transporter
(P5-ATPase, N=4)
Fisher's OR: 0; Bonferroni p-val: 1


P53 DNA-binding domain
(P53, N=3)
Fisher's OR: 3.53; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


P53 transactivation motif
(P53_TAD, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

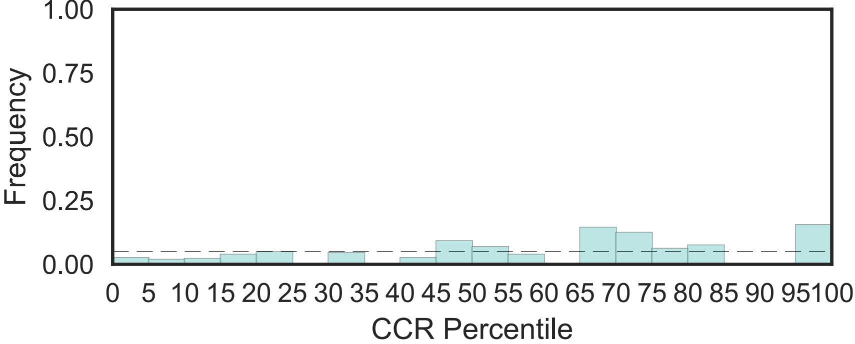


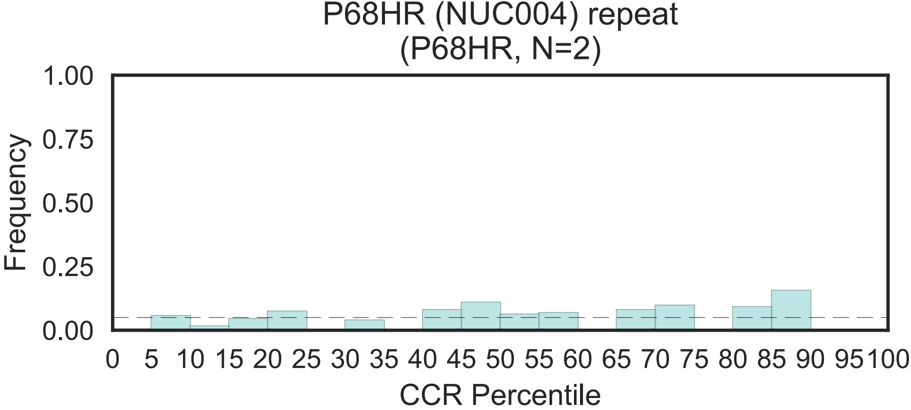
P53 tetramerisation motif
(P53_tetramer, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

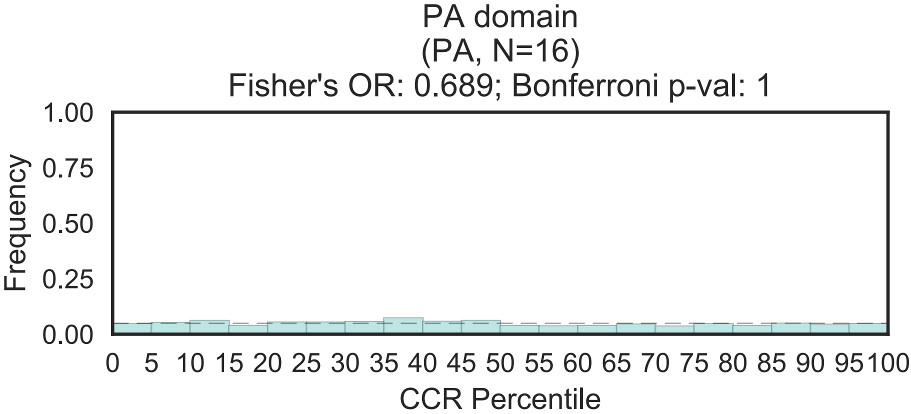


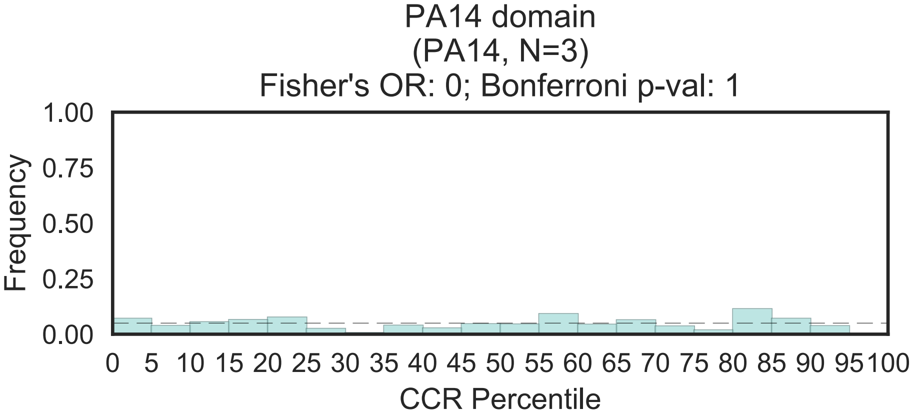
Pyrroline-5-carboxylate reductase dimerisation
(P5CR_dimer, N=5)
Fisher's OR: 0.581; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

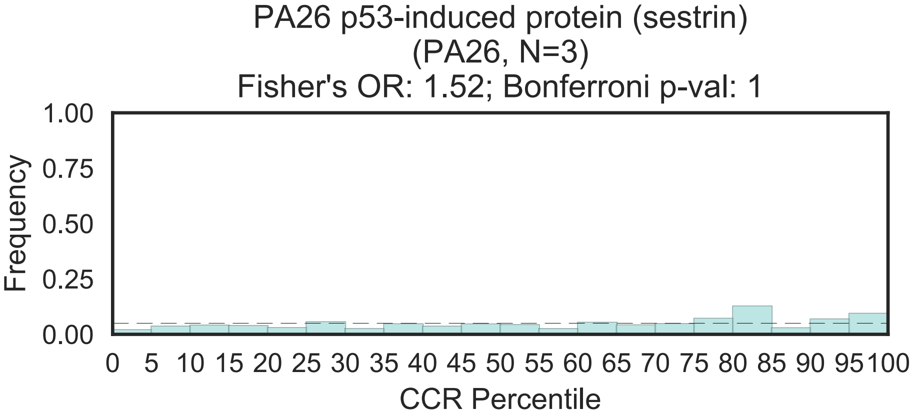
Coiled-coil and interaction region of P66A and P66B with MBD2 (P66_CC, N=2)

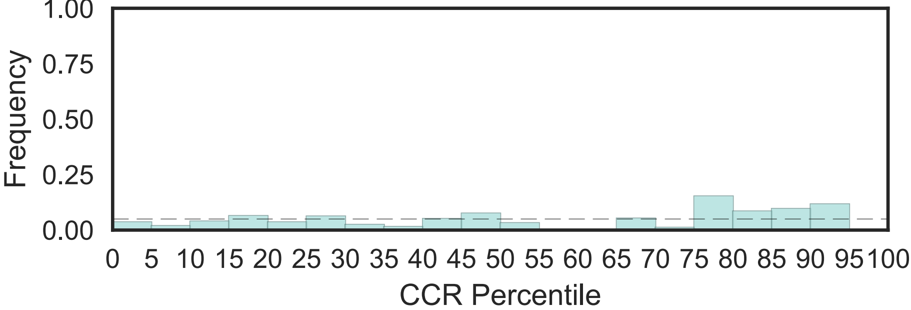



P68HR (NUC004) repeat
(P68HR, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

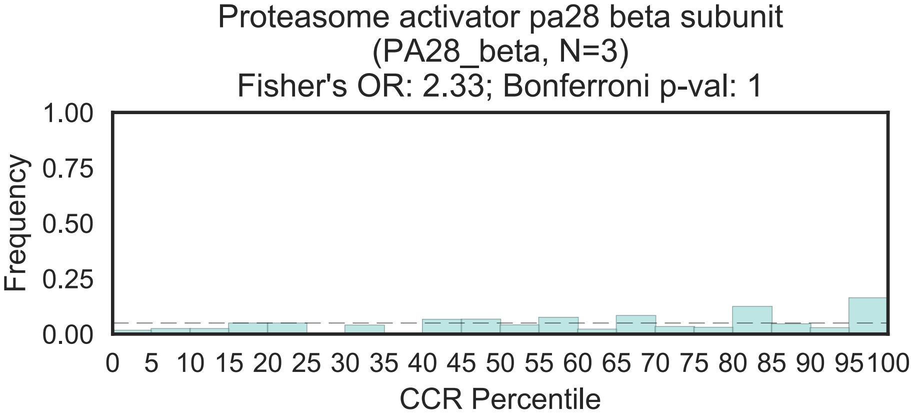

PA domain
(PA, N=16)
Fisher's OR: 0.689; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

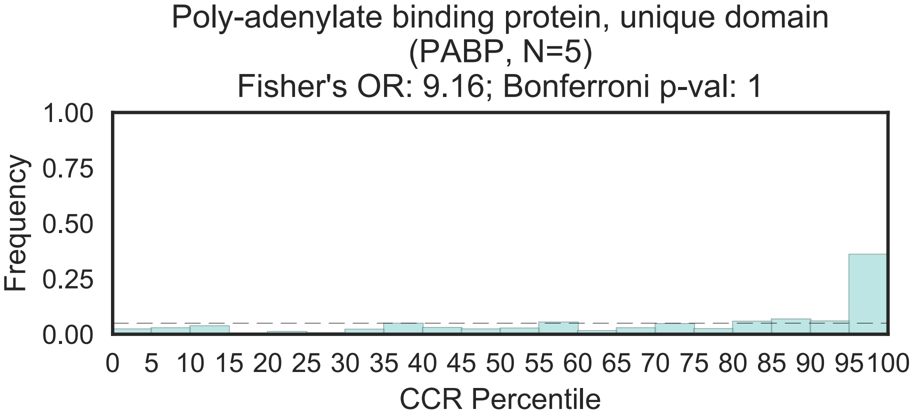

PA14 domain
(PA14, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

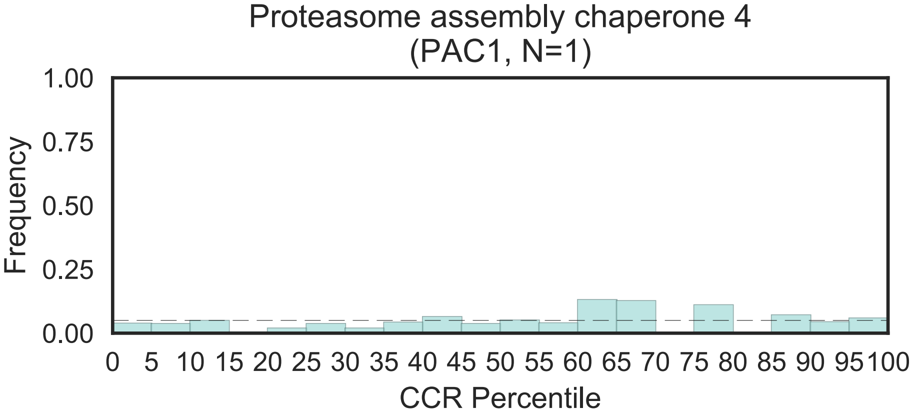

PA26 p53-induced protein (sestrin)
(PA26, N=3)
Fisher's OR: 1.52; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

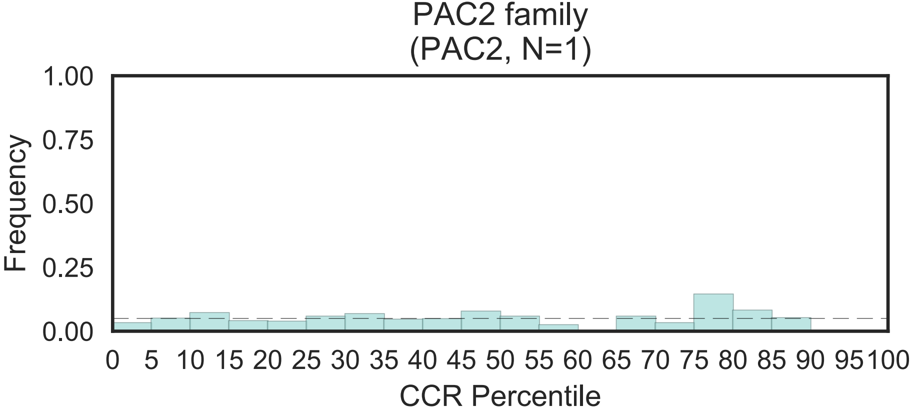


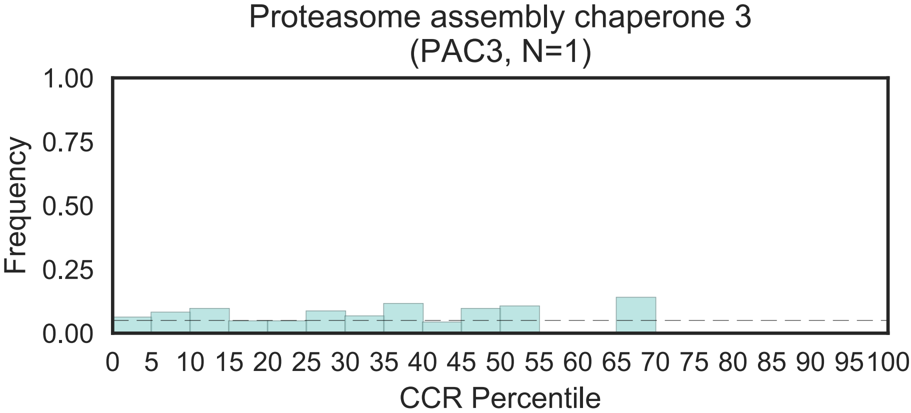
Proteasome activator pa28 alpha subunit
(PA28_alpha, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

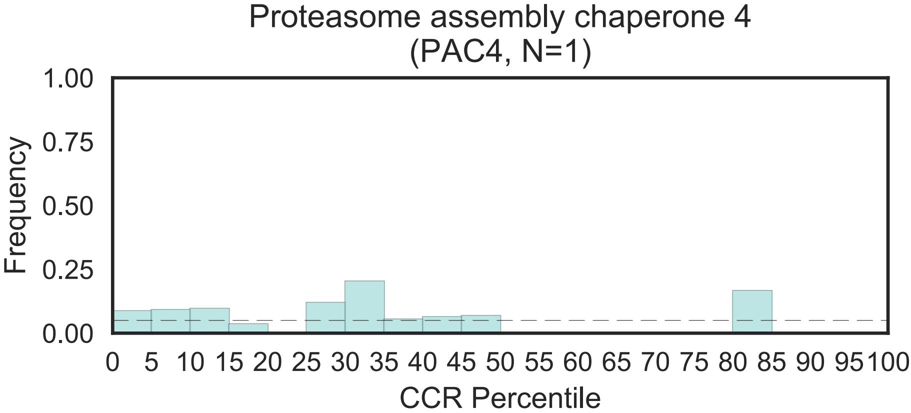

Proteasome activator pa28 beta subunit
(PA28_beta, N=3)
Fisher's OR: 2.33; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

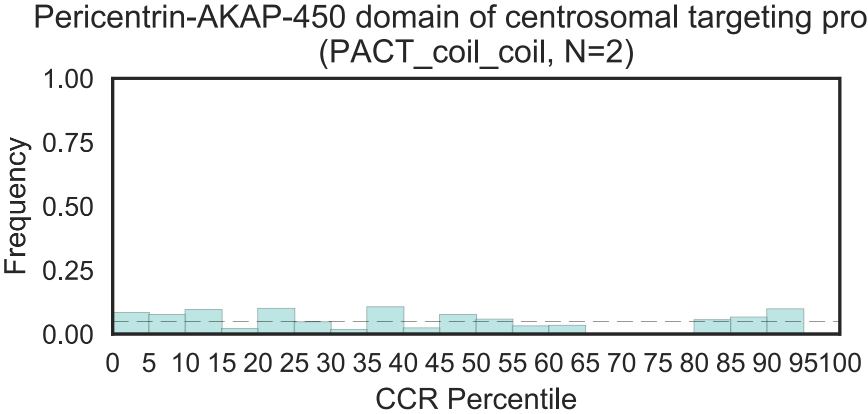

Poly-adenylate binding protein, unique domain
(PABP, N=5)
Fisher's OR: 9.16; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

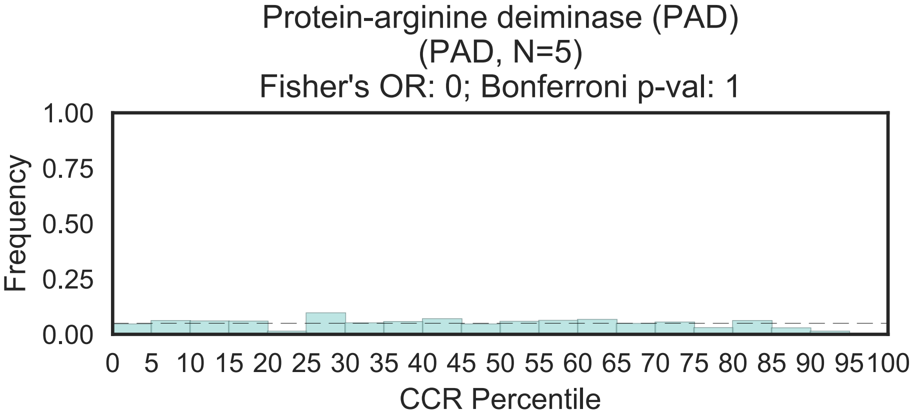

Proteasome assembly chaperone 4
(PAC1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

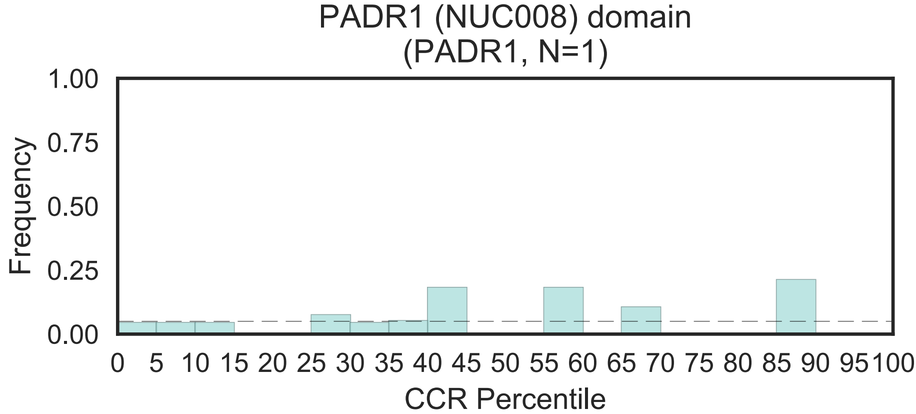

PAC2 family
(PAC2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


Proteasome assembly chaperone 3
(PAC3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

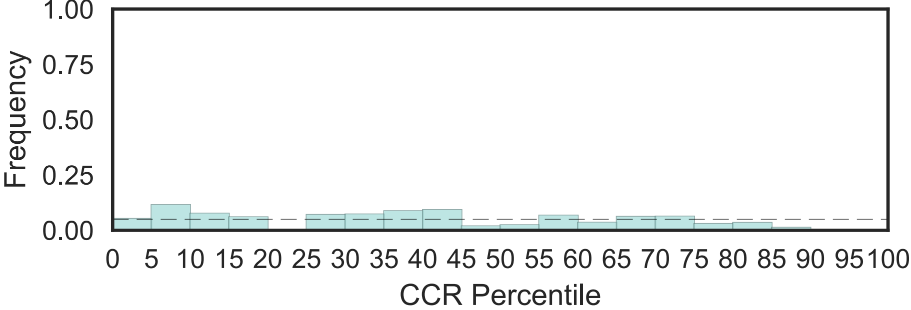

Proteasome assembly chaperone 4
(PAC4, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

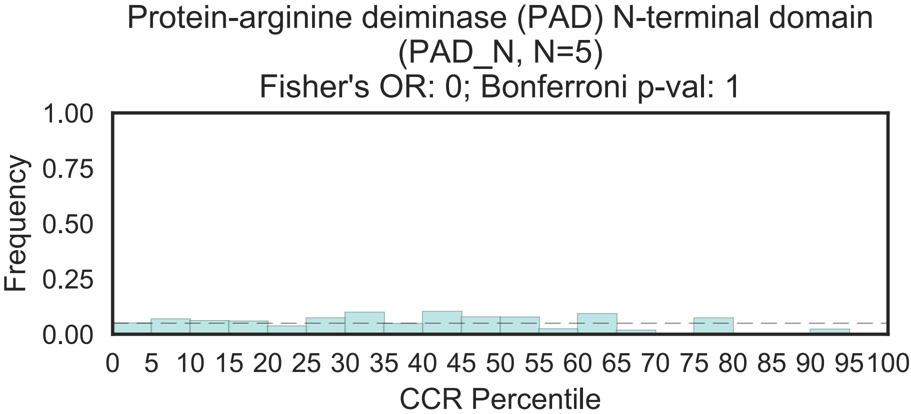

Pericentrin-AKAP-450 domain of centrosomal targeting protein
(PACT_coil_coil, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

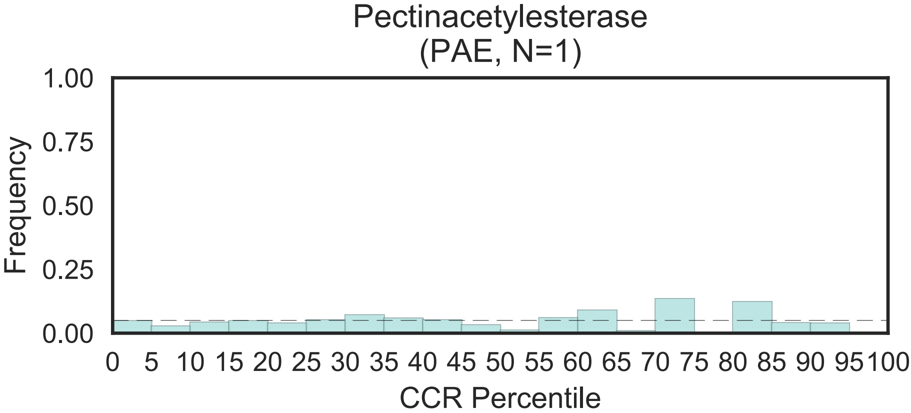

Protein-arginine deiminase (PAD)
(PAD, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

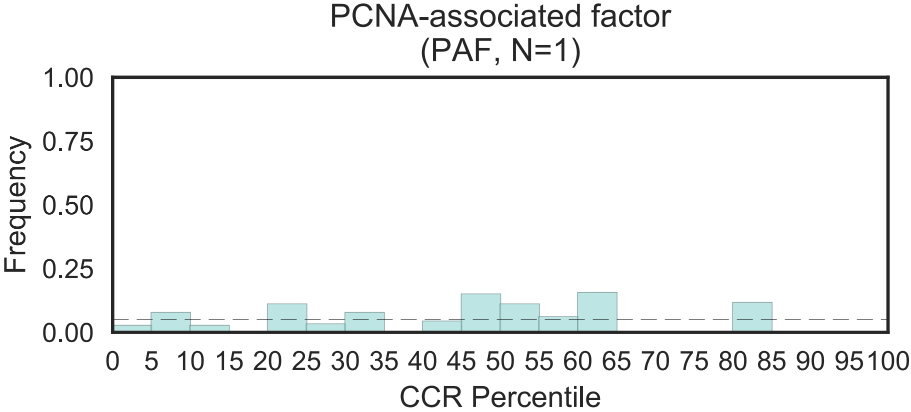

PADR1 (NUC008) domain
(PADR1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

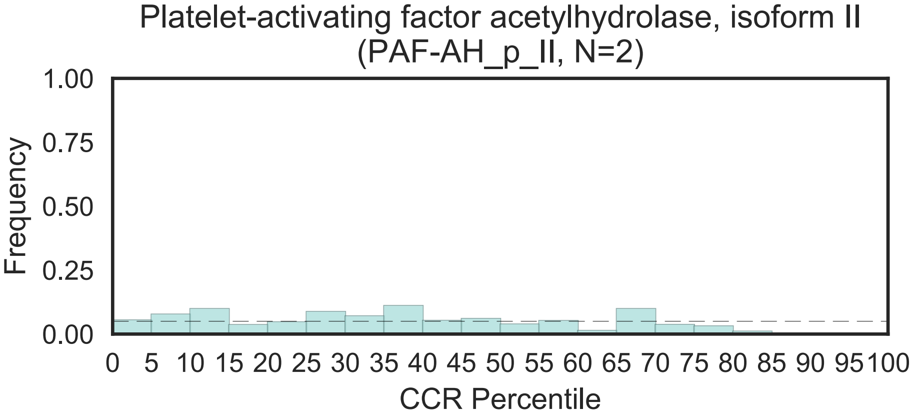
Protein-arginine deiminase (PAD) middle domain
(PAD_M, N=5)
Fisher's OR: 0; Bonferroni p-val: 1

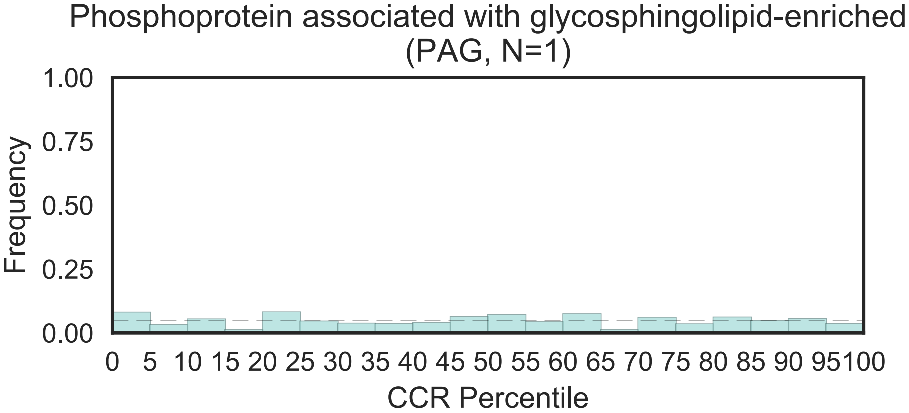


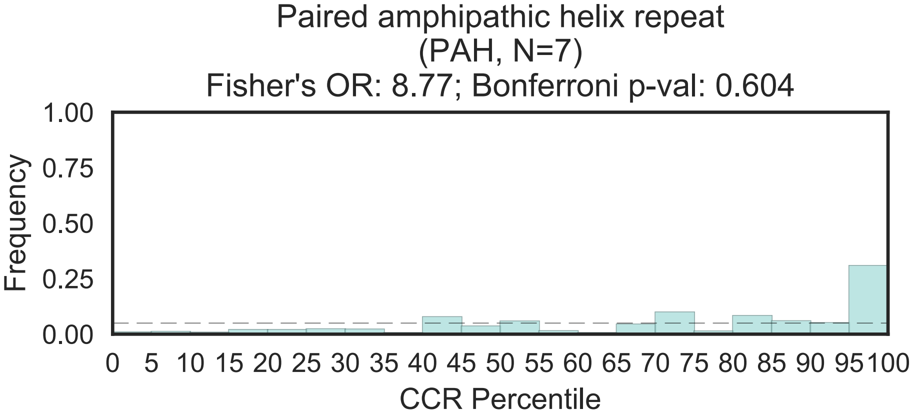

Protein-arginine deiminase (PAD) N-terminal domain
(PAD_N, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

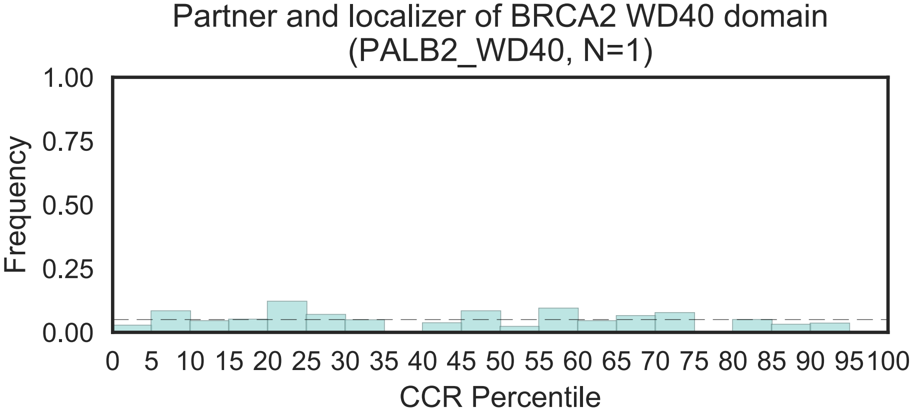

Pectinacetylesterase
(PAE, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

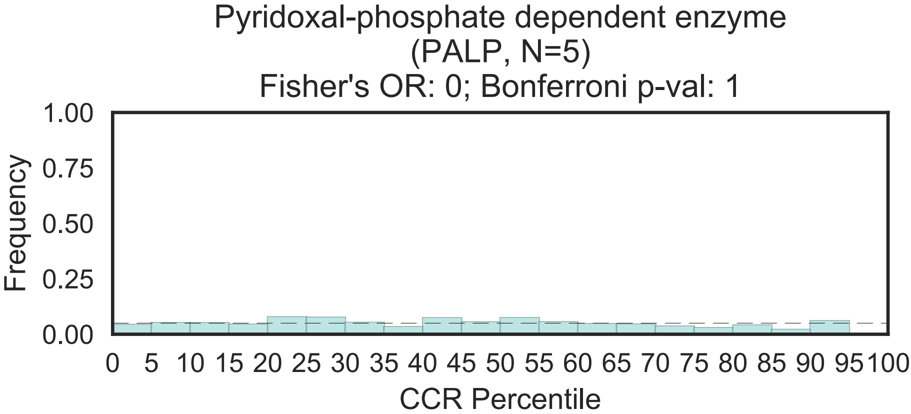

PCNA-associated factor
(PAF, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

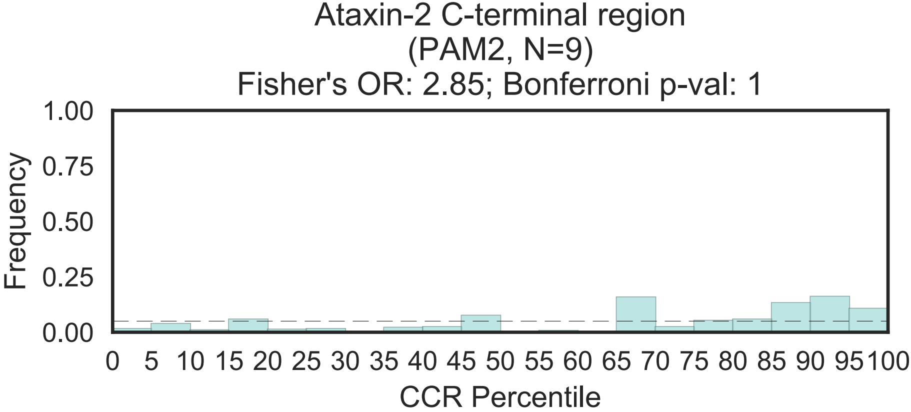

Platelet-activating factor acetylhydrolase, isoform II
(PAF-AH_p_II, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

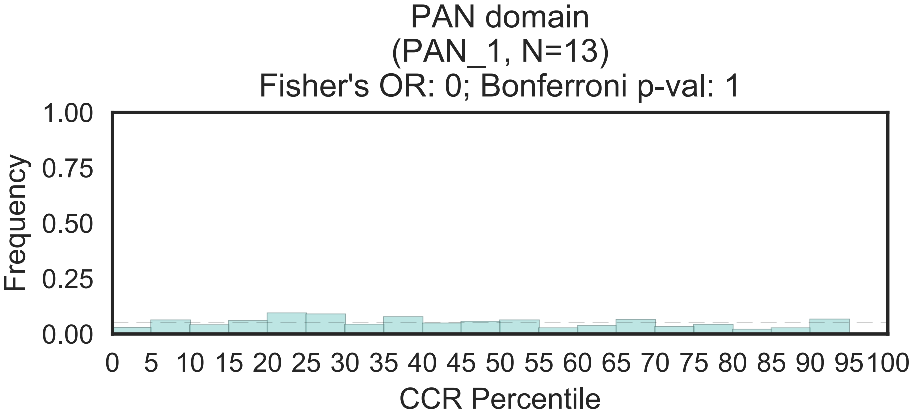

Phosphoprotein associated with glycosphingolipid-enriched
(PAG, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

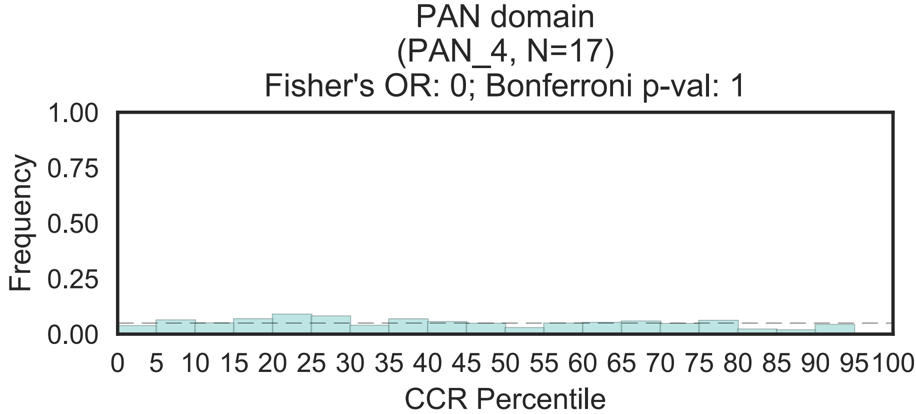

Paired amphipathic helix repeat
(PAH, N=7)
Fisher's OR: 8.77; Bonferroni p-val: 0.604
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

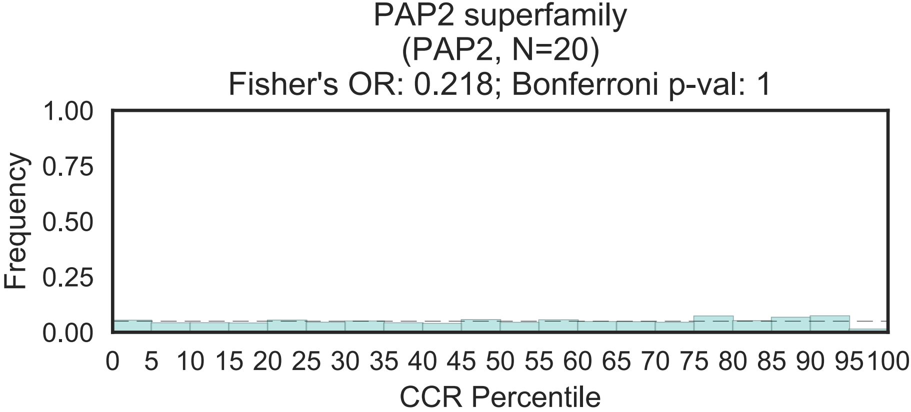

Partner and localizer of BRCA2 WD40 domain
(PALB2_WD40, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

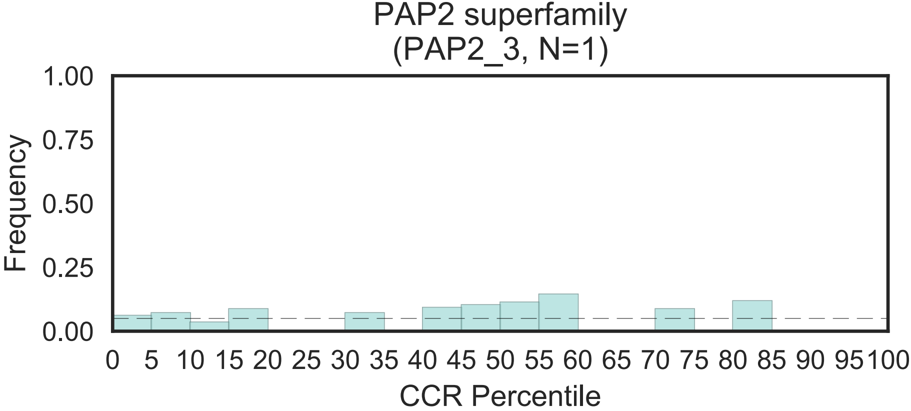

Pyridoxal-phosphate dependent enzyme
(PALP, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

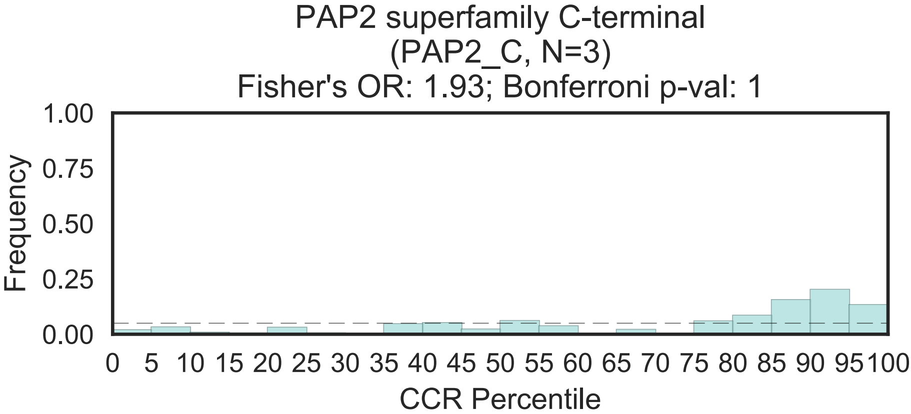

Ataxin-2 C-terminal region
(PAM2, N=9)
Fisher's OR: 2.85; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

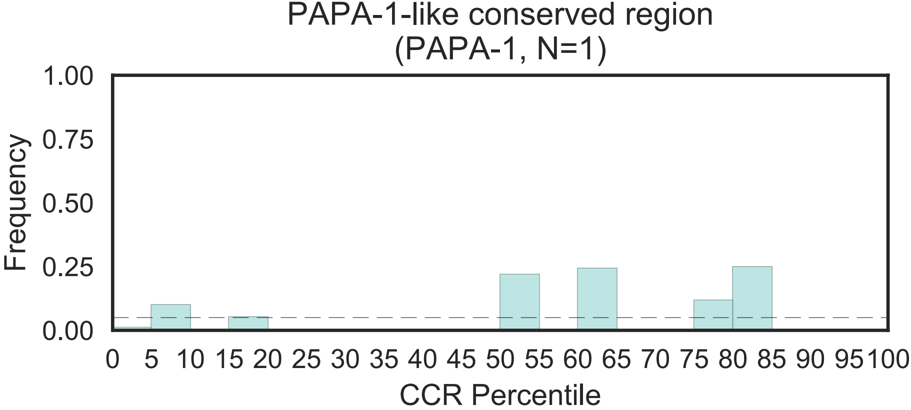

PAN domain
(PAN_1, N=13)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

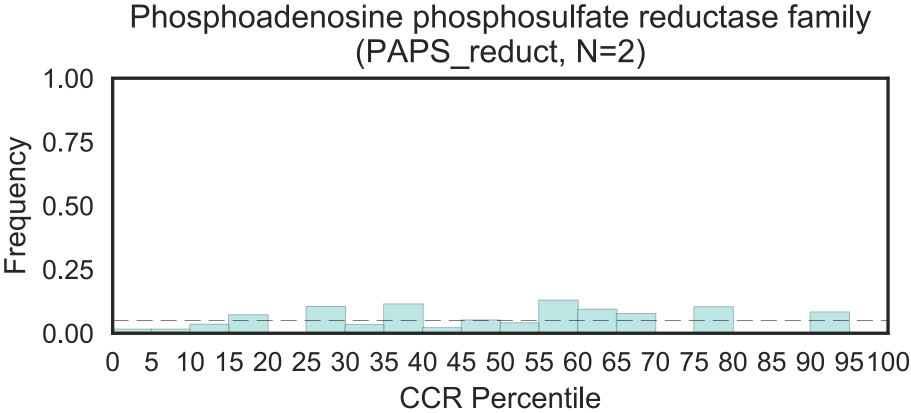

PAN domain
(PAN_4, N=17)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

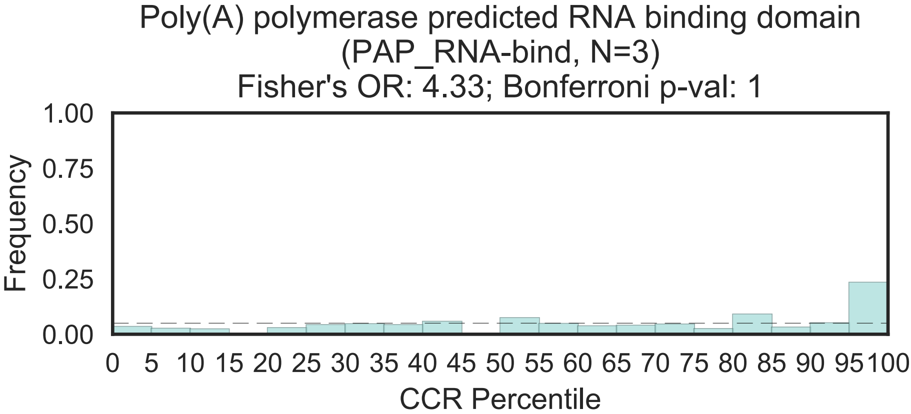

PAP2 superfamily
(PAP2, N=20)
Fisher's OR: 0.218; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

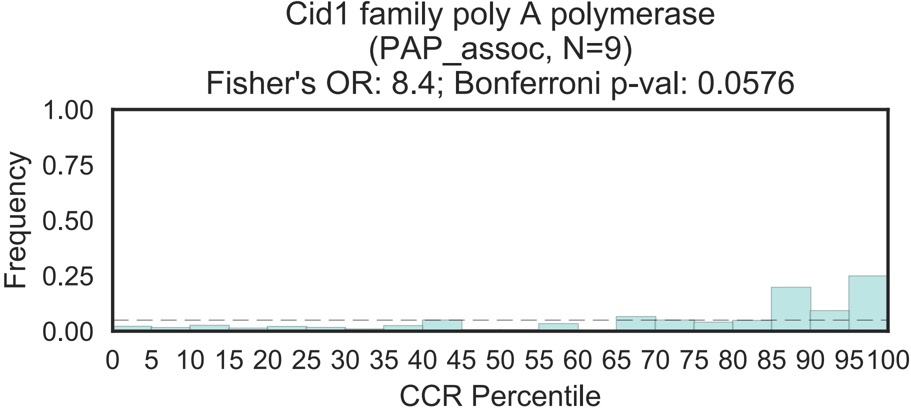

PAP2 superfamily
(PAP2_3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

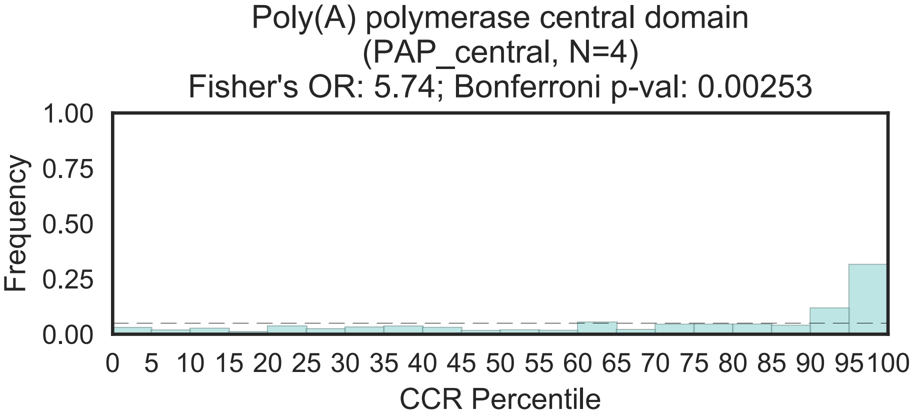

PAP2 superfamily C-terminal
(PAP2_C, N=3)
Fisher's OR: 1.93; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

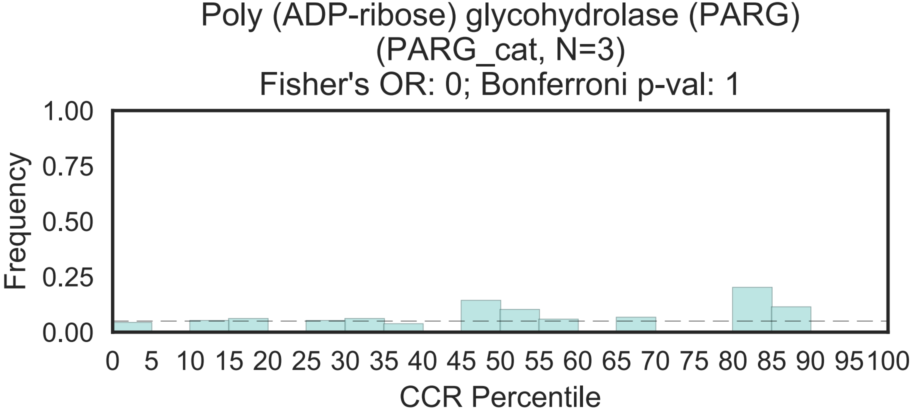

PAPA-1-like conserved region
(PAPA-1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

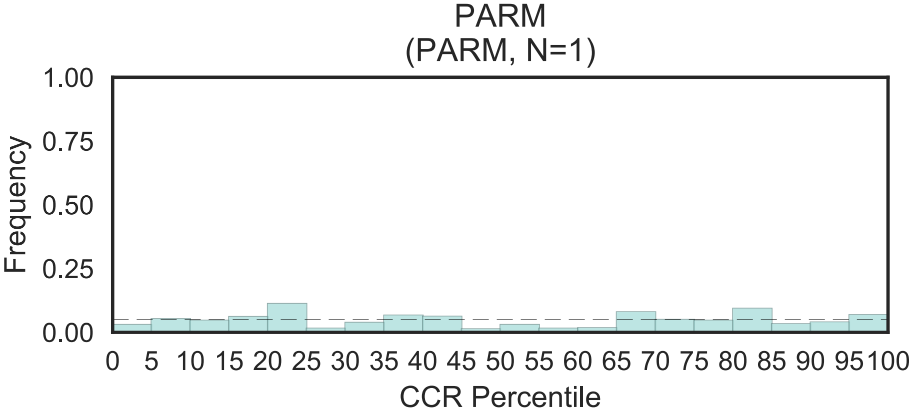

Phosphoadenosine phosphosulfate reductase family
(PAPS_reduct, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

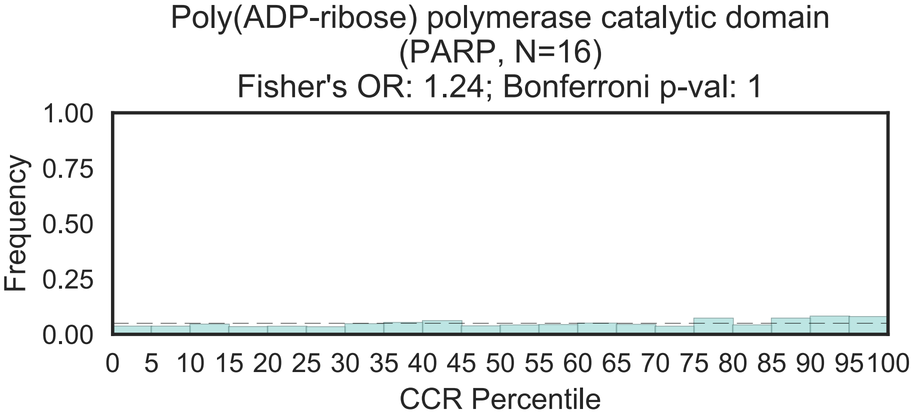

Poly(A) polymerase predicted RNA binding domain
(PAP_RNA-bind, N=3)
Fisher's OR: 4.33; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

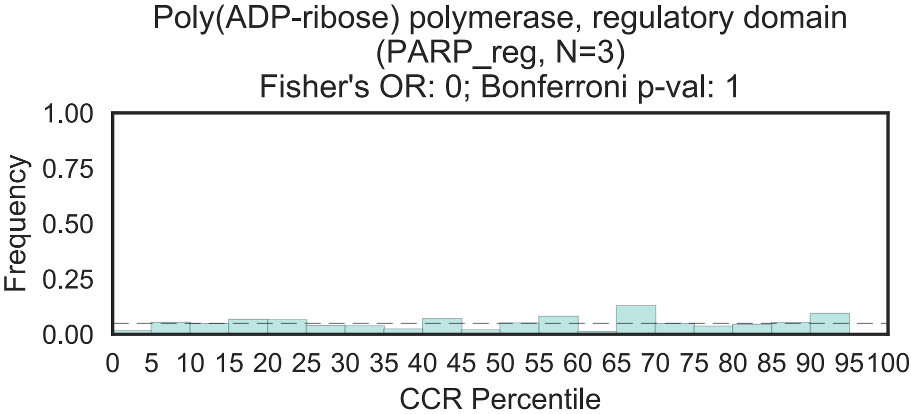

Cid1 family poly A polymerase
(PAP_assoc, N=9)
Fisher's OR: 8.4; Bonferroni p-val: 0.0576
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

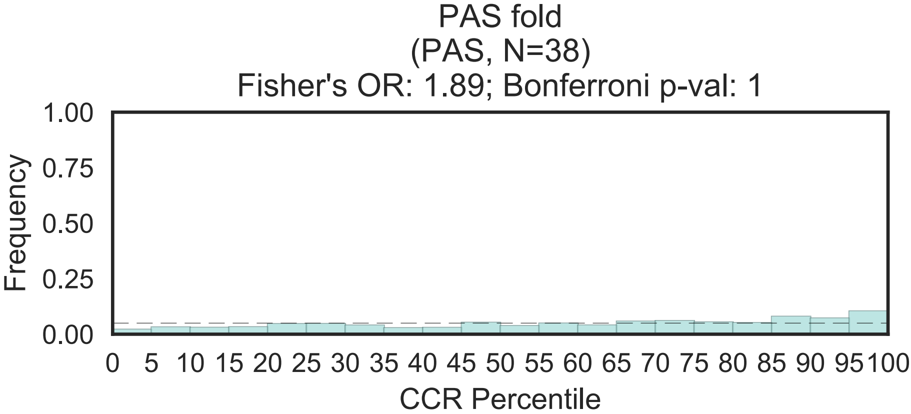

Poly(A) polymerase central domain
(PAP_central, N=4)
Fisher's OR: 5.74; Bonferroni p-val: 0.00253
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

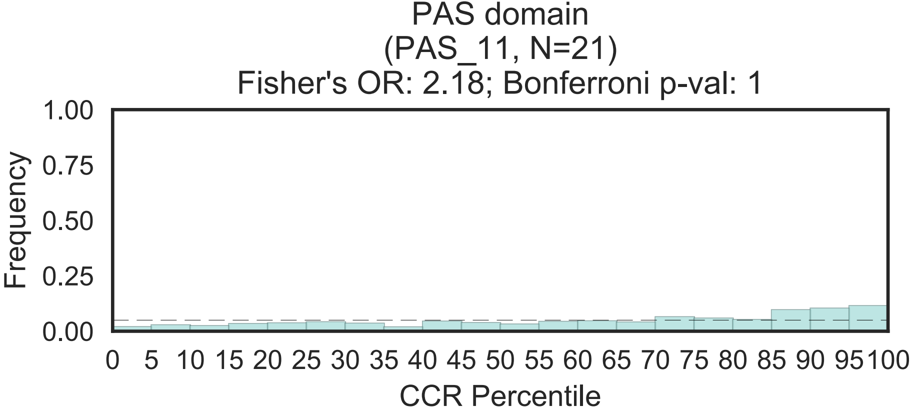

Poly (ADP-ribose) glycohydrolase (PARG)
(PARG_cat, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

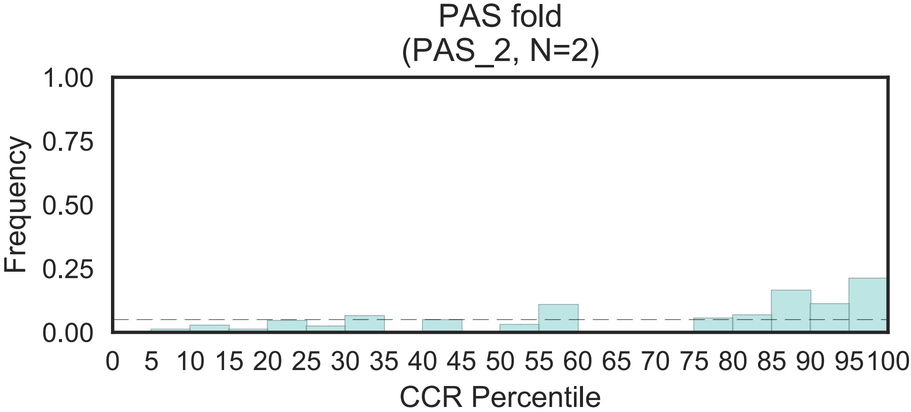

PARM
(PARM, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

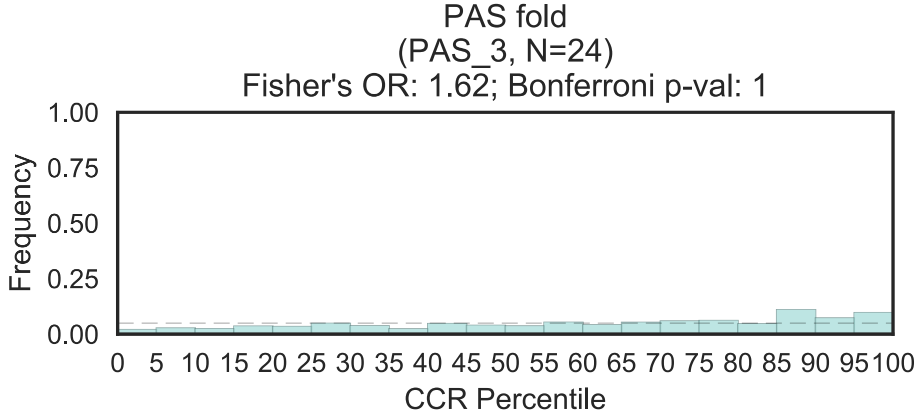

Poly(ADP-ribose) polymerase catalytic domain
(PARP, N=16)
Fisher's OR: 1.24; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

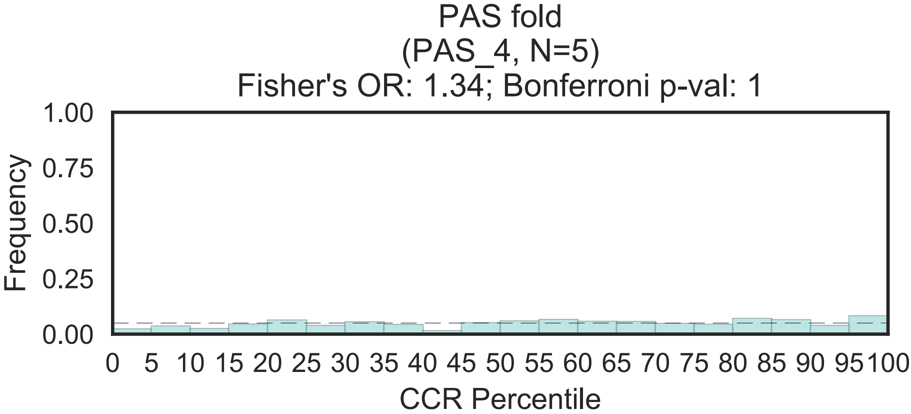

Poly(ADP-ribose) polymerase, regulatory domain
(PARP_reg, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

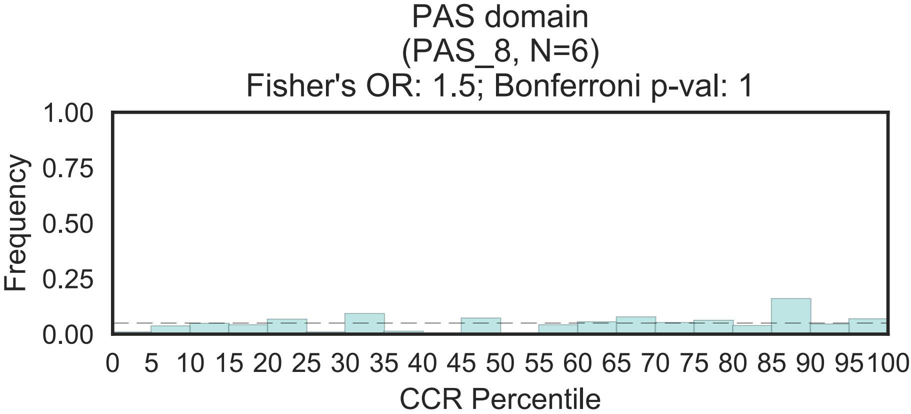

PAS fold
(PAS, N=38)
Fisher's OR: 1.89; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

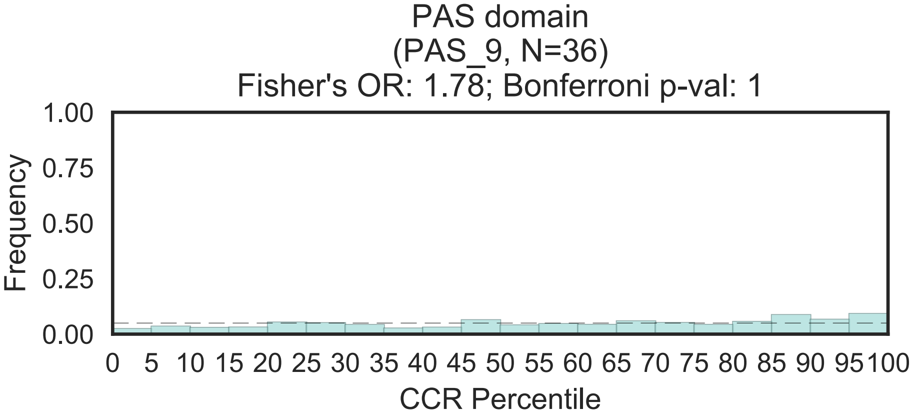

PAS domain
(PAS_11, N=21)
Fisher's OR: 2.18; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

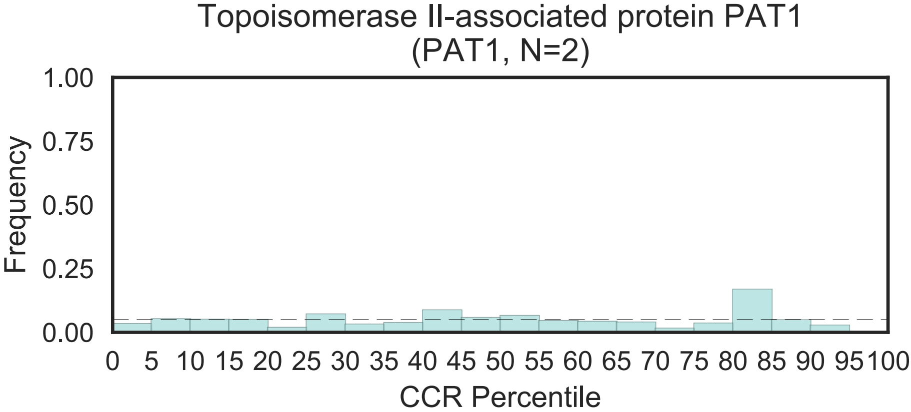

PAS fold
(PAS_2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

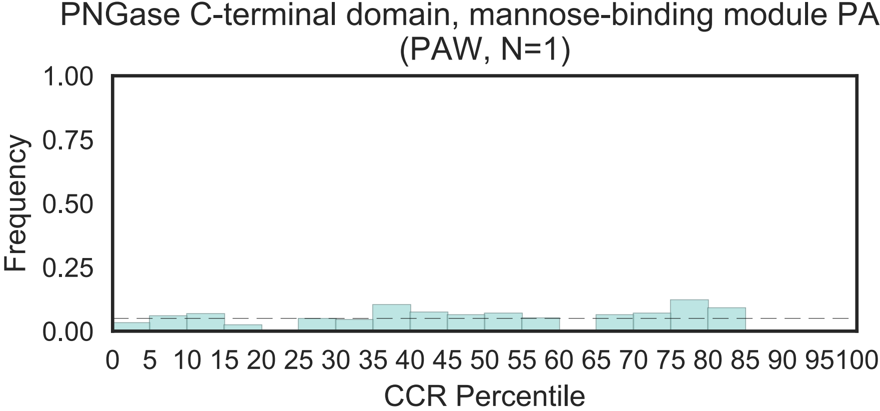

PAS fold
(PAS_3, N=24)
Fisher's OR: 1.62; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

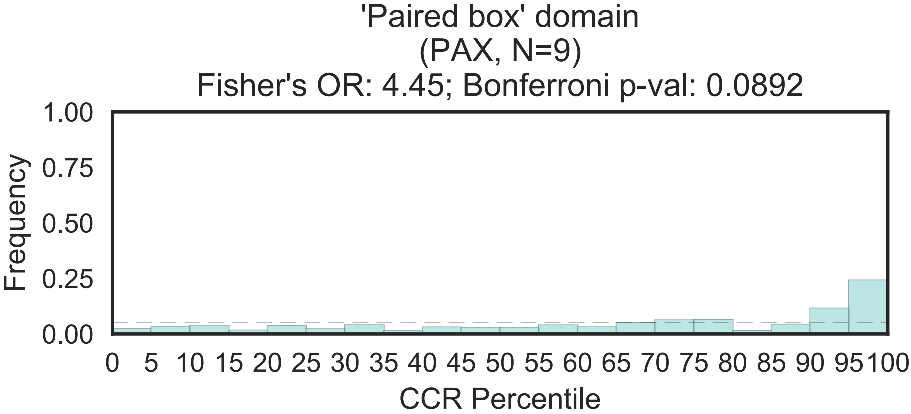

PAS fold
(PAS_4, N=5)
Fisher's OR: 1.34; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

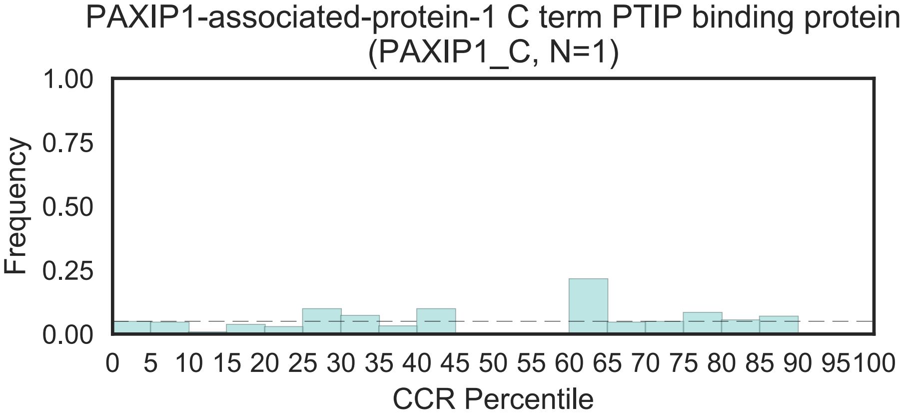

PAS domain
(PAS_8, N=6)
Fisher's OR: 1.5; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

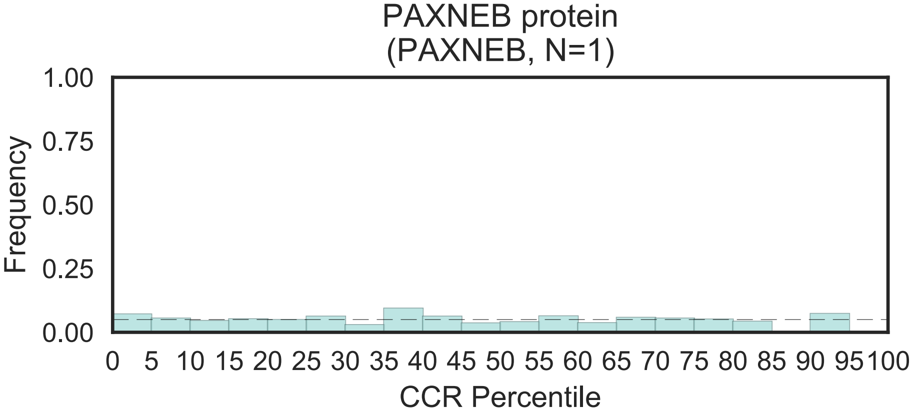

PAS domain
(PAS_9, N=36)
Fisher's OR: 1.78; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

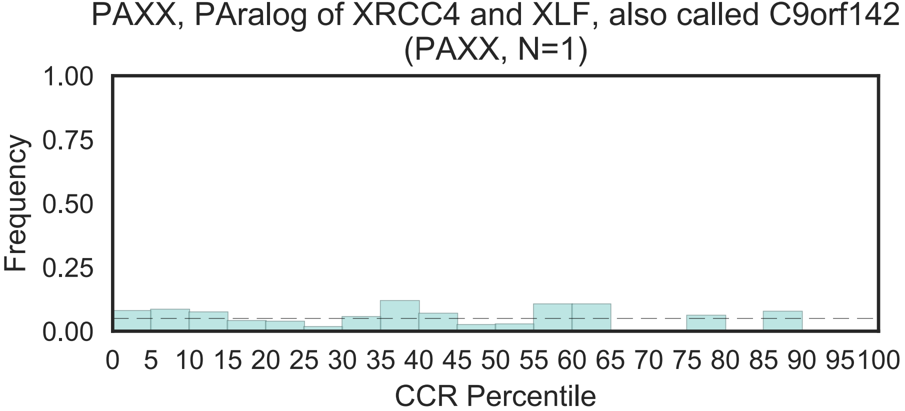

Topoisomerase II-associated protein PAT1
(PAT1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

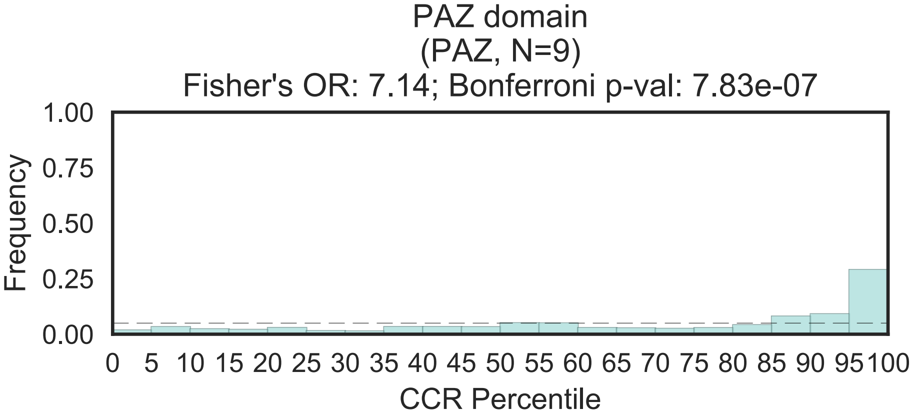

PNGase C-terminal domain, mannose-binding module PAW
(PAW, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

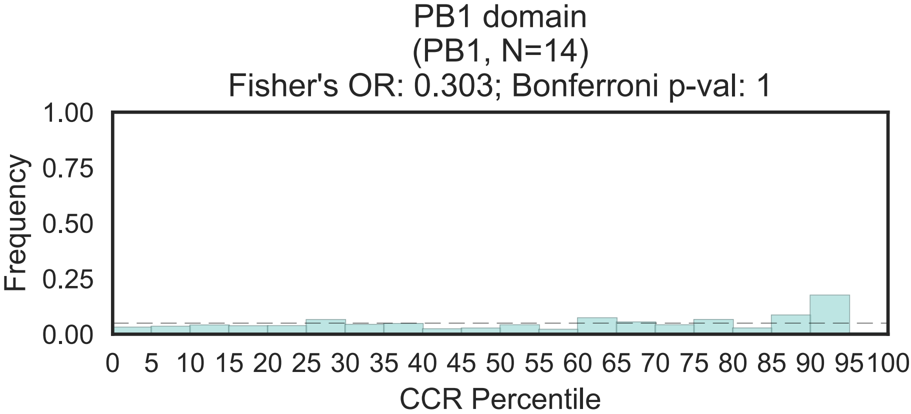

'Paired box' domain
(PAX, N=9)
Fisher's OR: 4.45; Bonferroni p-val: 0.0892
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

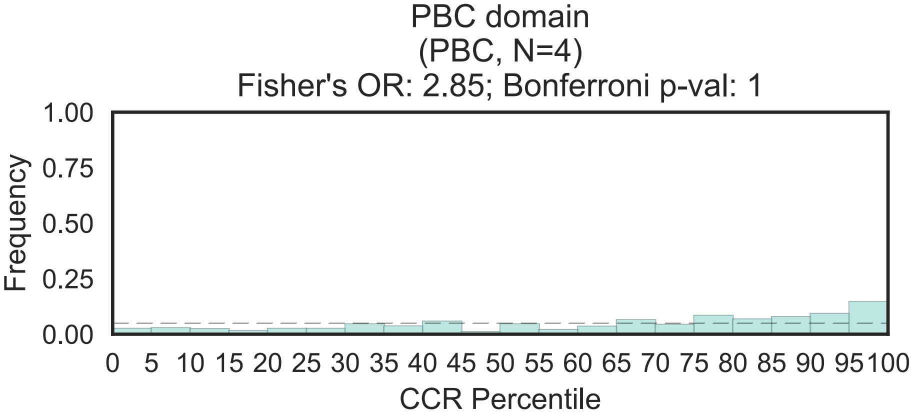

PAXIP1-associated-protein-1 C term PTIP binding protein
(PAXIP1_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

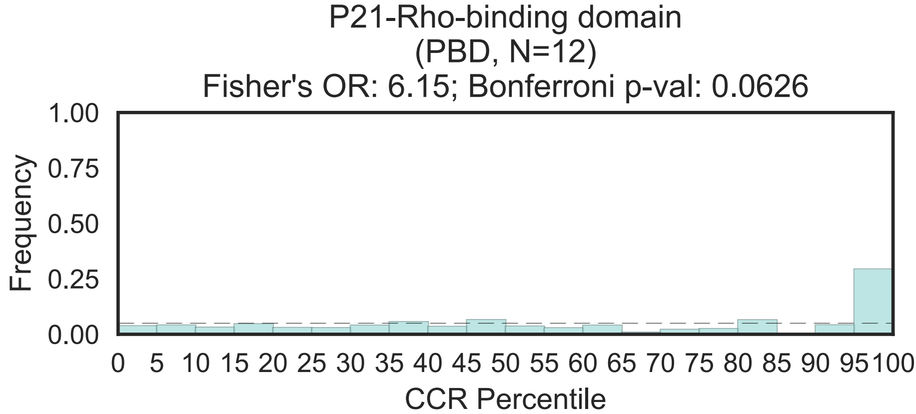

PAXNEB protein
(PAXNEB, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

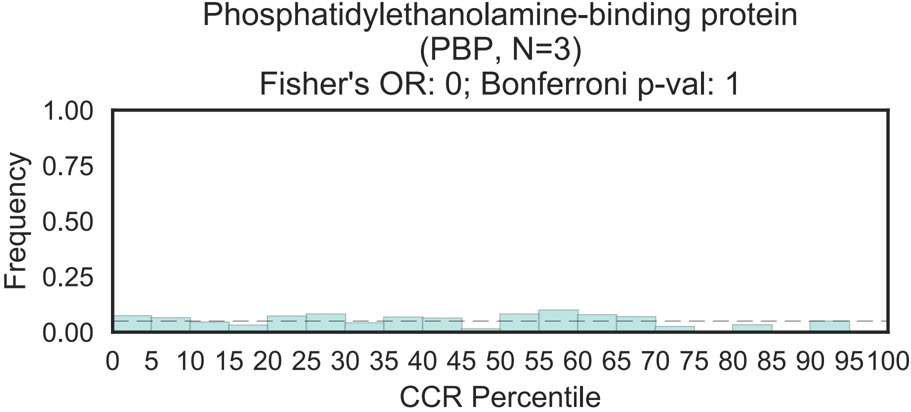

PAXX, PAralog of XRCC4 and XLF, also called C9orf142
(PAXX, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

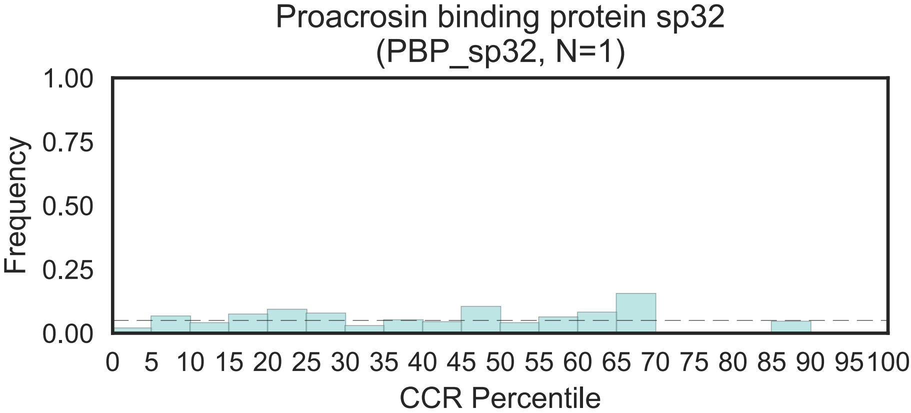

PAZ domain
(PAZ, N=9)
Fisher's OR: 7.14; Bonferroni p-val: 7.83e-07
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

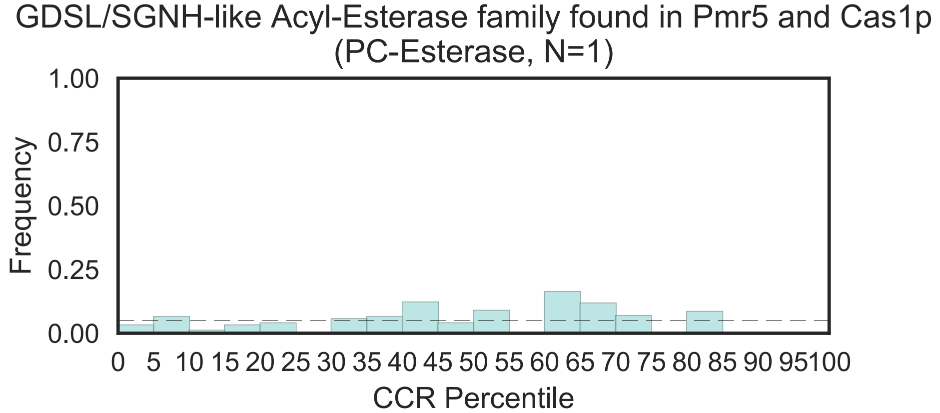

PB1 domain
(PB1, N=14)
Fisher's OR: 0.303; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

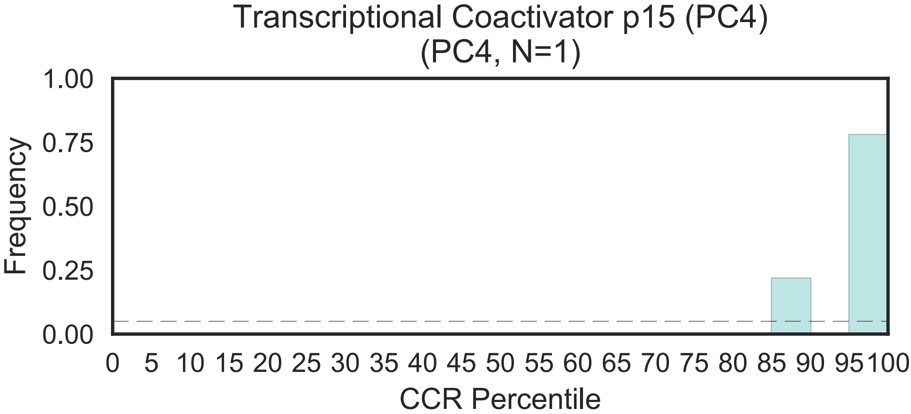

PBC domain
(PBC, N=4)
Fisher's OR: 2.85; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

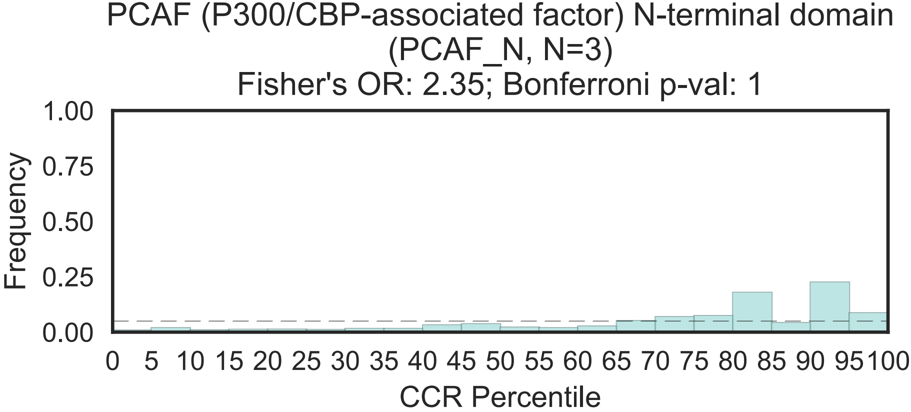

P21-Rho-binding domain
(PBD, N=12)
Fisher's OR: 6.15; Bonferroni p-val: 0.0626
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

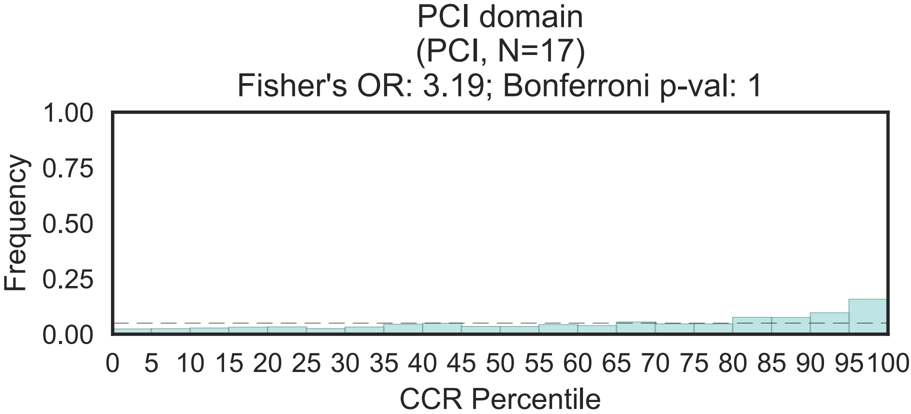

Phosphatidylethanolamine-binding protein
(PBP, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Proacrosin binding protein sp32
(PBP_sp32, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

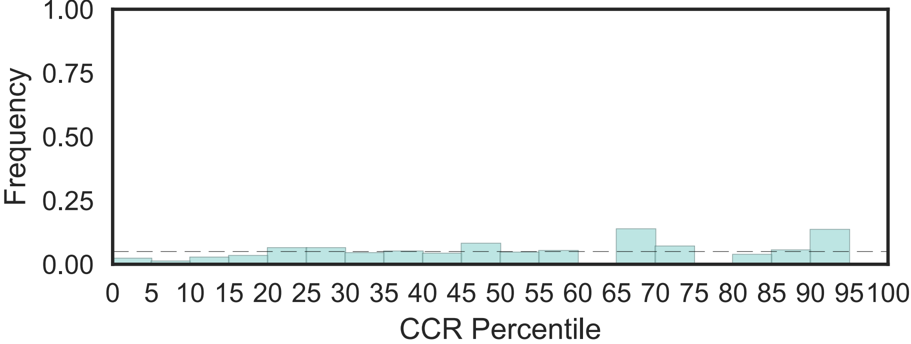

GDSL/SGNH-like Acyl-Esterase family found in Pmr5 and Cas1p
(PC-Esterase, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

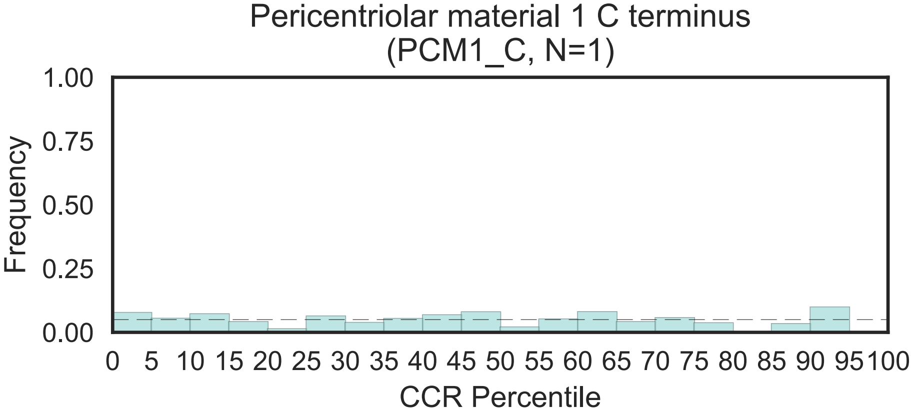

Transcriptional Coactivator p15 (PC4)
(PC4, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

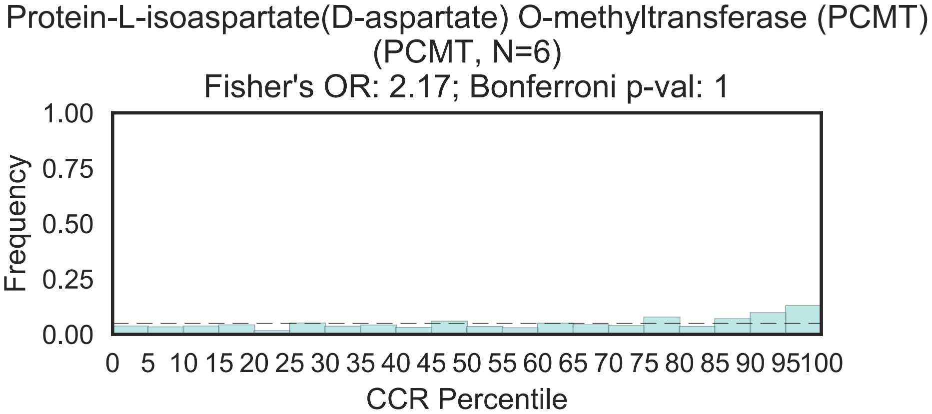

PCAF (P300/CBP-associated factor) N-terminal domain (PCAF_N, N=3)
Fisher's OR: 2.35; Bonferroni p-val: 1

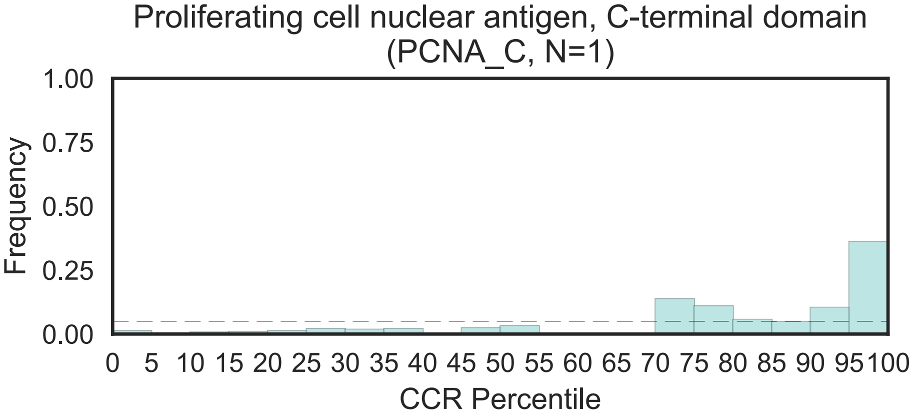

PCI domain
(PCI, N=17)
Fisher's OR: 3.19; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

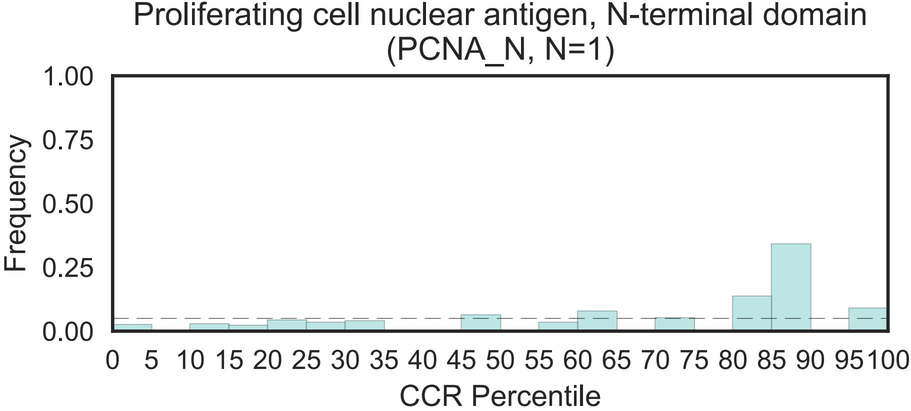
Phosphorylated CTD interacting factor 1 WW domain (PCIF1_WW, N=1)

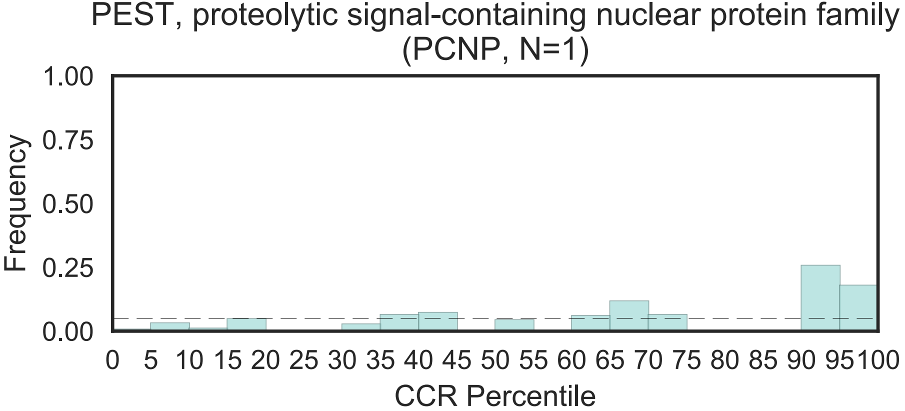


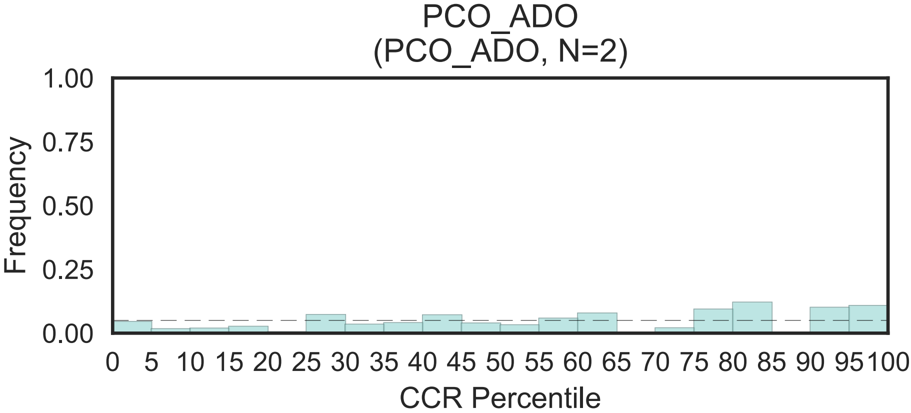

Pericentriolar material 1 C terminus
(PCM1_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

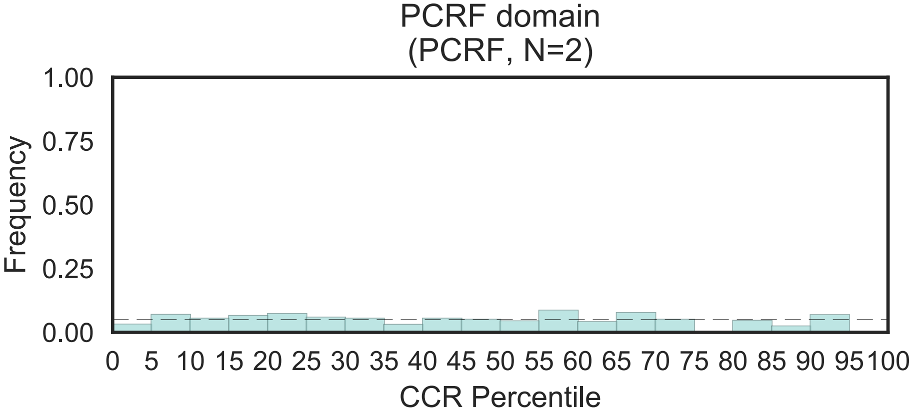

Protein-L-isoaspartate(D-aspartate) O-methyltransferase (PCMT)
(PCMT, N=6)
Fisher's OR: 2.17; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

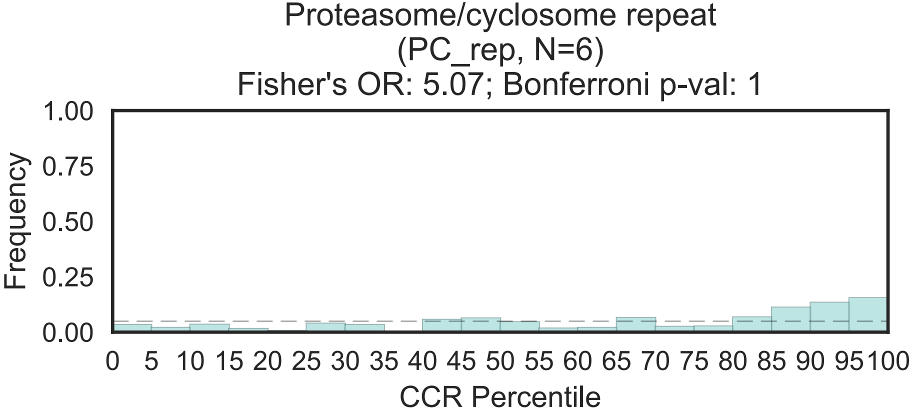

Proliferating cell nuclear antigen, C-terminal domain
(PCNA_C, N=1)

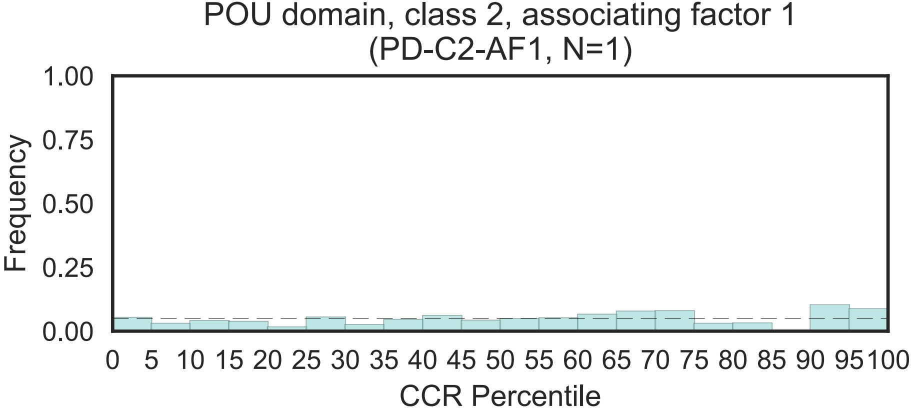

Proliferating cell nuclear antigen, N-terminal domain
(PCNA_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

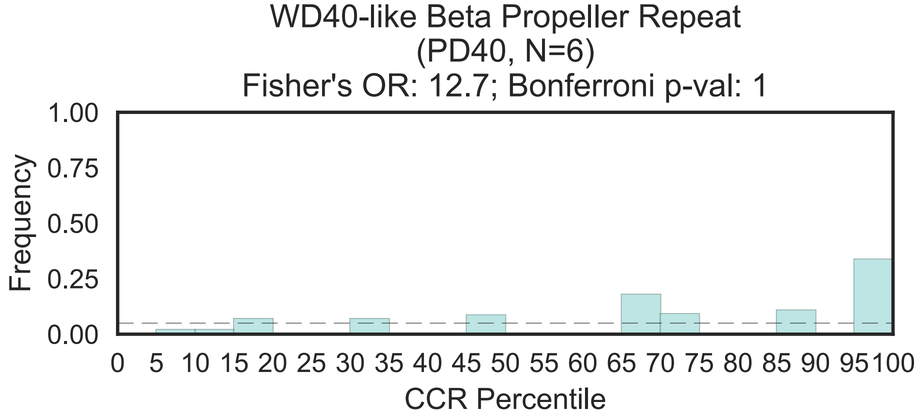

PEST, proteolytic signal-containing nuclear protein family
(PCNP, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


PCO_ADO
(PCO_ADO, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

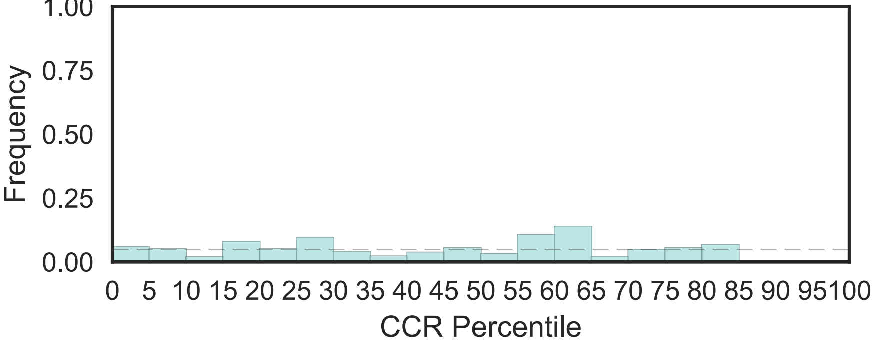

PCRF domain
(PCRF, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

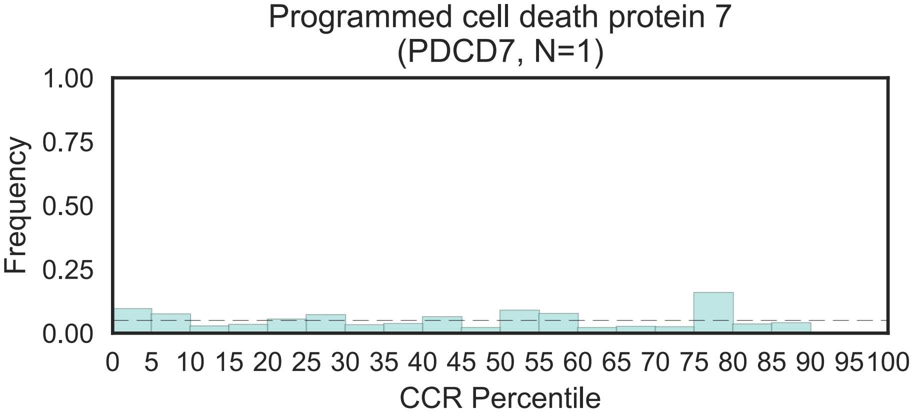

Proteasome/cyclosome repeat
(PC_rep, N=6)
Fisher's OR: 5.07; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

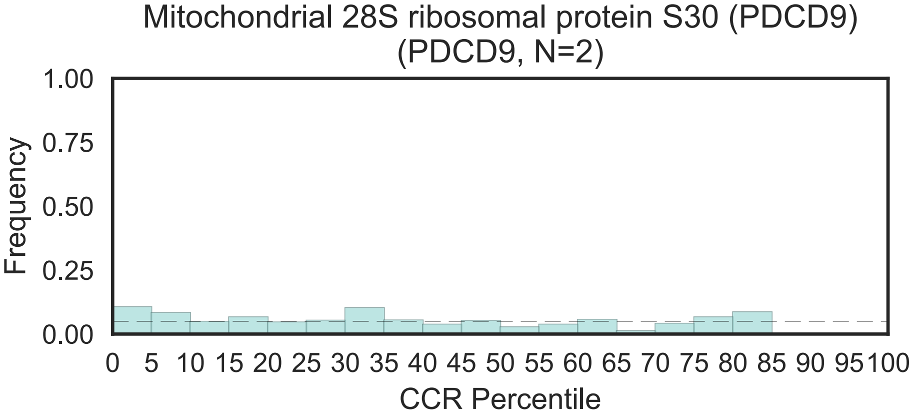

POU domain, class 2, associating factor 1
(PD-C2-AF1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

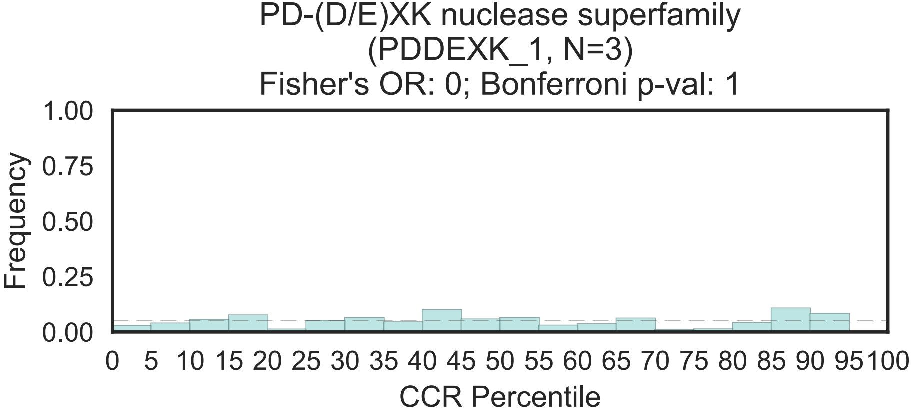

WD40-like Beta Propeller Repeat
(PD40, N=6)
Fisher's OR: 12.7; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

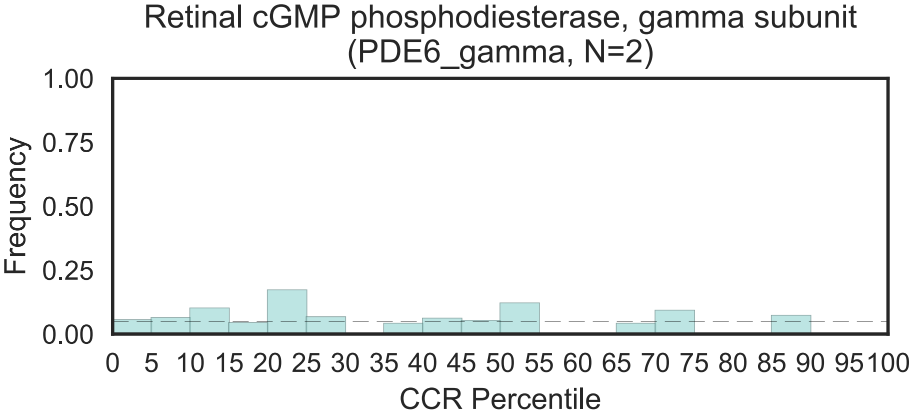
Programmed cell death protein 2, C-terminal putative domain
(PDCD2_C, N=2)

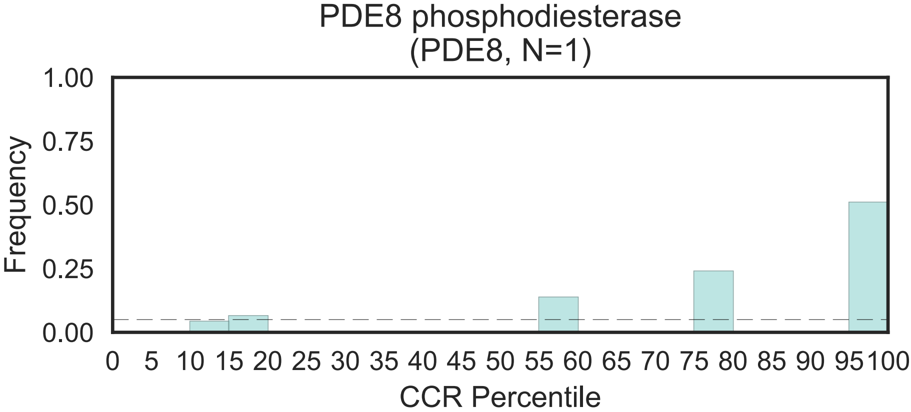


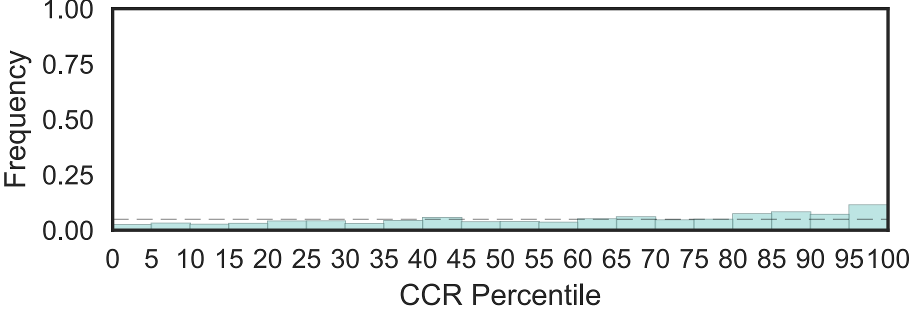

Programmed cell death protein 7
(PDCD7, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


Mitochondrial 28S ribosomal protein S30 (PDCD9)
(PDCD9, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

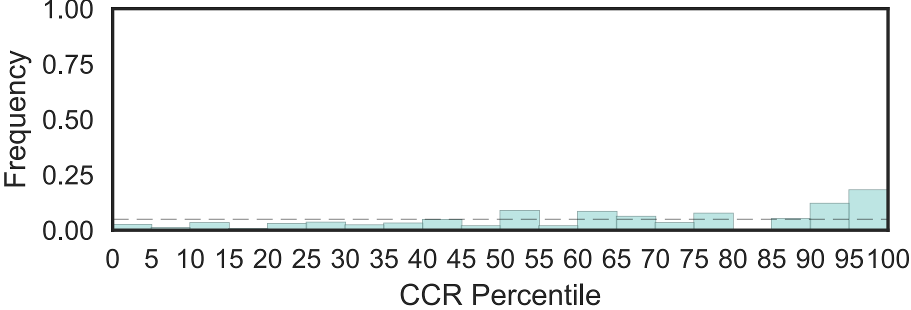

PD-(D/E)XK nuclease superfamily
(PDDEXK_1, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Retinal cGMP phosphodiesterase, gamma subunit
(PDE6_gamma, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

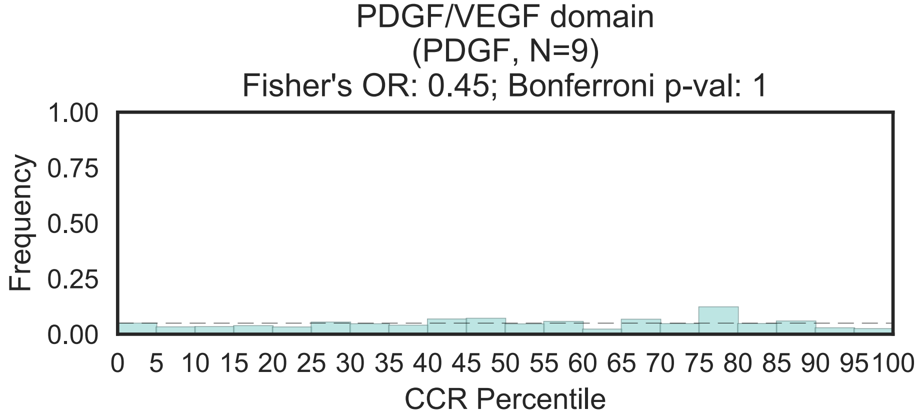

PDE8 phosphodiesterase
(PDE8, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

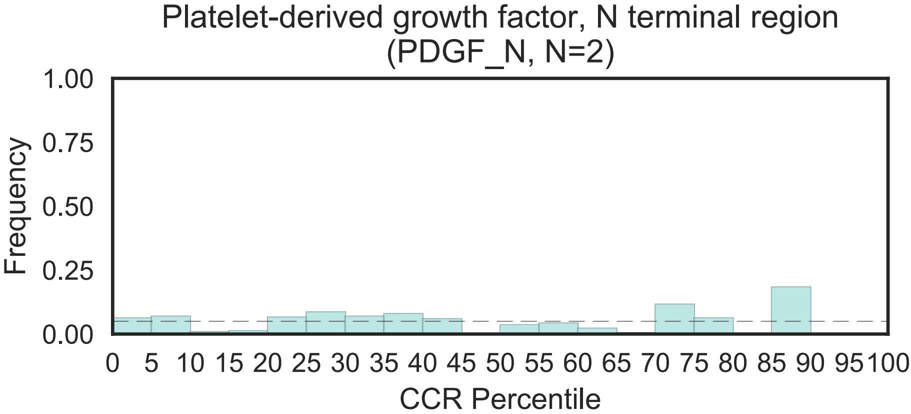


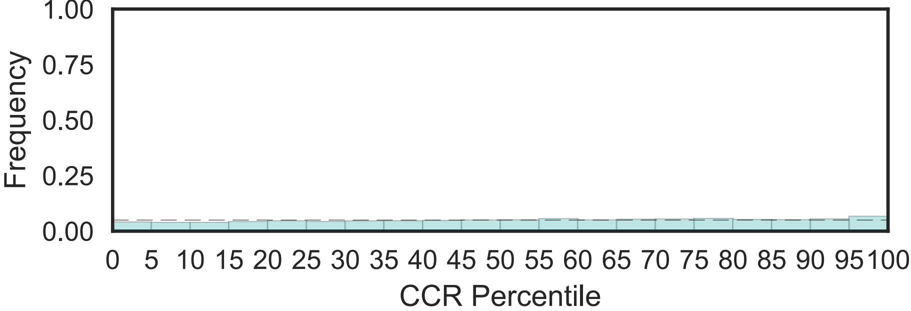
3'5'-cyclic nucleotide phosphodiesterase
(PDEase_I, N=22)
Fisher's OR: 1.93; Bonferroni p-val: 1

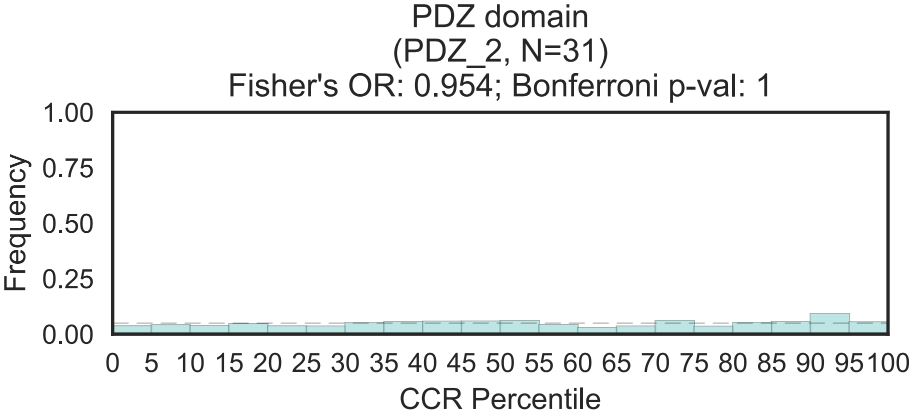


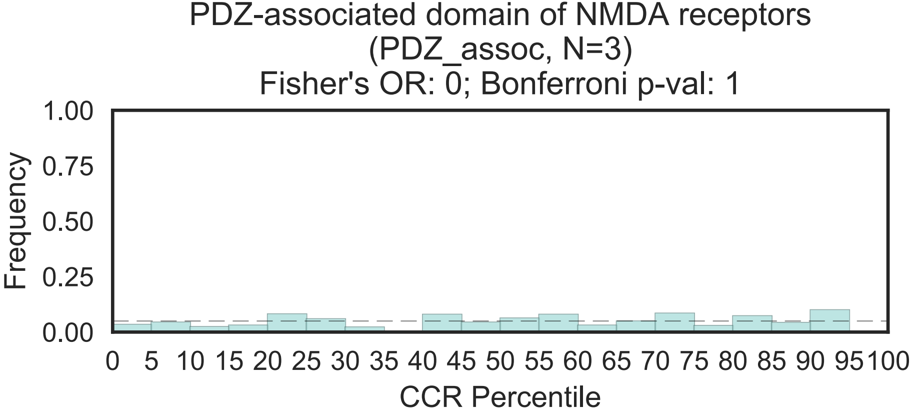
3'5'-cyclic nucleotide phosphodiesterase N-terminal
(PDEase_I_N, N=3)
Fisher's OR: 4.6; Bonferroni p-val: 1

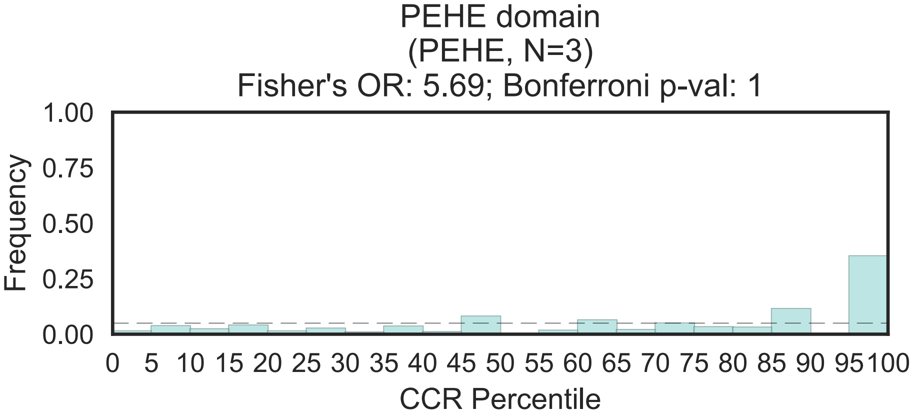

PDGF/VEGF domain
(PDGF, N=9)
Fisher's OR: 0.45; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

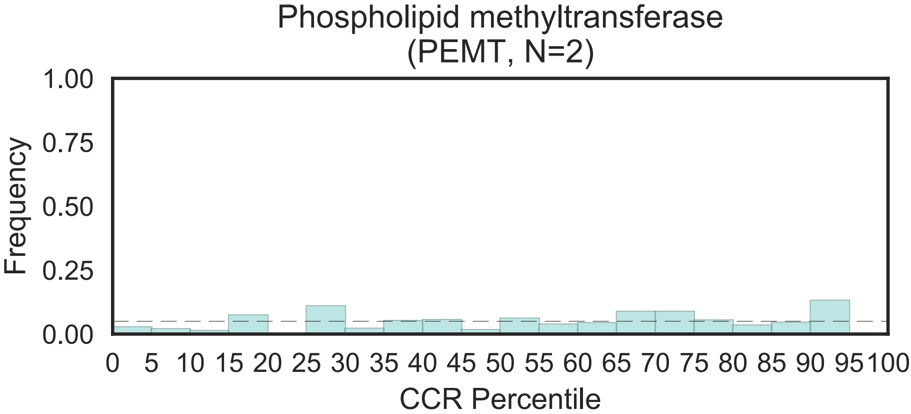

Platelet-derived growth factor, N terminal region
(PDGF_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


PDZ domain (Also known as DHR or GLGF)
(PDZ, N=215)
Fisher's OR: 1.01; Bonferroni p-val: 1


PDZ domain
(PDZ_2, N=31)
Fisher's OR: 0.954; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

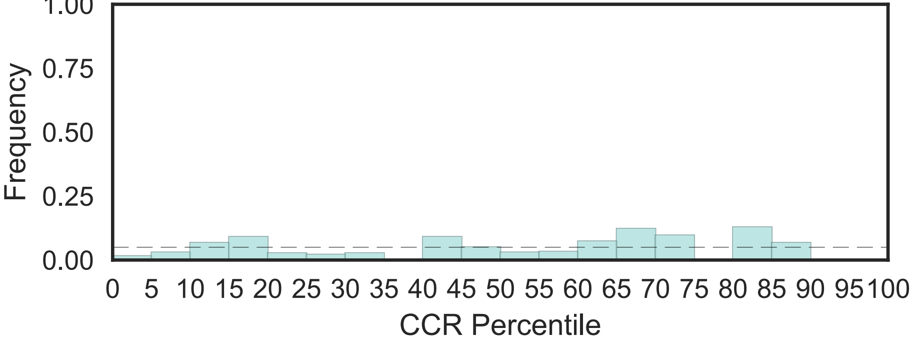

PDZ-associated domain of NMDA receptors
(PDZ_assoc, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

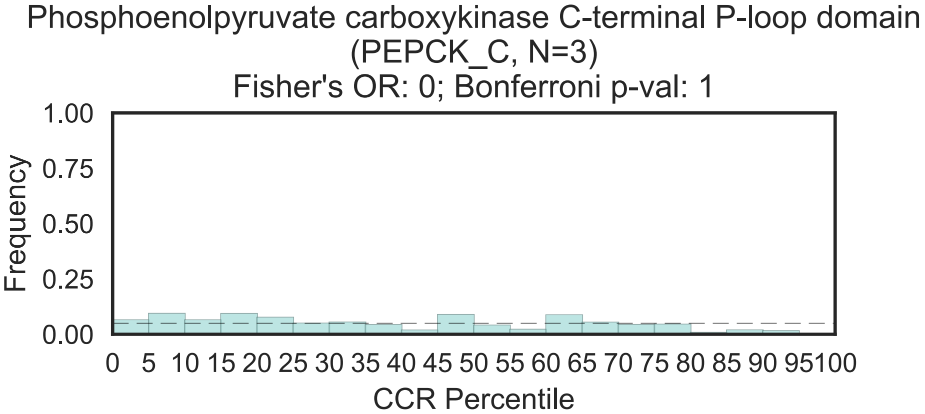

PEHE domain
(PEHE, N=3)
Fisher's OR: 5.69; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



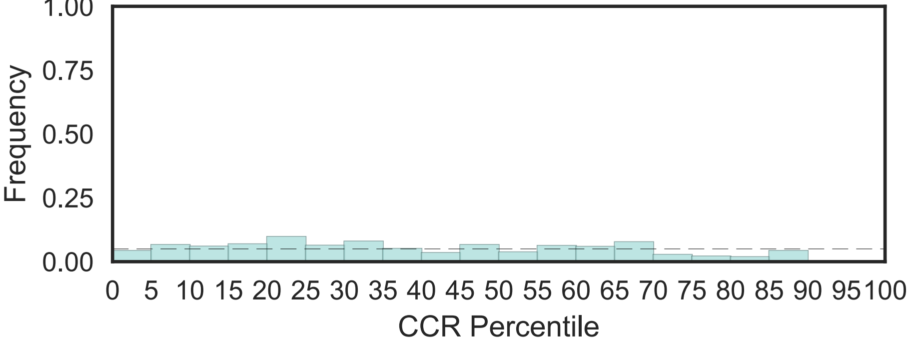
Phospholipid methyltransferase
(PEMT, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Presenilin enhancer-2 subunit of gamma secretase (PEN-2, N=1)

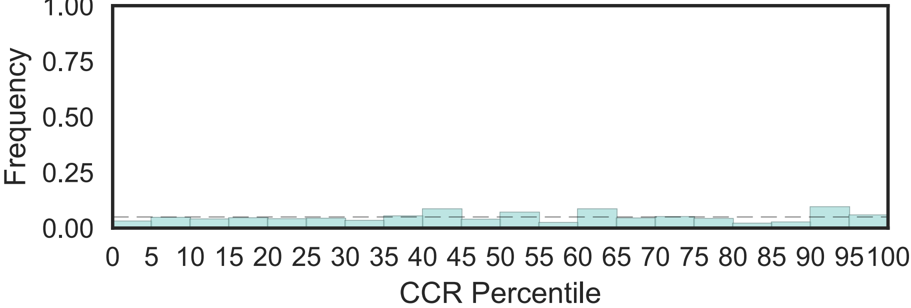


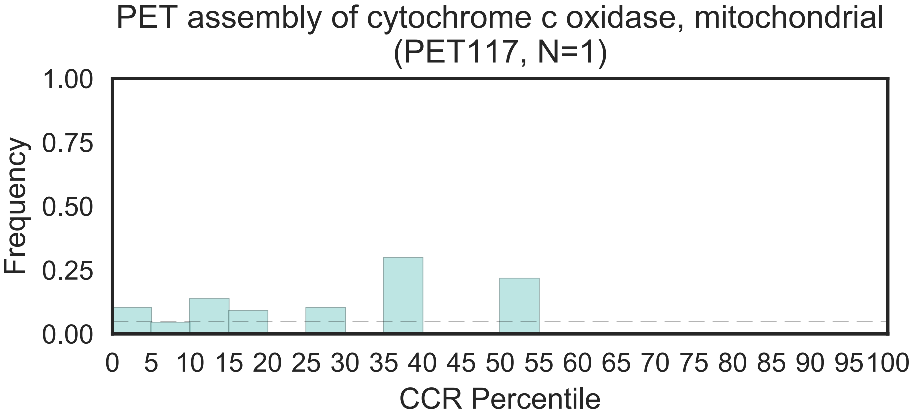

Phosphoenolpyruvate carboxykinase C-terminal P-loop domain
(PEPCK_C, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

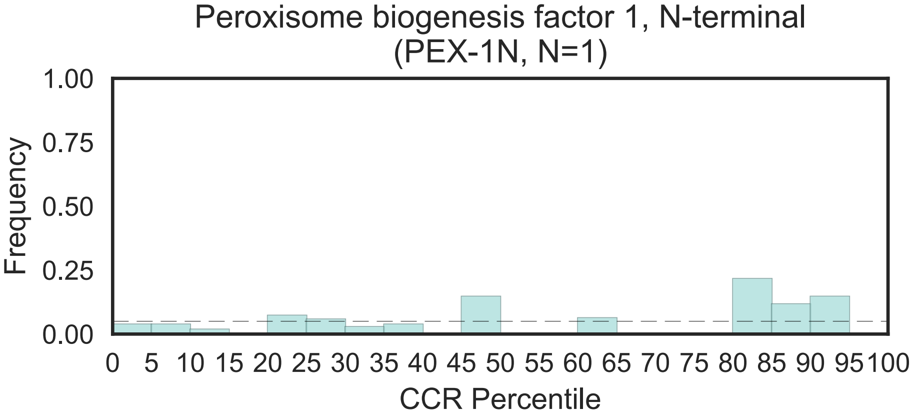
Phosphoenolpyruvate carboxykinase N-terminal domain (PEPCK_N, N=2)

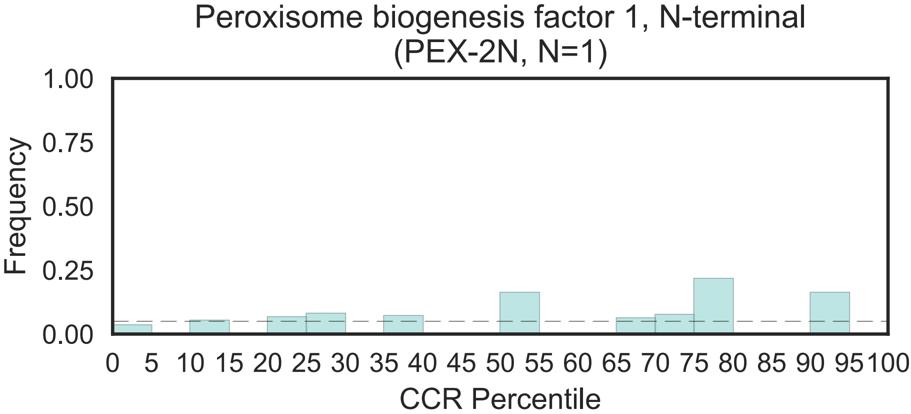


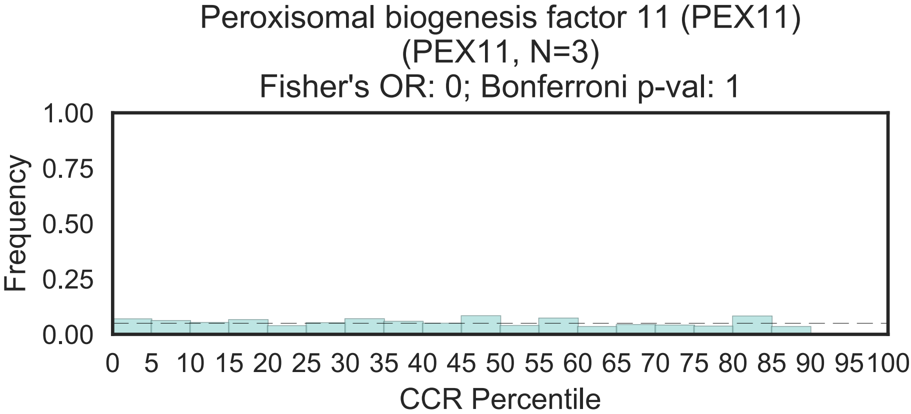
PET Domain
(PET, N=5)
Fisher's OR: 0.761; Bonferroni p-val: 1

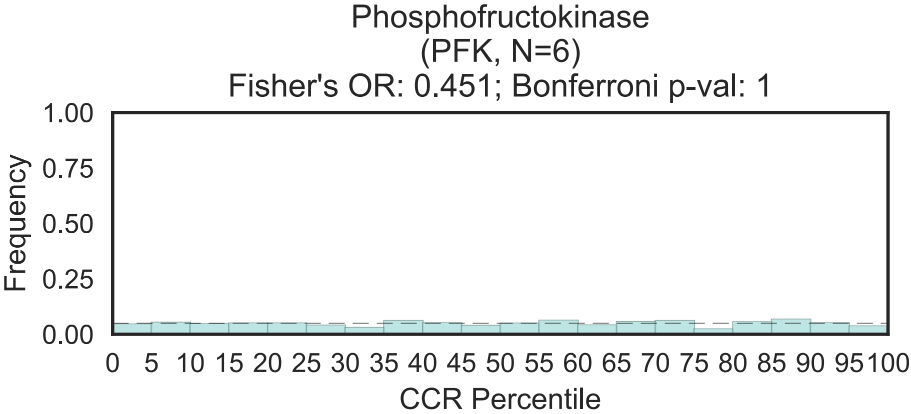


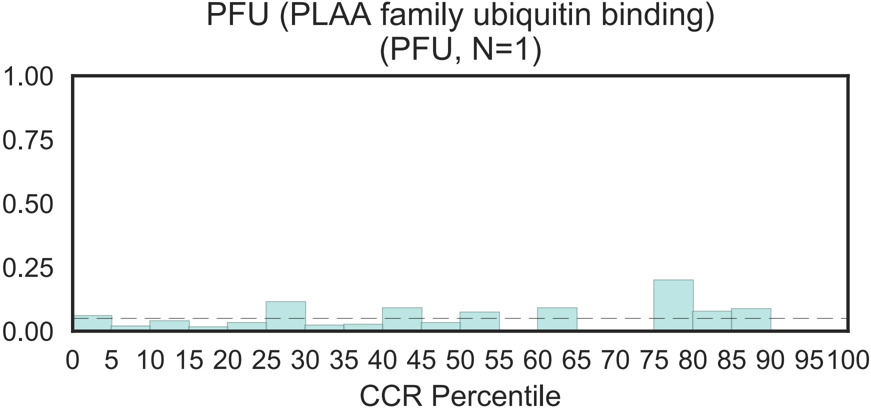

PET assembly of cytochrome c oxidase, mitochondrial
(PET117, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

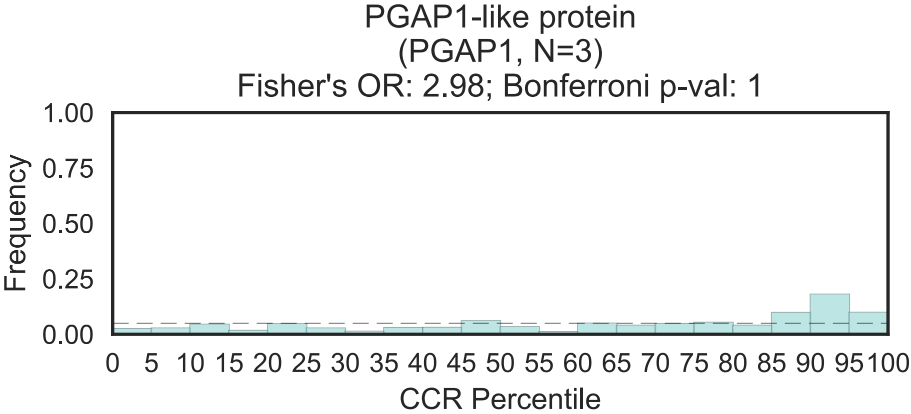

Peroxisome biogenesis factor 1, N-terminal
(PEX-1N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

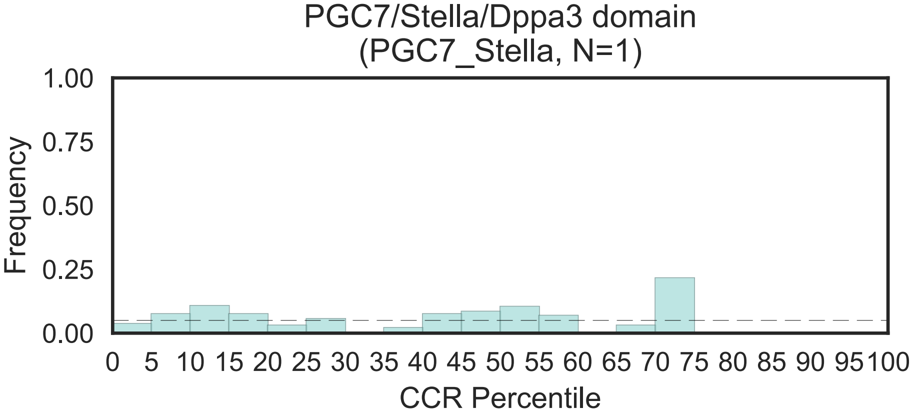

Peroxisome biogenesis factor 1, N-terminal
(PEX-2N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

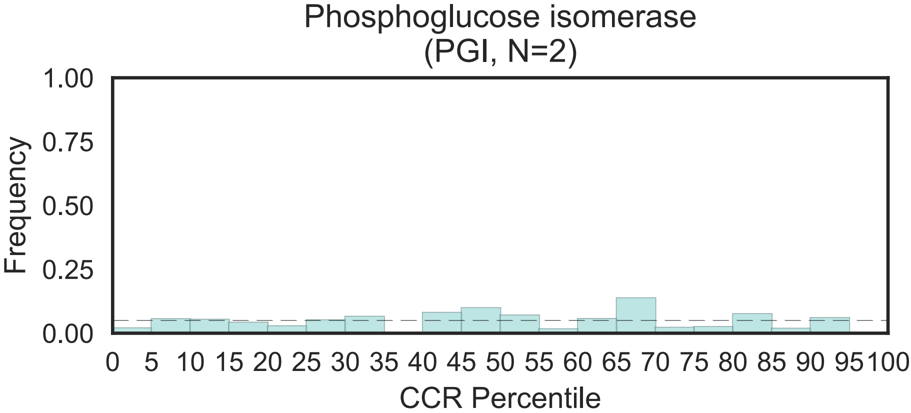

Peroxisomal biogenesis factor 11 (PEX11)
(PEX11, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

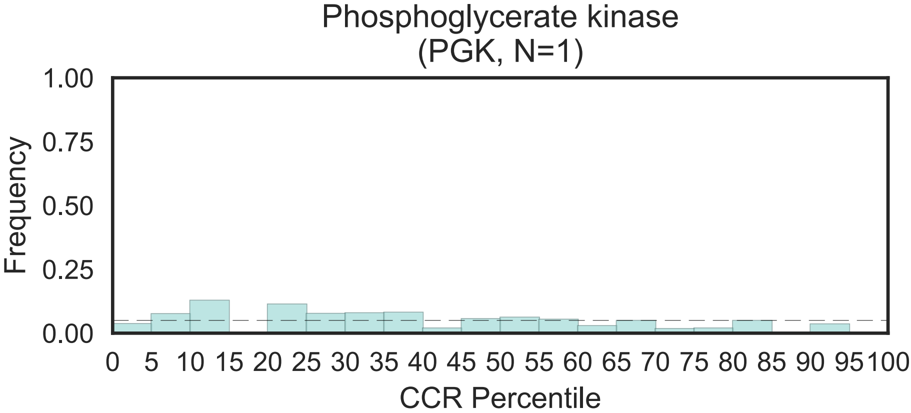

Phosphofructokinase
(PFK, N=6)
Fisher's OR: 0.451; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

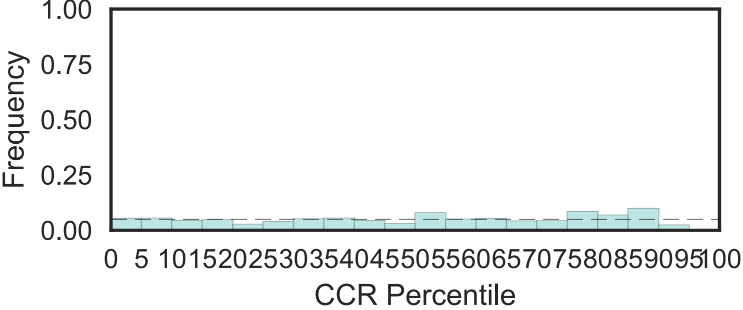

PFU (PLAA family ubiquitin binding)
(PFU, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


PGAP1-like protein
(PGAP1, N=3)
Fisher's OR: 2.98; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


PGC7/Stella/Dppa3 domain
(PGC7_Stella, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

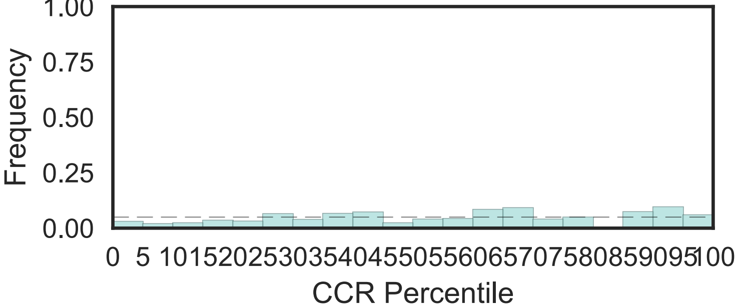

Phosphoglucose isomerase
(PGI, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

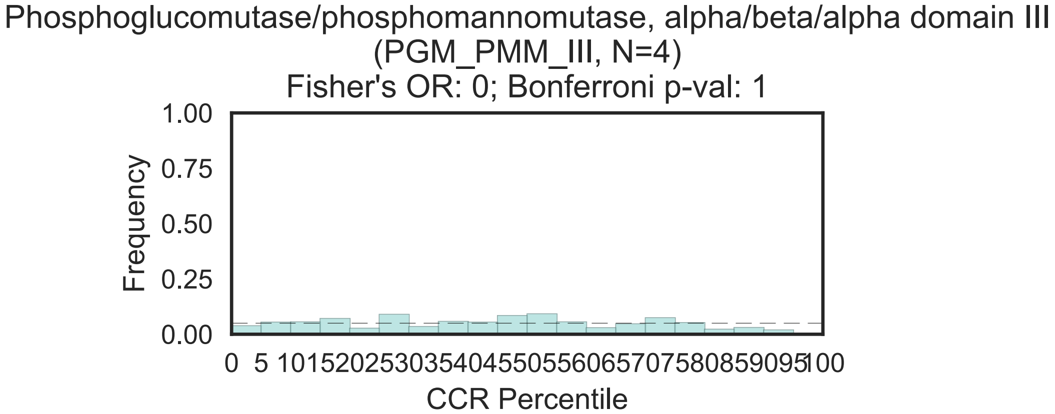

Phosphoglycerate kinase
(PGK, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

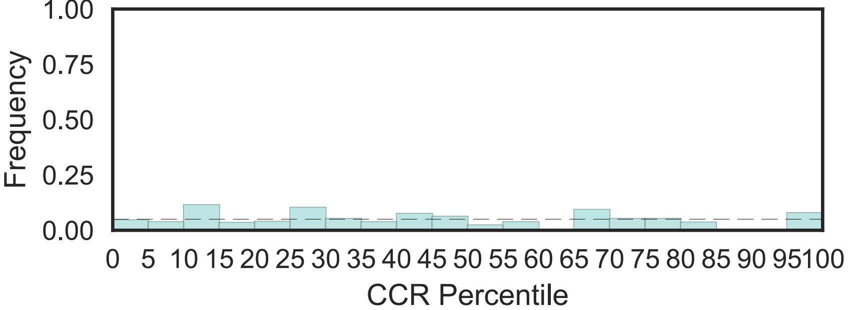


Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain I (PGM_PMM_I, N=6)
Fisher's OR: 0; Bonferroni p-val: 1

Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain II (PGM_PMM_II, N=4) Fisher's OR: 1.05; Bonferroni p-val: 1

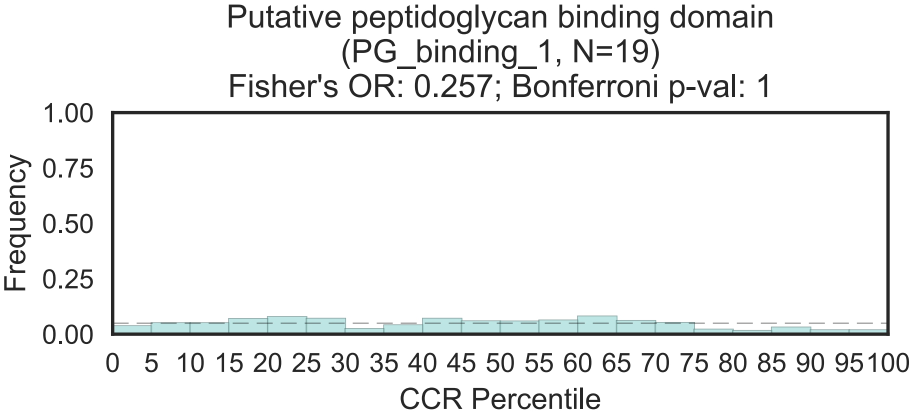


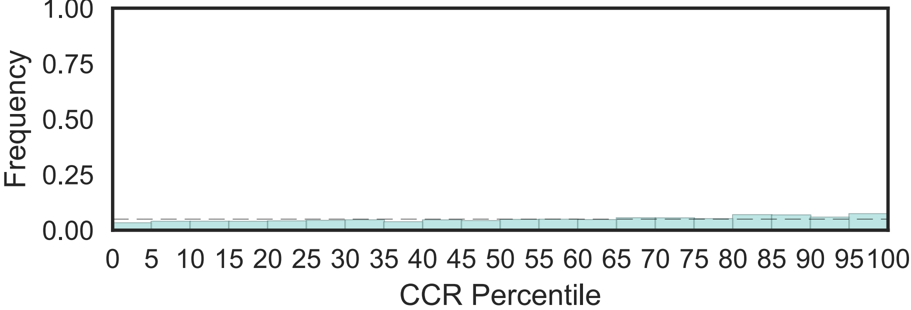

Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain III
(PGM_PMM_III, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



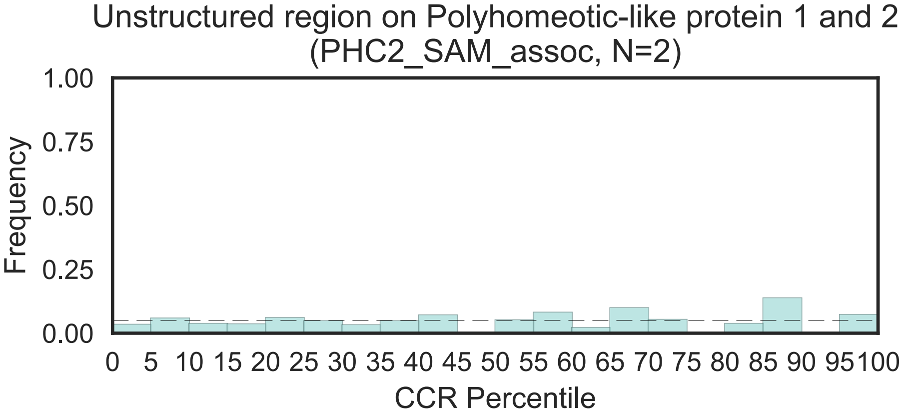
Phosphoglucomutase/phosphomannomutase, C-terminal domain (PGM_PMM_IV, N=4)

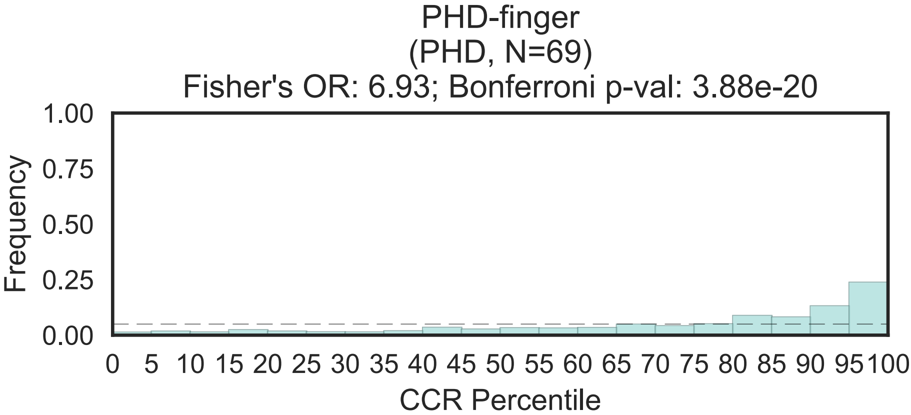
Fisher's OR: 1.07; Bonferroni p-val: 1


Putative peptidoglycan binding domain
(PG_binding_1, N=19)
Fisher's OR: 0.257; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

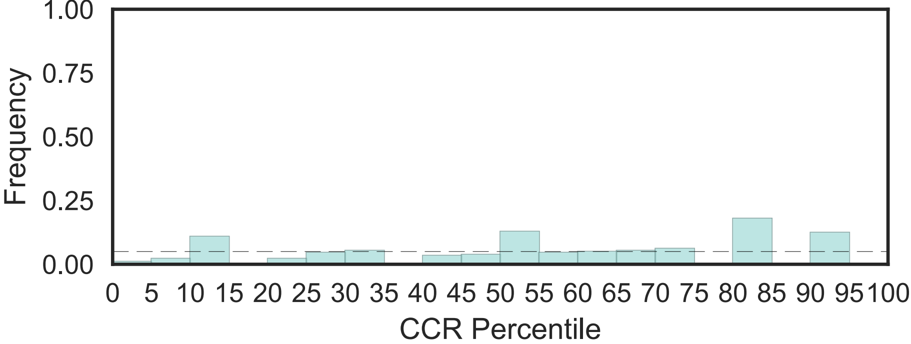


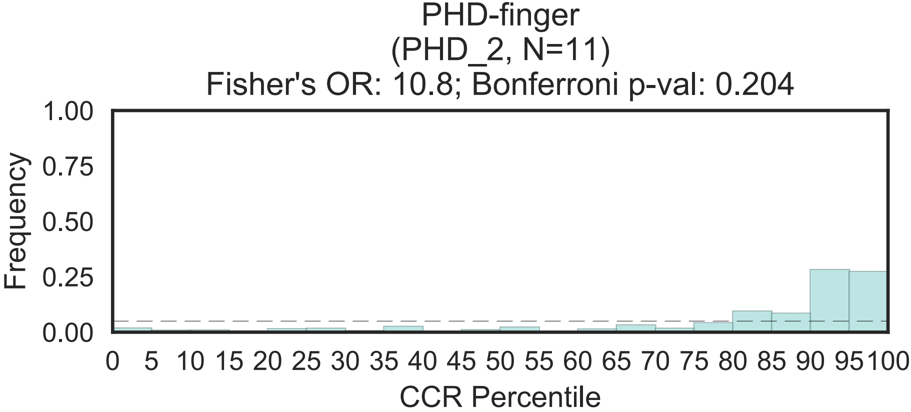
PH domain
(PH, N=215)
Fisher's OR: 1.26; Bonferroni p-val: 1

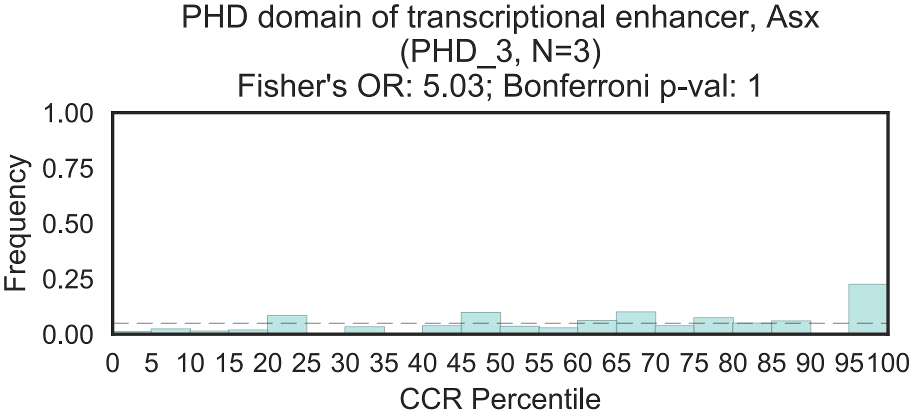

Unstructured region on Polyhomeotic-like protein 1 and 2
(PHC2_SAM_assoc, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


PHD-finger
(PHD, N=69)
Fisher's OR: 6.93; Bonferroni p-val: 3.88e-20
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

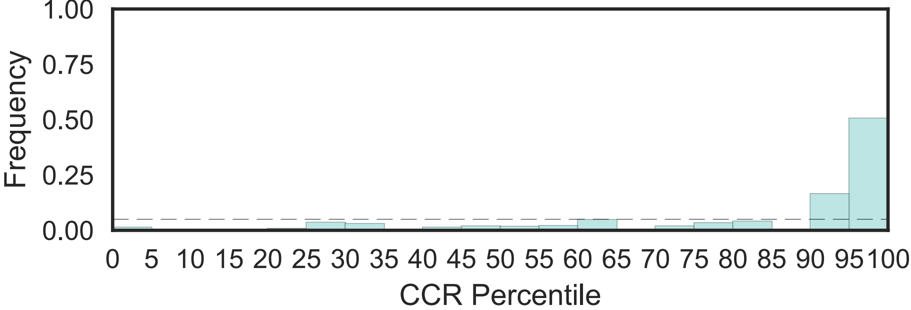
PHD finger protein 20-like protein 1
(PHD20L1_u1, N=1)

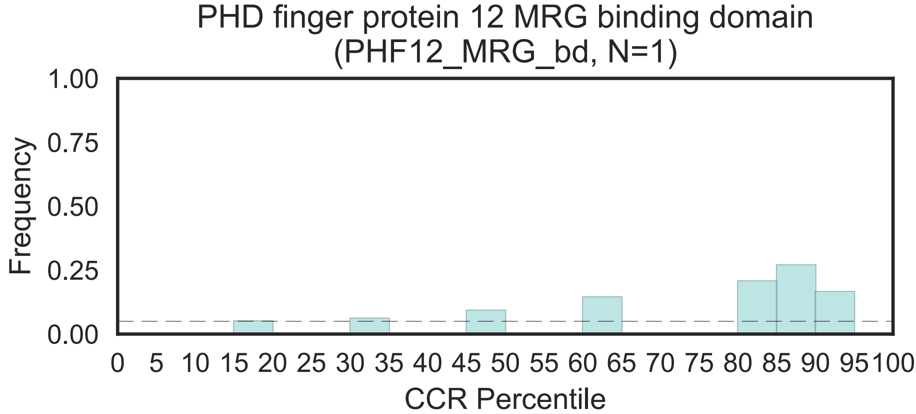


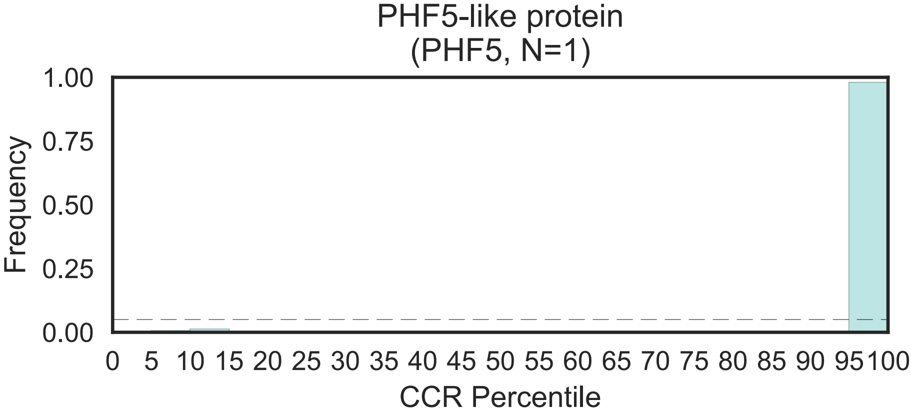

PHD-finger
(PHD_2, N=11)
Fisher's OR: 10.8; Bonferroni p-val: 0.204
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

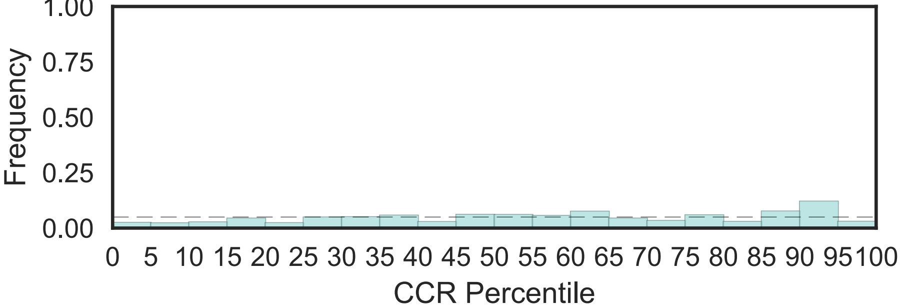

PHD domain of transcriptional enhancer, Asx
(PHD_3, N=3)
Fisher's OR: 5.03; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

PHD-finger
(PHD_4, N=3)
Fisher's OR: 25; Bonferroni p-val: 0.00265

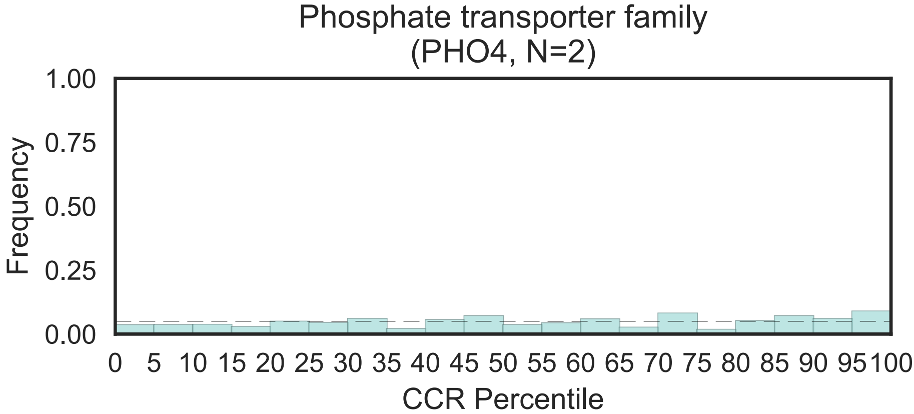


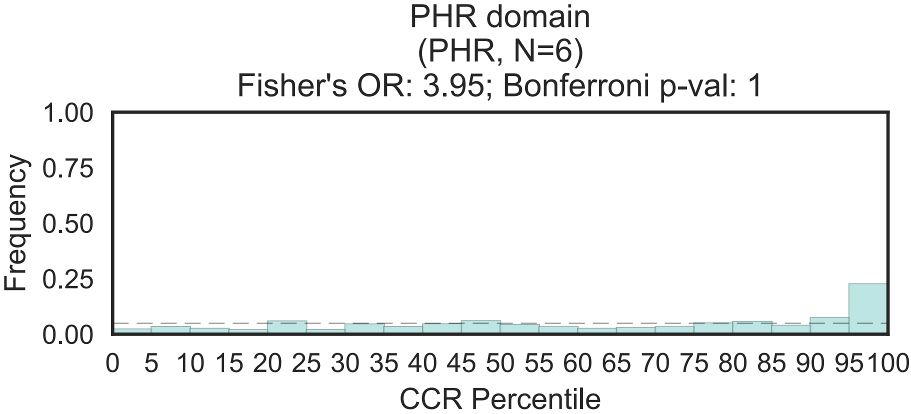

PHD finger protein 12 MRG binding domain
(PHF12_MRG_bd, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

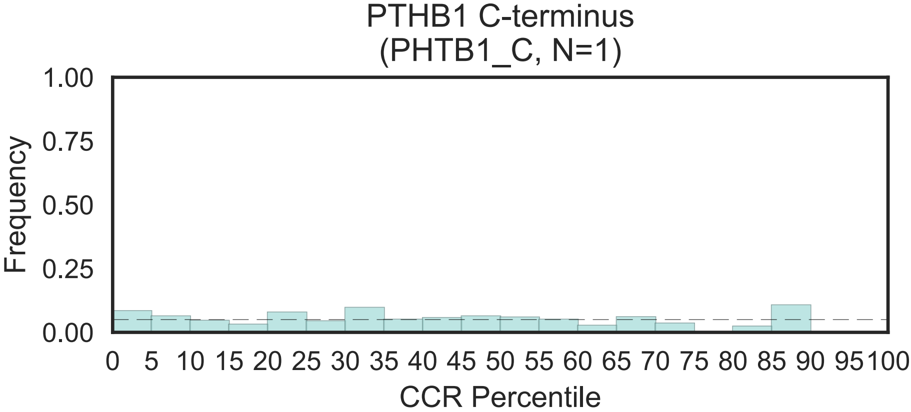

PHF5-like protein
(PHF5, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

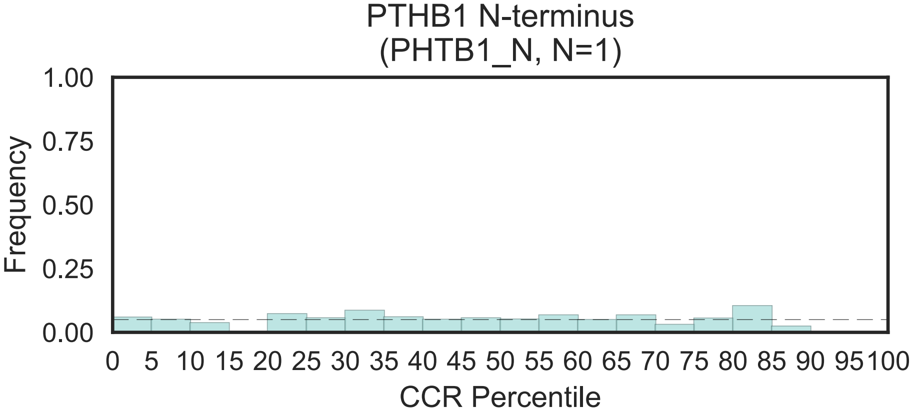


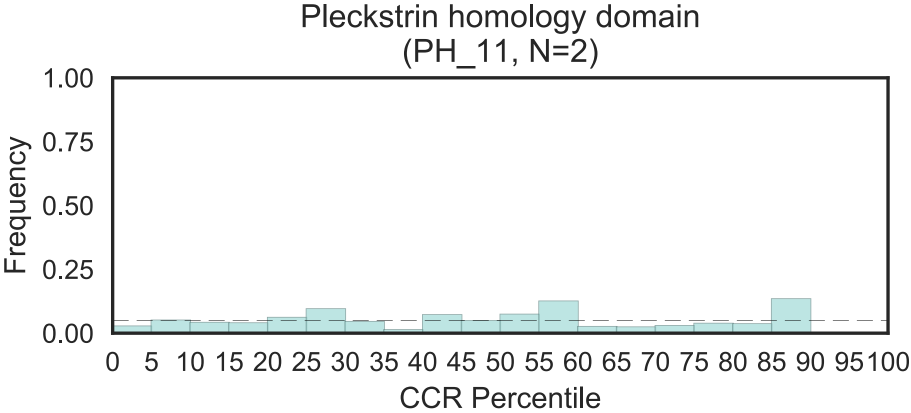
Cytosolic domain of 10TM putative phosphate transporter
(PHM7_cyt, N=3)
Fisher's OR: 0.597; Bonferroni p-val: 1

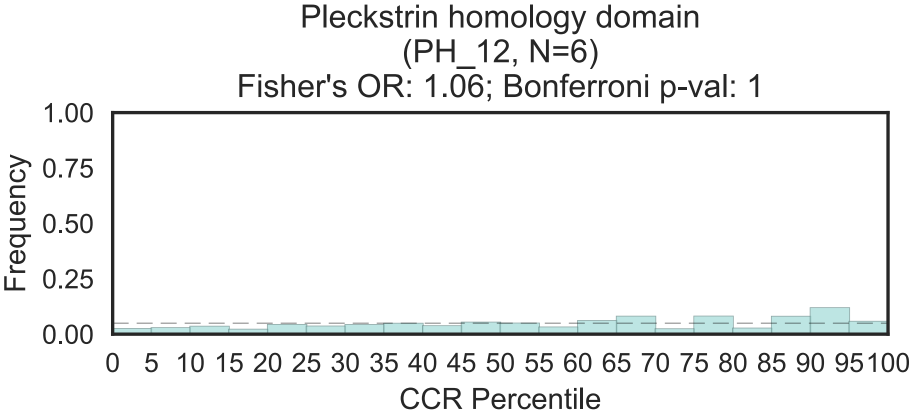

Phosphate transporter family
(PHO4, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

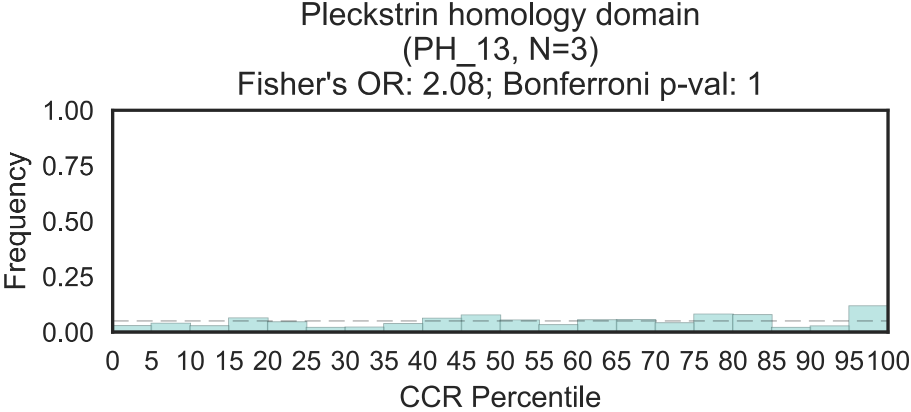

PHR domain
(PHR, N=6)
Fisher's OR: 3.95; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

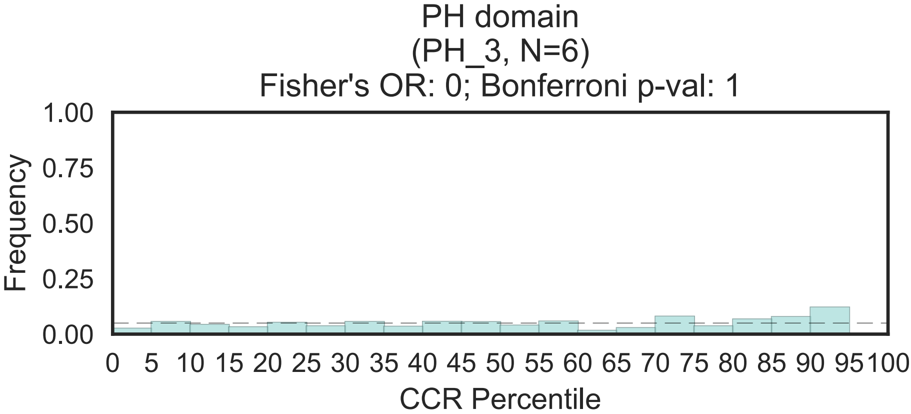

PTHB1 C-terminus
(PHTB1_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


PTHB1 N-terminus
(PHTB1_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

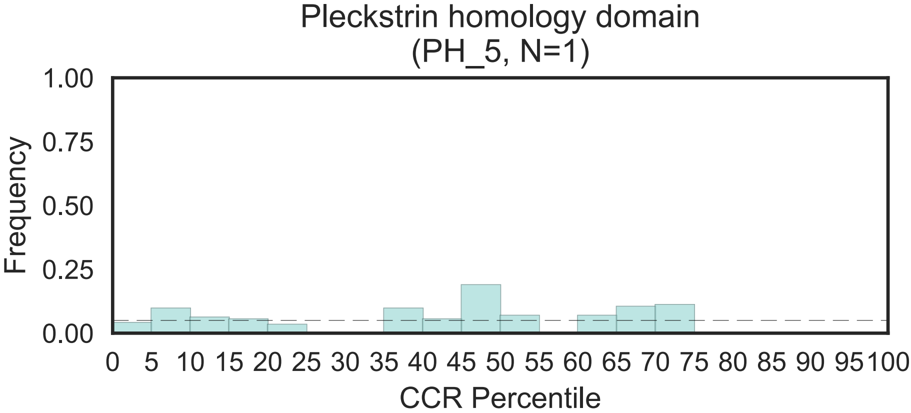

Pleckstrin homology domain
(PH_11, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

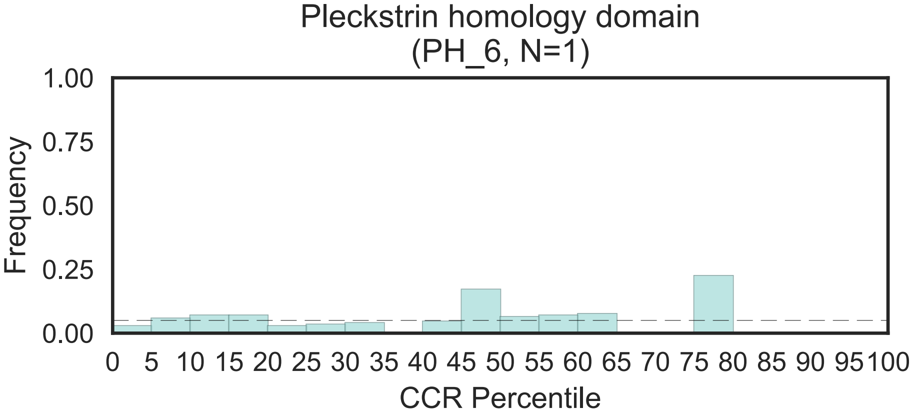

Pleckstrin homology domain
(PH_12, N=6)
Fisher's OR: 1.06; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

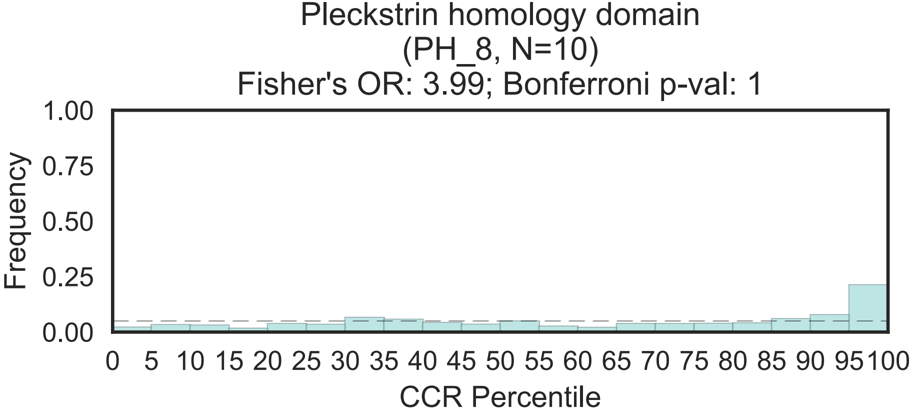

Pleckstrin homology domain
(PH_13, N=3)
Fisher's OR: 2.08; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

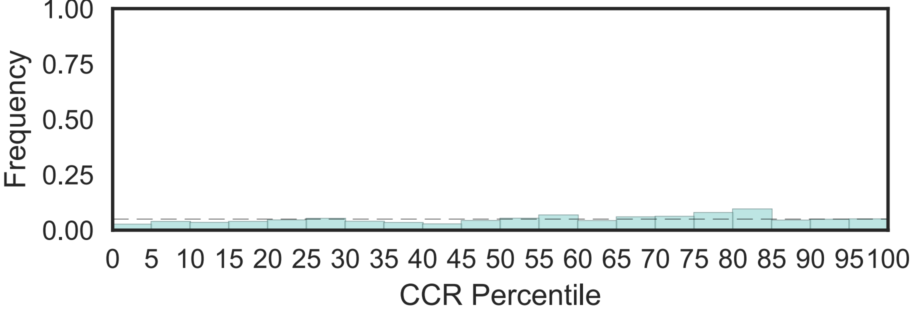


PH domain
(PH_3, N=6)
Fisher's OR: 0; Bonferroni p-val: 1

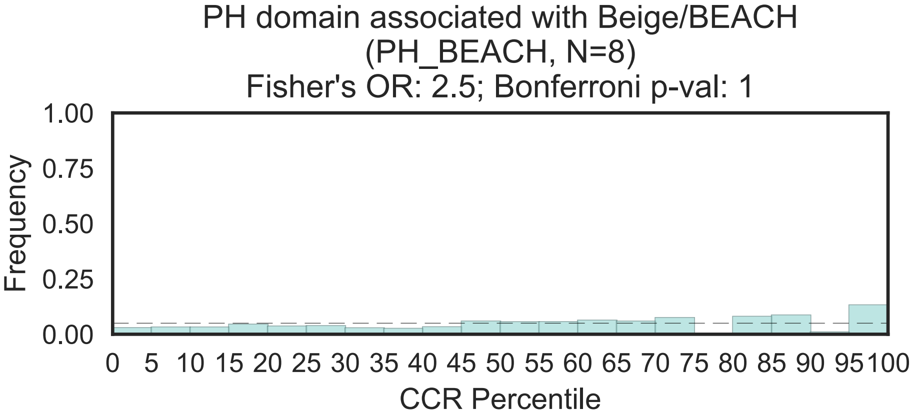

Pleckstrin homology domain
(PH_5, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

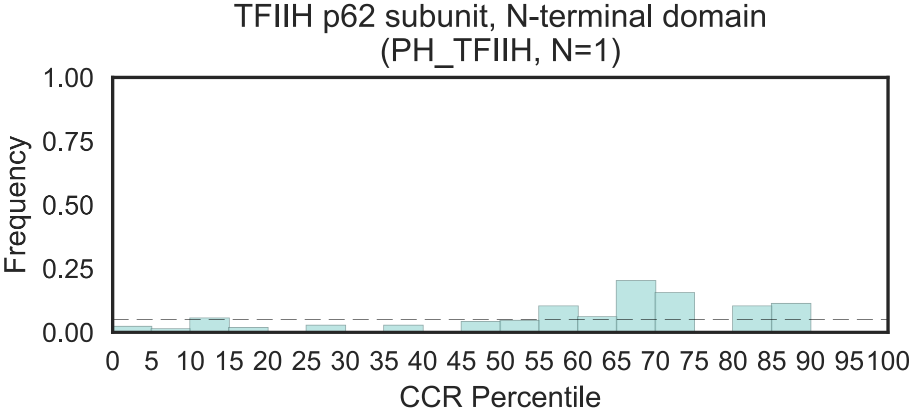

Pleckstrin homology domain
(PH_6, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


Pleckstrin homology domain
(PH_8, N=10)
Fisher's OR: 3.99; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

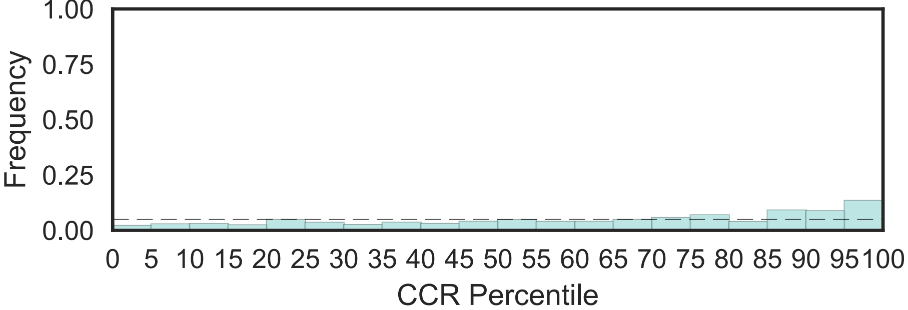


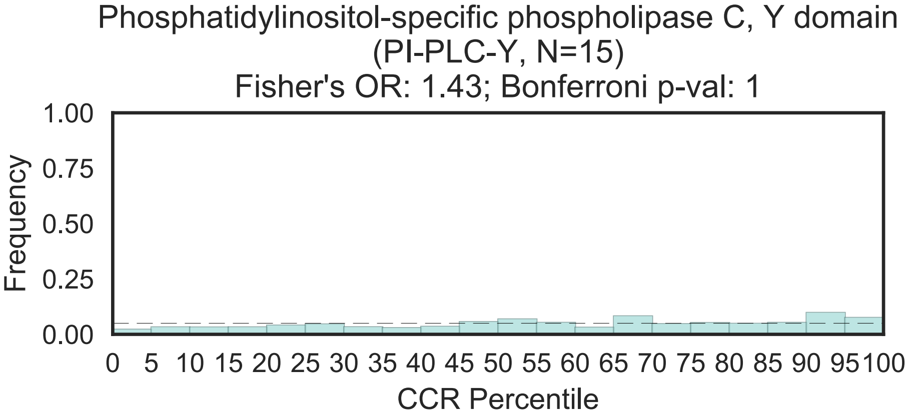
Pleckstrin homology domain
(PH_9, N=15)
Fisher's OR: 0.91; Bonferroni p-val: 1


PH domain associated with Beige/BEACH
(PH_BEACH, N=8)
Fisher's OR: 2.5; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

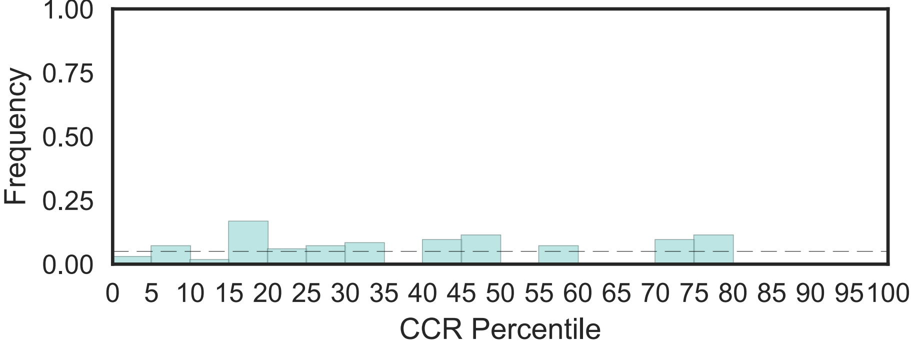

TFIIH p62 subunit, N-terminal domain
(PH_TFIIH, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

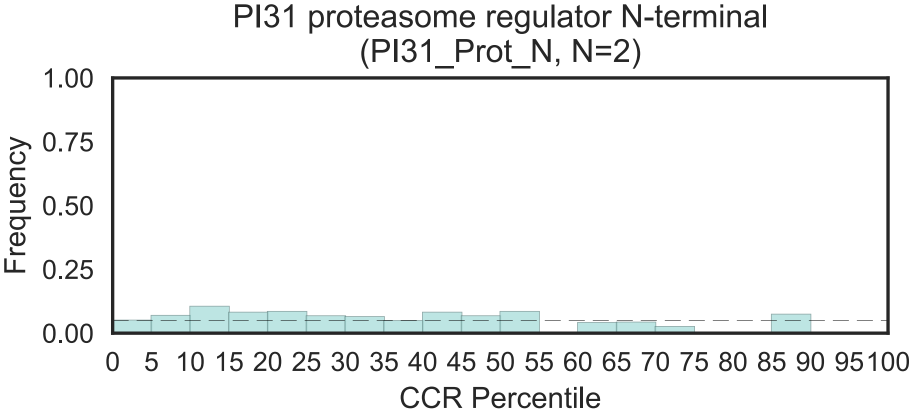
Phosphatidylinositol-specific phospholipase C, X domain
(PI-PLC-X, N=15)
Fisher's OR: 2.35; Bonferroni p-val: 1

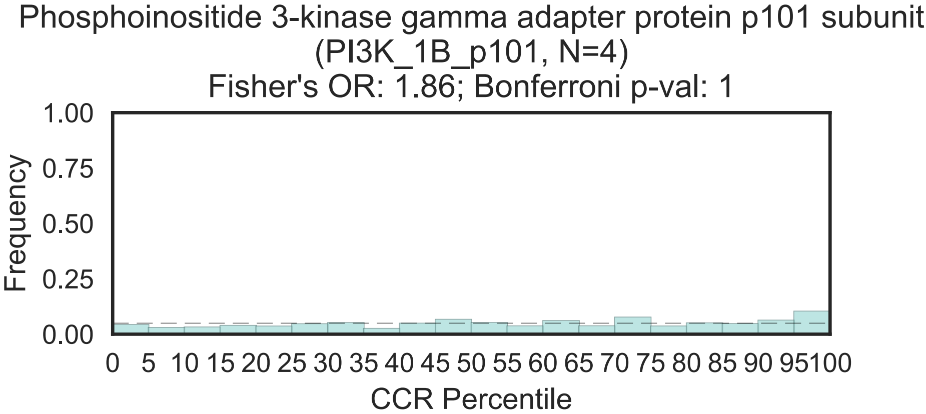


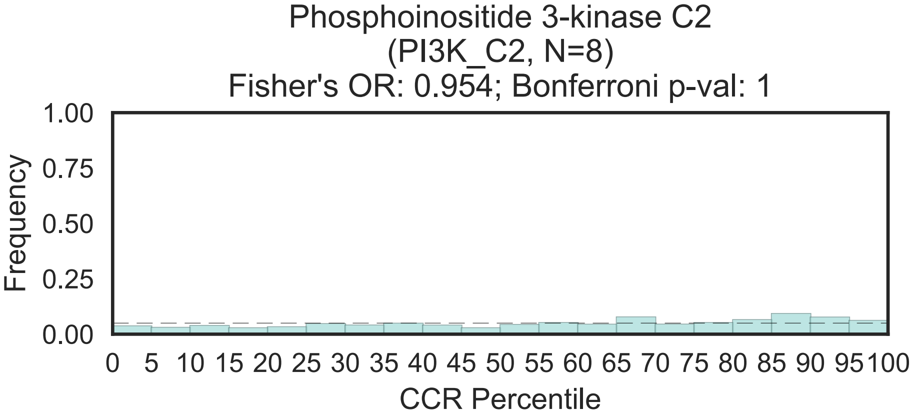

Phosphatidylinositol-specific phospholipase C, Y domain
(PI-PLC-Y, N=15)
Fisher's OR: 1.43; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

PI31 proteasome regulator (PI31_Prot_C, N=1)

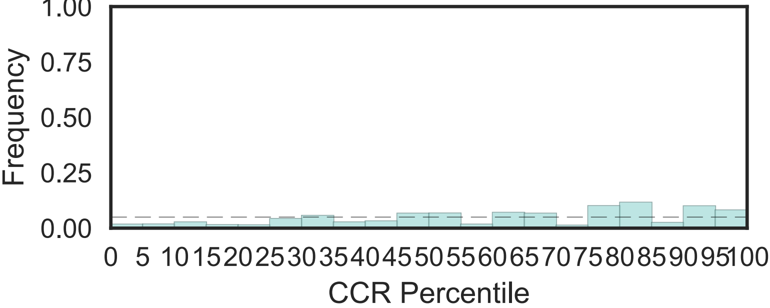


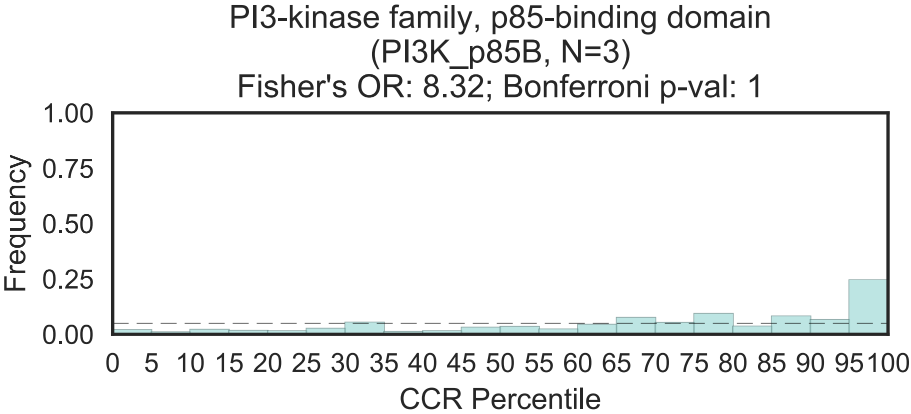

PI31 proteasome regulator N-terminal
(PI31_Prot_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

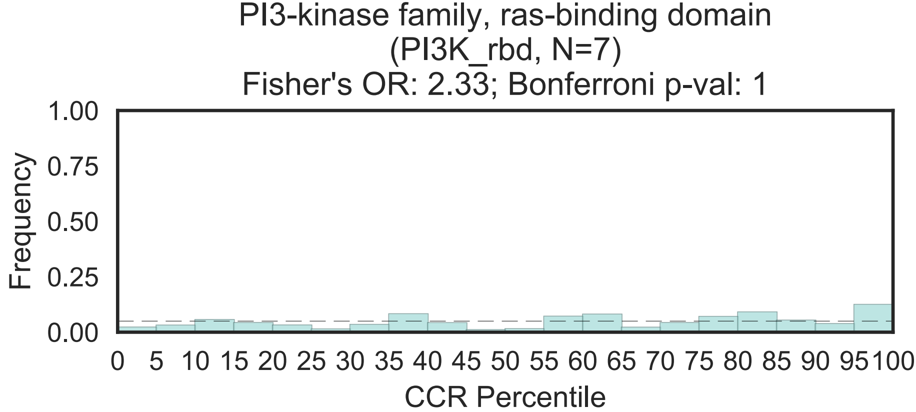

Phosphoinositide 3-kinase gamma adapter protein p101 subunit
(PI3K_1B_p101, N=4)
Fisher's OR: 1.86; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

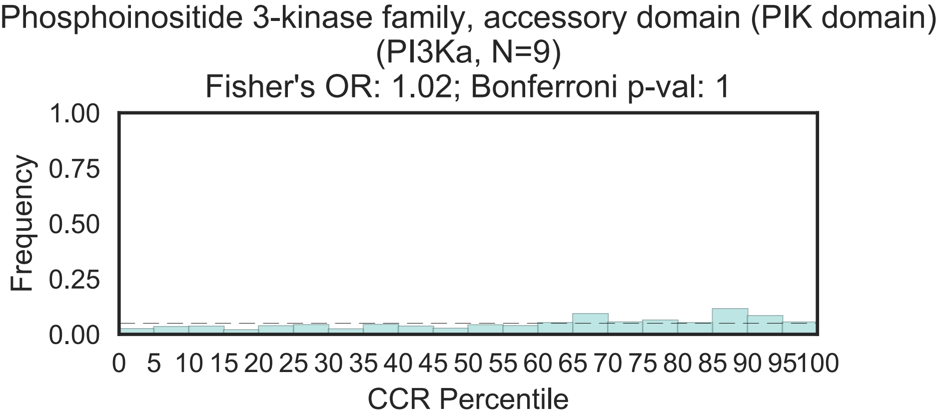

Phosphoinositide 3-kinase C2
(PI3K_C2, N=8)
Fisher's OR: 0.954; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Phosphatidylinositol 3-kinase regulatory subunit P85 inter-SH2 domain (PI3K_P85_iSH2, N=3)
Fisher's OR: 1.59; Bonferroni p-val: 1

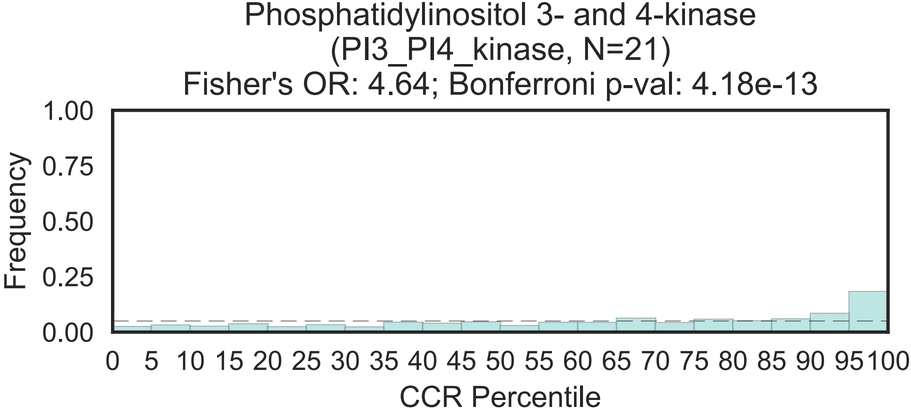


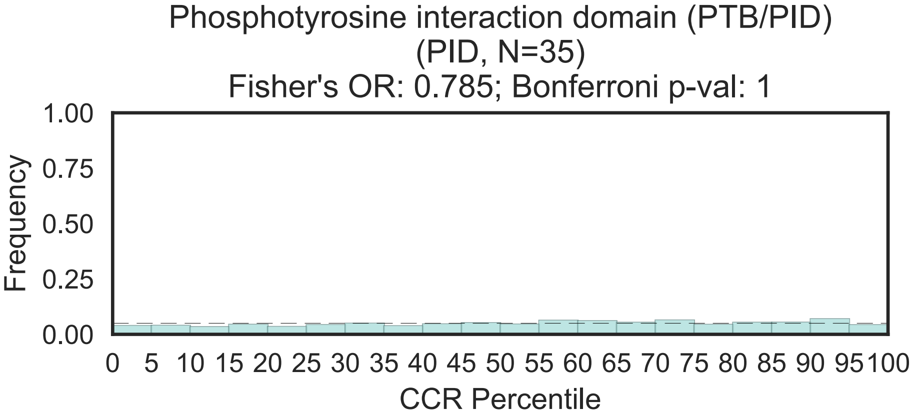

PI3-kinase family, p85-binding domain
(PI3K_p85B, N=3)
Fisher's OR: 8.32; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

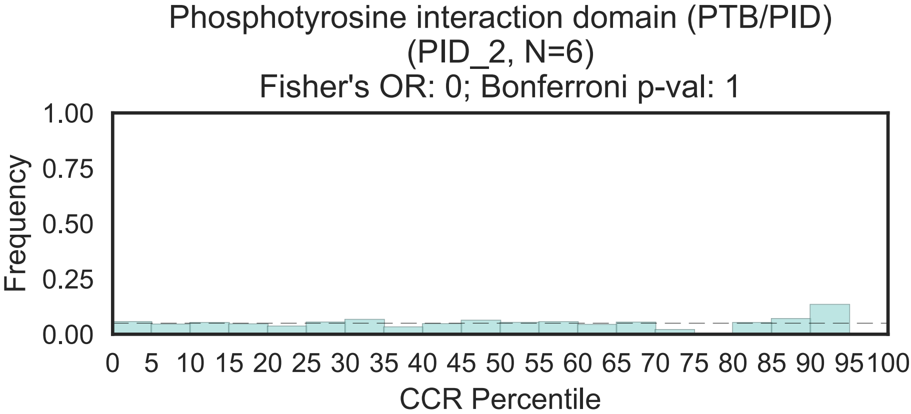

PI3-kinase family, ras-binding domain
(PI3K_rbd, N=7)
Fisher's OR: 2.33; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

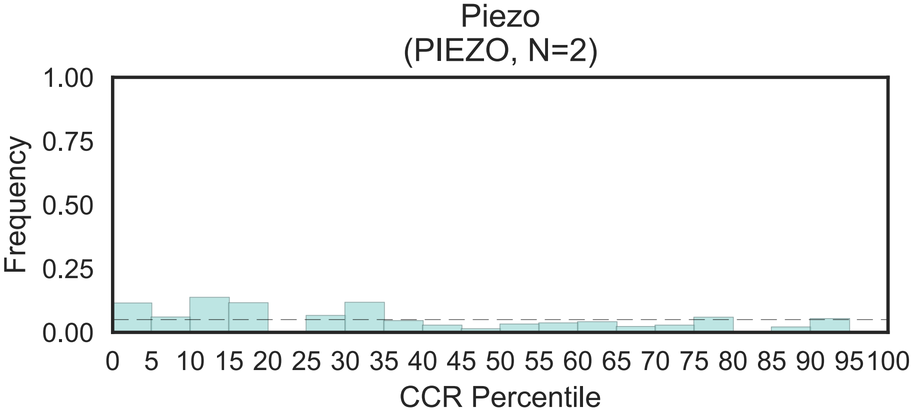


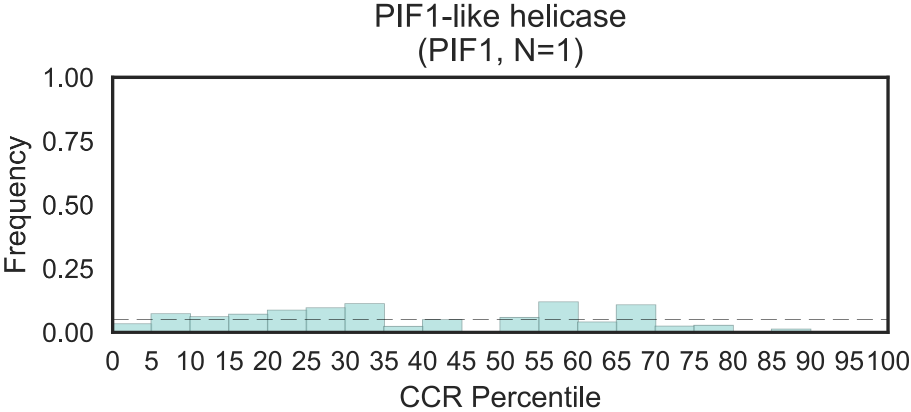
Phosphoinositide 3-kinase family, accessory domain (PIK domain)
(PI3Ka, N=9)
Fisher's OR: 1.02; Bonferroni p-val: 1

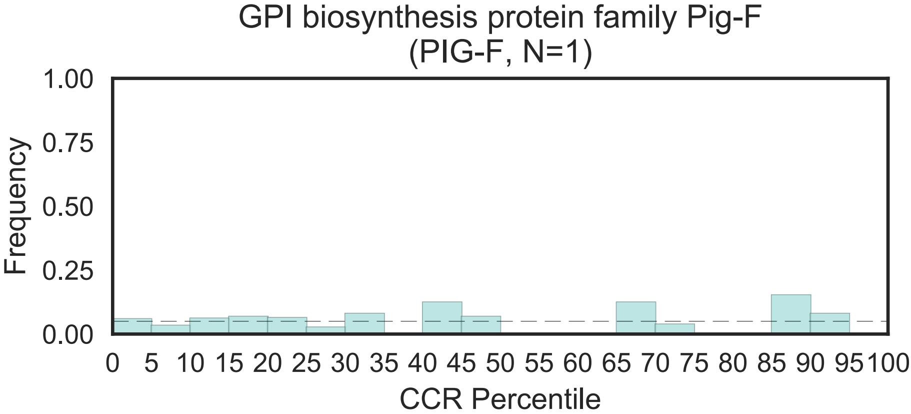

Phosphatidylinositol 3- and 4-kinase
(PI3_PI4_kinase, N=21)
Fisher's OR: 4.64; Bonferroni p-val: 4.18e-13
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

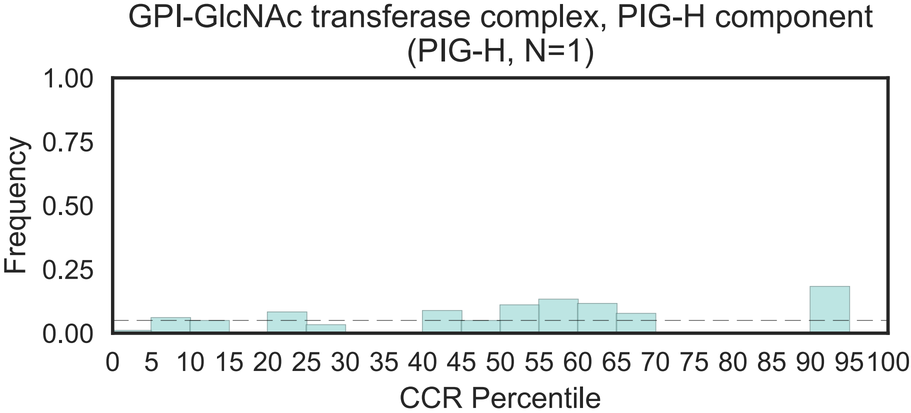

Phosphotyrosine interaction domain (PTB/PID)
(PID, N=35)
Fisher's OR: 0.785; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

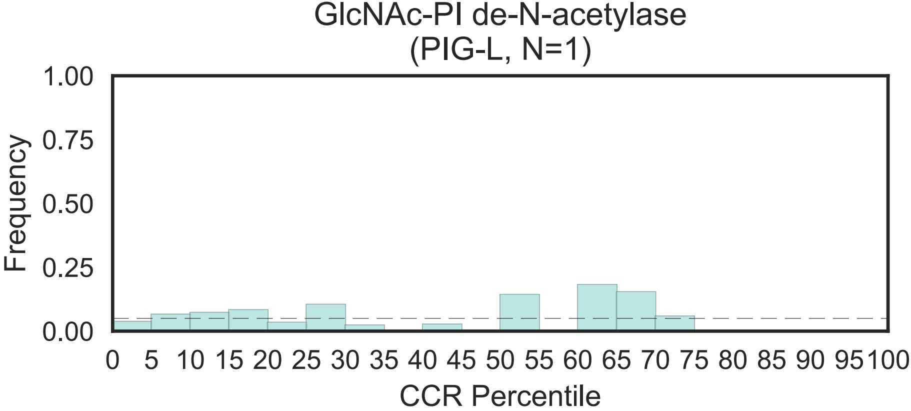

Phosphotyrosine interaction domain (PTB/PID)
(PID_2, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

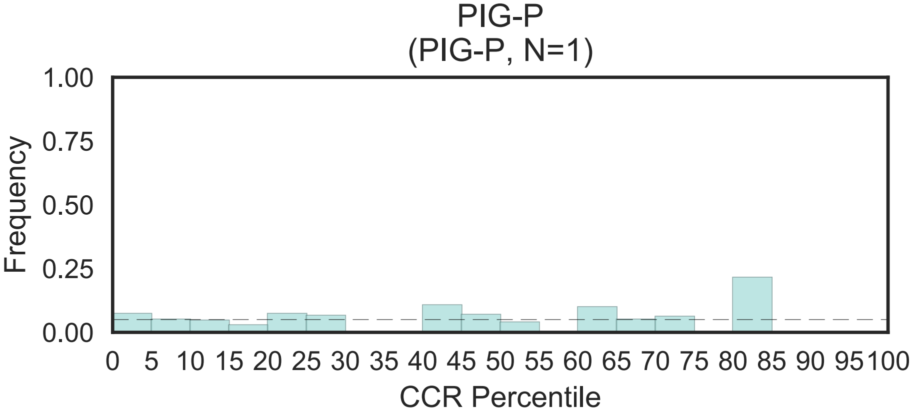

Piezo
(PIEZO, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

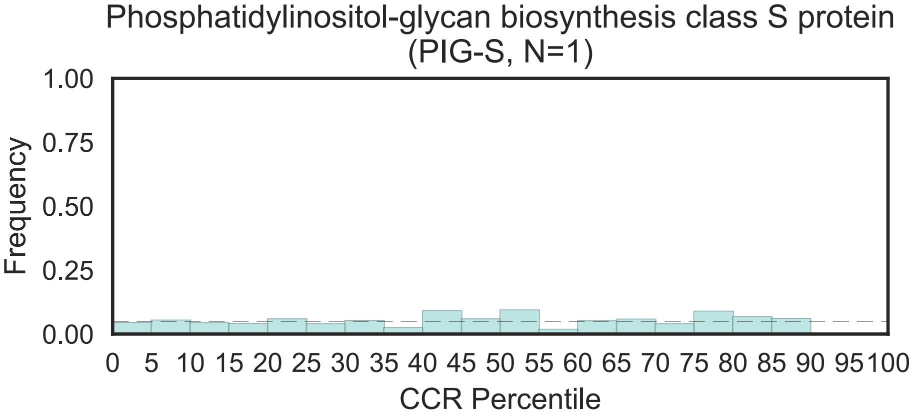

PIF1-like helicase
(PIF1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

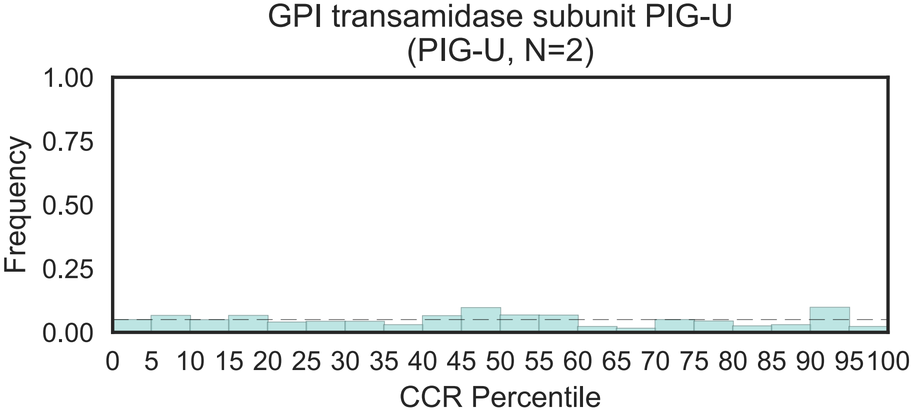

GPI biosynthesis protein family Pig-F
(PIG-F, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

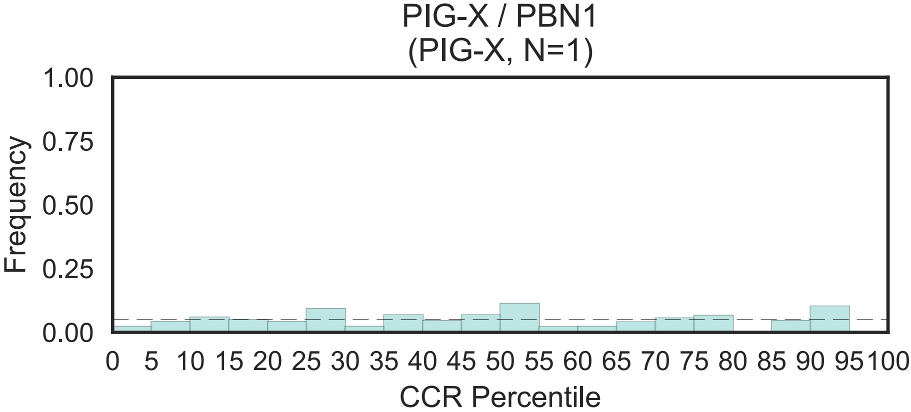

GPI-GlcNAc transferase complex, PIG-H component
(PIG-H, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

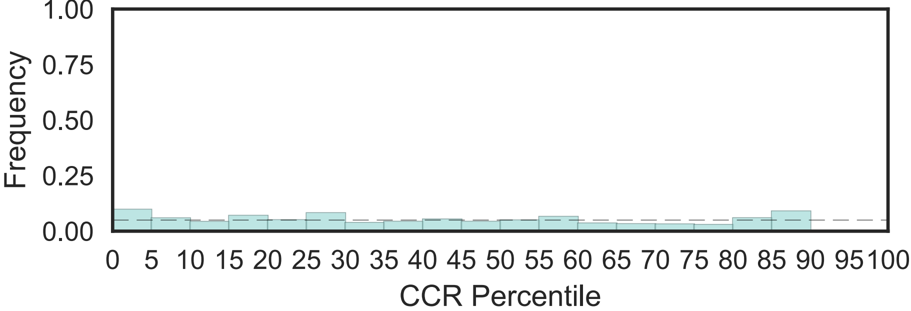

GlcNAc-PI de-N-acetylase
(PIG-L, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


PIG-P
(PIG-P, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

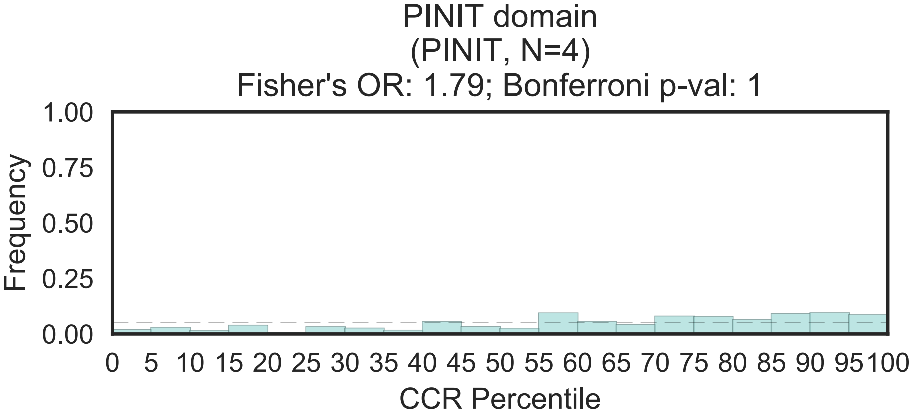

Phosphatidylinositol-glycan biosynthesis class S protein
(PIG-S, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

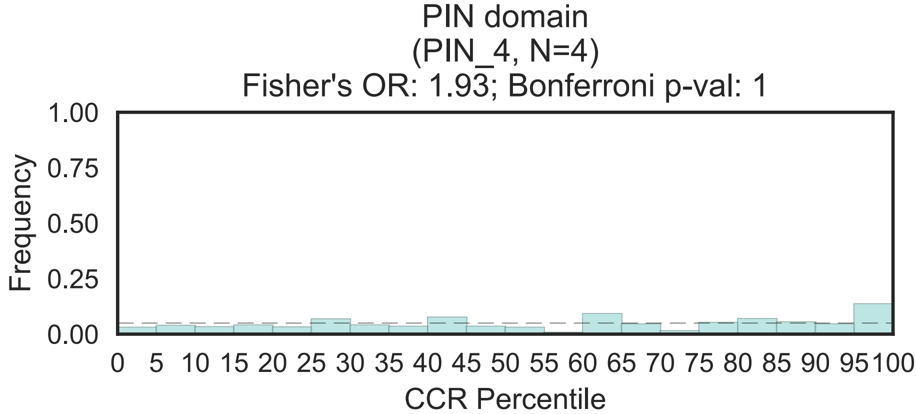

GPI transamidase subunit PIG-U
(PIG-U, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

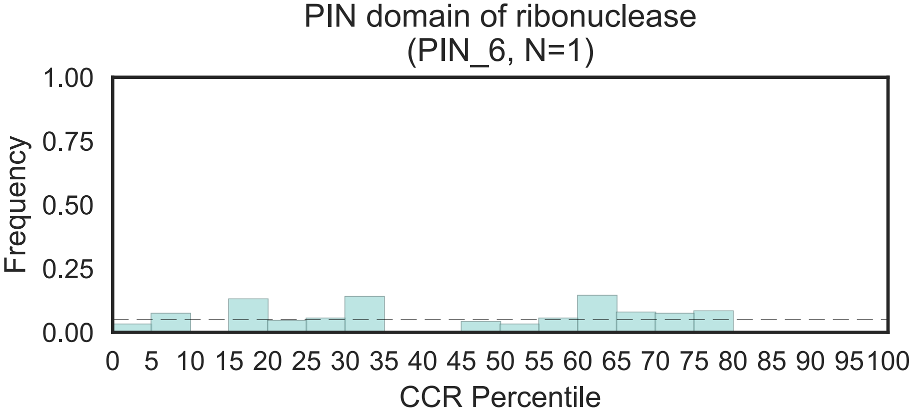

PIG-X / PBN1
(PIG-X, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

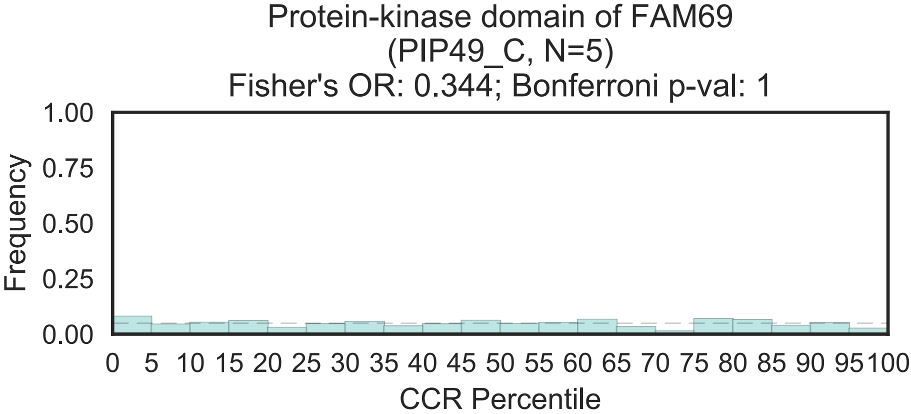


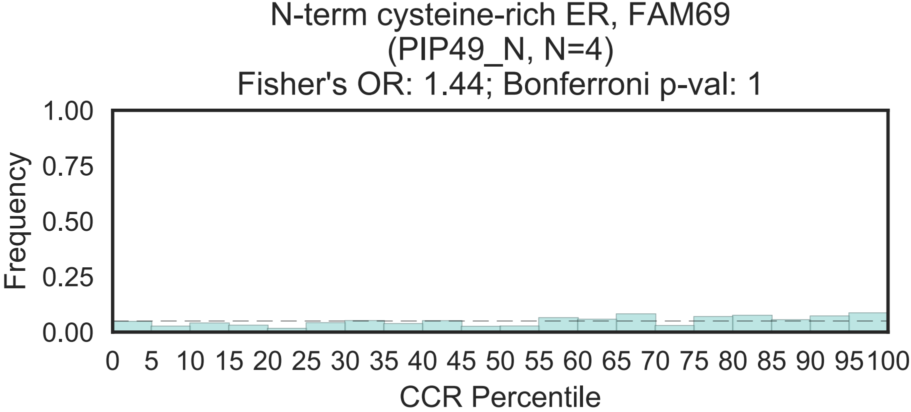
pre-RNA processing PIH1/Nop17
(PIH1, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

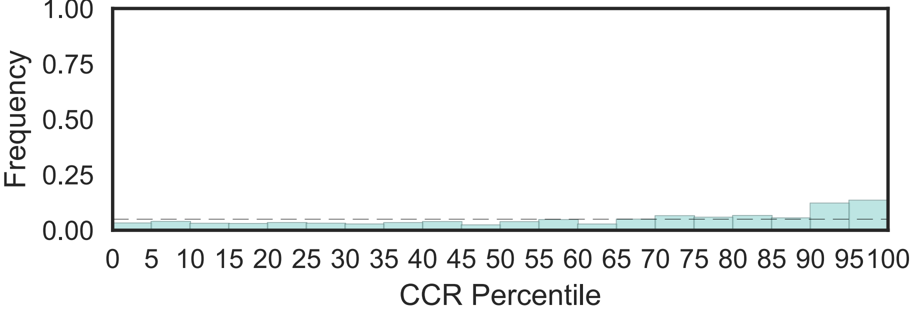

PINIT domain
(PINIT, N=4)
Fisher's OR: 1.79; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

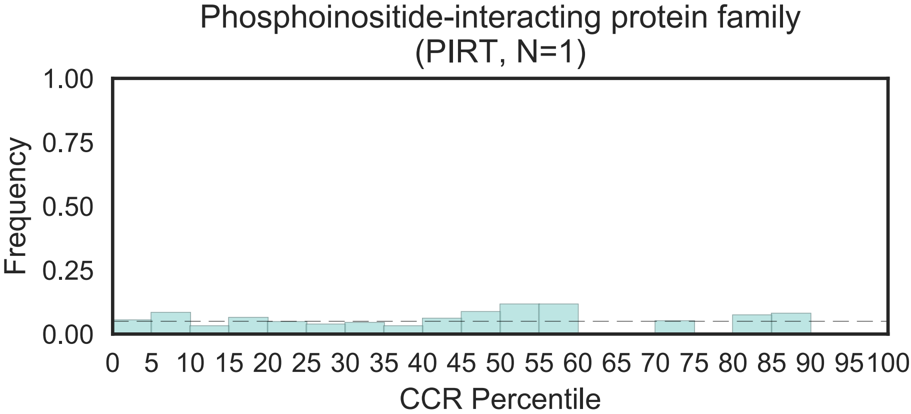

PIN domain
(PIN_4, N=4)
Fisher's OR: 1.93; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

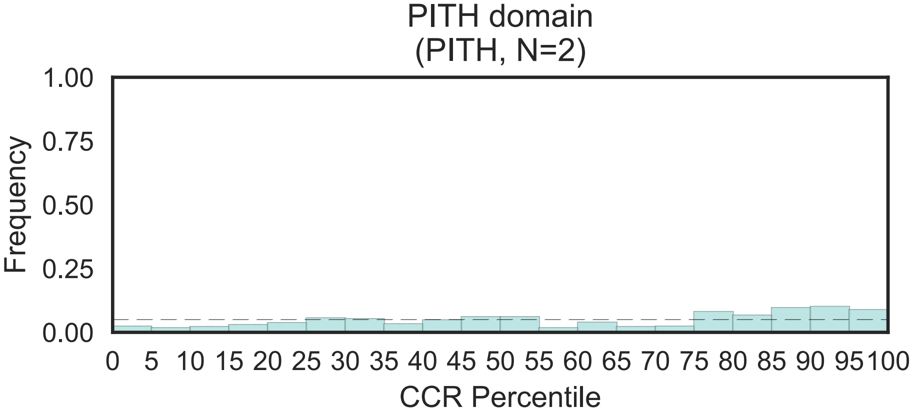

PIN domain of ribonuclease
(PIN_6, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

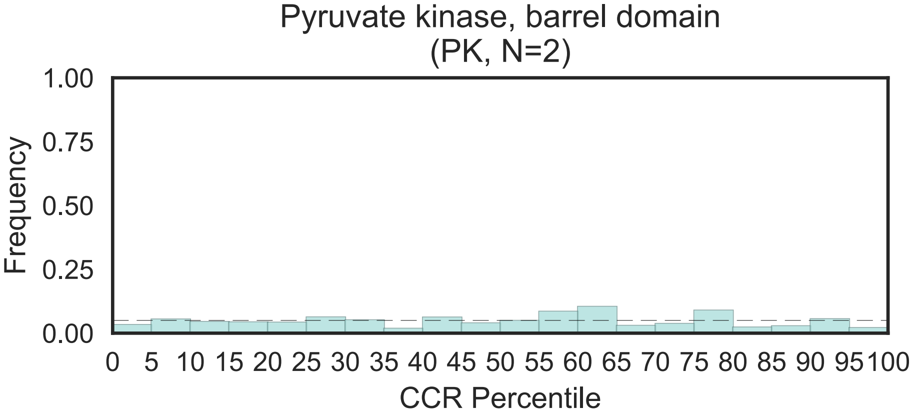

Protein-kinase domain of FAM69
(PIP49_C, N=5)
Fisher's OR: 0.344; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

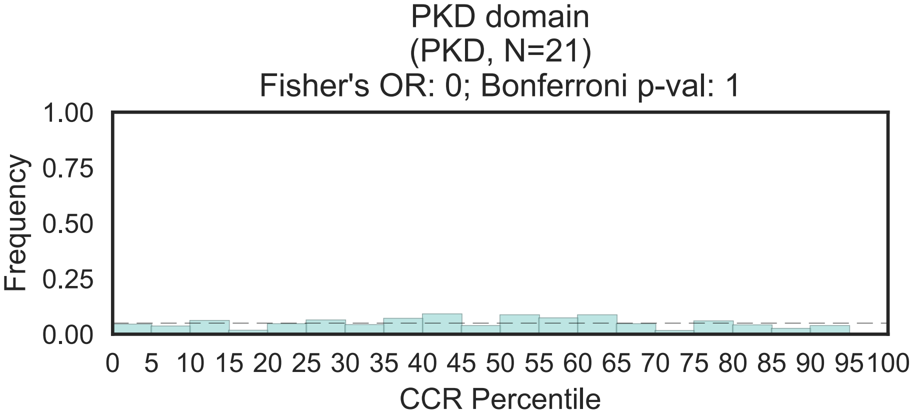

N-term cysteine-rich ER, FAM69
(PIP49_N, N=4)
Fisher's OR: 1.44; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

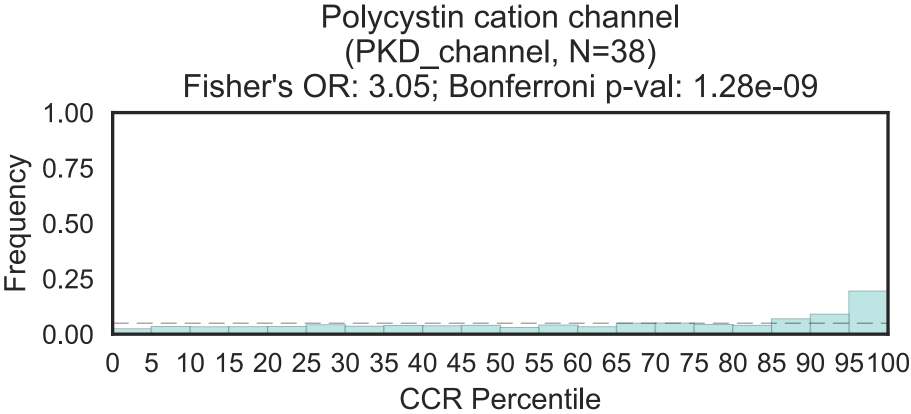

Phosphatidylinositol-4-phosphate 5-Kinase
(PIP5K, N=9)
Fisher's OR: 2.25; Bonferroni p-val: 1

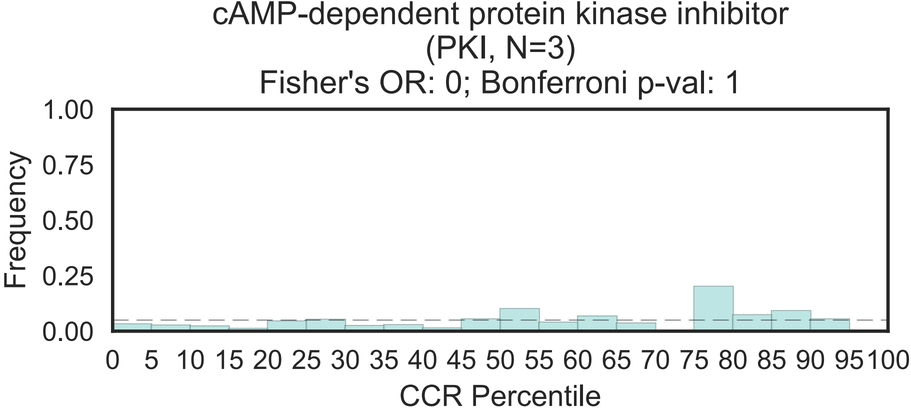

Phosphoinositide-interacting protein family
(PIRT, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

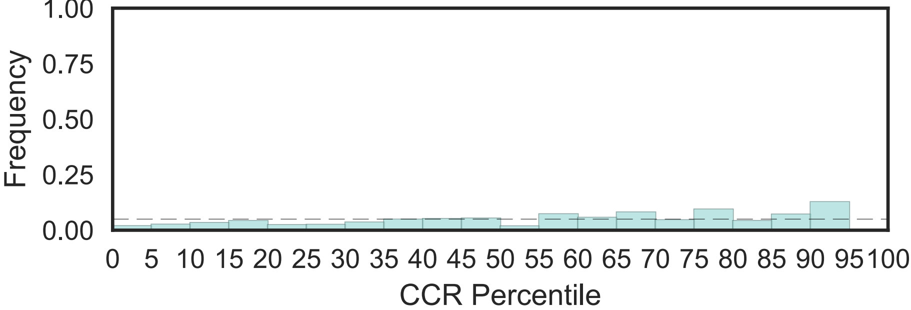

PITH domain
(PITH, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Pyruvate kinase, barrel domain
(PK, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

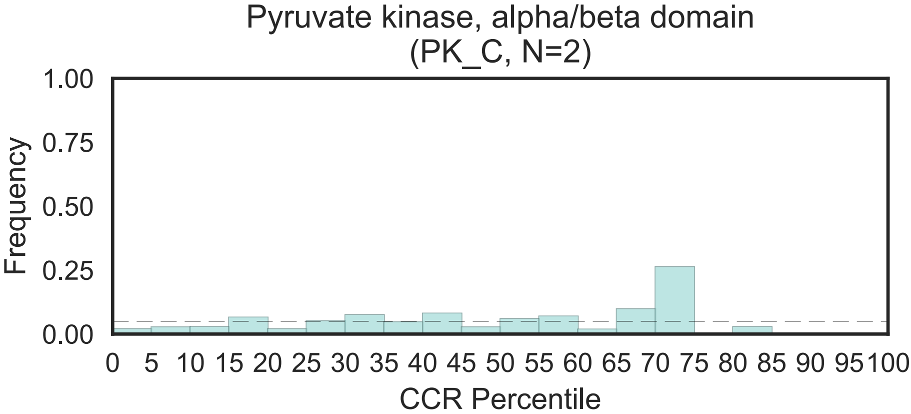

PKD domain
(PKD, N=21)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

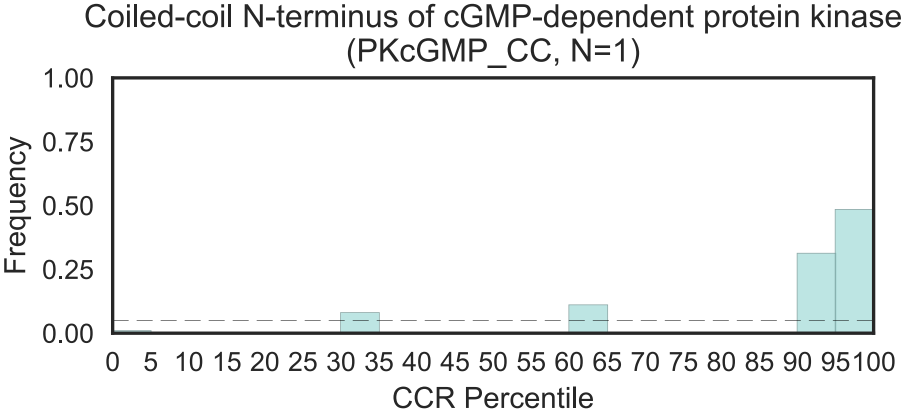

Polycystin cation channel
(PKD_channel, N=38)
Fisher's OR: 3.05; Bonferroni p-val: 1.28e-09
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

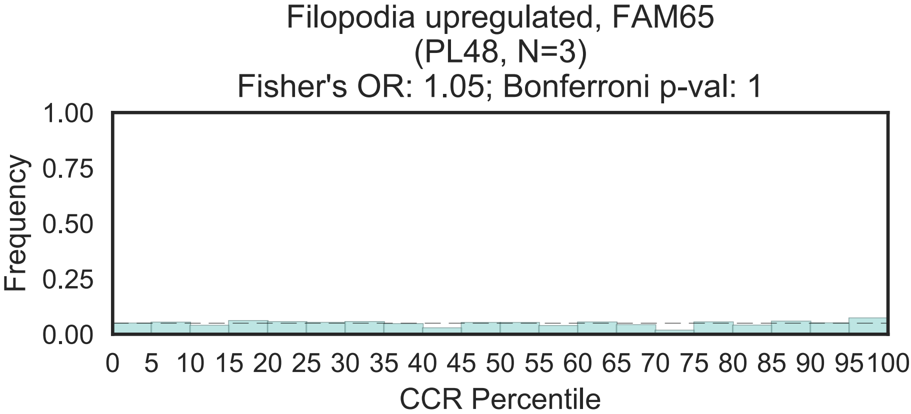

cAMP-dependent protein kinase inhibitor
(PKI, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

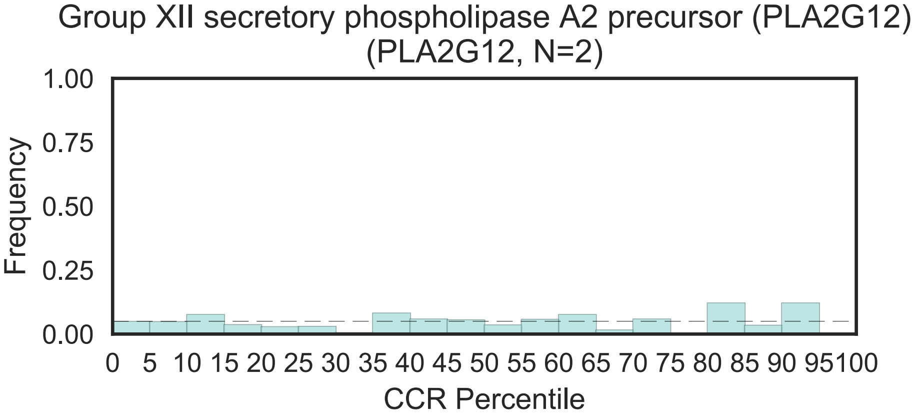


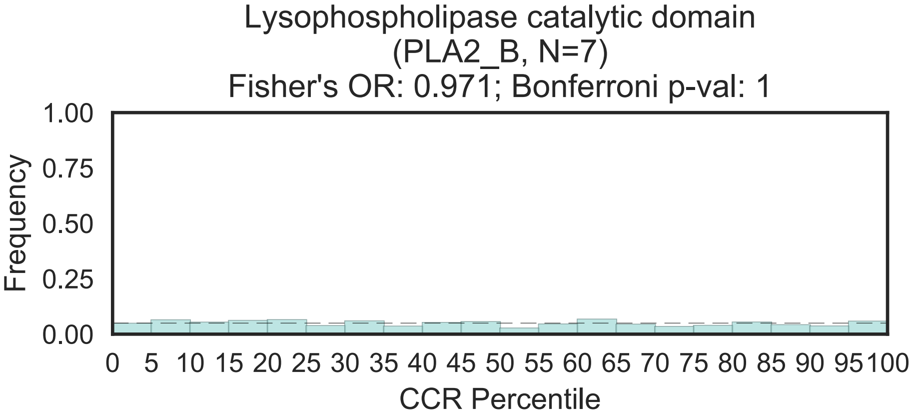
Polo kinase kinase
(PKK, N=4)
Fisher's OR: 0; Bonferroni p-val: 1


Pyruvate kinase, alpha/beta domain
(PK_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

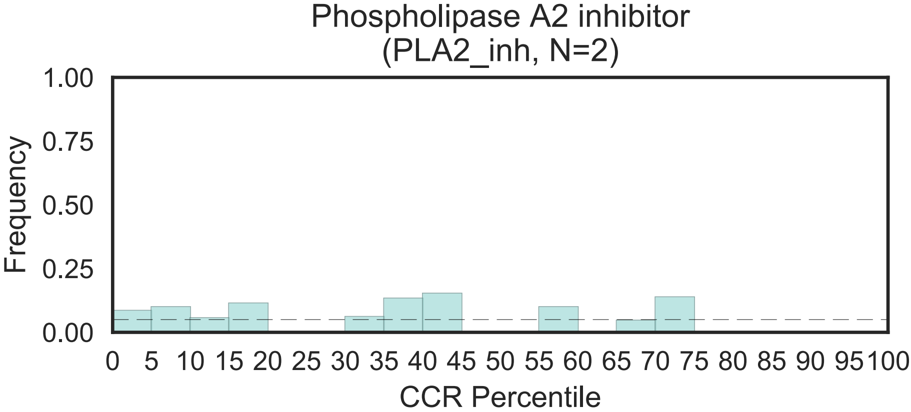

Coiled-coil N-terminus of cGMP-dependent protein kinase
(PKcGMP_CC, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

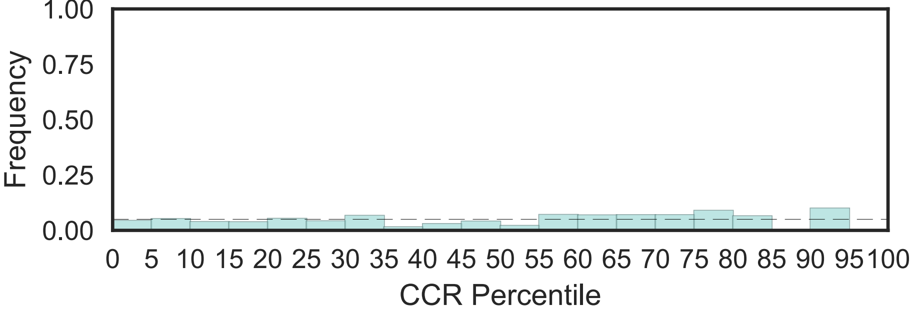

Filopodia upregulated, FAM65
(PL48, N=3)
Fisher's OR: 1.05; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

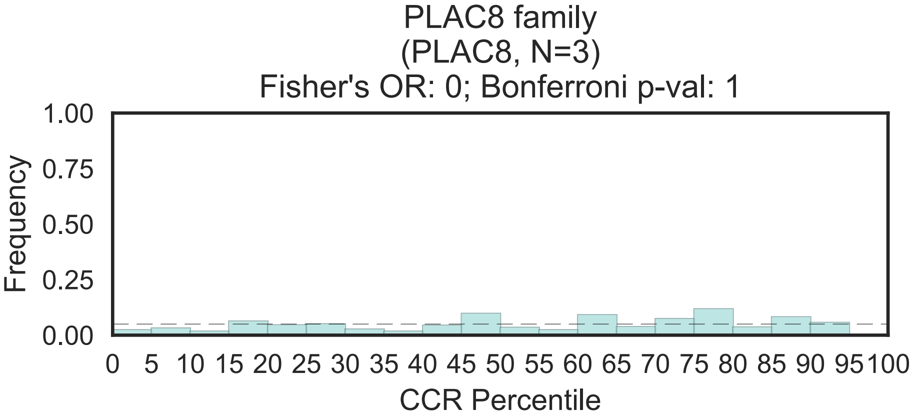

Group XII secretory phospholipase A2 precursor (PLA2G12)
(PLA2G12, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

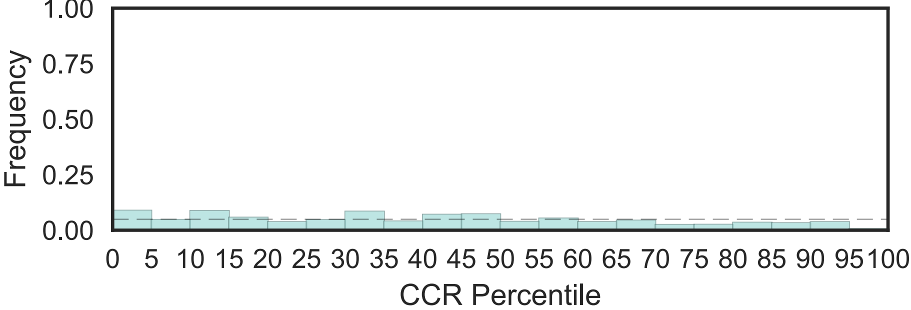


Lysophospholipase catalytic domain
(PLA2_B, N=7)
Fisher's OR: 0.971; Bonferroni p-val: 1

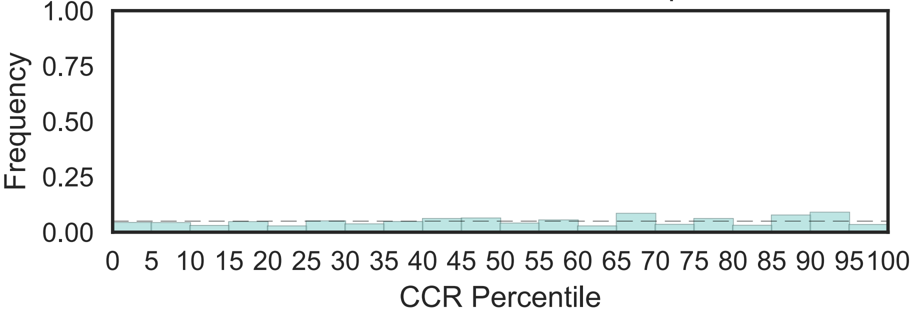

Phospholipase A2 inhibitor
(PLA2_inh, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


PLAC (protease and lacunin) domain
(PLAC, N=13)
Fisher's OR: 0; Bonferroni p-val: 1

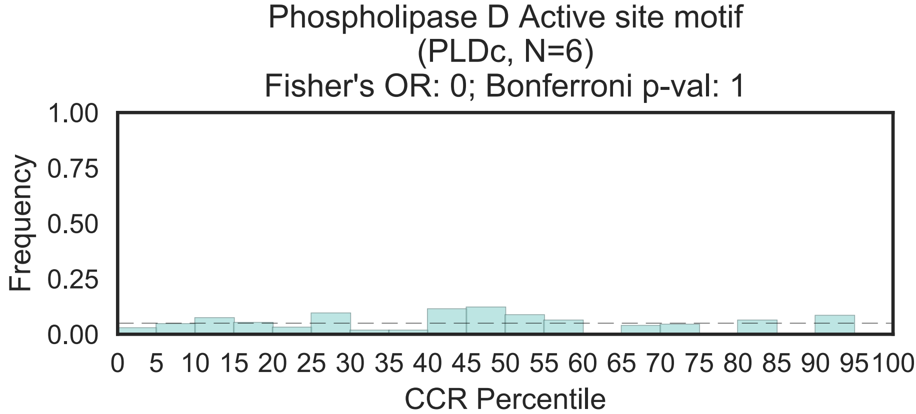

PLAC8 family
(PLAC8, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

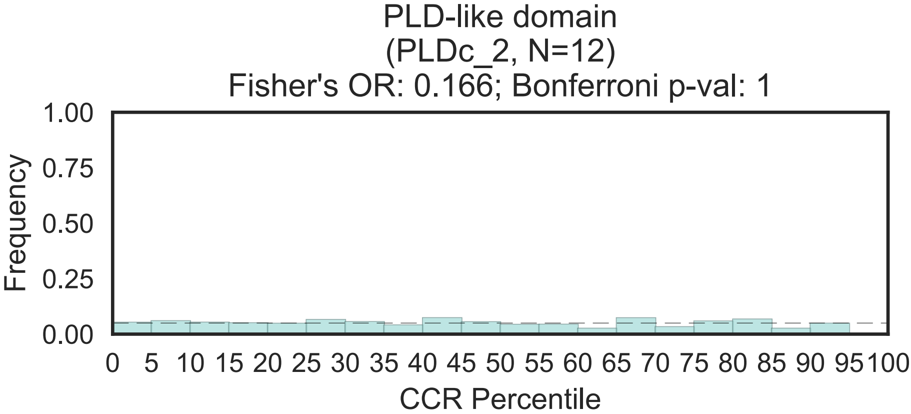


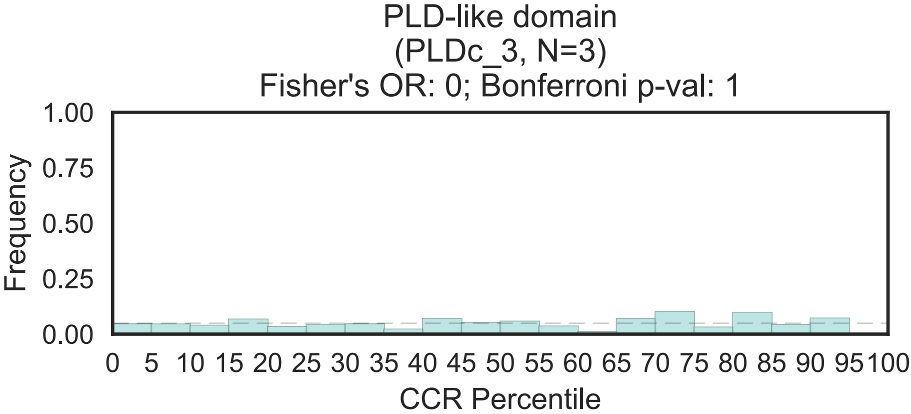
PLAT/LH2 domain
(PLAT, N=34)
Fisher's OR: 0.0832; Bonferroni p-val: 1

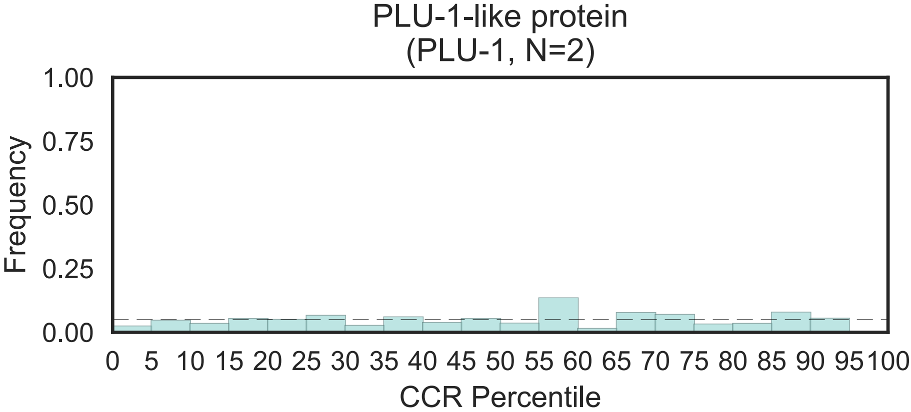


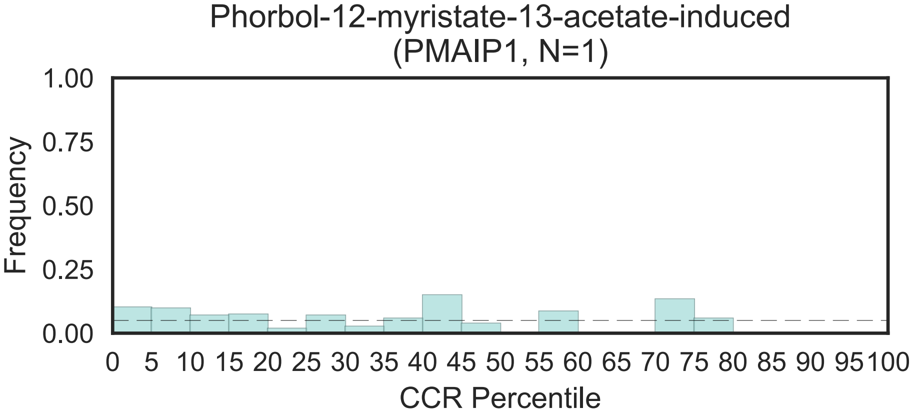
PLC-beta C terminal
(PLC-beta_C, N=3)
Fisher's OR: 0.578; Bonferroni p-val: 1

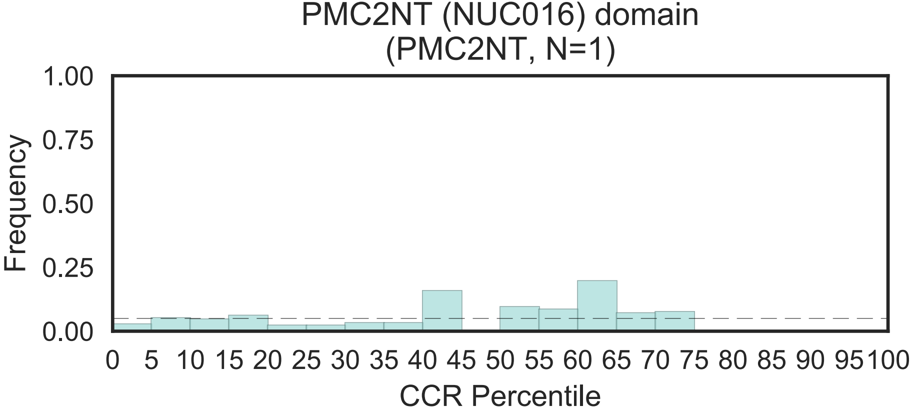

Phospholipase D Active site motif
(PLDc, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


PLD-like domain
(PLDc_2, N=12)
Fisher's OR: 0.166; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

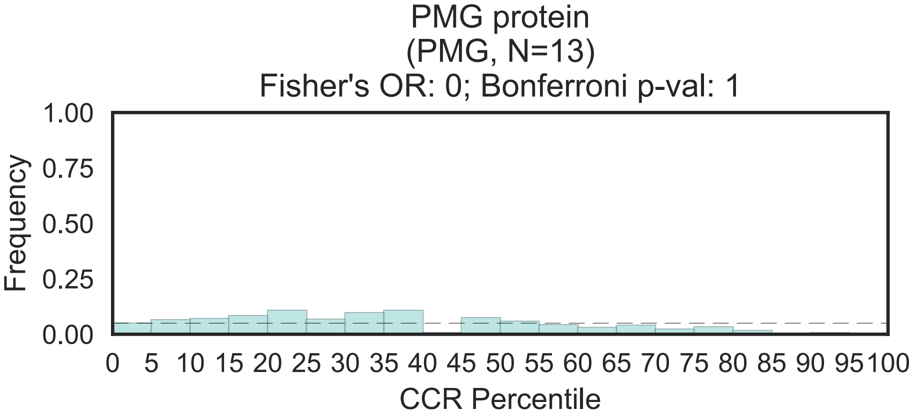

PLD-like domain
(PLDc_3, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

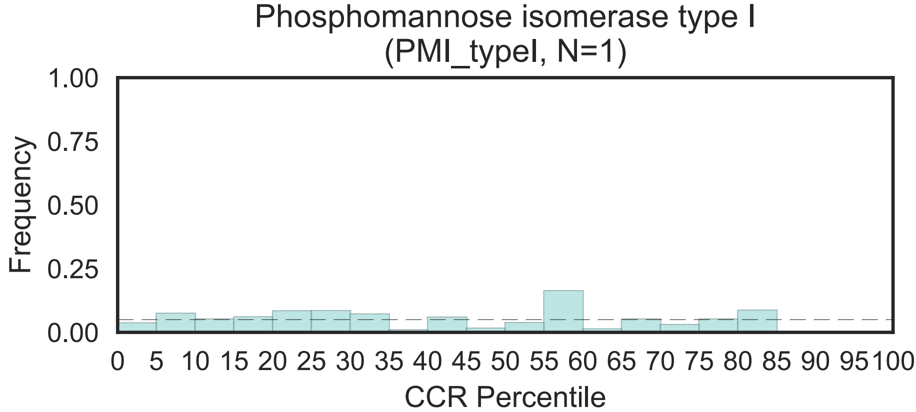

PLU-1-like protein
(PLU-1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

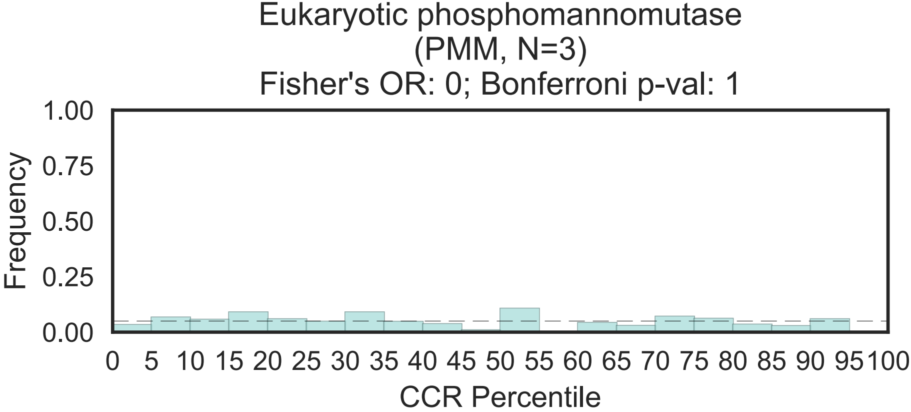

Phorbol-12-myristate-13-acetate-induced
(PMAIP1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

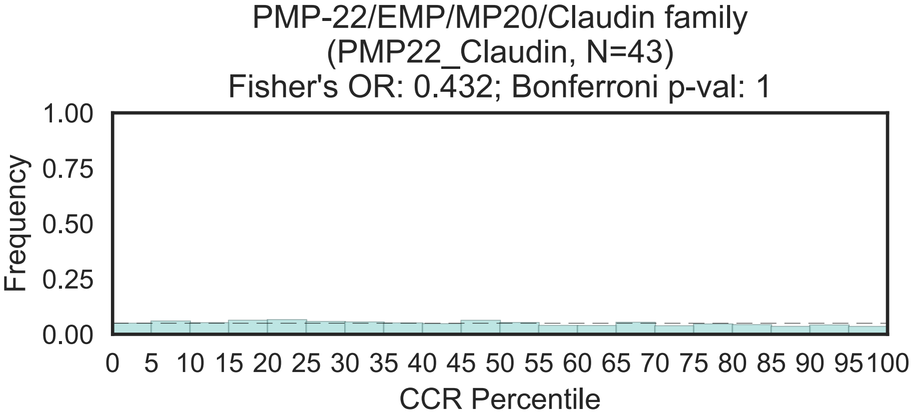


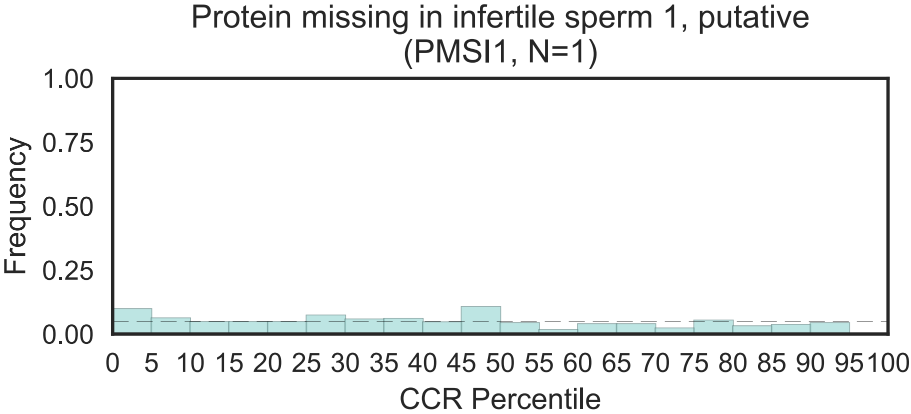
PMC2NT (NUC016) domain
(PMC2NT, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

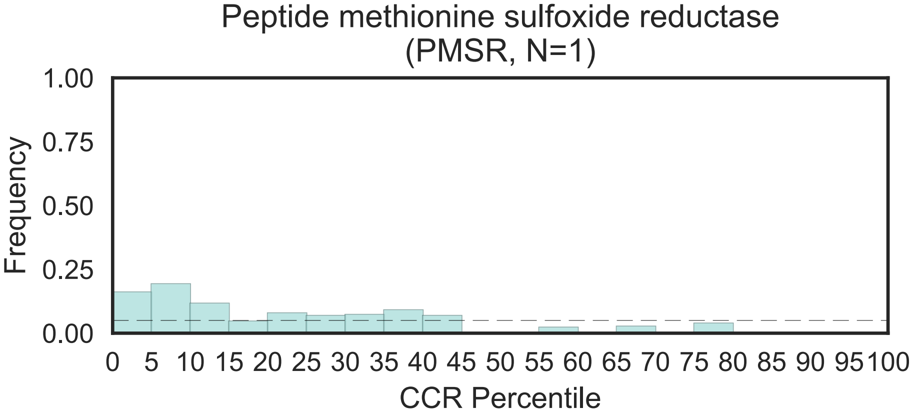

PMG protein
(PMG, N=13)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

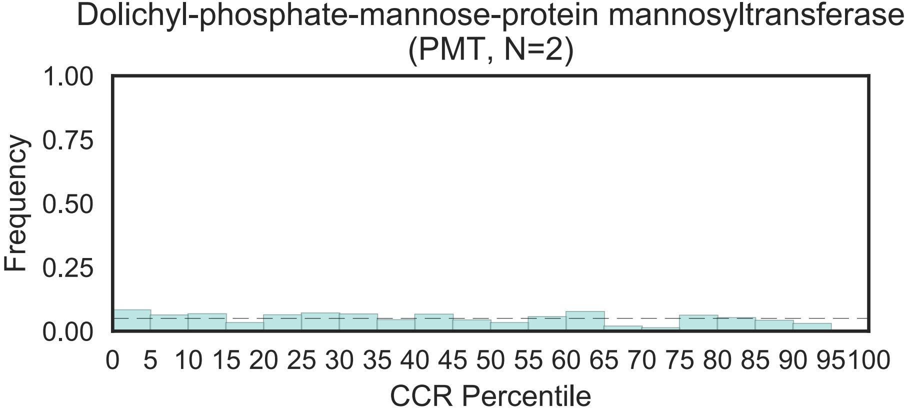

Phosphomannose isomerase type I
(PMI_typeI, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

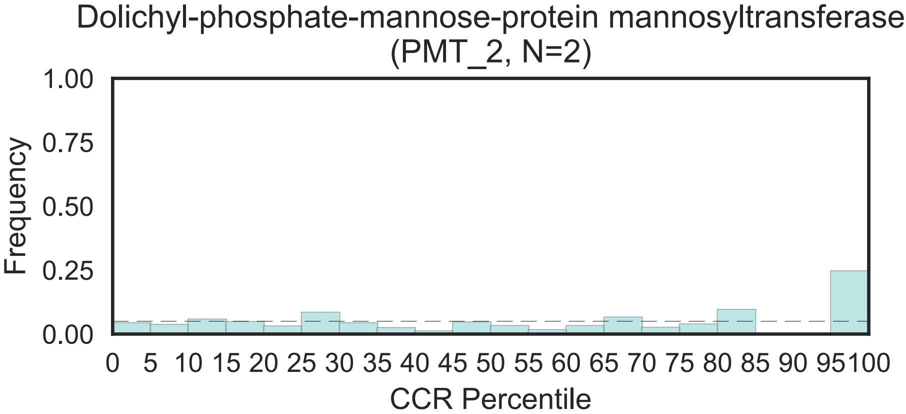

Eukaryotic phosphomannomutase
(PMM, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

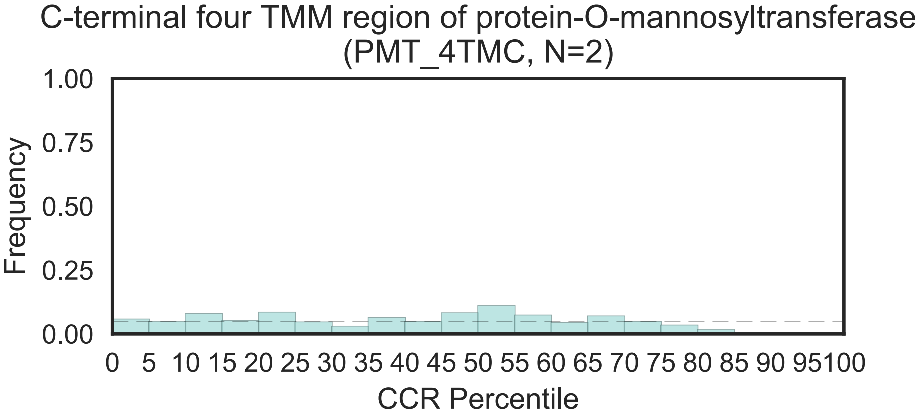

PMP-22/EMP/MP20/Claudin family
(PMP22_Claudin, N=43)
Fisher's OR: 0.432; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

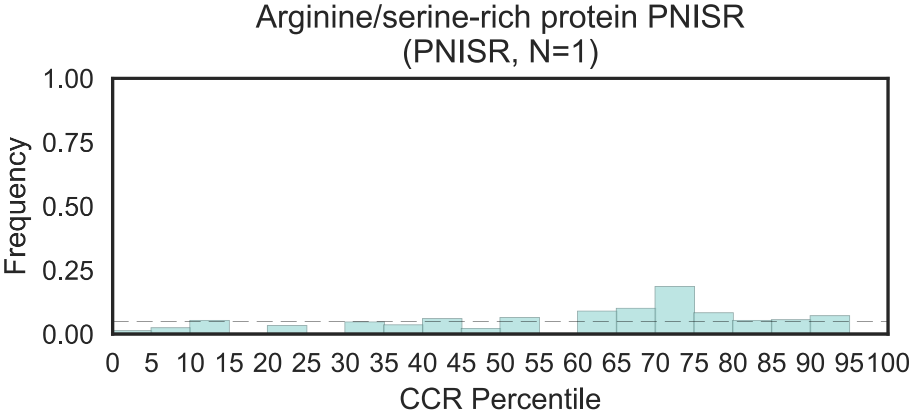

Protein missing in infertile sperm 1, putative
(PMSI1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

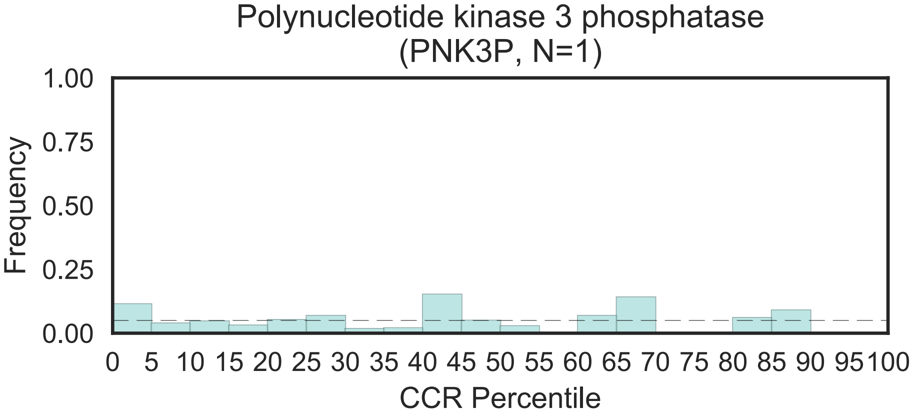

Peptide methionine sulfoxide reductase
(PMSR, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

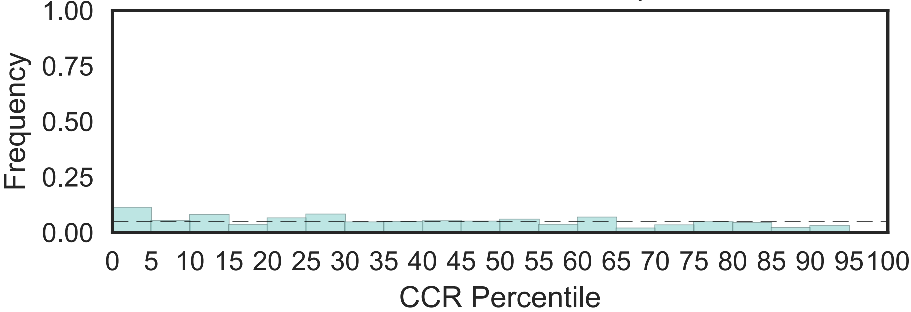

Dolichyl-phosphate-mannose-protein mannosyltransferase
(PMT, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

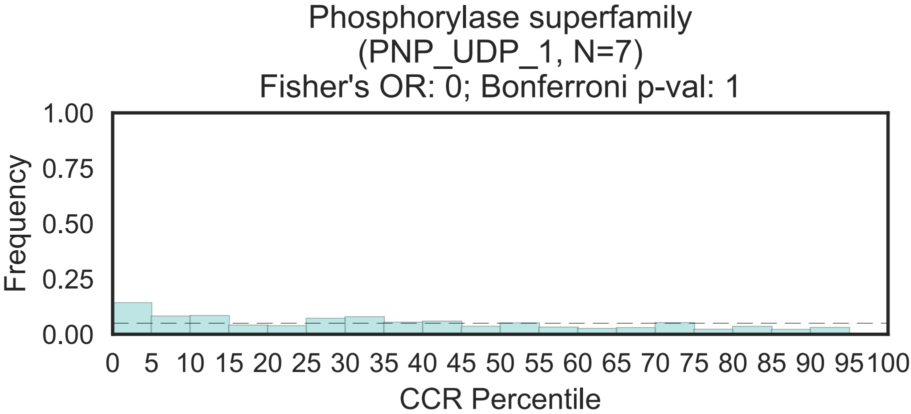

Dolichyl-phosphate-mannose-protein mannosyltransferase
(PMT_2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

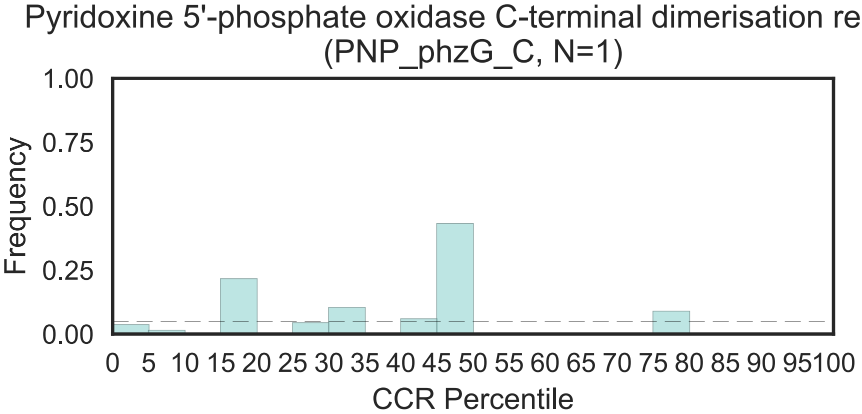

C-terminal four TMM region of protein-O-mannosyltransferase
(PMT_4TMC, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

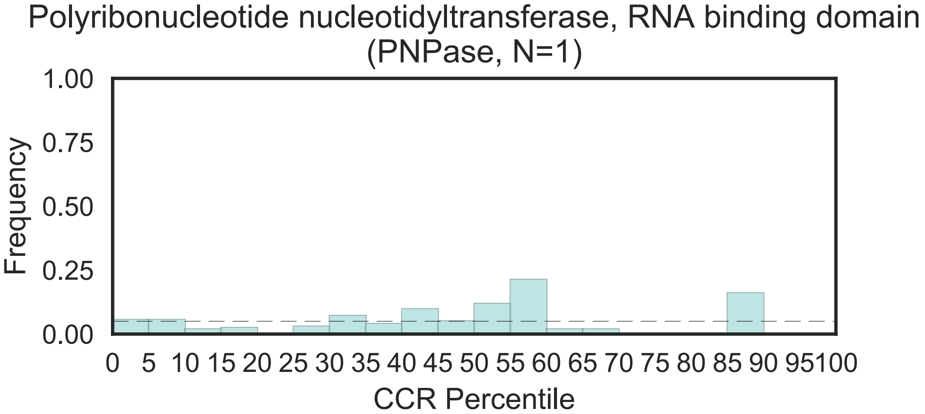

Arginine/serine-rich protein PNISR
(PNISR, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

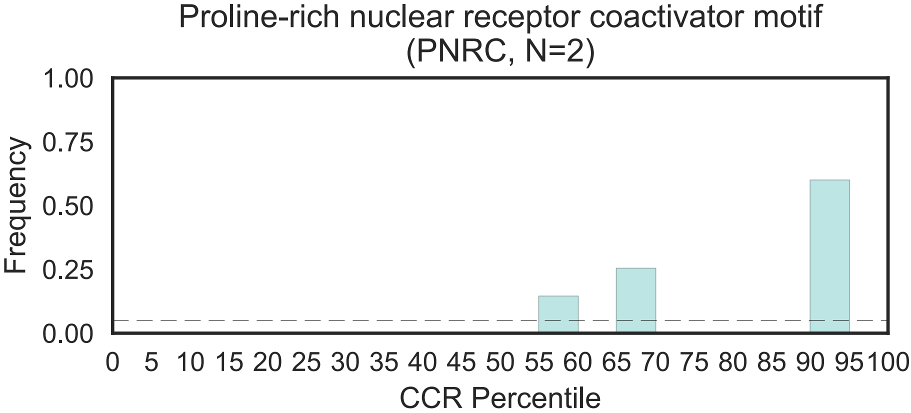

Polynucleotide kinase 3 phosphatase
(PNK3P, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

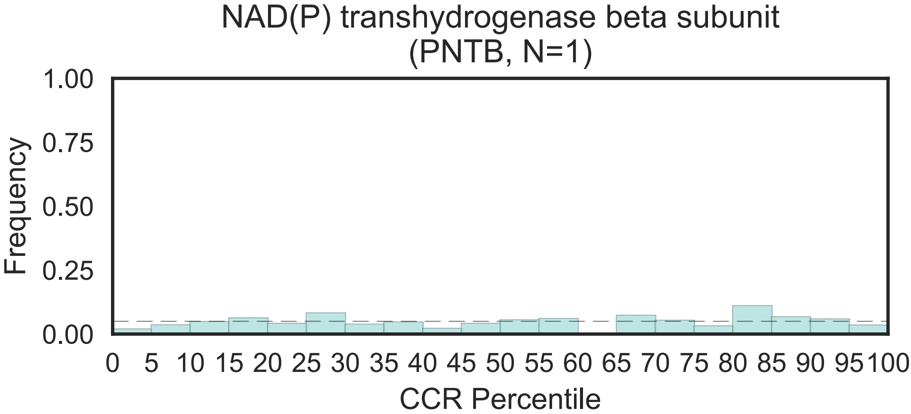

PNMA
(PNMA, N=7)
Fisher's OR: 0; Bonferroni p-val: 1

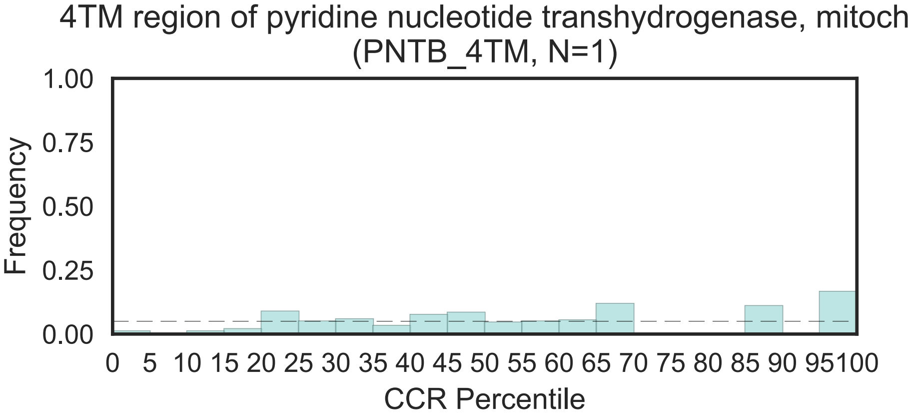

Phosphorylase superfamily
(PNP_UDP_1, N=7)
Fisher's OR: 0; Bonferroni p-val: 1

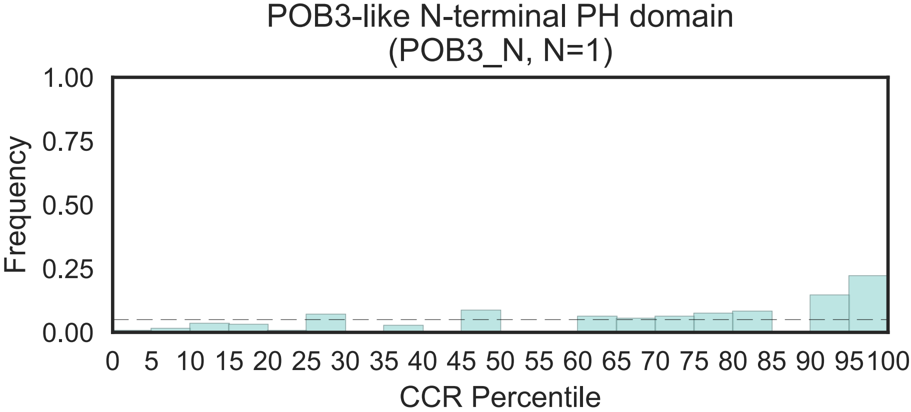

Pyridoxine 5'-phosphate oxidase C-terminal dimerisation region
(PNP_phzG_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95100
CCR Percentile

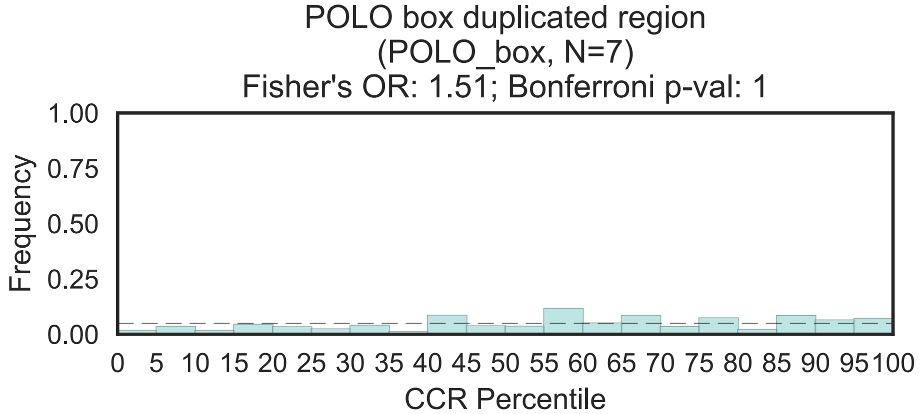

Polyribonucleotide nucleotidyltransferase, RNA binding domain
(PNPase, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

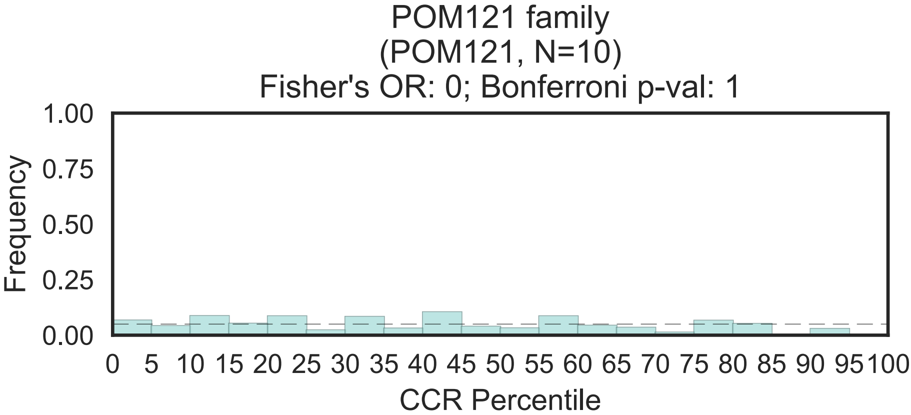

Proline-rich nuclear receptor coactivator motif
(PNRC, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

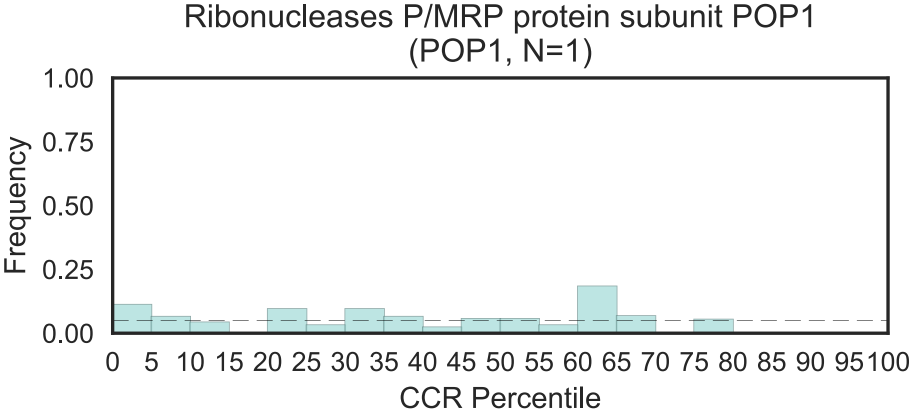

NAD(P) transhydrogenase beta subunit
(PNTB, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

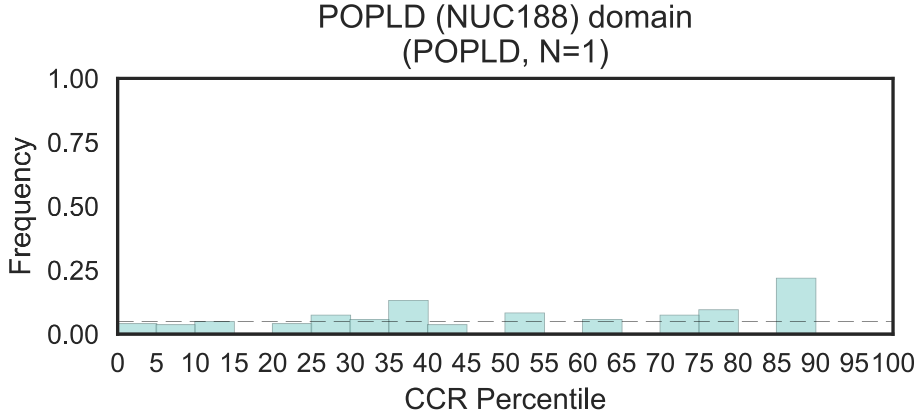

4TM region of pyridine nucleotide transhydrogenase, mitoch
(PNTB_4TM, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

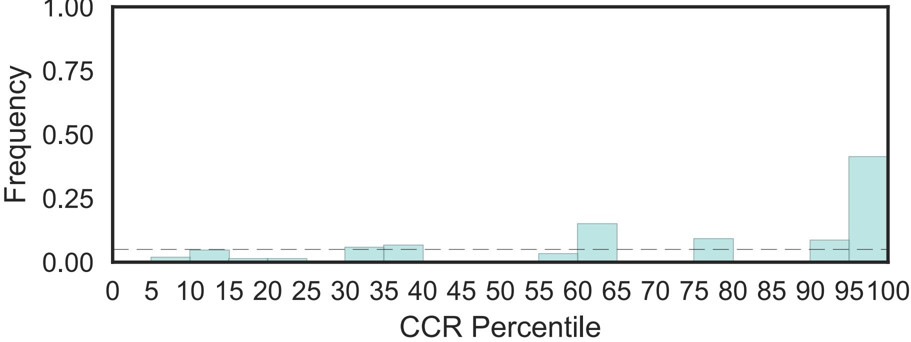

POB3-like N-terminal PH domain
(POB3_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


POLO box duplicated region
(POLO_box, N=7)
Fisher's OR: 1.51; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

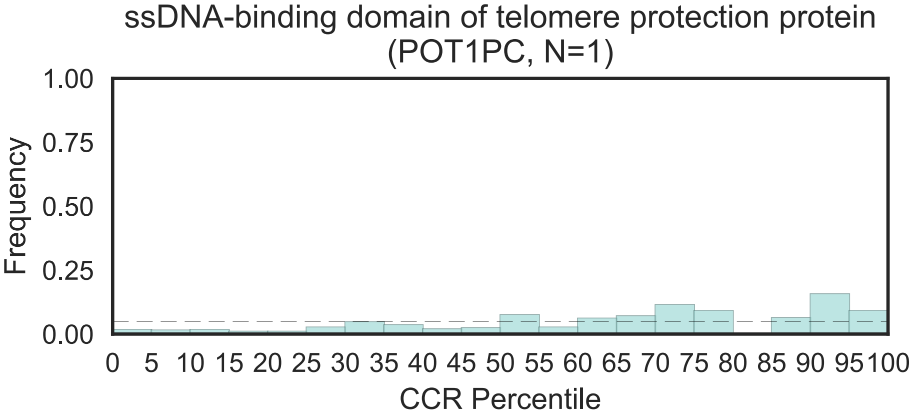

POM121 family
(POM121, N=10)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

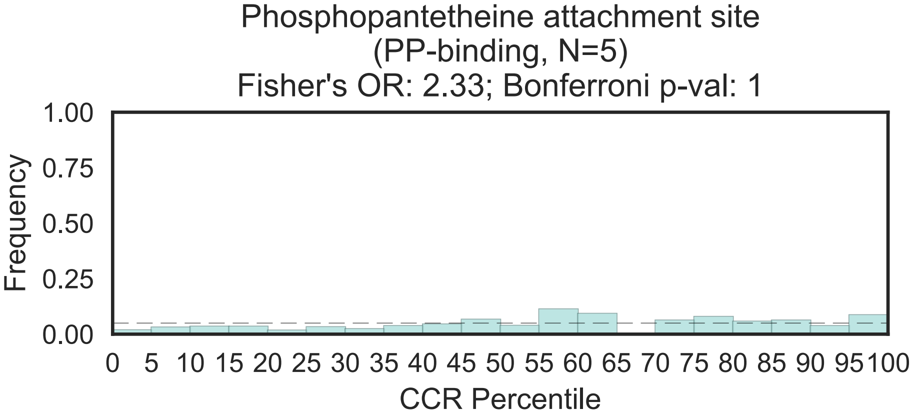

Ribonucleases P/MRP protein subunit POP1
(POP1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

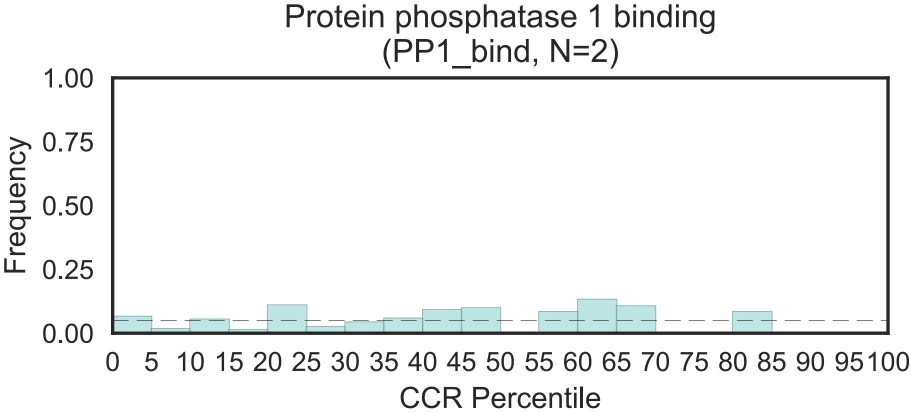

POPLD (NUC188) domain
(POPLD, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

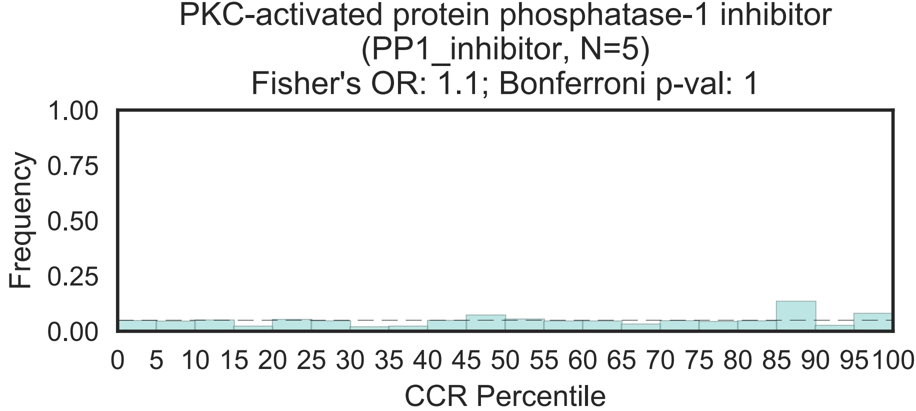


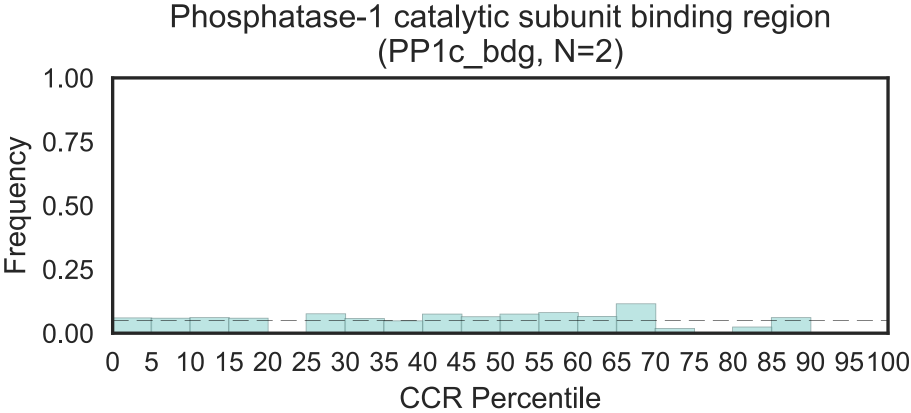
Telomeric single stranded DNA binding POT1/CDC13
(POT1, N=1)

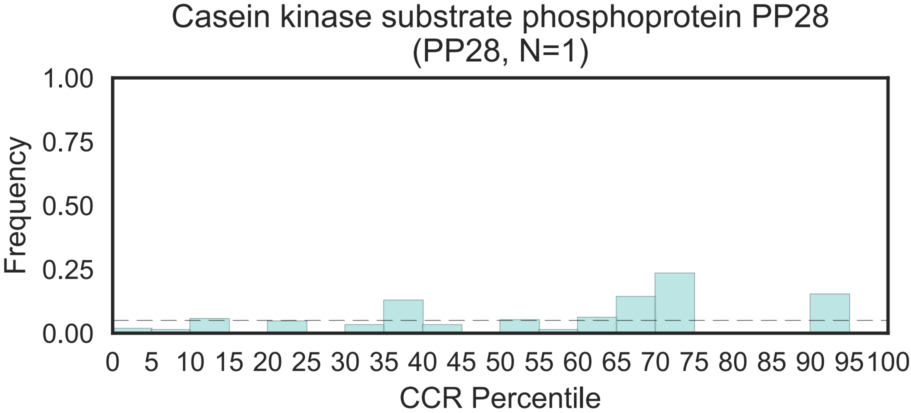

ssDNA-binding domain of telomere protection protein
(POT1PC, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Phosphopantetheine attachment site
(PP-binding, N=5)
Fisher's OR: 2.33; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

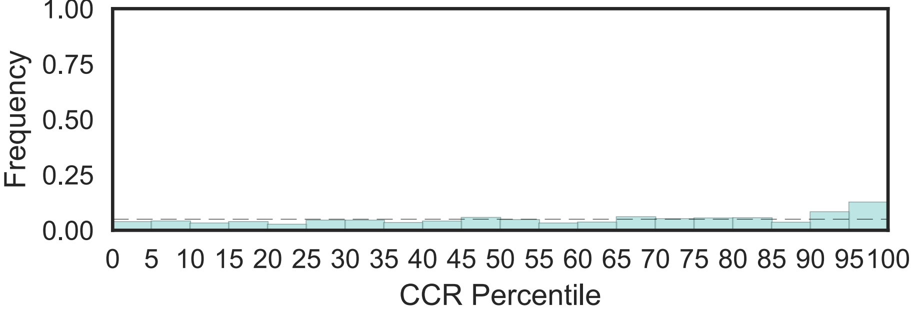

Protein phosphatase 1 binding
(PP1_bind, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

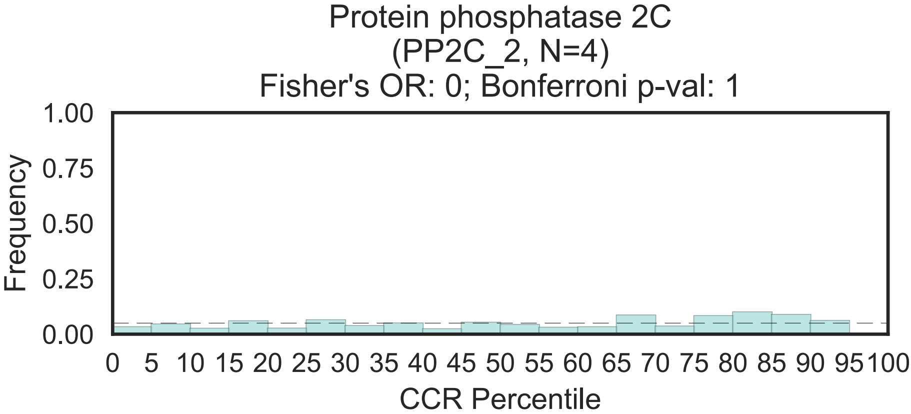

PKC-activated protein phosphatase-1 inhibitor
(PP1_inhibitor, N=5)
Fisher's OR: 1.1; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

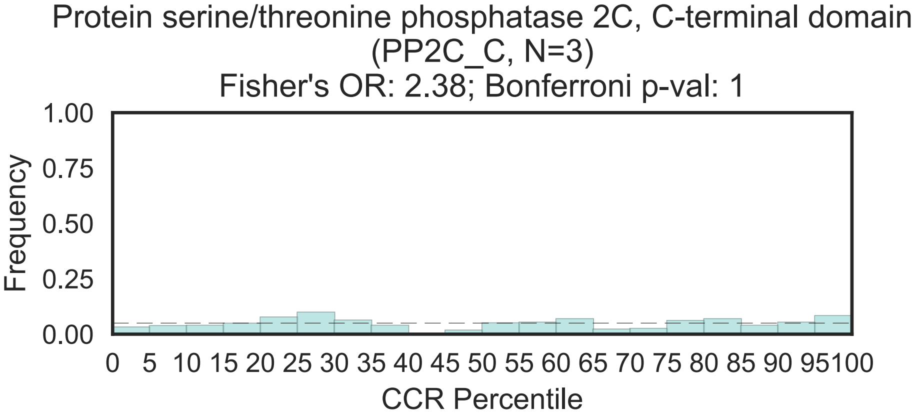

Phosphatase-1 catalytic subunit binding region
(PP1c_bdg, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

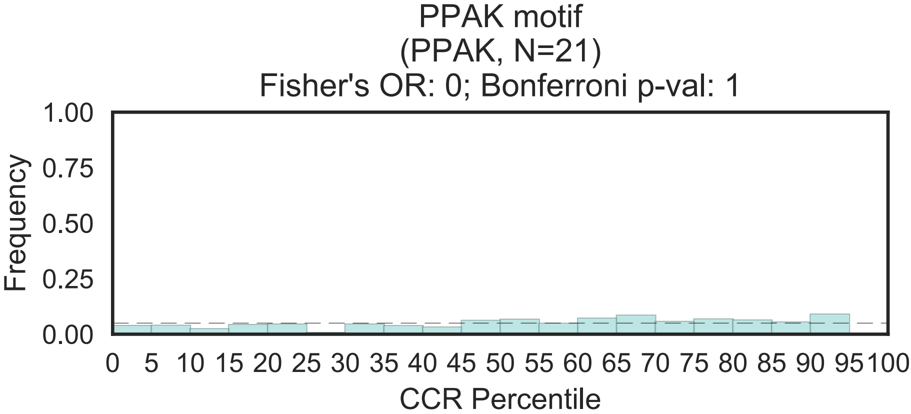

Casein kinase substrate phosphoprotein PP28
(PP28, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

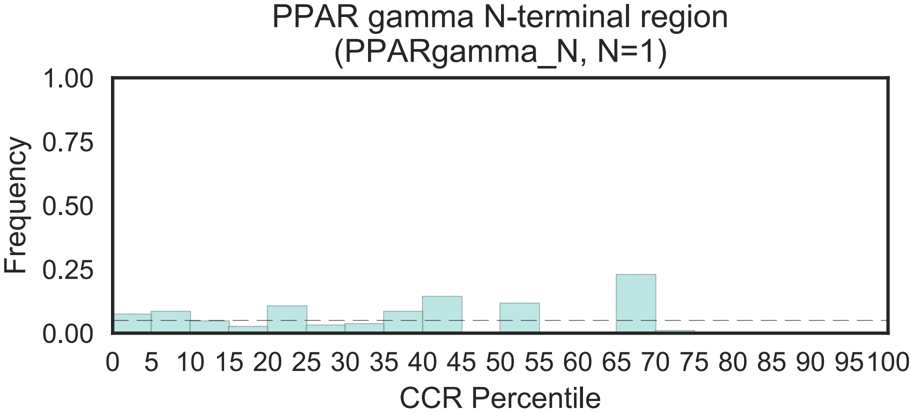
Protein phosphatase 2C
(PP2C, N=24)
Fisher's OR: 2.39; Bonferroni p-val: 0.0627

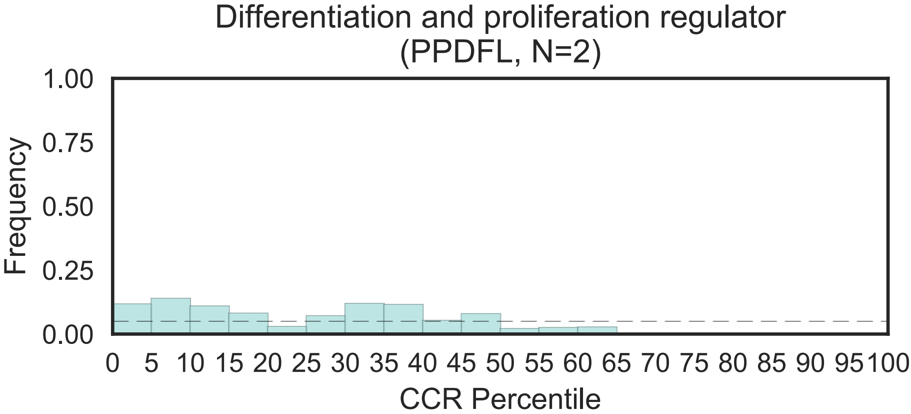


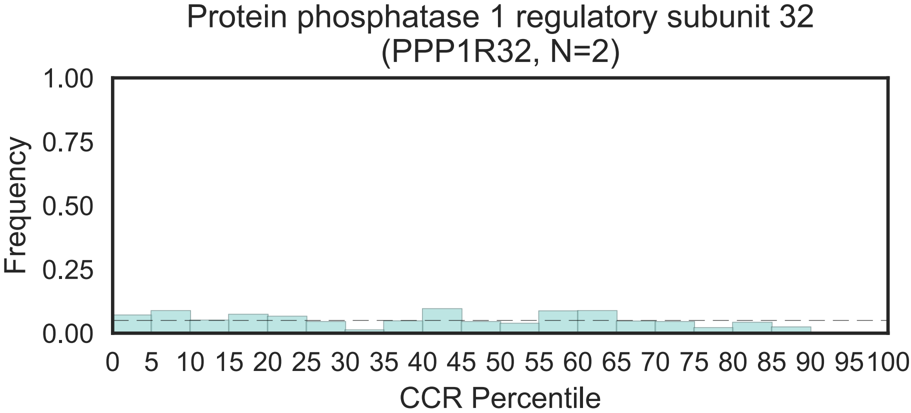

Protein phosphatase 2C
(PP2C_2, N=4)
Fisher's OR: 0; Bonferroni p-val: 1


Protein serine/threonine phosphatase 2C, C-terminal domain
(PP2C_C, N=3)
Fisher's OR: 2.38; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

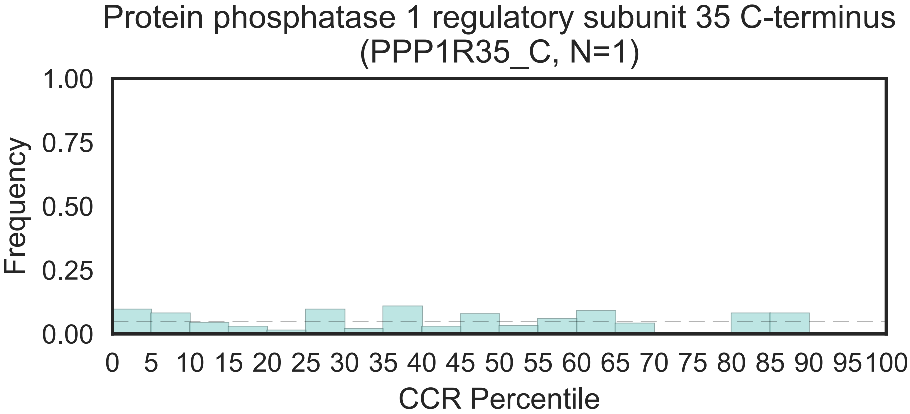

PPAK motif
(PPAK, N=21)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

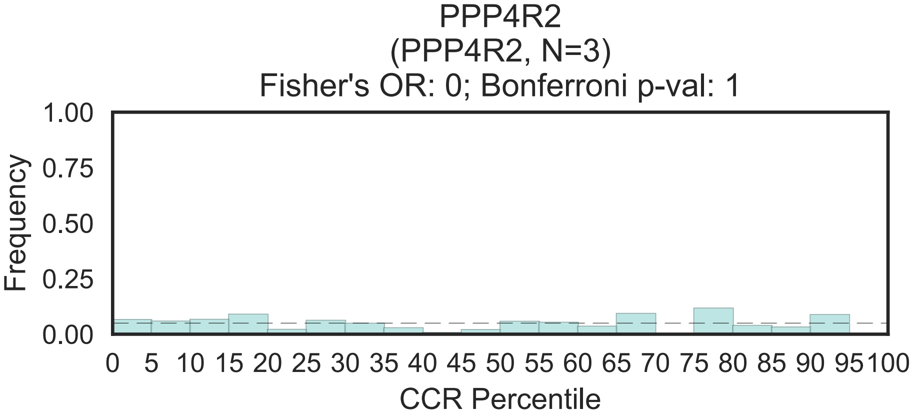

PPAR gamma N-terminal region
(PPARgamma_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

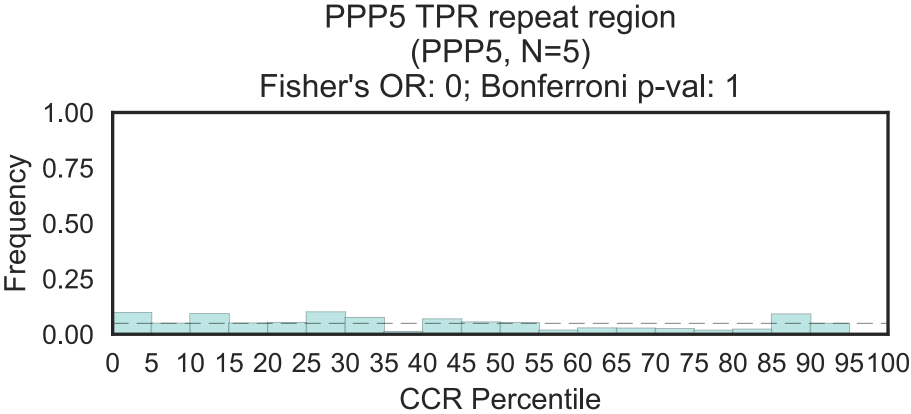

Differentiation and proliferation regulator
(PPDFL, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

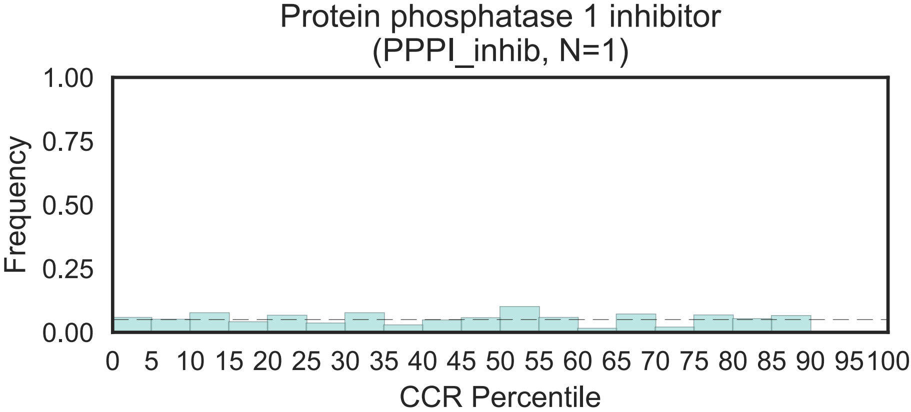


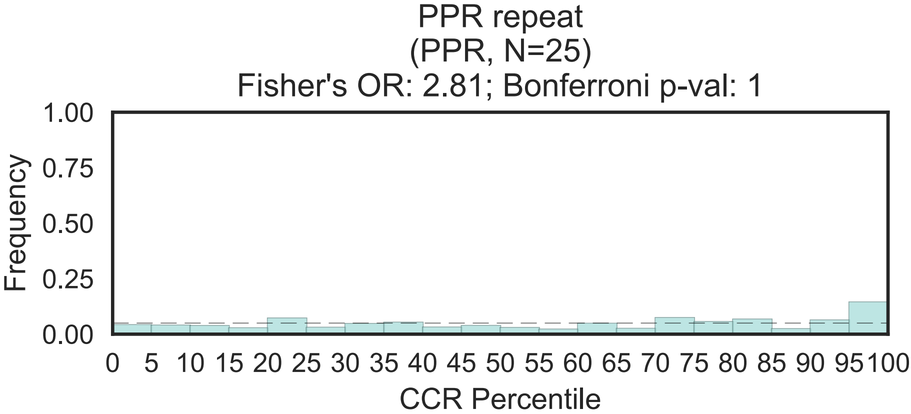
Protein phosphatase 1 regulatory subunit 32
(PPP1R32, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

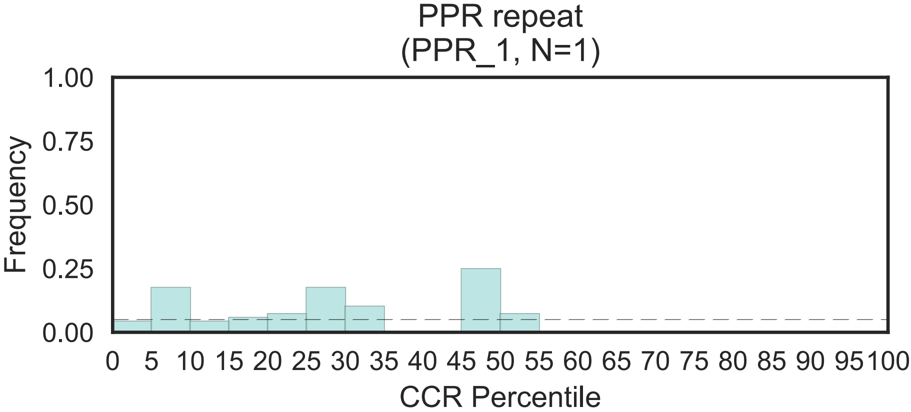

Protein phosphatase 1 regulatory subunit 35 C-terminus
(PPP1R35_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

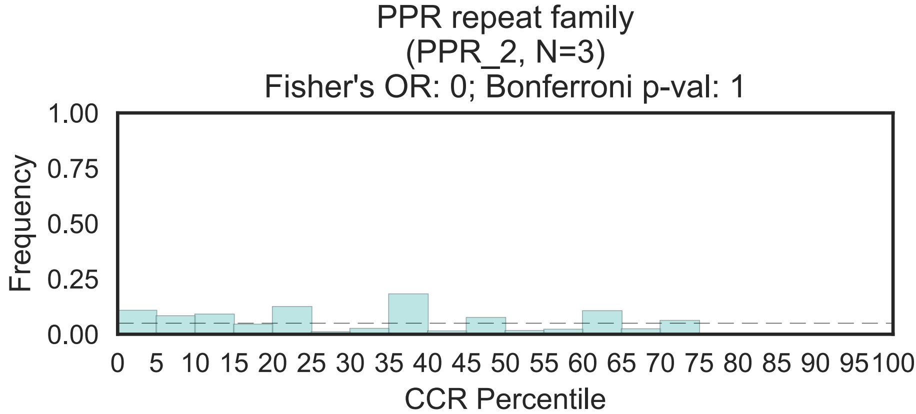

PPP4R2
(PPP4R2, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

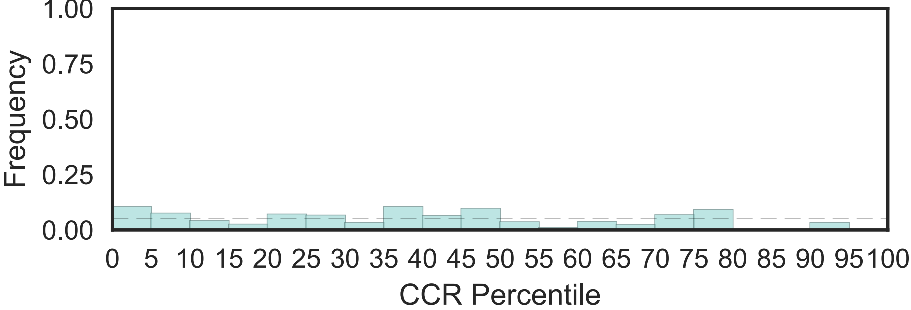

PPP5 TPR repeat region
(PPP5, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

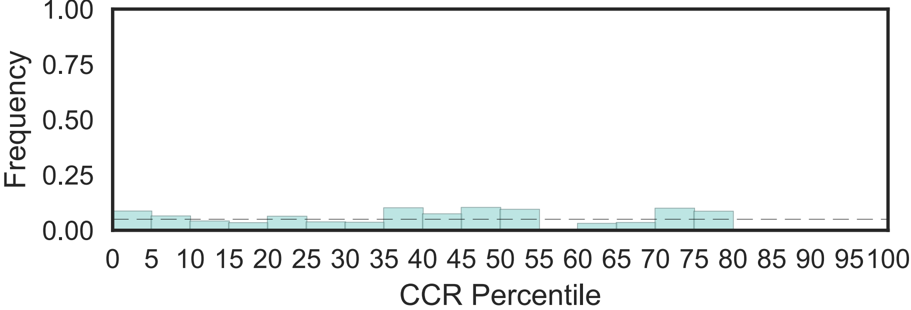

Protein phosphatase 1 inhibitor
(PPPI_inhib, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

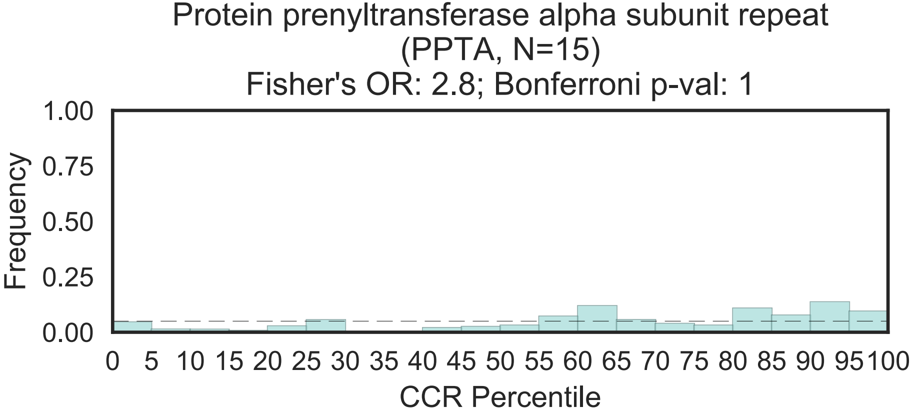

PPR repeat
(PPR, N=25)
Fisher's OR: 2.81; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

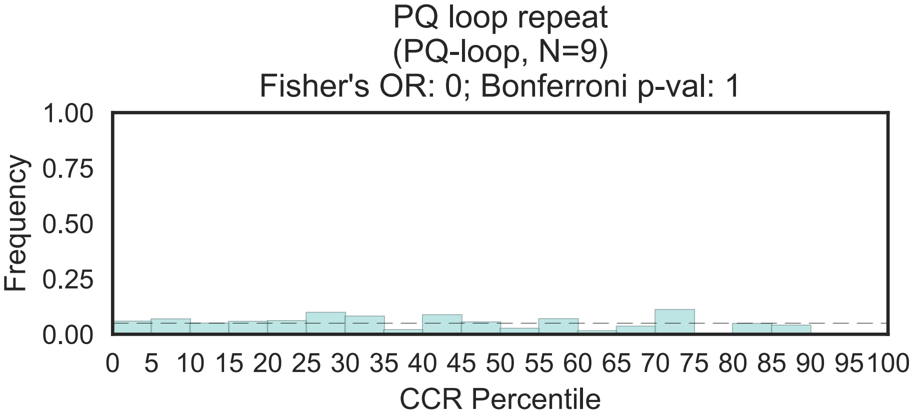

PPR repeat
(PPR_1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

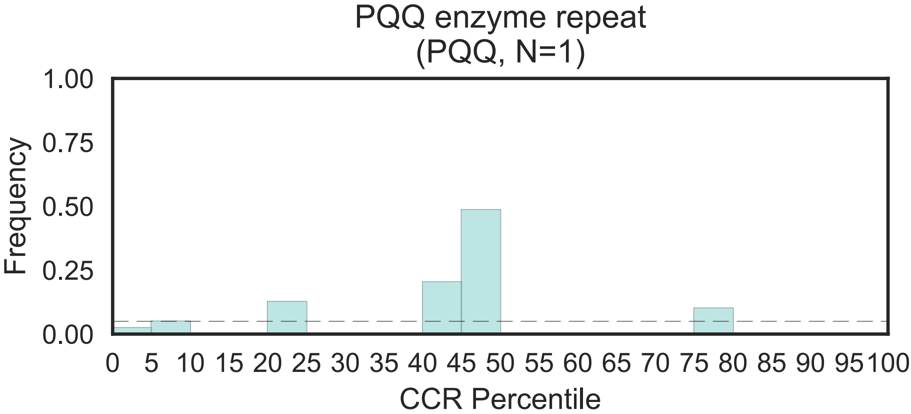

PPR repeat family
(PPR_2, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

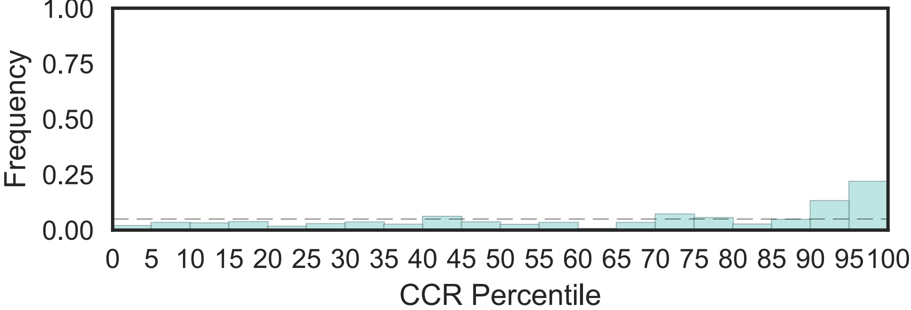

Pentatricopeptide repeat domain
(PPR_3, N=11)
Fisher's OR: 0; Bonferroni p-val: 1

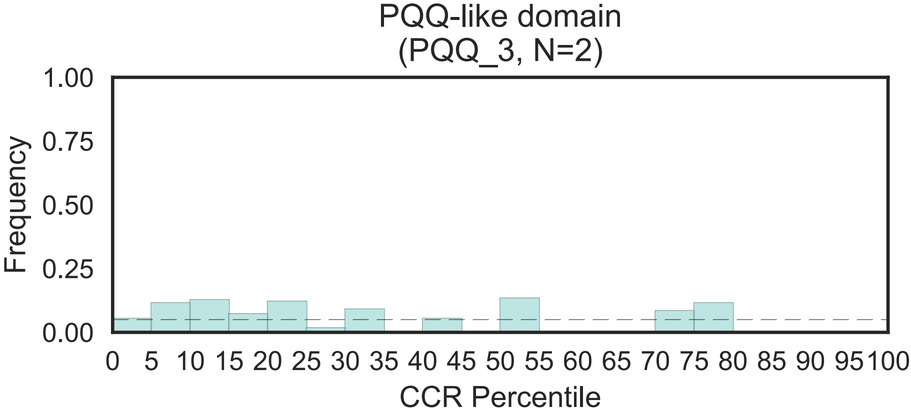

Pentacotripeptide-repeat region of PRORP
(PPR_long, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

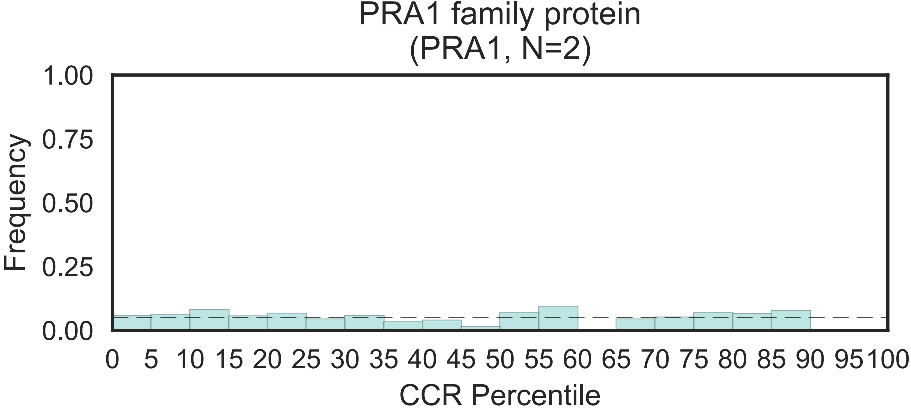

Protein prenyltransferase alpha subunit repeat
(PPTA, N=15)
Fisher's OR: 2.8; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

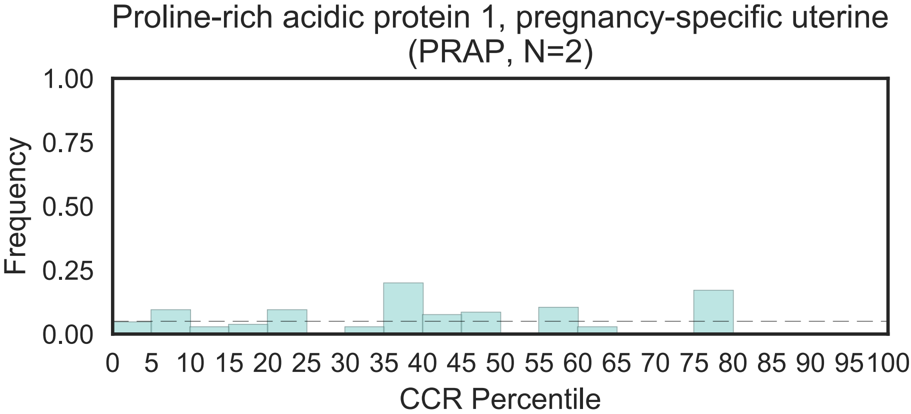

PQ loop repeat
(PQ-loop, N=9)
Fisher's OR: 0; Bonferroni p-val: 1

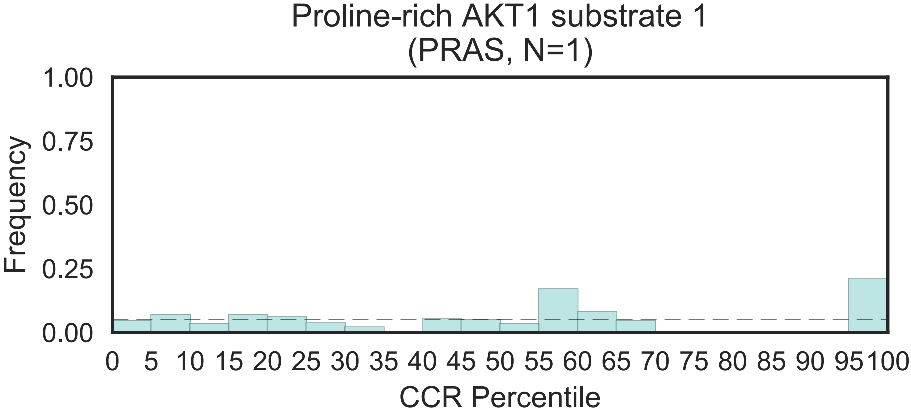

PQQ enzyme repeat
(PQQ, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


PQQ-like domain
(PQQ_2, N=4)
Fisher's OR: 3.79; Bonferroni p-val: 1

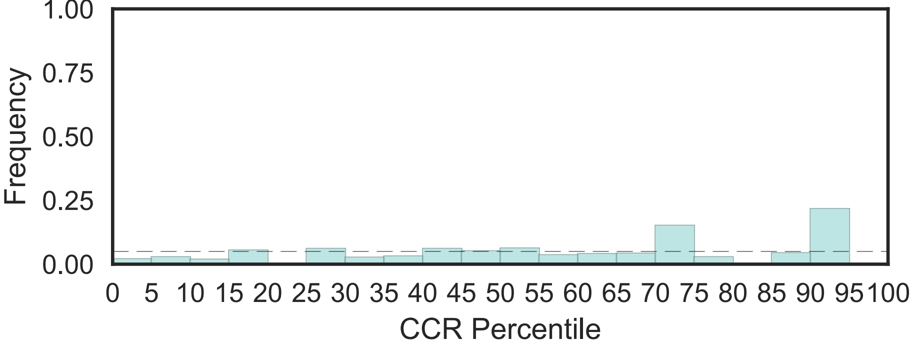

PQQ-like domain
(PQQ_3, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


PRA1 family protein
(PRA1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

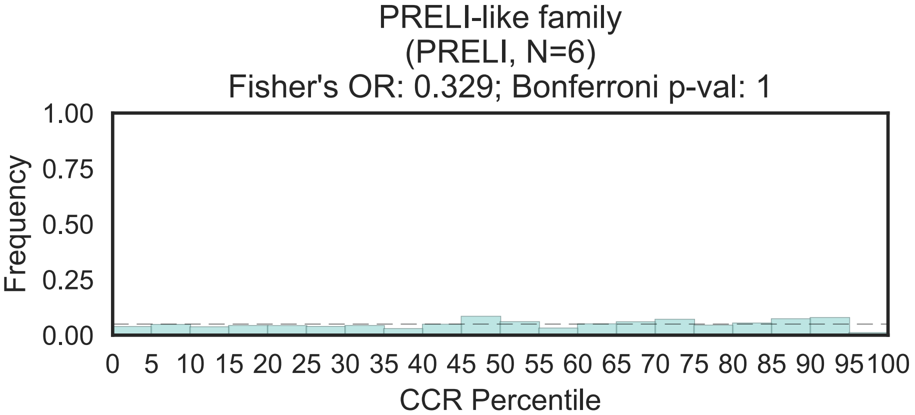

Proline-rich acidic protein 1, pregnancy-specific uterine
(PRAP, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

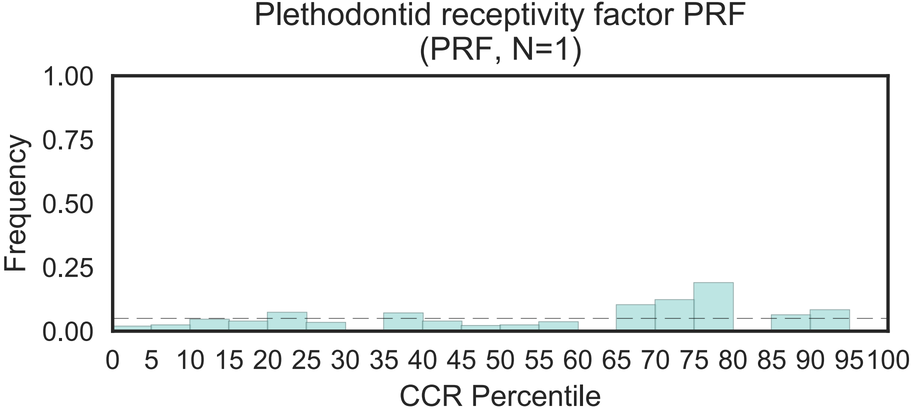


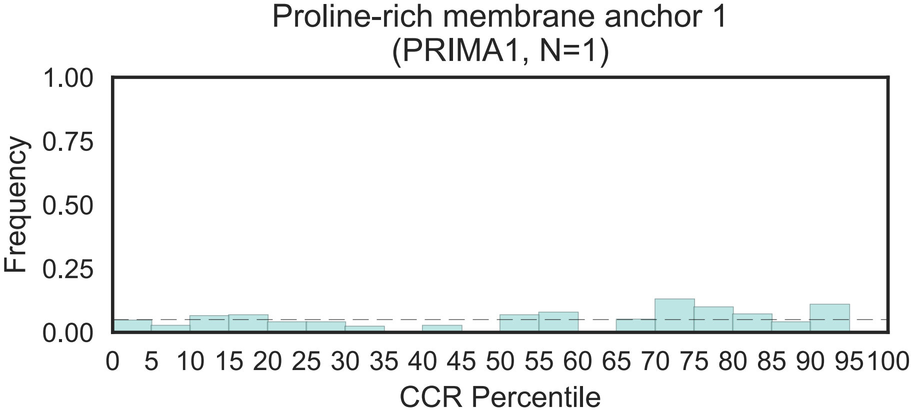
Proline-rich AKT1 substrate 1
(PRAS, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

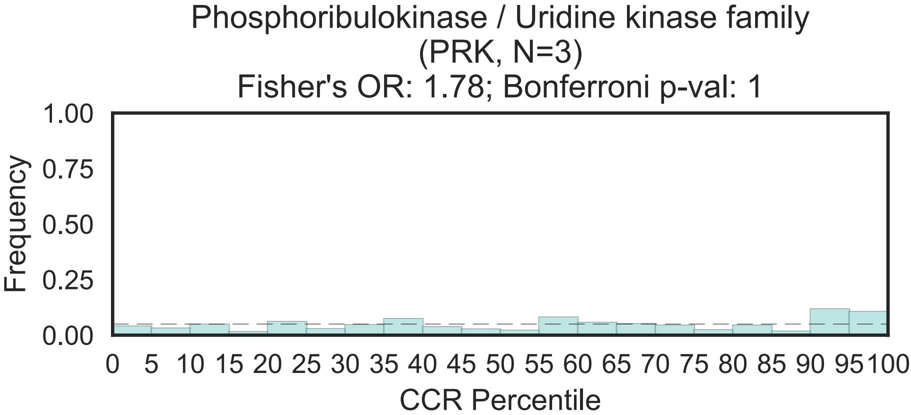


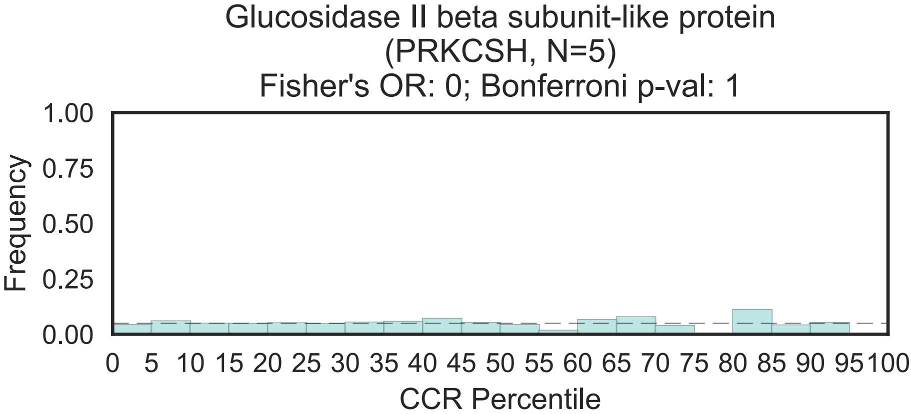
Mitotic checkpoint regulator, MAD2B-interacting
(PRCC, N=1)

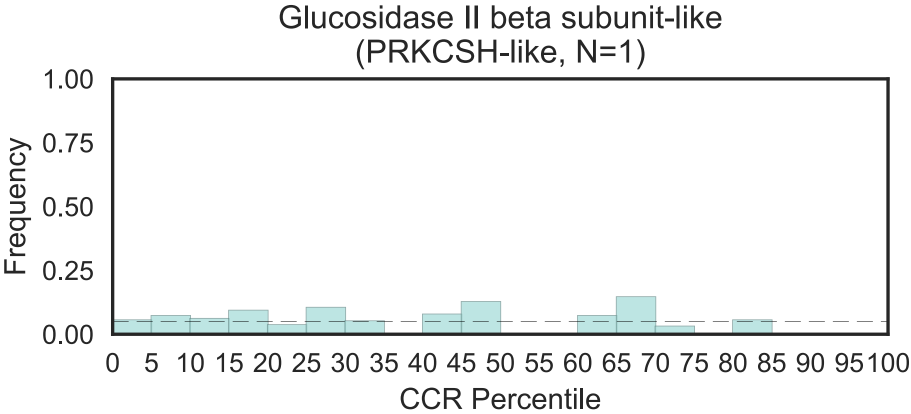

PRELI-like family
(PRELI, N=6)
Fisher's OR: 0.329; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Plethodontid receptivity factor PRF
(PRF, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Proline-rich membrane anchor 1
(PRIMA1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

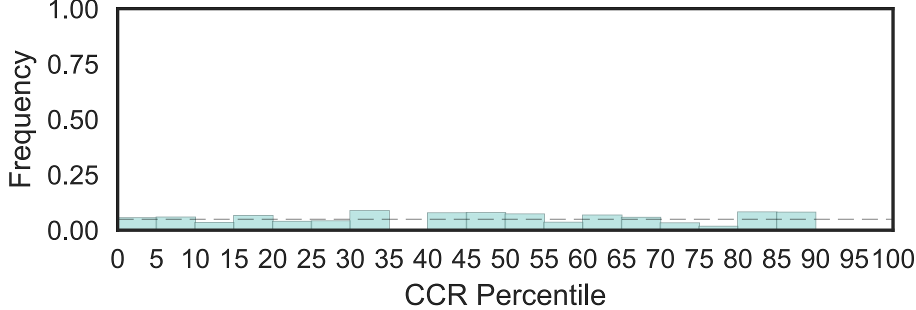

Phosphoribulokinase / Uridine kinase family
(PRK, N=3)
Fisher's OR: 1.78; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

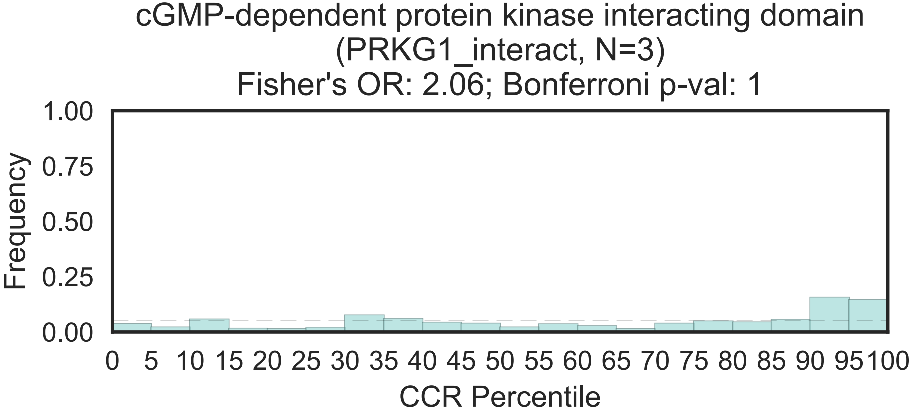

Glucosidase II beta subunit-like protein
(PRKCSH, N=5)
Fisher's OR: 0; Bonferroni p-val: 1

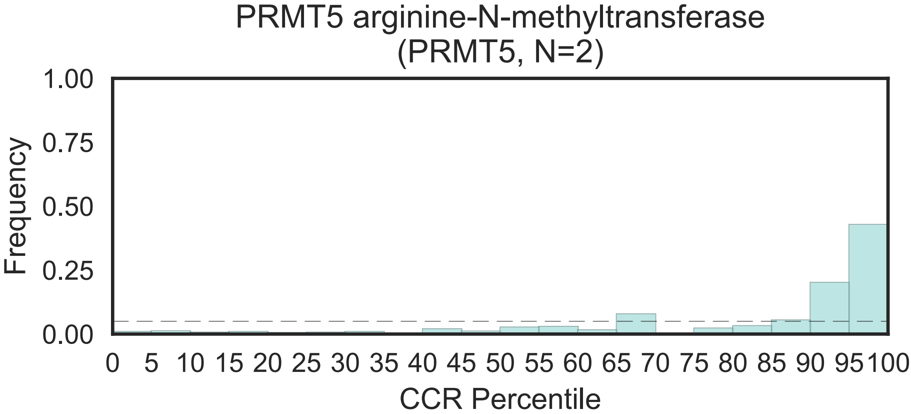


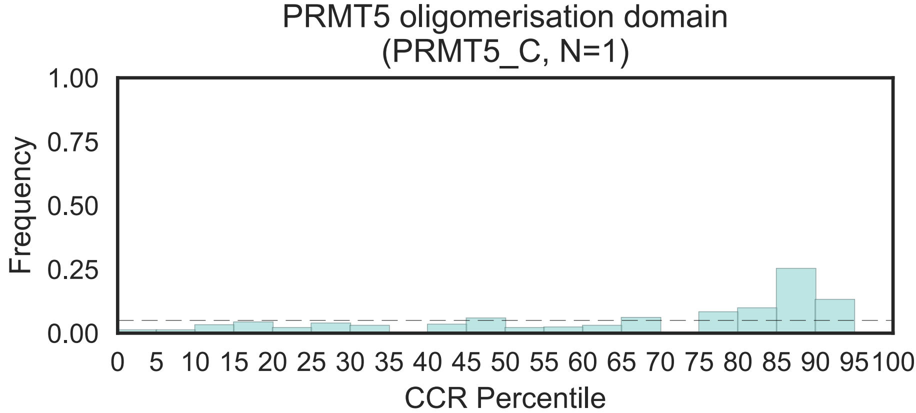
Glucosidase II beta subunit-like
(PRKCSH-like, N=1)

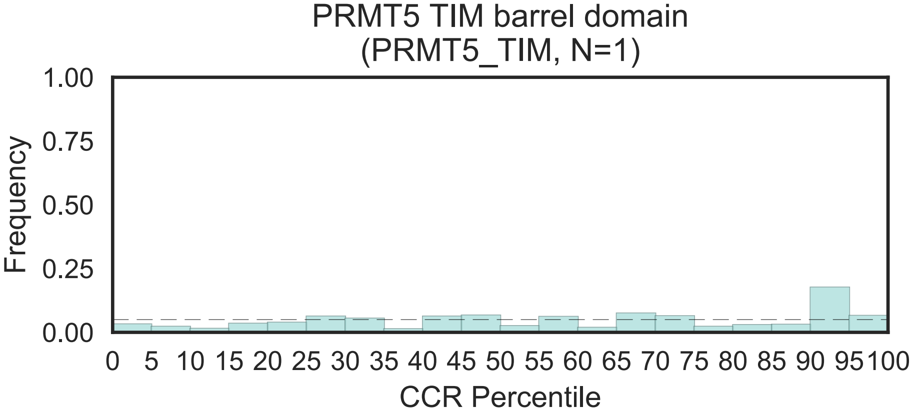
Glucosidase II beta subunit-like protein (PRKCSH_1, N=3) Fisher's OR: 0; Bonferroni p-val: 1

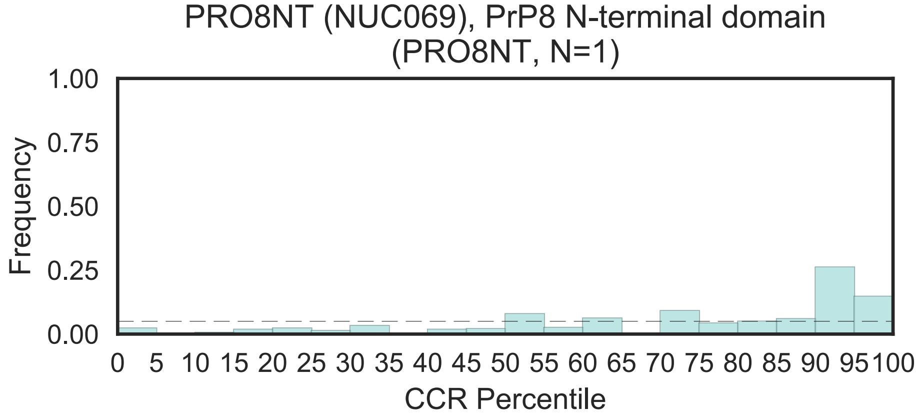


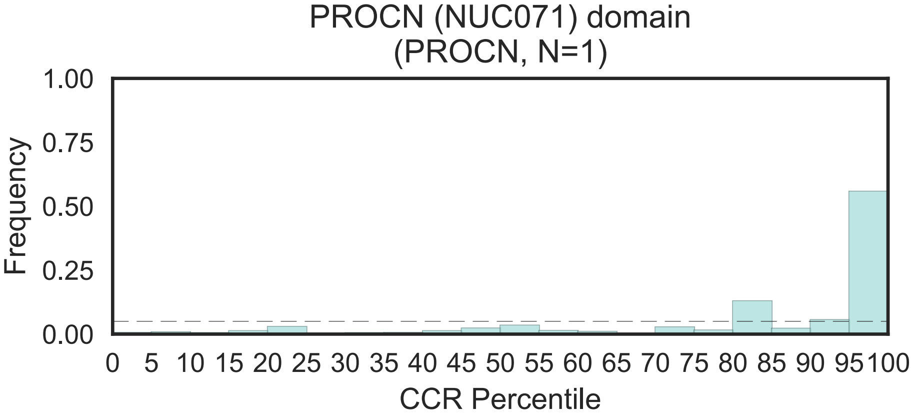

cGMP-dependent protein kinase interacting domain
(PRKG1_interact, N=3)
Fisher's OR: 2.06; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

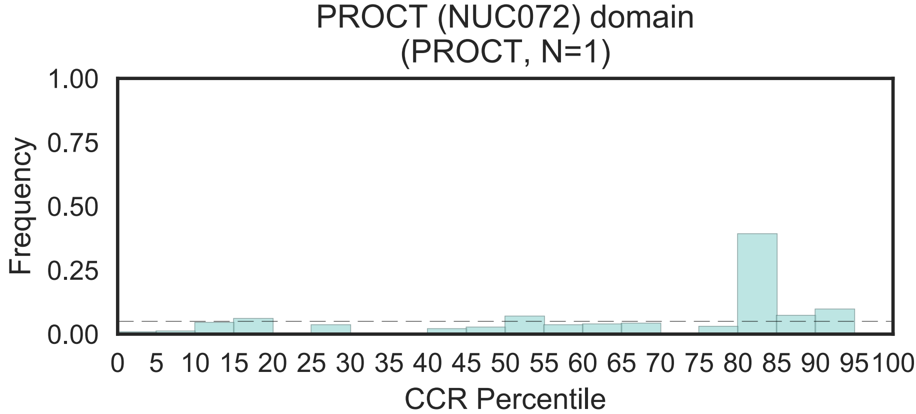

PRMT5 arginine-N-methyltransferase
(PRMT5, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

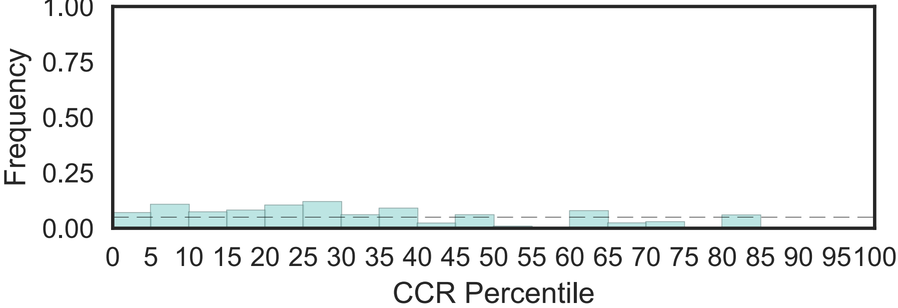

PRMT5 oligomerisation domain
(PRMT5_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


PRMT5 TIM barrel domain
(PRMT5_TIM, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

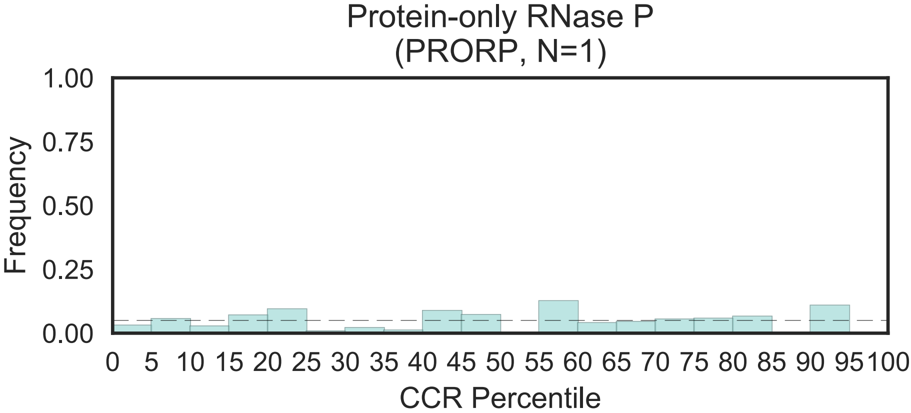

PRO8NT (NUC069), PrP8 N-terminal domain
(PRO8NT, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

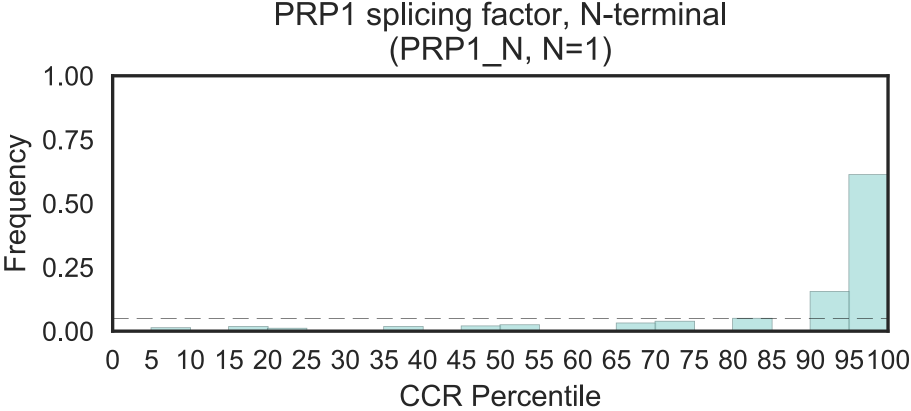

PROCN (NUC071) domain
(PROCN, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

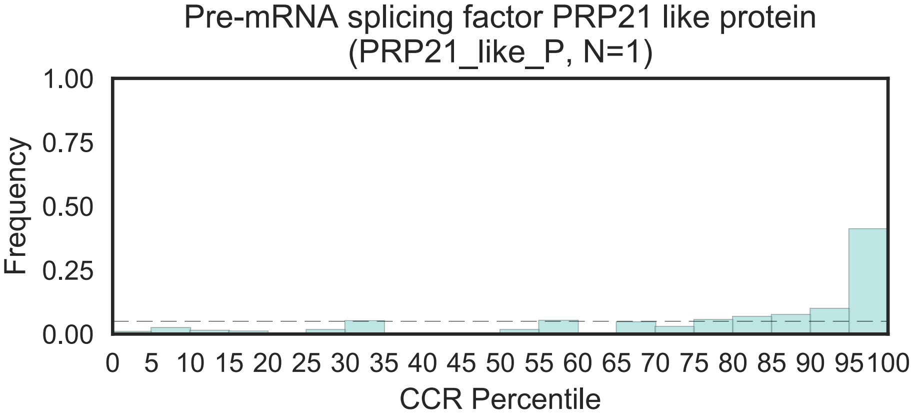

PROCT (NUC072) domain
(PROCT, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



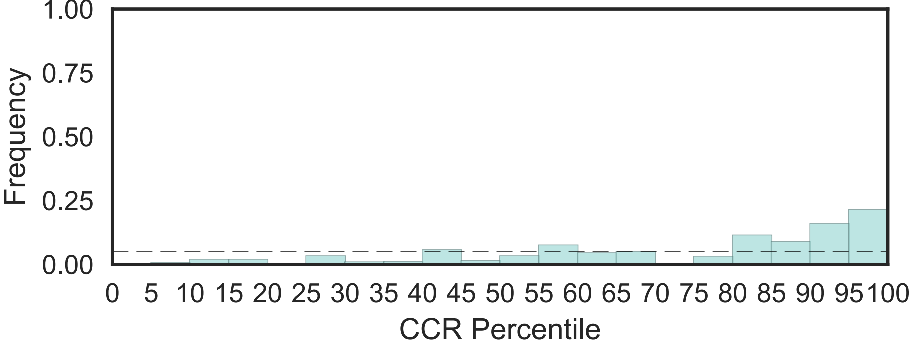
Proline-rich submaxillary gland androgen-regulated family
(PROL5-SMR, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

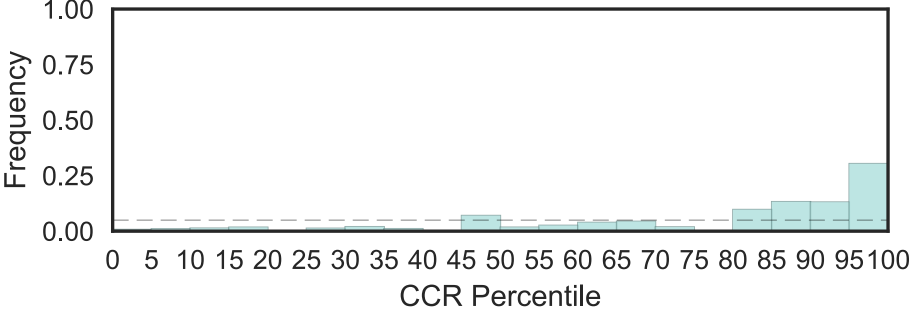

Protein-only RNase P
(PRORP, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

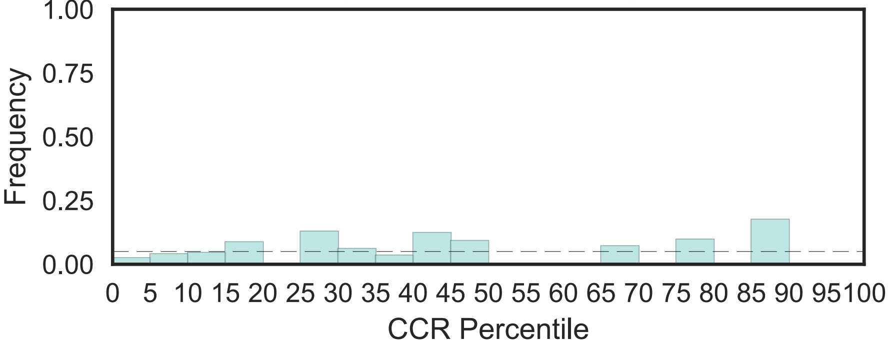

PRP1 splicing factor, N-terminal
(PRP1_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Pre-mRNA splicing factor PRP21 like protein
(PRP21_like_P, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

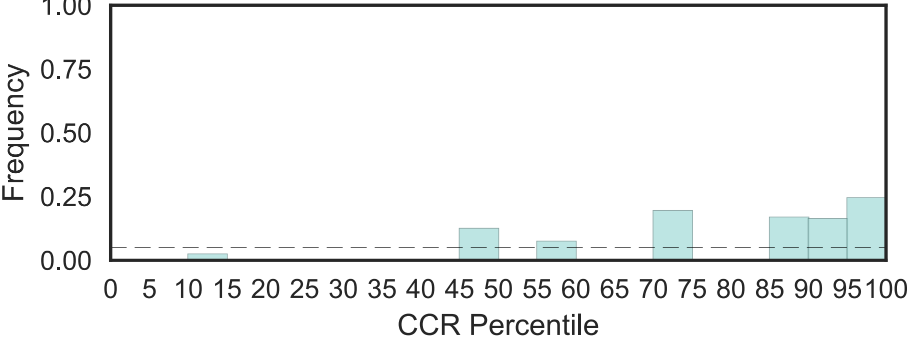
pre-mRNA processing factor 3 (PRP3)
(PRP3, N=1)

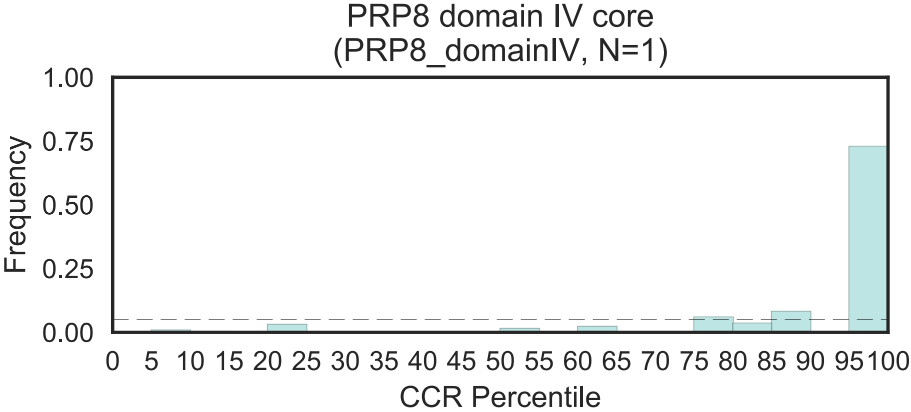


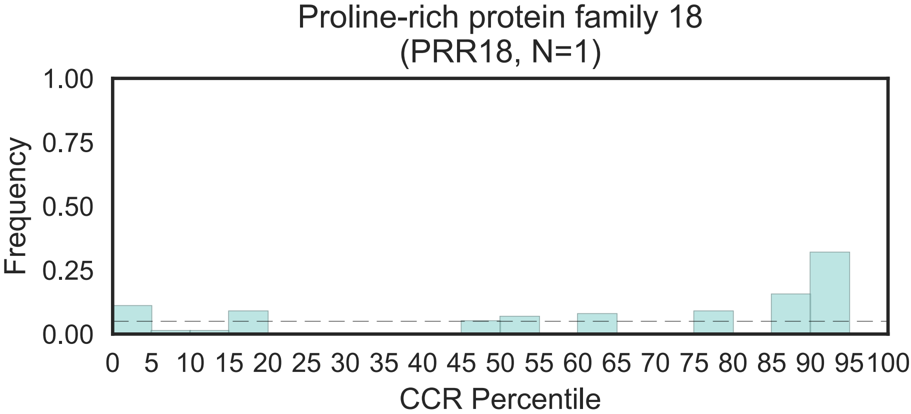

PRP38 family
(PRP38, N=3)
Fisher's OR: 13.5; Bonferroni p-val: 0.0116

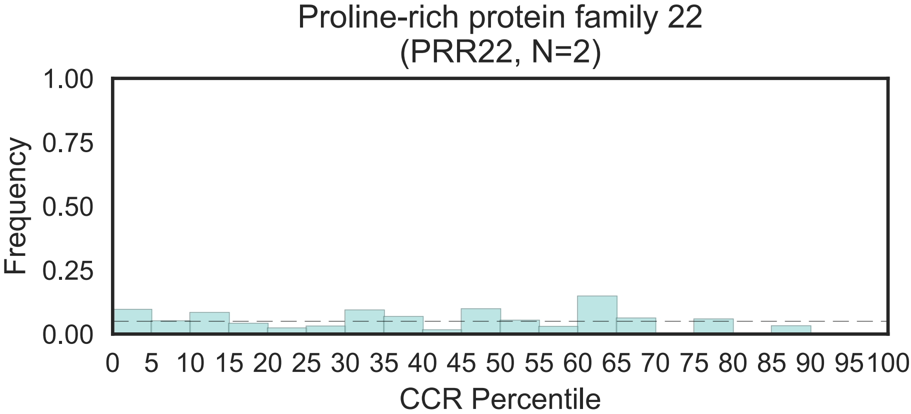

Pre-mRNA-splicing factor 38-associated hydrophilic C-term (PRP38_assoc, N=1)

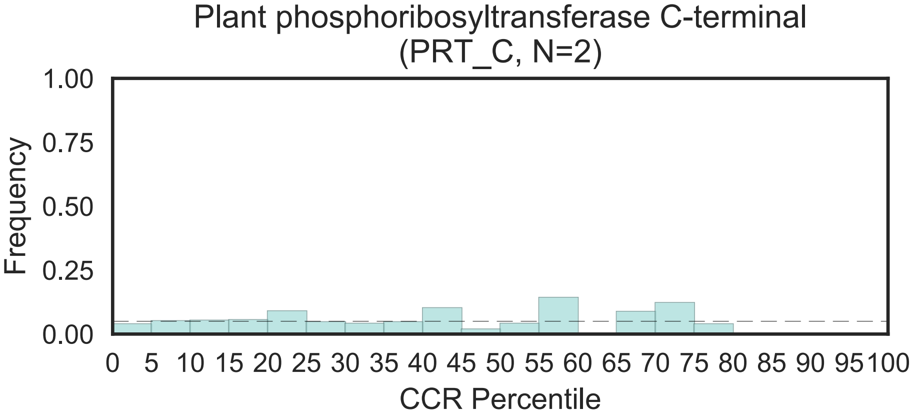
pre-mRNA processing factor 4 (PRP4) like
(PRP4, N=2)

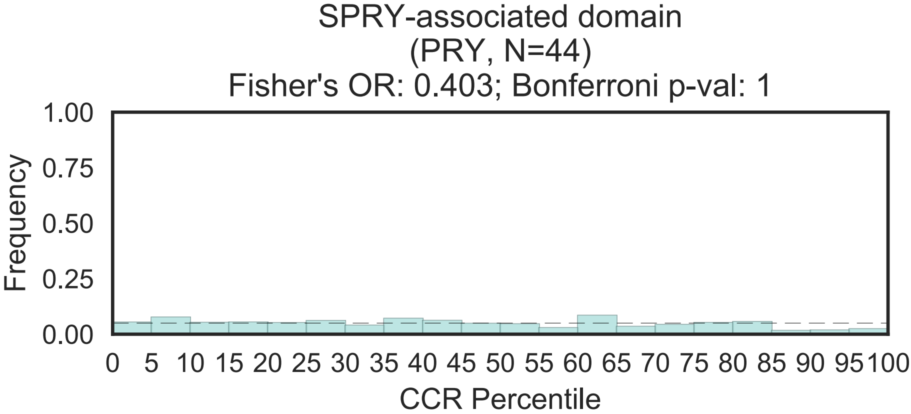


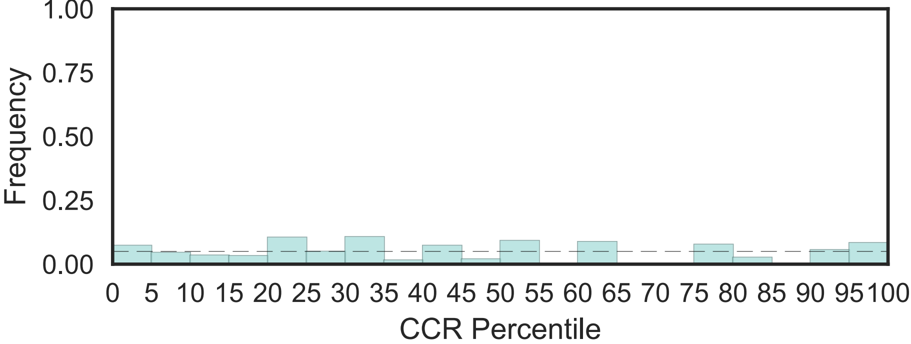

PRP8 domain IV core
(PRP8_domainIV, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Proline-rich protein family 18
(PRR18, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

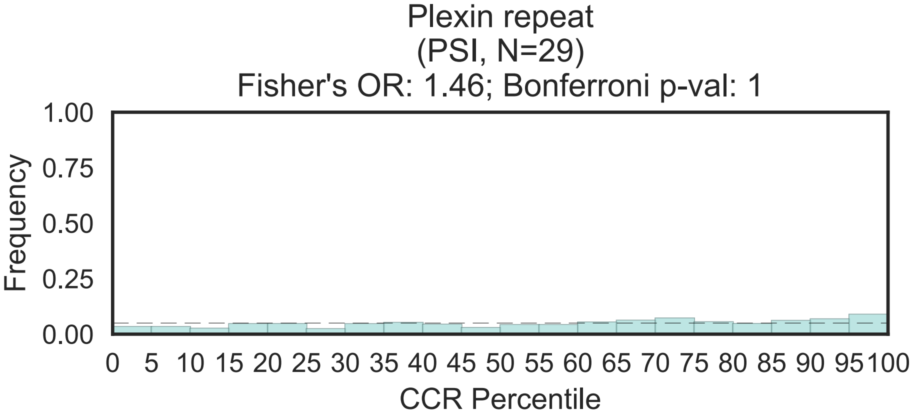

Proline-rich protein family 22
(PRR22, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

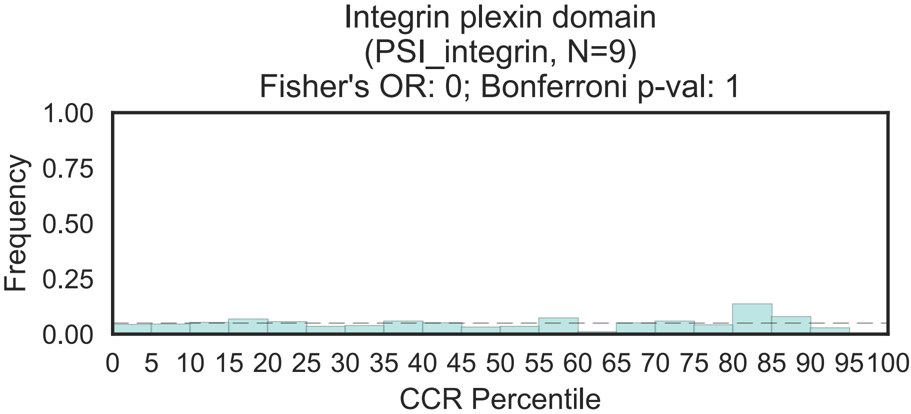

Plant phosphoribosyltransferase C-terminal
(PRT_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

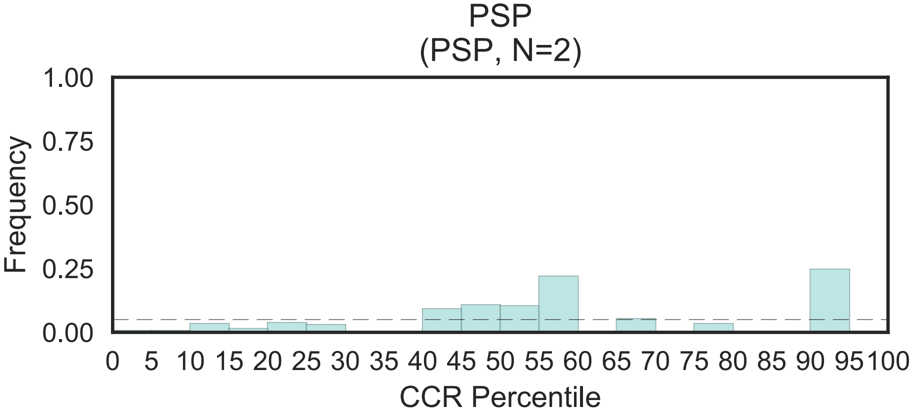

SPRY-associated domain
(PRY, N=44)
Fisher's OR: 0.403; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

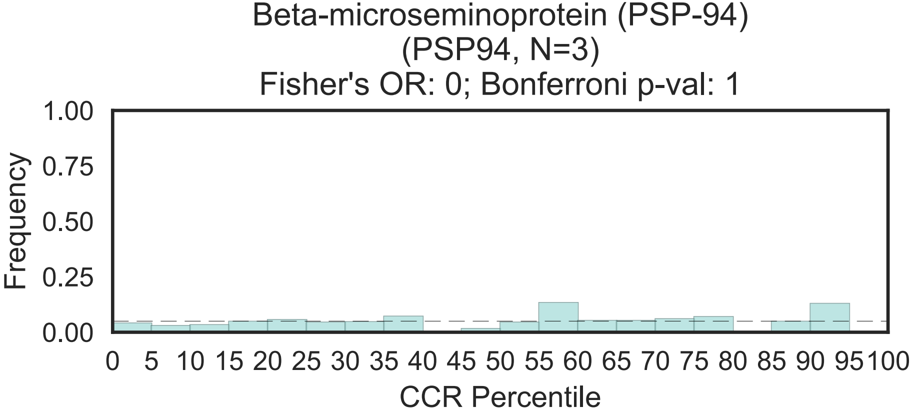


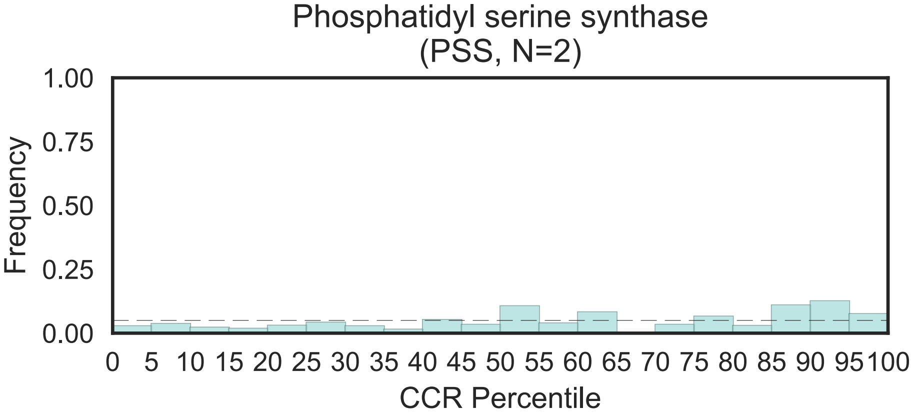
Polyketide synthase dehydratase
(PS-DH, N=1)

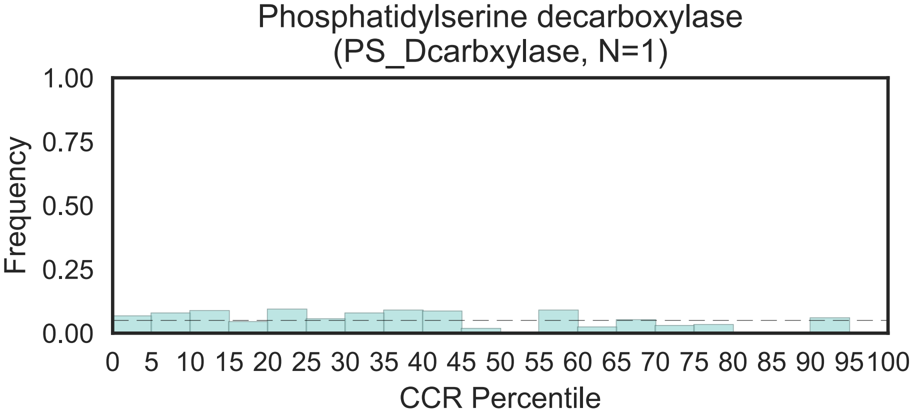

Plexin repeat
(PSI, N=29)
Fisher's OR: 1.46; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

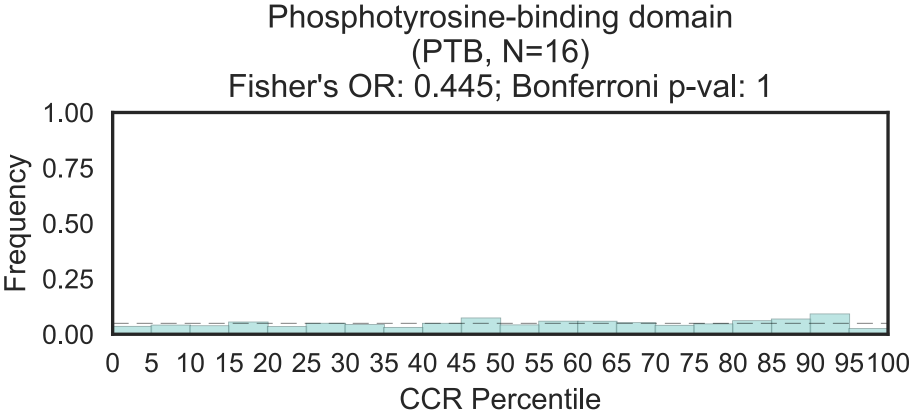

Integrin plexin domain
(PSI_integrin, N=9)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

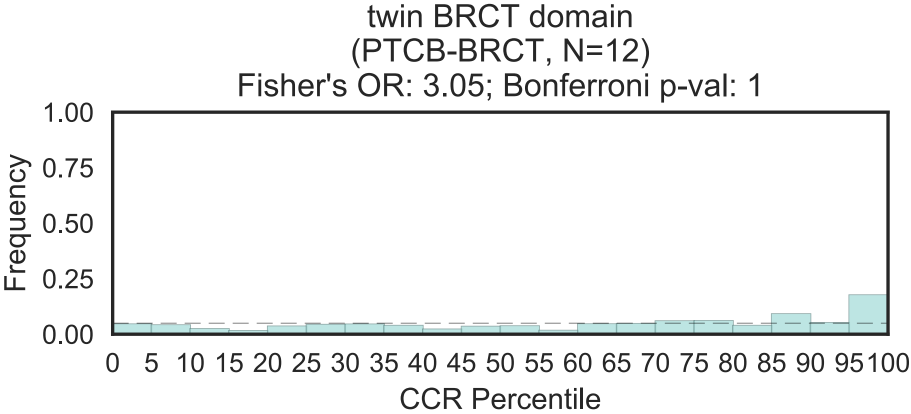

PSP
(PSP, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Beta-microseminoprotein (PSP-94)
(PSP94, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

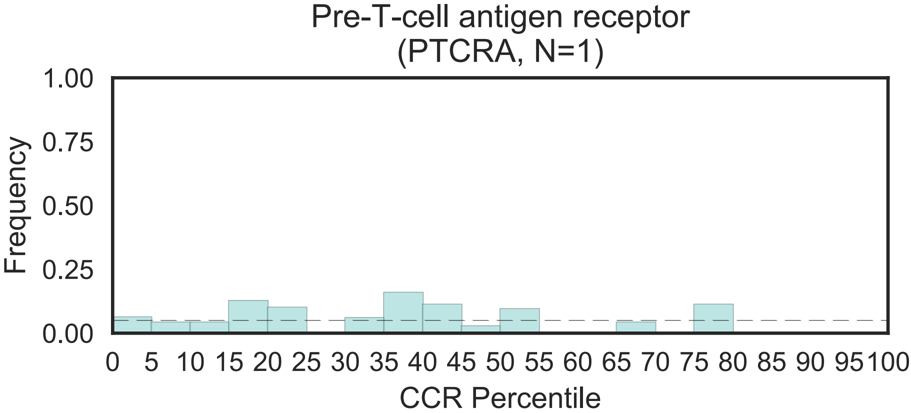

Phosphatidyl serine synthase
(PSS, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

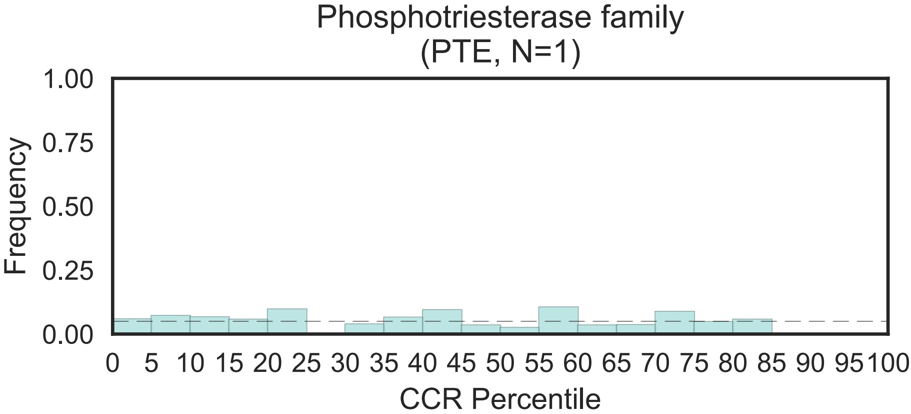

Phosphatidylserine decarboxylase
(PS_Dcarbxylase, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Phosphotyrosine-binding domain
(PTB, N=16)
Fisher's OR: 0.445; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

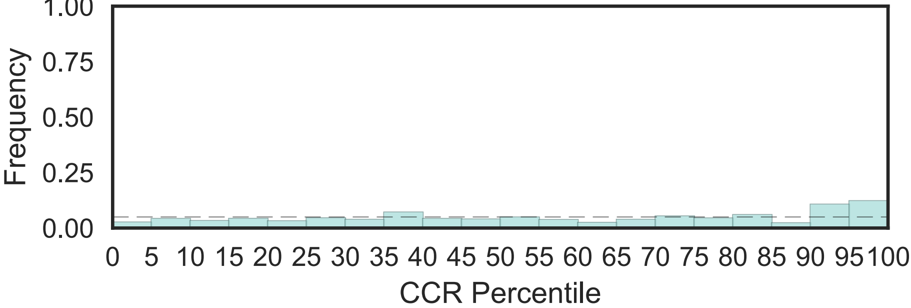


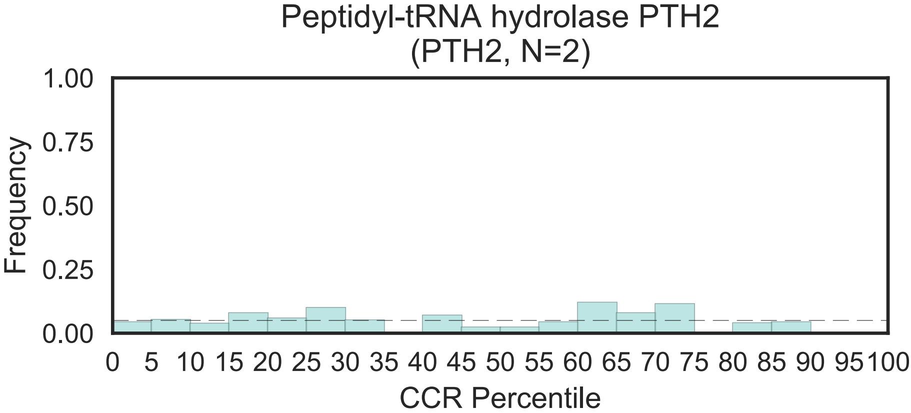
twin BRCT domain
(PTCB-BRCT, N=12)
Fisher's OR: 3.05; Bonferroni p-val: 1

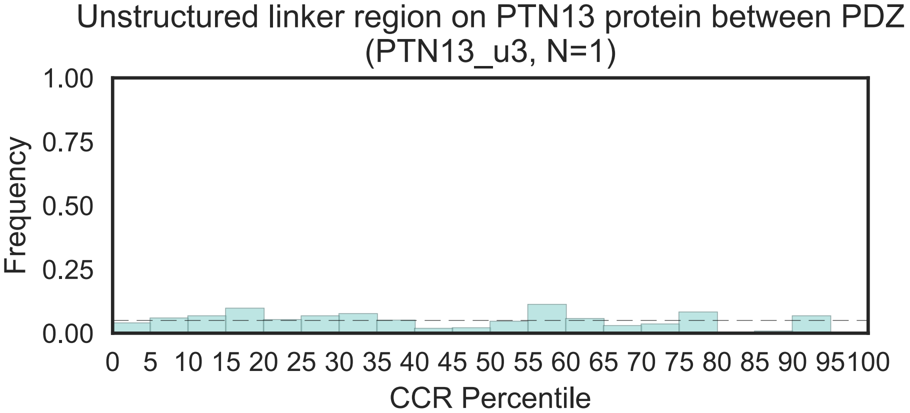

Pre-T-cell antigen receptor
(PTCRA, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

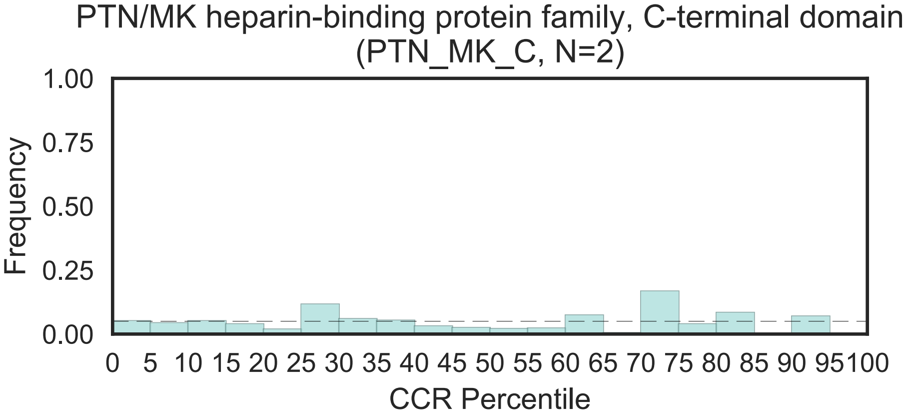

Phosphotriesterase family
(PTE, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

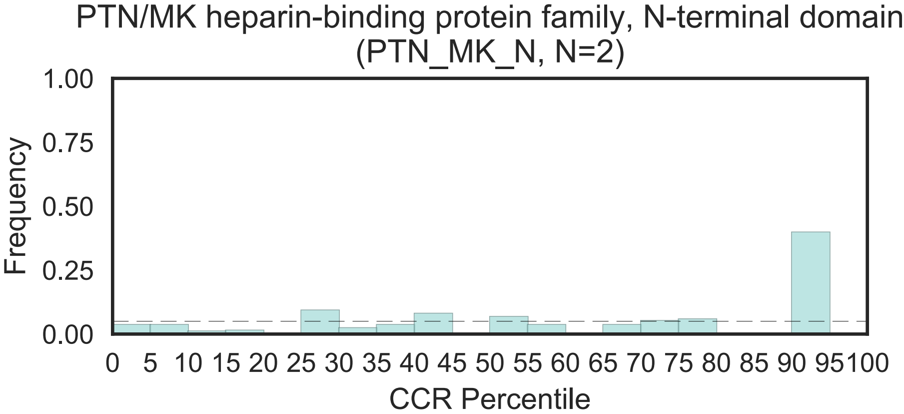
C2 domain of PTEN tumour-suppressor protein
(PTEN_C2, N=8)
Fisher's OR: 2.41; Bonferroni p-val: 1

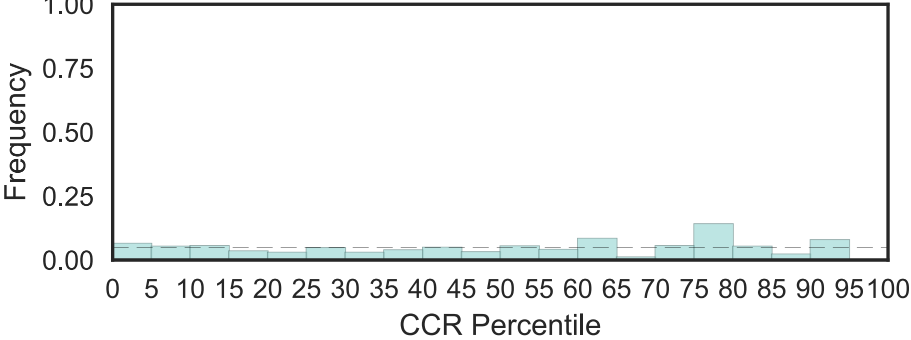



Peptidyl-tRNA hydrolase PTH2
(PTH2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

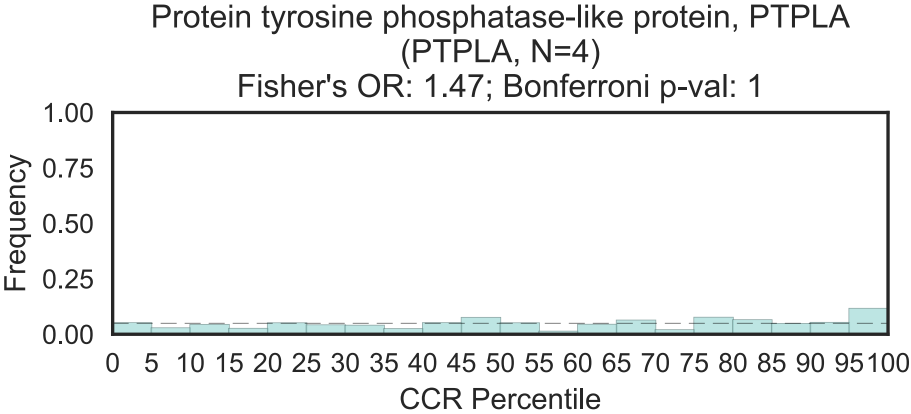

Unstructured linker region on PTN13 protein between PDZ
(PTN13_u3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


PTN/MK heparin-binding protein family, C-terminal domain
(PTN_MK_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

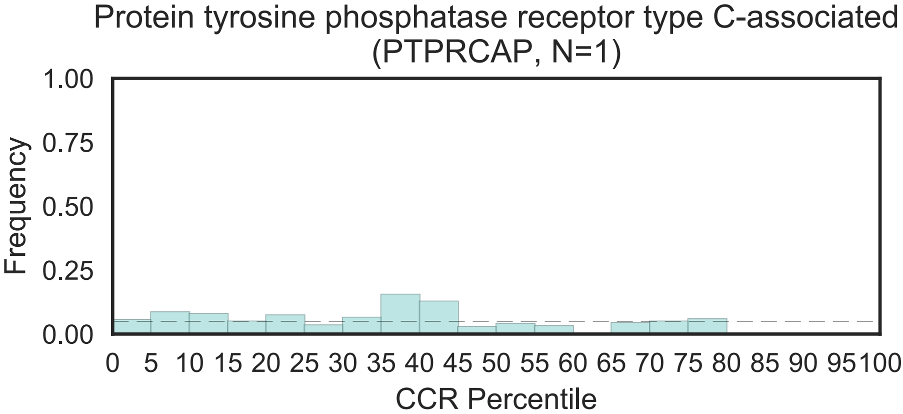
PTN/MK heparin-binding protein family, N-terminal domain
(PTN_MK_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

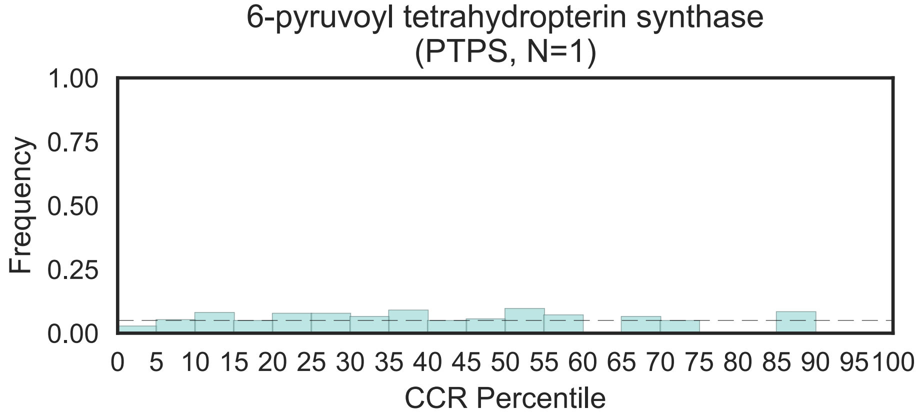


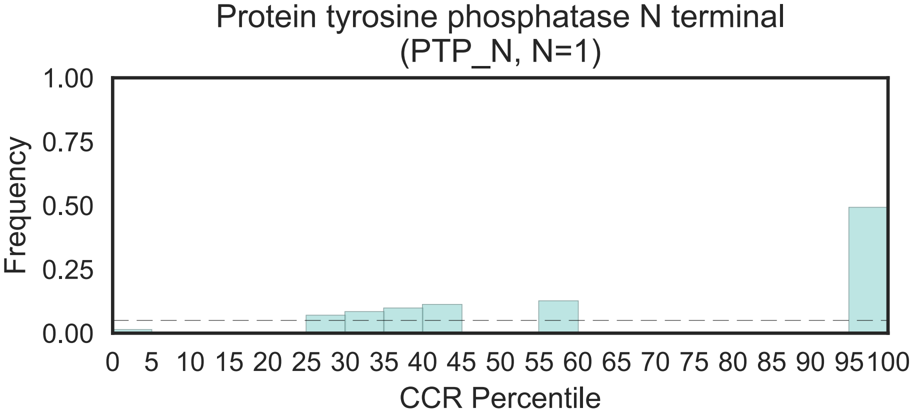
Phosphotyrosyl phosphate activator (PTPA) protein
(PTPA, N=1)

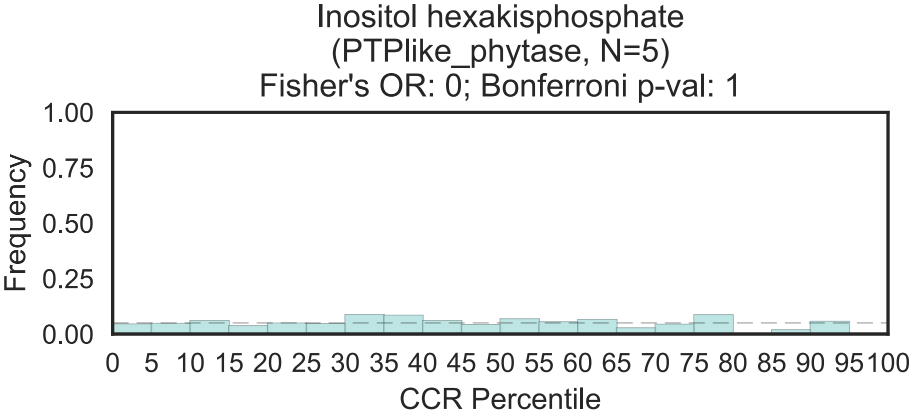


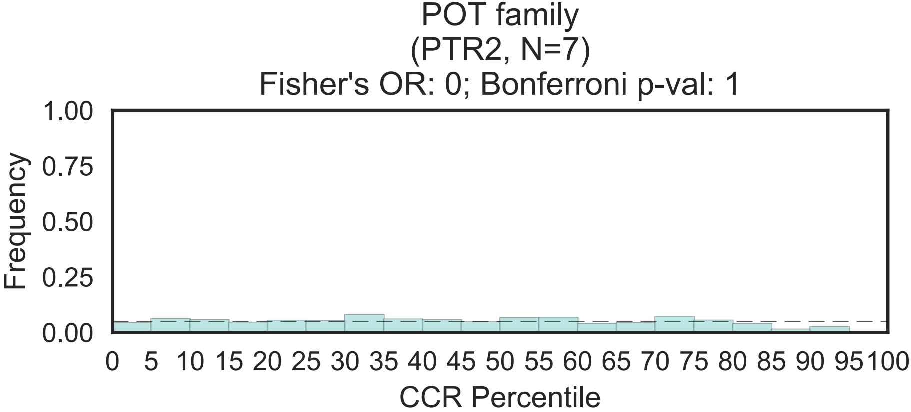
Protein tyrosine phosphatase-like protein, PTPLA
(PTPLA, N=4)
Fisher's OR: 1.47; Bonferroni p-val: 1

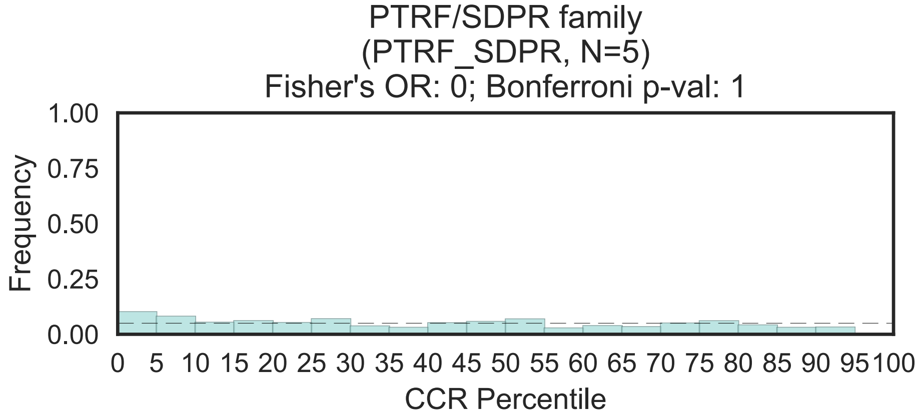

Protein tyrosine phosphatase receptor type C-associated (PTPRCAP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

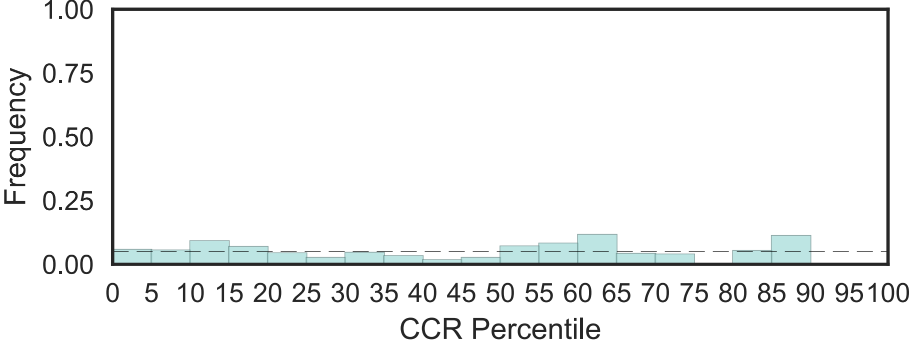

6-pyruvoyl tetrahydropterin synthase
(PTPS, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

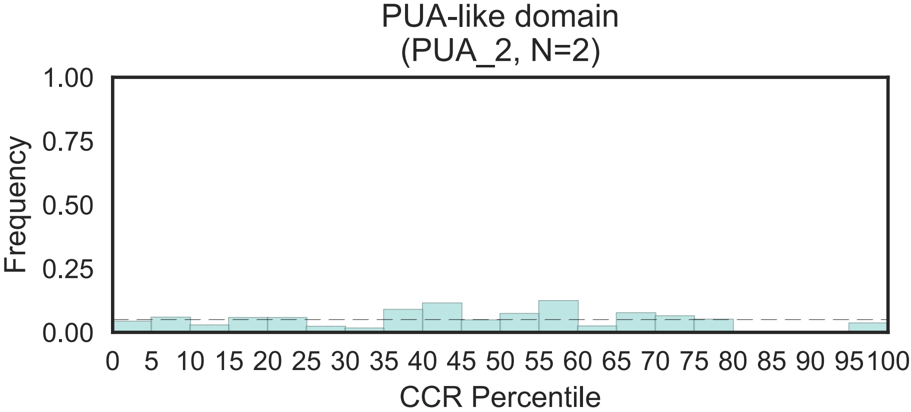

Protein tyrosine phosphatase N terminal
(PTP_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

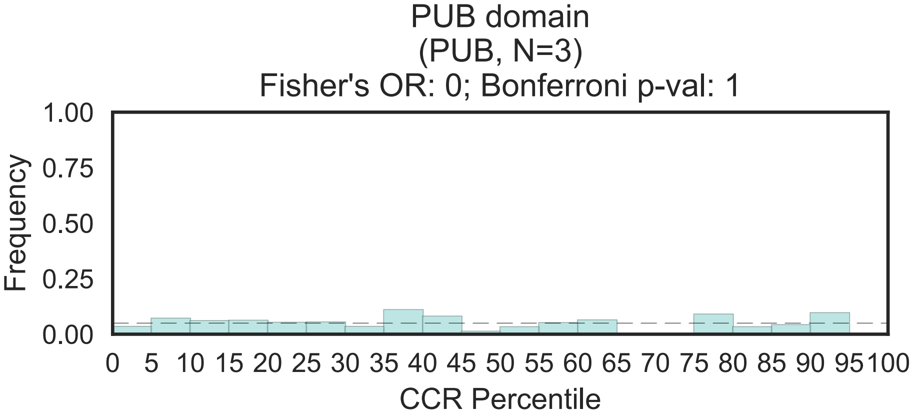

Inositol hexakisphosphate
(PTPlike_phytase, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

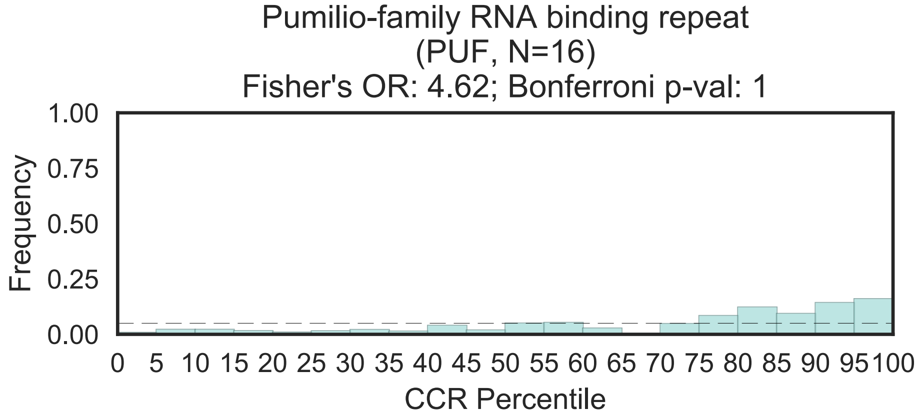

POT family
(PTR2, N=7)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

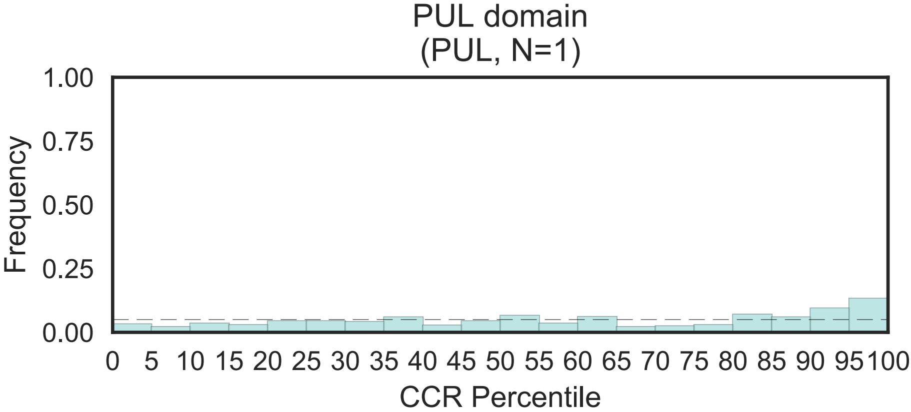

PTRF/SDPR family
(PTRF_SDPR, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

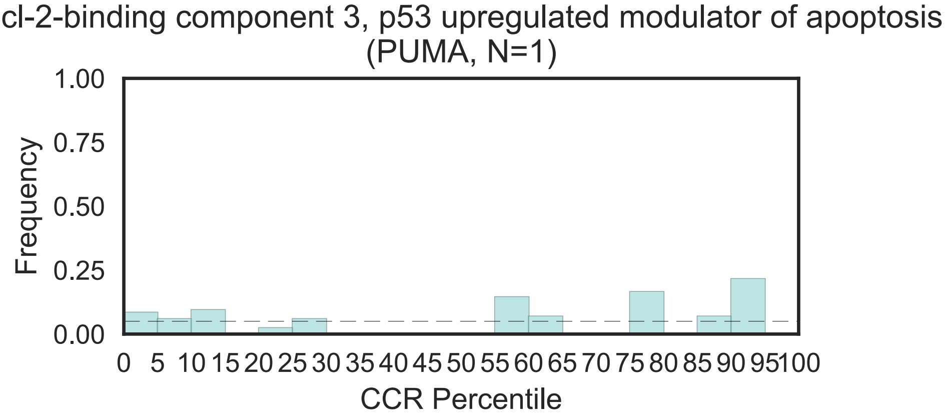

RNA 2'-phosphotransferase, Tpt1 / KptA family (PTS_2-RNA, N=1)

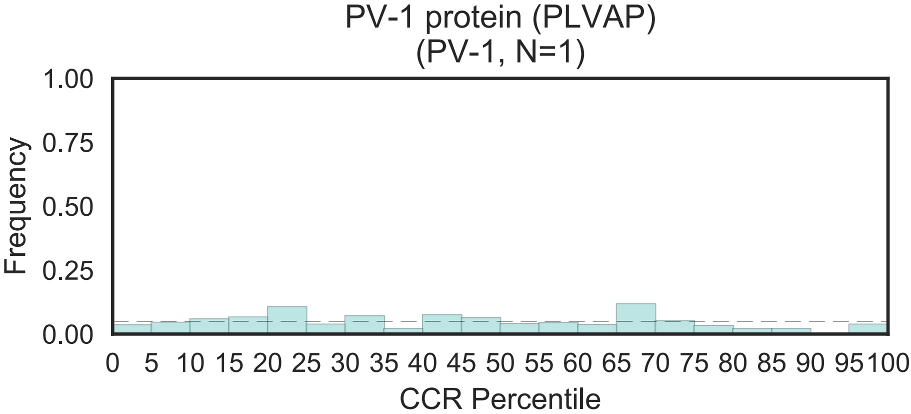

PUA-like domain
(PUA_2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


PUB domain
(PUB, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Pumilio-family RNA binding repeat
(PUF, N=16)
Fisher's OR: 4.62; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

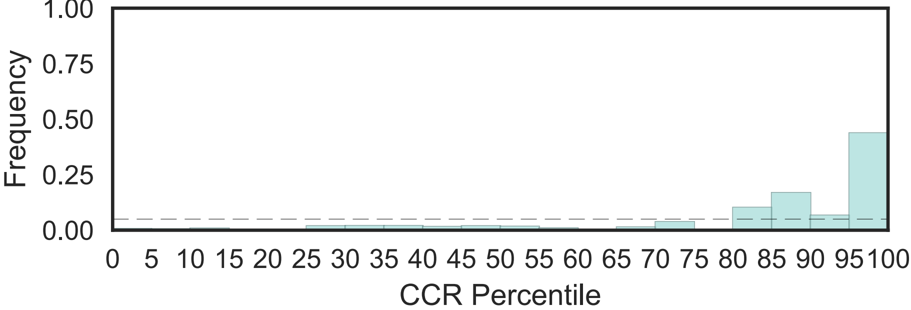

PUL domain
(PUL, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

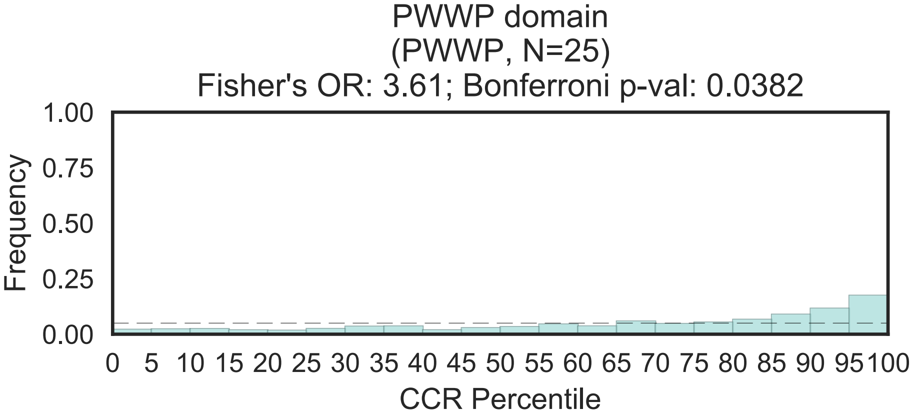

Bcl-2-binding component 3, p53 upregulated modulator of apoptosis
(PUMA, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

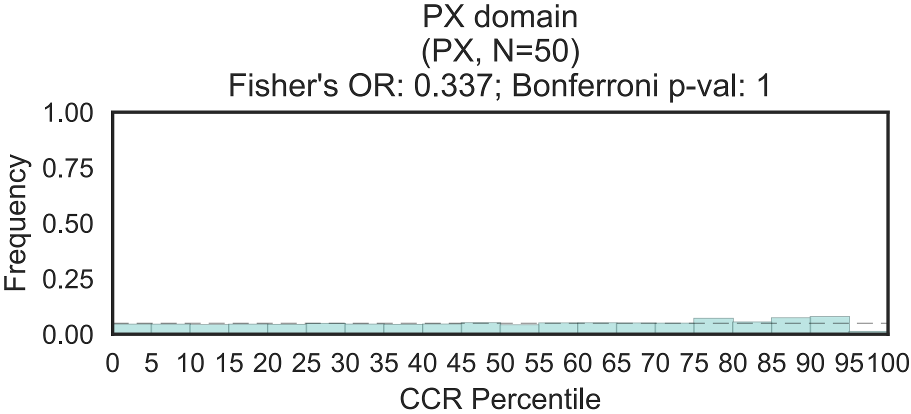


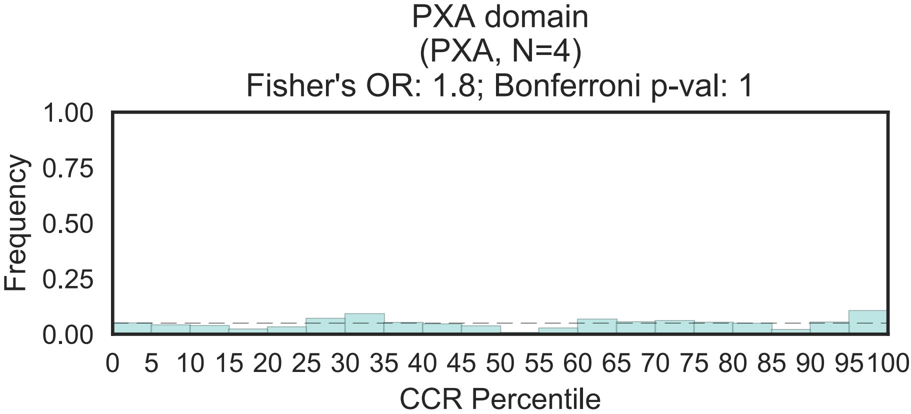
PV-1 protein (PLVAP)
(PV-1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

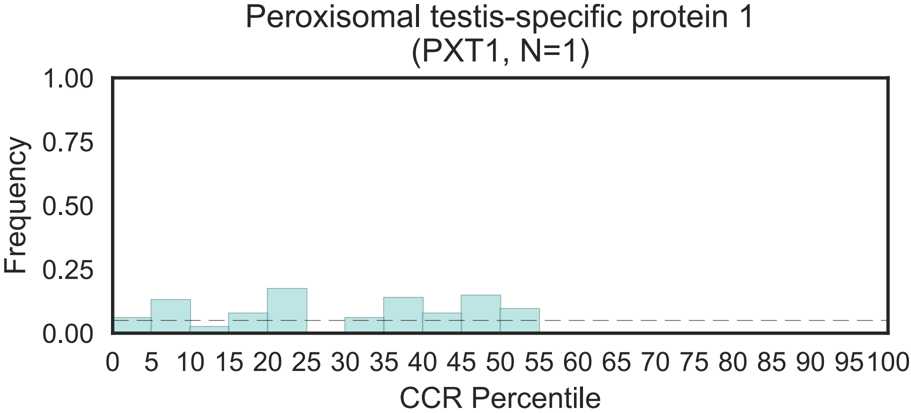
PWI domain
(PWI, N=5)
Fisher's OR: 19.7; Bonferroni p-val: 0.000158

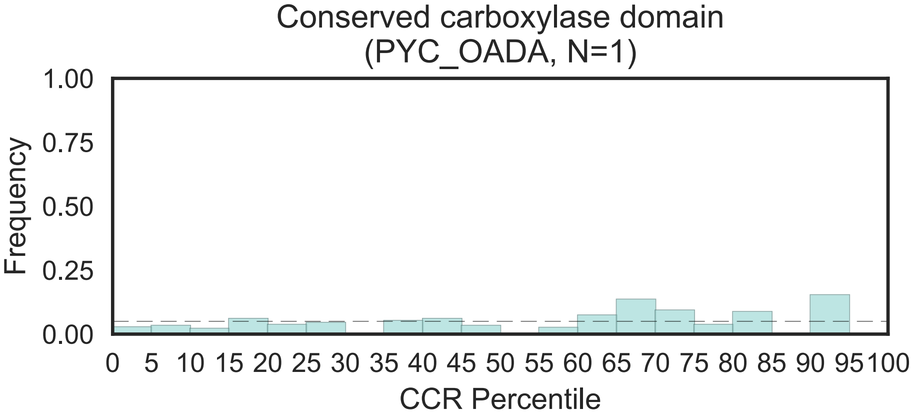


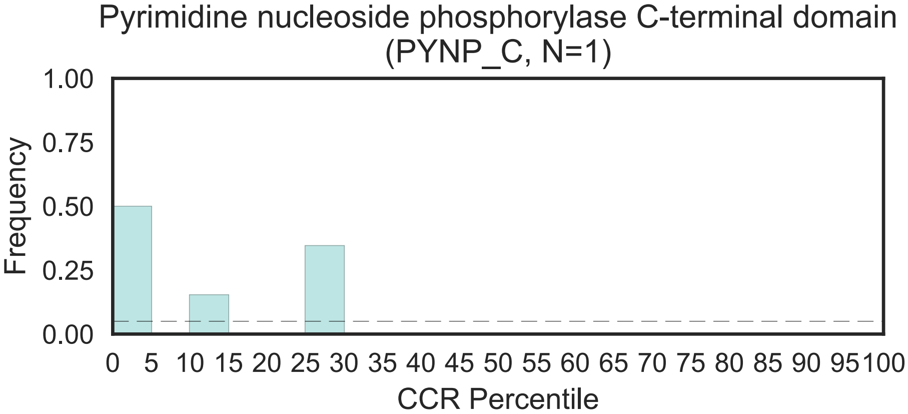

PWWP domain
(PWWP, N=25)
Fisher's OR: 3.61; Bonferroni p-val: 0.0382
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

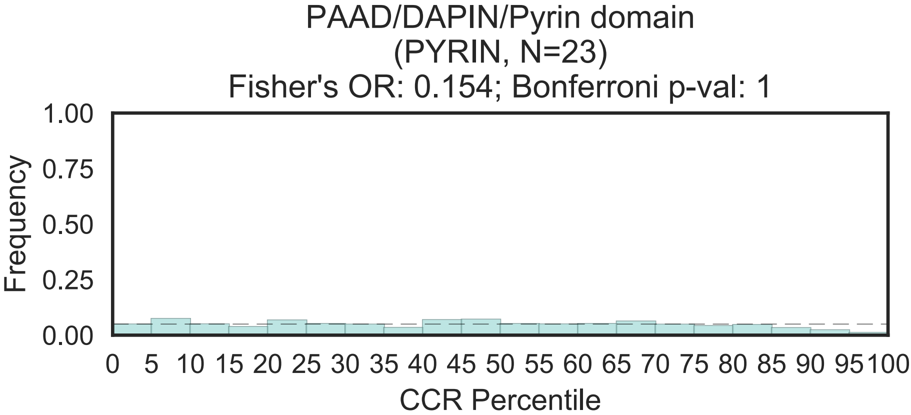

PX domain
(PX, N=50)
Fisher's OR: 0.337; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

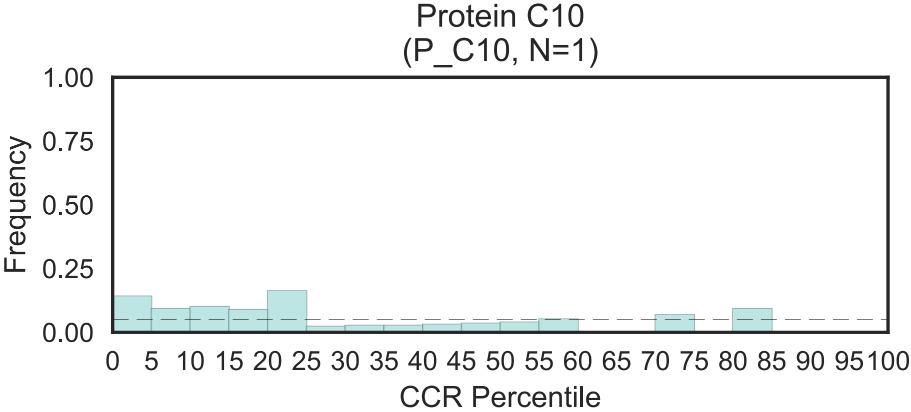

PXA domain
(PXA, N=4)
Fisher's OR: 1.8; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

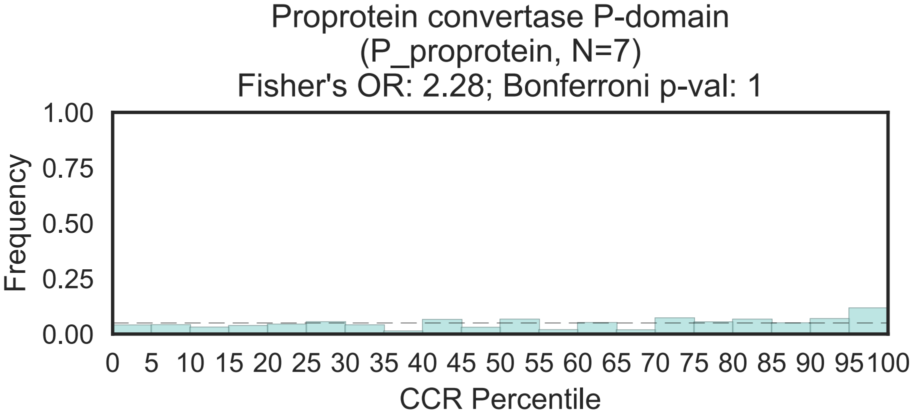

Peroxisomal testis-specific protein 1
(PXT1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

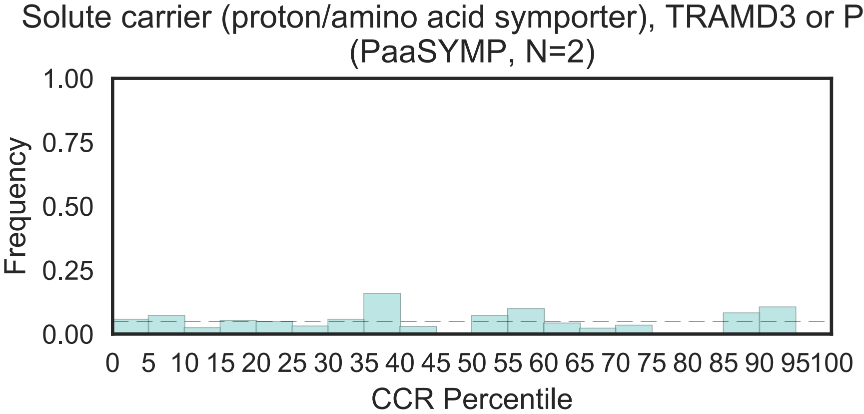

Conserved carboxylase domain
(PYC_OADA, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

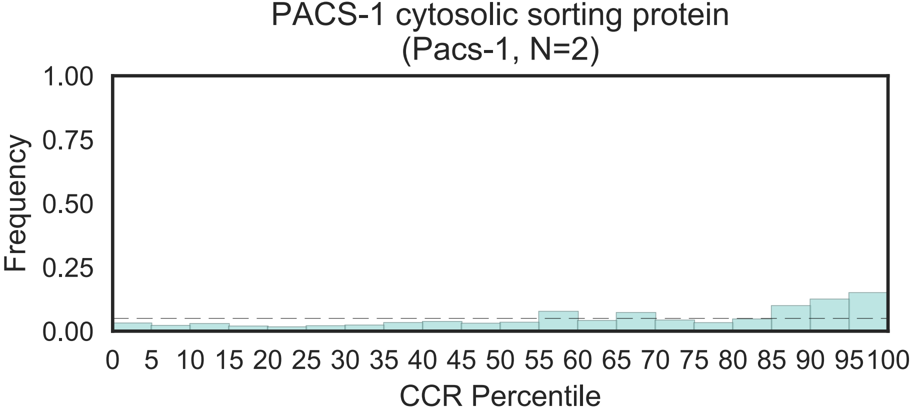

Pyrimidine nucleoside phosphorylase C-terminal domain
(PYNP_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

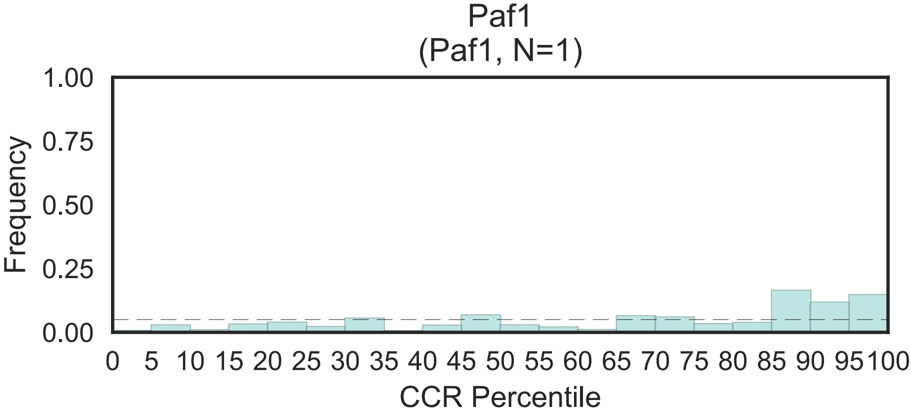

PAAD/DAPIN/Pyrin domain
(PYRIN, N=23)
Fisher's OR: 0.154; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

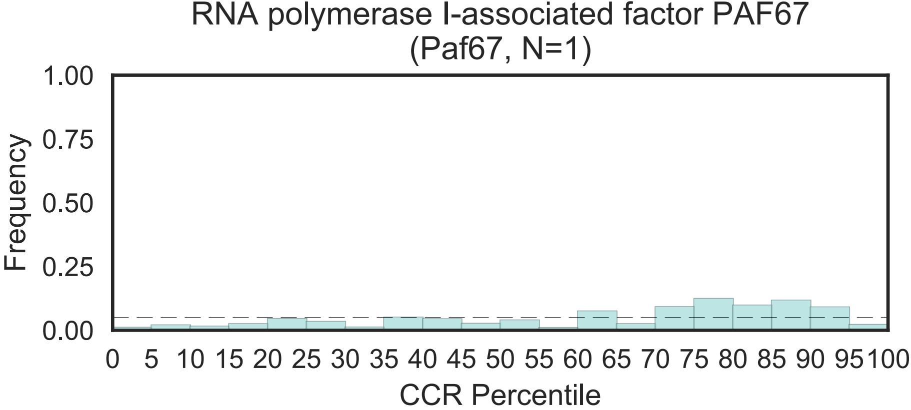

Protein C10
(P_C10, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

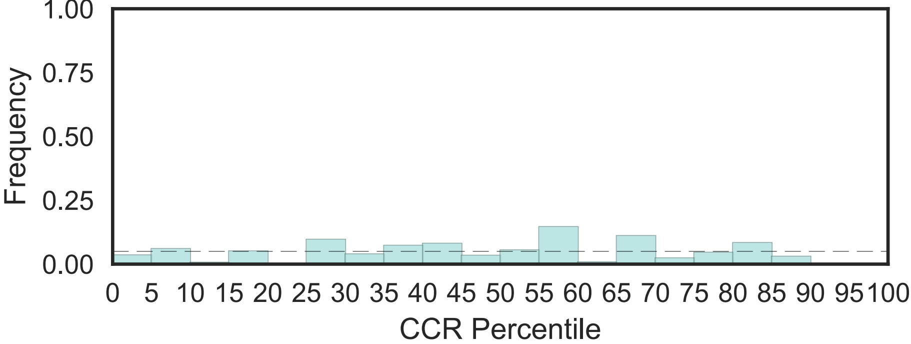

Proprotein convertase P-domain
(P_proprotein, N=7)
Fisher's OR: 2.28; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Solute carrier (proton/amino acid symporter), TRAMD3 or PAT1
(PaaSYMP, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

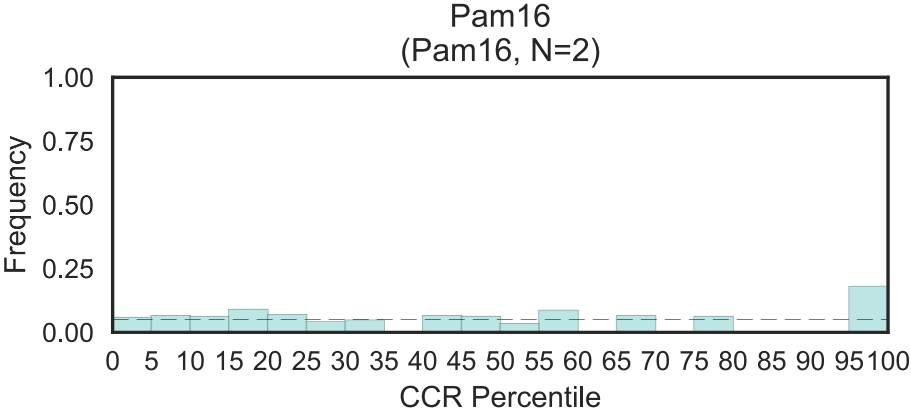

PACS-1 cytosolic sorting protein
(Pacs-1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

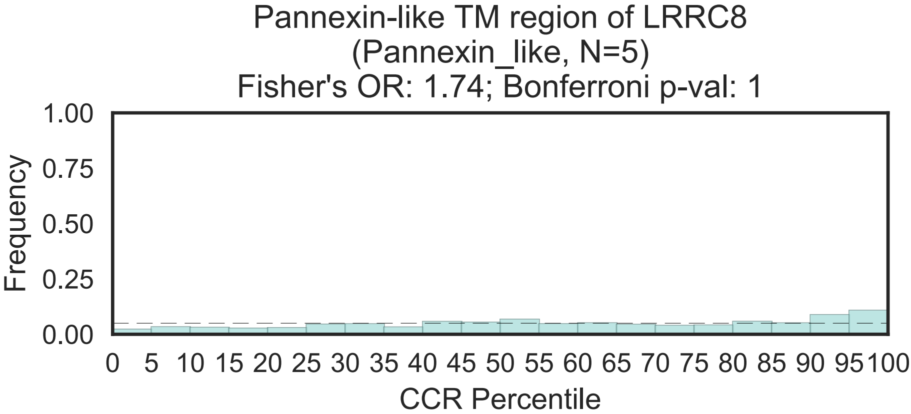

Paf1
(Paf1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

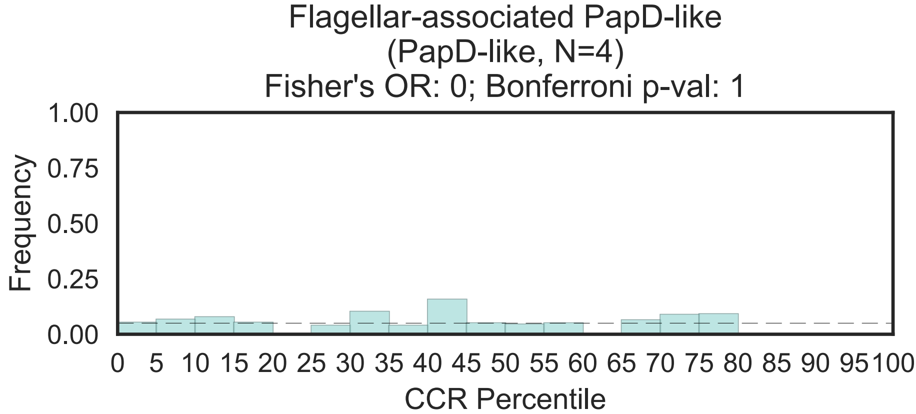

RNA polymerase I-associated factor PAF67
(Paf67, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

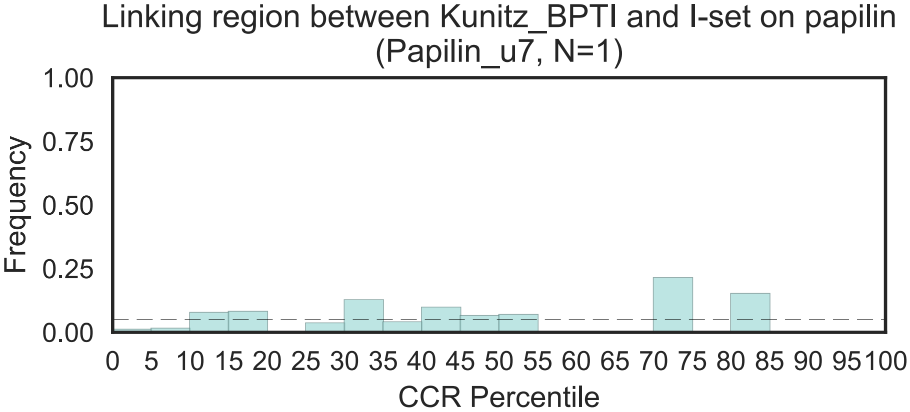


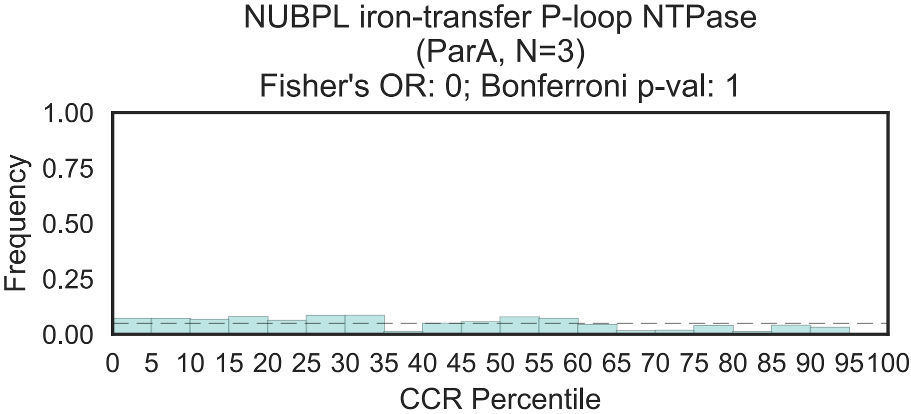
Palmitoyl protein thioesterase
(Palm_thioest, N=2)

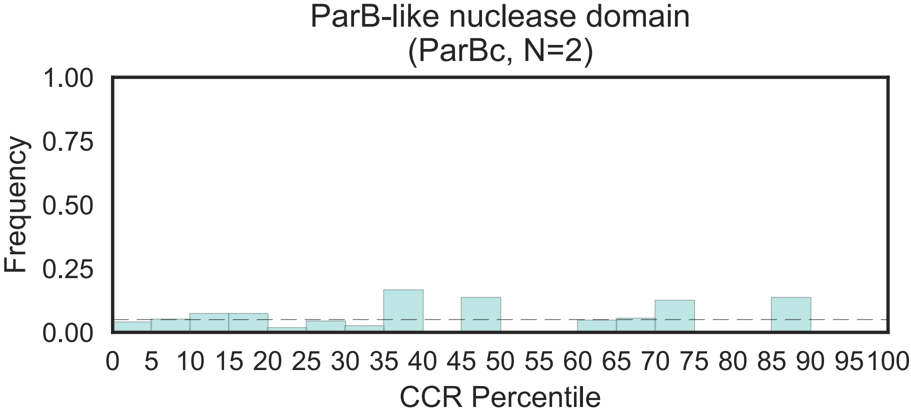

Pam16
(Pam16, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

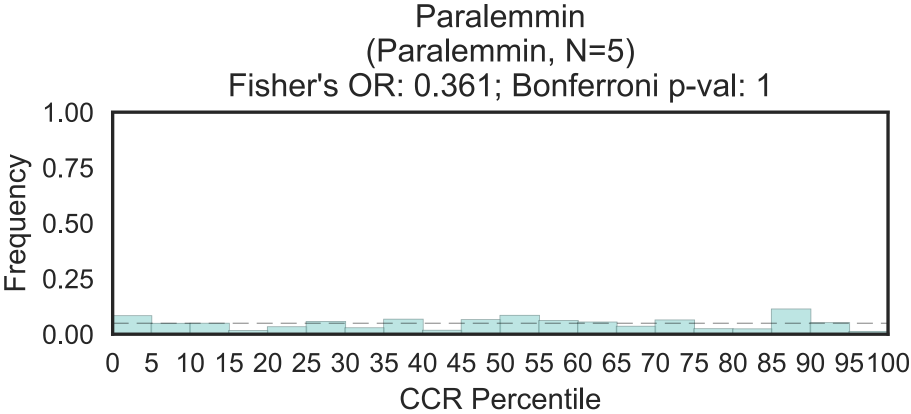

Pannexin-like TM region of LRRC8
(Pannexin_like, N=5)
Fisher's OR: 1.74; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

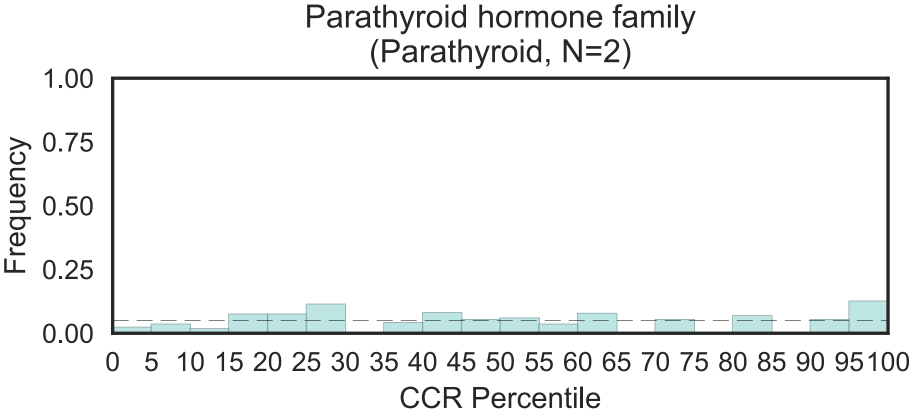

Flagellar-associated PapD-like
(PapD-like, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

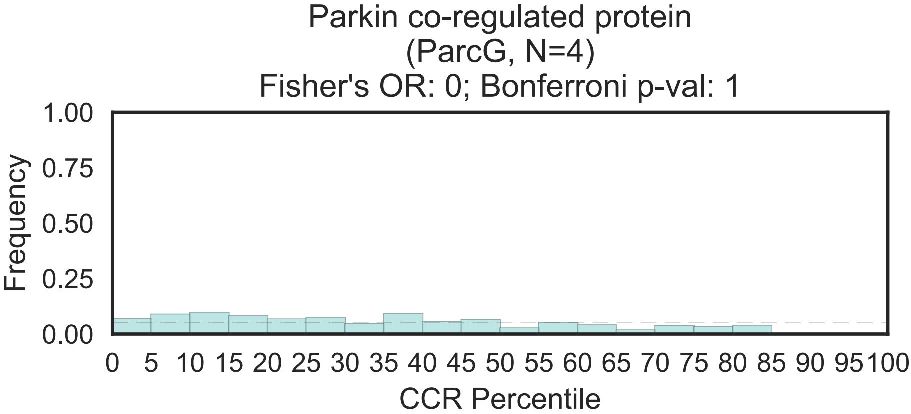

Linking region between Kunitz_BPTI and I-set on papilin
(Papilin_u7, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


NUBPL iron-transfer P-loop NTPase
(ParA, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

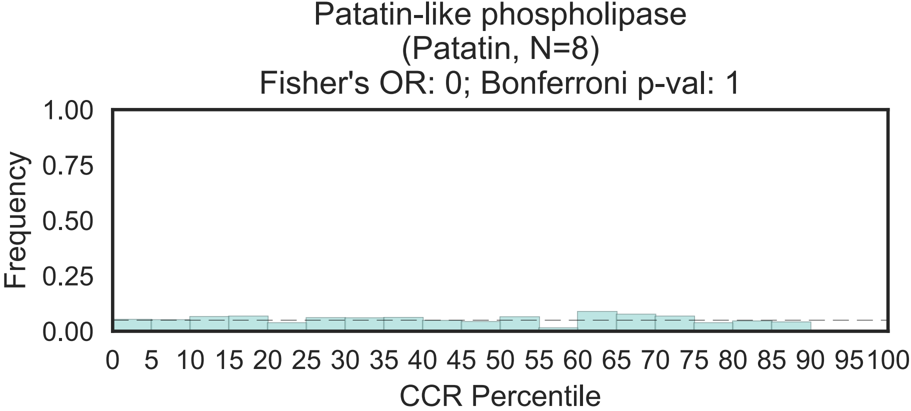

ParB-like nuclease domain
(ParBc, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Paralemmin
(Paralemmin, N=5)
Fisher's OR: 0.361; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

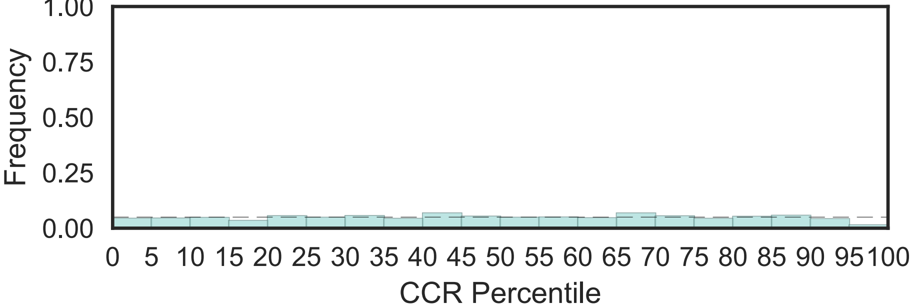

Parathyroid hormone family
(Parathyroid, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

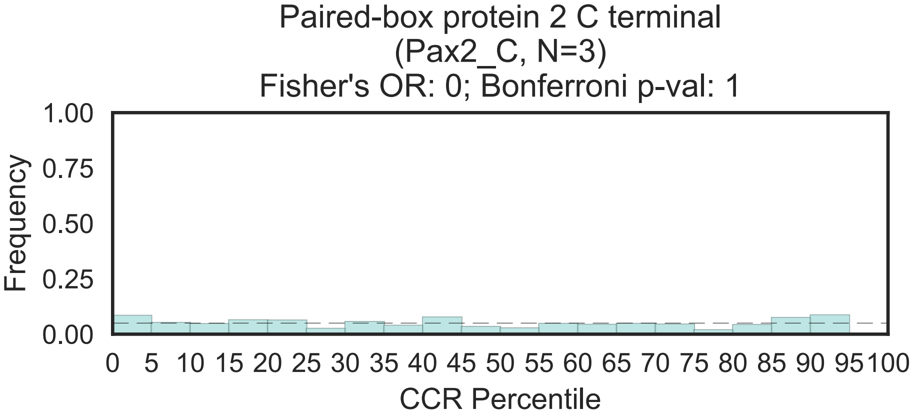


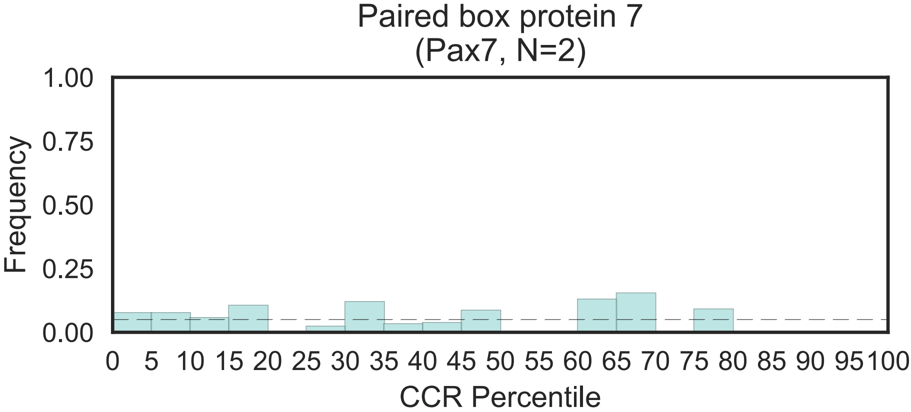
Parkin co-regulated protein
(ParcG, N=4)
Fisher's OR: 0; Bonferroni p-val: 1


Patatin-like phospholipase
(Patatin, N=8)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

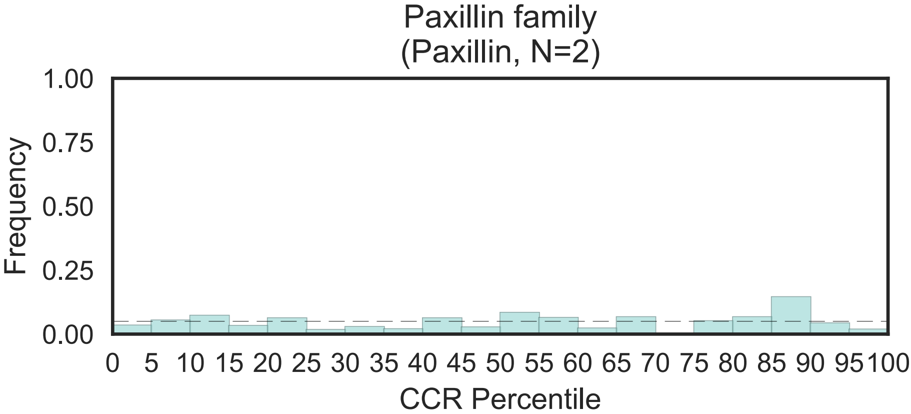
Patched family
(Patched, N=16)
Fisher's OR: 0.241; Bonferroni p-val: 1

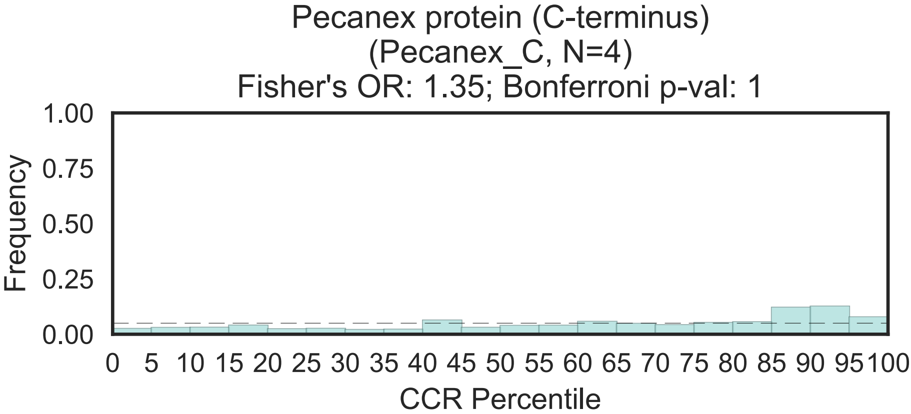


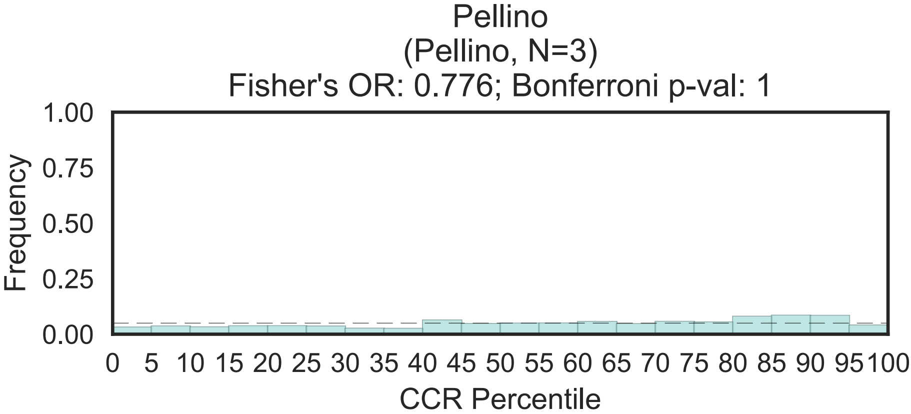

Paired-box protein 2 C terminal
(Pax2_C, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

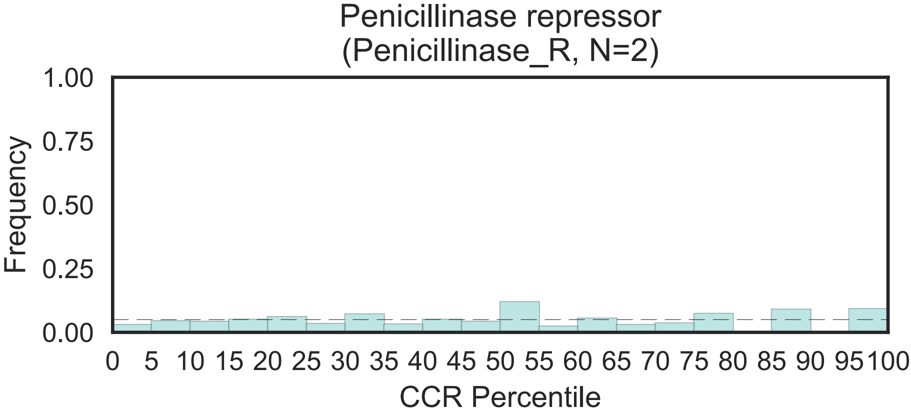


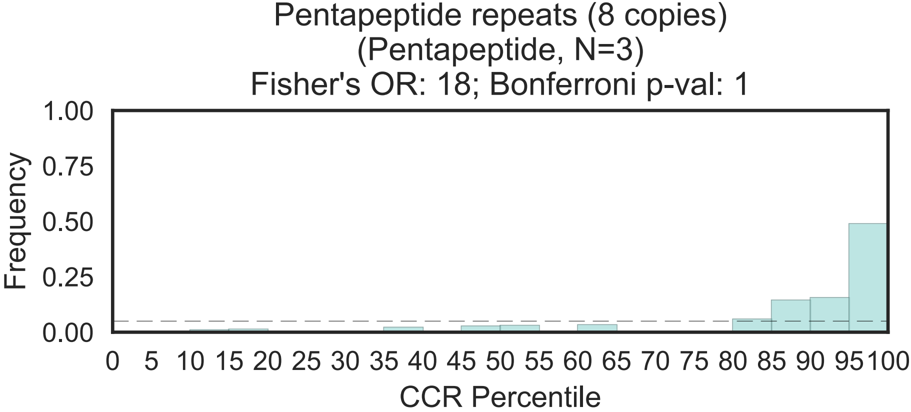
Paired box protein 7
(Pax7, N=2)

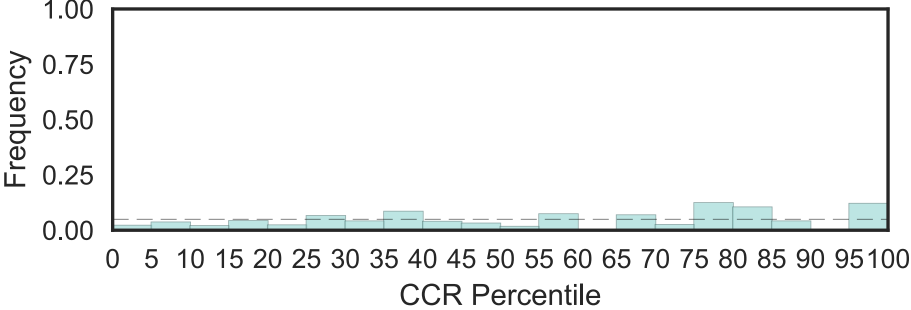

Paxillin family
(Paxillin, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Pecanex protein (C-terminus)
(Pecanex_C, N=4)
Fisher's OR: 1.35; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

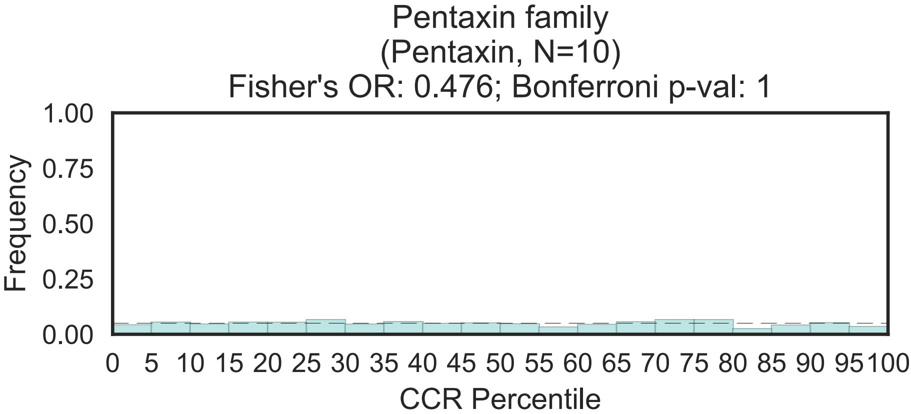

Pellino
(Pellino, N=3)
Fisher's OR: 0.776; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

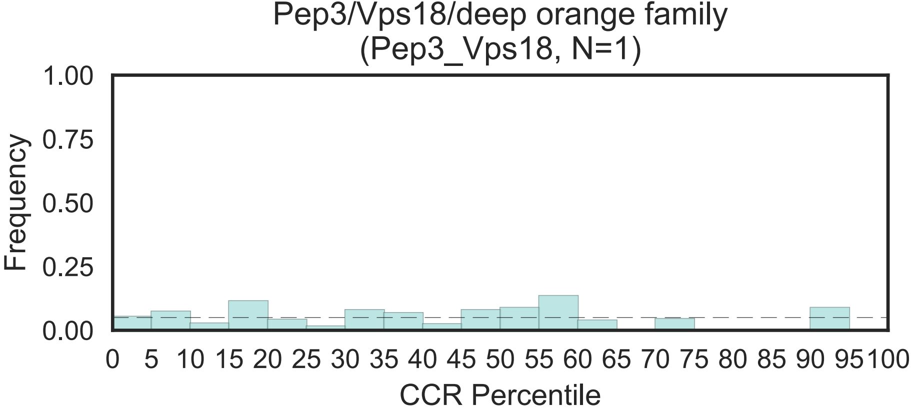

Penicillinase repressor
(Penicillinase_R, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

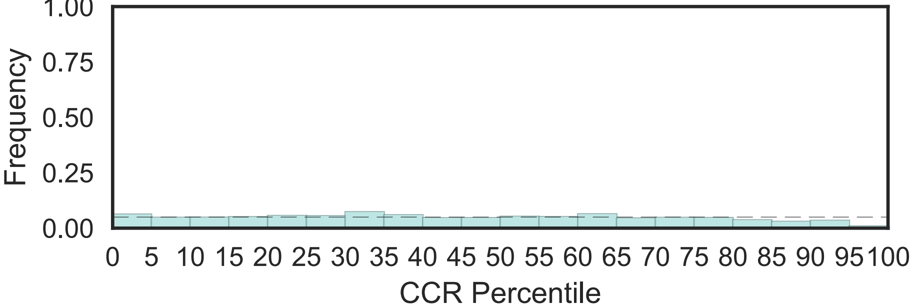

Pentapeptide repeats (8 copies)
(Pentapeptide, N=3)
Fisher's OR: 18; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



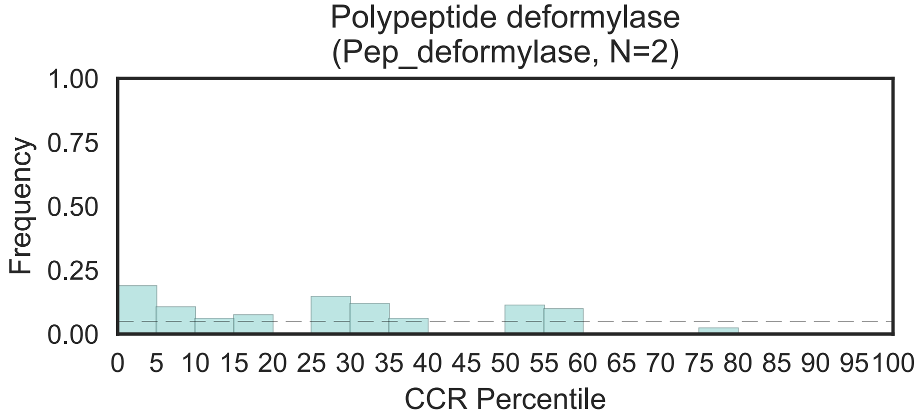
Pentapeptide repeats (9 copies)
(Pentapeptide_4, N=4)
Fisher's OR: 1.33; Bonferroni p-val: 1

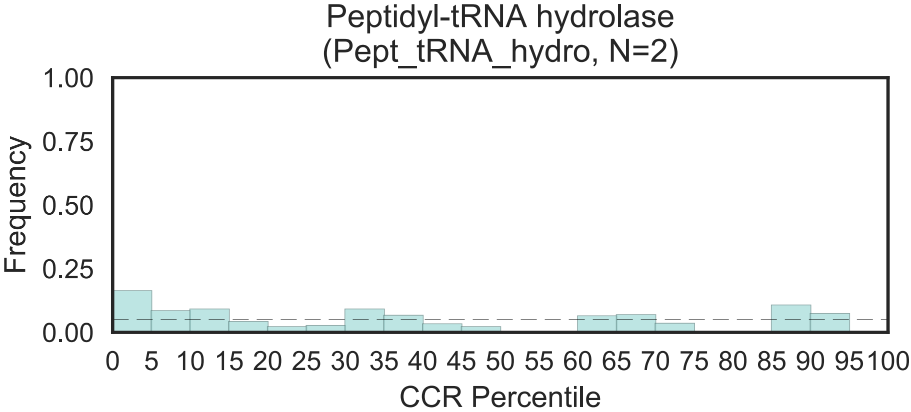

Pentaxin family
(Pentaxin, N=10)
Fisher's OR: 0.476; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

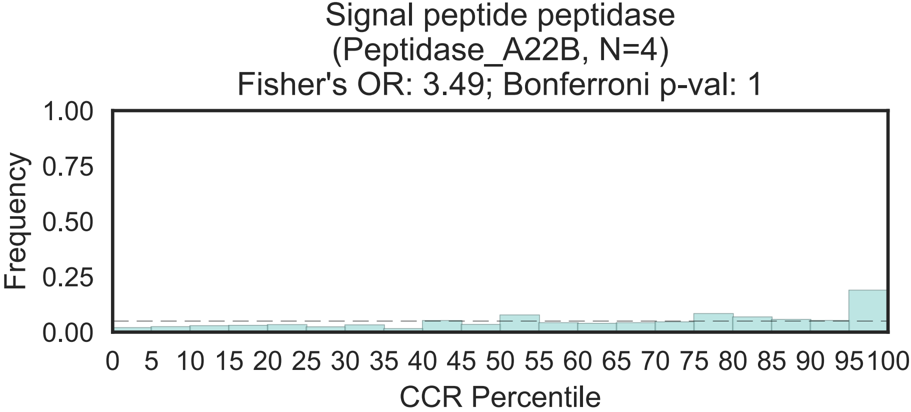

Pep3/Vps18/deep orange family
(Pep3_Vps18, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



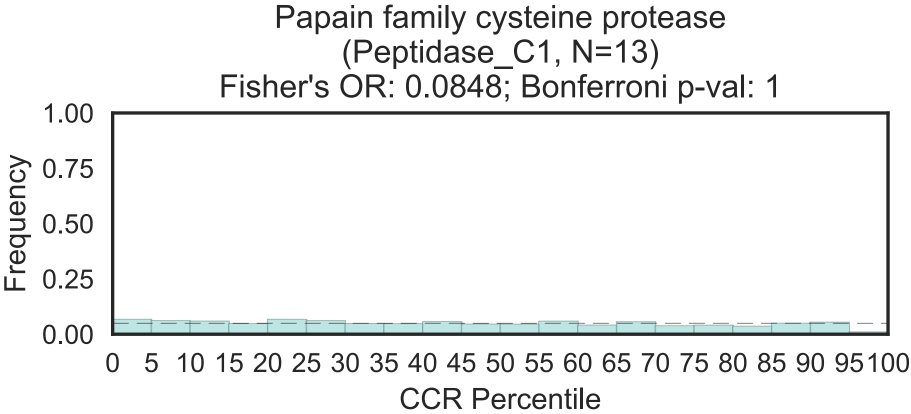
Reprolysin family propeptide
(Pep_M12B_propep, N=39)
Fisher's OR: 0.184; Bonferroni p-val: 0.865


Polypeptide deformylase
(Pep_deformylase, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

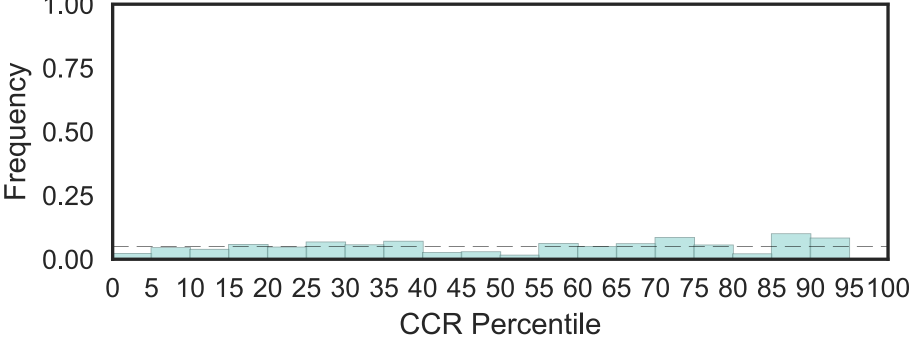

Peptidyl-tRNA hydrolase
(Pept_tRNA_hydro, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

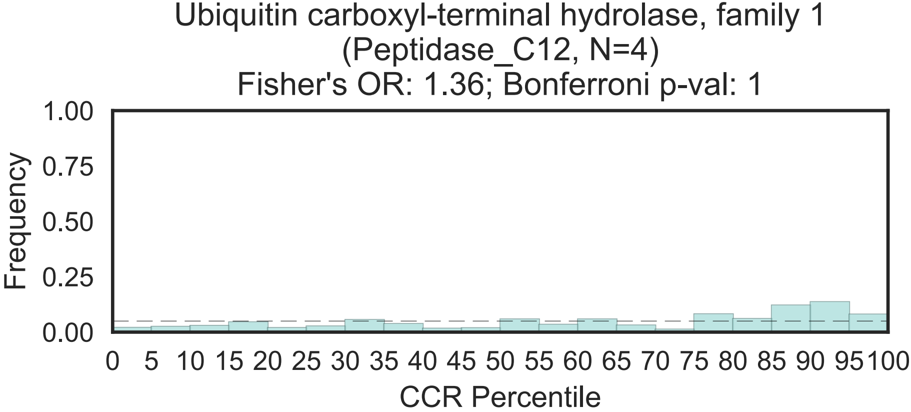


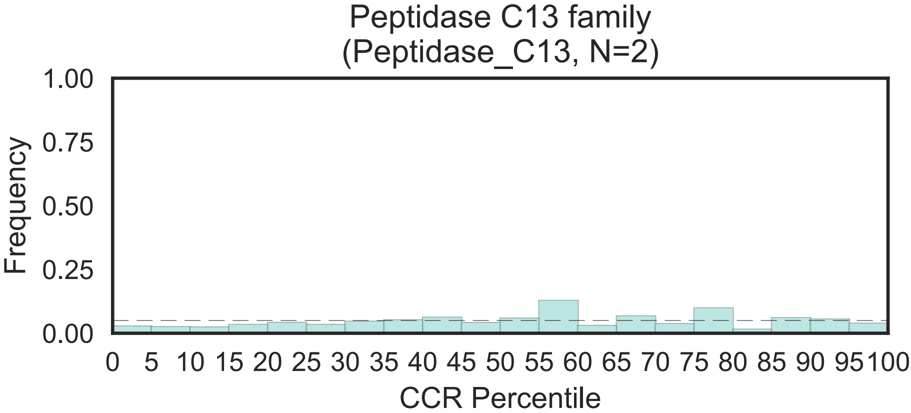
Signal peptide peptidase
(Peptidase_A22B, N=4)
Fisher's OR: 3.49; Bonferroni p-val: 1

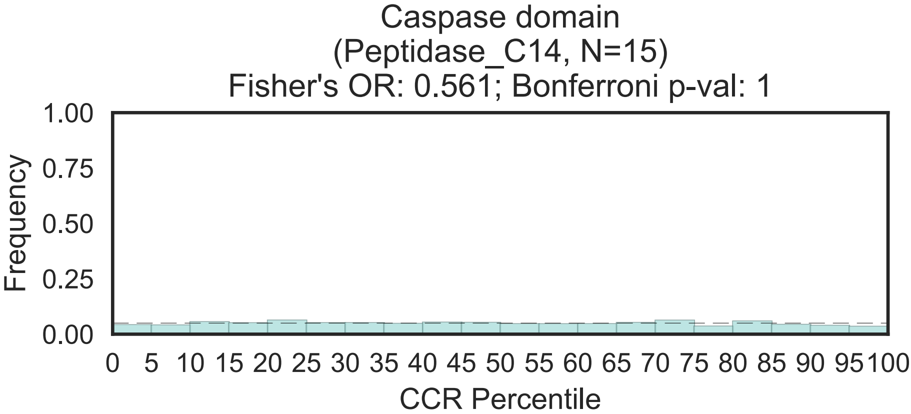

Papain family cysteine protease
(Peptidase_C1, N=13)
Fisher's OR: 0.0848; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

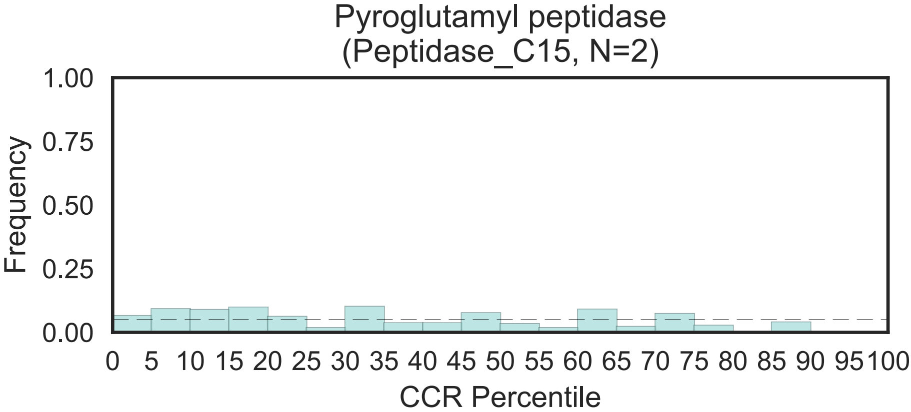
Peptidase family C101
(Peptidase_C101, N=2)

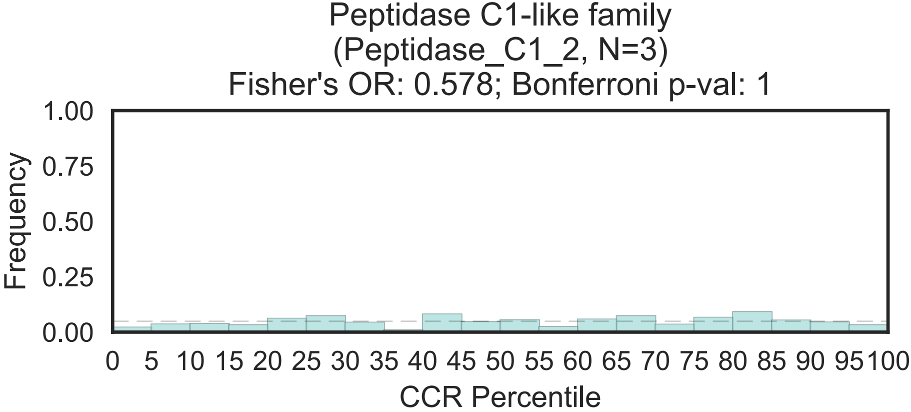



Ubiquitin carboxyl-terminal hydrolase, family 1
(Peptidase_C12, N=4)
Fisher's OR: 1.36; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

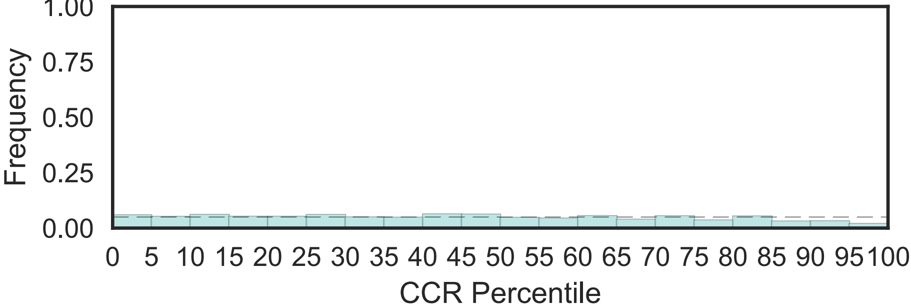

Peptidase C13 family
(Peptidase_C13, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

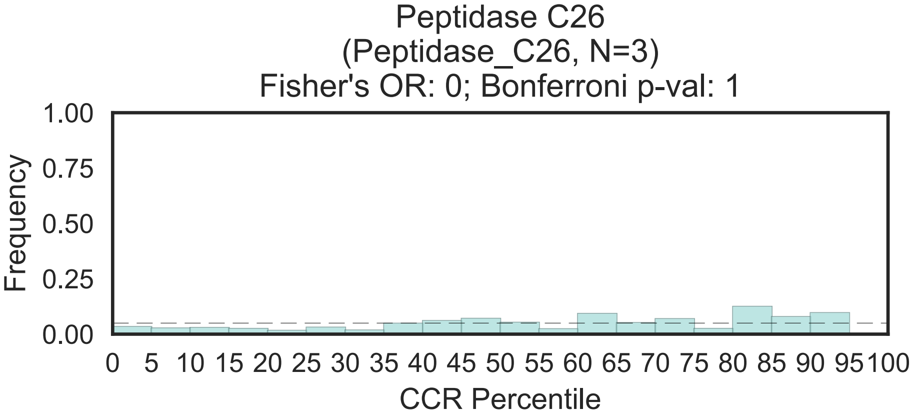

Caspase domain
(Peptidase_C14, N=15)
Fisher's OR: 0.561; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

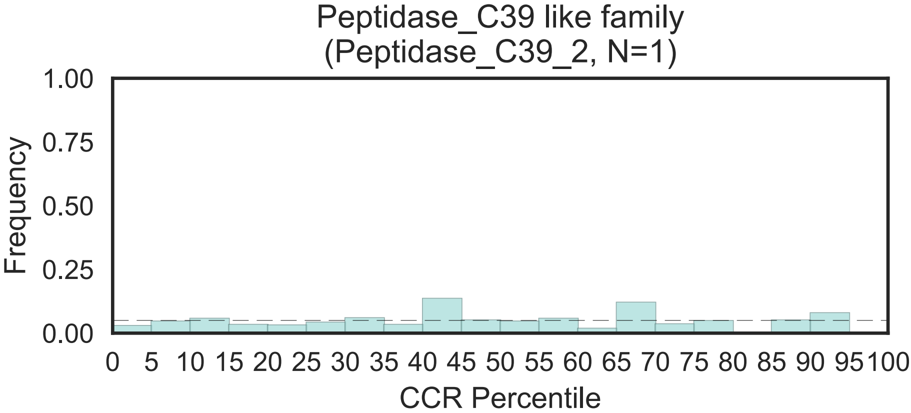

Pyroglutamyl peptidase
(Peptidase_C15, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

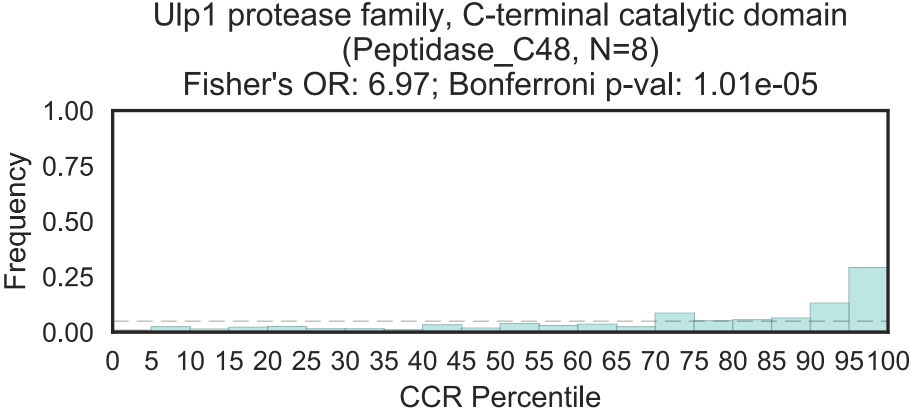

Peptidase C1-like family
(Peptidase_C1_2, N=3)
Fisher's OR: 0.578; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

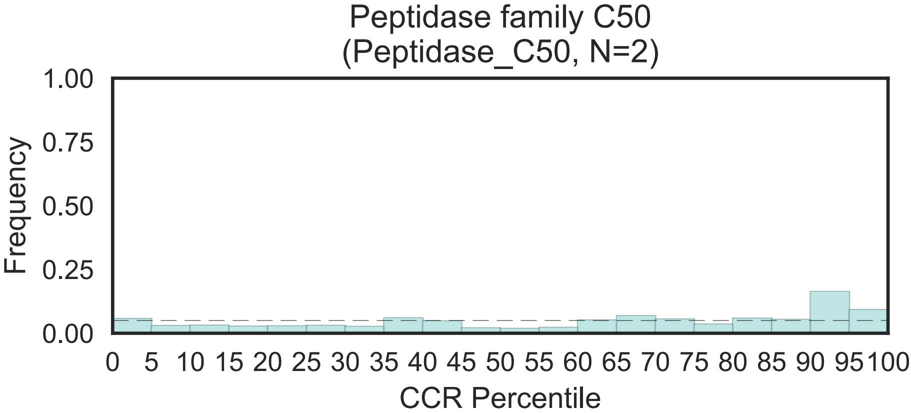
Calpain family cysteine protease
(Peptidase_C2, N=15)
Fisher's OR: 0.358; Bonferroni p-val: 1



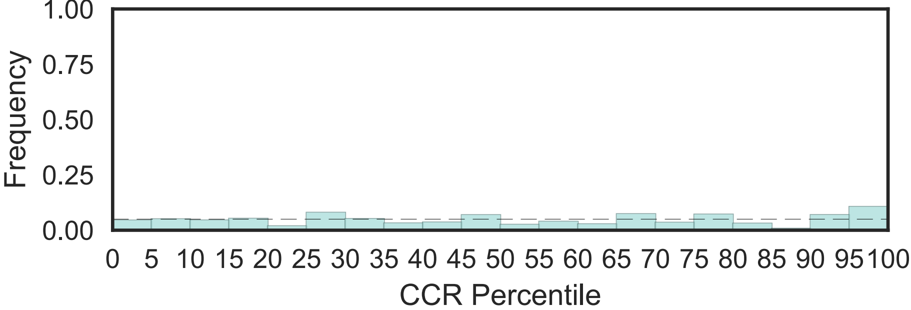

Peptidase C26
(Peptidase_C26, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

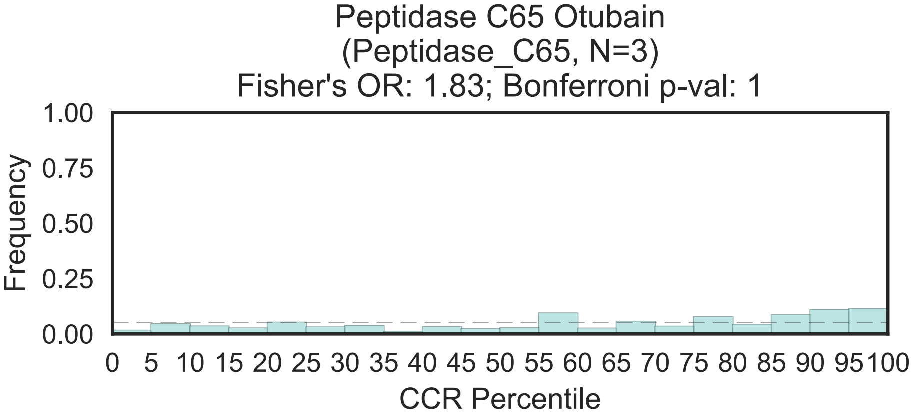

Peptidase_C39 like family
(Peptidase_C39_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ulp1 protease family, C-terminal catalytic domain
(Peptidase_C48, N=8)
Fisher's OR: 6.97; Bonferroni p-val: 1.01e-05
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

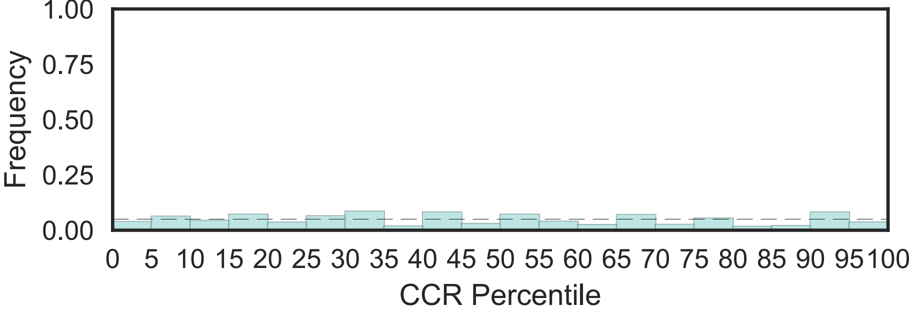

Peptidase family C50
(Peptidase_C50, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

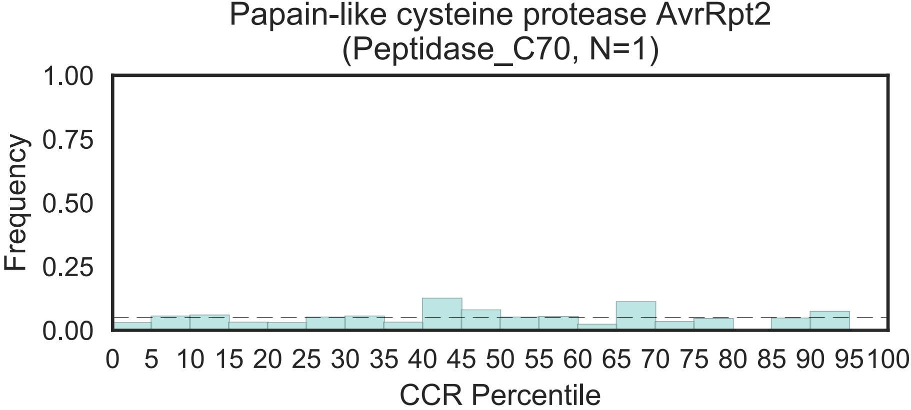
Peptidase family C54
(Peptidase_C54, N=3)
Fisher's OR: 1.14; Bonferroni p-val: 1

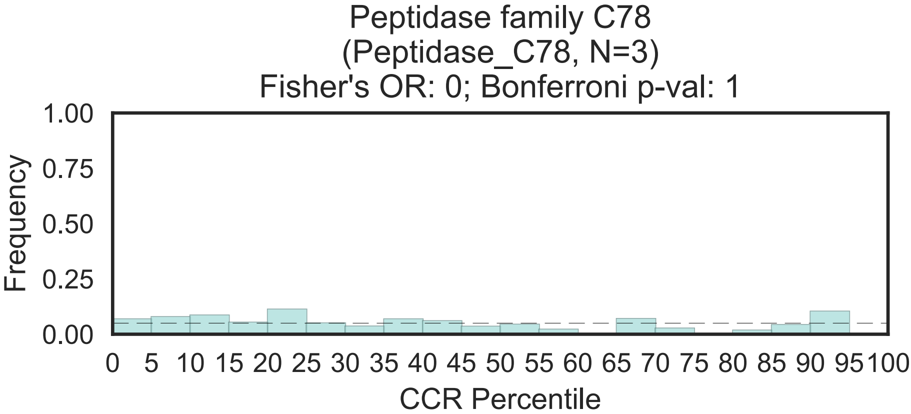


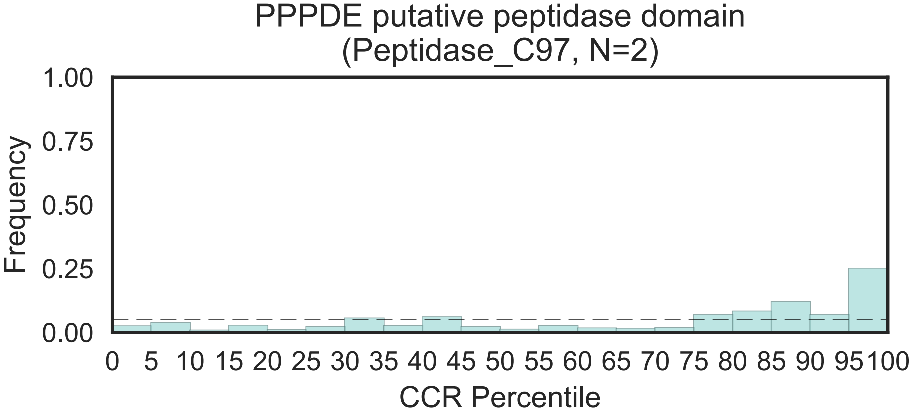


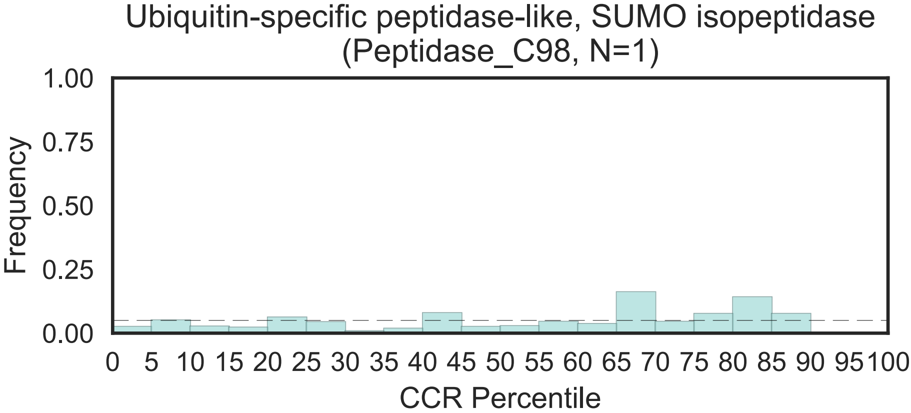
Peptidase C65 Otubain
(Peptidase_C65, N=3)
Fisher's OR: 1.83; Bonferroni p-val: 1

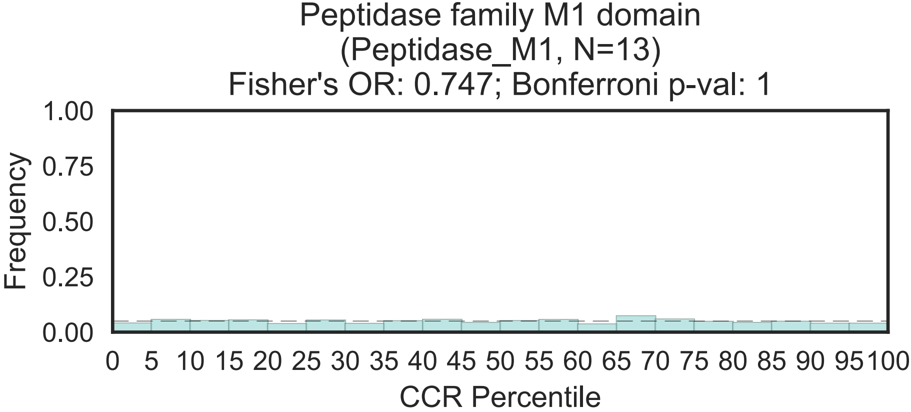

Peptidase family C69
(Peptidase_C69, N=3)
Fisher's OR: 0.56; Bonferroni p-val: 1

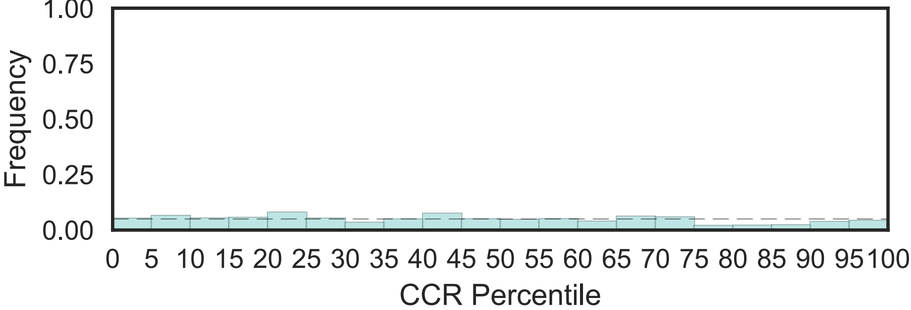

Papain-like cysteine protease AvrRpt2
(Peptidase_C70, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Peptidase family C78
(Peptidase_C78, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

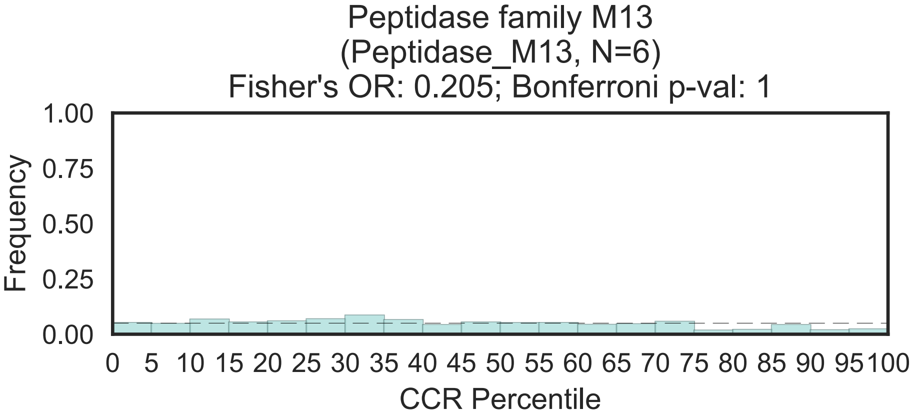

PPPDE putative peptidase domain
(Peptidase_C97, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

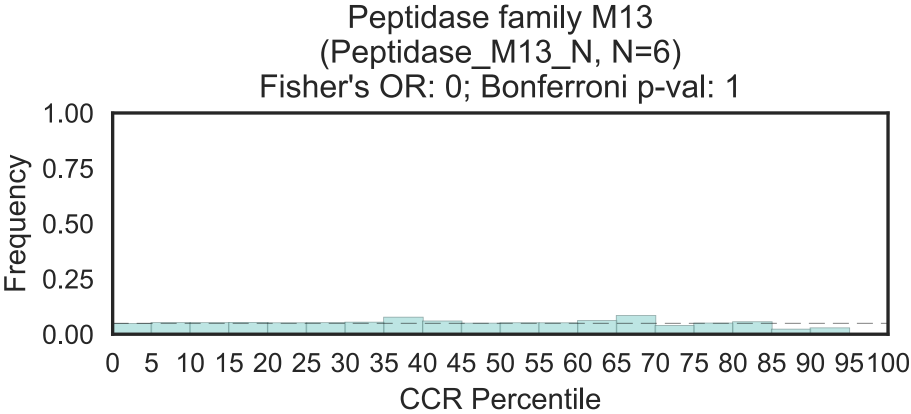

Ubiquitin-specific peptidase-like, SUMO isopeptidase
(Peptidase_C98, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

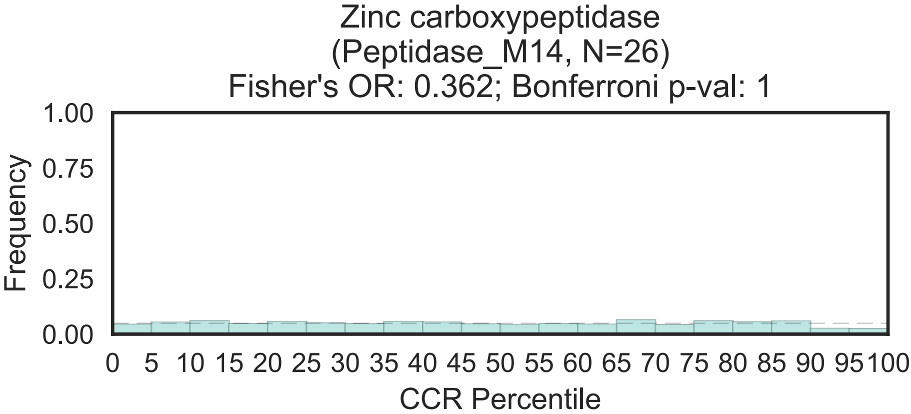

Peptidase family M1 domain
(Peptidase_M1, N=13)
Fisher's OR: 0.747; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

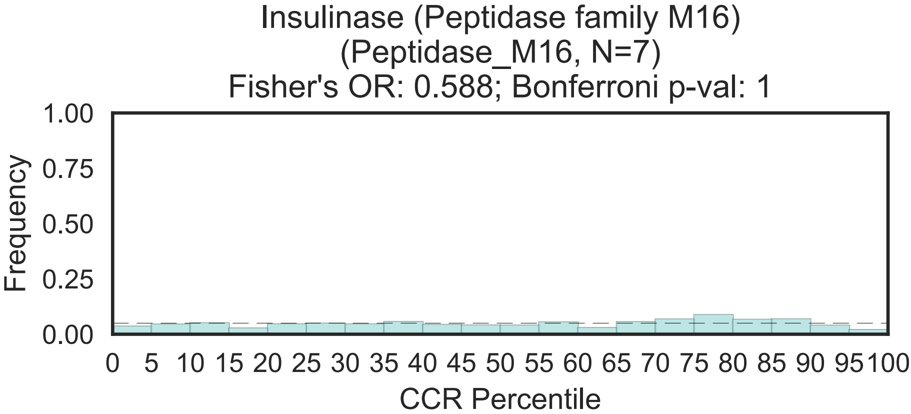


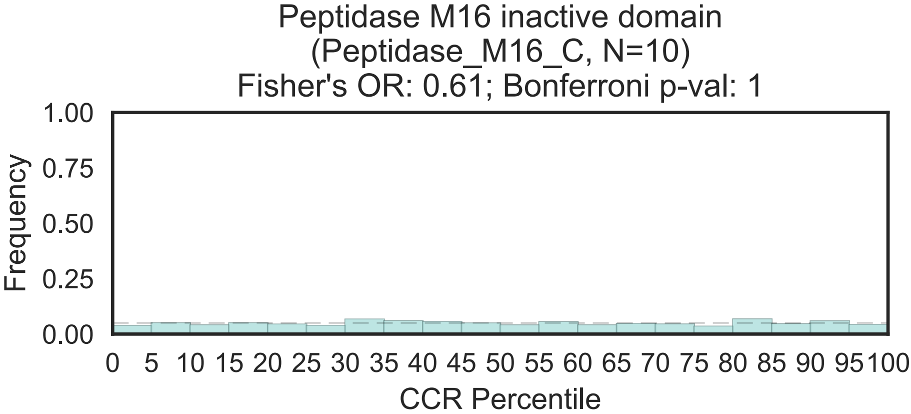
Matrixin
(Peptidase_M10, N=21)
Fisher's OR: 0.421; Bonferroni p-val: 1

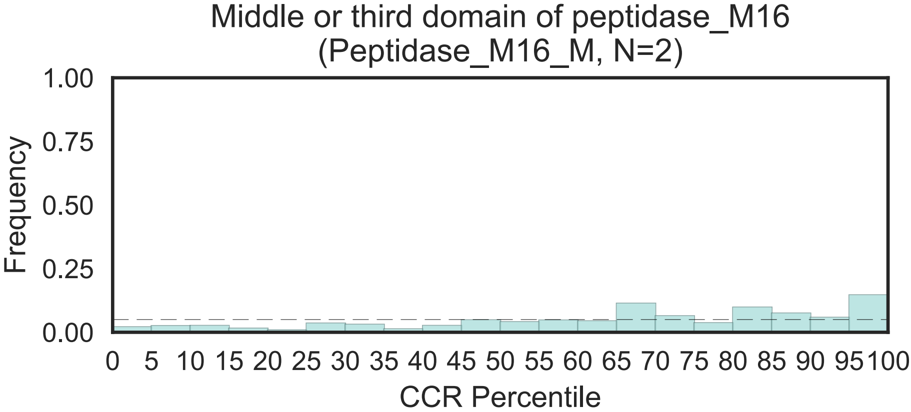

Peptidase family M13
(Peptidase_M13, N=6)
Fisher's OR: 0.205; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

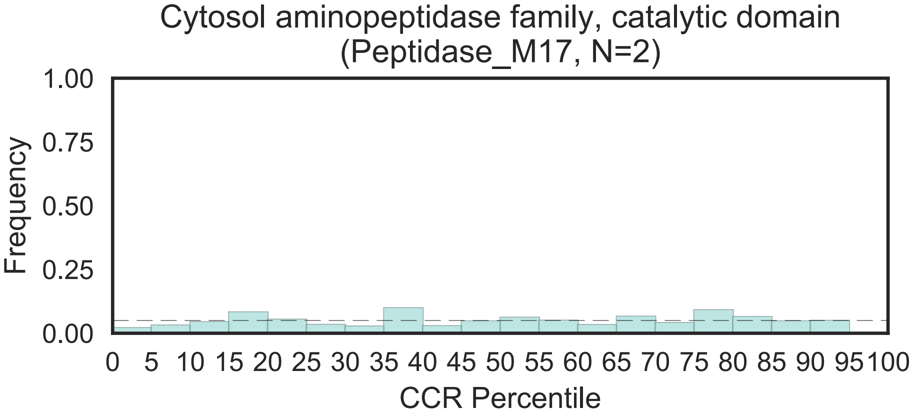

Peptidase family M13
(Peptidase_M13_N, N=6)
Fisher's OR: 0; Bonferroni p-val: 1

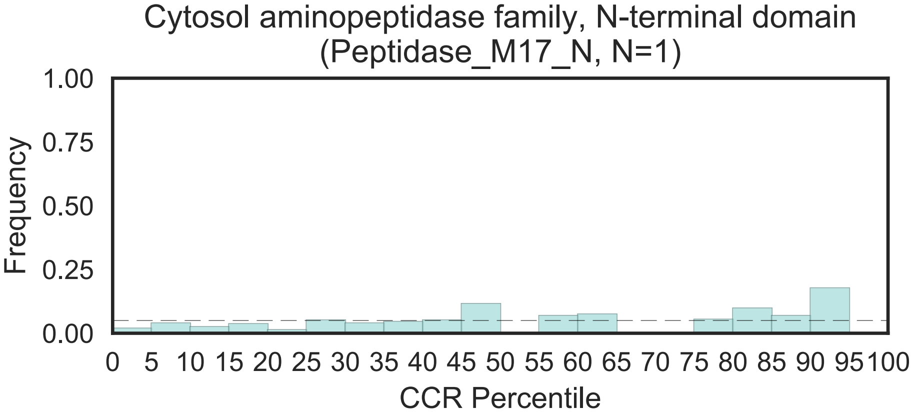

Zinc carboxypeptidase
(Peptidase_M14, N=26)
Fisher's OR: 0.362; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

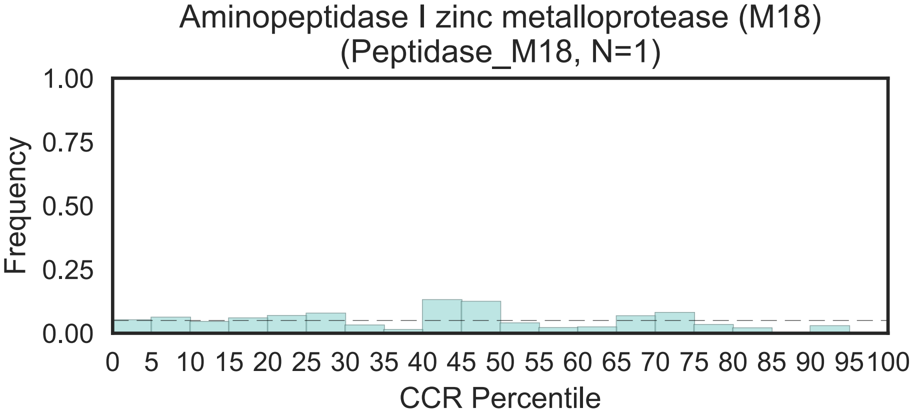

Insulinase (Peptidase family M16)
(Peptidase_M16, N=7)
Fisher's OR: 0.588; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Peptidase M16 inactive domain
(Peptidase_M16_C, N=10)
Fisher's OR: 0.61; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Middle or third domain of peptidase_M16
(Peptidase_M16_M, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

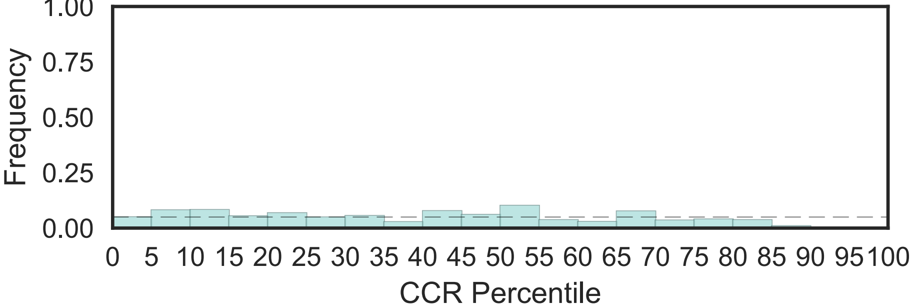

Cytosol aminopeptidase family, catalytic domain
(Peptidase_M17, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

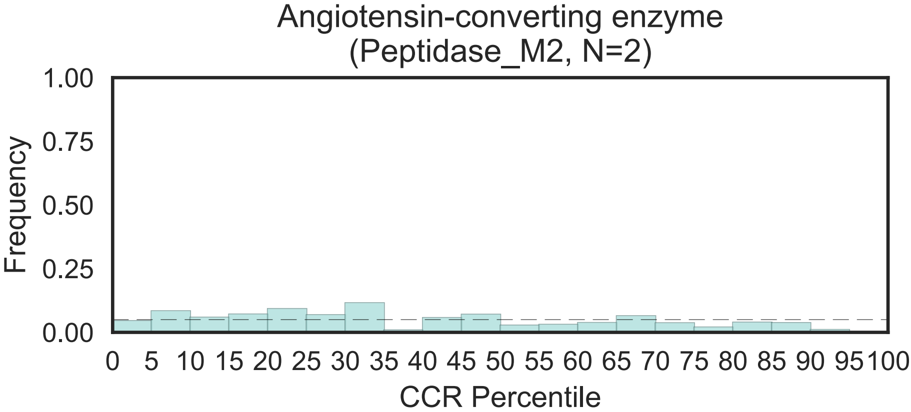

Cytosol aminopeptidase family, N-terminal domain
(Peptidase_M17_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



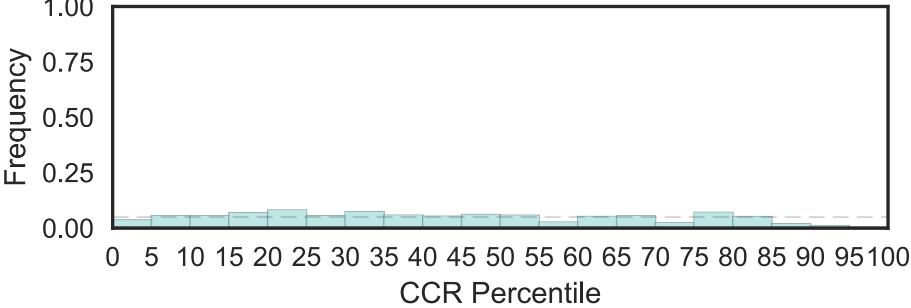
Aminopeptidase I zinc metalloprotease (M18)
(Peptidase_M18, N=1)

Membrane dipeptidase (Peptidase family M19)
(Peptidase_M19, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

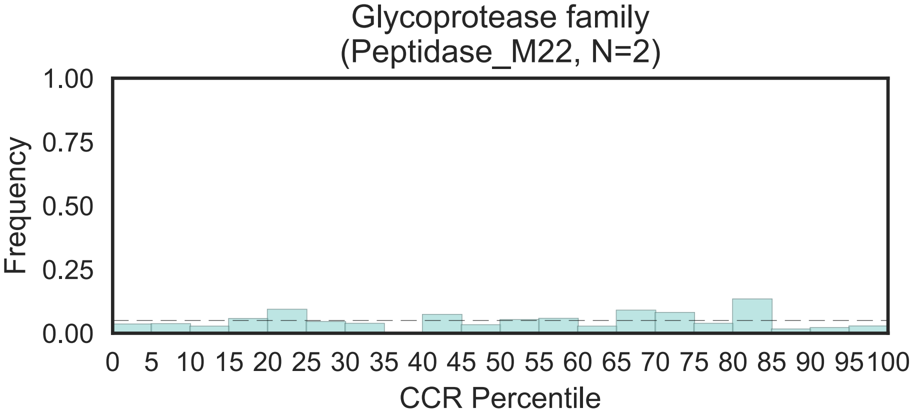


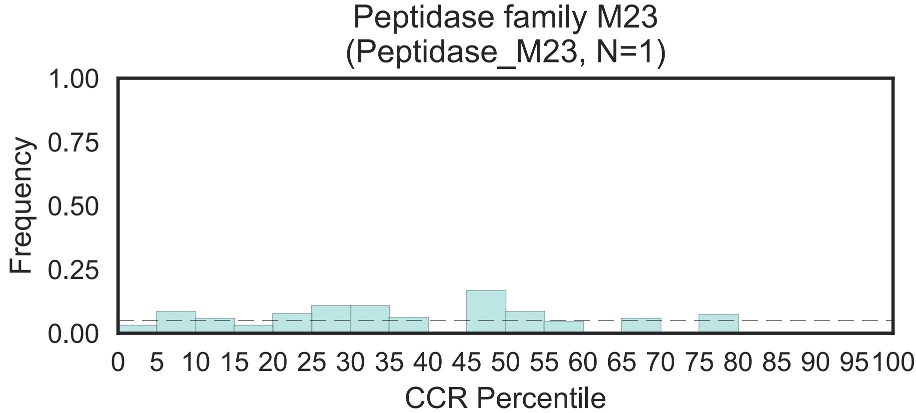


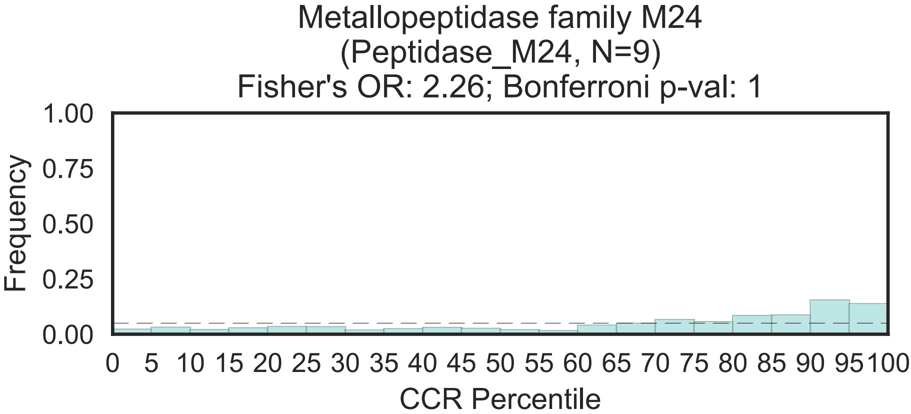
Angiotensin-converting enzyme
(Peptidase_M2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



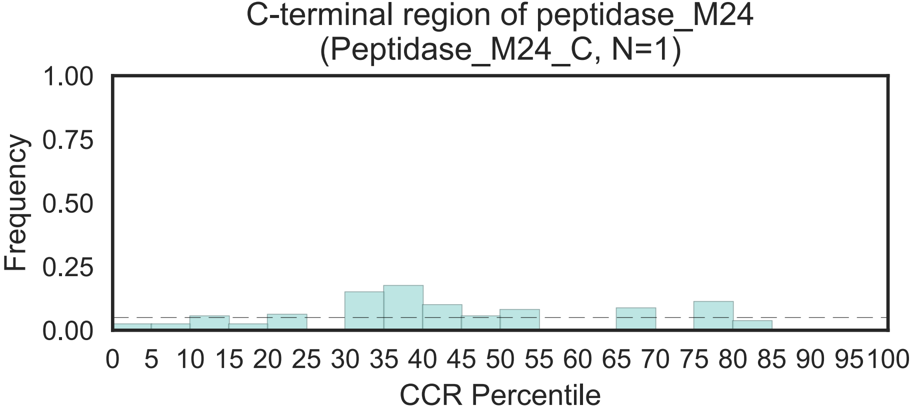
Peptidase family M20/M25/M40
(Peptidase_M20, N=7)
Fisher's OR: 0; Bonferroni p-val: 1

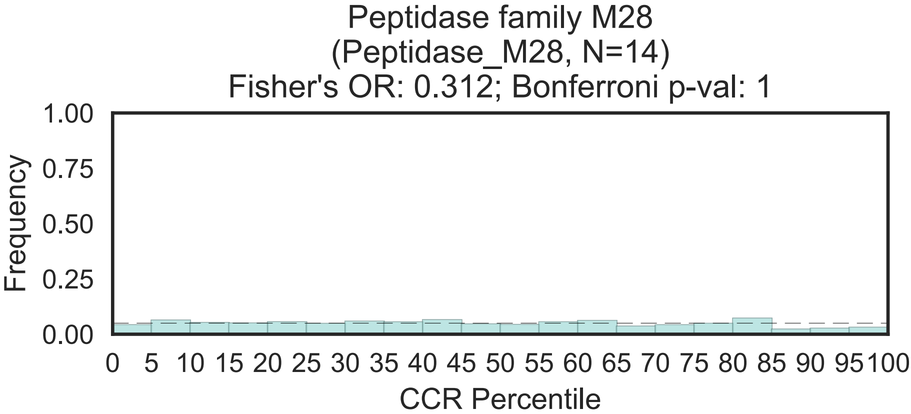

Glycoprotease family
(Peptidase_M22, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

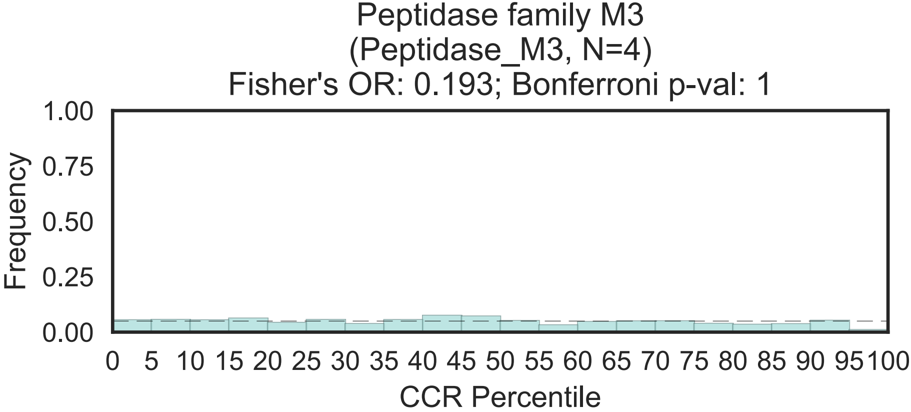

Peptidase family M23
(Peptidase_M23, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



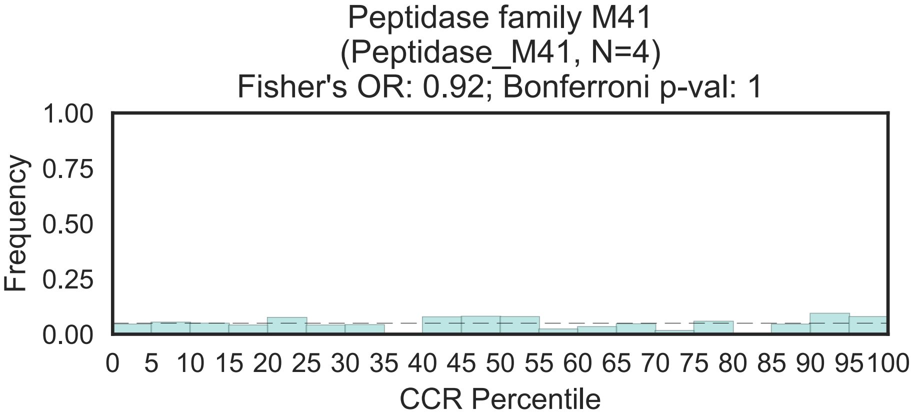
Metallopeptidase family M24
(Peptidase_M24, N=9)
Fisher's OR: 2.26; Bonferroni p-val: 1

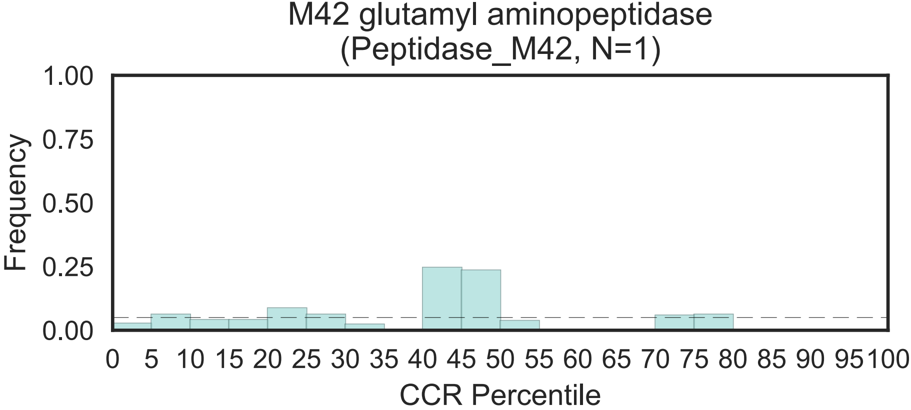

C-terminal region of peptidase_M24
(Peptidase_M24_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

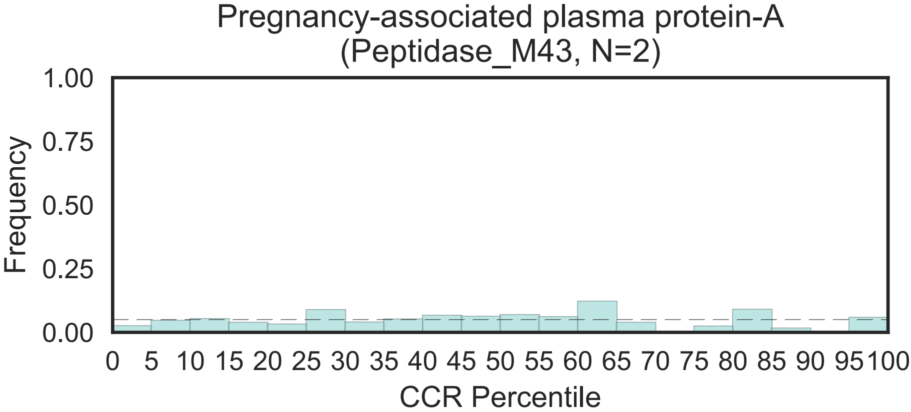

Peptidase family M28
(Peptidase_M28, N=14)
Fisher's OR: 0.312; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

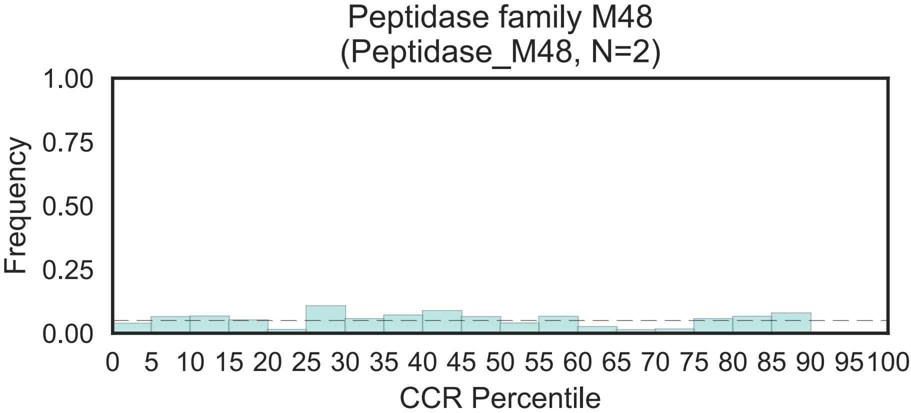


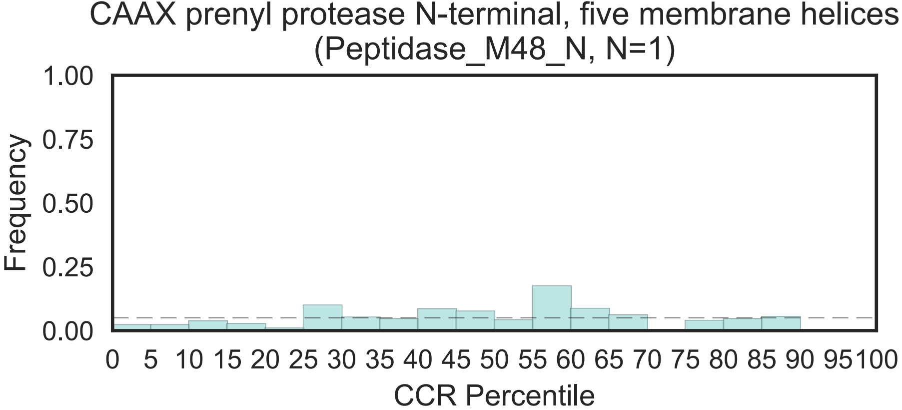
Peptidase family M3
(Peptidase_M3, N=4)
Fisher's OR: 0.193; Bonferroni p-val: 1

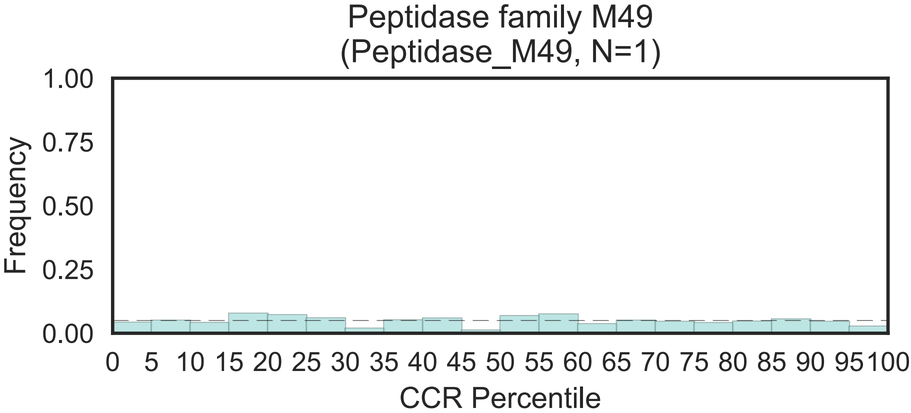

Peptidase family M41
(Peptidase_M41, N=4)
Fisher's OR: 0.92; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

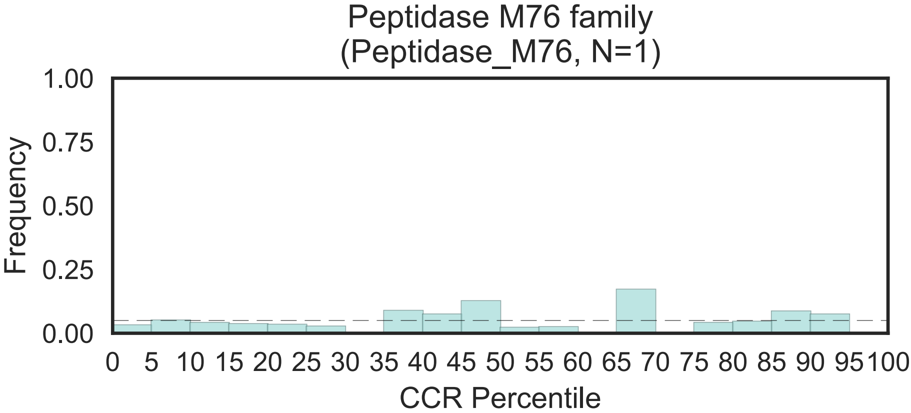

M42 glutamyl aminopeptidase
(Peptidase_M42, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

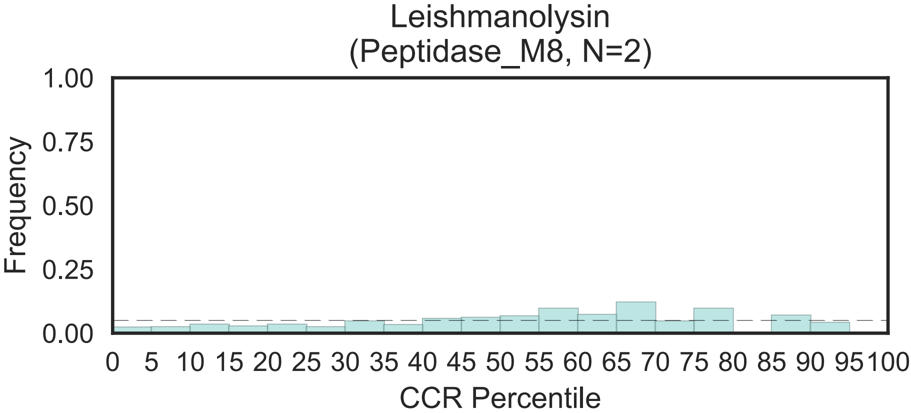

Pregnancy-associated plasma protein-A
(Peptidase_M43, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

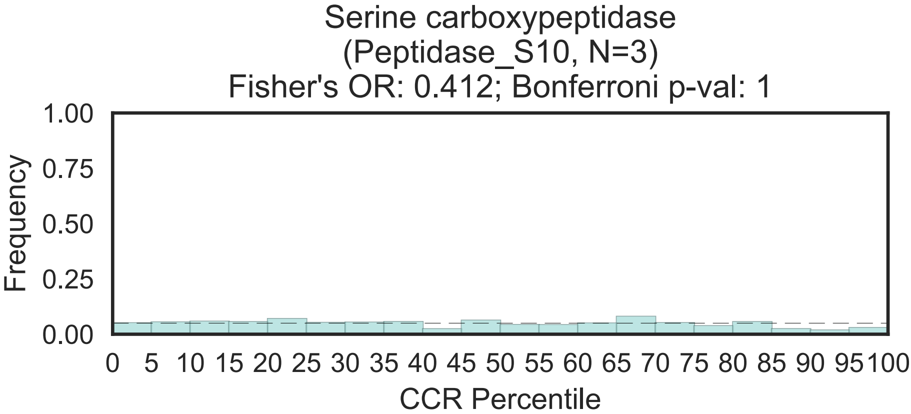

Peptidase family M48
(Peptidase_M48, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

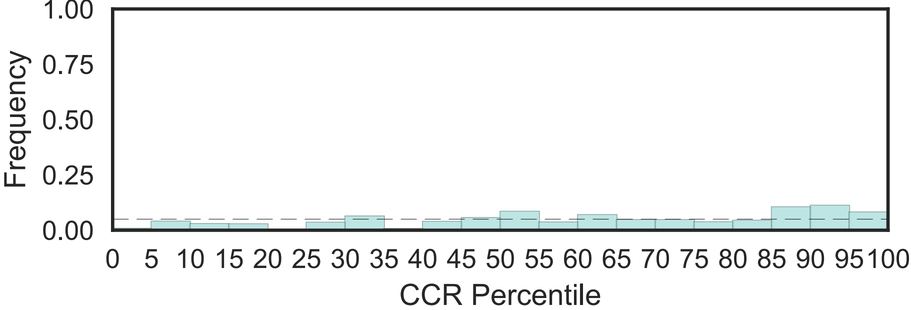

CAAX prenyl protease N-terminal, five membrane helices
(Peptidase_M48_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

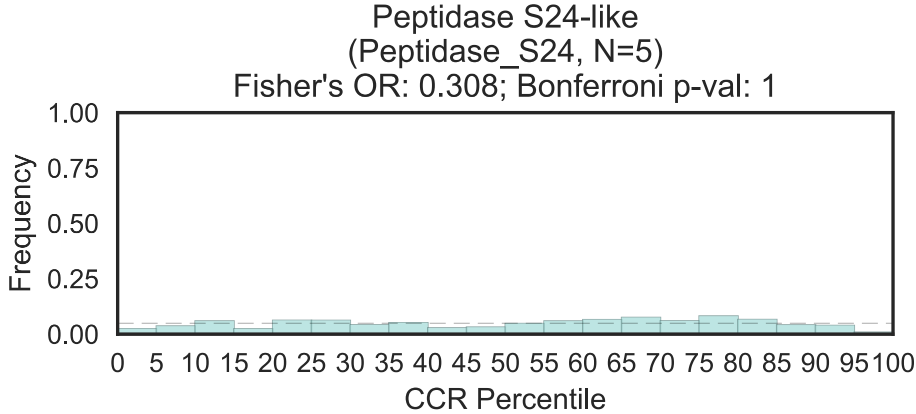

Peptidase family M49
(Peptidase_M49, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

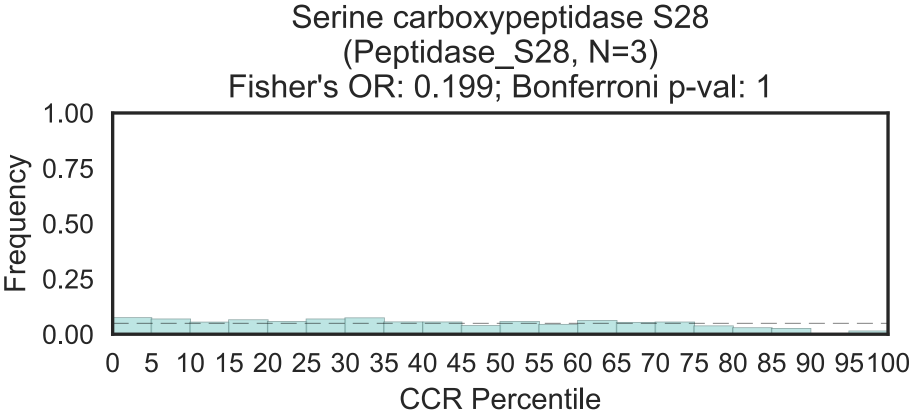

Peptidase M76 family
(Peptidase_M76, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Leishmanolysin
(Peptidase_M8, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

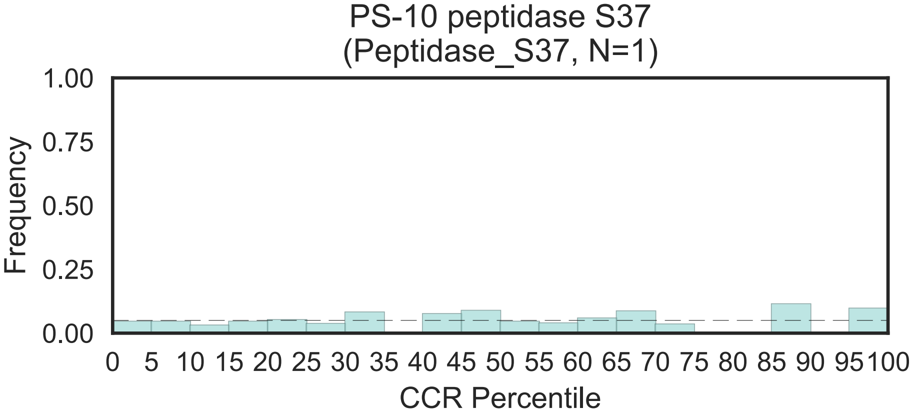

Serine carboxypeptidase
(Peptidase_S10, N=3)
Fisher's OR: 0.412; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

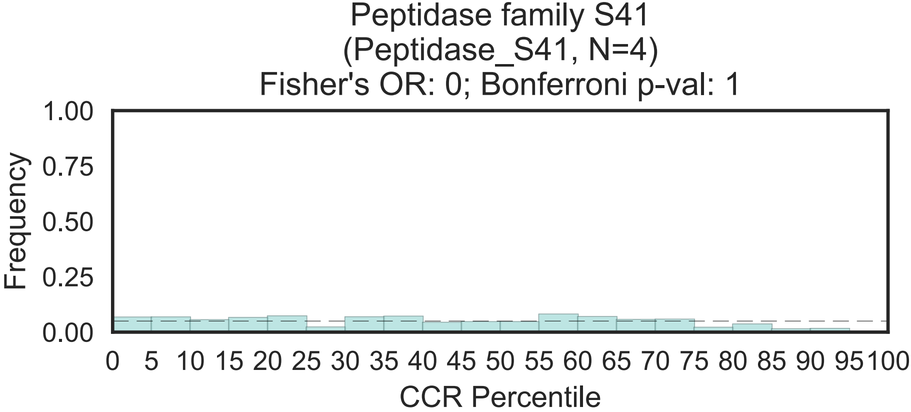

X-Pro dipeptidyl-peptidase (S15 family)
(Peptidase_S15, N=3)
Fisher's OR: 2.1; Bonferroni p-val: 1


Peptidase S24-like
(Peptidase_S24, N=5)
Fisher's OR: 0.308; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



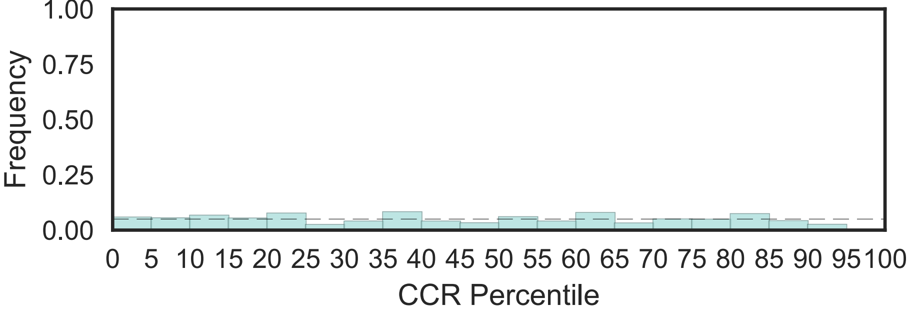
Serine carboxypeptidase S28
(Peptidase_S28, N=3)
Fisher's OR: 0.199; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

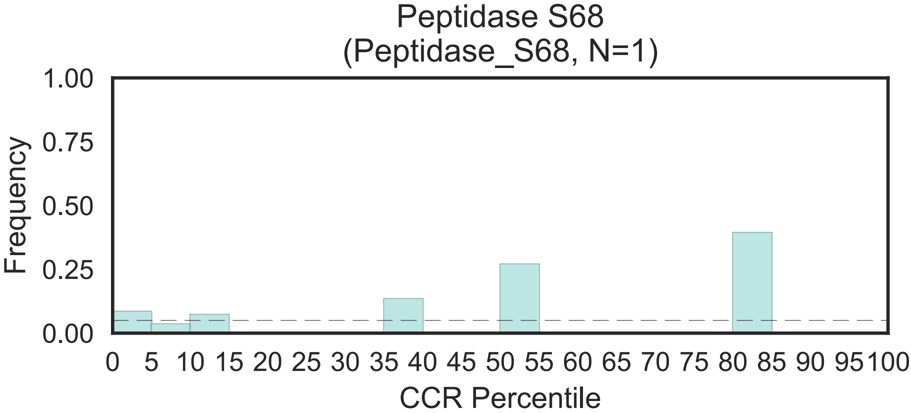

PS-10 peptidase S37
(Peptidase_S37, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

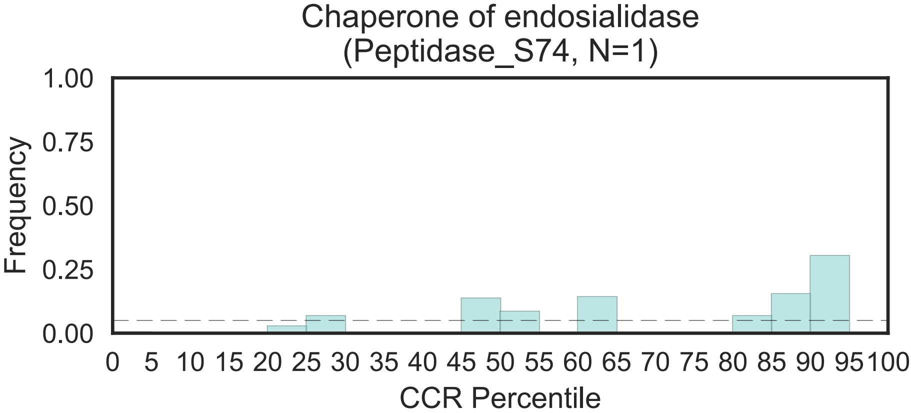


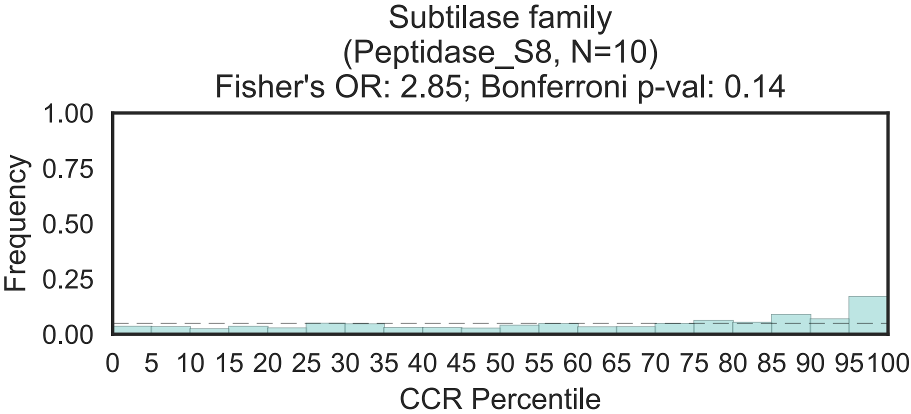
Peptidase family S41
(Peptidase_S41, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

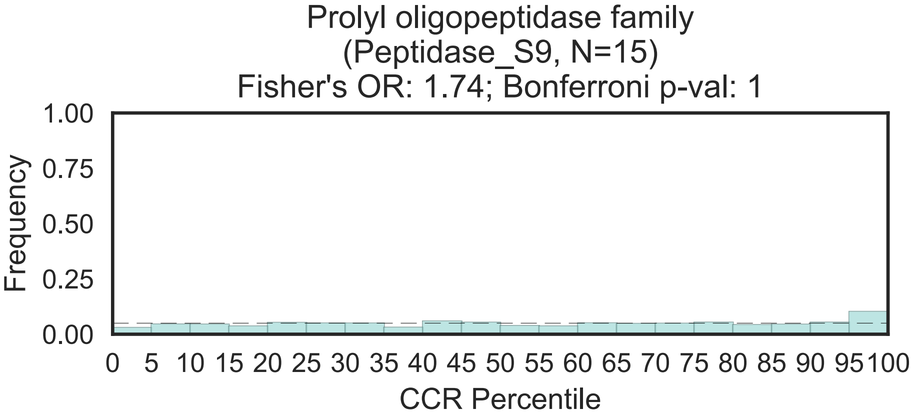
N-terminal domain of Peptidase_S41 in eukaryotic IRBP
(Peptidase_S41_N, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

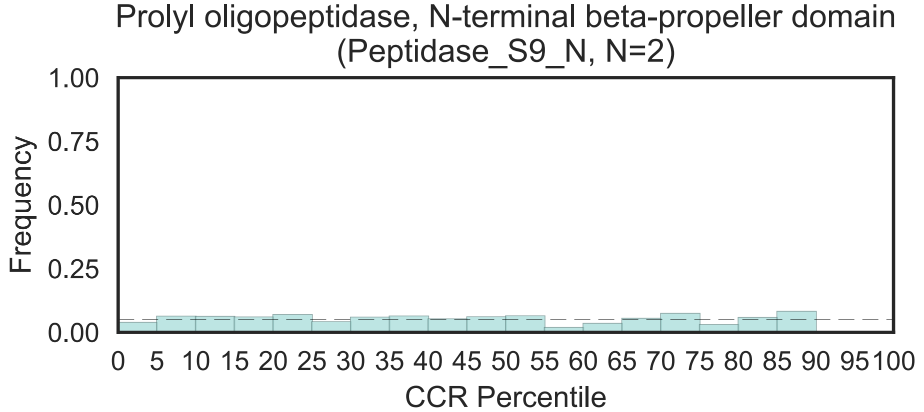


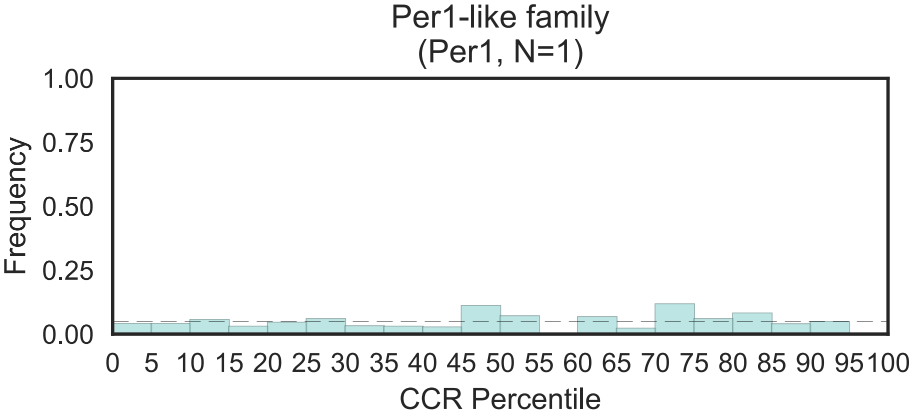

Peptidase S68
(Peptidase_S68, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

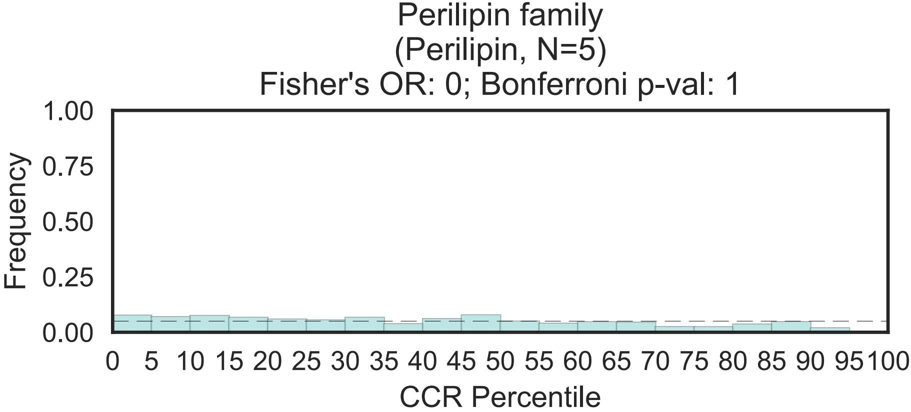

Chaperone of endosialidase
(Peptidase_S74, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

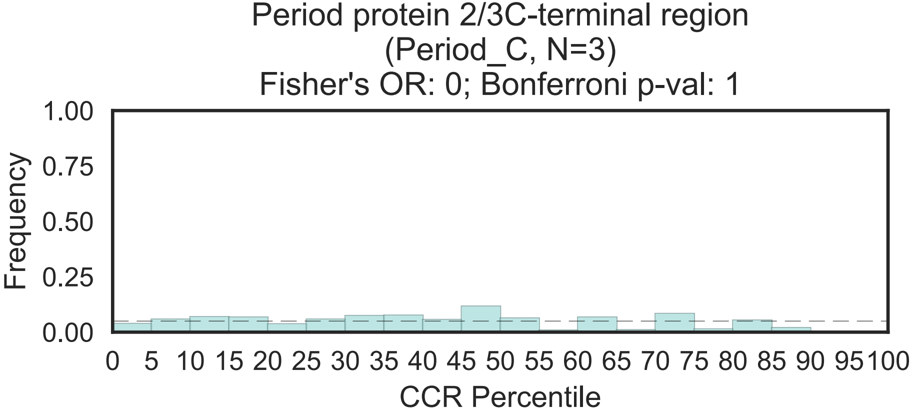

Subtilase family
(Peptidase_S8, N=10)
Fisher's OR: 2.85; Bonferroni p-val: 0.14
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

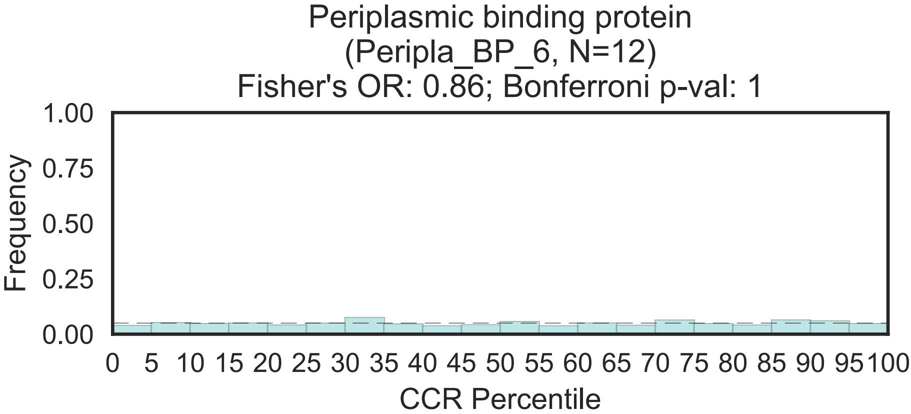

Prolyl oligopeptidase family
(Peptidase_S9, N=15)
Fisher's OR: 1.74; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

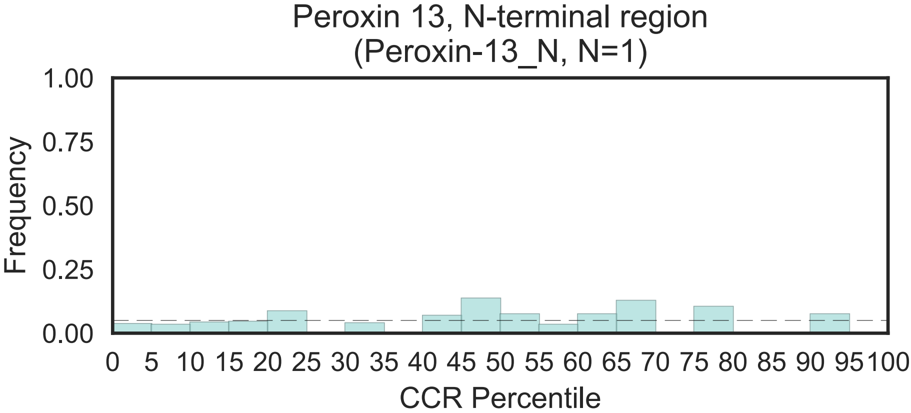

Prolyl oligopeptidase, N-terminal beta-propeller domain
(Peptidase_S9_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

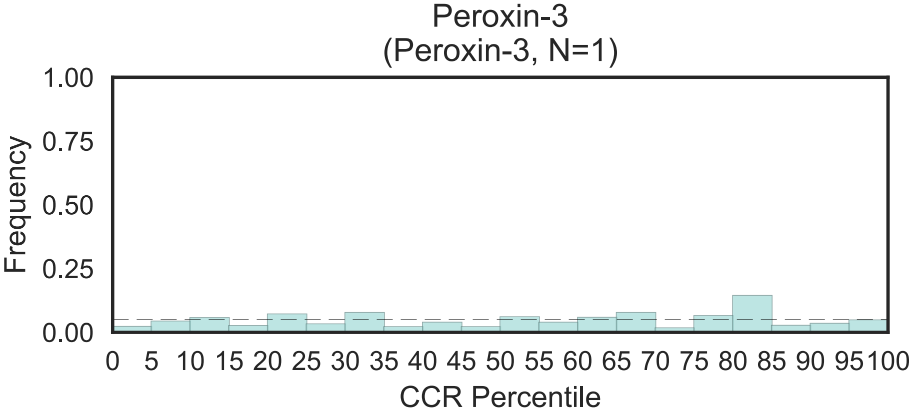

Per1-like family
(Per1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

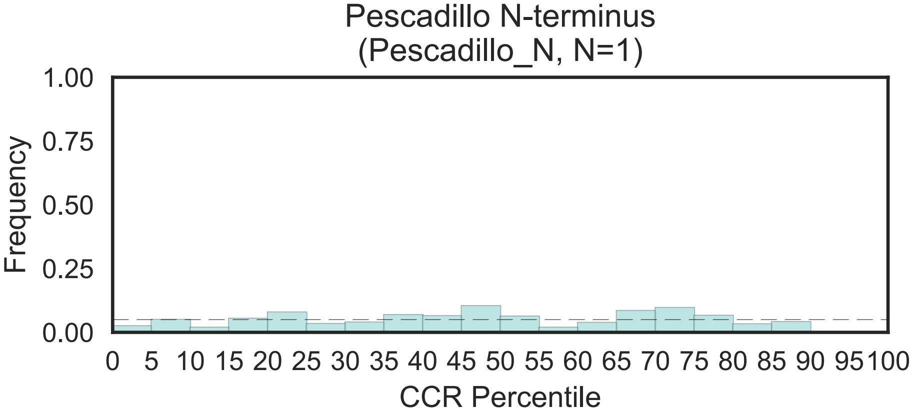

Perilipin family
(Perilipin, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

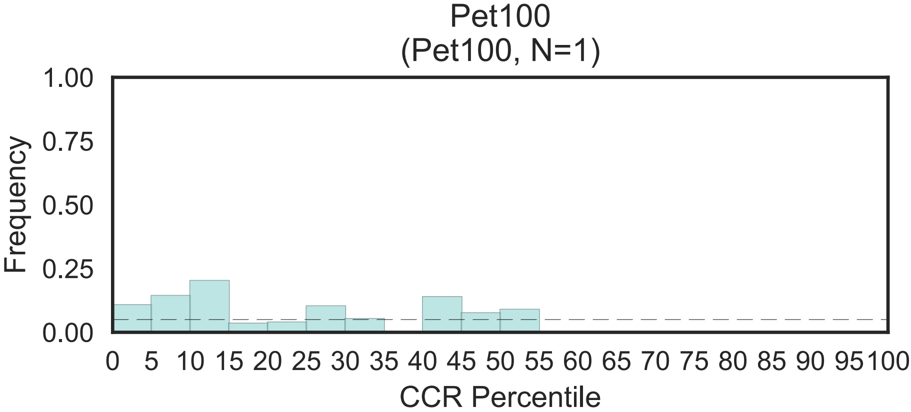

Period protein 2/3C-terminal region
(Period_C, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

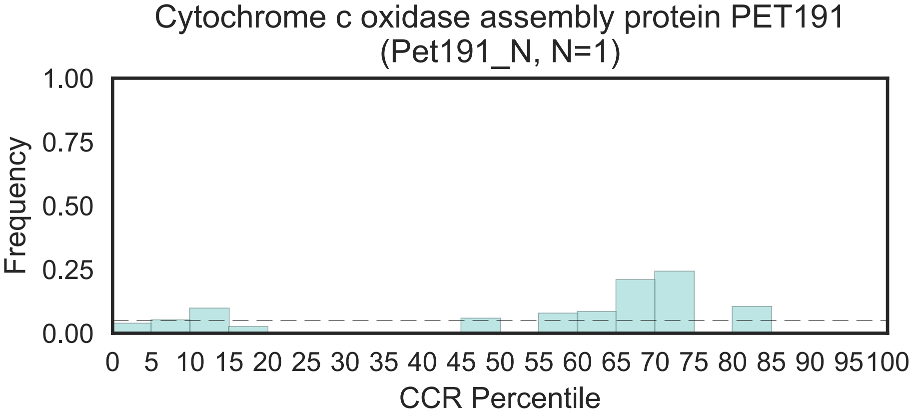

Periplasmic binding protein
(Peripla_BP_6, N=12)
Fisher's OR: 0.86; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Peroxin 13, N-terminal region
(Peroxin-13_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

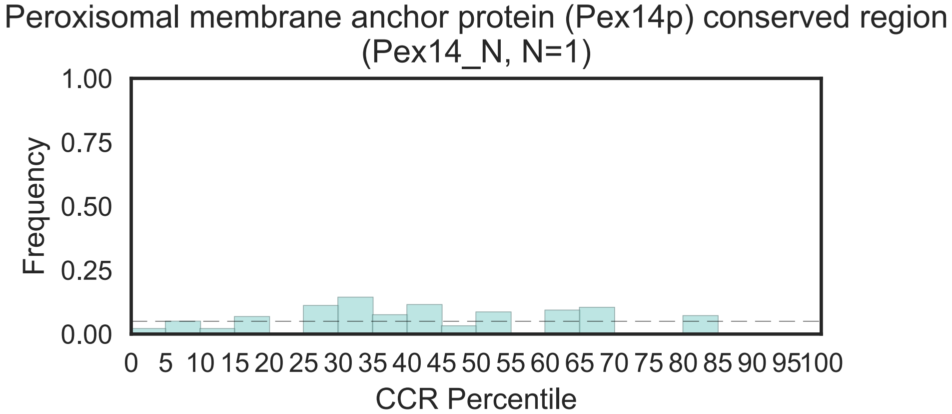

Peroxin-3
(Peroxin-3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

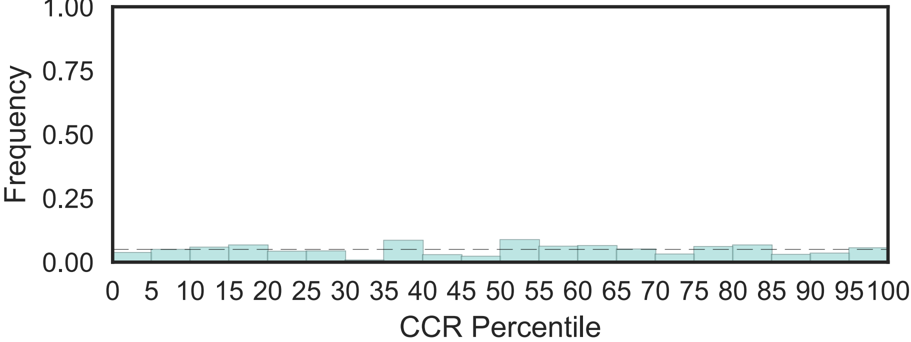

Pescadillo N-terminus
(Pescadillo_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

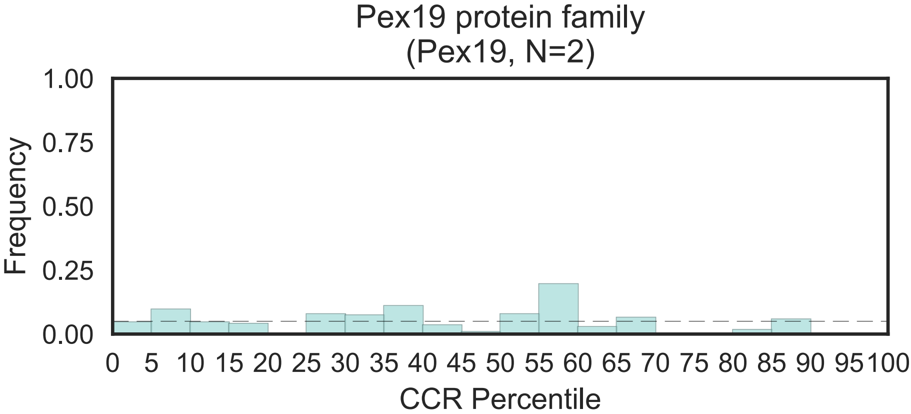

Pet100
(Pet100, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

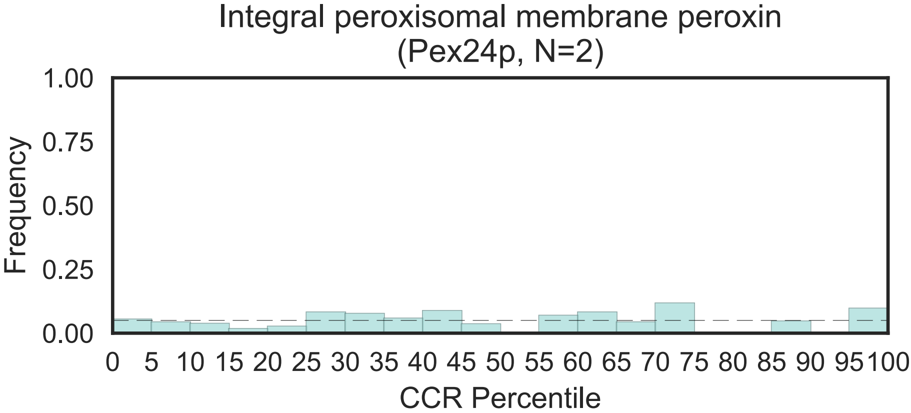


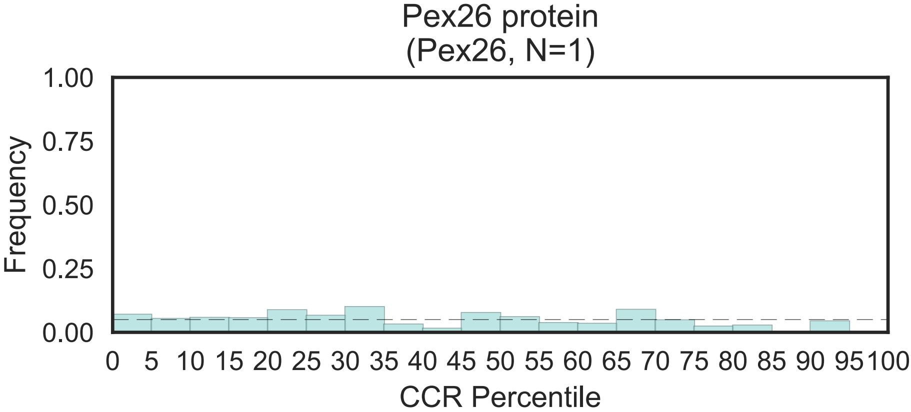
Cytochrome c oxidase assembly protein PET191
(Pet191_N, N=1)

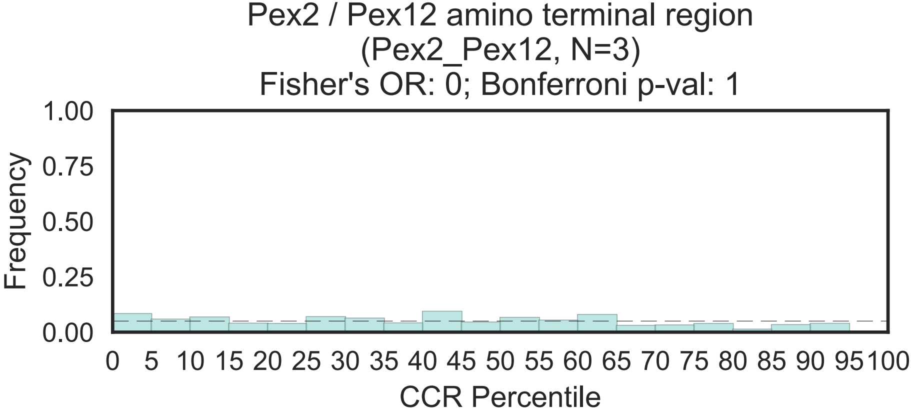

Peroxisomal membrane anchor protein (Pex14p) conserved region
(Pex14_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

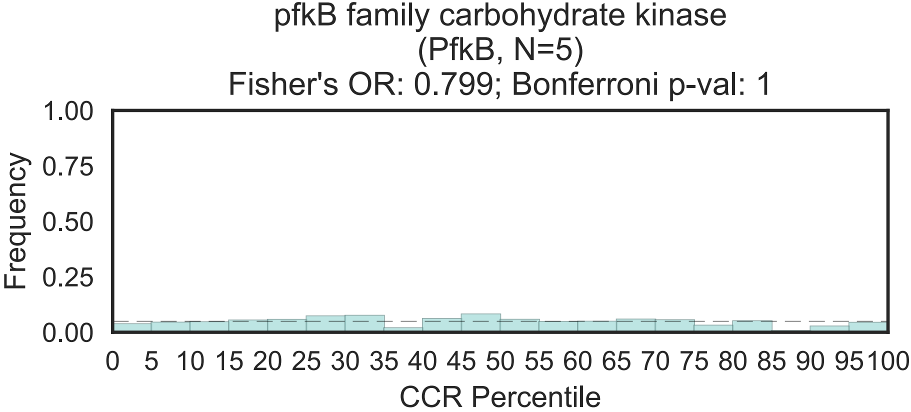

Peroxisomal membrane protein (Pex16)
(Pex16, N=1)

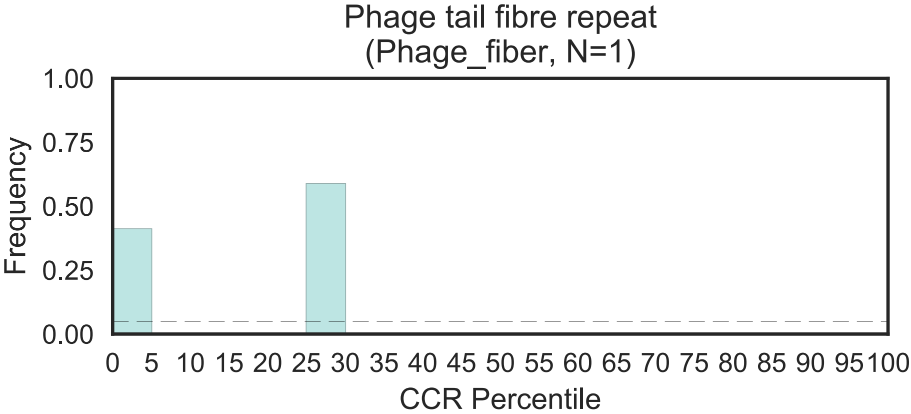

Pex19 protein family
(Pex19, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

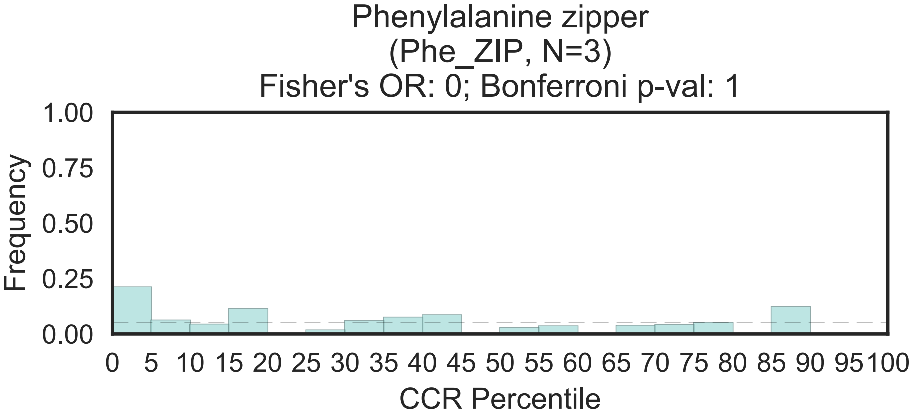

Integral peroxisomal membrane peroxin
(Pex24p, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

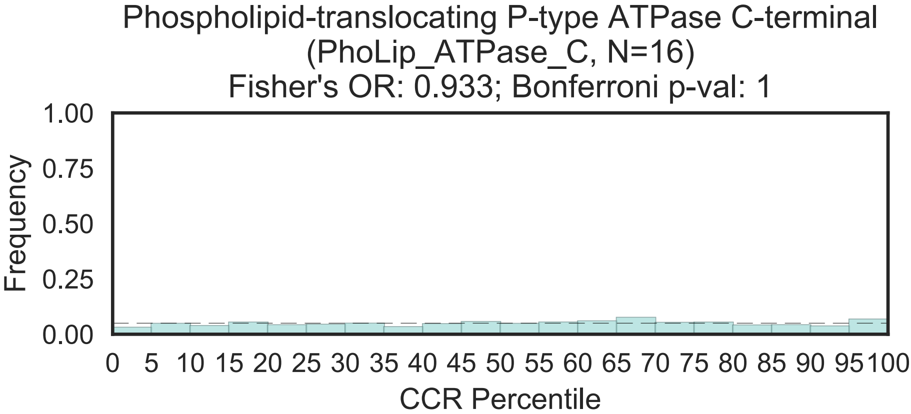

Pex26 protein
(Pex26, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

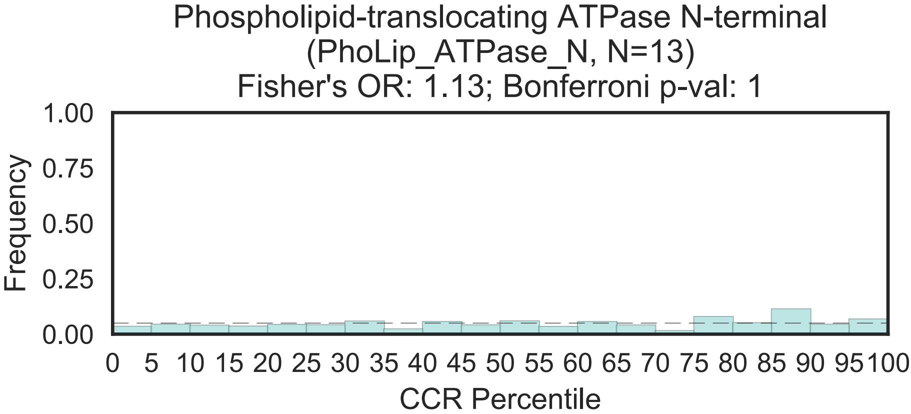

Pex2 / Pex12 amino terminal region
(Pex2_Pex12, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

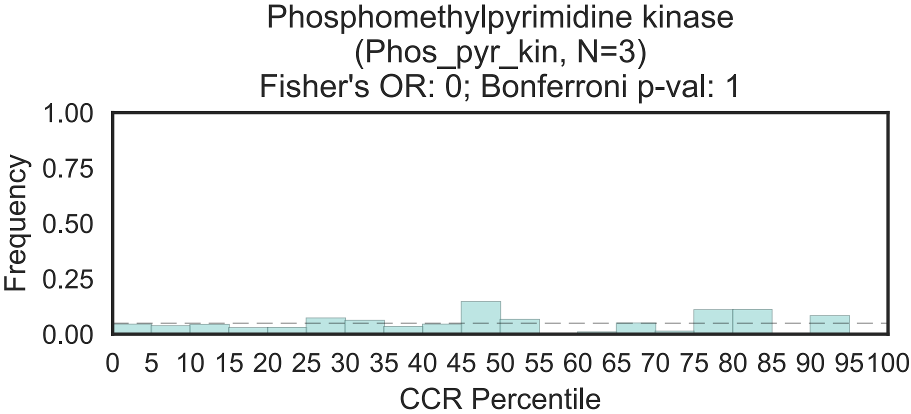

pfkB family carbohydrate kinase
(PfkB, N=5)
Fisher's OR: 0.799; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

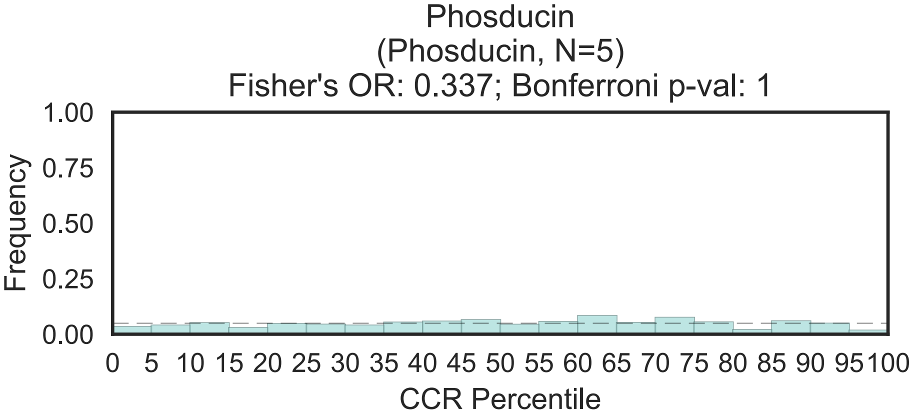

Phage tail fibre repeat
(Phage_fiber, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

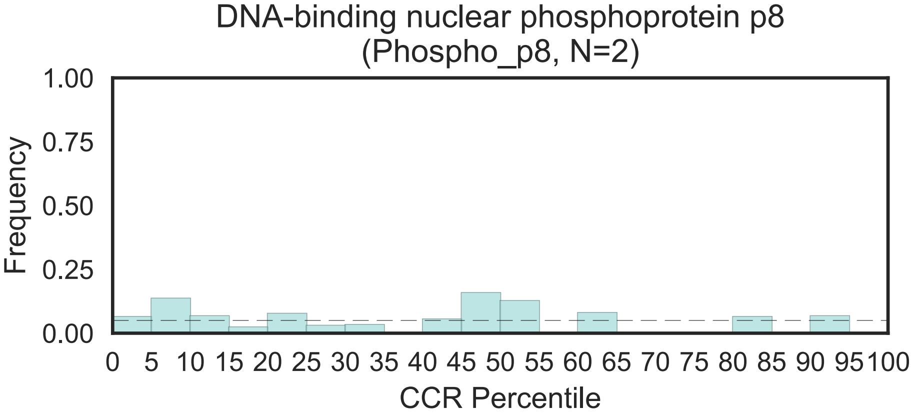

Phenylalanine zipper
(Phe_ZIP, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Phospholipid-translocating P-type ATPase C-terminal
(PhoLip_ATPase_C, N=16)
Fisher's OR: 0.933; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

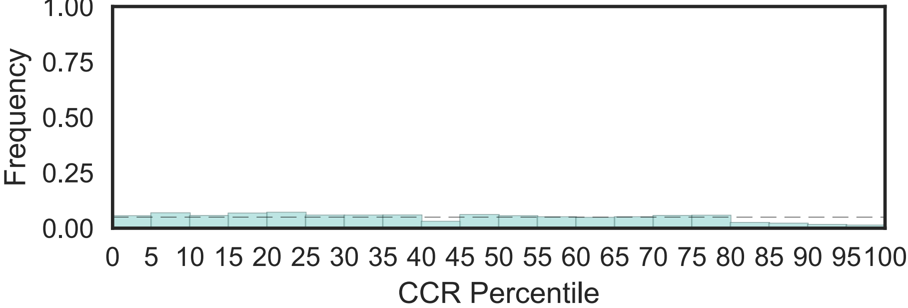

Phospholipid-translocating ATPase N-terminal
(PhoLip_ATPase_N, N=13)
Fisher's OR: 1.13; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

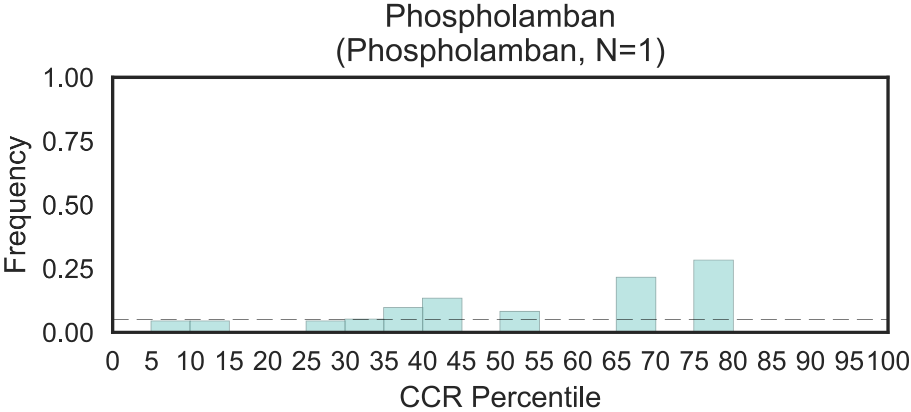

Phosphomethylpyrimidine kinase
(Phos_pyr_kin, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

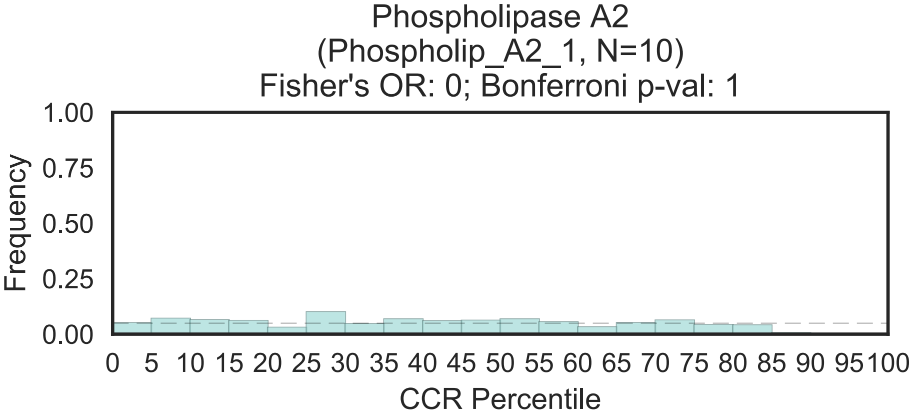

Phosducin
(Phosducin, N=5)
Fisher's OR: 0.337; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

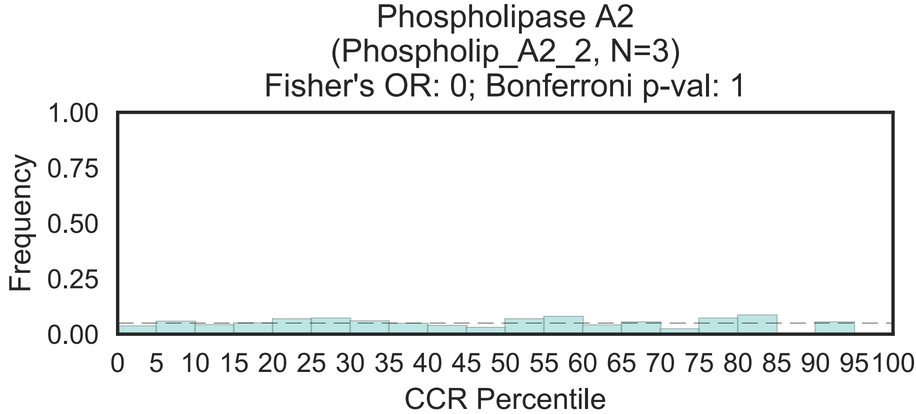

DNA-binding nuclear phosphoprotein p8
(Phospho_p8, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

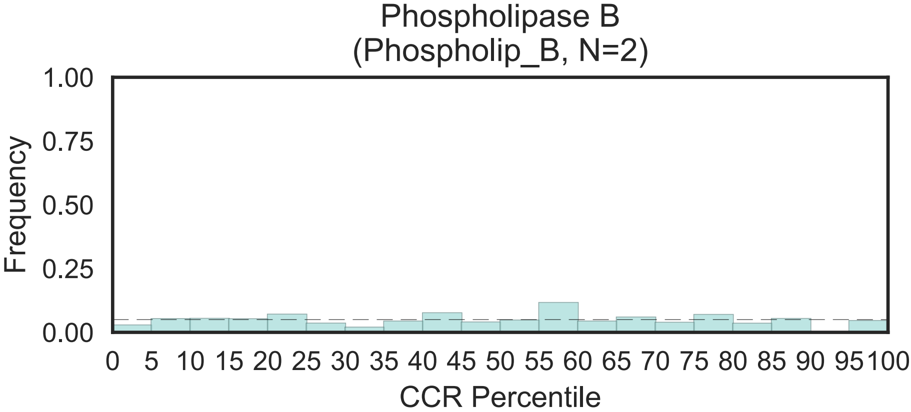
Type I phosphodiesterase / nucleotide pyrophosphatase
(Phosphodiest, N=15)
Fisher's OR: 0.235; Bonferroni p-val: 1

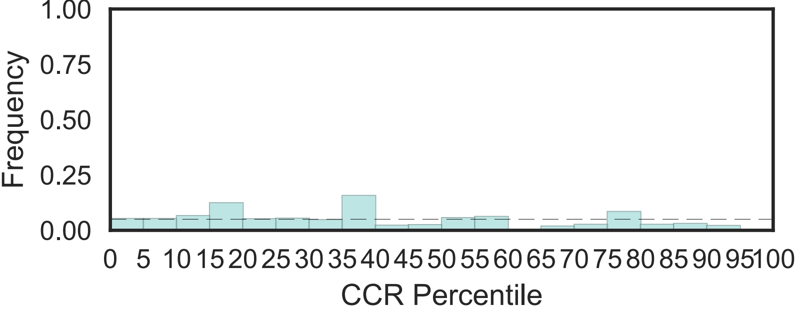



Phospholamban
(Phospholamban, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

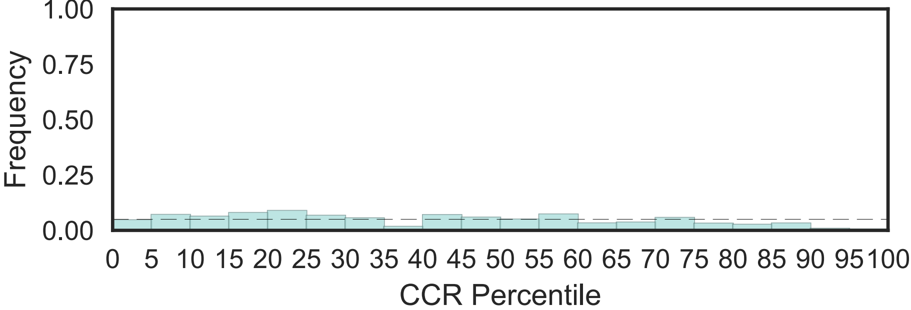

Phospholipase A2
(Phospholip_A2_1, N=10)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Phospholipase A2
(Phospholip_A2_2, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

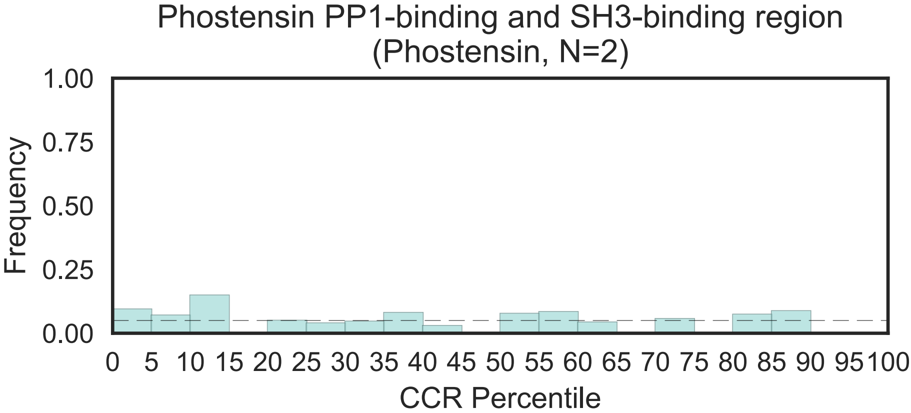

Phospholipase B
(Phospholip_B, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



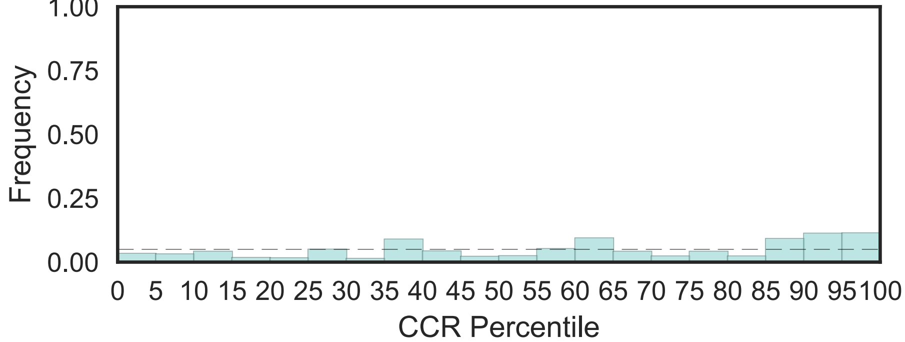
ABC transporter, phosphonate, periplasmic substrate-binding protein
(Phosphonate-bd, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

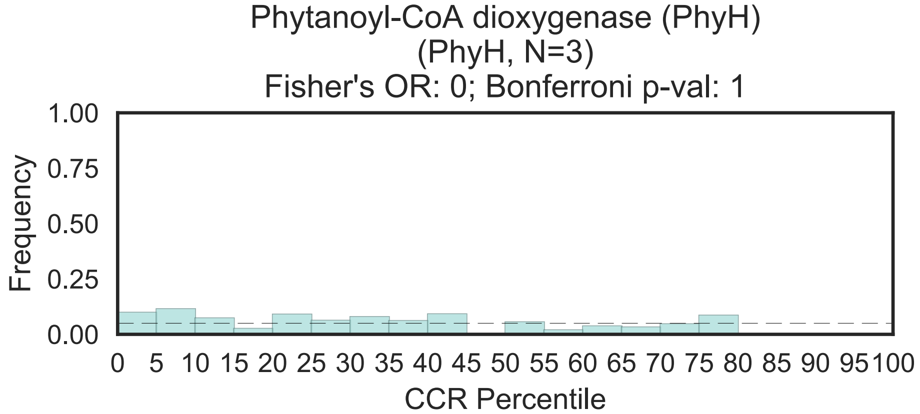


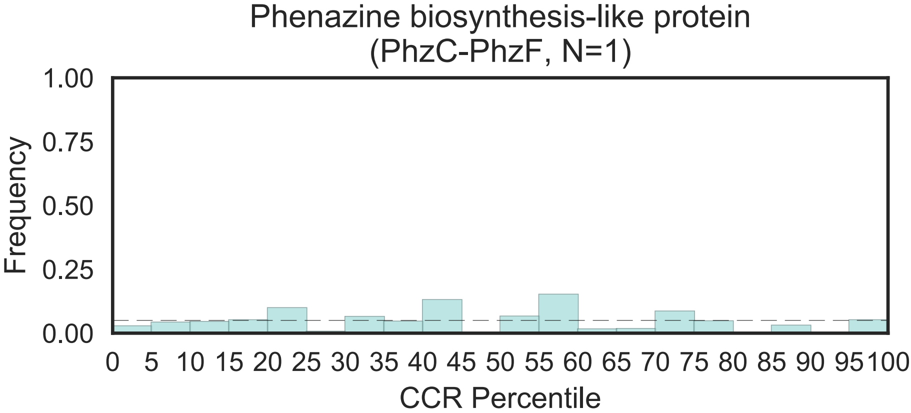
Carbohydrate phosphorylase
(Phosphorylase, N=4)
Fisher's OR: 0.108; Bonferroni p-val: 1

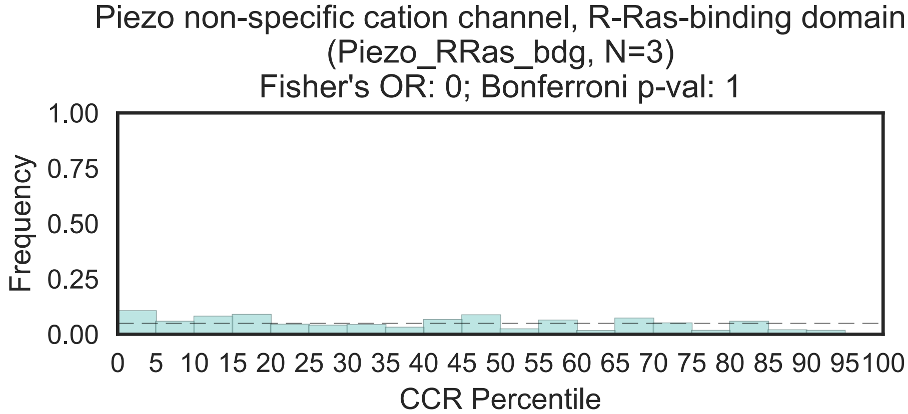

Phostensin PP1-binding and SH3-binding region
(Phostensin, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

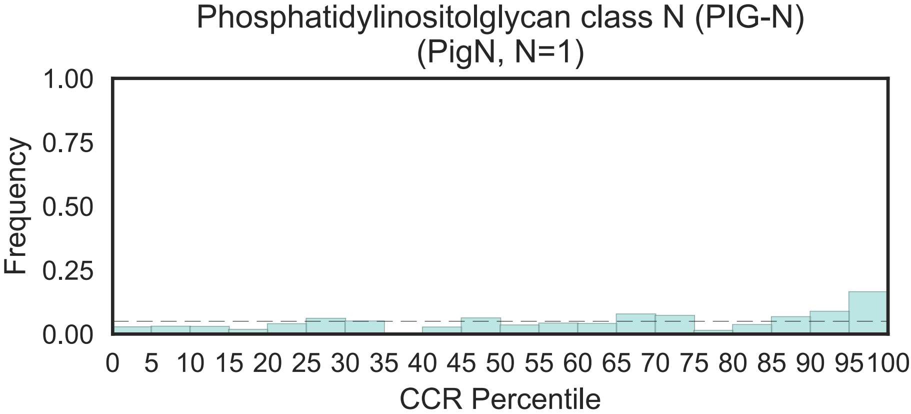
Male germ-cell putative homeodomain transcription factor (Phtf-FEM1B_bdg, N=2)

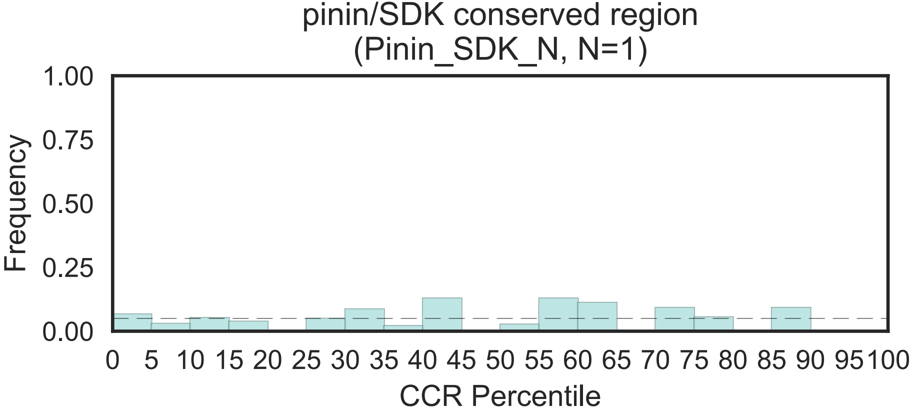


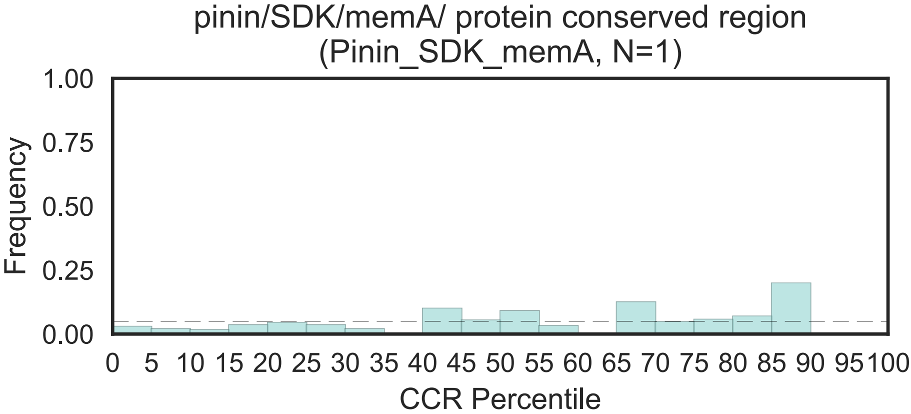

Phytanoyl-CoA dioxygenase (PhyH)
(PhyH, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

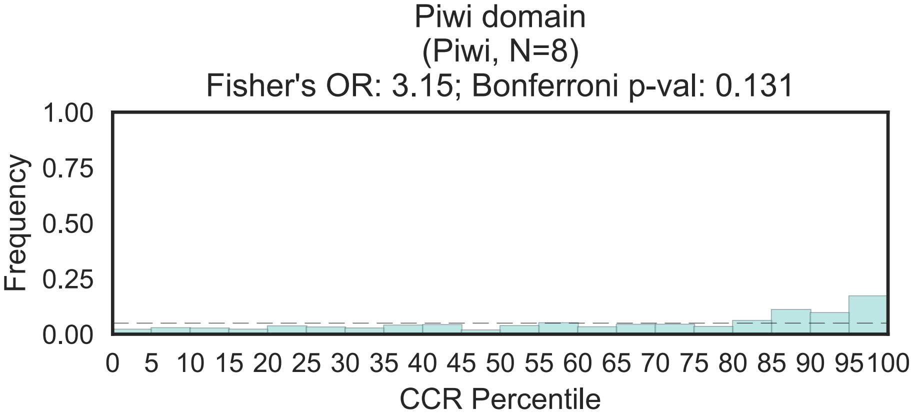

Phenazine biosynthesis-like protein
(PhzC-PhzF, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

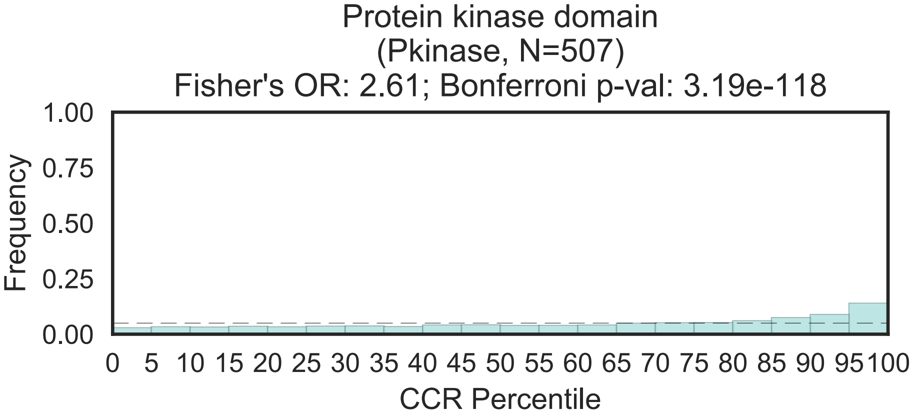

Piezo non-specific cation channel, R-Ras-binding domain
(Piezo_RRas_bdg, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

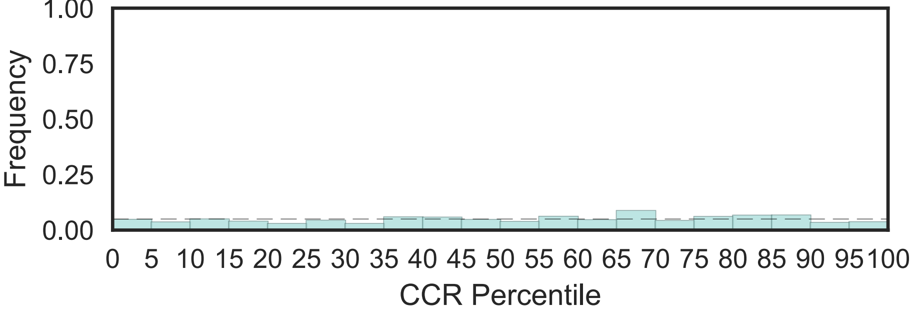

Phosphatidylinositolglycan class N (PIG-N)
(PigN, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


pinin/SDK conserved region
(Pinin_SDK_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

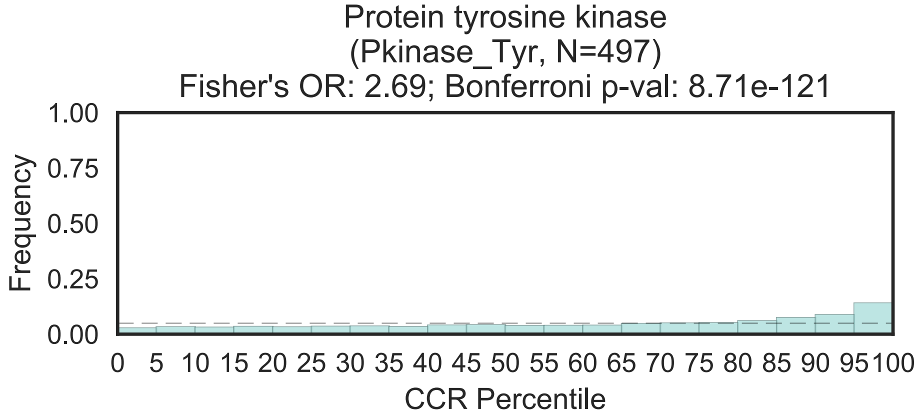

pinin/SDK/memA/ protein conserved region
(Pinin_SDK_memA, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

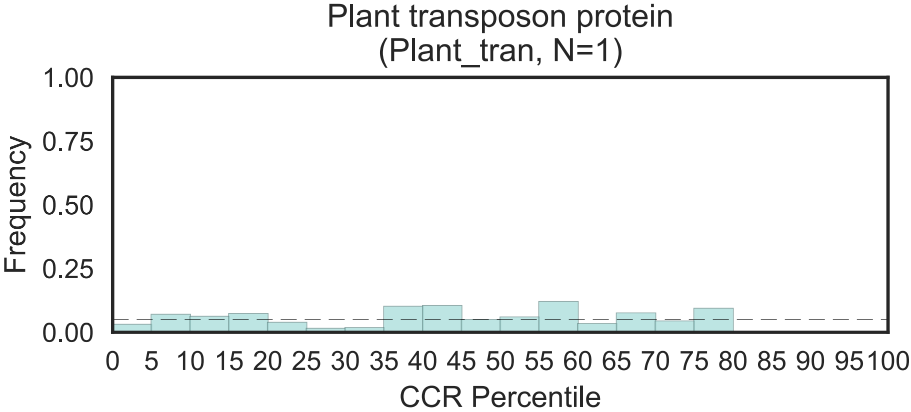

Piwi domain
(Piwi, N=8)
Fisher's OR: 3.15; Bonferroni p-val: 0.131
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

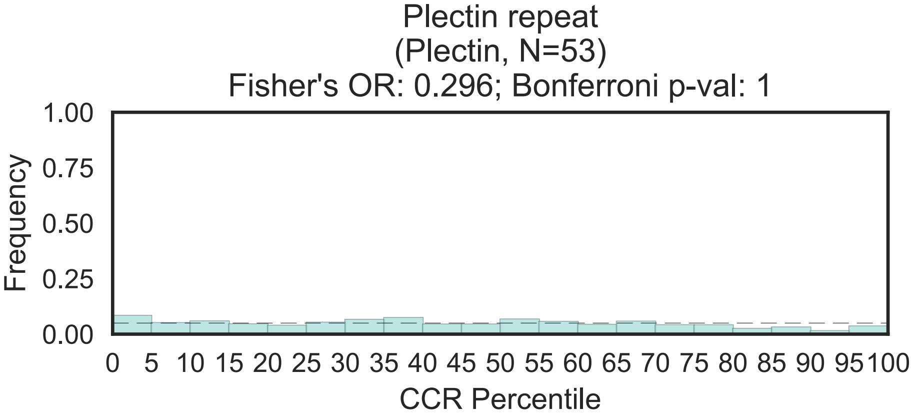

Protein kinase domain
(Pkinase, N=507)
Fisher's OR: 2.61; Bonferroni p-val: 3.19e-118
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

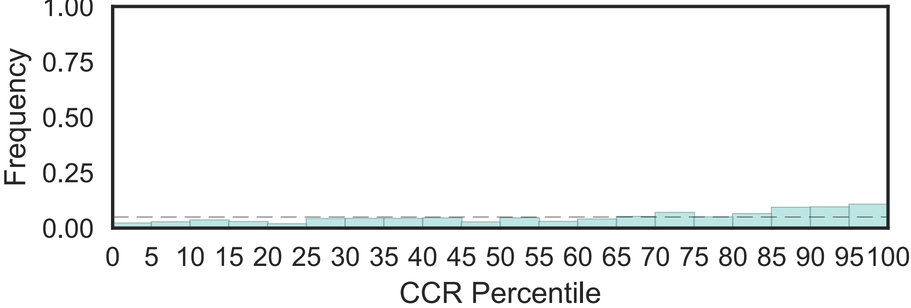


Protein kinase C terminal domain
(Pkinase_C, N=34)
Fisher's OR: 0.681; Bonferroni p-val: 1

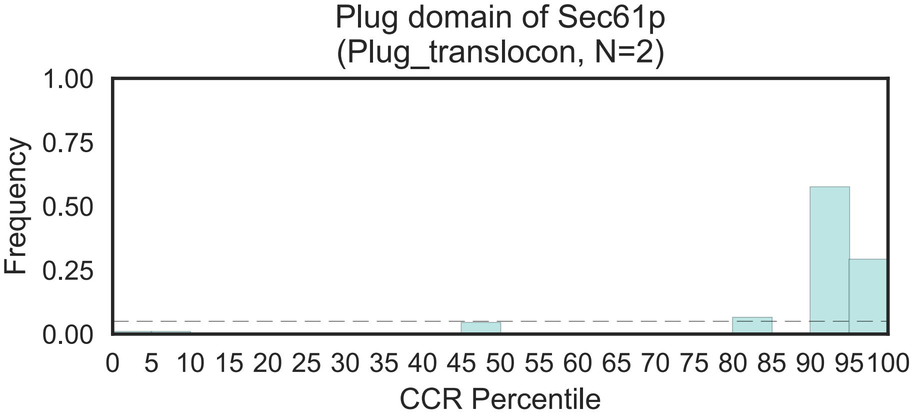

Protein tyrosine kinase
(Pkinase_Tyr, N=497)
Fisher's OR: 2.69; Bonferroni p-val: 8.71e-121
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

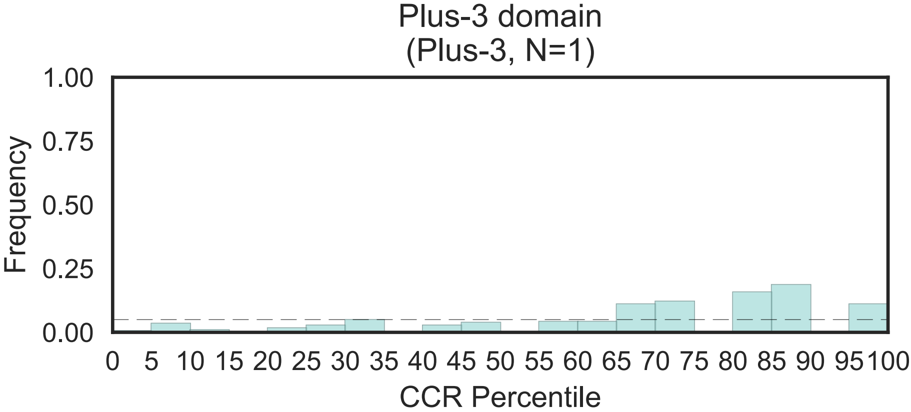

Plant transposon protein
(Plant_tran, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

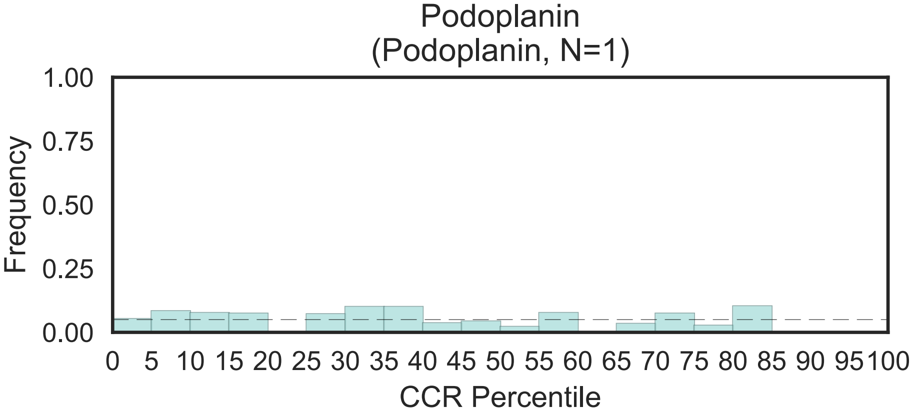

Plectin repeat
(Plectin, N=53)
Fisher's OR: 0.296; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

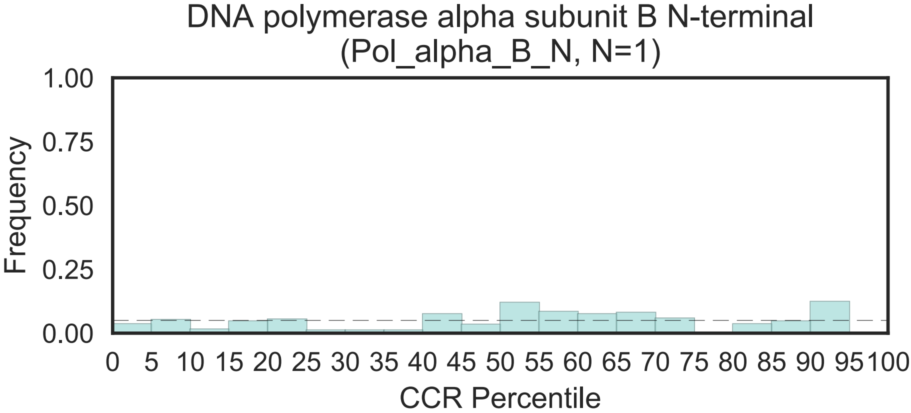


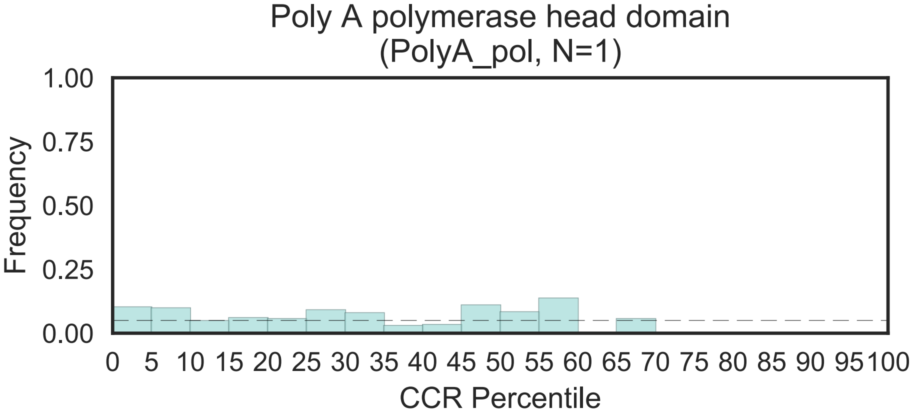
Plexin cytoplasmic RasGAP domain
(Plexin_cytopl, N=10)
Fisher's OR: 2.1; Bonferroni p-val: 1


Plug domain of Sec61p
(Plug_translocon, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

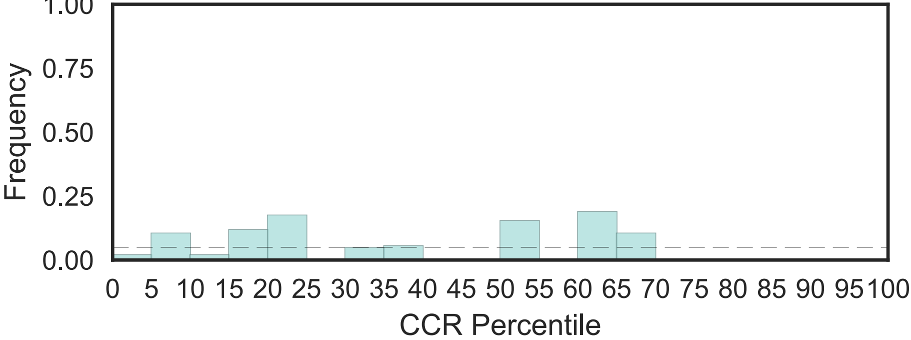

Plus-3 domain
(Plus-3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

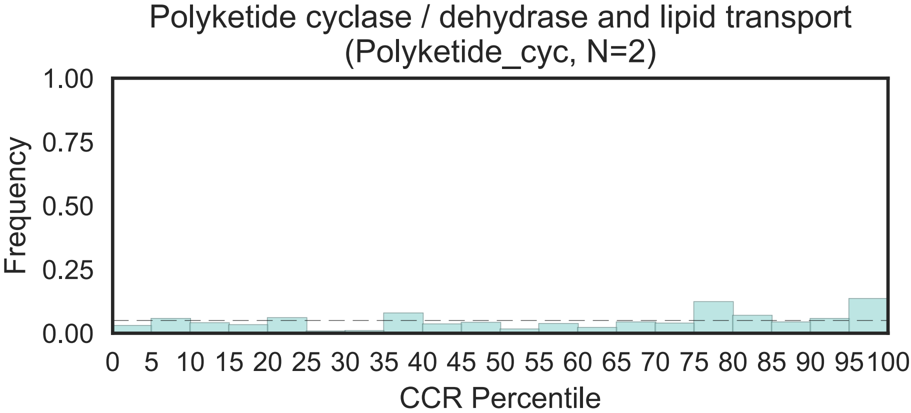

Podoplanin
(Podoplanin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

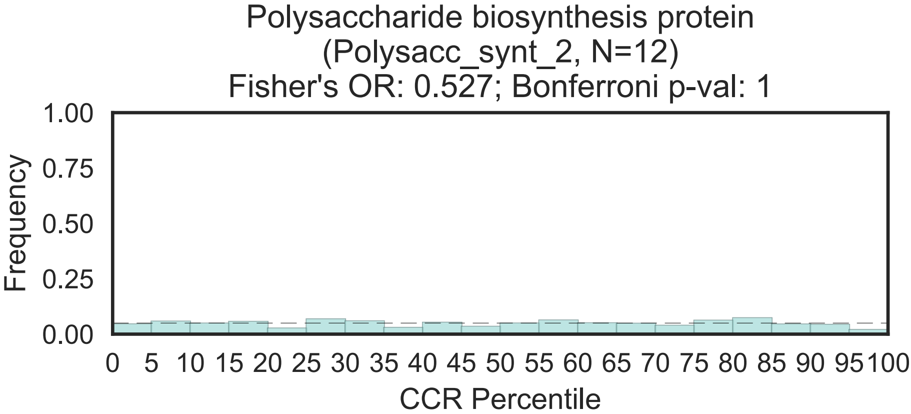

DNA polymerase alpha subunit B N-terminal
(Pol_alpha_B_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

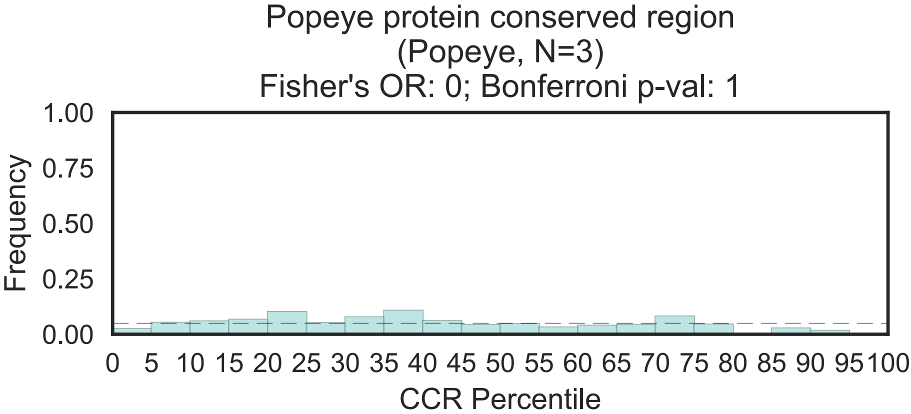

Poly A polymerase head domain
(PolyA_pol, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

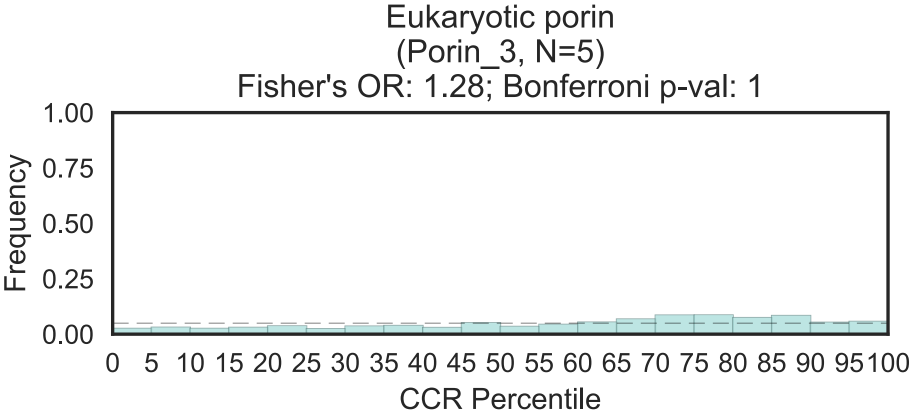
Probable RNA and SrmB- binding site of polymerase A (PolyA_pol_RNAbd, N=1)

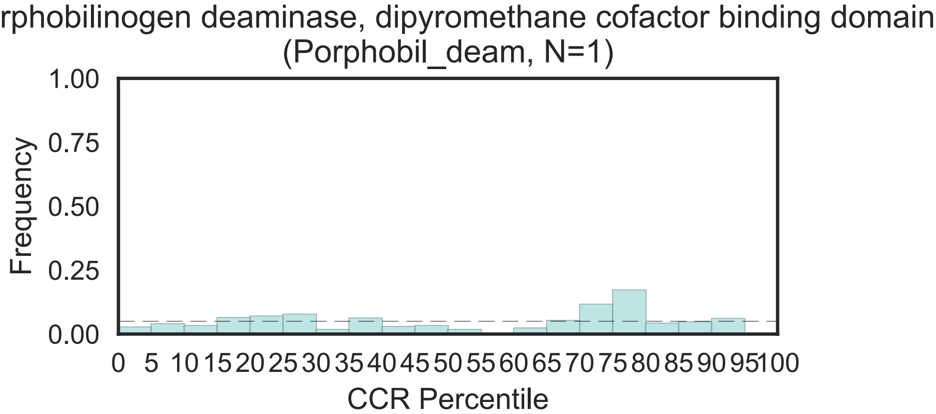


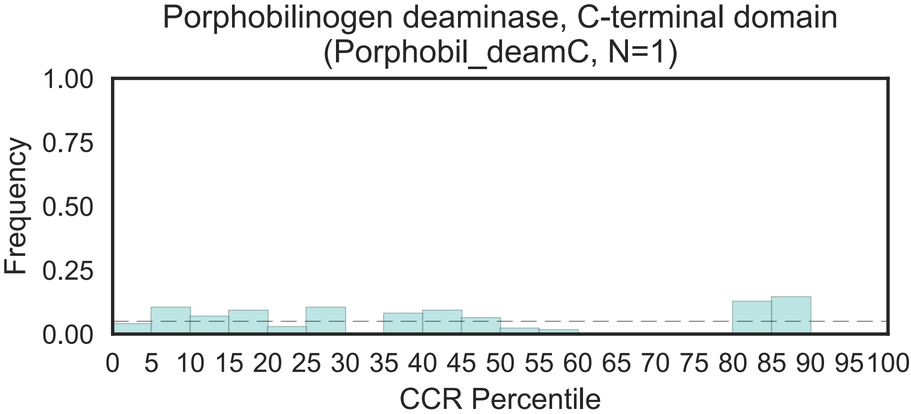

Polyketide cyclase / dehydrase and lipid transport
(Polyketide_cyc, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

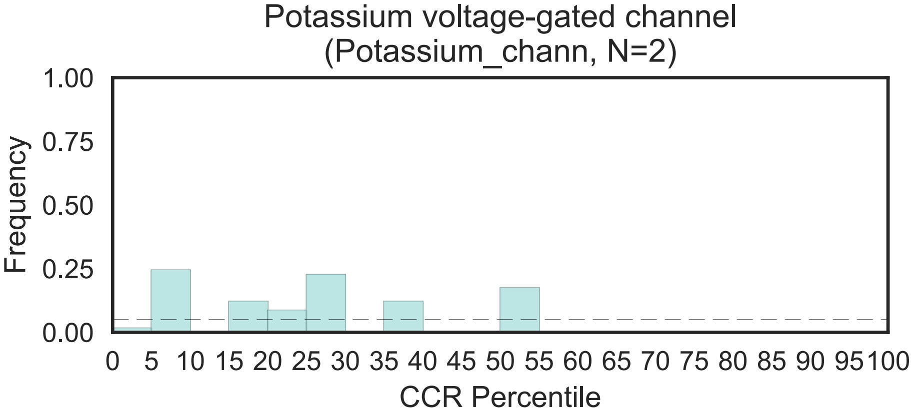

Polysaccharide biosynthesis protein
(Polysacc_synt_2, N=12)
Fisher's OR: 0.527; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

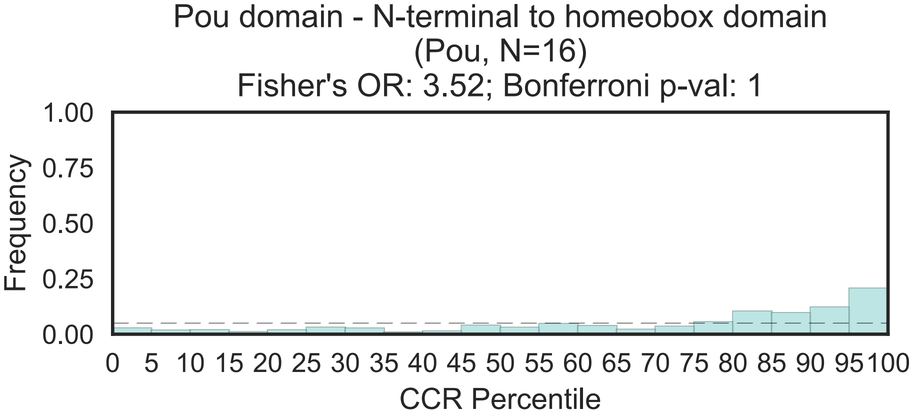

Popeye protein conserved region
(Popeye, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

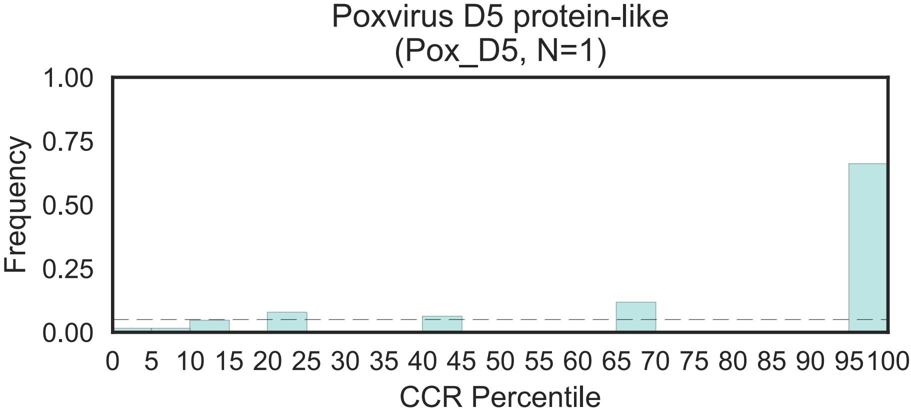

Eukaryotic porin
(Porin_3, N=5)
Fisher's OR: 1.28; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

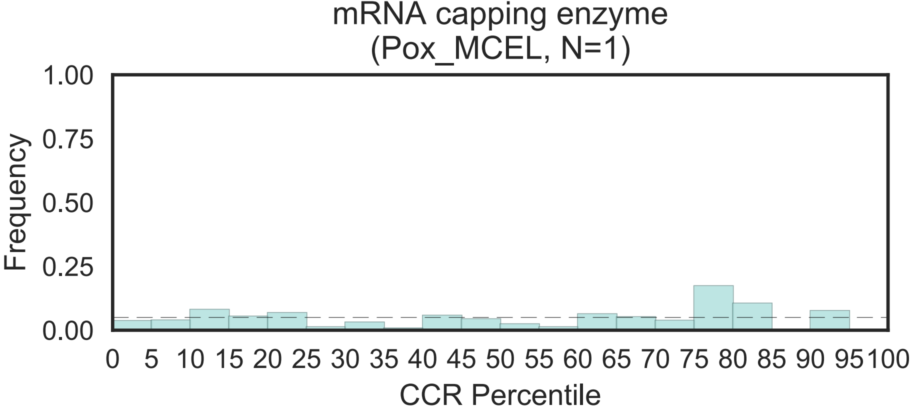

Porphobilinogen deaminase, dipyromethane cofactor binding domain
(Porphobil_deam, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

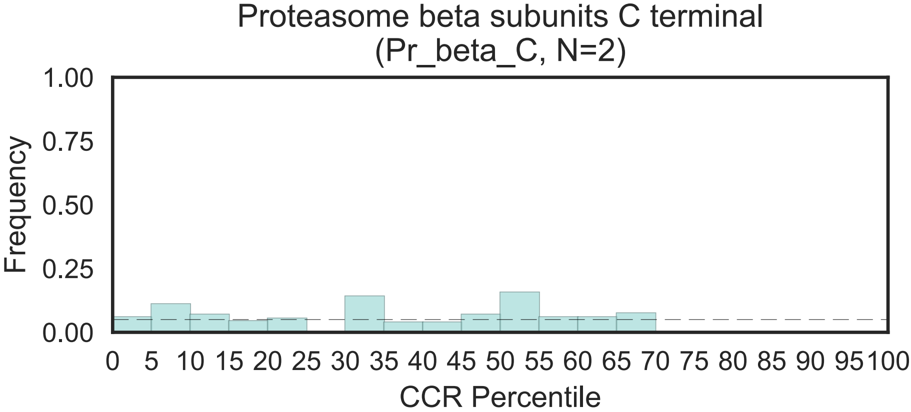

Porphobilinogen deaminase, C-terminal domain
(Porphobil_deamC, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

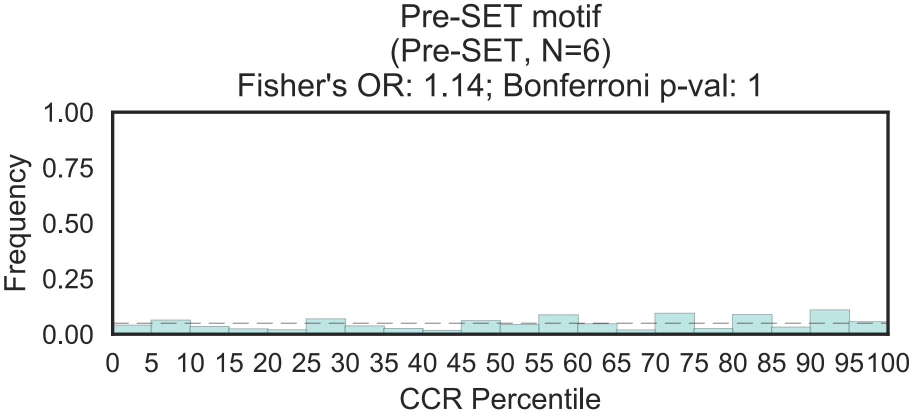

Potassium voltage-gated channel
(Potassium_chann, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

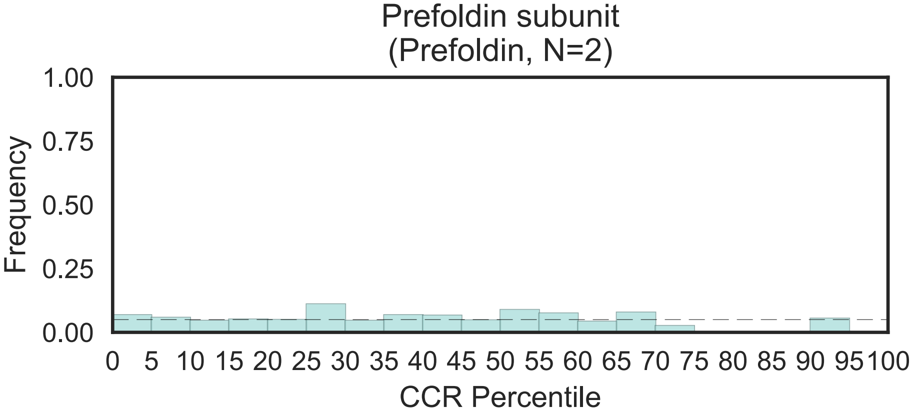

Pou domain - N-terminal to homeobox domain
(Pou, N=16)
Fisher's OR: 3.52; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

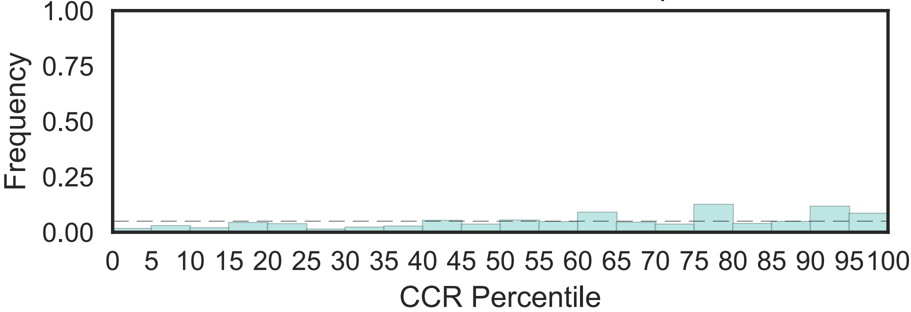

Poxvirus D5 protein-like
(Pox_D5, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

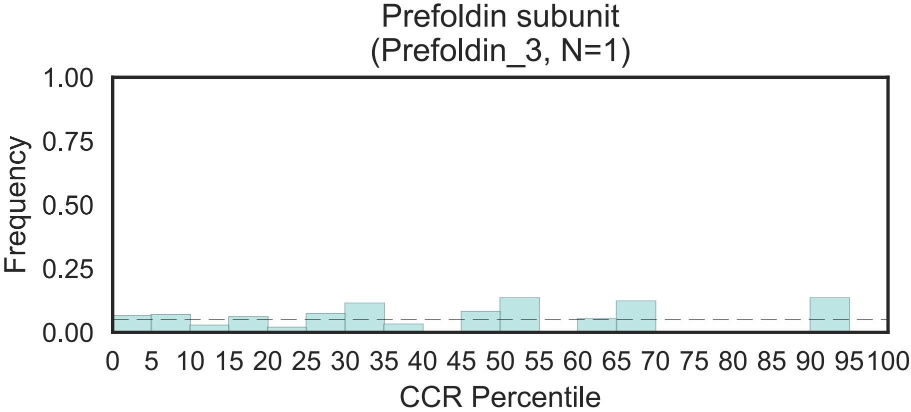

mRNA capping enzyme
(Pox_MCEL, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

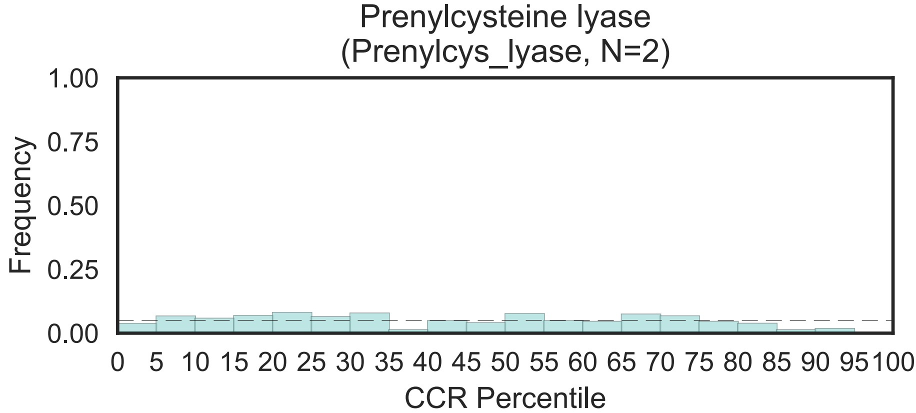

Proteasome beta subunits C terminal
(Pr_beta_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

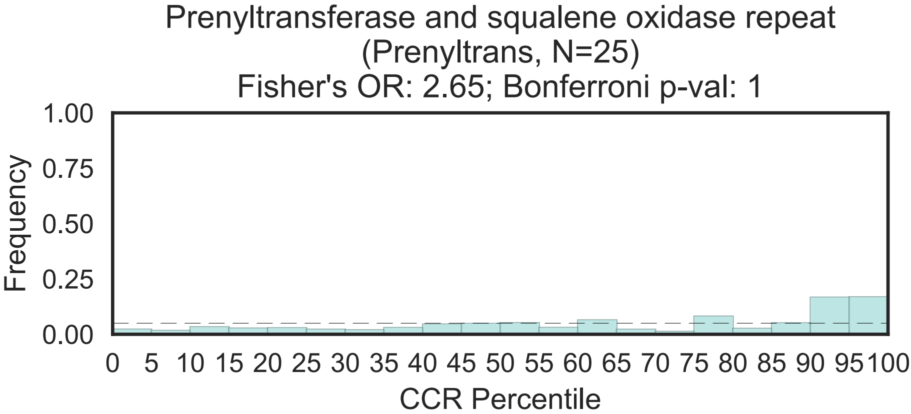

Pre-SET motif
(Pre-SET, N=6)
Fisher's OR: 1.14; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

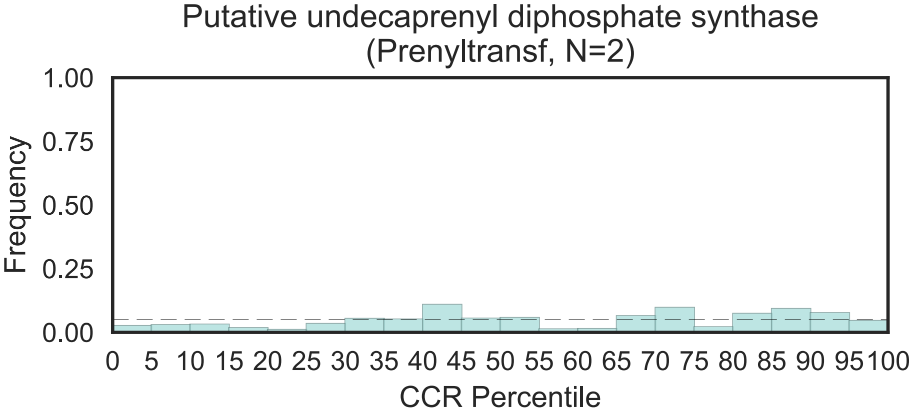

Prefoldin subunit
(Prefoldin, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

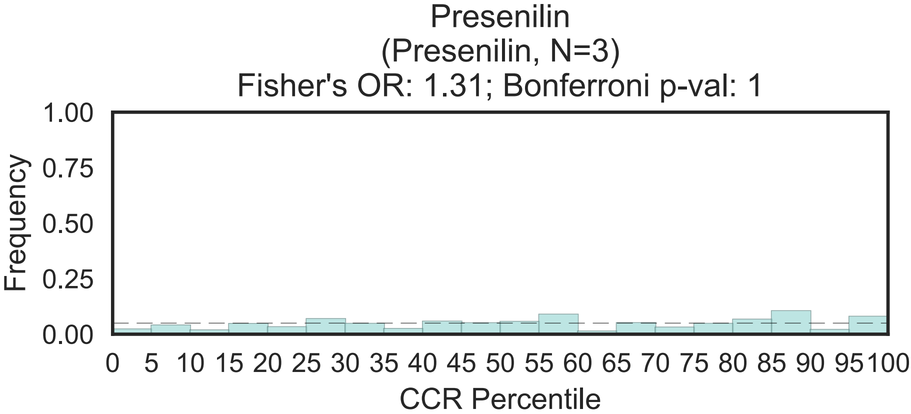

Prefoldin subunit
(Prefoldin_2, N=5)
Fisher's OR: 1.91; Bonferroni p-val: 1


Prefoldin subunit
(Prefoldin_3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

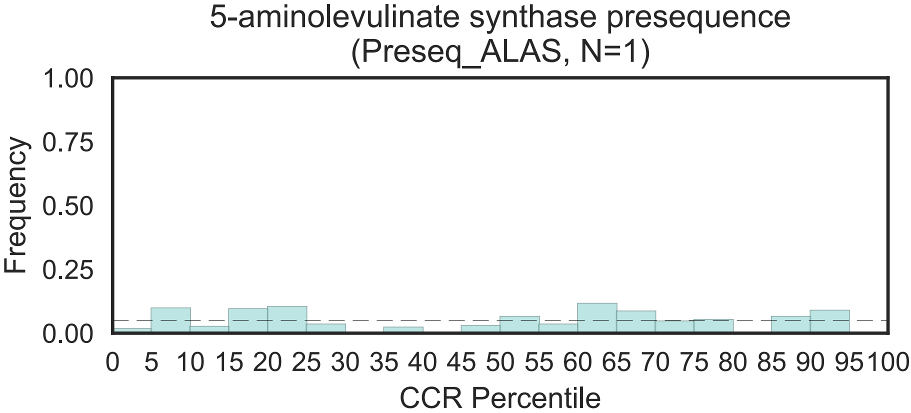

Prenylcysteine lyase
(Prenylcys_lyase, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

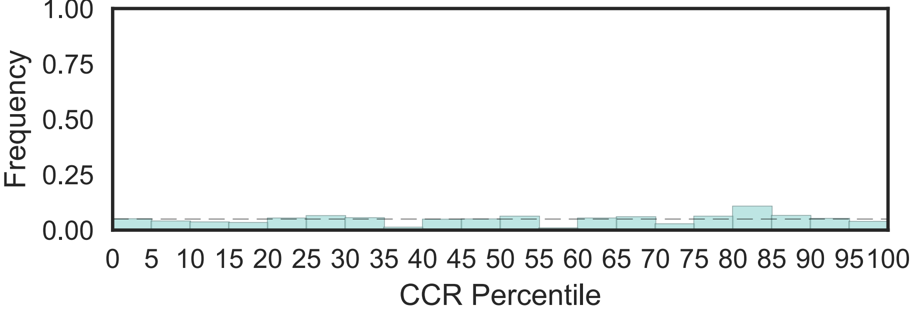

Prenyltransferase and squalene oxidase repeat
(Prenyltrans, N=25)
Fisher's OR: 2.65; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Putative undecaprenyl diphosphate synthase
(Prenyltransf, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

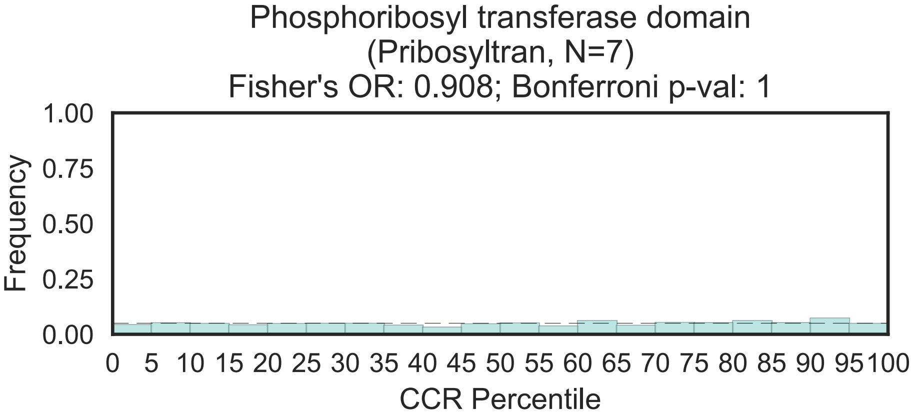


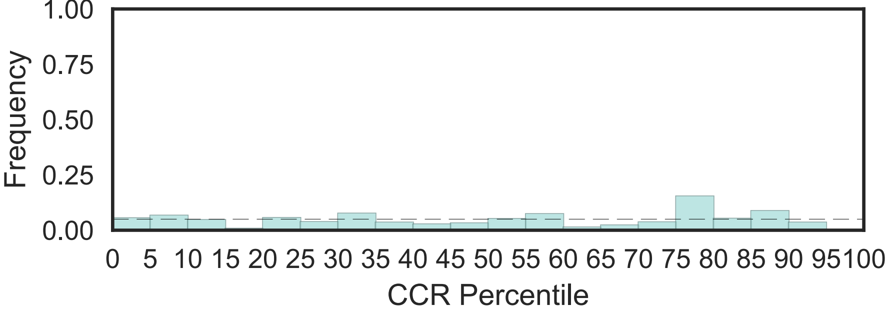
Presenilin
(Presenilin, N=3)
Fisher's OR: 1.31; Bonferroni p-val: 1


5-aminolevulinate synthase presequence
(Preseq_ALAS, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

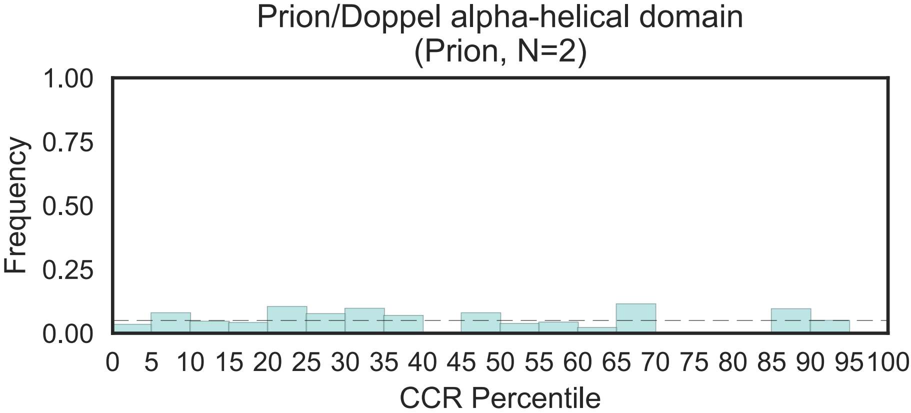


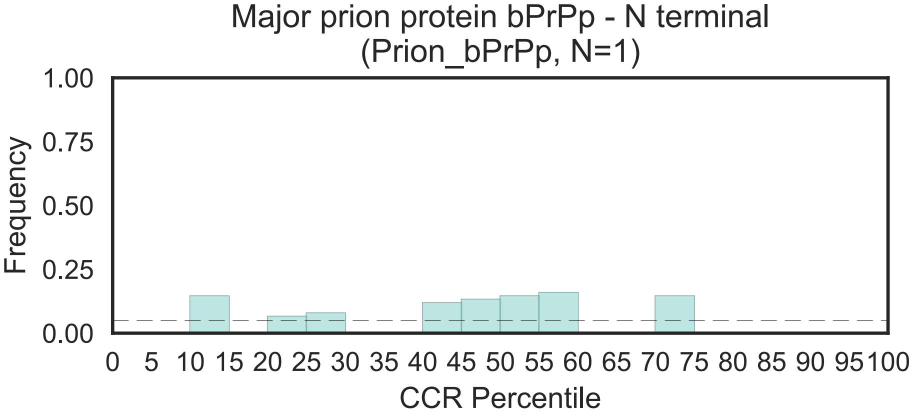
Phosphoribosyl synthetase-associated domain
(Pribosyl_synth, N=3)
Fisher's OR: 0.611; Bonferroni p-val: 1

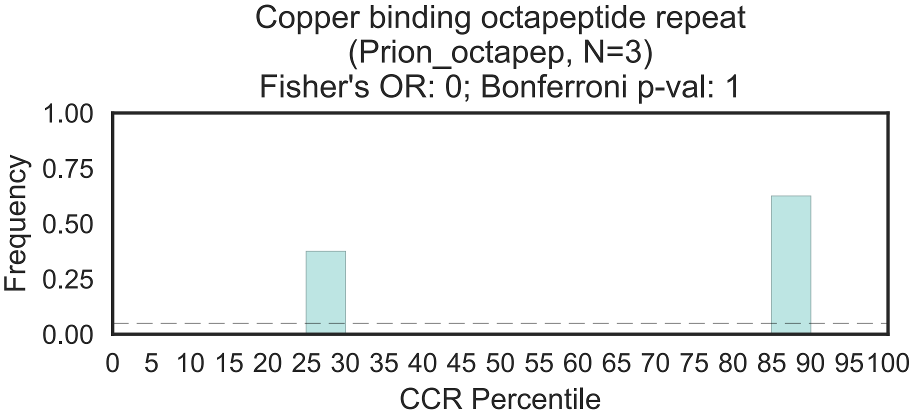

Phosphoribosyl transferase domain
(Pribosyltran, N=7)
Fisher's OR: 0.908; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

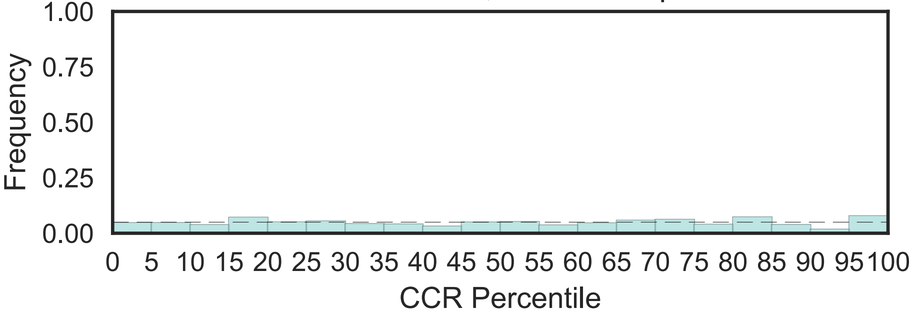


N-terminal domain of ribose phosphate pyrophosphokinase
(Pribosyltran_N, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

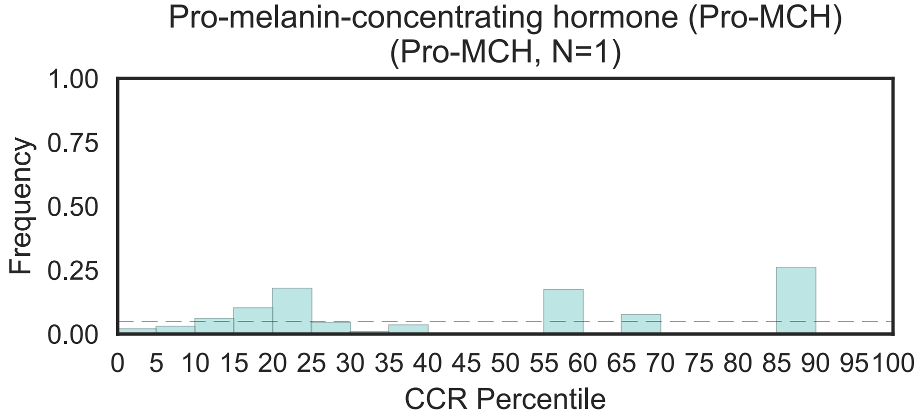

Prion/Doppel alpha-helical domain
(Prion, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

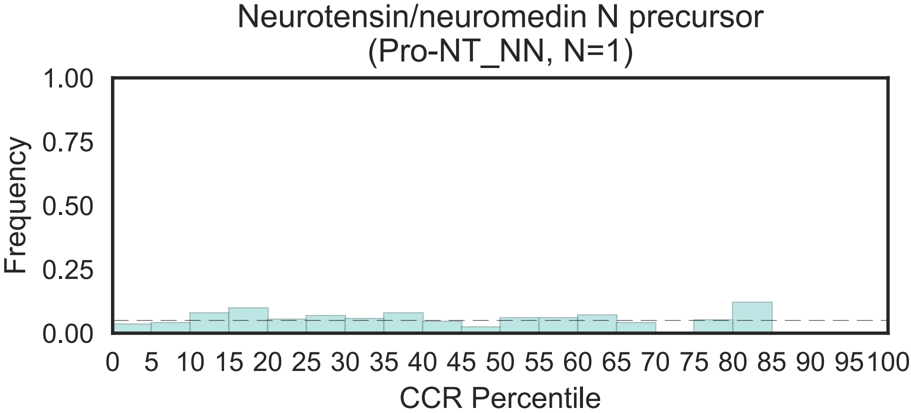

Major prion protein bPrPp - N terminal
(Prion_bPrPp, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

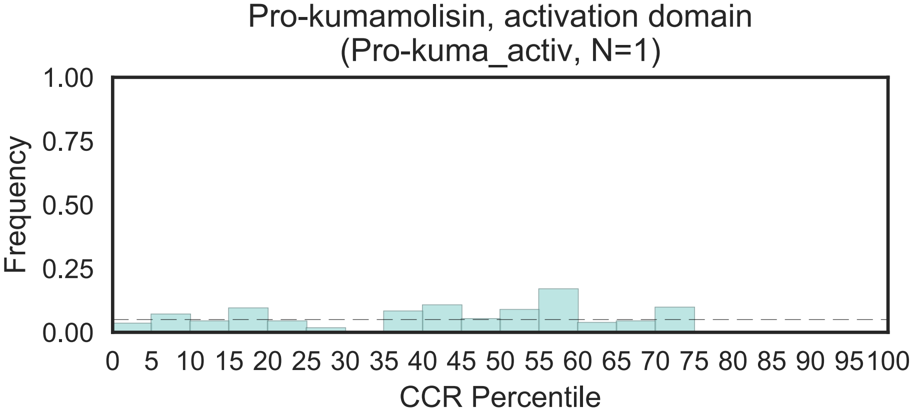

Copper binding octapeptide repeat
(Prion_octapep, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

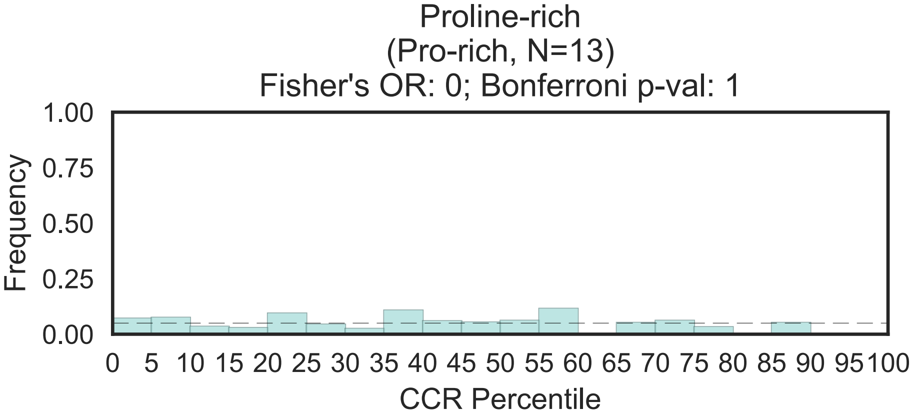


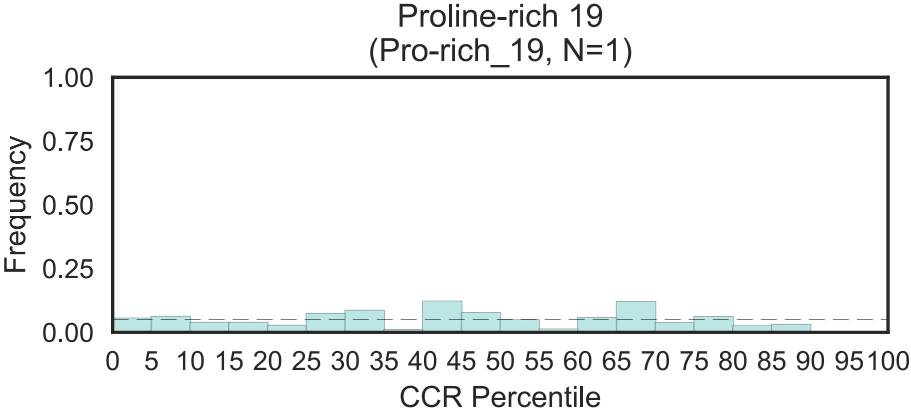
Ribosomal protein L11 methyltransferase (PrmA)
(PrmA, N=17)
Fisher's OR: 1.33; Bonferroni p-val: 1

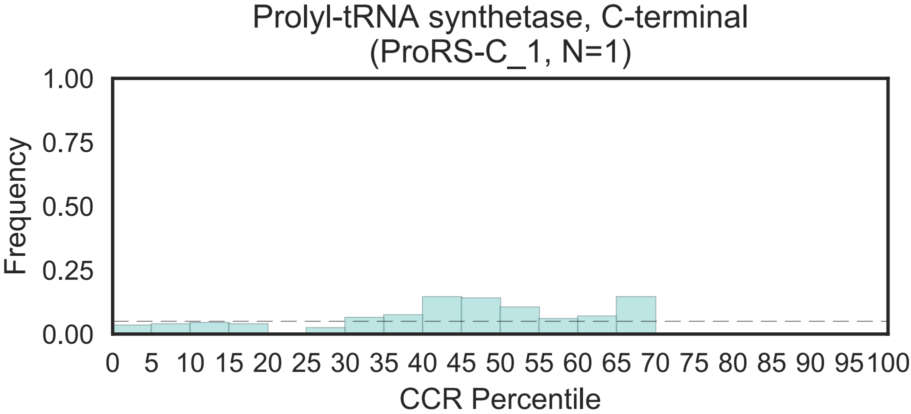

Pro-melanin-concentrating hormone (Pro-MCH)
(Pro-MCH, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

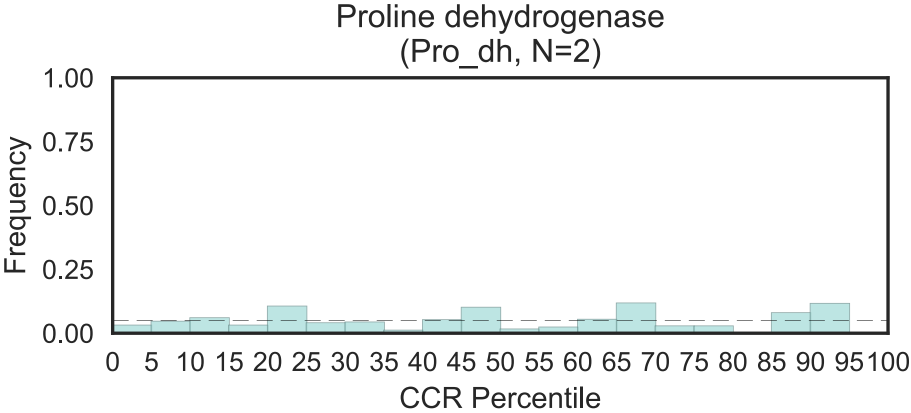

Neurotensin/neuromedin N precursor
(Pro-NT_NN, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

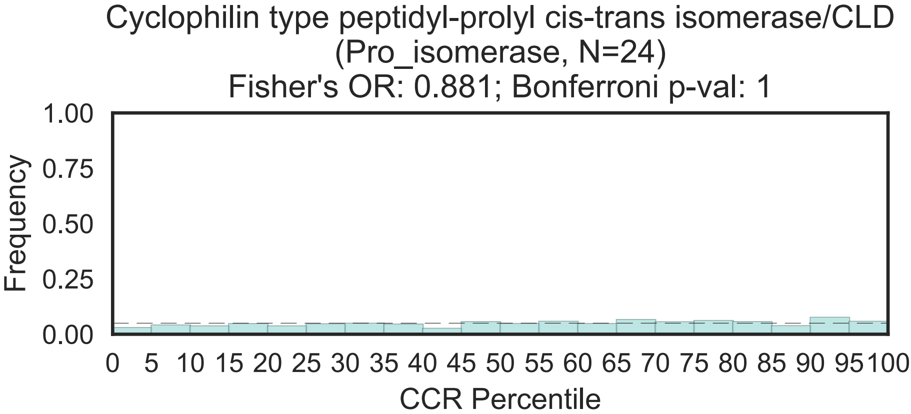

Pro-kumamolisin, activation domain
(Pro-kuma_activ, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

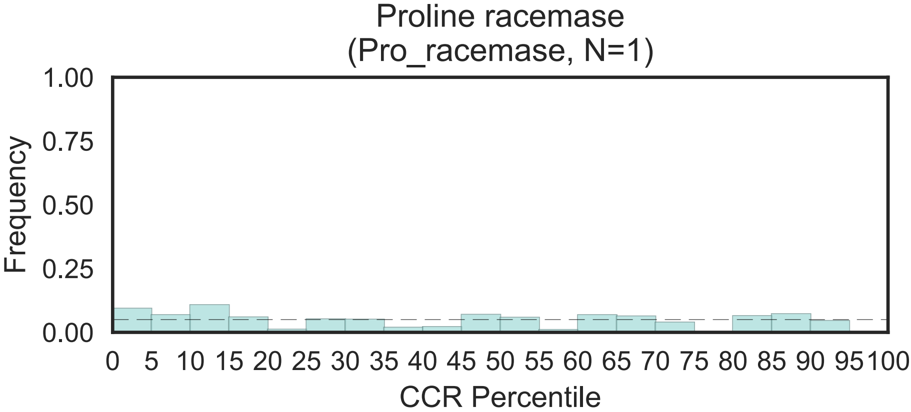

Proline-rich
(Pro-rich, N=13)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

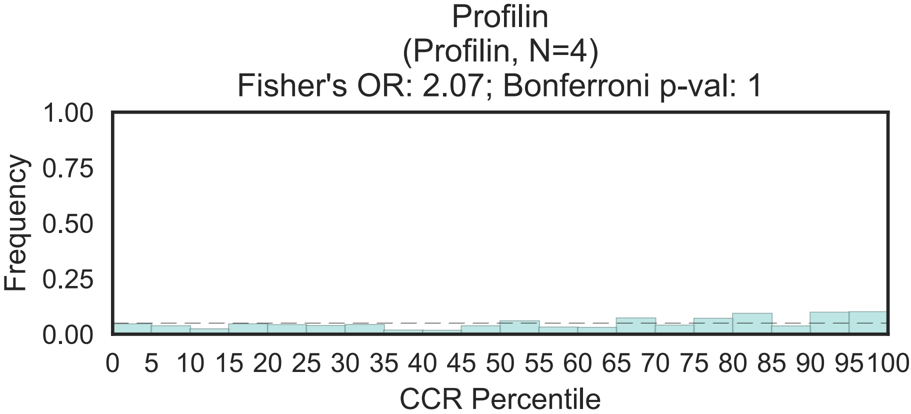

Proline-rich 19
(Pro-rich_19, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

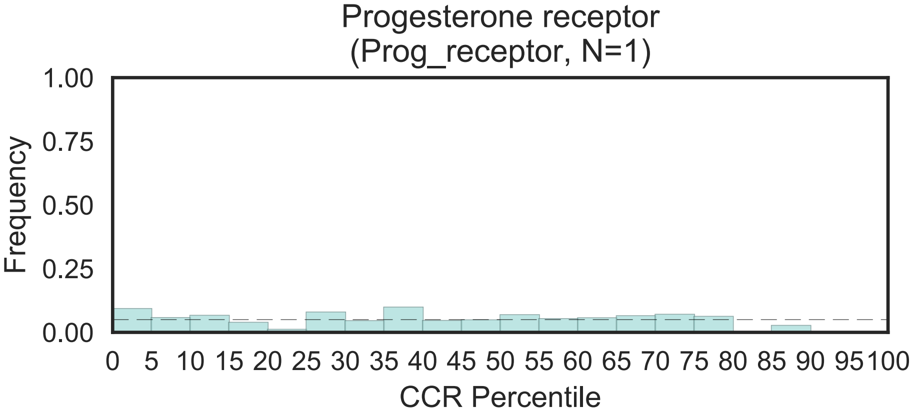

Prolyl-tRNA synthetase, C-terminal
(ProRS-C_1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

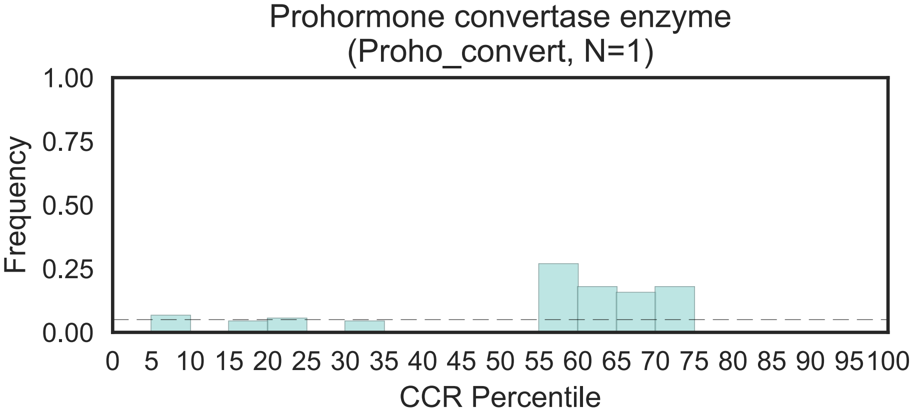

Proline dehydrogenase
(Pro_dh, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

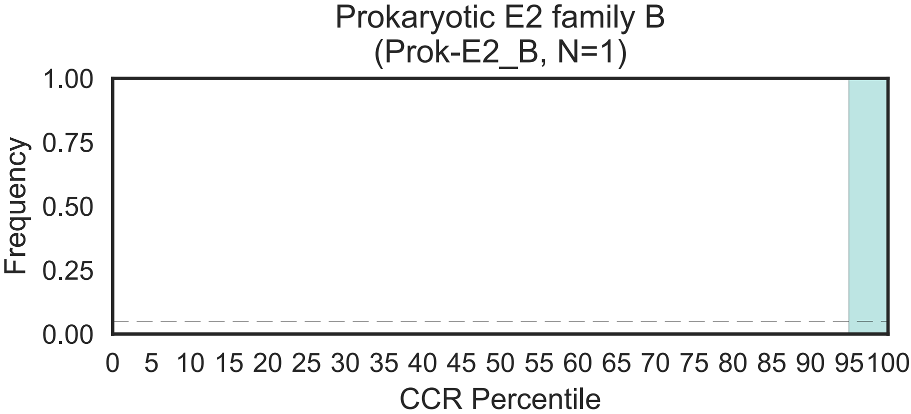

Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD
(Pro_isomerase, N=24)
Fisher's OR: 0.881; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

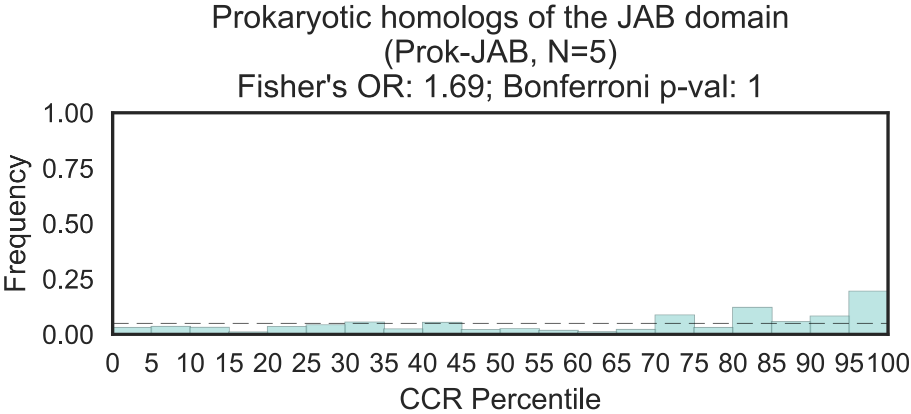

Proline racemase
(Pro_racemase, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

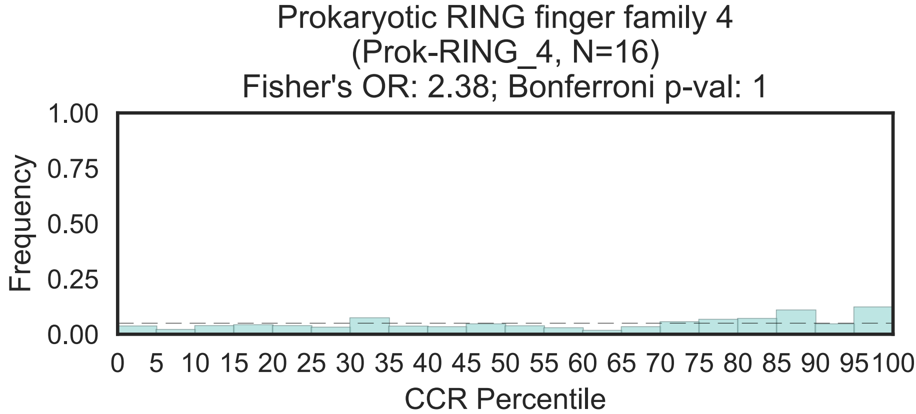

Profilin
(Profilin, N=4)
Fisher's OR: 2.07; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

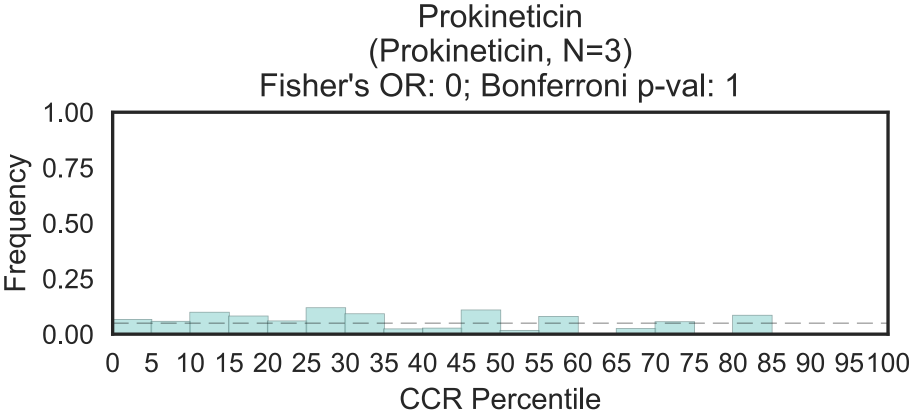

Progesterone receptor
(Prog_receptor, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

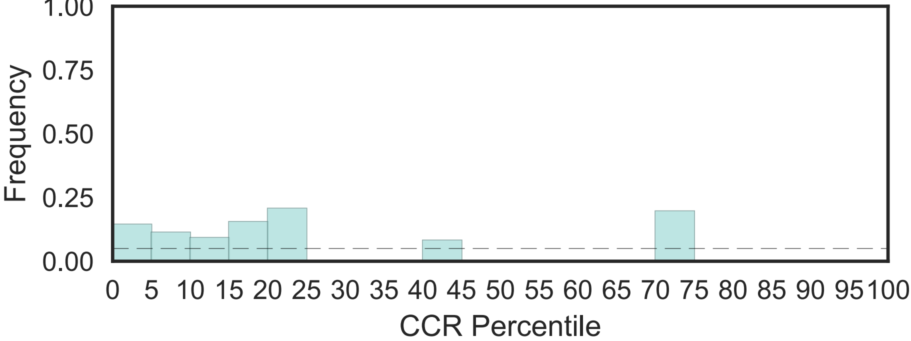

Prohormone convertase enzyme
(Proho_convert, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Prokaryotic E2 family B
(Prok-E2_B, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

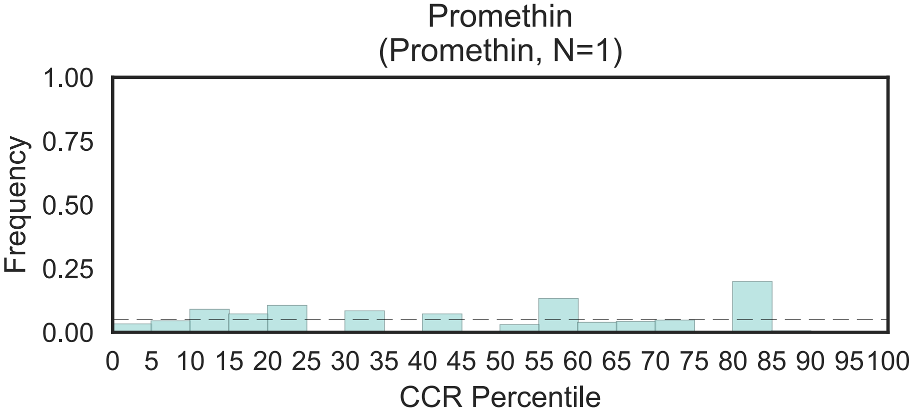

Prokaryotic homologs of the JAB domain
(Prok-JAB, N=5)
Fisher's OR: 1.69; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

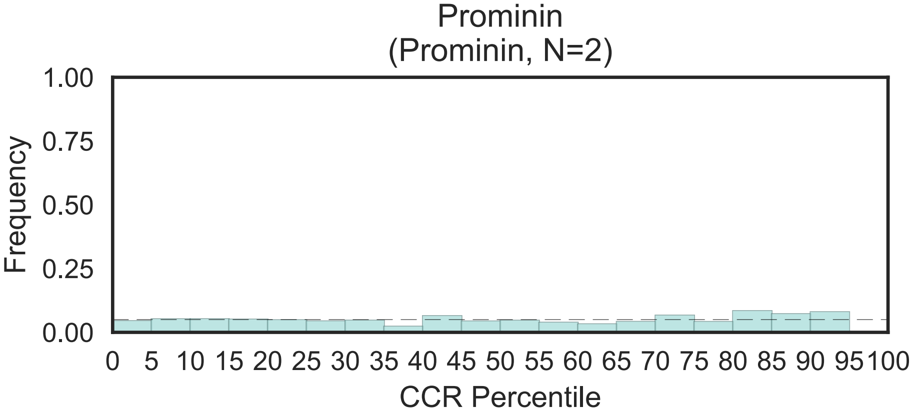

Prokaryotic RING finger family 4
(Prok-RING_4, N=16)
Fisher's OR: 2.38; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

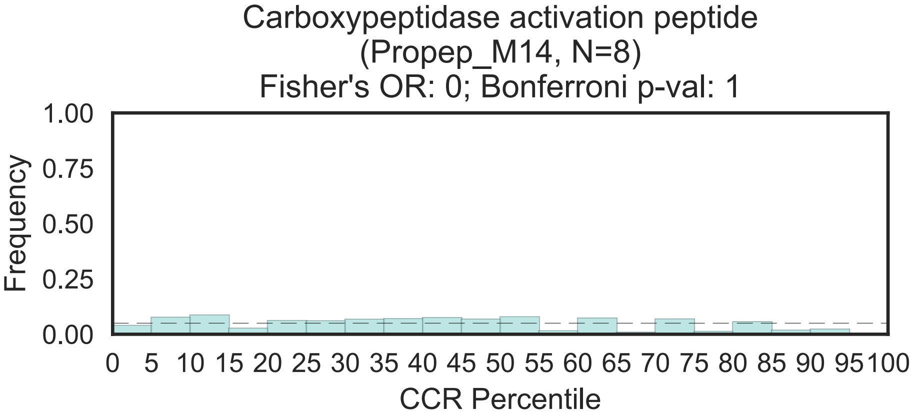

Prokineticin
(Prokineticin, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

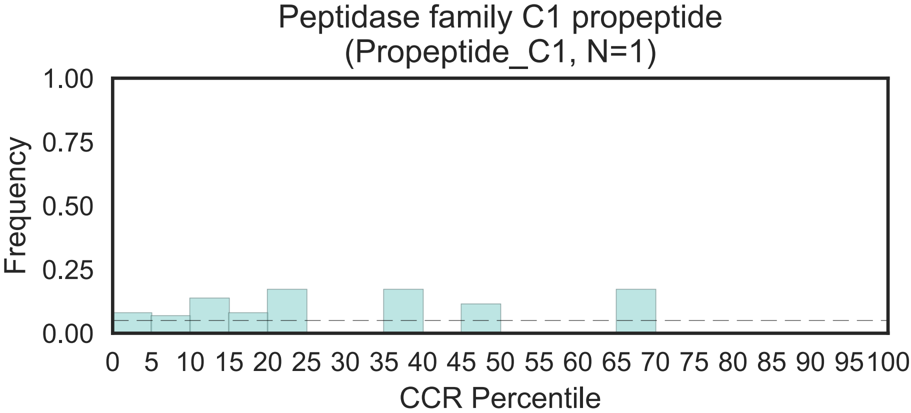


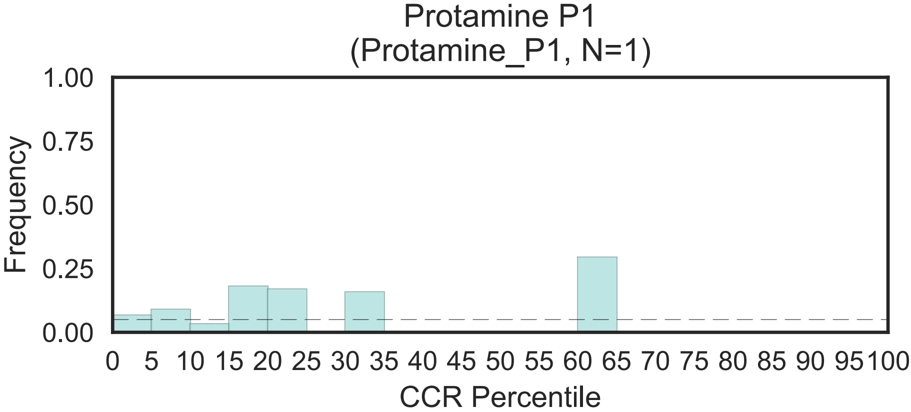
Prolactin-releasing peptide
(Prolactin_RP, N=1)

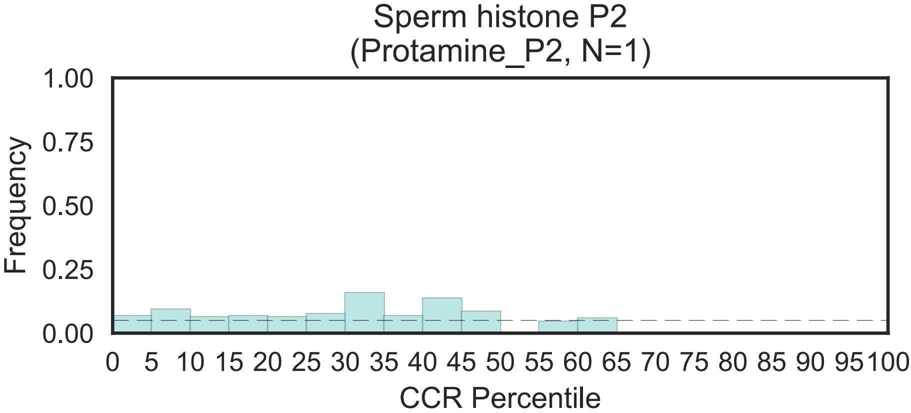

Promethin
(Promethin, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

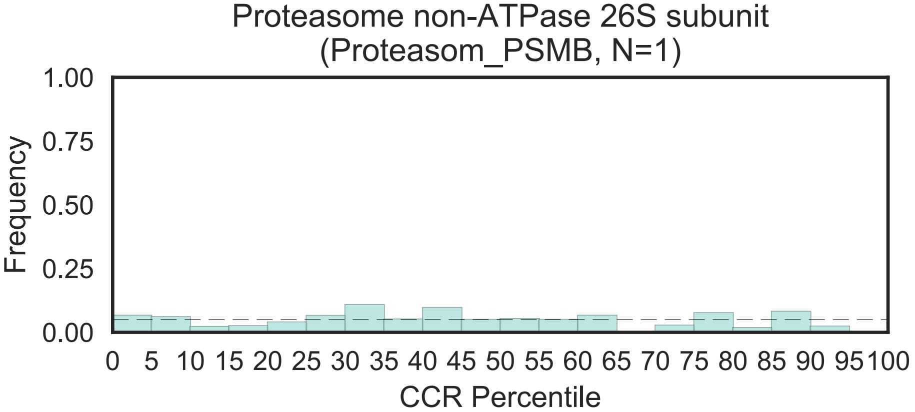

Prominin
(Prominin, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

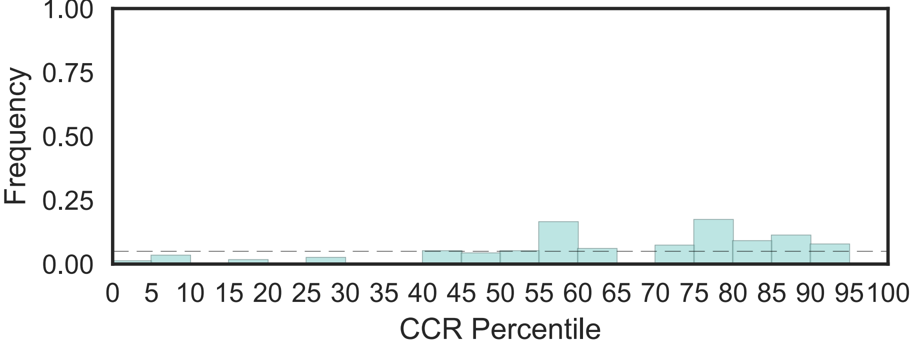

Carboxypeptidase activation peptide
(Propep_M14, N=8)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Peptidase family C1 propeptide
(Propeptide_C1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

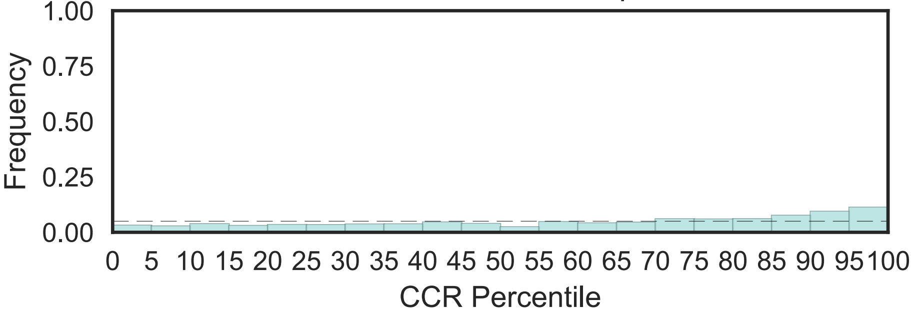

Protamine P1
(Protamine_P1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Sperm histone P2
(Protamine_P2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

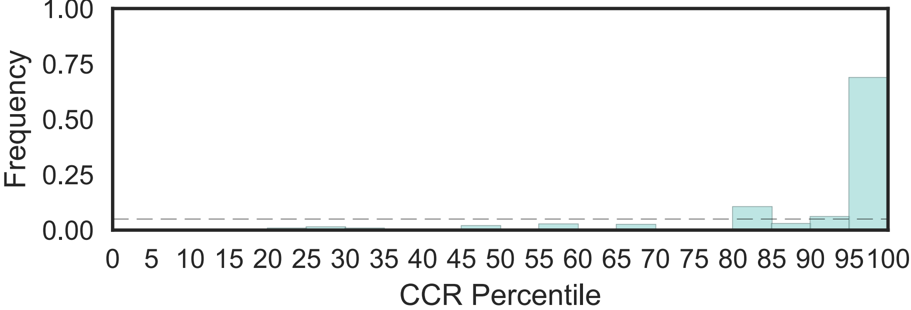

Proteasome non-ATPase 26S subunit
(Proteasom_PSMB, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



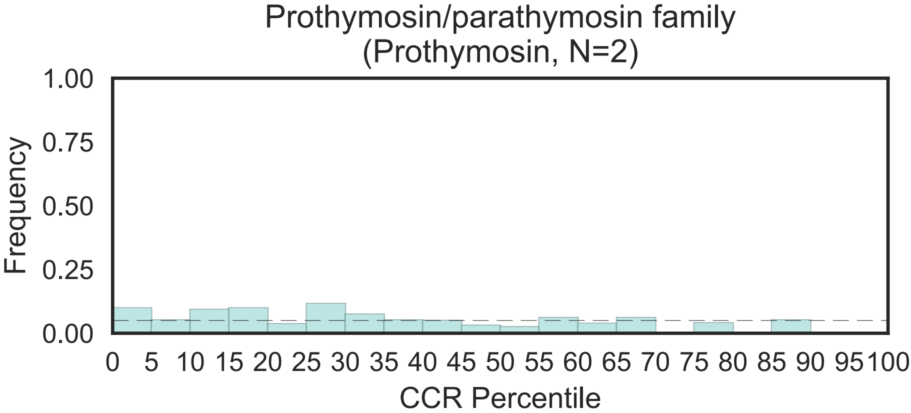
Proteasome complex subunit Rpn13 ubiquitin receptor
(Proteasom_Rpn13, N=1)

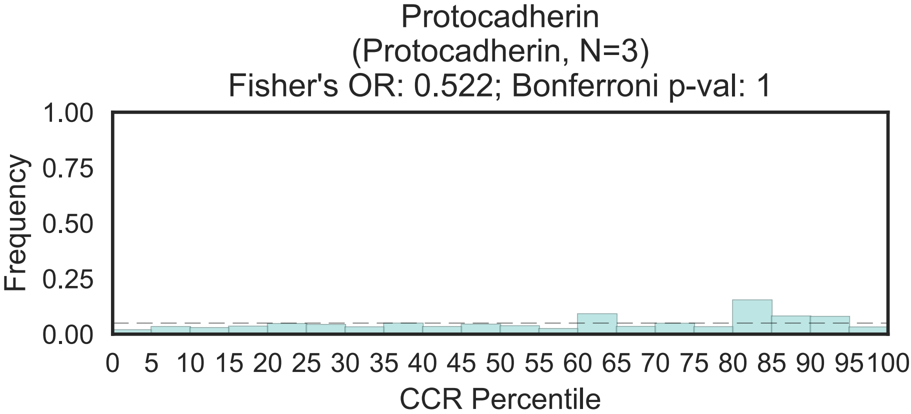


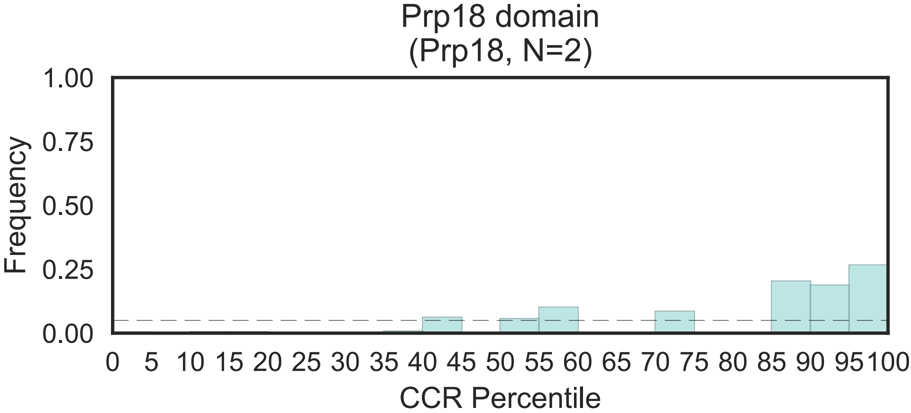
Proteasome subunit
(Proteasome, N=20)
Fisher's OR: 2.76; Bonferroni p-val: 0.0663

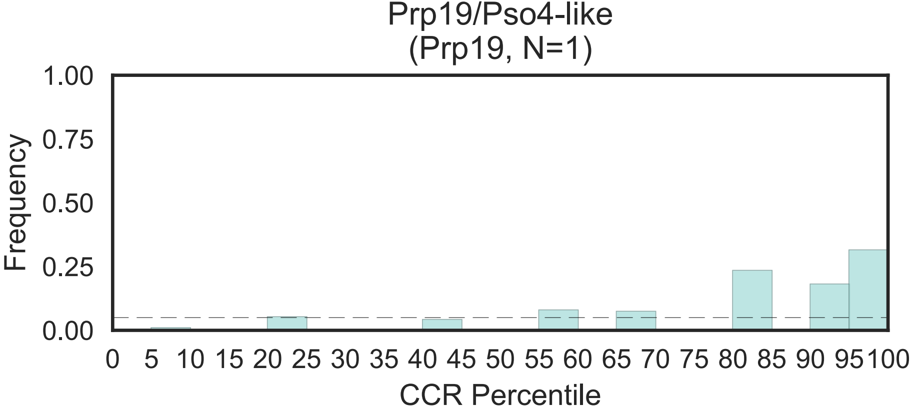


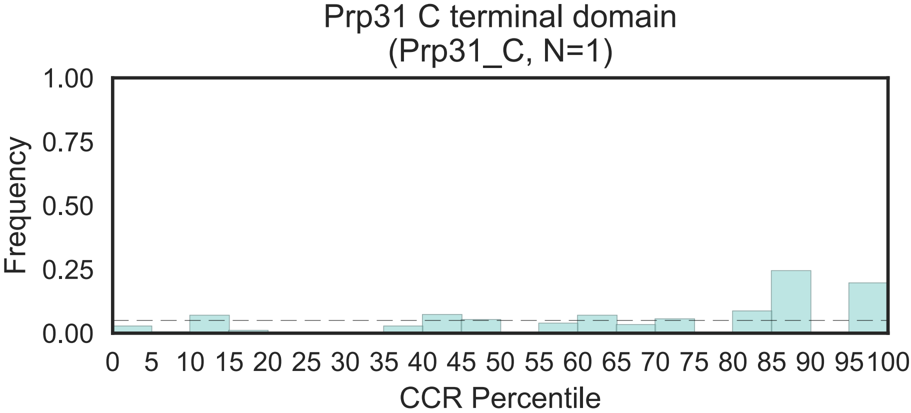
Proteasome subunit A N-terminal signature
(Proteasome_A_N, N=8)
Fisher's OR: 50.5; Bonferroni p-val: 4.97e-06


Prothymosin/parathymosin family
(Prothymosin, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

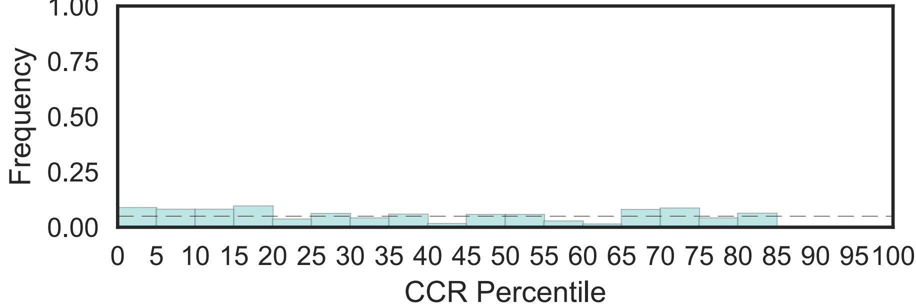

Protocadherin
(Protocadherin, N=3)
Fisher's OR: 0.522; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

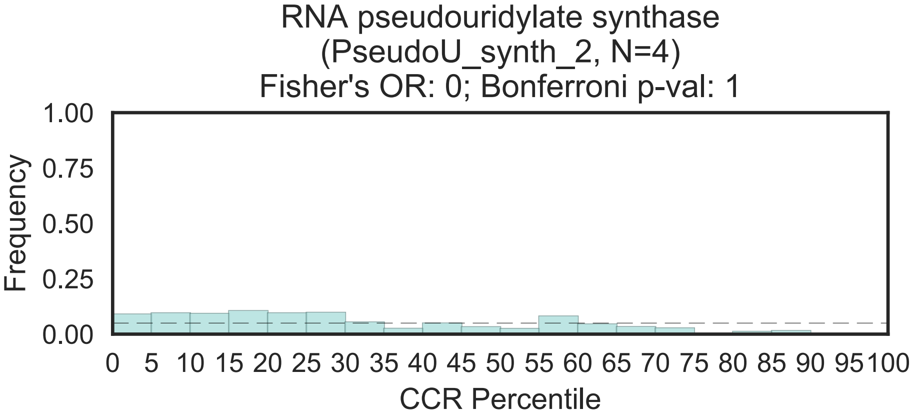

Prp18 domain
(Prp18, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

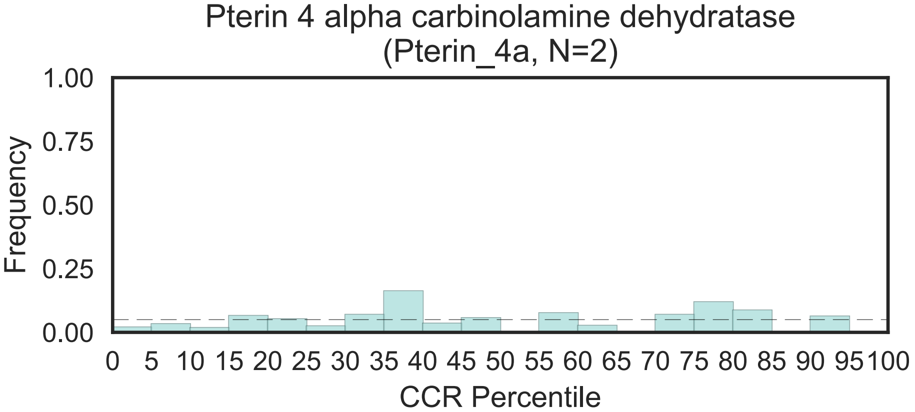

Prp19/Pso4-like
(Prp19, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

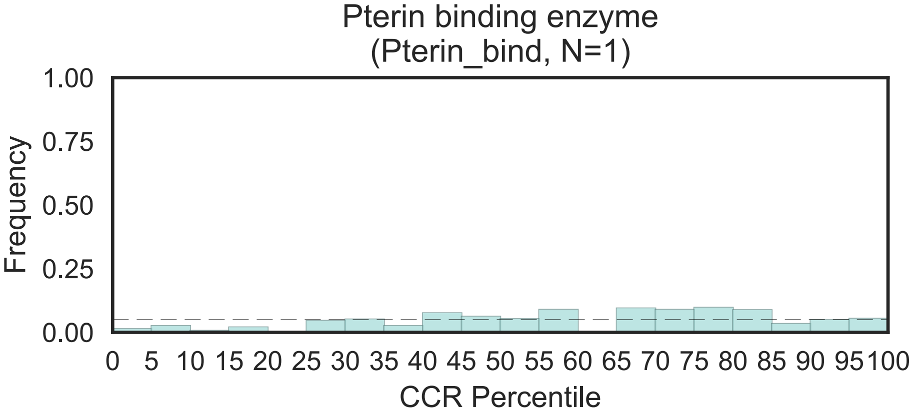

Prp31 C terminal domain
(Prp31_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

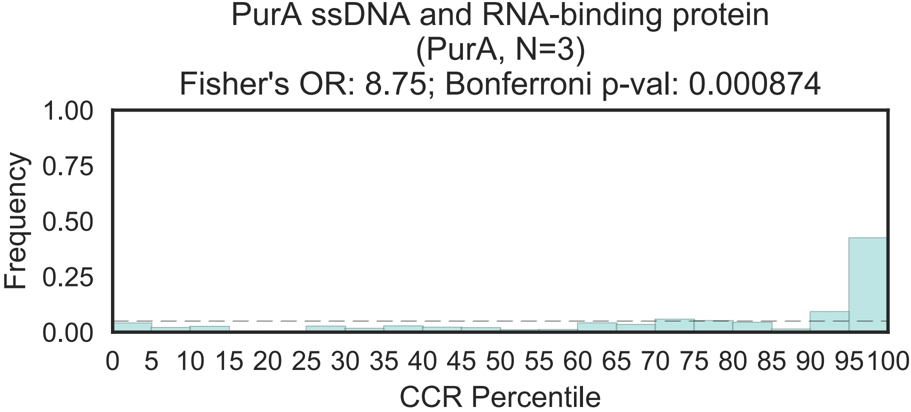
tRNA pseudouridine synthase (PseudoU_synth_1, N=4) Fisher's OR: 0; Bonferroni p-val: 1

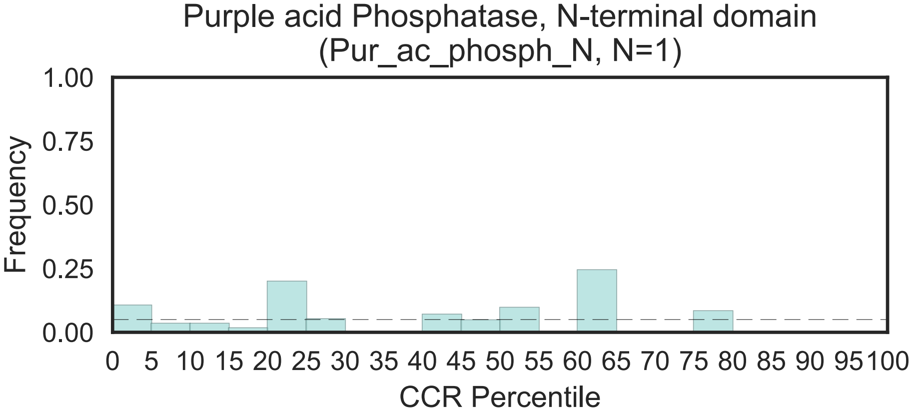


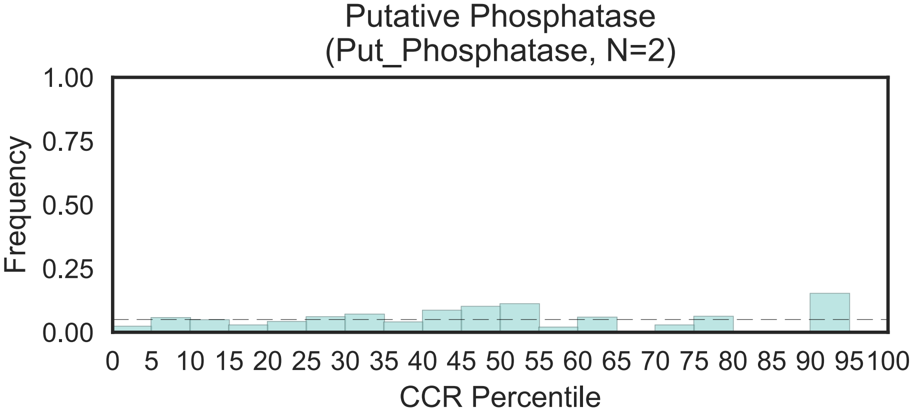

RNA pseudouridylate synthase
(PseudoU_synth_2, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

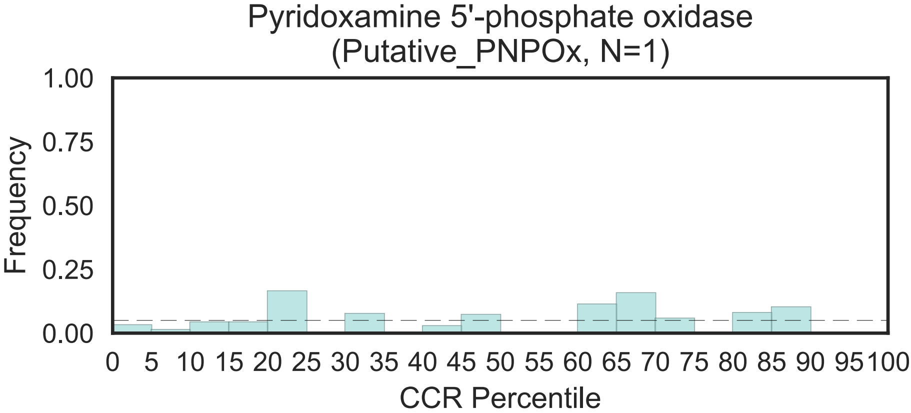

Pterin 4 alpha carbinolamine dehydratase
(Pterin_4a, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

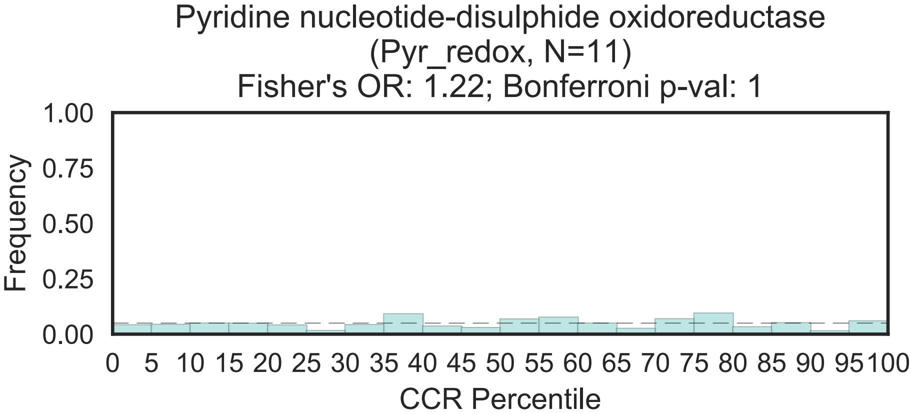

Pterin binding enzyme
(Pterin_bind, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

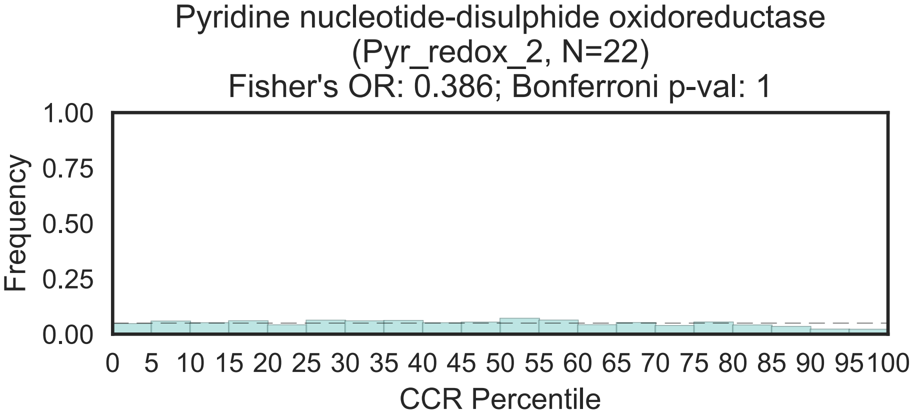

PurA ssDNA and RNA-binding protein
(PurA, N=3)
Fisher's OR: 8.75; Bonferroni p-val: 0.000874
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

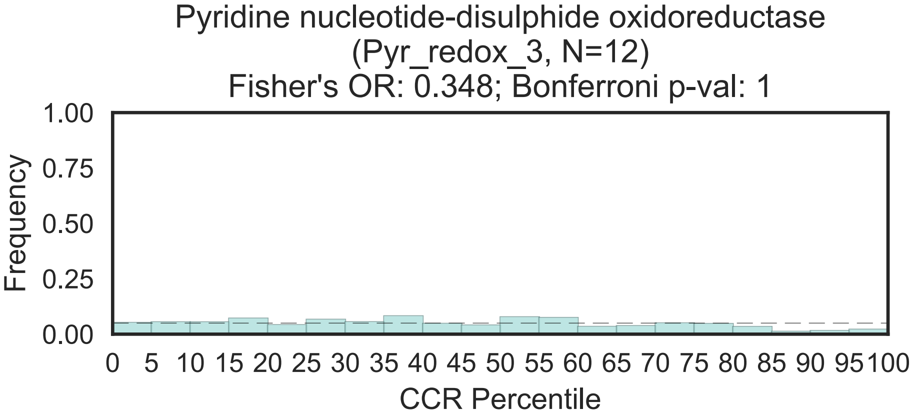

Purple acid Phosphatase, N-terminal domain
(Pur_ac_phosph_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

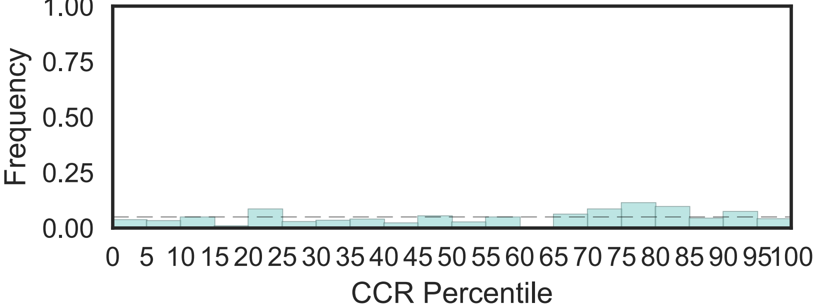

Putative Phosphatase
(Put_Phosphatase, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Pyridoxamine 5'-phosphate oxidase
(Putative_PNPOx, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

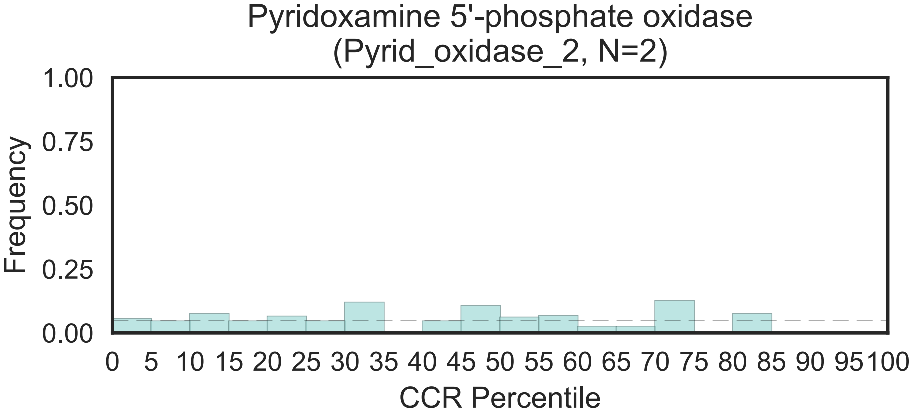

Pyridine nucleotide-disulphide oxidoreductase
(Pyr_redox, N=11)
Fisher's OR: 1.22; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

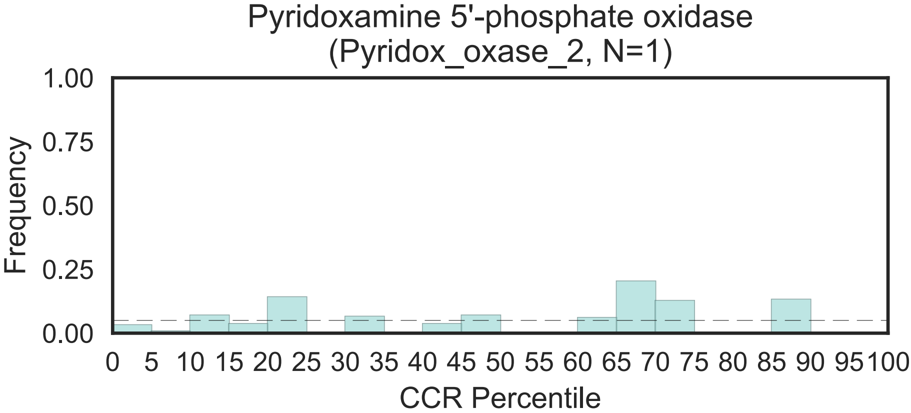

Pyridine nucleotide-disulphide oxidoreductase
(Pyr_redox_2, N=22)
Fisher's OR: 0.386; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

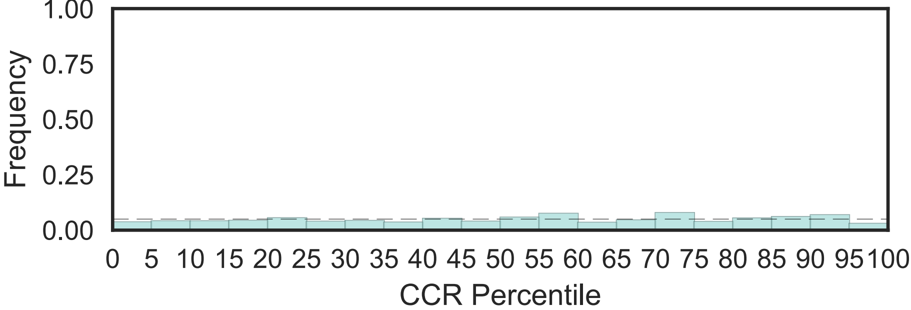

Pyridine nucleotide-disulphide oxidoreductase
(Pyr_redox_3, N=12)
Fisher's OR: 0.348; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

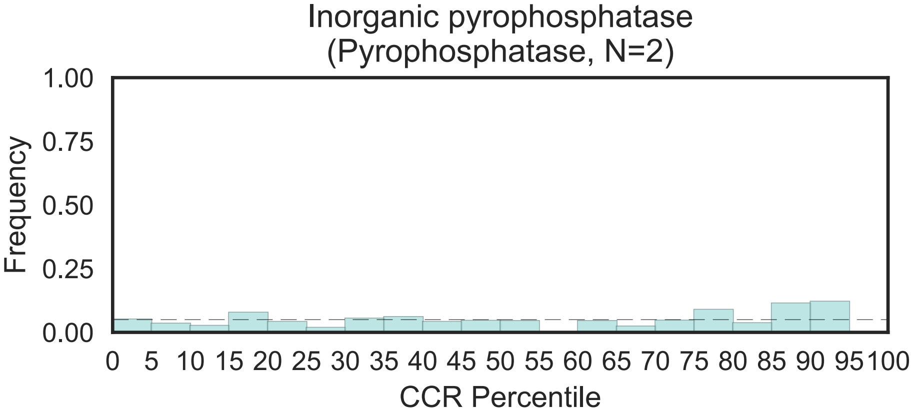


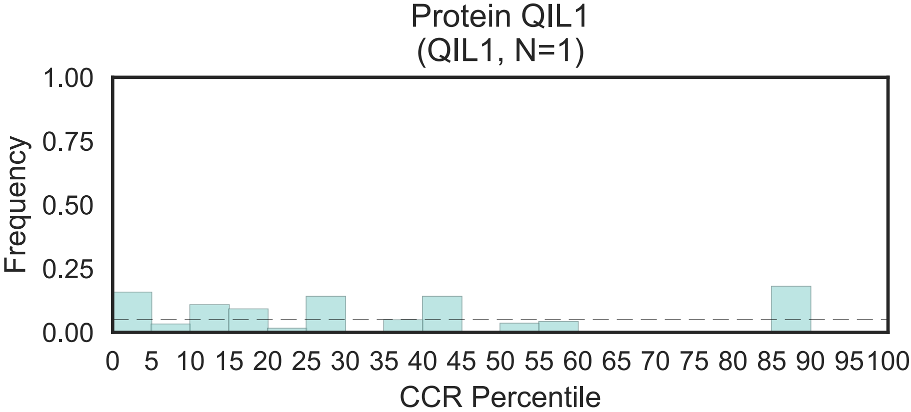
Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain
(Pyr_redox_dim, N=4)
Fisher's OR: 0.721; Bonferroni p-val: 1

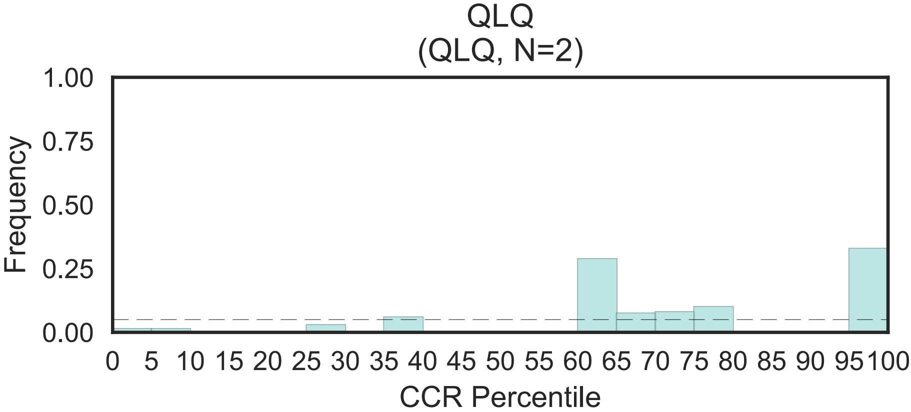

Pyridoxamine 5'-phosphate oxidase
(Pyrid_oxidase_2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

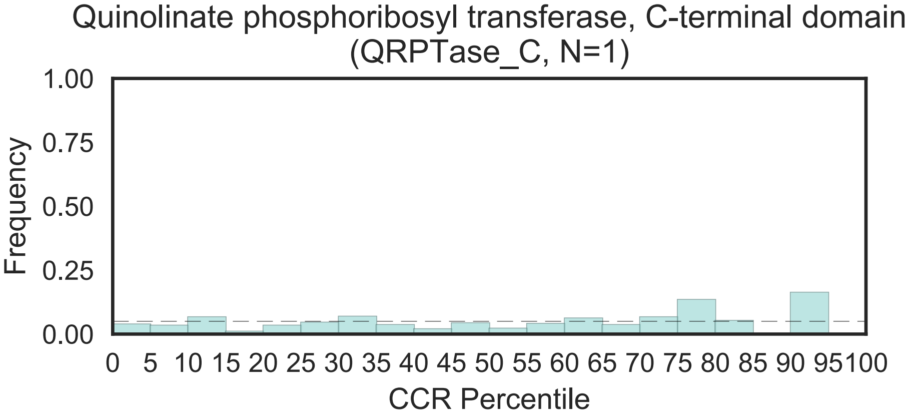

Pyridoxamine 5'-phosphate oxidase
(Pyridox_oxase_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

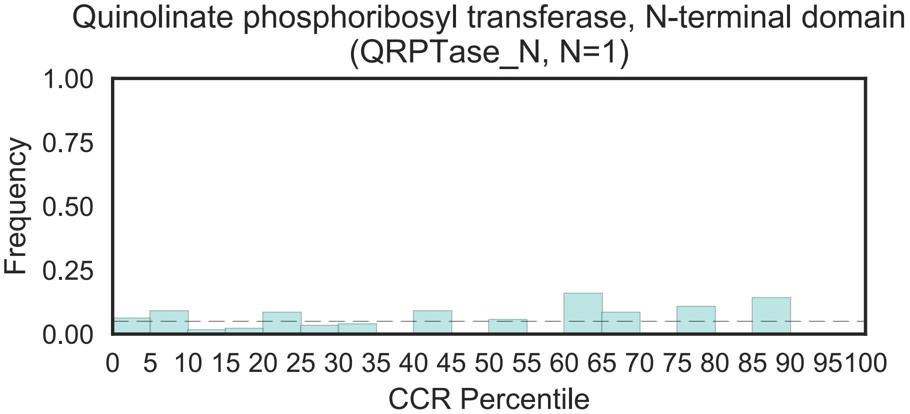

Pyridoxal-dependent decarboxylase conserved domain
(Pyridoxal_deC, N=11)
Fisher's OR: 0.465; Bonferroni p-val: 1

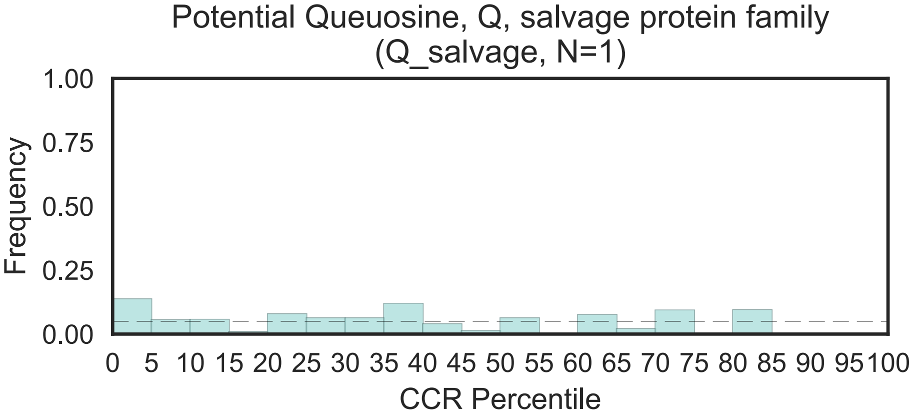

Inorganic pyrophosphatase
(Pyrophosphatase, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

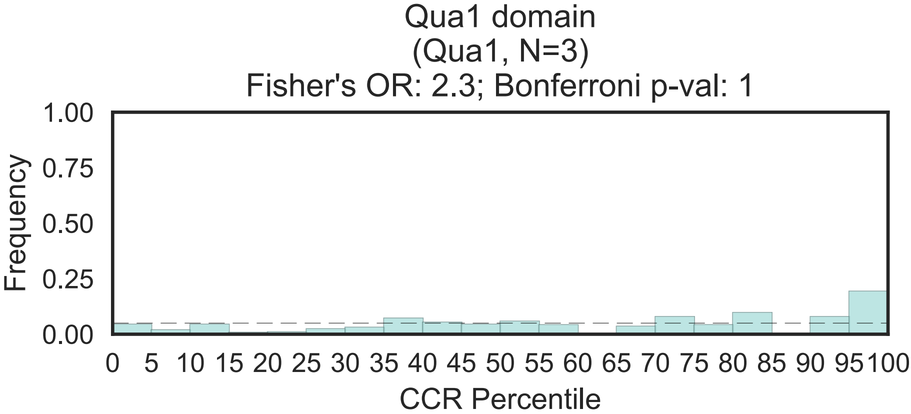

Protein QIL1
(QIL1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

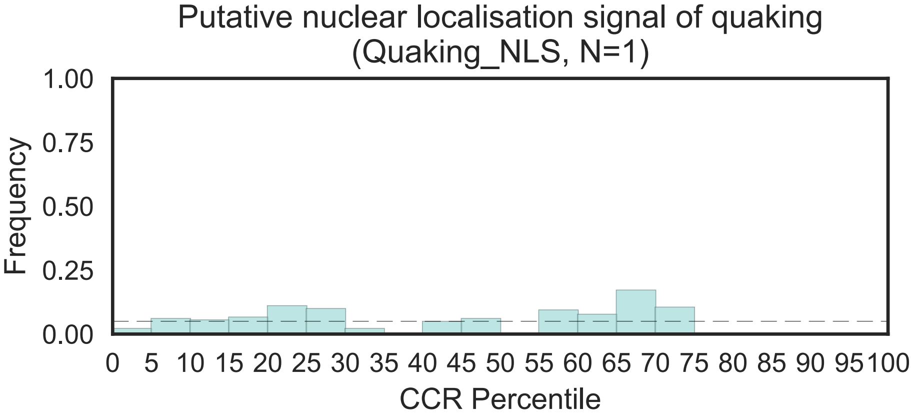

QLQ
(QLQ, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

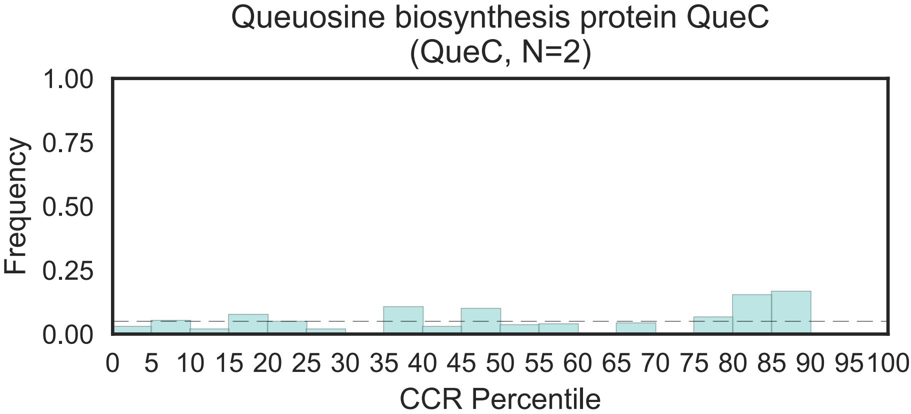

Quinolinate phosphoribosyl transferase, C-terminal domain
(QRPTase_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

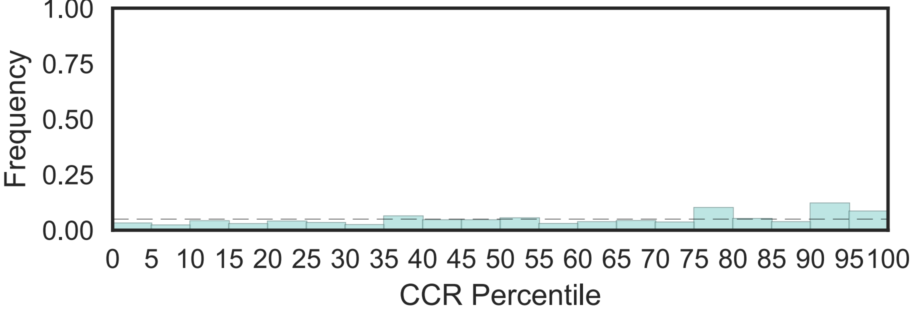

Quinolinate phosphoribosyl transferase, N-terminal domain (QRPTase_N, N=1)

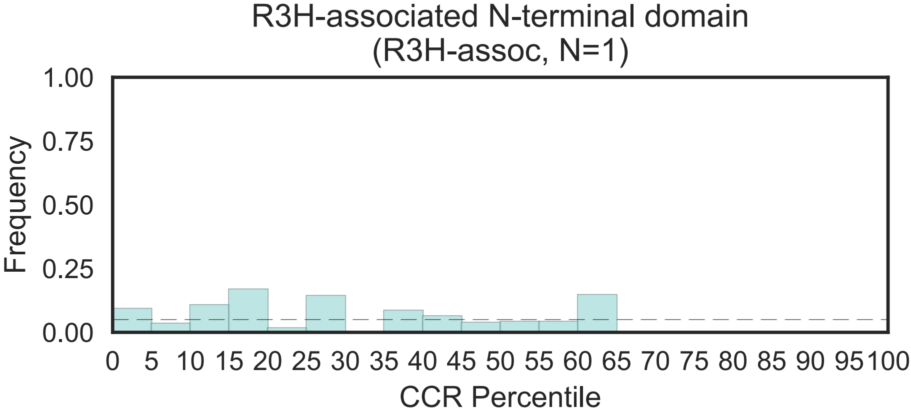

Potential Queuosine, Q, salvage protein family
(Q_salvage, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

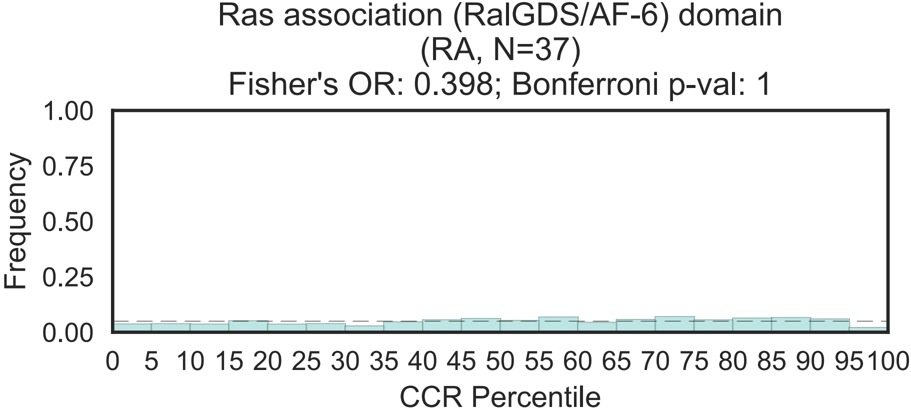

Qua1 domain
(Qua1, N=3)
Fisher's OR: 2.3; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Putative nuclear localisation signal of quaking
(Quaking_NLS, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

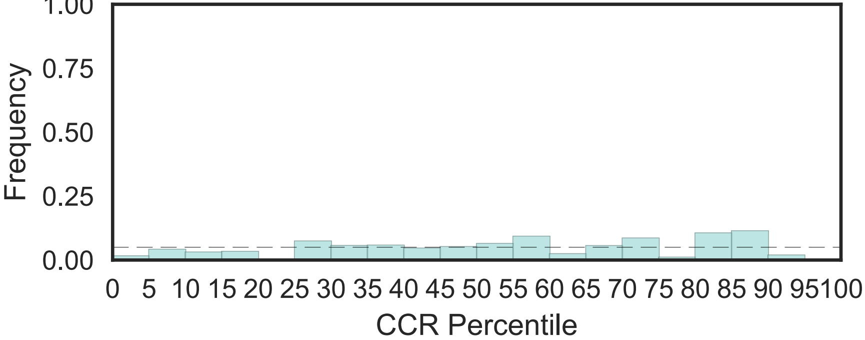

Queuosine biosynthesis protein QueC
(QueC, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

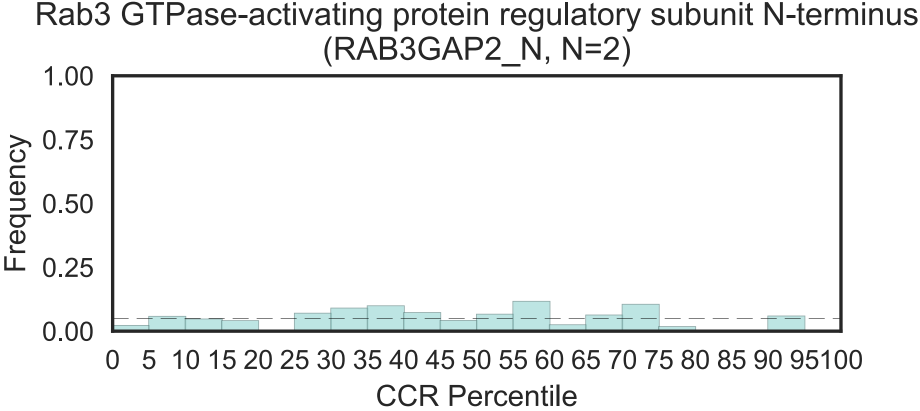

R3H domain
(R3H, N=9)
Fisher's OR: 2.07; Bonferroni p-val: 1

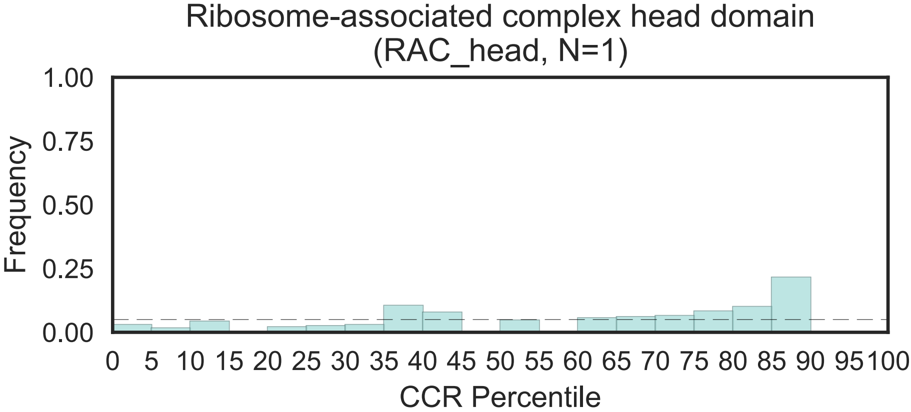

R3H-associated N-terminal domain
(R3H-assoc, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

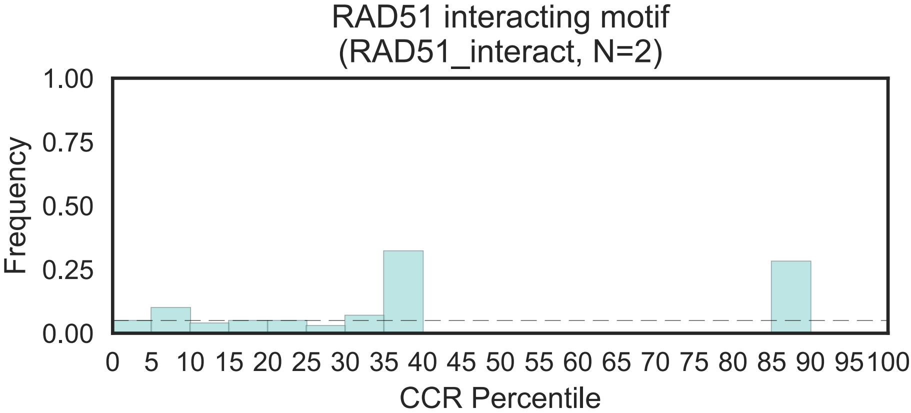

Ras association (RalGDS/AF-6) domain
(RA, N=37)
Fisher's OR: 0.398; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Rab3 GTPase-activating protein regulatory subunit C-terminus (RAB3GAP2_C, N=1)

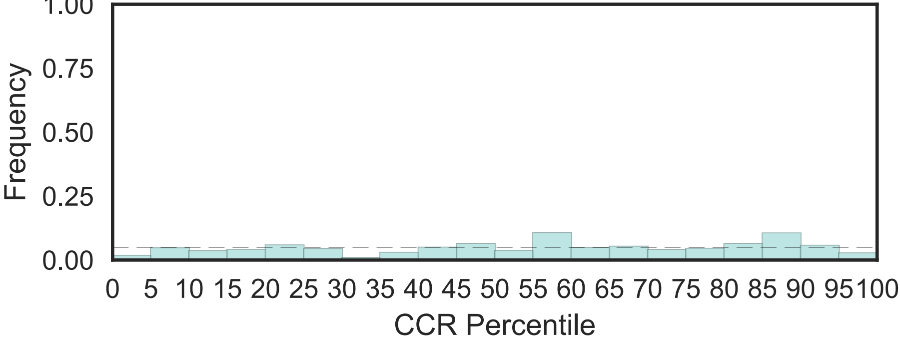


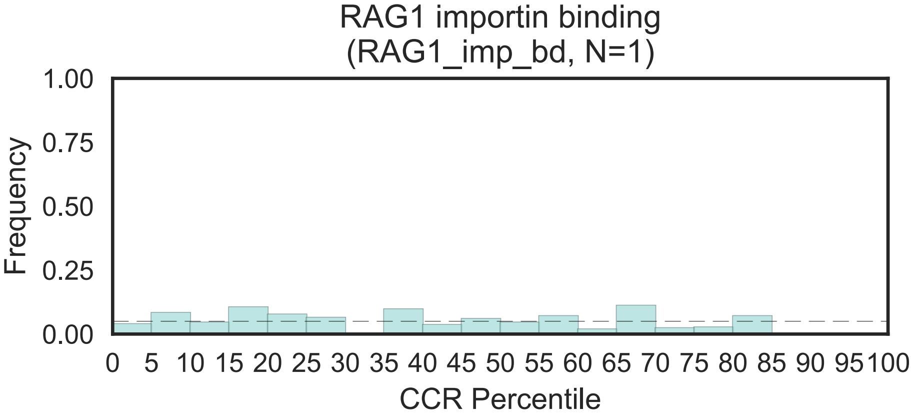

Rab3 GTPase-activating protein regulatory subunit N-terminus
(RAB3GAP2_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

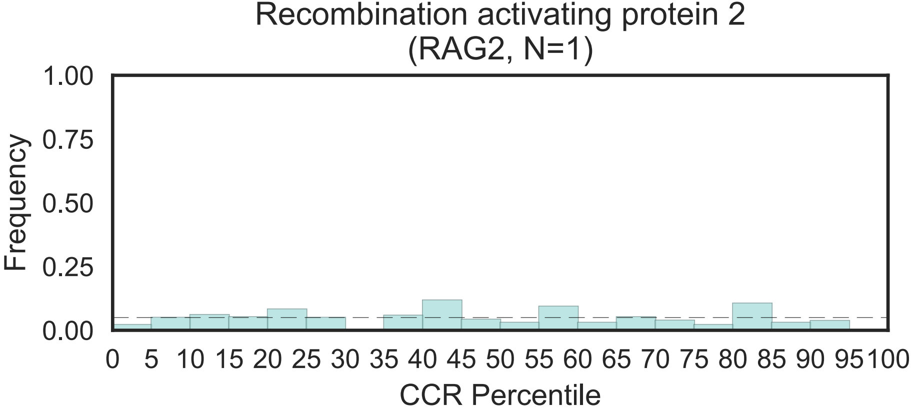

Ribosome-associated complex head domain
(RAC_head, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

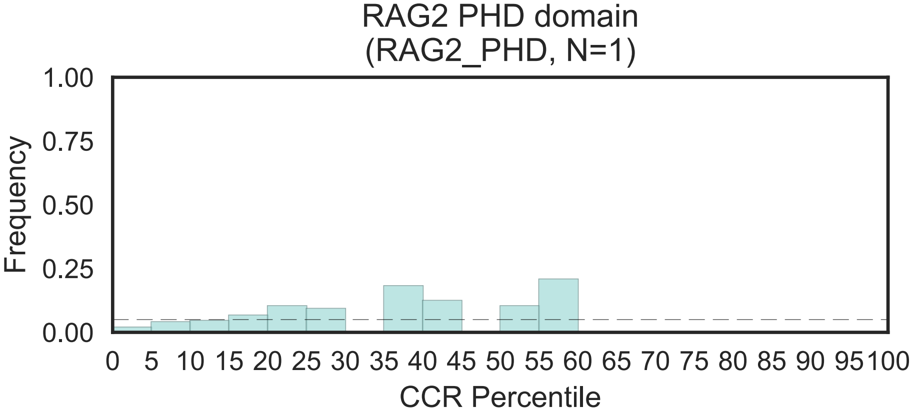

RAD51 interacting motif
(RAD51_interact, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

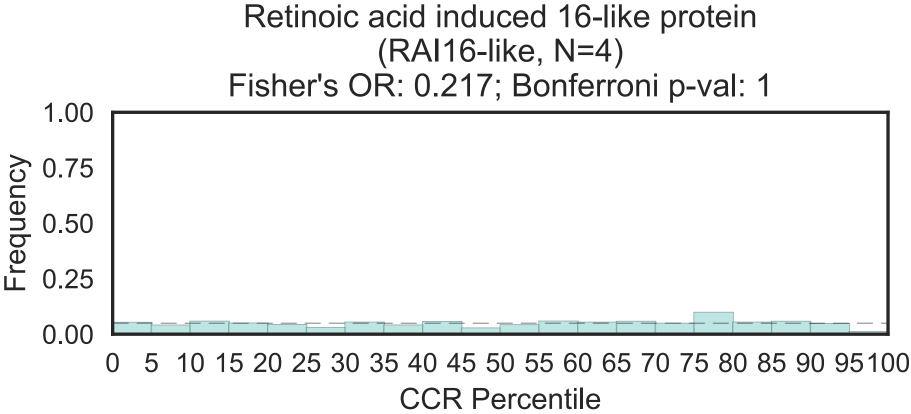
Recombination-activation protein 1 (RAG1), recombinase (RAG1, N=1)

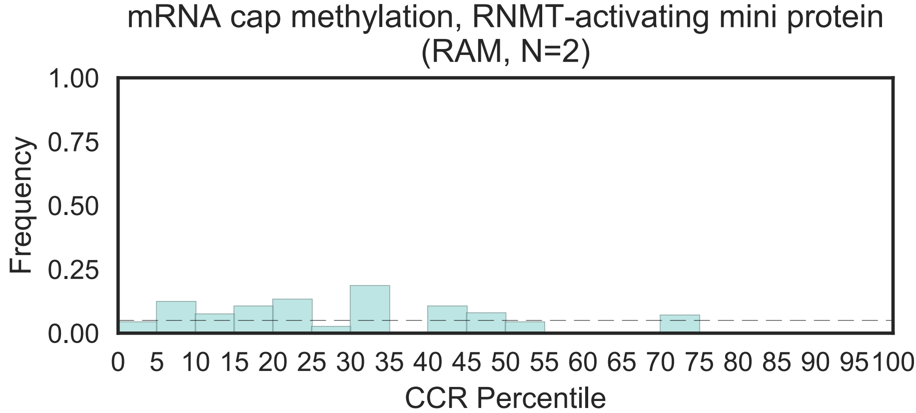


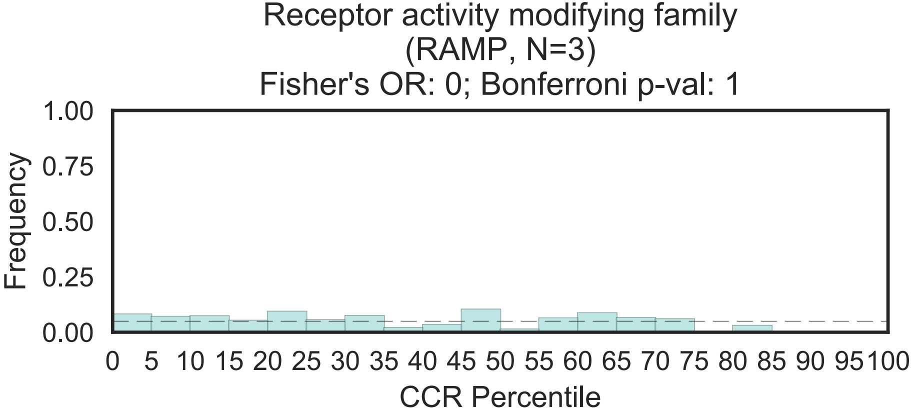

RAG1 importin binding
(RAG1_imp_bd, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

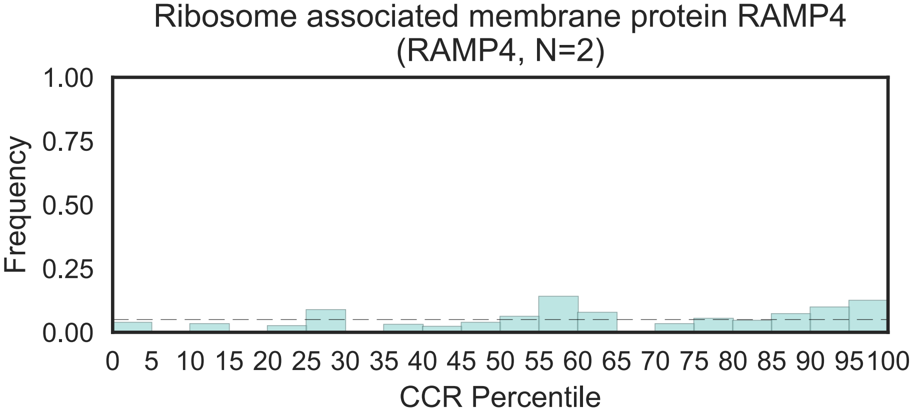

Recombination activating protein 2
(RAG2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

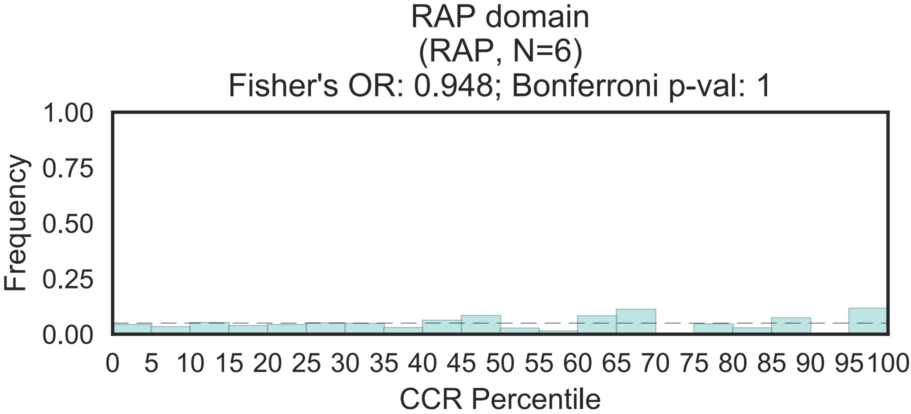

RAG2 PHD domain
(RAG2_PHD, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

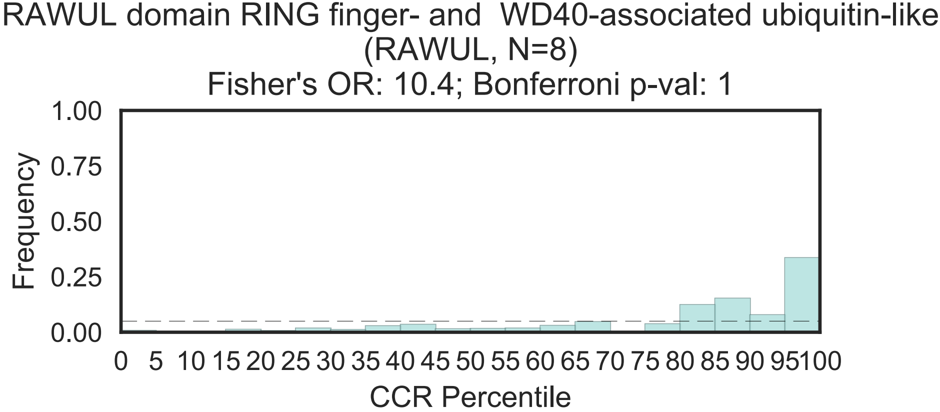

Retinoic acid induced 16-like protein
(RAI16-like, N=4)
Fisher's OR: 0.217; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

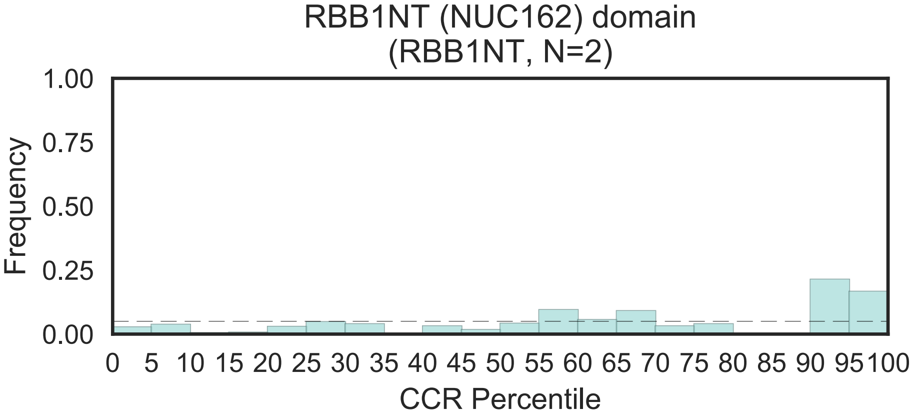

mRNA cap methylation, RNMT-activating mini protein
(RAM, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Receptor activity modifying family
(RAMP, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

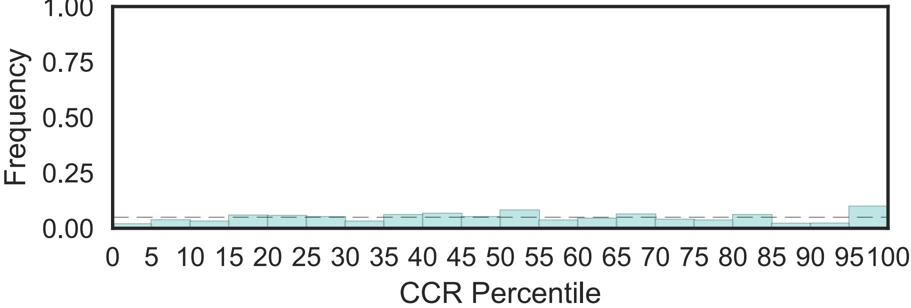

Ribosome associated membrane protein RAMP4
(RAMP4, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

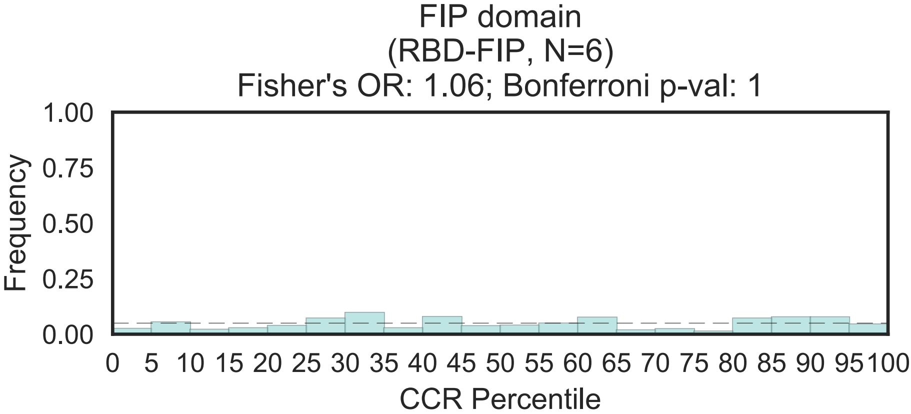

RAP domain
(RAP, N=6)
Fisher's OR: 0.948; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

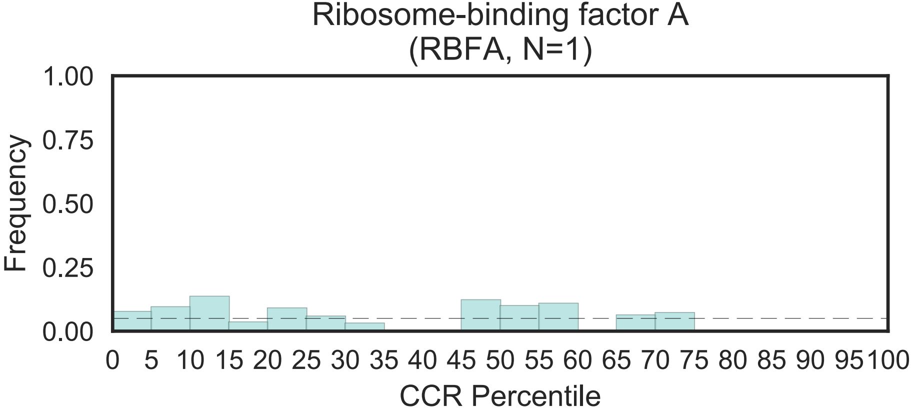

RAWUL domain RING finger- and WD40-associated ubiquitin-like
(RAWUL, N=8)
Fisher's OR: 10.4; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

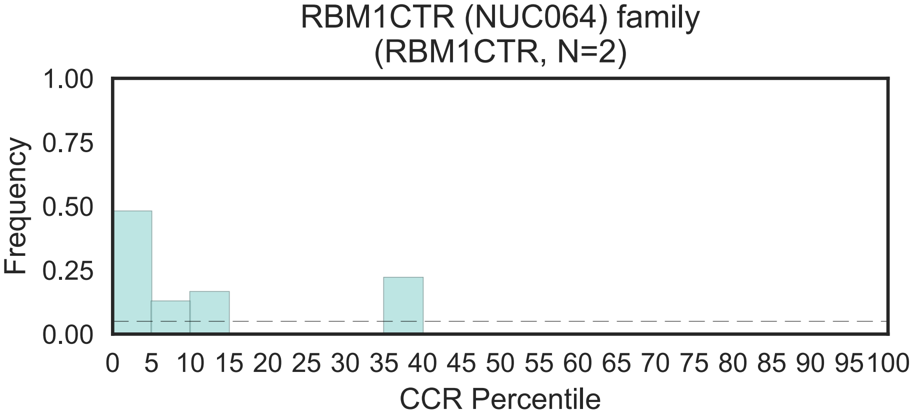

RBB1NT (NUC162) domain
(RBB1NT, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

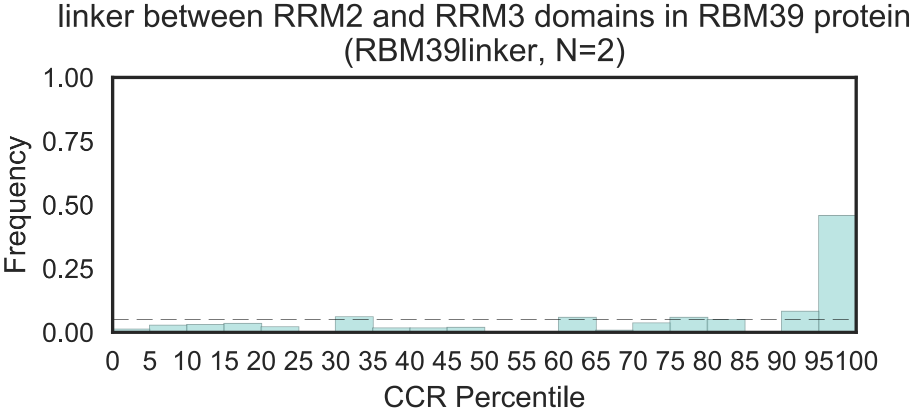
Raf-like Ras-binding domain
(RBD, N=7)
Fisher's OR: 1.94; Bonferroni p-val: 1

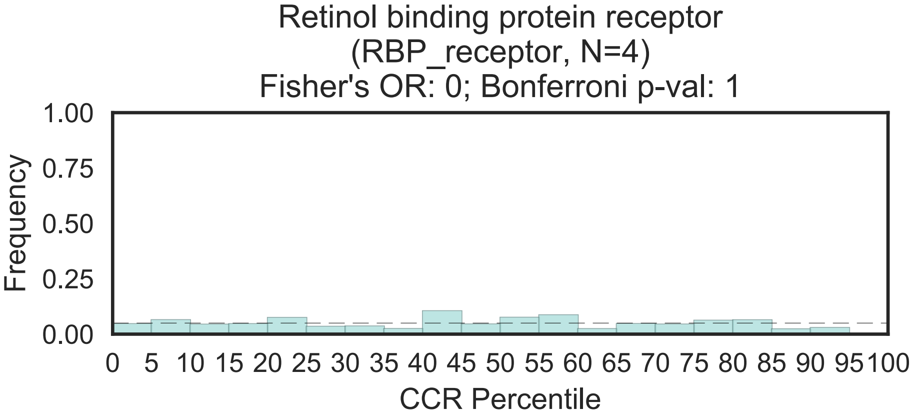


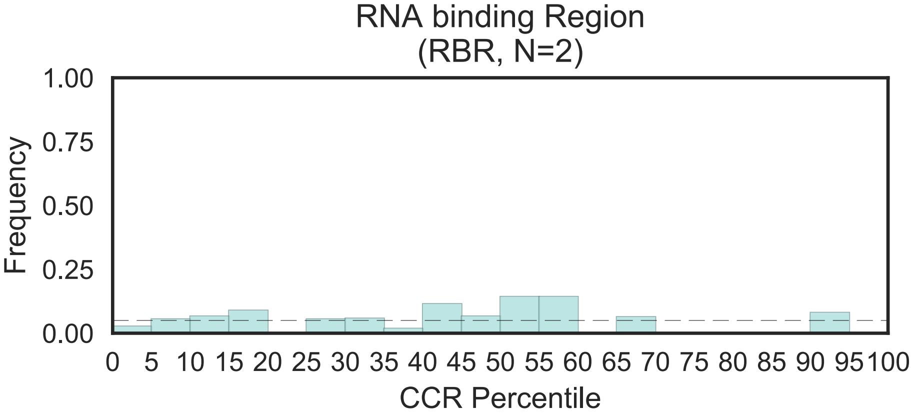

FIP domain
(RBD-FIP, N=6)
Fisher's OR: 1.06; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

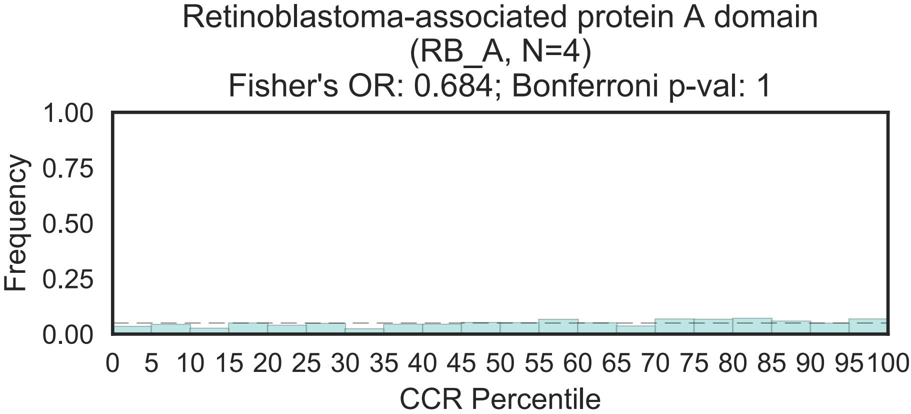

Ribosome-binding factor A
(RBFA, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

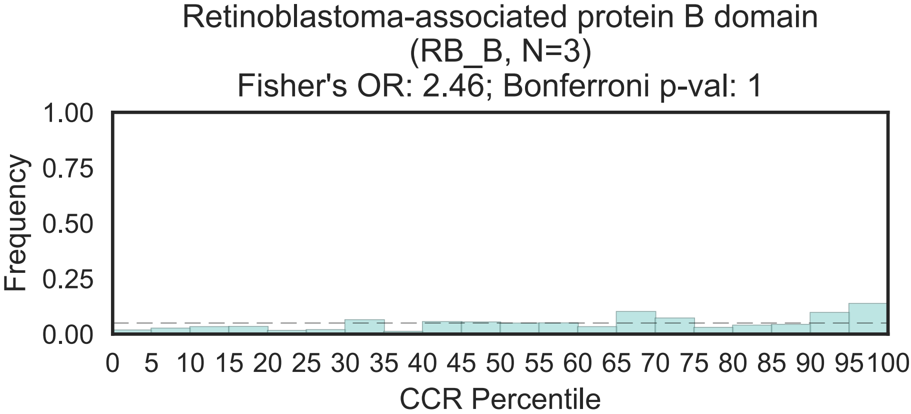

RBM1CTR (NUC064) family
(RBM1CTR, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


linker between RRM2 and RRM3 domains in RBM39 protein
(RBM39linker, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

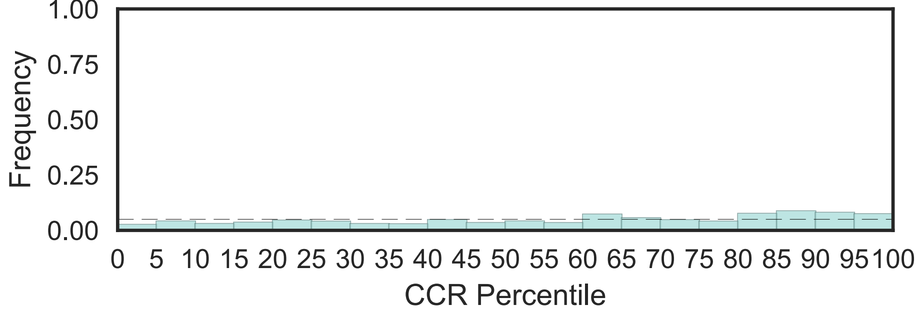

Retinol binding protein receptor
(RBP_receptor, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

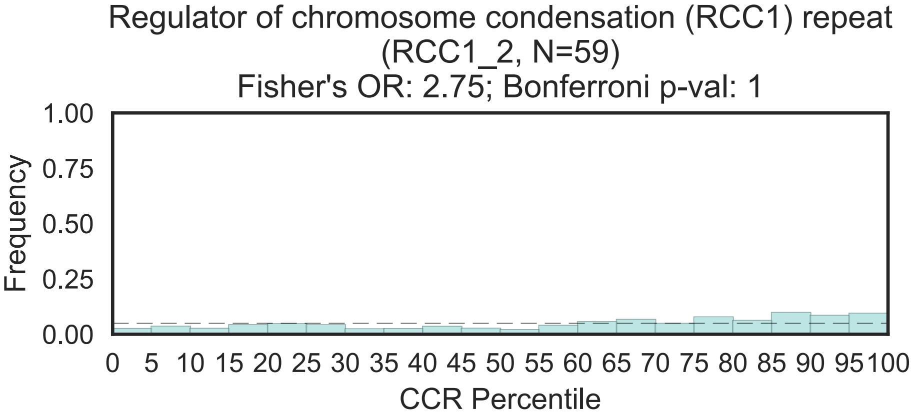

RNA binding Region
(RBR, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


Retinoblastoma-associated protein A domain
(RB_A, N=4)
Fisher's OR: 0.684; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

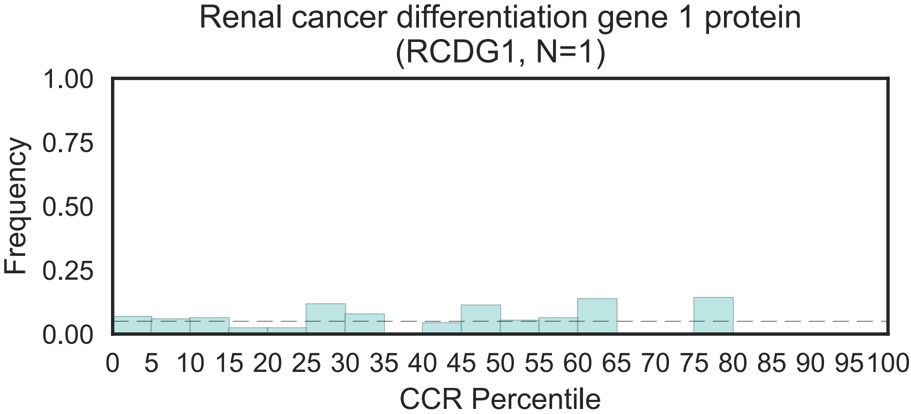

Retinoblastoma-associated protein B domain
(RB_B, N=3)
Fisher's OR: 2.46; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

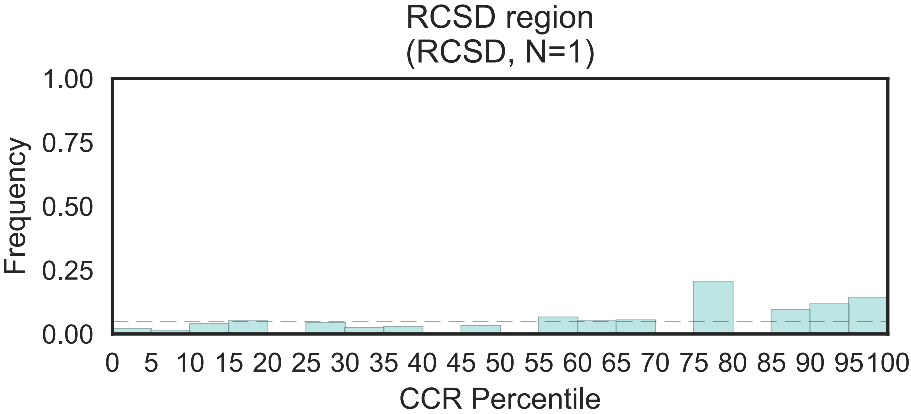
Regulator of chromosome condensation (RCC1) repeat
(RCC1, N=101)
Fisher's OR: 1.62; Bonferroni p-val: 1

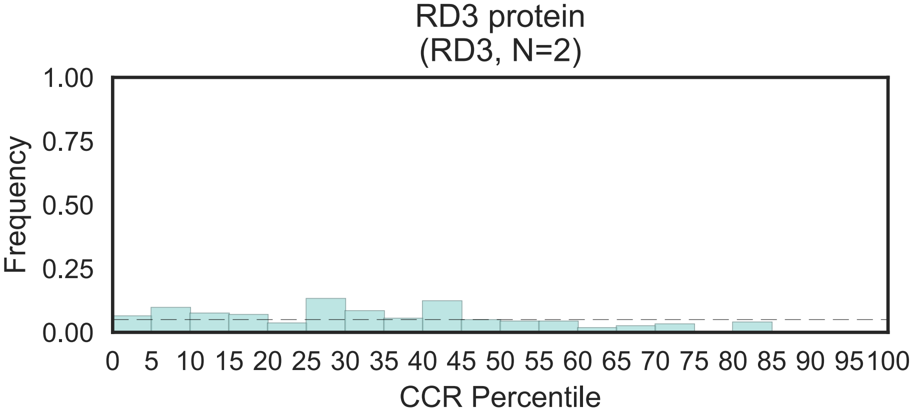


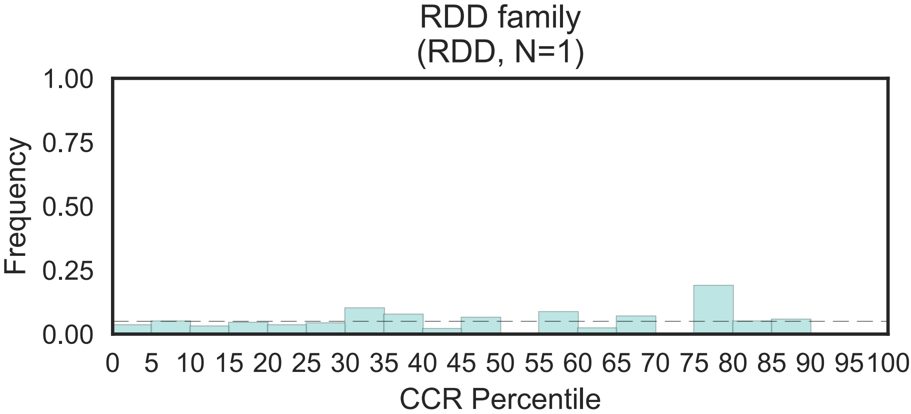


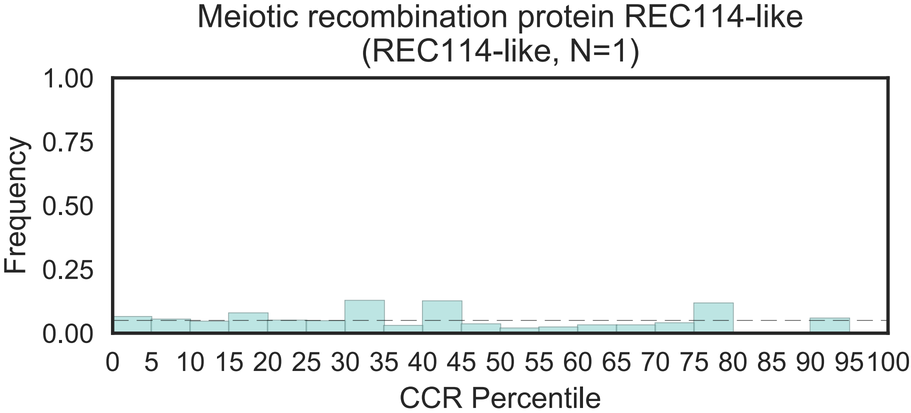
Regulator of chromosome condensation (RCC1) repeat
(RCC1_2, N=59)
Fisher's OR: 2.75; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

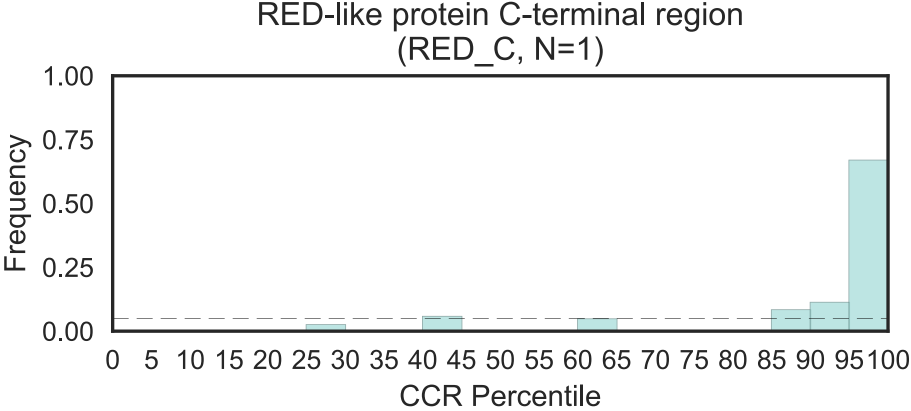

Renal cancer differentiation gene 1 protein
(RCDG1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

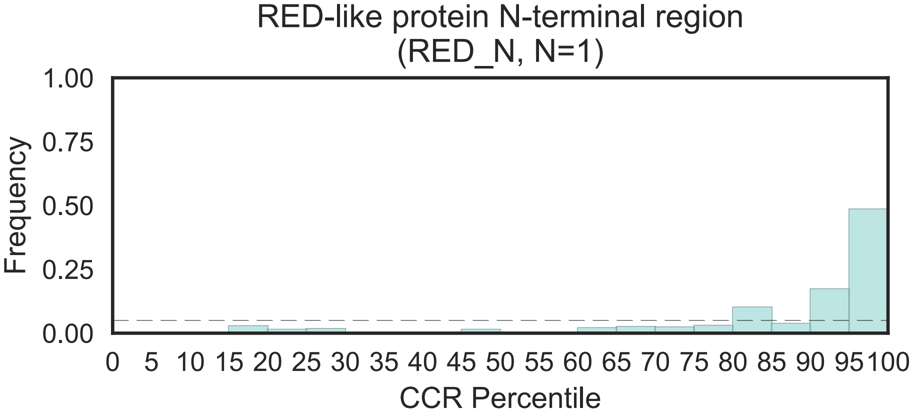

RCSD region
(RCSD, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

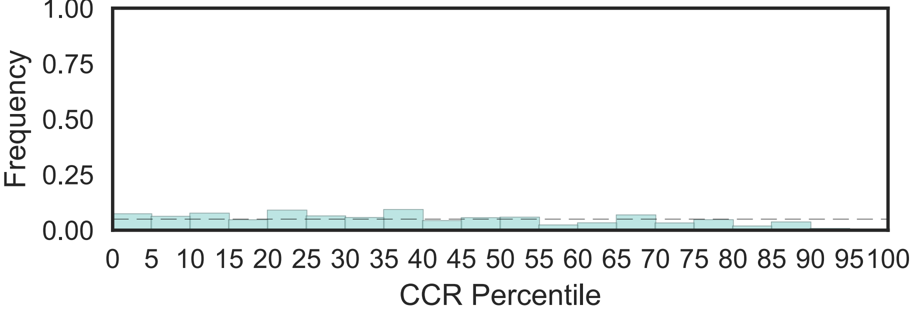

RD3 protein
(RD3, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


RDD family
(RDD, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Meiotic recombination protein REC114-like
(REC114-like, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

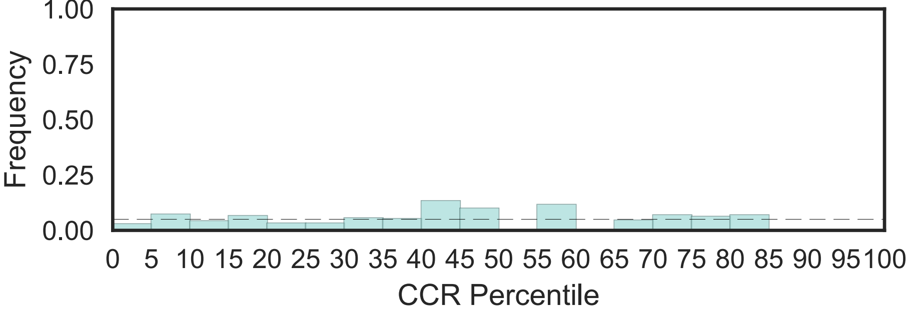

RED-like protein C-terminal region
(RED_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

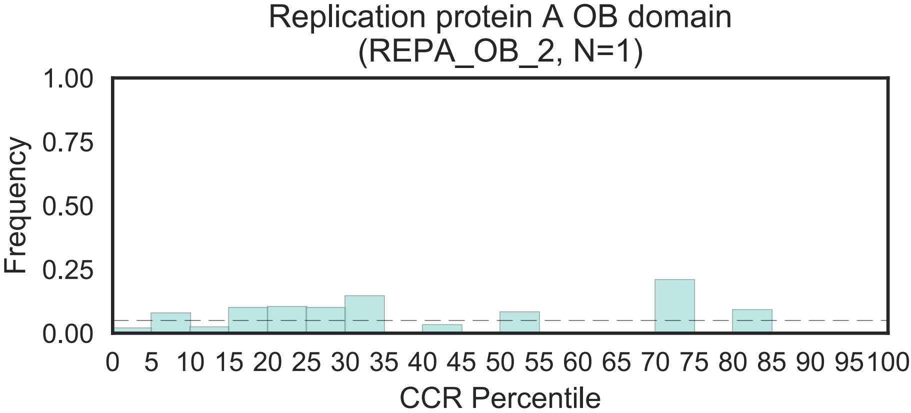

RED-like protein N-terminal region
(RED_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

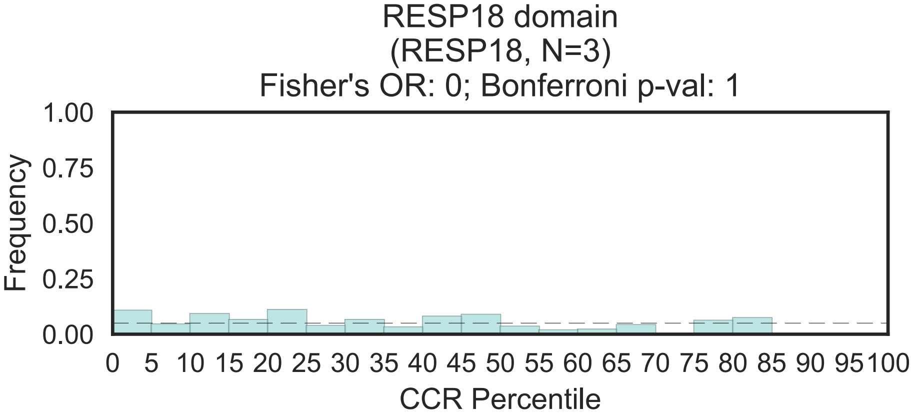


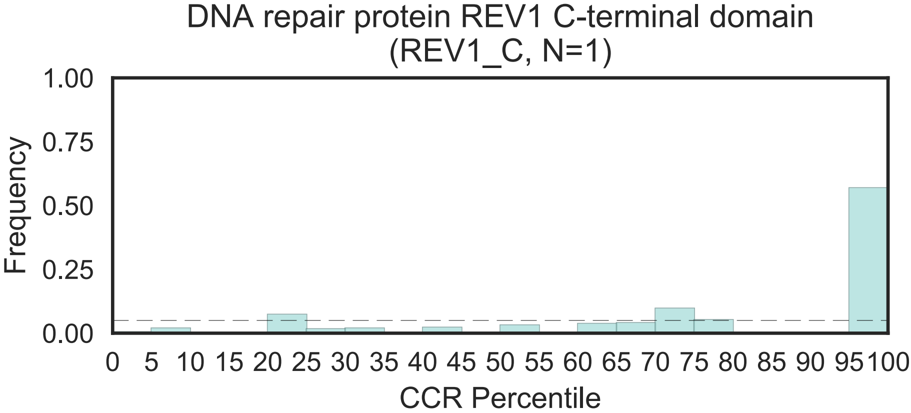
REJ domain
(REJ, N=5)
Fisher's OR: 0.157; Bonferroni p-val: 1

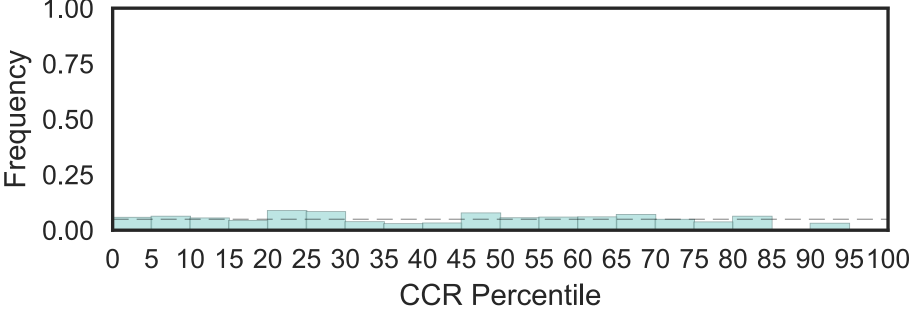
Tumour necrosis factor receptor superfamily member 19 (RELT, N=3)
Fisher's OR: 0; Bonferroni p-val: 1



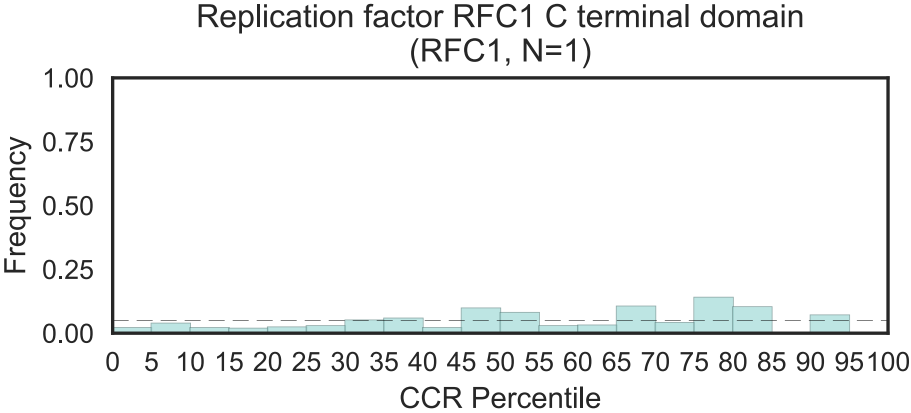

Replication protein A OB domain
(REPA_OB_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

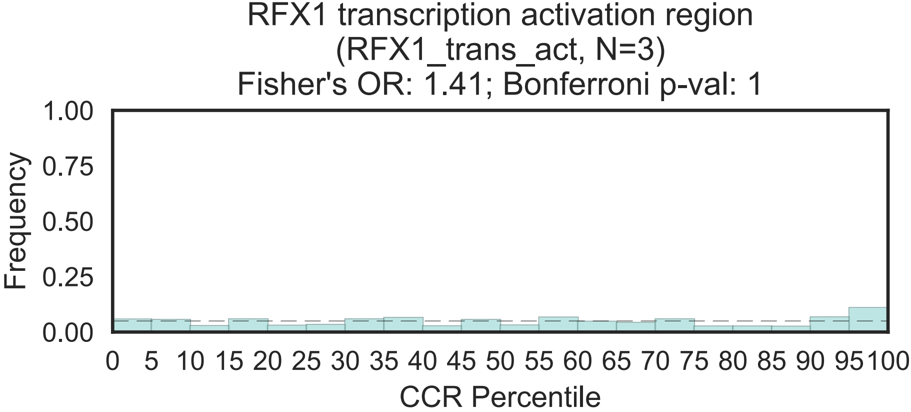

RESP18 domain
(RESP18, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

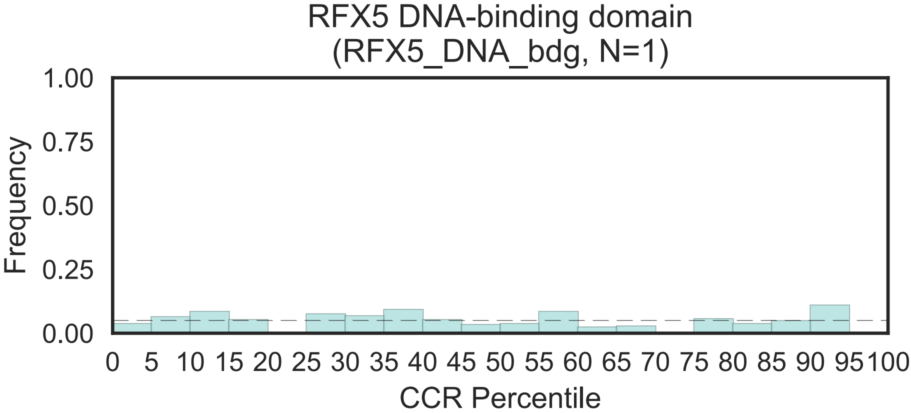

DNA repair protein REV1 C-terminal domain
(REV1_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

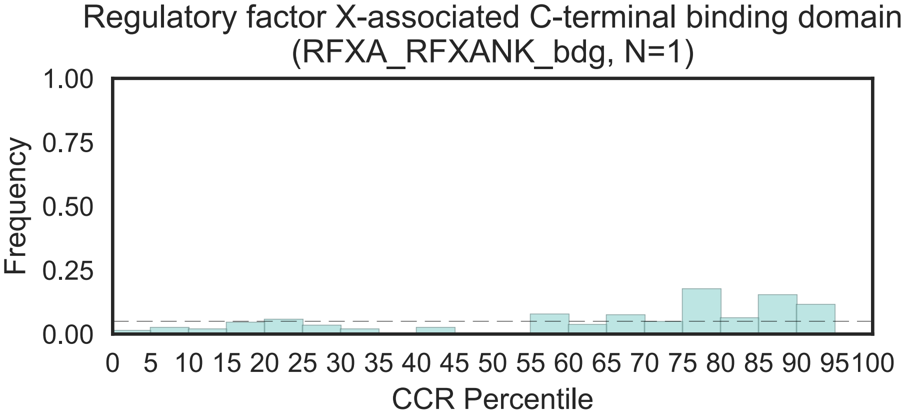


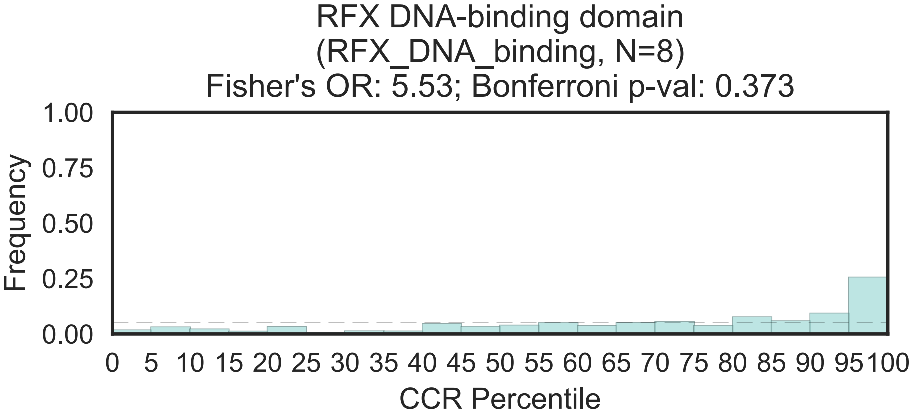
RF-1 domain
(RF-1, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

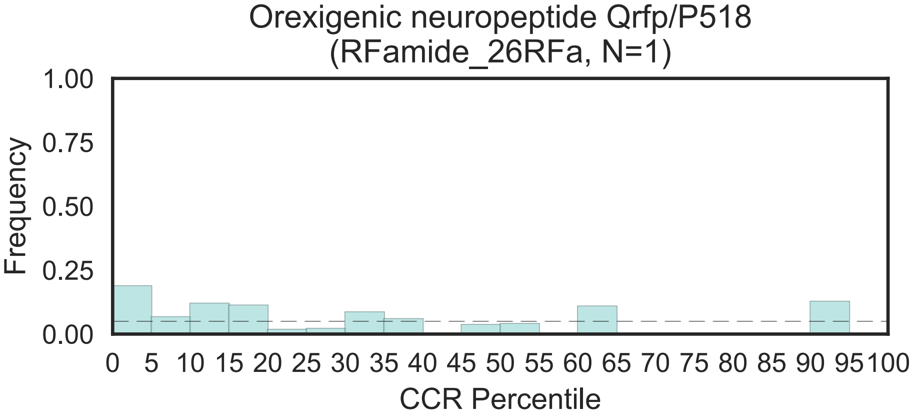

Replication factor RFC1 C terminal domain
(RFC1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

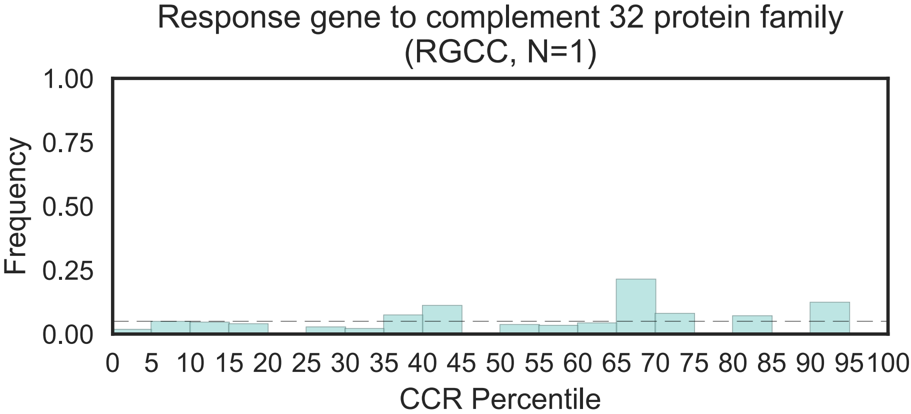

RFX1 transcription activation region
(RFX1_trans_act, N=3)
Fisher's OR: 1.41; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

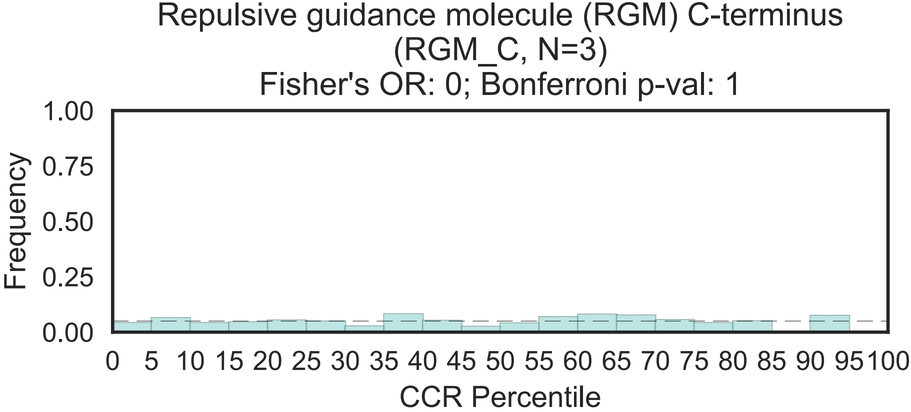

RFX5 DNA-binding domain
(RFX5_DNA_bdg, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Regulatory factor X-associated C-terminal binding domain
(RFXA_RFXANK_bdg, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


RFX DNA-binding domain
(RFX_DNA_binding, N=8)
Fisher's OR: 5.53; Bonferroni p-val: 0.373
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

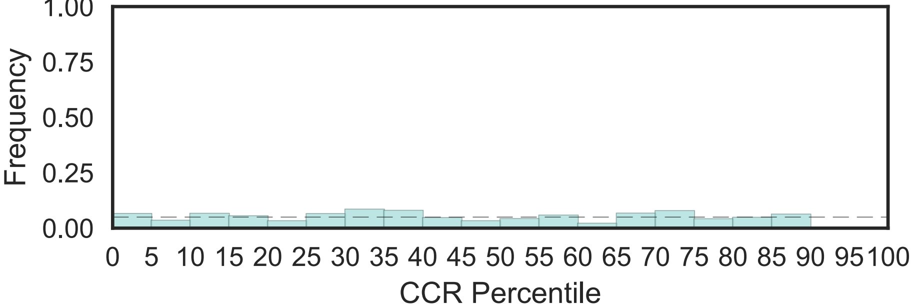

Orexigenic neuropeptide Qrfp/P518
(RFamide_26RFa, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

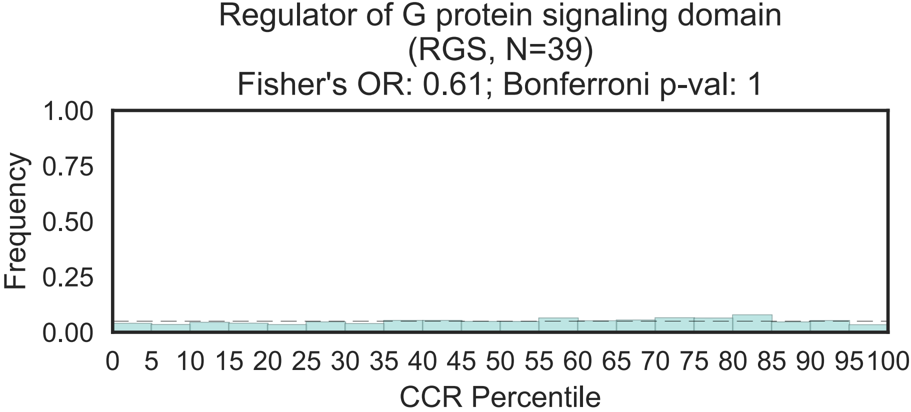

Response gene to complement 32 protein family
(RGCC, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

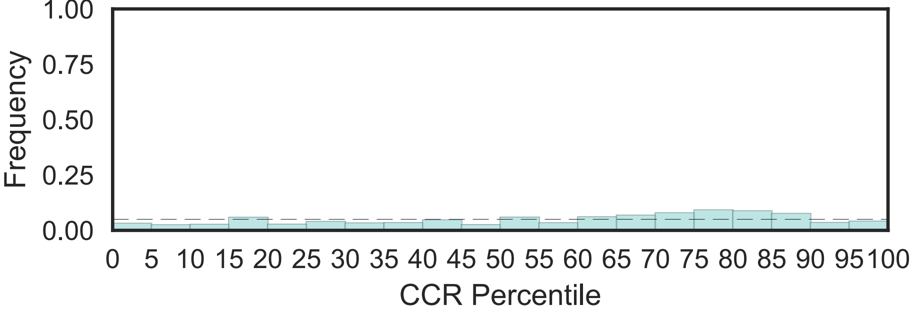


Repulsive guidance molecule (RGM) C-terminus
(RGM_C, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

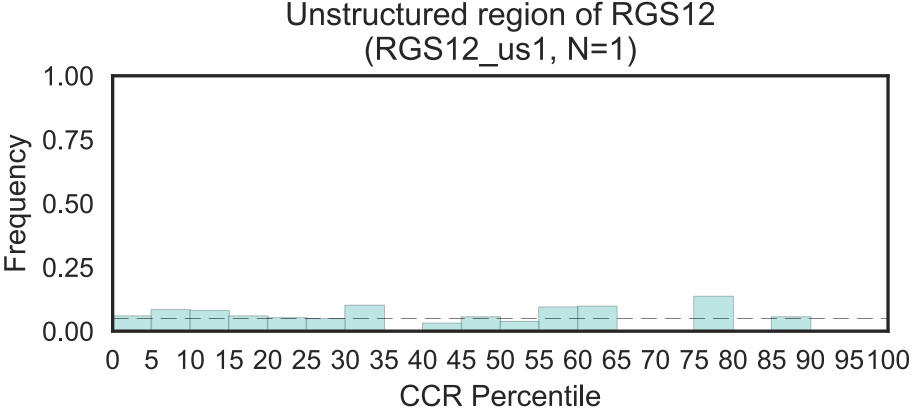
Repulsive guidance molecule (RGM) N-terminus (RGM_N, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

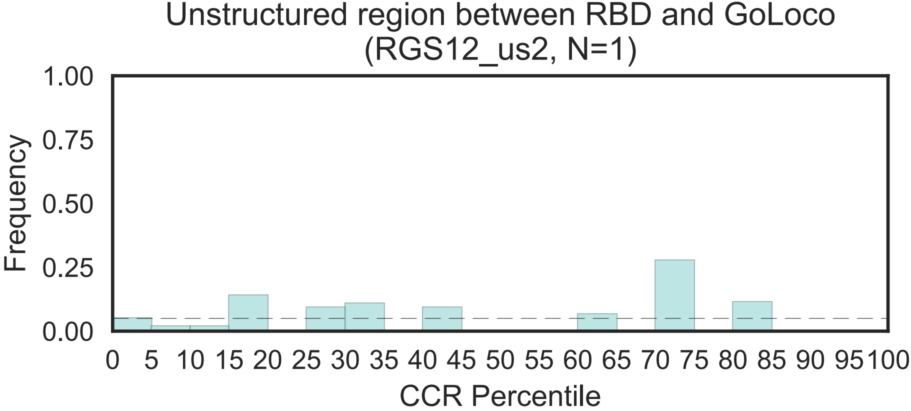


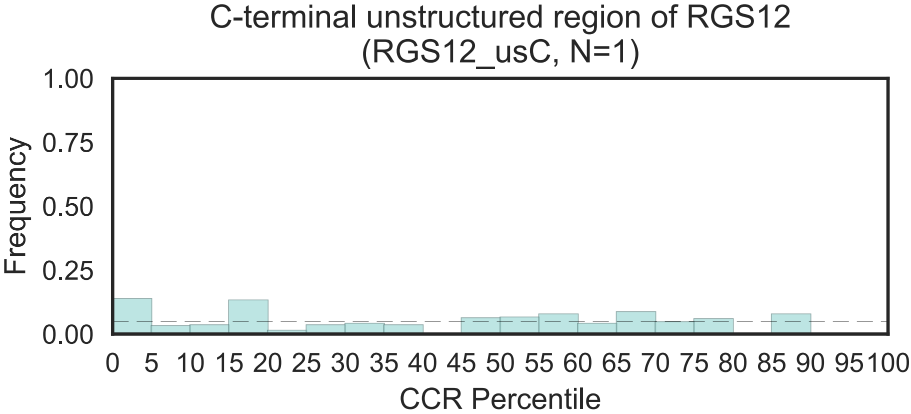

Regulator of G protein signaling domain
(RGS, N=39)
Fisher's OR: 0.61; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

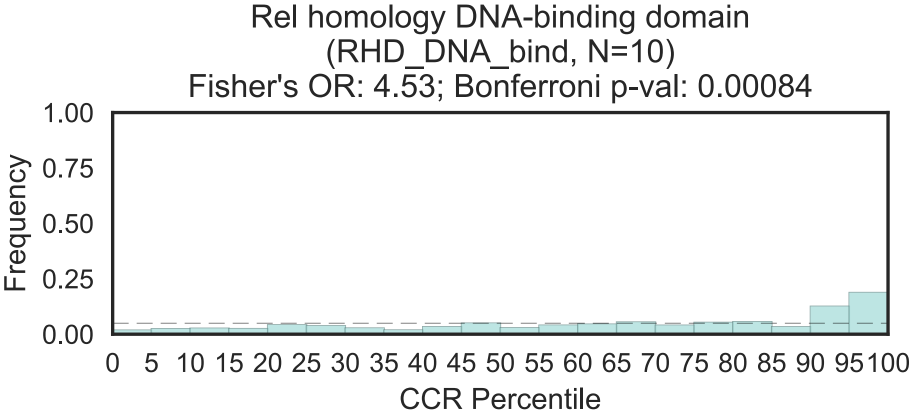


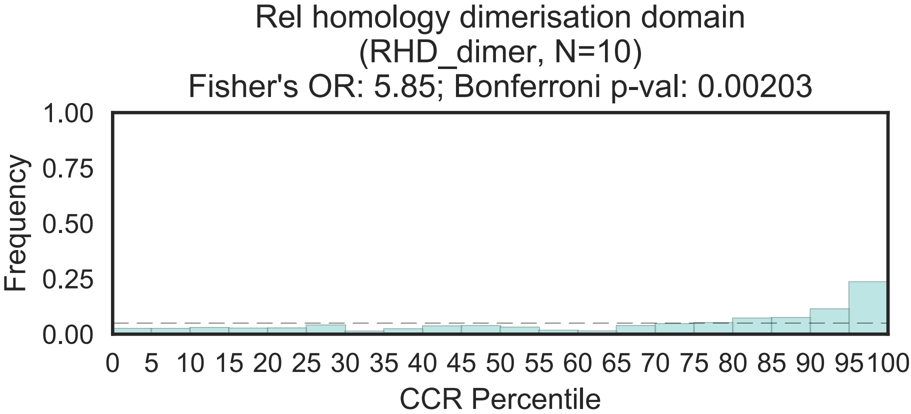
Regulator of G protein signalling-like domain
(RGS-like, N=3)
Fisher's OR: 0.597; Bonferroni p-val: 1


Unstructured region of RGS12
(RGS12_us1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

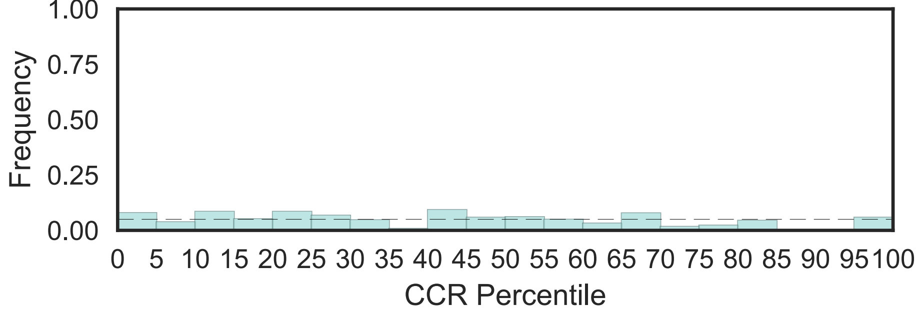

Unstructured region between RBD and GoLoco
(RGS12_us2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

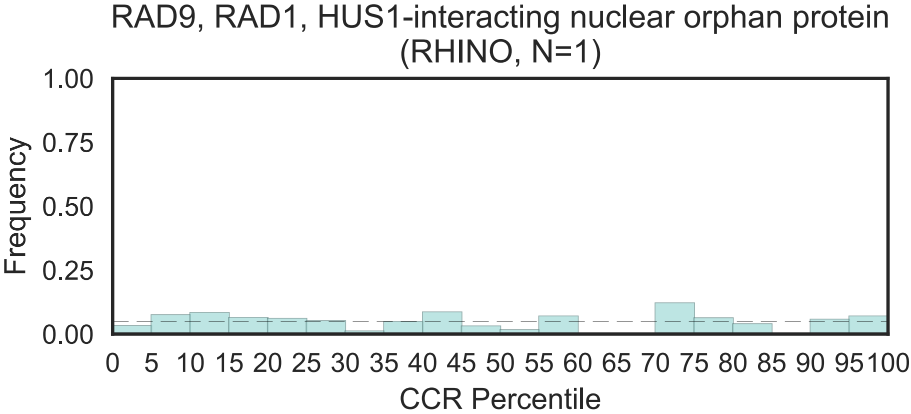

C-terminal unstructured region of RGS12
(RGS12_usC, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

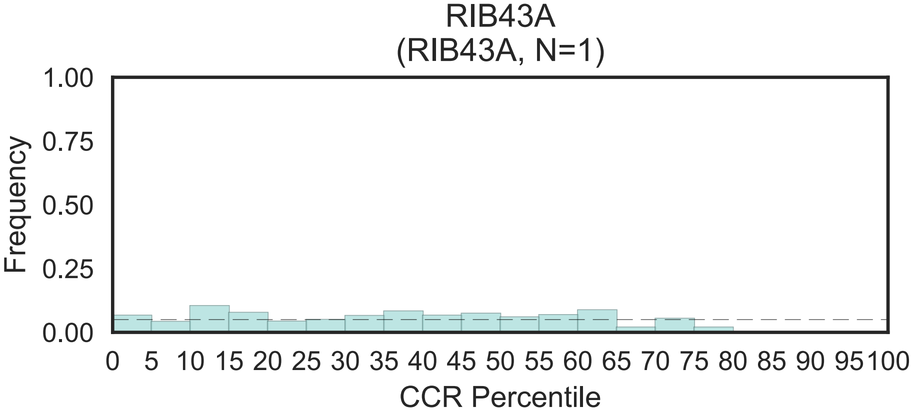

Rel homology DNA-binding domain
(RHD_DNA_bind, N=10)
Fisher's OR: 4.53; Bonferroni p-val: 0.00084
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

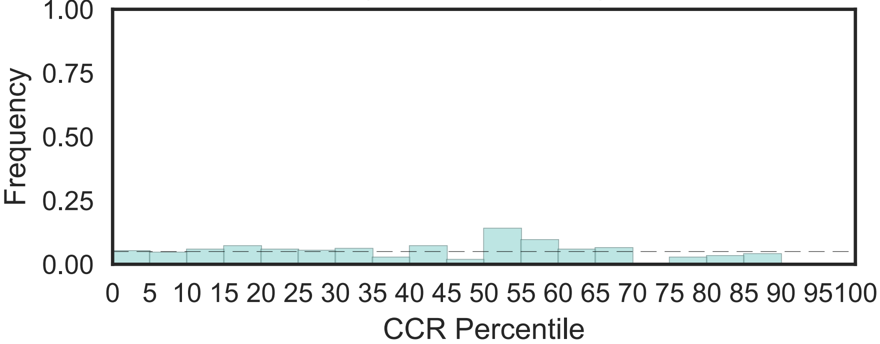

Rel homology dimerisation domain
(RHD_dimer, N=10)
Fisher's OR: 5.85; Bonferroni p-val: 0.00203
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

RIP homotypic interaction motif
(RHIM, N=6)
Fisher's OR: 0.948; Bonferroni p-val: 1

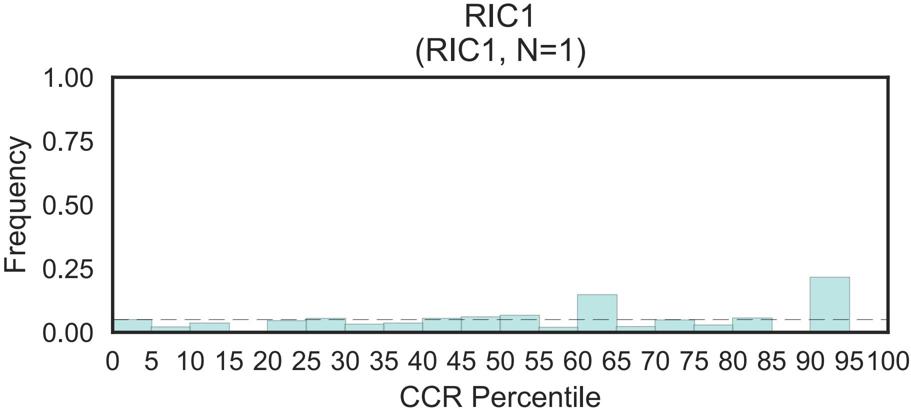


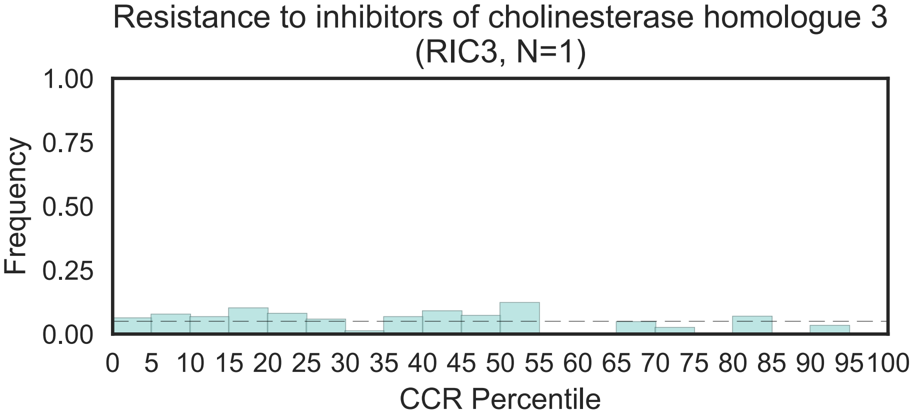

RAD9, RAD1, HUS1-interacting nuclear orphan protein
(RHINO, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

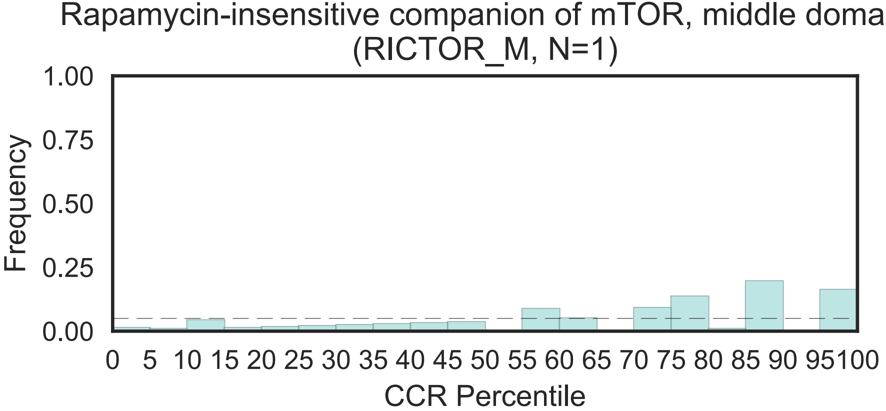

RIB43A
(RIB43A, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



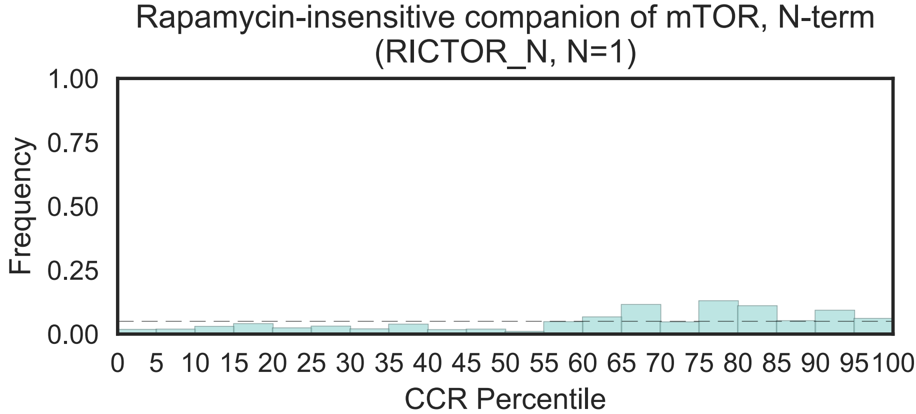
40S ribosome biogenesis protein Tsr1 and BMS1 C-terminal (RIBIOP_C, N=2)

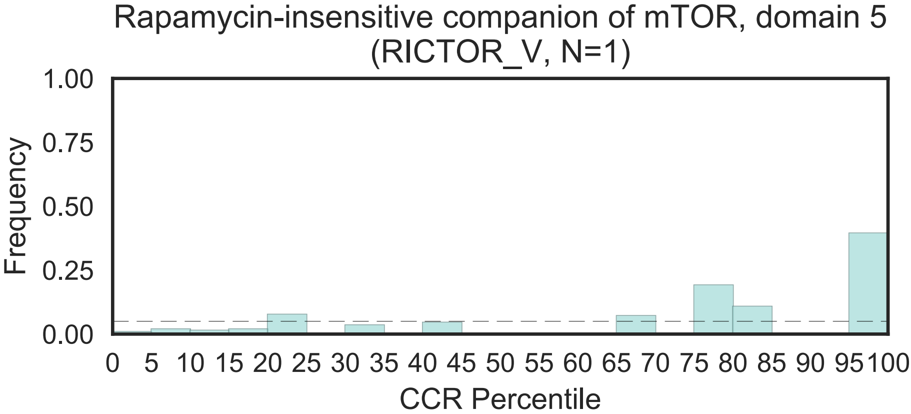

RIC1
(RIC1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

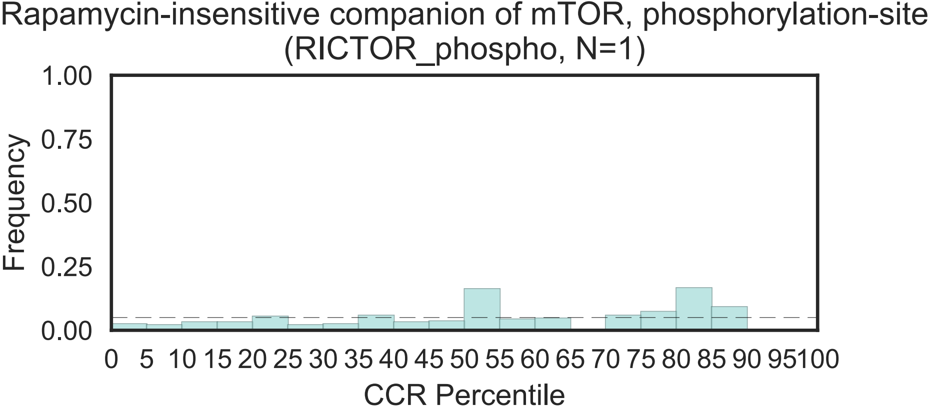

Resistance to inhibitors of cholinesterase homologue 3
(RIC3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

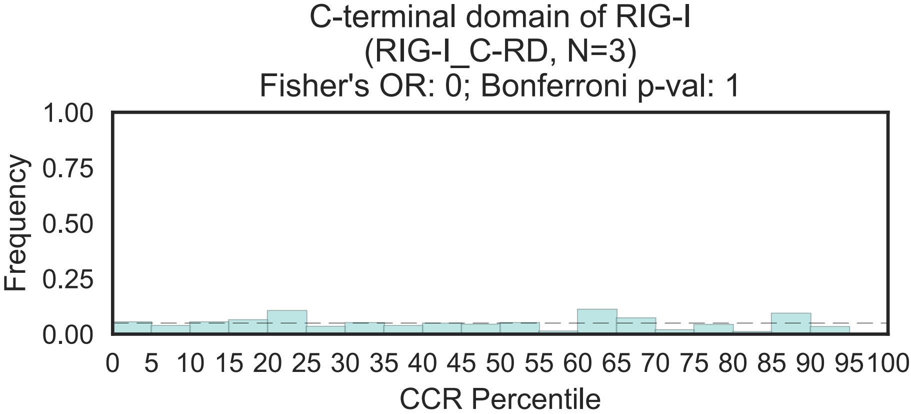


Rapamycin-insensitive companion of mTOR, middle domain
(RICTOR_M, N=1)

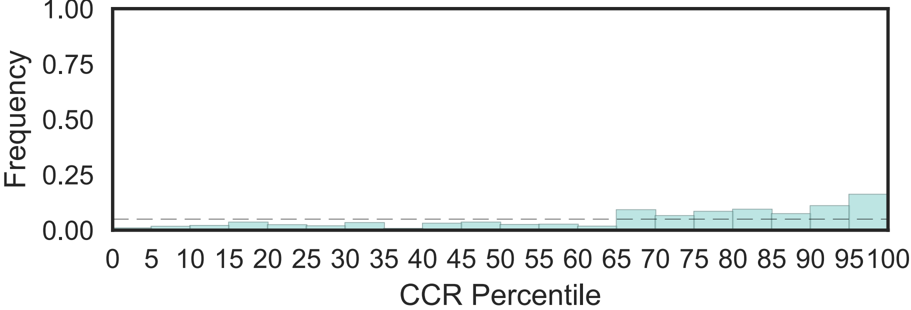

Rapamycin-insensitive companion of mTOR, N-term
(RICTOR_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Rapamycin-insensitive companion of mTOR, domain 5
(RICTOR_V, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

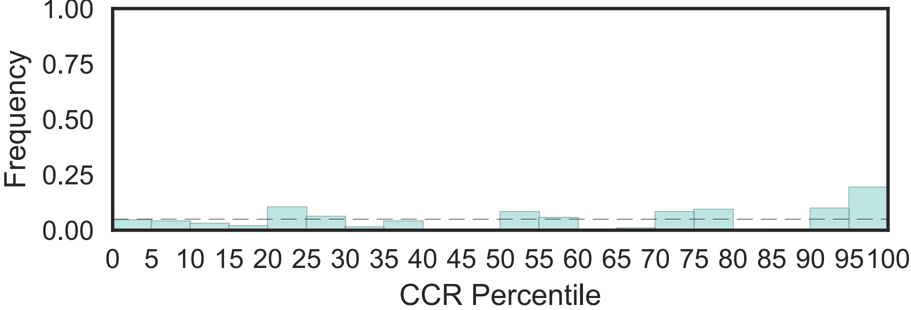

Rapamycin-insensitive companion of mTOR, phosphorylation-site
(RICTOR_phospho, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

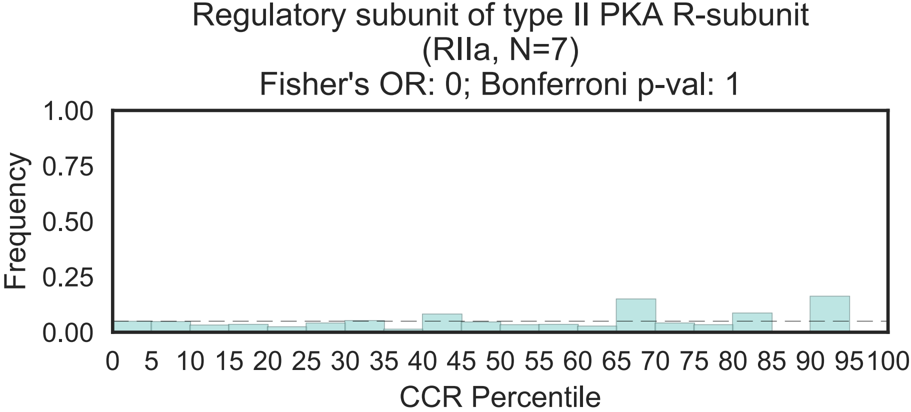

C-terminal domain of RIG-I
(RIG-I_C-RD, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

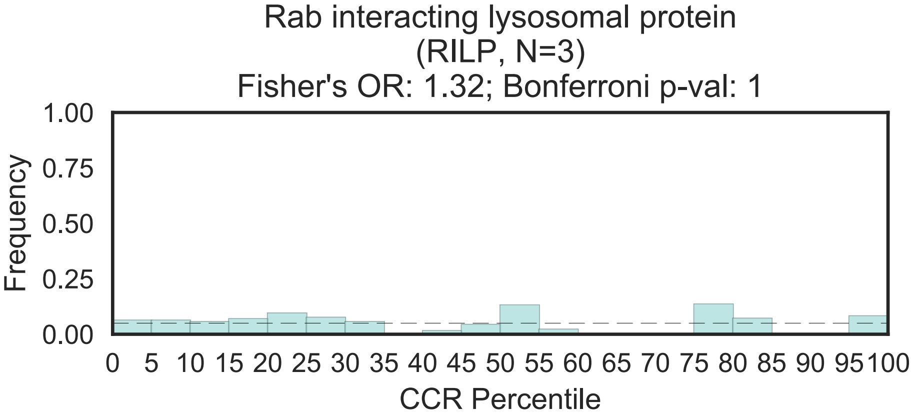
RyR and IP3R Homology associated
(RIH_assoc, N=6)
Fisher's OR: 2.74; Bonferroni p-val: 1

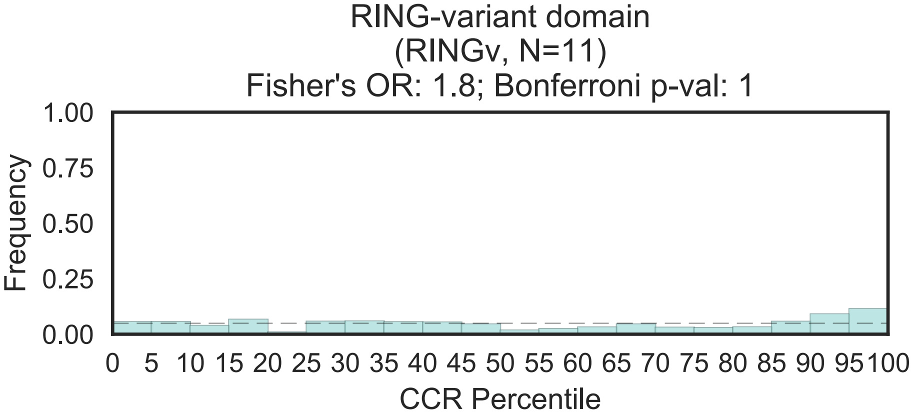


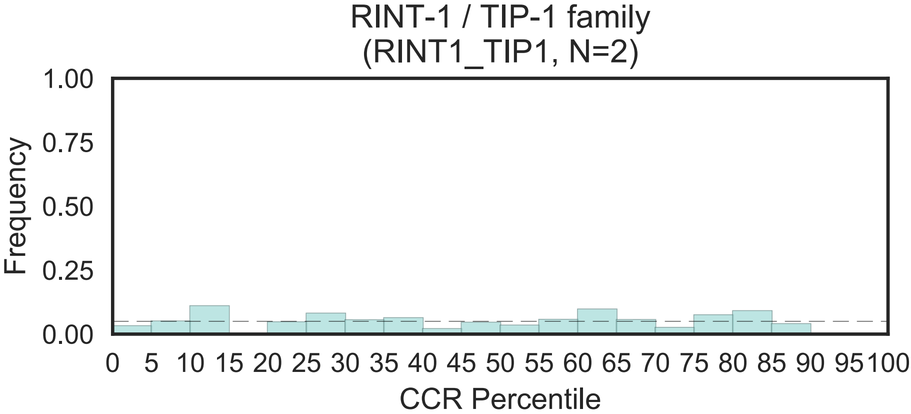
RII binding domain
(RII_binding_1, N=4)
Fisher's OR: 3.38; Bonferroni p-val: 1

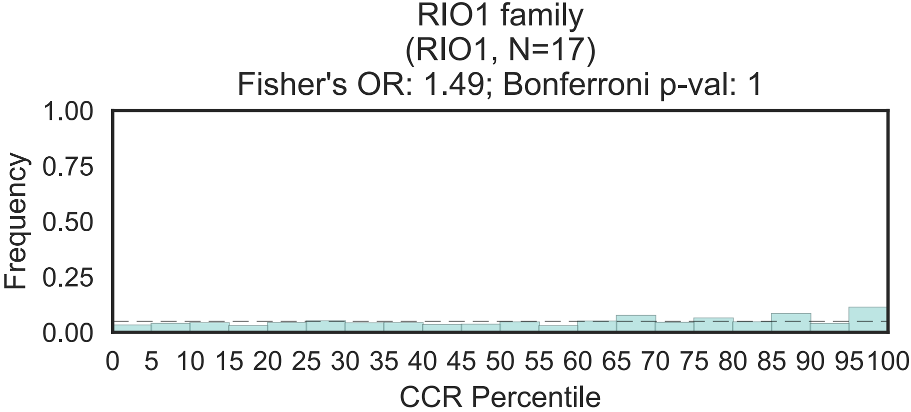


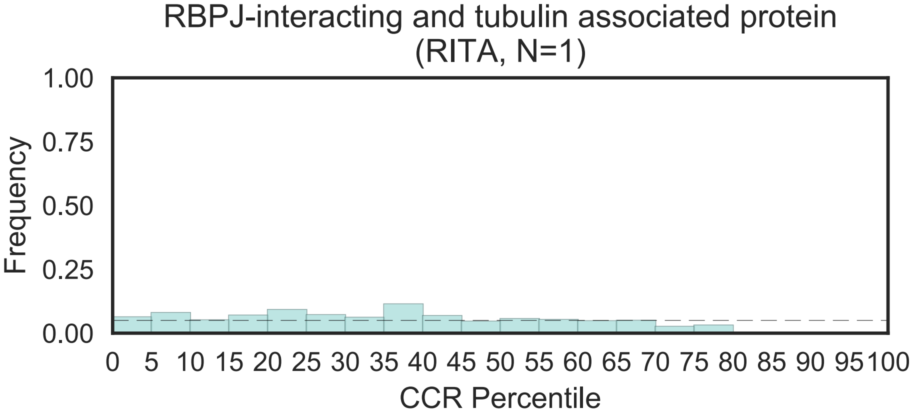

Regulatory subunit of type II PKA R-subunit
(RIIa, N=7)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

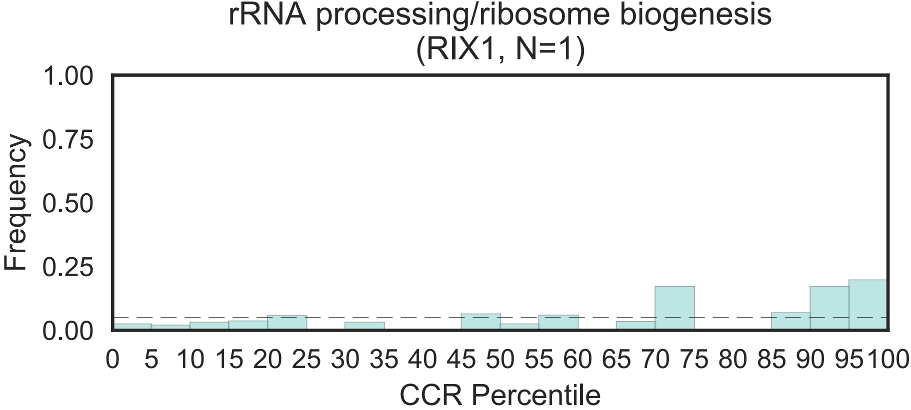

Rab interacting lysosomal protein
(RILP, N=3)
Fisher's OR: 1.32; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

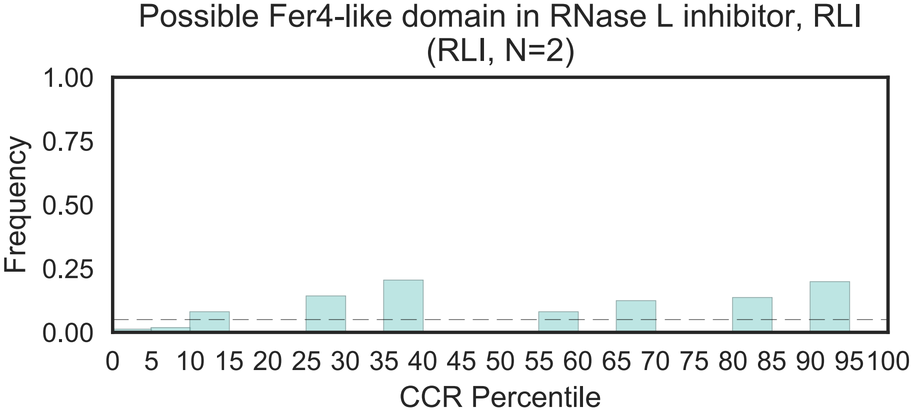

RING-variant domain
(RINGv, N=11)
Fisher's OR: 1.8; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

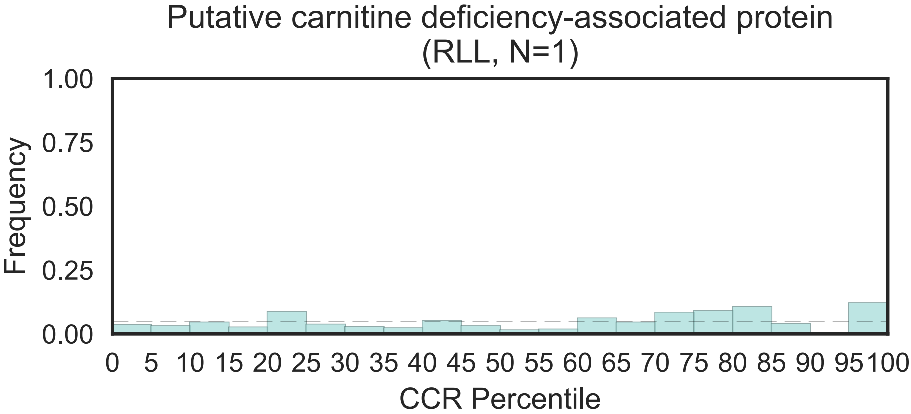

RINT-1 / TIP-1 family
(RINT1_TIP1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


RIO1 family
(RIO1, N=17)
Fisher's OR: 1.49; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

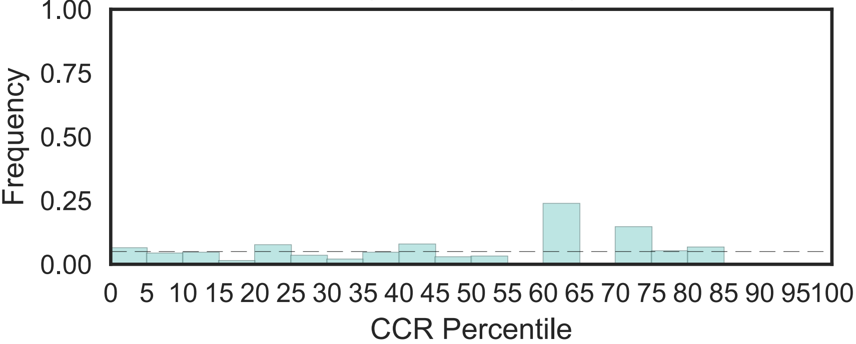

RBPJ-interacting and tubulin associated protein
(RITA, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

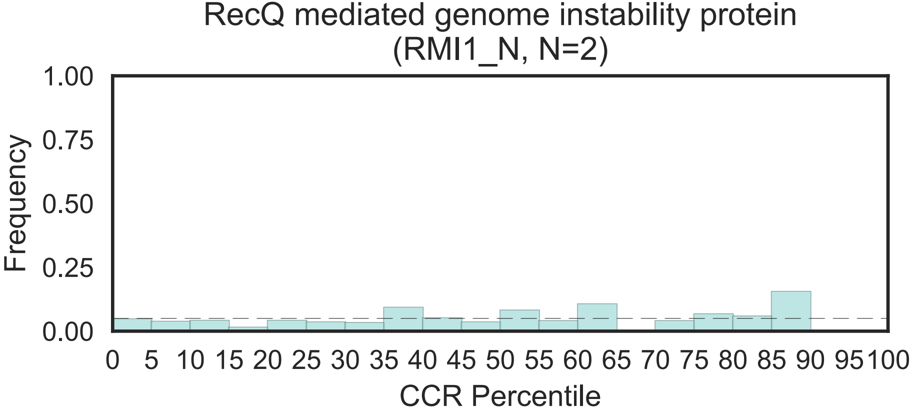

rRNA processing/ribosome biogenesis
(RIX1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

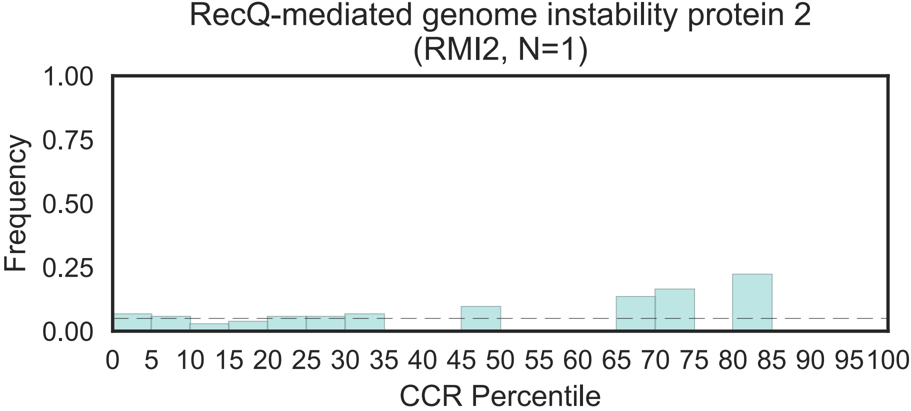

Possible Fer4-like domain in RNase L inhibitor, RLI
(RLI, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

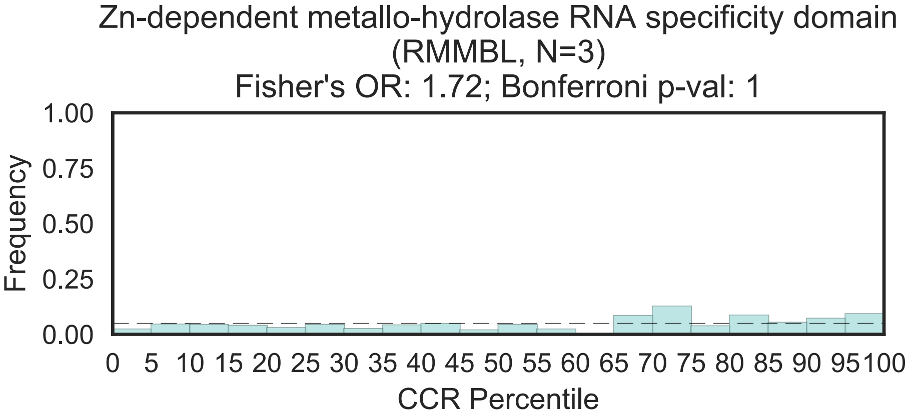

Putative carnitine deficiency-associated protein
(RLL, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

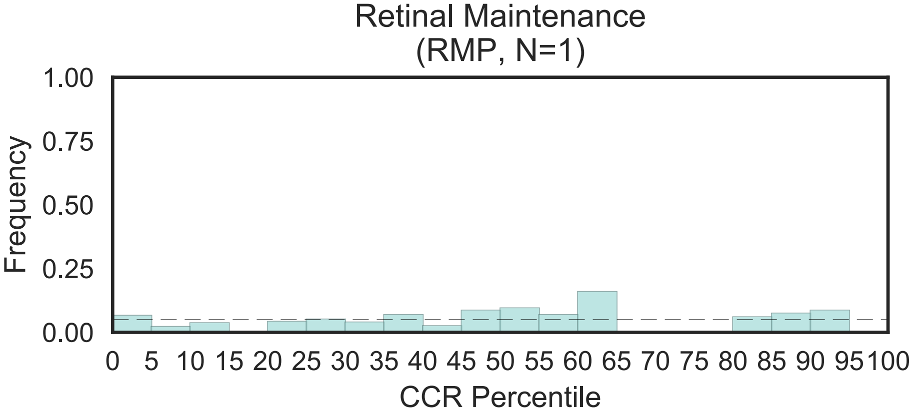
Recq-mediated genome instability protein 1, C-terminal OB-fold (RMI1_C, N=1)

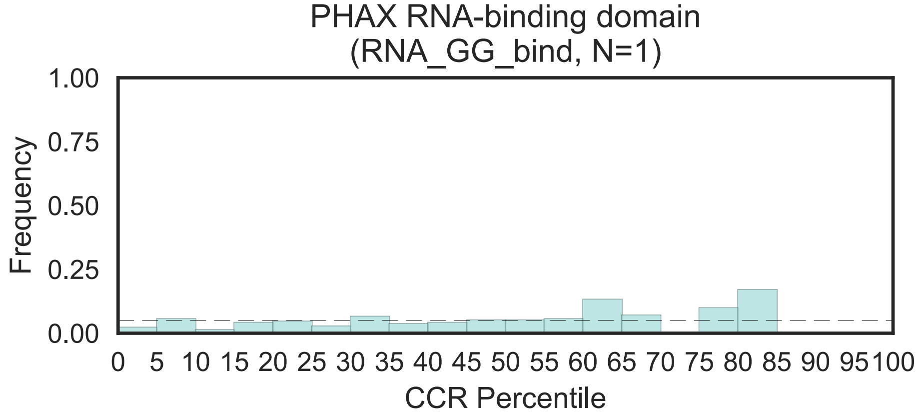


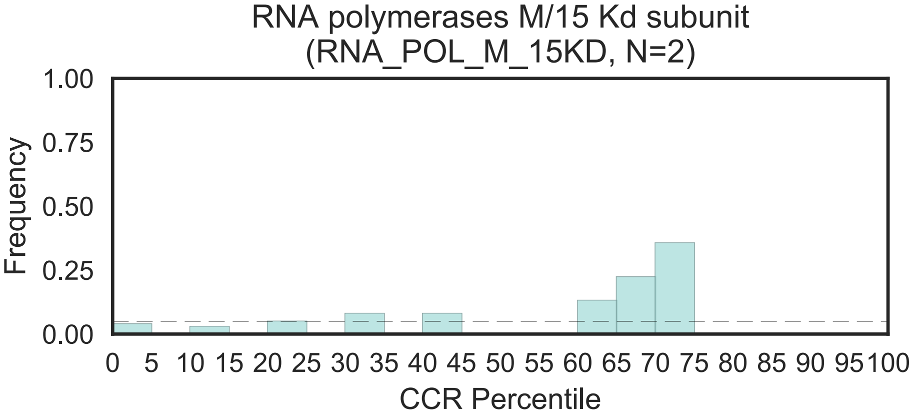

RecQ mediated genome instability protein
(RMI1_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

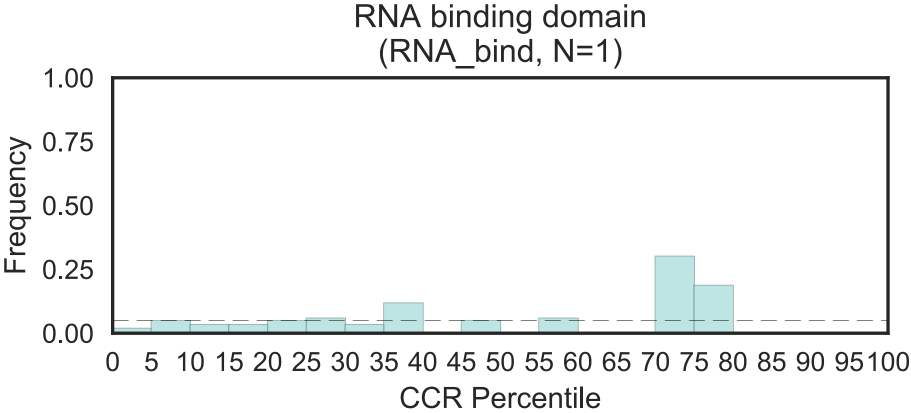

RecQ-mediated genome instability protein 2
(RMI2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

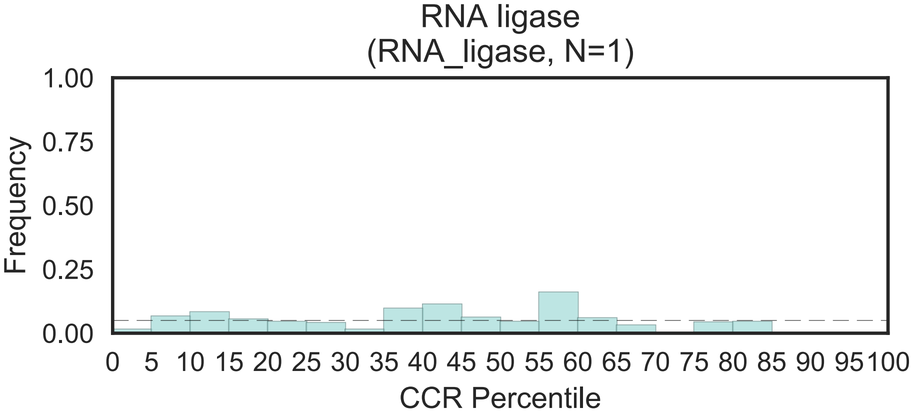

Zn-dependent metallo-hydrolase RNA specificity domain
(RMMBL, N=3)
Fisher's OR: 1.72; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

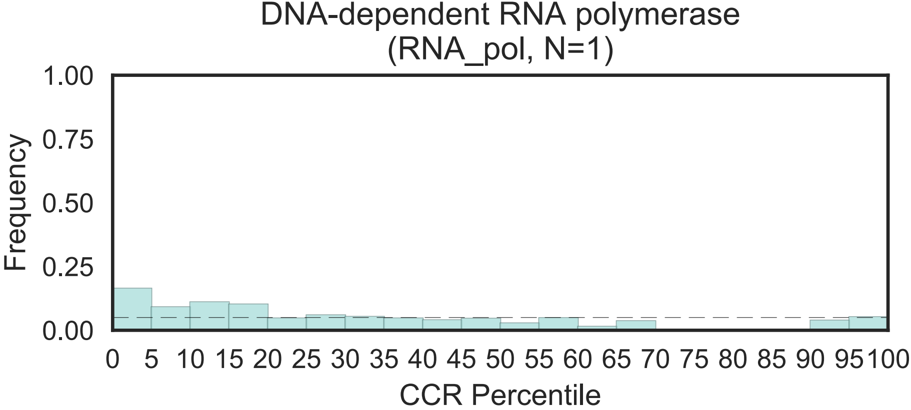

Retinal Maintenance
(RMP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

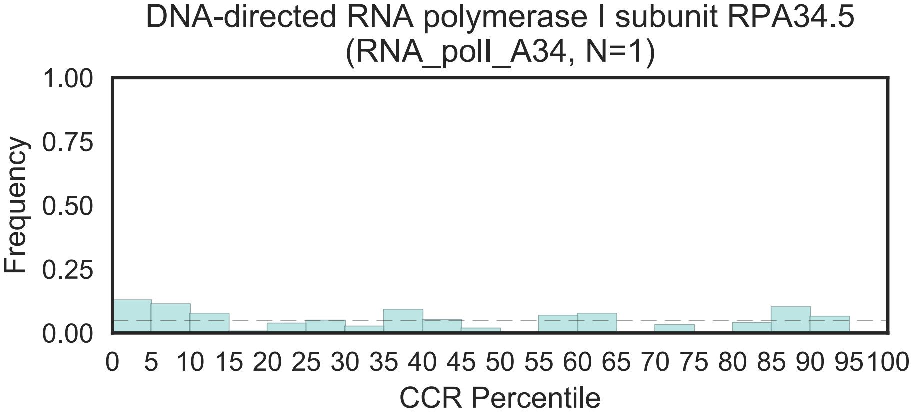

PHAX RNA-binding domain
(RNA_GG_bind, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

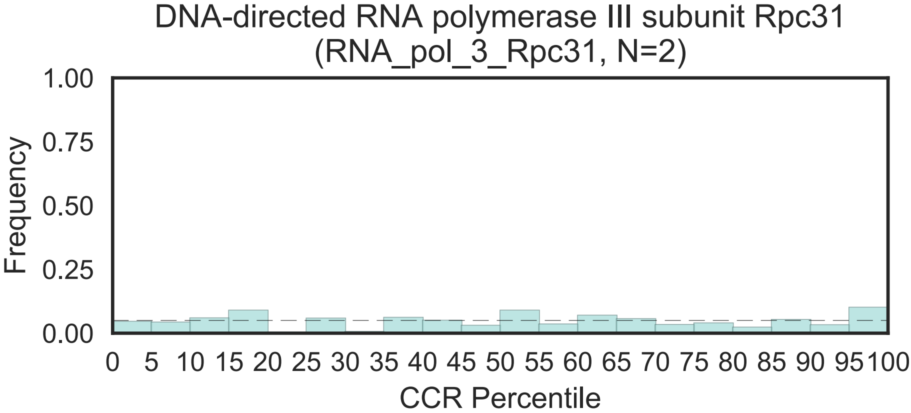

RNA polymerases M/15 Kd subunit
(RNA_POL_M_15KD, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

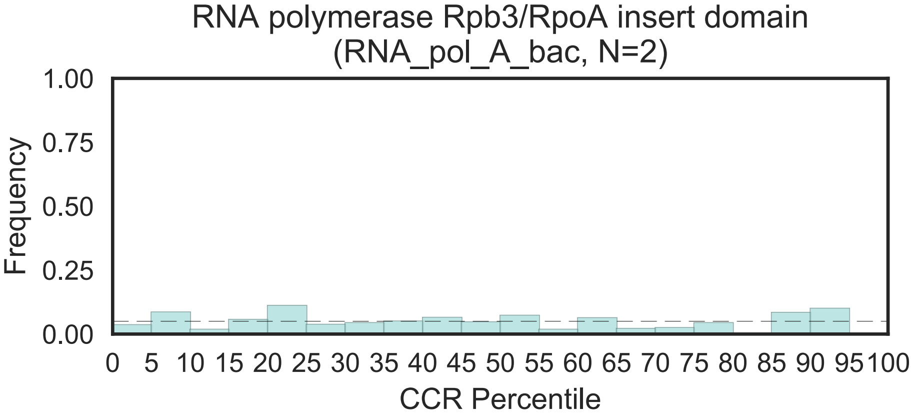

RNA binding domain
(RNA_bind, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

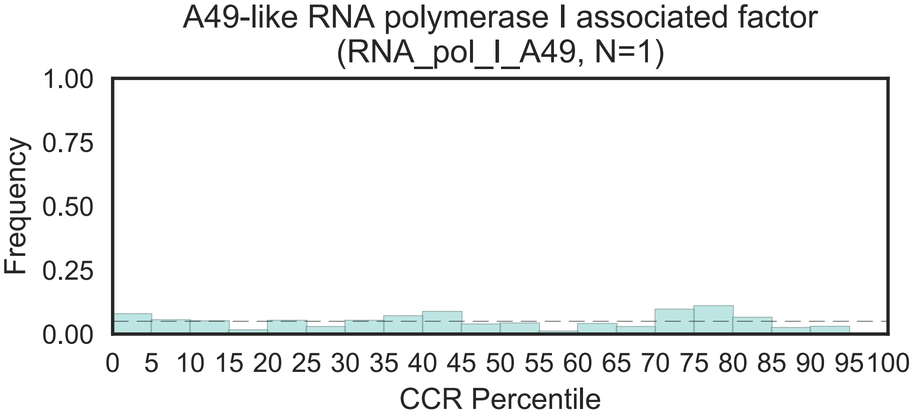

RNA ligase
(RNA_ligase, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

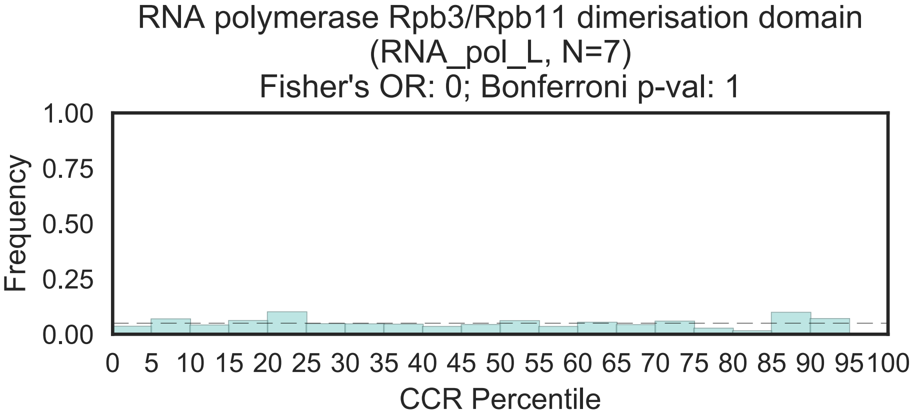

DNA-dependent RNA polymerase
(RNA_pol, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


DNA-directed RNA polymerase I subunit RPA34.5
(RNA_polI_A34, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

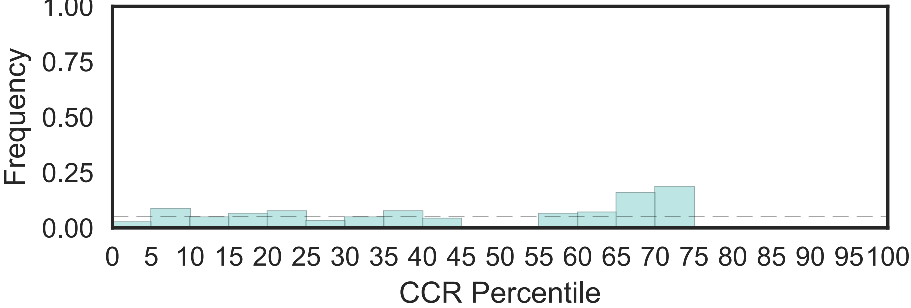

DNA-directed RNA polymerase III subunit Rpc31
(RNA_pol_3_Rpc31, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

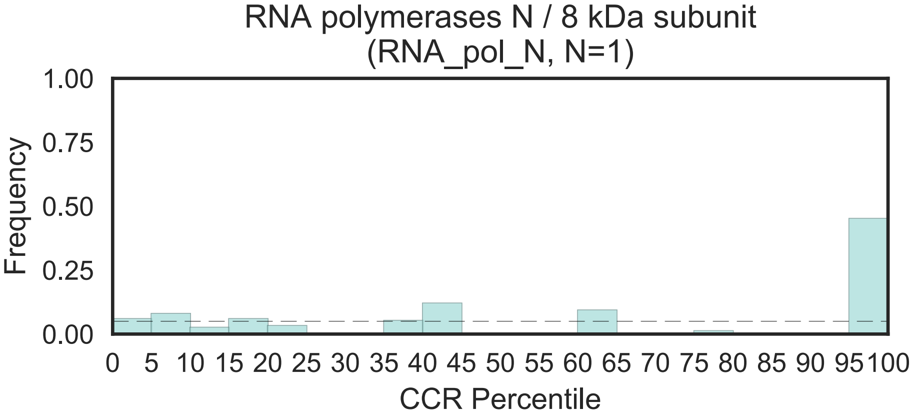

RNA polymerase Rpb3/RpoA insert domain
(RNA_pol_A_bac, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

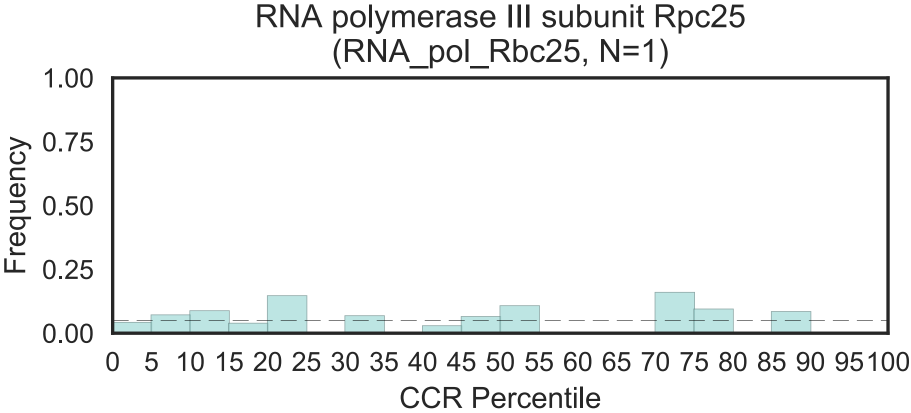

A49-like RNA polymerase I associated factor
(RNA_pol_I_A49, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

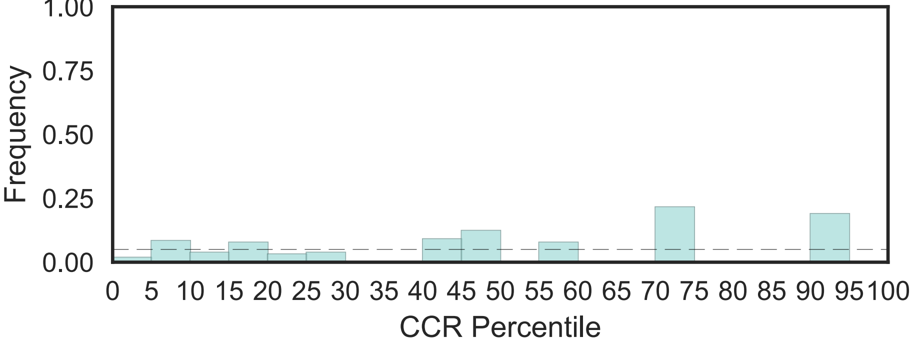

RNA polymerase Rpb3/Rpb11 dimerisation domain
(RNA_pol_L, N=7)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

RNA polymerase Rpb3/Rpb11 dimerisation domain (RNA_pol_L_2, N=5)
Fisher's OR: 0; Bonferroni p-val: 1

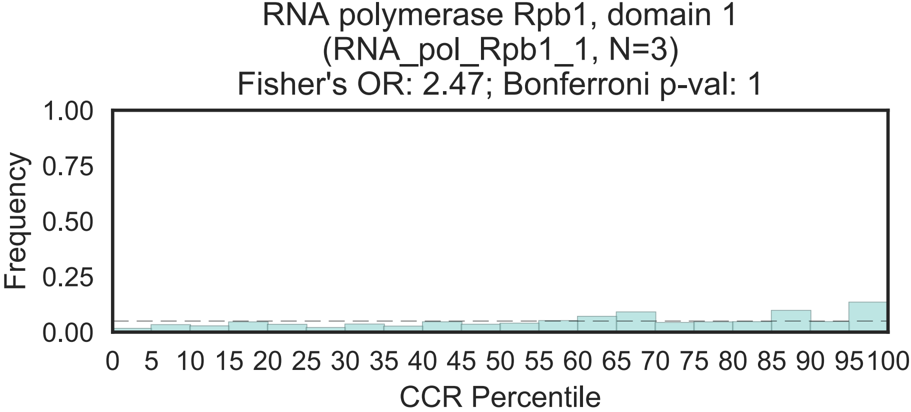



RNA polymerases N / 8 kDa subunit
(RNA_pol_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

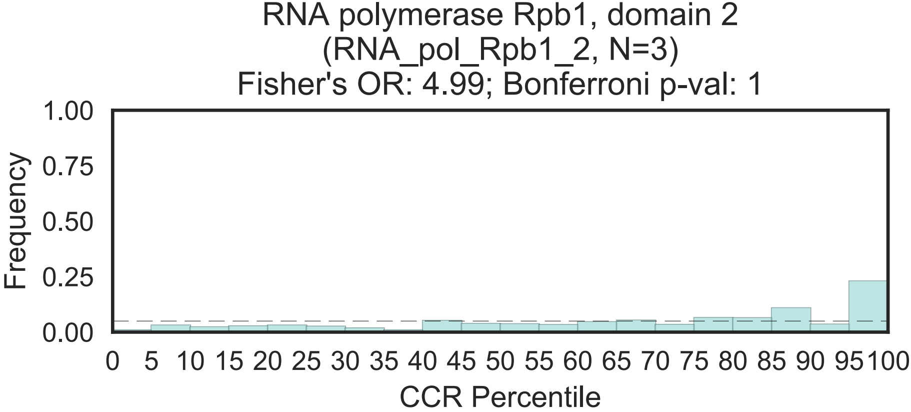

RNA polymerase III subunit Rpc25
(RNA_pol_Rbc25, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

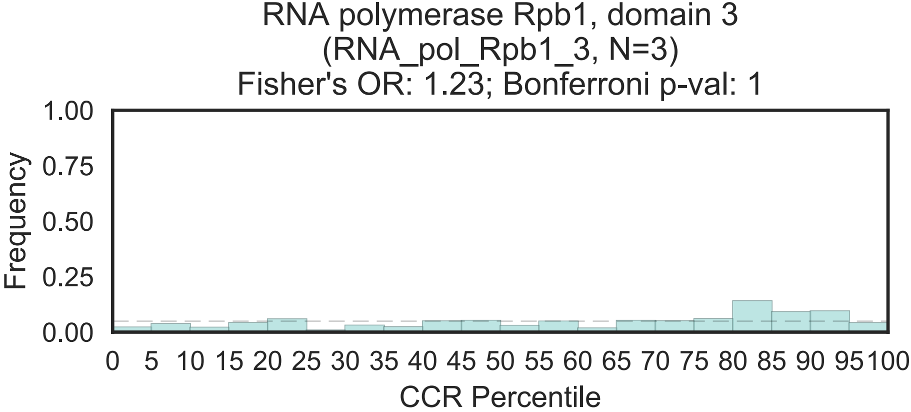


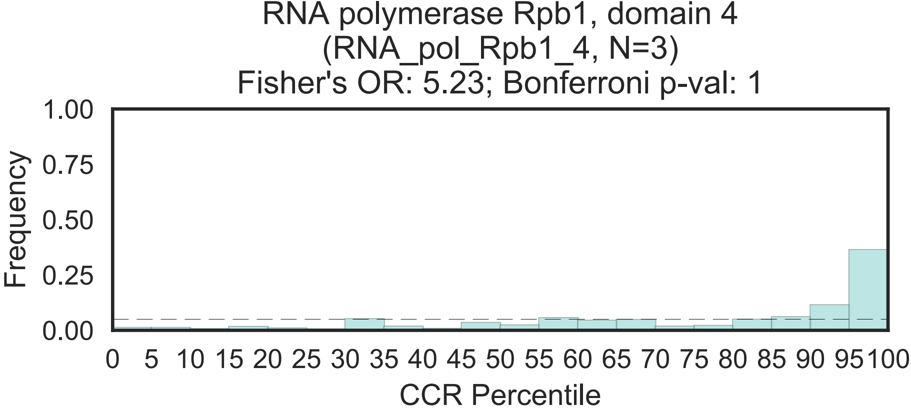
RNA polymerase I, Rpa2 specific domain
(RNA_pol_Rpa2_4, N=1)

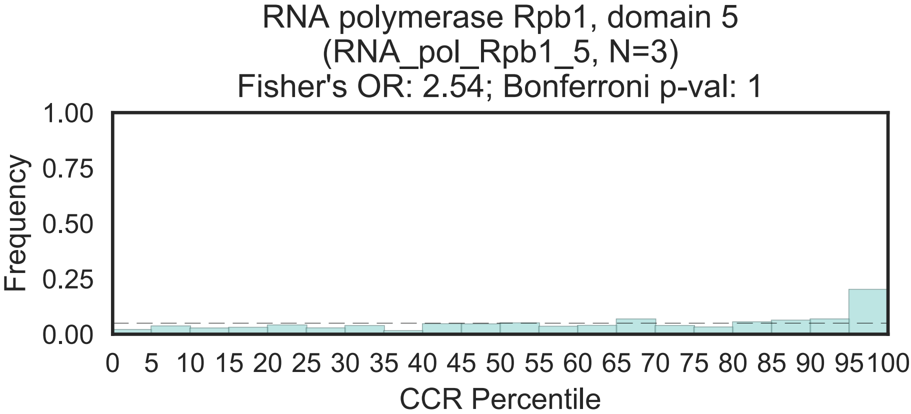


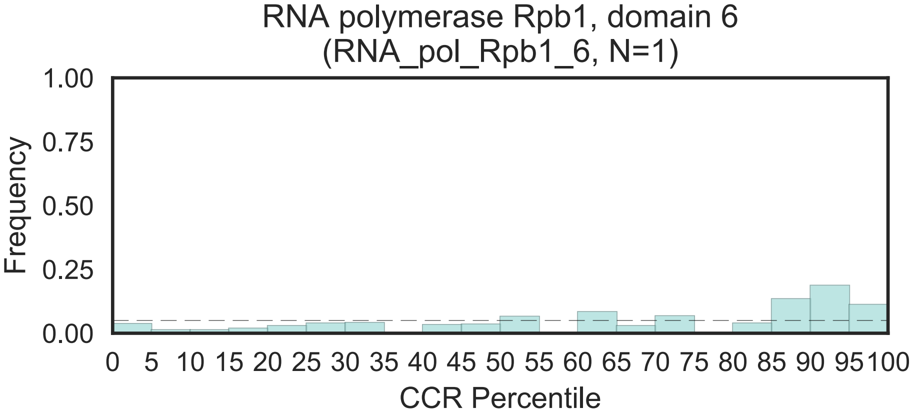
RNA polymerase Rpb1, domain 1
(RNA_pol_Rpb1_1, N=3)
Fisher's OR: 2.47; Bonferroni p-val: 1

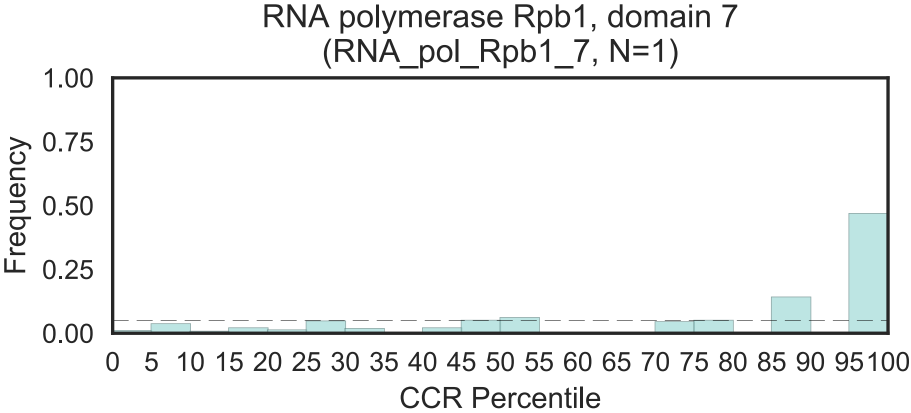

RNA polymerase Rpb1, domain 2
(RNA_pol_Rpb1_2, N=3)
Fisher's OR: 4.99; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


RNA polymerase Rpb1, domain 3
(RNA_pol_Rpb1_3, N=3)
Fisher's OR: 1.23; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

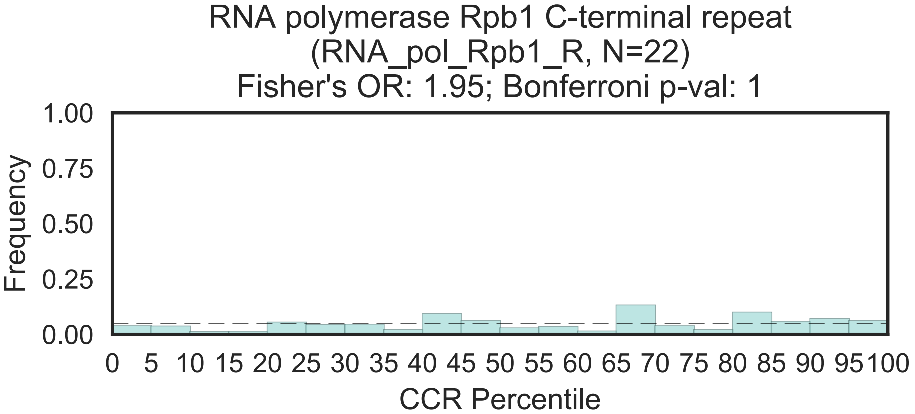

RNA polymerase Rpb1, domain 4
(RNA_pol_Rpb1_4, N=3)
Fisher's OR: 5.23; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

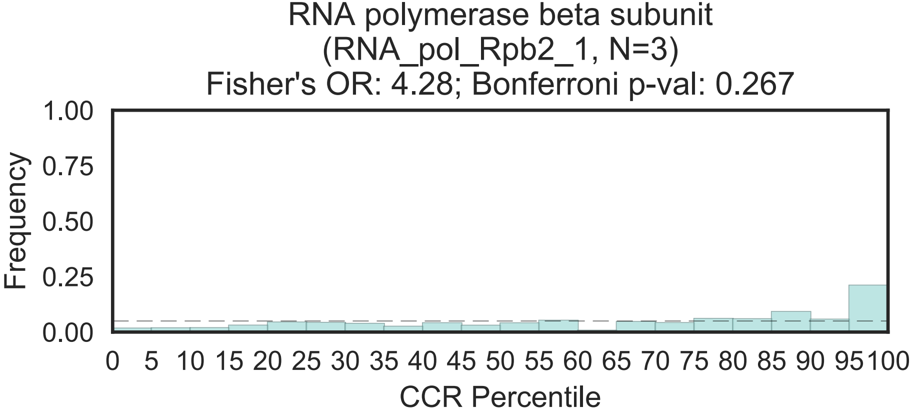

RNA polymerase Rpb1, domain 5
(RNA_pol_Rpb1_5, N=3)
Fisher's OR: 2.54; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

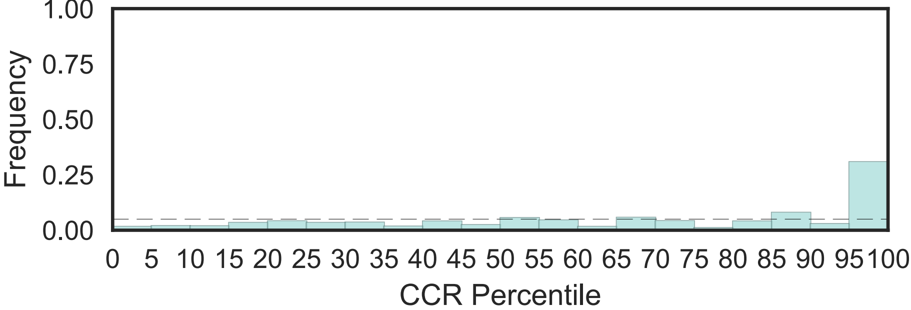

RNA polymerase Rpb1, domain 6
(RNA_pol_Rpb1_6, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



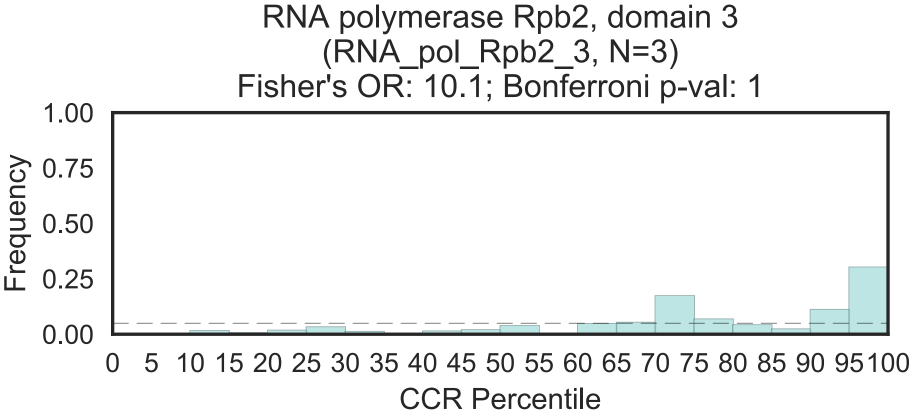
RNA polymerase Rpb1, domain 7
(RNA_pol_Rpb1_7, N=1)

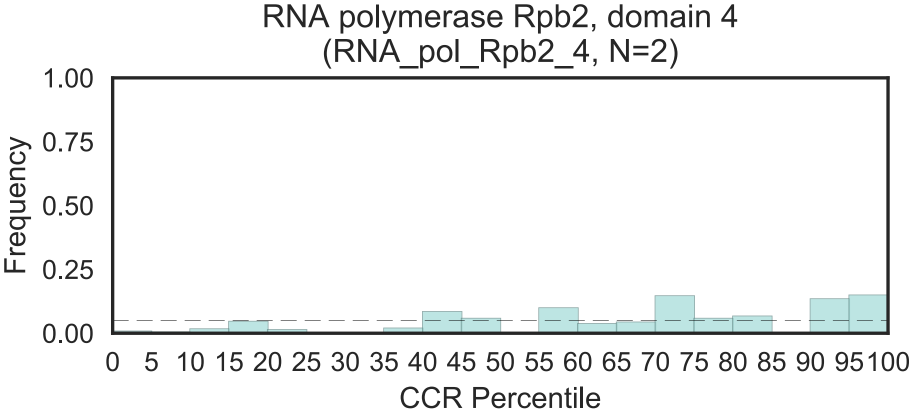

RNA polymerase Rpb1 C-terminal repeat
(RNA_pol_Rpb1_R, N=22)
Fisher's OR: 1.95; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

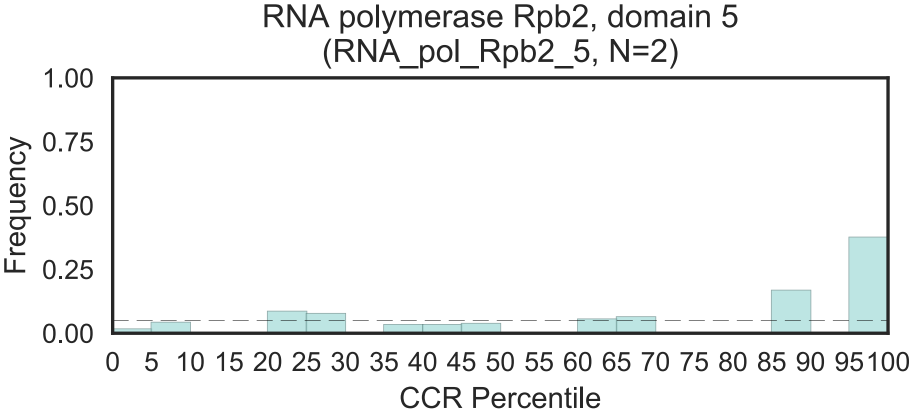

RNA polymerase beta subunit
(RNA_pol_Rpb2_1, N=3)
Fisher's OR: 4.28; Bonferroni p-val: 0.267
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

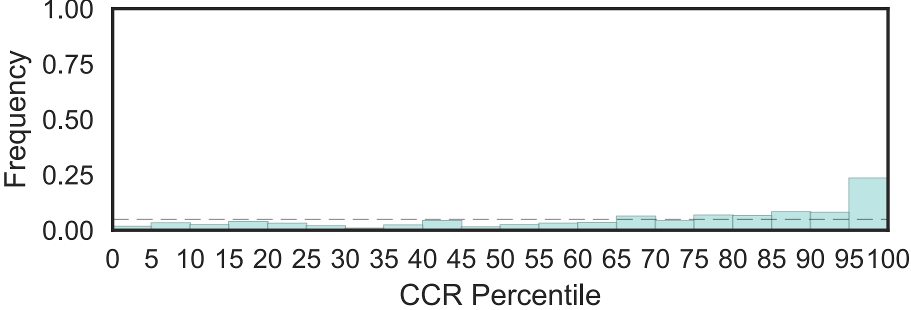


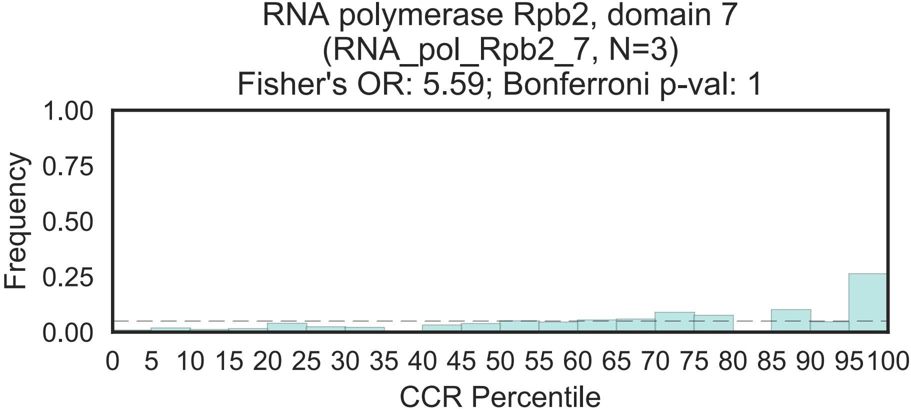
RNA polymerase Rpb2, domain 2
(RNA_pol_Rpb2_2, N=3)
Fisher's OR: 6.67; Bonferroni p-val: 0.0933


RNA polymerase Rpb2, domain 3
(RNA_pol_Rpb2_3, N=3)
Fisher's OR: 10.1; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

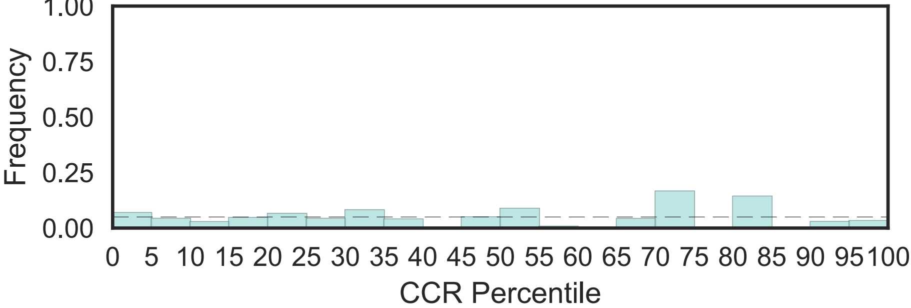

RNA polymerase Rpb2, domain 4
(RNA_pol_Rpb2_4, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

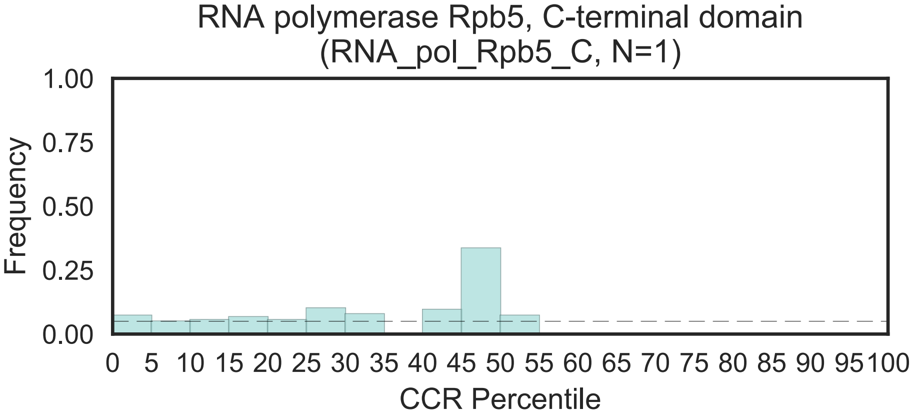

RNA polymerase Rpb2, domain 5
(RNA_pol_Rpb2_5, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

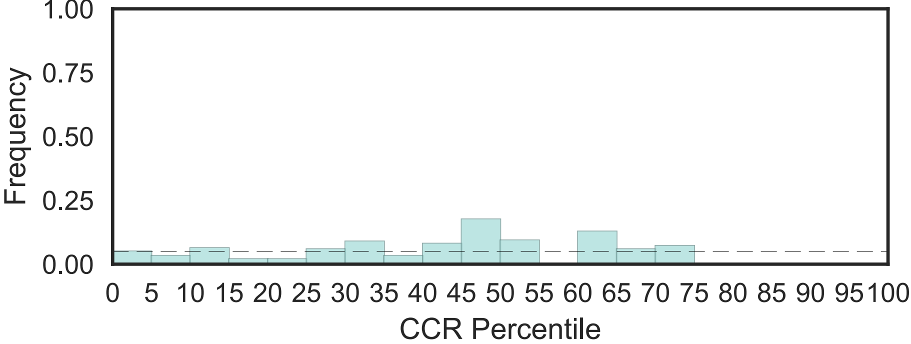

RNA polymerase Rpb2, domain 6
(RNA_pol_Rpb2_6, N=4)
Fisher's OR: 6.81; Bonferroni p-val: 1.39e-05

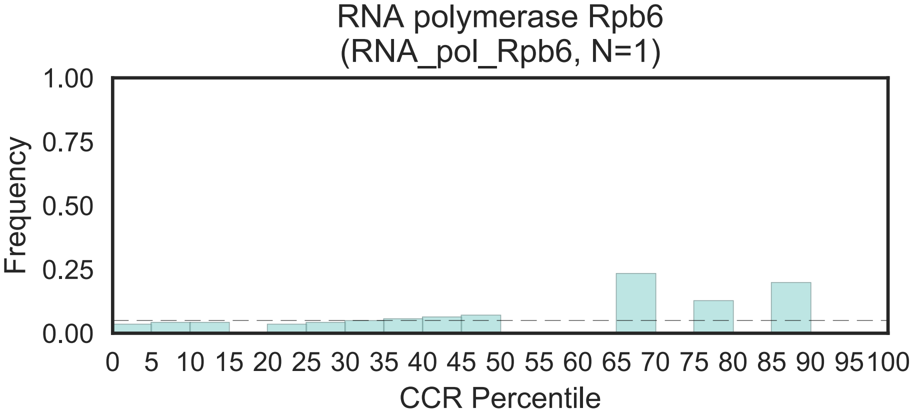

RNA polymerase Rpb2, domain 7
(RNA_pol_Rpb2_7, N=3)
Fisher's OR: 5.59; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

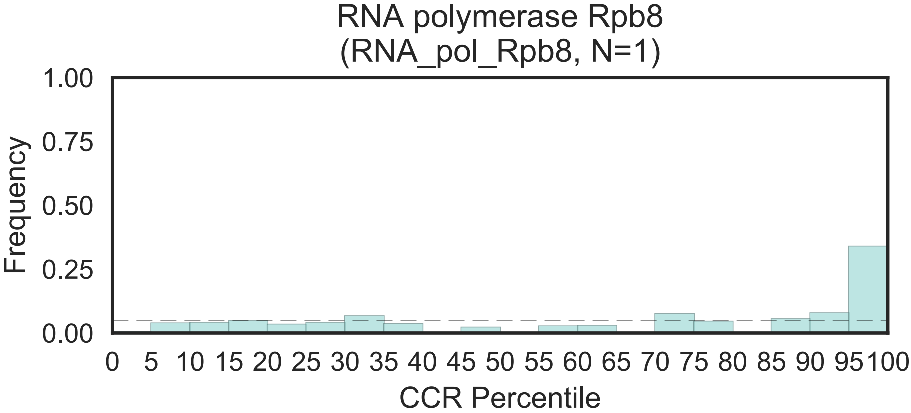
RNA polymerase Rpb4
(RNA_pol_Rpb4, N=3)
Fisher's OR: 0.932; Bonferroni p-val: 1

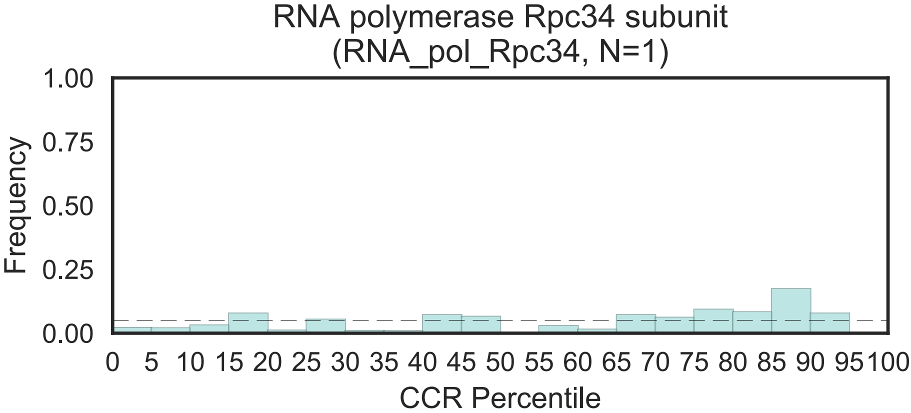



RNA polymerase Rpb5, C-terminal domain
(RNA_pol_Rpb5_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

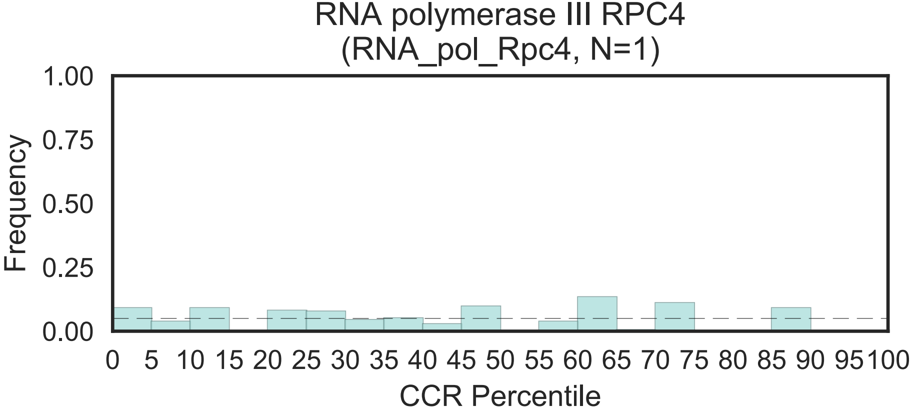

RNA polymerase Rpb5, N-terminal domain
(RNA_pol_Rpb5_N, N=1)

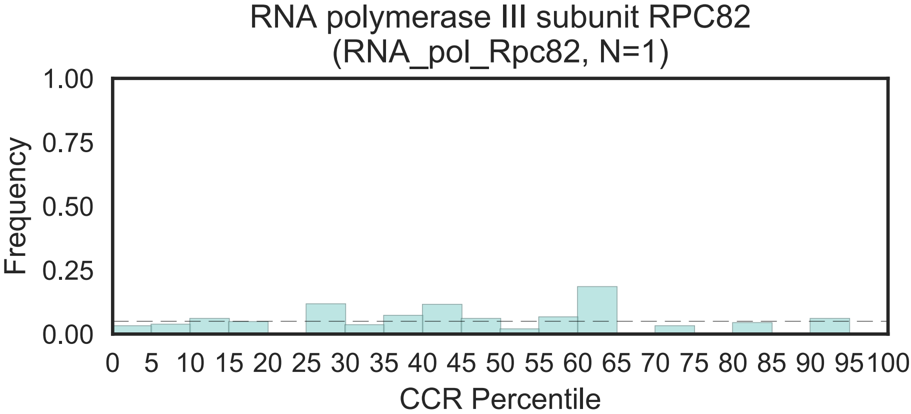

RNA polymerase Rpb6
(RNA_pol_Rpb6, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

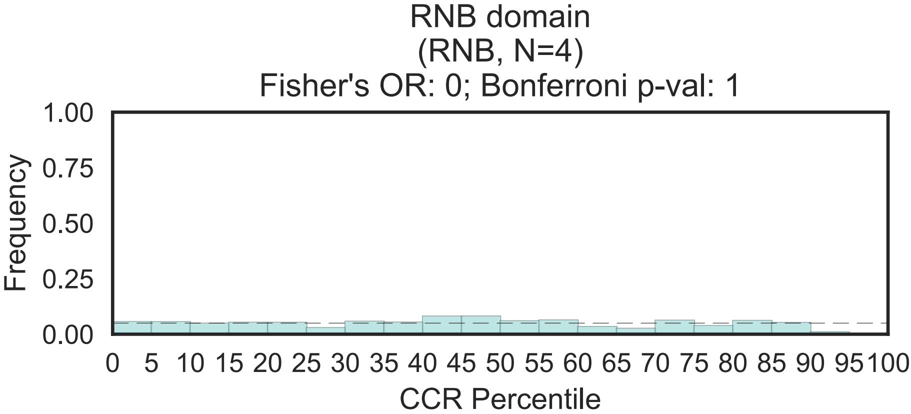

RNA polymerase Rpb8
(RNA_pol_Rpb8, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

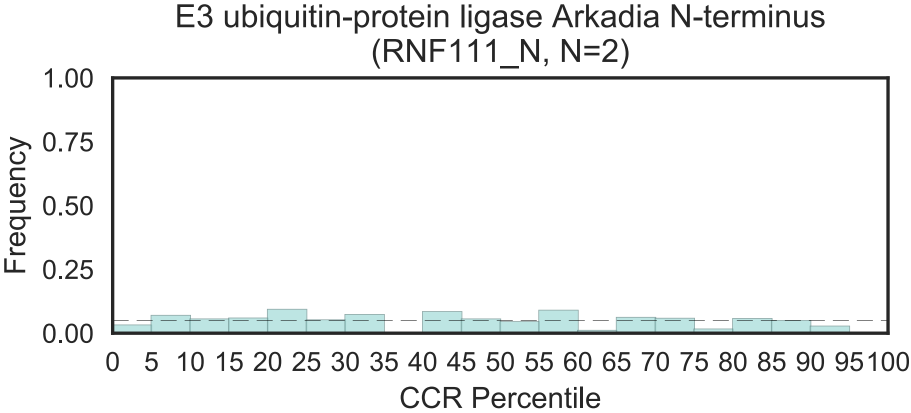


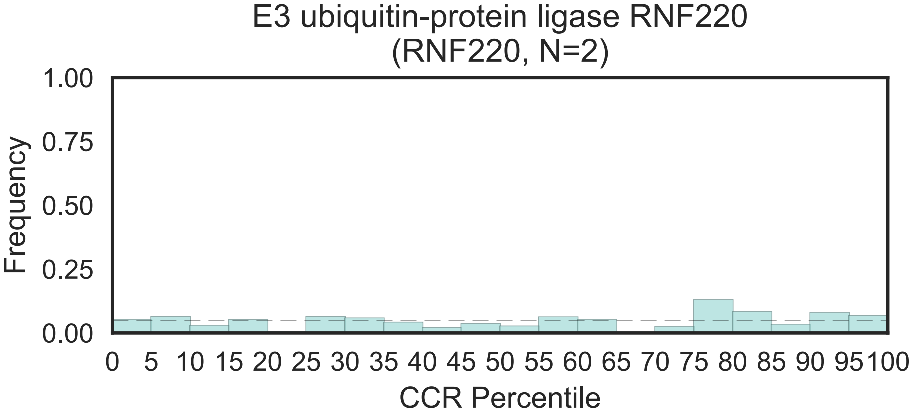
RNA polymerase Rpc34 subunit
(RNA_pol_Rpc34, N=1)

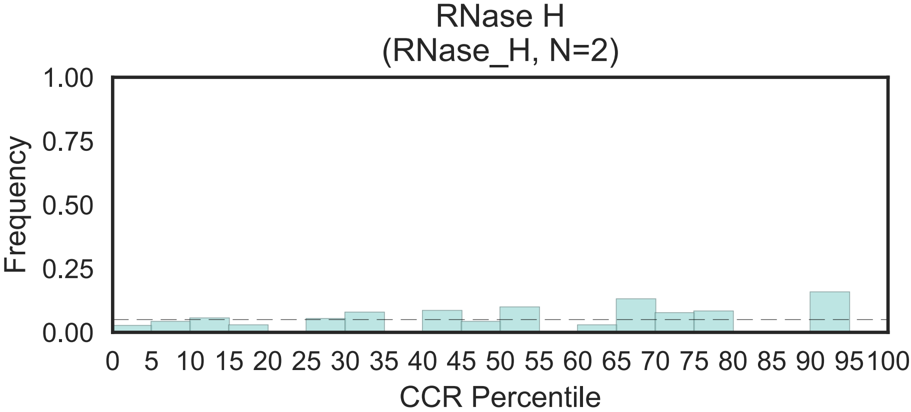

RNA polymerase III RPC4
(RNA_pol_Rpc4, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

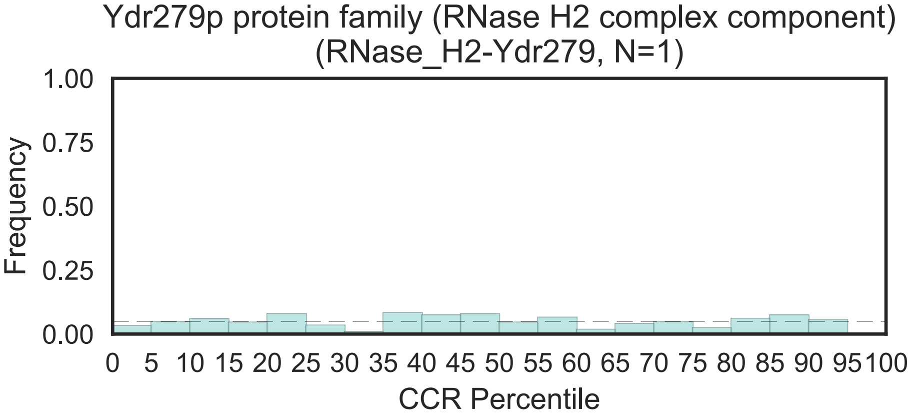

RNA polymerase III subunit RPC82
(RNA_pol_Rpc82, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

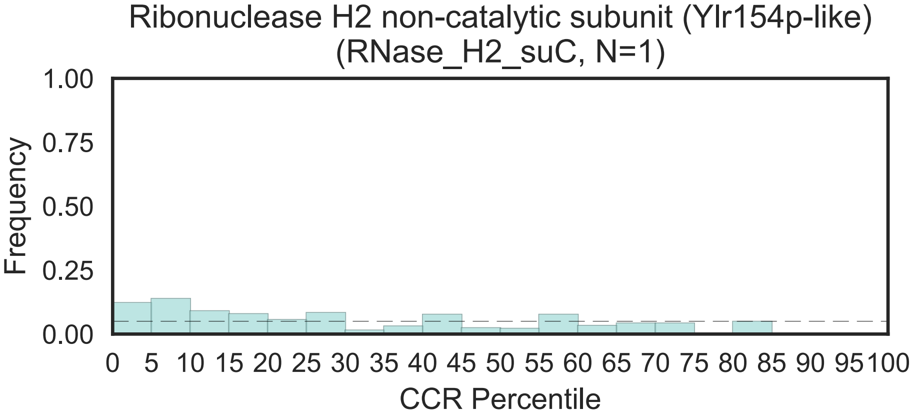

RNB domain
(RNB, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


E3 ubiquitin-protein ligase Arkadia N-terminus
(RNF111_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

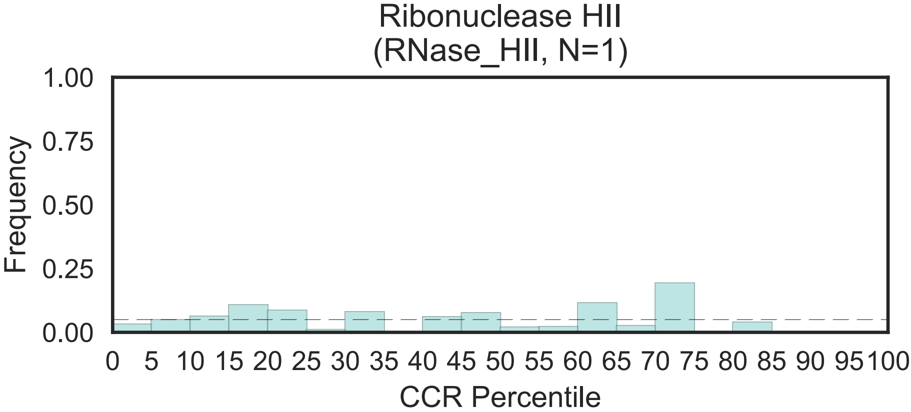

E3 ubiquitin-protein ligase RNF220
(RNF220, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


RNase H
(RNase_H, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

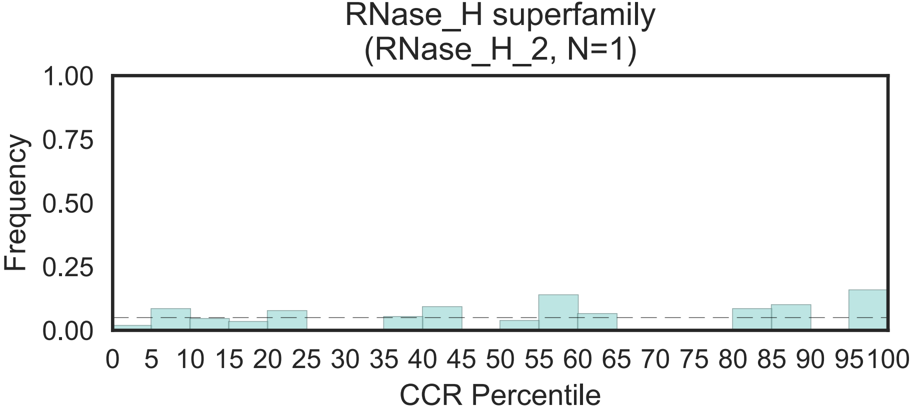

Ydr279p protein family (RNase H2 complex component)
(RNase_H2-Ydr279, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

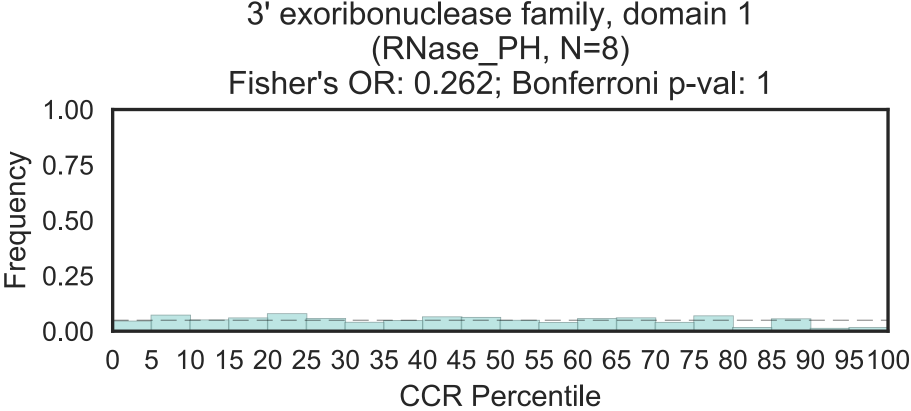


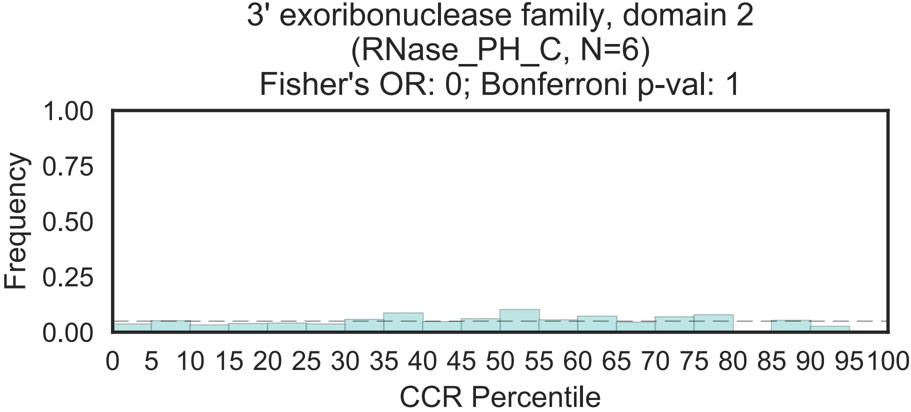
Ribonuclease H2 non-catalytic subunit (Ylr154p-like)
(RNase_H2_suC, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

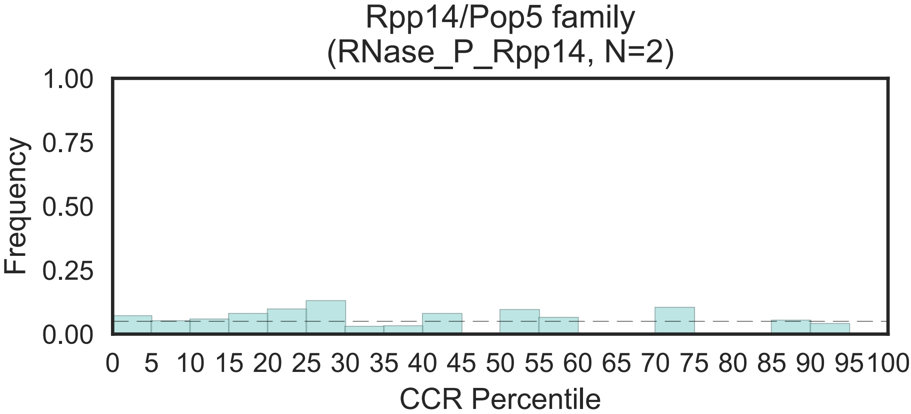


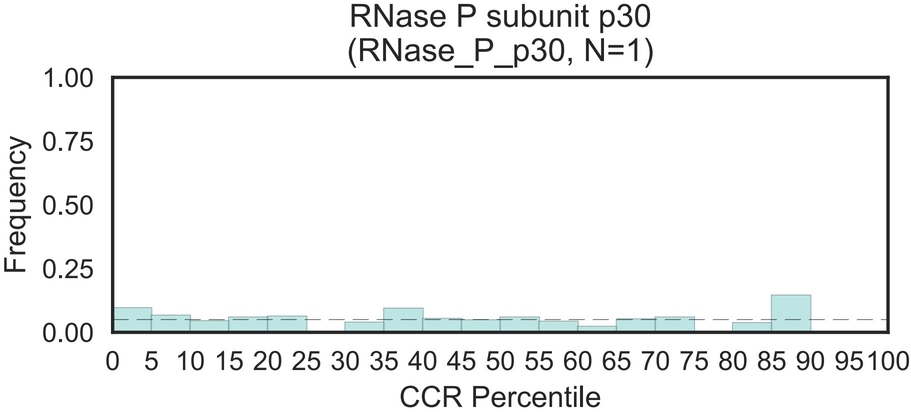
Ribonuclease HII
(RNase_HII, N=1)

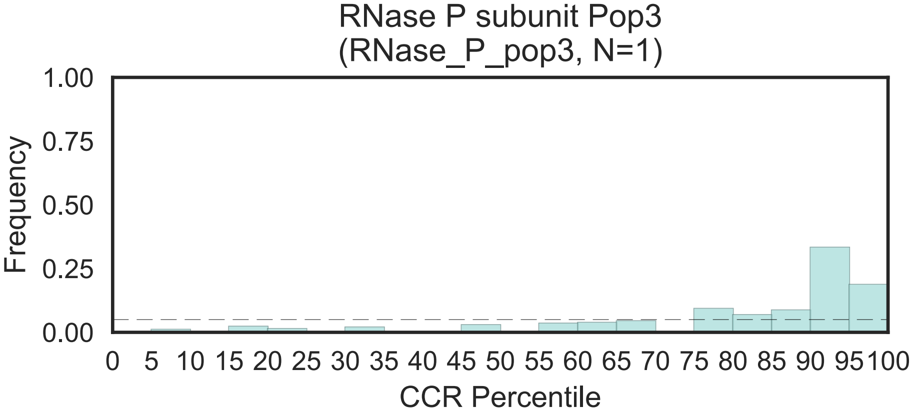

RNase_H superfamily
(RNase_H_2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

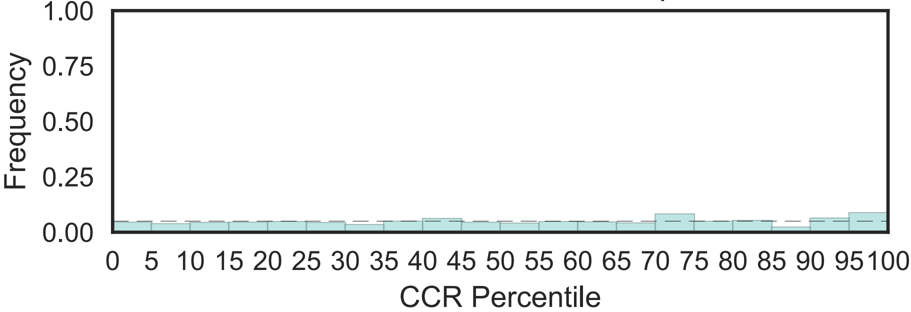

3' exoribonuclease family, domain 1
(RNase_PH, N=8)
Fisher's OR: 0.262; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


3' exoribonuclease family, domain 2
(RNase_PH_C, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

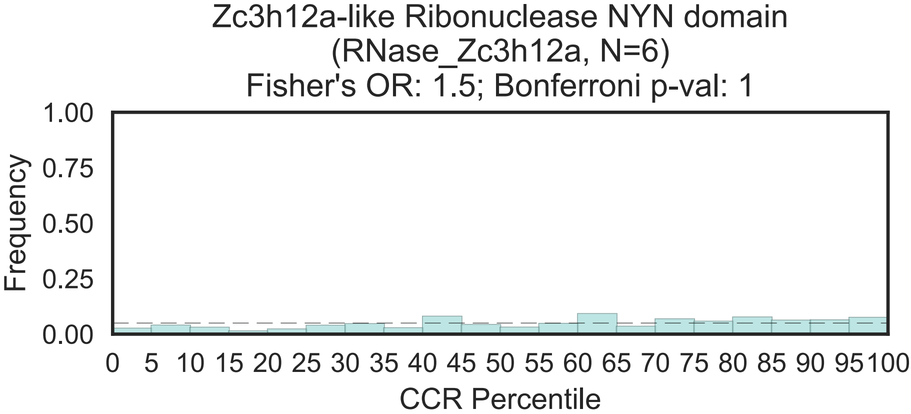

Rpp14/Pop5 family
(RNase_P_Rpp14, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

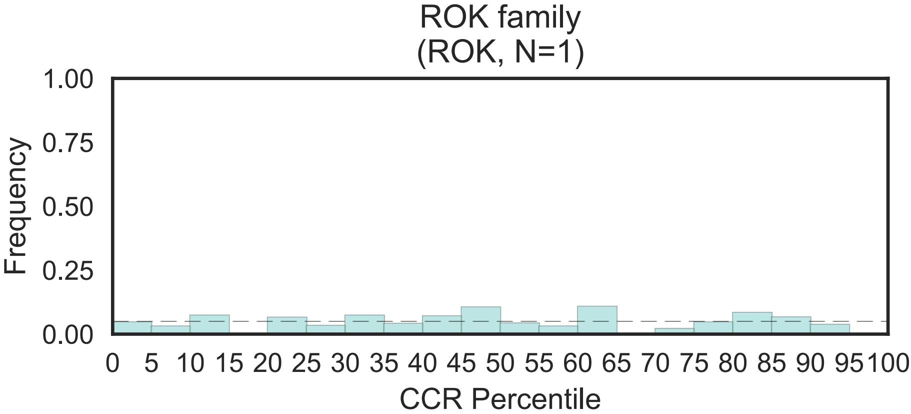

RNase P subunit p30
(RNase_P_p30, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

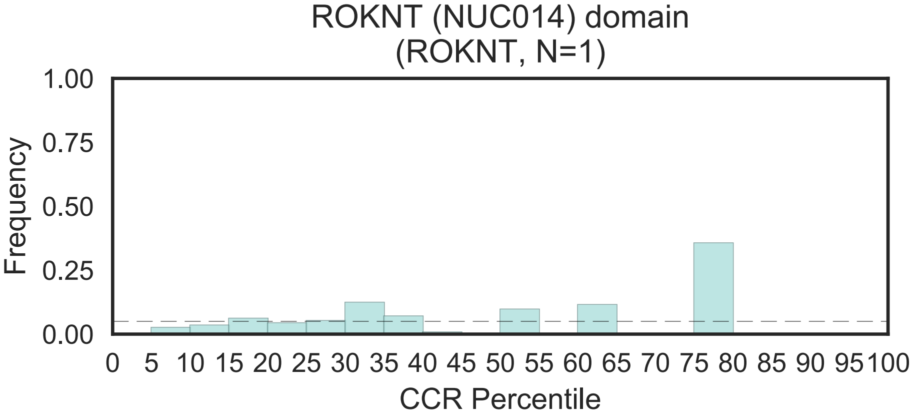

RNase P subunit Pop3
(RNase_P_pop3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

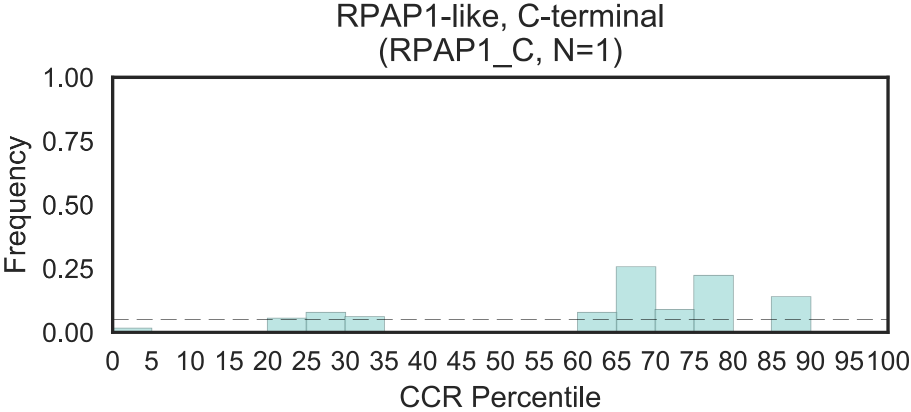


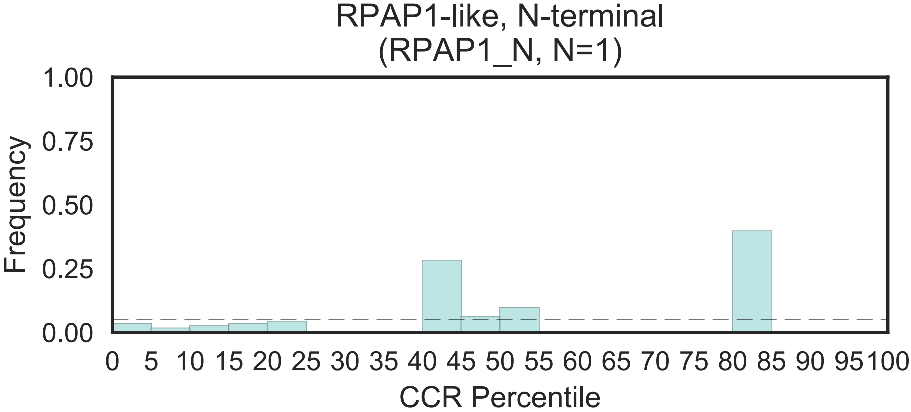
Exonuclease
(RNase_T, N=12)
Fisher's OR: 1.31; Bonferroni p-val: 1

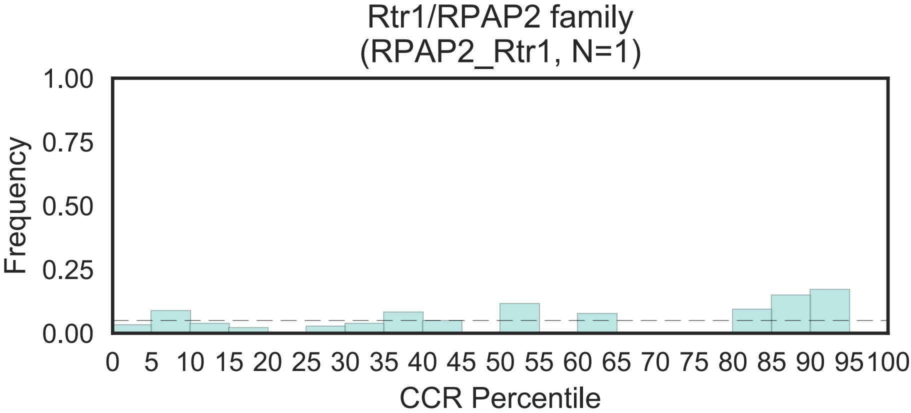

Zc3h12a-like Ribonuclease NYN domain
(RNase_Zc3h12a, N=6)
Fisher's OR: 1.5; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

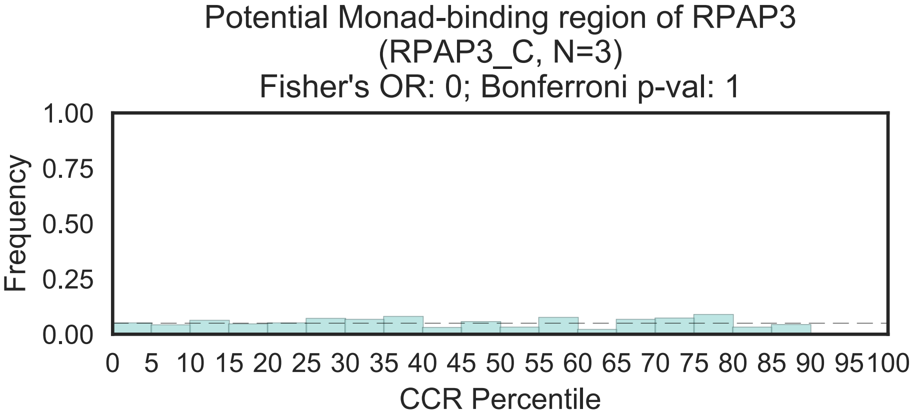

ROK family
(ROK, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


ROKNT (NUC014) domain
(ROKNT, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

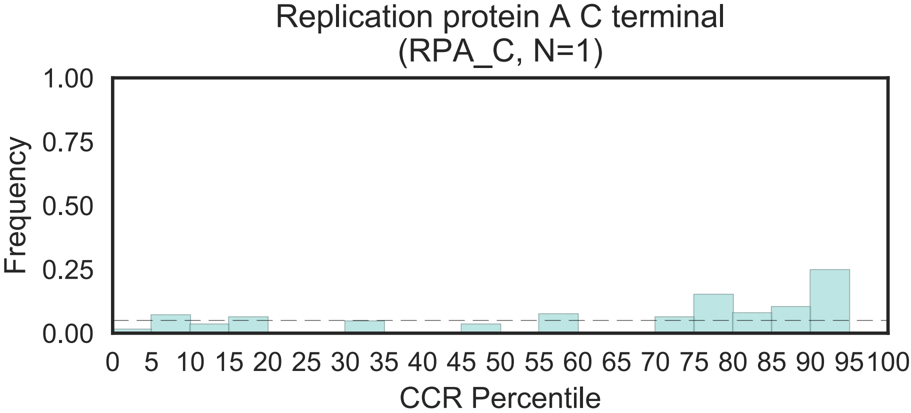

RPAP1-like, C-terminal
(RPAP1_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

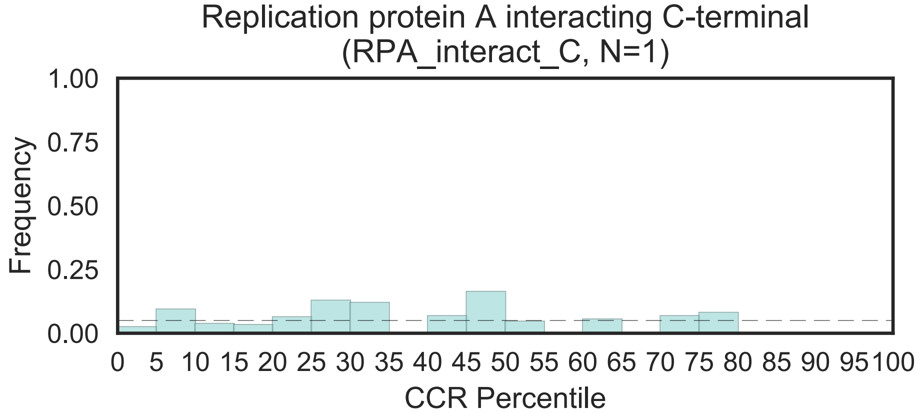

RPAP1-like, N-terminal
(RPAP1_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

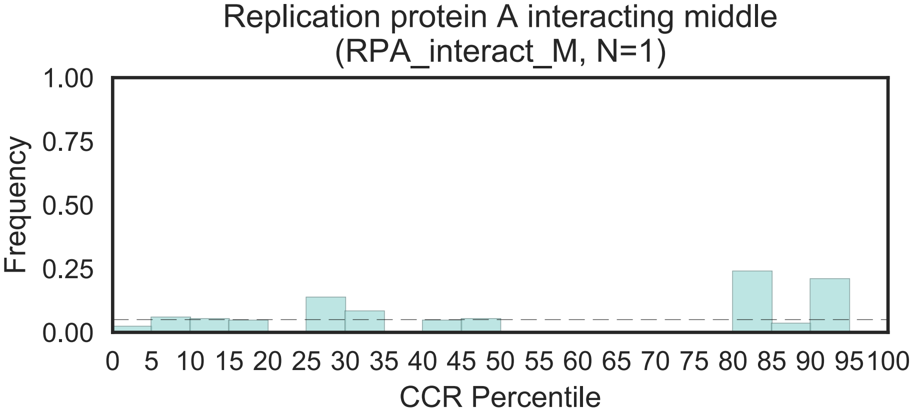

Rtr1/RPAP2 family
(RPAP2_Rtr1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

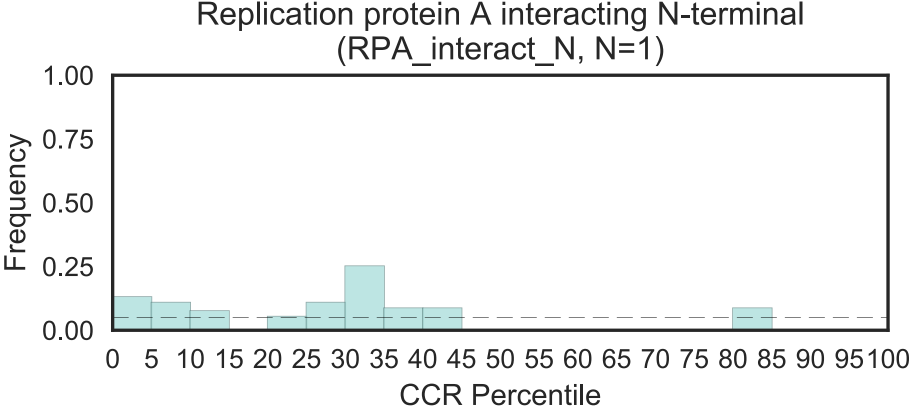


Potential Monad-binding region of RPAP3
(RPAP3_C, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Replication protein A C terminal
(RPA_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

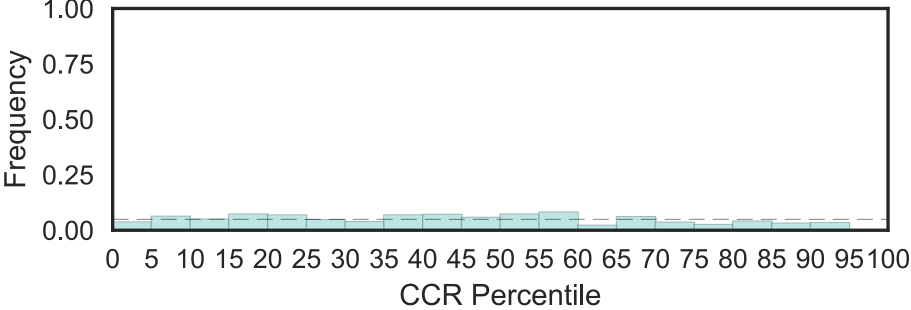

Replication protein A interacting C-terminal
(RPA_interact_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

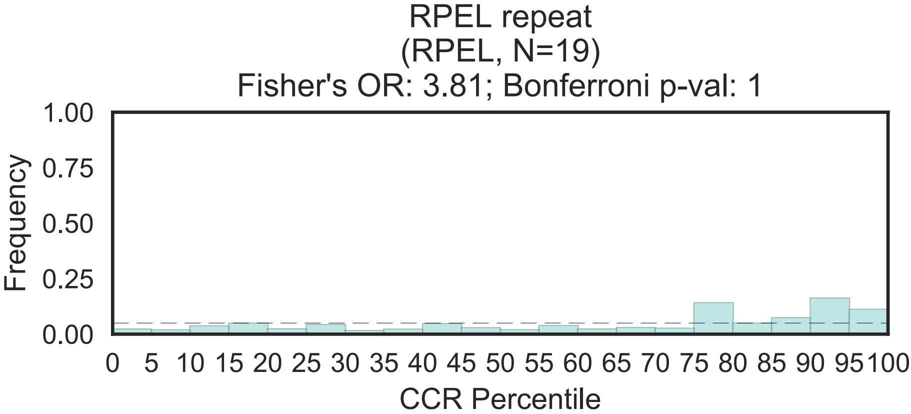

Replication protein A interacting middle
(RPA_interact_M, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

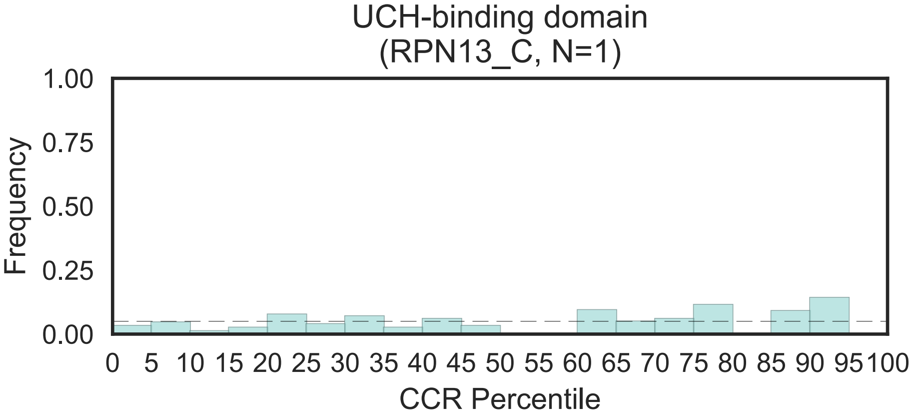


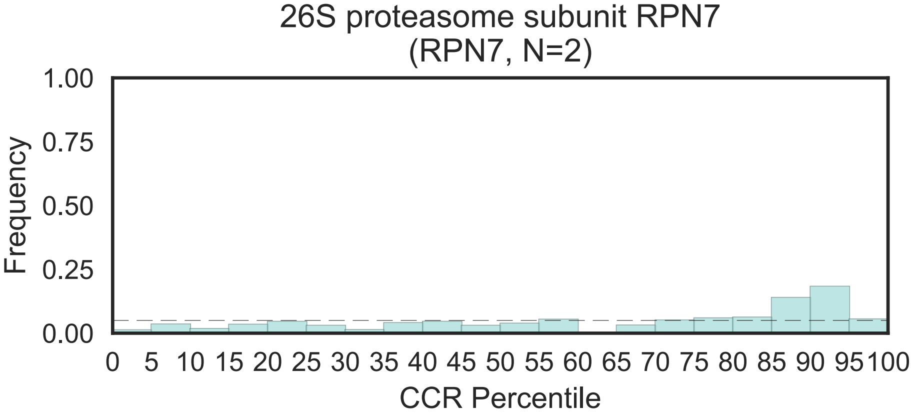
Replication protein A interacting N-terminal
(RPA_interact_N, N=1)

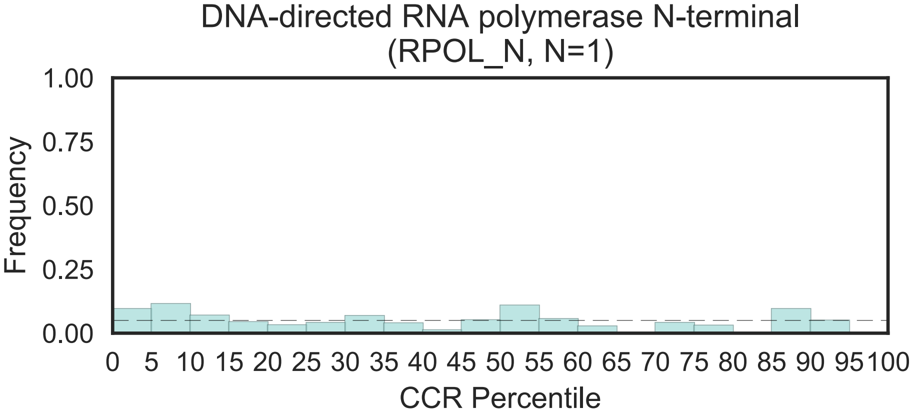
Retinal pigment epithelial membrane protein
(RPE65, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

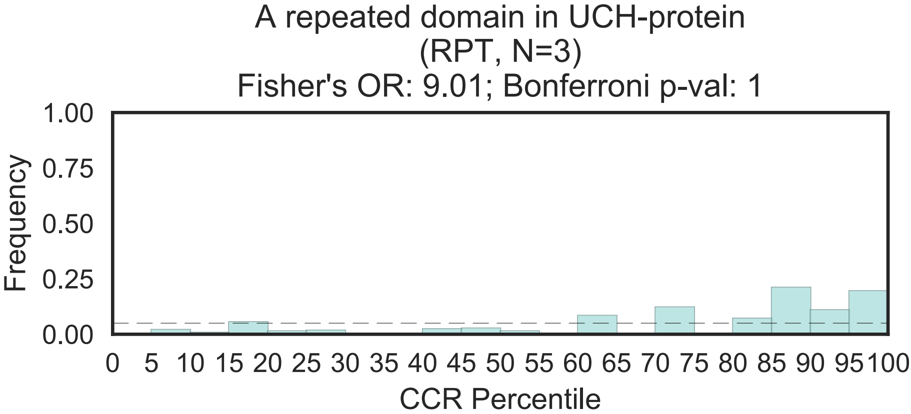


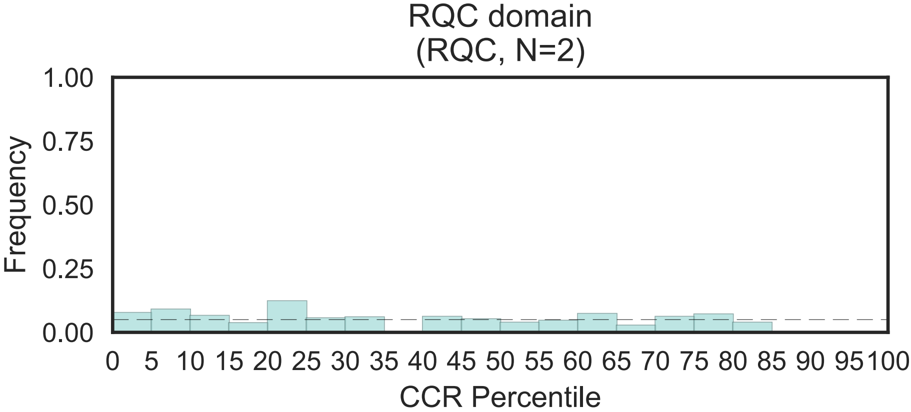

RPEL repeat
(RPEL, N=19)
Fisher's OR: 3.81; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

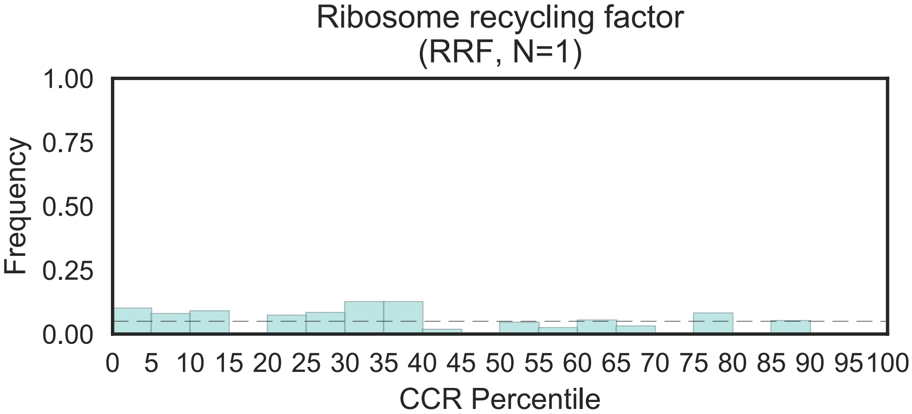

UCH-binding domain
(RPN13_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

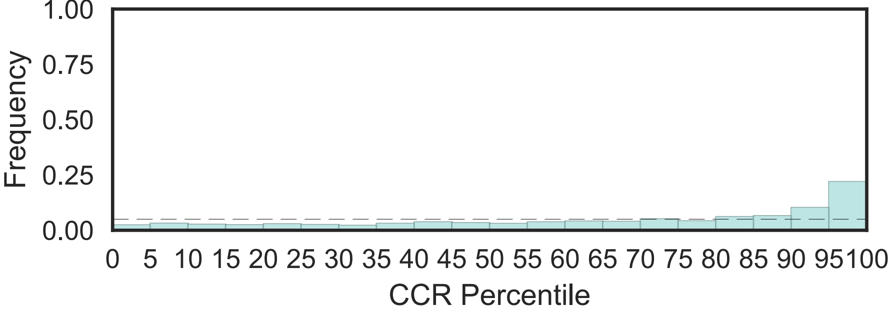

26S proteasome subunit RPN7
(RPN7, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


DNA-directed RNA polymerase N-terminal
(RPOL_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

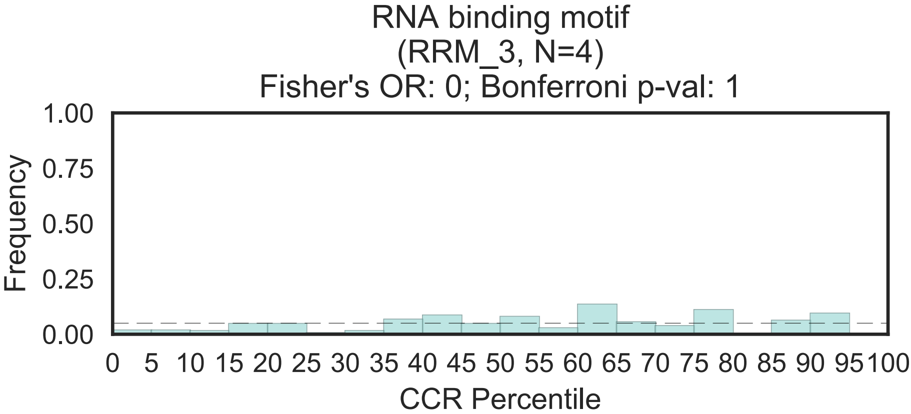

A repeated domain in UCH-protein
(RPT, N=3)
Fisher's OR: 9.01; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


RQC domain
(RQC, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

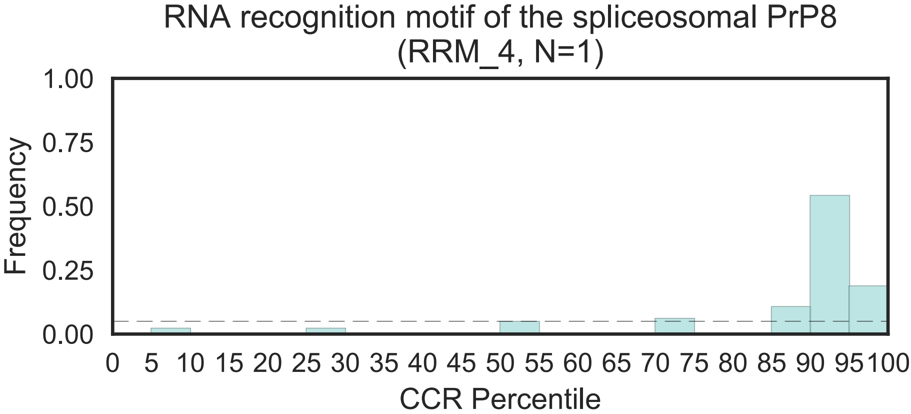

Ribosome recycling factor
(RRF, N=1)

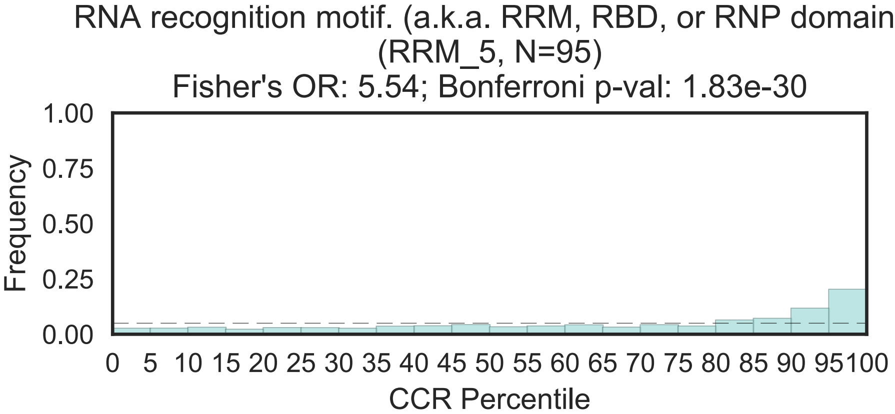


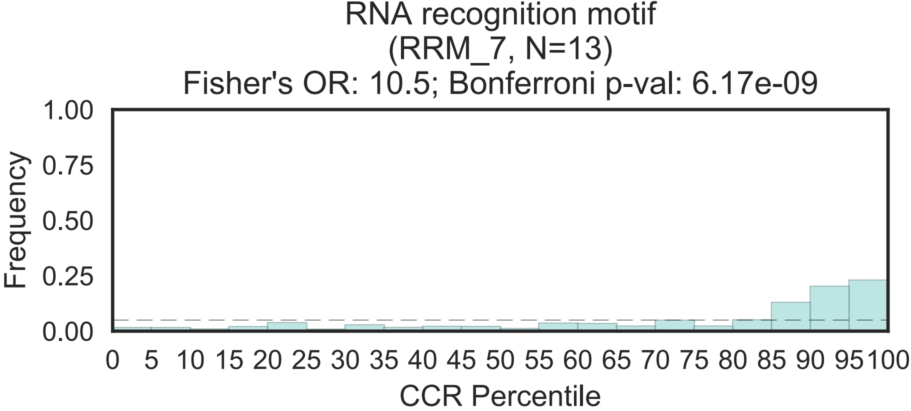
RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
(RRM_1, N=321)
Fisher's OR: 6.39; Bonferroni p-val: 6.57e-118

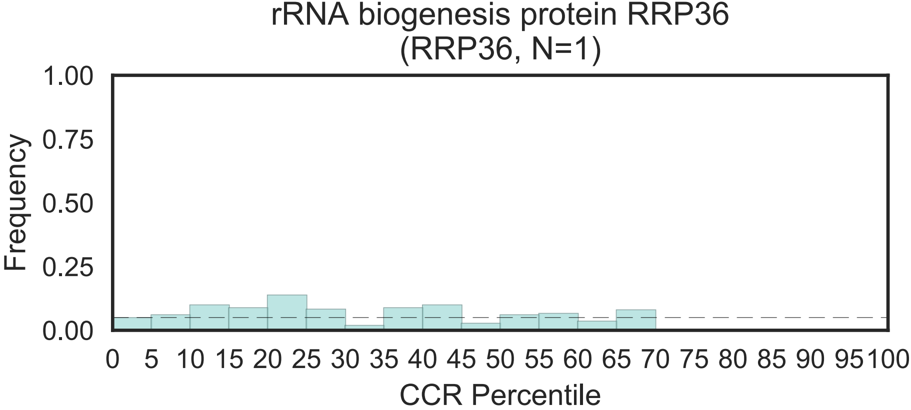


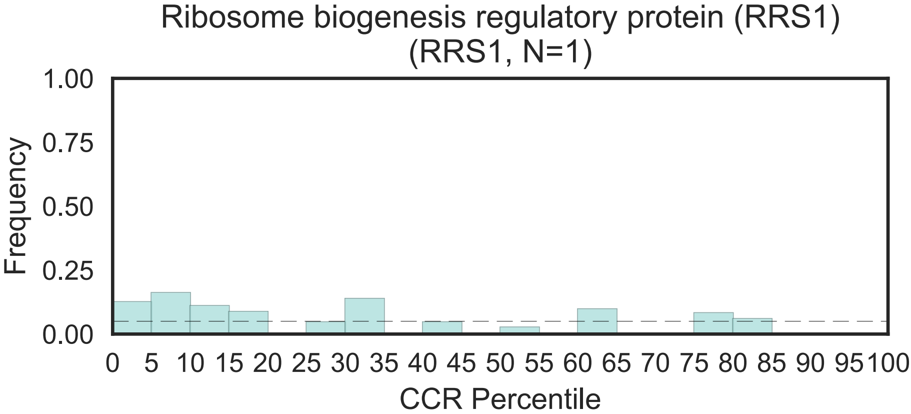
RNA binding motif
(RRM_3, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

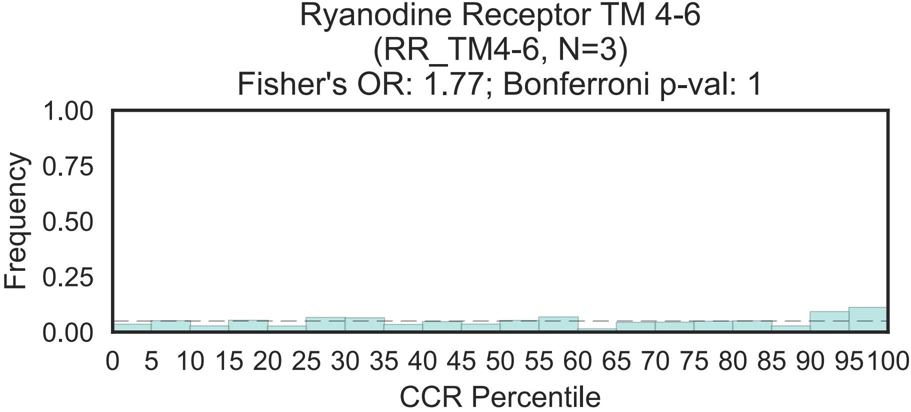

RNA recognition motif of the spliceosomal PrP8
(RRM_4, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

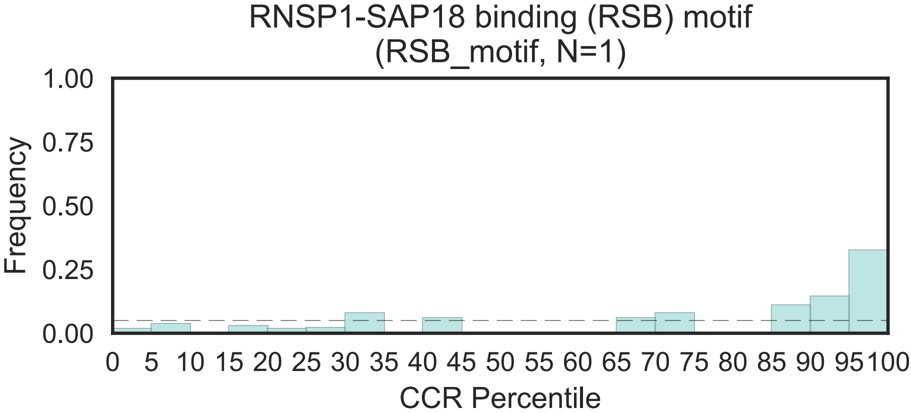

RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
(RRM_5, N=95)
Fisher's OR: 5.54; Bonferroni p-val: 1.83e-30
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

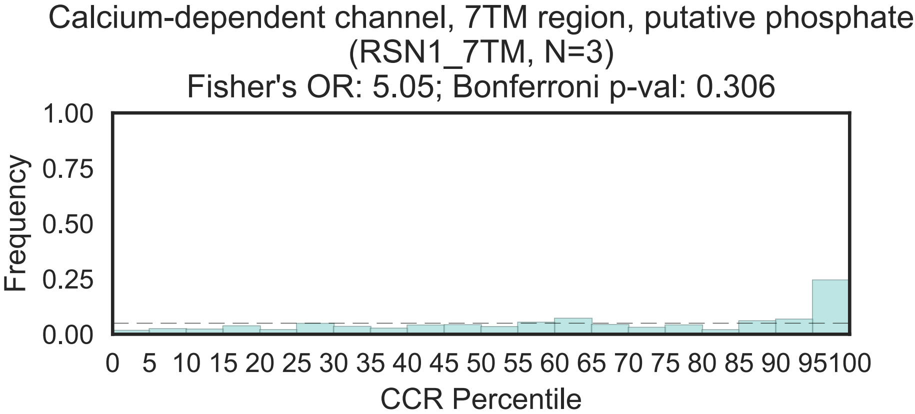

RNA recognition motif
(RRM_7, N=13)
Fisher's OR: 10.5; Bonferroni p-val: 6.17e-09
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

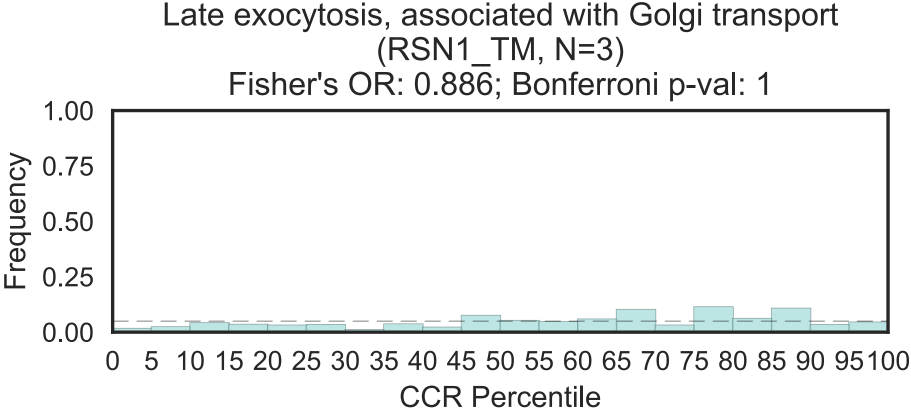

rRNA biogenesis protein RRP36
(RRP36, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

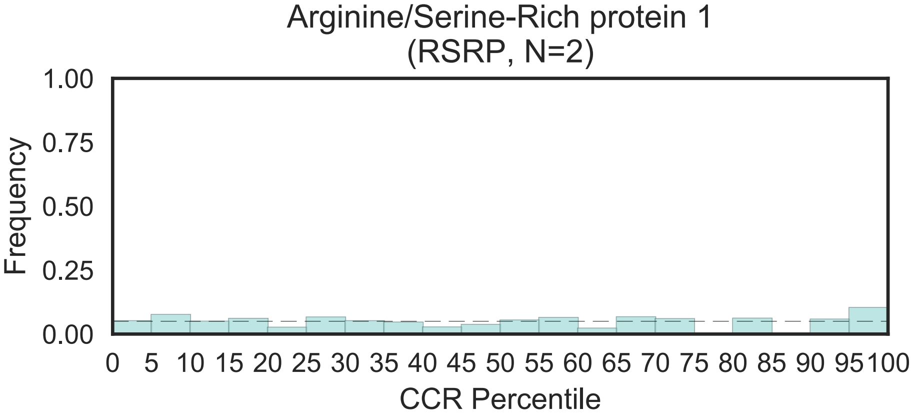

Ribosome biogenesis regulatory protein (RRS1)
(RRS1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

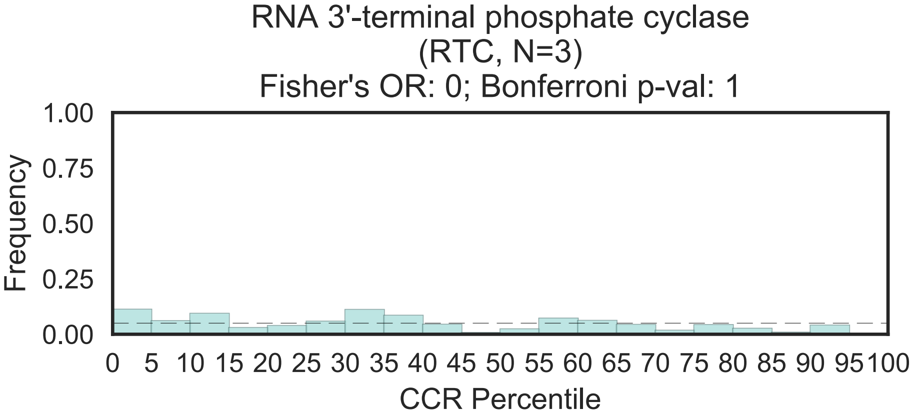

Ryanodine Receptor TM 4-6
(RR_TM4-6, N=3)
Fisher's OR: 1.77; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


RNSP1-SAP18 binding (RSB) motif
(RSB_motif, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

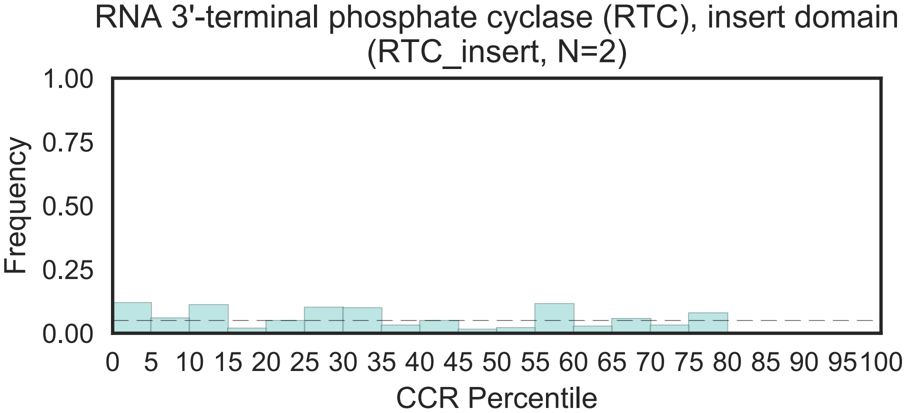

Calcium-dependent channel, 7TM region, putative phosphate
(RSN1_7TM, N=3)
Fisher's OR: 5.05; Bonferroni p-val: 0.306
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

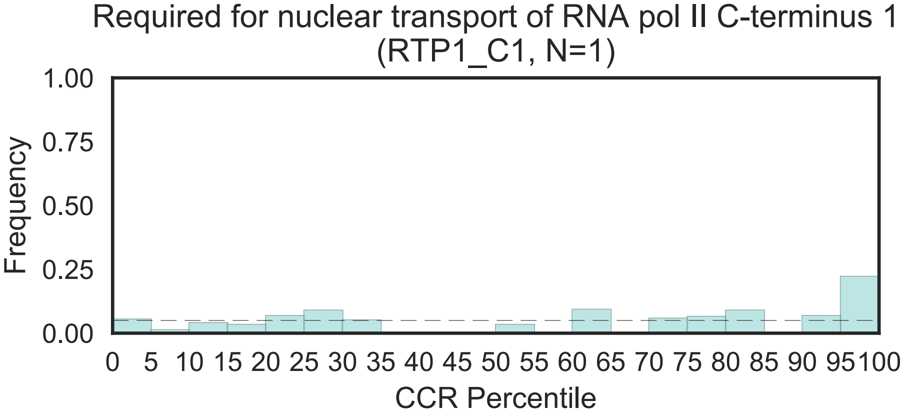

Late exocytosis, associated with Golgi transport
(RSN1_TM, N=3)
Fisher's OR: 0.886; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Arginine/Serine-Rich protein 1
(RSRP, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

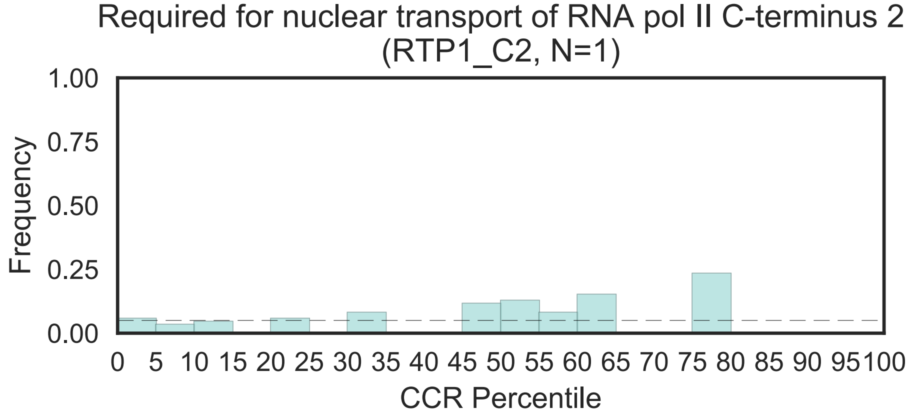


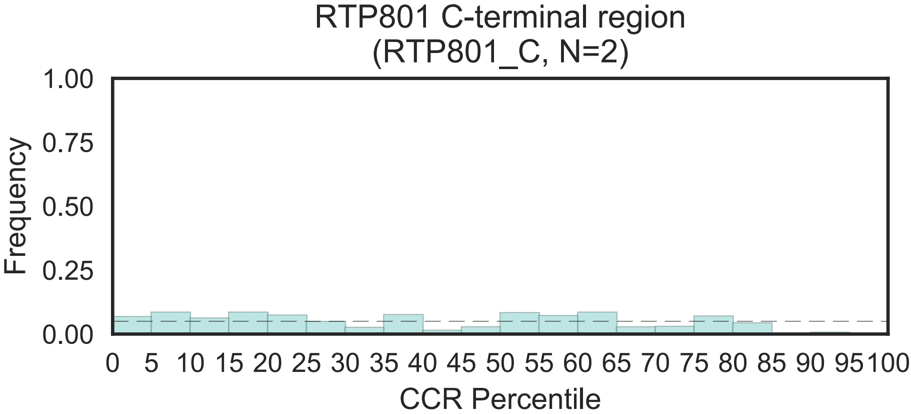
RNA 3'-terminal phosphate cyclase
(RTC, N=3)
Fisher's OR: 0; Bonferroni p-val: 1


RNA 3'-terminal phosphate cyclase (RTC), insert domain
(RTC_insert, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

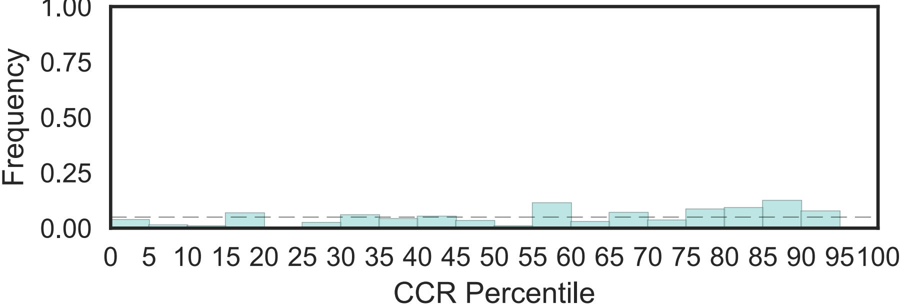


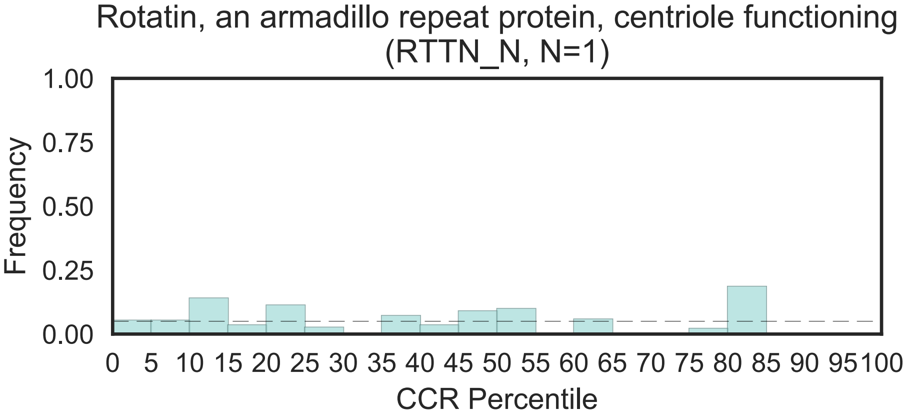
Required for nuclear transport of RNA pol II C-terminus 1
(RTP1_C1, N=1)

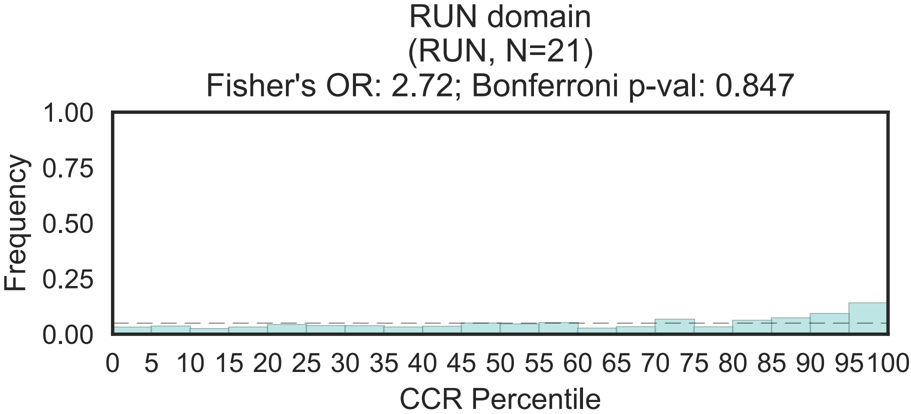

Required for nuclear transport of RNA pol II C-terminus 2
(RTP1_C2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

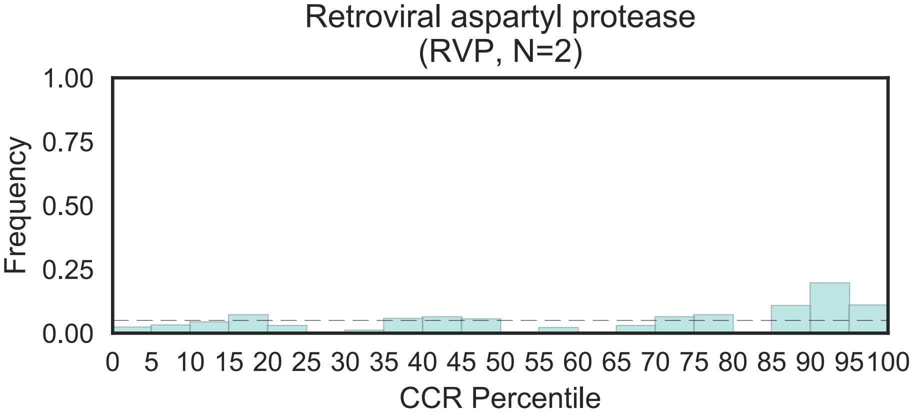

RTP801 C-terminal region
(RTP801_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

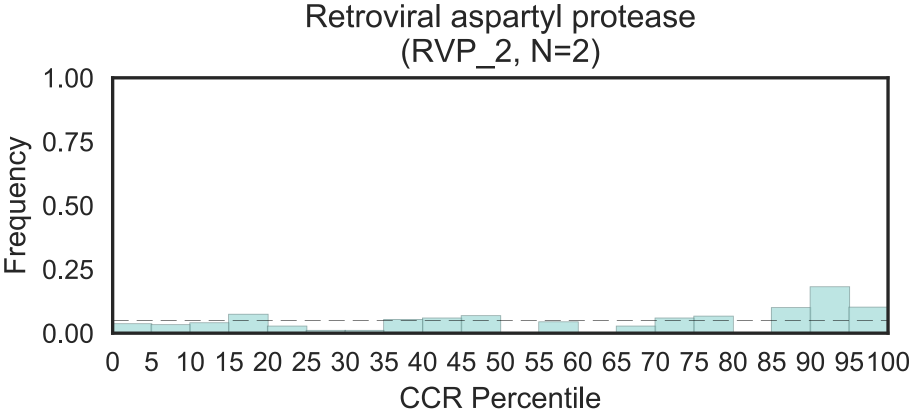
Regulator of Ty1 transposition protein 107 BRCT domain
(RTT107_BRCT_5, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

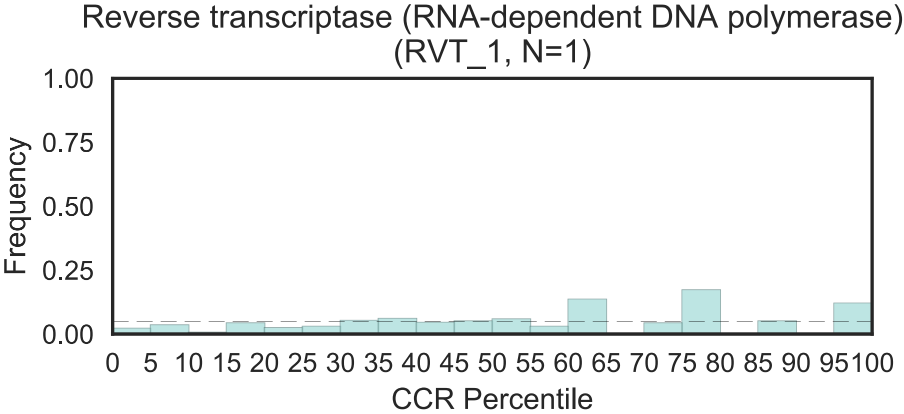



Rotatin, an armadillo repeat protein, centriole functioning
(RTTN_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

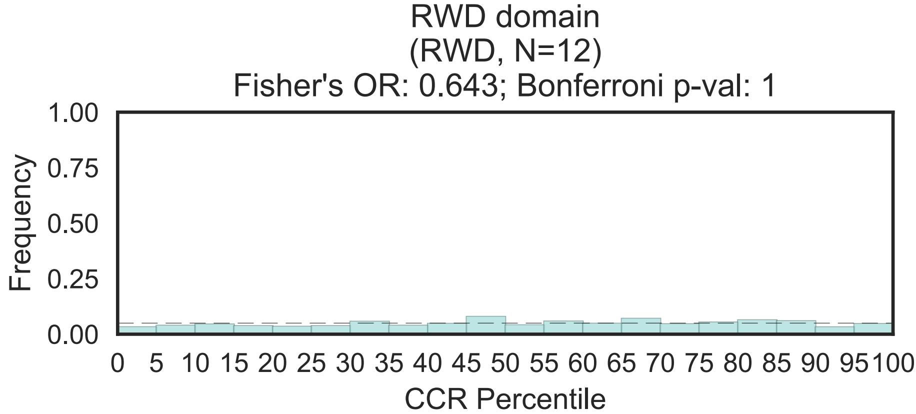

RUN domain
(RUN, N=21)
Fisher's OR: 2.72; Bonferroni p-val: 0.847
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Retroviral aspartyl protease
(RVP, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

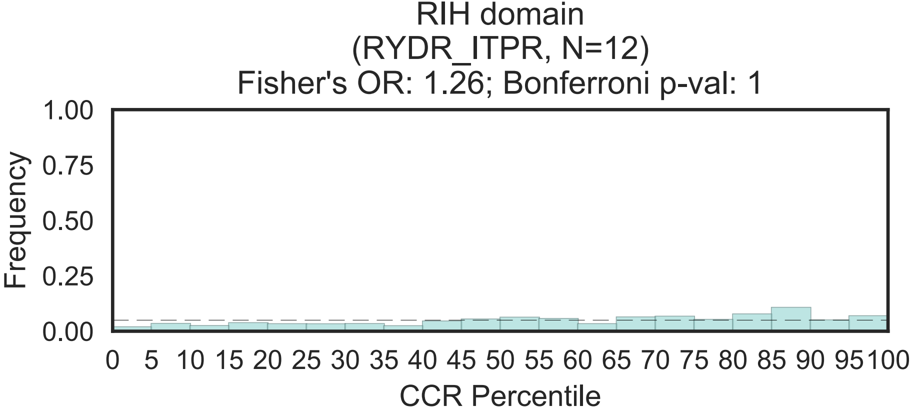

Retroviral aspartyl protease
(RVP_2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

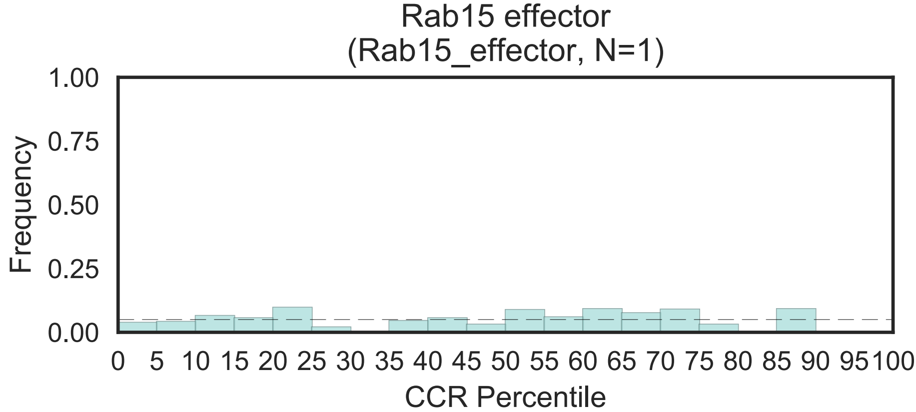


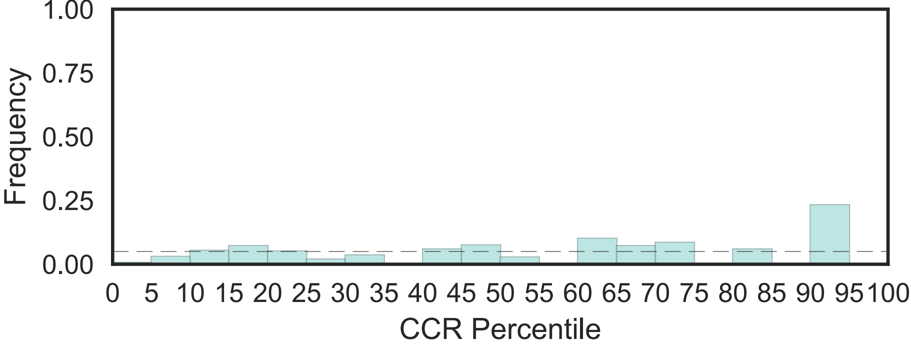
Reverse transcriptase (RNA-dependent DNA polymerase)
(RVT_1, N=1)



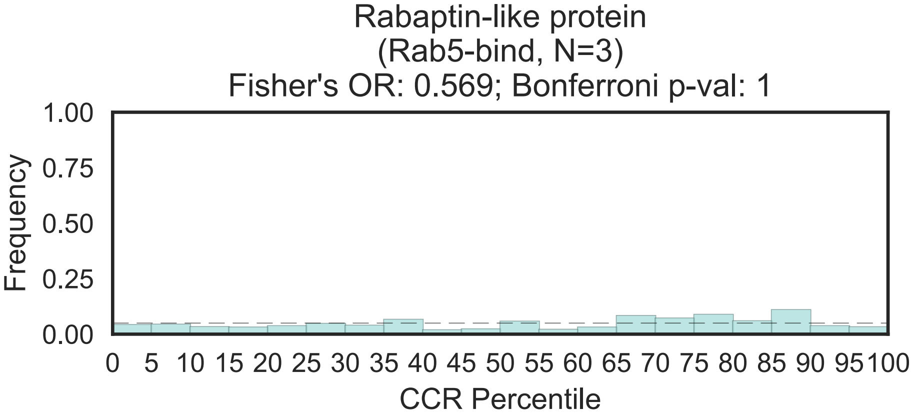
RWD domain
(RWD, N=12)
Fisher's OR: 0.643; Bonferroni p-val: 1

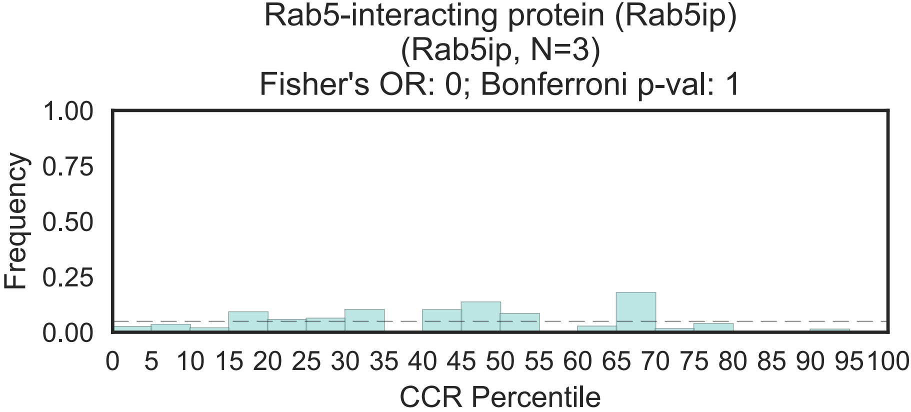

RIH domain
(RYDR_ITPR, N=12)
Fisher's OR: 1.26; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

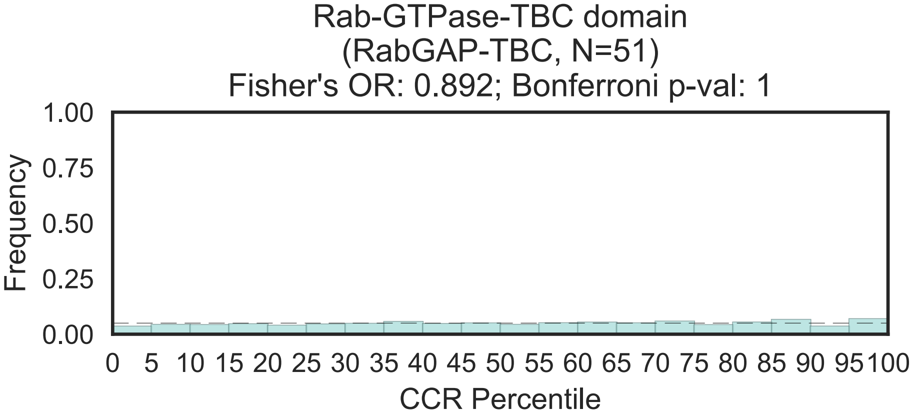

Rab15 effector
(Rab15_effector, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

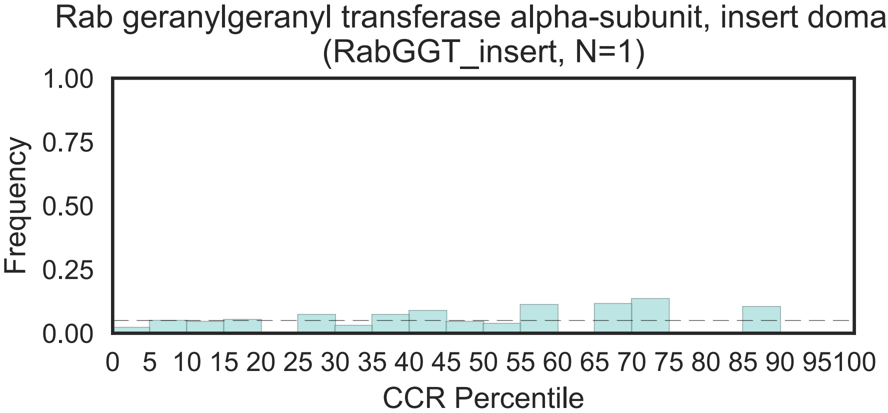


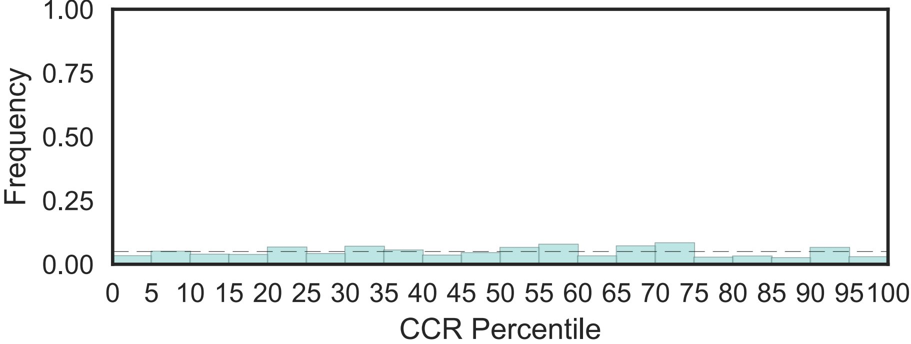
Rab3 GTPase-activating protein catalytic subunit
(Rab3-GTPase_cat, N=1)


Rabaptin-like protein
(Rab5-bind, N=3)
Fisher's OR: 0.569; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

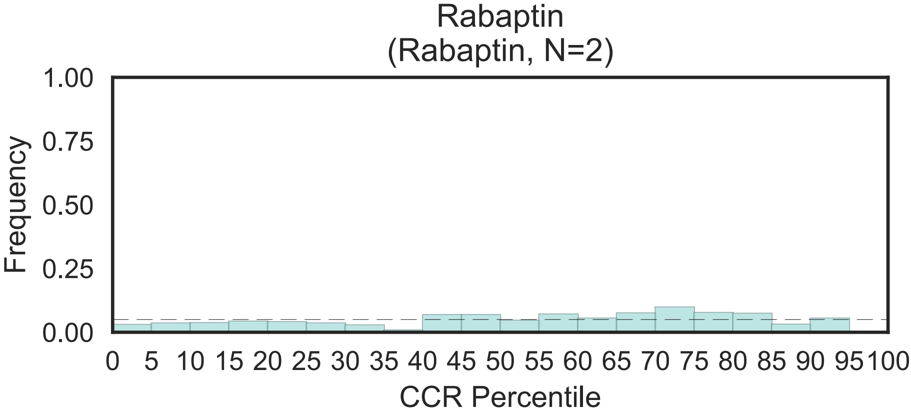

Rab5-interacting protein (Rab5ip)
(Rab5ip, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

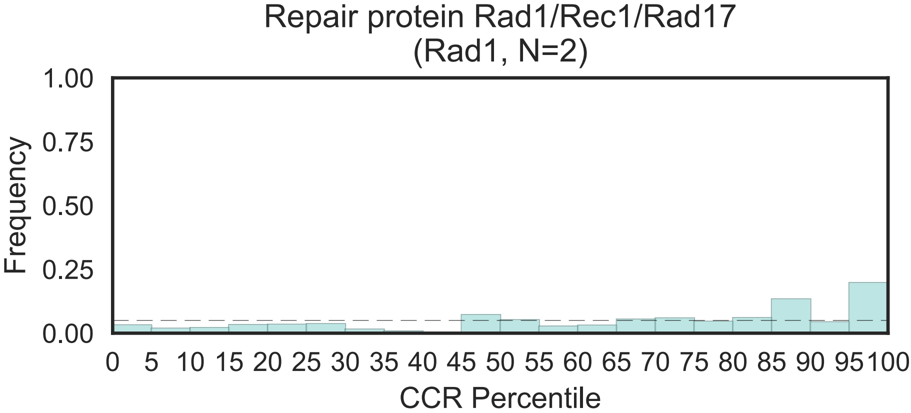

Rab-GTPase-TBC domain
(RabGAP-TBC, N=51)
Fisher's OR: 0.892; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

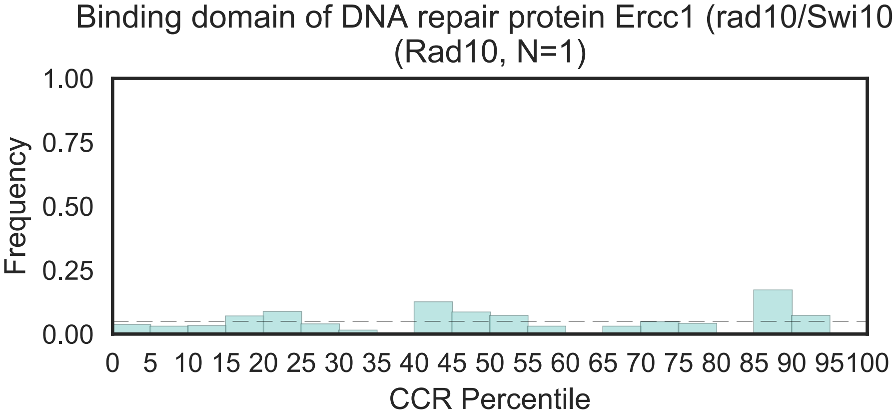

Rab geranylgeranyl transferase alpha-subunit, insert domain
(RabGGT_insert, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



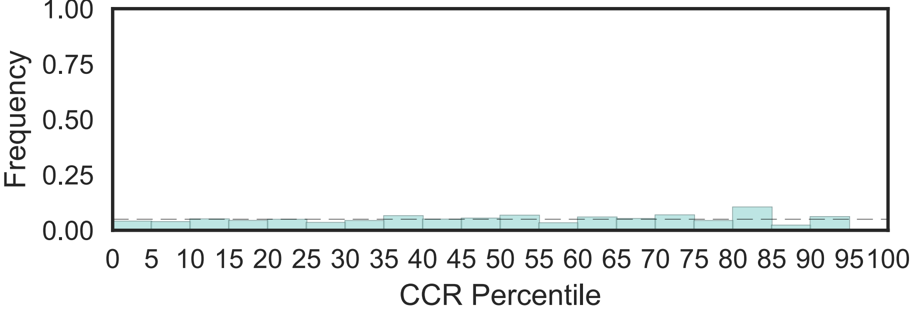
Rab effector MyRIP/melanophilin C-terminus
(Rab_eff_C, N=2)


Rabaptin
(Rabaptin, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Repair protein Rad1/Rec1/Rad17
(Rad1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

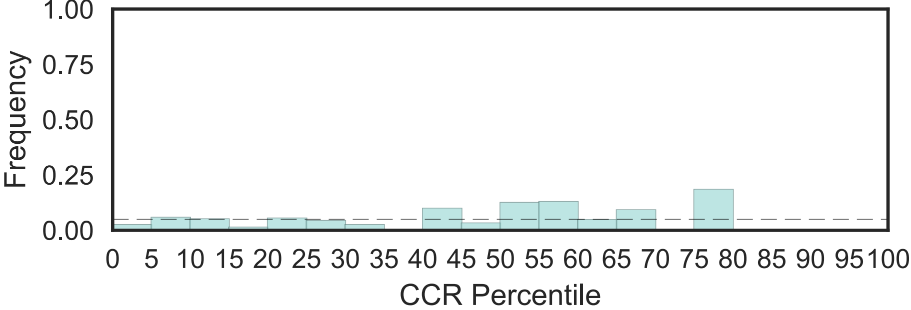


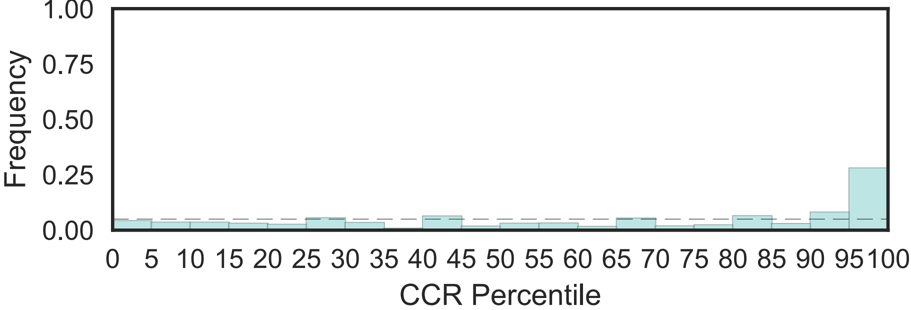
Binding domain of DNA repair protein Ercc1 (rad10/Swi10)
(Rad10, N=1)



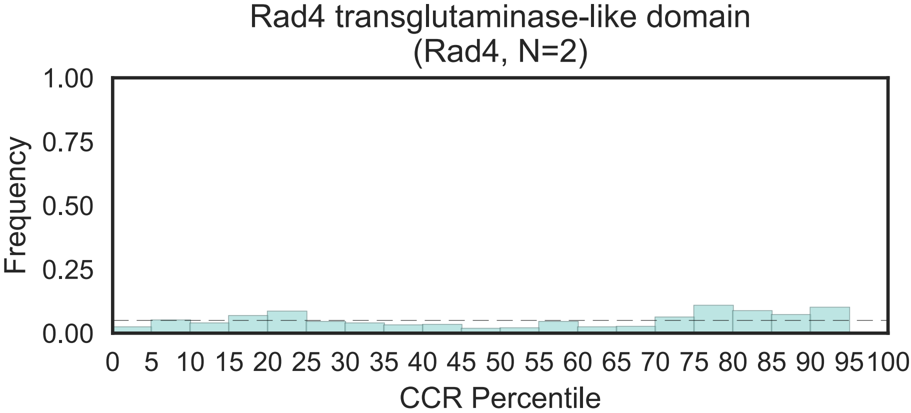
Rad17 cell cycle checkpoint protein
(Rad17, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

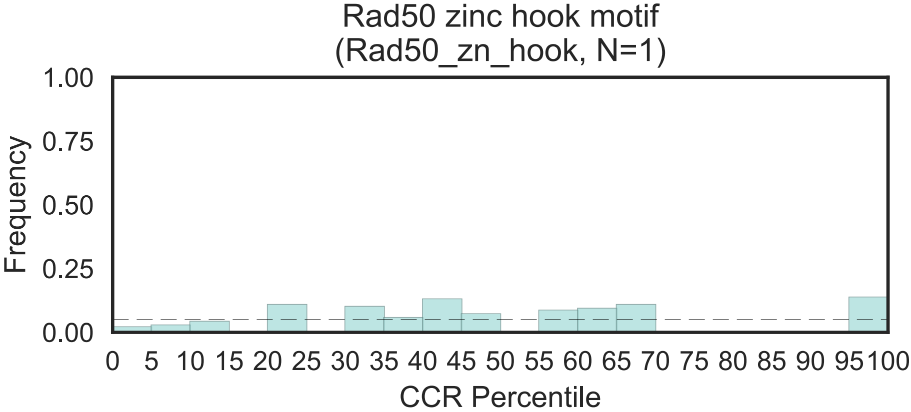
Conserved region of Rad21 / Rec8 like protein
(Rad21_Rec8, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

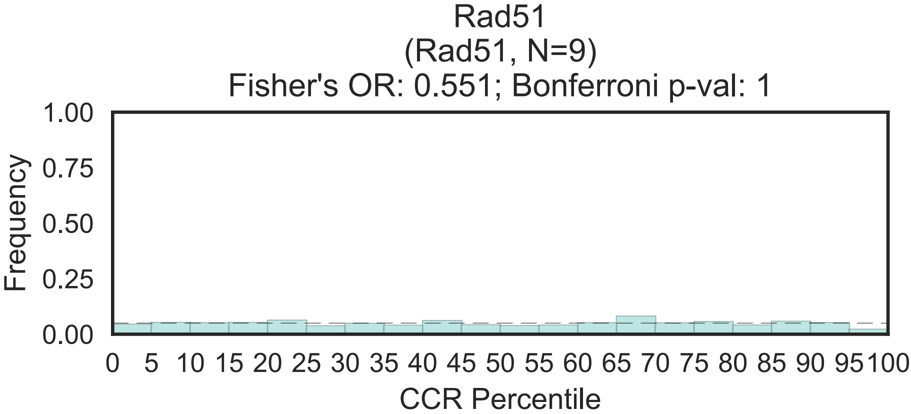




N terminus of Rad21 / Rec8 like protein
(Rad21_Rec8_N, N=3)
Fisher's OR: 6.09; Bonferroni p-val: 1

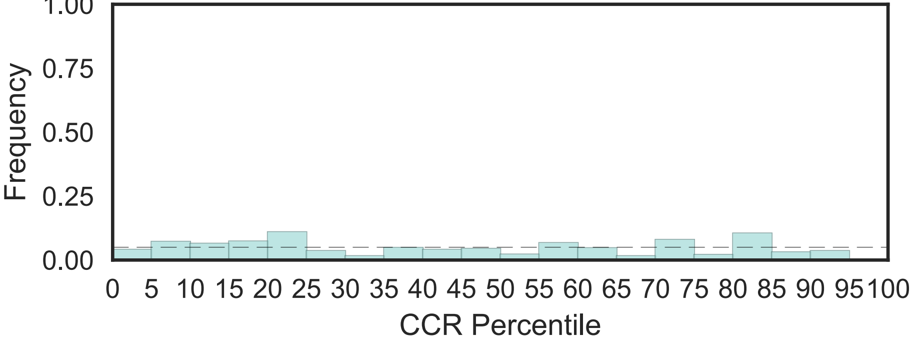

Rad4 transglutaminase-like domain
(Rad4, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

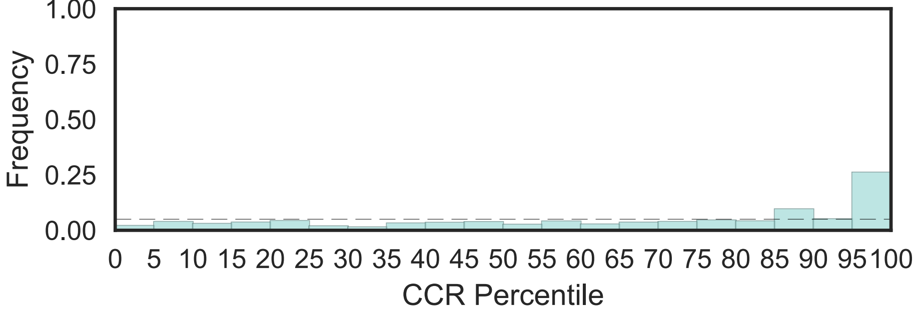

Rad50 zinc hook motif
(Rad50_zn_hook, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



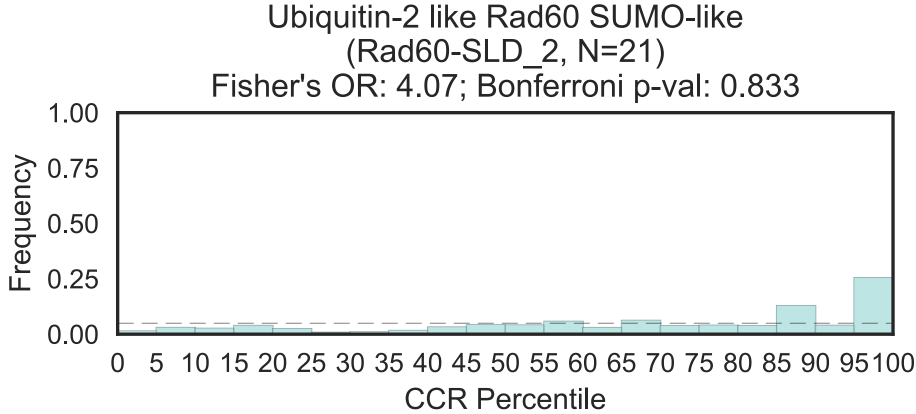
Rad51
(Rad51, N=9)
Fisher's OR: 0.551; Bonferroni p-val: 1

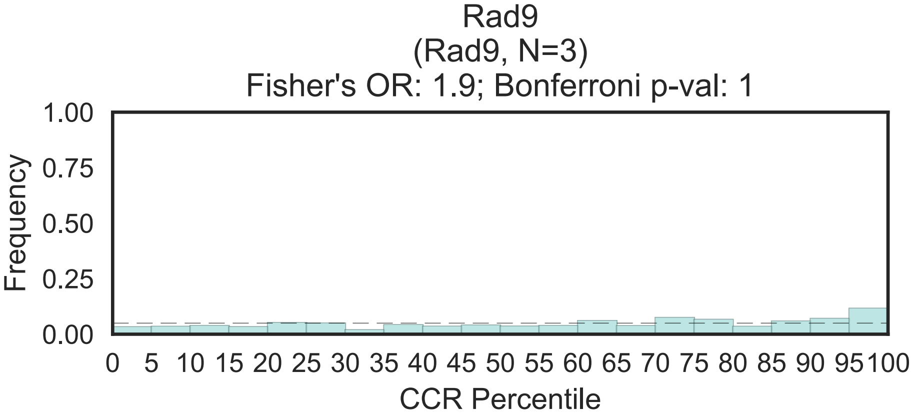
Rad52/22 family double-strand break repair protein (Rad52_Rad22, N=2)

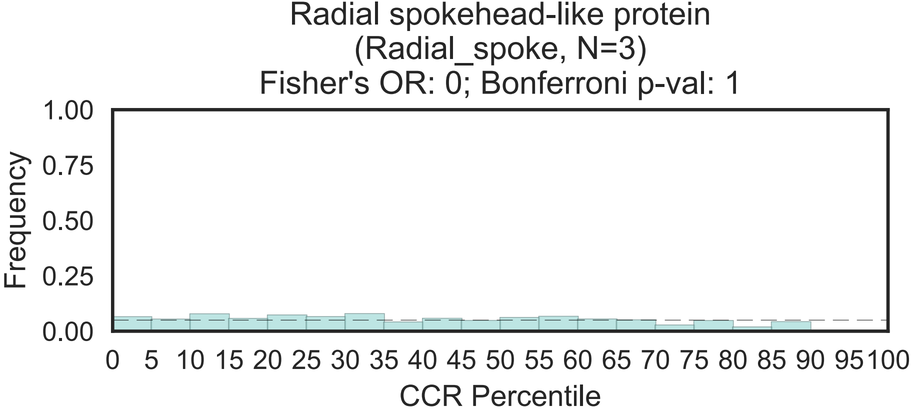




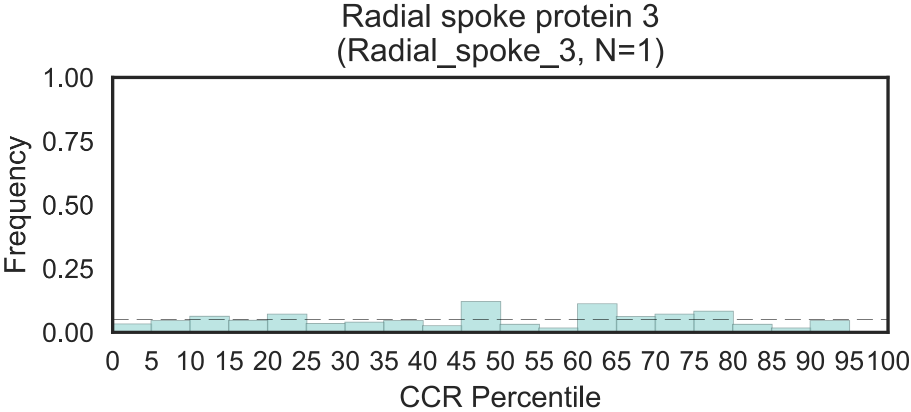
Ubiquitin-2 like Rad60 SUMO-like
(Rad60-SLD, N=32)
Fisher's OR: 3.02; Bonferroni p-val: 1

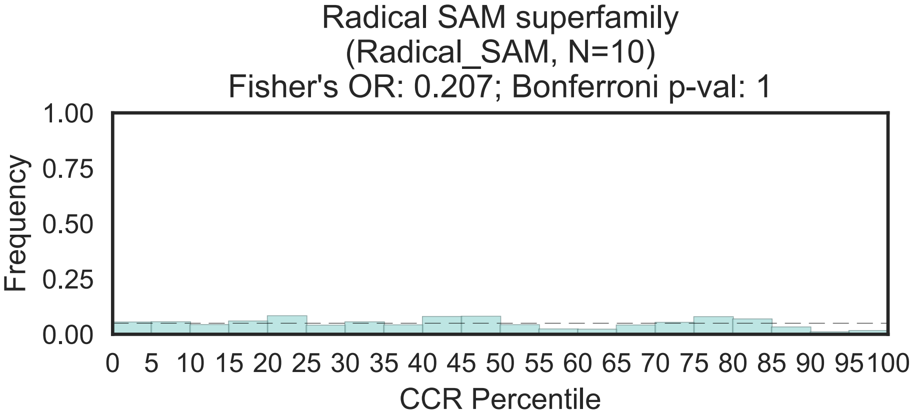

Ubiquitin-2 like Rad60 SUMO-like
(Rad60-SLD_2, N=21)
Fisher's OR: 4.07; Bonferroni p-val: 0.833
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

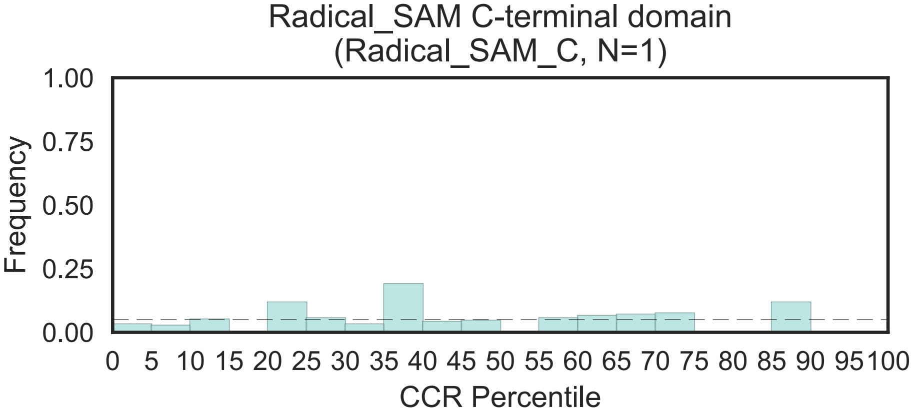

Rad9
(Rad9, N=3)
Fisher's OR: 1.9; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



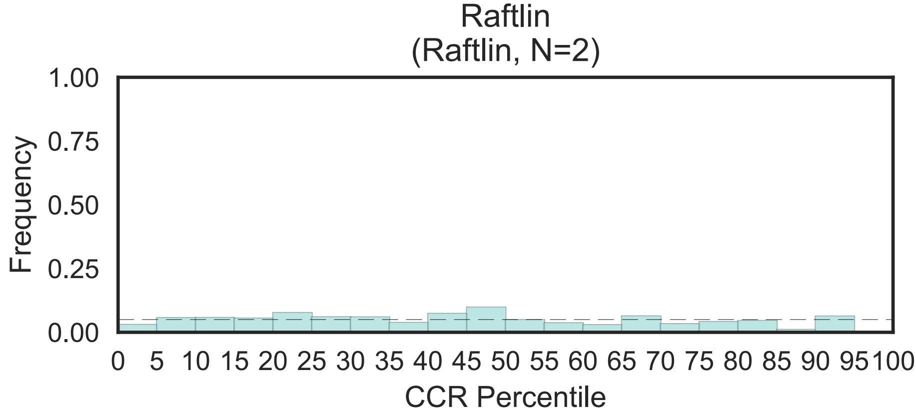
Radial spokehead-like protein
(Radial_spoke, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

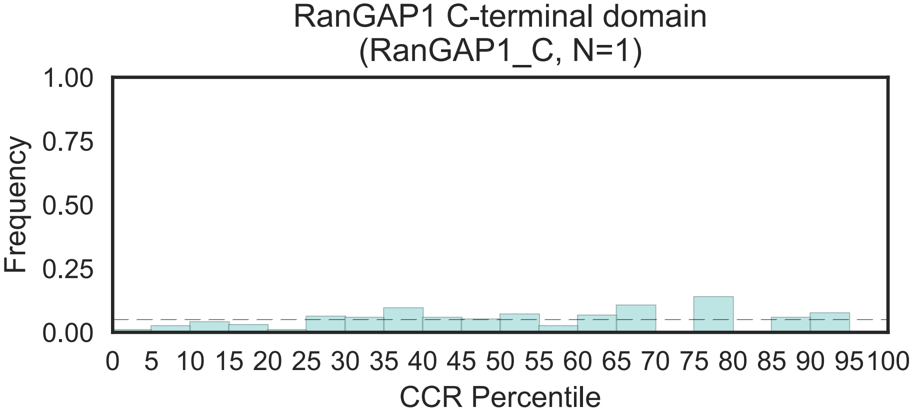

Radial spoke protein 3
(Radial_spoke_3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

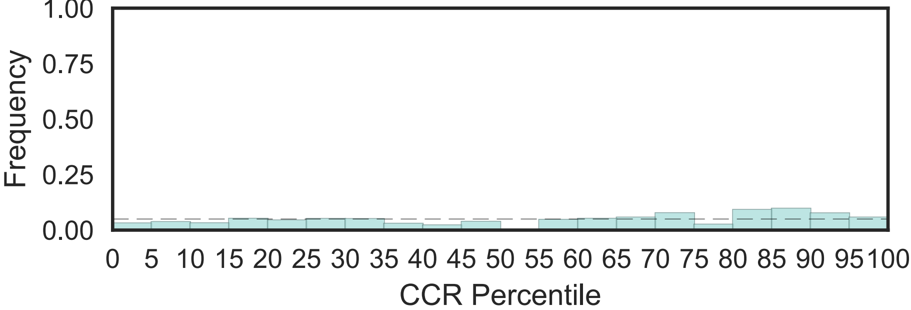

Radical SAM superfamily
(Radical_SAM, N=10)
Fisher's OR: 0.207; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



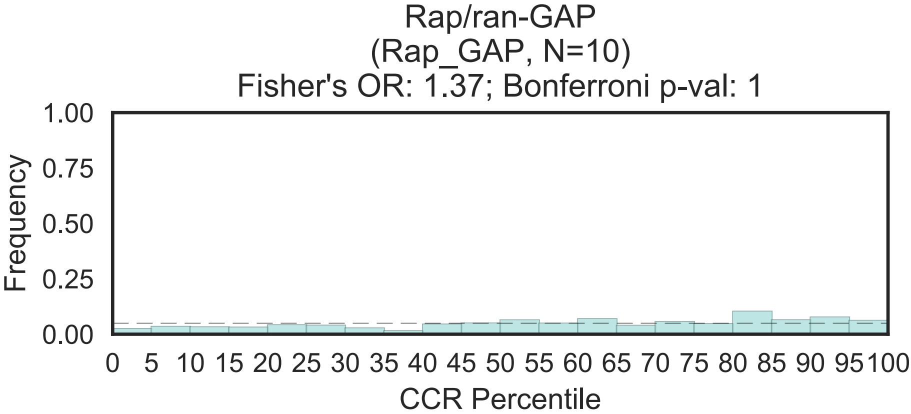
Radical_SAM C-terminal domain
(Radical_SAM_C, N=1)

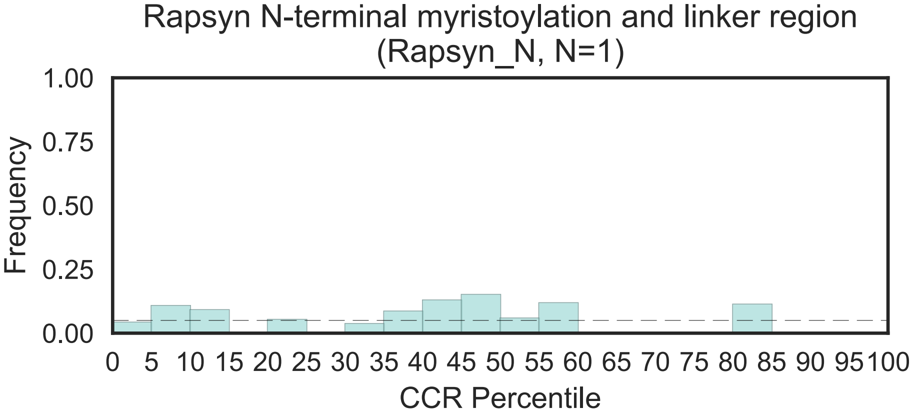

Raftlin
(Raftlin, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

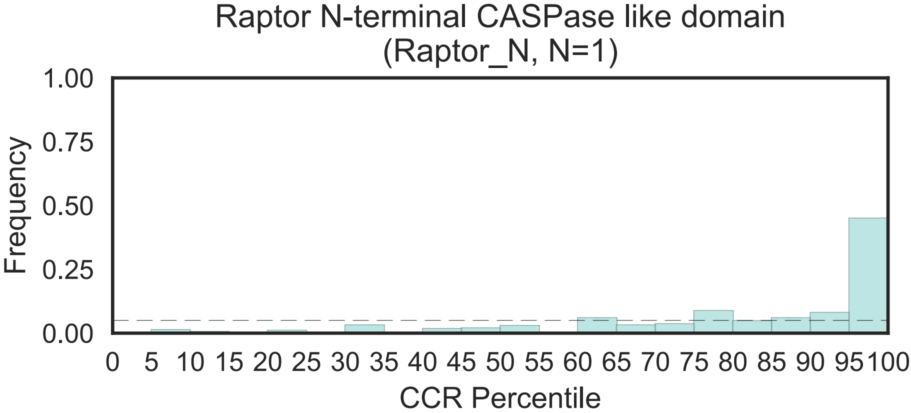

RanGAP1 C-terminal domain
(RanGAP1_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



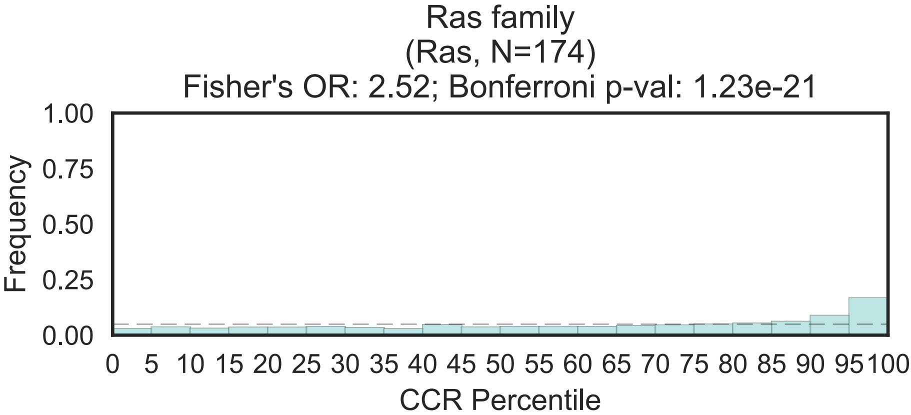
RanBP1 domain
(Ran_BP1, N=22)
Fisher's OR: 1.17; Bonferroni p-val: 1


Rap/ran-GAP
(Rap_GAP, N=10)
Fisher's OR: 1.37; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

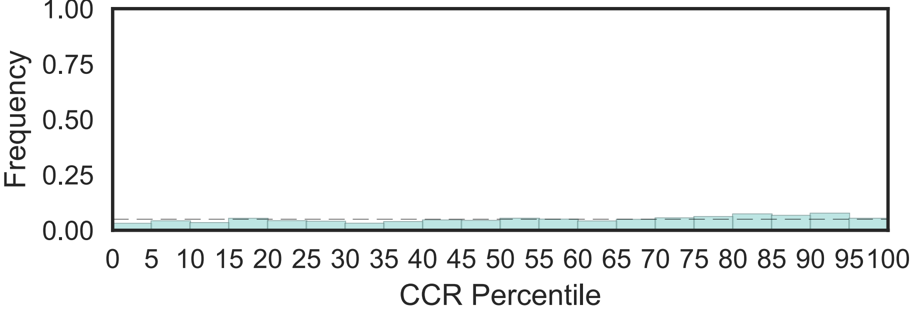

Rapsyn N-terminal myristoylation and linker region
(Rapsyn_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

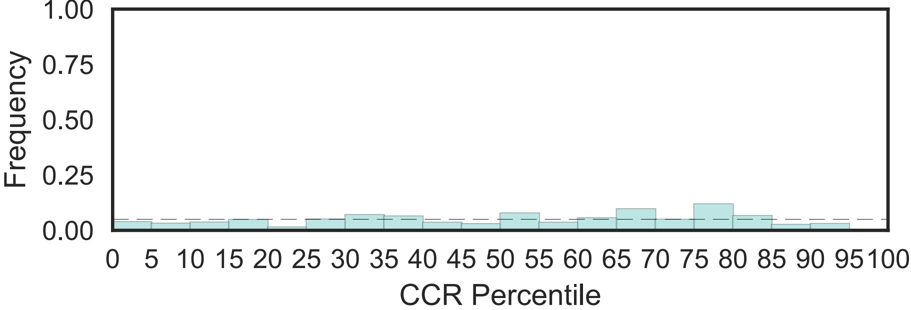


Raptor N-terminal CASPase like domain
(Raptor_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

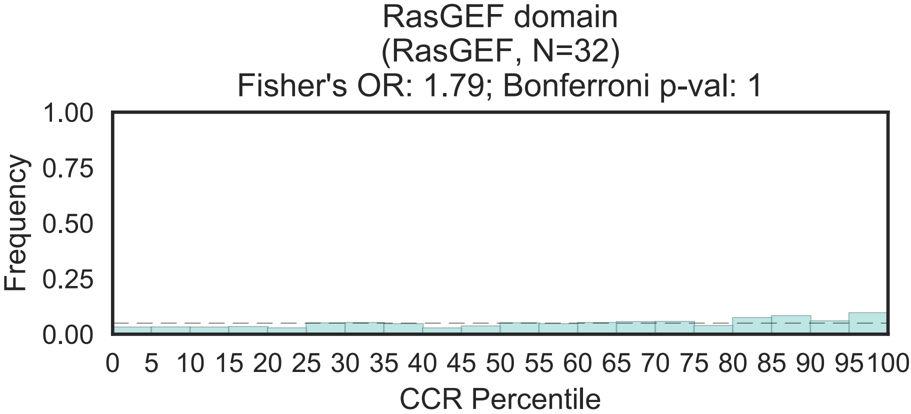

Ras family
(Ras, N=174)
Fisher's OR: 2.52; Bonferroni p-val: 1.23e-21
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

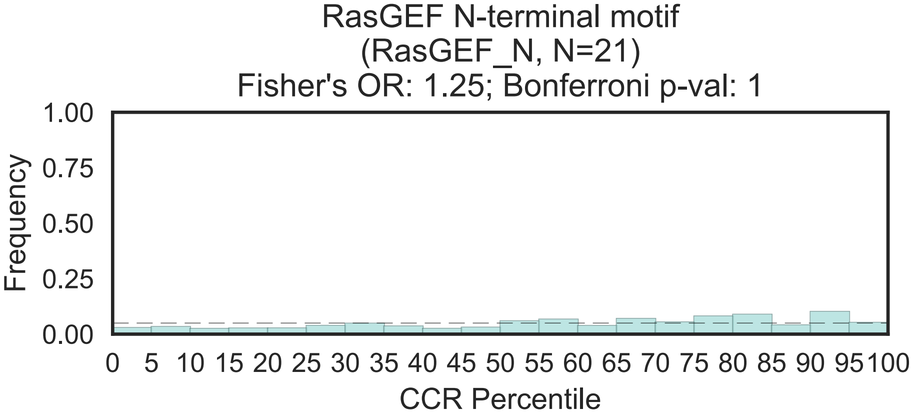
GTPase-activator protein for Ras-like GTPase
(RasGAP, N=20)
Fisher's OR: 0.955; Bonferroni p-val: 1

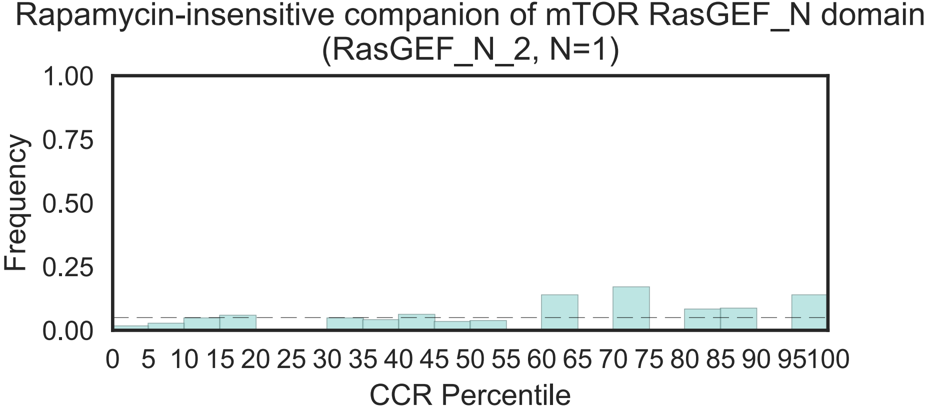




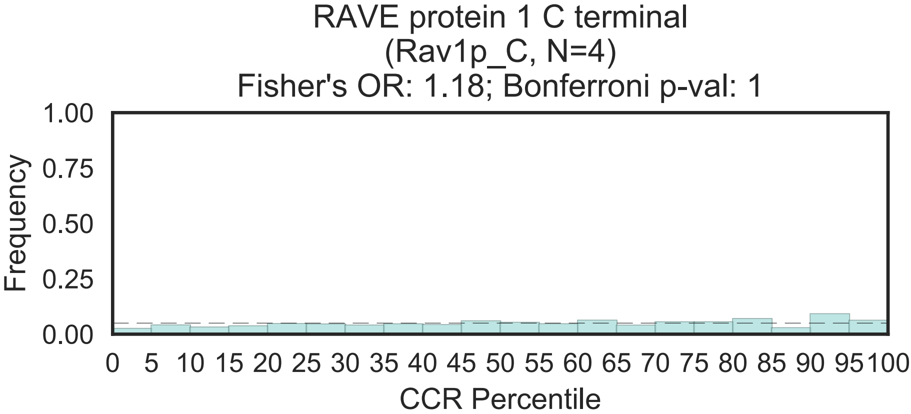
RasGAP C-terminus
(RasGAP_C, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

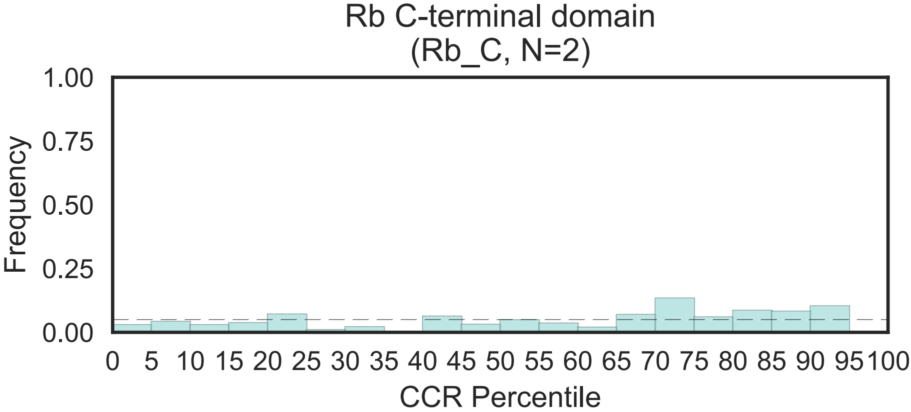

RasGEF domain
(RasGEF, N=32)
Fisher's OR: 1.79; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

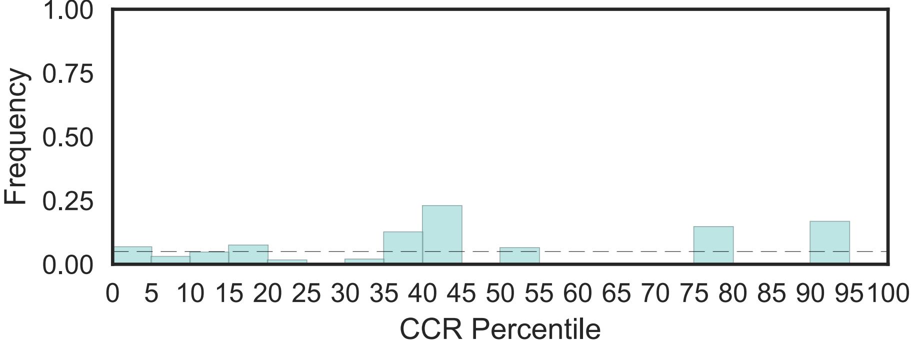

RasGEF N-terminal motif
(RasGEF_N, N=21)
Fisher's OR: 1.25; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



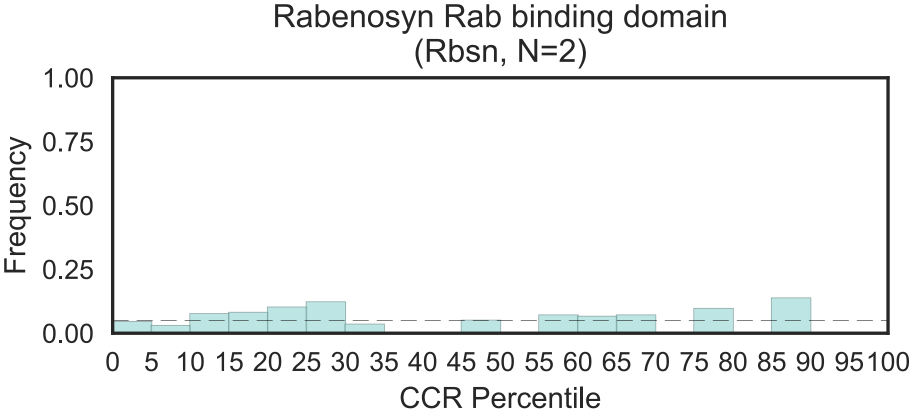
Rapamycin-insensitive companion of mTOR RasGEF_N domain (RasGEF_N_2, N=1)

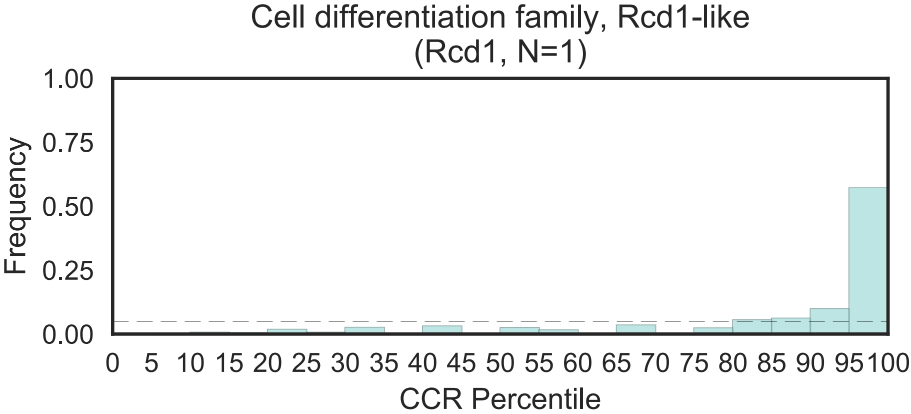

RAVE protein 1 C terminal
(Rav1p_C, N=4)
Fisher's OR: 1.18; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

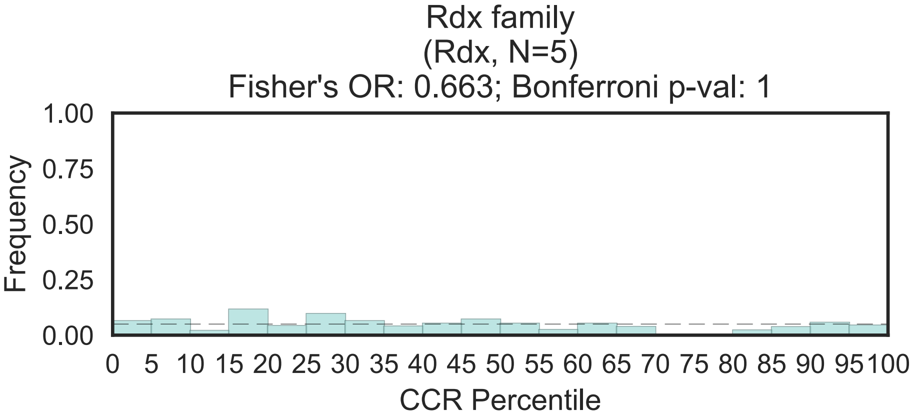

Rb C-terminal domain
(Rb_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

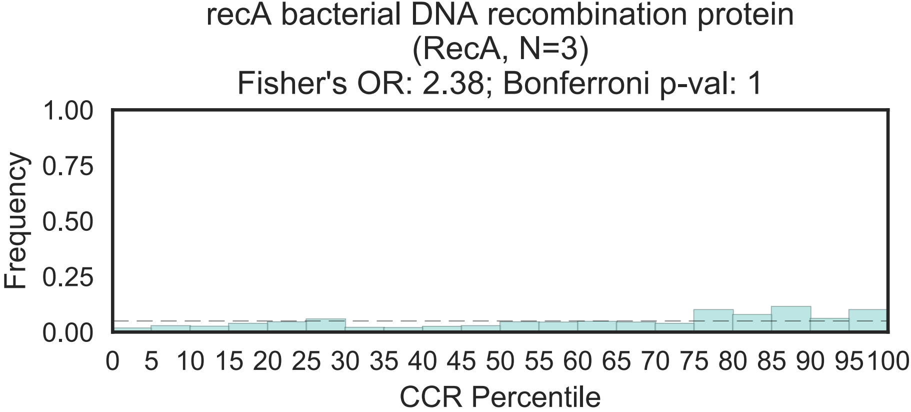


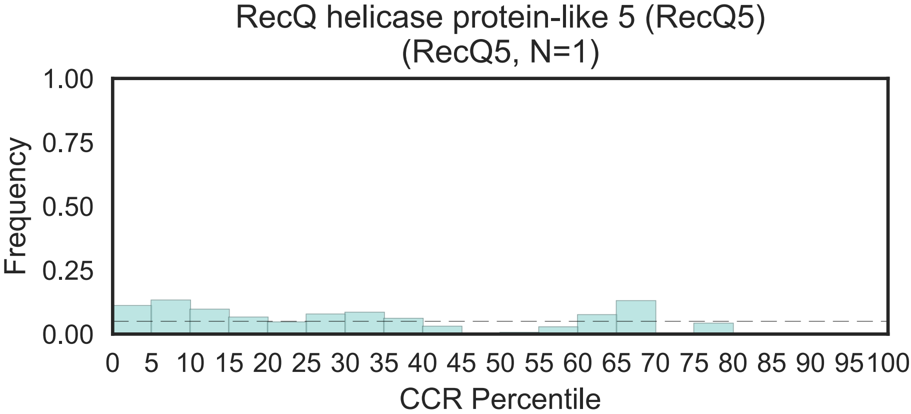
RbsD / FucU transport protein family
(RbsD_FucU, N=1)

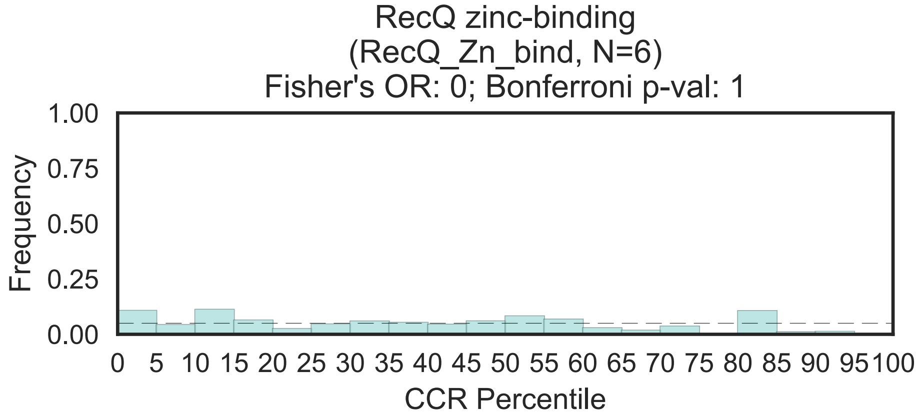

Rabenosyn Rab binding domain
(Rbsn, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

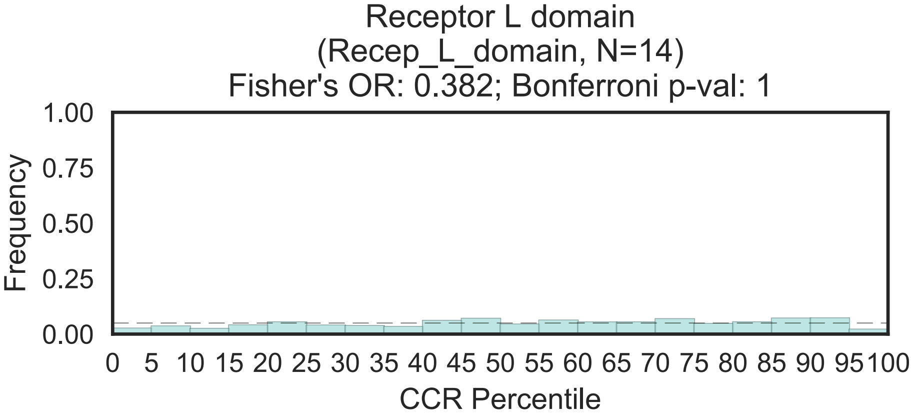

Cell differentiation family, Rcd1-like
(Rcd1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

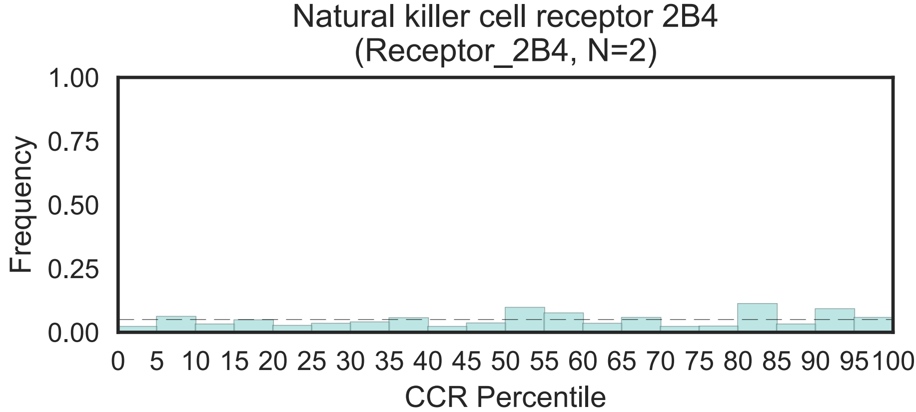

Rdx family
(Rdx, N=5)
Fisher's OR: 0.663; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

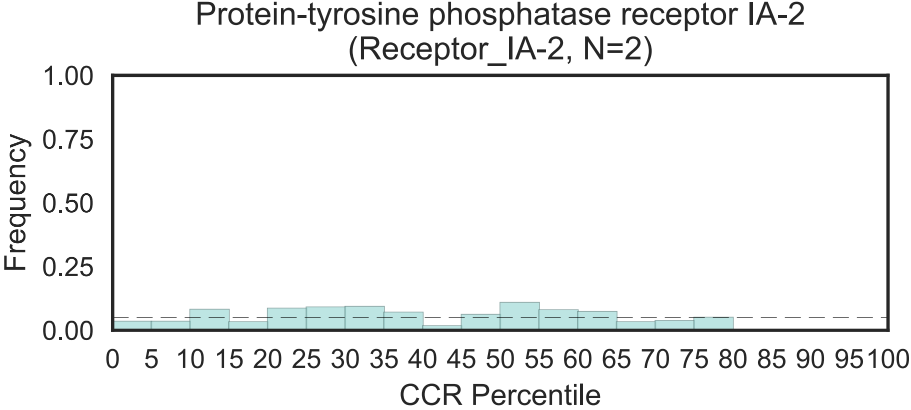

recA bacterial DNA recombination protein
(RecA, N=3)
Fisher's OR: 2.38; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

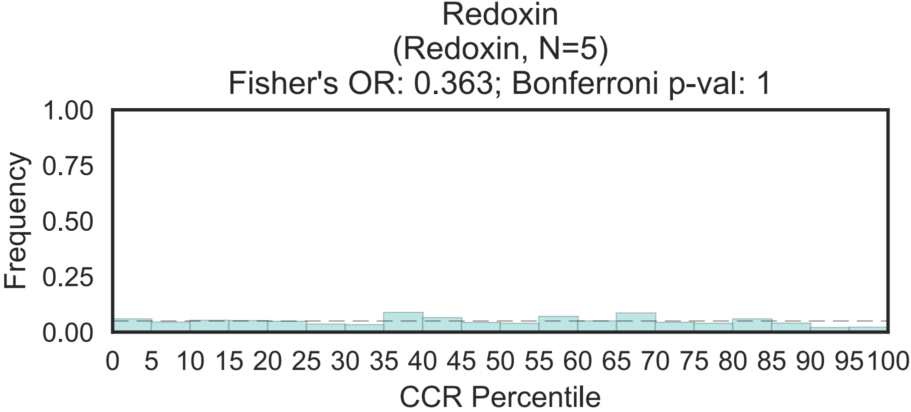

RecQ helicase protein-like 5 (RecQ5)
(RecQ5, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

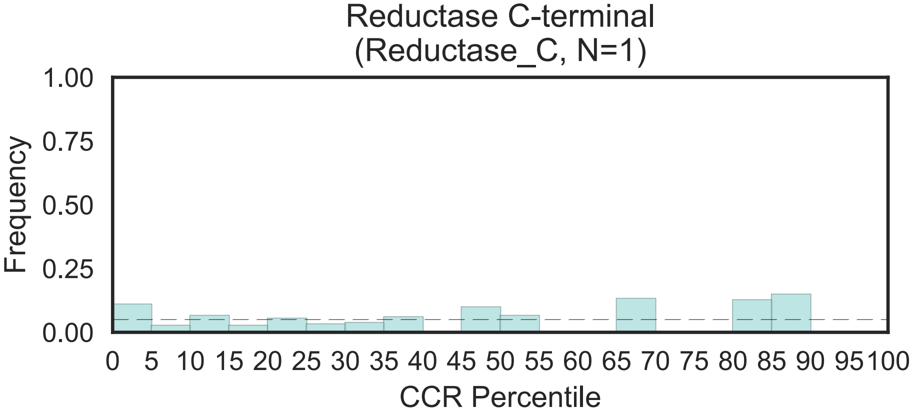

RecQ zinc-binding
(RecQ_Zn_bind, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

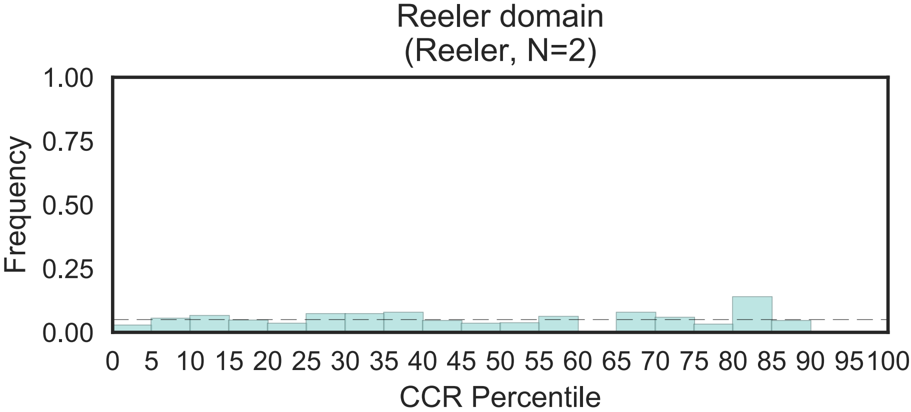

Receptor L domain
(Recep_L_domain, N=14)
Fisher's OR: 0.382; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Natural killer cell receptor 2B4
(Receptor_2B4, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

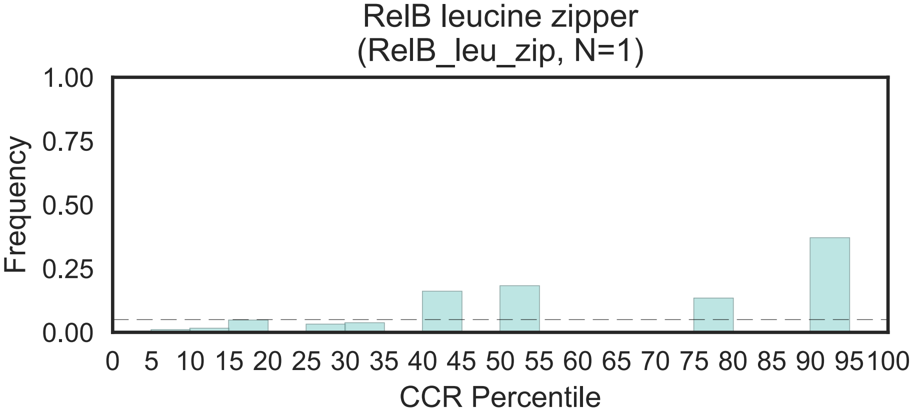

Protein-tyrosine phosphatase receptor IA-2
(Receptor_IA-2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Redoxin
(Redoxin, N=5)
Fisher's OR: 0.363; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

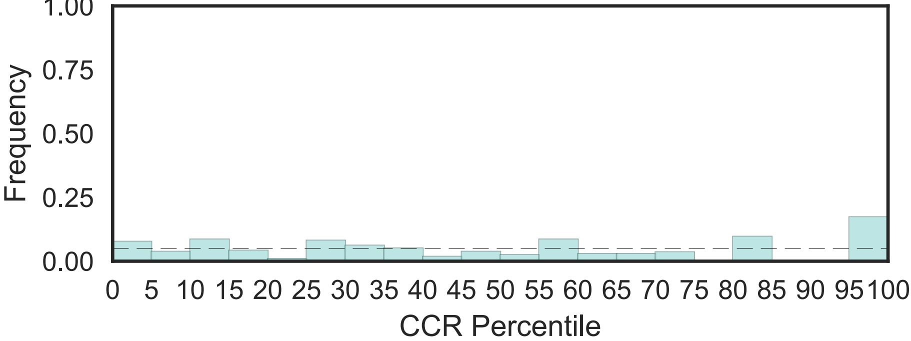

Reductase C-terminal
(Reductase_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

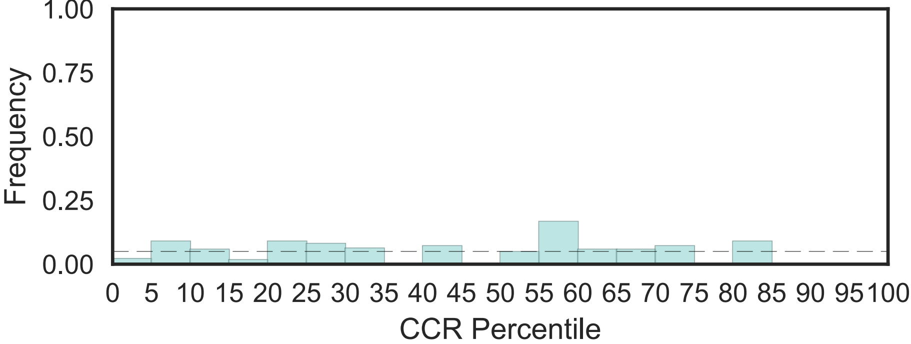


Reeler domain
(Reeler, N=2)

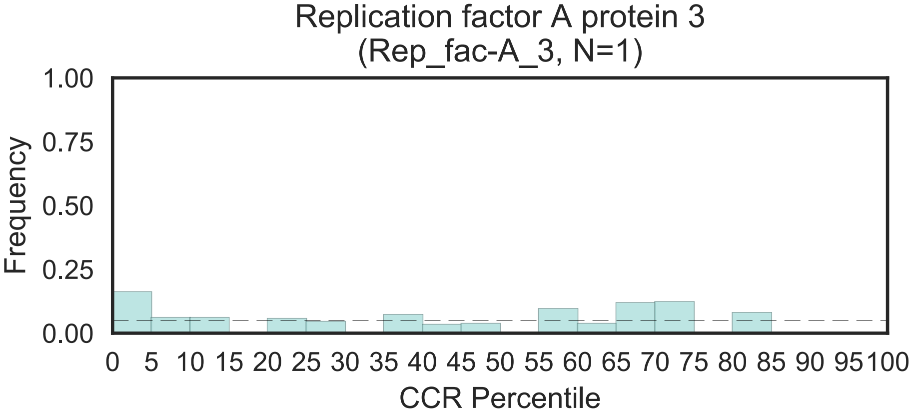

RelB leucine zipper
(RelB_leu_zip, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

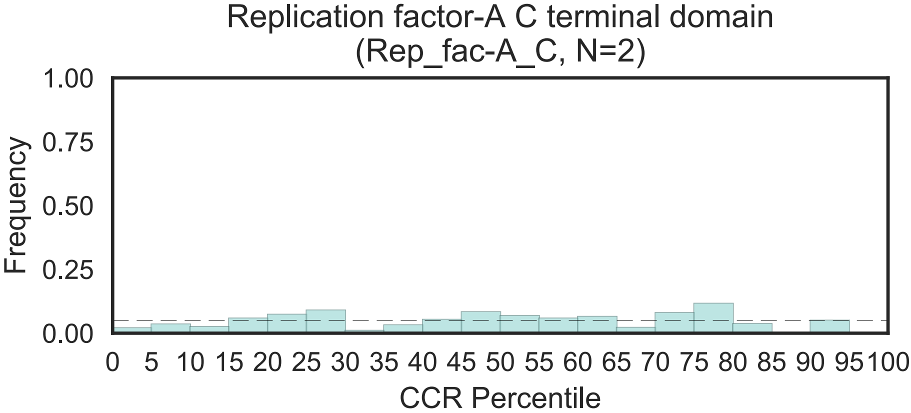
RelB transactivation domain (RelB_transactiv, N=1)

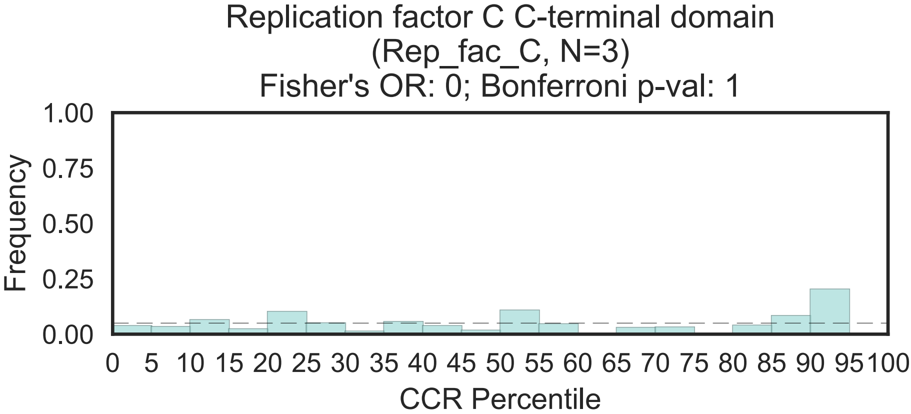


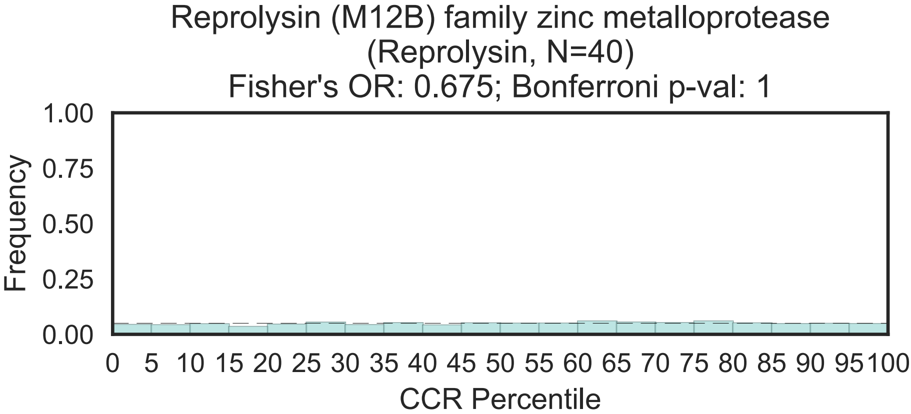


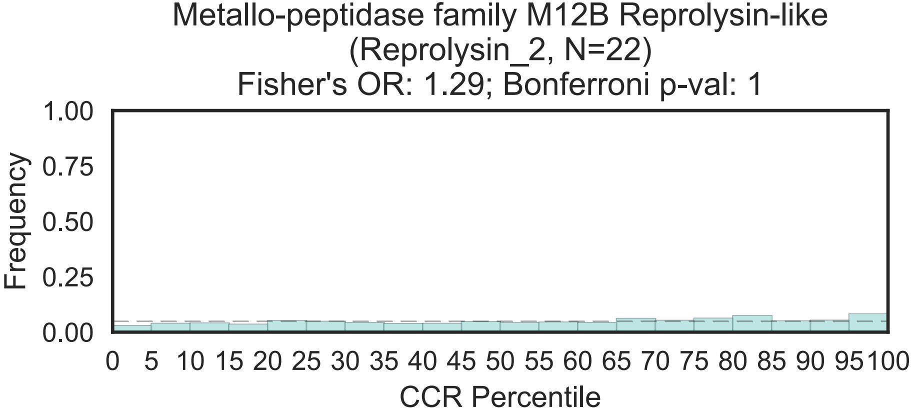
Replication factor-A protein 1, N-terminal domain
(Rep-A_N, N=1)

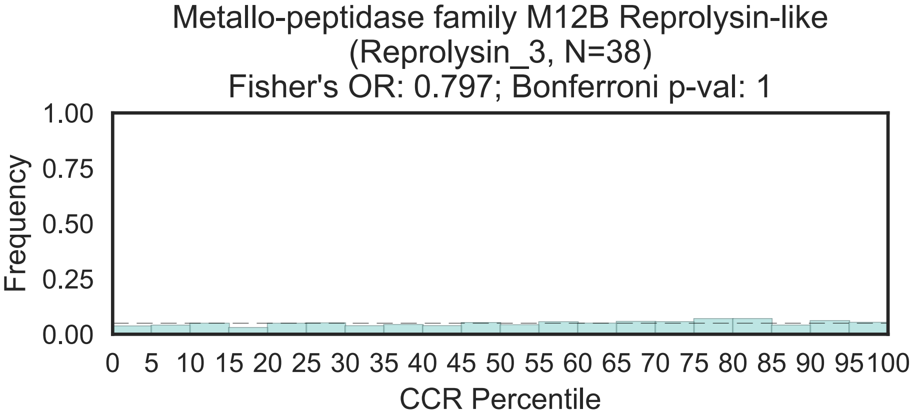

Replication factor A protein 3
(Rep_fac-A_3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

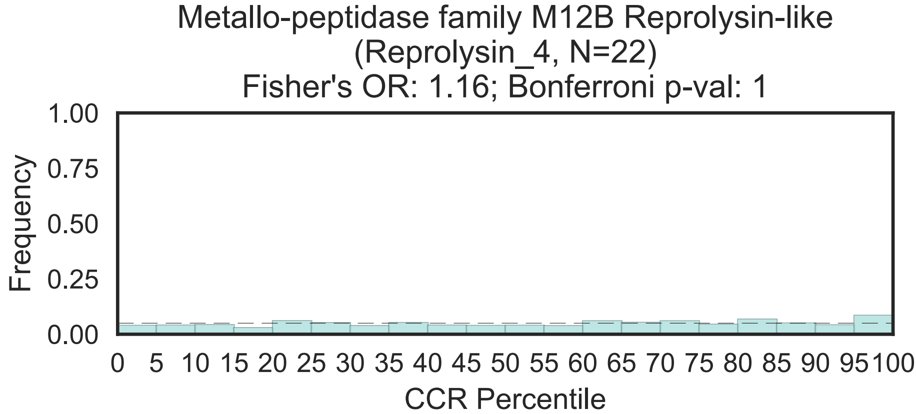

Replication factor-A C terminal domain
(Rep_fac-A_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

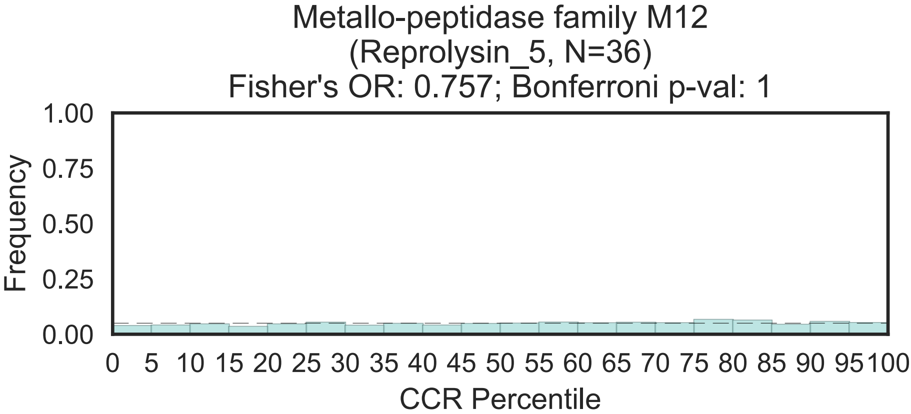

Replication factor C C-terminal domain
(Rep_fac_C, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

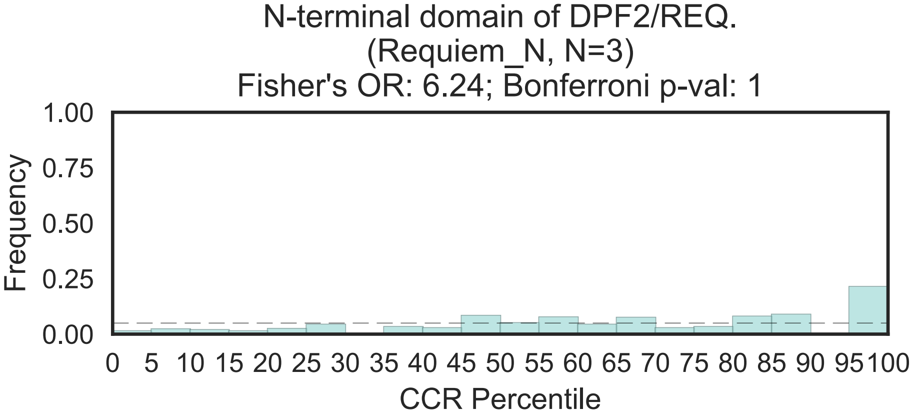

Reprolysin (M12B) family zinc metalloprotease
(Reprolysin, N=40)
Fisher's OR: 0.675; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

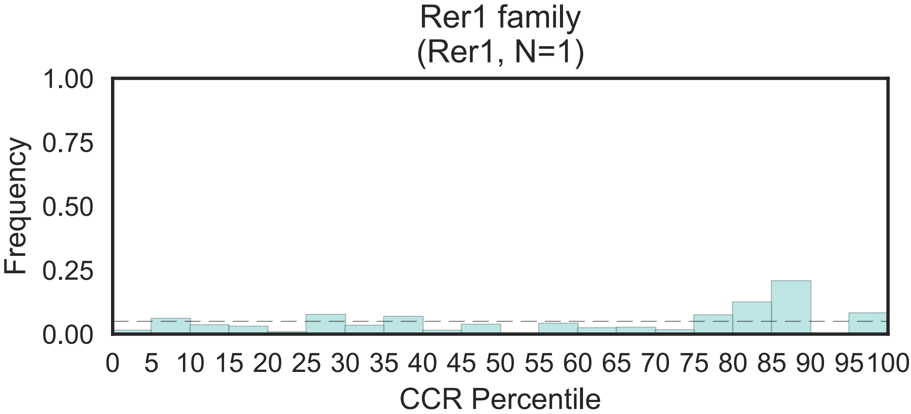

Metallo-peptidase family M12B Reprolysin-like
(Reprolysin_2, N=22)
Fisher's OR: 1.29; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

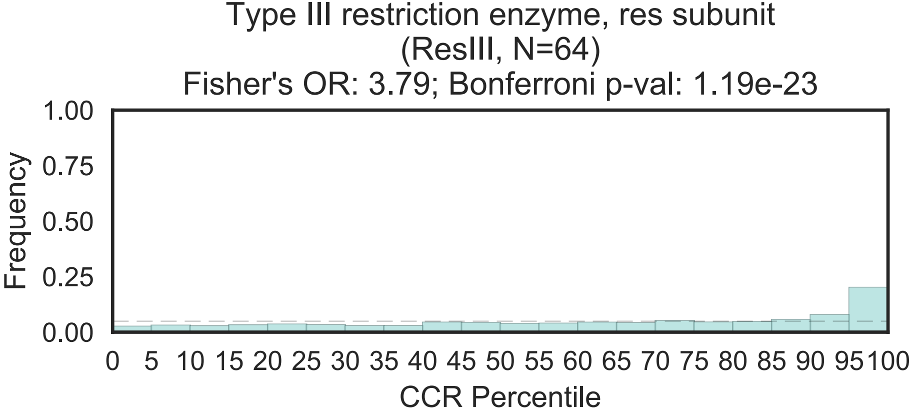

Metallo-peptidase family M12B Reprolysin-like
(Reprolysin_3, N=38)
Fisher's OR: 0.797; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Metallo-peptidase family M12B Reprolysin-like
(Reprolysin_4, N=22)
Fisher's OR: 1.16; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

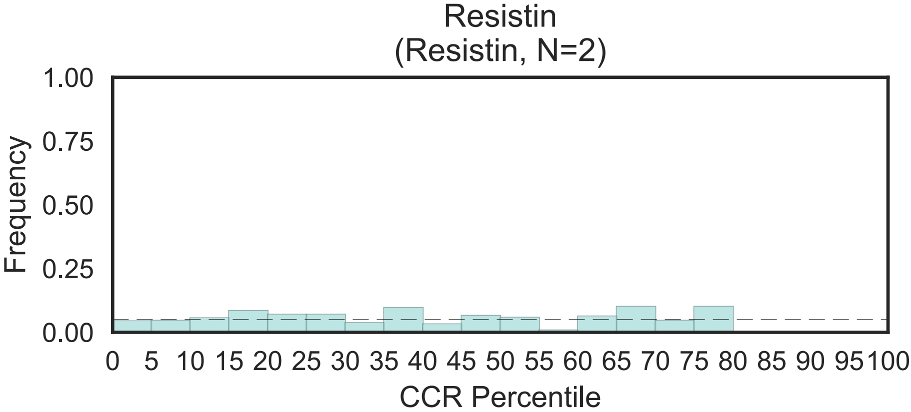

Metallo-peptidase family M12
(Reprolysin_5, N=36)
Fisher's OR: 0.757; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


N-terminal domain of DPF2/REQ.
(Requiem_N, N=3)
Fisher's OR: 6.24; Bonferroni p-val: 1

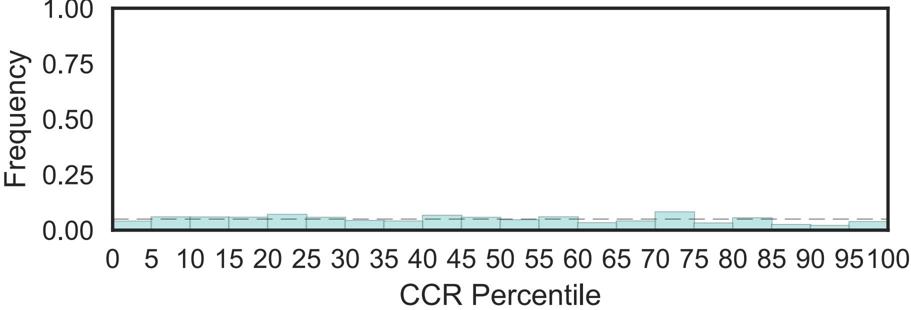

Rer1 family
(Rer1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

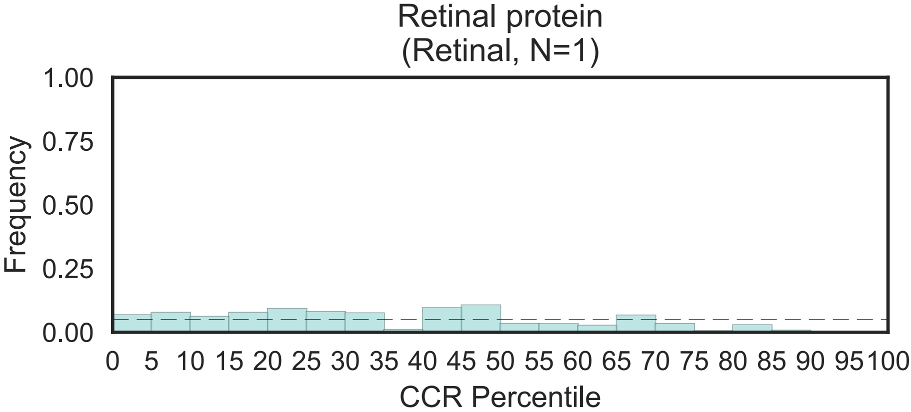


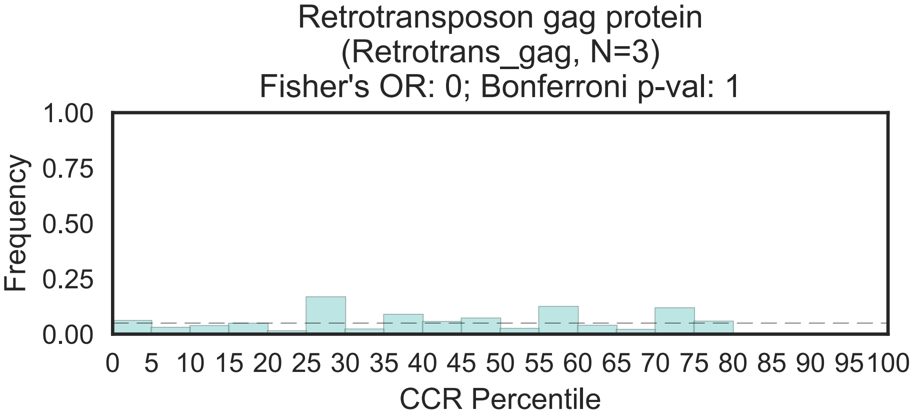
Type III restriction enzyme, res subunit
(ResIII, N=64)
Fisher's OR: 3.79; Bonferroni p-val: 1.19e-23

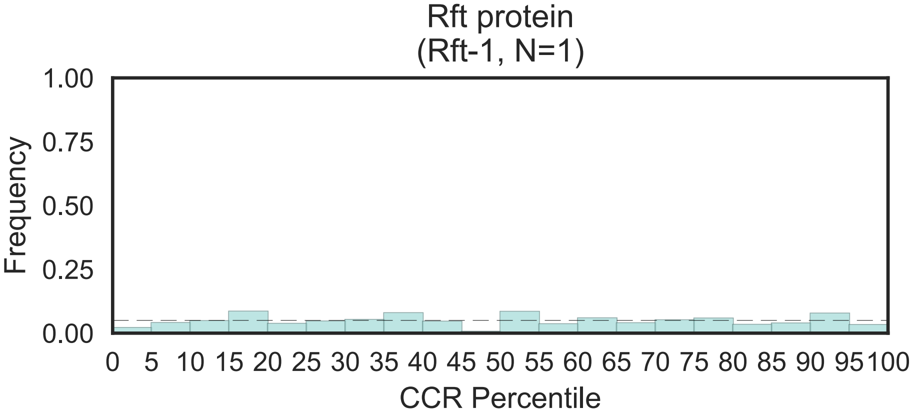

Resistin
(Resistin, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

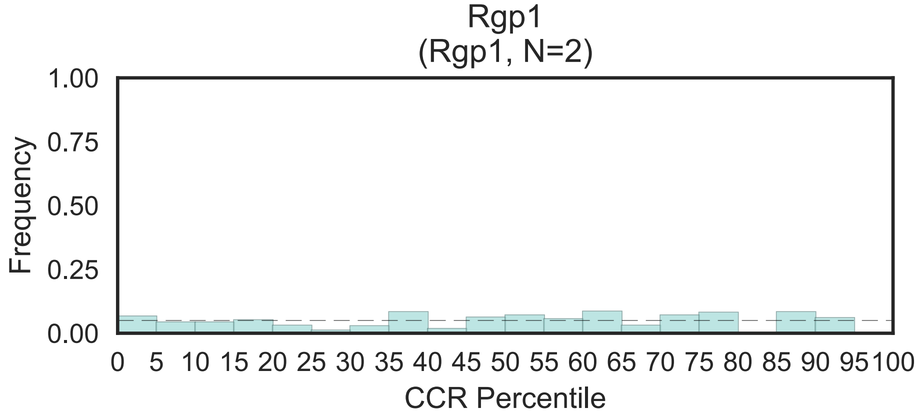
Reticulon
(Reticulon, N=4)
Fisher's OR: 0.553; Bonferroni p-val: 1

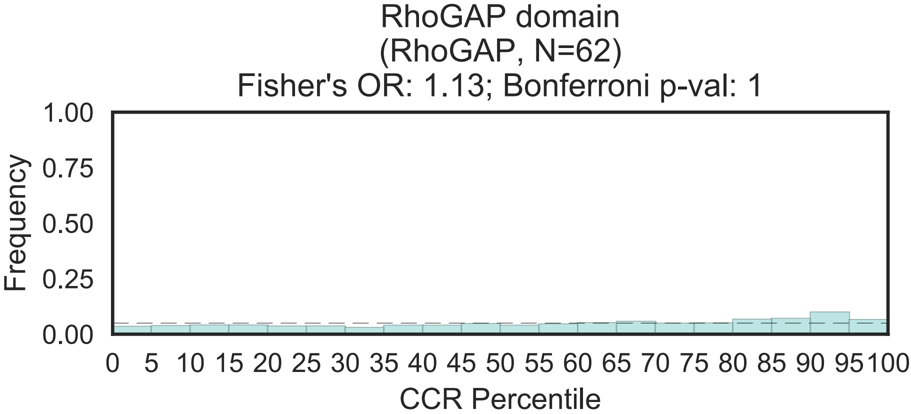


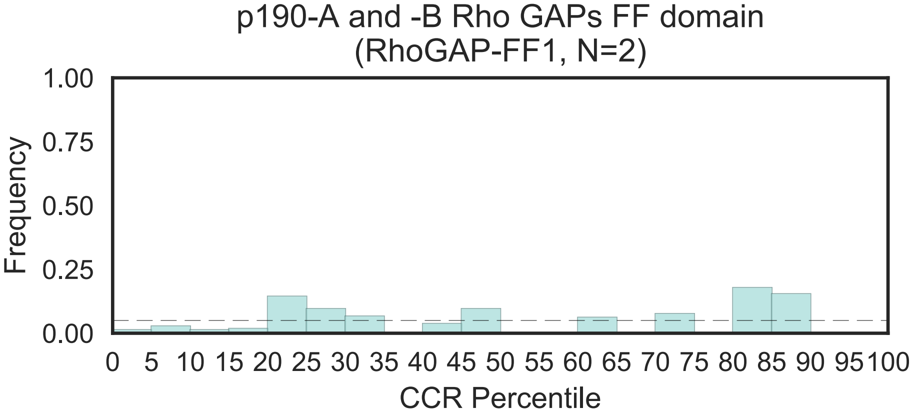

Retinal protein
(Retinal, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

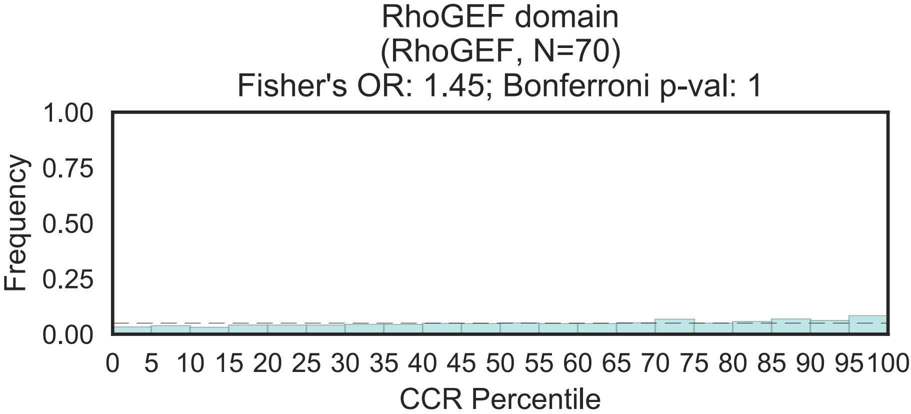

Retrotransposon gag protein
(Retrotrans_gag, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

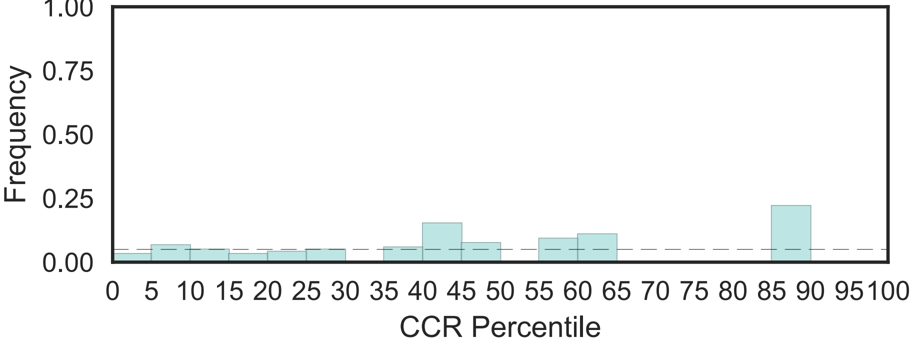

Rft protein
(Rft-1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Rgp1
(Rgp1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

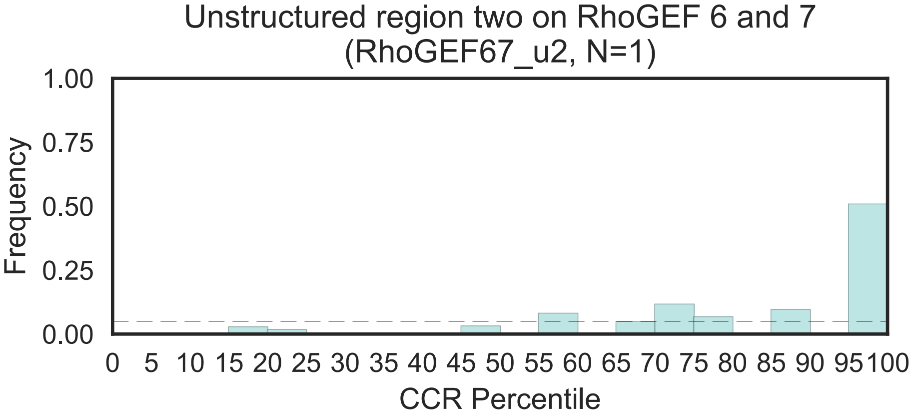

RhoGAP domain
(RhoGAP, N=62)
Fisher's OR: 1.13; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

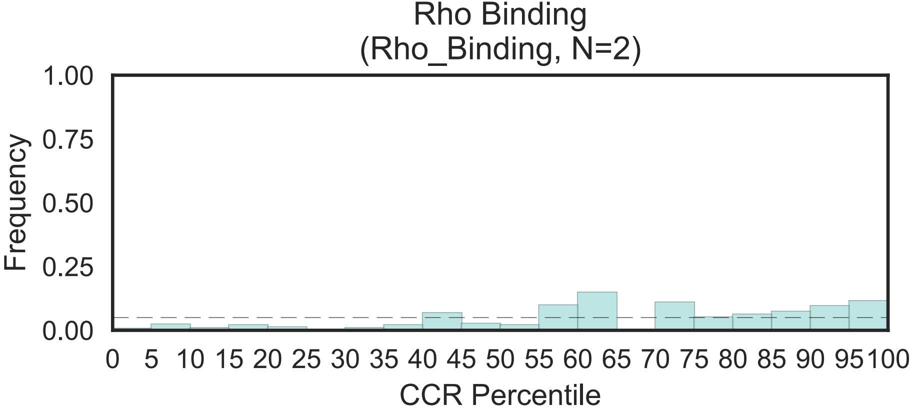

p190-A and -B Rho GAPs FF domain
(RhoGAP-FF1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

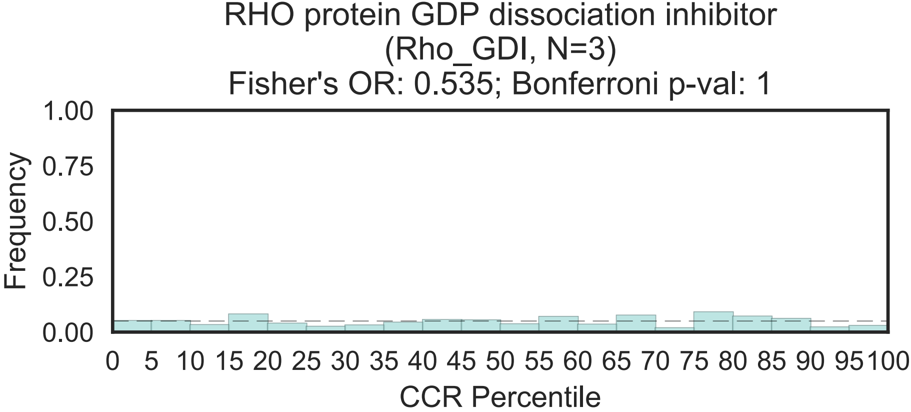

RhoGEF domain
(RhoGEF, N=70)
Fisher's OR: 1.45; Bonferroni p-val: 1



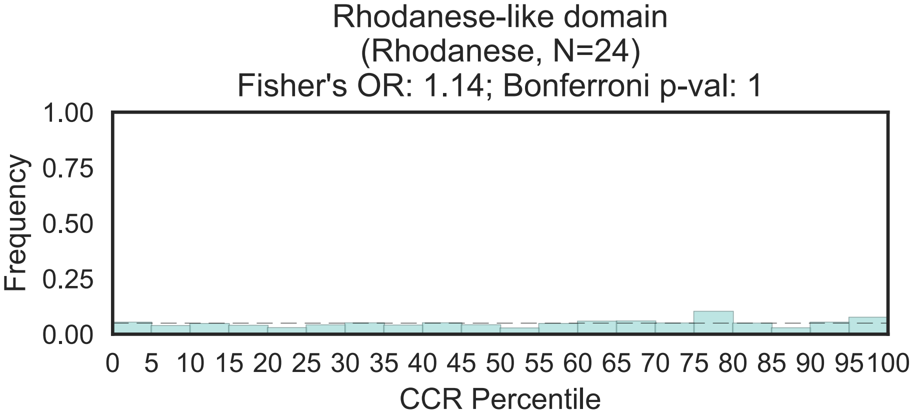
Unstructured region one on RhoGEF 6 and 7
(RhoGEF67_u1, N=1)

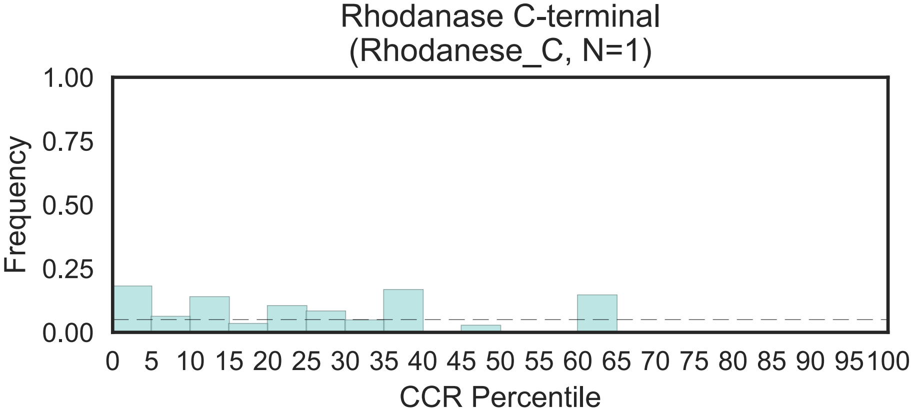

Unstructured region two on RhoGEF 6 and 7
(RhoGEF67_u2, N=1)

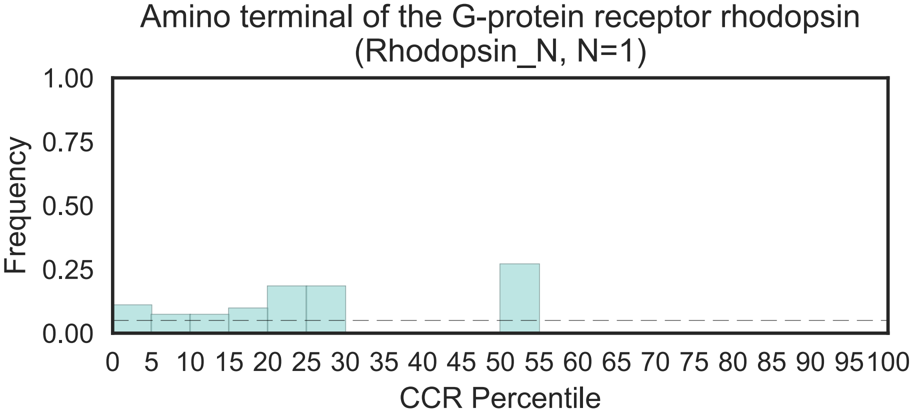

Rho Binding
(Rho_Binding, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



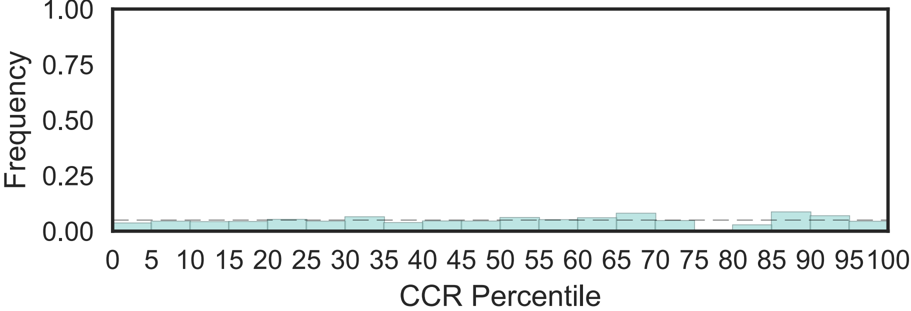
RHO protein GDP dissociation inhibitor
(Rho_GDI, N=3)
Fisher's OR: 0.535; Bonferroni p-val: 1


Rhodanese-like domain
(Rhodanese, N=24)
Fisher's OR: 1.14; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

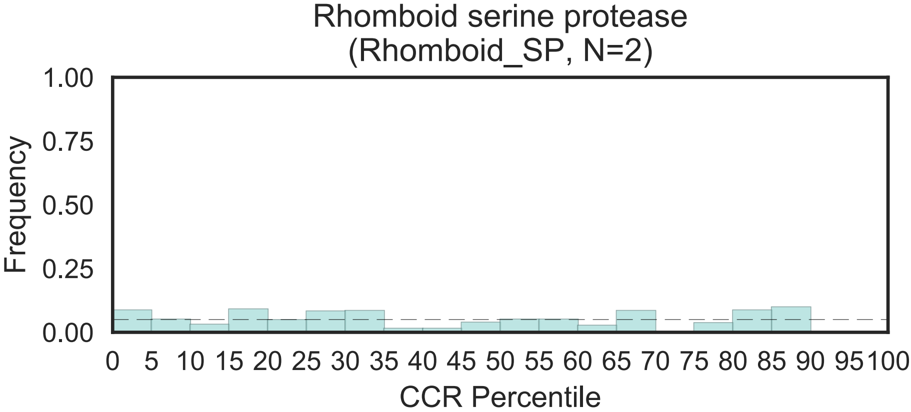

Rhodanase C-terminal
(Rhodanese_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

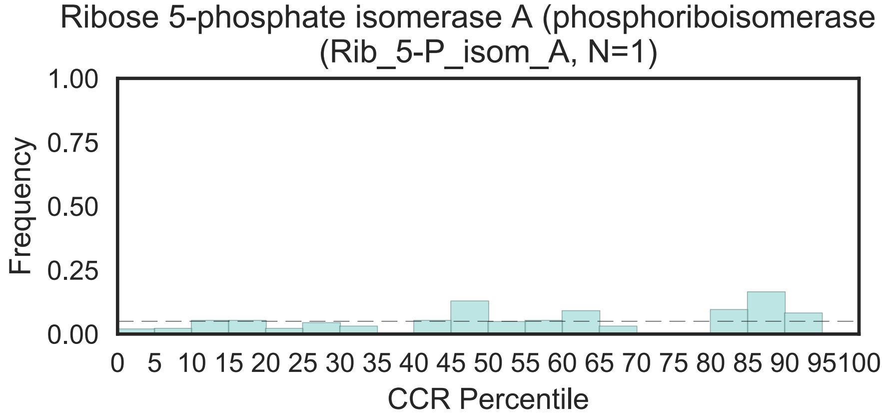


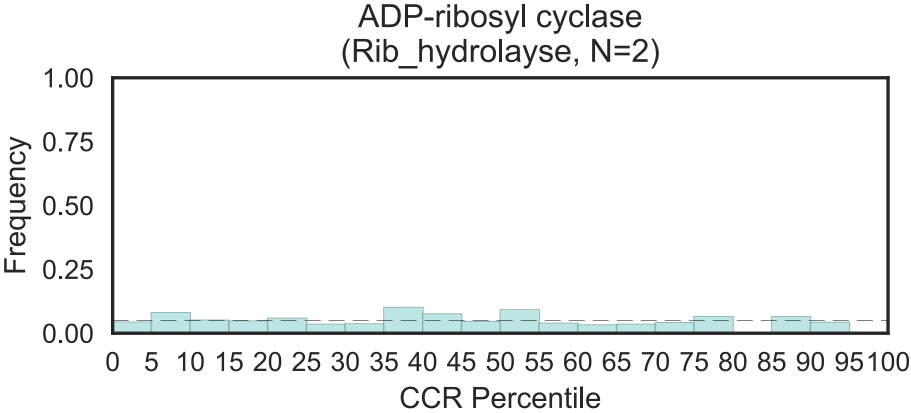
Amino terminal of the G-protein receptor rhodopsin
(Rhodopsin_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

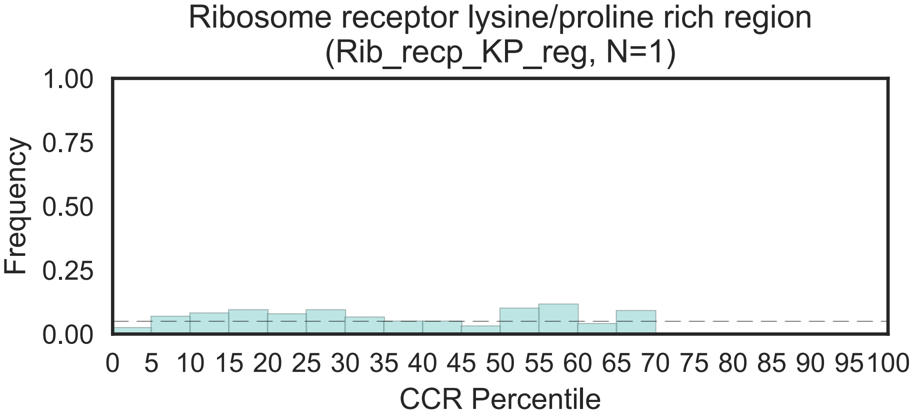


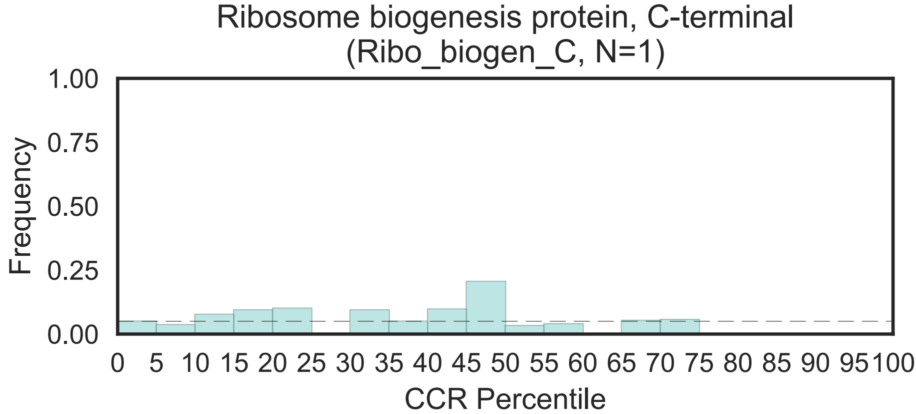
Rhomboid family
(Rhomboid, N=9)
Fisher's OR: 0.781; Bonferroni p-val: 1

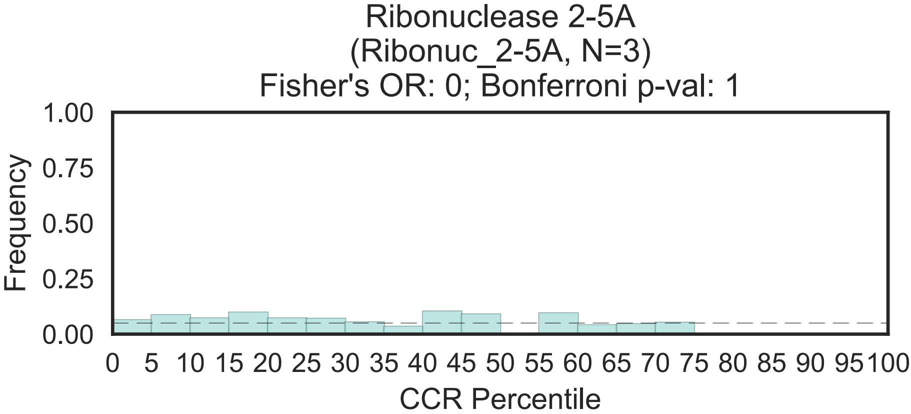
Rhomboid serine protease
(Rhomboid_SP, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribose 5-phosphate isomerase A (phosphoriboisomerase A)
(Rib_5-P_isom_A, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

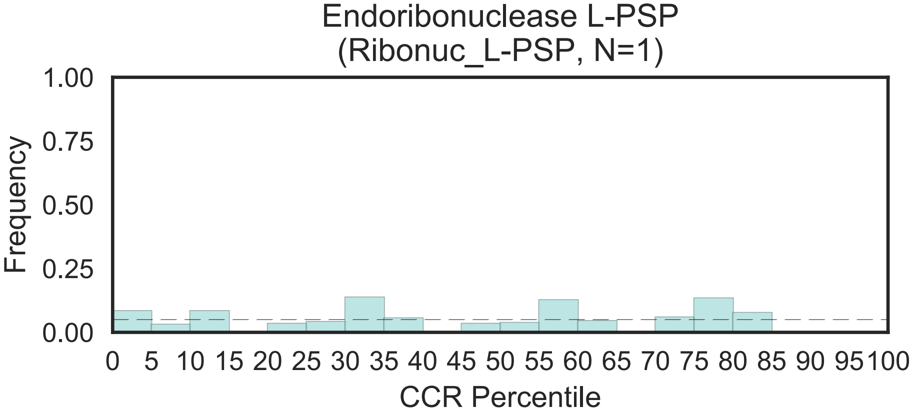

ADP-ribosyl cyclase
(Rib_hydrolayse, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

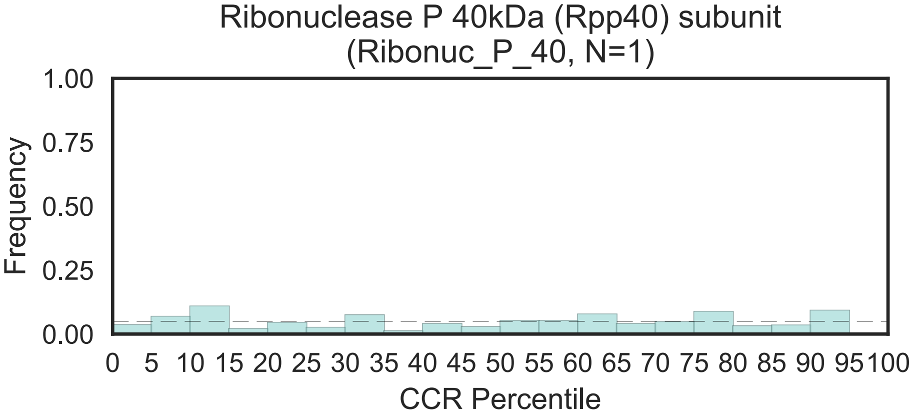

Ribosome receptor lysine/proline rich region
(Rib_recp_KP_reg, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

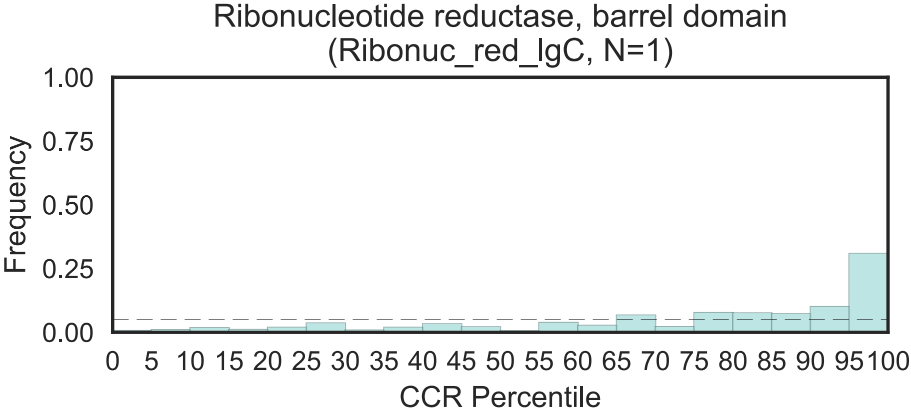

Ribosome biogenesis protein, C-terminal
(Ribo_biogen_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

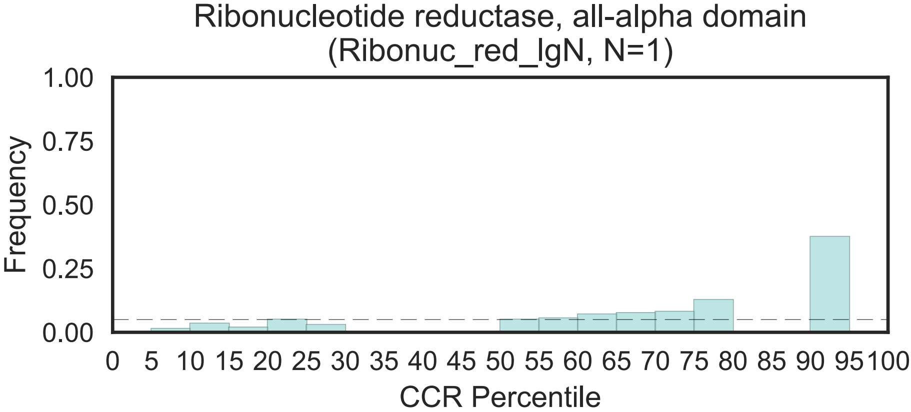


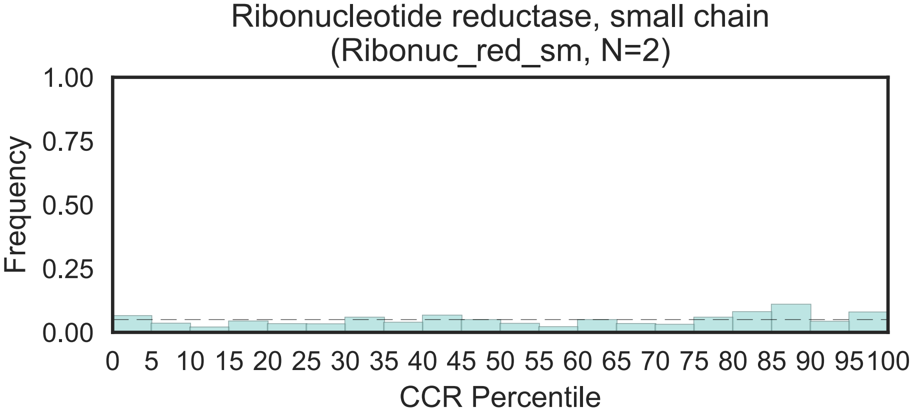
Ribonuclease 2-5A
(Ribonuc_2-5A, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

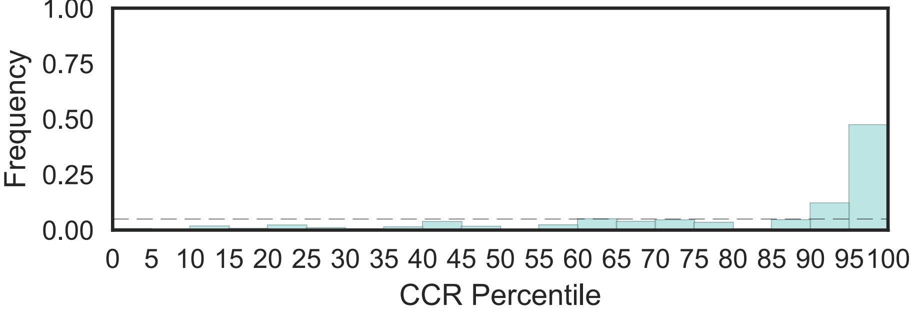

Endoribonuclease L-PSP
(Ribonuc_L-PSP, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribonuclease P 40kDa (Rpp40) subunit
(Ribonuc_P_40, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

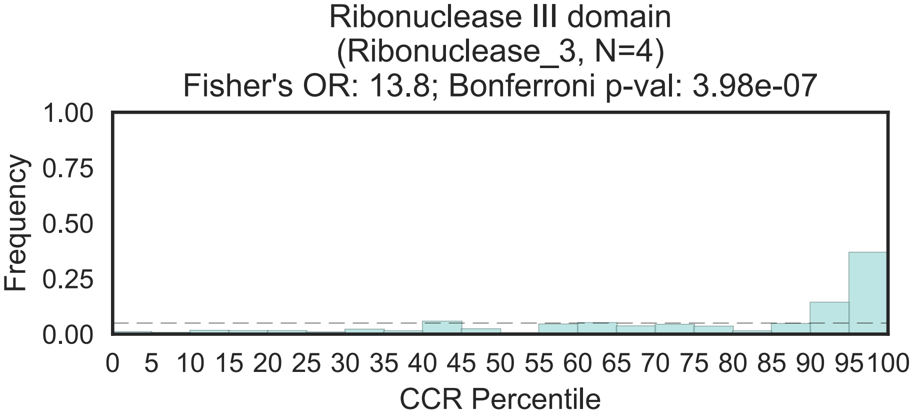

Ribonucleotide reductase, barrel domain
(Ribonuc_red_lgC, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribonucleotide reductase, all-alpha domain
(Ribonuc_red_lgN, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

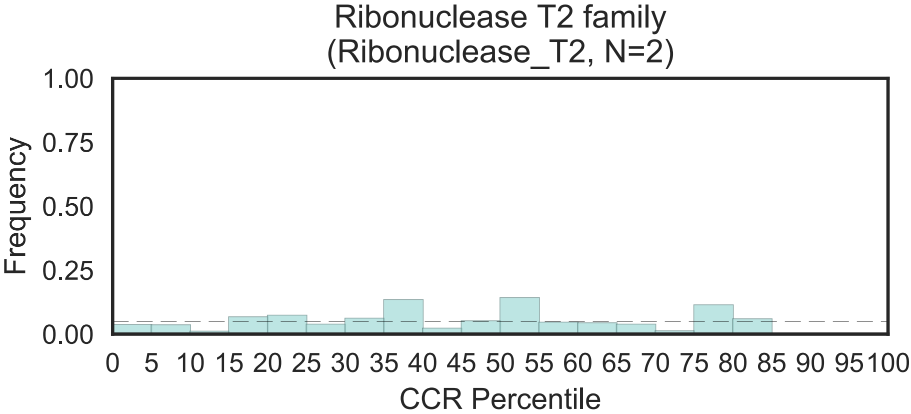

Ribonucleotide reductase, small chain
(Ribonuc_red_sm, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

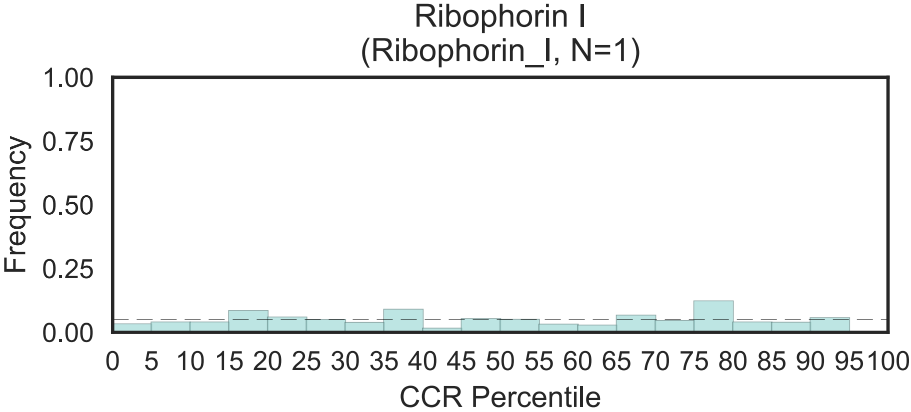


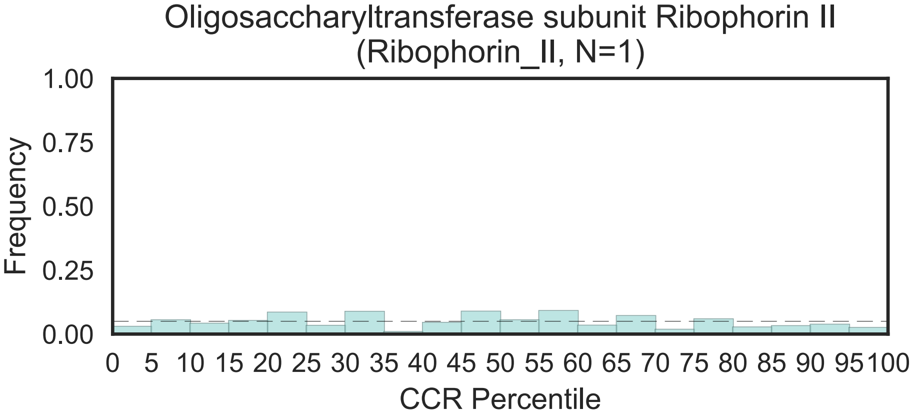
Ribonuclease-III-like
(Ribonucleas_3_3, N=3)
Fisher's OR: 19.3; Bonferroni p-val: 3.34e-06

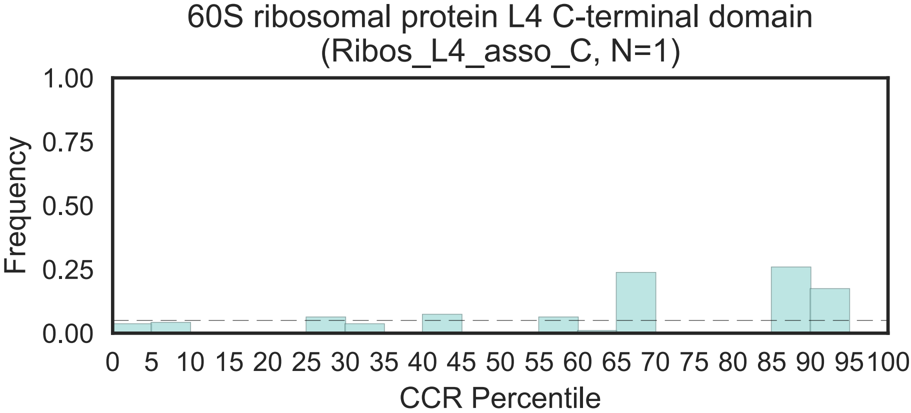


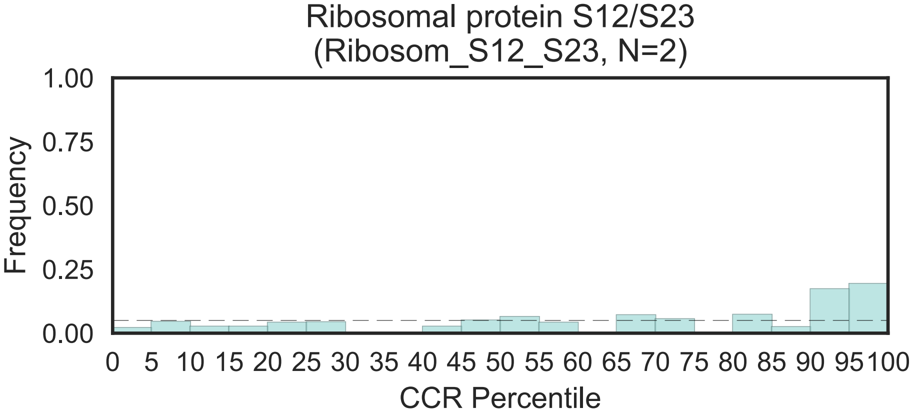
Ribonuclease III domain
(Ribonuclease_3, N=4)
Fisher's OR: 13.8; Bonferroni p-val: 3.98e-07

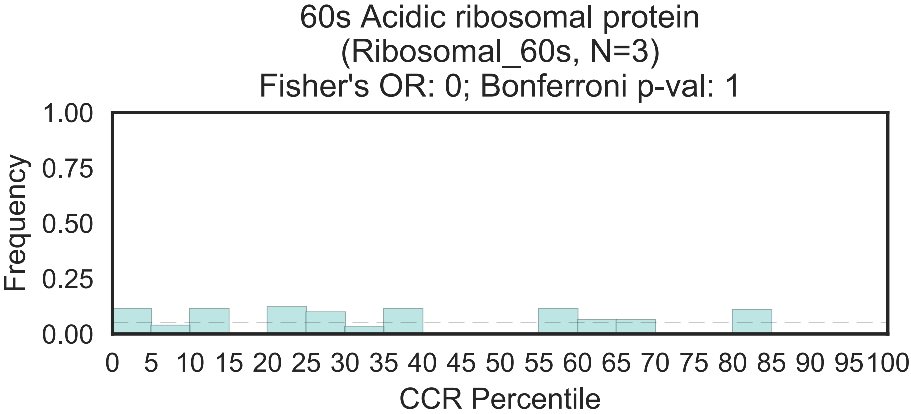

Ribonuclease T2 family
(Ribonuclease_T2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribophorin I
(Ribophorin_I, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

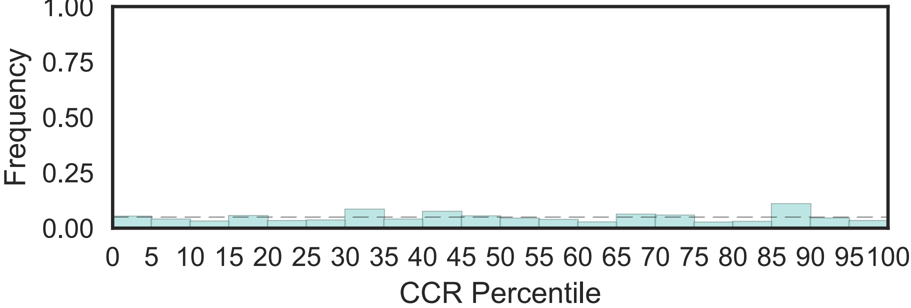

Oligosaccharyltransferase subunit Ribophorin II
(Ribophorin_II, N=1)

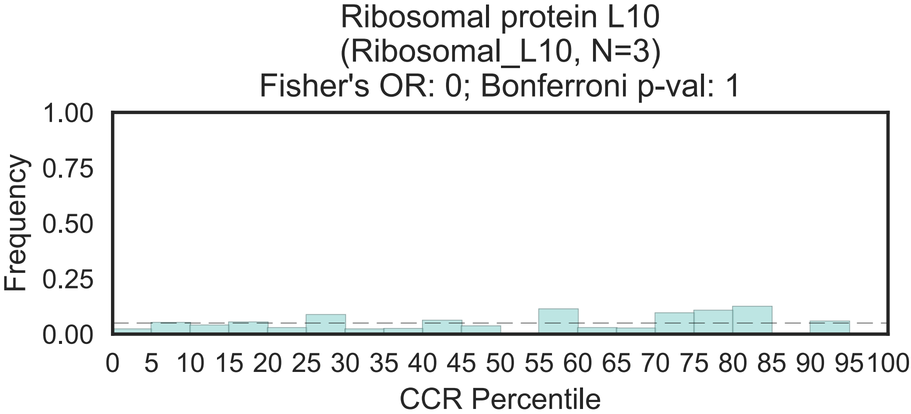

60S ribosomal protein L4 C-terminal domain
(Ribos_L4_asso_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribosomal protein S12/S23
(Ribosom_S12_S23, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

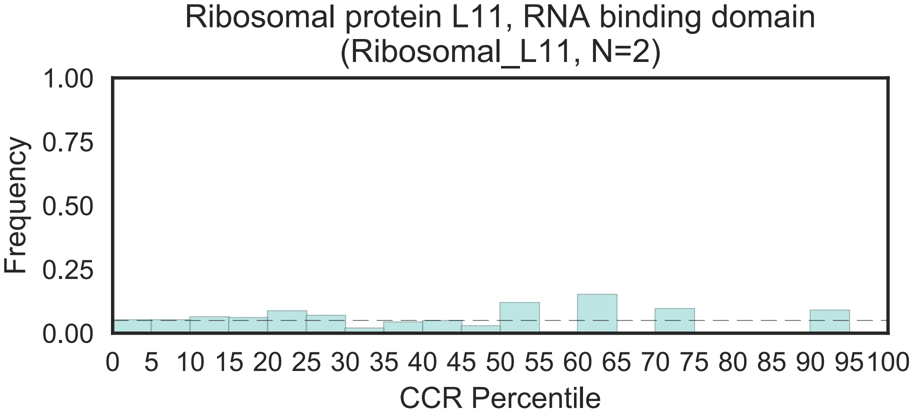

60s Acidic ribosomal protein
(Ribosomal_60s, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

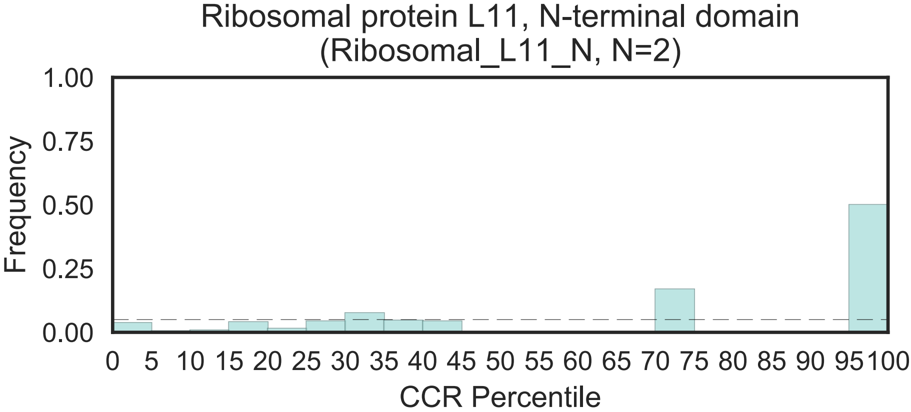
Ribosomal protein L1p/L10e family
(Ribosomal_L1, N=3)
Fisher's OR: 0.489; Bonferroni p-val: 1

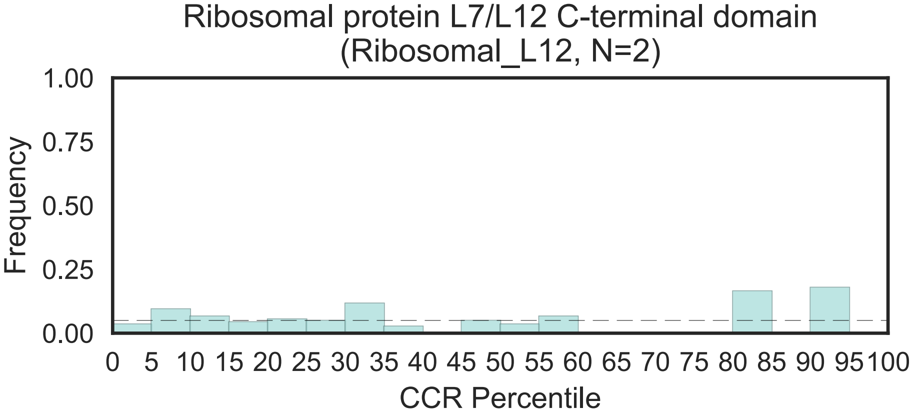


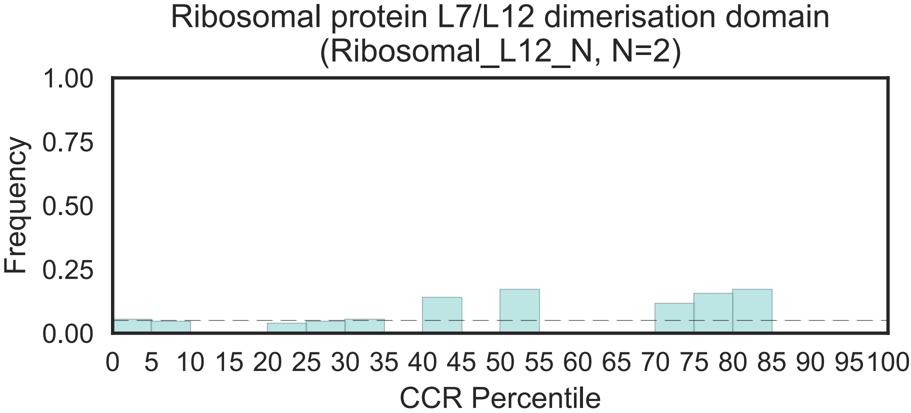


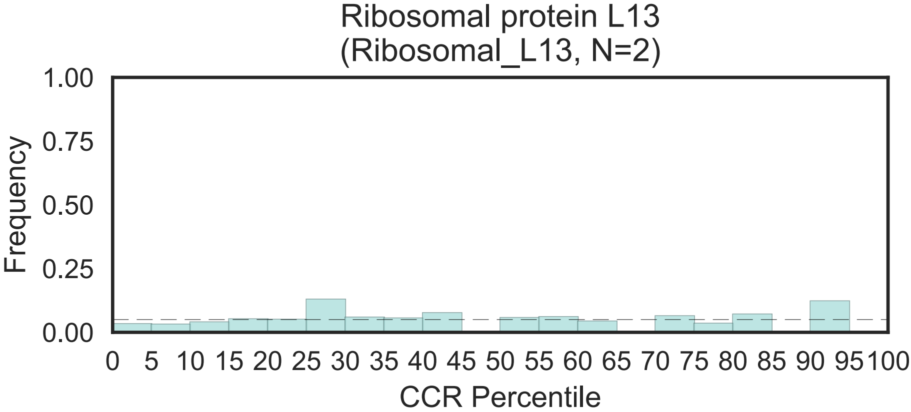
Ribosomal protein L10
(Ribosomal_L10, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

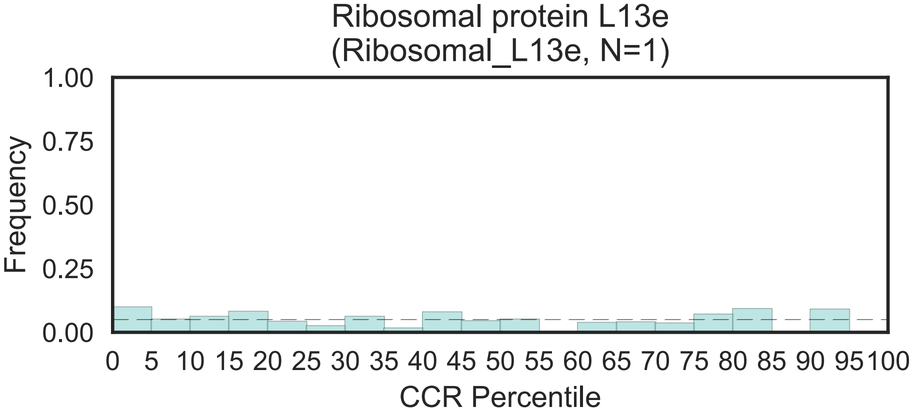

Ribosomal protein L11, RNA binding domain
(Ribosomal_L11, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

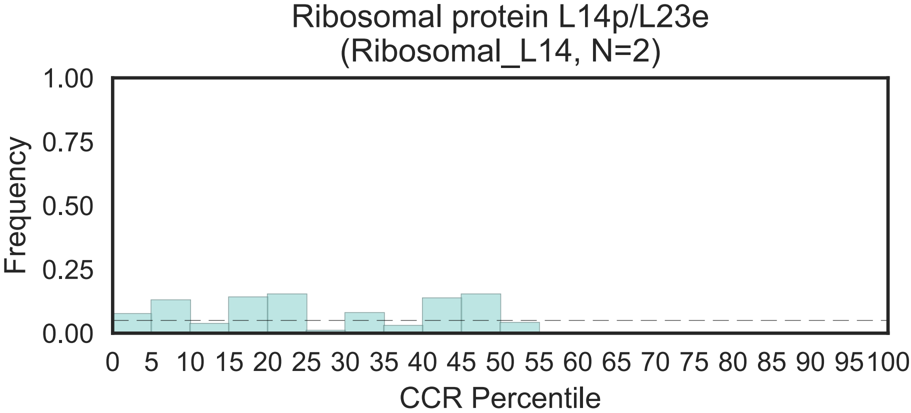

Ribosomal protein L11, N-terminal domain
(Ribosomal_L11_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

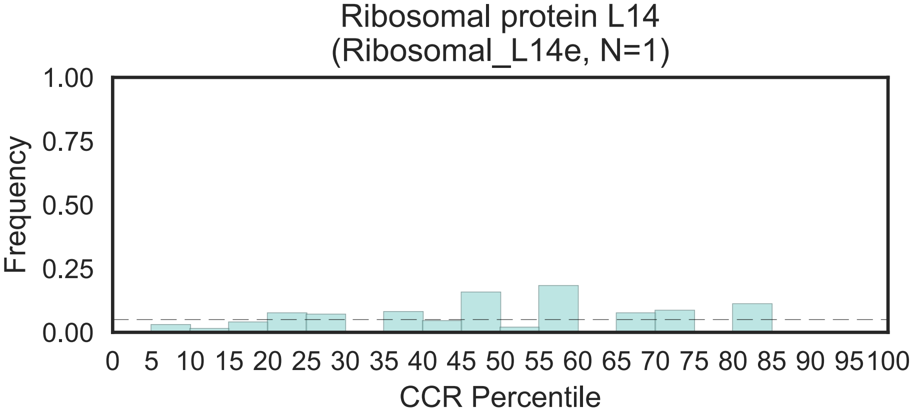

Ribosomal protein L7/L12 C-terminal domain
(Ribosomal_L12, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

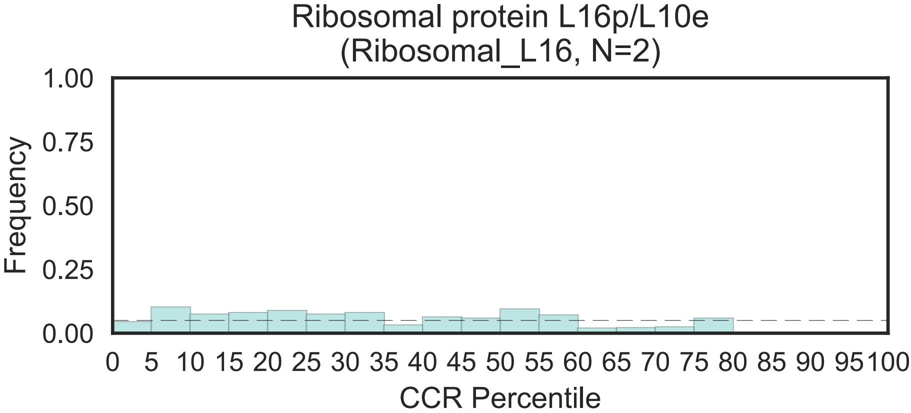

Ribosomal protein L7/L12 dimerisation domain
(Ribosomal_L12_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

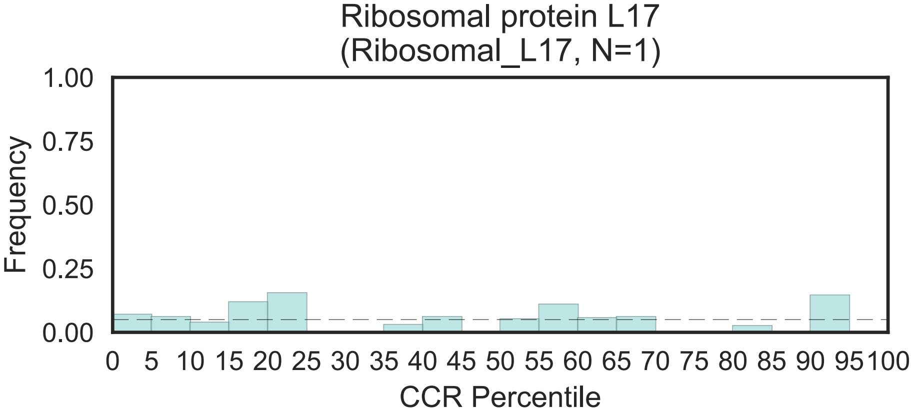

Ribosomal protein L13
(Ribosomal_L13, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

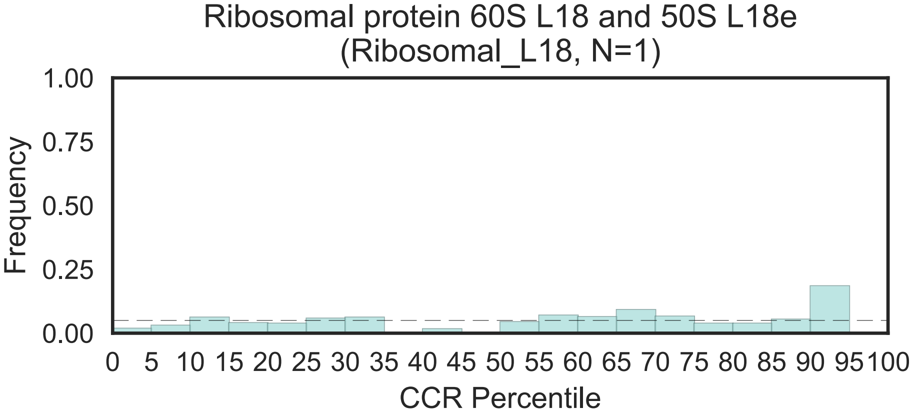

Ribosomal protein L13e
(Ribosomal_L13e, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

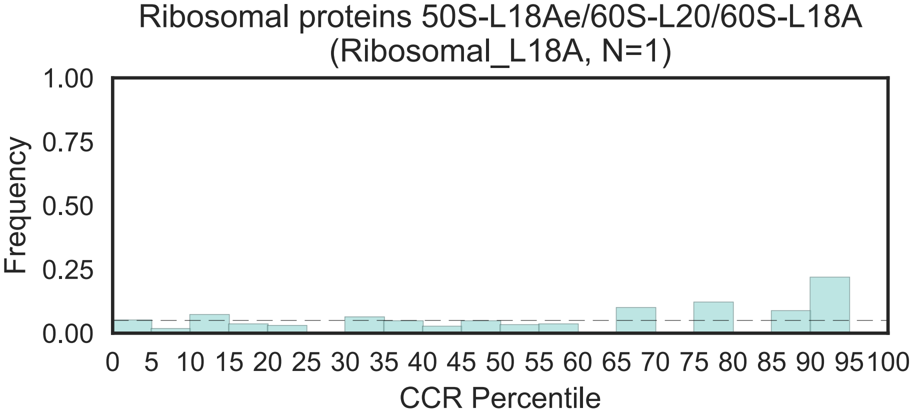

Ribosomal protein L14p/L23e
(Ribosomal_L14, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

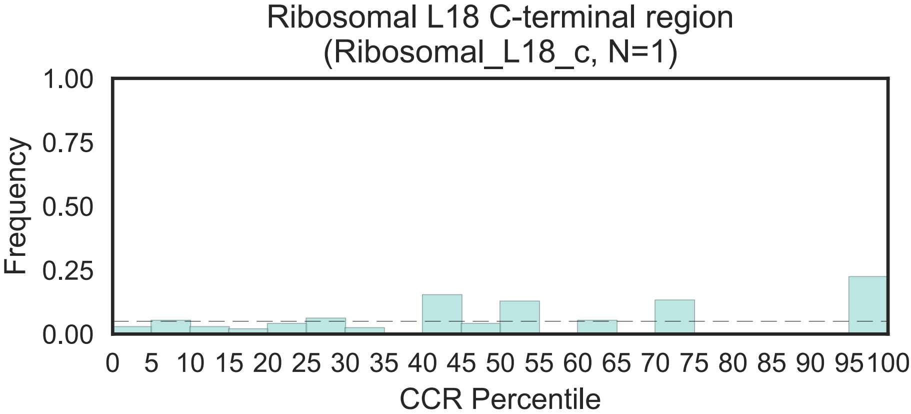

Ribosomal protein L14
(Ribosomal_L14e, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribosomal protein L16p/L10e
(Ribosomal_L16, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribosomal protein L17
(Ribosomal_L17, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribosomal protein 60S L18 and 50S L18e
(Ribosomal_L18, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribosomal proteins 50S-L18Ae/60S-L20/60S-L18A
(Ribosomal_L18A, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribosomal L18 C-terminal region
(Ribosomal_L18_c, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
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35
40
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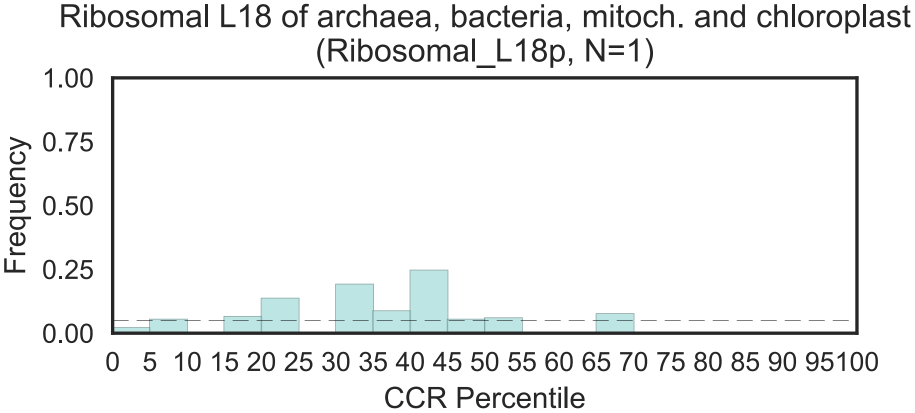
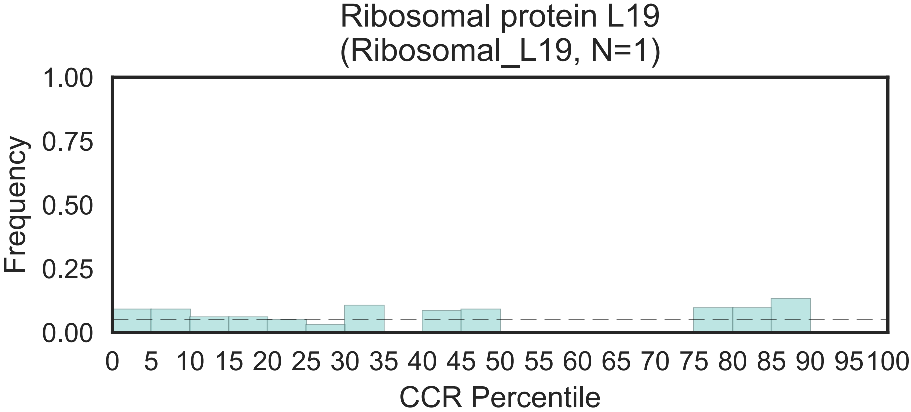
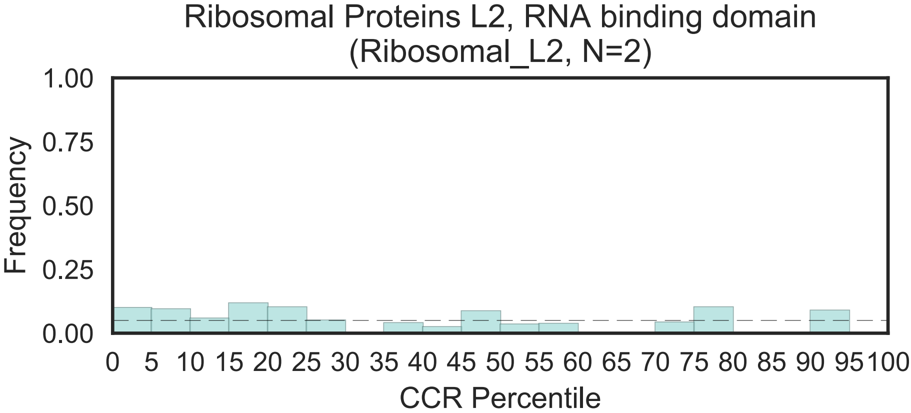
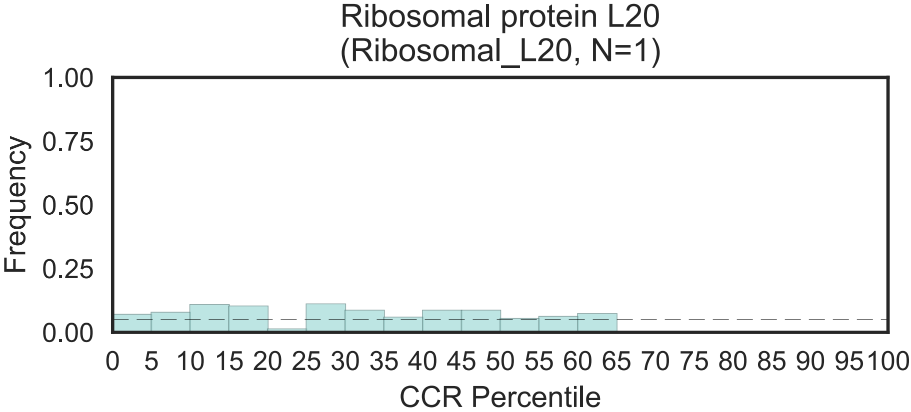
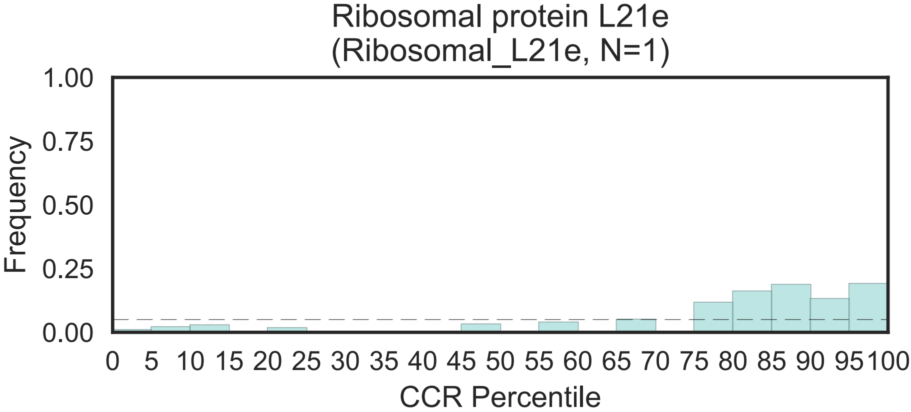
55
60
65
70
75
80
85
90
95
100
CCR Percentile

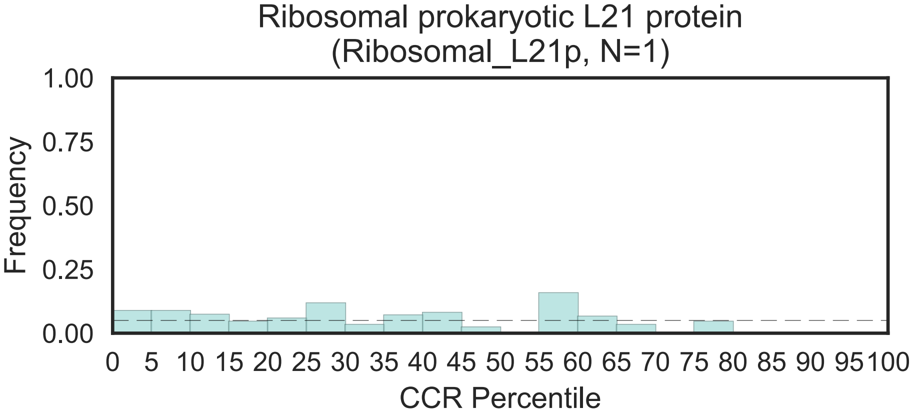

Ribosomal L18 of archaea, bacteria, mitoch. and chloroplast
(Ribosomal_L18p, N=1)

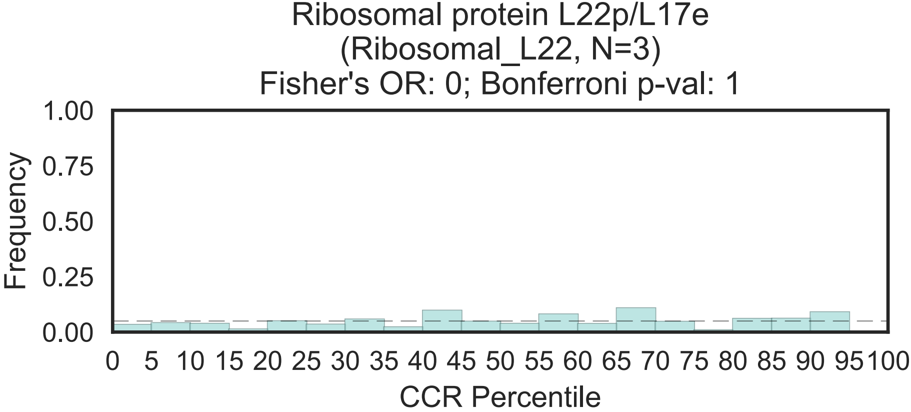

Ribosomal protein L19
(Ribosomal_L19, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

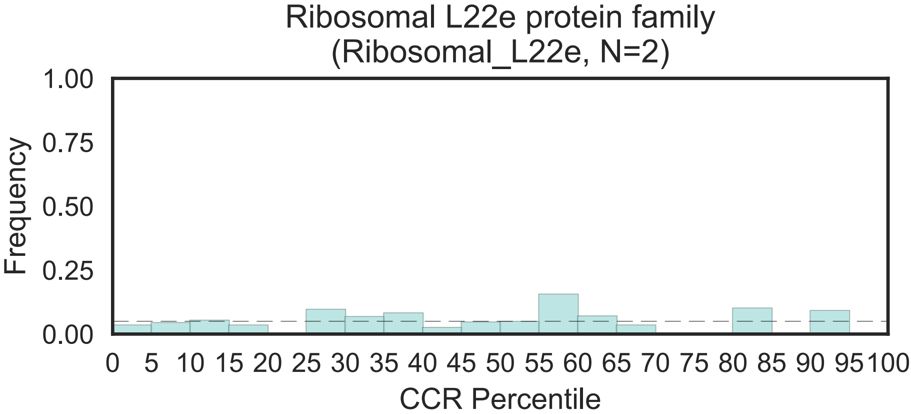

Ribosomal Proteins L2, RNA binding domain
(Ribosomal_L2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

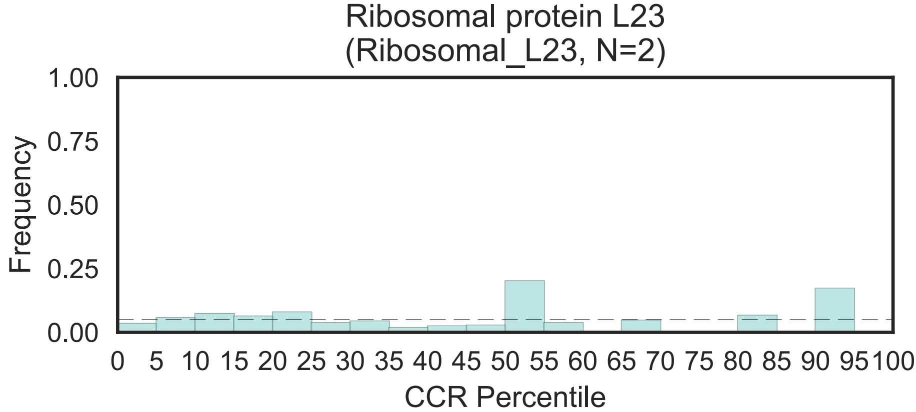

Ribosomal protein L20
(Ribosomal_L20, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

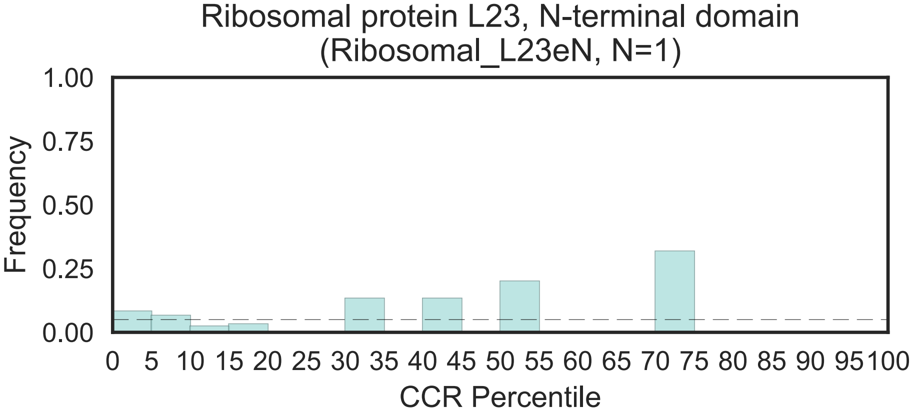

Ribosomal protein L21e
(Ribosomal_L21e, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

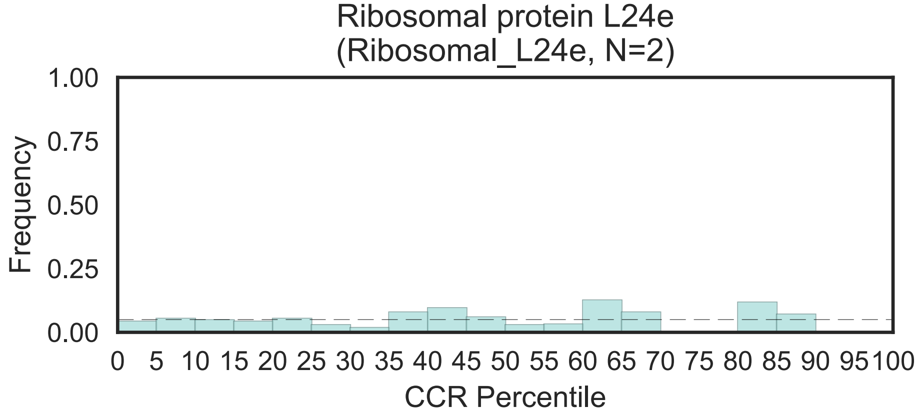

Ribosomal prokaryotic L21 protein
(Ribosomal_L21p, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

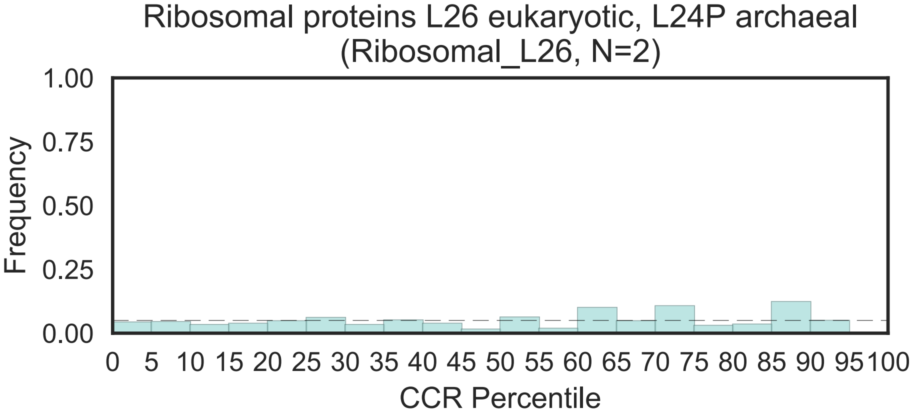

Ribosomal protein L22p/L17e
(Ribosomal_L22, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

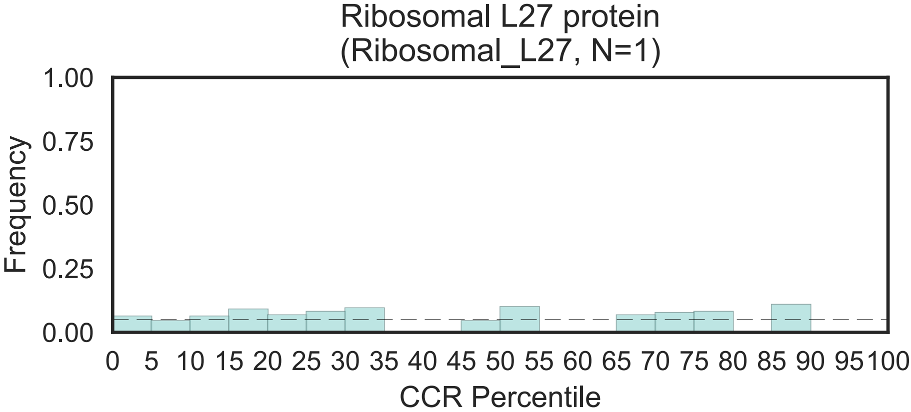

Ribosomal L22e protein family
(Ribosomal_L22e, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

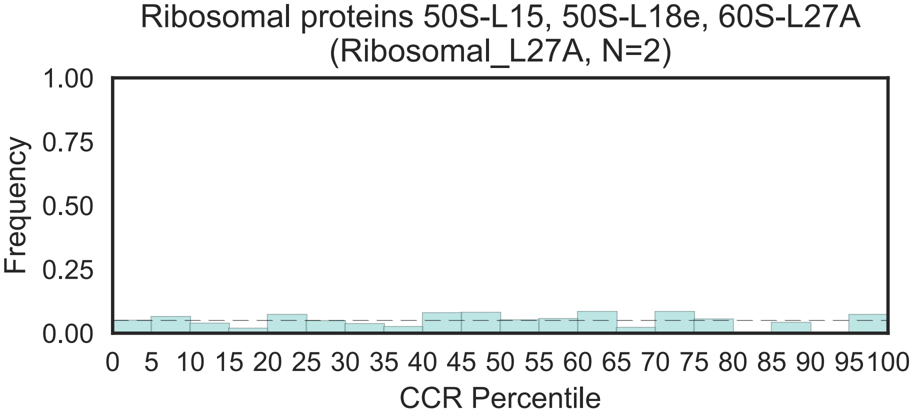

Ribosomal protein L23
(Ribosomal_L23, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

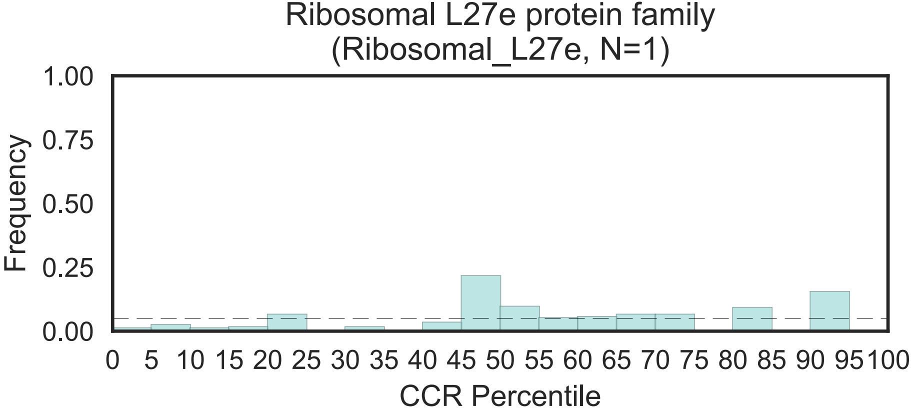
Ribosomal protein L23, N-terminal domain
(Ribosomal_L23eN, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

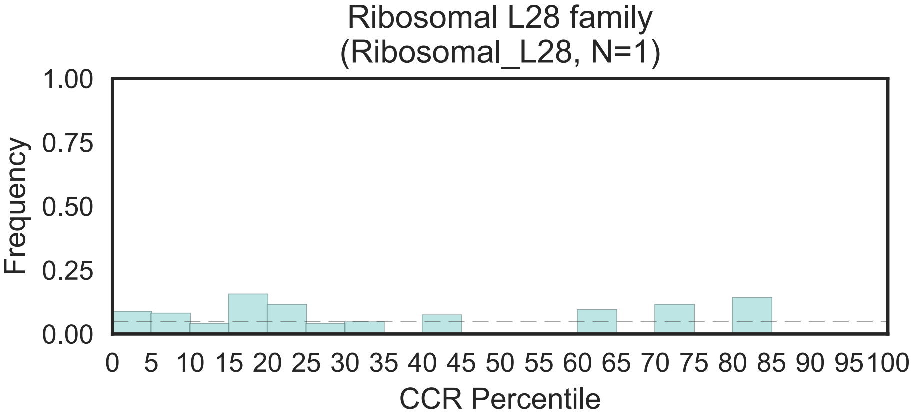

Ribosomal protein L24e
(Ribosomal_L24e, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

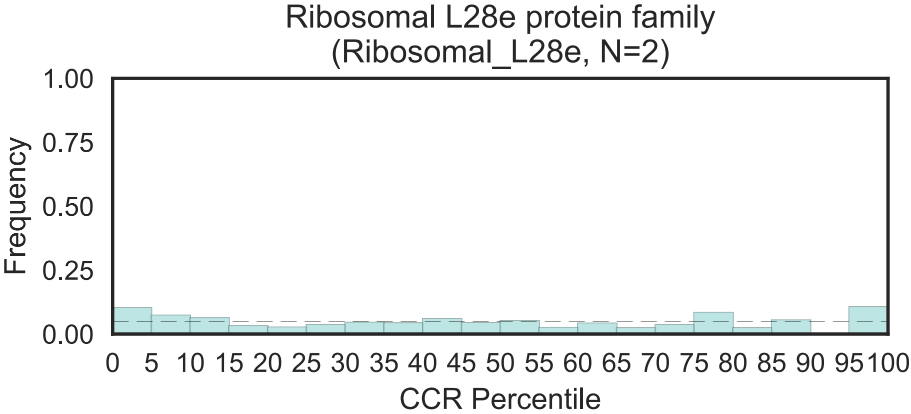

Ribosomal proteins L26 eukaryotic, L24P archaeal
(Ribosomal_L26, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

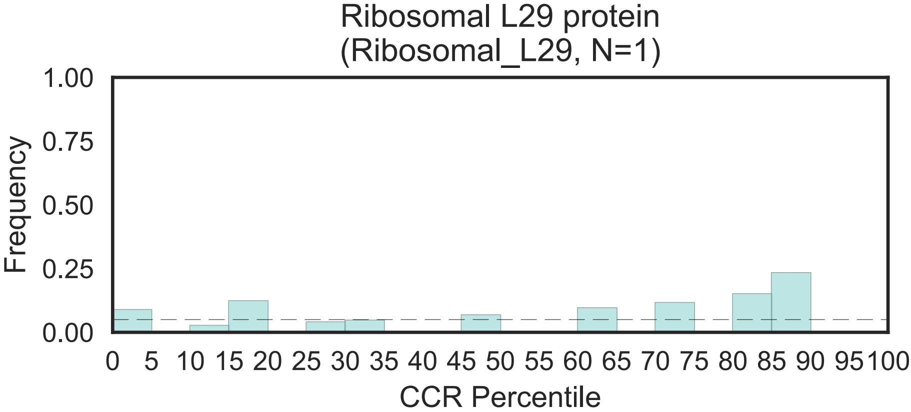

Ribosomal L27 protein
(Ribosomal_L27, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

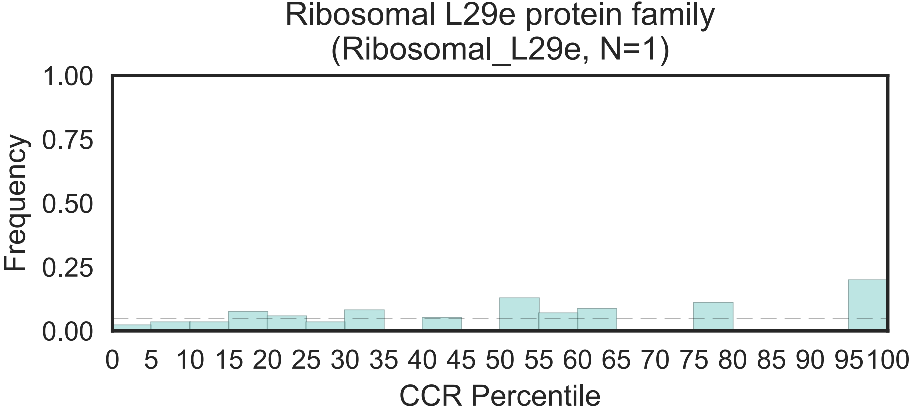

Ribosomal proteins 50S-L15, 50S-L18e, 60S-L27A
(Ribosomal_L27A, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

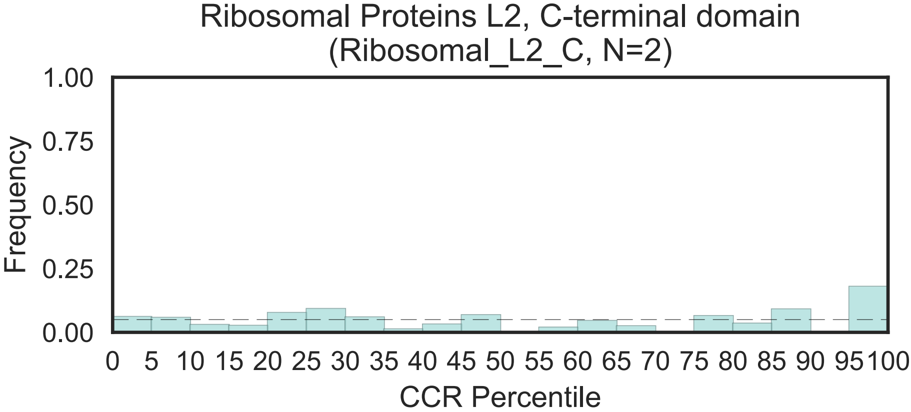

Ribosomal L27e protein family
(Ribosomal_L27e, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

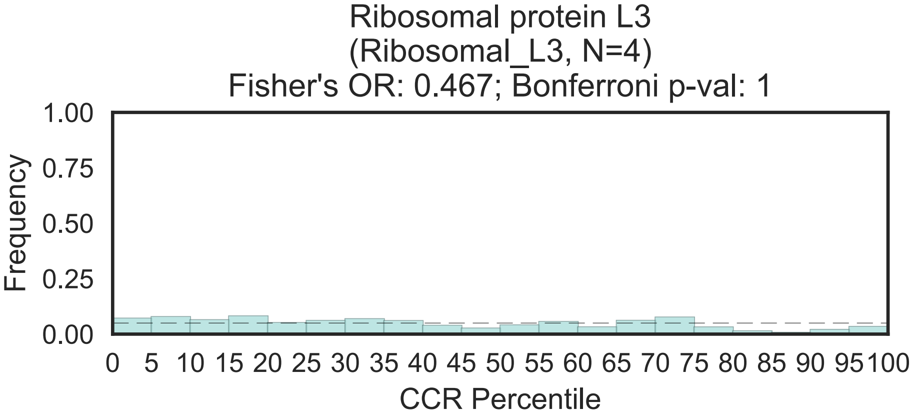

Ribosomal L28 family
(Ribosomal_L28, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

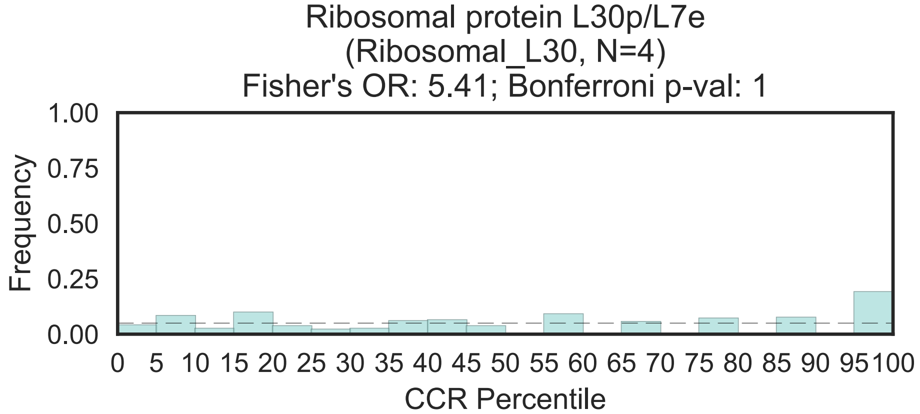

Ribosomal L28e protein family
(Ribosomal_L28e, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribosomal L29 protein
(Ribosomal_L29, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribosomal L29e protein family
(Ribosomal_L29e, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribosomal Proteins L2, C-terminal domain
(Ribosomal_L2_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribosomal protein L3
(Ribosomal_L3, N=4)
Fisher's OR: 0.467; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribosomal protein L30p/L7e
(Ribosomal_L30, N=4)
Fisher's OR: 5.41; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
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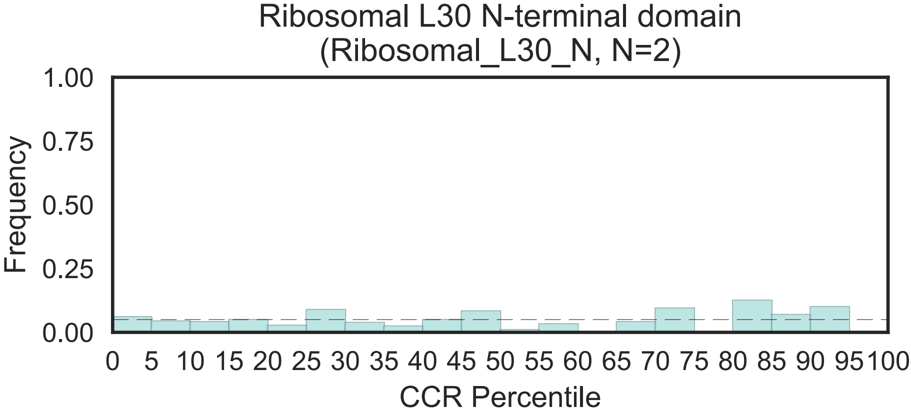
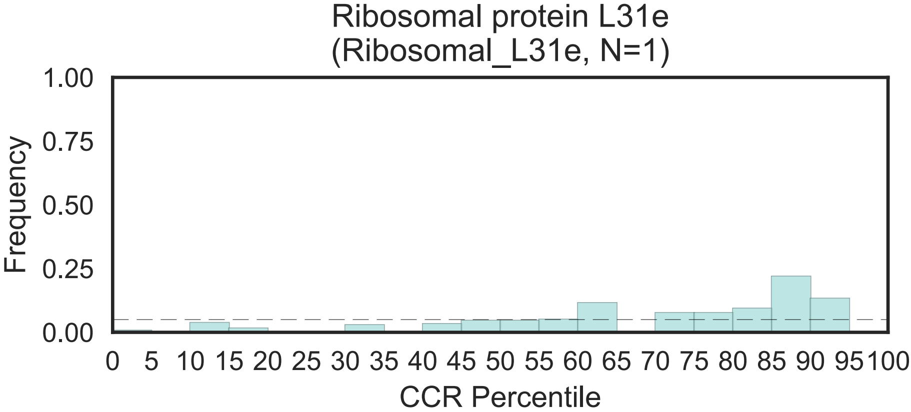
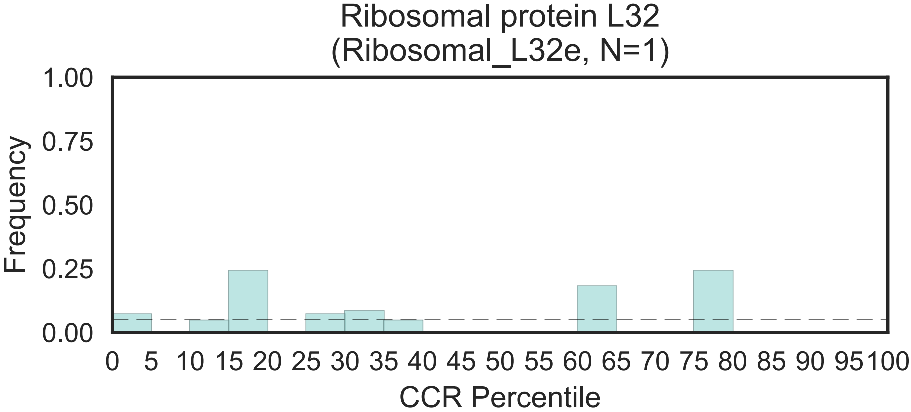
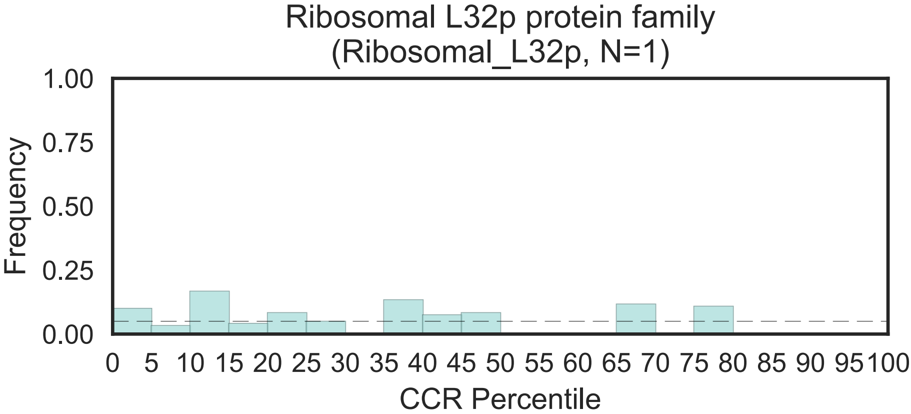
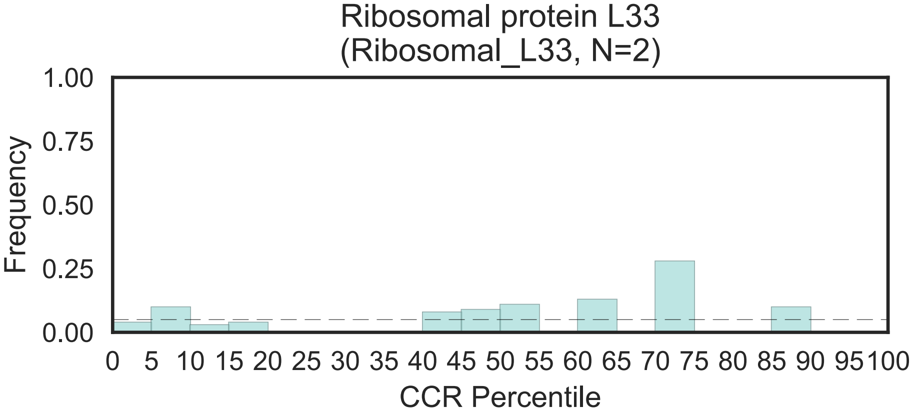
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

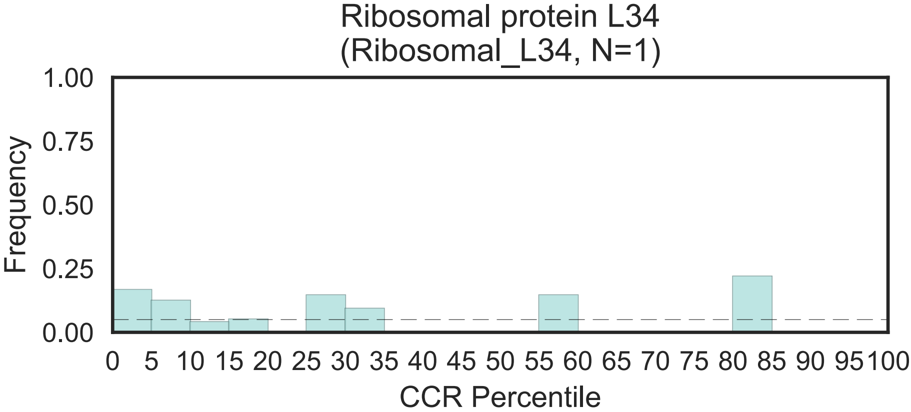

Ribosomal L30 N-terminal domain
(Ribosomal_L30_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

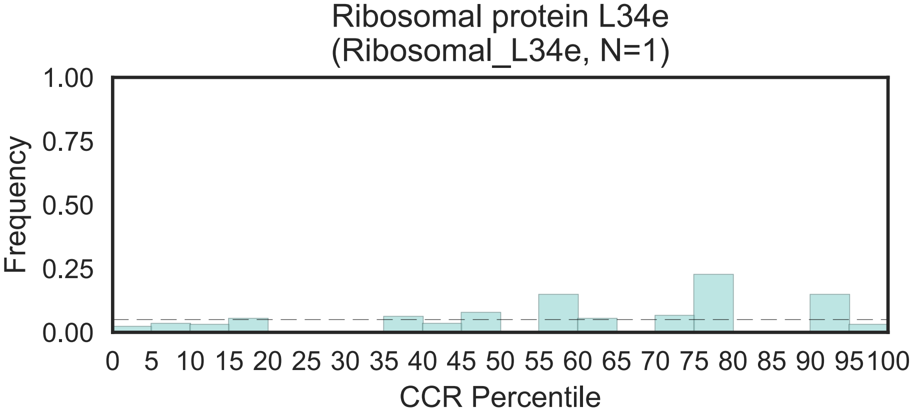

Ribosomal protein L31e
(Ribosomal_L31e, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

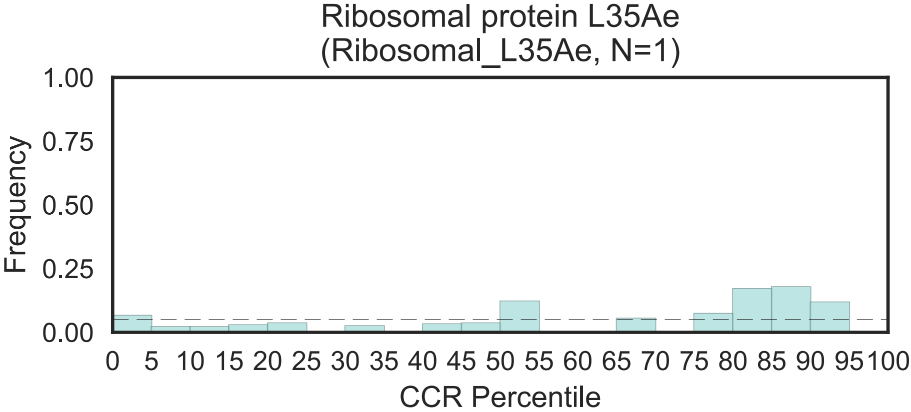

Ribosomal protein L32
(Ribosomal_L32e, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

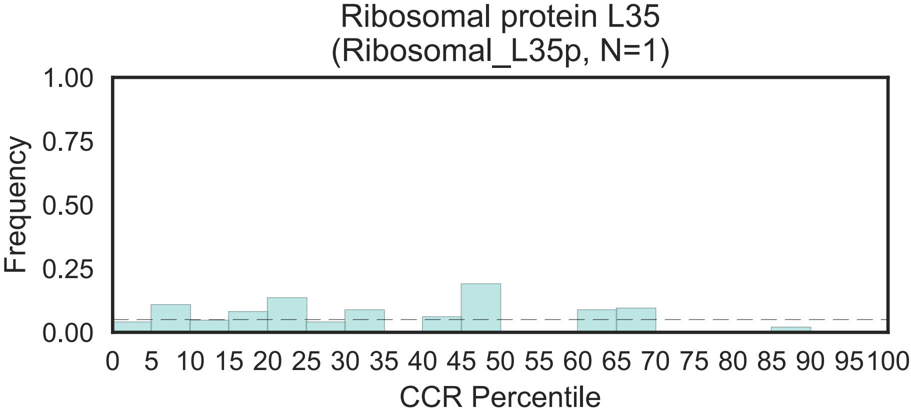

Ribosomal L32p protein family
(Ribosomal_L32p, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribosomal protein L33
(Ribosomal_L33, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribosomal protein L34
(Ribosomal_L34, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribosomal protein L34e
(Ribosomal_L34e, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


Ribosomal protein L35Ae
(Ribosomal_L35Ae, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribosomal protein L35
(Ribosomal_L35p, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
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15
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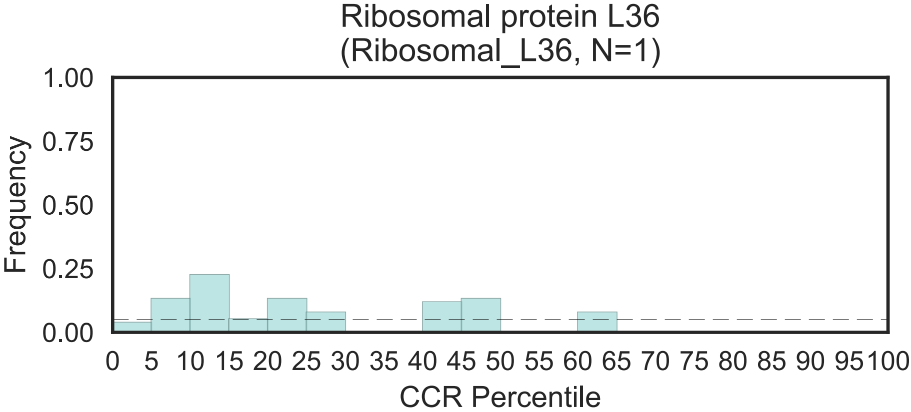
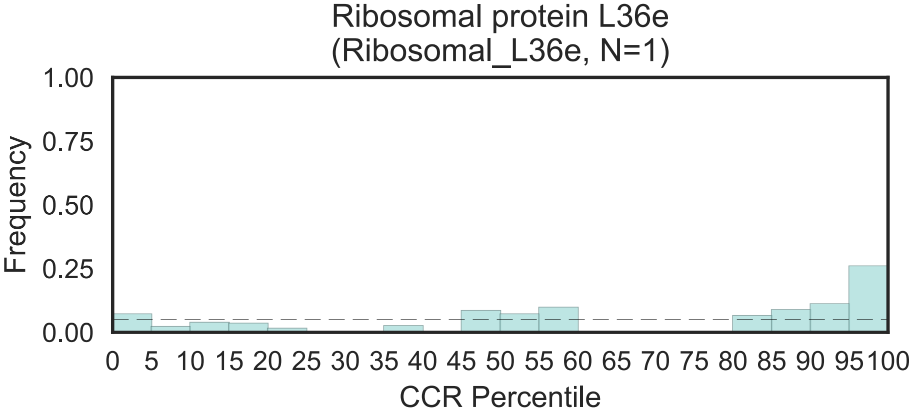
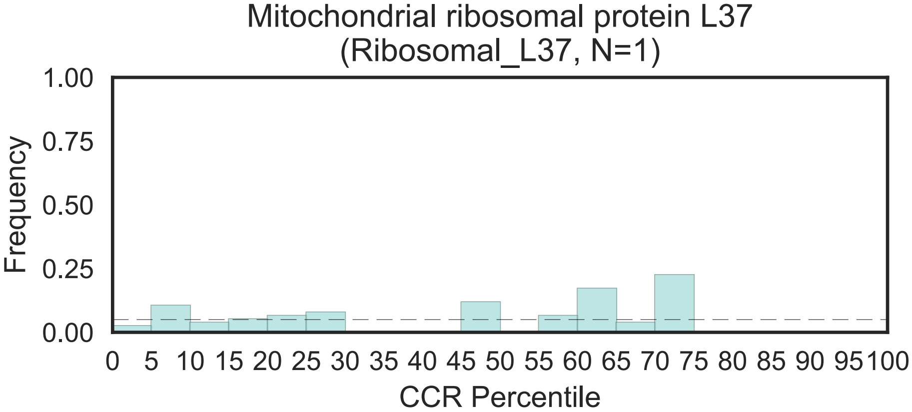
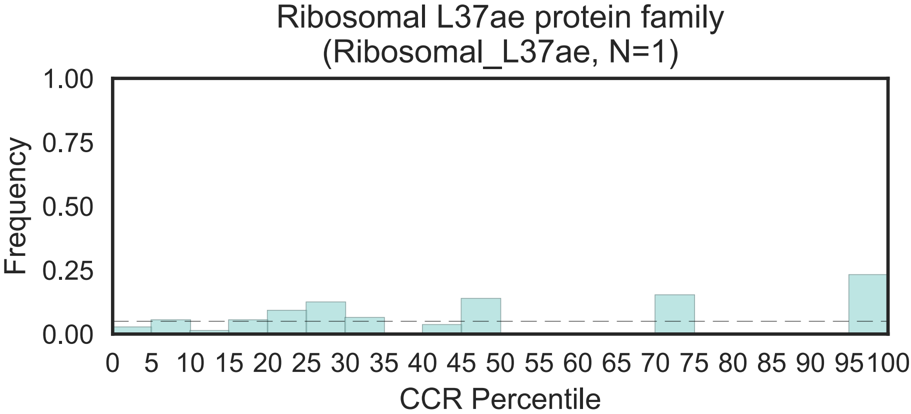
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

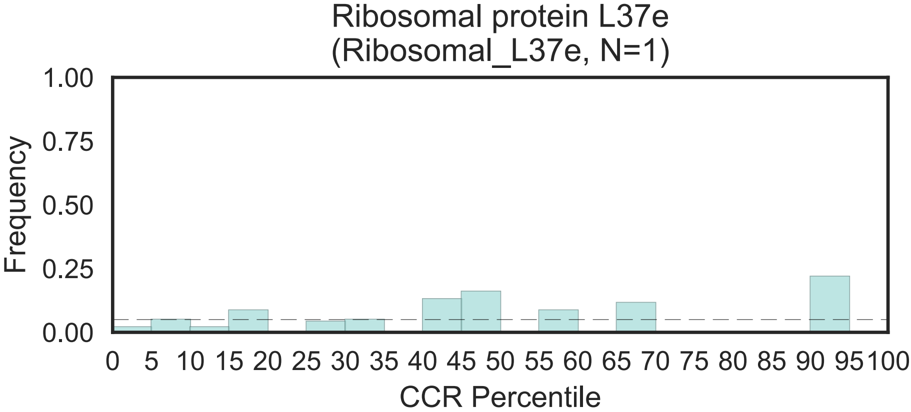


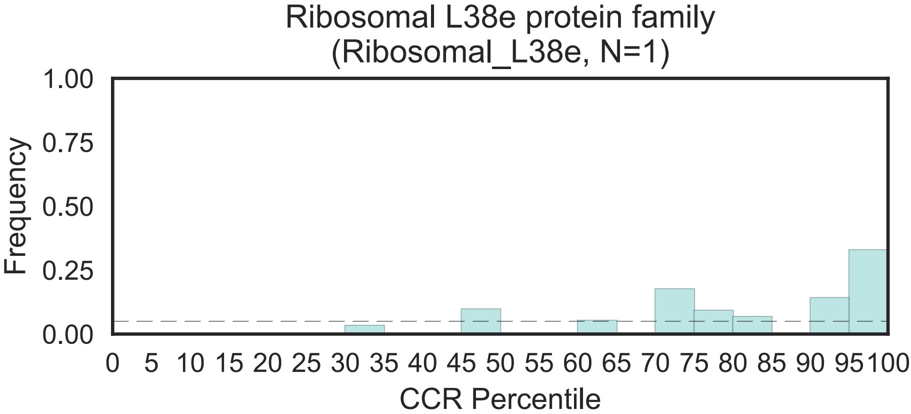
Ribosomal protein L36
(Ribosomal_L36, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

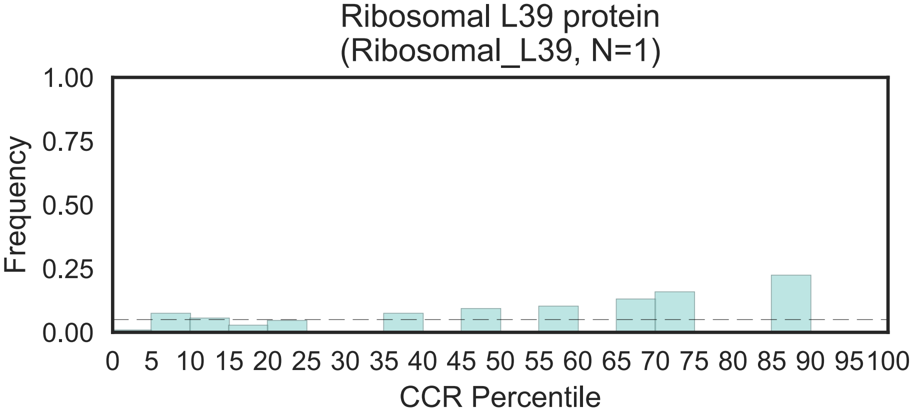

Ribosomal protein L36e
(Ribosomal_L36e, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

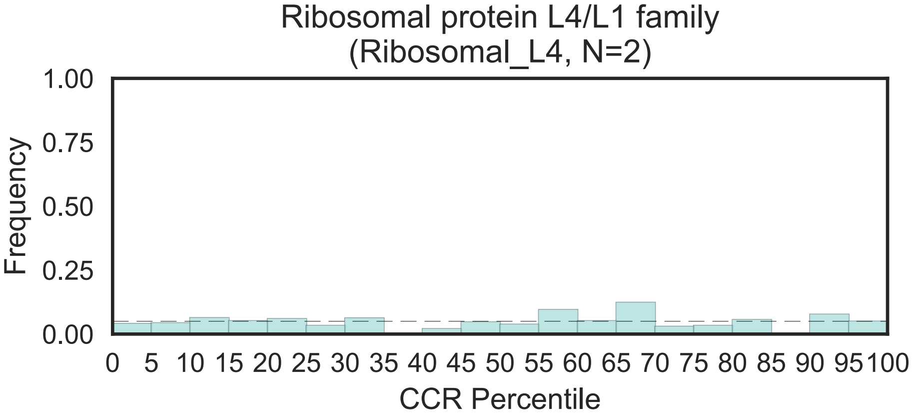

Mitochondrial ribosomal protein L37
(Ribosomal_L37, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

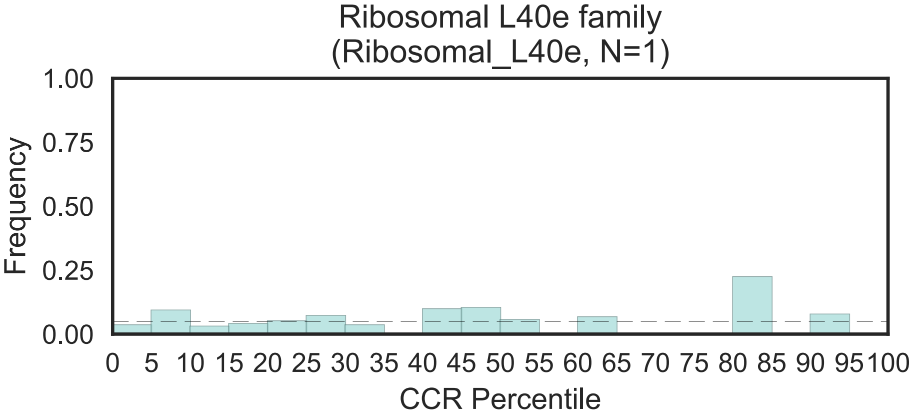

Ribosomal L37ae protein family
(Ribosomal_L37ae, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribosomal protein L37e
(Ribosomal_L37e, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

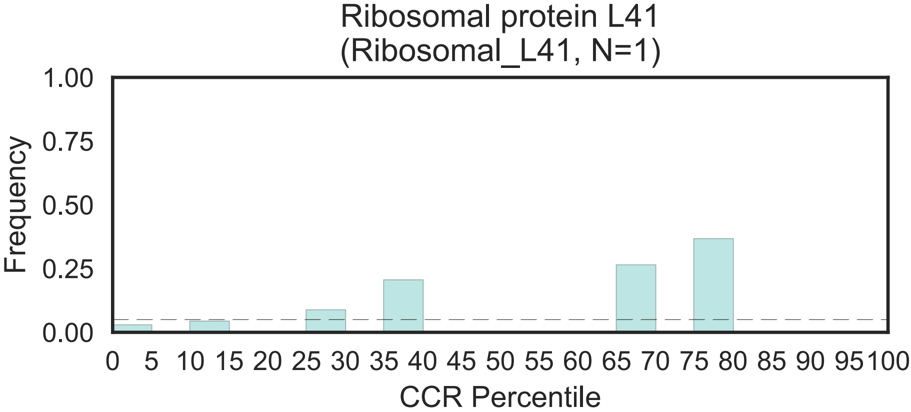

Ribosomal L38e protein family
(Ribosomal_L38e, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribosomal L39 protein
(Ribosomal_L39, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

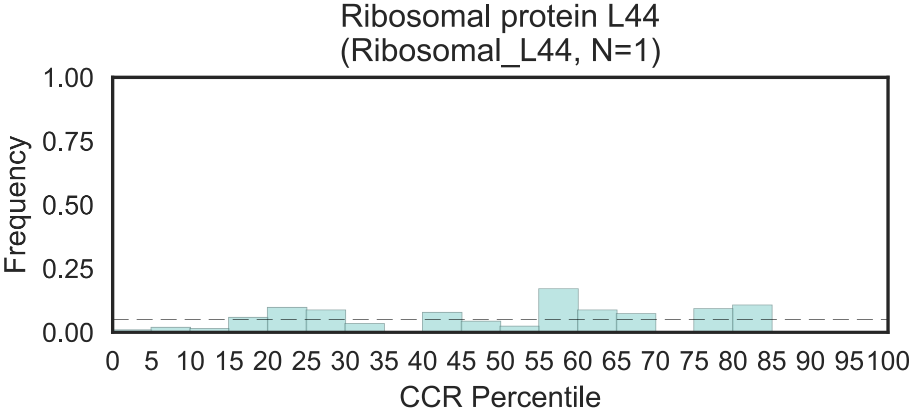

Ribosomal protein L4/L1 family
(Ribosomal_L4, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

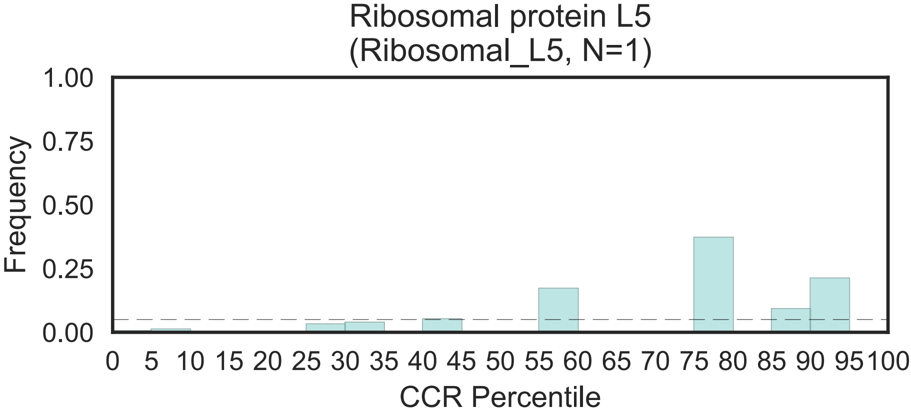


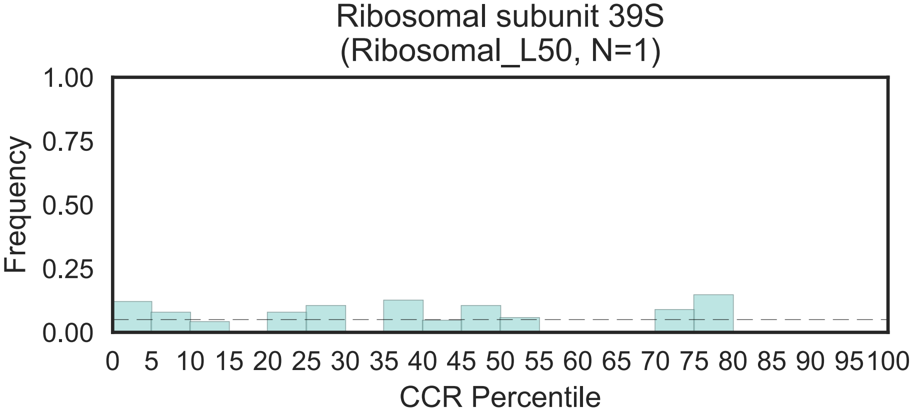
Ribosomal L40e family
(Ribosomal_L40e, N=1)

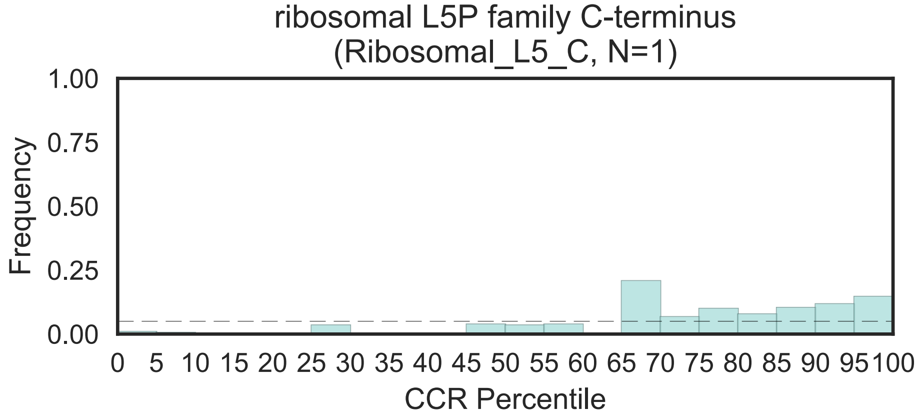


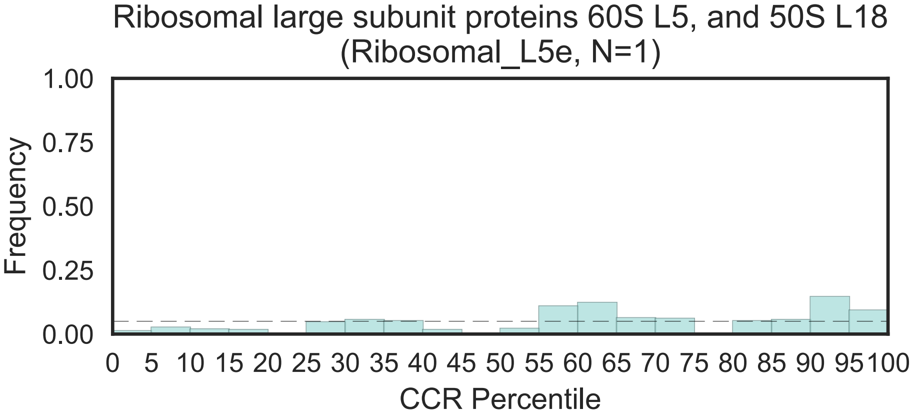
Ribosomal protein L41
(Ribosomal_L41, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

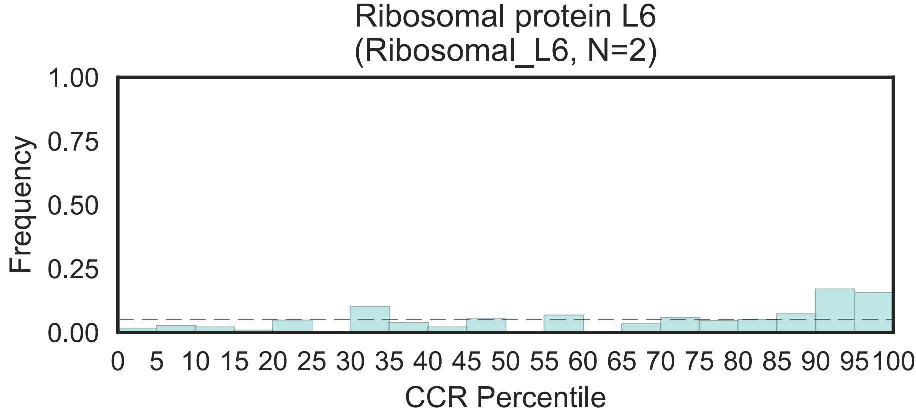

Ribosomal protein L44
(Ribosomal_L44, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

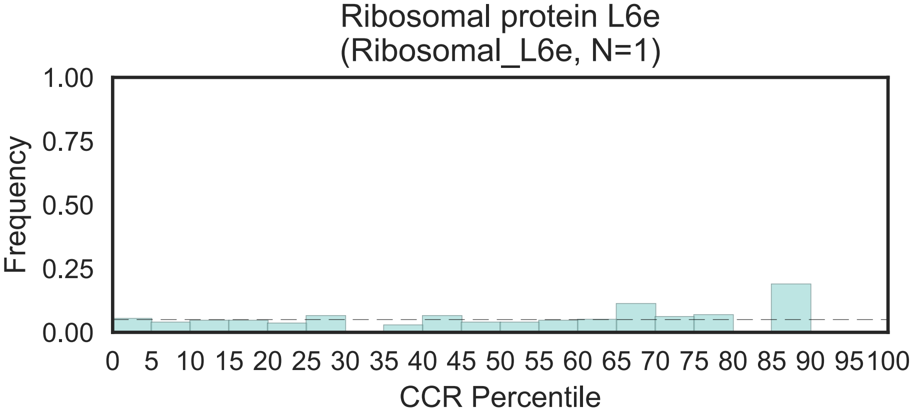

Ribosomal protein L5
(Ribosomal_L5, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

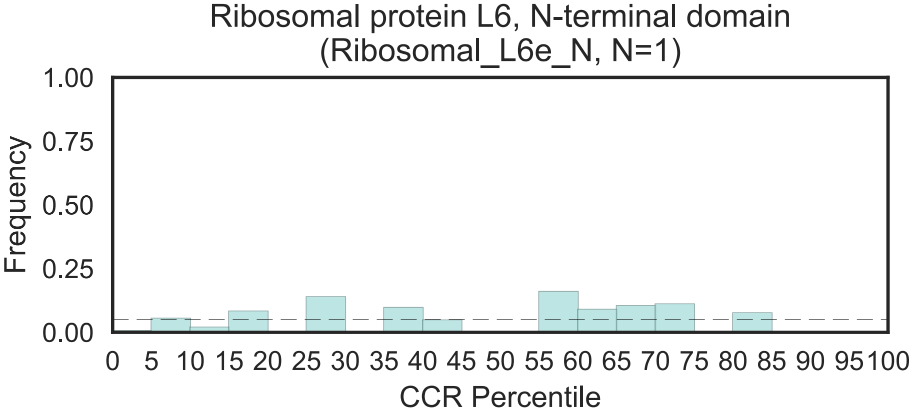

Ribosomal subunit 39S
(Ribosomal_L50, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

