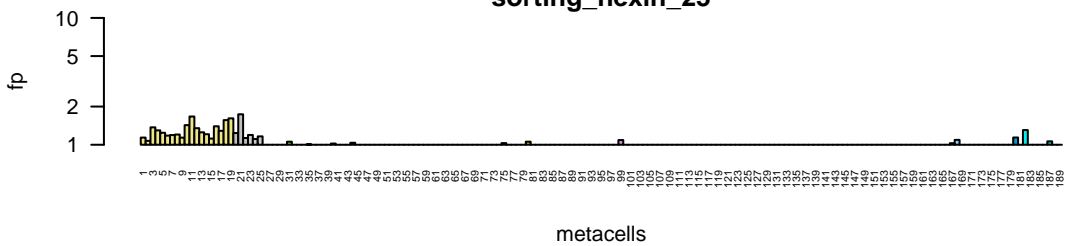
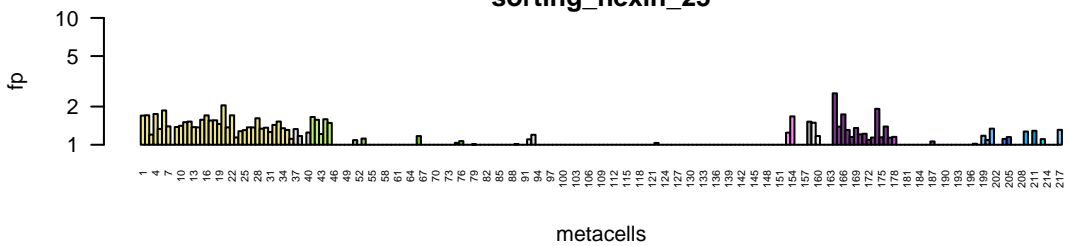


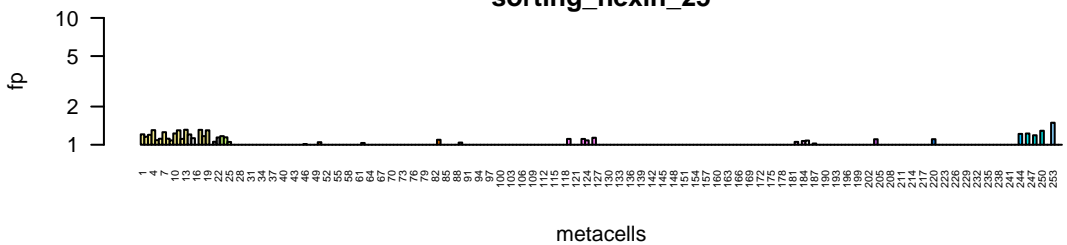
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Tadh_TriadT56593
sorting_nexin_25



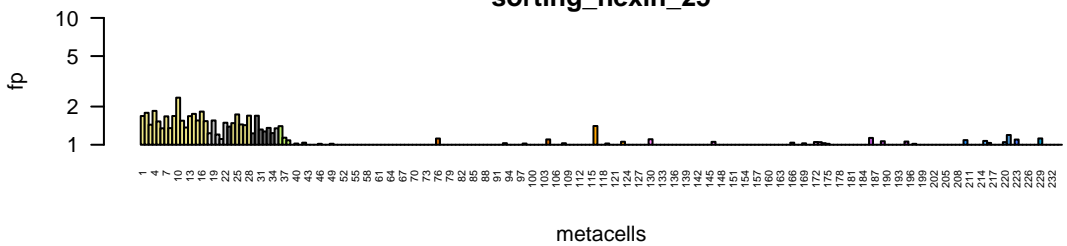
TrH2 OG_4176
TrH2_TrispH2_005862-RA
sorting_nexin_25

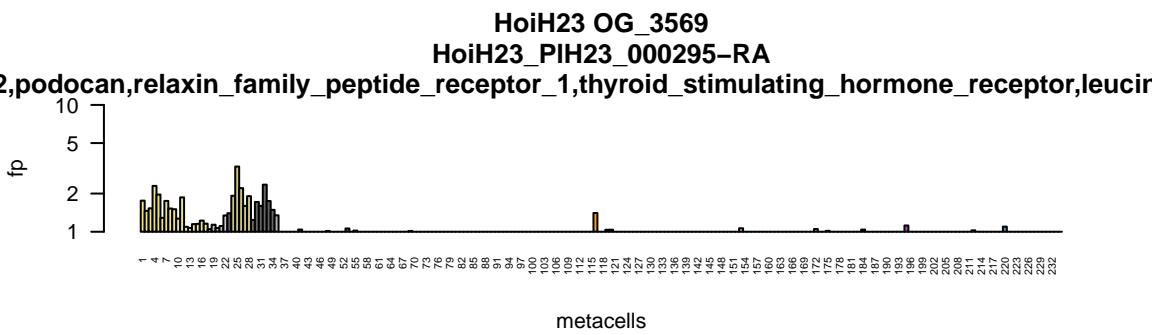
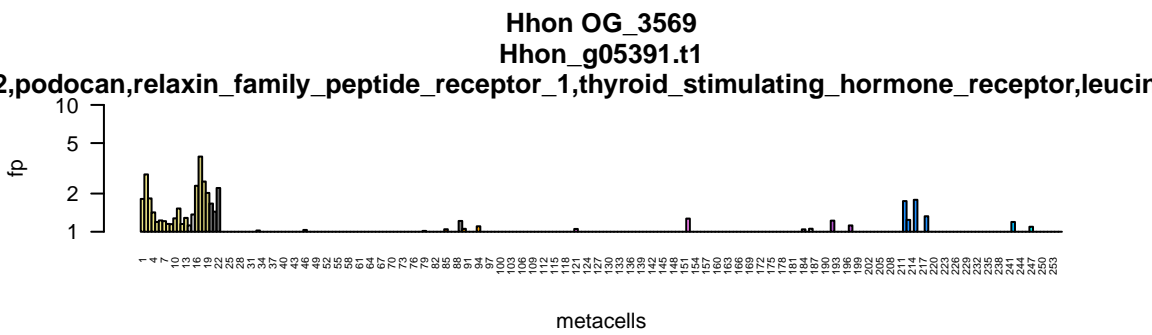
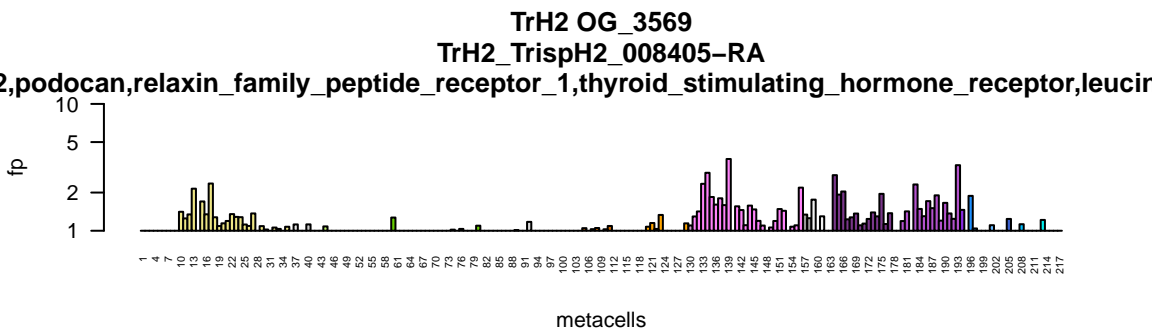


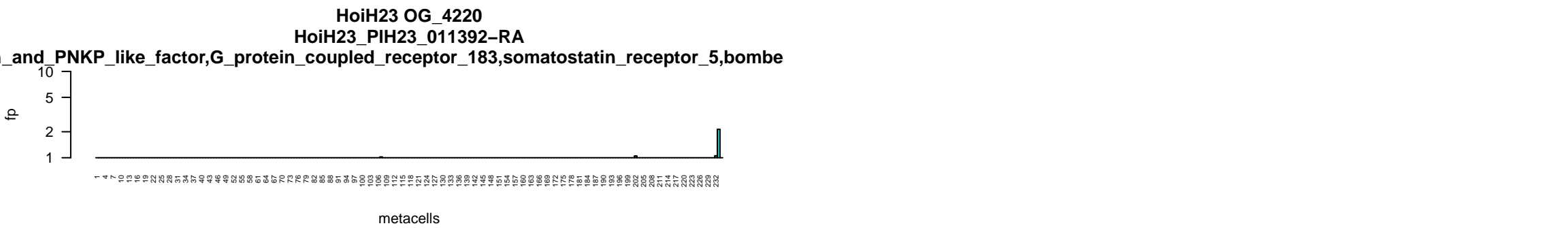
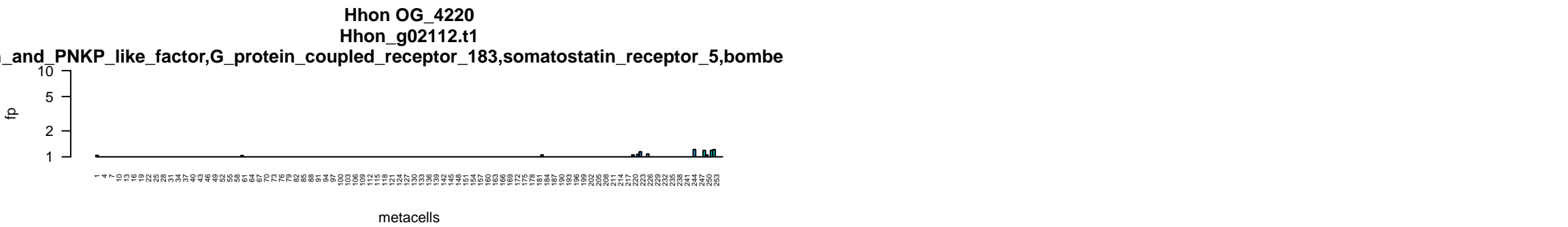
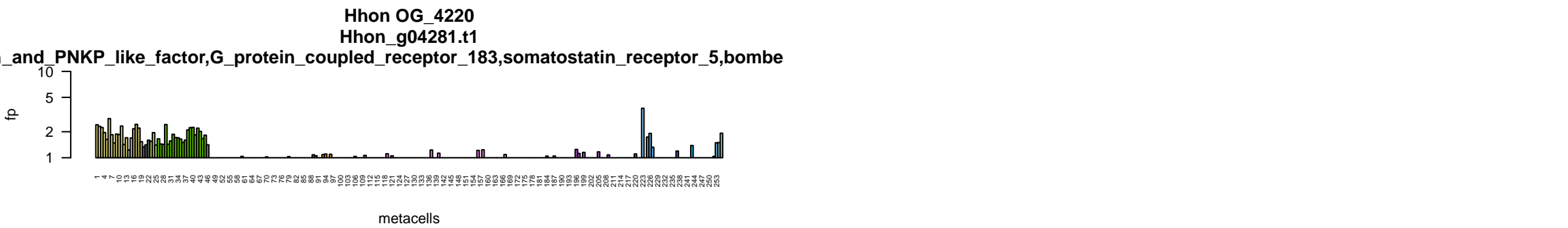
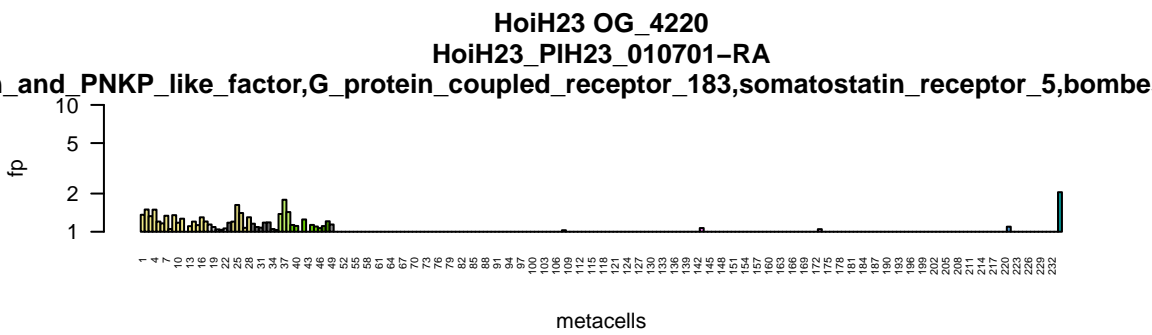
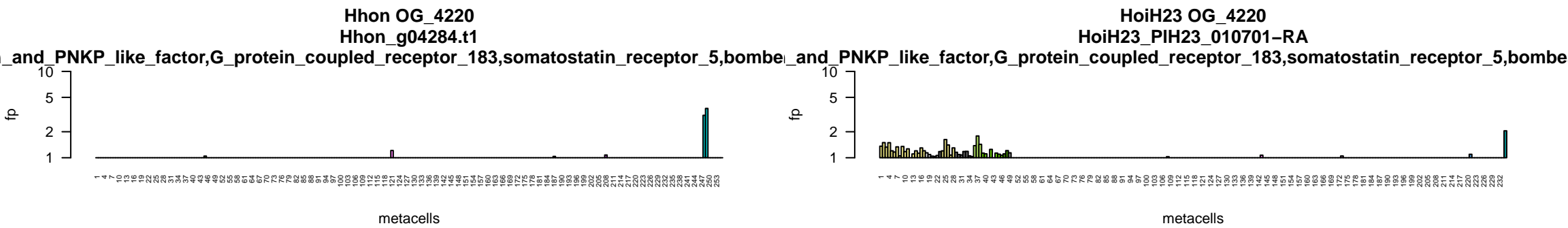
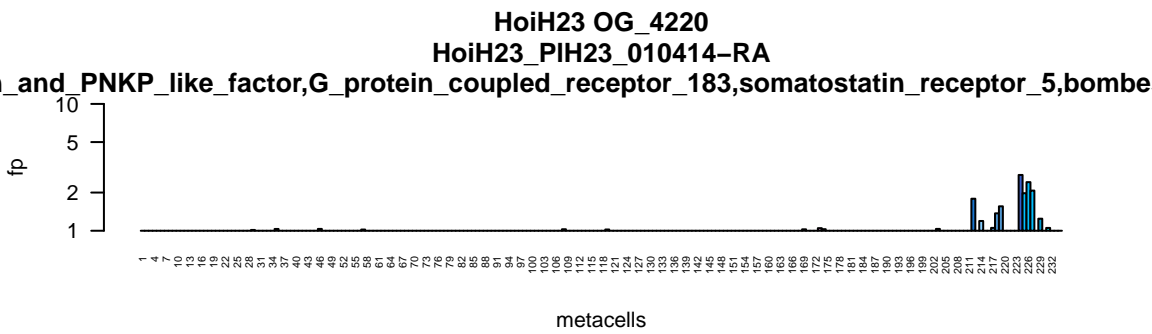
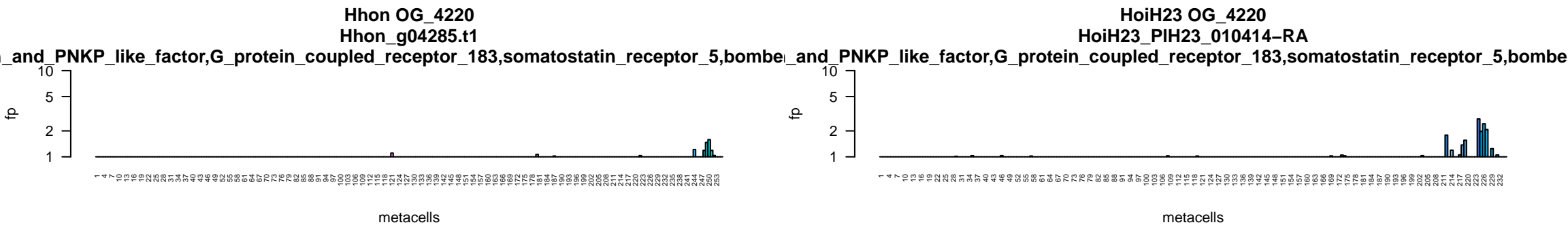
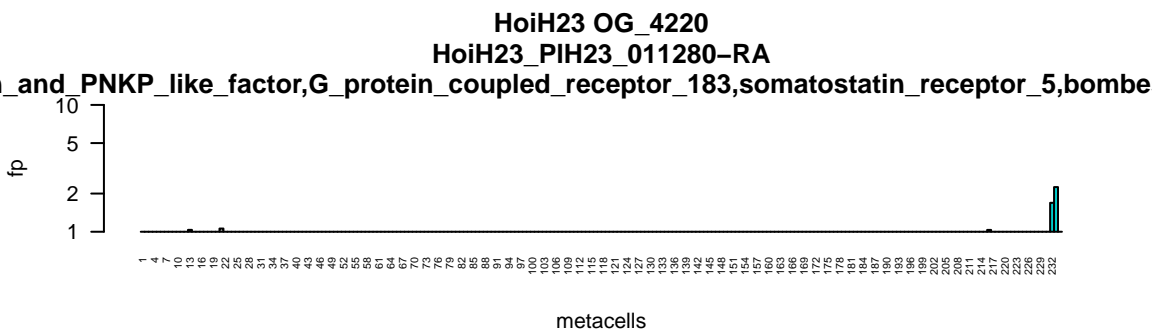
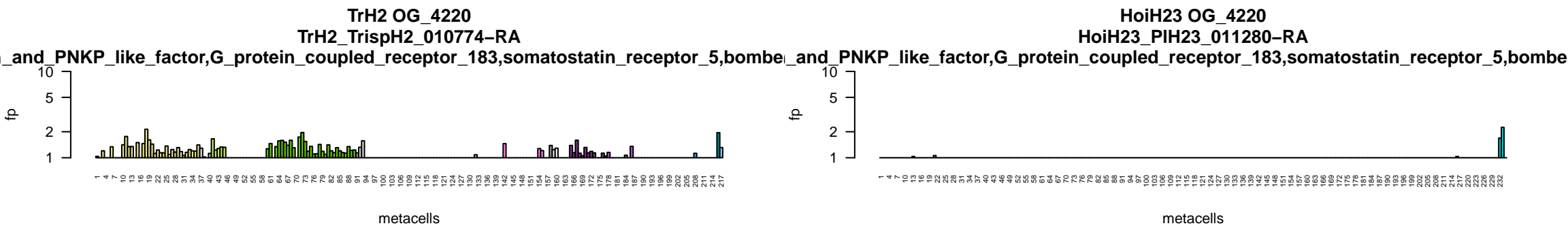
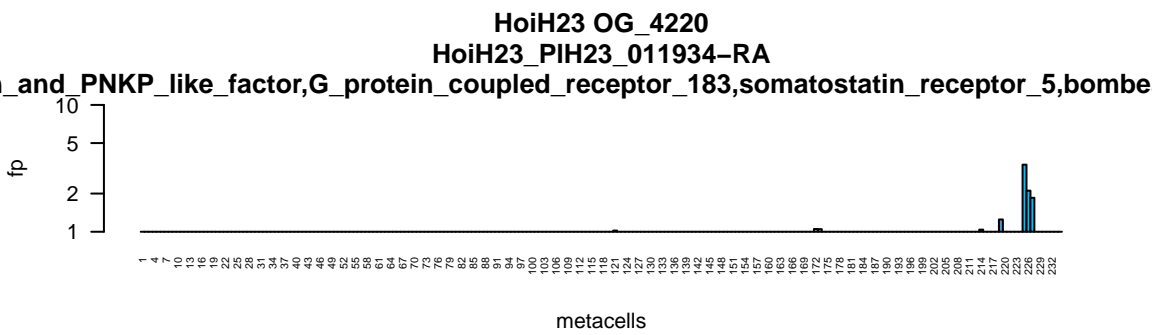
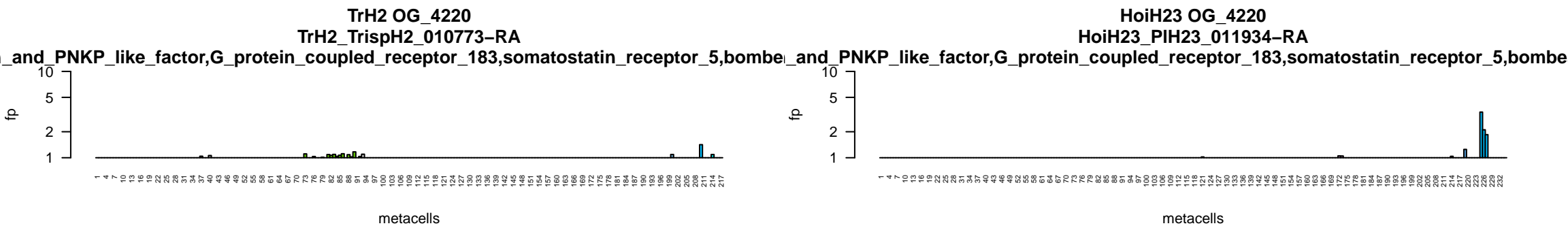
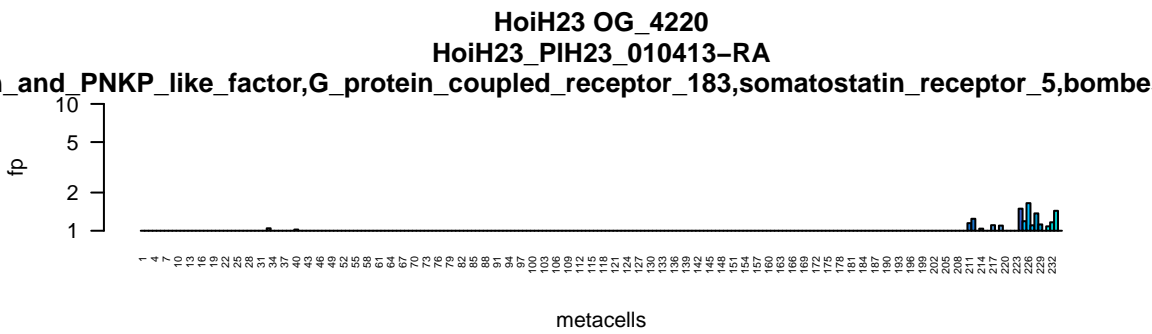
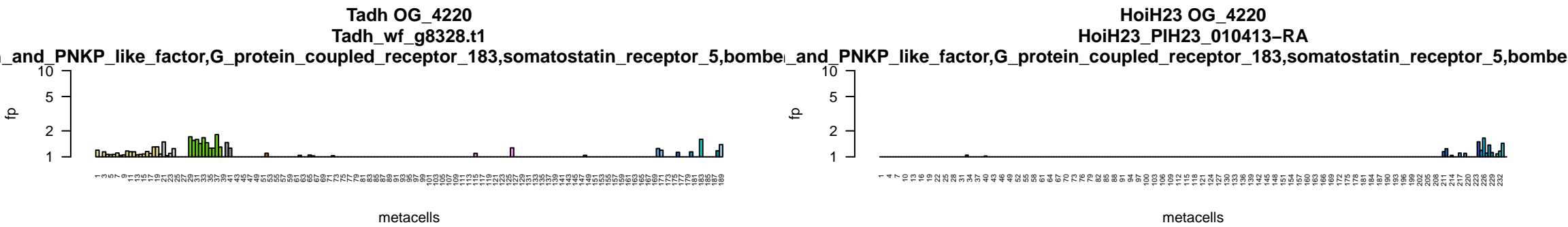
Hhon OG_4176
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sorting_nexin_25



HoiH23 OG_4176
HoiH23_PIH23_009291-RA
sorting_nexin_25

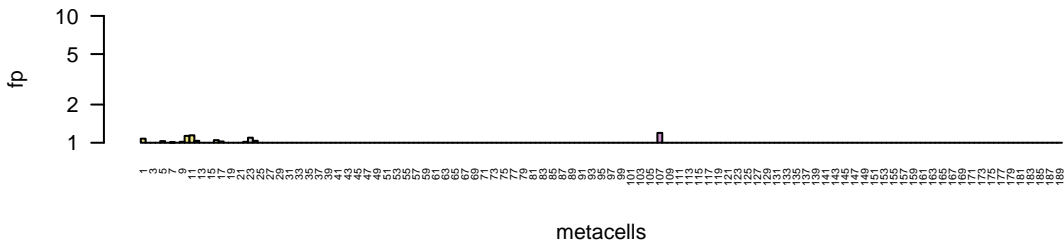






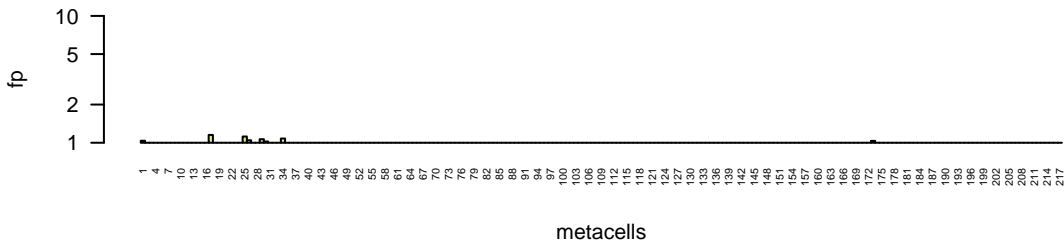
Tadh OG_6016

Tadh_TriadT53133



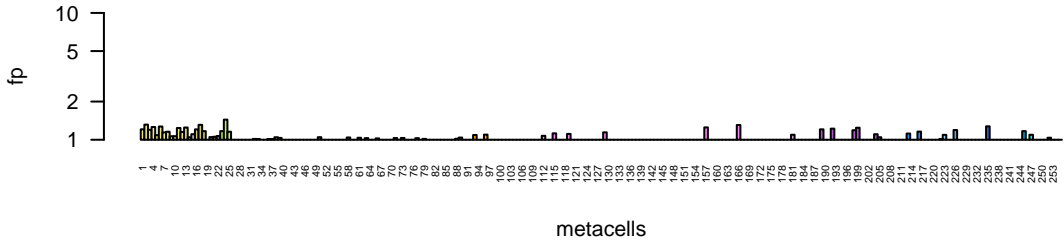
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TrH2_TrispH2_003058-RA



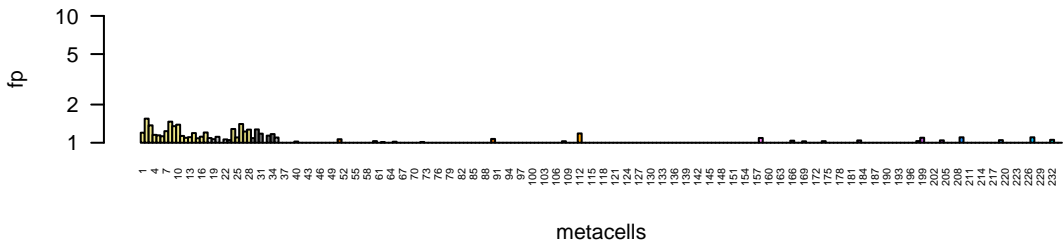
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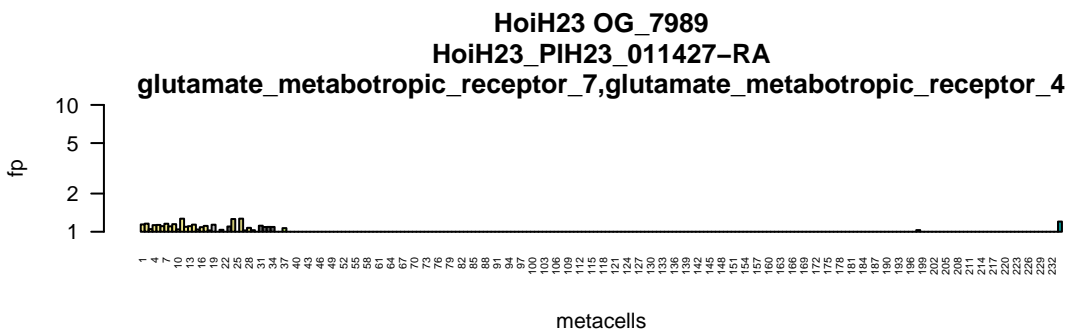
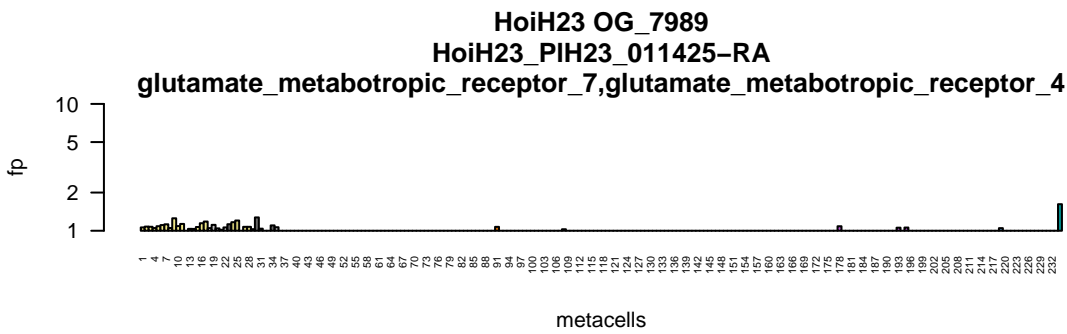
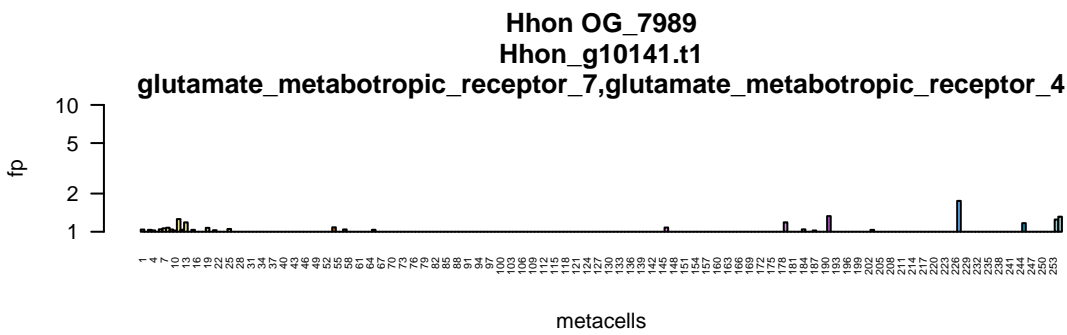
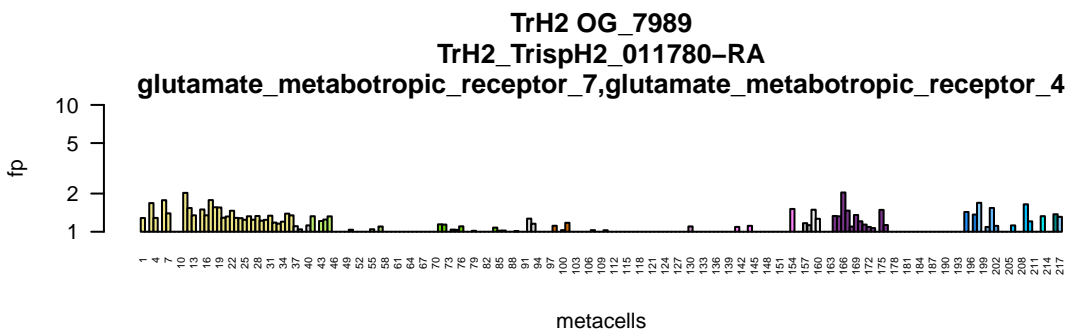
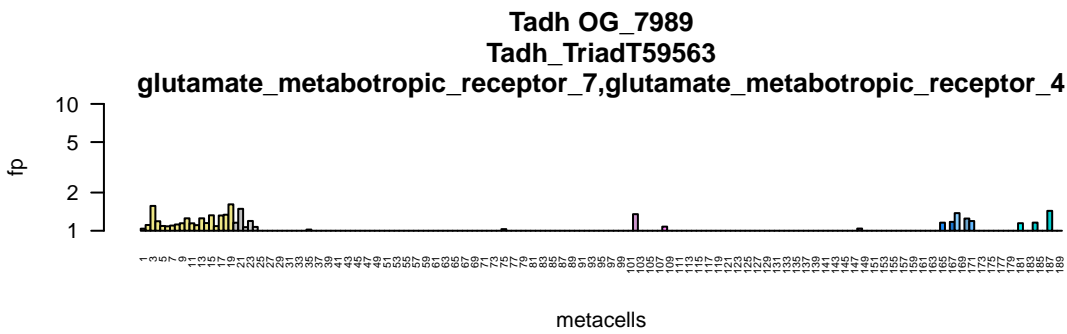
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HoiH23 OG_6016

HoiH23_PIH23_000013-RA

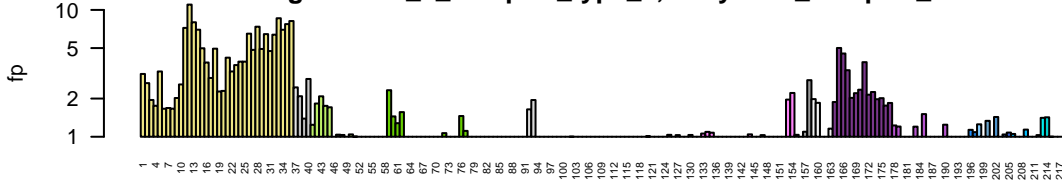




angiotensin_II_receptor_type_2,tachykinin_receptor_1
Tadh | no data

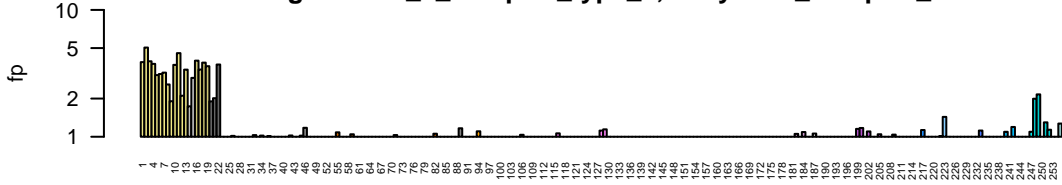


TrH2 OG_9264
TrH2_TrispH2_002603-RA
angiotensin_II_receptor_type_2,tachykinin_receptor_1



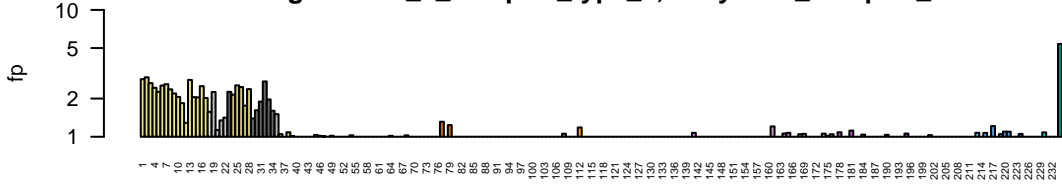
metacells

Hhon OG_9264
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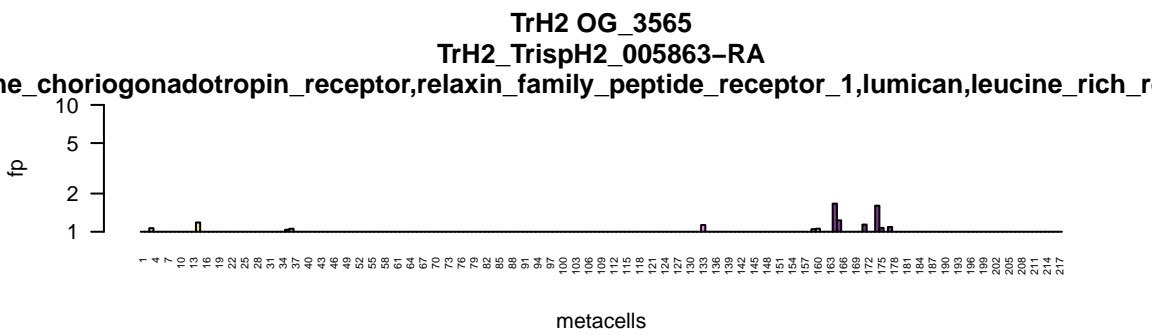
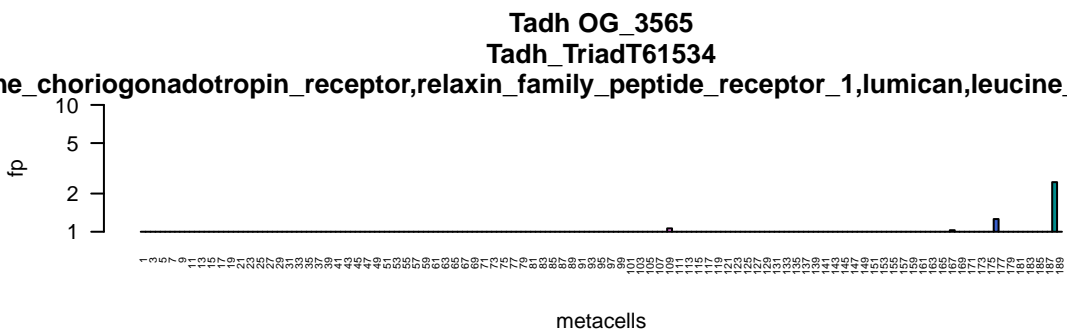
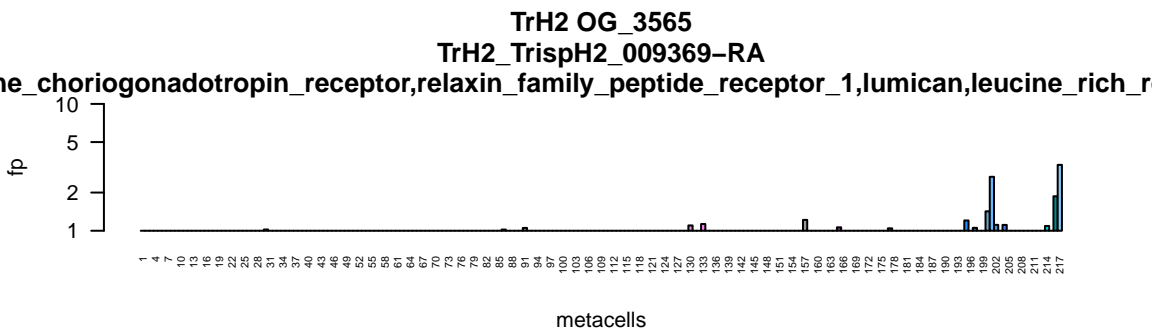
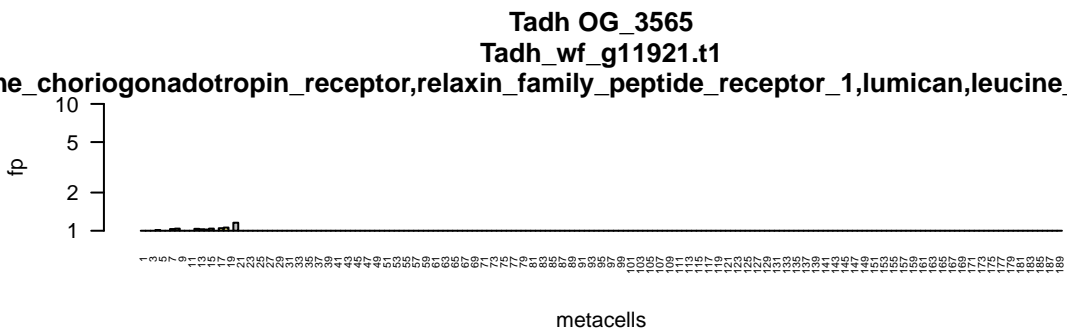
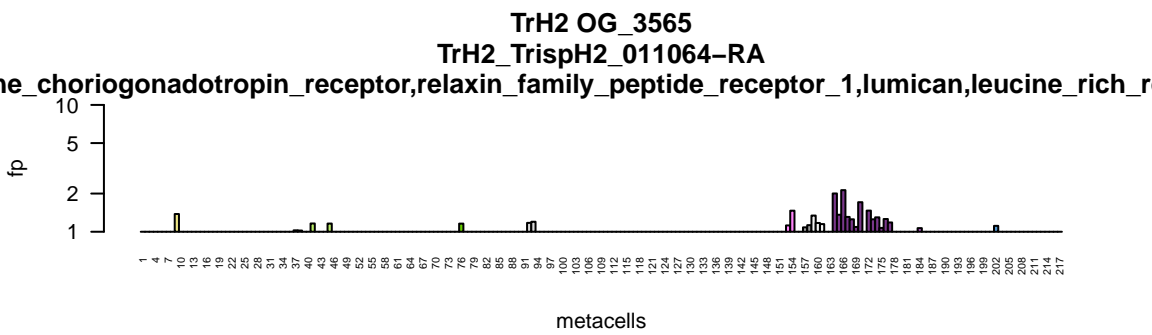
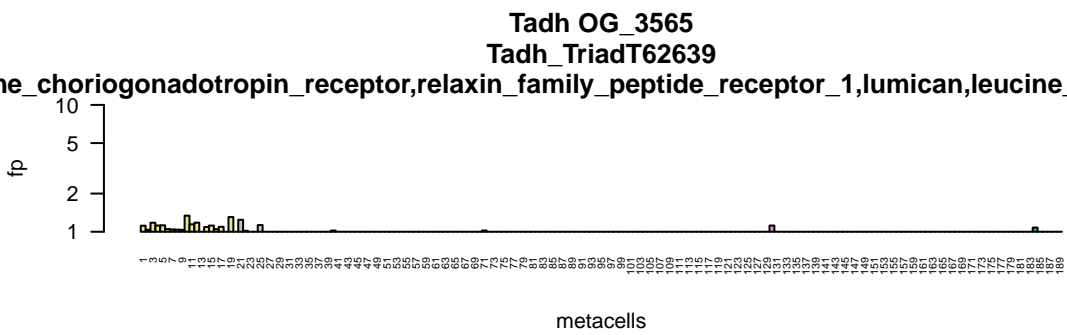
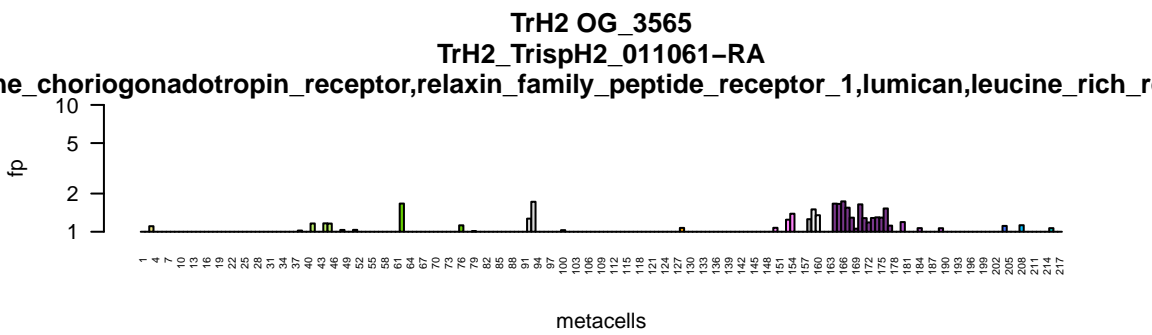
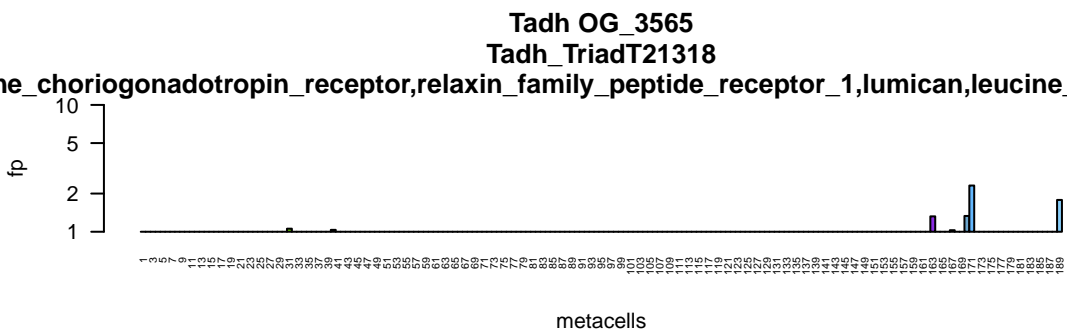
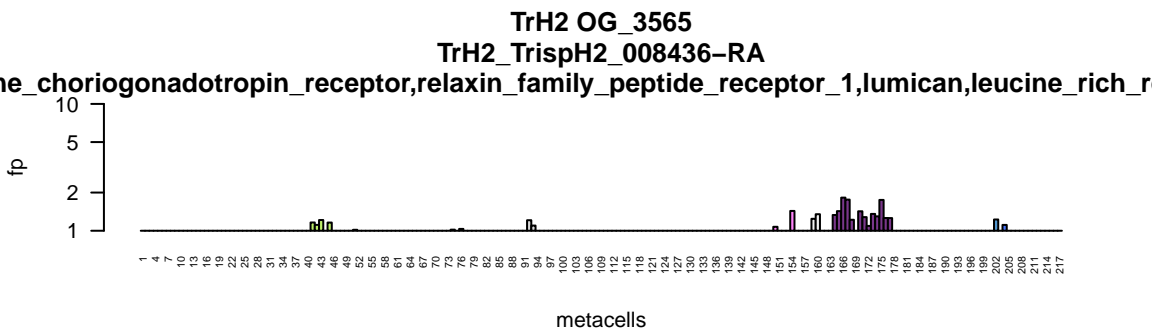
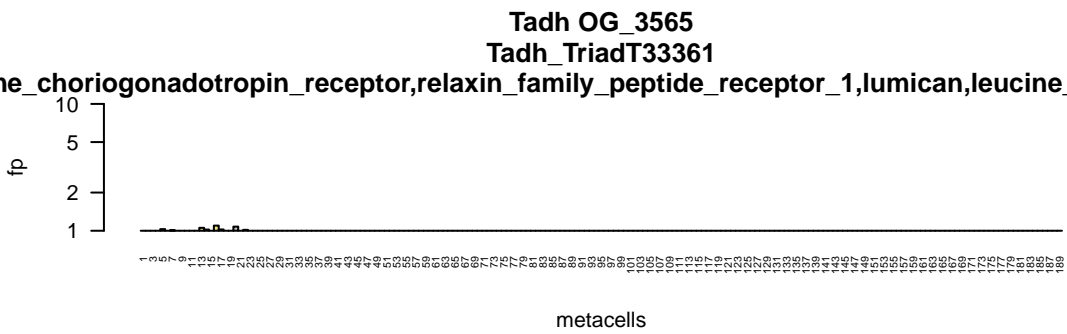
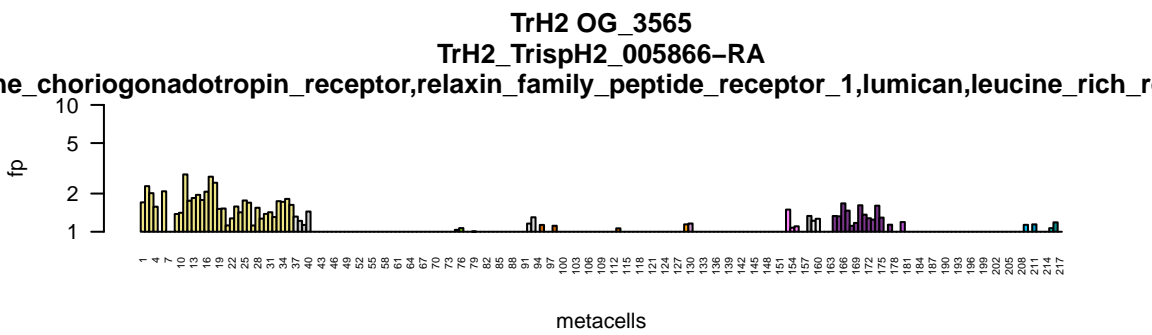
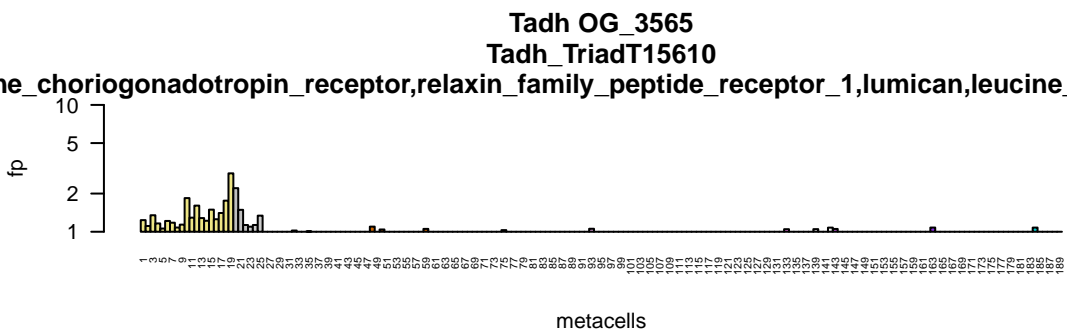
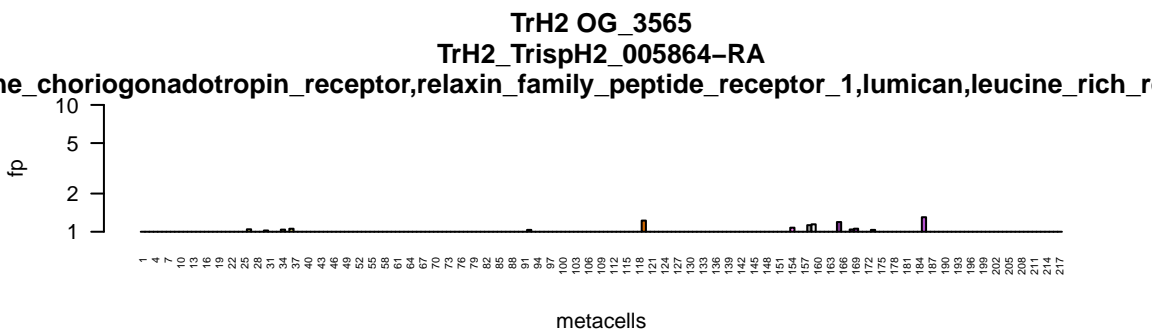
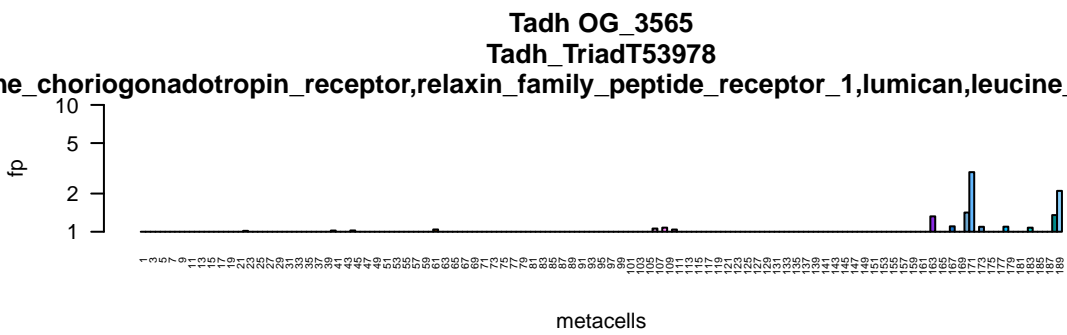
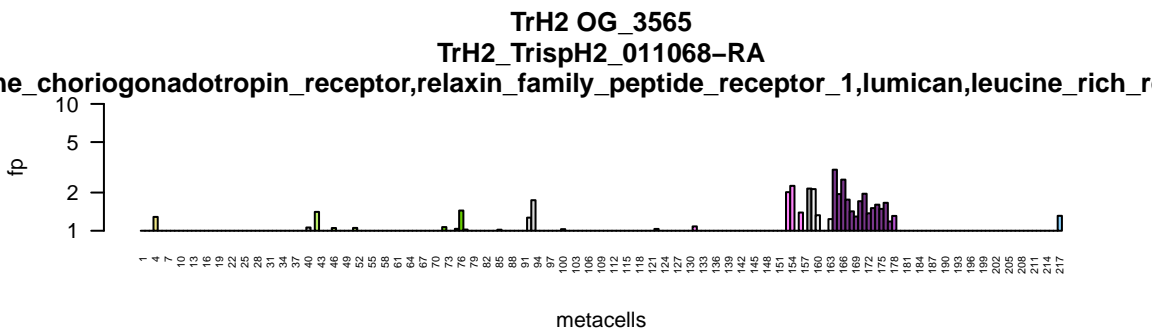
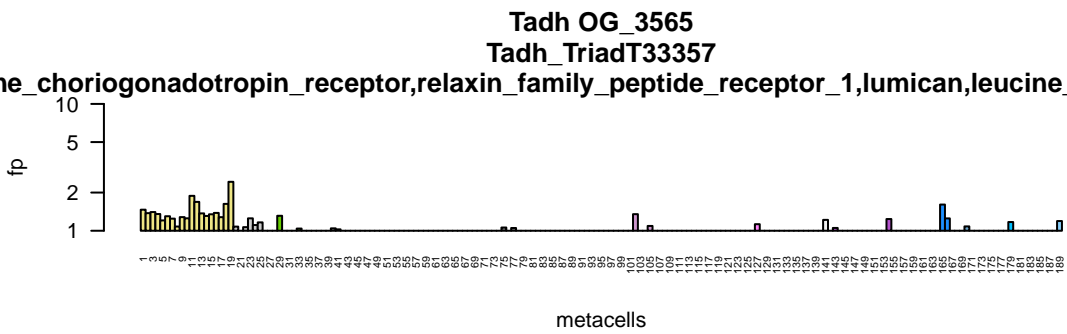


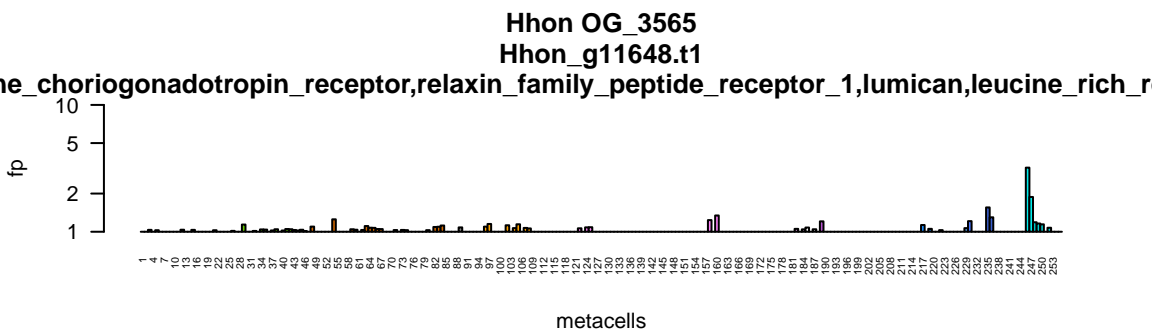
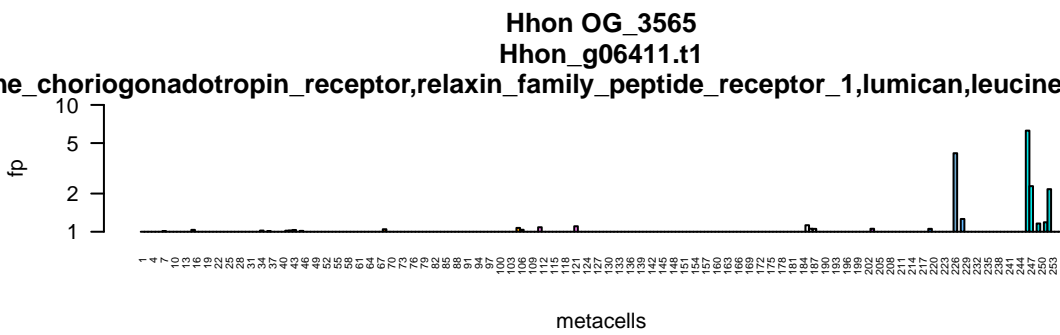
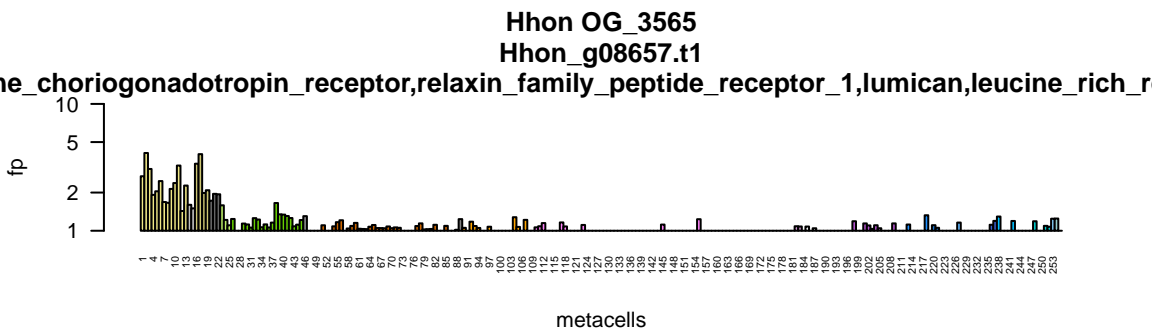
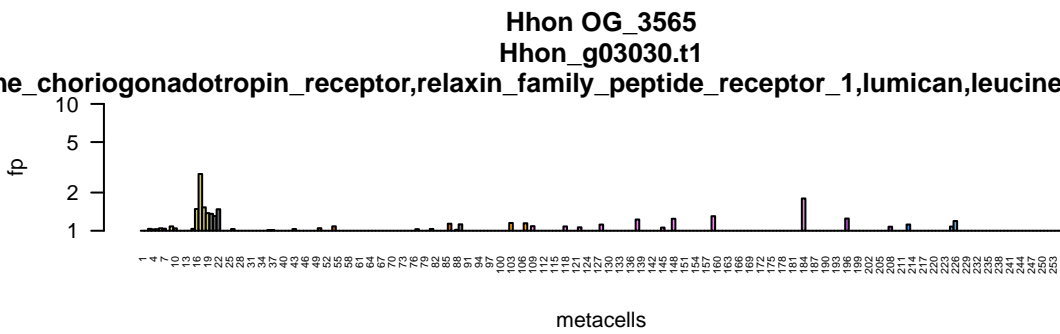
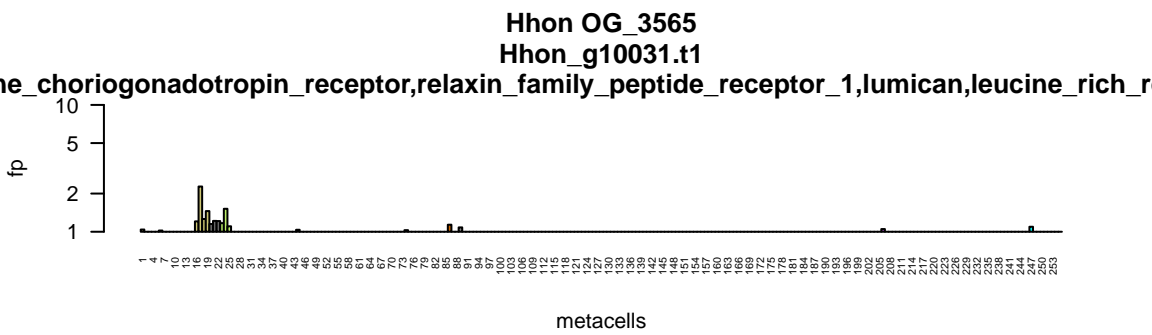
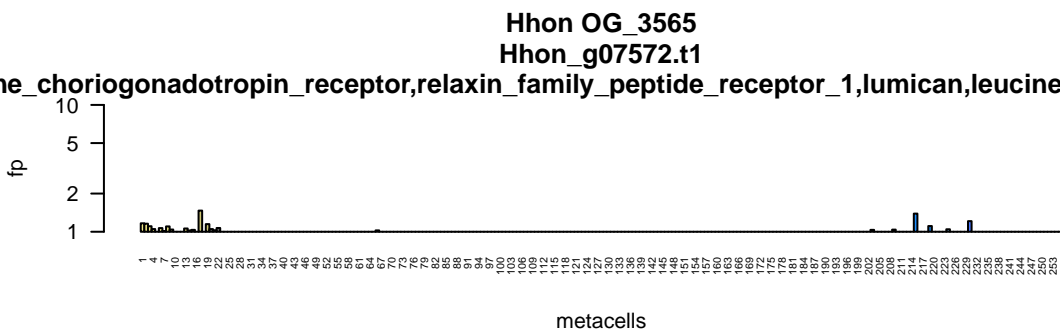
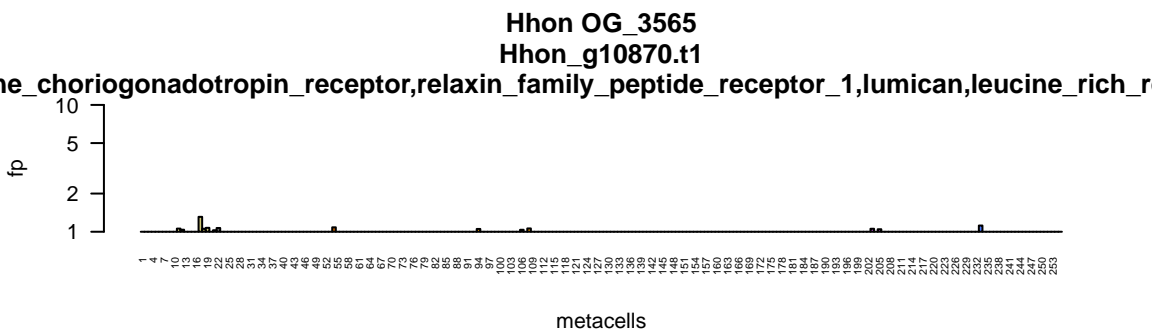
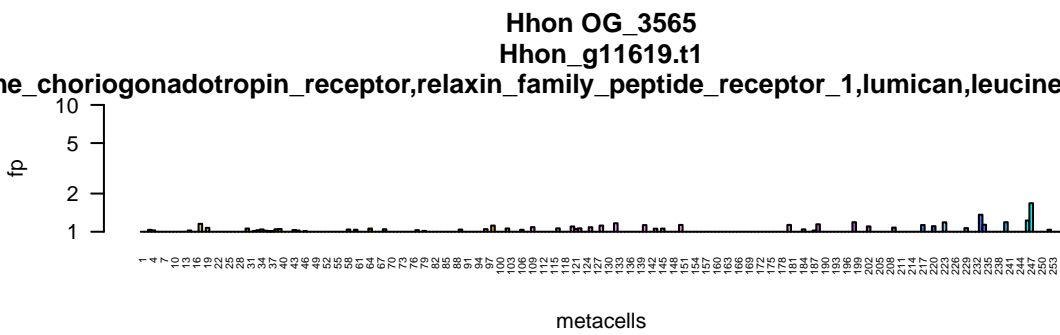
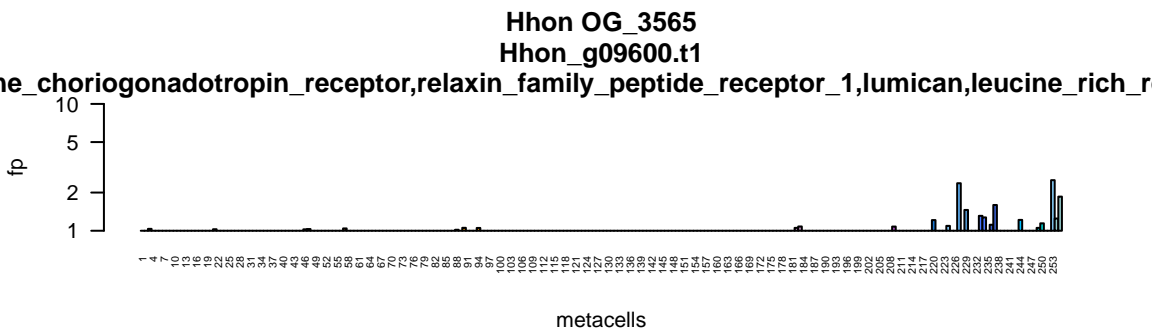
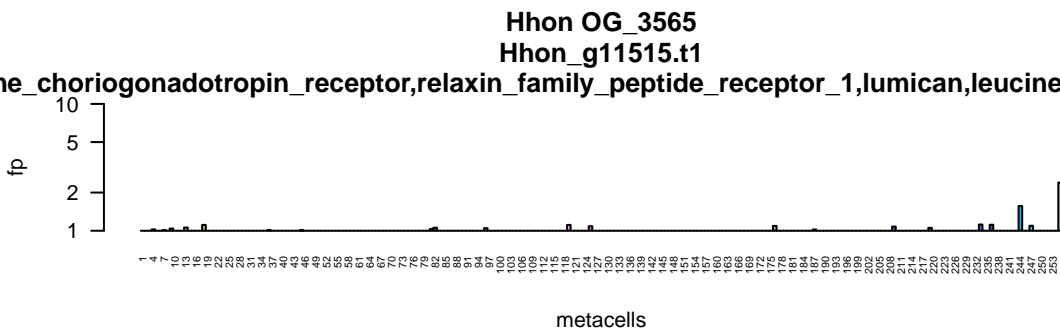
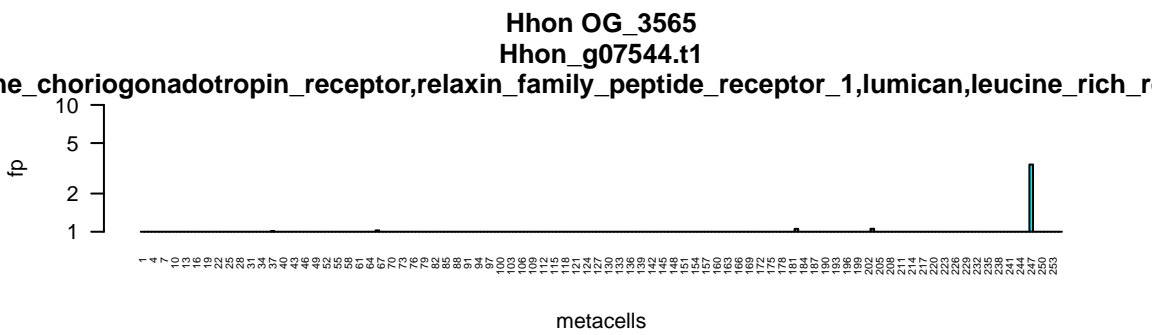
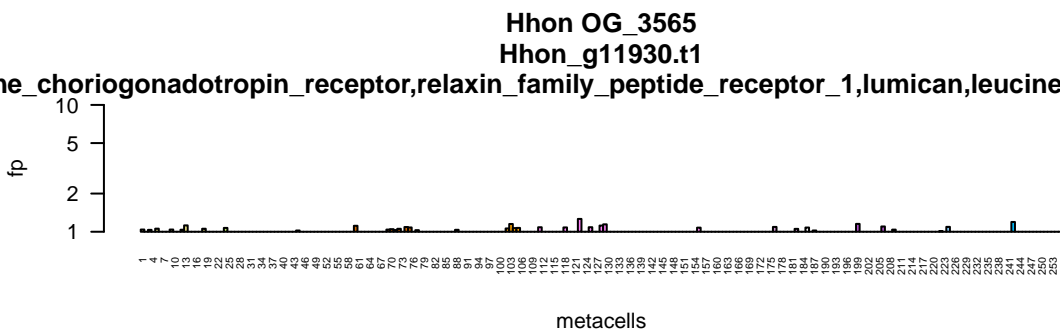
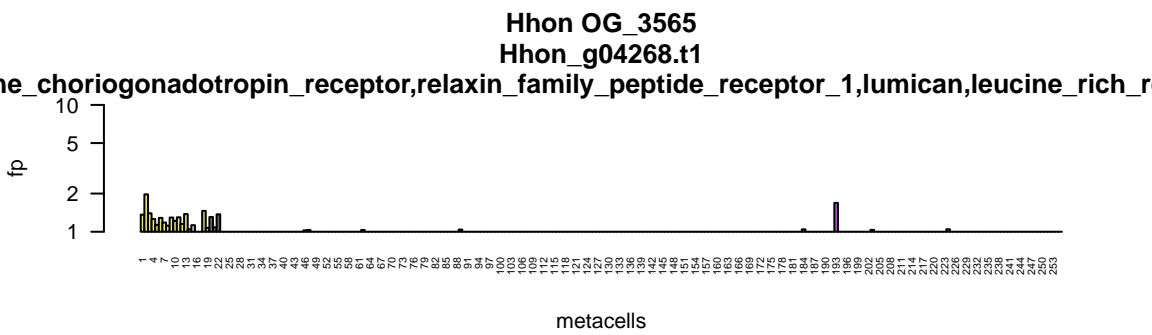
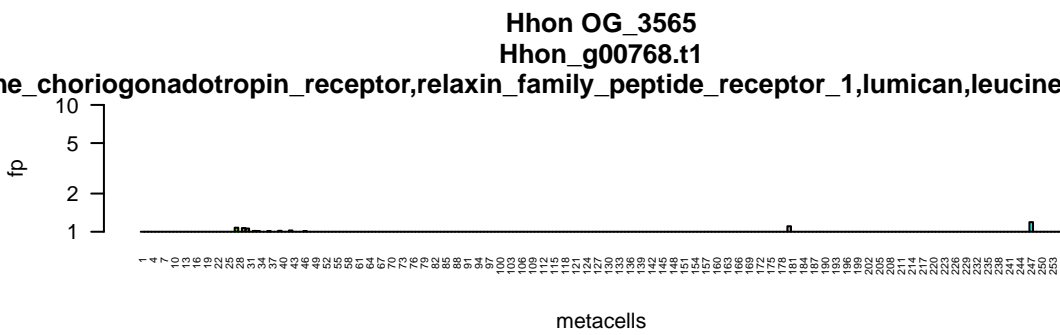
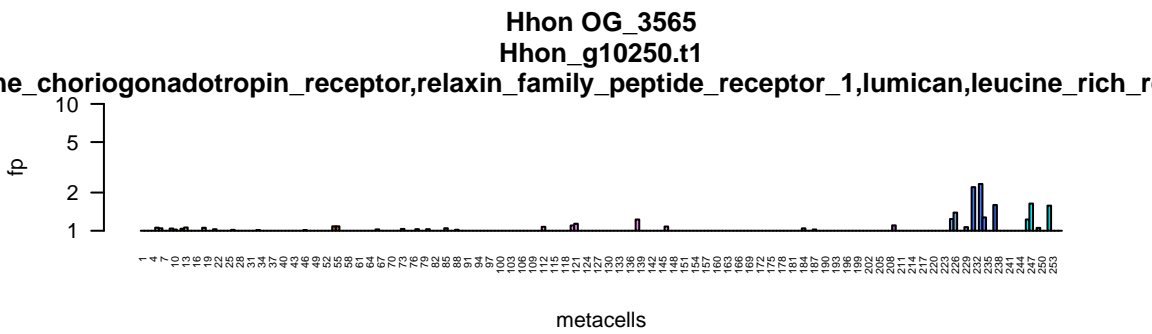
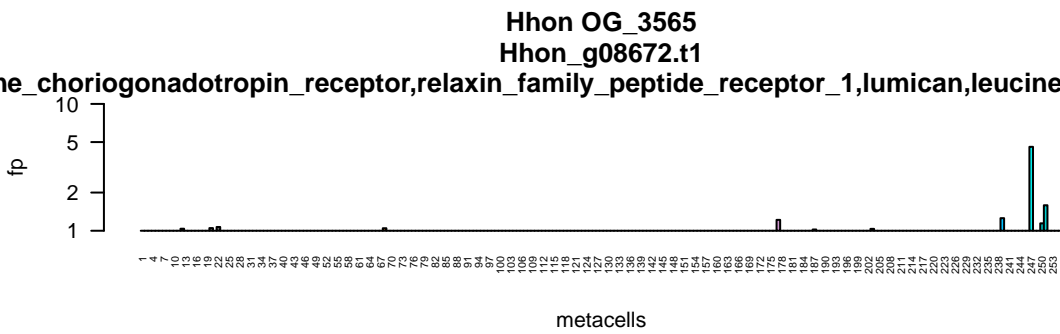
metacells

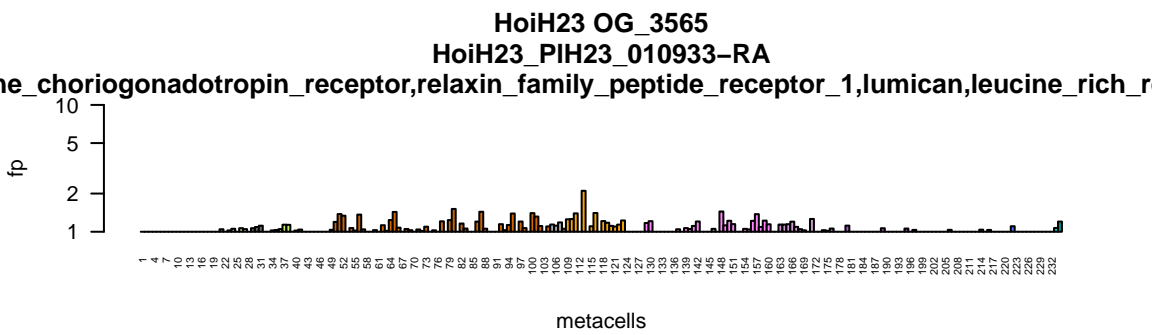
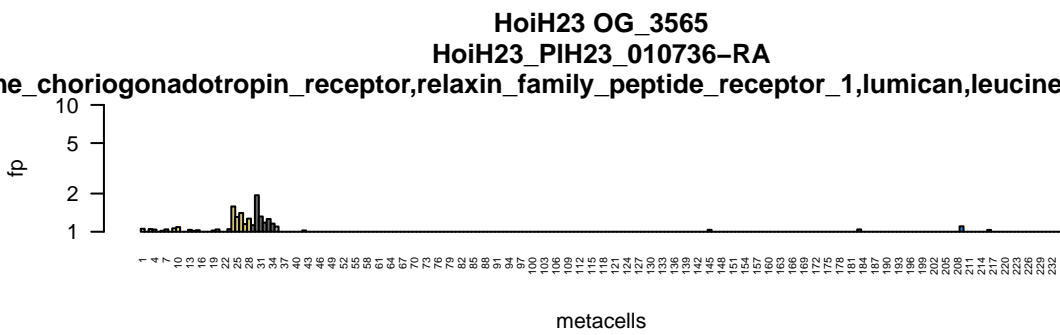
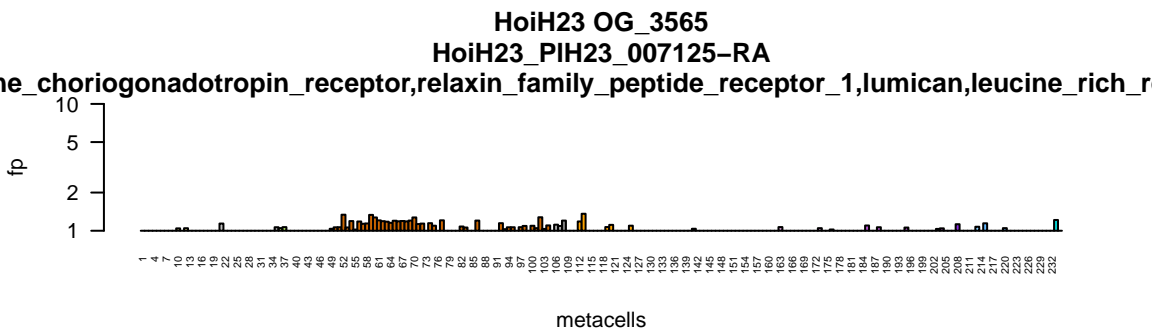
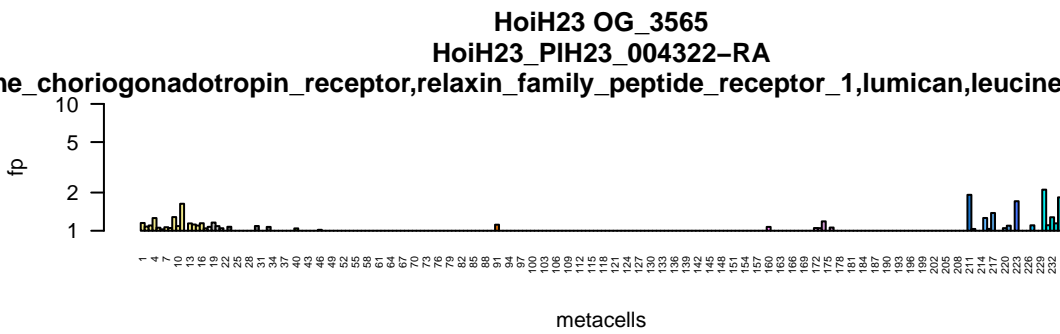
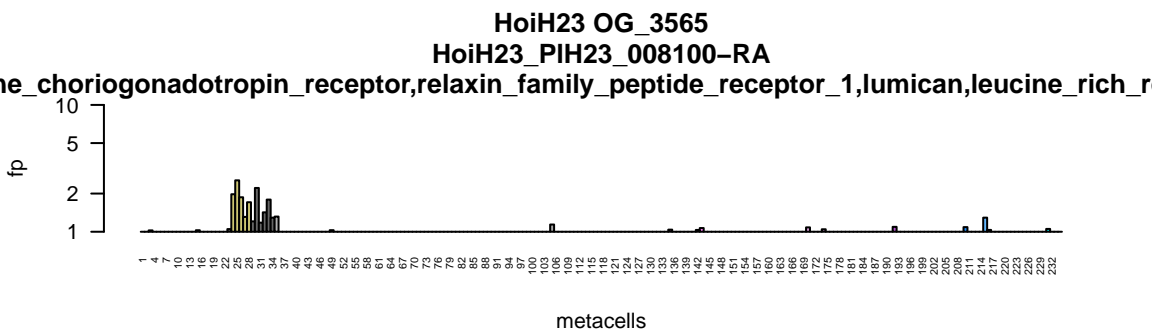
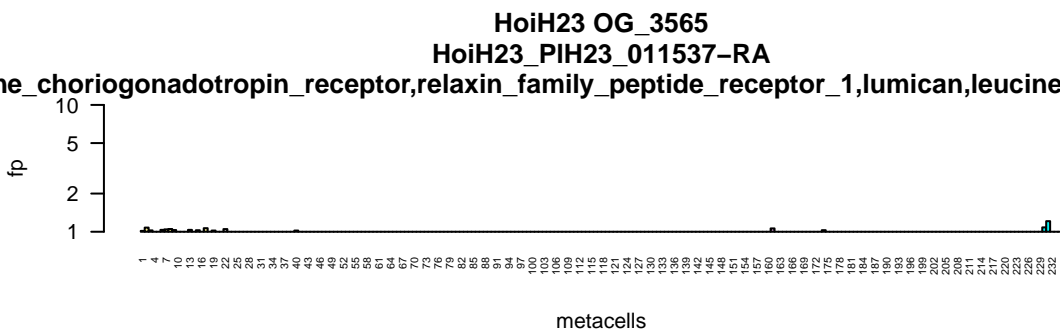
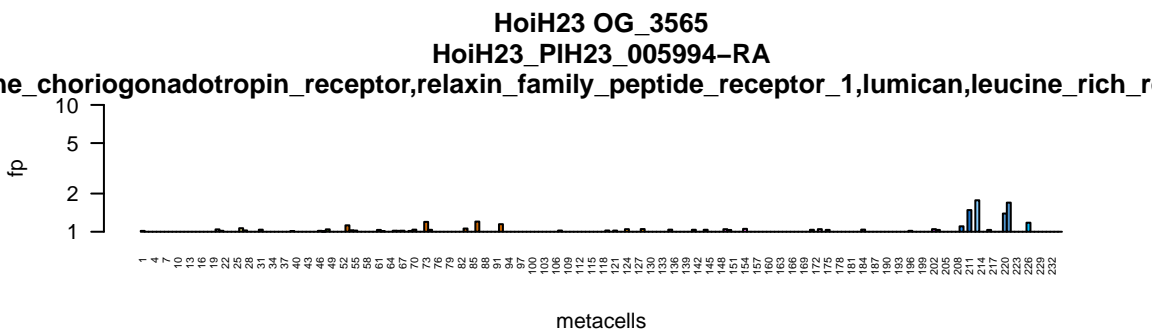
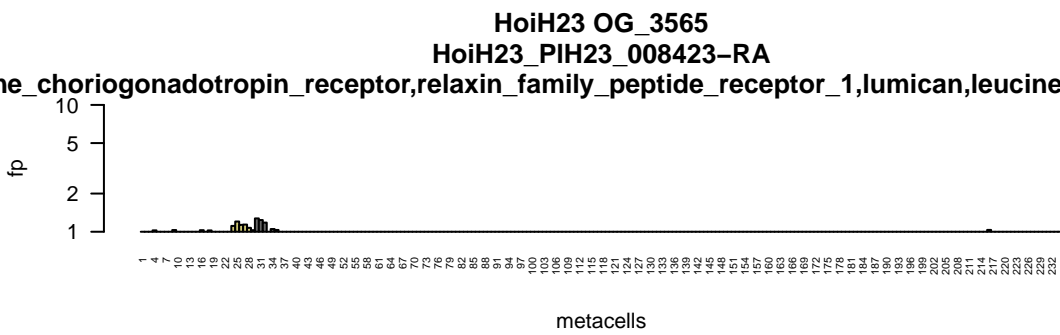
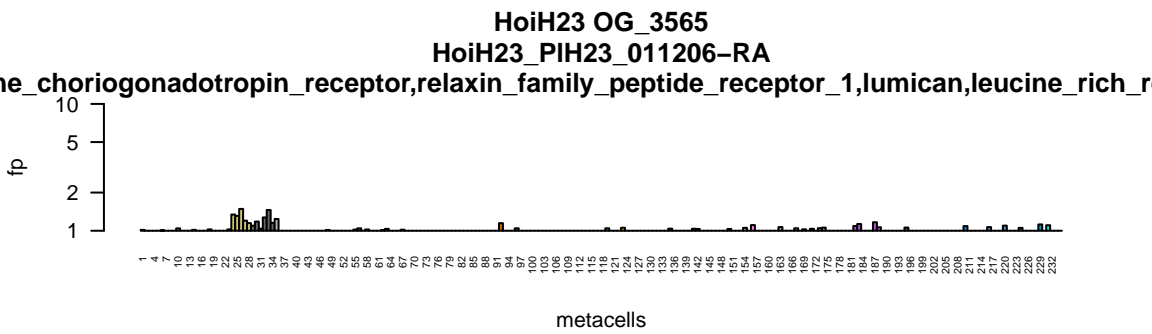
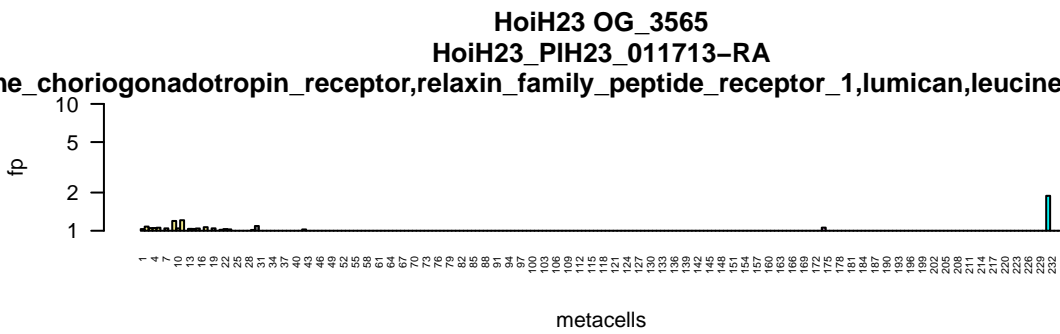
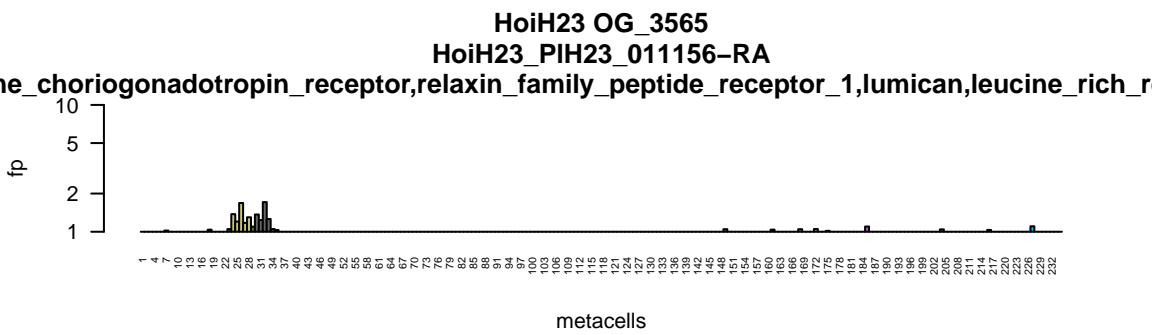
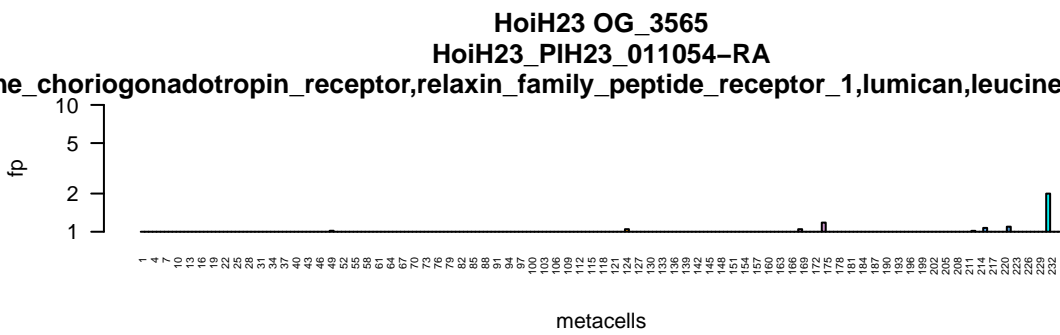
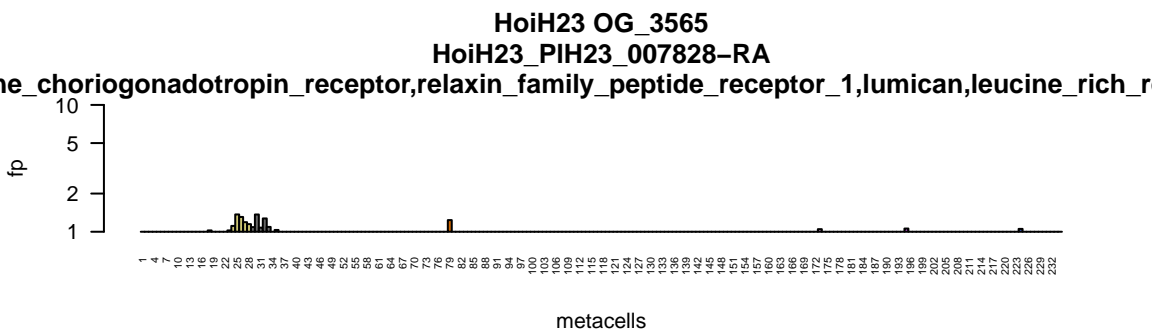
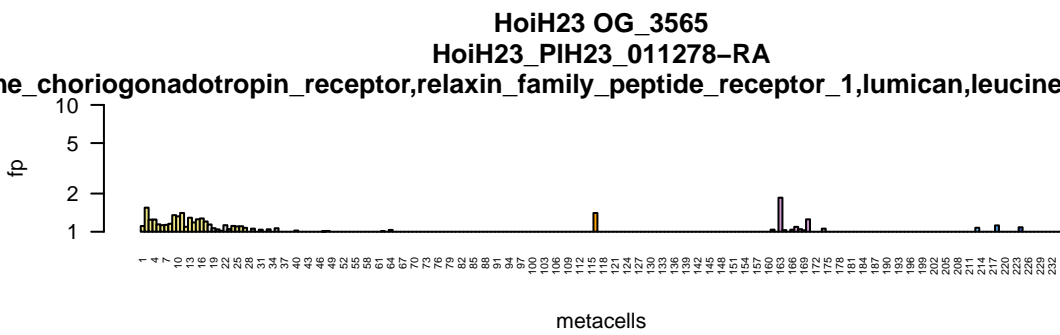
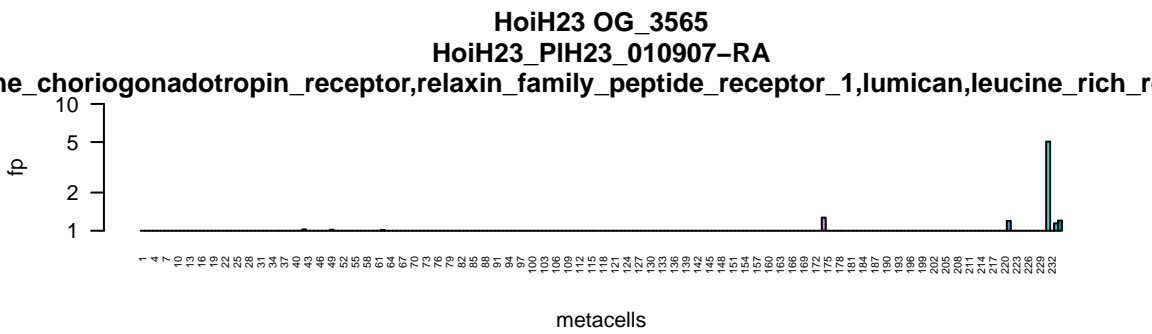
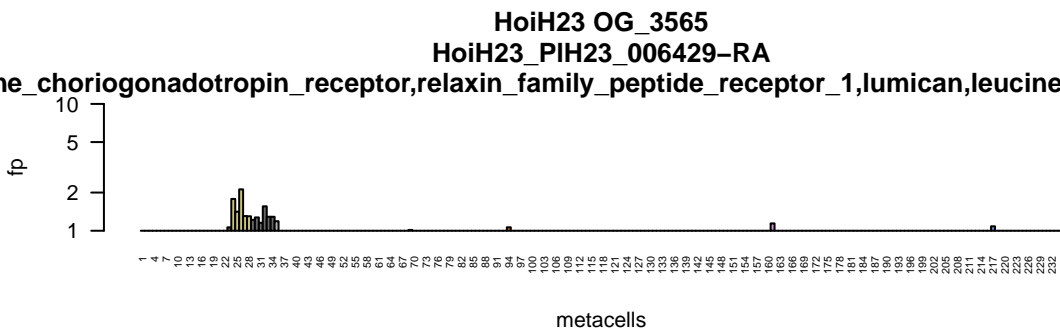
HoiH23 OG_9264
HoiH23_PIH23_008322-RA
angiotensin_II_receptor_type_2,tachykinin_receptor_1

