Bioinformatic project

Project title: Complex clonal CNAs

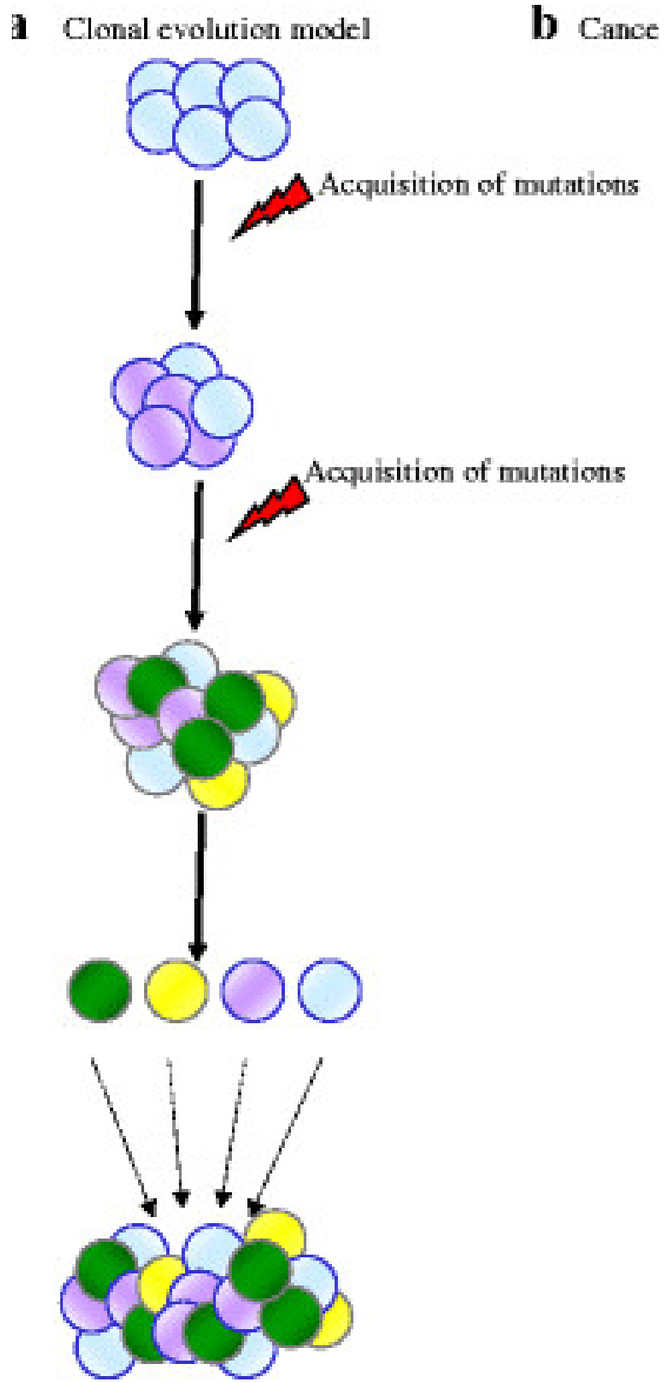
Project Description

- Compute all the evolutionary trajectories for a certain set of complex sets starting from wildtype 1:1
- Test all different complex karyotypes up to a certain ploidy (6) simulating their trajectory up to a certain length
- For each of these simulations, find the proportion of trajectories that have the same peak composition and make some plots (pie plots)
- Examine the data and identify the path that aligns with the peak composition

Creating a trajectory of complex copy number alteration

CCNAs are defined as regions of the genome that have a combination of multiple copy number changes such as :

- Amplifications,
- Deletions, (only deletion is allowed at each step)
- and/or copy-neutral events which we will not consider
- At each step, we consider a new mutation



- This process helps us understand which mutation occurs first and later during clonal/disease evolution.
- The idea is that if we are able to understand this, we will be able to look at the genomic profile of a given patient and try to predict the evolution of the disease.
- We can also find the relation between treatment and clonal evolution.

Creating a trajectory of complex copy number alteration

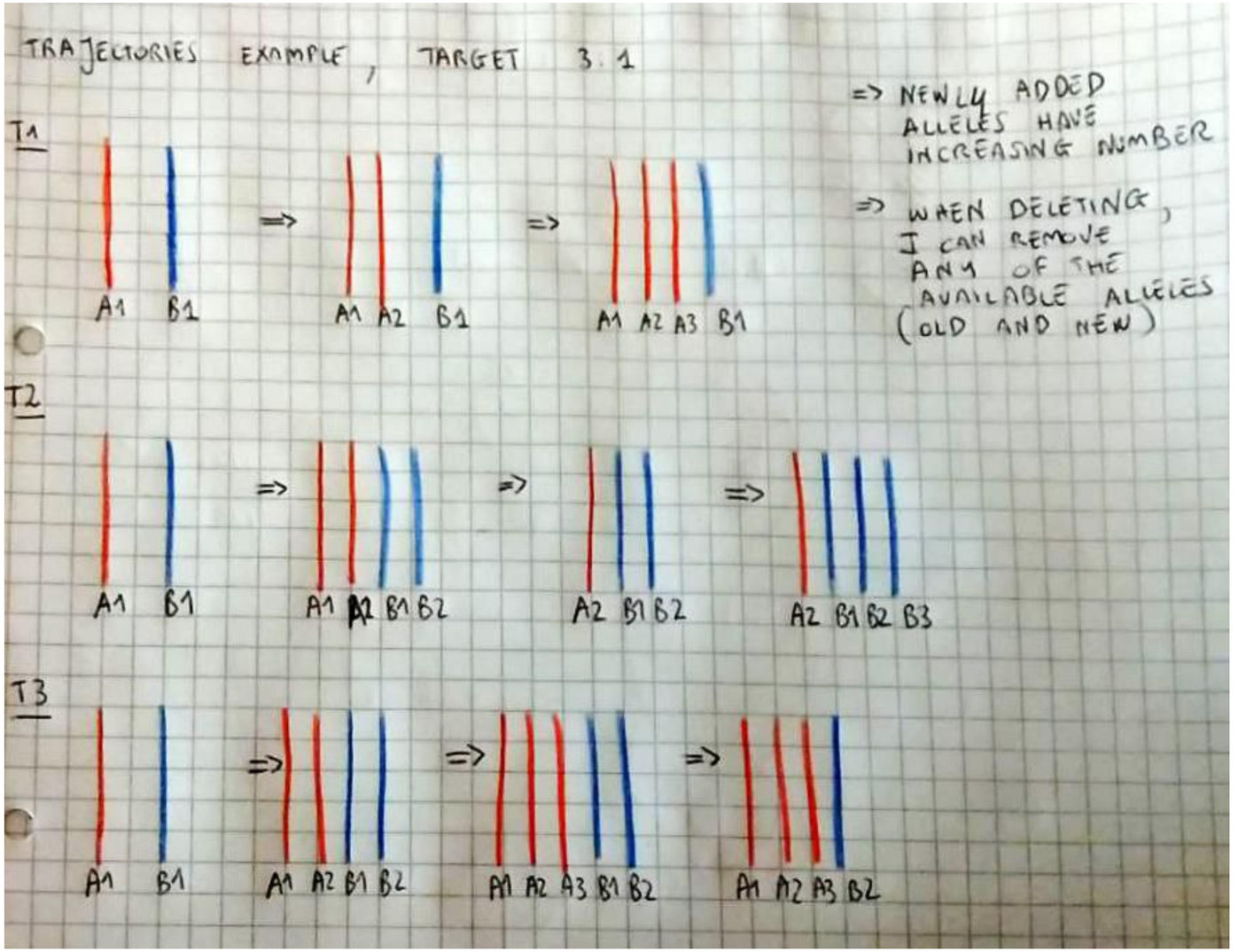
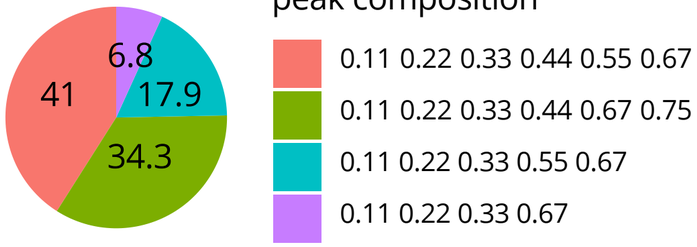


