The genotypes in the file c32p9l have NOT been standardized with other laboratories. The allele length estimates for each locus in this data set should be standardized if the intent is to combine this data set with other data sets (i.e. to assure you are combining apples with apples).

The genotypes were derived by estimating the microsatellite allele lengths in base pairs for each locus. These estimates were made using electrophoresis to separate allele copies (from PCR) in a 6% denaturing polyacrylamide gel (constant power, 60 W). This PCR was performed with a RoboCycler (Stratagene, La Jolla, CA, USA) in a volume of 25 μl with a final concentration of 10 mM Tris (pH 8.5), 2.0 mM $MgCl_2$, 50 mM KCL, 0.01% pectin, 200 μM each dNTP, 10 pmol HEX-labeled forward primer, 10 pmol reverse primer, 0.25 units *Taq* polymerase (Stratagene) and approximately 100 ng genomic DNA. The microsatellites were visualized by scanning for fluorescence at 585 nm using the Hitachi FMBIO II flat bed scanner. Microsatellite allele lengths were estimated using a MapMarker™ Low 70-400 bp size standard (BioVentures Inc., Myrfreesboro, TN, USA) and Gene Profiler software (Scanalytics Inc., Fairfax, VA, USA).