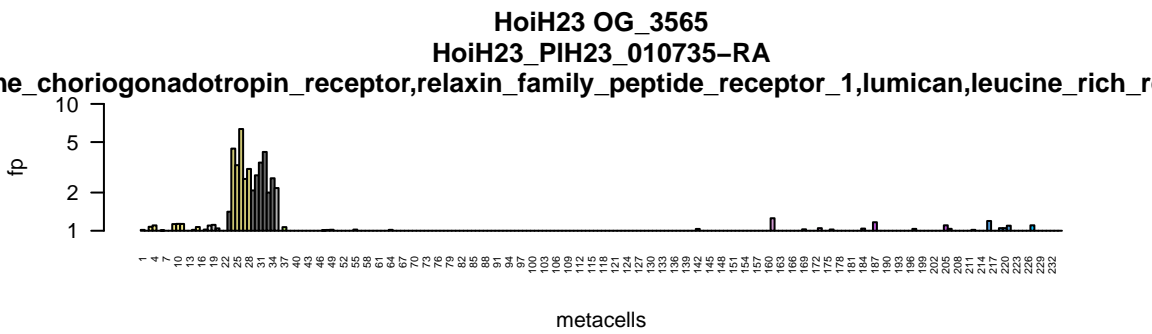
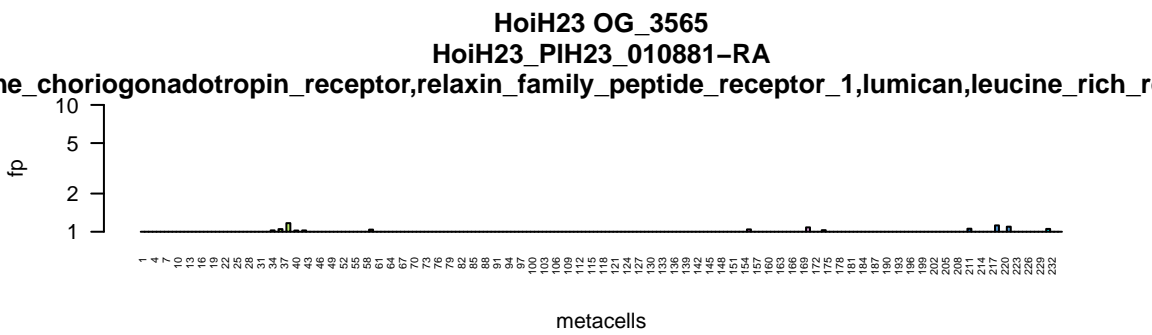
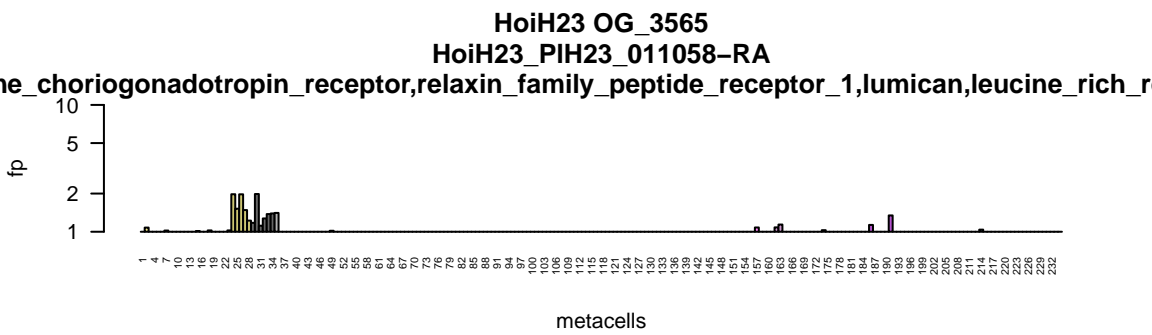
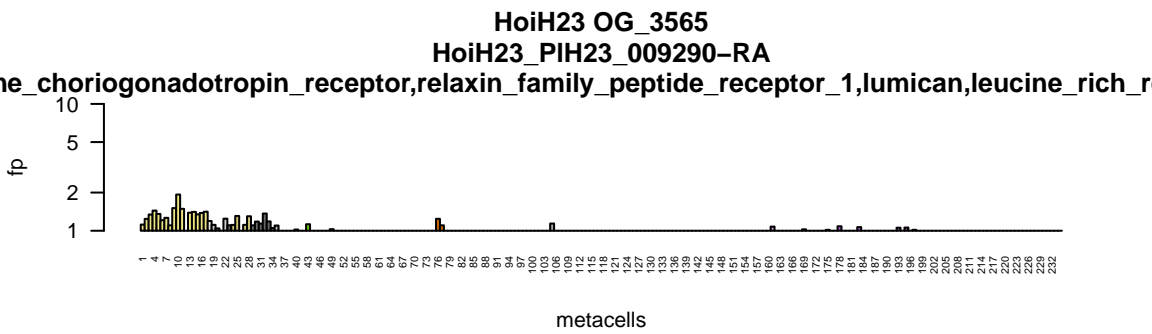


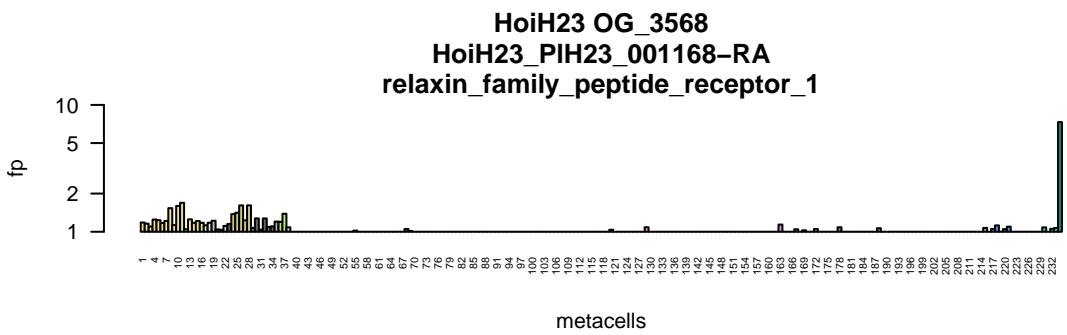
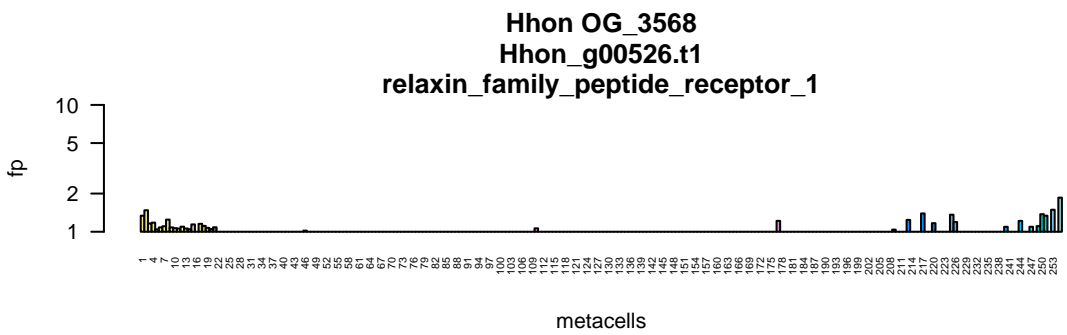
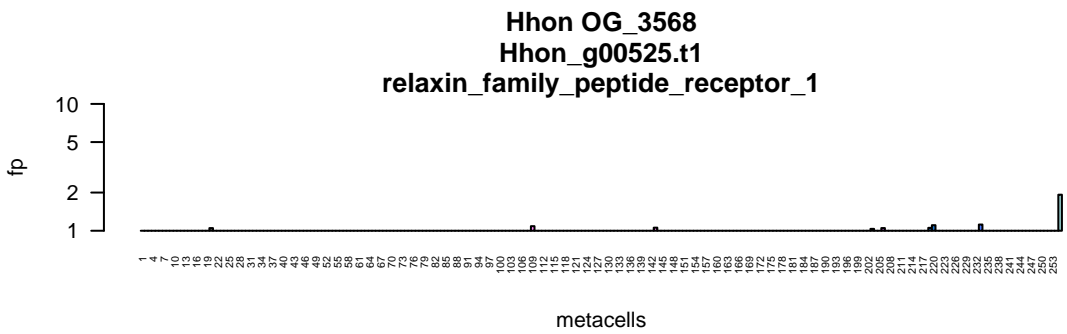
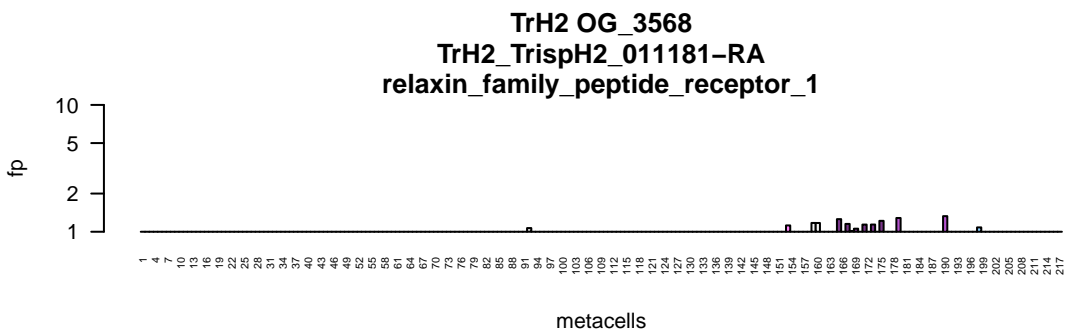
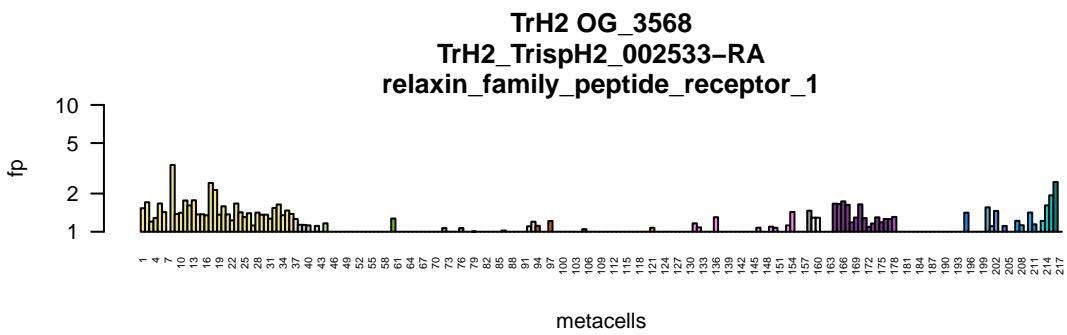
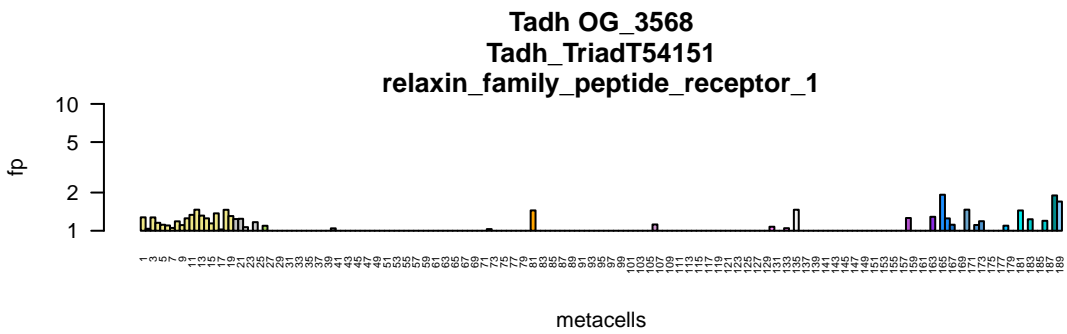
metacells

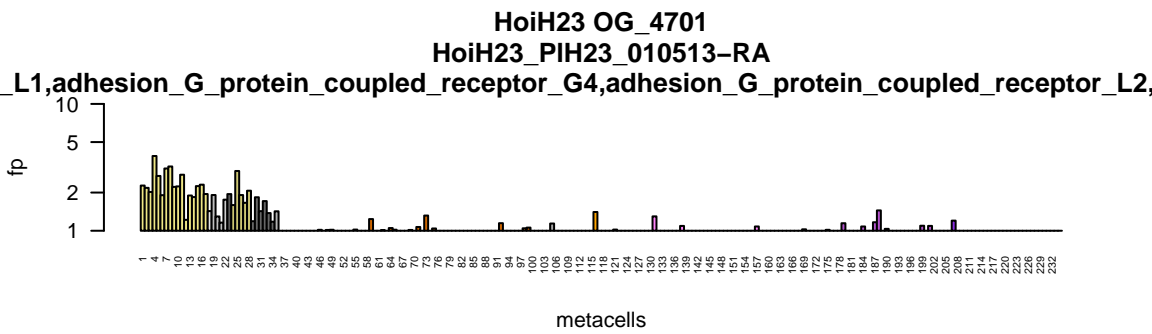
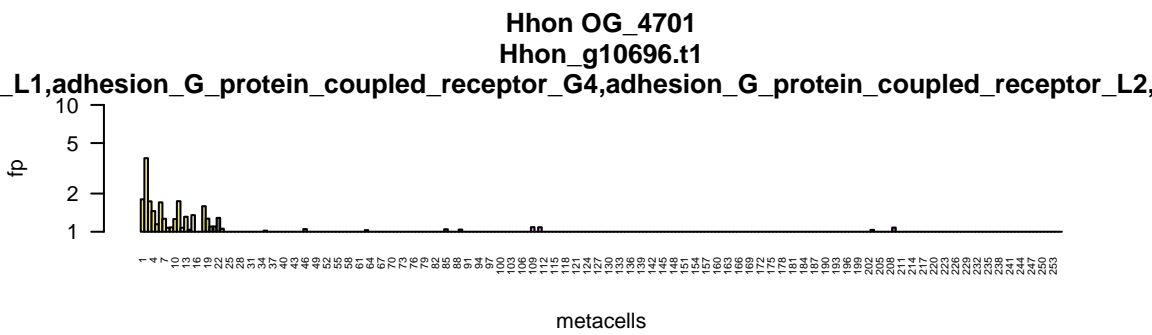
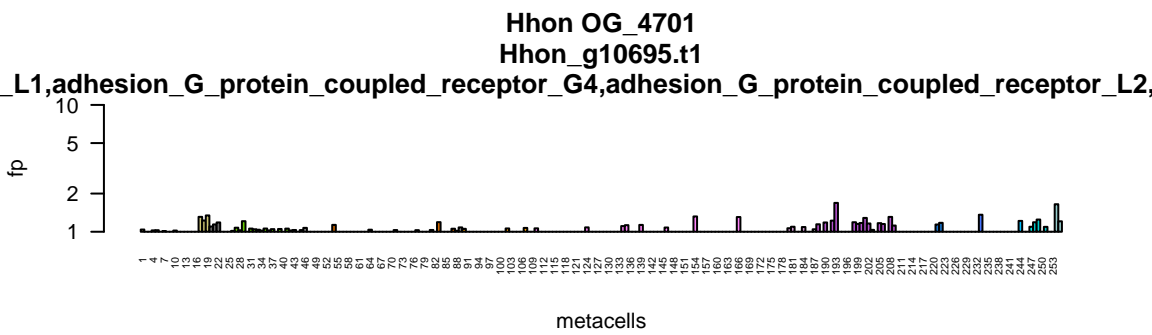
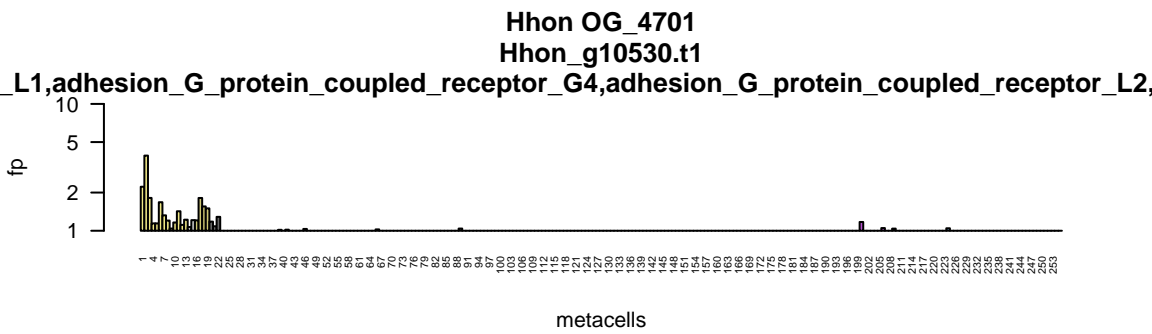
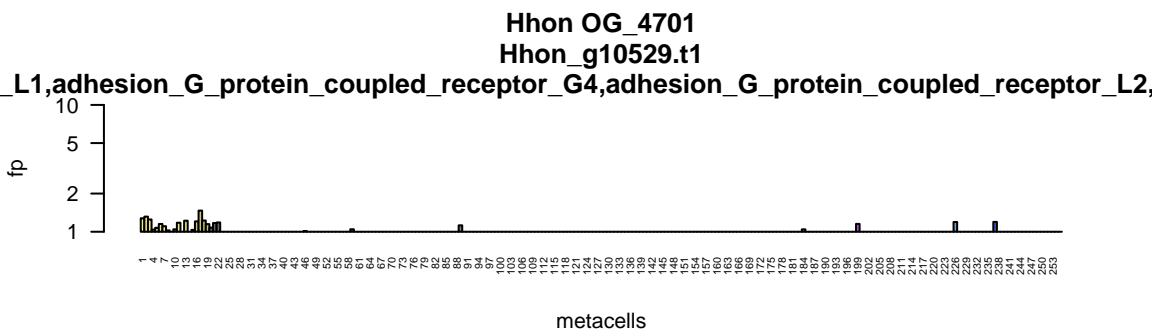
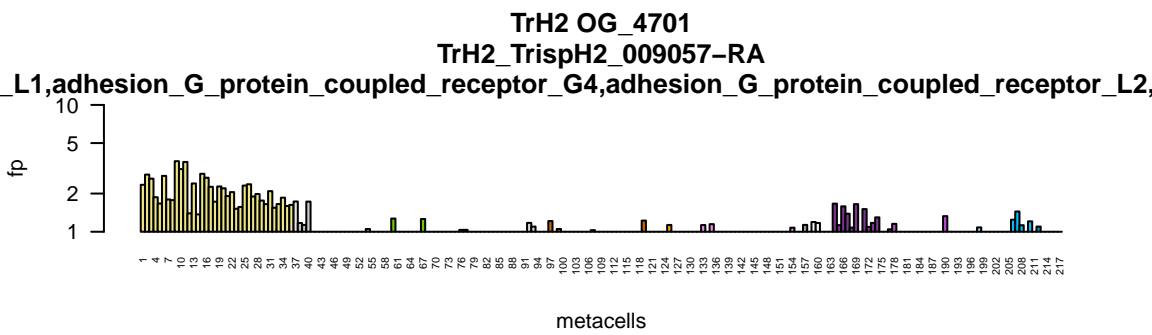
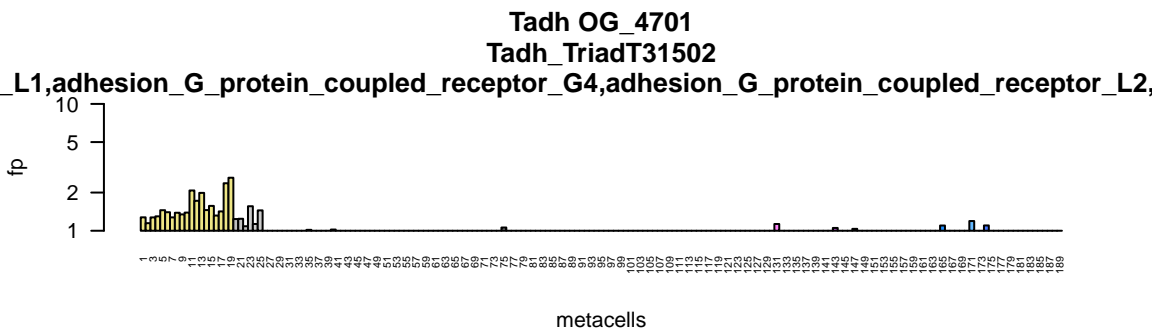


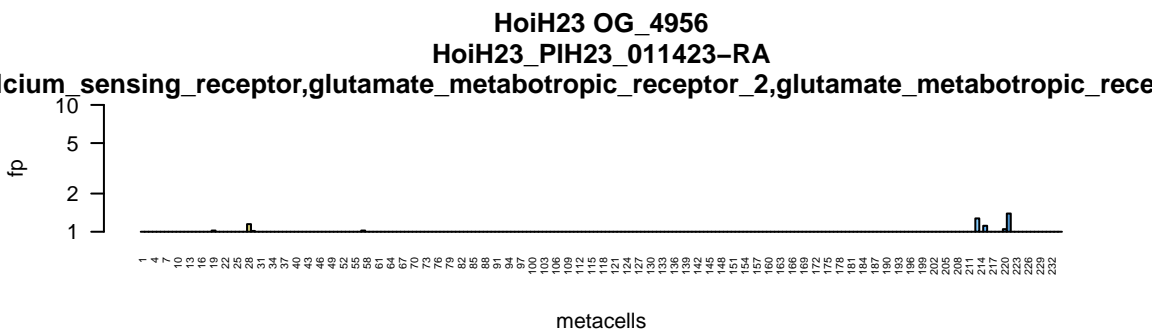
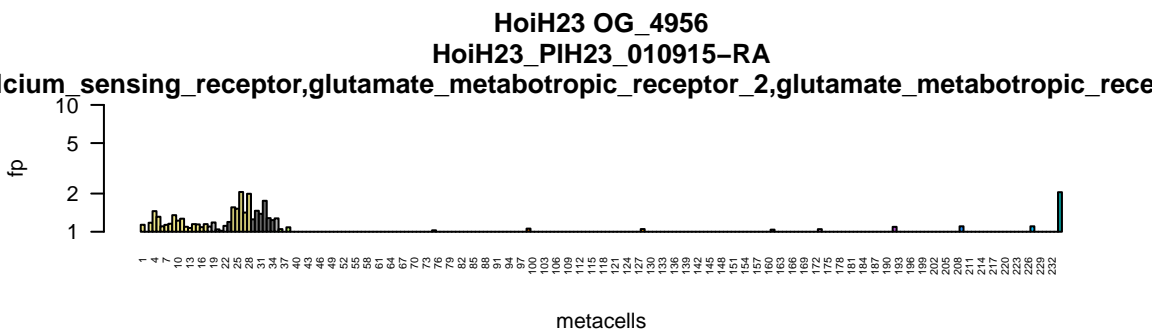
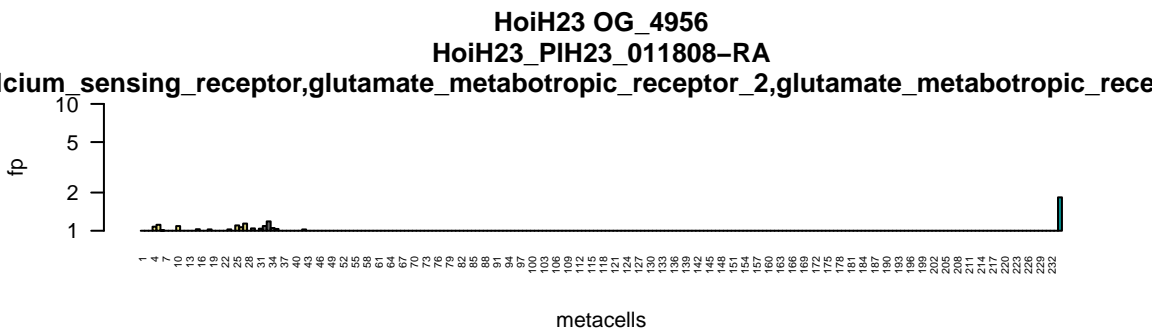
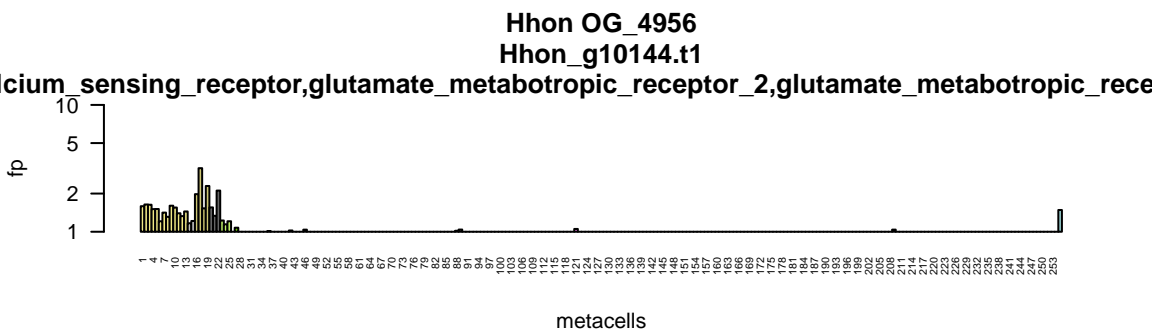
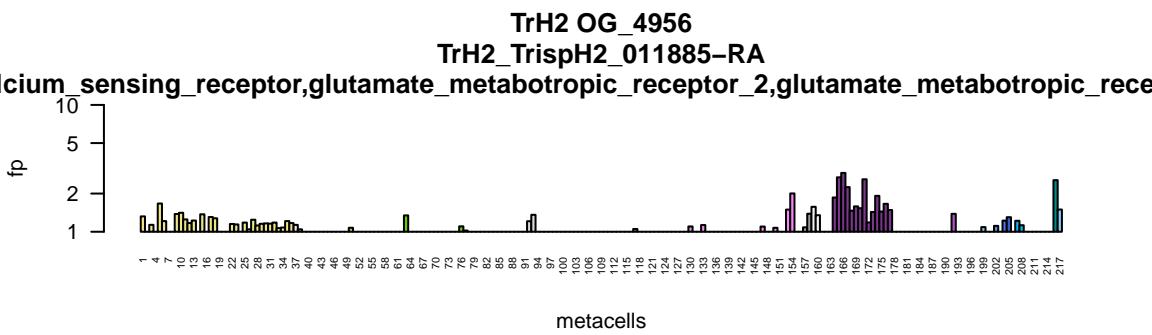
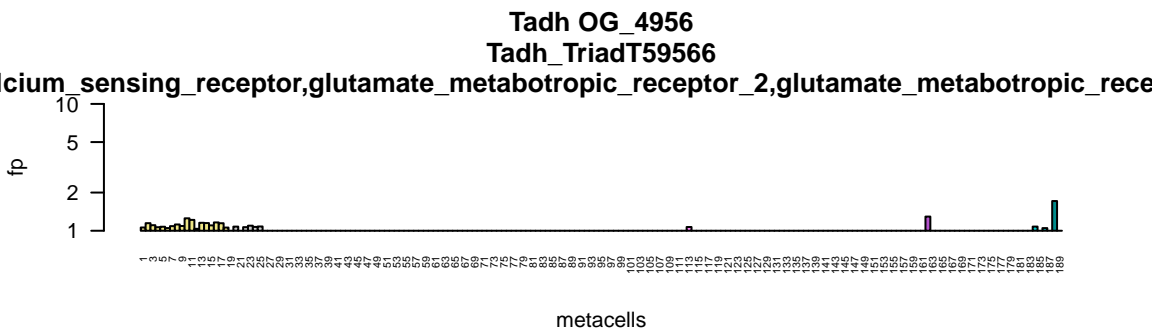


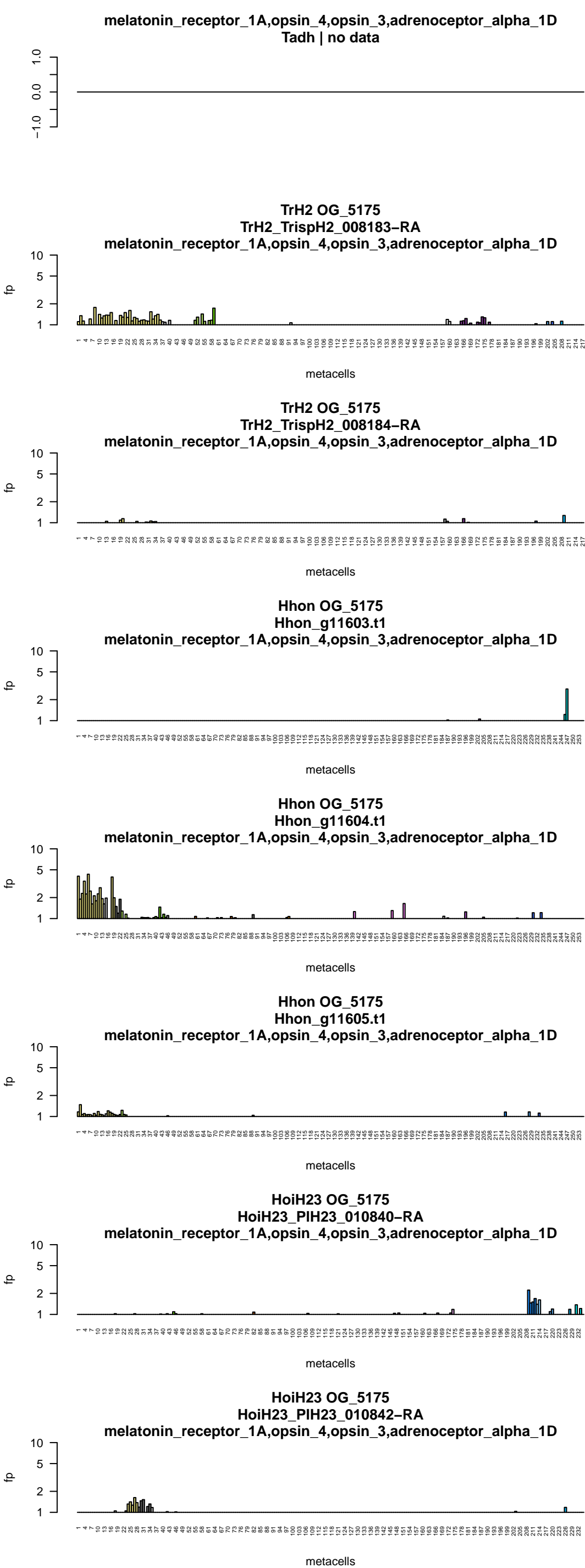


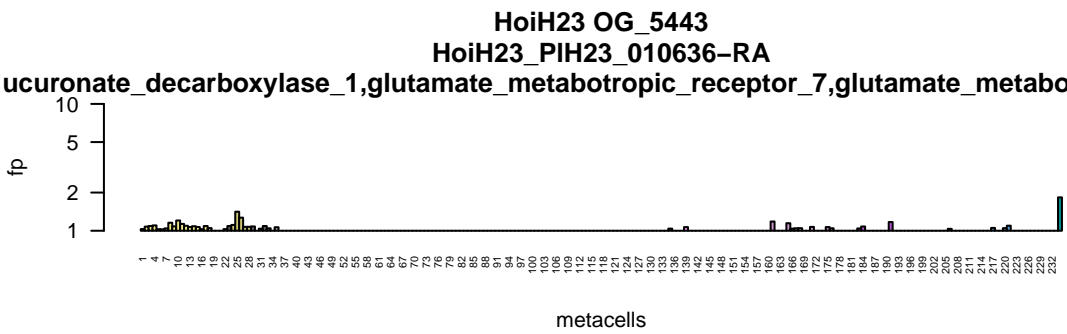
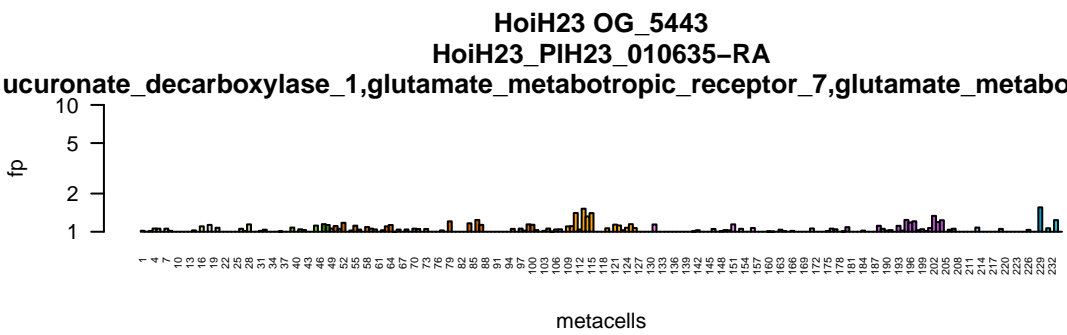
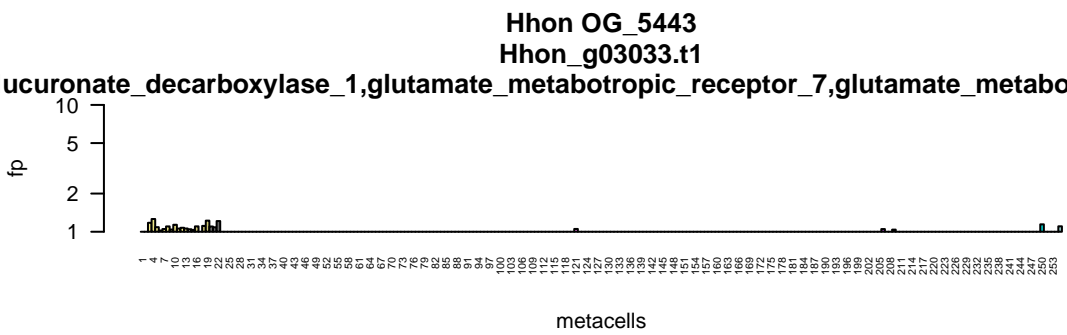
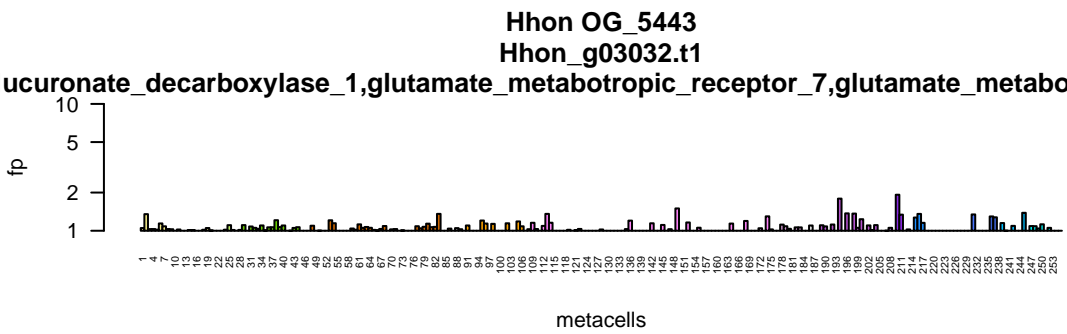
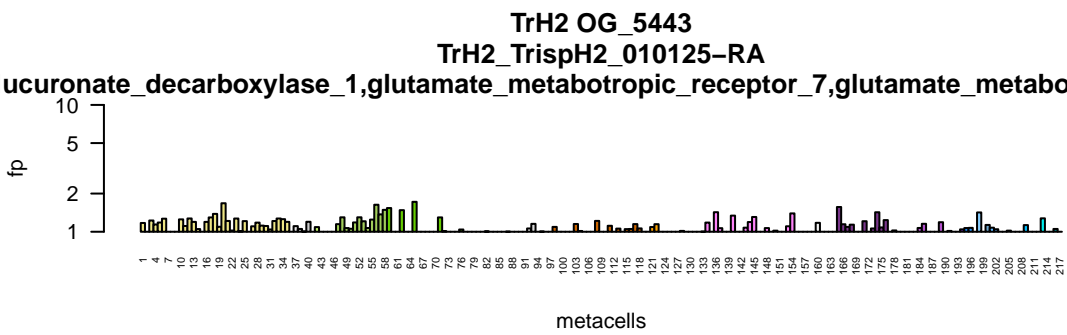
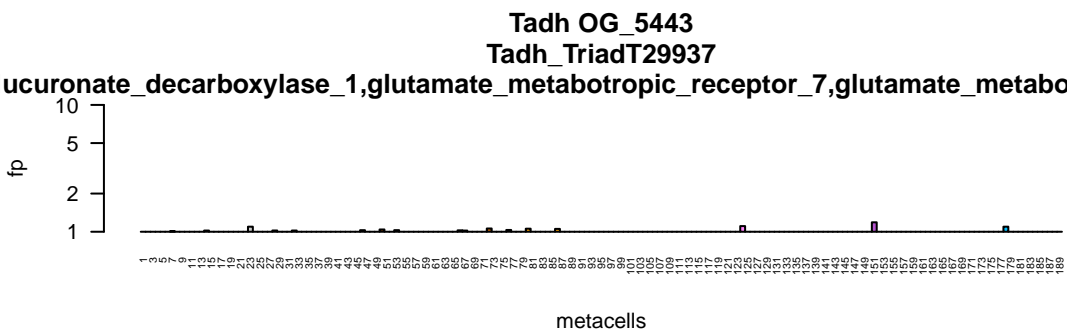
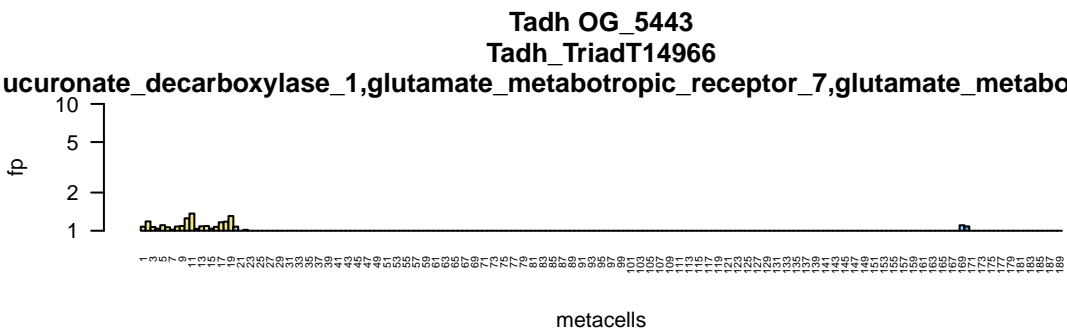


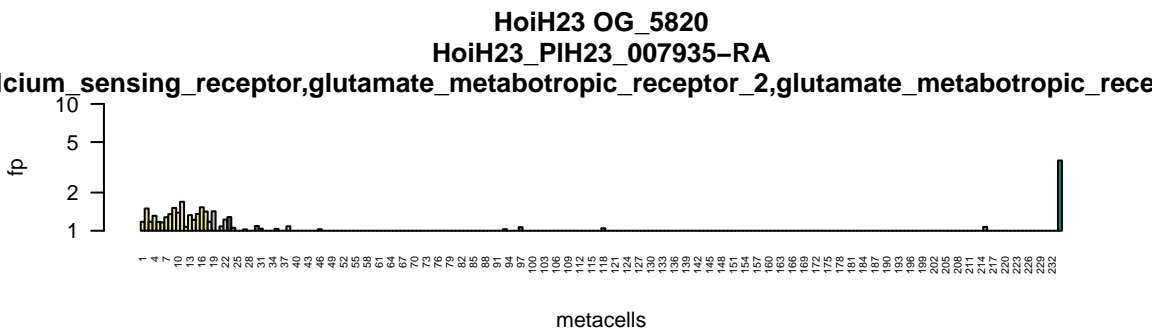
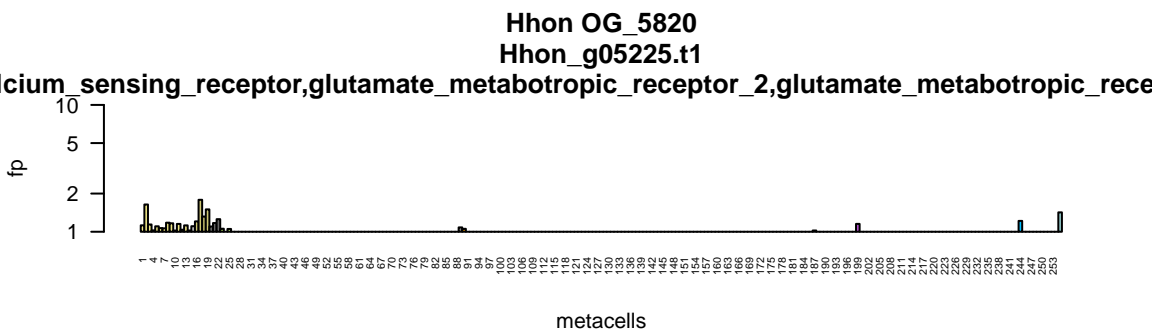
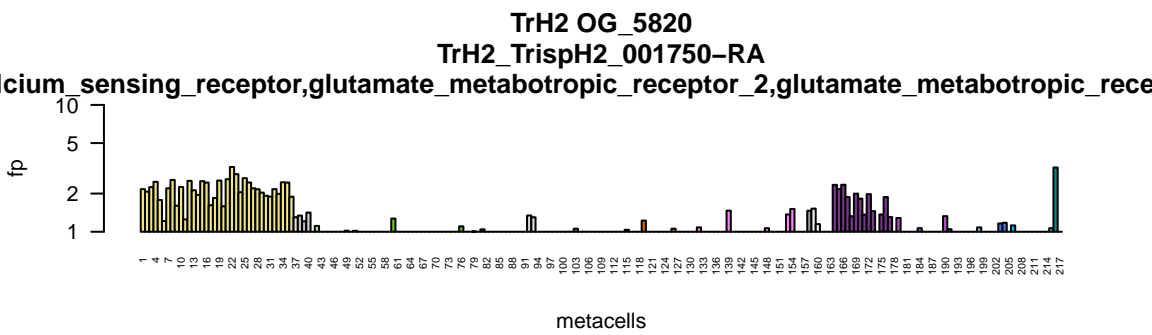
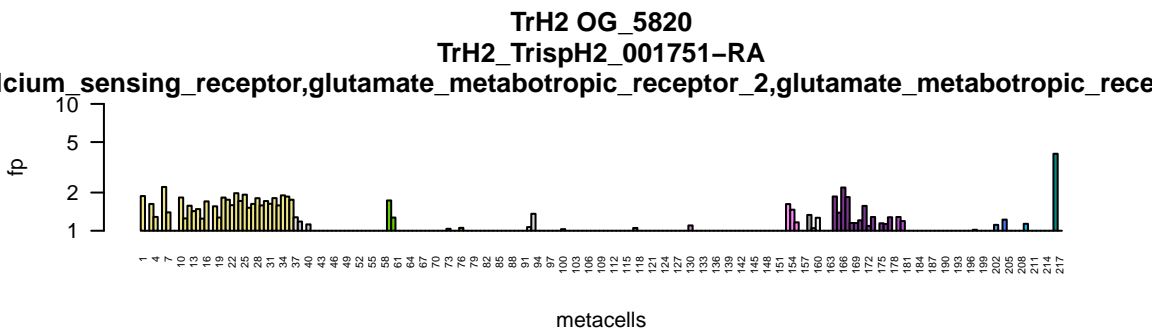
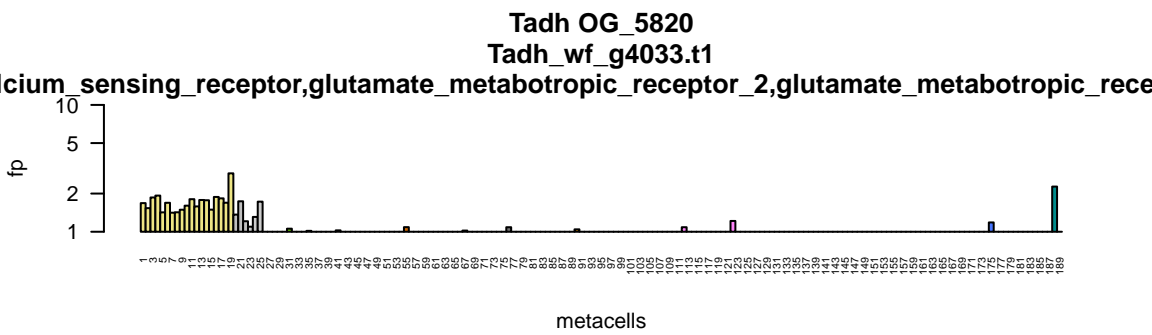
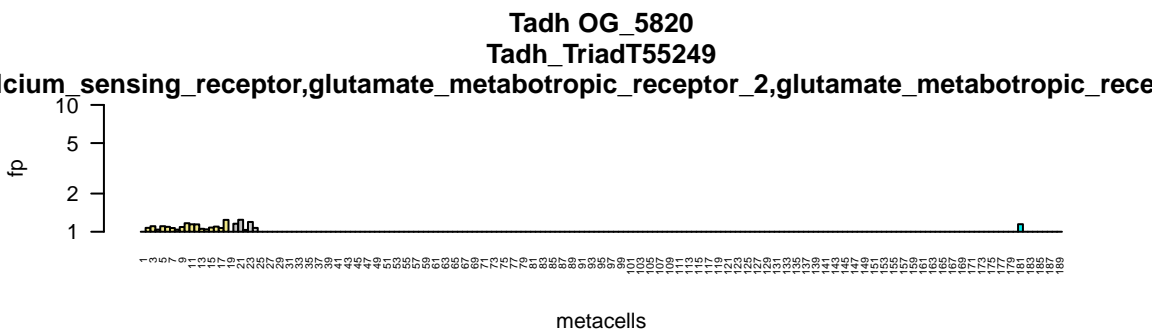
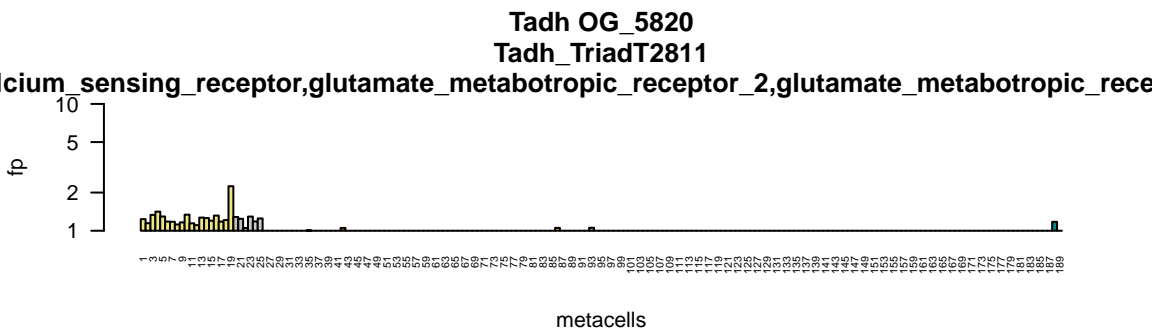












Tadh_TriadT62222

Bar chart showing the number of false positives (fp) for each metacell. The y-axis is labeled 'fp' and ranges from 0 to 10. The x-axis is labeled 'metacells' and lists 189 metacells. Most metacells have 0 false positives, but metacell 169 has 10 false positives, and metacell 168 has 1 false positive. Other metacells have 1 or 2 false positives.

metacell	fp
1	0
3	0
7	0
11	0
13	0
17	0
21	1
23	0
27	0
31	0
35	0
37	0
41	0
45	0
47	0
51	1
55	0
57	0
61	0
65	0
69	0
71	1
75	0
77	0
81	0
85	0
89	1
91	0
95	1
97	0
101	0
105	0
109	0
113	0
115	0
119	0
123	0
125	0
129	0
133	0
135	0
139	0
143	0
145	0
149	0
153	0
155	1
159	0
163	0
165	1
167	1
169	10
173	0
177	0
179	0
183	1
187	0
189	1

TrH2_TrispH2_008367-RA

metacell	fp
1	0
4	0
7	0
10	0
13	0
16	0
19	0
22	0
25	0
28	0
31	0
34	0
37	0
40	0
43	0
46	0
49	0
52	0
55	0
58	0
61	0
64	0
67	0
70	0
73	0
76	0
79	0
82	0
85	0
88	0
91	0
94	0
97	0
100	0
103	0
106	0
109	0
112	0
115	0
118	0
121	0
124	0
127	0
130	0
133	0
136	0
139	0
142	0
145	0
148	0
151	0
154	0
157	0
160	1.5
163	1
166	0
169	0
172	0
175	0
179	0
182	0
184	0
187	0
190	0
193	0
196	0
199	2
202	10
205	0
208	0
211	0
213	1
214	0.5
217	0

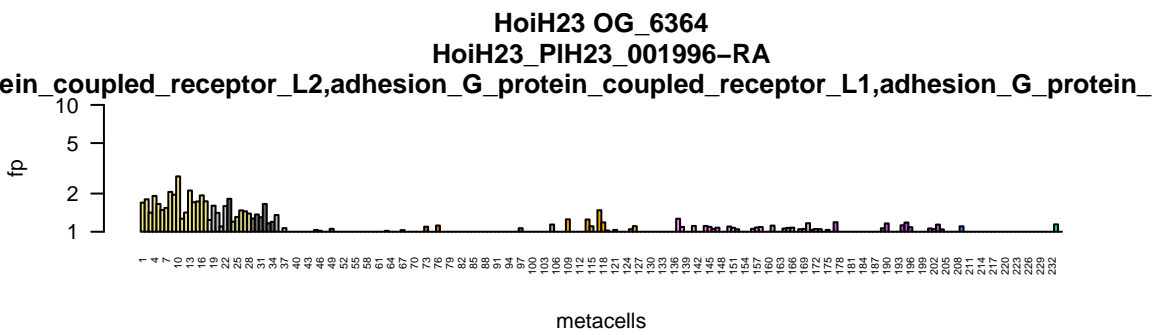
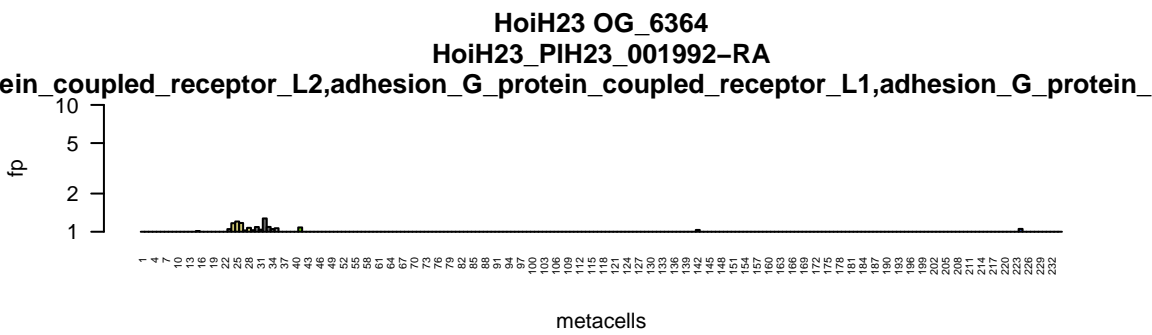
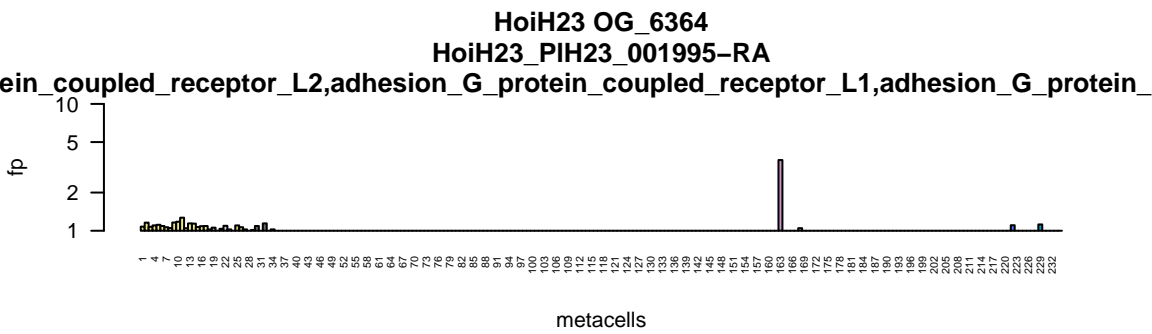
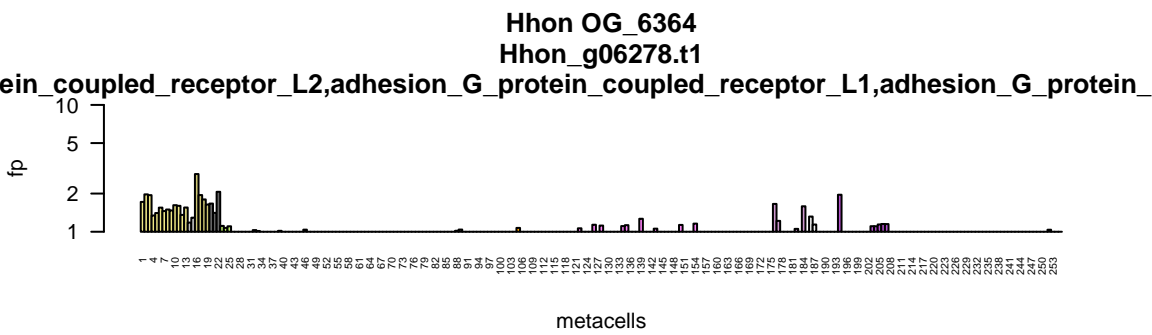
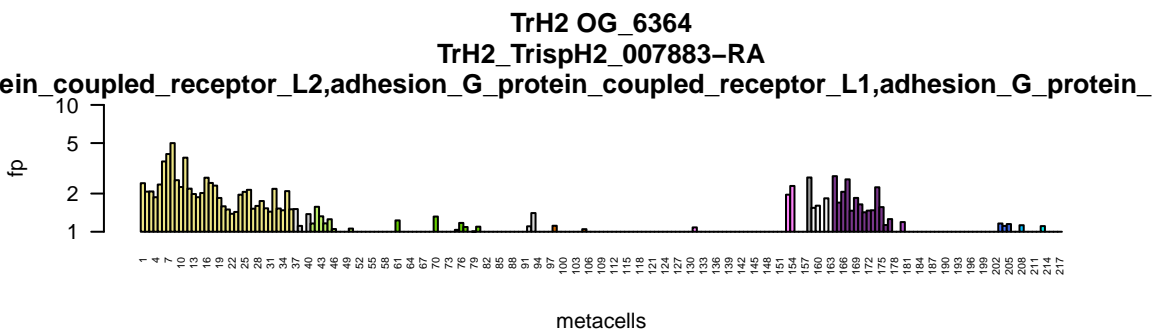
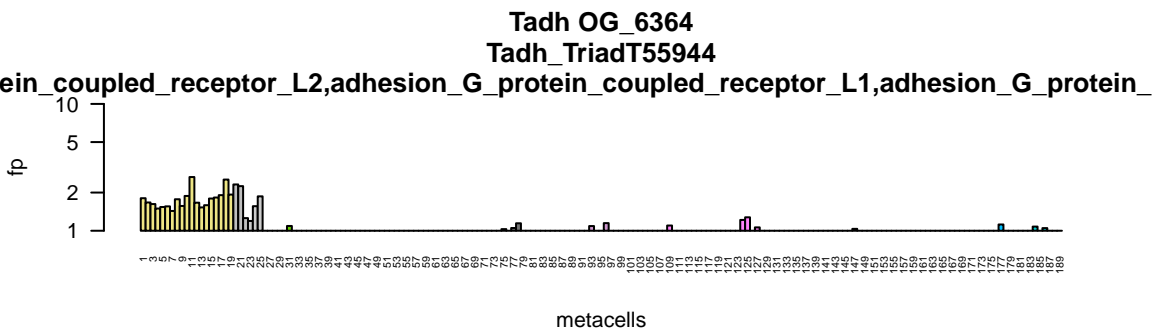
Bar chart showing the frequency of metacells (x-axis) versus the number of features (y-axis, fp). The x-axis ranges from 1 to 253, and the y-axis ranges from 1 to 10. The chart shows a distribution of feature counts across metacells, with most metacells having 1 or 2 features. A notable peak is observed at metacell 223, which has 5 features.

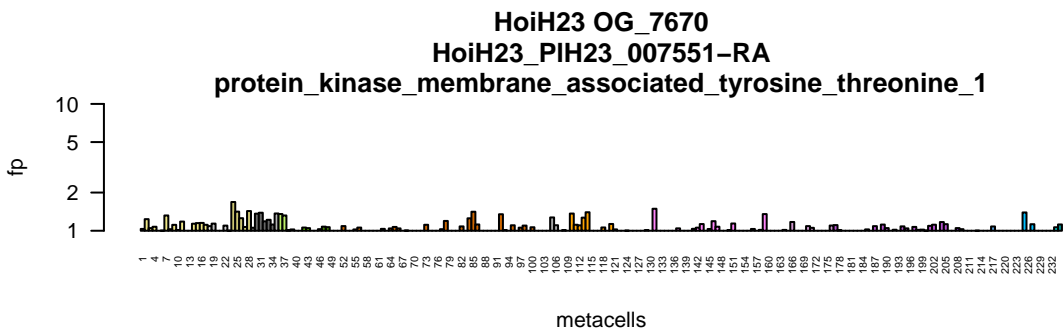
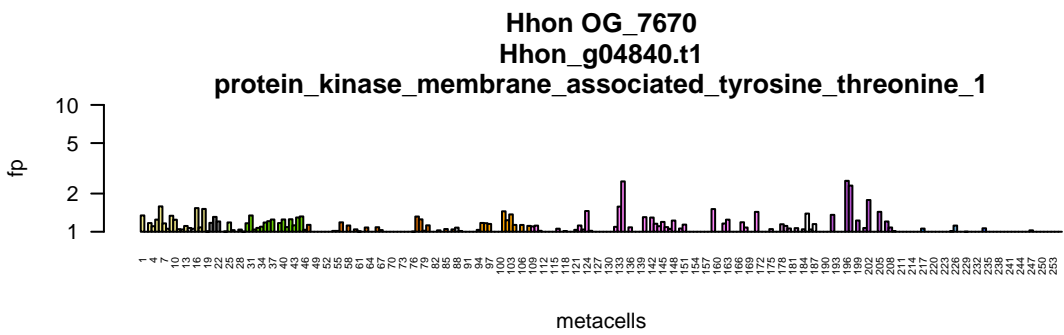
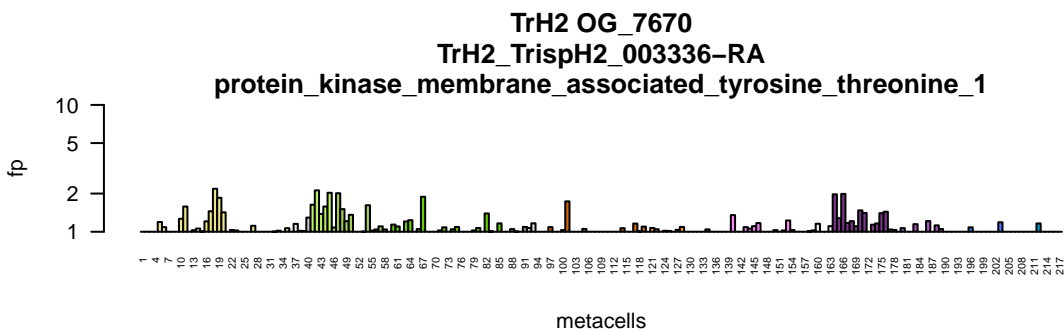
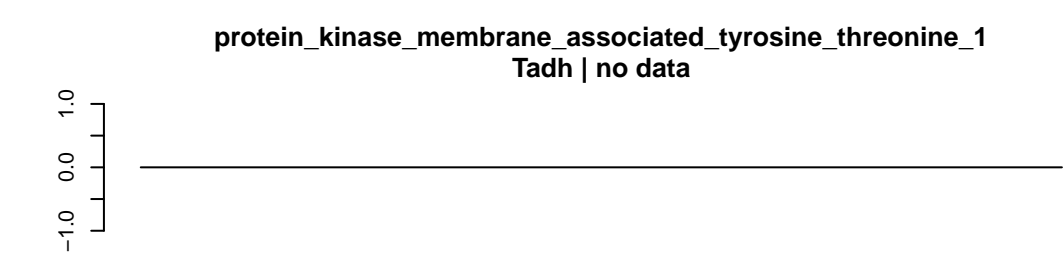
A bar chart showing the frequency of metacells (x-axis) versus the number of features (fp, y-axis). The x-axis is labeled 'metacells' and ranges from 1 to 232. The y-axis is labeled 'fp' and ranges from 1 to 10. The chart shows that most metacells have a frequency of 1, with a few outliers reaching up to 2.

Bar chart showing the frequency of metacells (x-axis) versus the number of features (fp, y-axis). The x-axis ranges from 1 to 232, and the y-axis ranges from 1 to 10. The distribution is highly skewed, with most metacells having 1 or 2 features. The highest frequency is 2 features, occurring for metacells 25, 26, and 27.

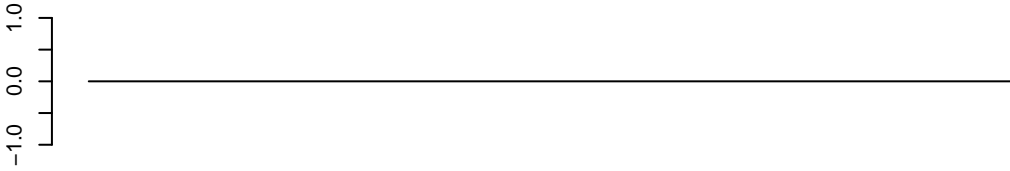
Bar chart showing the frequency of metacells (x-axis) for the number of features (fp, y-axis). The x-axis ranges from 1 to 232, and the y-axis ranges from 1 to 10. The distribution is highly skewed, with most metacells having 1 or 2 features. A notable peak occurs at metacell 218, which has 4 features.

Bar chart showing the number of reads (fp) for each metacell. The y-axis is logarithmic, ranging from 1 to 10. The x-axis lists metacells from 1 to 232. Most metacells have 1 read, but metacell 214 has a significantly higher value, exceeding 10 reads.

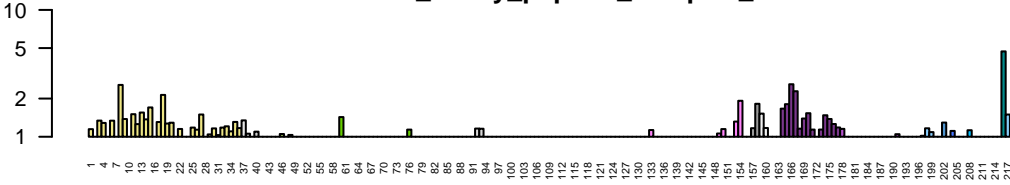




relaxin_family_peptide_receptor_1
Tadh | no data

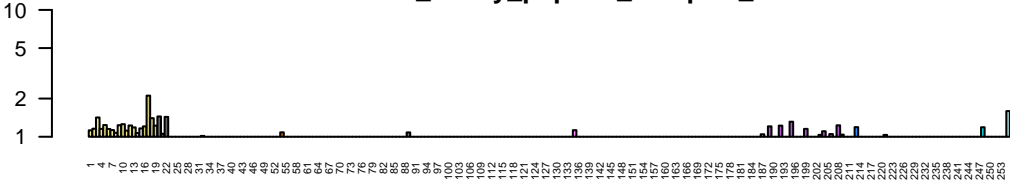


TrH2 OG_8036
TrH2_TrispH2_007969-RA
relaxin_family_peptide_receptor_1



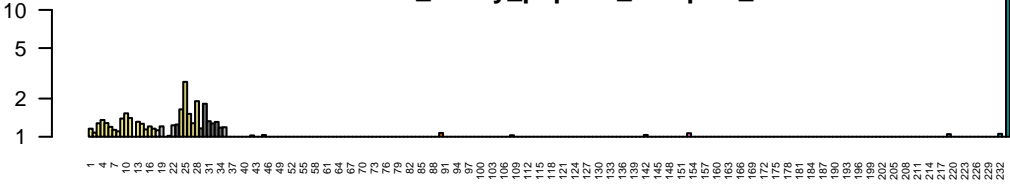
metacells

Hhon OG_8036
Hhon_g05641.t1
relaxin_family_peptide_receptor_1

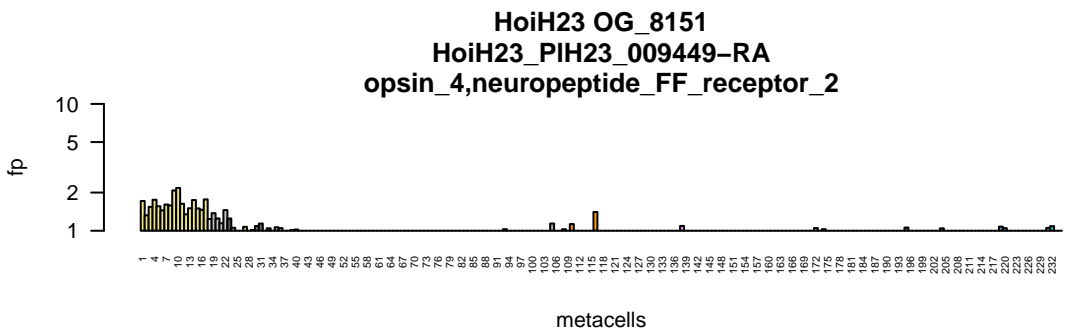
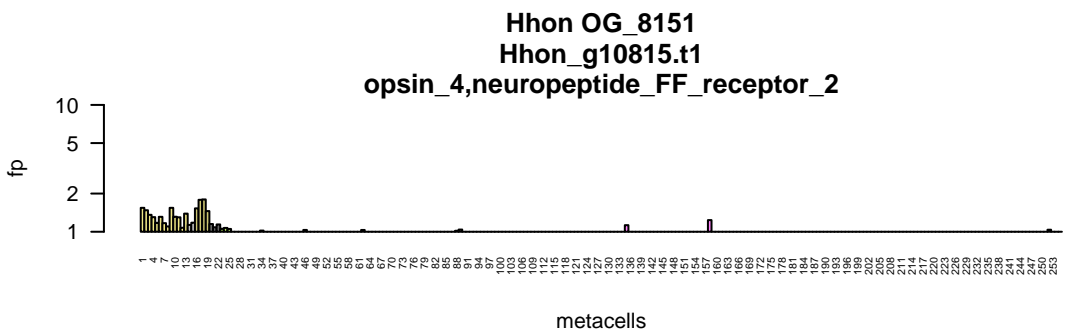
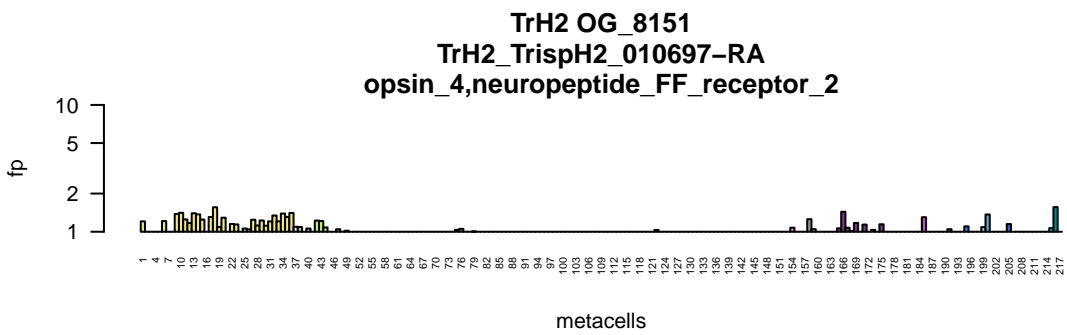
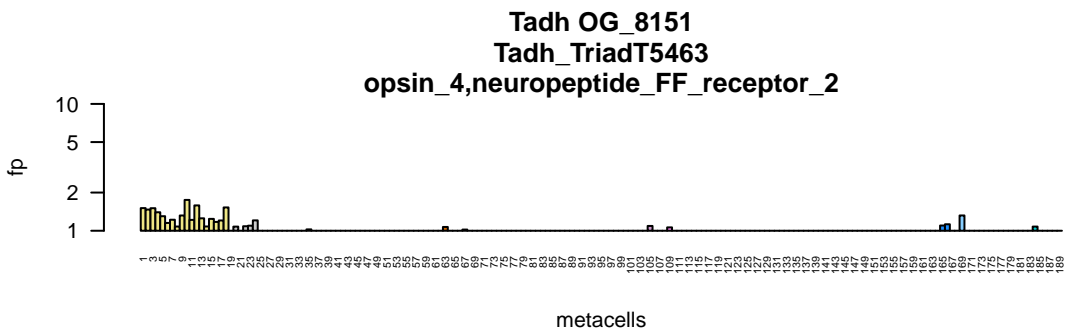


metacells

HoiH23 OG_8036
HoiH23_PIH23_005185-RA
relaxin_family_peptide_receptor_1



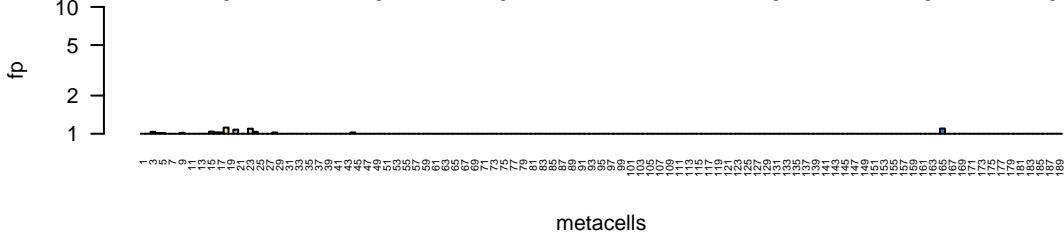
metacells



Tadh OG_8767

Tadh_hyp_clust6751.t1

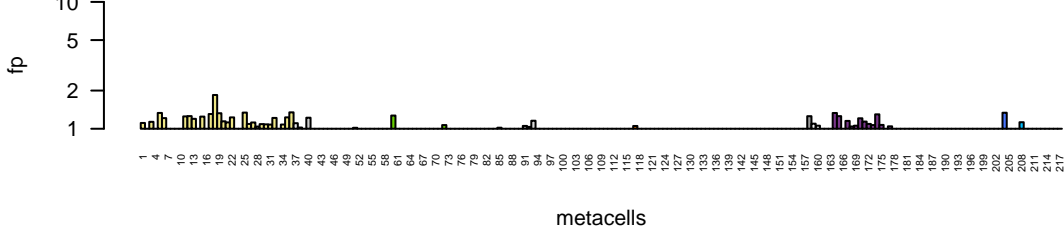
adhesion_G_protein_coupled_receptor_L2,adhesion_G_protein_coupled_receptor_L3



TrH2 OG_8767

TrH2_TrispH2_011408-RA

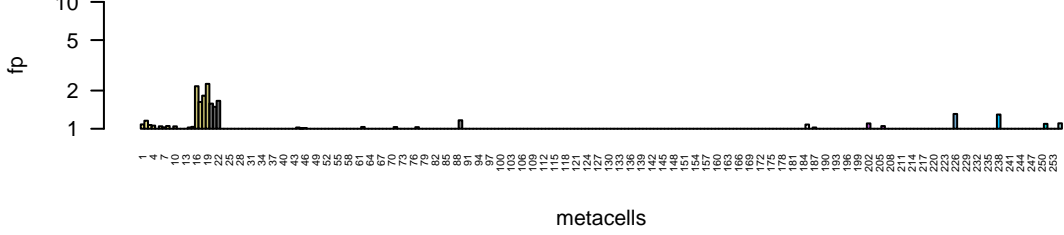
adhesion_G_protein_coupled_receptor_L2,adhesion_G_protein_coupled_receptor_L3



Hhon OG_8767

Hhon_g09539.t1

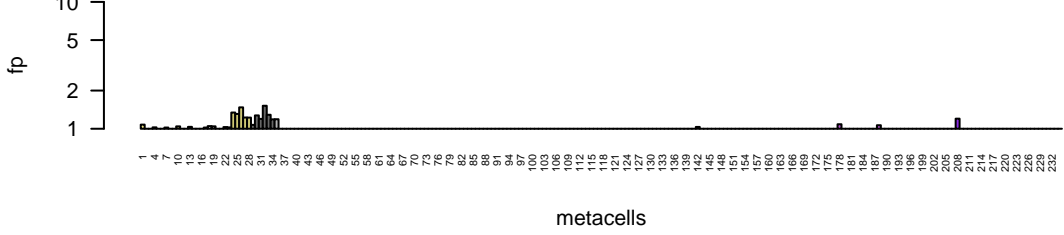
adhesion_G_protein_coupled_receptor_L2,adhesion_G_protein_coupled_receptor_L3



HoiH23 OG_8767

HoiH23_PIH23_007683-RA

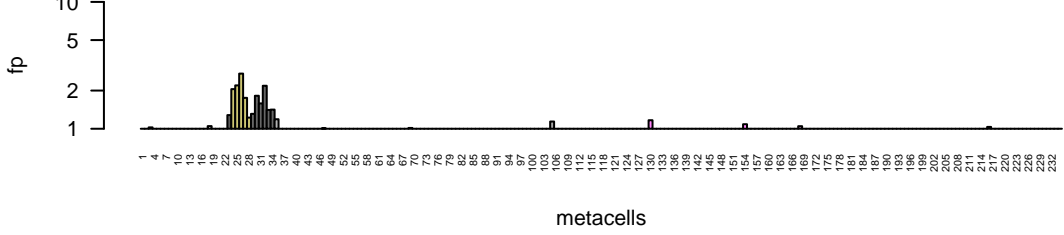
adhesion_G_protein_coupled_receptor_L2,adhesion_G_protein_coupled_receptor_L3



HoiH23 OG_8767

HoiH23_PIH23_007684-RA

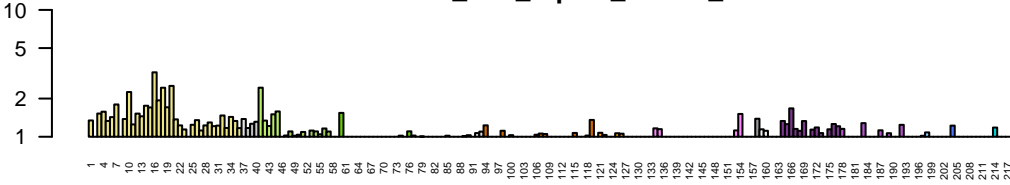
adhesion_G_protein_coupled_receptor_L2,adhesion_G_protein_coupled_receptor_L3



leucine_rich_repeat_kinase_1
Tadh | no data

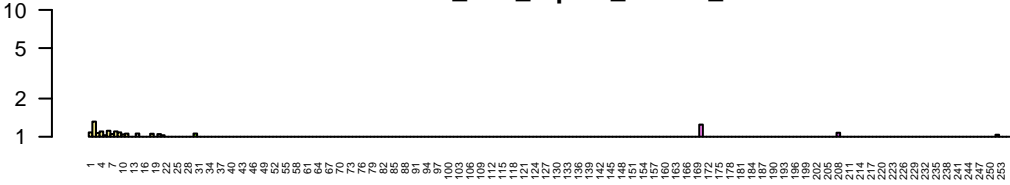


TrH2 OG_10615
TrH2_TrispH2_004289-RA
leucine_rich_repeat_kinase_1



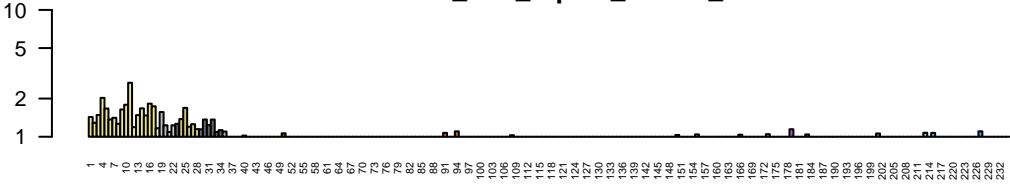
metacells

Hhon OG_10615
Hhon_g06459.t1
leucine_rich_repeat_kinase_1



metacells

HoiH23 OG_10615
HoiH23_PIH23_003918-RA
leucine_rich_repeat_kinase_1



metacells