Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 00:59:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004091.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_SRR6004091 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004091.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 00:59:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004091.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,227,196
Mapped reads	1,830,524 / 82.19%
Unmapped reads	396,672 / 17.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,654 / 1.2%
Read min/max/mean length	30 / 76 / 76.42
Duplicated reads (estimated)	214,287 / 9.62%
Duplication rate	9.32%
Clipped reads	997,868 / 44.8%

2.2. ACGT Content

Number/percentage of A's	32,482,907 / 27.5%
Number/percentage of C's	21,372,474 / 18.1%
Number/percentage of T's	37,853,025 / 32.05%
Number/percentage of G's	26,355,645 / 22.31%
Number/percentage of N's	45,780 / 0.04%
GC Percentage	40.41%

2.3. Coverage

Mean	0.0382

Standard Deviation	0.3892

2.4. Mapping Quality

Mean Mapping Quality	42.53

2.5. Mismatches and indels

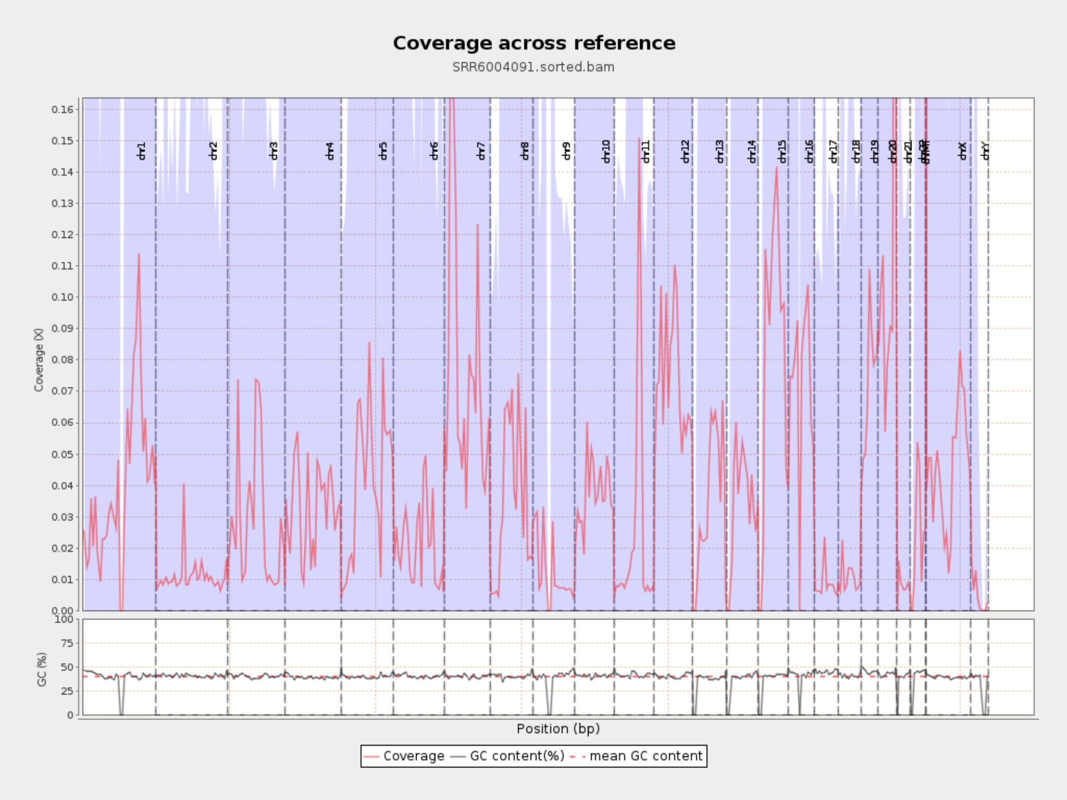
General error rate	0.85%
Mismatches	990,686
Insertions	8,183
Mapped reads with at least one insertion	0.44%
Deletions	37,592
Mapped reads with at least one deletion	2.03%
Homopolymer indels	44.91%

2.6. Chromosome stats

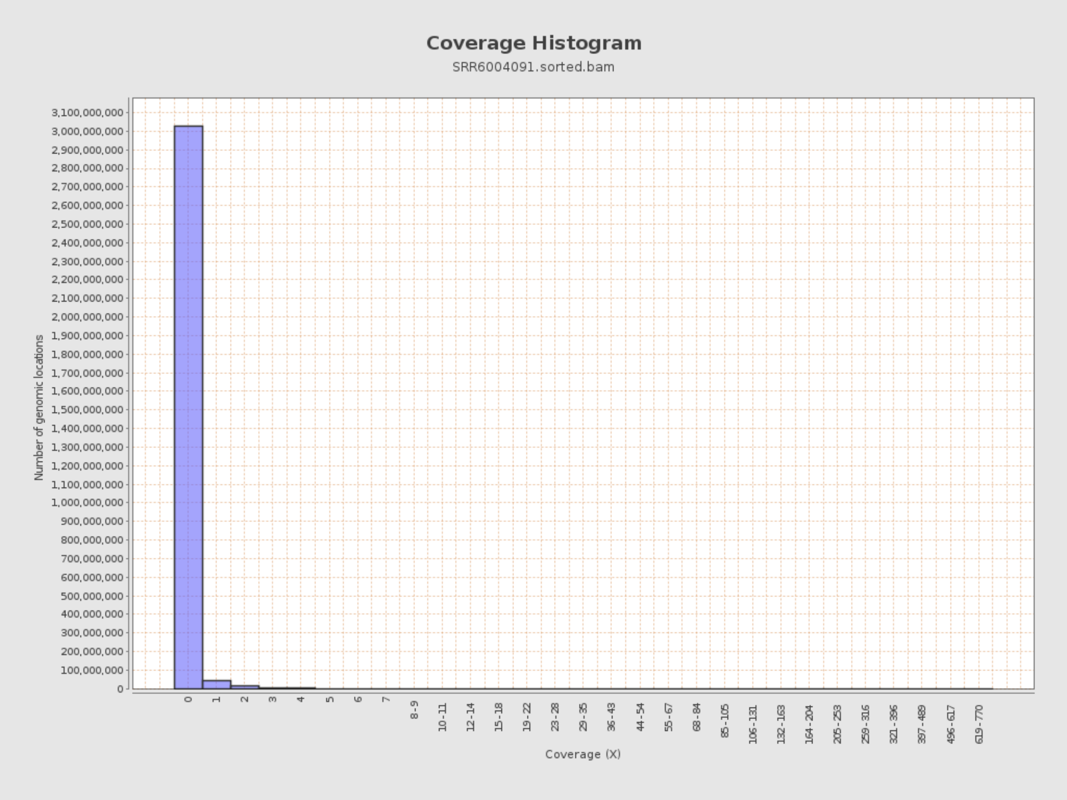
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9905705	0.0397	0.6937
chr2	243199373	2652569	0.0109	0.3454
chr3	198022430	5614546	0.0284	0.2555
chr4	191154276	6290501	0.0329	0.2796
chr5	180915260	7475471	0.0413	0.3155
chr6	171115067	3633415	0.0212	0.2352
chr7	159138663	12385712	0.0778	0.5099

chr8	146364022	5113252	0.0349	0.5046
chr9	141213431	1705195	0.0121	0.2137
chr10	135534747	5082854	0.0375	0.3945
chr11	135006516	3266961	0.0242	0.2525
chr12	133851895	9940243	0.0743	0.4208
chr13	115169878	4162422	0.0361	0.2926
chr14	107349540	3715830	0.0346	0.2884
chr15	102531392	8491909	0.0828	0.4482
chr16	90354753	6450171	0.0714	0.4188
chr17	81195210	680103	0.0084	0.1299
chr18	78077248	813108	0.0104	0.3463
chr19	59128983	4337625	0.0734	0.5577
chr20	63025520	7445841	0.1181	0.5417
chr21	48129895	395687	0.0082	0.1325
chr22	51304566	1173930	0.0229	0.224
chrMT	16571	33950	2.0488	2.54
chrX	155270560	7118822	0.0458	0.331
chrY	59373566	286368	0.0048	0.1258

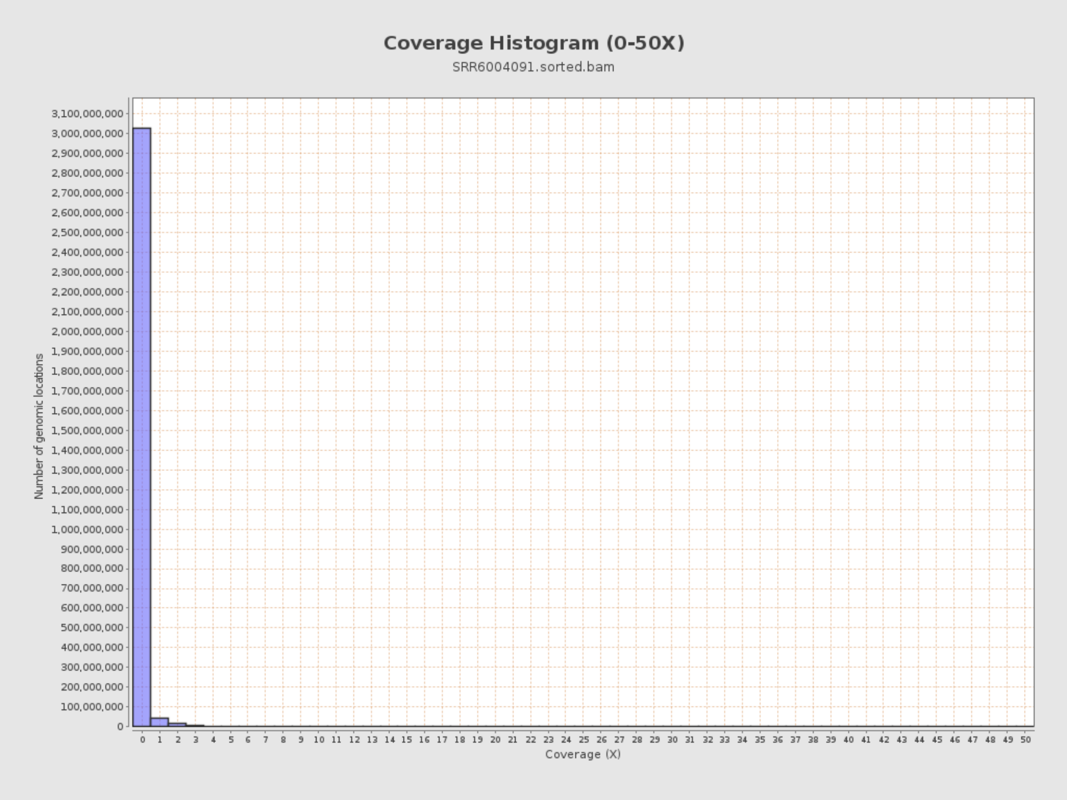
3. Results : Coverage across reference



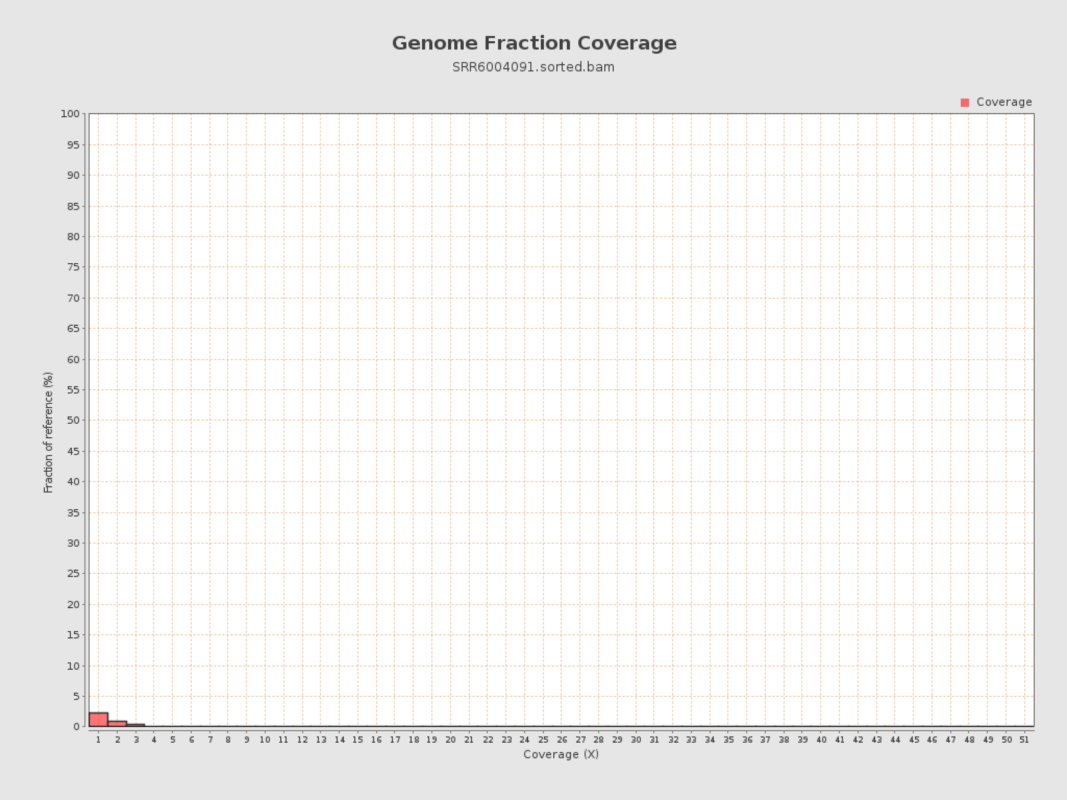
4. Results : Coverage Histogram



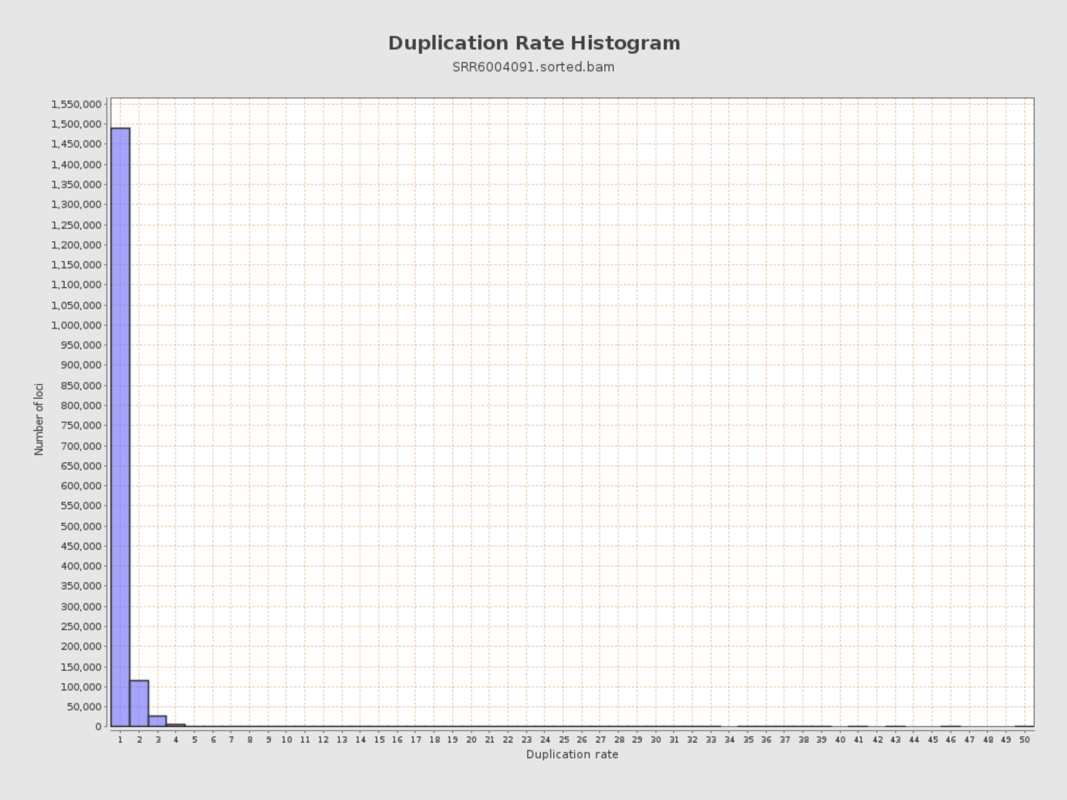
5. Results : Coverage Histogram (0-50X)



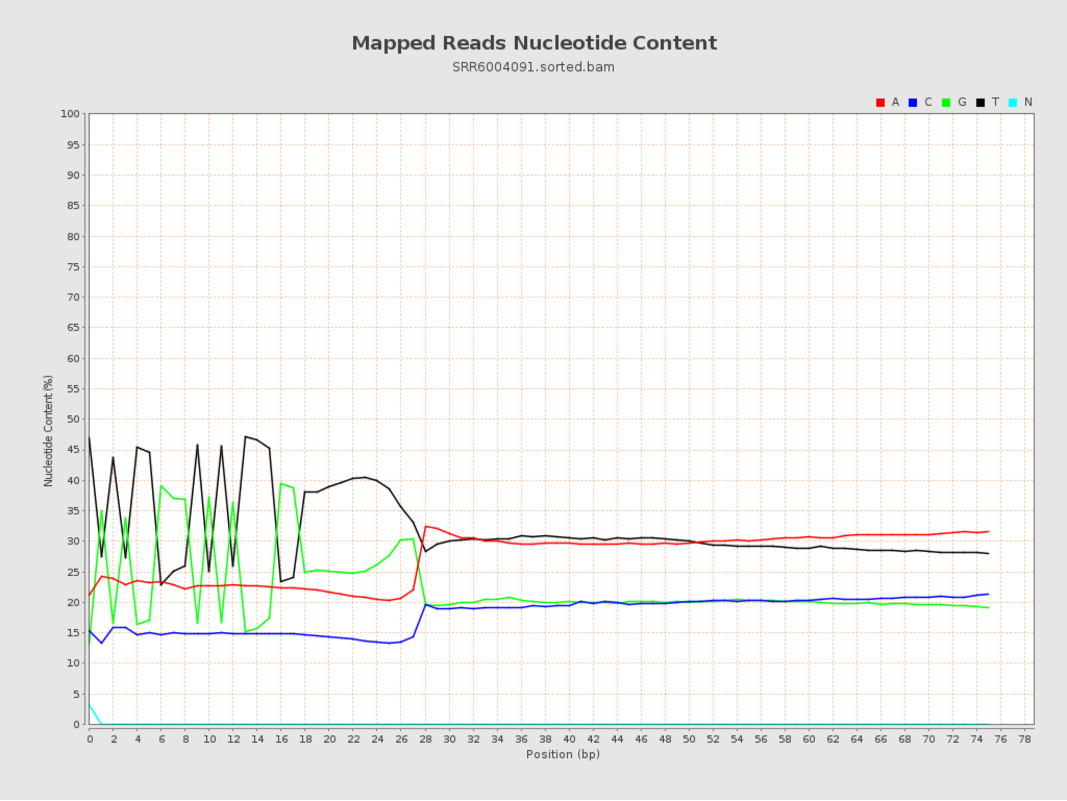
6. Results : Genome Fraction Coverage



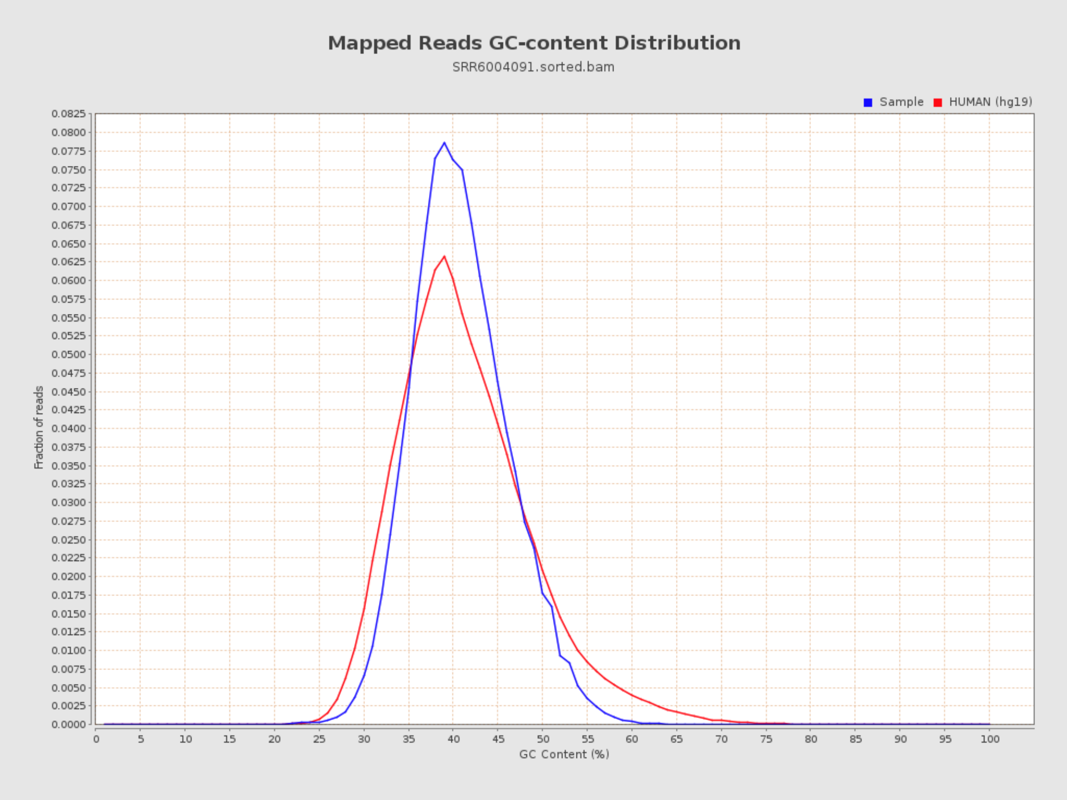
7. Results : Duplication Rate Histogram



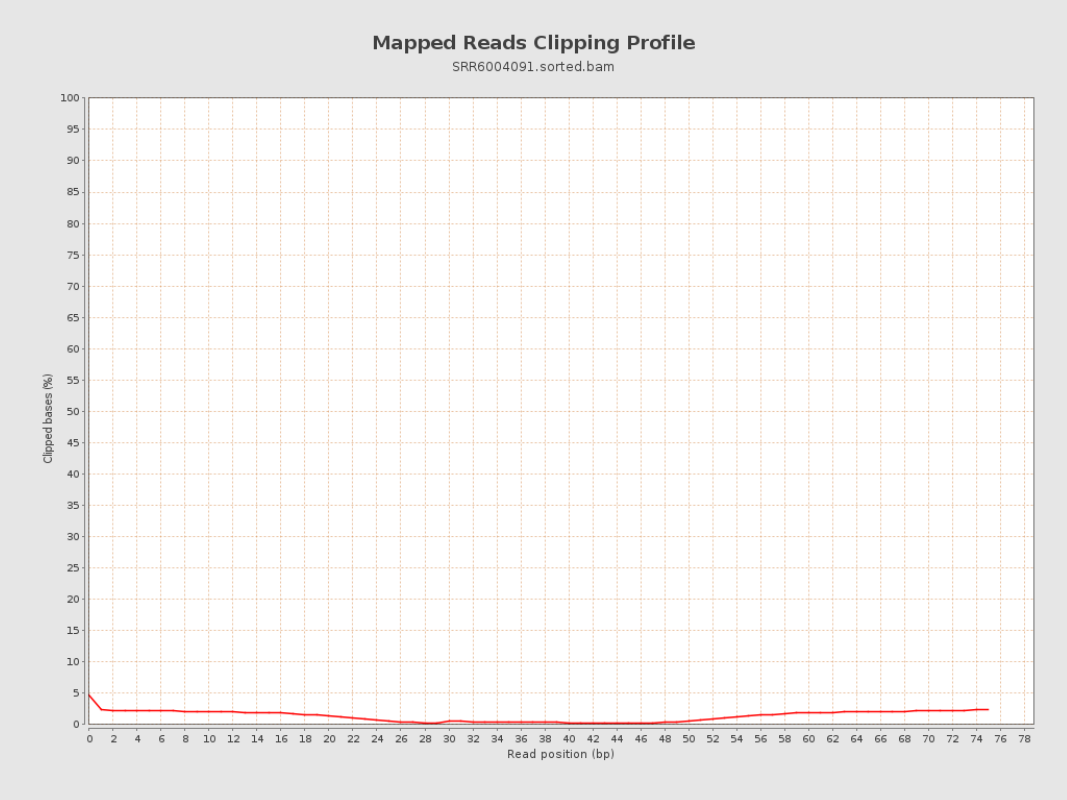
8. Results : Mapped Reads Nucleotide Content



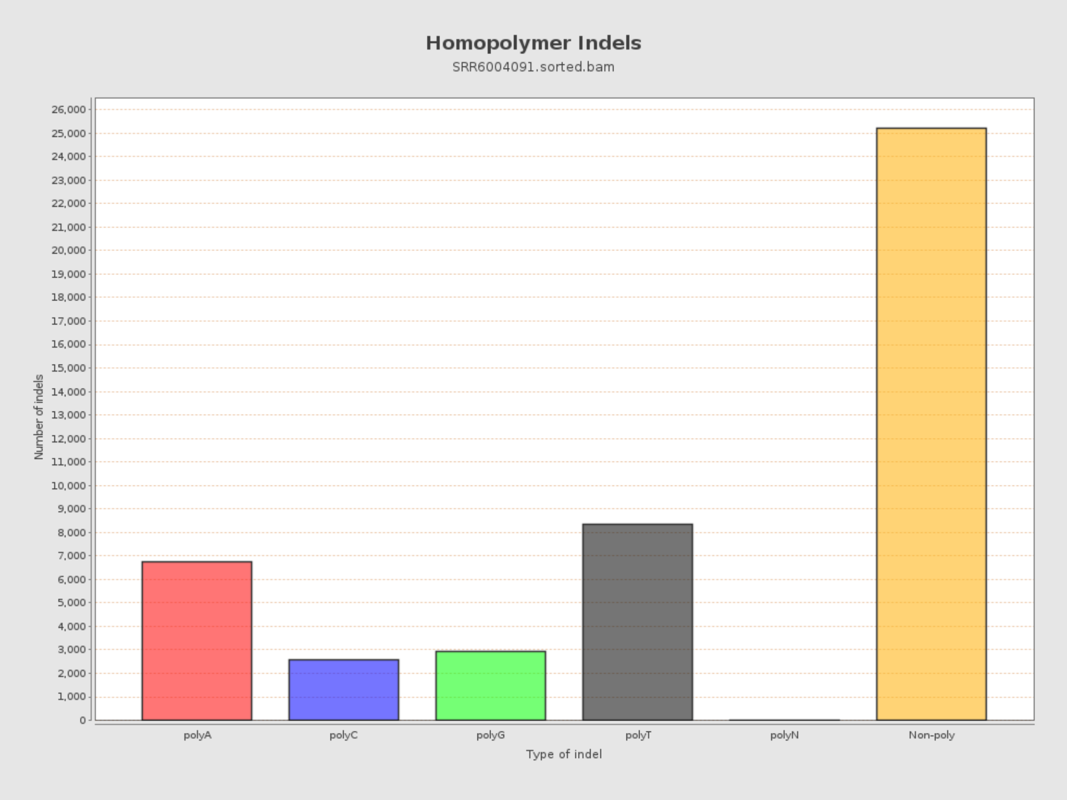
9. Results : Mapped Reads GC-content Distribution



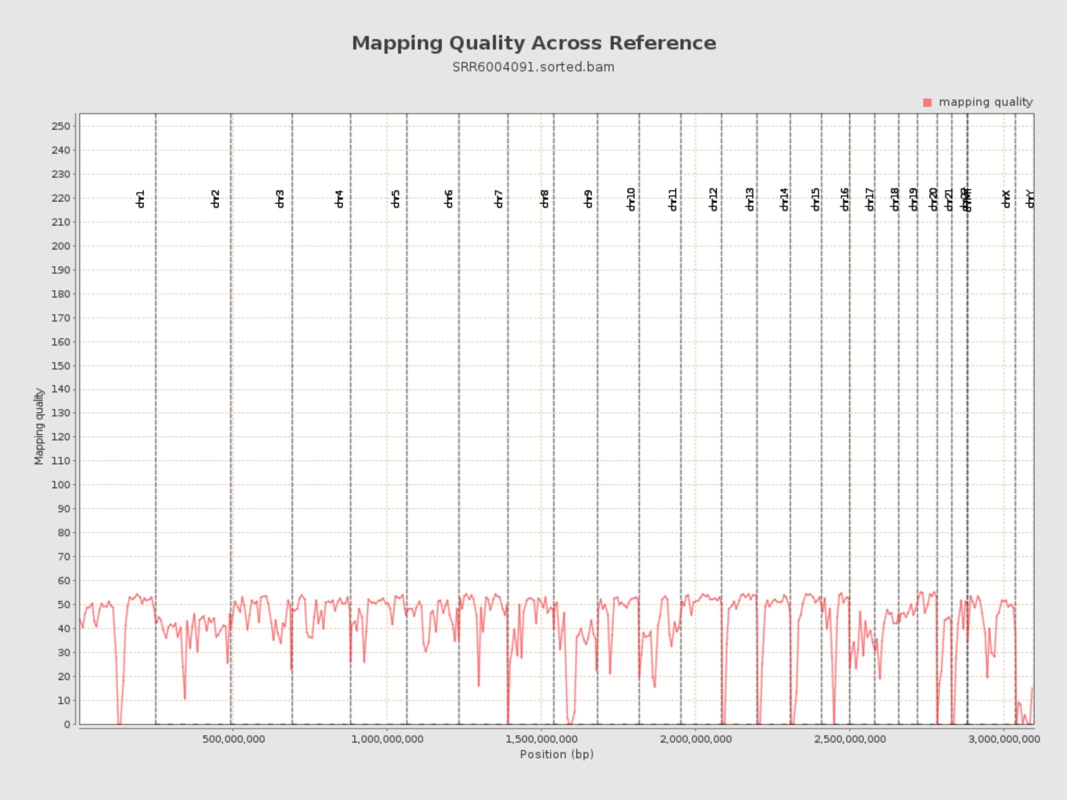
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram