Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 10:42:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068109.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_SRR6068109 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068109.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 10:42:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068109.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,888,026
Mapped reads	3,662,064 / 94.19%
Unmapped reads	225,962 / 5.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,820 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	1,446,588 / 37.21%
Duplication rate	18.97%
Clipped reads	1,997,308 / 51.37%

2.2. ACGT Content

Number/percentage of A's	62,288,327 / 26.35%
Number/percentage of C's	42,805,629 / 18.11%
Number/percentage of T's	76,601,924 / 32.4%
Number/percentage of G's	54,674,206 / 23.13%
Number/percentage of N's	26,708 / 0.01%
GC Percentage	41.24%

2.3. Coverage

Mean	0.0764

Standard Deviation	0.954

2.4. Mapping Quality

Mean Mapping Quality	46.32

2.5. Mismatches and indels

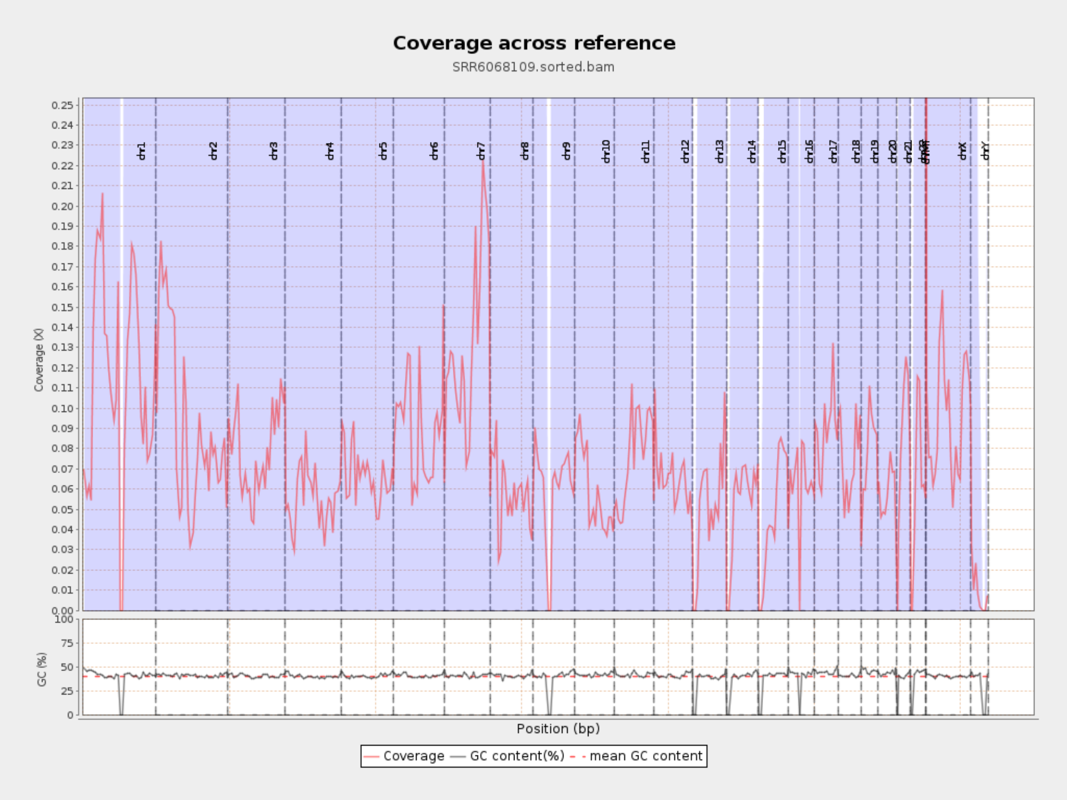
General error rate	0.52%
Mismatches	1,191,764
Insertions	15,770
Mapped reads with at least one insertion	0.43%
Deletions	52,051
Mapped reads with at least one deletion	1.4%
Homopolymer indels	44.33%

2.6. Chromosome stats

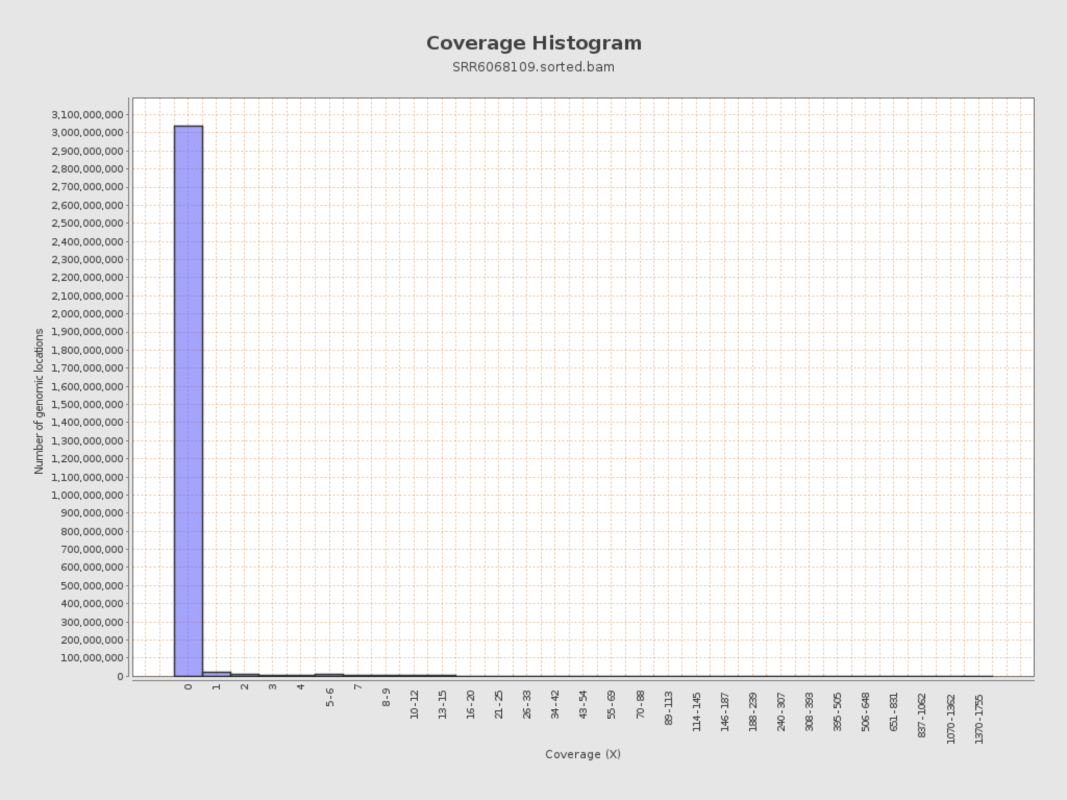
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28495997	0.1143	1.5417
chr2	243199373	22823983	0.0938	1.0445
chr3	198022430	15510466	0.0783	0.7904
chr4	191154276	10605205	0.0555	0.7467
chr5	180915260	12153650	0.0672	0.7413
chr6	171115067	15394442	0.09	0.8657
chr7	159138663	21415179	0.1346	1.1645

chr8	146364022	8330609	0.0569	1.0681
chr9	141213431	8537347	0.0605	0.7389
chr10	135534747	7960459	0.0587	1.2628
chr11	135006516	10356927	0.0767	0.8601
chr12	133851895	8825297	0.0659	0.7363
chr13	115169878	5927371	0.0515	0.6441
chr14	107349540	5617871	0.0523	0.6477
chr15	102531392	4664148	0.0455	0.5965
chr16	90354753	5515747	0.061	0.7073
chr17	81195210	7316088	0.0901	0.8747
chr18	78077248	5787611	0.0741	0.9629
chr19	59128983	4732057	0.08	1.0934
chr20	63025520	3713623	0.0589	0.6962
chr21	48129895	4034726	0.0838	0.8247
chr22	51304566	3114253	0.0607	0.7065
chrMT	16571	340843	20.5686	27.9
chrX	155270560	14760393	0.0951	1.0139
chrY	59373566	554869	0.0093	0.2465

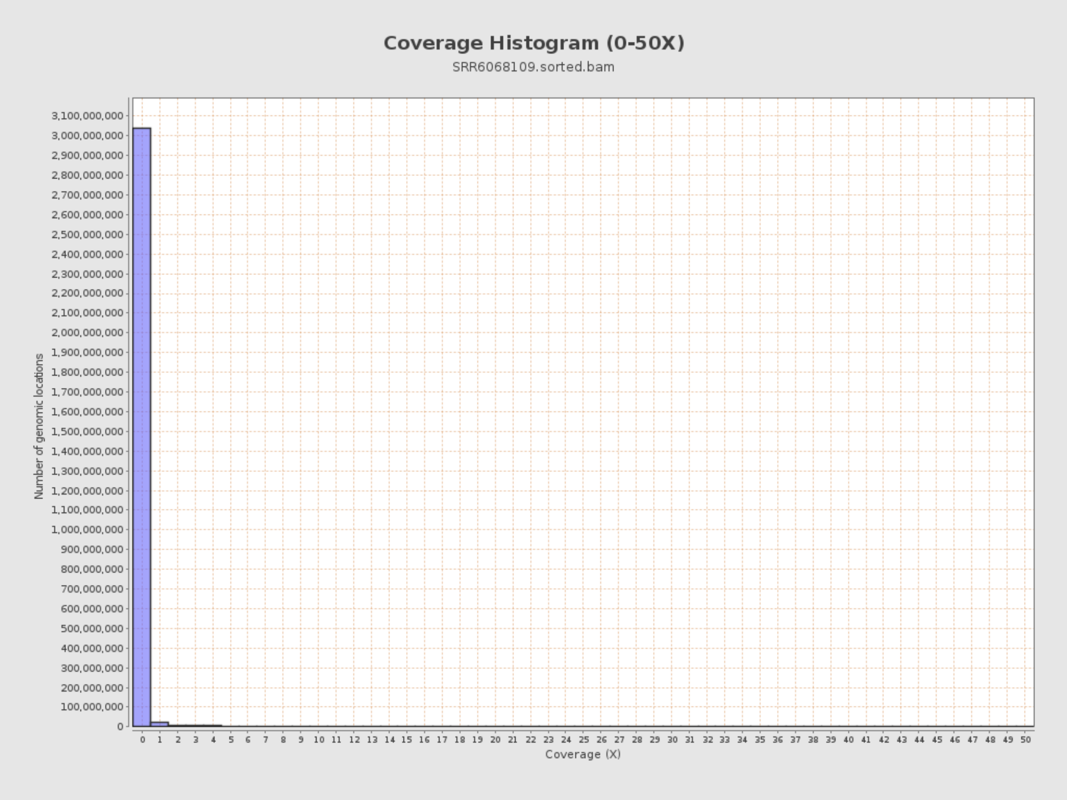
3. Results : Coverage across reference



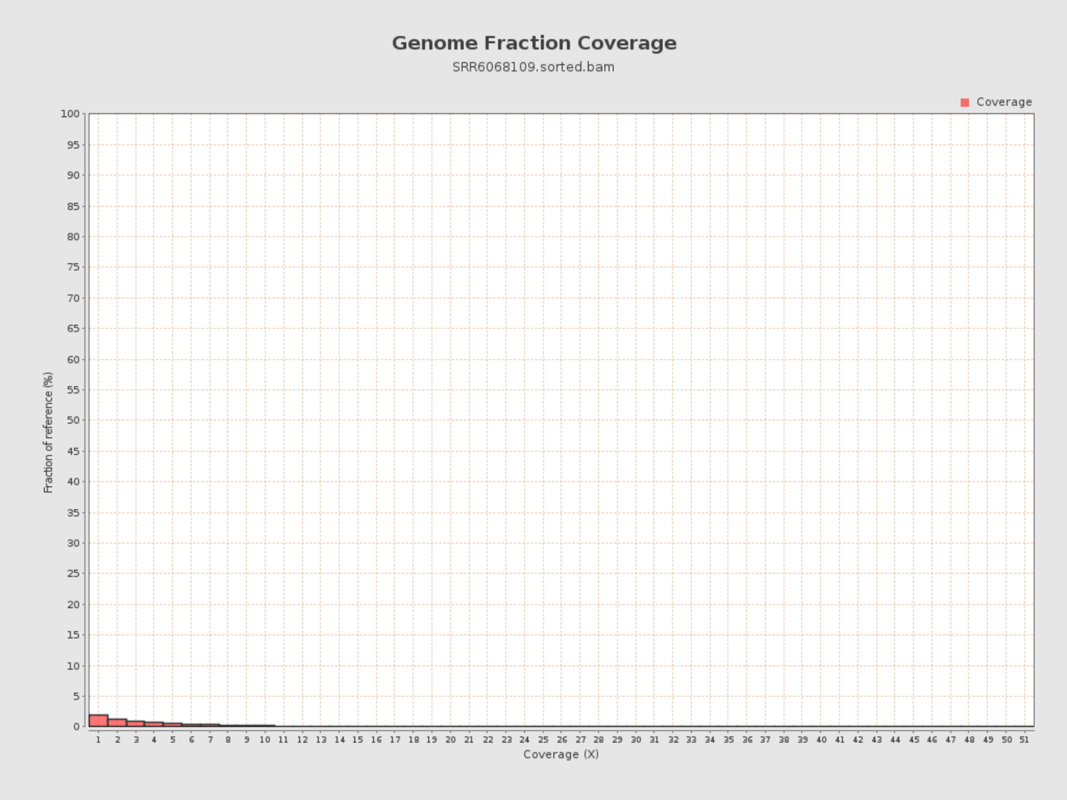
4. Results : Coverage Histogram



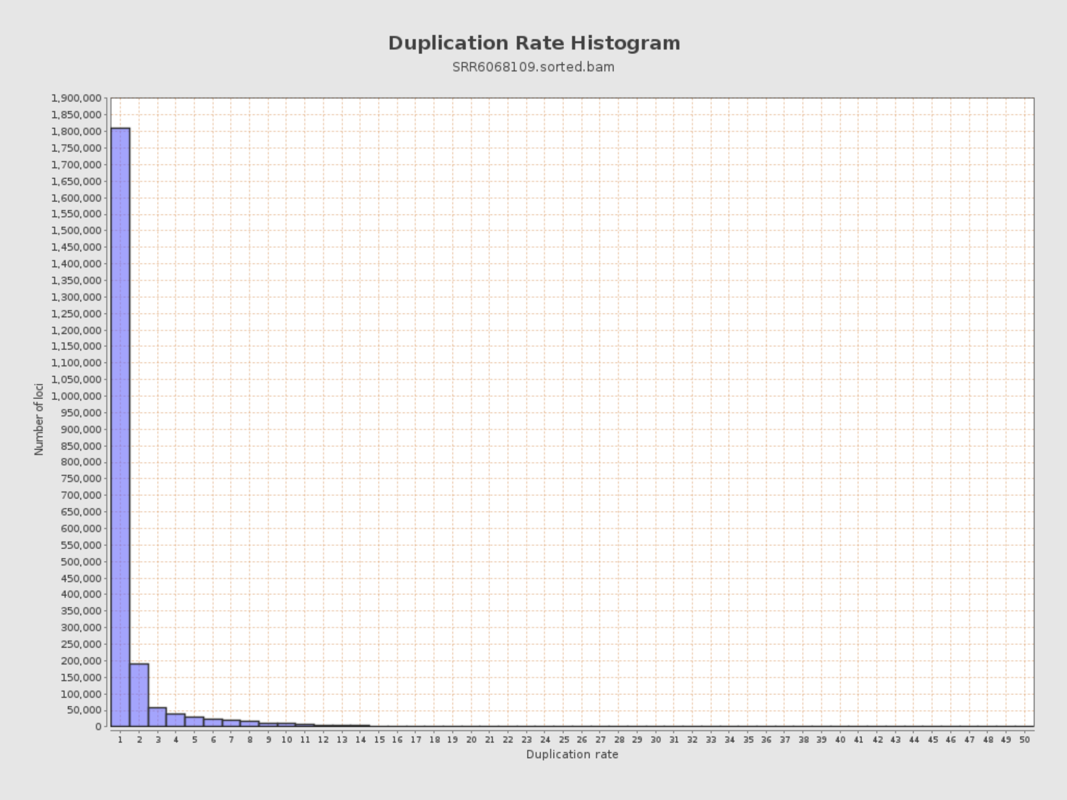
5. Results : Coverage Histogram (0-50X)



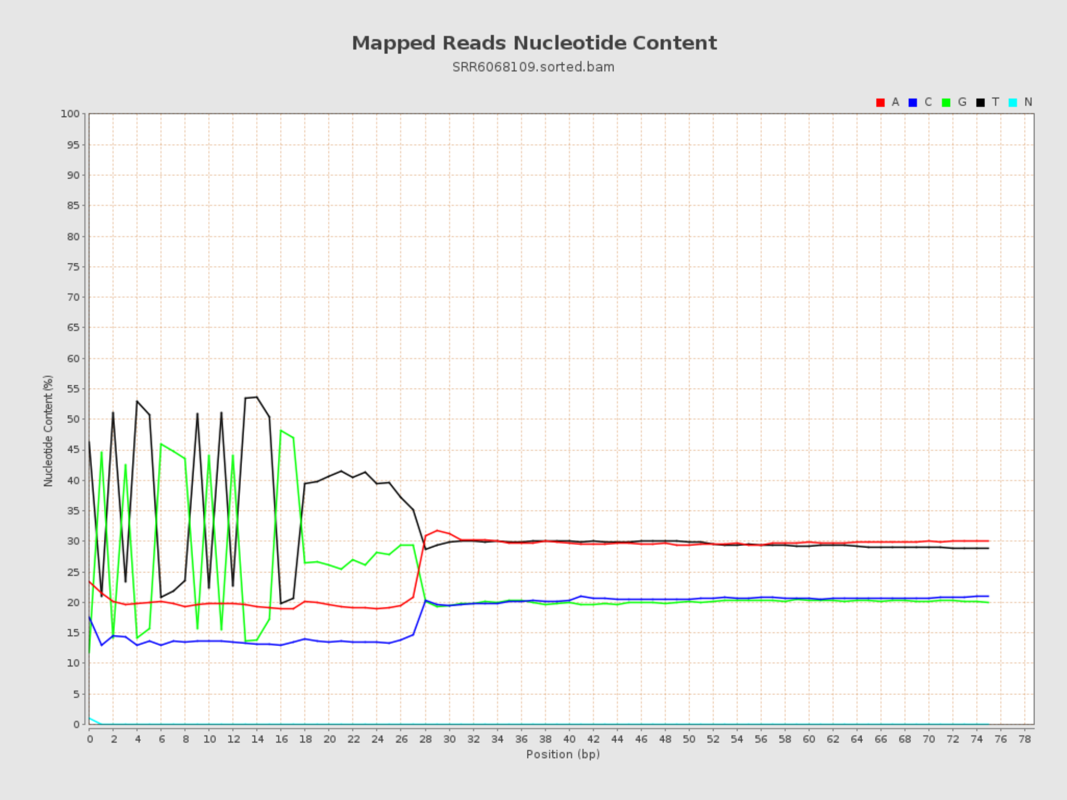
6. Results : Genome Fraction Coverage



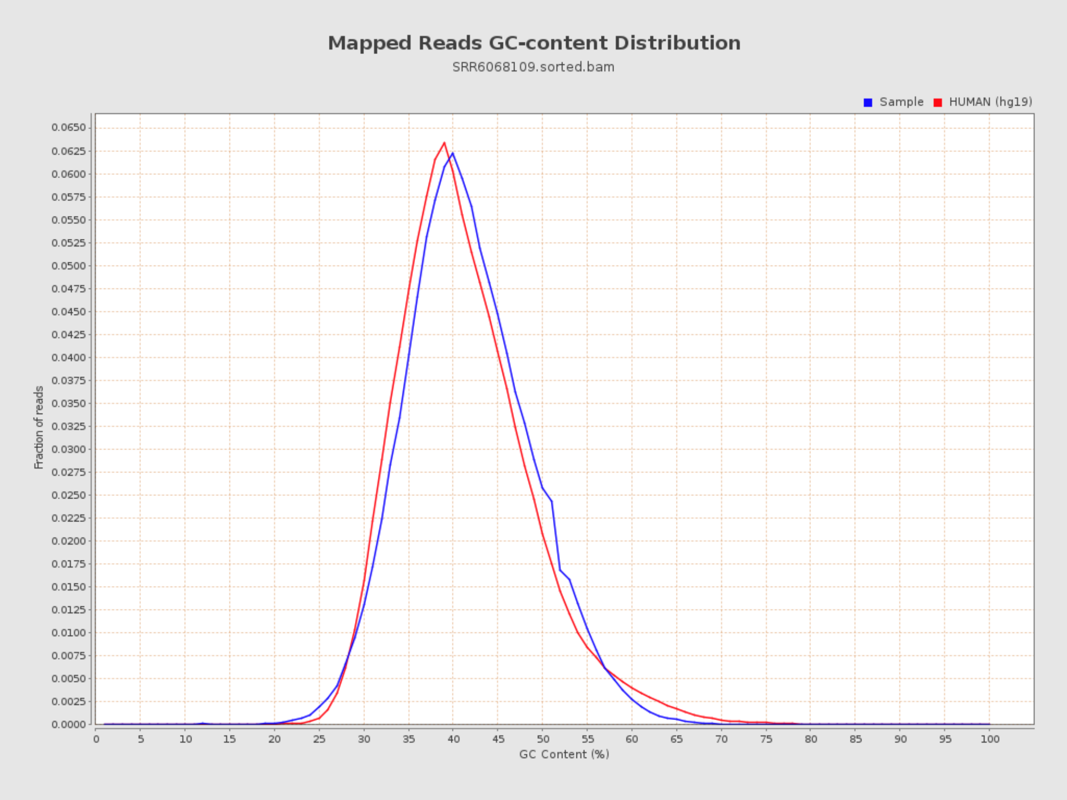
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



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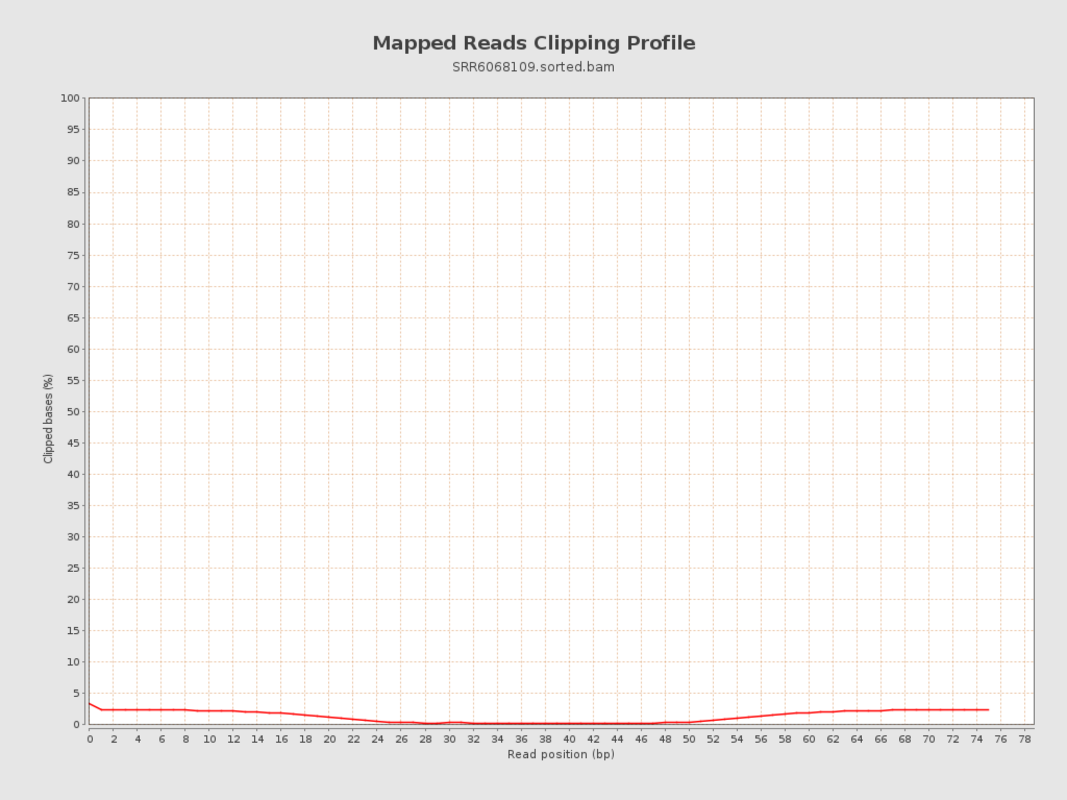
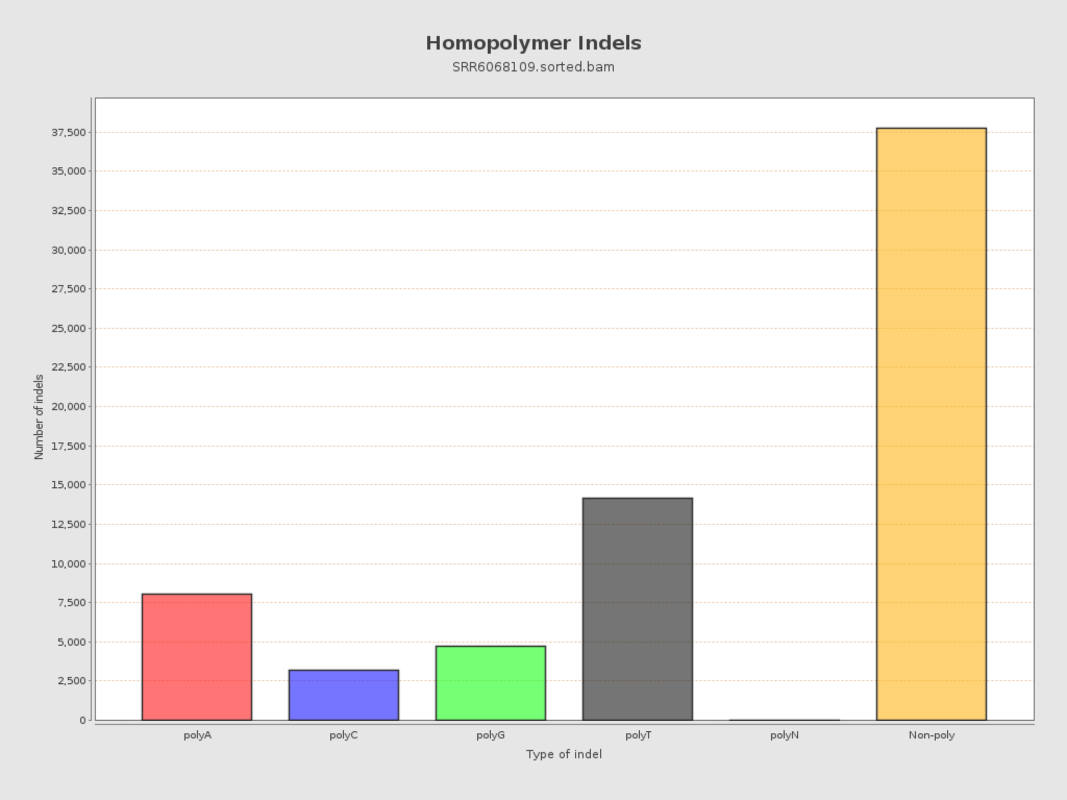
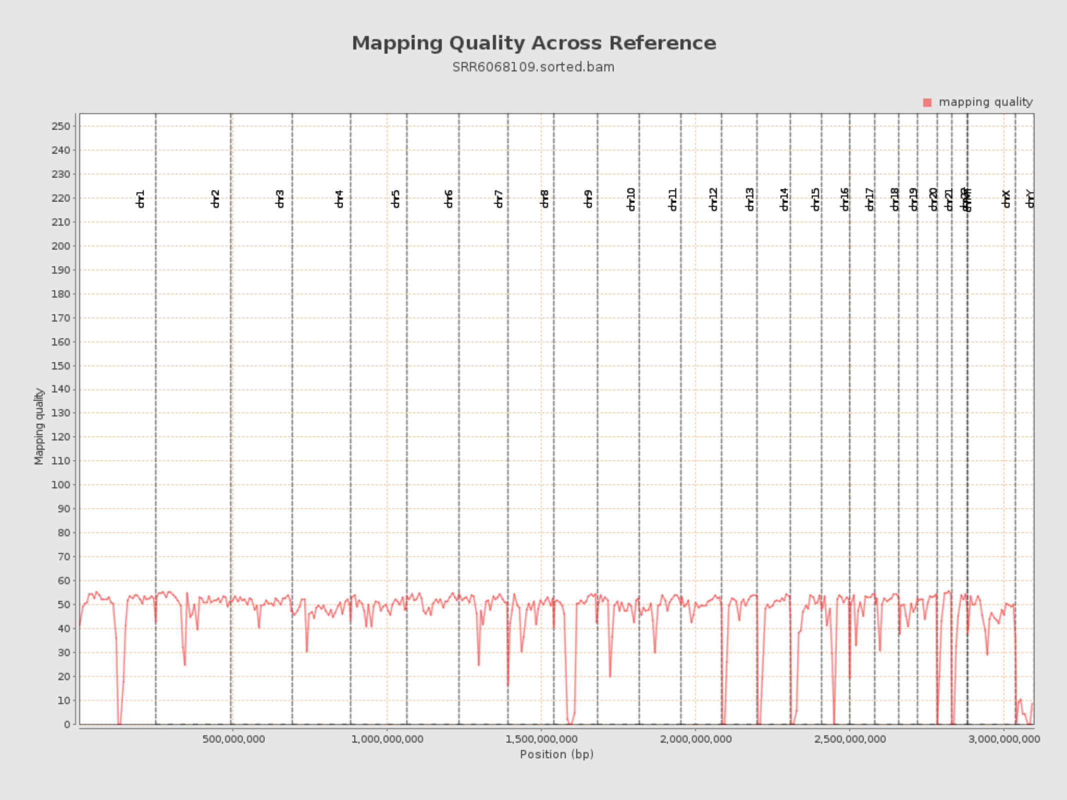
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram