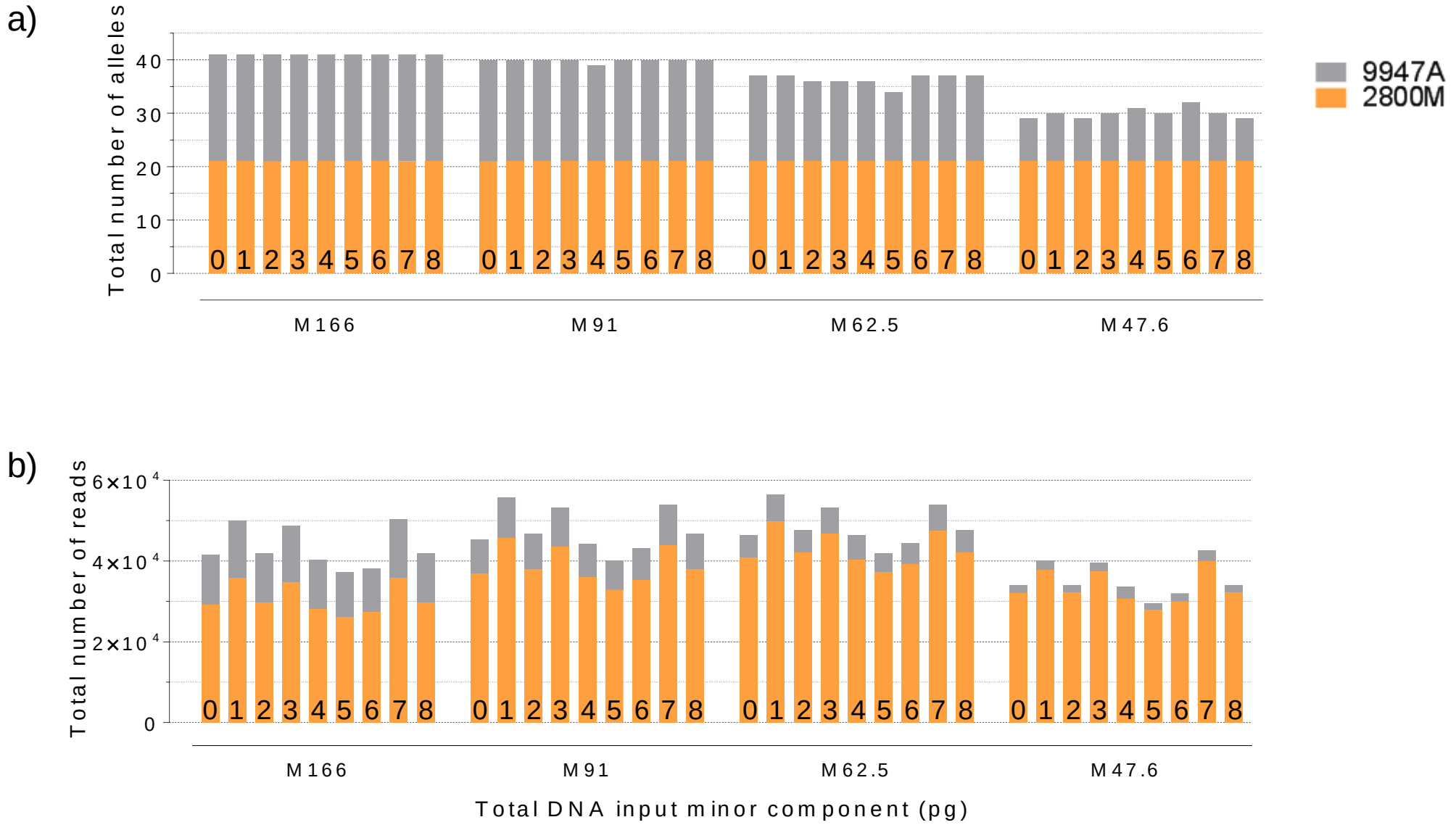

Figure S2. Total number of a) correctly typed alleles and b) observed reads/mixture-component. Mixtures M166, M91, M62.5 and M47.6 were prepared at ratios 83.3:16.7, 90.9:9.1, 93.7:6.3 and 95.2:4.8 using control DNAs 9947A (minor contributor) and 2800M (major contributor) and amplified with 1 ng total DNA input. Only STR markers that were distinguishable from one another were included for analysis (D1S1656, TPOX, D2S1338, D3S1358, D5S818, D8S1179, vWA, PentaE, D16S539, D18S51, D21S11 and D22S1045). Numbers on the bottom of each bar denote the associated sequencing run.

Müller P., Sell C., Hadrys T., Hedman J., Bredemeyer S., Laurent F.X., Roewer L., Achtruth S., Sidstedt S., Sijen T., Trimborn M., Weiler N., Willuweit S., Bastisch I., Parson W., and the SeqForSTR-Consortium. Inter-laboratory study on standardized MPS libraries: Evaluation of performance, concordance and sensitivity using mixtures and degraded DNA