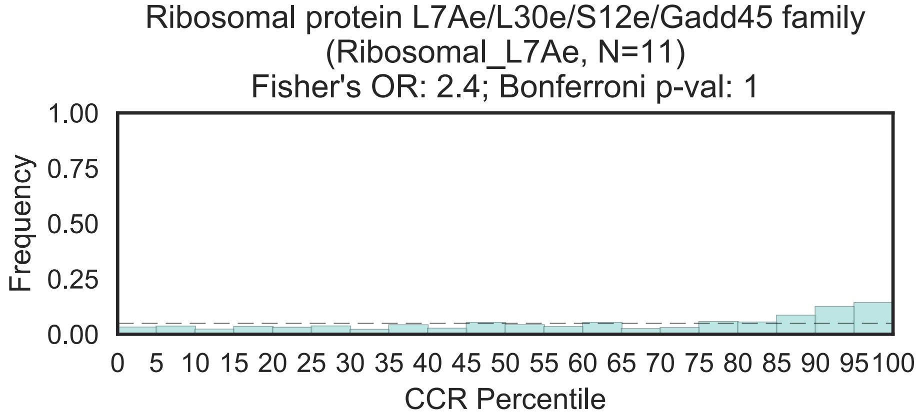

ribosomal L5P family C-terminus
(Ribosomal_L5_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

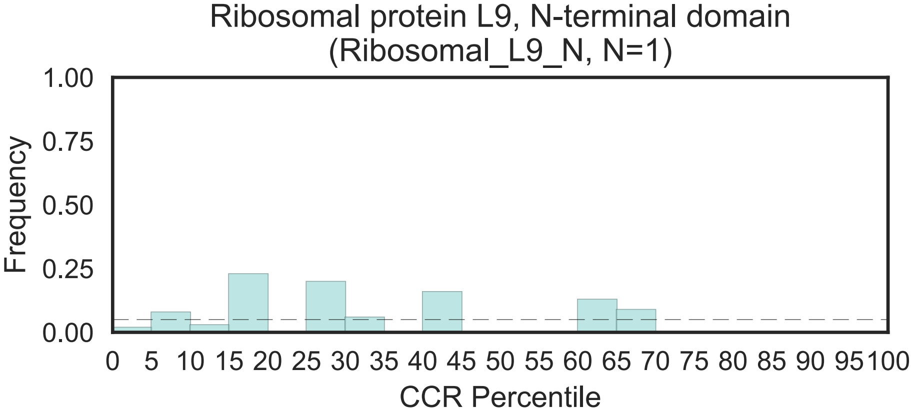

Ribosomal large subunit proteins 60S L5, and 50S L18
(Ribosomal_L5e, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

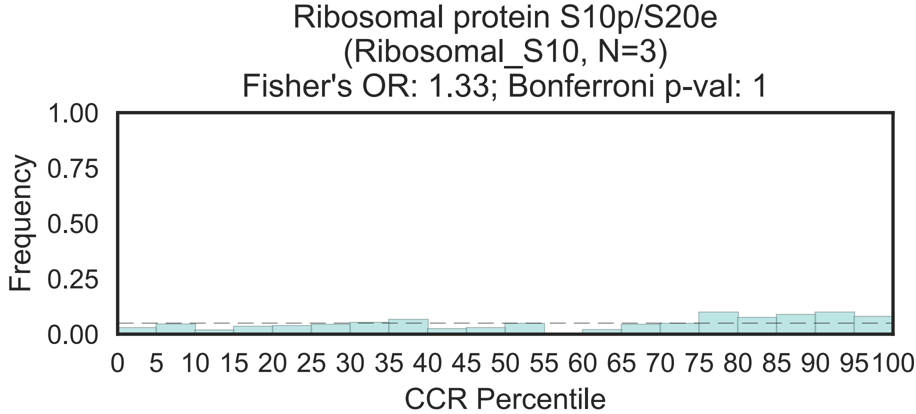

Ribosomal protein L6
(Ribosomal_L6, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

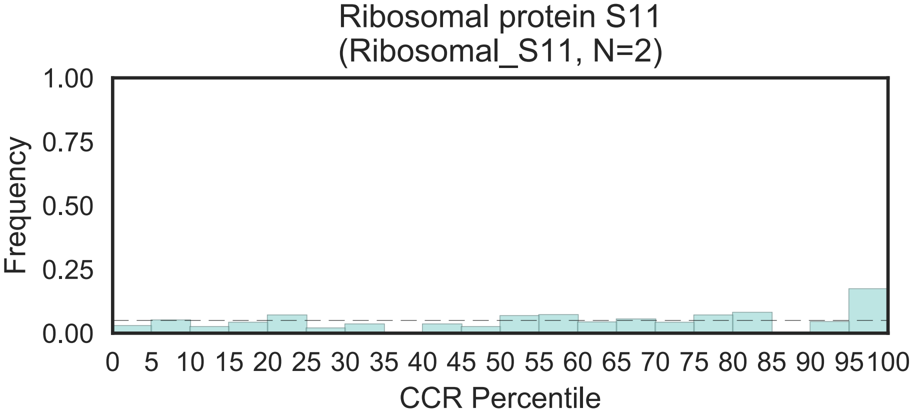

Ribosomal protein L6e
(Ribosomal_L6e, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

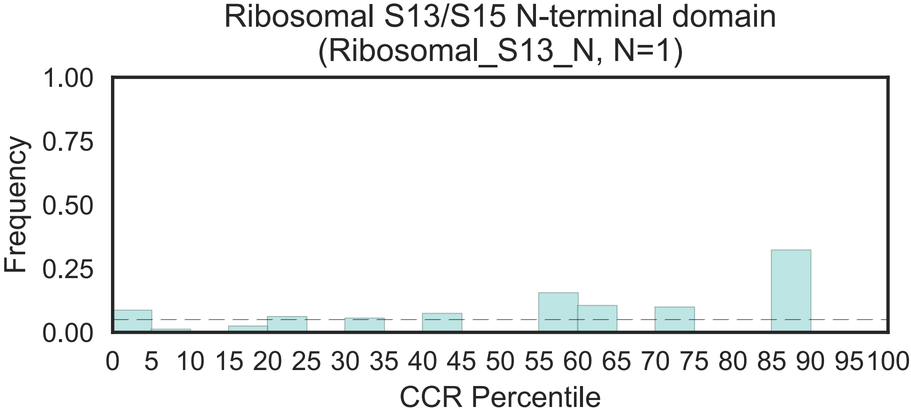

Ribosomal protein L6, N-terminal domain
(Ribosomal_L6e_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribosomal protein L7Ae/L30e/S12e/Gadd45 family
(Ribosomal_L7Ae, N=11)
Fisher's OR: 2.4; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

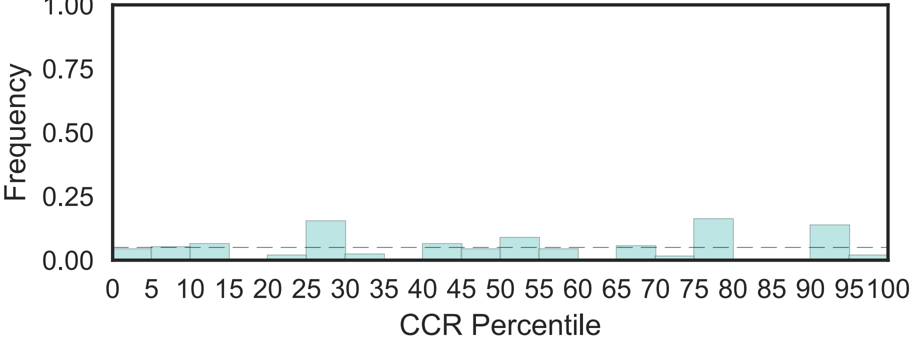

Ribosomal protein L9, N-terminal domain
(Ribosomal_L9_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

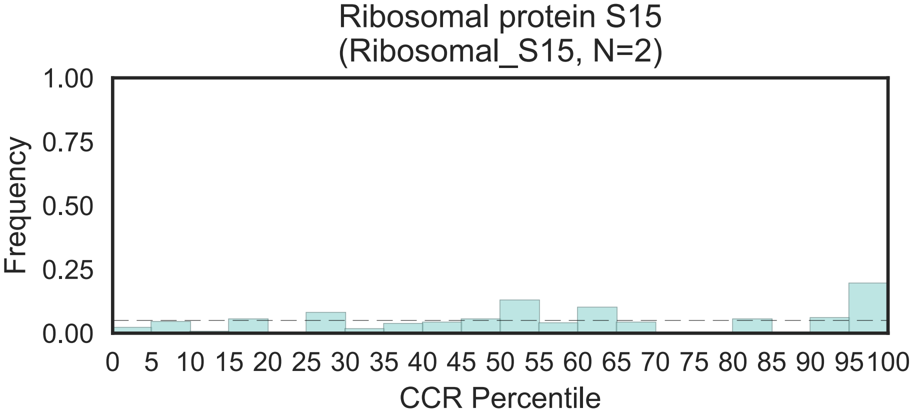

Ribosomal protein S10p/S20e
(Ribosomal_S10, N=3)
Fisher's OR: 1.33; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

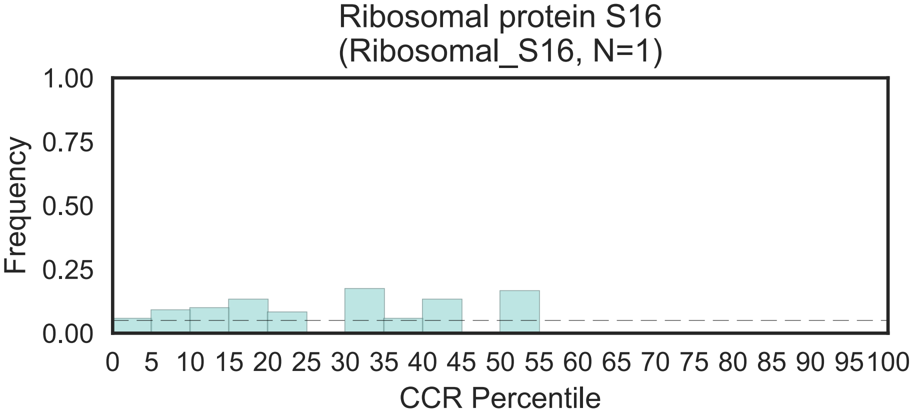

Ribosomal protein S11
(Ribosomal_S11, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

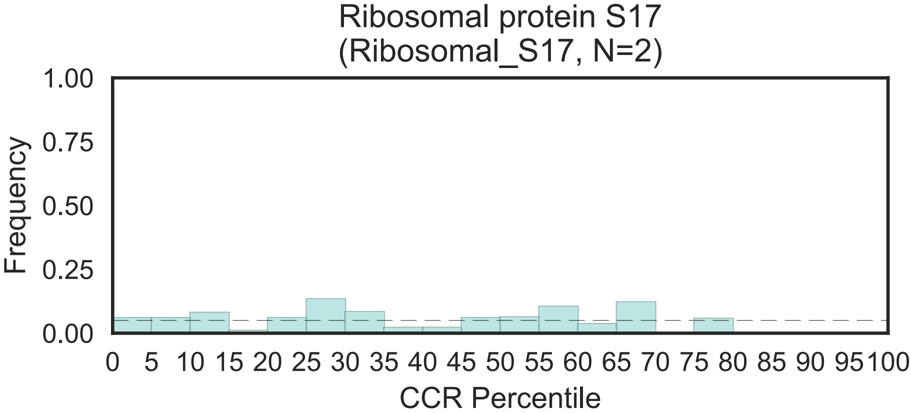

Ribosomal S13/S15 N-terminal domain
(Ribosomal_S13_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

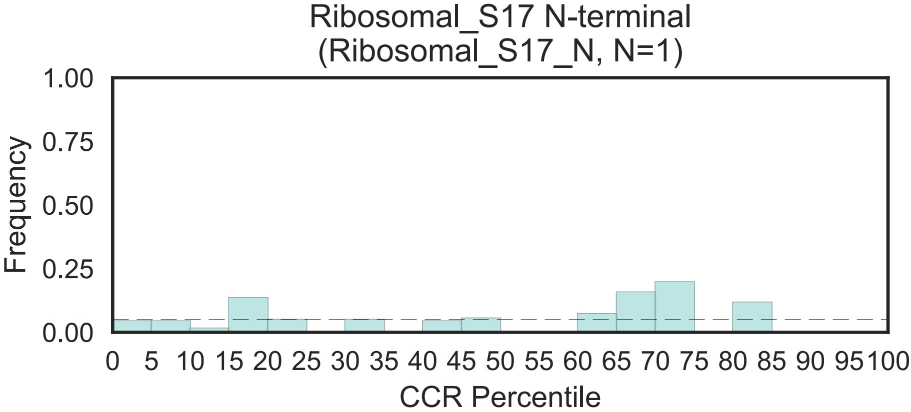
Ribosomal protein S14p/S29e (Ribosomal_S14, N=2)

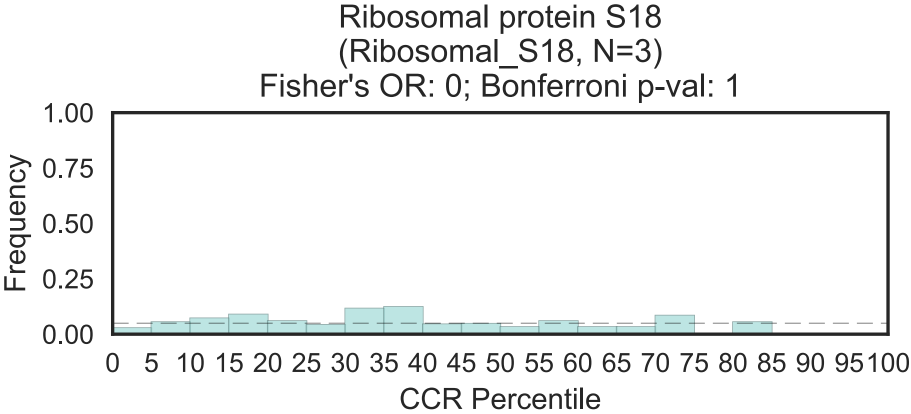



Ribosomal protein S15
(Ribosomal_S15, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

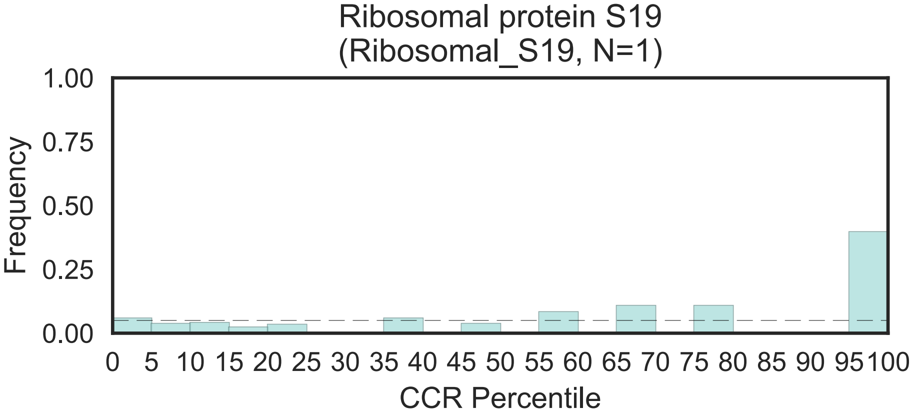

Ribosomal protein S16
(Ribosomal_S16, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

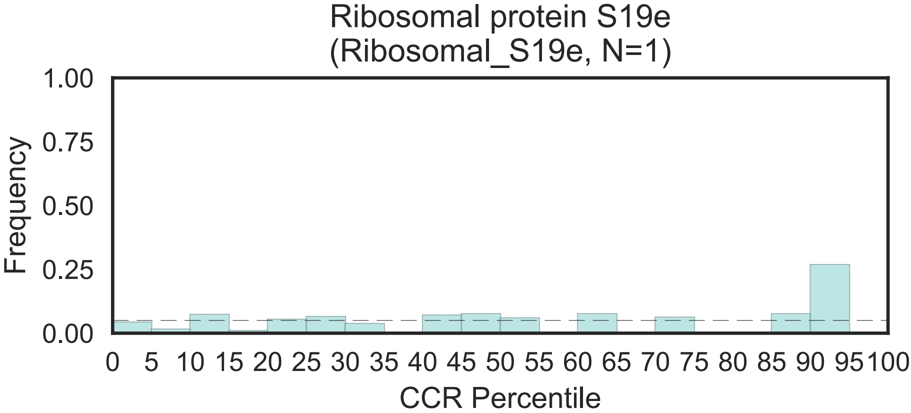

Ribosomal protein S17
(Ribosomal_S17, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribosomal_S17 N-terminal
(Ribosomal_S17_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

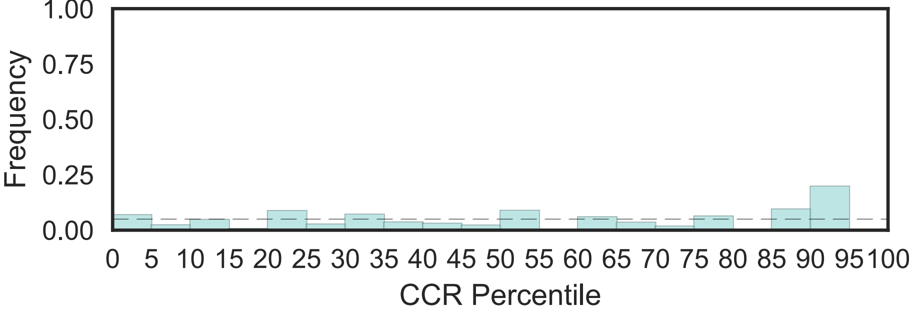


Ribosomal protein S18
(Ribosomal_S18, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

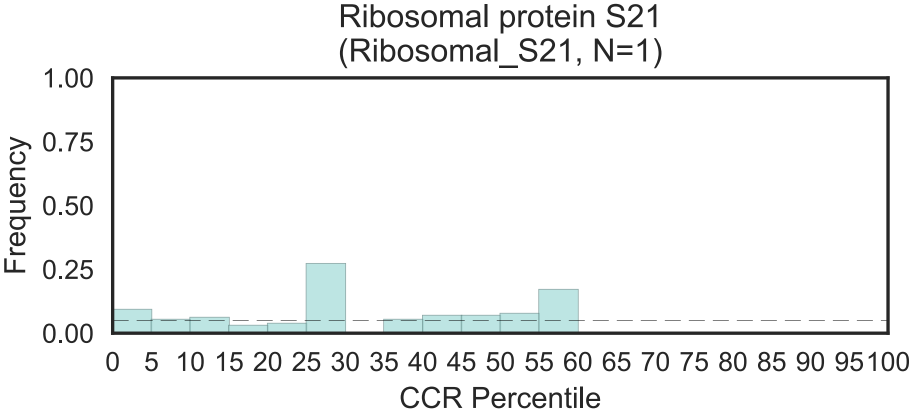

Ribosomal protein S19
(Ribosomal_S19, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

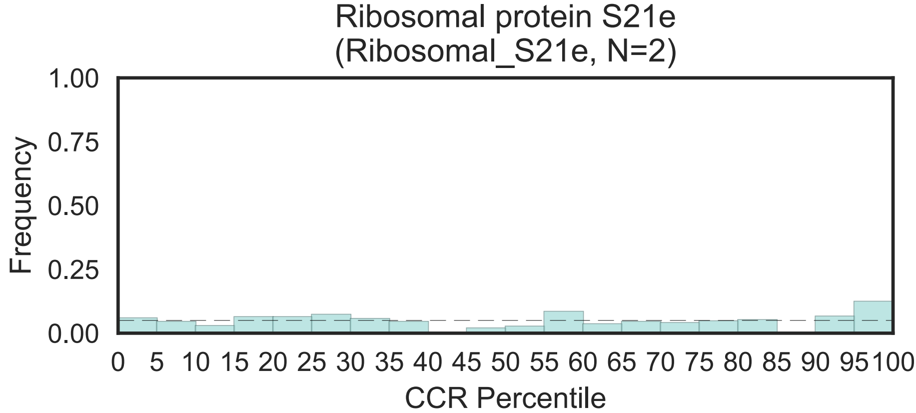


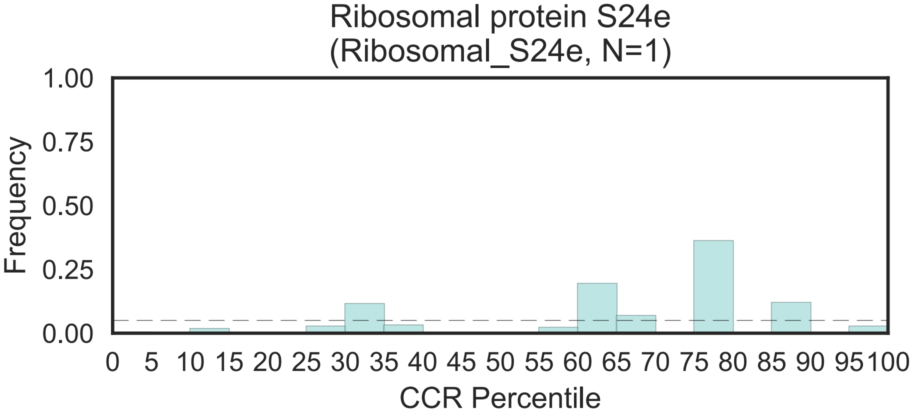
Ribosomal protein S19e
(Ribosomal_S19e, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

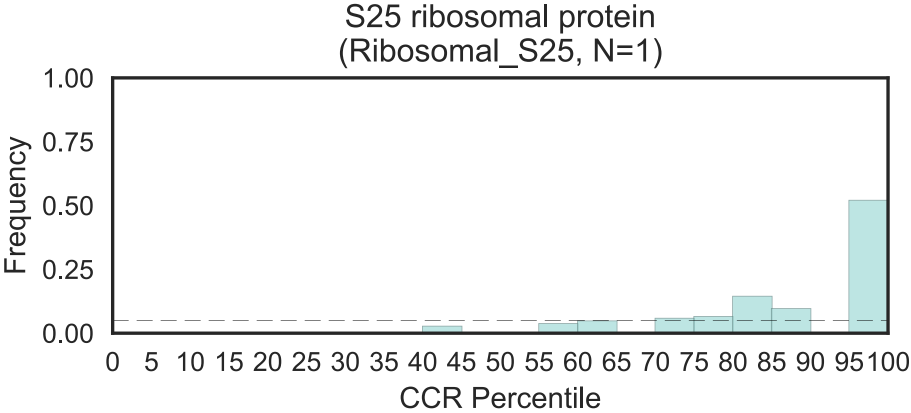


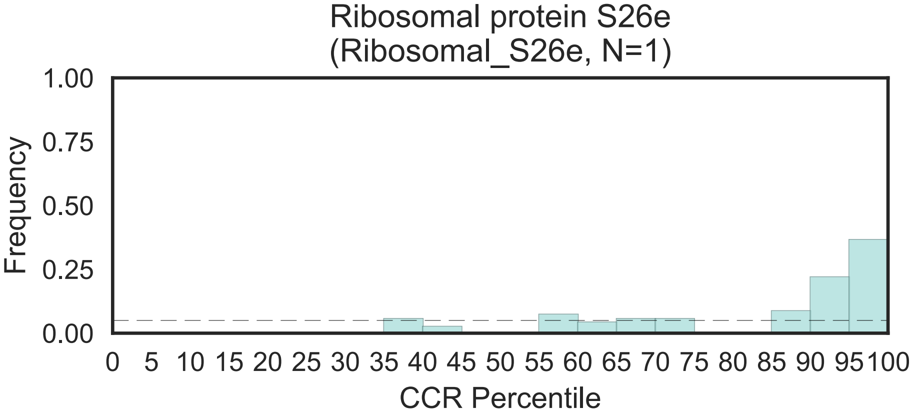
Ribosomal protein S2
(Ribosomal_S2, N=6)
Fisher's OR: 0; Bonferroni p-val: 1

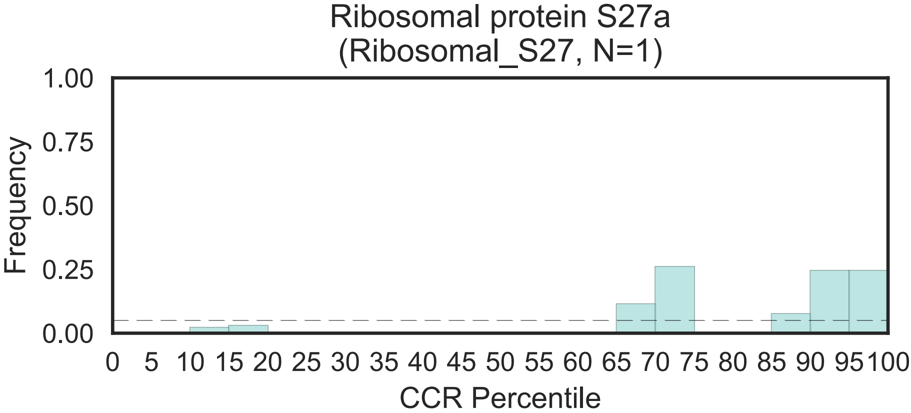

Ribosomal protein S21
(Ribosomal_S21, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

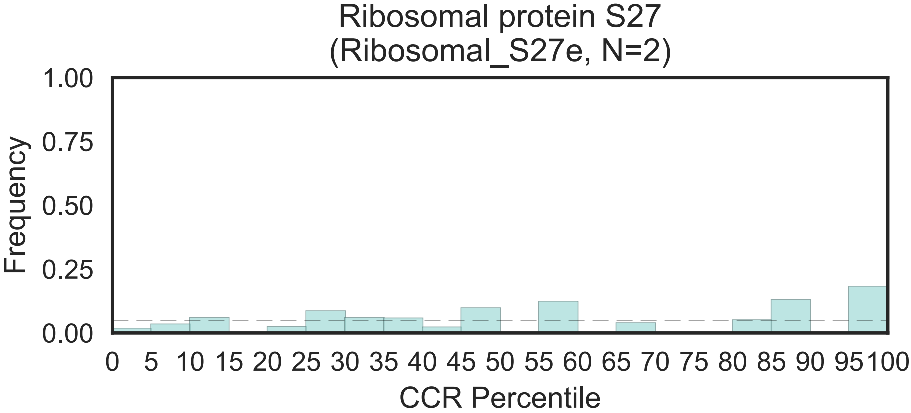

Ribosomal protein S21e
(Ribosomal_S21e, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

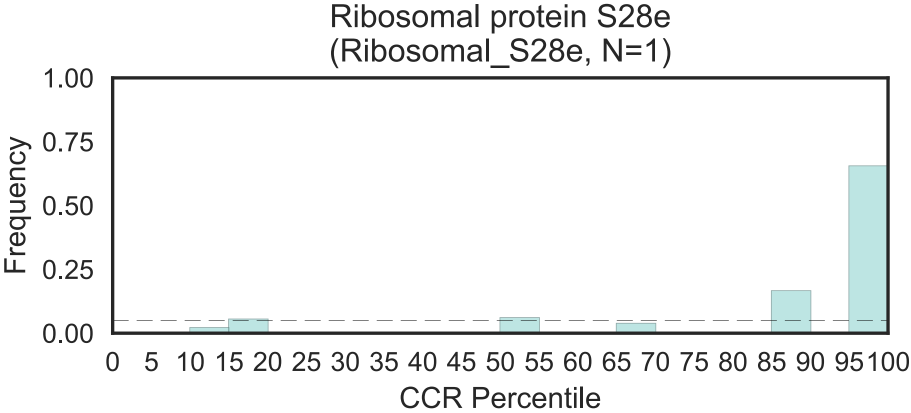

Ribosomal protein S24e
(Ribosomal_S24e, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


S25 ribosomal protein
(Ribosomal_S25, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

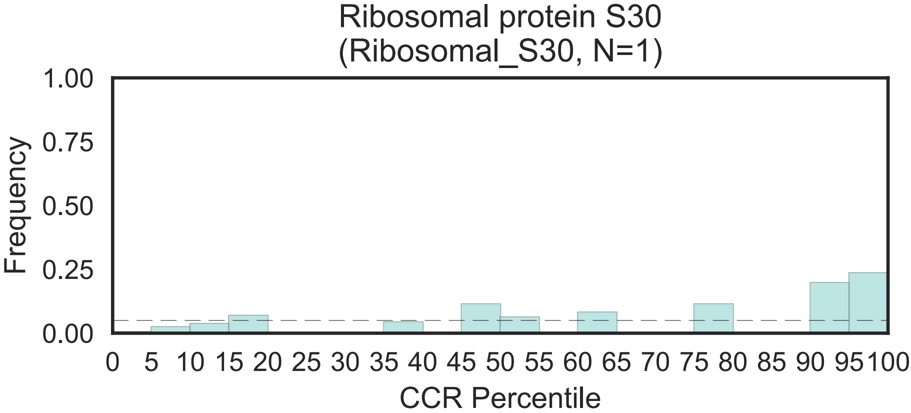

Ribosomal protein S26e
(Ribosomal_S26e, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribosomal protein S27a
(Ribosomal_S27, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

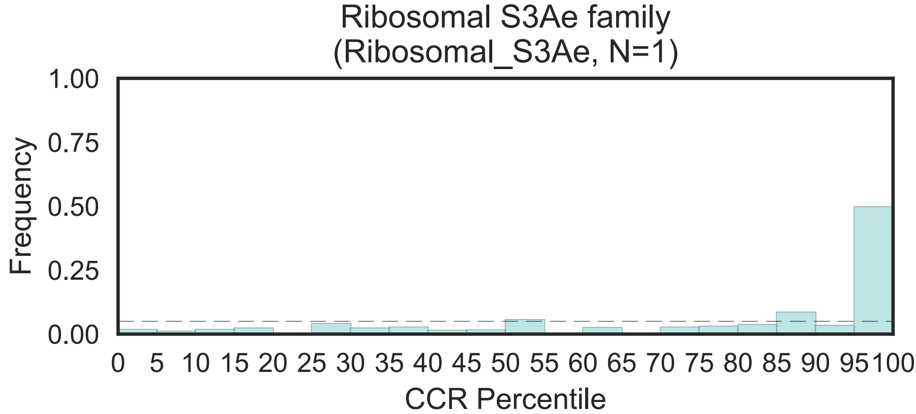

Ribosomal protein S27
(Ribosomal_S27e, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

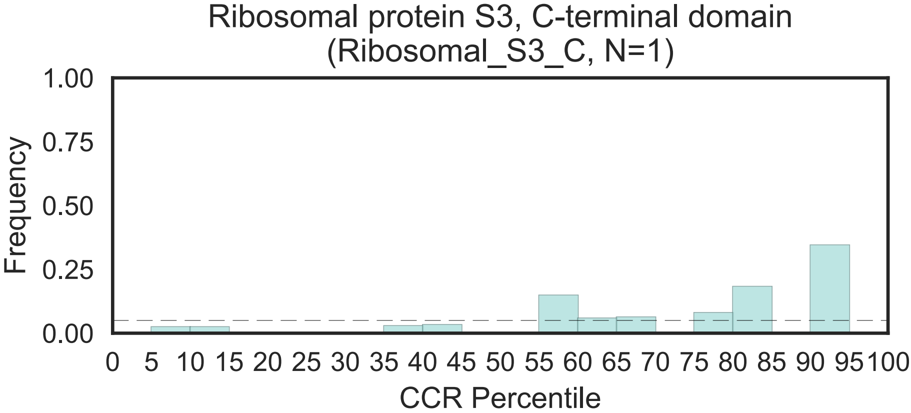


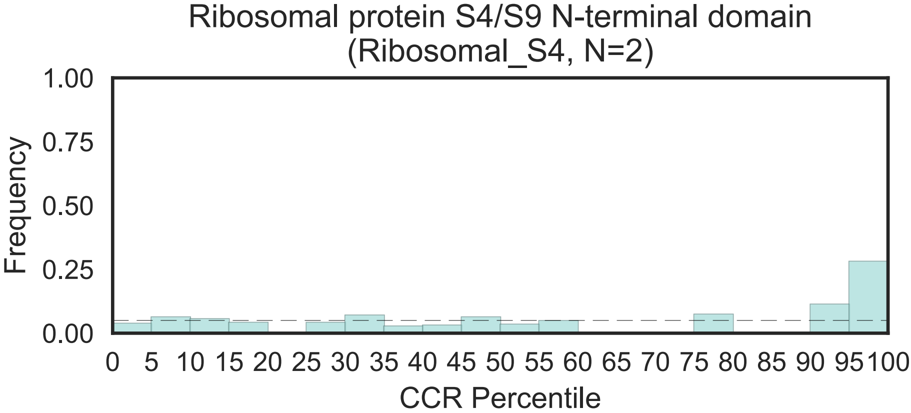
Ribosomal protein S28e
(Ribosomal_S28e, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

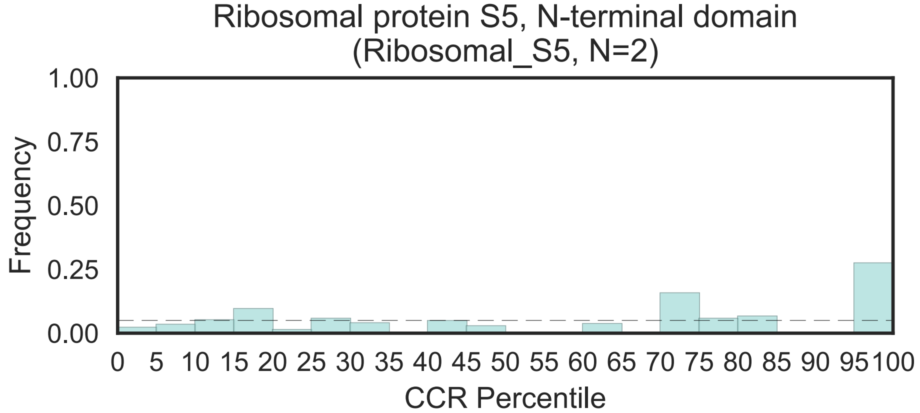


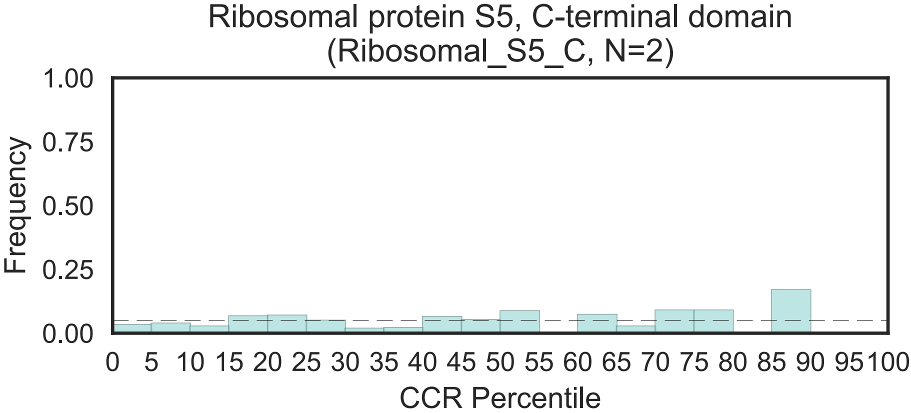
Ribosomal protein S30
(Ribosomal_S30, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

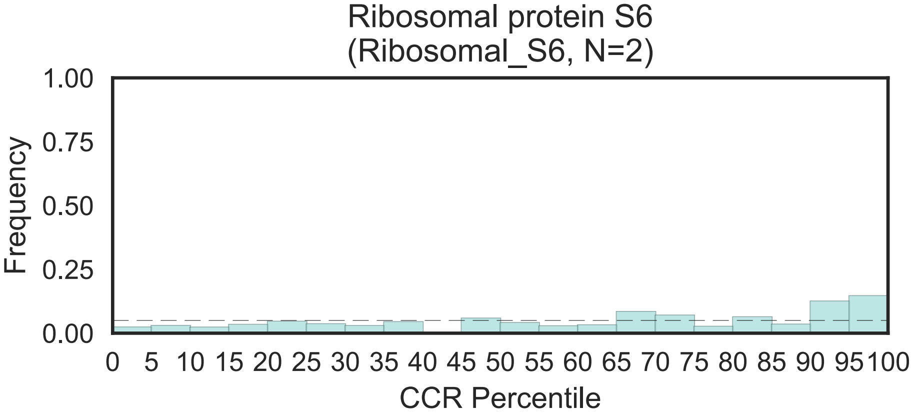

Ribosomal S3Ae family
(Ribosomal_S3Ae, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

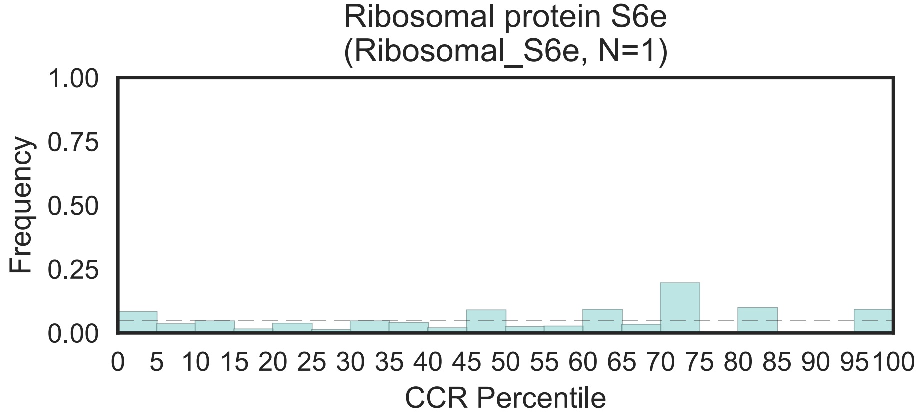

Ribosomal protein S3, C-terminal domain
(Ribosomal_S3_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

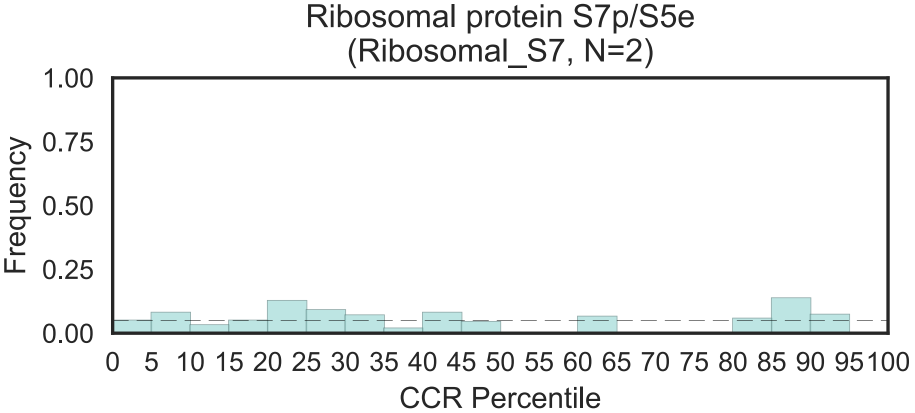

Ribosomal protein S4/S9 N-terminal domain
(Ribosomal_S4, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribosomal protein S5, N-terminal domain
(Ribosomal_S5, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

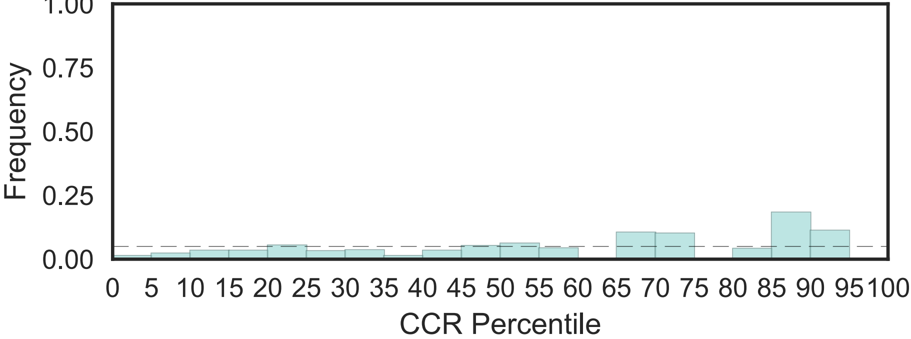

Ribosomal protein S5, C-terminal domain
(Ribosomal_S5_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

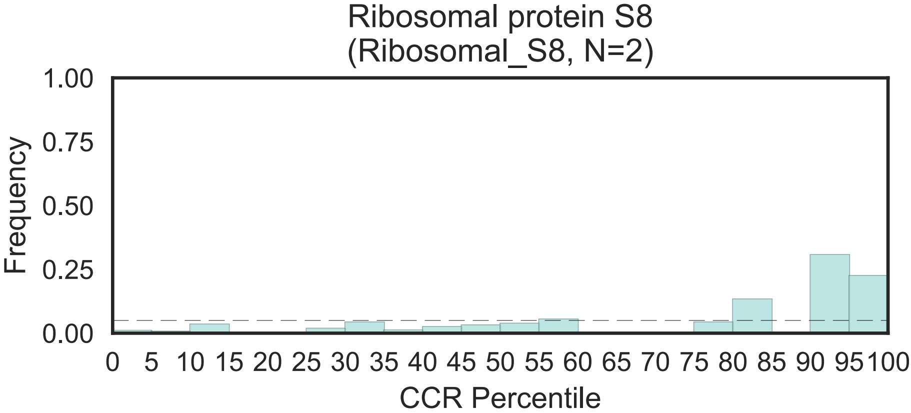

Ribosomal protein S6
(Ribosomal_S6, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

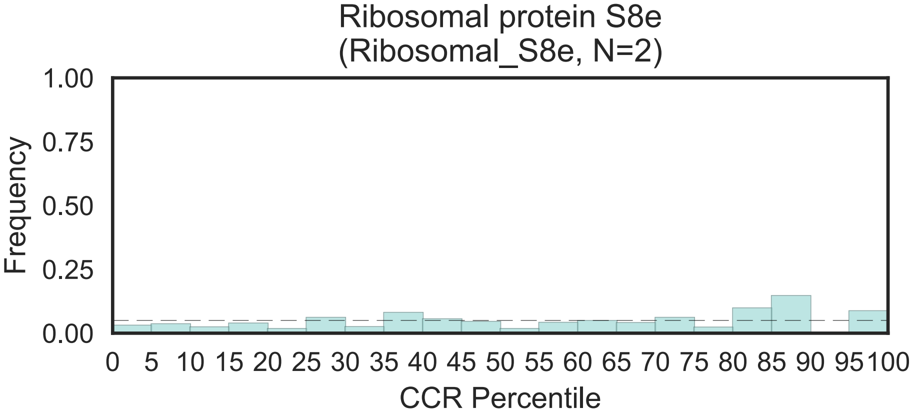

Ribosomal protein S6e
(Ribosomal_S6e, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

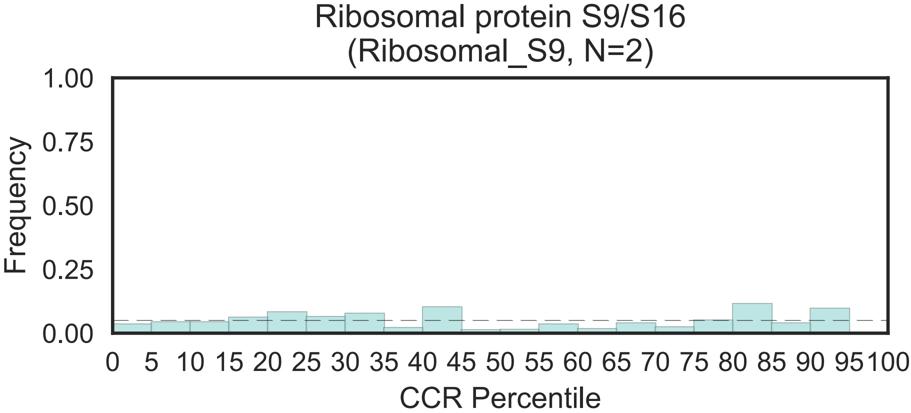

Ribosomal protein S7p/S5e
(Ribosomal_S7, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

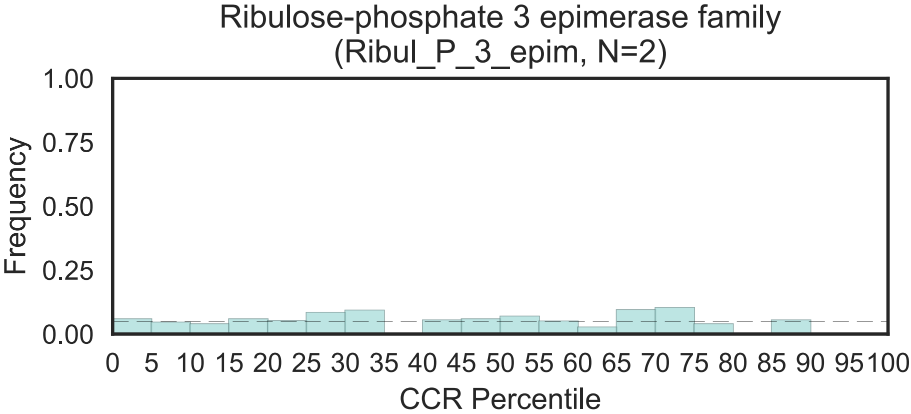
Ribosomal protein S7e
(Ribosomal_S7e, N=1)

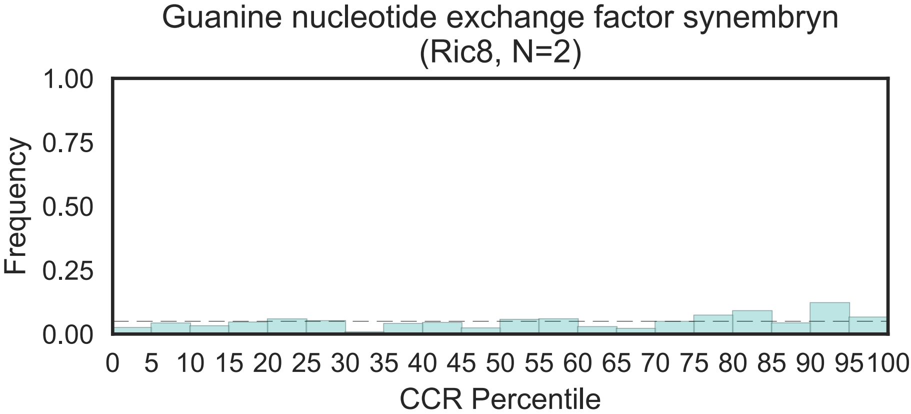


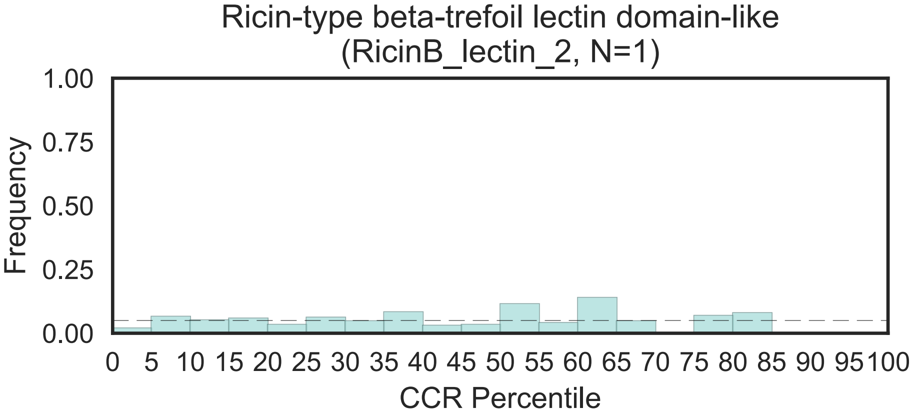

Ribosomal protein S8
(Ribosomal_S8, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

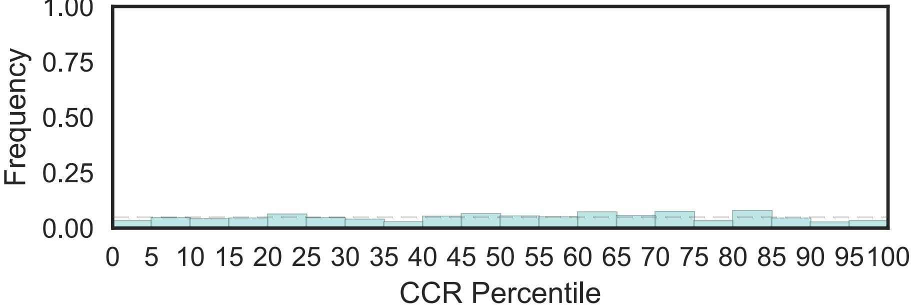

Ribosomal protein S8e
(Ribosomal_S8e, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ribosomal protein S9/S16
(Ribosomal_S9, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

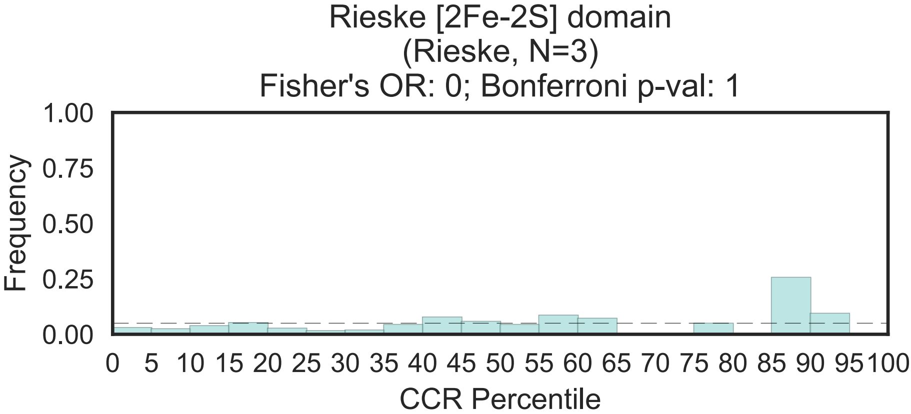

Ribulose-phosphate 3 epimerase family
(Ribul_P_3_epim, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

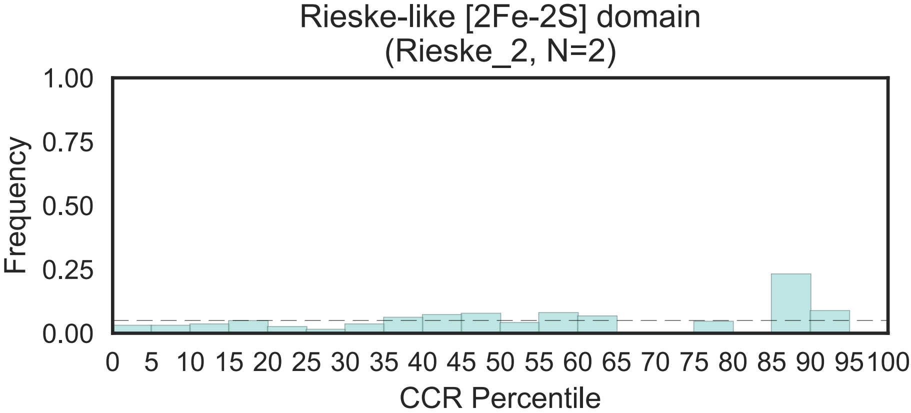

Guanine nucleotide exchange factor synembryn
(Ric8, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

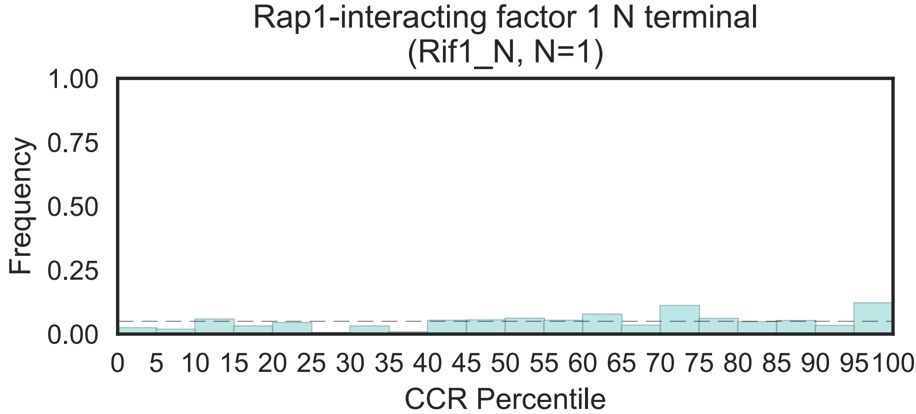

Ricin-type beta-trefoil lectin domain-like
(RicinB_lectin_2, N=1)

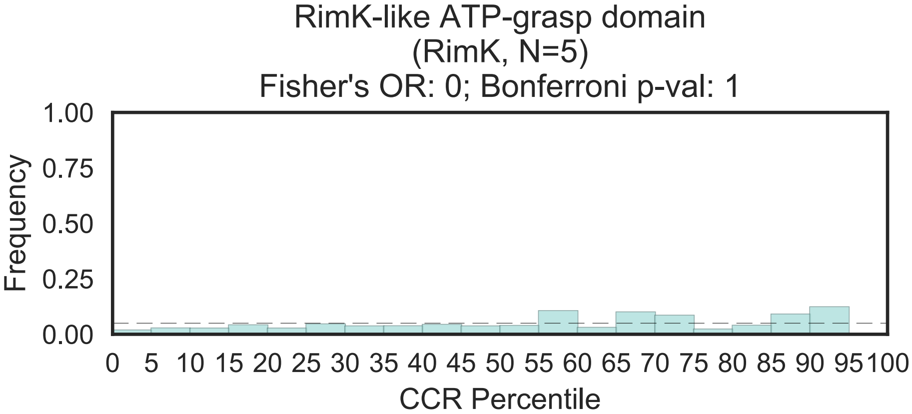


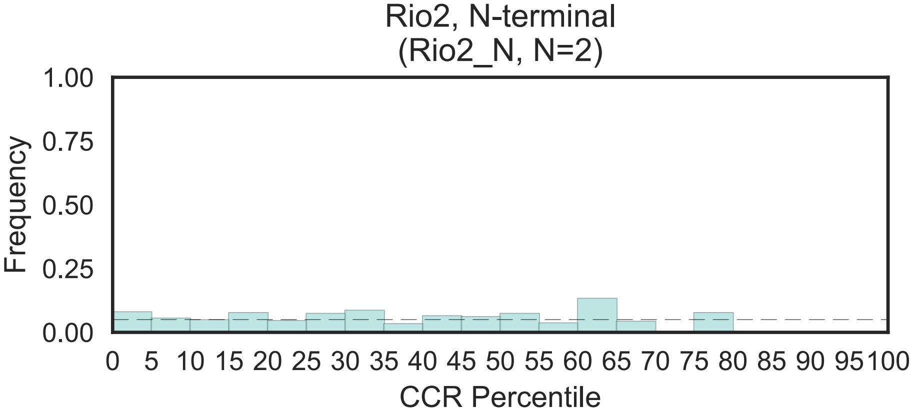
Ricin-type beta-trefoil lectin domain
(Ricin_B_lectin, N=24)
Fisher's OR: 0.544; Bonferroni p-val: 1


Rieske [2Fe-2S] domain
(Rieske, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

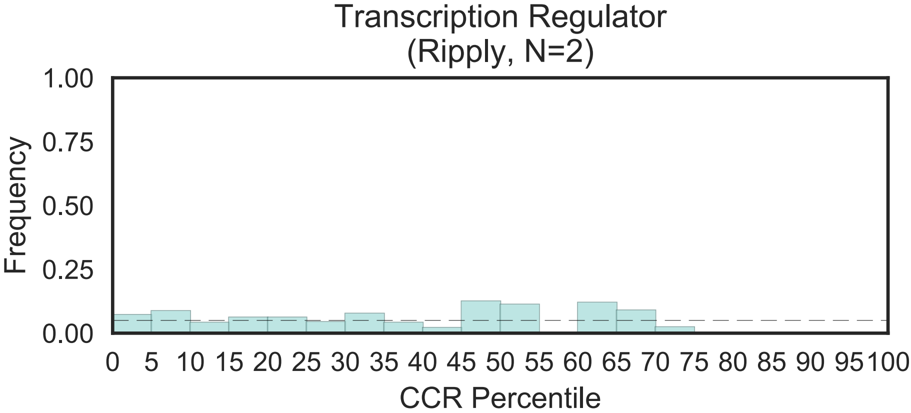

Rieske-like [2Fe-2S] domain
(Rieske_2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

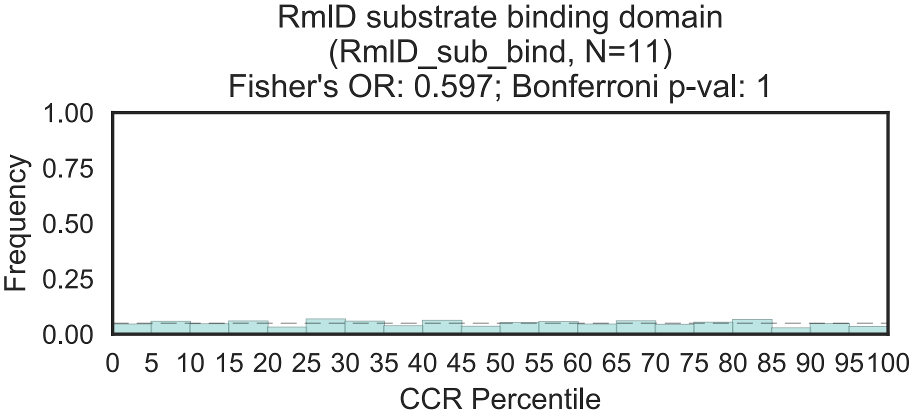

Rap1-interacting factor 1 N terminal
(Rif1_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

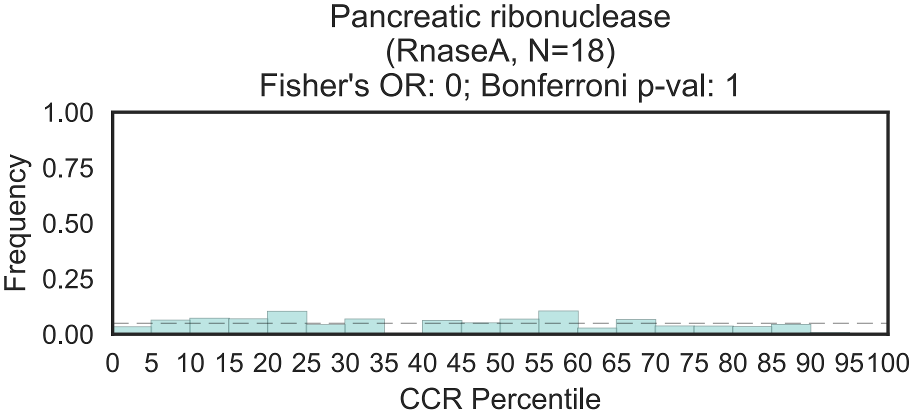

RimK-like ATP-grasp domain
(RimK, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

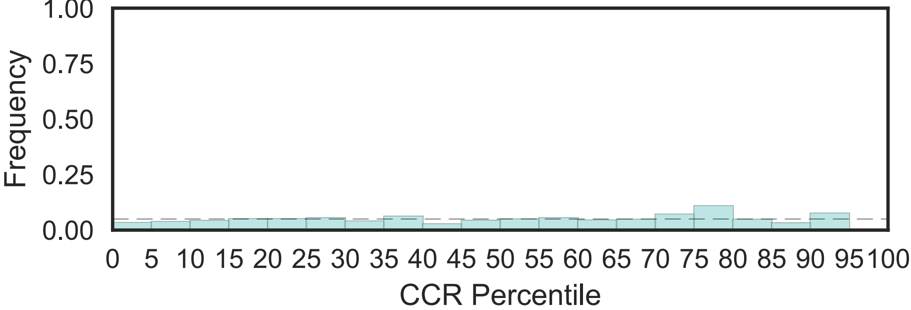


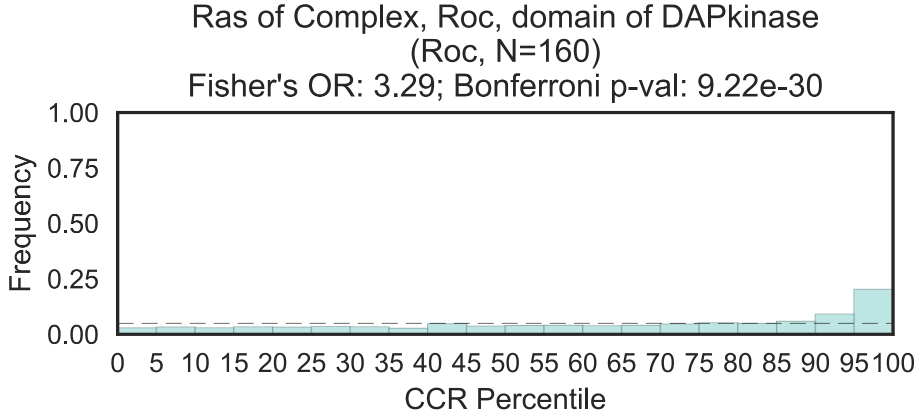
Rio2, N-terminal
(Rio2_N, N=2)

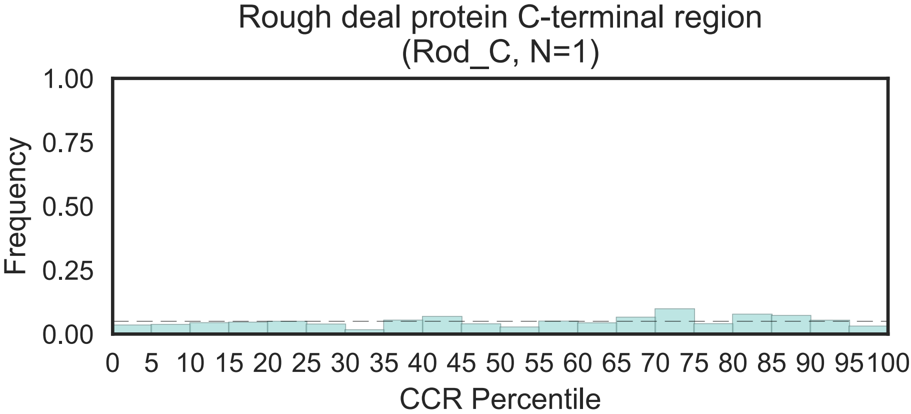

Transcription Regulator
(Ripply, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

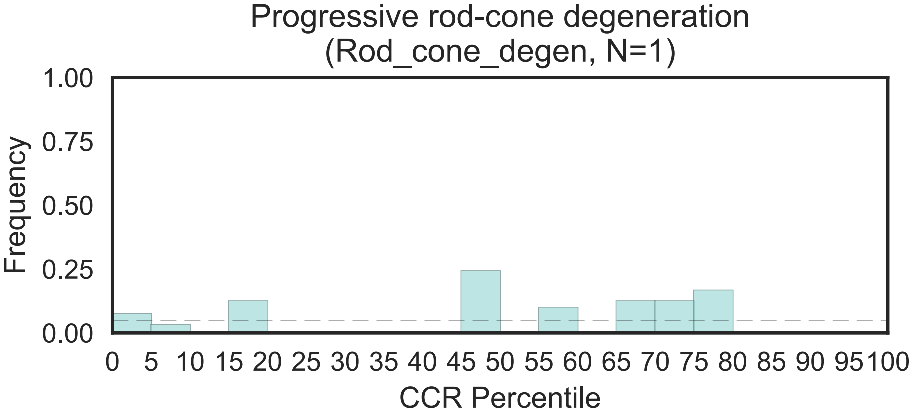

RmlD substrate binding domain
(RmlD_sub_bind, N=11)
Fisher's OR: 0.597; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

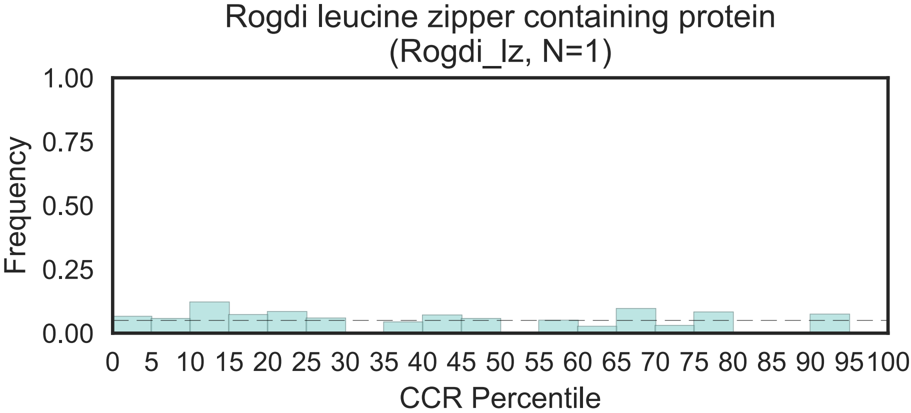

Pancreatic ribonuclease
(RnaseA, N=18)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

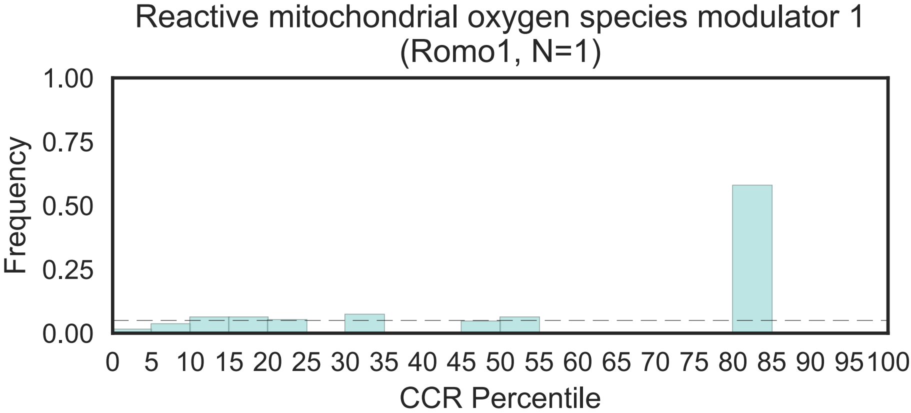

Roadblock/LC7 domain
(Robl_LC7, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

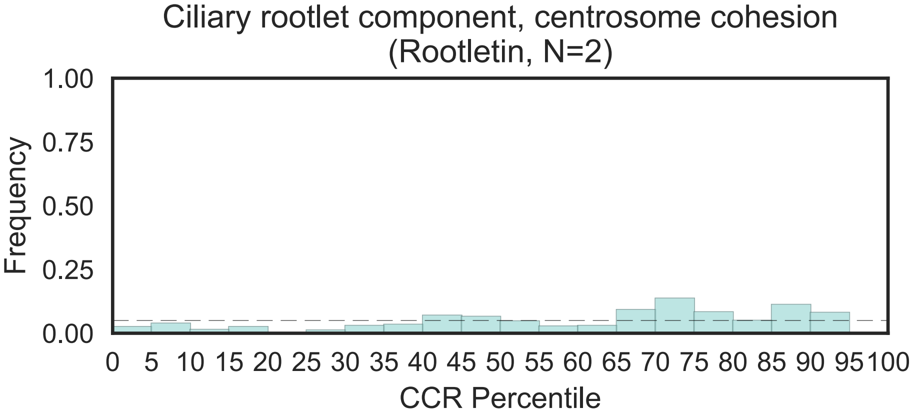

Ras of Complex, Roc, domain of DAPkinase
(Roc, N=160)
Fisher's OR: 3.29; Bonferroni p-val: 9.22e-30
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

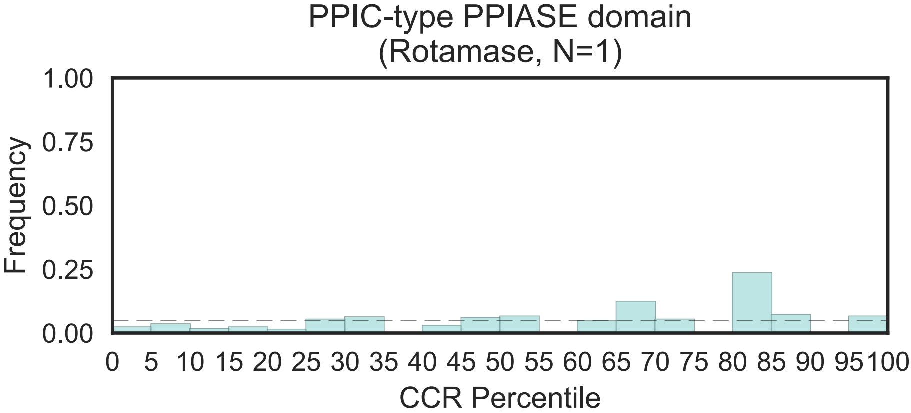

Rough deal protein C-terminal region
(Rod_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

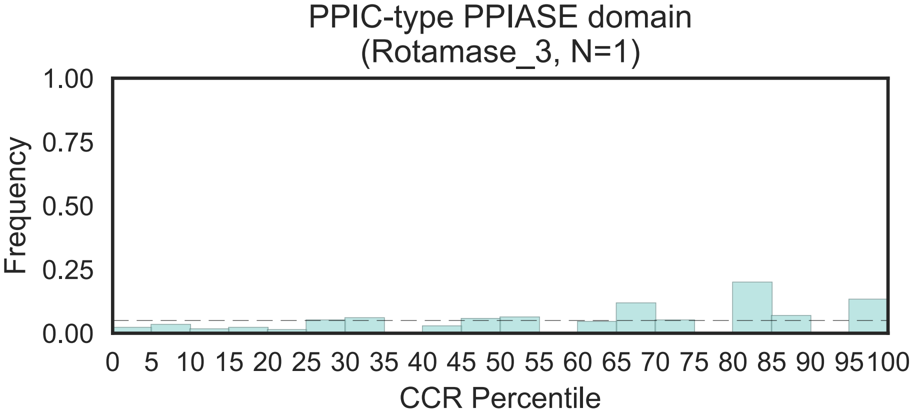

Progressive rod-cone degeneration
(Rod_cone_degen, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

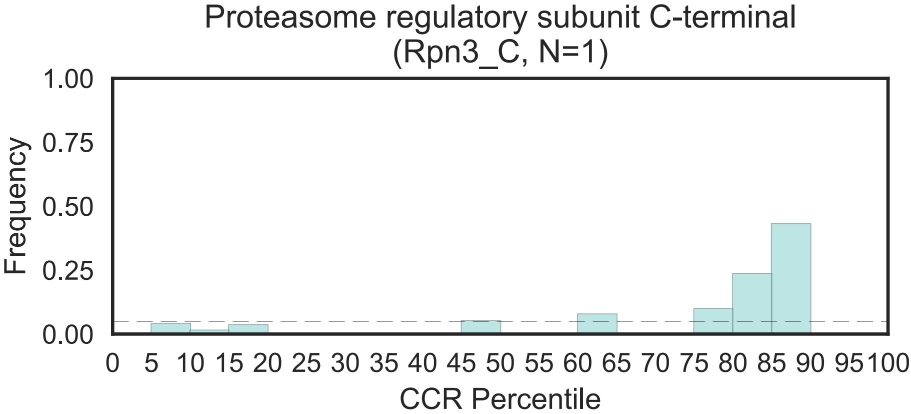

Rogdi leucine zipper containing protein
(Rogdi_lz, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

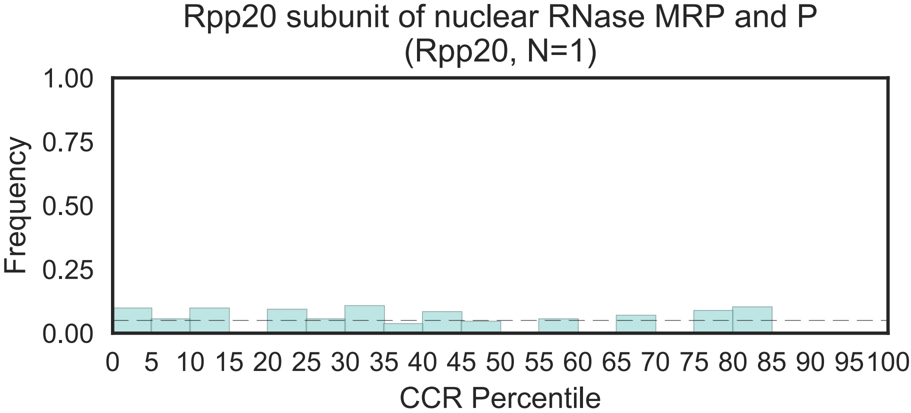

Reactive mitochondrial oxygen species modulator 1
(Romo1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

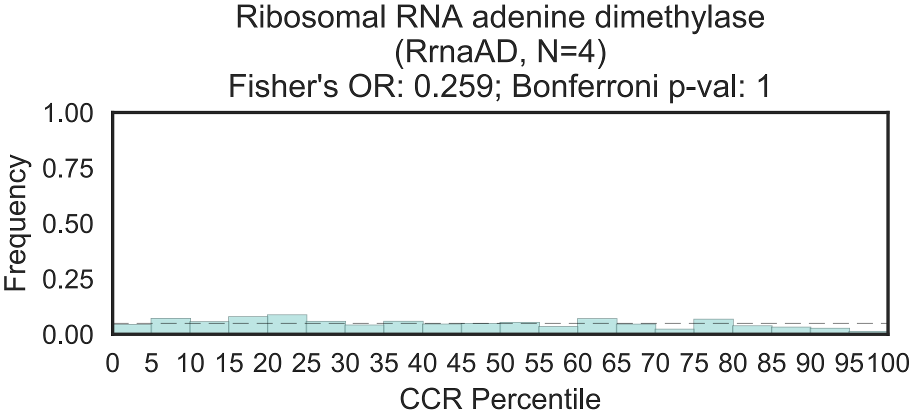

Ciliary rootlet component, centrosome cohesion
(Rootletin, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

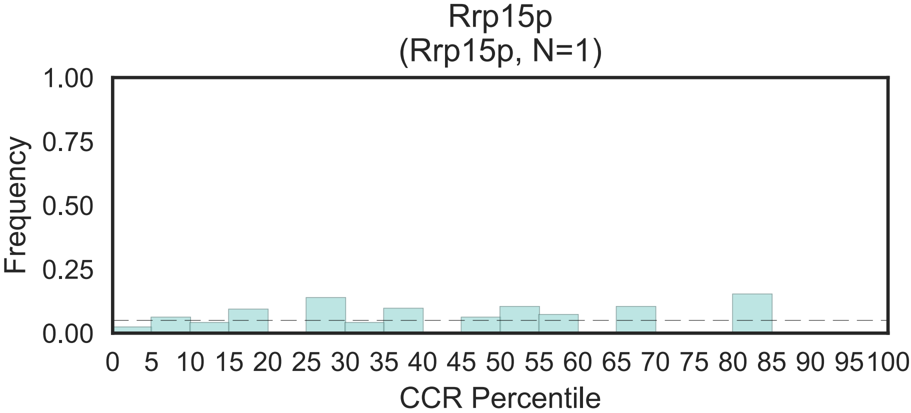

PPIC-type PPIASE domain
(Rotamase, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


PPIC-type PPIASE domain
(Rotamase_3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

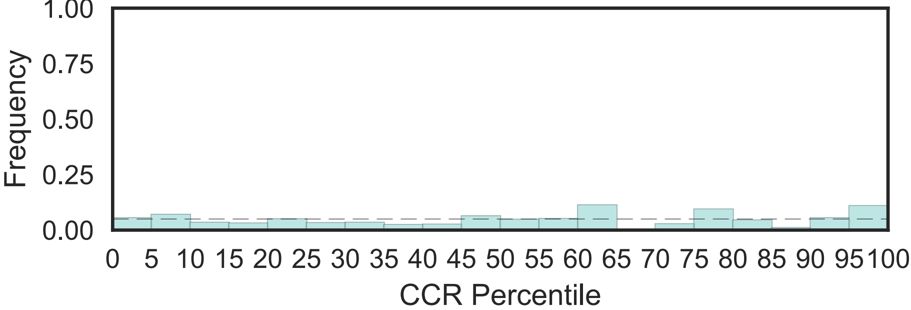

Proteasome regulatory subunit C-terminal
(Rpn3_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

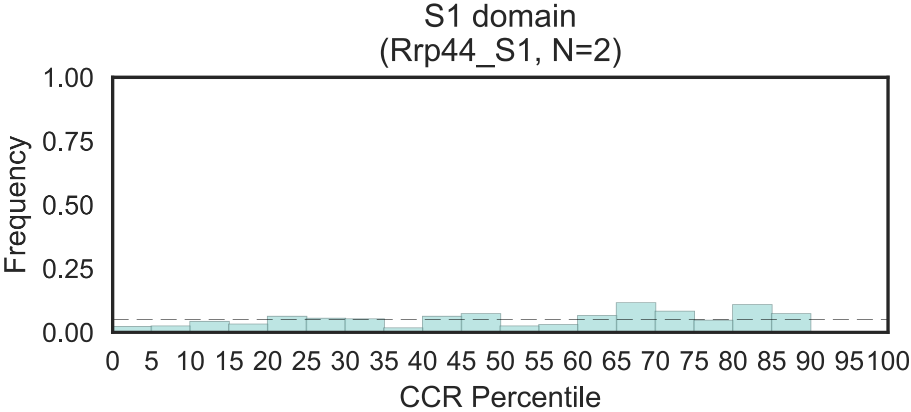

Rpp20 subunit of nuclear RNase MRP and P
(Rpp20, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

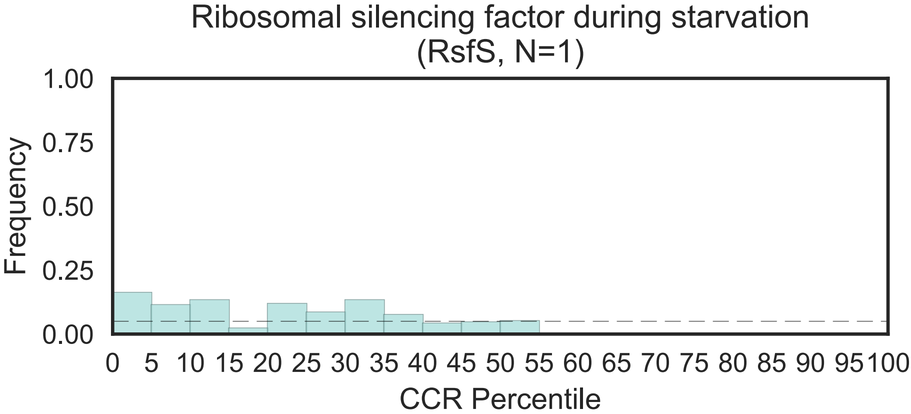

Ribosomal RNA adenine dimethylase
(RrnaAD, N=4)
Fisher's OR: 0.259; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

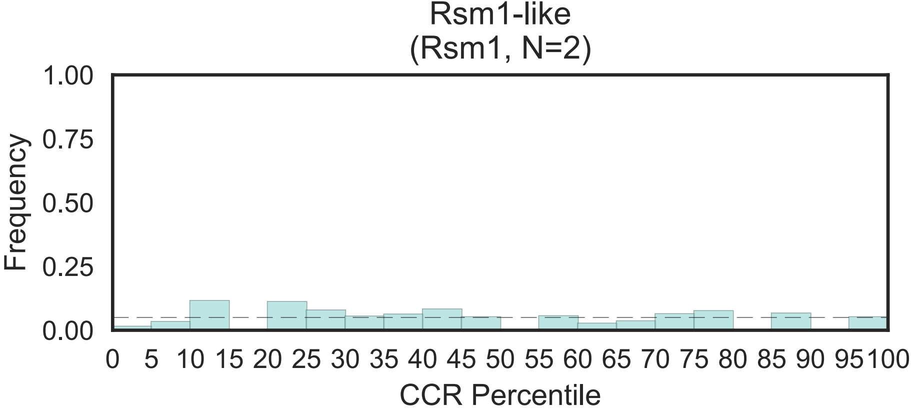

Rrp15p
(Rrp15p, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

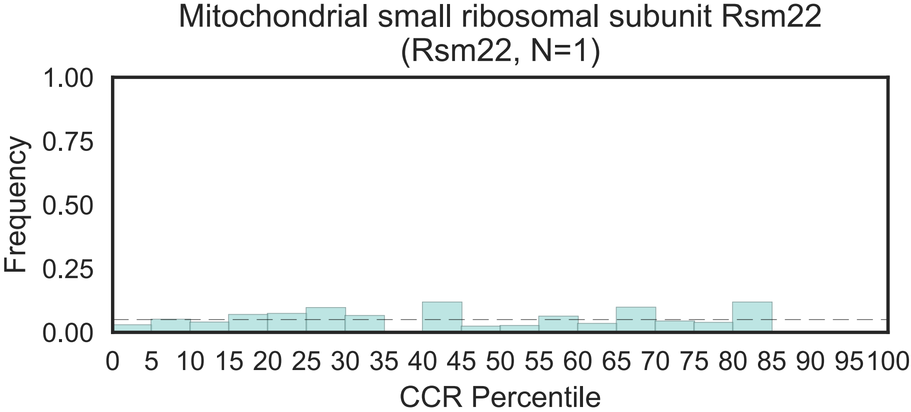
Rrp44-like cold shock domain (Rrp44_CSD1, N=3) Fisher's OR: 1.2; Bonferroni p-val: 1

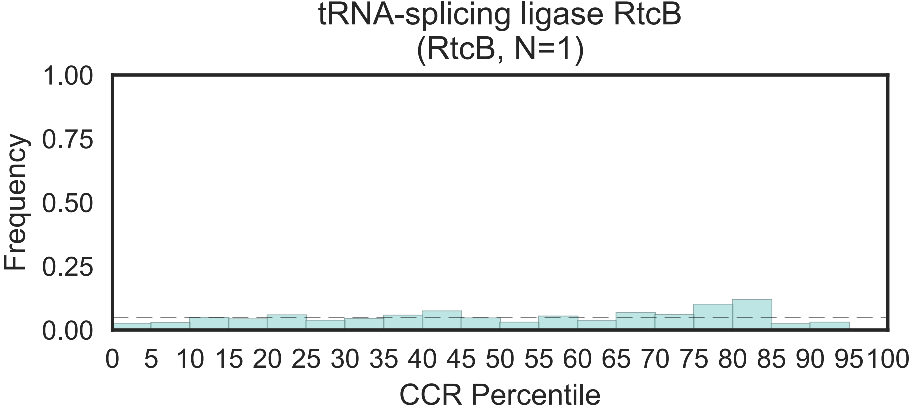


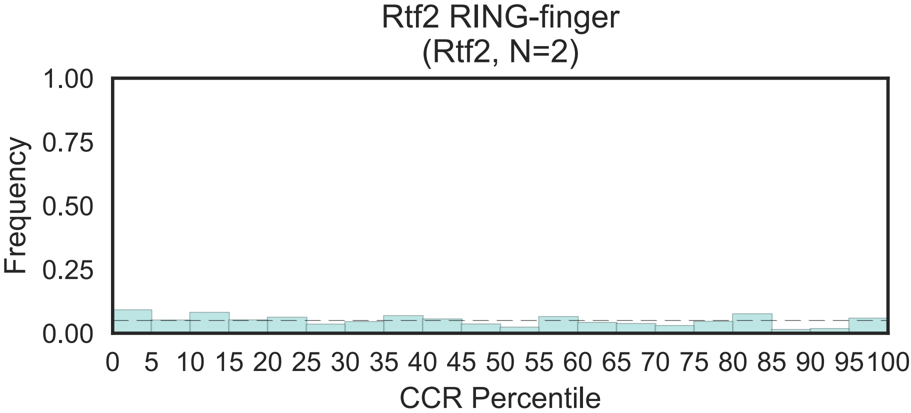

S1 domain
(Rrp44_S1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

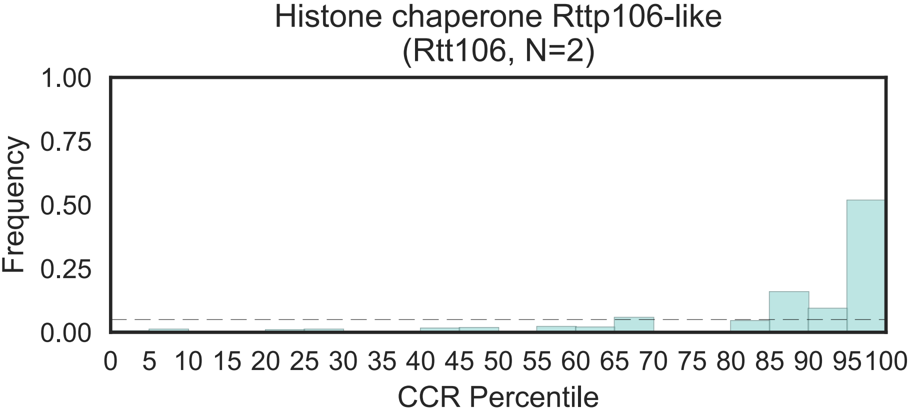

Ribosomal silencing factor during starvation
(RsfS, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

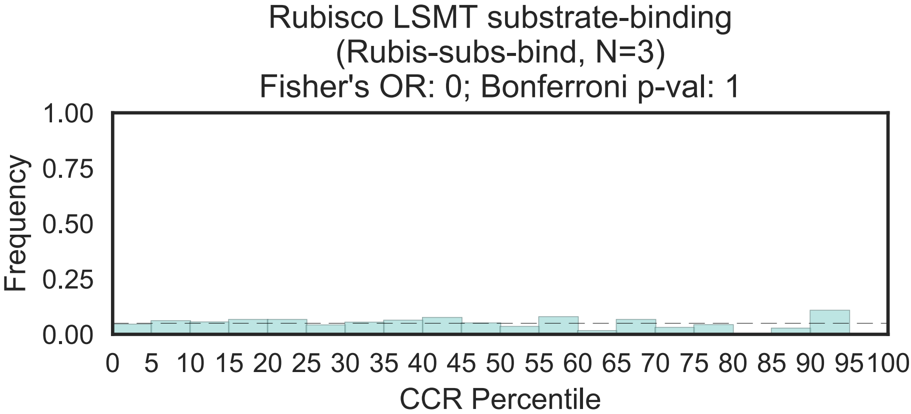

Rsm1-like
(Rsm1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

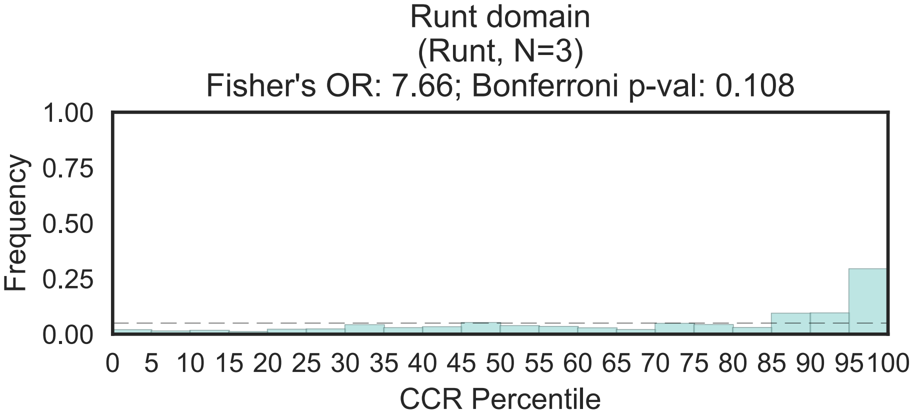

Mitochondrial small ribosomal subunit Rsm22
(Rsm22, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

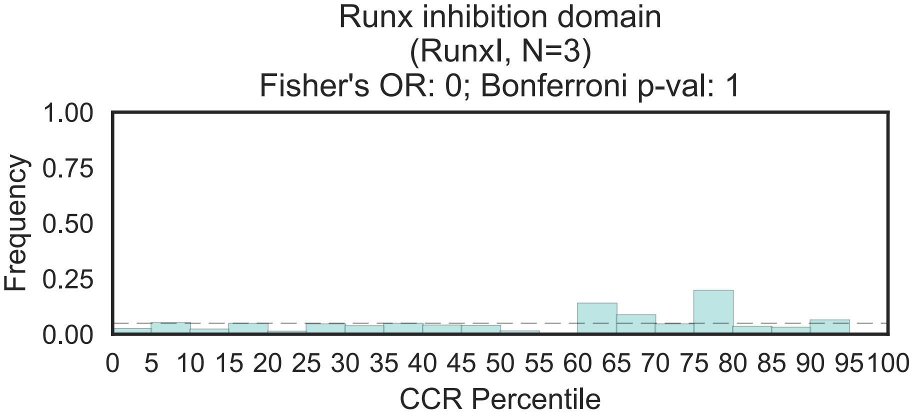

tRNA-splicing ligase RtcB
(RtcB, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Rtf2 RING-finger
(Rtf2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

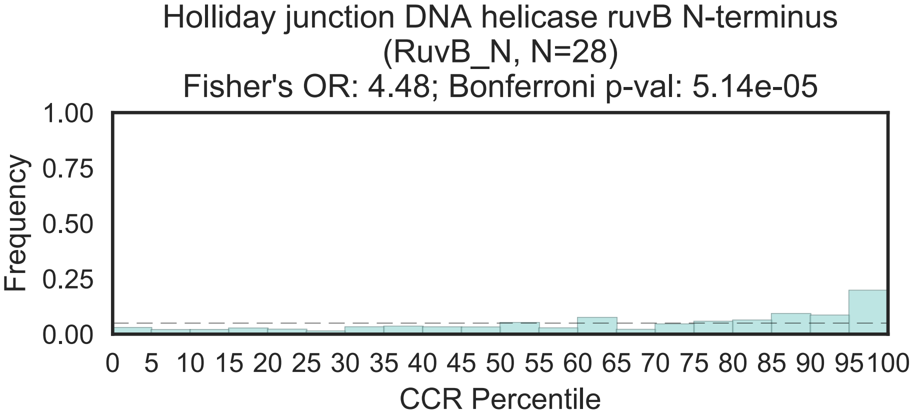

Histone chaperone Rttp106-like
(Rtt106, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

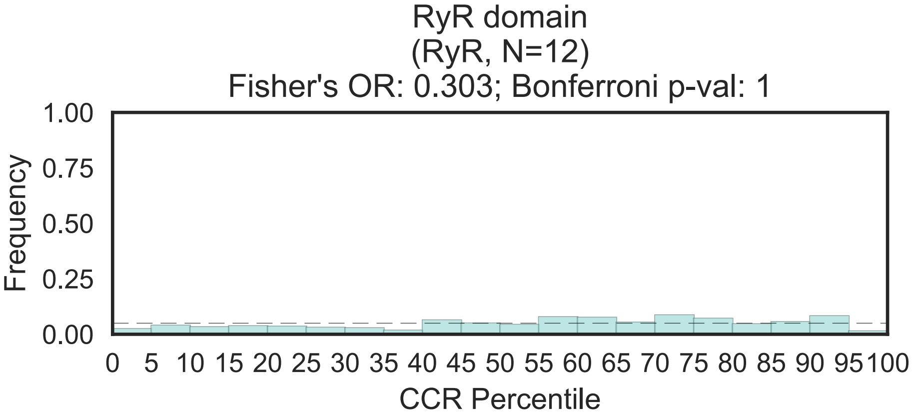

Rubisco LSMT substrate-binding
(Rubis-subs-bind, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

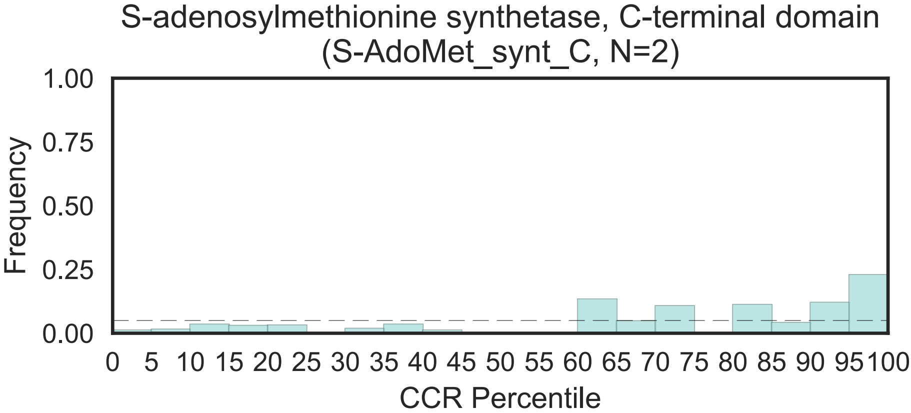

Runt domain
(Runt, N=3)
Fisher's OR: 7.66; Bonferroni p-val: 0.108
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

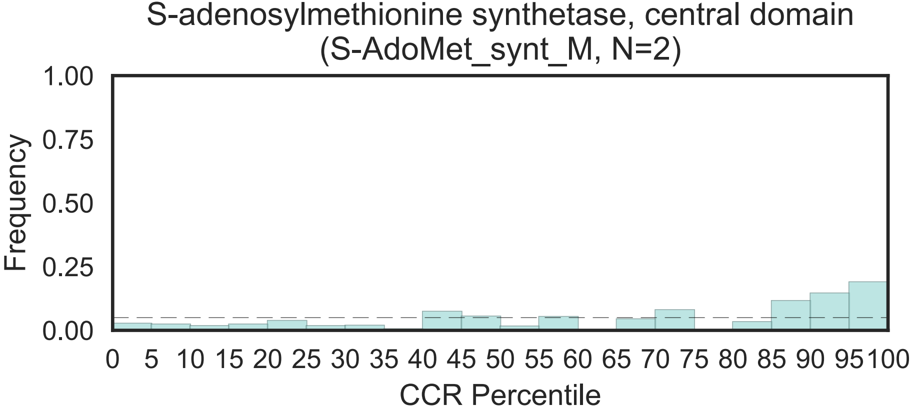


Runx inhibition domain
(RunxI, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

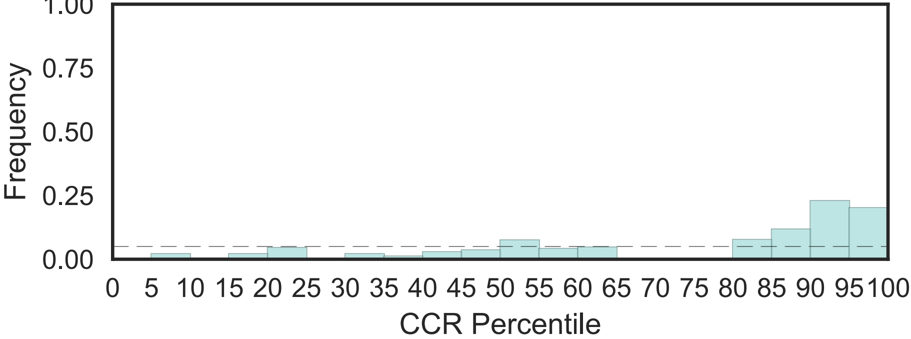

Holliday junction DNA helicase ruvB N-terminus
(RuvB_N, N=28)
Fisher's OR: 4.48; Bonferroni p-val: 5.14e-05
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

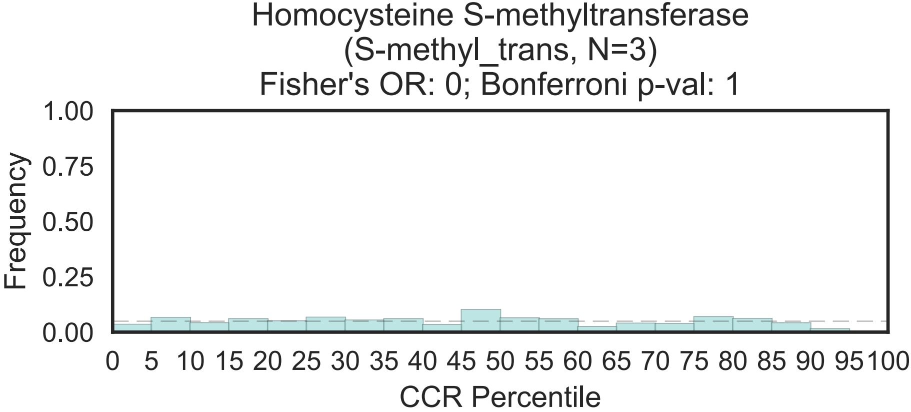

RyR domain
(RyR, N=12)
Fisher's OR: 0.303; Bonferroni p-val: 1

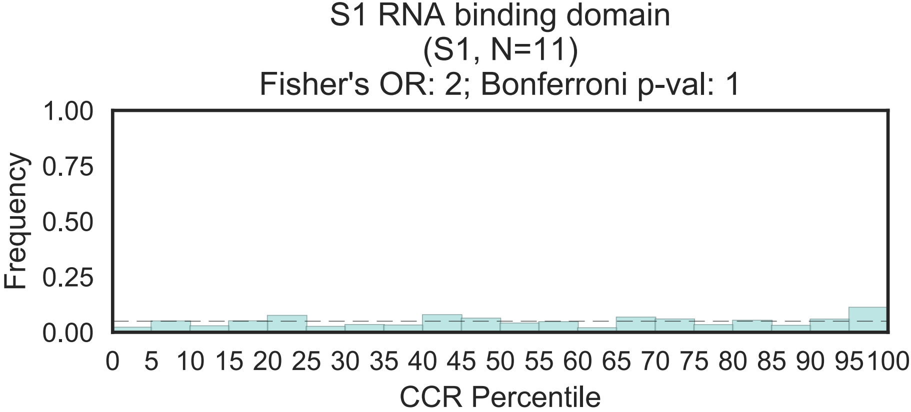

S-adenosylmethionine synthetase, C-terminal domain
(S-AdoMet_synt_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

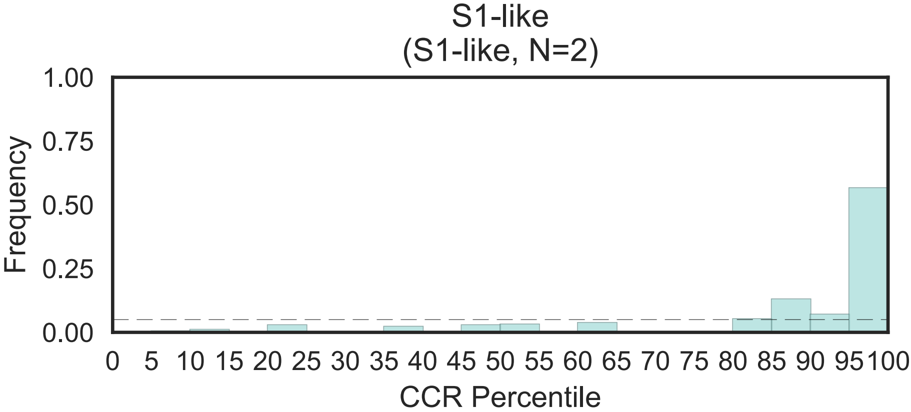

S-adenosylmethionine synthetase, central domain
(S-AdoMet_synt_M, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

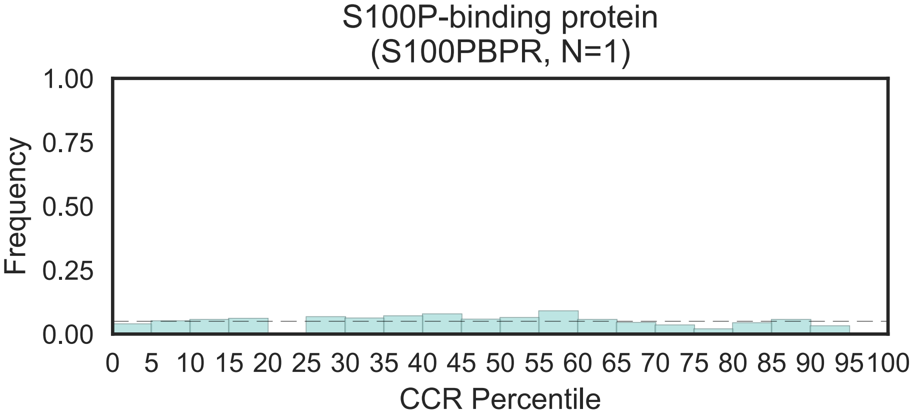
S-adenosylmethionine synthetase, N-terminal domain (S-AdoMet_synt_N, N=2)

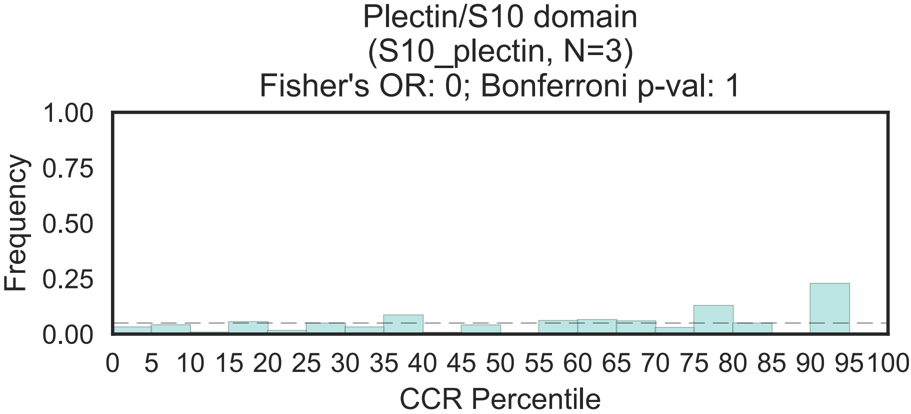


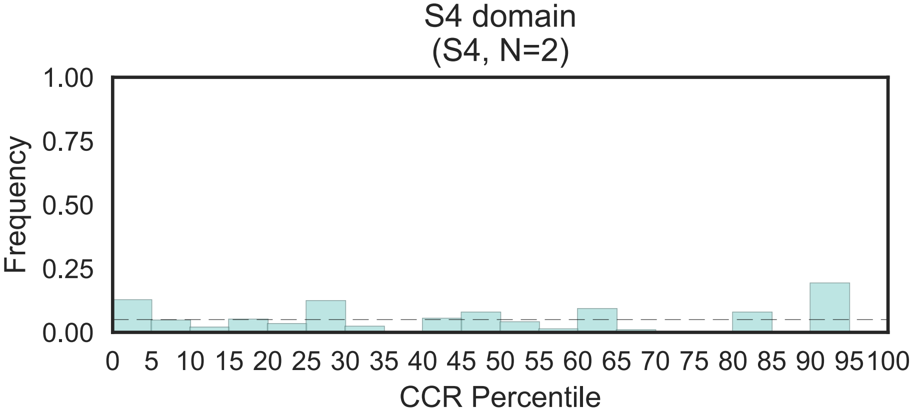

Homocysteine S-methyltransferase
(S-methyl_trans, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

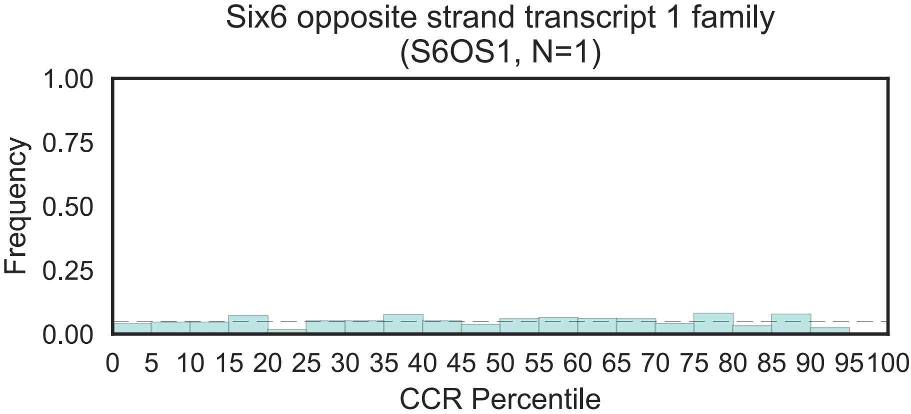

S1 RNA binding domain
(S1, N=11)
Fisher's OR: 2; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


S1-like
(S1-like, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

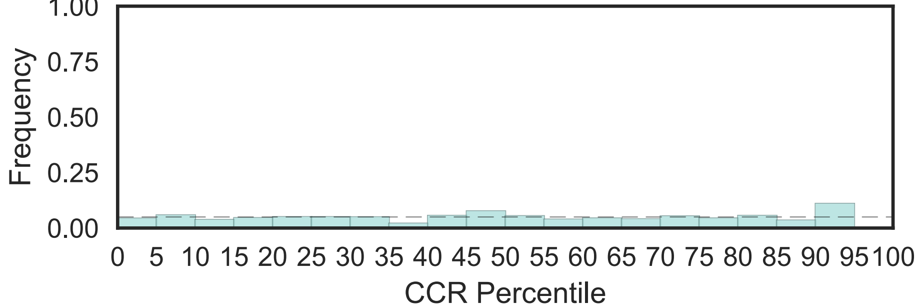

S100P-binding protein
(S100PBPR, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

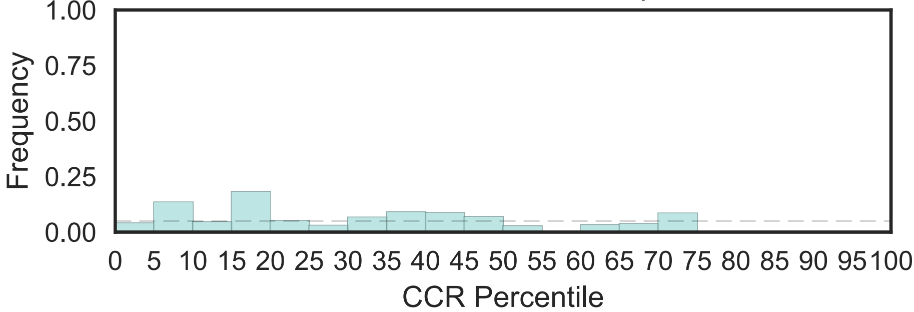

Plectin/S10 domain
(S10_plectin, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


S4 domain
(S4, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

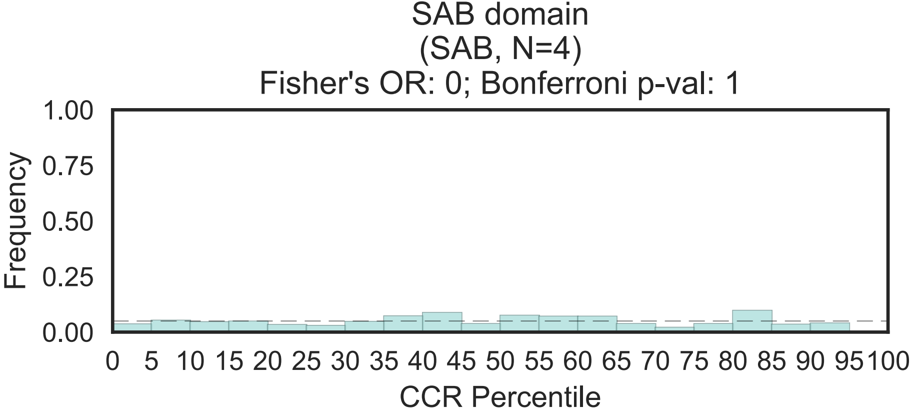

Six6 opposite strand transcript 1 family
(S6OS1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

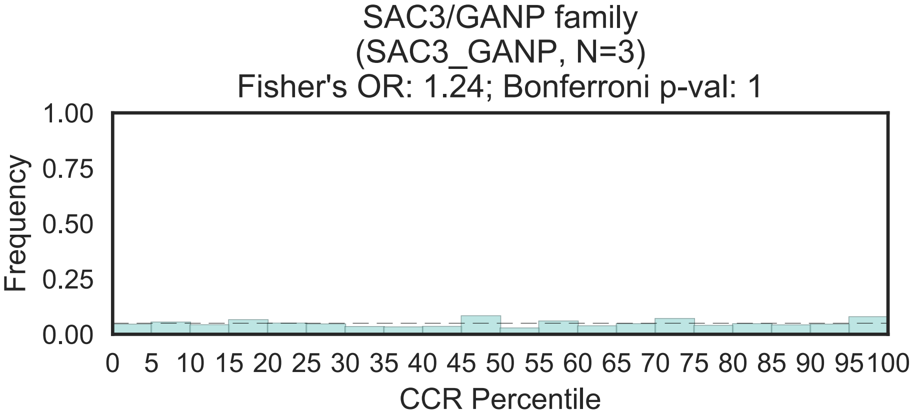
Peptidase S8 pro-domain
(S8_pro-domain, N=7)
Fisher's OR: 0; Bonferroni p-val: 1

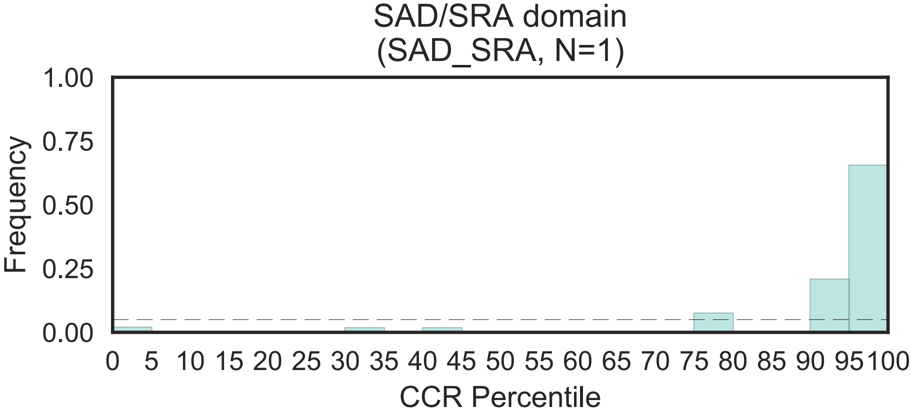


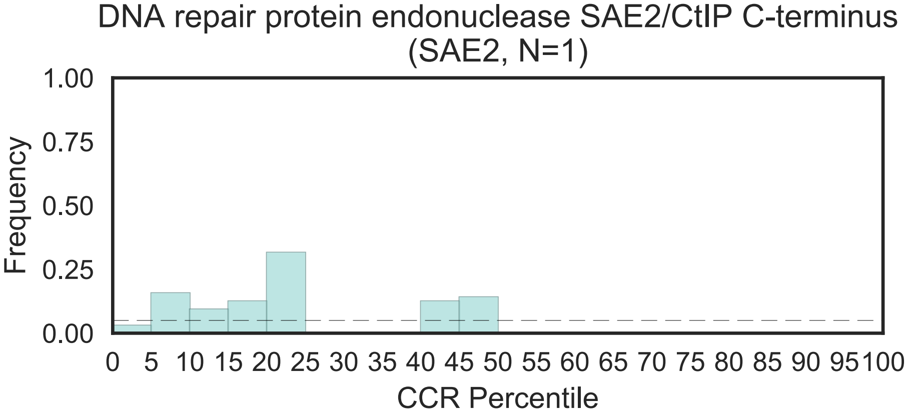


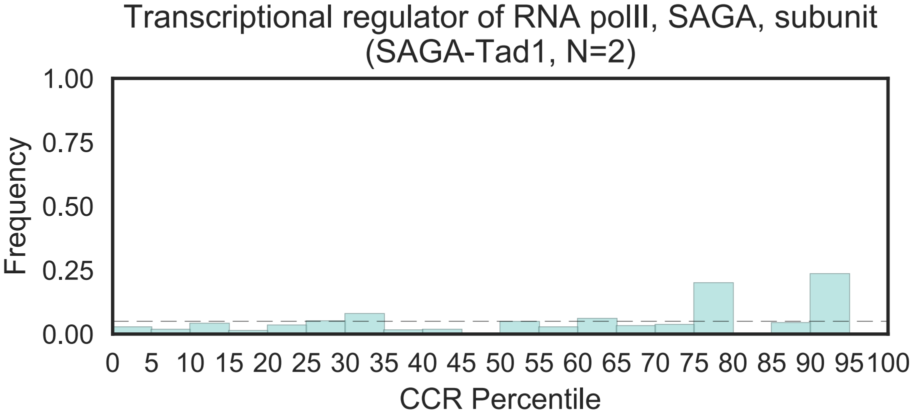
Serum amyloid A protein
(SAA, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

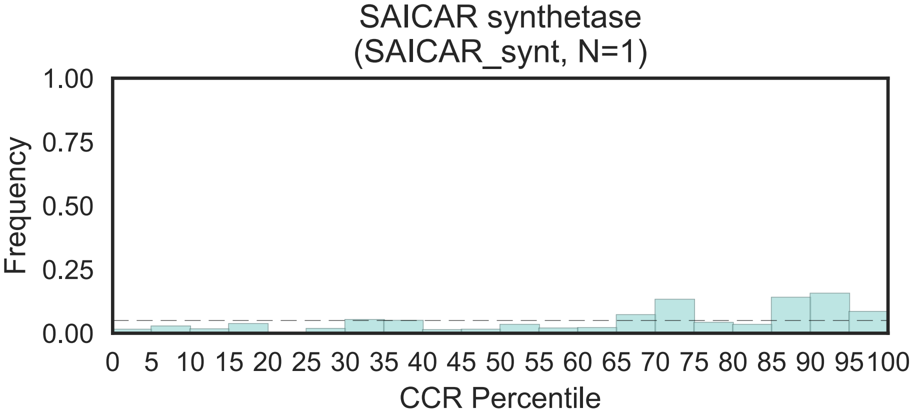

SAB domain
(SAB, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

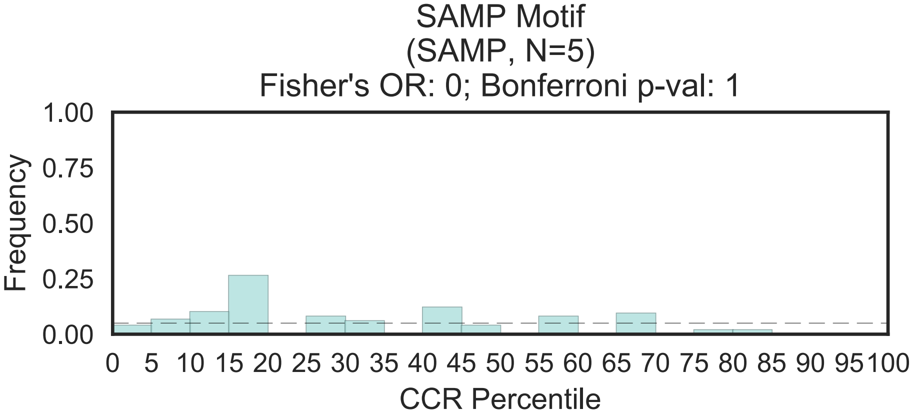

SAC3/GANP family
(SAC3_GANP, N=3)
Fisher's OR: 1.24; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


SAD/SRA domain
(SAD_SRA, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

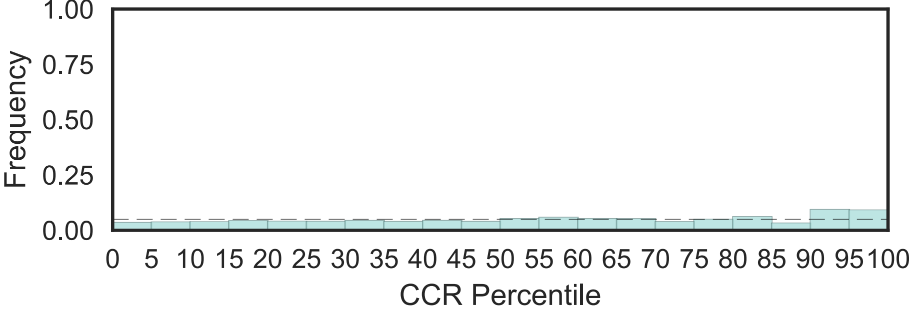

DNA repair protein endonuclease SAE2/CtIP C-terminus
(SAE2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Transcriptional regulator of RNA polII, SAGA, subunit
(SAGA-Tad1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

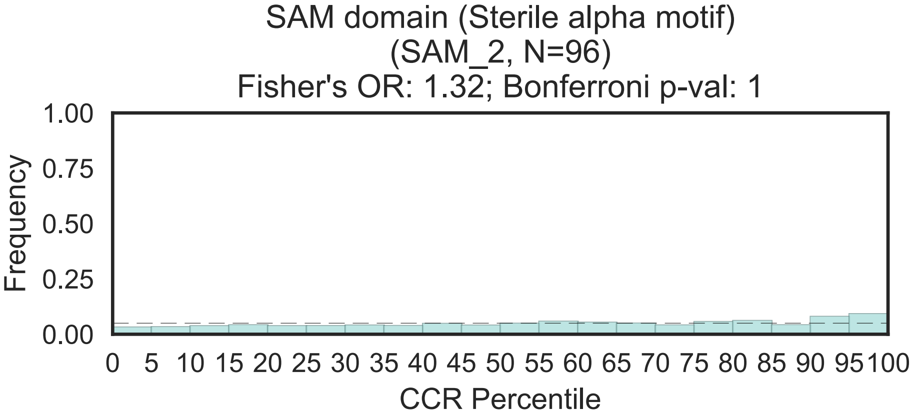

SAICAR synthetase
(SAICAR_synt, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

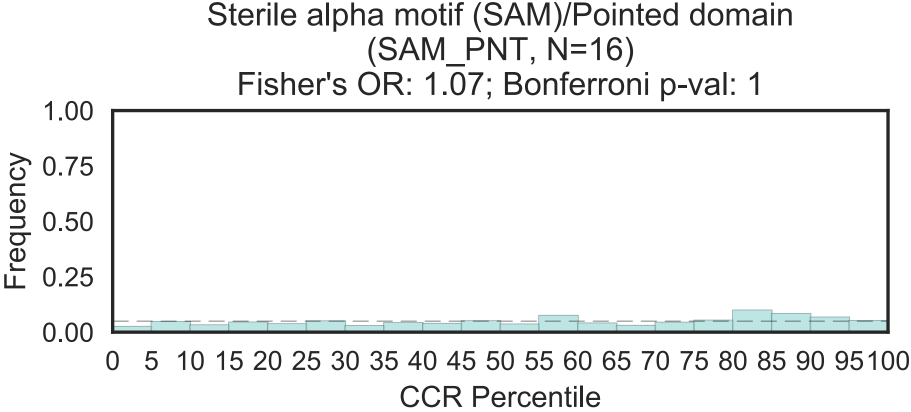


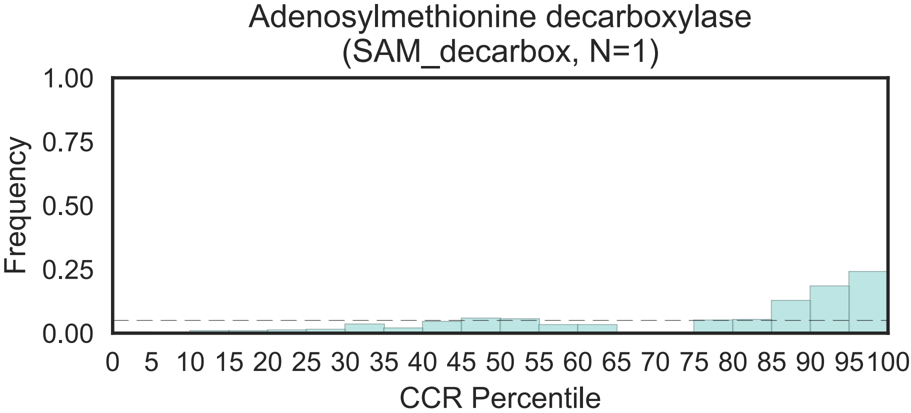
SAMP Motif
(SAMP, N=5)
Fisher's OR: 0; Bonferroni p-val: 1



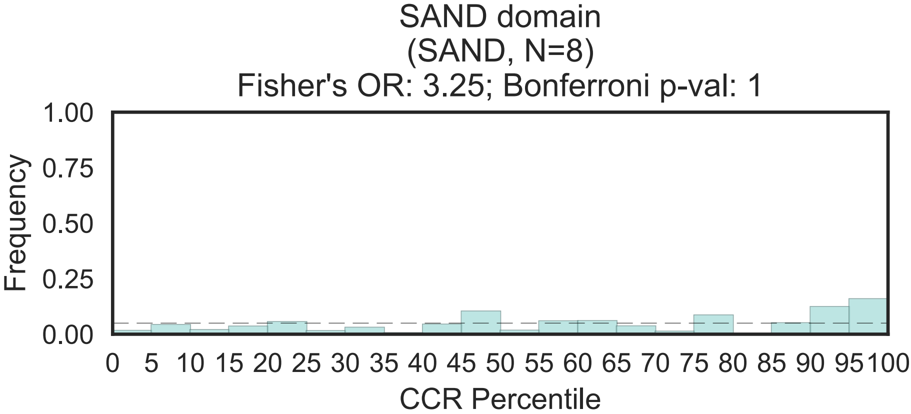
SAM domain (Sterile alpha motif)
(SAM_1, N=92)
Fisher's OR: 1.36; Bonferroni p-val: 1

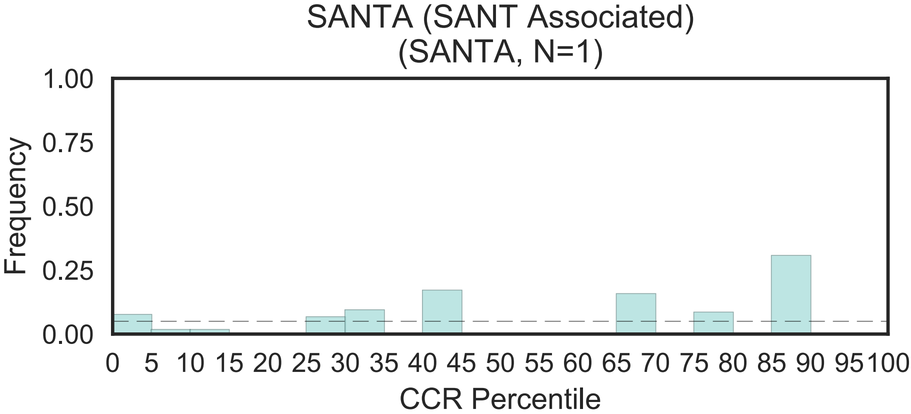

SAM domain (Sterile alpha motif)
(SAM_2, N=96)
Fisher's OR: 1.32; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

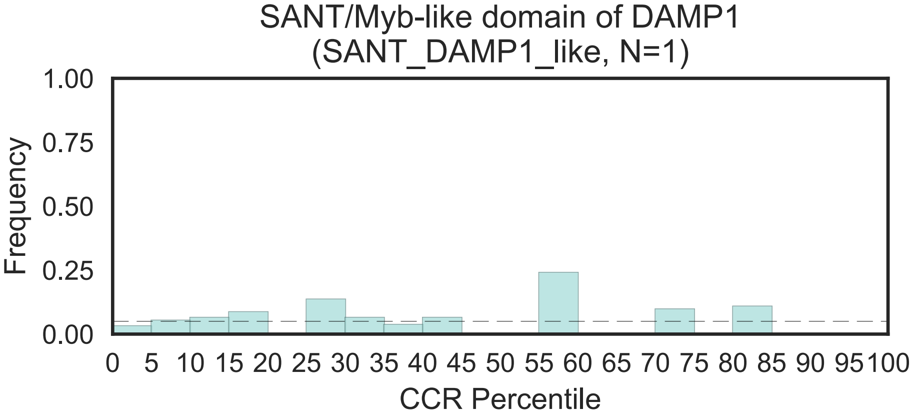

Sterile alpha motif (SAM)/Pointed domain
(SAM_PNT, N=16)
Fisher's OR: 1.07; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

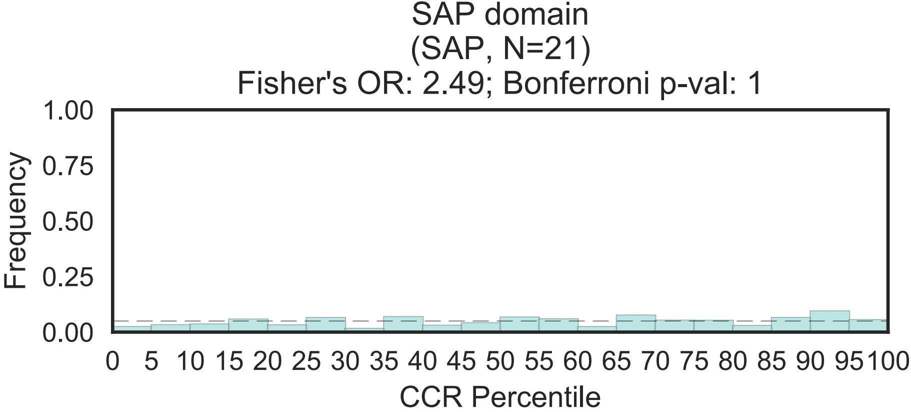


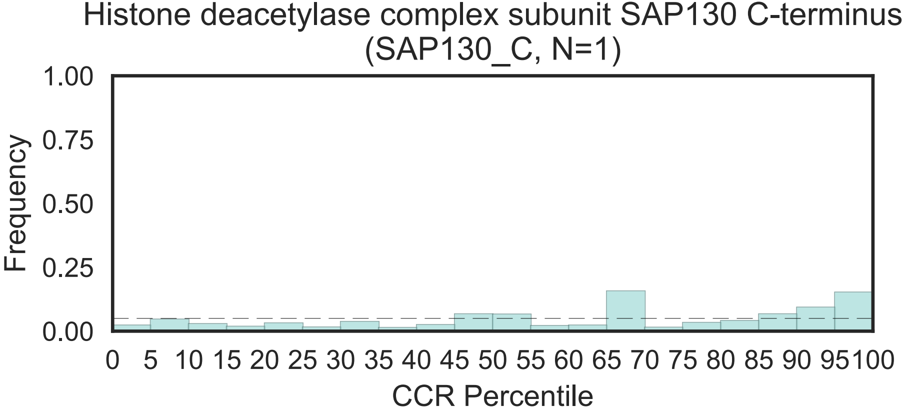
Adenosylmethionine decarboxylase
(SAM_decarbox, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

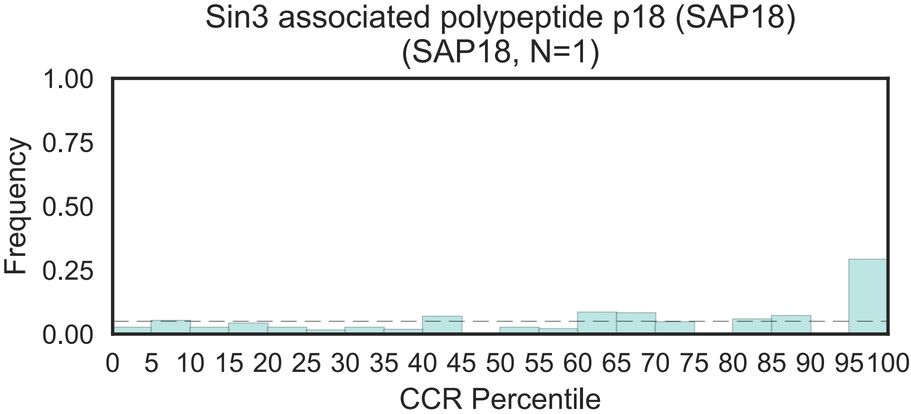

SAND domain
(SAND, N=8)
Fisher's OR: 3.25; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


SANTA (SANT Associated)
(SANTA, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

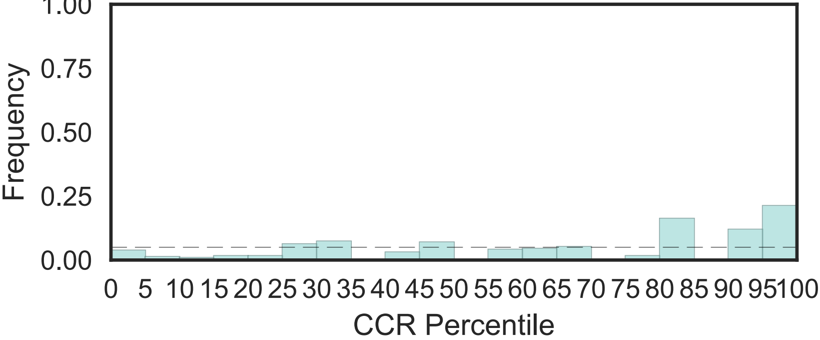

SANT/Myb-like domain of DAMP1
(SANT_DAMP1_like, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

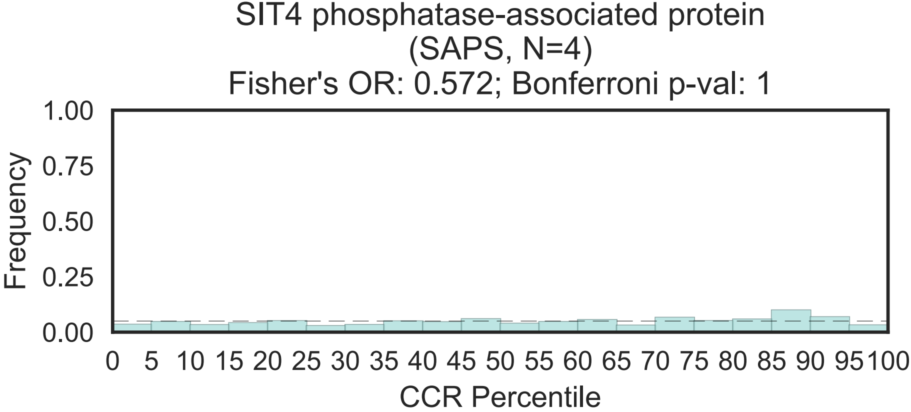

SAP domain
(SAP, N=21)
Fisher's OR: 2.49; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

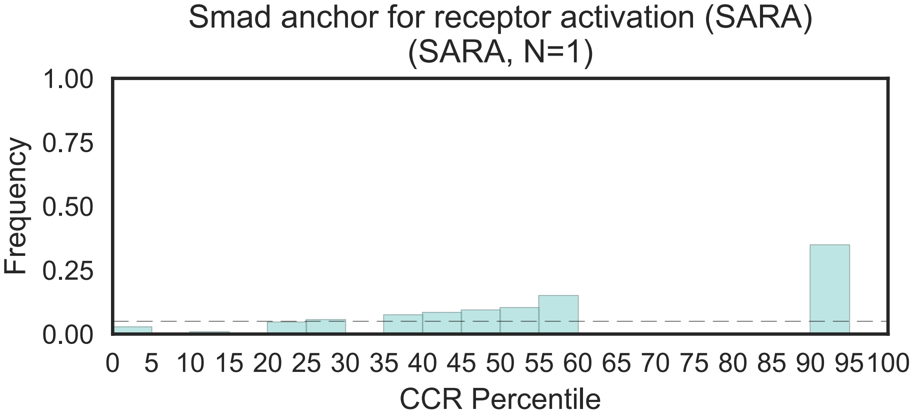

Histone deacetylase complex subunit SAP130 C-terminus
(SAP130_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

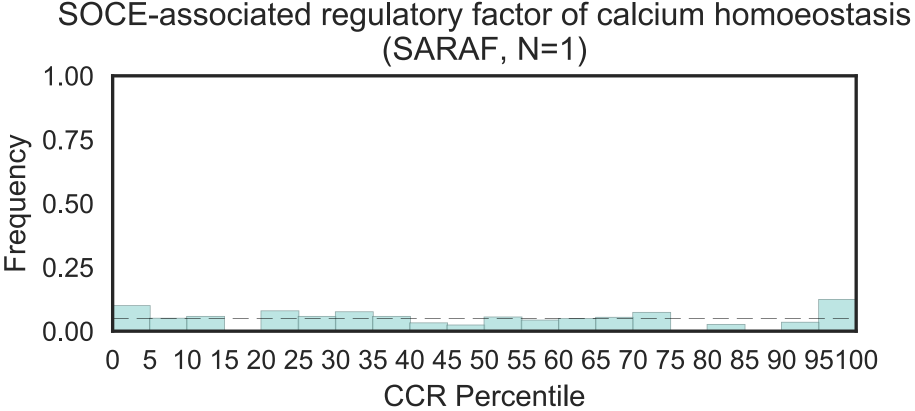

Sin3 associated polypeptide p18 (SAP18)
(SAP18, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

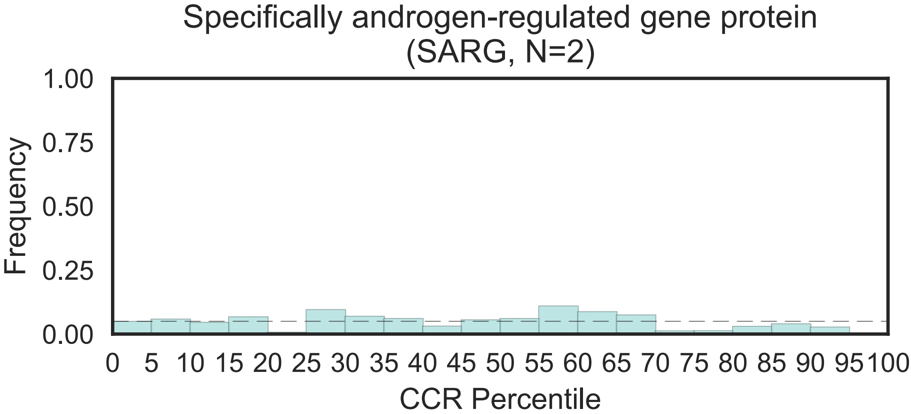
Sin3 binding region of histone deacetylase complex subunit SAP30 (SAP30_Sin3_bdg, N=2)

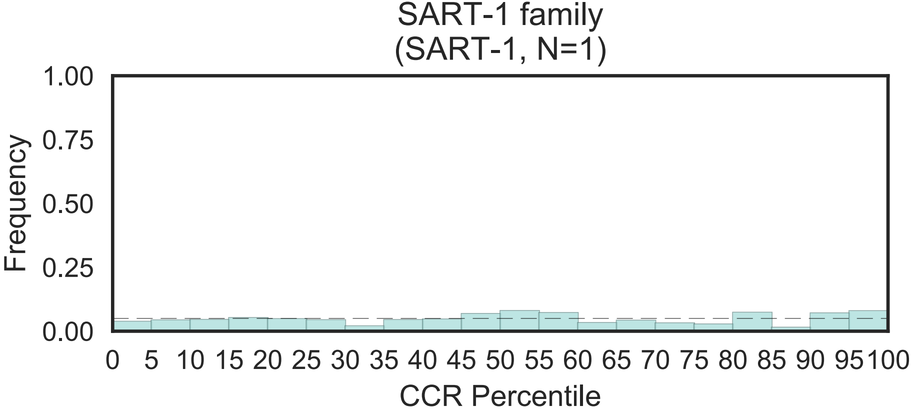


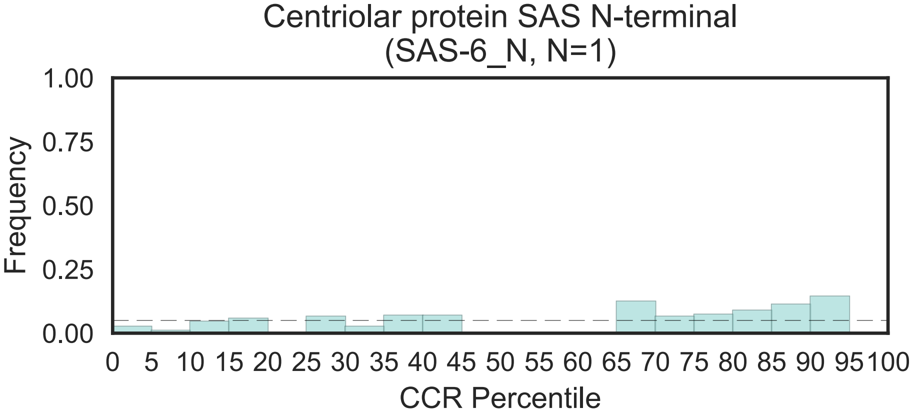

SIT4 phosphatase-associated protein
(SAPS, N=4)
Fisher's OR: 0.572; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

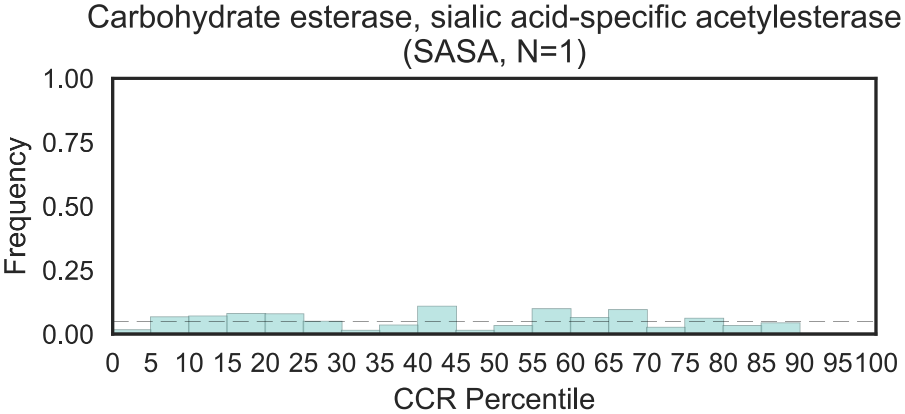

Smad anchor for receptor activation (SARA)
(SARA, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

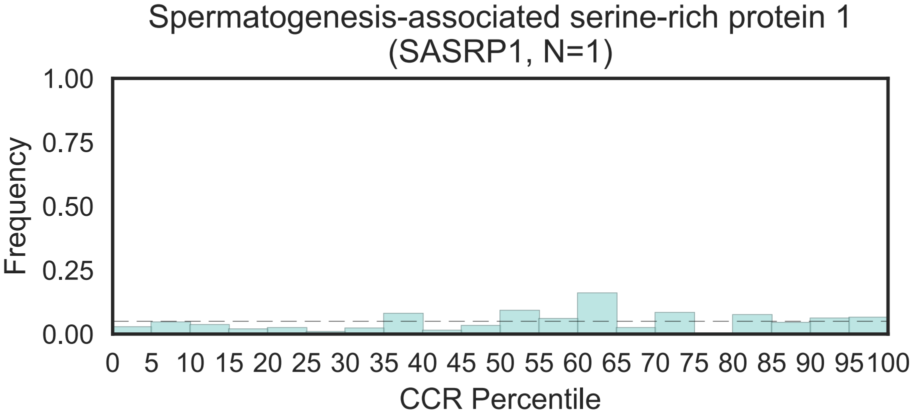

SOCE-associated regulatory factor of calcium homoeostasis
(SARAF, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

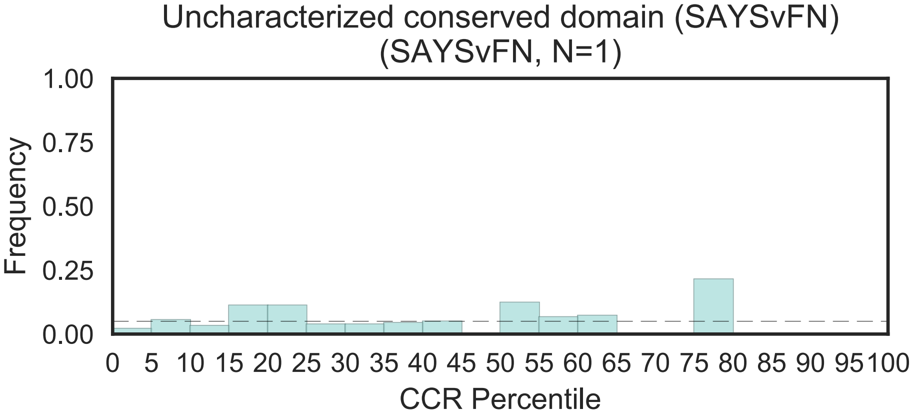

Specifically androgen-regulated gene protein
(SARG, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

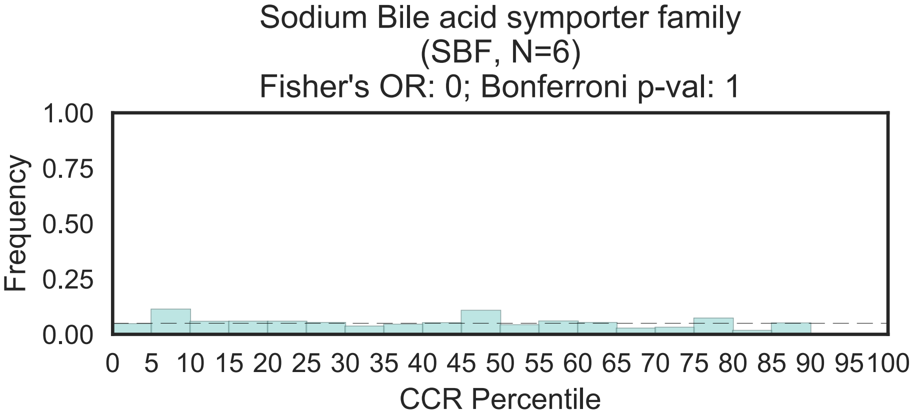

SART-1 family
(SART-1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


Centriolar protein SAS N-terminal
(SAS-6_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

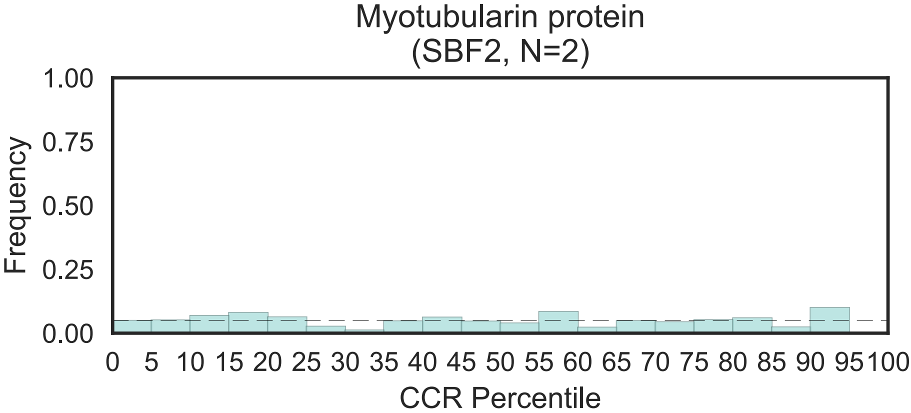

Carbohydrate esterase, sialic acid-specific acetylesterase (SASA, N=1)

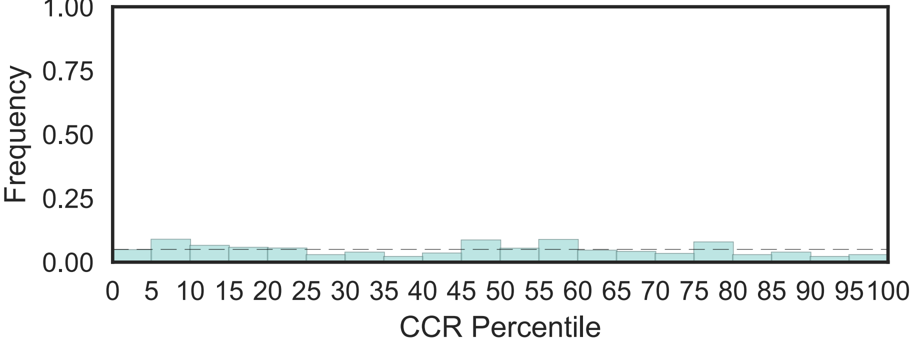

Spermatogenesis-associated serine-rich protein 1
(SASRP1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Uncharacterized conserved domain (SAYSvFN)
(SAYSvFN, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

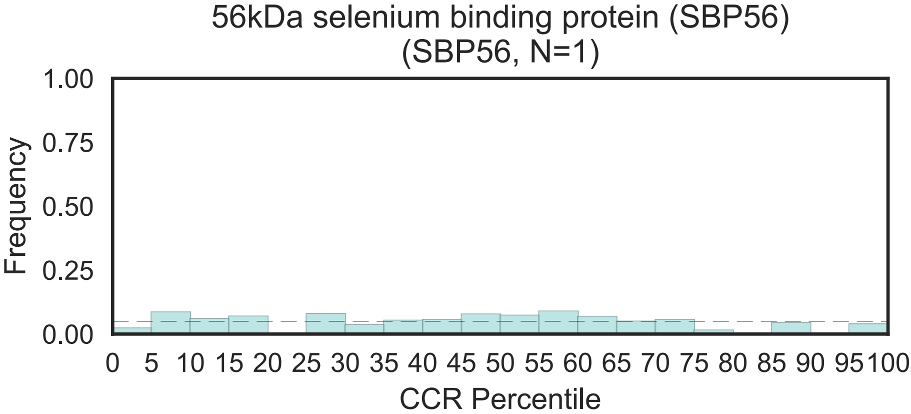


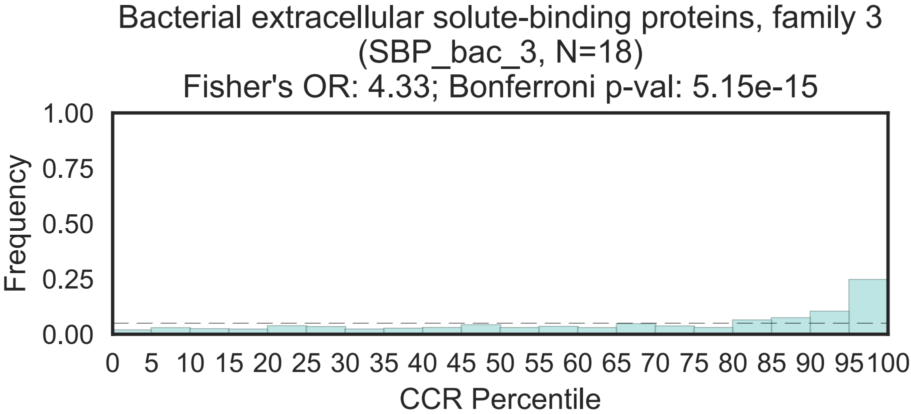
Sodium Bile acid symporter family
(SBF, N=6)
Fisher's OR: 0; Bonferroni p-val: 1


Myotubularin protein
(SBF2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

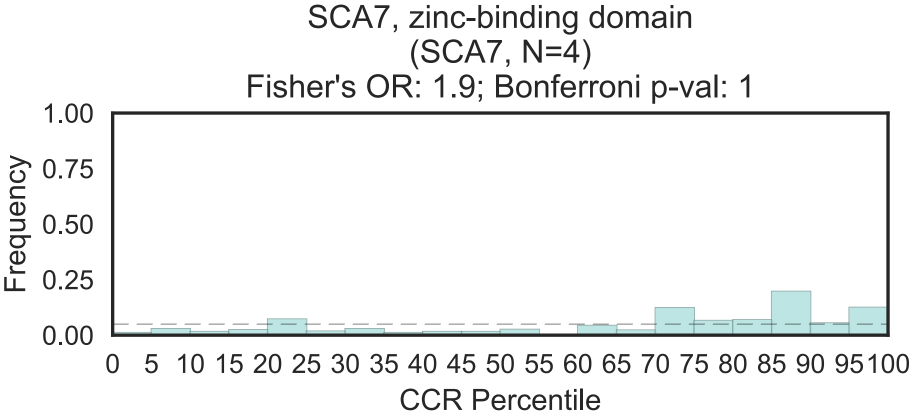


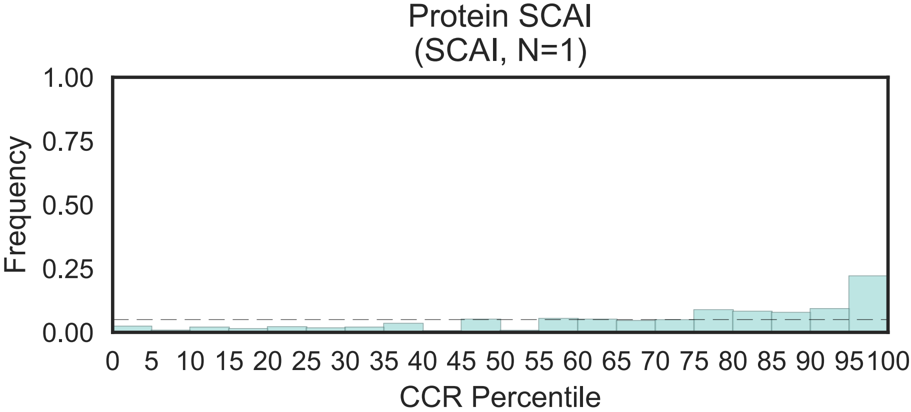
SBF-like CPA transporter family (DUF4137)
(SBF_like, N=2)

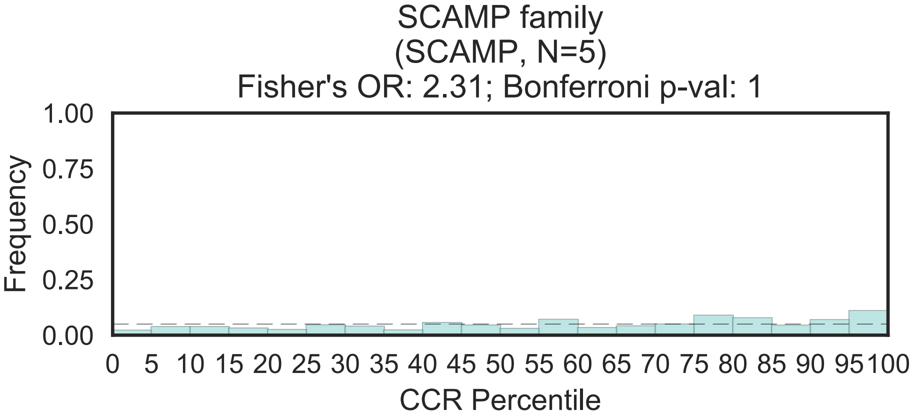

56kDa selenium binding protein (SBP56)
(SBP56, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

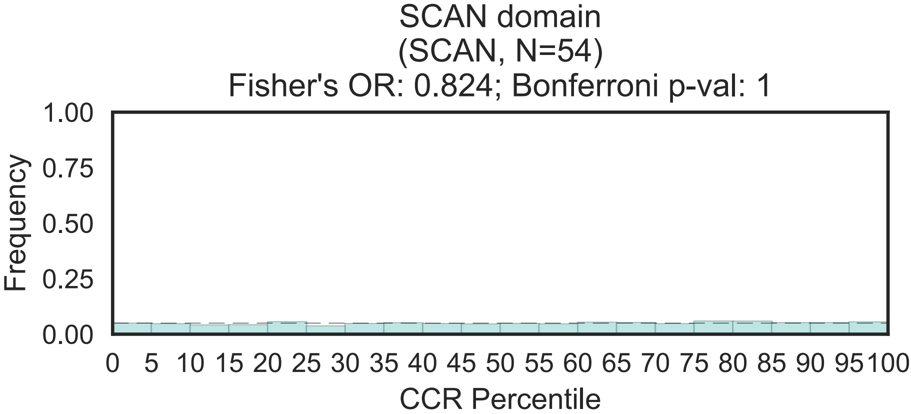


Bacterial extracellular solute-binding proteins, family 3
(SBP_bac_3, N=18)
Fisher's OR: 4.33; Bonferroni p-val: 5.15e-15

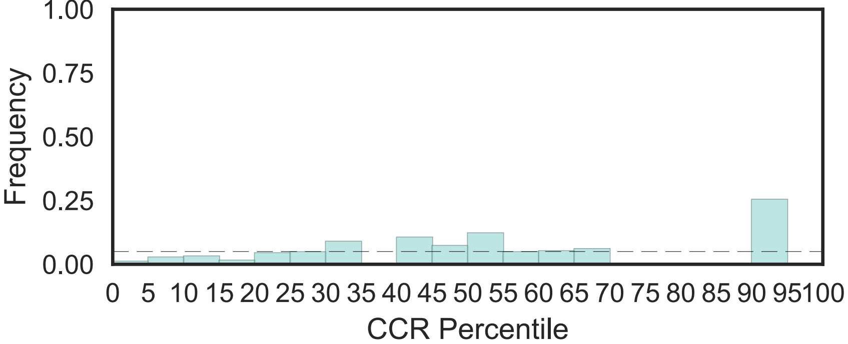

SCA7, zinc-binding domain
(SCA7, N=4)
Fisher's OR: 1.9; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

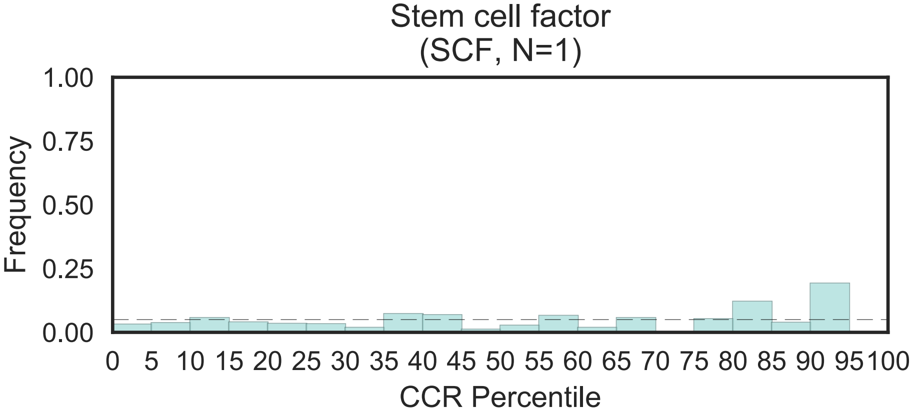

Protein SCAI
(SCAI, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

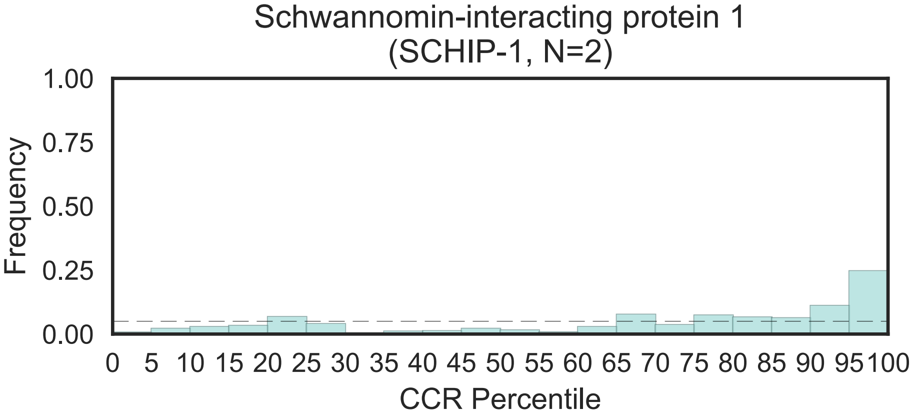

SCAMP family
(SCAMP, N=5)
Fisher's OR: 2.31; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

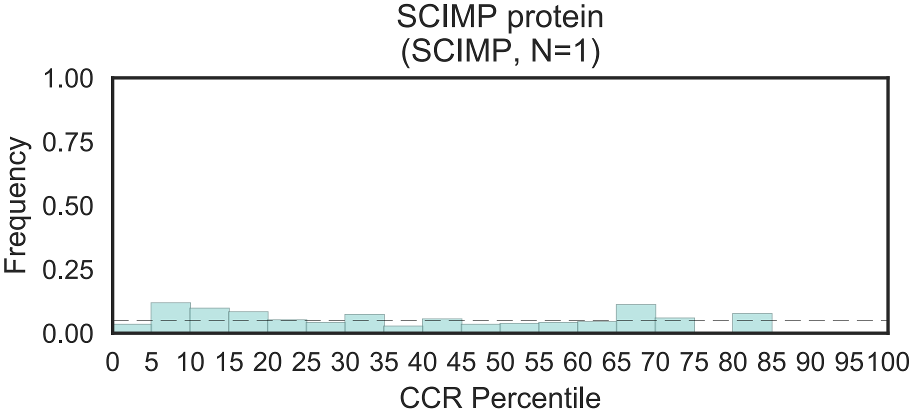

SCAN domain
(SCAN, N=54)
Fisher's OR: 0.824; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

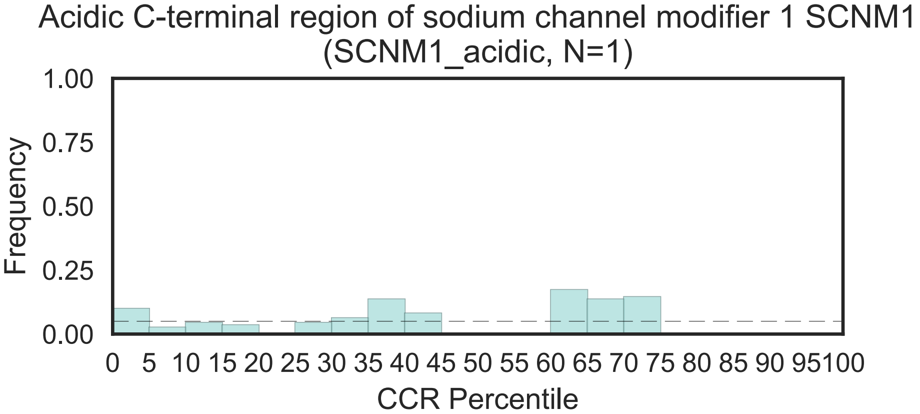
S phase cyclin A-associated protein in the endoplasmic reticulum (SCAPER_N, N=1)

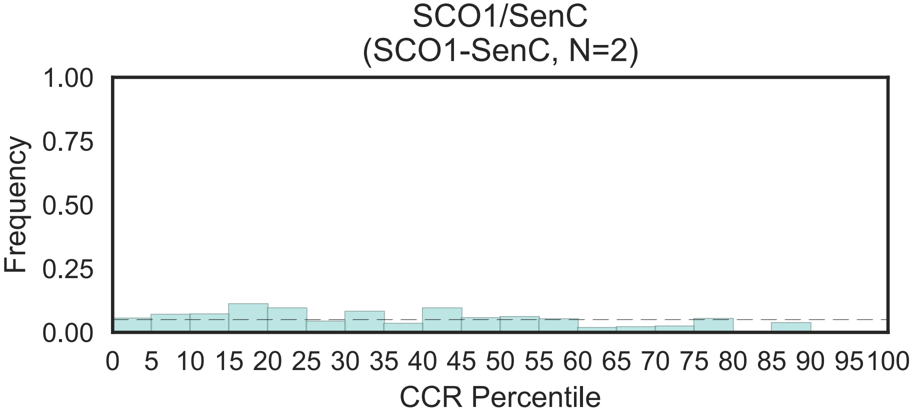


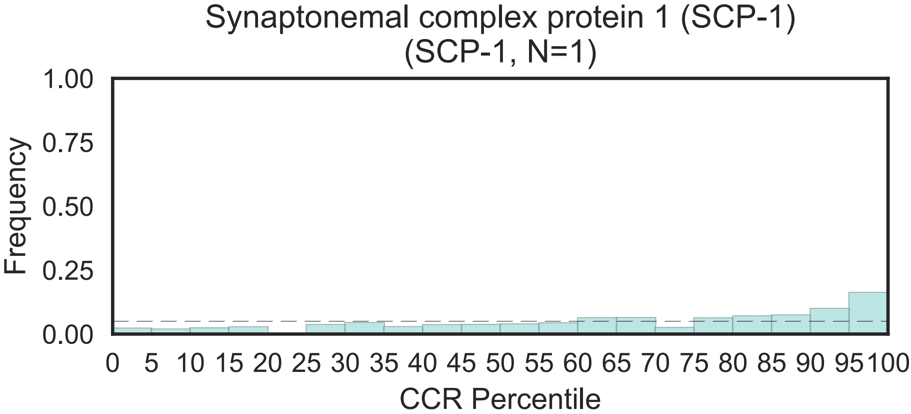

Stem cell factor
(SCF, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

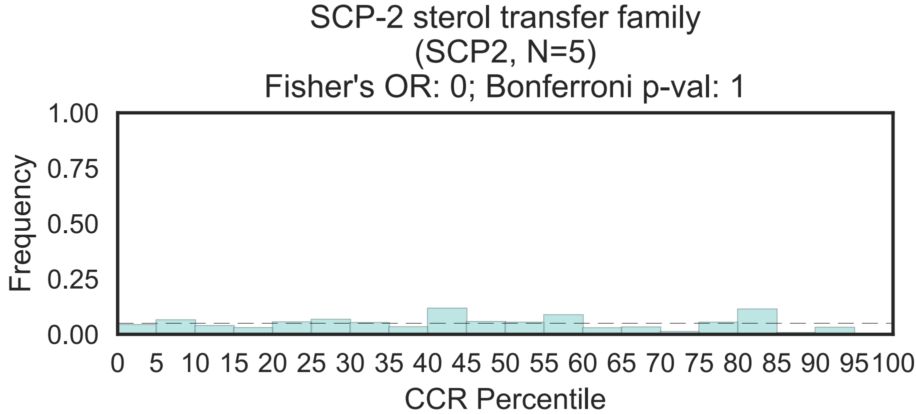
Schwannomin-interacting protein 1
(SCHIP-1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

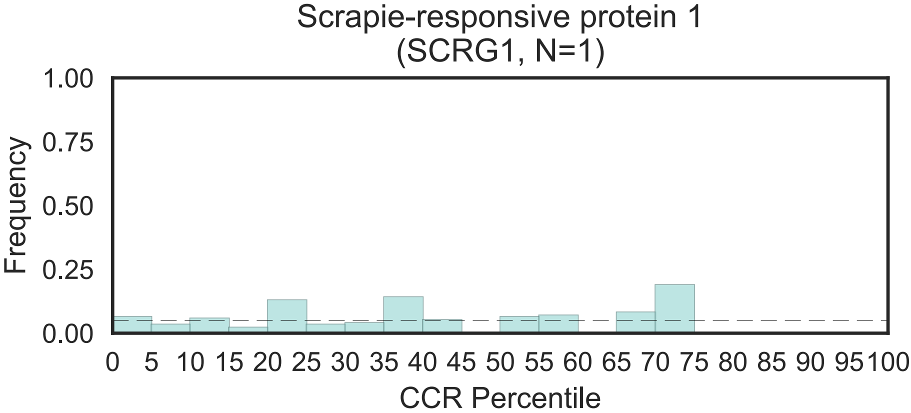

SCIMP protein
(SCIMP, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

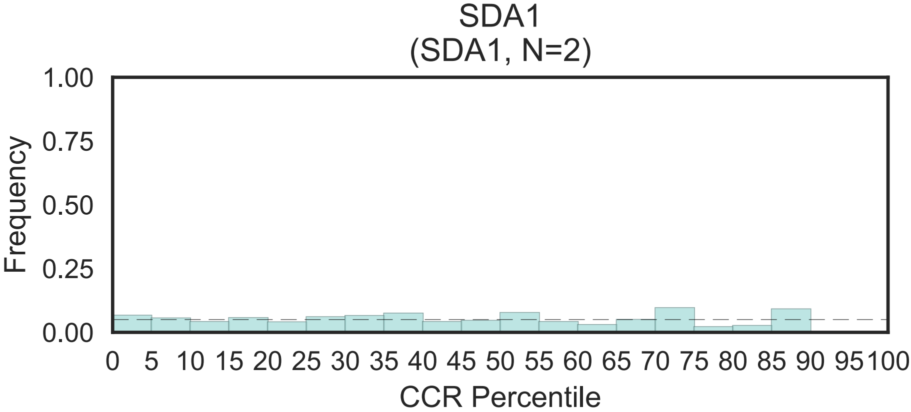

Acidic C-terminal region of sodium channel modifier 1 SCNM1 (SCNM1_acidic, N=1)

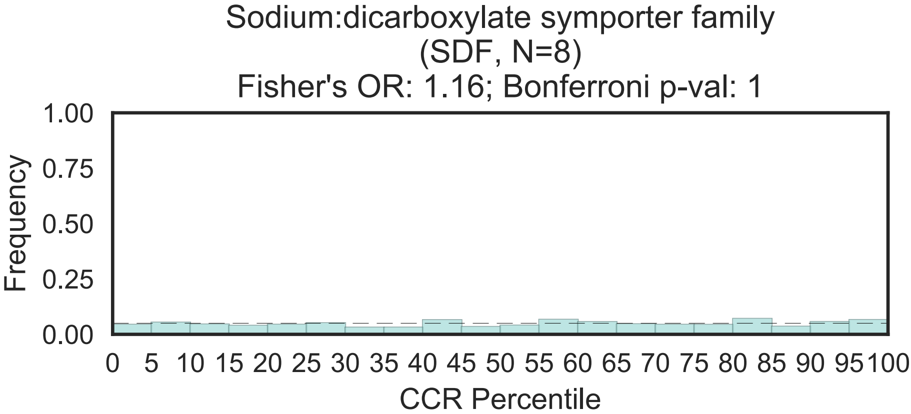

SCO1/SenC
(SCO1-SenC, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


Synaptonemal complex protein 1 (SCP-1)
(SCP-1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

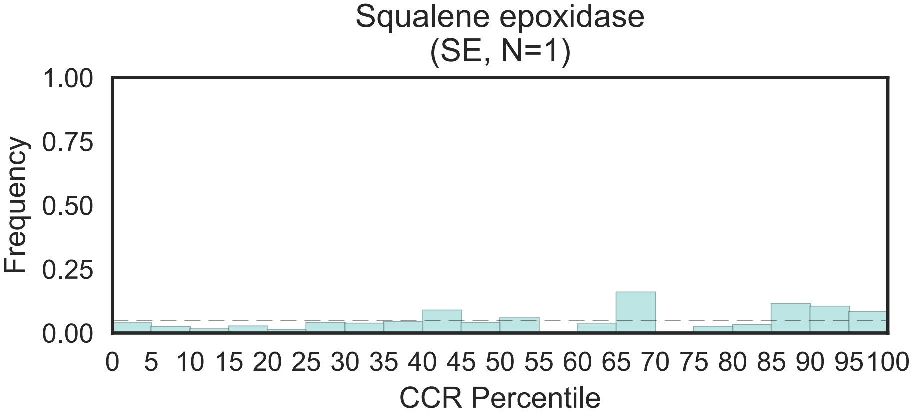

SCP-2 sterol transfer family
(SCP2, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

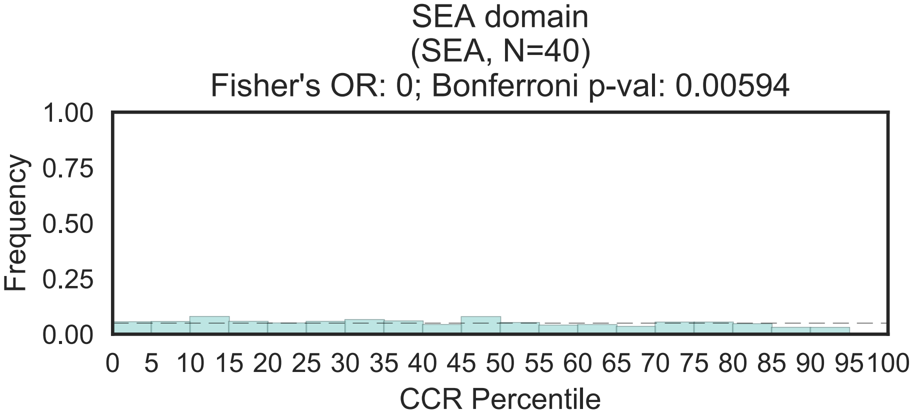

Scrapie-responsive protein 1
(SCRG1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

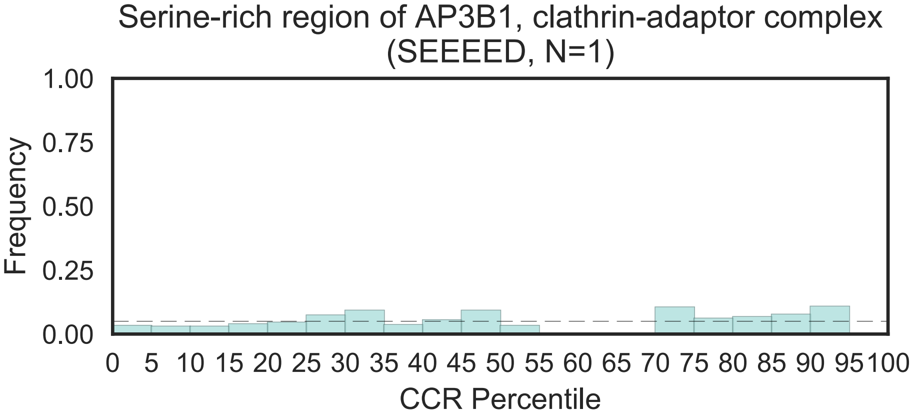

SDA1
(SDA1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

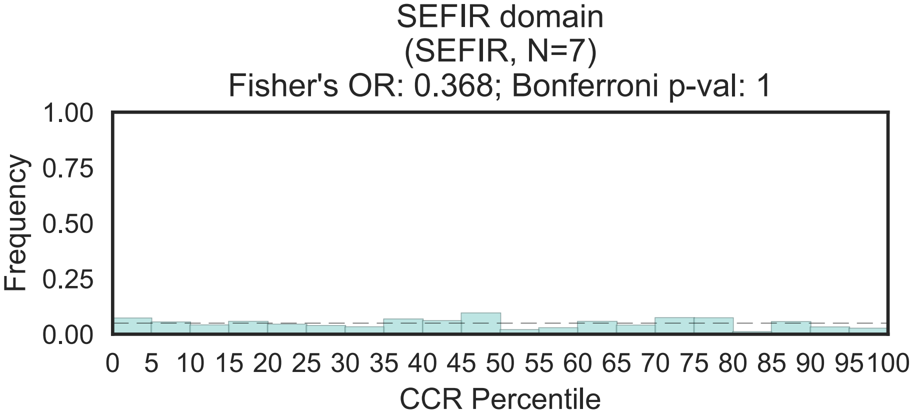


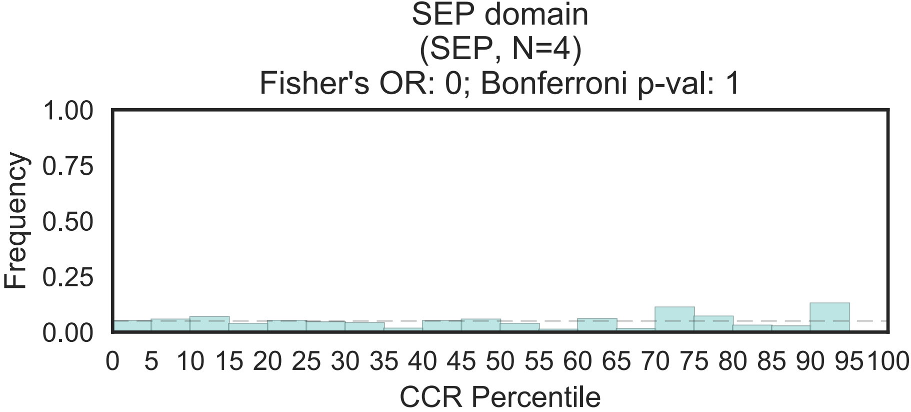
Sodium:dicarboxylate symporter family
(SDF, N=8)
Fisher's OR: 1.16; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

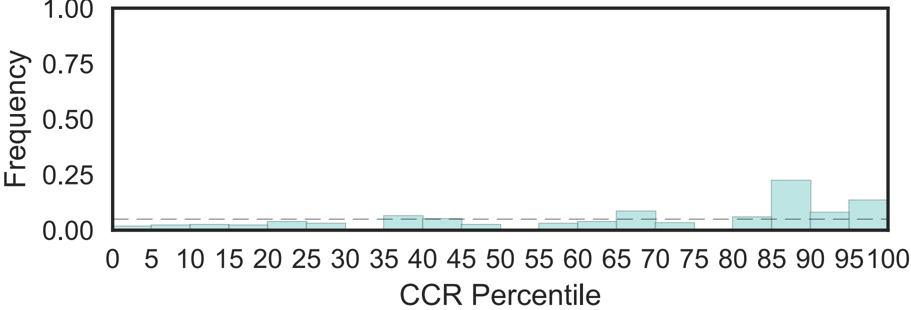

Squalene epoxidase
(SE, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

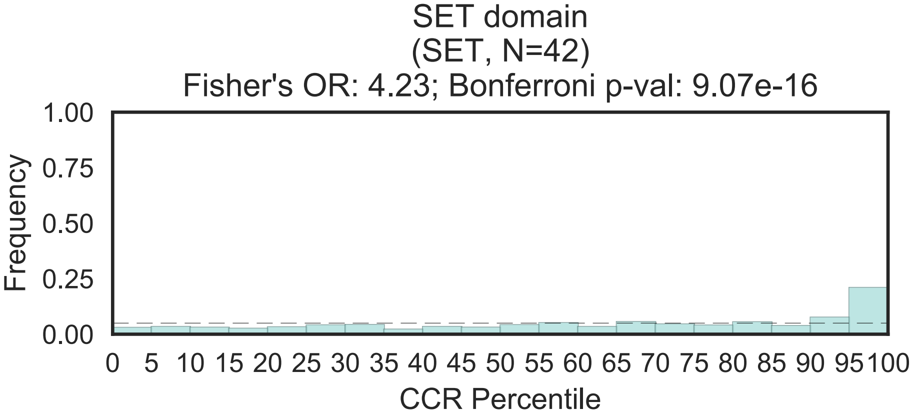

SEA domain
(SEA, N=40)
Fisher's OR: 0; Bonferroni p-val: 0.00594
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

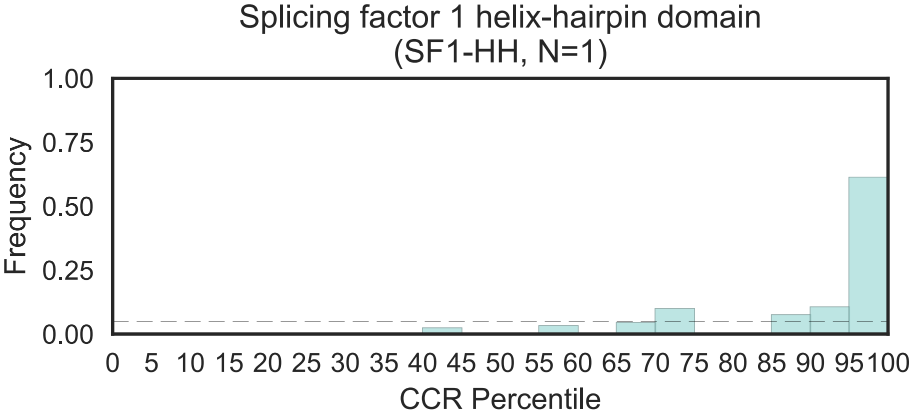

Serine-rich region of AP3B1, clathrin-adaptor complex
(SEEEED, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


SEFIR domain
(SEFIR, N=7)
Fisher's OR: 0.368; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

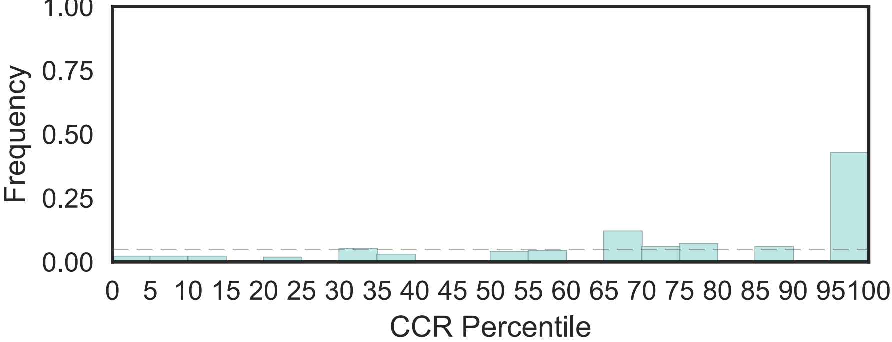

SEP domain
(SEP, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

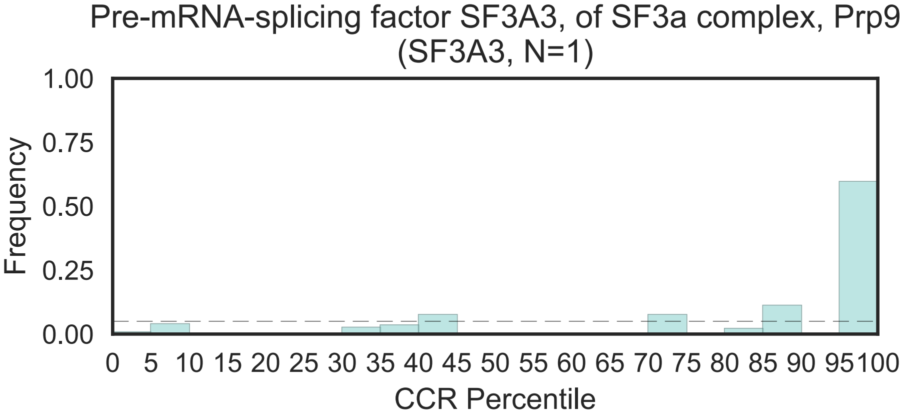

SERTA motif
(SERTA, N=5)
Fisher's OR: 3; Bonferroni p-val: 1

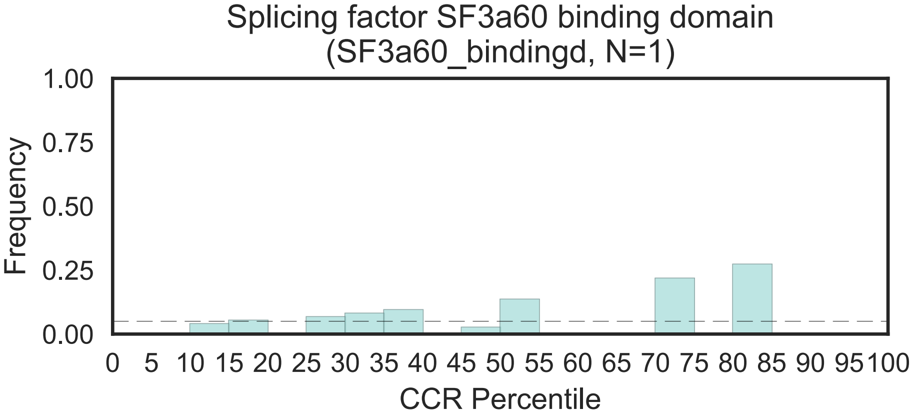

SET domain
(SET, N=42)
Fisher's OR: 4.23; Bonferroni p-val: 9.07e-16
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

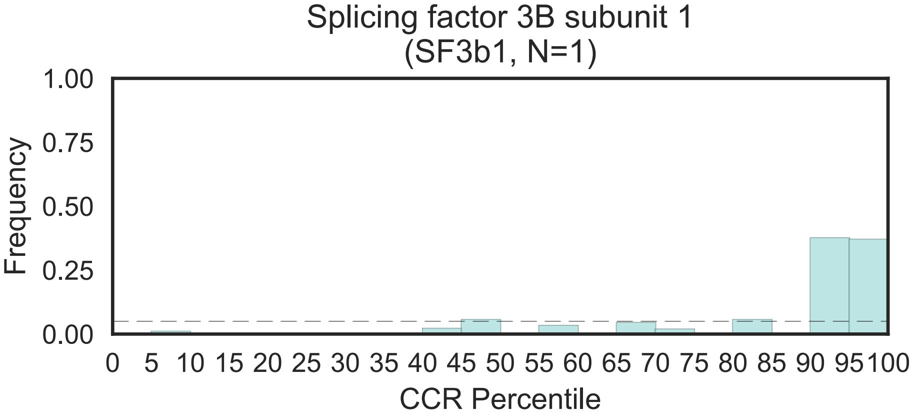

Splicing factor 1 helix-hairpin domain
(SF1-HH, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

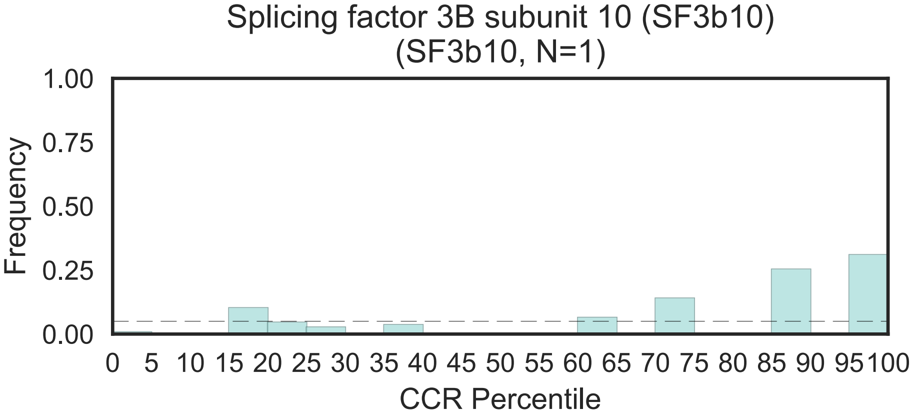
Pre-mRNA-splicing factor SF3a complex subunit 2 (Prp11) (SF3A2, N=1)

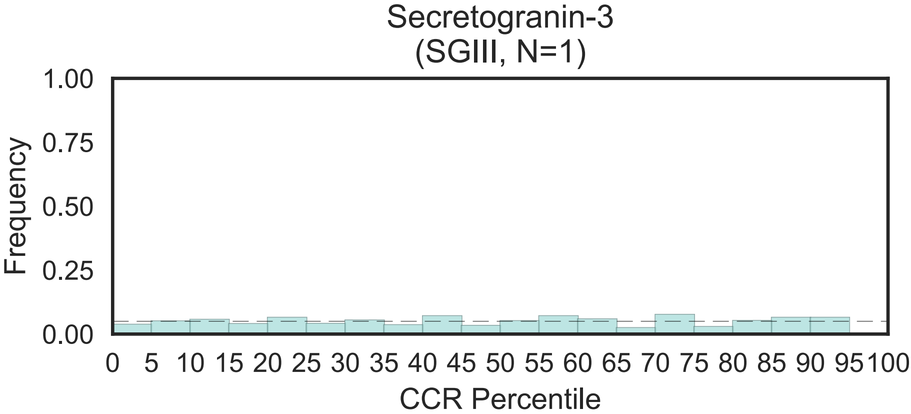


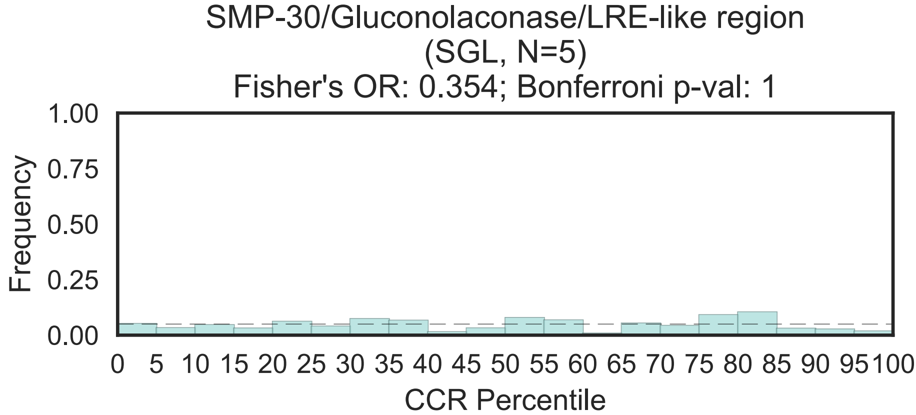

Pre-mRNA-splicing factor SF3A3, of SF3a complex, Prp9
(SF3A3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

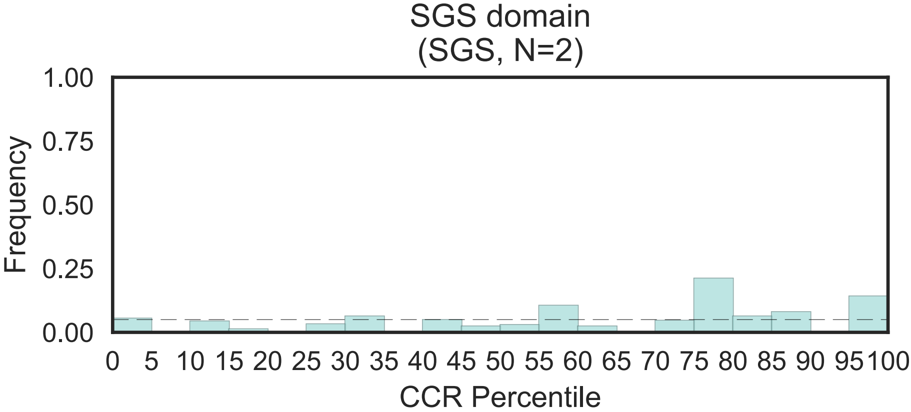

Splicing factor SF3a60 binding domain
(SF3a60_bindingd, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

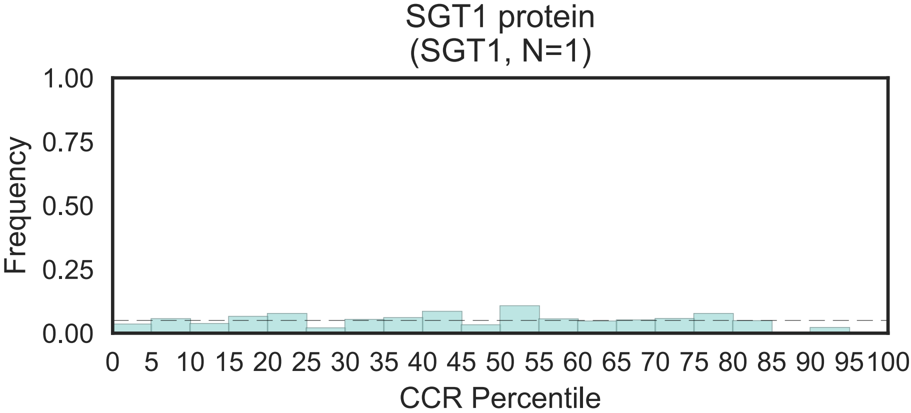

Splicing factor 3B subunit 1
(SF3b1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

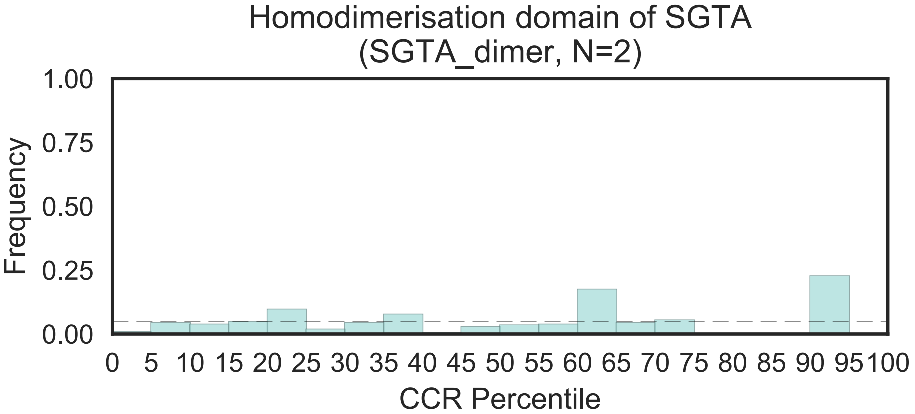

Splicing factor 3B subunit 10 (SF3b10)
(SF3b10, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

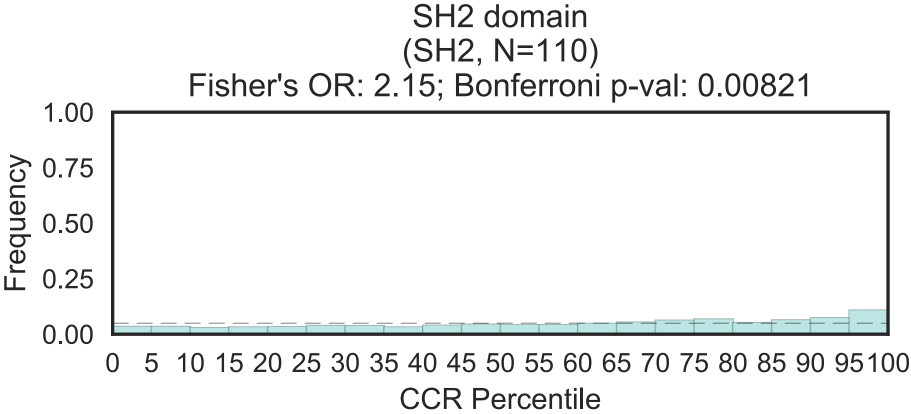

Secretogranin-3
(SGIII, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

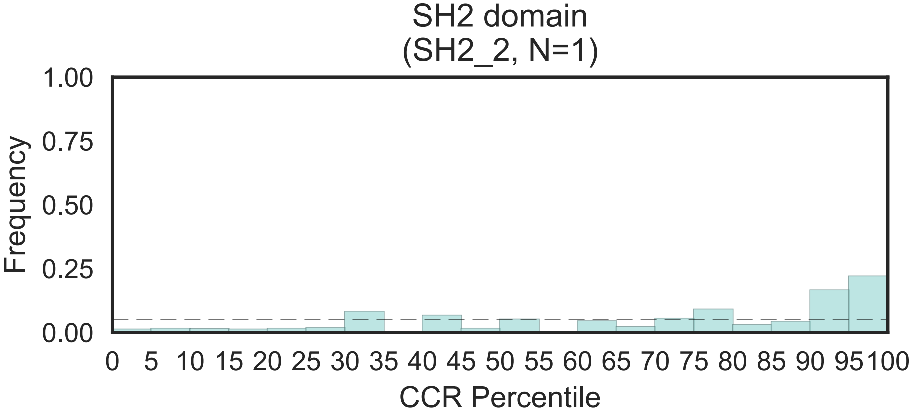

SMP-30/Gluconolaconase/LRE-like region
(SGL, N=5)
Fisher's OR: 0.354; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

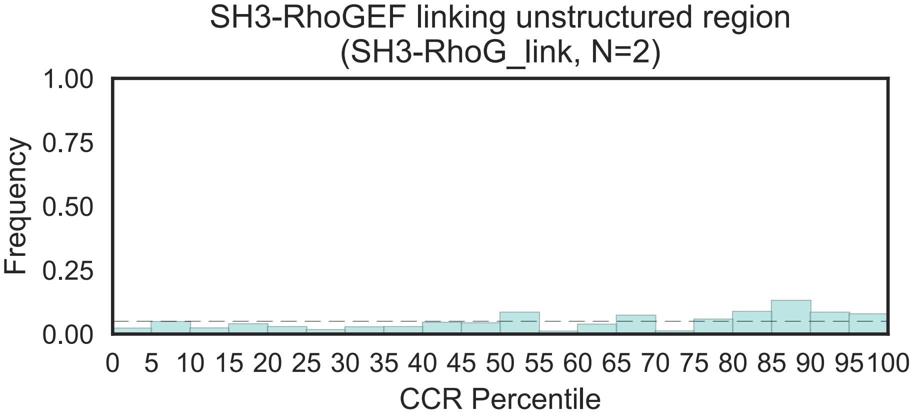

SGS domain
(SGS, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

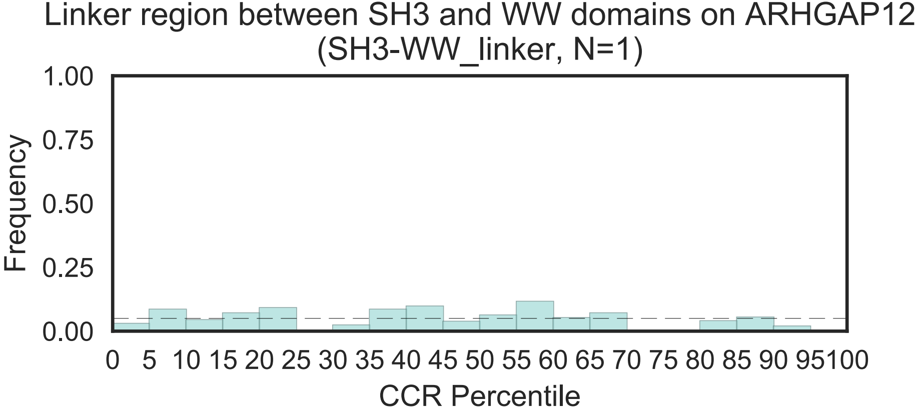

SGT1 protein
(SGT1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

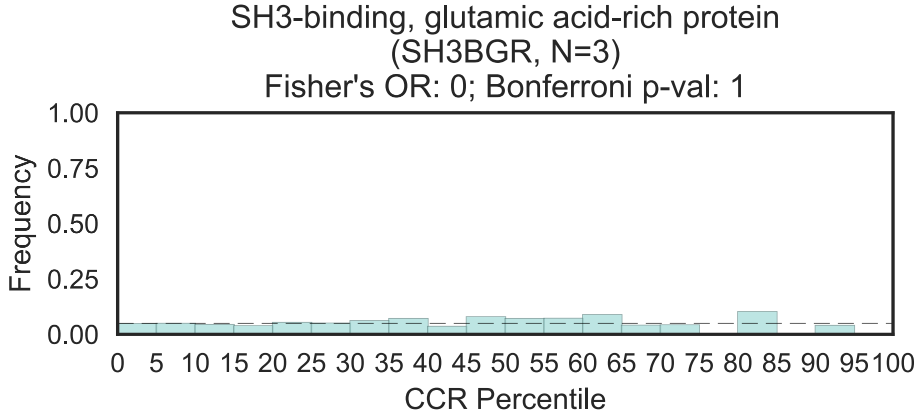

Homodimerisation domain of SGTA
(SGTA_dimer, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

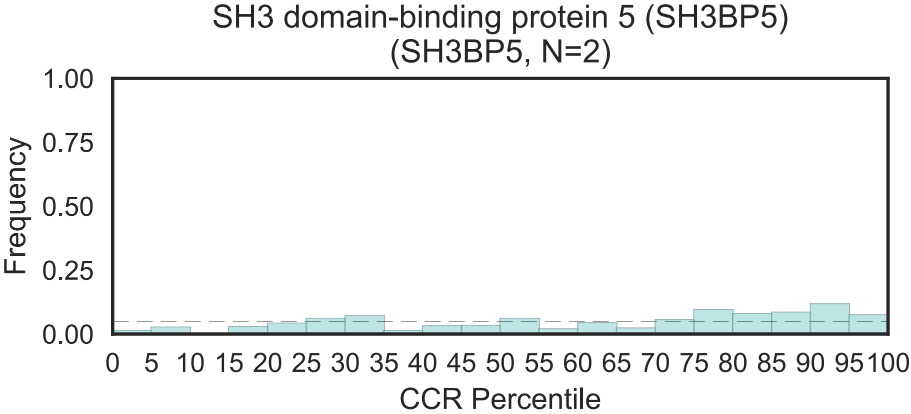

SH2 domain
(SH2, N=110)
Fisher's OR: 2.15; Bonferroni p-val: 0.00821
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

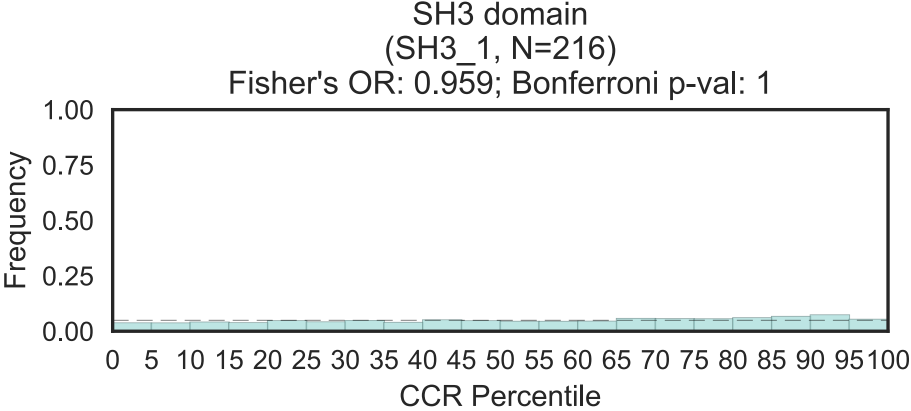

SH2 domain
(SH2_2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

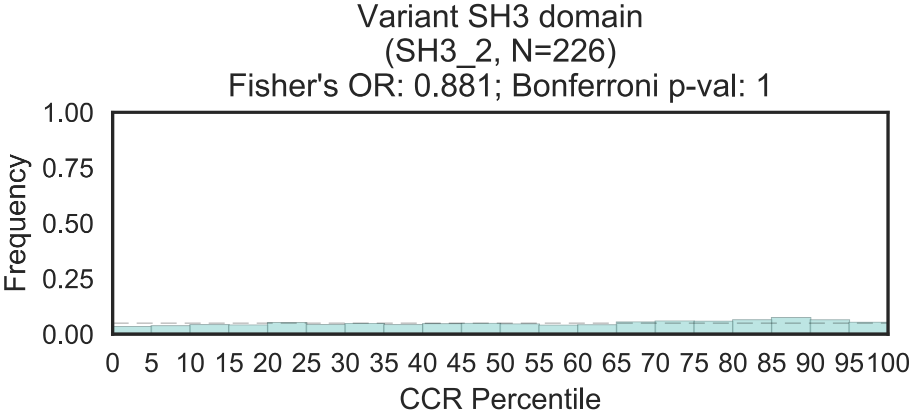

SH3-RhoGEF linking unstructured region
(SH3-RhoG_link, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

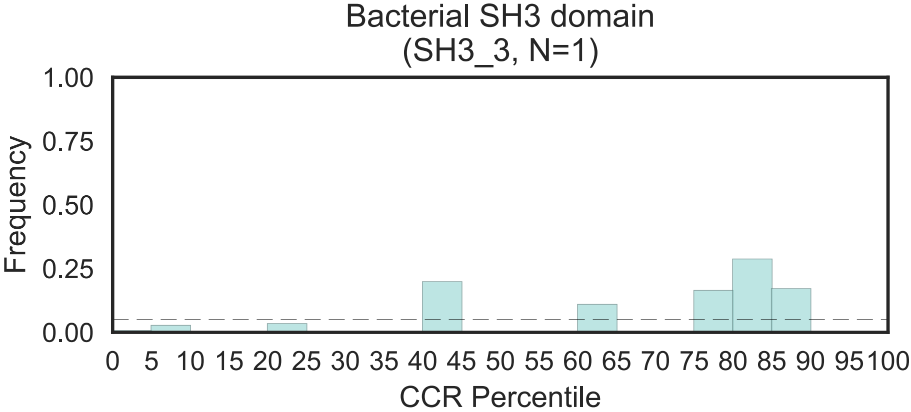

Linker region between SH3 and WW domains on ARHGAP12
(SH3-WW_linker, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

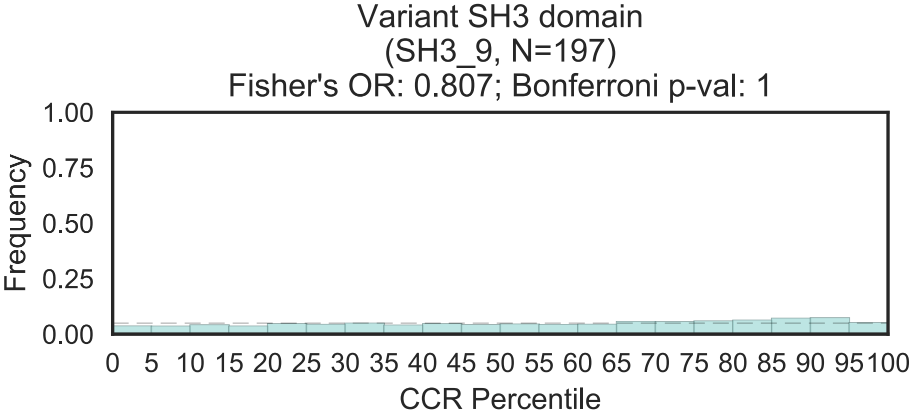

SH3-binding, glutamic acid-rich protein
(SH3BGR, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


SH3 domain-binding protein 5 (SH3BP5)
(SH3BP5, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

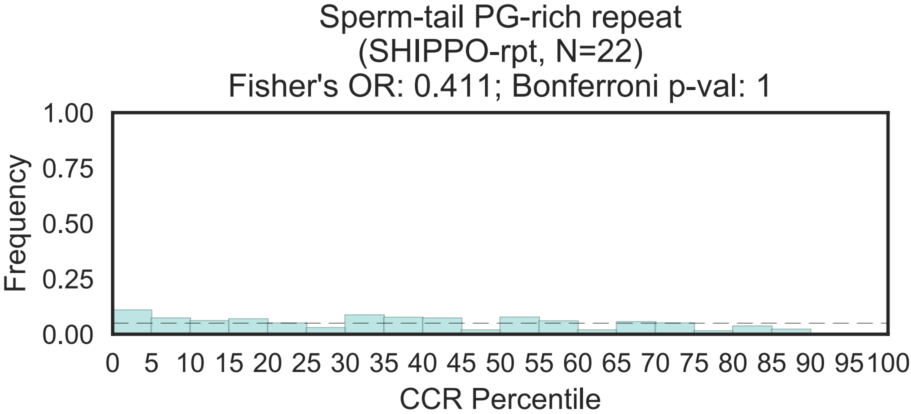

SH3 domain
(SH3_1, N=216)
Fisher's OR: 0.959; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

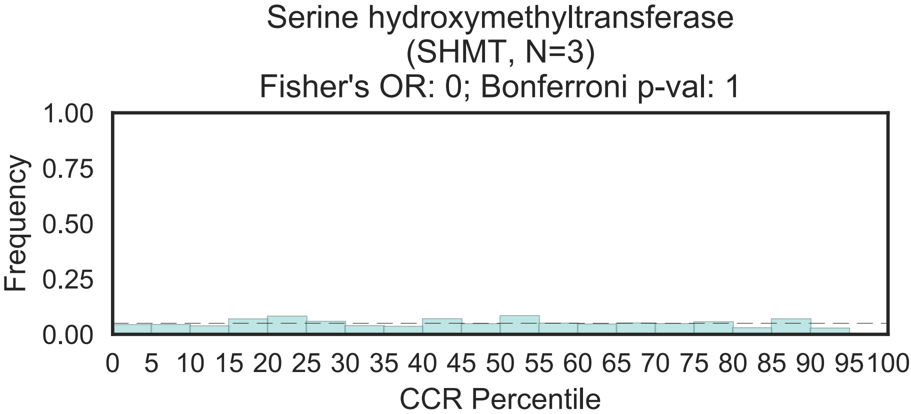

Variant SH3 domain
(SH3_2, N=226)
Fisher's OR: 0.881; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

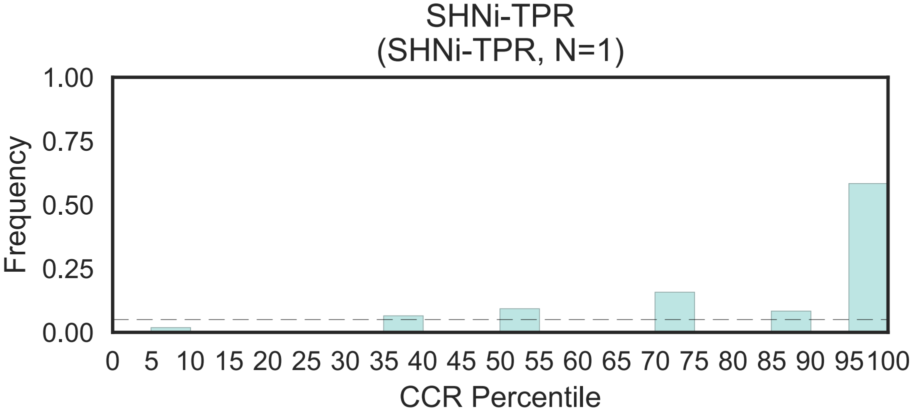

Bacterial SH3 domain
(SH3_3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

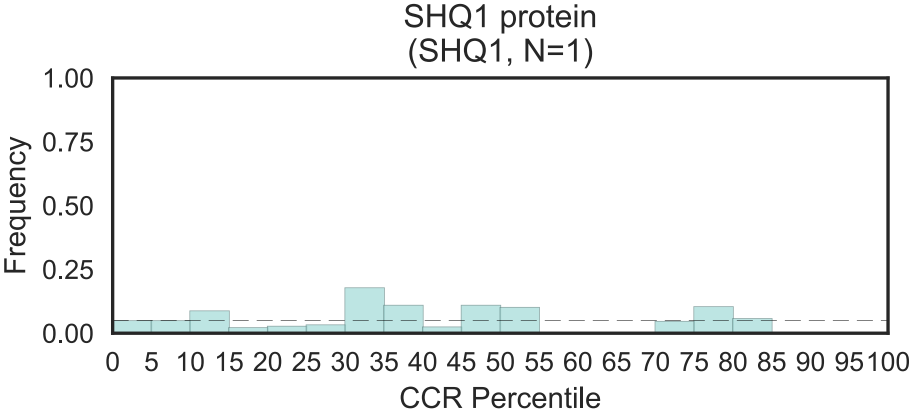


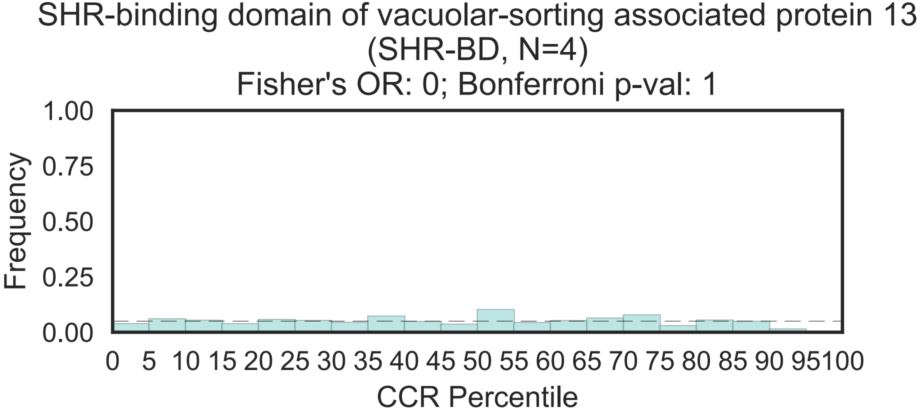
Variant SH3 domain
(SH3_9, N=197)
Fisher's OR: 0.807; Bonferroni p-val: 1

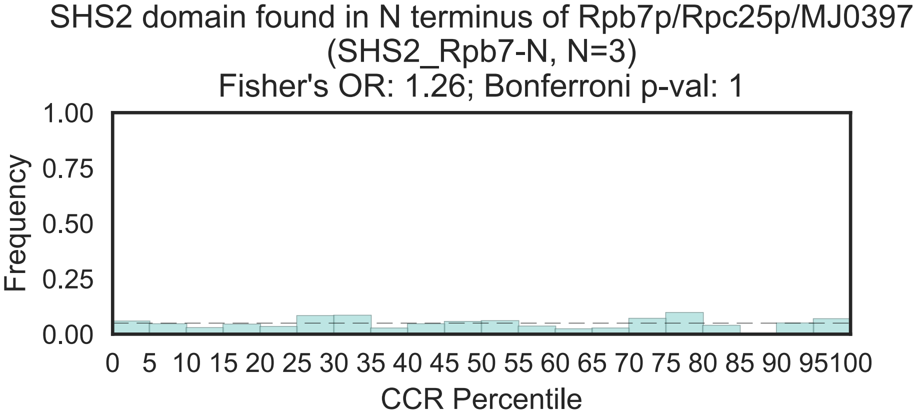

Sperm-tail PG-rich repeat
(SHIPPO-rpt, N=22)
Fisher's OR: 0.411; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

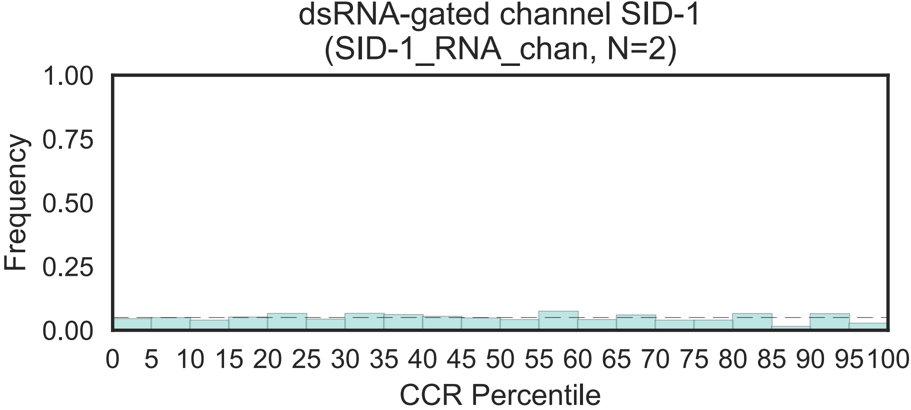

Serine hydroxymethyltransferase
(SHMT, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

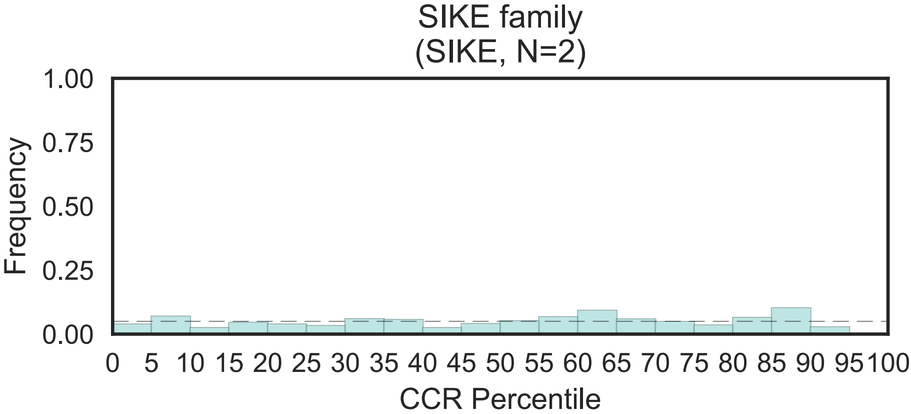

SHNi-TPR
(SHNi-TPR, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


SHQ1 protein
(SHQ1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

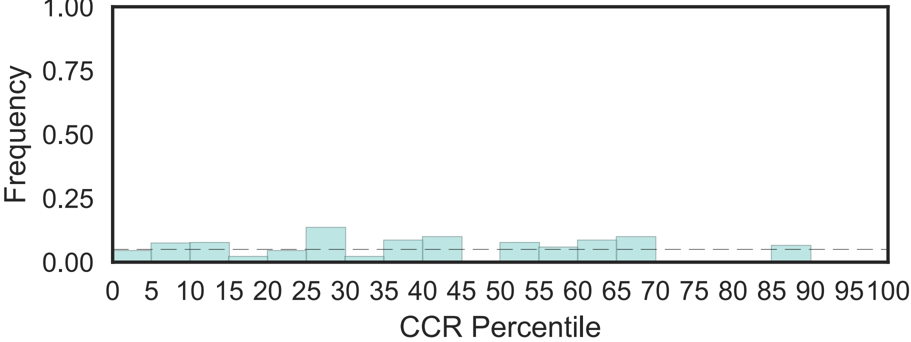

SHR-binding domain of vacuolar-sorting associated protein 13
(SHR-BD, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

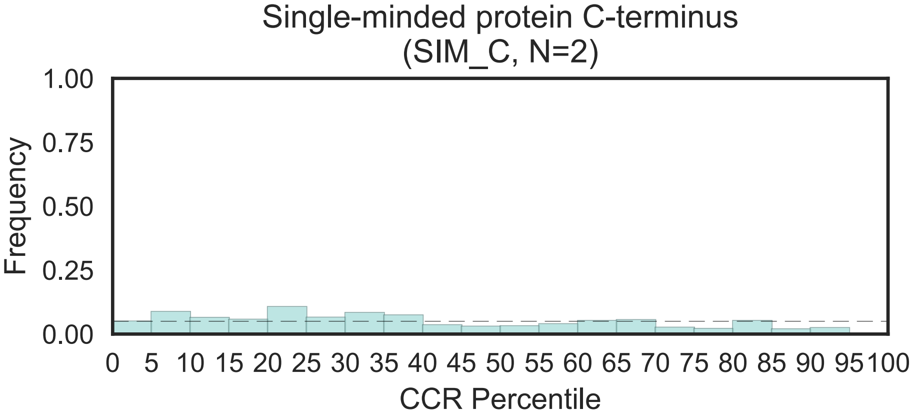

SHS2 domain found in N terminus of Rpb7p/Rpc25p/MJ0397
(SHS2_Rpb7-N, N=3)
Fisher's OR: 1.26; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

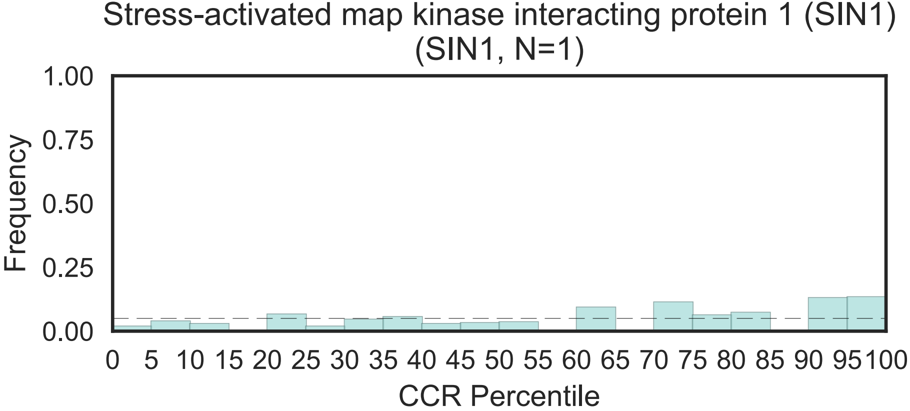

dsRNA-gated channel SID-1
(SID-1_RNA_chan, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


SIKE family
(SIKE, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

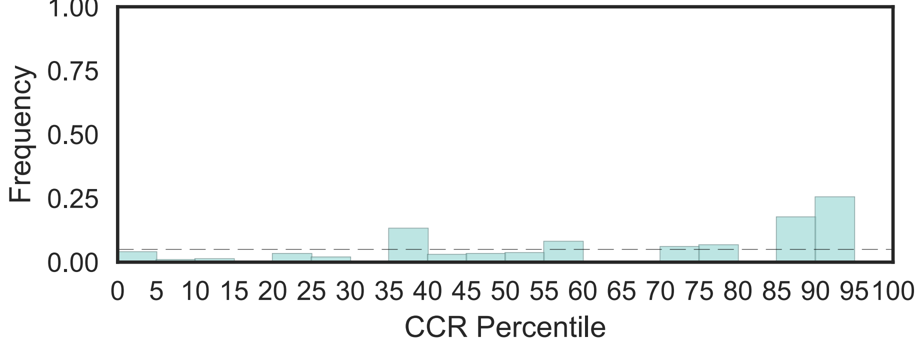
Protein of unknown function (DUF541)
(SIMPL, N=1)

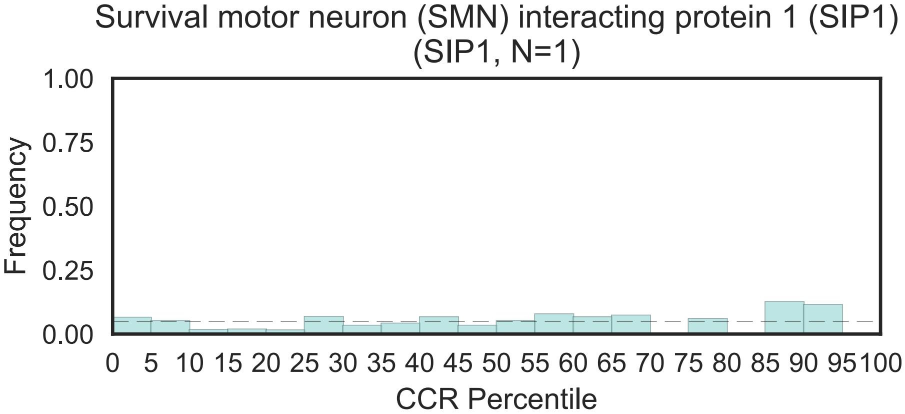


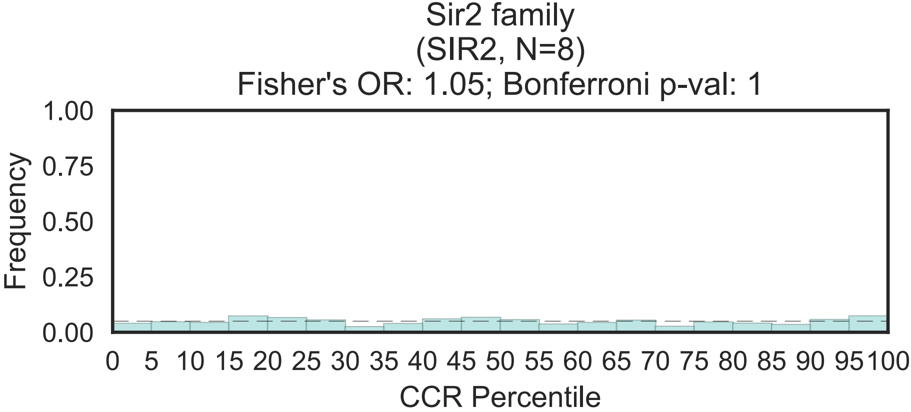

Single-minded protein C-terminus
(SIM_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

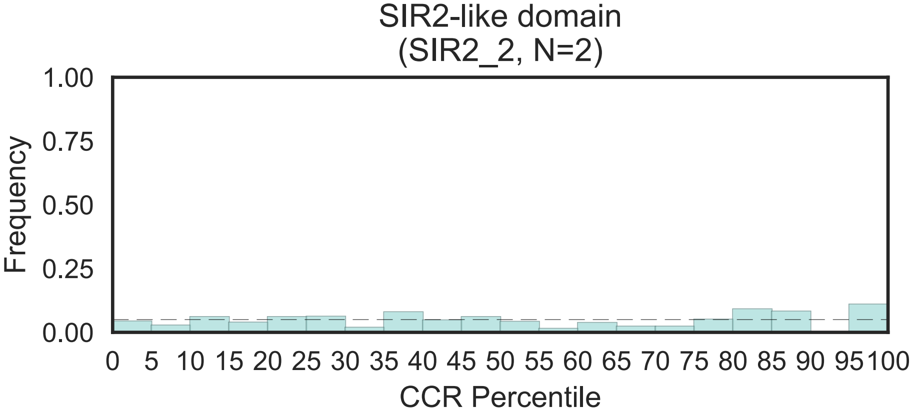

Stress-activated map kinase interacting protein 1 (SIN1)
(SIN1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

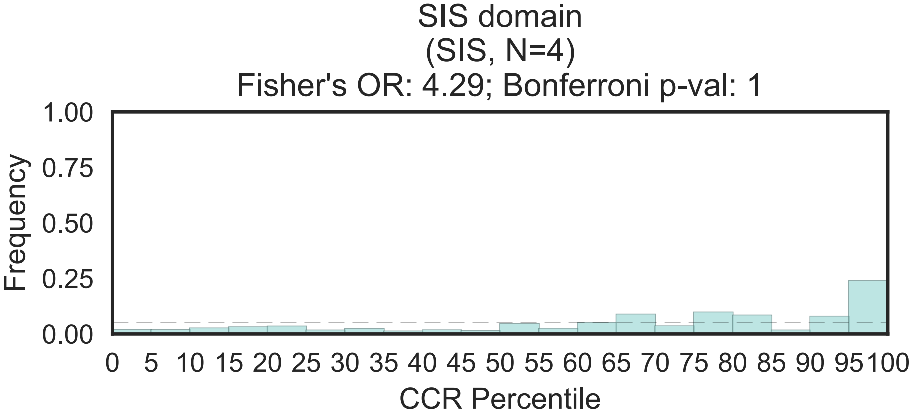
SAPK-interacting protein 1 (Sin1), Pleckstrin-homology (SIN1_PH, N=1)

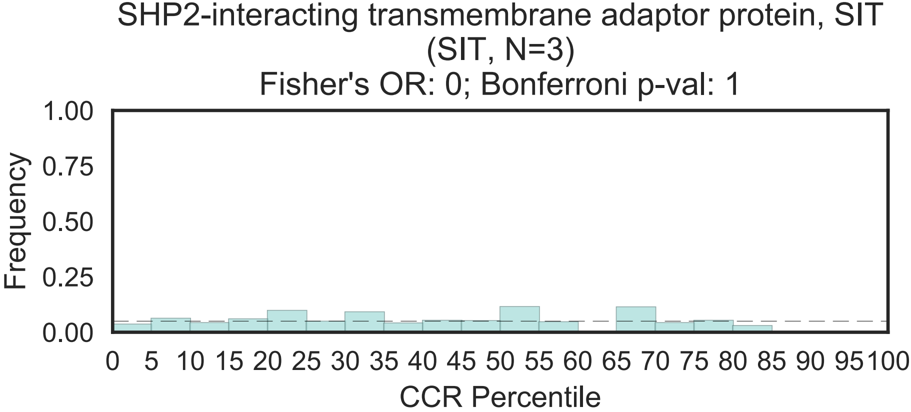


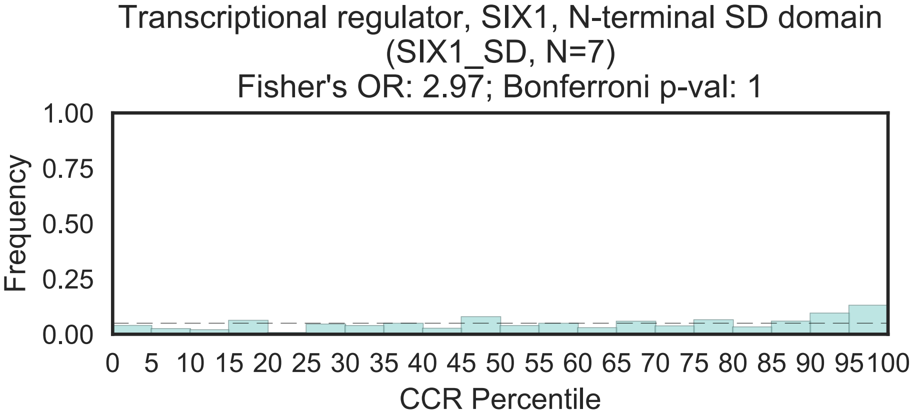

Survival motor neuron (SMN) interacting protein 1 (SIP1)
(SIP1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

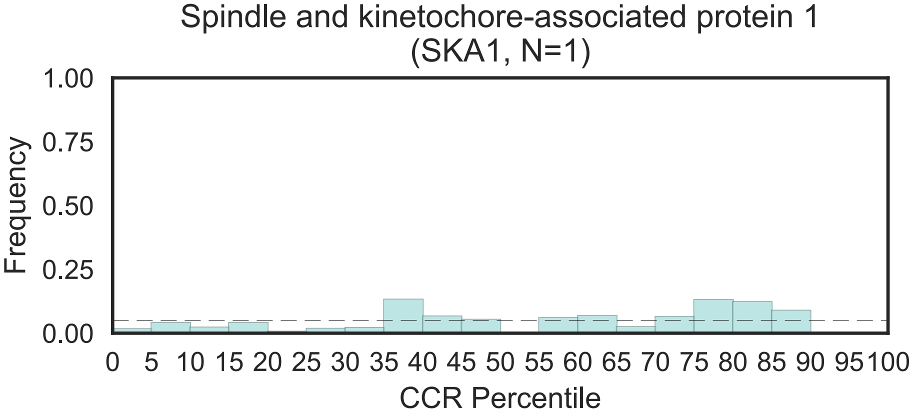

Sir2 family
(SIR2, N=8)
Fisher's OR: 1.05; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

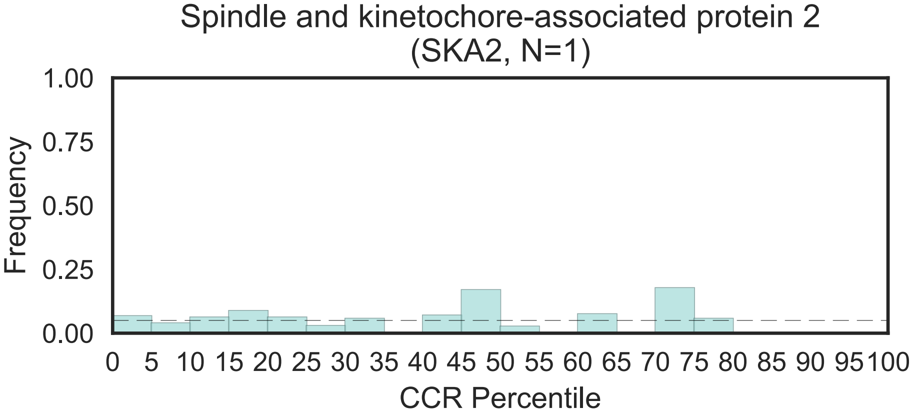

SIR2-like domain
(SIR2_2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

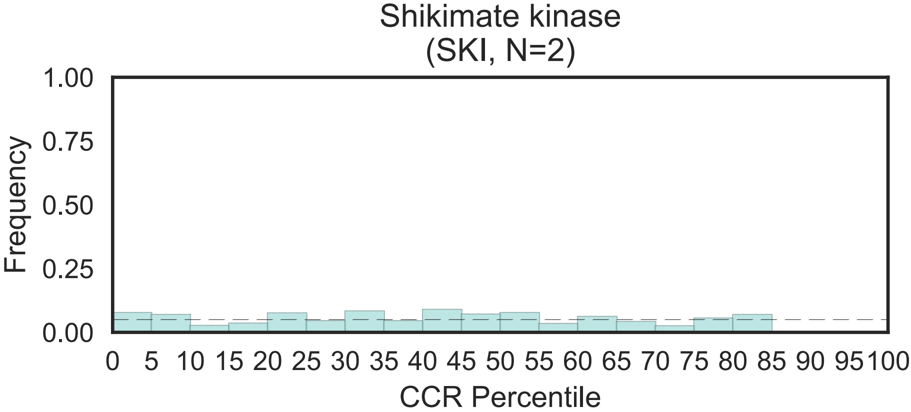

SIS domain
(SIS, N=4)
Fisher's OR: 4.29; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

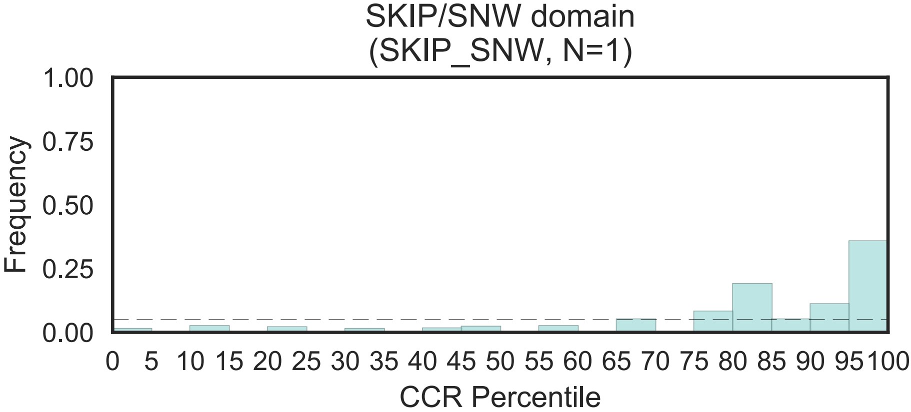

SHP2-interacting transmembrane adaptor protein, SIT
(SIT, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Transcriptional regulator, SIX1, N-terminal SD domain
(SIX1_SD, N=7)
Fisher's OR: 2.97; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

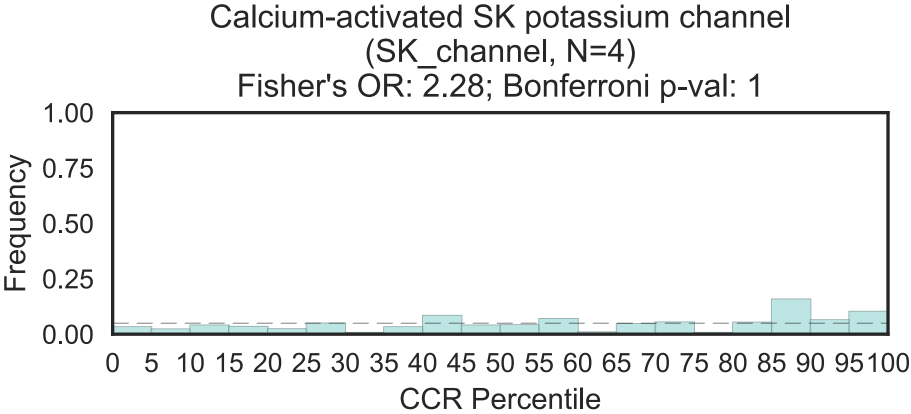

Spindle and kinetochore-associated protein 1
(SKA1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

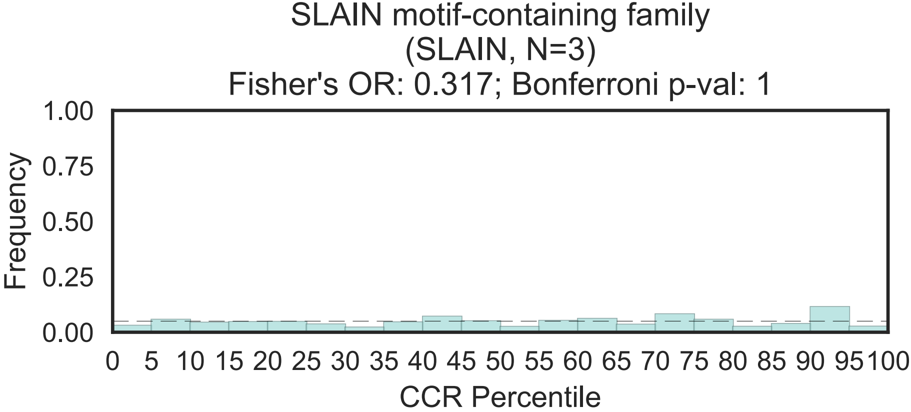

Spindle and kinetochore-associated protein 2
(SKA2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

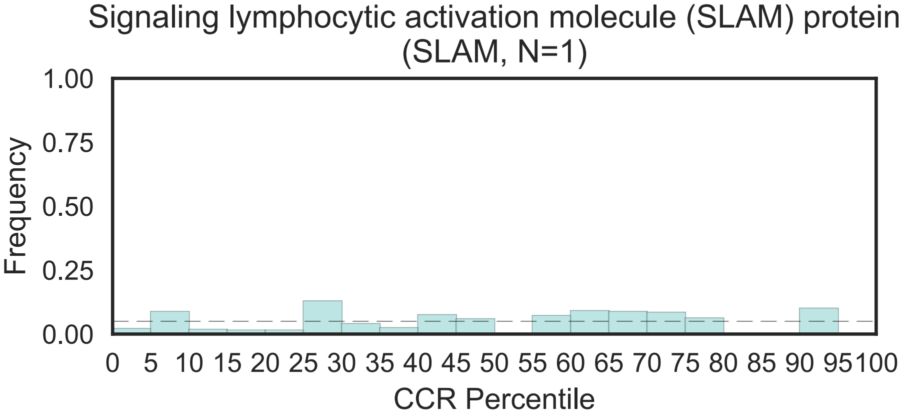

Shikimate kinase
(SKI, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

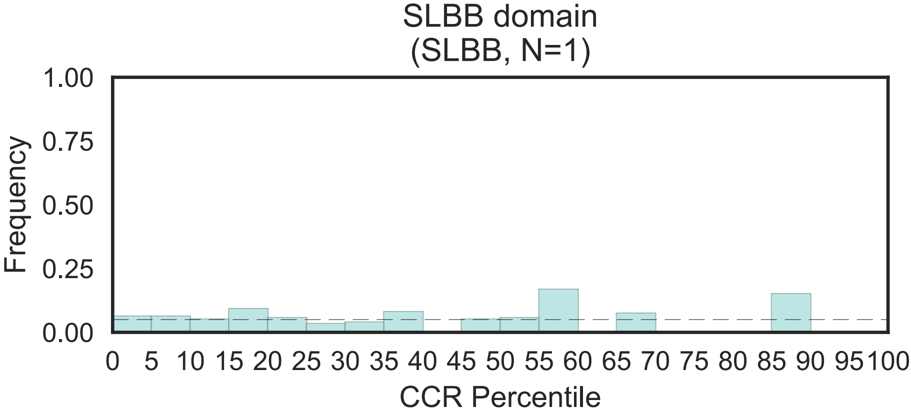


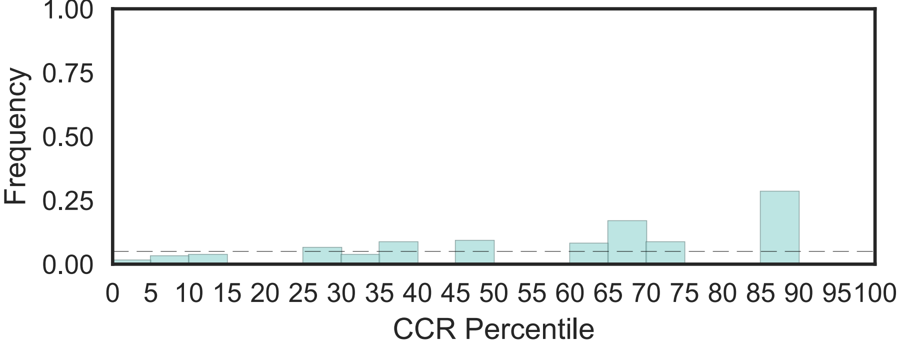
SKIP/SNW domain
(SKIP_SNW, N=1)


Calcium-activated SK potassium channel
(SK_channel, N=4)
Fisher's OR: 2.28; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

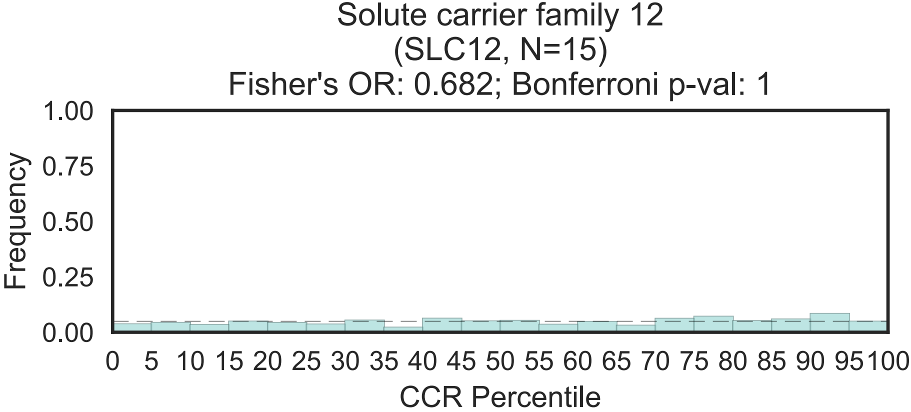

SLAIN motif-containing family
(SLAIN, N=3)
Fisher's OR: 0.317; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

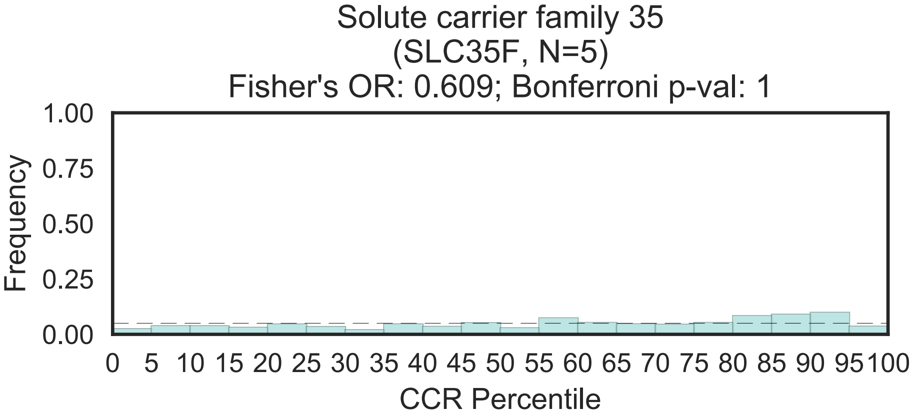

Signaling lymphocytic activation molecule (SLAM) protein
(SLAM, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


SLBB domain
(SLBB, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

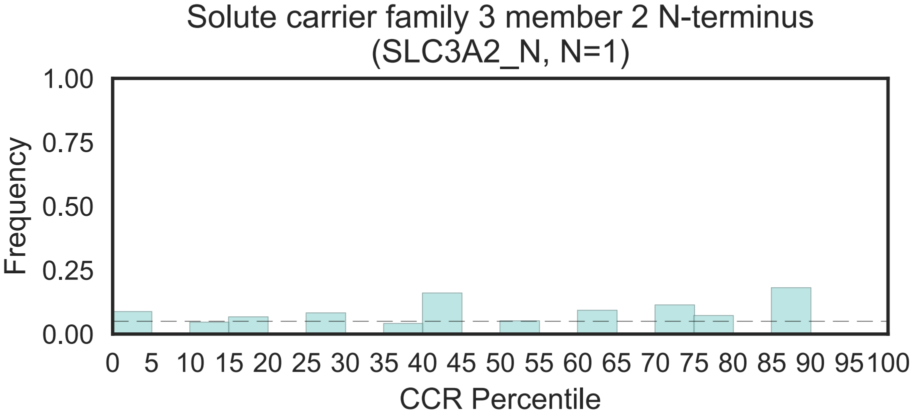


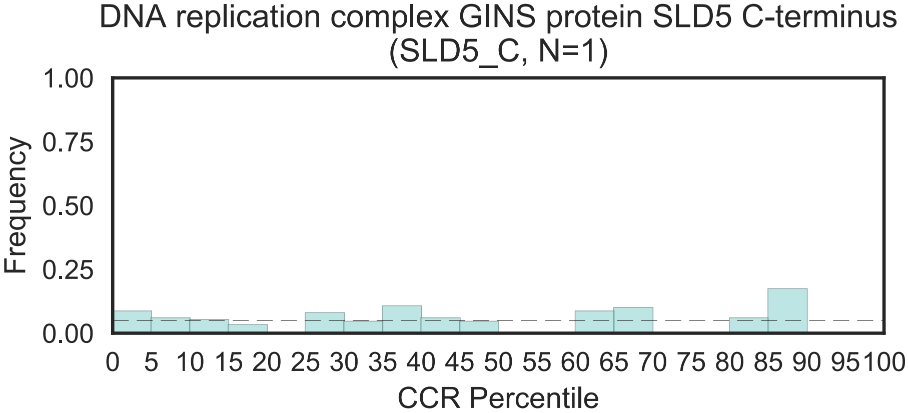
Histone RNA hairpin-binding protein RNA-binding domain (SLBP_RNA_bind, N=1)

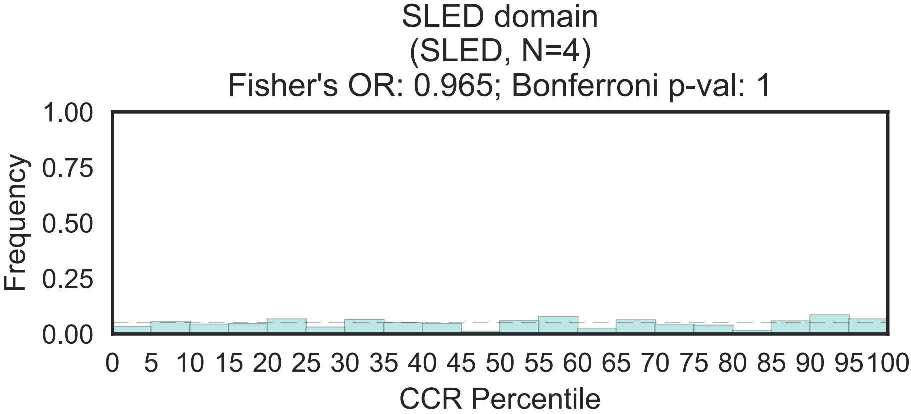

Solute carrier family 12
(SLC12, N=15)
Fisher's OR: 0.682; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

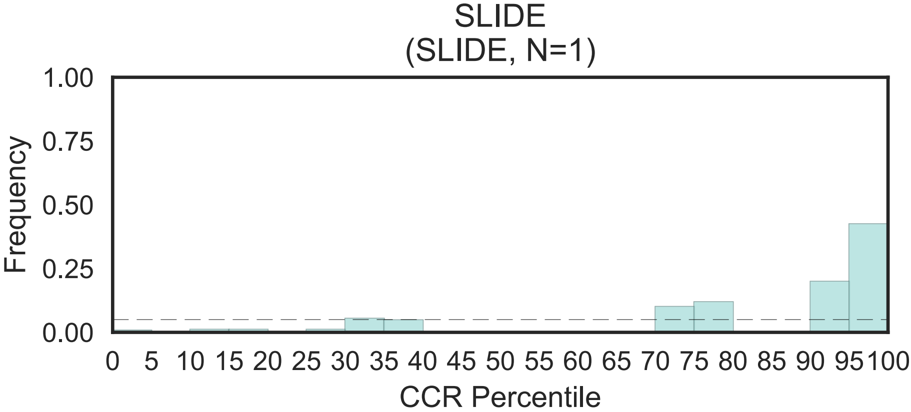


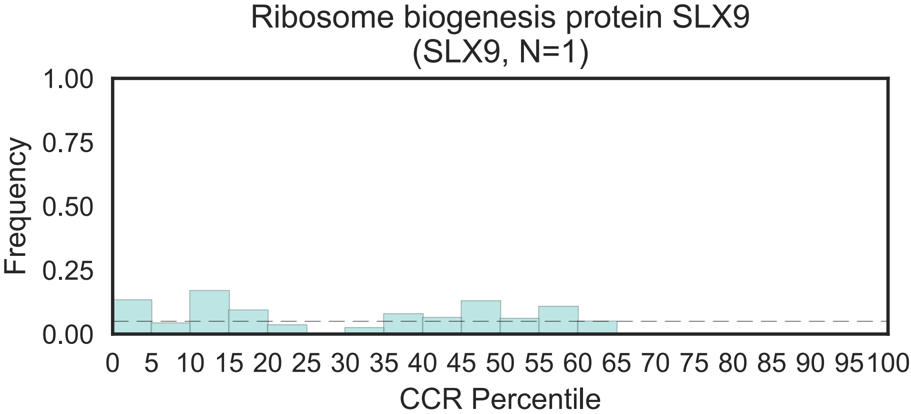
Solute carrier family 35
(SLC35F, N=5)
Fisher's OR: 0.609; Bonferroni p-val: 1

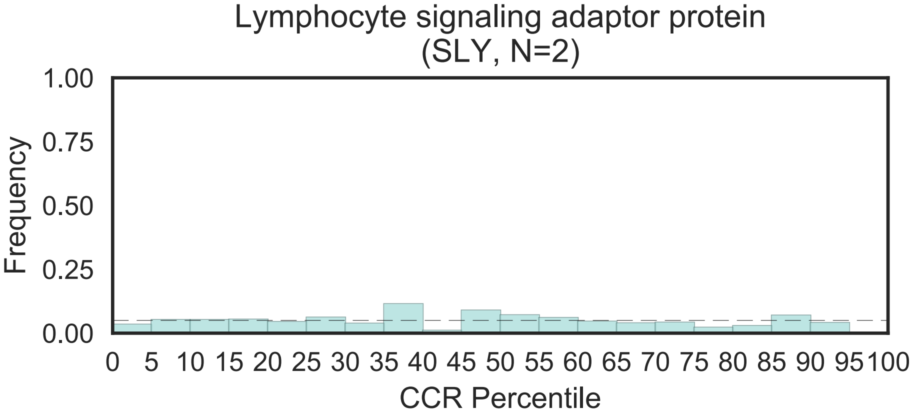

Solute carrier family 3 member 2 N-terminus
(SLC3A2_N, N=1)

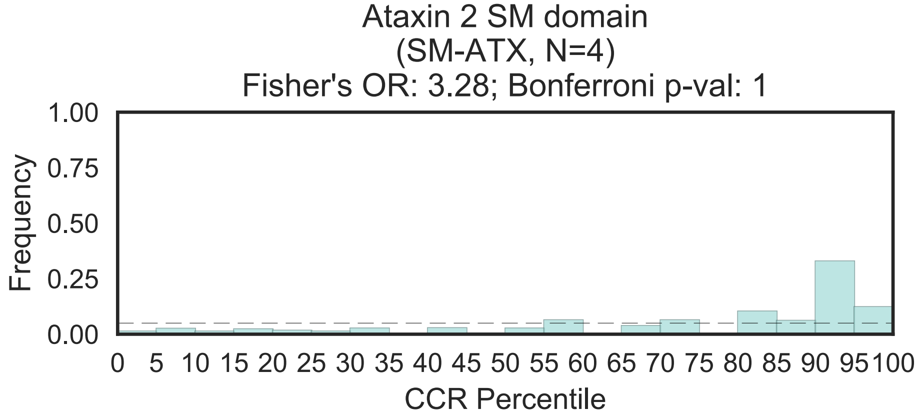

DNA replication complex GINS protein SLD5 C-terminus
(SLD5_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

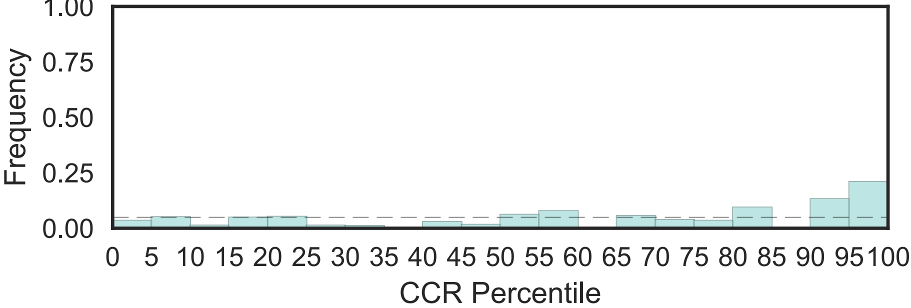

SLED domain
(SLED, N=4)
Fisher's OR: 0.965; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


SLIDE
(SLIDE, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

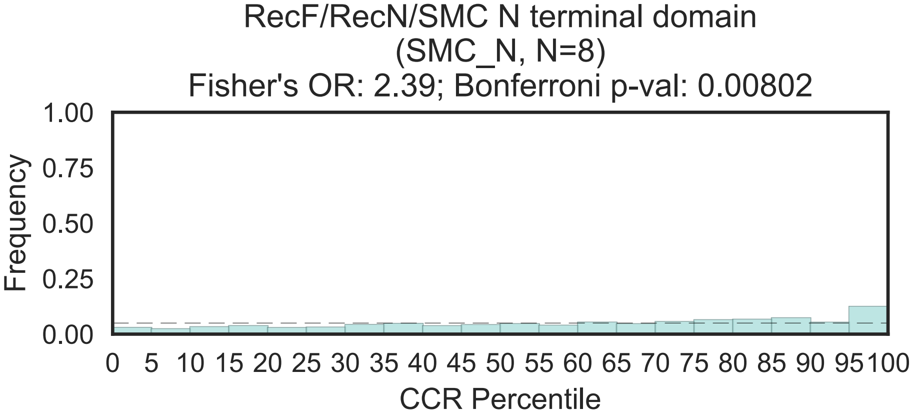

Ribosome biogenesis protein SLX9
(SLX9, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

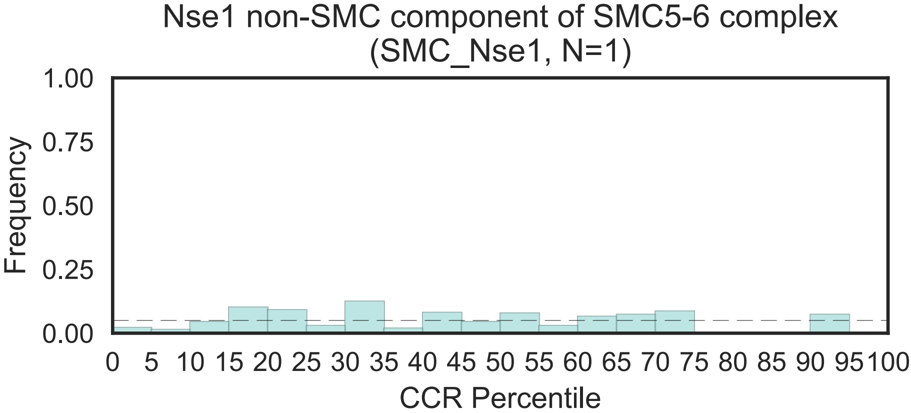

Lymphocyte signaling adaptor protein
(SLY, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

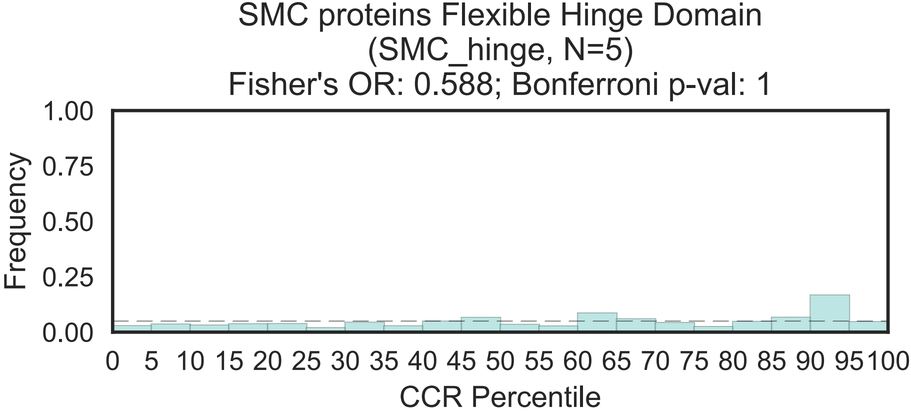

Ataxin 2 SM domain
(SM-ATX, N=4)
Fisher's OR: 3.28; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

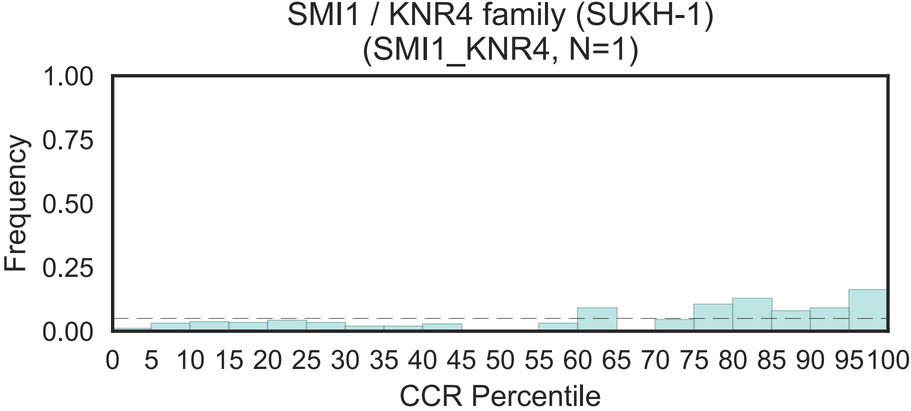


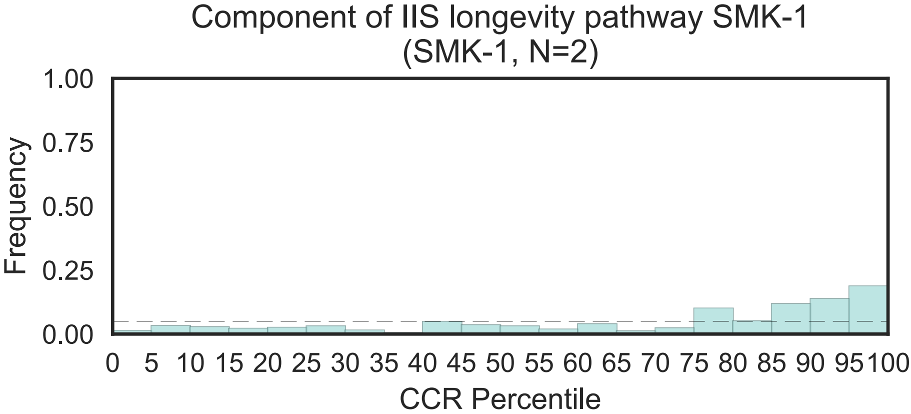
Small acidic protein family
(SMAP, N=3)
Fisher's OR: 3.09; Bonferroni p-val: 1


RecF/RecN/SMC N terminal domain
(SMC_N, N=8)
Fisher's OR: 2.39; Bonferroni p-val: 0.00802
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

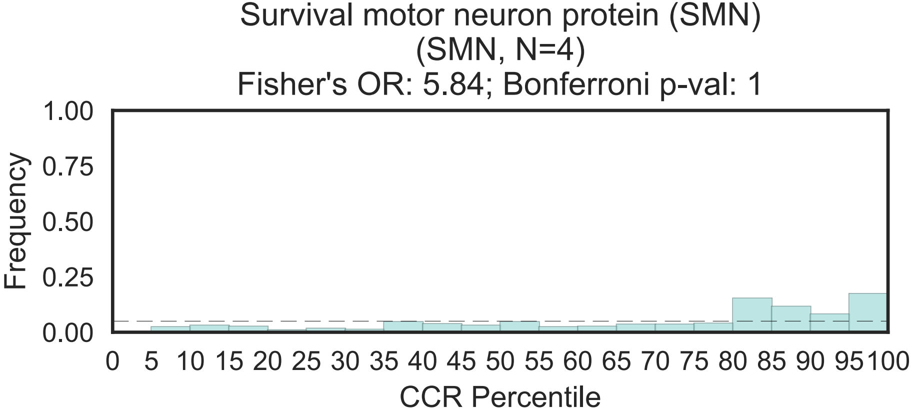

Nse1 non-SMC component of SMC5-6 complex
(SMC_Nse1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

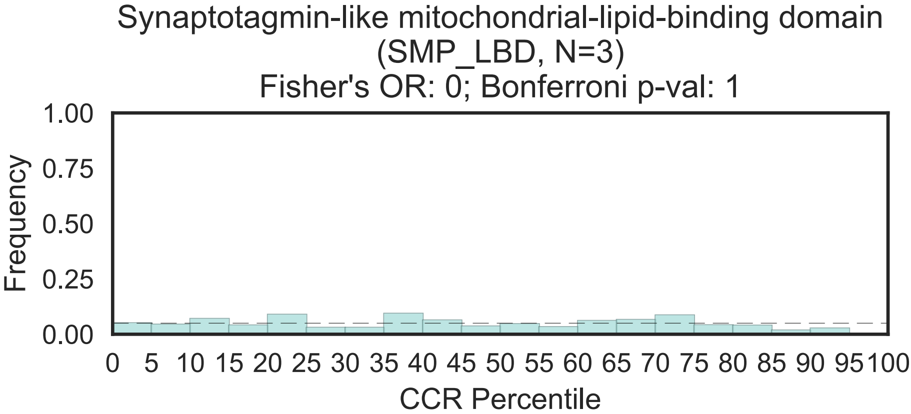

SMC proteins Flexible Hinge Domain
(SMC_hinge, N=5)
Fisher's OR: 0.588; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

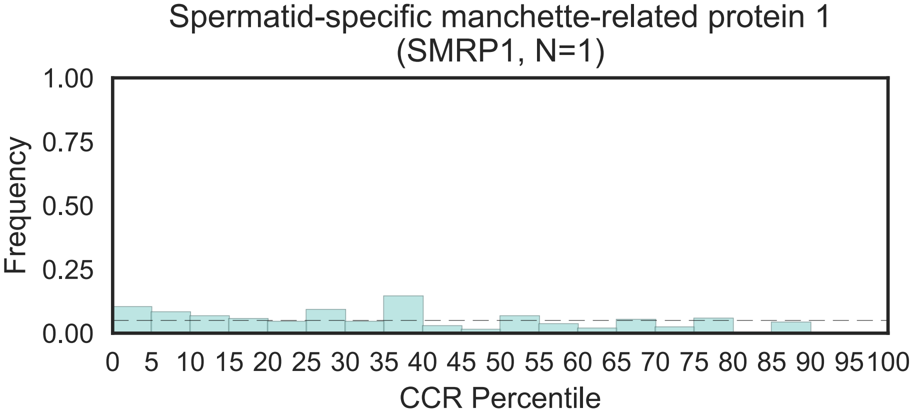

SMI1 / KNR4 family (SUKH-1)
(SMI1_KNR4, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



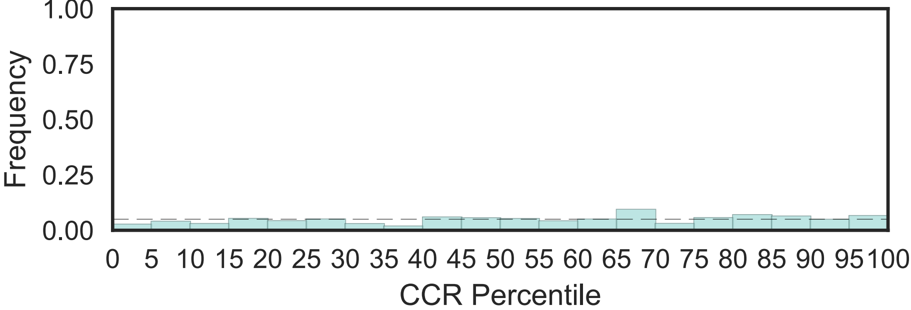
Component of IIS longevity pathway SMK-1
(SMK-1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

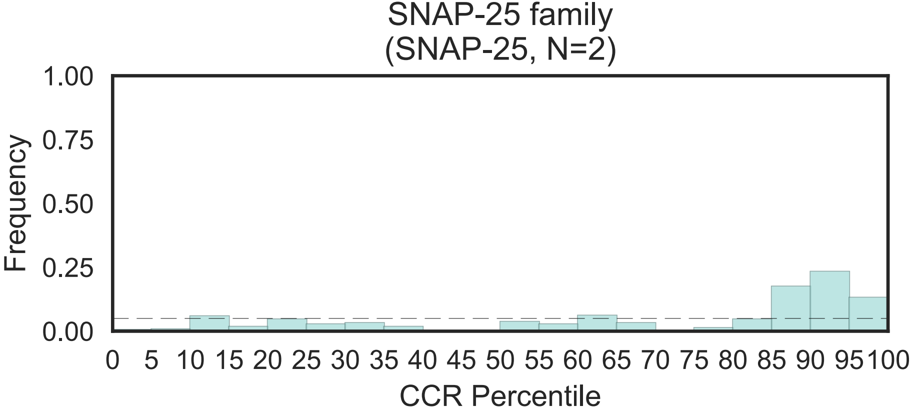

Survival motor neuron protein (SMN)
(SMN, N=4)
Fisher's OR: 5.84; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

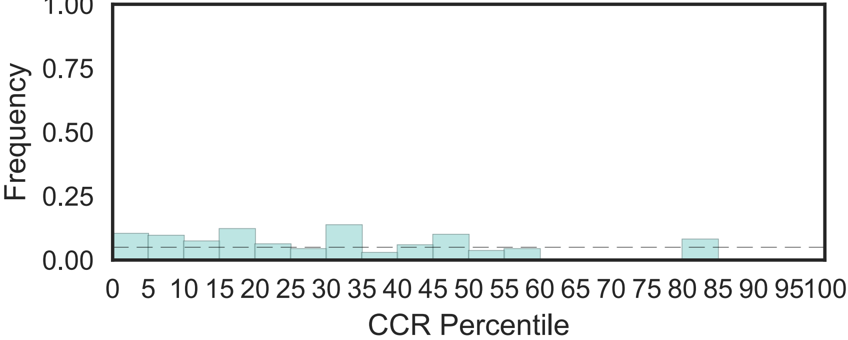

Synaptotagmin-like mitochondrial-lipid-binding domain
(SMP_LBD, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

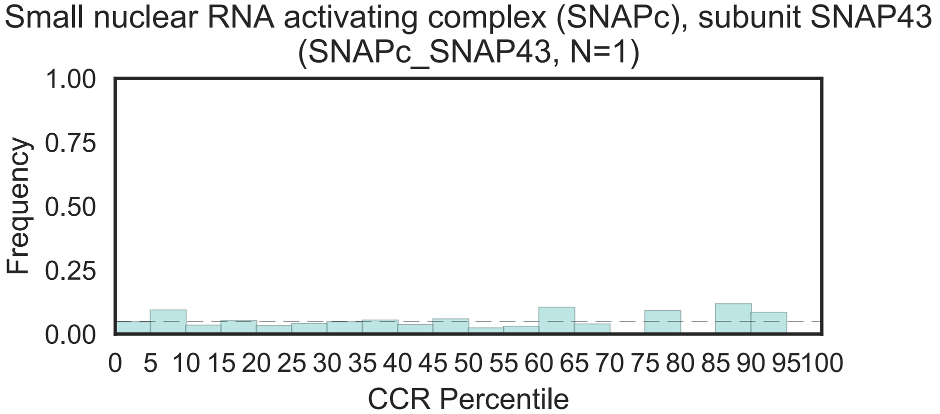

Spermatid-specific manchette-related protein 1
(SMRP1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

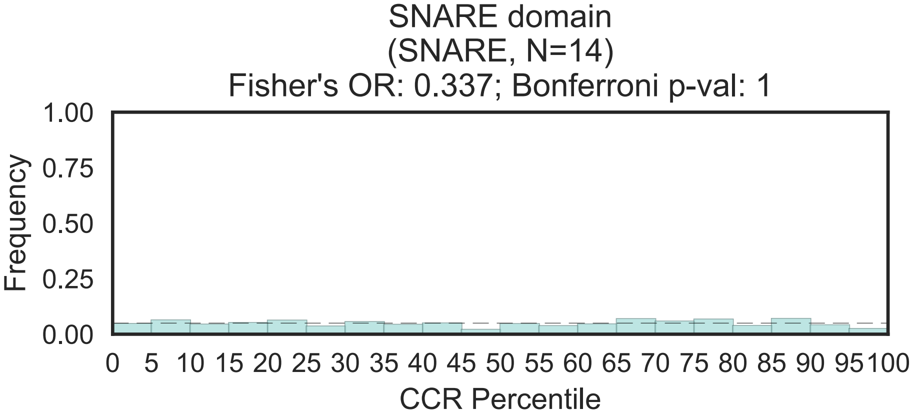
Soluble NSF attachment protein, SNAP
(SNAP, N=5)
Fisher's OR: 1.18; Bonferroni p-val: 1

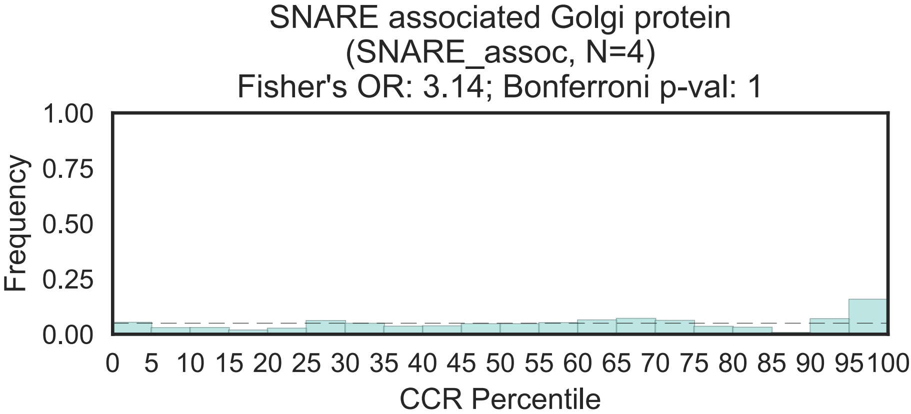


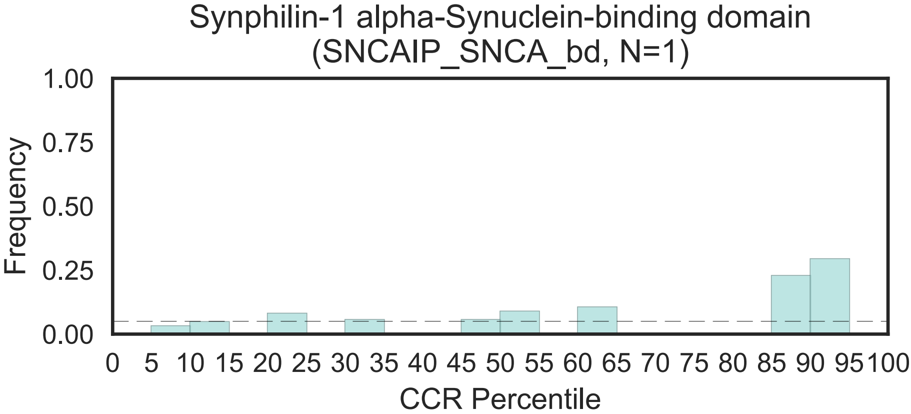

SNAP-25 family
(SNAP-25, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

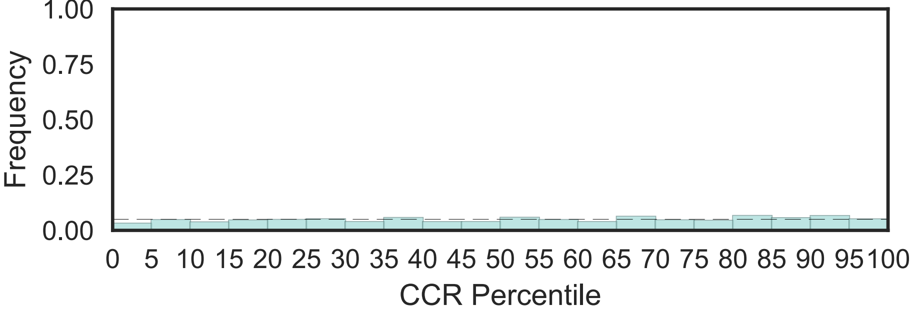

snRNA-activating protein complex subunit 19, SNAPc subunit 19 (SNAPc19, N=1)

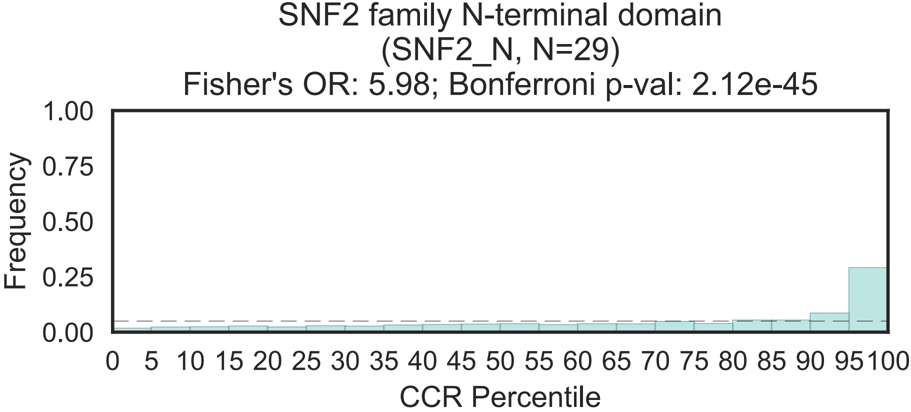

Small nuclear RNA activating complex (SNAPc), subunit SNAP43
(SNAPc_SNAP43, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

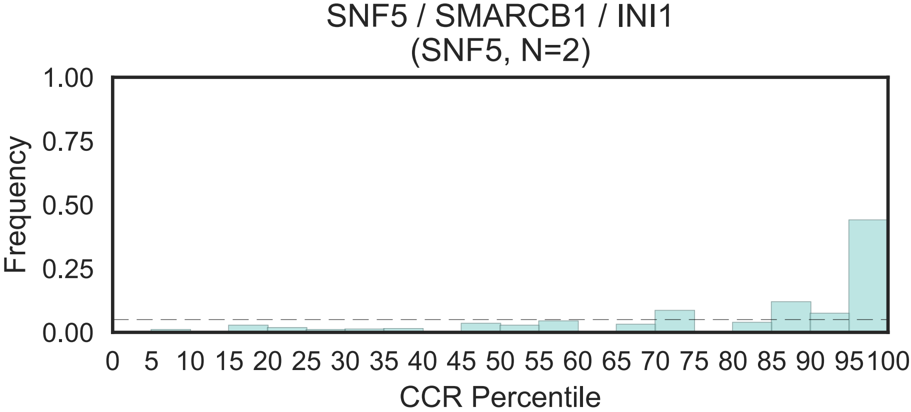

SNARE domain
(SNARE, N=14)
Fisher's OR: 0.337; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

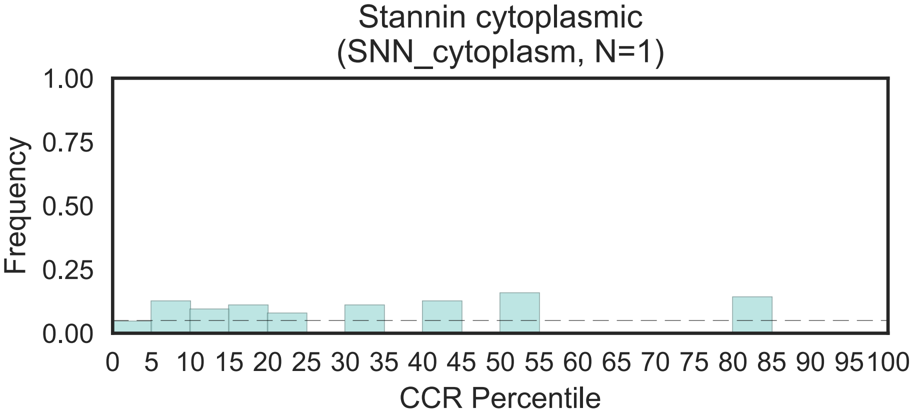

SNARE associated Golgi protein
(SNARE_assoc, N=4)
Fisher's OR: 3.14; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

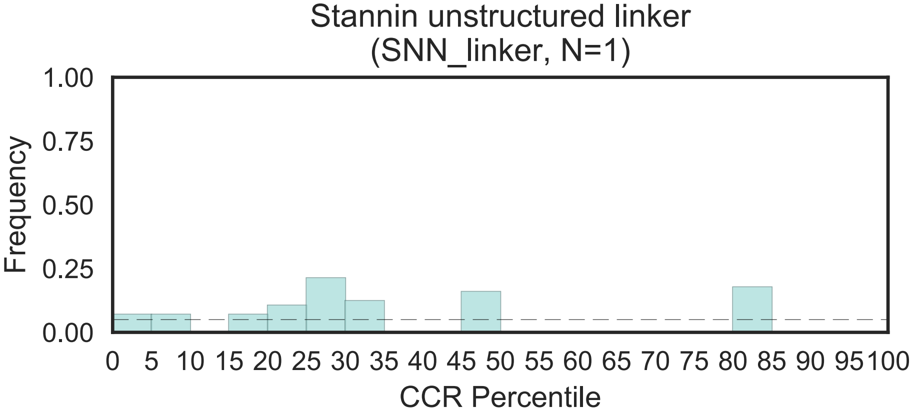

Synphilin-1 alpha-Synuclein-binding domain
(SNCAIP_SNCA_bd, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

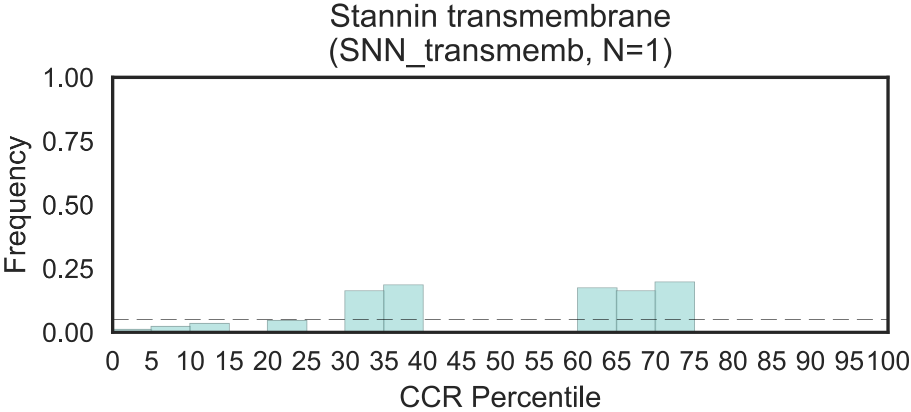

Sodium:neurotransmitter symporter family
(SNF, N=19)
Fisher's OR: 0.79; Bonferroni p-val: 1

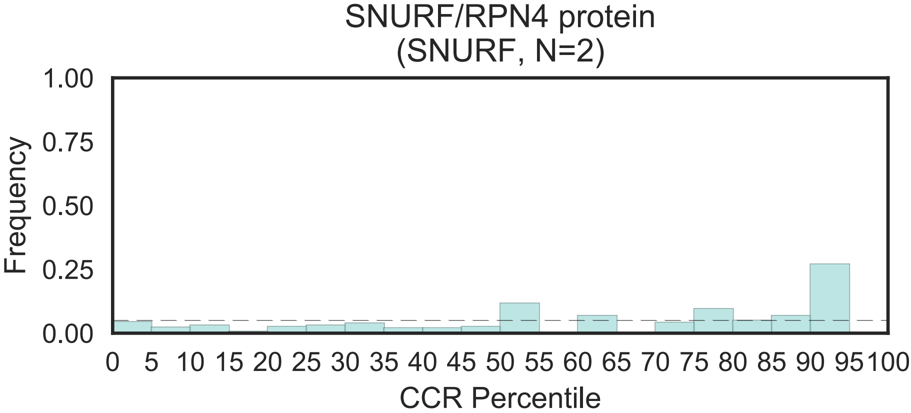

SNF2 family N-terminal domain
(SNF2_N, N=29)
Fisher's OR: 5.98; Bonferroni p-val: 2.12e-45
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

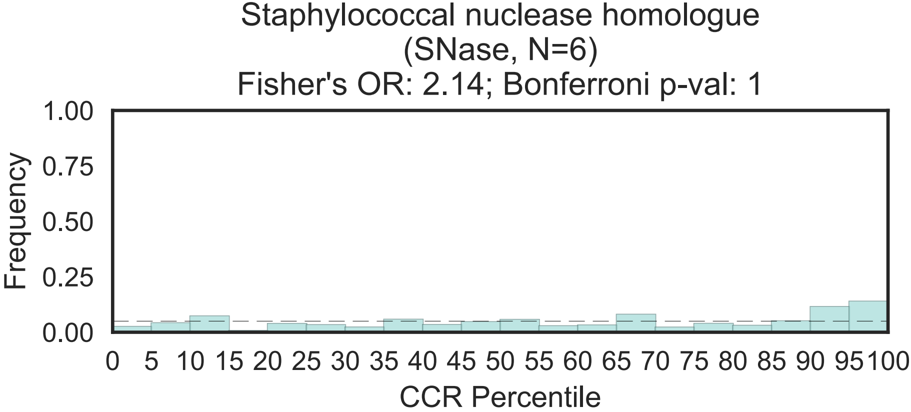

SNF5 / SMARCB1 / INI1
(SNF5, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

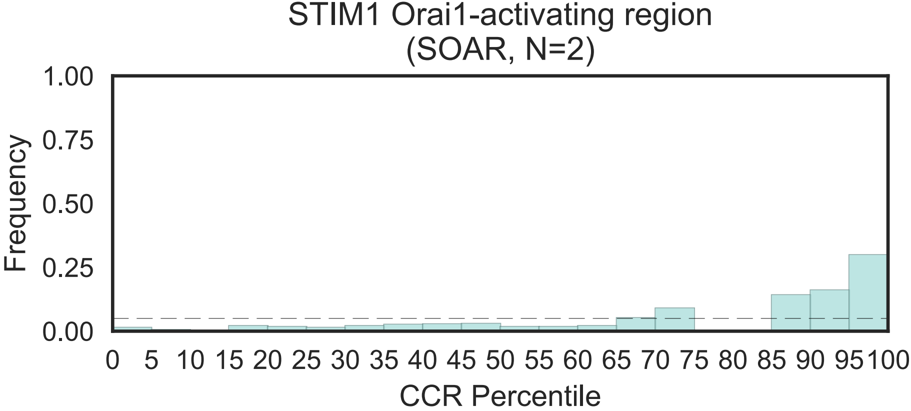

Stannin cytoplasmic
(SNN_cytoplasm, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

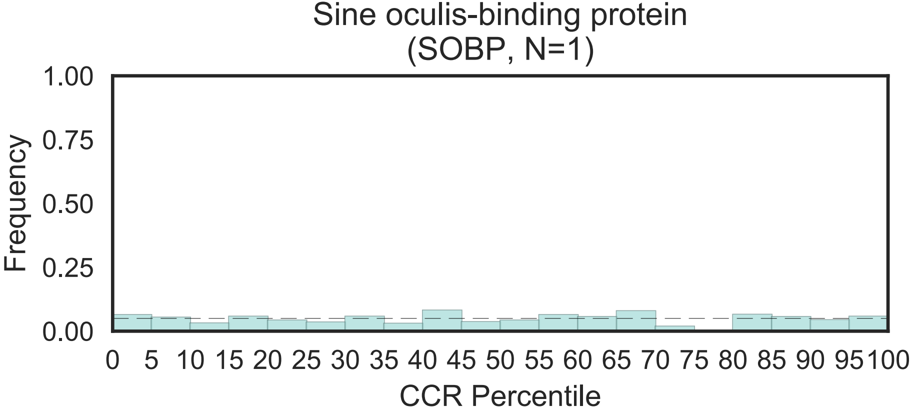

Stannin unstructured linker
(SNN_linker, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

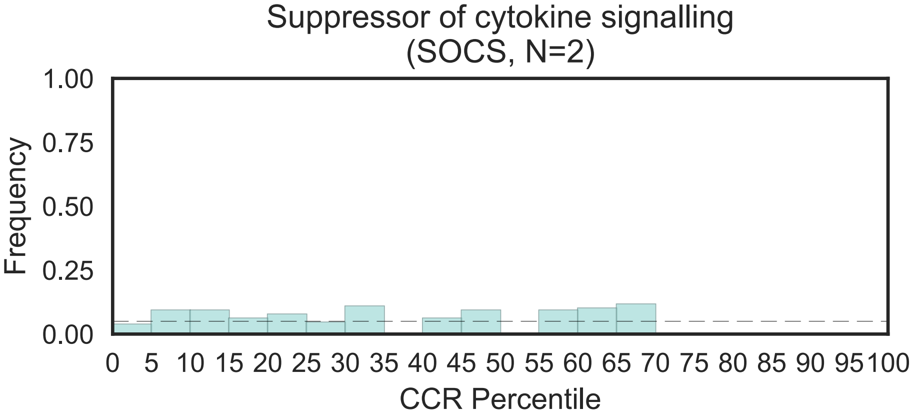

Stannin transmembrane
(SNN_transmemb, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

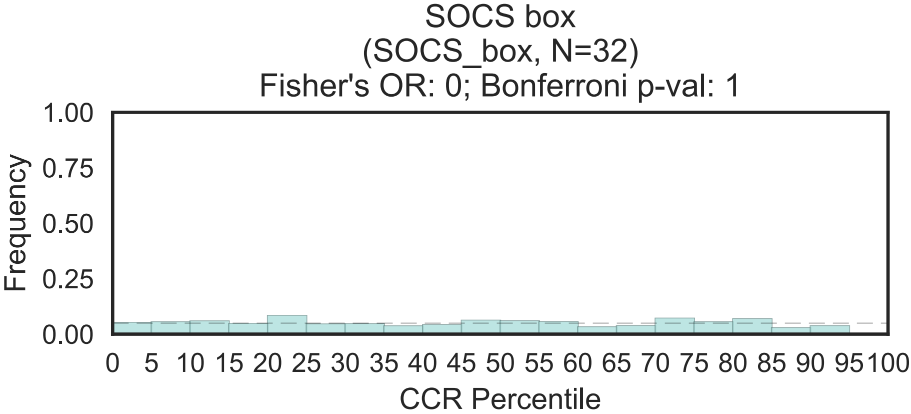

SNURF/RPN4 protein
(SNURF, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

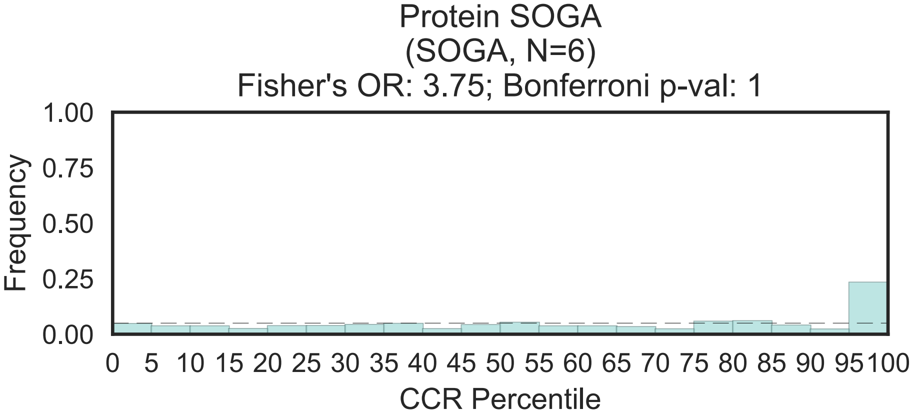

Staphylococcal nuclease homologue
(SNase, N=6)
Fisher's OR: 2.14; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

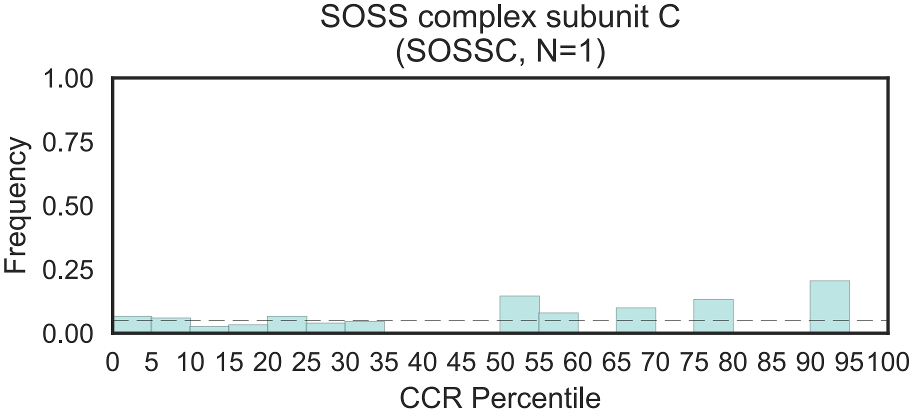

STIM1 Orai1-activating region
(SOAR, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

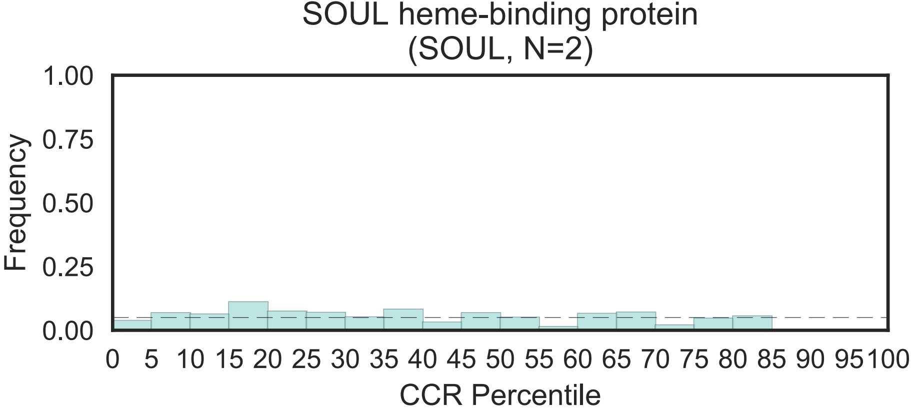

Sine oculis-binding protein
(SOBP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

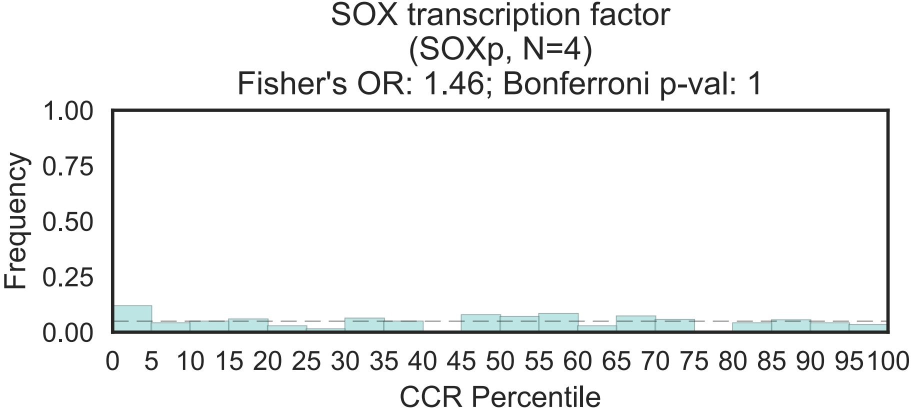

Suppressor of cytokine signalling
(SOCS, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

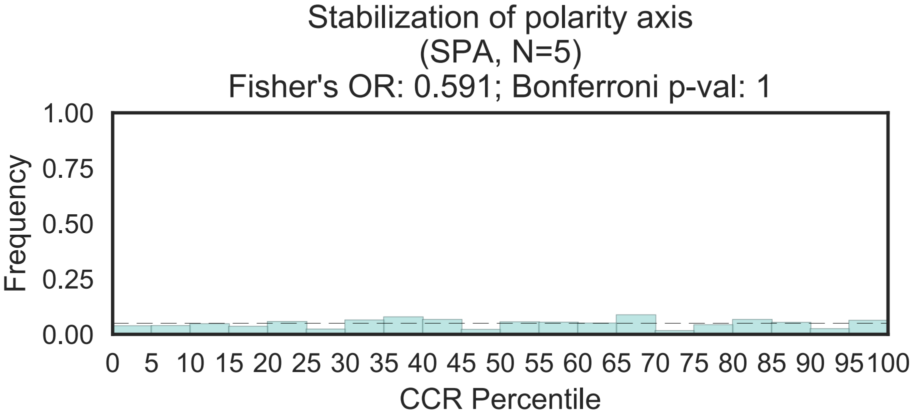

SOCS box
(SOCS_box, N=32)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

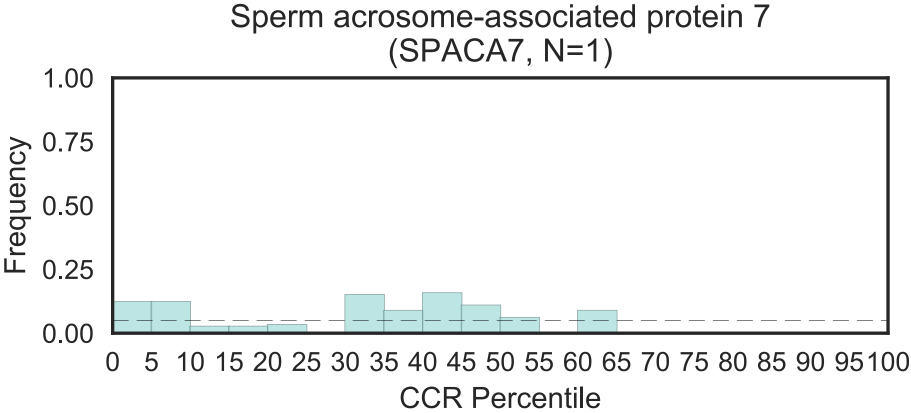

Protein SOGA
(SOGA, N=6)
Fisher's OR: 3.75; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

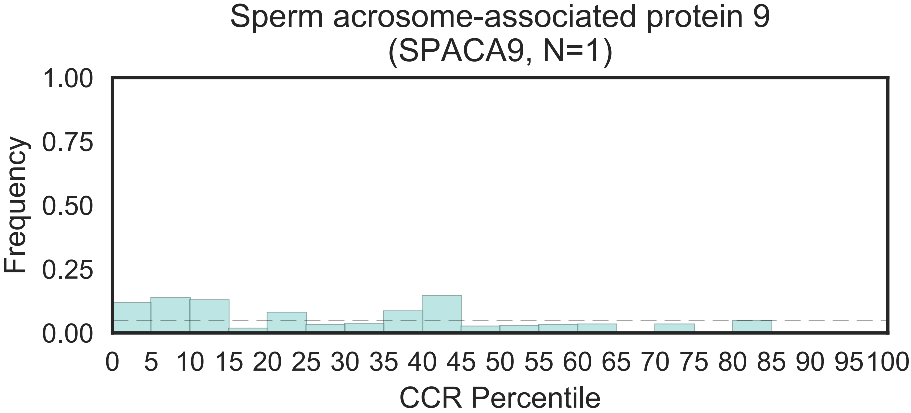

SOSS complex subunit C
(SOSSC, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

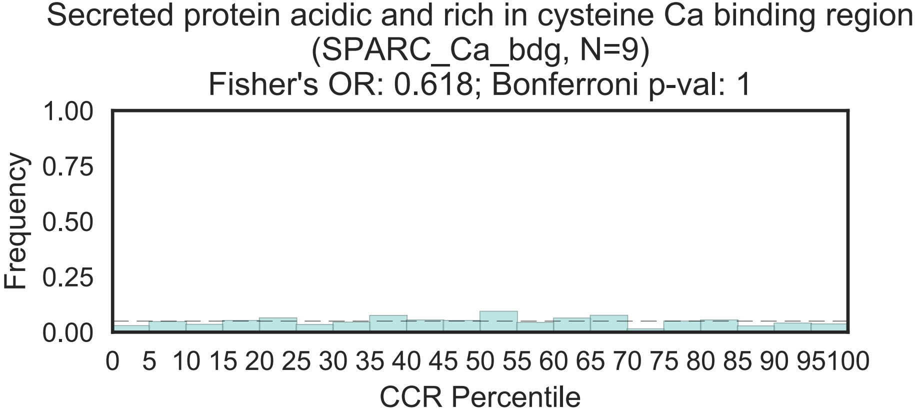

SOUL heme-binding protein
(SOUL, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

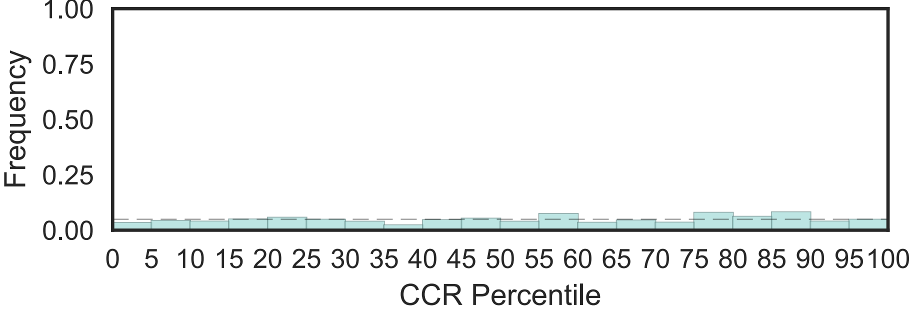

SOX transcription factor
(SOXp, N=4)
Fisher's OR: 1.46; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Stabilization of polarity axis
(SPA, N=5)
Fisher's OR: 0.591; Bonferroni p-val: 1

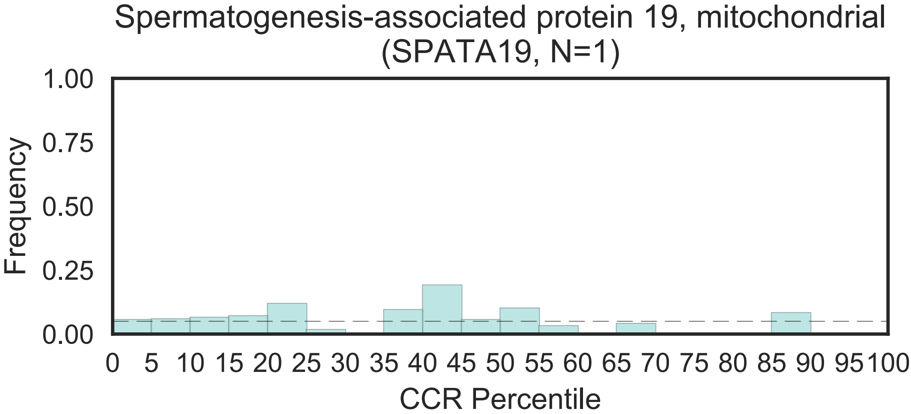

Sperm acrosome-associated protein 7
(SPACA7, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

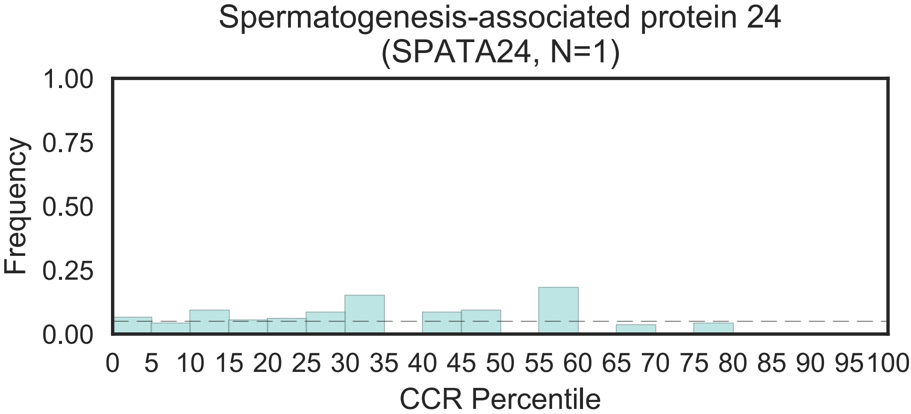
Sperm acrosome-associated protein 9
(SPACA9, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

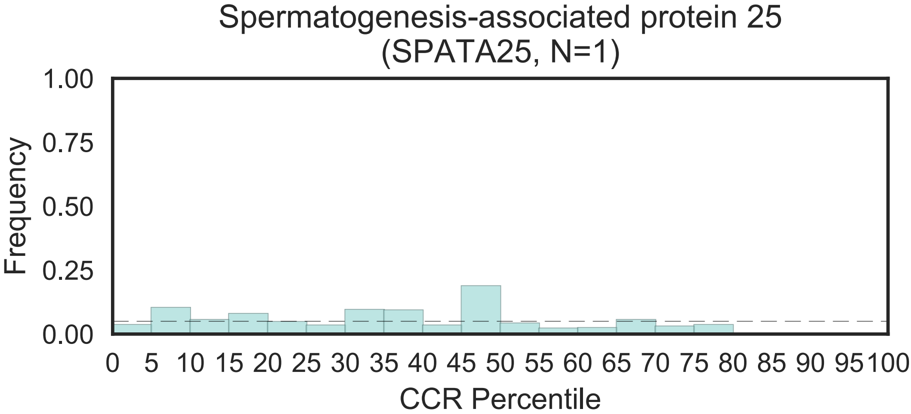

Secreted protein acidic and rich in cysteine Ca binding region
(SPARC_Ca_bdg, N=9)
Fisher's OR: 0.618; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



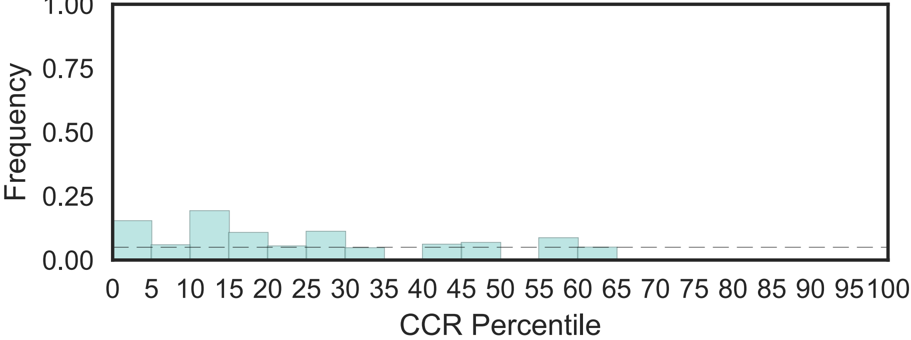
C-terminal domain of SPAR protein
(SPAR_C, N=3)
Fisher's OR: 0.832; Bonferroni p-val: 1

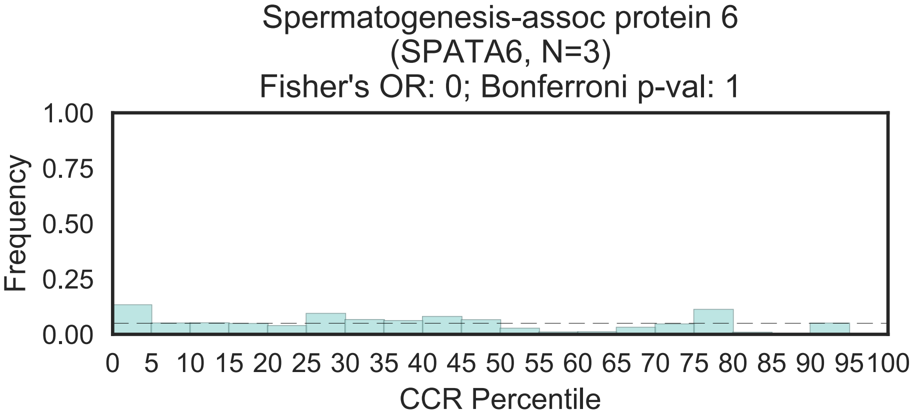
Spermatogenesis-associated protein 19, mitochondrial
(SPATA19, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Spermatogenesis-associated protein 24
(SPATA24, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

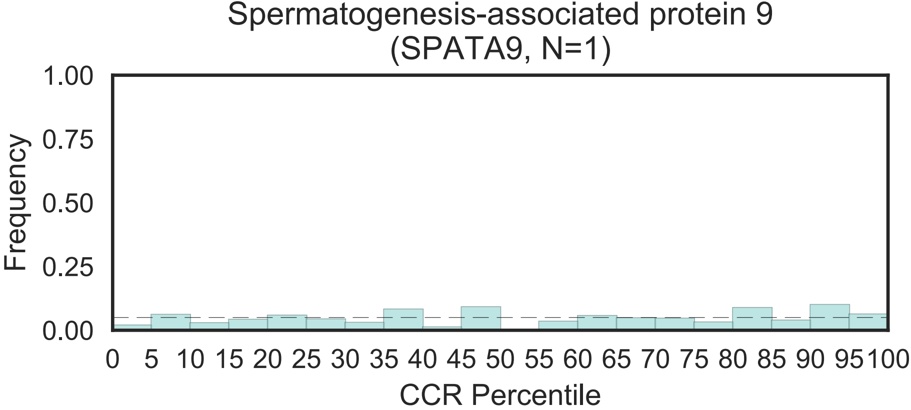

Spermatogenesis-associated protein 25
(SPATA25, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

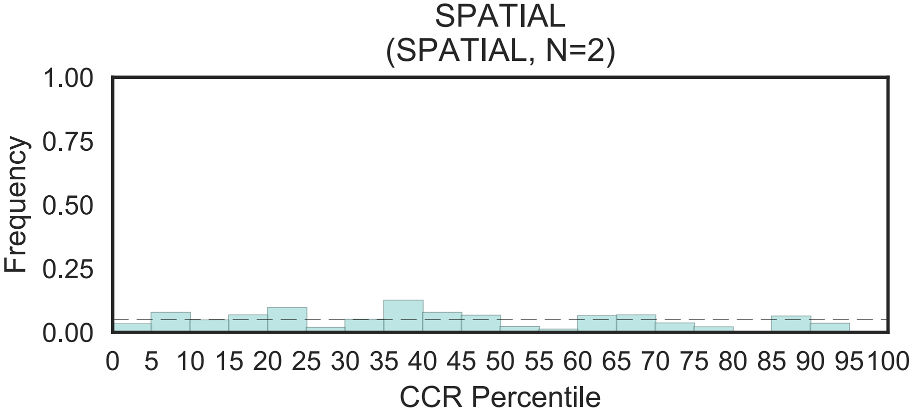
Spermatogenesis-associated protein 3 family (SPATA3, N=1)

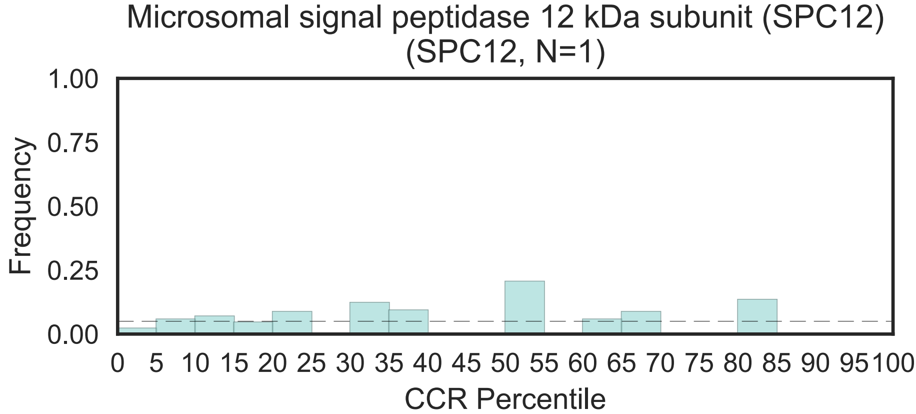


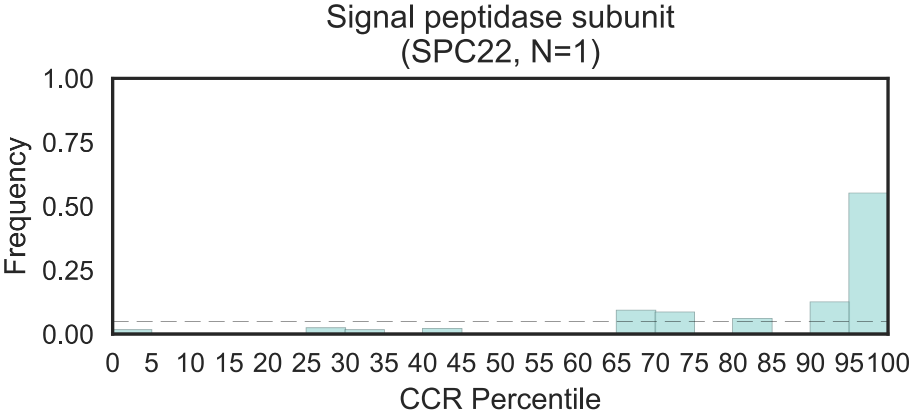


Spermatogenesis-assoc protein 6
(SPATA6, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

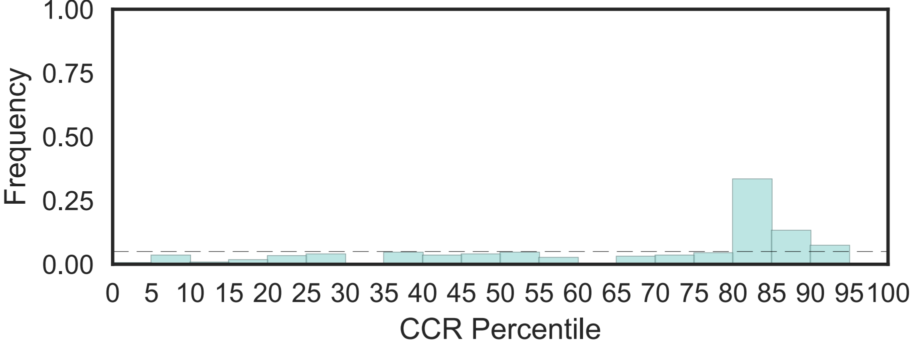

Spermatogenesis-associated protein 9
(SPATA9, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

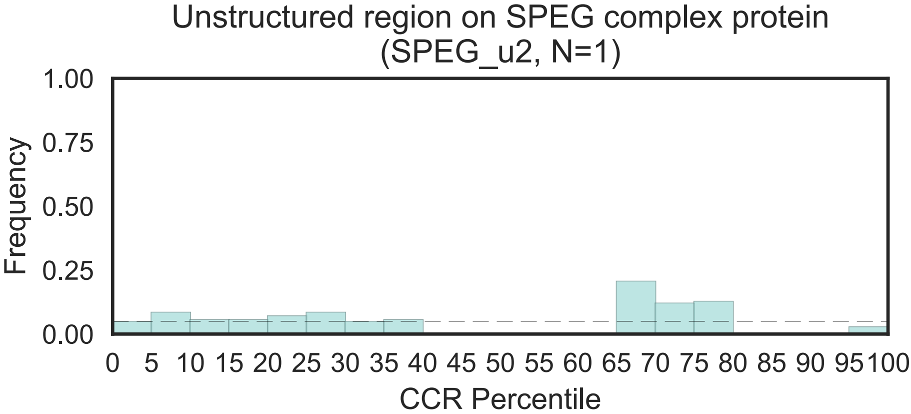

SPATIAL
(SPATIAL, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

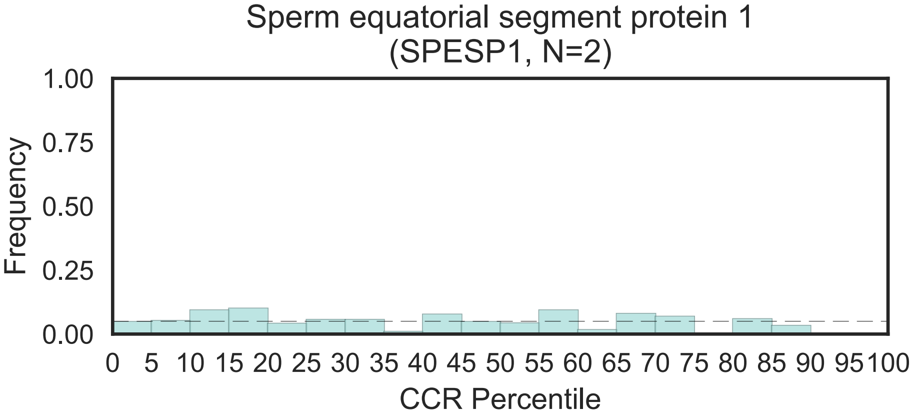

Microsomal signal peptidase 12 kDa subunit (SPC12)
(SPC12, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

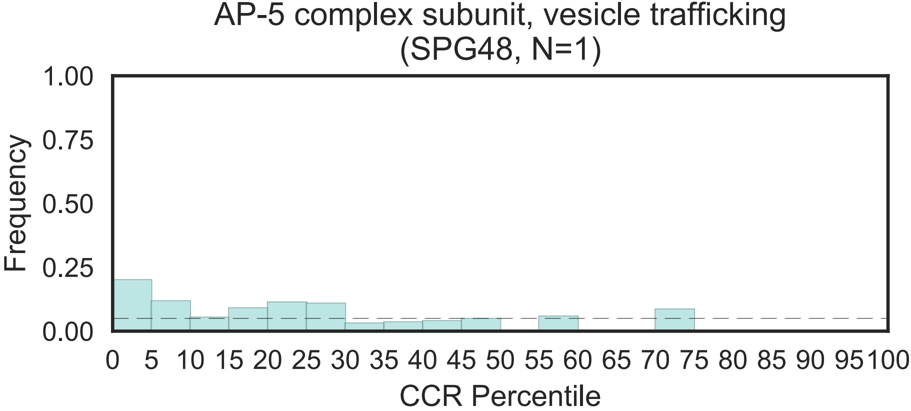

Signal peptidase subunit
(SPC22, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Microsomal signal peptidase 25 kDa subunit (SPC25) (SPC25, N=1)

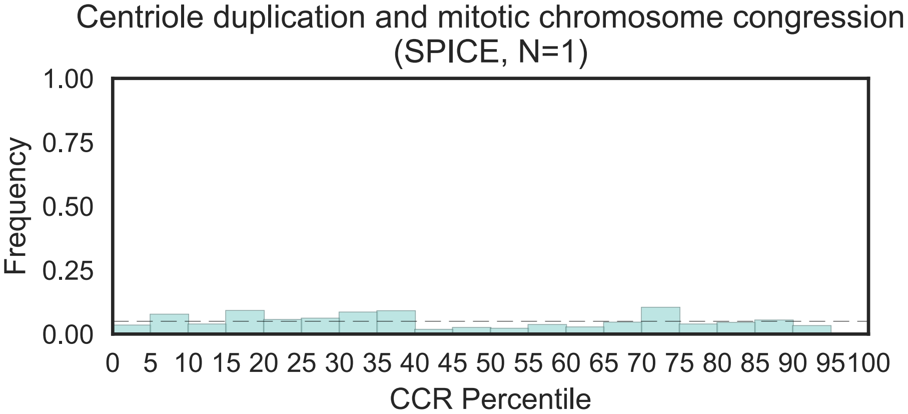


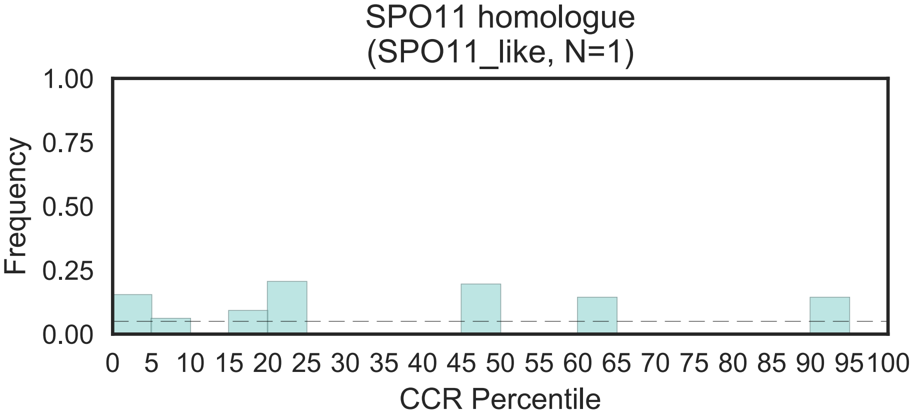

Unstructured region on SPEG complex protein
(SPEG_u2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

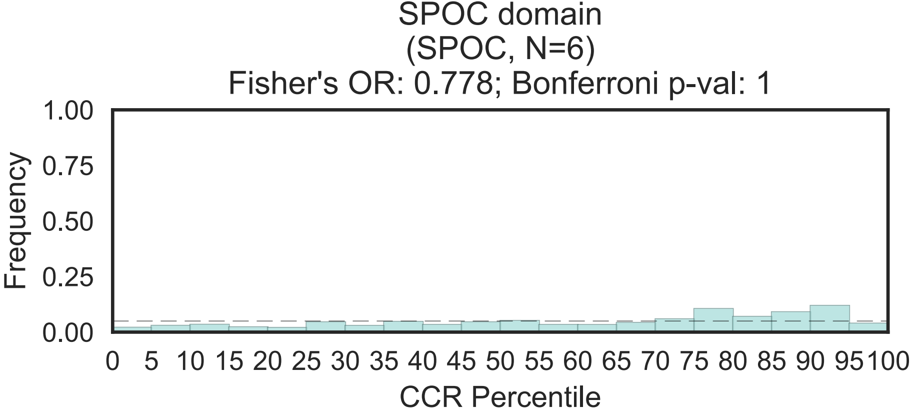

Sperm equatorial segment protein 1
(SPESP1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

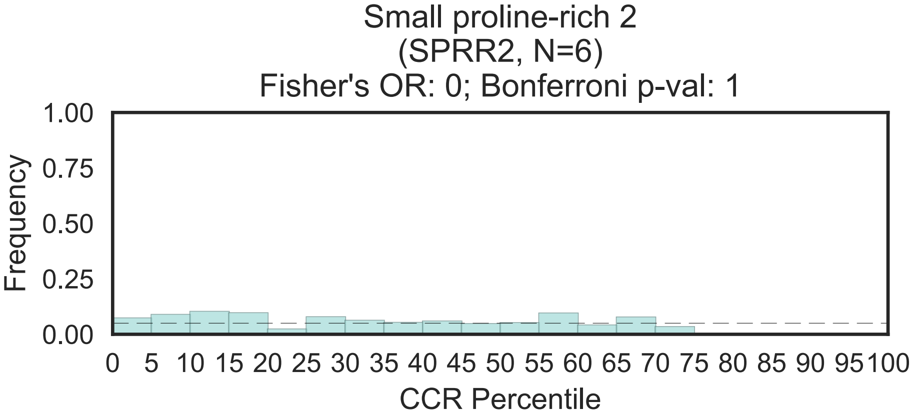


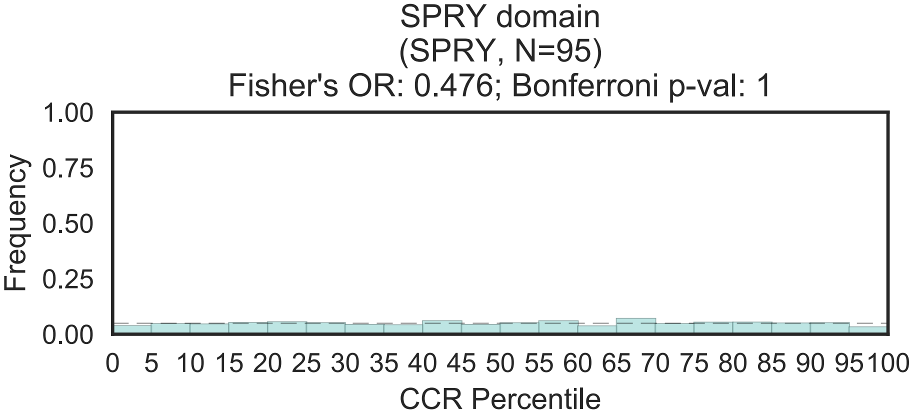
AP-5 complex subunit, vesicle trafficking
(SPG48, N=1)

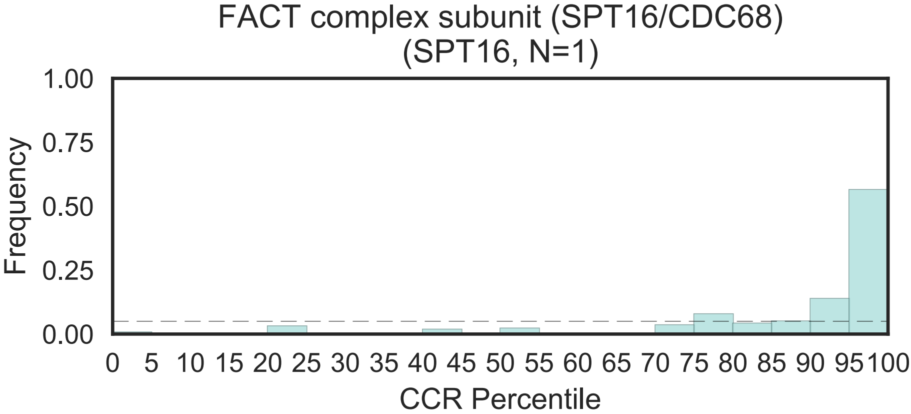

Centriole duplication and mitotic chromosome congression
(SPICE, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


SPO11 homologue
(SPO11_like, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

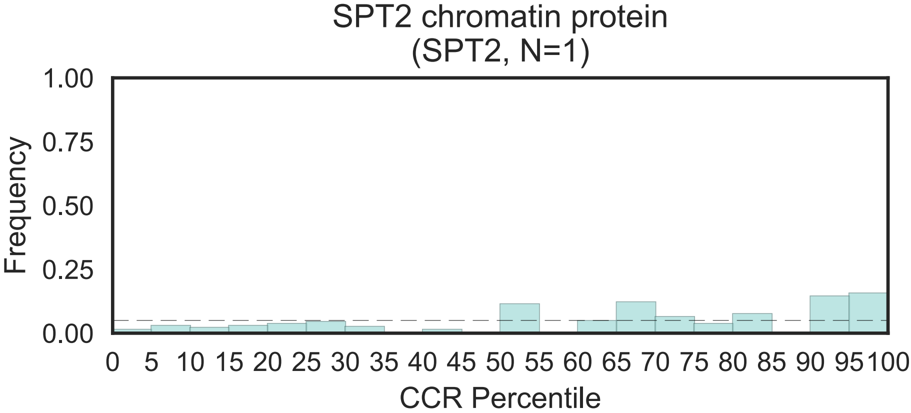

SPOC domain
(SPOC, N=6)
Fisher's OR: 0.778; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

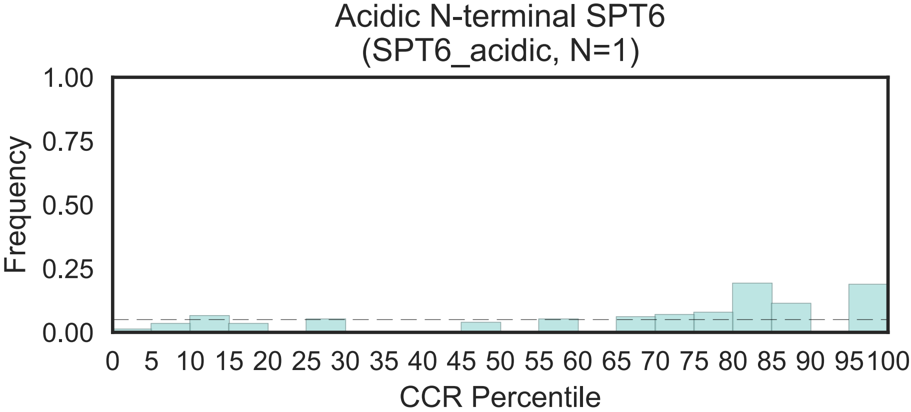

Small proline-rich 2
(SPRR2, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

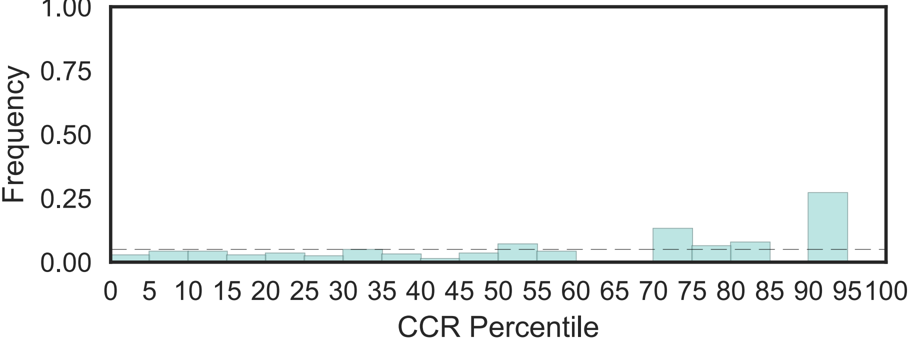

SPRY domain
(SPRY, N=95)
Fisher's OR: 0.476; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

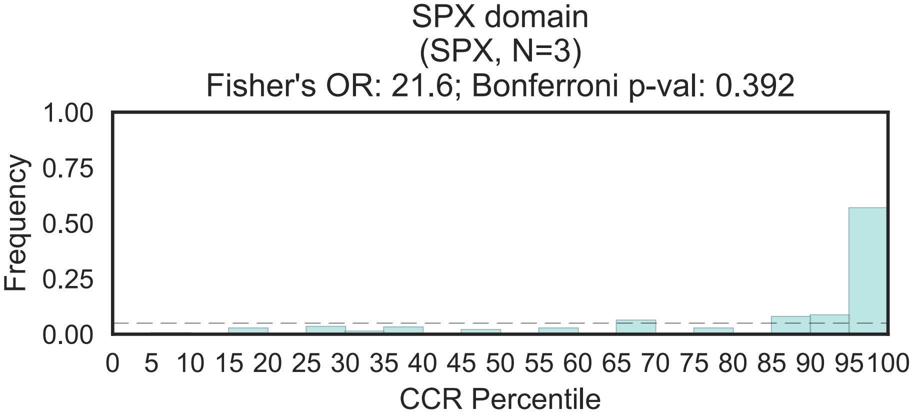


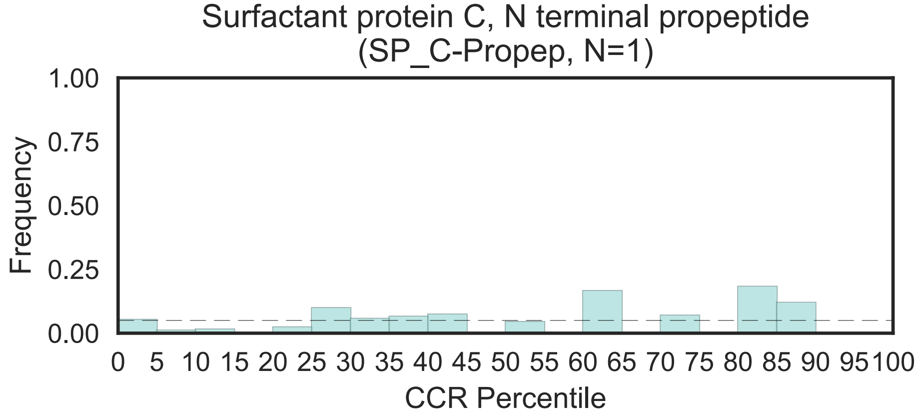
FACT complex subunit (SPT16/CDC68)
(SPT16, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

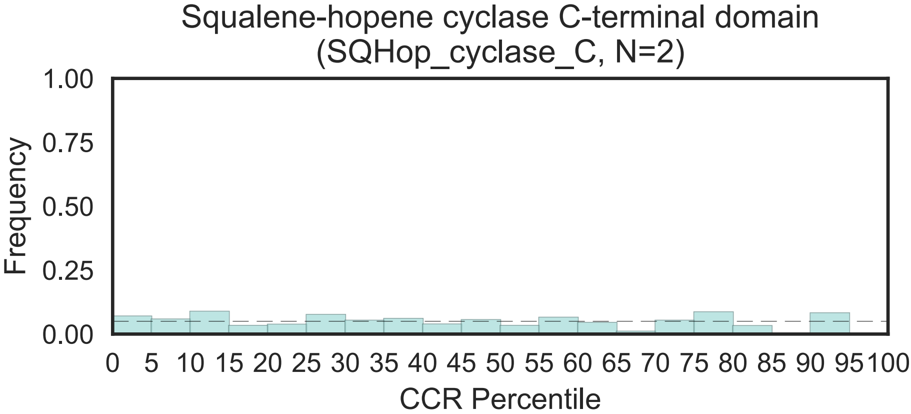

SPT2 chromatin protein
(SPT2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

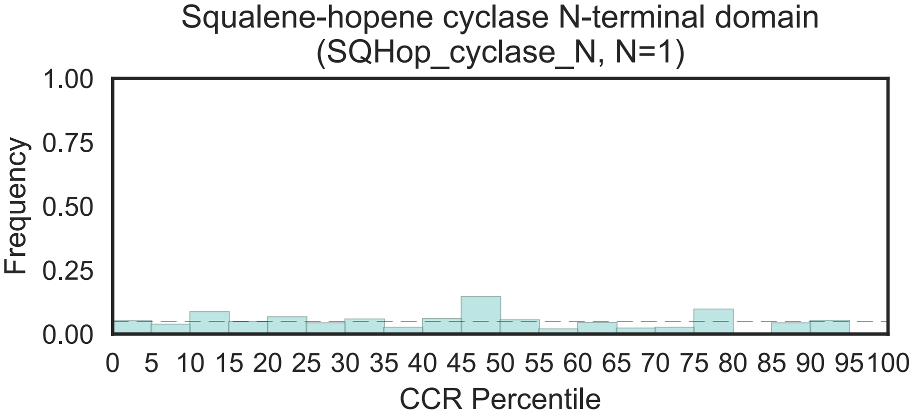

Acidic N-terminal SPT6
(SPT6_acidic, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

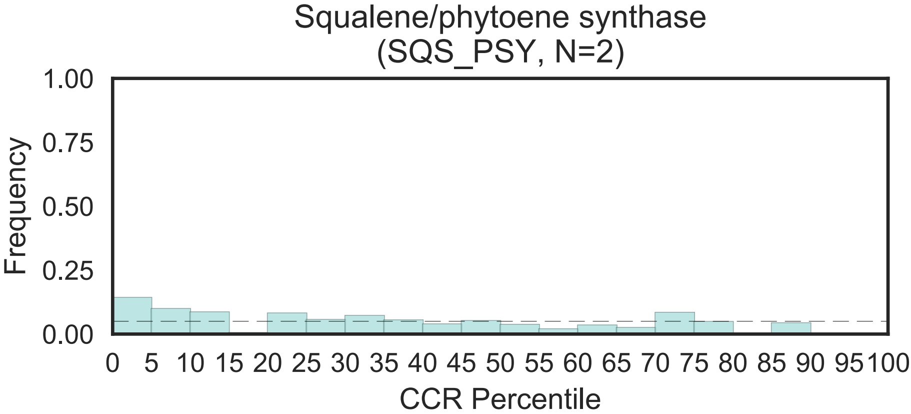

Small subunit of serine palmitoyltransferase-like
(SPT_ssu-like, N=2)

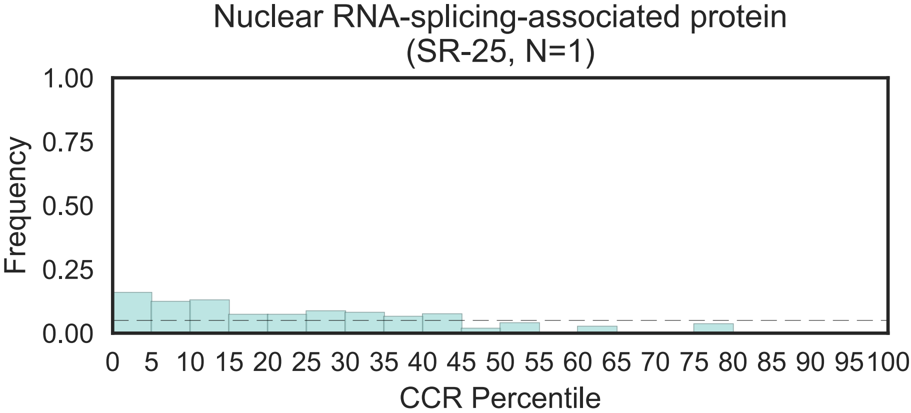

SPX domain
(SPX, N=3)
Fisher's OR: 21.6; Bonferroni p-val: 0.392
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

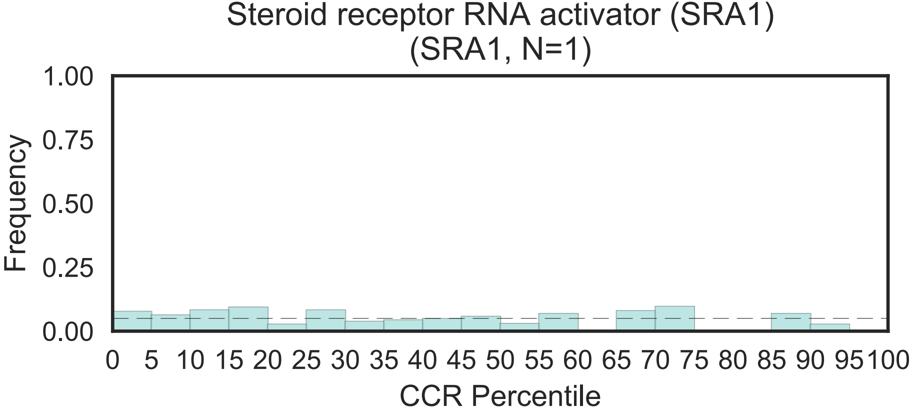

Surfactant protein C, N terminal propeptide
(SP_C-Propep, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

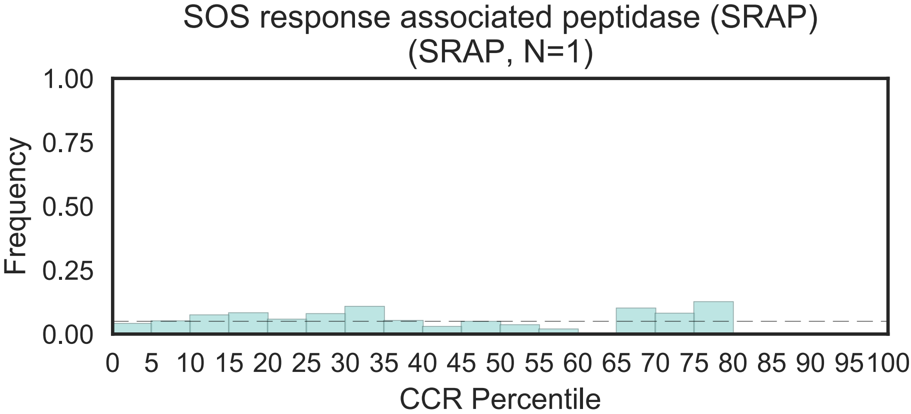

Squalene-hopene cyclase C-terminal domain
(SQHop_cyclase_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

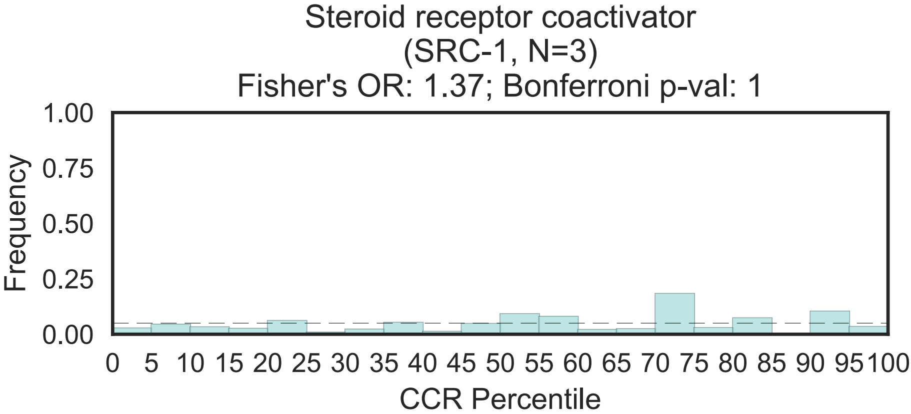

Squalene-hopene cyclase N-terminal domain
(SQHop_cyclase_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

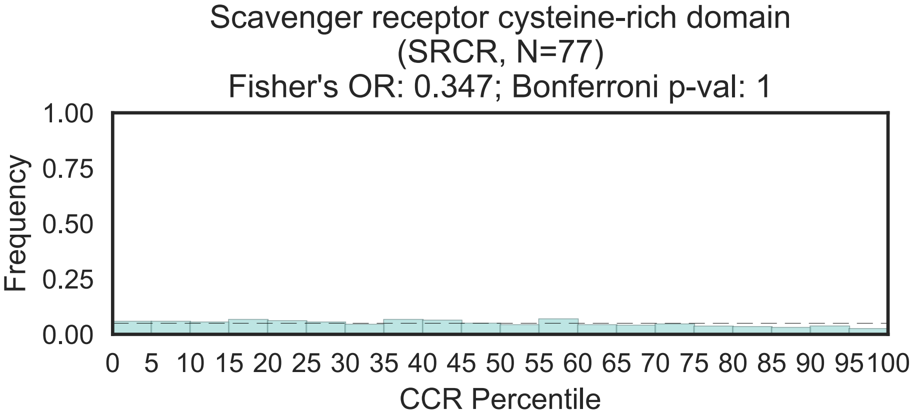

Squalene/phytoene synthase
(SQS_PSY, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

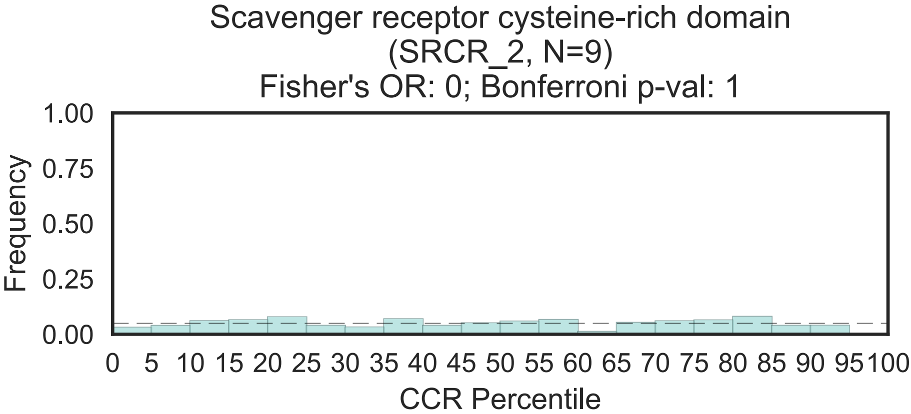

Nuclear RNA-splicing-associated protein
(SR-25, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

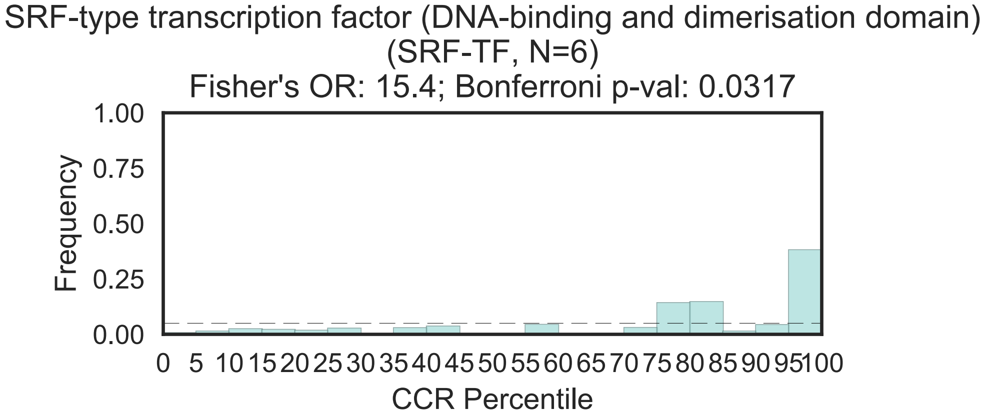

Steroid receptor RNA activator (SRA1)
(SRA1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

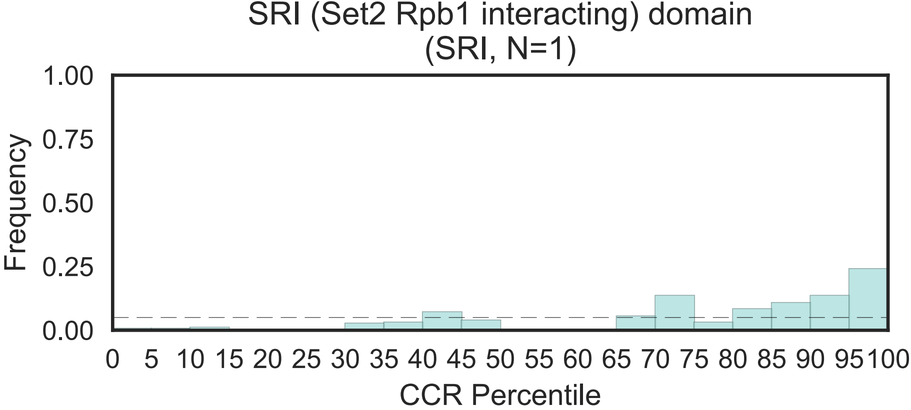

SOS response associated peptidase (SRAP)
(SRAP, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


Steroid receptor coactivator
(SRC-1, N=3)
Fisher's OR: 1.37; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

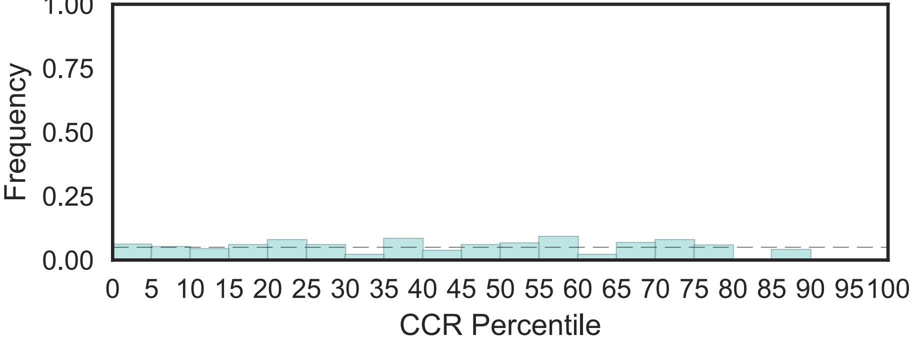

Scavenger receptor cysteine-rich domain
(SRCR, N=77)
Fisher's OR: 0.347; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

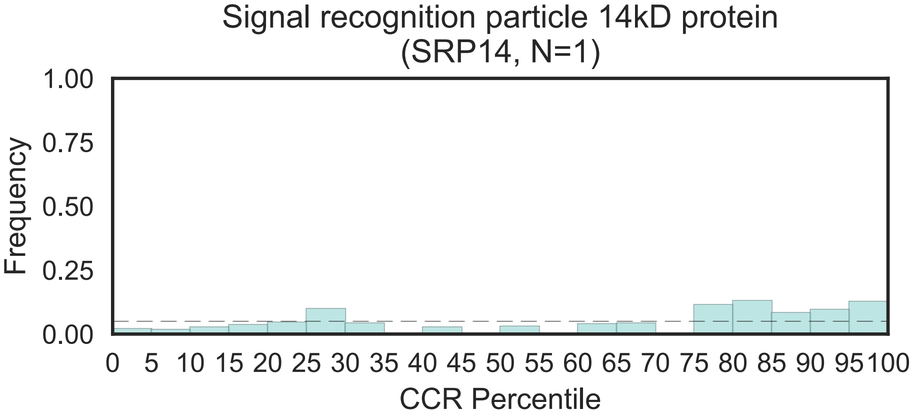

Scavenger receptor cysteine-rich domain
(SRCR_2, N=9)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


SRF-type transcription factor (DNA-binding and dimerisation domain)
(SRF-TF, N=6)
Fisher's OR: 15.4; Bonferroni p-val: 0.0317
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

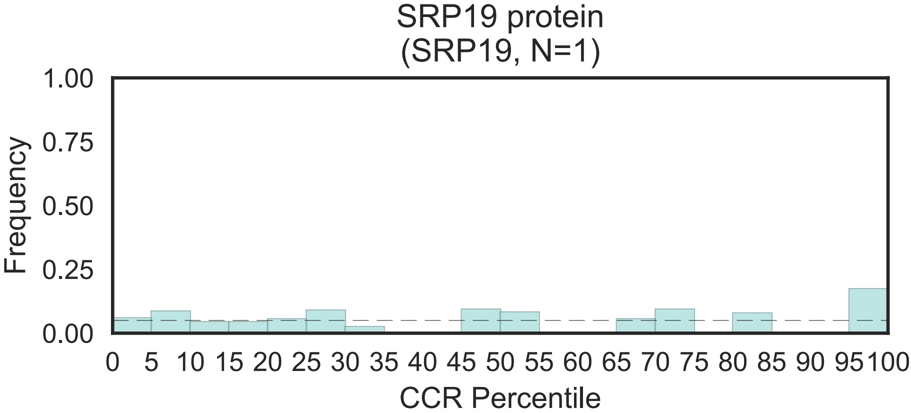

SRI (Set2 Rpb1 interacting) domain
(SRI, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

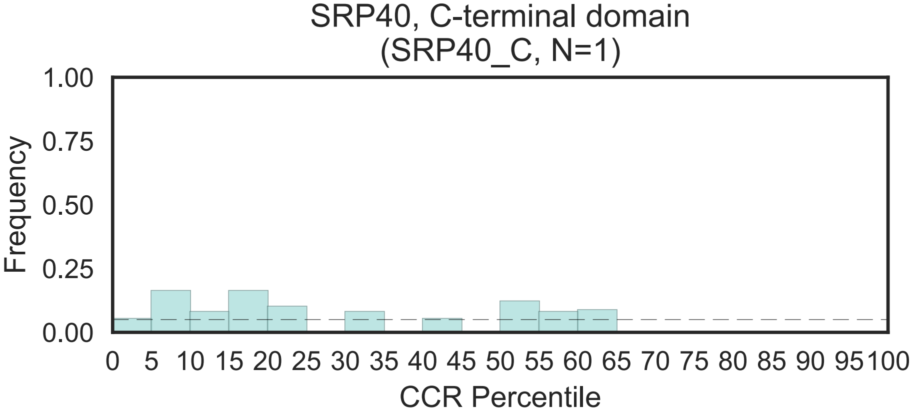
Signal recognition particle, alpha subunit, N-terminal (SRP-alpha_N, N=1)

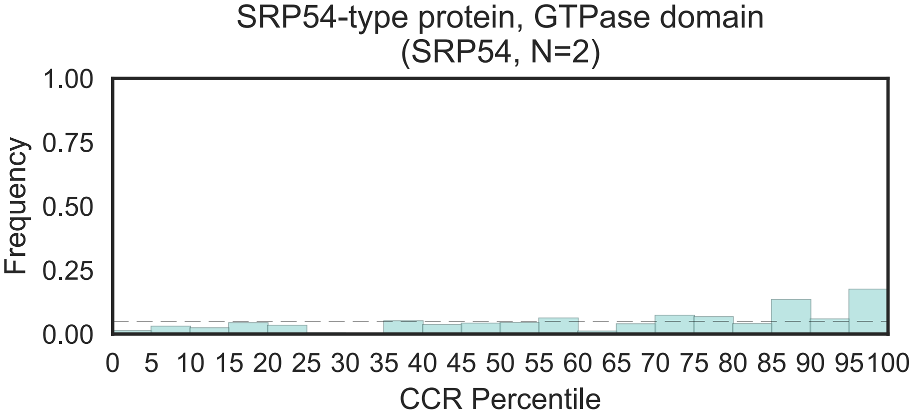


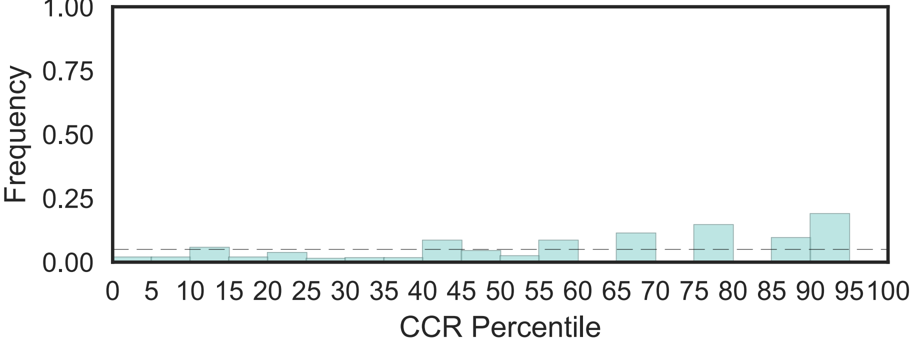


Signal recognition particle 14kD protein
(SRP14, N=1)


SRP19 protein
(SRP19, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

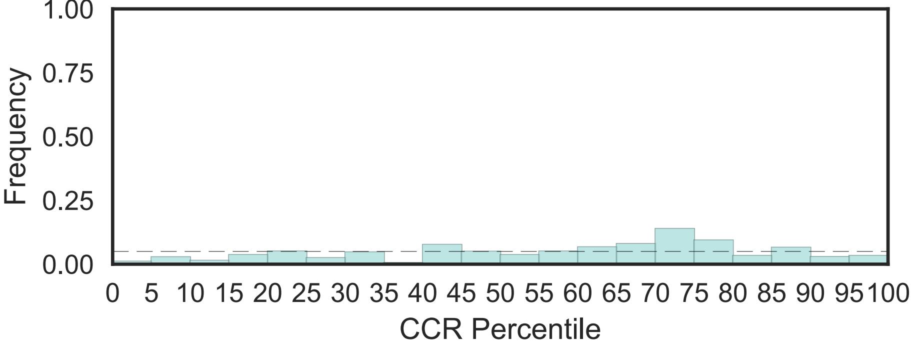

SRP40, C-terminal domain
(SRP40_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

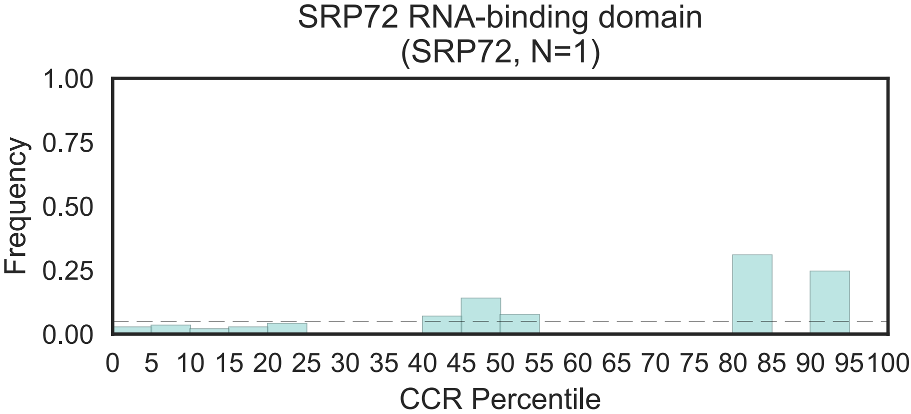

SRP54-type protein, GTPase domain
(SRP54, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

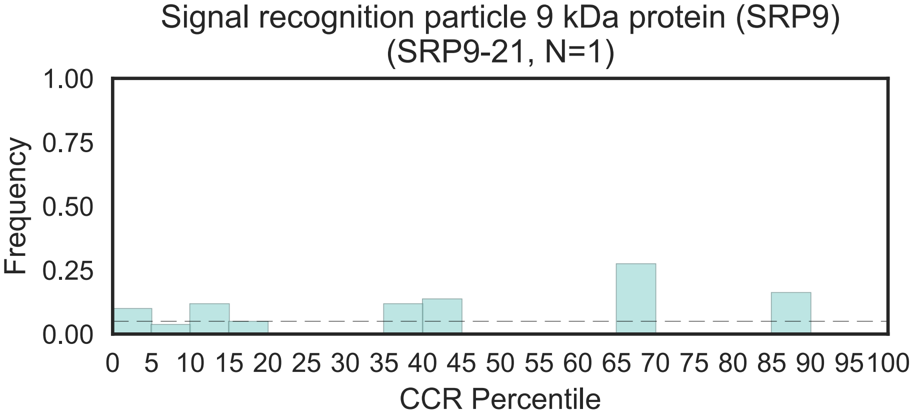


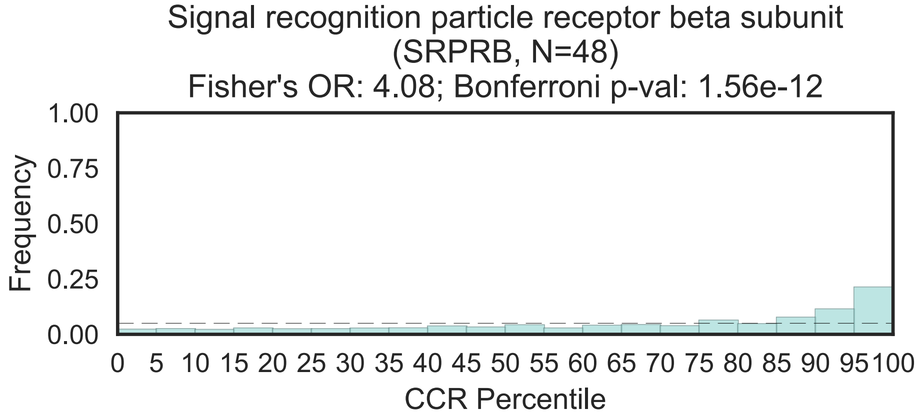
SRP54-type protein, helical bundle domain
(SRP54_N, N=2)

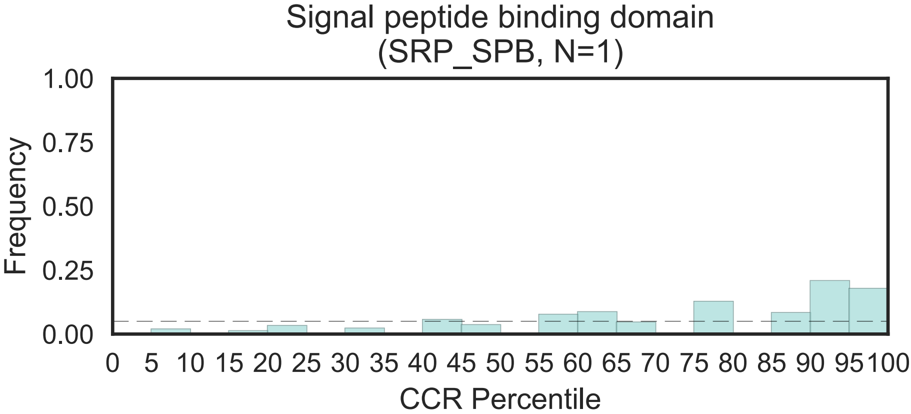
RNA-binding signal recognition particle 68 (SRP68, N=1)

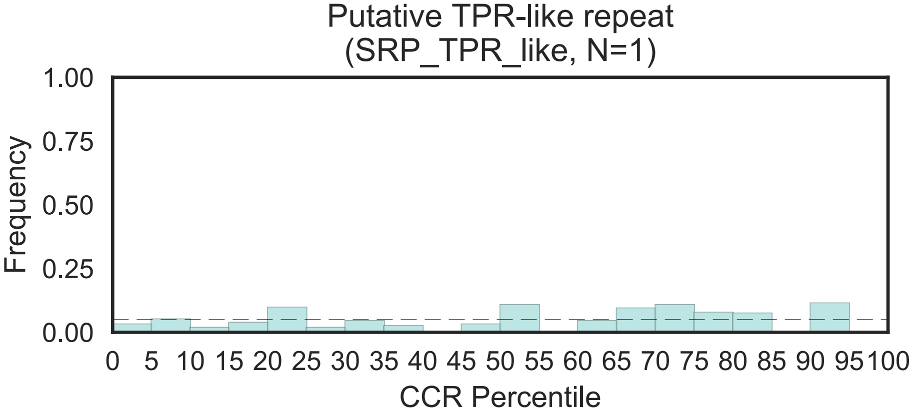


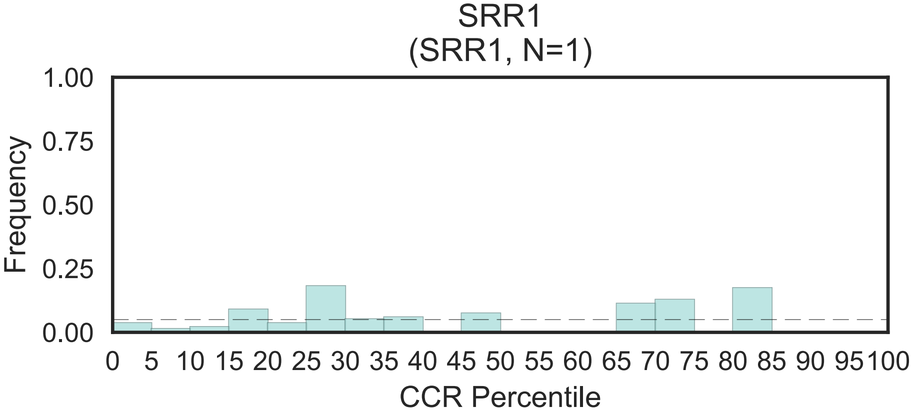

SRP72 RNA-binding domain
(SRP72, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

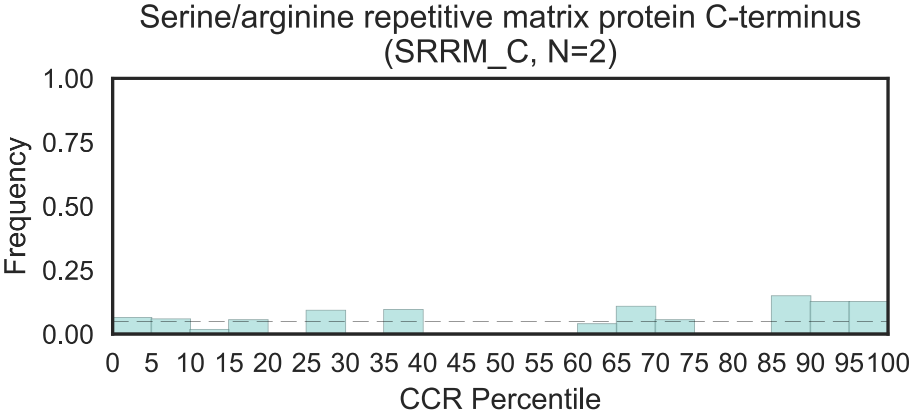

Signal recognition particle 9 kDa protein (SRP9)
(SRP9-21, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

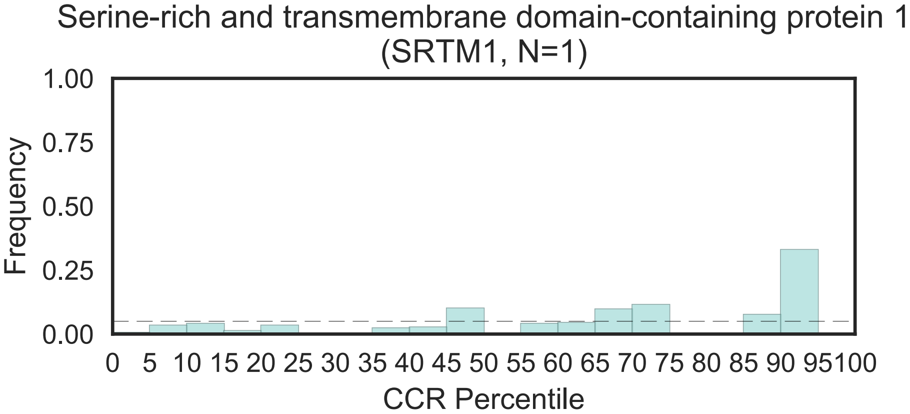

Signal recognition particle receptor beta subunit
(SRPRB, N=48)
Fisher's OR: 4.08; Bonferroni p-val: 1.56e-12
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

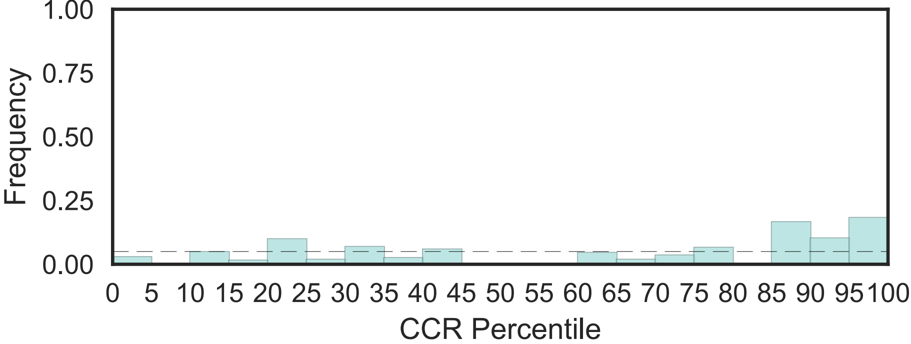

Signal peptide binding domain
(SRP_SPB, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Putative TPR-like repeat
(SRP_TPR_like, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

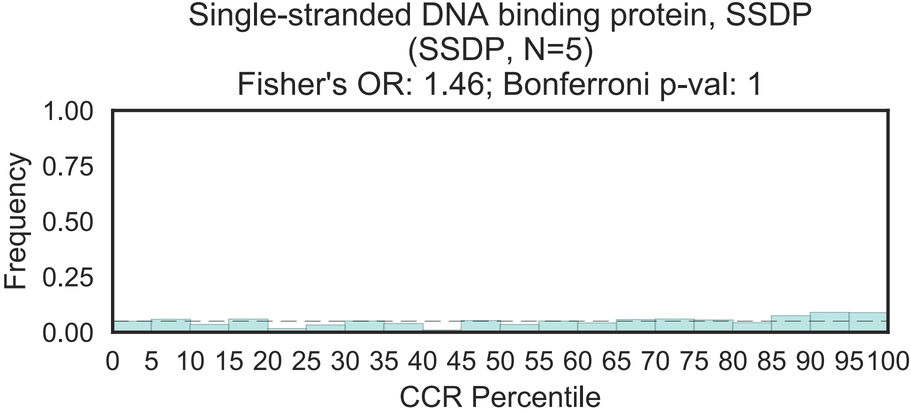

SRR1
(SRR1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

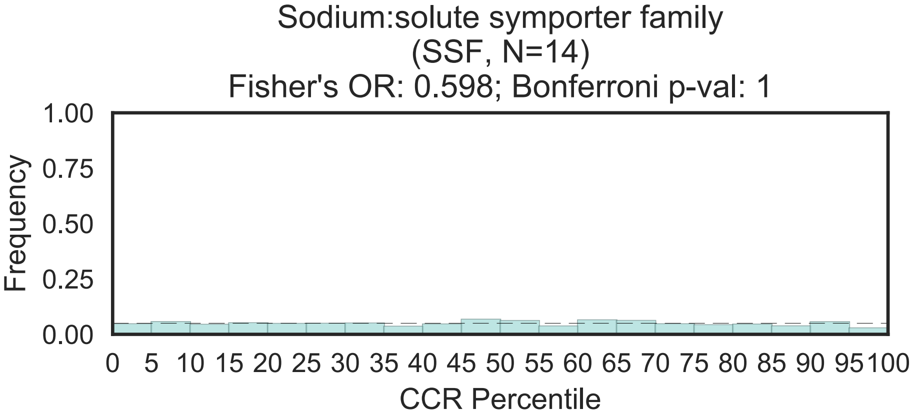

Serine/arginine repetitive matrix protein C-terminus
(SRRM_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

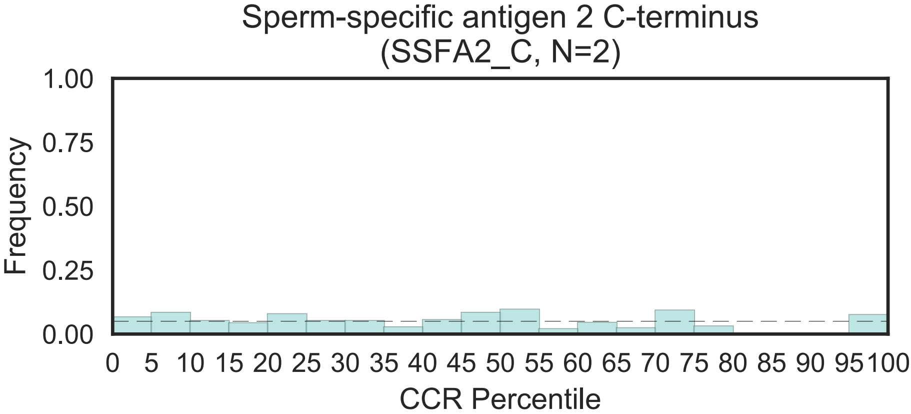

Serine-rich and transmembrane domain-containing protein 1
(SRTM1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

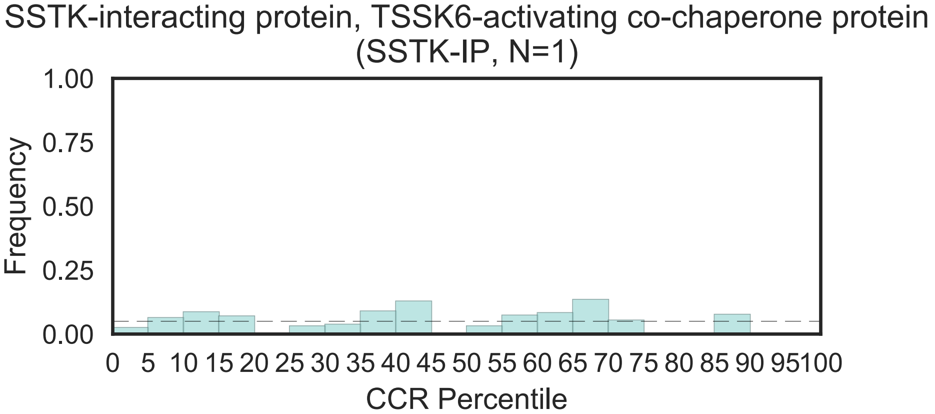


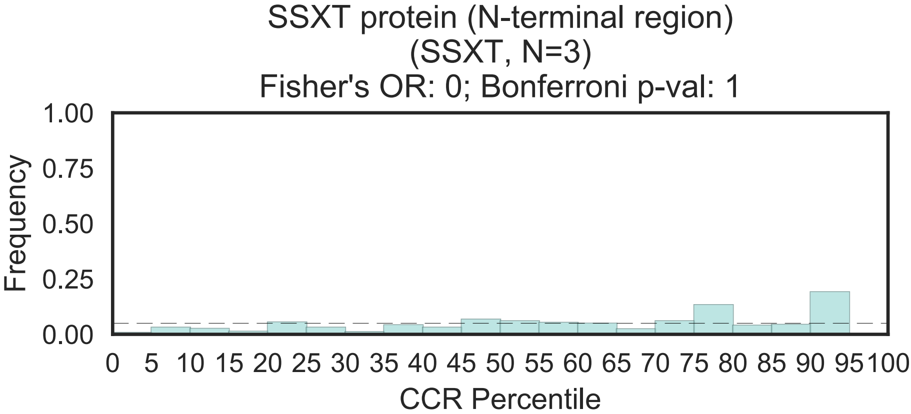
Single-strand binding protein family
(SSB, N=1)

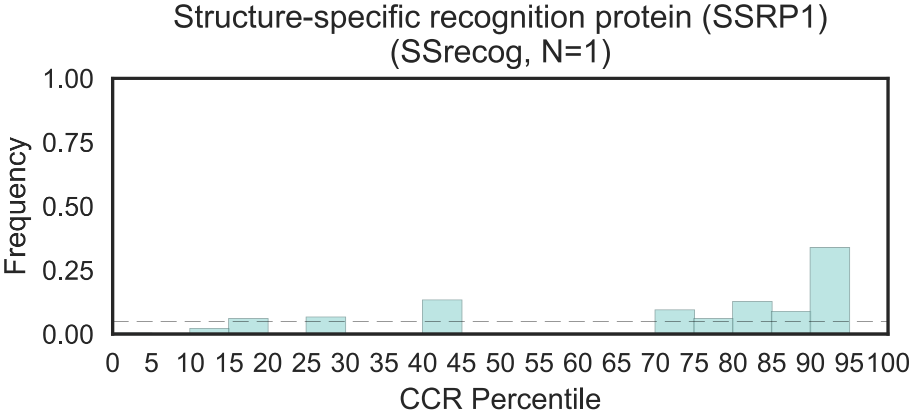

Single-stranded DNA binding protein, SSDP
(SSDP, N=5)
Fisher's OR: 1.46; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Sodium:solute symporter family
(SSF, N=14)
Fisher's OR: 0.598; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

