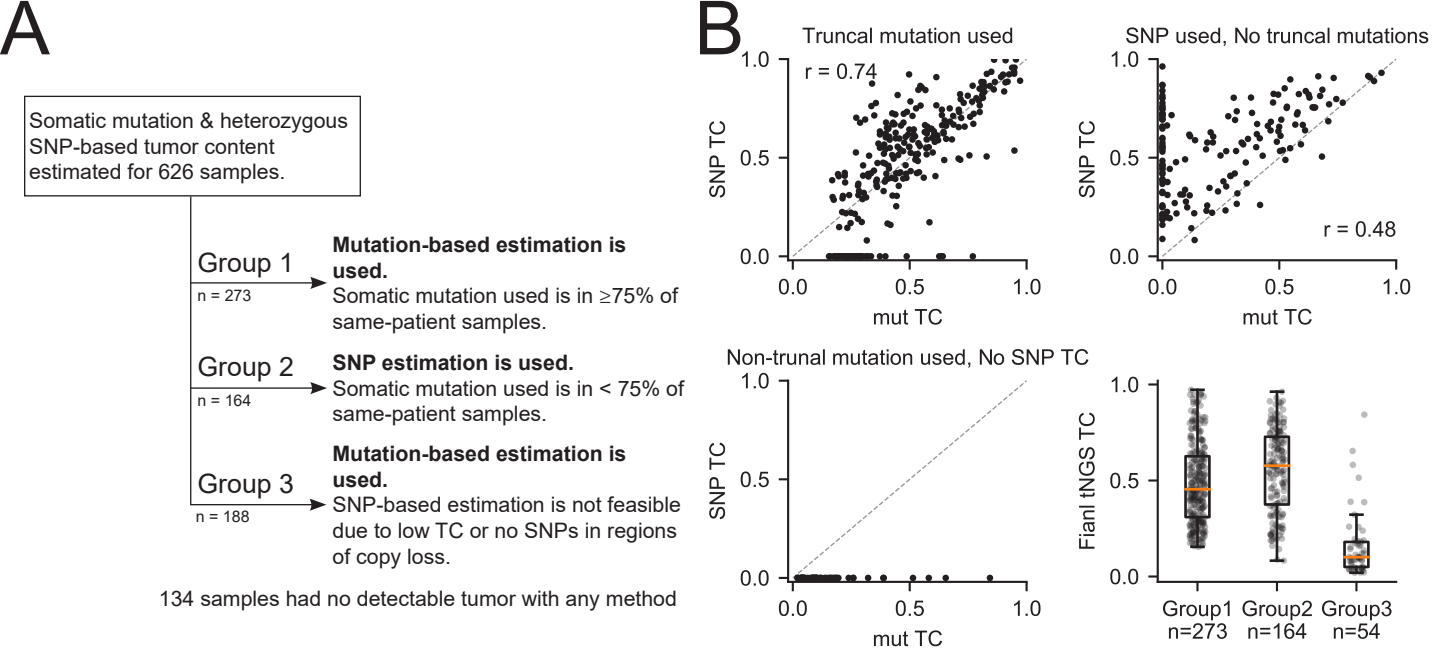
A
Somatic mutation & heterozygous SNP-based tumor content estimated for 626 samples.
Group 1
n = 273
Mutation-based estimation is used.
Somatic mutation used is in ≥75% of same-patient samples.
Group 2
n = 164
SNP estimation is used.
Somatic mutation used is in < 75% of same-patient samples.
Group 3
n = 188
Mutation-based estimation is used.
SNP-based estimation is not feasible due to low TC or no SNPs in regions of copy loss.
134 samples had no detectable tumor with any method
B
Truncal mutation used
r = 0.74
SNP TC
mut TC
SNP used, No truncal mutations
r = 0.48
Non-trunal mutation used, No SNP TC
Fianl tNGS TC
Group1 n=273
Group2 n=164
Group3 n=54