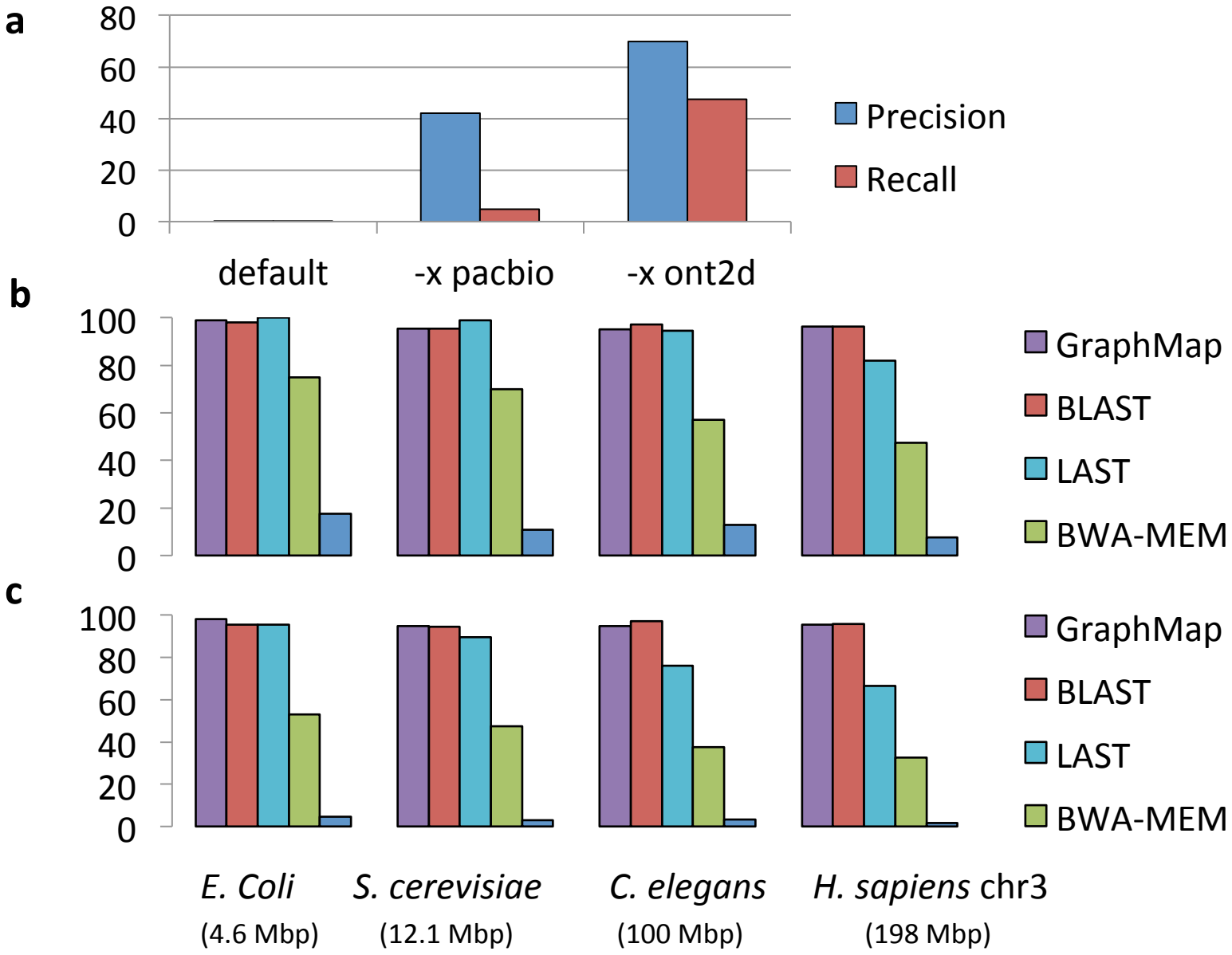
Supplementary Table 1. Precision and recall of alignment for GraphMap using various read alignment settings. Results are reported in the format: precision-for-2D-reads/recall-for-2D-reads; precision-for-1D-reads/recall-for-1D-reads.

