

FIG. 1

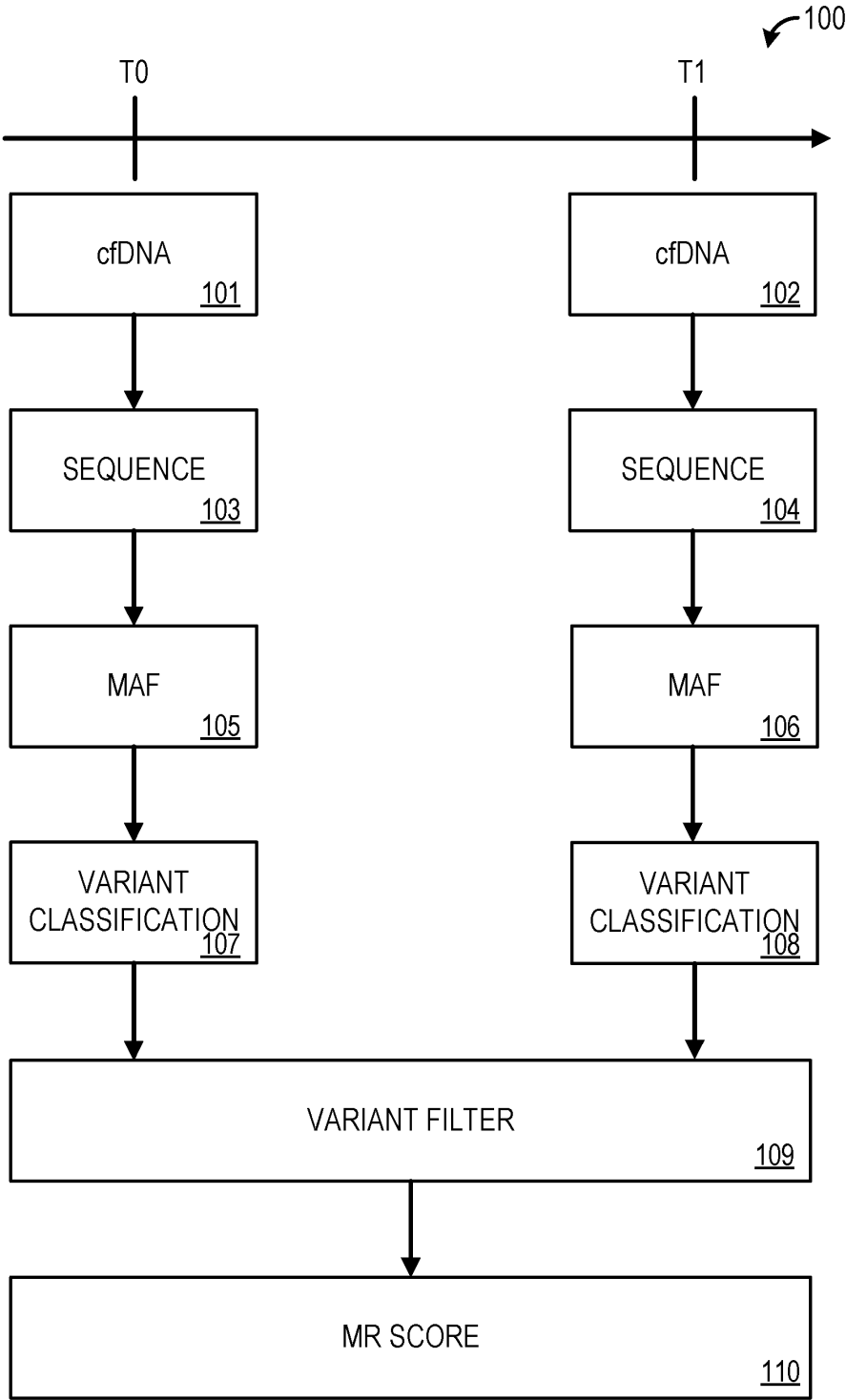


FIG. 2

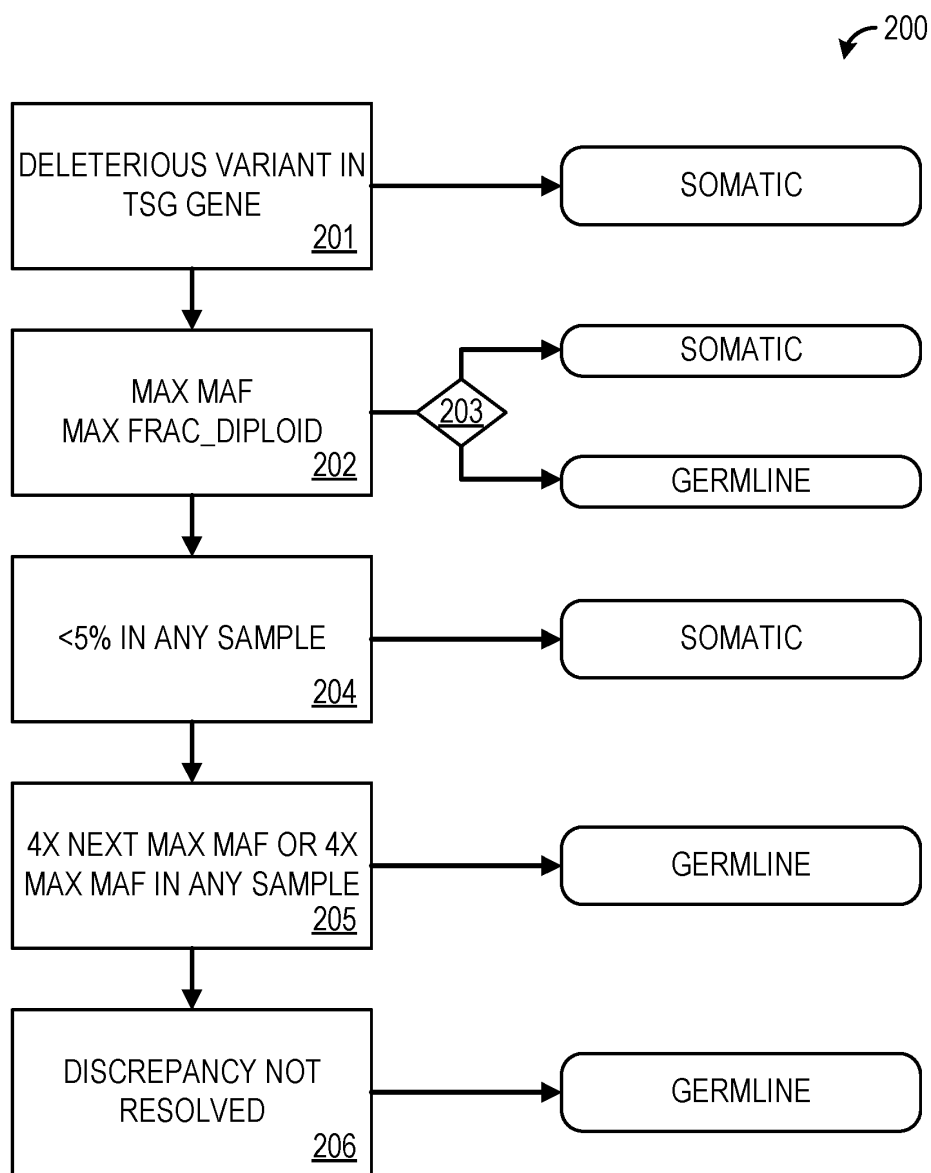
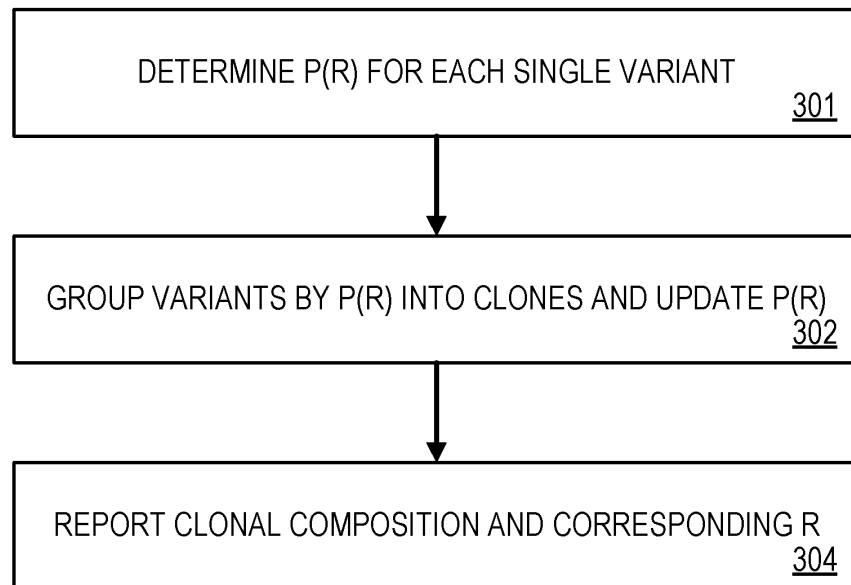


