Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/03 00:02:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714200.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_ERR9714200 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714200.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 03 00:02:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	ERR9714200.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	123,164
Mapped reads	19,225 / 15.61%
Unmapped reads	103,939 / 84.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	750 / 0.61%
Read min/max/mean length	30 / 151 / 59.62
Duplicated reads (estimated)	17,284 / 14.03%
Duplication rate	46.56%
Clipped reads	12,510 / 10.16%

2.2. ACGT Content

Number/percentage of A's	186,986 / 9.4%
Number/percentage of C's	134,608 / 6.77%
Number/percentage of T's	159,474 / 8.02%
Number/percentage of G's	1,507,022 / 75.8%
Number/percentage of N's	70 / 0%
GC Percentage	82.57%

2.3. Coverage

Mean	0.0006

Standard Deviation	1.7008

2.4. Mapping Quality

Mean Mapping Quality	26.49

2.5. Mismatches and indels

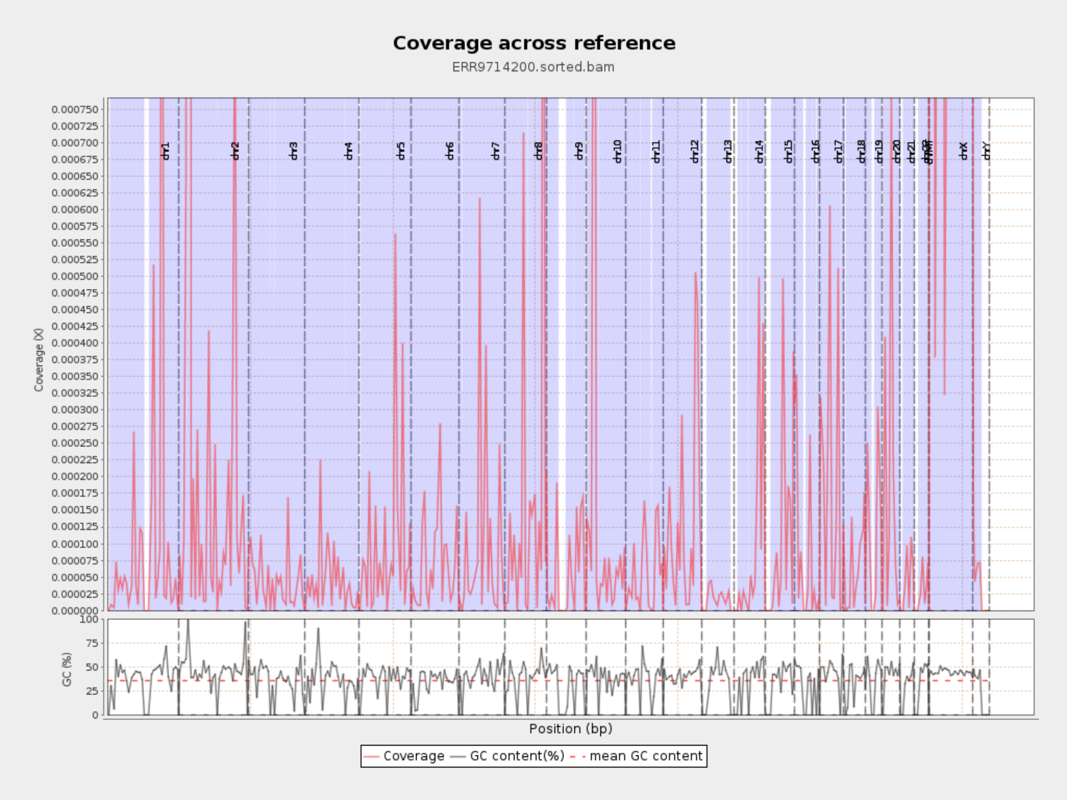
General error rate	3.73%
Mismatches	56,104
Insertions	2,525
Mapped reads with at least one insertion	8.64%
Deletions	2,402
Mapped reads with at least one deletion	12.02%
Homopolymer indels	52.89%