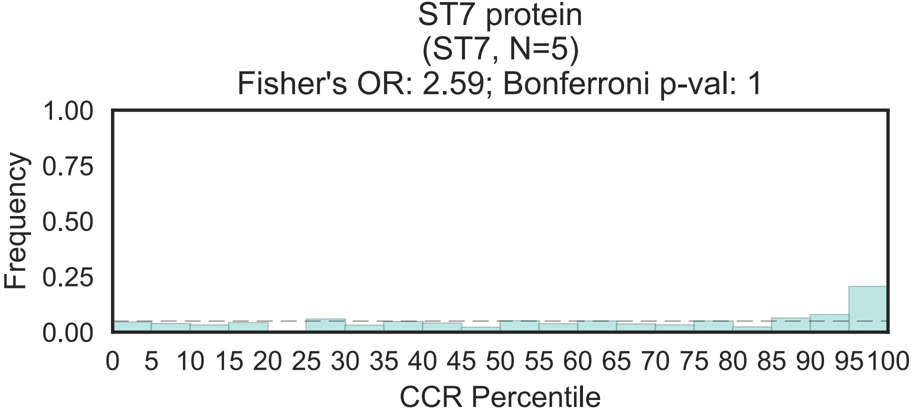

Sperm-specific antigen 2 C-terminus
(SSFA2_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

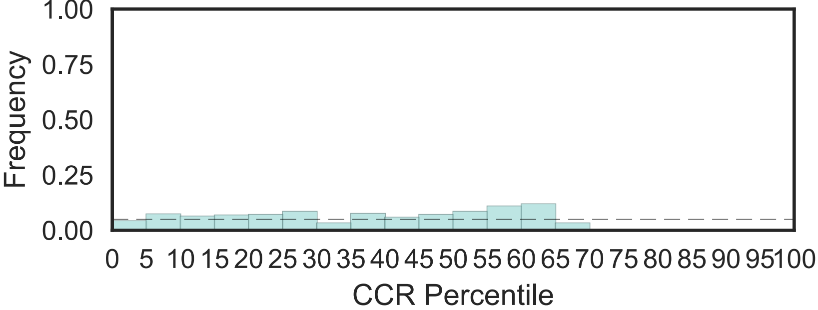

SSTK-interacting protein, TSSK6-activating co-chaperone protein
(SSTK-IP, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


SSXT protein (N-terminal region)
(SSXT, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

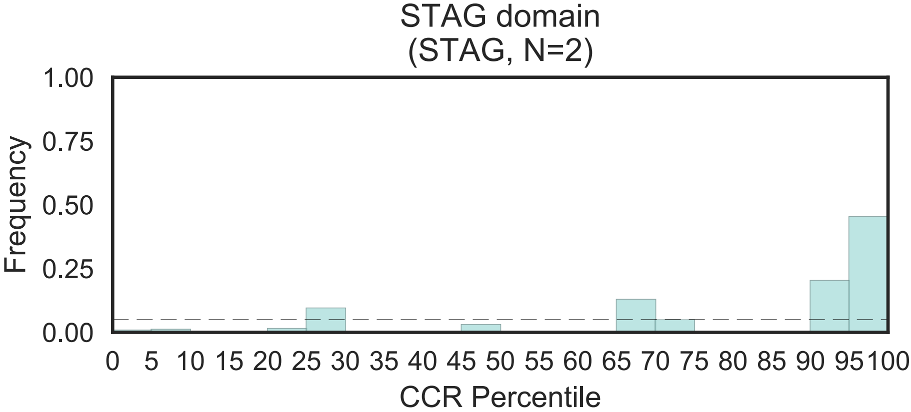


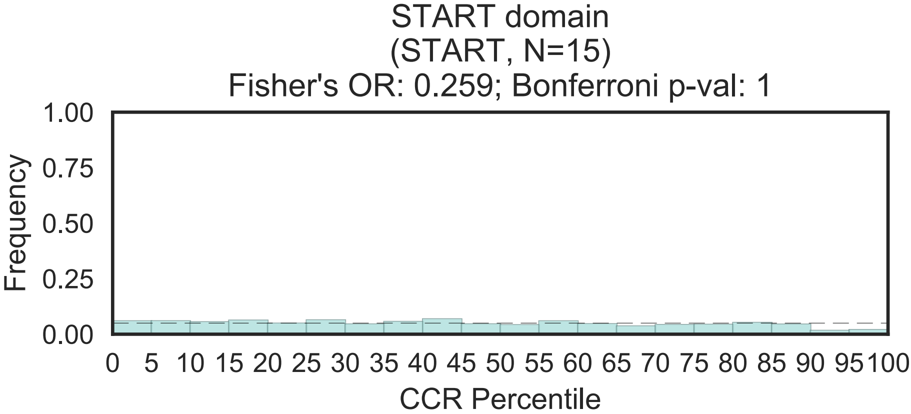
Structure-specific recognition protein (SSRP1)
(SSrecog, N=1)


ST7 protein
(ST7, N=5)
Fisher's OR: 2.59; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

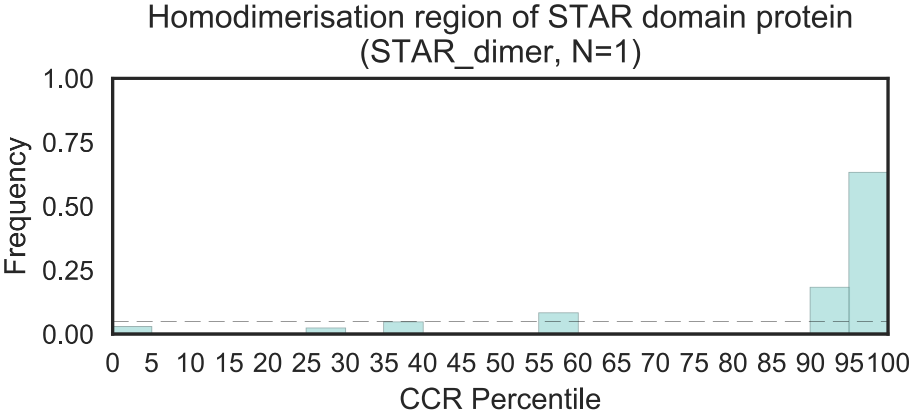


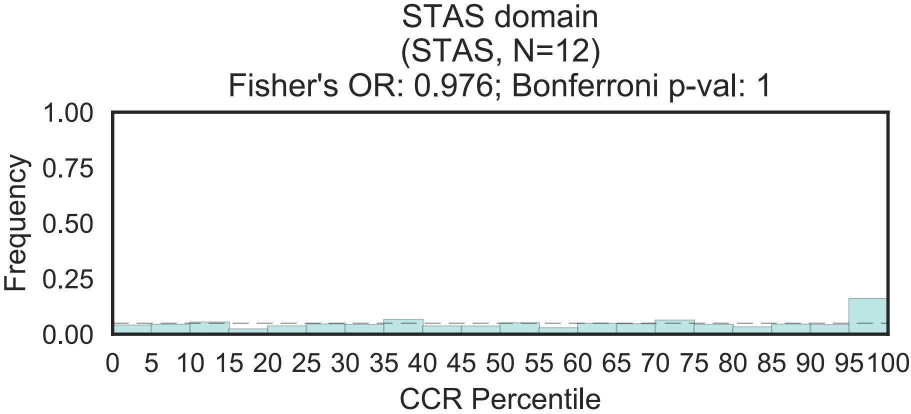
Unstructured on SH3 and cysteine-rich domain-containing protein 2
(STAC2_u1, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

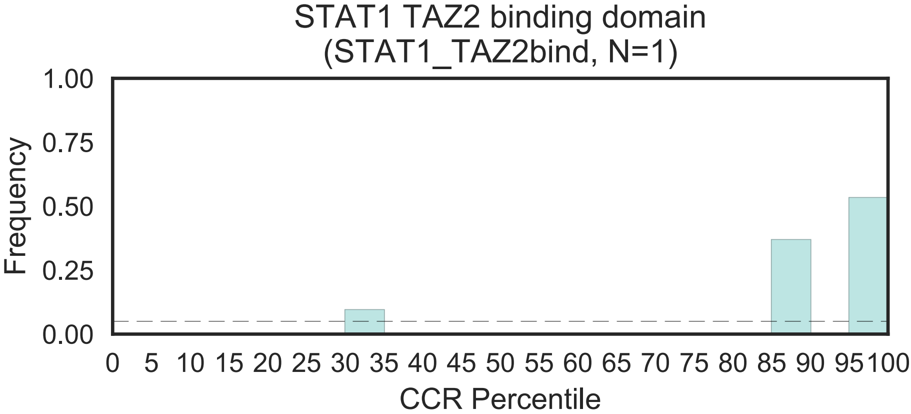

STAG domain
(STAG, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

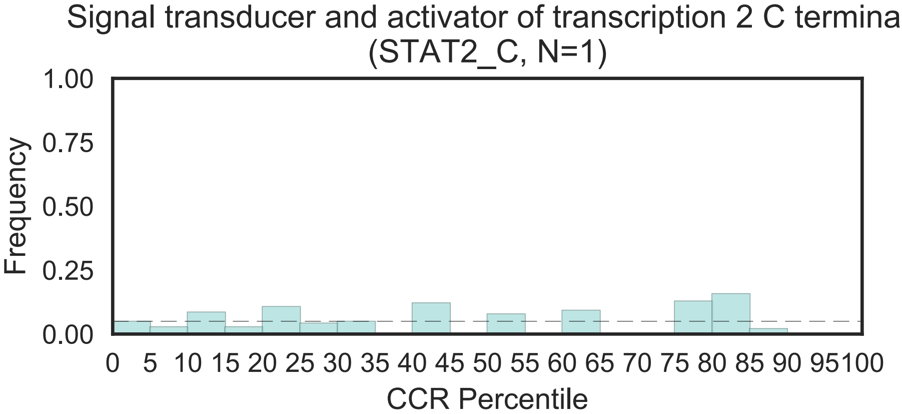


START domain
(START, N=15)
Fisher's OR: 0.259; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

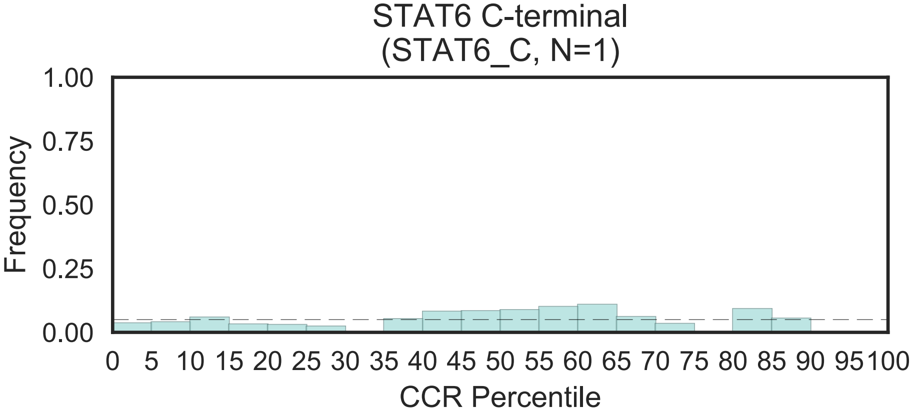

Homodimerisation region of STAR domain protein
(STAR_dimer, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

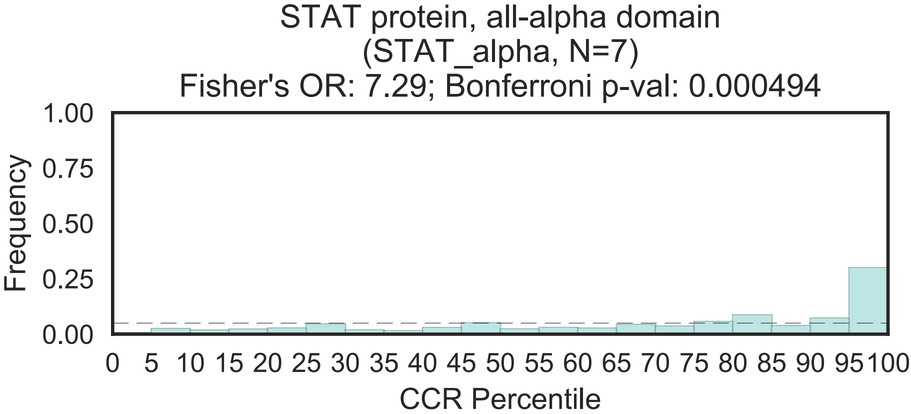

STAS domain
(STAS, N=12)
Fisher's OR: 0.976; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


STAT1 TAZ2 binding domain
(STAT1_TAZ2bind, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

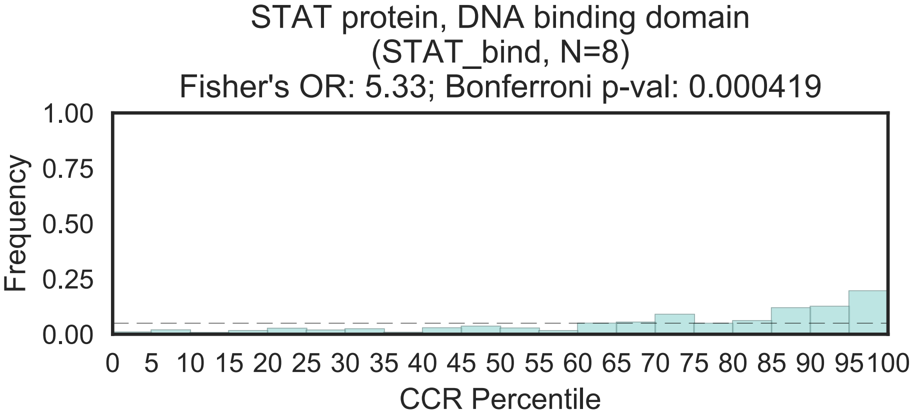


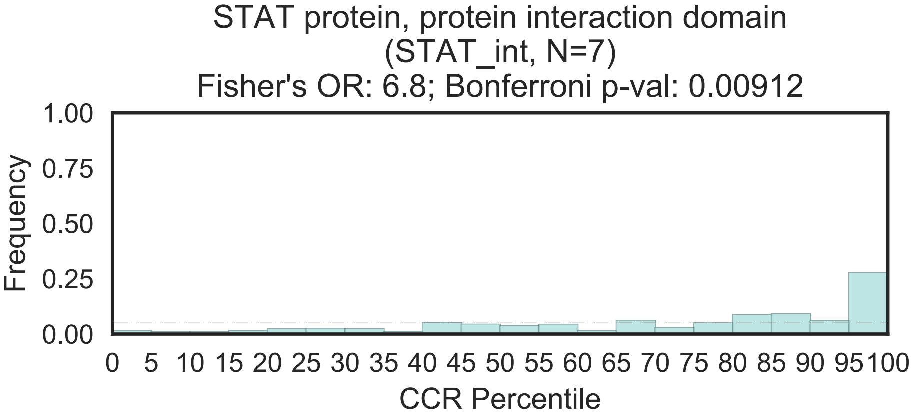
Signal transducer and activator of transcription 2 C terminal (STAT2_C, N=1)

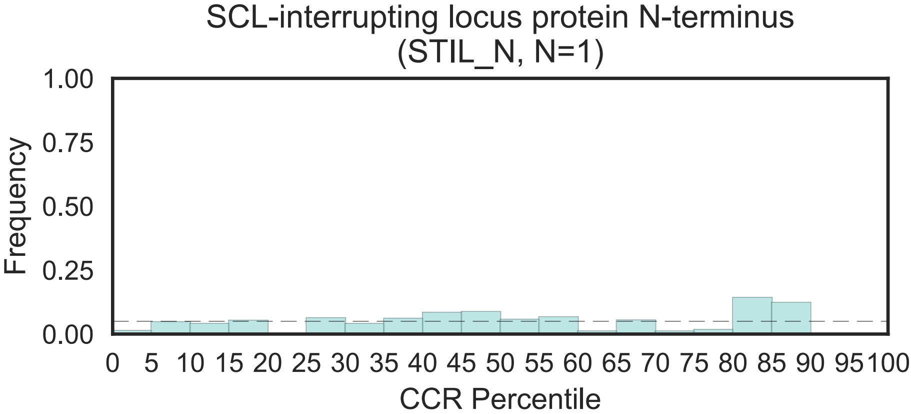

STAT6 C-terminal
(STAT6_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

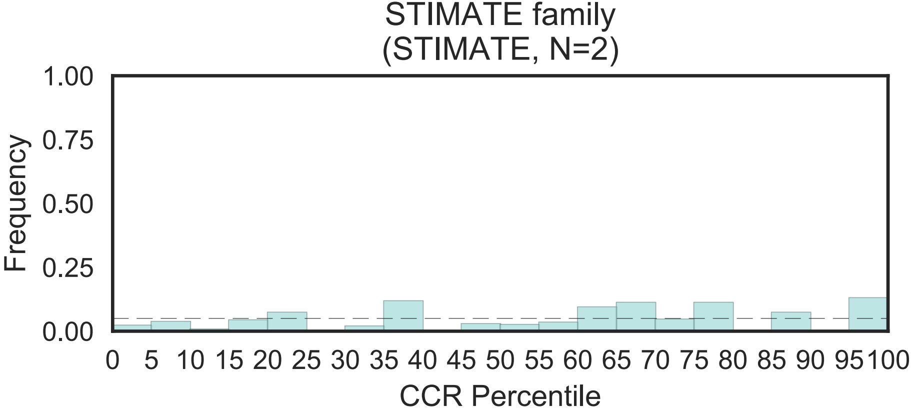


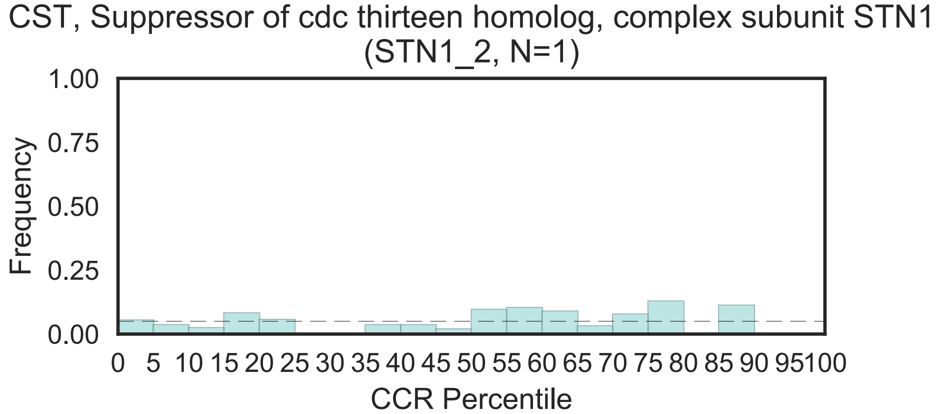
STAT protein, all-alpha domain
(STAT_alpha, N=7)
Fisher's OR: 7.29; Bonferroni p-val: 0.000494
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

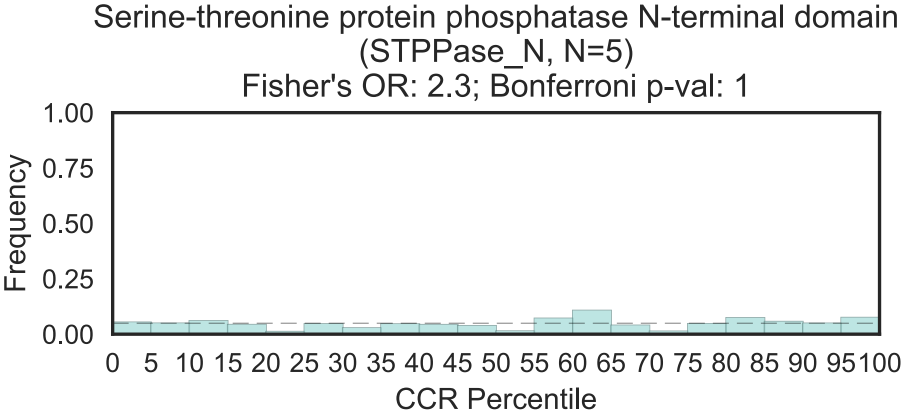

STAT protein, DNA binding domain
(STAT_bind, N=8)
Fisher's OR: 5.33; Bonferroni p-val: 0.000419
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


STAT protein, protein interaction domain
(STAT_int, N=7)
Fisher's OR: 6.8; Bonferroni p-val: 0.00912
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

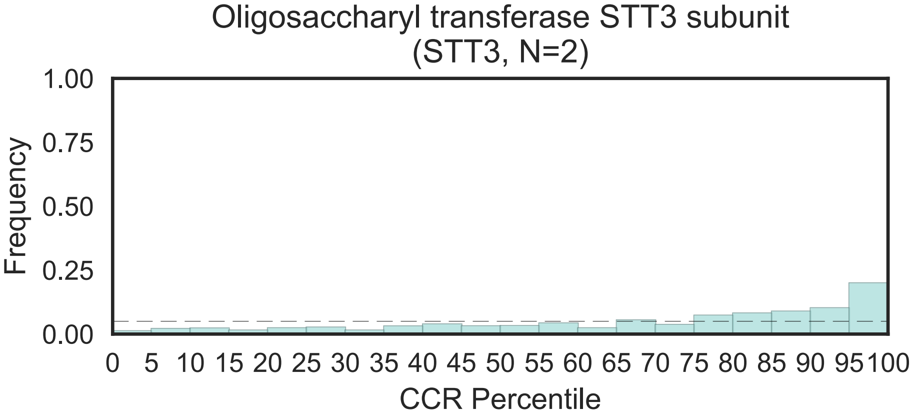

SCL-interrupting locus protein N-terminus
(STIL_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

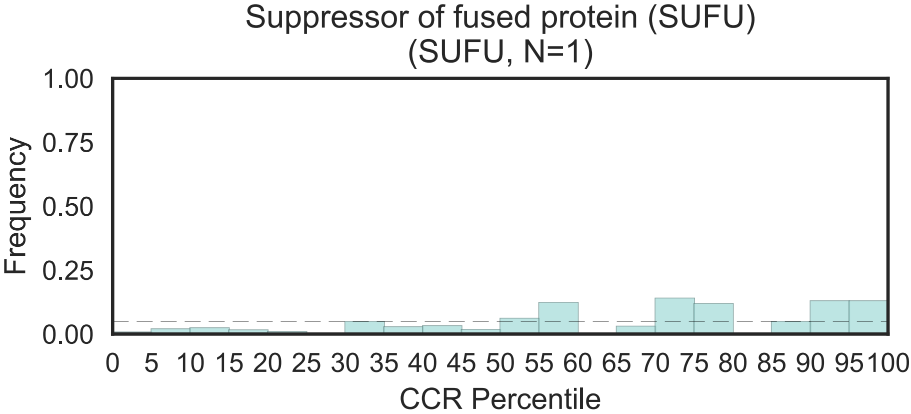

STIMATE family
(STIMATE, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

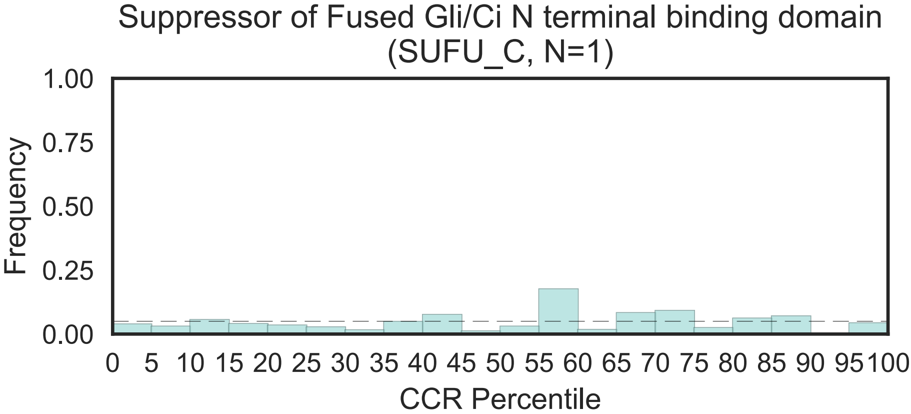

CST, Suppressor of cdc thirteen homolog, complex subunit STN1
(STN1_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



Serine-threonine protein phosphatase N-terminal domain
(STPPase_N, N=5)
Fisher's OR: 2.3; Bonferroni p-val: 1

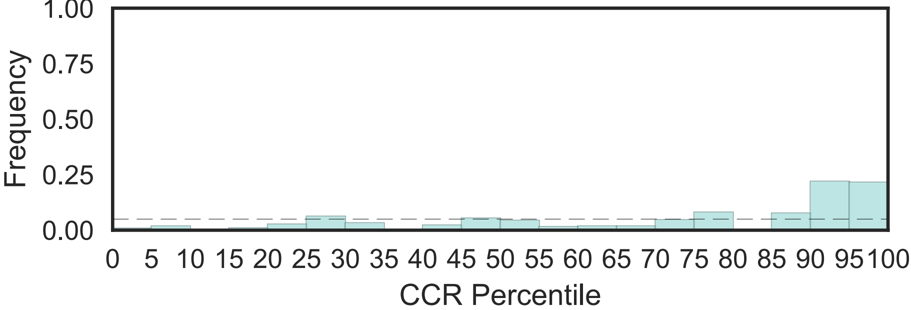

Oligosaccharyl transferase STT3 subunit
(STT3, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

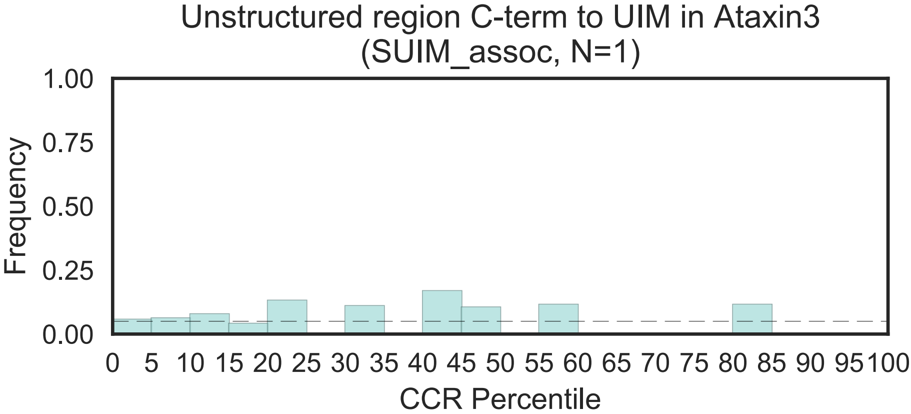

Suppressor of fused protein (SUFU)
(SUFU, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

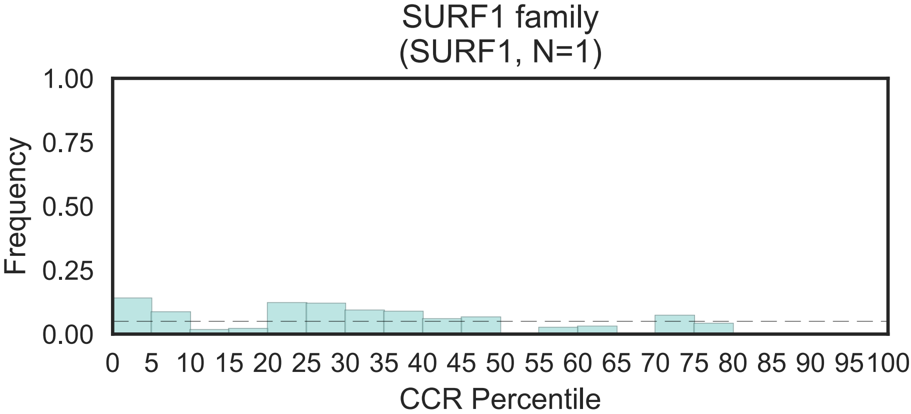


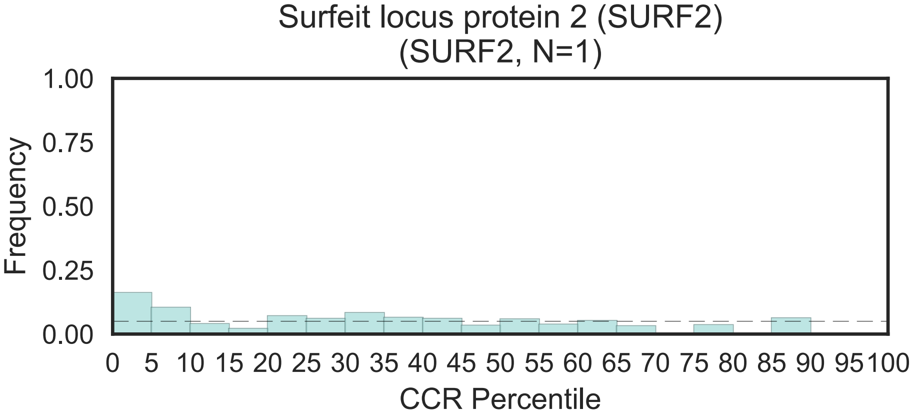
Suppressor of Fused Gli/Ci N terminal binding domain (SUFU_C, N=1)

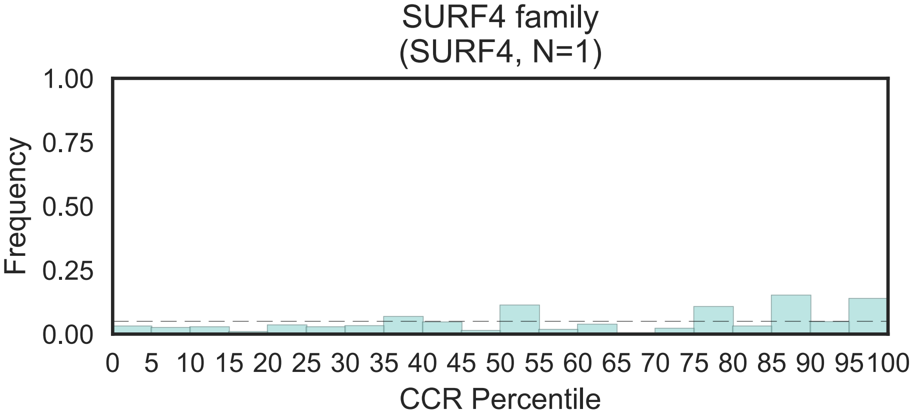
Translation initiation factor SUI1
(SUI1, N=4)
Fisher's OR: 7.72; Bonferroni p-val: 1

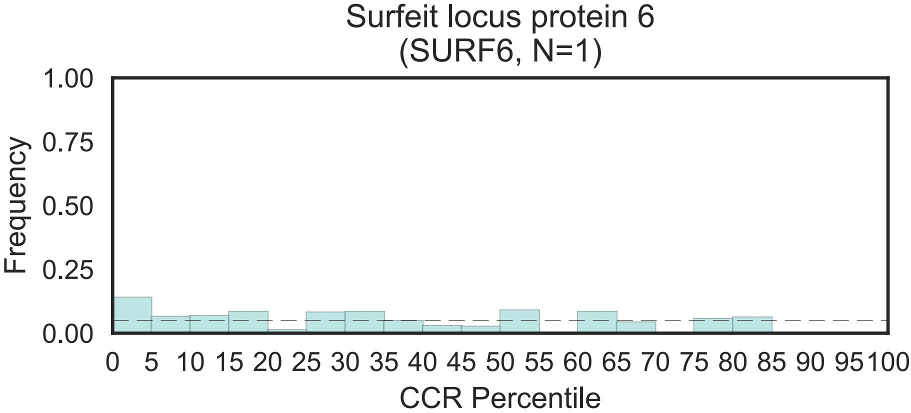


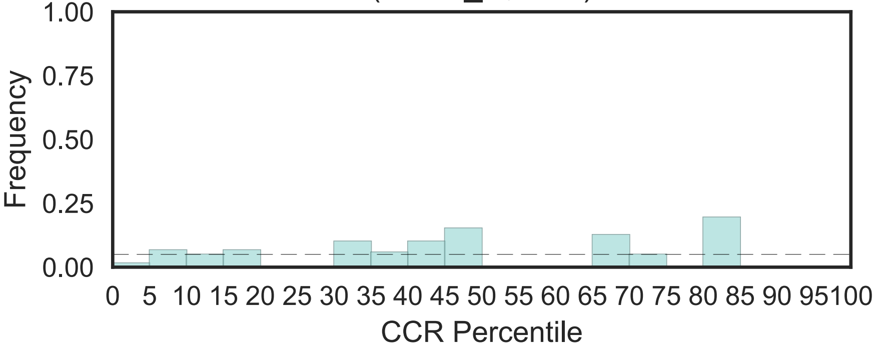

Unstructured region C-term to UIM in Ataxin3
(SUIM_assoc, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

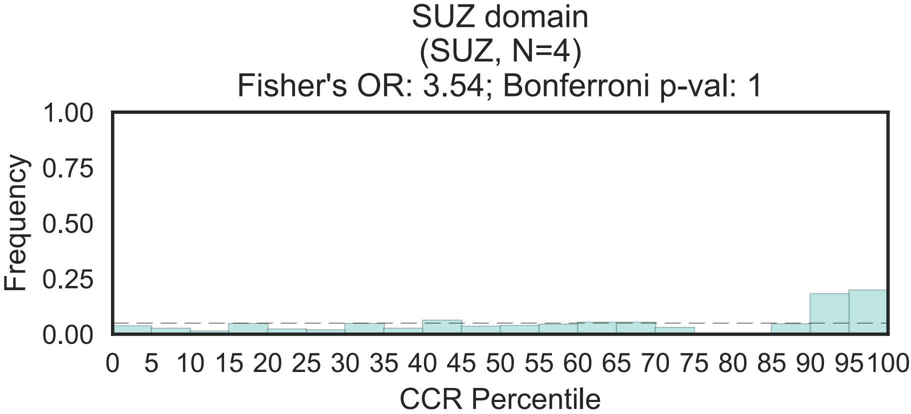

SURF1 family
(SURF1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

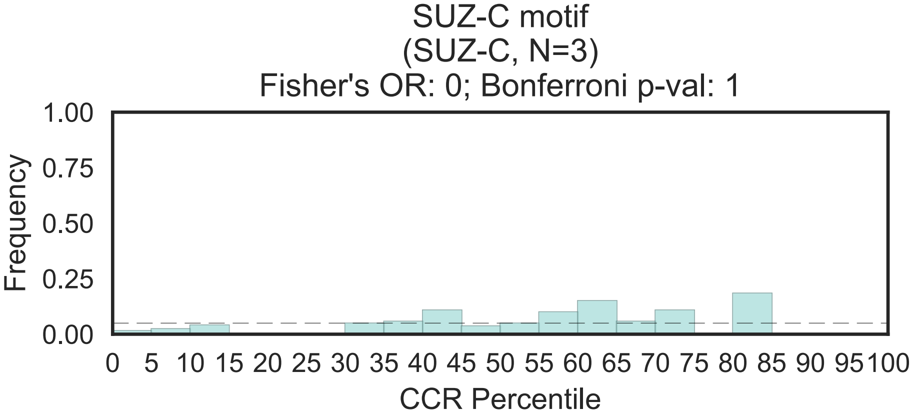

Surfeit locus protein 2 (SURF2)
(SURF2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

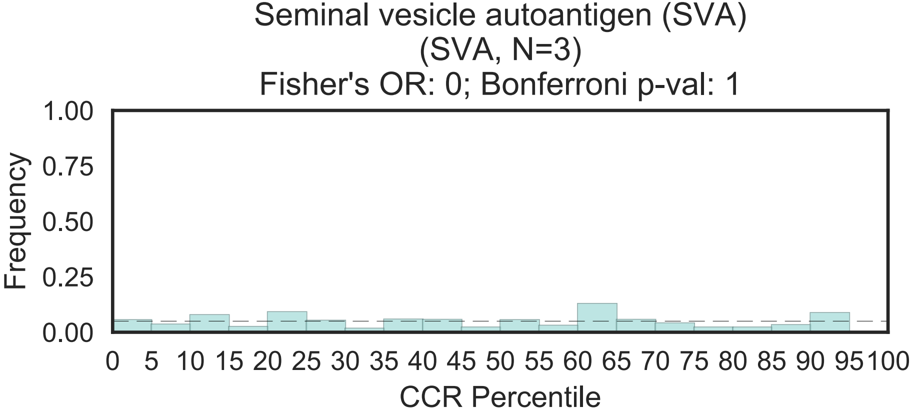

SURF4 family
(SURF4, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

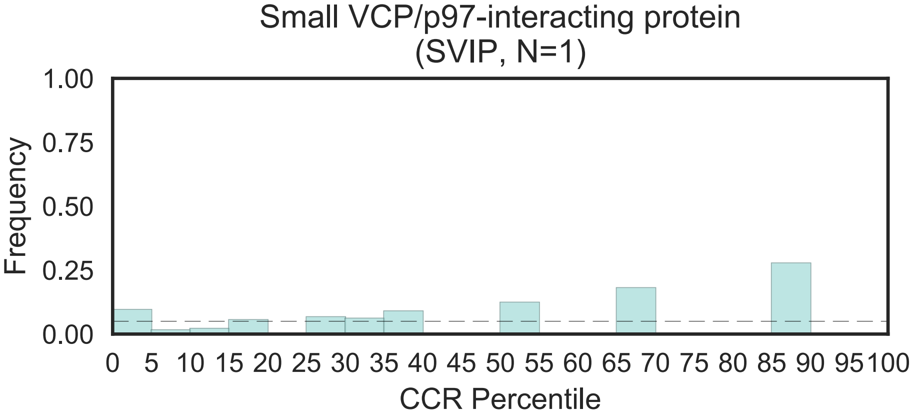

Surfeit locus protein 6
(SURF6, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

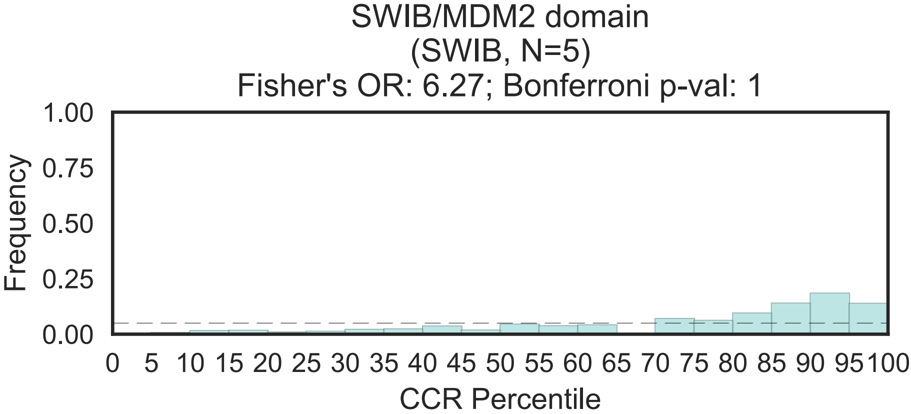

Mitochondrial degradasome RNA helicase subunit C terminal (SUV3_C, N=1)

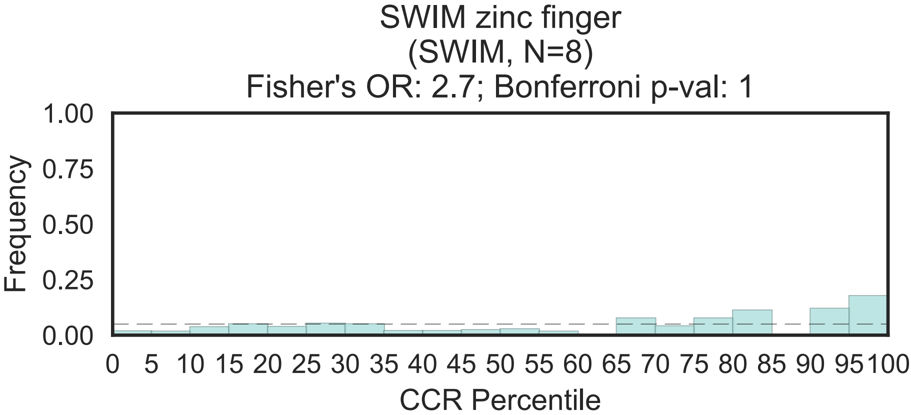

SUZ domain
(SUZ, N=4)
Fisher's OR: 3.54; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


SUZ-C motif
(SUZ-C, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

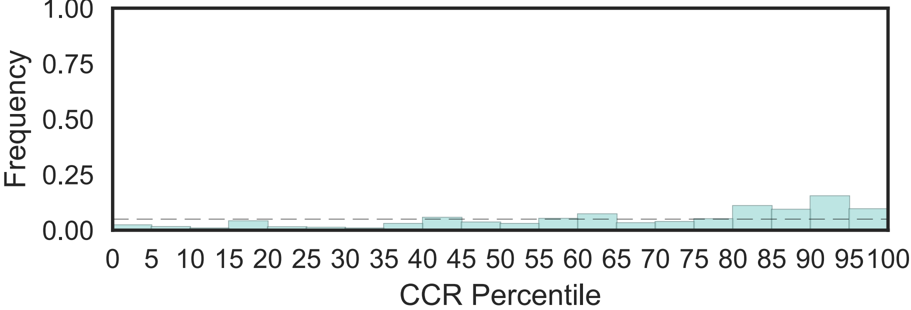

Seminal vesicle autoantigen (SVA)
(SVA, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

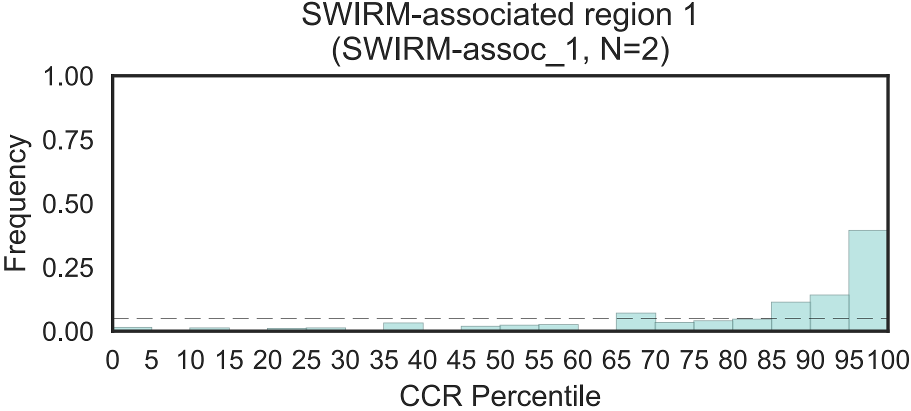

Small VCP/p97-interacting protein
(SVIP, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


SWIB/MDM2 domain
(SWIB, N=5)
Fisher's OR: 6.27; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

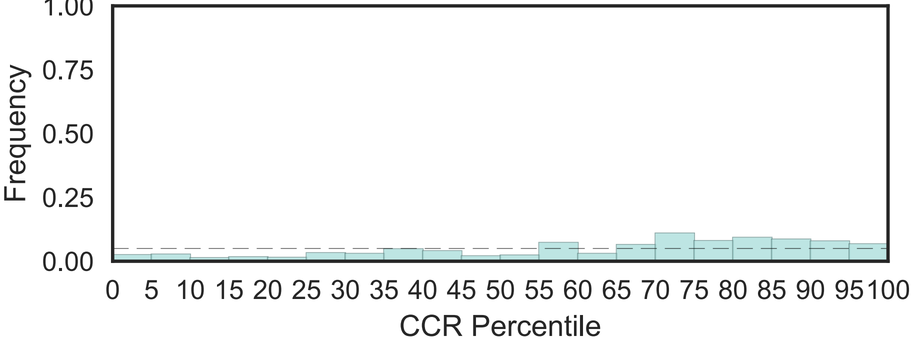

SWIM zinc finger
(SWIM, N=8)
Fisher's OR: 2.7; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

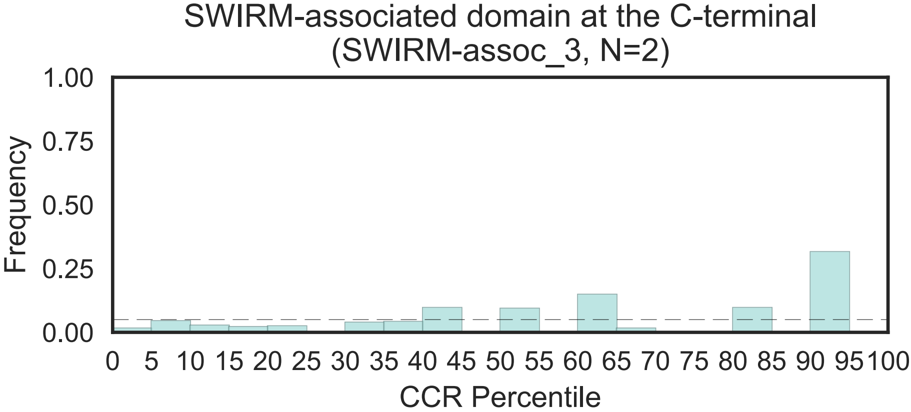
SWIRM domain
(SWIRM, N=6)
Fisher's OR: 2.66; Bonferroni p-val: 1

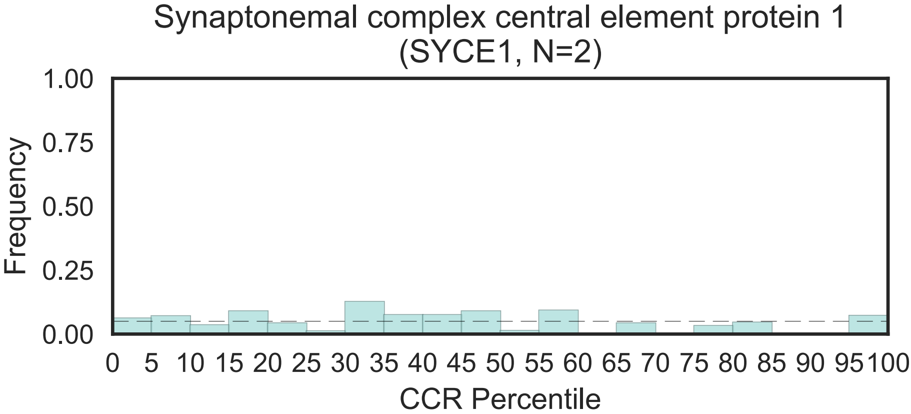



SWIRM-associated region 1
(SWIRM-assoc_1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

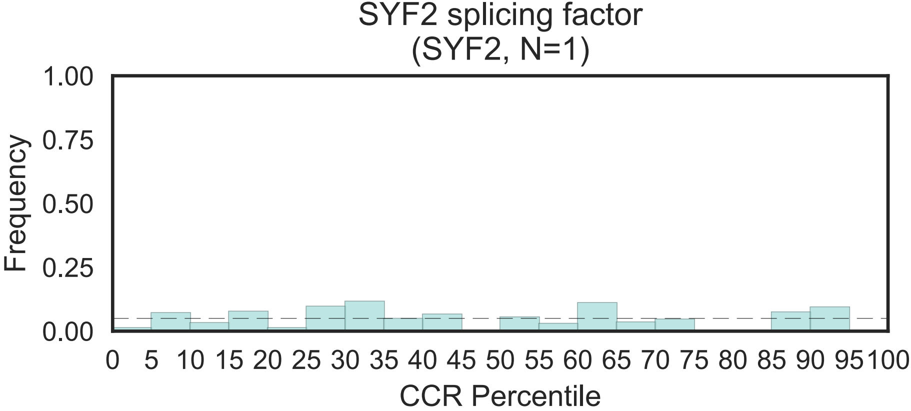
SWIRM-associated domain at the N-terminal (SWIRM-assoc_2, N=2)



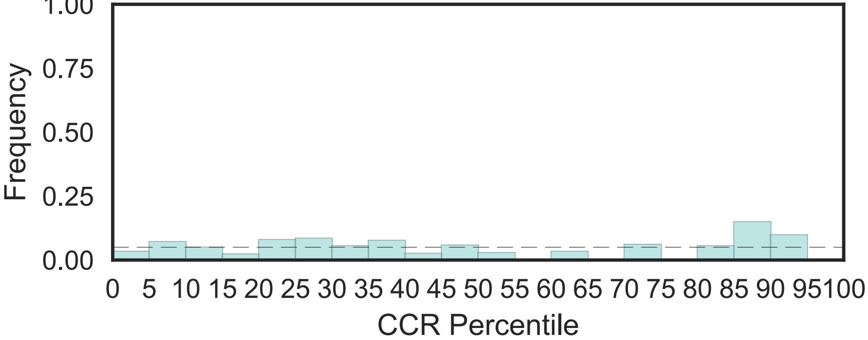

SWIRM-associated domain at the C-terminal
(SWIRM-assoc_3, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

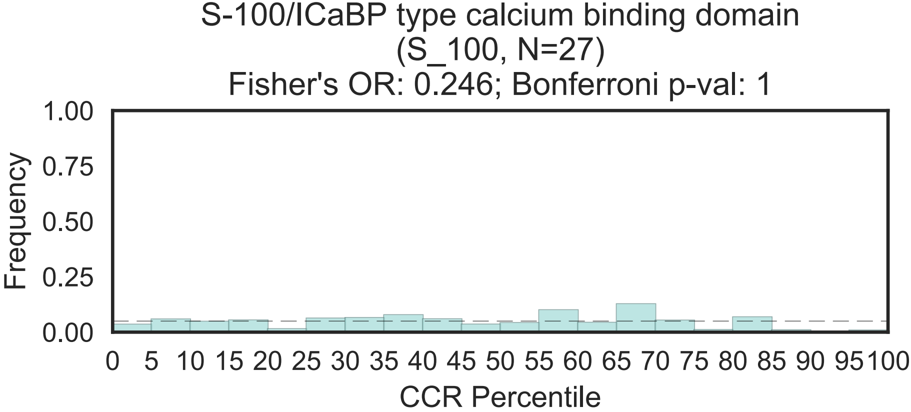


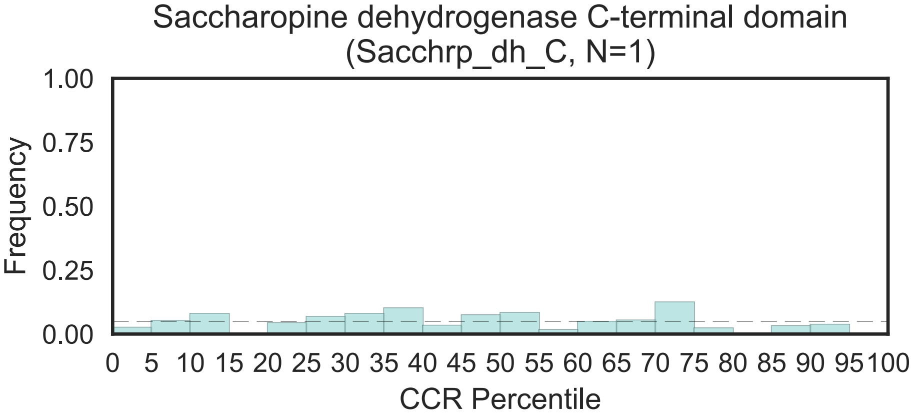
Synaptonemal complex central element protein 1
(SYCE1, N=2)

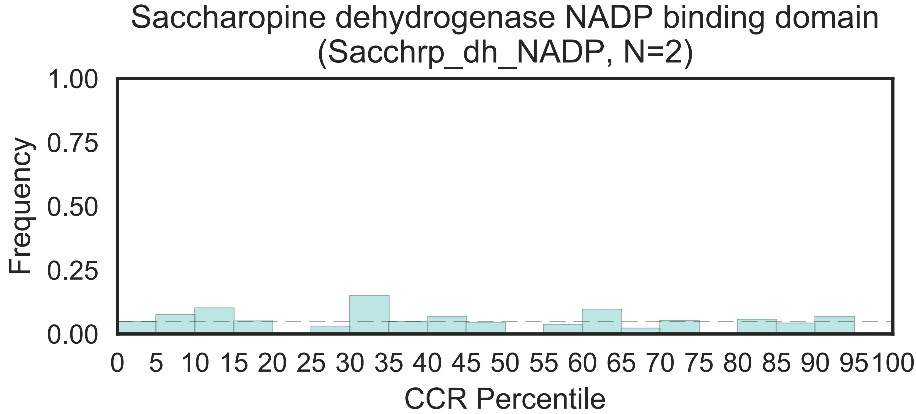

SYF2 splicing factor
(SYF2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

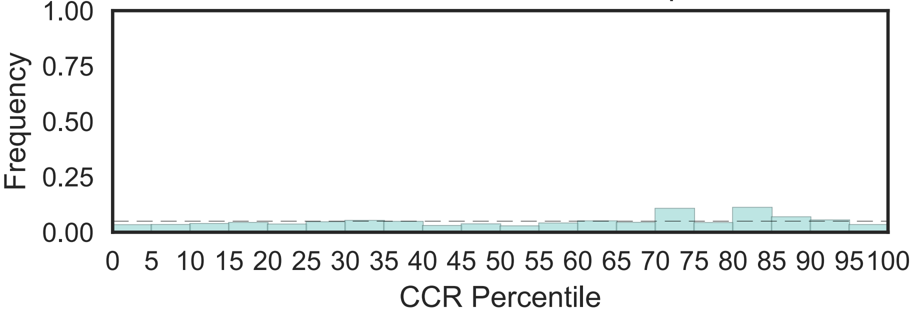
Integral membrane protein S linking to the trans Golgi network (SYS1, N=1)

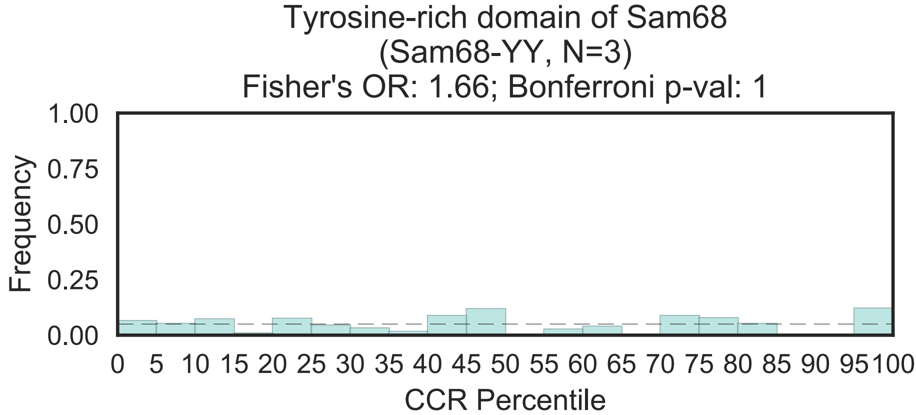


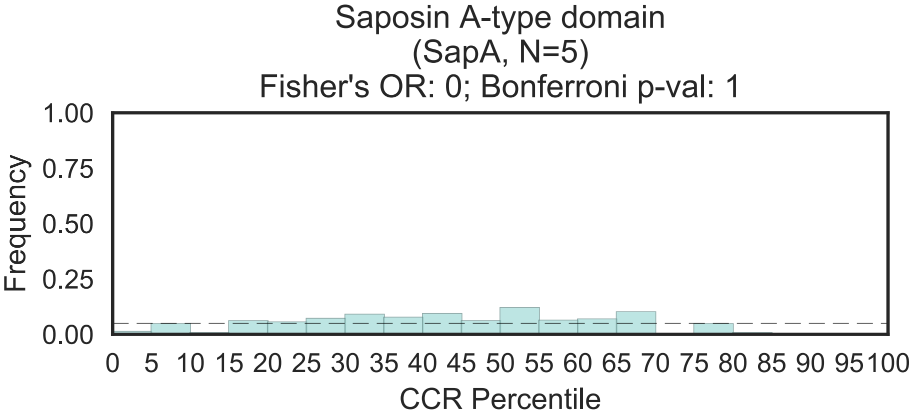

S-100/ICaBP type calcium binding domain
(S_100, N=27)
Fisher's OR: 0.246; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

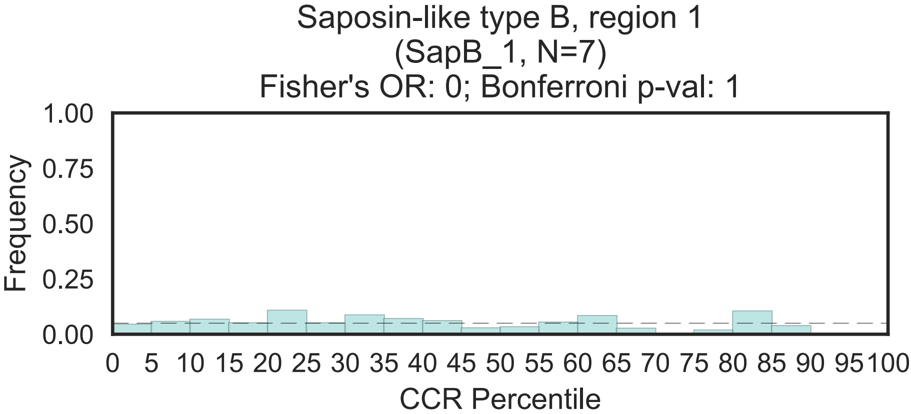

Saccharopine dehydrogenase C-terminal domain
(Sacchrp_dh_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Saccharopine dehydrogenase NADP binding domain
(Sacchrp_dh_NADP, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

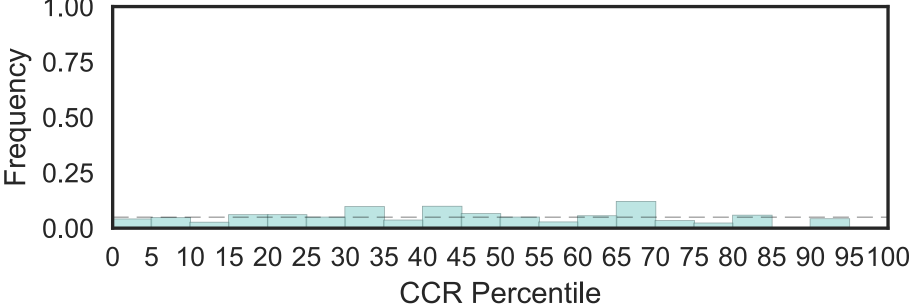

Sad1 / UNC-like C-terminal
(Sad1_UNC, N=8)
Fisher's OR: 0.995; Bonferroni p-val: 1

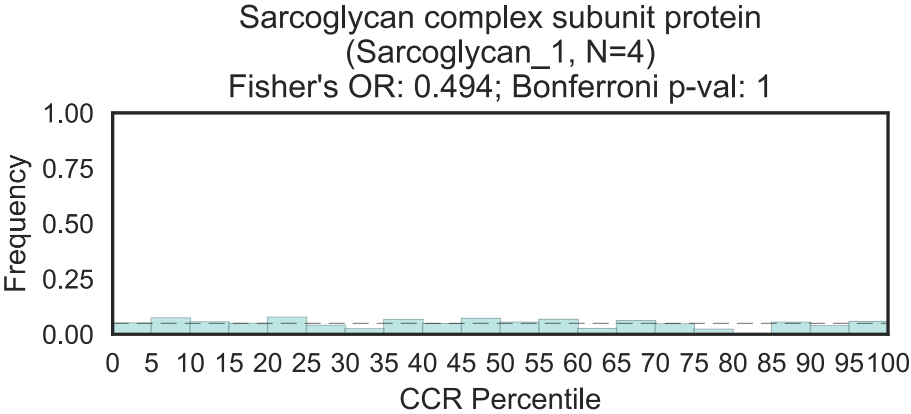

Tyrosine-rich domain of Sam68
(Sam68-YY, N=3)
Fisher's OR: 1.66; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

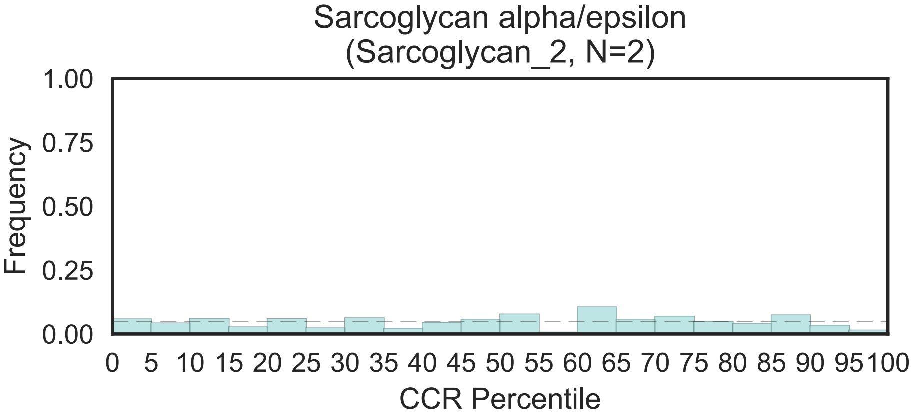

Saposin A-type domain
(SapA, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

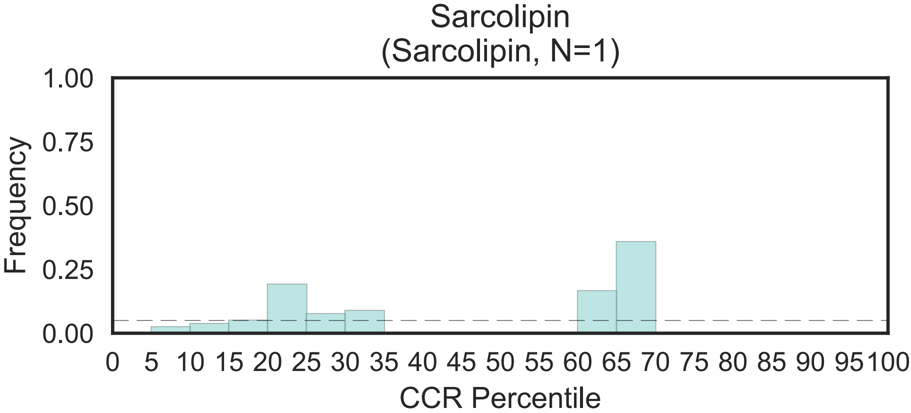

Saposin-like type B, region 1
(SapB_1, N=7)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

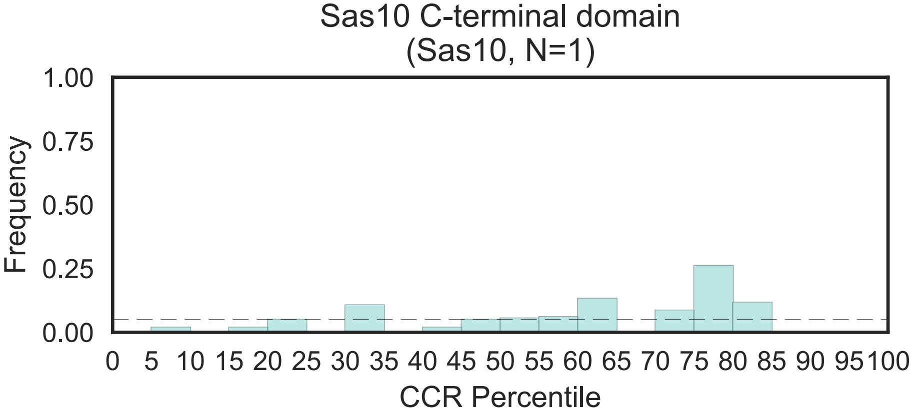
Saposin-like type B, region 2
(SapB_2, N=10)
Fisher's OR: 0; Bonferroni p-val: 1

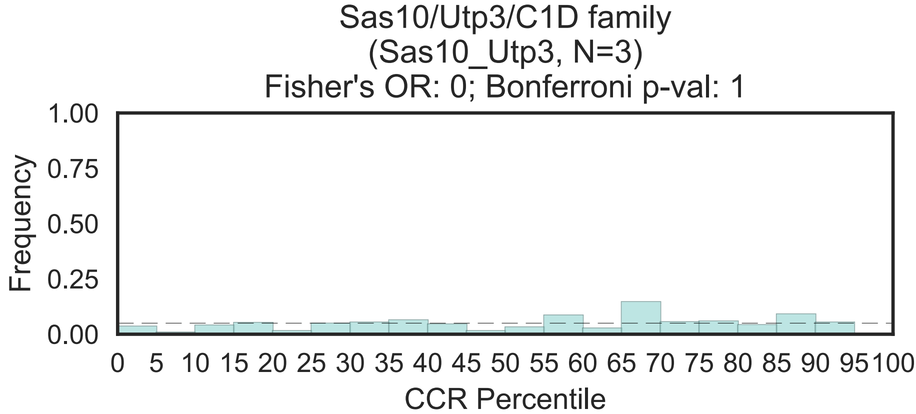


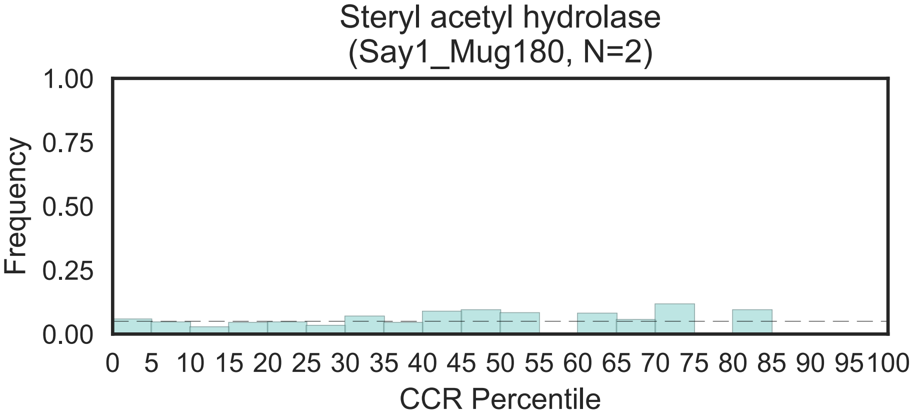

Sarcoglycan complex subunit protein
(Sarcoglycan_1, N=4)
Fisher's OR: 0.494; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

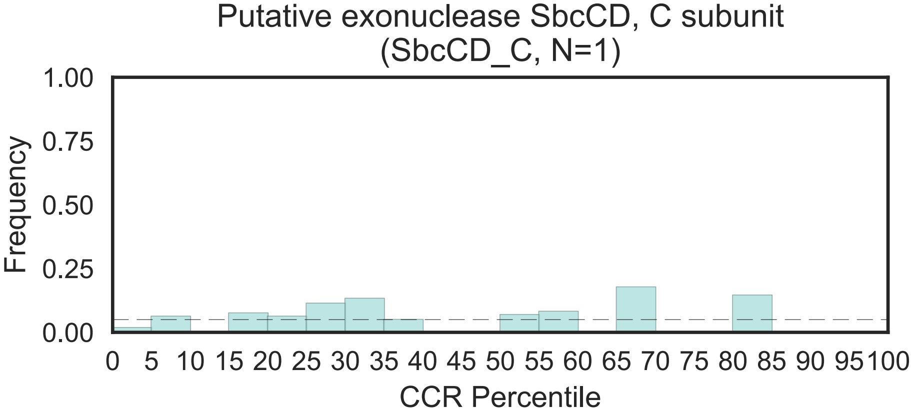

Sarcoglycan alpha/epsilon
(Sarcoglycan_2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

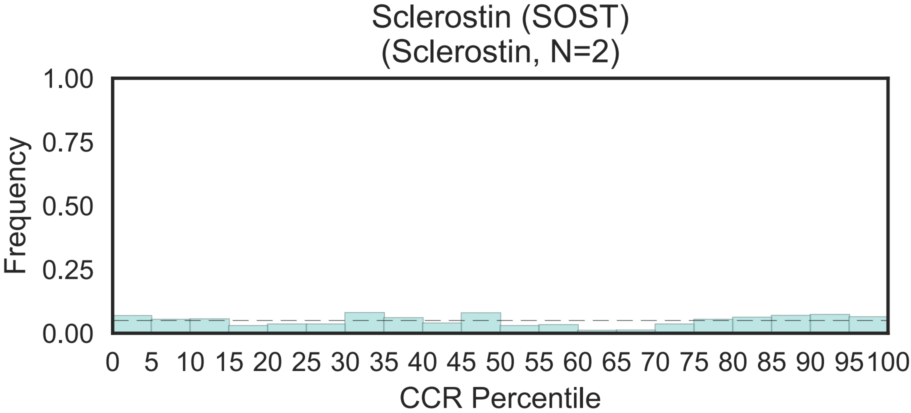

Sarcolipin
(Sarcolipin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

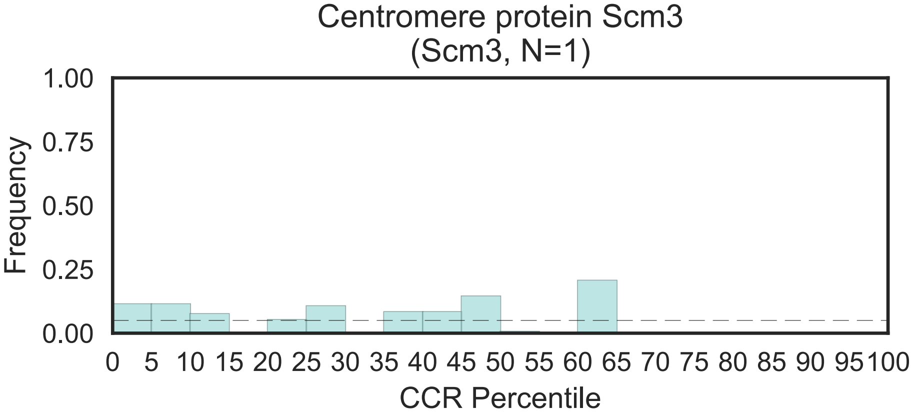

Sas10 C-terminal domain
(Sas10, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

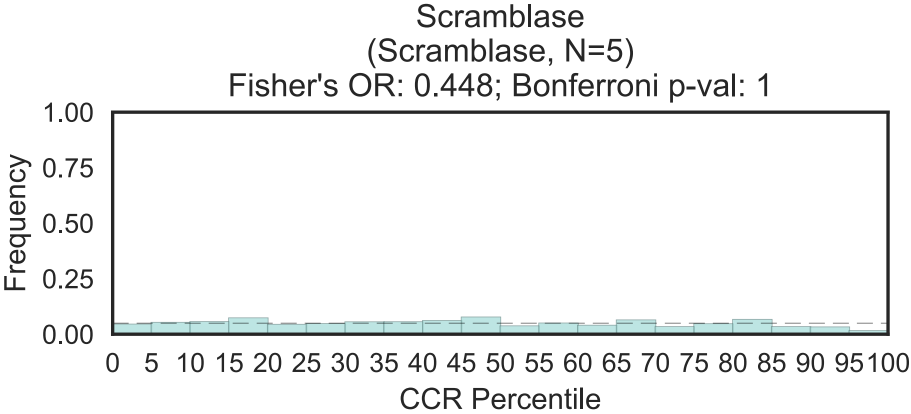

Sas10/Utp3/C1D family
(Sas10_Utp3, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

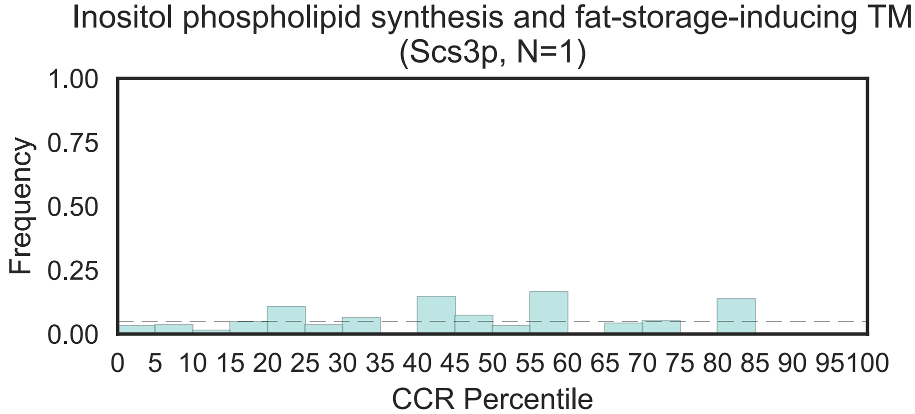

Steryl acetyl hydrolase
(Say1_Mug180, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

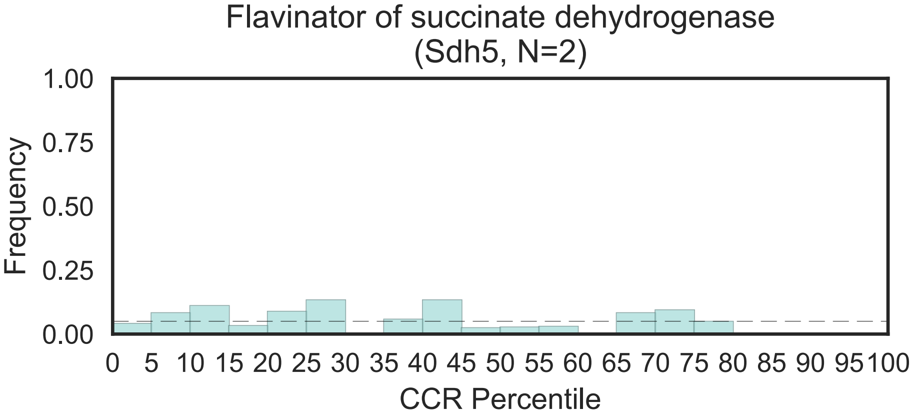

Putative exonuclease SbcCD, C subunit
(SbcCD_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

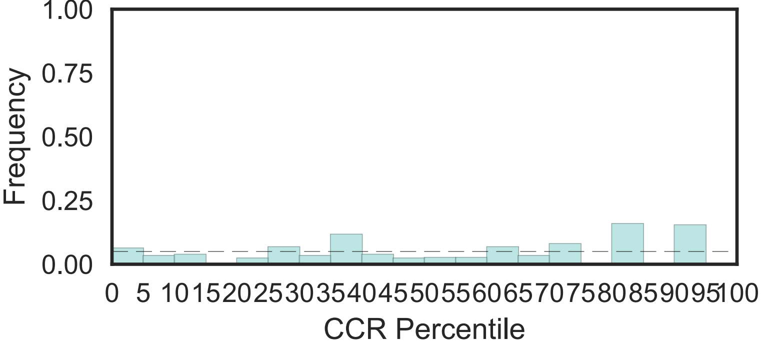

Sclerostin (SOST)
(Sclerostin, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Centromere protein Scm3
(Scm3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

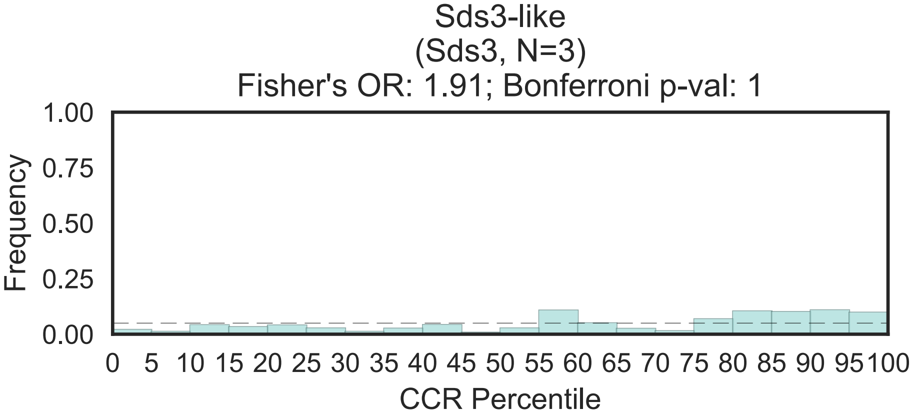

Scramblase
(Scramblase, N=5)
Fisher's OR: 0.448; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

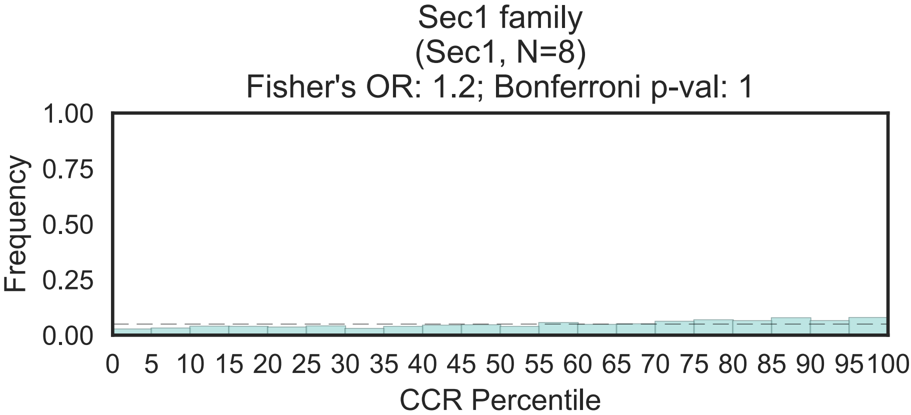

Inositol phospholipid synthesis and fat-storage-inducing TM
(Scs3p, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

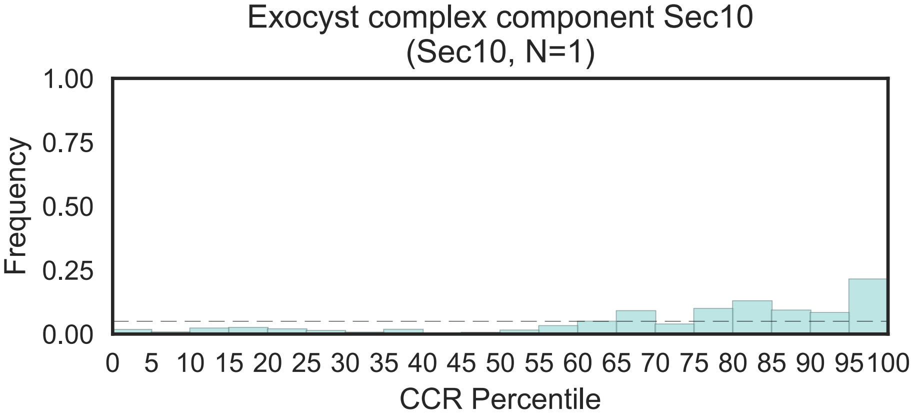

Flavinator of succinate dehydrogenase
(Sdh5, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

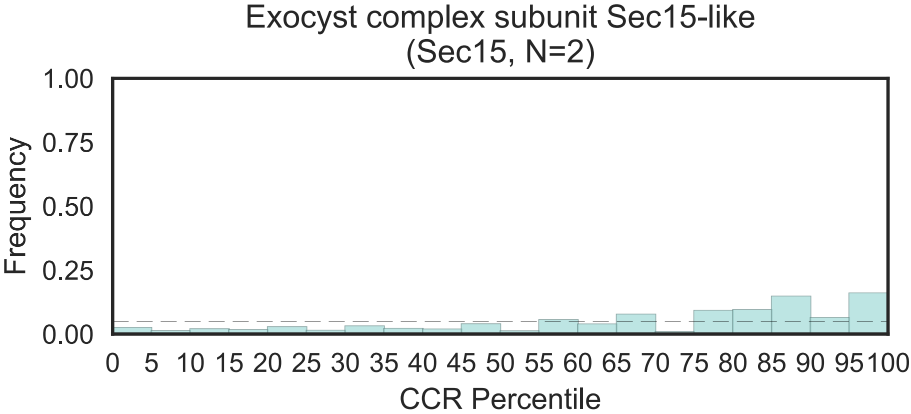


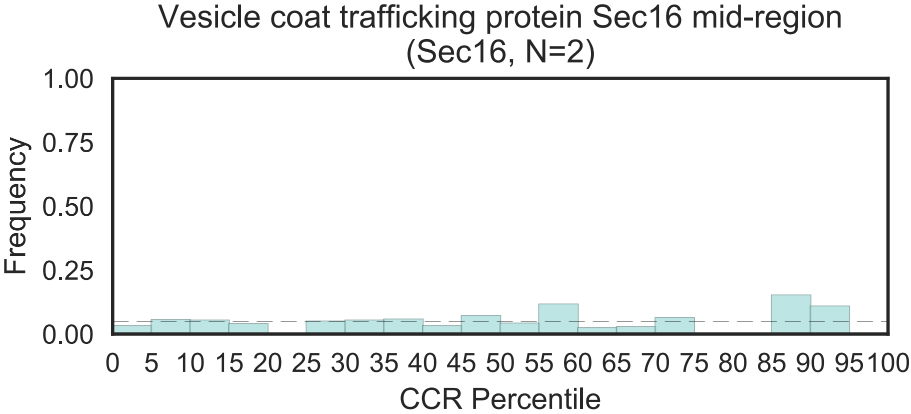
Succinate dehydrogenase/Fumarate reductase transmembrane subunit
(Sdh_cyt, N=1)

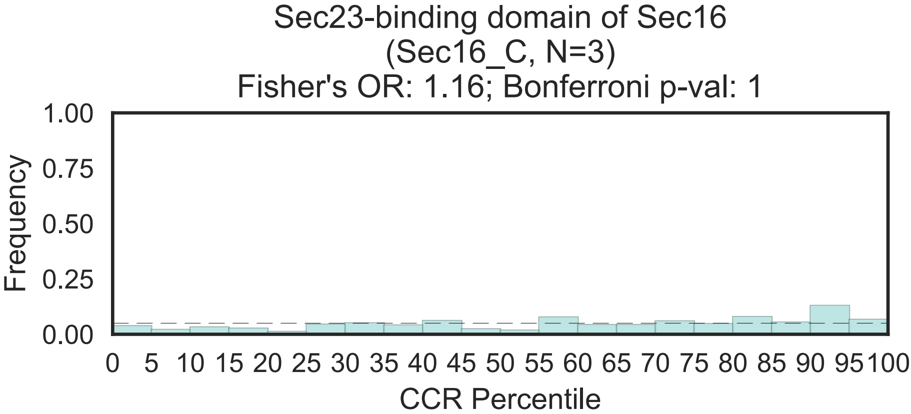

Sds3-like
(Sds3, N=3)
Fisher's OR: 1.91; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

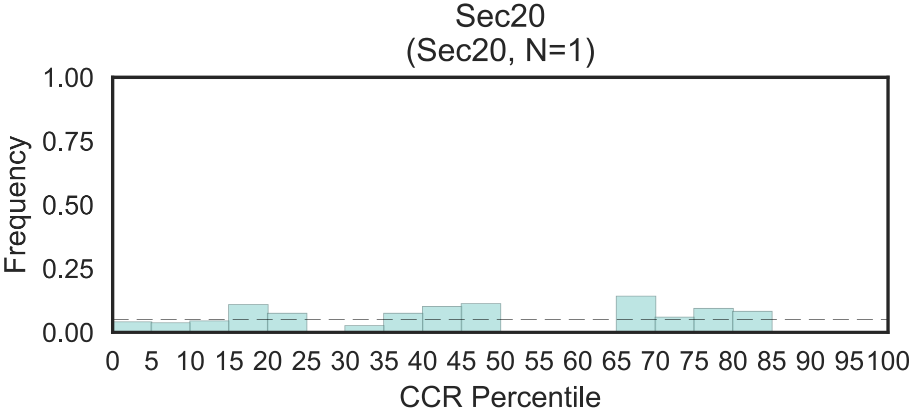

Sec1 family
(Sec1, N=8)
Fisher's OR: 1.2; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

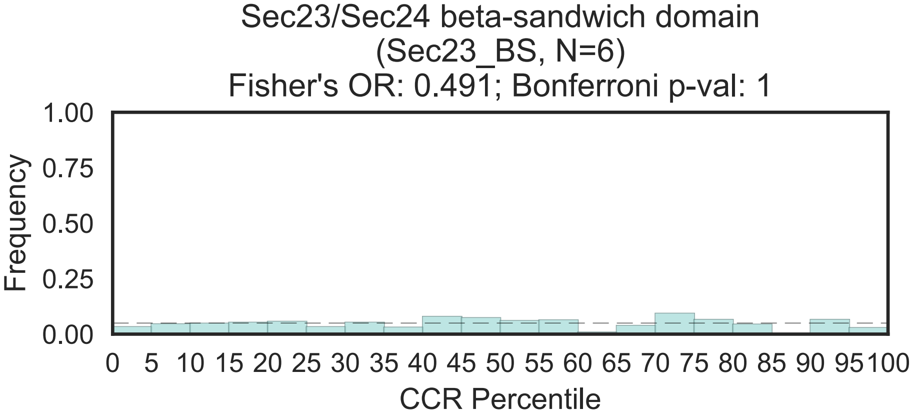

Exocyst complex component Sec10
(Sec10, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Exocyst complex subunit Sec15-like
(Sec15, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

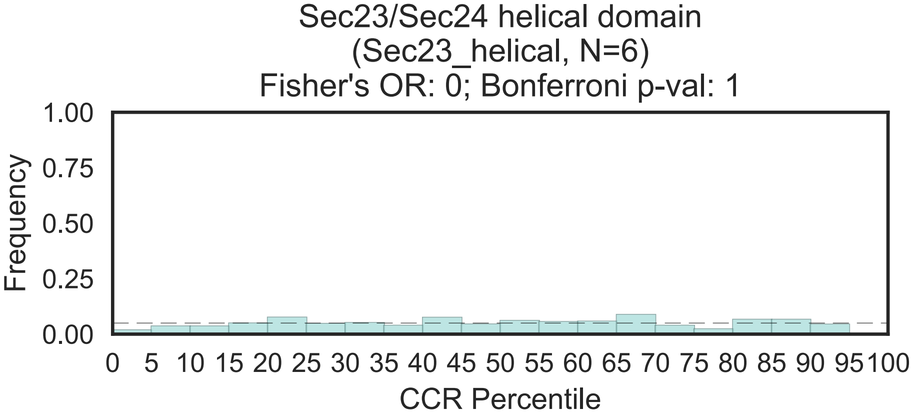

Vesicle coat trafficking protein Sec16 mid-region
(Sec16, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Sec23-binding domain of Sec16
(Sec16_C, N=3)
Fisher's OR: 1.16; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

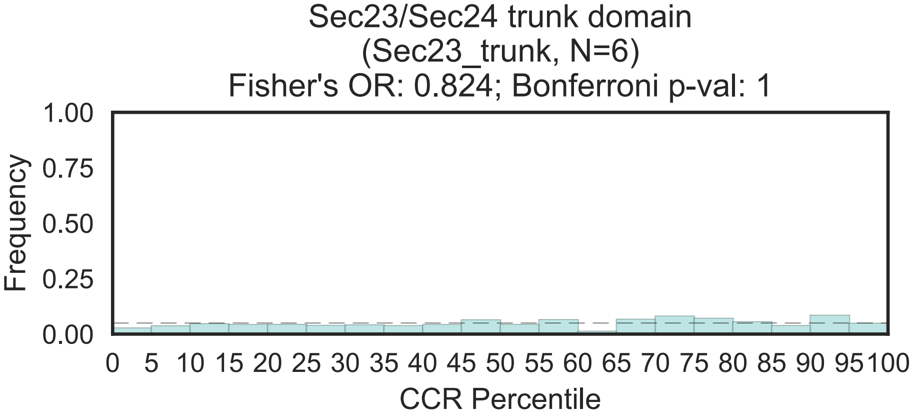

Sec20
(Sec20, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

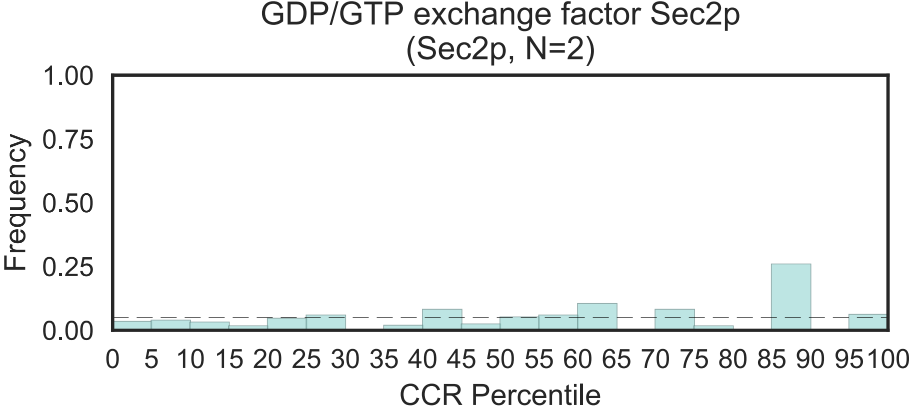


Sec23/Sec24 beta-sandwich domain
(Sec23_BS, N=6)
Fisher's OR: 0.491; Bonferroni p-val: 1

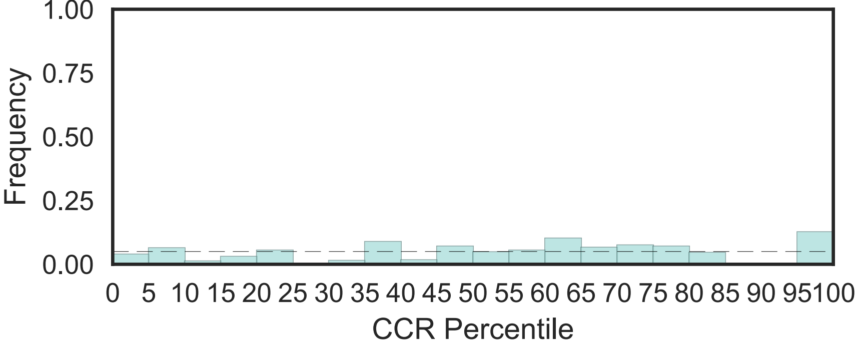


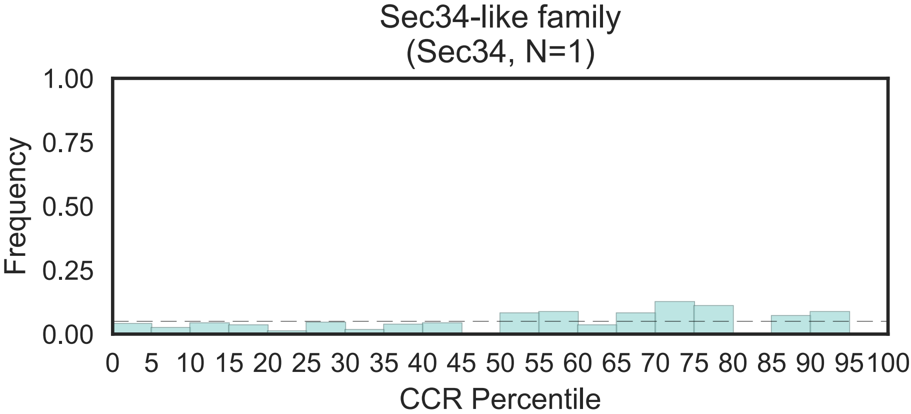
Sec23/Sec24 helical domain
(Sec23_helical, N=6)
Fisher's OR: 0; Bonferroni p-val: 1

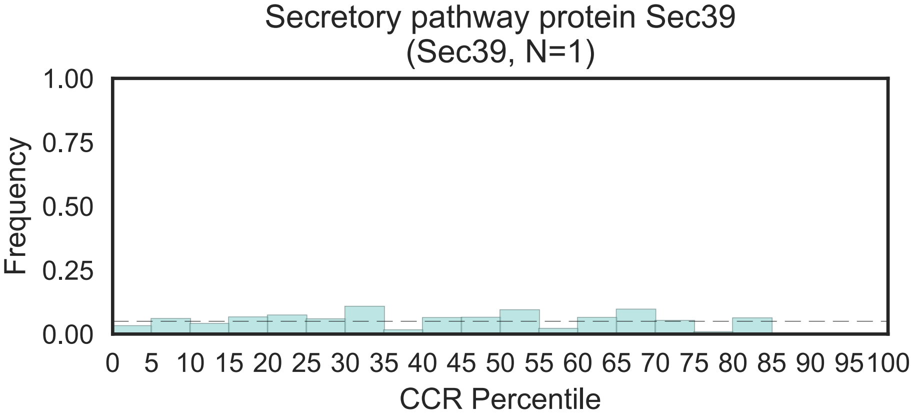

Sec23/Sec24 trunk domain
(Sec23_trunk, N=6)
Fisher's OR: 0.824; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

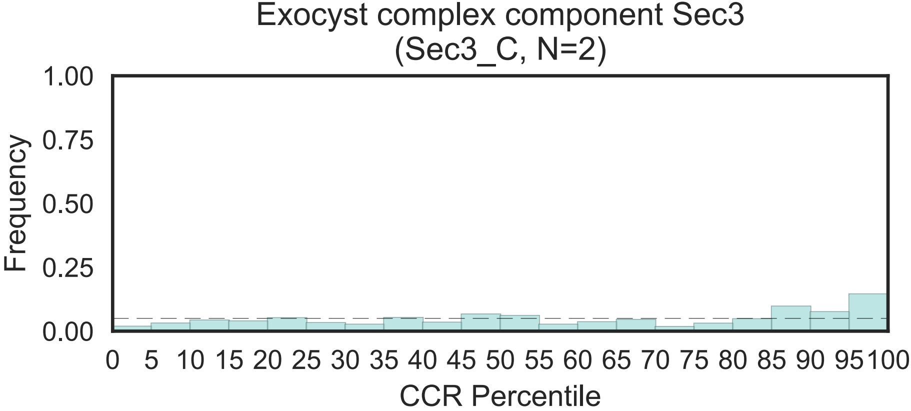

GDP/GTP exchange factor Sec2p
(Sec2p, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

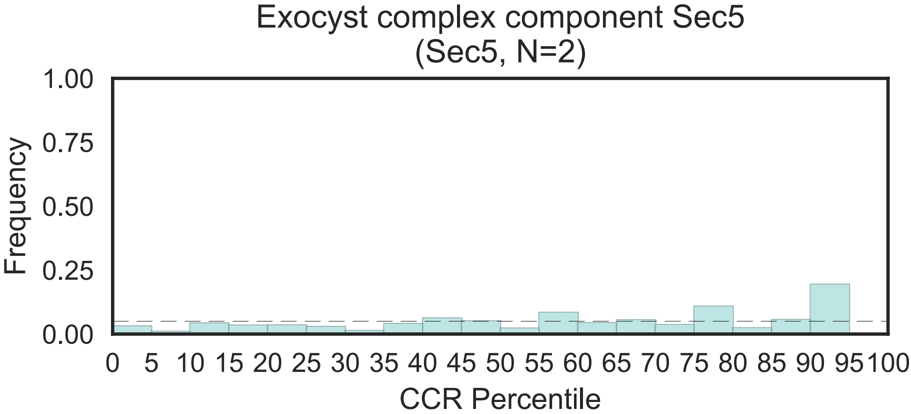
Exocyst complex component SEC3 N-terminal PIP2 binding PH (Sec3-PIP2_bind, N=2)

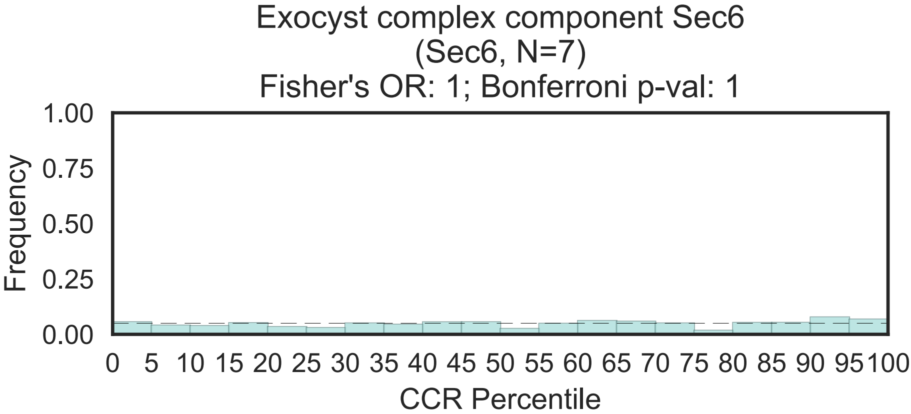


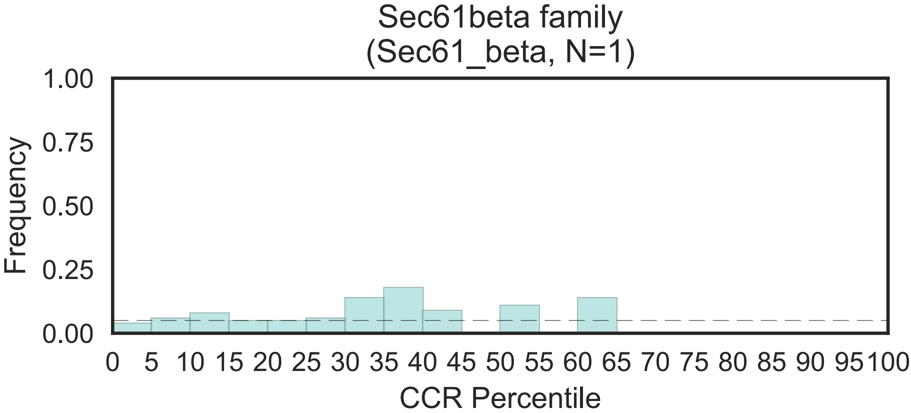

Sec34-like family
(Sec34, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

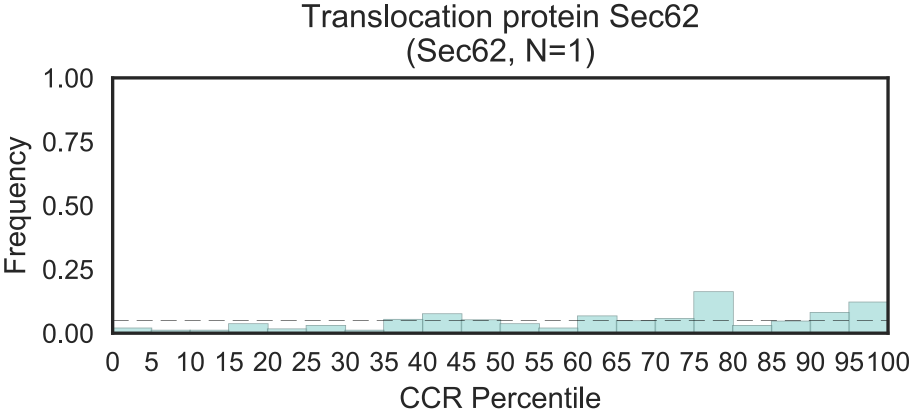

Secretory pathway protein Sec39
(Sec39, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

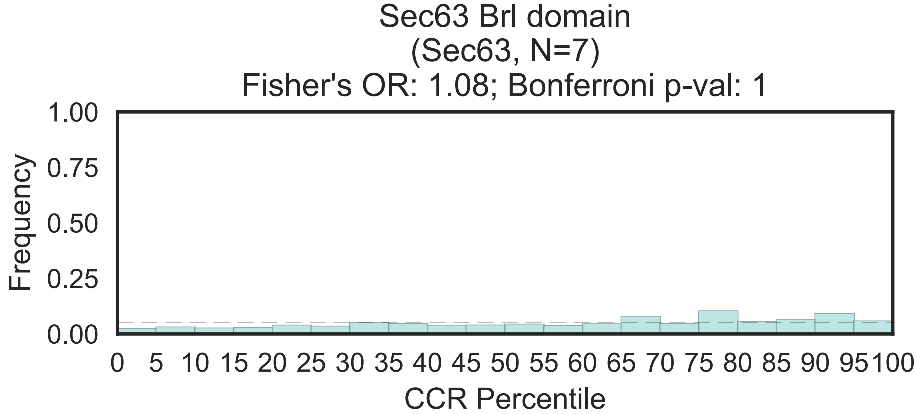

Exocyst complex component Sec3
(Sec3_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Exocyst complex component Sec5
(Sec5, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

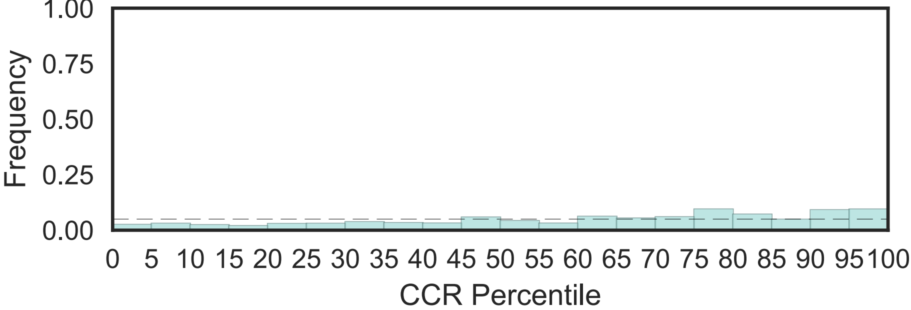

Exocyst complex component Sec6
(Sec6, N=7)
Fisher's OR: 1; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

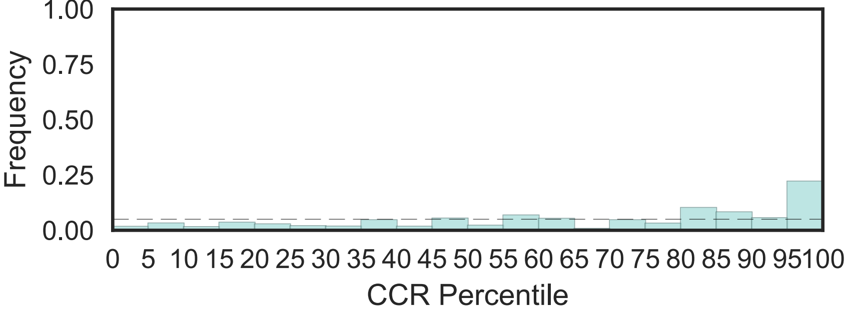

Sec61beta family
(Sec61_beta, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

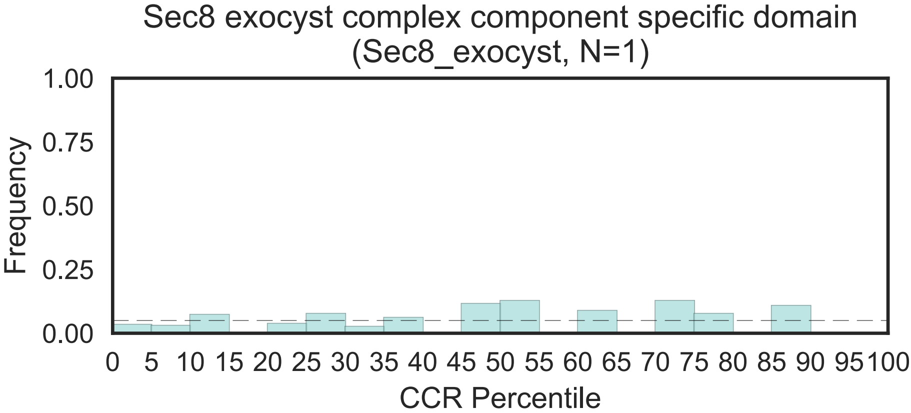

Translocation protein Sec62
(Sec62, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

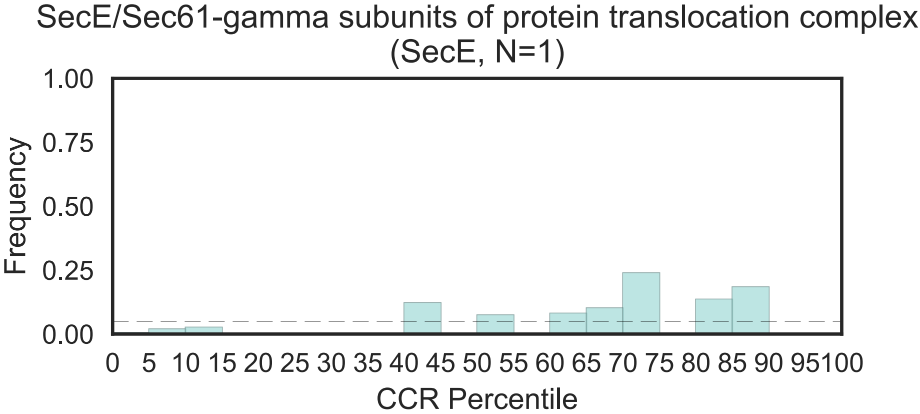

Sec63 Brl domain
(Sec63, N=7)
Fisher's OR: 1.08; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Sec7 domain
(Sec7, N=15)
Fisher's OR: 2.4; Bonferroni p-val: 1

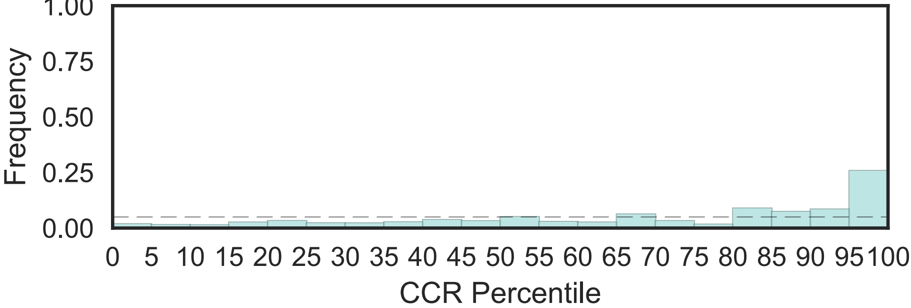


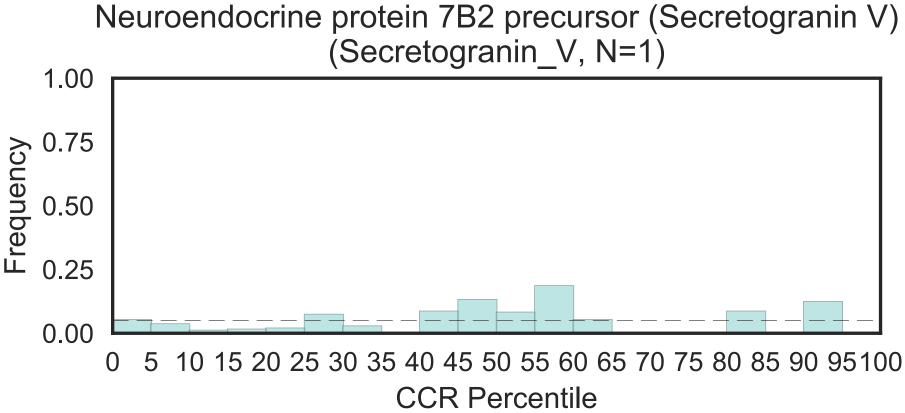

Guanine nucleotide exchange factor in Golgi transport N-terminal (Sec7_N, N=4)
Fisher's OR: 5; Bonferroni p-val: 1

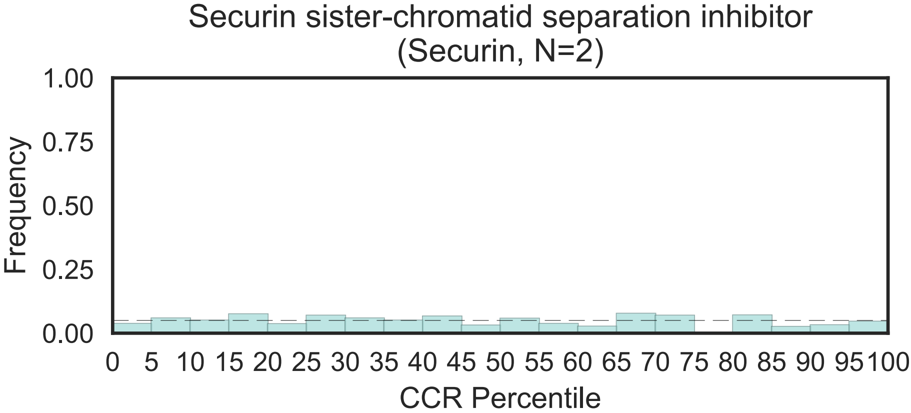

Sec8 exocyst complex component specific domain
(Sec8_exocyst, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

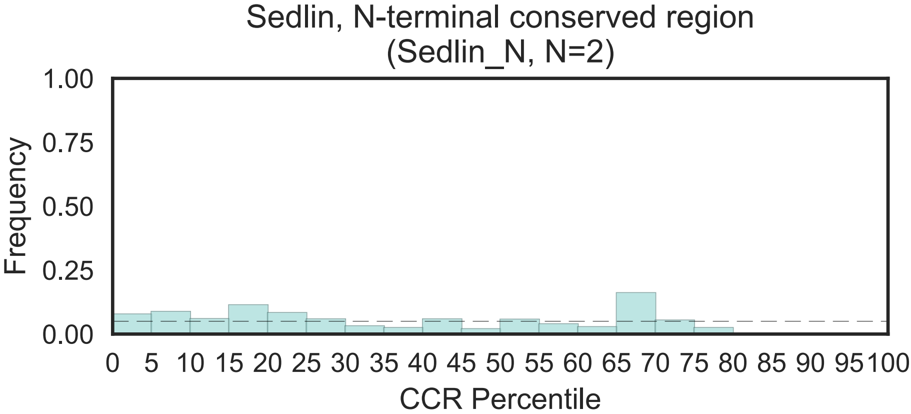

SecE/Sec61-gamma subunits of protein translocation complex
(SecE, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

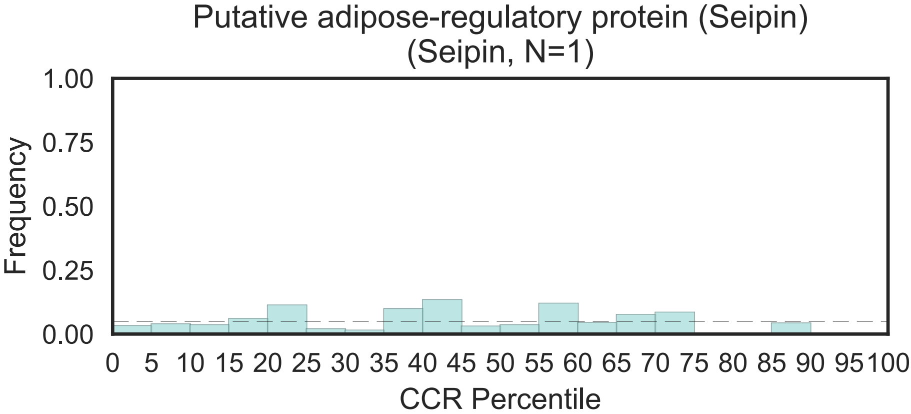
SecY translocase
(SecY, N=4)
Fisher's OR: 5.53; Bonferroni p-val: 0.0588

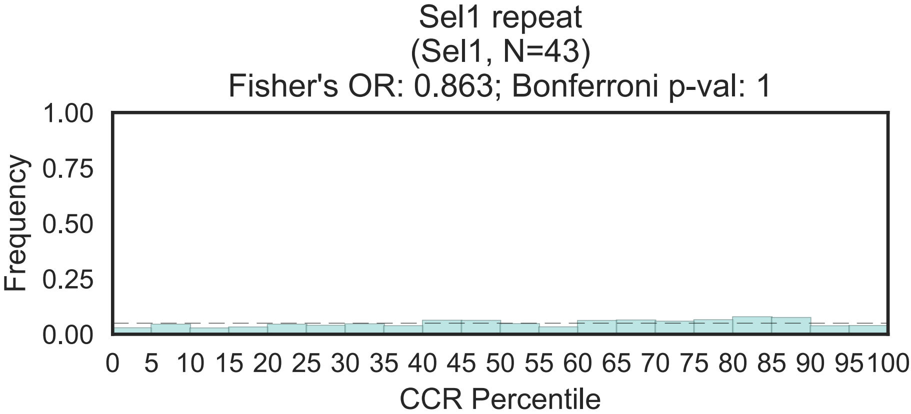


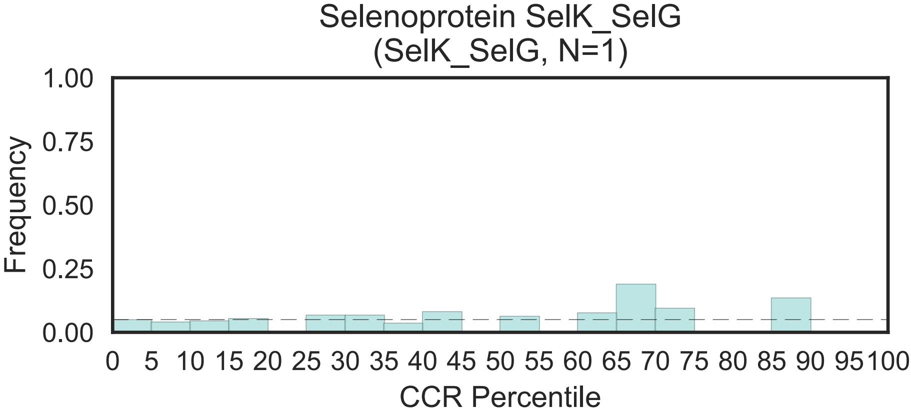

Neuroendocrine protein 7B2 precursor (Secretogranin V)
(Secretogranin_V, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

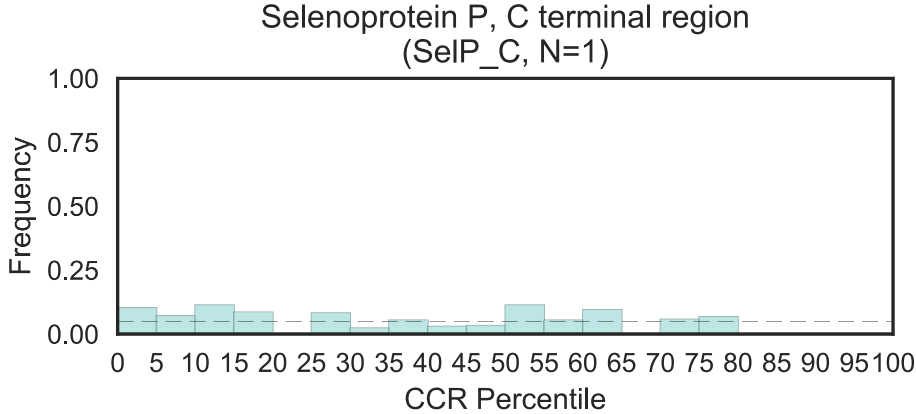

Securin sister-chromatid separation inhibitor
(Securin, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

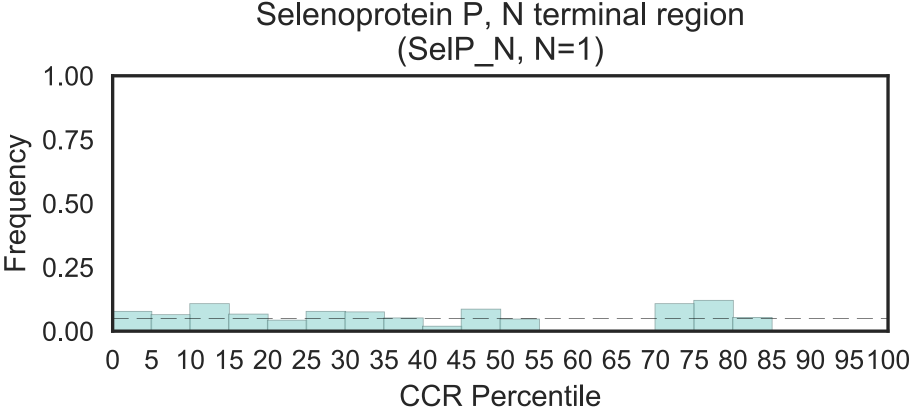

Sedlin, N-terminal conserved region
(Sedlin_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

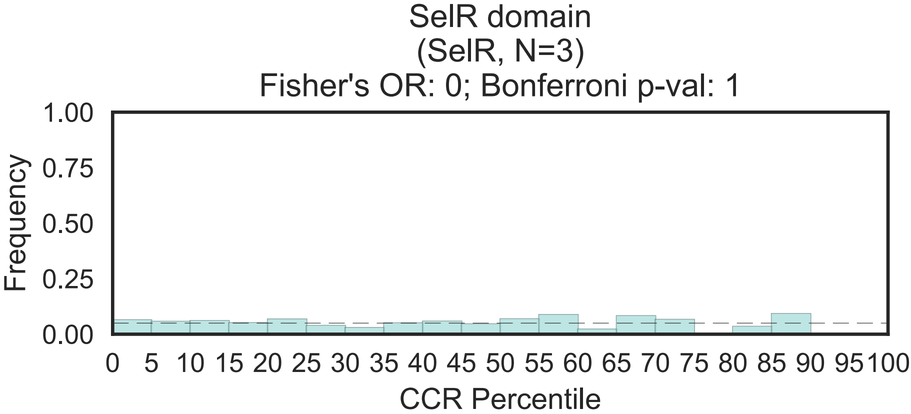

Putative adipose-regulatory protein (Seipin)
(Seipin, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

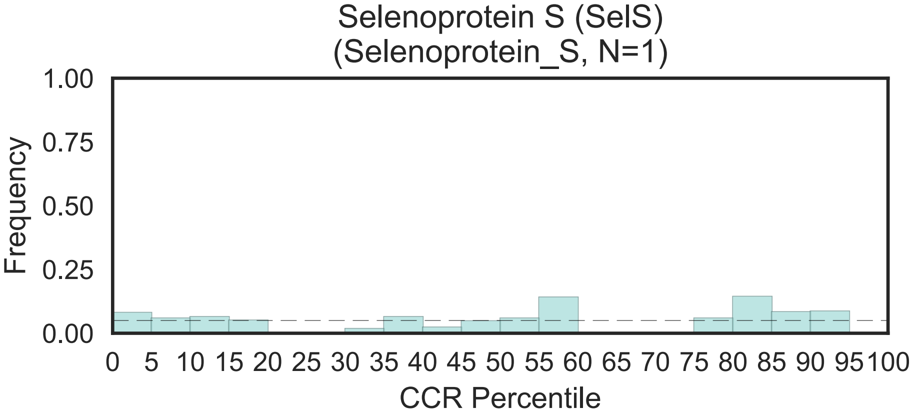

Sel1 repeat
(Sel1, N=43)
Fisher's OR: 0.863; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

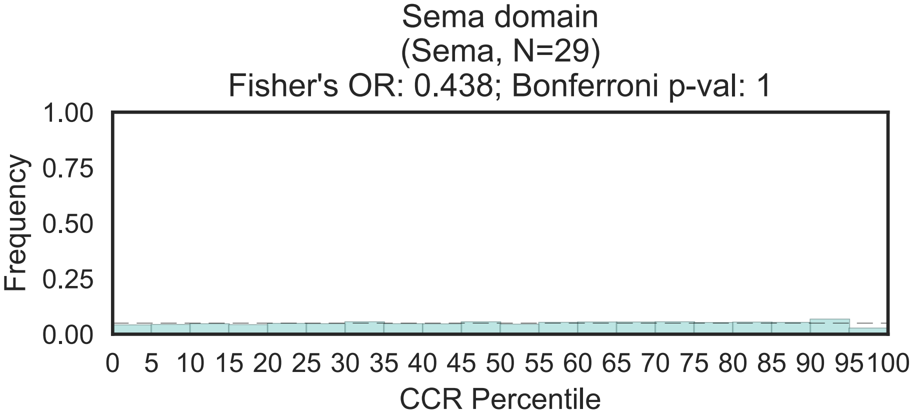

Selenoprotein SelK_SelG
(SelK_SelG, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

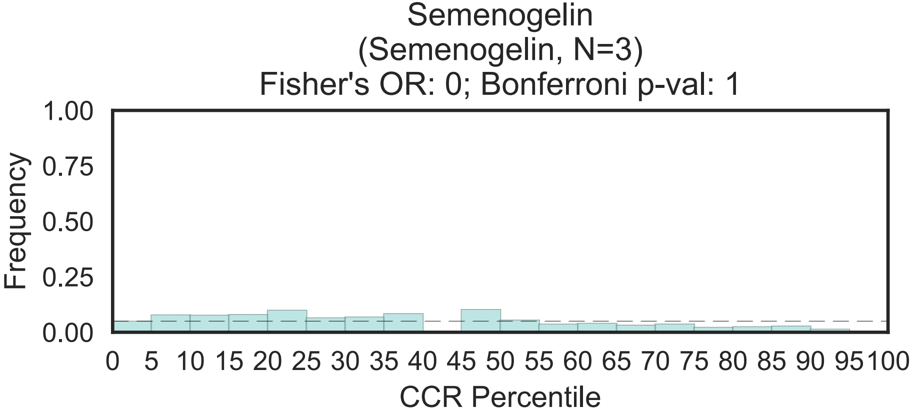

Selenoprotein P, C terminal region
(SelP_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

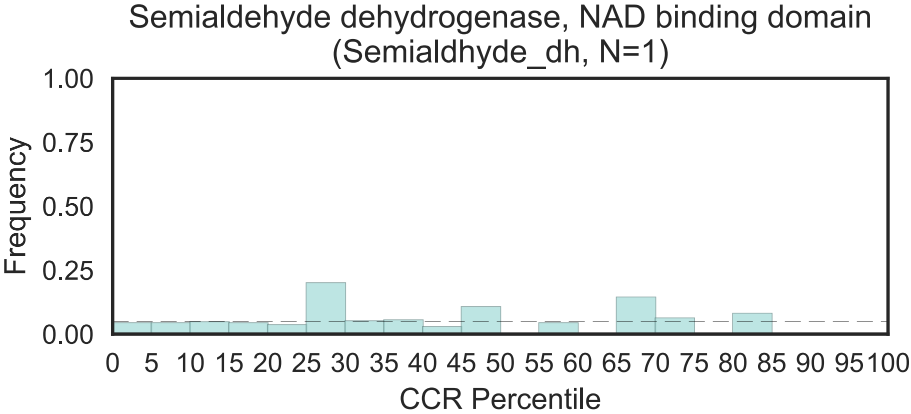

Selenoprotein P, N terminal region
(SelP_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

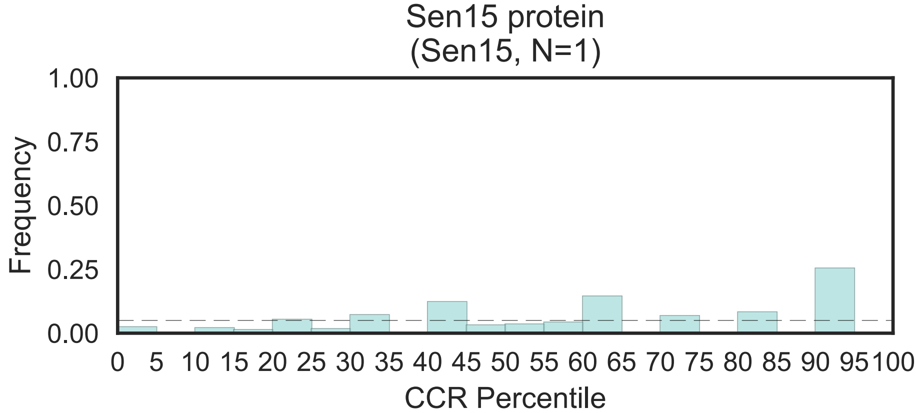

SelR domain
(SelR, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

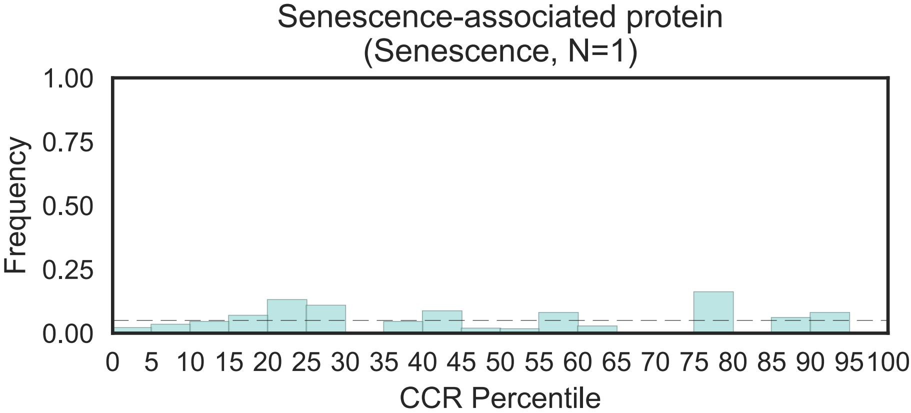

Selenoprotein S (SelS)
(Selenoprotein_S, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

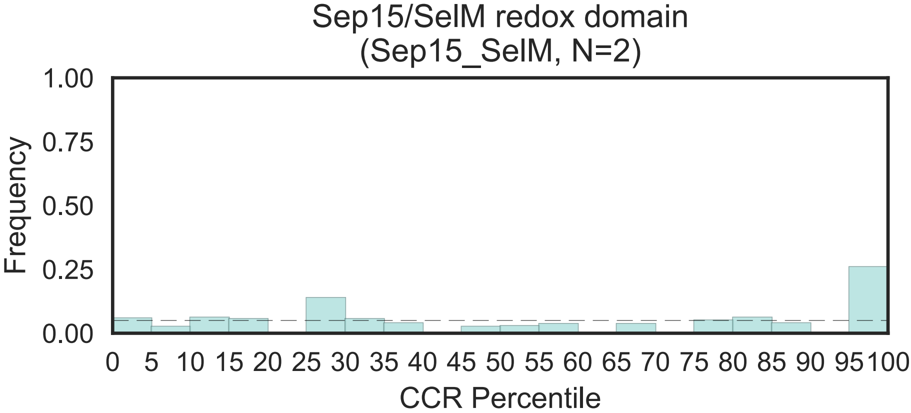

Sema domain
(Sema, N=29)
Fisher's OR: 0.438; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

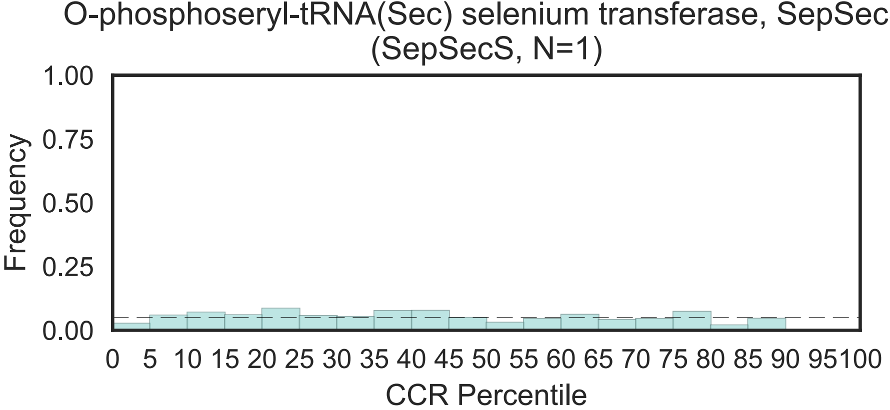

Semenogelin
(Semenogelin, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

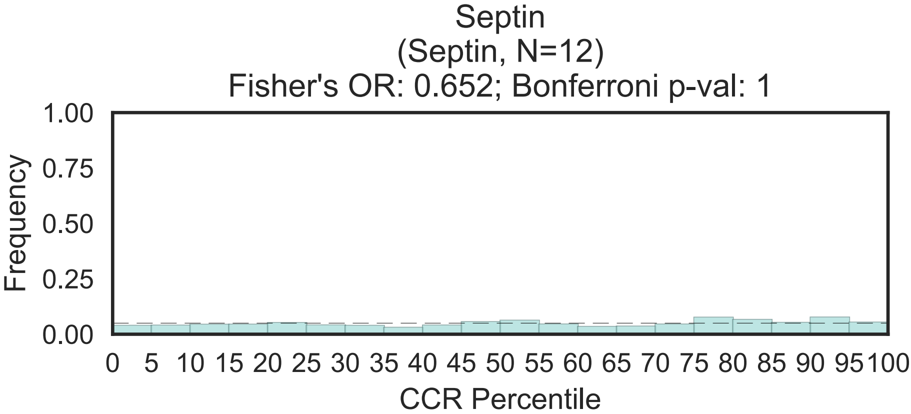

Semialdehyde dehydrogenase, NAD binding domain
(Semialdhyde_dh, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

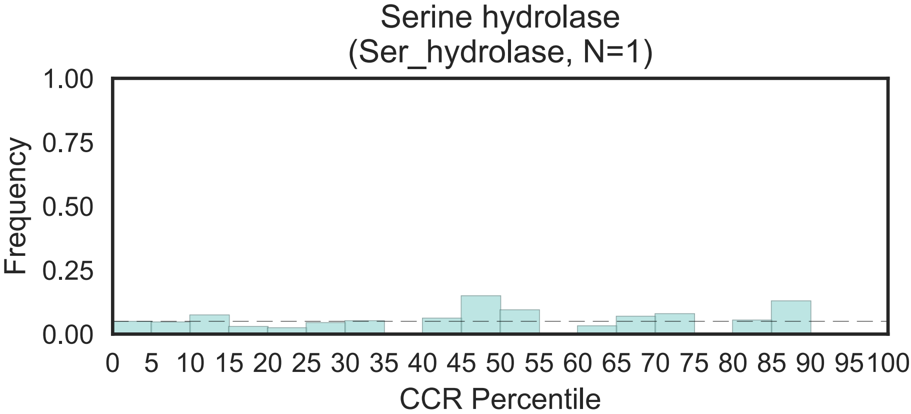

Sen15 protein
(Sen15, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

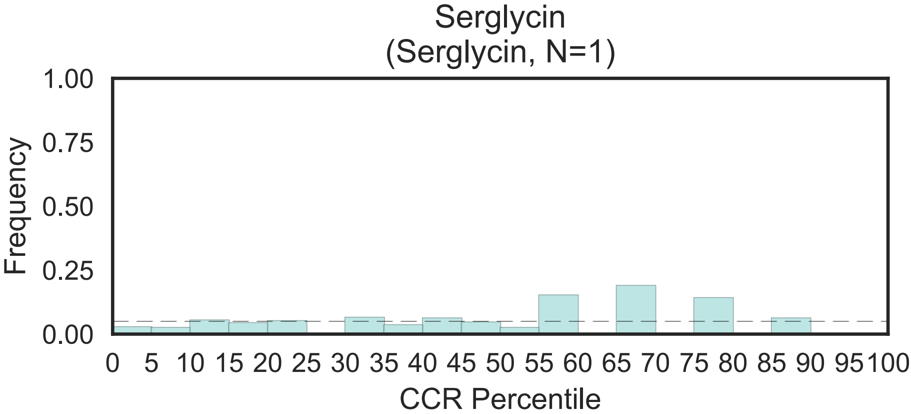

Senescence-associated protein
(Senescence, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

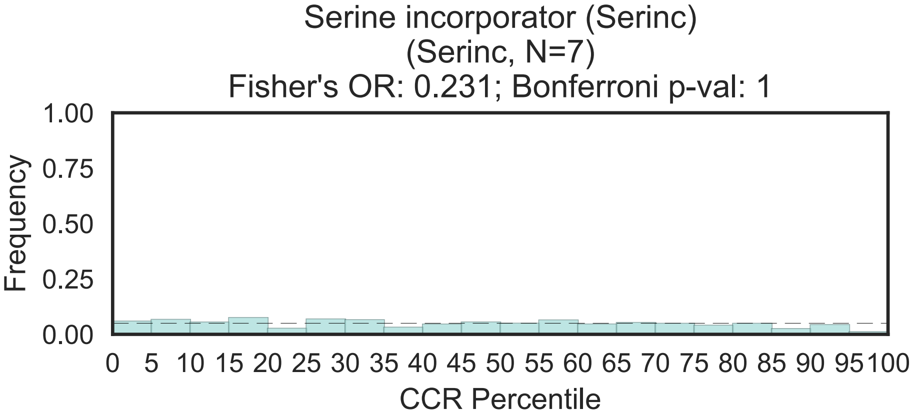

Sep15/SelM redox domain
(Sep15_SelM, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

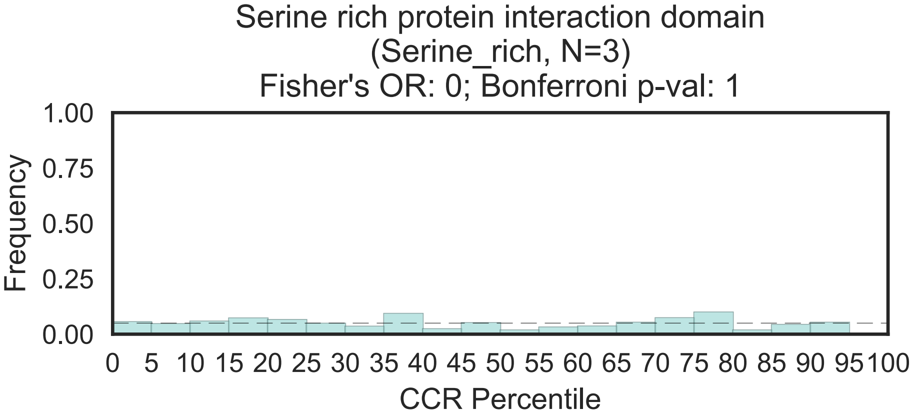

O-phosphoseryl-tRNA(Sec) selenium transferase, SepSecS
(SepSecS, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

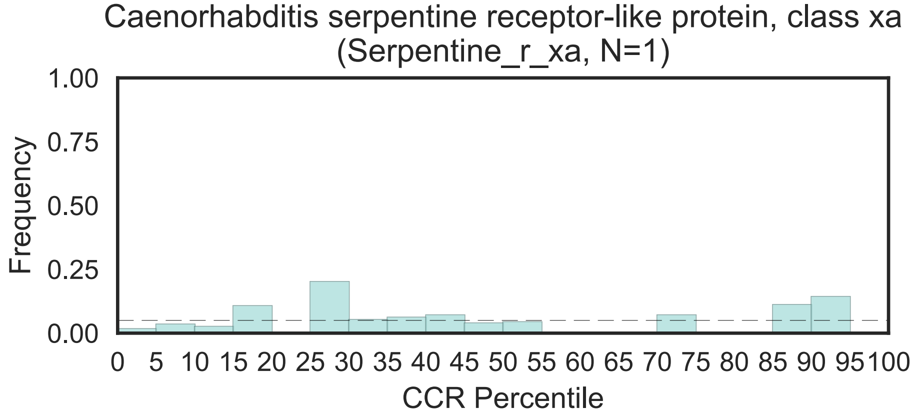

Septin
(Septin, N=12)
Fisher's OR: 0.652; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

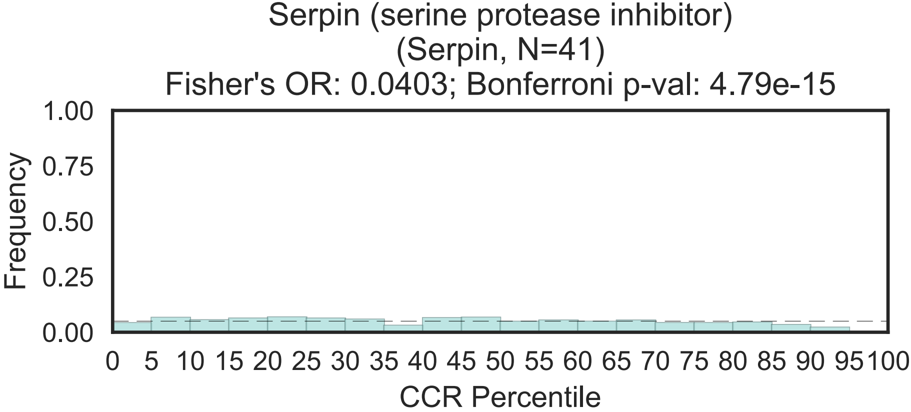

Serine hydrolase
(Ser_hydrolase, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Serglycin
(Serglycin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

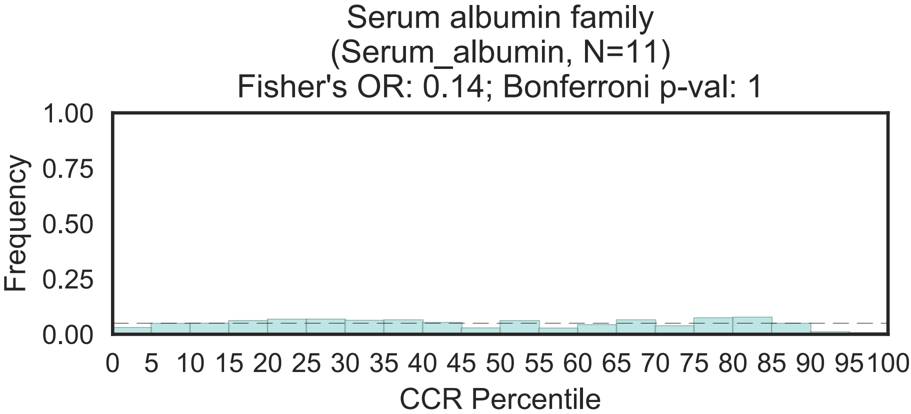

Serine incorporator (Serinc)
(Serinc, N=7)
Fisher's OR: 0.231; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Serine rich protein interaction domain
(Serine_rich, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

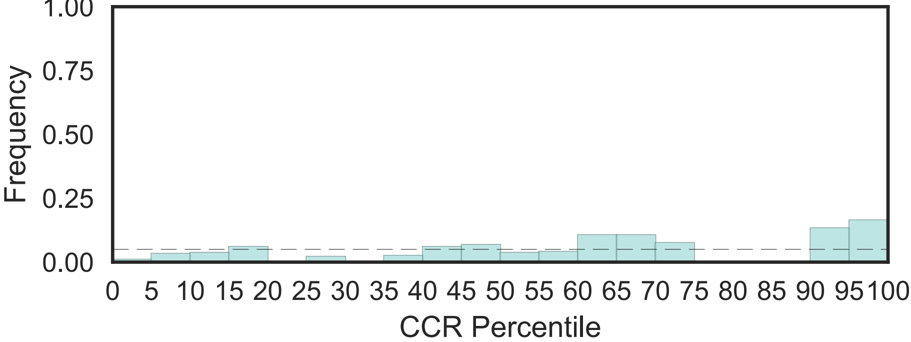

Caenorhabditis serpentine receptor-like protein, class xa
(Serpentine_r_xa, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

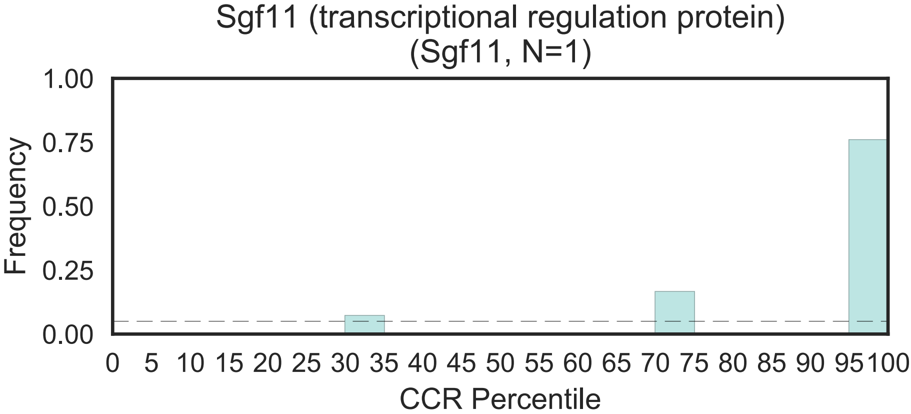


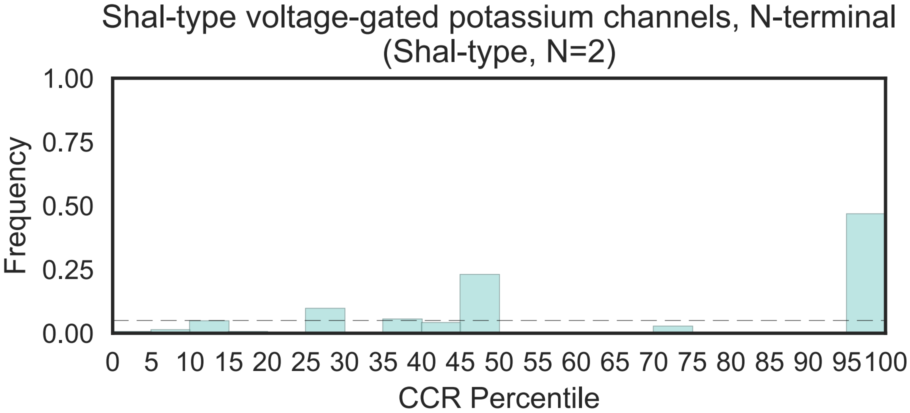
Serpin (serine protease inhibitor)
(Serpin, N=41)
Fisher's OR: 0.0403; Bonferroni p-val: 4.79e-15

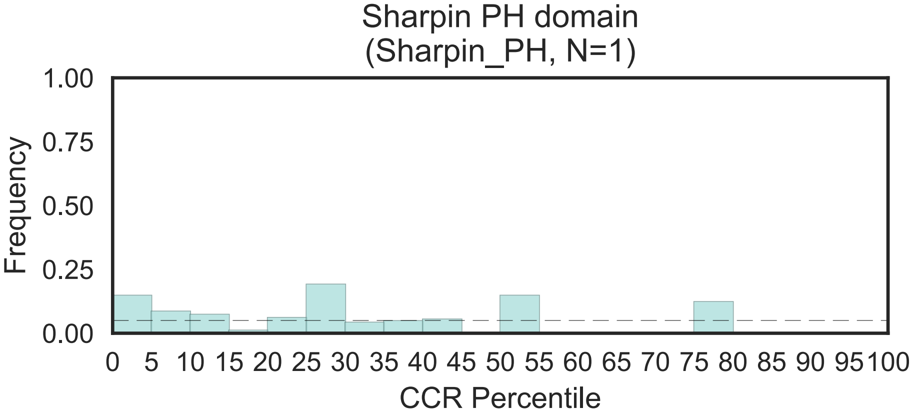

Serum albumin family
(Serum_albumin, N=11)
Fisher's OR: 0.14; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

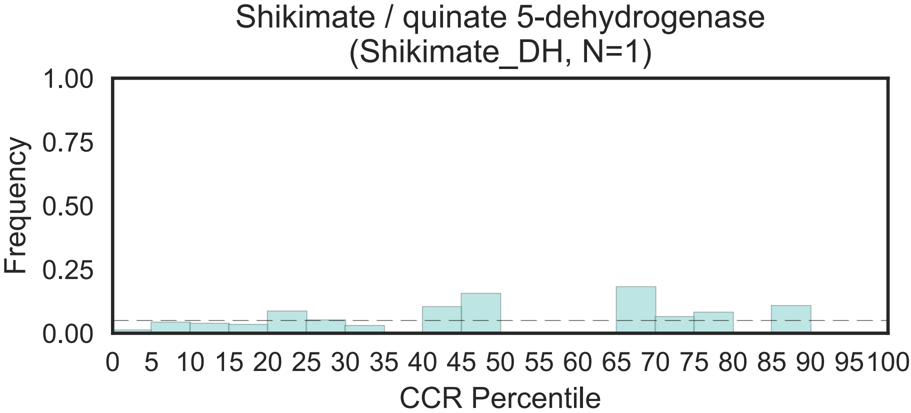
Seryl-tRNA synthetase N-terminal domain (Seryl_tRNA_N, N=1)

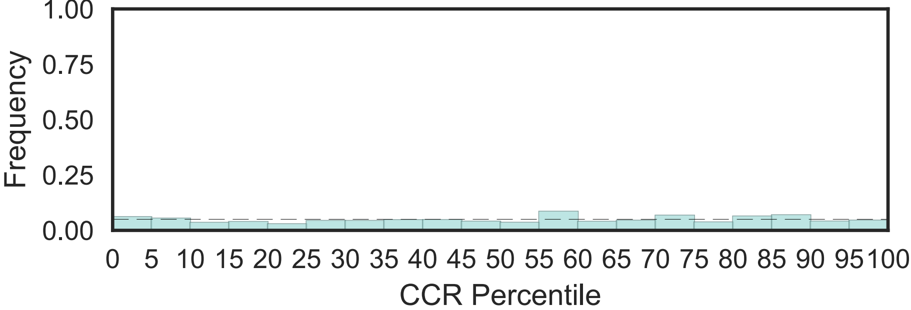



Sgf11 (transcriptional regulation protein)
(Sgf11, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

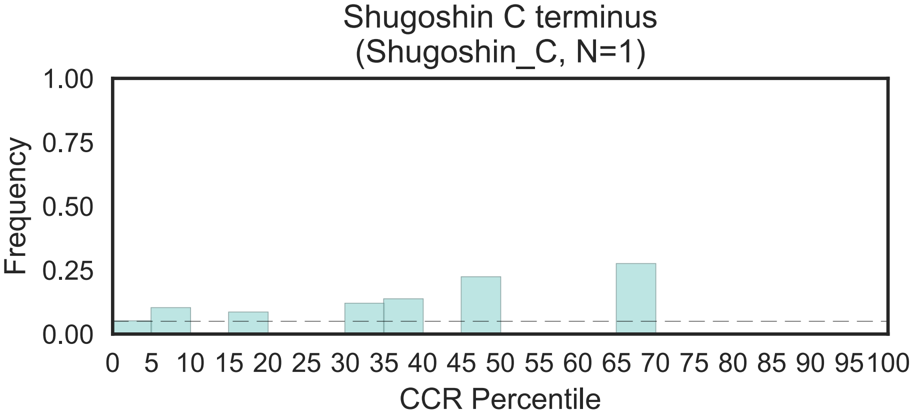

Shal-type voltage-gated potassium channels, N-terminal
(Shal-type, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

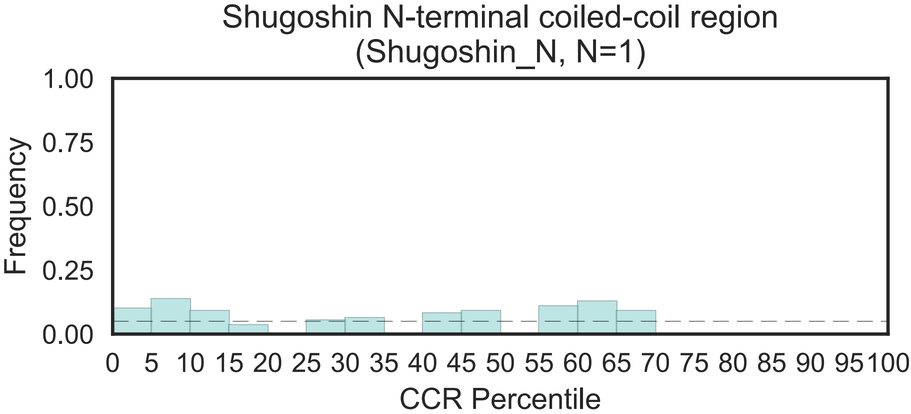

Sharpin PH domain
(Sharpin_PH, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


Shikimate / quinate 5-dehydrogenase
(Shikimate_DH, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

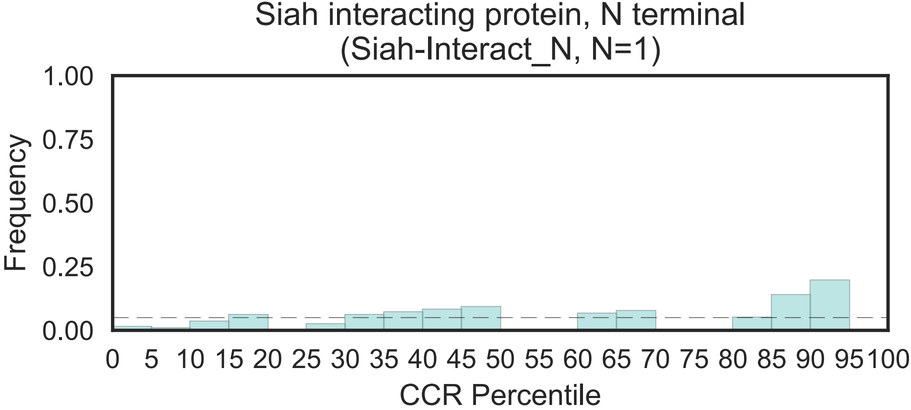


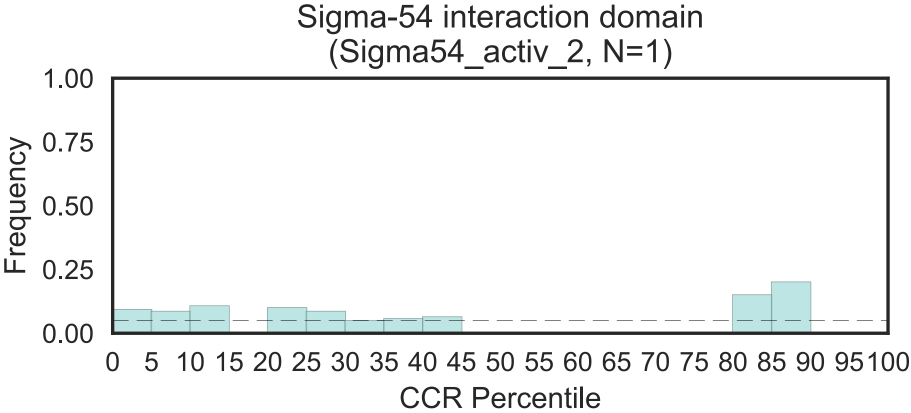
Wnt and FGF inhibitory regulator
(Shisa, N=9)
Fisher's OR: 0.707; Bonferroni p-val: 1

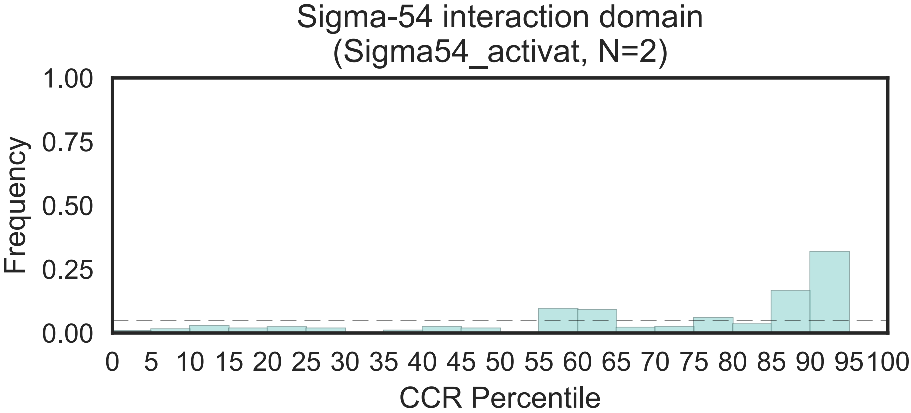

Shugoshin C terminus
(Shugoshin_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



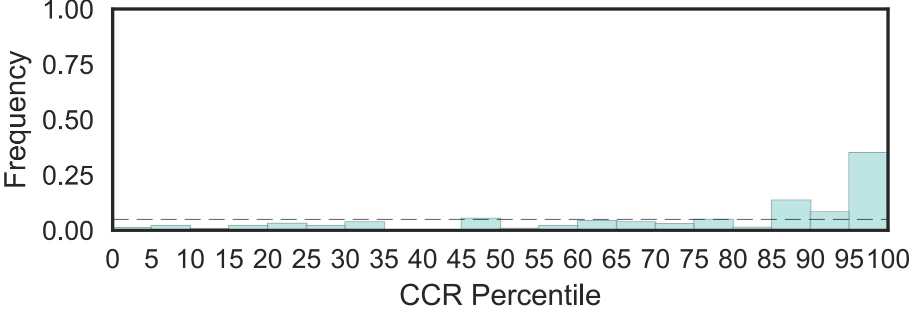
Shugoshin N-terminal coiled-coil region
(Shugoshin_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

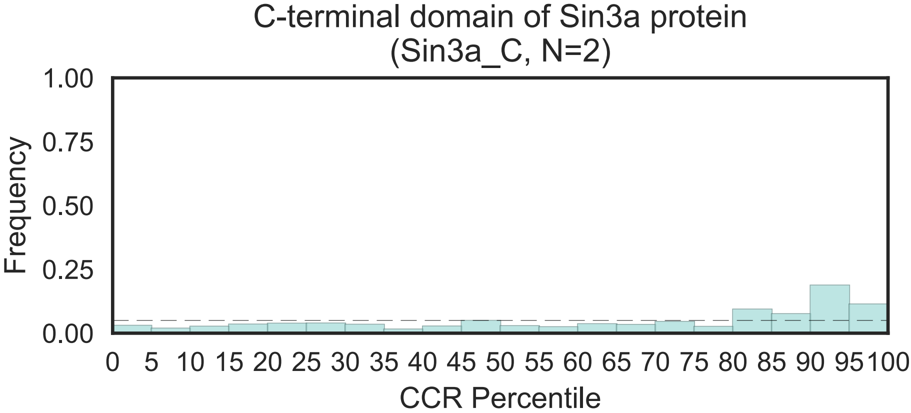

Siah interacting protein, N terminal
(Siah-Interact_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

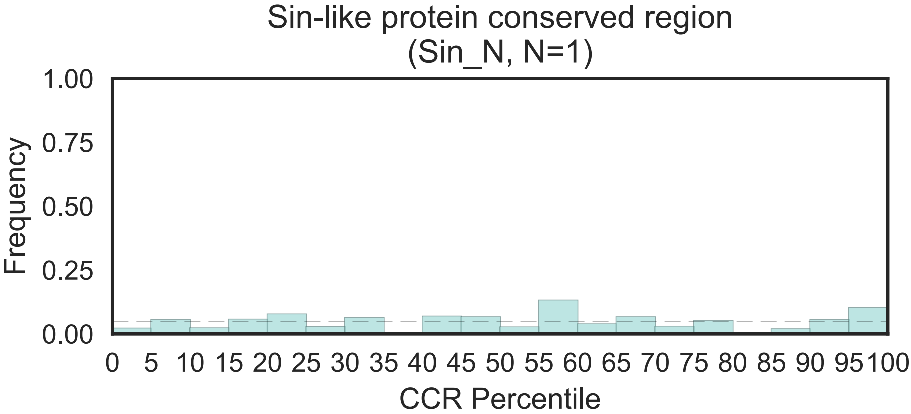

Sigma-54 interaction domain
(Sigma54_activ_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

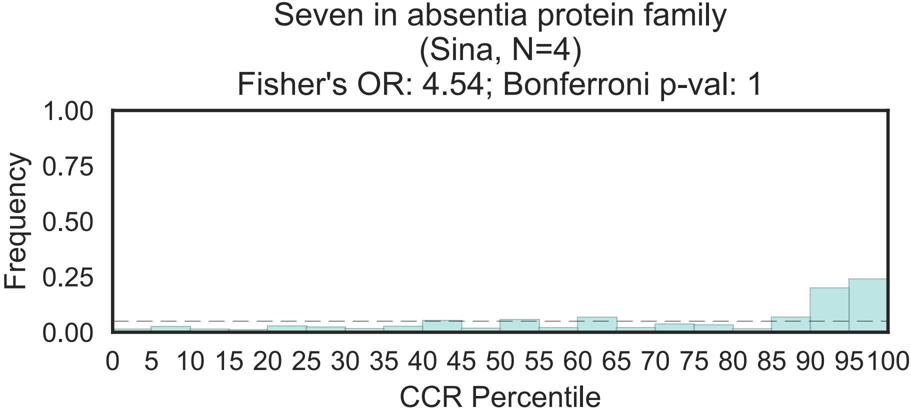

Sigma-54 interaction domain
(Sigma54_activat, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Sin3 family co-repressor (Sin3_corepress, N=3) Fisher's OR: 10; Bonferroni p-val: 1

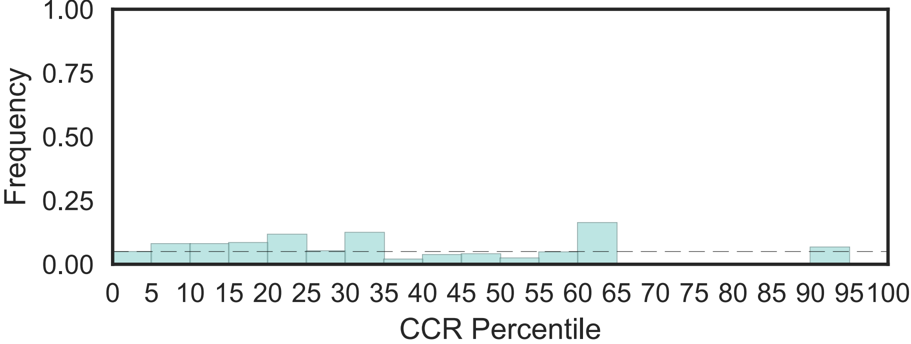


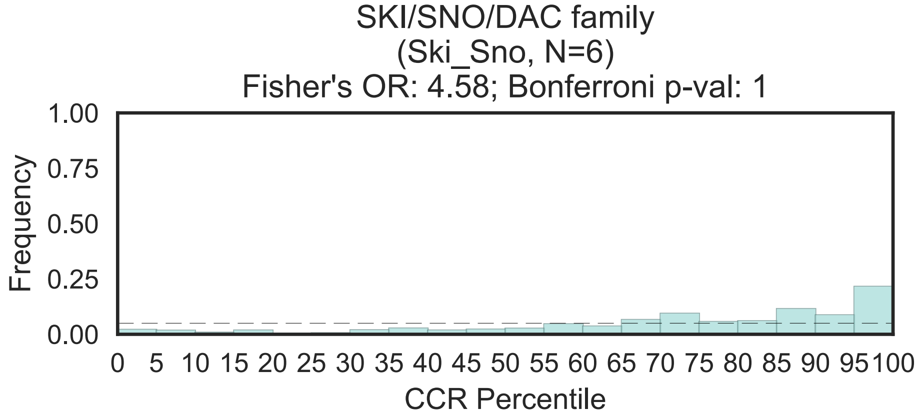

C-terminal domain of Sin3a protein
(Sin3a_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

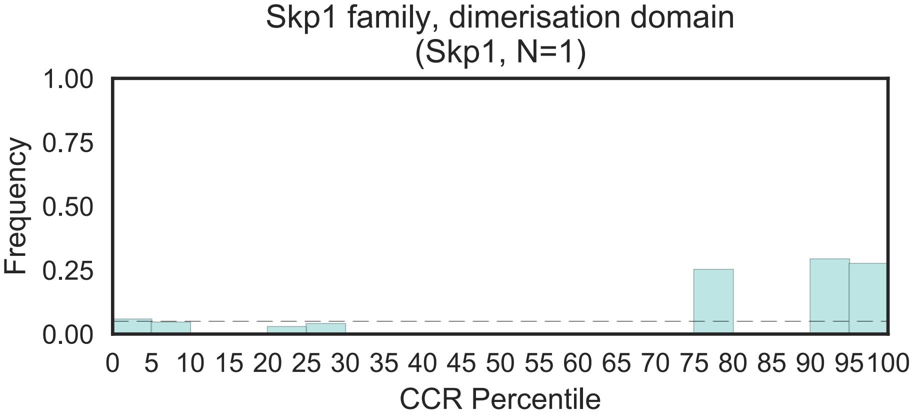

Sin-like protein conserved region
(Sin_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

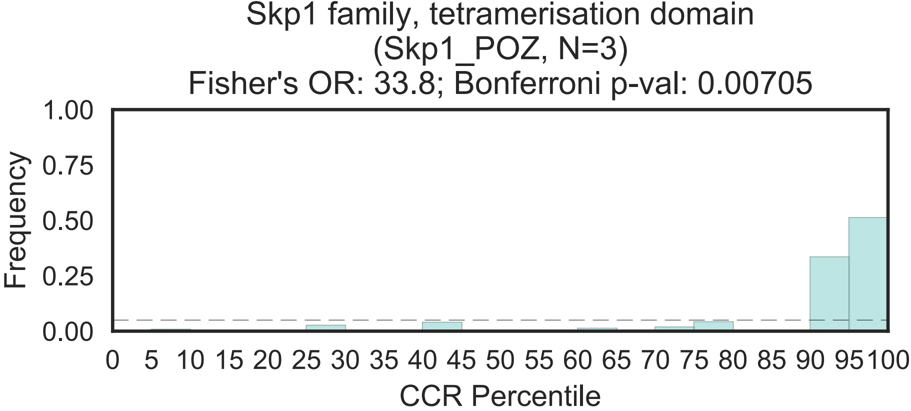

Seven in absentia protein family
(Sina, N=4)
Fisher's OR: 4.54; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

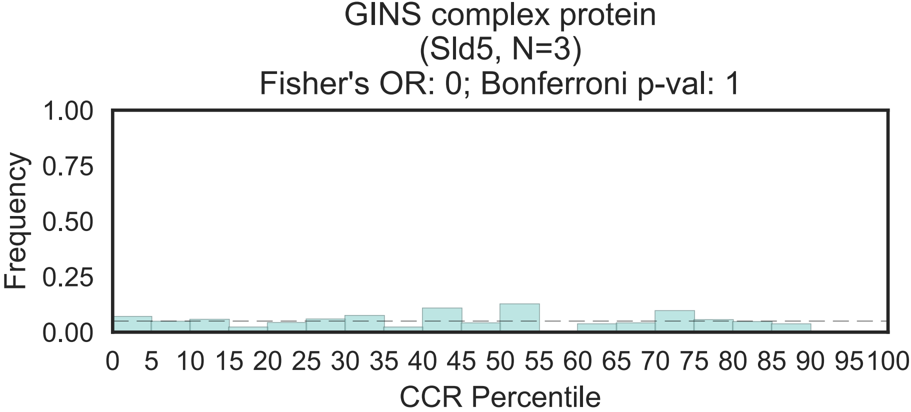
Cd27 binding protein (Siva)
(Siva, N=2)

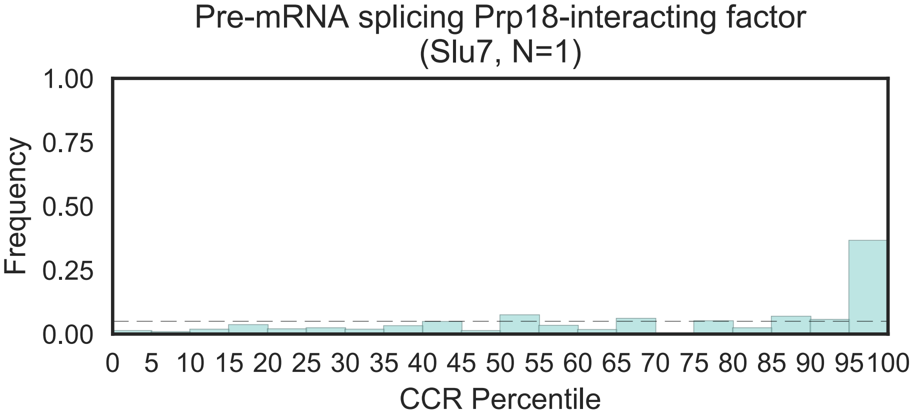


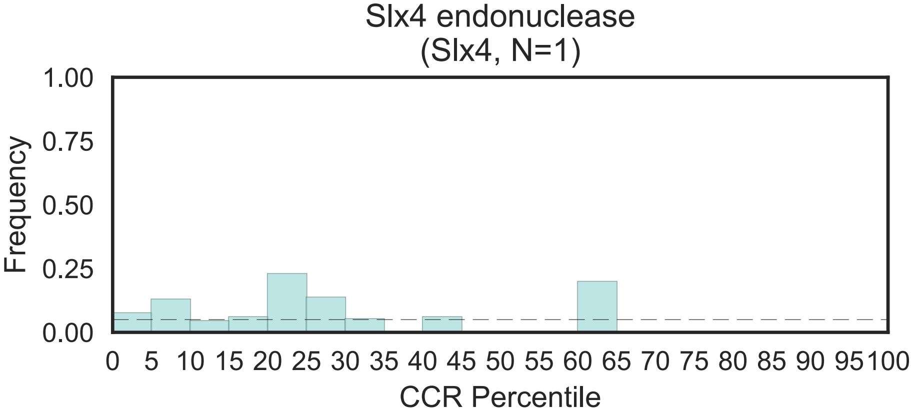

SKI/SNO/DAC family
(Ski_Sno, N=6)
Fisher's OR: 4.58; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

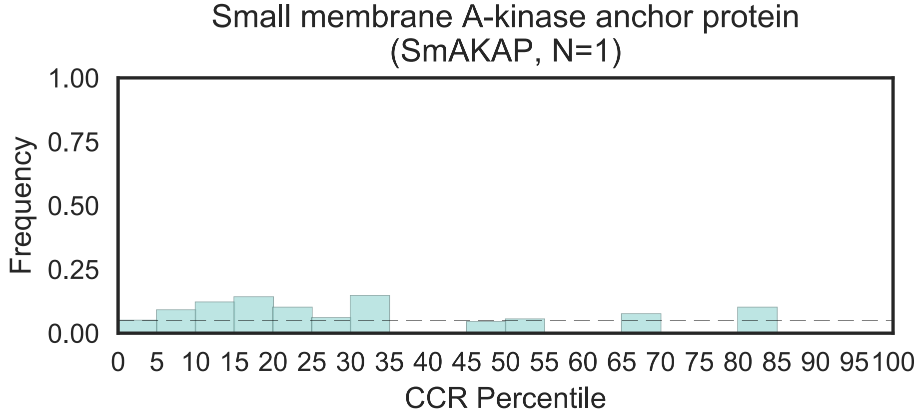

Skp1 family, dimerisation domain
(Skp1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

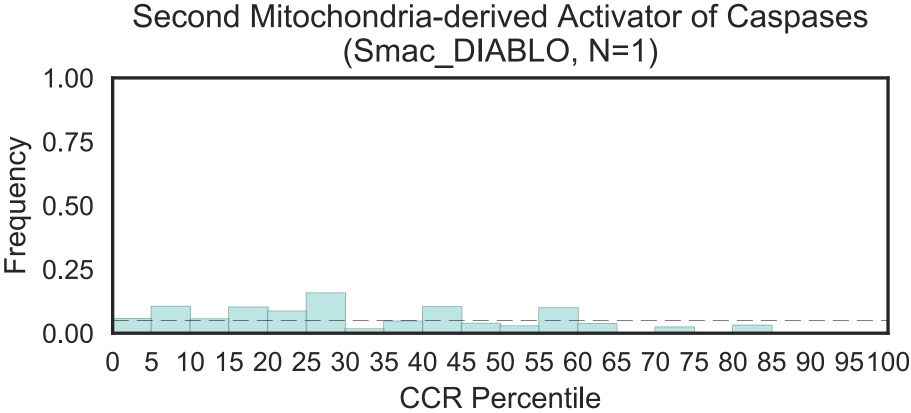

Skp1 family, tetramerisation domain
(Skp1_POZ, N=3)
Fisher's OR: 33.8; Bonferroni p-val: 0.00705
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

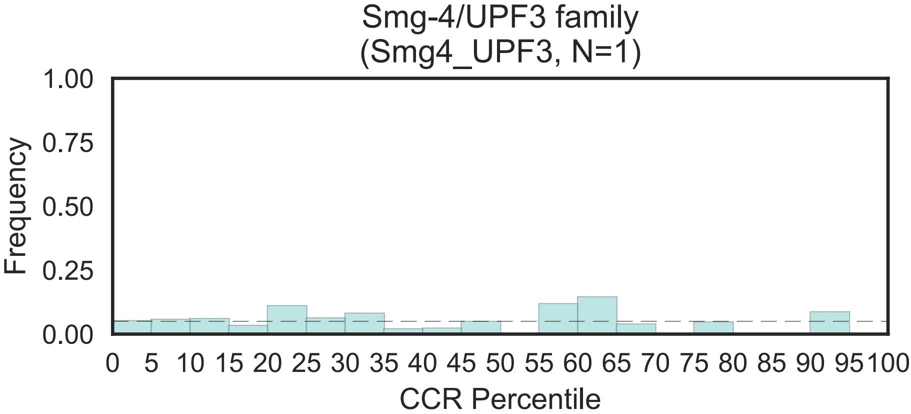

GINS complex protein
(Sld5, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

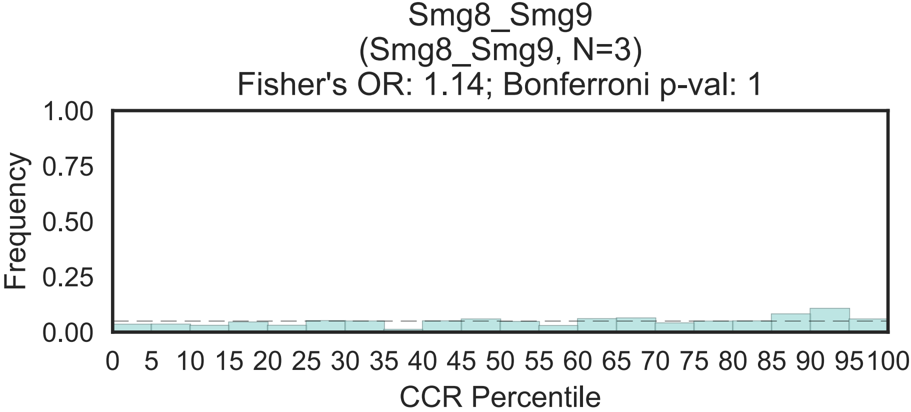

Pre-mRNA splicing Prp18-interacting factor
(Slu7, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

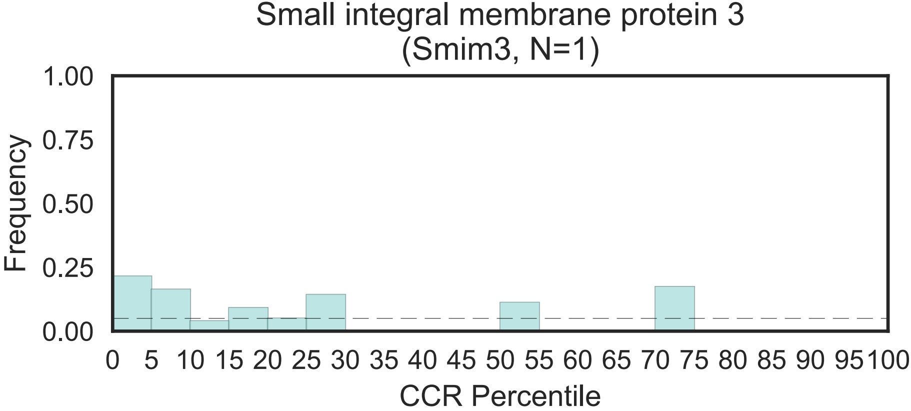

Slx4 endonuclease
(Slx4, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

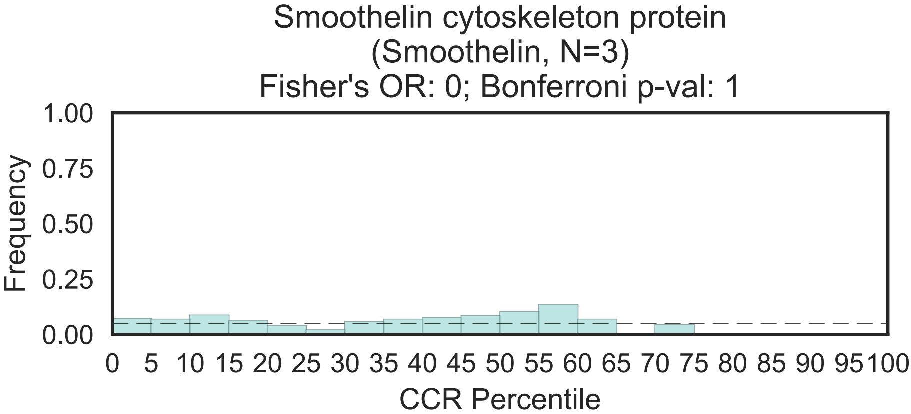

Small membrane A-kinase anchor protein
(SmAKAP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

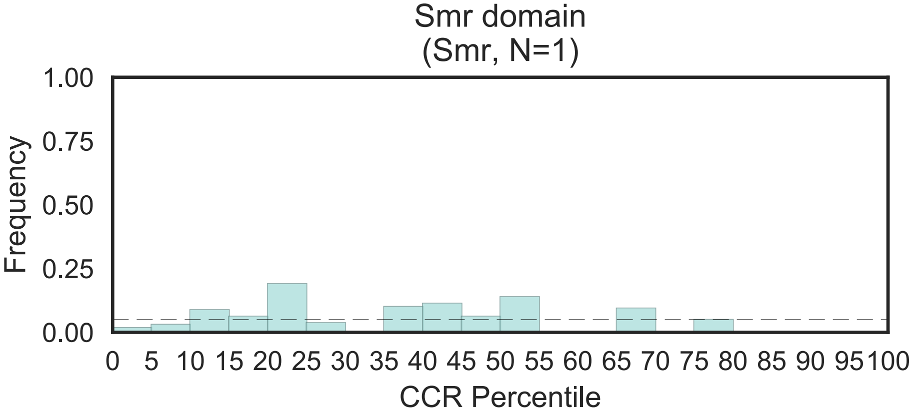

Second Mitochondria-derived Activator of Caspases
(Smac_DIABLO, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

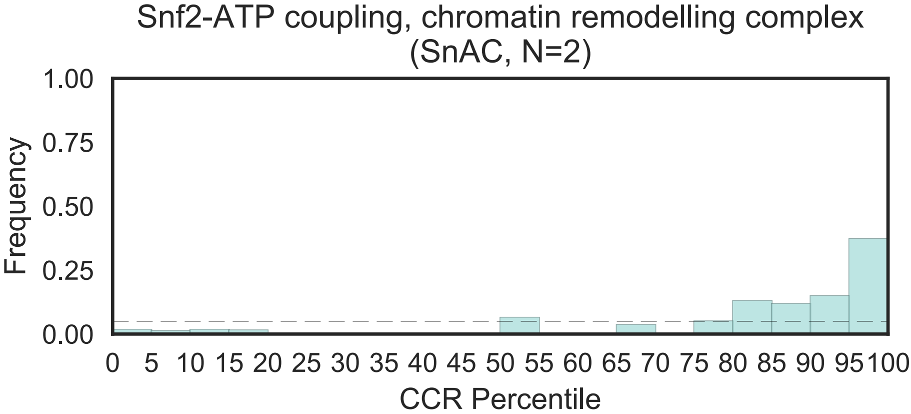

Smg-4/UPF3 family
(Smg4_UPF3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Smg8_Smg9
(Smg8_Smg9, N=3)
Fisher's OR: 1.14; Bonferroni p-val: 1

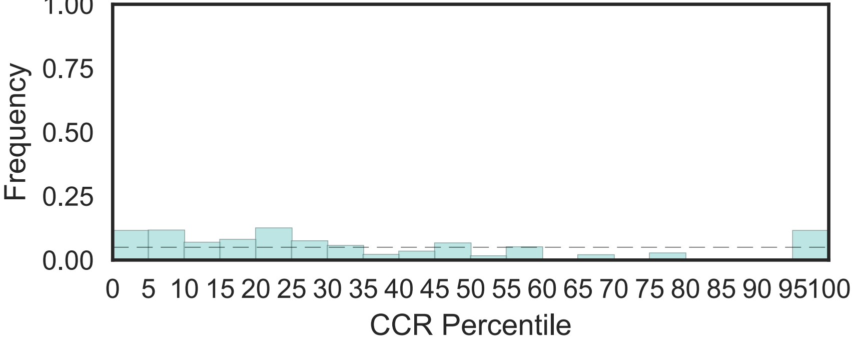

Small integral membrane protein 3
(Smim3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

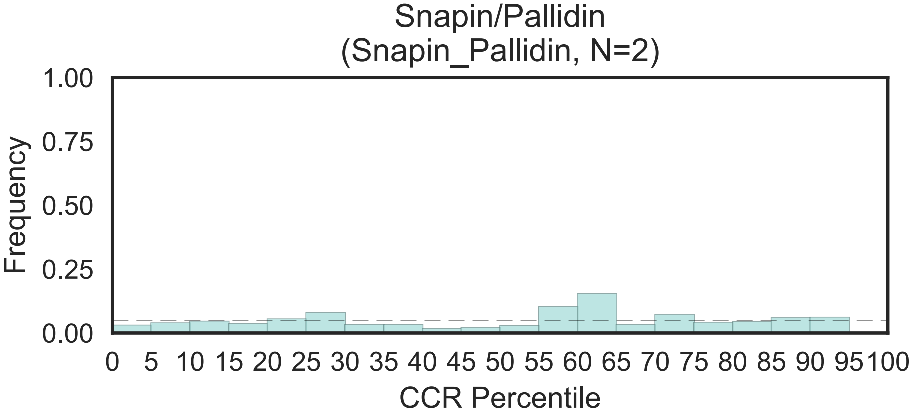

Smoothelin cytoskeleton protein
(Smoothelin, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

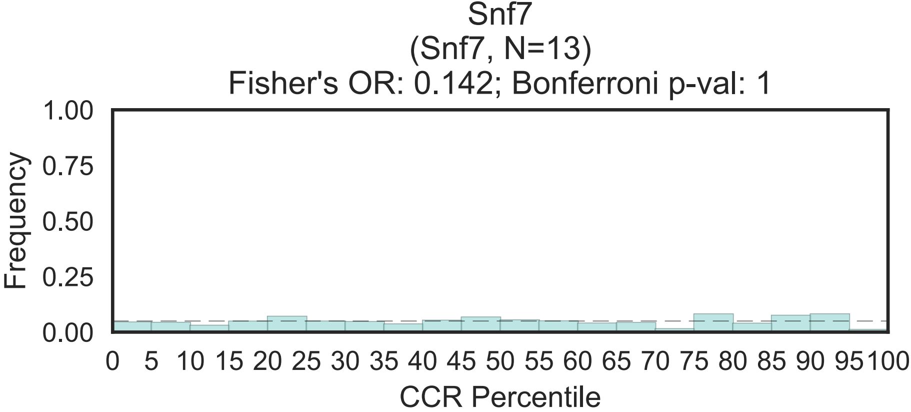

Smr domain
(Smr, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

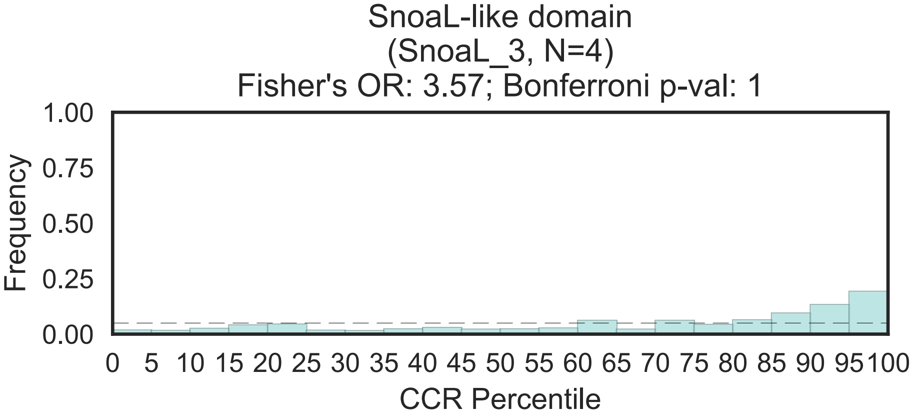

Snf2-ATP coupling, chromatin remodelling complex
(SnAC, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

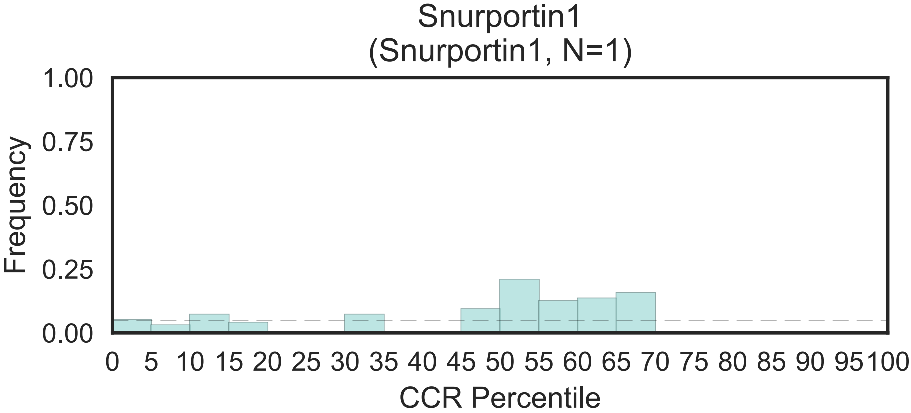
Small nuclear RNA activating complex subunit 2, SNAP190 Myb (SnAPC_2_like, N=1)

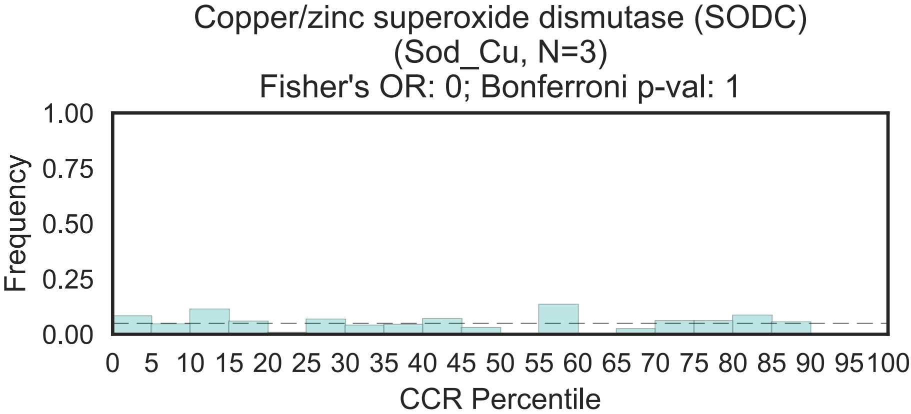


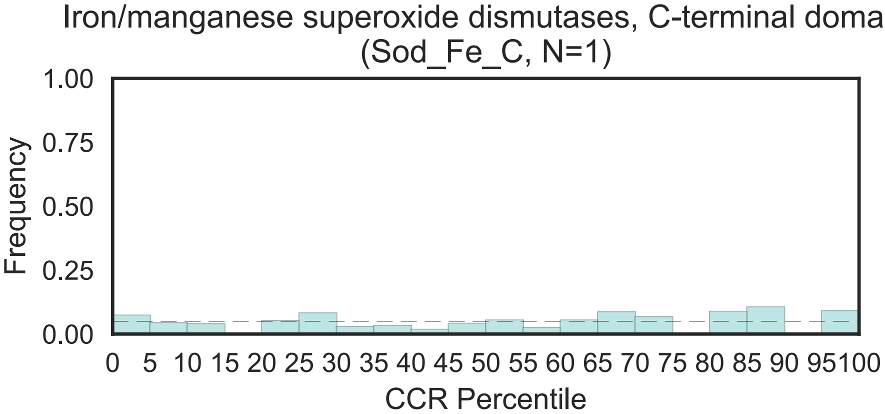

Snapin/Pallidin
(Snapin_Pallidin, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

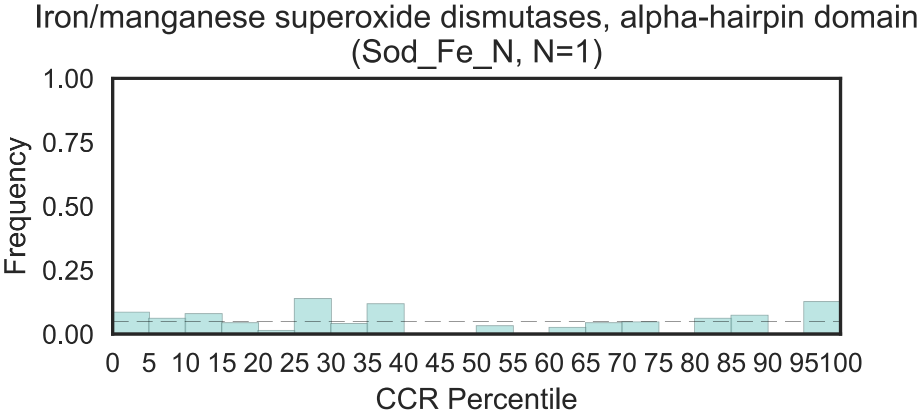

Snf7
(Snf7, N=13)
Fisher's OR: 0.142; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

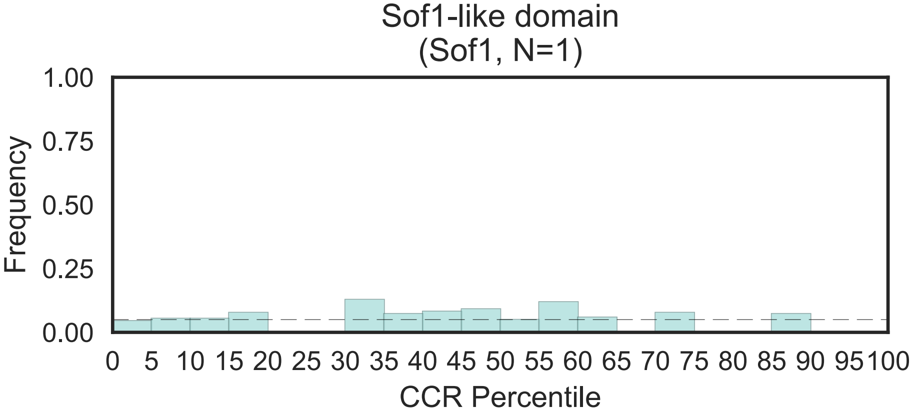

SnoaL-like domain
(SnoaL_3, N=4)
Fisher's OR: 3.57; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

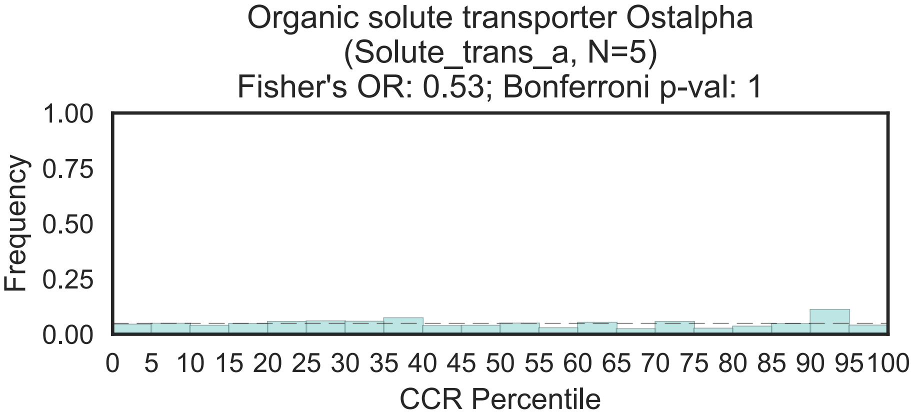

Snurportin1
(Snurportin1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

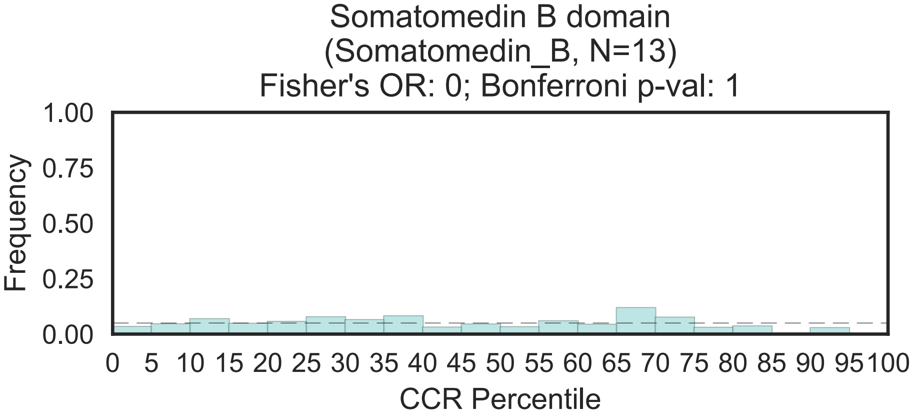

Copper/zinc superoxide dismutase (SODC)
(Sod_Cu, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

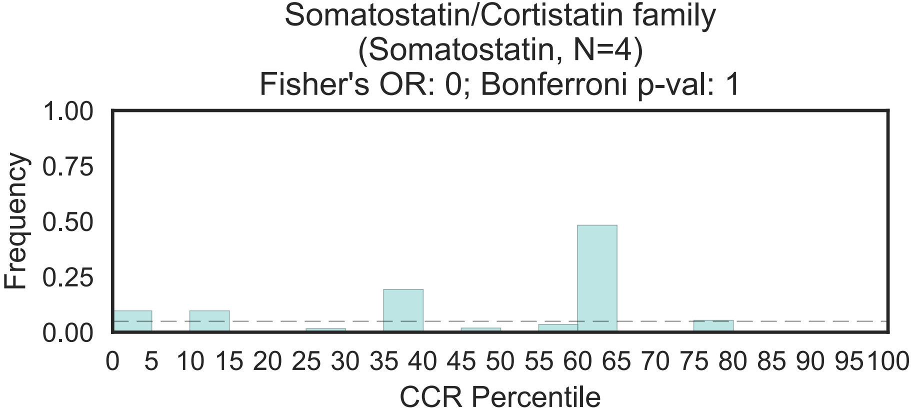

Iron/manganese superoxide dismutases, C-terminal domain
(Sod_Fe_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

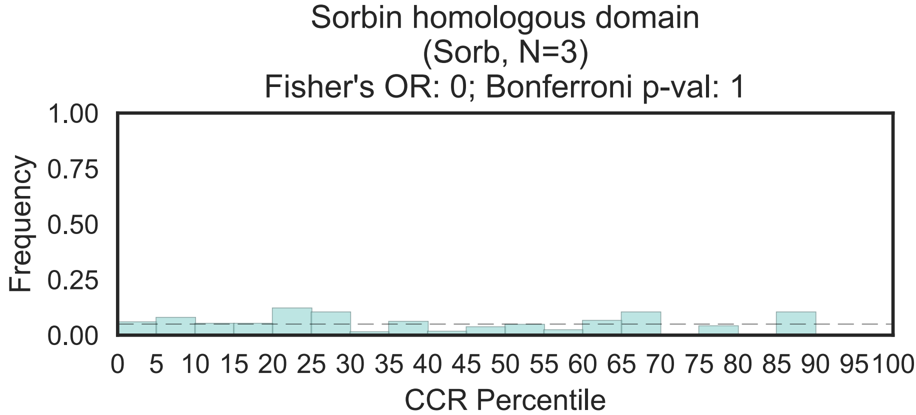

Iron/manganese superoxide dismutases, alpha-hairpin domain
(Sod_Fe_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

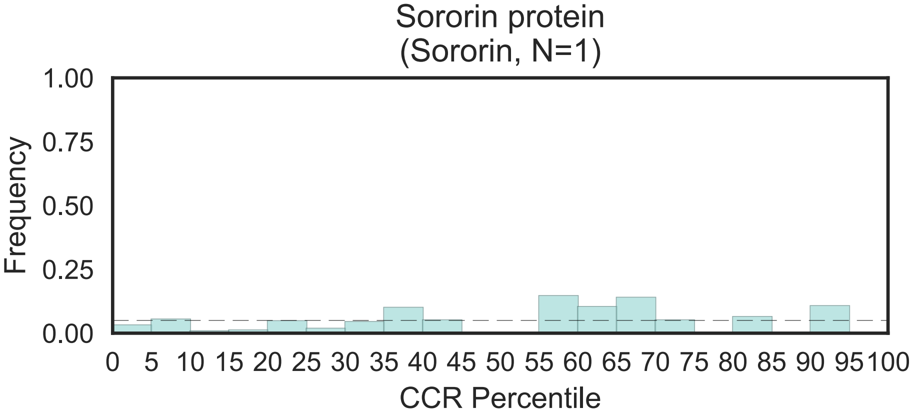

Sof1-like domain
(Sof1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

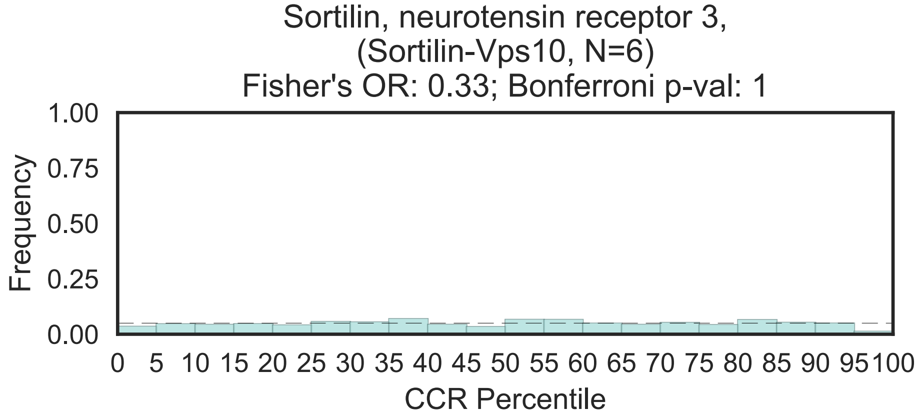

Organic solute transporter Ostalpha
(Solute_trans_a, N=5)
Fisher's OR: 0.53; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Somatomedin B domain
(Somatomedin_B, N=13)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Somatostatin/Cortistatin family
(Somatostatin, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

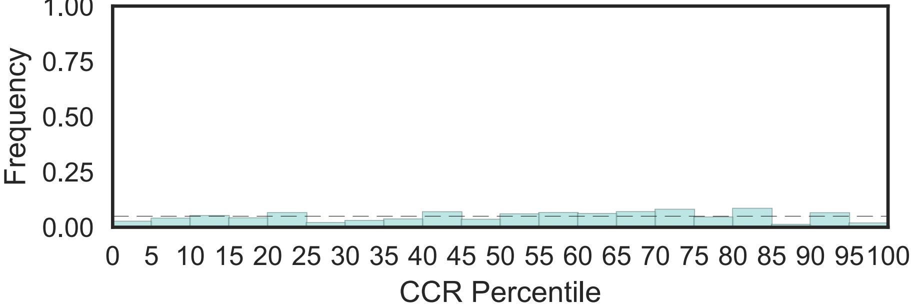

Sorbin homologous domain
(Sorb, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

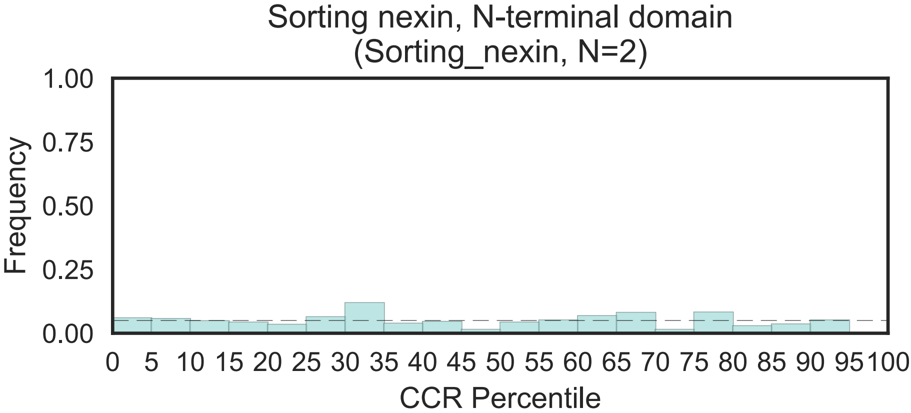

Sororin protein
(Sororin, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



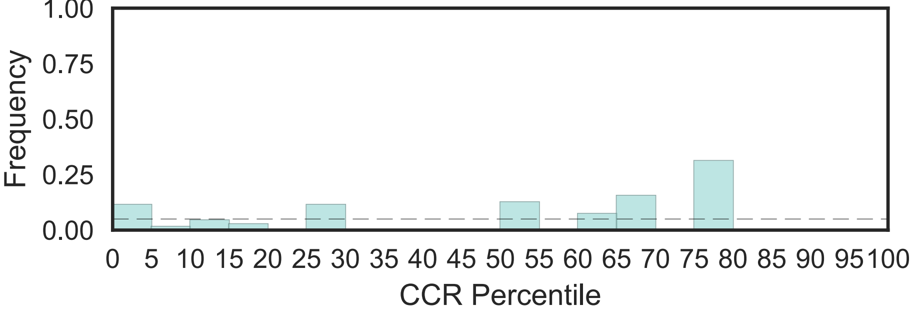
Sortilin, neurotensin receptor 3,
(Sortilin-Vps10, N=6)
Fisher's OR: 0.33; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

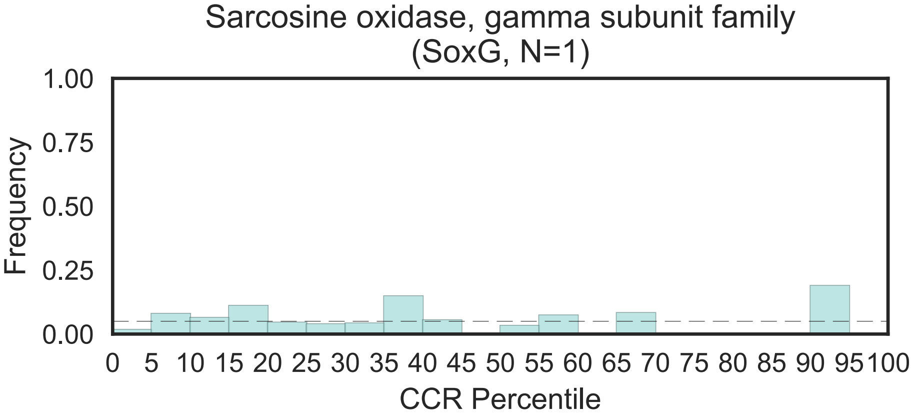
Sortilin, neurotensin receptor 3, C-terminal
(Sortilin_C, N=5)
Fisher's OR: 0.377; Bonferroni p-val: 1



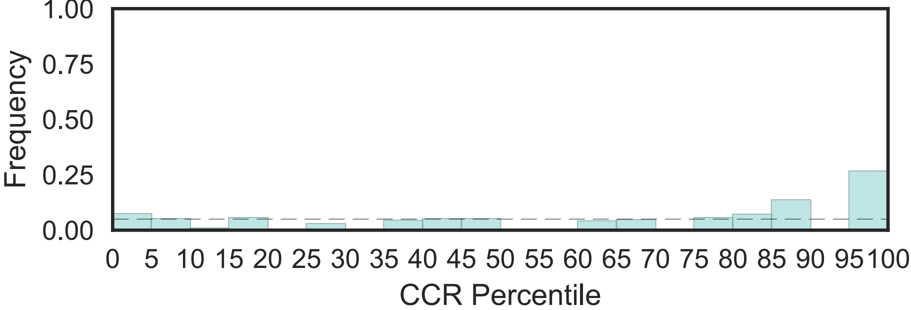

Sorting nexin, N-terminal domain
(Sorting_nexin, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

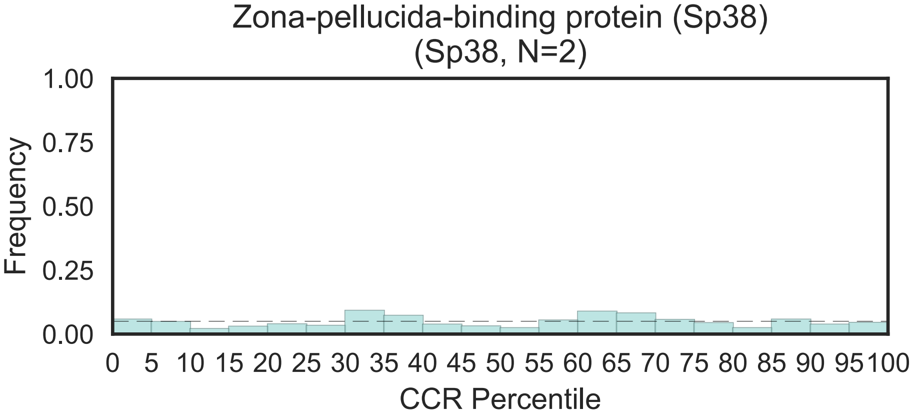
Sox 17/18 central domain
(Sox17_18_mid, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

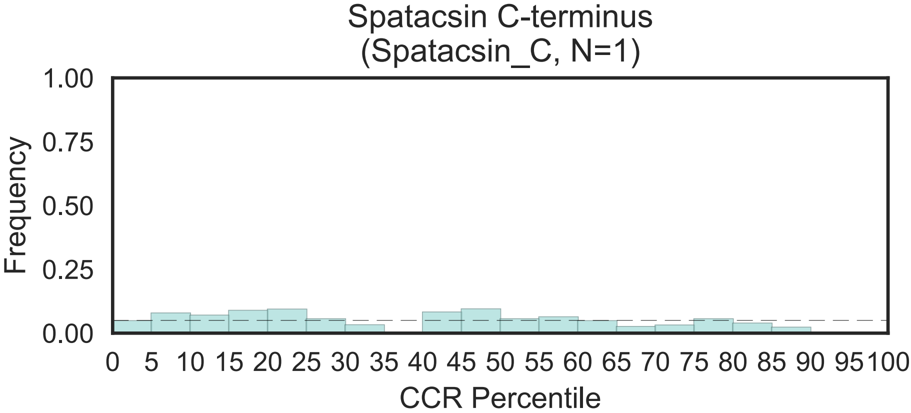


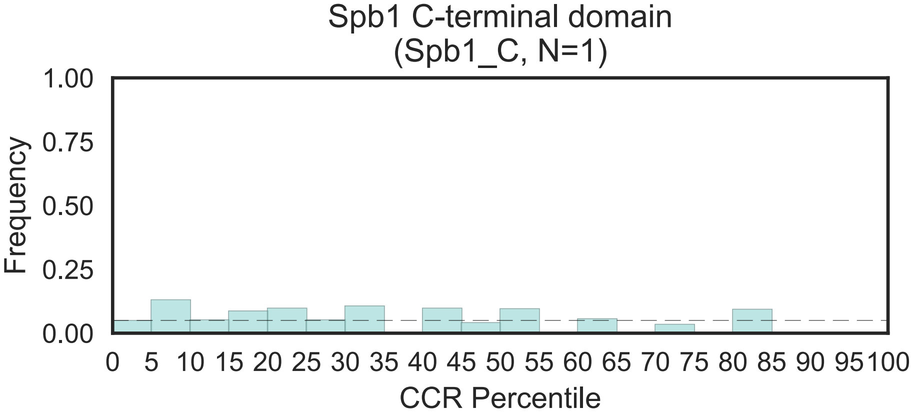

Sarcosine oxidase, gamma subunit family
(SoxG, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

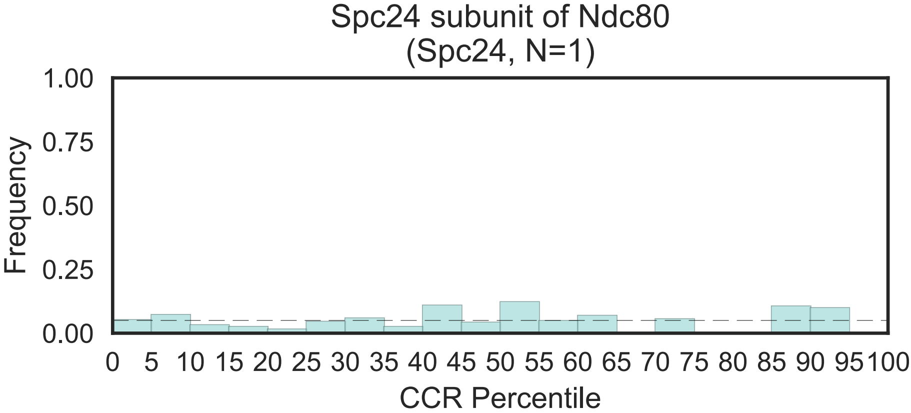
Sox developmental protein N terminal (Sox_N, N=3) Fisher's OR: 6.98; Bonferroni p-val: 1

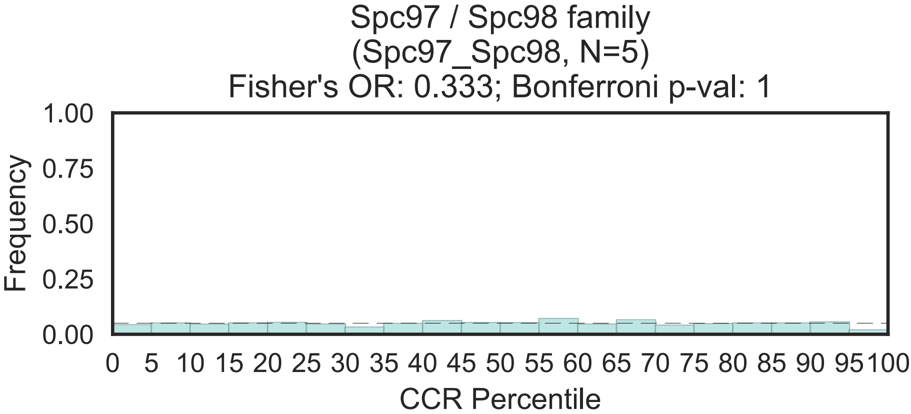


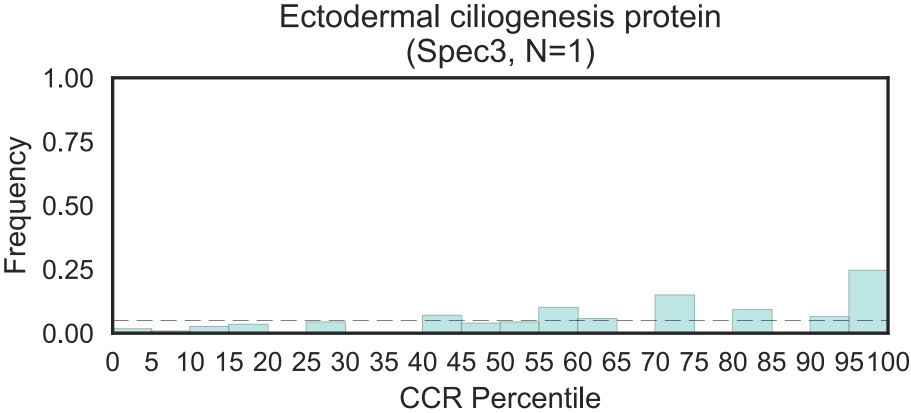

Zona-pellucida-binding protein (Sp38)
(Sp38, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Spatacsin C-terminus
(Spatacsin_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

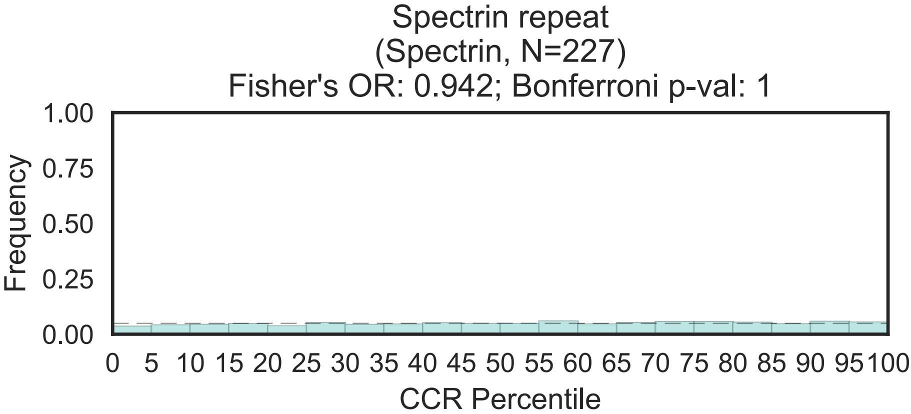

Spb1 C-terminal domain
(Spb1_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

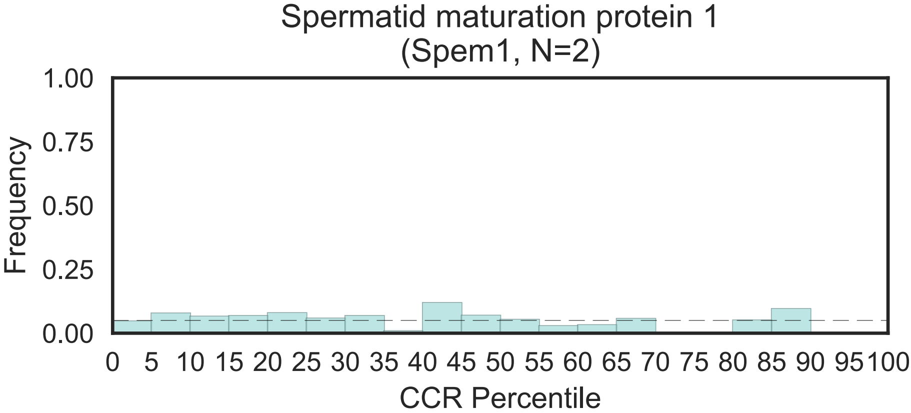

Spc24 subunit of Ndc80
(Spc24, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

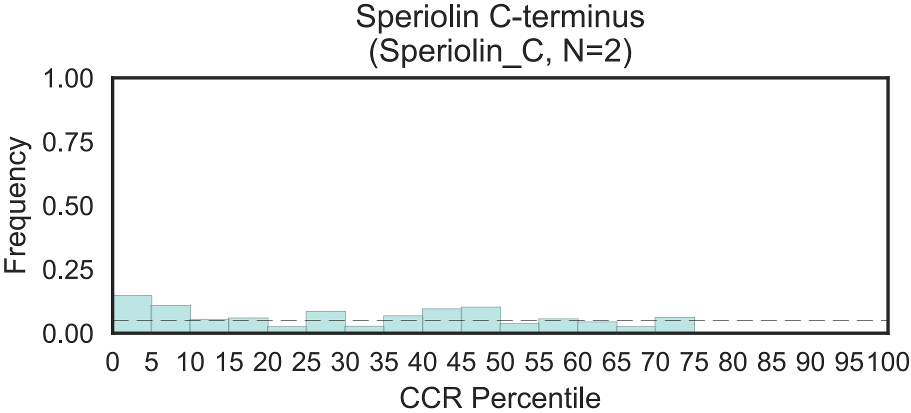

Spc97 / Spc98 family
(Spc97_Spc98, N=5)
Fisher's OR: 0.333; Bonferroni p-val: 1

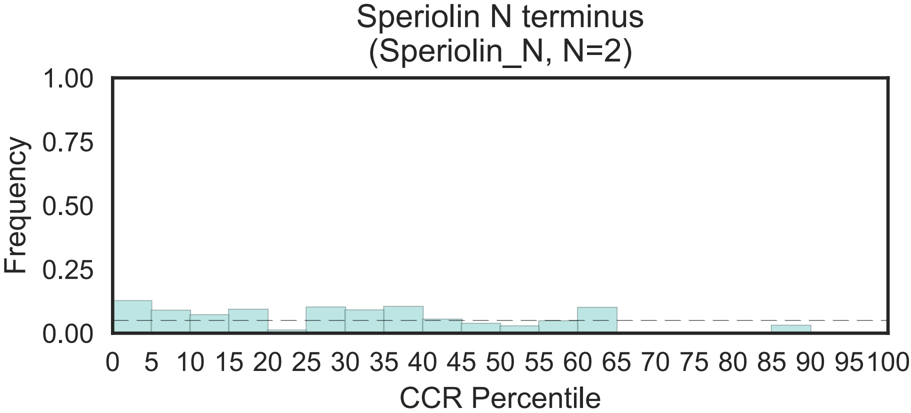


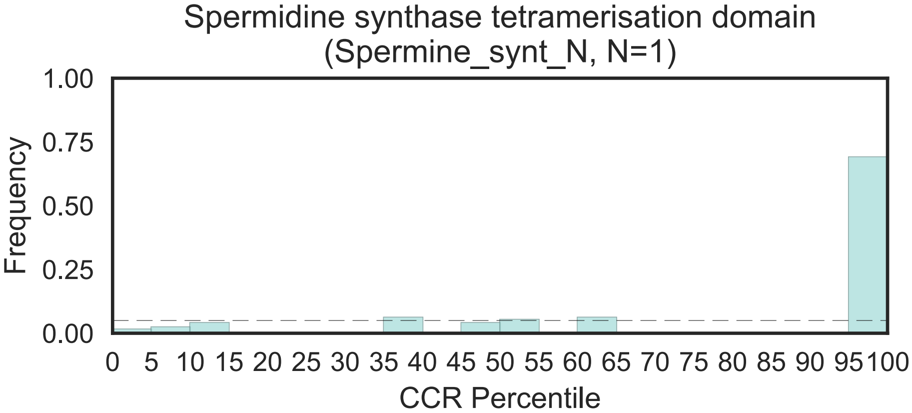
Ectodermal ciliogenesis protein
(Spec3, N=1)

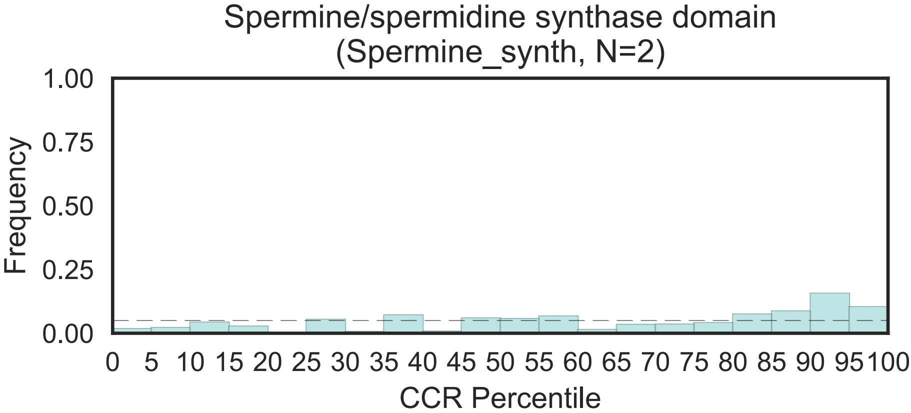

Spectrin repeat
(Spectrin, N=227)
Fisher's OR: 0.942; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

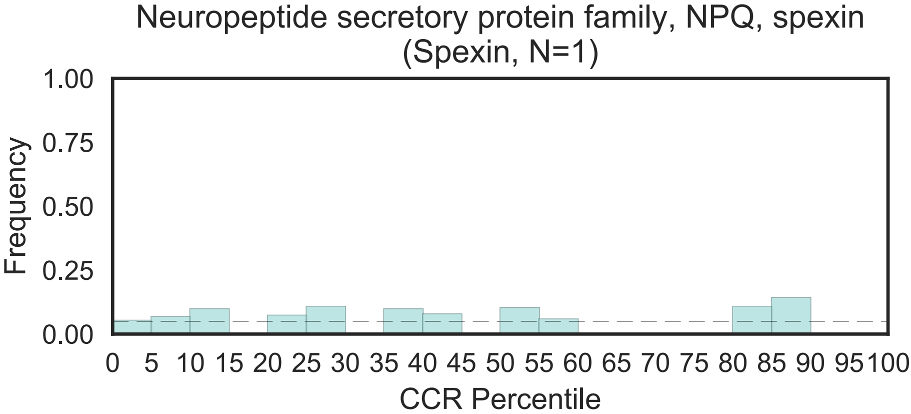

Spermatid maturation protein 1
(Spem1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

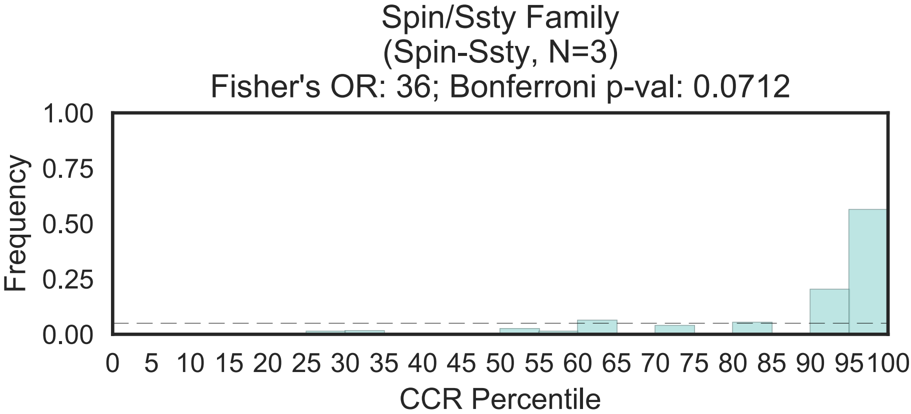

Speriolin C-terminus
(Speriolin_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

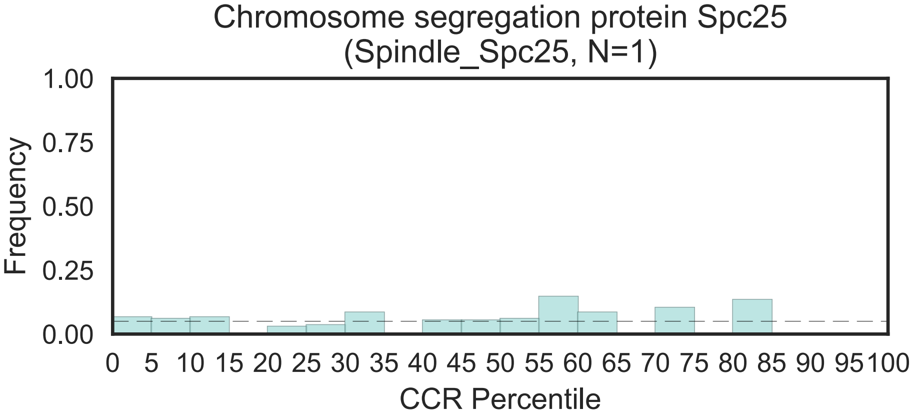

Speriolin N terminus
(Speriolin_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

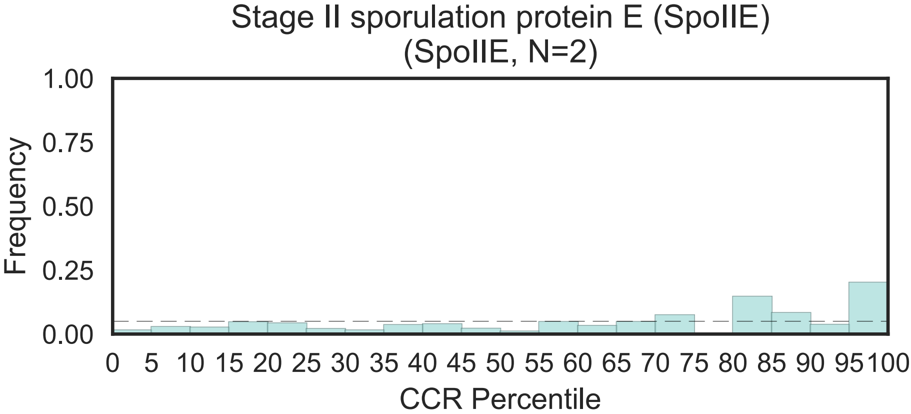

Spermidine synthase tetramerisation domain
(Spermine_synt_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

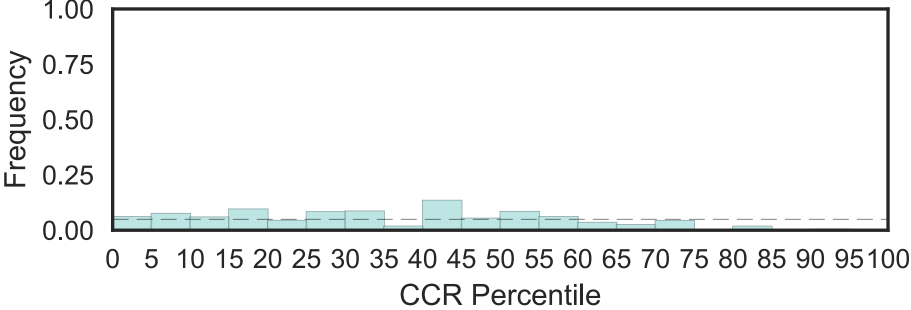

Spermine/spermidine synthase domain
(Spermine_synth, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

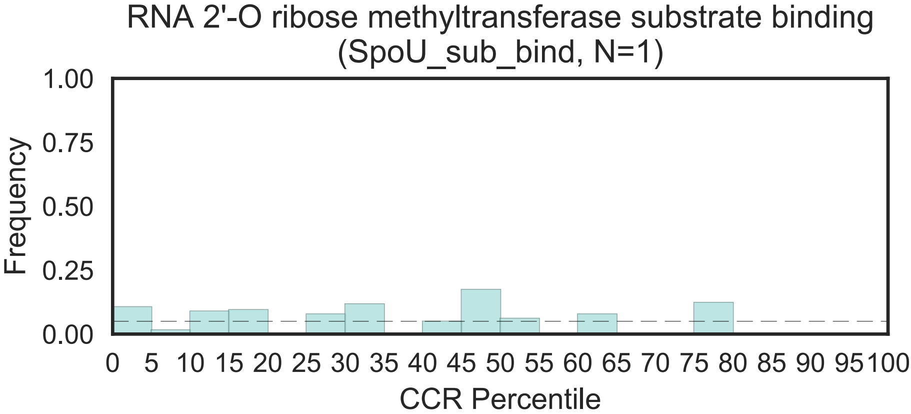

Neuropeptide secretory protein family, NPQ, spexin
(Spexin, N=1)

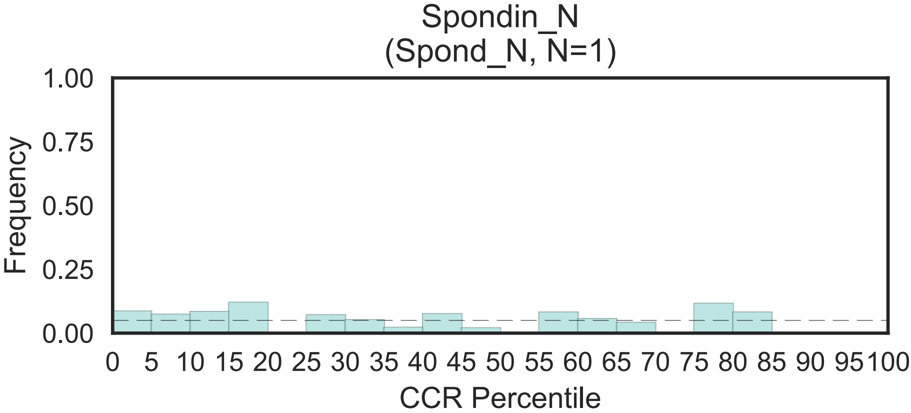

Spin/Ssty Family
(Spin-Ssty, N=3)
Fisher's OR: 36; Bonferroni p-val: 0.0712
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

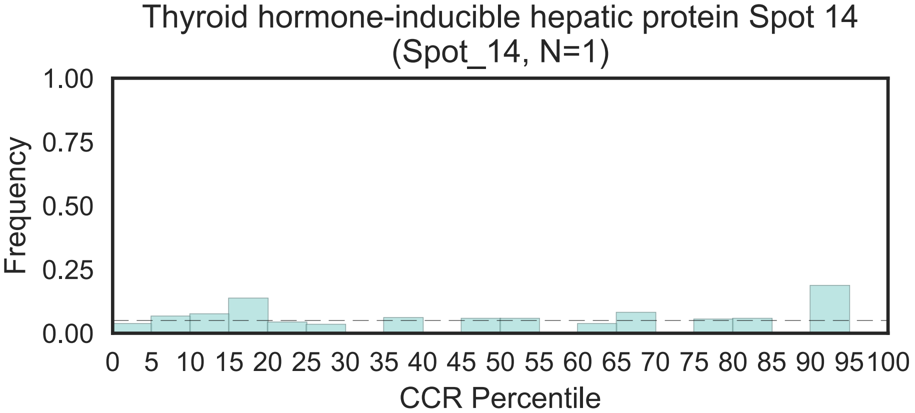

Chromosome segregation protein Spc25
(Spindle_Spc25, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Stage II sporulation protein E (SpoIIE)
(SpoIIE, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

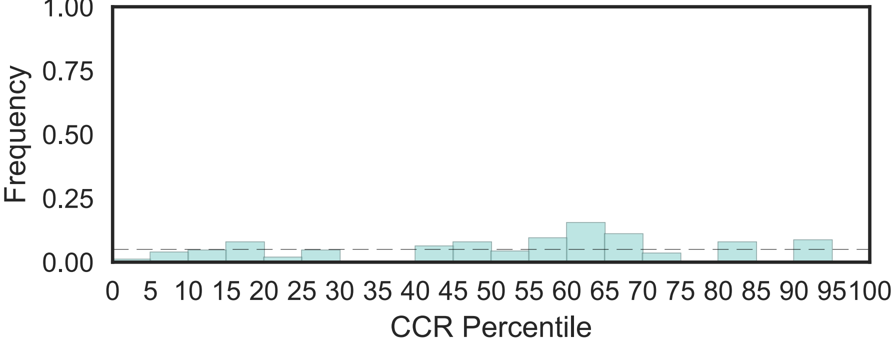

SpoU rRNA Methylase family
(SpoU_methylase, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

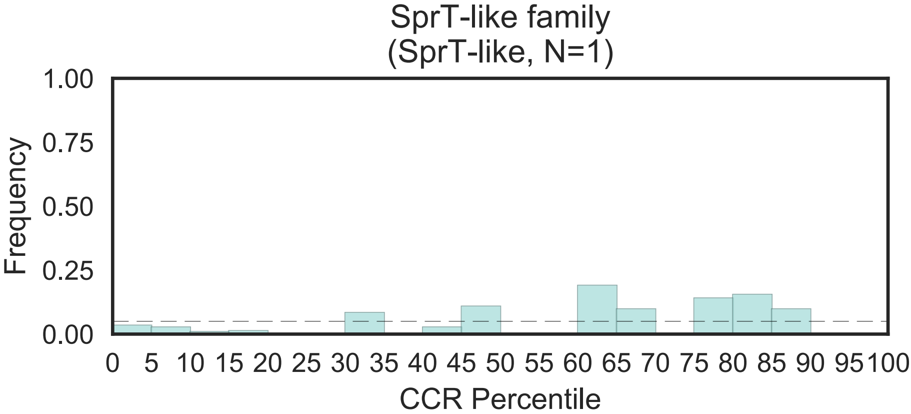

RNA 2'-O ribose methyltransferase substrate binding
(SpoU_sub_bind, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

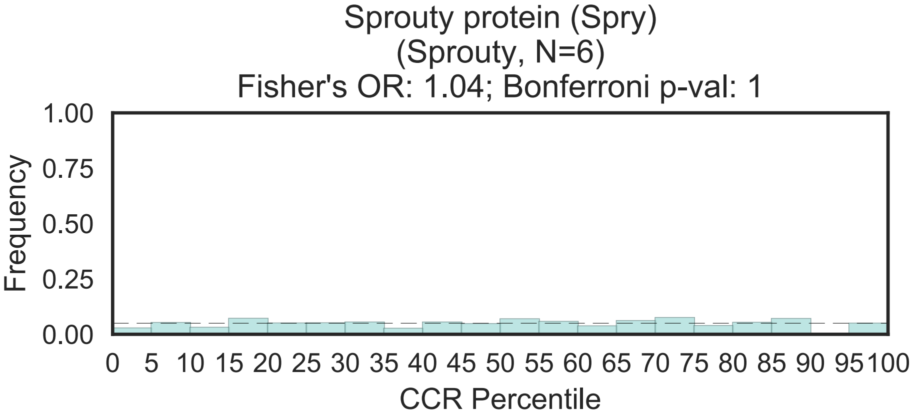

Spondin_N
(Spond_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

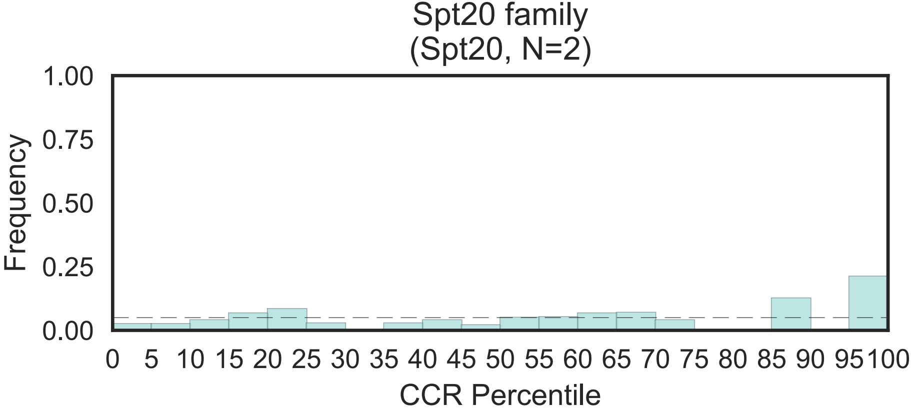

Thyroid hormone-inducible hepatic protein Spot 14
(Spot_14, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

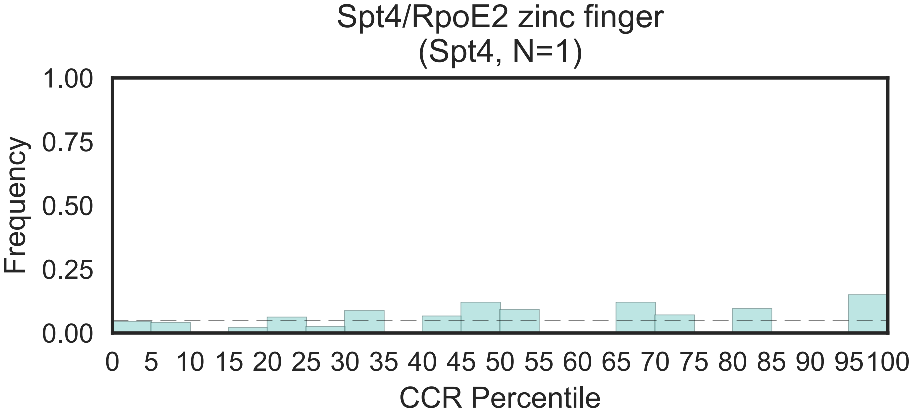
Secreted phosphoprotein 24 (Spp-24) cystatin-like domain (Spp-24, N=2)

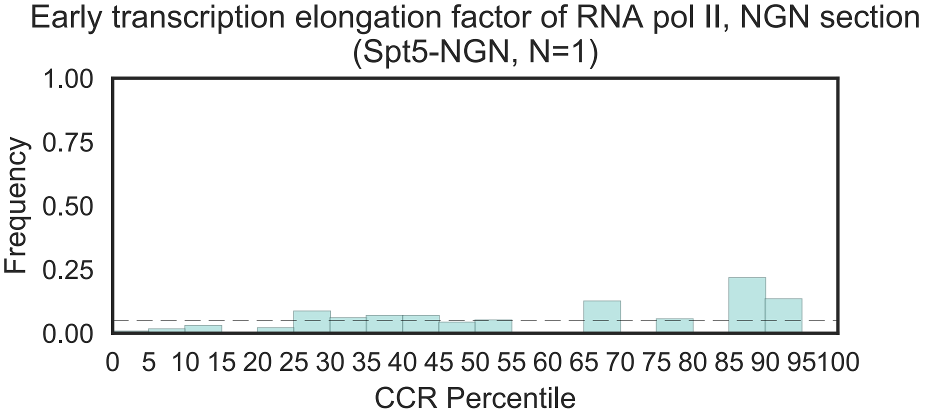


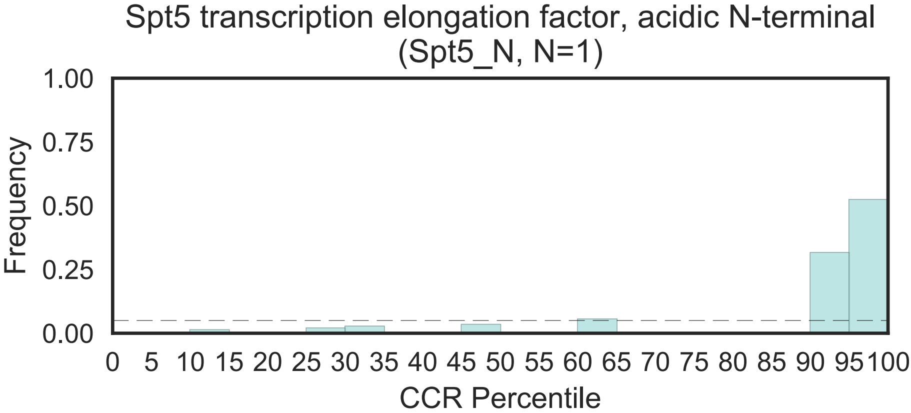

SprT-like family
(SprT-like, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

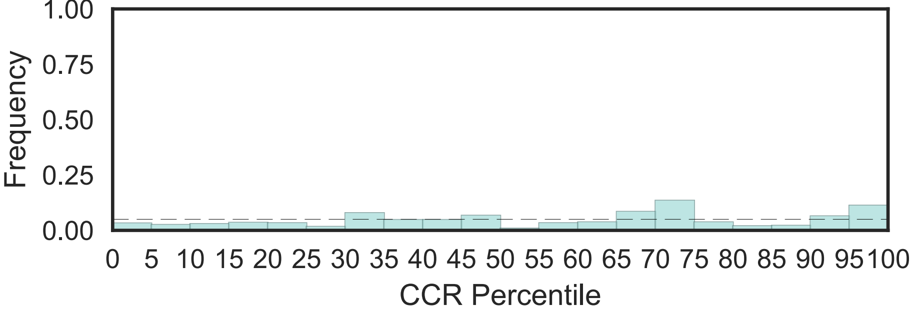

Sprouty protein (Spry)
(Sprouty, N=6)
Fisher's OR: 1.04; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Spt20 family
(Spt20, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Spt4/RpoE2 zinc finger
(Spt4, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

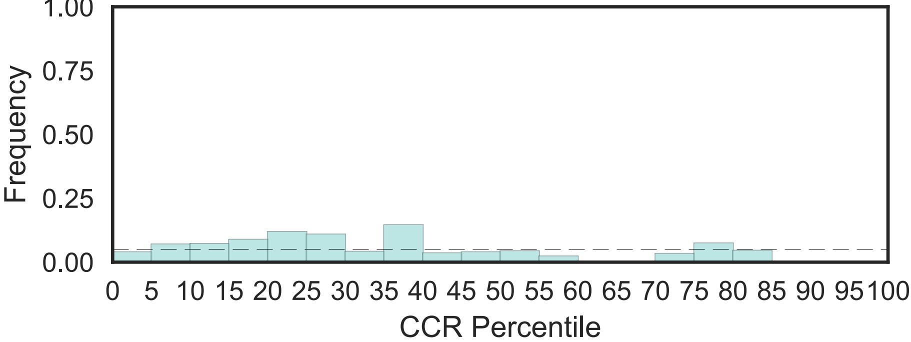

Early transcription elongation factor of RNA pol II, NGN section
(Spt5-NGN, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

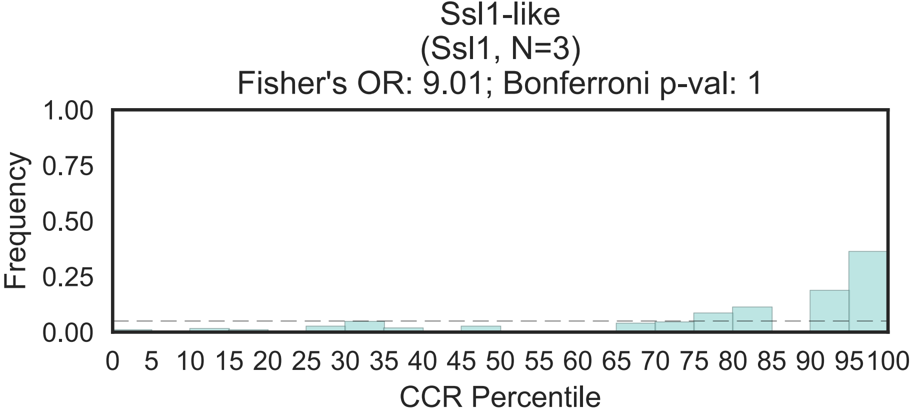

Spt5 transcription elongation factor, acidic N-terminal
(Spt5_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

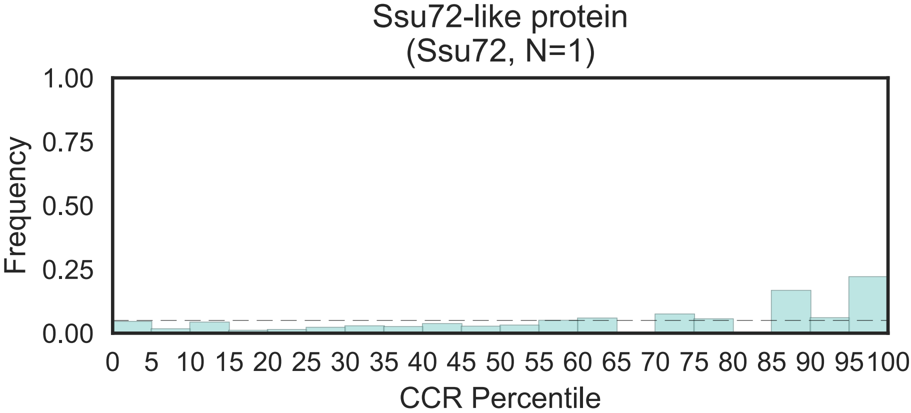


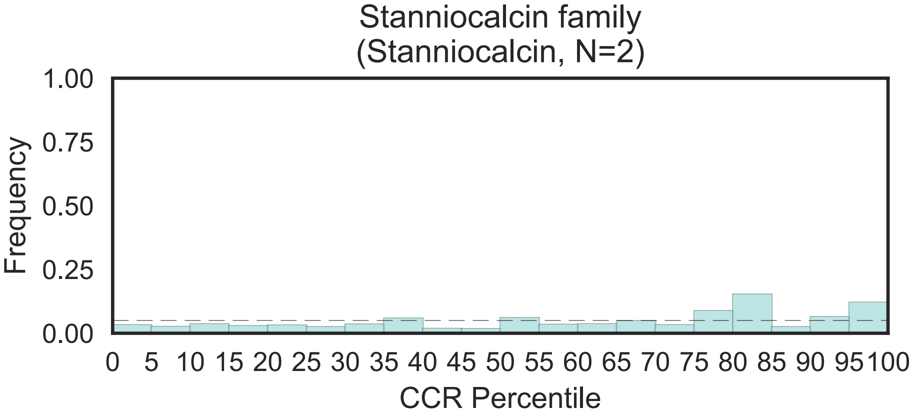
Cell cycle regulatory protein
(Spy1, N=11)
Fisher's OR: 1.76; Bonferroni p-val: 1

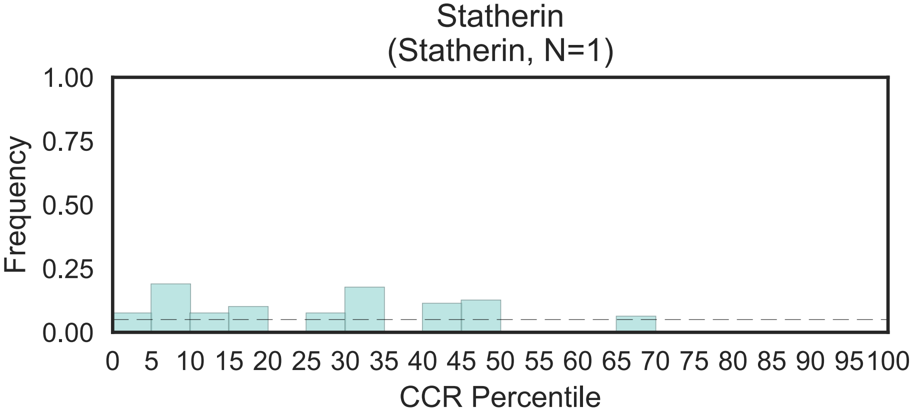
Srg family chemoreceptor
(Srg, N=1)



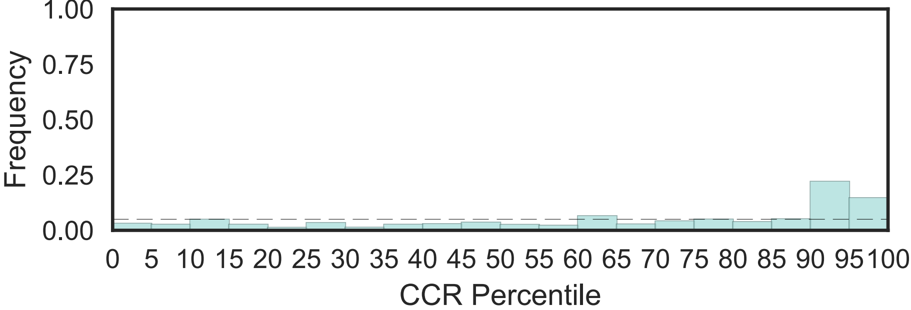

Ssl1-like
(Ssl1, N=3)
Fisher's OR: 9.01; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

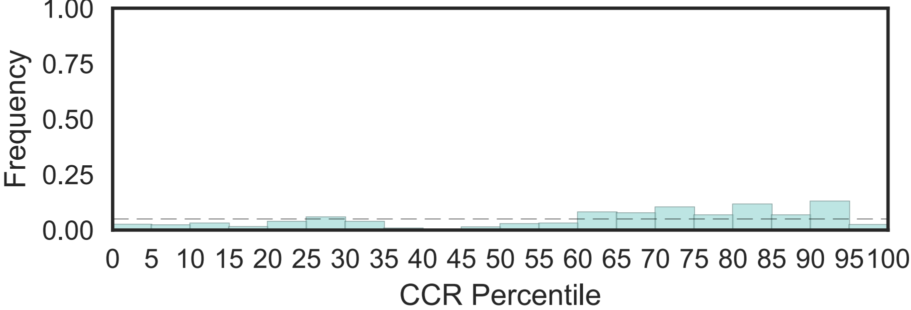

Ssu72-like protein
(Ssu72, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Stanniocalcin family
(Stanniocalcin, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

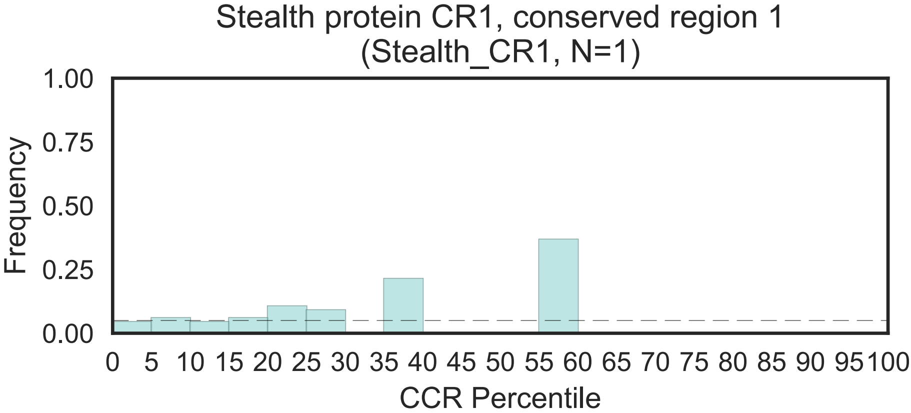

Statherin
(Statherin, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

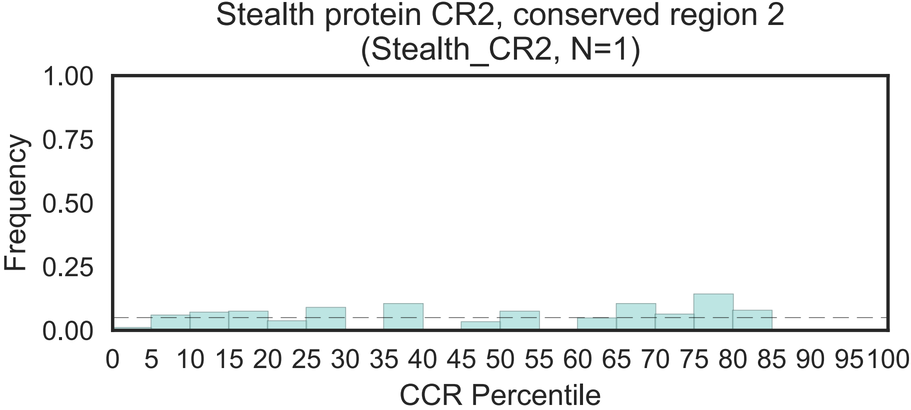
Stathmin family
(Stathmin, N=5)
Fisher's OR: 3.92; Bonferroni p-val: 1

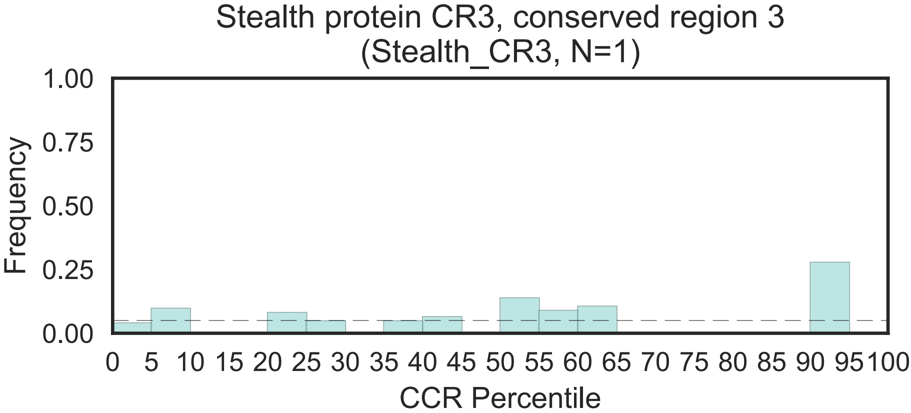


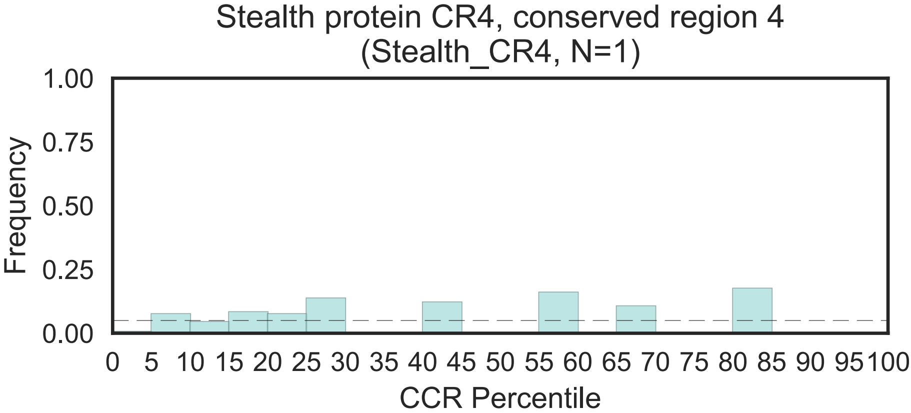


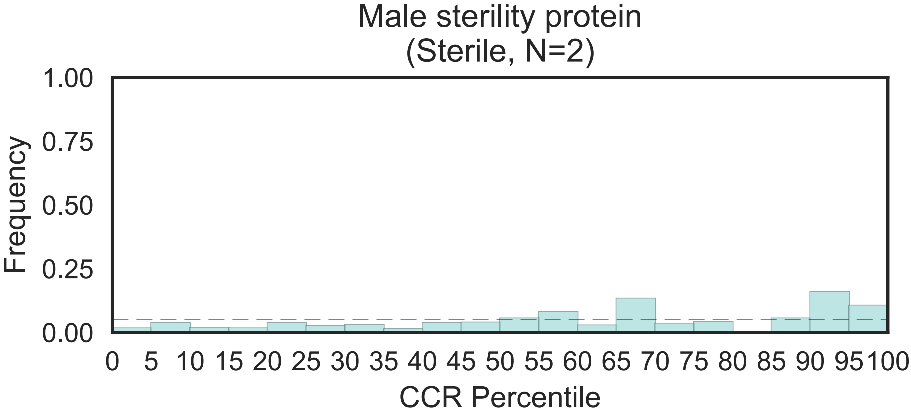
Staufen C-terminal domain
(Staufen_C, N=4)
Fisher's OR: 1.33; Bonferroni p-val: 1

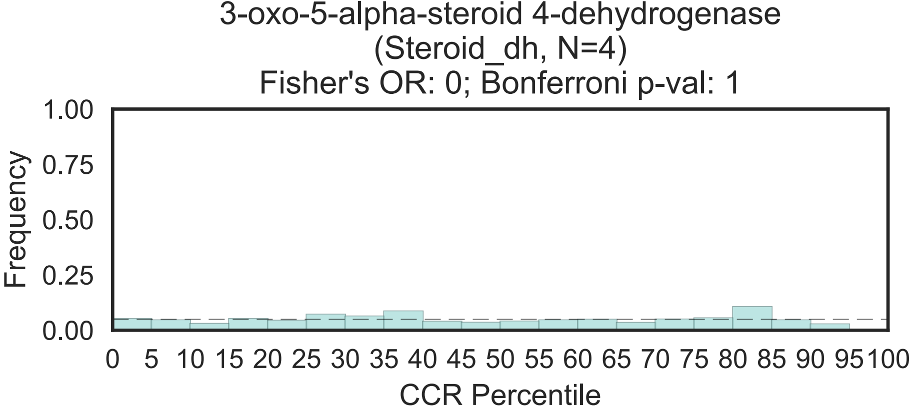

Stealth protein CR1, conserved region 1
(Stealth_CR1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

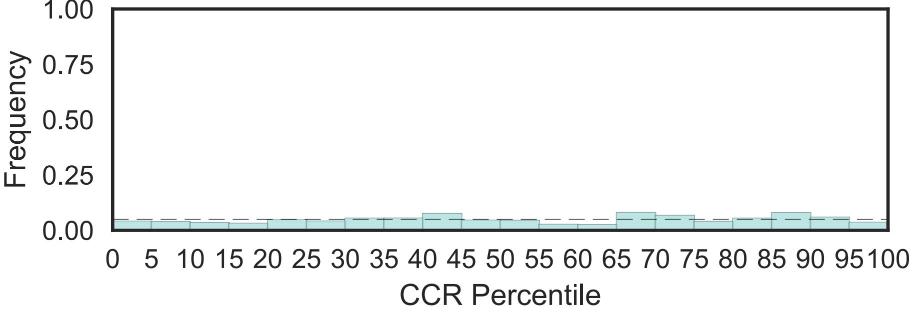

Stealth protein CR2, conserved region 2
(Stealth_CR2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Stealth protein CR3, conserved region 3
(Stealth_CR3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

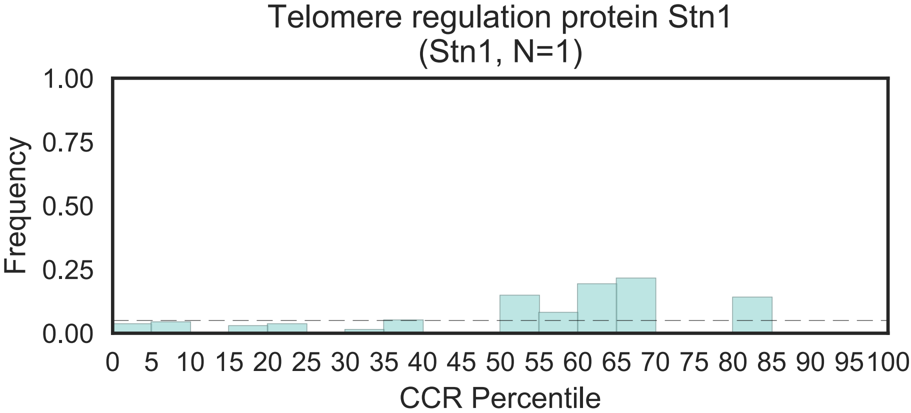

Stealth protein CR4, conserved region 4
(Stealth_CR4, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

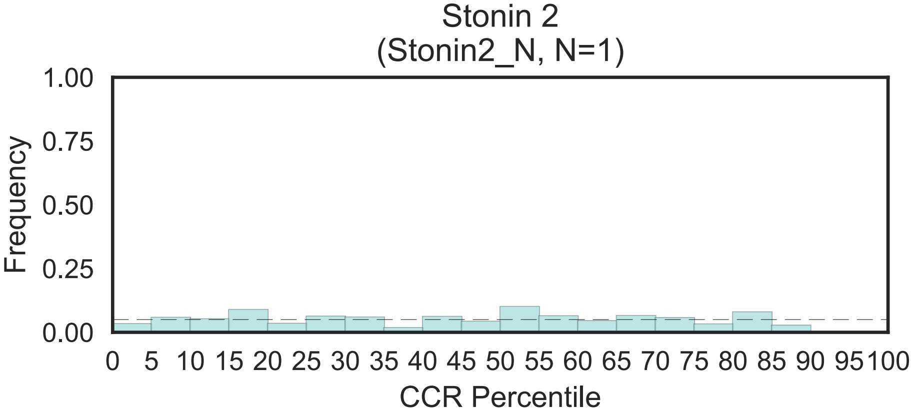

Male sterility protein
(Sterile, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

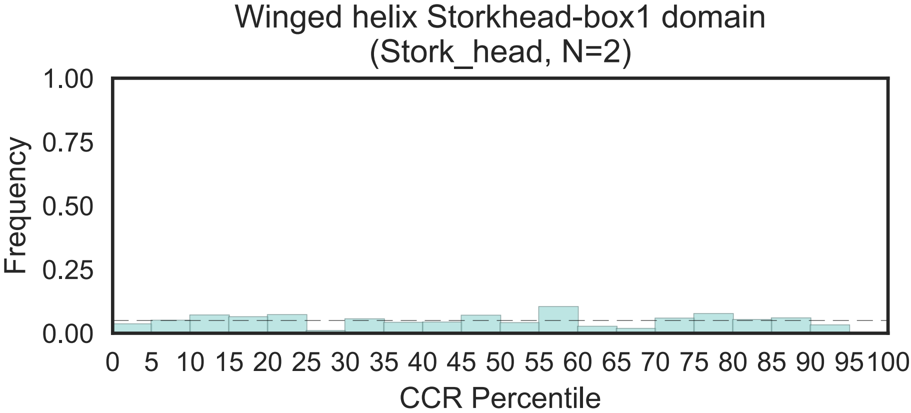

3-oxo-5-alpha-steroid 4-dehydrogenase
(Steroid_dh, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

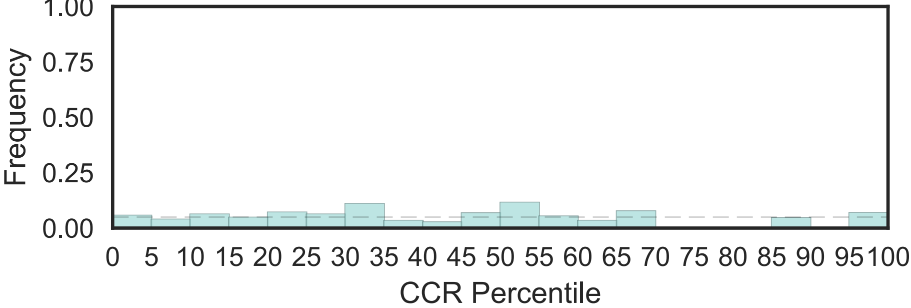


Sterol-sensing domain of SREBP cleavage-activation
(Sterol-sensing, N=10)
Fisher's OR: 0.599; Bonferroni p-val: 1

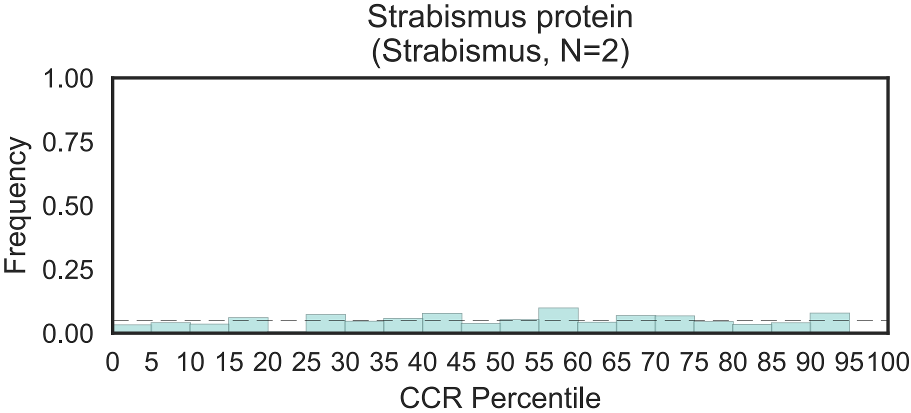

Telomere regulation protein Stn1
(Stn1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

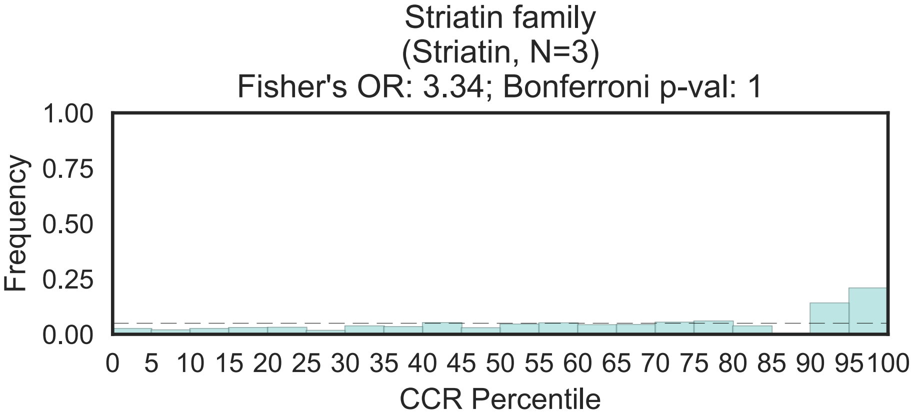

Stonin 2
(Stonin2_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

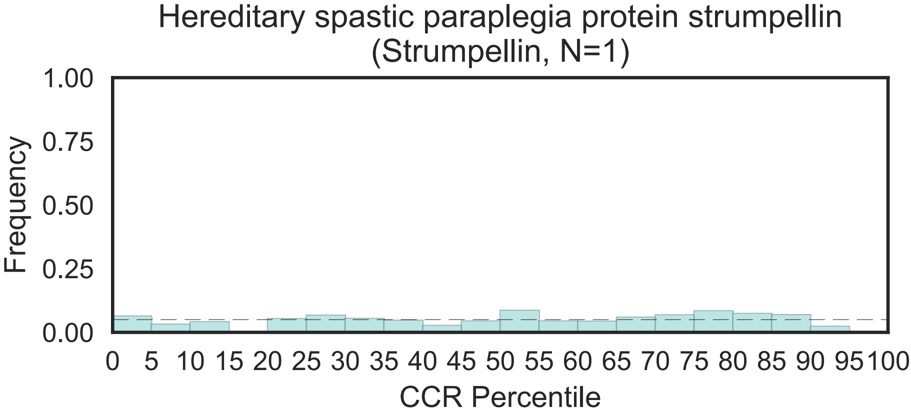

Winged helix Storkhead-box1 domain
(Stork_head, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

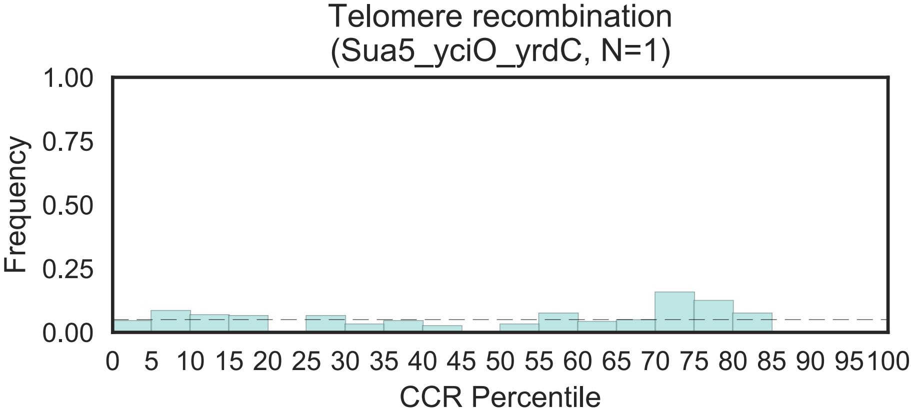


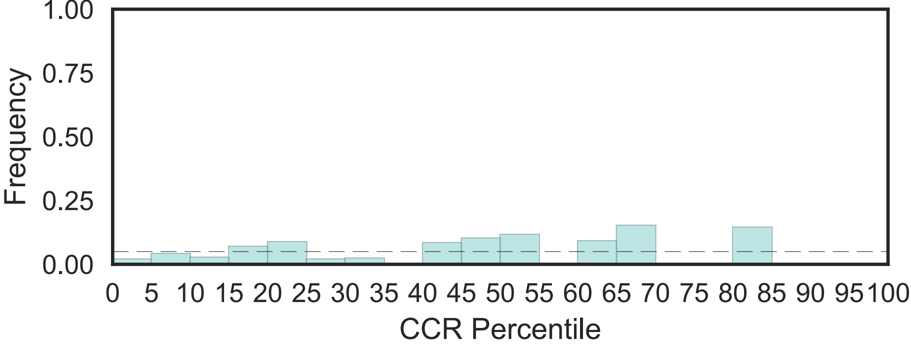
Strictosidine synthase
(Str_synth, N=3)
Fisher's OR: 1.13; Bonferroni p-val: 1


Strabismus protein
(Strabismus, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

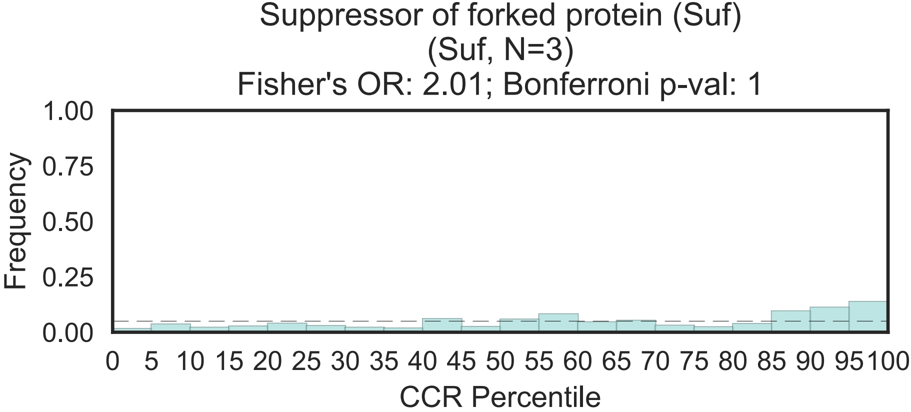

Striatin family
(Striatin, N=3)
Fisher's OR: 3.34; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

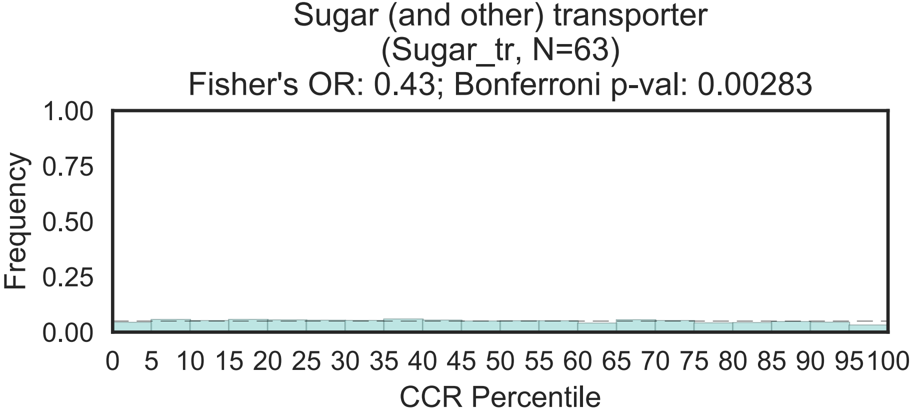

Hereditary spastic paraplegia protein strumpellin
(Strumpellin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Telomere recombination
(Sua5_yciO_yrdC, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

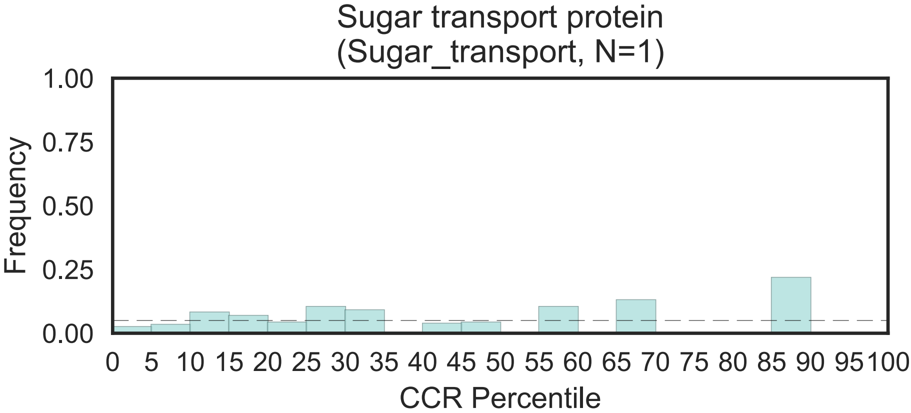


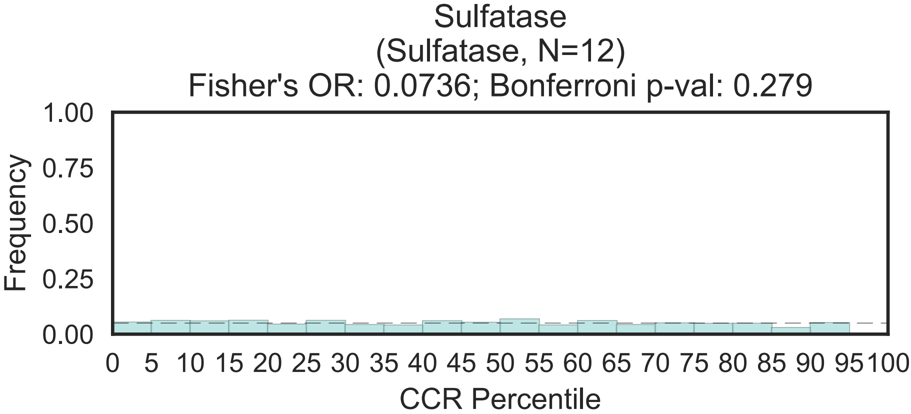
Succinyl-CoA ligase like flavodoxin domain
(Succ_CoA_lig, N=1)

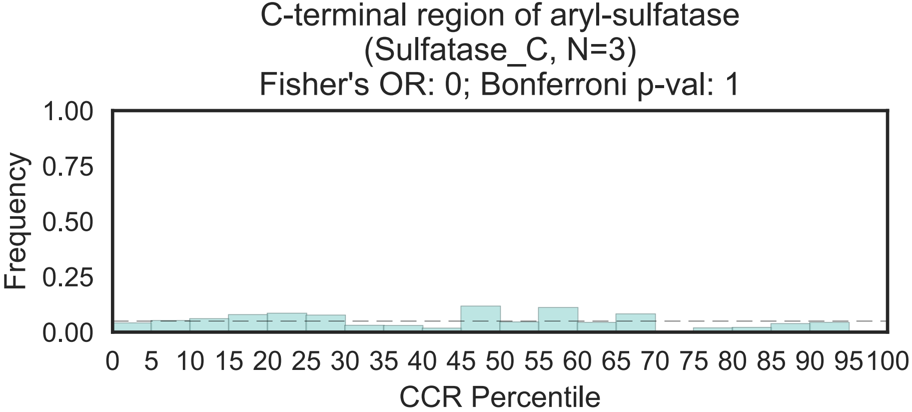

Suppressor of forked protein (Suf)
(Suf, N=3)
Fisher's OR: 2.01; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

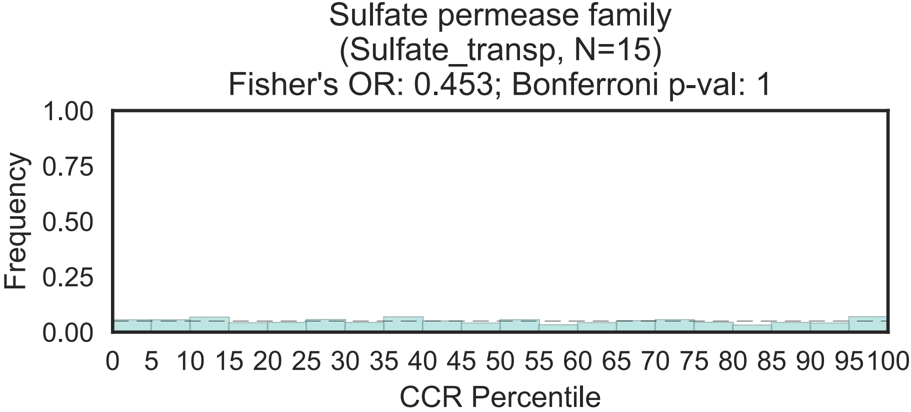


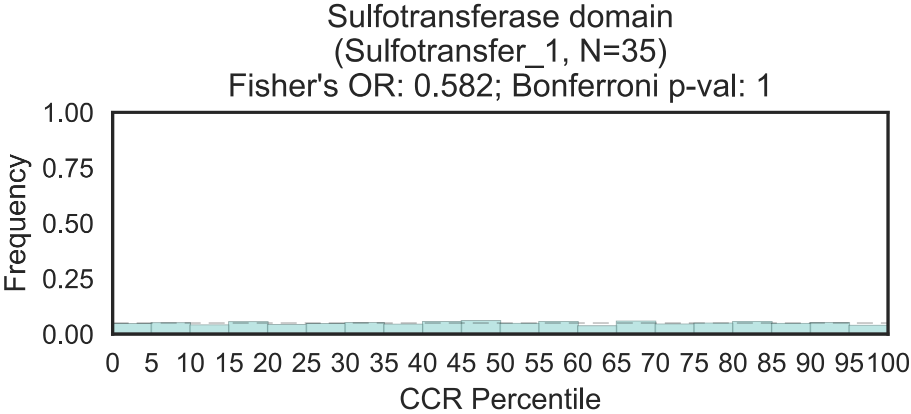
Sugar (and other) transporter
(Sugar_tr, N=63)
Fisher's OR: 0.43; Bonferroni p-val: 0.00283


Sugar transport protein
(Sugar_transport, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

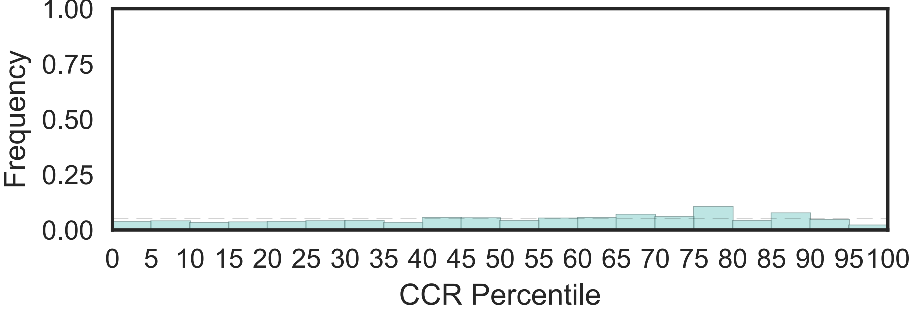

Sulfatase
(Sulfatase, N=12)
Fisher's OR: 0.0736; Bonferroni p-val: 0.279
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


C-terminal region of aryl-sulfatase
(Sulfatase_C, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

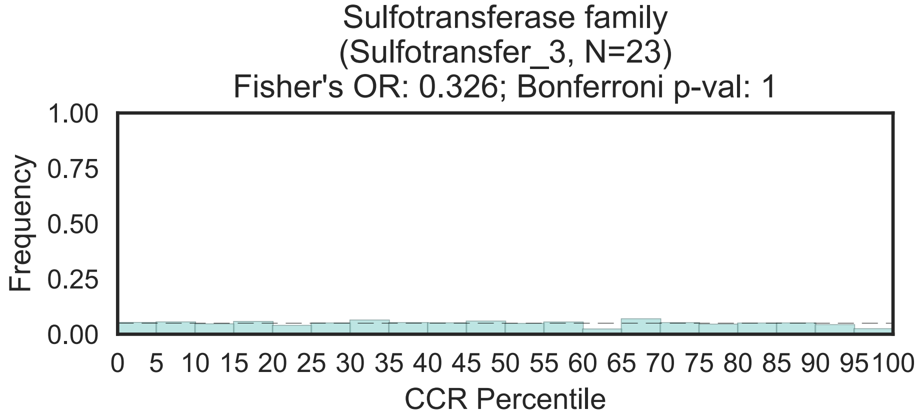

Sulfate permease family
(Sulfate_transp, N=15)
Fisher's OR: 0.453; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

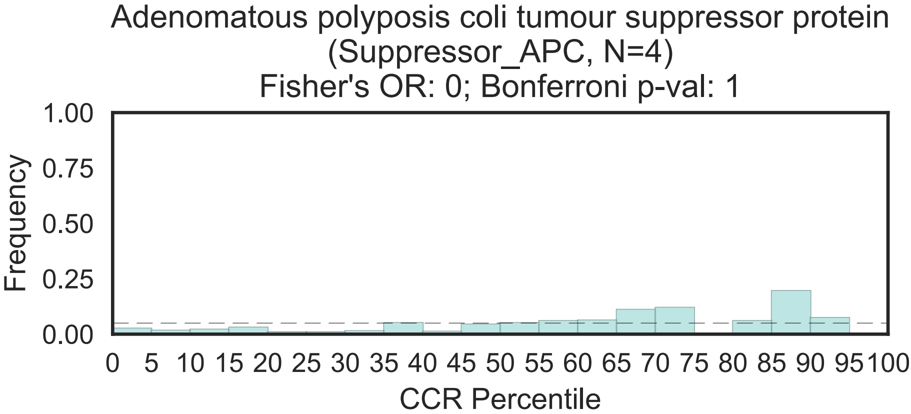


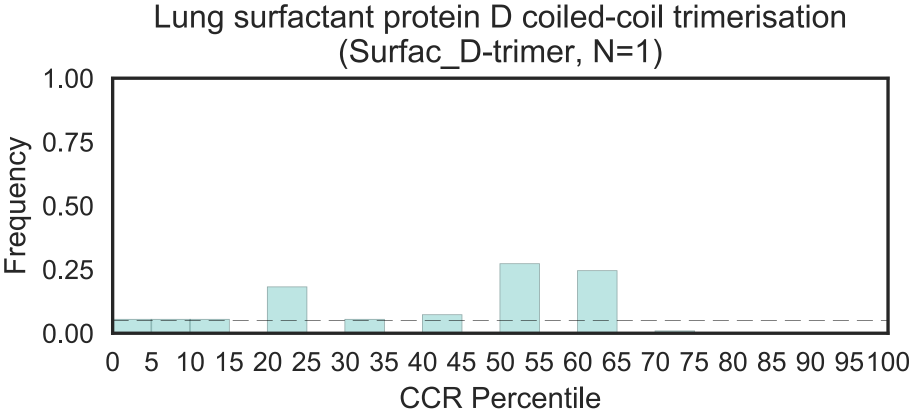
Sulfotransferase domain
(Sulfotransfer_1, N=35)
Fisher's OR: 0.582; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

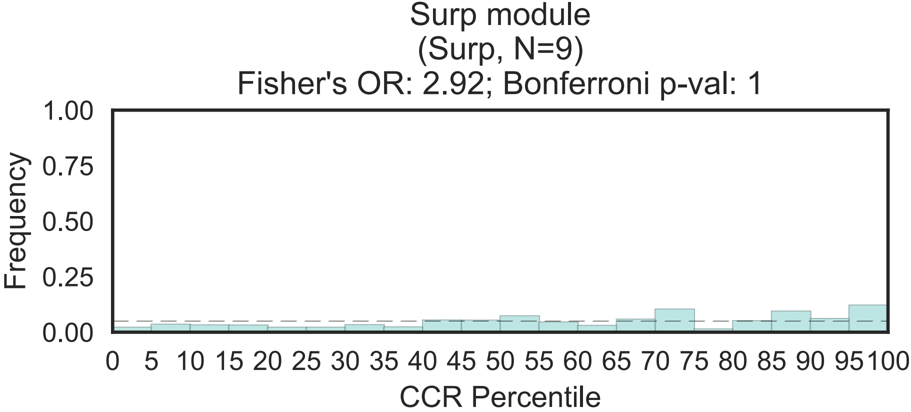


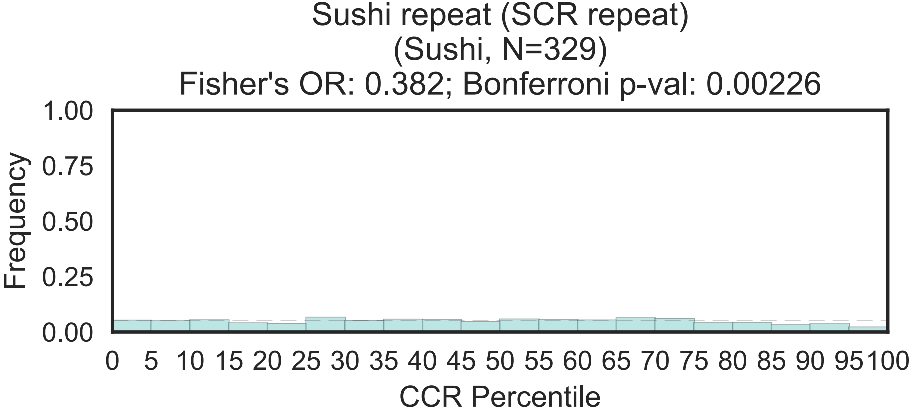
Sulfotransferase family
(Sulfotransfer_2, N=12)
Fisher's OR: 0.47; Bonferroni p-val: 1


Sulfotransferase family
(Sulfotransfer_3, N=23)
Fisher's OR: 0.326; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

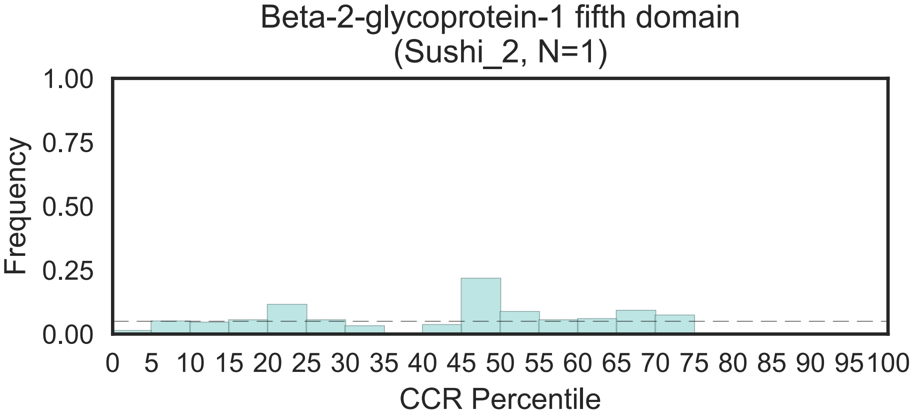

Adenomatous polyposis coli tumour suppressor protein
(Suppressor_APC, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

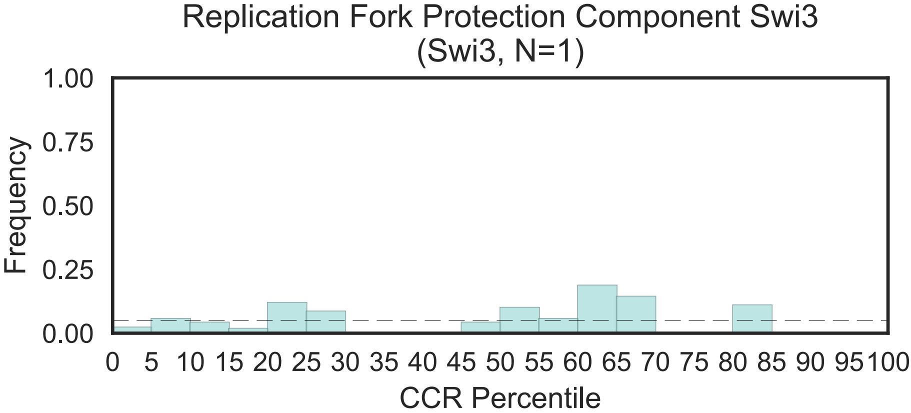

Lung surfactant protein D coiled-coil trimerisation
(Surfac_D-trimer, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

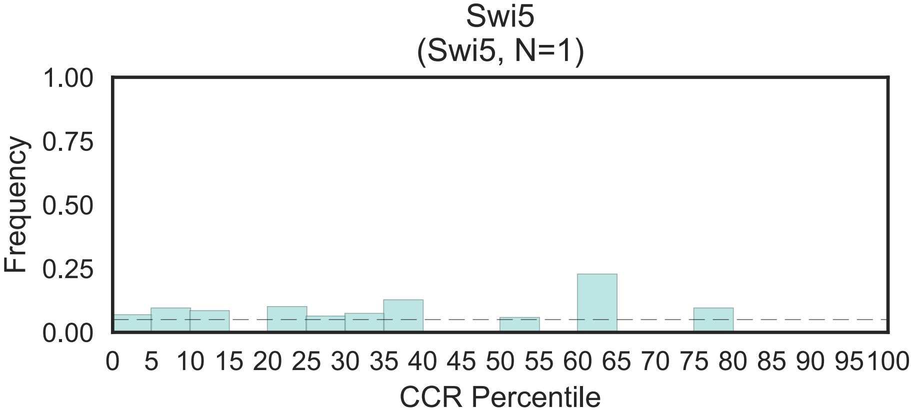

Surp module
(Surp, N=9)
Fisher's OR: 2.92; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

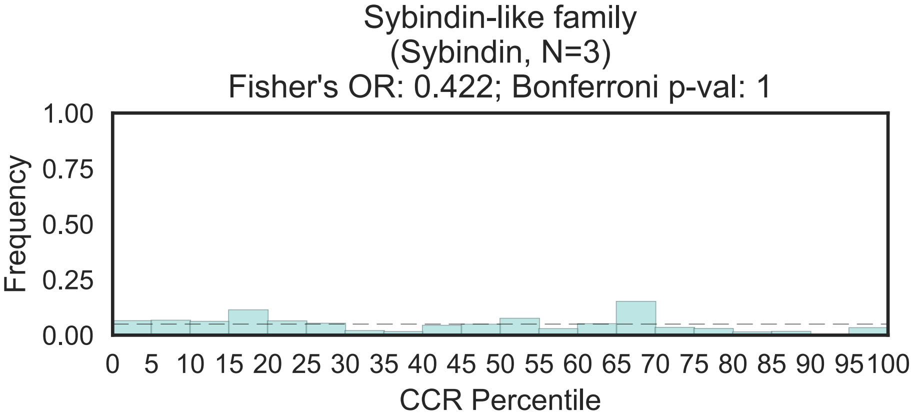


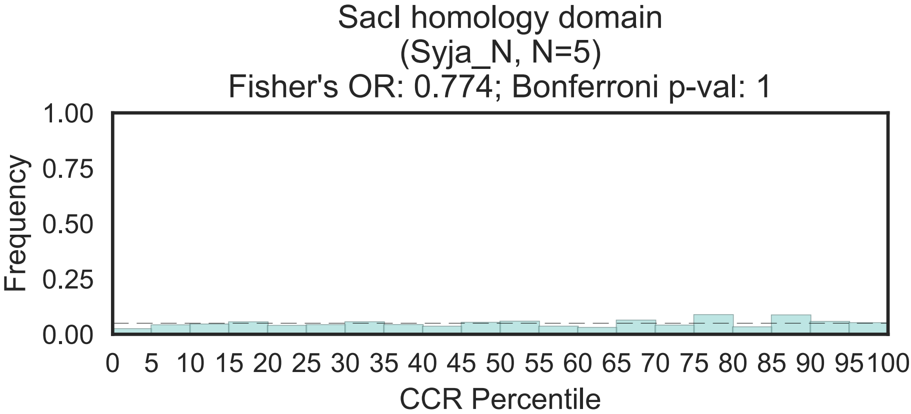
Sushi repeat (SCR repeat)
(Sushi, N=329)
Fisher's OR: 0.382; Bonferroni p-val: 0.00226


Beta-2-glycoprotein-1 fifth domain
(Sushi_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

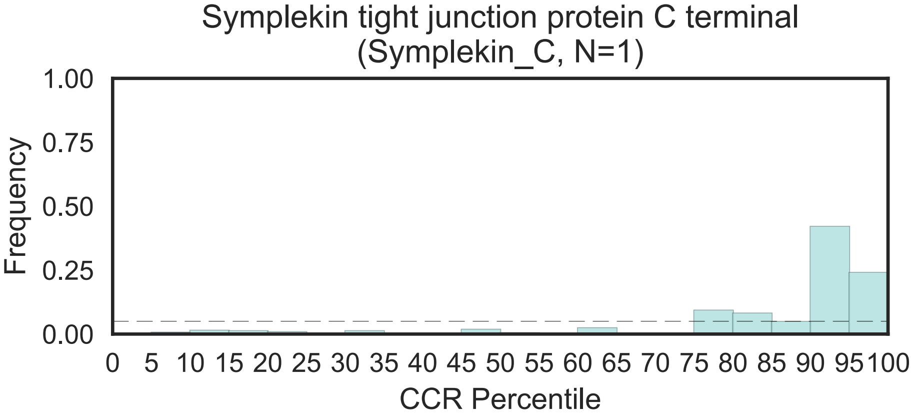

Replication Fork Protection Component Swi3
(Swi3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

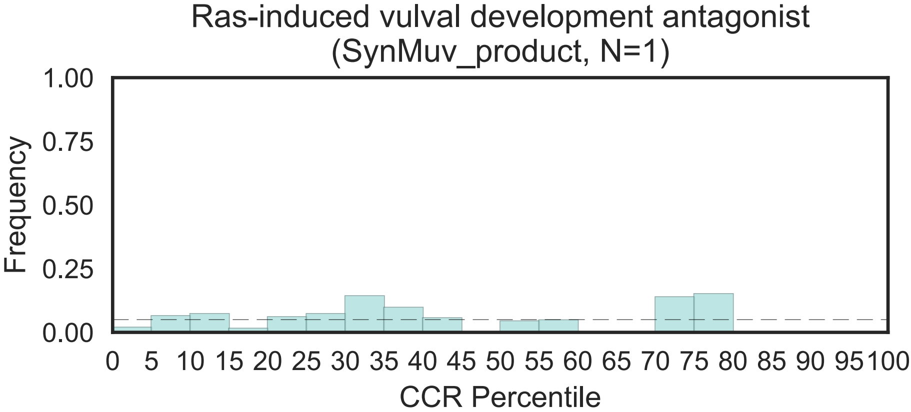

Swi5
(Swi5, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

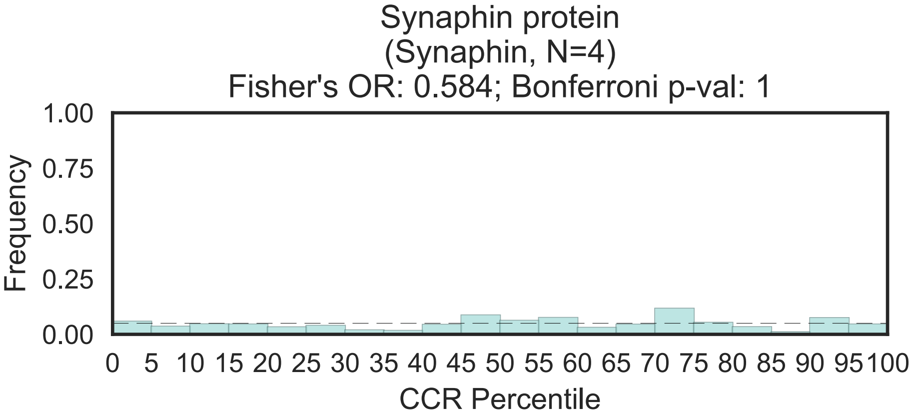

Sybindin-like family
(Sybindin, N=3)
Fisher's OR: 0.422; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

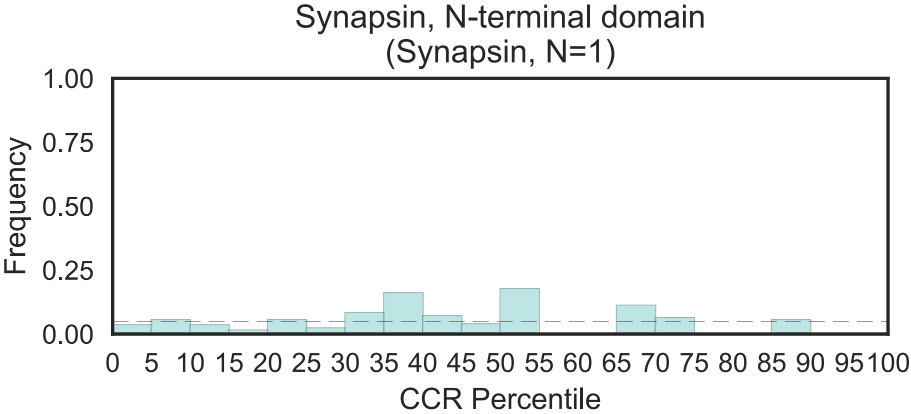


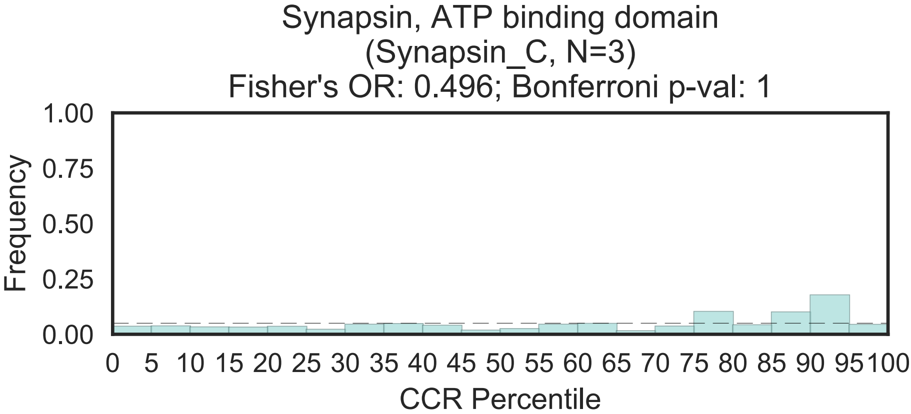
SacI homology domain
(Syja_N, N=5)
Fisher's OR: 0.774; Bonferroni p-val: 1

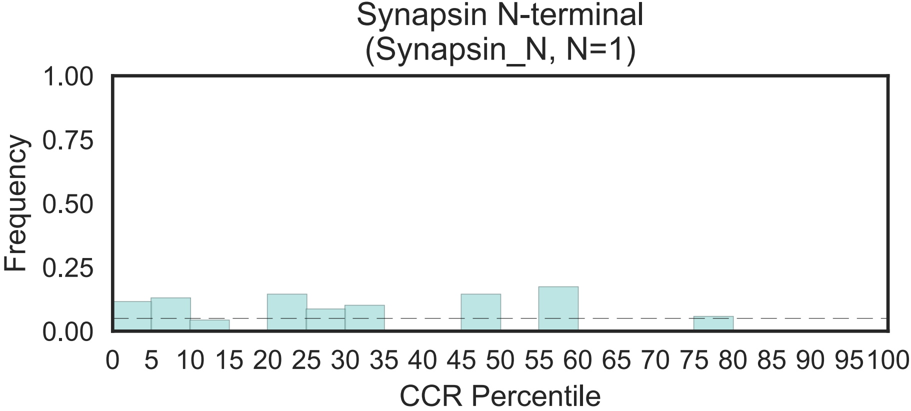

Symplekin tight junction protein C terminal
(Symplekin_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

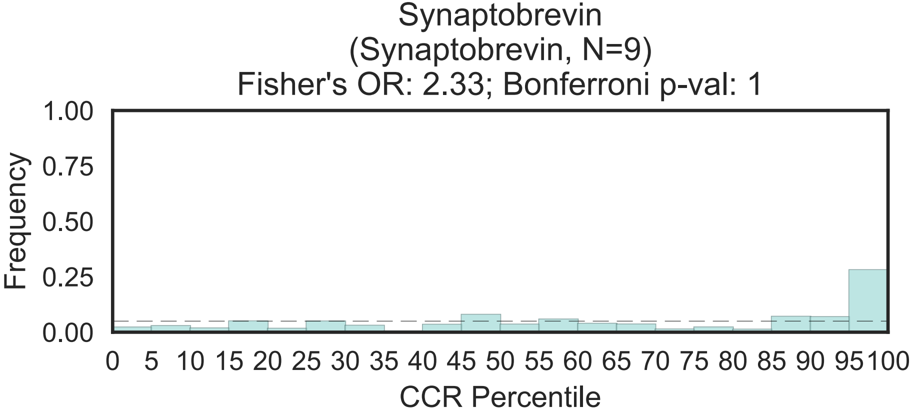

Ras-induced vulval development antagonist
(SynMuv_product, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

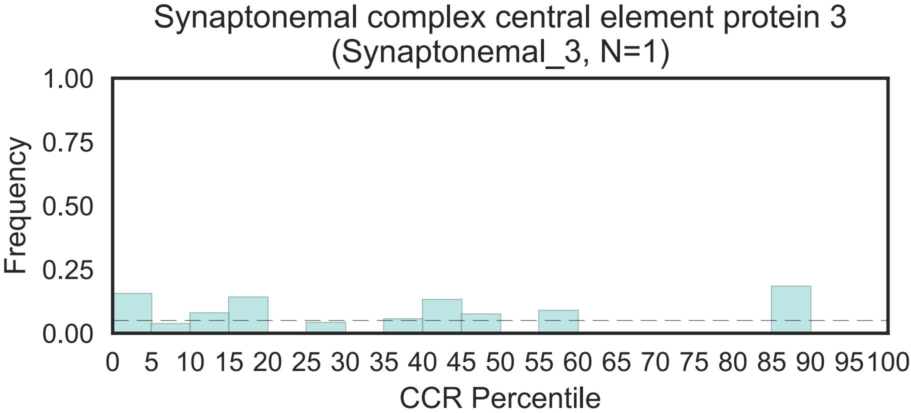

Synaphin protein
(Synaphin, N=4)
Fisher's OR: 0.584; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

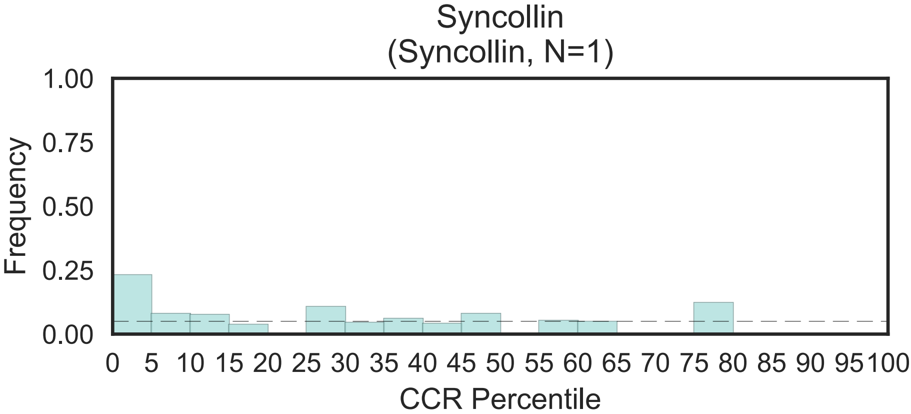

Synapsin, N-terminal domain
(Synapsin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

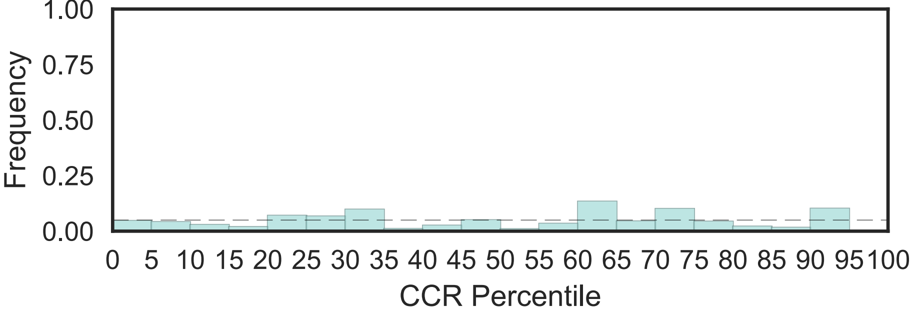

Synapsin, ATP binding domain
(Synapsin_C, N=3)
Fisher's OR: 0.496; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Synapsin N-terminal
(Synapsin_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

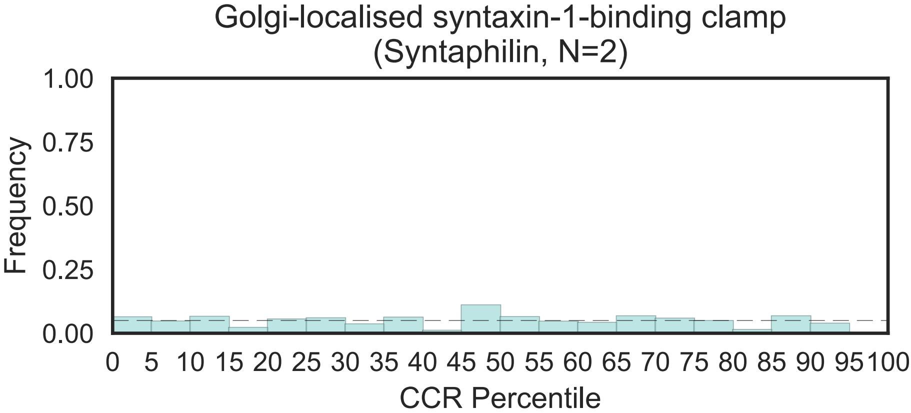

Synaptobrevin
(Synaptobrevin, N=9)
Fisher's OR: 2.33; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

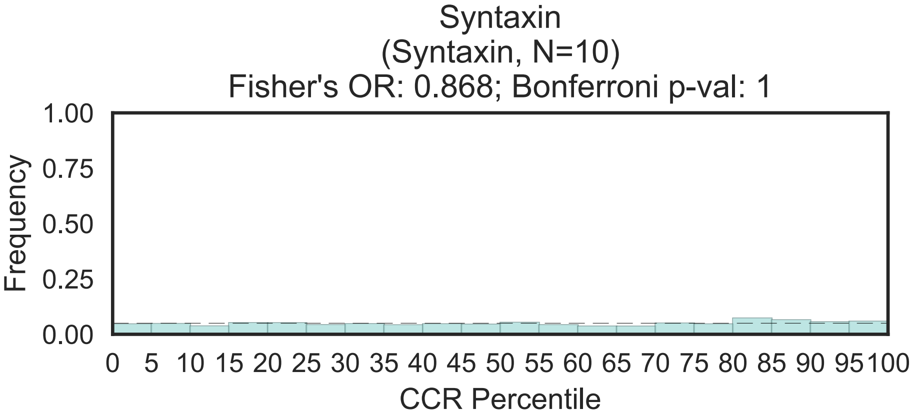

Synaptonemal complex central element protein 3
(Synaptonemal_3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

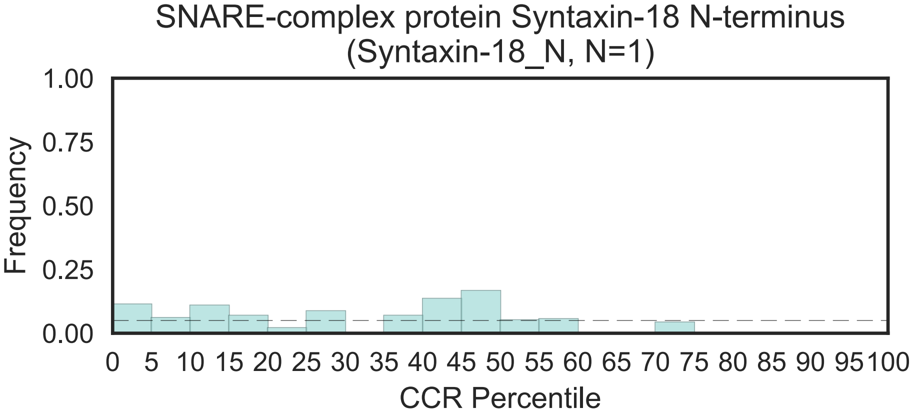

Syncollin
(Syncollin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

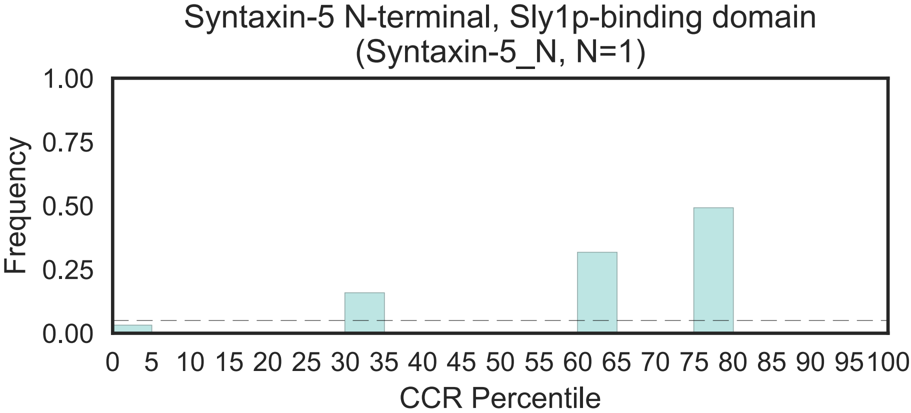


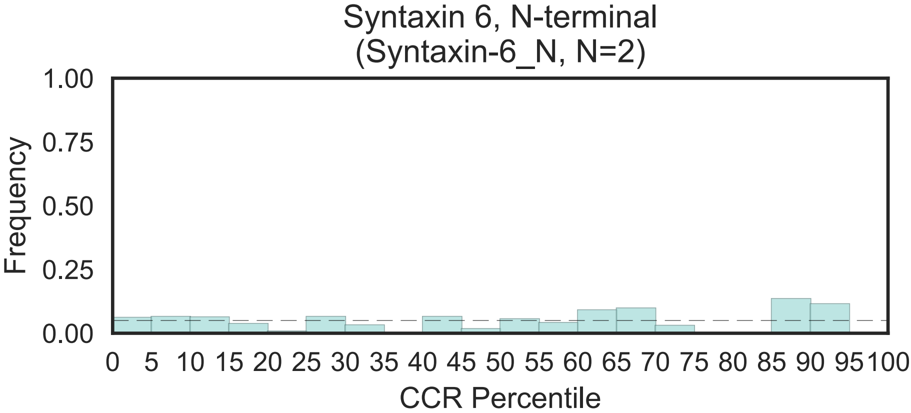
Syndecan domain
(Syndecan, N=7)
Fisher's OR: 0; Bonferroni p-val: 1

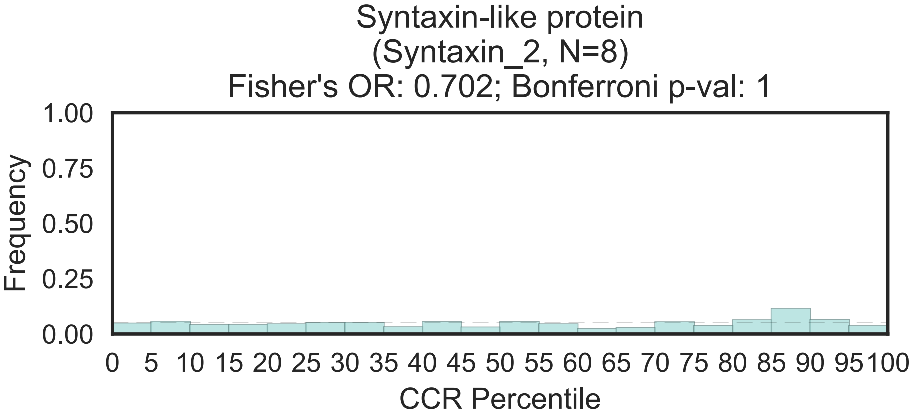

Golgi-localised syntaxin-1-binding clamp
(Syntaphilin, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

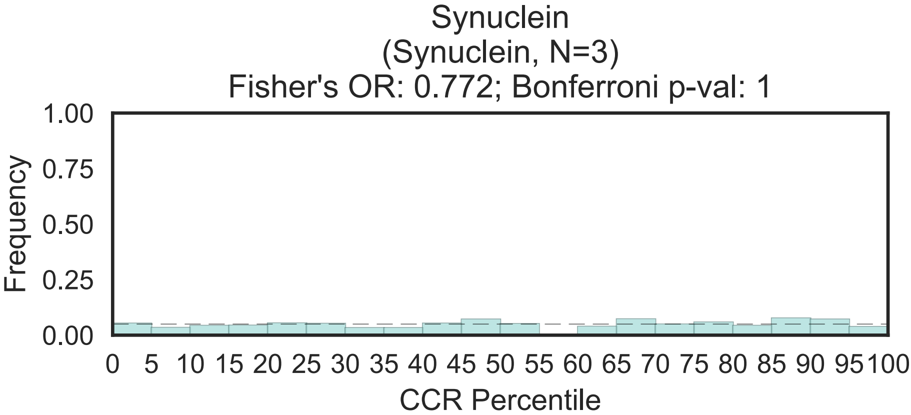

Syntaxin
(Syntaxin, N=10)
Fisher's OR: 0.868; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

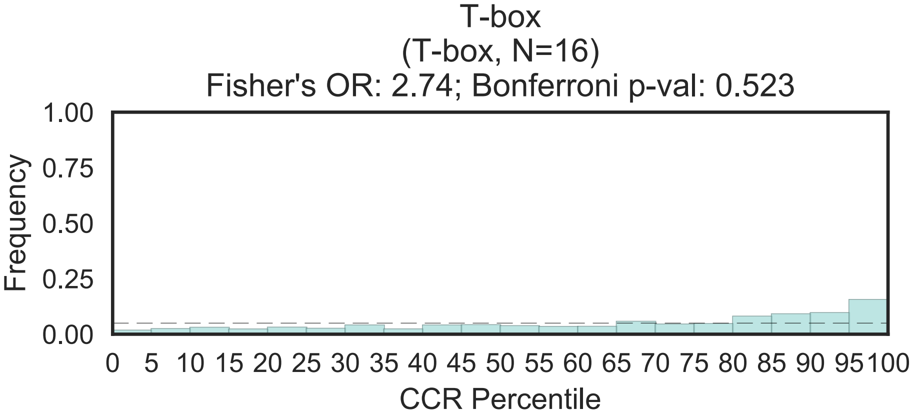

SNARE-complex protein Syntaxin-18 N-terminus
(Syntaxin-18_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Syntaxin-5 N-terminal, Sly1p-binding domain
(Syntaxin-5_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

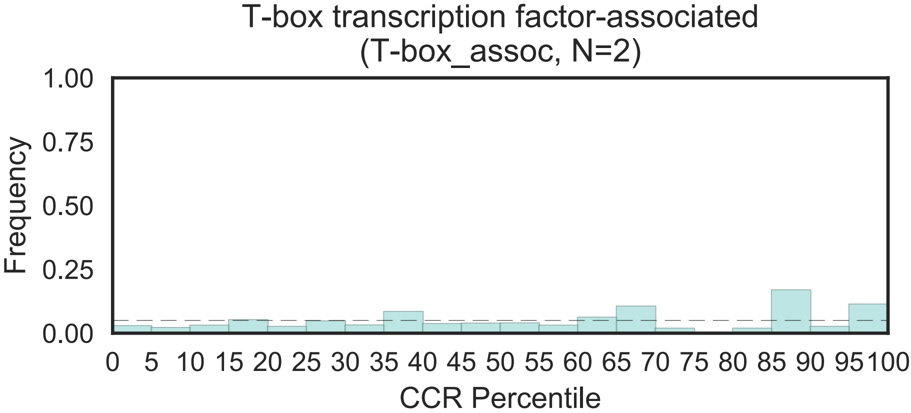

Syntaxin 6, N-terminal
(Syntaxin-6_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Syntaxin-like protein
(Syntaxin_2, N=8)
Fisher's OR: 0.702; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

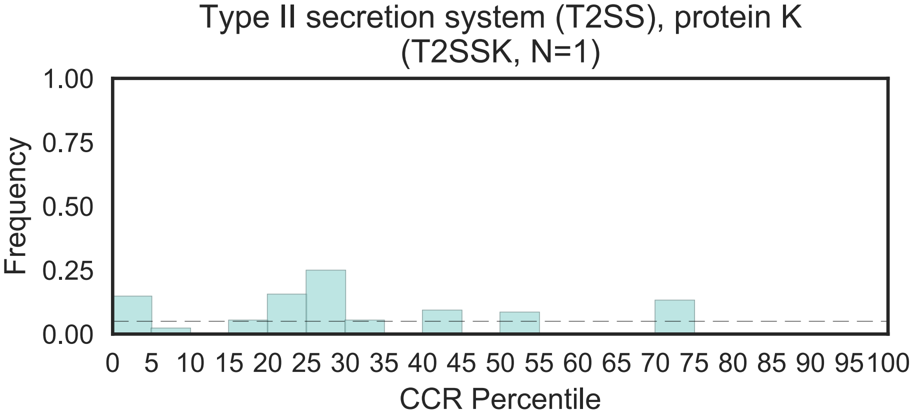

Synuclein
(Synuclein, N=3)
Fisher's OR: 0.772; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

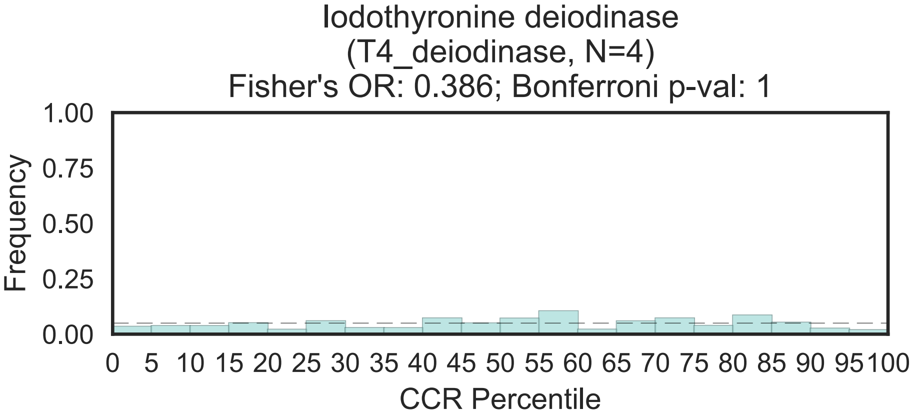


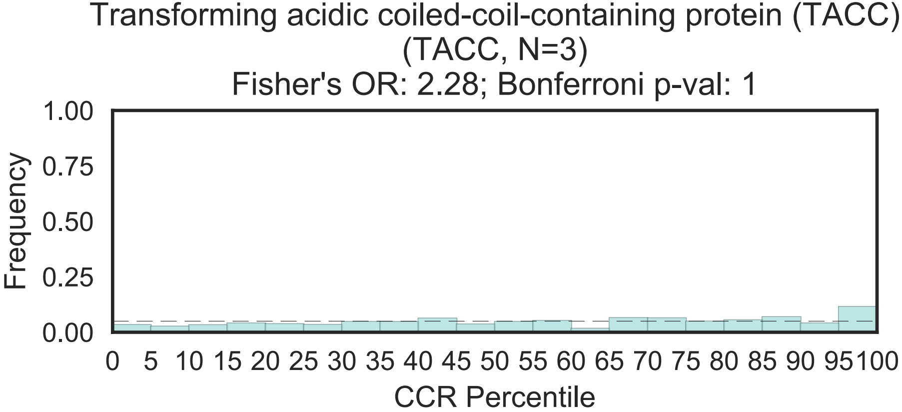
T-box
(T-box, N=16)
Fisher's OR: 2.74; Bonferroni p-val: 0.523

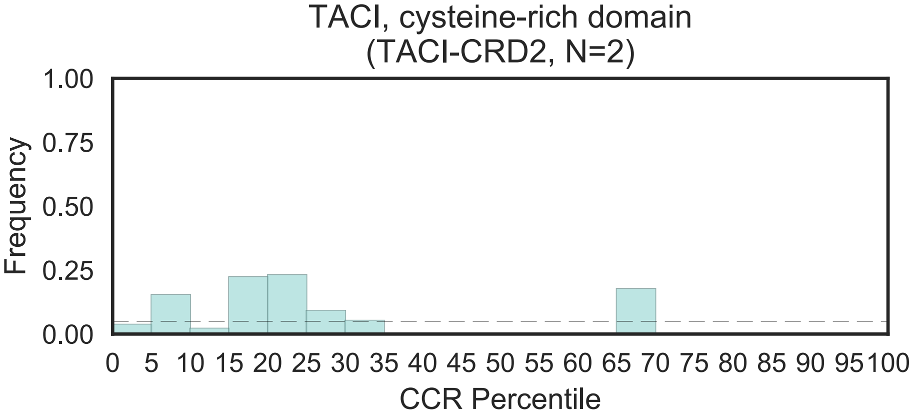


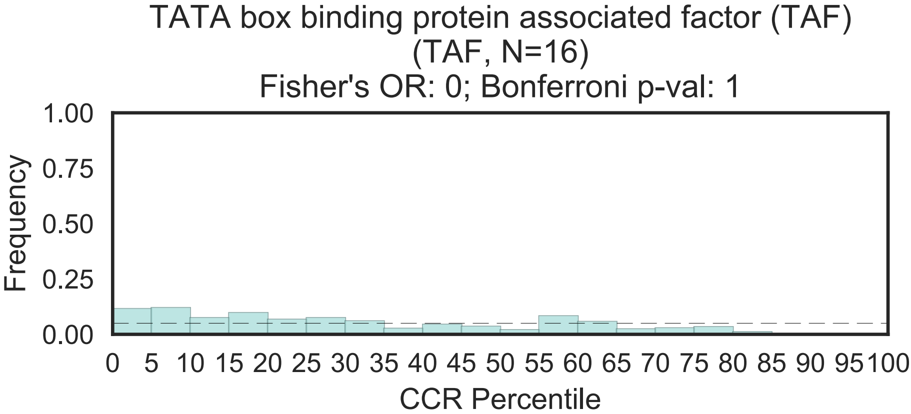
T-box transcription factor-associated
(T-box_assoc, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

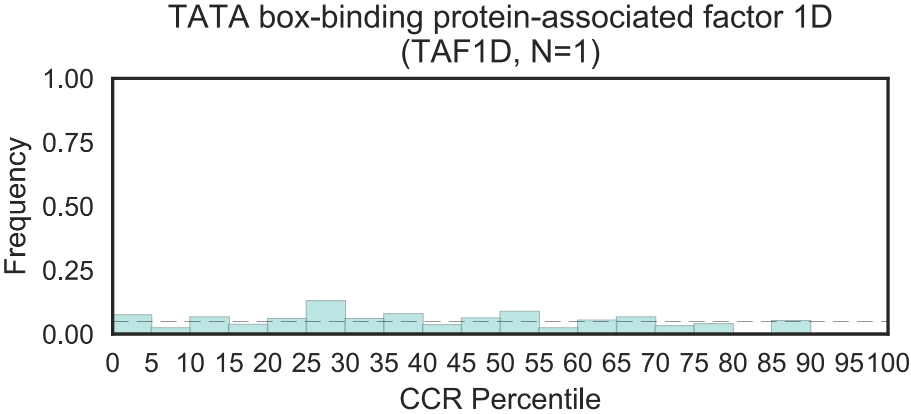

Type II secretion system (T2SS), protein K
(T2SSK, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

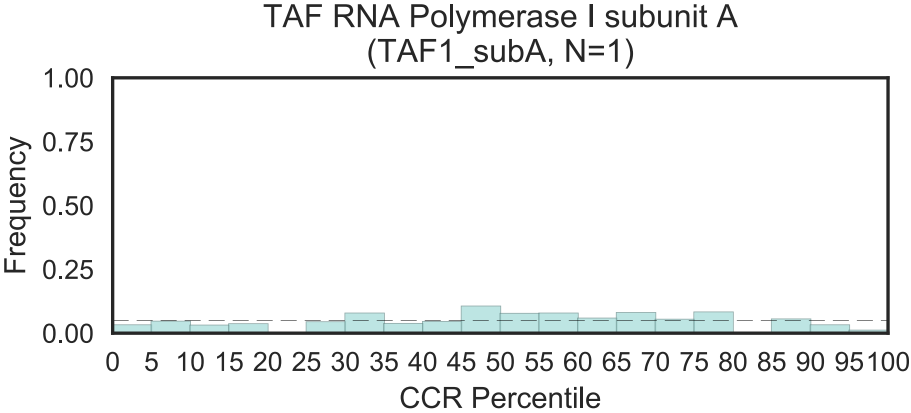

Iodothyronine deiodinase
(T4_deiodinase, N=4)
Fisher's OR: 0.386; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Transforming acidic coiled-coil-containing protein (TACC)
(TACC, N=3)
Fisher's OR: 2.28; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

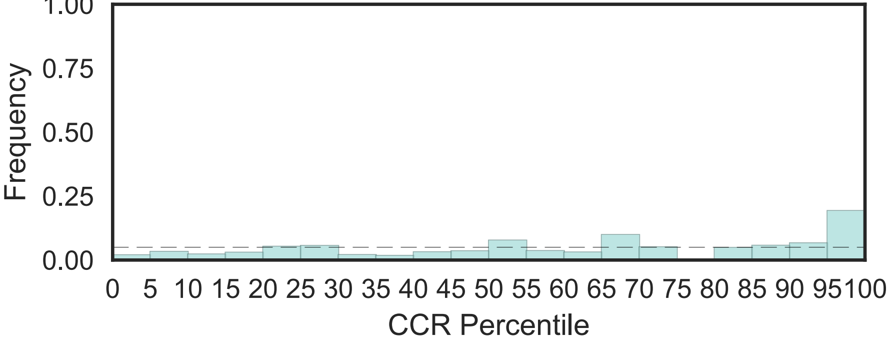

TACI, cysteine-rich domain
(TACI-CRD2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

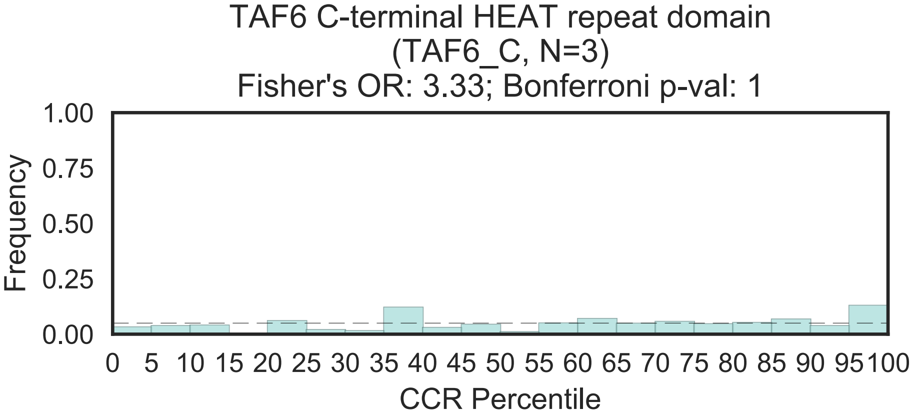

TATA box binding protein associated factor (TAF)
(TAF, N=16)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

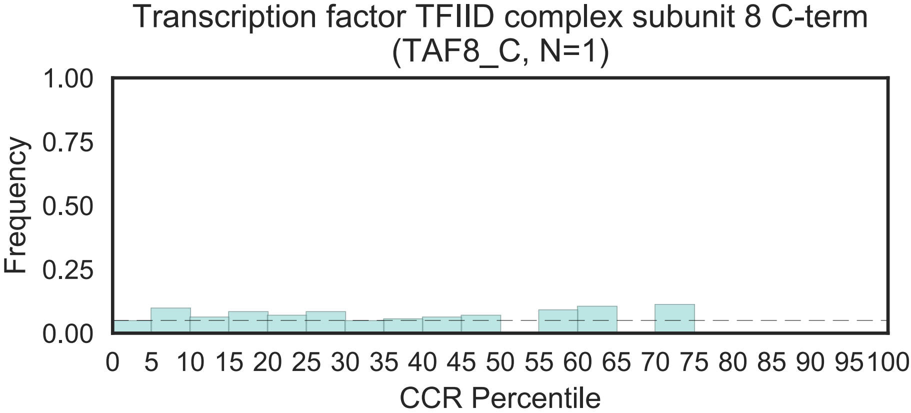

TATA box-binding protein-associated factor 1D
(TAF1D, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

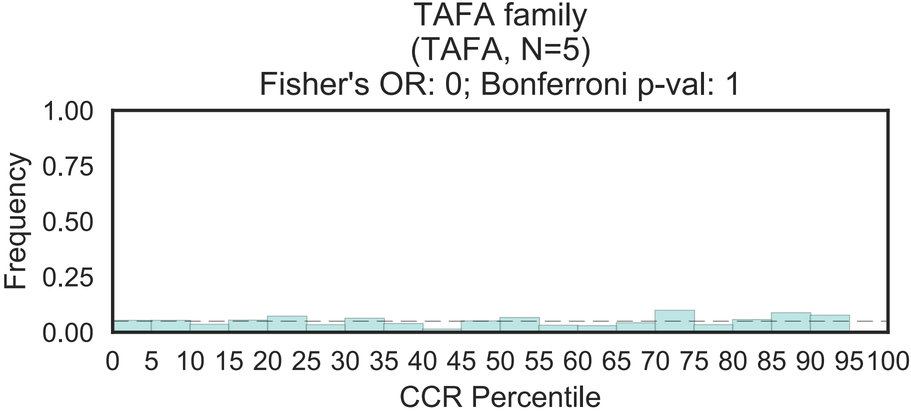

TAF RNA Polymerase I subunit A
(TAF1_subA, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

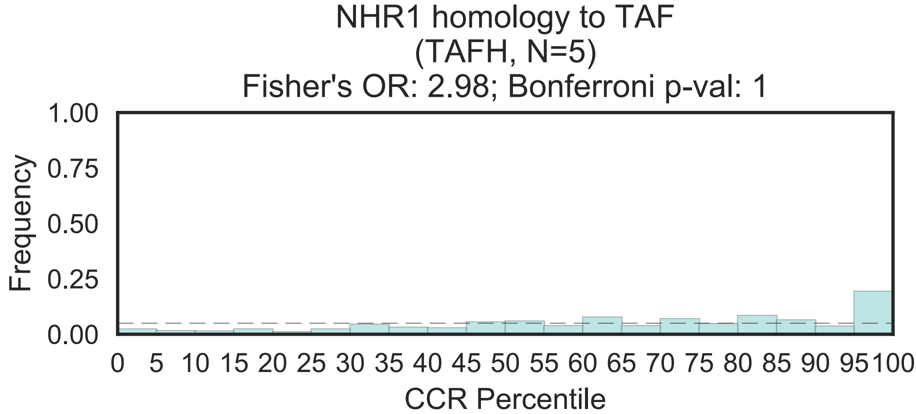
Transcription initiation factor TFIID component TAF4 family (TAF4, N=2)

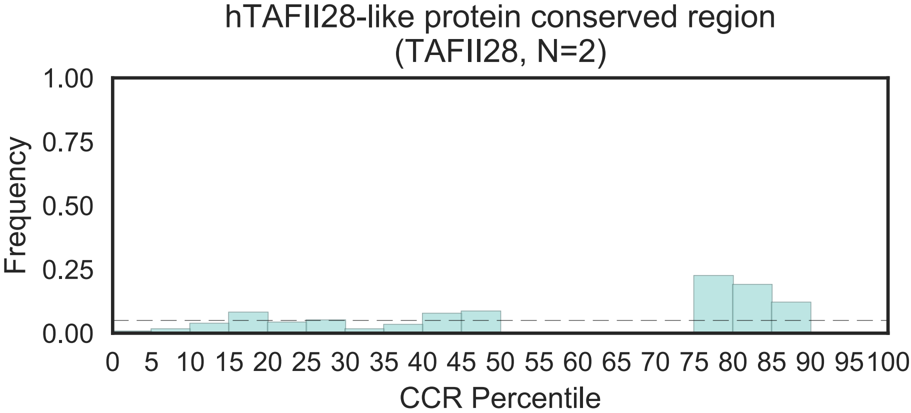


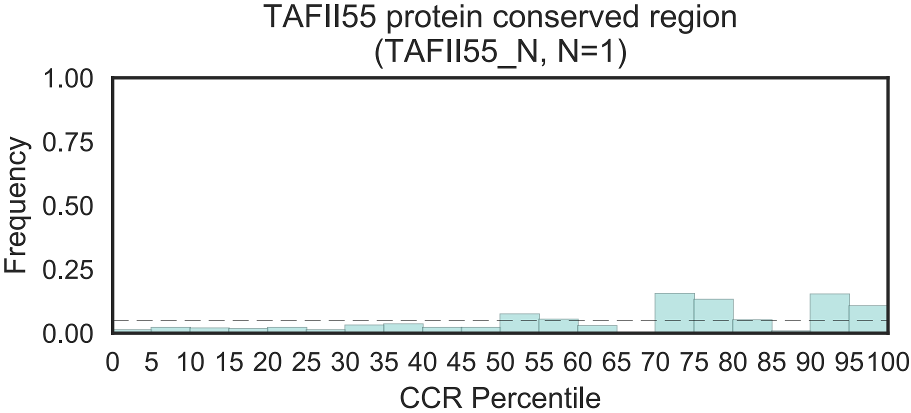

TAF6 C-terminal HEAT repeat domain
(TAF6_C, N=3)
Fisher's OR: 3.33; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

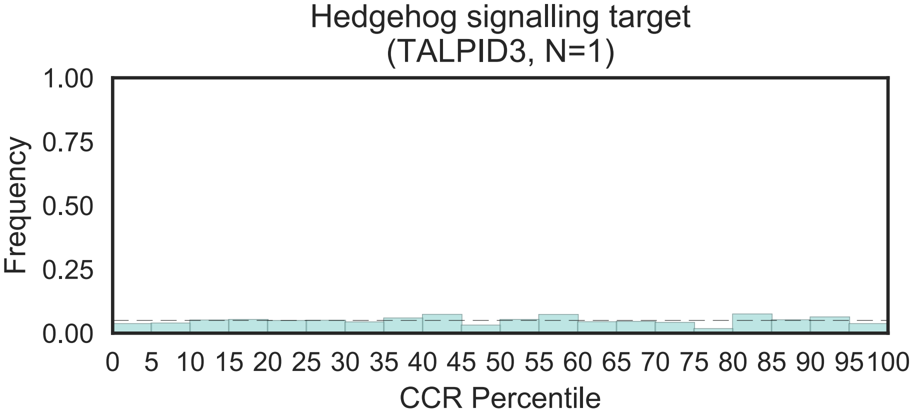

Transcription factor TFIID complex subunit 8 C-term
(TAF8_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

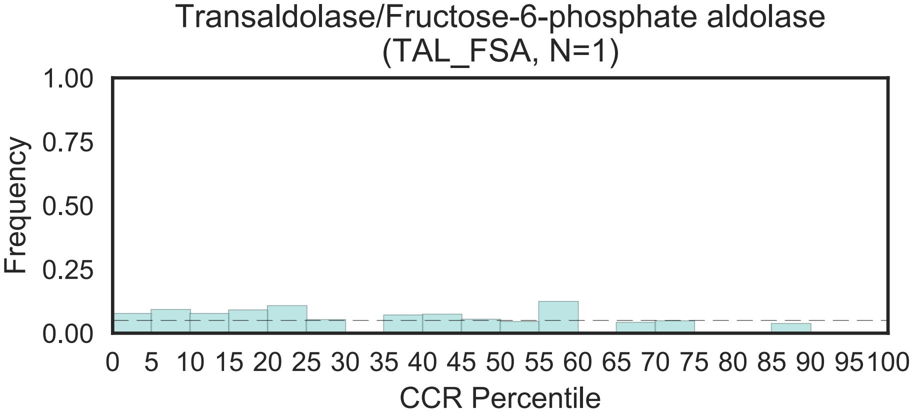

TAFA family
(TAFA, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

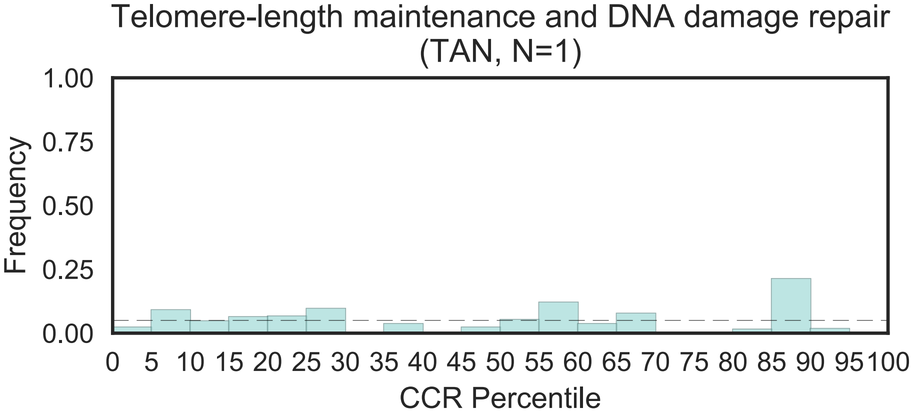

NHR1 homology to TAF
(TAFH, N=5)
Fisher's OR: 2.98; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

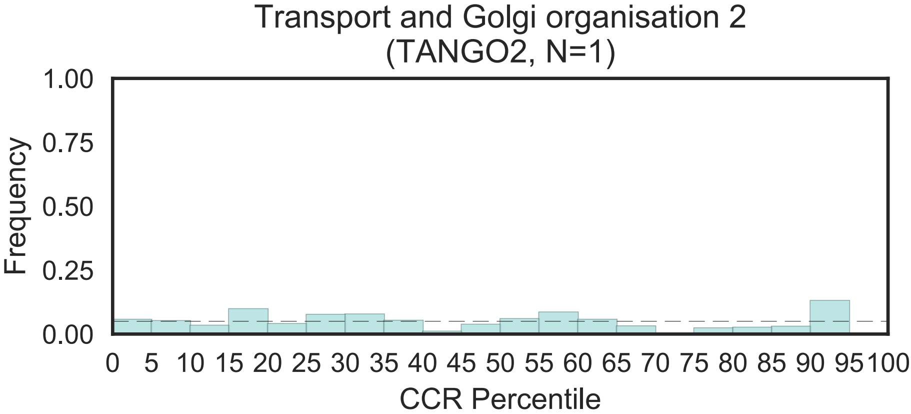

hTAFII28-like protein conserved region
(TAFII28, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

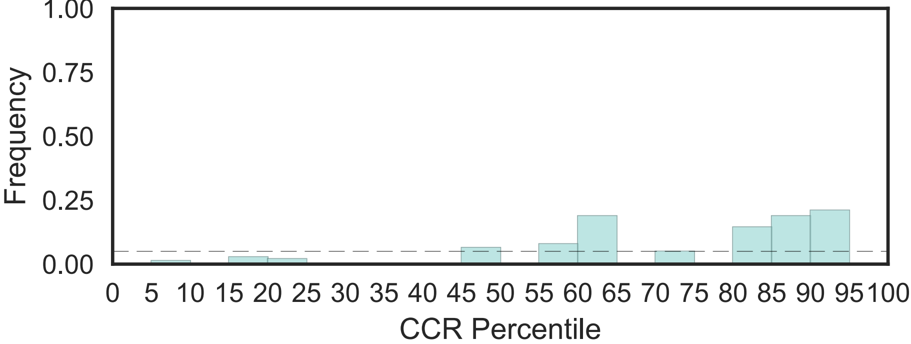

TAFII55 protein conserved region
(TAFII55_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Hedgehog signalling target
(TALPID3, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

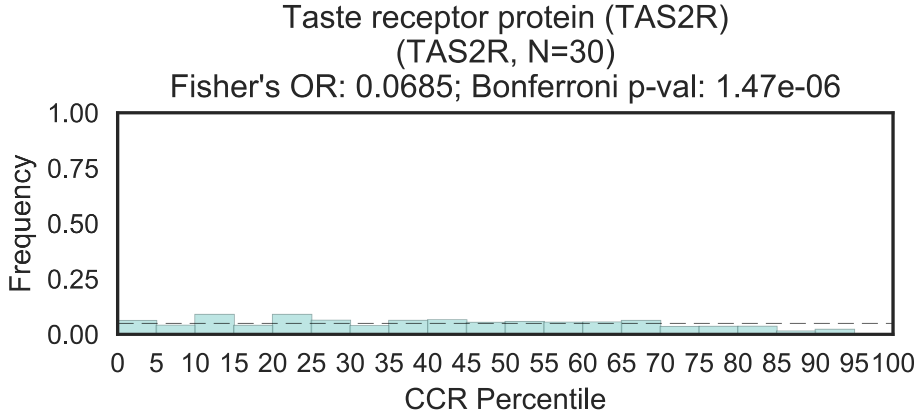

Transaldolase/Fructose-6-phosphate aldolase
(TAL_FSA, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

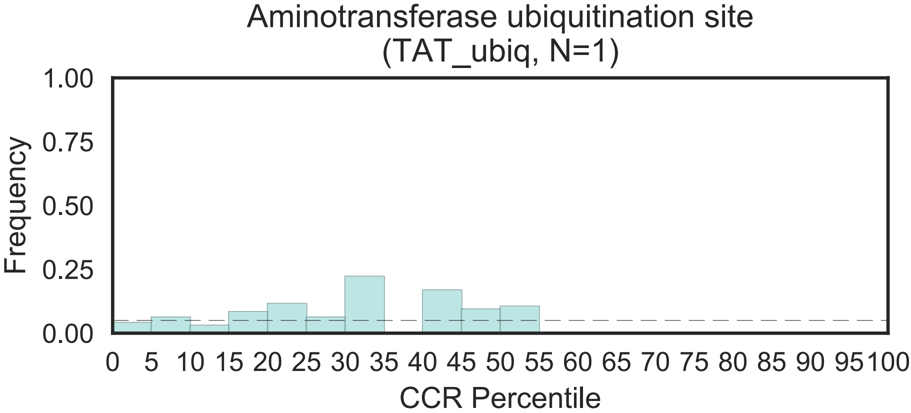

Telomere-length maintenance and DNA damage repair
(TAN, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

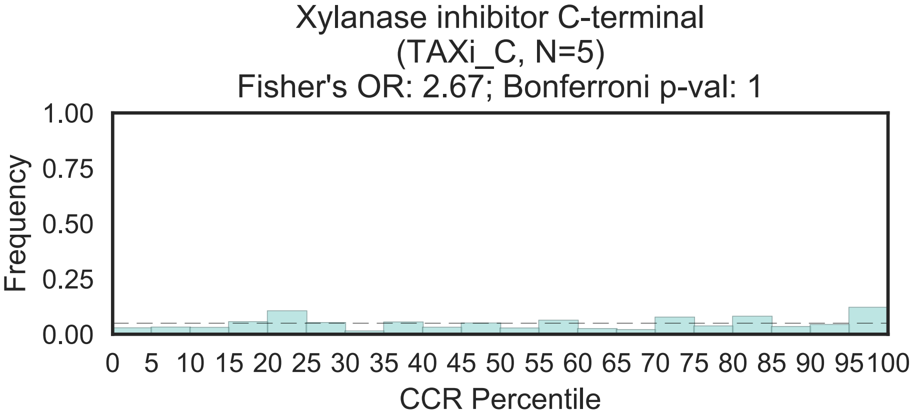

Transport and Golgi organisation 2
(TANGO2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

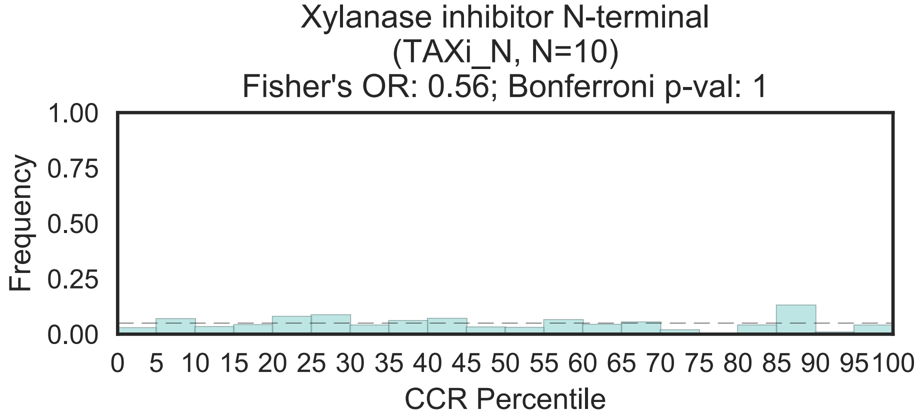


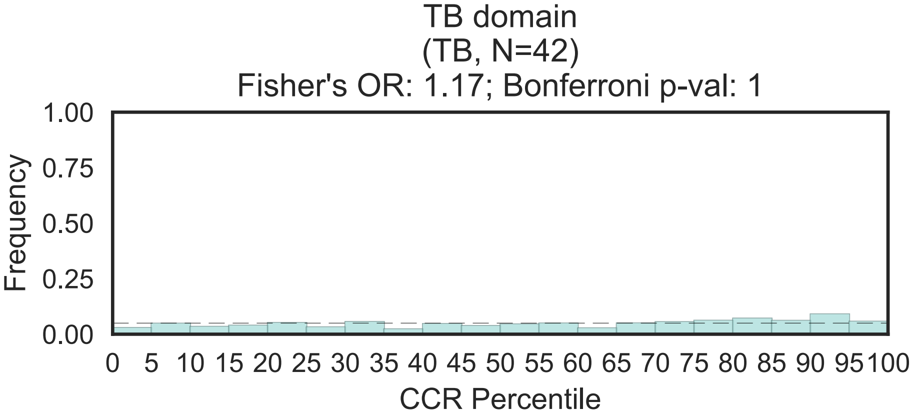
TAP C-terminal domain
(TAP_C, N=1)

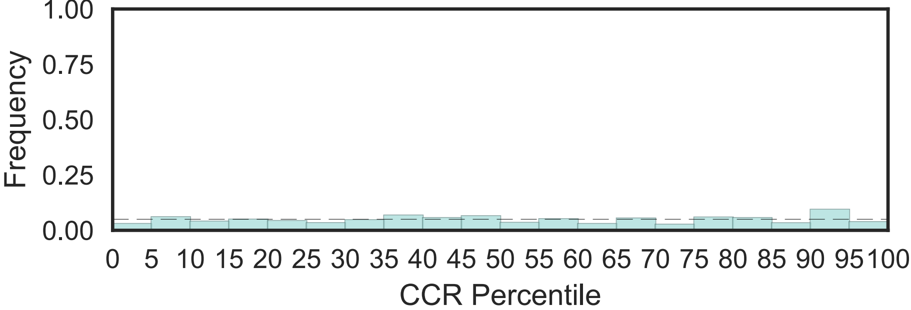

Taste receptor protein (TAS2R)
(TAS2R, N=30)
Fisher's OR: 0.0685; Bonferroni p-val: 1.47e-06
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Aminotransferase ubiquitination site
(TAT_ubiq, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

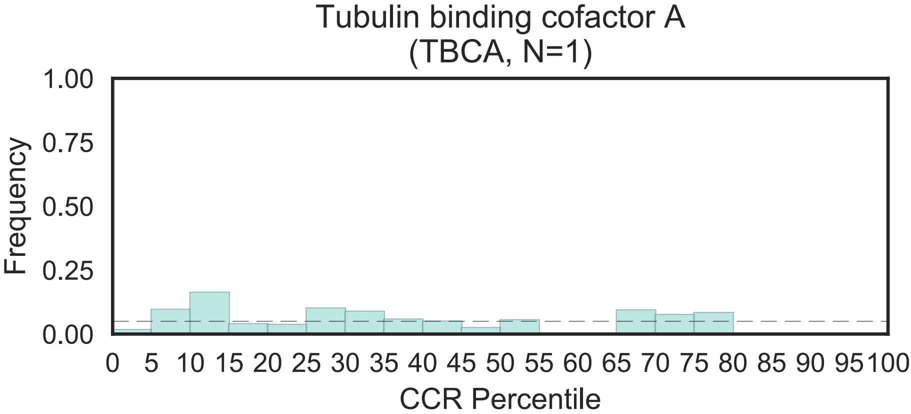

Xylanase inhibitor C-terminal
(TAXi_C, N=5)
Fisher's OR: 2.67; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

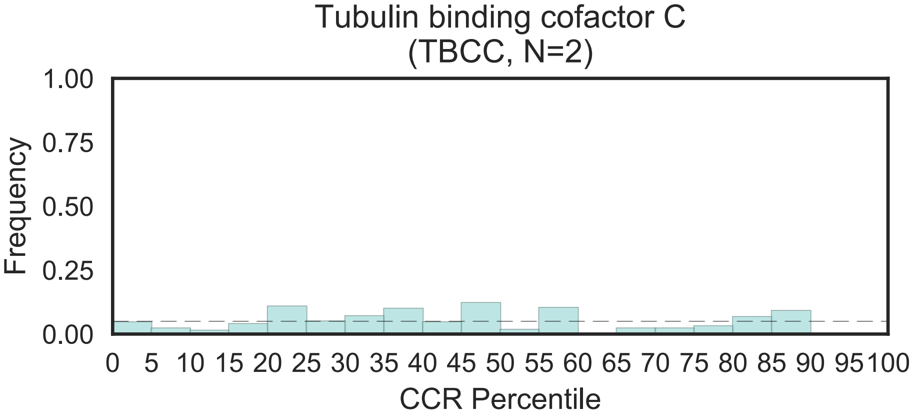

Xylanase inhibitor N-terminal
(TAXi_N, N=10)
Fisher's OR: 0.56; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


TB domain
(TB, N=42)
Fisher's OR: 1.17; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

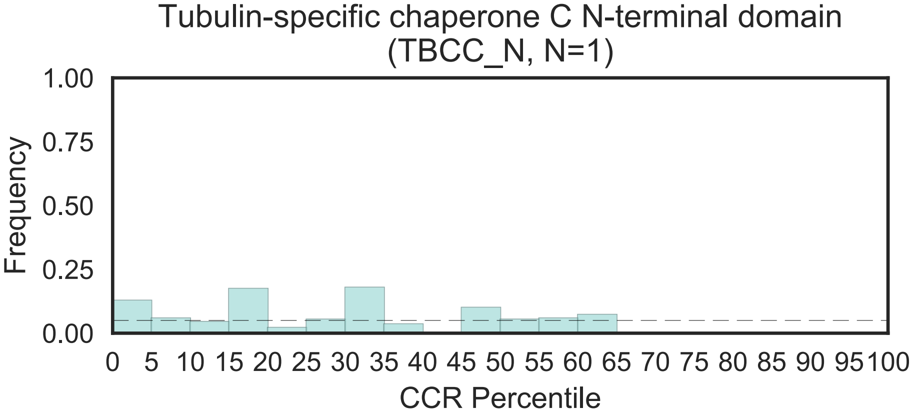


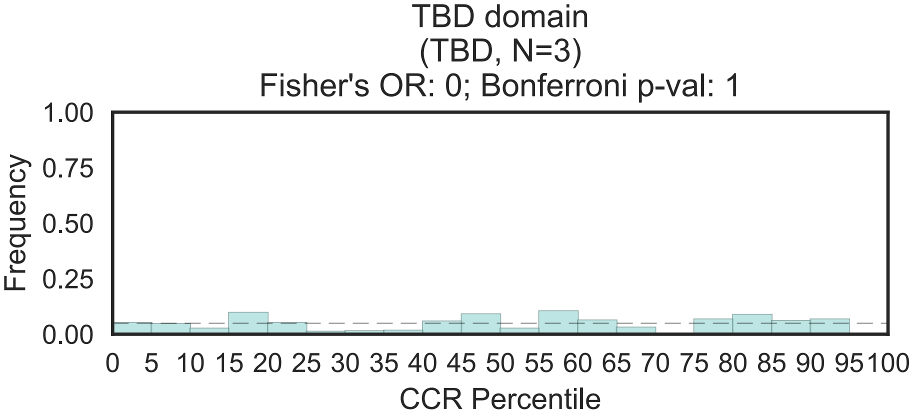
TB2/DP1, HVA22 family
(TB2_DP1_HVA22, N=7)
Fisher's OR: 0.569; Bonferroni p-val: 1

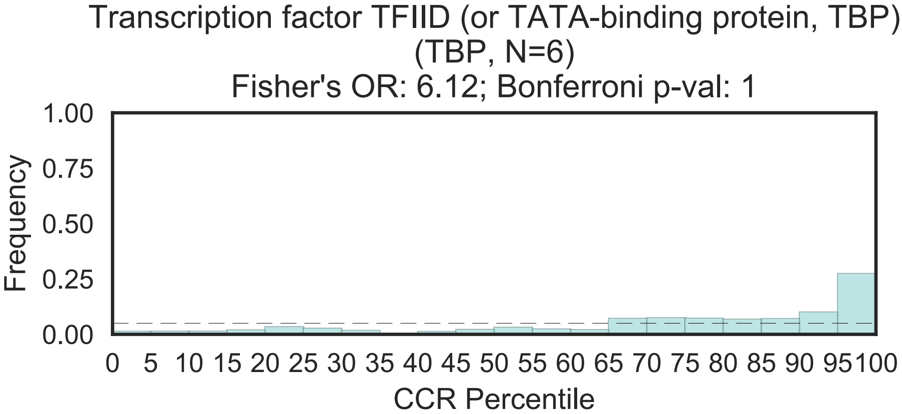

Tubulin binding cofactor A
(TBCA, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile



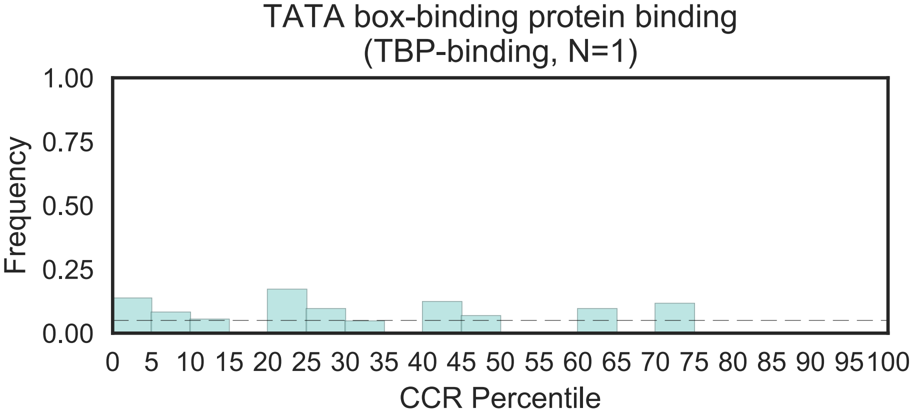
Tubulin binding cofactor C
(TBCC, N=2)

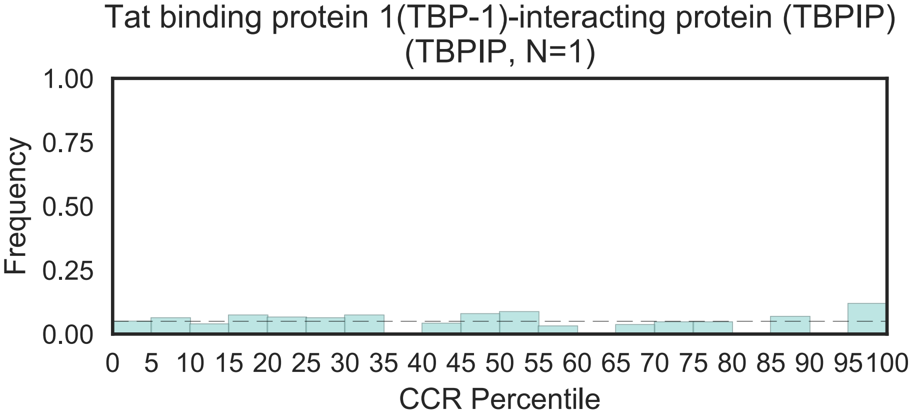

Tubulin-specific chaperone C N-terminal domain
(TBCC_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


TBD domain
(TBD, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

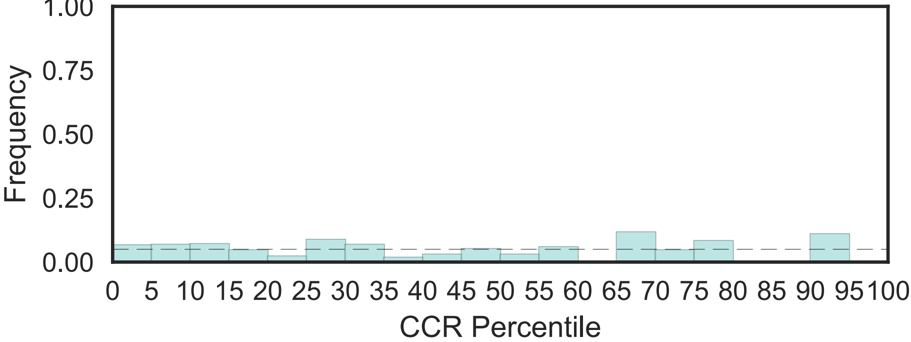


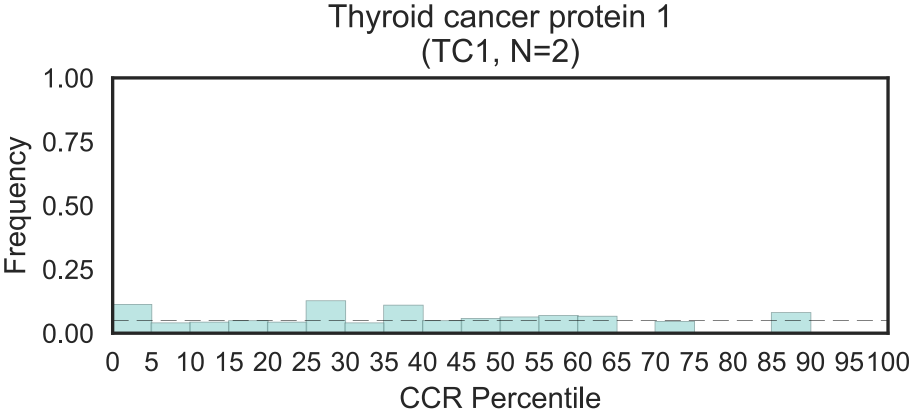
Transcription factor TFIID (or TATA-binding protein, TBP)
(TBP, N=6)
Fisher's OR: 6.12; Bonferroni p-val: 1

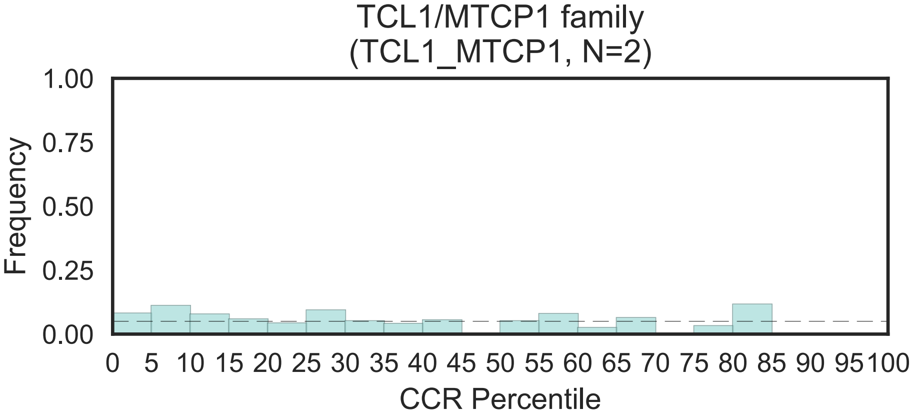

TATA box-binding protein binding
(TBP-binding, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

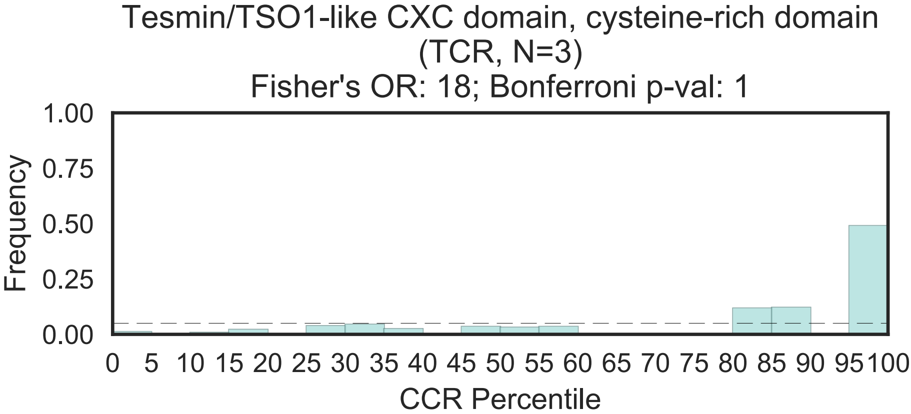

Tat binding protein 1(TBP-1)-interacting protein (TBPIP)
(TBPIP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

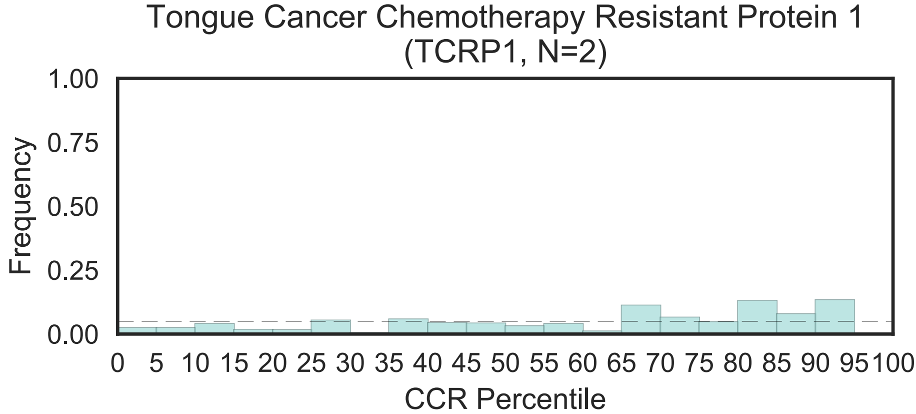
T-box transcription factor
(TBX, N=2)

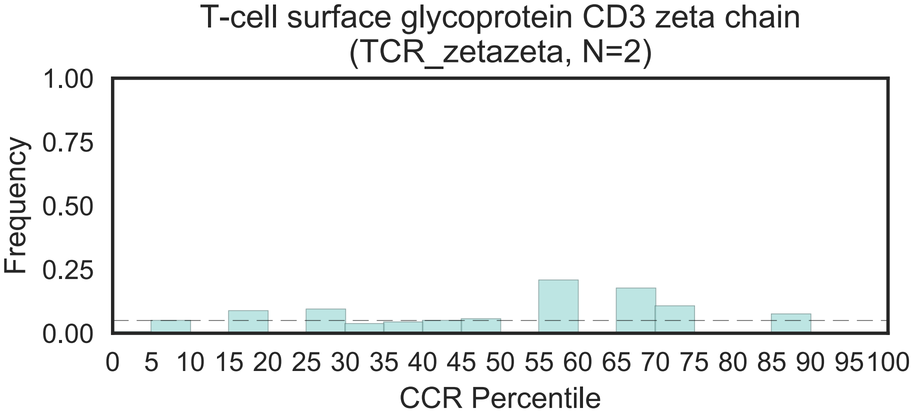


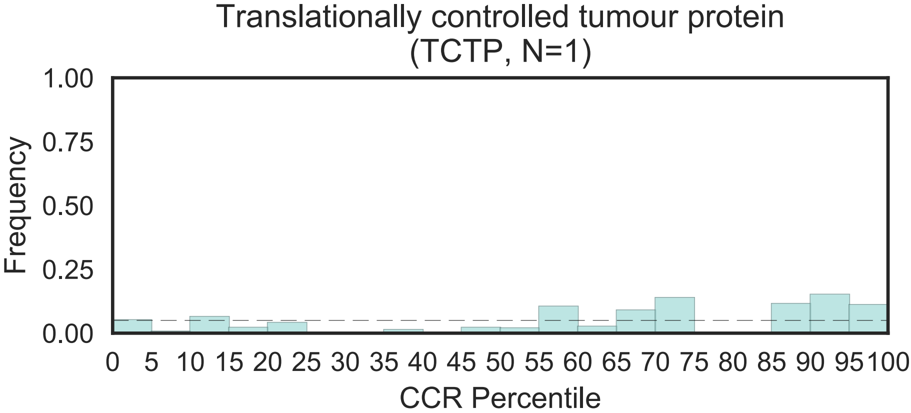

Thyroid cancer protein 1
(TC1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

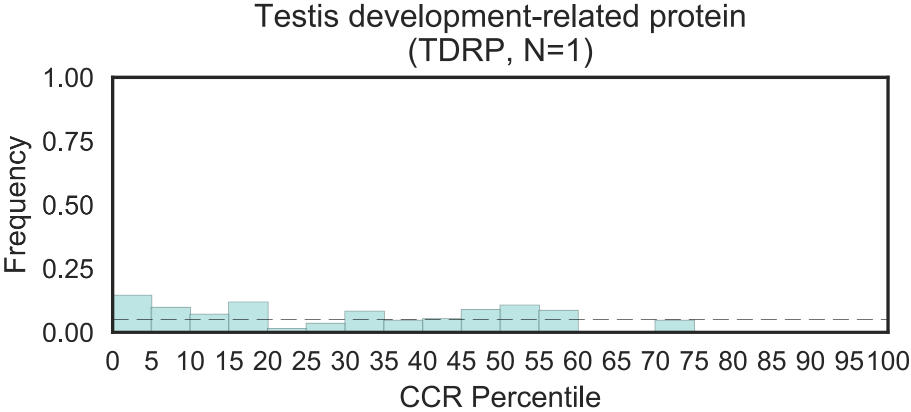

TCL1/MTCP1 family
(TCL1_MTCP1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

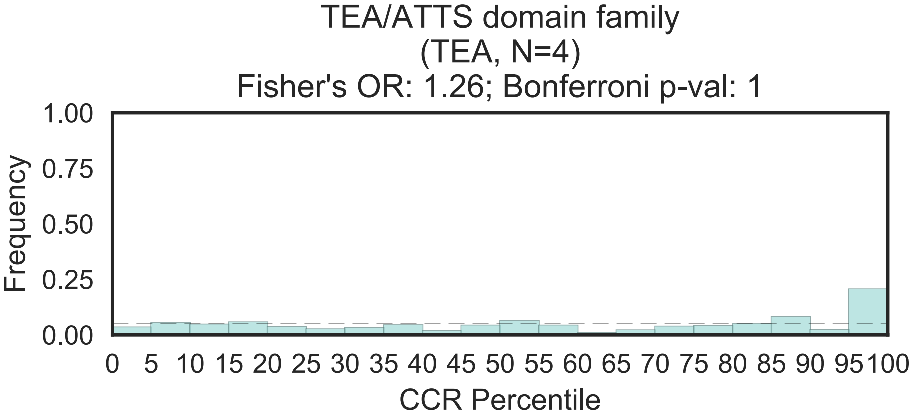

Tesmin/TSO1-like CXC domain, cysteine-rich domain
(TCR, N=3)
Fisher's OR: 18; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Tongue Cancer Chemotherapy Resistant Protein 1
(TCRP1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

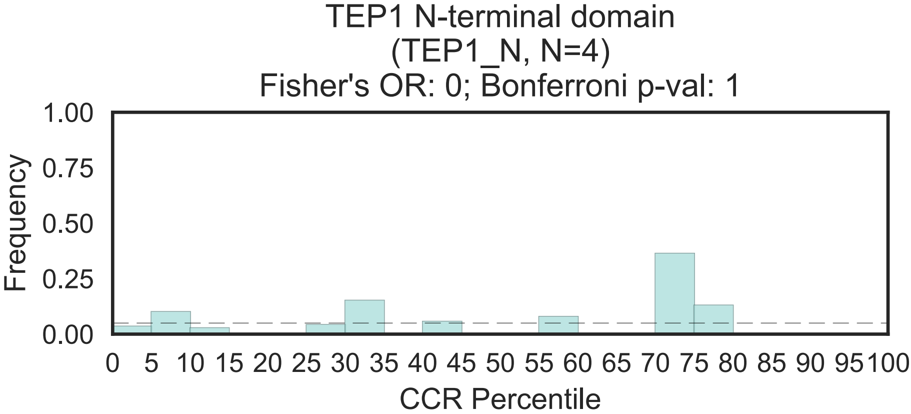

T-cell surface glycoprotein CD3 zeta chain
(TCR_zetazeta, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Translationally controlled tumour protein
(TCTP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

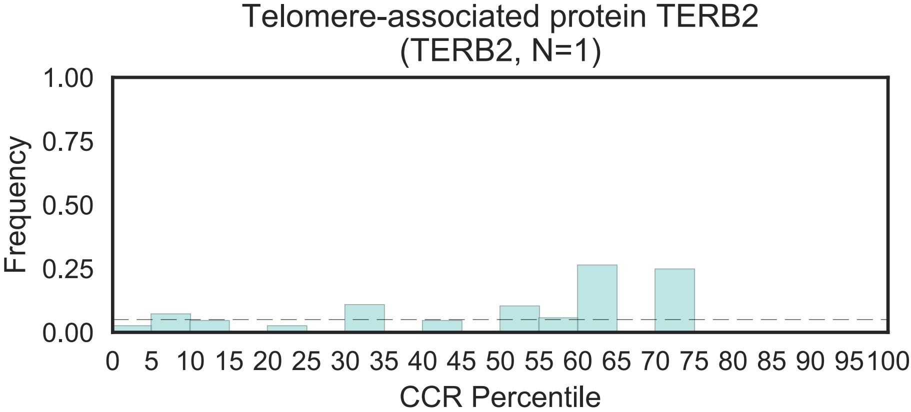

Testis development-related protein
(TDRP, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

