

*Abstract:*

TrueAllele System 2 and GT/GS peaks heights differ 13% for SGMplus data and 11% for Identifiler data.

*Materials and Methods:*

TrueAllele System 2, in order to model peaks accurately, first models and sets the baseline according to the data. It uses each quantitated marker window (marker window +5 bp on each side) to determine the baseline for each experiment (i.e. one marker for one lane). TrueAllele System 2 models the baseline in order to include the base of the true data peaks. Generally the true baseline is not zero but slightly above. TrueAllele System 2 then fits a gaussian curve to each peak above threshold. The peak height is the difference of the modeled gaussian curve from the modeled baseline.

The comparison uses TrueAllele-quantitated peak heights from five SGMplus injections (plate HC06.4066) and from six Identifiler injections (plate 18012006-1). The peak heights collected for each peak are within 0.2 base pairs of the TrueAllele peak size. Genotyper and Genescan were used to gather peak heights for the SGMplus and Identifiler data respectively. Five-dye data is not supported in the Genotyper version used; the Genescan and Genotyper peak heights were found to be equivalent.

For SGMplus, the scatter plot shows all peaks greater than 110 bp. Peaks below 110 bp contain amelogenin-pull up peaks that produced outliers, and so were removed from the analysis. For Identifiler, injections B10 and D10 were excluded as peak sizes for the two sets were discordant.

*Results:*

For SGMplus, the plot demonstrates that TrueAllele peak heights are 87% of the Genotyper peak heights (see Figure 1). The Identifiler TrueAllele peak heights are 89% of the Genescan peak heights (see Figure 2).

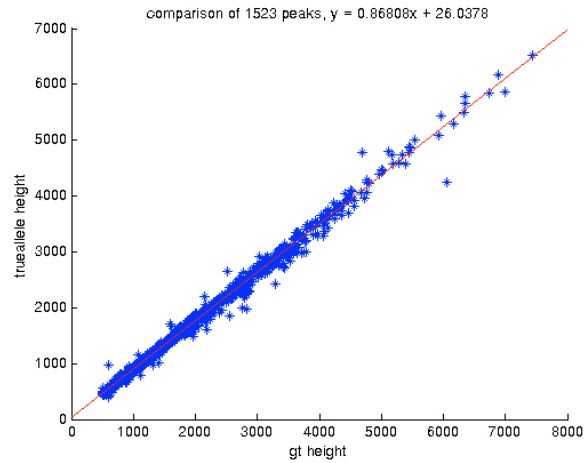


Figure 1. TrueAllele and Genotyper peak heights for all SGMplus peaks greater than 110 bp.

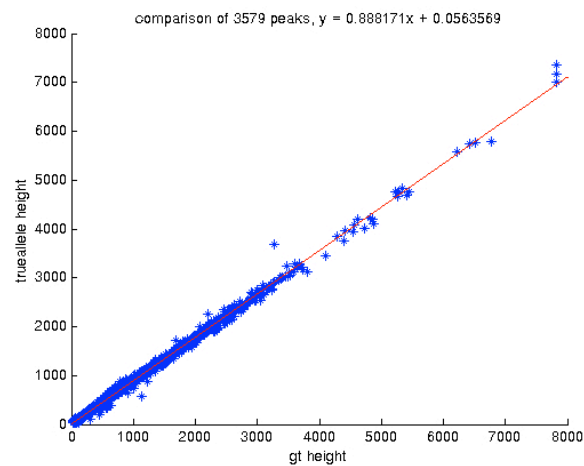


Figure 2. TrueAllele and Genescan peak heights for Identifiler peaks.

*Conclusions:*

The linear regression curves show strong correlations between peak heights for TrueAllele System 2 and GS/GT for the SGMplus and Identifiler kits. The regression lines provide adjustment values for each data type that can be used when determining thresholds.