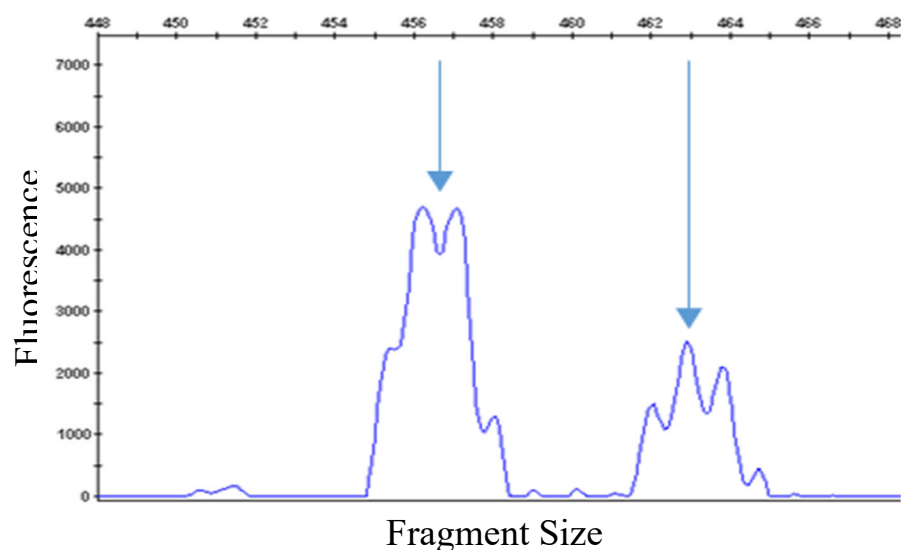


Figure e-1. Fragment analysis trace for a *TOMM40*-523' allele heterozygote



Alleles contained an average of 4 peaks. The mode of each allele was chosen as the “true” allele size (right). In cases where the mode was shared by two peaks, the average of the two peaks was used (left). Peak size was rounded to the nearest integer, which was subsequently subtracted from 439bp to determine number of T's.