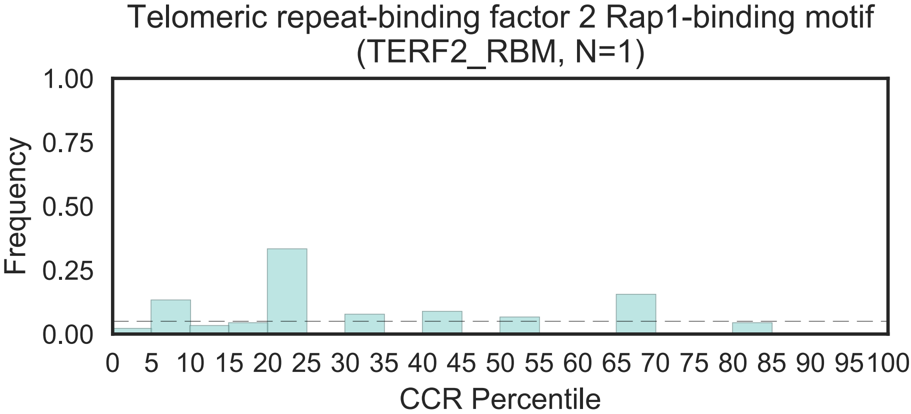


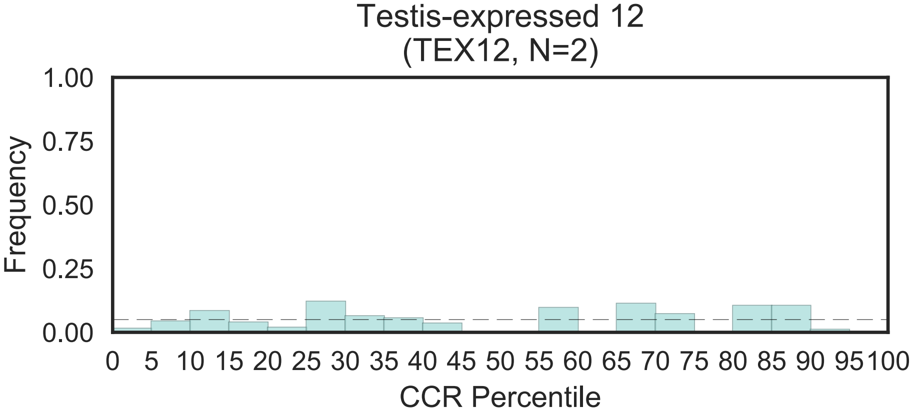
TEA/ATTS domain family
(TEA, N=4)
Fisher's OR: 1.26; Bonferroni p-val: 1

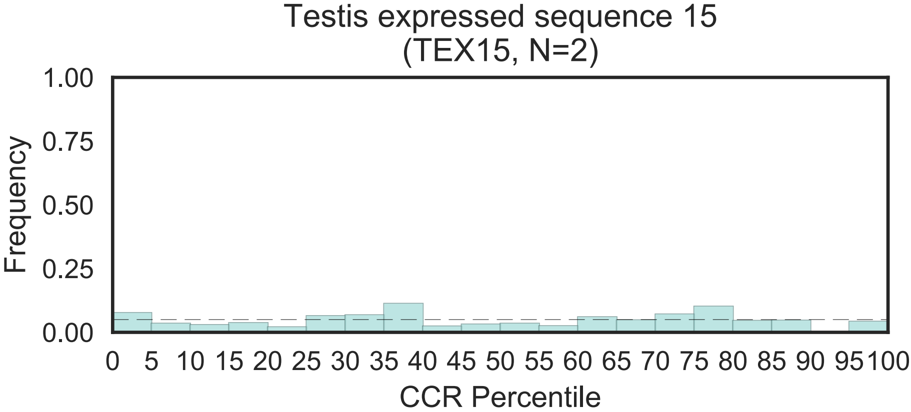


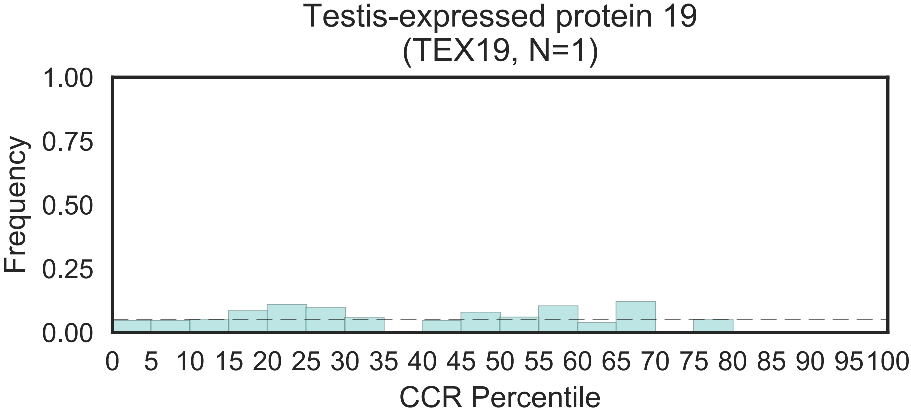
TEP1 N-terminal domain
(TEP1_N, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

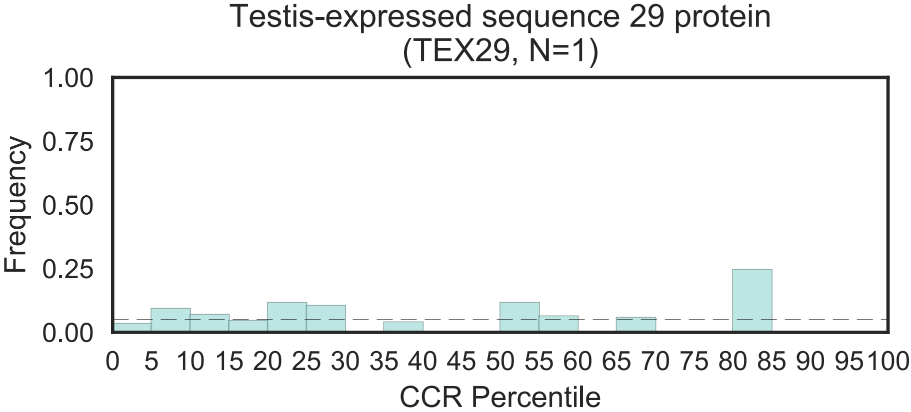

Telomere-associated protein TERB2
(TERB2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

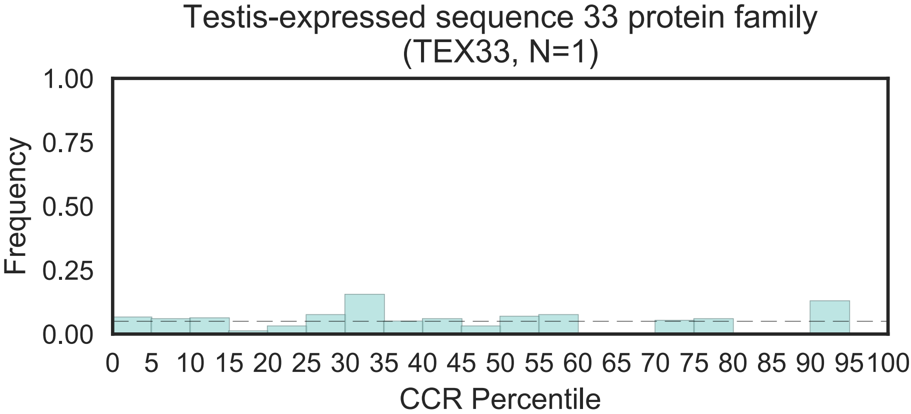

Telomeric repeat-binding factor 2 Rap1-binding motif
(TERF2_RBM, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

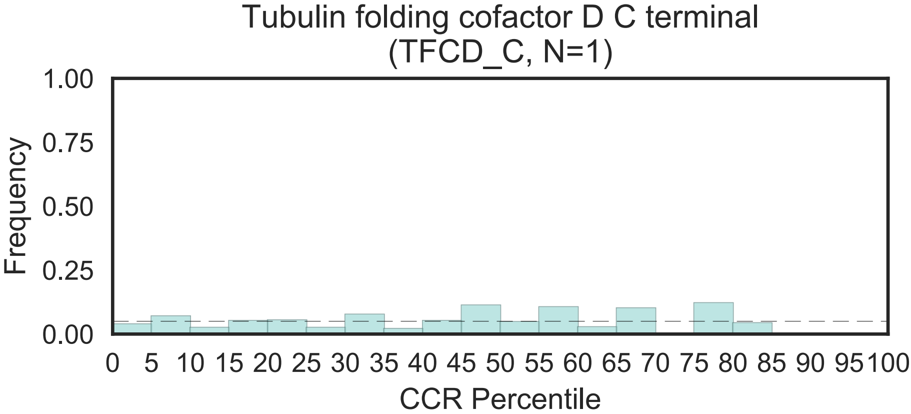

Testis-expressed 12
(TEX12, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

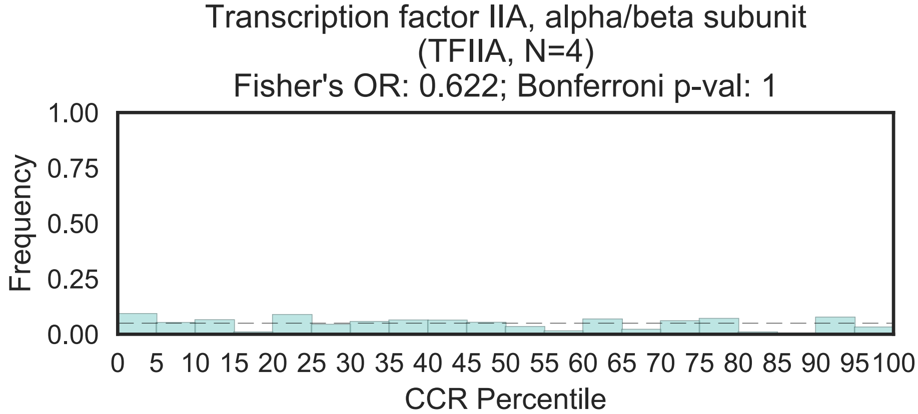

Testis expressed sequence 15
(TEX15, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

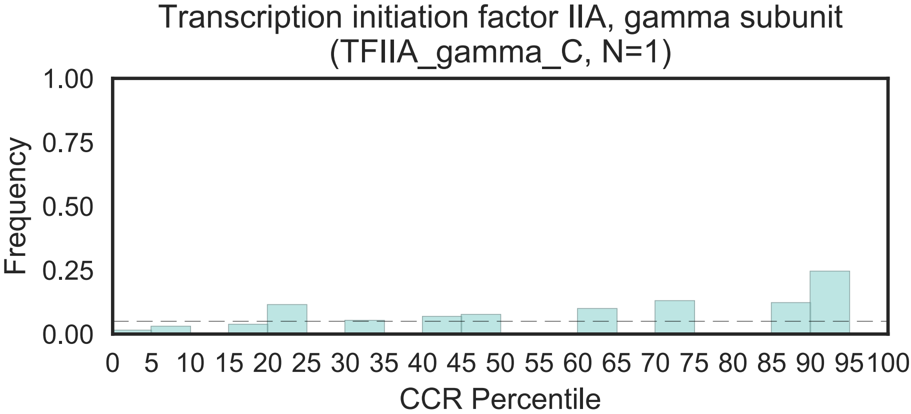

Testis-expressed protein 19
(TEX19, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

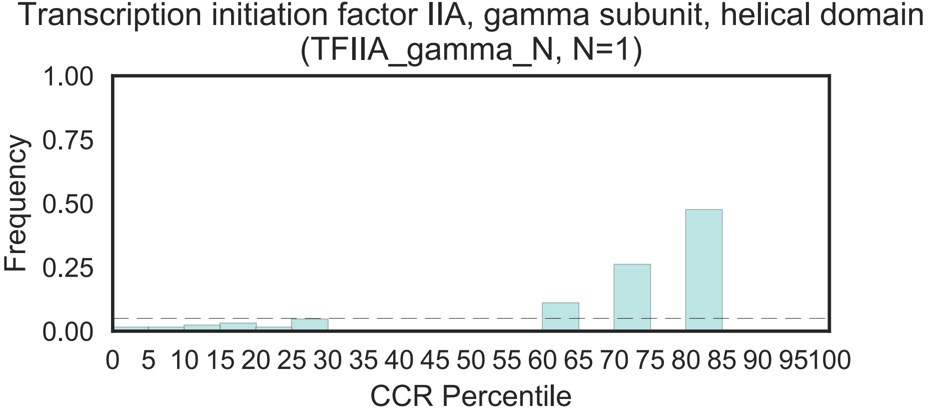

Testis-expressed sequence 29 protein
(TEX29, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

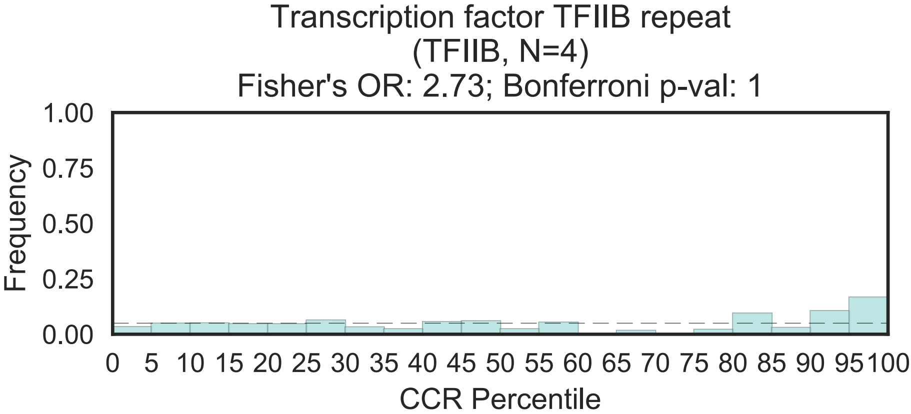

Testis-expressed sequence 33 protein family
(TEX33, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

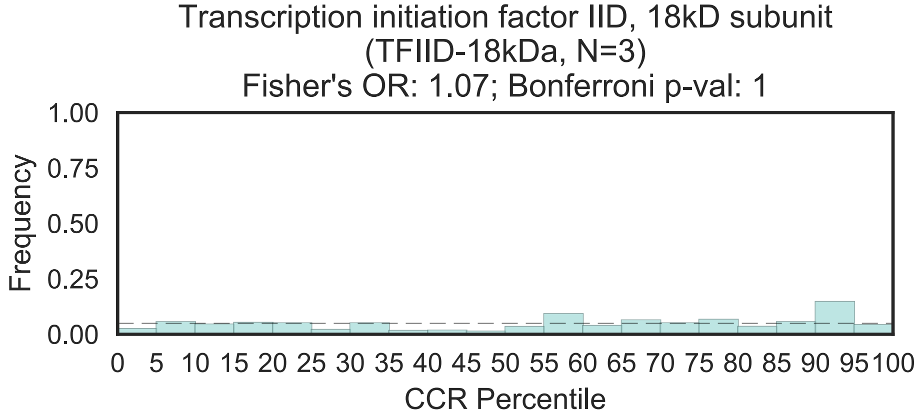

Tubulin folding cofactor D C terminal
(TFCD_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

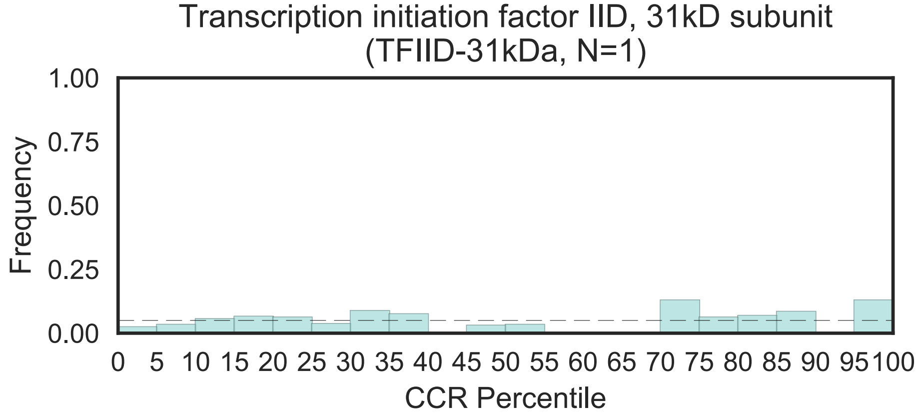

Transcription factor IIA, alpha/beta subunit
(TFIIA, N=4)
Fisher's OR: 0.622; Bonferroni p-val: 1

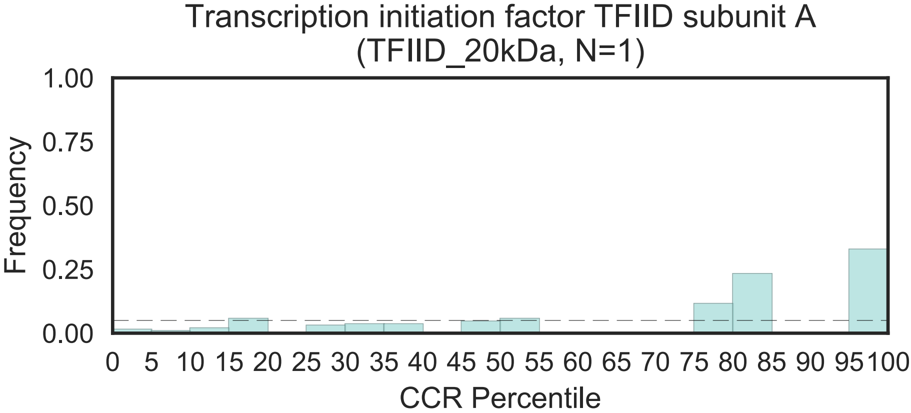

Transcription initiation factor IIA, gamma subunit
(TFIIA_gamma_C, N=1)

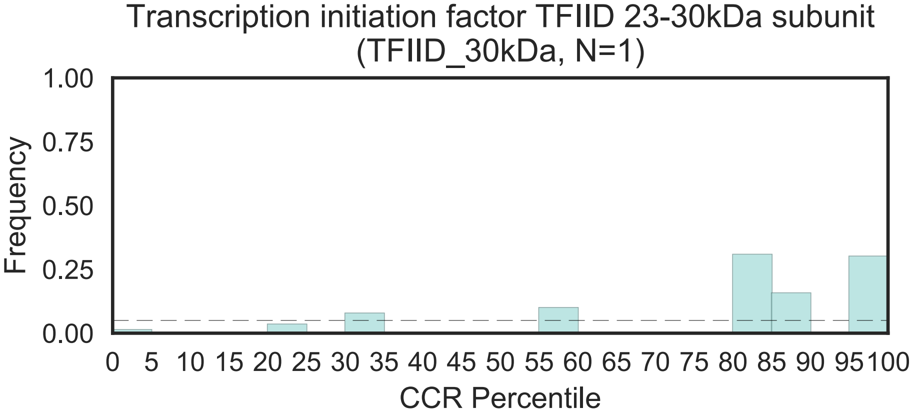

Transcription initiation factor IIA, gamma subunit, helical domain
(TFIIA_gamma_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Transcription factor TFIIB repeat
(TFIIB, N=4)
Fisher's OR: 2.73; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

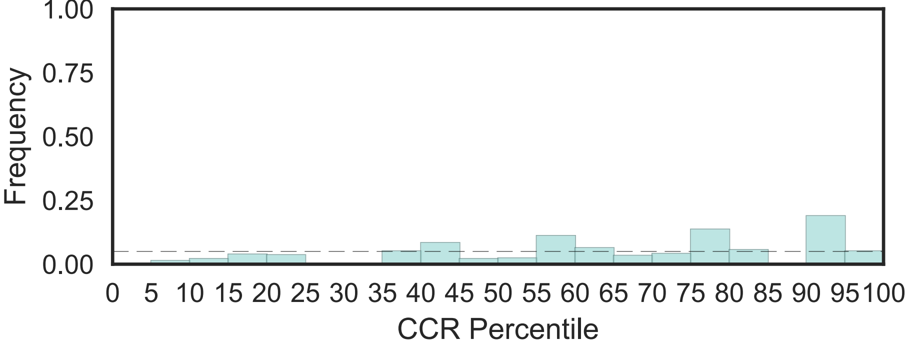

Transcription initiation factor IID, 18kD subunit
(TFIID-18kDa, N=3)
Fisher's OR: 1.07; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

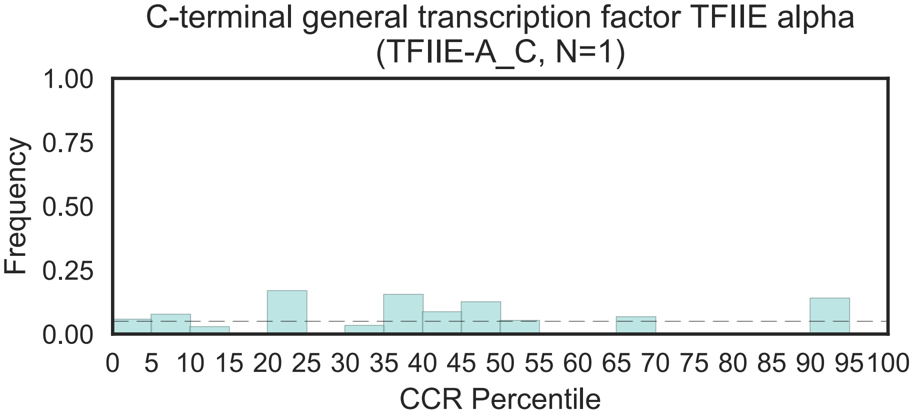

Transcription initiation factor IID, 31kD subunit
(TFIID-31kDa, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

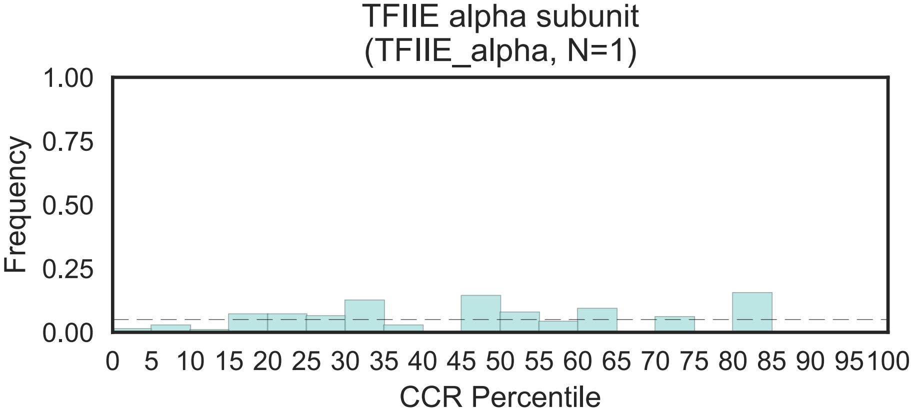

Transcription initiation factor TFIID subunit A
(TFIID_20kDa, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

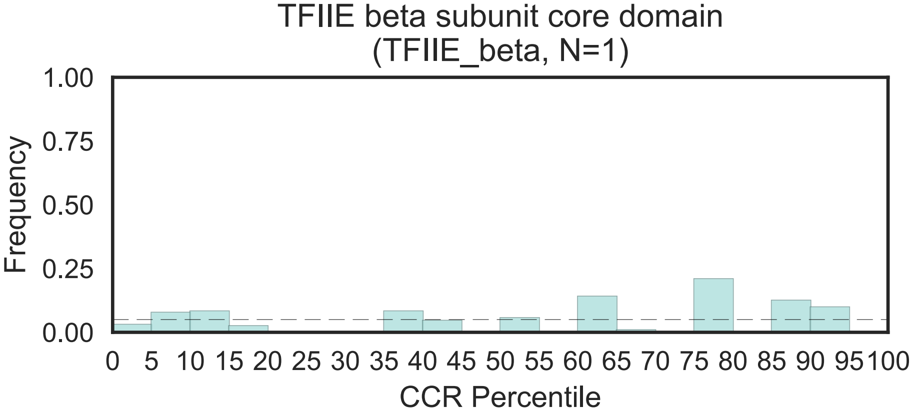

Transcription initiation factor TFIID 23-30kDa subunit
(TFIID_30kDa, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

WD40 associated region in TFIID subunit, NTD2 domain
(TFIID_NTD2, N=2)

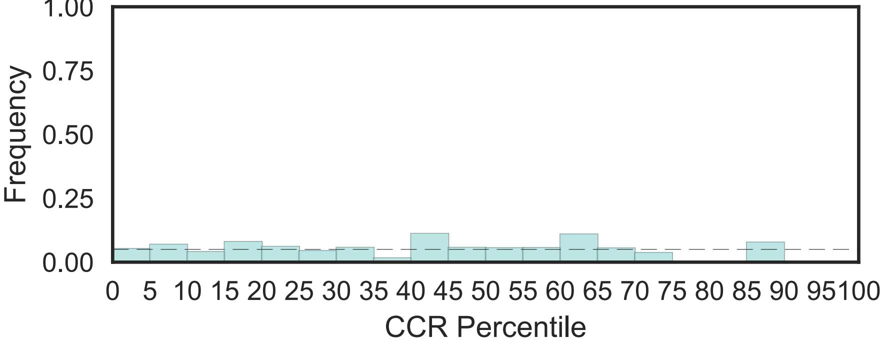


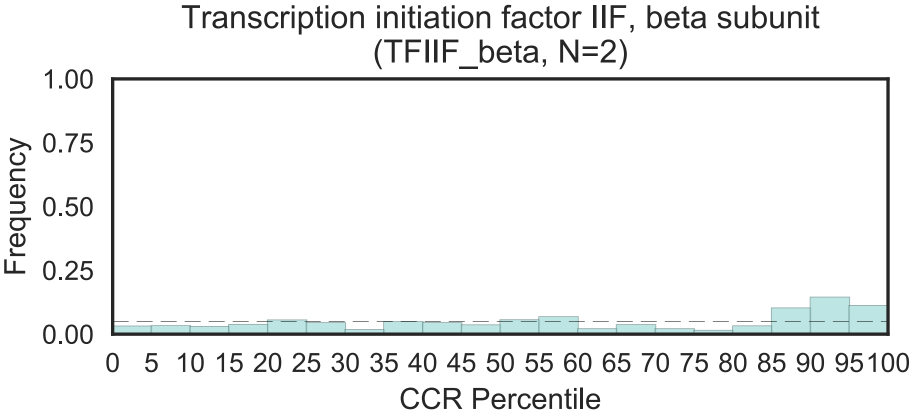

C-terminal general transcription factor TFIIE alpha
(TFIIE-A_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

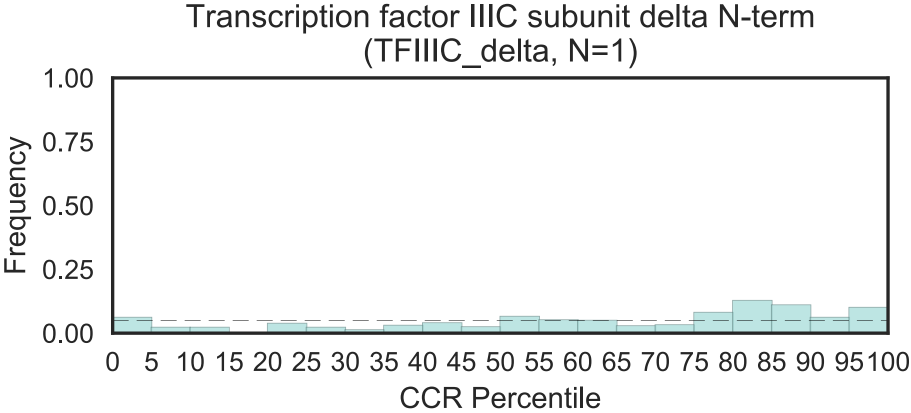

TFIIE alpha subunit
(TFIIE_alpha, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

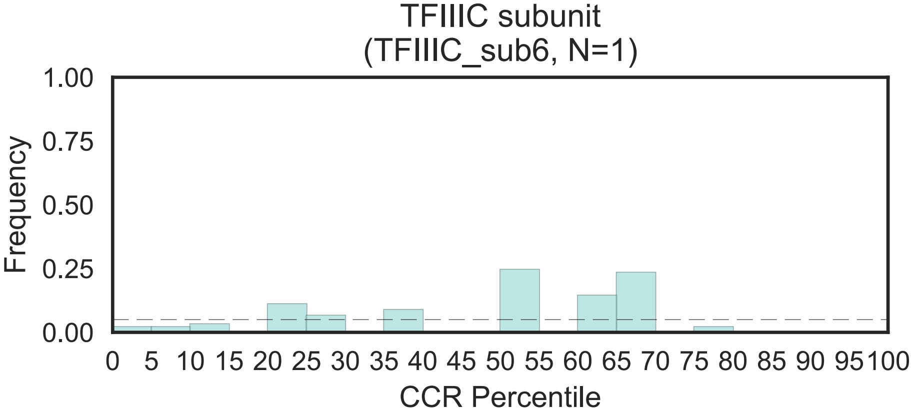

TFIIE beta subunit core domain
(TFIIE_beta, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

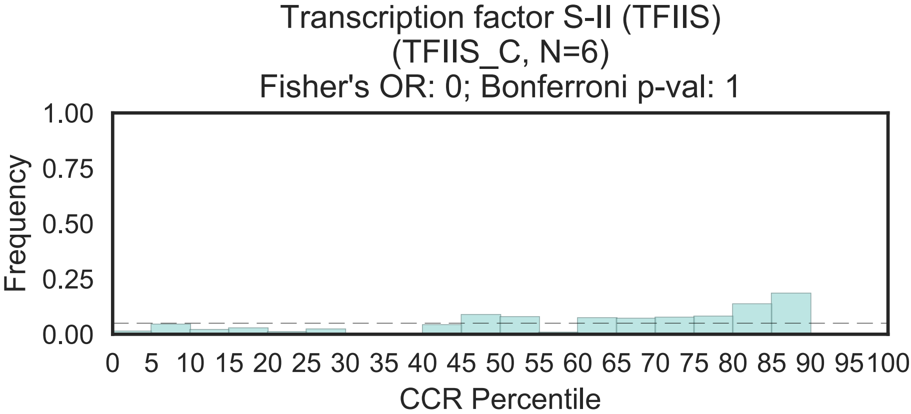
Transcription initiation factor IIF, alpha subunit (TFIIF-alpha) (TFIIF_alpha, N=1)

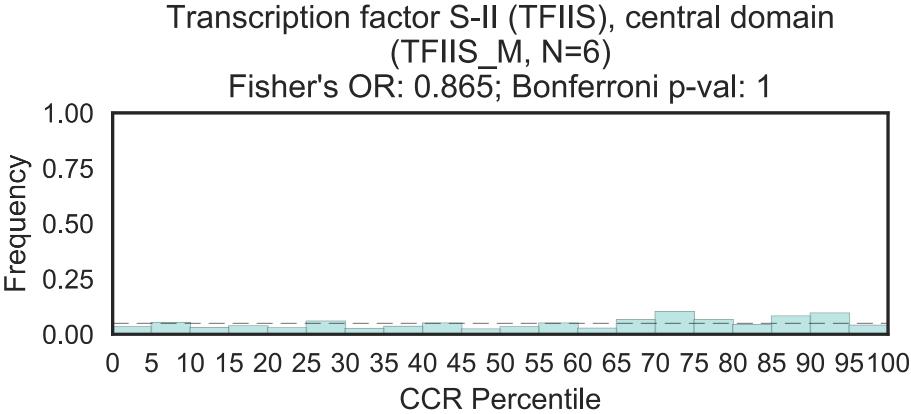


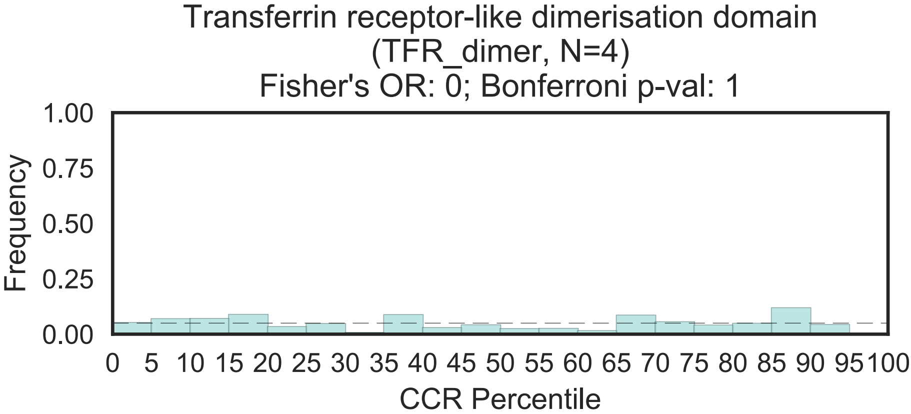

Transcription initiation factor IIF, beta subunit
(TFIIF_beta, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Transcription factor IIIC subunit delta N-term
(TFIIIC_delta, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

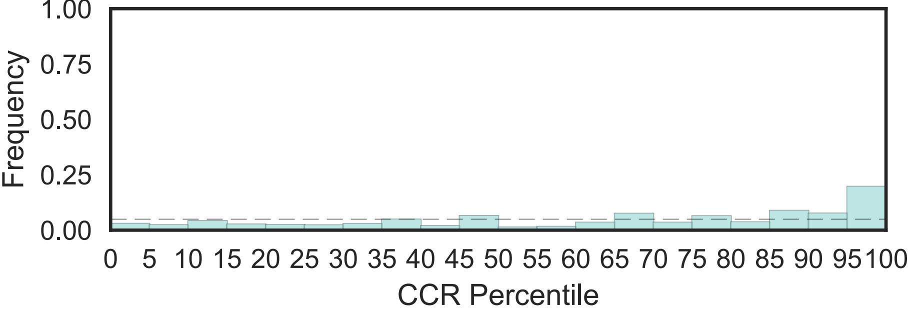

TFIIIC subunit
(TFIIIC_sub6, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

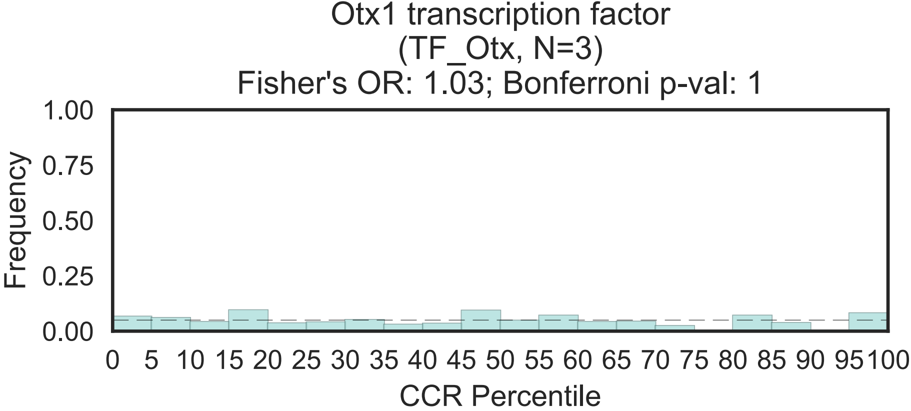

Transcription factor S-II (TFIIS)
(TFIIS_C, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

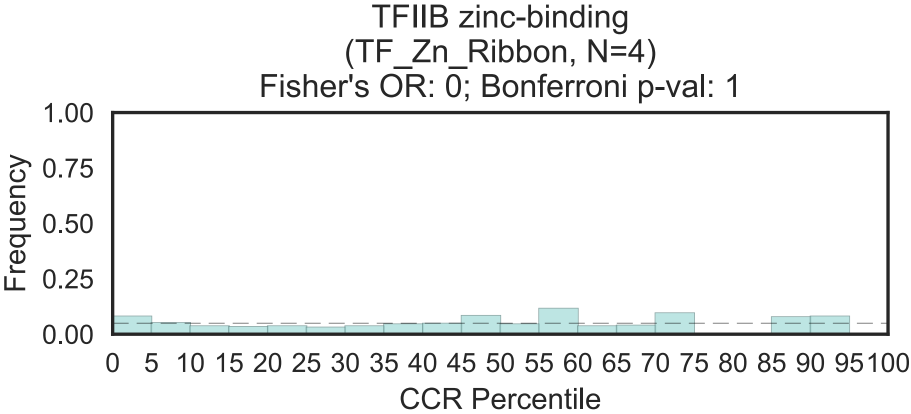

Transcription factor S-II (TFIIS), central domain
(TFIIS_M, N=6)
Fisher's OR: 0.865; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

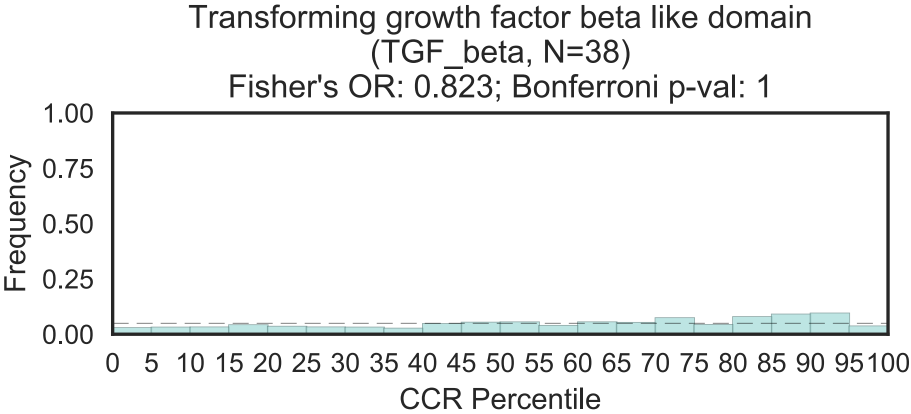


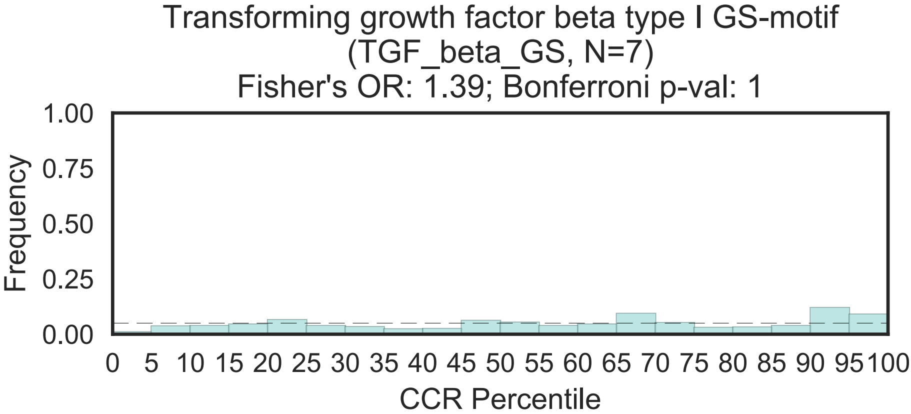
Transferrin receptor-like dimerisation domain
(TFR_dimer, N=4)
Fisher's OR: 0; Bonferroni p-val: 1


Transcription factor AP-2
(TF_AP-2, N=5)
Fisher's OR: 4.07; Bonferroni p-val: 1

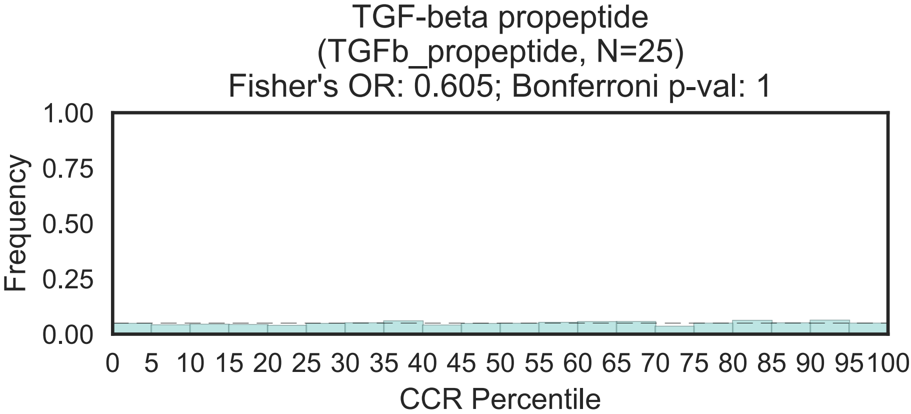

Otx1 transcription factor
(TF_Otx, N=3)
Fisher's OR: 1.03; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

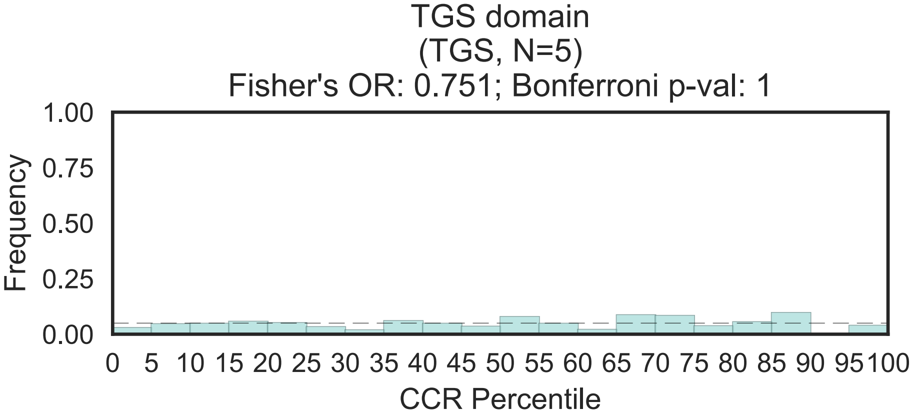

TFIIB zinc-binding
(TF_Zn_Ribbon, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

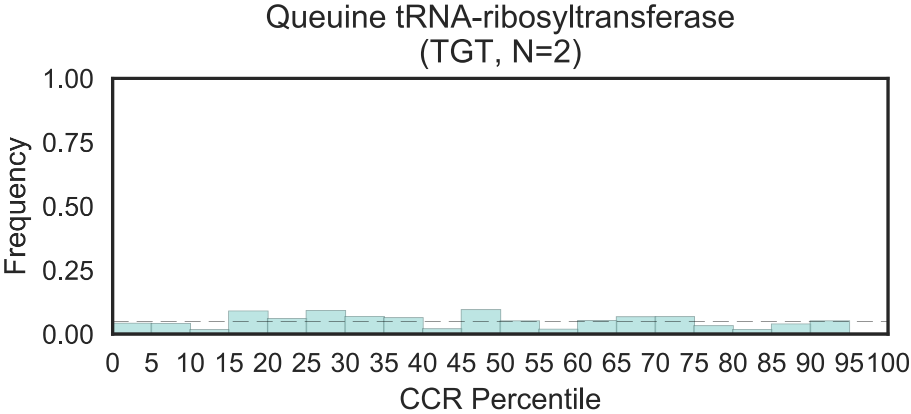

Transforming growth factor beta like domain
(TGF_beta, N=38)
Fisher's OR: 0.823; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

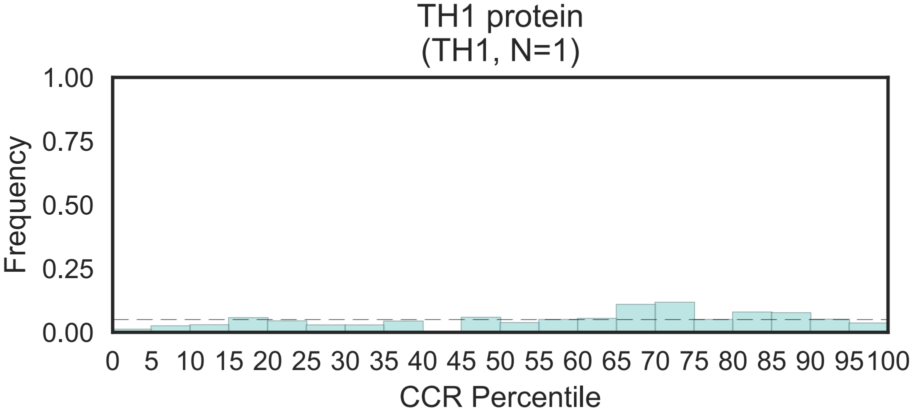


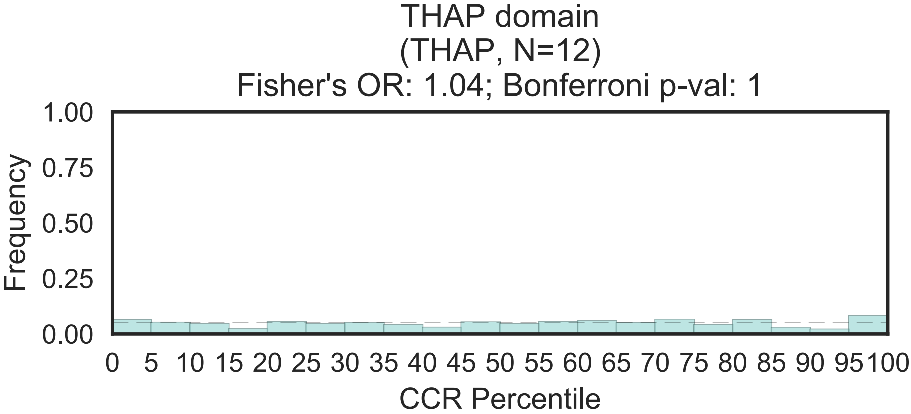
Transforming growth factor beta type I GS-motif
(TGF_beta_GS, N=7)
Fisher's OR: 1.39; Bonferroni p-val: 1

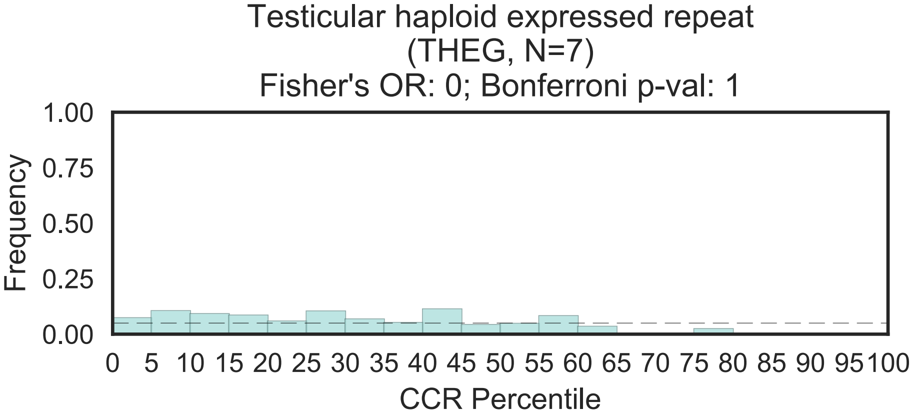

TGF-beta propeptide
(TGFb_propeptide, N=25)
Fisher's OR: 0.605; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

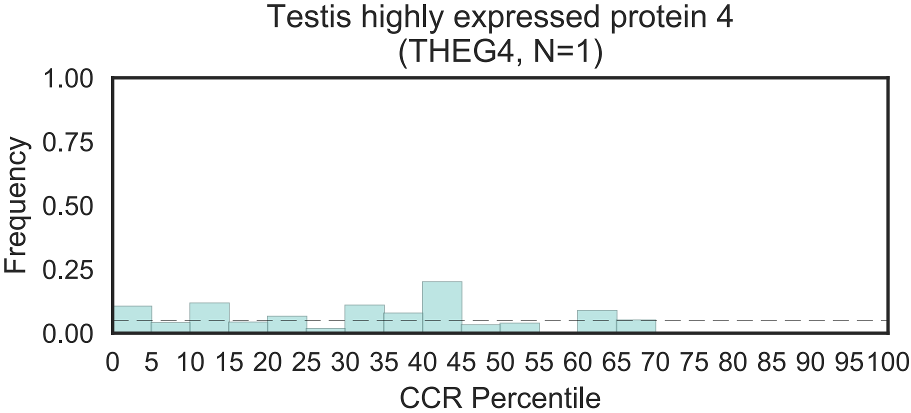

TGS domain
(TGS, N=5)
Fisher's OR: 0.751; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

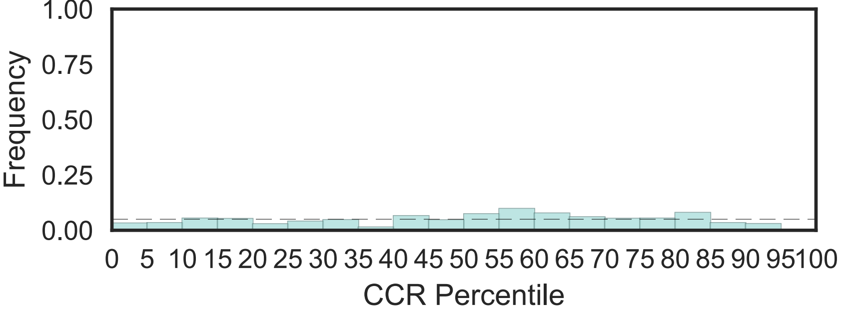

Queuine tRNA-ribosyltransferase
(TGT, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


TH1 protein
(TH1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

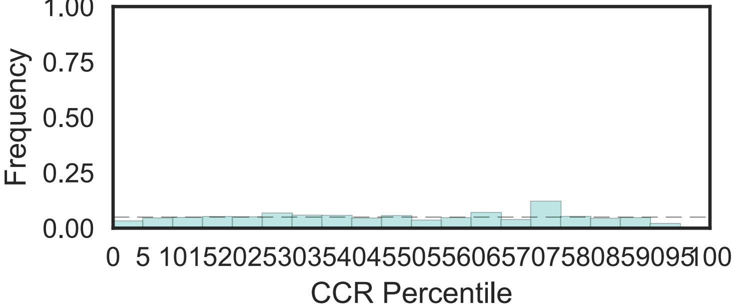

THAP domain
(THAP, N=12)
Fisher's OR: 1.04; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Testicular haploid expressed repeat
(THEG, N=7)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

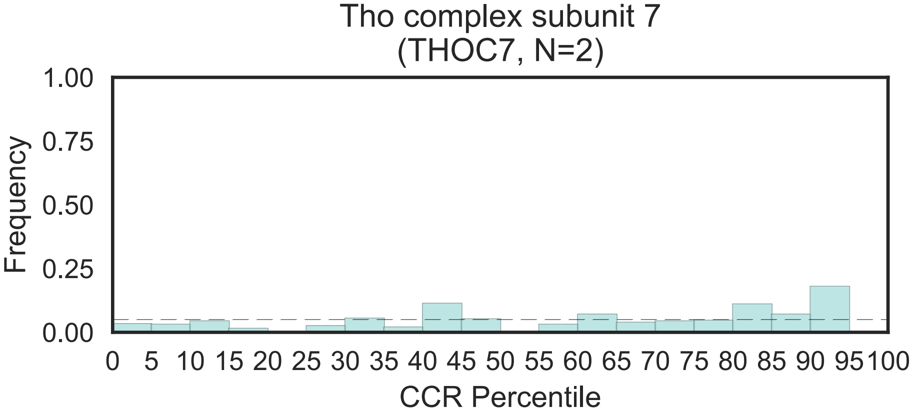

Testis highly expressed protein 4
(THEG4, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

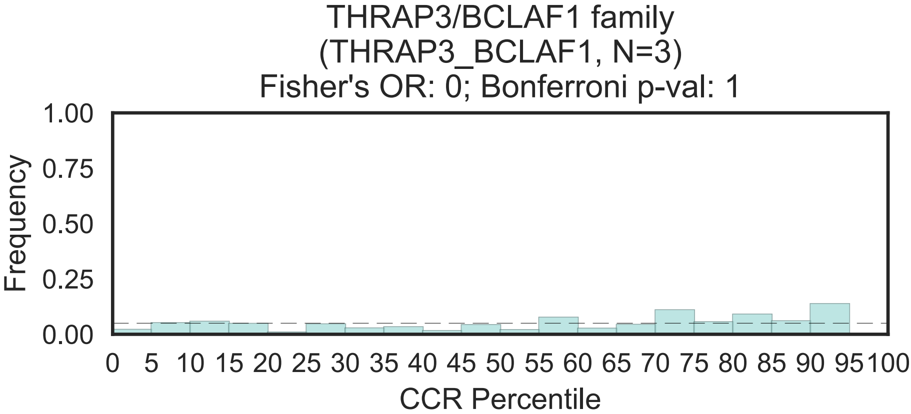


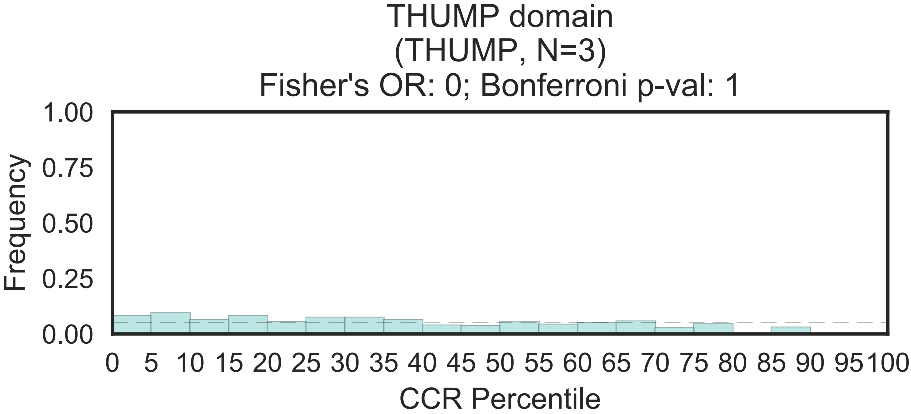
Tetrahydrofolate dehydrogenase/cyclohydrolase, catalytic domain (THF_DHG_CYH, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

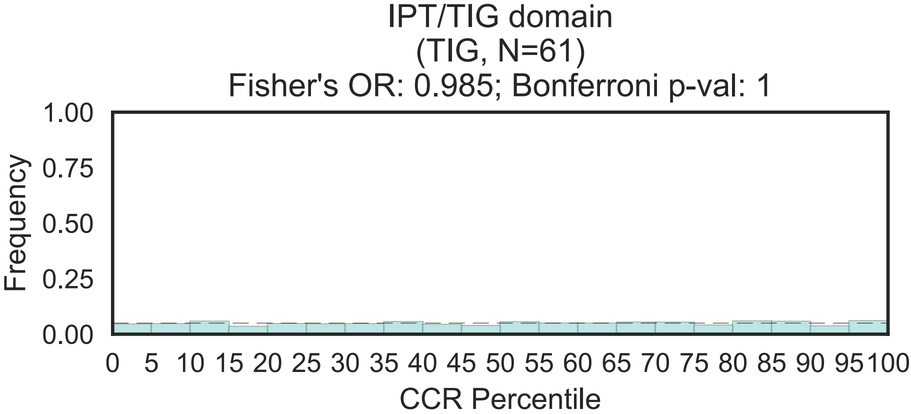


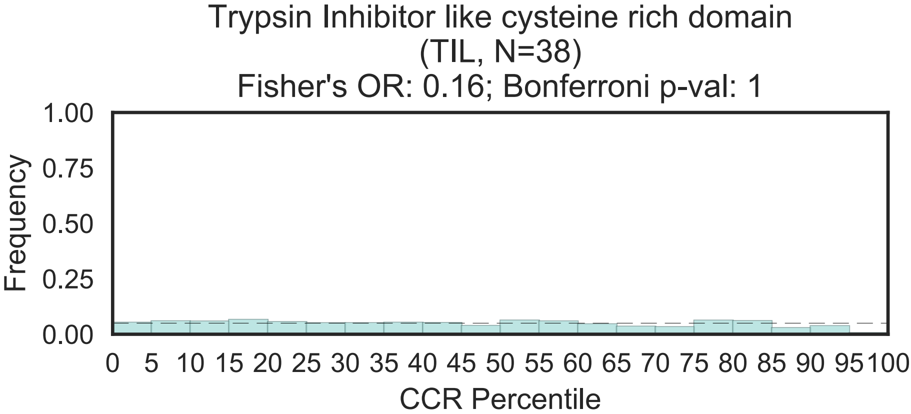
Tetrahydrofolate dehydrogenase/cyclohydrolase, NAD(P)-binding domain (THF_DHG_CYH_C, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

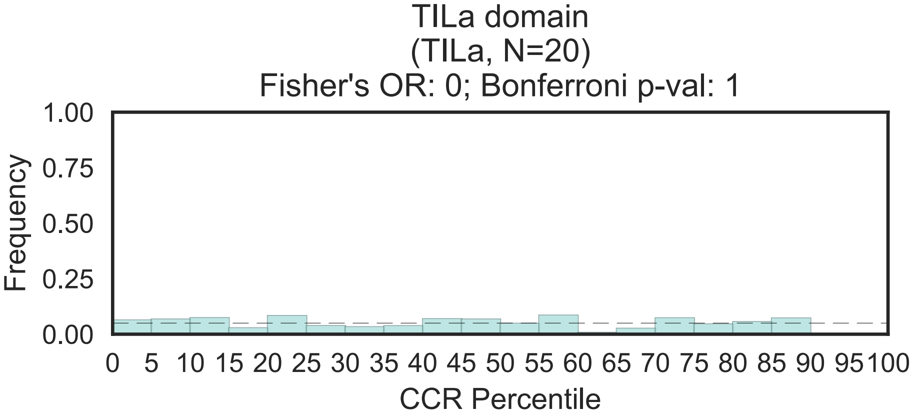

Tho complex subunit 7
(THOC7, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

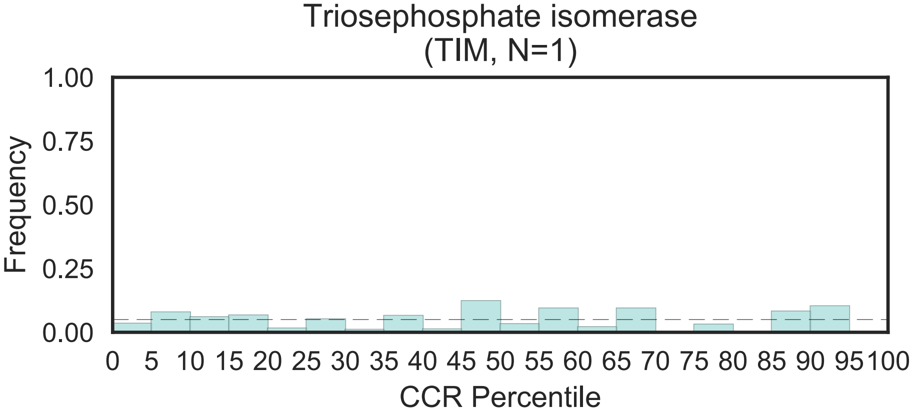

THRAP3/BCLAF1 family
(THRAP3_BCLAF1, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

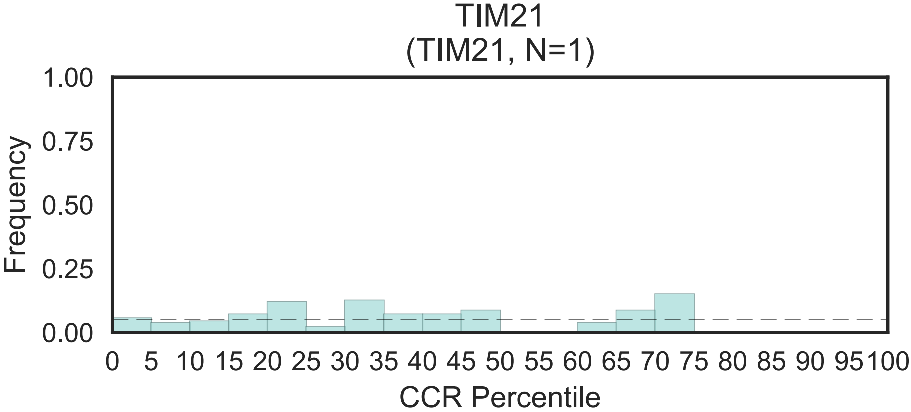

THUMP domain
(THUMP, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

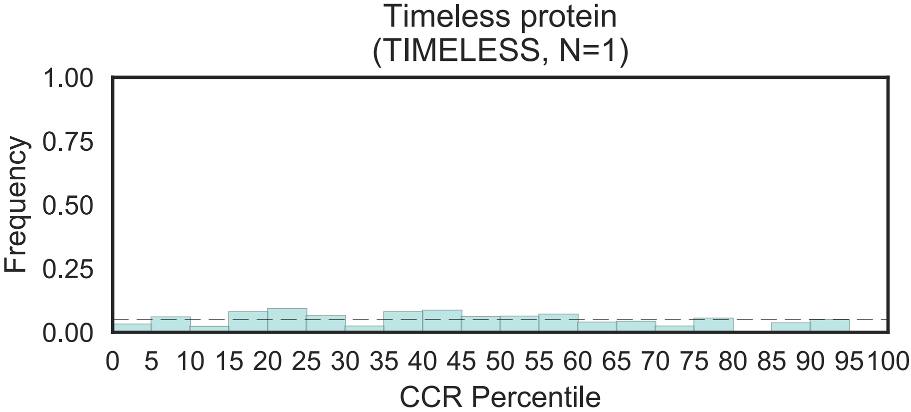

IPT/TIG domain
(TIG, N=61)
Fisher's OR: 0.985; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Trypsin Inhibitor like cysteine rich domain
(TIL, N=38)
Fisher's OR: 0.16; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

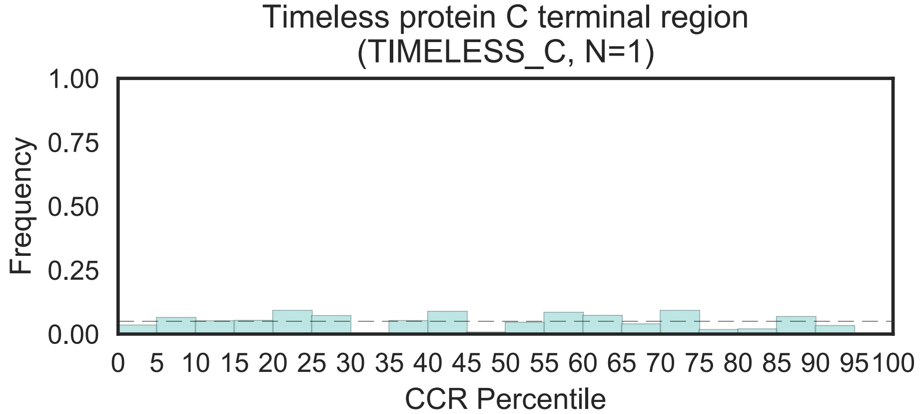

TILa domain
(TILa, N=20)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

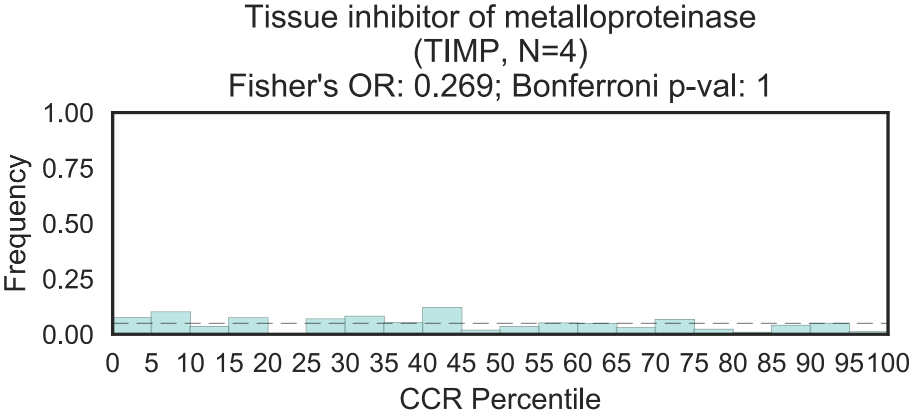

Triosephosphate isomerase
(TIM, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


TIM21
(TIM21, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

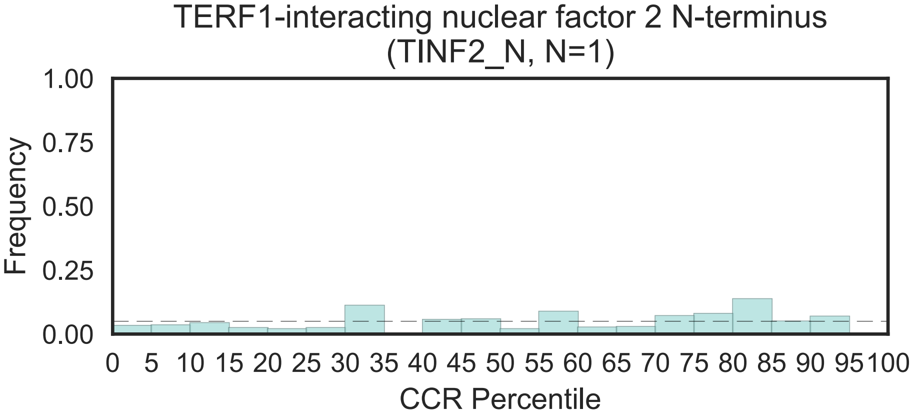


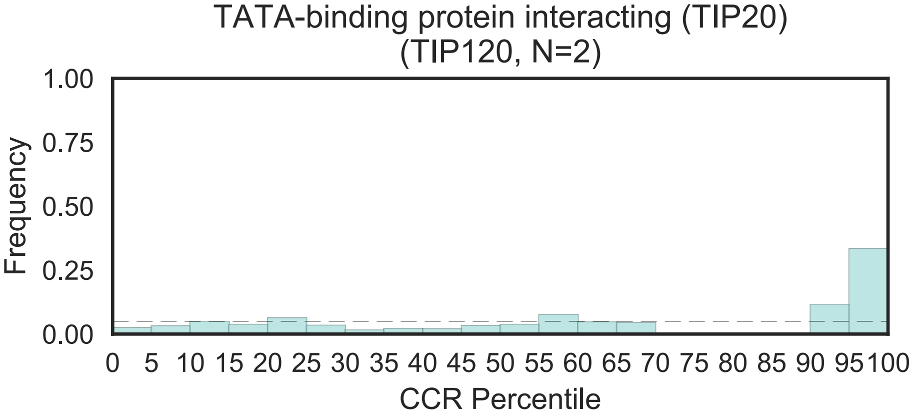
Timeless protein
(TIMELESS, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

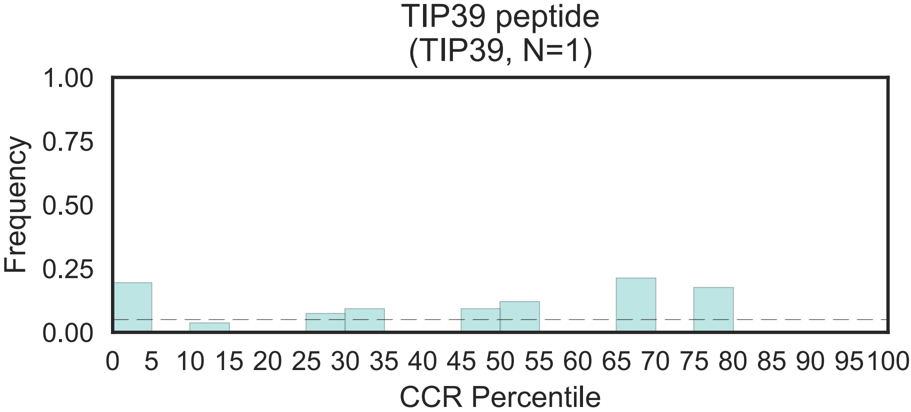

Timeless protein C terminal region
(TIMELESS_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

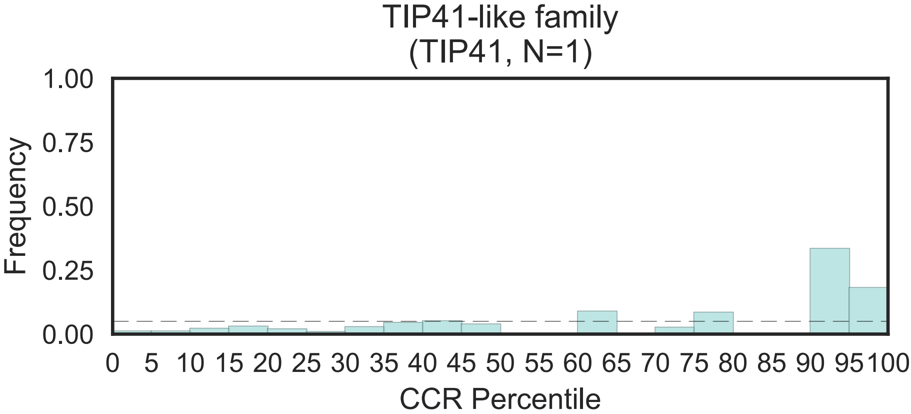


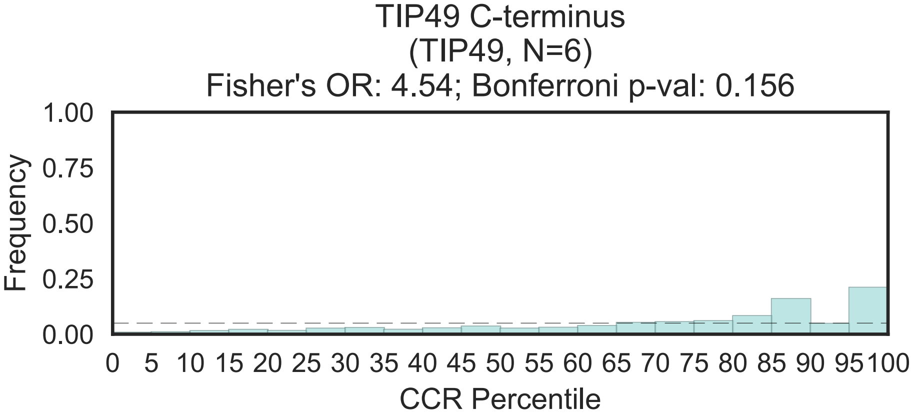
Tissue inhibitor of metalloproteinase
(TIMP, N=4)
Fisher's OR: 0.269; Bonferroni p-val: 1

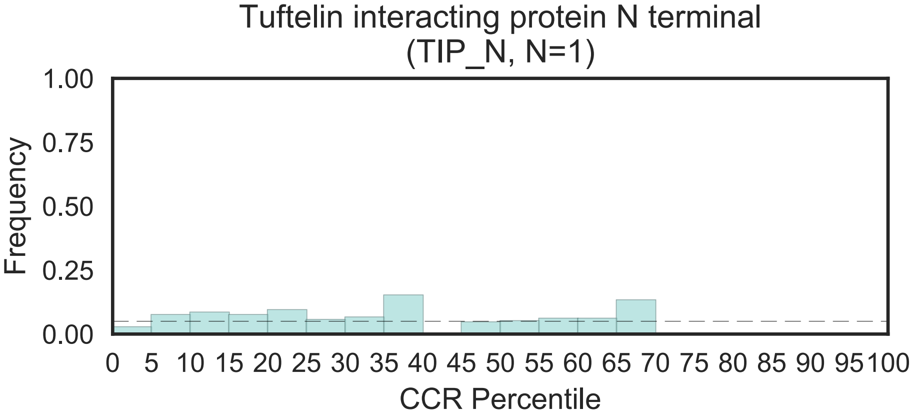

TERF1-interacting nuclear factor 2 N-terminus
(TINF2_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

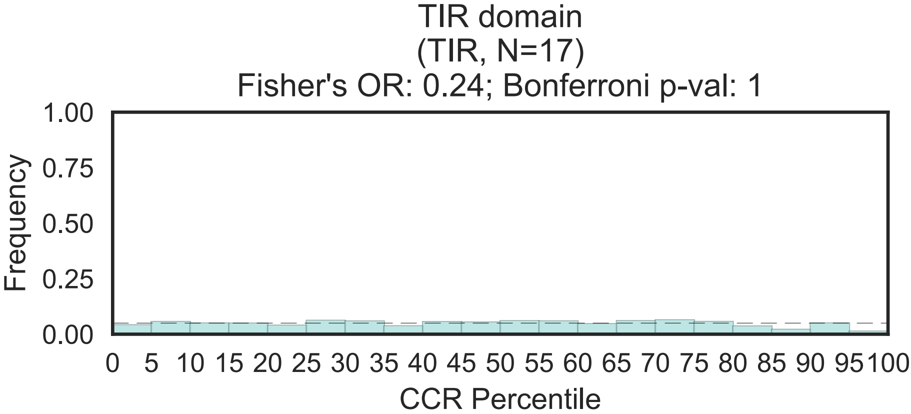

TATA-binding protein interacting (TIP20)
(TIP120, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

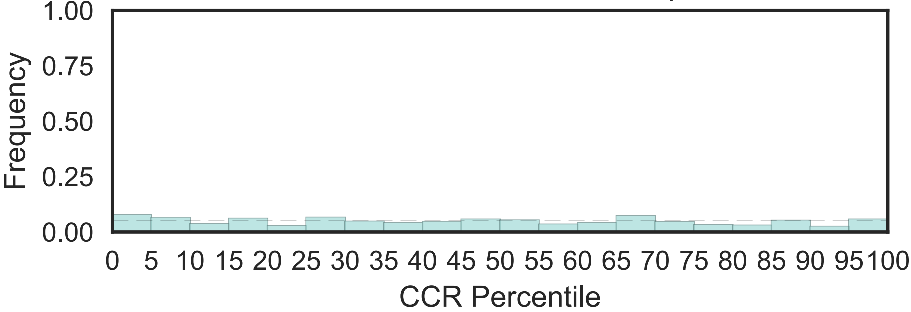

TIP39 peptide
(TIP39, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


TIP41-like family
(TIP41, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

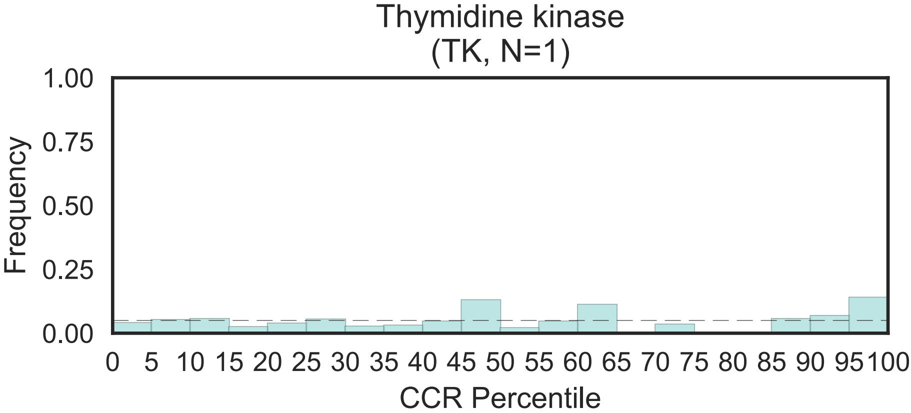

TIP49 C-terminus
(TIP49, N=6)
Fisher's OR: 4.54; Bonferroni p-val: 0.156
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

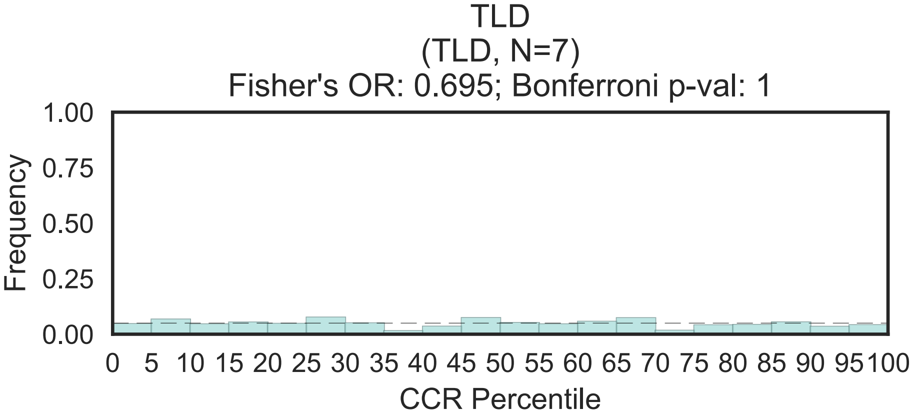

Tuftelin interacting protein N terminal
(TIP_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

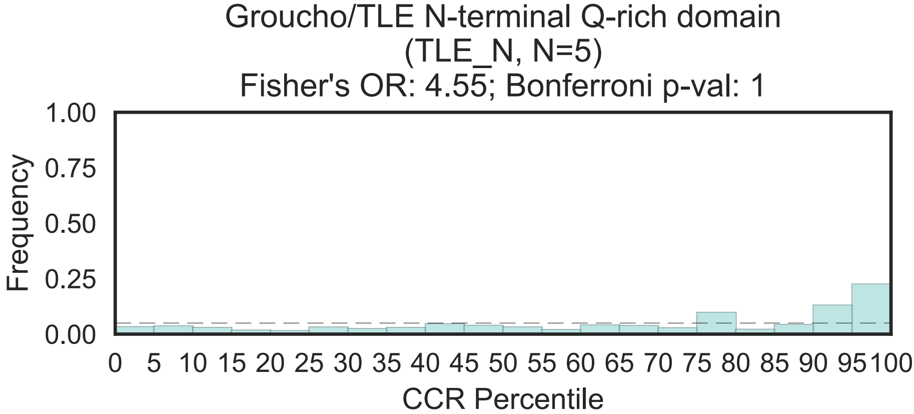

TIR domain
(TIR, N=17)
Fisher's OR: 0.24; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

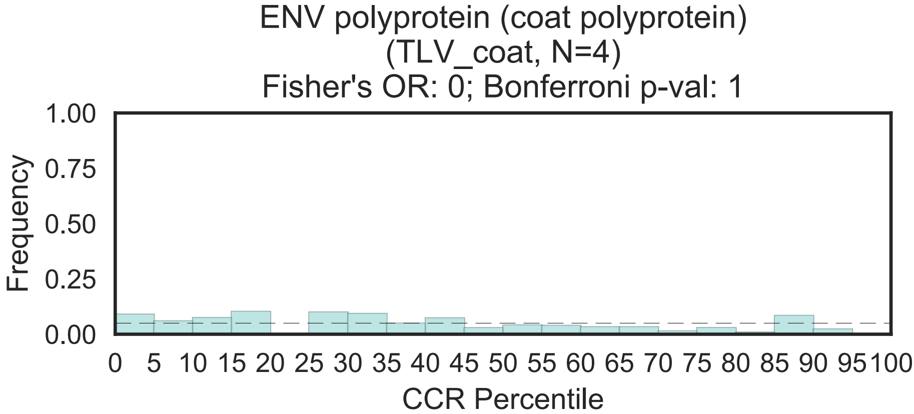


TIR domain
(TIR_2, N=11)
Fisher's OR: 0.562; Bonferroni p-val: 1

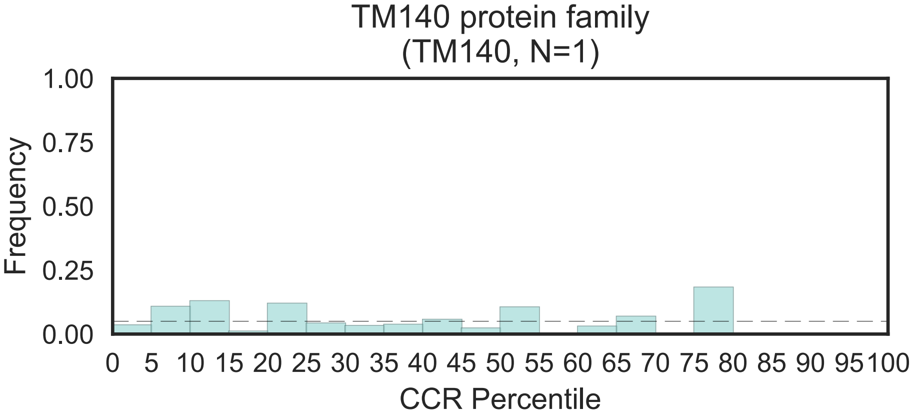

Thymidine kinase
(TK, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

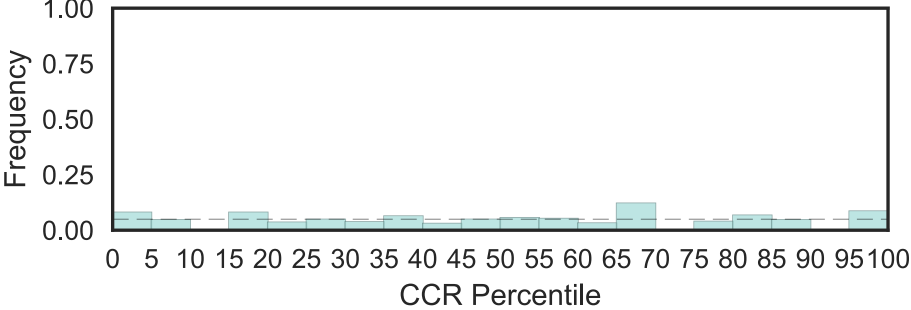

TLD
(TLD, N=7)
Fisher's OR: 0.695; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

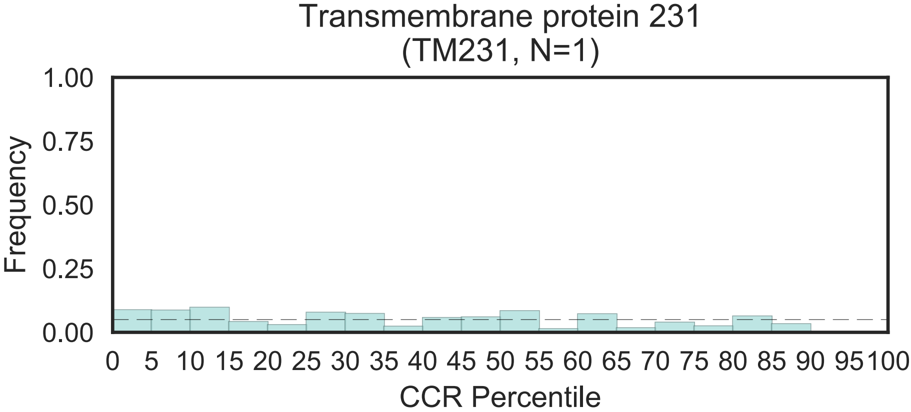

Groucho/TLE N-terminal Q-rich domain
(TLE_N, N=5)
Fisher's OR: 4.55; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

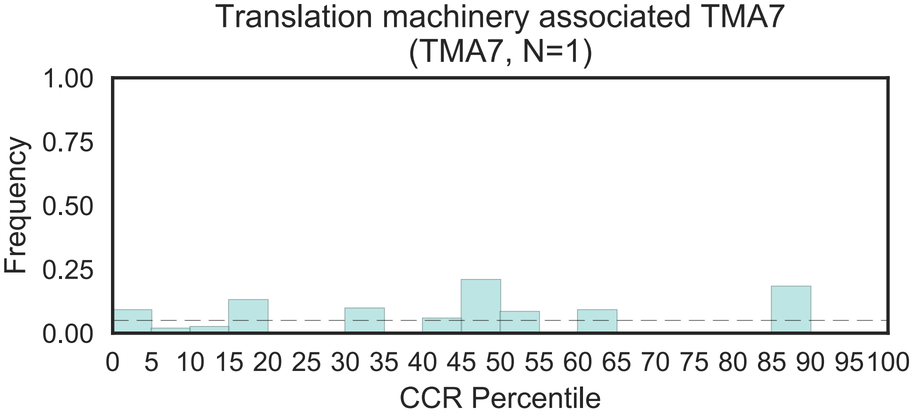


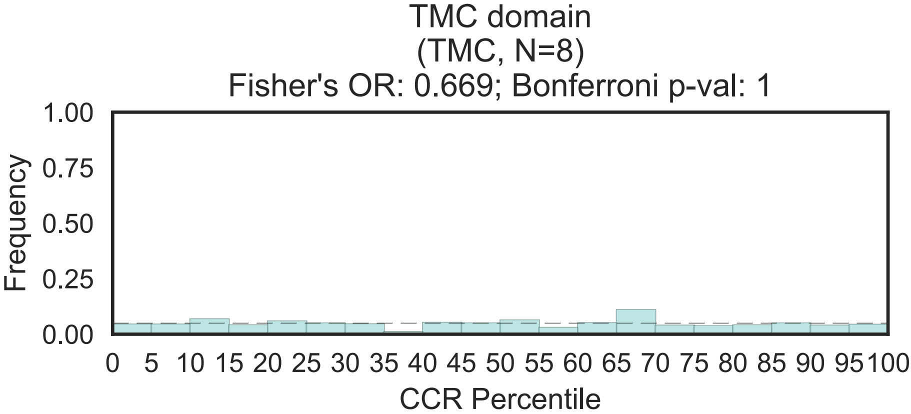
ENV polyprotein (coat polyprotein)
(TLV_coat, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

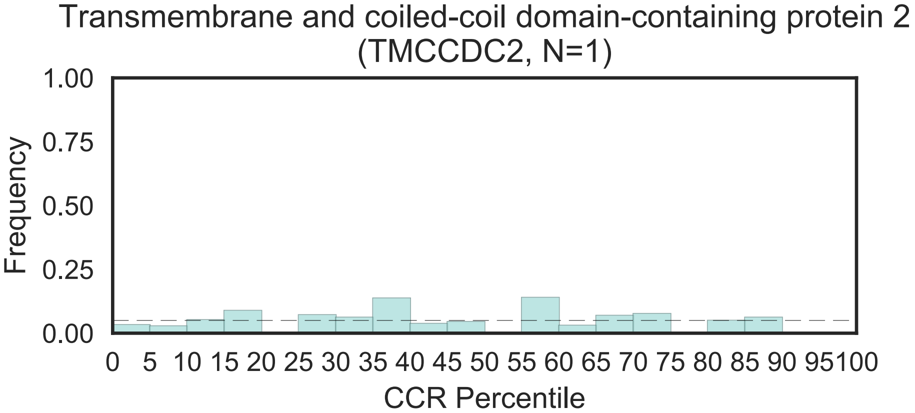

TM140 protein family
(TM140, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

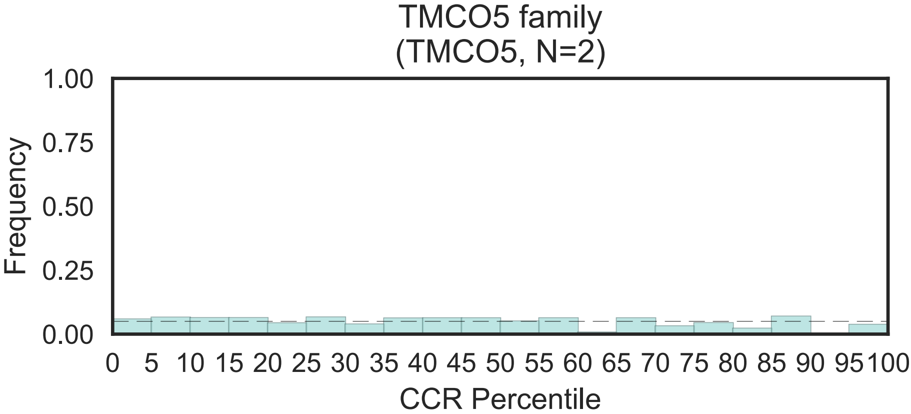

TM2 domain
(TM2, N=4)
Fisher's OR: 1.46; Bonferroni p-val: 1


Transmembrane protein 231
(TM231, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

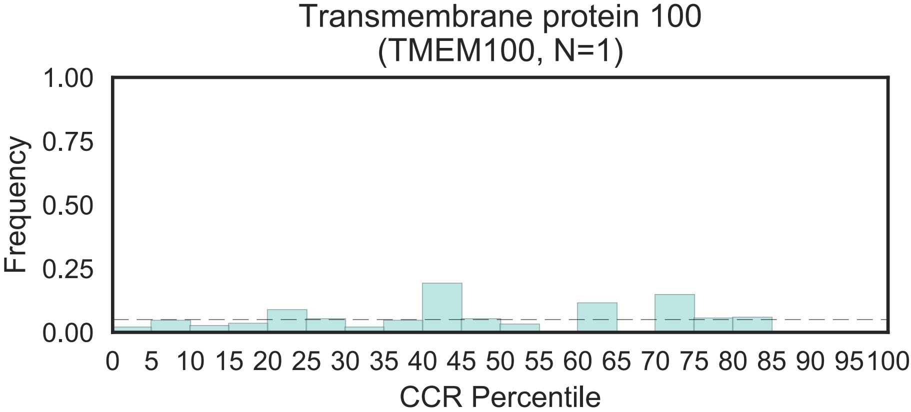

Translation machinery associated TMA7
(TMA7, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

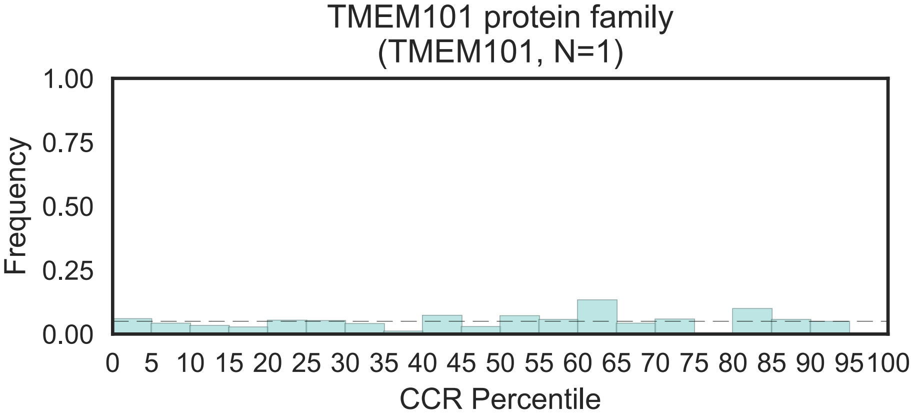

TMC domain
(TMC, N=8)
Fisher's OR: 0.669; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

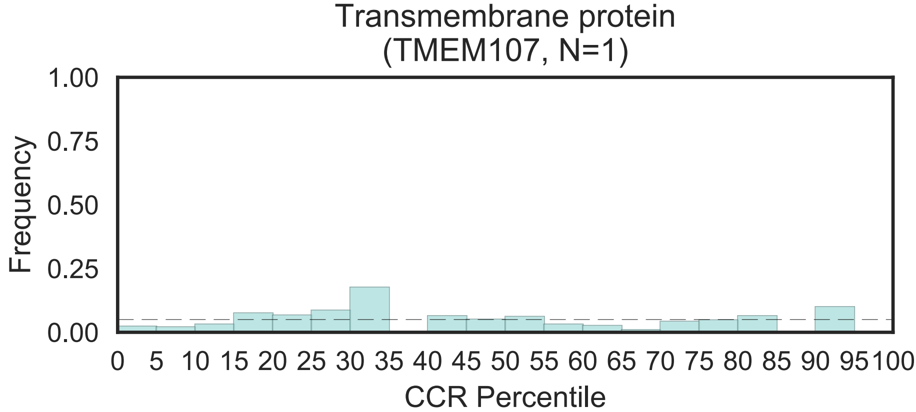

Transmembrane and coiled-coil domain-containing protein 2
(TMCCDC2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

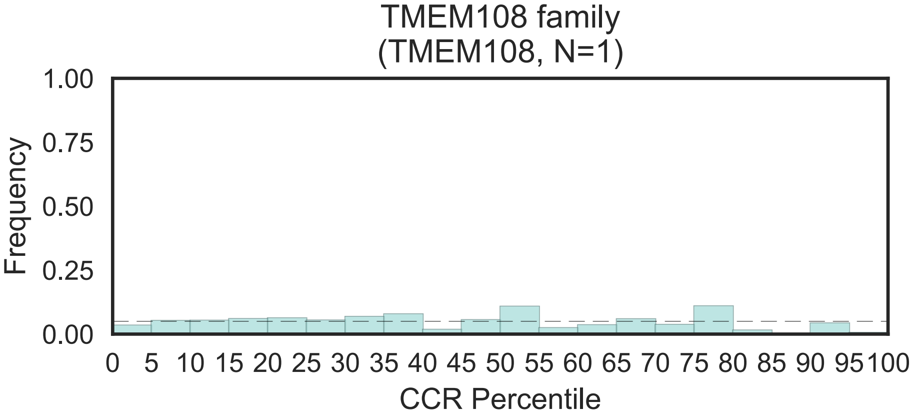


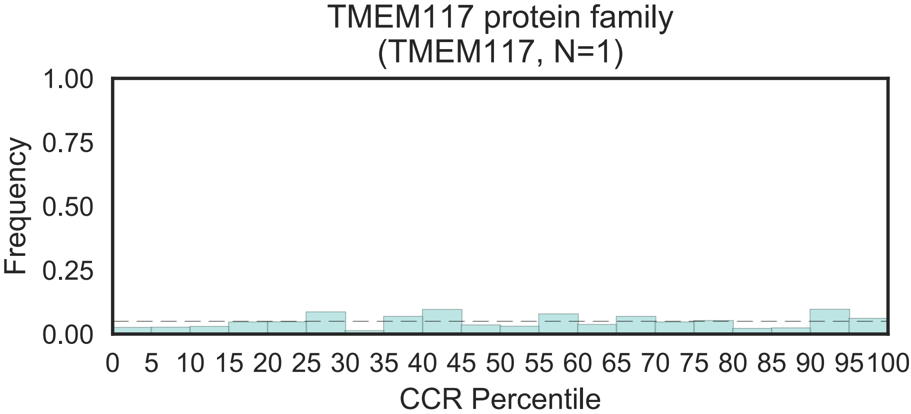
TMCO5 family
(TMCO5, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

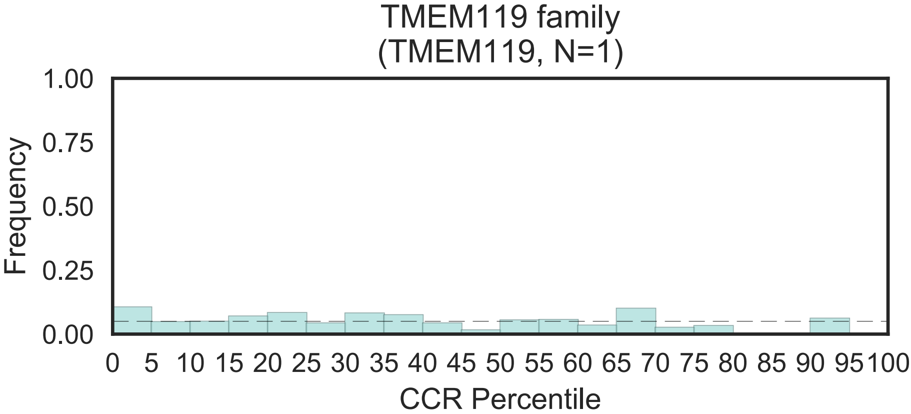

Transmembrane protein 100
(TMEM100, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

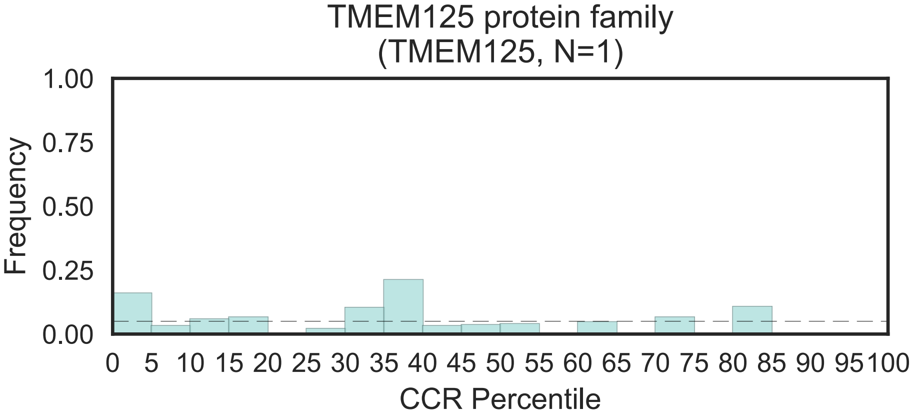

TMEM101 protein family
(TMEM101, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Transmembrane protein
(TMEM107, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

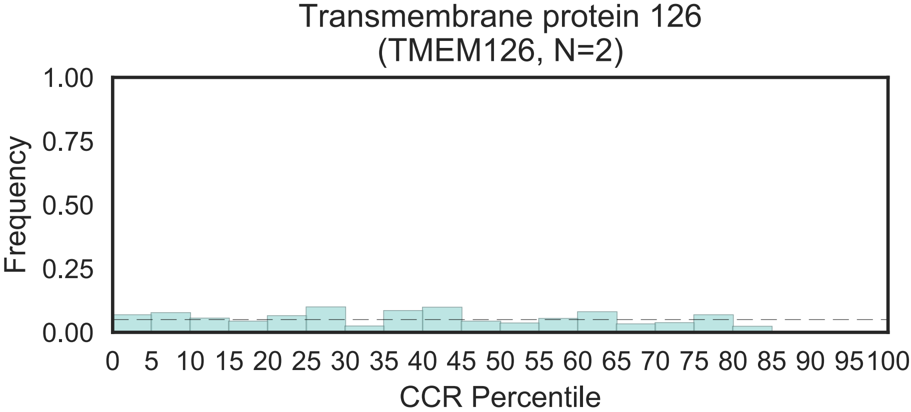

TMEM108 family
(TMEM108, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

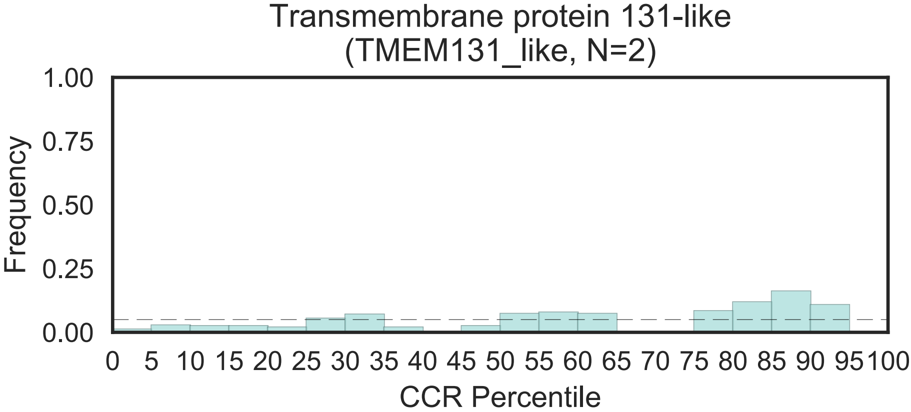

TMEM117 protein family
(TMEM117, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

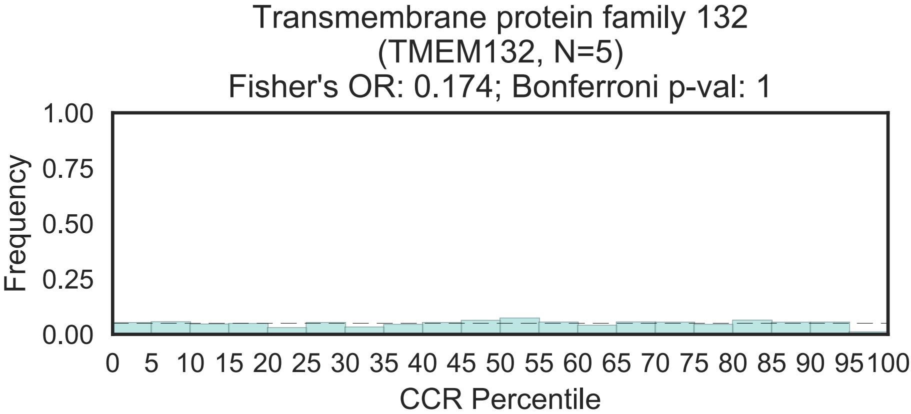

TMEM119 family
(TMEM119, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



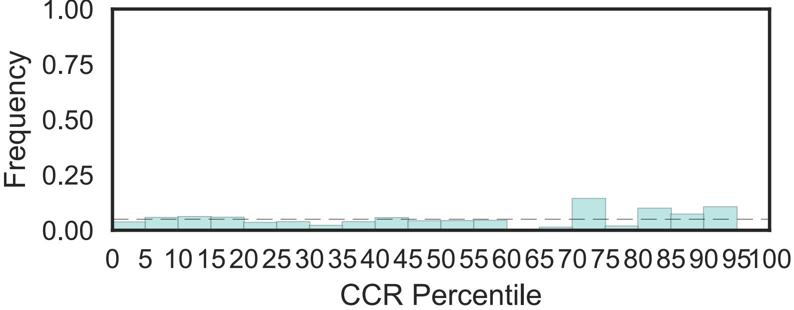
TMEM125 protein family
(TMEM125, N=1)


Transmembrane protein 126
(TMEM126, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

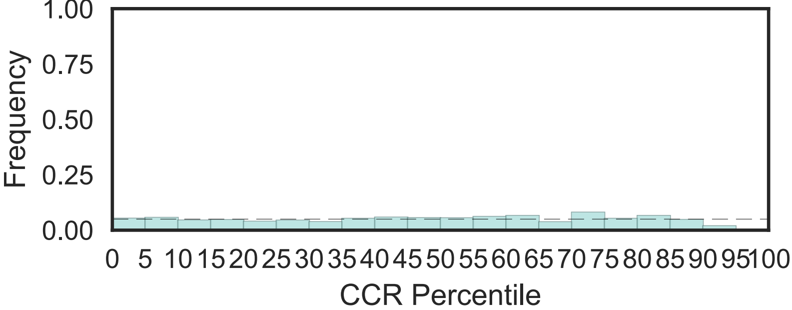

Transmembrane protein 131-like
(TMEM131_like, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

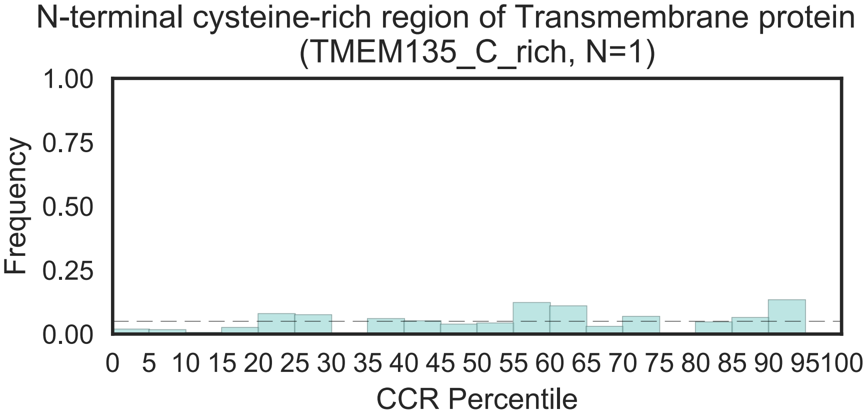

Transmembrane protein family 132
(TMEM132, N=5)
Fisher's OR: 0.174; Bonferroni p-val: 1

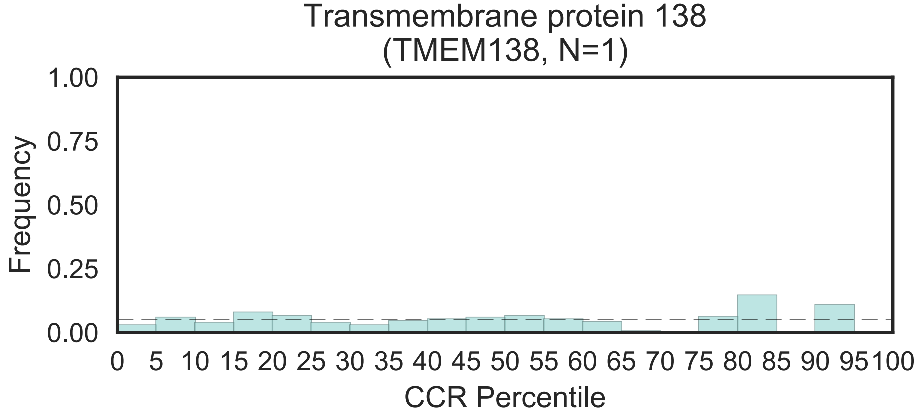
Mature oligodendrocyte transmembrane protein, TMEM132D, C-term
(TMEM132D_C, N=5)
Fisher's OR: 0; Bonferroni p-val: 1

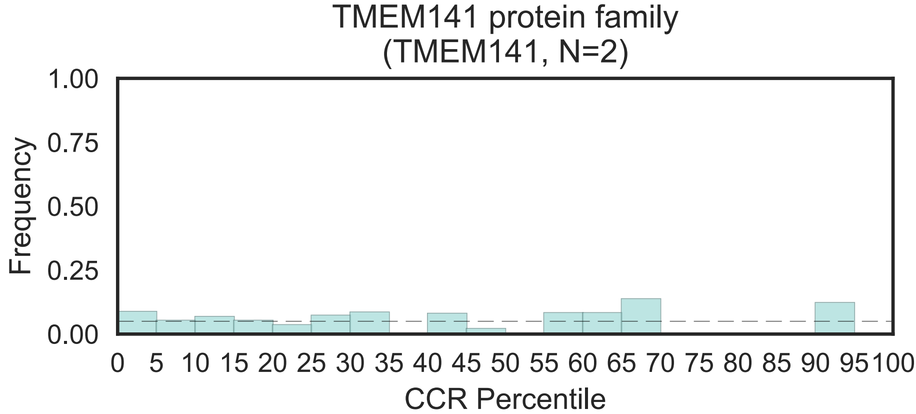


Mature oligodendrocyte transmembrane protein, TMEM132D, N-term
(TMEM132D_N, N=5)
Fisher's OR: 0; Bonferroni p-val: 1

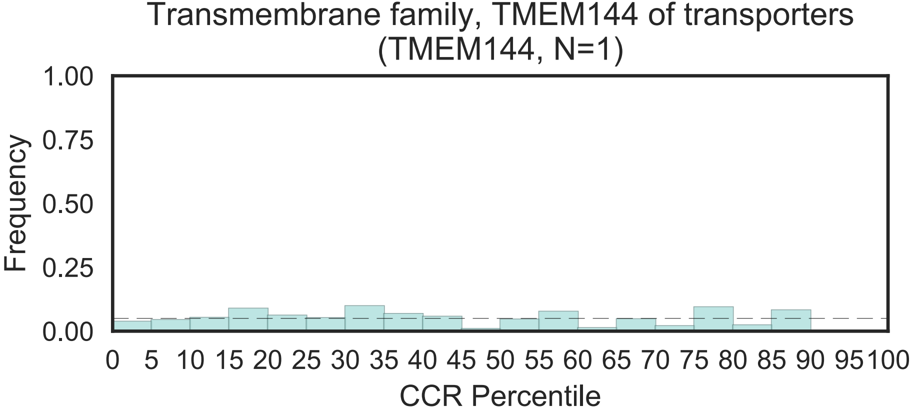


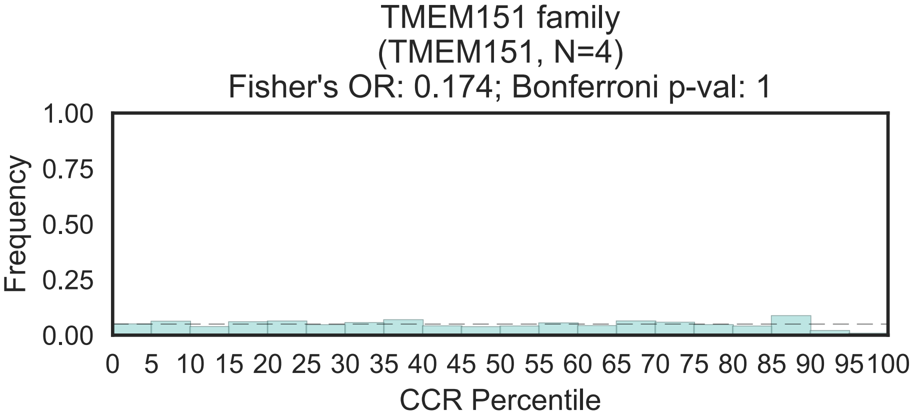

N-terminal cysteine-rich region of Transmembrane protein 135
(TMEM135_C_rich, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

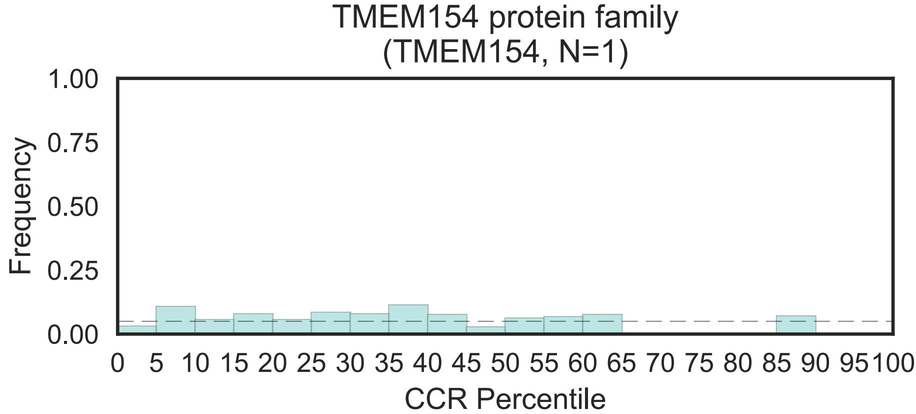

Transmembrane protein 138
(TMEM138, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



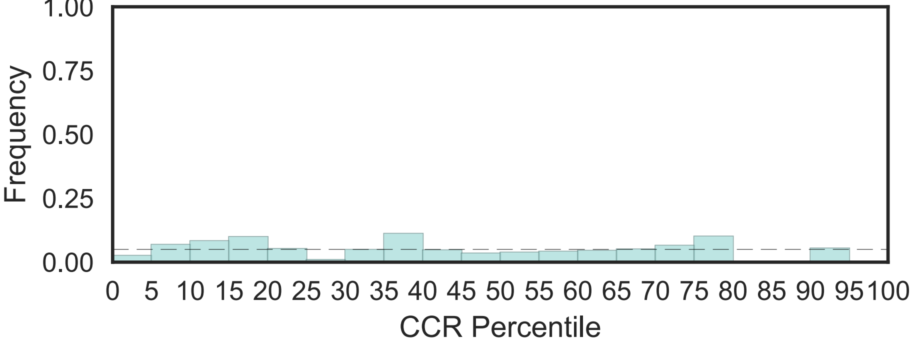
TMEM141 protein family
(TMEM141, N=2)

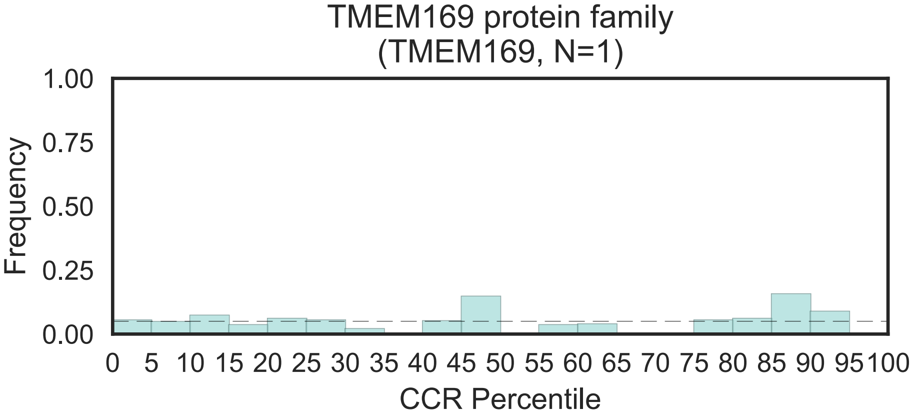

Transmembrane family, TMEM144 of transporters
(TMEM144, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

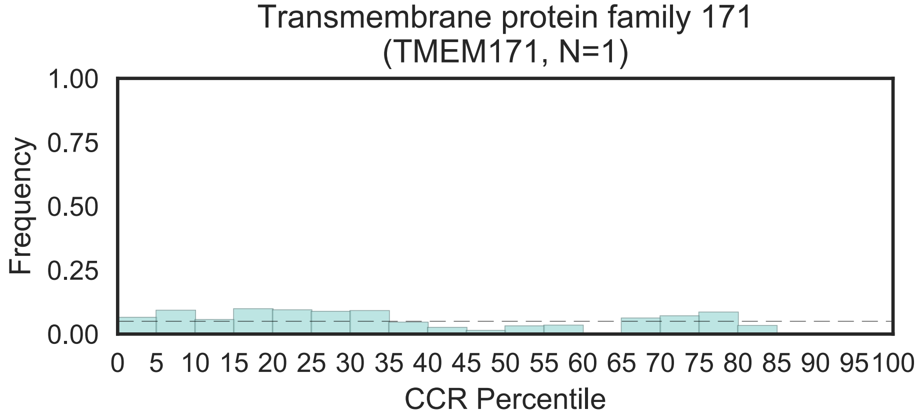

TMEM151 family
(TMEM151, N=4)
Fisher's OR: 0.174; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


TMEM154 protein family
(TMEM154, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

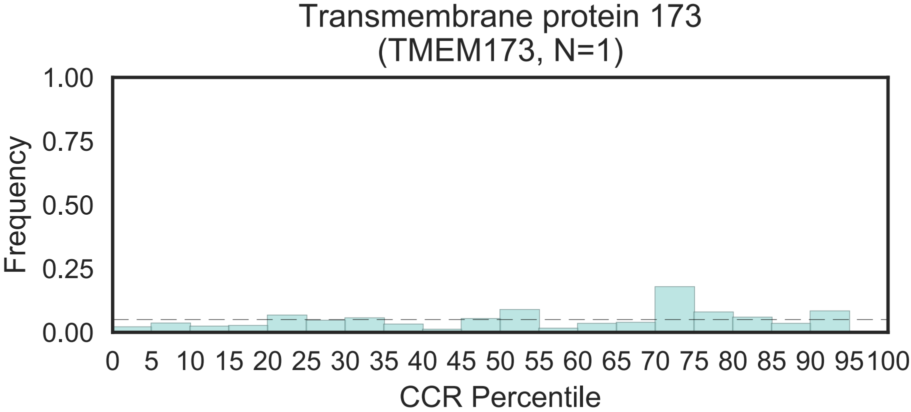
TMEM156 protein family
(TMEM156, N=1)



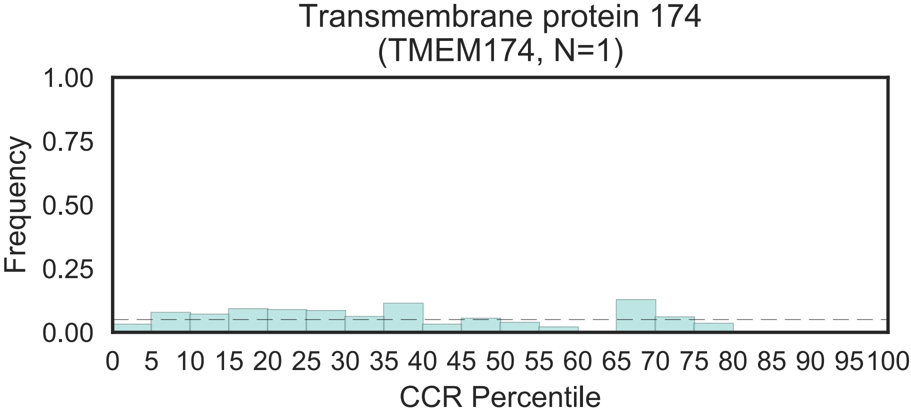

TMEM169 protein family
(TMEM169, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



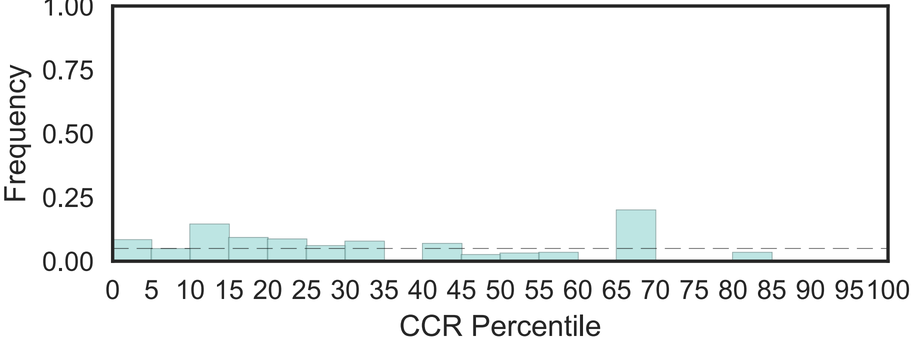
Transmembrane protein family 171
(TMEM171, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



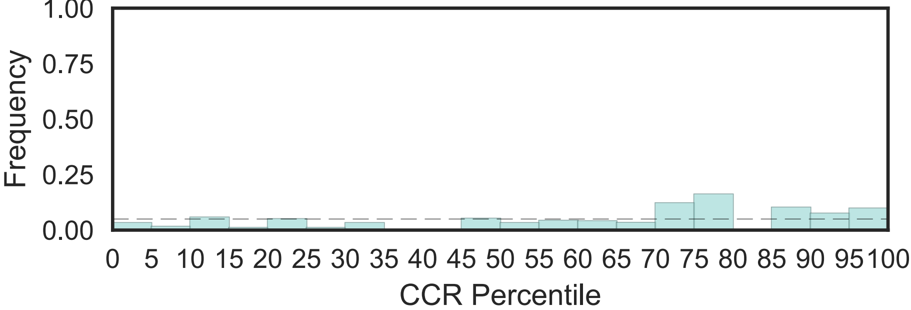
Transmembrane protein 173
(TMEM173, N=1)

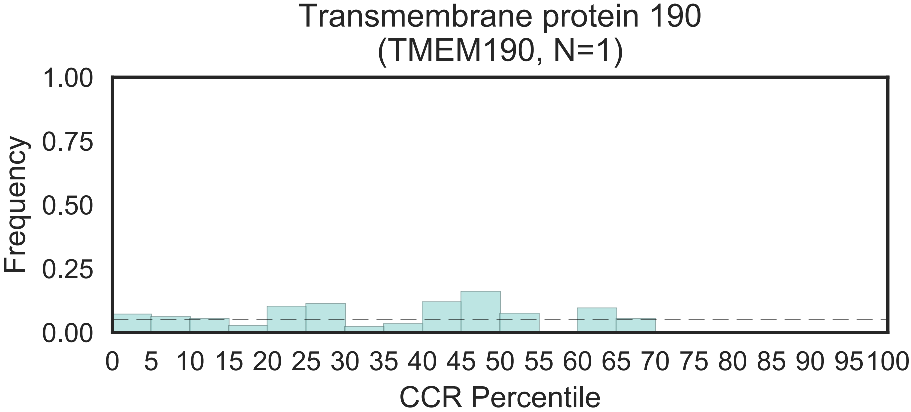

Transmembrane protein 174
(TMEM174, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

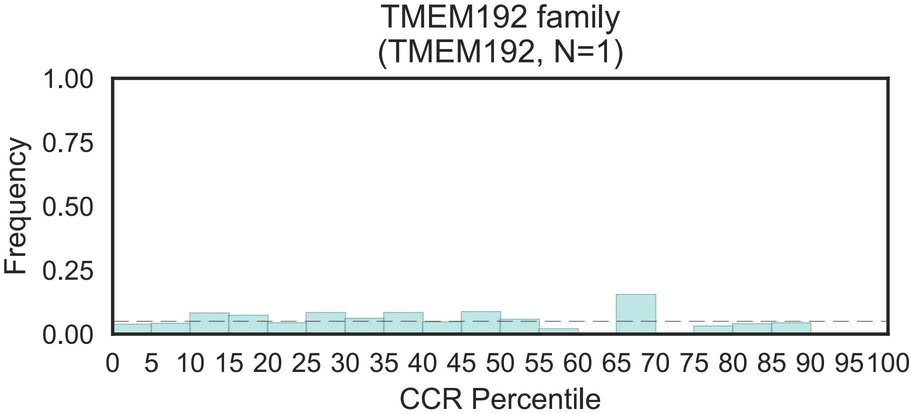
Transmembrane protein 18
(TMEM18, N=1)

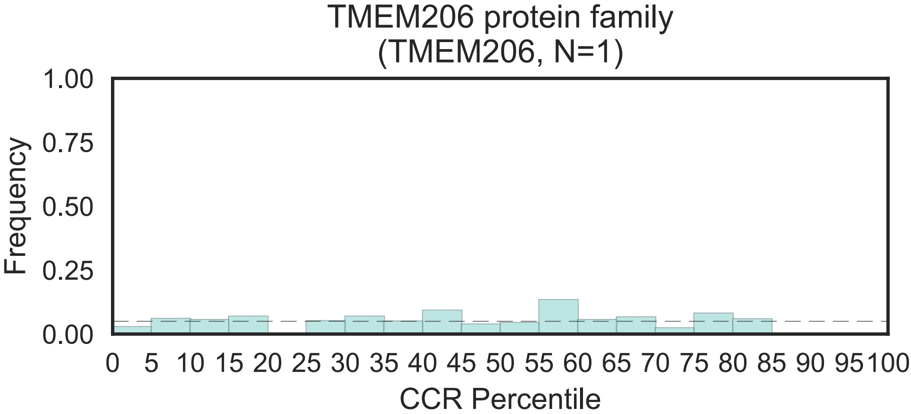


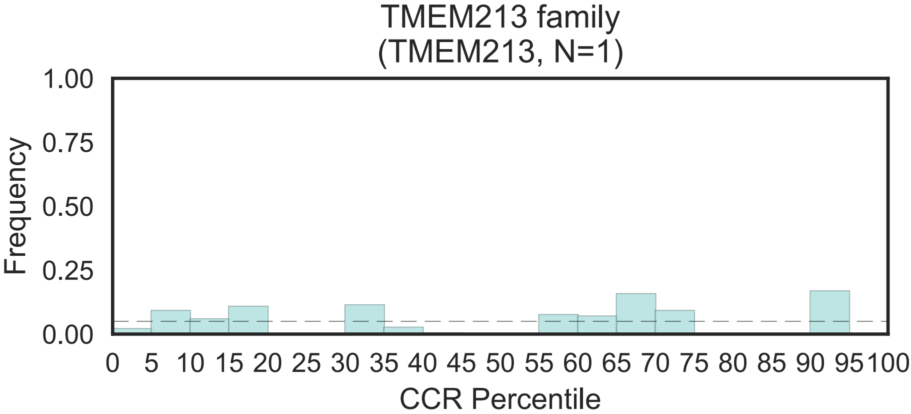
B domain of TMEM189, localisation domain
(TMEM189_B_dmain, N=3)
Fisher's OR: 2.1; Bonferroni p-val: 1

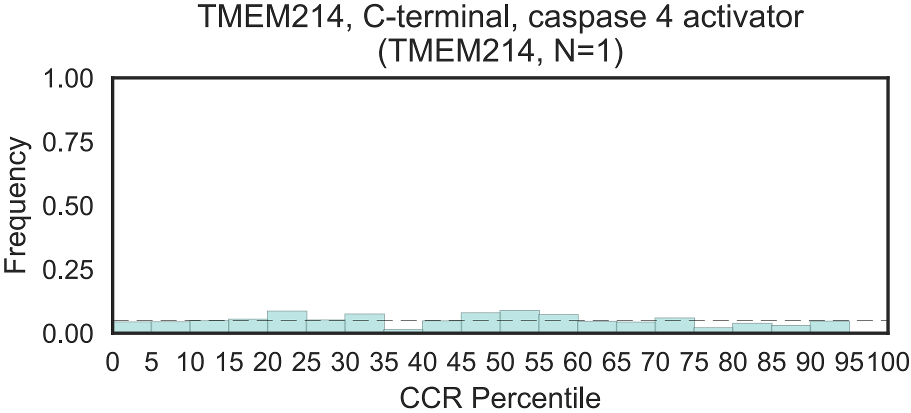


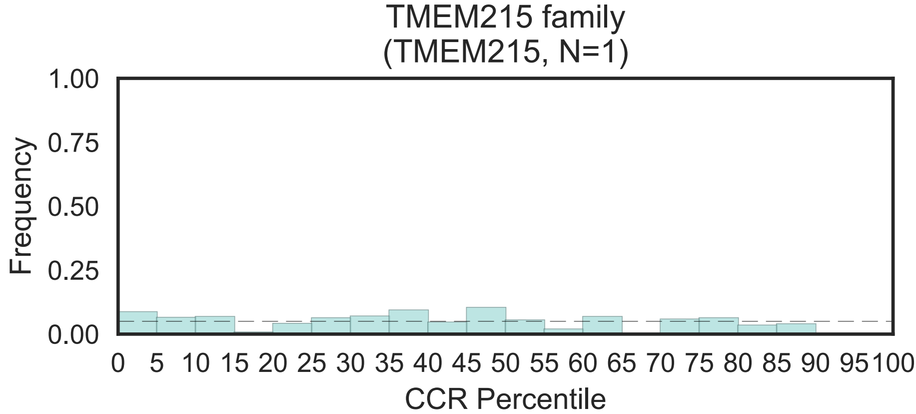

Transmembrane protein 190
(TMEM190, N=1)

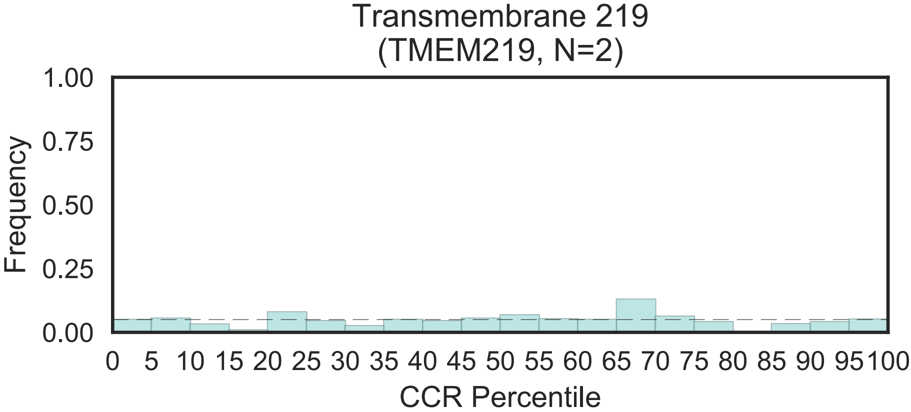

TMEM192 family
(TMEM192, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

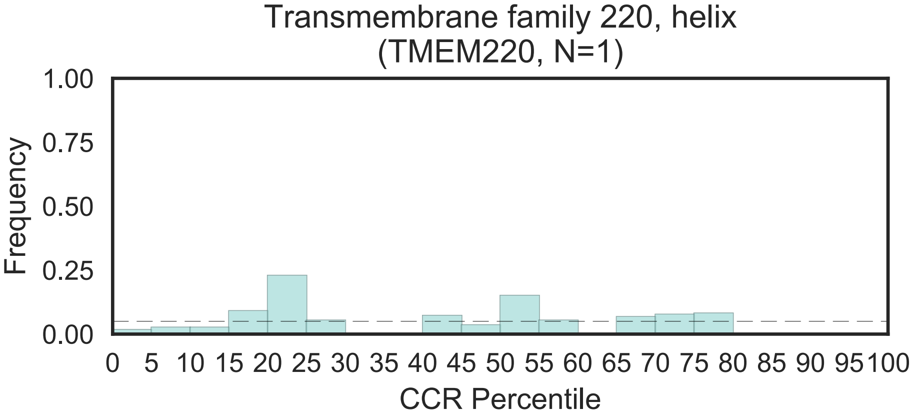

TMEM206 protein family
(TMEM206, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

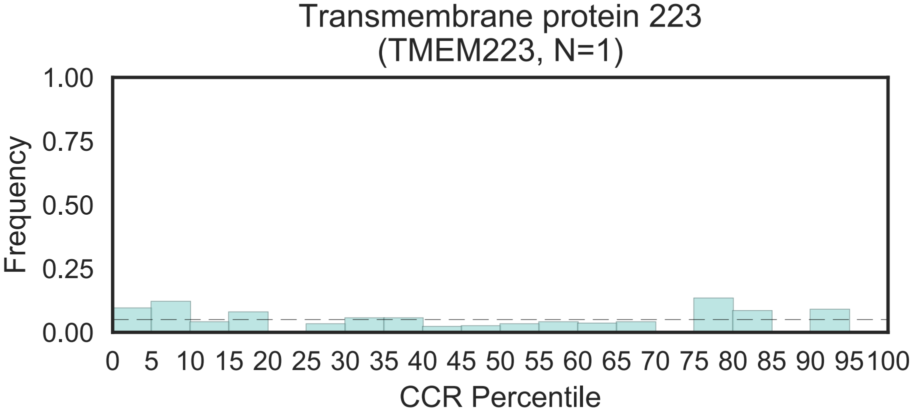

TMEM213 family
(TMEM213, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

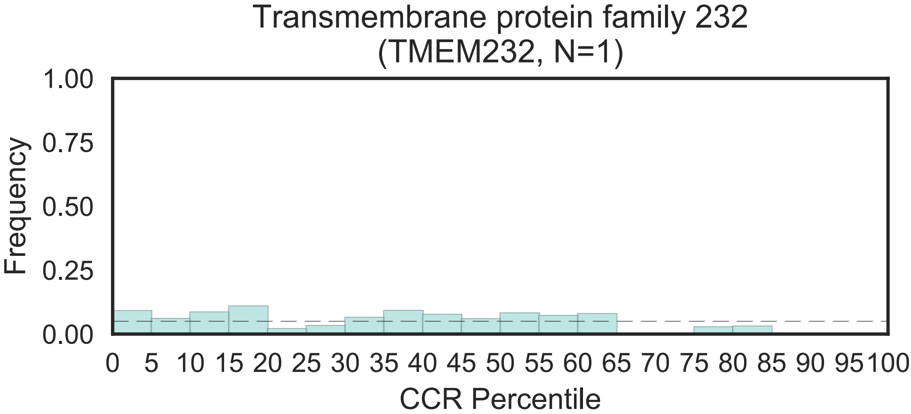

TMEM214, C-terminal, caspase 4 activator
(TMEM214, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

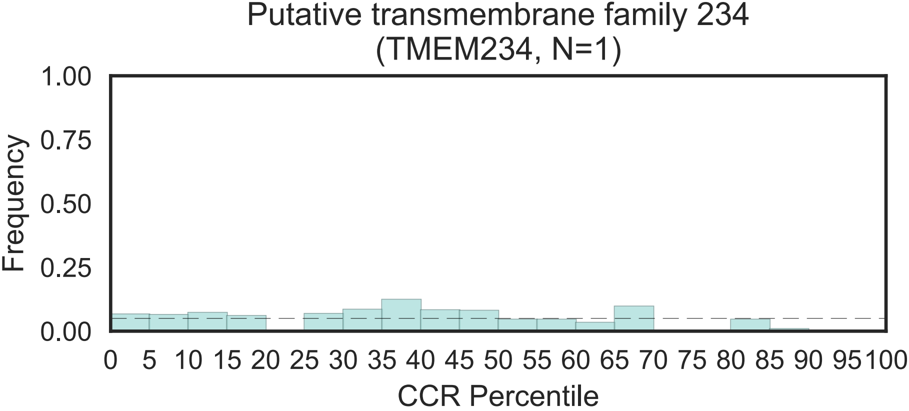

TMEM215 family
(TMEM215, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

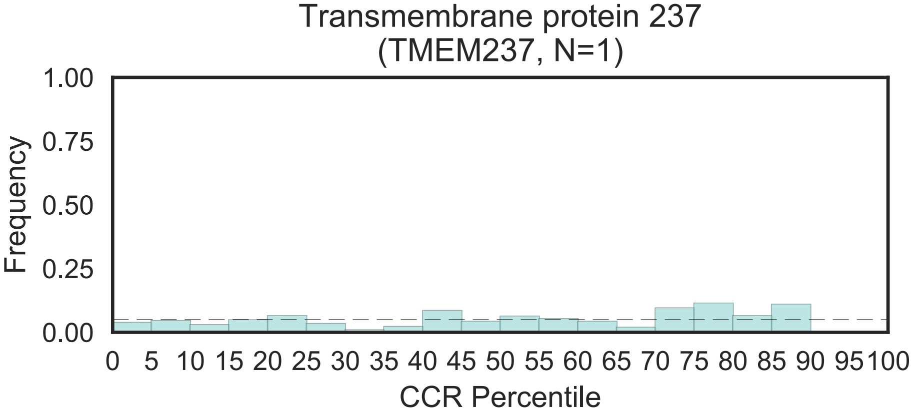

Transmembrane 219
(TMEM219, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

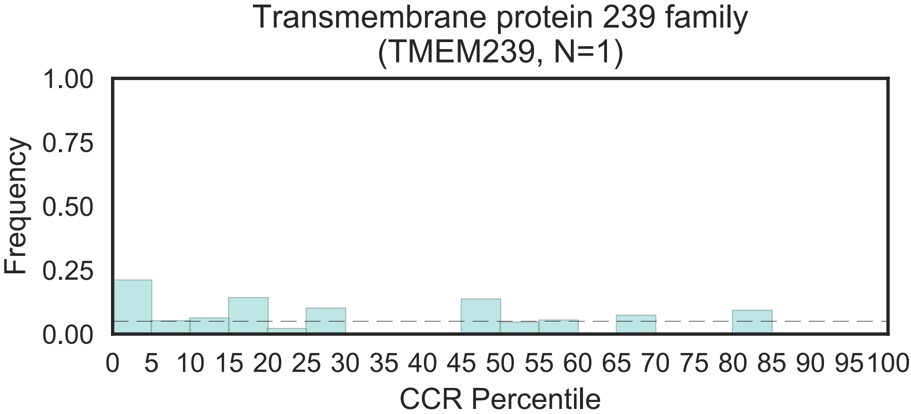

Transmembrane family 220, helix
(TMEM220, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

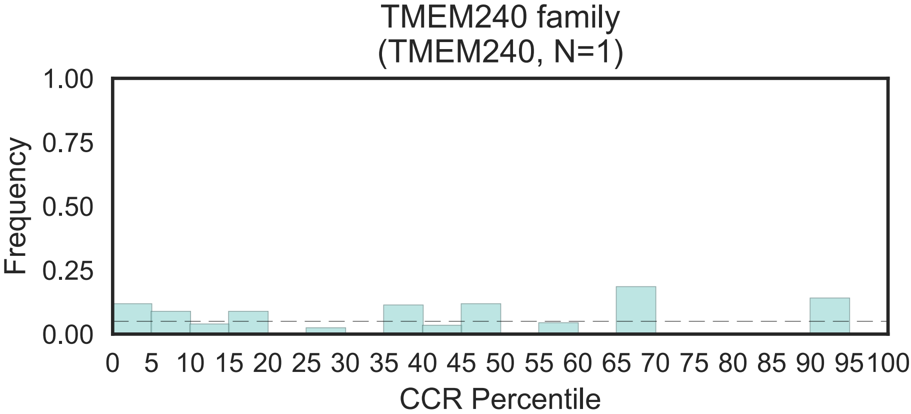

Transmembrane protein 223
(TMEM223, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

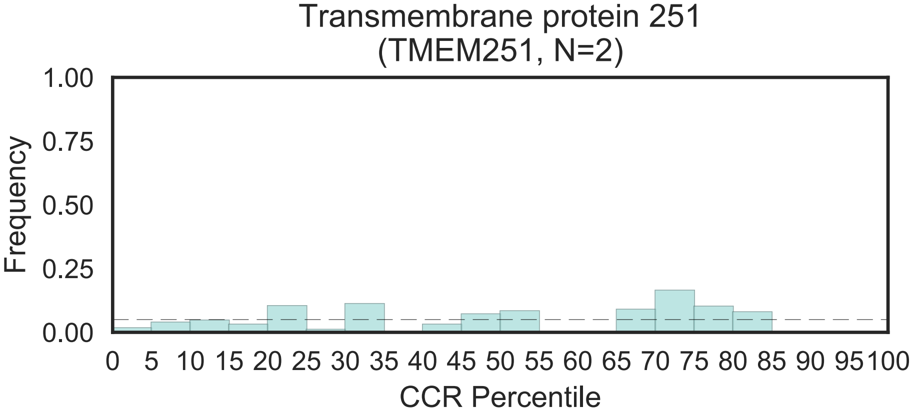

Transmembrane protein family 232
(TMEM232, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

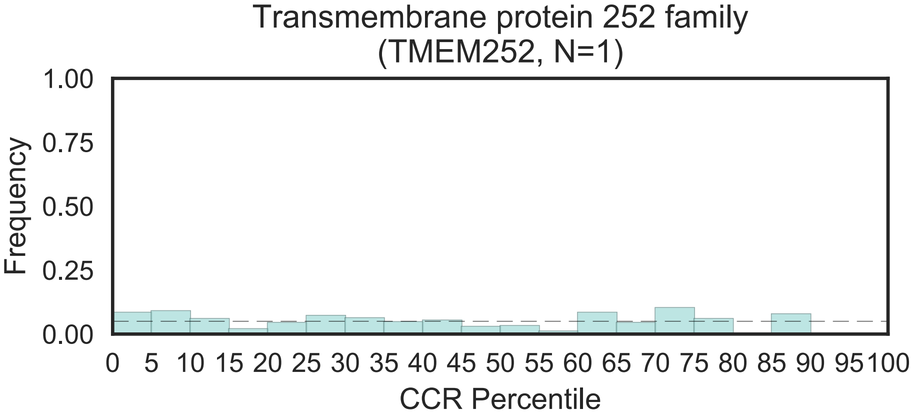

Putative transmembrane family 234
(TMEM234, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

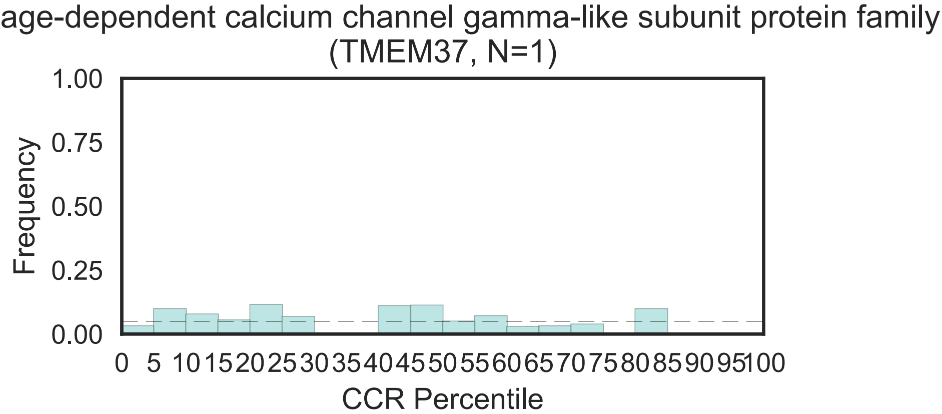

Transmembrane protein 237
(TMEM237, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

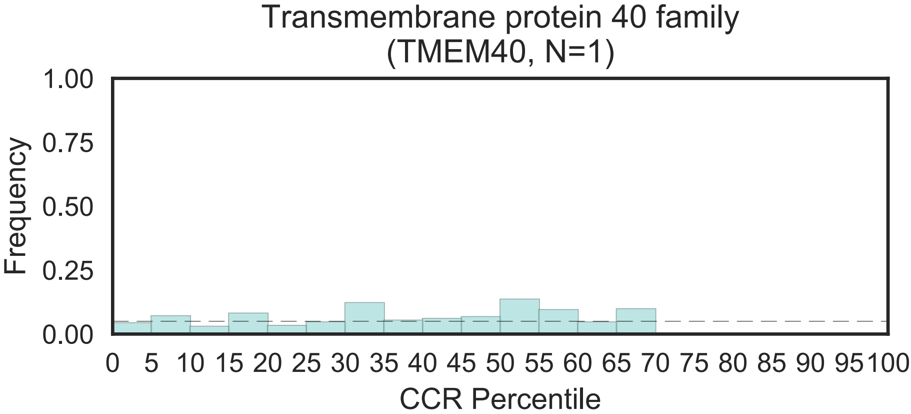

Transmembrane protein 239 family
(TMEM239, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

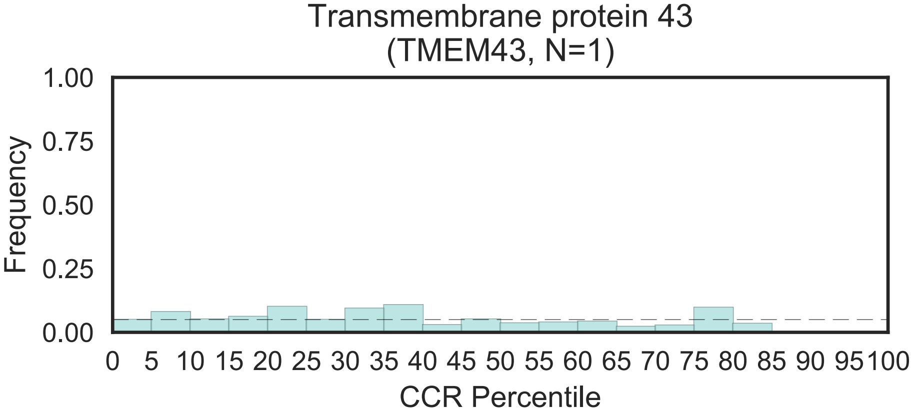

TMEM240 family
(TMEM240, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

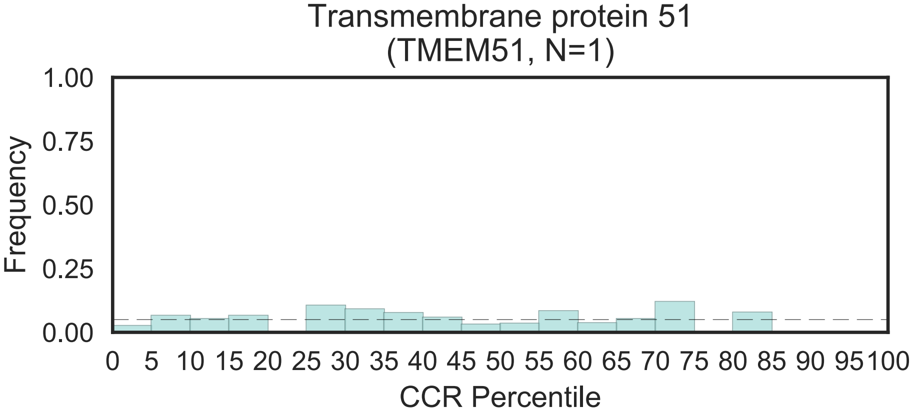

Transmembrane protein 251
(TMEM251, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

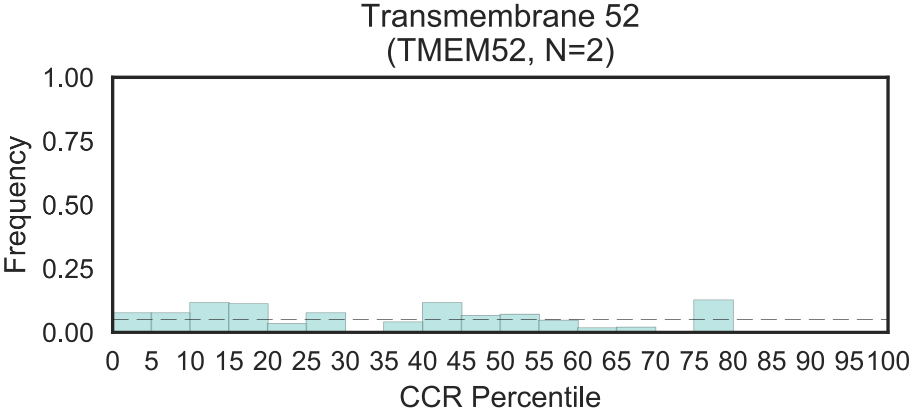

Transmembrane protein 252 family
(TMEM252, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

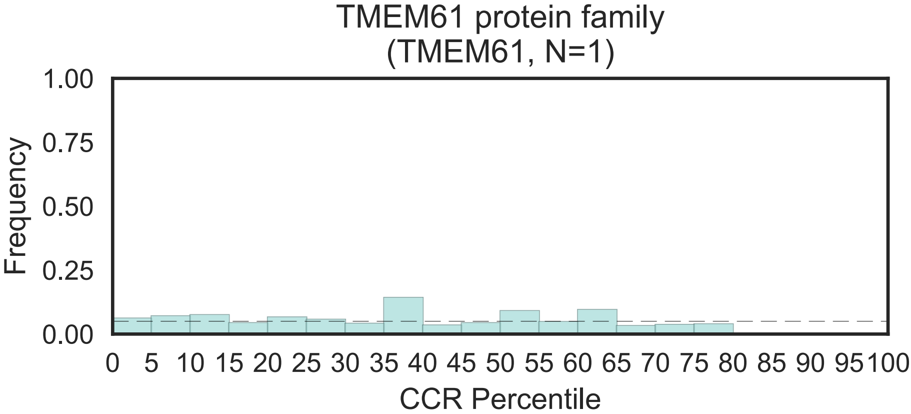

Voltage-dependent calcium channel gamma-like subunit protein family
(TMEM37, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

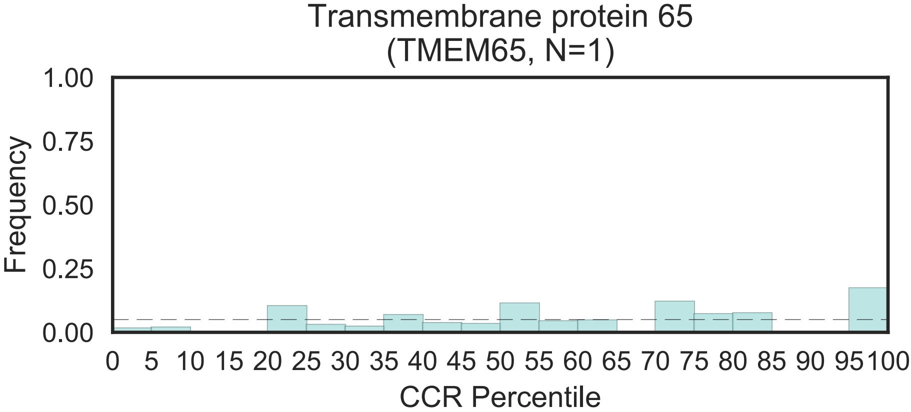

Transmembrane protein 40 family
(TMEM40, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

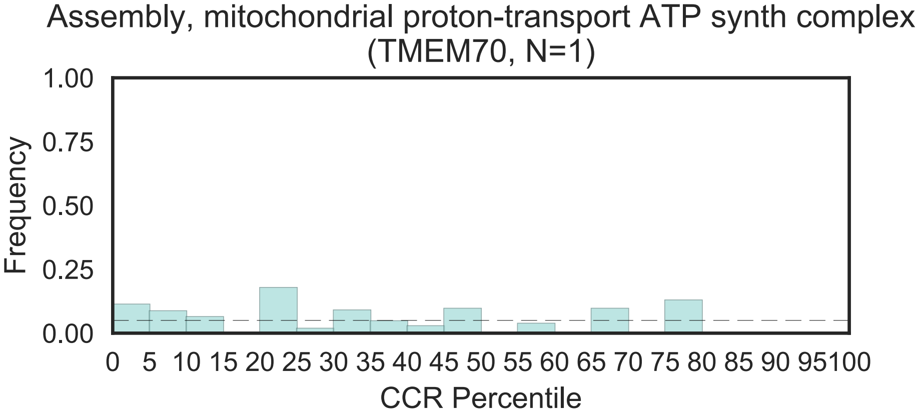

Transmembrane protein 43
(TMEM43, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Transmembrane protein 51
(TMEM51, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

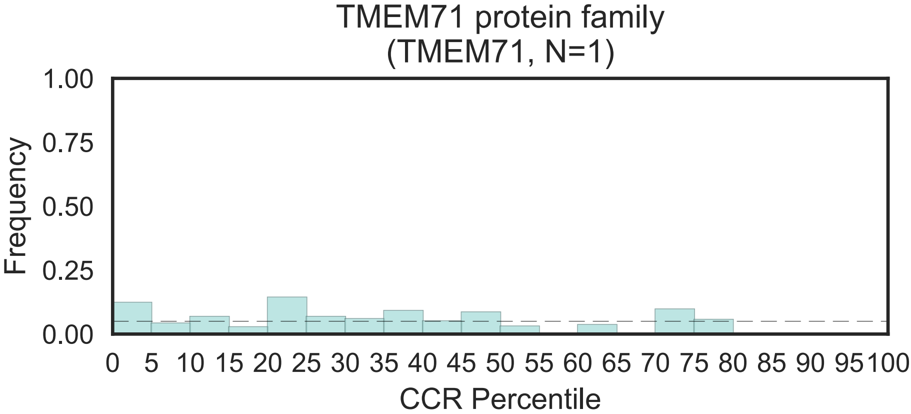

Transmembrane 52
(TMEM52, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

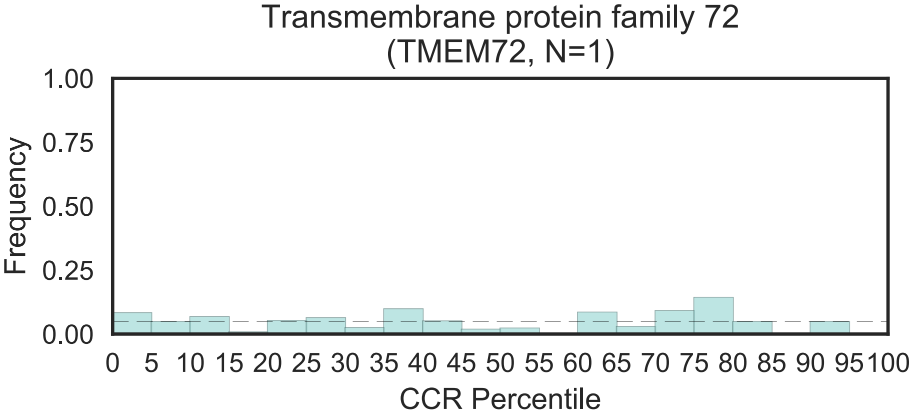

TMEM61 protein family
(TMEM61, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Transmembrane protein 65
(TMEM65, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

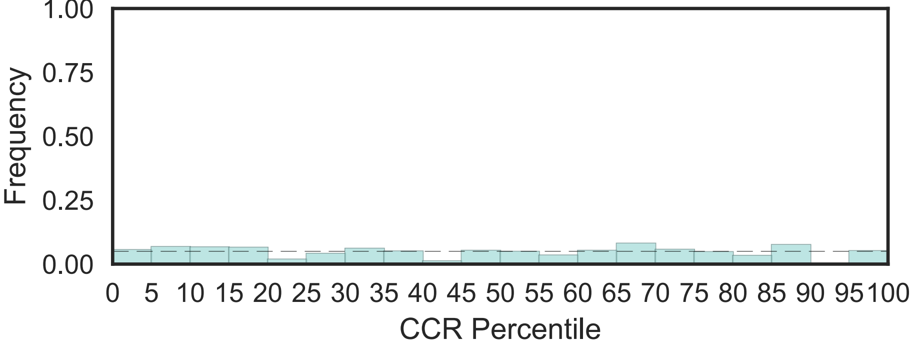


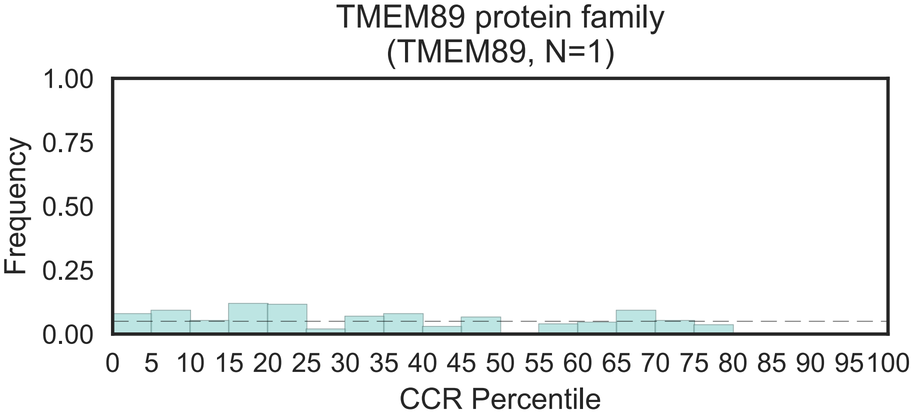
Assembly, mitochondrial proton-transport ATP synth complex (TMEM70, N=1)

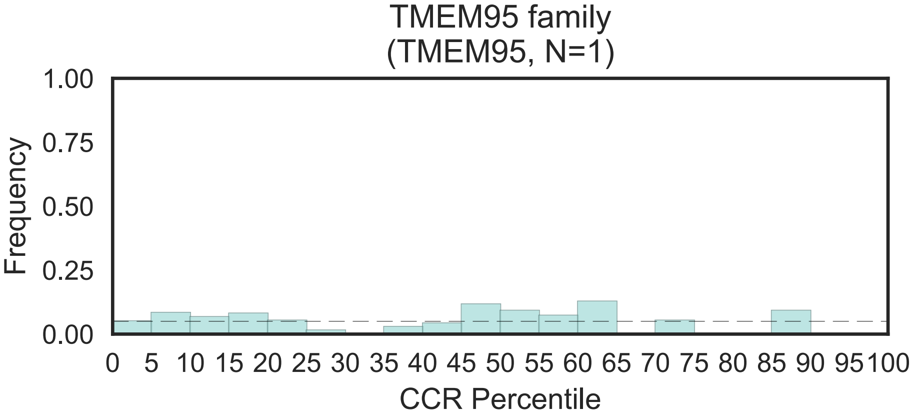

TMEM71 protein family
(TMEM71, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

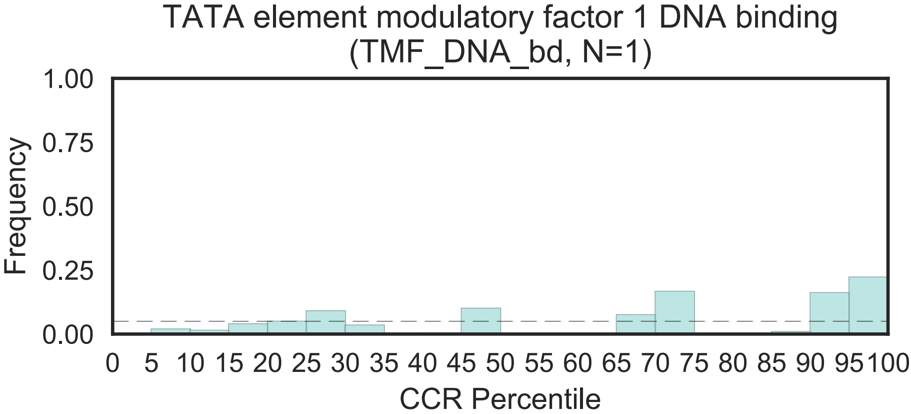

Transmembrane protein family 72
(TMEM72, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

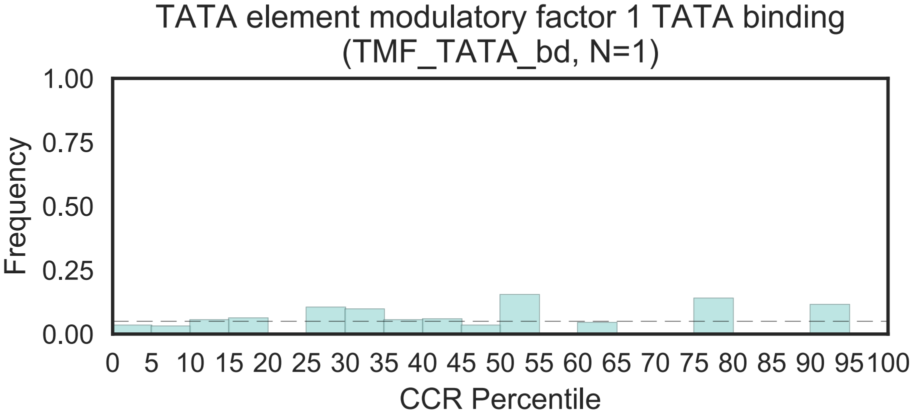
Transmembrane protein 82
(TMEM82, N=1)

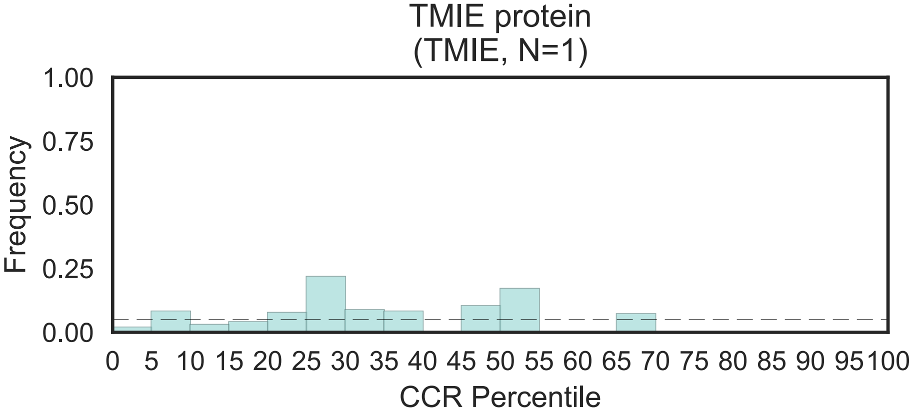


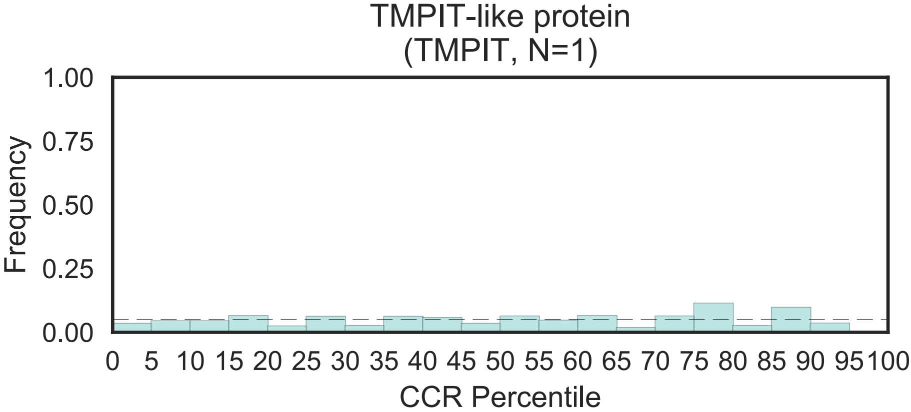

TMEM89 protein family
(TMEM89, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

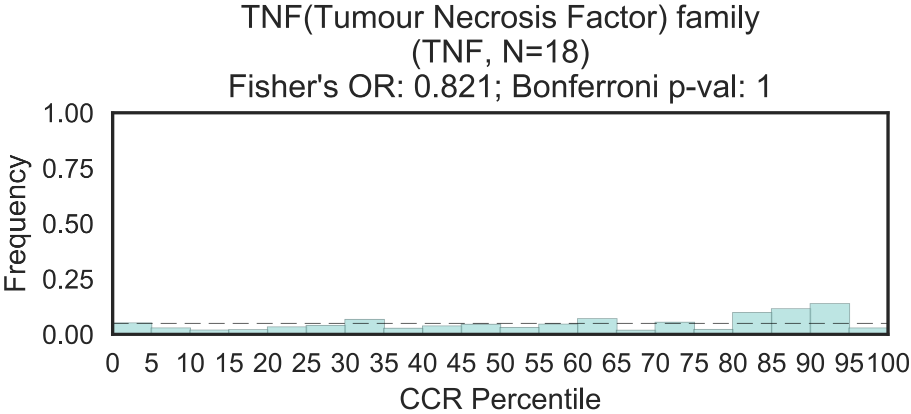

TMEM95 family
(TMEM95, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

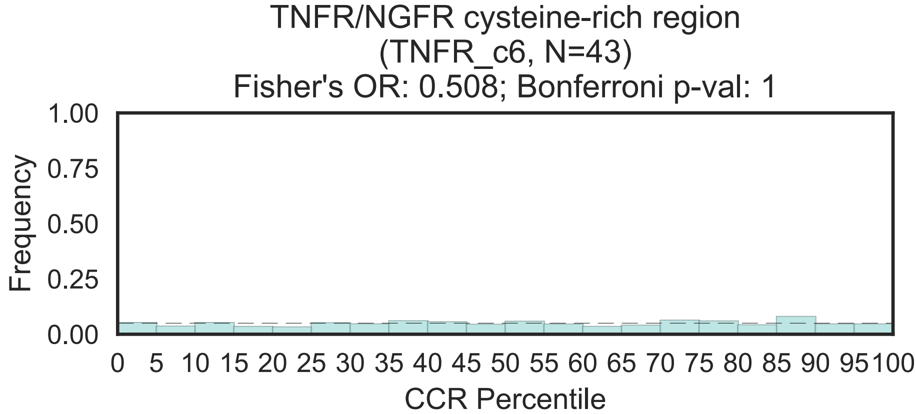

TATA element modulatory factor 1 DNA binding
(TMF_DNA_bd, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

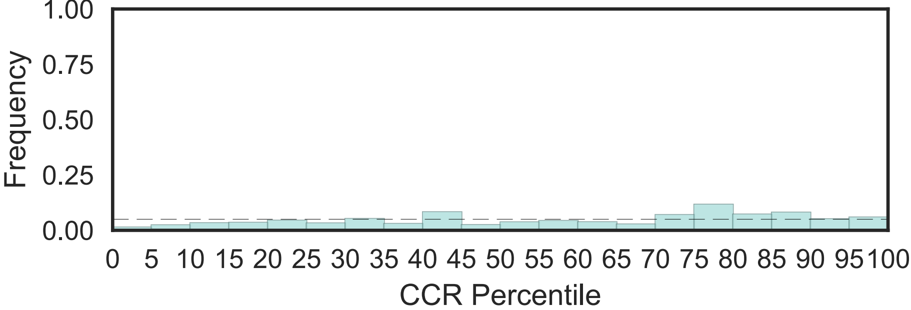

TATA element modulatory factor 1 TATA binding
(TMF_TATA_bd, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


TMIE protein
(TMIE, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

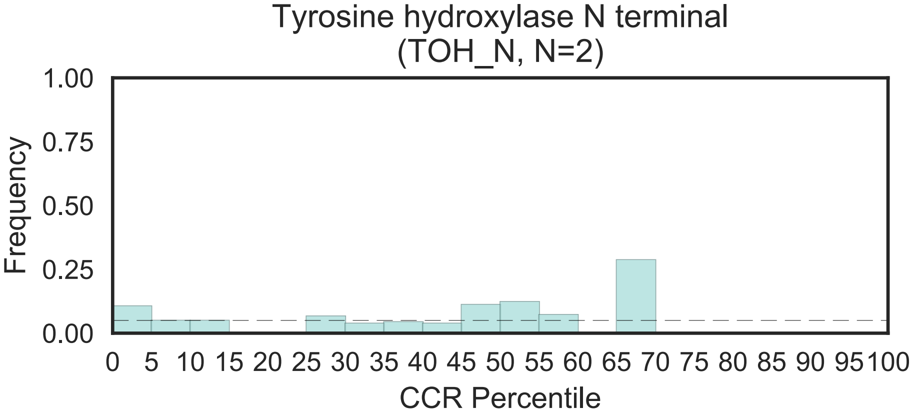

TMPIT-like protein
(TMPIT, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


TNF(Tumour Necrosis Factor) family
(TNF, N=18)
Fisher's OR: 0.821; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

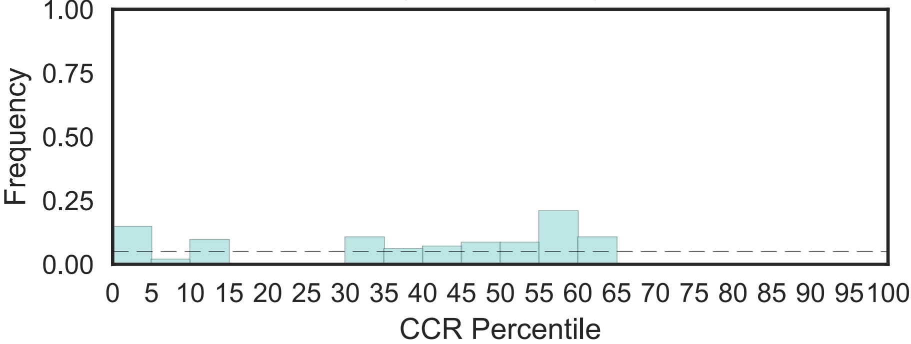

TNFR/NGFR cysteine-rich region
(TNFR_c6, N=43)
Fisher's OR: 0.508; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

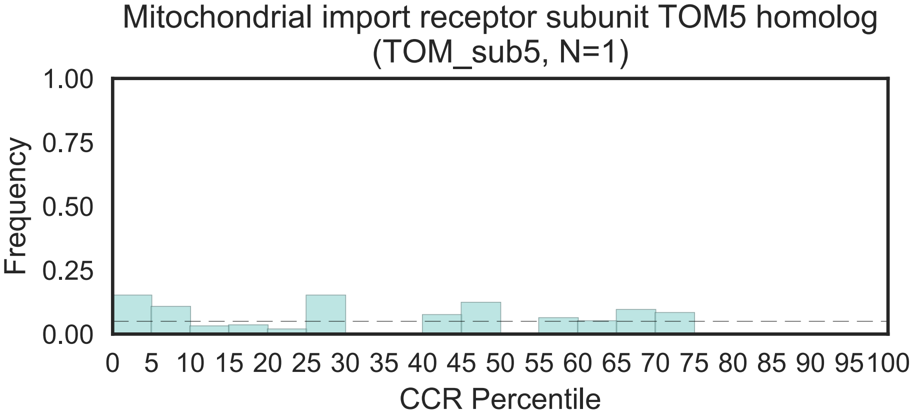


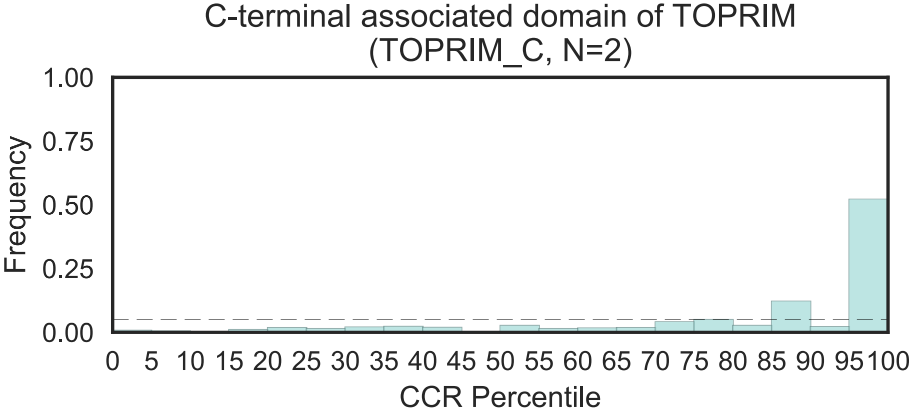
TNRC6-PABC binding domain
(TNRC6-PABC_bdg, N=4)
Fisher's OR: 1.3; Bonferroni p-val: 1

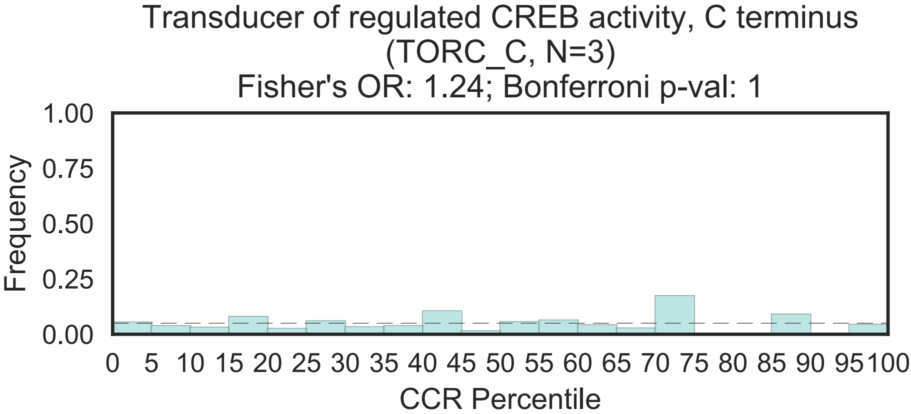

Tyrosine hydroxylase N terminal
(TOH_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

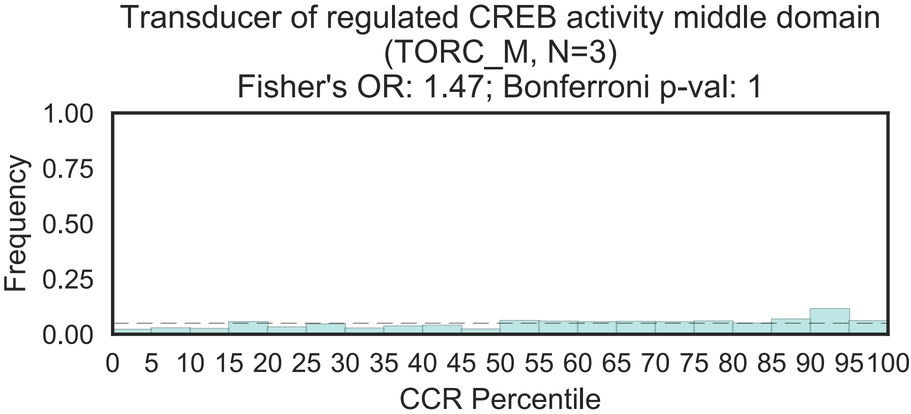
Mitochondrial import receptor subunit TOM6 homolog (TOM6p, N=1)

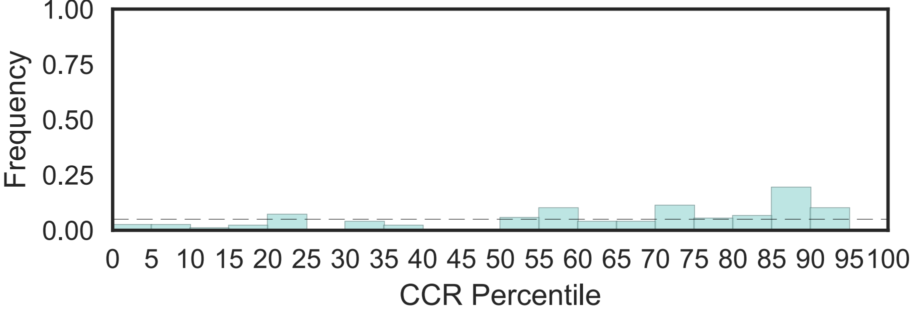



Mitochondrial import receptor subunit TOM5 homolog (TOM_sub5, N=1)

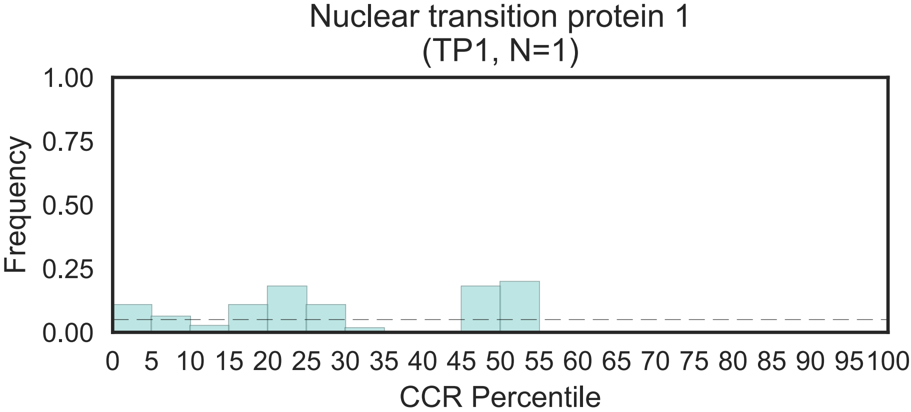

C-terminal associated domain of TOPRIM
(TOPRIM_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

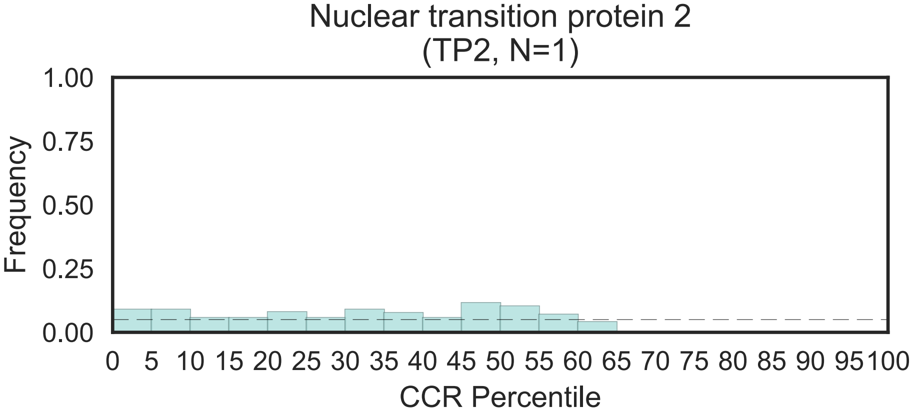

Transducer of regulated CREB activity, C terminus
(TORC_C, N=3)
Fisher's OR: 1.24; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

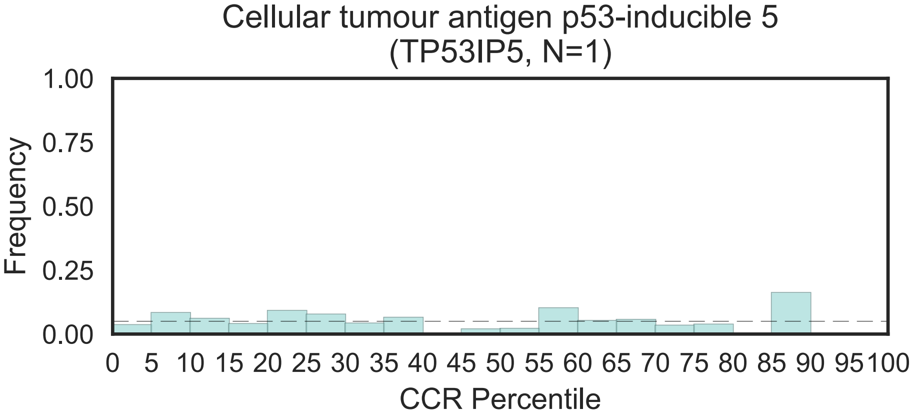

Transducer of regulated CREB activity middle domain
(TORC_M, N=3)
Fisher's OR: 1.47; Bonferroni p-val: 1

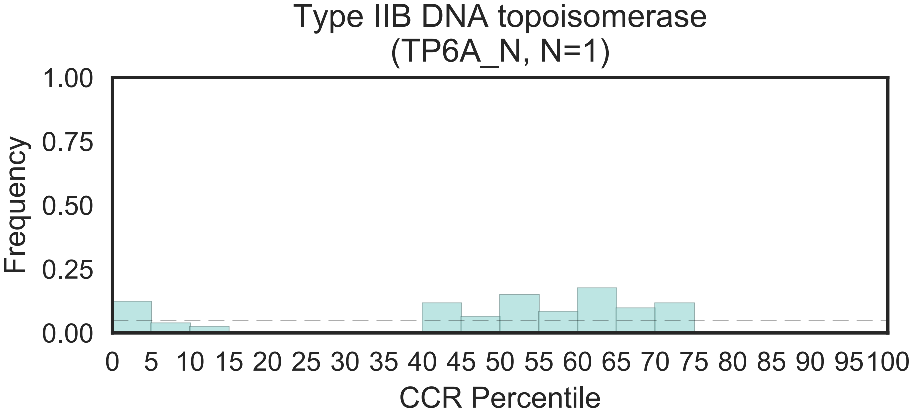


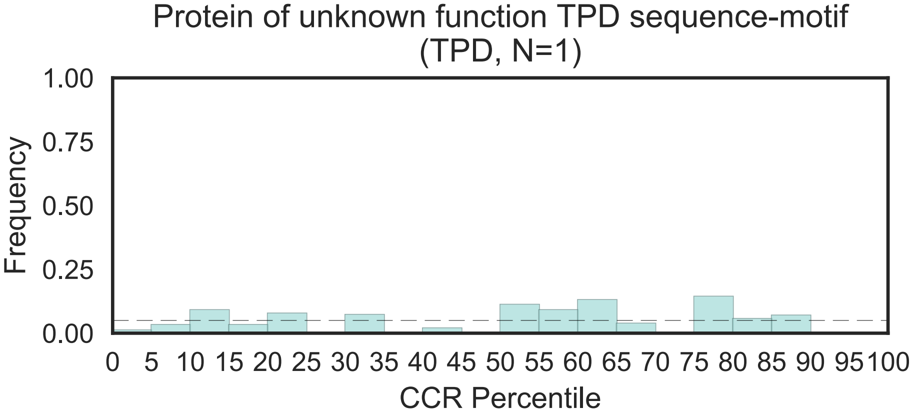
Transducer of regulated CREB activity, N terminus
(TORC_N, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

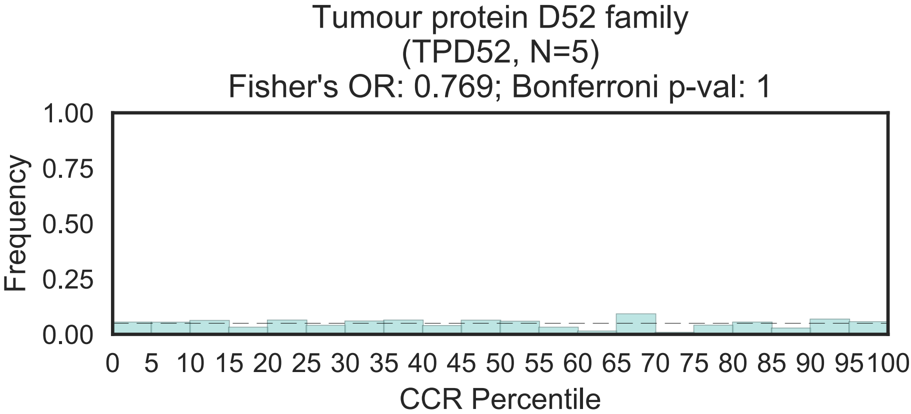

Nuclear transition protein 1
(TP1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

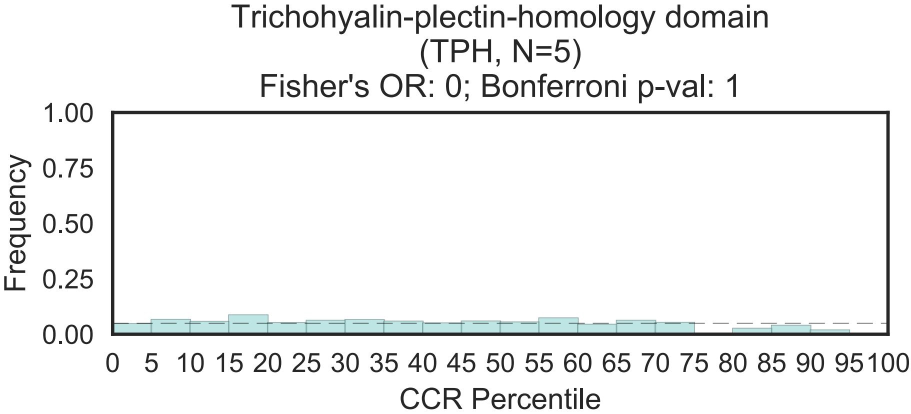

Nuclear transition protein 2
(TP2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Cellular tumour antigen p53-inducible 5
(TP53IP5, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

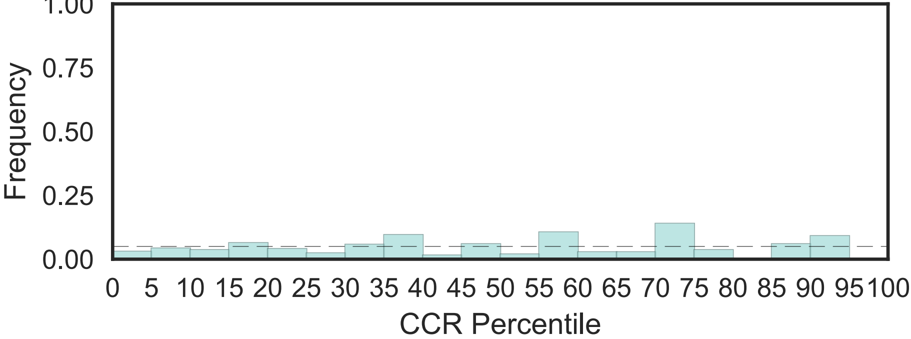

Type IIB DNA topoisomerase
(TP6A_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Protein of unknown function TPD sequence-motif
(TPD, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

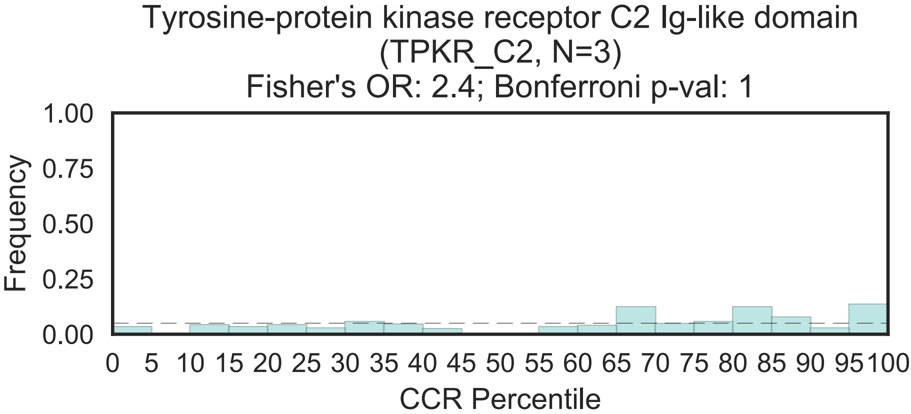

Tumour protein D52 family
(TPD52, N=5)
Fisher's OR: 0.769; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



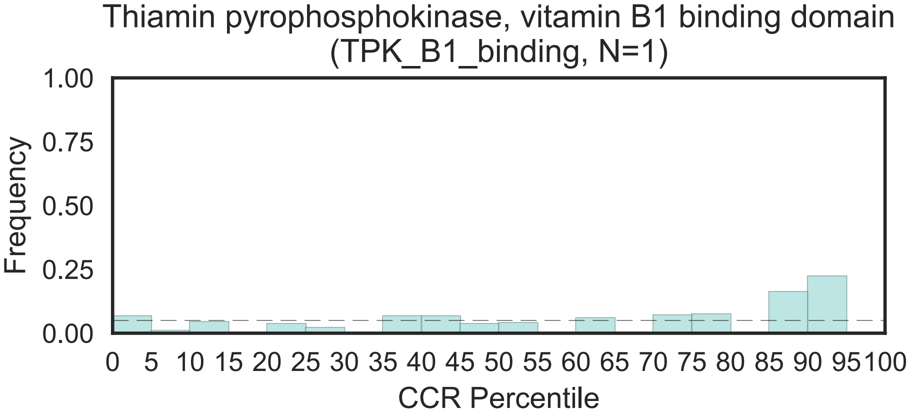
Trichohyalin-plectin-homology domain
(TPH, N=5)
Fisher's OR: 0; Bonferroni p-val: 1

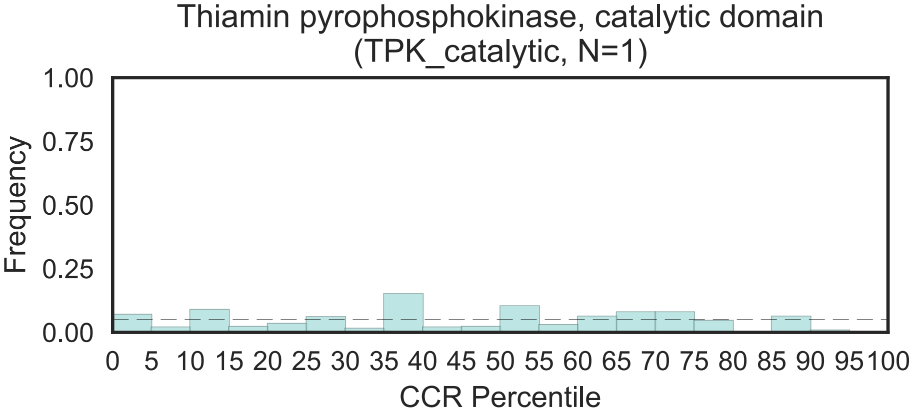


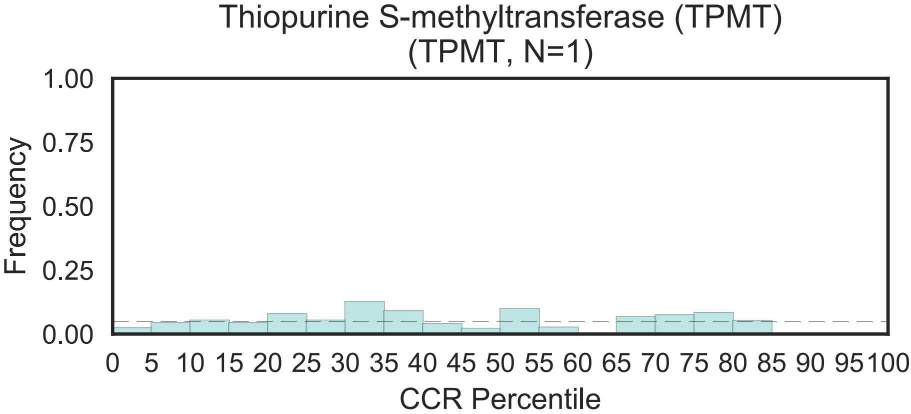
p53-regulated apoptosis-inducing protein 1
(TPIP1, N=1)

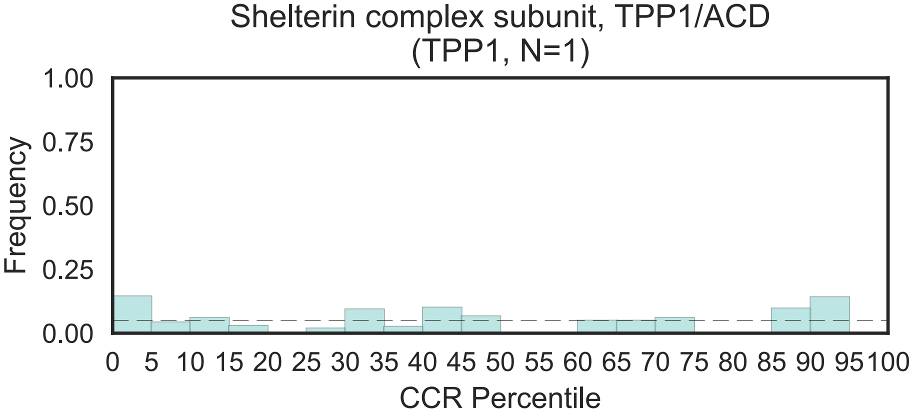


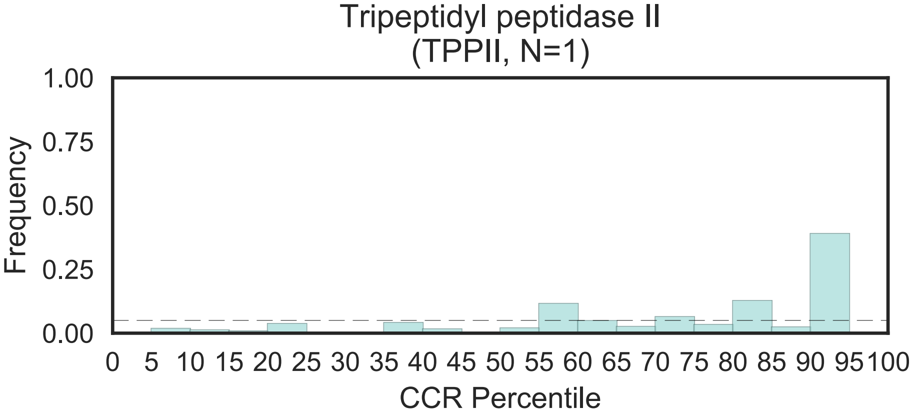
Tyrosine-protein kinase receptor C2 Ig-like domain
(TPKR_C2, N=3)
Fisher's OR: 2.4; Bonferroni p-val: 1

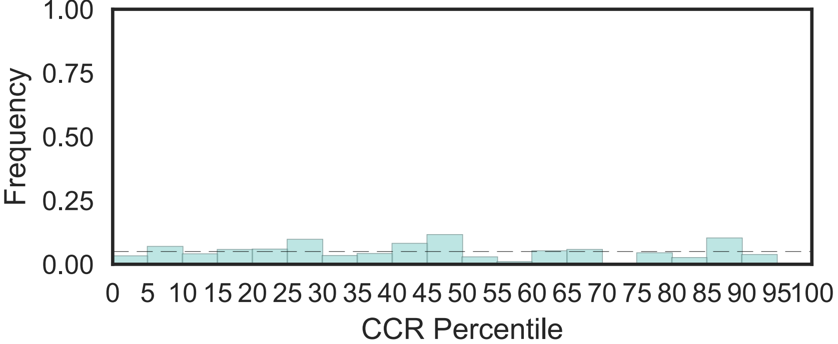

Thiamin pyrophosphokinase, vitamin B1 binding domain
(TPK_B1_binding, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Thiamin pyrophosphokinase, catalytic domain
(TPK_catalytic, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

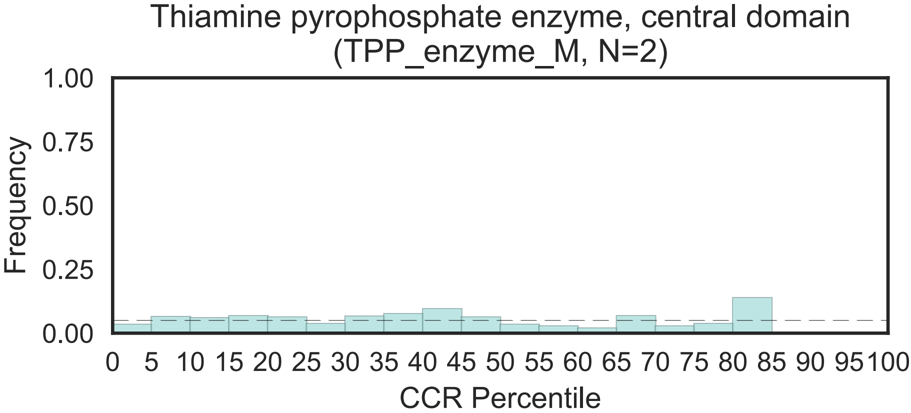

Thiopurine S-methyltransferase (TPMT)
(TPMT, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

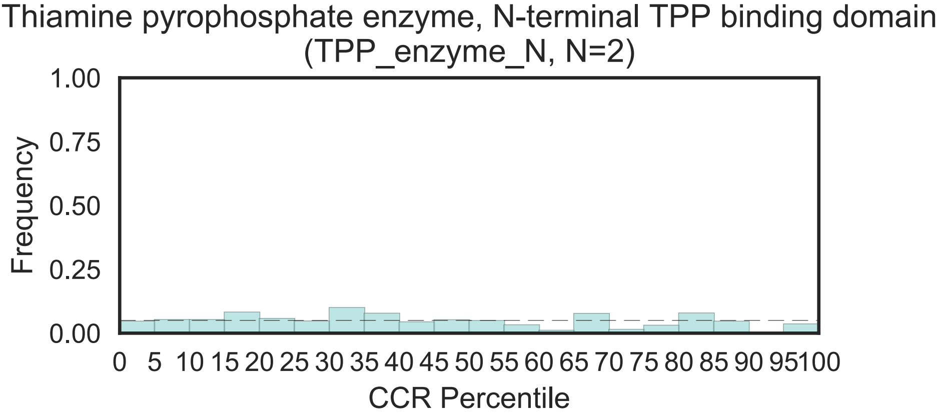

Shelterin complex subunit, TPP1/ACD
(TPP1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Tripeptidyl peptidase II
(TPPII, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

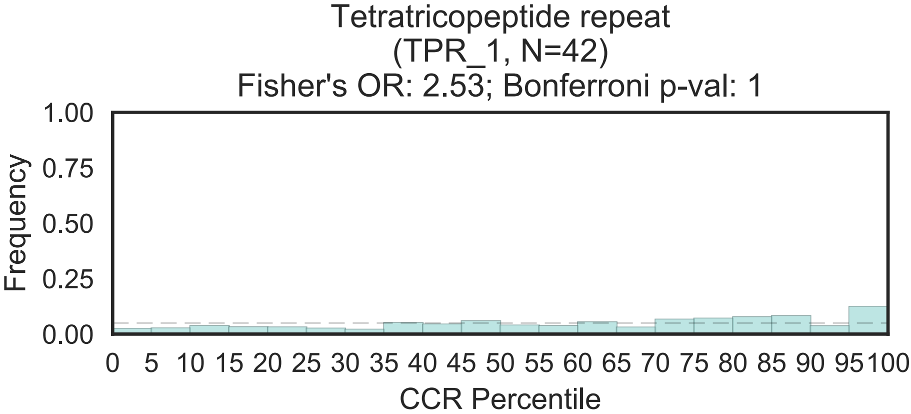


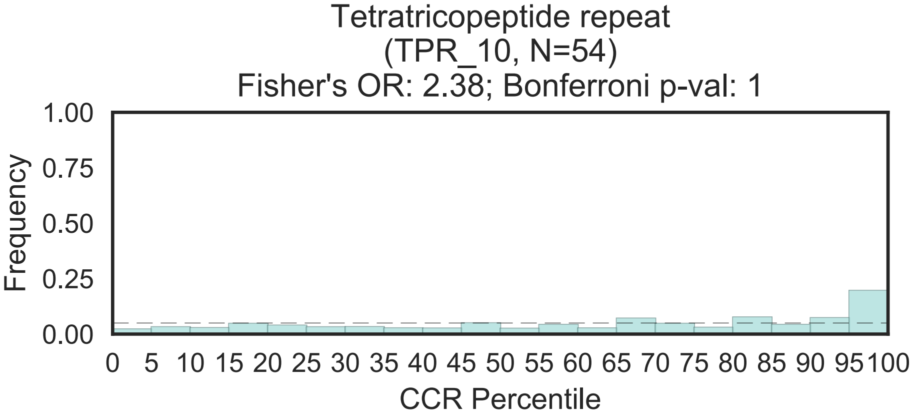
Thiamine pyrophosphate enzyme, C-terminal TPP binding domain
(TPP_enzyme_C, N=2)

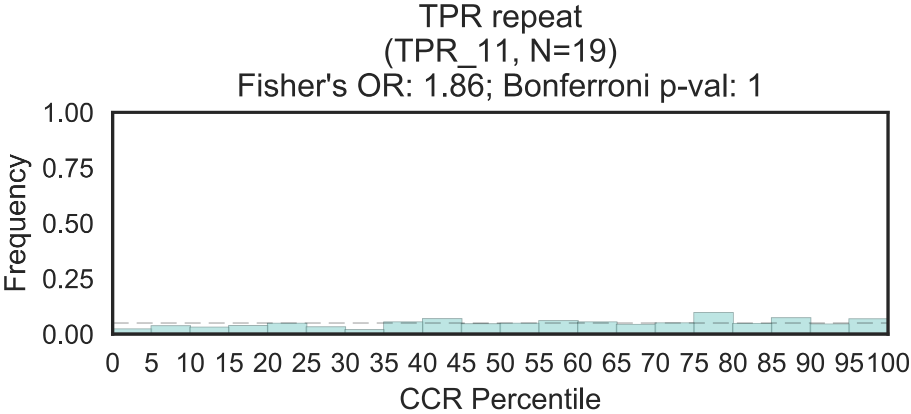

Thiamine pyrophosphate enzyme, central domain
(TPP_enzyme_M, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



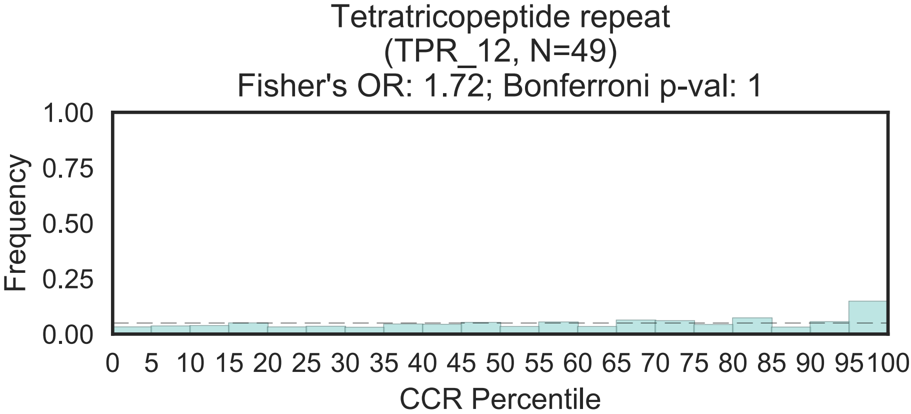
Thiamine pyrophosphate enzyme, N-terminal TPP binding domain (TPP_enzyme_N, N=2)

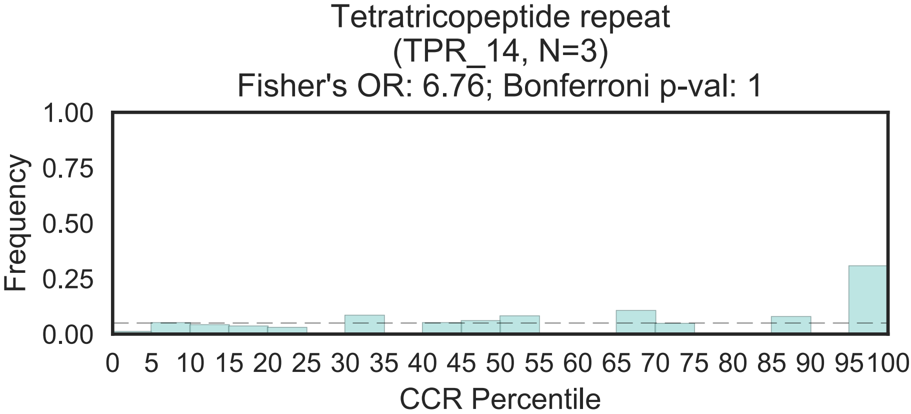

Tetratricopeptide repeat
(TPR_1, N=42)
Fisher's OR: 2.53; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

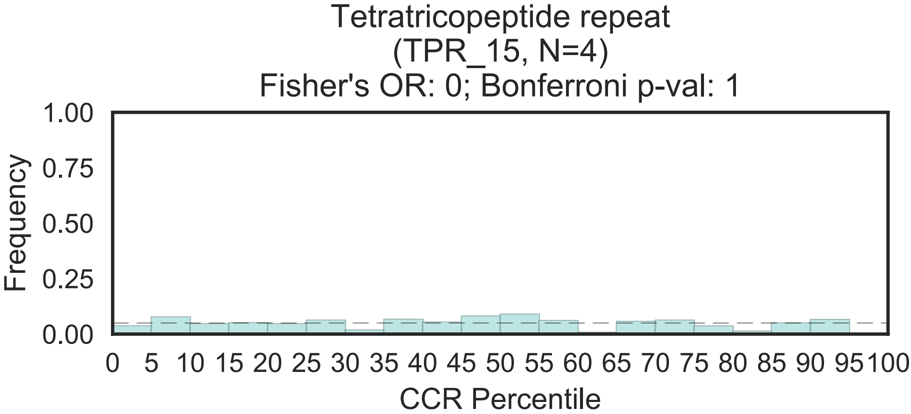

Tetratricopeptide repeat
(TPR_10, N=54)
Fisher's OR: 2.38; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

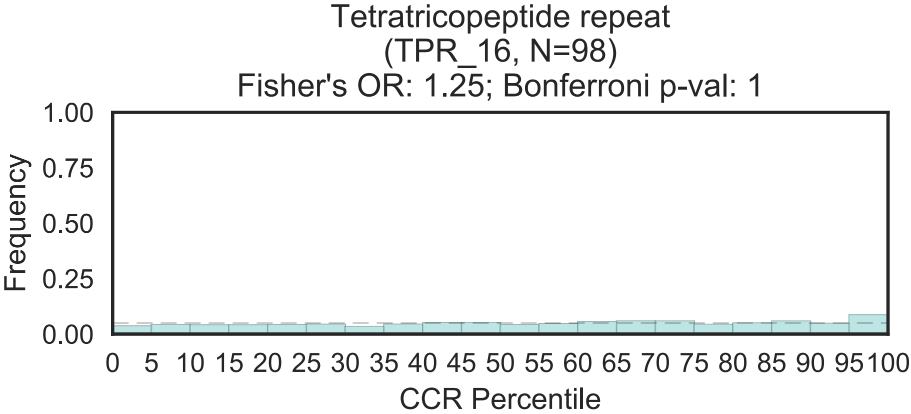


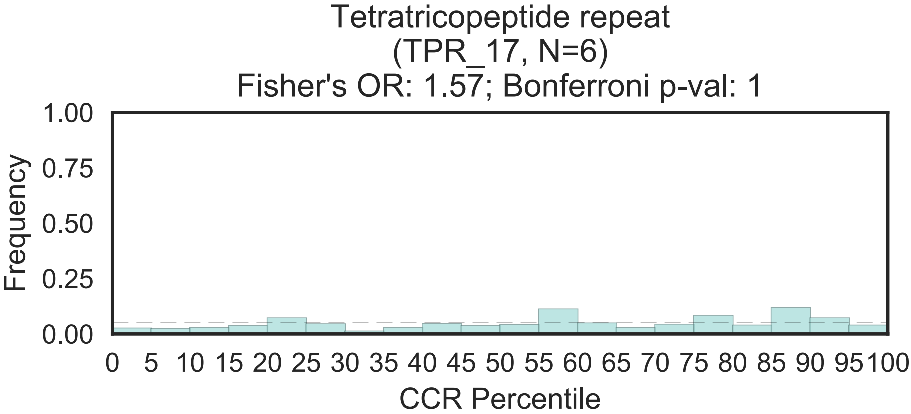
TPR repeat
(TPR_11, N=19)
Fisher's OR: 1.86; Bonferroni p-val: 1


Tetratricopeptide repeat
(TPR_12, N=49)
Fisher's OR: 1.72; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

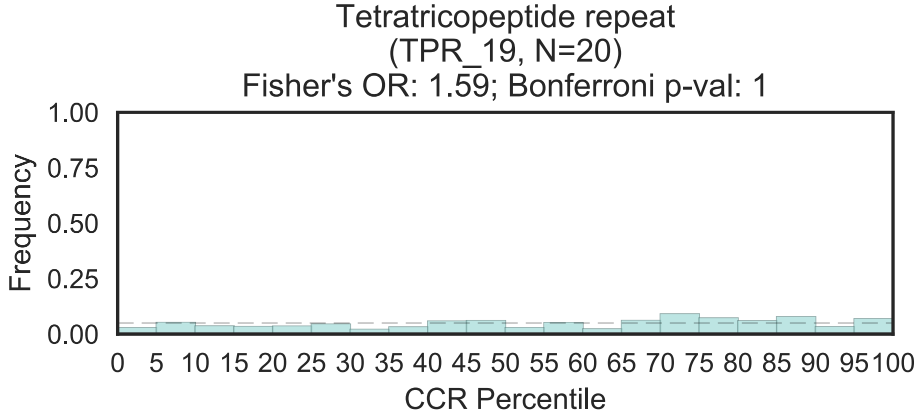

Tetratricopeptide repeat
(TPR_14, N=3)
Fisher's OR: 6.76; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

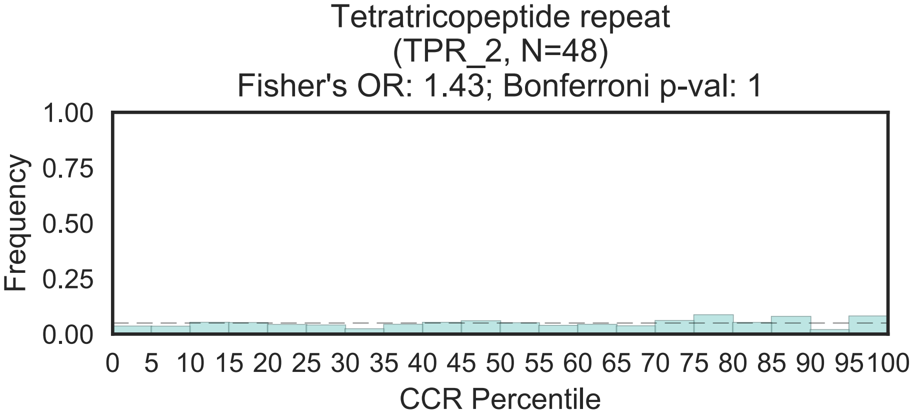

Tetratricopeptide repeat
(TPR_15, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

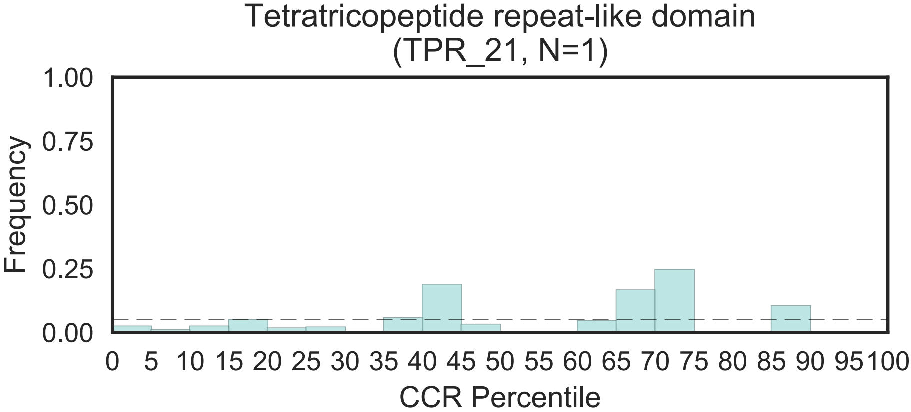

Tetratricopeptide repeat
(TPR_16, N=98)
Fisher's OR: 1.25; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

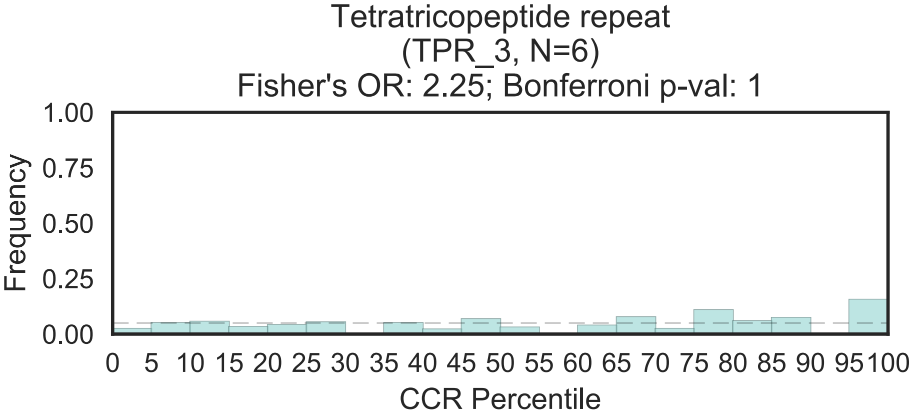


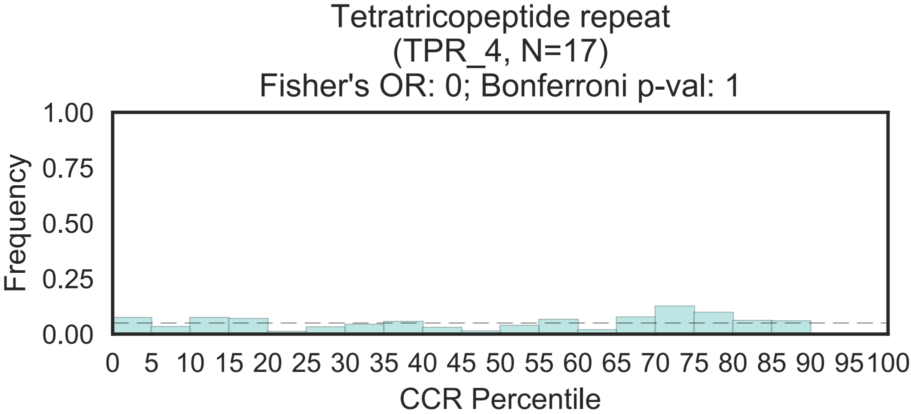
Tetratricopeptide repeat
(TPR_17, N=6)
Fisher's OR: 1.57; Bonferroni p-val: 1

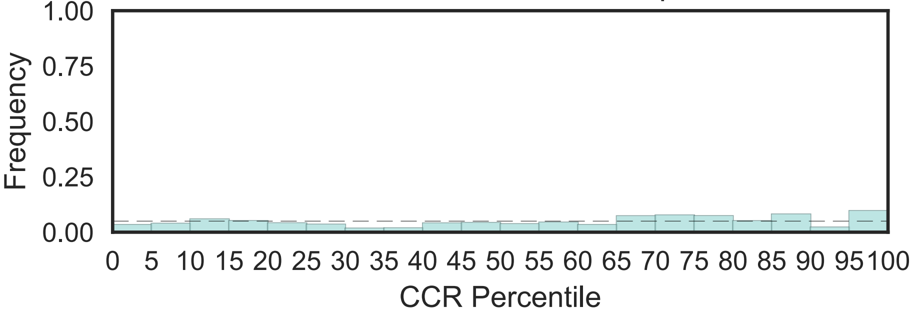

Tetratricopeptide repeat
(TPR_19, N=20)
Fisher's OR: 1.59; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Tetratricopeptide repeat
(TPR_2, N=48)
Fisher's OR: 1.43; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

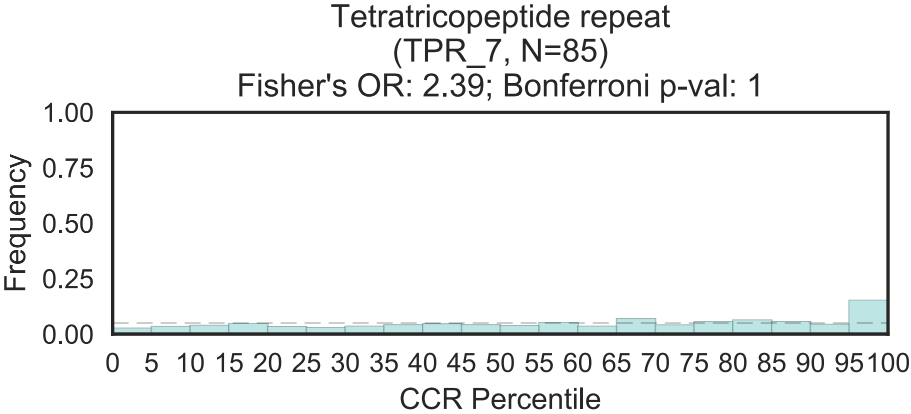

Tetratricopeptide repeat-like domain
(TPR_21, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

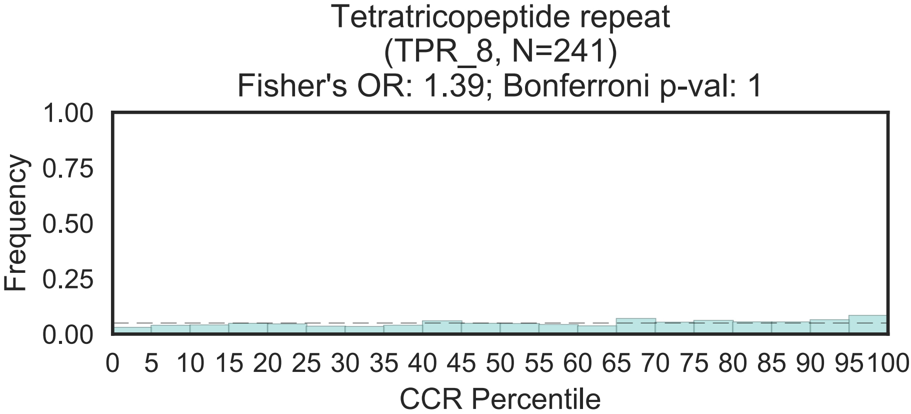

Tetratricopeptide repeat
(TPR_3, N=6)
Fisher's OR: 2.25; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

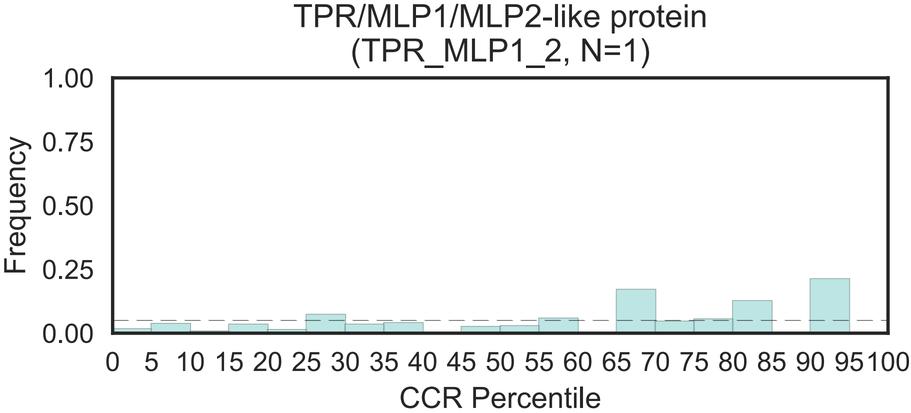

Tetratricopeptide repeat
(TPR_4, N=17)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

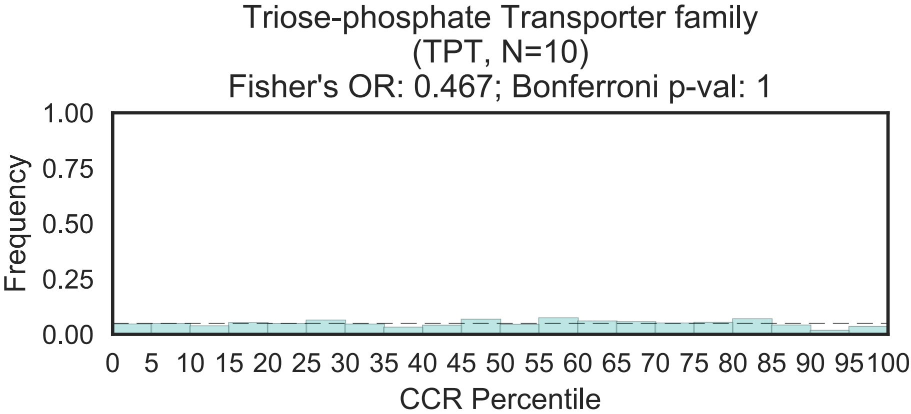


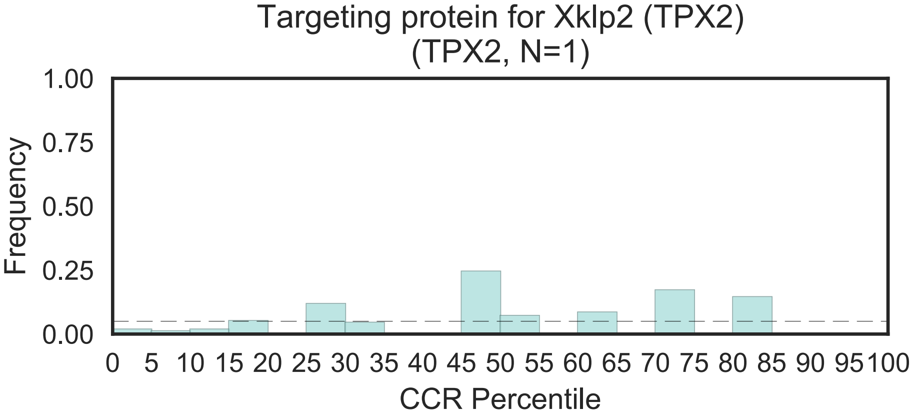
Tetratricopeptide repeat
(TPR_6, N=37)
Fisher's OR: 1.86; Bonferroni p-val: 1

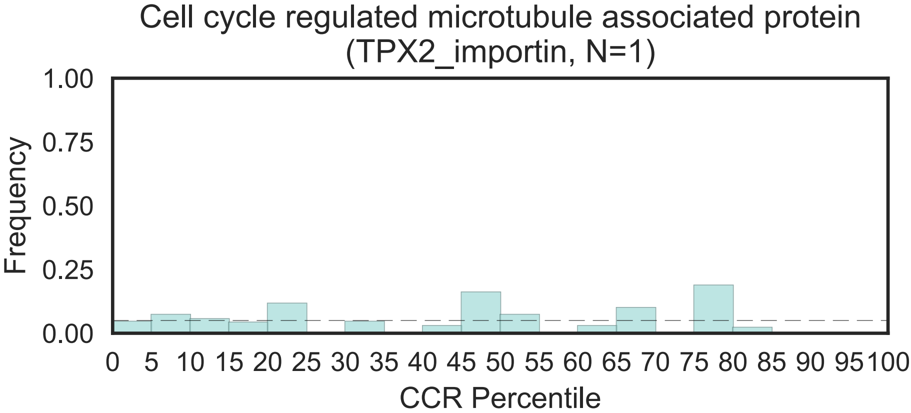

Tetratricopeptide repeat
(TPR_7, N=85)
Fisher's OR: 2.39; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

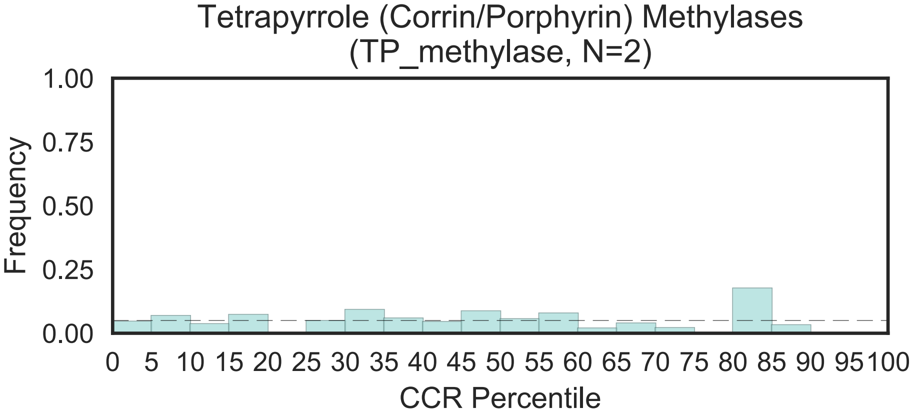

Tetratricopeptide repeat
(TPR_8, N=241)
Fisher's OR: 1.39; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

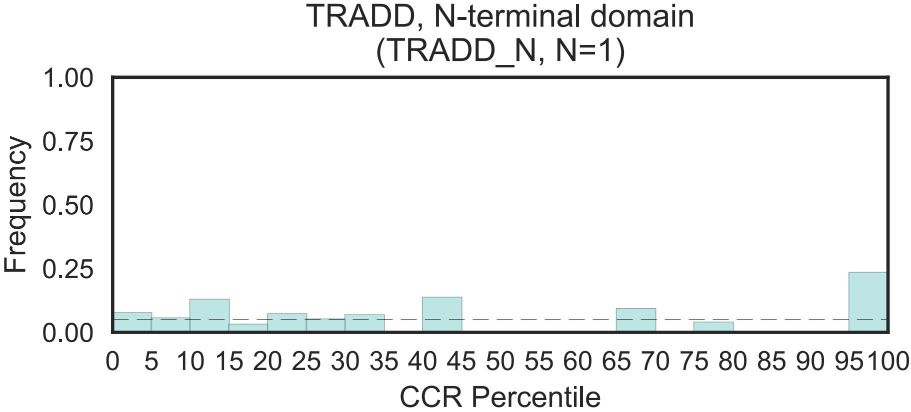

TPR/MLP1/MLP2-like protein
(TPR_MLP1_2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

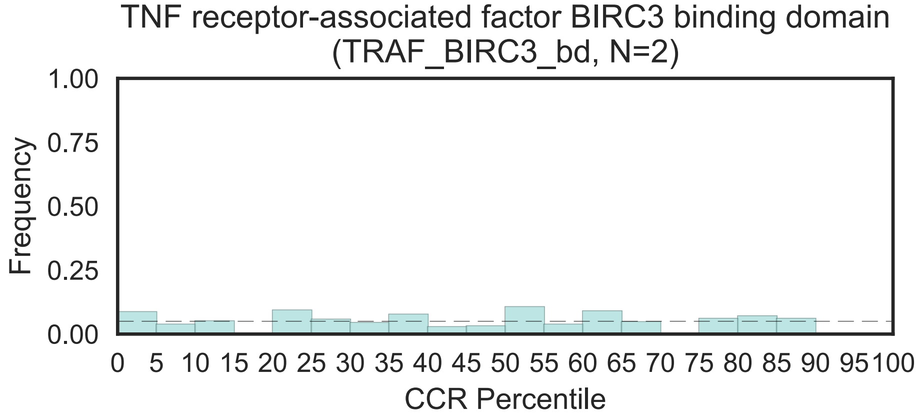

Triose-phosphate Transporter family
(TPT, N=10)
Fisher's OR: 0.467; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

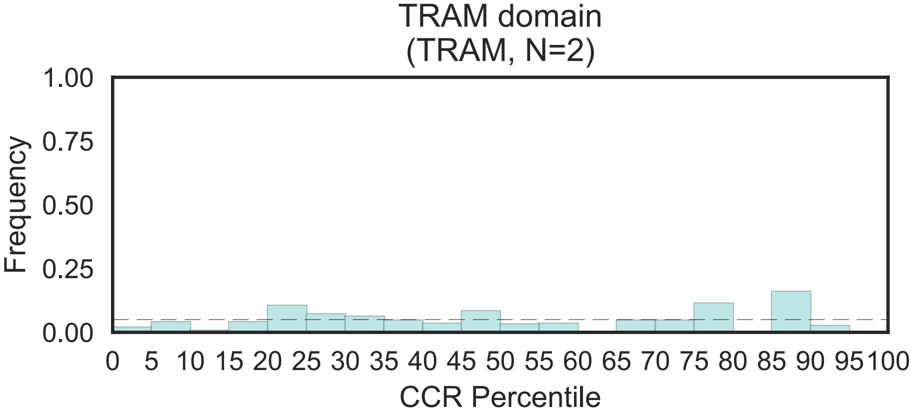

Targeting protein for Xklp2 (TPX2)
(TPX2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

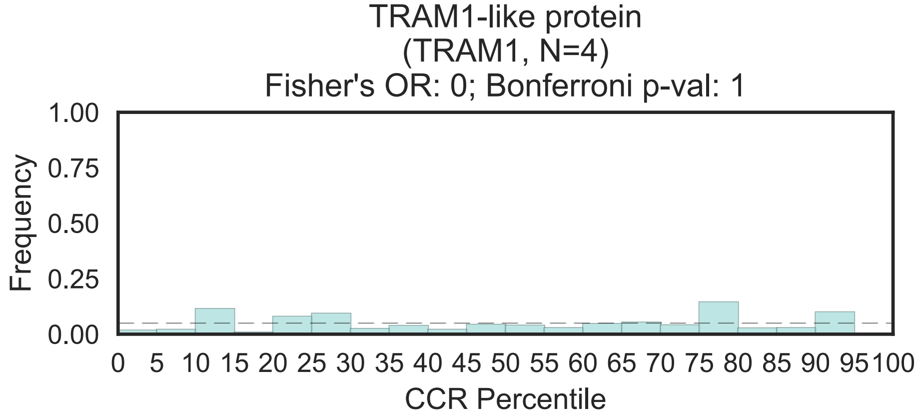

Cell cycle regulated microtubule associated protein
(TPX2_importin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

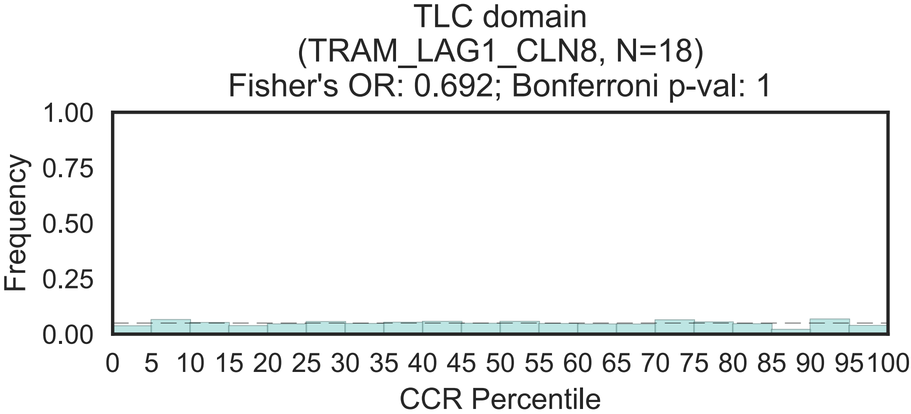

Tetrapyrrole (Corrin/Porphyrin) Methylases
(TP_methylase, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

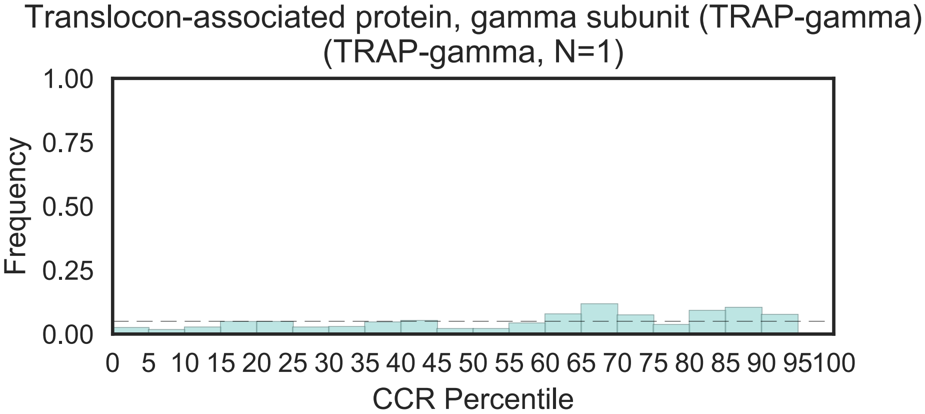

TRADD, N-terminal domain
(TRADD_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


TNF receptor-associated factor BIRC3 binding domain
(TRAF_BIRC3_bd, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

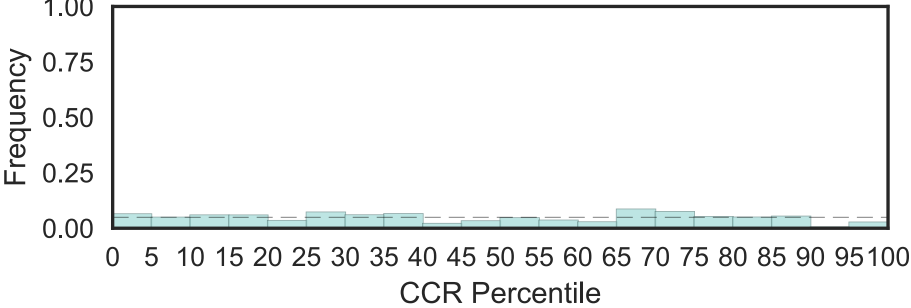

TRAM domain
(TRAM, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

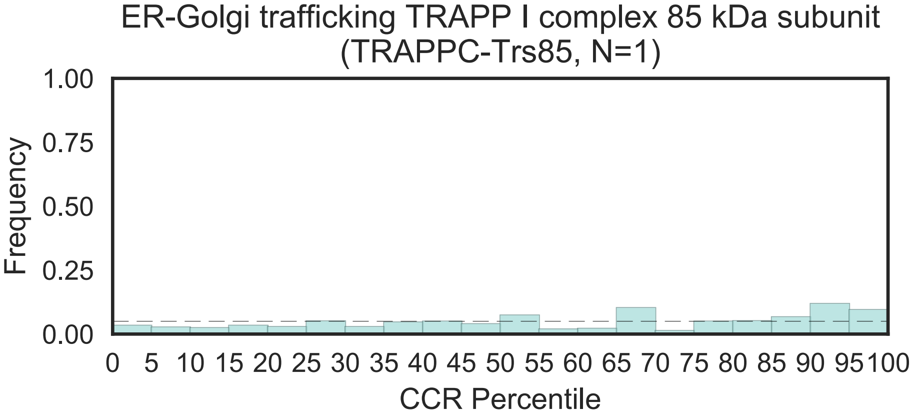

TRAM1-like protein
(TRAM1, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

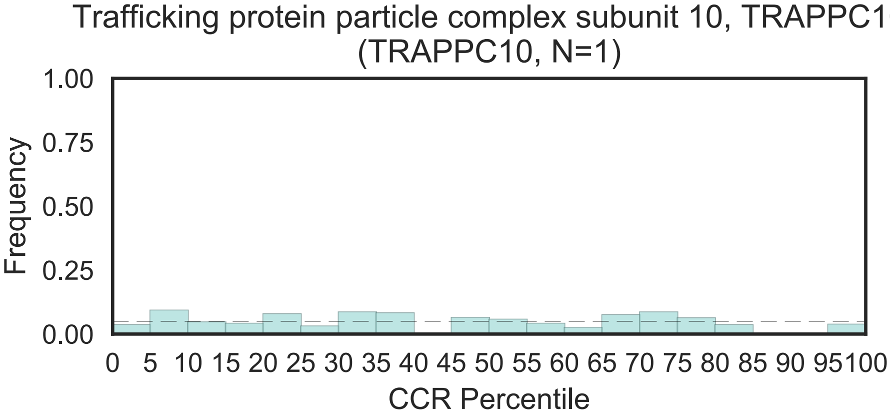

TLC domain
(TRAM_LAG1_CLN8, N=18)
Fisher's OR: 0.692; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

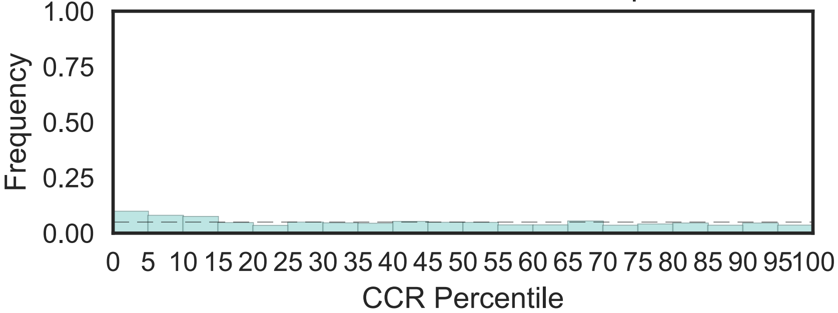

Translocon-associated protein, gamma subunit (TRAP-gamma)
(TRAP-gamma, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Transport protein particle (TRAPP) component
(TRAPP, N=7)
Fisher's OR: 0.511; Bonferroni p-val: 1

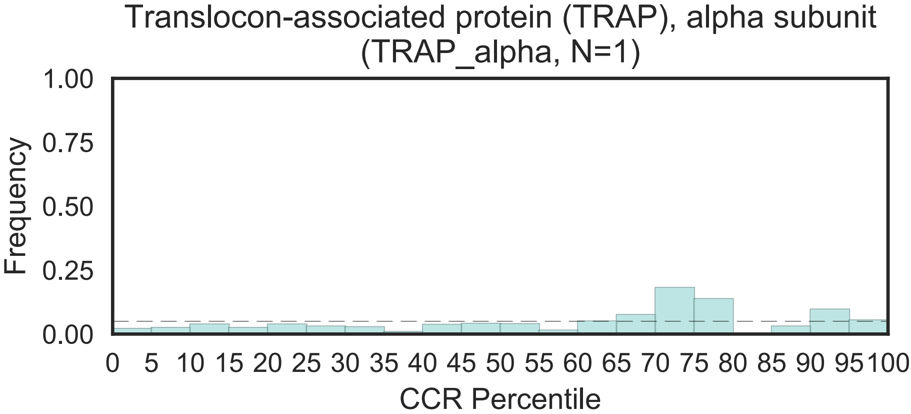


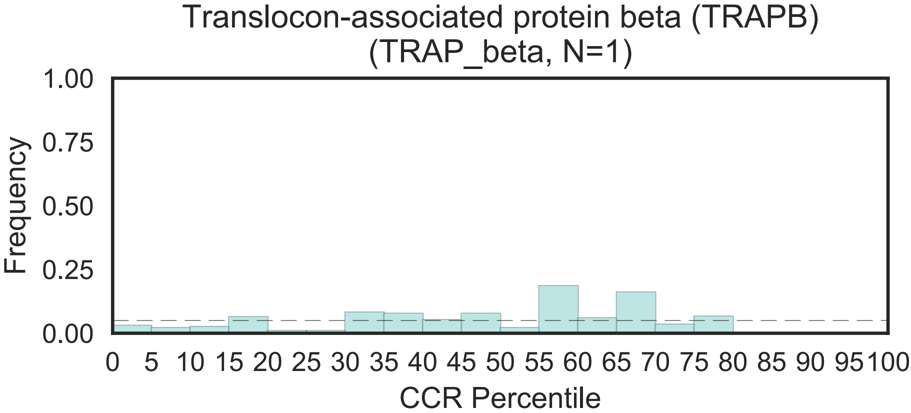

ER-Golgi trafficking TRAPP I complex 85 kDa subunit
(TRAPPC-Trs85, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

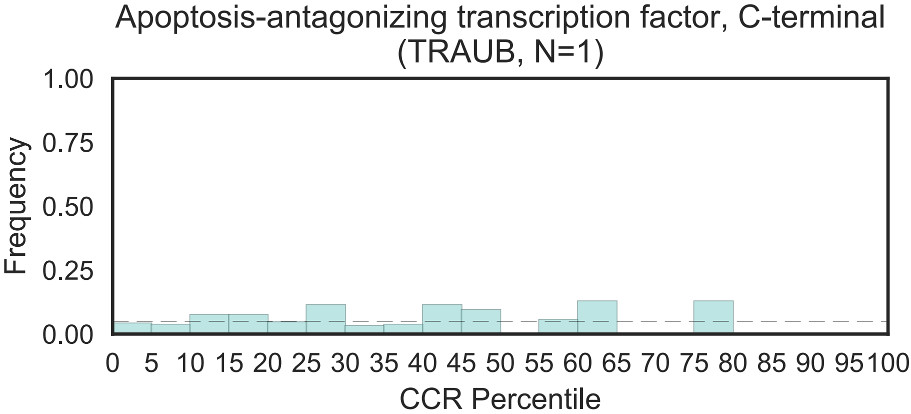

Trafficking protein particle complex subunit 10, TRAPPC10
(TRAPPC10, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

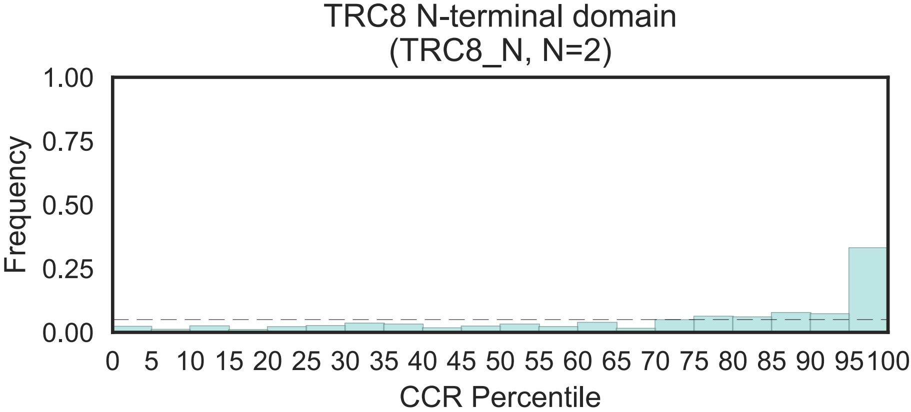


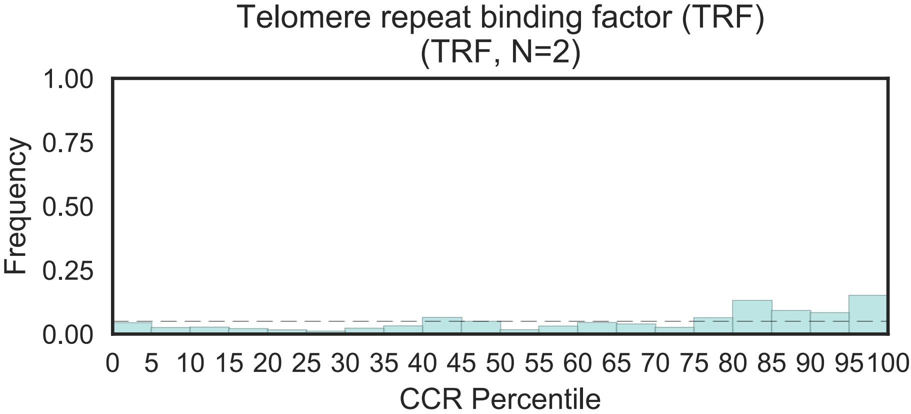
Transport protein Trs120 or TRAPPC9, TRAPP II complex subunit
(TRAPPC9-Trs120, N=4)
Fisher's OR: 0.718; Bonferroni p-val: 1

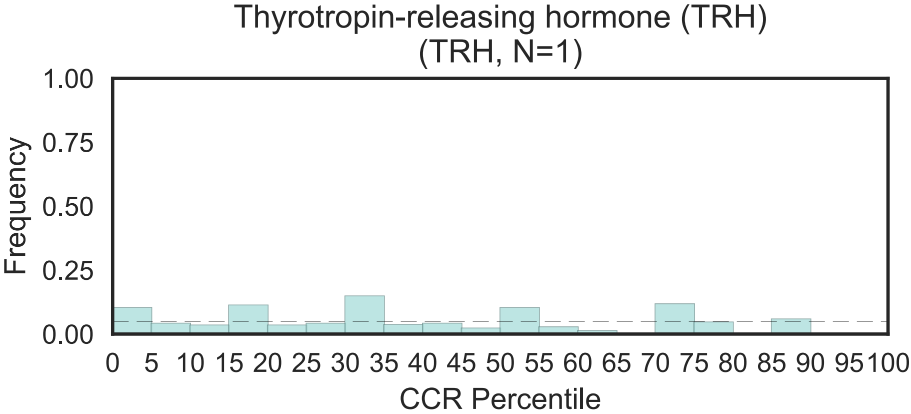

Translocon-associated protein (TRAP), alpha subunit
(TRAP_alpha, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

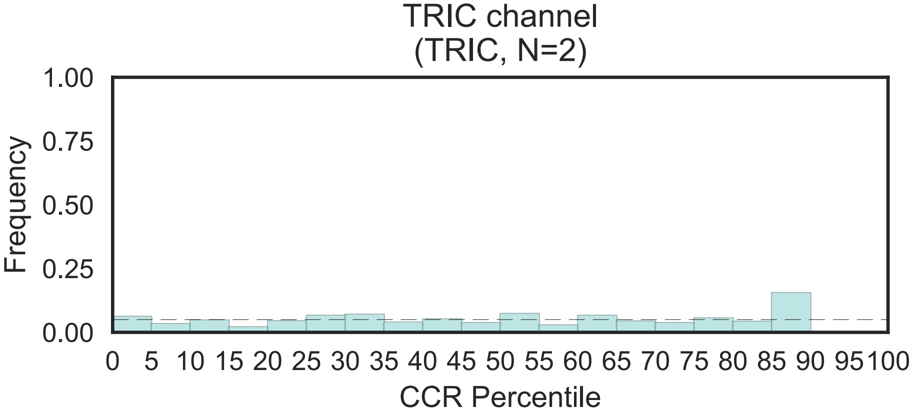

Translocon-associated protein beta (TRAPB)
(TRAP_beta, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

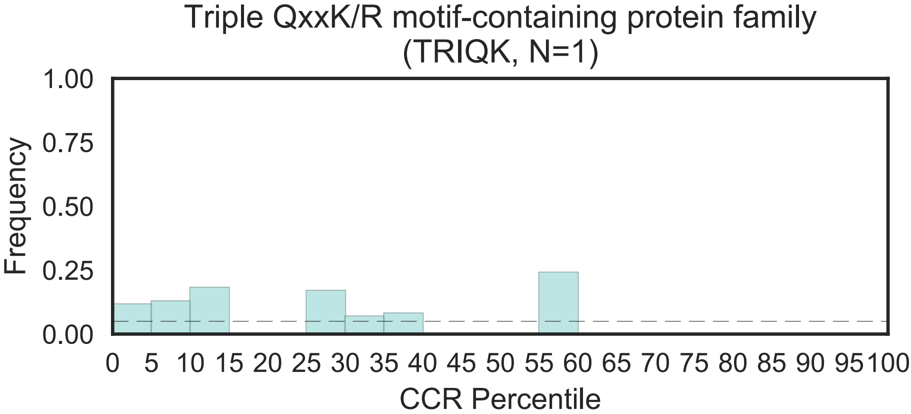

Apoptosis-antagonizing transcription factor, C-terminal
(TRAUB, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

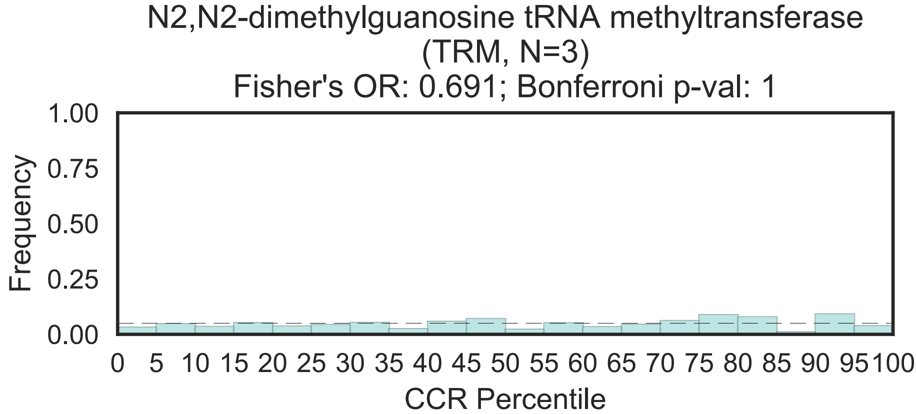

TRC8 N-terminal domain
(TRC8_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

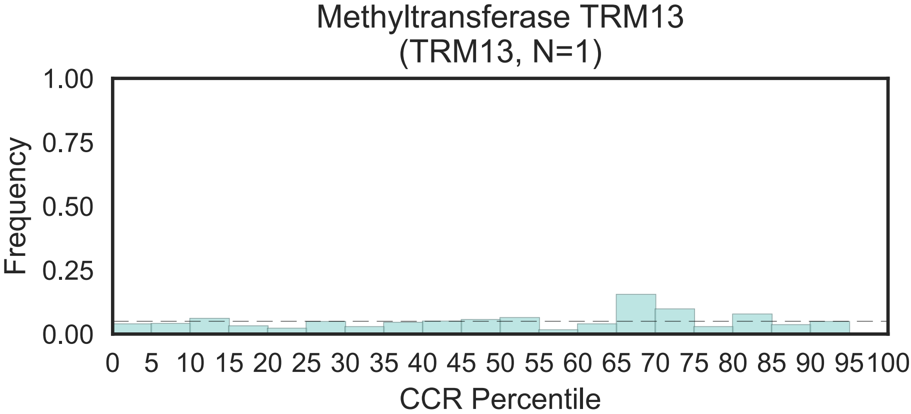

Telomere repeat binding factor (TRF)
(TRF, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

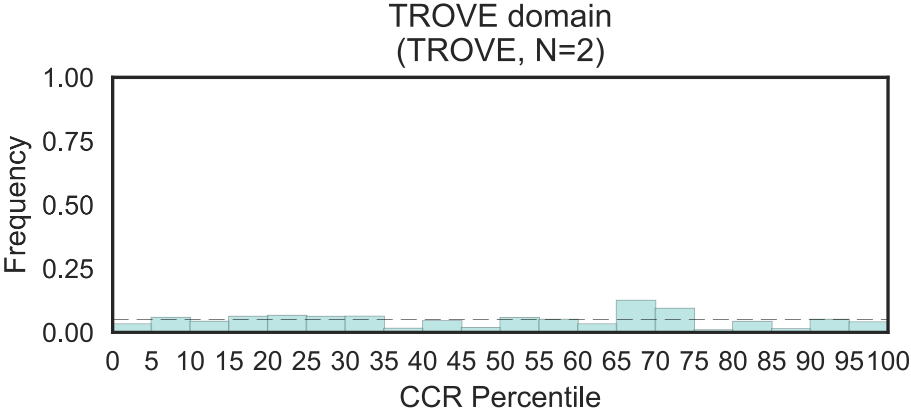

Thyrotropin-releasing hormone (TRH)
(TRH, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

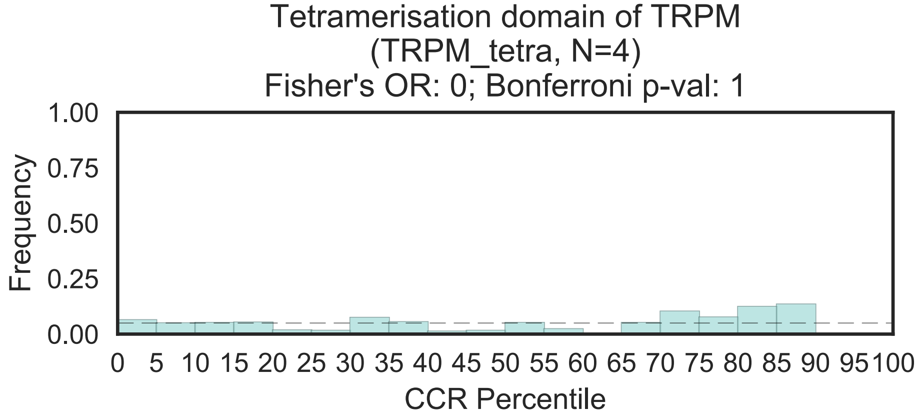

TRIC channel
(TRIC, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Triple QxxK/R motif-containing protein family
(TRIQK, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

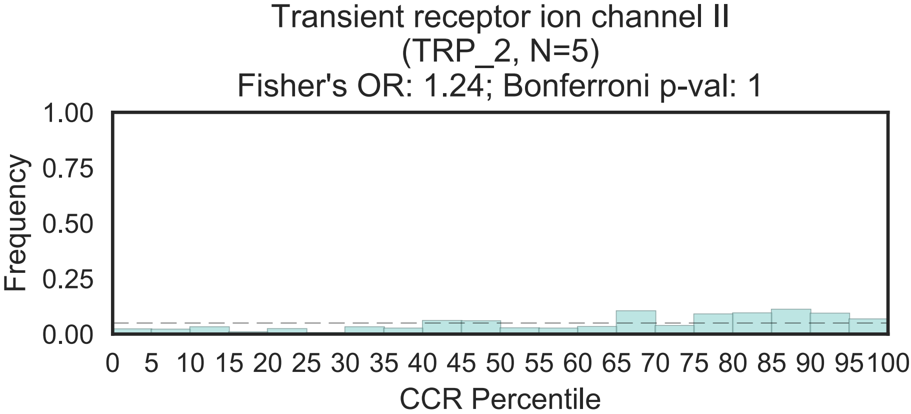

N2,N2-dimethylguanosine tRNA methyltransferase
(TRM, N=3)
Fisher's OR: 0.691; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

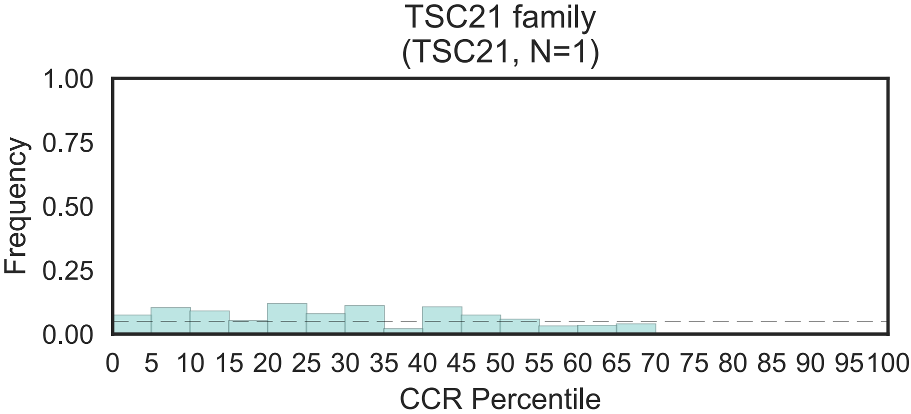

Methyltransferase TRM13
(TRM13, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

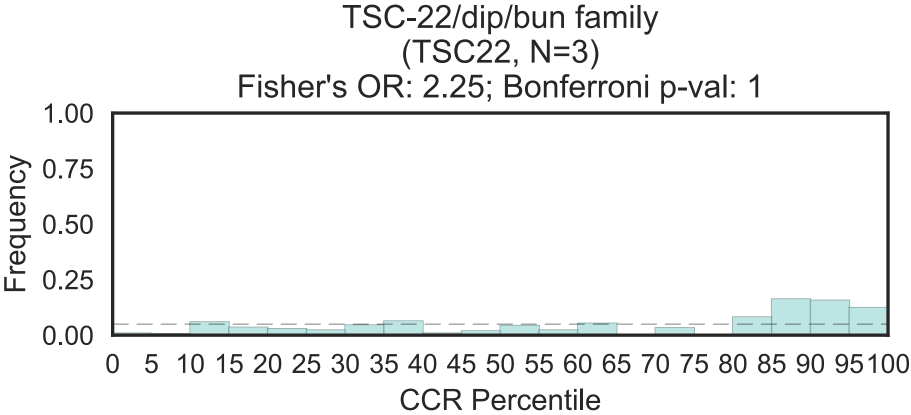

TROVE domain
(TROVE, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

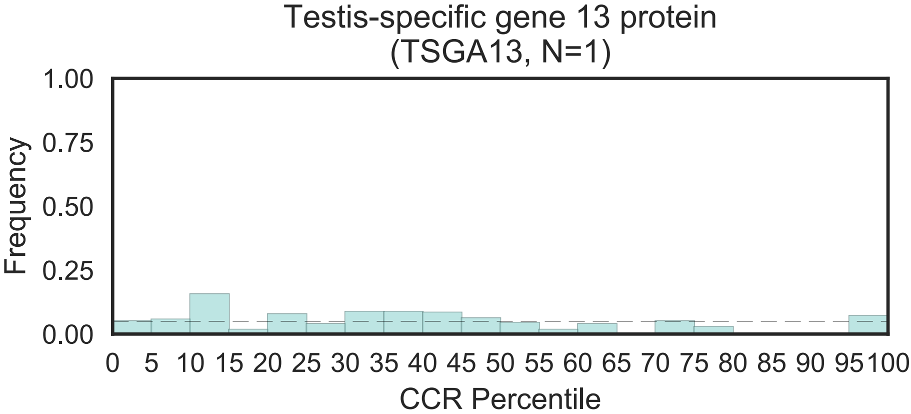


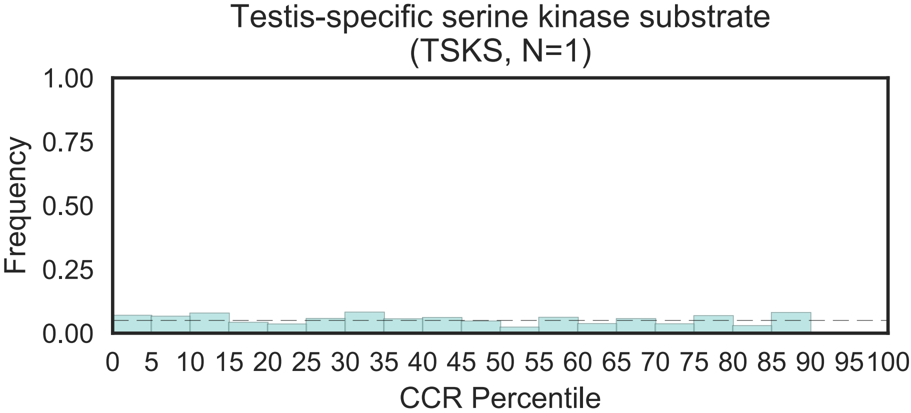
Tetramerisation domain of TRPM
(TRPM_tetra, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

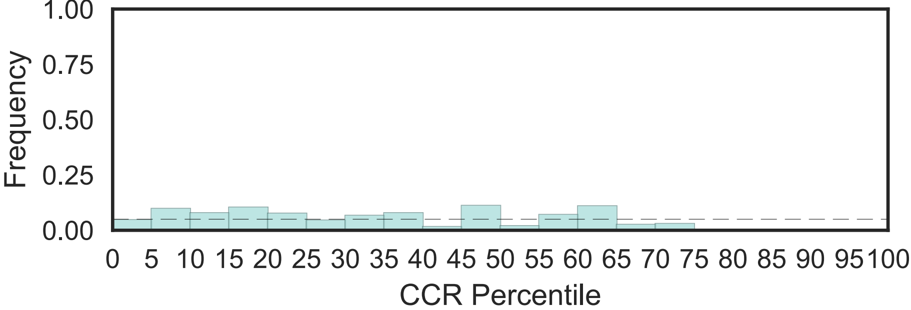

Transient receptor ion channel II
(TRP_2, N=5)
Fisher's OR: 1.24; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

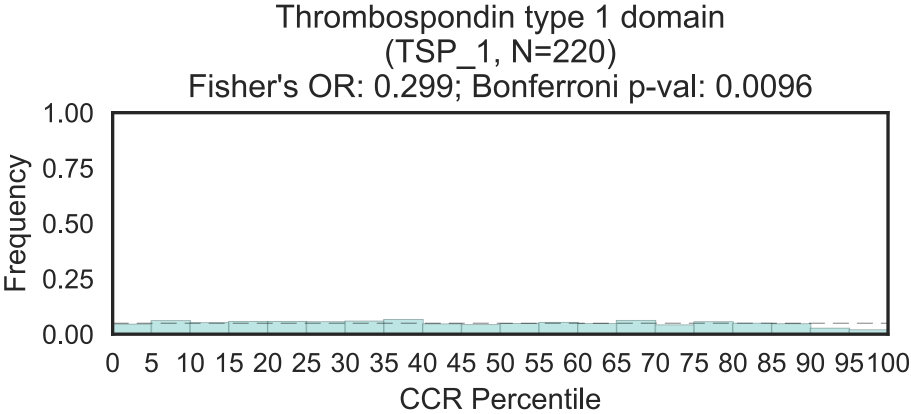

TSC21 family
(TSC21, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

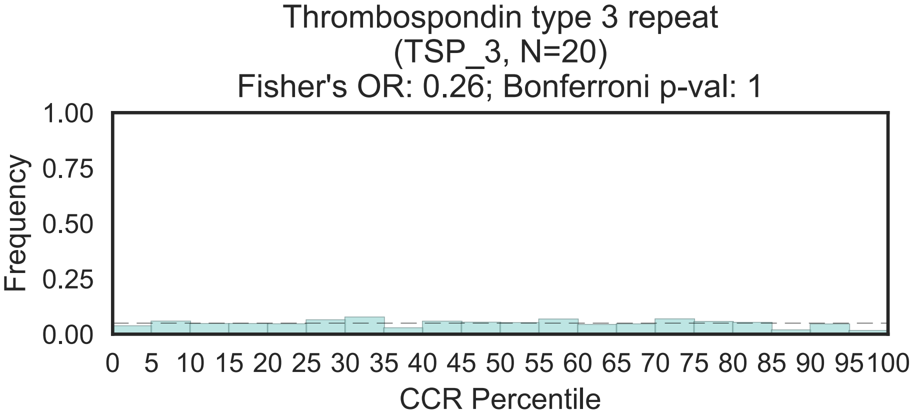

TSC-22/dip/bun family
(TSC22, N=3)
Fisher's OR: 2.25; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

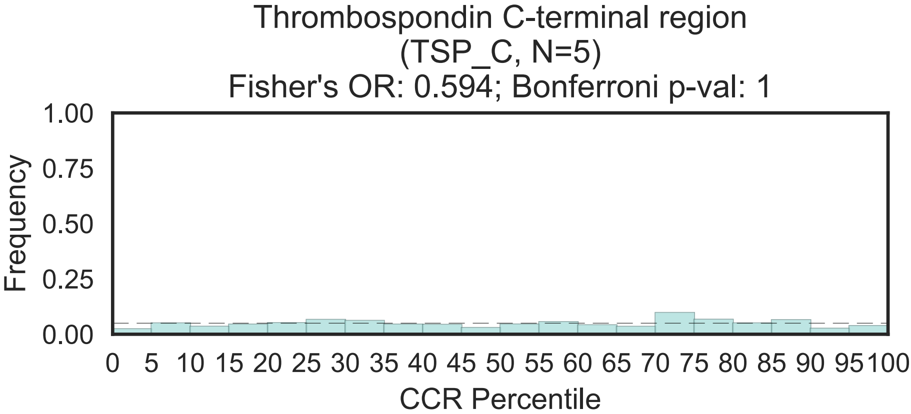

Testis-specific gene 13 protein
(TSGA13, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

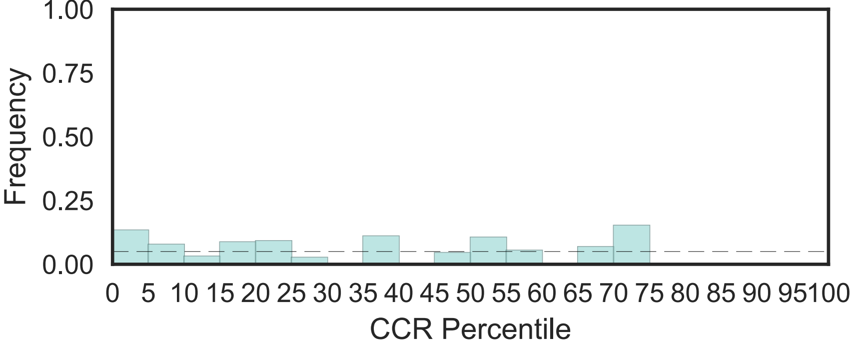

Testis-specific serine kinase substrate
(TSKS, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Translin-associated factor X-interacting N-terminus
(TSNAXIP1_N, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

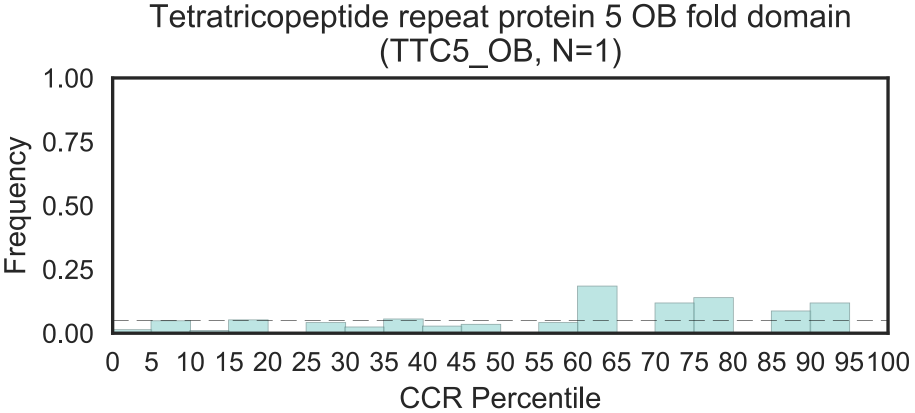

Thrombospondin type 1 domain
(TSP_1, N=220)
Fisher's OR: 0.299; Bonferroni p-val: 0.0096
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

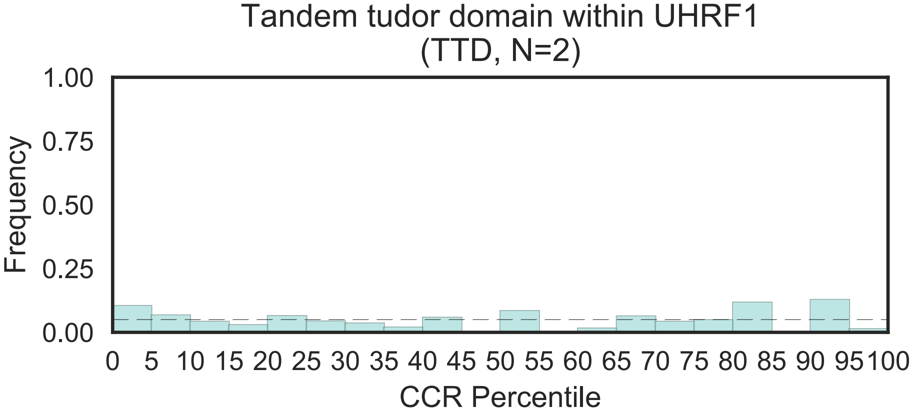

Thrombospondin type 3 repeat
(TSP_3, N=20)
Fisher's OR: 0.26; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

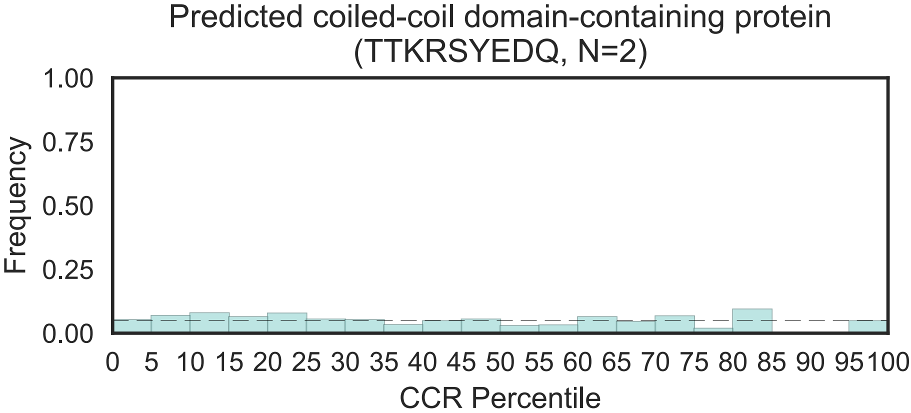

Thrombospondin C-terminal region
(TSP_C, N=5)
Fisher's OR: 0.594; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

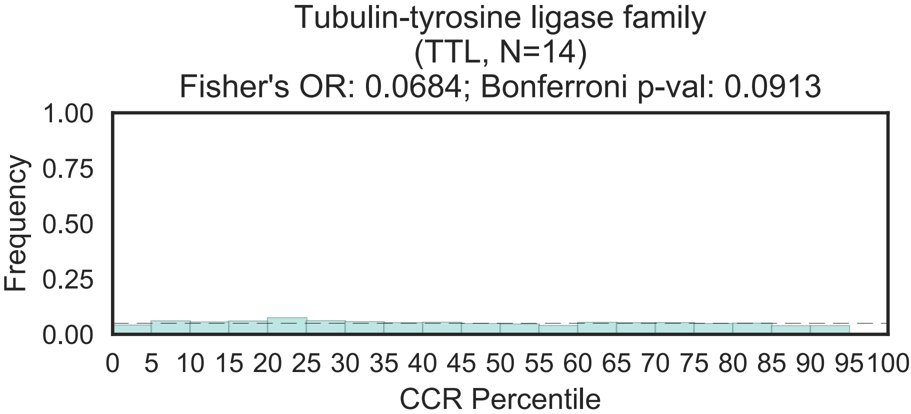


Tumour suppressing sub-chromosomal transferable candidate 4 (TSSC4, N=1)

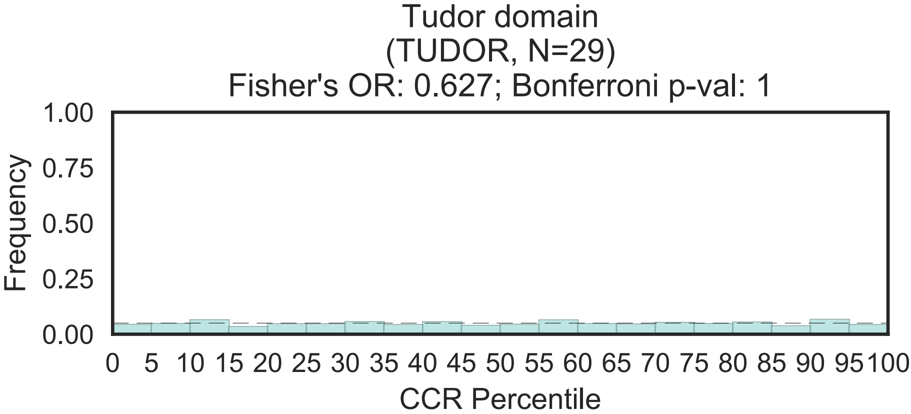

Tetratricopeptide repeat protein 5 OB fold domain
(TTC5_OB, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

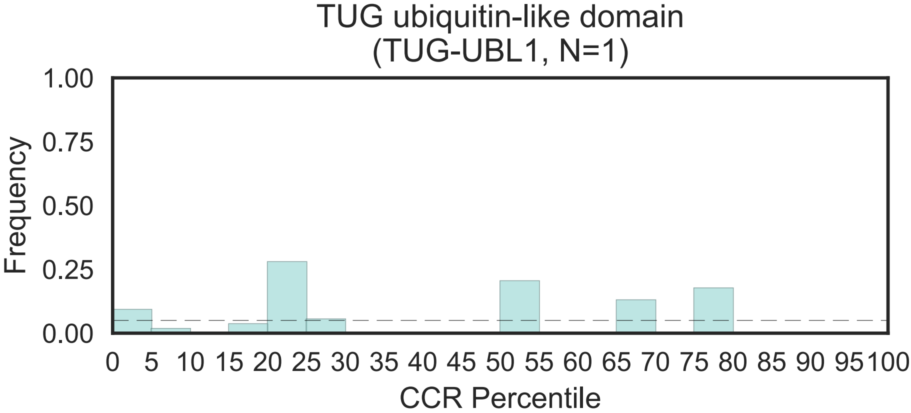

Tandem tudor domain within UHRF1
(TTD, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

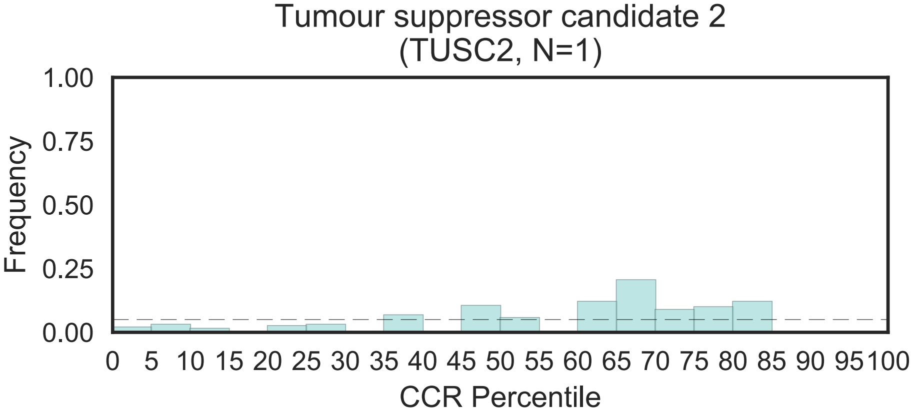

Predicted coiled-coil domain-containing protein
(TTKRSYEDQ, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

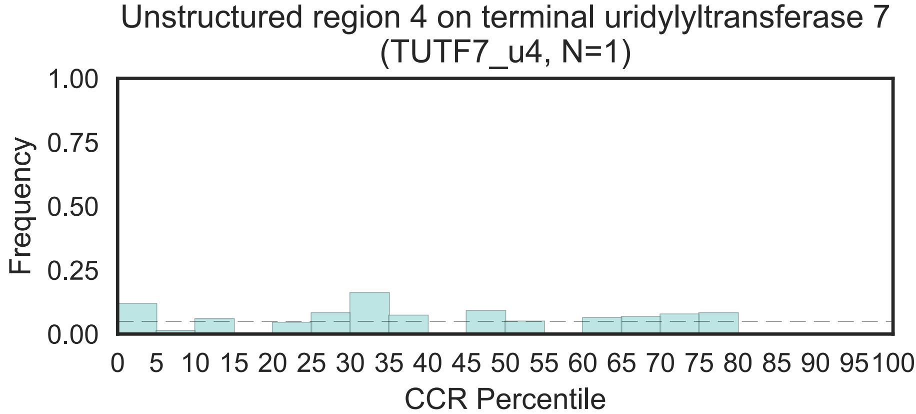


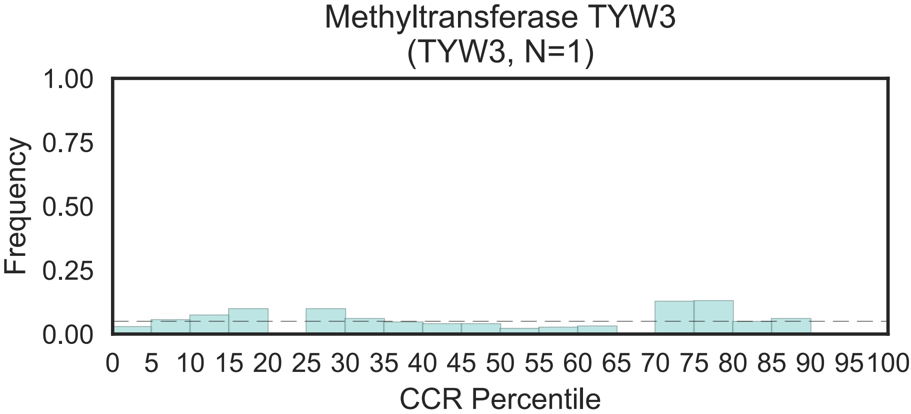
Tubulin-tyrosine ligase family
(TTL, N=14)
Fisher's OR: 0.0684; Bonferroni p-val: 0.0913

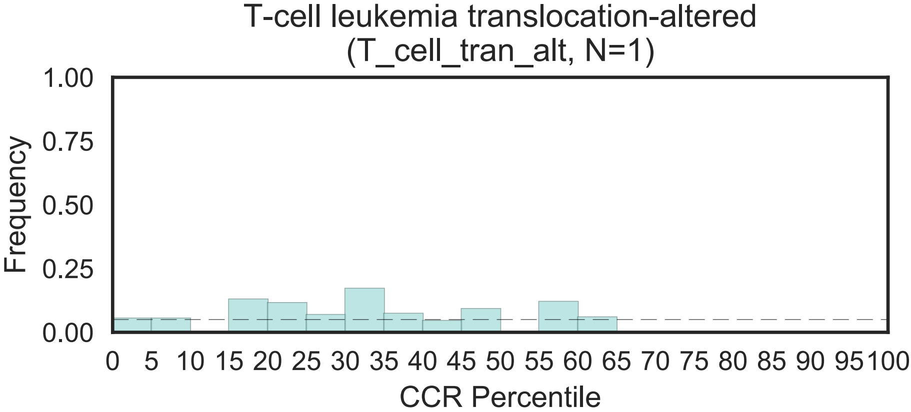

Tudor domain
(TUDOR, N=29)
Fisher's OR: 0.627; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

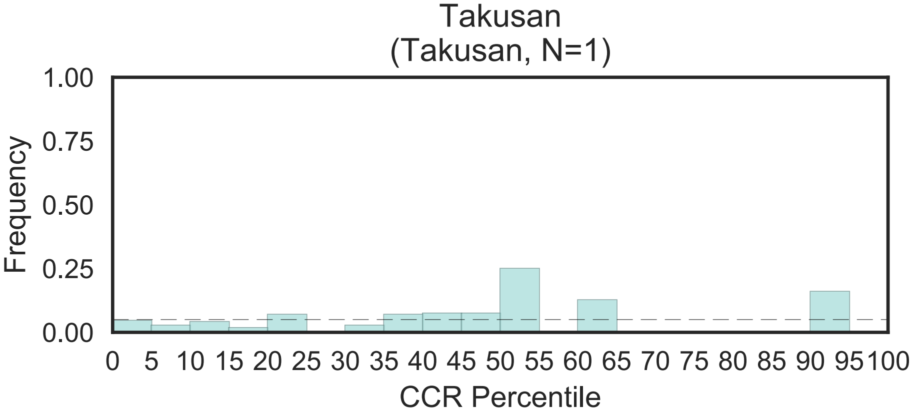

TUG ubiquitin-like domain
(TUG-UBL1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

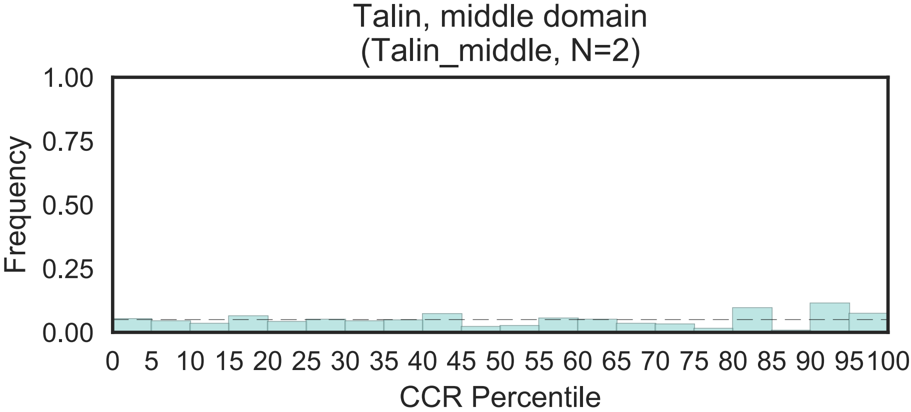

Tumour suppressor candidate 2
(TUSC2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

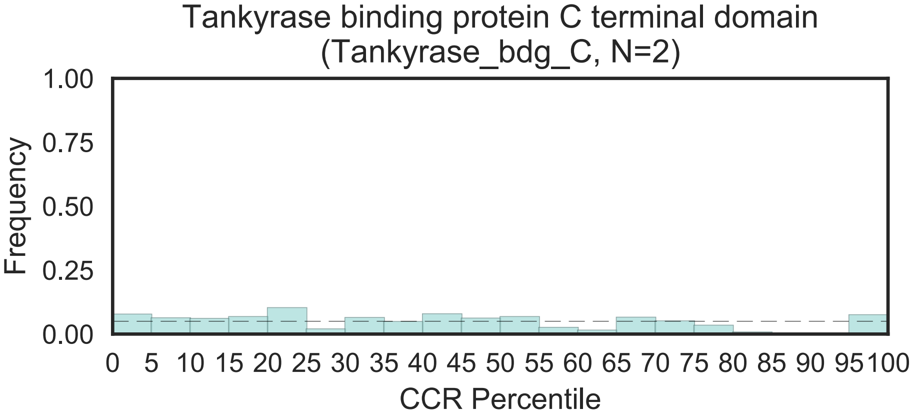

Unstructured region 4 on terminal uridylyltransferase 7
(TUTF7_u4, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

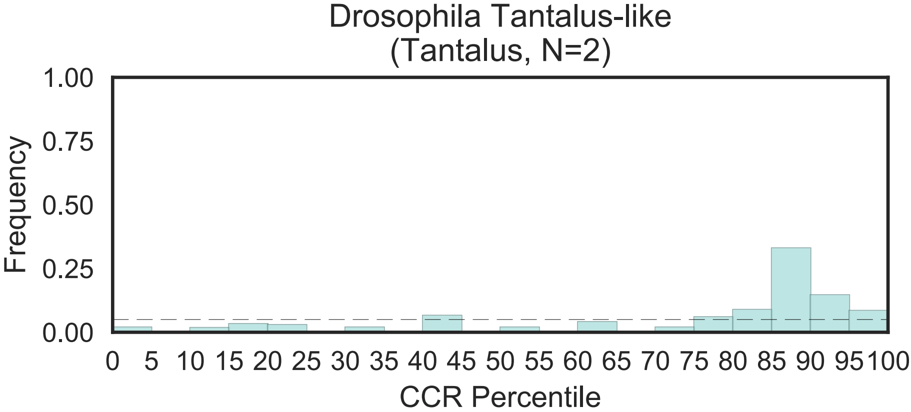

Methyltransferase TYW3
(TYW3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

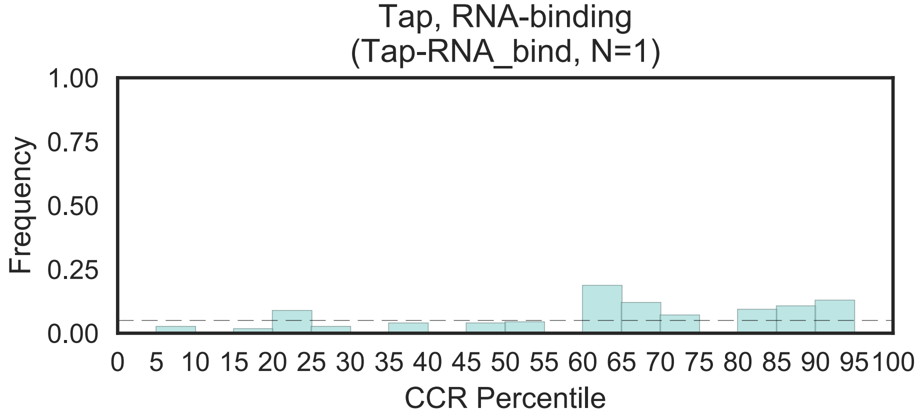

T-cell leukemia translocation-altered
(T_cell_tran_alt, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

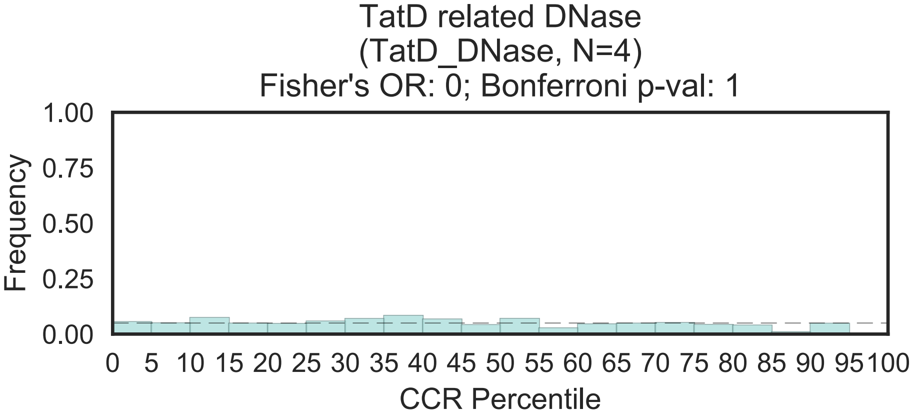

Takusan
(Takusan, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Talin, middle domain
(Talin_middle, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

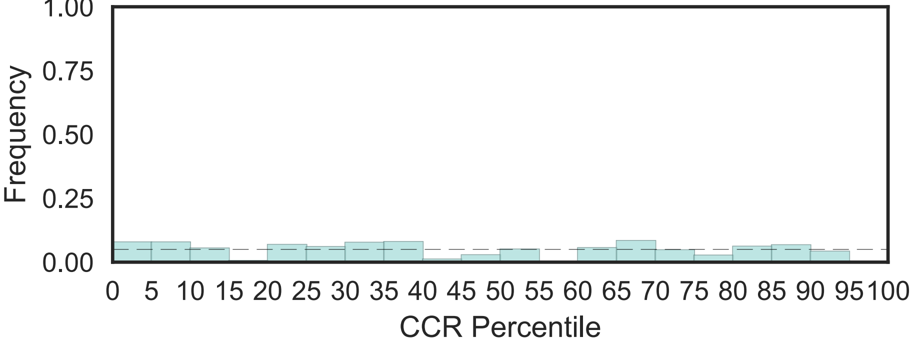

Tankyrase binding protein C terminal domain
(Tankyrase_bdg_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Drosophila Tantalus-like
(Tantalus, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

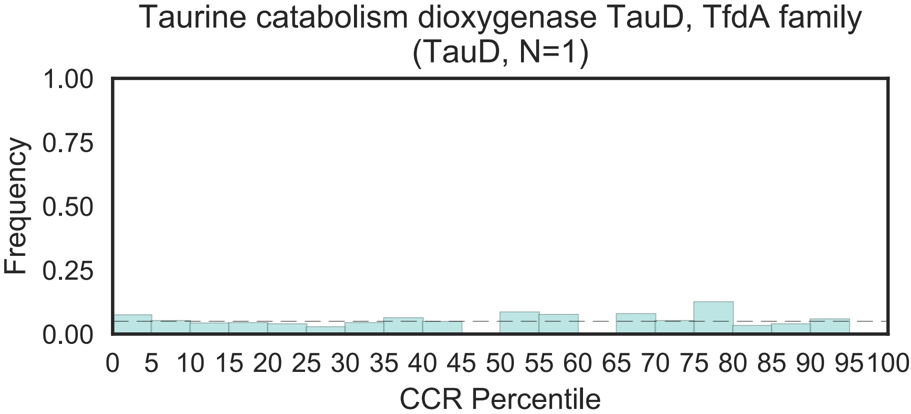

Tap, RNA-binding
(Tap-RNA_bind, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

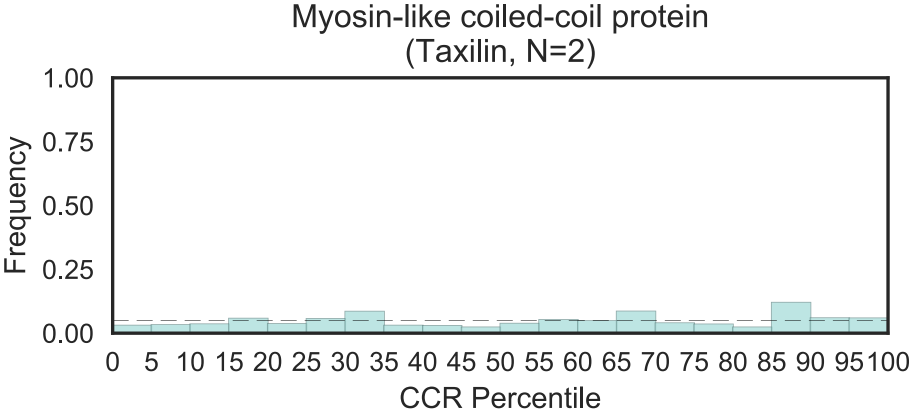


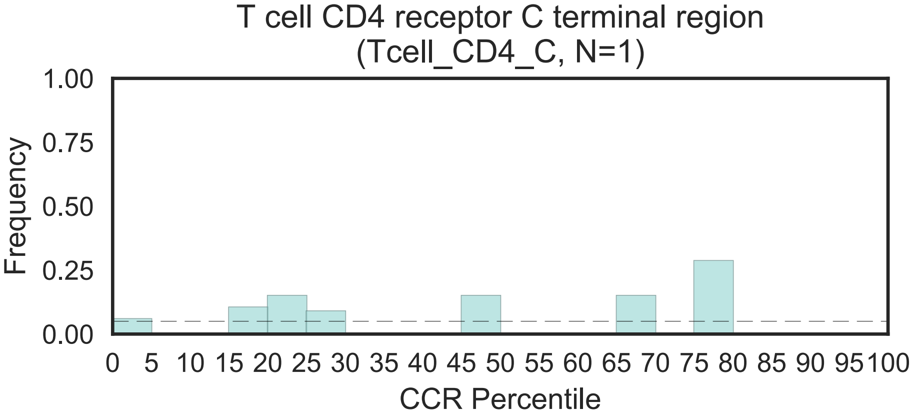
TatD related DNase
(TatD_DNase, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

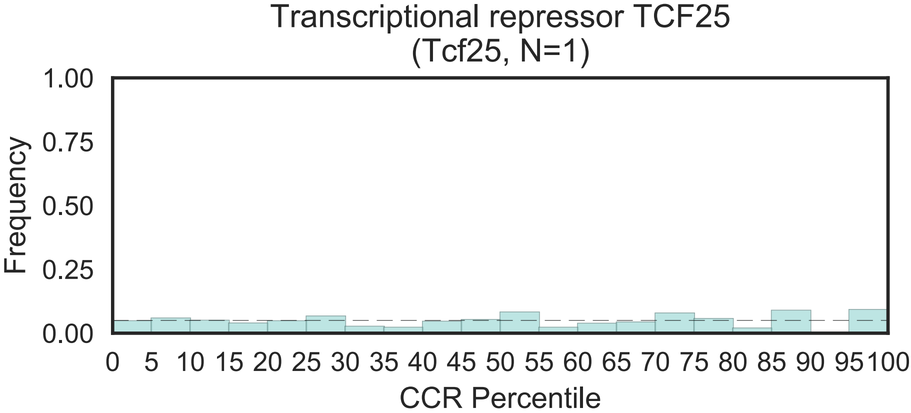


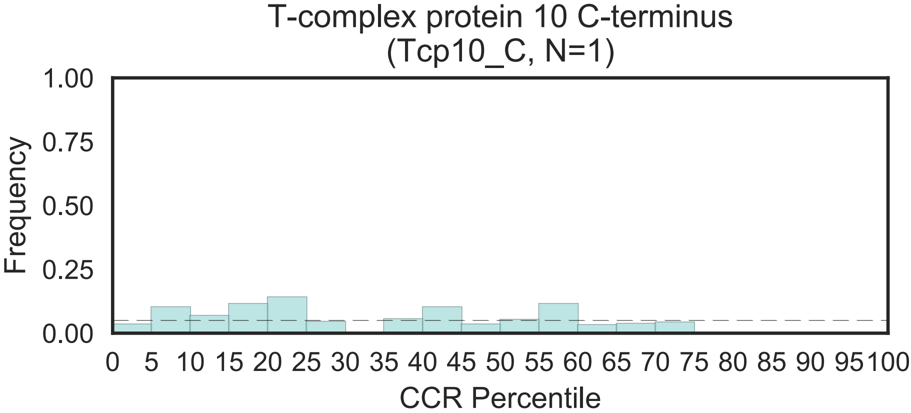
RNA polymerase III transcription factor (TF)IIIC subunit
(Tau95, N=1)

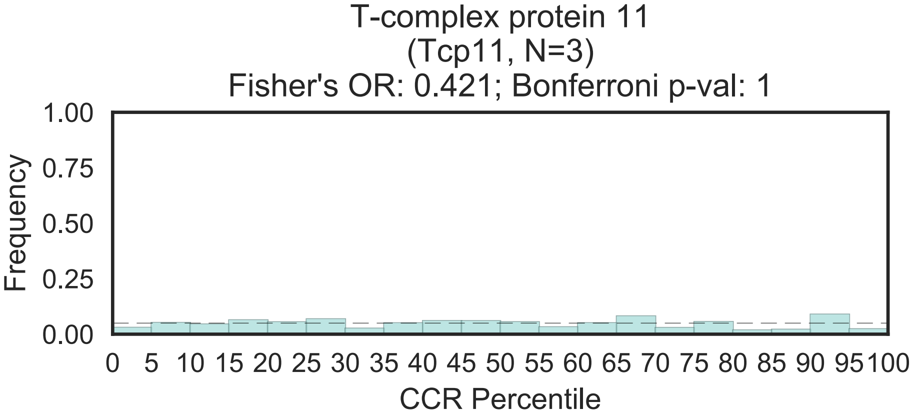

Taurine catabolism dioxygenase TauD, TfdA family
(TauD, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

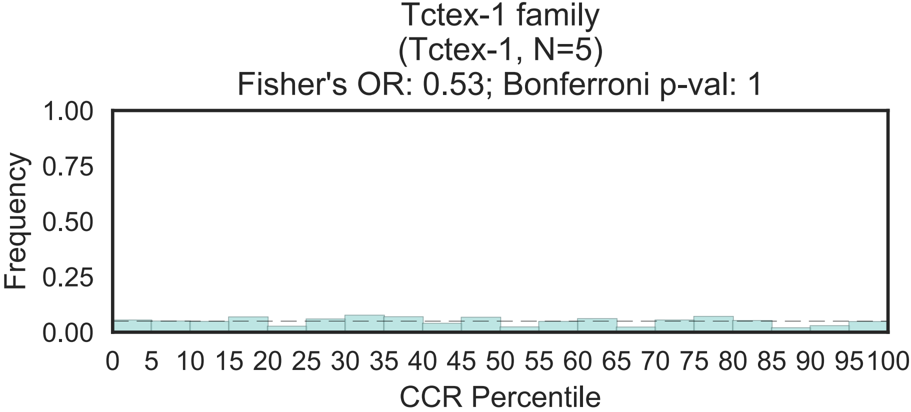

Myosin-like coiled-coil protein
(Taxilin, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

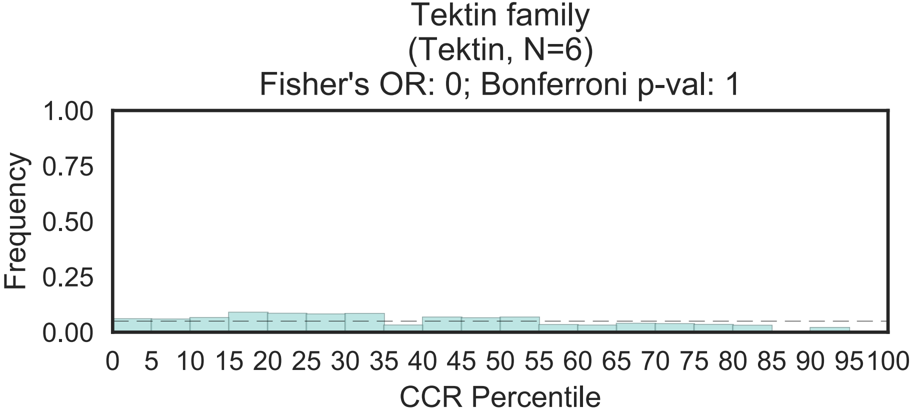

T cell CD4 receptor C terminal region
(Tcell_CD4_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

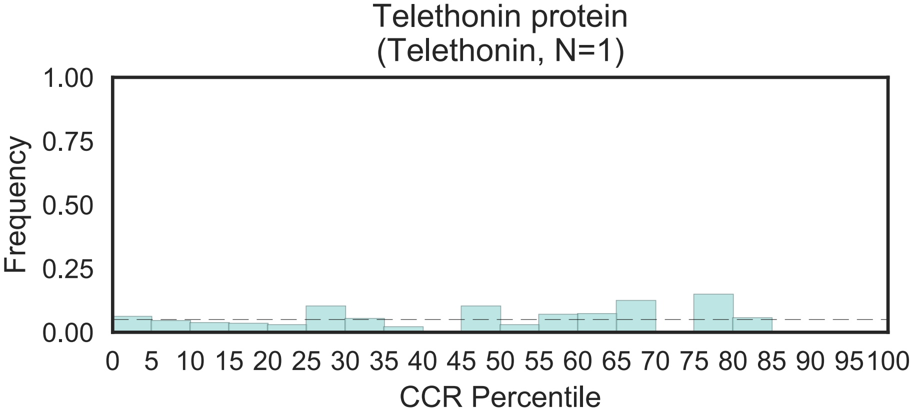

Transcriptional repressor TCF25
(Tcf25, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

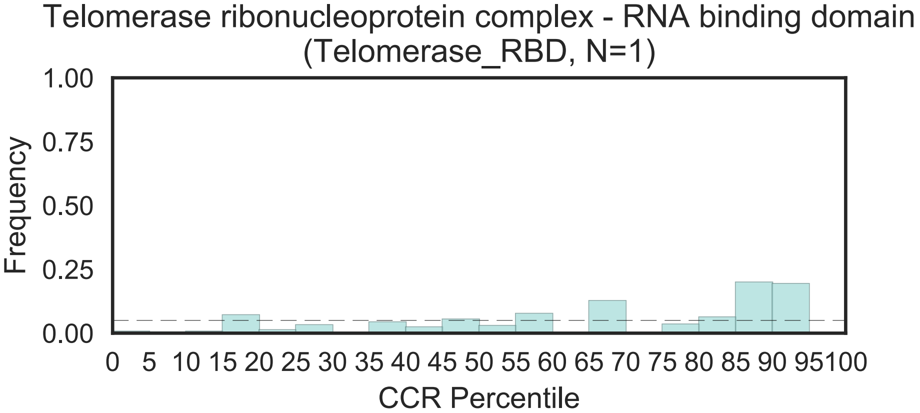

T-complex protein 10 C-terminus
(Tcp10_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

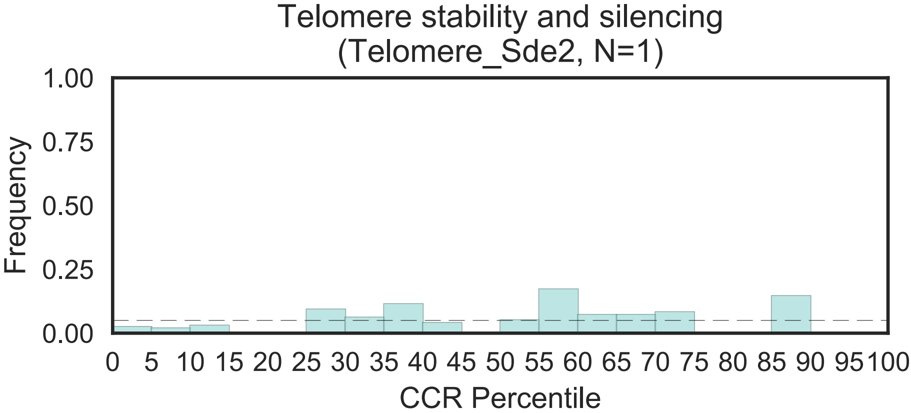

T-complex protein 11
(Tcp11, N=3)
Fisher's OR: 0.421; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

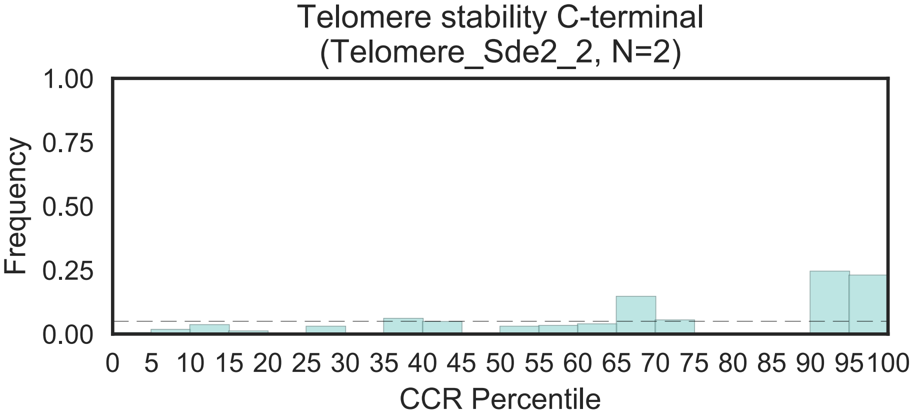

Tctex-1 family
(Tctex-1, N=5)
Fisher's OR: 0.53; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

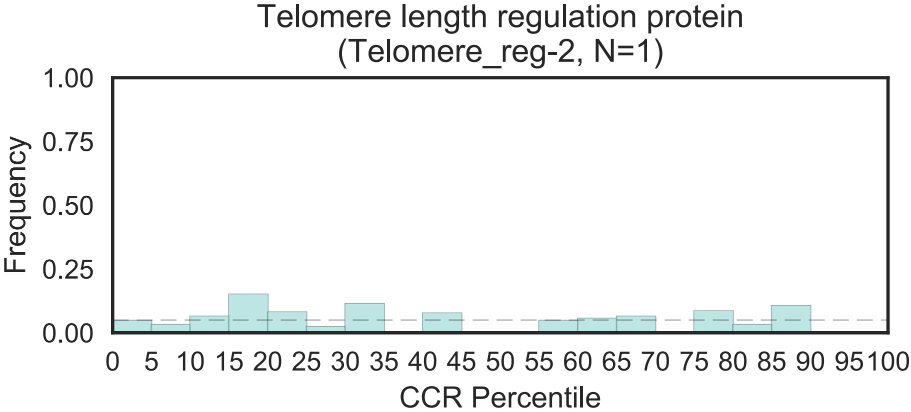

Tektin family
(Tektin, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

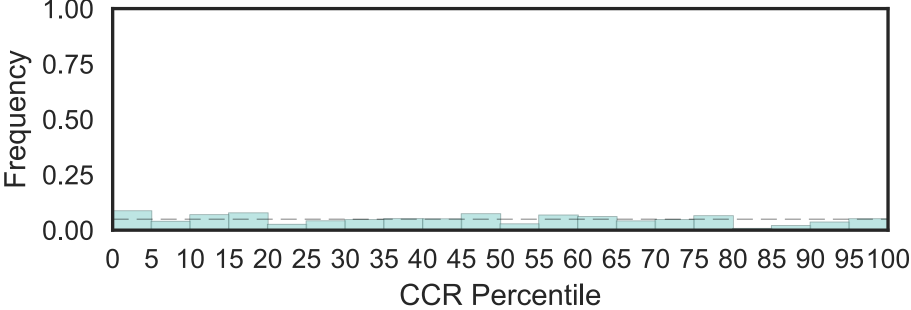

Telethonin protein
(Telethonin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Telomerase ribonucleoprotein complex - RNA binding domain
(Telomerase_RBD, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

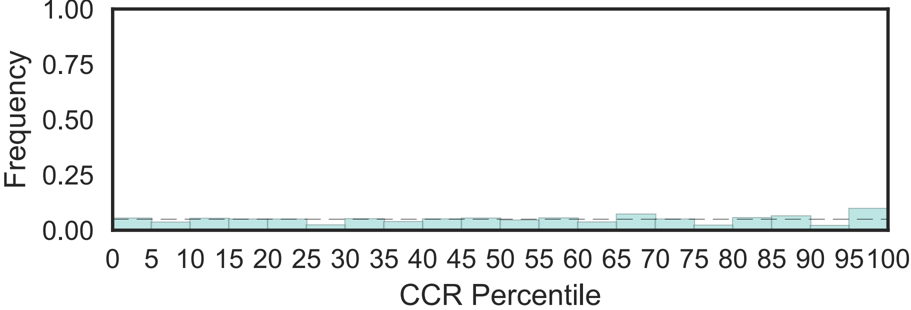

Telomere stability and silencing
(Telomere_Sde2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

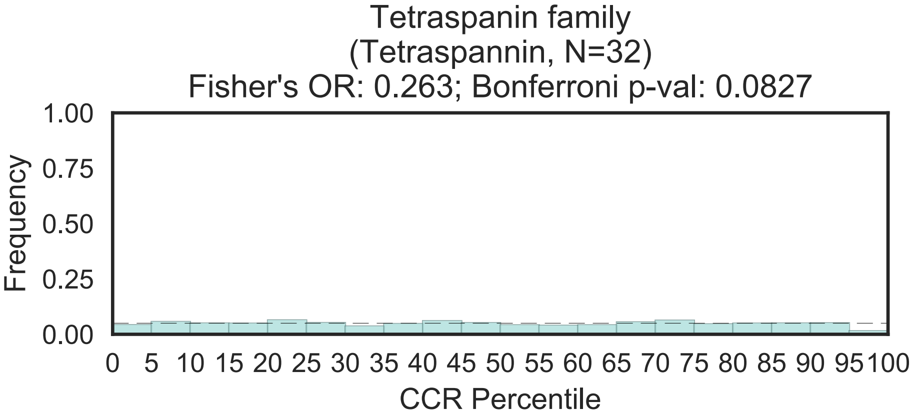

Telomere stability C-terminal
(Telomere_Sde2_2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

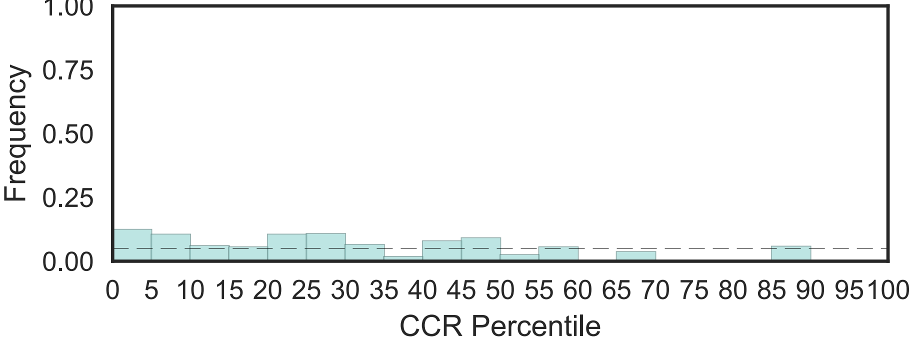

Telomere length regulation protein
(Telomere_reg-2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



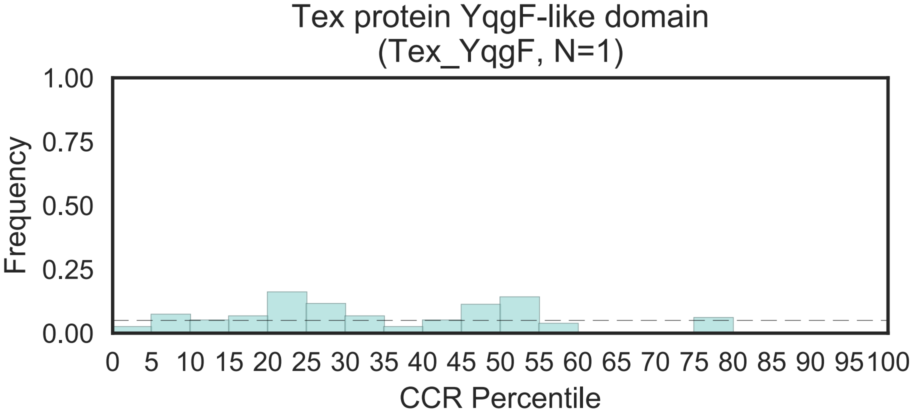
Teneurin Intracellular Region
(Ten_N, N=3)
Fisher's OR: 0.642; Bonferroni p-val: 1


Oxygenase domain of the 2OGFeDO superfamily
(Tet_JBP, N=3)
Fisher's OR: 1.55; Bonferroni p-val: 1

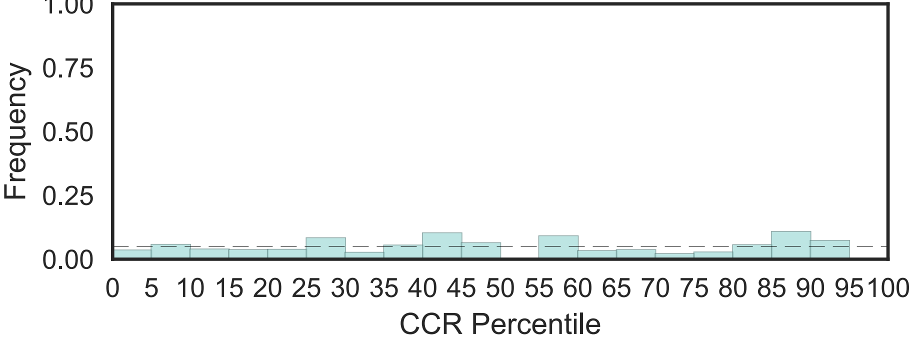

Tetraspanin family
(Tetraspannin, N=32)
Fisher's OR: 0.263; Bonferroni p-val: 0.0827
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

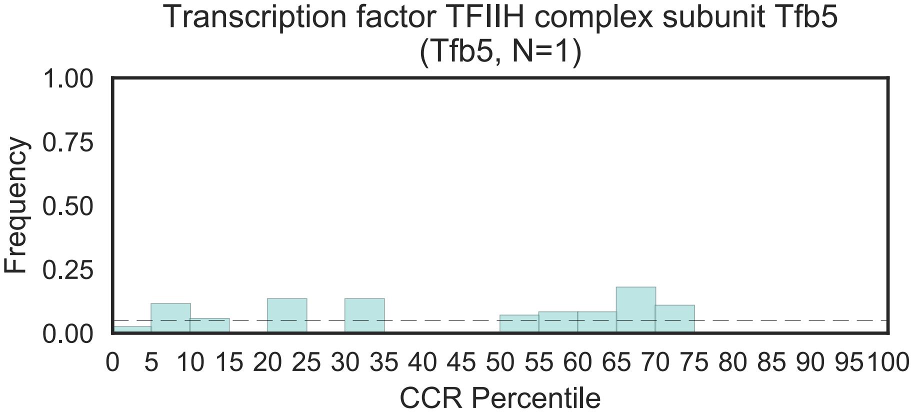


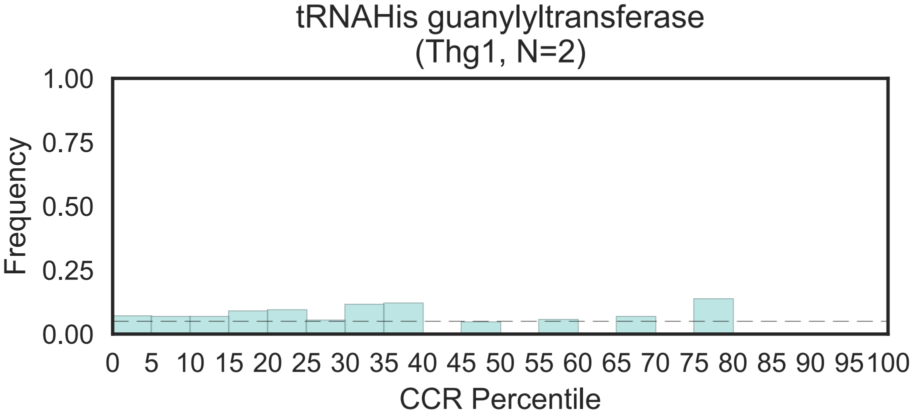
Tex-like protein N-terminal domain
(Tex_N, N=1)

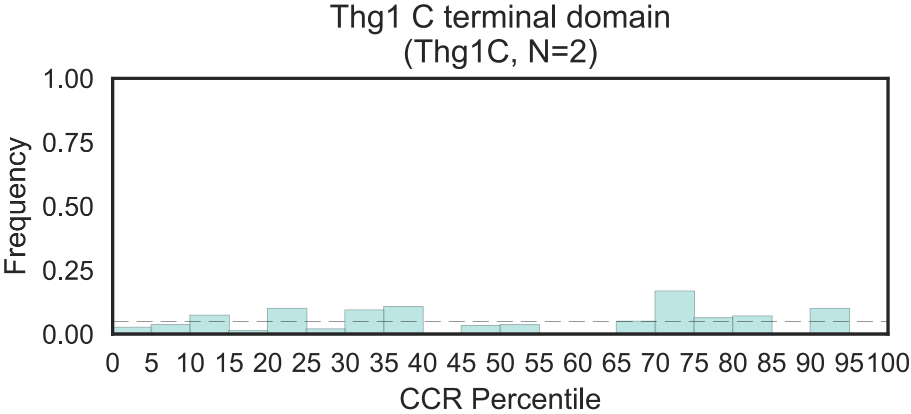

Tex protein YqgF-like domain
(Tex_YqgF, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

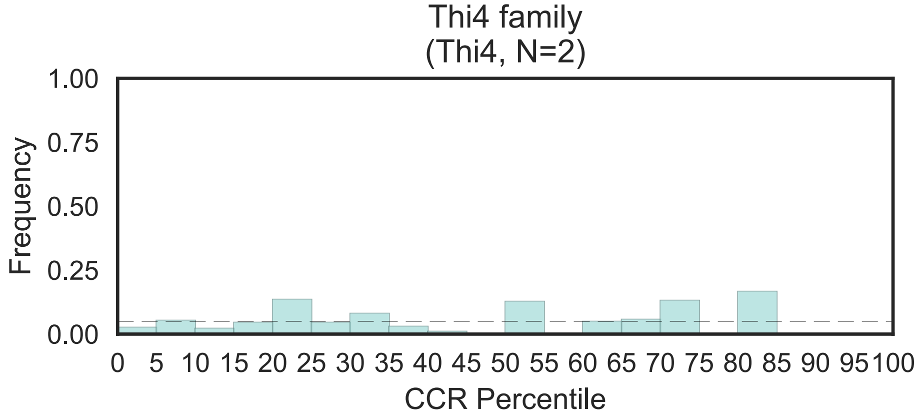
Transcription factor Tfb4
(Tfb4, N=1)

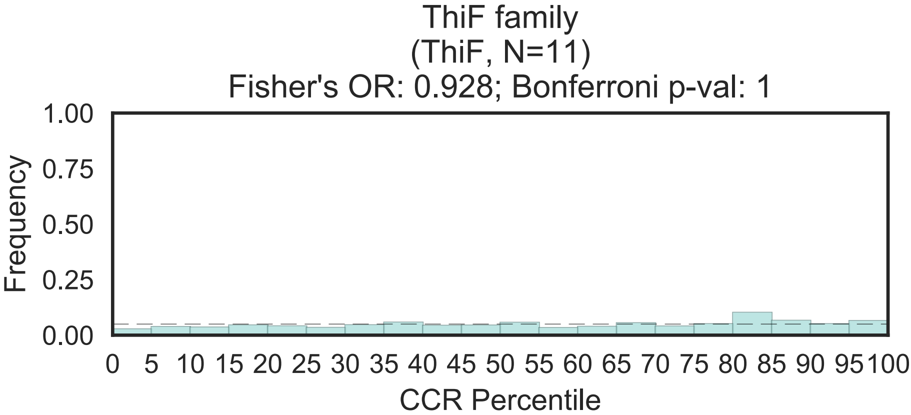


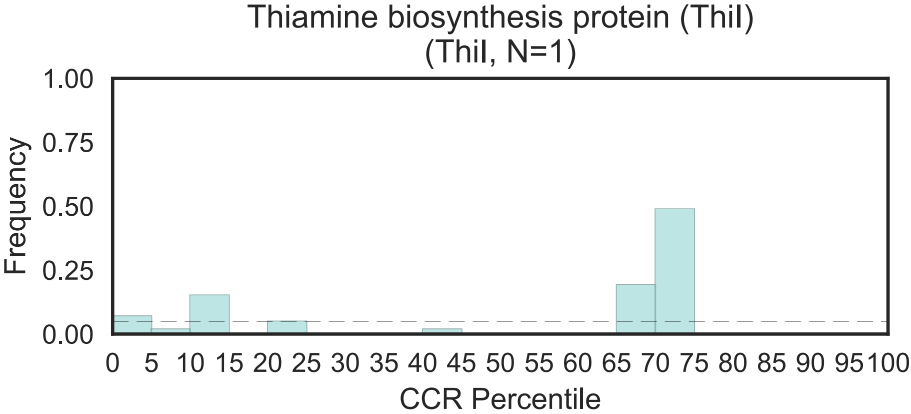

Transcription factor TFIIH complex subunit Tfb5
(Tfb5, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

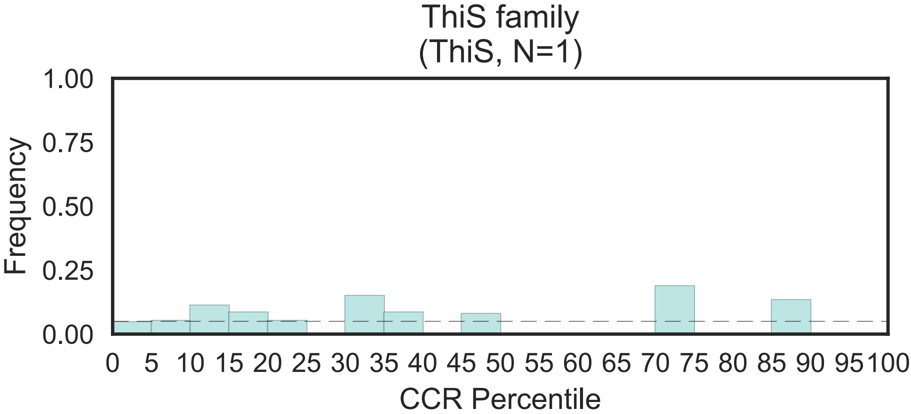

tRNAHis guanylyltransferase
(Thg1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

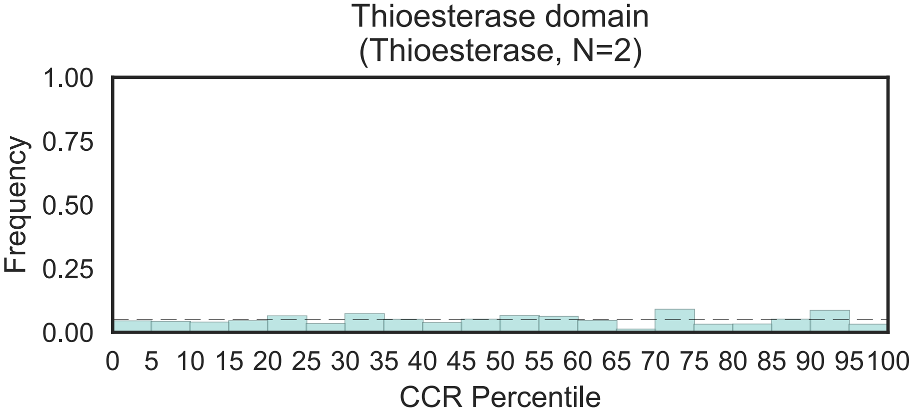

Thg1 C terminal domain
(Thg1C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

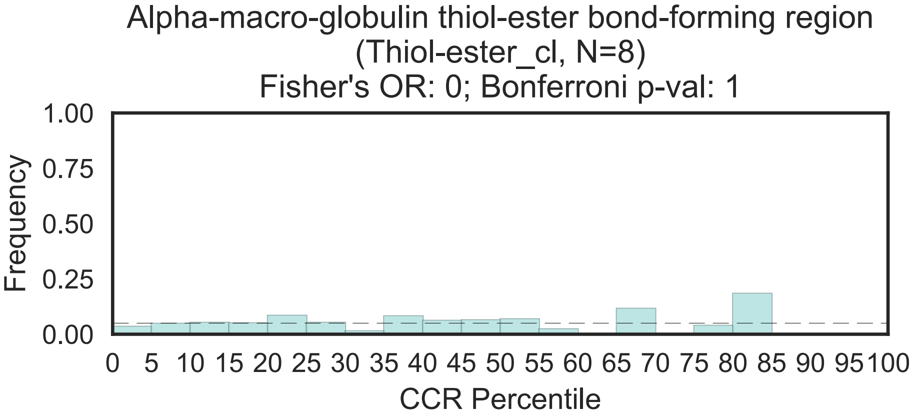

Thi4 family
(Thi4, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

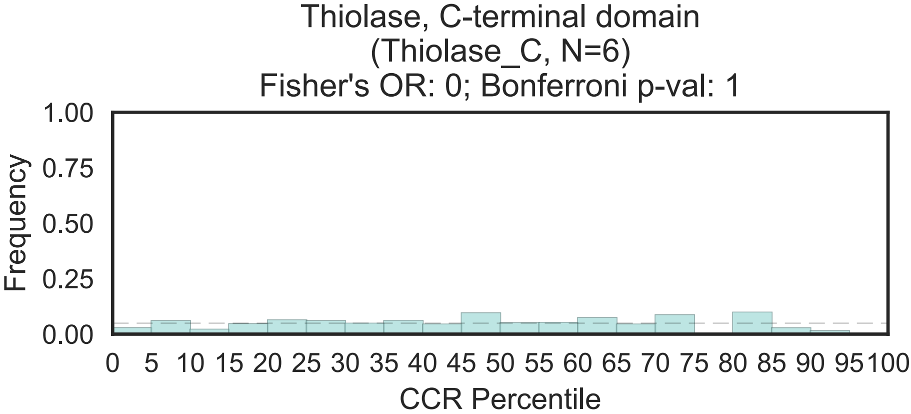

ThiF family
(ThiF, N=11)
Fisher's OR: 0.928; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

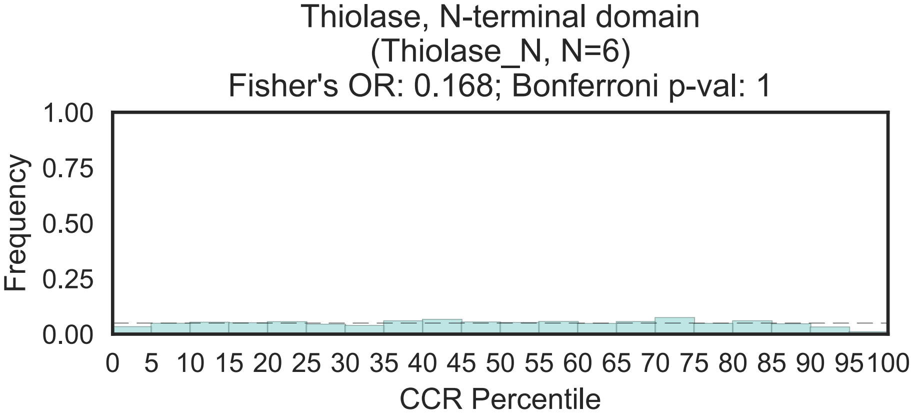

Thiamine biosynthesis protein (ThiI)
(ThiI, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


ThiS family
(ThiS, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

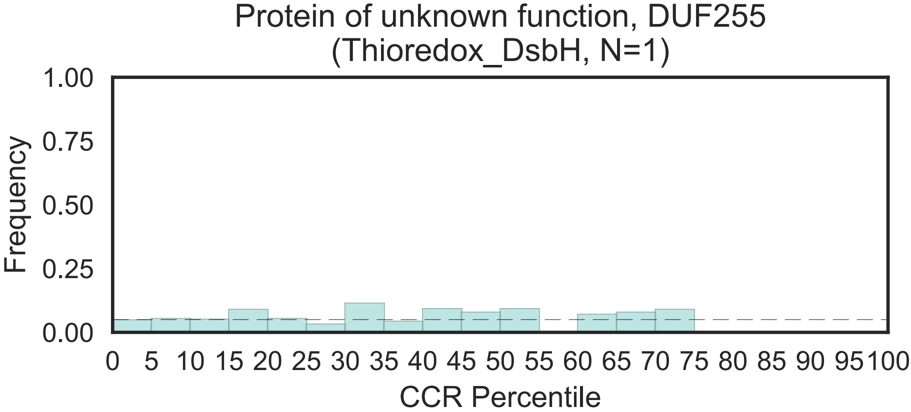

Thioesterase domain
(Thioesterase, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

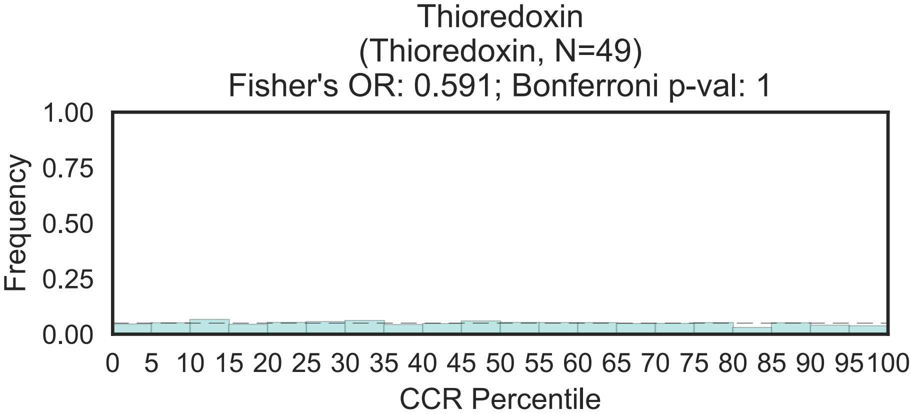

Alpha-macro-globulin thiol-ester bond-forming region
(Thiol-ester_cl, N=8)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

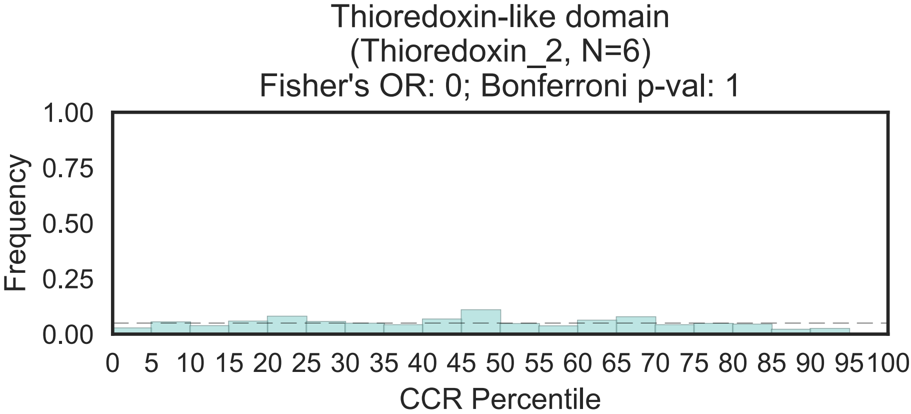

Thiolase, C-terminal domain
(Thiolase_C, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

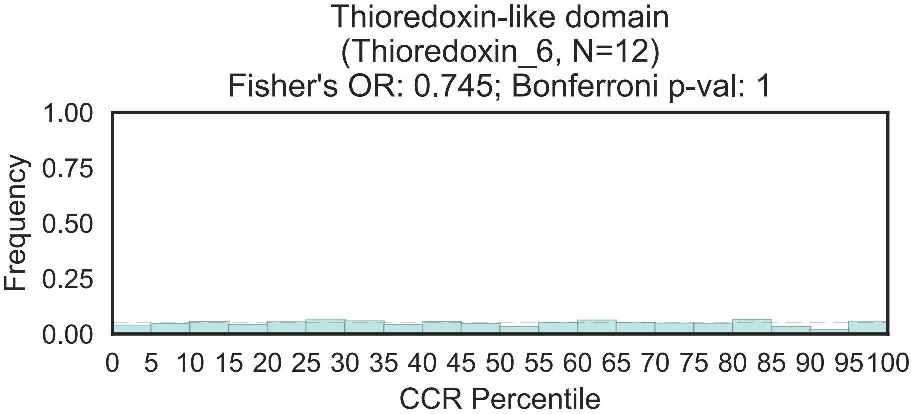


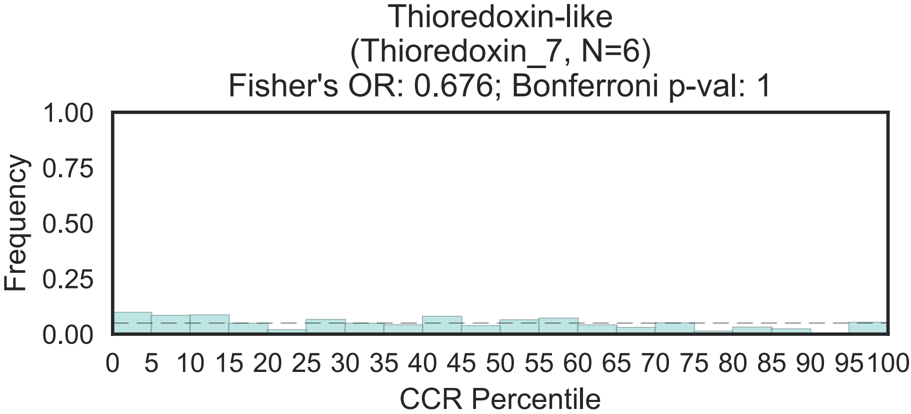
Thiolase, N-terminal domain
(Thiolase_N, N=6)
Fisher's OR: 0.168; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

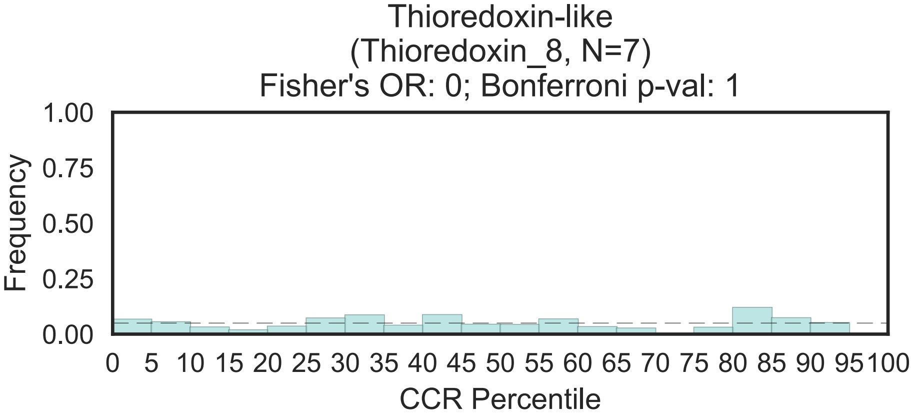

Protein of unknown function, DUF255
(Thioredox_DsbH, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Thioredoxin
(Thioredoxin, N=49)
Fisher's OR: 0.591; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

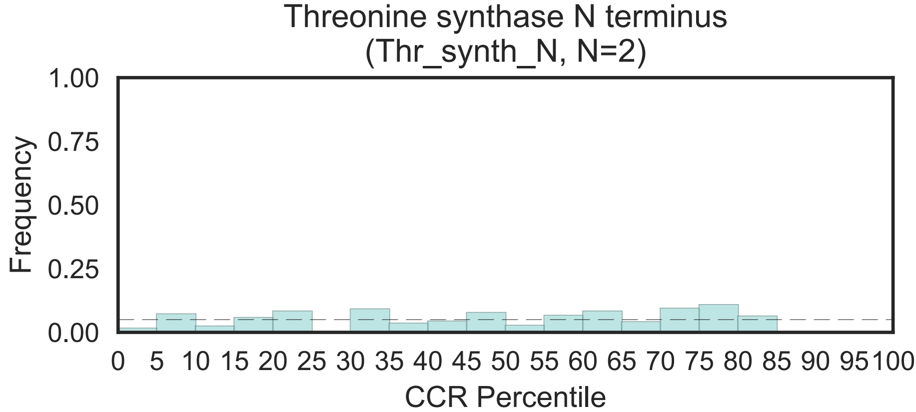

Thioredoxin-like domain
(Thioredoxin_2, N=6)
Fisher's OR: 0; Bonferroni p-val: 1

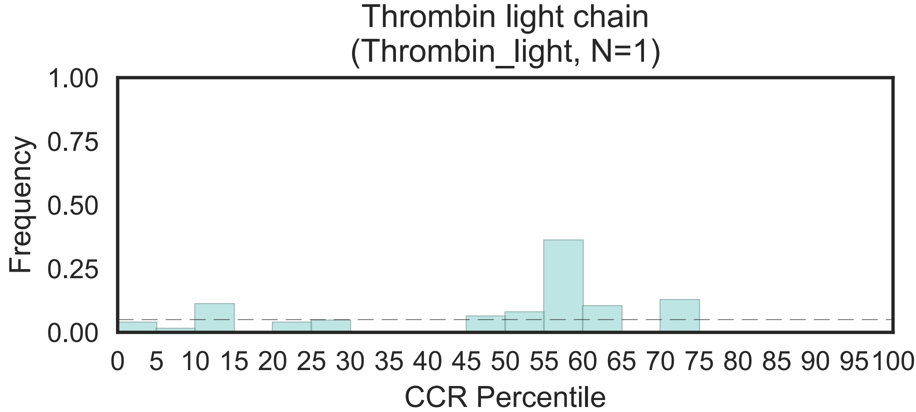

Thioredoxin-like domain
(Thioredoxin_6, N=12)
Fisher's OR: 0.745; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

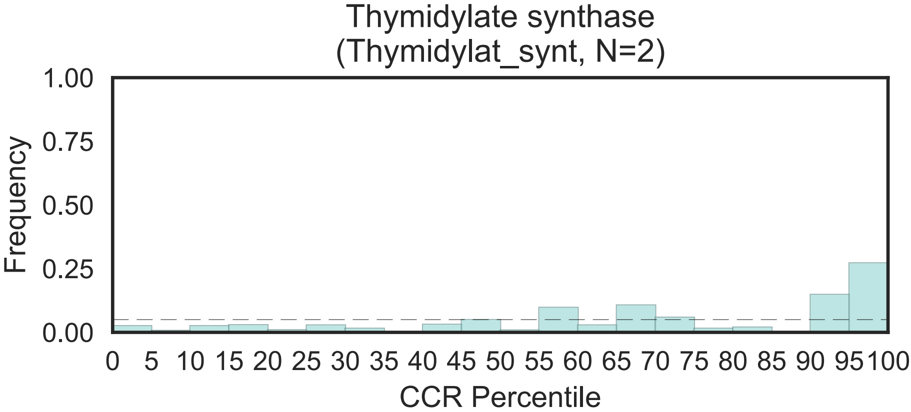

Thioredoxin-like
(Thioredoxin_7, N=6)
Fisher's OR: 0.676; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

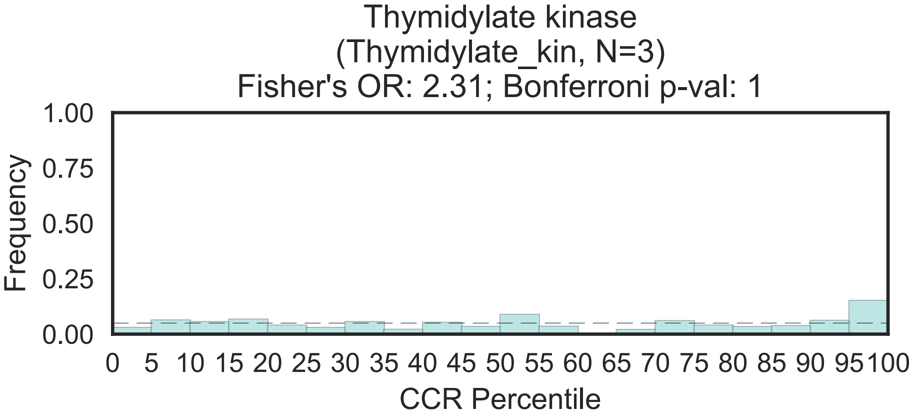


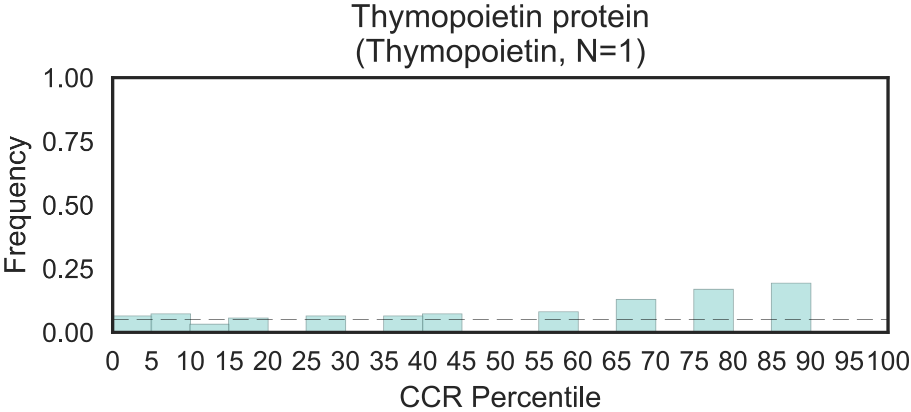
Thioredoxin-like
(Thioredoxin_8, N=7)
Fisher's OR: 0; Bonferroni p-val: 1

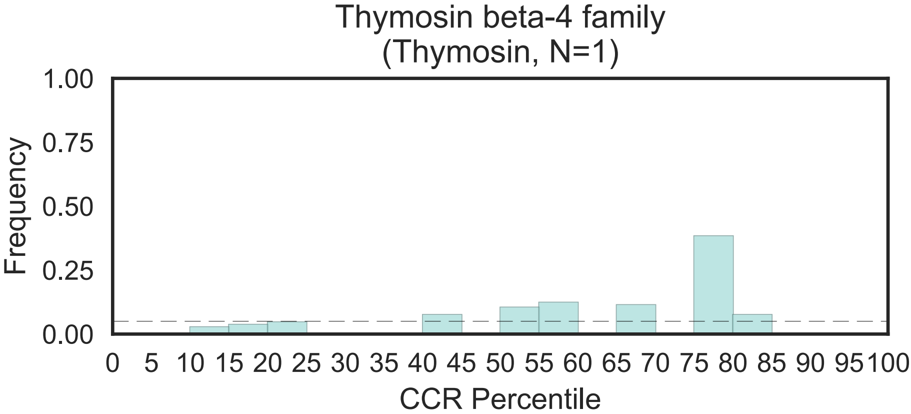

Threonine synthase N terminus
(Thr_synth_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

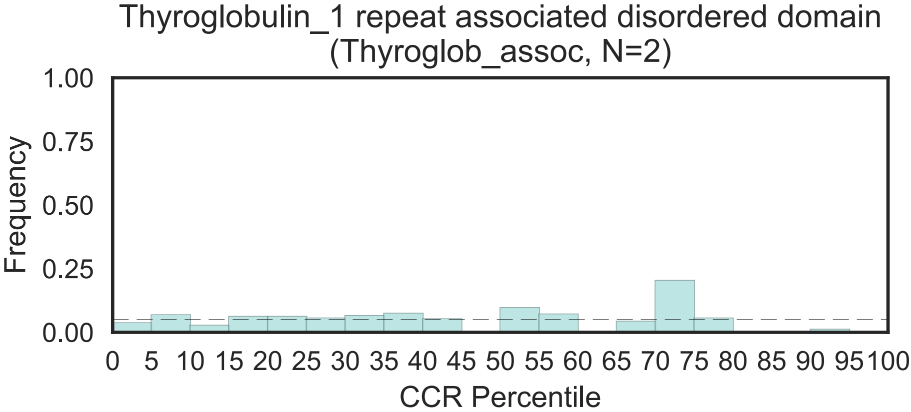

Thrombin light chain
(Thrombin_light, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

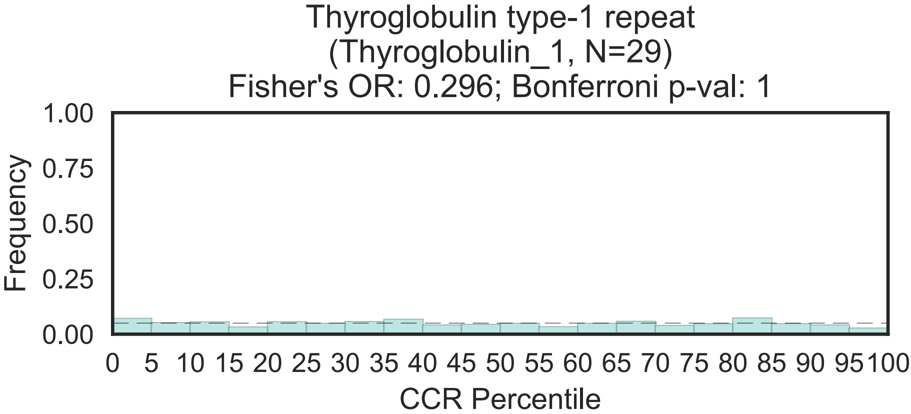

Thymidylate synthase
(Thymidylat_synt, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

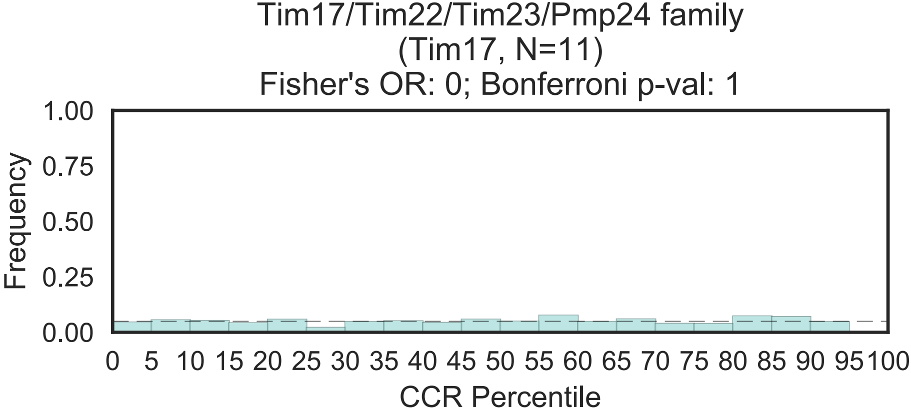

Thymidylate kinase
(Thymidylate_kin, N=3)
Fisher's OR: 2.31; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

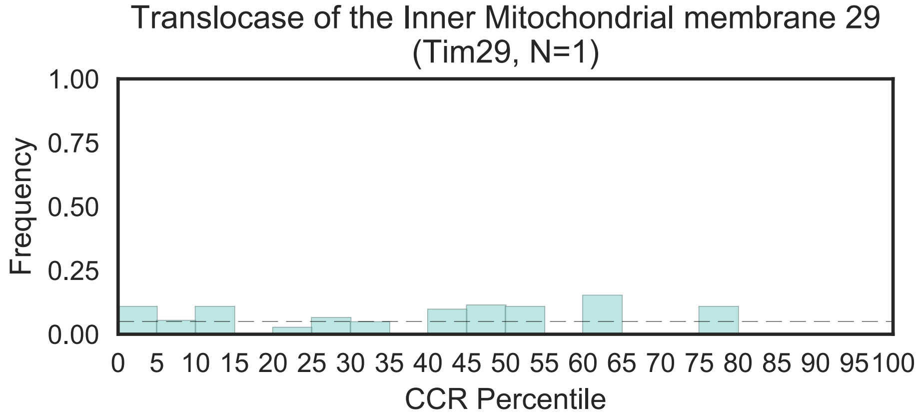

Thymopoietin protein
(Thymopoietin, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

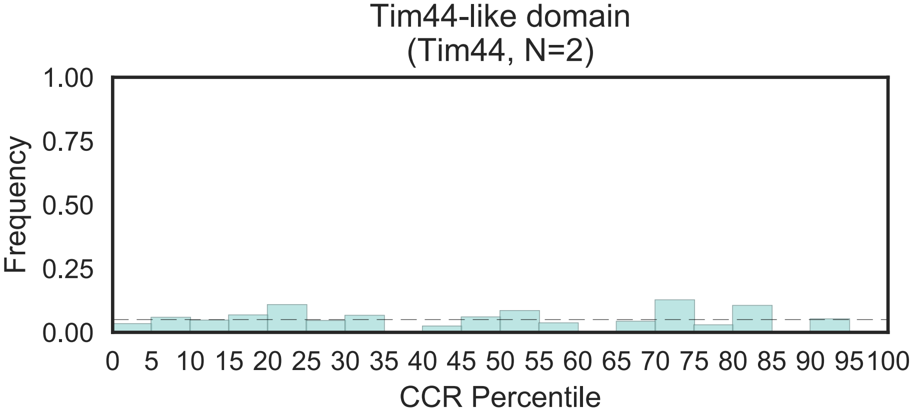

Thymosin beta-4 family
(Thymosin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

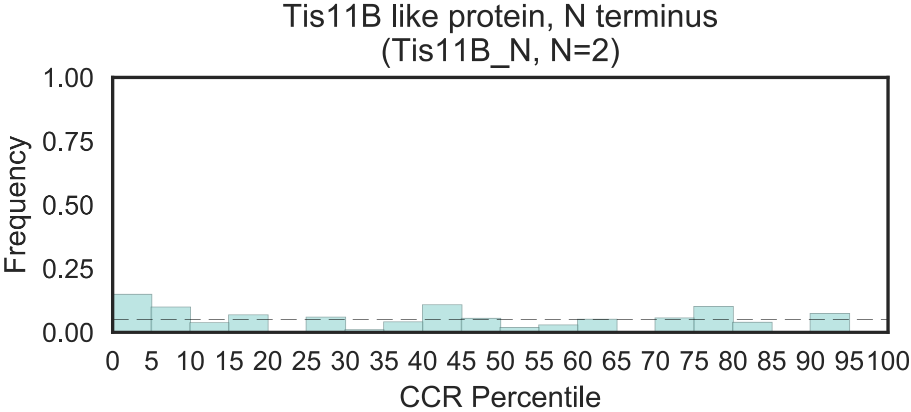

Thyroglobulin_1 repeat associated disordered domain
(Thyroglob_assoc, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

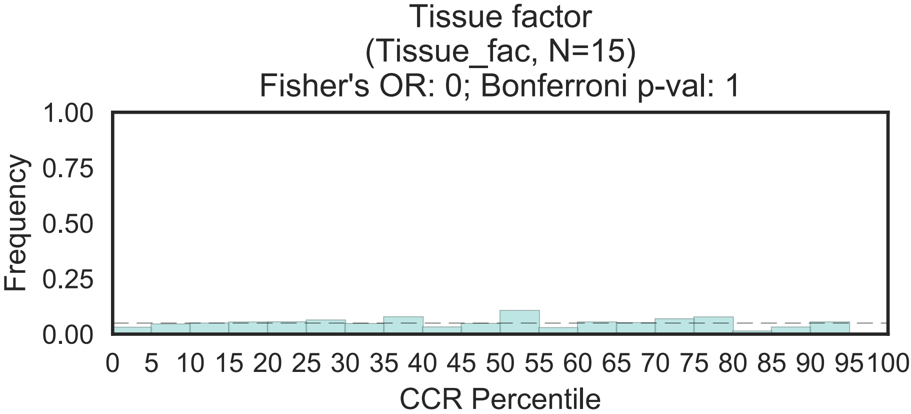

Thyroglobulin type-1 repeat
(Thyroglobulin_1, N=29)
Fisher's OR: 0.296; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

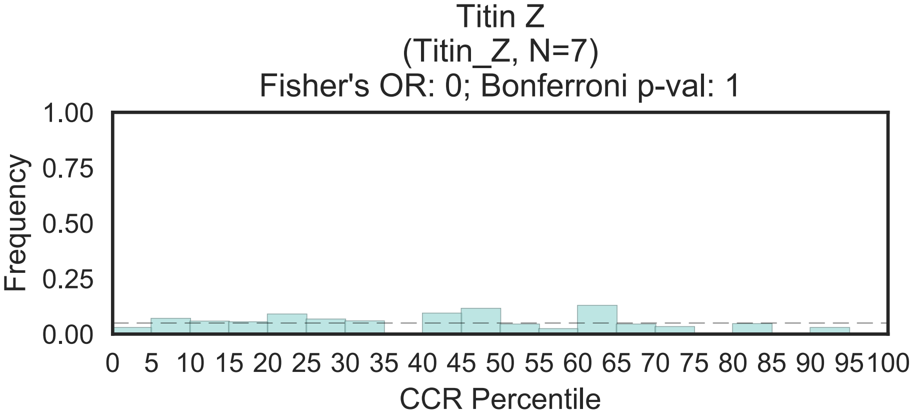

Tim17/Tim22/Tim23/Pmp24 family
(Tim17, N=11)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

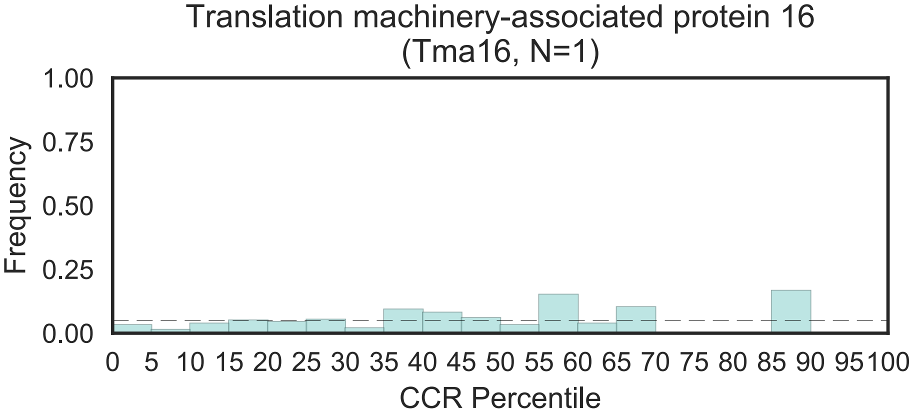

Translocase of the Inner Mitochondrial membrane 29
(Tim29, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

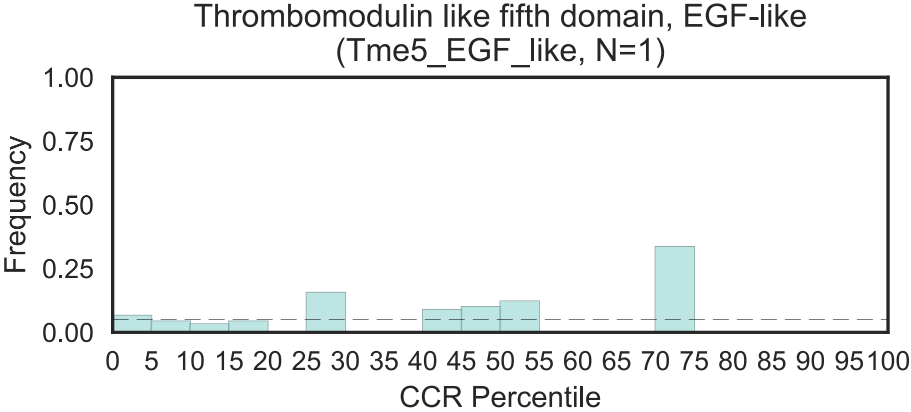

Tim44-like domain
(Tim44, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

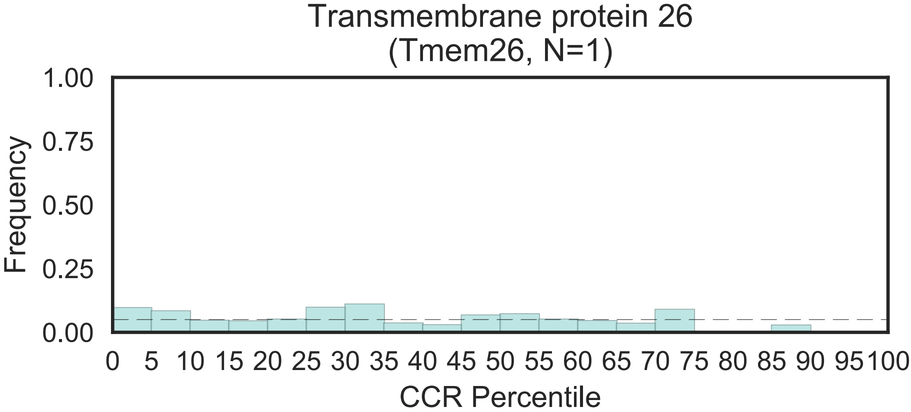

Tis11B like protein, N terminus
(Tis11B_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

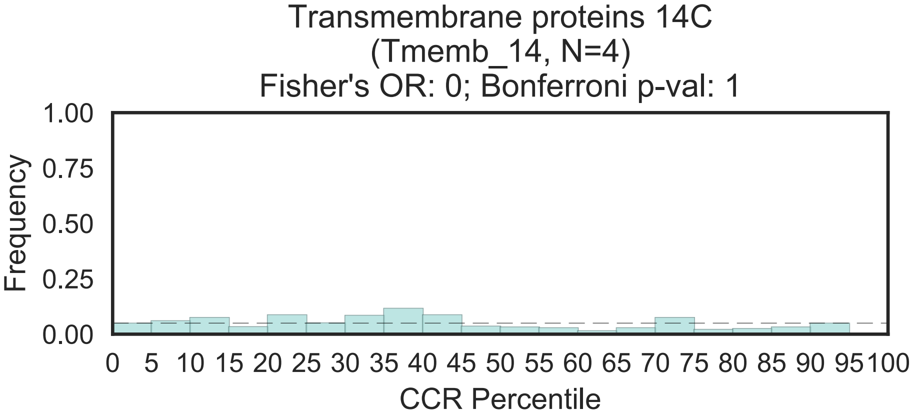

Tissue factor
(Tissue_fac, N=15)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

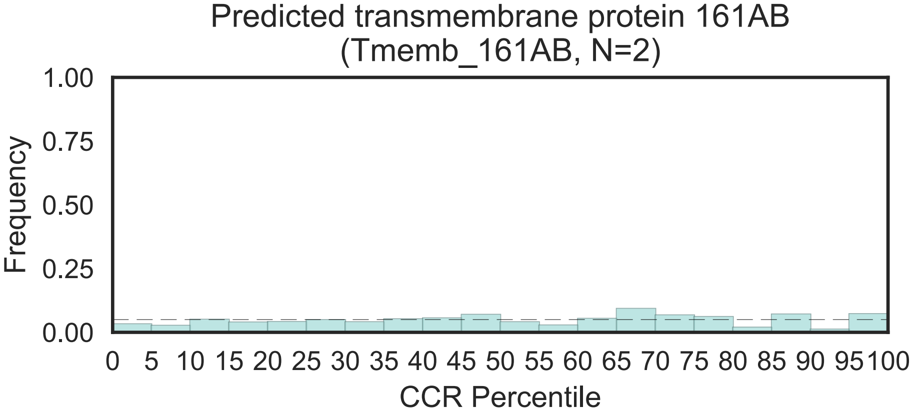

Titin Z
(Titin_Z, N=7)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Translation machinery-associated protein 16
(Tma16, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

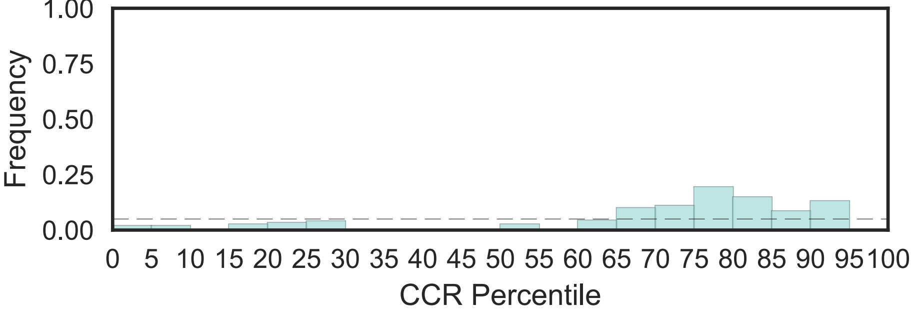

Thrombomodulin like fifth domain, EGF-like
(Tme5_EGF_like, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

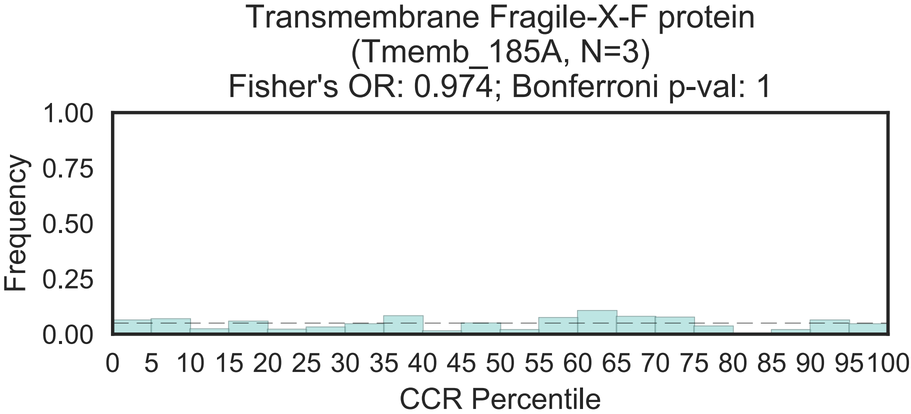

Transmembrane protein 26
(Tmem26, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

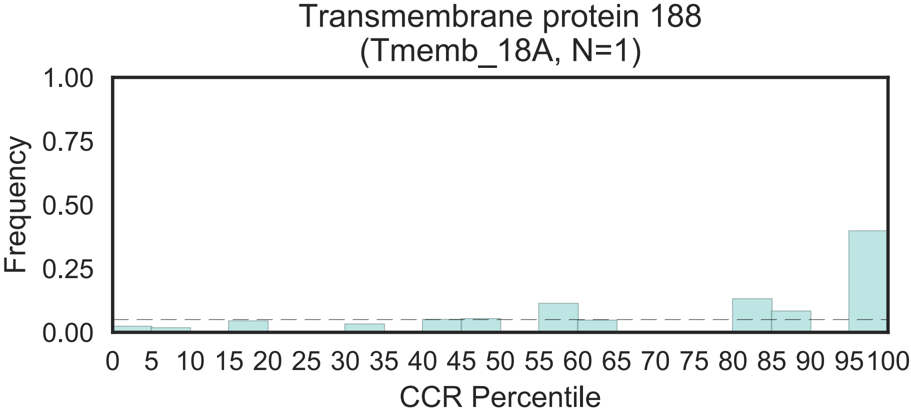

Transmembrane proteins 14C
(Tmemb_14, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

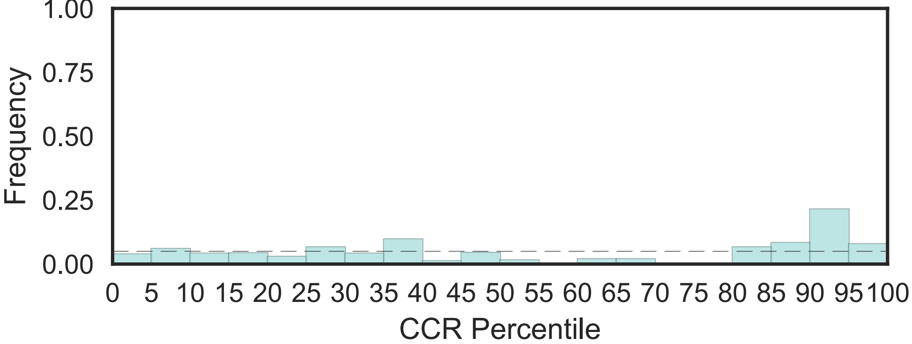

Predicted transmembrane protein 161AB
(Tmemb_161AB, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Putative transmembrane protein 170
(Tmemb_170, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

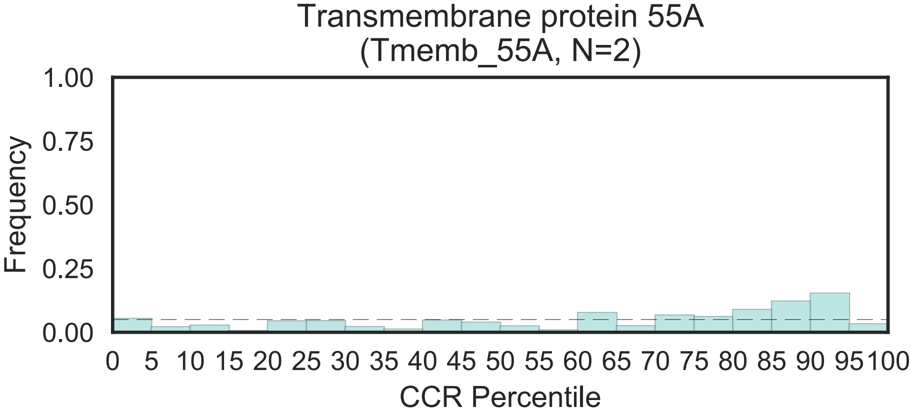


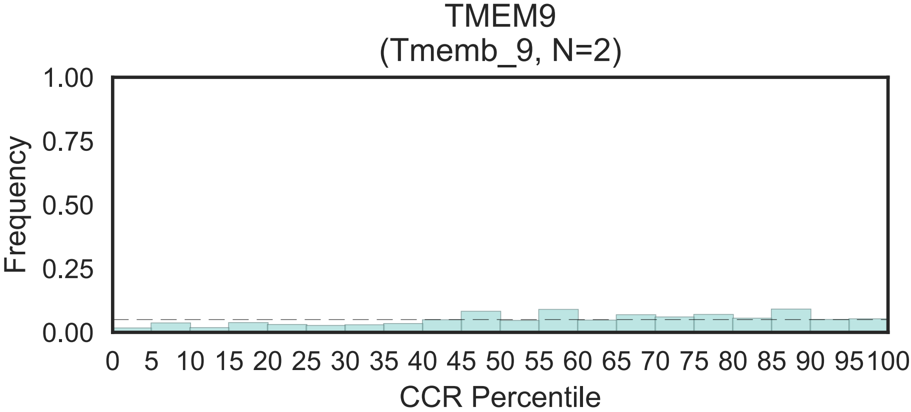

Transmembrane Fragile-X-F protein
(Tmemb_185A, N=3)
Fisher's OR: 0.974; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

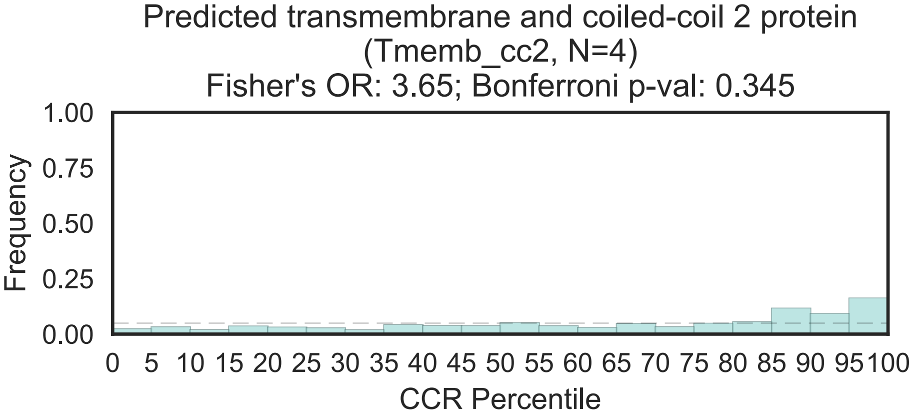

Transmembrane protein 188
(Tmemb_18A, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



Predicted membrane protein
(Tmemb_40, N=1)


Transmembrane protein 55A
(Tmemb_55A, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


TMEM9
(Tmemb_9, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Predicted transmembrane and coiled-coil 2 protein
(Tmemb_cc2, N=4)
Fisher's OR: 3.65; Bonferroni p-val: 0.345
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
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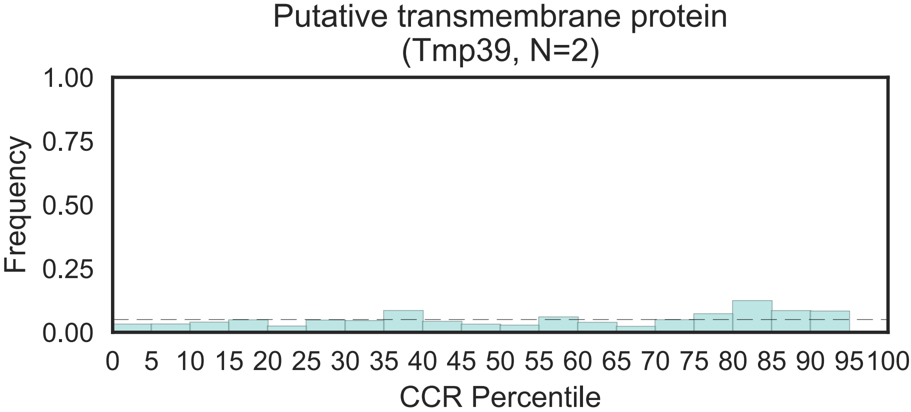
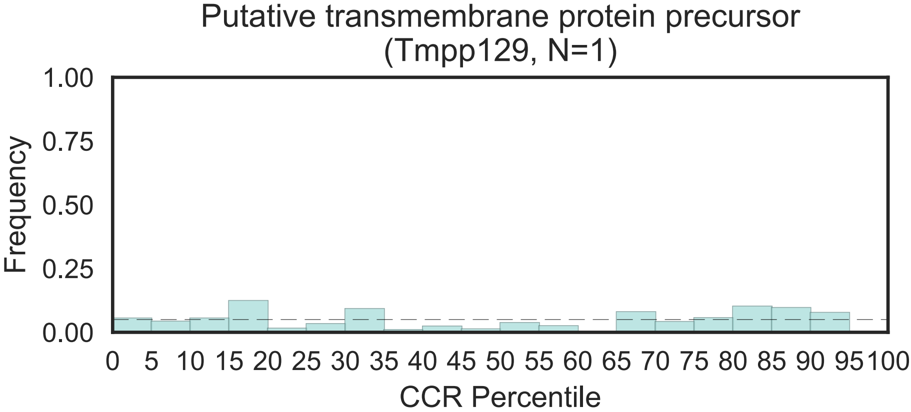
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Putative transmembrane protein
(Tmp39, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Putative transmembrane protein precursor
(Tmpp129, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
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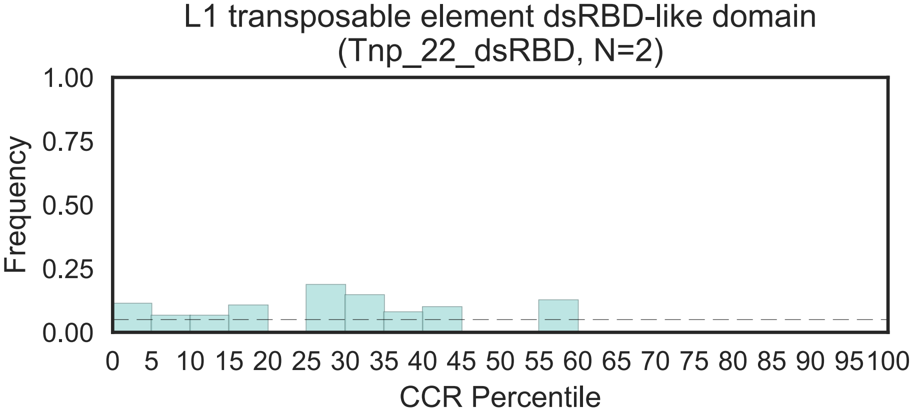
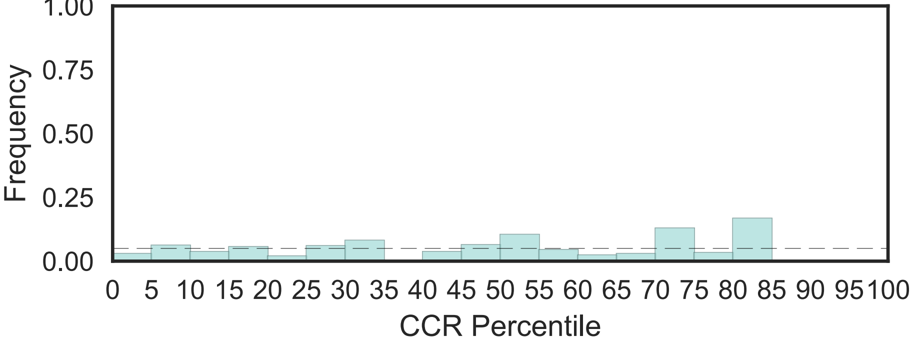
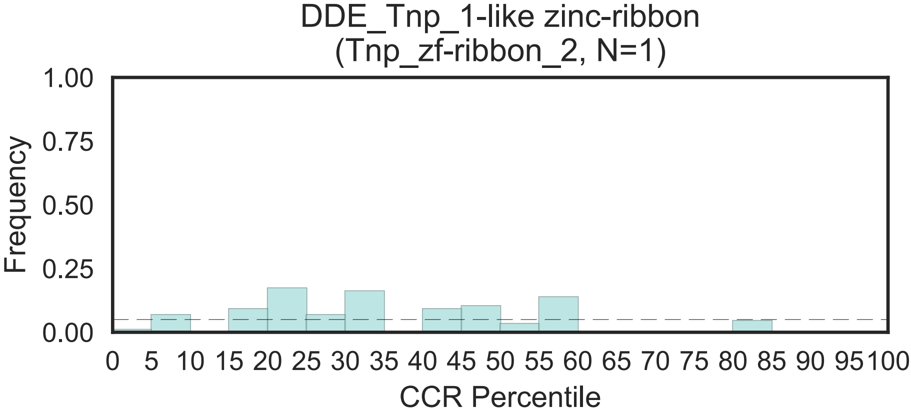
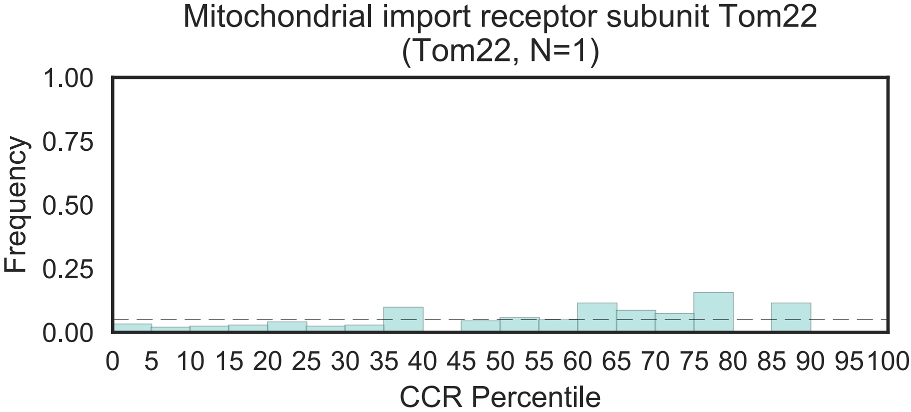
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