FIG. 3

300



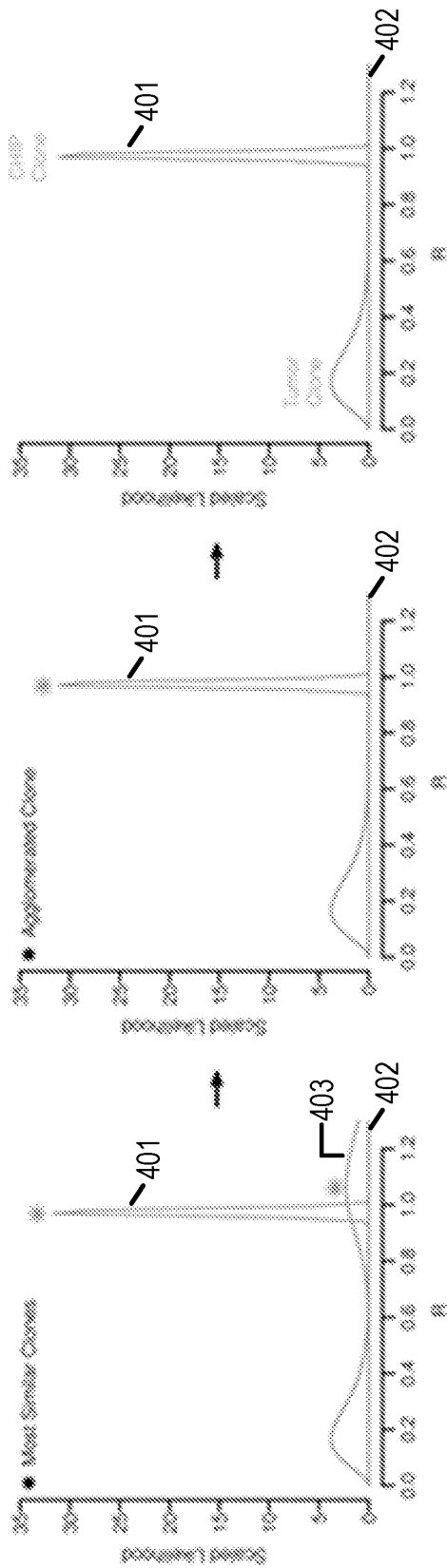


FIG. 4

FIG. 5

500

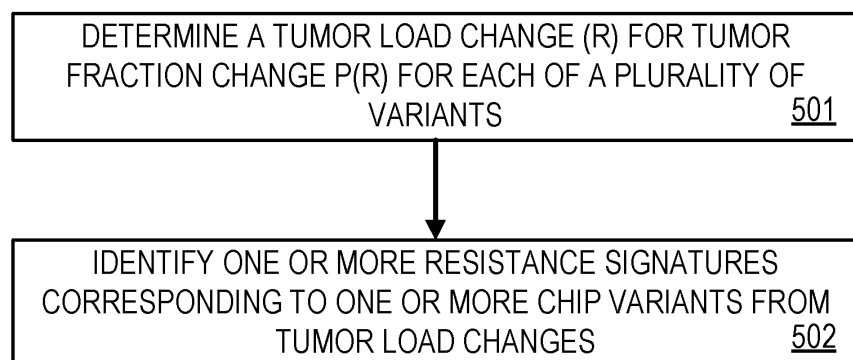


FIG. 6A

600

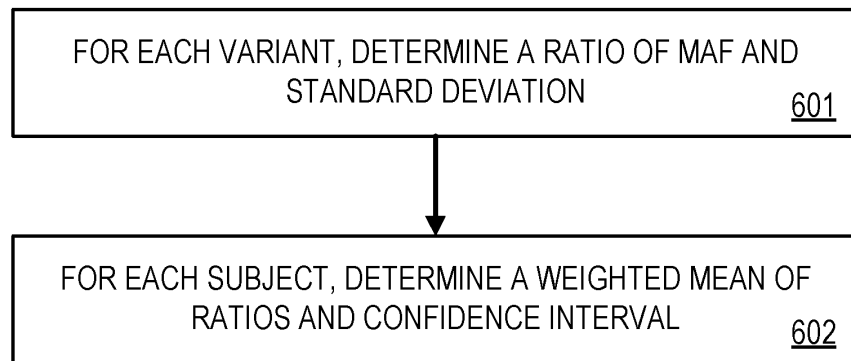


FIG. 6B

610

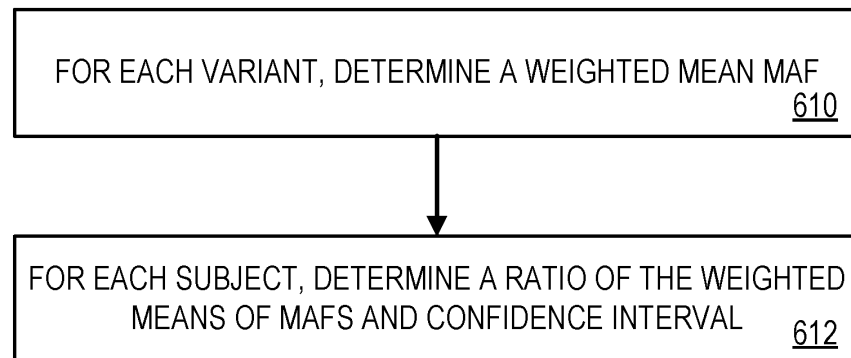


