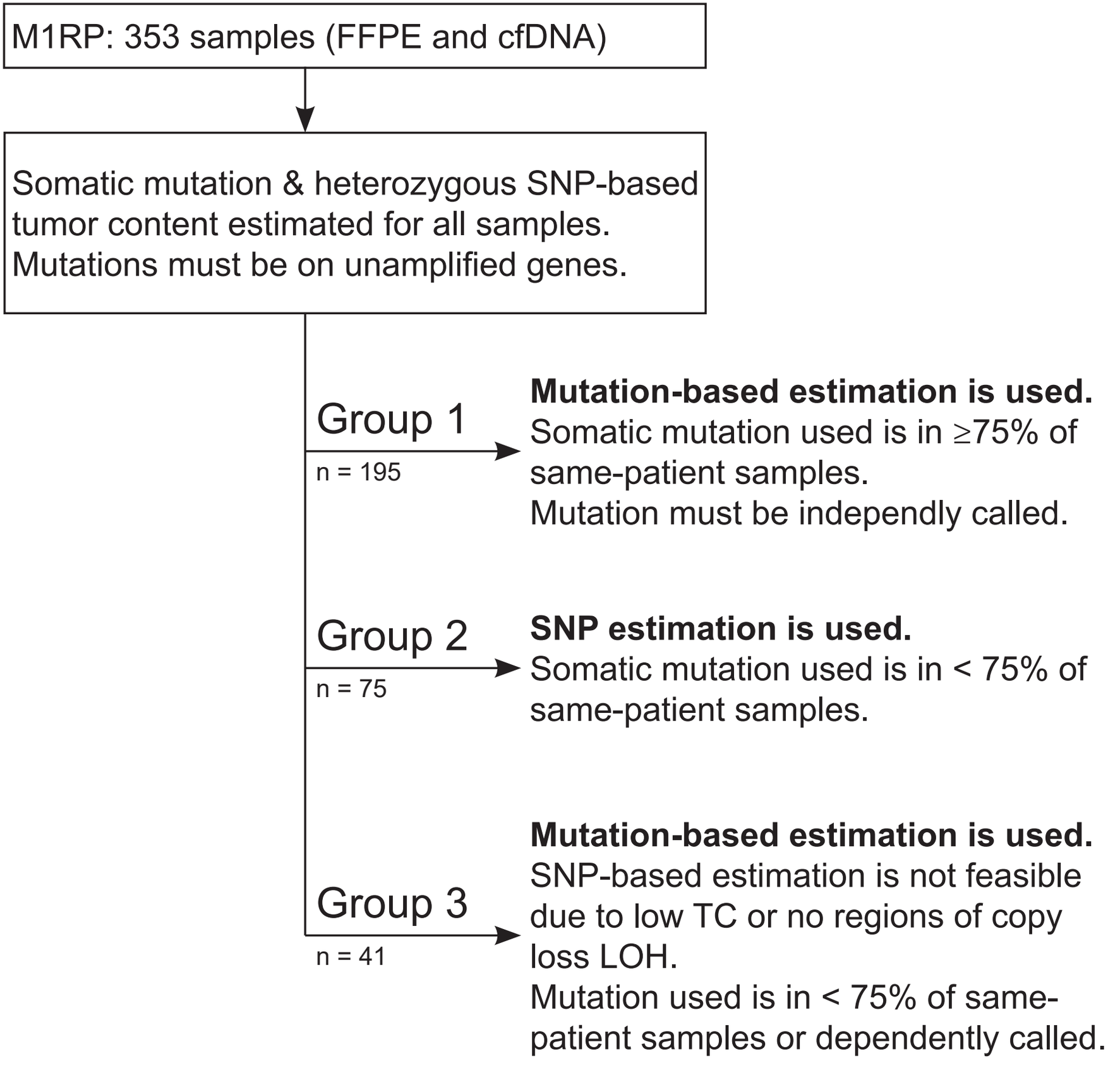
M1RP: 353 samples (FFPE and cfDNA)
Somatic mutation & heterozygous SNP-based tumor content estimated for all samples.
Mutations must be on unamplified genes.
Group 1
n = 195
Mutation-based estimation is used.
Somatic mutation used is in ≥75% of same-patient samples.
Mutation must be independly called.
Group 2
n = 75
SNP estimation is used.
Somatic mutation used is in < 75% of same-patient samples.
Group 3
n = 41
Mutation-based estimation is used.
SNP-based estimation is not feasible due to low TC or no regions of copy loss LOH.
Mutation used is in < 75% of same-patient samples or dependently called.
42 samples had no detectable tumor with any method