Table 1. Analysis of human genomic DNA for G551D and ΔF508 mutations

Sample	[DNA] (ng/μL) [a]	G551D Genotyping [b]	ΔF508 Genotyping [c]	Known Genotype
01	112.0	G551D/N	ΔF508/N	ΔF508/G551D
02	18.5	G551D/N	ΔF508/N	ΔF508/G551D
03	6.4	G551D/N	ΔF508/N	ΔF508/G551D
04	5.5	N/N	ΔF508/ΔF508	ΔF508/ΔF508
05	17.0	G551D/G551D	N/N	G551D/G551D
06	19.0	G551D/N	N/N	G551D/P67L
07	142.0	G551D/N	ΔF508/N	ΔF508/G551D
08	110.5	G551D/N	N/N	G542X/G551D
09	157.5	N/N	ΔF508/ ΔF508	ΔF508/ΔF508
10	377.5	N/N	ΔF508/ ΔF508	ΔF508/ΔF508
11	145.5	N/N	ΔF508/ ΔF508	ΔF508/ΔF508
12	107.0	N/N	ΔF508/ ΔF508	ΔF508/ΔF508

[a] Measured using GE Healthcare Nanovue.

[b] N/N = homozygous wild-type; G551D/N = heterozygous mutant; G551D/G551D = homozygous mutant. As peaks of < 5 % relative intensity were disregarded, the threshold minor:major allele peak ratio for heterozygote calling was ≥ 0.05, although the lowest recorded ratio was 0.25.

[c] N/N = homozygous wild-type; ΔF508/N = heterozygous mutant; ΔF508/ΔF508 = homozygous mutant. Again, the threshold minor:major allele peak ratio for heterozygote calling was ≥ 0.05, although the lowest recorded ratio was 0.51.

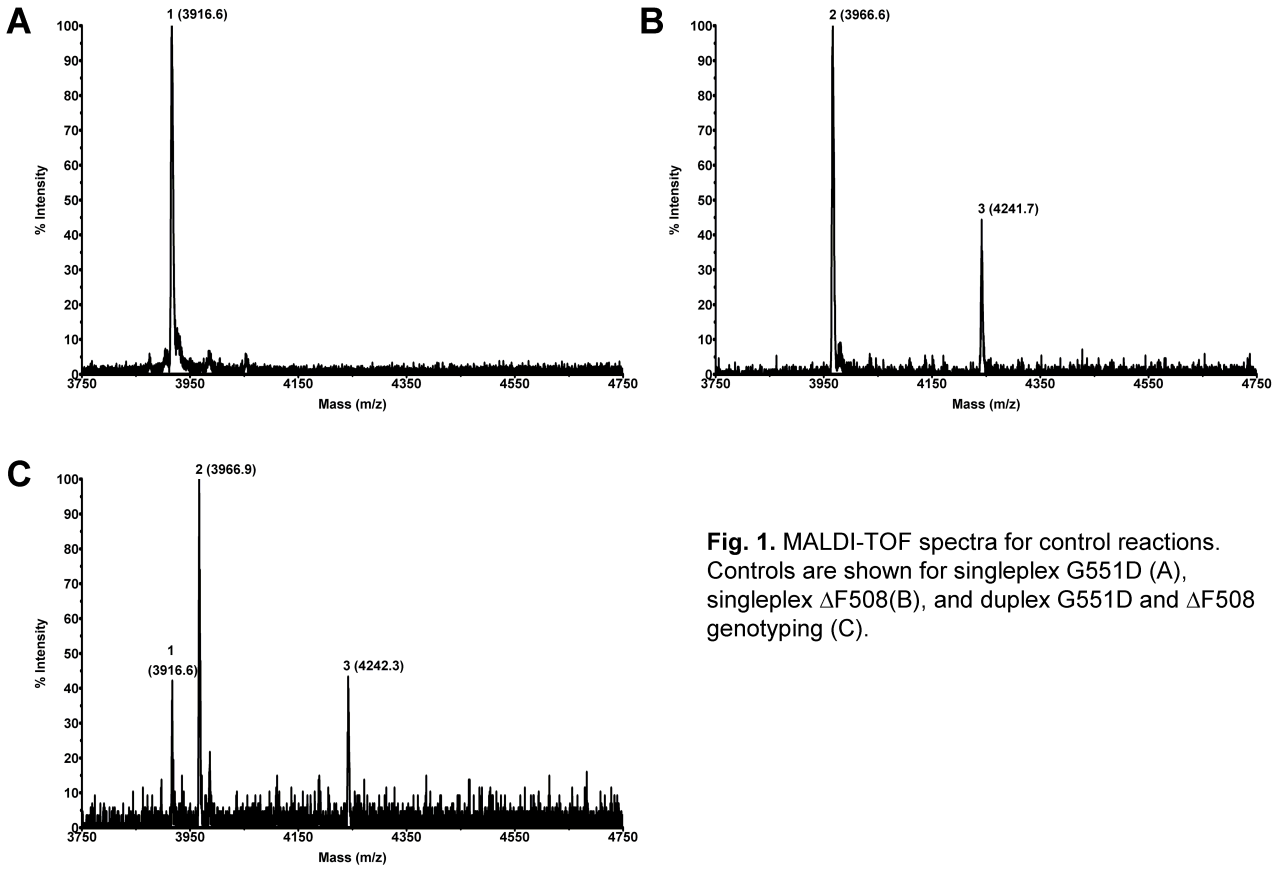

Fig. 1. MALDI-TOF spectra for control reactions. Controls are shown for singleplex G551D (A), singleplex ΔF508(B), and duplex G551D and ΔF508 genotyping (C).