THE DIFFERENCE BETWEEN RUTAND RUTAND



Revealing the Genome through SMRT® Biology: Discoveries and Applications

Long-Read Single Molecule Sequencing in an Academic Medical Hospital Professor Johan den Dunnen, Leiden University Medical Centre

Applying the PacBio® RS in Human Genetics - Case Studies Dr. Kerstin Stangier, GATC Biotech

Simplified Characterization of Large Deletions using the PacBio Sequencing Platform

Dr. Gabor Matyas, Center for Cardiovascular Genetics and Gene Diagnostics

Saturday, June 23

14:00 - 15:30

Location: Instanbul Room

ARE YOU PLAGUED BY FALSE POSITIVES?

When investigating genes or regions associated with disease you need to know you've found all the SNPs, and that they are real. The PacBio *RS* provides highly accurate sequence information with better context to determine true SNPs, with high sensitivity for SNP calling. Other approaches routinely call false positives or miss variants altogether, giving you only part of the picture.

SO WHAT ELSE ARE YOU MISSING?