Table storing trajectory information

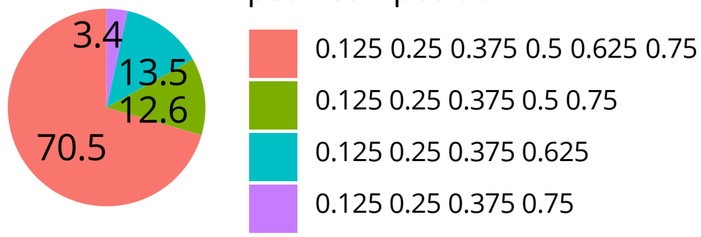
1	trajectory	subtrajectory	peakcomposition
2	1:1 2:2 2:1 3:1 4:1 4:2	A1B1/A1A2B1B2/A1B1B2/A1B1B2B3/A1B1B2B3B4/A1A2B1B2B3B4	0.166666666666667 0.333333333333333 0.5 0.666666666666667
3	1:1 2:2 2:1 3:1 4:1 4:2	A1B1/A1A2B1B2/A1A2B1/A1A2A3B1/A1A2A3A4B1/A1A2A3A4B1B2	0.166666666666667 0.333333333333333 0.5 0.666666666666667
4	1:1 2:2 2:1 3:1 4:1 4:2	A1B1/A1A2B1B2/A1A2B2/A1A2A3B2/A1A2A3A4B2/A1A2A3A4B2B3	0.166666666666667 0.333333333333333 0.5 0.666666666666667
5	1:1 2:1 3:2 3:1 2:2 3:3 4:2	A1B1/A1B1B2/A1A2B1B3B4/A2B1B3B4/A2A3B3B4/A2A3A4B3B4B5/A2A3B3B4B5B6	0.166666666666667 0.333333333333333 0.5 0.666666666666667
6	1:1 2:1 3:2 3:1 2:2 3:3 4:2	A1B1/A1A2B1/A1A2A3B1B2/A1A2A3B1/A1A3B1B2/A1A3A4B1B2B3/A1A2A3A4B1B2	0.166666666666667 0.333333333333333 0.666666666666667
7	1:1 2:1 3:2 3:1 2:2 3:3 4:2	A1B1/A1A2B1/A1A2A3B1B2/A1A2A3B2/A1A3B2B3/A1A3A4B2B3B4/A1A2A3A4B2B3	0.166666666666667 0.333333333333333 0.666666666666667
8	1:1 2:1 3:2 3:1 2:2 3:3 4:2	A1B1/A1B1B2/A1A2B1B3B4/A2B1B3B4/A2A3B1B4/A2A3A4B1B4B5/A3A4B1B2B4B5	0.166666666666667 0.333333333333333 0.666666666666667
9	1:1 2:1 3:2 3:1 2:2 3:3 4:2	A1B1/A1A2B1/A1A2A4B1B2/A1A2A4B1/A1A4B1B2/A1A4A5B1B2B3/A1A2A4A5B2B3	0.166666666666667 0.333333333333333 0.666666666666667
10	1:1 2:1 3:2 3:1 2:2 3:3 4:2	A1B1/A1A2B1/A1A2A4B1B2/A1A2A4B2/A1A4B2B3/A1A4A5B2B3B4/A1A4B2B3B4B5	0.166666666666667 0.333333333333333 0.5 0.666666666666667
11	1:1 2:1 3:2 3:1 2:2 3:3 4:2	A1B1/A1B1B2/A1A2B1B2B3/A1B1B2B3/A1A2B1B3/A1A2A3B1B2B3/A2A3B1B2B3B4	0.166666666666667 0.333333333333333 0.5 0.666666666666667
12	1:1 2:1 3:2 3:1 2:2 3:3 4:2	A1B1/A1A2B1/A1A3A4B1B2/A1A3A4B2/A1A4B2B3/A1A2A4B2B3B4/A1A2A3A4B3B4	0.166666666666667 0.333333333333333 0.5 0.666666666666667
13	1:1 2:1 3:2 3:1 2:2 3:3 4:2	A1B1/A1B1B2/A1A2B1B2B4/A2B1B2B4/A2A3B1B2/A2A3A4B1B2B3/A2A4B1B2B3B4	0.166666666666667 0.333333333333333 0.5 0.666666666666667
14	1:1 2:1 3:2 3:1 2:2 3:3 4:2	A1B1/A1B1B2/A1A2B2B3B4/A1B2B3B4/A1A2B2B3/A1A2A3B2B3B4/A1A2B2B3B4B5	0.166666666666667 0.333333333333333 0.5 0.666666666666667
15	1:1 2:1 3:2 3:1 2:2 3:3 4:2	A1B1/A1B1B2/A1A2B1B3B4/A2B1B3B4/A2A3B1B4/A2A3A4B1B4B5/A2A3A4A5B1B5	0.166666666666667 0.333333333333333 0.5 0.666666666666667
16	1:1 2:1 3:2 3:1 2:2 3:3 4:2	A1B1/A1B1B2/A1A2B1B2B4/A1B1B2B4/A1A2B1B2/A1A2A3B1B2B3/A1A3B1B2B3B4	0.166666666666667 0.333333333333333 0.5 0.666666666666667
17	1:1 2:1 3:2 3:1 2:2 3:3 4:2	A1B1/A1B1B2/A1A2B1B3B4/A1B1B3B4/A1A2B1B4/A1A2A3B1B4B5/A1A2B1B2B4B5	0.166666666666667 0.333333333333333 0.666666666666667
18	1:1 2:1 3:2 3:1 2:2 3:3 4:2	A1B1/A1B1B2/A1A2B1B3B4/A1B1B3B4/A1A2B3B4/A1A2A3B3B4B5/A1A2A3A4B3B5	0.166666666666667 0.333333333333333 0.5 0.666666666666667
19	1:1 2:1 3:2 3:1 2:2 3:3 4:2	A1B1/A1A2B1/A2A3A4B1B2/A2A3A4B1/A2A4B1B2/A2A4A5B1B2B3/A2A5B1B2B3B4	0.166666666666667 0.333333333333333 0.5 0.666666666666667
20	1:1 2:1 3:2 3:1 2:2 3:3 4:2	A1B1/A1B1B2/A1A2B1B2B3/A2B1B2B3/A2A3B1B3/A2A3A4B1B3B4/A2A3B1B3B4B5	0.166666666666667 0.333333333333333 0.5 0.666666666666667

A peak composition for a complex state

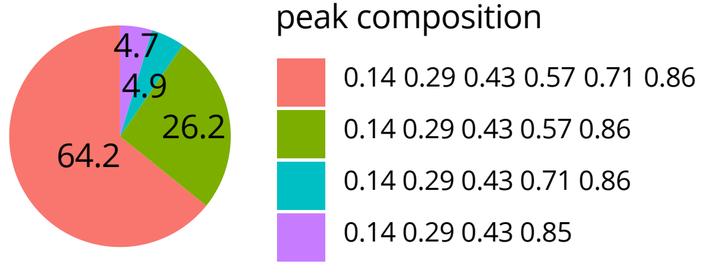
complex state 6:3



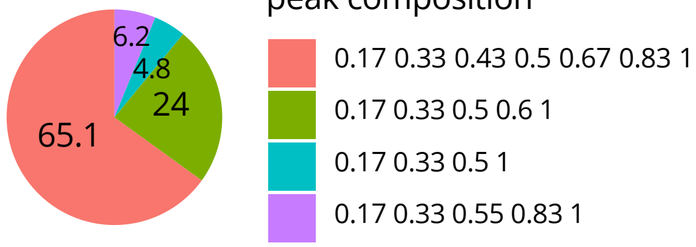
complex state 6:2



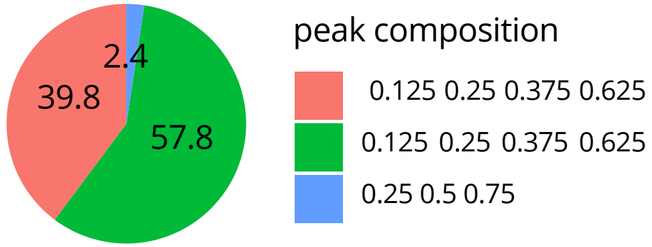
complex state 6:1



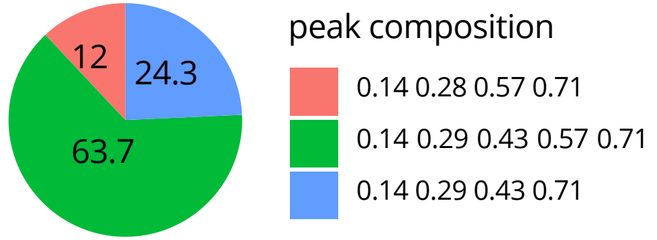
complex state 6:0



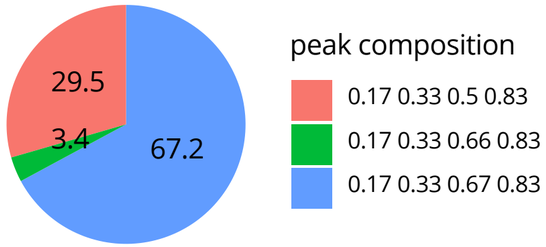
complex state 5:3



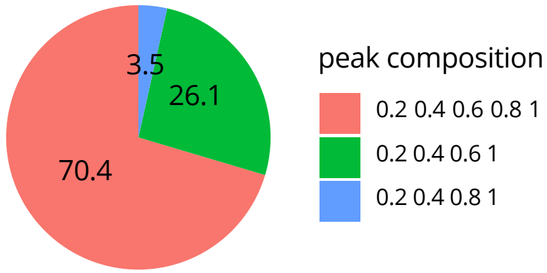
complex state 5:2



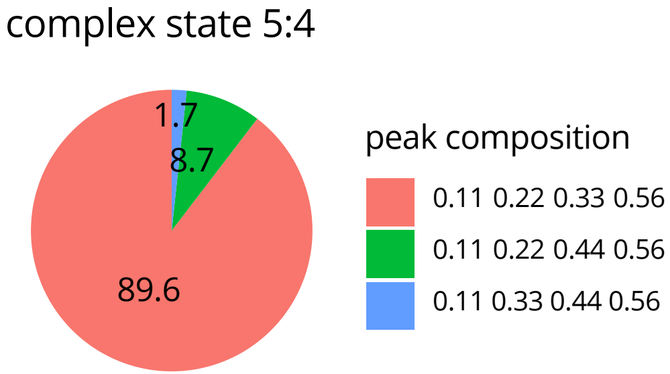
complex state 5:1



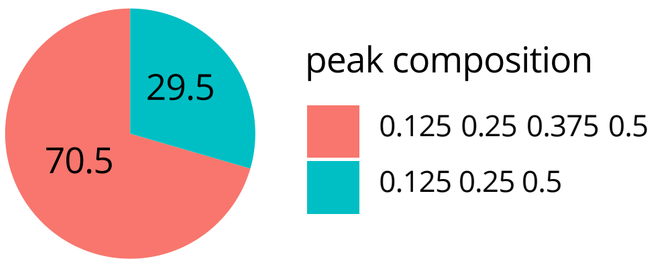
complex state 5:0



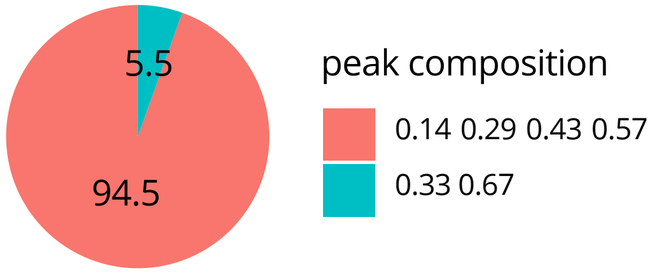
complex state 5:4



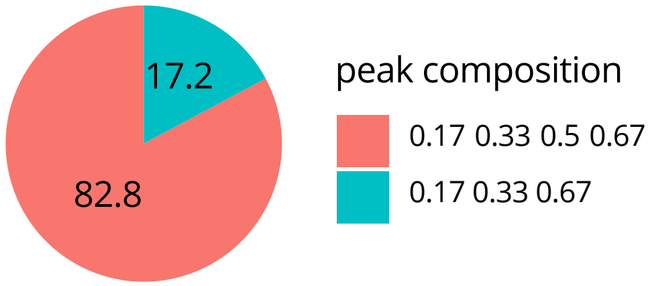
complex state 4:4



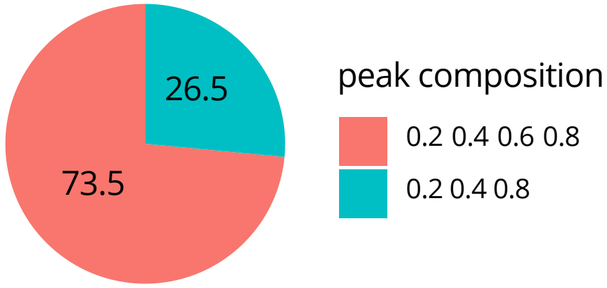
complex state 4:3



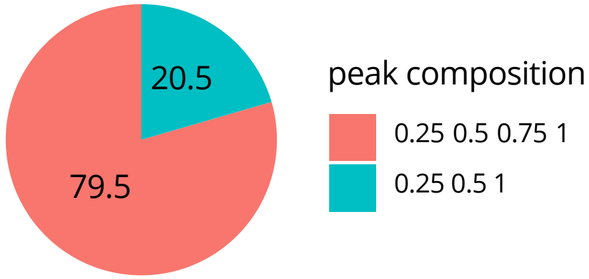
complex state 4:2



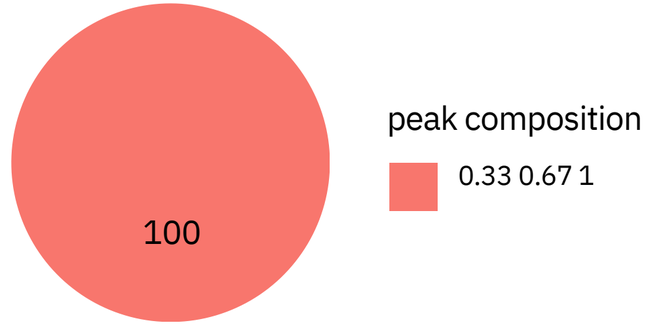
complex state 4:1



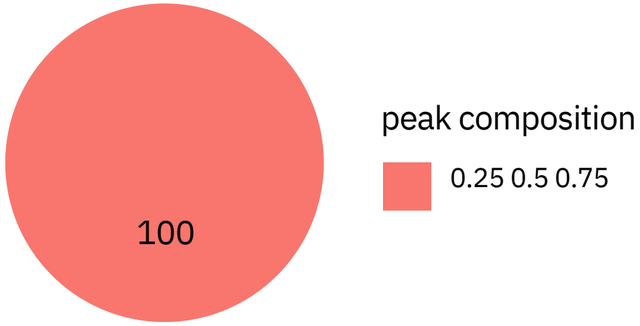
complex state 4:0



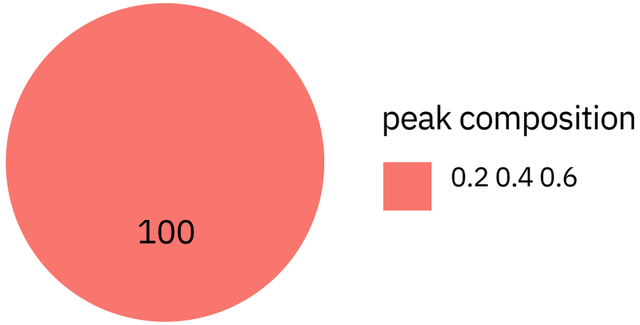
complex stat 3:0



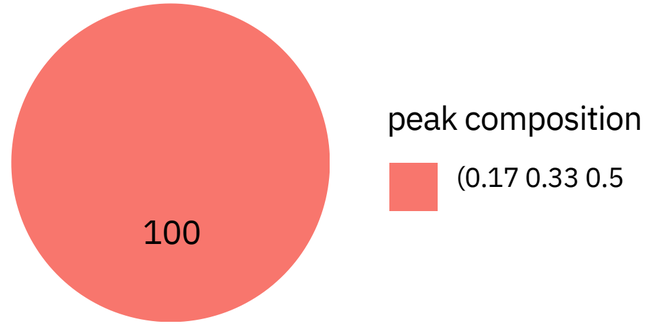
complex stat 3:1

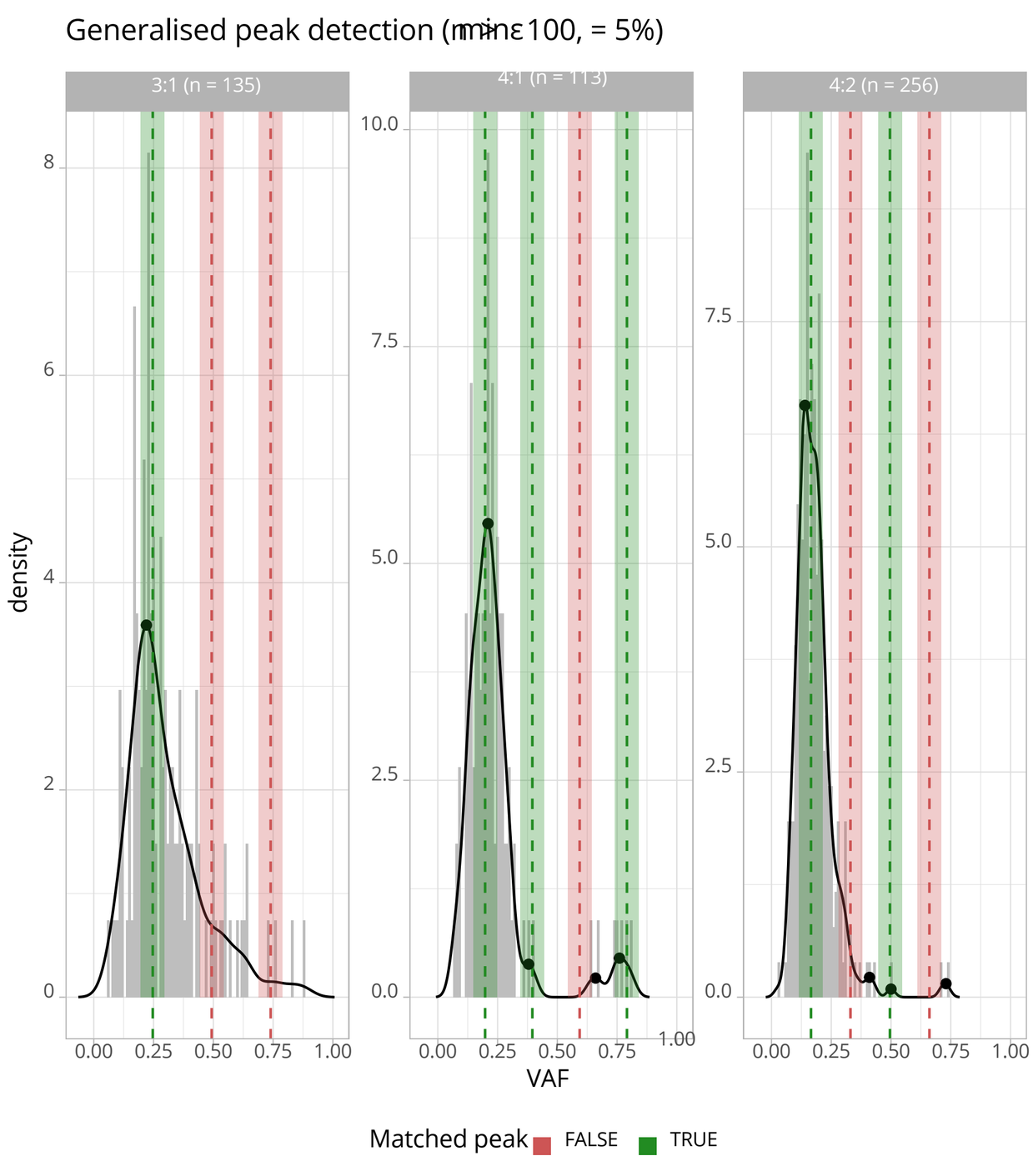


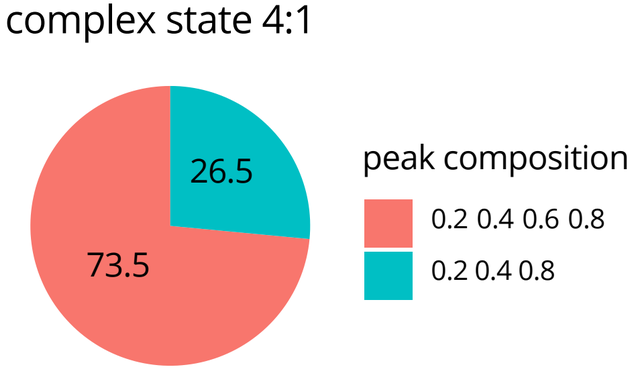
complex stat 3:2



complex stat 3:3





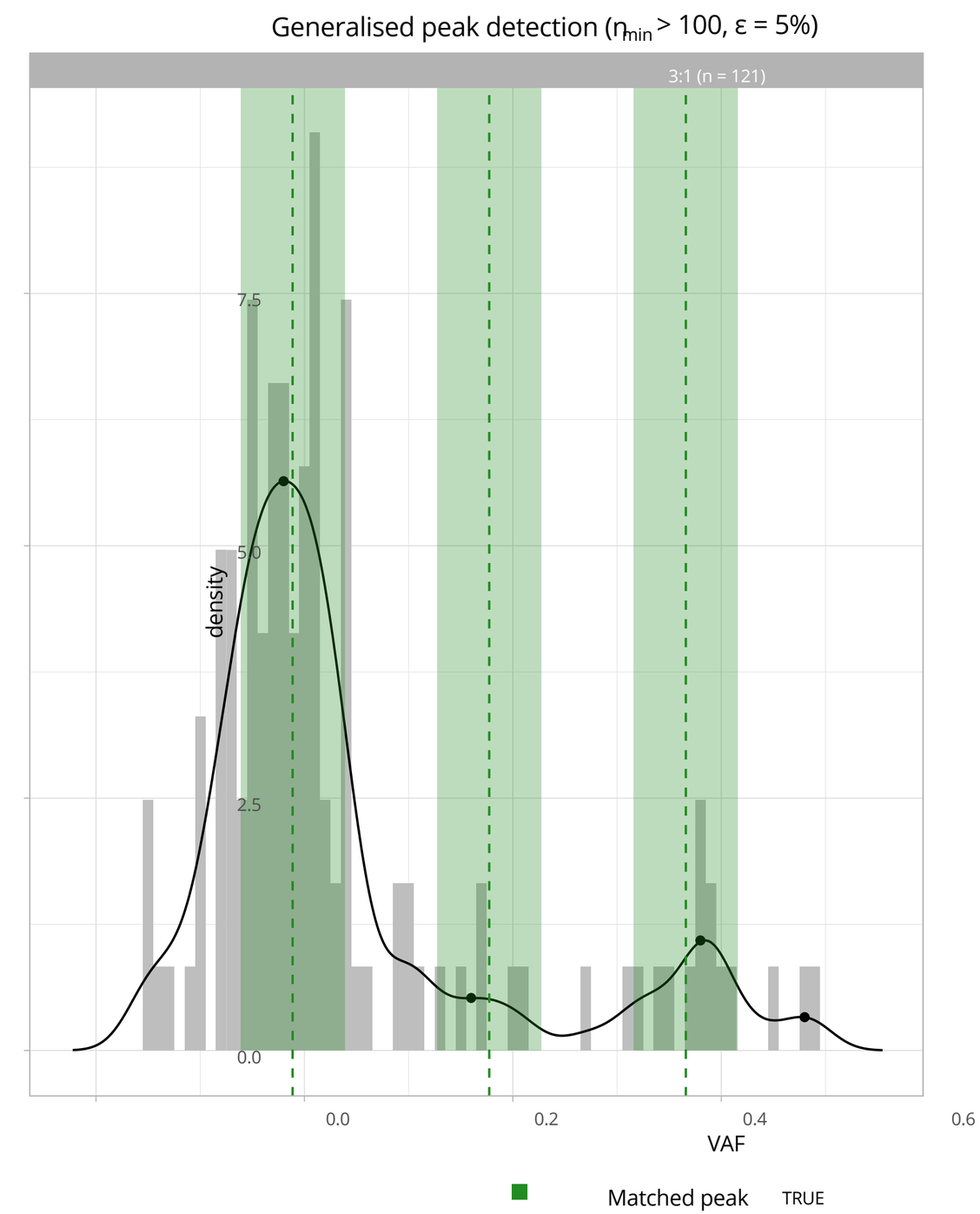


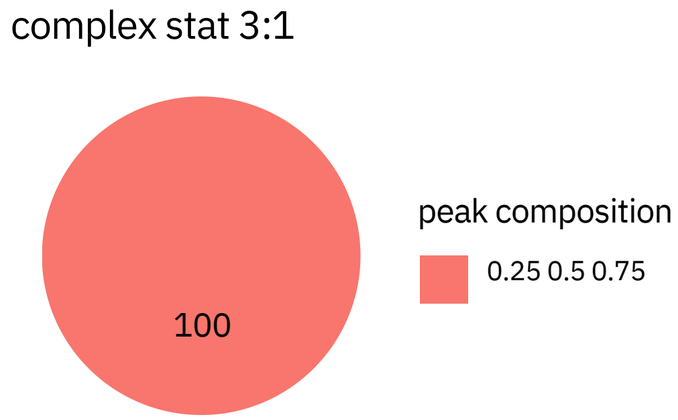
1. A1B1/A1A2B1B2/A1B1B2B3/A1A2B2B3B4B5/A1B2B3B4B5

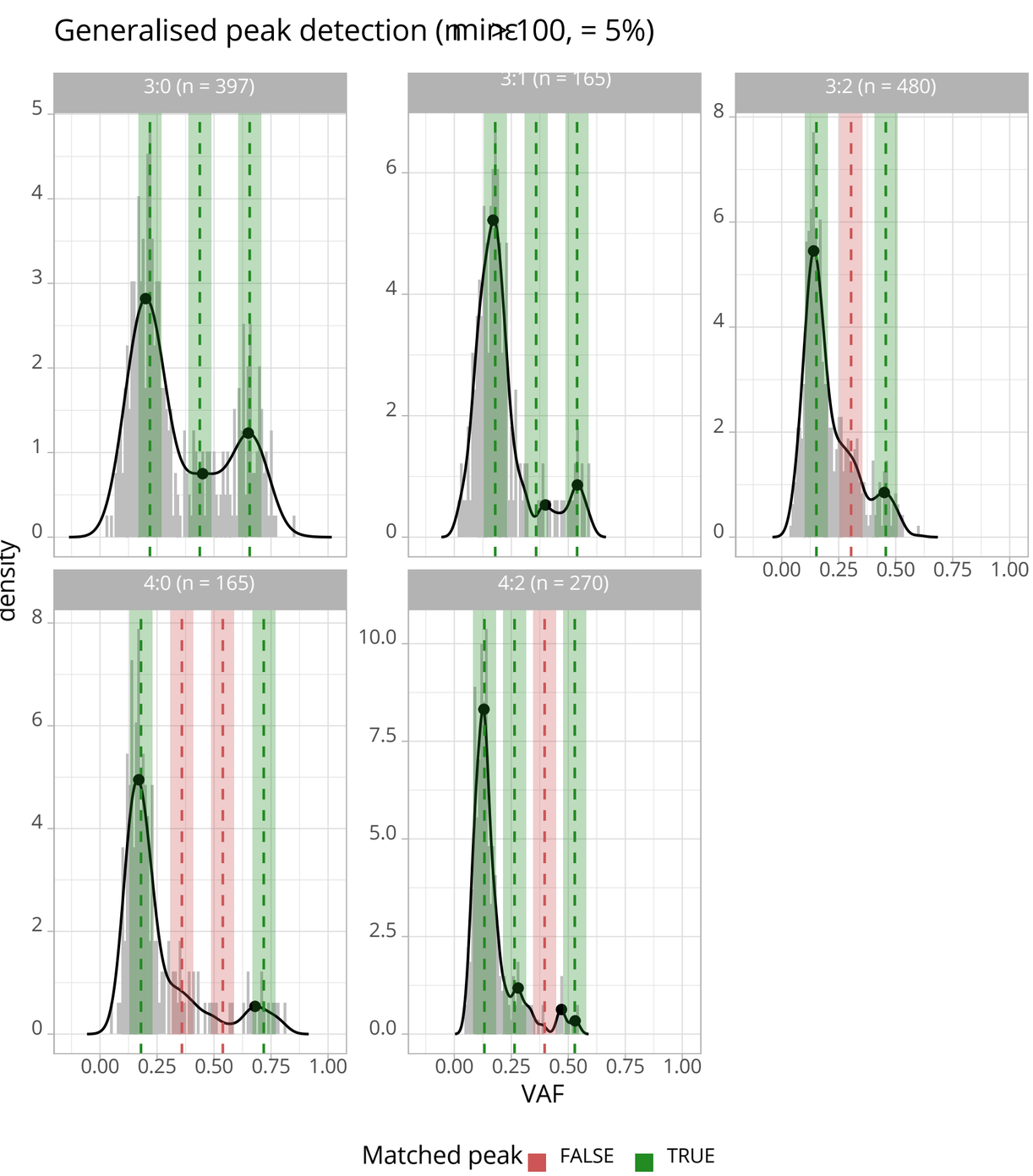
2. A1B1/A1A2B1B2/A2B1B2B3/A2B1B2/A2A3B1B2B4/A2A3B1B2B3B4/A2B1B2B3B4

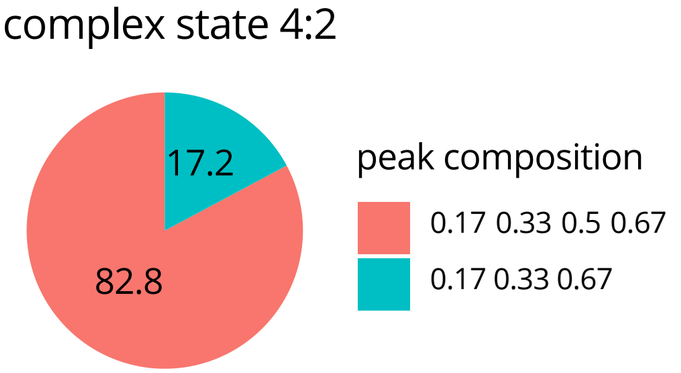
3. A1B1/A1A2B1/A1A2A4B1B2/A1A2A3A4B2

A complex state's evolution can be inferred from its VAF.


Generalised peak detection (n_{min} > 100, ε = 5%)
3:1 (n = 121)
7.5
5.0
2.5
0.0
density
0.0
0.2
0.4
0.6
VAF
Matched peak
TRUE


complex stat 3:1
100
peak composition
0.25 0.5 0.75





A1B1/A1A2B1B2/A1A2B1/A1A3A4B1B2/A1A3A4B2/A3A4A5A6B2B3

A1B1/A1A2B1/A1A3A4B1B2/A1A3A4A5B1/A1A2A3A4A5B1/A1A2A3A5B1B2

Thank you for your attention