

Figure S1. Concordance score and number of matching and discordant results for each locus and gene

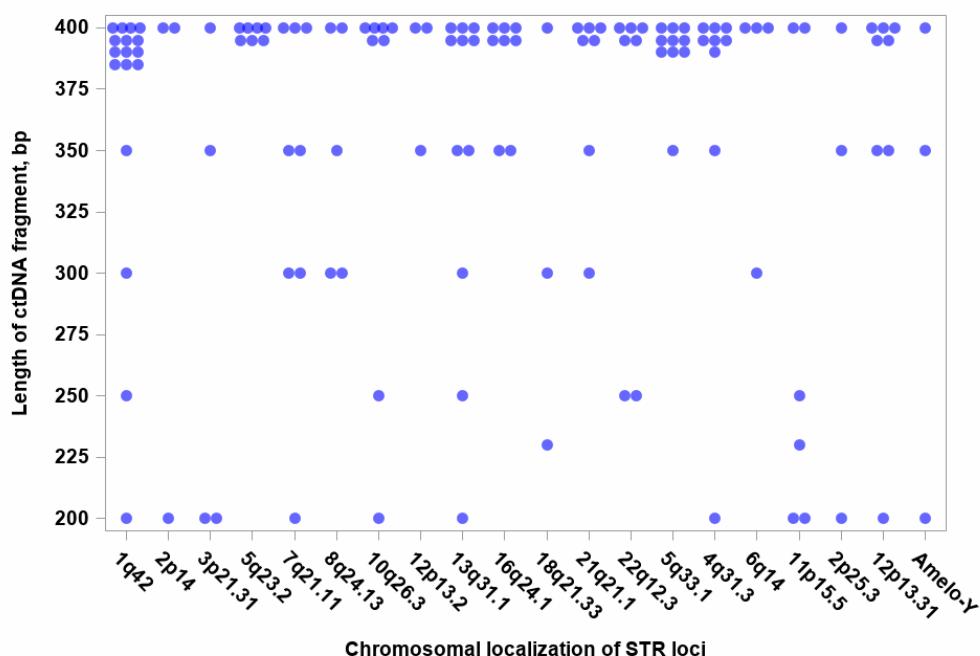


Figure S2. Distribution of LOH loci depending on the length of the ctDNA fragment

Table S1. Spectrum of high-risk aberrations in MM patients

Cytogenetic abnormality	Patients with MM (n=49)
t(4;14)	6 (12,3%)
t(14;16)	1 (2%)
Gain 1q	25 (51%)
del17p13	6 (12,3%)
Double-hit	10 (20,4%)
t(4;14) and gain 1q	2
t(4;14) and del17p13	2
t(14;16) and gain 1q	2
t(14;16) and del17p13	2
del17p13 and gain 1q	2
Triple-hit del17p13, t(14;16) and gain 1q	1 (2%)

TableS2. Comparison of the mutation status of RAS-ERK cascade genes and LOH in MM

	0-4 LOH loci (n=71)	5-8 LOH loci (n=15)	p
Mutations in RAS-ERK genes	31(44%)	11 (73%)	0.048