FIG. 7

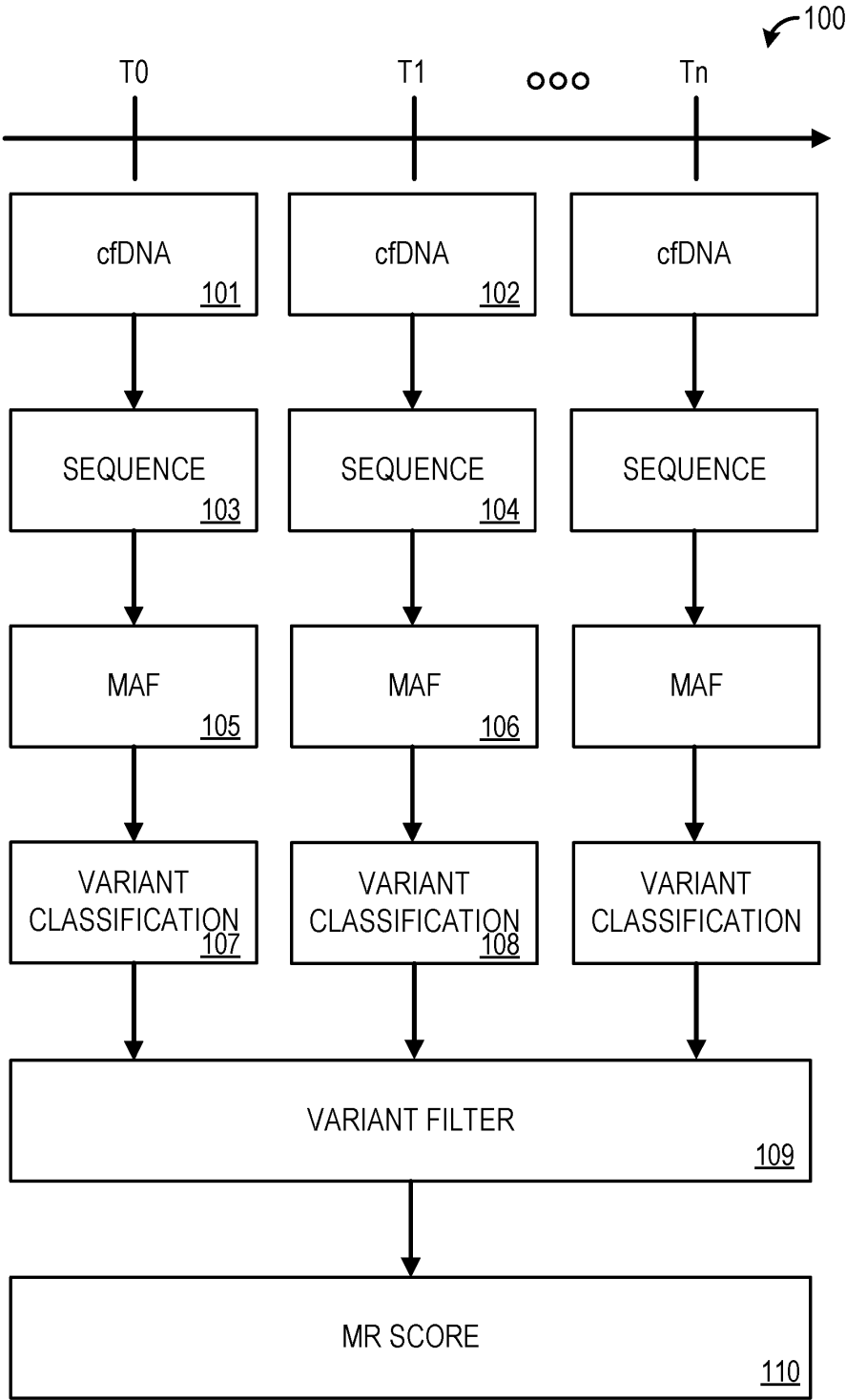


FIG. 8

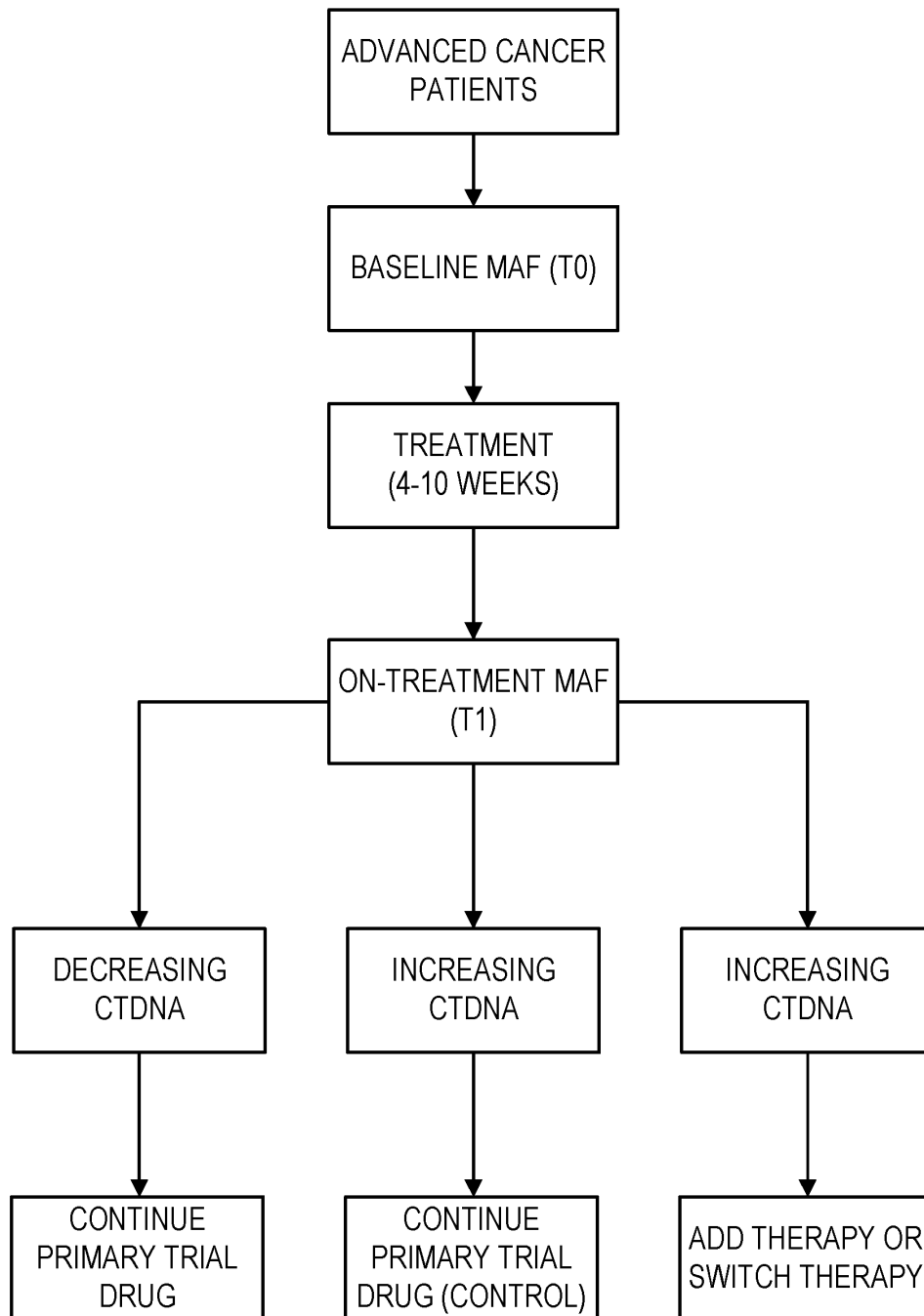


FIG. 9

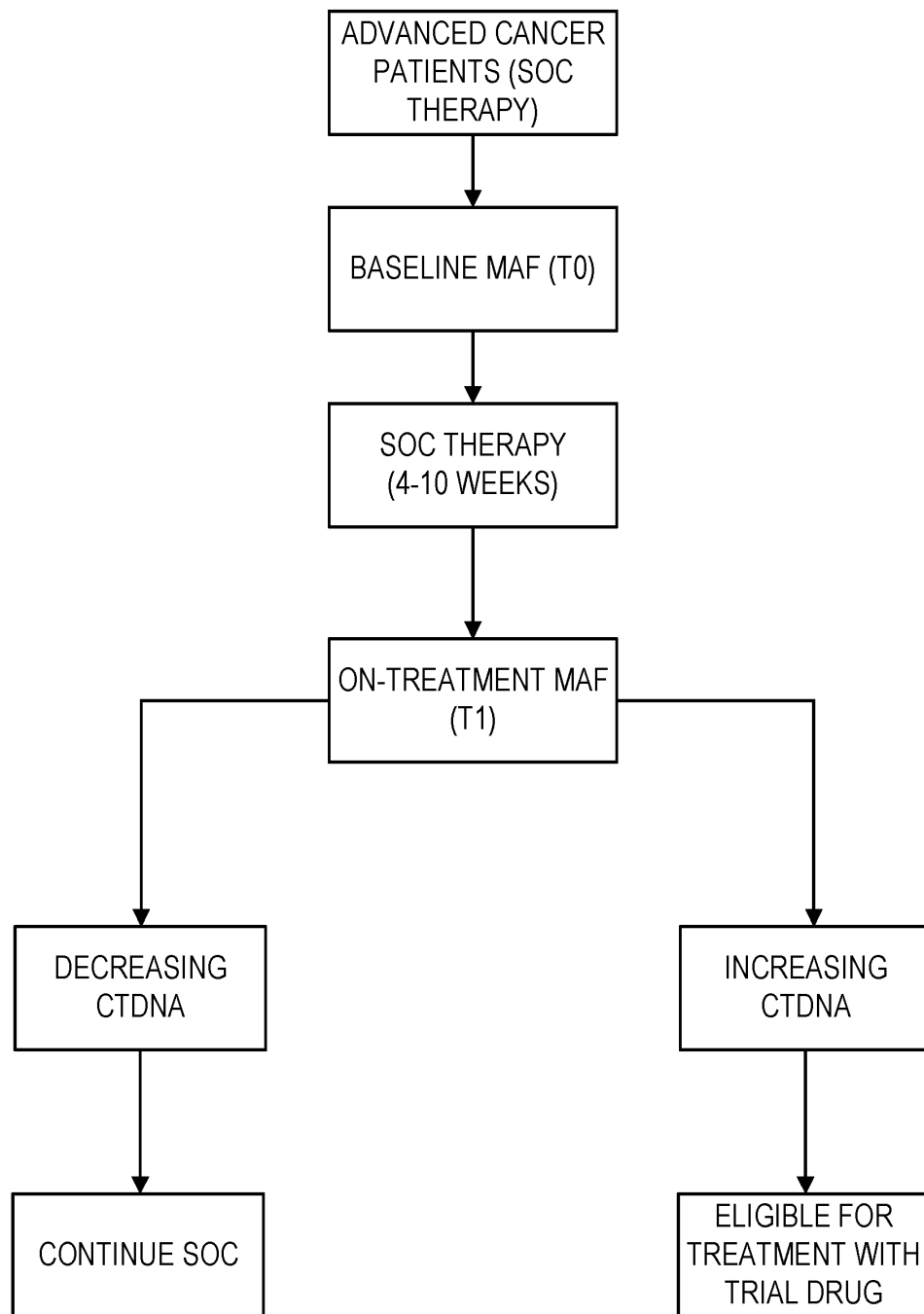


FIG. 10

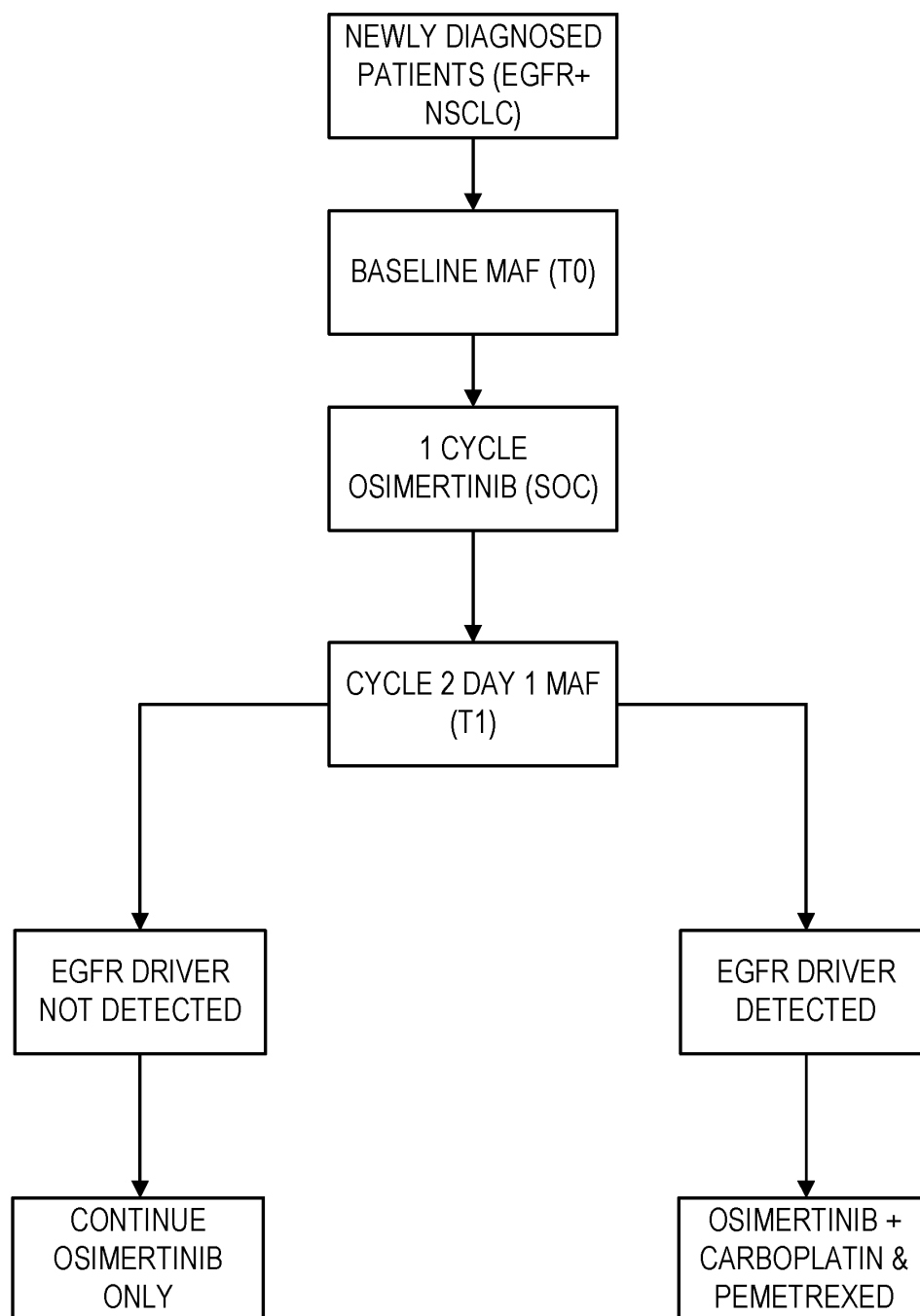


