
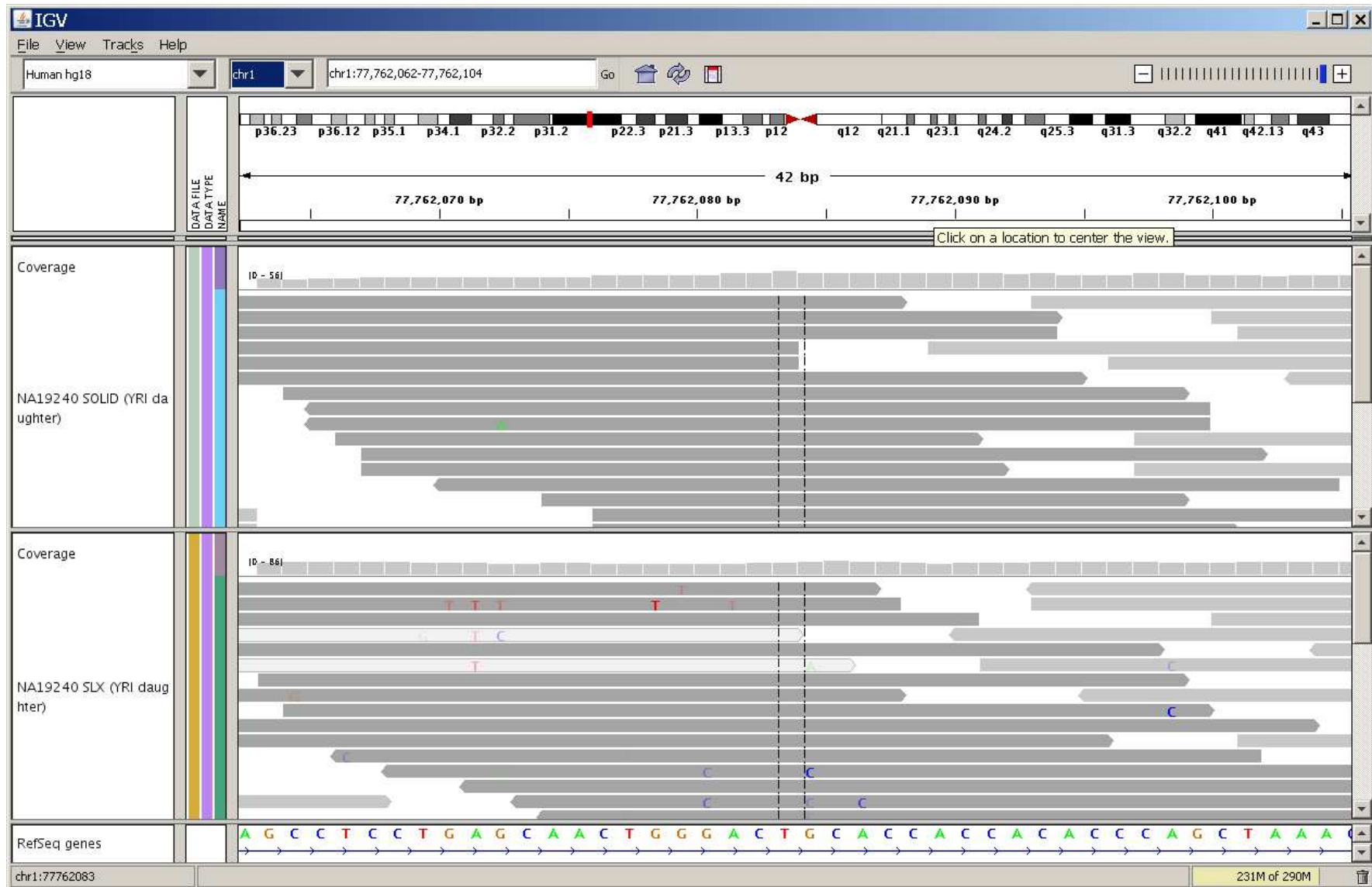


# 1000 Genome Project Data Error Rate Comparison

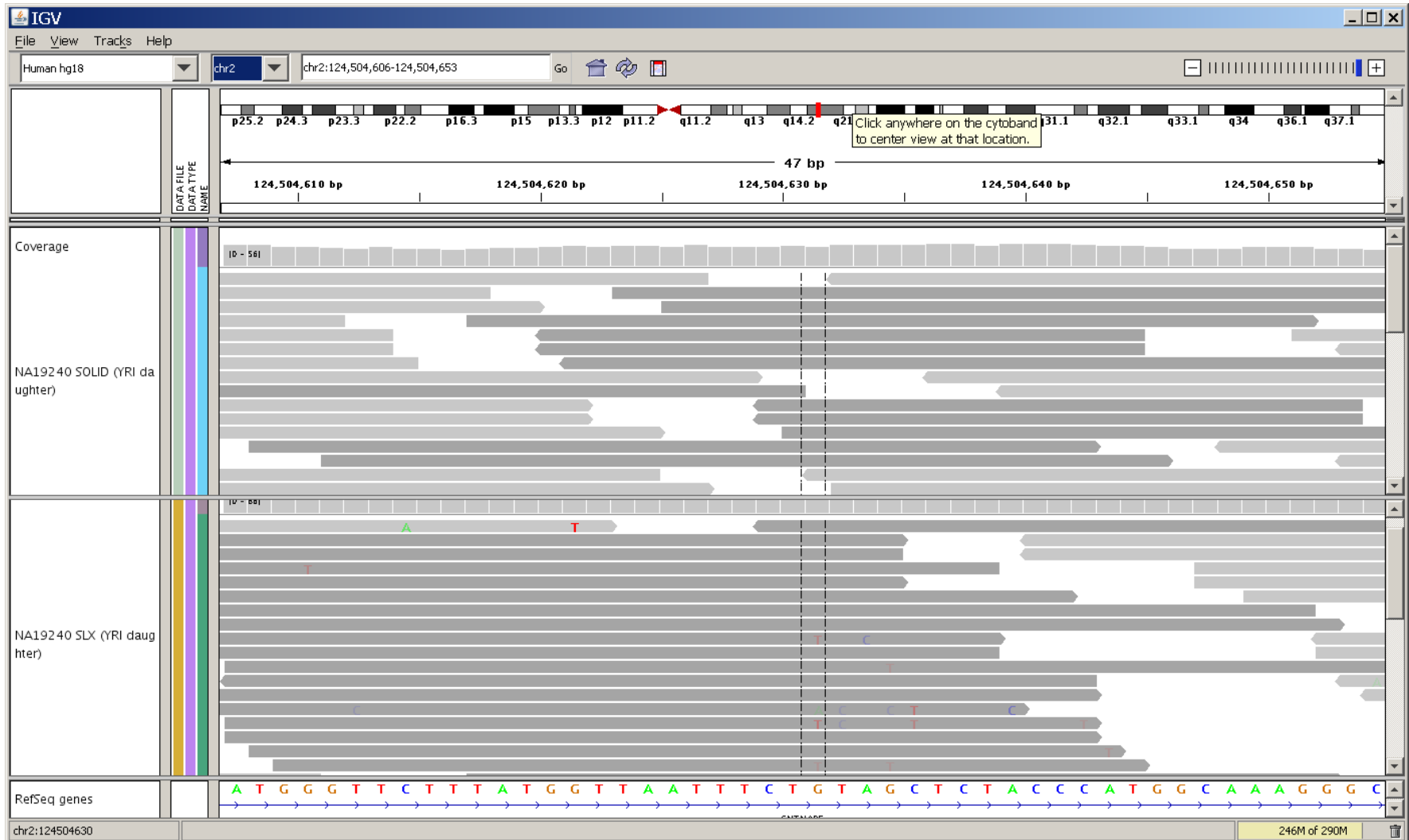
- Using Broad IGV
- NA19240 SOLID YRI Daughter
- NA NA19240 SLX(Illumina) YRI Daughter
  
- Install IGV and See the SOLID and SLX (Illumina) data
  - Download and install <http://www.broadinstitute.org/igv/> (need register)
  - Open IGV and Select Human hg18
  - Go to File --> Load from server ( be connected to internet)
  - Under Available Datasets pop up window, Expand 1000 Genomes
  - Expand YRI Trio
  - Select NA19240 SOLID YRI Daughter and NA NA19240 SLX(Illumina) YRI Daughter
  - Pick any chr, move the blue zoom bar (minus plus sign on top right) to the most right (closest to ⊕)
  - Randomly move the solid-red  to any region on the chr
  - Count SNP/Error calls by counting the colored base

# Random Pick #1



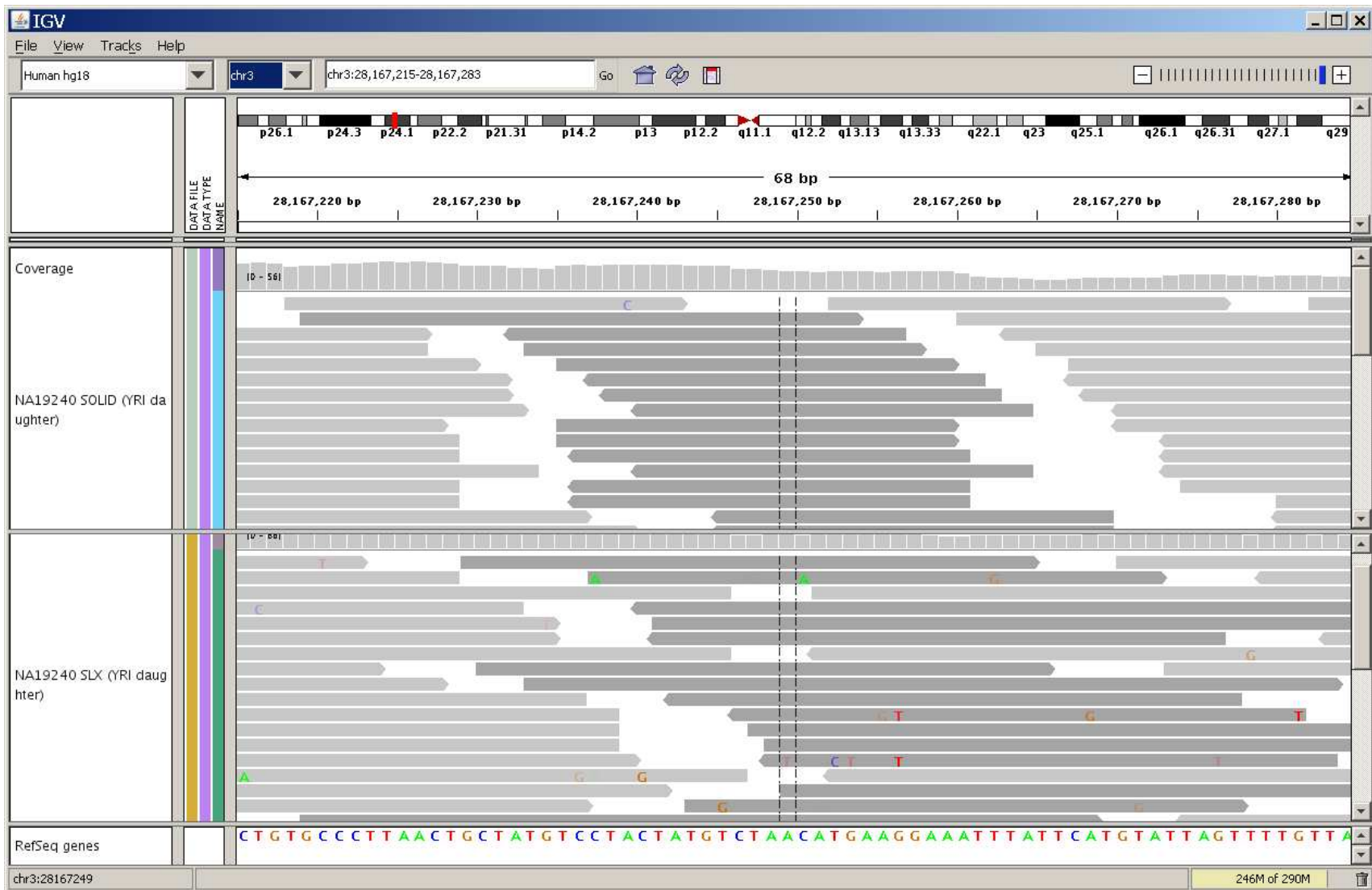
In chr1:77,762,062-77,762,104, a 42 bp region, Illumina has 29 SNP/Error calls, and SOLiD has 1 SNP/Error call.

# Random Pick #2



In chr2:124,504,606 -124,504,653, a 47 bp region, Illumina has 15 SNP/Error calls, and SOLiD has none.

# Random Pick #3



In chr3:28,167,215-28,167,283, a 68 bp region, Illumina has 22 SNP/Error calls, and SOLiD has 1 SNP/Error call.