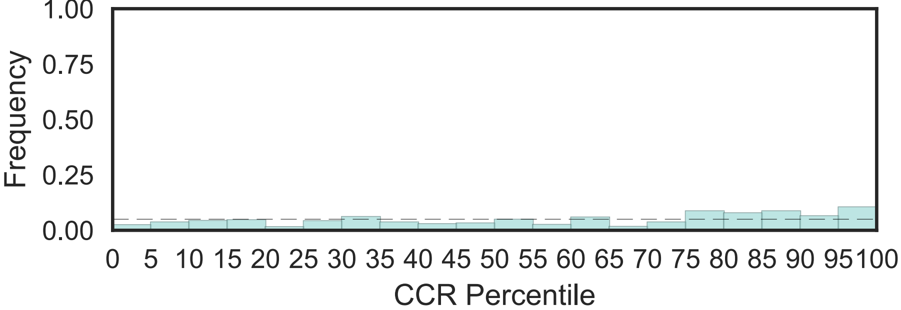

L1 transposable element dsRBD-like domain
(Tnp_22_dsRBD, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



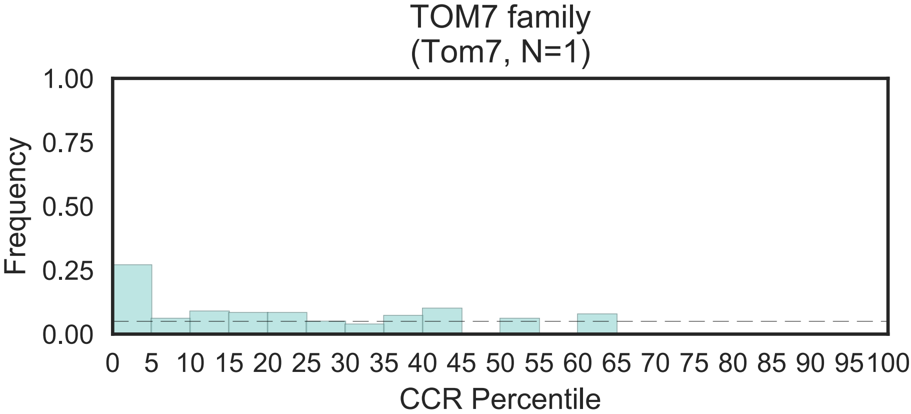
Transposase protein
(Tnp_P_element, N=1)

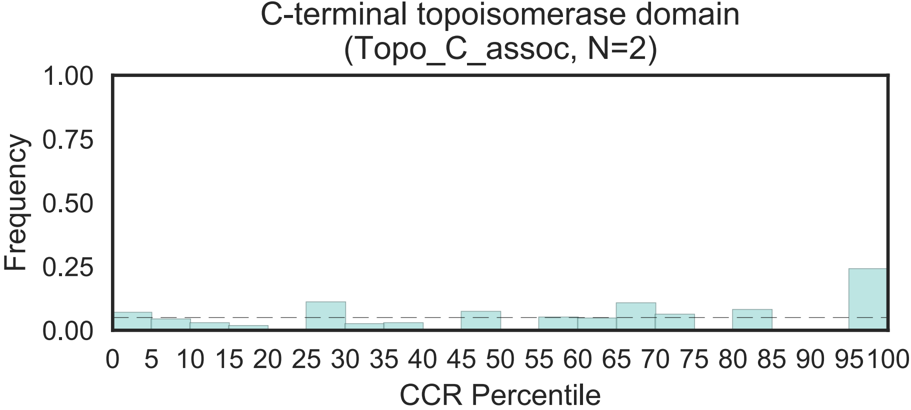

DDE_Tnp_1-like zinc-ribbon
(Tnp_zf-ribbon_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

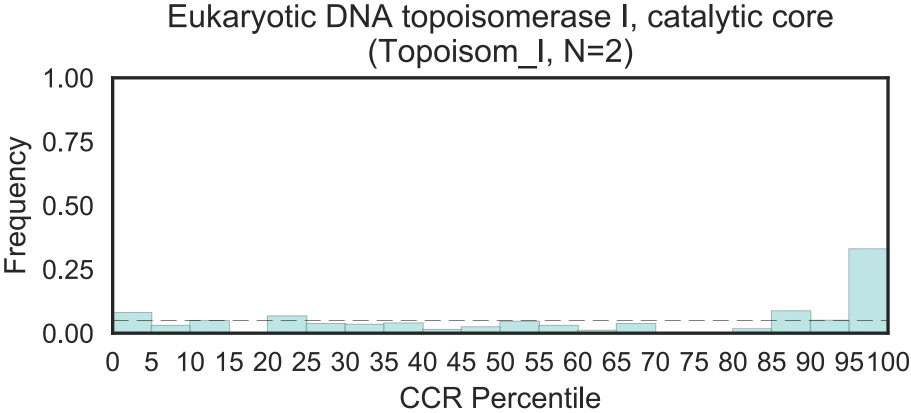

Mitochondrial import receptor subunit Tom22
(Tom22, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

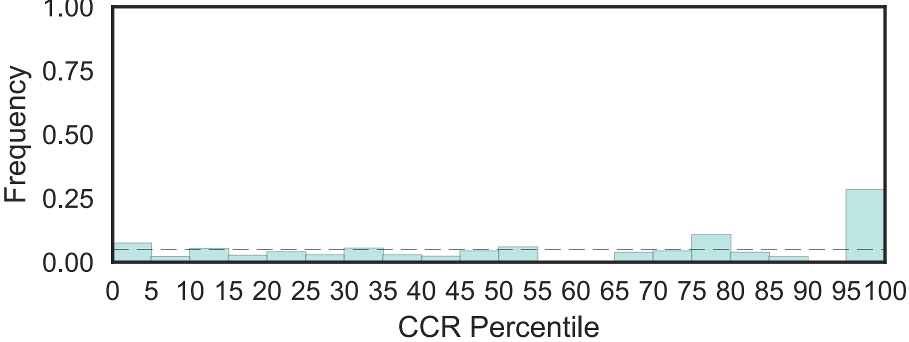


Outer mitochondrial membrane transport complex protein
(Tom37, N=4)
Fisher's OR: 2.08; Bonferroni p-val: 1

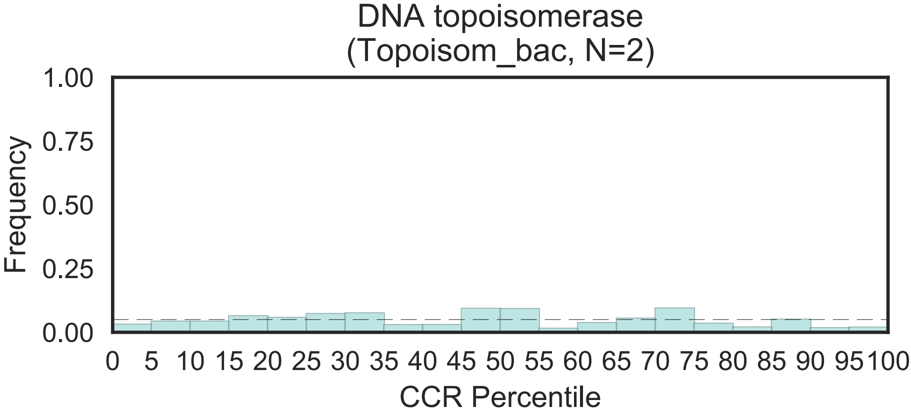

TOM7 family
(Tom7, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

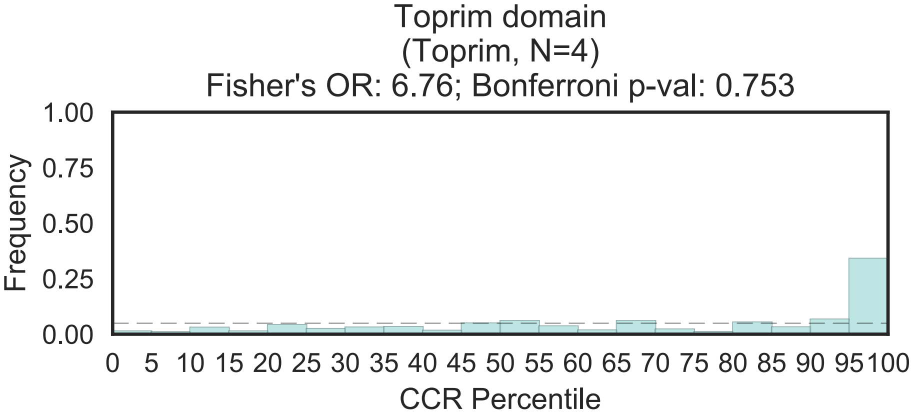

C-terminal topoisomerase domain
(Topo_C_assoc, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

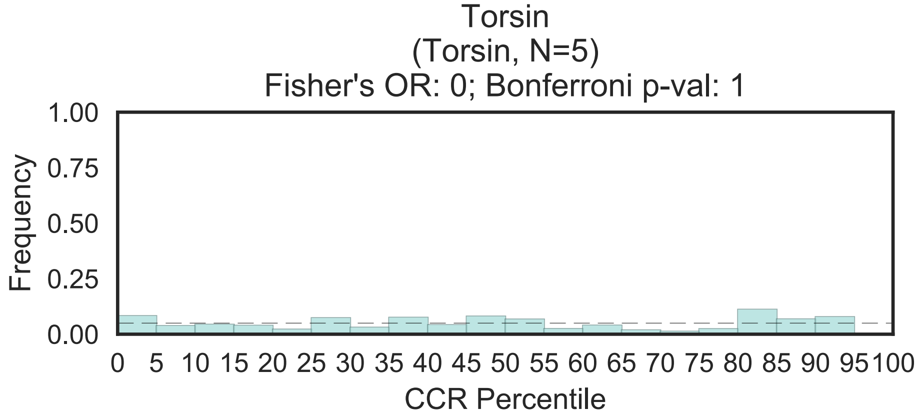

Eukaryotic DNA topoisomerase I, catalytic core
(Topoisom_I, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

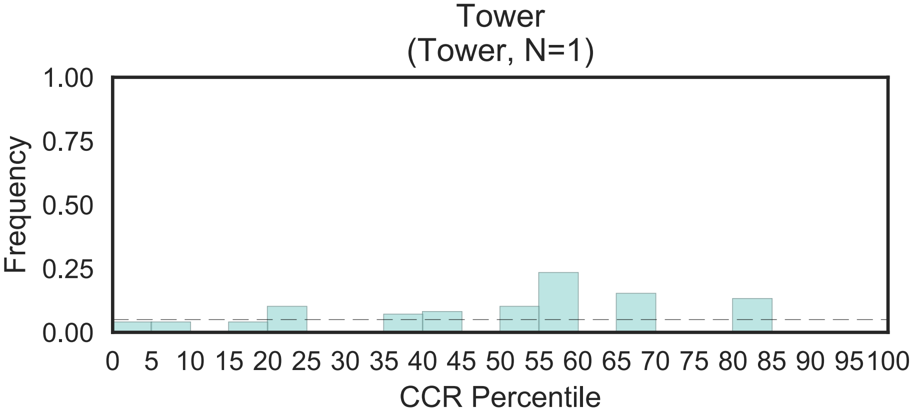


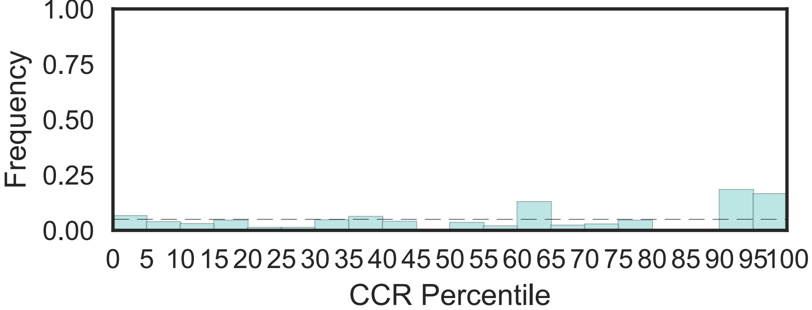
Eukaryotic DNA topoisomerase I, DNA binding fragment (Topoisom_I_N, N=2)

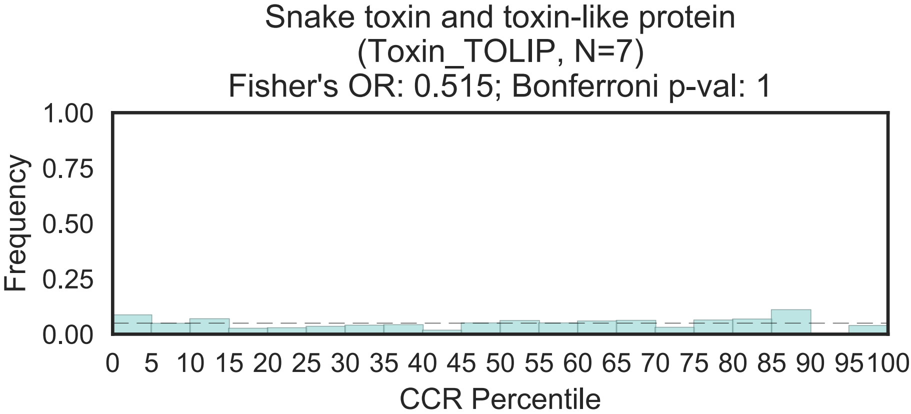

DNA topoisomerase
(Topoisom_bac, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

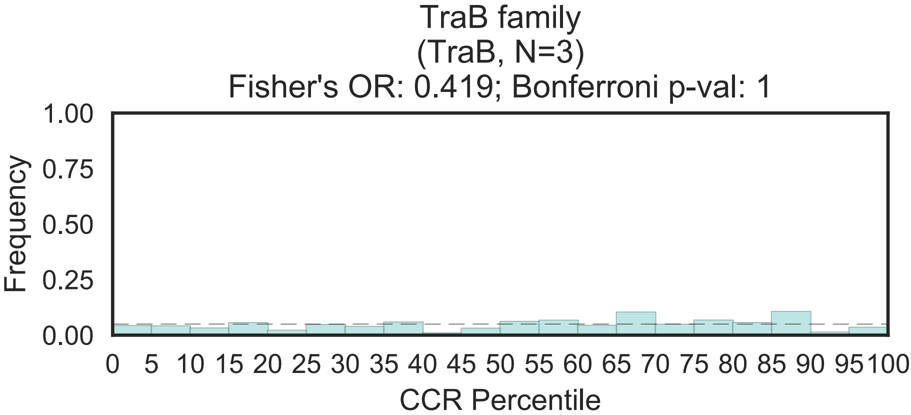

Toprim domain
(Toprim, N=4)
Fisher's OR: 6.76; Bonferroni p-val: 0.753
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

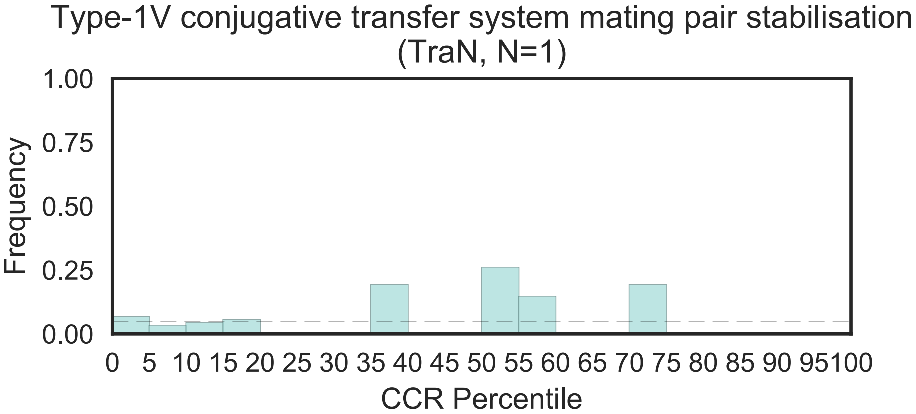

Torsin
(Torsin, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

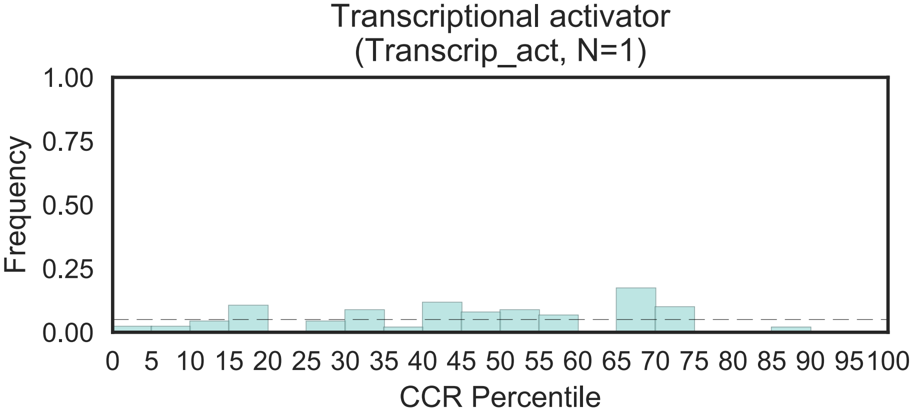

Tower
(Tower, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

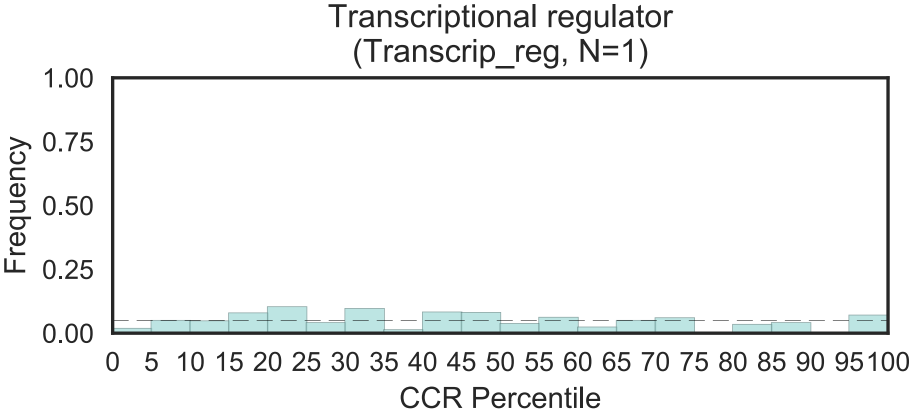

GHH signature containing HNH/Endo VII superfamily nuclease toxin (Tox-GHH, N=3)
Fisher's OR: 3.33; Bonferroni p-val: 1

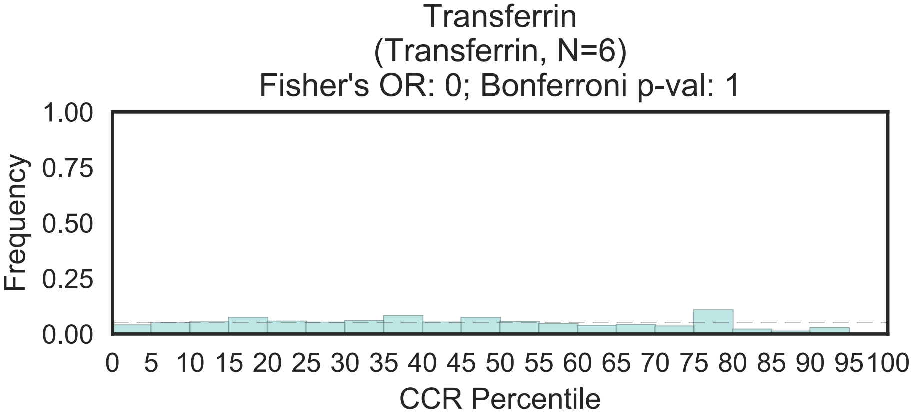

Snake toxin and toxin-like protein
(Toxin_TOLIP, N=7)
Fisher's OR: 0.515; Bonferroni p-val: 1

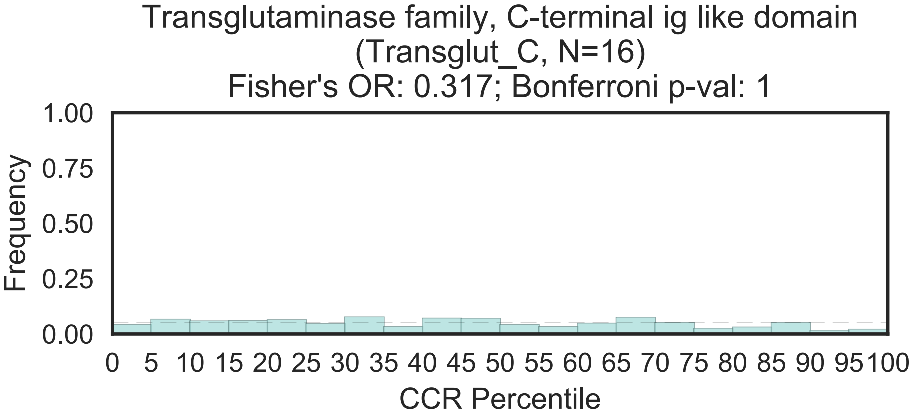

TraB family
(TraB, N=3)
Fisher's OR: 0.419; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

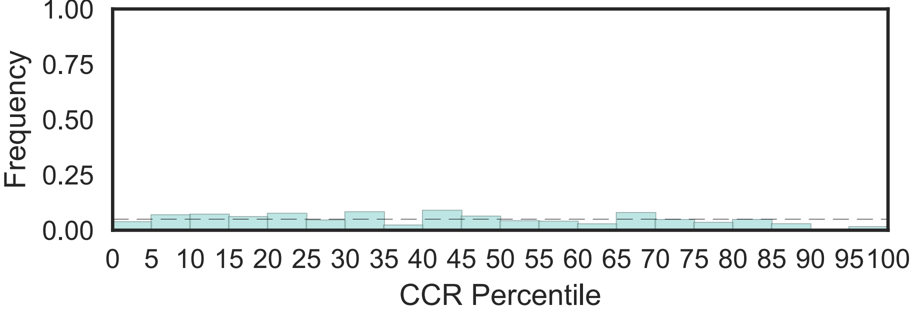

Type-1V conjugative transfer system mating pair stabilisation
(TraN, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95100
CCR Percentile


Transcriptional activator
(Transcrip_act, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

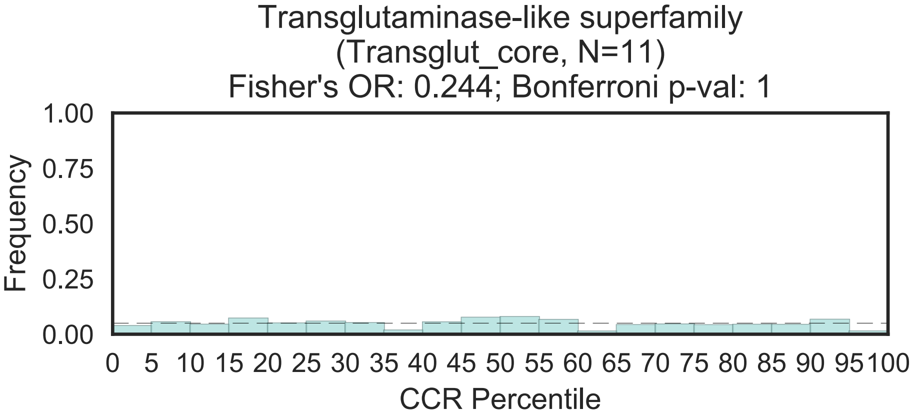

Transcriptional regulator
(Transcrip_reg, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

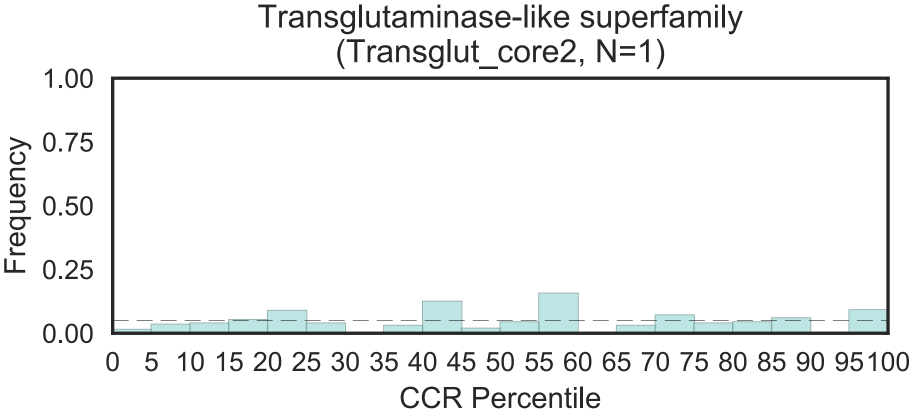

Transferrin
(Transferrin, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

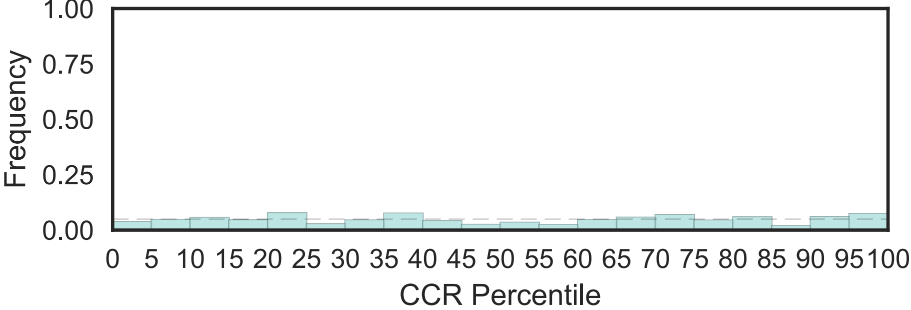

Transglutaminase family, C-terminal ig like domain
(Transglut_C, N=16)
Fisher's OR: 0.317; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



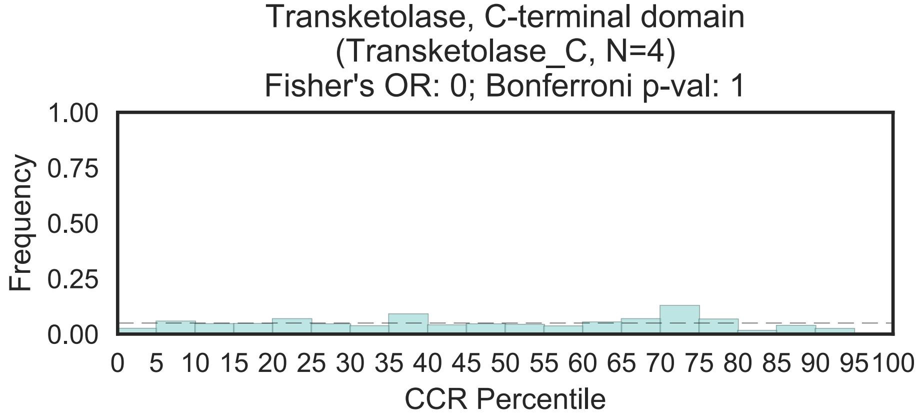
Transglutaminase family
(Transglut_N, N=9)
Fisher's OR: 0.215; Bonferroni p-val: 1

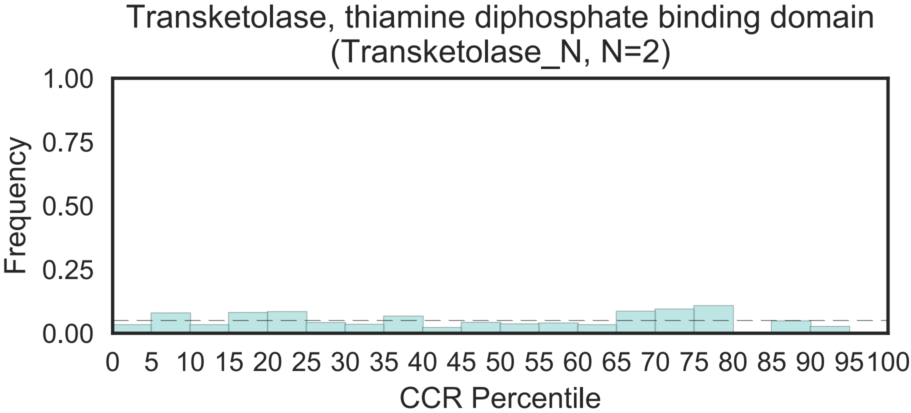

Transglutaminase-like superfamily
(Transglut_core, N=11)
Fisher's OR: 0.244; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

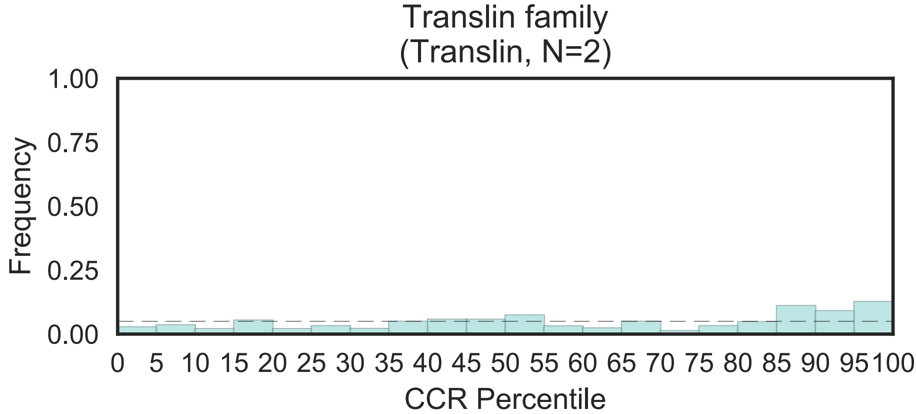

Transglutaminase-like superfamily
(Transglut_core2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

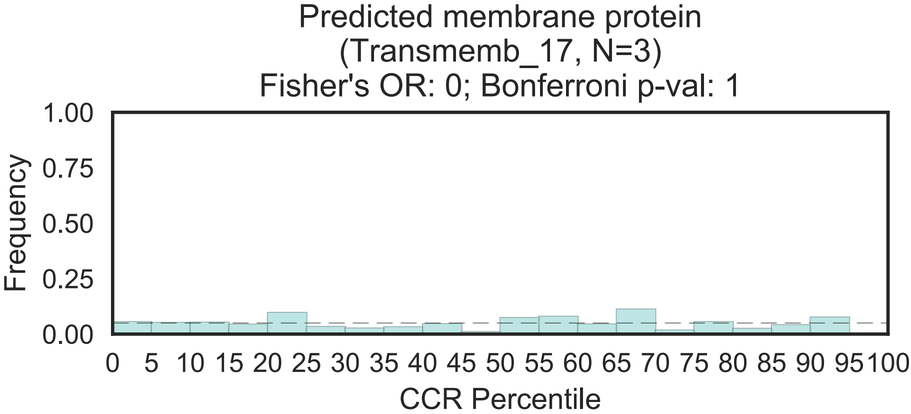


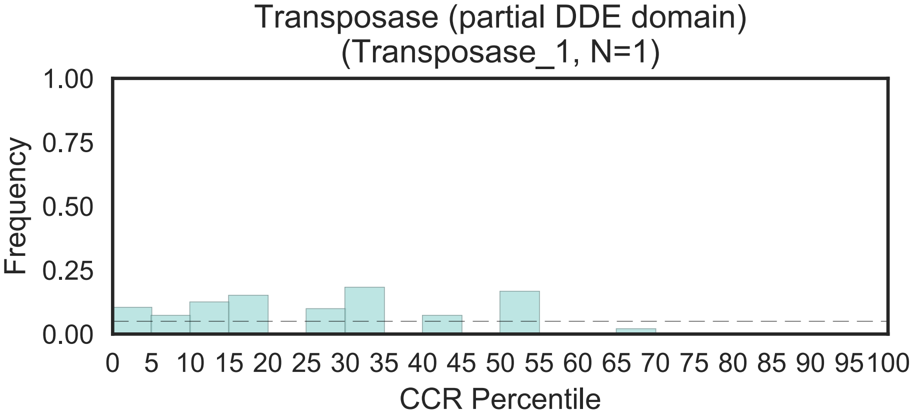
Transketolase, pyrimidine binding domain
(Transket_pyr, N=7)
Fisher's OR: 1.07; Bonferroni p-val: 1


Transketolase, C-terminal domain
(Transketolase_C, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

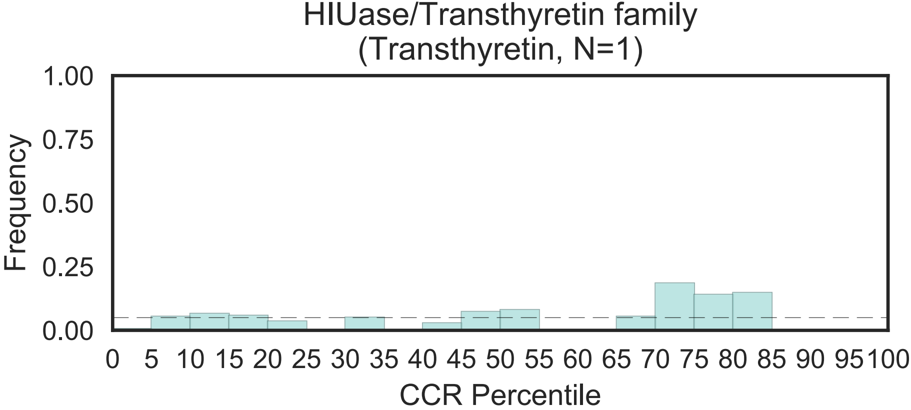

Transketolase, thiamine diphosphate binding domain
(Transketolase_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

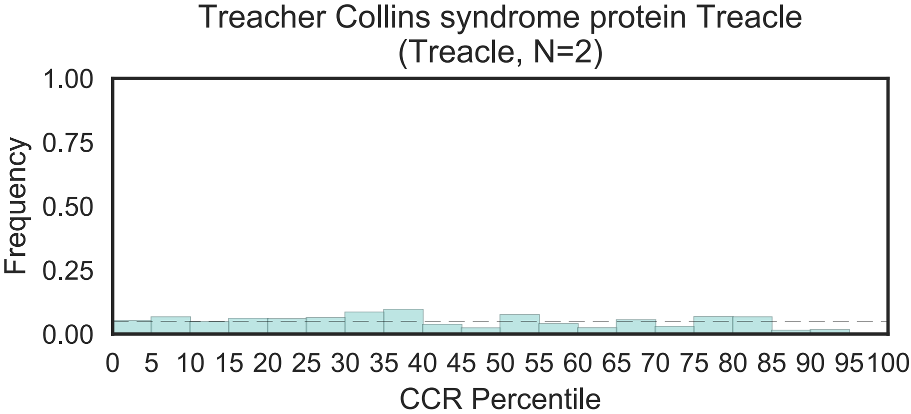

Translin family
(Translin, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

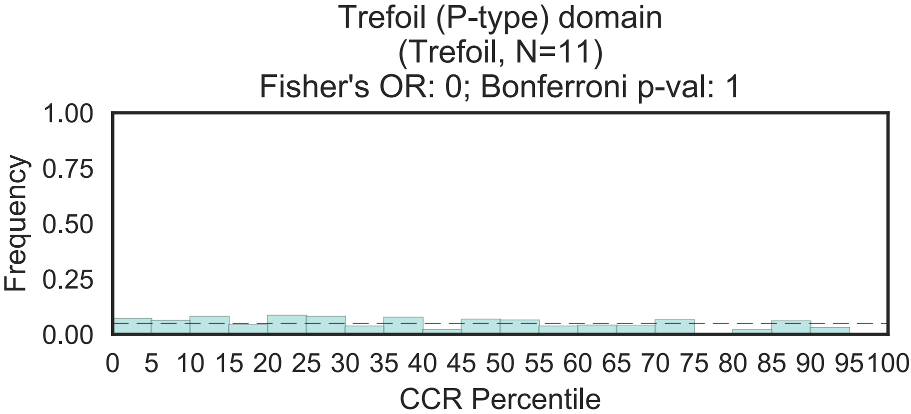

Predicted membrane protein
(Transmemb_17, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

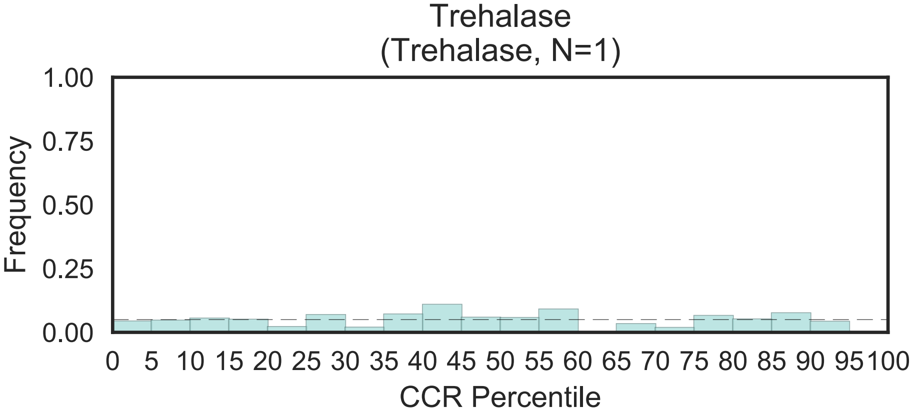


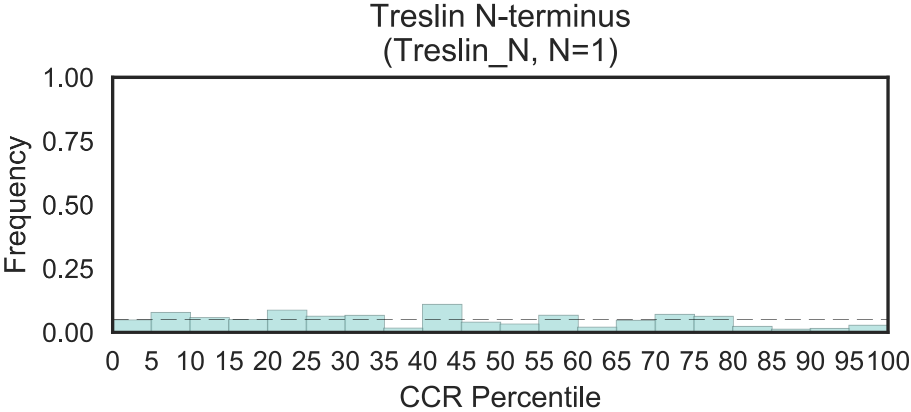
Transposase (partial DDE domain)
(Transposase_1, N=1)

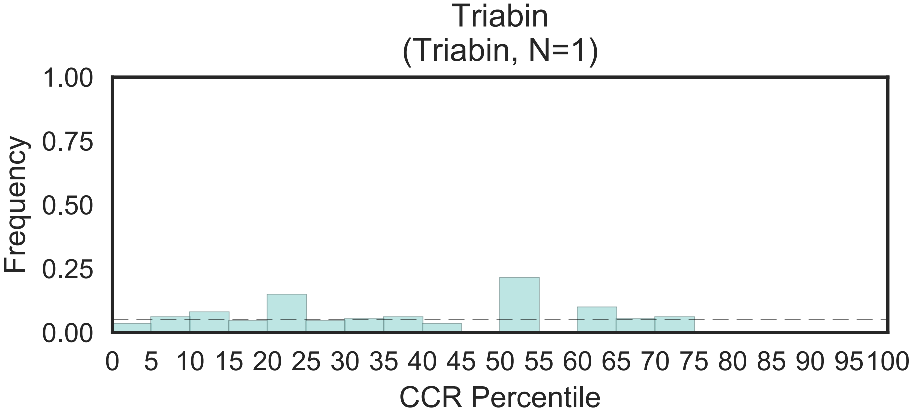

HIUase/Transthyretin family
(Transthyretin, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

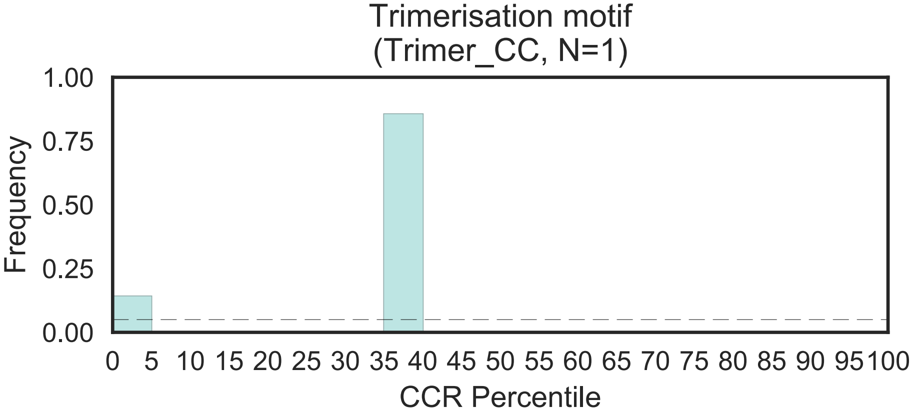

Treacher Collins syndrome protein Treacle
(Treacle, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

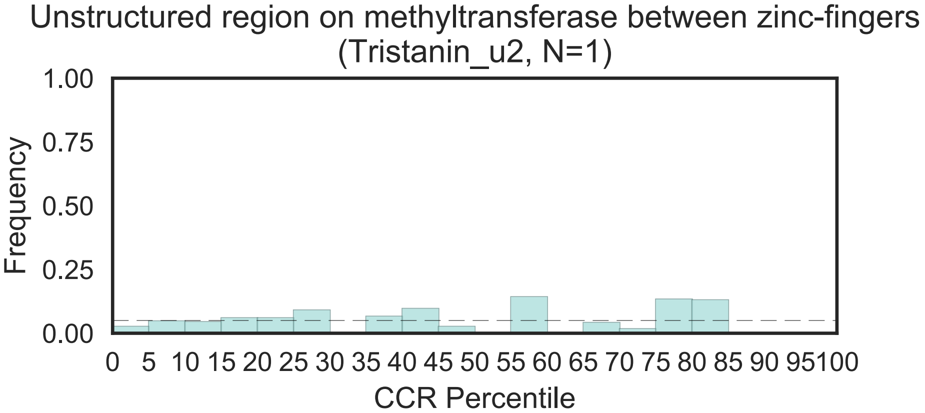

Trefoil (P-type) domain
(Trefoil, N=11)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

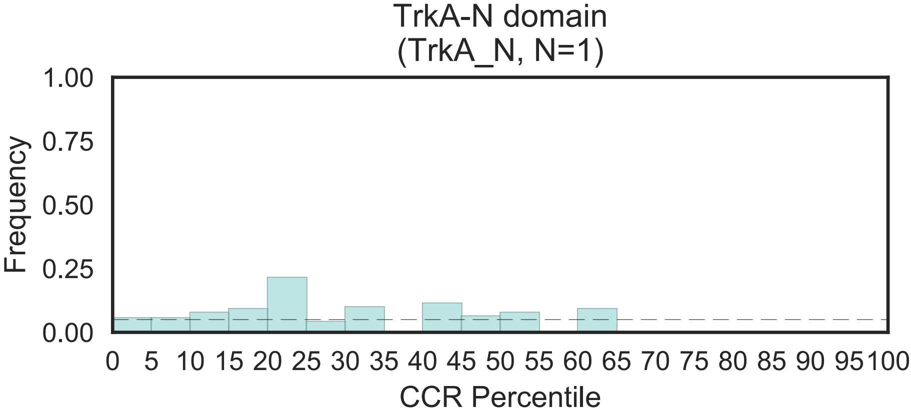

Trehalase
(Trehalase, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

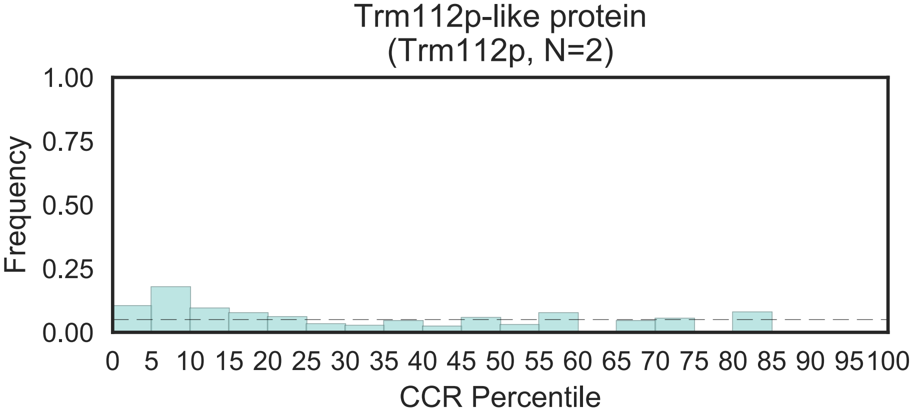

Treslin N-terminus
(Treslin_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

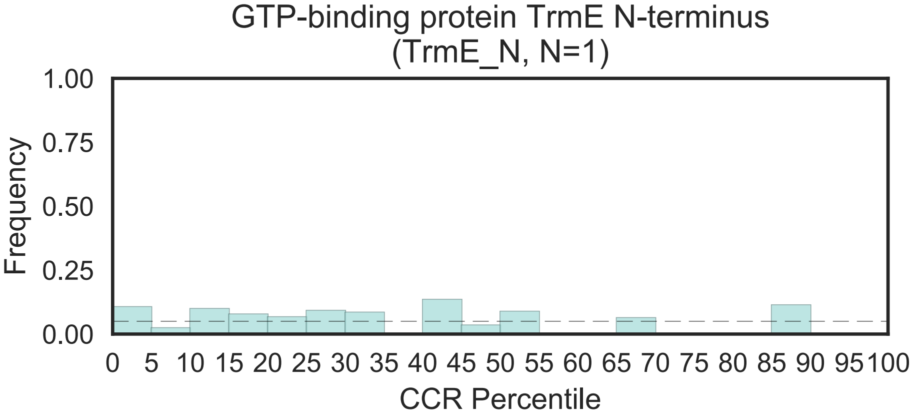

Triabin
(Triabin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

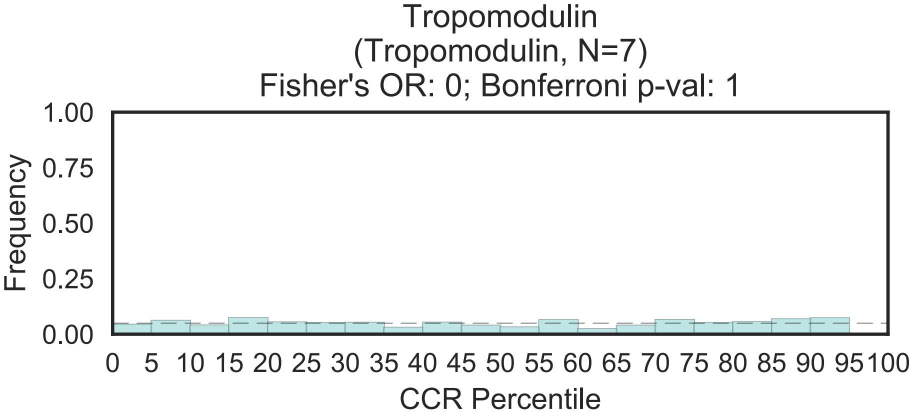

Trimerisation motif
(Trimer_CC, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

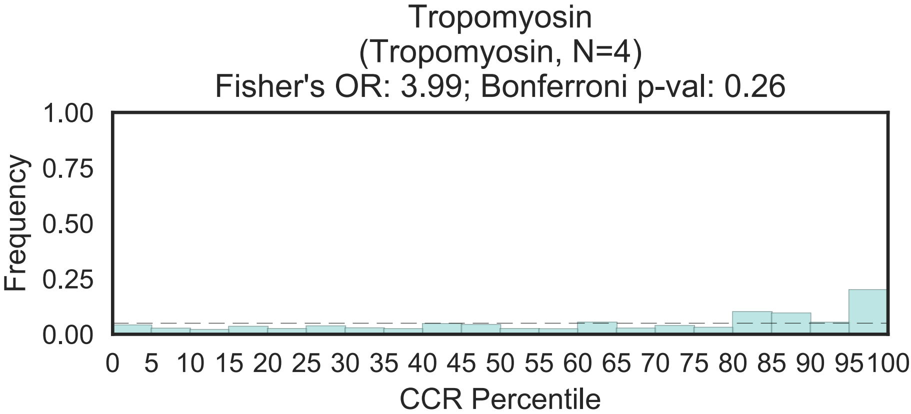

Unstructured region on methyltransferase between zinc-fingers
(Tristanin_u2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

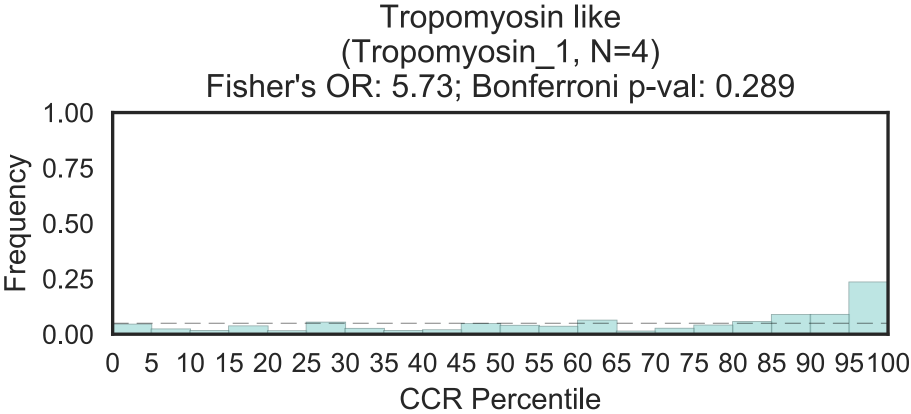

TrkA-N domain
(TrkA_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

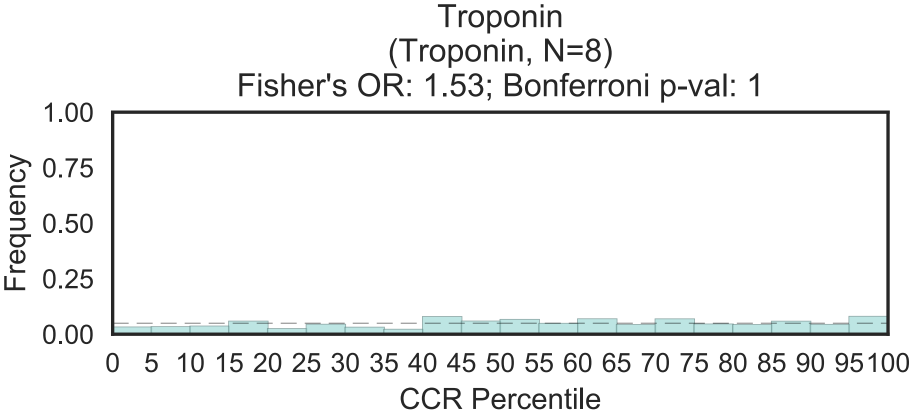

Trm112p-like protein
(Trm112p, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

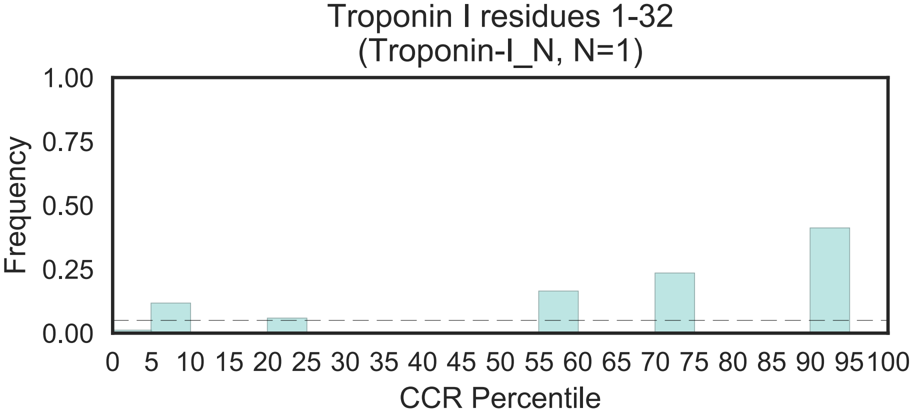

GTP-binding protein TrmE N-terminus
(TrmE_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

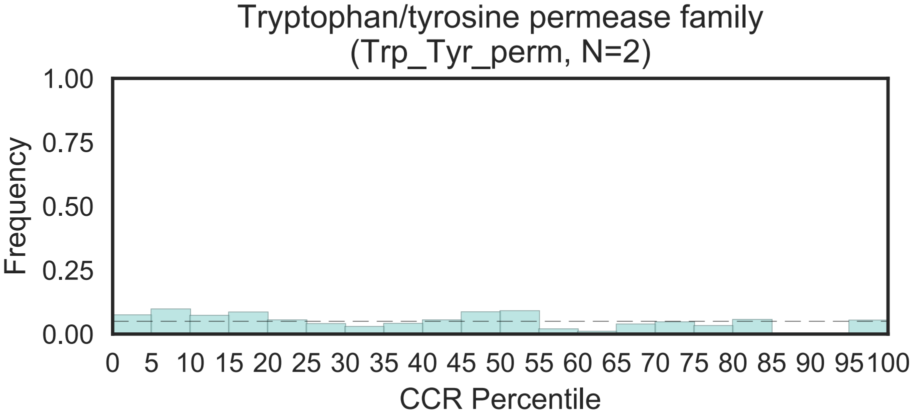

Tropomodulin
(Tropomodulin, N=7)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

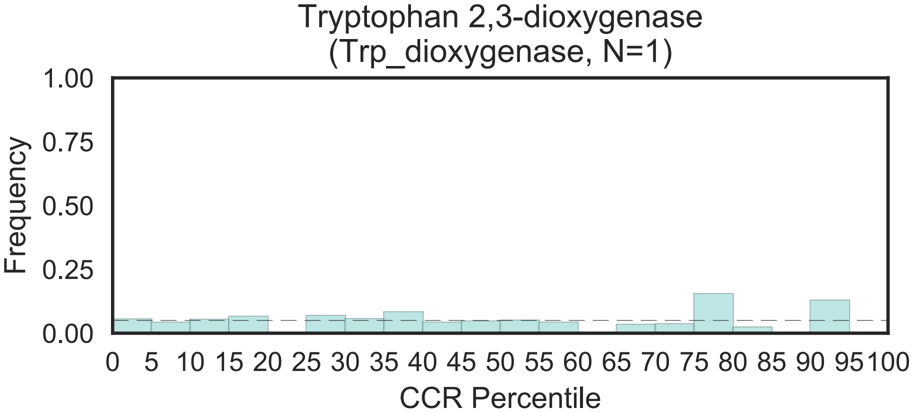

Tropomyosin
(Tropomyosin, N=4)
Fisher's OR: 3.99; Bonferroni p-val: 0.26
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

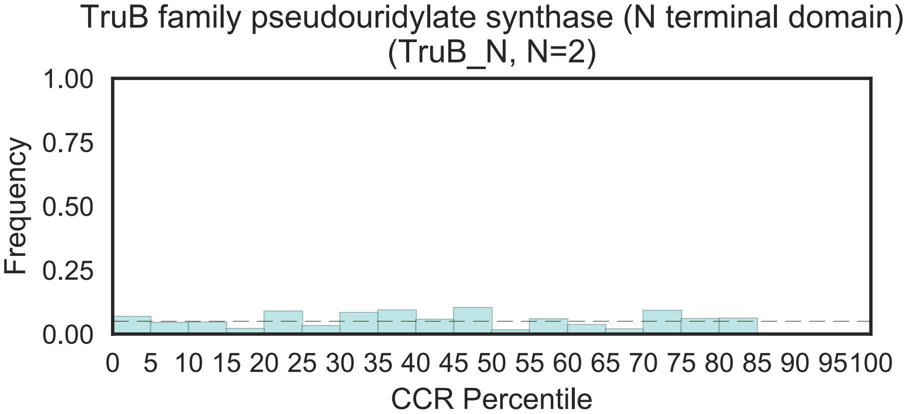

Tropomyosin like
(Tropomyosin_1, N=4)
Fisher's OR: 5.73; Bonferroni p-val: 0.289
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

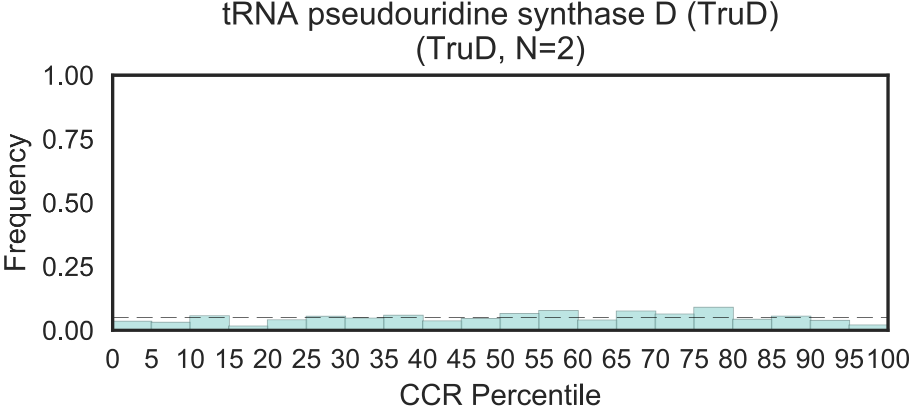

Troponin
(Troponin, N=8)
Fisher's OR: 1.53; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

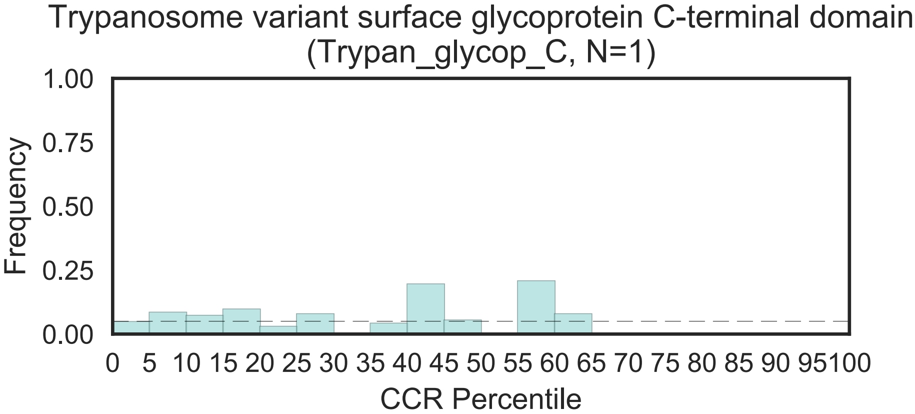

Troponin I residues 1-32
(Troponin-I_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

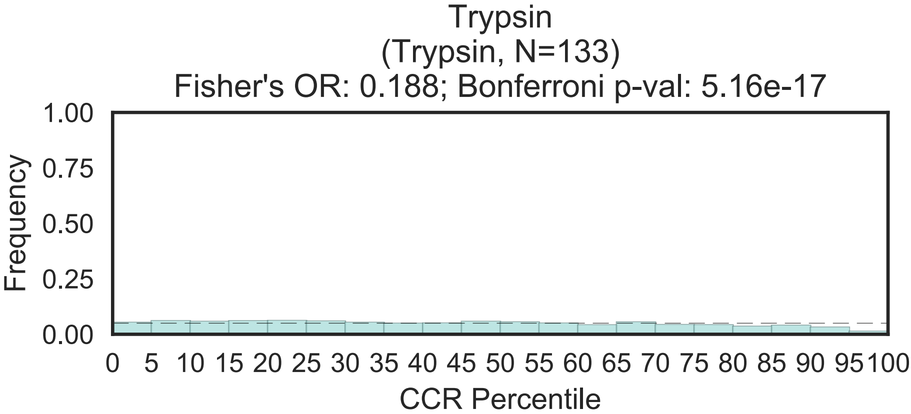

Tryptophan/tyrosine permease family
(Trp_Tyr_perm, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

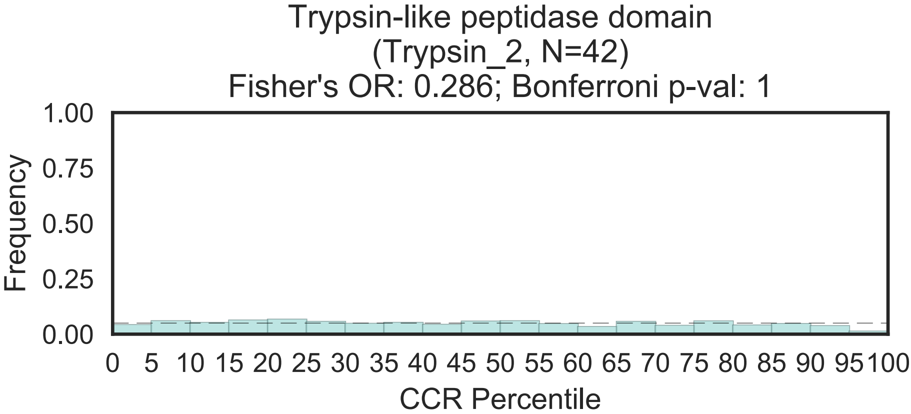

Tryptophan 2,3-dioxygenase
(Trp_dioxygenase, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

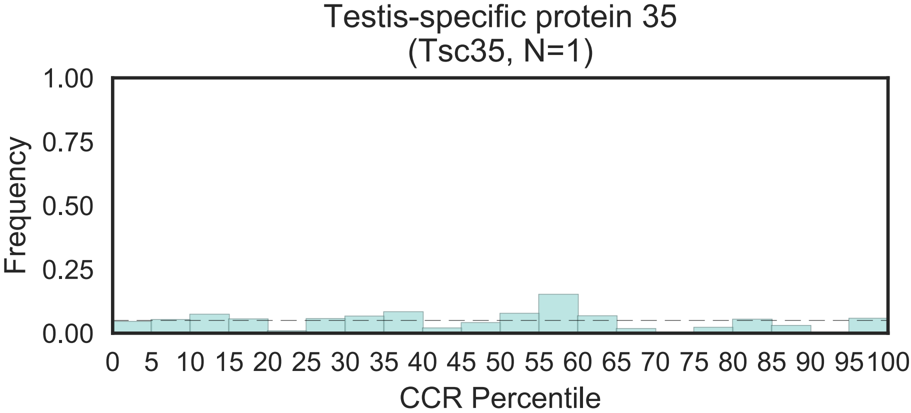

TruB family pseudouridylate synthase (N terminal domain)
(TruB_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

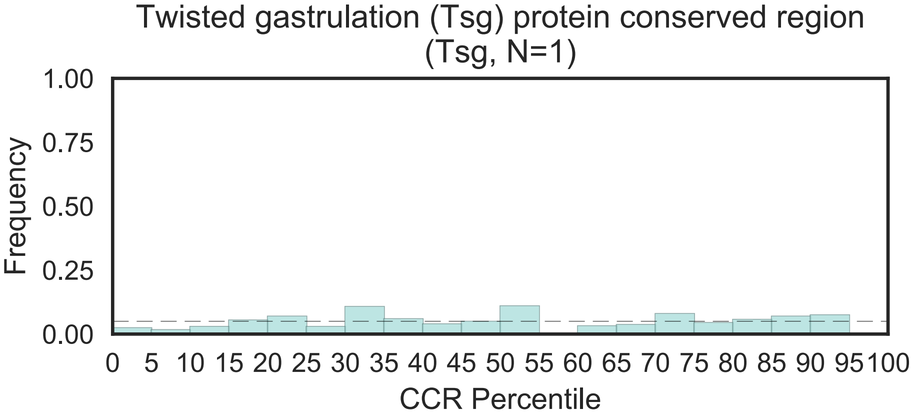

tRNA pseudouridine synthase D (TruD)
(TruD, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

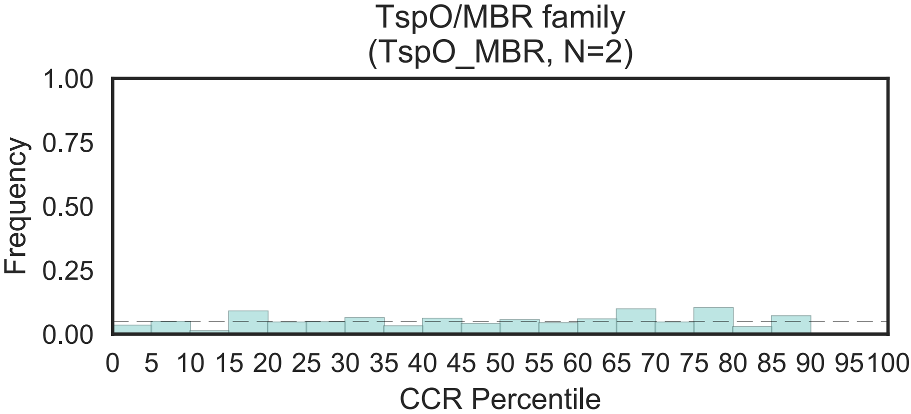

Trypanosome variant surface glycoprotein C-terminal domain
(Trypan_glycop_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

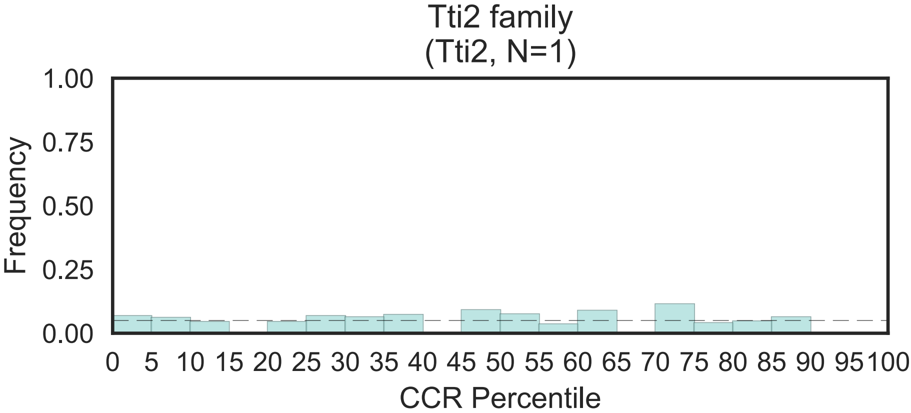

Trypsin
(Trypsin, N=133)
Fisher's OR: 0.188; Bonferroni p-val: 5.16e-17
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

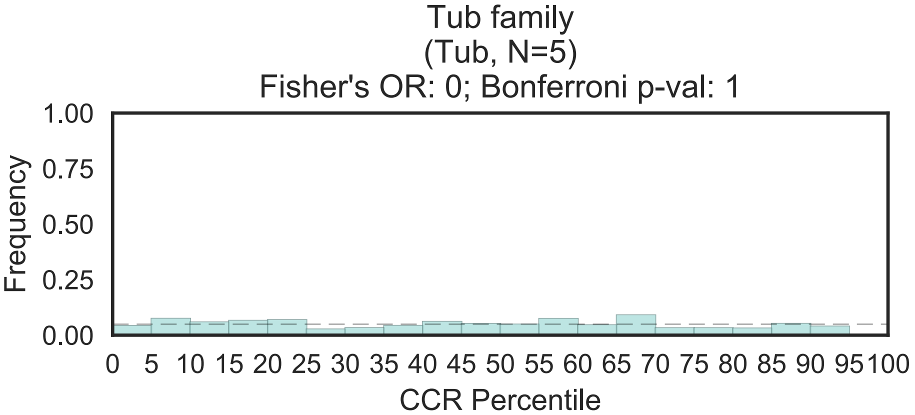

Trypsin-like peptidase domain
(Trypsin_2, N=42)
Fisher's OR: 0.286; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

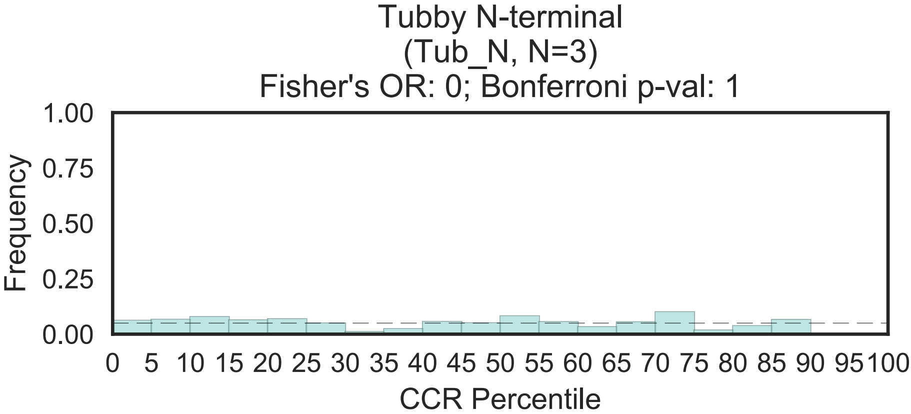

Testis-specific protein 35
(Tsc35, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

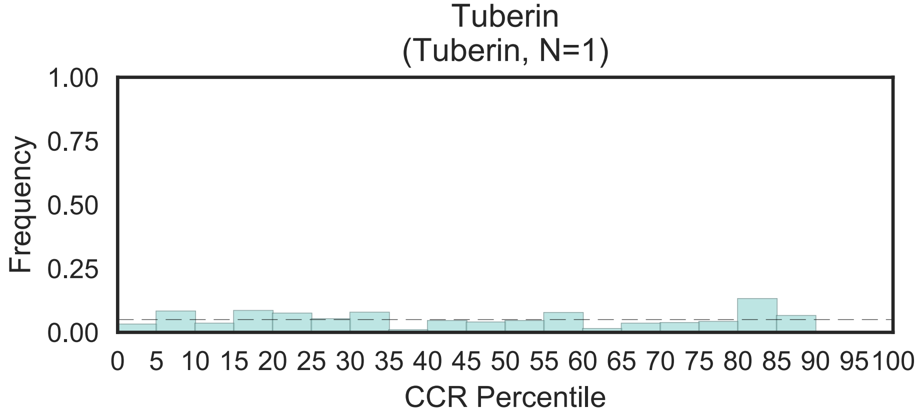

Twisted gastrulation (Tsg) protein conserved region
(Tsg, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

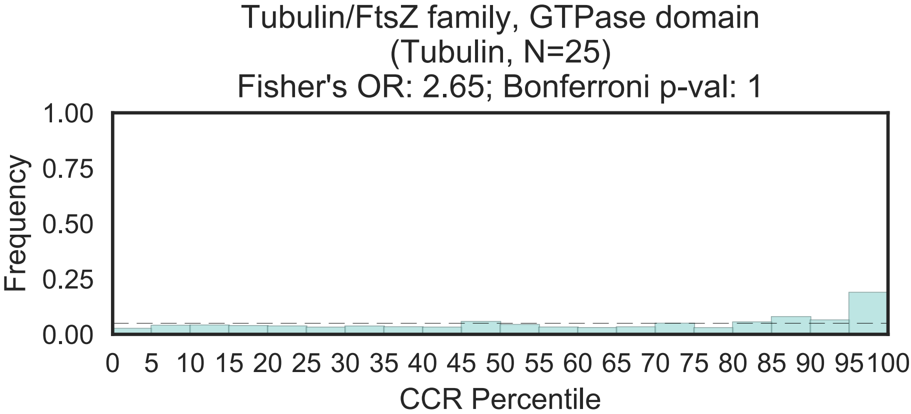

TspO/MBR family
(TspO_MBR, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


Tti2 family
(Tti2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

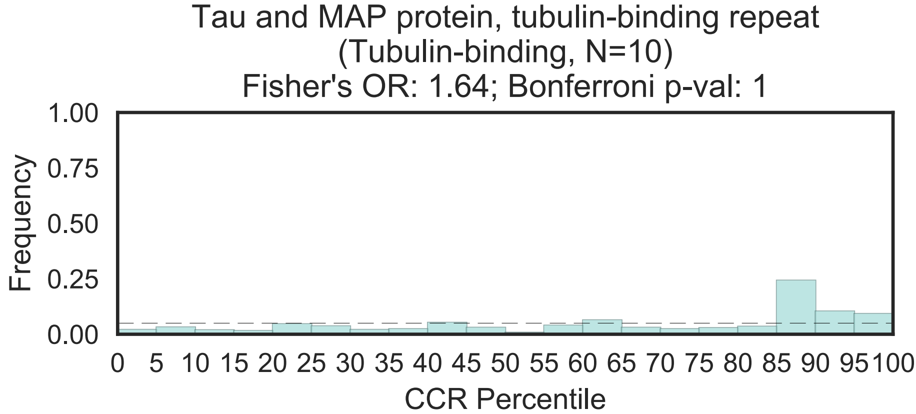

Tub family
(Tub, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Tubby N-terminal
(Tub_N, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

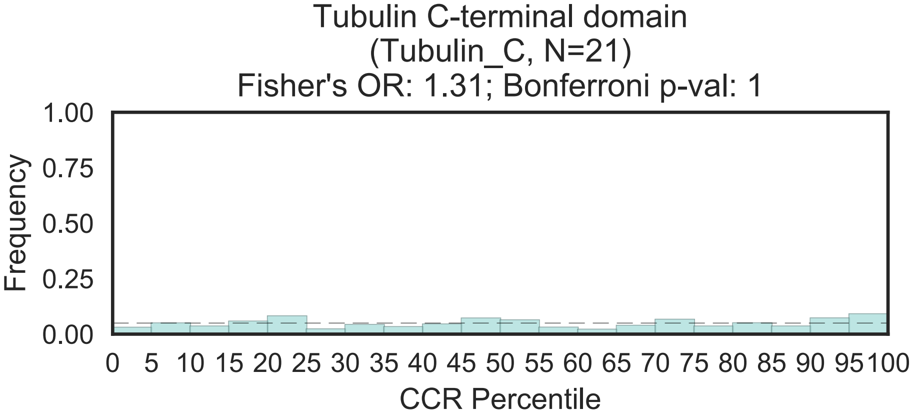

Tuberin
(Tuberin, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

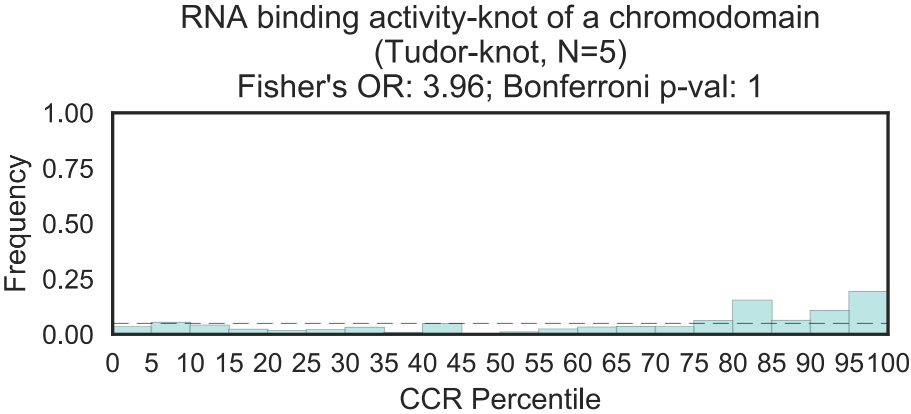


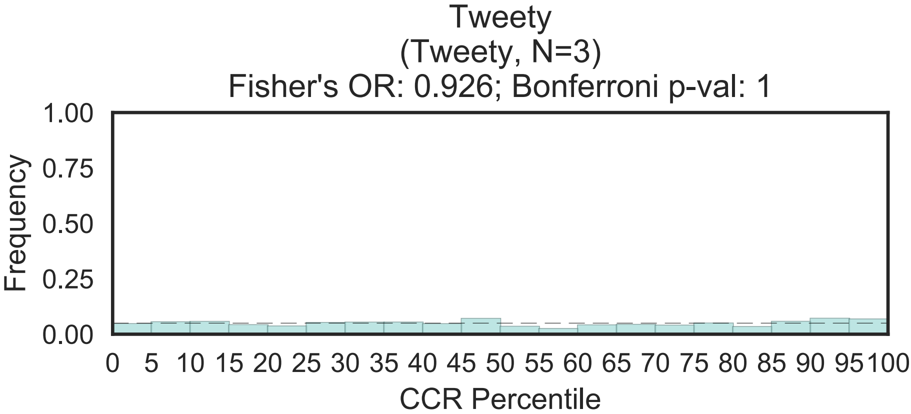
Tubulin/FtsZ family, GTPase domain
(Tubulin, N=25)
Fisher's OR: 2.65; Bonferroni p-val: 1

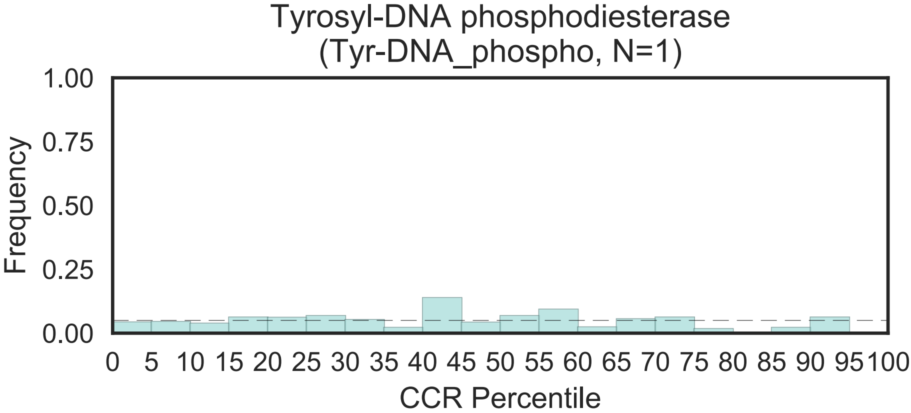


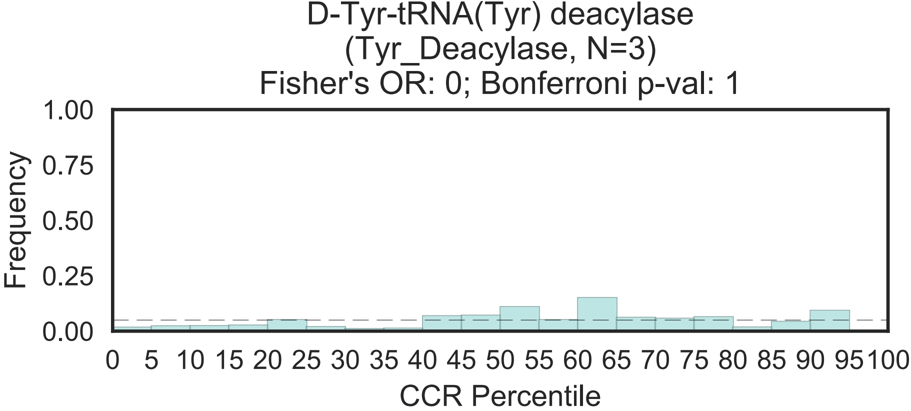
Tau and MAP protein, tubulin-binding repeat
(Tubulin-binding, N=10)
Fisher's OR: 1.64; Bonferroni p-val: 1


Tubulin C-terminal domain
(Tubulin_C, N=21)
Fisher's OR: 1.31; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

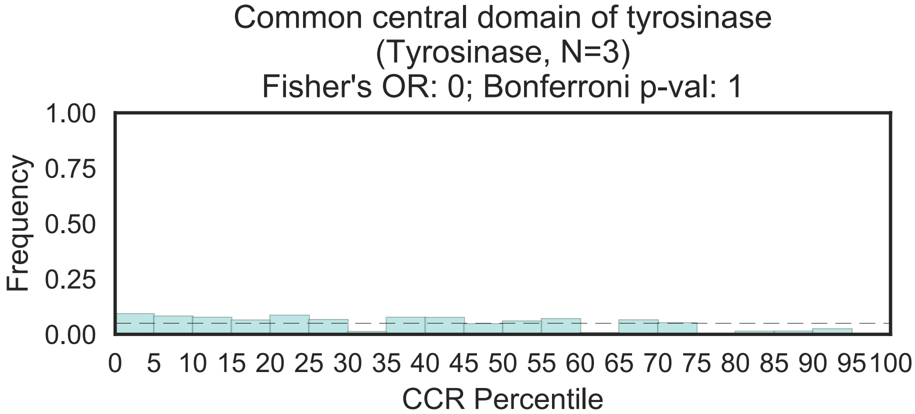

RNA binding activity-knot of a chromodomain
(Tudor-knot, N=5)
Fisher's OR: 3.96; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Tweety
(Tweety, N=3)
Fisher's OR: 0.926; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

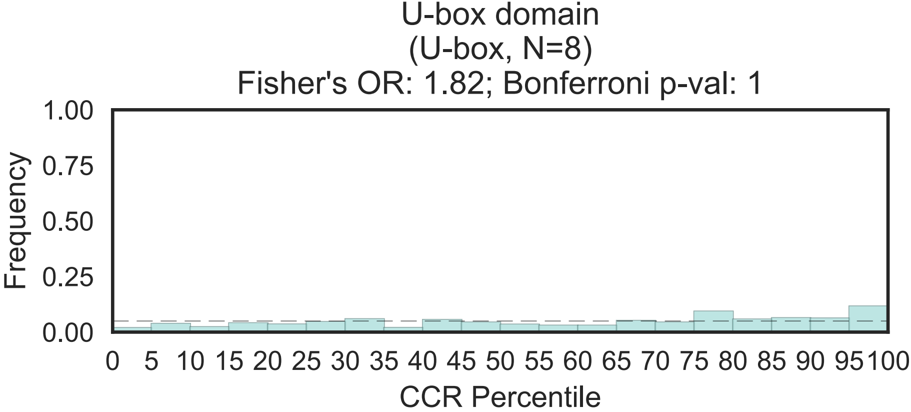

Tyrosyl-DNA phosphodiesterase
(Tyr-DNA_phospho, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

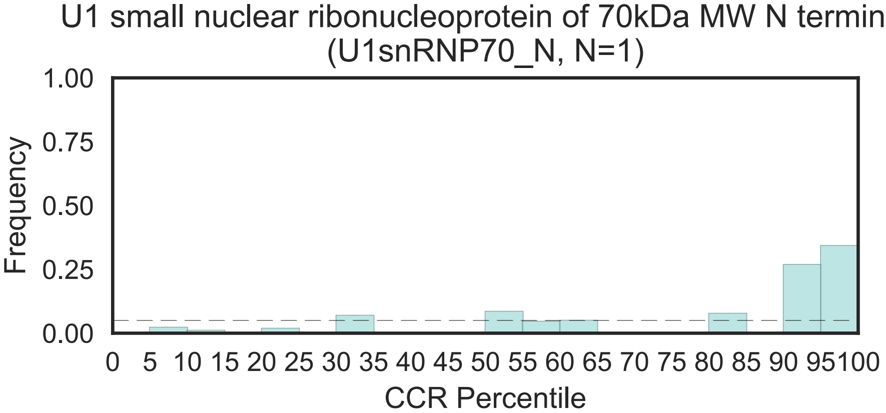


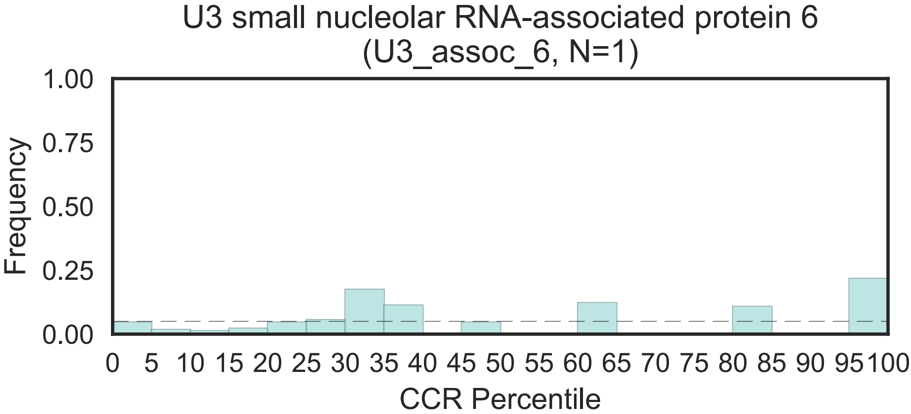
D-Tyr-tRNA(Tyr) deacylase
(Tyr_Deacylase, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

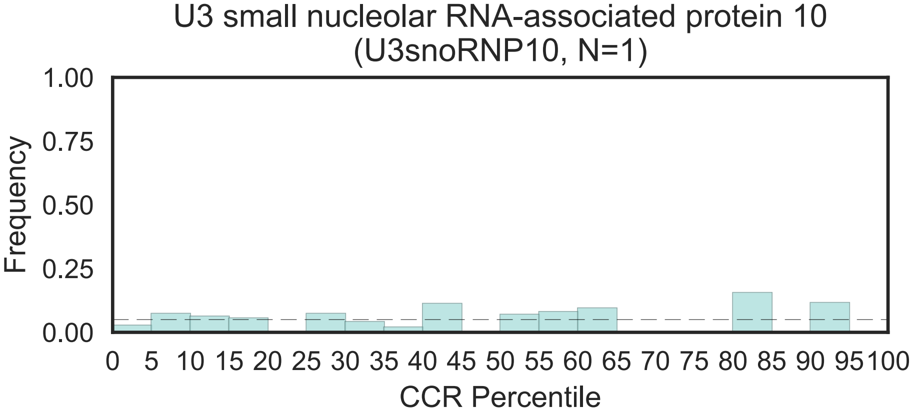


Common central domain of tyrosinase
(Tyrosinase, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

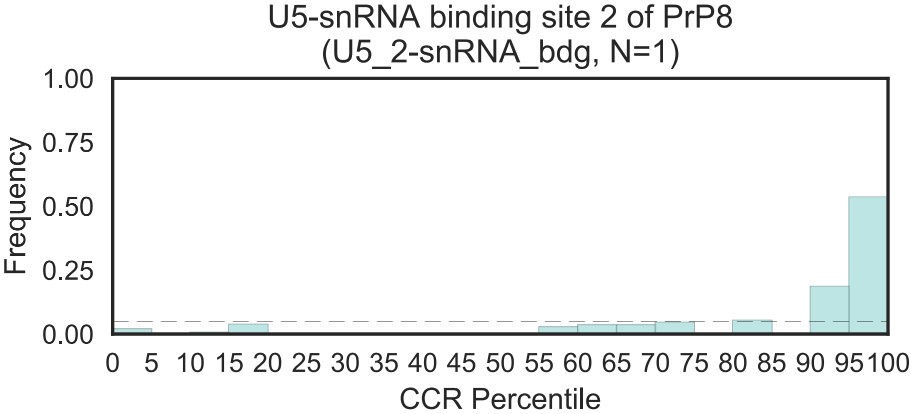

U-box domain
(U-box, N=8)
Fisher's OR: 1.82; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

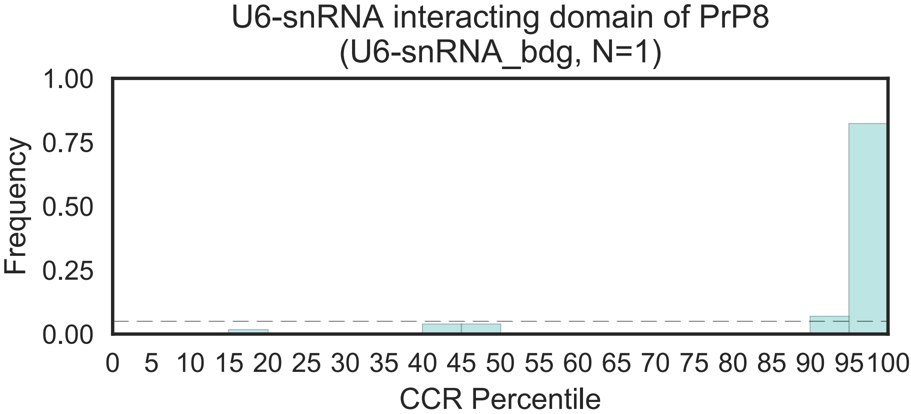

U1 small nuclear ribonucleoprotein of 70kDa MW N terminal
(U1snRNP70_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

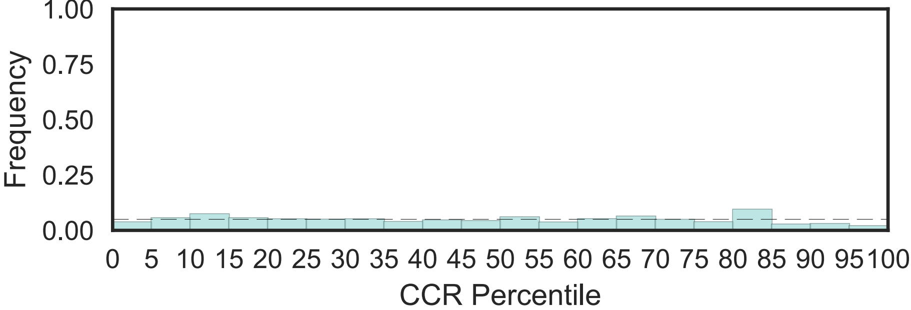

U3 small nucleolar RNA-associated protein 6
(U3_assoc_6, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



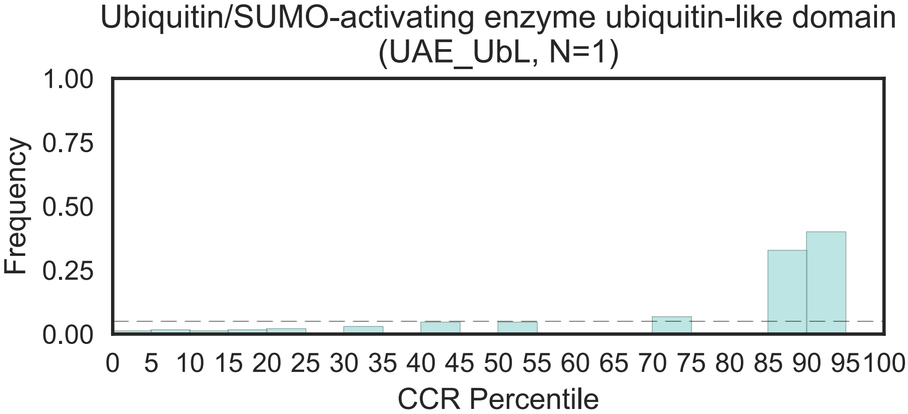
U3 small nucleolar RNA-associated protein 10
(U3snoRNP10, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

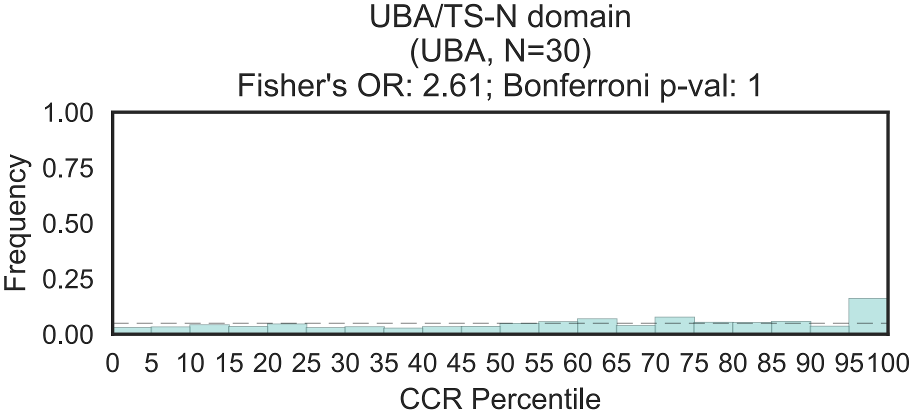

U5-snRNA binding site 2 of PrP8
(U5_2-snRNA_bdg, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


U6-snRNA interacting domain of PrP8
(U6-snRNA_bdg, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

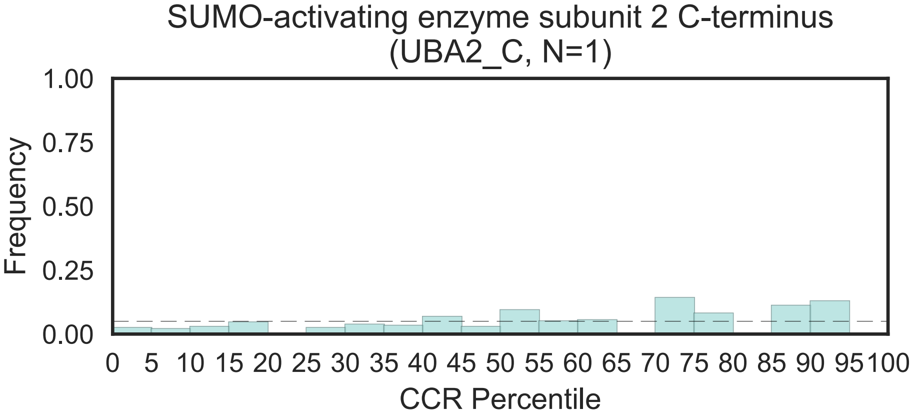


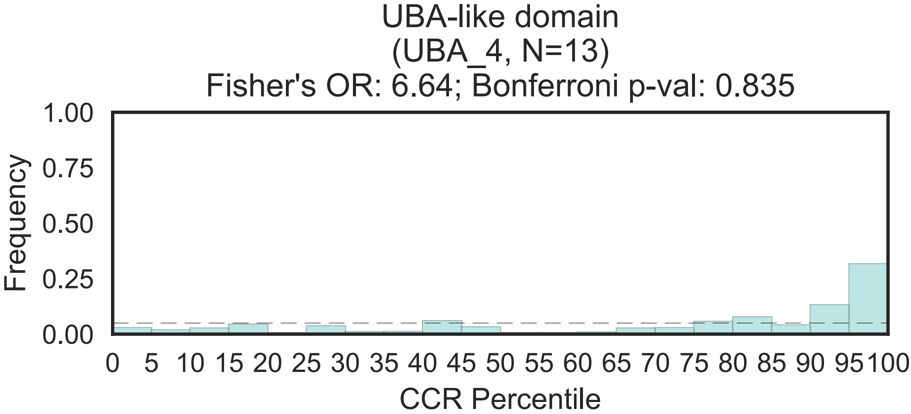
UAA transporter family
(UAA, N=7)
Fisher's OR: 0.332; Bonferroni p-val: 1


Ubiquitin/SUMO-activating enzyme ubiquitin-like domain
(UAE_UbL, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

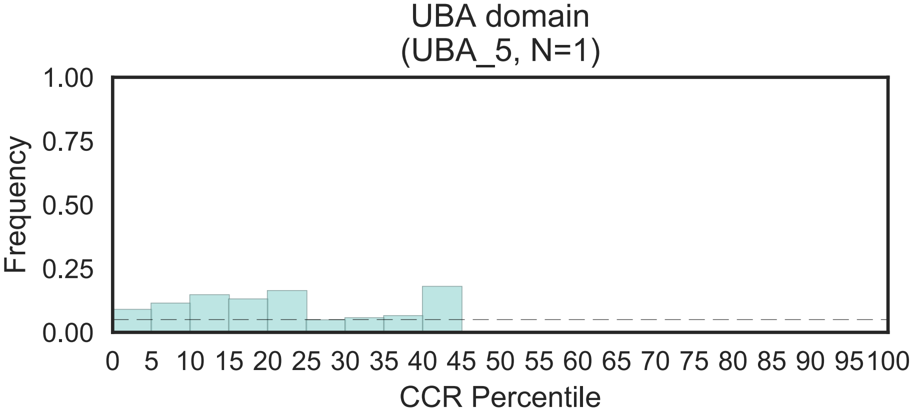


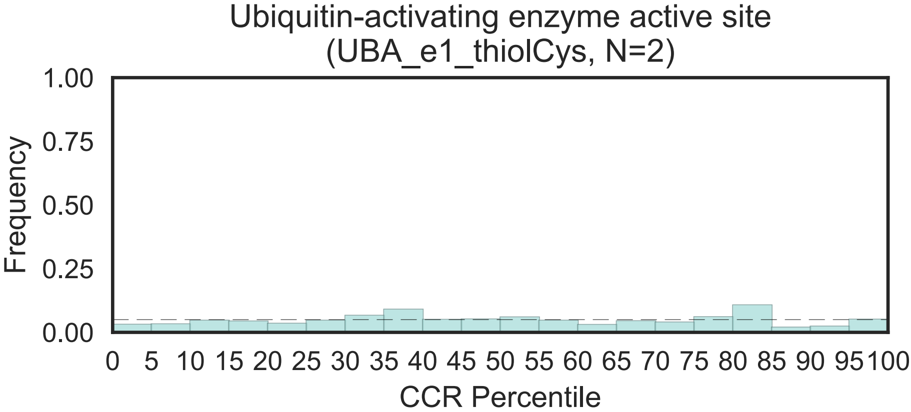
UBA/TS-N domain
(UBA, N=30)
Fisher's OR: 2.61; Bonferroni p-val: 1

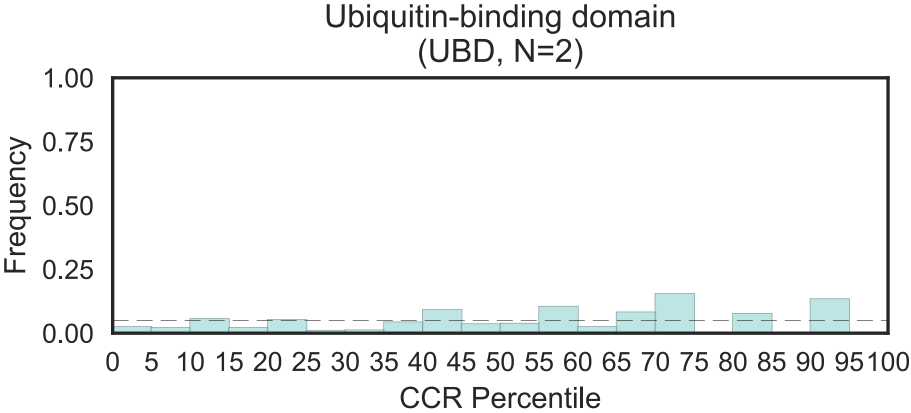

SUMO-activating enzyme subunit 2 C-terminus
(UBA2_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

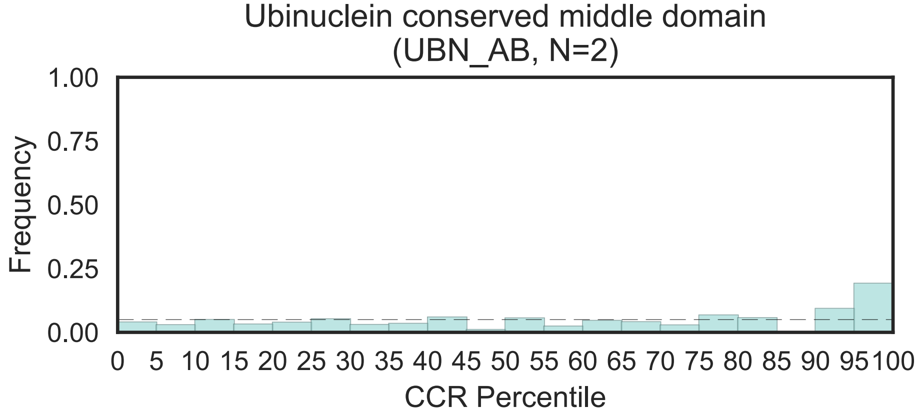


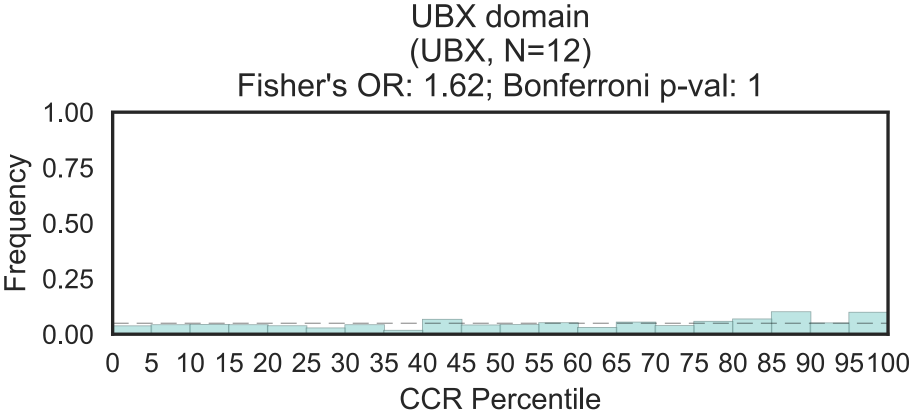
UBA-like domain
(UBA_4, N=13)
Fisher's OR: 6.64; Bonferroni p-val: 0.835

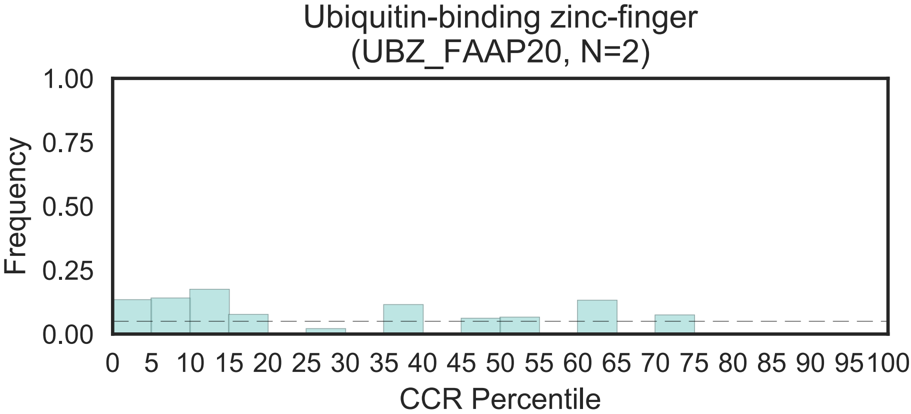

UBA domain
(UBA_5, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

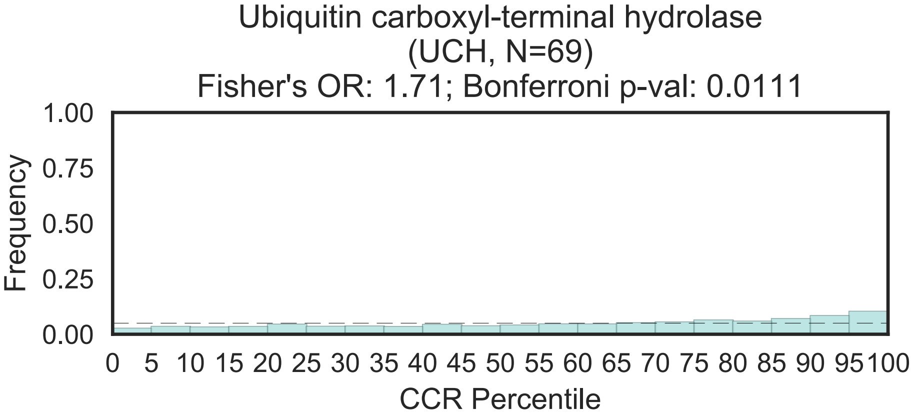

Ubiquitin-activating enzyme active site
(UBA_e1_thiolCys, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

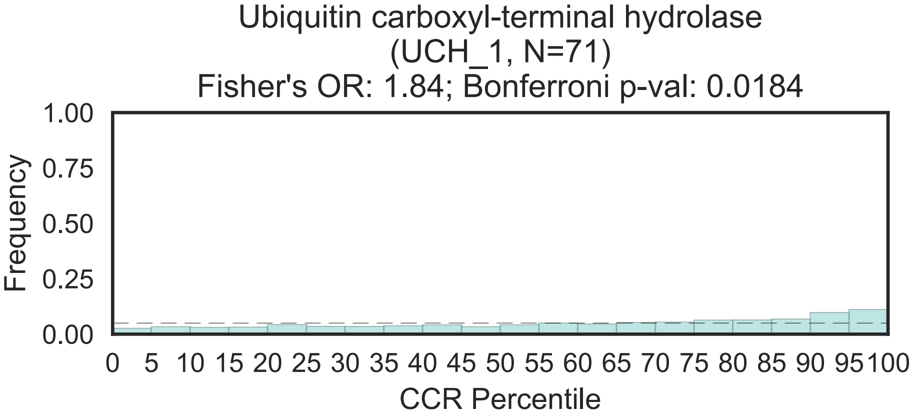

Ubiquitin-binding domain
(UBD, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

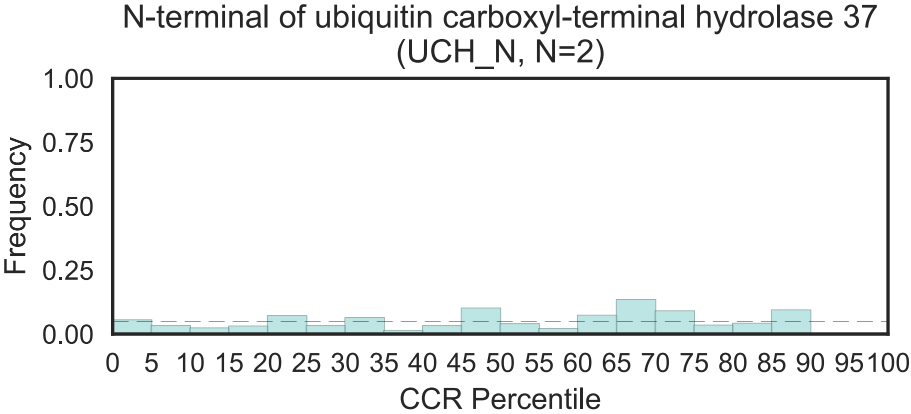

Ubinuclein conserved middle domain
(UBN_AB, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

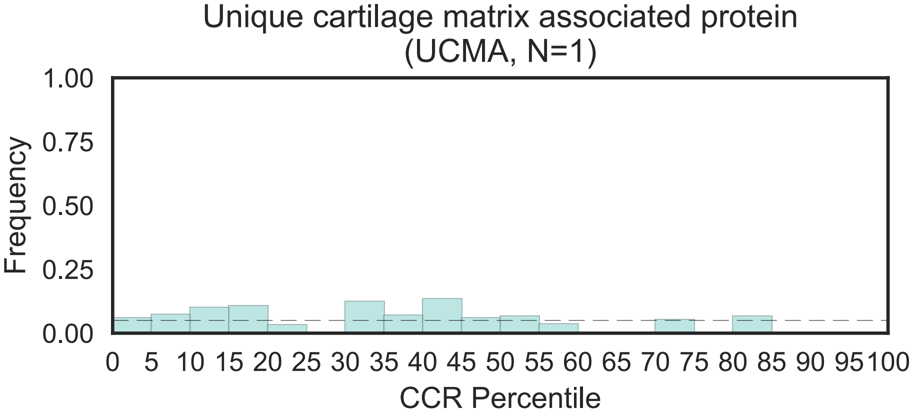

UBX domain
(UBX, N=12)
Fisher's OR: 1.62; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ubiquitin-binding zinc-finger
(UBZ_FAAP20, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ubiquitin carboxyl-terminal hydrolase
(UCH, N=69)
Fisher's OR: 1.71; Bonferroni p-val: 0.0111
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

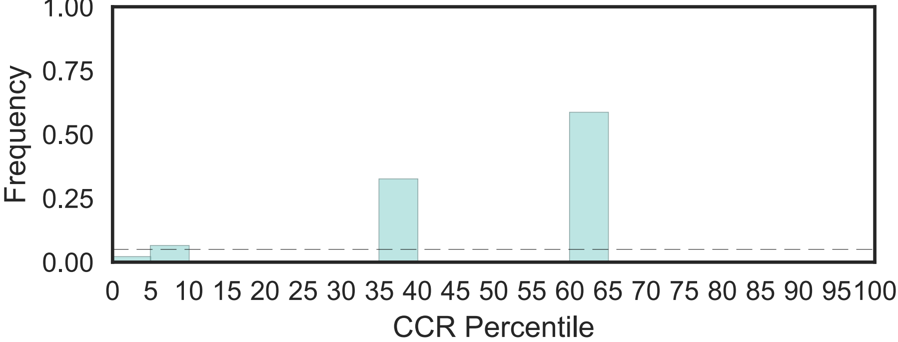

Ubiquitin carboxyl-terminal hydrolase
(UCH_1, N=71)
Fisher's OR: 1.84; Bonferroni p-val: 0.0184
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


N-terminal of ubiquitin carboxyl-terminal hydrolase 37
(UCH_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

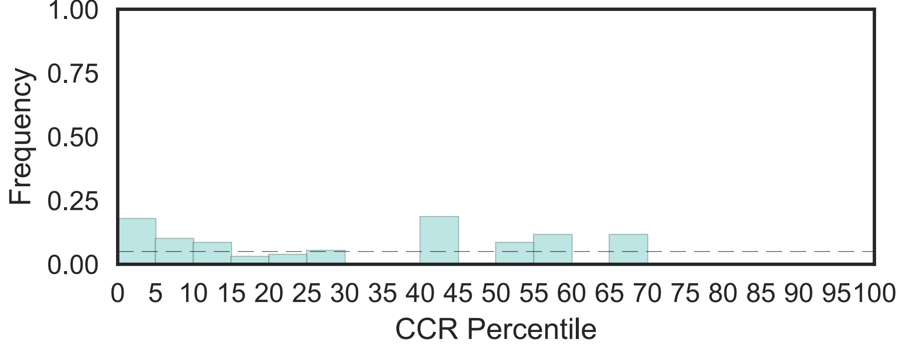


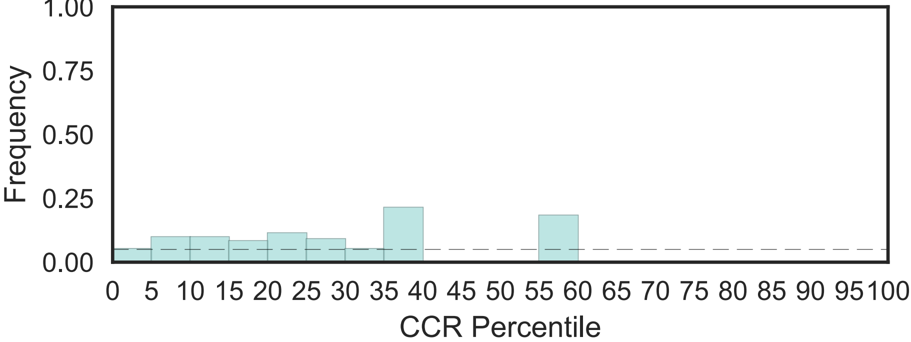
Unique cartilage matrix associated protein
(UCMA, N=1)

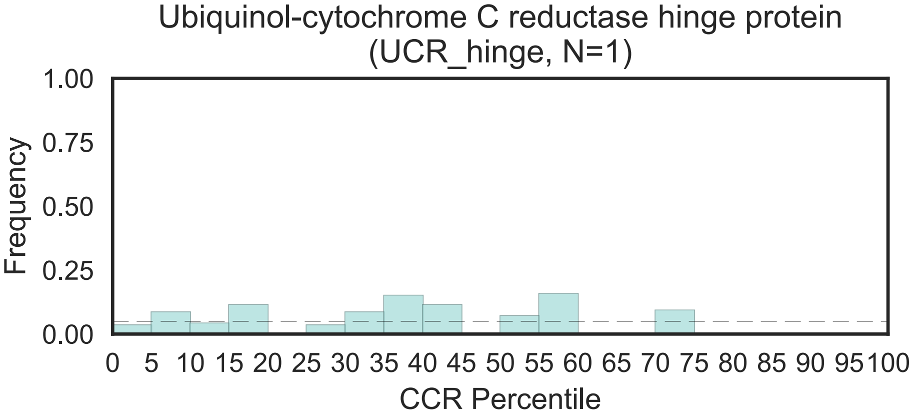
Ubiquinol-cytochrome C reductase complex 14kD subunit (UCR_14kD, N=1)

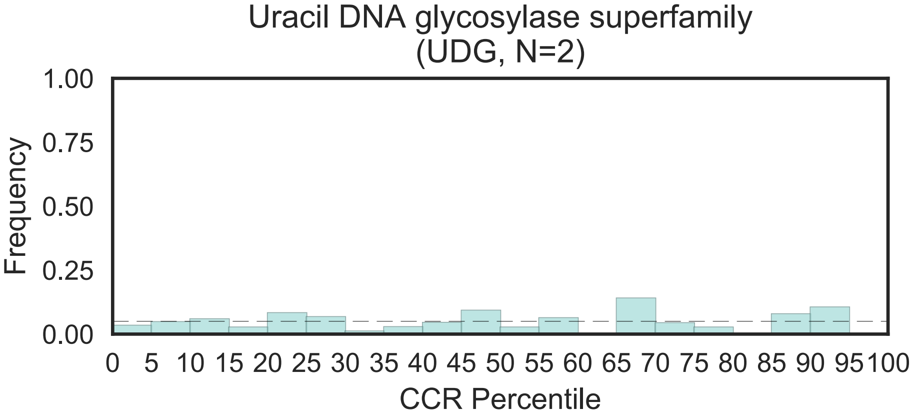


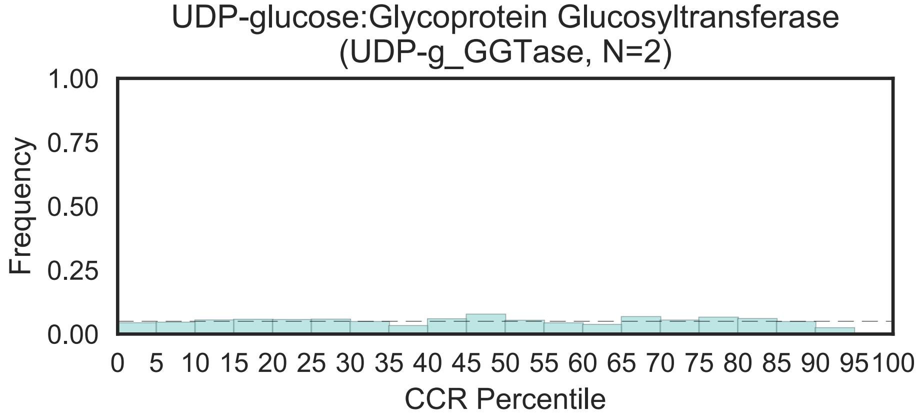
Ubiquinol-cytochrome C reductase complex, 6.4kD protein (UCR_6-4kD, N=1)

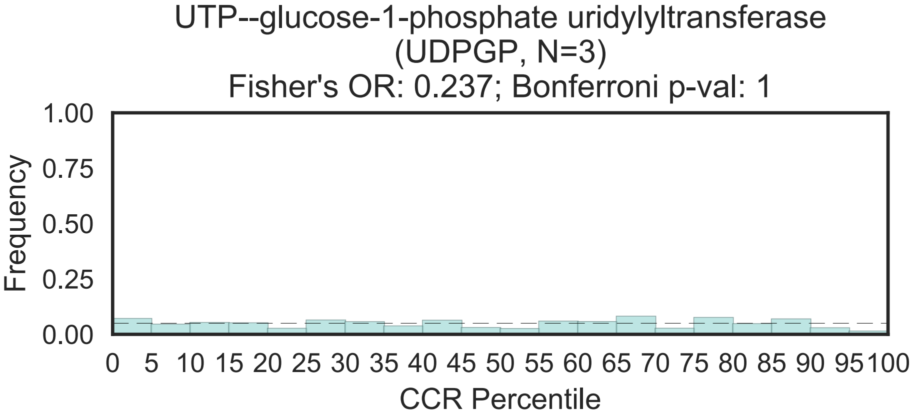


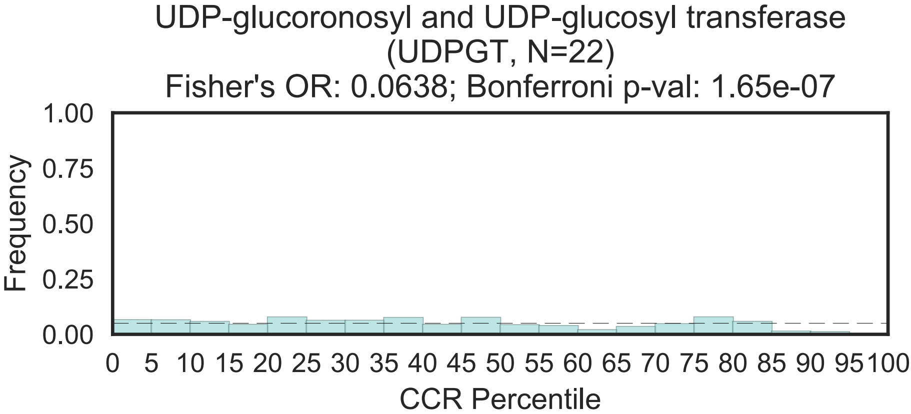

Ubiquinol-cytochrome C reductase, UQCRX/QCR9 like (UCR_UQCRX_QCR9, N=1)

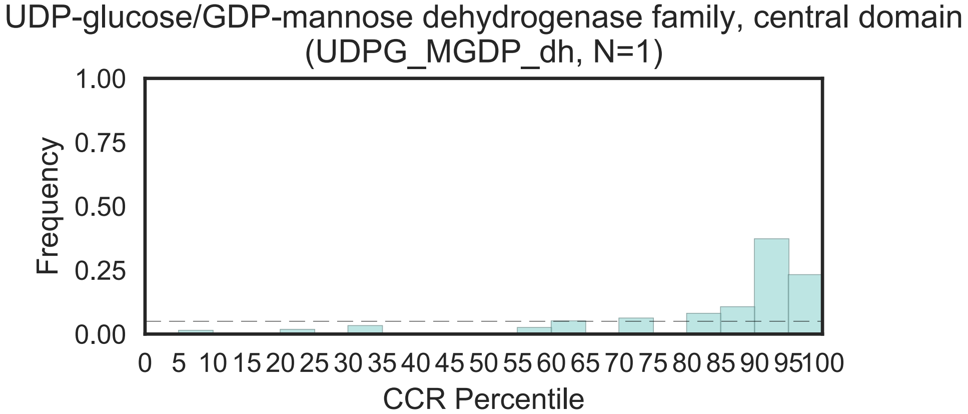

Ubiquinol-cytochrome C reductase hinge protein
(UCR_hinge, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Uracil DNA glycosylase superfamily
(UDG, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

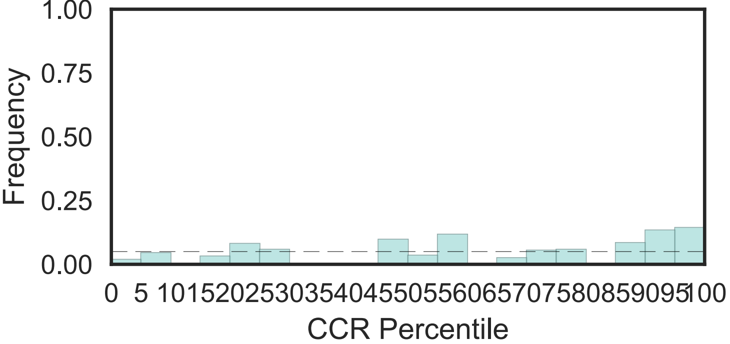

UDP-glucose:Glycoprotein Glucosyltransferase
(UDP-g_GGTase, N=2)

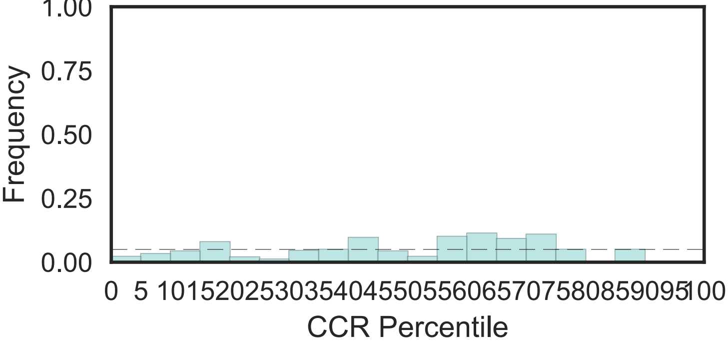

UTP--glucose-1-phosphate uridylyltransferase
(UDPGP, N=3)
Fisher's OR: 0.237; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


UDP-glucoronosyl and UDP-glucosyl transferase
(UDPGT, N=22)
Fisher's OR: 0.0638; Bonferroni p-val: 1.65e-07
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

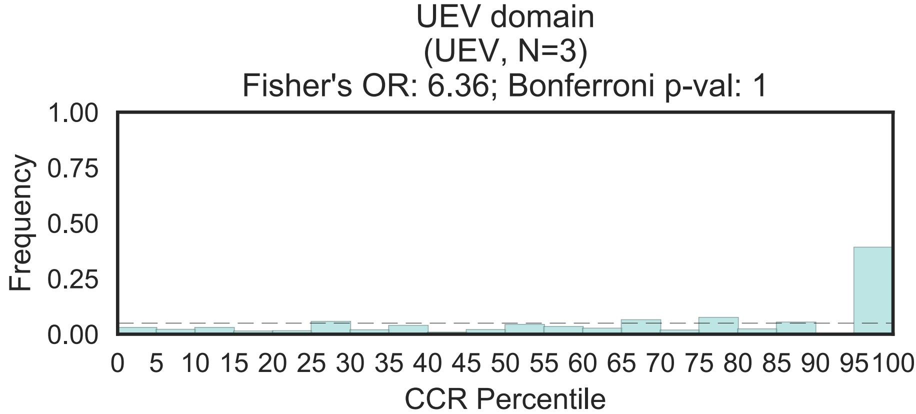

UDP-glucose/GDP-mannose dehydrogenase family, central domain
(UDPG_MGDP_dh, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

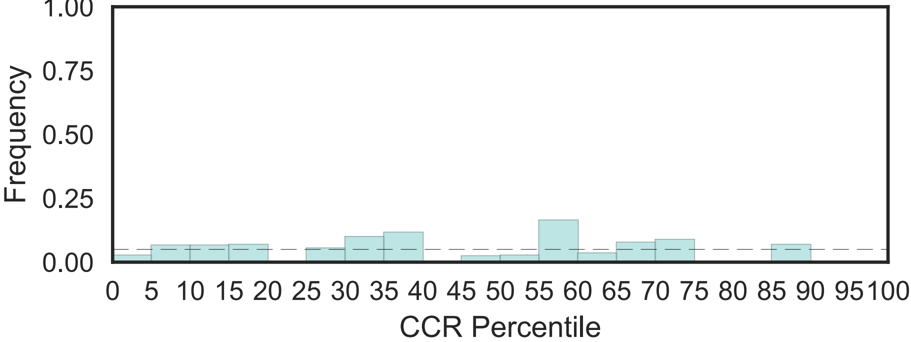
UDP-glucose/GDP-mannose dehydrogenase family, UDP binding domain (UDPG_MGDP_dh_C, N=1)



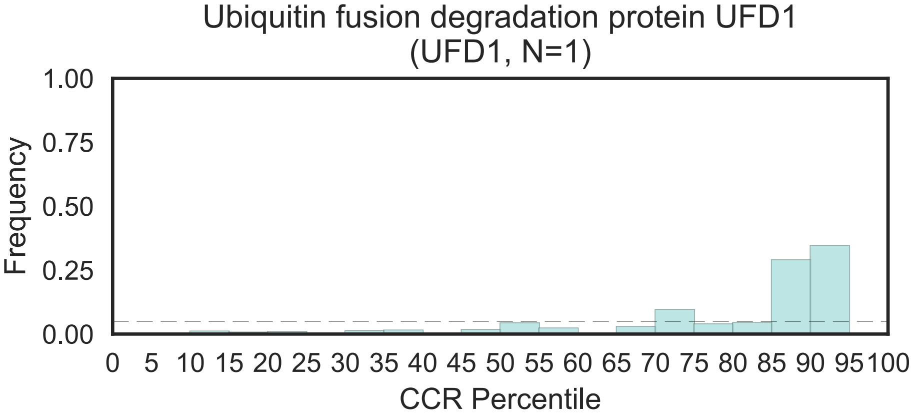


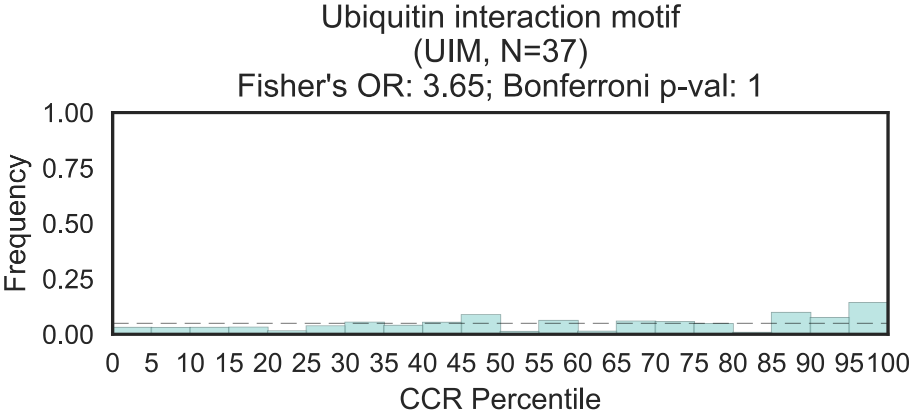
UDP-glucose/GDP-mannose dehydrogenase family, NAD binding domain (UDPG_MGDP_dh_N, N=1)

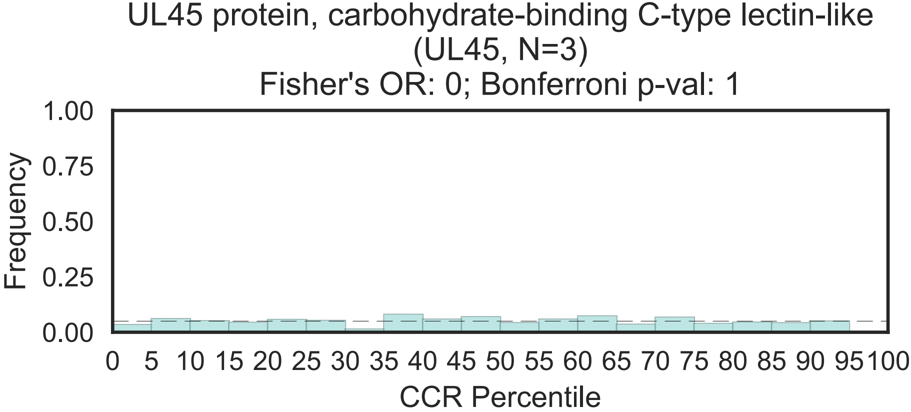

UEV domain
(UEV, N=3)
Fisher's OR: 6.36; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

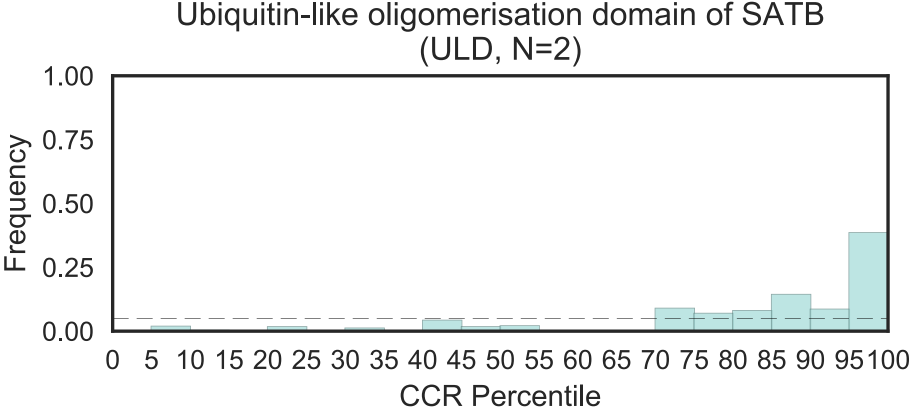


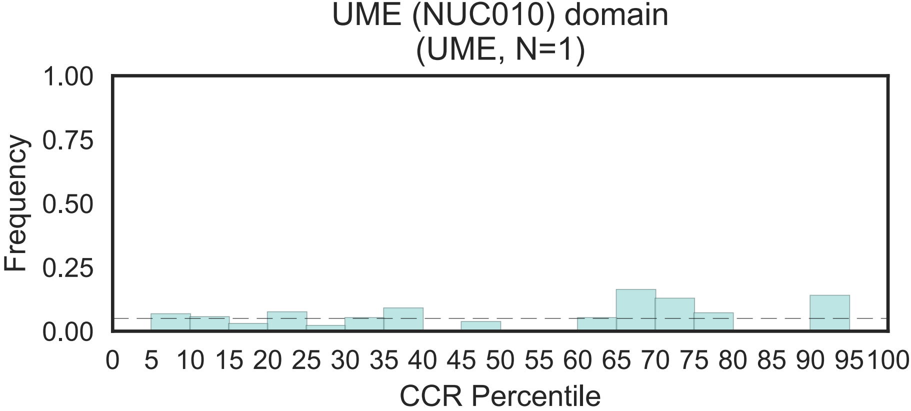
Ubiquitin-fold modifier-conjugating enzyme 1
(UFC1, N=1)

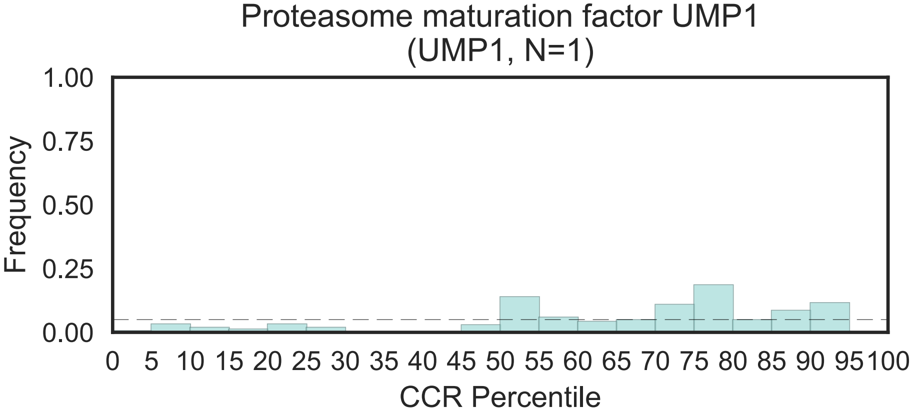

Ubiquitin fusion degradation protein UFD1
(UFD1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ubiquitin interaction motif
(UIM, N=37)
Fisher's OR: 3.65; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

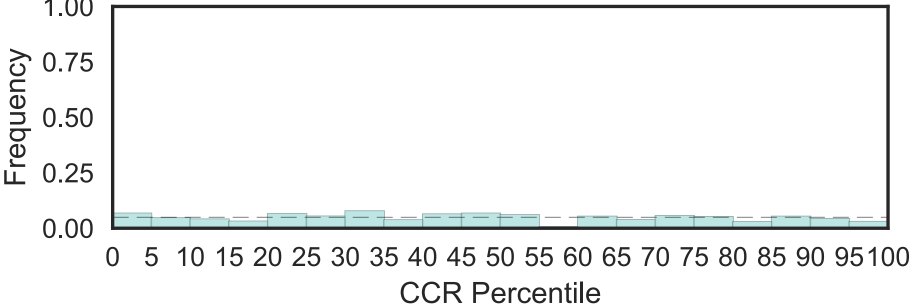

UL45 protein, carbohydrate-binding C-type lectin-like
(UL45, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

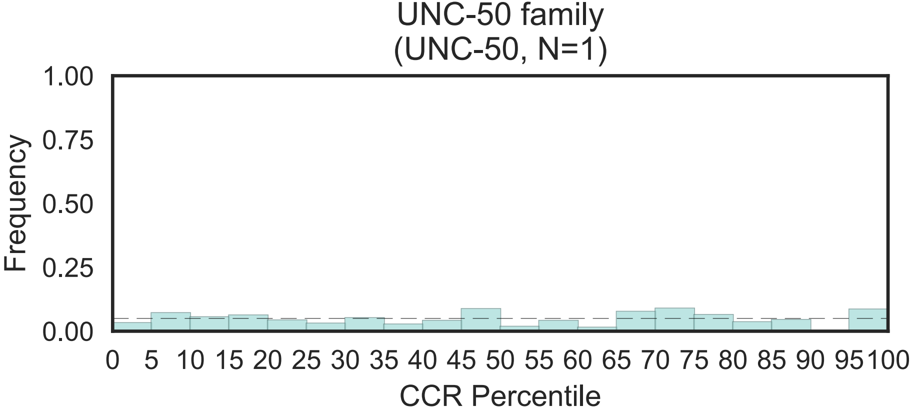

Ubiquitin-like oligomerisation domain of SATB
(ULD, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

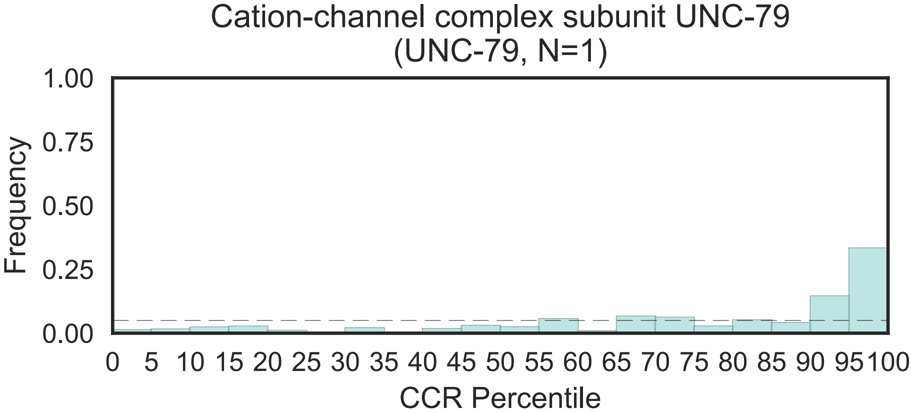

UME (NUC010) domain
(UME, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Proteasome maturation factor UMP1
(UMP1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

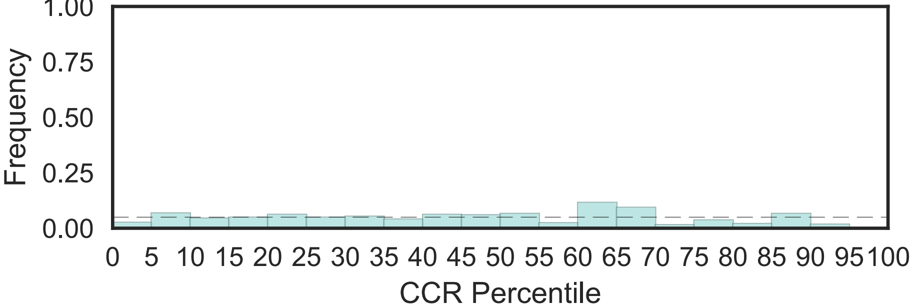
Pyrimidine 5'-nucleotidase (UMPH-1)
(UMPH-1, N=3)
Fisher's OR: 0.449; Bonferroni p-val: 1

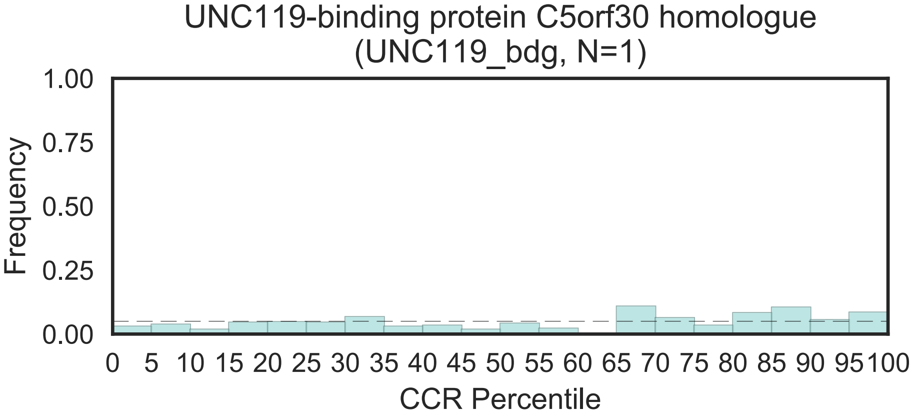


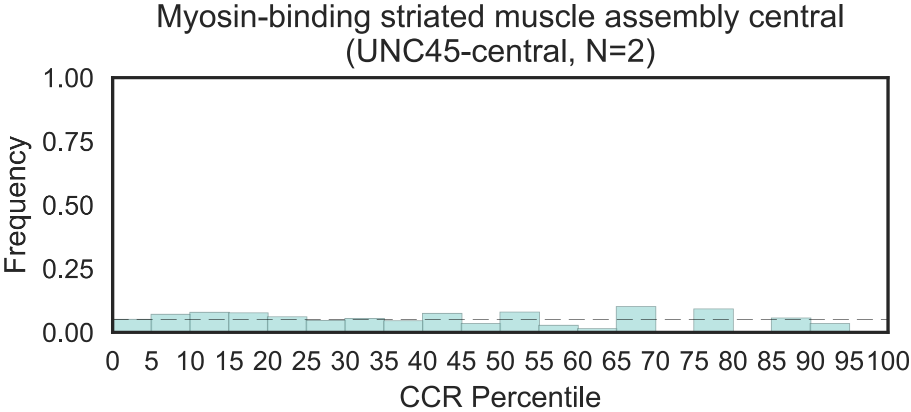

UNC-50 family
(UNC-50, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Cation-channel complex subunit UNC-79
(UNC-79, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

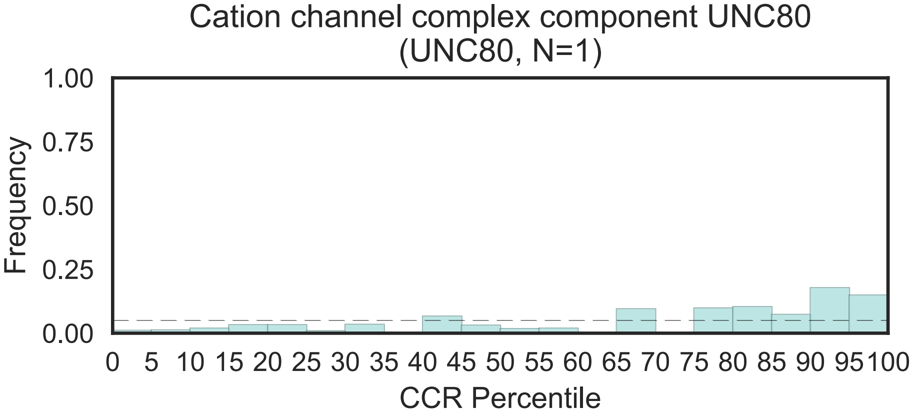
Ion channel regulatory protein UNC-93
(UNC-93, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

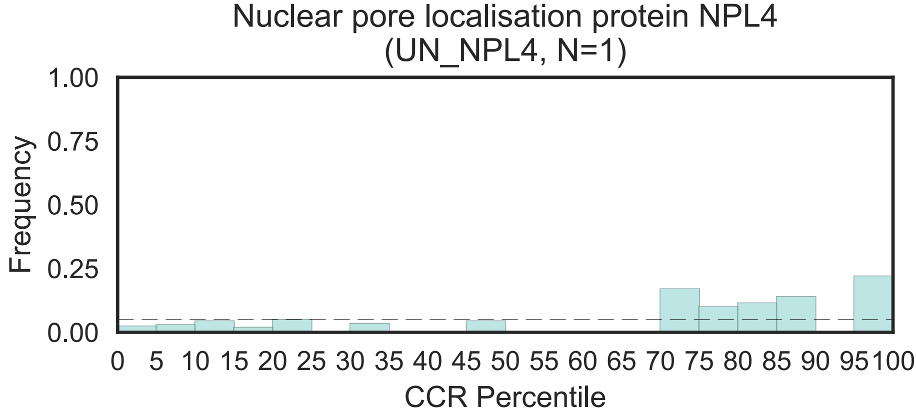


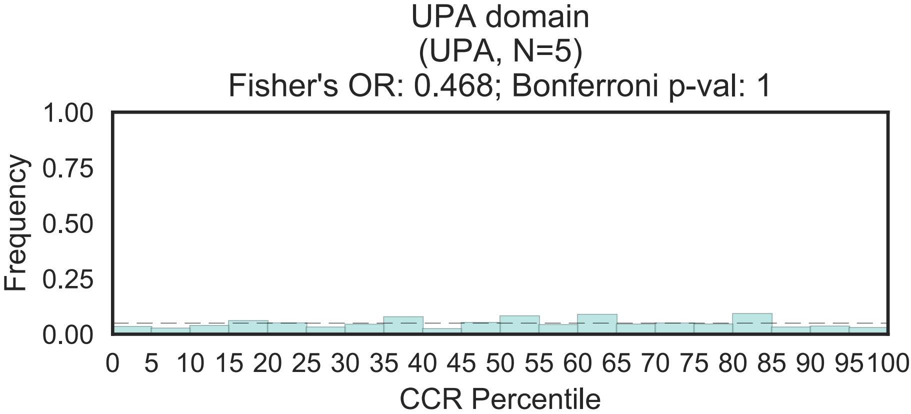

UNC119-binding protein C5orf30 homologue
(UNC119_bdg, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

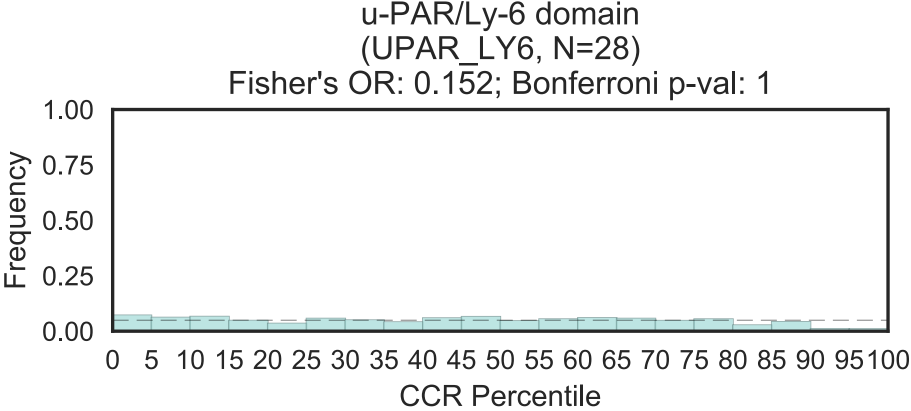


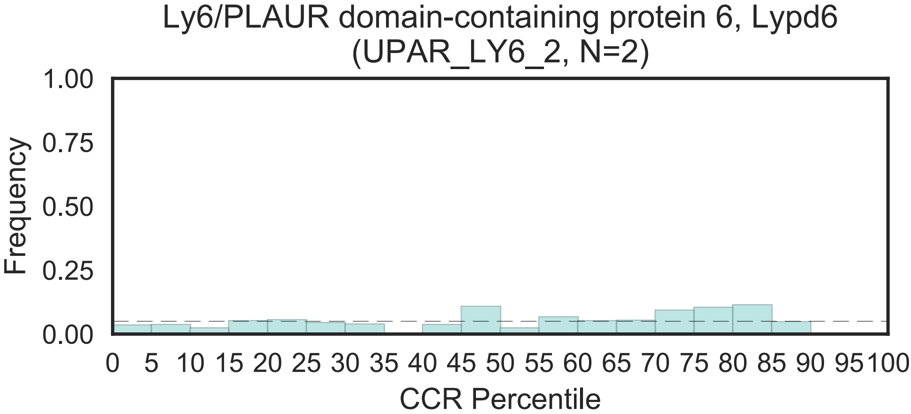
Myosin-binding striated muscle assembly central (UNC45-central, N=2)

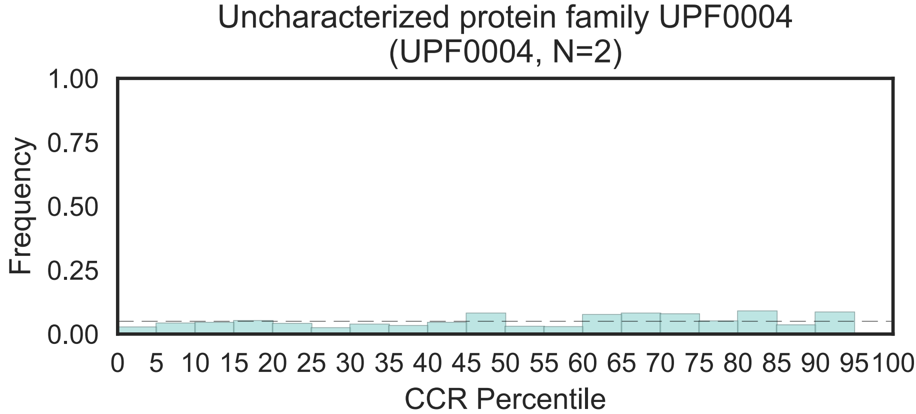

Cation channel complex component UNC80
(UNC80, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


Nuclear pore localisation protein NPL4
(UN_NPL4, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

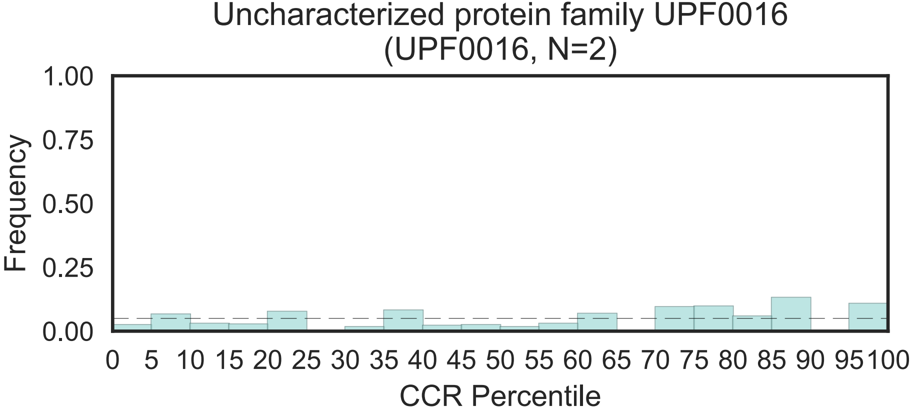

UPA domain
(UPA, N=5)
Fisher's OR: 0.468; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

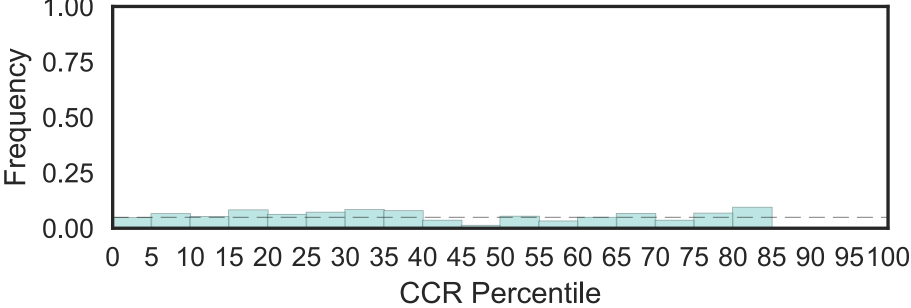

u-PAR/Ly-6 domain
(UPAR_LY6, N=28)
Fisher's OR: 0.152; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Ly6/PLAUR domain-containing protein 6, Lypd6
(UPAR_LY6_2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

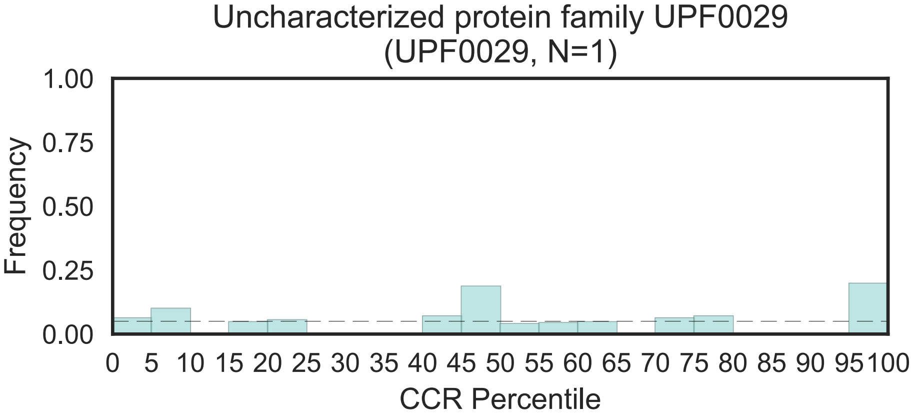


Uncharacterized protein family UPF0004
(UPF0004, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Uncharacterized protein family UPF0016
(UPF0016, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile



Putative RNA methylase family UPF0020
(UPF0020, N=5)
Fisher's OR: 0; Bonferroni p-val: 1


Uncharacterized protein family UPF0029
(UPF0029, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
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55
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75
80
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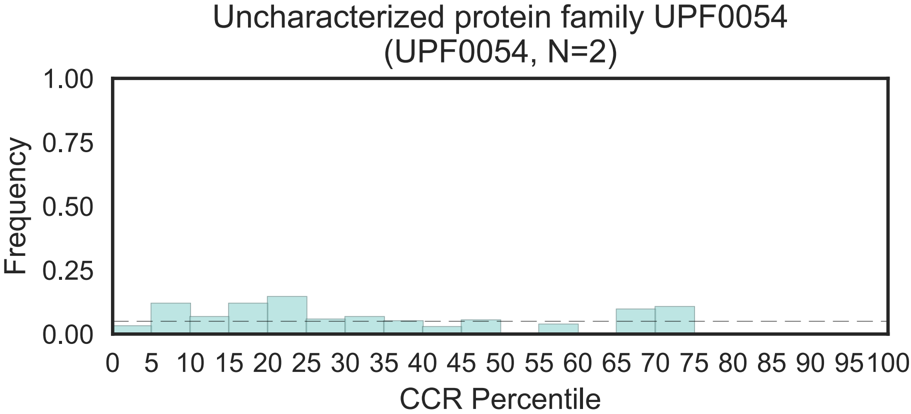
90
95
100
CCR Percentile


Uncharacterized protein family UPF0054
(UPF0054, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
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25
30
35
40
45
50
55
60
65
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75
80
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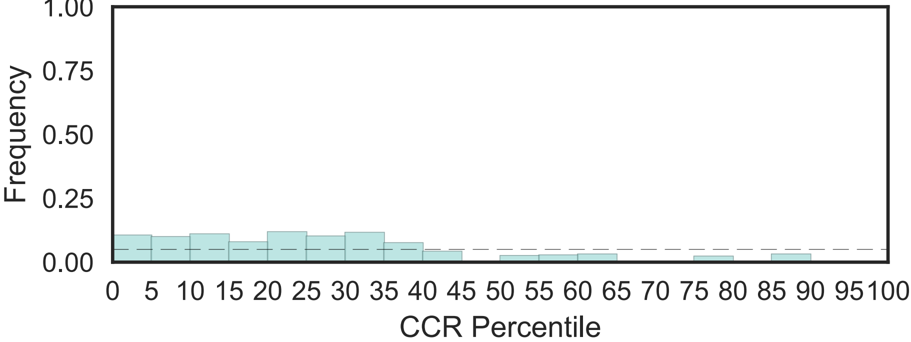
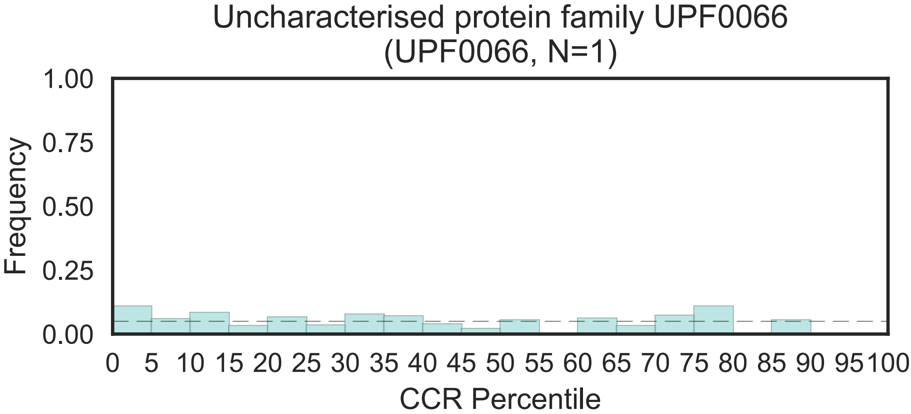
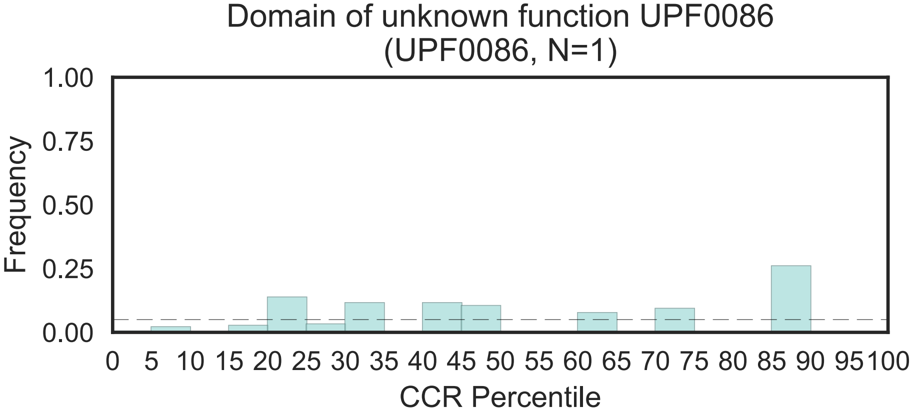
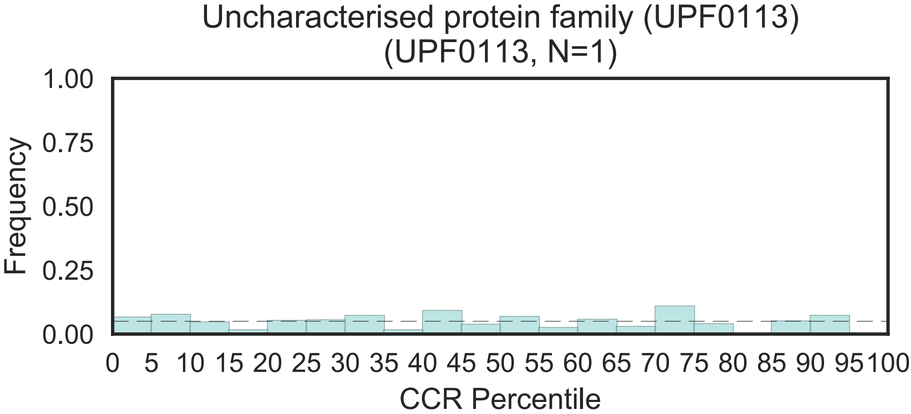
95
100
CCR Percentile

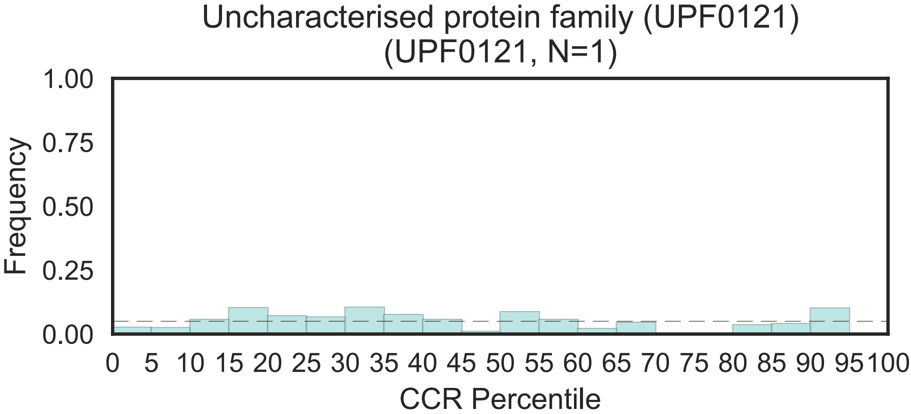


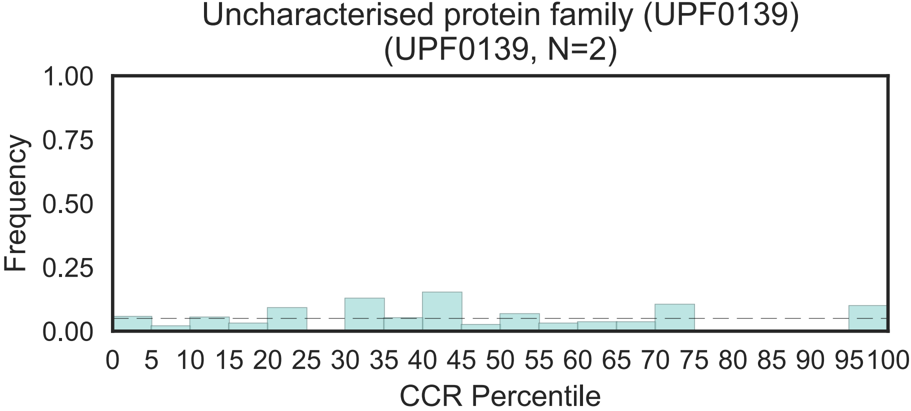
Uncharacterized ACR, YdiU/UPF0061 family (UPF0061, N=1)

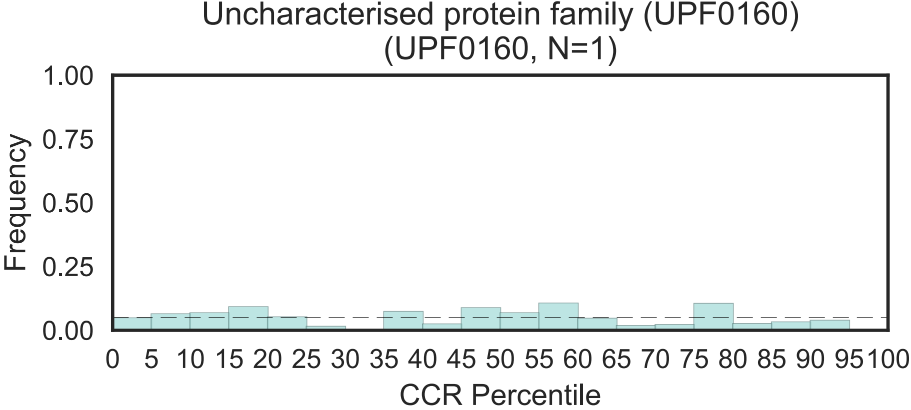

Uncharacterised protein family UPF0066
(UPF0066, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

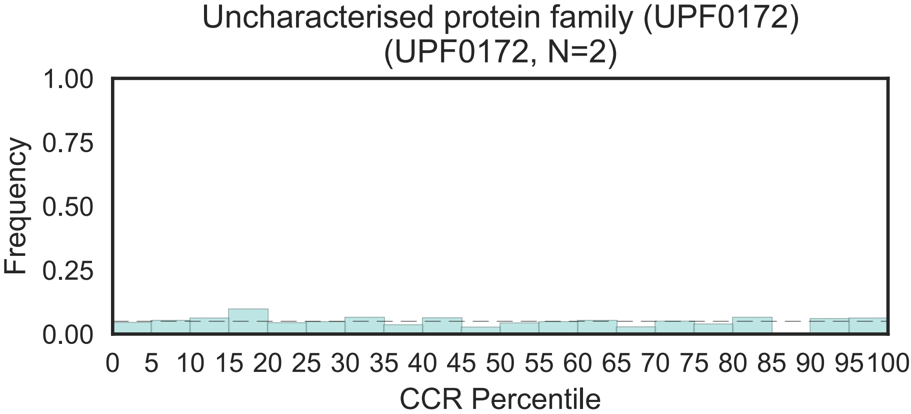

Domain of unknown function UPF0086
(UPF0086, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

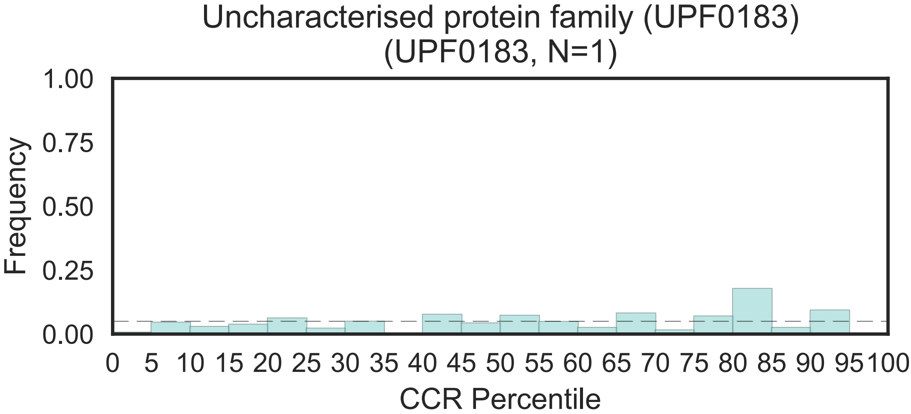

Uncharacterised protein family (UPF0113)
(UPF0113, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

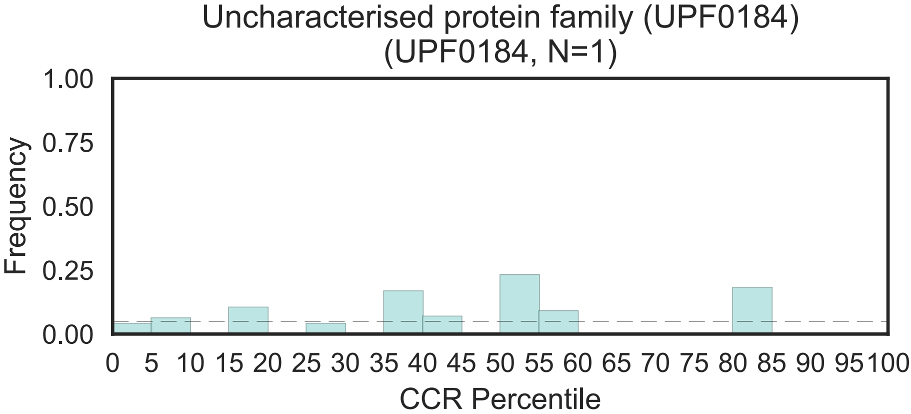

Uncharacterised protein family (UPF0121)
(UPF0121, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

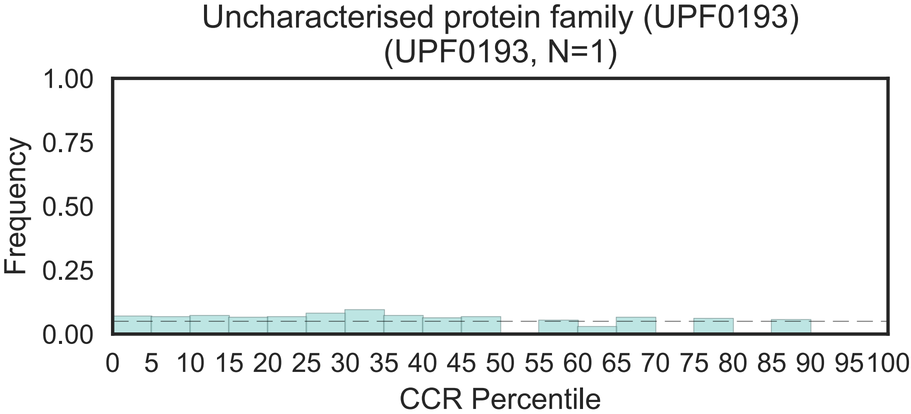

Uncharacterised protein family (UPF0139)
(UPF0139, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

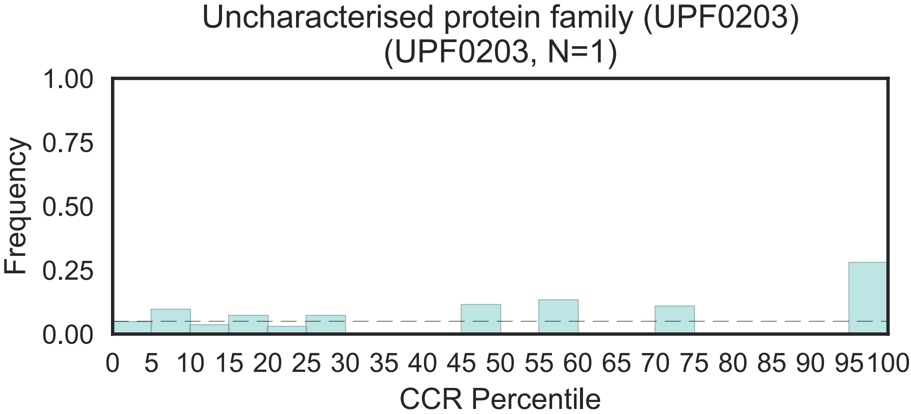

Uncharacterised protein family (UPF0160)
(UPF0160, N=1)

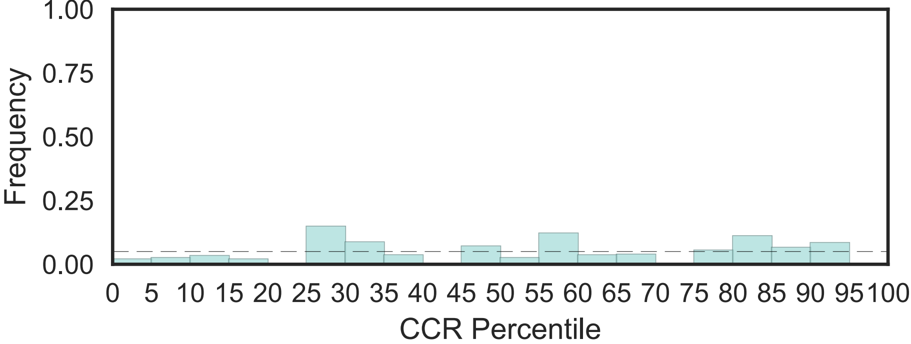

Uncharacterised protein family (UPF0172)
(UPF0172, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Uncharacterised protein family (UPF0183)
(UPF0183, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

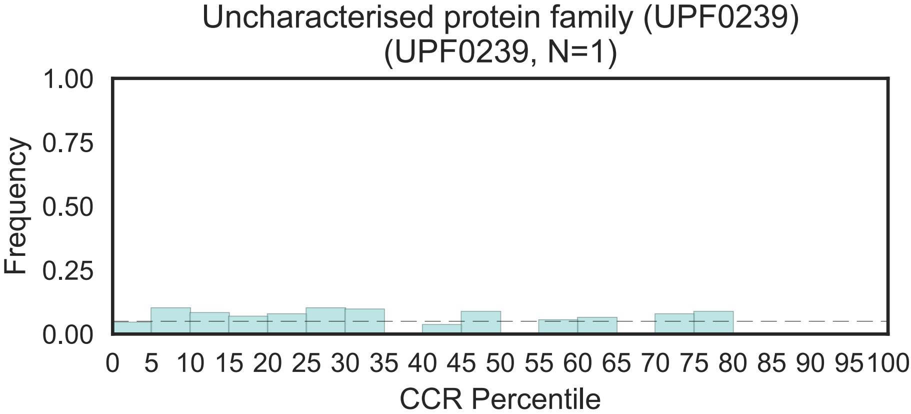

Uncharacterised protein family (UPF0184)
(UPF0184, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

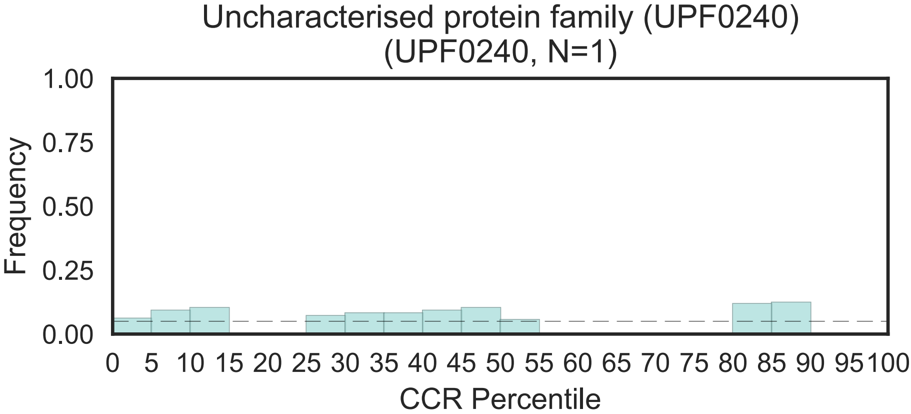

Uncharacterised protein family (UPF0193)
(UPF0193, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

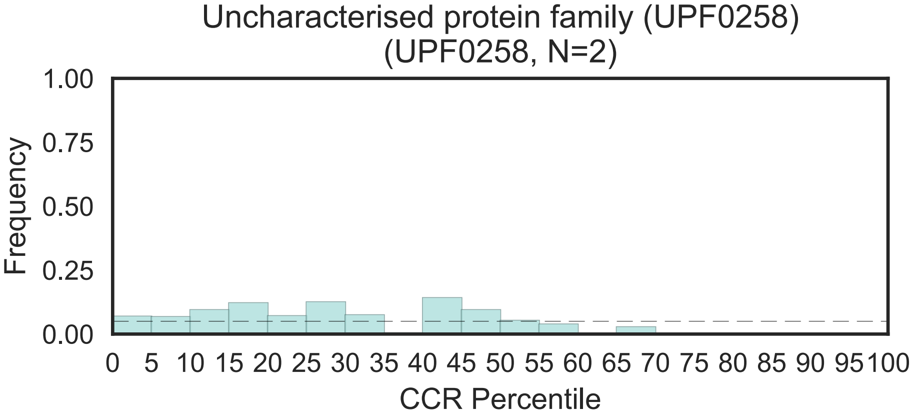

Uncharacterised protein family (UPF0203)
(UPF0203, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



Uncharacterised protein family (UPF0220)
(UPF0220, N=1)


Uncharacterised protein family (UPF0239)
(UPF0239, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Uncharacterised protein family (UPF0240)
(UPF0240, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Uncharacterised protein family (UPF0258)
(UPF0258, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
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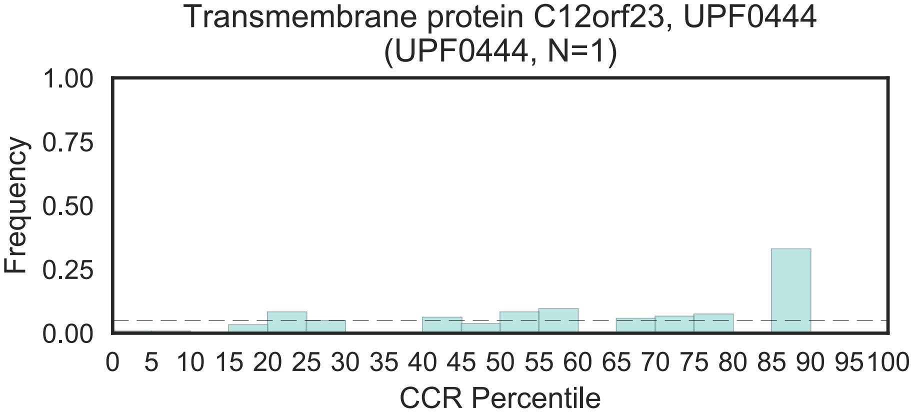
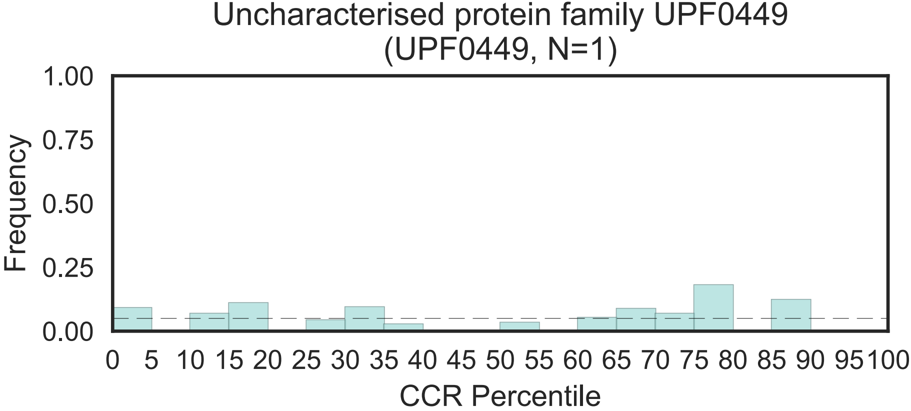
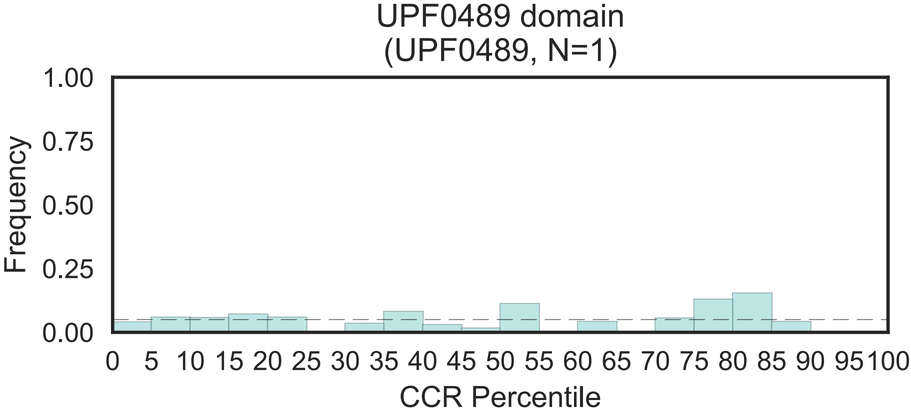
95
100
CCR Percentile


Transmembrane protein C12orf23, UPF0444
(UPF0444, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Uncharacterised protein family UPF0449
(UPF0449, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


UPF0489 domain
(UPF0489, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
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20
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30
35
40
45
50
55
60
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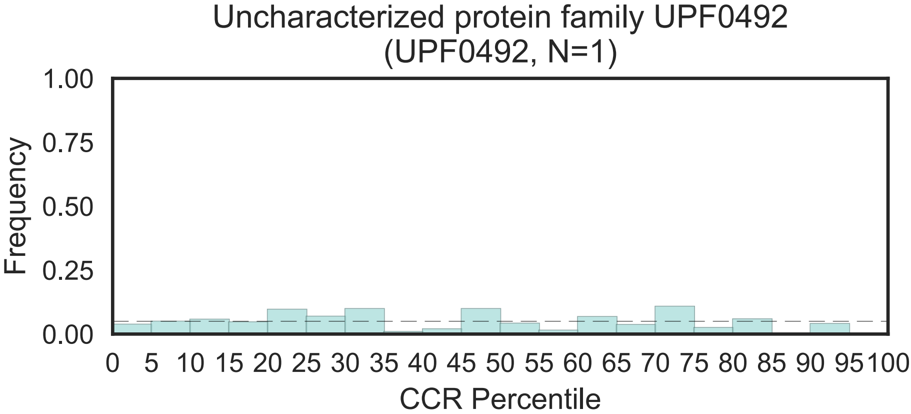
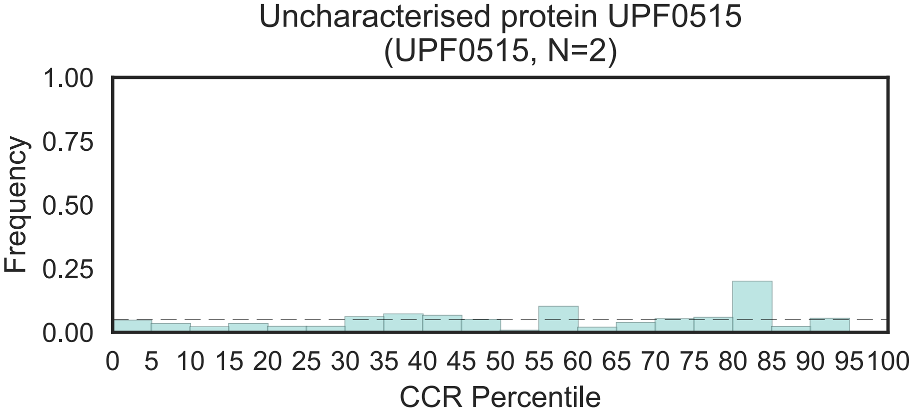
70
75
80
85
90
95
100
CCR Percentile


Uncharacterized protein family UPF0492
(UPF0492, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Uncharacterised protein UPF0515
(UPF0515, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
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25
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35
40
45
50
55
60
65
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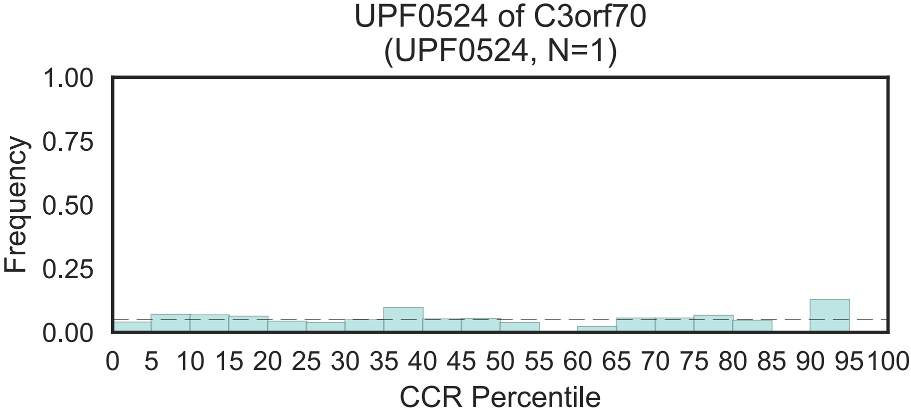
75
80
85
90
95
100
CCR Percentile


UPF0524 of C3orf70
(UPF0524, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
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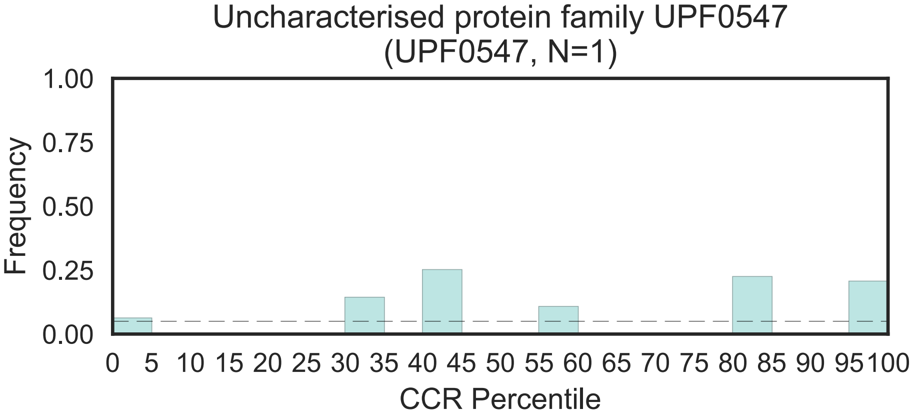
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Uncharacterised protein family UPF0547
(UPF0547, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
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25
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35
40
45
50
55
60
65
70
75
80
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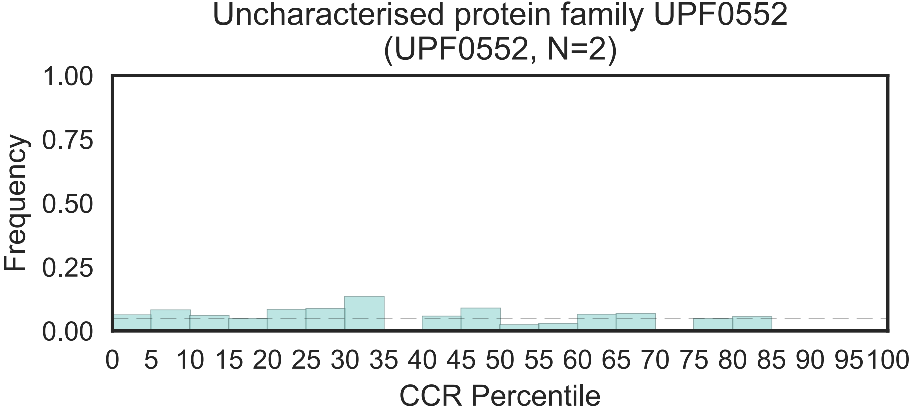
95
100
CCR Percentile


Uncharacterised protein family UPF0552
(UPF0552, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
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20
25
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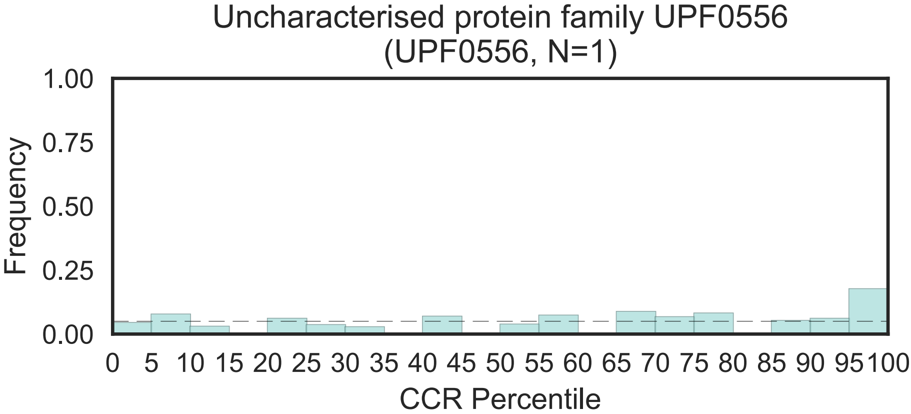
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Uncharacterised protein family UPF0556
(UPF0556, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
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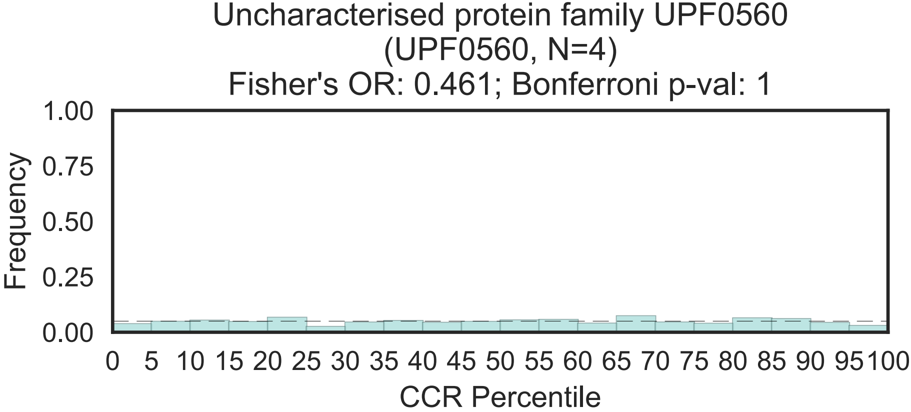
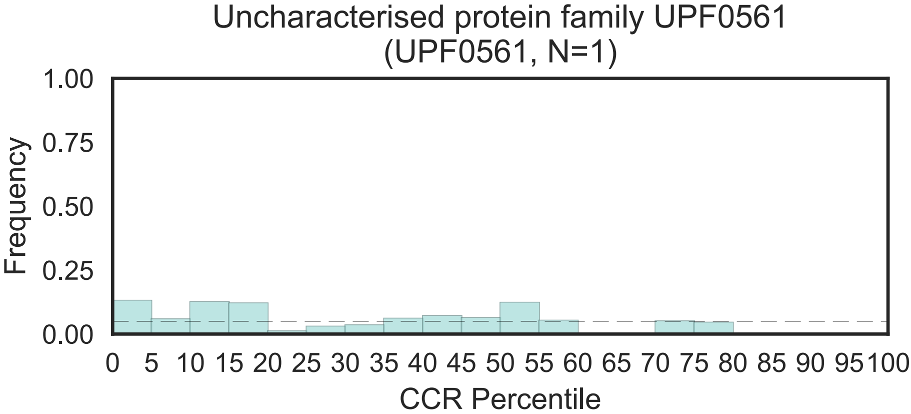
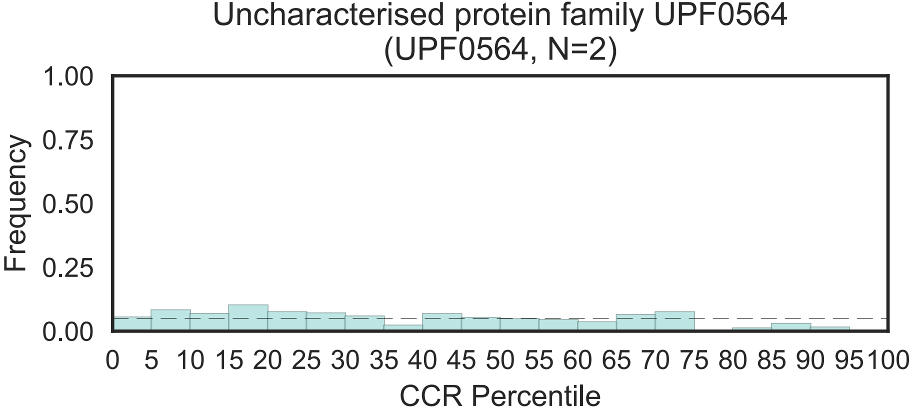
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



Uncharacterised protein family UPF0560
(UPF0560, N=4)
Fisher's OR: 0.461; Bonferroni p-val: 1


Uncharacterised protein family UPF0561
(UPF0561, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Uncharacterised protein family UPF0564
(UPF0564, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
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15
20
25
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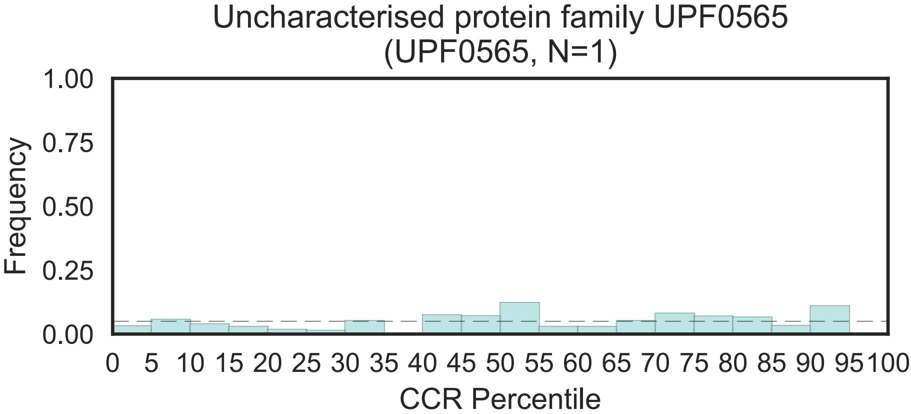
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Uncharacterised protein family UPF0565
(UPF0565, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
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25
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35
40
45
50
55
60
65
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75
80
85
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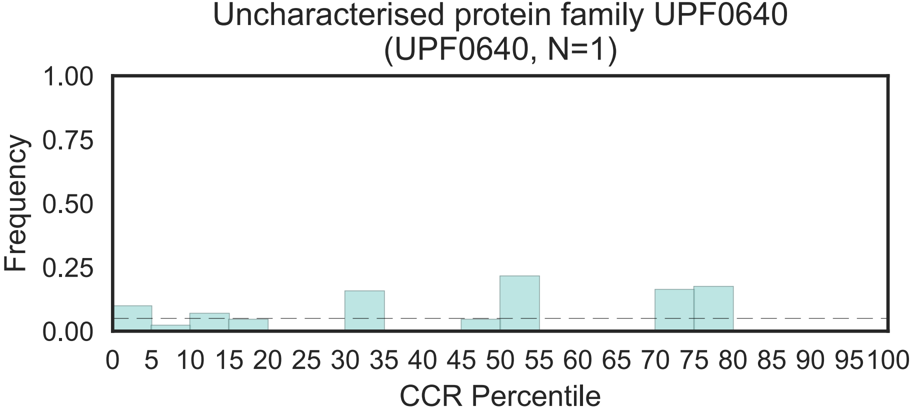
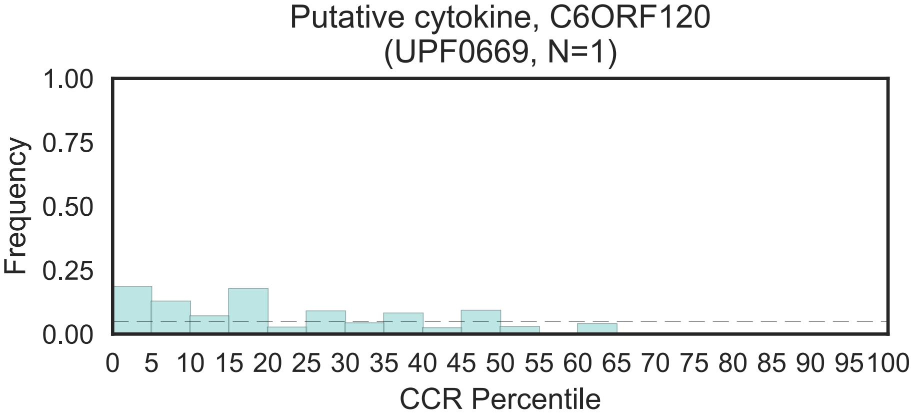
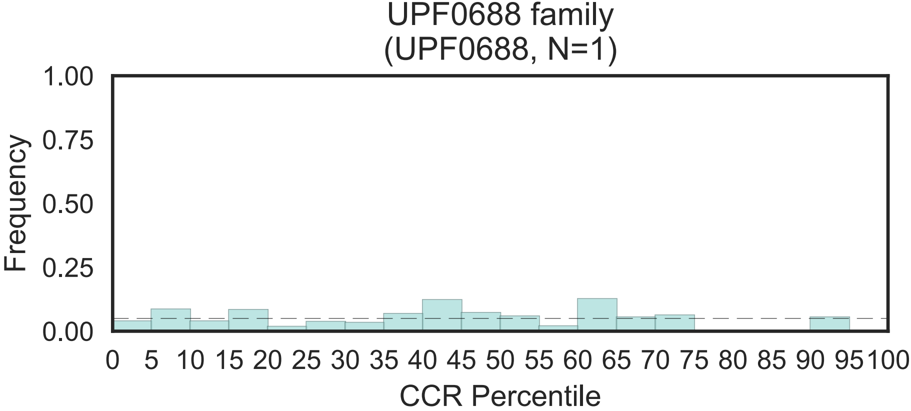
95
100
CCR Percentile


Uncharacterised protein family UPF0640
(UPF0640, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Putative cytokine, C6ORF120
(UPF0669, N=1)


UPF0688 family
(UPF0688, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
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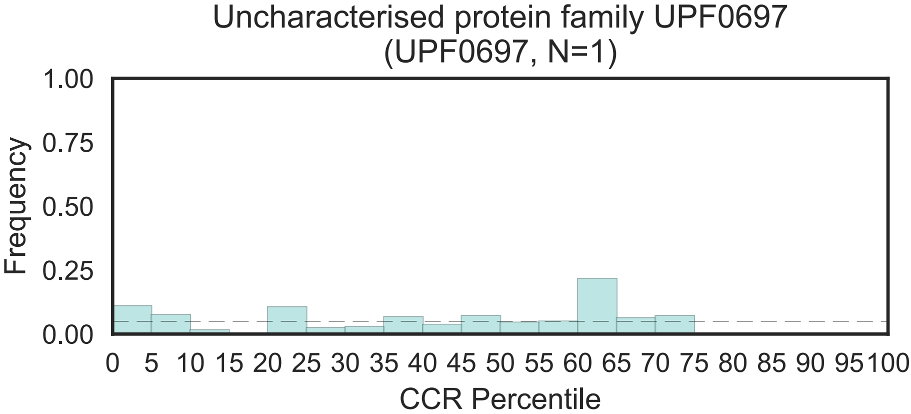
75
80
85
90
95
100
CCR Percentile


Uncharacterised protein family UPF0697
(UPF0697, N=1)
Frequency
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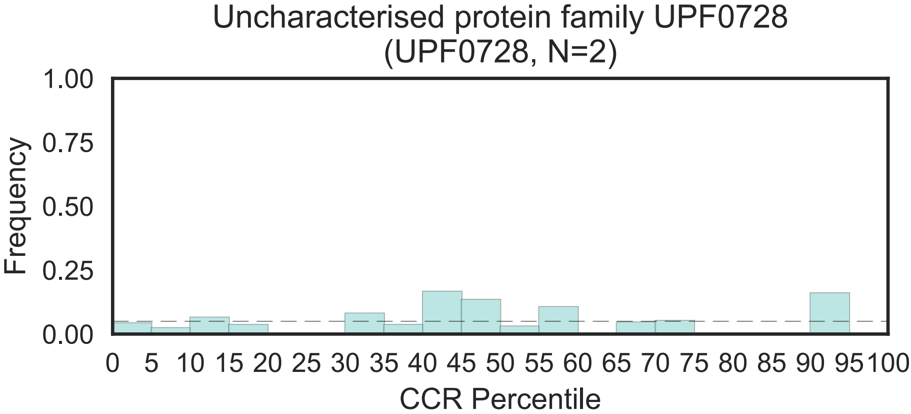
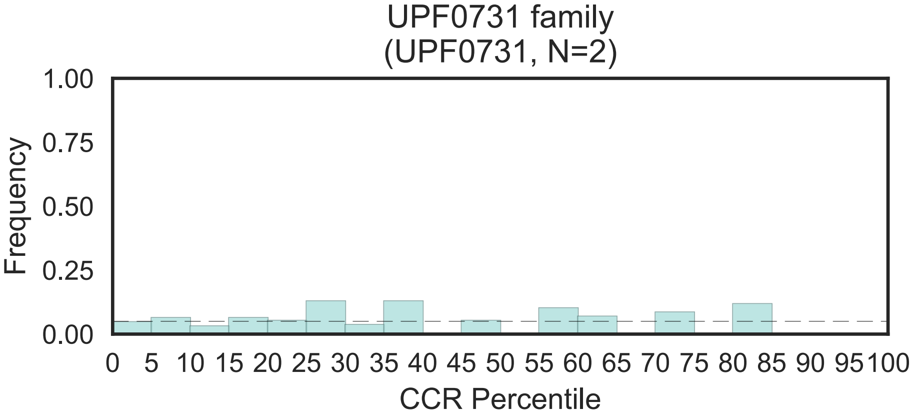
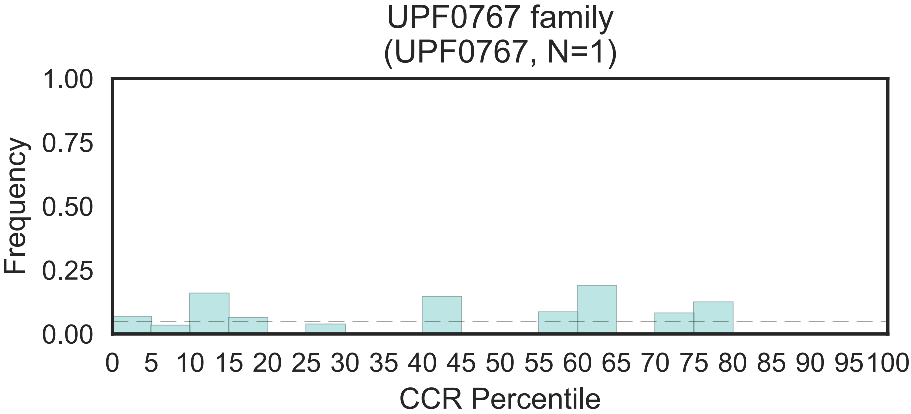
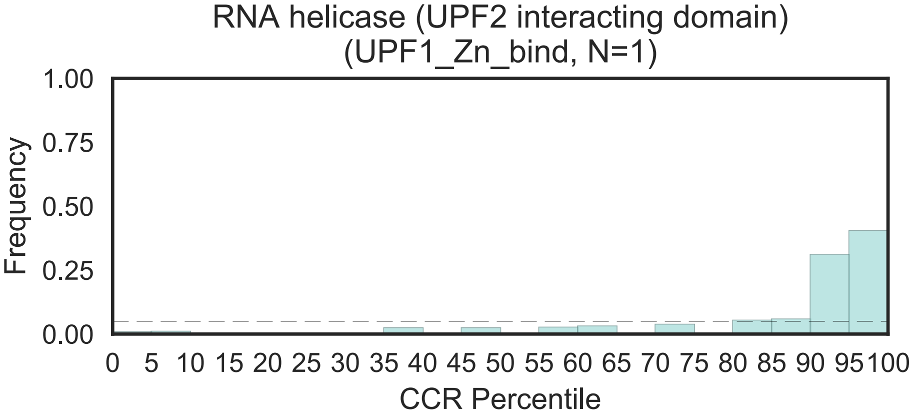
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

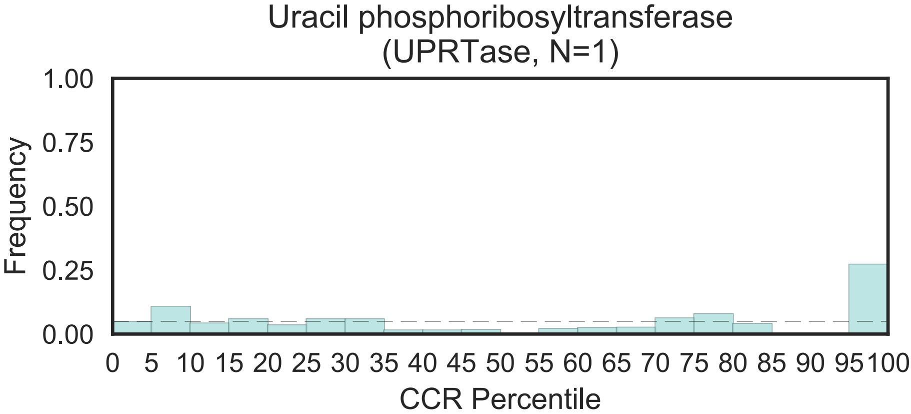

Uncharacterised protein family UPF0728
(UPF0728, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

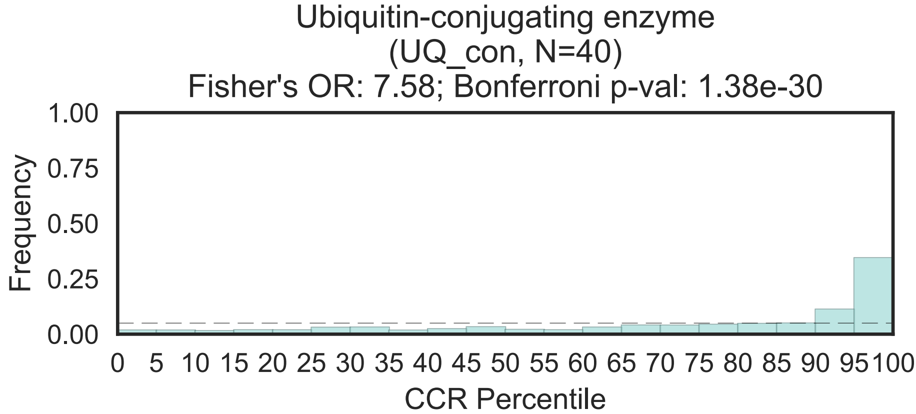

UPF0731 family
(UPF0731, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

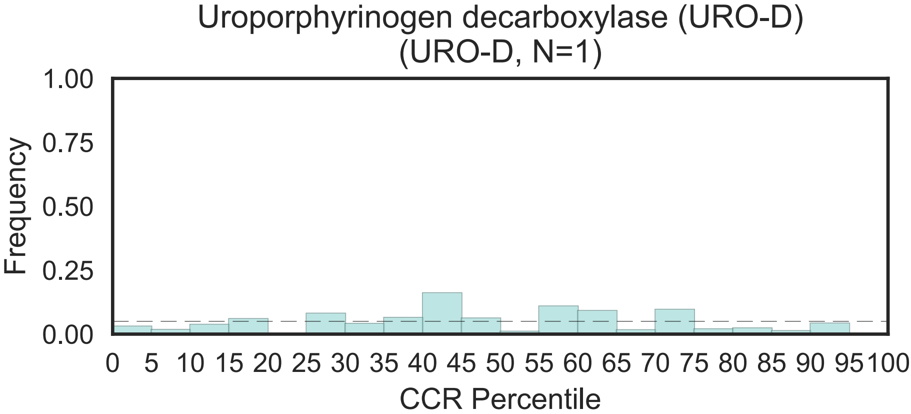

UPF0767 family
(UPF0767, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

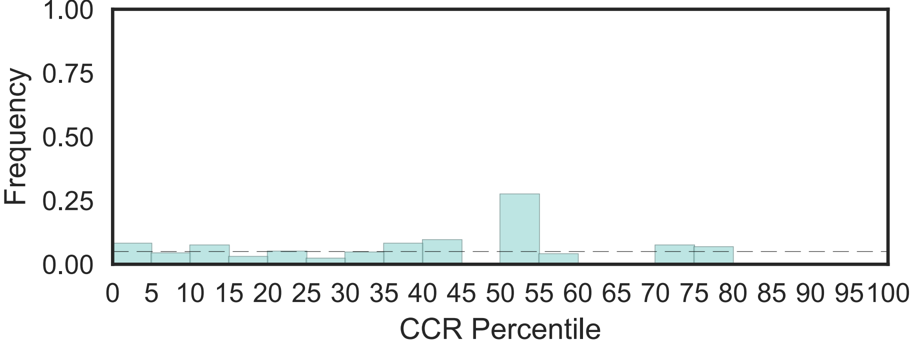


RNA helicase (UPF2 interacting domain)
(UPF1_Zn_bind, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

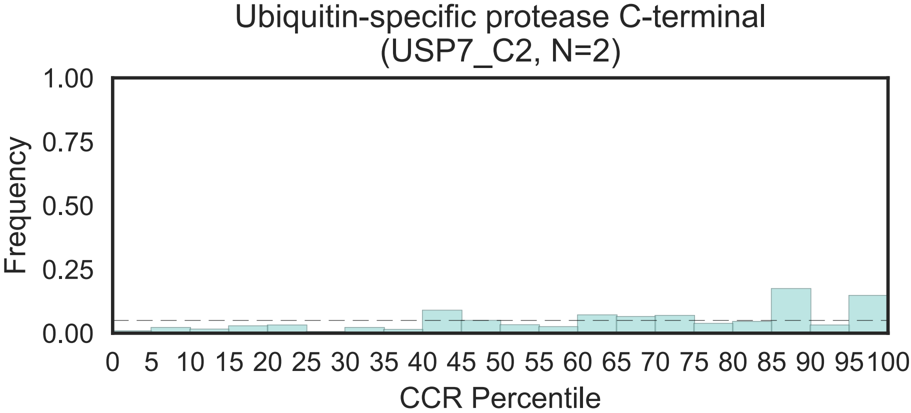

Uracil phosphoribosyltransferase
(UPRTase, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

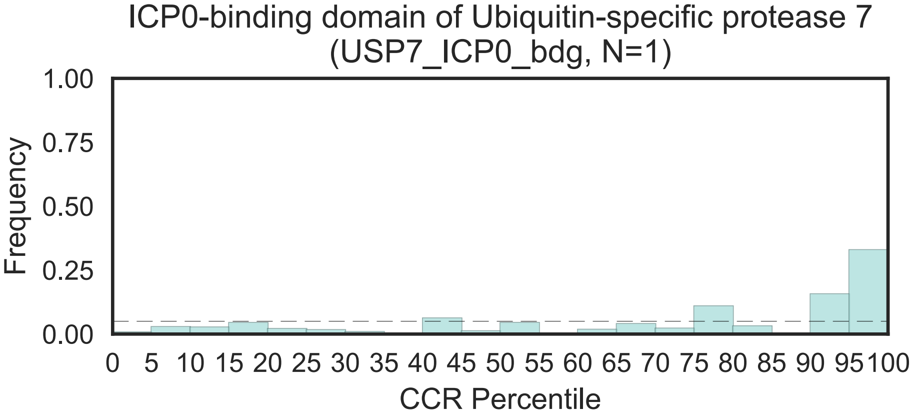

Ubiquitin-conjugating enzyme
(UQ_con, N=40)
Fisher's OR: 7.58; Bonferroni p-val: 1.38e-30
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

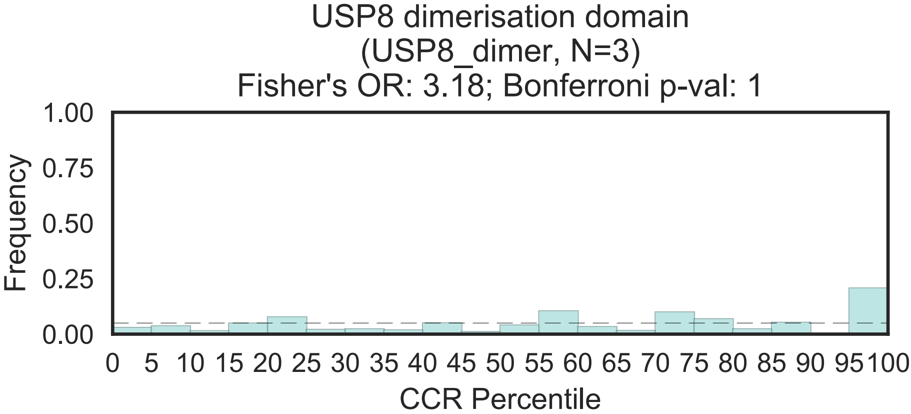

Uroporphyrinogen decarboxylase (URO-D)
(URO-D, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

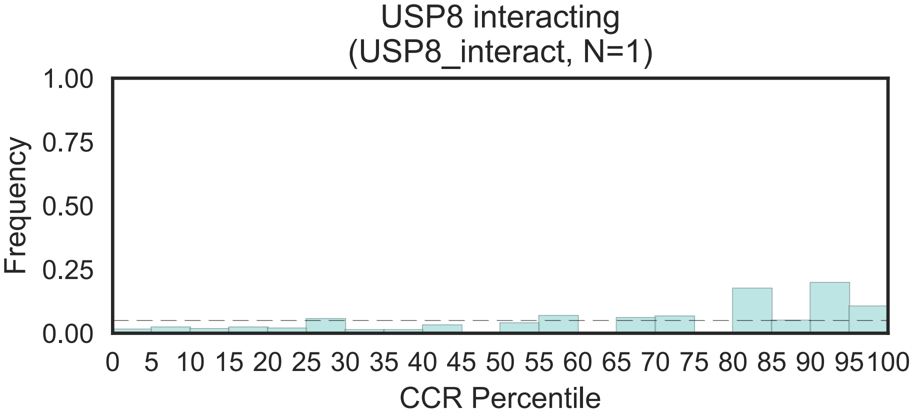


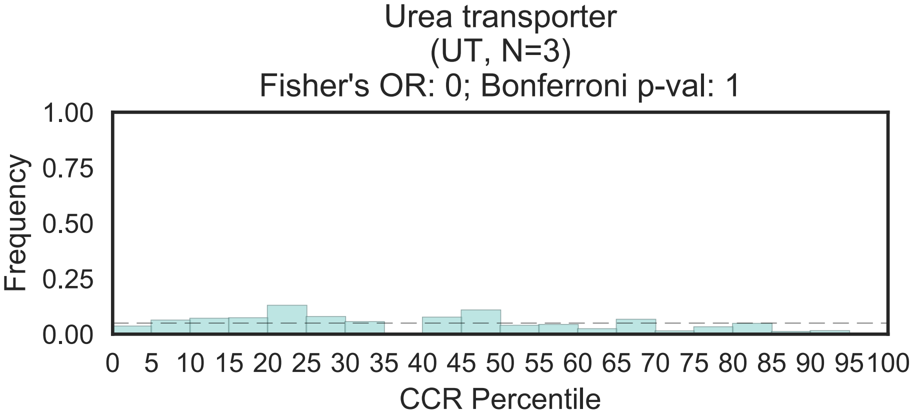
Linker region of USP19 deubiquitinase
(USP19_linker, N=1)

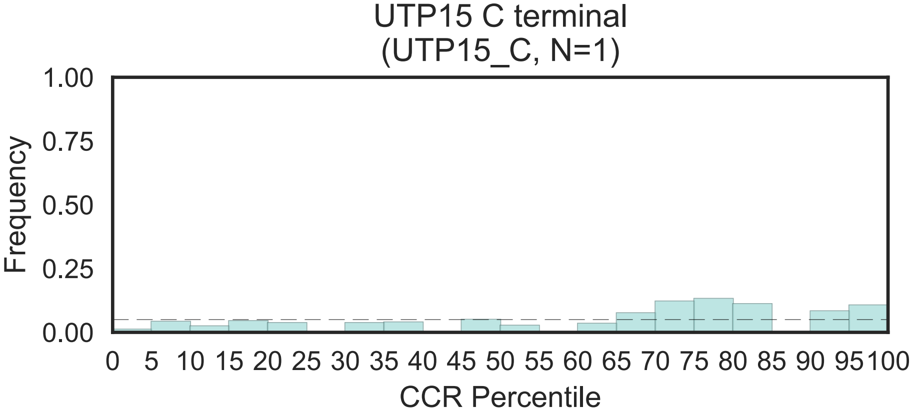

Ubiquitin-specific protease C-terminal
(USP7_C2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

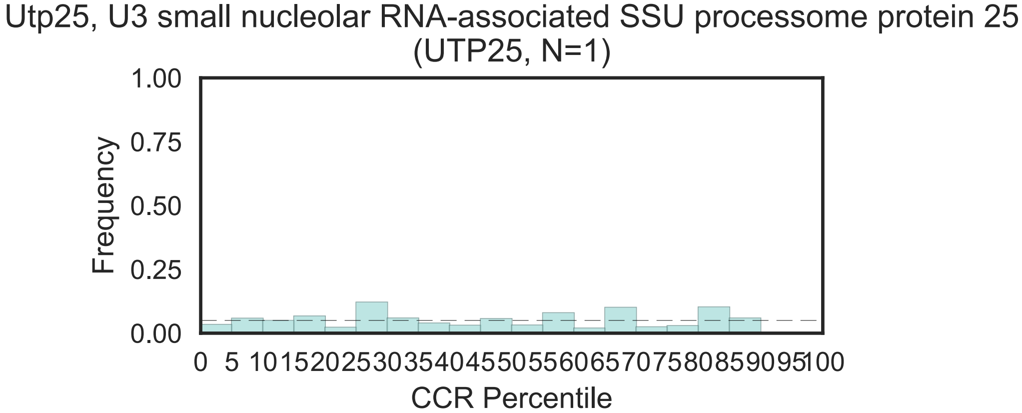

ICP0-binding domain of Ubiquitin-specific protease 7
(USP7_ICP0_bdg, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

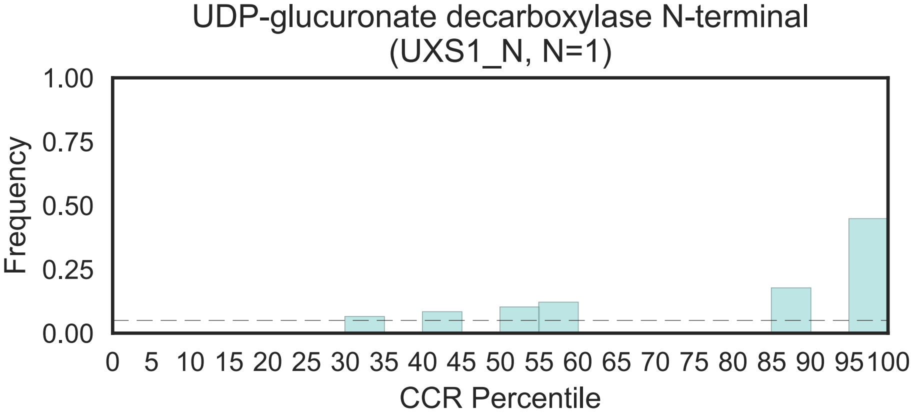

USP8 dimerisation domain
(USP8_dimer, N=3)
Fisher's OR: 3.18; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

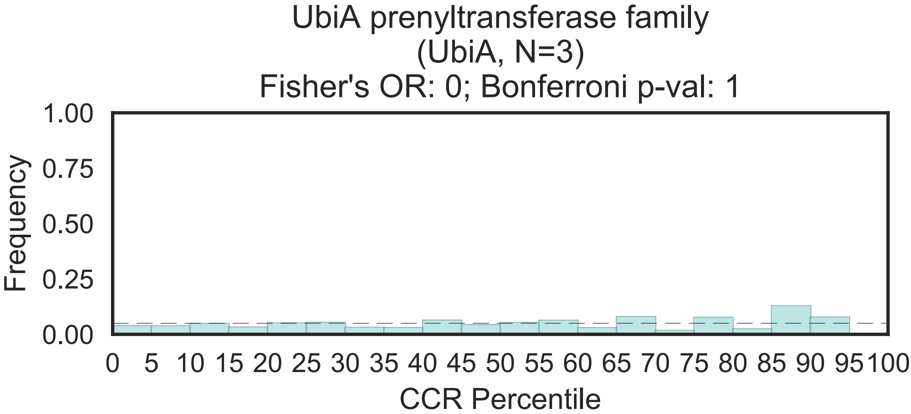

USP8 interacting
(USP8_interact, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

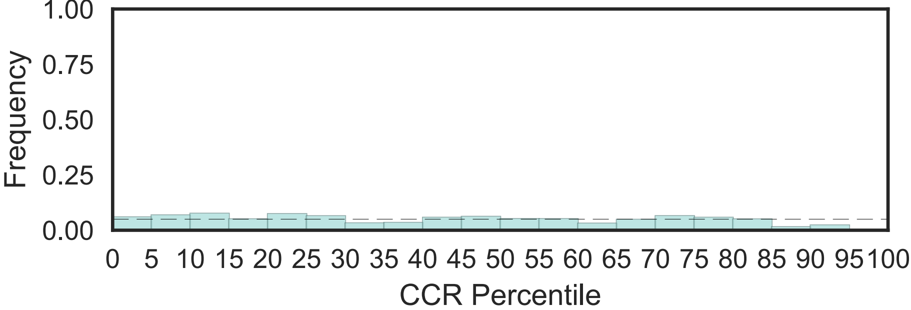

Urea transporter
(UT, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


UTP15 C terminal
(UTP15_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

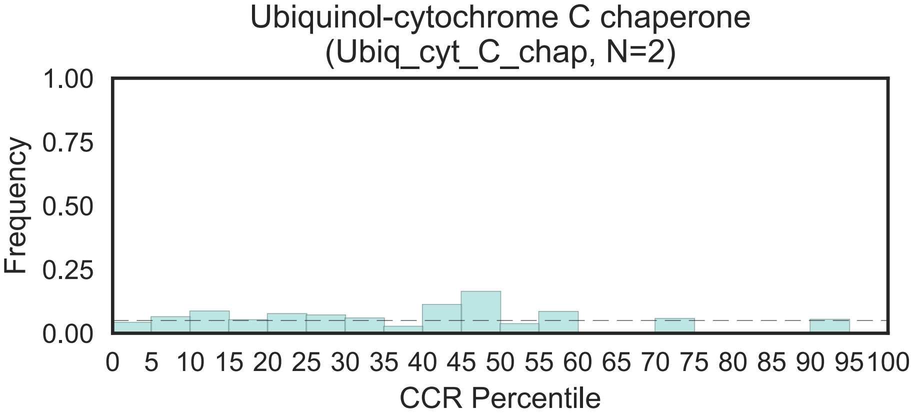

Utp25, U3 small nucleolar RNA-associated SSU processome protein 25
(UTP25, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

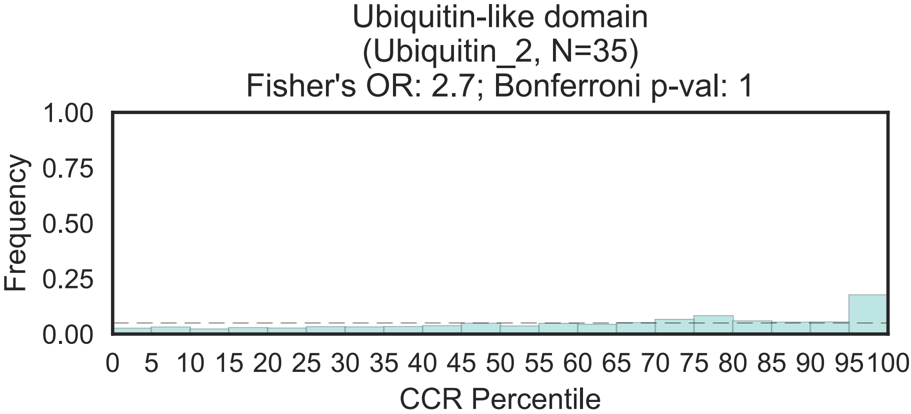

UDP-glucuronate decarboxylase N-terminal
(UXS1_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

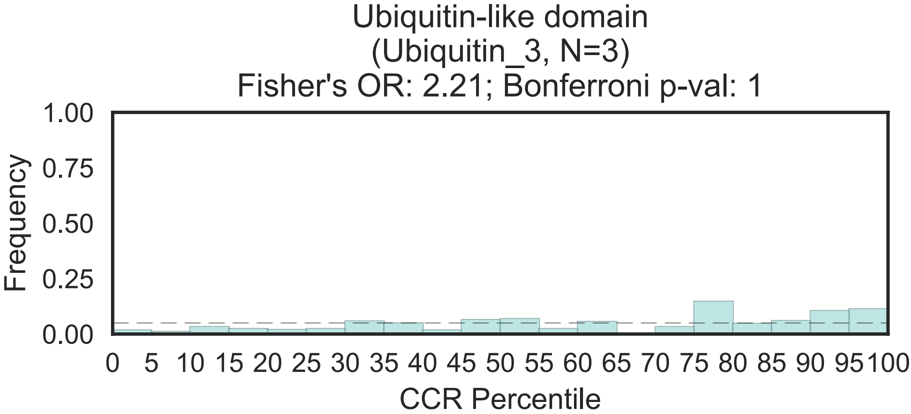

UbiA prenyltransferase family
(UbiA, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

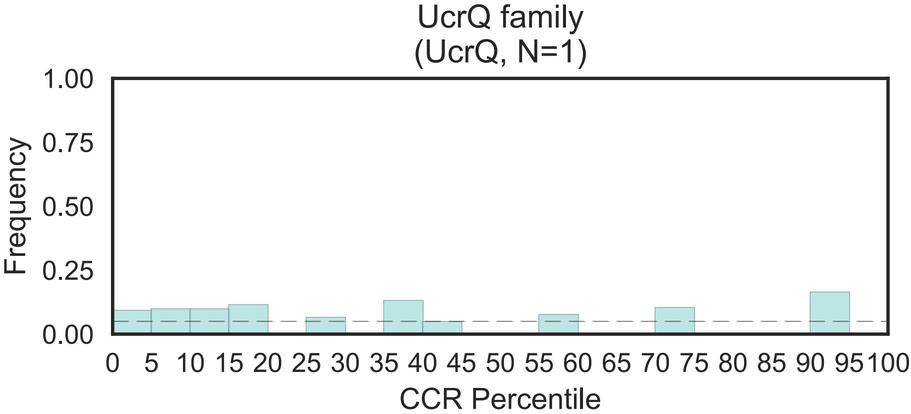


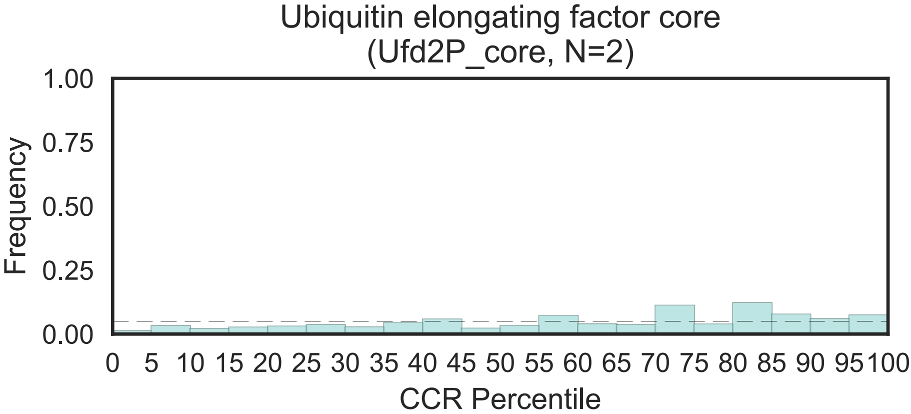
ubiE/COQ5 methyltransferase family
(Ubie_methyltran, N=13)
Fisher's OR: 0; Bonferroni p-val: 1

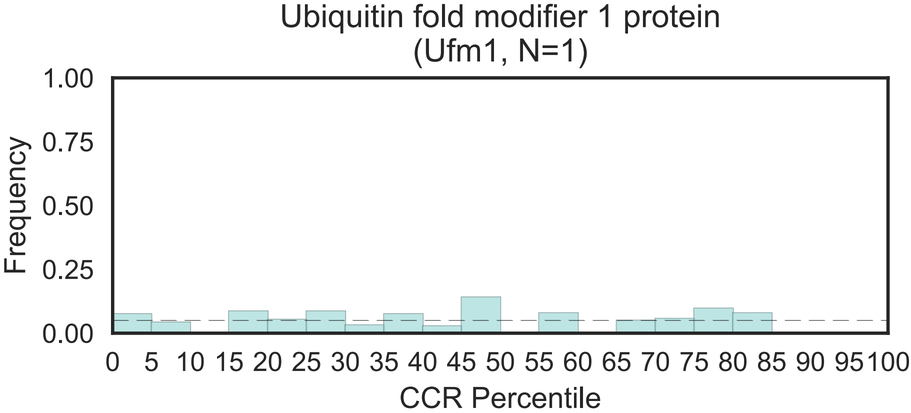

Ubiquinol-cytochrome C chaperone
(Ubiq_cyt_C_chap, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

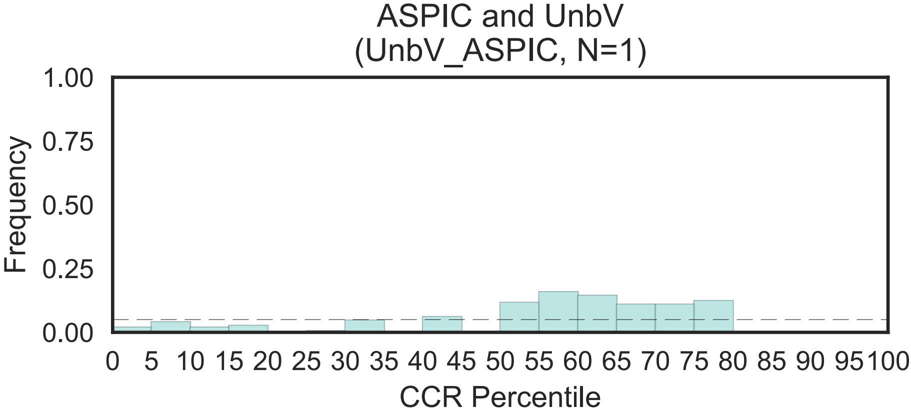

Ubiquitin-like domain
(Ubiquitin_2, N=35)
Fisher's OR: 2.7; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

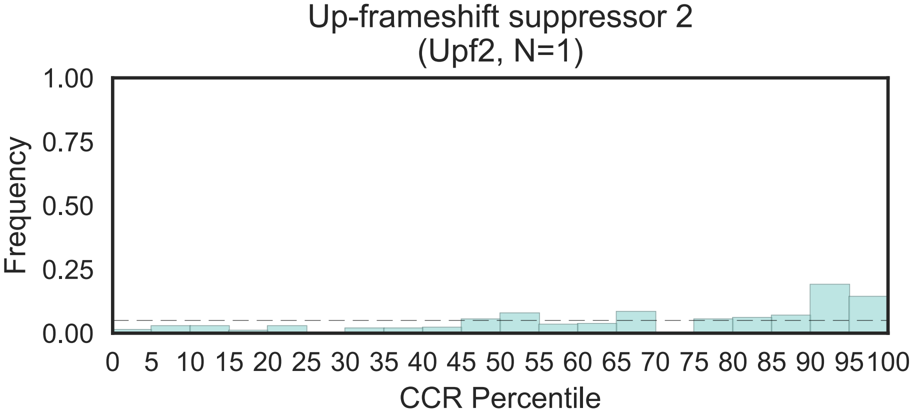

Ubiquitin-like domain
(Ubiquitin_3, N=3)
Fisher's OR: 2.21; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

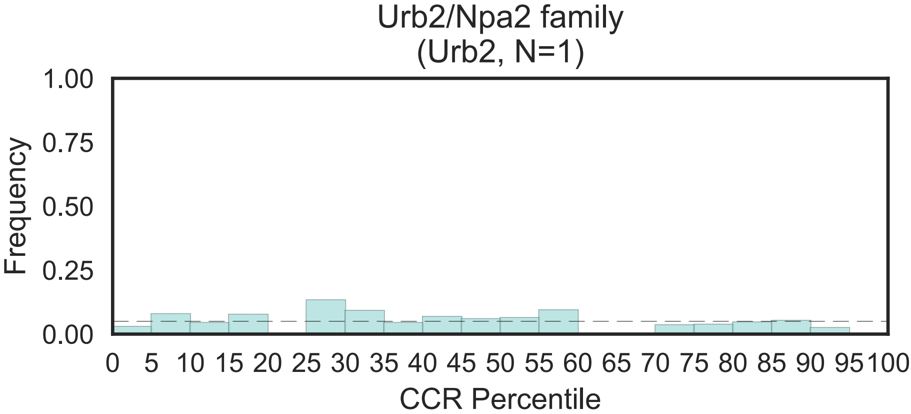

UcrQ family
(UcrQ, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

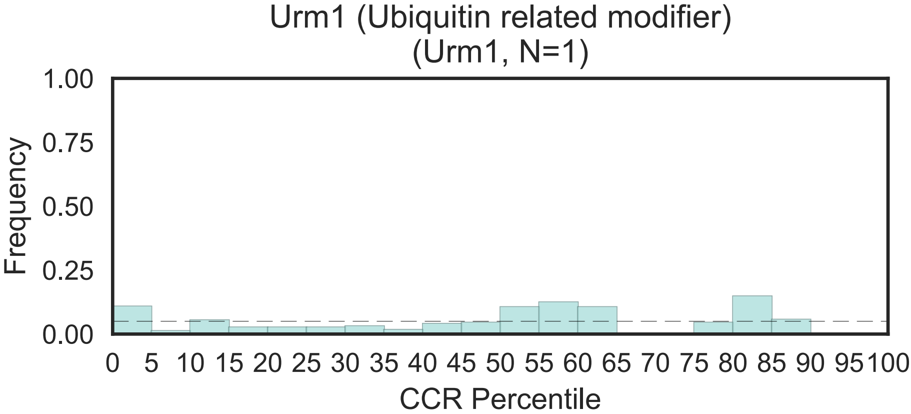

Ubiquitin elongating factor core
(Ufd2P_core, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

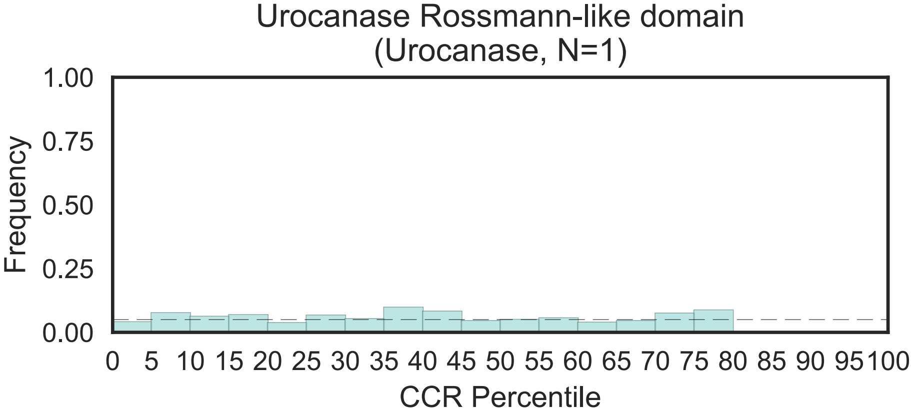

Ubiquitin fold modifier 1 protein
(Ufm1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

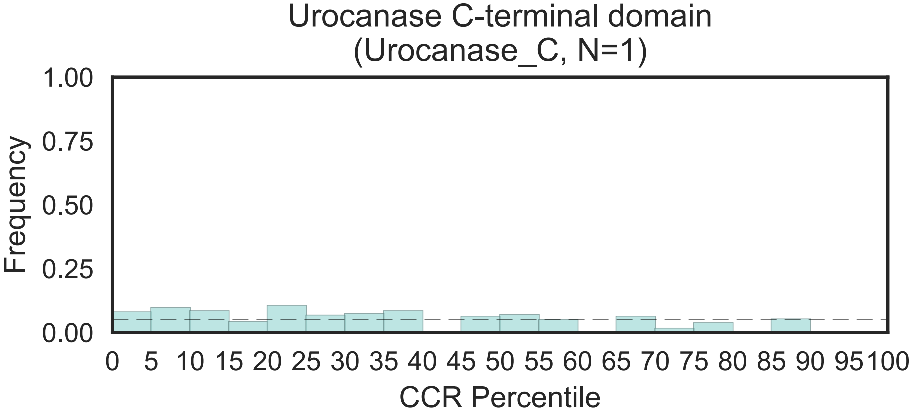

ASPIC and UnbV
(UnbV_ASPIC, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

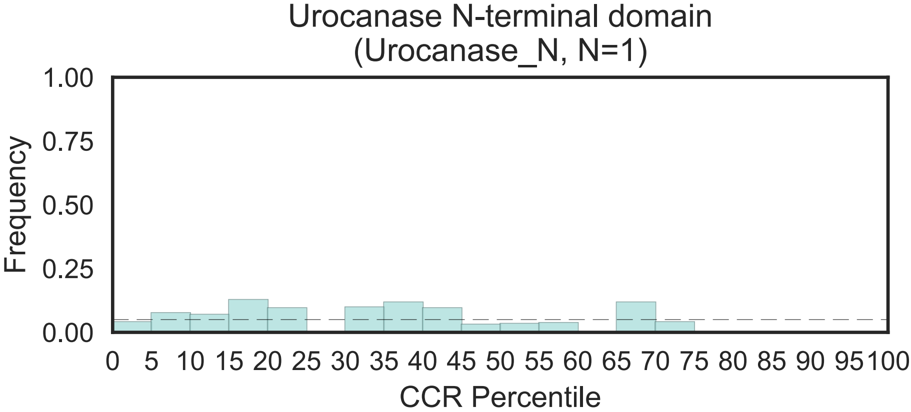

Up-frameshift suppressor 2
(Upf2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

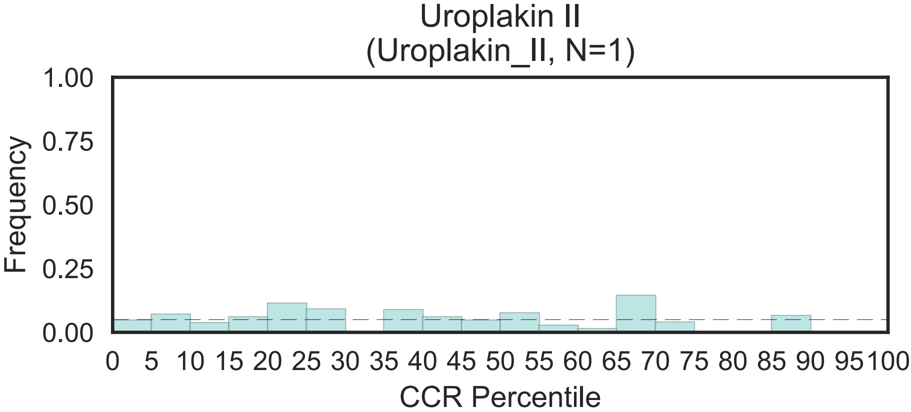

Urb2/Npa2 family
(Urb2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

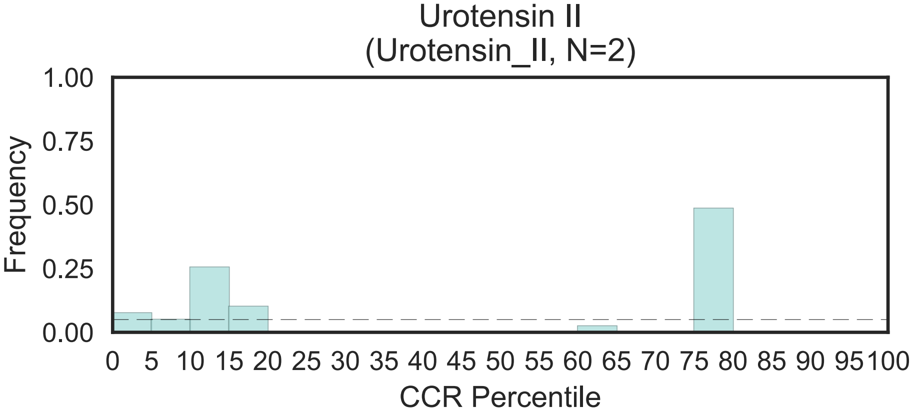

Urm1 (Ubiquitin related modifier)
(Urm1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

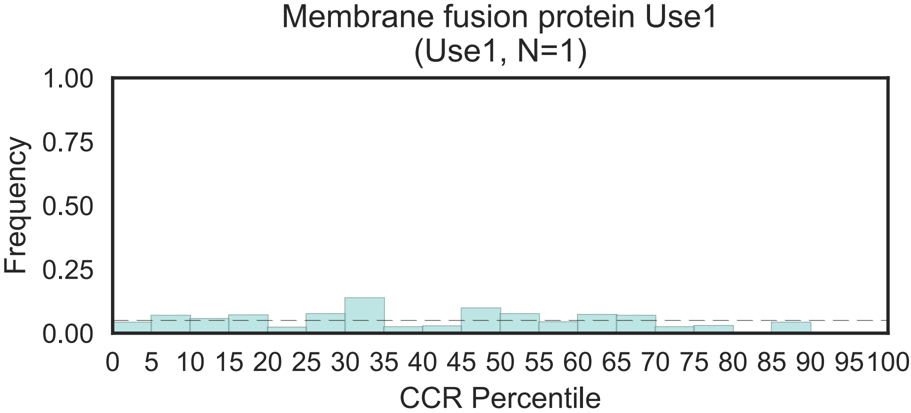

Urocanase Rossmann-like domain
(Urocanase, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

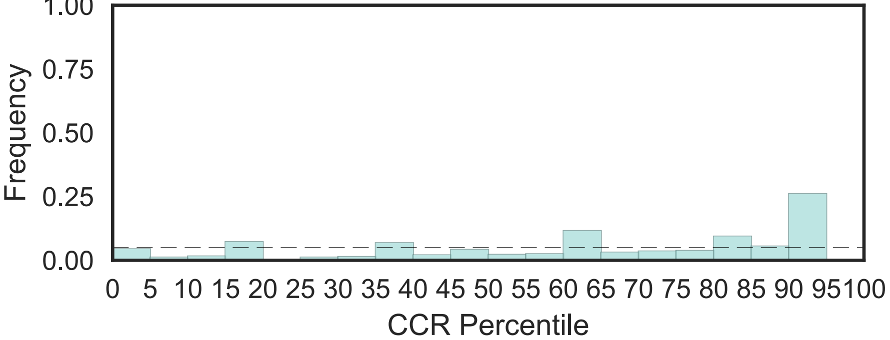

Urocanase C-terminal domain
(Urocanase_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Urocanase N-terminal domain
(Urocanase_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

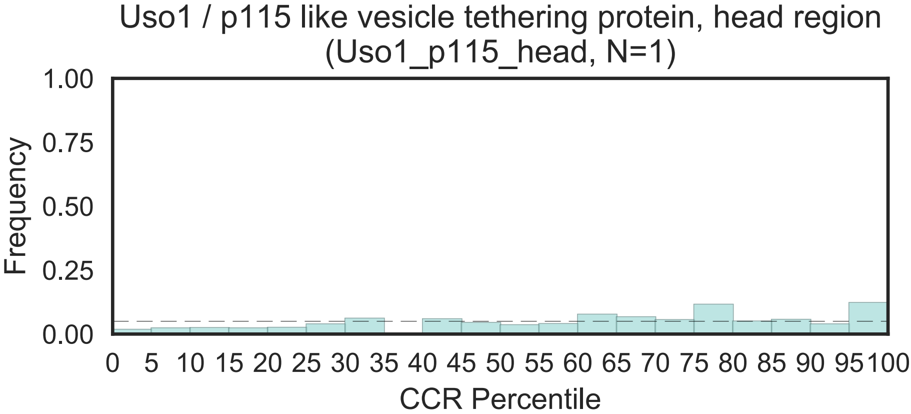

Uroplakin II
(Uroplakin_II, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

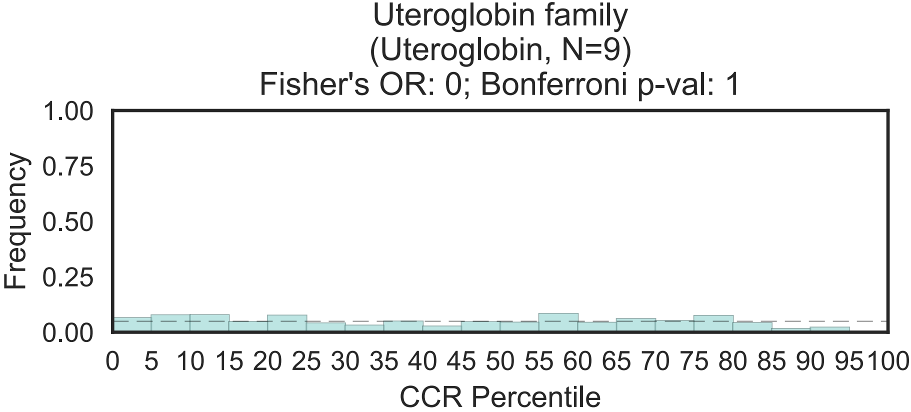

Urotensin II
(Urotensin_II, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

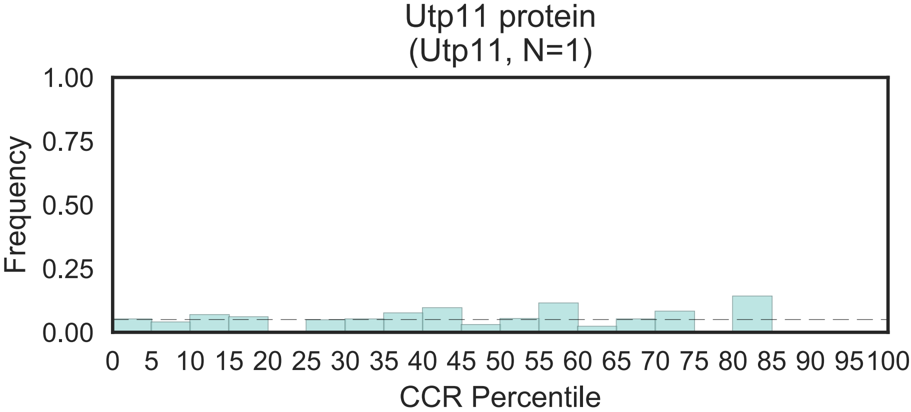

Membrane fusion protein Use1
(Use1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

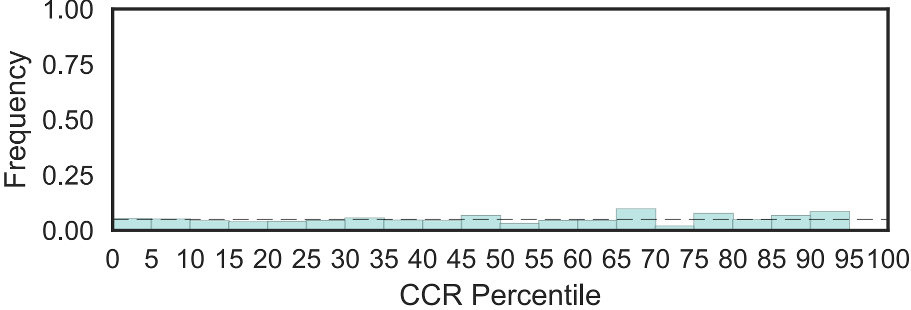


Uso1 / p115 like vesicle tethering protein, C terminal region (Uso1_p115_C, N=1)

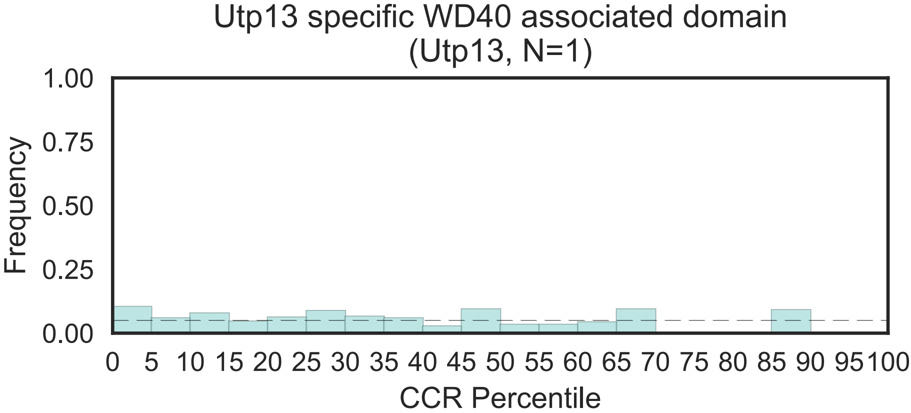

Uso1 / p115 like vesicle tethering protein, head region
(Uso1_p115_head, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

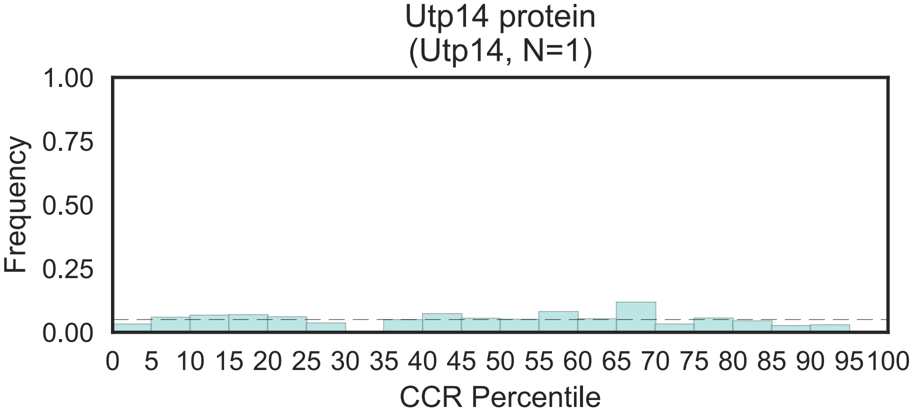

Uteroglobin family
(Uteroglobin, N=9)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

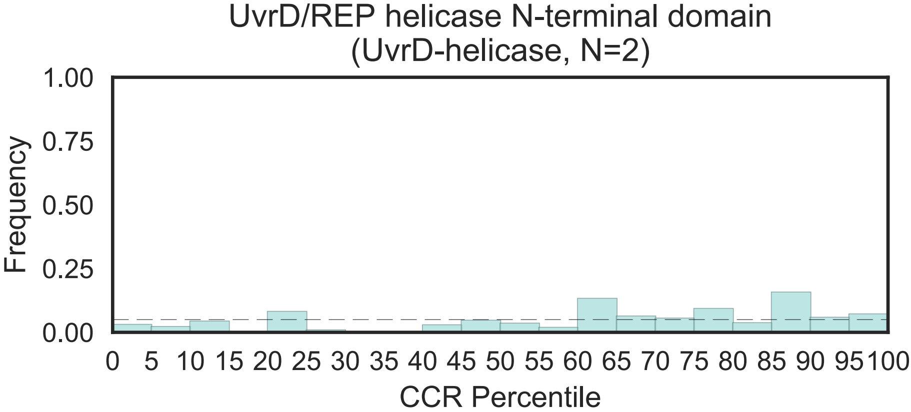

Utp11 protein
(Utp11, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

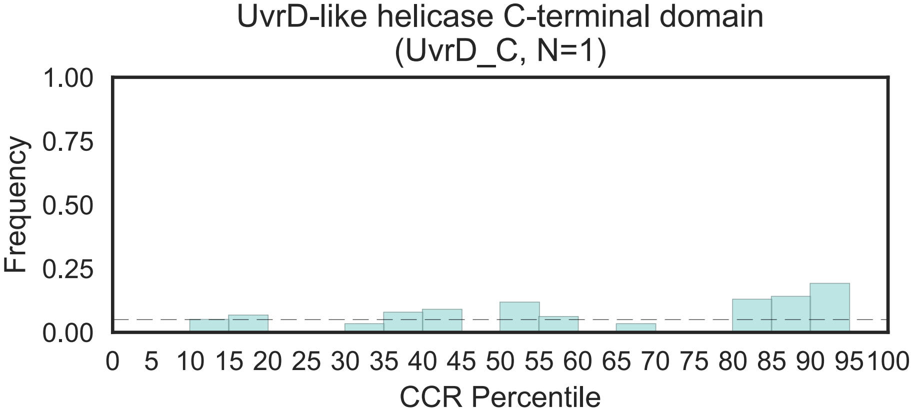


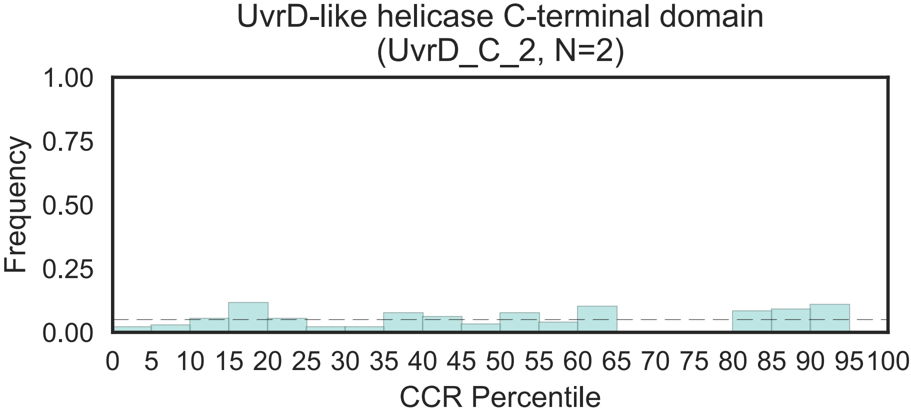
Dip2/Utp12 Family
(Utp12, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

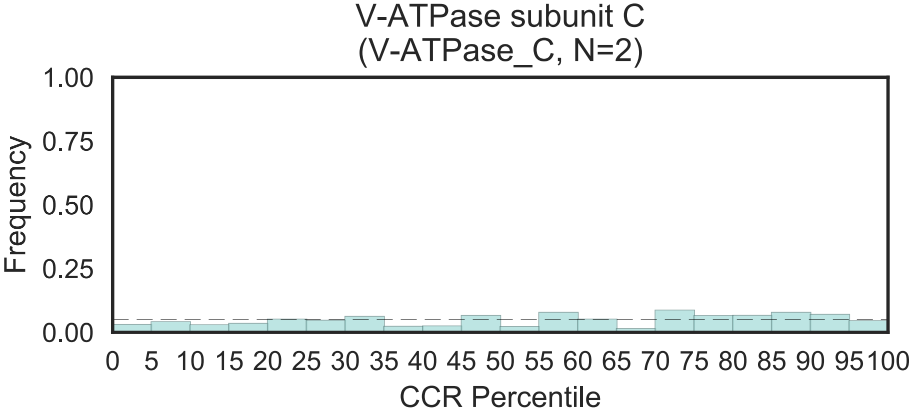

Utp13 specific WD40 associated domain
(Utp13, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

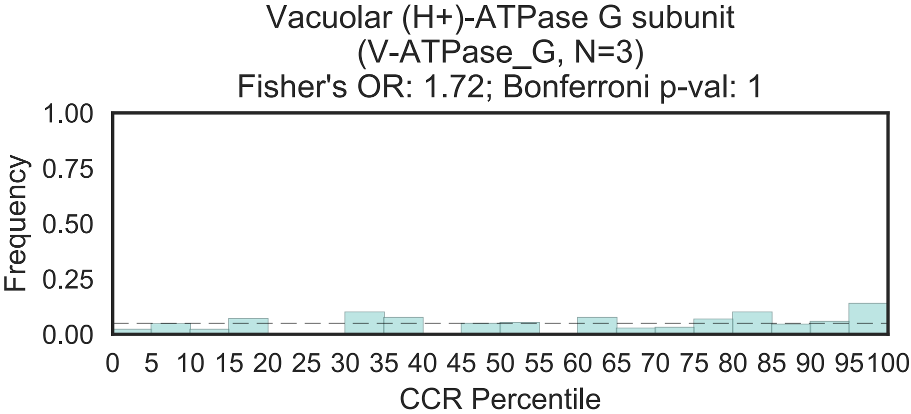

Utp14 protein
(Utp14, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

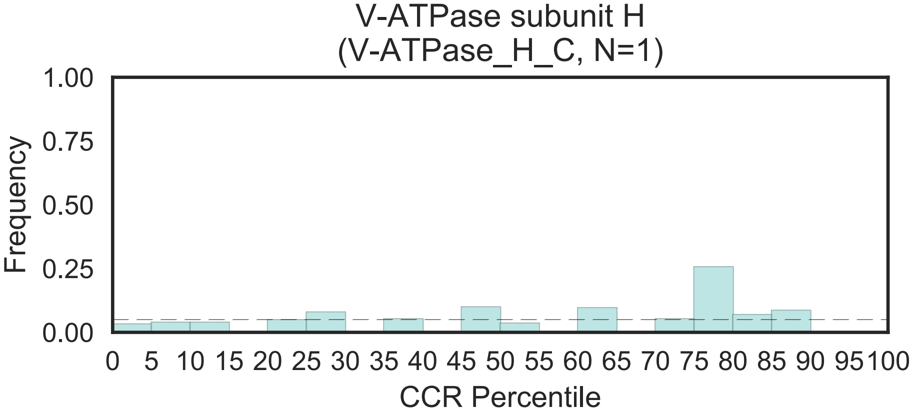

UvrD/REP helicase N-terminal domain
(UvrD-helicase, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

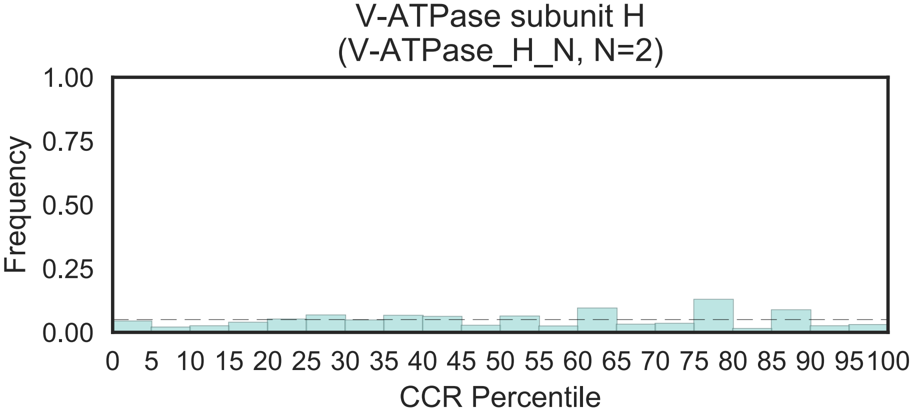

UvrD-like helicase C-terminal domain
(UvrD_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

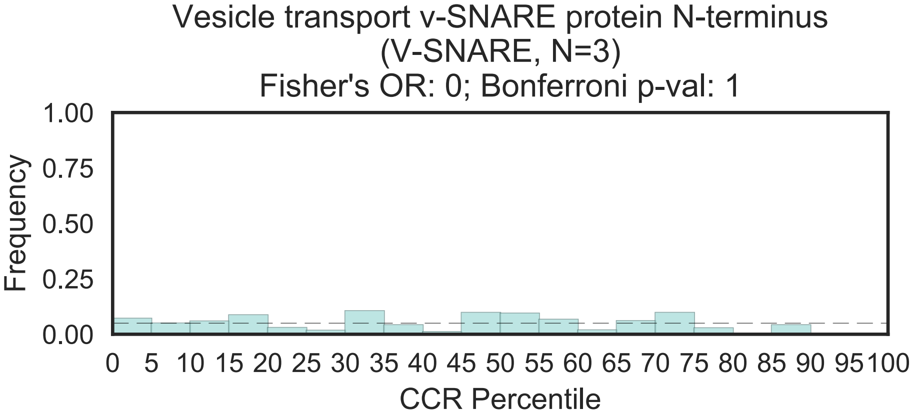

UvrD-like helicase C-terminal domain
(UvrD_C_2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

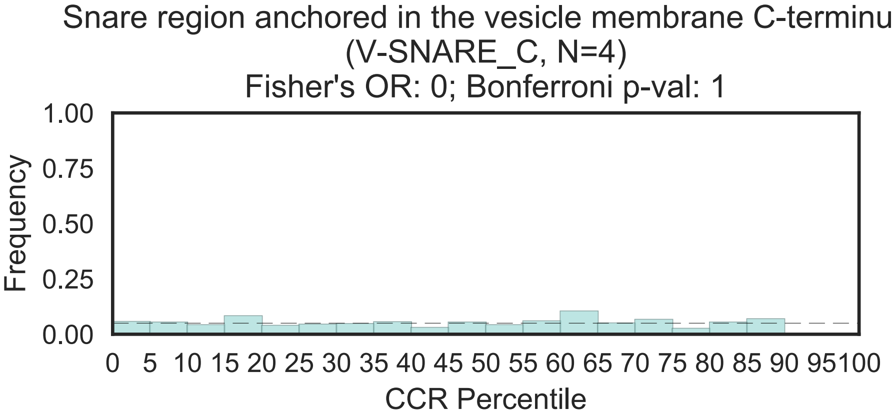

V-ATPase subunit C
(V-ATPase_C, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Vacuolar (H+)-ATPase G subunit
(V-ATPase_G, N=3)
Fisher's OR: 1.72; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

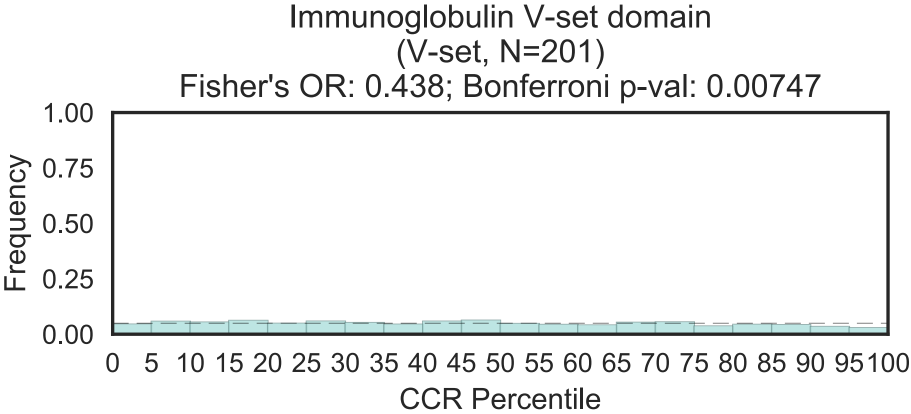

V-ATPase subunit H
(V-ATPase_H_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

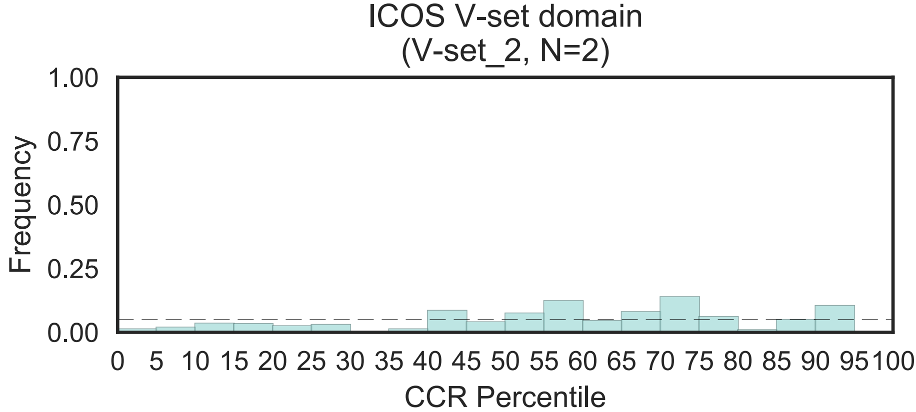

V-ATPase subunit H
(V-ATPase_H_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

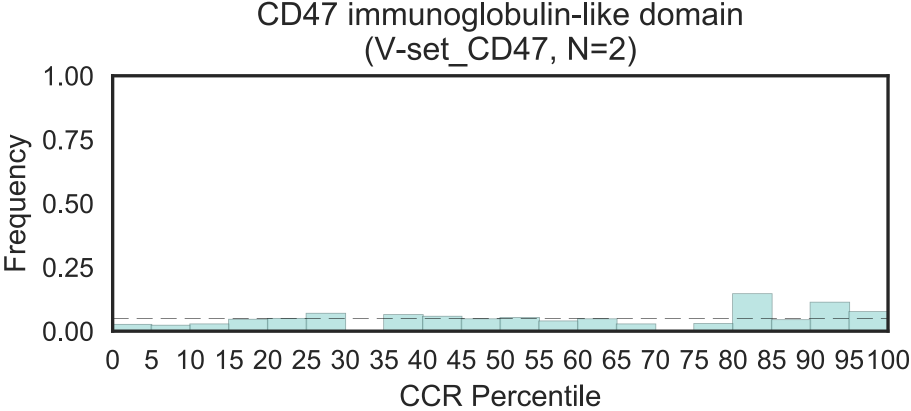

Vesicle transport v-SNARE protein N-terminus
(V-SNARE, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

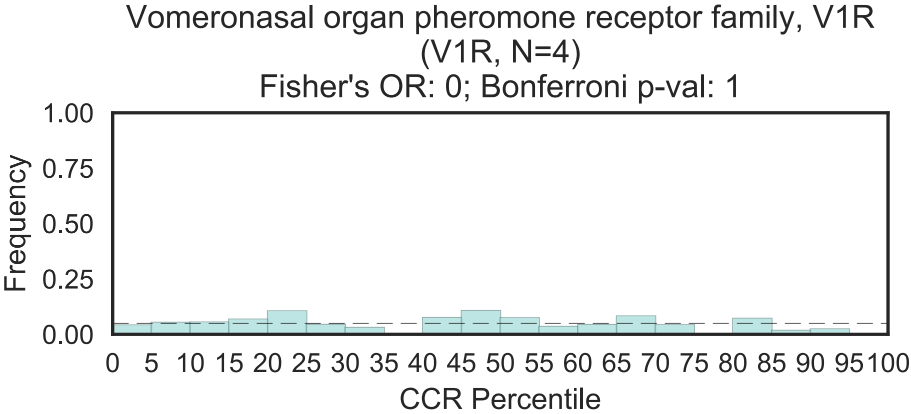


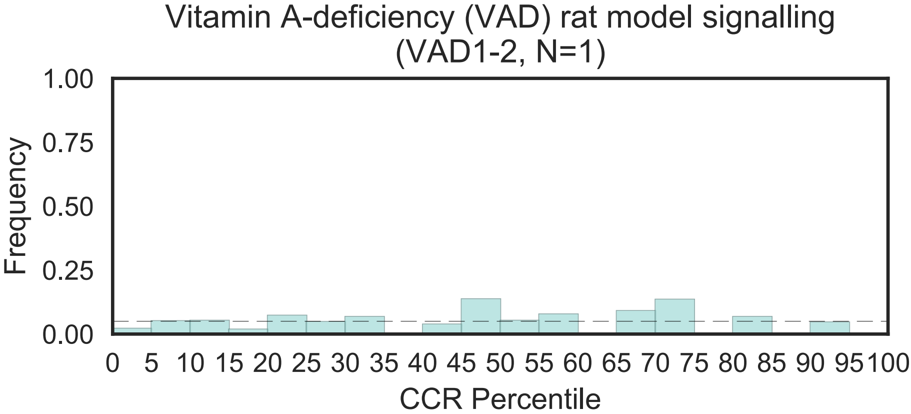
Snare region anchored in the vesicle membrane C-terminus
(V-SNARE_C, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Immunoglobulin V-set domain
(V-set, N=201)
Fisher's OR: 0.438; Bonferroni p-val: 0.00747
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

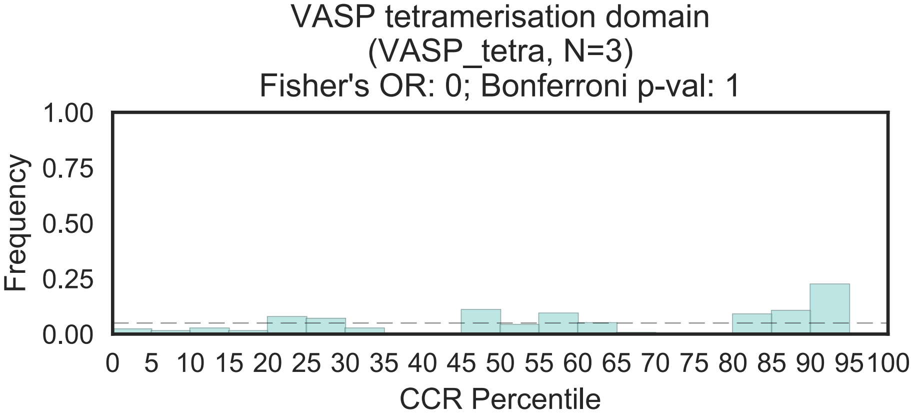

ICOS V-set domain
(V-set_2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

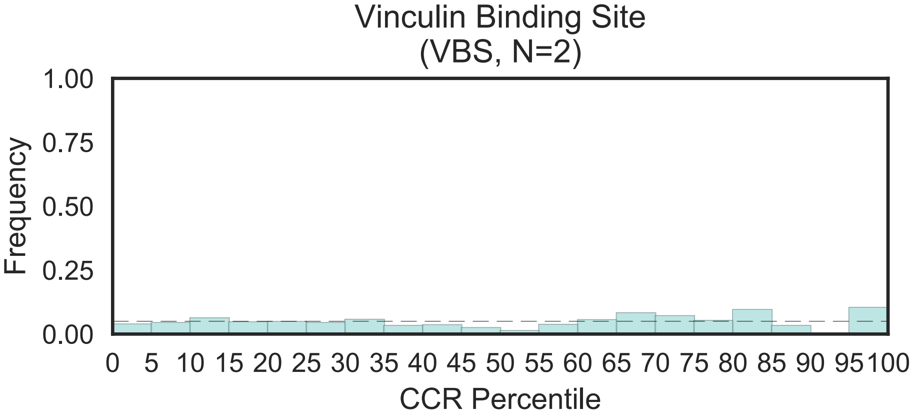

CD47 immunoglobulin-like domain
(V-set_CD47, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

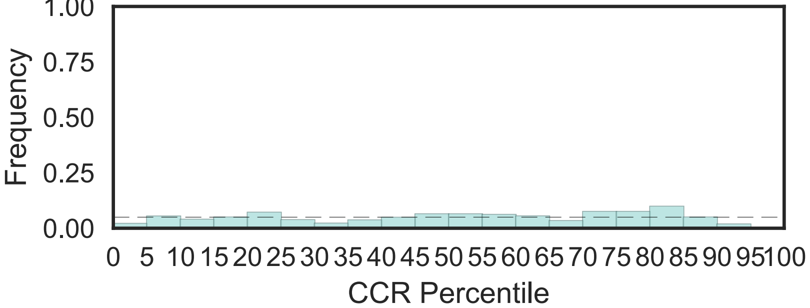

Vomeronasal organ pheromone receptor family, V1R
(V1R, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

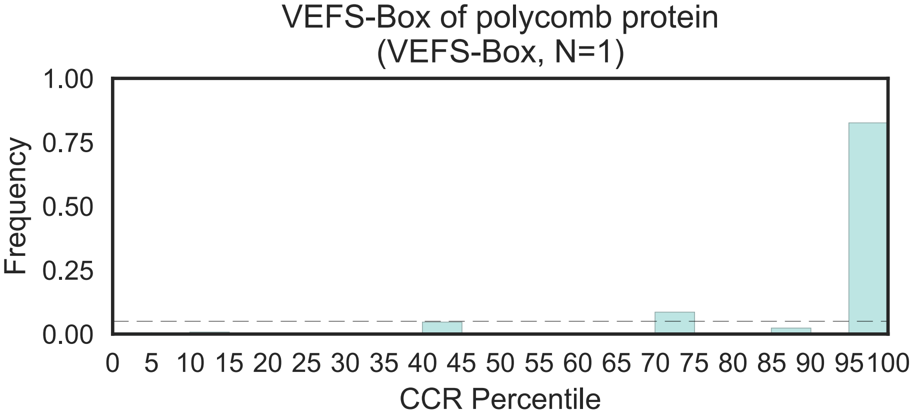


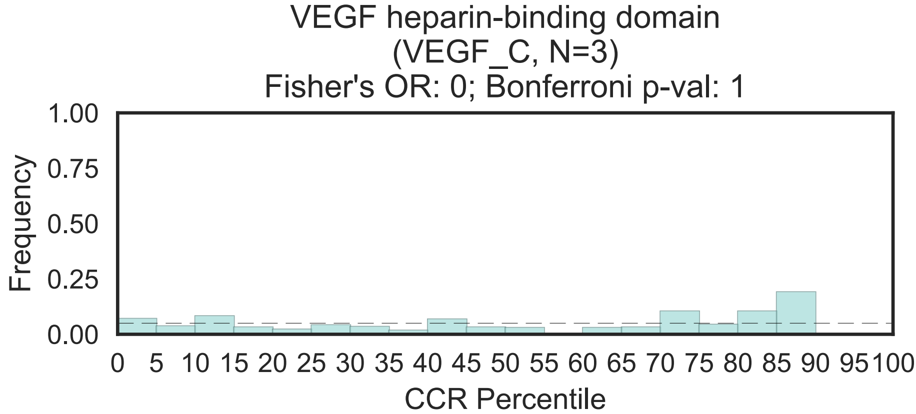
Vitamin A-deficiency (VAD) rat model signalling
(VAD1-2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

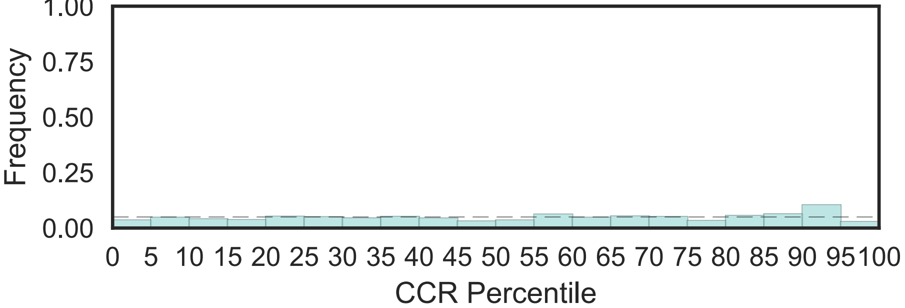

VASP tetramerisation domain
(VASP_tetra, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Vinculin Binding Site
(VBS, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

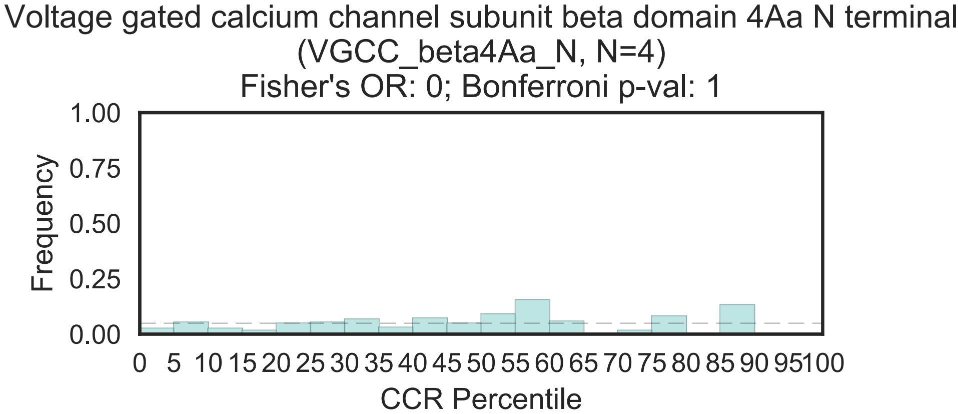

Repeat domain in Vibrio, Colwellia, Bradyrhizobium and Shewanella
(VCBS, N=10)
Fisher's OR: 0.377; Bonferroni p-val: 1

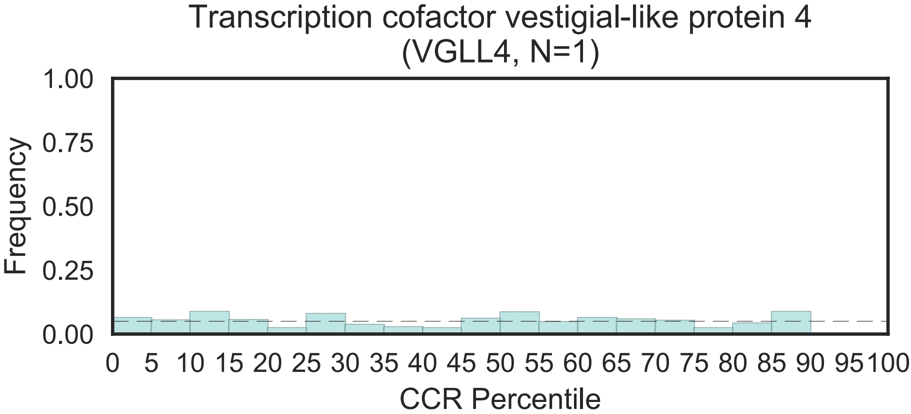

VEFS-Box of polycomb protein
(VEFS-Box, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

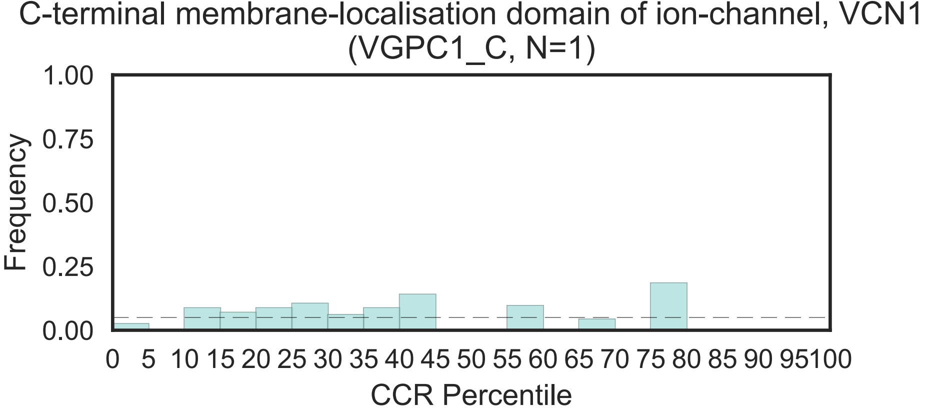

VEGF heparin-binding domain
(VEGF_C, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

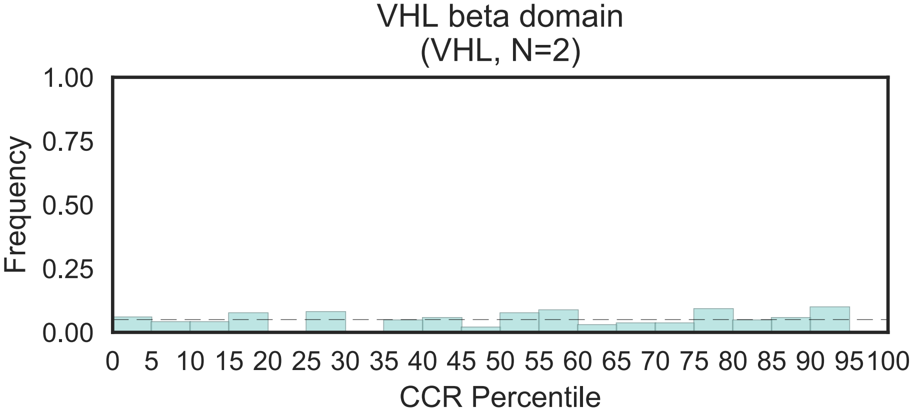


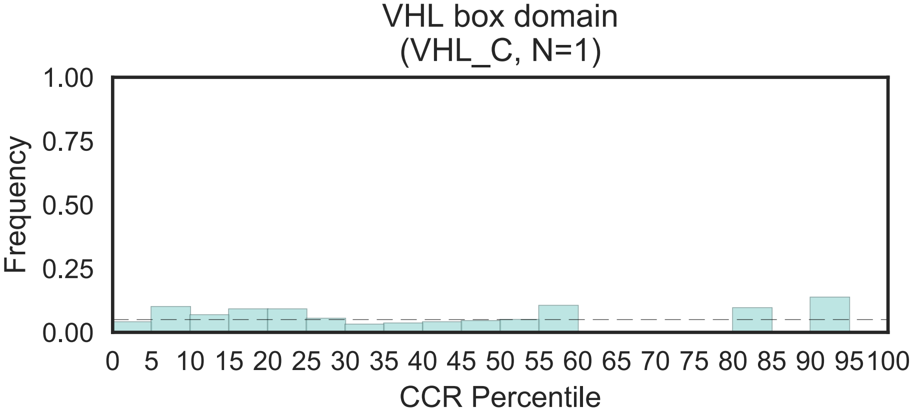
Neuronal voltage-dependent calcium channel alpha 2acd
(VGCC_alpha2, N=7)
Fisher's OR: 0.507; Bonferroni p-val: 1

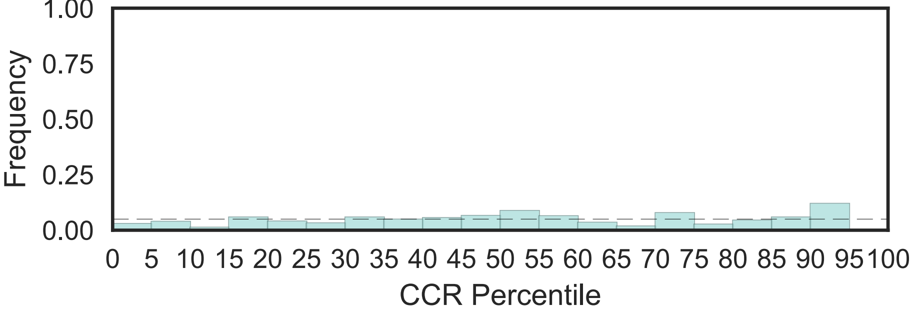

Voltage gated calcium channel subunit beta domain 4Aa N terminal
(VGCC_beta4Aa_N, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Transcription cofactor vestigial-like protein 4
(VGLL4, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

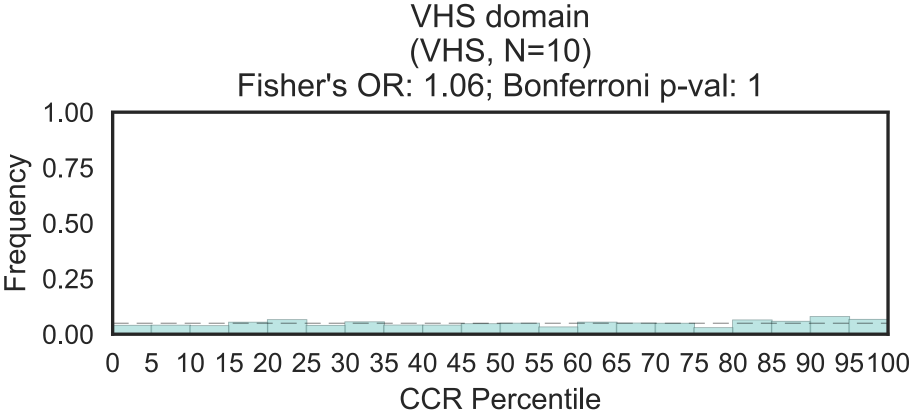

C-terminal membrane-localisation domain of ion-channel, VCN1
(VGPC1_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

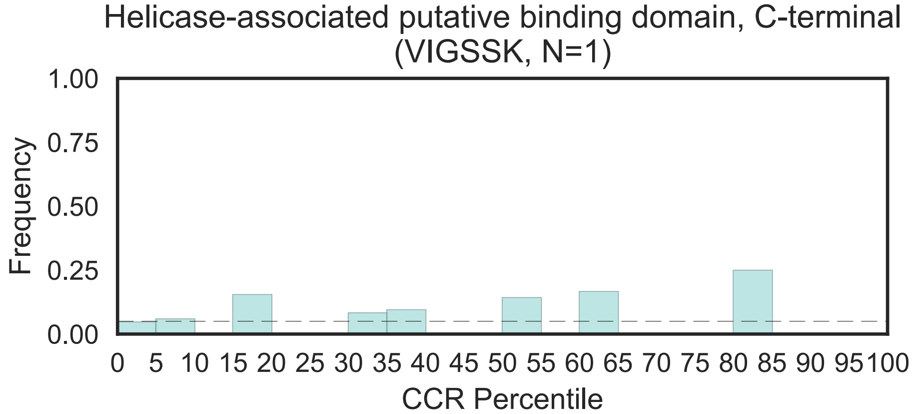

VHL beta domain
(VHL, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

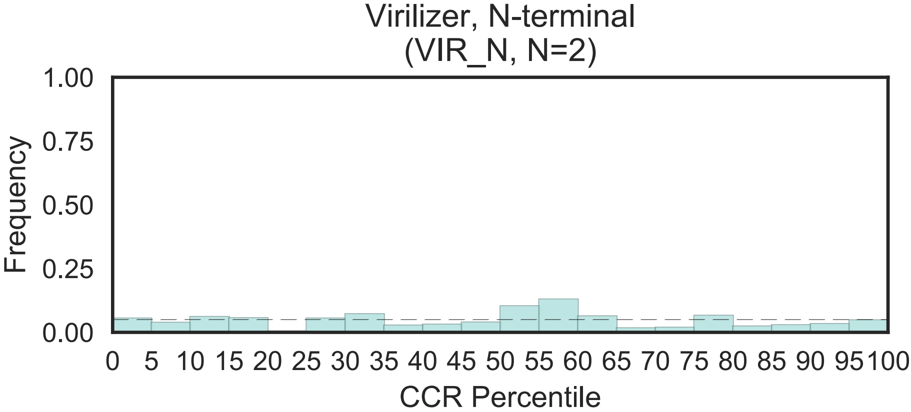

VHL box domain
(VHL_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

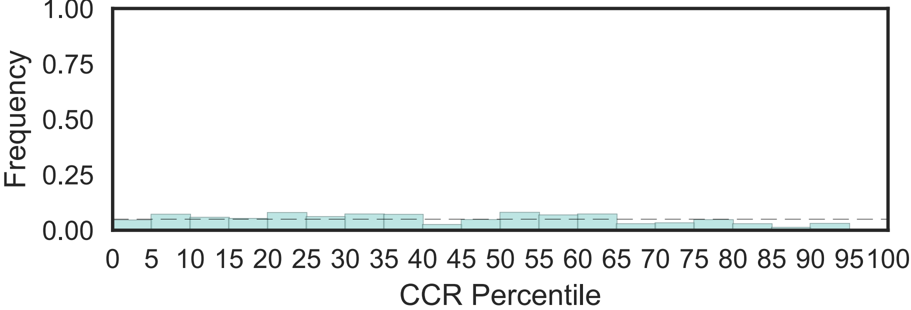


Villin headpiece domain
(VHP, N=8)
Fisher's OR: 0; Bonferroni p-val: 1

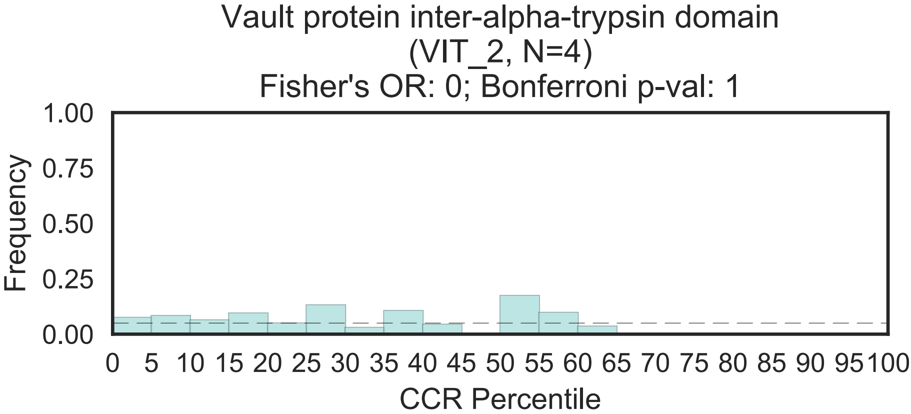

VHS domain
(VHS, N=10)
Fisher's OR: 1.06; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

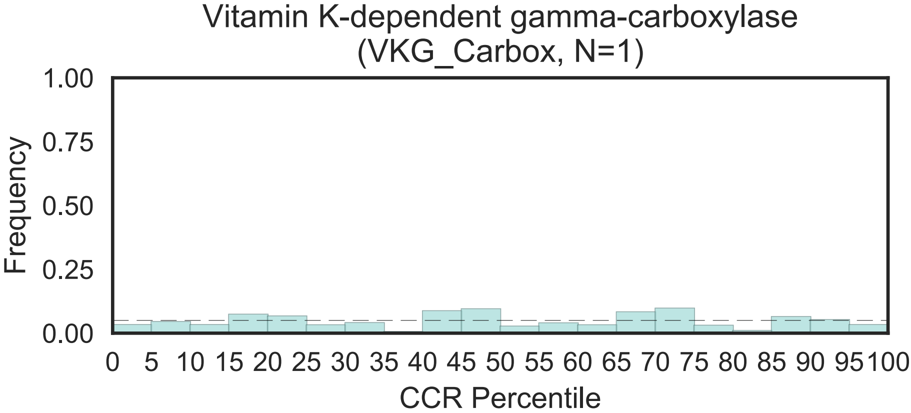

Helicase-associated putative binding domain, C-terminal
(VIGSSK, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

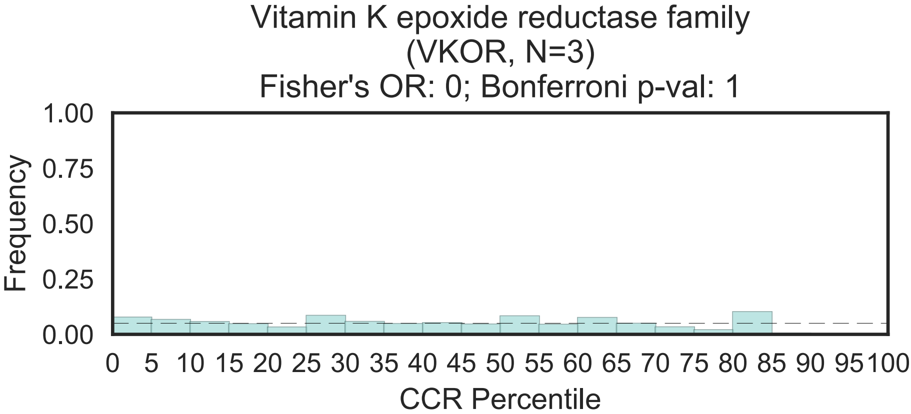

Virilizer, N-terminal
(VIR_N, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

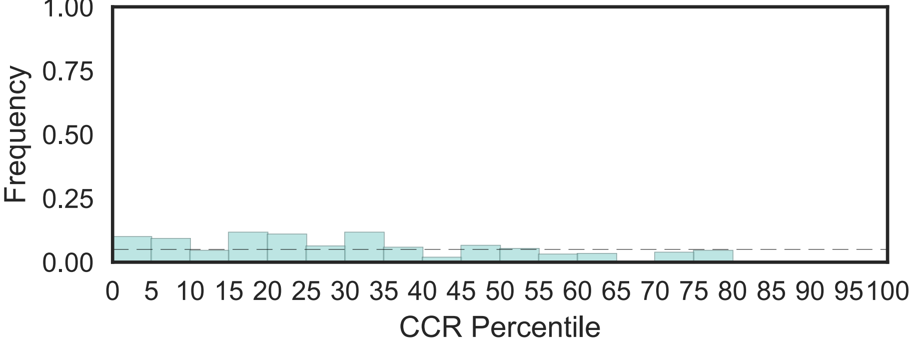


Vault protein inter-alpha-trypsin domain
(VIT, N=9)
Fisher's OR: 0; Bonferroni p-val: 1

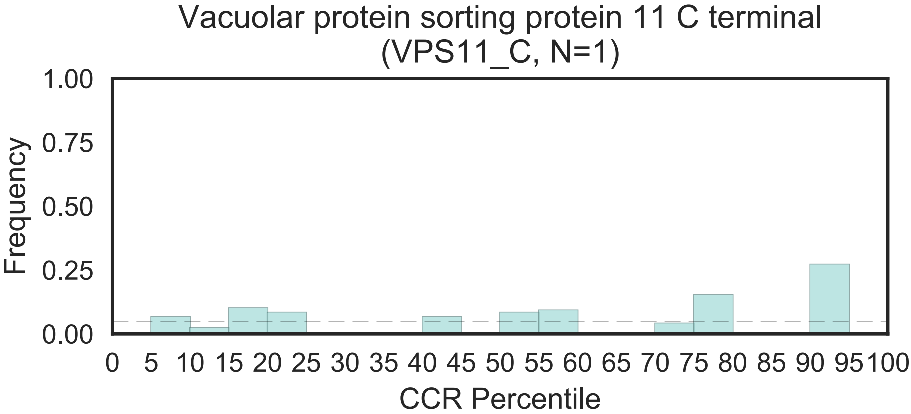

Vault protein inter-alpha-trypsin domain
(VIT_2, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

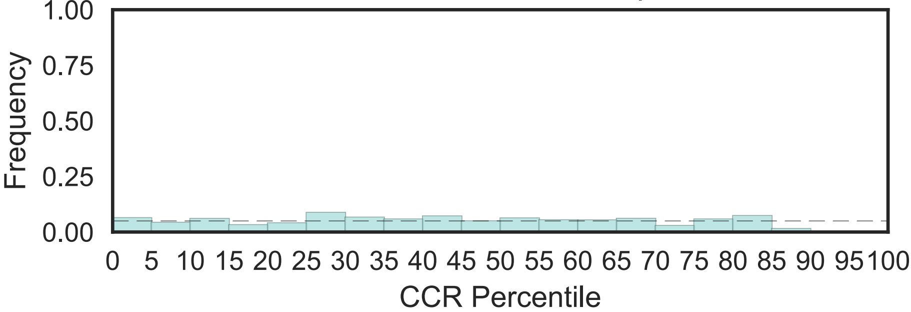

Vitamin K-dependent gamma-carboxylase
(VKG_Carbox, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

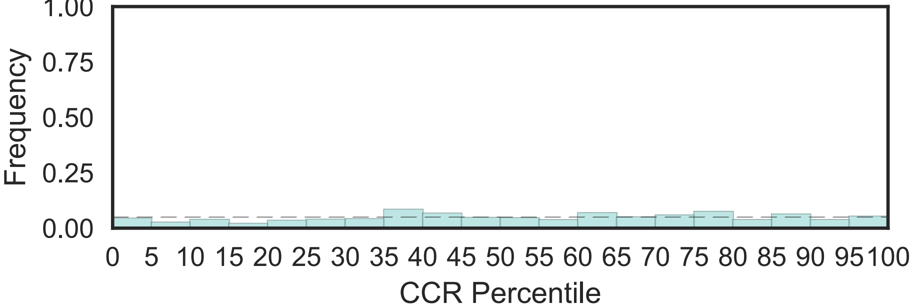

Vitamin K epoxide reductase family
(VKOR, N=3)
Fisher's OR: 0; Bonferroni p-val: 1



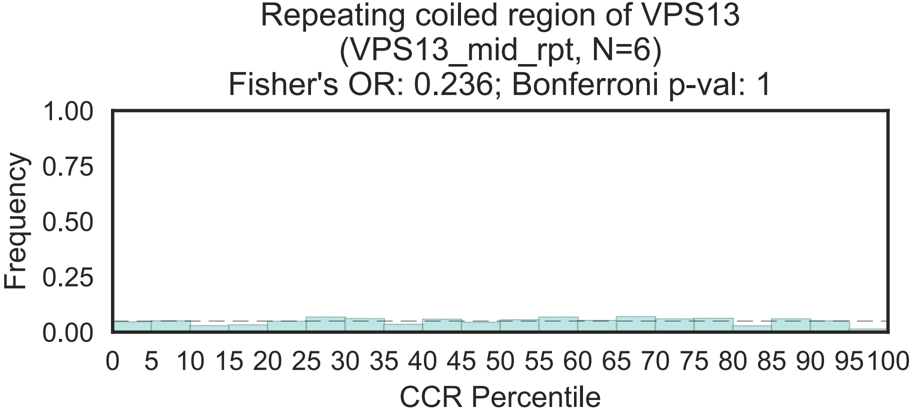
Vitelline membrane outer layer protein I (VOMI)
(VOMI, N=1)


Vacuolar protein sorting protein 11 C terminal
(VPS11_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

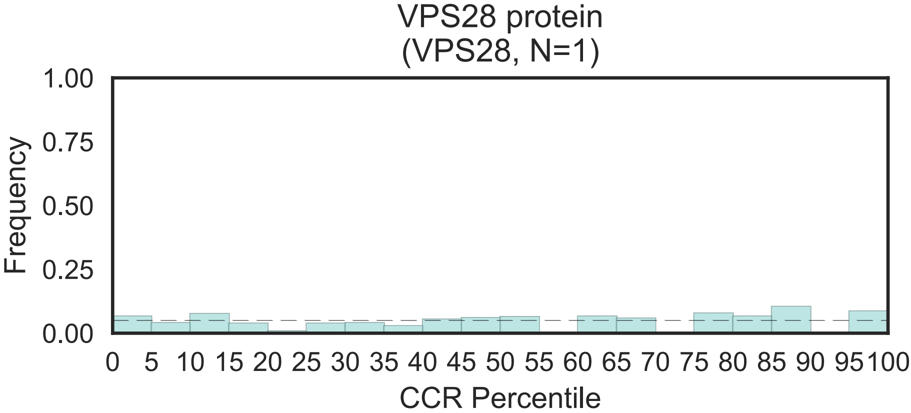

Vacuolar sorting-associated protein 13, N-terminal
(VPS13, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

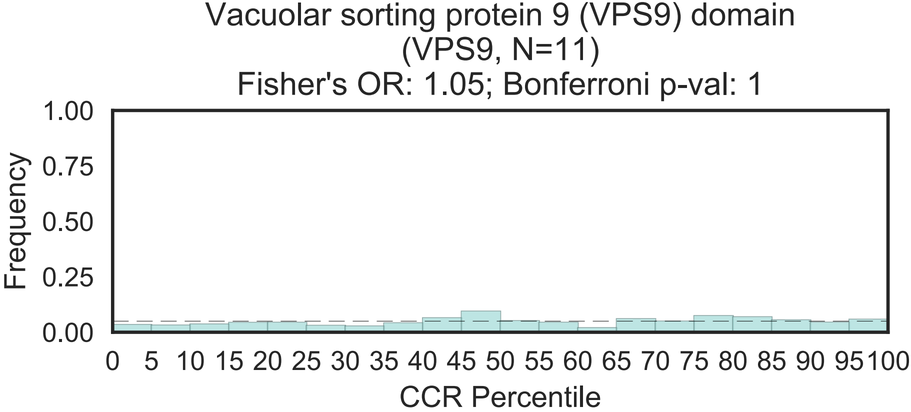


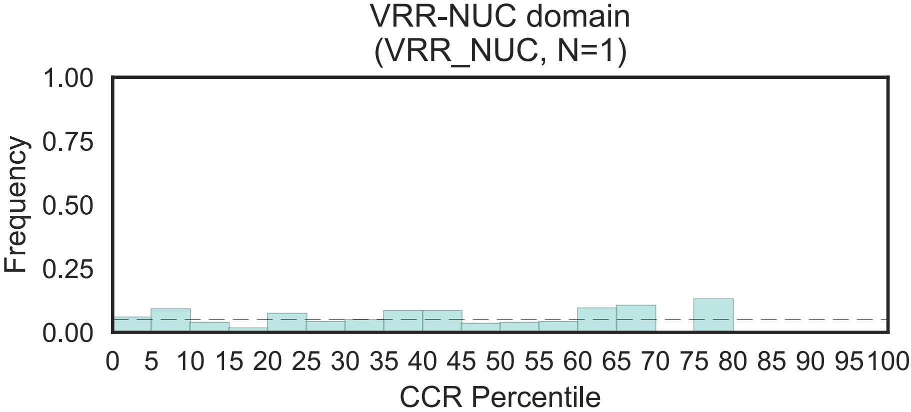
Vacuolar-sorting-associated 13 protein C-terminal
(VPS13_C, N=4)
Fisher's OR: 1.01; Bonferroni p-val: 1

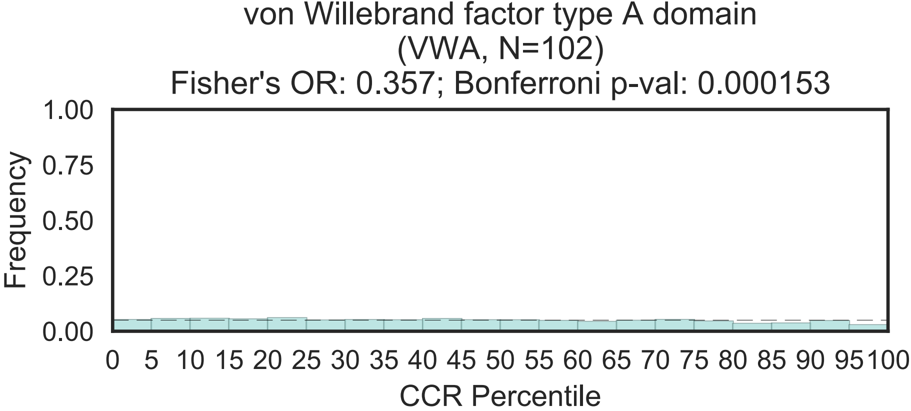


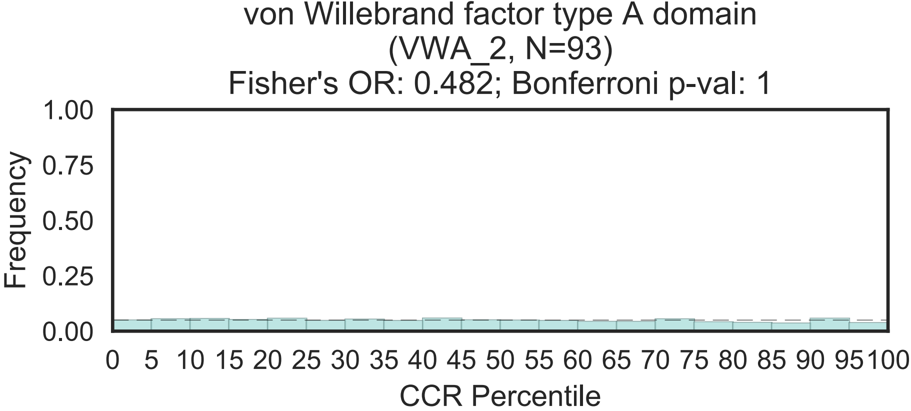
Repeating coiled region of VPS13
(VPS13_mid_rpt, N=6)
Fisher's OR: 0.236; Bonferroni p-val: 1

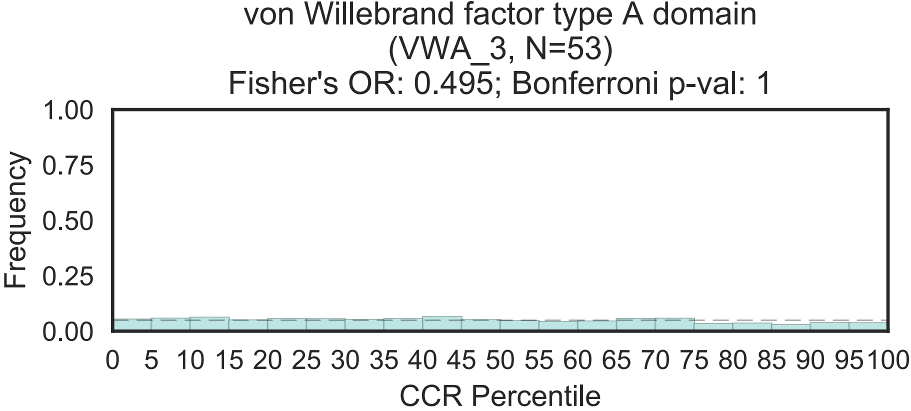

VPS28 protein
(VPS28, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

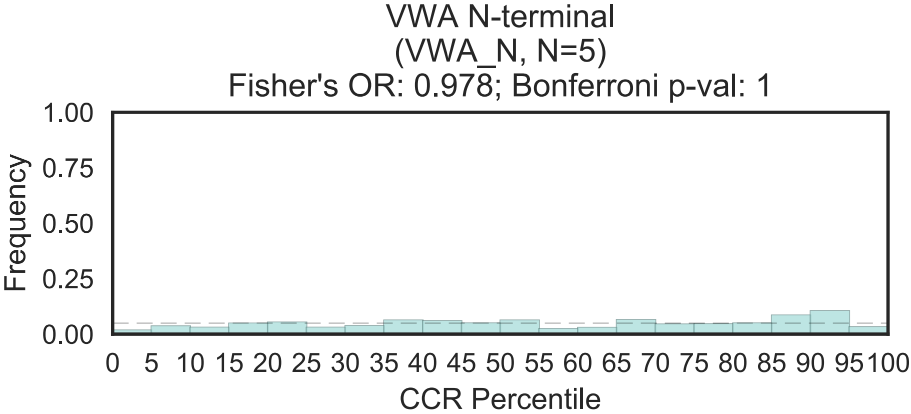

Vacuolar sorting protein 9 (VPS9) domain
(VPS9, N=11)
Fisher's OR: 1.05; Bonferroni p-val: 1

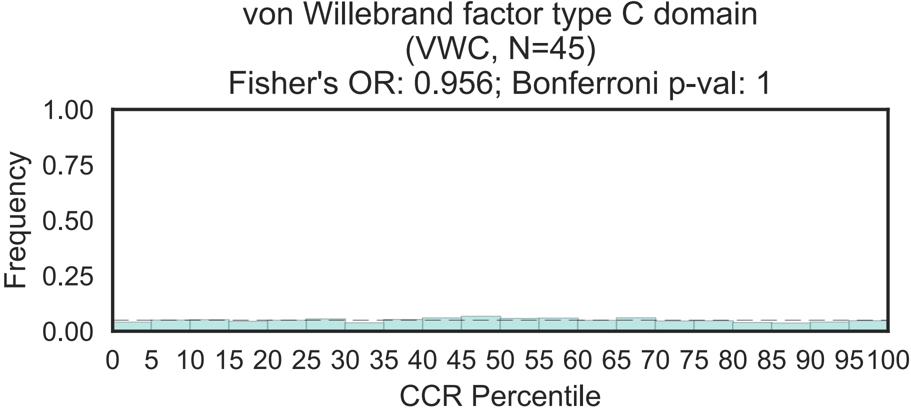

VRR-NUC domain
(VRR_NUC, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

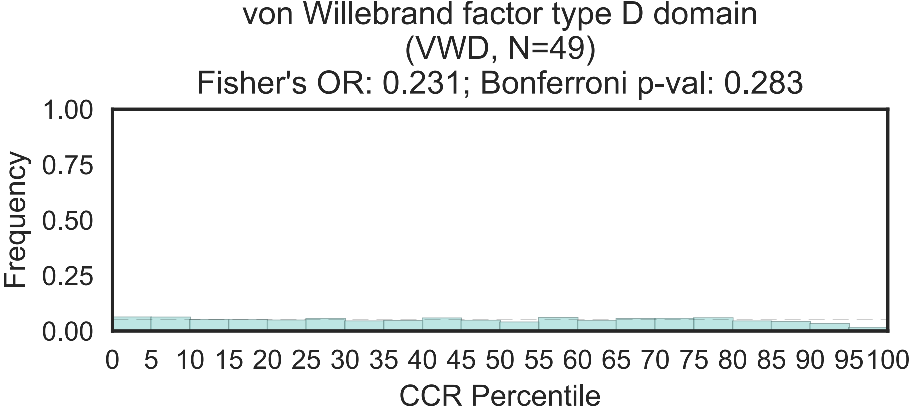

von Willebrand factor type A domain
(VWA, N=102)
Fisher's OR: 0.357; Bonferroni p-val: 0.000153
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

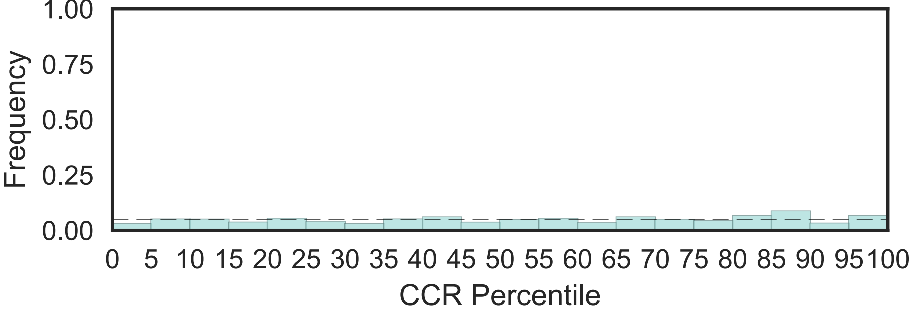

von Willebrand factor type A domain
(VWA_2, N=93)
Fisher's OR: 0.482; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


von Willebrand factor type A domain
(VWA_3, N=53)
Fisher's OR: 0.495; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

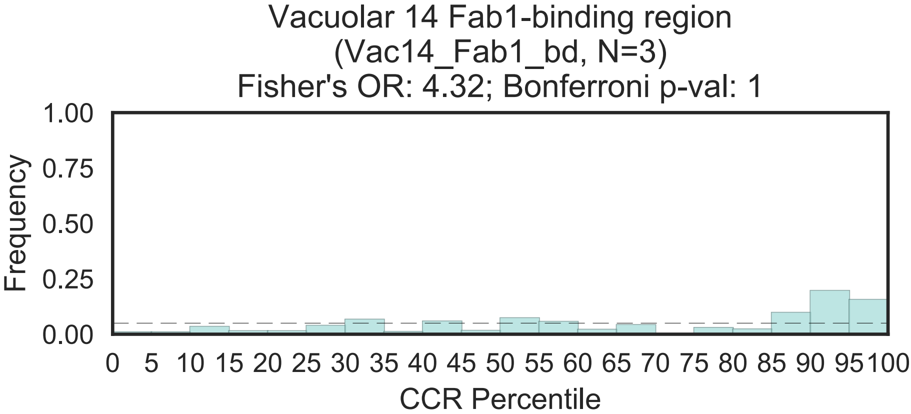

VWA N-terminal
(VWA_N, N=5)
Fisher's OR: 0.978; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

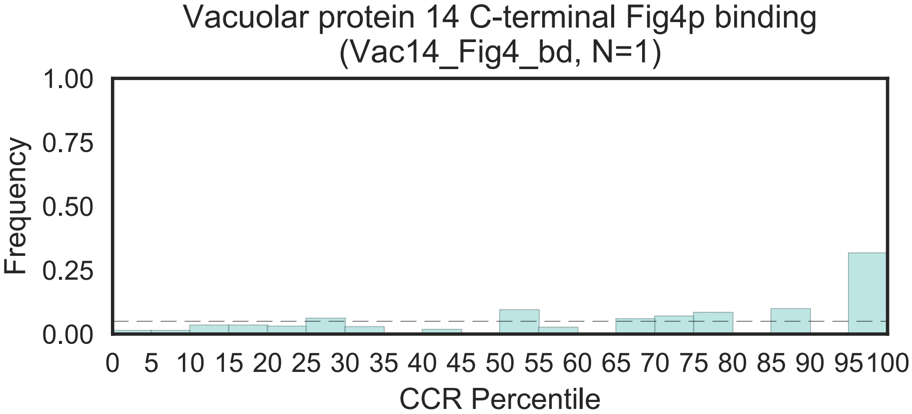

von Willebrand factor type C domain
(VWC, N=45)
Fisher's OR: 0.956; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

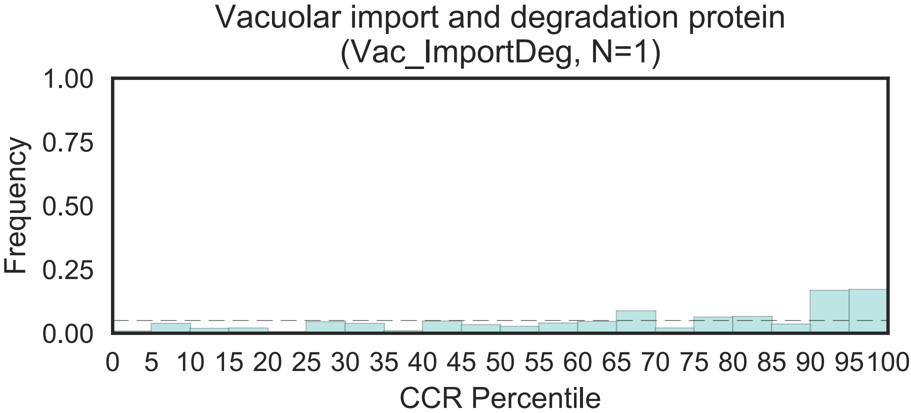

von Willebrand factor type D domain
(VWD, N=49)
Fisher's OR: 0.231; Bonferroni p-val: 0.283
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

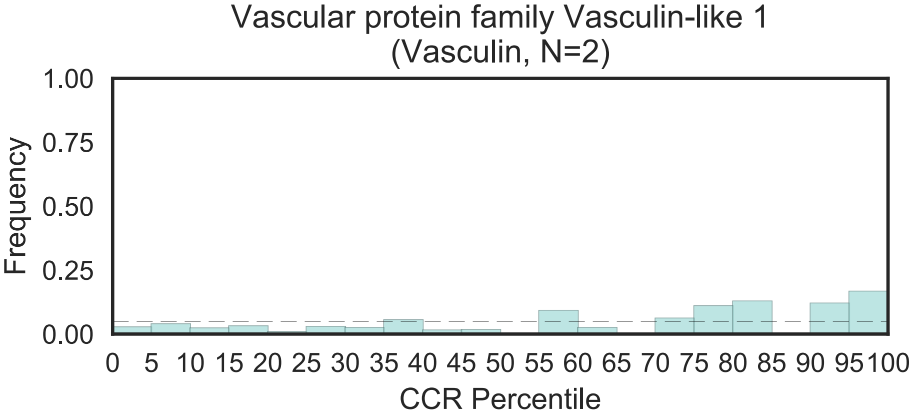


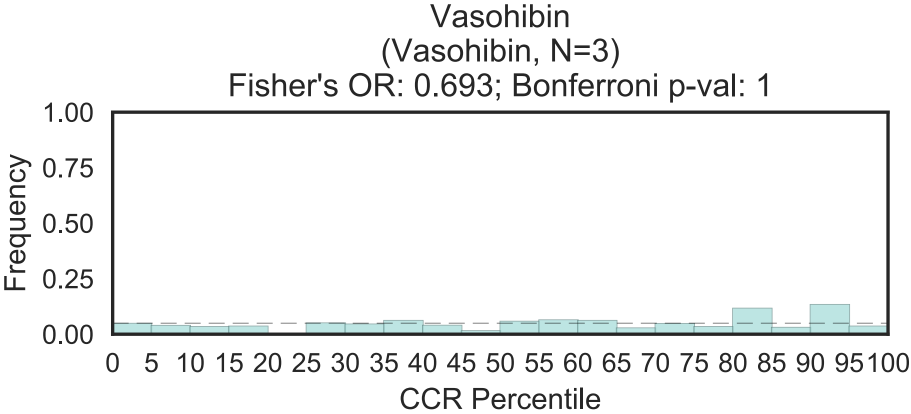
V-type ATPase 116kDa subunit family
(V_ATPase_I, N=6)
Fisher's OR: 0.743; Bonferroni p-val: 1


Vacuolar 14 Fab1-binding region
(Vac14_Fab1_bd, N=3)
Fisher's OR: 4.32; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

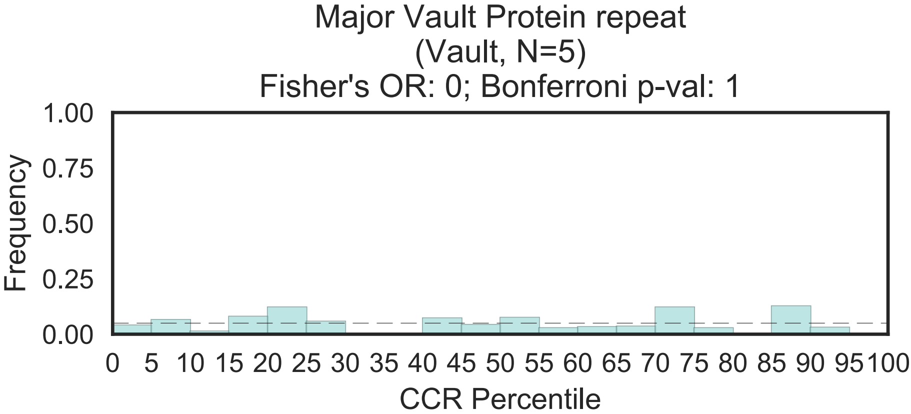

Vacuolar protein 14 C-terminal Fig4p binding
(Vac14_Fig4_bd, N=1)


Vacuolar import and degradation protein
(Vac_ImportDeg, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

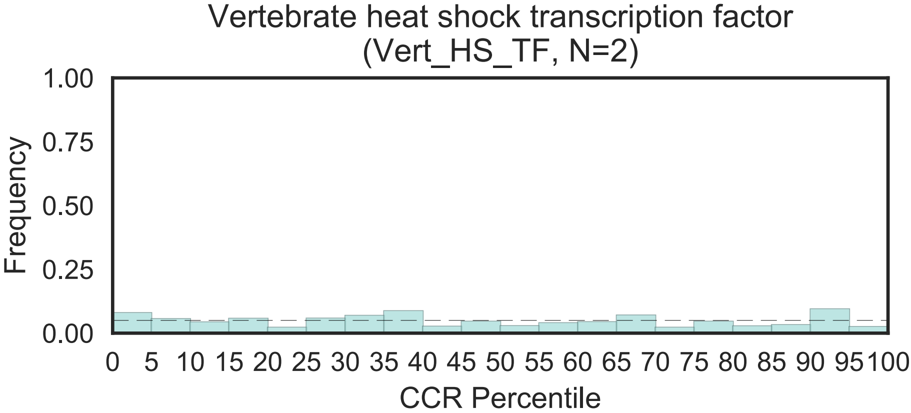

Vascular protein family Vasculin-like 1
(Vasculin, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

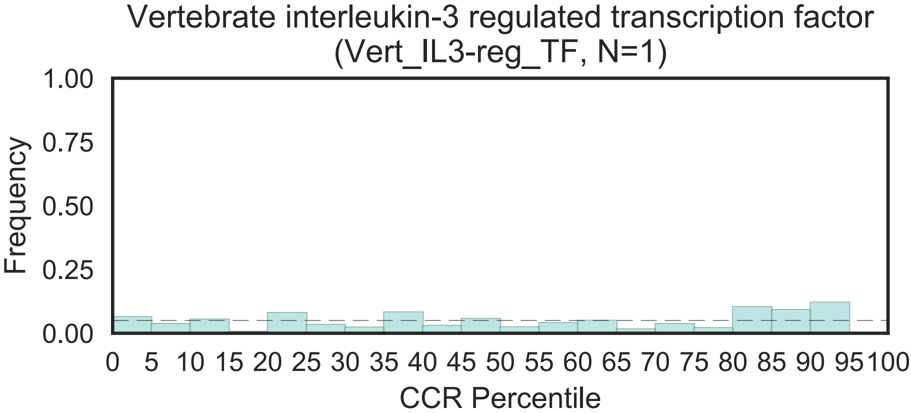


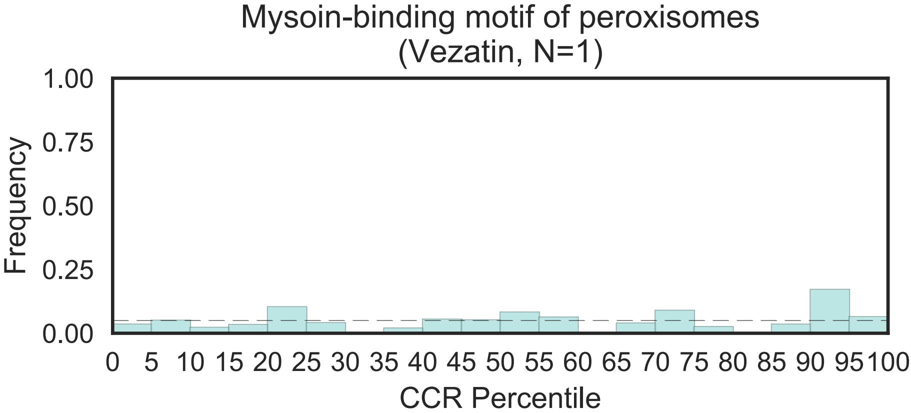
Vasohibin
(Vasohibin, N=3)
Fisher's OR: 0.693; Bonferroni p-val: 1

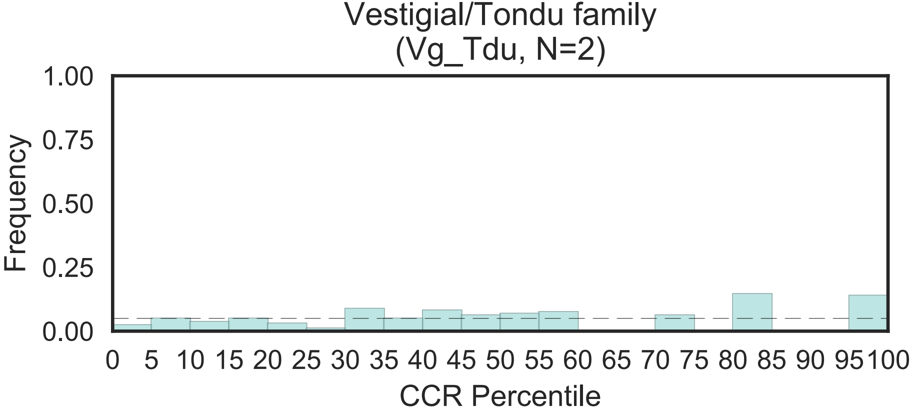


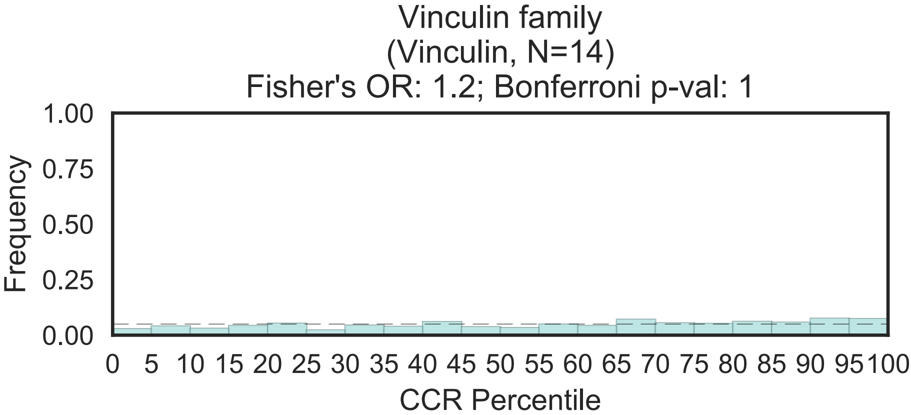
Major Vault Protein repeat
(Vault, N=5)
Fisher's OR: 0; Bonferroni p-val: 1

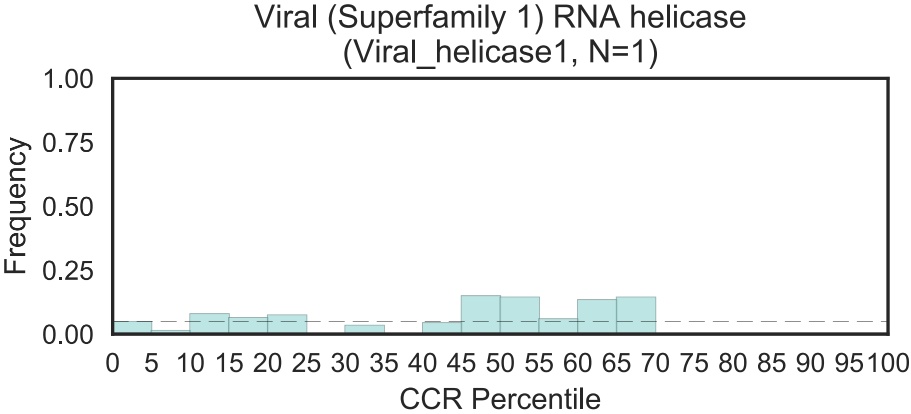

Vertebrate heat shock transcription factor
(Vert_HS_TF, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

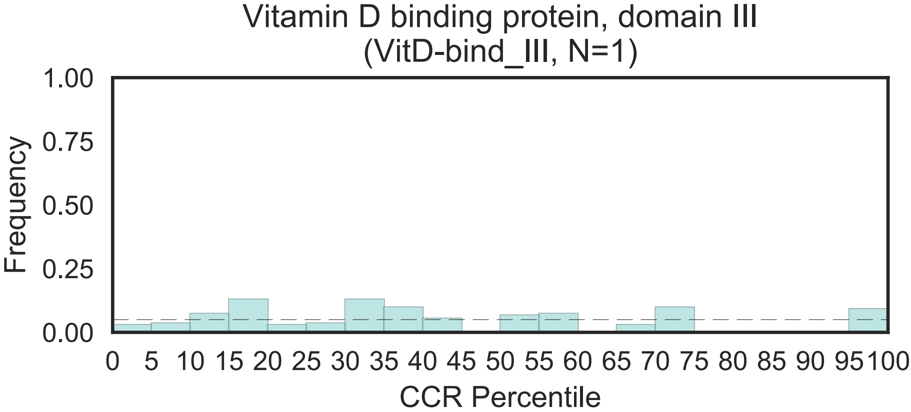

Vertebrate interleukin-3 regulated transcription factor
(Vert_IL3-reg_TF, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

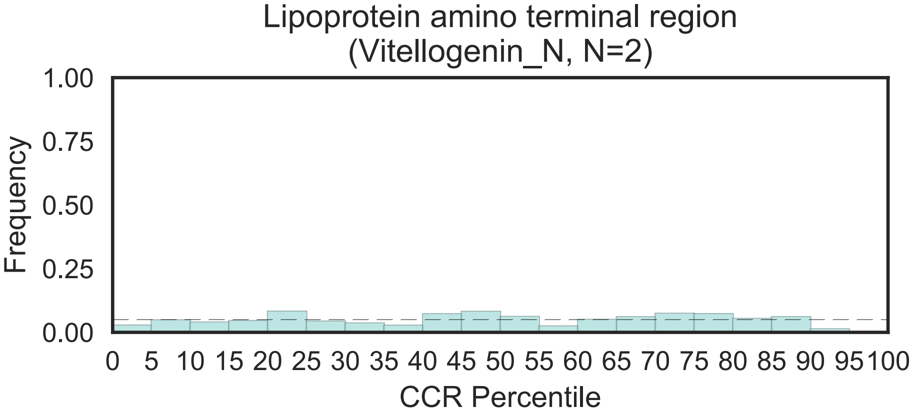

Mysoin-binding motif of peroxisomes
(Vezatin, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Vestigial/Tondu family
(Vg_Tdu, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

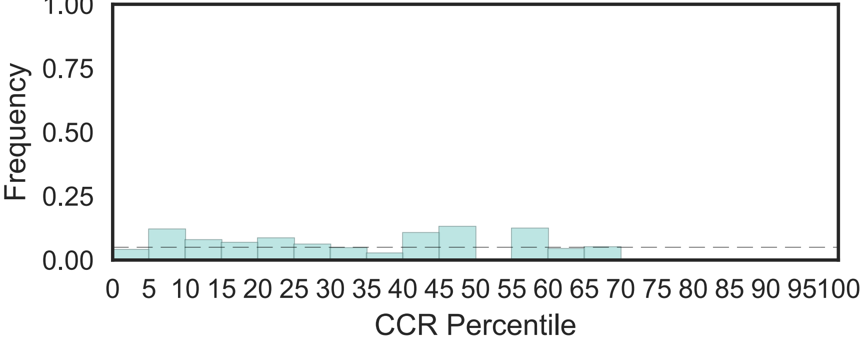

Vinculin family
(Vinculin, N=14)
Fisher's OR: 1.2; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

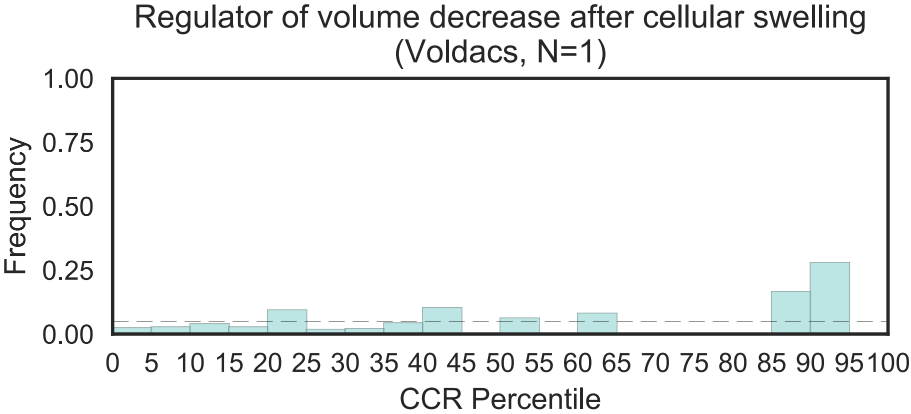

Viral (Superfamily 1) RNA helicase
(Viral_helicase1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

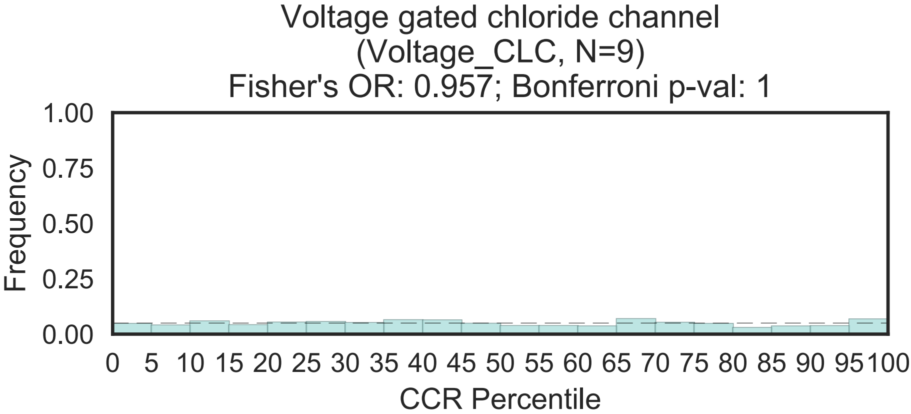

Vitamin D binding protein, domain III
(VitD-bind_III, N=1)

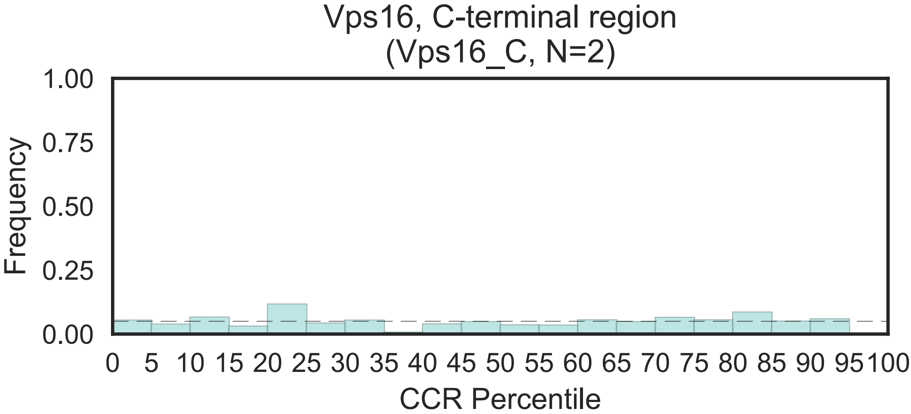

Lipoprotein amino terminal region
(Vitellogenin_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

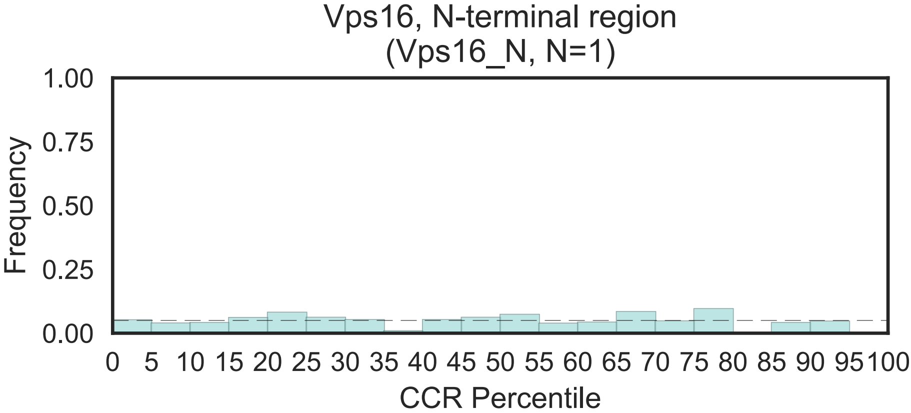
Endoplasmic reticulum-based factor for assembly of V-ATPase (Vma12, N=1)

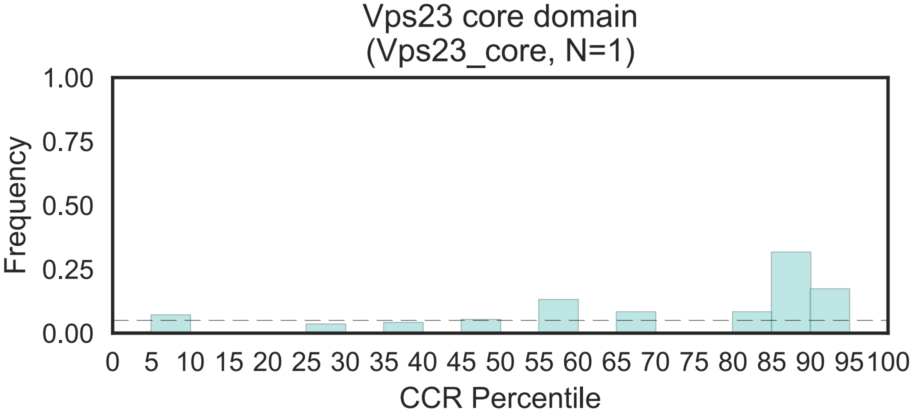


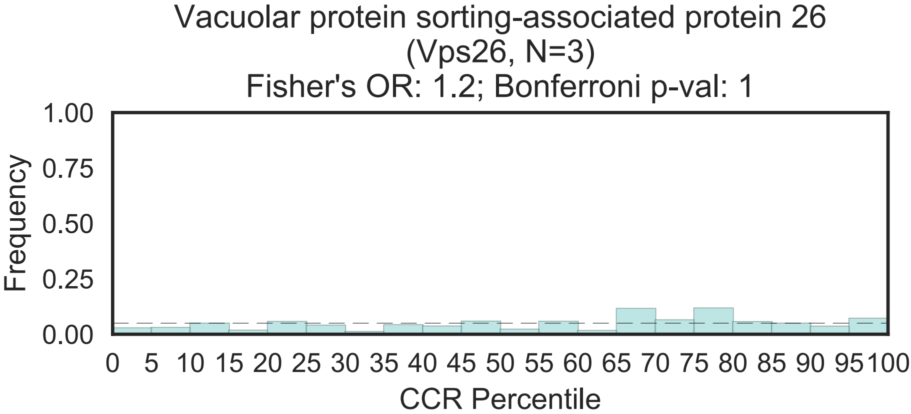

Regulator of volume decrease after cellular swelling
(Voldacs, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

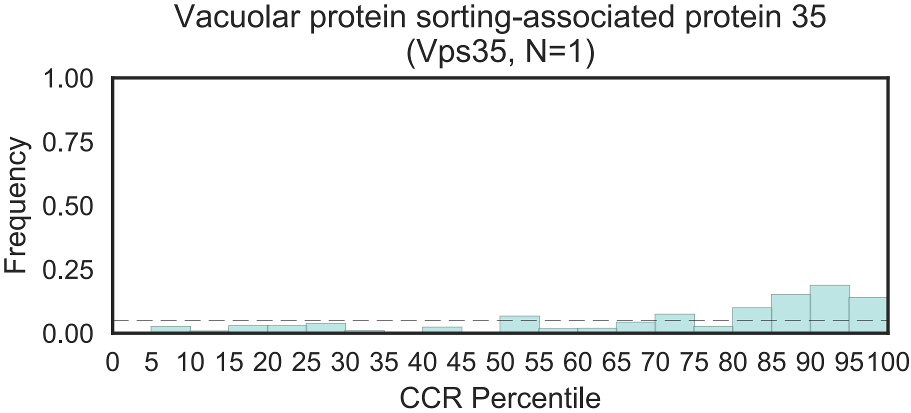

Voltage gated chloride channel
(Voltage_CLC, N=9)
Fisher's OR: 0.957; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Vps16, C-terminal region
(Vps16_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

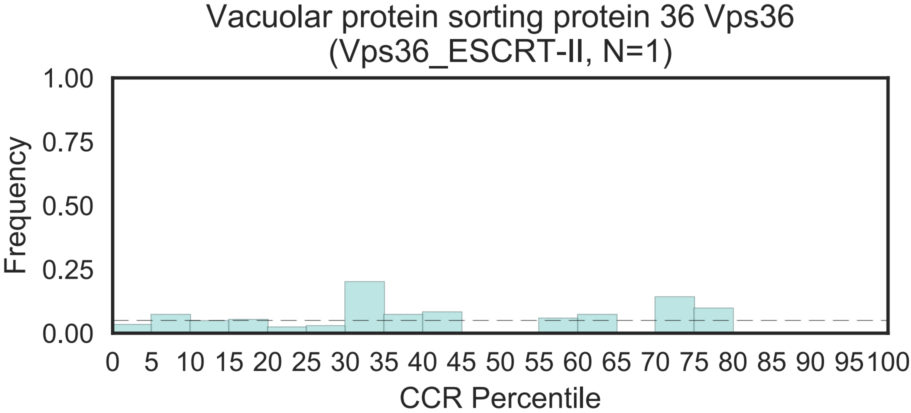

Vps16, N-terminal region
(Vps16_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

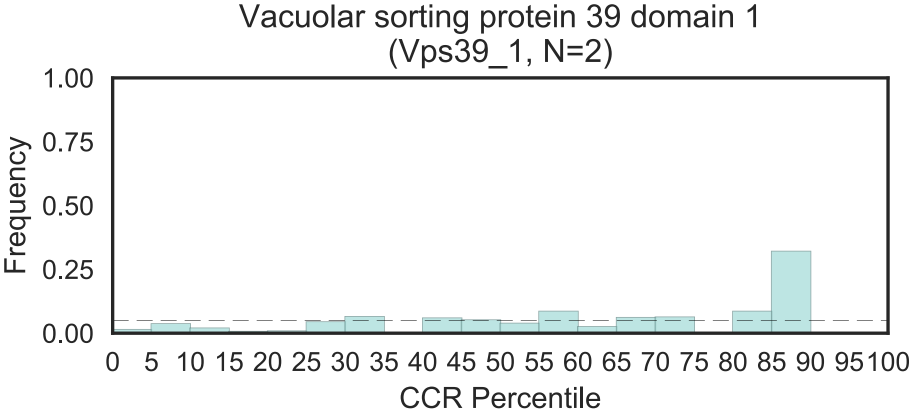

Vps23 core domain
(Vps23_core, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

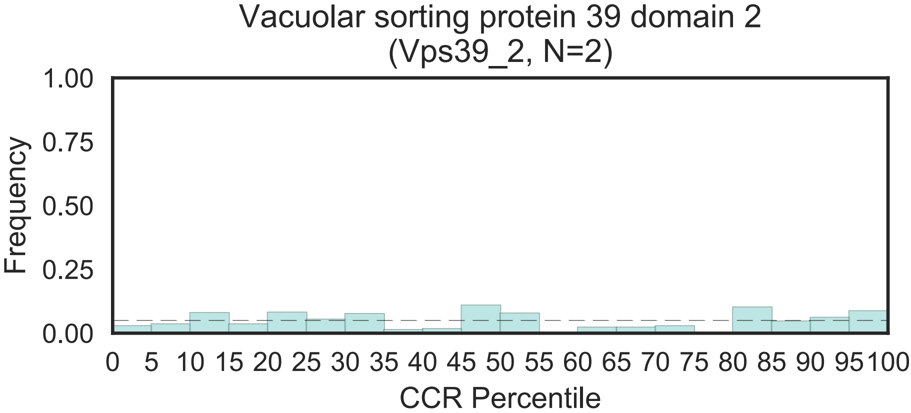

Vacuolar protein sorting-associated protein 26
(Vps26, N=3)
Fisher's OR: 1.2; Bonferroni p-val: 1

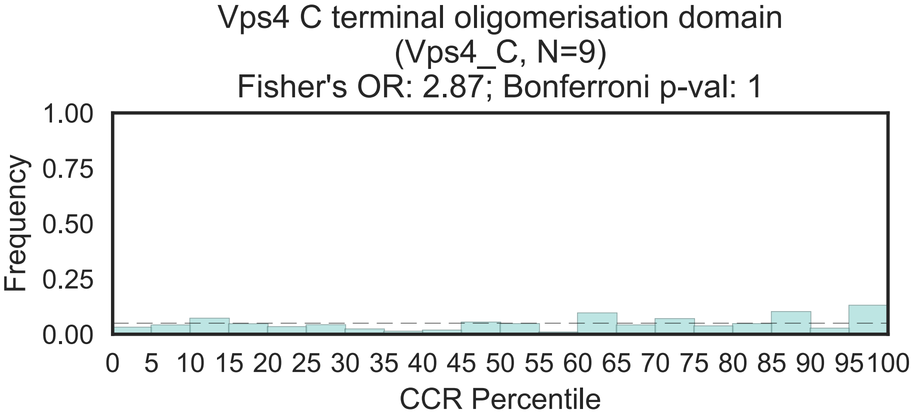


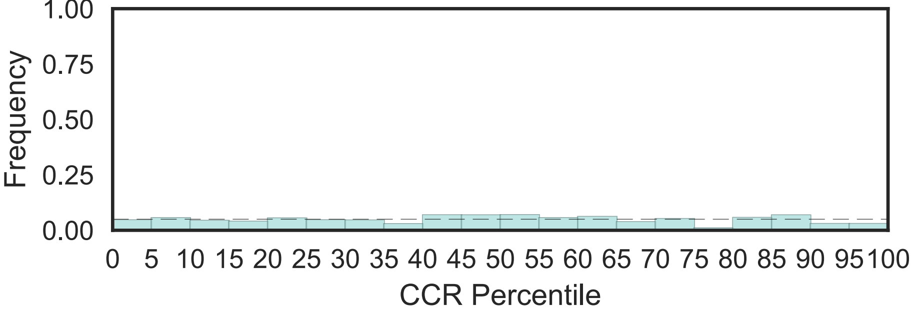
Vacuolar protein sorting-associated protein 35 (Vps35, N=1)

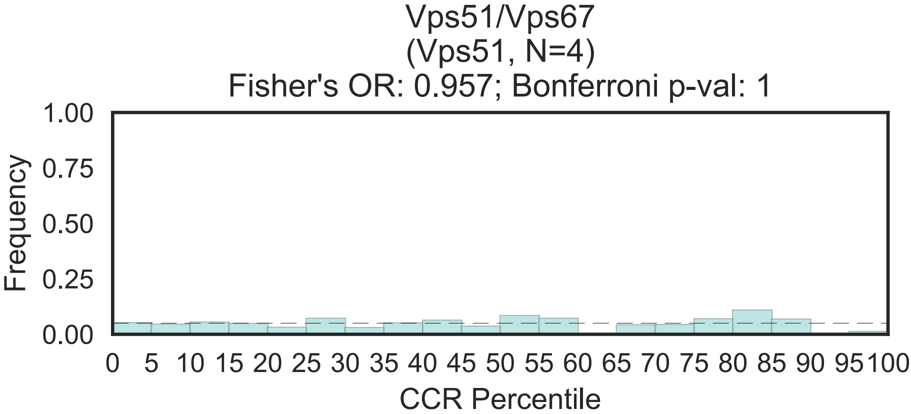

Vacuolar protein sorting protein 36 Vps36
(Vps36_ESCRT-II, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

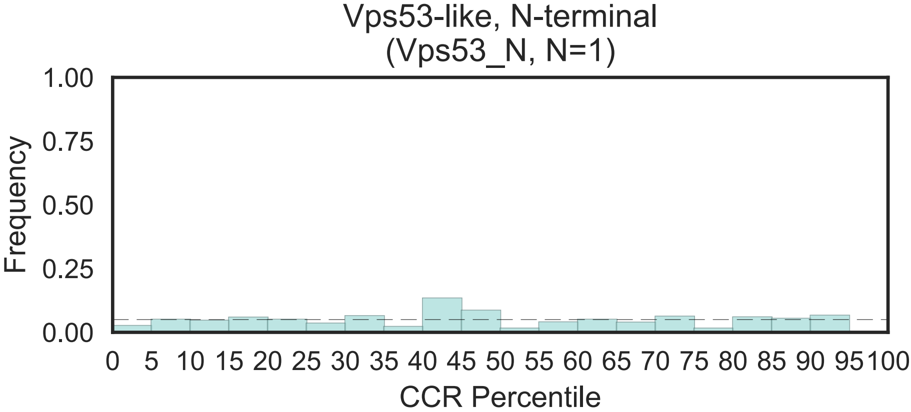

Vacuolar sorting protein 39 domain 1
(Vps39_1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

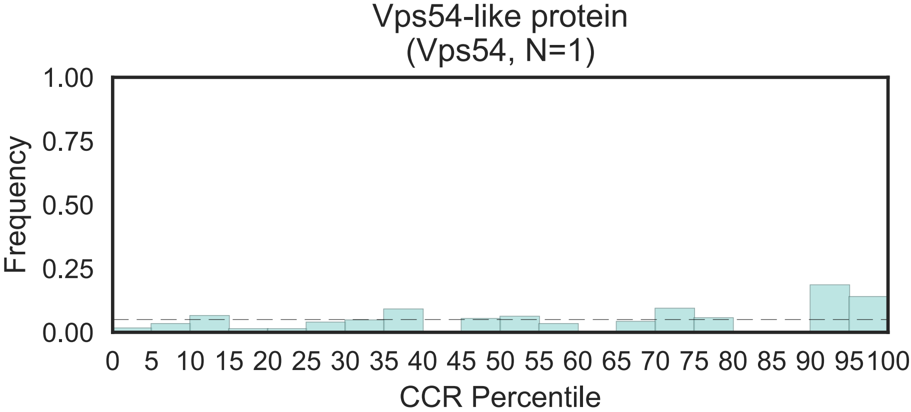

Vacuolar sorting protein 39 domain 2
(Vps39_2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

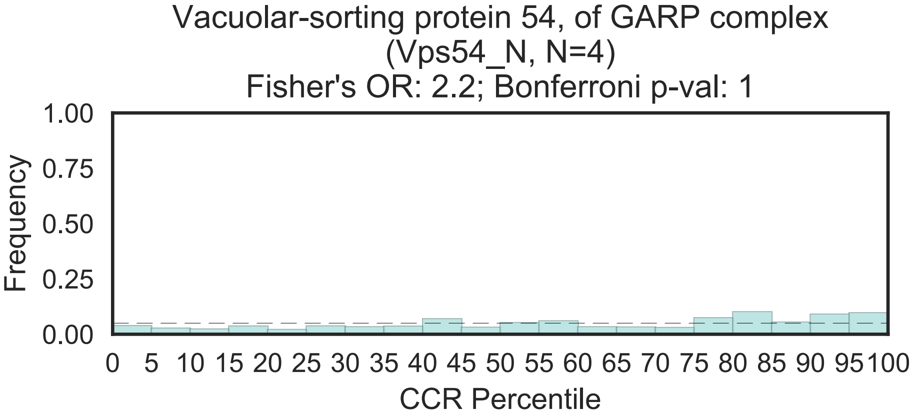

Vps4 C terminal oligomerisation domain
(Vps4_C, N=9)
Fisher's OR: 2.87; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Vps5 C terminal like
(Vps5, N=6)
Fisher's OR: 0.434; Bonferroni p-val: 1

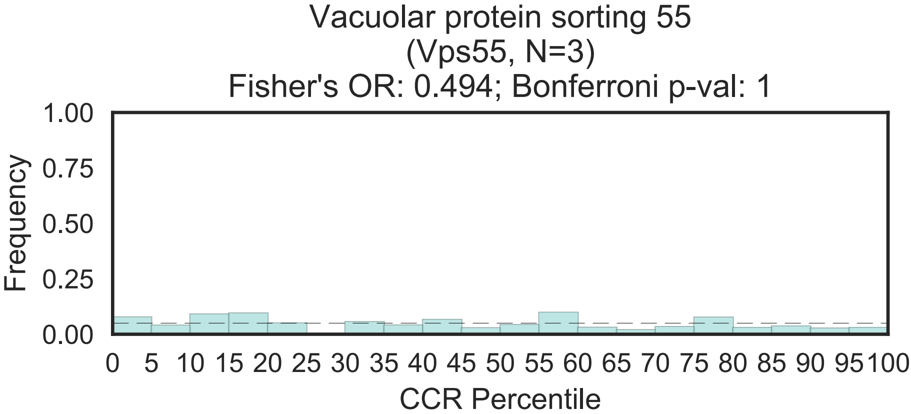

Vps51/Vps67
(Vps51, N=4)
Fisher's OR: 0.957; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

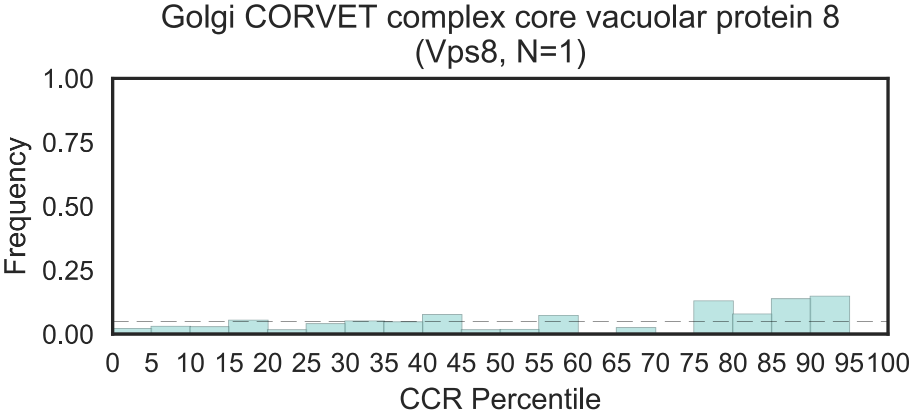

Vps53-like, N-terminal
(Vps53_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

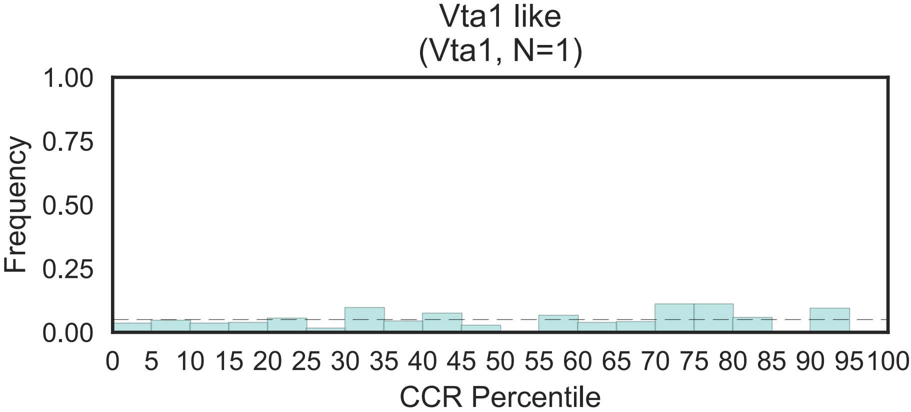

Vps54-like protein
(Vps54, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

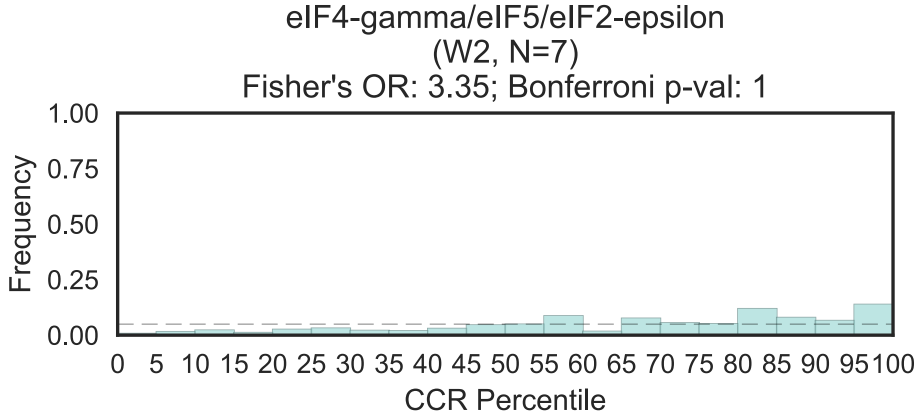


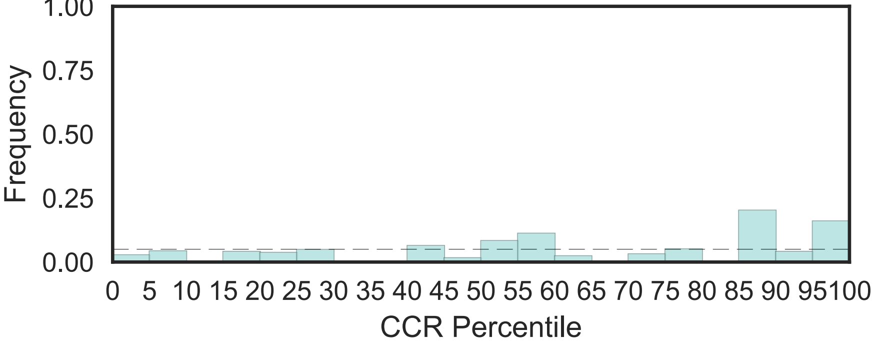
Vacuolar-sorting protein 54, of GARP complex
(Vps54_N, N=4)
Fisher's OR: 2.2; Bonferroni p-val: 1

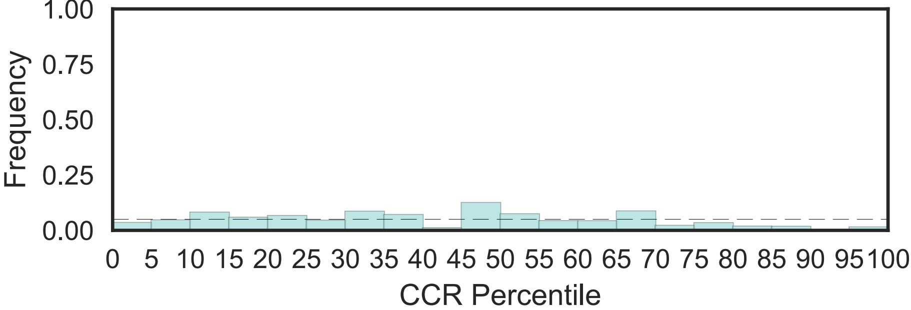

Vacuolar protein sorting 55
(Vps55, N=3)
Fisher's OR: 0.494; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Golgi CORVET complex core vacuolar protein 8
(Vps8, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

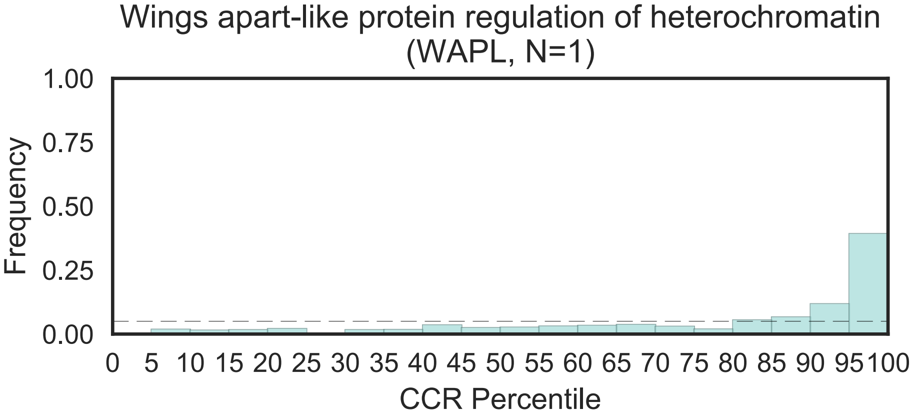

Vta1 like
(Vta1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

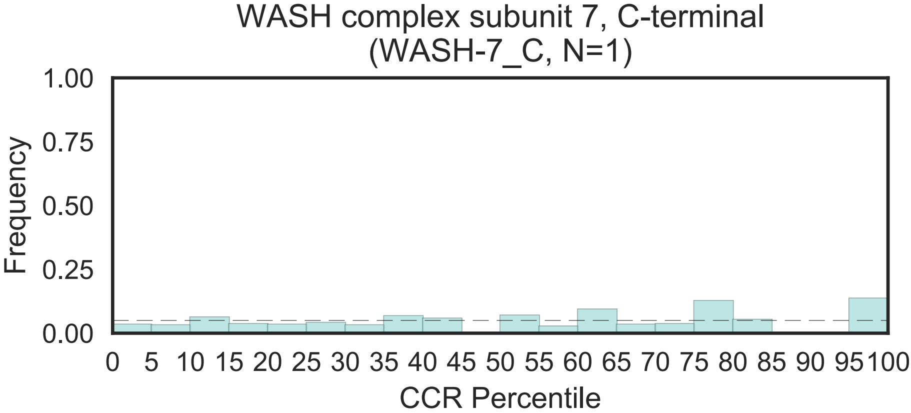

eIF4-gamma/eIF5/eIF2-epsilon
(W2, N=7)
Fisher's OR: 3.35; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

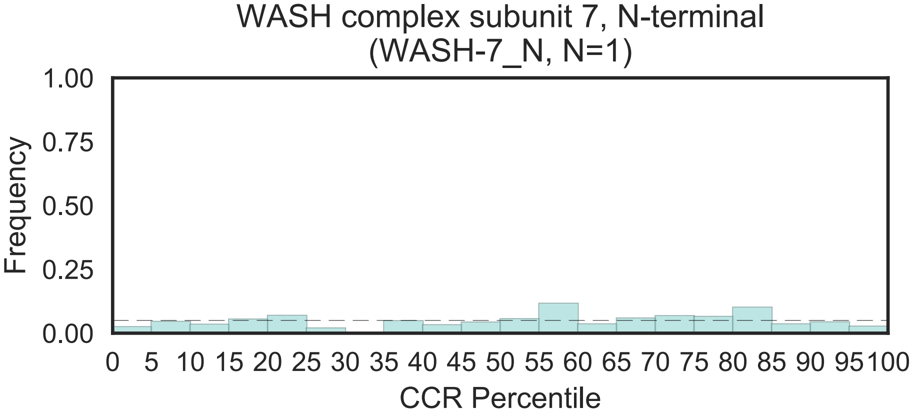

ATP-utilising chromatin assembly and remodelling N-terminal
(WAC_Acf1_DNA_bd, N=2)

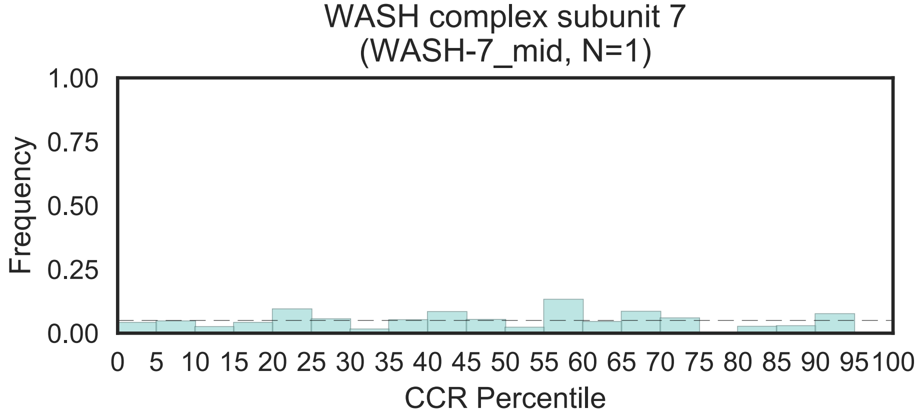


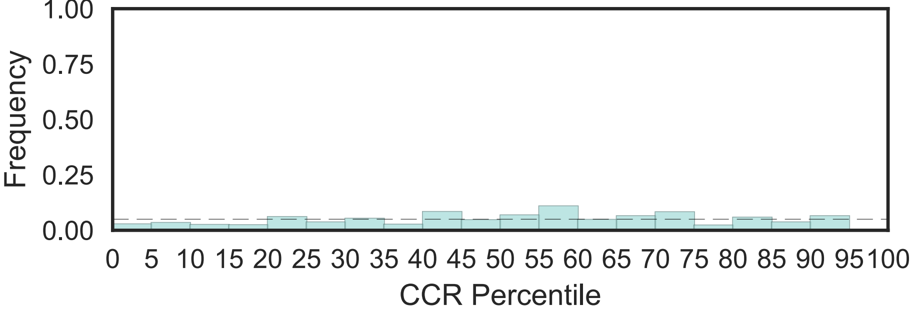
WAP-type (Whey Acidic Protein) 'four-disulfide core'
(WAP, N=25)
Fisher's OR: 0.251; Bonferroni p-val: 1


Wings apart-like protein regulation of heterochromatin
(WAPL, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


WASH complex subunit 7, C-terminal
(WASH-7_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

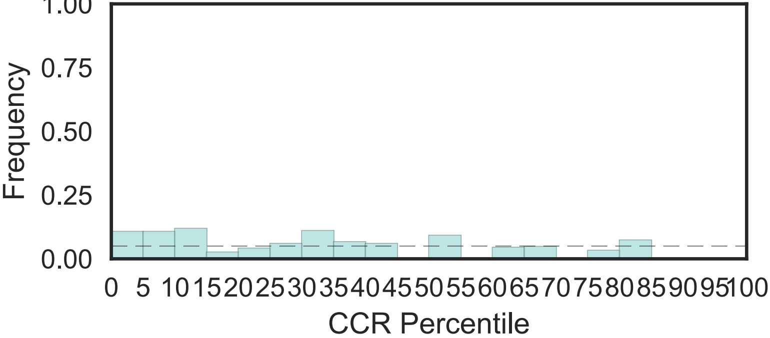

WASH complex subunit 7, N-terminal
(WASH-7_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

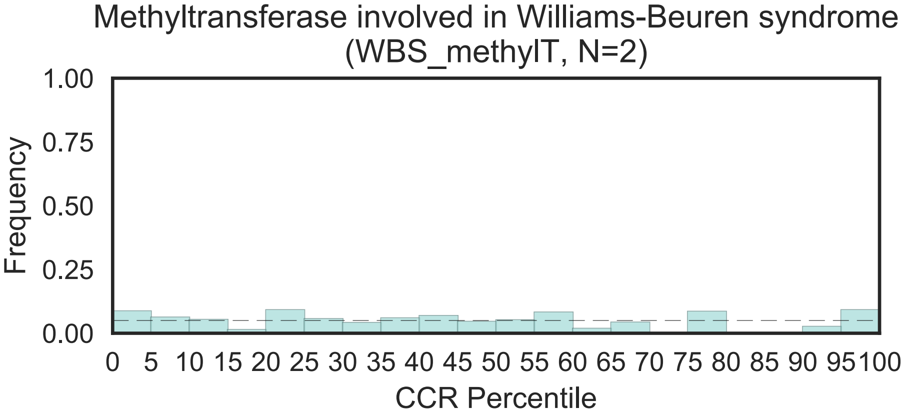

WASH complex subunit 7
(WASH-7_mid, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

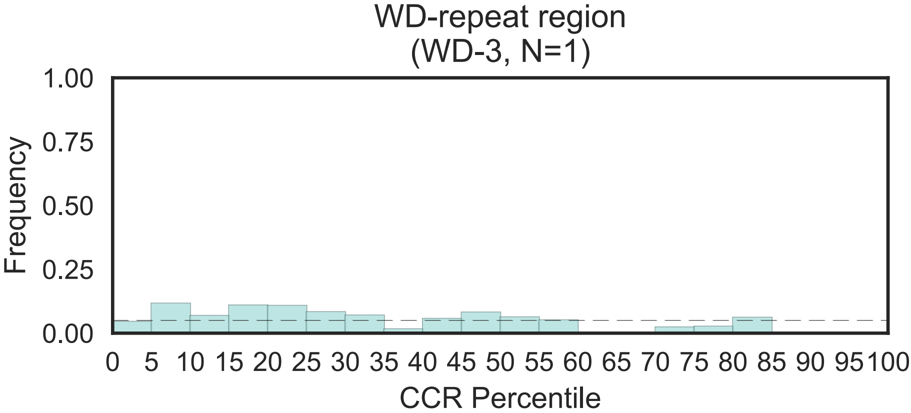


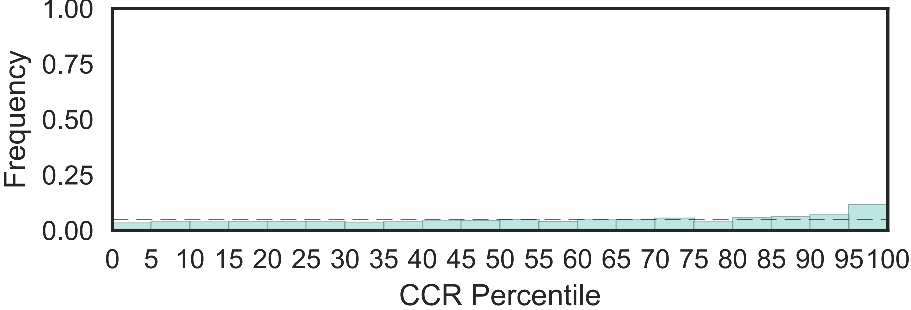
WW domain-binding protein 1
(WBP-1, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

Williams-Beuren syndrome chromosomal region 28 protein homologue (WBS28, N=1)

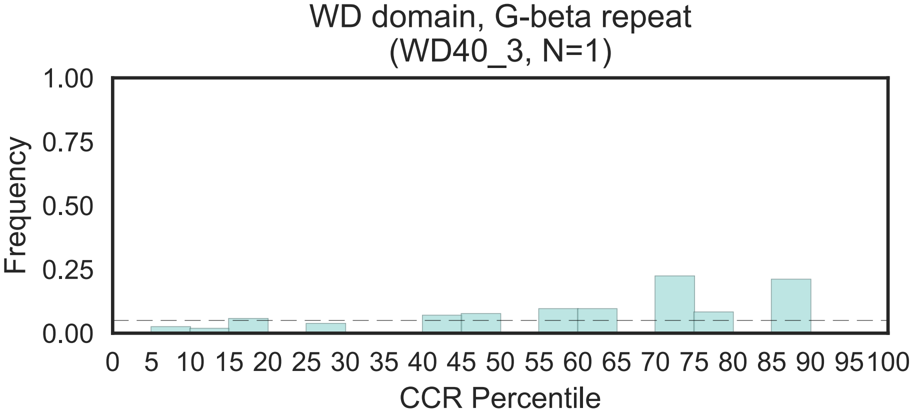


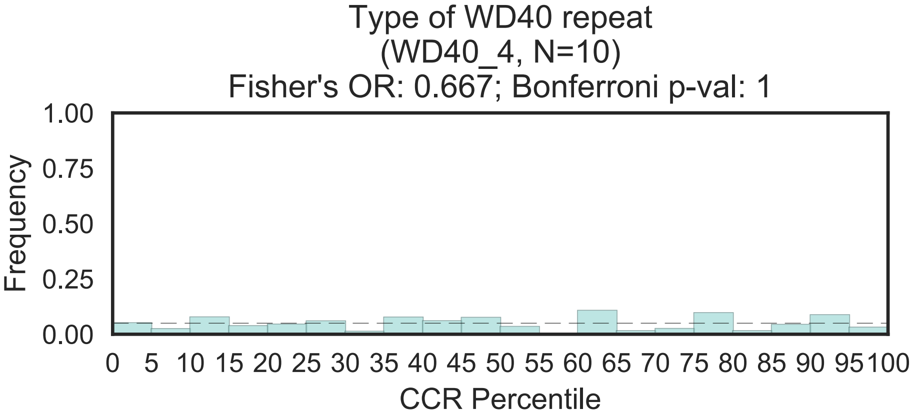

Methyltransferase involved in Williams-Beuren syndrome
(WBS_methylT, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