FIG. 11

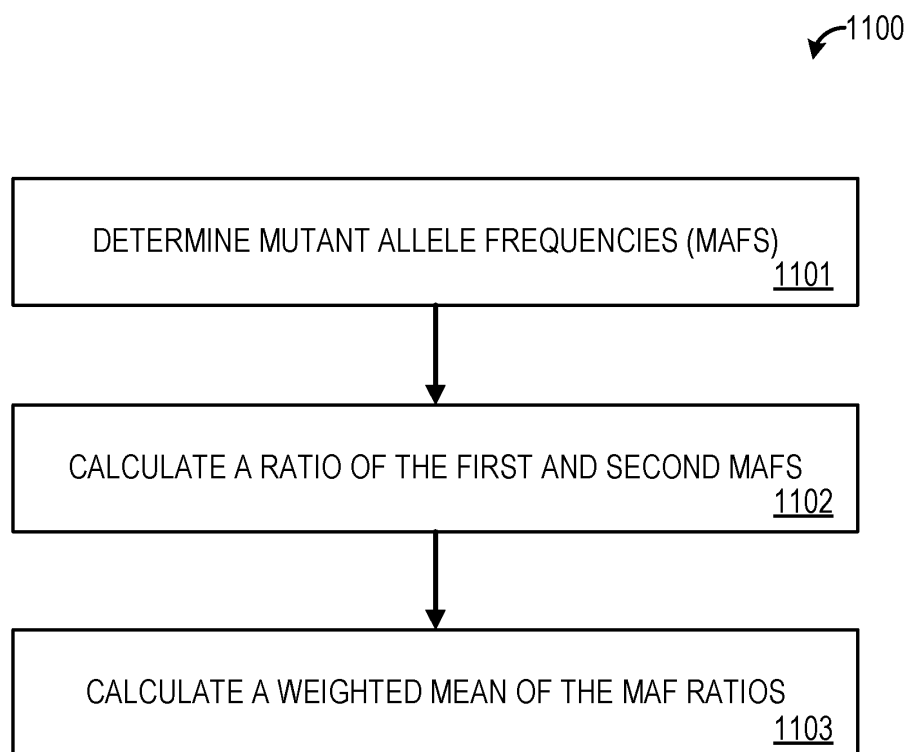


FIG. 12A

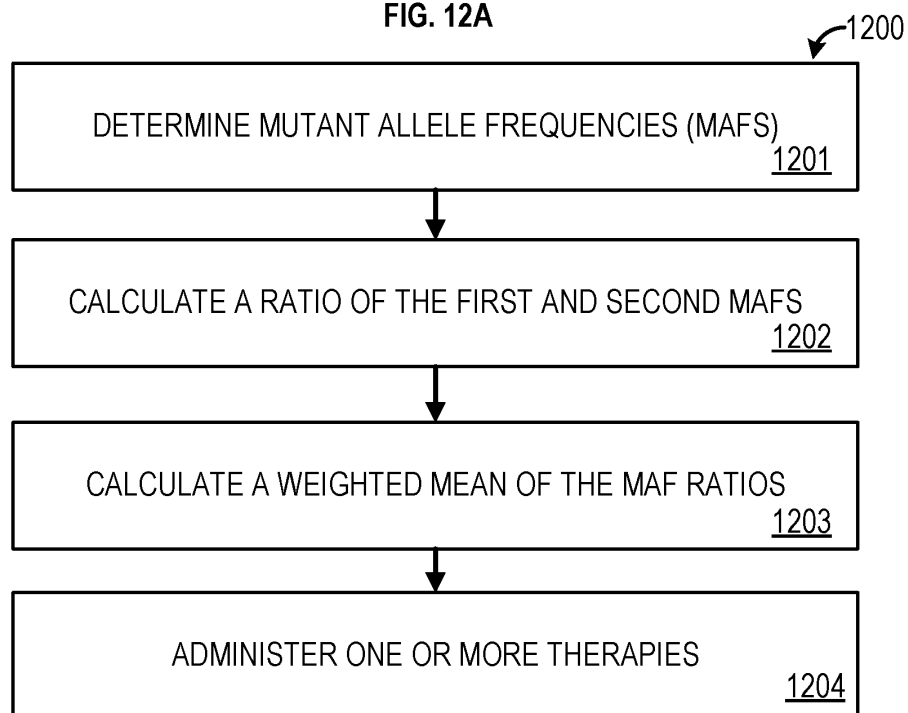


FIG. 12B

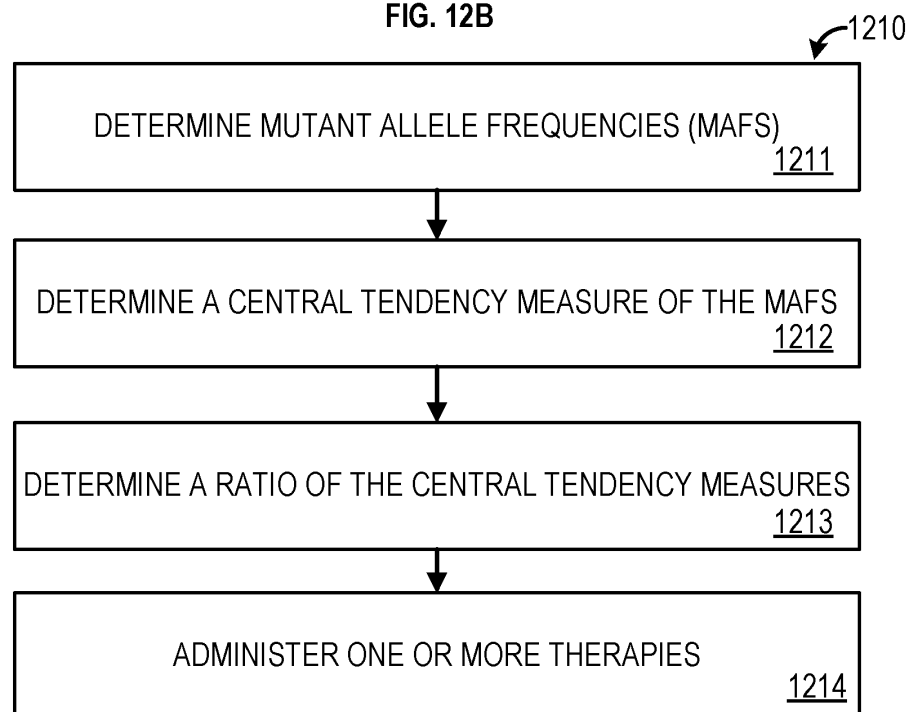


FIG. 13

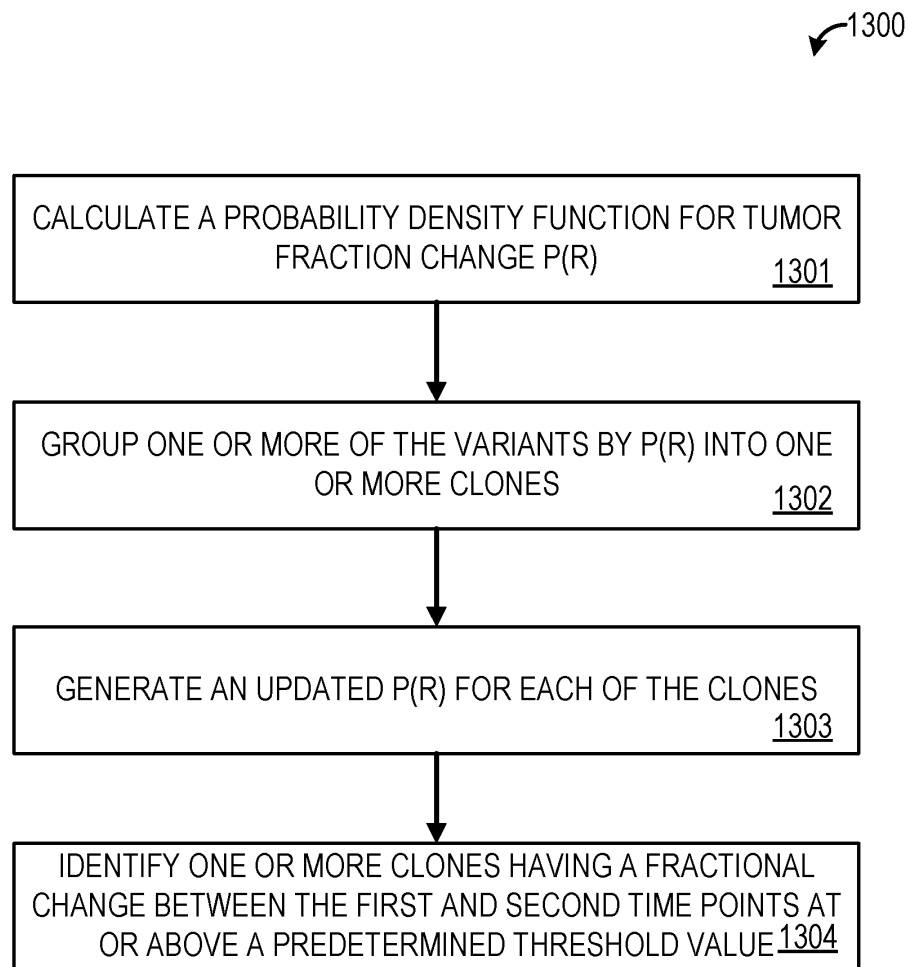


