Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 01:47:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004103.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_SRR6004103 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004103.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 01:47:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004103.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,638,221
Mapped reads	2,442,667 / 67.14%
Unmapped reads	1,195,554 / 32.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,836 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	296,480 / 8.15%
Duplication rate	9.21%
Clipped reads	1,021,323 / 28.07%

2.2. ACGT Content

Number/percentage of A's	46,644,310 / 28.18%
Number/percentage of C's	31,030,088 / 18.75%
Number/percentage of T's	52,740,915 / 31.86%
Number/percentage of G's	35,091,527 / 21.2%
Number/percentage of N's	22,419 / 0.01%
GC Percentage	39.95%

2.3. Coverage

Mean	0.0535

Standard Deviation	0.5586

2.4. Mapping Quality

Mean Mapping Quality	46.42

2.5. Mismatches and indels

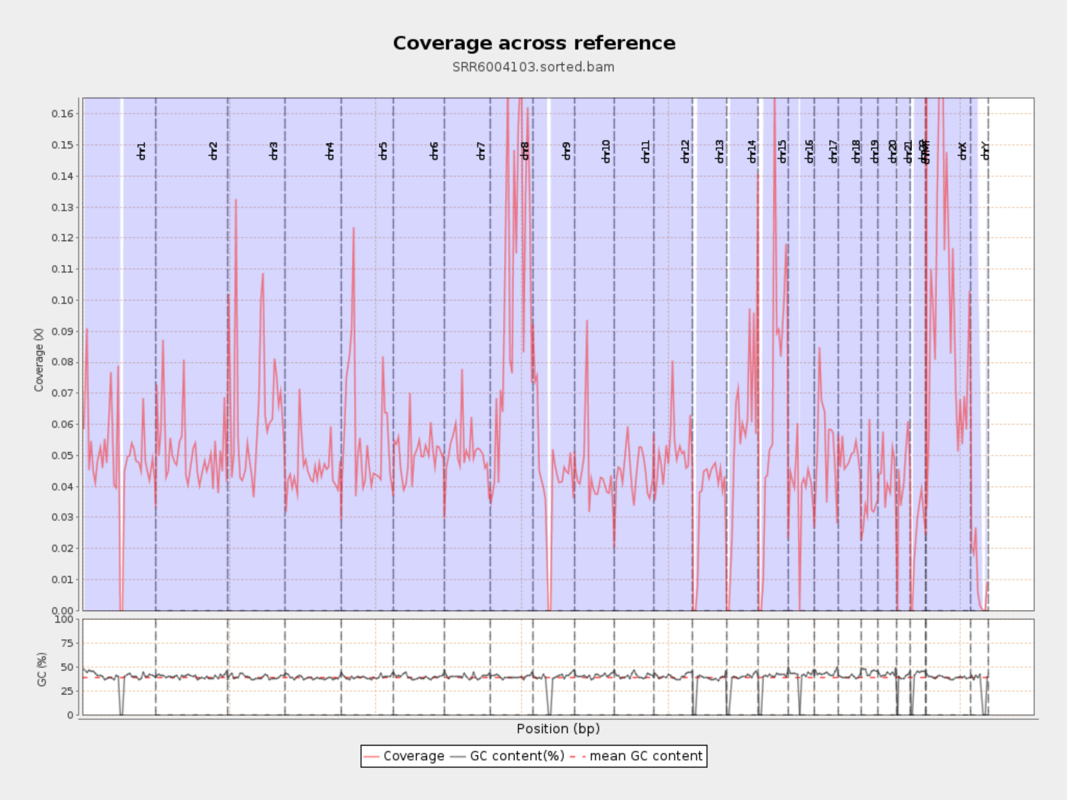
General error rate	0.97%
Mismatches	1,579,580
Insertions	13,707
Mapped reads with at least one insertion	0.56%
Deletions	45,966
Mapped reads with at least one deletion	1.86%
Homopolymer indels	47.58%

2.6. Chromosome stats

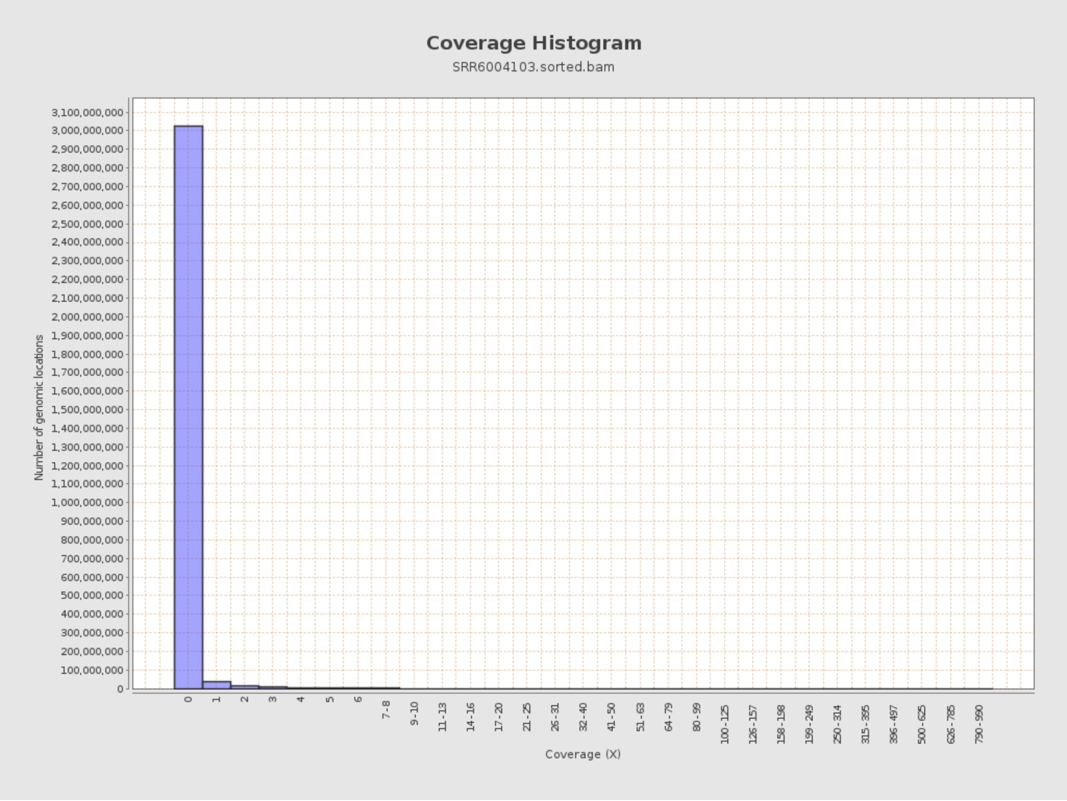
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12185393	0.0489	0.8846
chr2	243199373	12465827	0.0513	0.5561
chr3	198022430	12739860	0.0643	0.5041
chr4	191154276	8718351	0.0456	0.4215
chr5	180915260	10165563	0.0562	0.4628
chr6	171115067	8693921	0.0508	0.4933
chr7	159138663	8137417	0.0511	0.5974

chr8	146364022	14934454	0.102	0.7721
chr9	141213431	6025207	0.0427	0.4589
chr10	135534747	5917214	0.0437	0.5383
chr11	135006516	6001687	0.0445	0.4557
chr12	133851895	6832657	0.051	0.4375
chr13	115169878	4122868	0.0358	0.3633
chr14	107349540	5979537	0.0557	0.4755
chr15	102531392	6918319	0.0675	0.5178
chr16	90354753	3449507	0.0382	0.3944
chr17	81195210	4422353	0.0545	0.4788
chr18	78077248	3892533	0.0499	0.7486
chr19	59128983	2087315	0.0353	0.6549
chr20	63025520	2799364	0.0444	0.4099
chr21	48129895	2031802	0.0422	0.4024
chr22	51304566	1224448	0.0239	0.2811
chrMT	16571	177970	10.7398	8.3816
chrX	155270560	15096149	0.0972	0.6556
chrY	59373566	585846	0.0099	0.2055

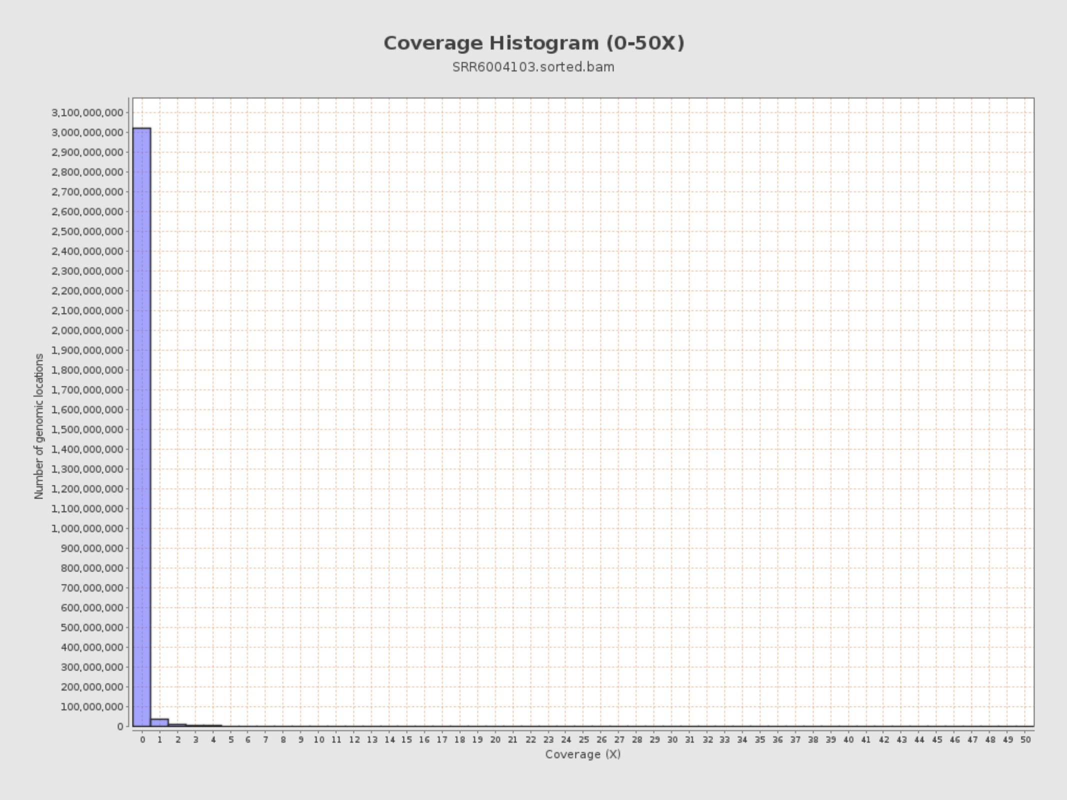
3. Results : Coverage across reference



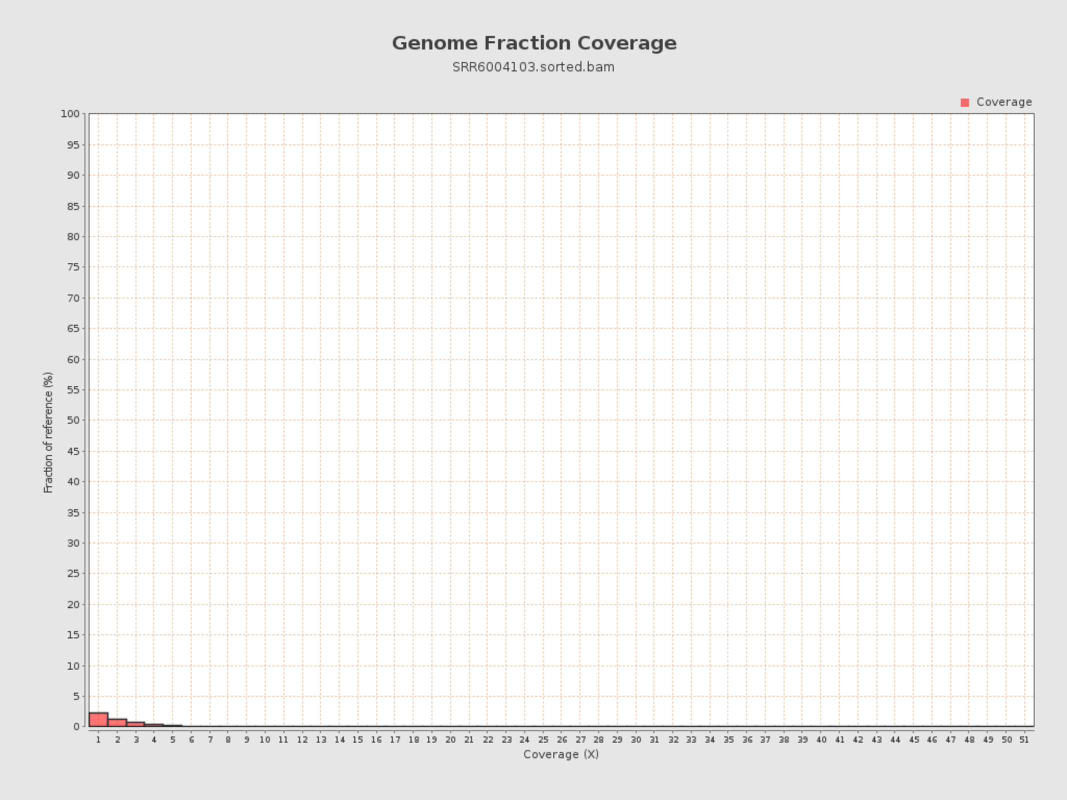
4. Results : Coverage Histogram



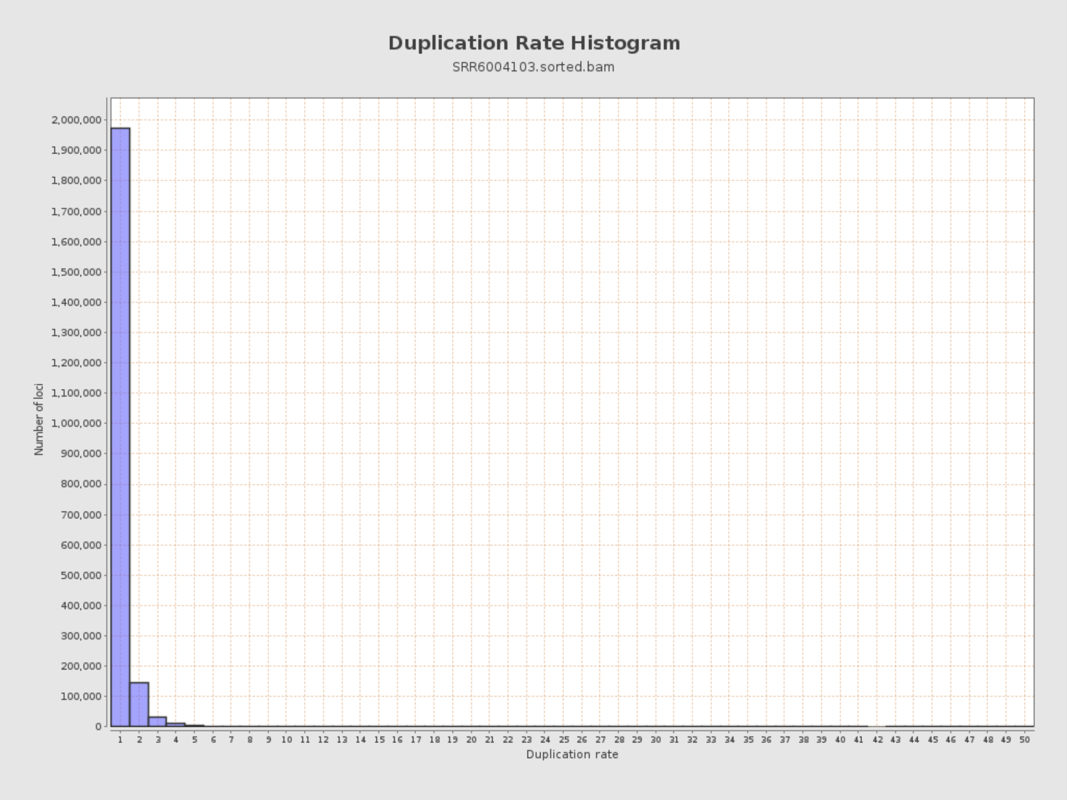
5. Results : Coverage Histogram (0-50X)



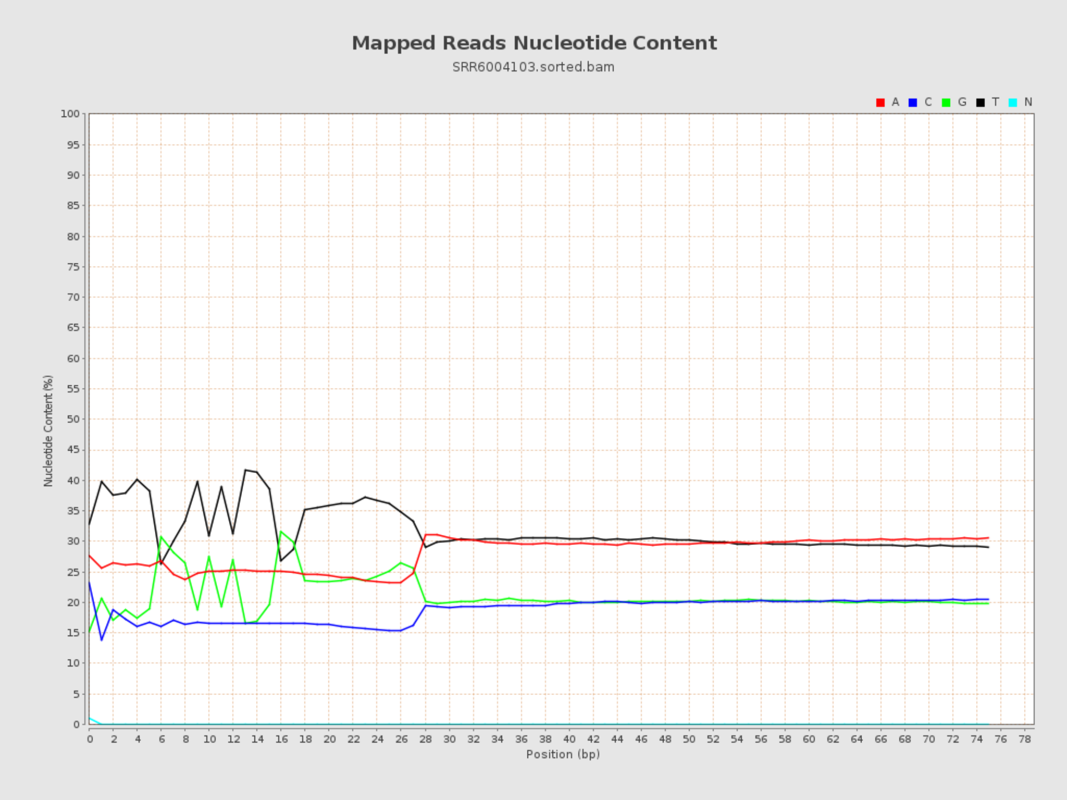
6. Results : Genome Fraction Coverage



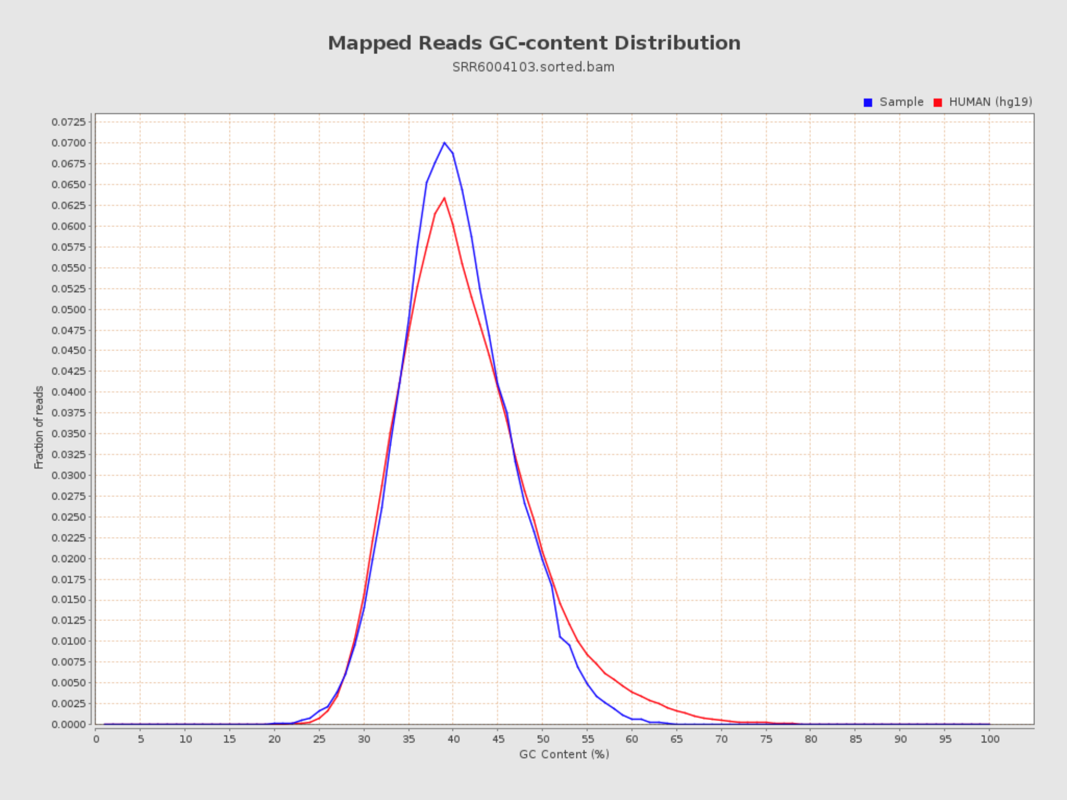
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



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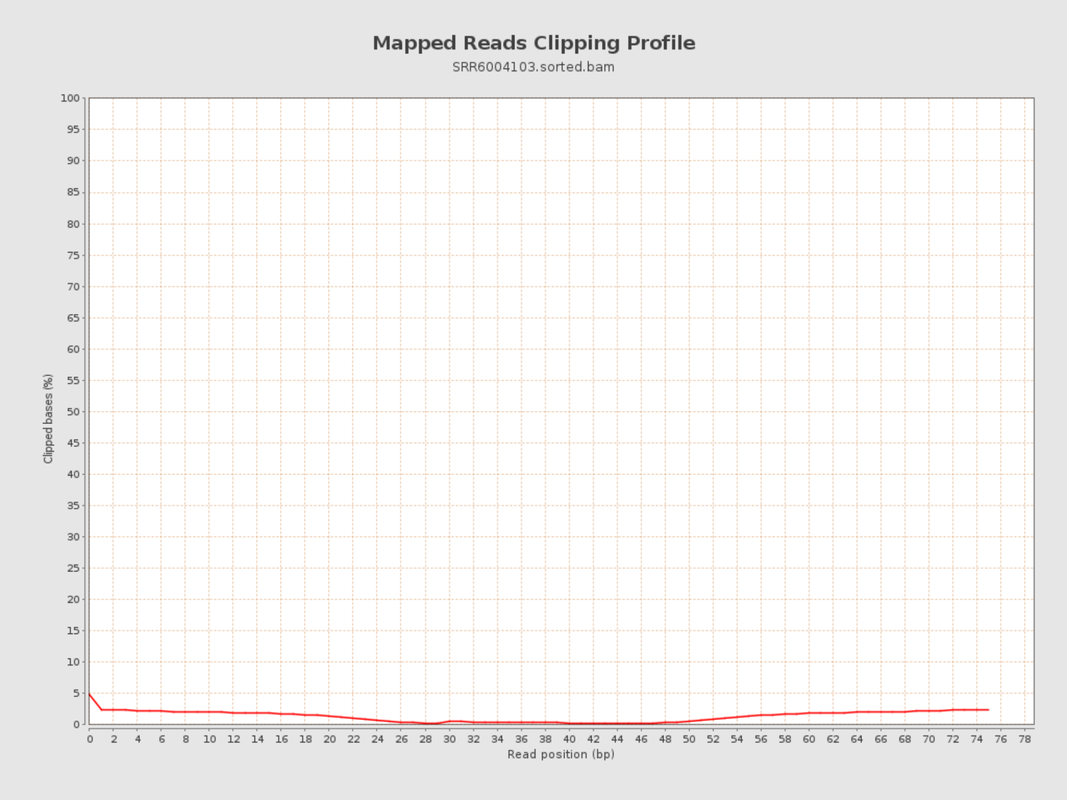
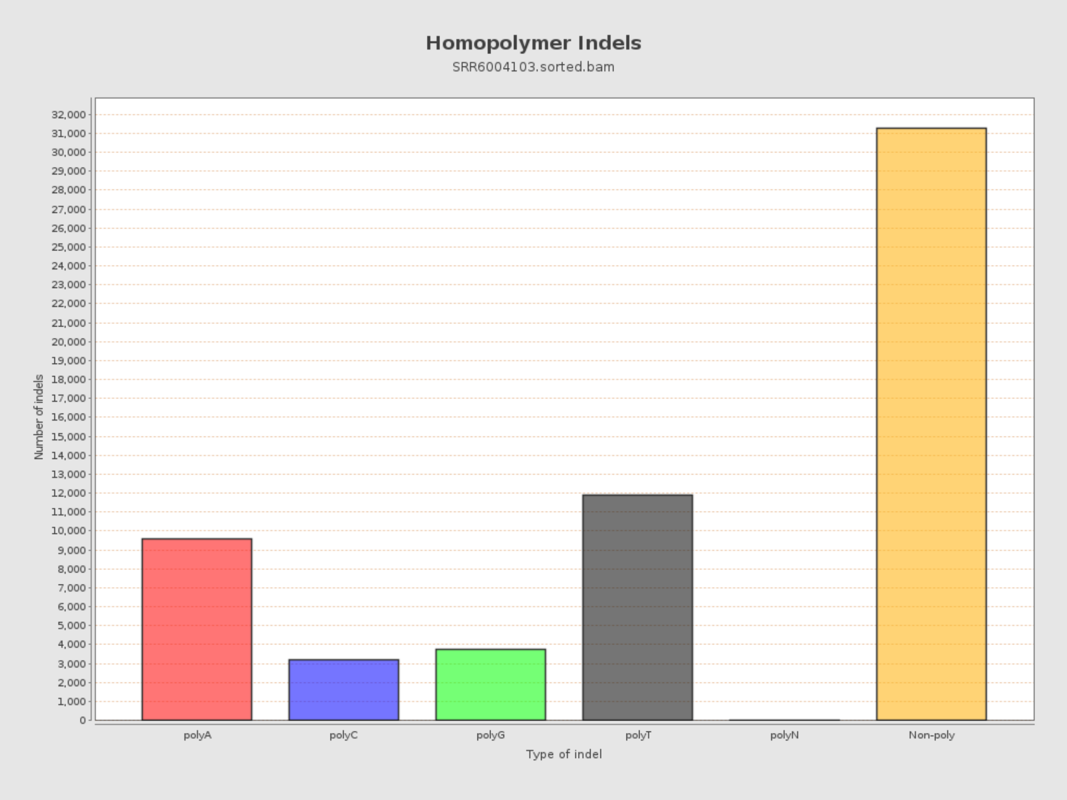
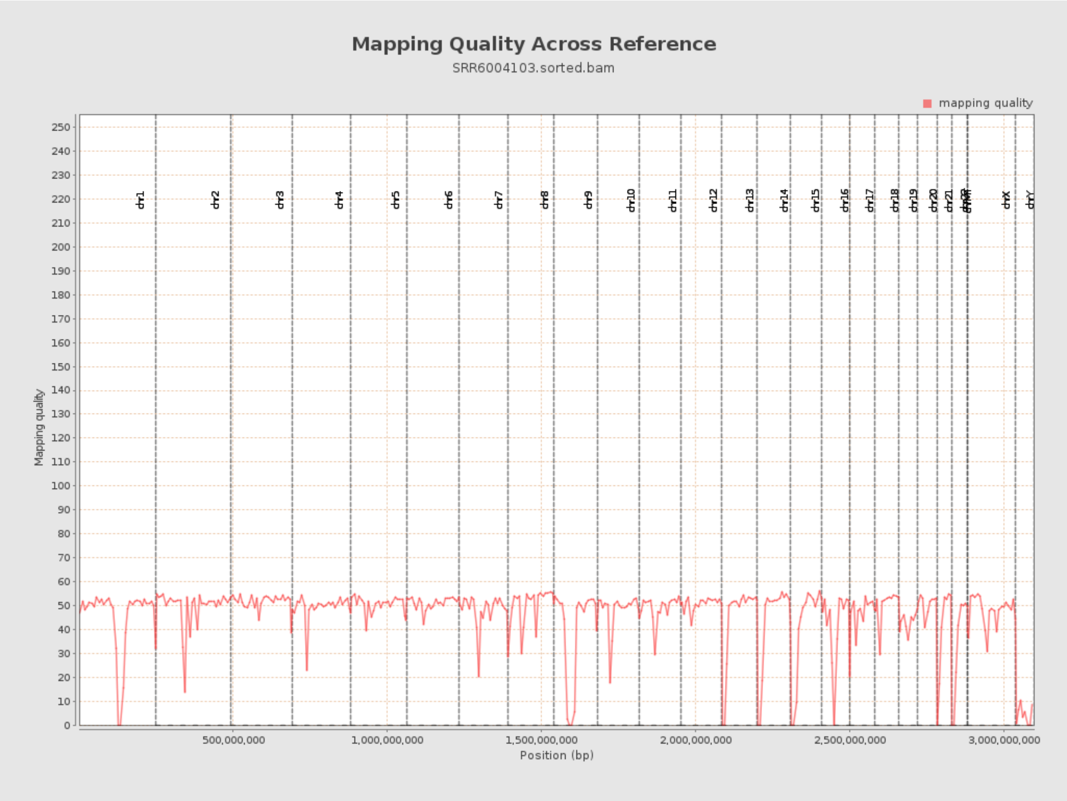
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram