VAF deconvolution by karyotype

Major allele · minor allele · 2:0 · 1:0 · 1:1 · 2:1

Ploidy 2; Purity 0.74; n = 1927 mutations in 31 segments; 10 fragmented arms

1:0 (n = 90, 4.7%)   **1:1** (n = 270, 14%)   **2:0** (n = 630, 32.7%)   **2:1** (n = 936, 48.6%)

1:0 (closest)   1:1 (closest)   2:0 (closest)   2:1 (closest)

QC FAIL p_{PASS} = 0.1   QC PASS p_{PASS} = 0.   QC PASS p_{PASS} = 0.   QC PASS p_{PASS} = 0.

n = 90; Tail 27.7%, C1 7:   n = 270; Tail 25.5%, C1 :   n = 630; Tail 28.4%, C1 :   n = 936; Tail 0%, C2 10.:

Cluster ■ C1 ■ Tail   Cluster ■ C1 ■ Tail   Cluster ■ C1 ■ Tail   Cluster ■ C1 ■ C2

MM (61 steps; ε = 1e−09), z_{nk} > 0   MM (31 steps; ε = 2e−05), z_{nk} > 0   MM (29 steps; ε = 3e−05), z_{nk} > 0   MM (46 steps; ε = 2e−05), z_{nk} > 0

n = 68, Bin 1 80%, Bin   n = 207, Bin 1 100%   n = 480, BBin 1 100%   n = 936, BBin 1 100%

Cluster ■ Bin 1 ■ Bin 2   Cluster ■ Bin 1   Cluster ■ BBin 1   Cluster ■ BBin 1

2021−01−31 17:14:51. evoverse pipeline for deconvolution from raw VAF and karyotypes: with fits TRUE