WD-repeat region
(WD-3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

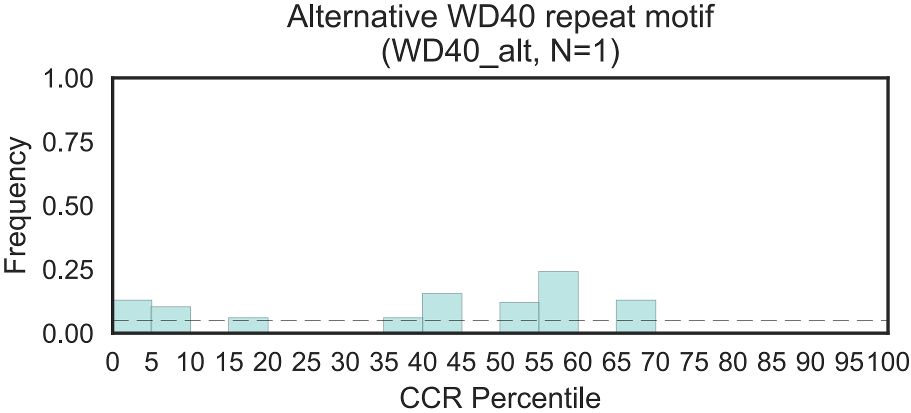


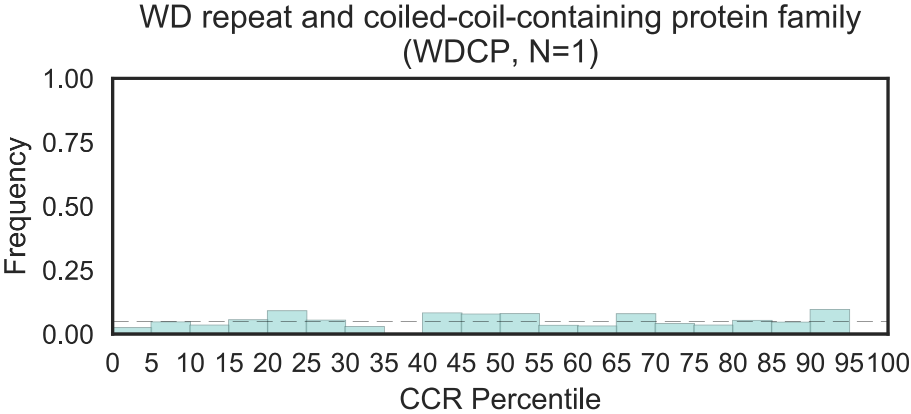
WD domain, G-beta repeat
(WD40, N=770)
Fisher's OR: 2.29; Bonferroni p-val: 6.71e-20

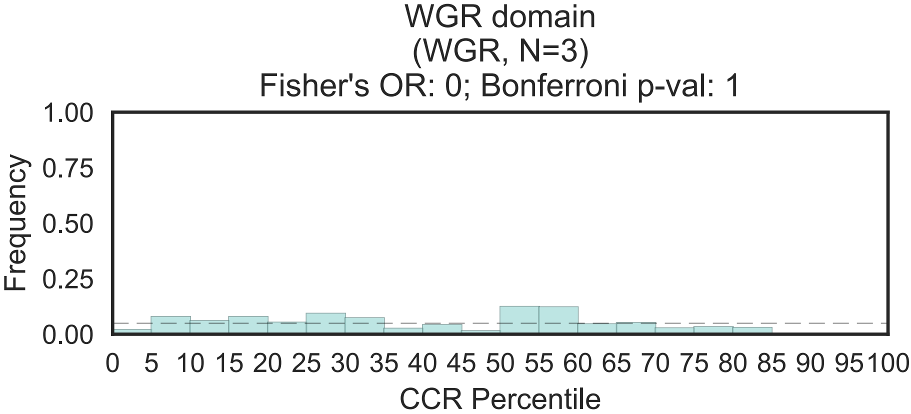

WD domain, G-beta repeat
(WD40_3, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

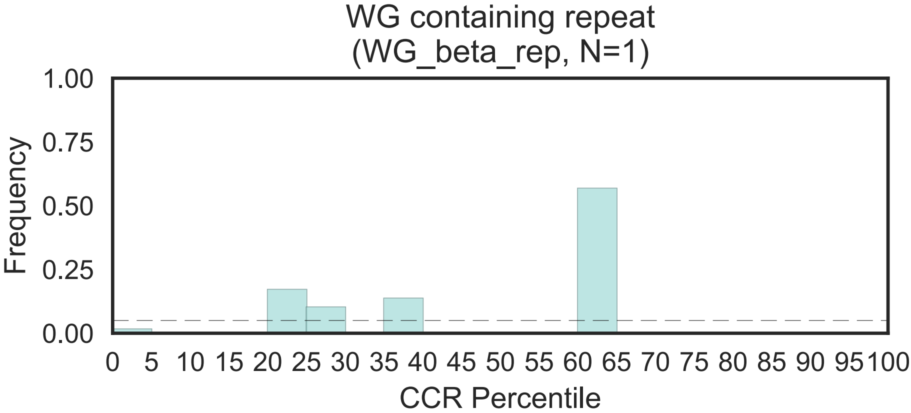


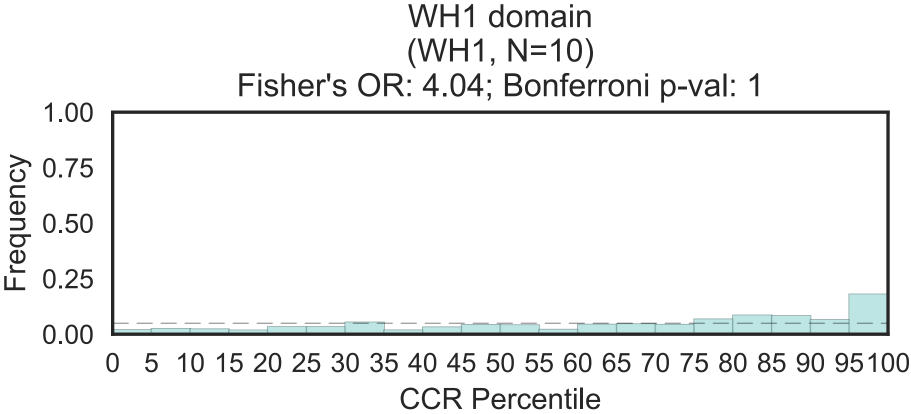
Type of WD40 repeat
(WD40_4, N=10)
Fisher's OR: 0.667; Bonferroni p-val: 1

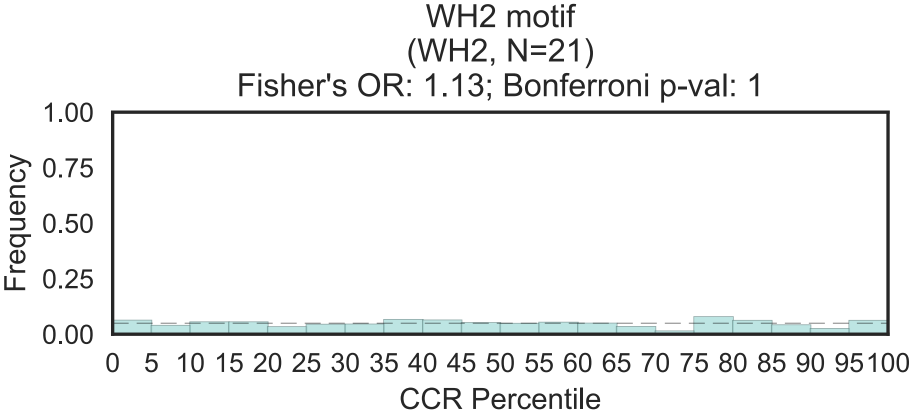

Alternative WD40 repeat motif
(WD40_alt, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

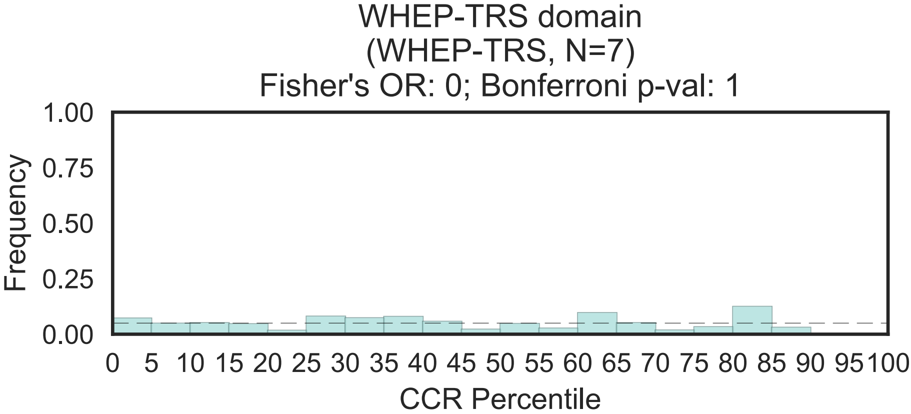

WD repeat and coiled-coil-containing protein family
(WDCP, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

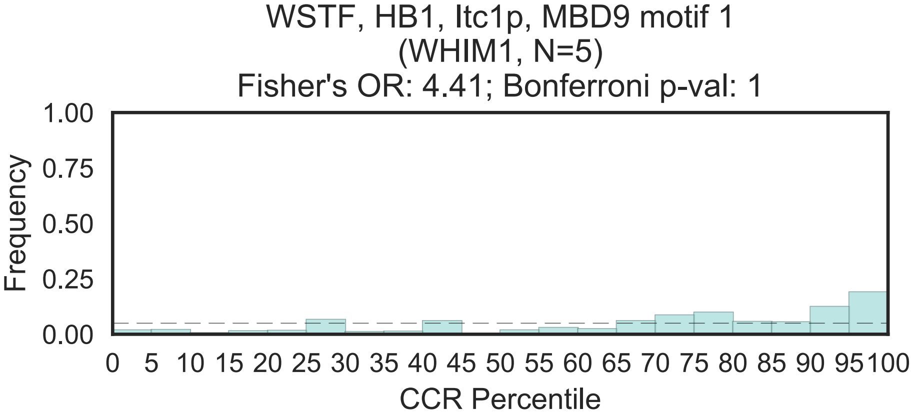

WGR domain
(WGR, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

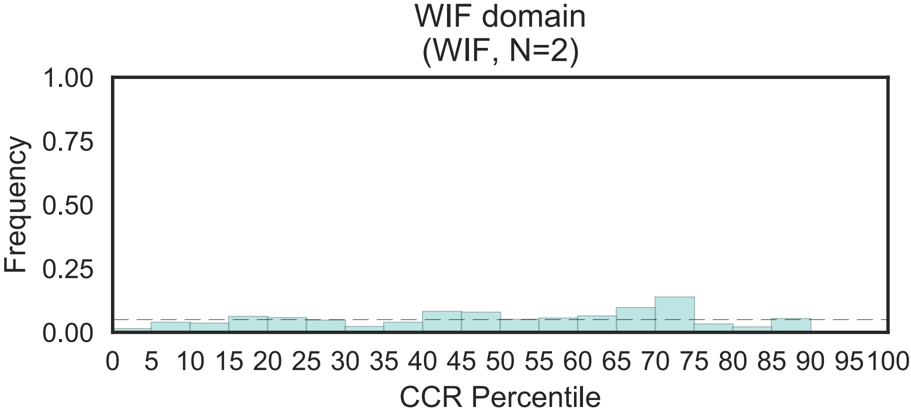

WG containing repeat
(WG_beta_rep, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

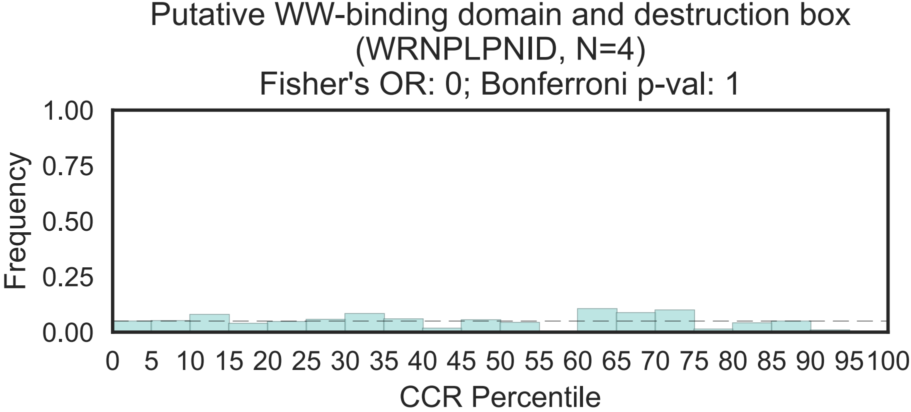

WH1 domain
(WH1, N=10)
Fisher's OR: 4.04; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


WH2 motif
(WH2, N=21)
Fisher's OR: 1.13; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

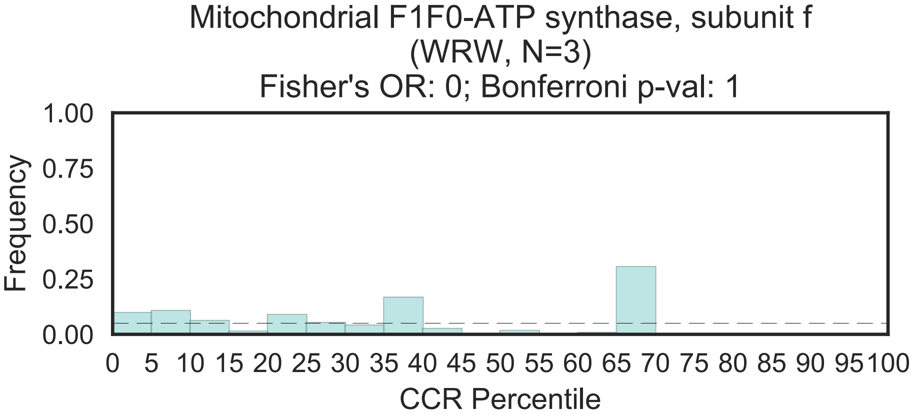

WHEP-TRS domain
(WHEP-TRS, N=7)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

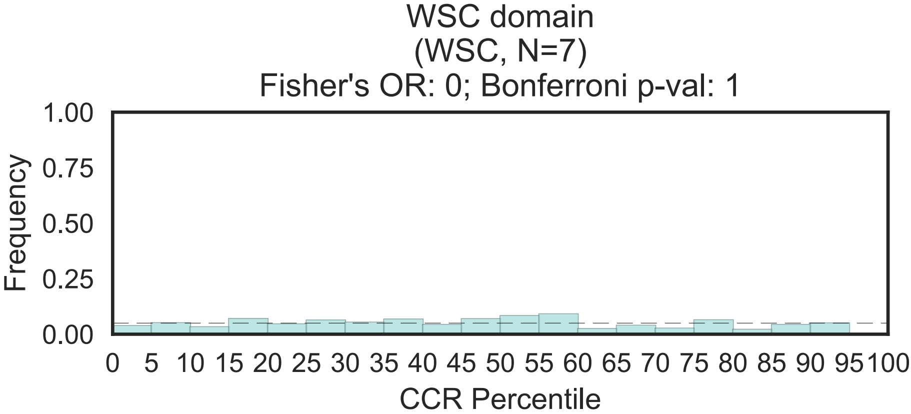

WSTF, HB1, Itc1p, MBD9 motif 1
(WHIM1, N=5)
Fisher's OR: 4.41; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

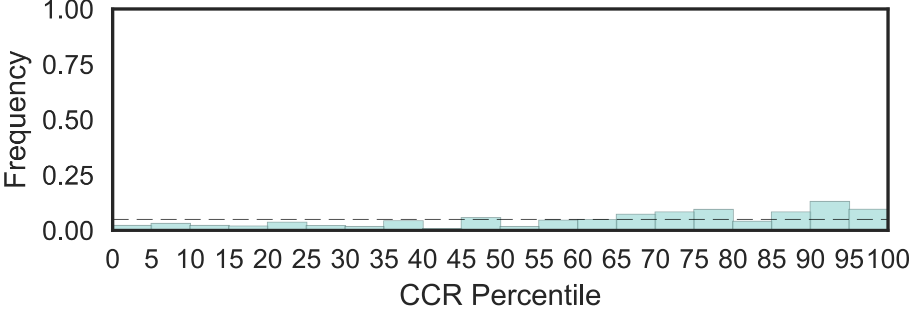

WIF domain
(WIF, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

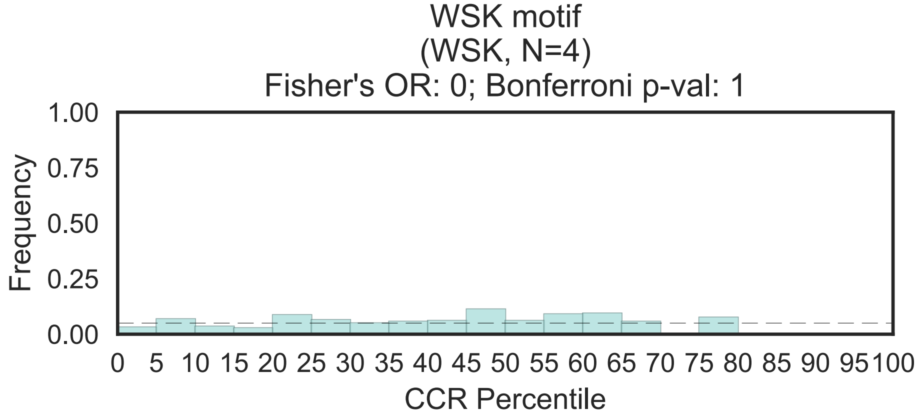


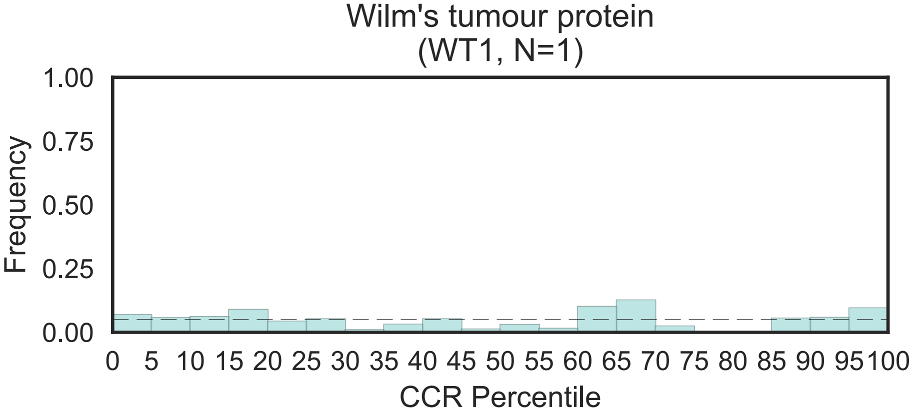
Putative WW-binding domain and destruction box
(WRNPLPNID, N=4)
Fisher's OR: 0; Bonferroni p-val: 1

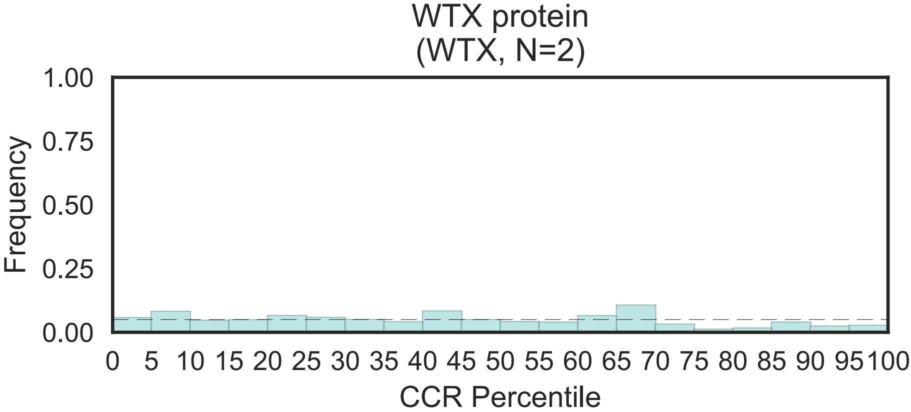

Mitochondrial F1F0-ATP synthase, subunit f
(WRW, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

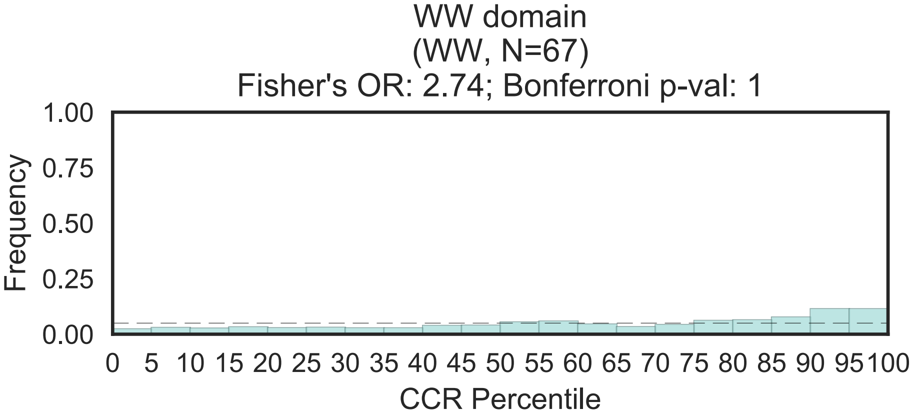

WSC domain
(WSC, N=7)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

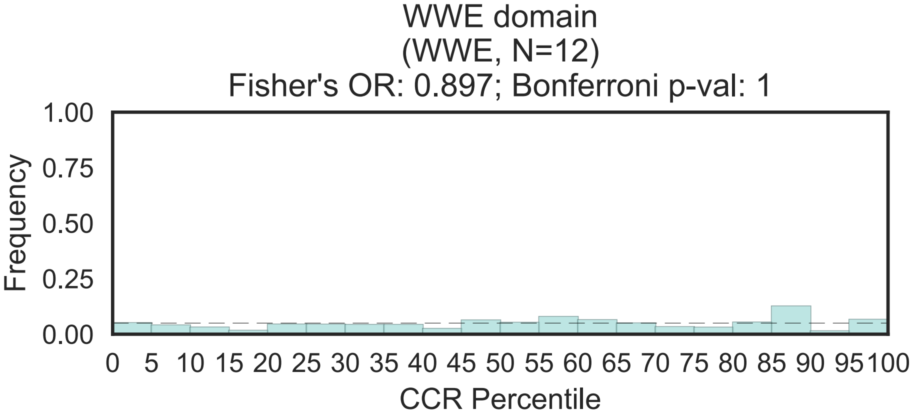

Williams-Beuren syndrome DDT (WSD), D-TOX E motif (WSD, N=6)
Fisher's OR: 2.68; Bonferroni p-val: 1

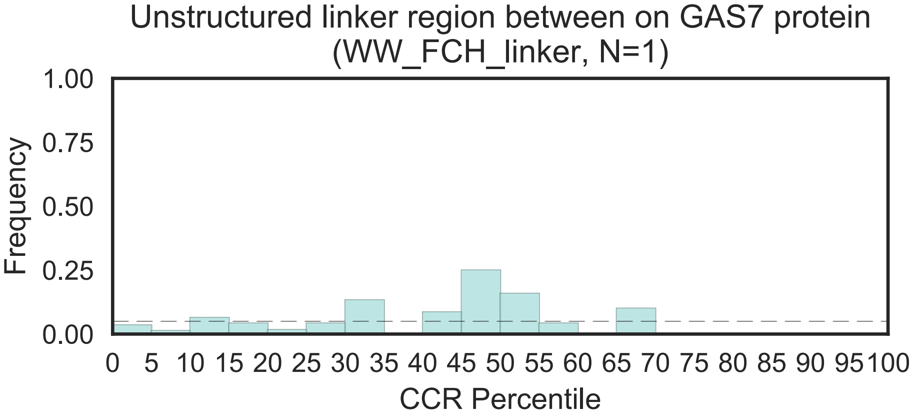

WSK motif
(WSK, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

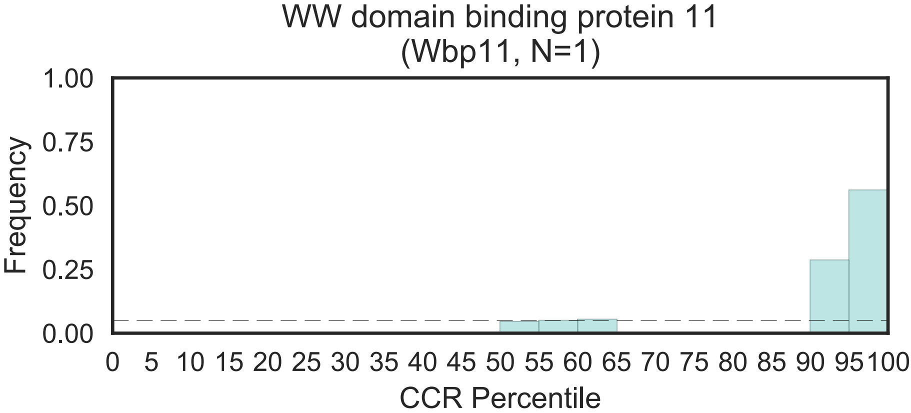

Wilm's tumour protein
(WT1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

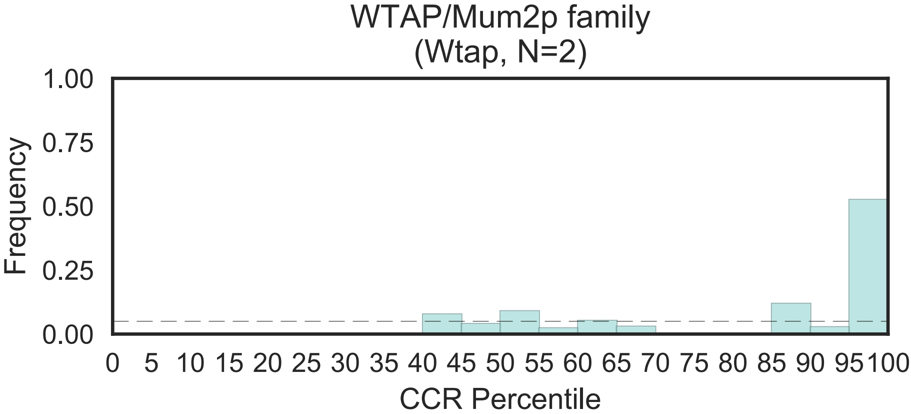

WTX protein
(WTX, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


WW domain
(WW, N=67)
Fisher's OR: 2.74; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

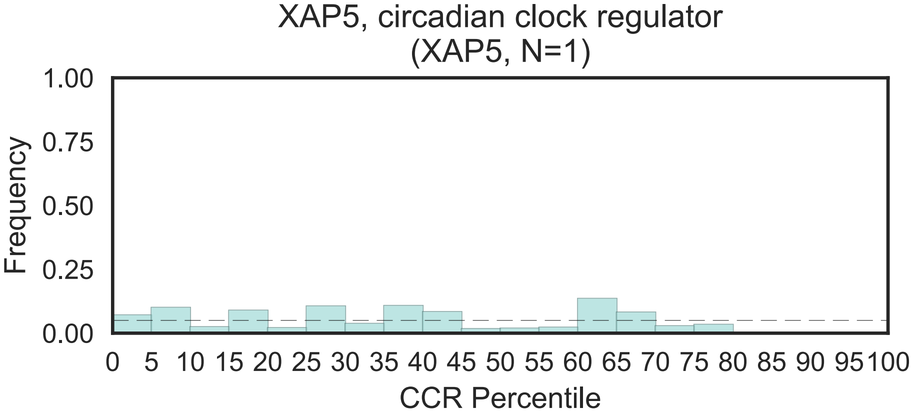

WWE domain
(WWE, N=12)
Fisher's OR: 0.897; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

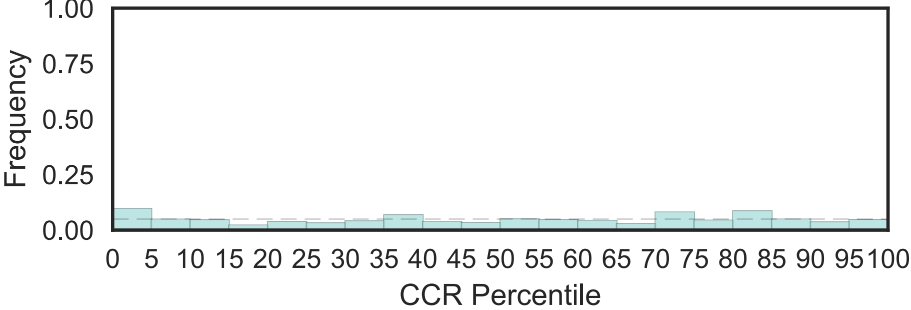

Unstructured linker region between on GAS7 protein
(WW_FCH_linker, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


WW domain binding protein 11
(Wbp11, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

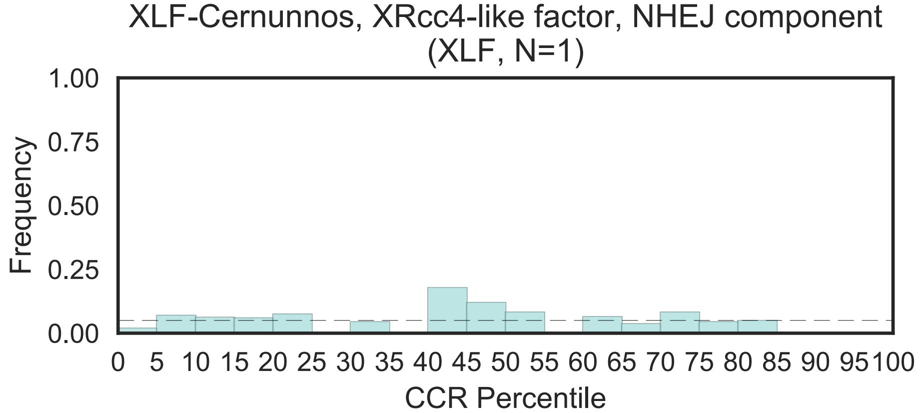


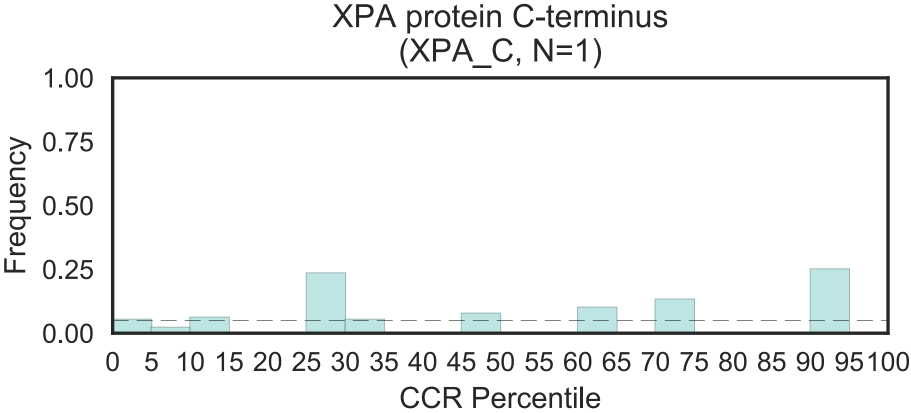
WTAP/Mum2p family
(Wtap, N=2)

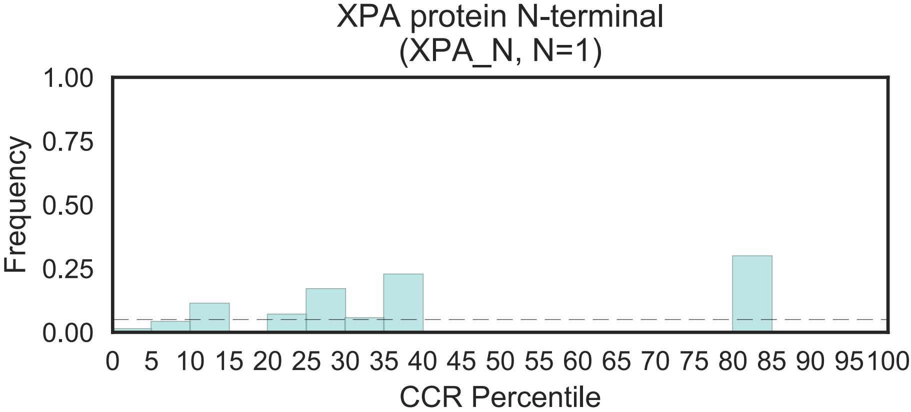

XAP5, circadian clock regulator
(XAP5, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

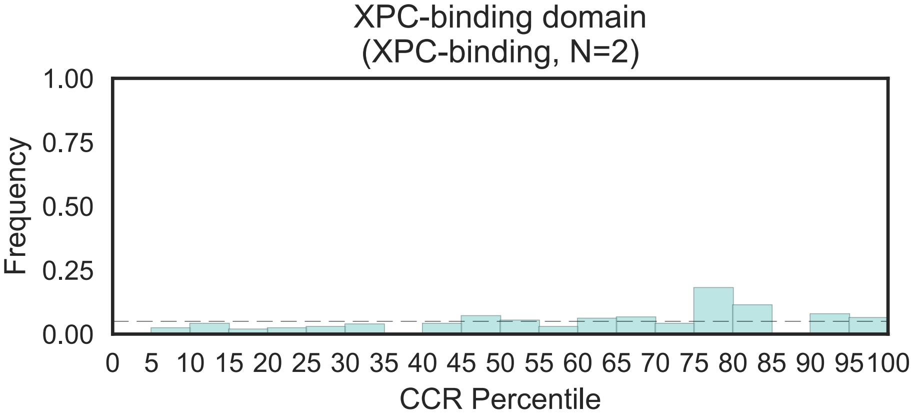


XK-related protein
(XK-related, N=9)
Fisher's OR: 0.633; Bonferroni p-val: 1

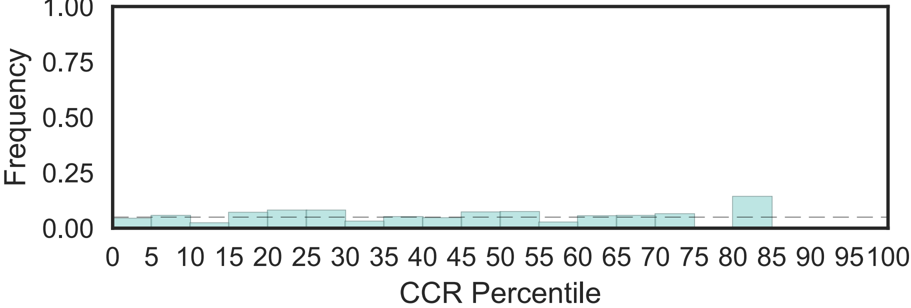

XLF-Cernunnos, XRcc4-like factor, NHEJ component
(XLF, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

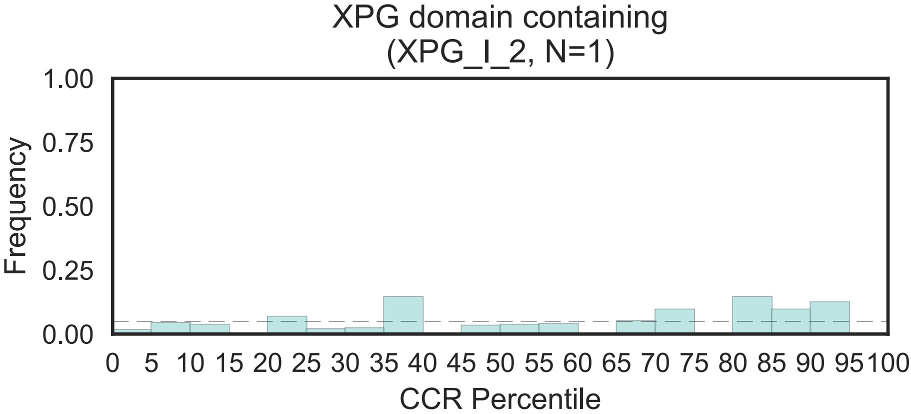

XPA protein C-terminus
(XPA_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

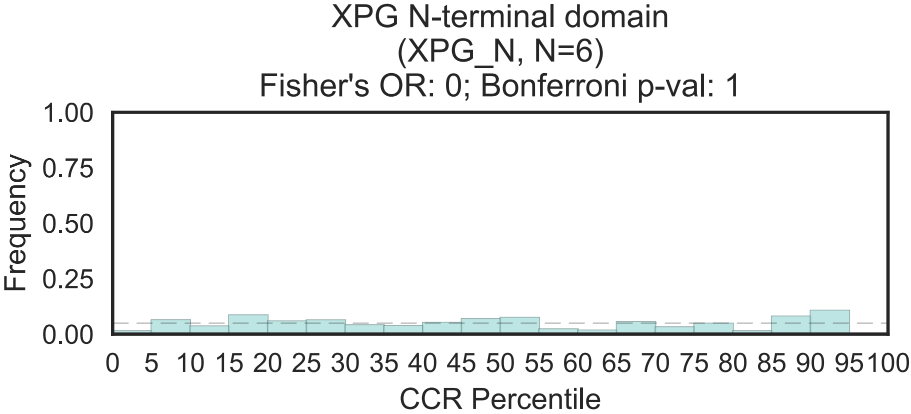

XPA protein N-terminal
(XPA_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

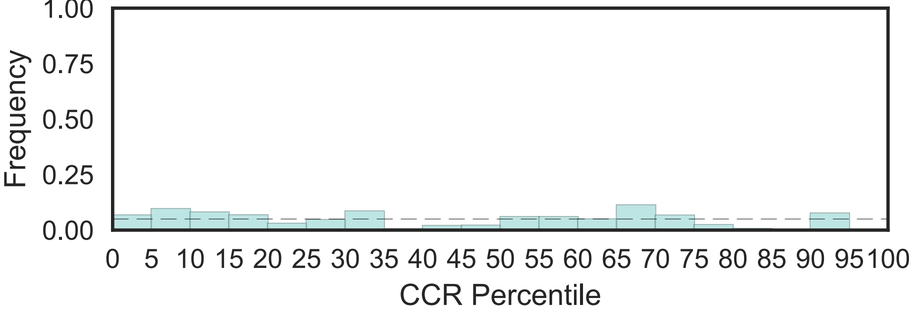

XPC-binding domain
(XPC-binding, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

XPG I-region
(XPG_I, N=5)
Fisher's OR: 0; Bonferroni p-val: 1

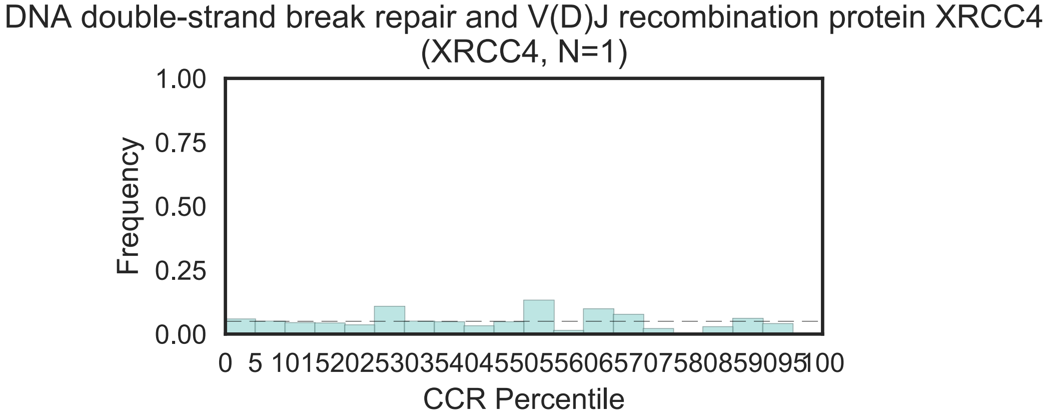


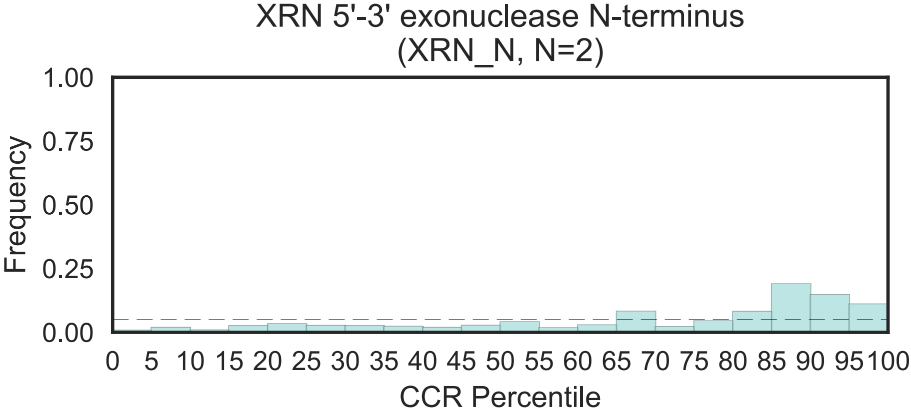

XPG domain containing
(XPG_I_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

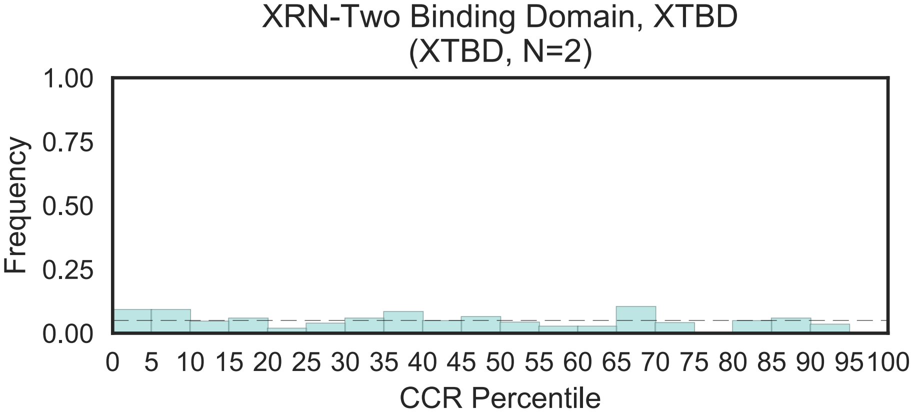

XPG N-terminal domain
(XPG_N, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

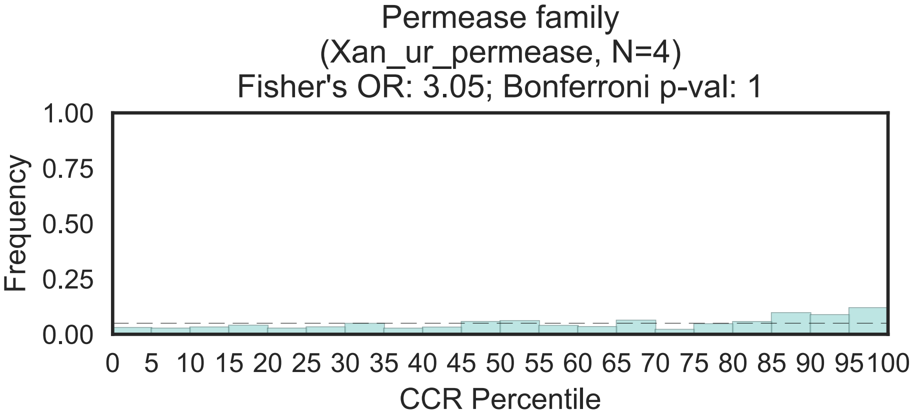


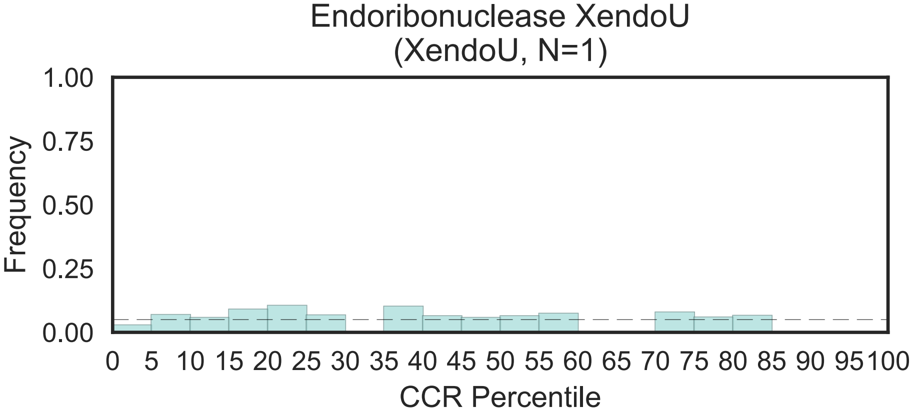
XRCC1 N terminal domain
(XRCC1_N, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

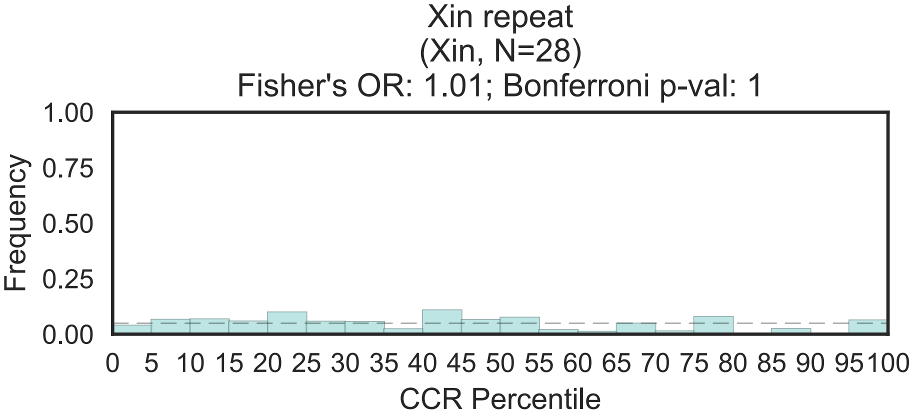

DNA double-strand break repair and V(D)J recombination protein XRCC4
(XRCC4, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

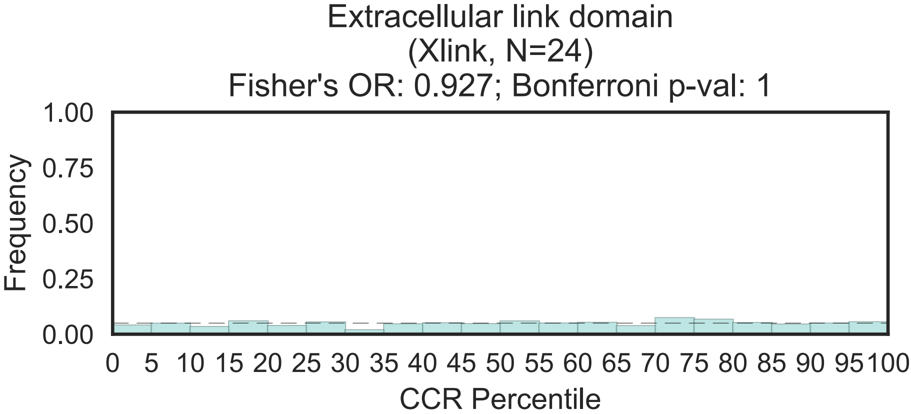

XRN 5'-3' exonuclease N-terminus
(XRN_N, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


XRN-Two Binding Domain, XTBD
(XTBD, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

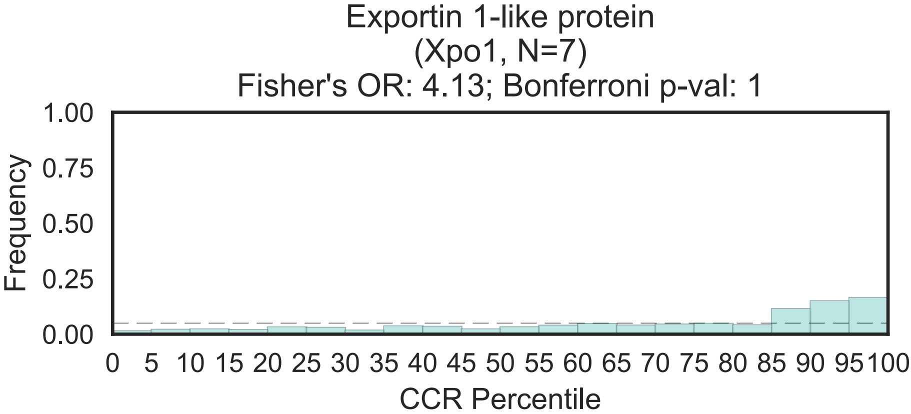

Permease family
(Xan_ur_permease, N=4)
Fisher's OR: 3.05; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Endoribonuclease XendoU
(XendoU, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

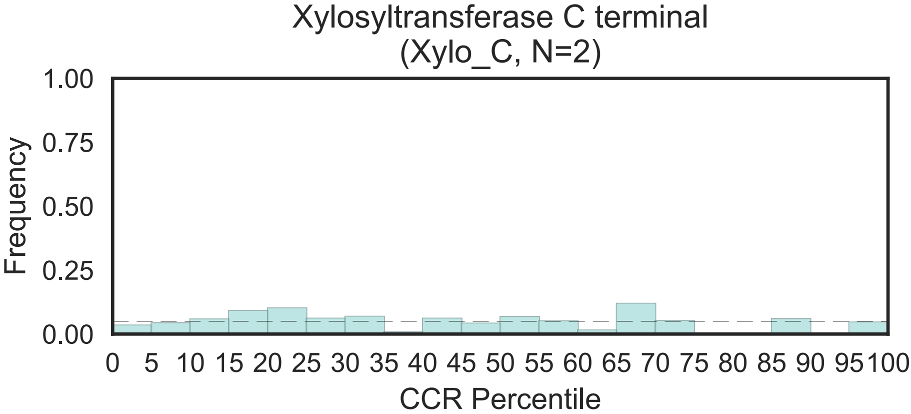

Xin repeat
(Xin, N=28)
Fisher's OR: 1.01; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

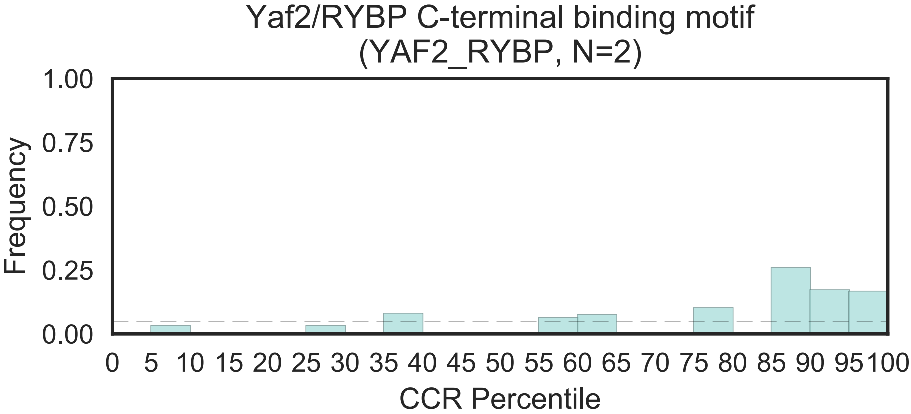


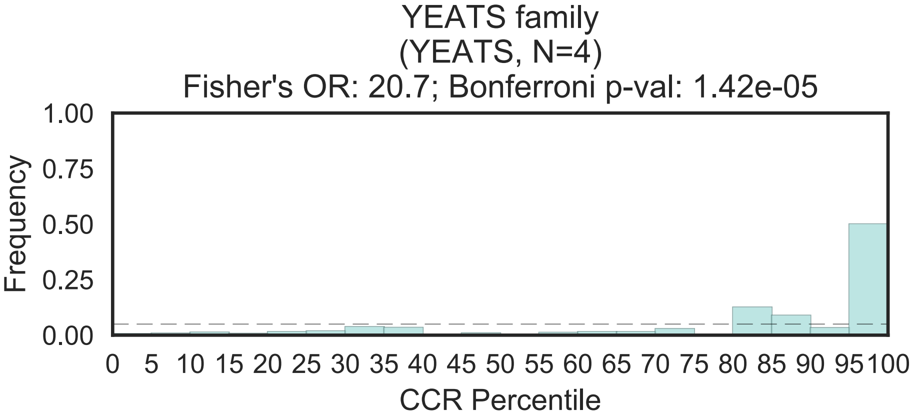
Extracellular link domain
(Xlink, N=24)
Fisher's OR: 0.927; Bonferroni p-val: 1

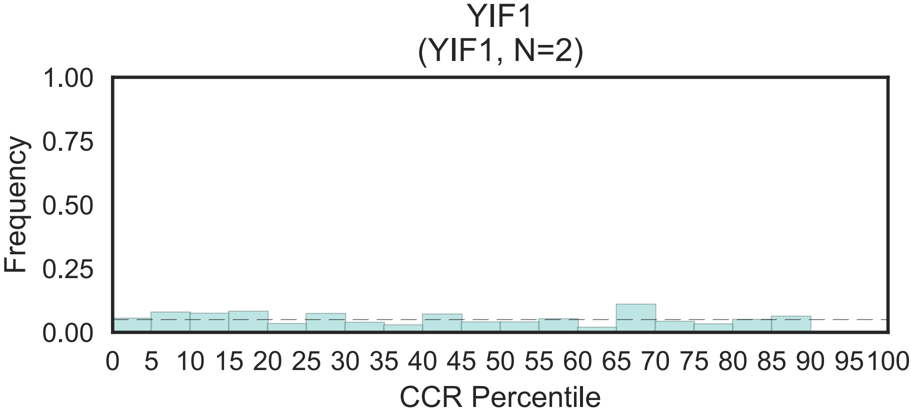


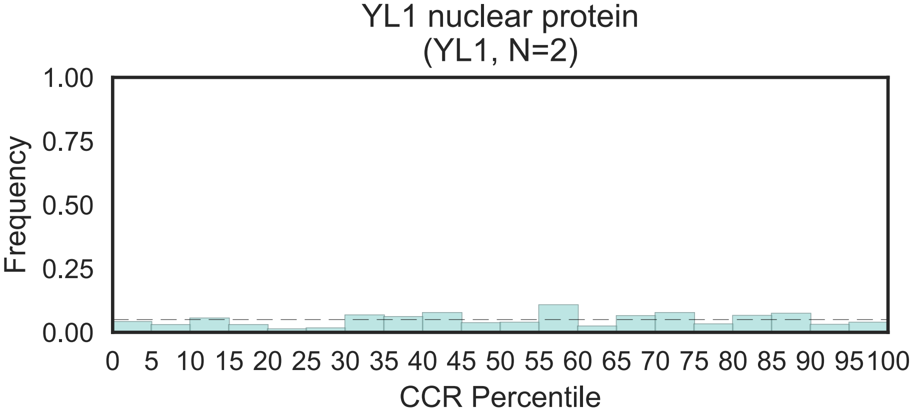
Exportin 1-like protein
(Xpo1, N=7)
Fisher's OR: 4.13; Bonferroni p-val: 1


Xylosyltransferase C terminal
(Xylo_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

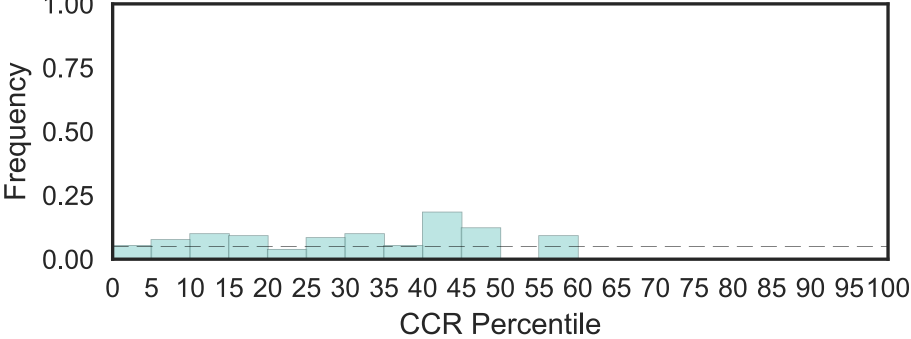

Yaf2/RYBP C-terminal binding motif
(YAF2_RYBP, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

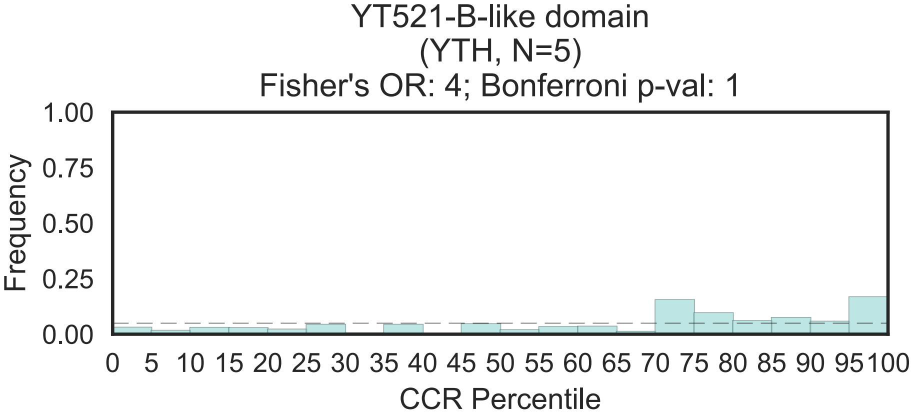

YEATS family
(YEATS, N=4)
Fisher's OR: 20.7; Bonferroni p-val: 1.42e-05
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

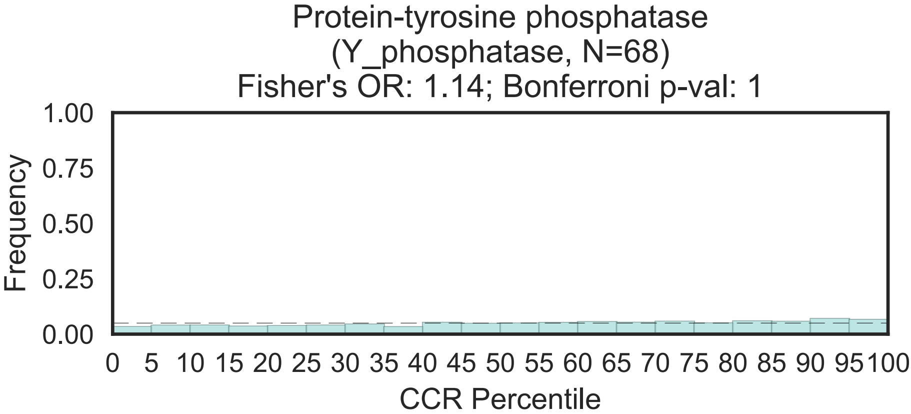

YIF1
(YIF1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

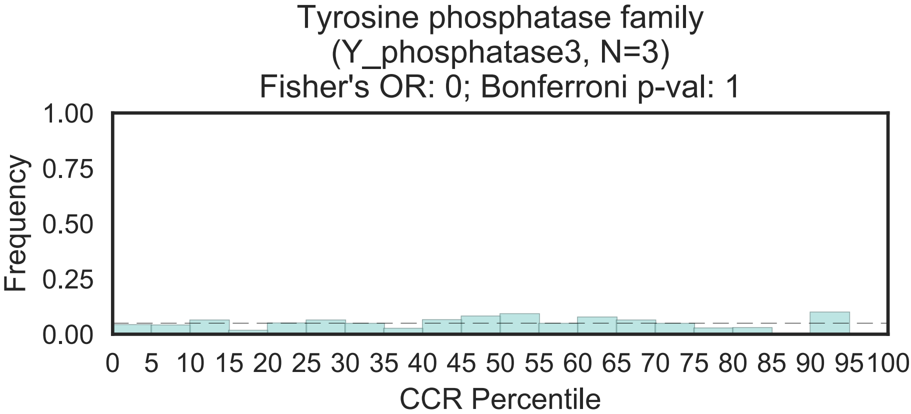

YL1 nuclear protein
(YL1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

YL1 nuclear protein C-terminal domain (YL1_C, N=2)

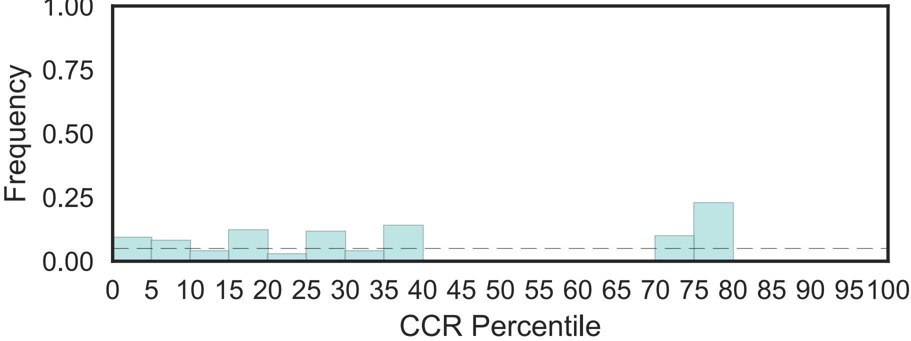



YT521-B-like domain
(YTH, N=5)
Fisher's OR: 4; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

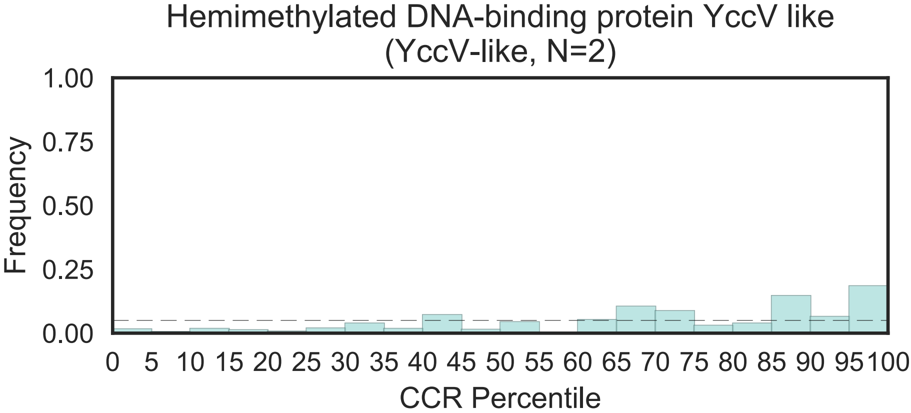

Protein-tyrosine phosphatase
(Y_phosphatase, N=68)
Fisher's OR: 1.14; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



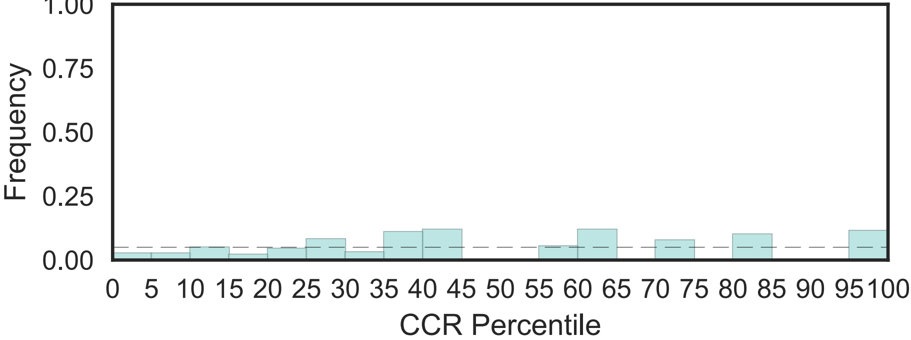
Tyrosine phosphatase family
(Y_phosphatase3, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

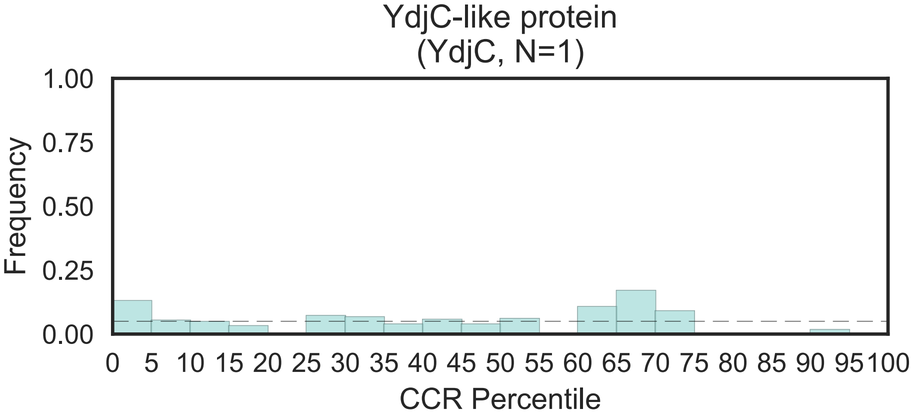


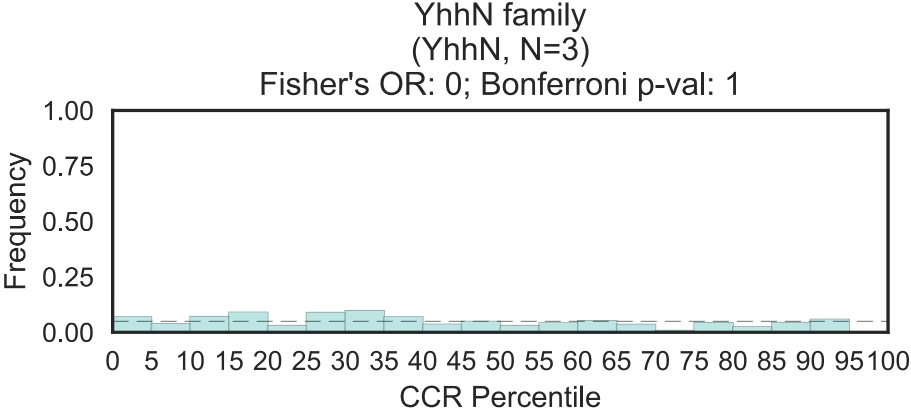
Essential protein Yae1, N terminal
(Yae1_N, N=2)

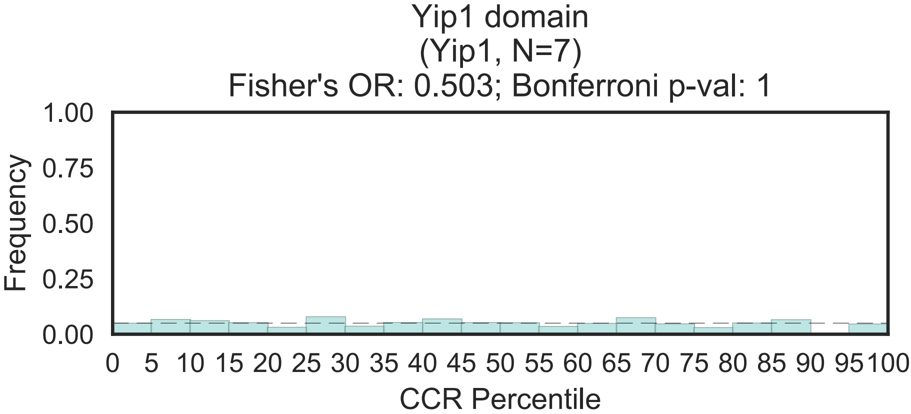

Hemimethylated DNA-binding protein YccV like
(YccV-like, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

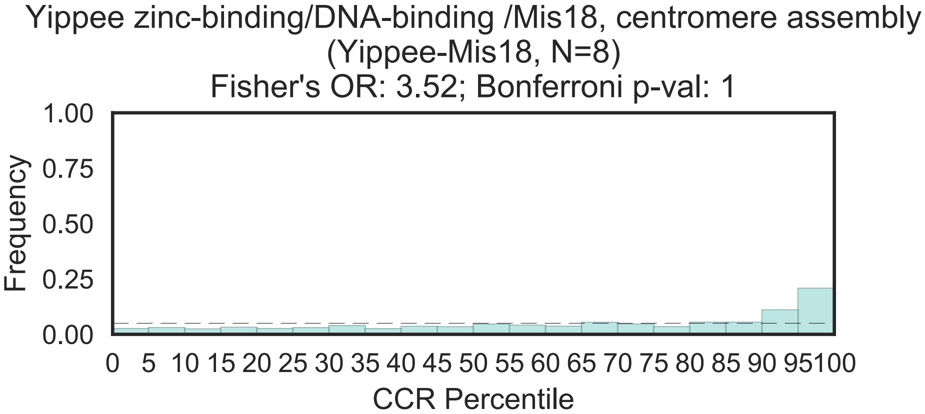
Protein of unknown function (DUF933) (YchF-GTPase_C, N=1)

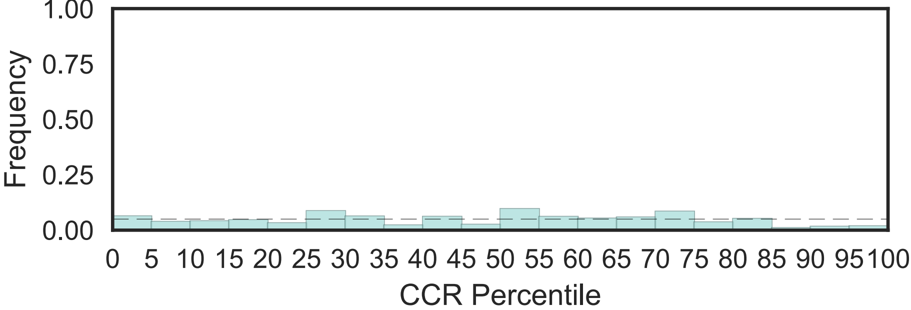



YdjC-like protein
(YdjC, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


YhhN family
(YhhN, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

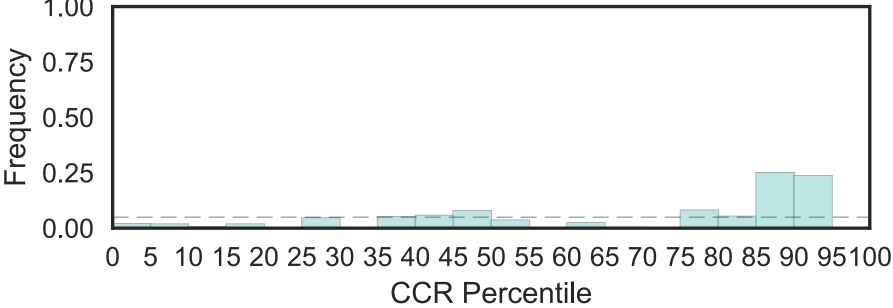

Yip1 domain
(Yip1, N=7)
Fisher's OR: 0.503; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

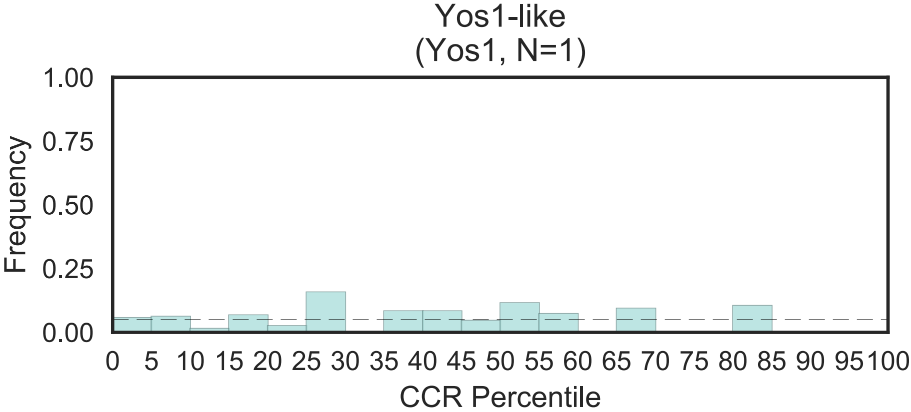

Yippee zinc-binding/DNA-binding /Mis18, centromere assembly
(Yippee-Mis18, N=8)
Fisher's OR: 3.52; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95100
CCR Percentile

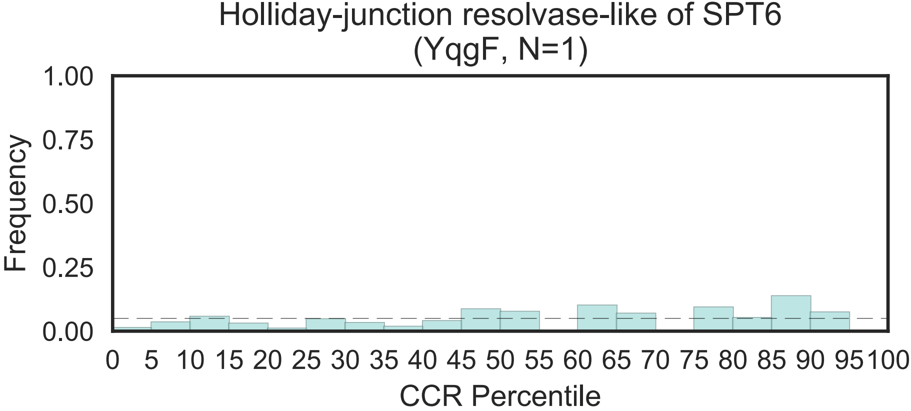


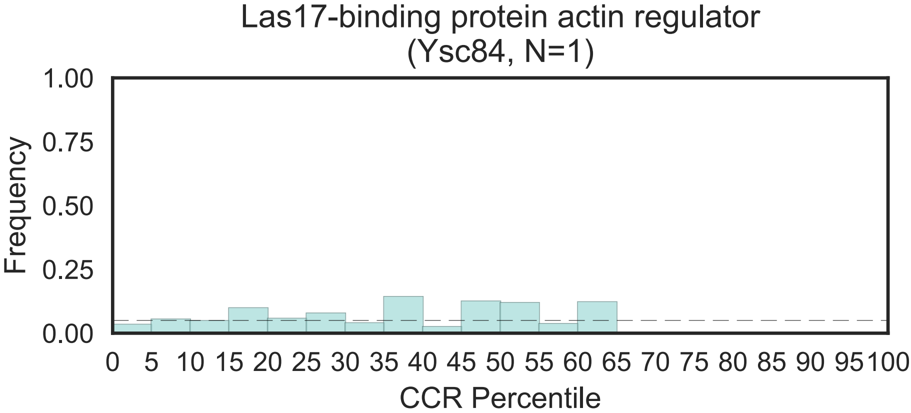
YjeF-related protein N-terminus
(YjeF_N, N=6)
Fisher's OR: 0.373; Bonferroni p-val: 1

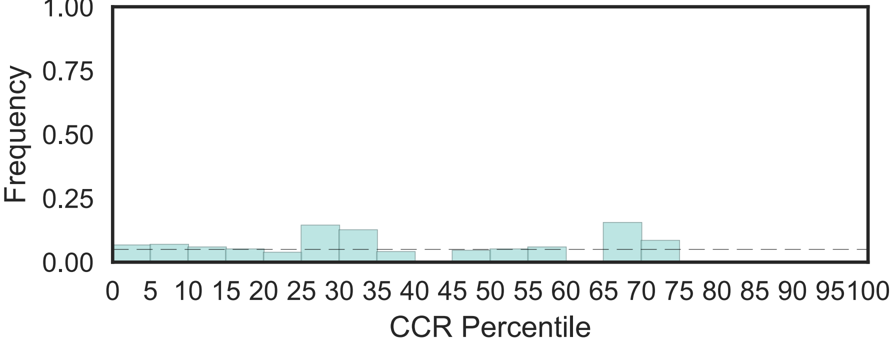
Inner membrane component of T3SS, cytoplasmic domain (Yop-YscD_cpl, N=3) Fisher's OR: 0; Bonferroni p-val: 1



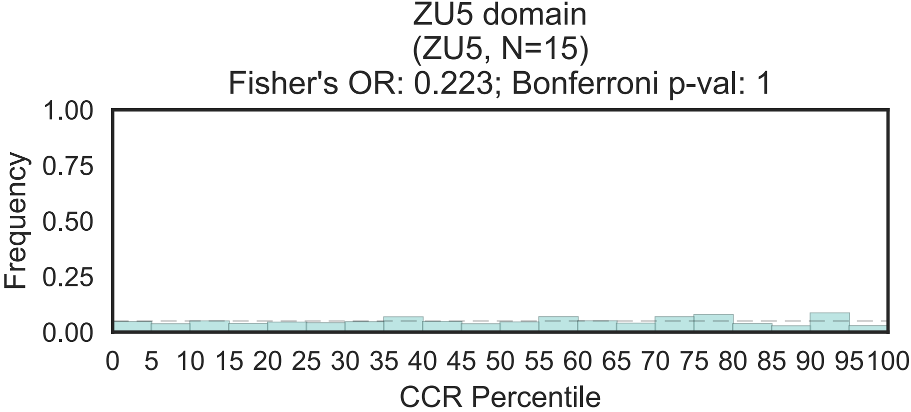

Yos1-like
(Yos1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Holliday-junction resolvase-like of SPT6
(YqgF, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

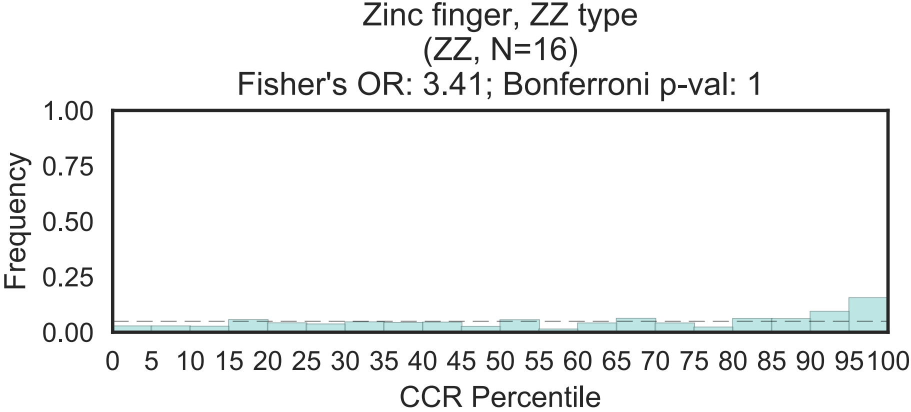

Las17-binding protein actin regulator
(Ysc84, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

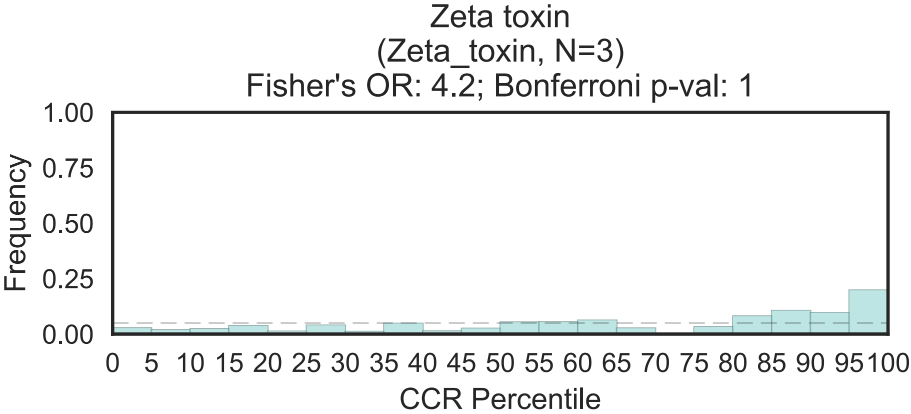


Zinc finger FYVE domain-containing protein 21 C-terminus
(ZFYVE21_C, N=1)

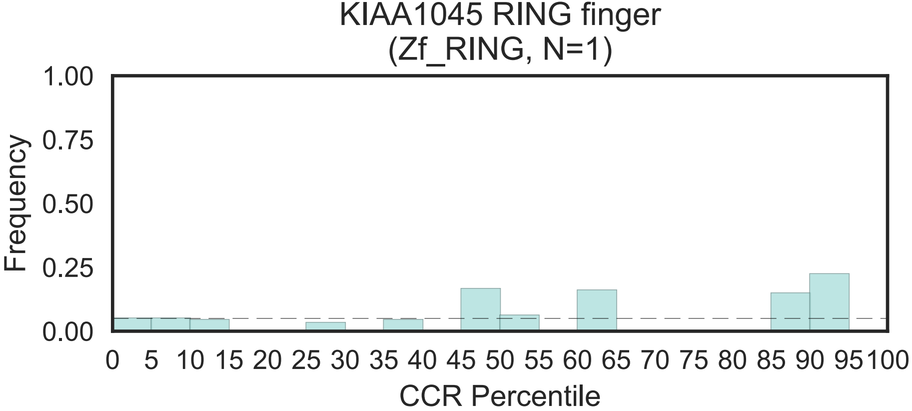


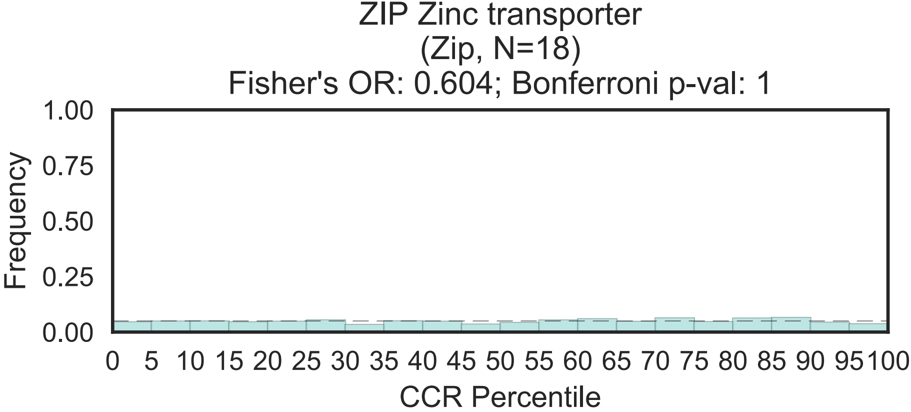
ZU5 domain
(ZU5, N=15)
Fisher's OR: 0.223; Bonferroni p-val: 1

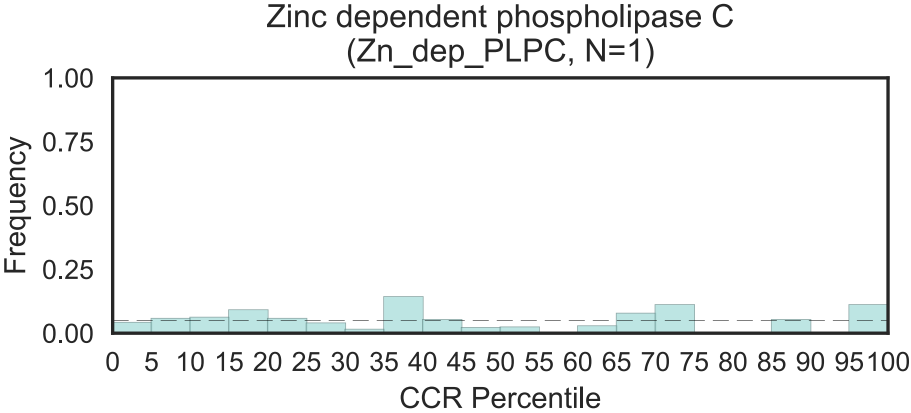

Zinc finger, ZZ type
(ZZ, N=16)
Fisher's OR: 3.41; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

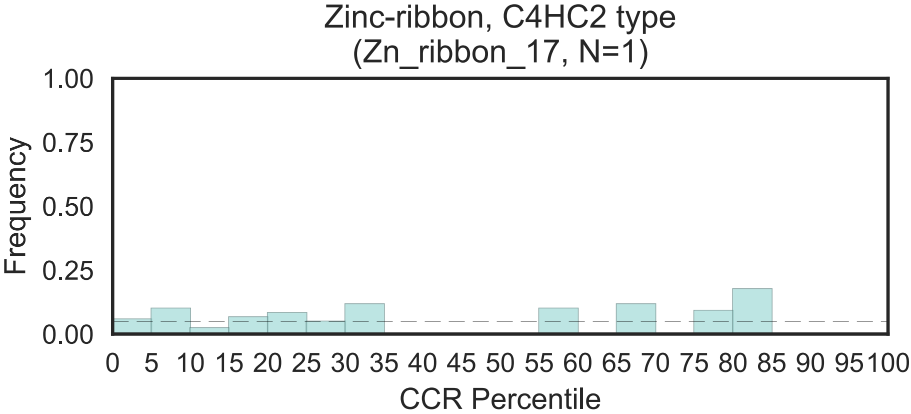


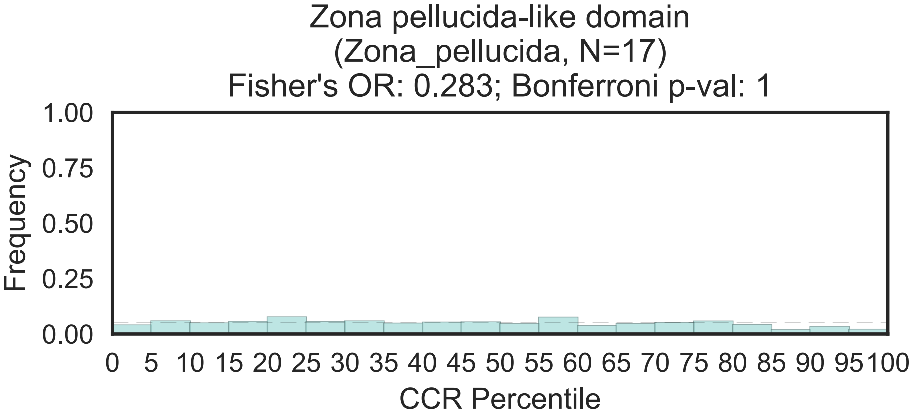
Zeta toxin
(Zeta_toxin, N=3)
Fisher's OR: 4.2; Bonferroni p-val: 1

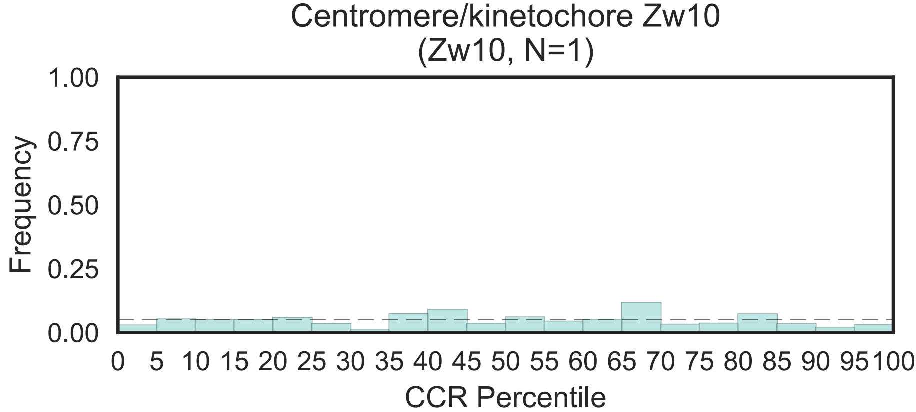

KIAA1045 RING finger
(Zf_RING, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

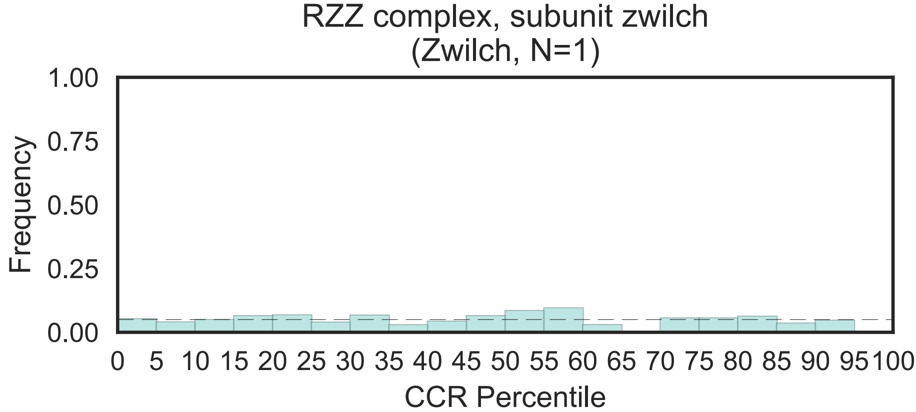

ZIP Zinc transporter
(Zip, N=18)
Fisher's OR: 0.604; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

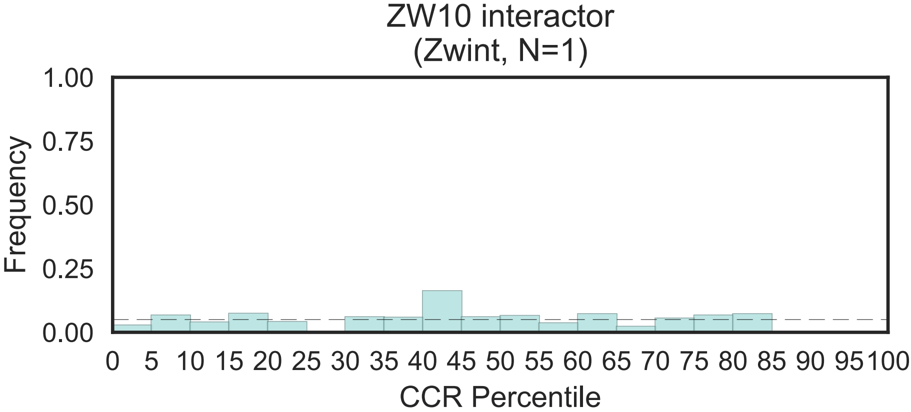

Zinc dependent phospholipase C
(Zn_dep_PLPC, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

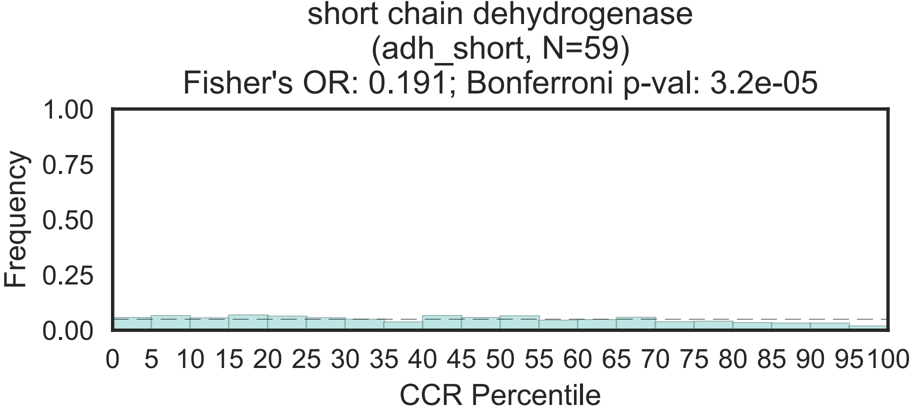

Zinc-ribbon, C4HC2 type
(Zn_ribbon_17, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Zona pellucida-like domain
(Zona_pellucida, N=17)
Fisher's OR: 0.283; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

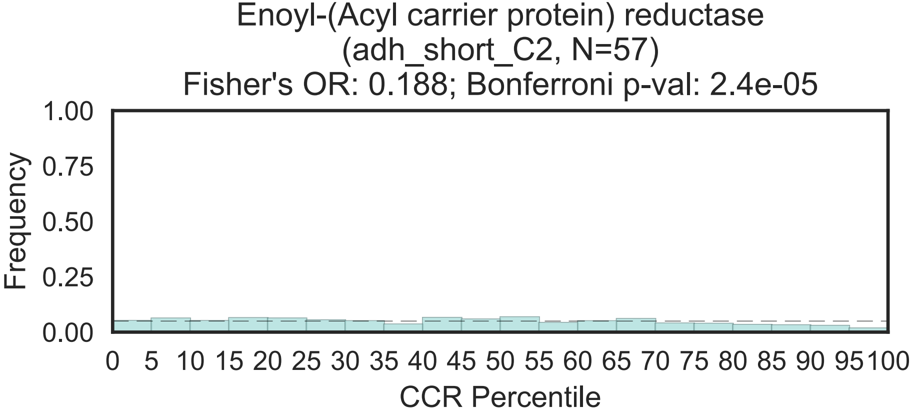

Centromere/kinetochore Zw10
(Zw10, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

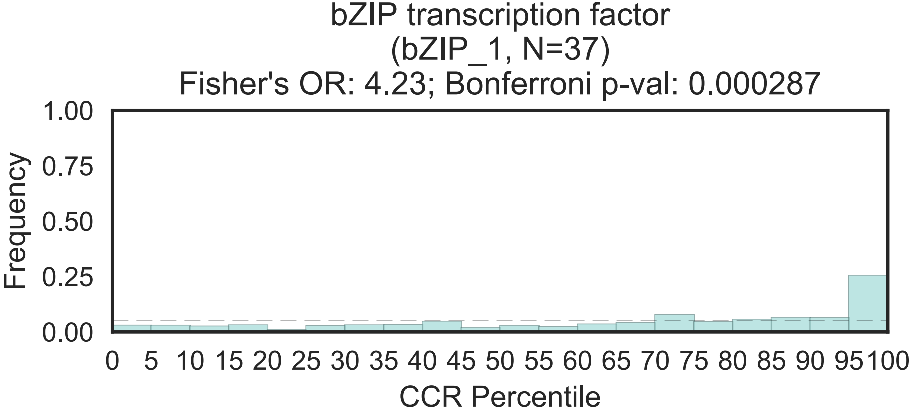

RZZ complex, subunit zwilch
(Zwilch, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

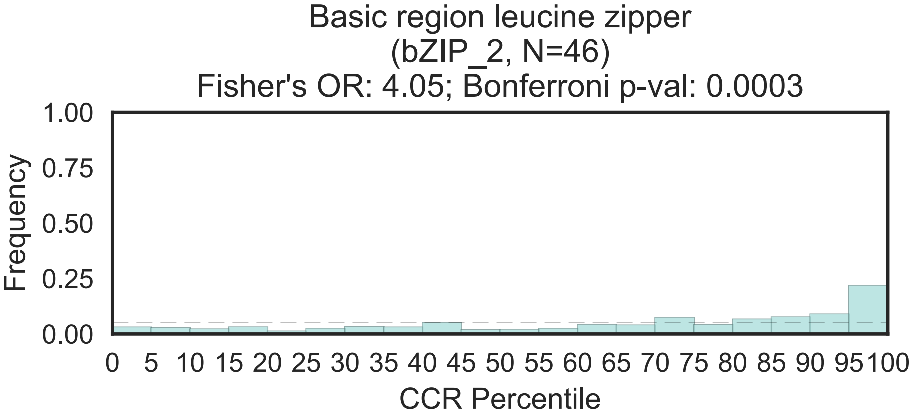

ZW10 interactor
(Zwint, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

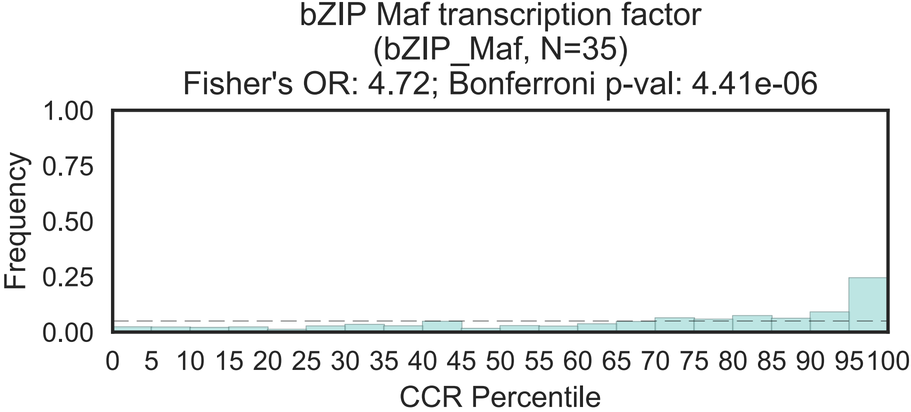


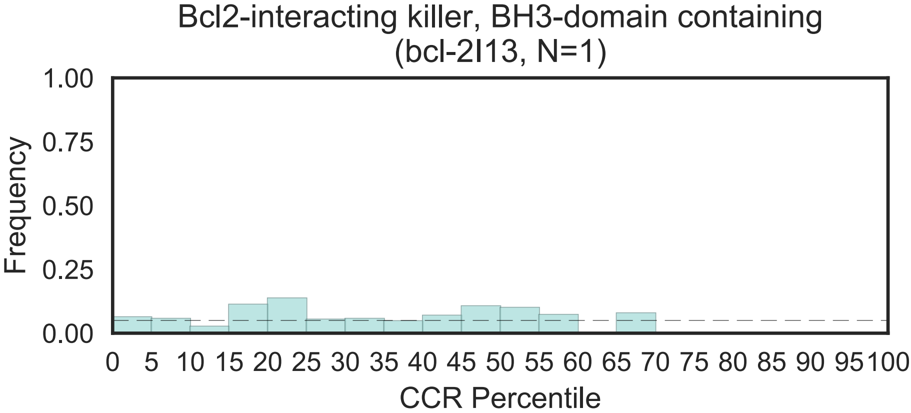
short chain dehydrogenase
(adh_short, N=59)
Fisher's OR: 0.191; Bonferroni p-val: 3.2e-05

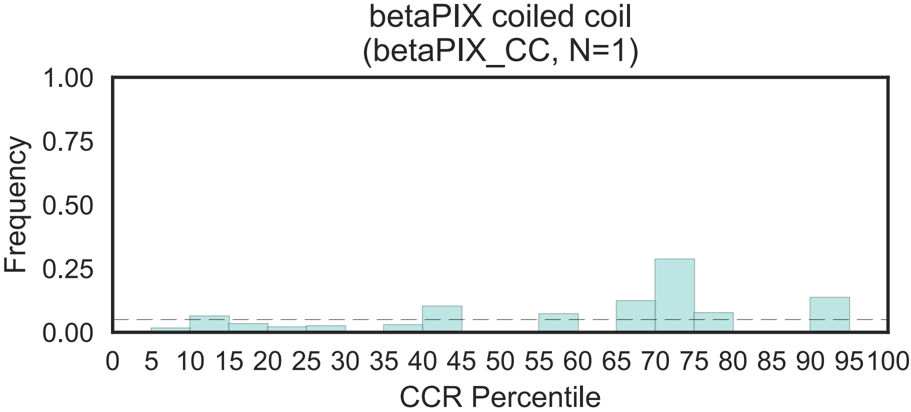

Enoyl-(Acyl carrier protein) reductase
(adh_short_C2, N=57)
Fisher's OR: 0.188; Bonferroni p-val: 2.4e-05
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

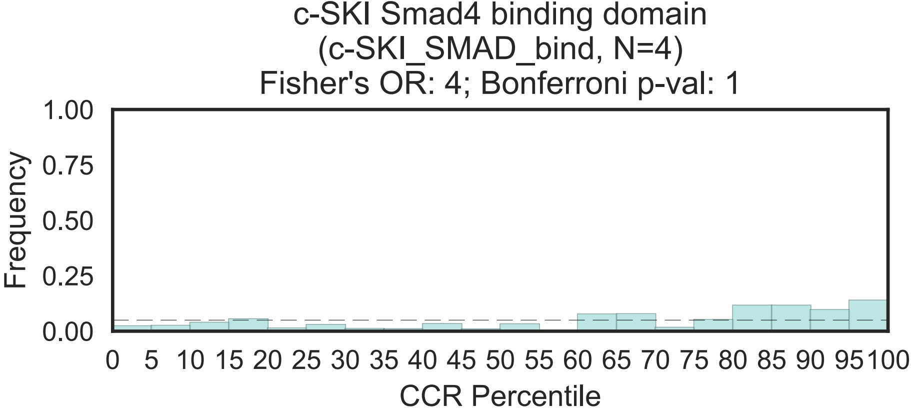

bZIP transcription factor
(bZIP_1, N=37)
Fisher's OR: 4.23; Bonferroni p-val: 0.000287
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

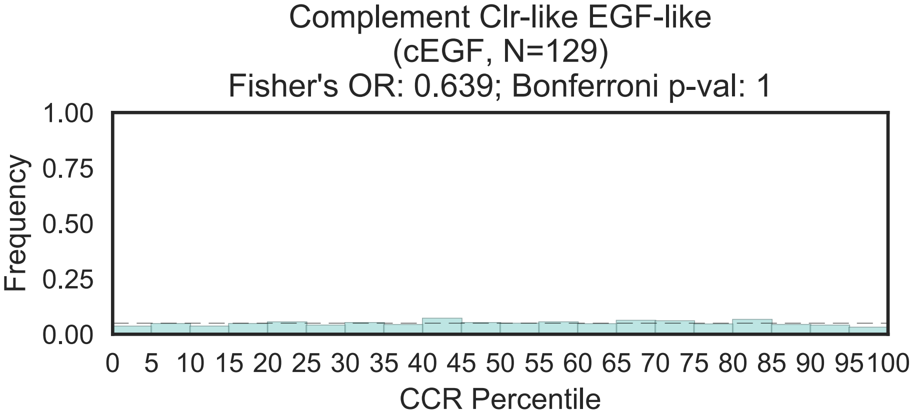

Basic region leucine zipper
(bZIP_2, N=46)
Fisher's OR: 4.05; Bonferroni p-val: 0.0003
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

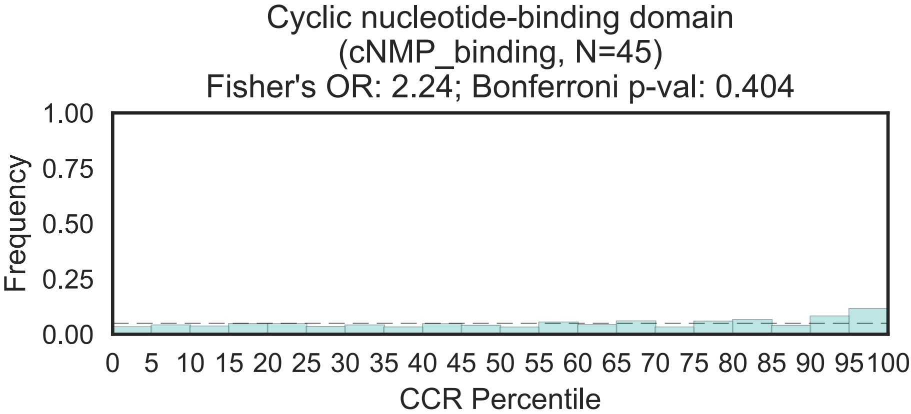

bZIP Maf transcription factor
(bZIP_Maf, N=35)
Fisher's OR: 4.72; Bonferroni p-val: 4.41e-06
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

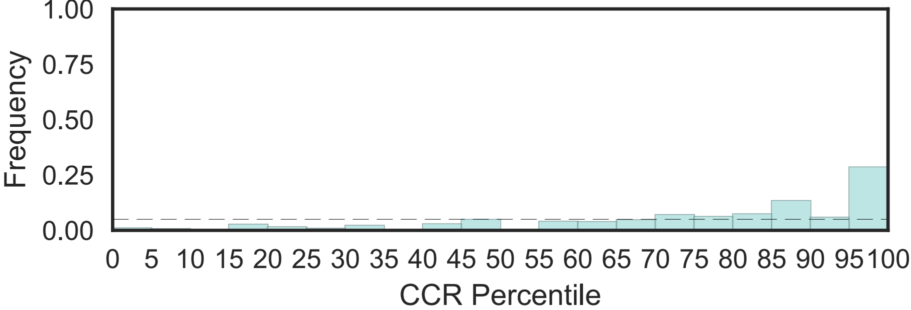

Bcl2-interacting killer, BH3-domain containing
(bcl-2l13, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

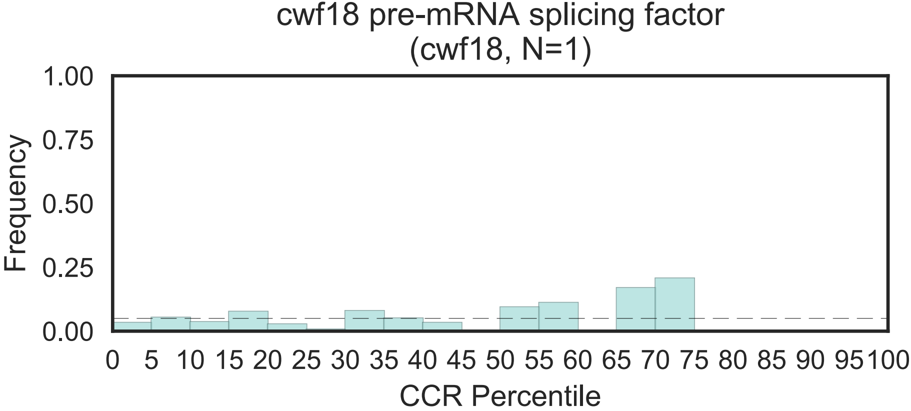

betaPIX coiled coil
(betaPIX_CC, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

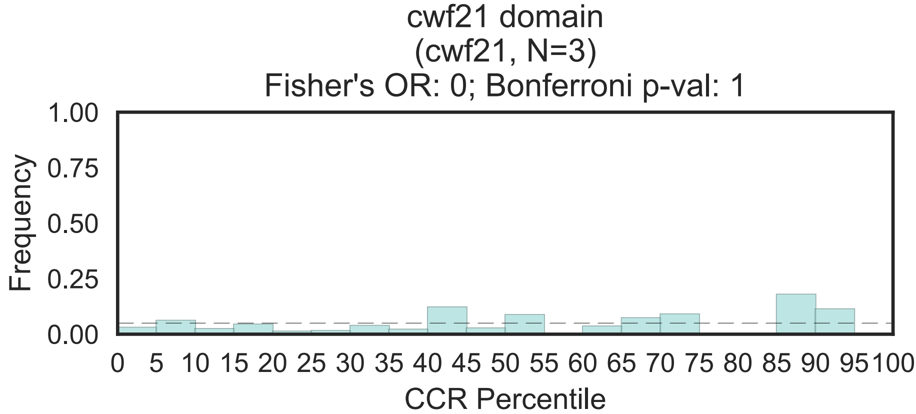

c-SKI Smad4 binding domain
(c-SKI_SMAD_bind, N=4)
Fisher's OR: 4; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Complement Clr-like EGF-like
(cEGF, N=129)
Fisher's OR: 0.639; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

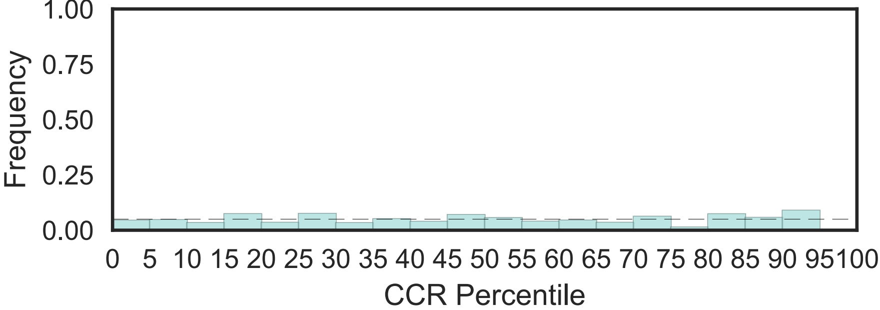

Cyclic nucleotide-binding domain
(cNMP_binding, N=45)
Fisher's OR: 2.24; Bonferroni p-val: 0.404
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

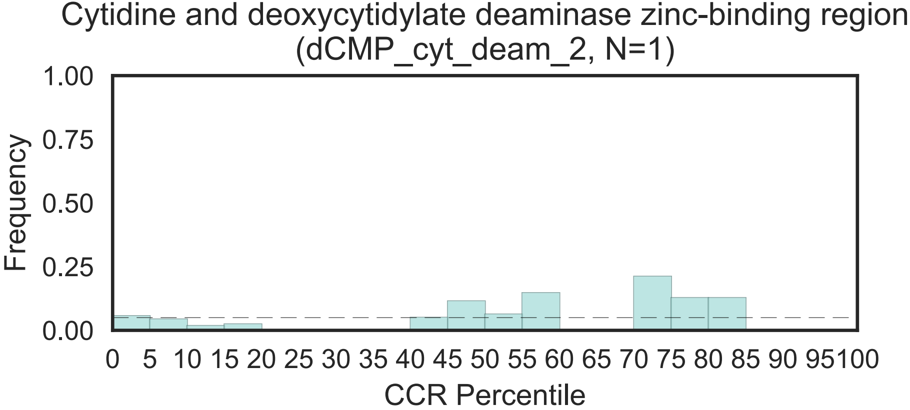

CobW/HypB/UreG, nucleotide-binding domain
(cobW, N=10)
Fisher's OR: 11.4; Bonferroni p-val: 1

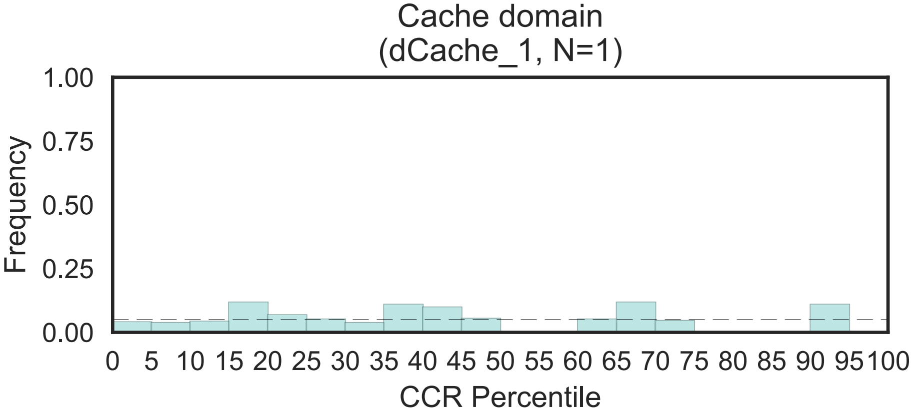

cwf18 pre-mRNA splicing factor
(cwf18, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

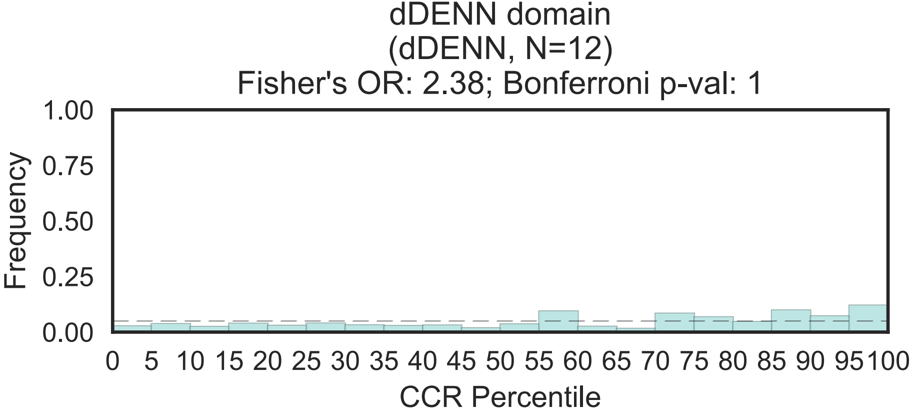

cwf21 domain
(cwf21, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

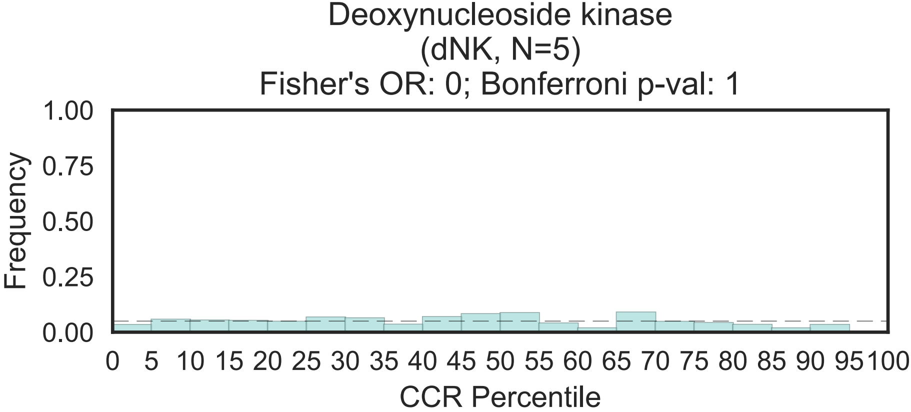
Cytidine and deoxycytidylate deaminase zinc-binding region
(dCMP_cyt_deam_1, N=8)
Fisher's OR: 0; Bonferroni p-val: 1

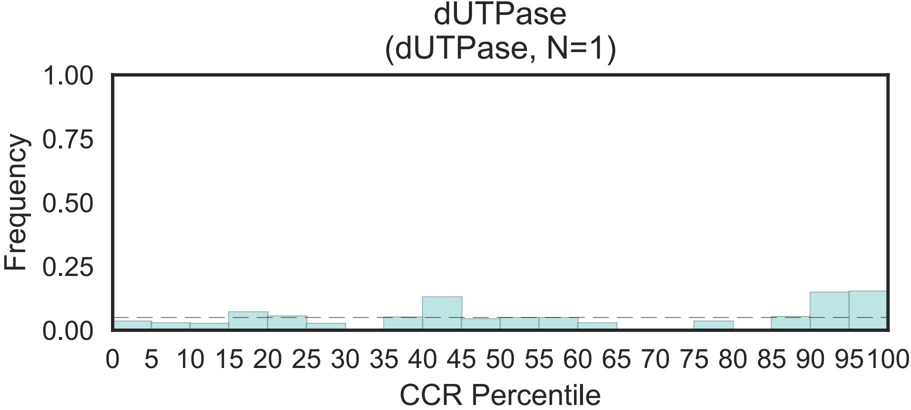


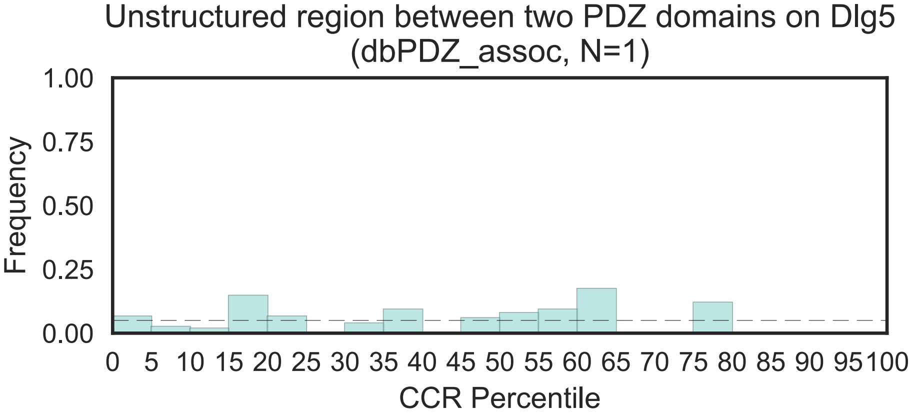

Cytidine and deoxycytidylate deaminase zinc-binding region
(dCMP_cyt_deam_2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

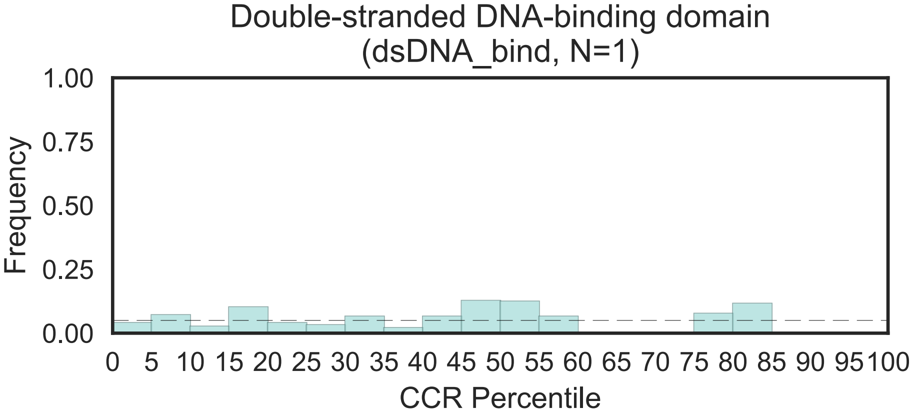

Cache domain
(dCache_1, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

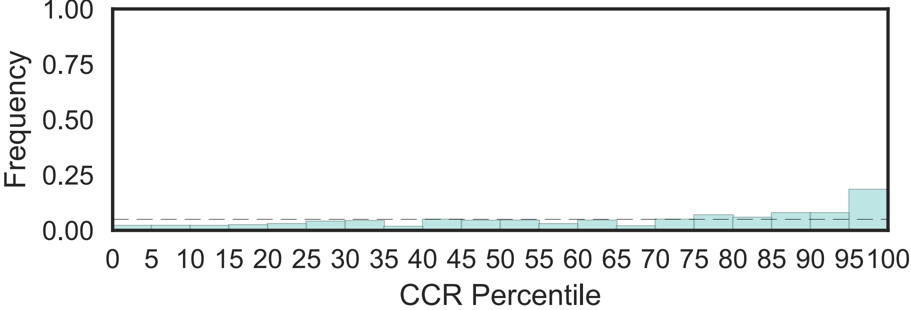

dDENN domain
(dDENN, N=12)
Fisher's OR: 2.38; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Deoxynucleoside kinase
(dNK, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

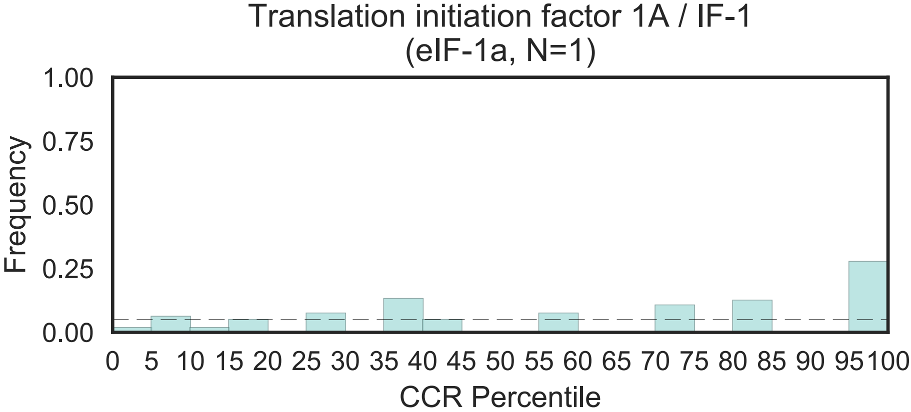

dUTPase
(dUTPase, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

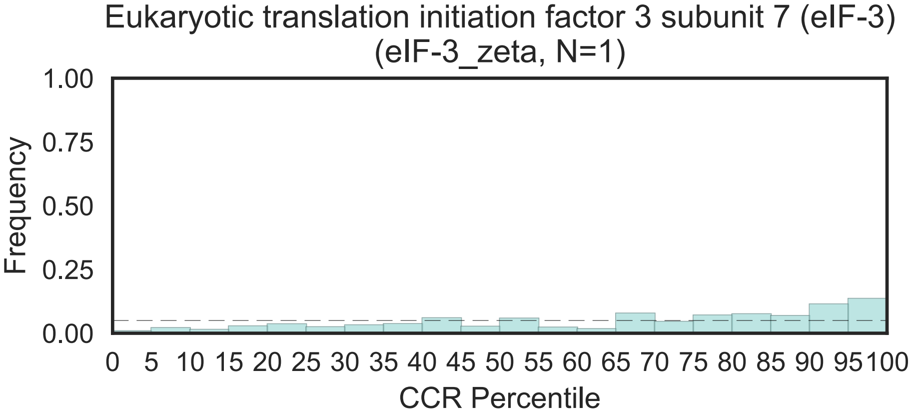

Unstructured region between two PDZ domains on Dlg5
(dbPDZ_assoc, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

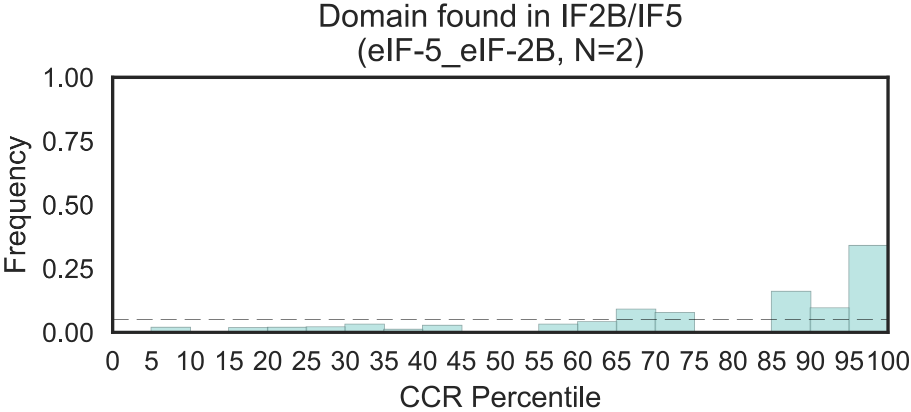

Double-stranded DNA-binding domain
(dsDNA_bind, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



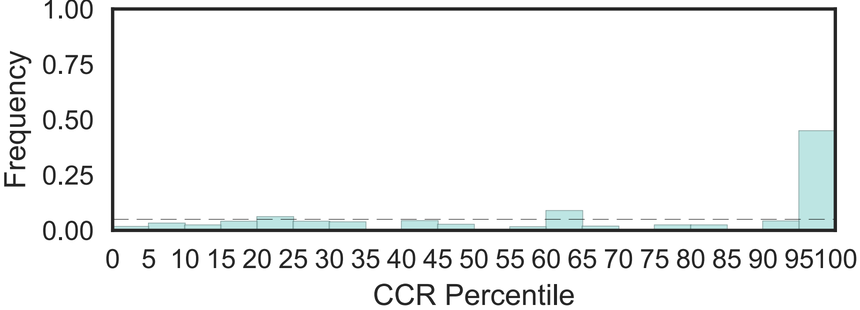
Double-stranded RNA binding motif
(dsrm, N=34)
Fisher's OR: 3.75; Bonferroni p-val: 0.0124

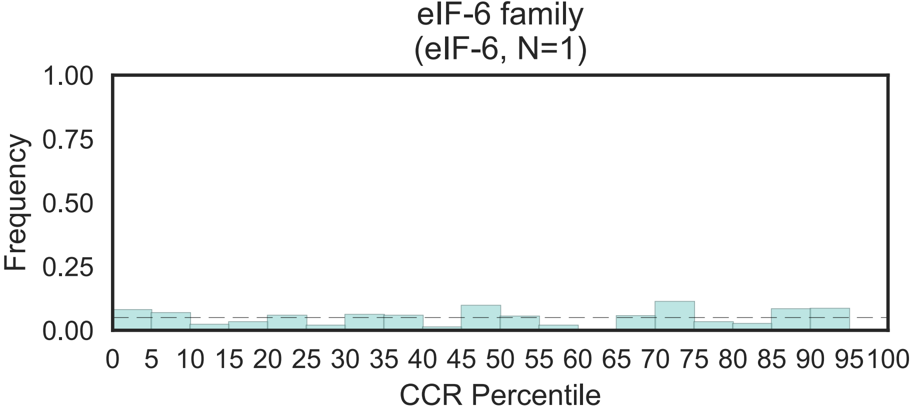

Translation initiation factor 1A / IF-1
(eIF-1a, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Eukaryotic translation initiation factor 3 subunit 7 (eIF-3)
(eIF-3_zeta, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

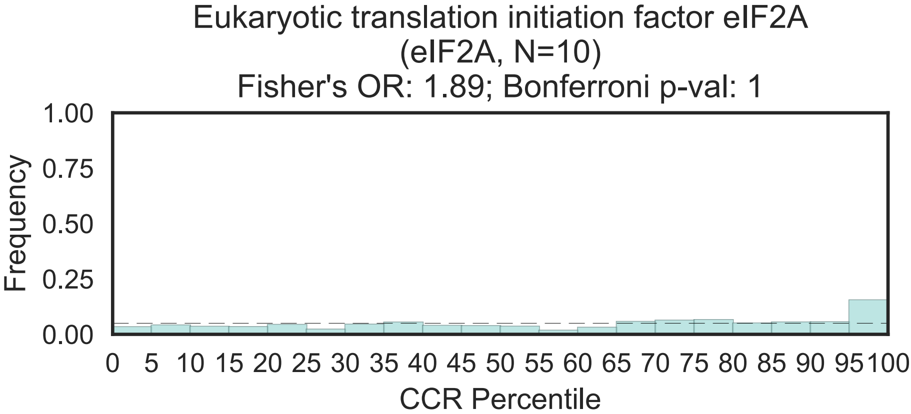

Domain found in IF2B/IF5
(eIF-5_eIF-2B, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

Eukaryotic elongation factor 5A hypusine, DNA-binding OB fold
(eIF-5a, N=4)
Fisher's OR: 6.49; Bonferroni p-val: 1

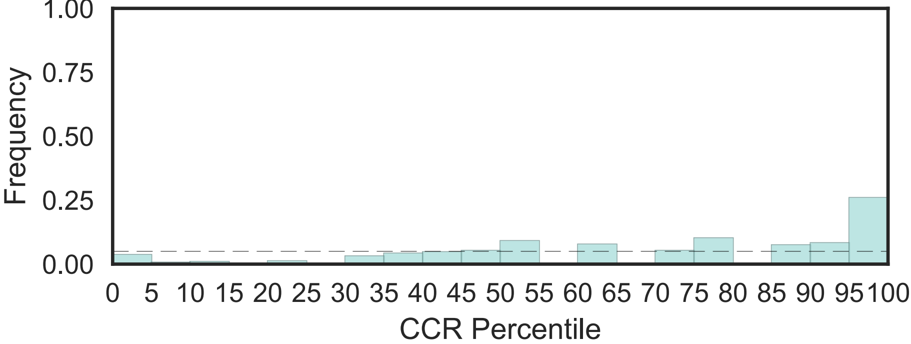


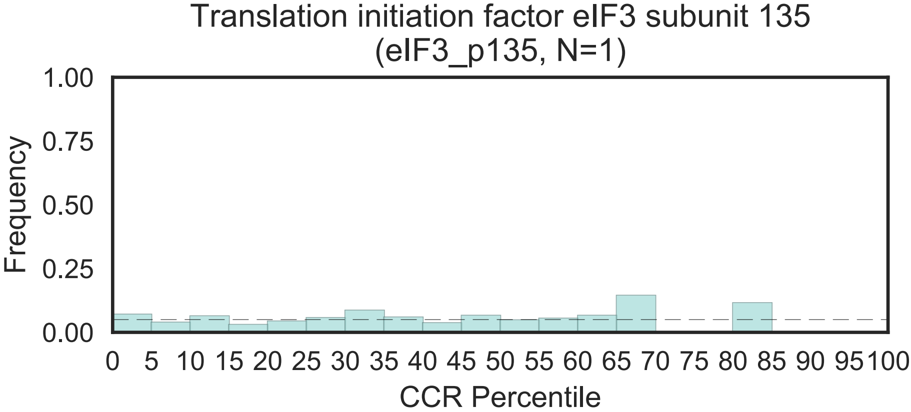


eIF-6 family
(eIF-6, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

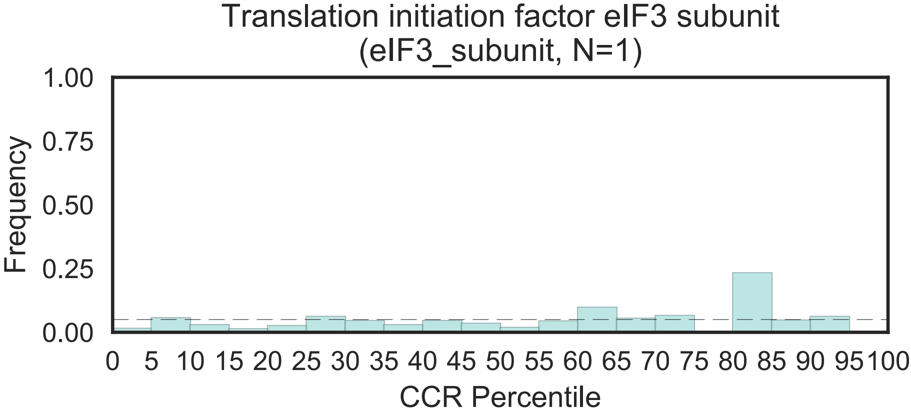

Eukaryotic translation initiation factor eIF2A
(eIF2A, N=10)
Fisher's OR: 1.89; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

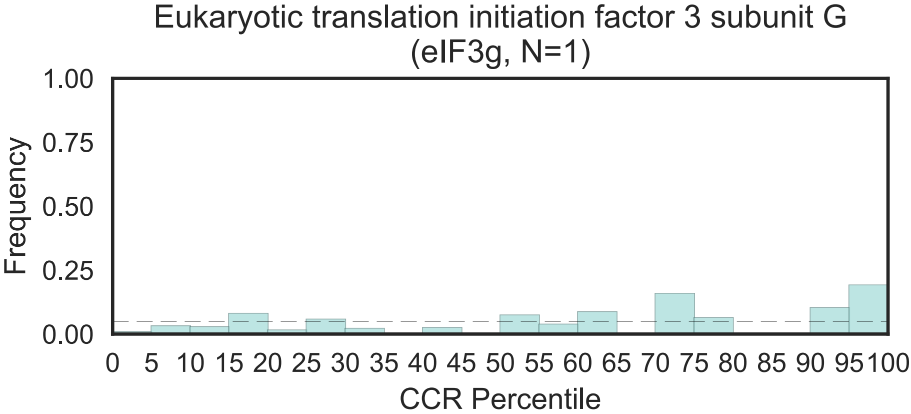
eIF3 subunit 6 N terminal domain (eIF3_N, N=1)

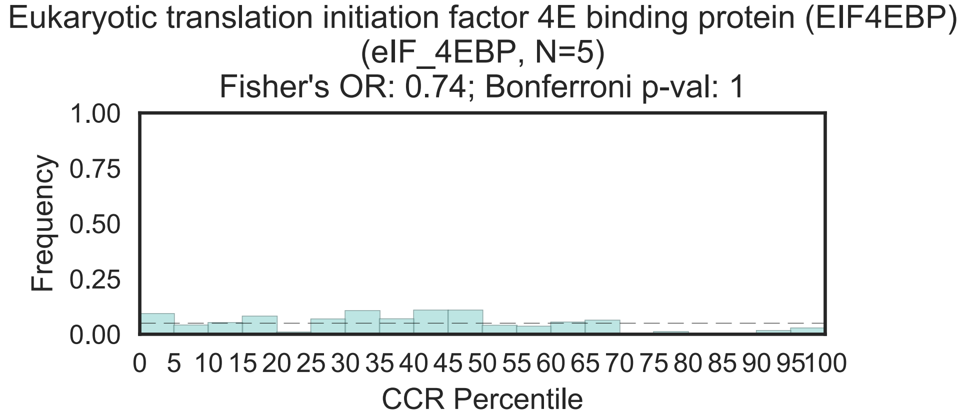




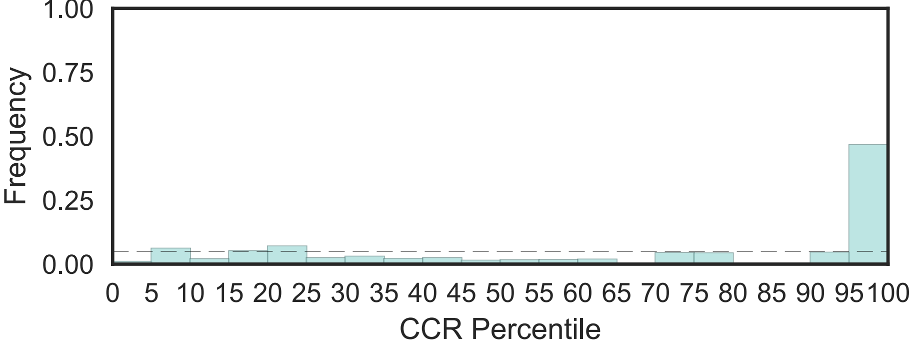
Translation initiation factor eIF3 subunit 135
(eIF3_p135, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

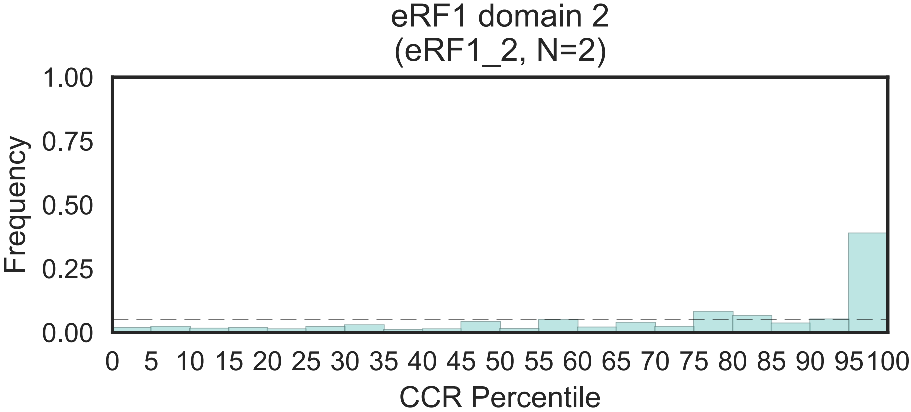

Translation initiation factor eIF3 subunit
(eIF3_subunit, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

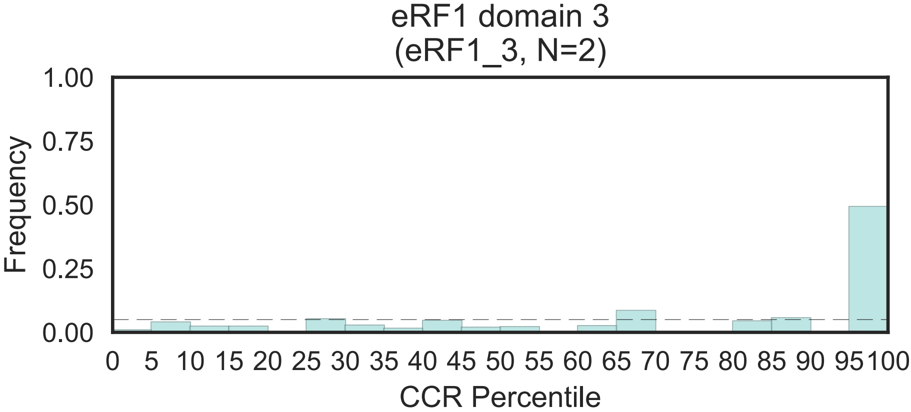

Eukaryotic translation initiation factor 3 subunit G
(eIF3g, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

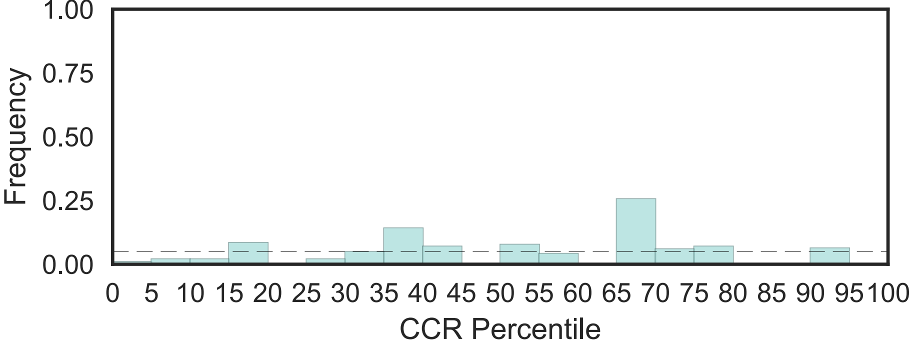

Eukaryotic translation initiation factor 4E binding protein (EIF4EBP)
(eIF_4EBP, N=5)
Fisher's OR: 0.74; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

eRF1 domain 1
(eRF1_1, N=2)

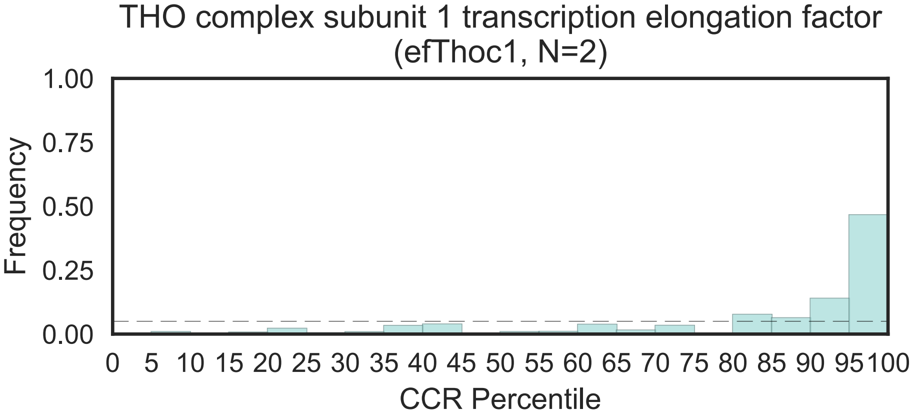


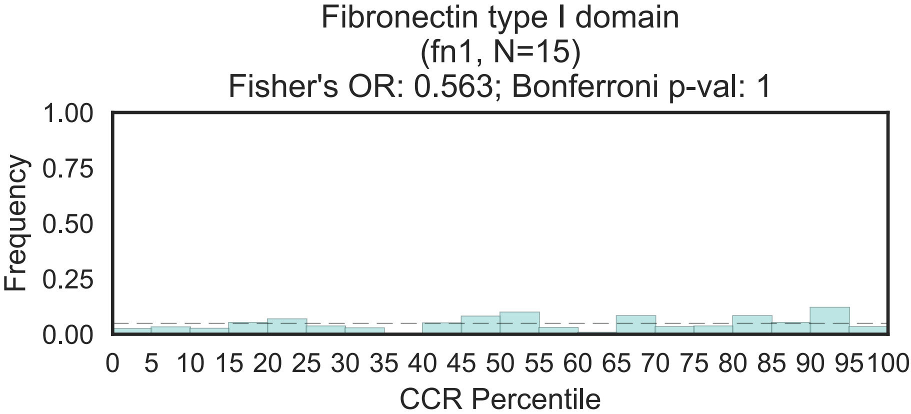

eRF1 domain 2
(eRF1_2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

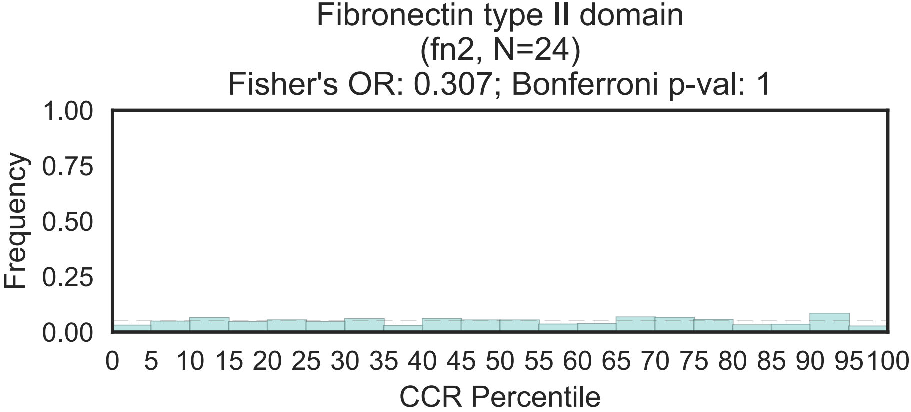

eRF1 domain 3
(eRF1_3, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

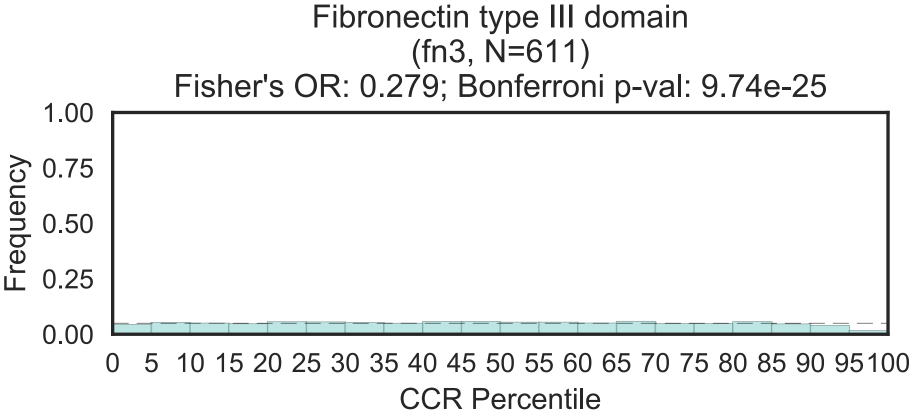


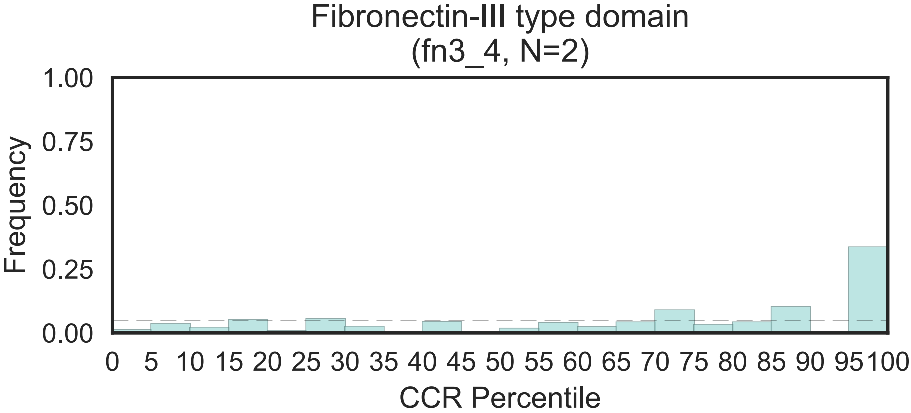
Transforming growth factor beta receptor 2 ectodomain
(ecTbetaR2, N=1)

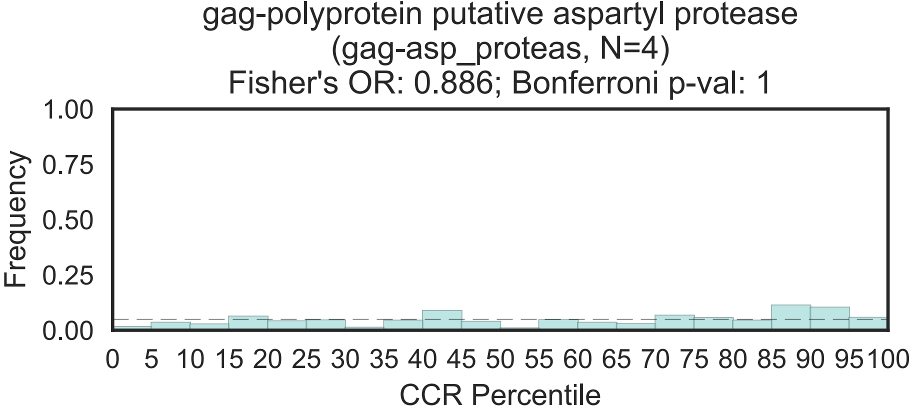

THO complex subunit 1 transcription elongation factor
(efThoc1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


Fibronectin type I domain
(fn1, N=15)
Fisher's OR: 0.563; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

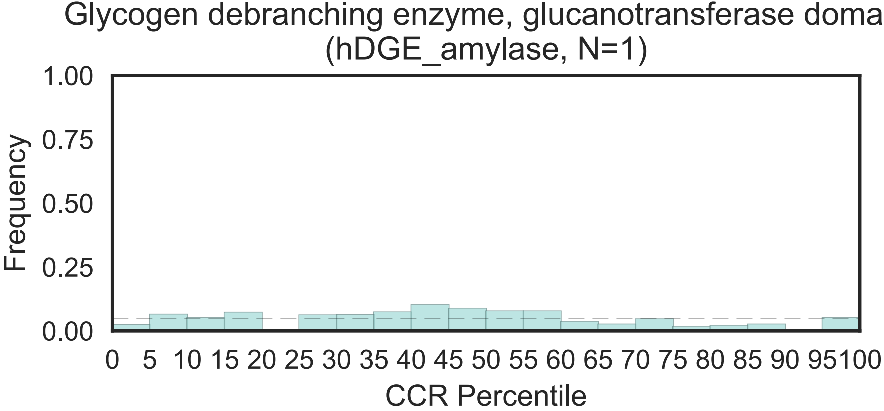

Fibronectin type II domain
(fn2, N=24)
Fisher's OR: 0.307; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

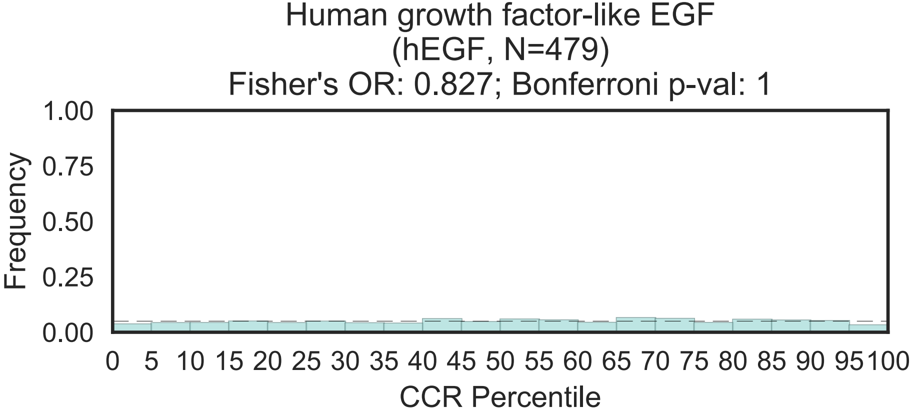

Fibronectin type III domain
(fn3, N=611)
Fisher's OR: 0.279; Bonferroni p-val: 9.74e-25
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

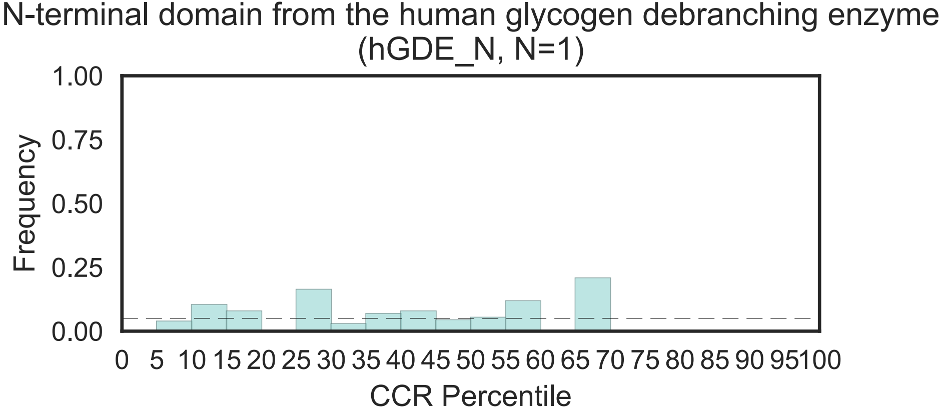

Fibronectin-III type domain
(fn3_4, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

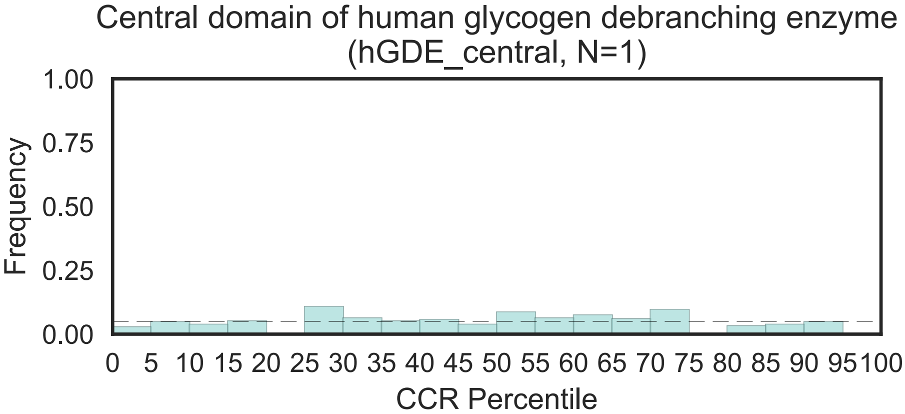


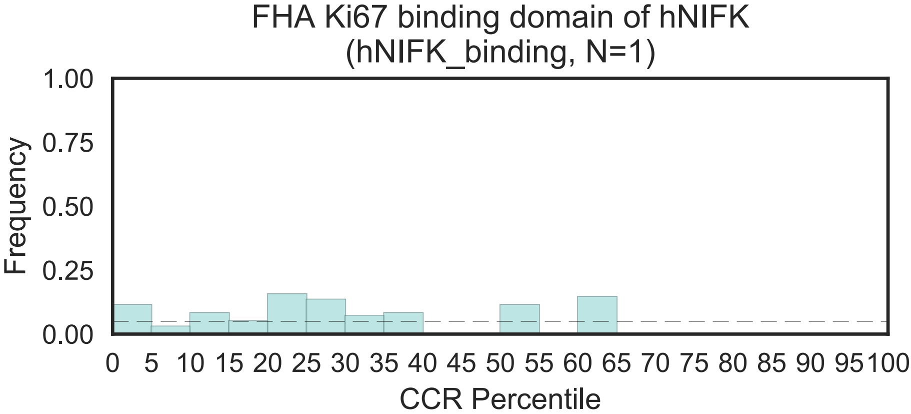
gag-polyprotein putative aspartyl protease
(gag-asp_proteas, N=4)
Fisher's OR: 0.886; Bonferroni p-val: 1

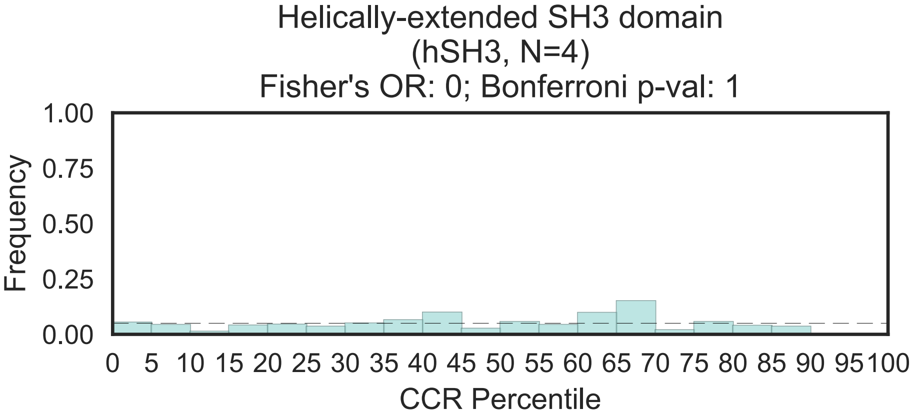

Glycogen debranching enzyme, glucanotransferase domain
(hDGE_amylase, N=1)

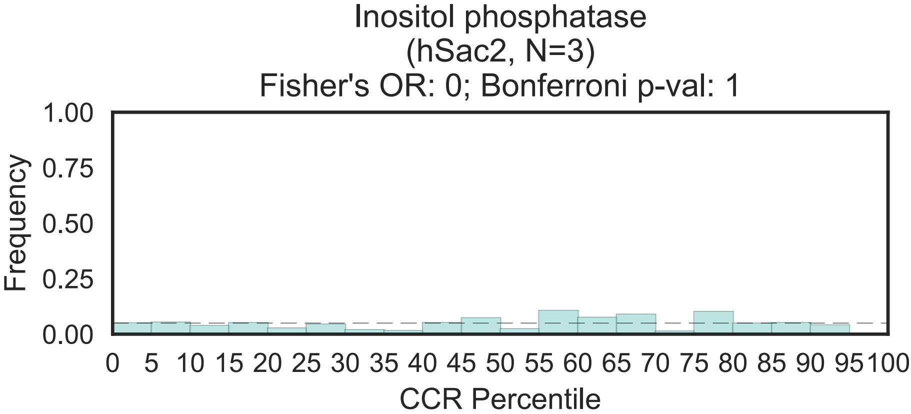

Human growth factor-like EGF
(hEGF, N=479)
Fisher's OR: 0.827; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

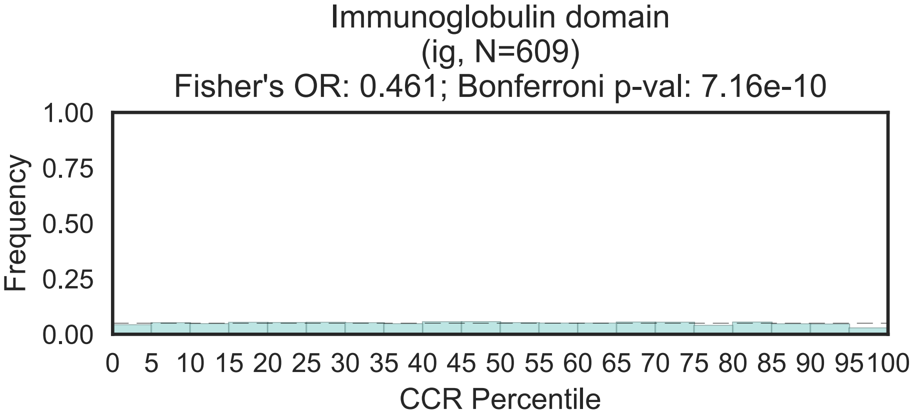

N-terminal domain from the human glycogen debranching enzyme
(hGDE_N, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Central domain of human glycogen debranching enzyme
(hGDE_central, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

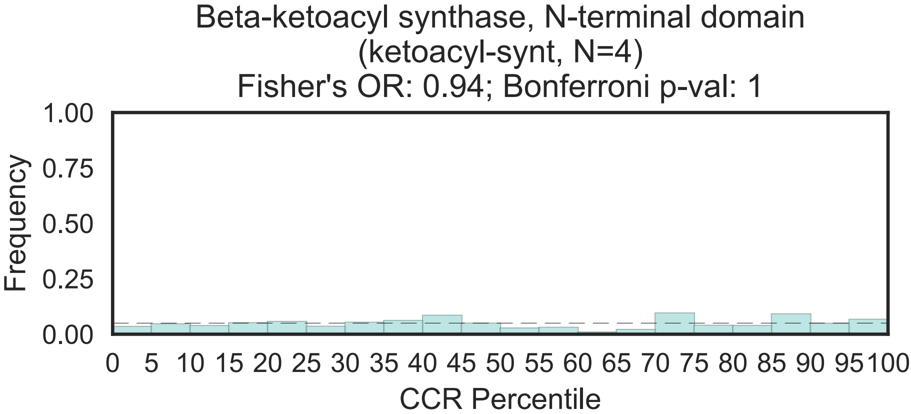

FHA Ki67 binding domain of hNIFK
(hNIFK_binding, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

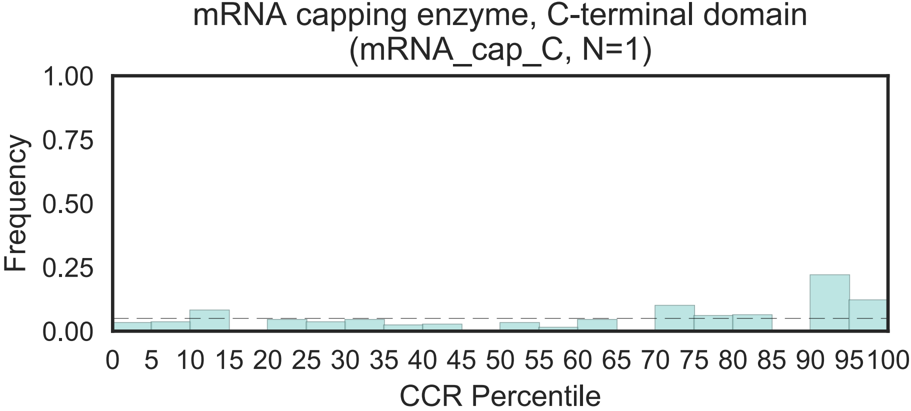

Helically-extended SH3 domain
(hSH3, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

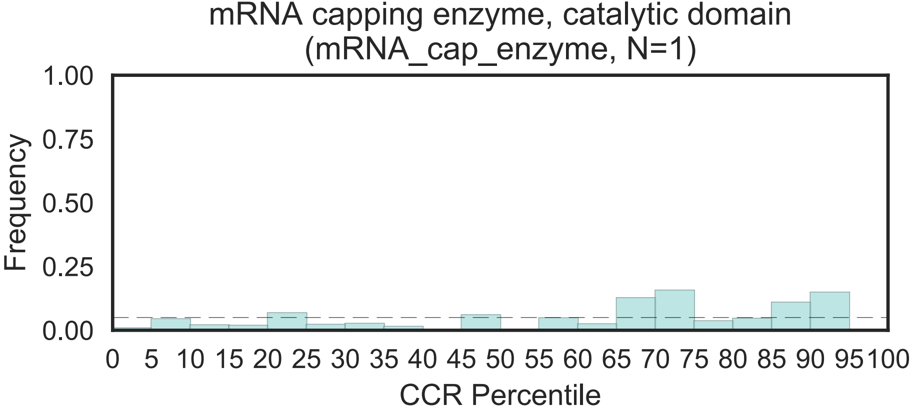

Inositol phosphatase
(hSac2, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



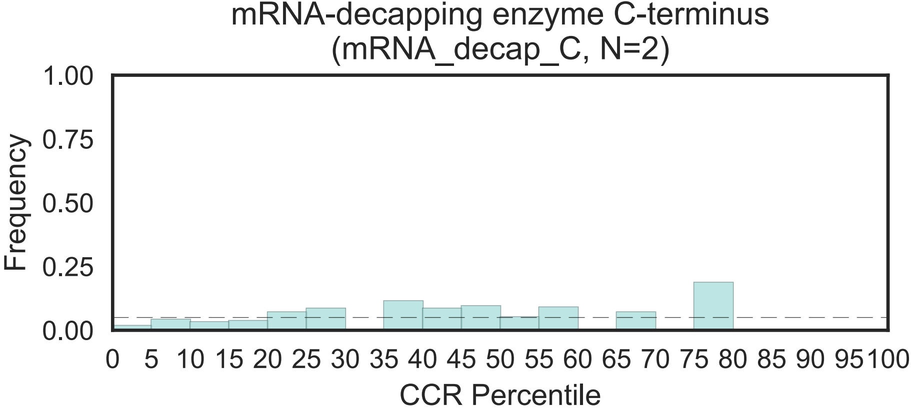
Immunoglobulin domain
(ig, N=609)
Fisher's OR: 0.461; Bonferroni p-val: 7.16e-10

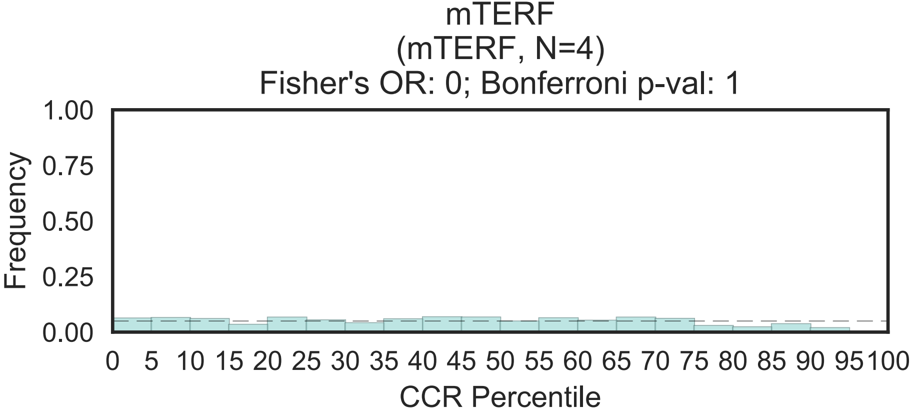

Beta-ketoacyl synthase, N-terminal domain
(ketoacyl-synt, N=4)
Fisher's OR: 0.94; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

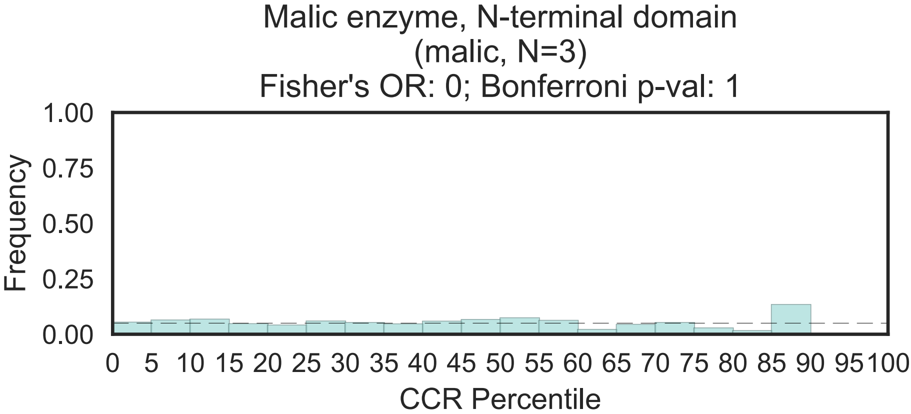

mRNA capping enzyme, C-terminal domain
(mRNA_cap_C, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

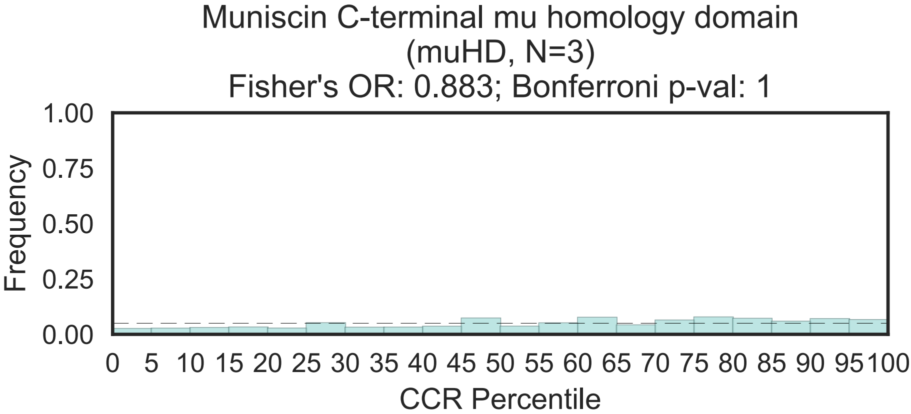


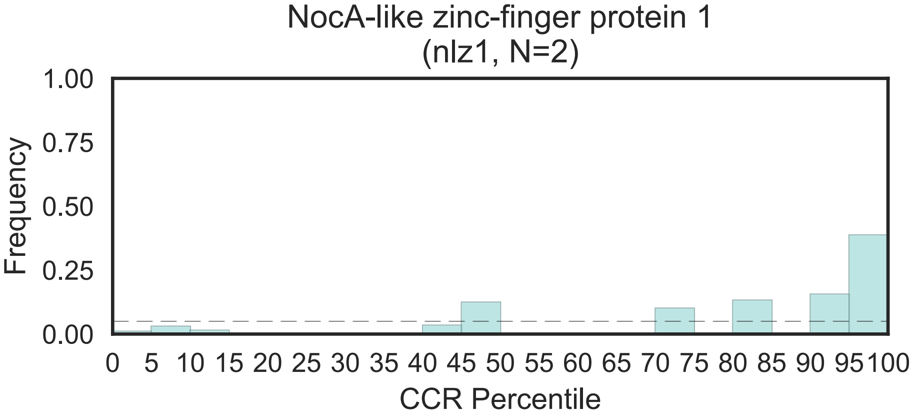
mRNA capping enzyme, catalytic domain (mRNA_cap_enzyme, N=1)

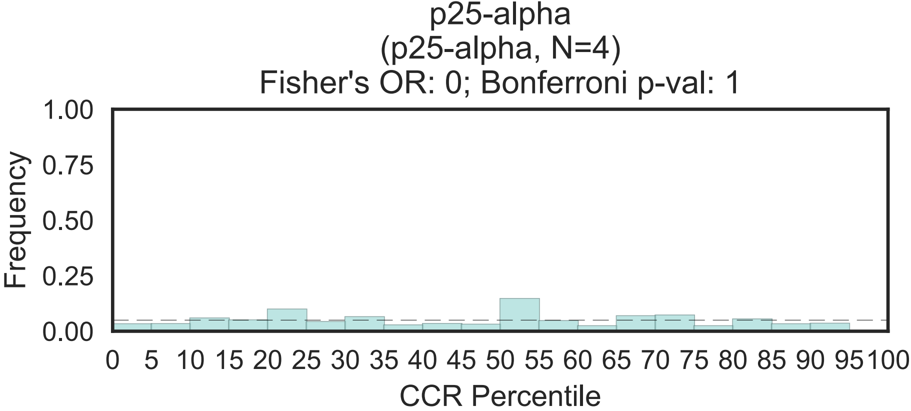

mRNA-decapping enzyme C-terminus
(mRNA_decap_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

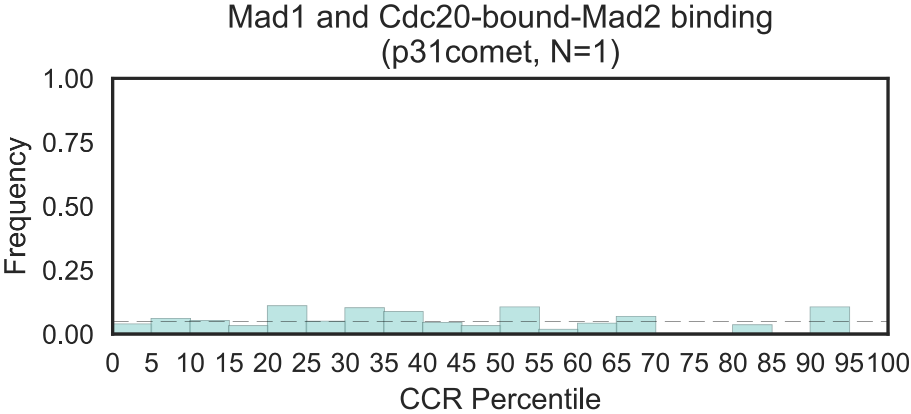

mTERF
(mTERF, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

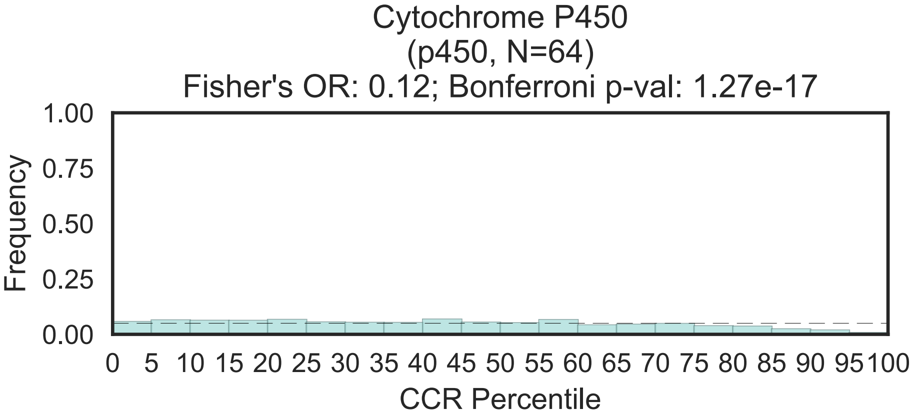

Malic enzyme, N-terminal domain
(malic, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

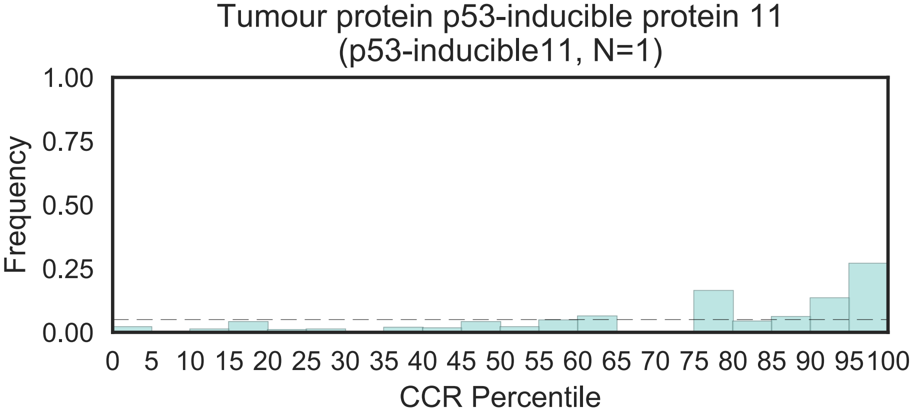

Muniscin C-terminal mu homology domain
(muHD, N=3)
Fisher's OR: 0.883; Bonferroni p-val: 1

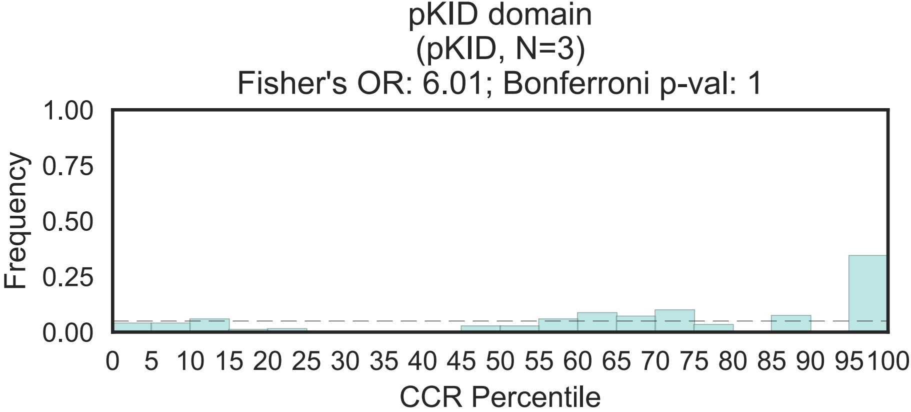

NocA-like zinc-finger protein 1
(nlz1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


p25-alpha
(p25-alpha, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

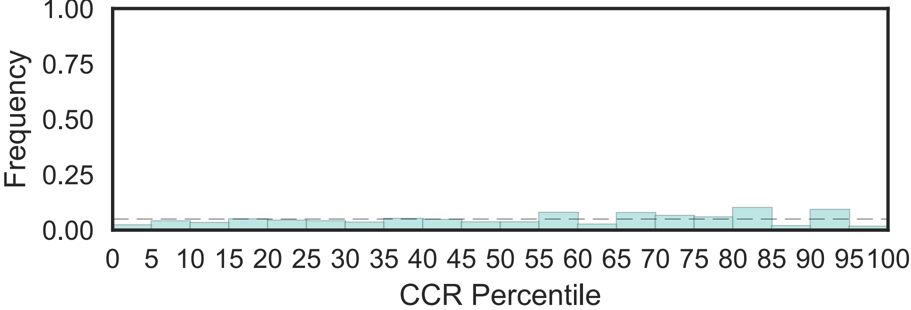

Mad1 and Cdc20-bound-Mad2 binding
(p31comet, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

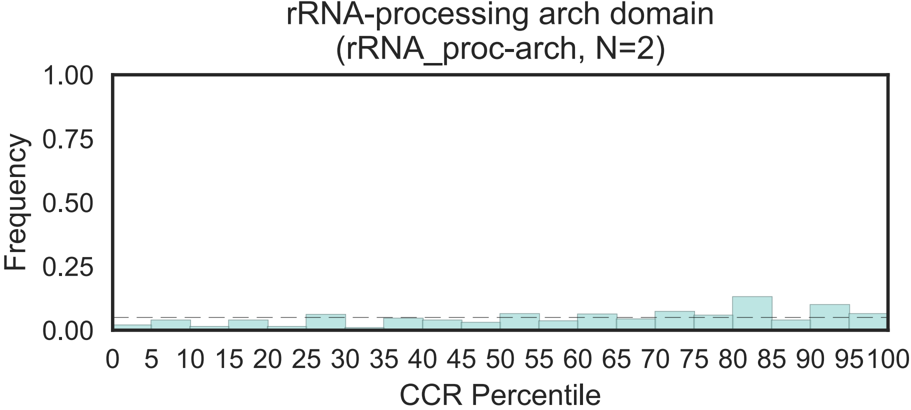

Cytochrome P450
(p450, N=64)
Fisher's OR: 0.12; Bonferroni p-val: 1.27e-17
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

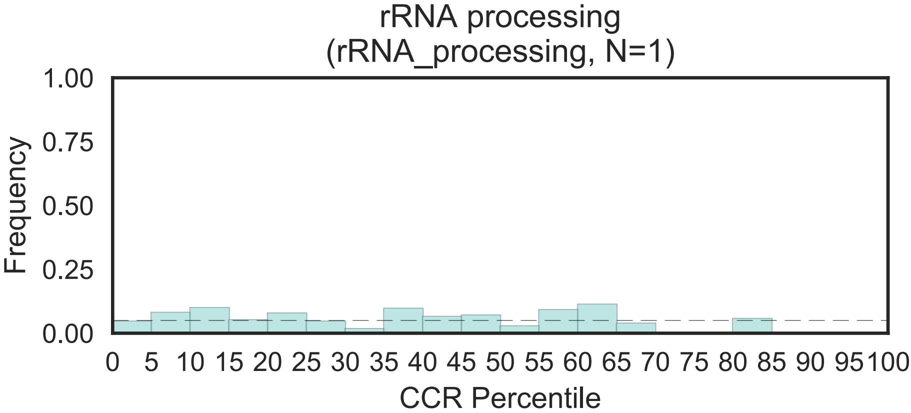

Tumour protein p53-inducible protein 11
(p53-inducible11, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

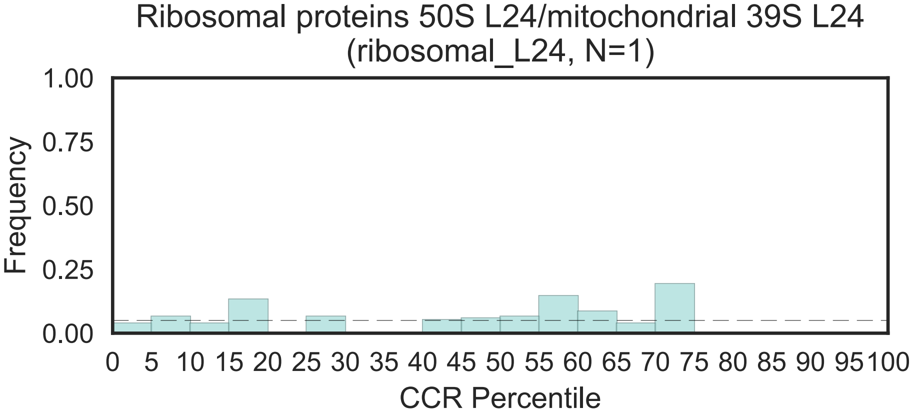

pKID domain
(pKID, N=3)
Fisher's OR: 6.01; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

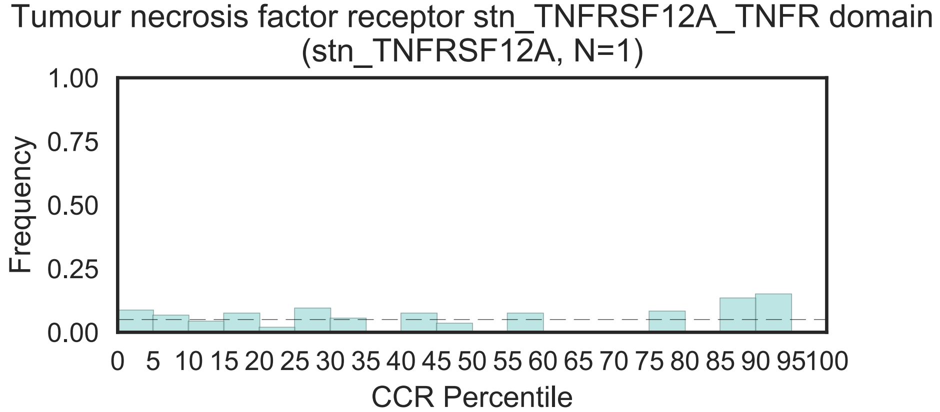
Polyprenyl synthetase
(polyprenyl_synt, N=4)
Fisher's OR: 0.316; Bonferroni p-val: 1

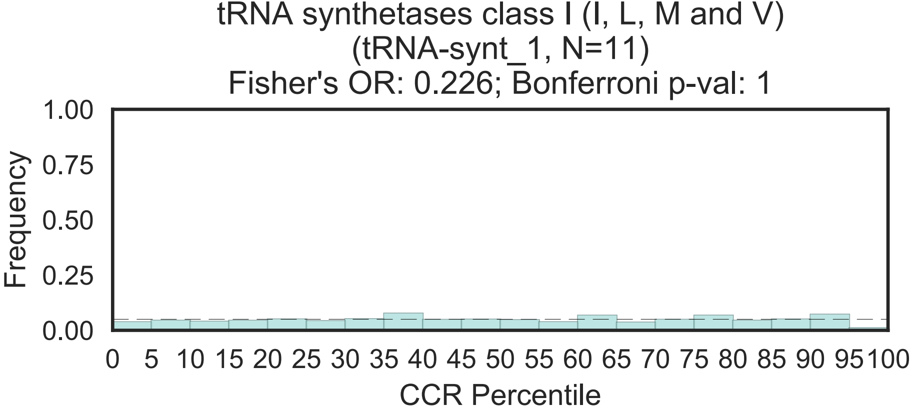



rRNA-processing arch domain
(rRNA_proc-arch, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

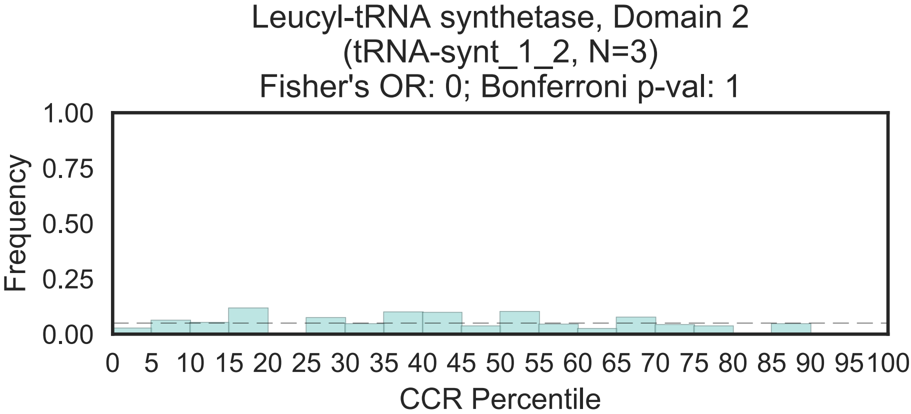

rRNA processing
(rRNA_processing, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

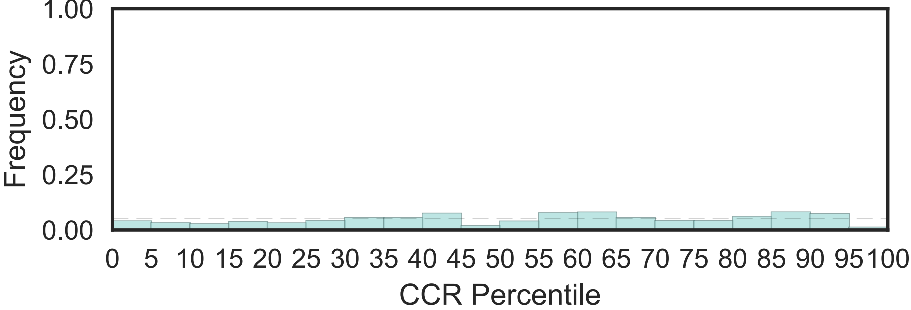

Ribosomal proteins 50S L24/mitochondrial 39S L24
(ribosomal_L24, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Tumour necrosis factor receptor stn_TNFRSF12A_TNFR domain
(stn_TNFRSF12A, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

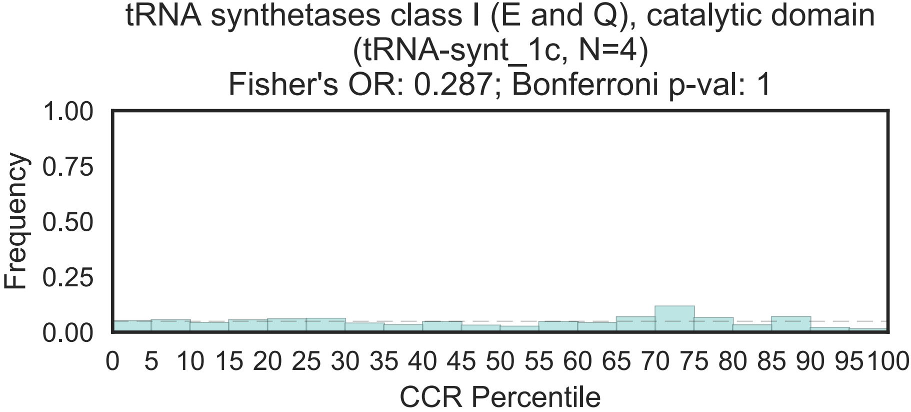


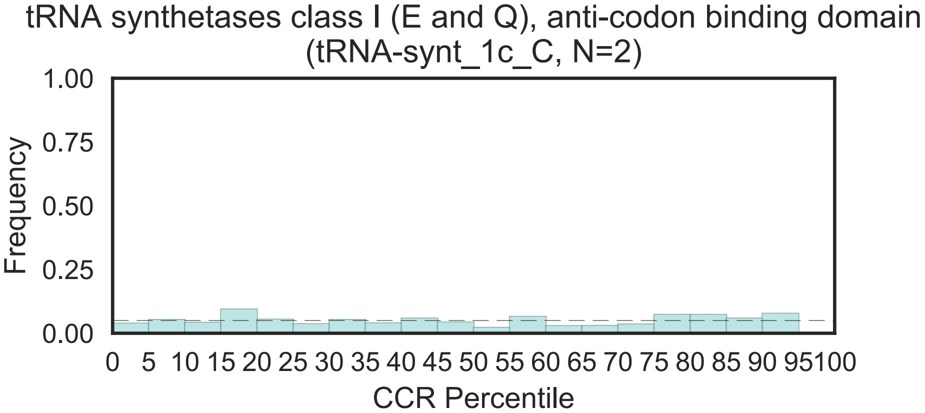
tRNA synthetases class I (I, L, M and V)
(tRNA-synt_1, N=11)
Fisher's OR: 0.226; Bonferroni p-val: 1

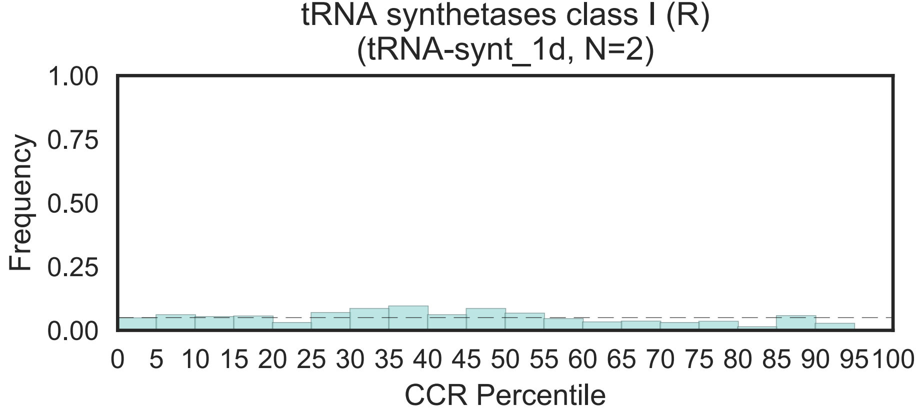

Leucyl-tRNA synthetase, Domain 2
(tRNA-synt_1_2, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

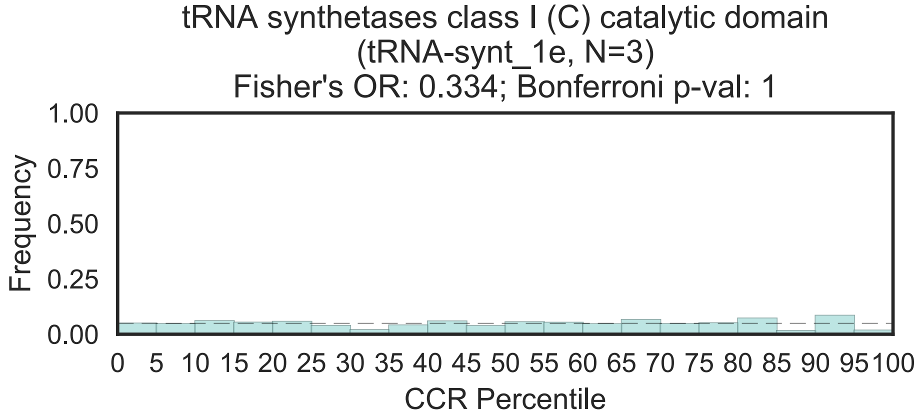


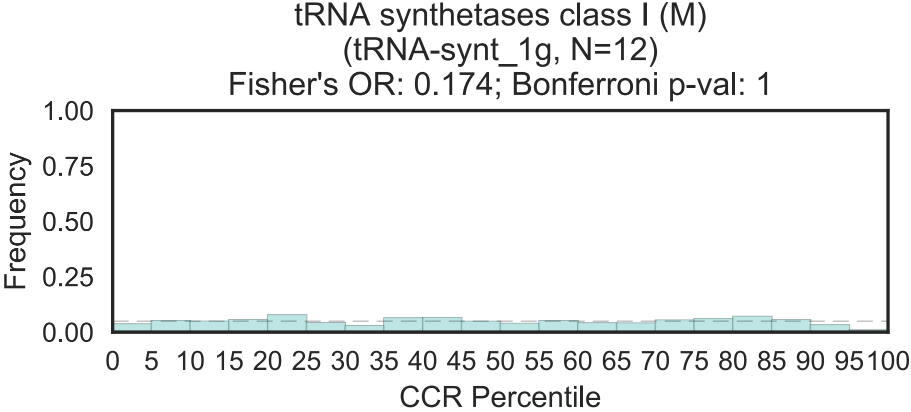
tRNA synthetases class I (W and Y)
(tRNA-synt_1b, N=4)
Fisher's OR: 0.251; Bonferroni p-val: 1


tRNA synthetases class I (E and Q), catalytic domain
(tRNA-synt_1c, N=4)
Fisher's OR: 0.287; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

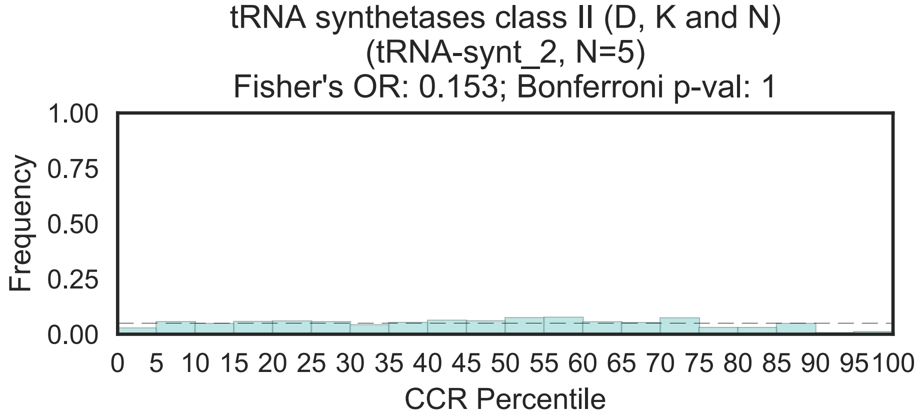

tRNA synthetases class I (E and Q), anti-codon binding domain
(tRNA-synt_1c_C, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

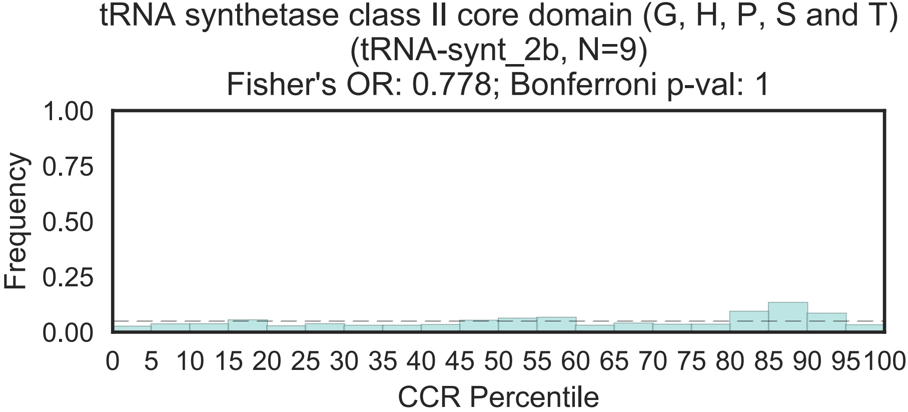

tRNA synthetases class I (R)
(tRNA-synt_1d, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

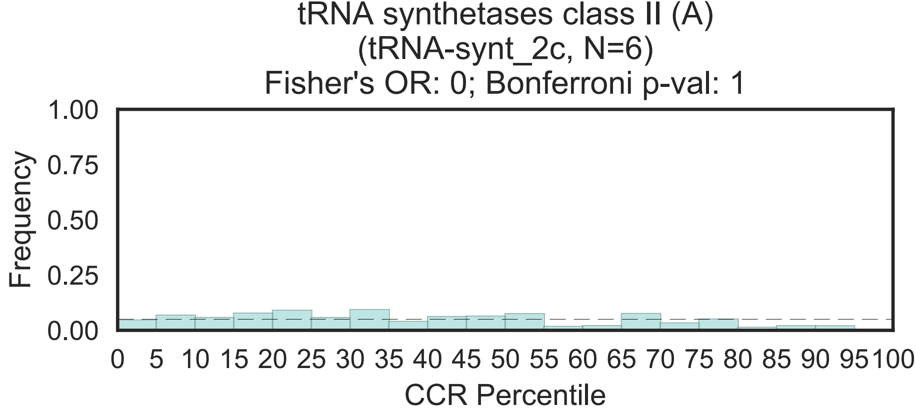

tRNA synthetases class I (C) catalytic domain
(tRNA-synt_1e, N=3)
Fisher's OR: 0.334; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

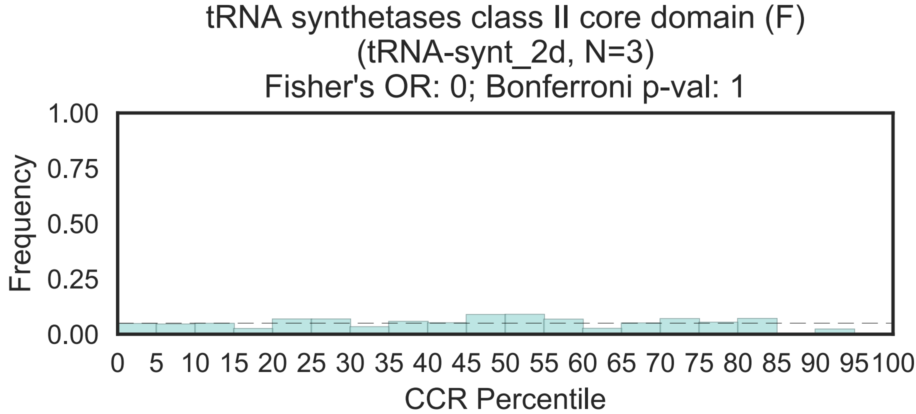


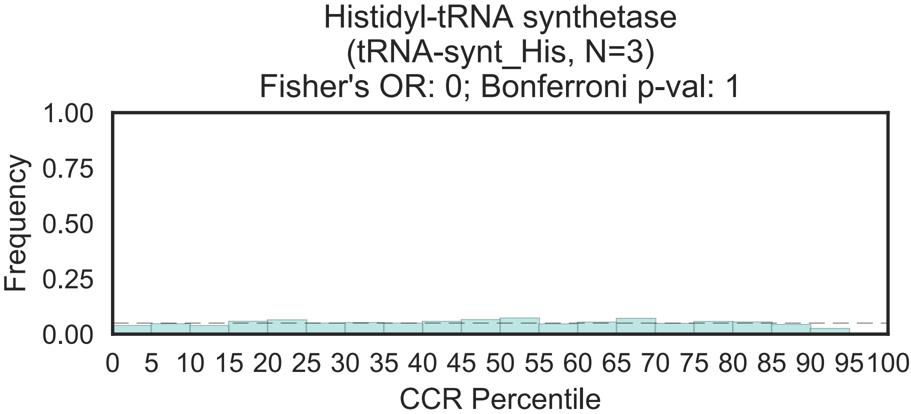
tRNA synthetases class I (M)
(tRNA-synt_1g, N=12)
Fisher's OR: 0.174; Bonferroni p-val: 1

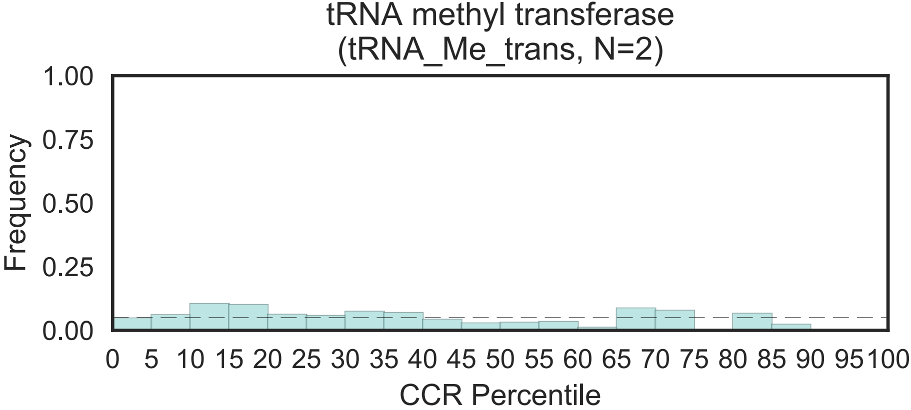

tRNA synthetases class II (D, K and N)
(tRNA-synt_2, N=5)
Fisher's OR: 0.153; Bonferroni p-val: 1

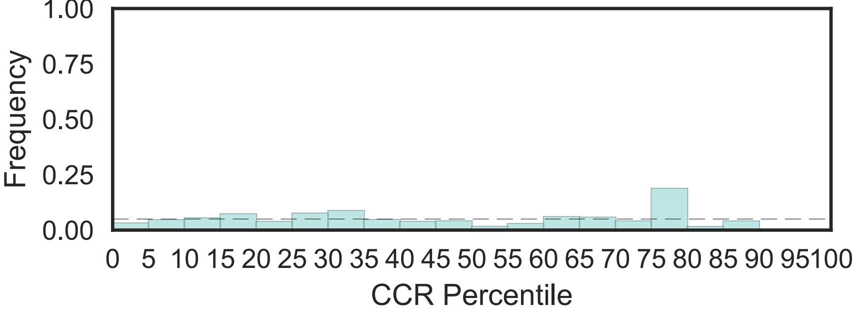

tRNA synthetase class II core domain (G, H, P, S and T)
(tRNA-synt_2b, N=9)
Fisher's OR: 0.778; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


tRNA synthetases class II (A)
(tRNA-synt_2c, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

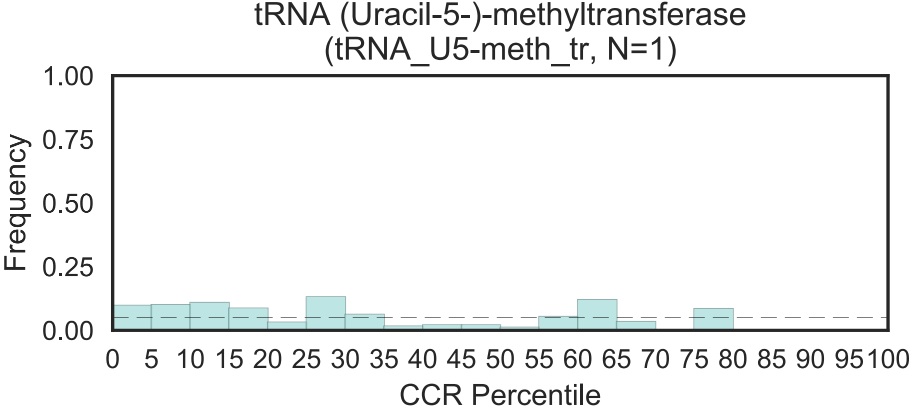

tRNA synthetases class II core domain (F)
(tRNA-synt_2d, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

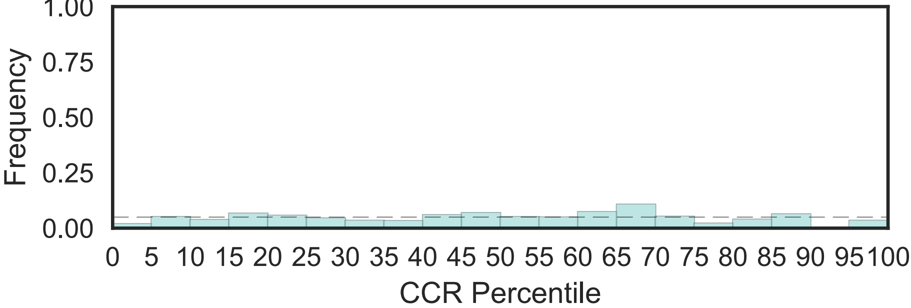

Histidyl-tRNA synthetase
(tRNA-synt_His, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


tRNA methyl transferase
(tRNA_Me_trans, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile

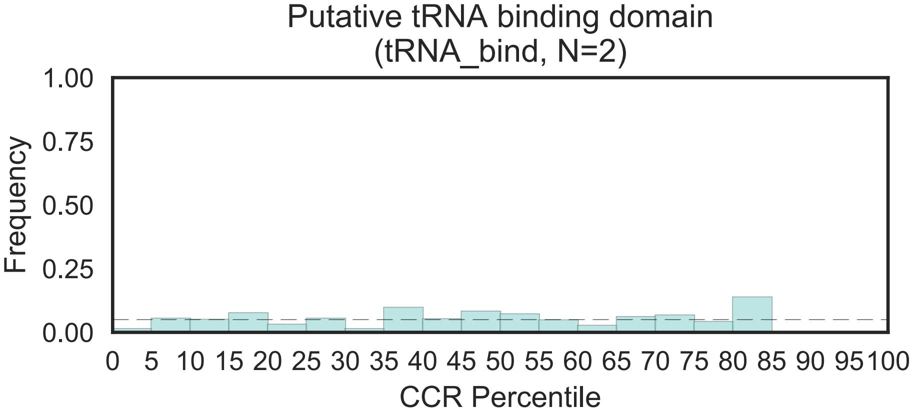


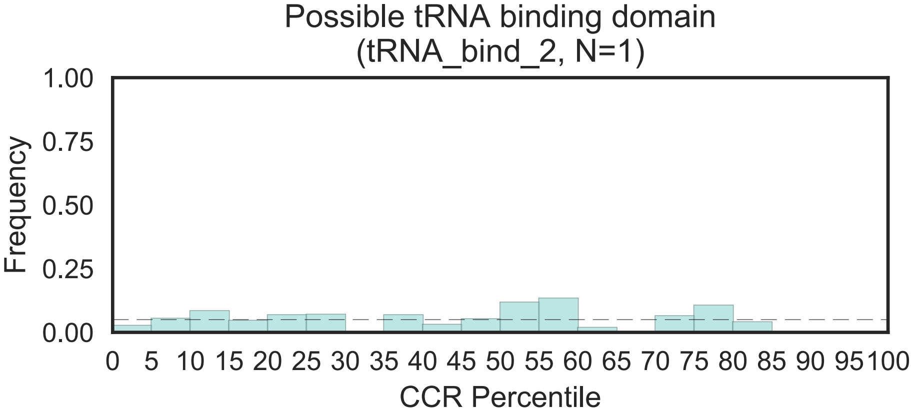
Threonyl and Alanyl tRNA synthetase second additional domain
(tRNA_SAD, N=7)
Fisher's OR: 0; Bonferroni p-val: 1


tRNA (Uracil-5-)-methyltransferase
(tRNA_U5-meth_tr, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

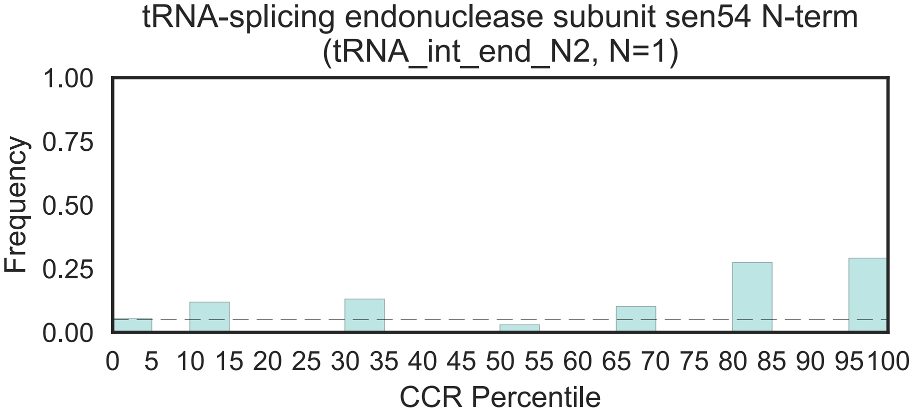


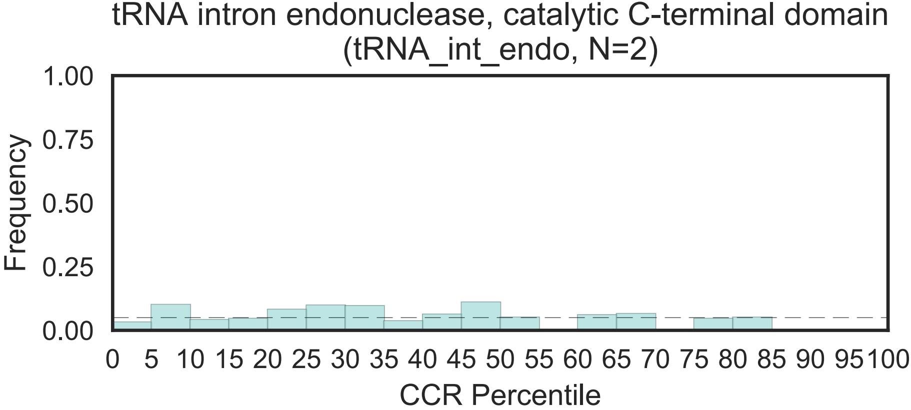
OB-fold nucleic acid binding domain
(tRNA_anti-codon, N=8)
Fisher's OR: 0.432; Bonferroni p-val: 1

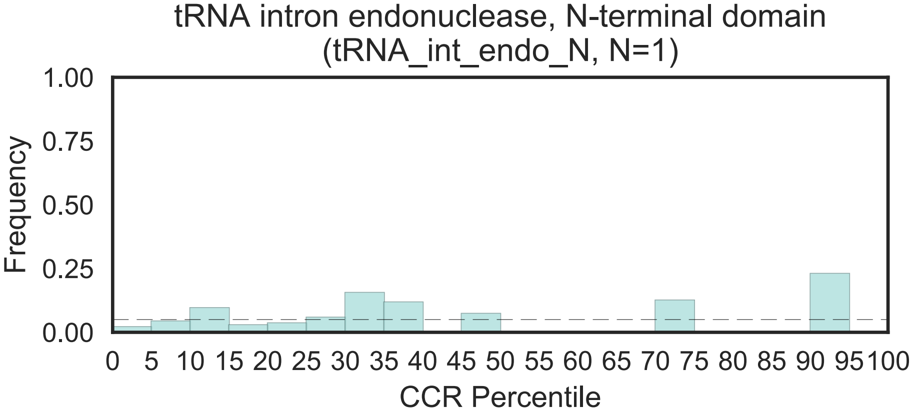

Putative tRNA binding domain
(tRNA_bind, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



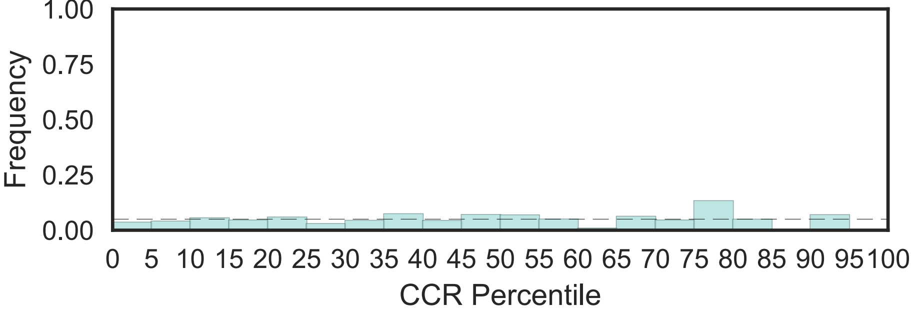
Possible tRNA binding domain
(tRNA_bind_2, N=1)

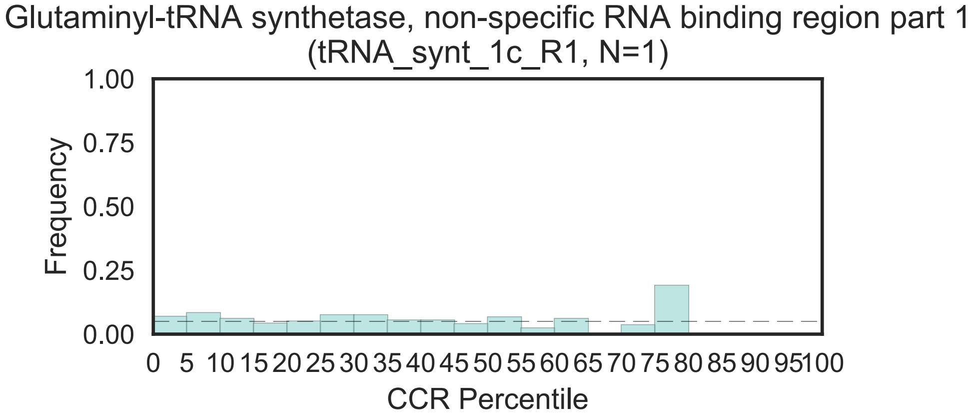

tRNA-splicing endonuclease subunit sen54 N-term
(tRNA_int_end_N2, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


tRNA intron endonuclease, catalytic C-terminal domain
(tRNA_int_endo, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

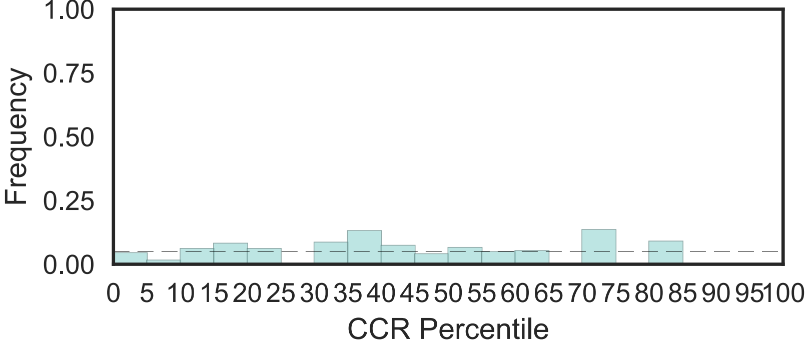

tRNA intron endonuclease, N-terminal domain
(tRNA_int_endo_N, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

tRNA (Guanine-1)-methyltransferase
(tRNA_m1G_MT, N=3)
Fisher's OR: 0; Bonferroni p-val: 1

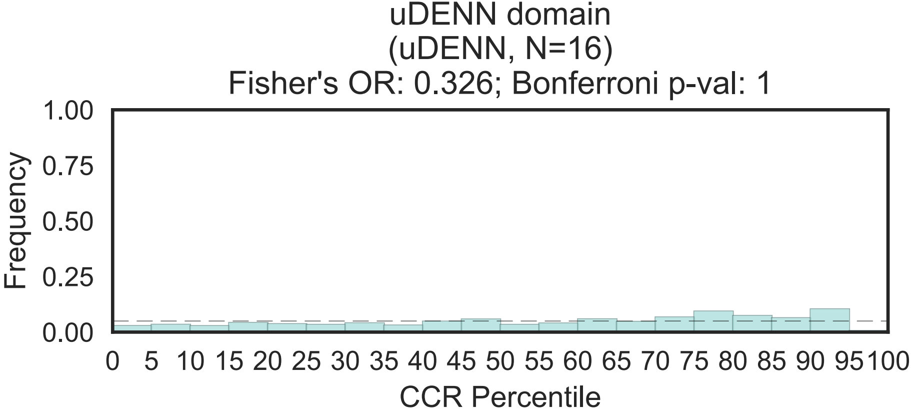


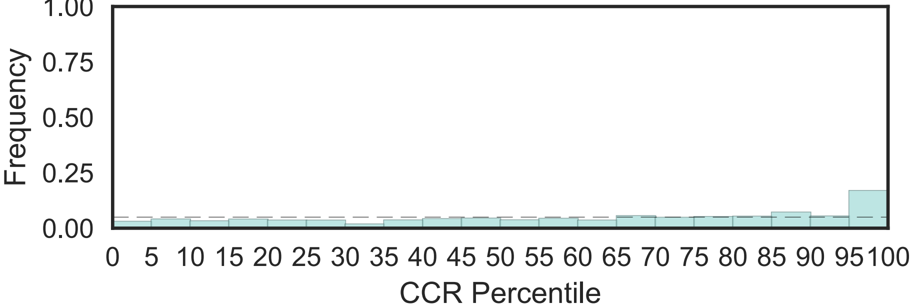


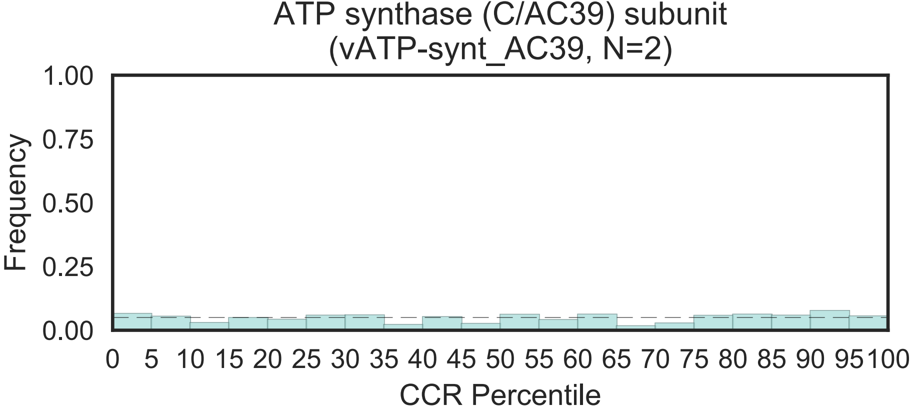
Glutaminyl-tRNA synthetase, non-specific RNA binding region part 1
(tRNA_synt_1c_R1, N=1)

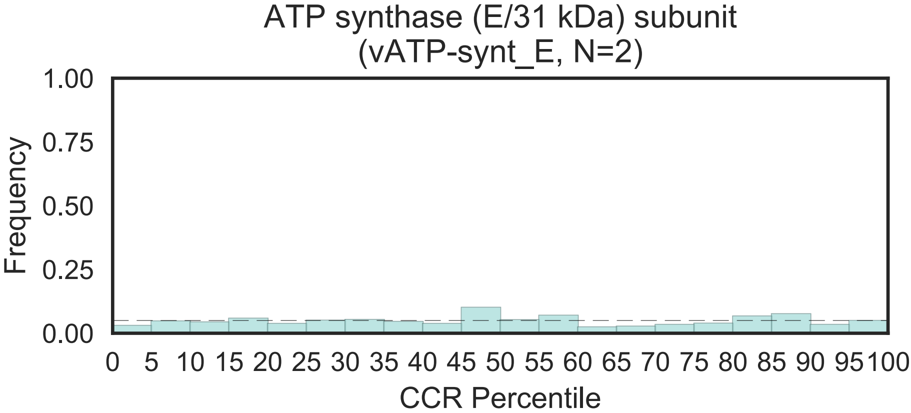


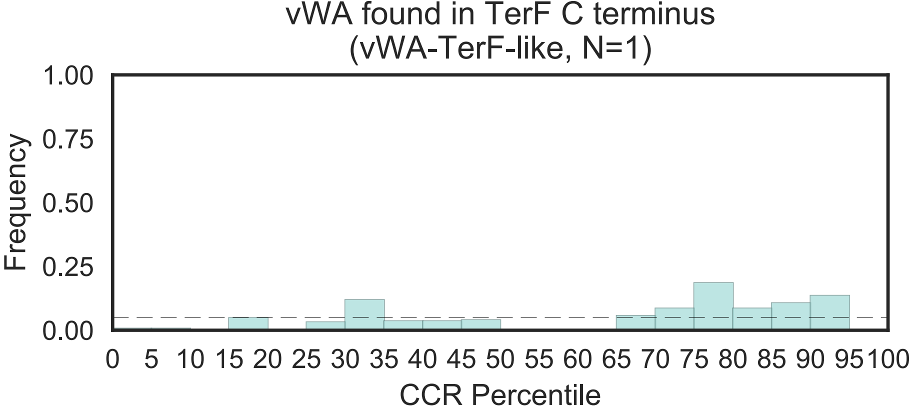
Glutaminyl-tRNA synthetase, non-specific RNA binding region part 2
(tRNA_synt_1c_R2, N=1)

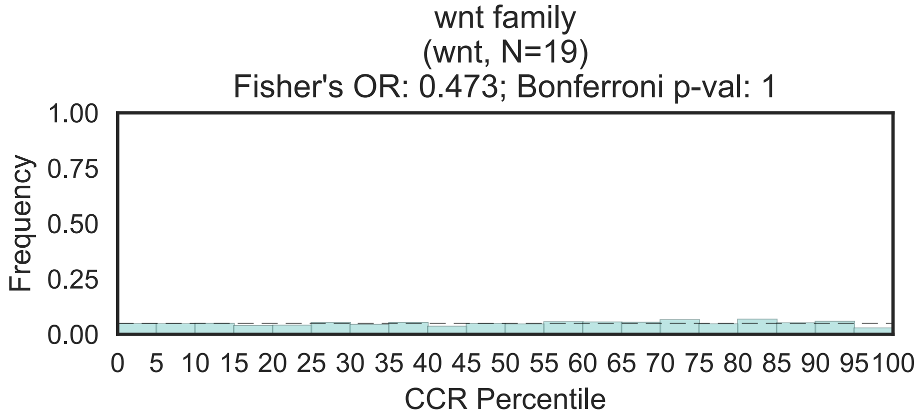

uDENN domain
(uDENN, N=16)
Fisher's OR: 0.326; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

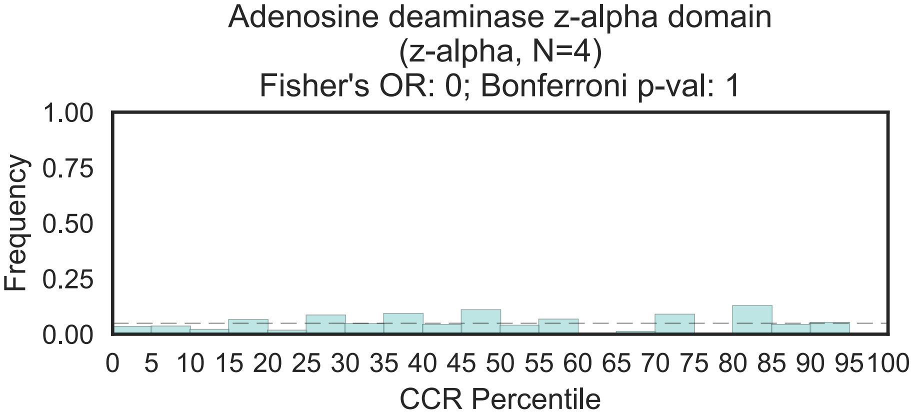

Ubiquitin family
(ubiquitin, N=63)
Fisher's OR: 2.03; Bonferroni p-val: 1

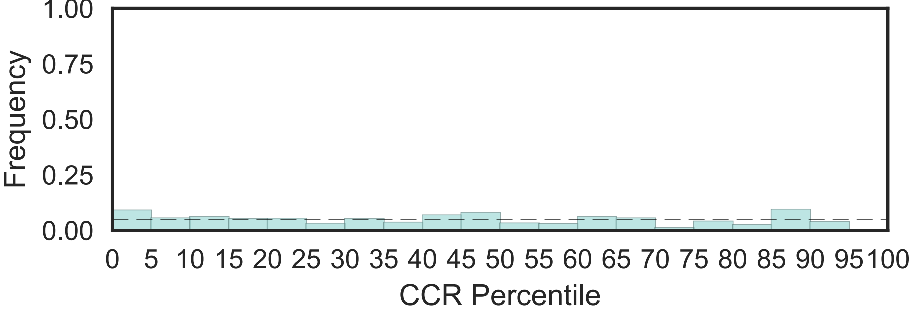

ATP synthase (C/AC39) subunit
(vATP-synt_AC39, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

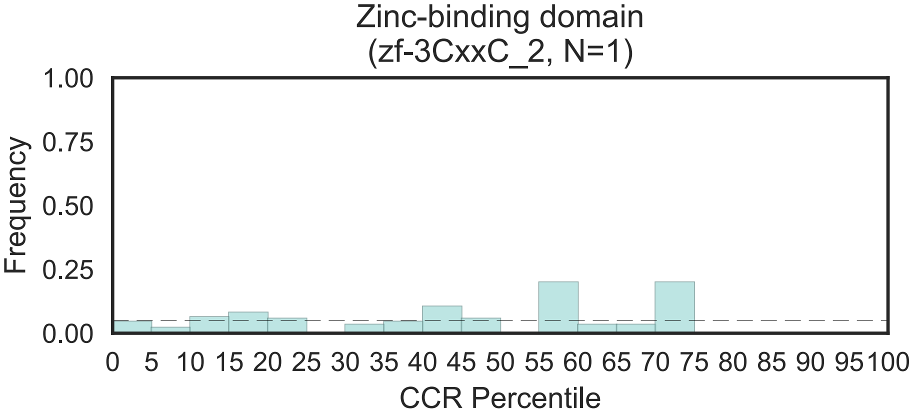

ATP synthase (E/31 kDa) subunit
(vATP-synt_E, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

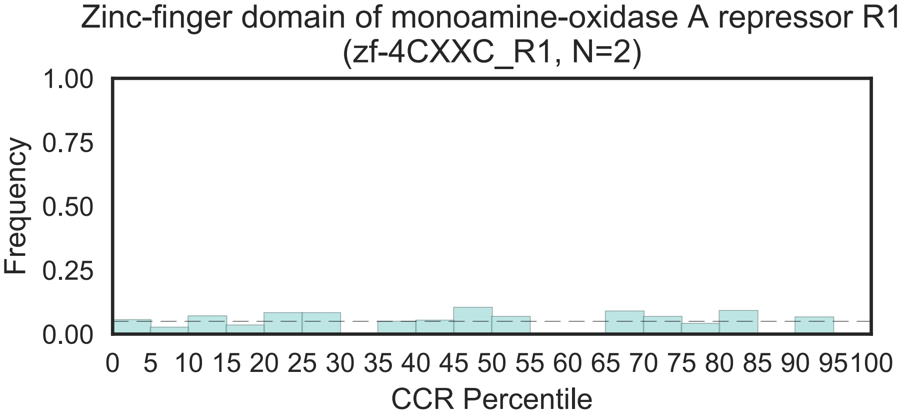

vWA found in TerF C terminus
(vWA-TerF-like, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

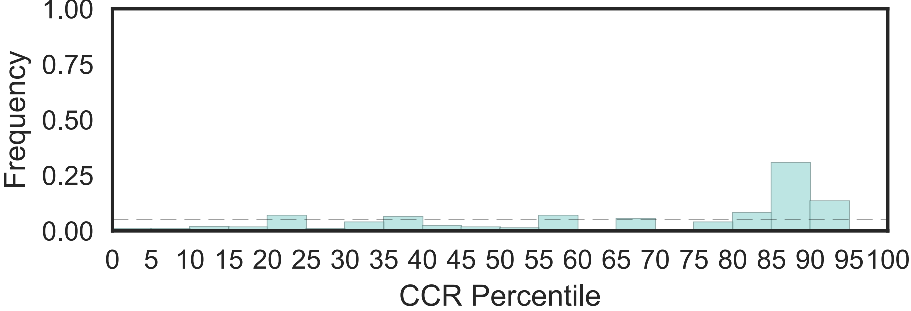

wnt family
(wnt, N=19)
Fisher's OR: 0.473; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Adenosine deaminase z-alpha domain
(z-alpha, N=4)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

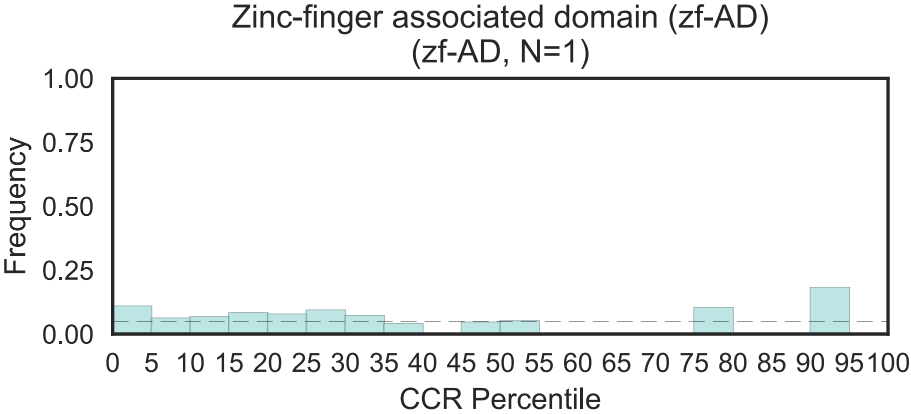

Zinc-binding domain
(zf-3CxxC, N=7)
Fisher's OR: 0; Bonferroni p-val: 1


Zinc-binding domain
(zf-3CxxC_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Zinc-finger domain of monoamine-oxidase A repressor R1
(zf-4CXXC_R1, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

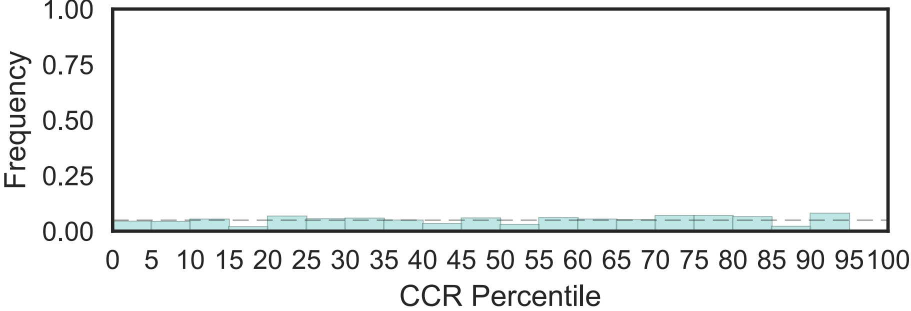


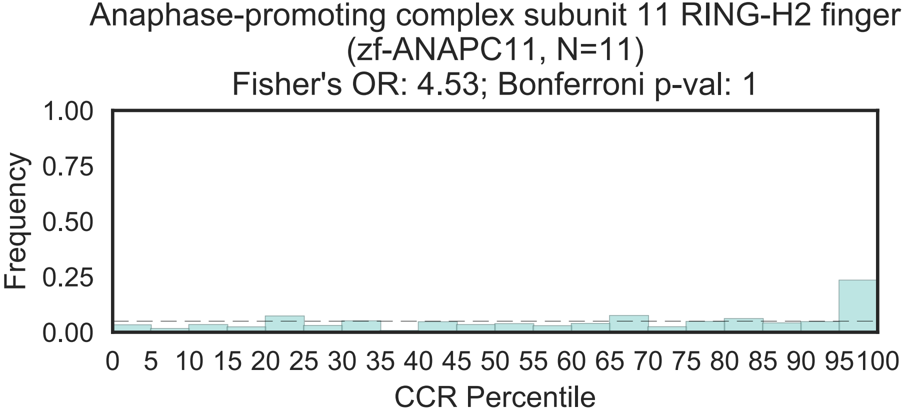
A20-like zinc finger
(zf-A20, N=11)
Fisher's OR: 0; Bonferroni p-val: 1



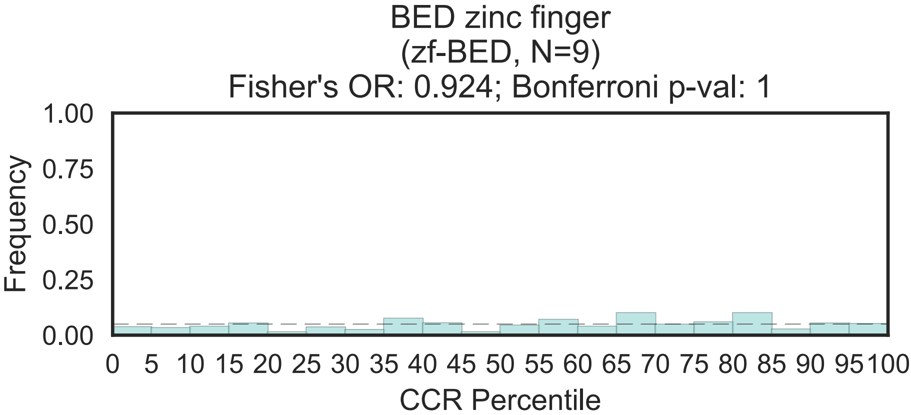
Zinc-finger associated domain (zf-AD)
(zf-AD, N=1)

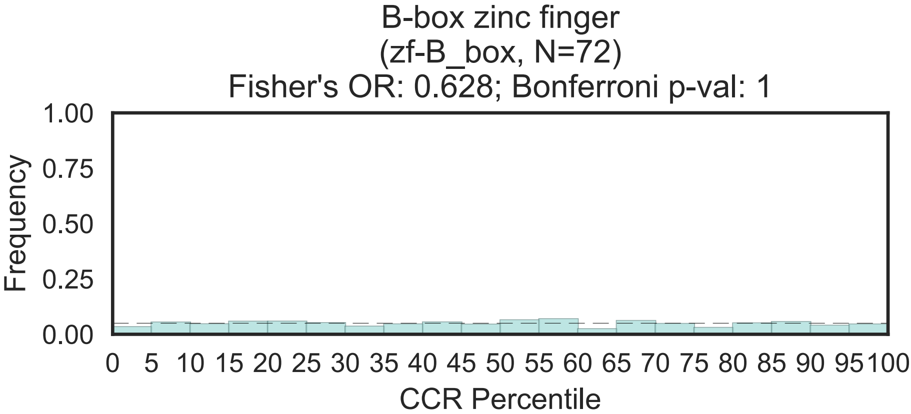
AN1-like Zinc finger
(zf-AN1, N=11)
Fisher's OR: 0; Bonferroni p-val: 1

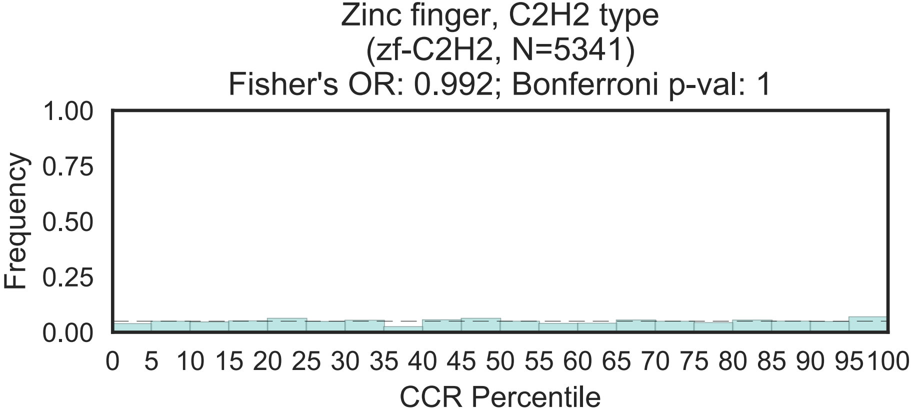




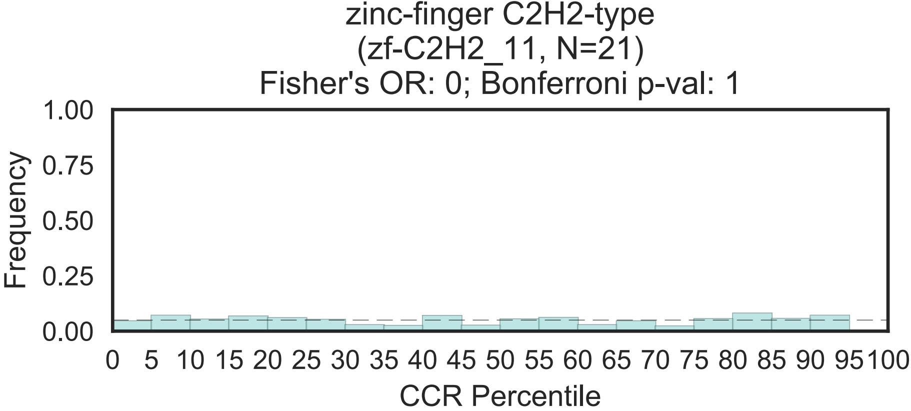
Anaphase-promoting complex subunit 11 RING-H2 finger
(zf-ANAPC11, N=11)
Fisher's OR: 4.53; Bonferroni p-val: 1

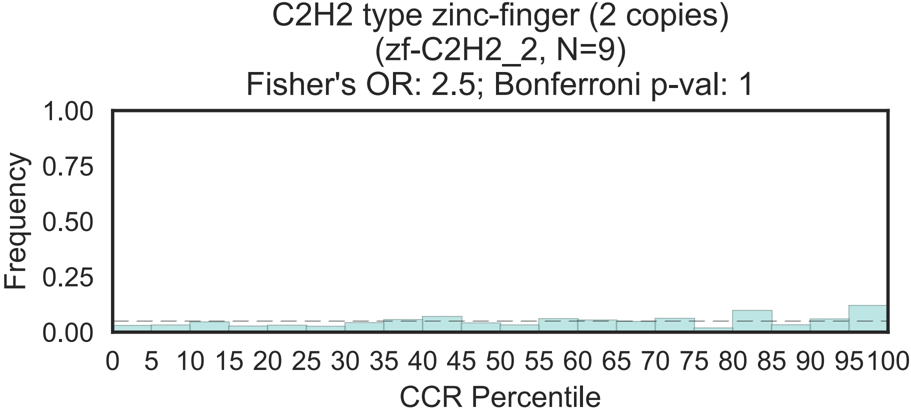

BED zinc finger
(zf-BED, N=9)
Fisher's OR: 0.924; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

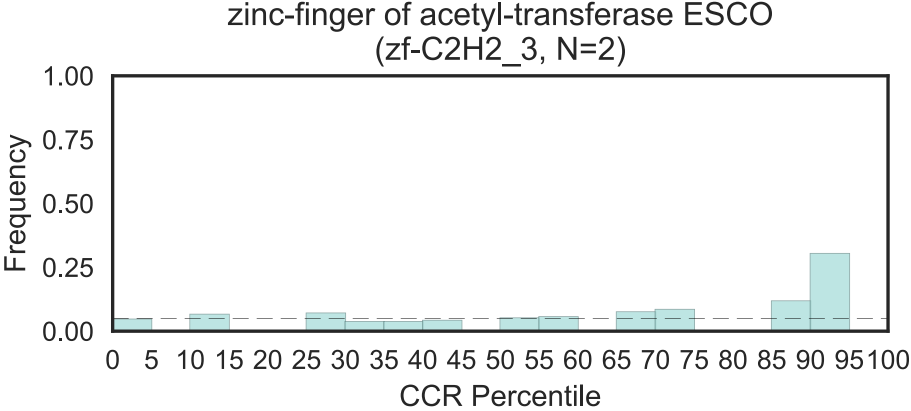

B-box zinc finger
(zf-B_box, N=72)
Fisher's OR: 0.628; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

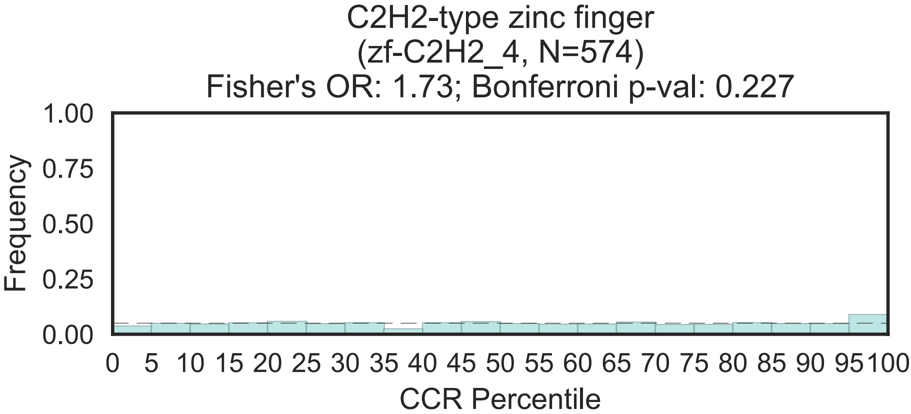


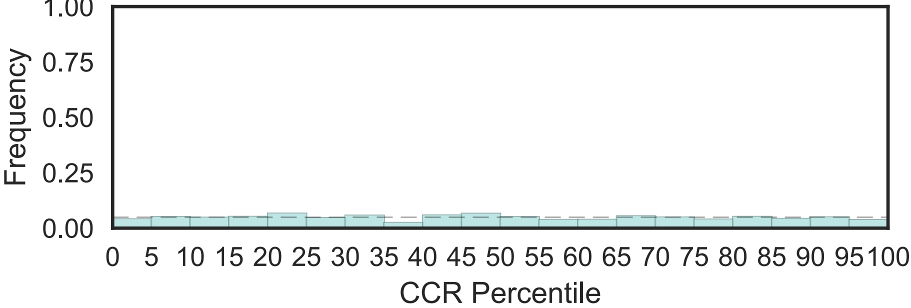
Zinc finger, C2H2 type
(zf-C2H2, N=5341)
Fisher's OR: 0.992; Bonferroni p-val: 1


zinc-finger C2H2-type
(zf-C2H2_11, N=21)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

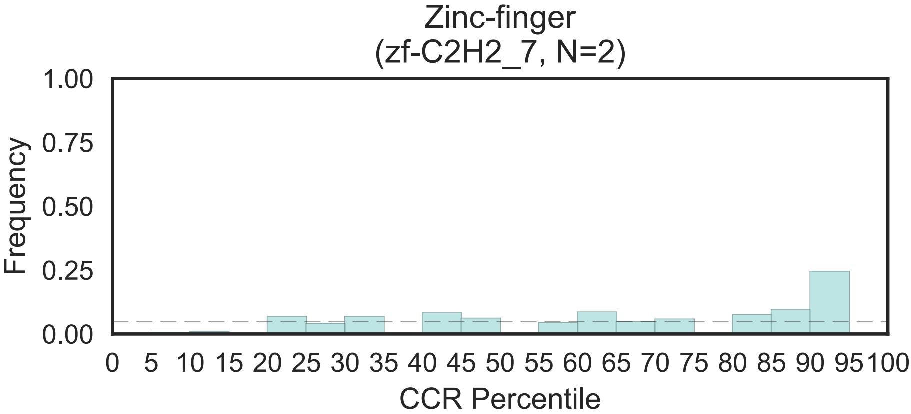

C2H2 type zinc-finger (2 copies)
(zf-C2H2_2, N=9)
Fisher's OR: 2.5; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

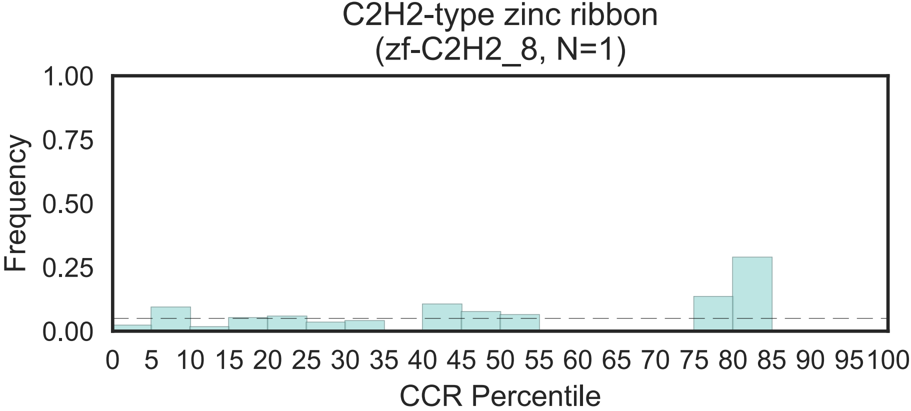

zinc-finger of acetyl-transferase ESCO
(zf-C2H2_3, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

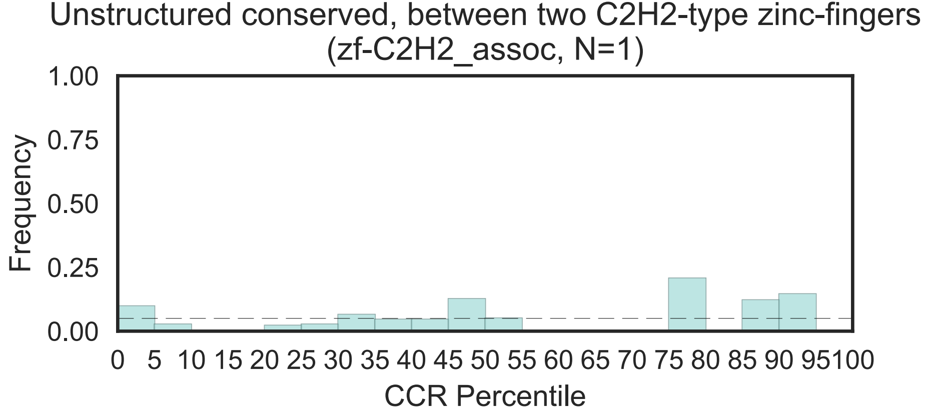

C2H2-type zinc finger
(zf-C2H2_4, N=574)
Fisher's OR: 1.73; Bonferroni p-val: 0.227
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile



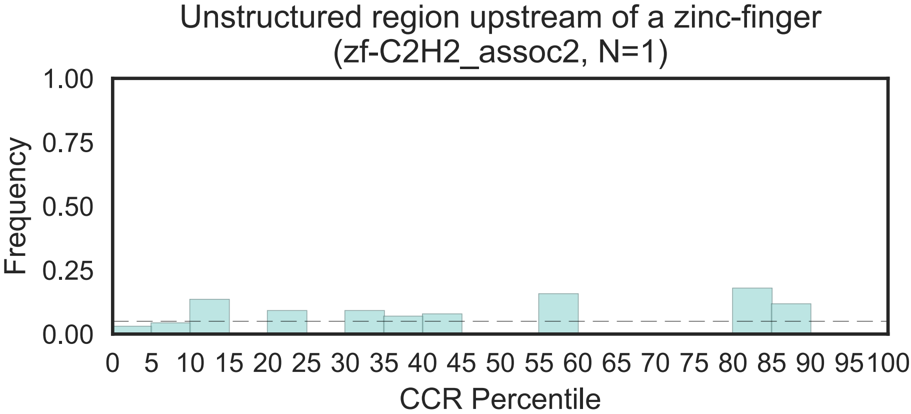
C2H2-type zinc finger
(zf-C2H2_6, N=1717)
Fisher's OR: 0.711; Bonferroni p-val: 1


Zinc-finger
(zf-C2H2_7, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

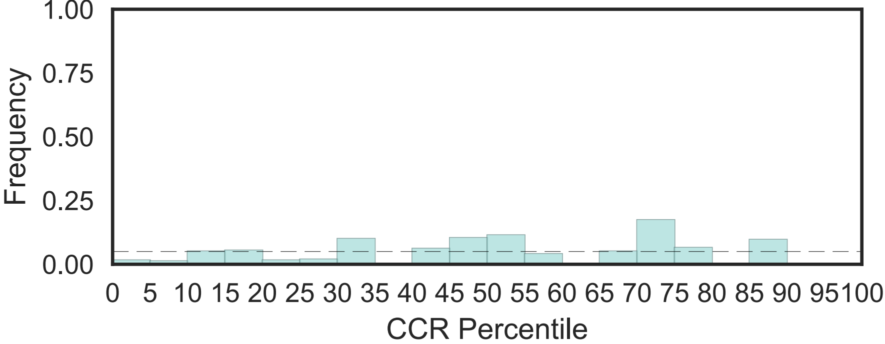

C2H2-type zinc ribbon
(zf-C2H2_8, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

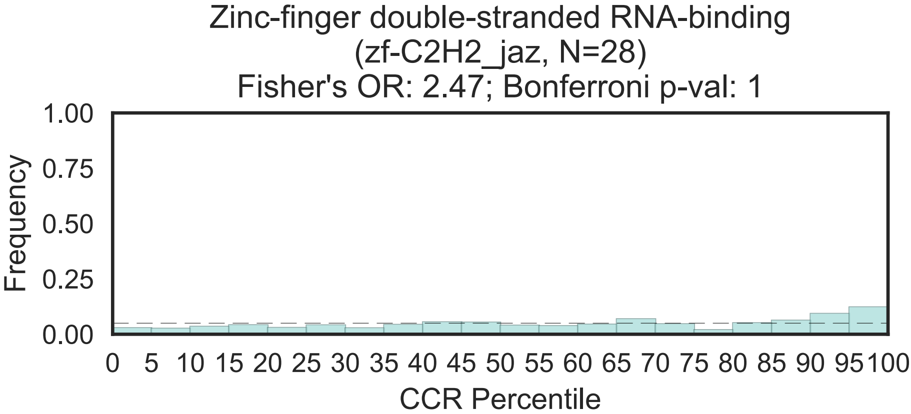


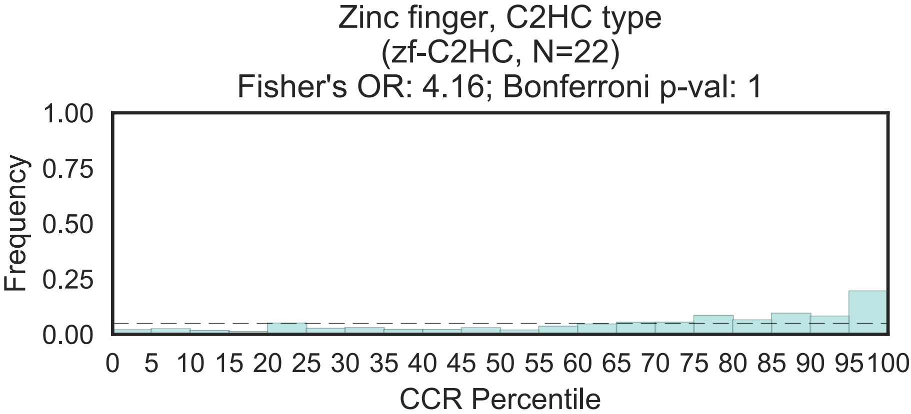
Unstructured conserved, between two C2H2-type zinc-fingers (zf-C2H2_assoc, N=1)

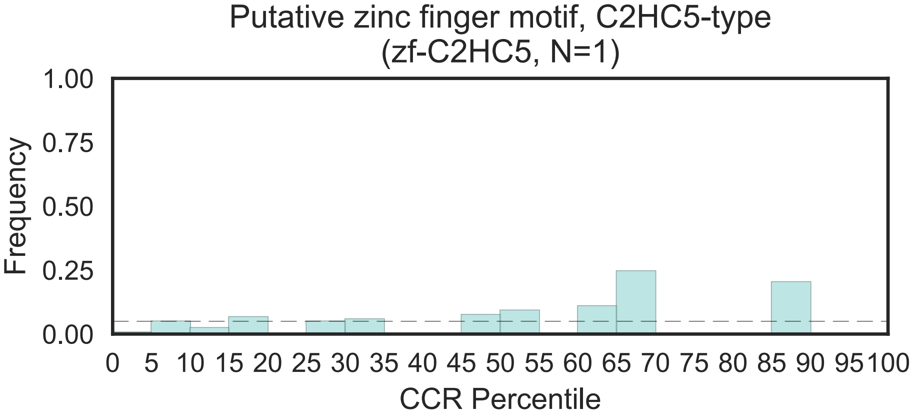


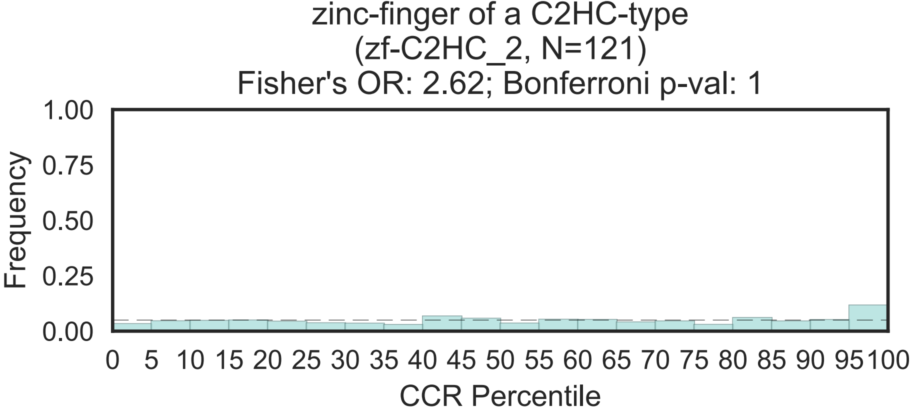
Unstructured region upstream of a zinc-finger
(zf-C2H2_assoc2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

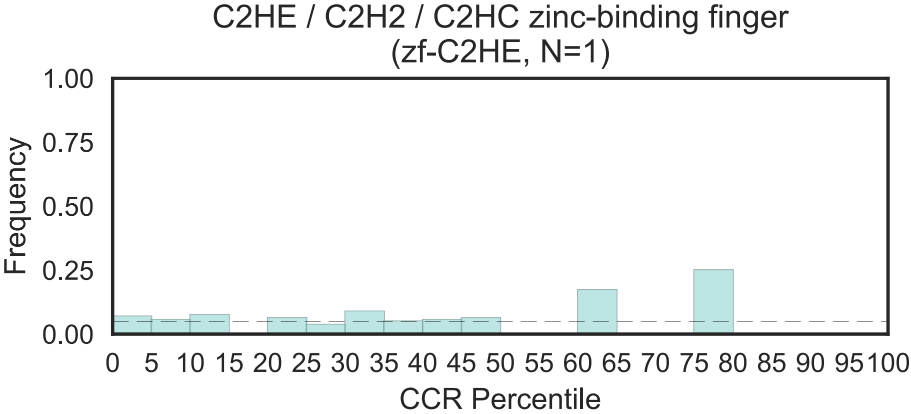

Putative zinc-finger between two C2H2 zinc-fingers on Patz
(zf-C2H2_assoc3, N=1)

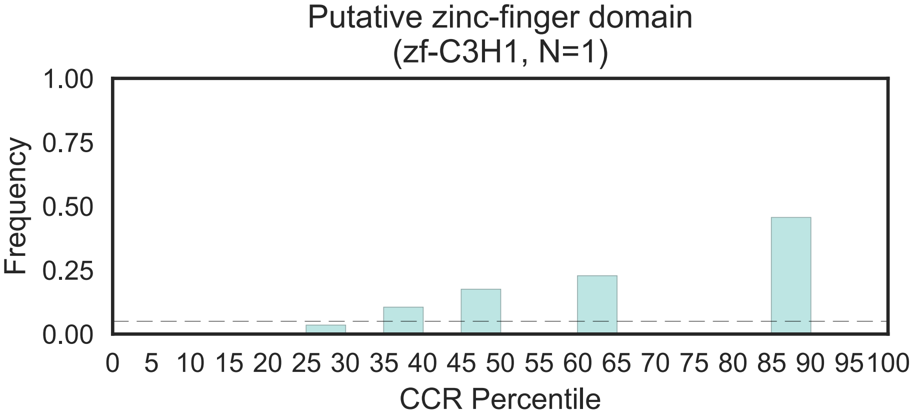

Zinc-finger double-stranded RNA-binding
(zf-C2H2_jaz, N=28)
Fisher's OR: 2.47; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

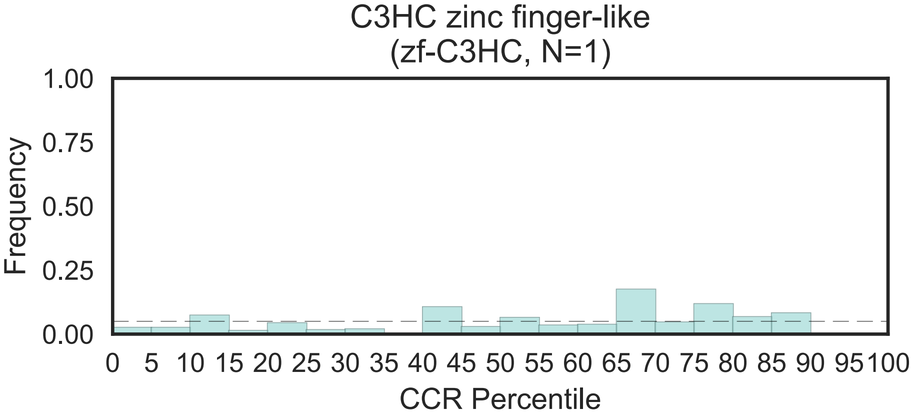

Zinc finger, C2HC type
(zf-C2HC, N=22)
Fisher's OR: 4.16; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

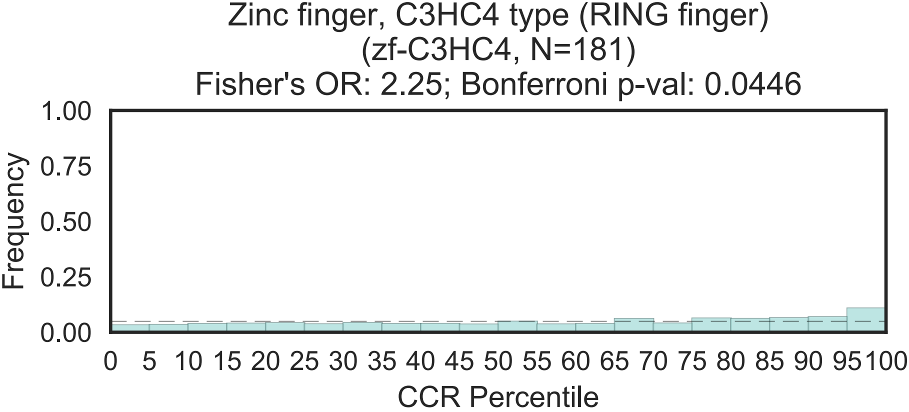

Putative zinc finger motif, C2HC5-type
(zf-C2HC5, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

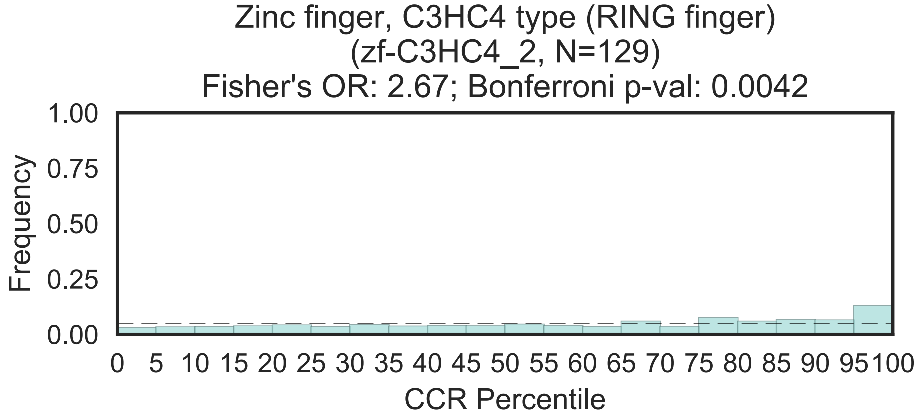

zinc-finger of a C2HC-type
(zf-C2HC_2, N=121)
Fisher's OR: 2.62; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

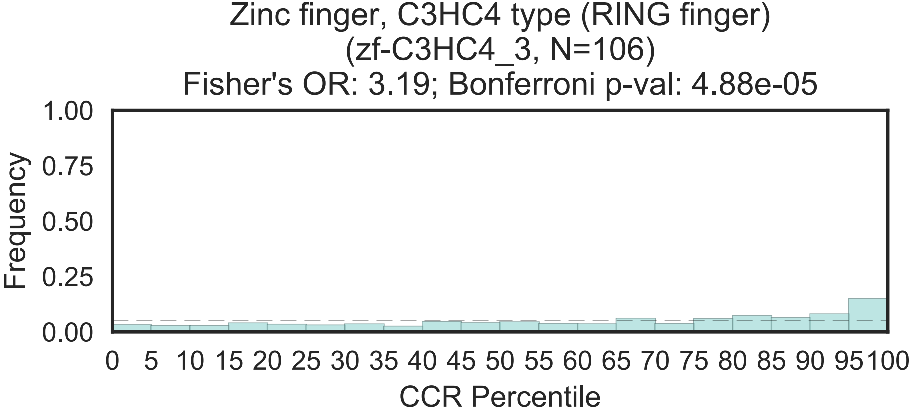

C2HE / C2H2 / C2HC zinc-binding finger
(zf-C2HE, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

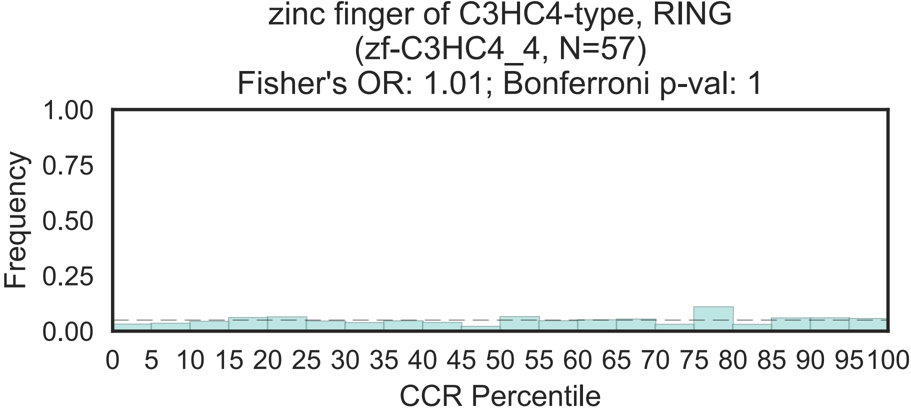

Putative zinc-finger domain
(zf-C3H1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

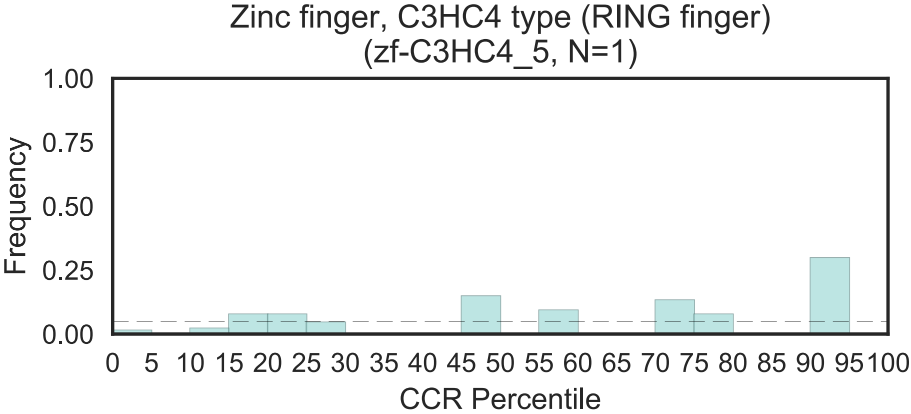

C3HC zinc finger-like
(zf-C3HC, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

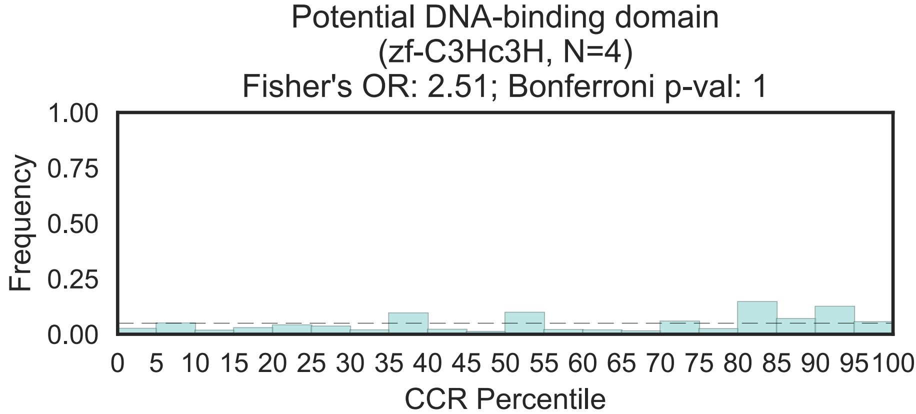

Zinc finger, C3HC4 type (RING finger)
(zf-C3HC4, N=181)
Fisher's OR: 2.25; Bonferroni p-val: 0.0446
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

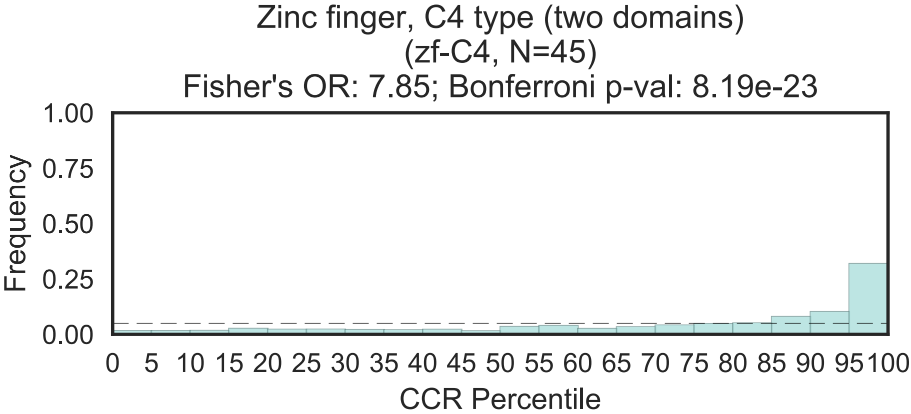

Zinc finger, C3HC4 type (RING finger)
(zf-C3HC4_2, N=129)
Fisher's OR: 2.67; Bonferroni p-val: 0.0042
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Zinc finger, C3HC4 type (RING finger)
(zf-C3HC4_3, N=106)
Fisher's OR: 3.19; Bonferroni p-val: 4.88e-05
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

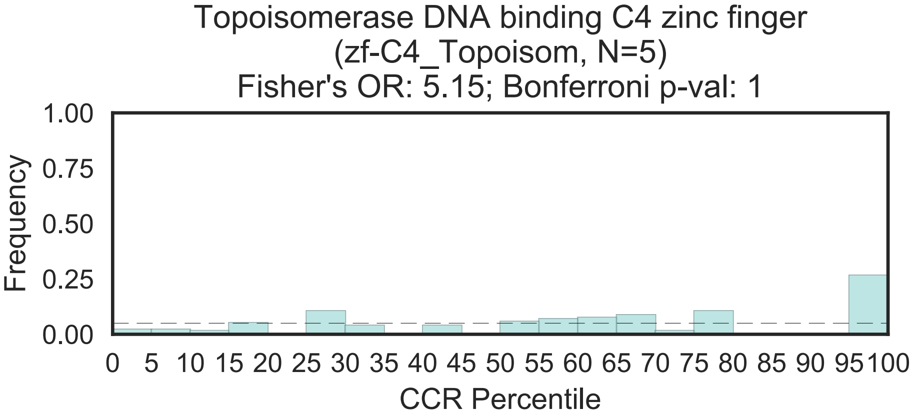

zinc finger of C3HC4-type, RING
(zf-C3HC4_4, N=57)
Fisher's OR: 1.01; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

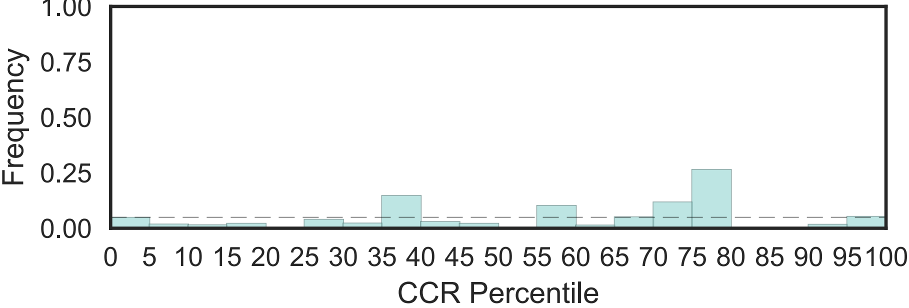

Zinc finger, C3HC4 type (RING finger)
(zf-C3HC4_5, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Potential DNA-binding domain
(zf-C3Hc3H, N=4)
Fisher's OR: 2.51; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

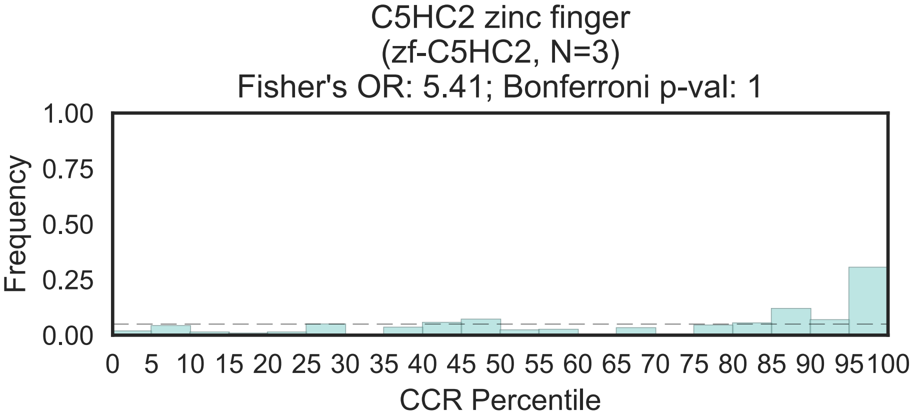


Zinc finger, C4 type (two domains)
(zf-C4, N=45)
Fisher's OR: 7.85; Bonferroni p-val: 8.19e-23

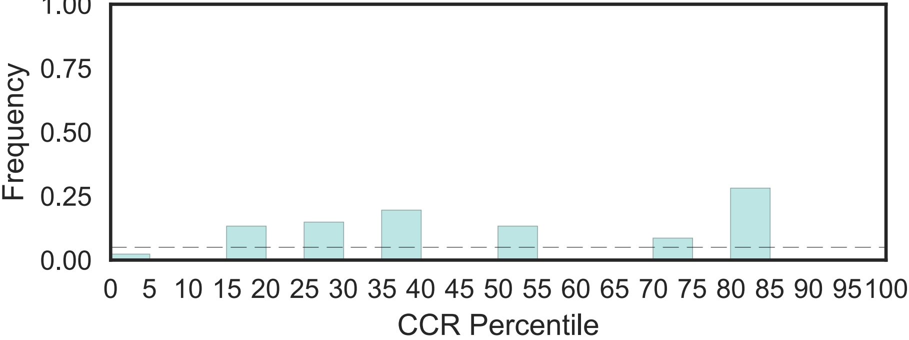

Topoisomerase DNA binding C4 zinc finger
(zf-C4_Topoisom, N=5)
Fisher's OR: 5.15; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

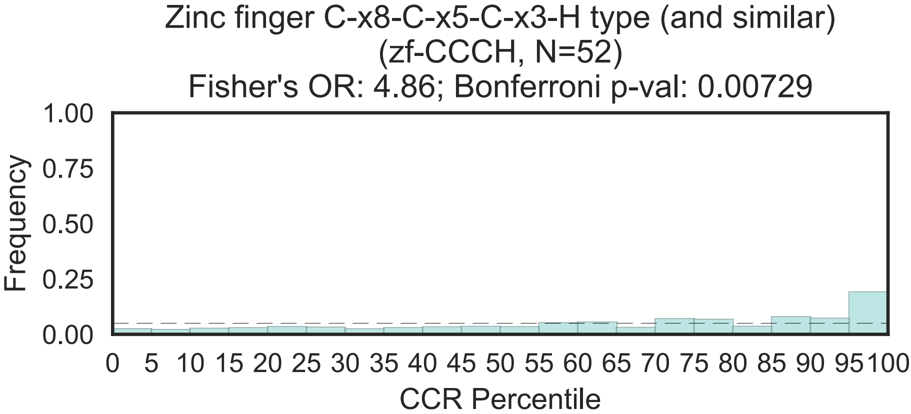


C4-type zinc-finger of DNA polymerase delta
(zf-C4pol, N=3)
Fisher's OR: 2.04; Bonferroni p-val: 1

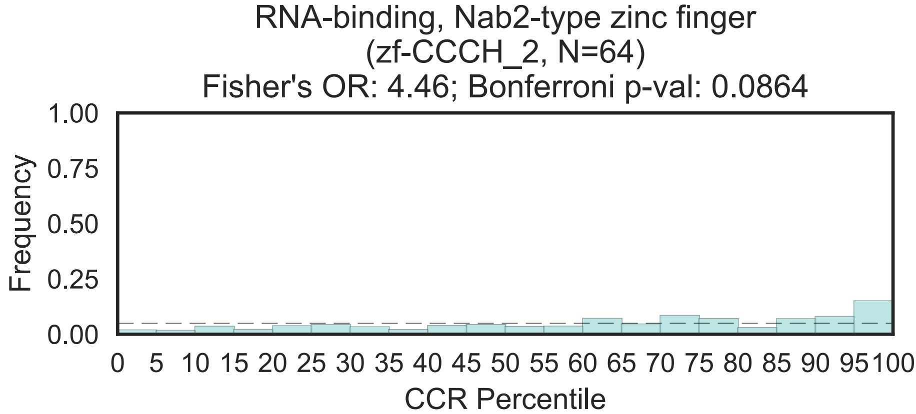

C5HC2 zinc finger
(zf-C5HC2, N=3)
Fisher's OR: 5.41; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

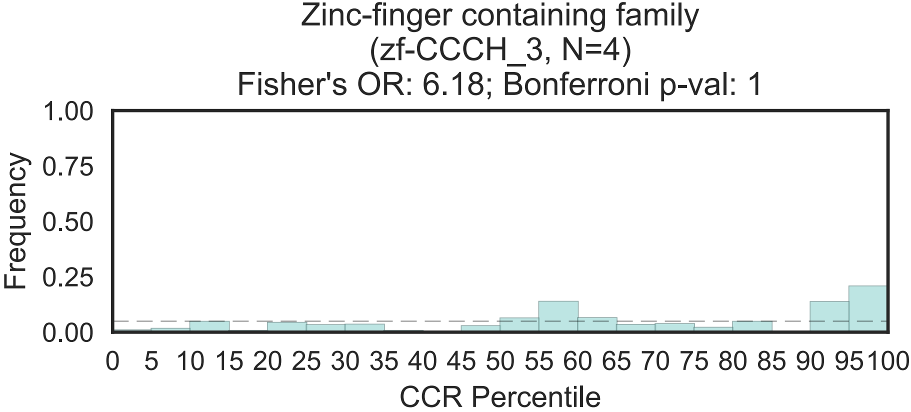
zf-MYND-like zinc finger, mRNA-binding (zf-C6H2, N=1)

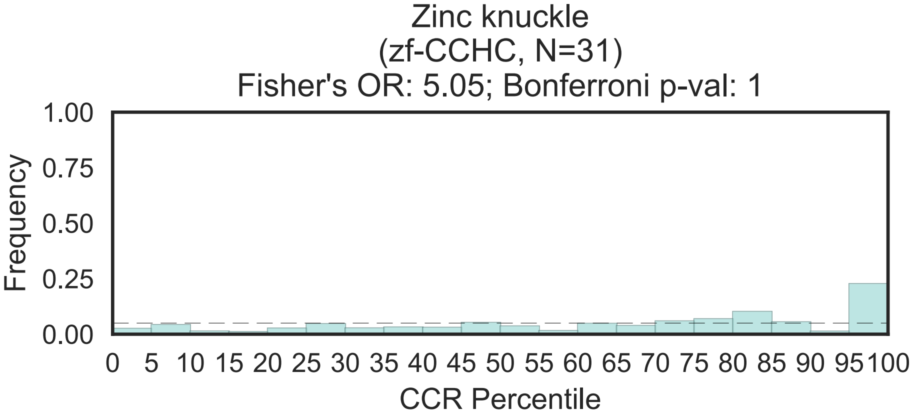


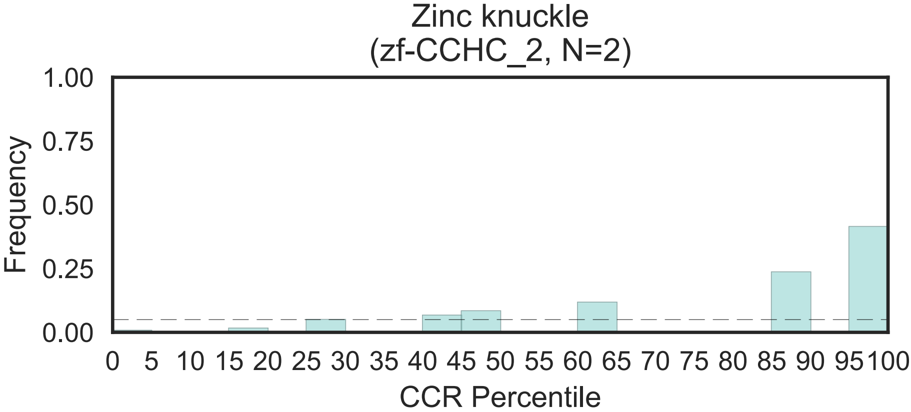


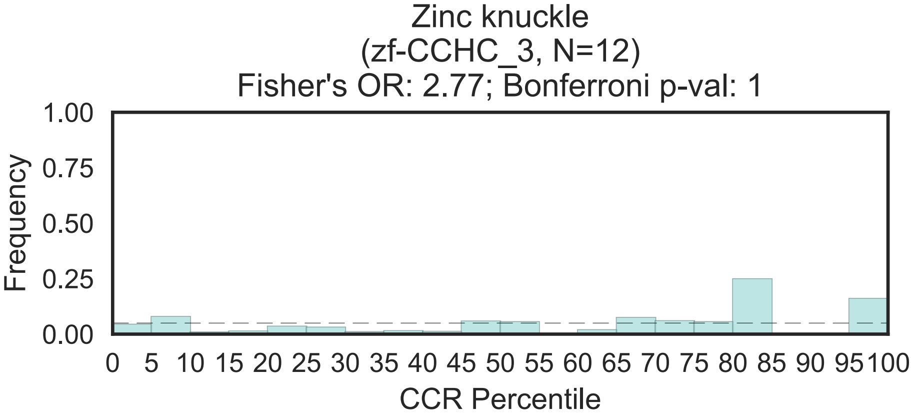
Zinc finger C-x8-C-x5-C-x3-H type (and similar)
(zf-CCCH, N=52)
Fisher's OR: 4.86; Bonferroni p-val: 0.00729

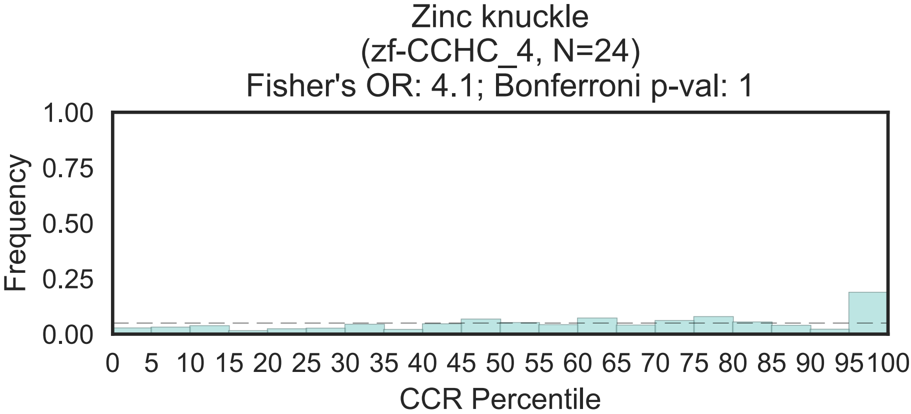

RNA-binding, Nab2-type zinc finger
(zf-CCCH_2, N=64)
Fisher's OR: 4.46; Bonferroni p-val: 0.0864
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

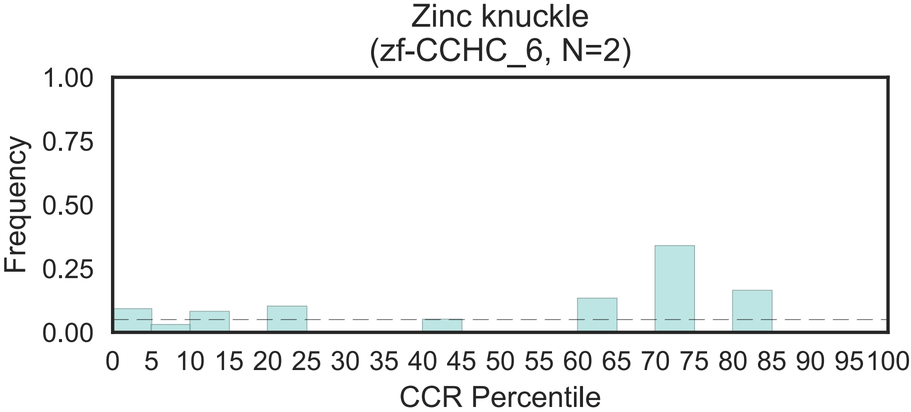

Zinc-finger containing family
(zf-CCCH_3, N=4)
Fisher's OR: 6.18; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

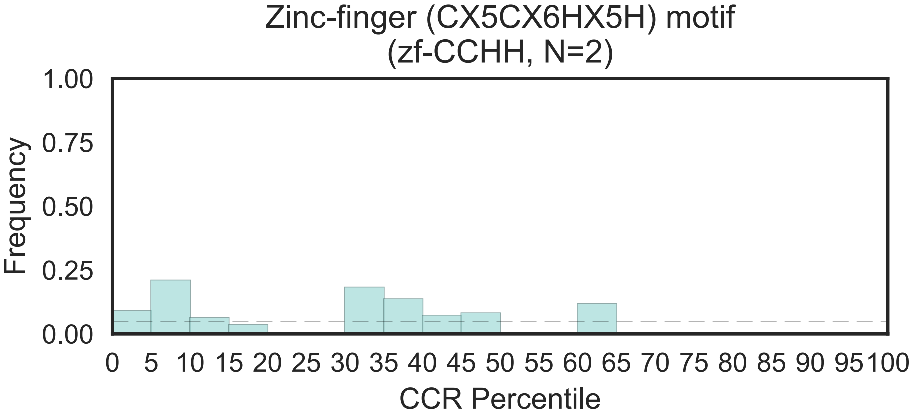

Zinc knuckle
(zf-CCHC, N=31)
Fisher's OR: 5.05; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

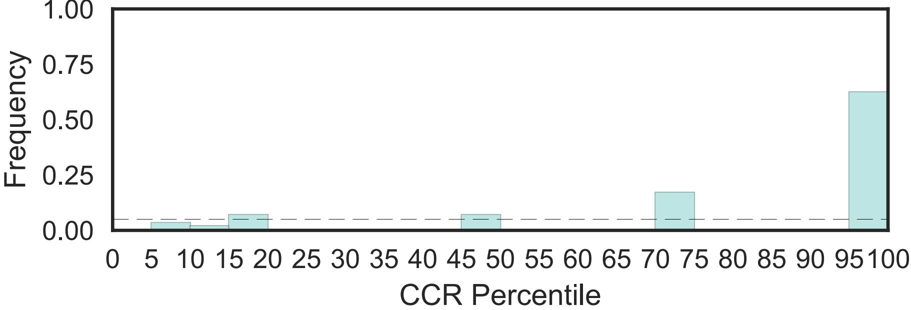

Zinc knuckle
(zf-CCHC_2, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
CCR Percentile


Zinc knuckle
(zf-CCHC_3, N=12)
Fisher's OR: 2.77; Bonferroni p-val: 1

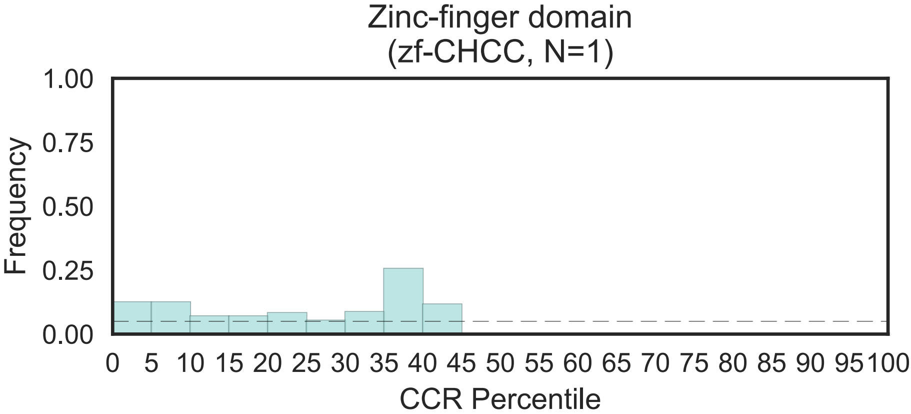

Zinc knuckle
(zf-CCHC_4, N=24)
Fisher's OR: 4.1; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

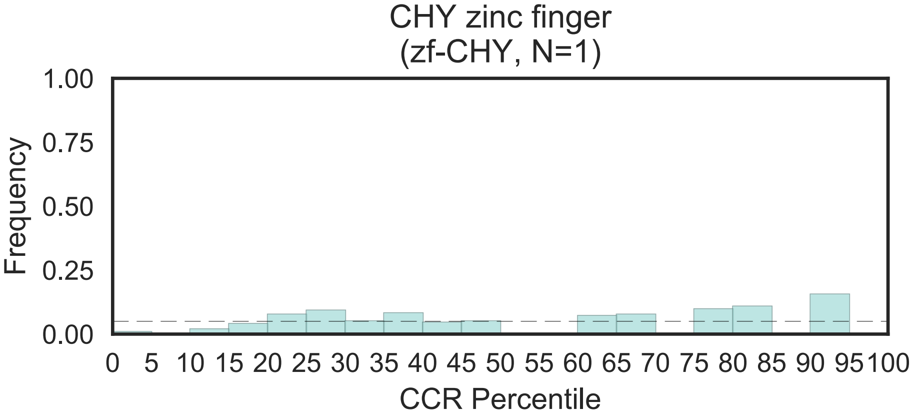

Zinc knuckle
(zf-CCHC_6, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

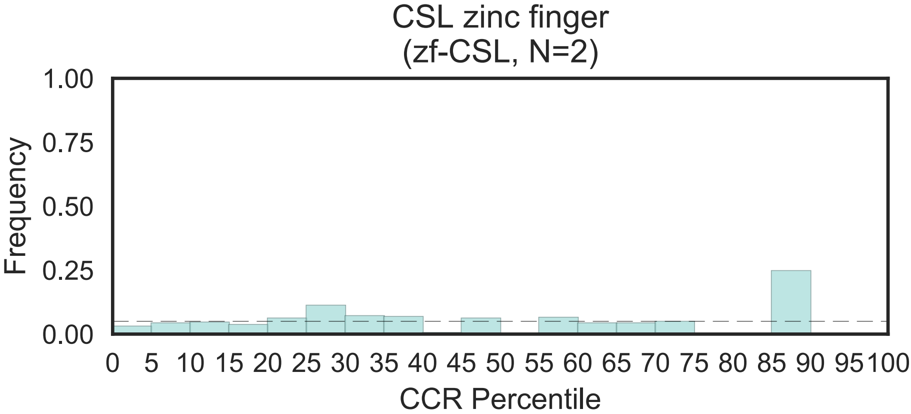

Zinc-finger (CX5CX6HX5H) motif
(zf-CCHH, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

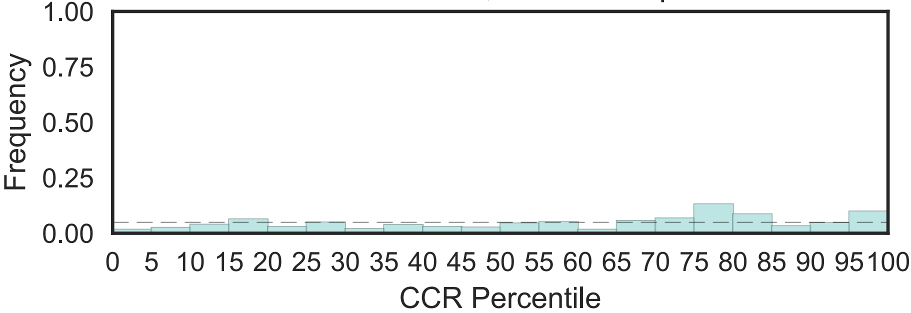


Iron-binding zinc finger CDGSH type
(zf-CDGSH, N=4)
Fisher's OR: 27; Bonferroni p-val: 1

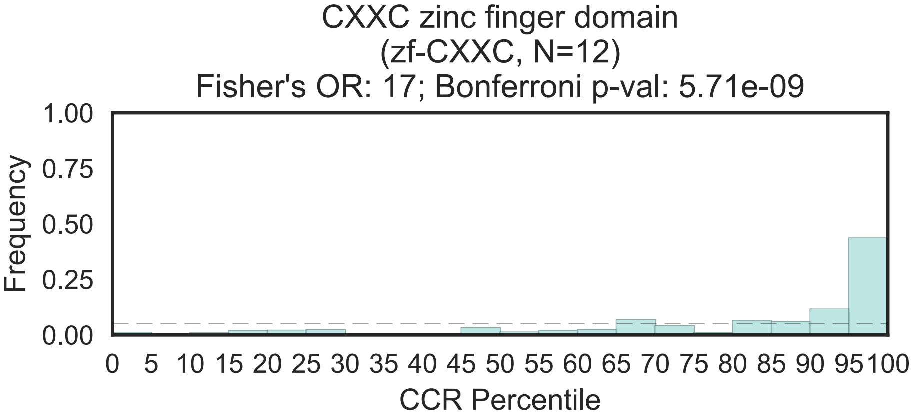

Zinc-finger domain
(zf-CHCC, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


CHY zinc finger
(zf-CHY, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

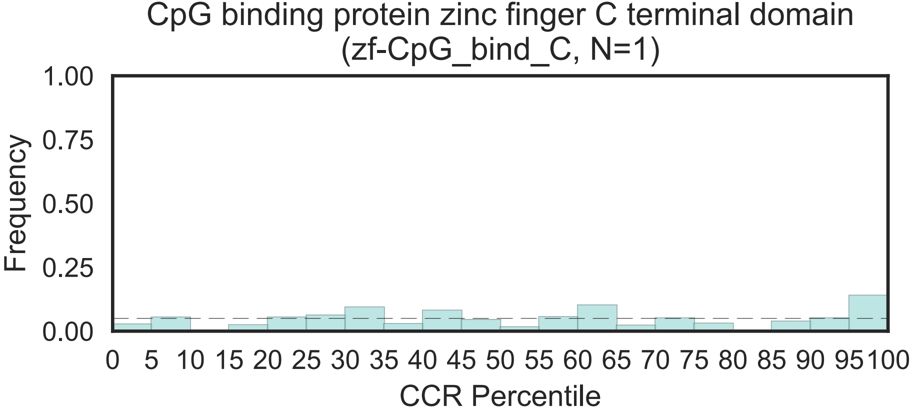

CSL zinc finger
(zf-CSL, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

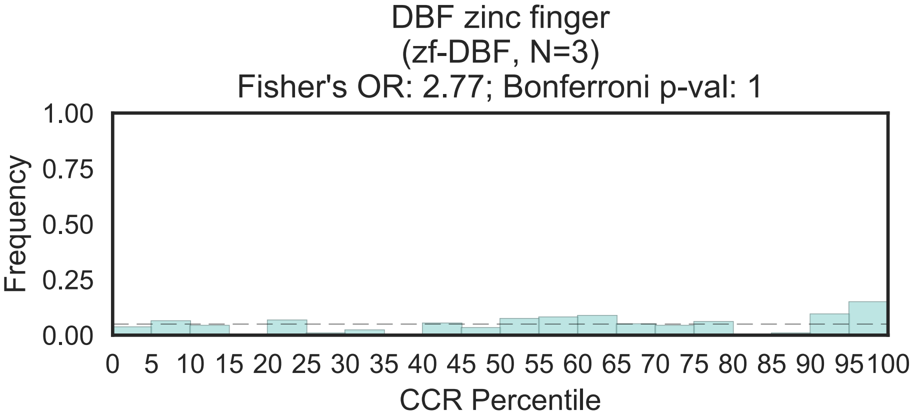


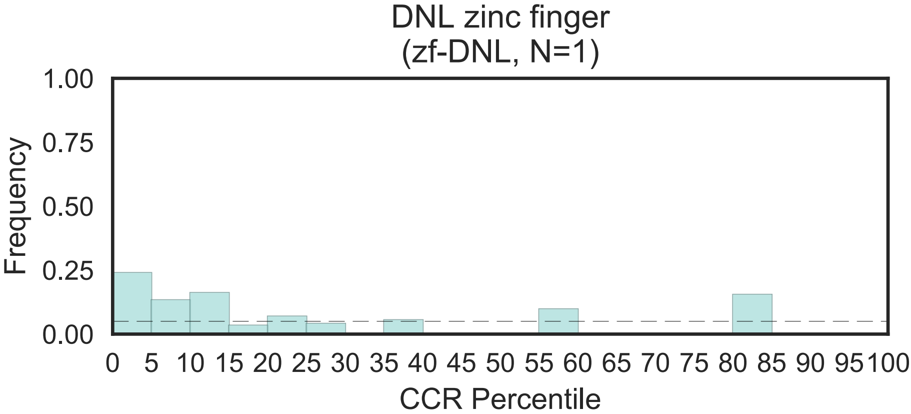
CW-type Zinc Finger
(zf-CW, N=6)
Fisher's OR: 2.49; Bonferroni p-val: 1

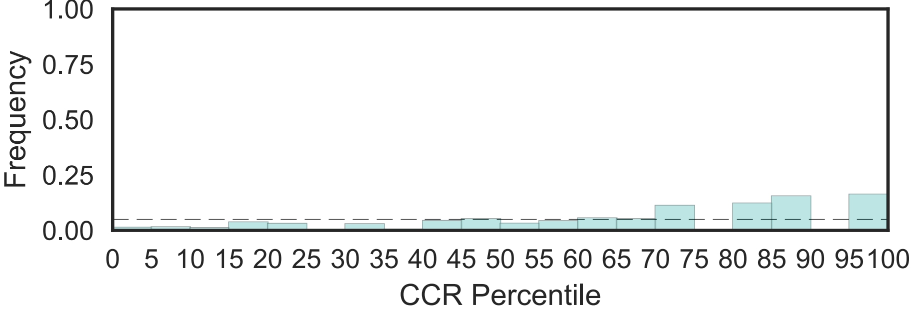


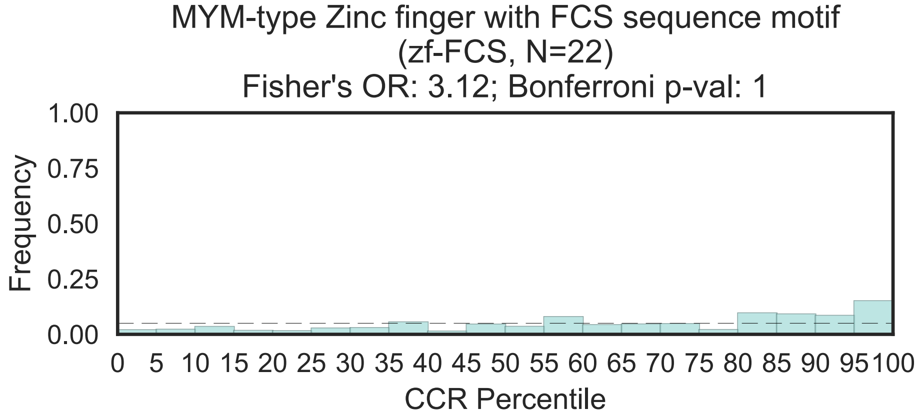
CXXC zinc finger domain
(zf-CXXC, N=12)
Fisher's OR: 17; Bonferroni p-val: 5.71e-09

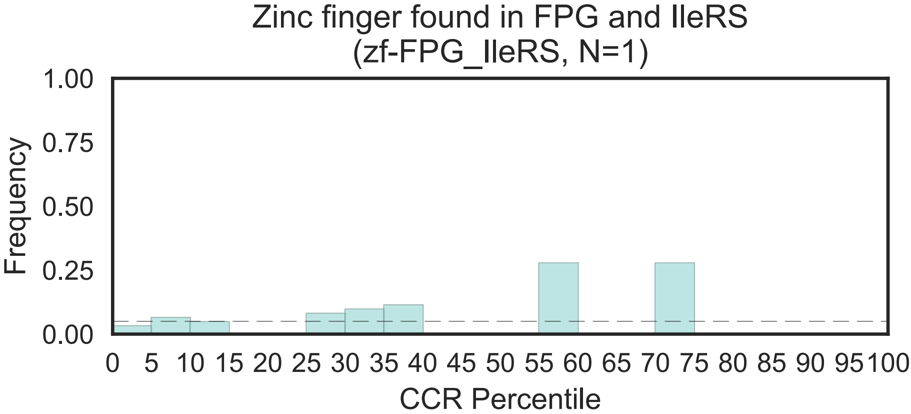

CpG binding protein zinc finger C terminal domain
(zf-CpG_bind_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

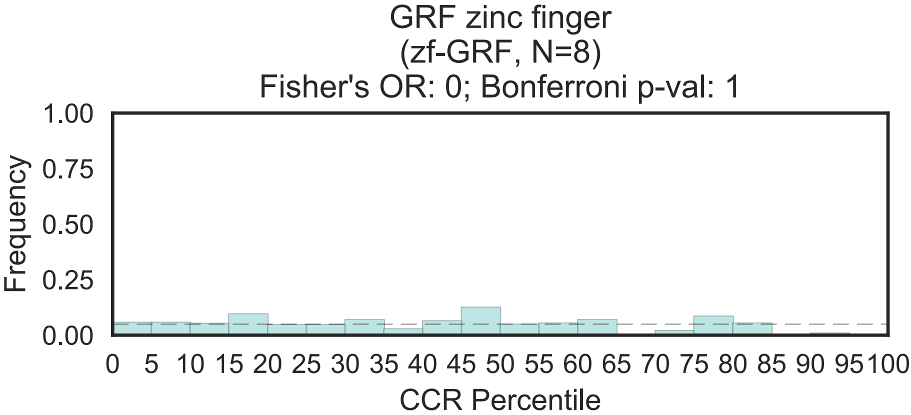

DBF zinc finger
(zf-DBF, N=3)
Fisher's OR: 2.77; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

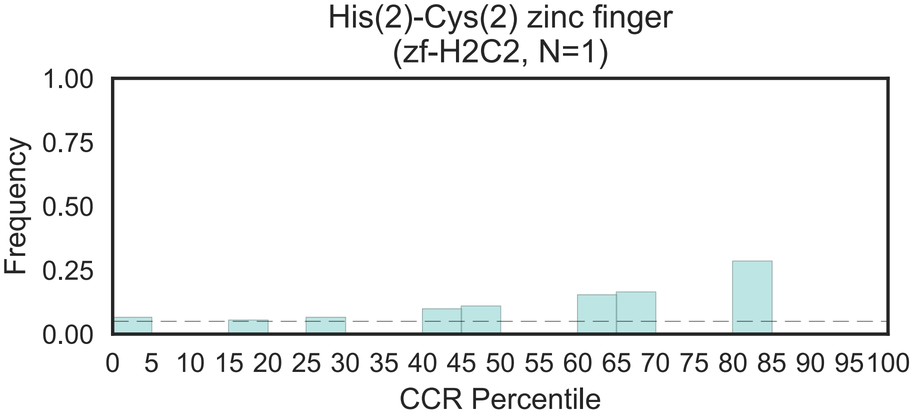

DNL zinc finger
(zf-DNL, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

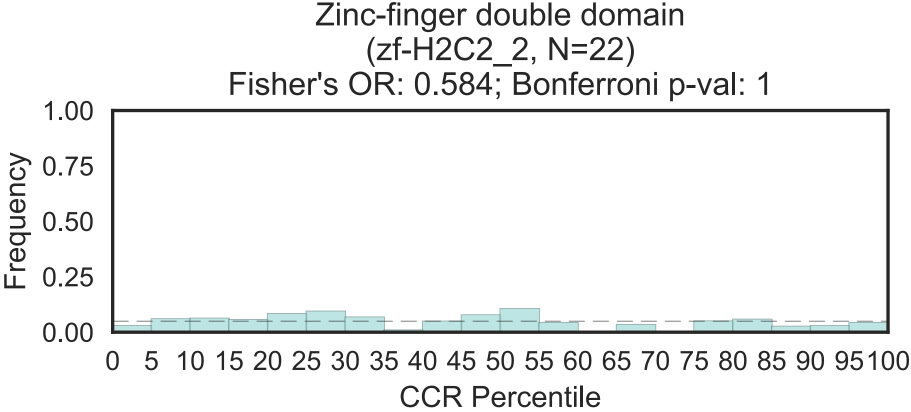

Drought induced 19 protein (Di19), zinc-binding
(zf-Di19, N=7)
Fisher's OR: 5.41; Bonferroni p-val: 1


MYM-type Zinc finger with FCS sequence motif
(zf-FCS, N=22)
Fisher's OR: 3.12; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

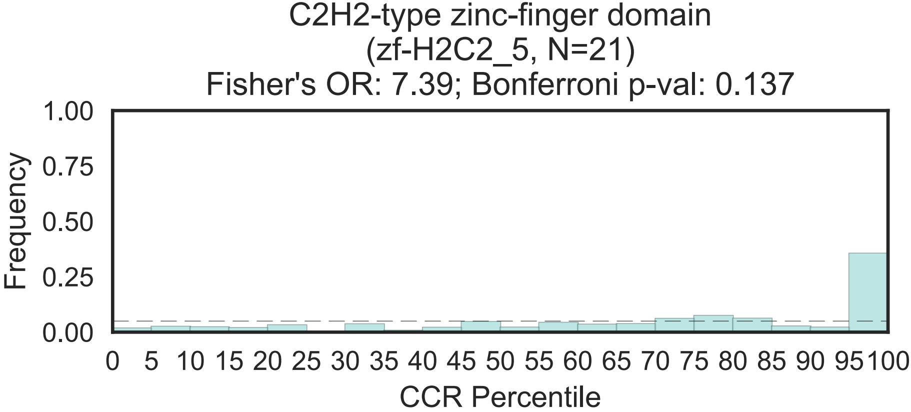

Zinc finger found in FPG and IleRS
(zf-FPG_IleRS, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

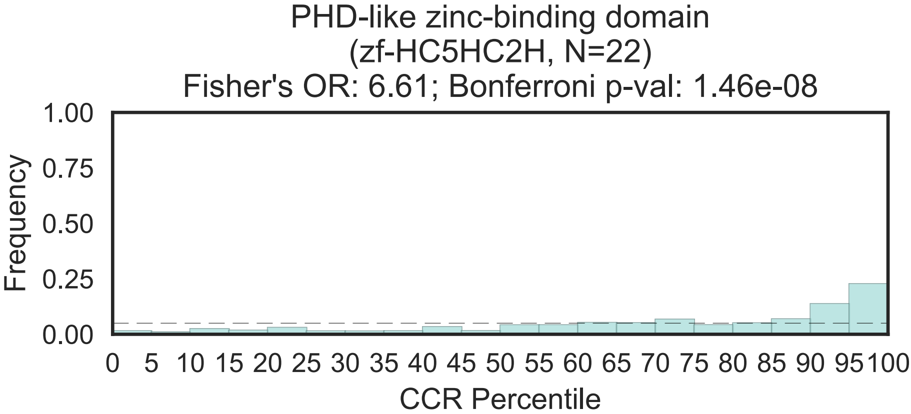

GRF zinc finger
(zf-GRF, N=8)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

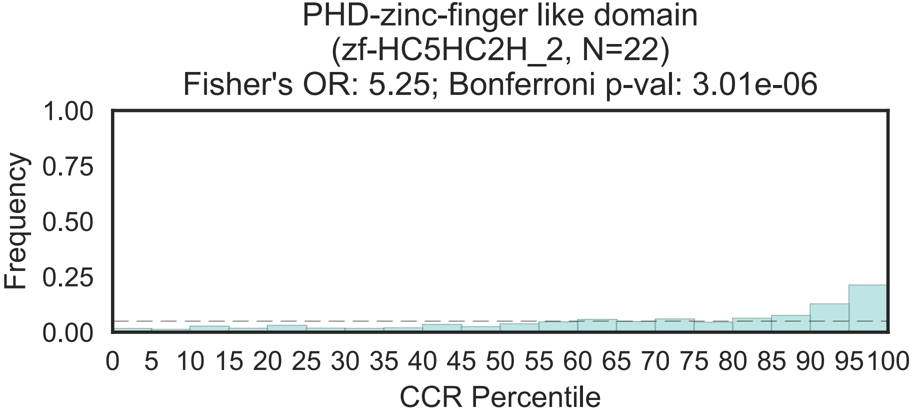

His(2)-Cys(2) zinc finger
(zf-H2C2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

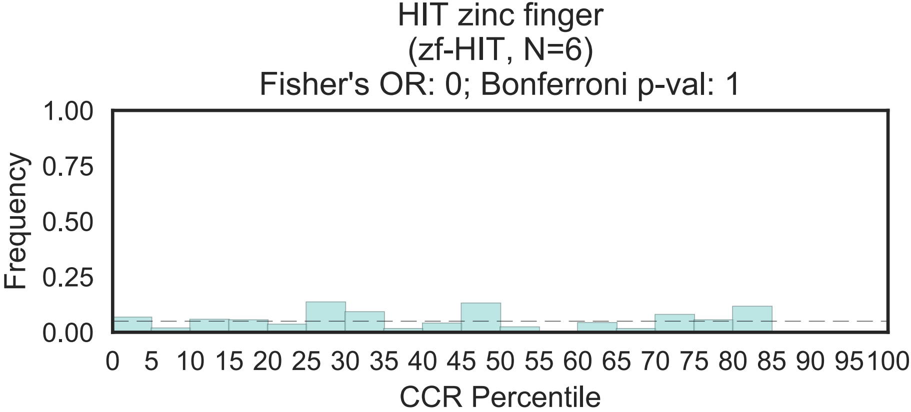


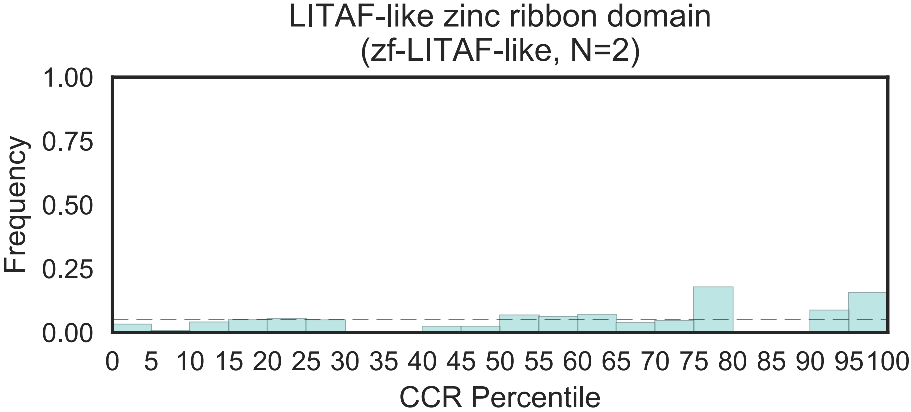
Zinc-finger double domain
(zf-H2C2_2, N=22)
Fisher's OR: 0.584; Bonferroni p-val: 1

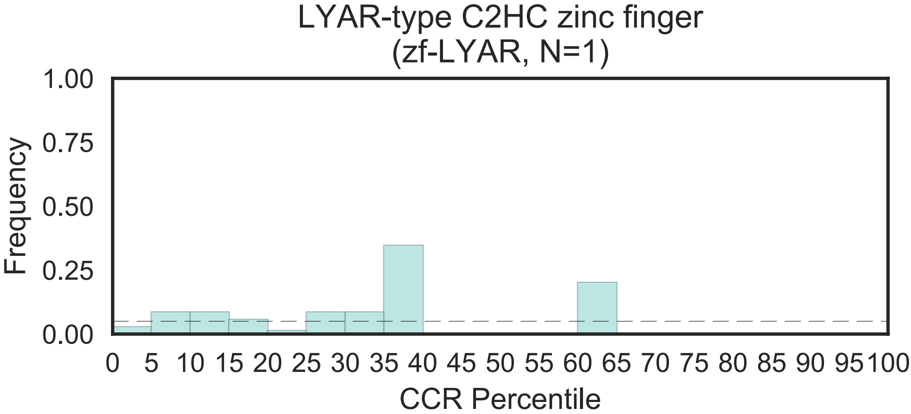

C2H2-type zinc-finger domain
(zf-H2C2_5, N=21)
Fisher's OR: 7.39; Bonferroni p-val: 0.137
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

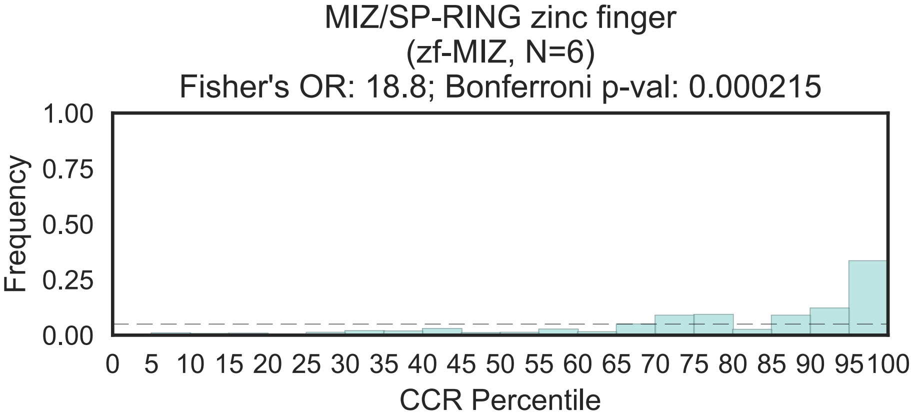

PHD-like zinc-binding domain
(zf-HC5HC2H, N=22)
Fisher's OR: 6.61; Bonferroni p-val: 1.46e-08
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

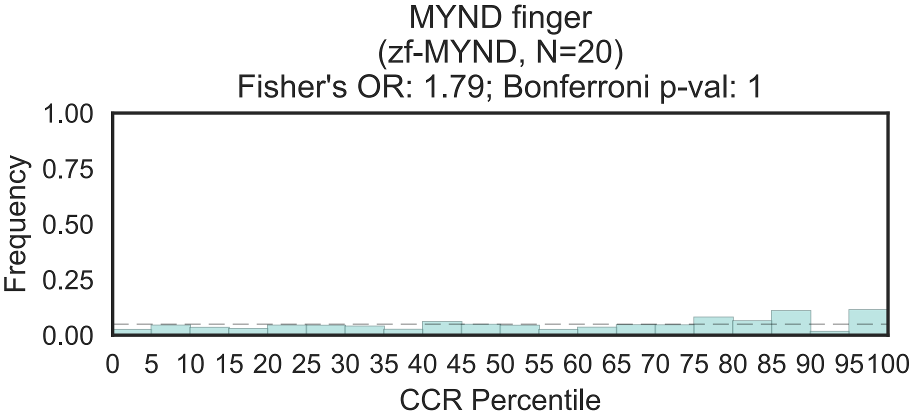

PHD-zinc-finger like domain
(zf-HC5HC2H_2, N=22)
Fisher's OR: 5.25; Bonferroni p-val: 3.01e-06
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

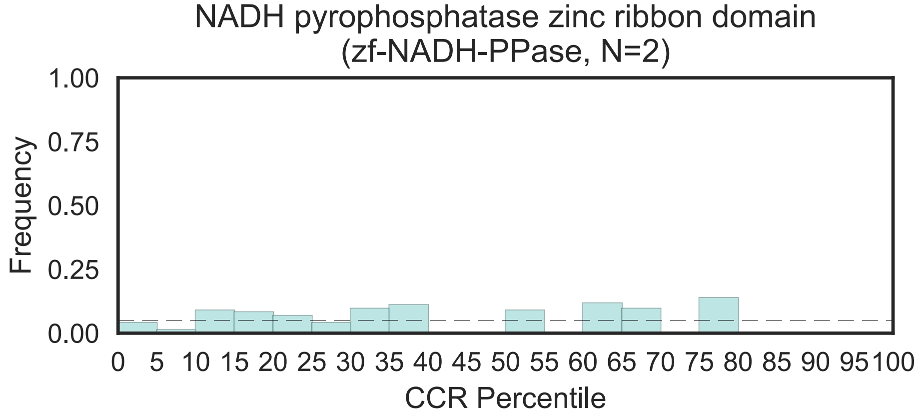

HIT zinc finger
(zf-HIT, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

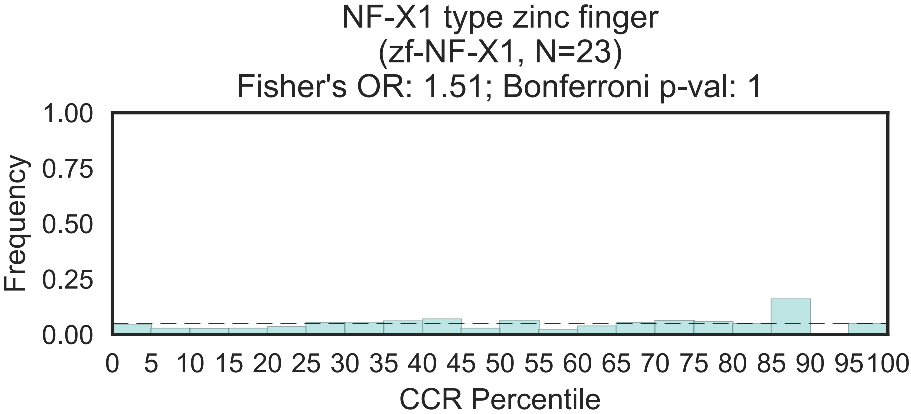

LITAF-like zinc ribbon domain
(zf-LITAF-like, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

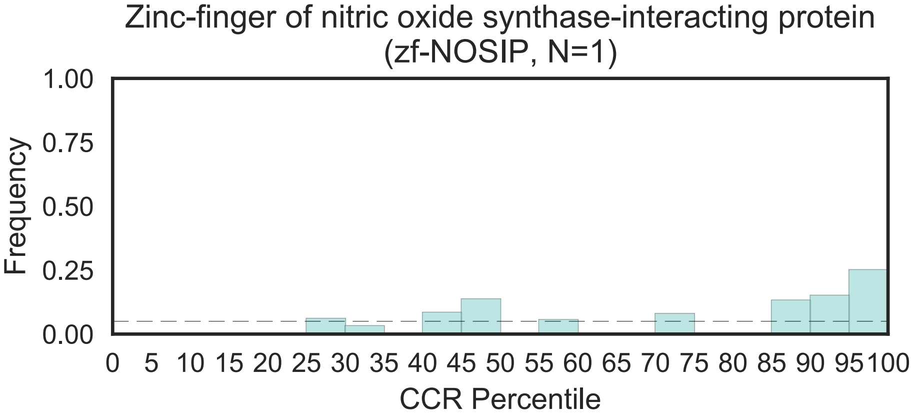

LYAR-type C2HC zinc finger
(zf-LYAR, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

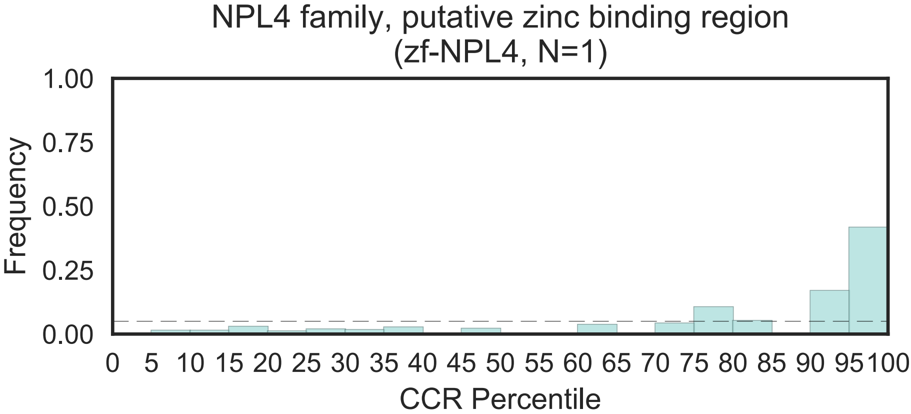

MIZ/SP-RING zinc finger
(zf-MIZ, N=6)
Fisher's OR: 18.8; Bonferroni p-val: 0.000215
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

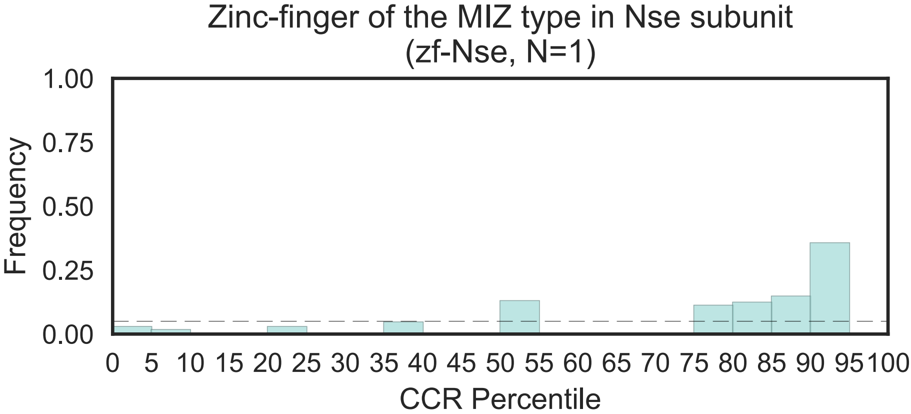

MYND finger
(zf-MYND, N=20)
Fisher's OR: 1.79; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

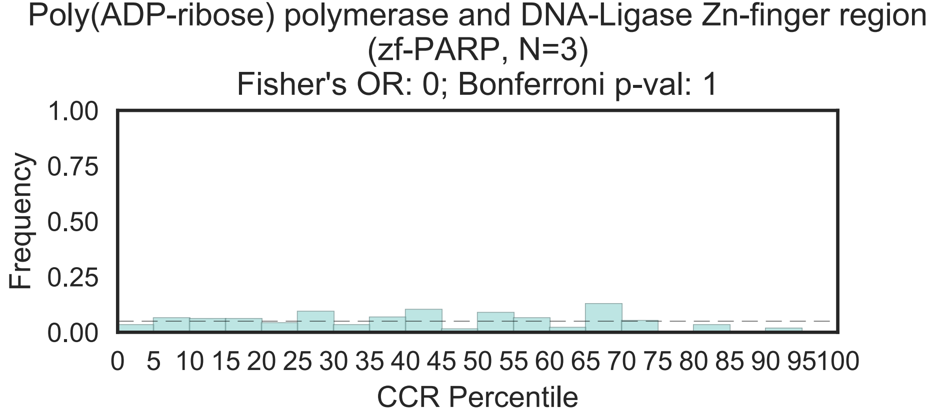

NADH pyrophosphatase zinc ribbon domain
(zf-NADH-PPase, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

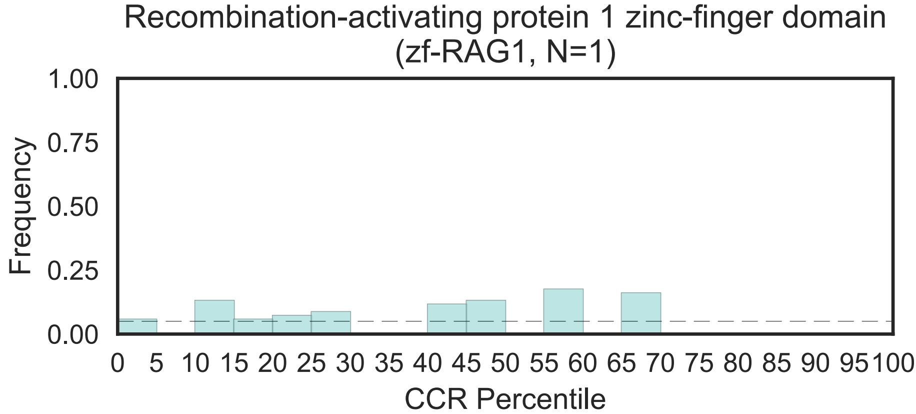

NF-X1 type zinc finger
(zf-NF-X1, N=23)
Fisher's OR: 1.51; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Zinc-finger of nitric oxide synthase-interacting protein
(zf-NOSIP, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

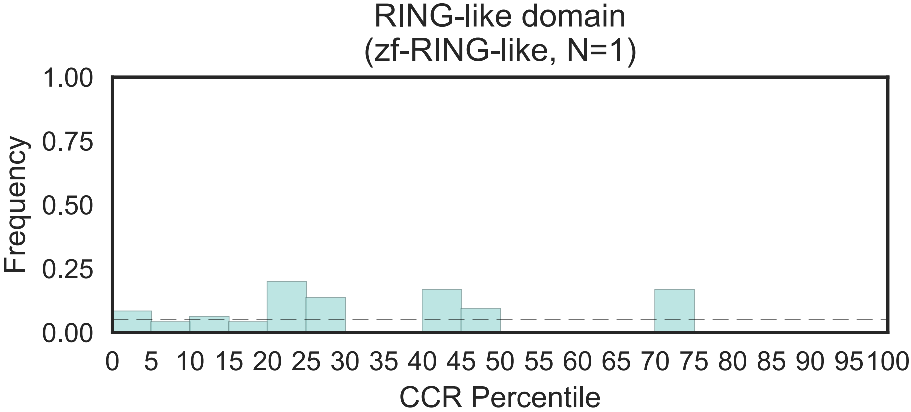

NPL4 family, putative zinc binding region
(zf-NPL4, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

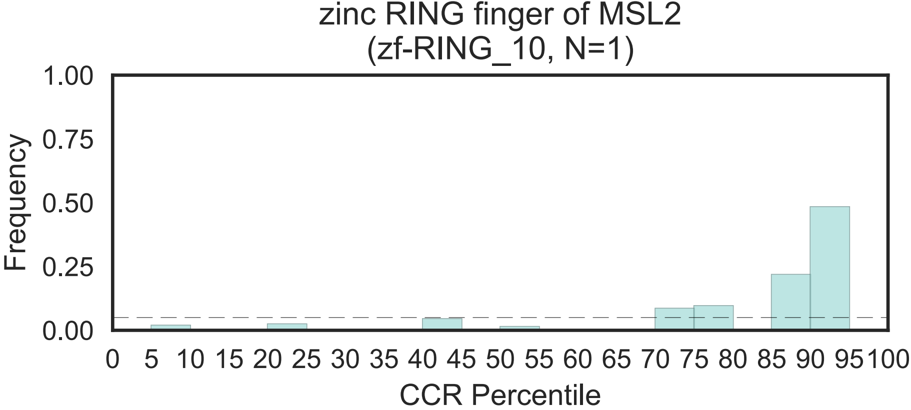

Zinc-finger of the MIZ type in Nse subunit
(zf-Nse, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Poly(ADP-ribose) polymerase and DNA-Ligase Zn-finger region
(zf-PARP, N=3)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

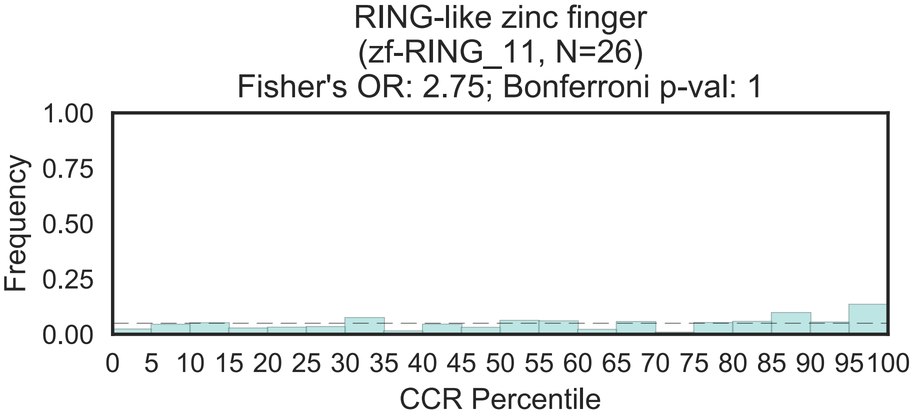


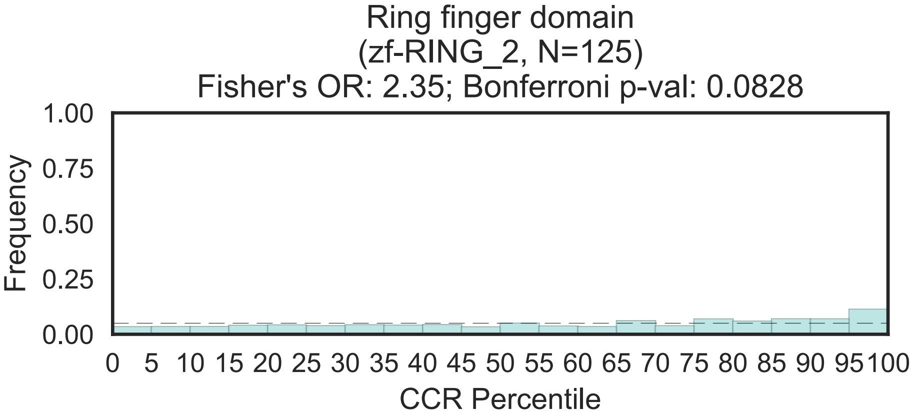
Recombination-activating protein 1 zinc-finger domain
(zf-RAG1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

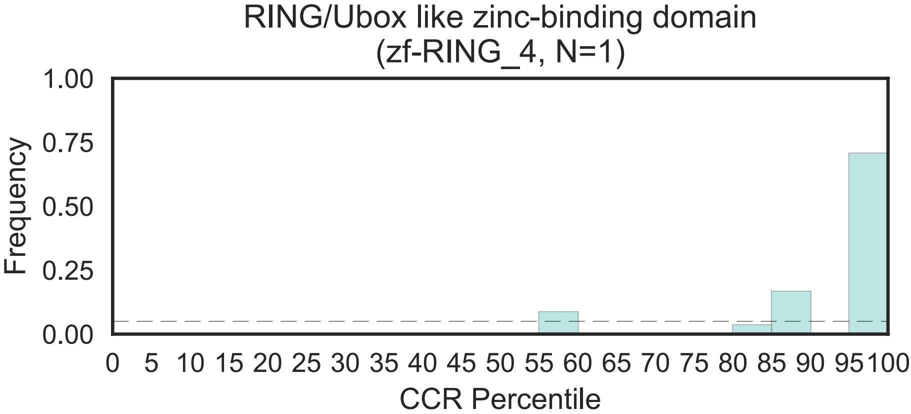

RING-like domain
(zf-RING-like, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

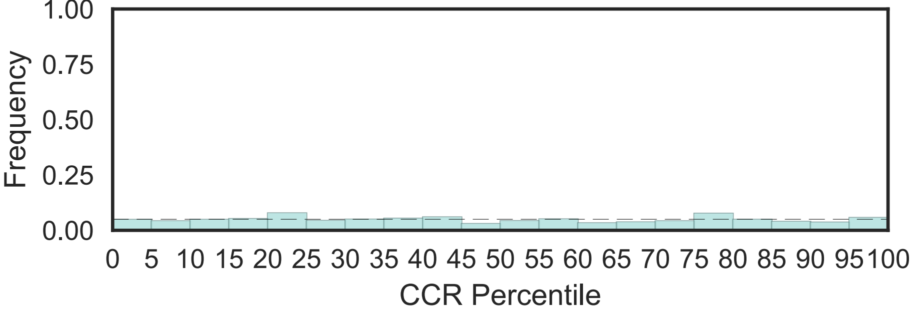


zinc RING finger of MSL2
(zf-RING_10, N=1)

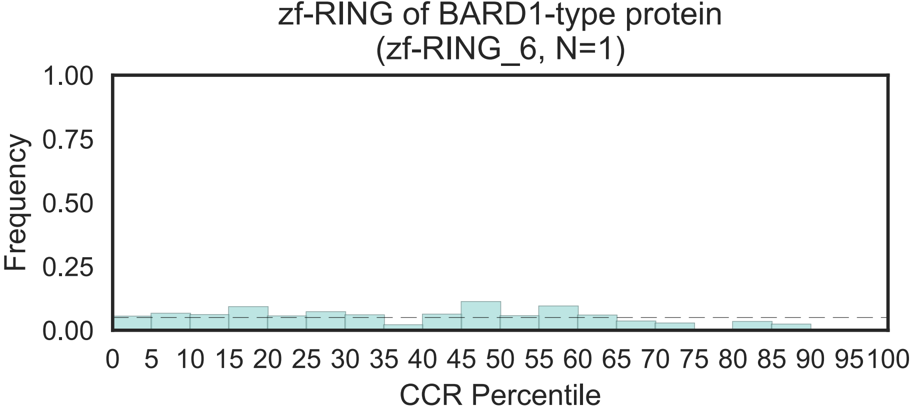

RING-like zinc finger
(zf-RING_11, N=26)
Fisher's OR: 2.75; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

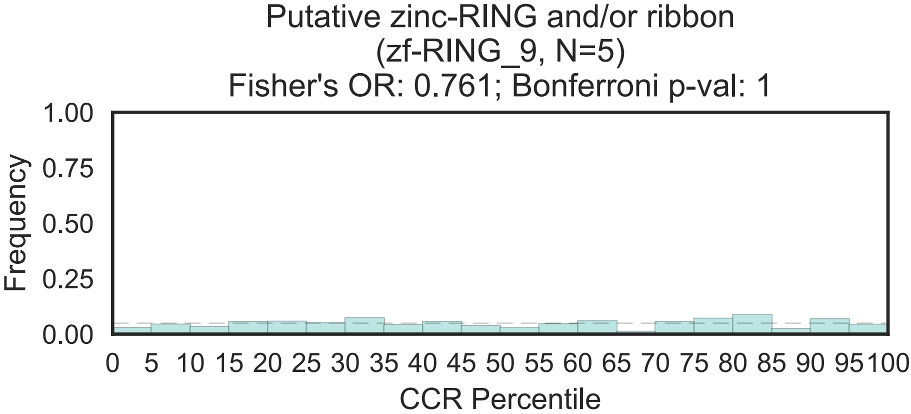

Ring finger domain
(zf-RING_2, N=125)
Fisher's OR: 2.35; Bonferroni p-val: 0.0828
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


RING/Ubox like zinc-binding domain
(zf-RING_4, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

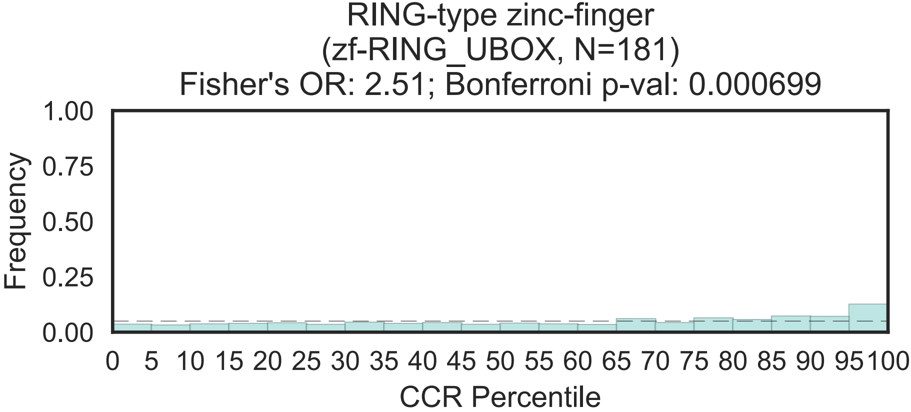


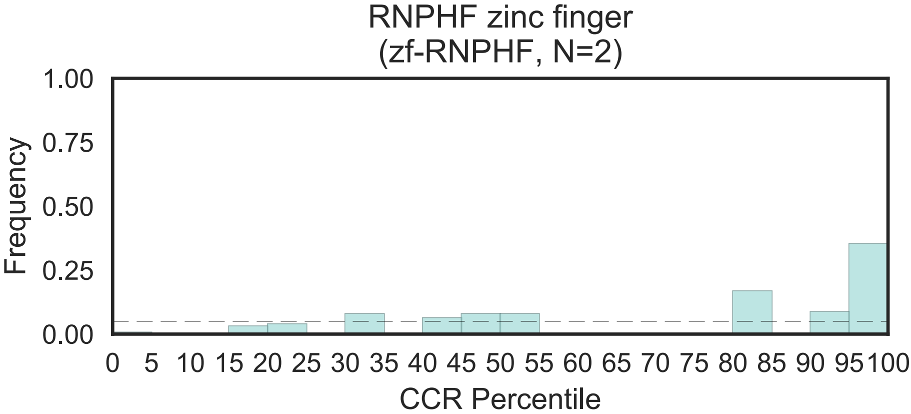
zinc-RING finger domain
(zf-RING_5, N=41)
Fisher's OR: 1.1; Bonferroni p-val: 1

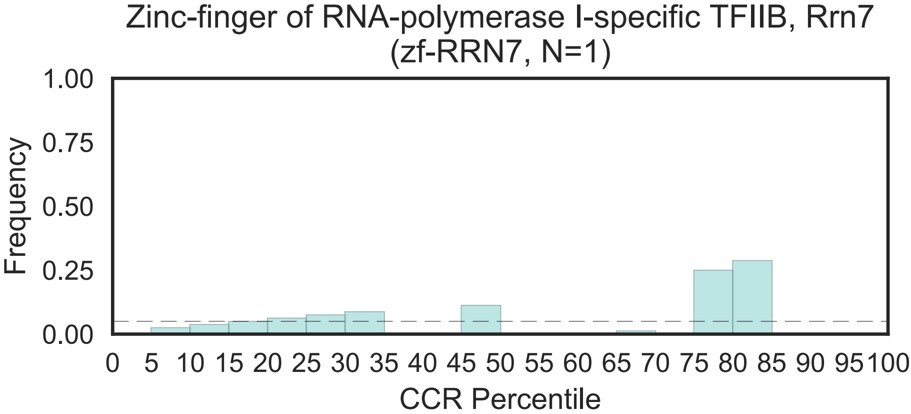

zf-RING of BARD1-type protein
(zf-RING_6, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

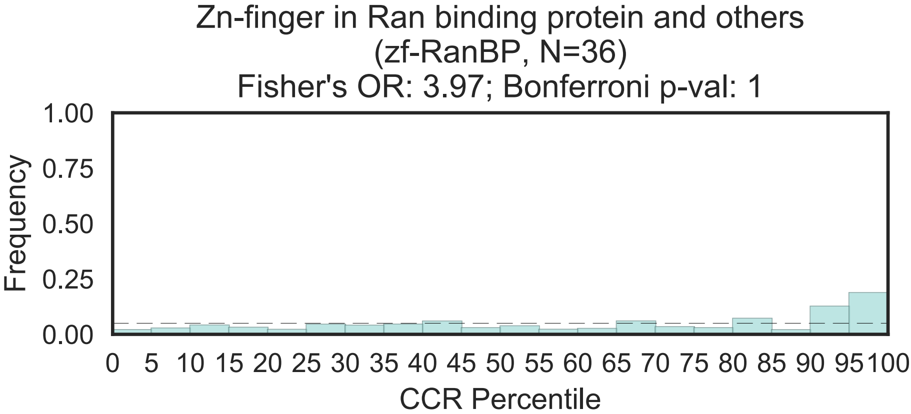


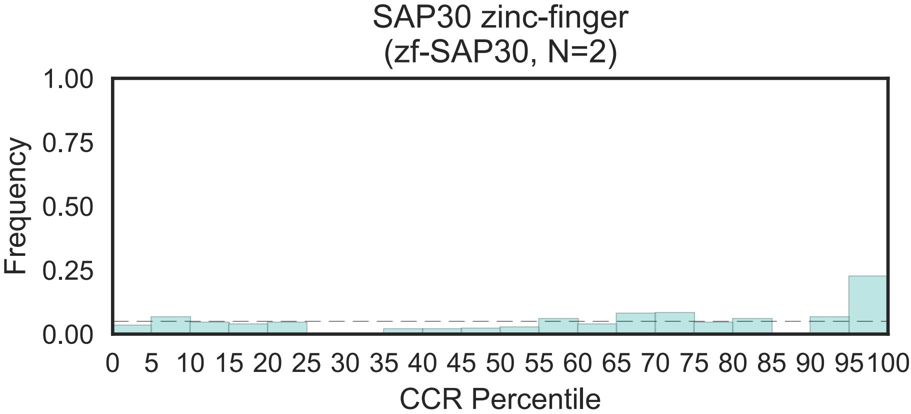
Putative zinc-RING and/or ribbon
(zf-RING_9, N=5)
Fisher's OR: 0.761; Bonferroni p-val: 1

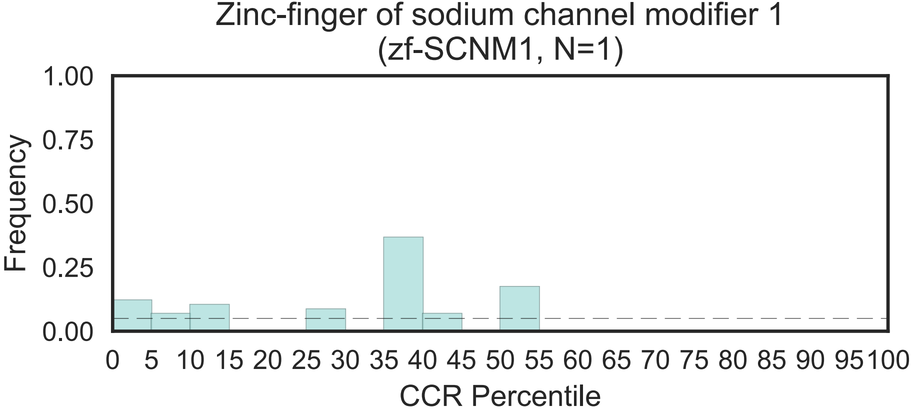

RING-type zinc-finger
(zf-RING_UBOX, N=181)
Fisher's OR: 2.51; Bonferroni p-val: 0.000699
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

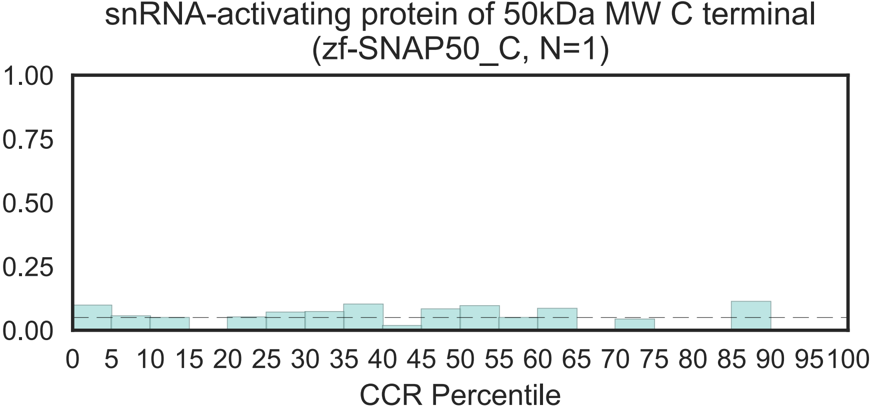

RNPHF zinc finger
(zf-RNPHF, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

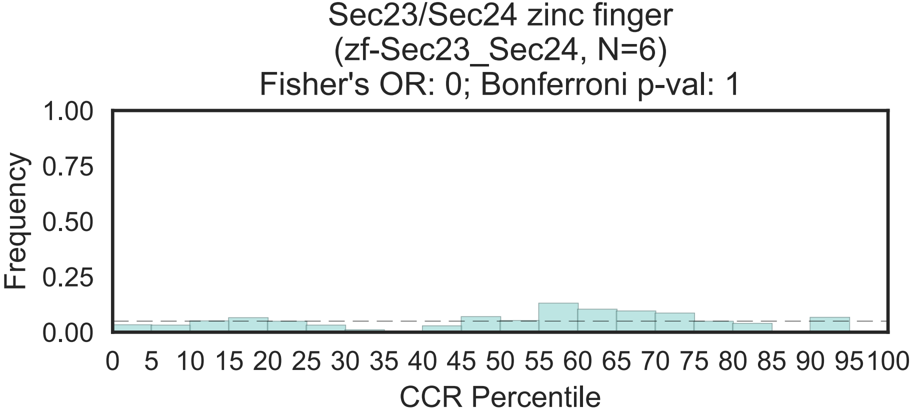

Zinc-finger of RNA-polymerase I-specific TFIIB, Rrn7
(zf-RRN7, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

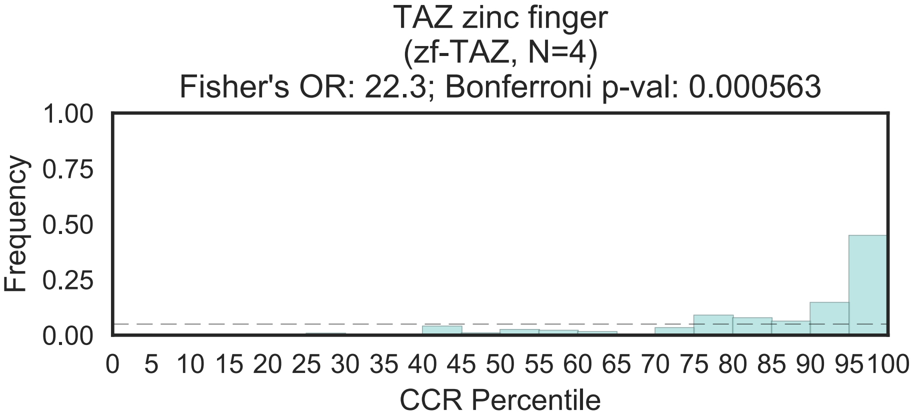

Zn-finger in Ran binding protein and others
(zf-RanBP, N=36)
Fisher's OR: 3.97; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

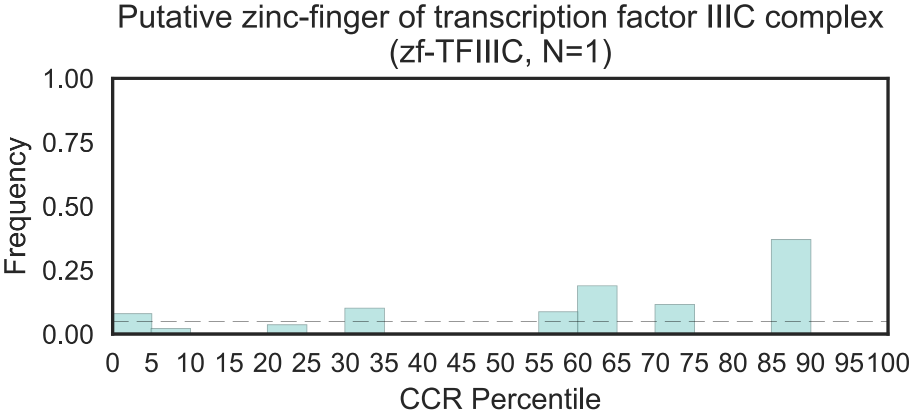

SAP30 zinc-finger
(zf-SAP30, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

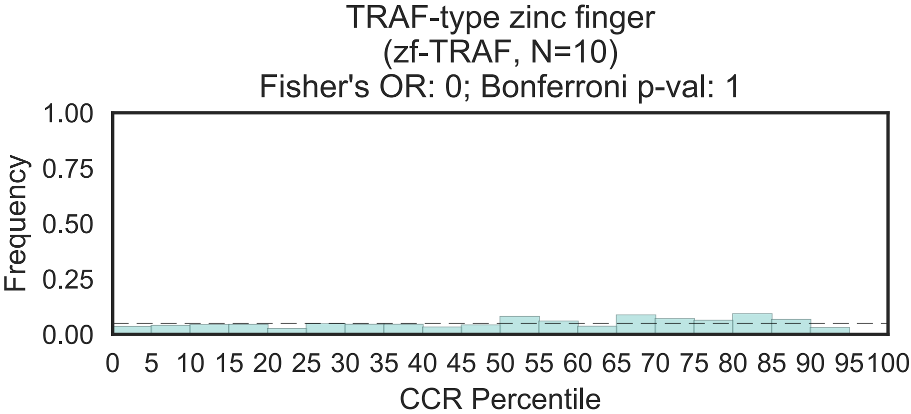

Zinc-finger of sodium channel modifier 1
(zf-SCNM1, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

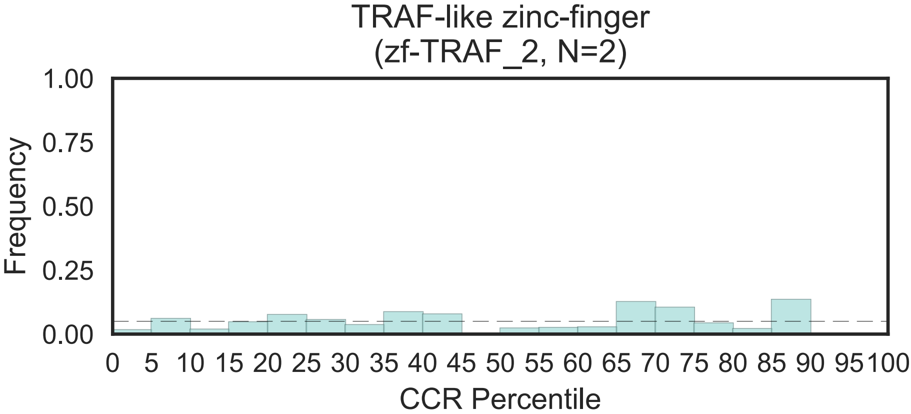

snRNA-activating protein of 50kDa MW C terminal
(zf-SNAP50_C, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

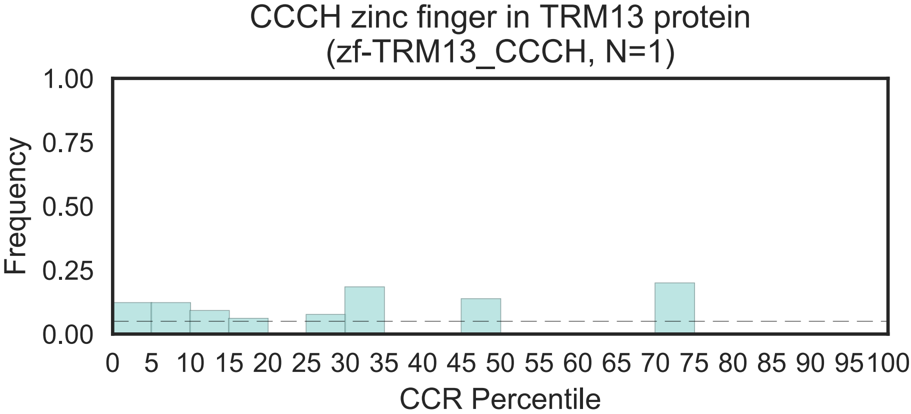

Sec23/Sec24 zinc finger
(zf-Sec23_Sec24, N=6)
Fisher's OR: 0; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

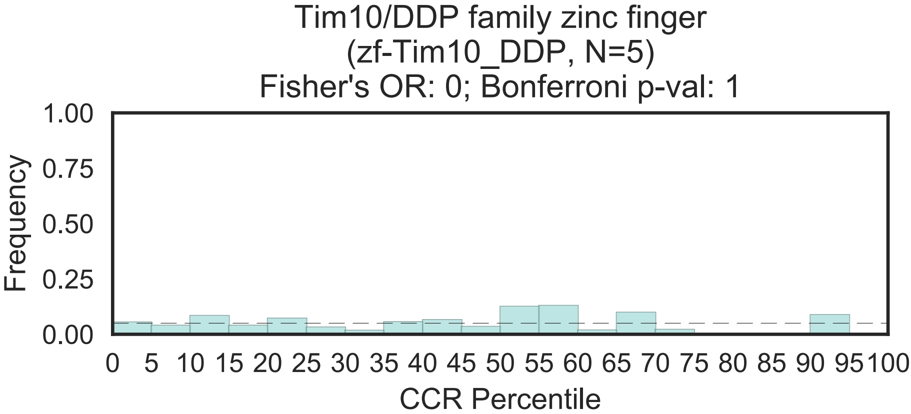

TAZ zinc finger
(zf-TAZ, N=4)
Fisher's OR: 22.3; Bonferroni p-val: 0.000563
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

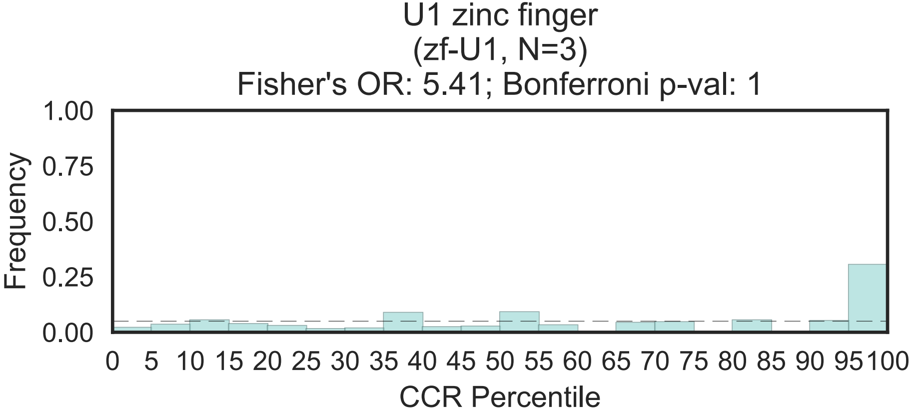

Putative zinc-finger of transcription factor IIIC complex
(zf-TFIIIC, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


TRAF-type zinc finger
(zf-TRAF, N=10)
Fisher's OR: 0; Bonferroni p-val: 1

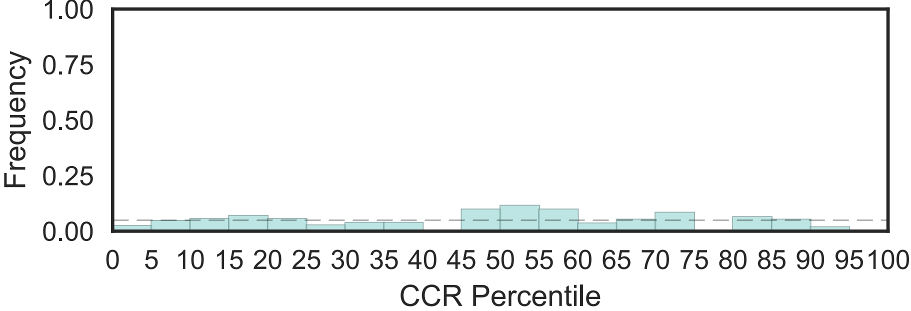

TRAF-like zinc-finger
(zf-TRAF_2, N=2)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


CCCH zinc finger in TRM13 protein
(zf-TRM13_CCCH, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

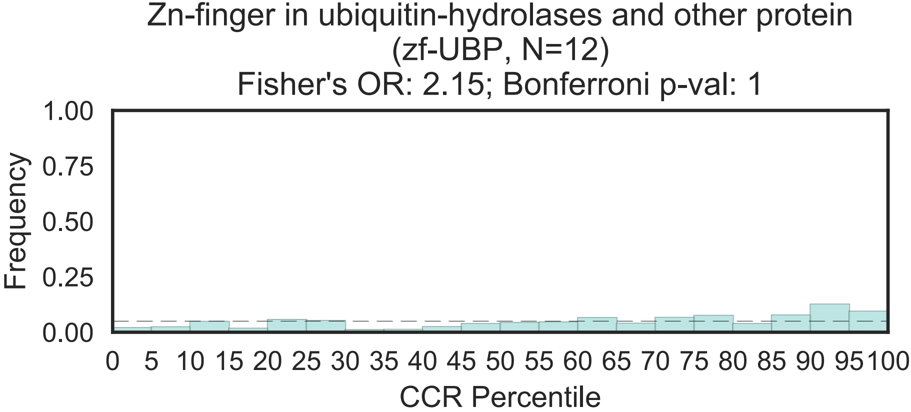

Tim10/DDP family zinc finger
(zf-Tim10_DDP, N=5)
Fisher's OR: 0; Bonferroni p-val: 1
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

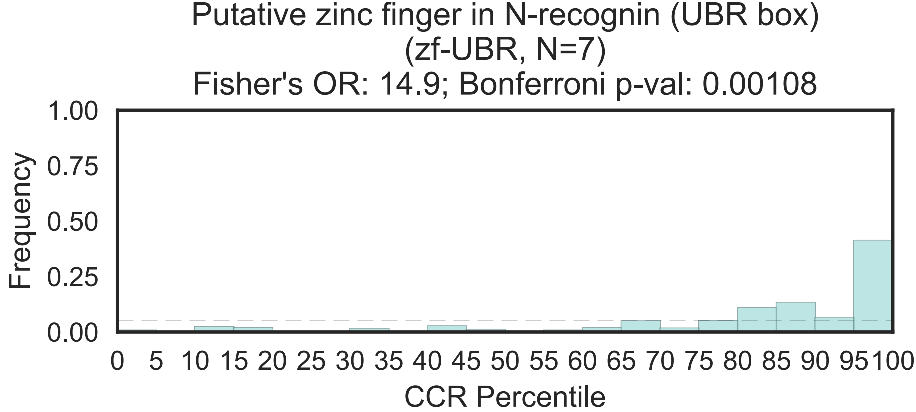


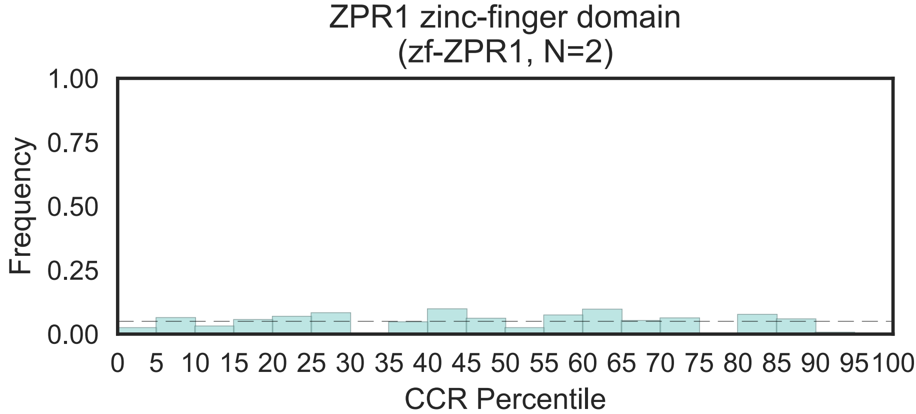
U1 zinc finger
(zf-U1, N=3)
Fisher's OR: 5.41; Bonferroni p-val: 1

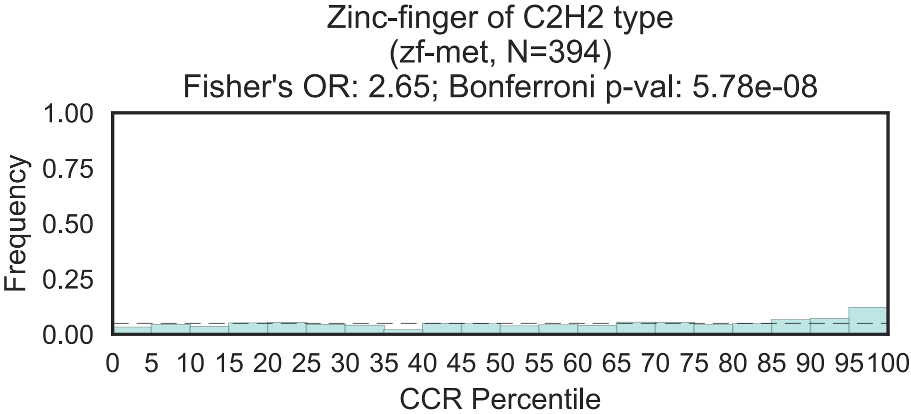


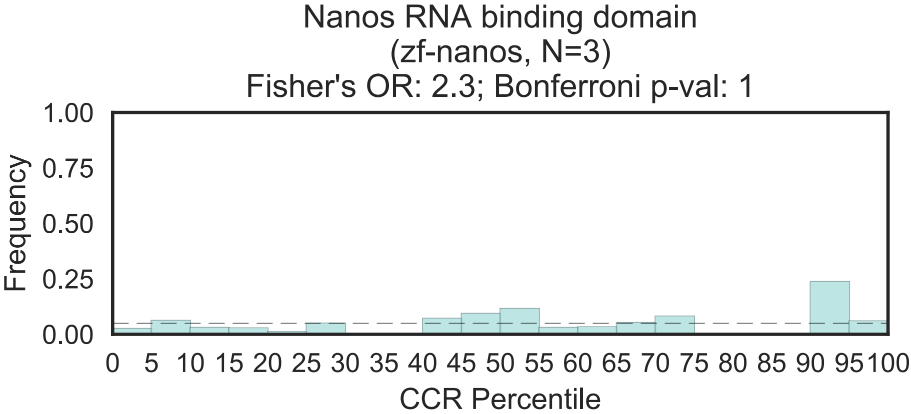
U11-48K-like CHHC zinc finger
(zf-U11-48K, N=6)
Fisher's OR: 0; Bonferroni p-val: 1


Zn-finger in ubiquitin-hydrolases and other protein
(zf-UBP, N=12)
Fisher's OR: 2.15; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

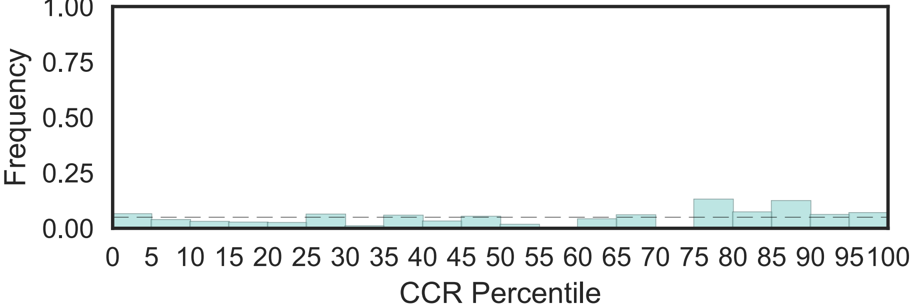

Putative zinc finger in N-recognin (UBR box)
(zf-UBR, N=7)
Fisher's OR: 14.9; Bonferroni p-val: 0.00108
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

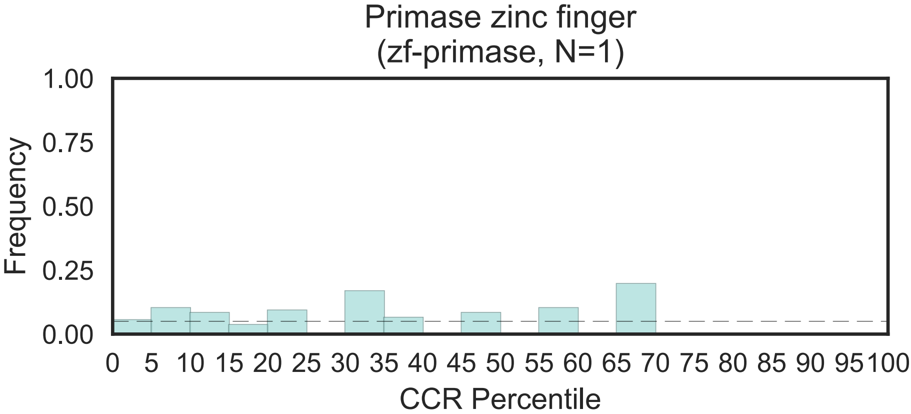

ZPR1 zinc-finger domain
(zf-ZPR1, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

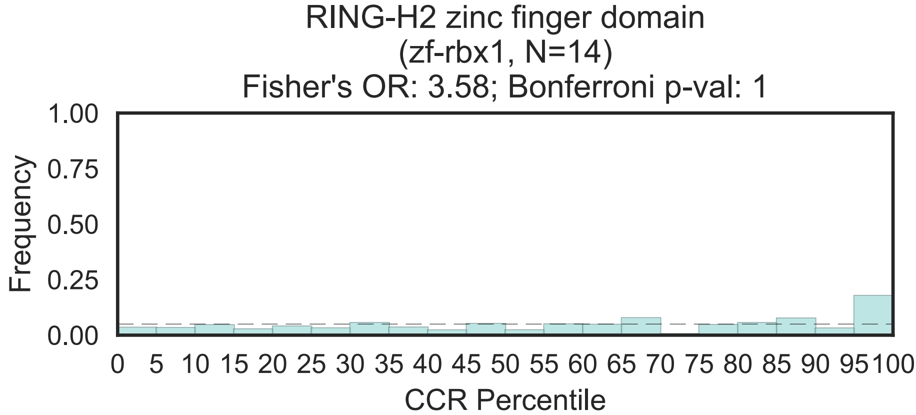

Zinc-finger of C2H2 type
(zf-met, N=394)
Fisher's OR: 2.65; Bonferroni p-val: 5.78e-08
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Nanos RNA binding domain
(zf-nanos, N=3)
Fisher's OR: 2.3; Bonferroni p-val: 1
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

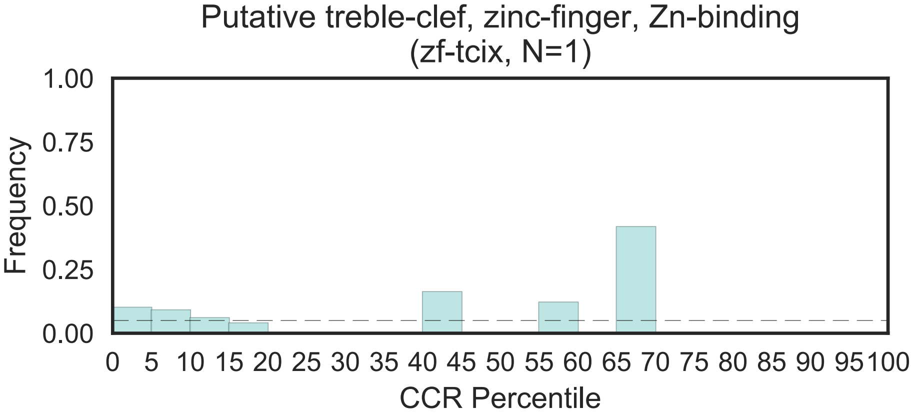
Piccolo Zn-finger
(zf-piccolo, N=4)
Fisher's OR: 1.39; Bonferroni p-val: 1

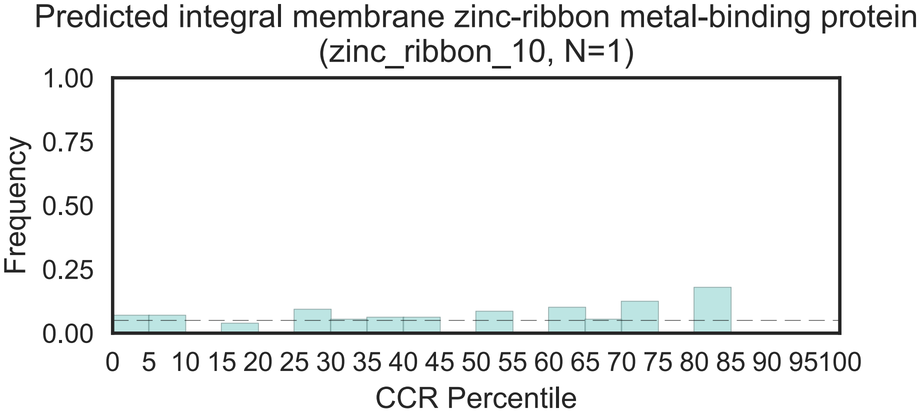


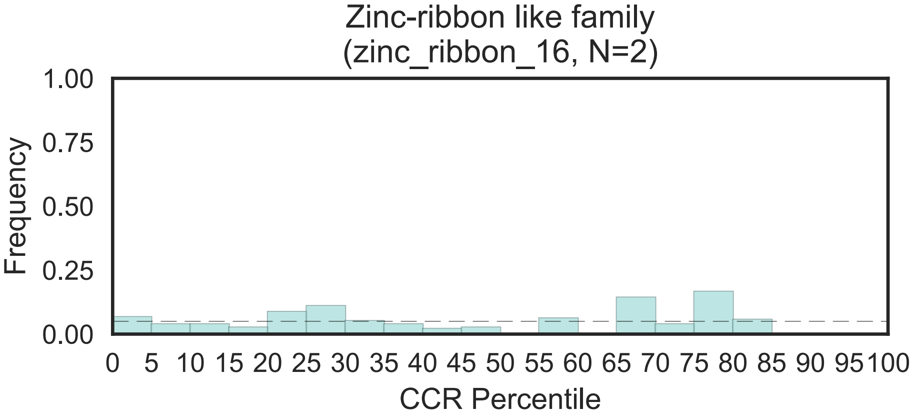

Primase zinc finger
(zf-primase, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile

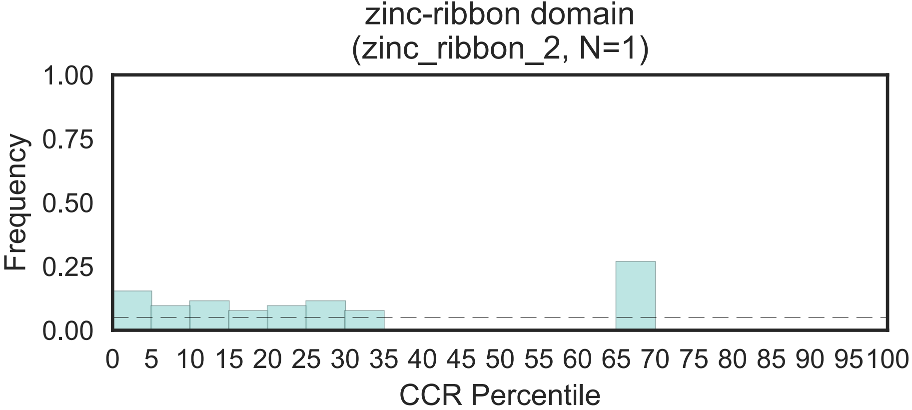


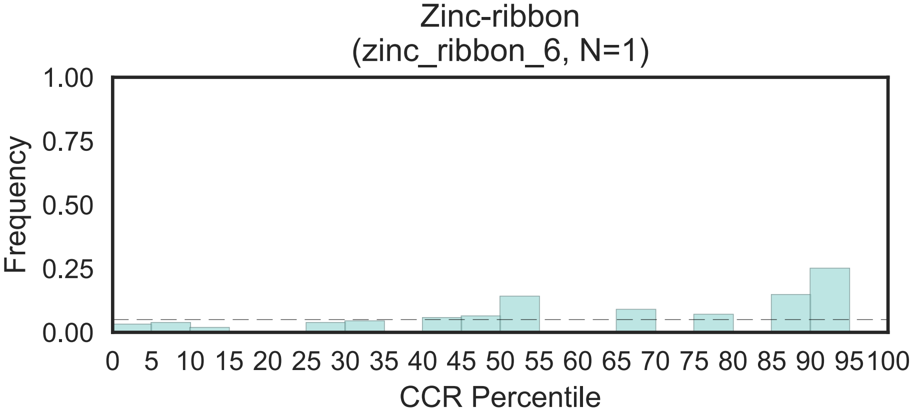
RING-H2 zinc finger domain
(zf-rbx1, N=14)
Fisher's OR: 3.58; Bonferroni p-val: 1

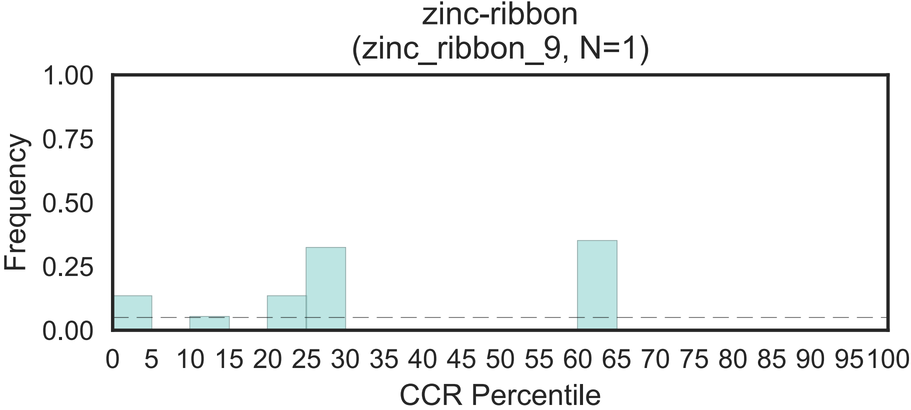

Putative treble-clef, zinc-finger, Zn-binding
(zf-tcix, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Predicted integral membrane zinc-ribbon metal-binding protein
(zinc_ribbon_10, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Zinc-ribbon like family
(zinc_ribbon_16, N=2)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


zinc-ribbon domain
(zinc_ribbon_2, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


Zinc-ribbon
(zinc_ribbon_6, N=1)
1.00
0.75
0.50
0.25
0.00
Frequency
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile


zinc-ribbon
(zinc_ribbon_9, N=1)
Frequency
1.00
0.75
0.50
0.25
0.00
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
CCR Percentile