FIG. 14

1400

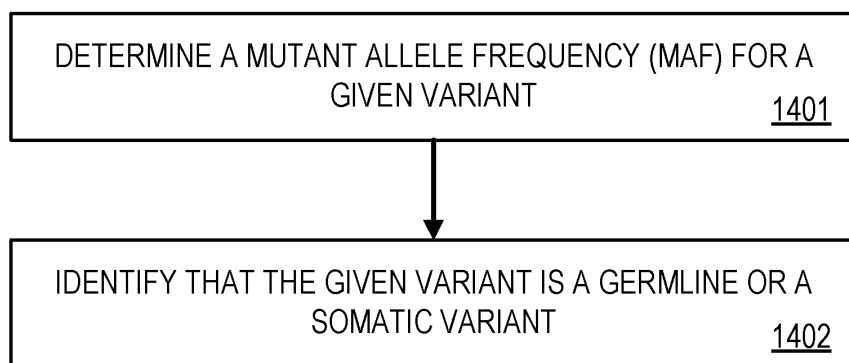


FIG. 15

1500

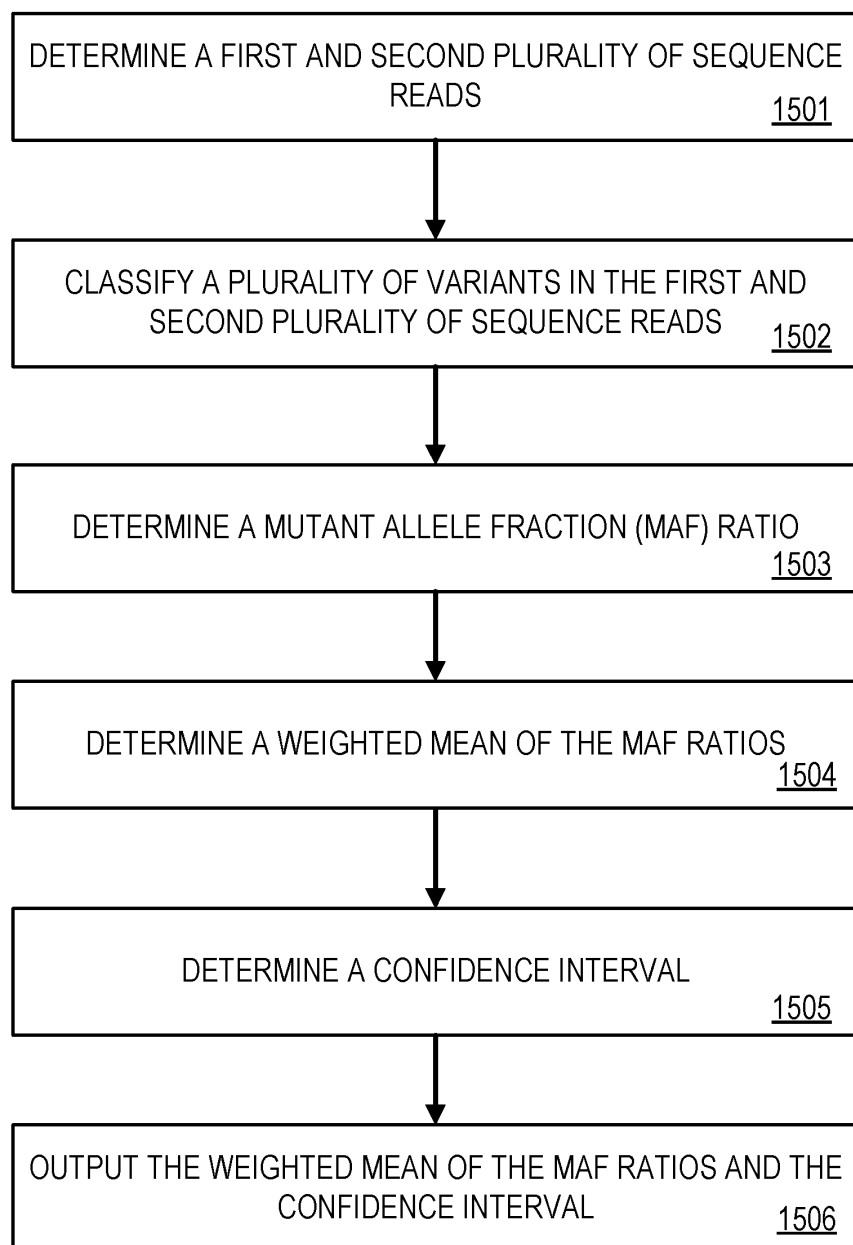


FIG. 16

1600

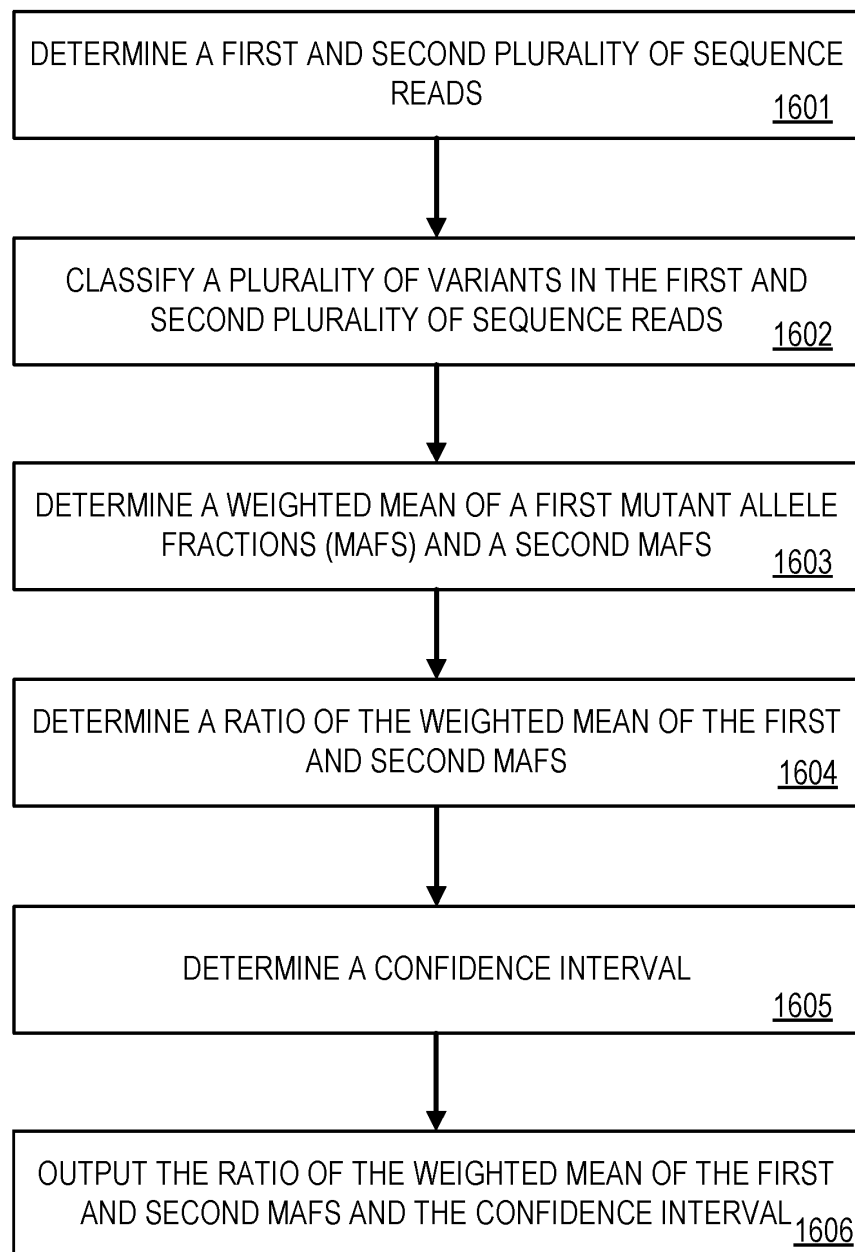


FIG. 17

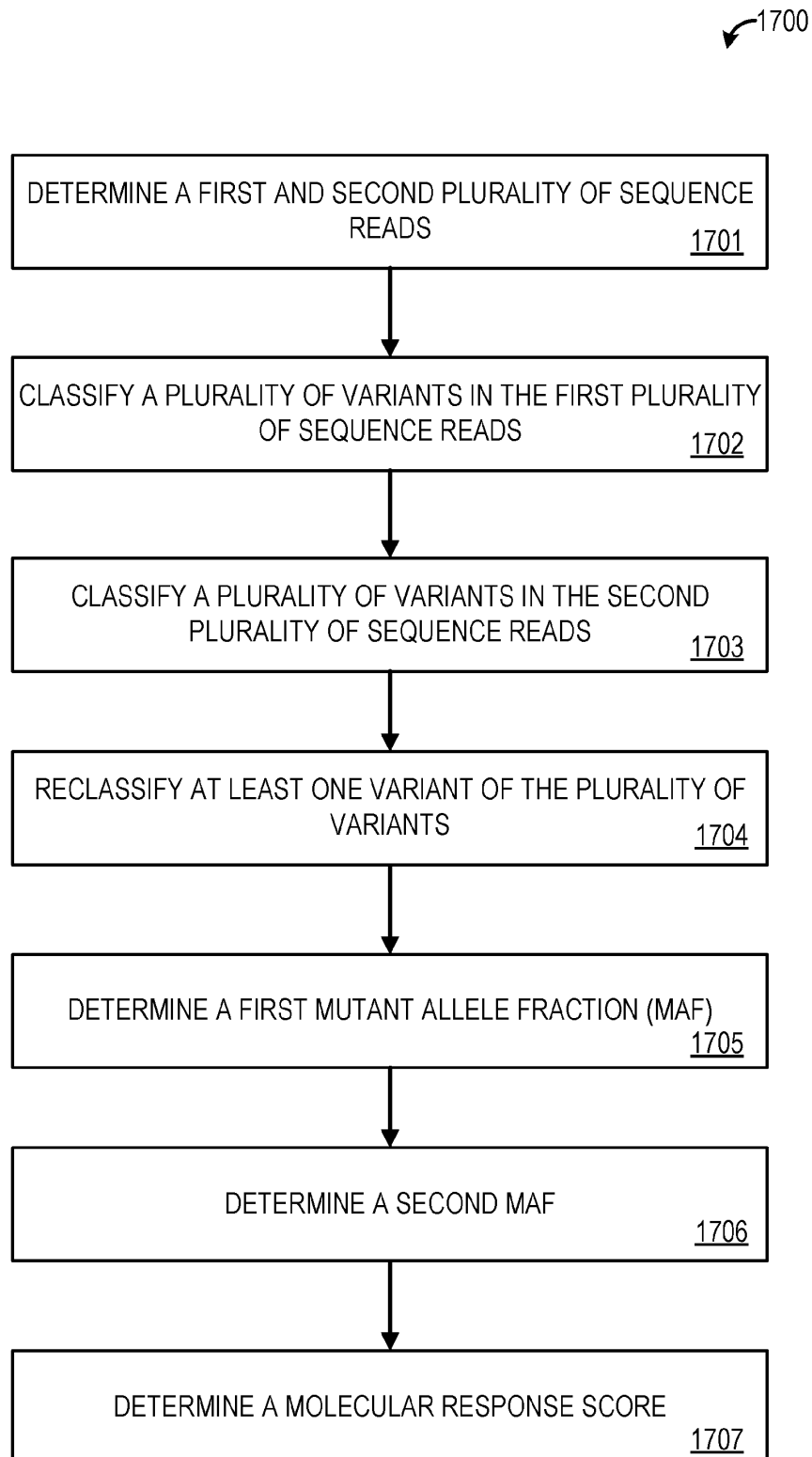