2.6. Chromosome stats

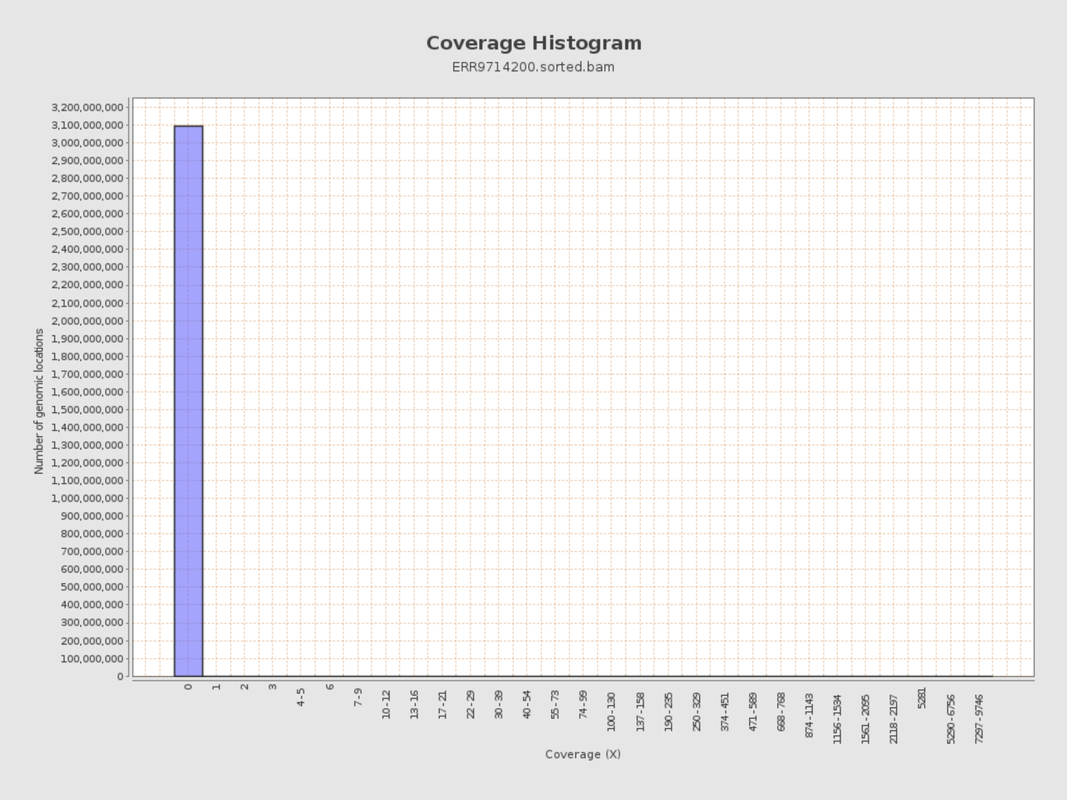
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27863	0.0001	0.147
chr2	243199373	1421538	0.0058	6.0599
chr3	198022430	8927	0	0.0113
chr4	191154276	8539	0	0.0118
chr5	180915260	17642	0.0001	0.0367
chr6	171115067	12097	0.0001	0.0212
chr7	159138663	16320	0.0001	0.0417

chr8	146364022	26954	0.0002	0.0812
chr9	141213431	7550	0.0001	0.0199
chr10	135534747	19737	0.0001	0.1966
chr11	135006516	7710	0.0001	0.015
chr12	133851895	17679	0.0001	0.038
chr13	115169878	1826	0	0.005
chr14	107349540	10688	0.0001	0.0398
chr15	102531392	9556	0.0001	0.0332
chr16	90354753	7671	0.0001	0.0292
chr17	81195210	15950	0.0002	0.0536
chr18	78077248	4903	0.0001	0.0153
chr19	59128983	6515	0.0001	0.0313
chr20	63025520	12278	0.0002	0.056
chr21	48129895	2243	0	0.0117
chr22	51304566	1354	0	0.0063
chrMT	16571	0	0	0
chrX	155270560	336760	0.0022	0.2586
chrY	59373566	2082	0	0.0097

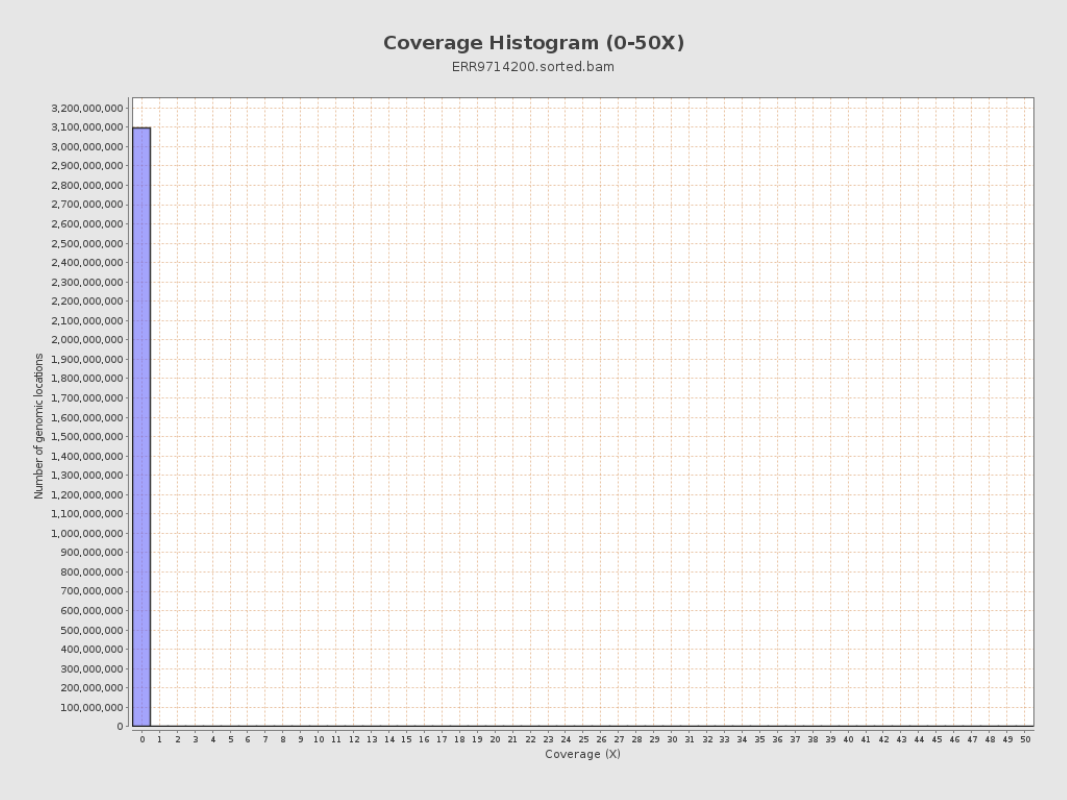
3. Results : Coverage across reference



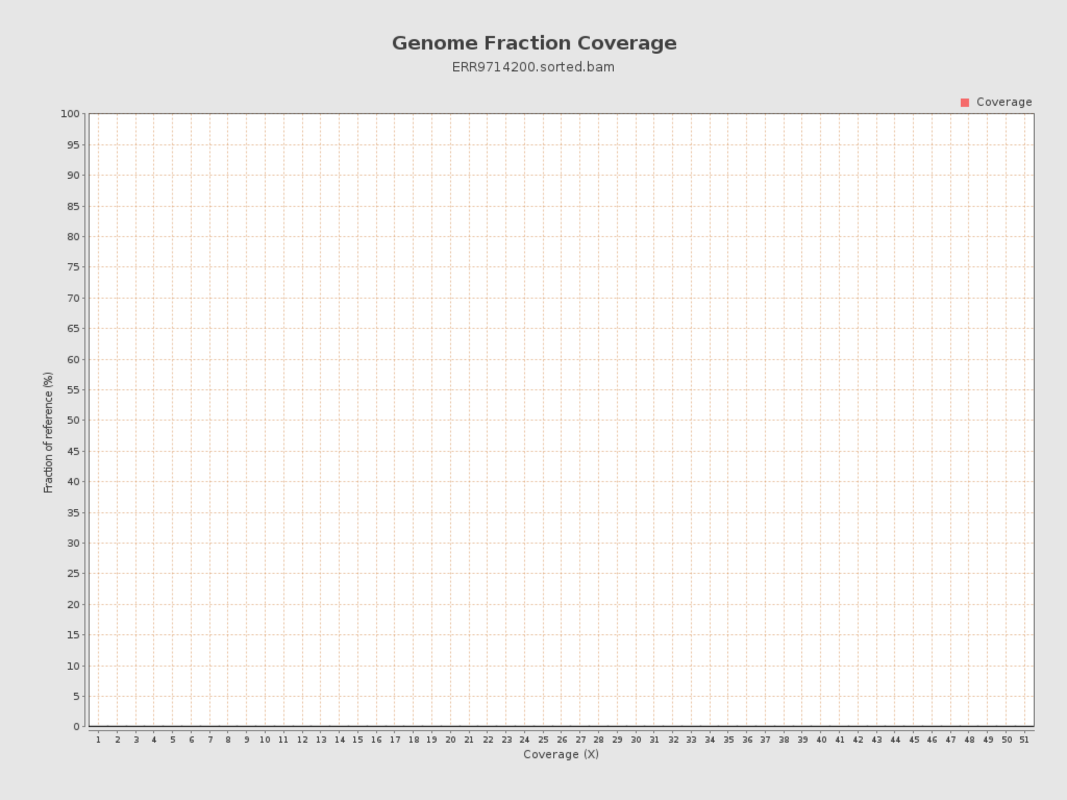
