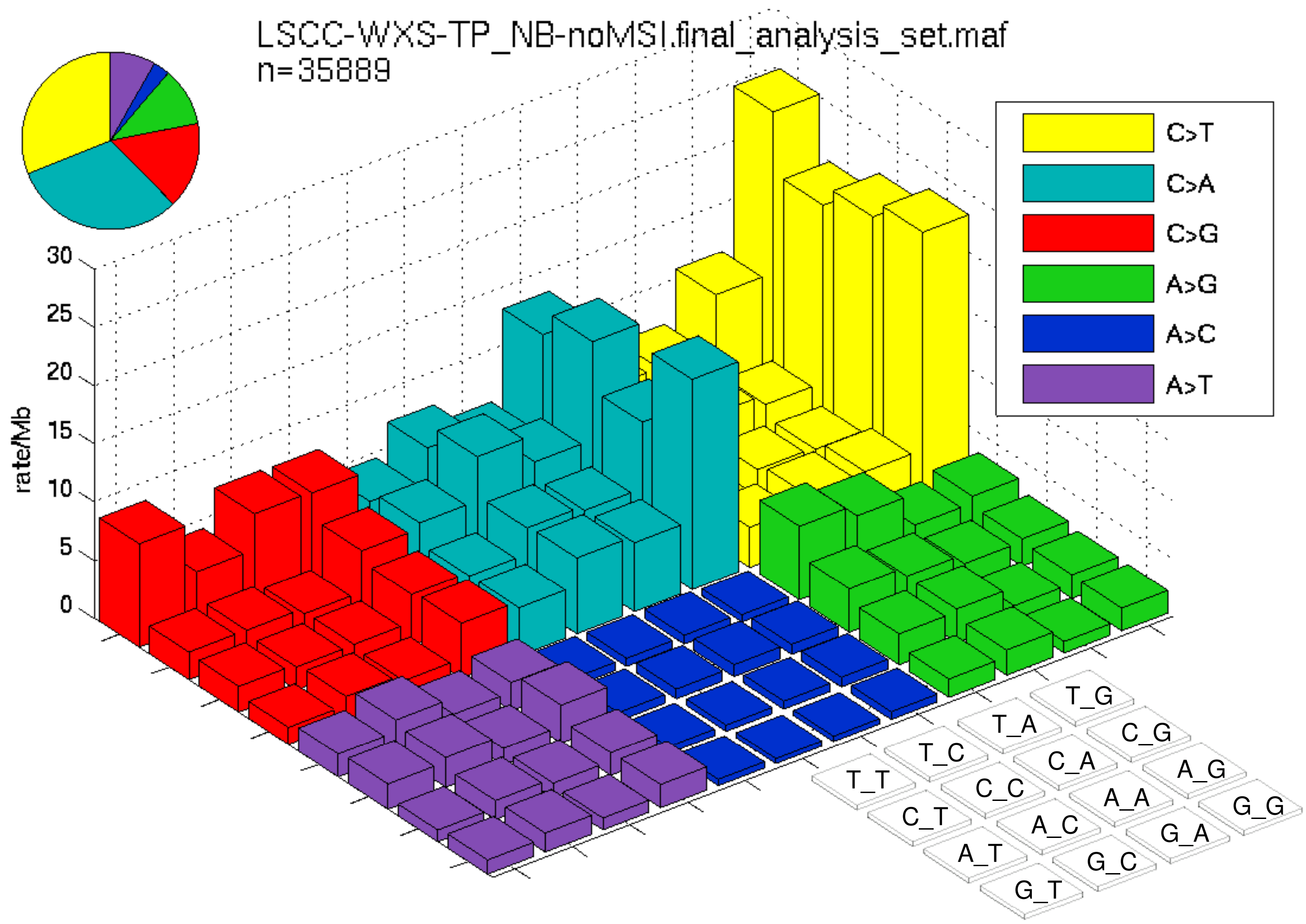
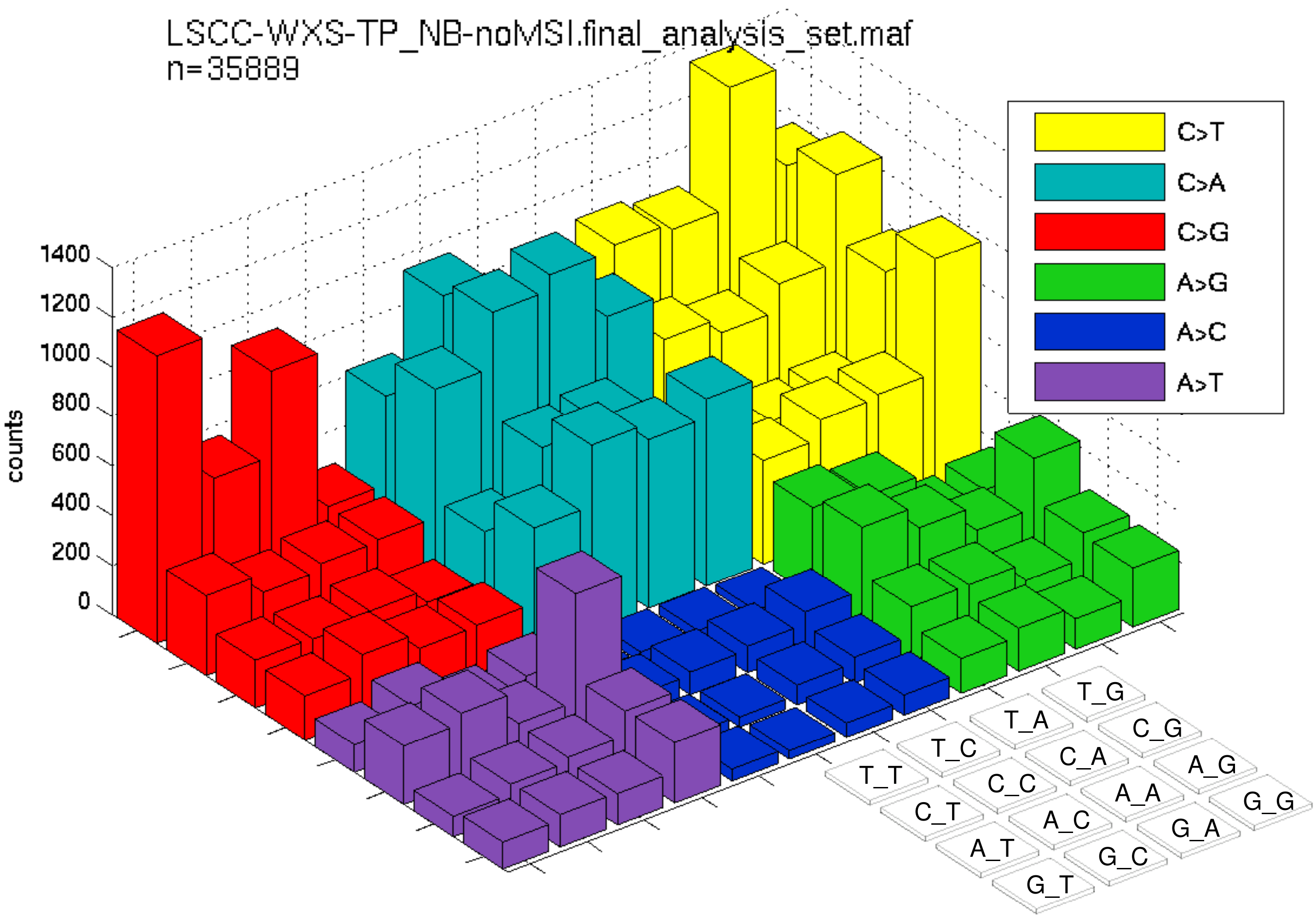
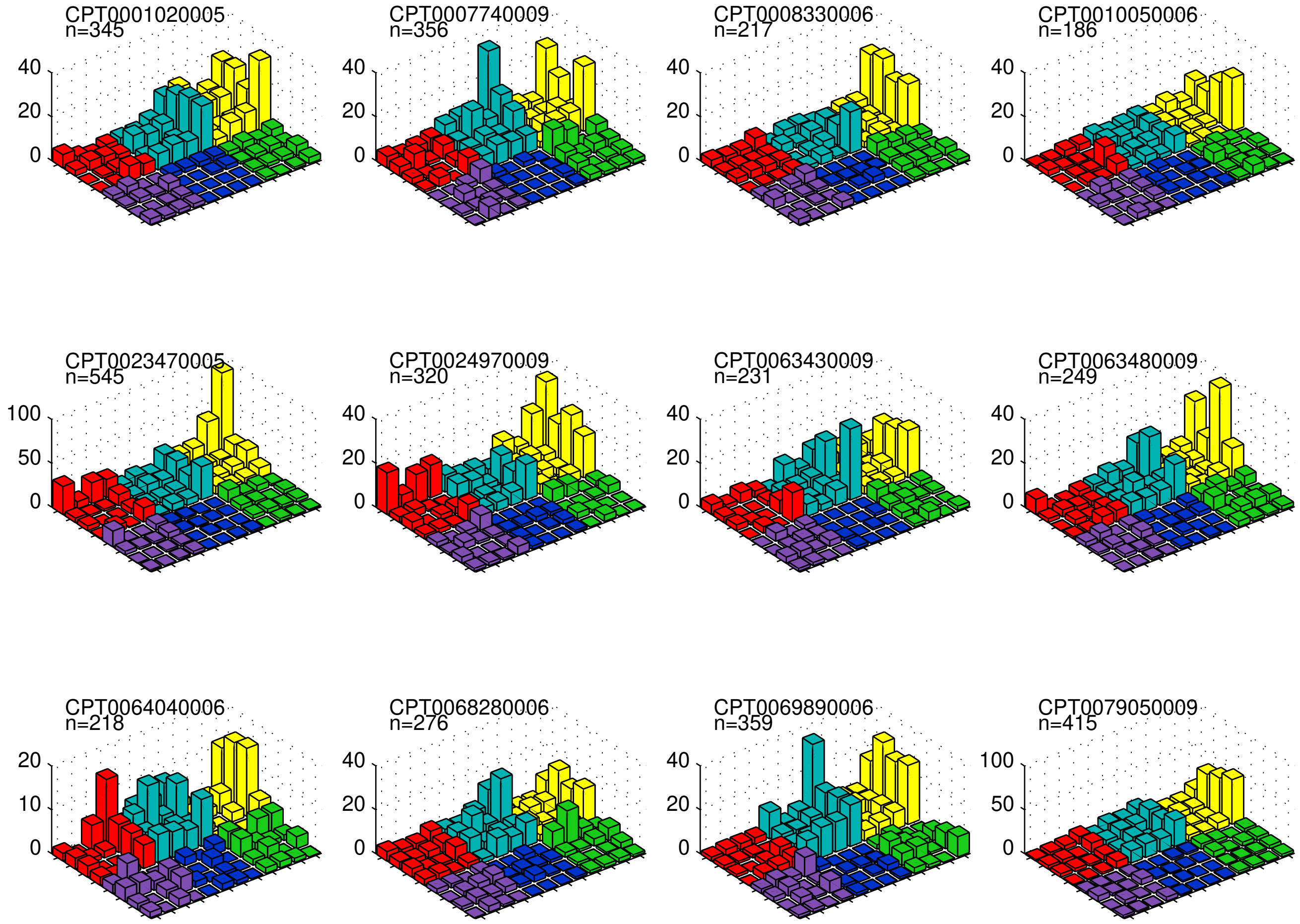
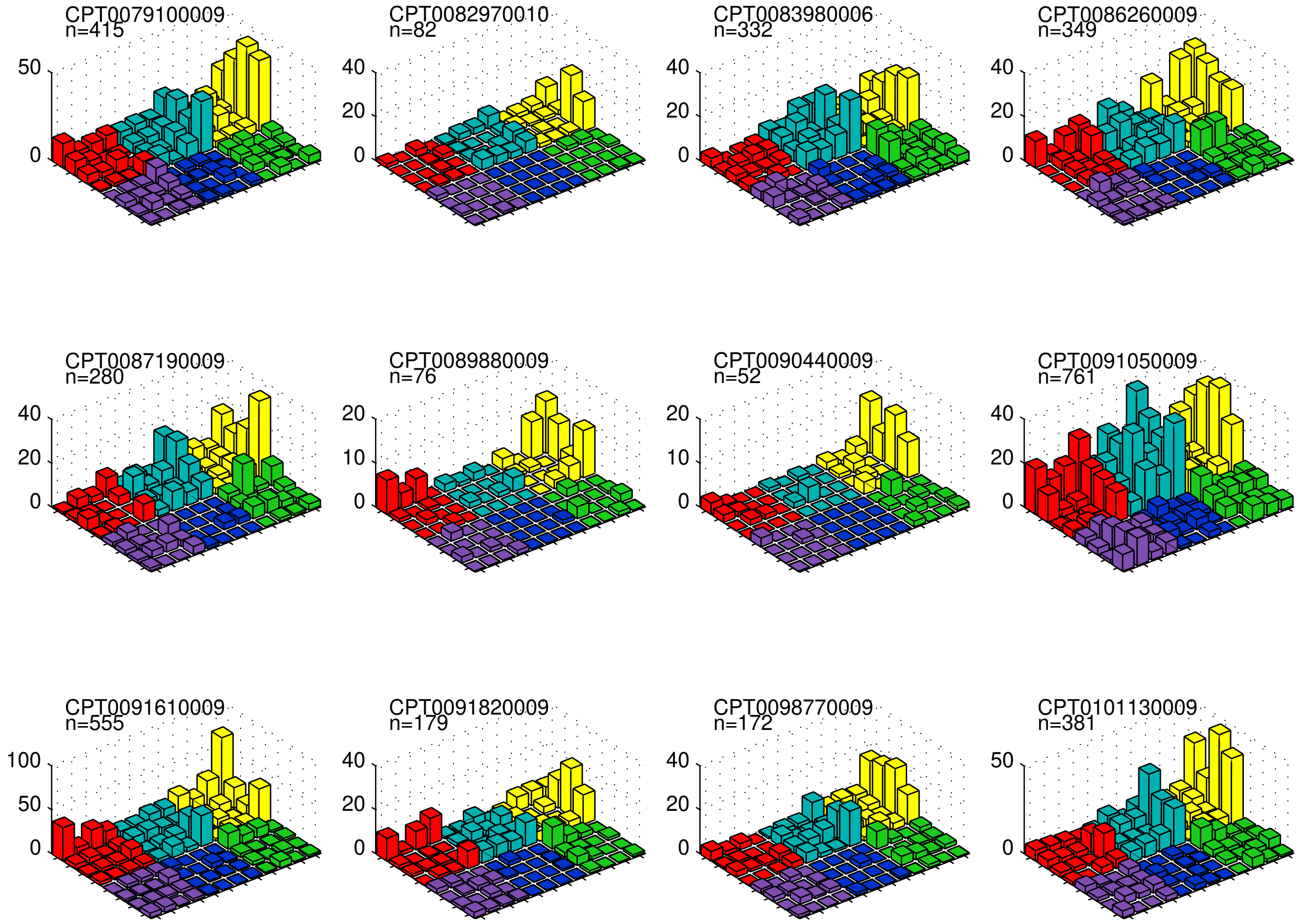


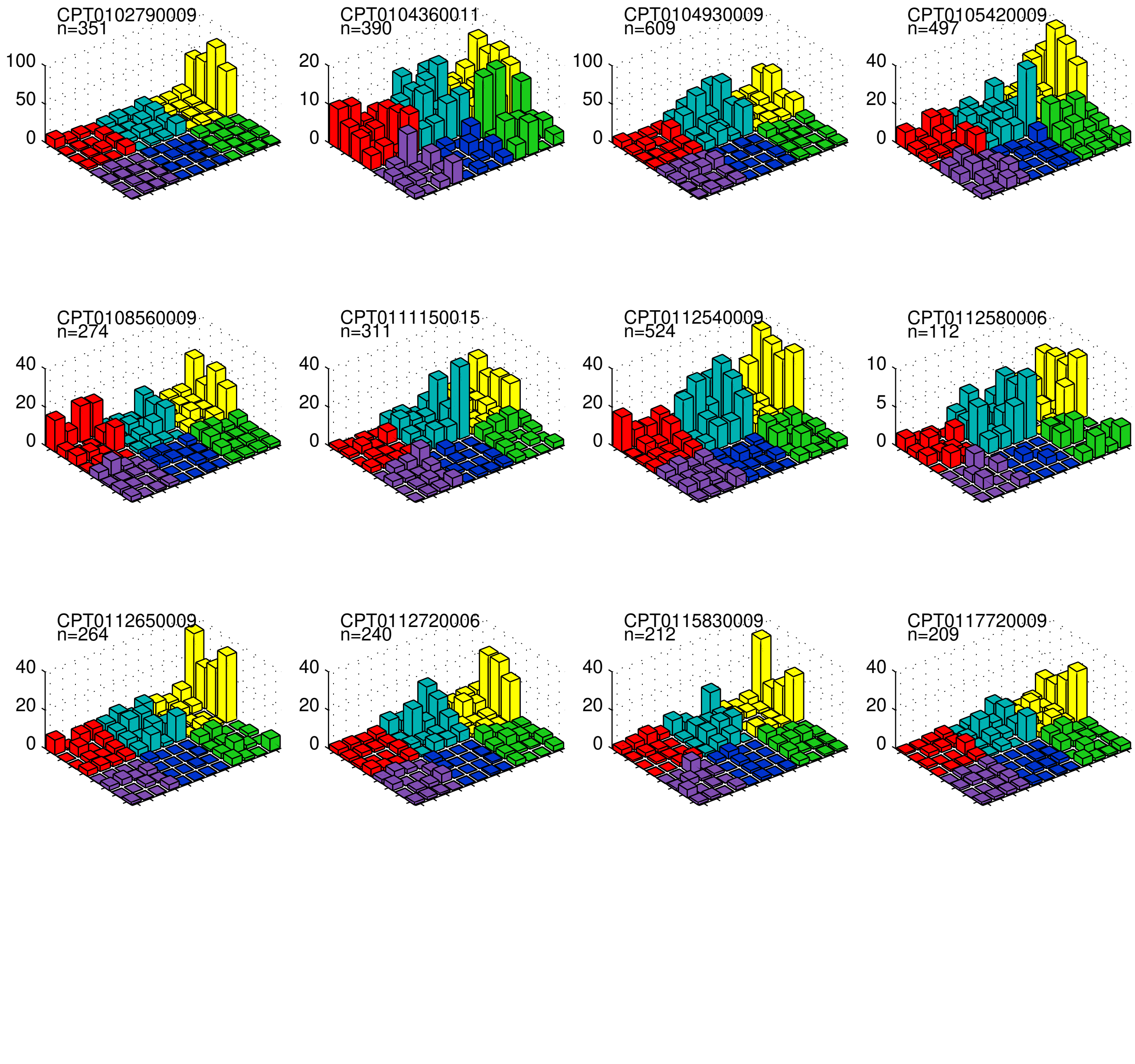
LSCC-WXS-TP_NB-noMSI.final_analysis_set.maf
n=35889
rate/Mb
30
25
20
15
10
5
0
C>T
C>A
C>G
A>G
A>C
A>T
T_T
C_T
A_T
G_T
T_C
C_C
A_C
G_C
T_A
C_A
A_A
G_A
T_G
C_G
A_G
G_G

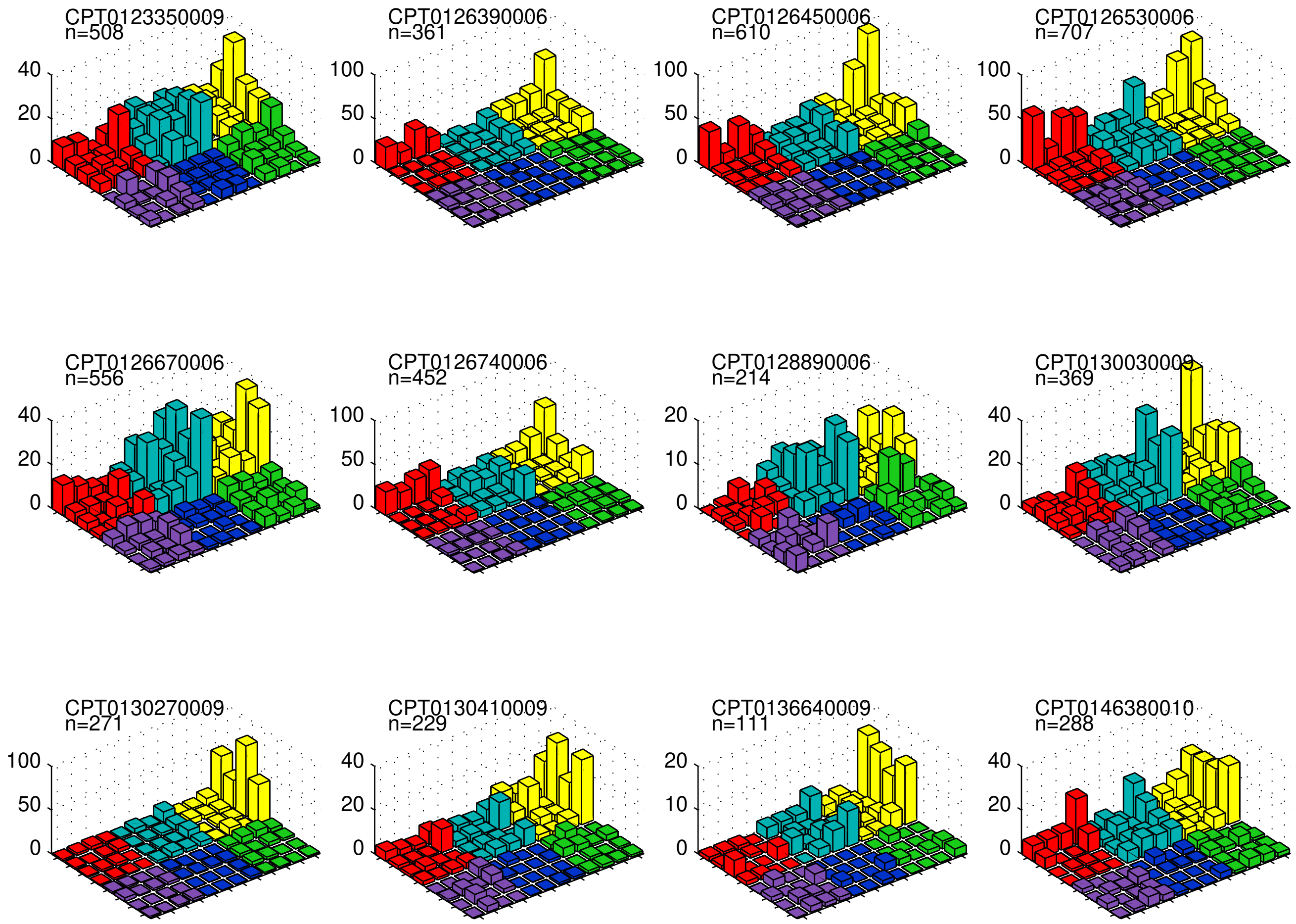


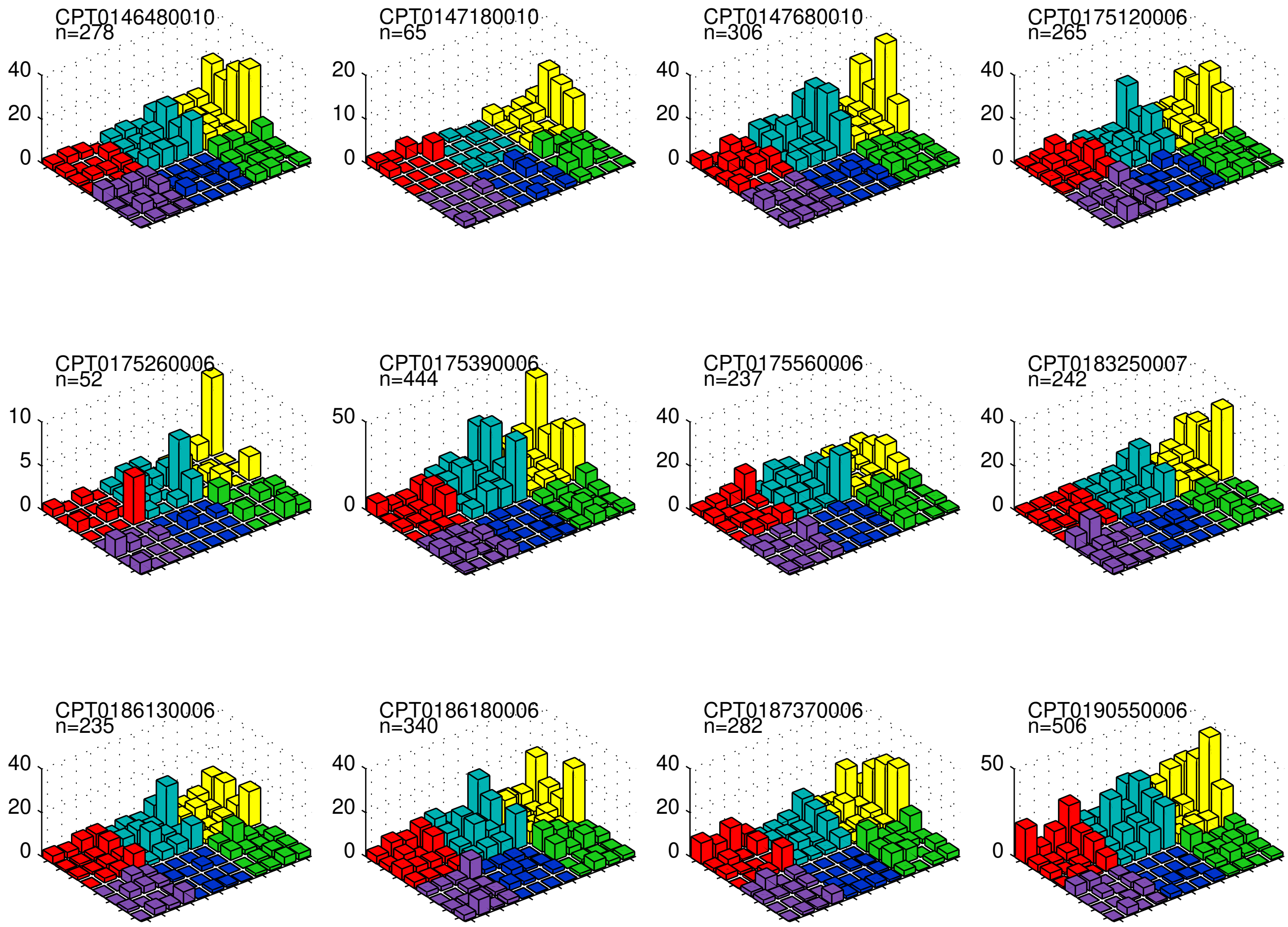
LSCC-WXS-TP_NB-noMSI.final_analysis_set.maf
n=35889
C>T
C>A
C>G
A>G
A>C
A>T
counts
1400
1200
1000
800
600
400
200
0
T_G
T_A
C_G
T_C
C_A
A_G
T_T
C_C
A_A
G_G
C_T
A_C
G_A
A_T
G_C
G_T

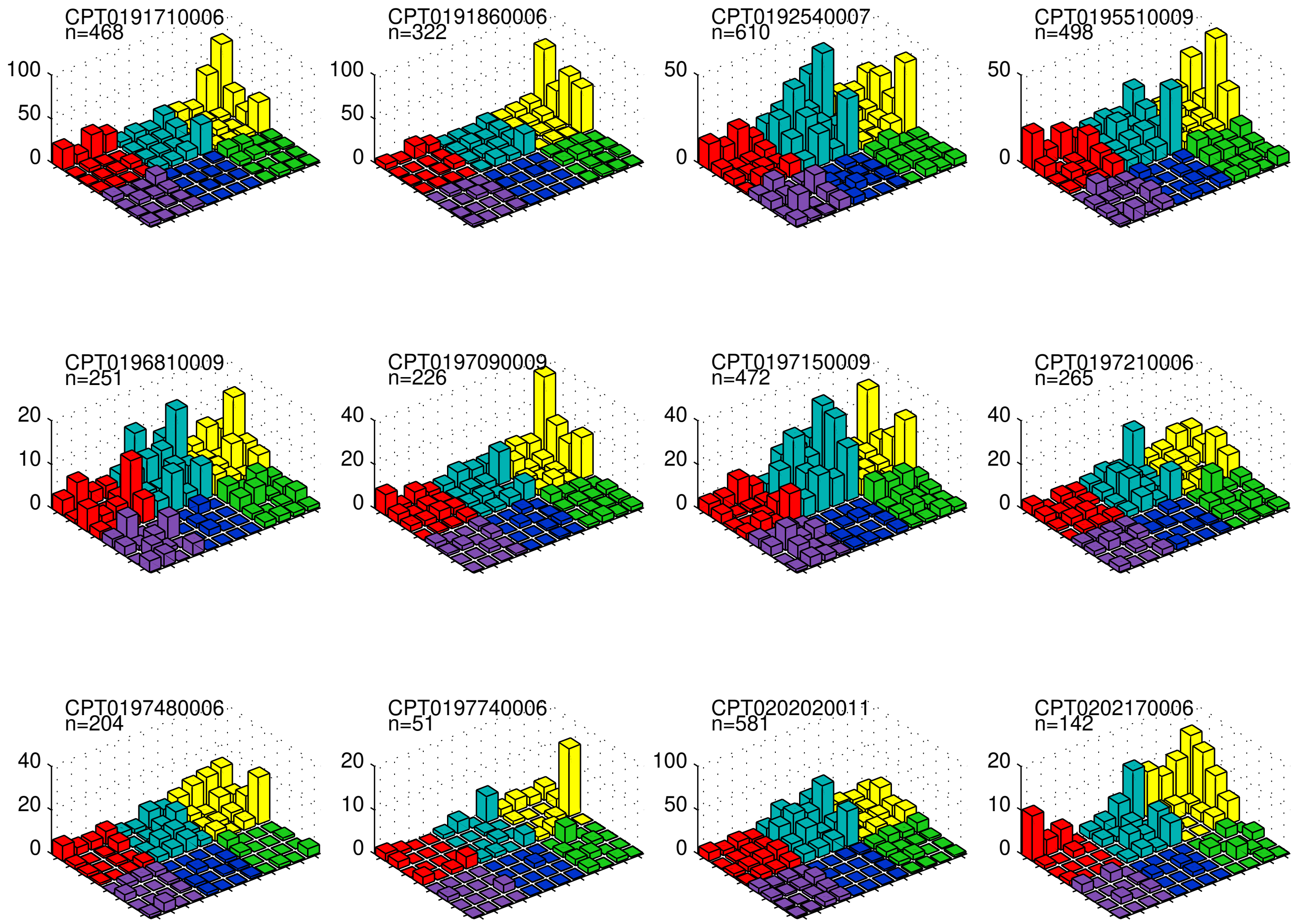

CPT0001020005
n=345
CPT0007740009
n=356
CPT0008330006
n=217
CPT0010050006
n=186
CPT0023470005
n=545
CPT0024970009
n=320
CPT0063430009
n=231
CPT0063480009
n=249
CPT0064040006
n=218
CPT0068280006
n=276
CPT0069890006
n=359
CPT0079050009
n=415

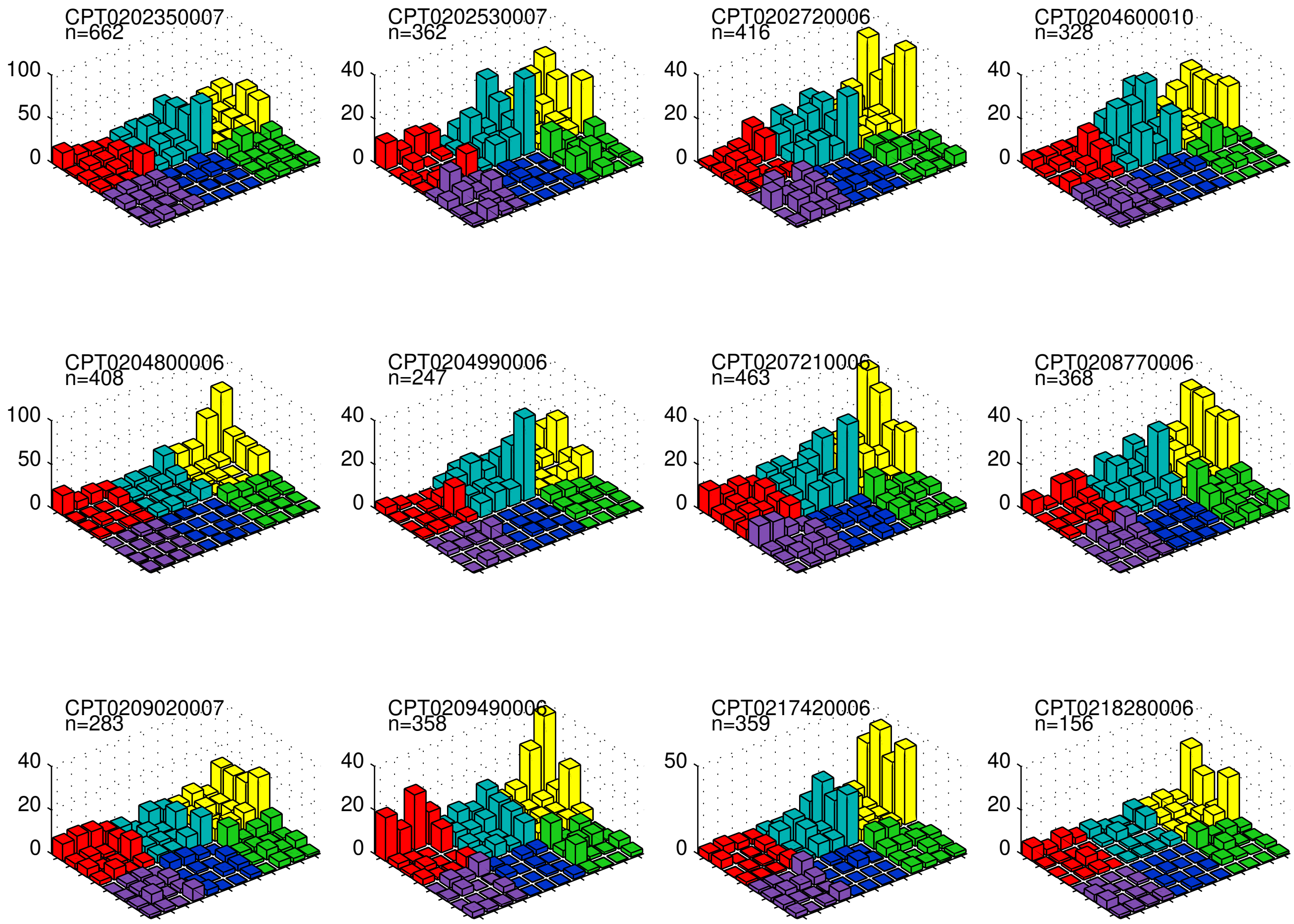

CPT0079100009
n=415
CPT0082970010
n=82
CPT0083980006
n=332
CPT0086260009
n=349
CPT0087190009
n=280
CPT0089880009
n=76
CPT0090440009
n=52
CPT0091050009
n=761
CPT0091610009
n=555
CPT0091820009
n=179
CPT0098770009
n=172
CPT0101130009
n=381

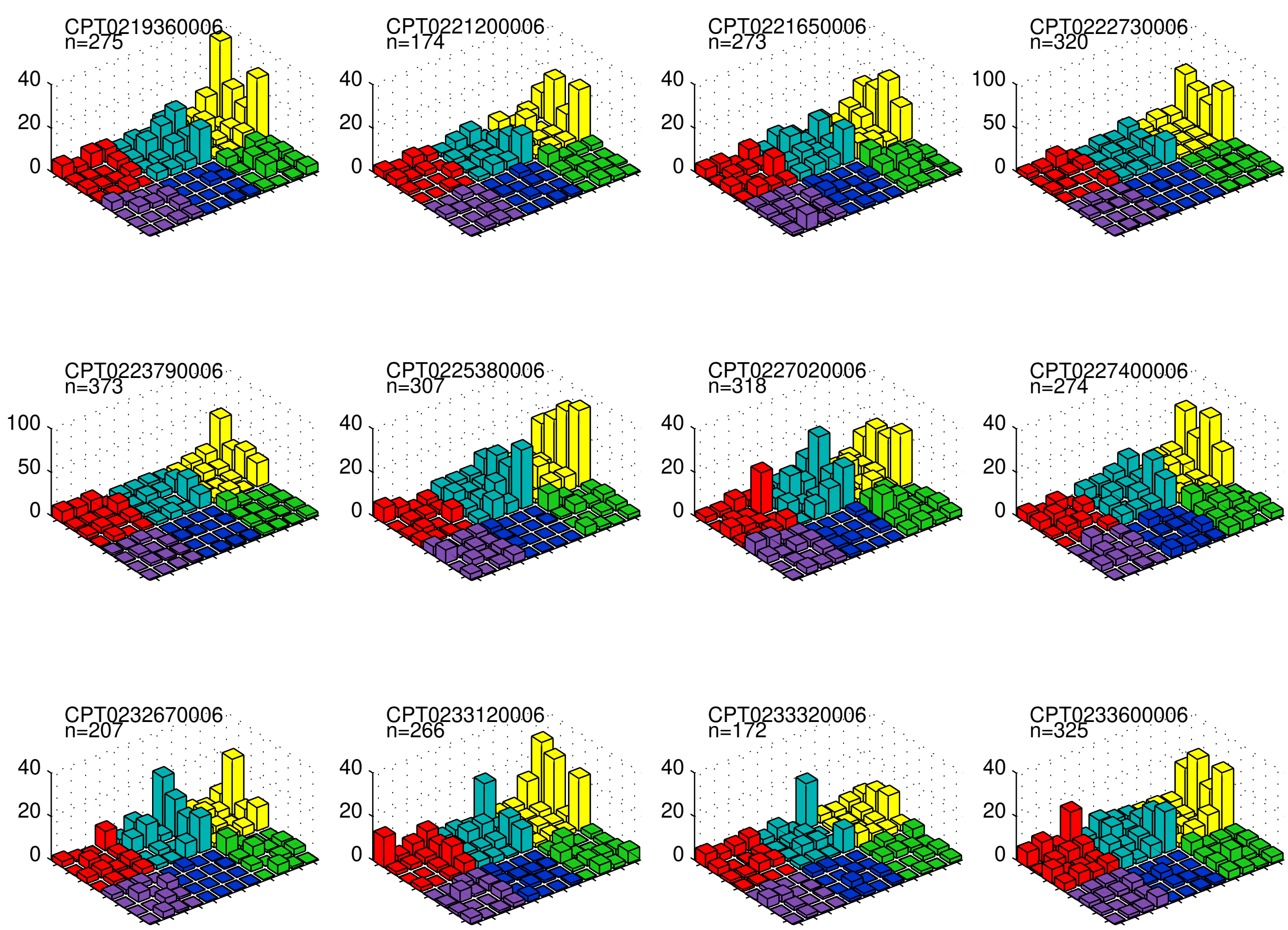

CPT0102790009
n=351
100
50
0
CPT0104360011
n=390
20
10
0
CPT0104930009
n=609
100
50
0
CPT0105420009
n=497
40
20
0
CPT0108560009
n=274
40
20
0
CPT0111150015
n=311
40
20
0
CPT0112540009
n=524
40
20
0
CPT0112580006
n=112
10
5
0
CPT0112650009
n=264
40
20
0
CPT0112720006
n=240
40
20
0
CPT0115830009
n=212
40
20
0
CPT0117720009
n=209
40
20
0

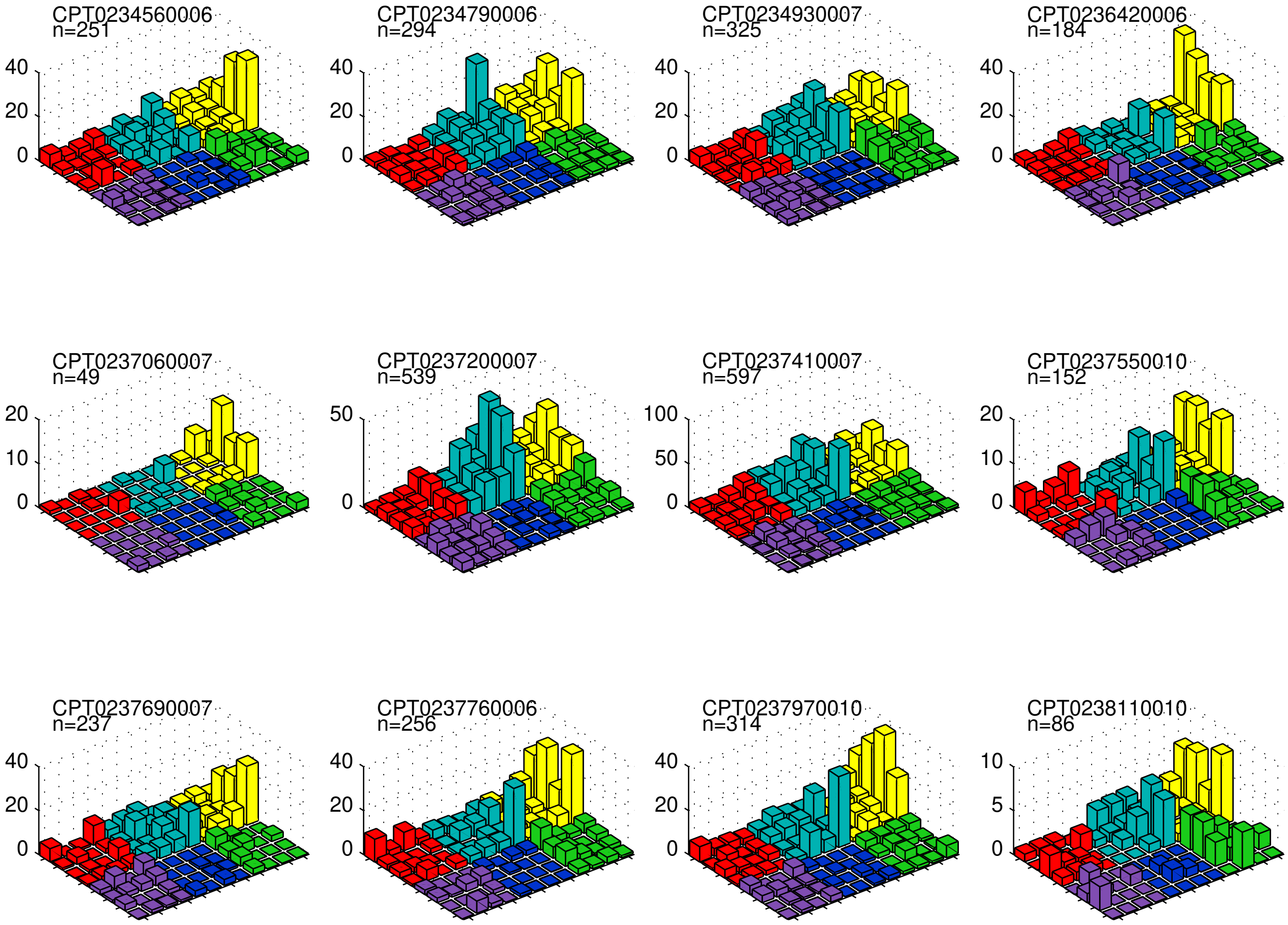

CPT0123350009
n=508
40
20
0
CPT0126390006
n=361
100
50
0
CPT0126450006
n=610
100
50
0
CPT0126530006
n=707
100
50
0
CPT0126670006
n=556
40
20
0
CPT0126740006
n=452
100
50
0
CPT0128890006
n=214
20
10
0
CPT0130030009
n=369
40
20
0
CPT0130270009
n=271
100
50
0
CPT0130410009
n=229
40
20
0
CPT0136640009
n=111
20
10
0
CPT0146380010
n=288
40
20
0


CPT0146480010
n=278
CPT0147180010
n=65
CPT0147680010
n=306
CPT0175120006
n=265
CPT0175260006
n=52
CPT0175390006
n=444
CPT0175560006
n=237
CPT0183250007
n=242
CPT0186130006
n=235
CPT0186180006
n=340
CPT0187370006
n=282
CPT0190550006
n=506

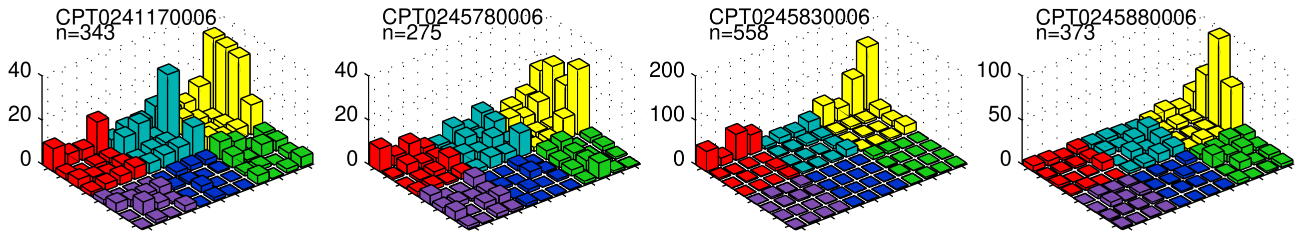

CPT0191710006
n=468
100
50
0
CPT0191860006
n=322
100
50
0
CPT0192540007
n=610
50
0
CPT0195510009
n=498
50
0
CPT0196810009
n=251
20
10
0
CPT0197090009
n=226
40
20
0
CPT0197150009
n=472
40
20
0
CPT0197210006
n=265
40
20
0
CPT0197480006
n=204
40
20
0
CPT0197740006
n=51
20
10
0
CPT0202020011
n=581
100
50
0
CPT0202170006
n=142
20
10
0

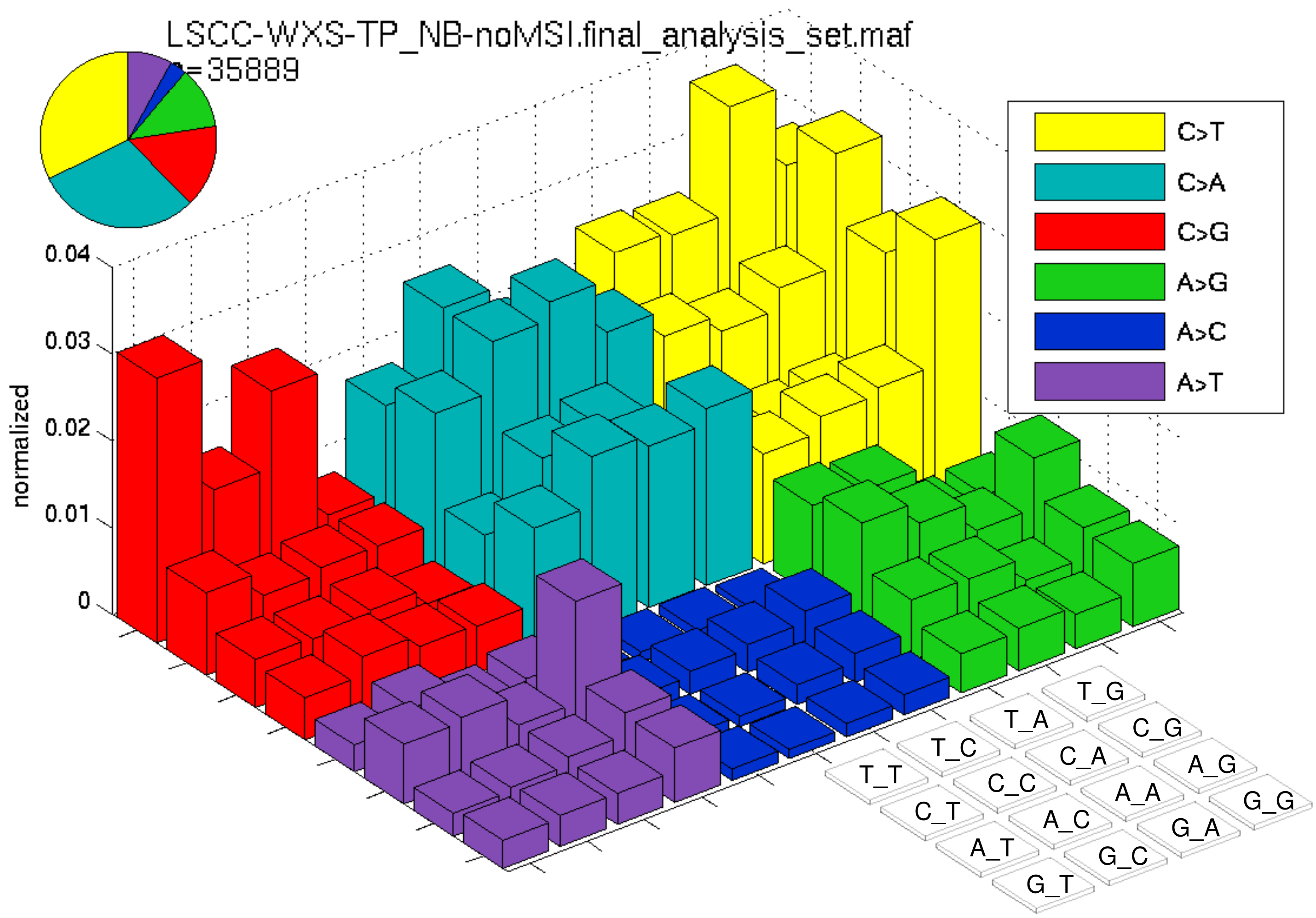

CPT0202350007
n=662
100
50
0
CPT0202530007
n=362
40
20
0
CPT0202720006
n=416
40
20
0
CPT0204600010
n=328
40
20
0
CPT0204800006
n=408
100
50
0
CPT0204990006
n=247
40
20
0
CPT0207210006
n=463
40
20
0
CPT0208770006
n=368
40
20
0
CPT0209020007
n=283
40
20
0
CPT0209490006
n=358
40
20
0
CPT0217420006
n=359
50
0
CPT0218280006
n=156
40
20
0


CPT0219360006
n=275
CPT0221200006
n=174
CPT0221650006
n=273
CPT0222730006
n=320
CPT0223790006
n=373
CPT0225380006
n=307
CPT0227020006
n=318
CPT0227400006
n=274
CPT0232670006
n=207
CPT0233120006
n=266
CPT0233320006
n=172
CPT0233600006
n=325
0
20
40
50
100



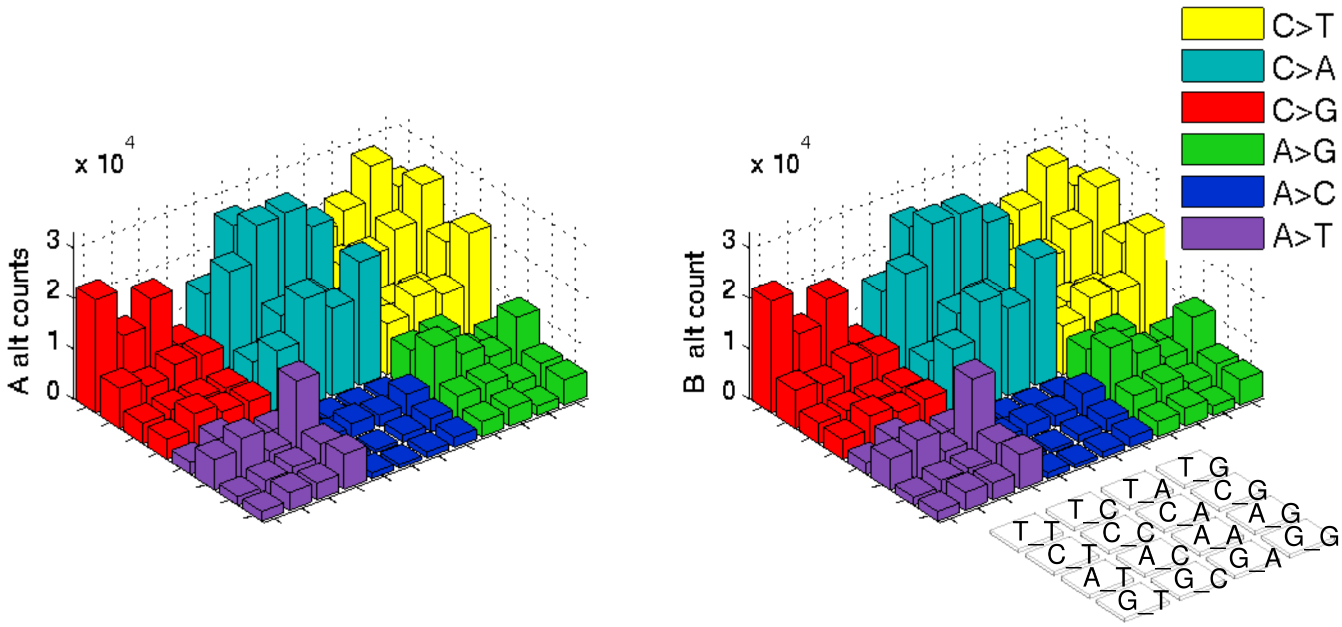
CPT0234560006
n=251
40
20
0
CPT0234790006
n=294
40
20
0
CPT0234930007
n=325
40
20
0
CPT0236420006
n=184
40
20
0
CPT0237060007
n=49
20
10
0
CPT0237200007
n=539
50
0
CPT0237410007
n=597
100
50
0
CPT0237550010
n=152
20
10
0
CPT0237690007
n=237
40
20
0
CPT0237760006
n=256
40
20
0
CPT0237970010
n=314
40
20
0
CPT0238110010
n=86
10
5
0


CPT0241170006
n=343
40
20
0
CPT0245780006
n=275
40
20
0
CPT0245830006
n=558
200
100
0
CPT0245880006
n=373
100
50
0


LSCC-WXS-TP_NB-noMSI.final_analysis_set.maf
n=35889
normalized
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

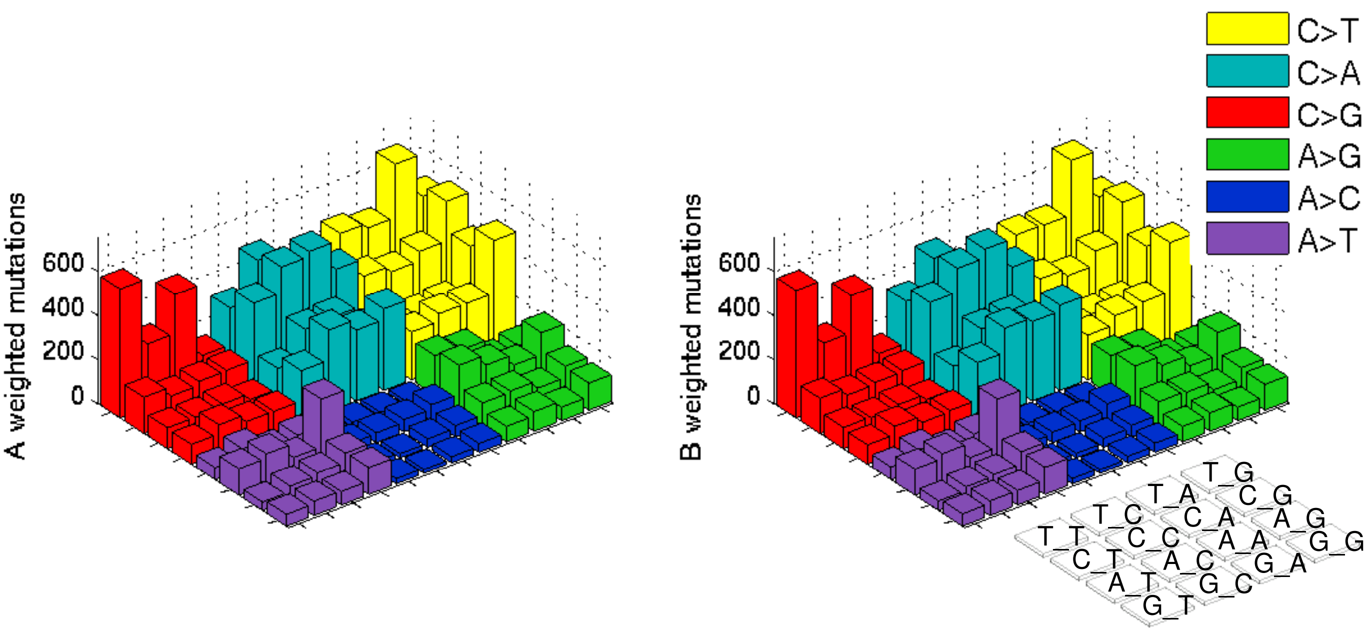
Orientation Bias: LSCC-WXS-TP$_N$B-noMSI.final$_a$nalysis$_s$et.maf

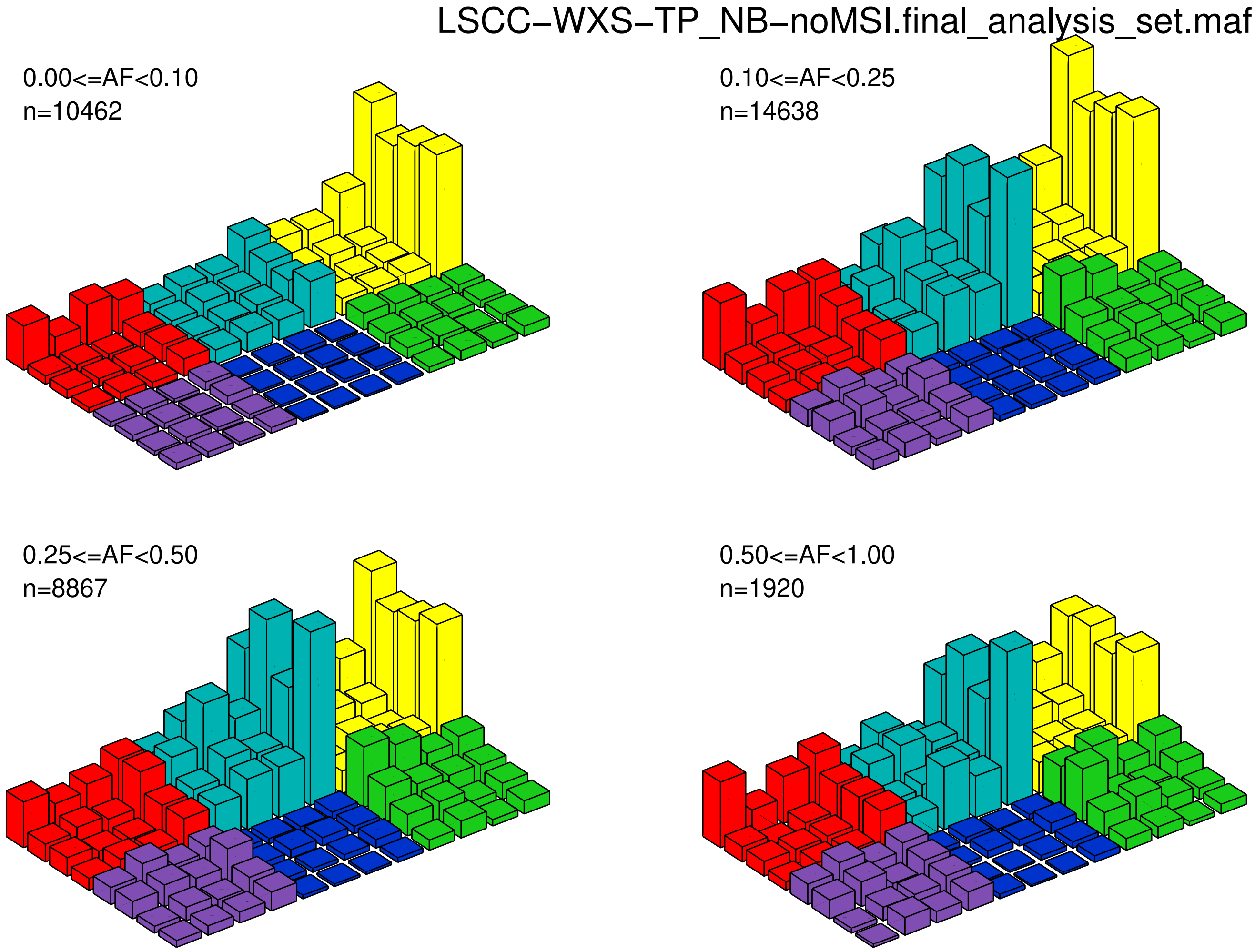
A = alt counts REF>ALT F1R2 + reverse complement F2R1; B = alt counts REF>ALT F2R1 + reverse cc



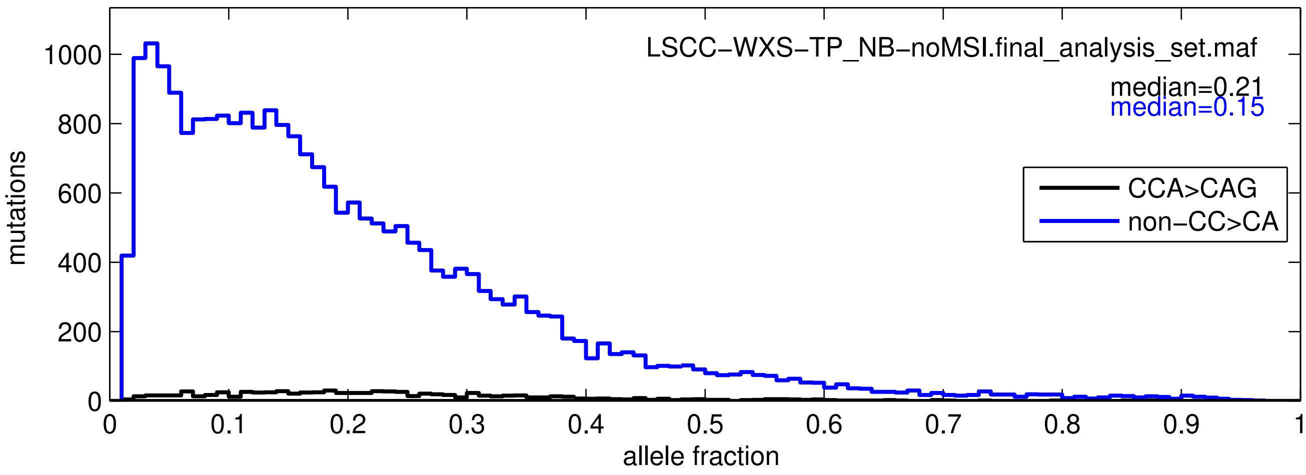
Orientation Bias weighted mutations: LSCC-WXS-TP$_N$B-noMSI.final$_a$nalysis$_s$et.maf

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

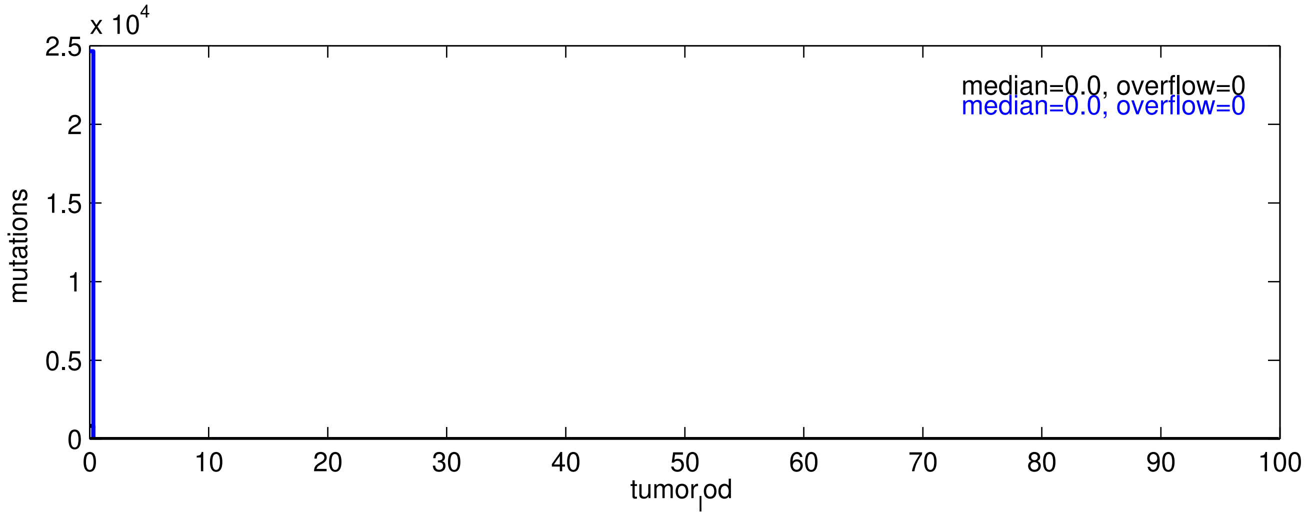




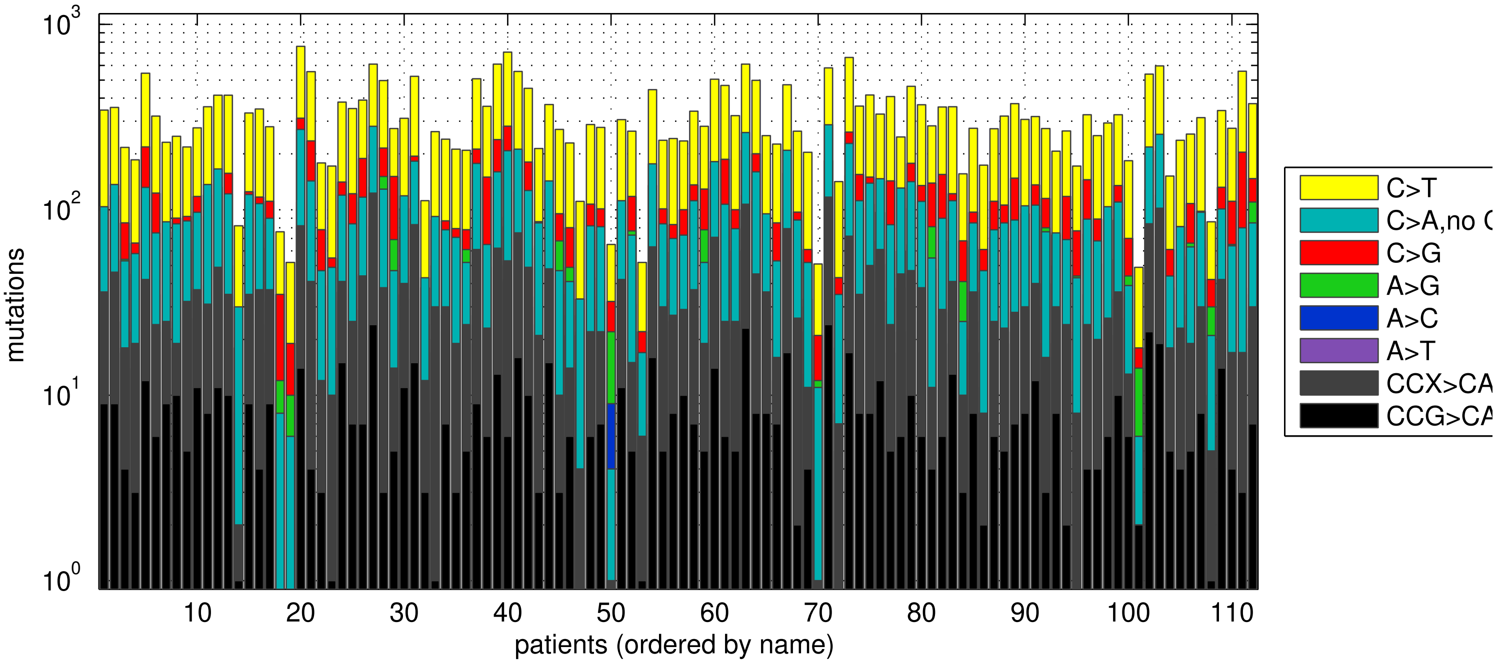
LSCC−WXS−TP_NB−noMSI.final_analysis_set.maf
0.00<=AF<0.10
n=10462
0.10<=AF<0.25
n=14638
0.25<=AF<0.50
n=8867
0.50<=AF<1.00
n=1920



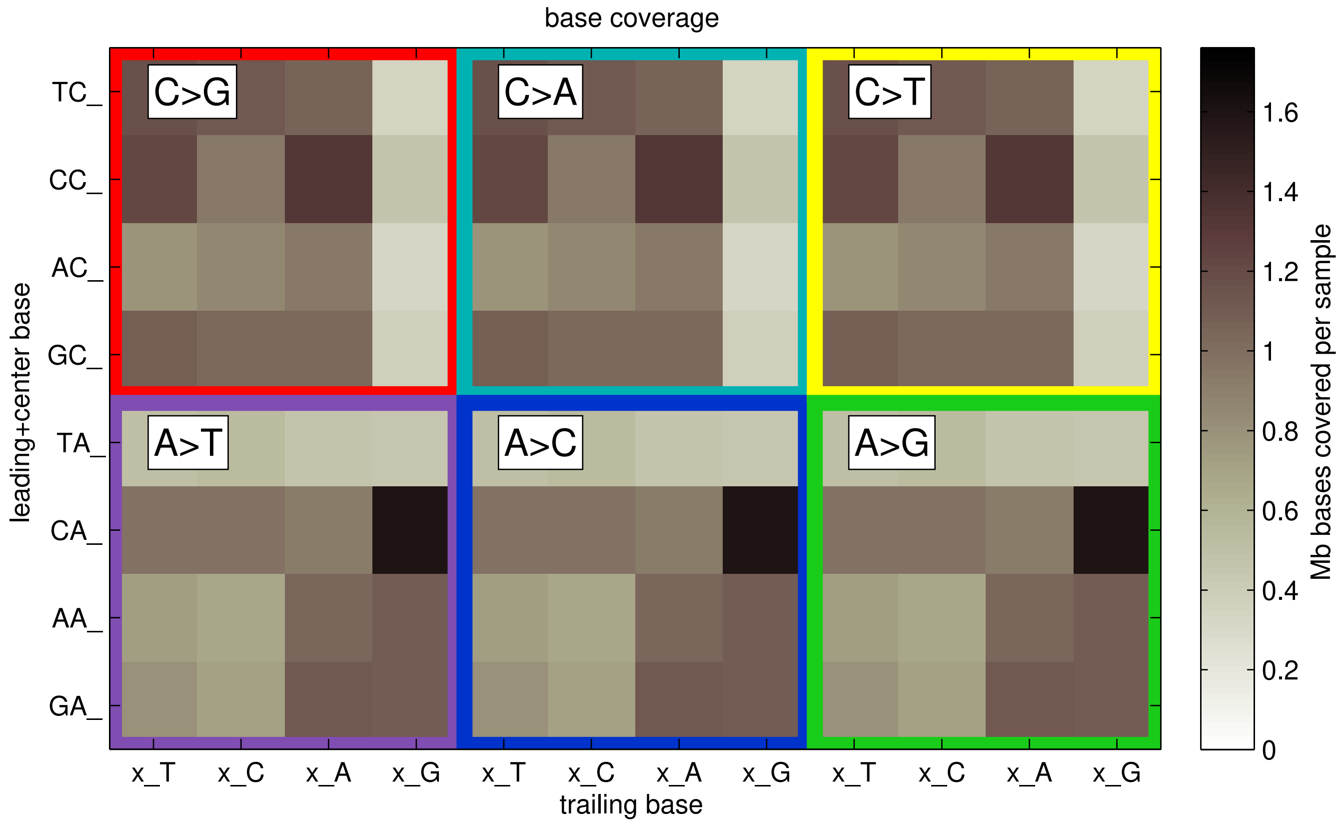
LSCC−WXS−TP_NB−noMSI.final_analysis_set.maf
median=0.21
median=0.15
CCA>CAG
non−CC>CA
mutations
allele fraction
0
200
400
600
800
1000
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1



x 10^4
median=0.0, overflow=0
median=0.0, overflow=0
mutations
tumor_lod
0
0.5
1
1.5
2
2.5
0
10
20
30
40
50
60
70
80
90
100



10^3
10^2
10^1
10^0
mutations
10
20
30
40
50
60
70
80
90
100
110
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