FIG. 18

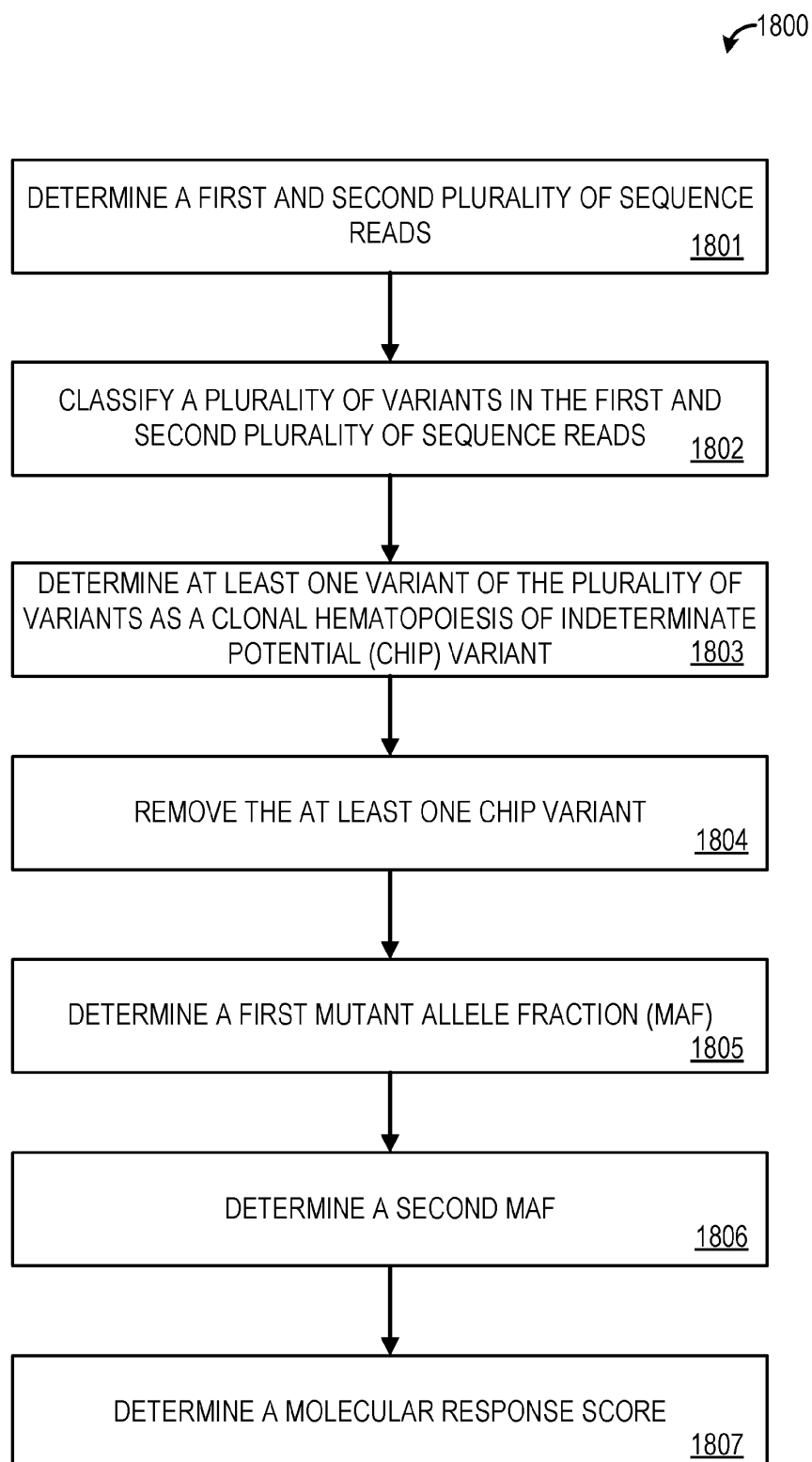


FIG. 19

1900

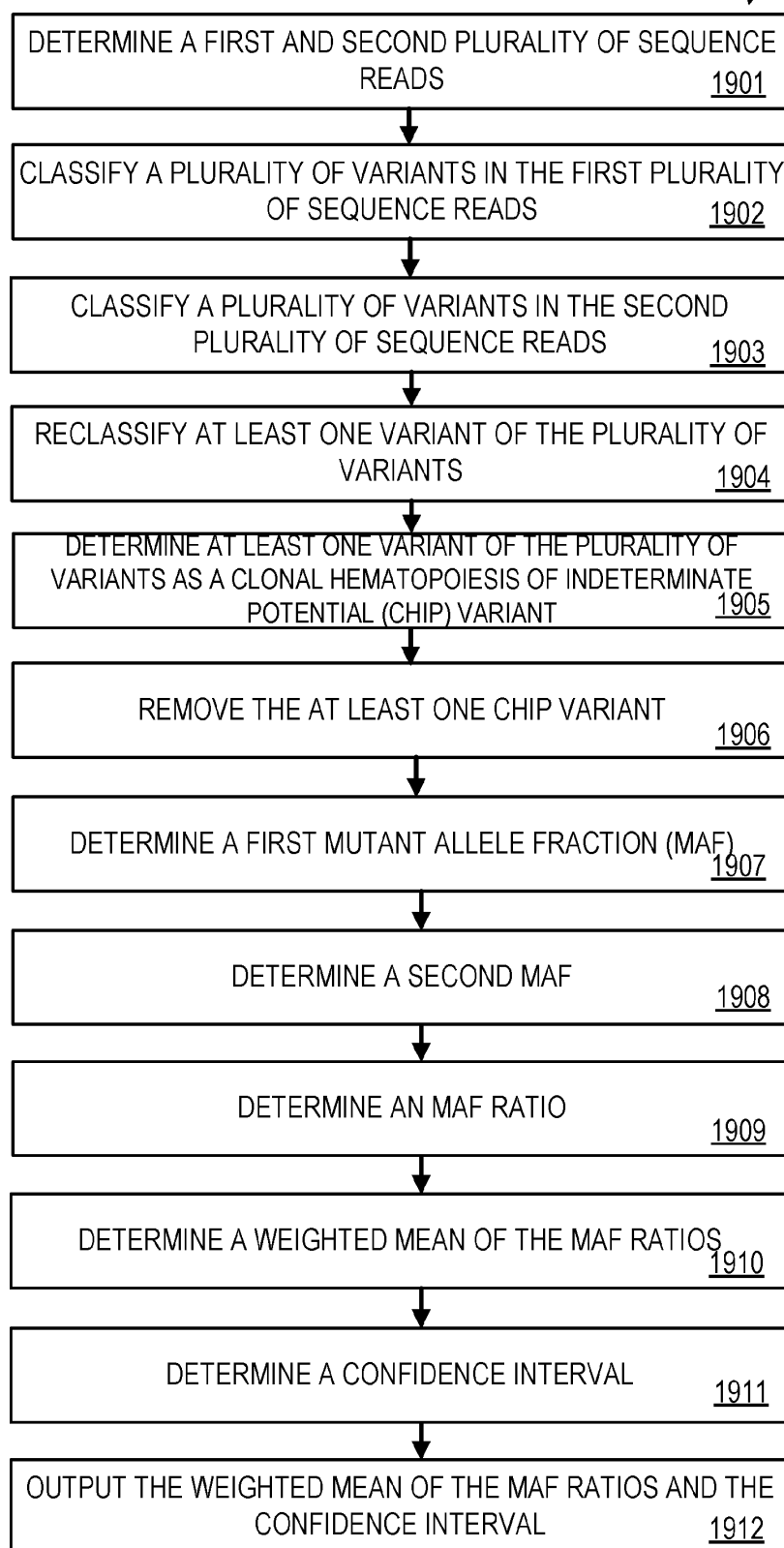


FIG. 20

2000

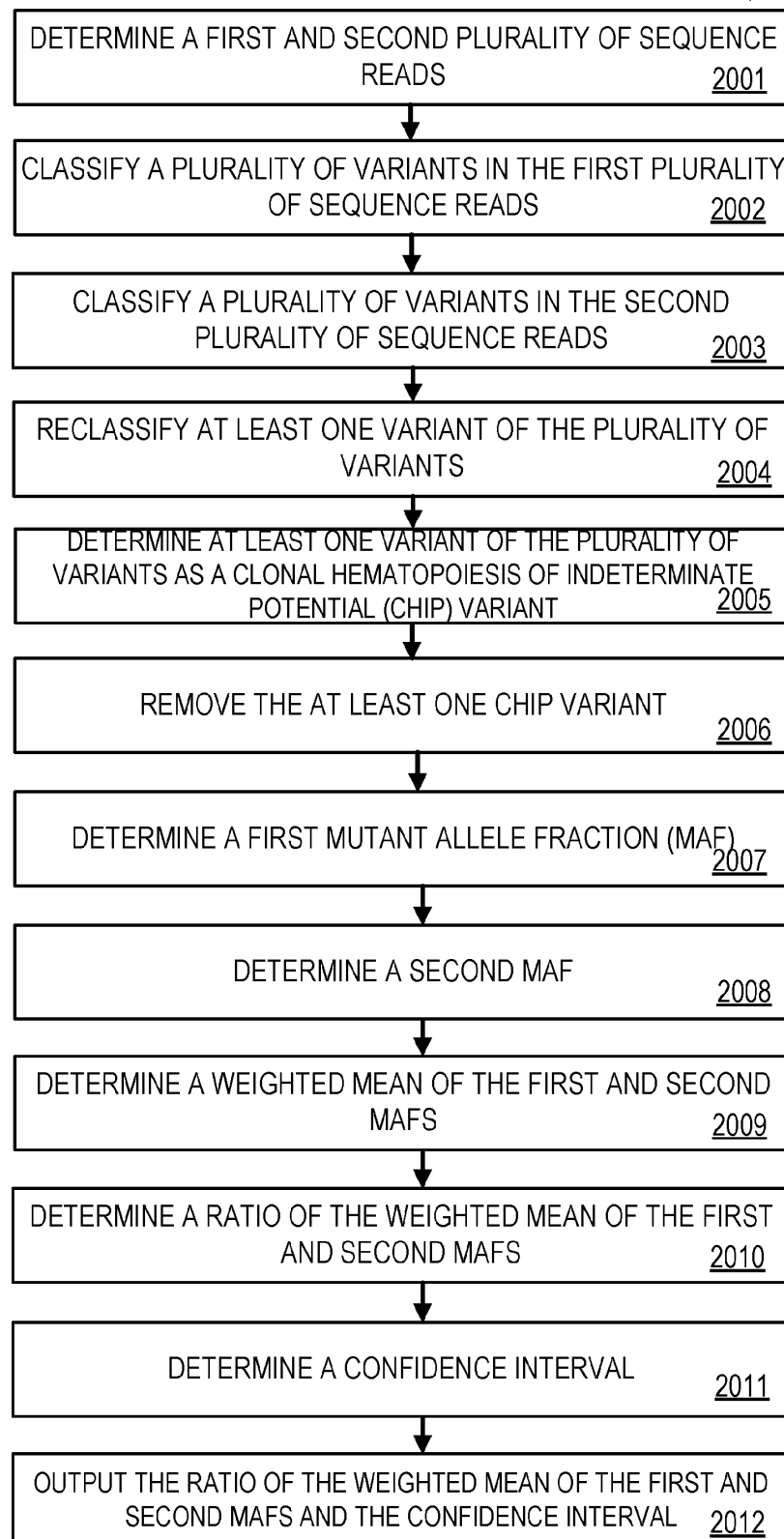
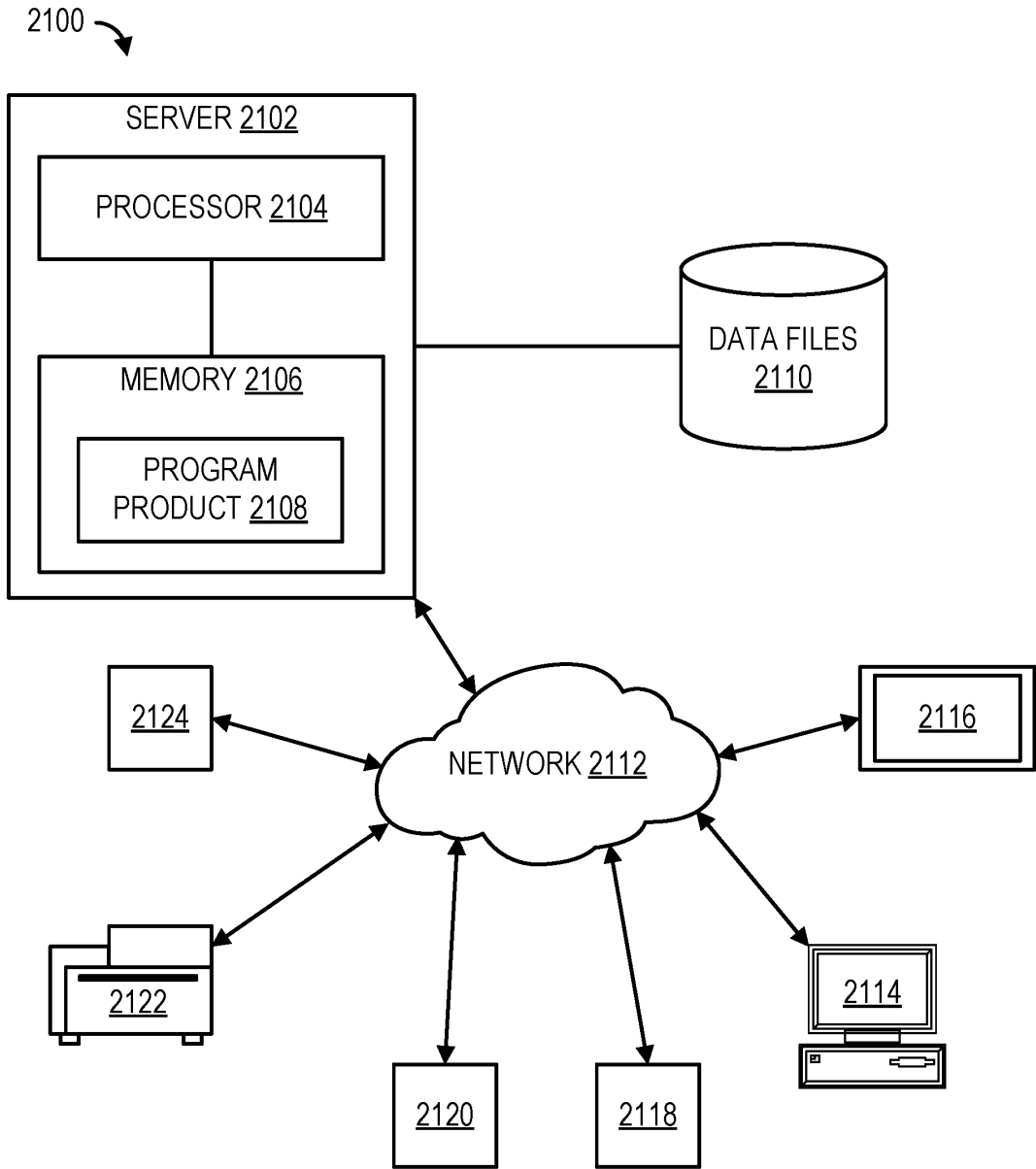


FIG. 21



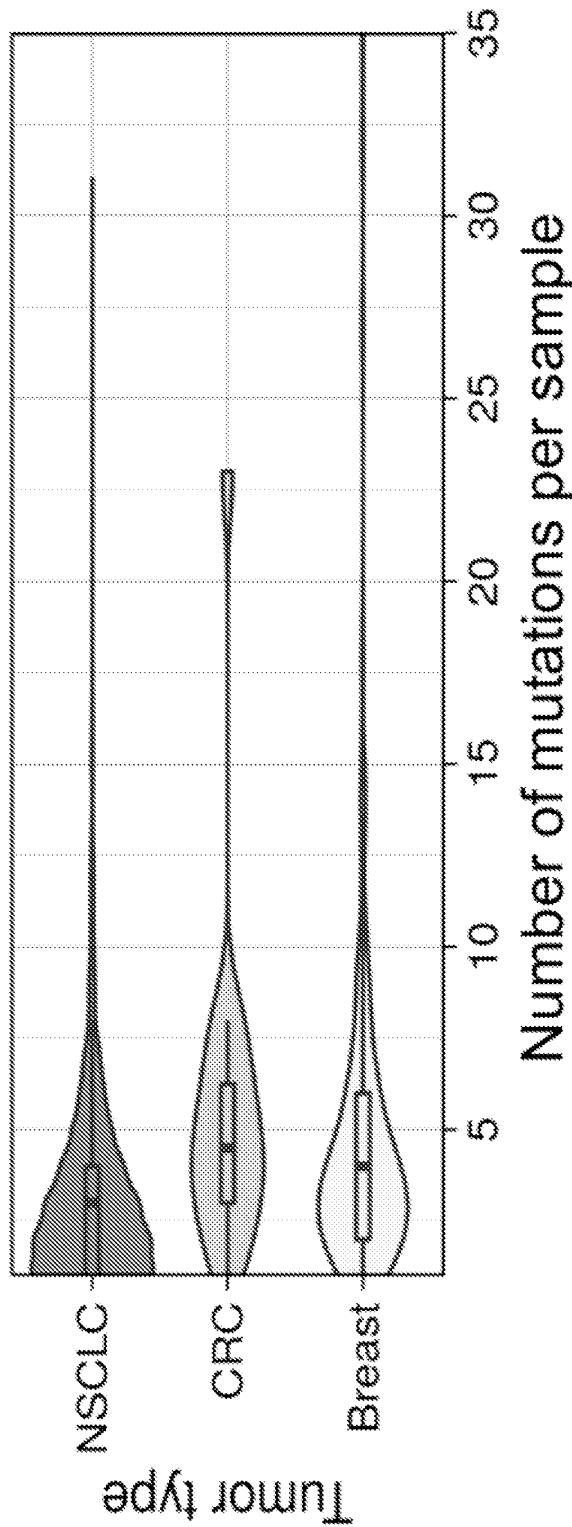
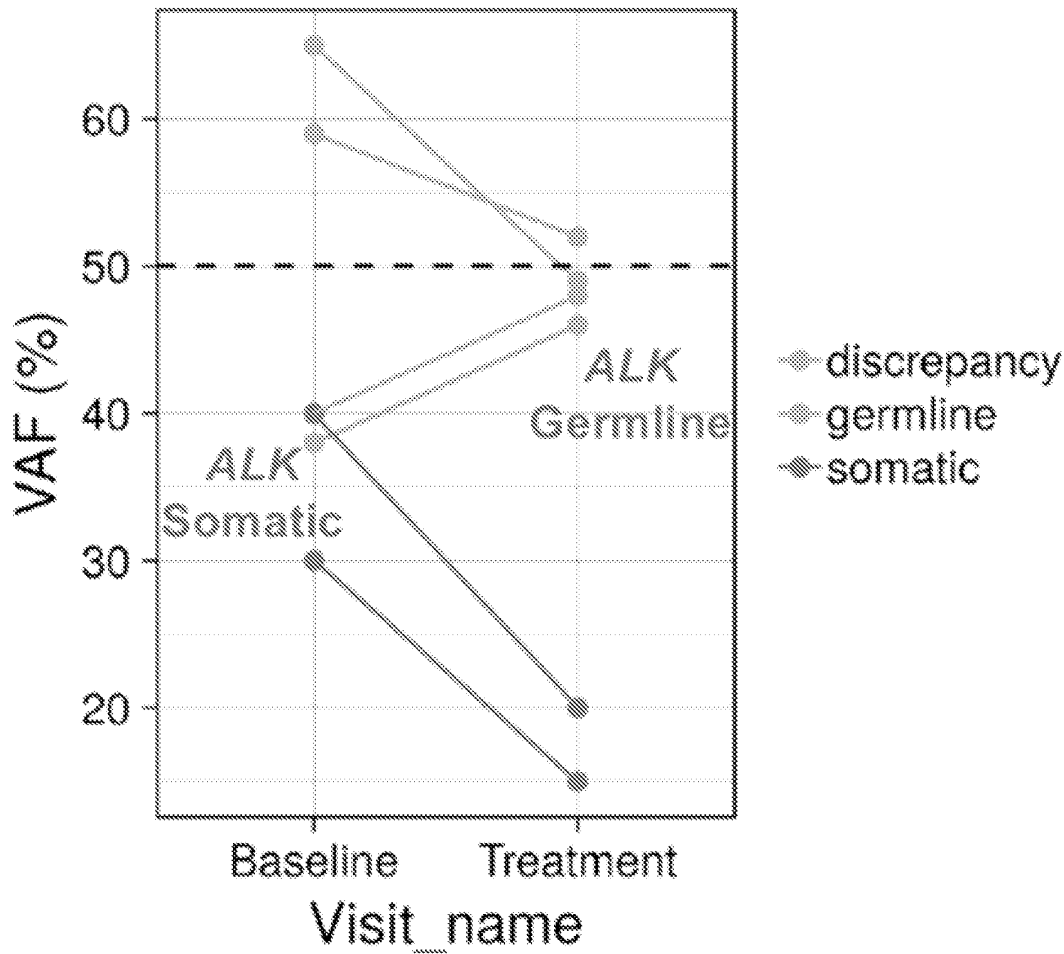


FIG. 22

FIG. 23



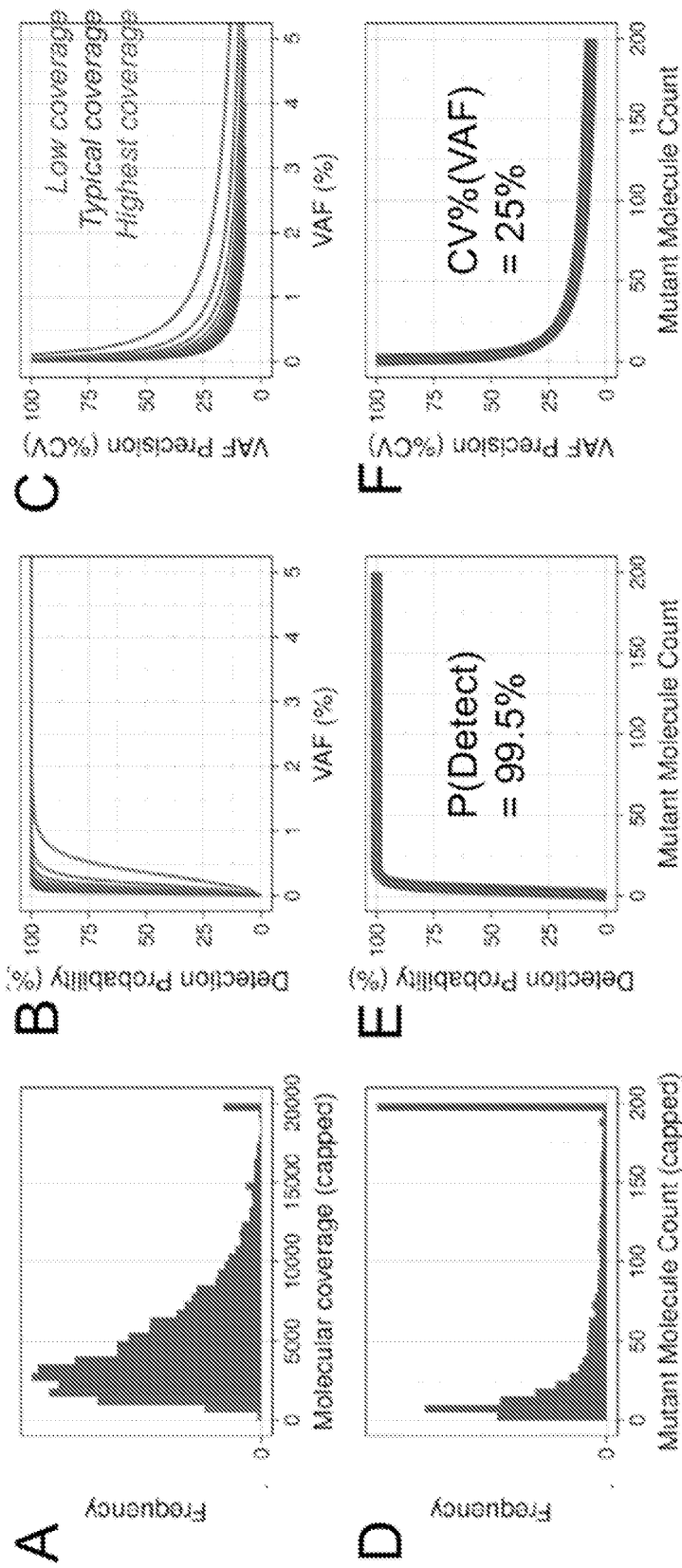


FIG. 24

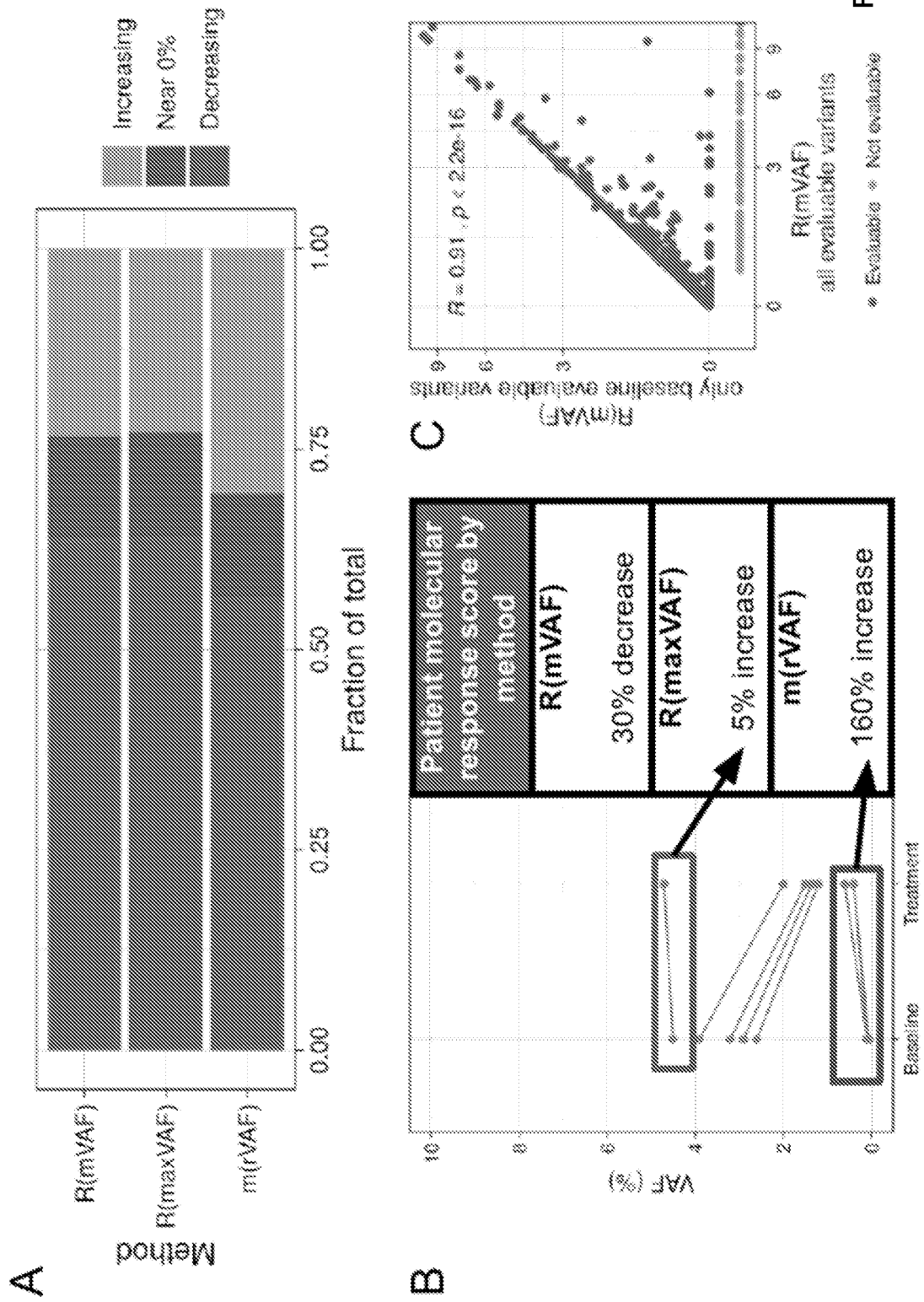


FIG. 25

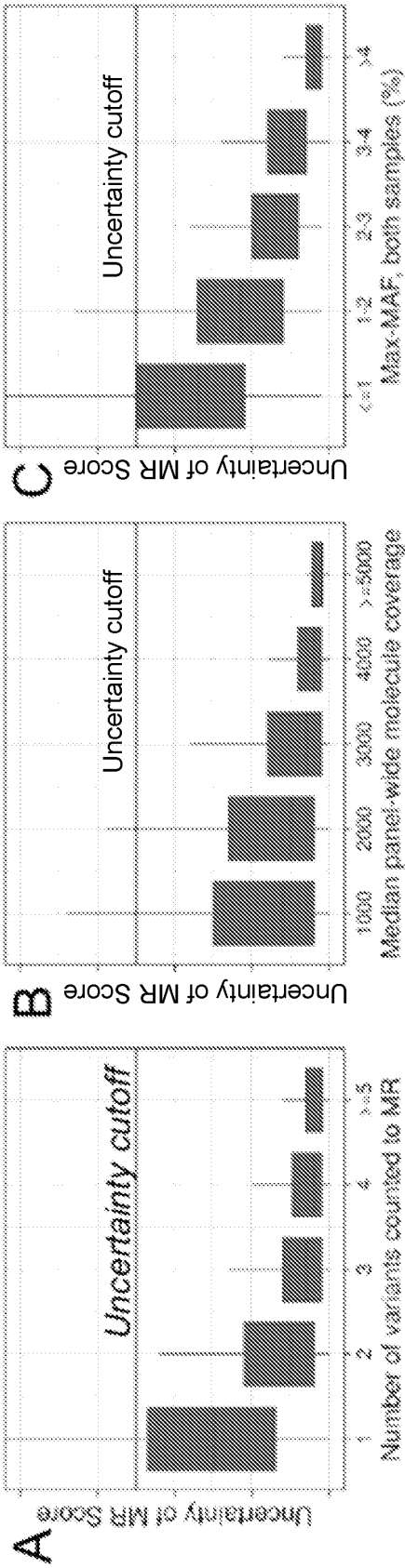


FIG. 26

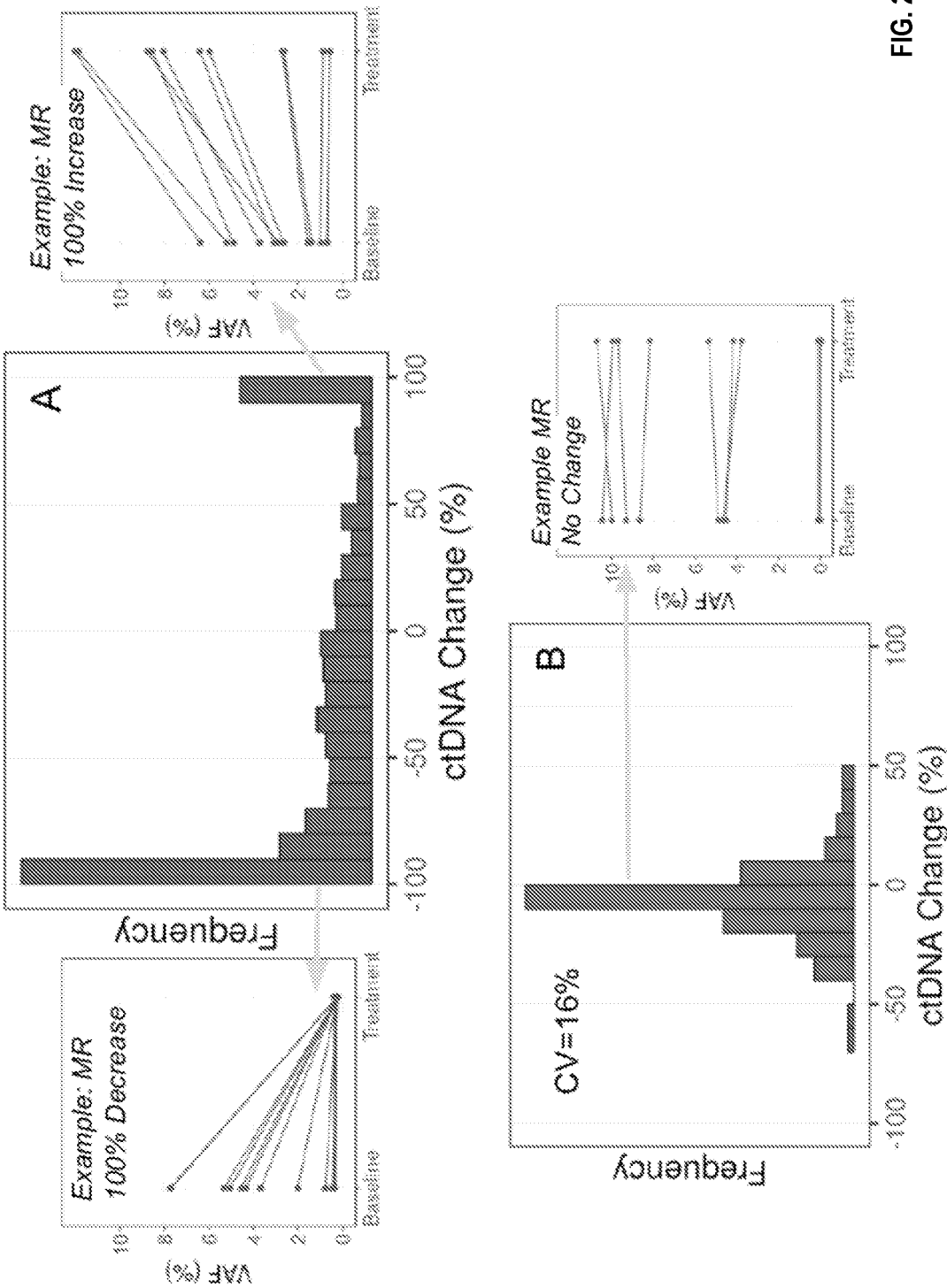


FIG. 27

sample_1	sample_2	chrom	position	gene	nucleotide mutation	amino acid mutation	somatic_call	percentage_1	percentage_2	max_maf_1	max_maf_2	change_flags
S10001	S10002	4	55139876	PDGFRA	G>A	E513K	germline	39.11	45.61	23.06	3.06	No discrepancy found
S10001	S10002	1	156849047	NTRK1	G>T	V647L	germline	24.74	44.38	23.06	3.06	No discrepancy found
S10001	S10002	4	55133574	PDGFRA	G>T	R293L	somatic	21.64	2.76	23.06	3.06	No discrepancy found
S10001	S10002	11	108236087	ATM	G>A	R3008H	somatic	0.32	0.44	23.06	3.06	No discrepancy found
S10001	S10002	17	7577559	TP53	G>A	S241F	somatic	0	0.1	23.06	3.06	No discrepancy found
S10001	S10002	10	43610031	RET	CA>C	K662fs	somatic	21.89	3.06	23.06	3.06	No discrepancy found
S10001	S10002	17	7577514	TP53	G>GT	T256fs	somatic	23.06	2.24	23.06	3.06	No discrepancy found
S10001	S10002	7	55249049	EGFR	ACCT>A	S784del	somatic	0	0.02	23.06	3.06	No discrepancy found

sample_1	sample_2	chrom	position	gene	nucleotide mutation	amino acid mutation	somatic_call	percentage_1	percentage_2	molecule count1	molecule count2	max_maf_1	max_maf_2	mutant molecule count1
S10001	S10002	4	55133574	PDGFRA	G>T	R293L	somatic	21.64	2.76	6444	7746	23.06	3.06	1394
S10001	S10002	17	7577559	TP53	G>A	S241F	somatic	0	0.1	9347	9347	23.06	3.06	0
S10001	S10002	10	43610031	RET	CA>C	K662fs	somatic	21.89	3.06	6896	10190	23.06	3.06	1510
S10001	S10002	17	7577514	TP53	G>GT	T256fs	somatic	23.06	2.24	6429	9654	23.06	3.06	1483
S10001	S10002	7	55249049	EGFR	ACCT>A	S784del	somatic	0	0.02	9976	9976	23.06	3.06	0

sample_1	sample_2	chrom	position	gene	nucleotide mutation	amino acid mutation	somatic_call	percentage_1	percentage_2	maf1	maf2	molecule count1	molecule count2	mutant molecule count1	mutant molecule count2
S10001	S10002	4	55133574	PDGFRA	G>T	R293L	somatic	21.64	2.76	0.2164	0.0276	6444	7746	1394.4816	213.7896
S10001	S10002	10	43610031	RET	CA>C	K662fs	somatic	21.89	3.06	0.2189	0.0306	6896	10190	1509.5344	311.814
S10001	S10002	17	7577514	TP53	G>GT	T256fs	somatic	23.06	2.24	0.2306	0.0224	6429	9654	1482.5274	216.2496

n_muts_in_mr	max_maf1	max_maf2	mean_maf1	mean_maf2	mr_score	sd_mr_inv_mr_score	mr_evaluable	mr_evaluable_comment
3	0.2306	0.0306	0.222	0.0269	0.12	0	Evaluable	

FIG. 28