	Myers bit vector (default)	**Gotoh**	**Anchored Alignment**
N. meningitidis	79/79; 73/73	82/82; 75/73	80/79; 73/71
E. coli	80/80; 74/74	83/83; 76/76	80/79; 74/73
S. cerevisiae	77/77; 70/70	80/80; 72/72	79/76; 72/70
C. elegans	78/78; 68/68	81/81; 70/70	78/76; 71/67
H. sapiens **chr 3**	78/78; 71/71	81/81; 73/73	78/77; 71/69

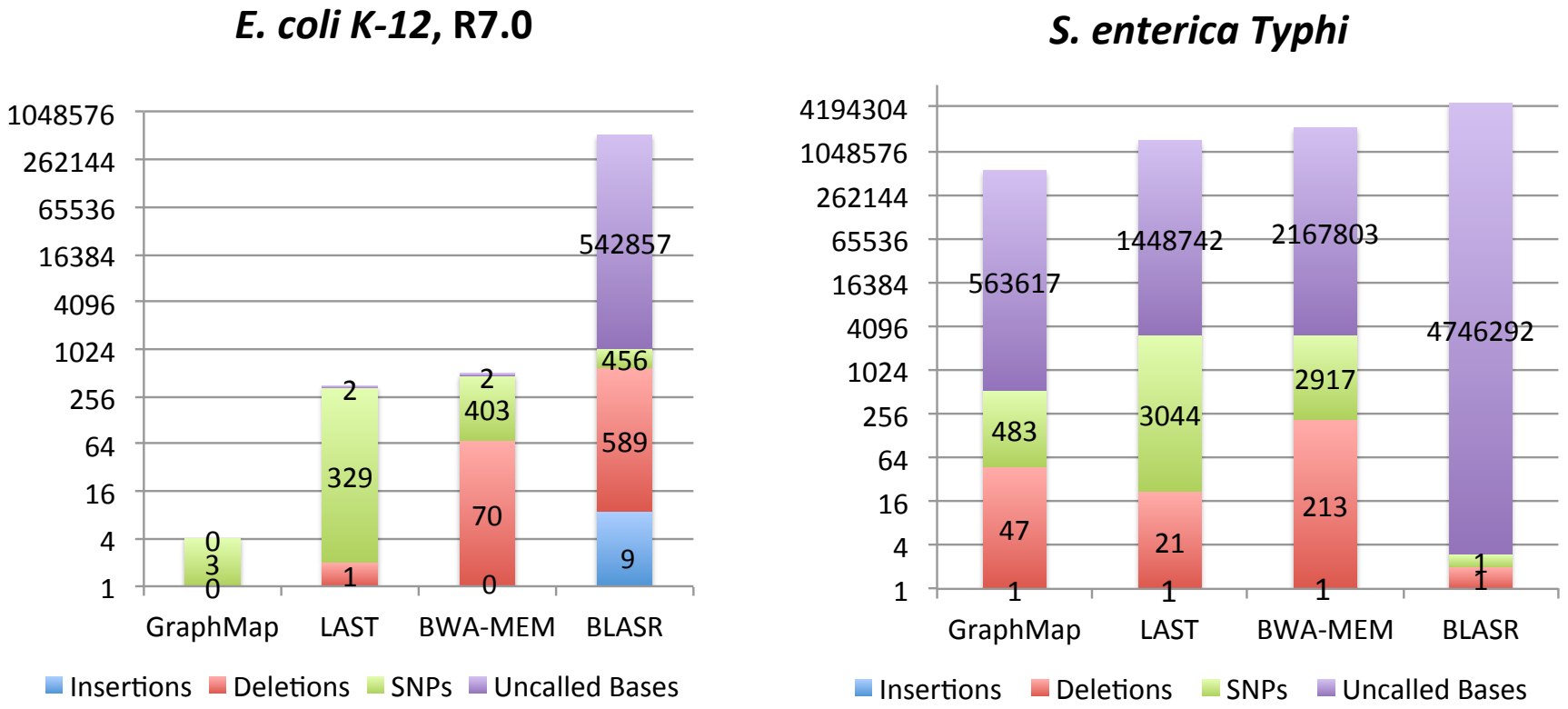
Supplementary Table 2. Runtime comparison between GraphMap and BLAST across a range of genomes. Results reported are CPU time for mapping a 1000 simulated 2D and 1D ONT reads for each genome (fastest runtimes for each dataset are marked in bold).

Genome	Size	ONT 2D			ONT 1D		
		BWA-MEM (s)	GraphMap [s]	BLAST [s]	BWA-MEM (s)	GraphMap [s]	BLAST [s]
N. meningitidis	2.2 Mbp	79	**60**	534	108	**55**	106
E. coli	4.6 Mbp	68	**63**	78	89	56	**36**
S. cerevisiae	12.1 Mbp	**89**	90	378	121	**80**	178
C. elegans	100 Mbp	**110**	302	15244	**78**	245	3727
H. sapiens chr 3	198 Mbp	**168**	500	110670	**83**	376	20592

Supplementary Figure 1. Performance in terms of finding the correct mapping location for various mappers using simulated ONT 1D reads. (a) for BWA-MEM with different parameter settings on *S. cerevisiae*. For all mappers with ONT settings (b) Precision and (c) Recall.



Supplementary Figure 2. Consensus calling errors and uncalled bases using MinION datasets and different mappers. Note that in the case of the *S. enterica* Typhi dataset, some of the observed variants (typically a few hundred SNPs and a handful of indels) could be true variants from the *S. enterica* Typhi Ty2 strain that was used as reference. Average coverage of the genome is reported in the table below.

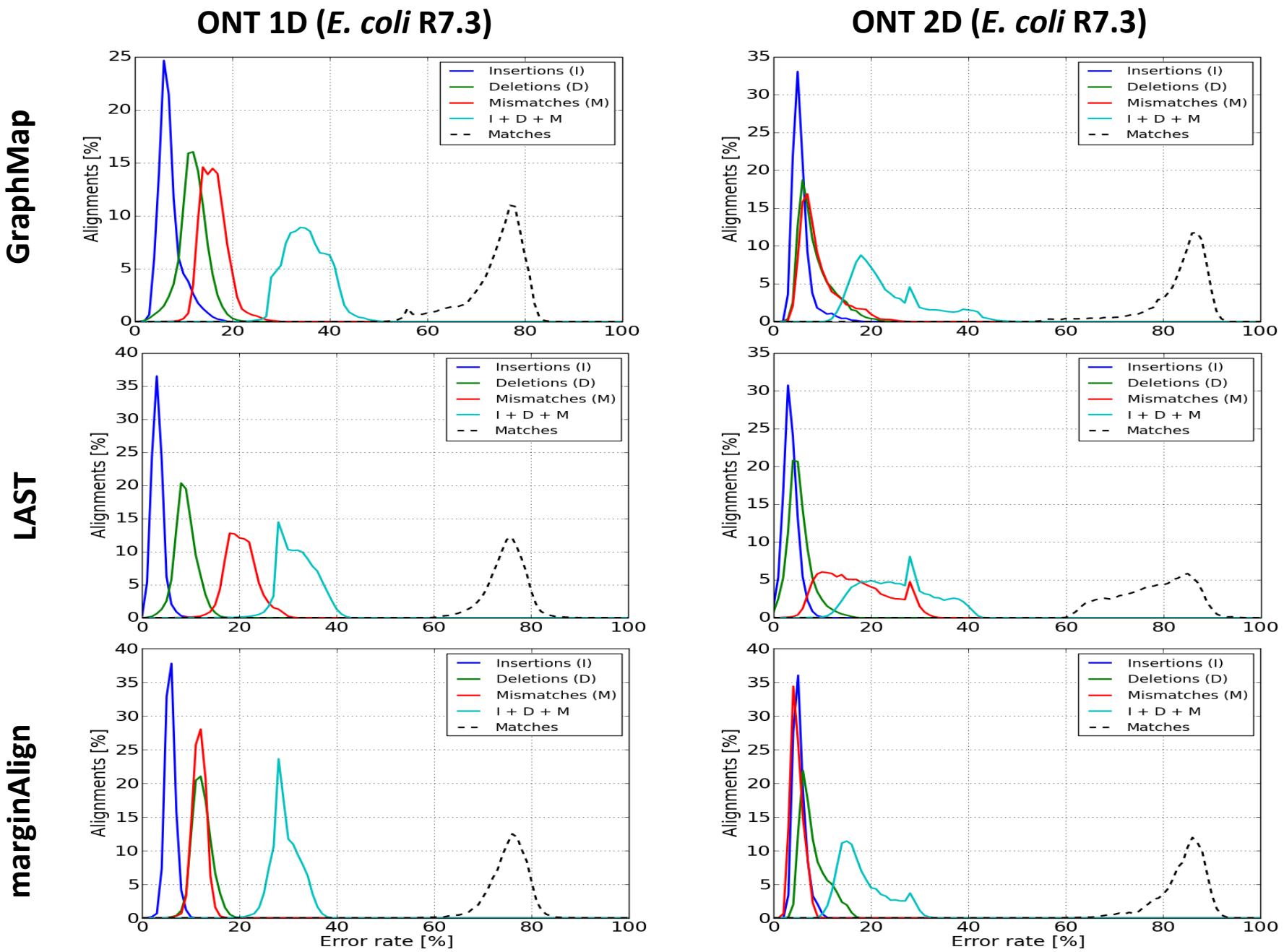


	E. coli K-12 coverage	*S. enterica* Typhi coverage
GraphMap	135	33
LAST	117	26
BWA-MEM	90	21
BLASR	24	7

Supplementary Table 3. Speed comparison across mappers on real datasets. Results are reported in terms of kilobases mapped per second to account for the wide variation in the number of bases aligned by different mappers.

	Lambda phage	*E. coli R7.3*	*E. coli* R7.0	*E. coli* UTI89
GraphMap	91	43	50	123
LAST	71	87	110	155
BWA-MEM	28	30	31	49
BLASR	2	14	20	43

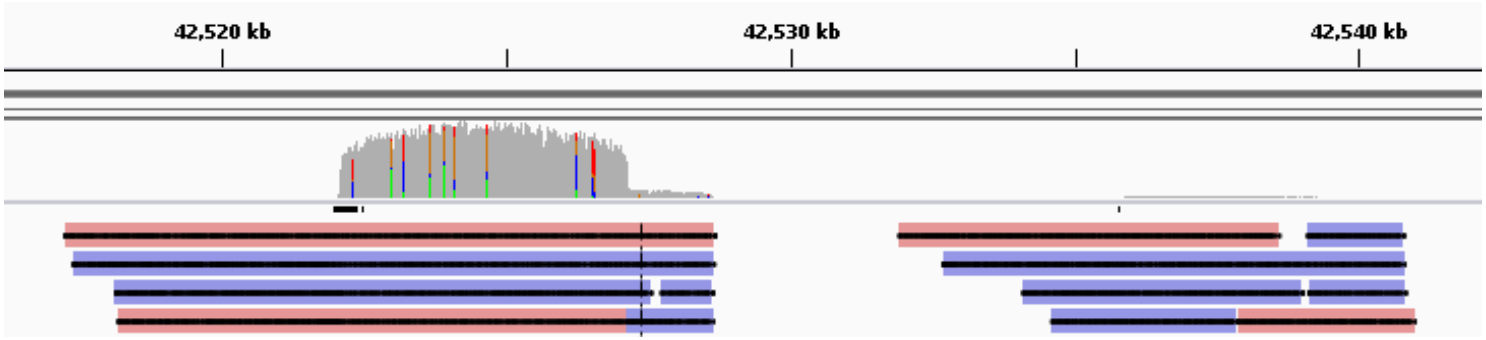
Supplementary Figure 3. Error rate distributions estimated using different aligners for ONT data.



Supplementary Table 4. Parameters used for generating simulated ONT reads.
Parameters were estimated using LAST alignments using E. Coli K-12 R7.3 data.

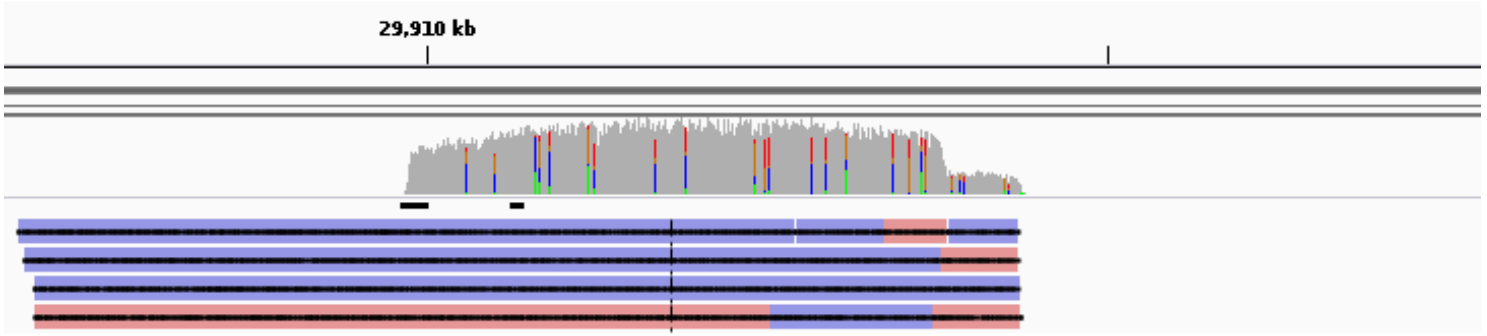
	2D reads	**1D reads**
Accuracy mean	0.69	0.59
Accuracy std	0.09	0.05
Accuracy min	0.40	0.40
Length mean	5600	4400
Length std	3500	3900
Length min	100	50
Length max	100000	100000
Error types ratio (mismatch:insertion:deletion)	55:17:28	51:11:38

Supplementary Figure 4. Mapping of targeted sequencing reads from Ammar et al.



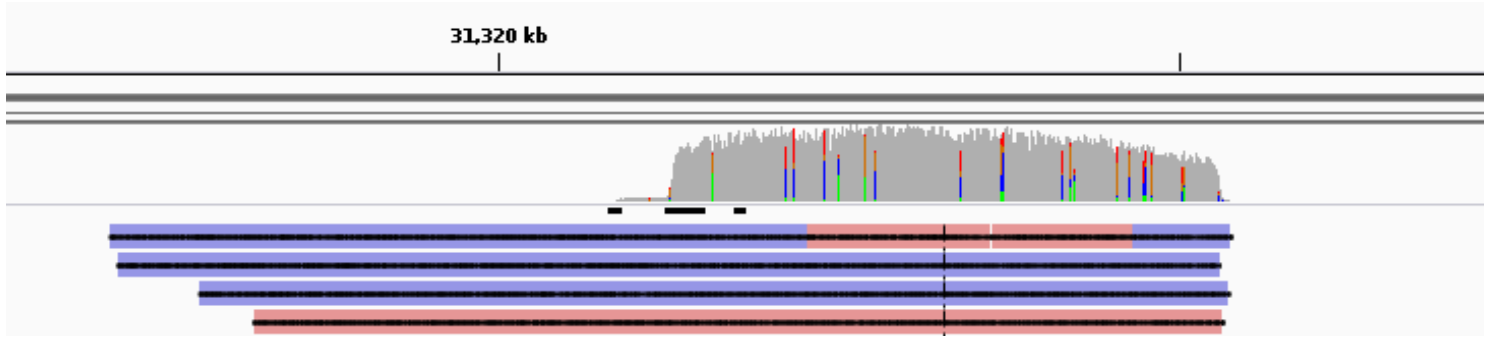
***CYP2D6* (chr22)**

# of on-target reads
GraphMap: 7231
BWA-MEM: 6287
LAST: 5204
BLASR: 3553



***HLA-A* (chr6)**

# of on-target reads
GraphMap: 5163
BWA-MEM: 4400
LAST: 3705
BLASR: 2096



***HLA-B* (chr6)**

# of on-target reads
GraphMap: 9013
BWA-MEM: 7567
LAST: 6237
BLASR: 3478