4. Results : Coverage Histogram



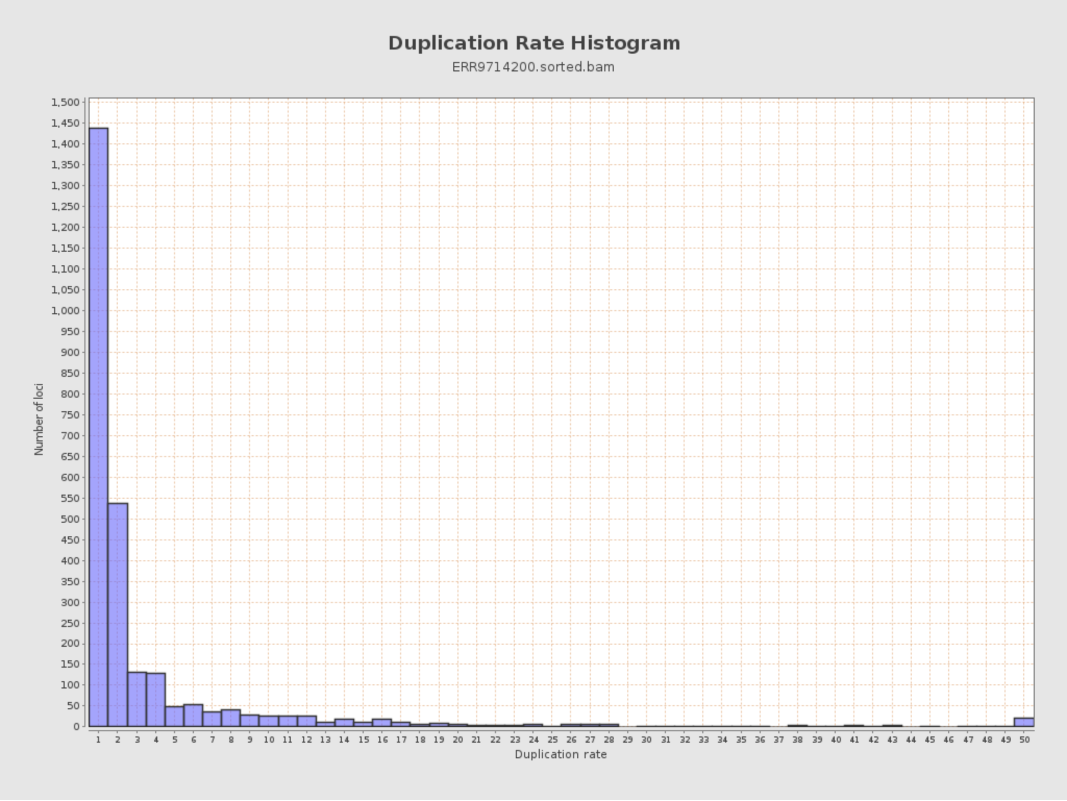
5. Results : Coverage Histogram (0-50X)



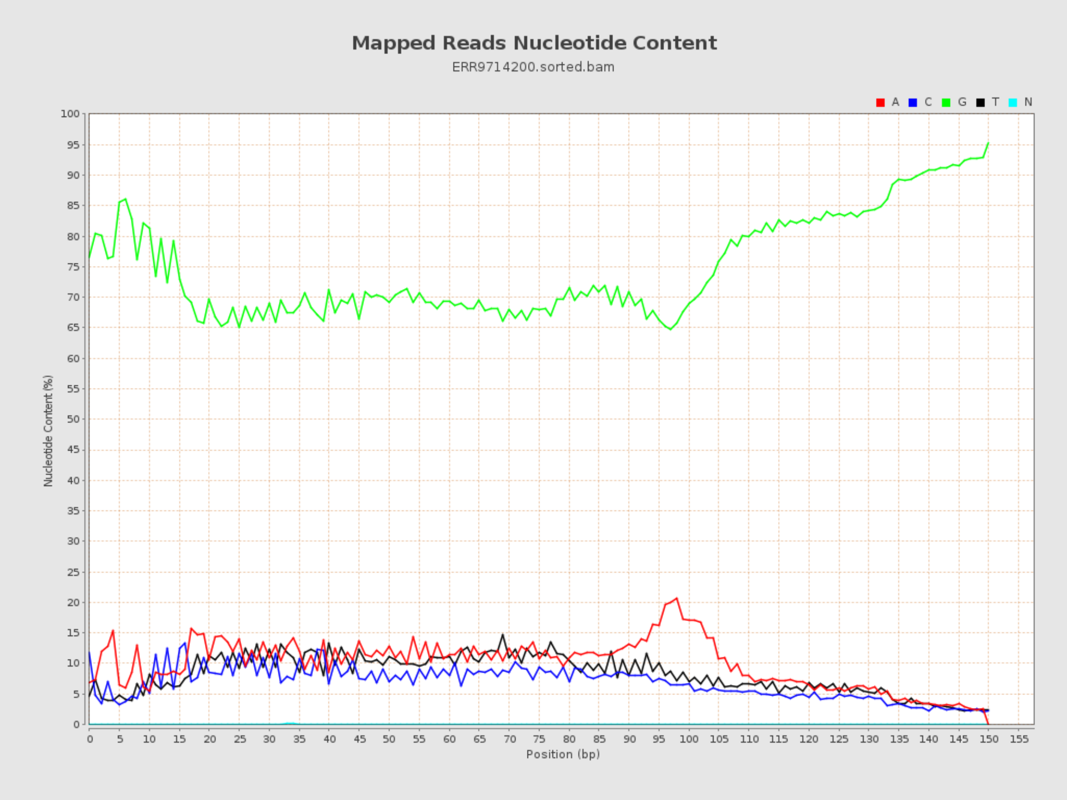
6. Results : Genome Fraction Coverage



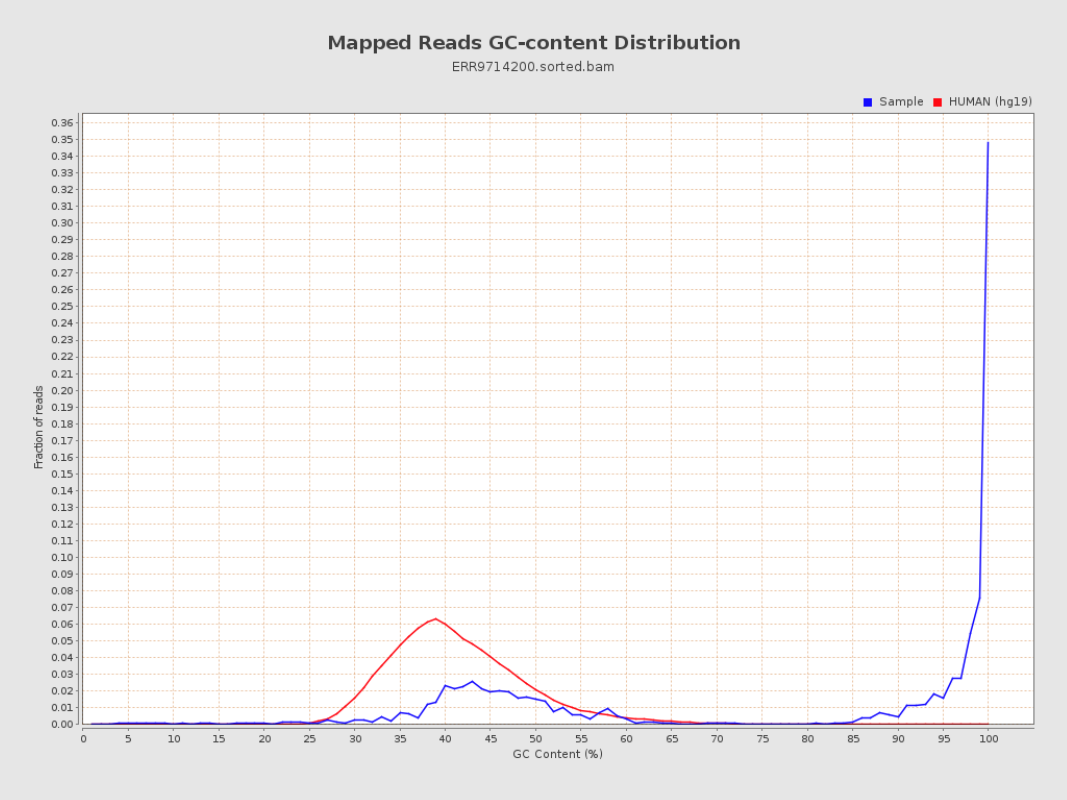
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



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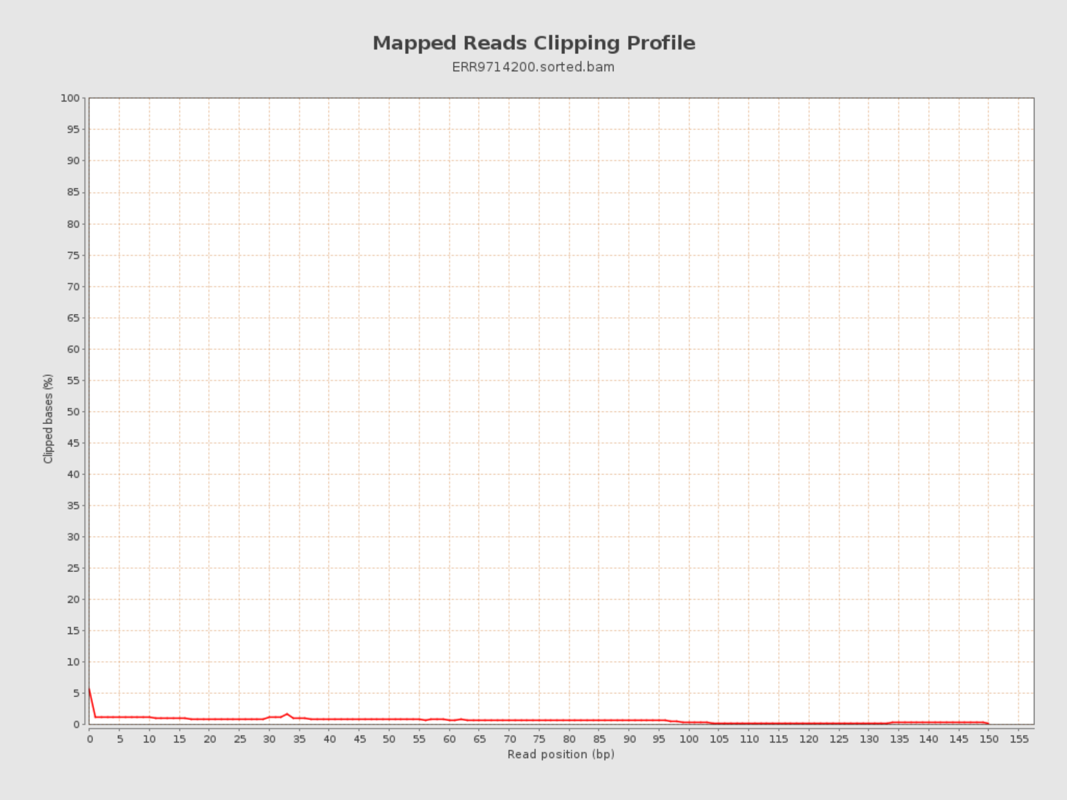
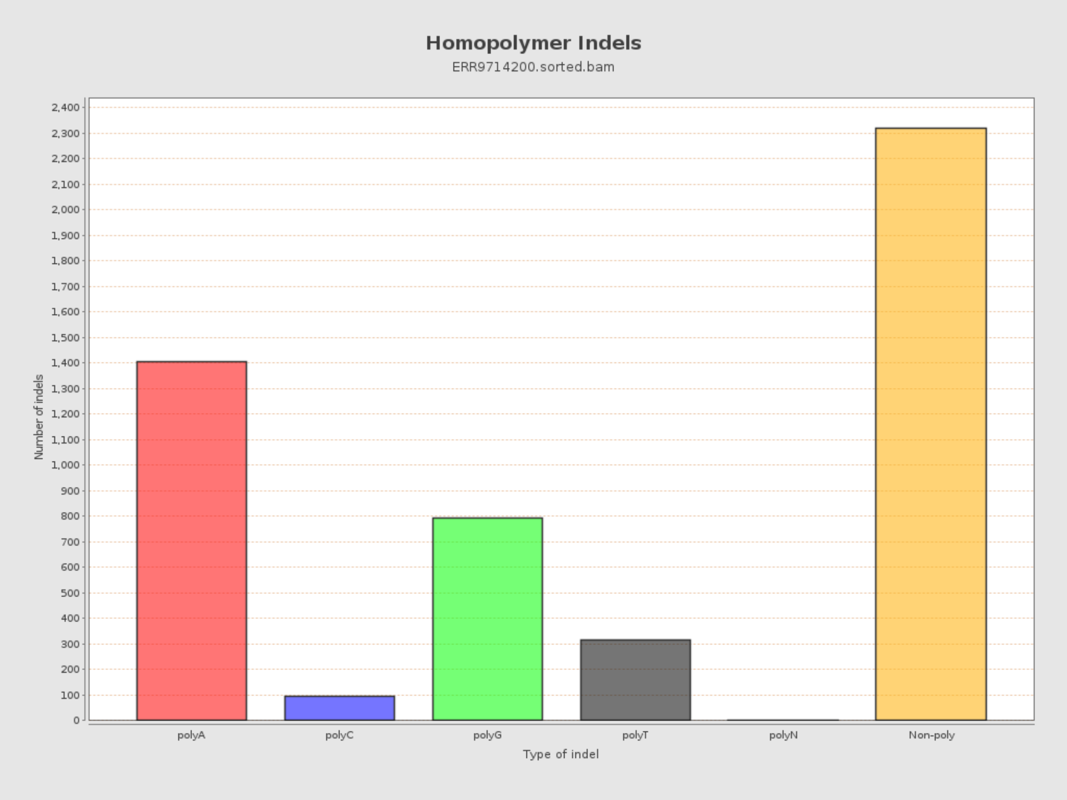
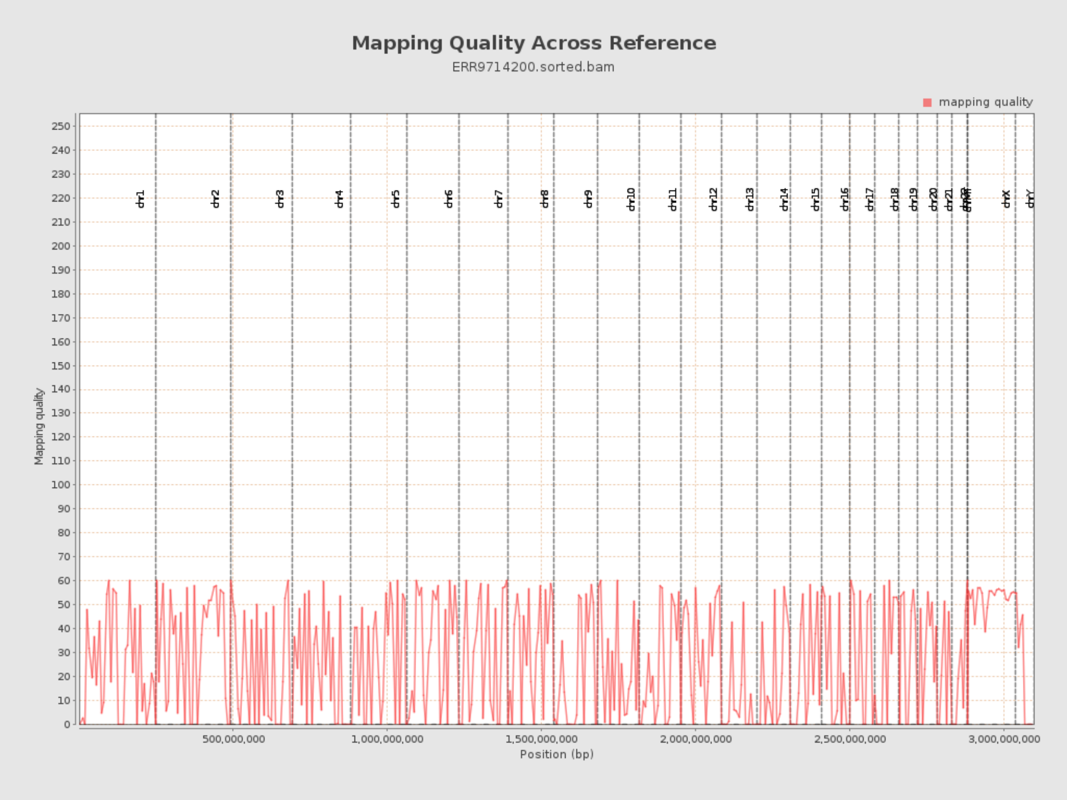
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram