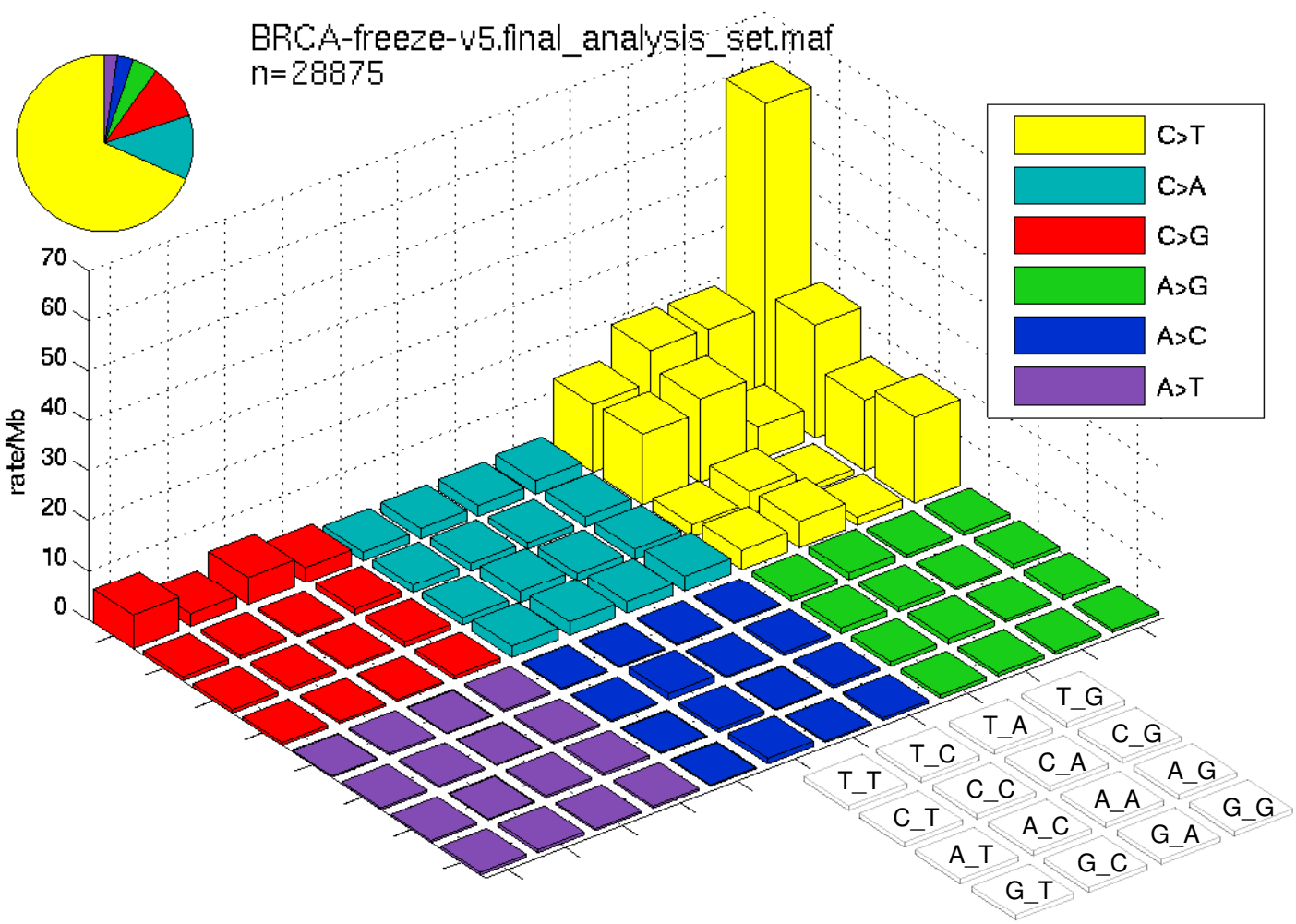
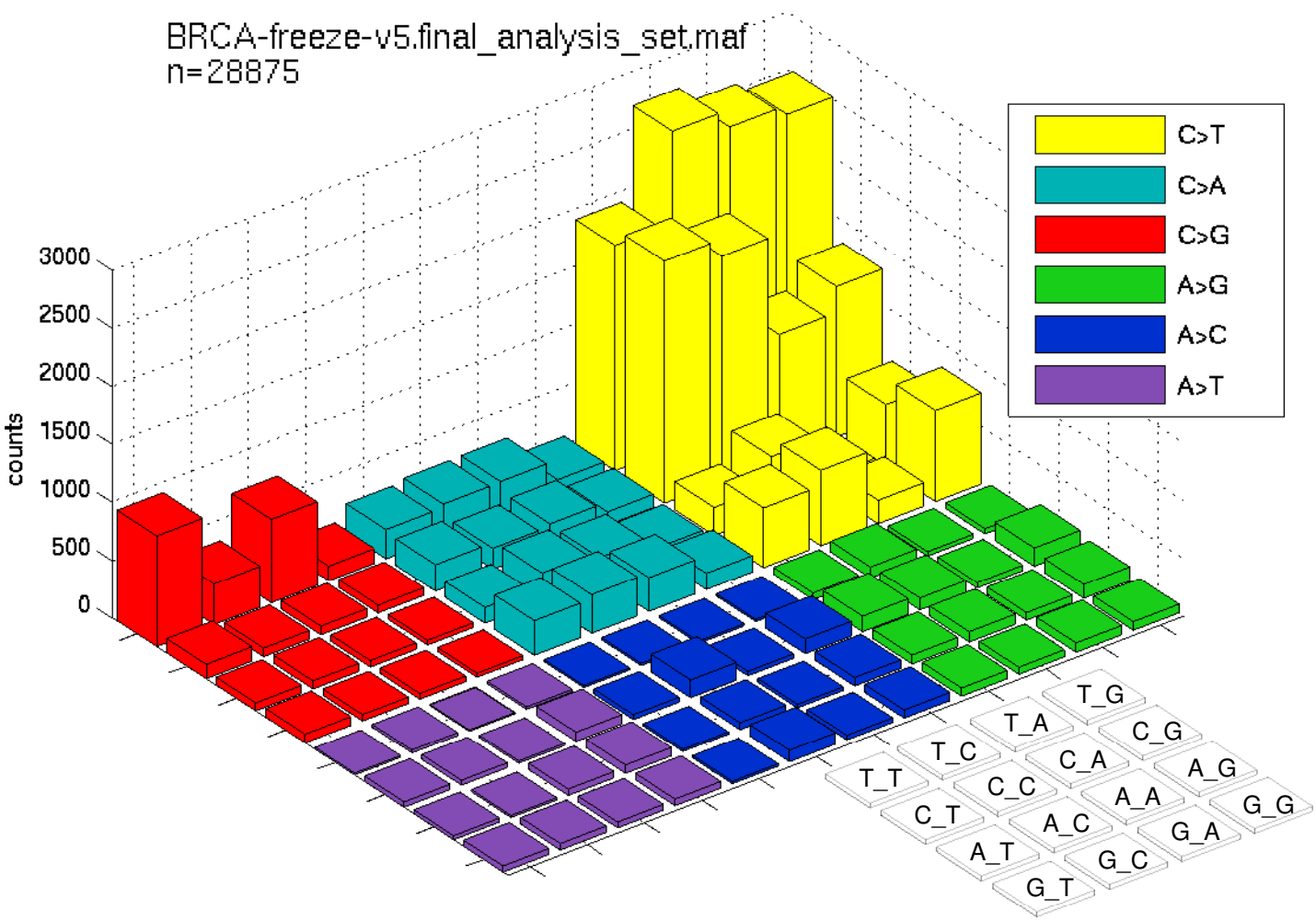
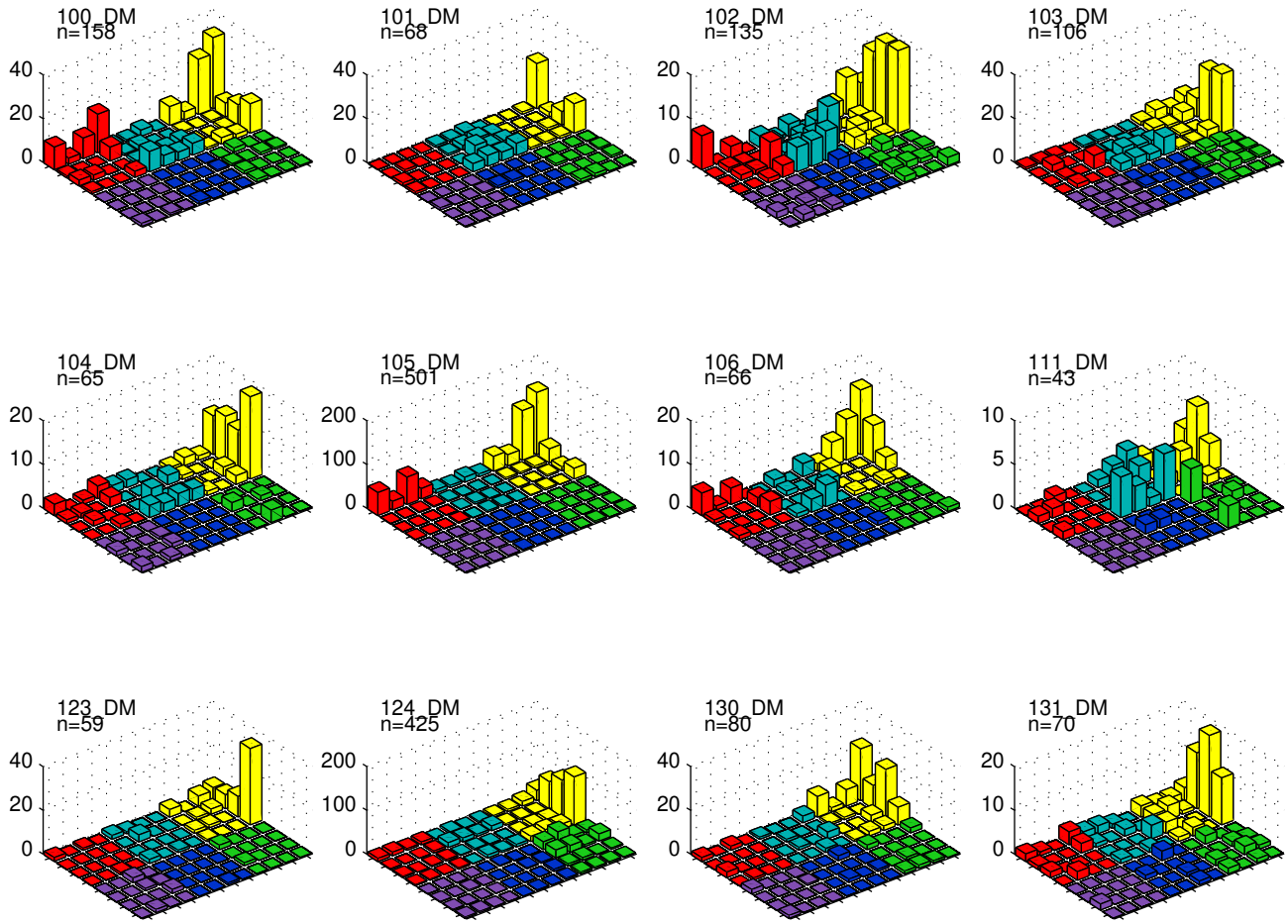
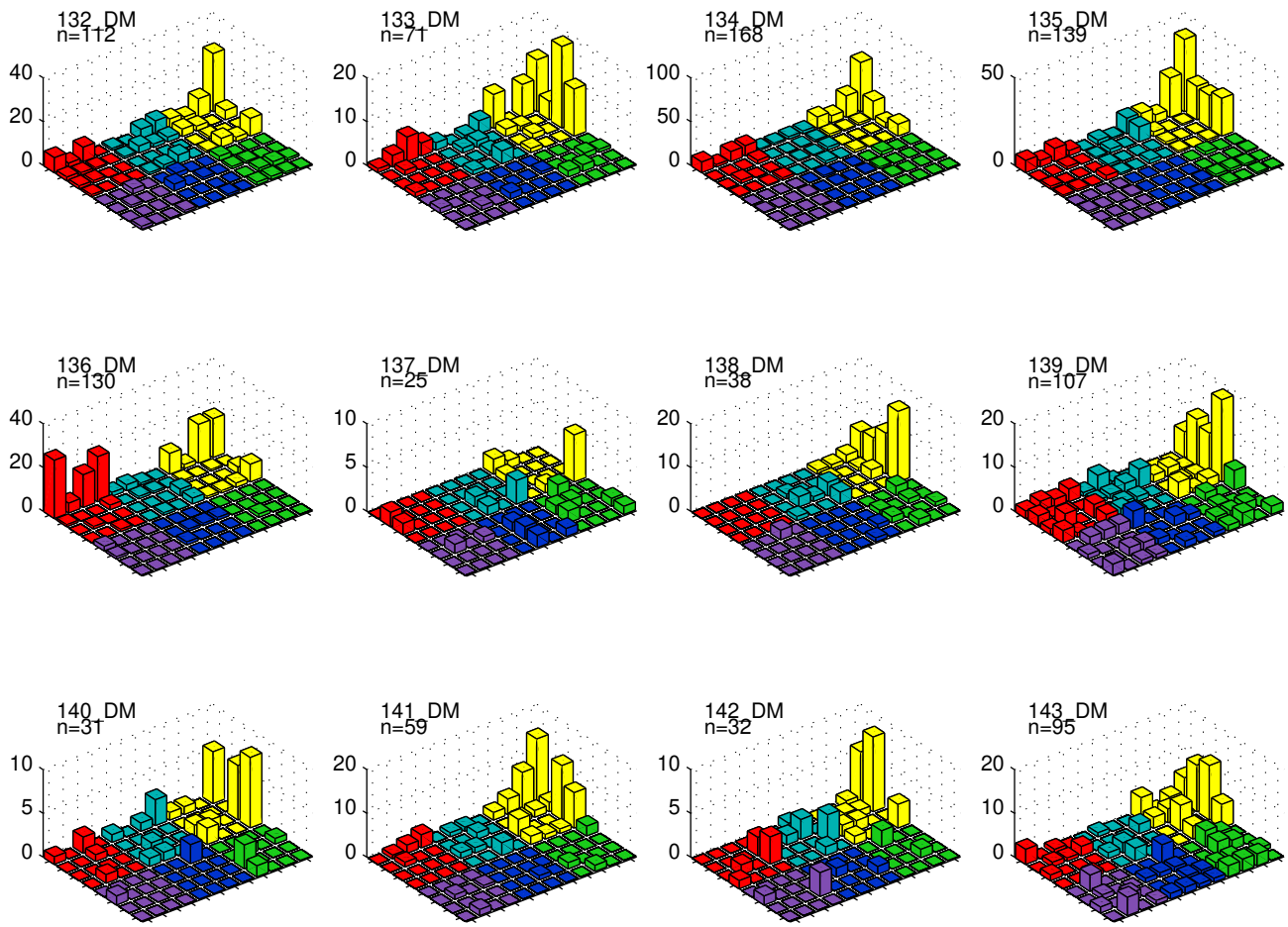
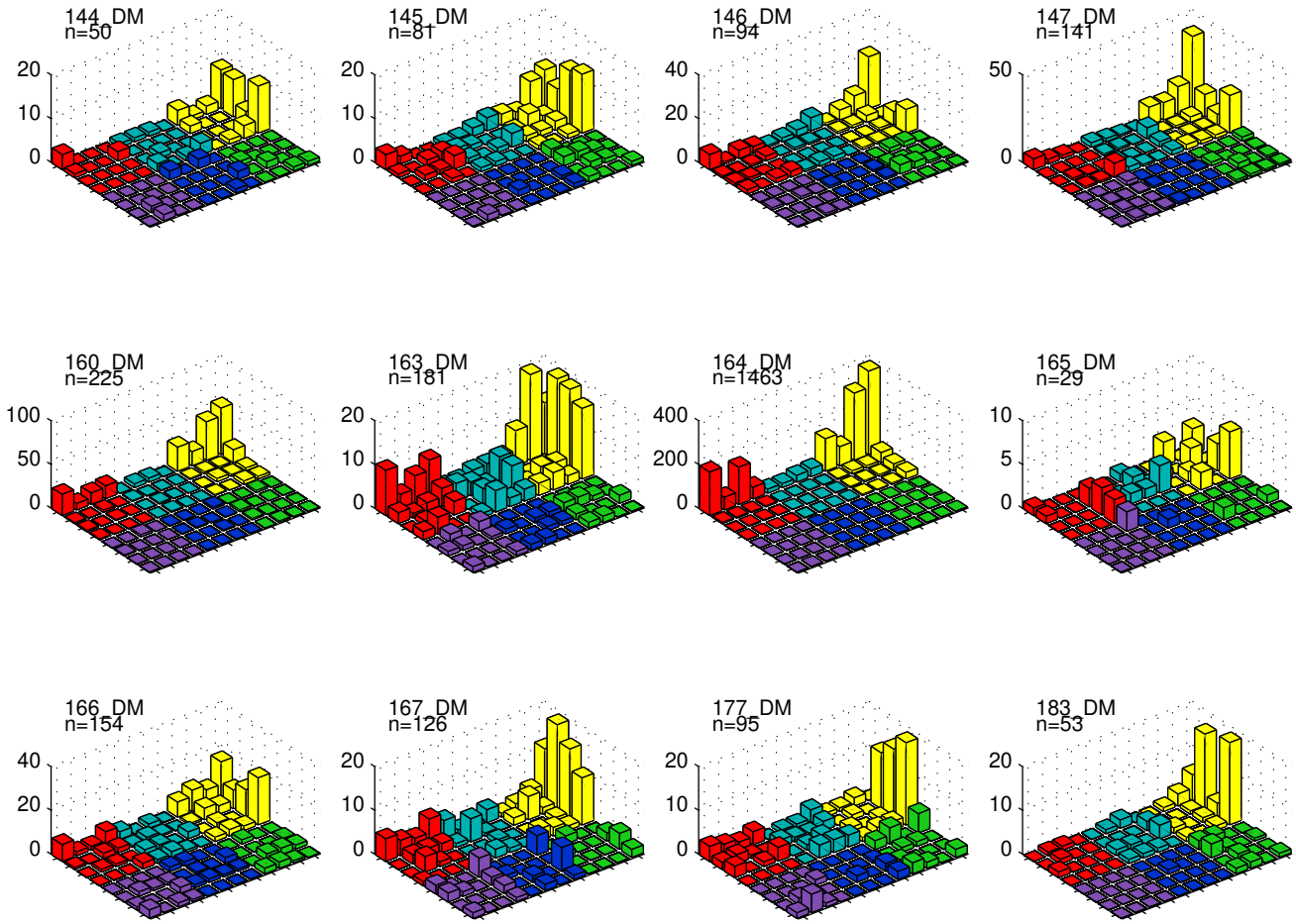
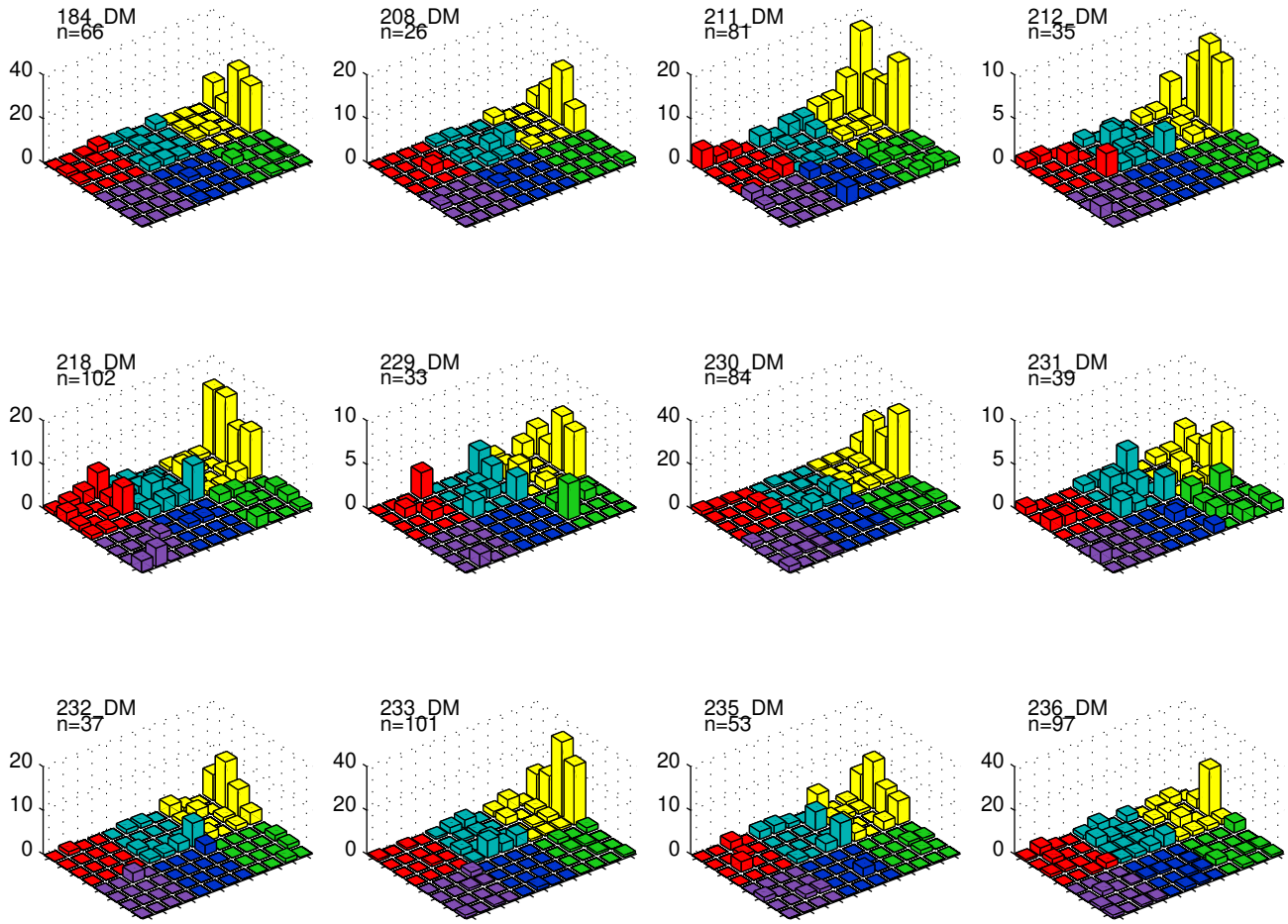

BRCA-freeze-v5.final_analysis_set.maf
n=28875
rate/Mb
70
60
50
40
30
20
10
0
C>T
C>A
C>G
A>G
A>C
A>T
T_G
T_A
C_G
T_C
C_A
A_G
T_T
C_C
A_A
G_G
C_T
A_C
G_A
A_T
G_C
G_T

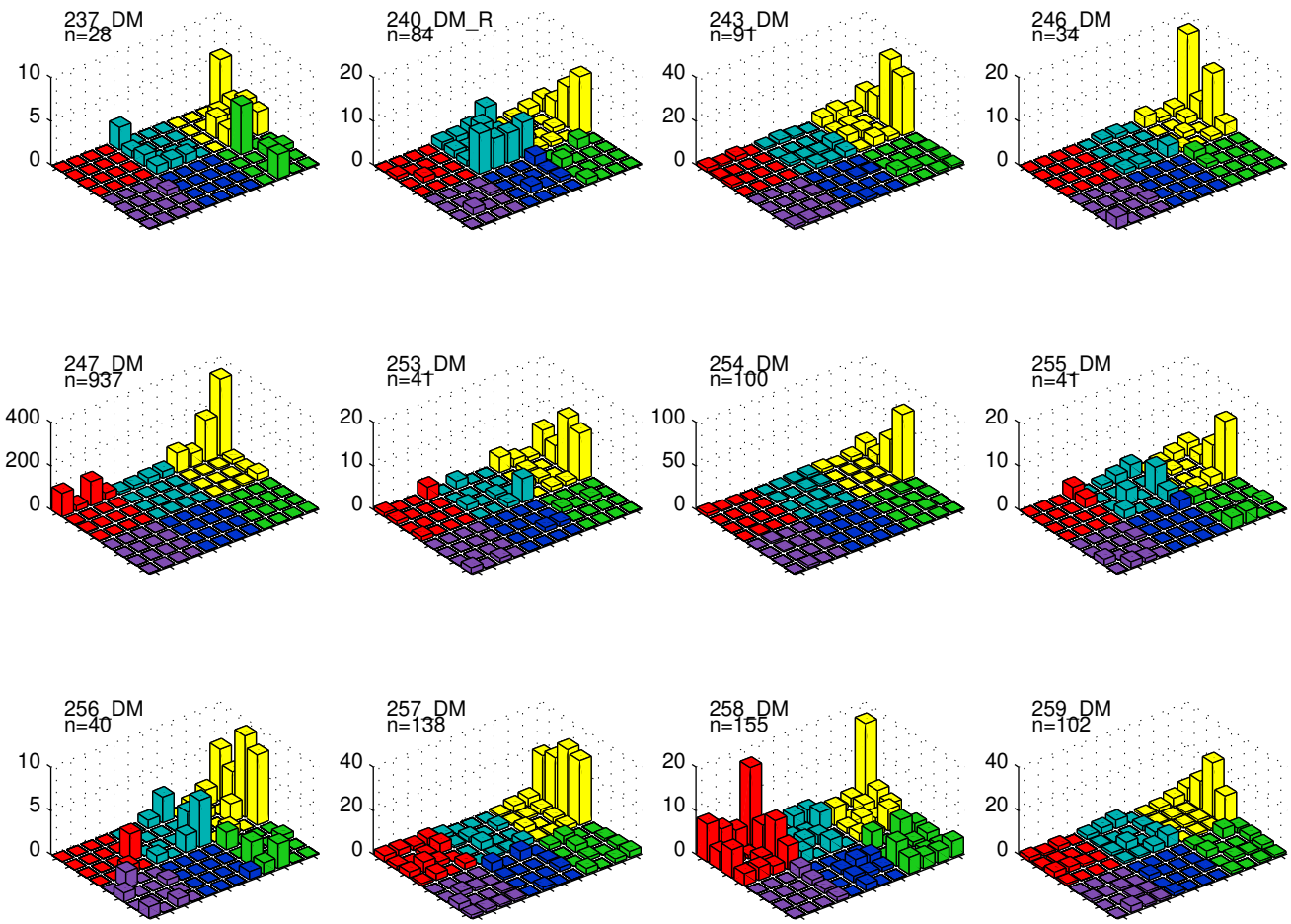

BRCA-freeze-v5.final_analysis_set.maf
n=28875
counts
3000
2500
2000
1500
1000
500
0
C>T
C>A
C>G
A>G
A>C
A>T
T_G
T_A
C_G
T_C
C_A
A_G
T_T
C_C
A_A
G_G
C_T
A_C
G_A
A_T
G_C
G_T

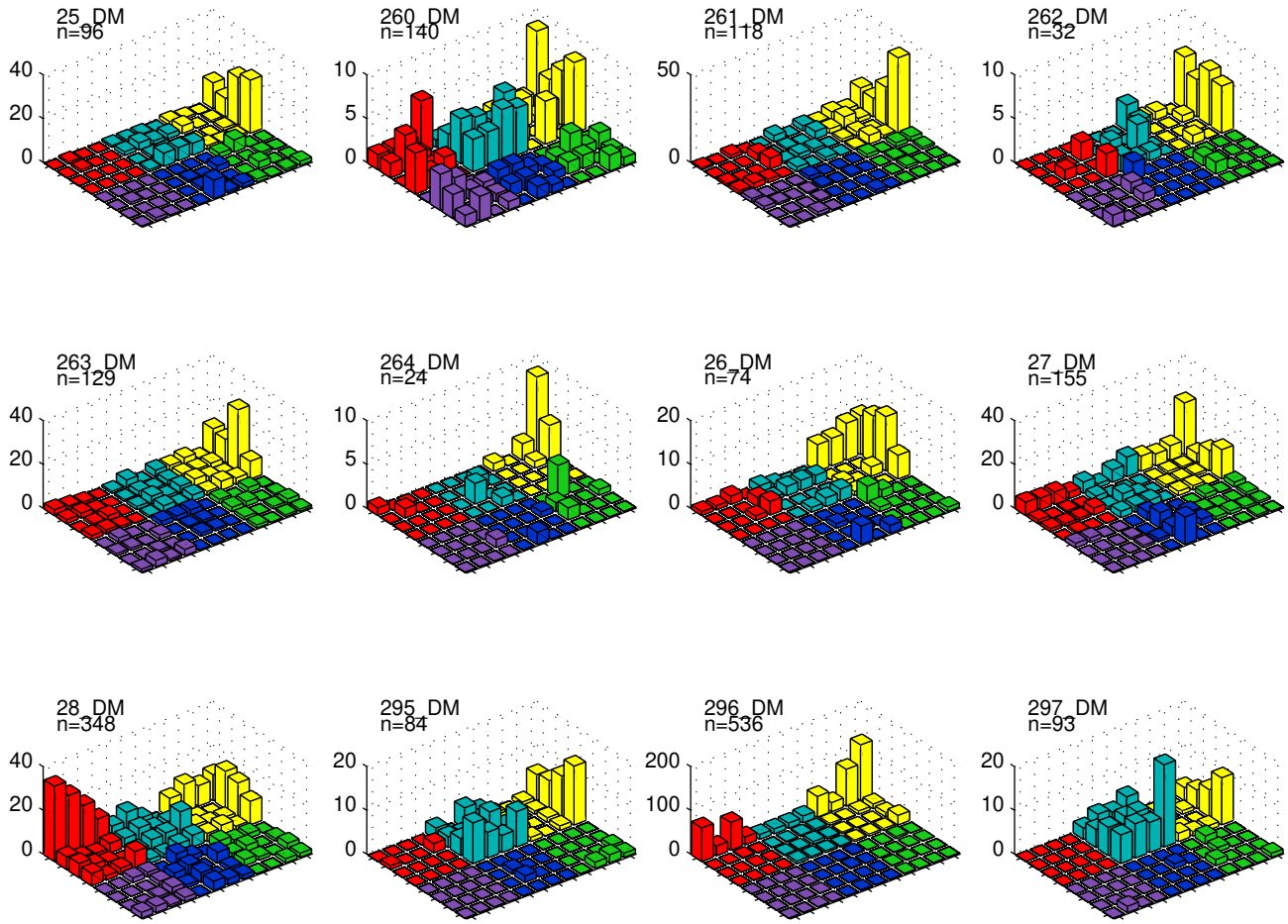

100_DM
n=158
40
20
0
101_DM
n=68
40
20
0
102_DM
n=135
20
10
0
103_DM
n=106
40
20
0
104_DM
n=65
20
10
0
105_DM
n=501
200
100
0
106_DM
n=66
20
10
0
111_DM
n=43
10
5
0
123_DM
n=59
40
20
0
124_DM
n=425
200
100
0
130_DM
n=80
40
20
0
131_DM
n=70
20
10
0

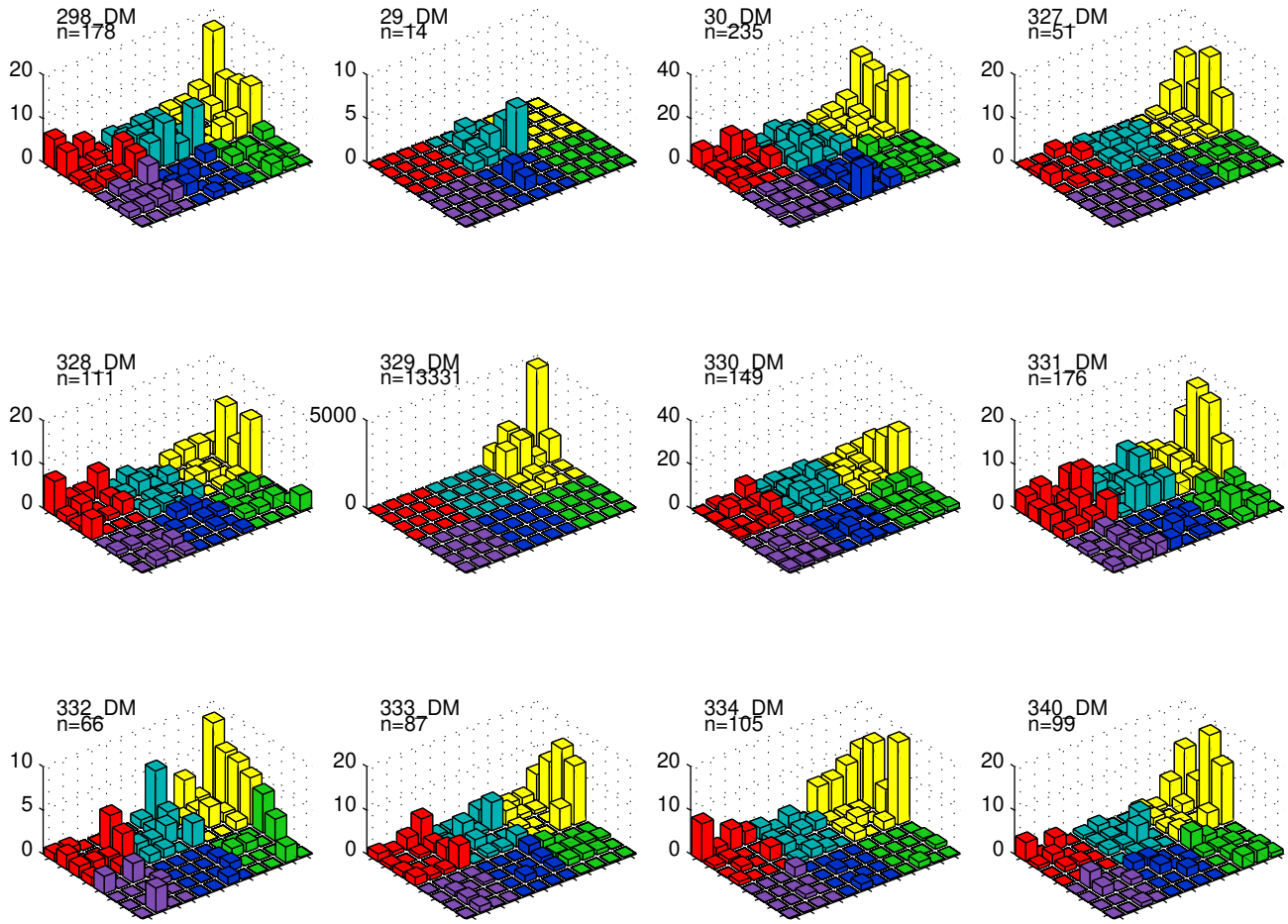

132_DM
n=112
40
20
0
133_DM
n=71
20
10
0
134_DM
n=168
100
50
0
135_DM
n=139
50
0
136_DM
n=130
40
20
0
137_DM
n=25
10
5
0
138_DM
n=38
20
10
0
139_DM
n=107
20
10
0
140_DM
n=31
10
5
0
141_DM
n=59
20
10
0
142_DM
n=32
10
5
0
143_DM
n=95
20
10
0

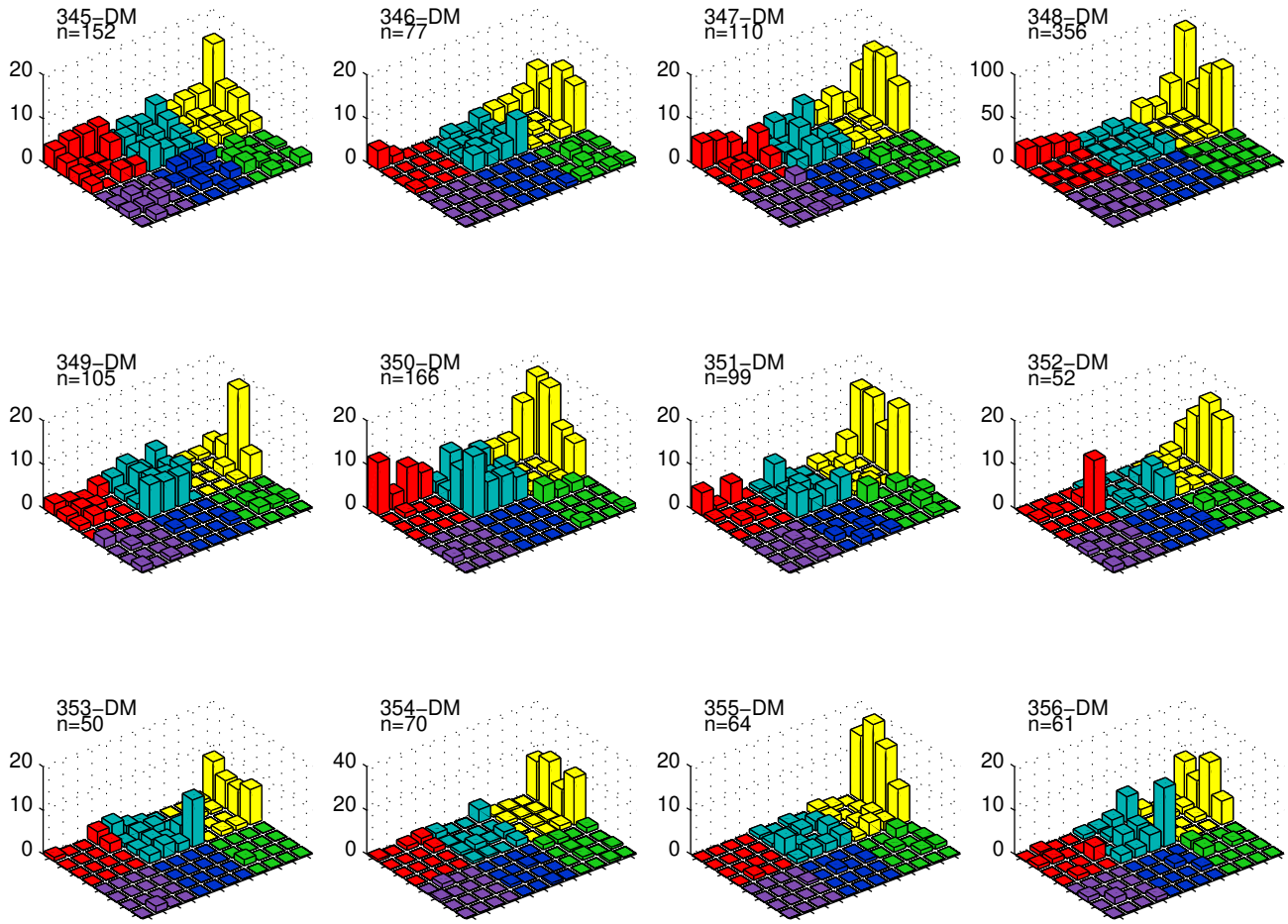

144_DM
n=50
20
10
0
145_DM
n=81
20
10
0
146_DM
n=94
40
20
0
147_DM
n=141
50
0
160_DM
n=225
100
50
0
163_DM
n=181
20
10
0
164_DM
n=1463
400
200
0
165_DM
n=29
10
5
0
166_DM
n=154
40
20
0
167_DM
n=126
20
10
0
177_DM
n=95
20
10
0
183_DM
n=53
20
10
0

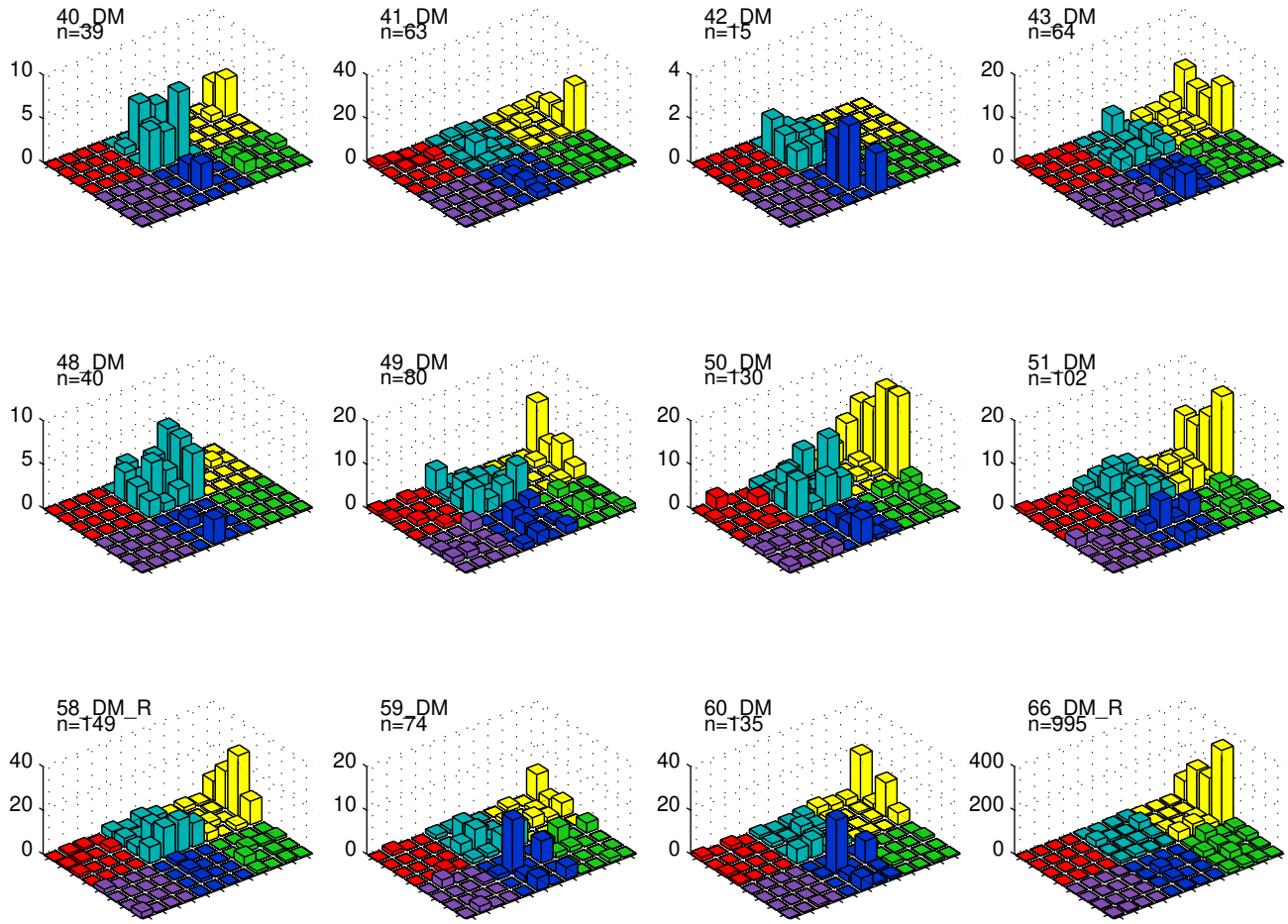

184_DM
n=66
208_DM
n=26
211_DM
n=81
212_DM
n=35
218_DM
n=102
229_DM
n=33
230_DM
n=84
231_DM
n=39
232_DM
n=37
233_DM
n=101
235_DM
n=53
236_DM
n=97

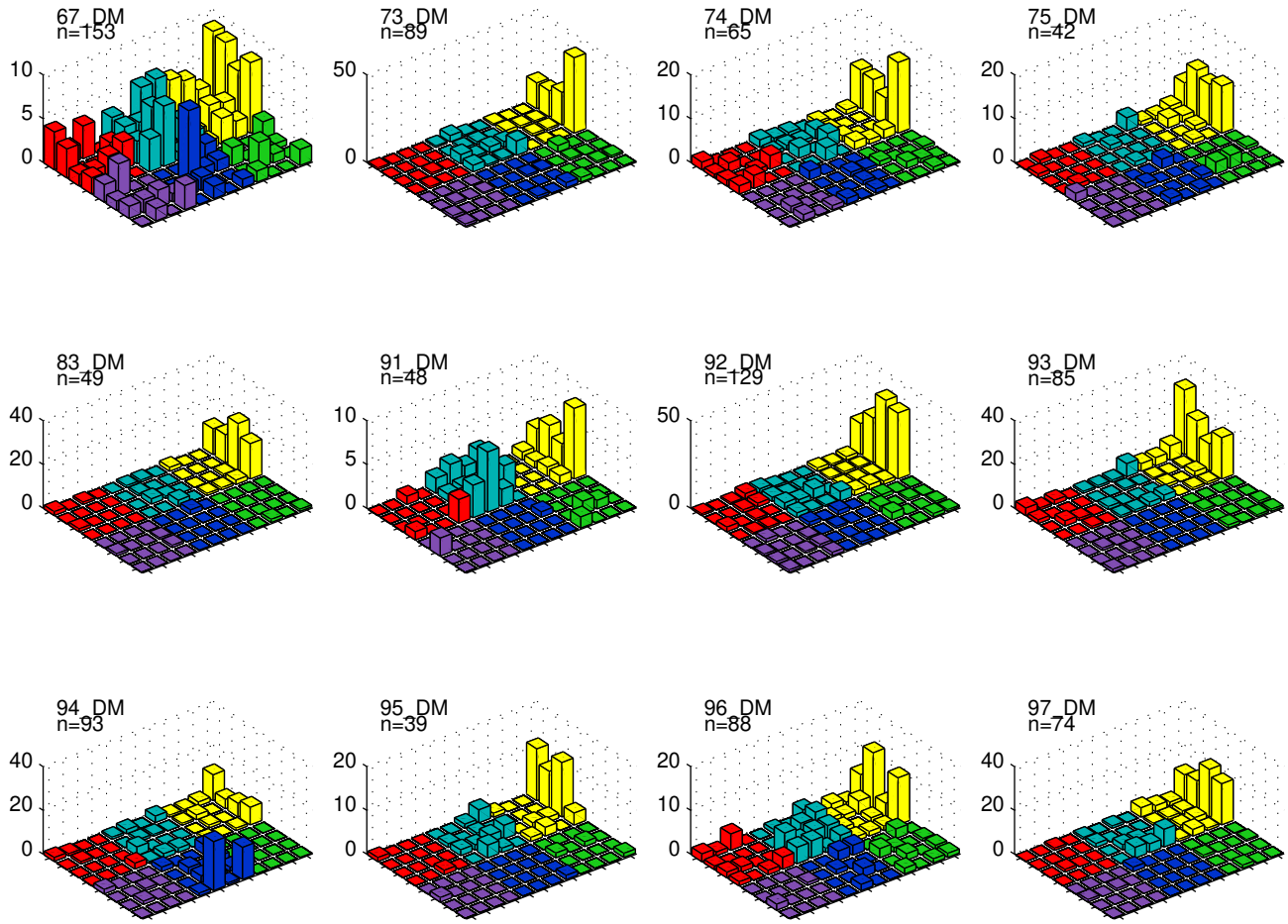

237_DM
n=28
10
5
0
240_DM_R
n=84
20
10
0
243_DM
n=91
40
20
0
246_DM
n=34
20
10
0
247_DM
n=937
400
200
0
253_DM
n=41
20
10
0
254_DM
n=100
100
50
0
255_DM
n=41
20
10
0
256_DM
n=40
10
5
0
257_DM
n=138
40
20
0
258_DM
n=155
20
10
0
259_DM
n=102
40
20
0

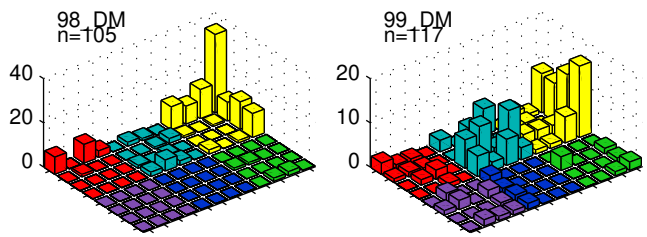

25_DM
n=96
40
20
0
260_DM
n=140
10
5
0
261_DM
n=118
50
0
262_DM
n=32
10
5
0
263_DM
n=129
40
20
0
264_DM
n=24
10
5
0
26_DM
n=74
20
10
0
27_DM
n=155
40
20
0
28_DM
n=348
40
20
0
295_DM
n=84
20
10
0
296_DM
n=536
200
100
0
297_DM
n=93
20
10
0

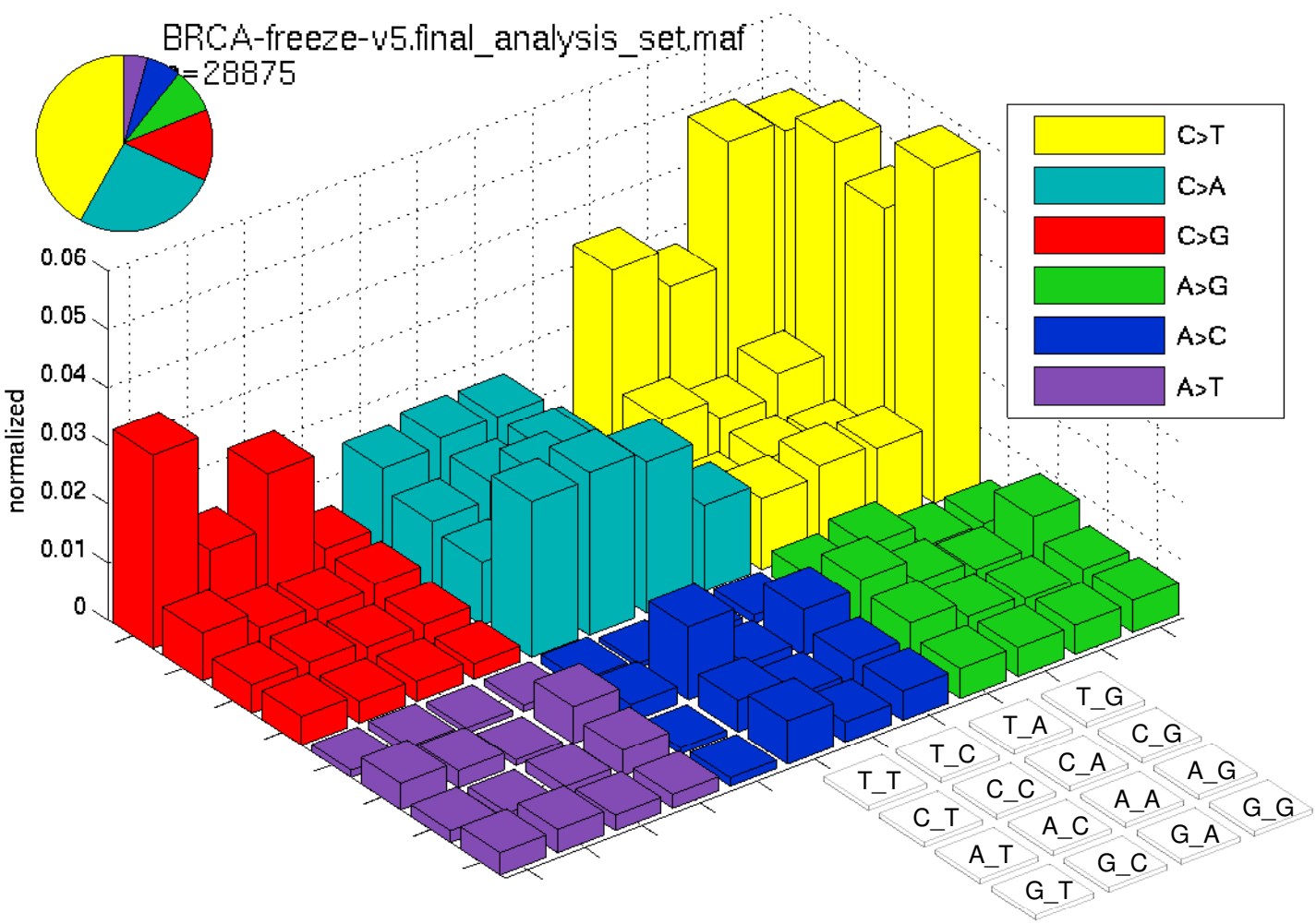

298_DM
n=178
20
10
0
29_DM
n=14
10
5
0
30_DM
n=235
40
20
0
327_DM
n=51
20
10
0
328_DM
n=111
20
10
0
329_DM
n=13331
5000
0
330_DM
n=149
40
20
0
331_DM
n=176
20
10
0
332_DM
n=66
10
5
0
333_DM
n=87
20
10
0
334_DM
n=105
20
10
0
340_DM
n=99
20
10
0


345–DM
n=152
20
10
0
346–DM
n=77
20
10
0
347–DM
n=110
20
10
0
348–DM
n=356
100
50
0
349–DM
n=105
20
10
0
350–DM
n=166
20
10
0
351–DM
n=99
20
10
0
352–DM
n=52
20
10
0
353–DM
n=50
20
10
0
354–DM
n=70
40
20
0
355–DM
n=64
20
10
0
356–DM
n=61
20
10
0


40_DM
n=39
10
5
0
41_DM
n=63
40
20
0
42_DM
n=15
4
2
0
43_DM
n=64
20
10
0
48_DM
n=40
10
5
0
49_DM
n=80
20
10
0
50_DM
n=130
20
10
0
51_DM
n=102
20
10
0
58_DM_R
n=149
40
20
0
59_DM
n=74
20
10
0
60_DM
n=135
40
20
0
66_DM_R
n=995
400
200
0

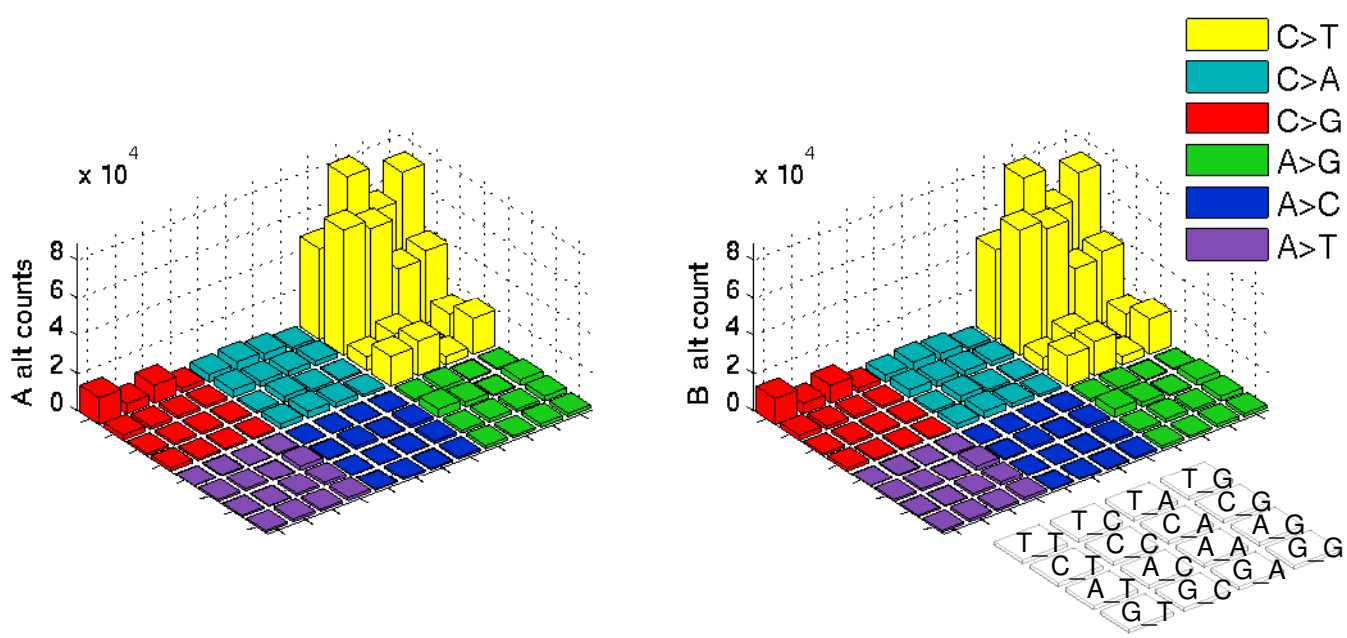

67_DM
n=153
10
5
0
73_DM
n=89
50
0
74_DM
n=65
20
10
0
75_DM
n=42
20
10
0
83_DM
n=49
40
20
0
91_DM
n=48
10
5
0
92_DM
n=129
50
0
93_DM
n=85
40
20
0
94_DM
n=93
40
20
0
95_DM
n=39
20
10
0
96_DM
n=88
20
10
0
97_DM
n=74
40
20
0


98_DM
n=105
40
20
0
99_DM
n=117
20
10
0


BRCA-freeze-v5.final_analysis_set.maf
=28875
normalized
0.06
0.05
0.04
0.03
0.02
0.01
0
C>T
C>A
C>G
A>G
A>C
A>T
T_G
T_A
C_G
T_C
C_A
A_G
T_T
C_C
A_A
G_G
C_T
A_C
G_A
A_T
G_C
G_T

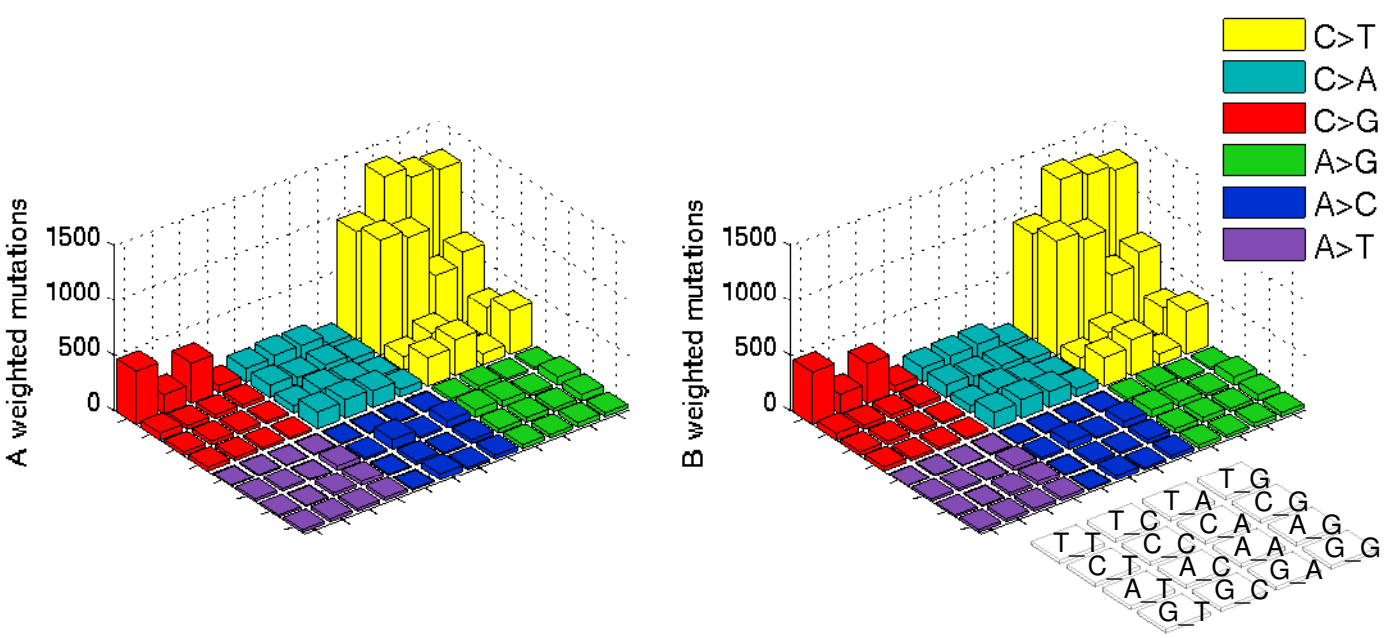
Orientation Bias: BRCA-freeze-v5.final_analysis_set.maf

A = alt counts REF>ALT F1R2 + reverse complement F2R1; B = alt counts REF>ALT F2R1 + reverse co



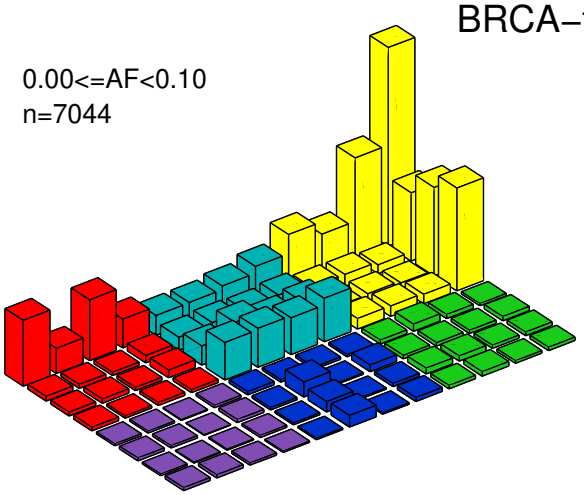
Orientation Bias weighted mutations: BRCA-freeze-v5.final_analysis_set.maf

A = alt counts REF>ALT F1R2 + reverse complement F2R1; B = alt counts REF>ALT F2R1 + reverse co

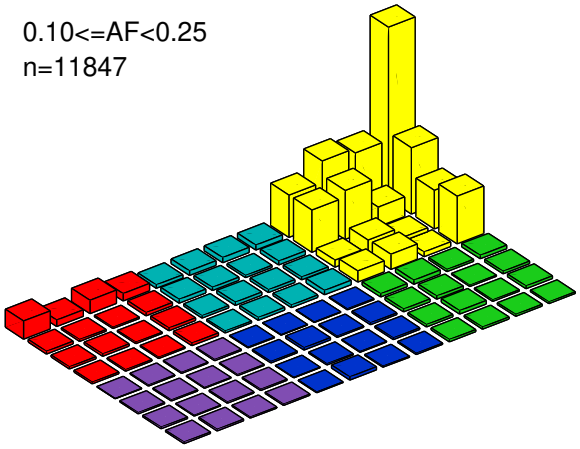


BRCA−freeze−v5.final_analysis_set.maf

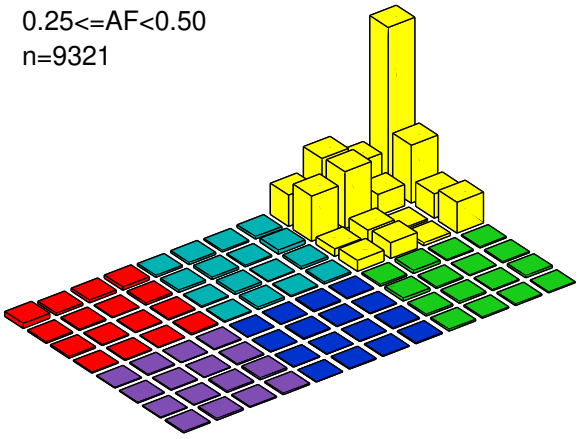
0.00<=AF<0.10
n=7044



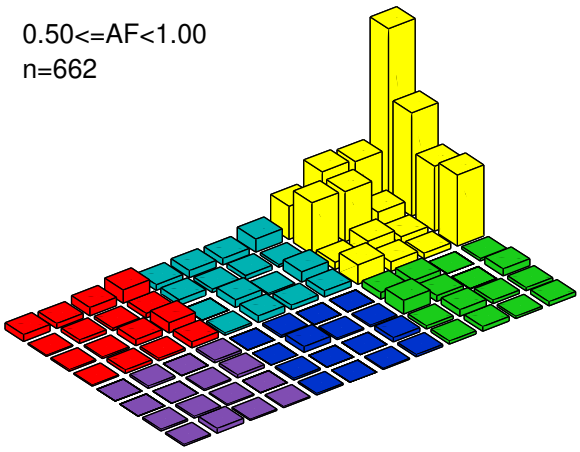
0.10<=AF<0.25
n=11847

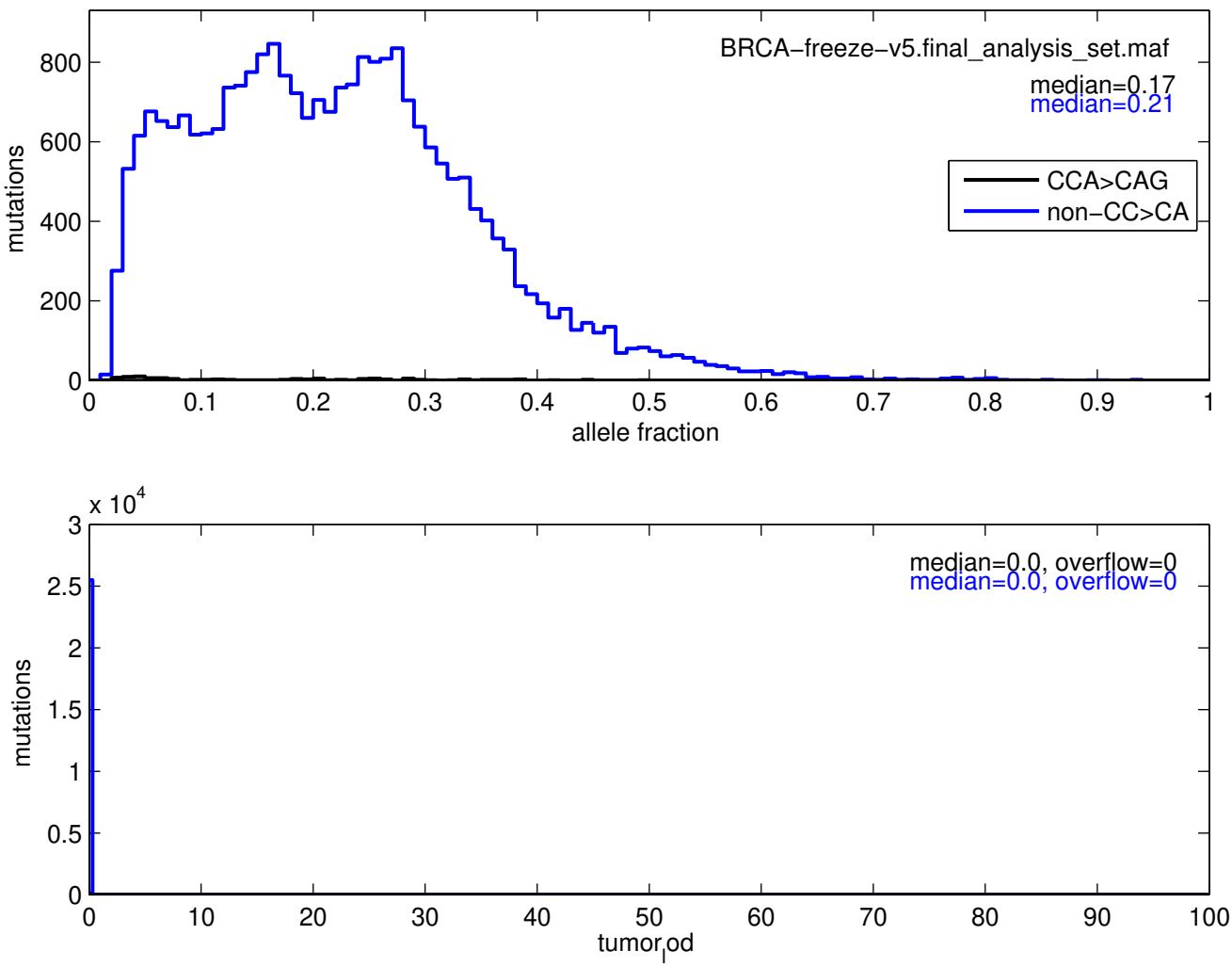


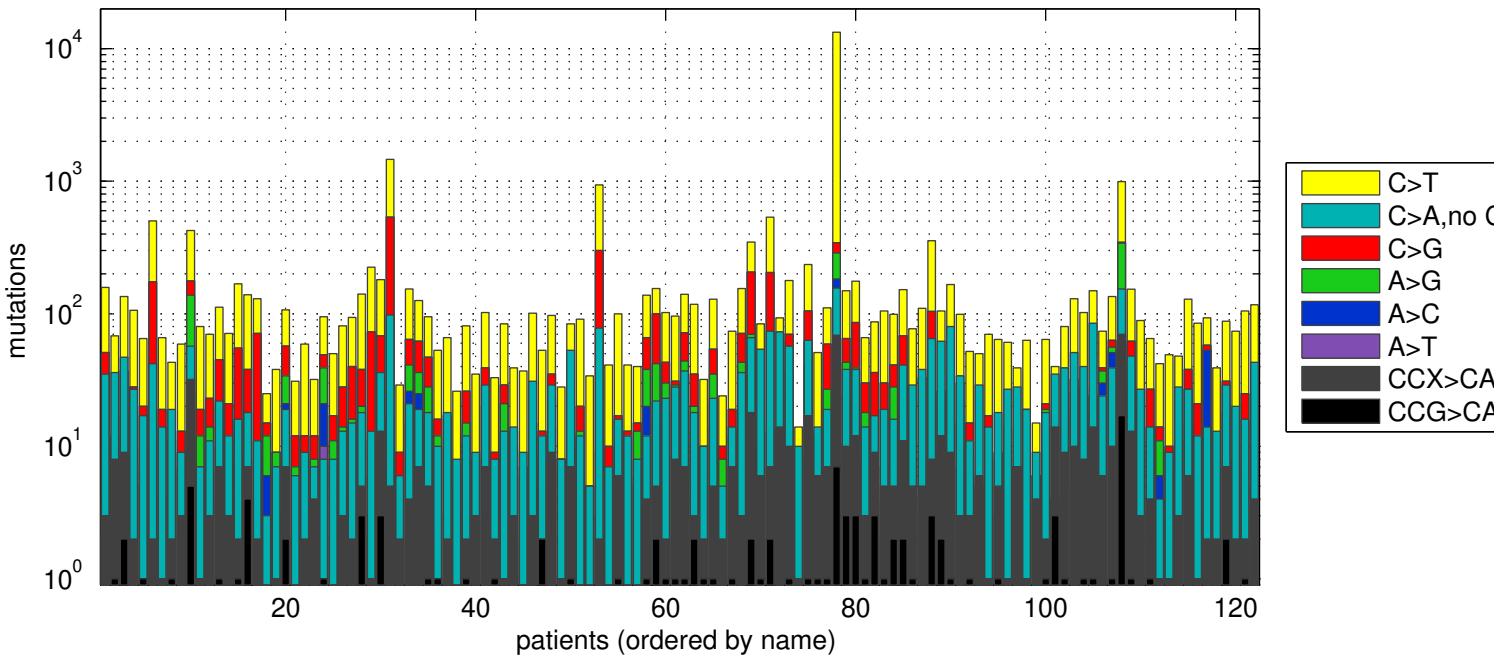
0.25<=AF<0.50
n=9321

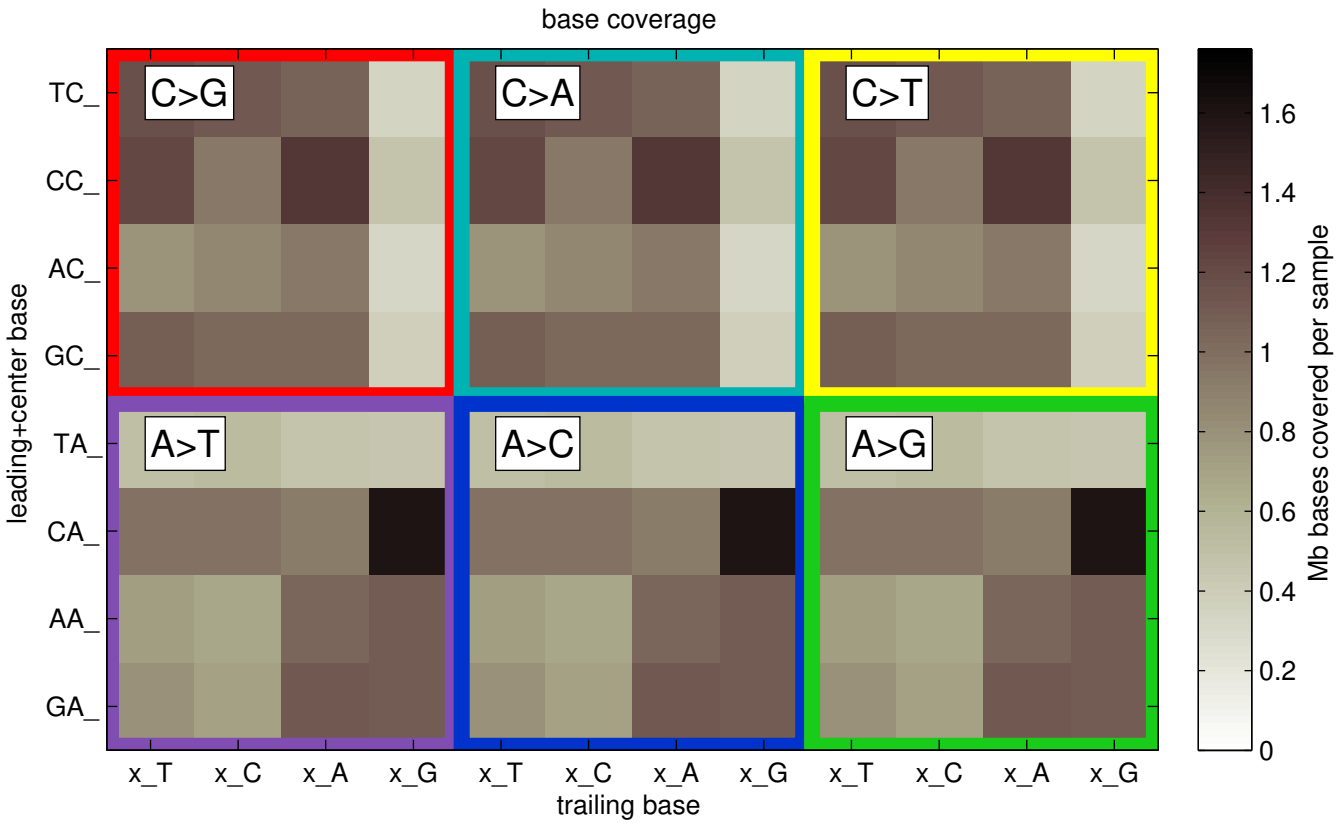


0.50<=AF<1.00
n=662




BRCA−freeze−v5.final_analysis_set.maf
median=0.17
median=0.21
CCA>CAG
non−CC>CA
mutations
allele fraction
x 10^4
median=0.0, overflow=0
median=0.0, overflow=0
mutations
tumor_od


mutations
10^4
10^3
10^2
10^1
10^0
20
40
60
80
100
120
patients (ordered by name)
C>T
C>A,no C
C>G
A>G
A>C
A>T
CCX>CA
CCG>CA


base coverage
C>G
C>A
C>T
A>T
A>C
A>G
TC_
CC_
AC_
GC_
TA_
CA_
AA_
GA_
leading+center base
x_T
x_C
x_A
x_G
trailing base
Mb bases covered per sample
0
0.2
0.4
0.6
0.8
1
1.2
1.4
1.6