Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 22:25:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004045.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_SRR6004045 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004045.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 22:25:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004045.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,711,427
Mapped reads	2,465,052 / 90.91%
Unmapped reads	246,375 / 9.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,781 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	108,086 / 3.99%
Duplication rate	3.44%
Clipped reads	1,168,604 / 43.1%

2.2. ACGT Content

Number/percentage of A's	44,814,110 / 27.55%
Number/percentage of C's	30,543,088 / 18.77%
Number/percentage of T's	50,646,908 / 31.13%
Number/percentage of G's	36,660,166 / 22.53%
Number/percentage of N's	18,175 / 0.01%
GC Percentage	41.31%

2.3. Coverage

Mean	0.0526

Standard Deviation	0.4174

2.4. Mapping Quality

Mean Mapping Quality	45.84

2.5. Mismatches and indels

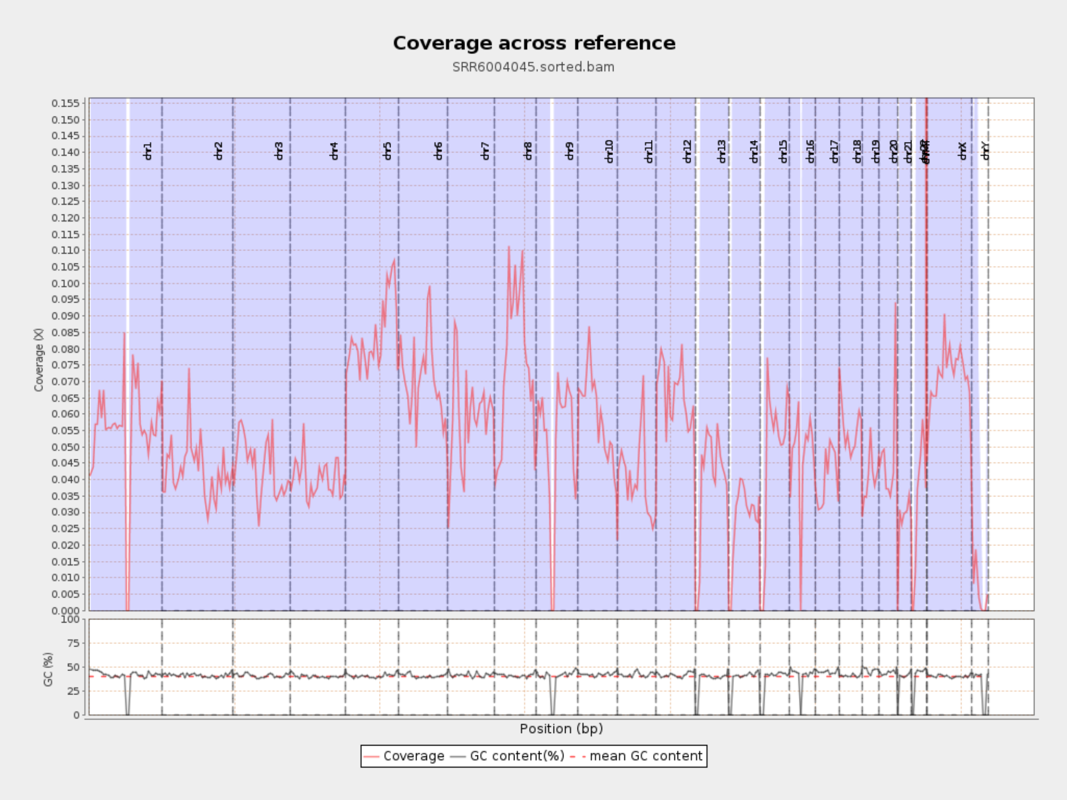
General error rate	0.75%
Mismatches	1,202,820
Insertions	11,230
Mapped reads with at least one insertion	0.45%
Deletions	44,967
Mapped reads with at least one deletion	1.8%
Homopolymer indels	45.15%

2.6. Chromosome stats

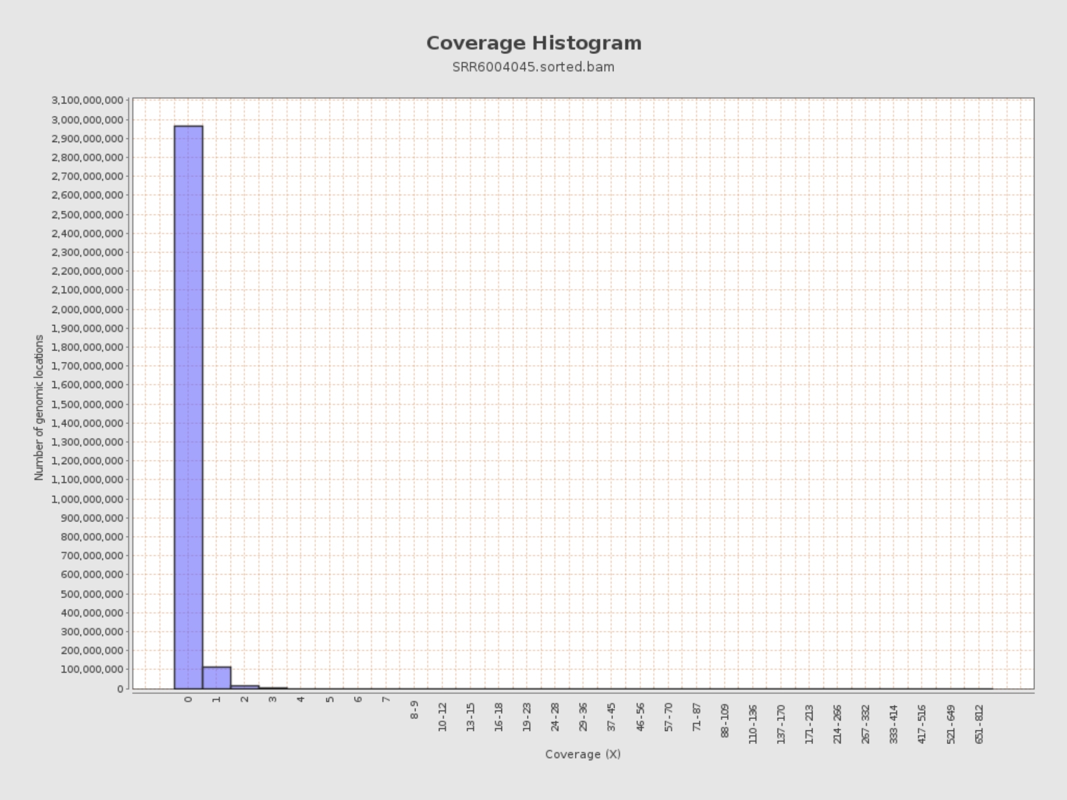
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13677067	0.0549	0.7567
chr2	243199373	10456450	0.043	0.4604
chr3	198022430	8714366	0.044	0.245
chr4	191154276	7718361	0.0404	0.2623
chr5	180915260	15212856	0.0841	0.3473
chr6	171115067	12110049	0.0708	0.3786
chr7	159138663	9544639	0.06	0.5152

chr8	146364022	11024382	0.0753	0.5191
chr9	141213431	7271090	0.0515	0.3876
chr10	135534747	8141294	0.0601	0.4238
chr11	135006516	5465511	0.0405	0.3161
chr12	133851895	8845257	0.0661	0.3085
chr13	115169878	4468686	0.0388	0.2304
chr14	107349540	2977231	0.0277	0.2292
chr15	102531392	4886985	0.0477	0.268
chr16	90354753	4256132	0.0471	0.2864
chr17	81195210	3309137	0.0408	0.2538
chr18	78077248	4343201	0.0556	0.6326
chr19	59128983	2435252	0.0412	0.5396
chr20	63025520	3099628	0.0492	0.2686
chr21	48129895	1314161	0.0273	0.2207
chr22	51304566	1653936	0.0322	0.2087
chrMT	16571	341472	20.6066	12.4644
chrX	155270560	11108833	0.0715	0.3524
chrY	59373566	385300	0.0065	0.1391

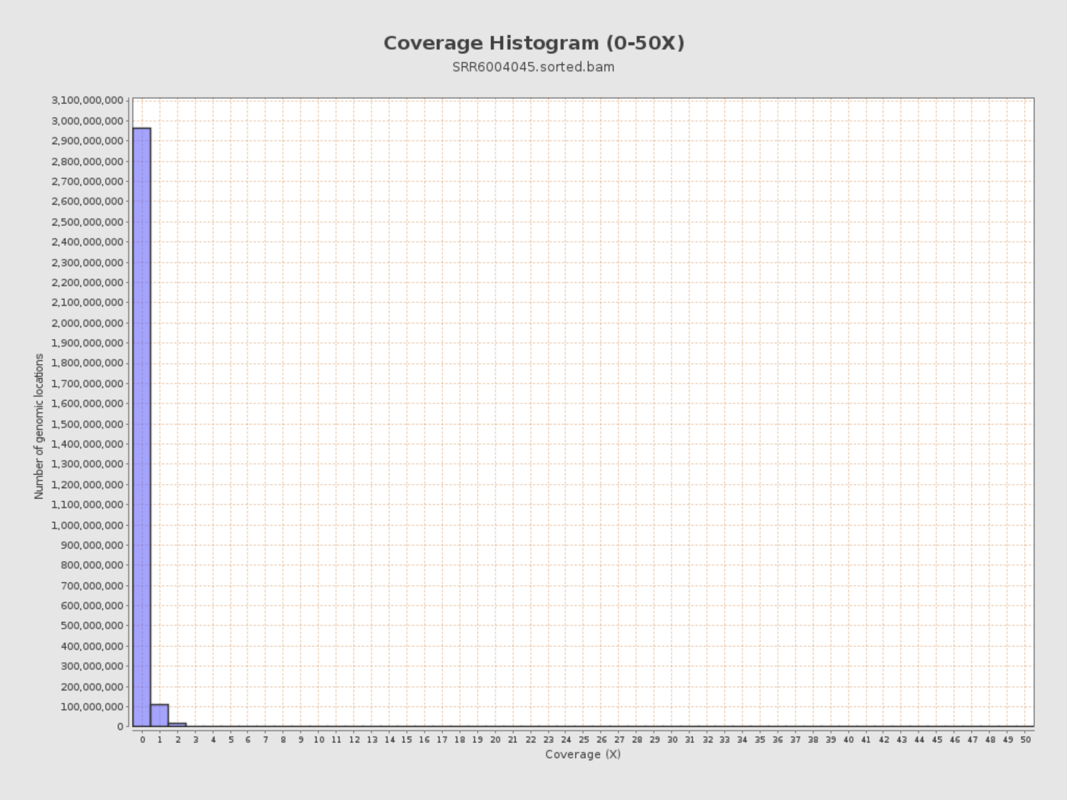
3. Results : Coverage across reference



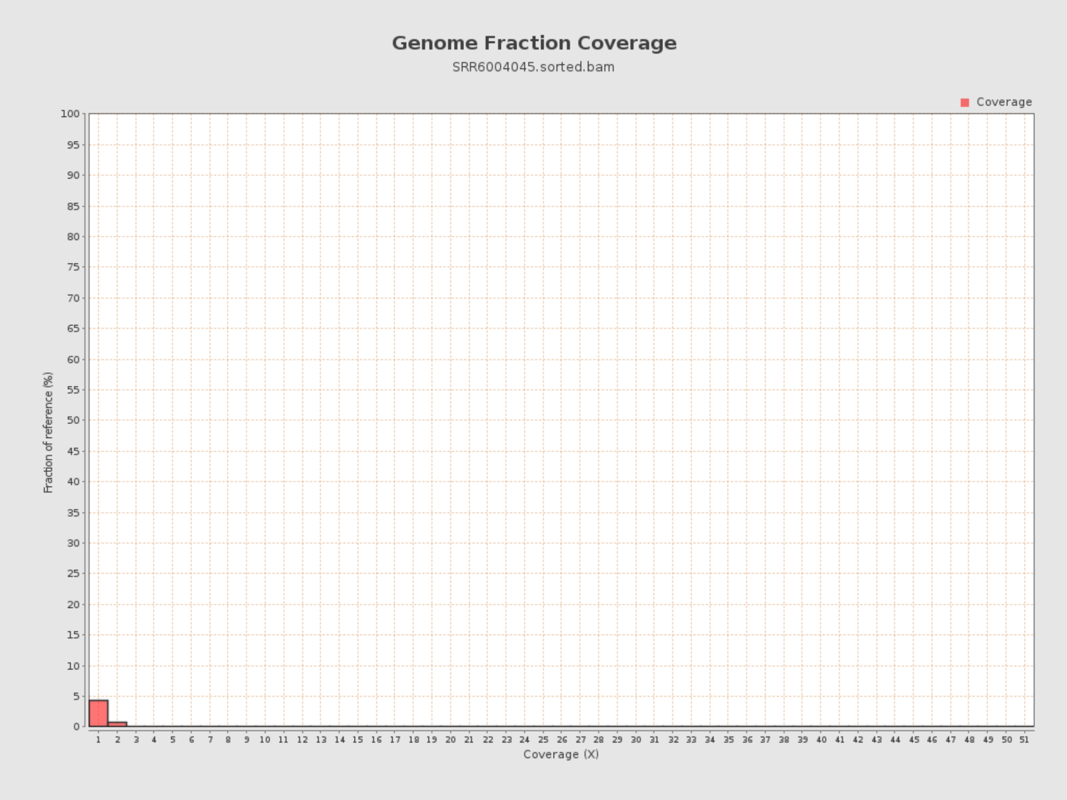
4. Results : Coverage Histogram



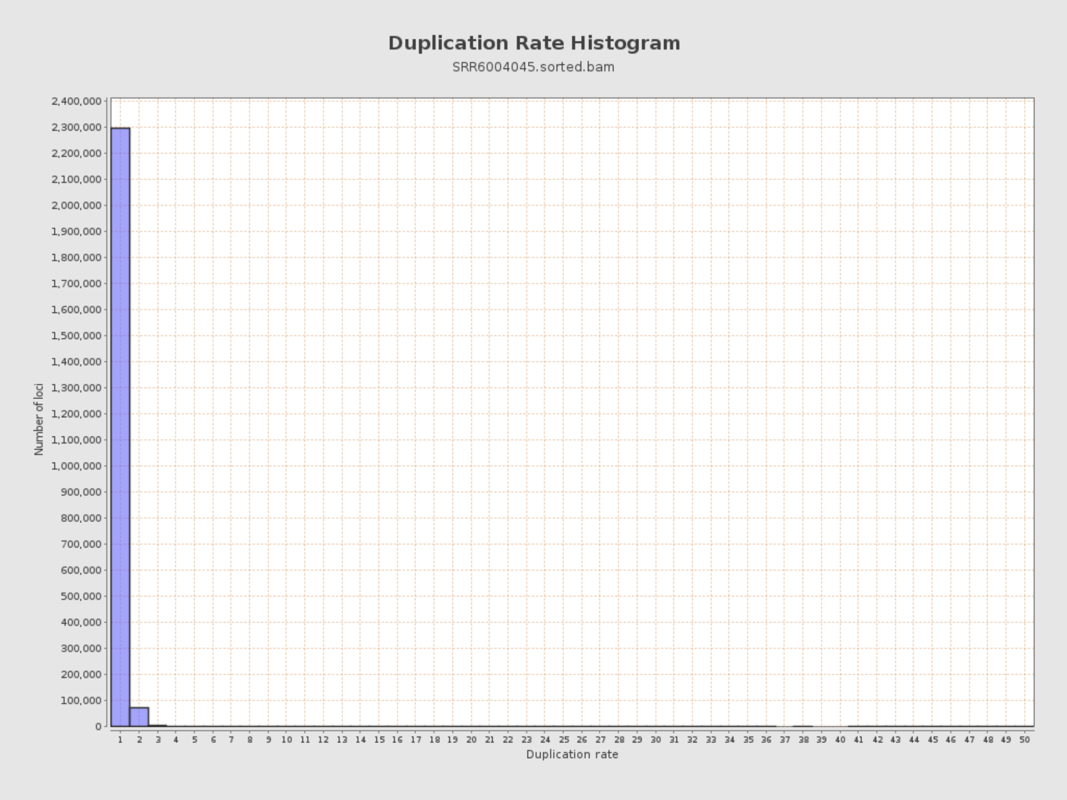
5. Results : Coverage Histogram (0-50X)



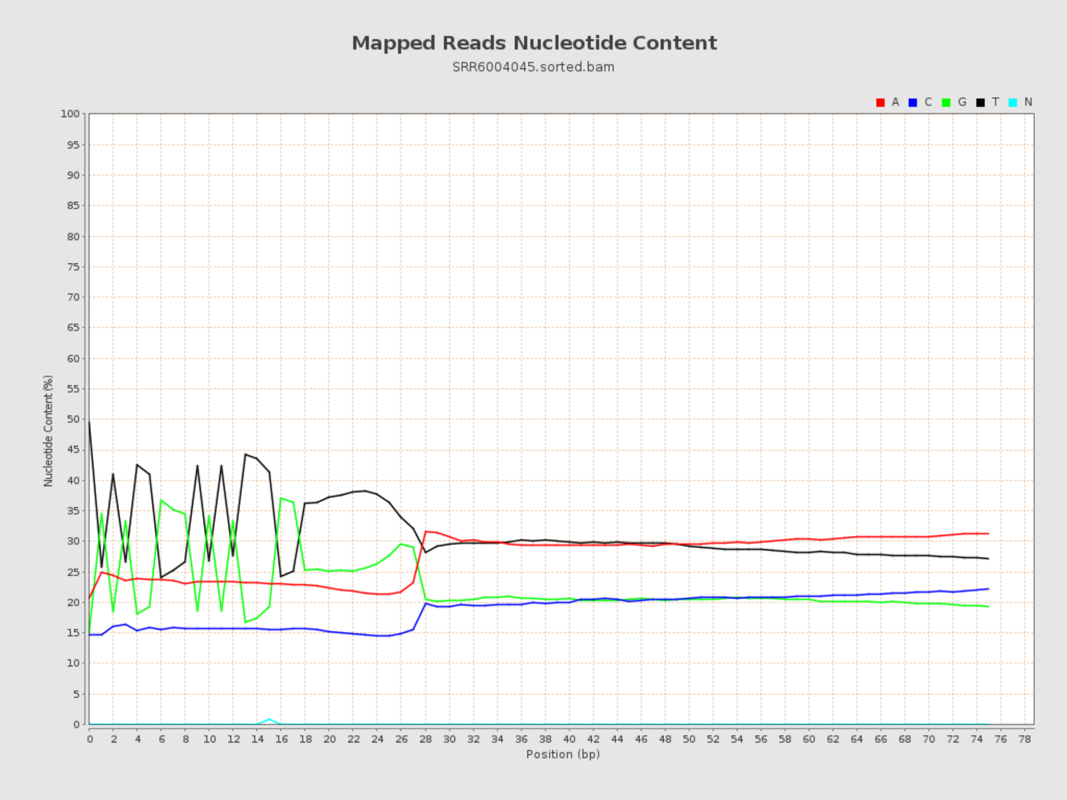
6. Results : Genome Fraction Coverage



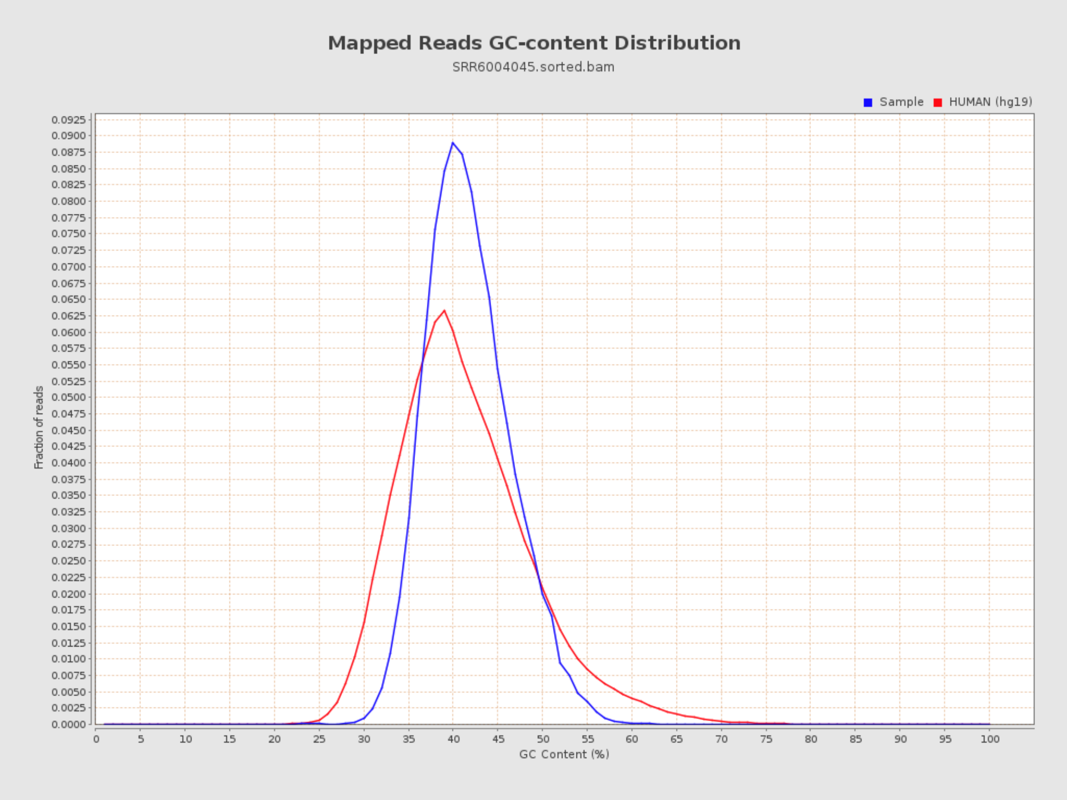
7. Results : Duplication Rate Histogram



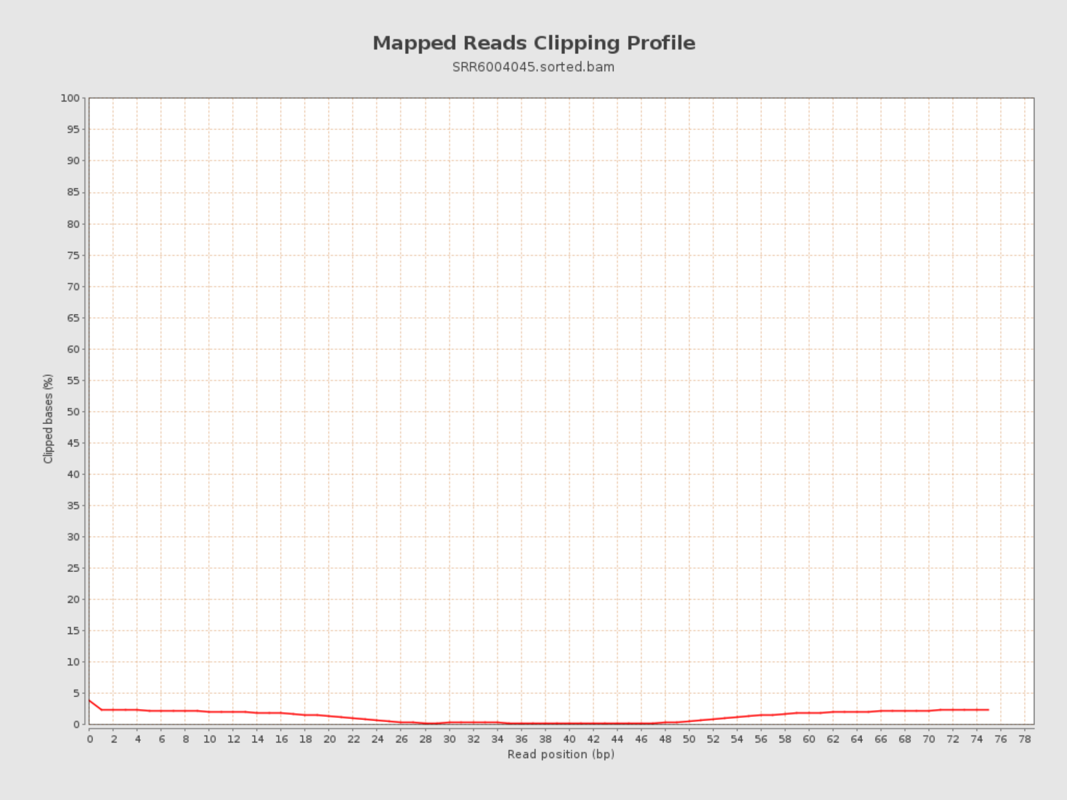
8. Results : Mapped Reads Nucleotide Content



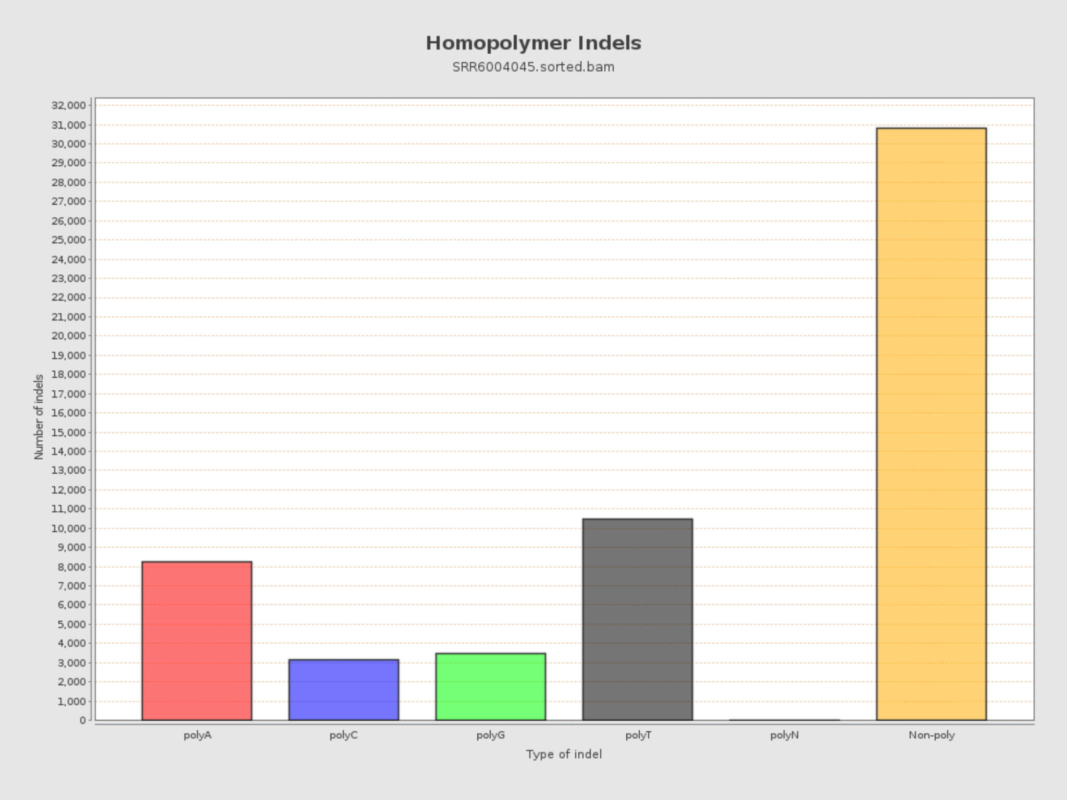
9. Results : Mapped Reads GC-content Distribution



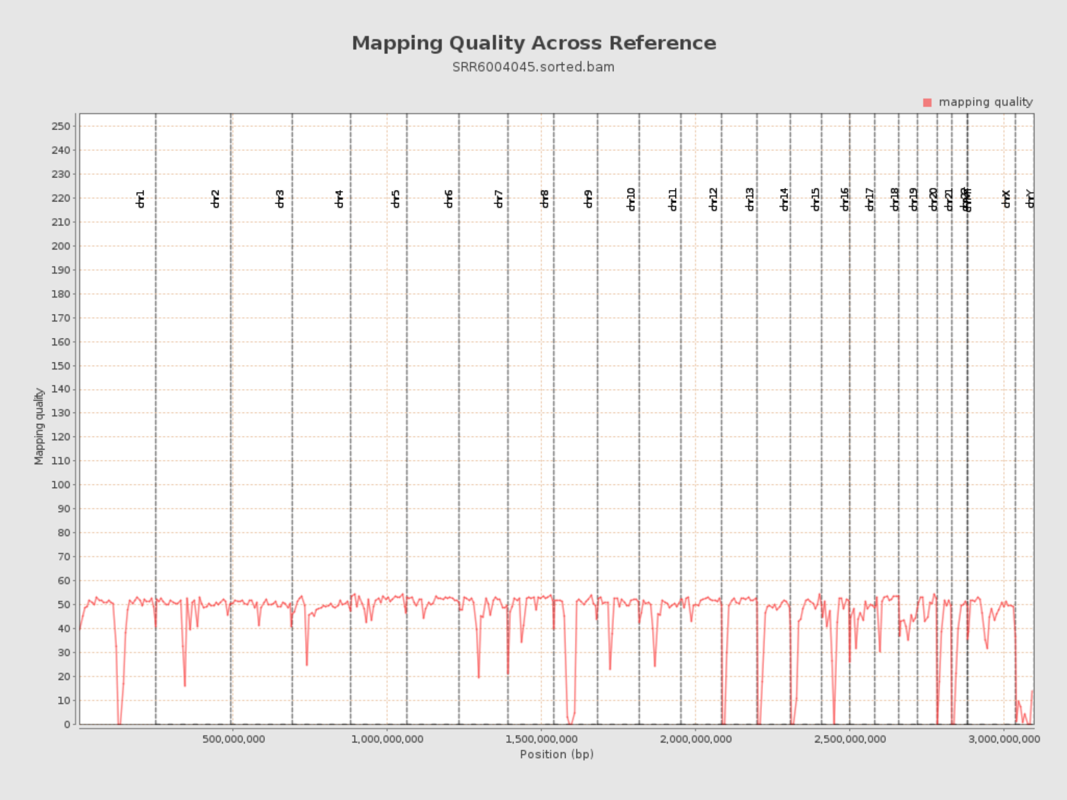
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram