Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 21:23:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004025.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_SRR6004025 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004025.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 21:23:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004025.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,292,018
Mapped reads	2,983,964 / 90.64%
Unmapped reads	308,054 / 9.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,675 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	81,912 / 2.49%
Duplication rate	1.96%
Clipped reads	1,576,405 / 47.89%

2.2. ACGT Content

Number/percentage of A's	53,341,689 / 27.55%
Number/percentage of C's	38,315,282 / 19.79%
Number/percentage of T's	56,834,108 / 29.36%
Number/percentage of G's	45,064,048 / 23.28%
Number/percentage of N's	36,700 / 0.02%
GC Percentage	43.07%

2.3. Coverage

Mean	0.0626

Standard Deviation	0.4457

2.4. Mapping Quality

Mean Mapping Quality	41.5

2.5. Mismatches and indels

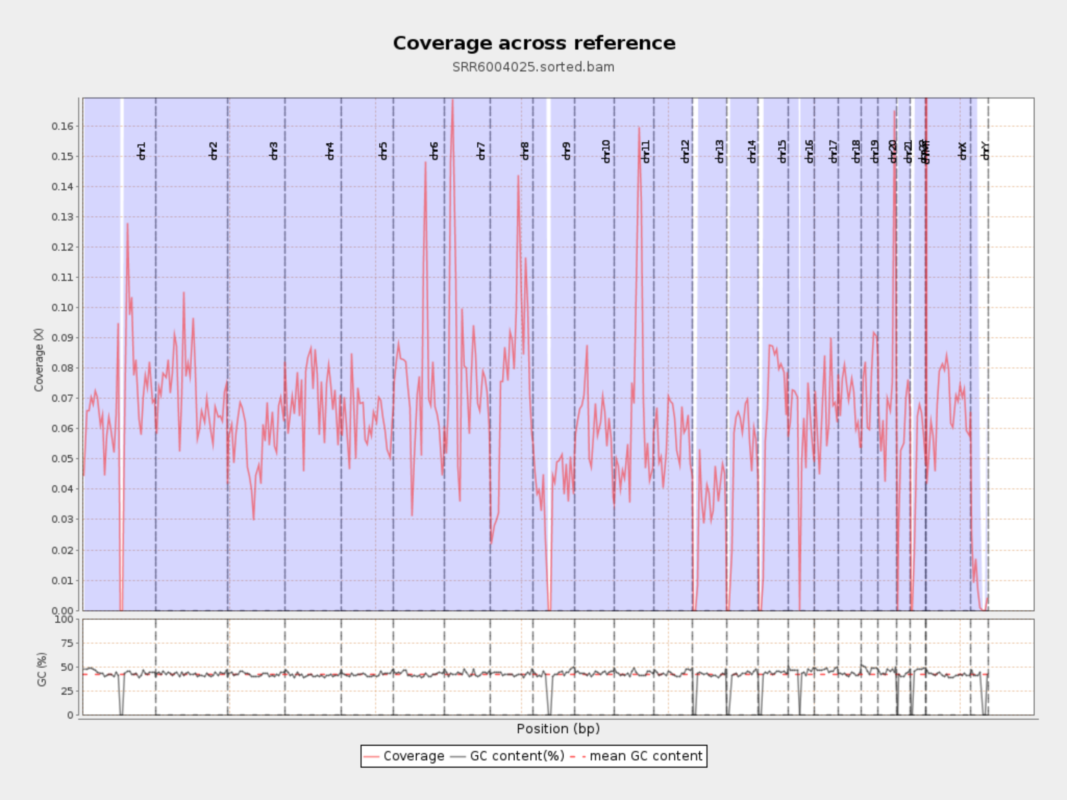
General error rate	0.84%
Mismatches	1,603,295
Insertions	15,727
Mapped reads with at least one insertion	0.52%
Deletions	49,962
Mapped reads with at least one deletion	1.66%
Homopolymer indels	44.31%

2.6. Chromosome stats

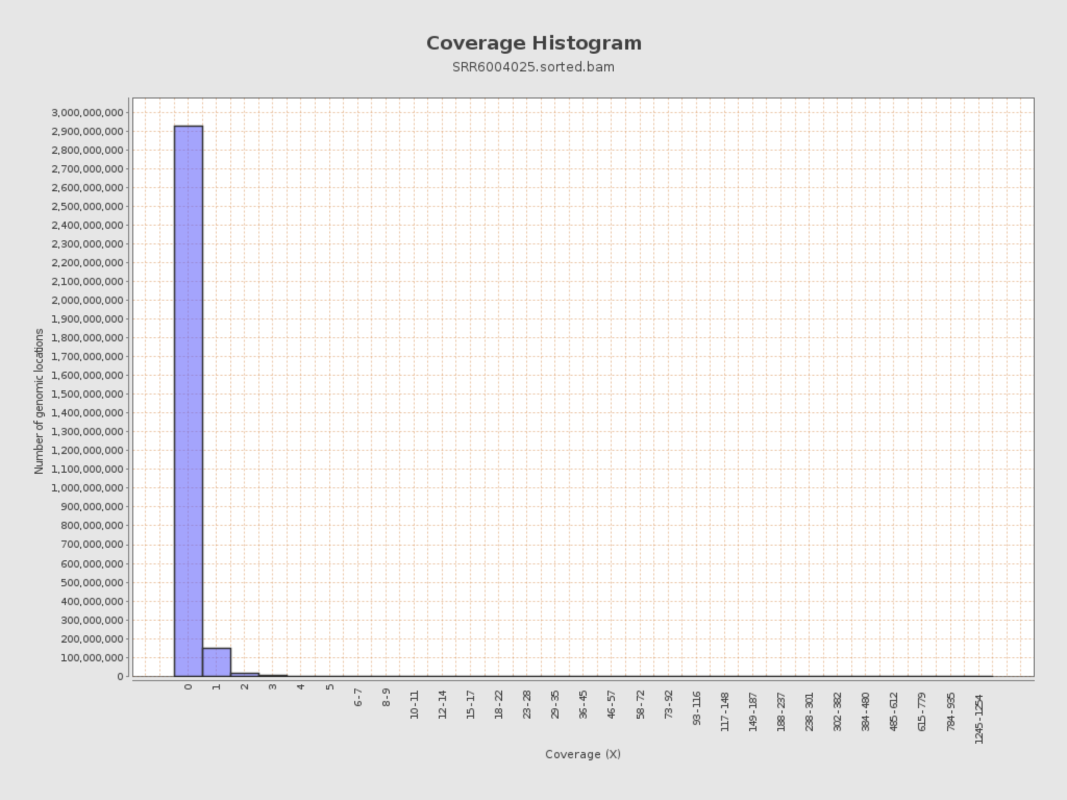
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16597111	0.0666	0.7826
chr2	243199373	17560709	0.0722	0.659
chr3	198022430	11070867	0.0559	0.2644
chr4	191154276	13523983	0.0707	0.3053
chr5	180915260	11324648	0.0626	0.2795
chr6	171115067	12641537	0.0739	0.3529
chr7	159138663	12881175	0.0809	0.6508

chr8	146364022	11283926	0.0771	0.4551
chr9	141213431	5323380	0.0377	0.3375
chr10	135534747	8395275	0.0619	0.4341
chr11	135006516	8828323	0.0654	0.3679
chr12	133851895	7766063	0.058	0.2712
chr13	115169878	3849084	0.0334	0.2063
chr14	107349540	5356968	0.0499	0.2732
chr15	102531392	6289145	0.0613	0.2937
chr16	90354753	5131809	0.0568	0.3044
chr17	81195210	5364951	0.0661	0.3125
chr18	78077248	5466965	0.07	0.636
chr19	59128983	4511039	0.0763	0.6047
chr20	63025520	4922406	0.0781	0.3294
chr21	48129895	2513890	0.0522	0.2675
chr22	51304566	2217034	0.0432	0.2318
chrMT	16571	75893	4.5799	4.1992
chrX	155270560	10352672	0.0667	0.3166
chrY	59373566	425521	0.0072	0.1239

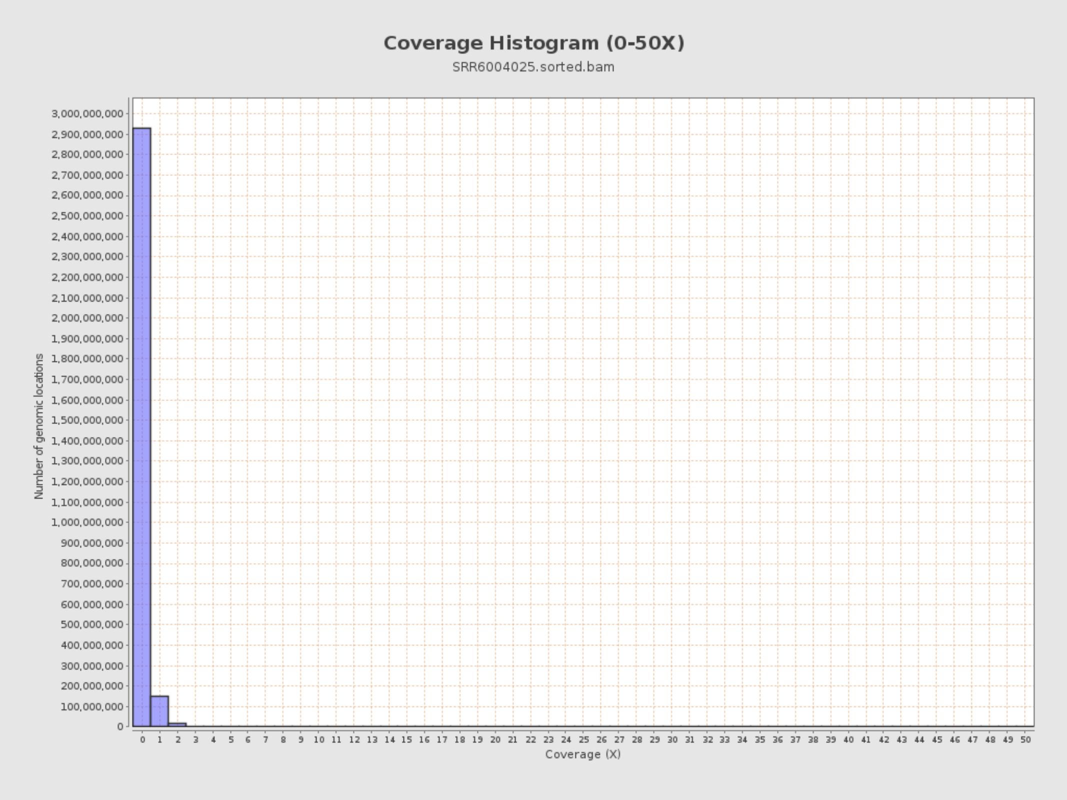
3. Results : Coverage across reference



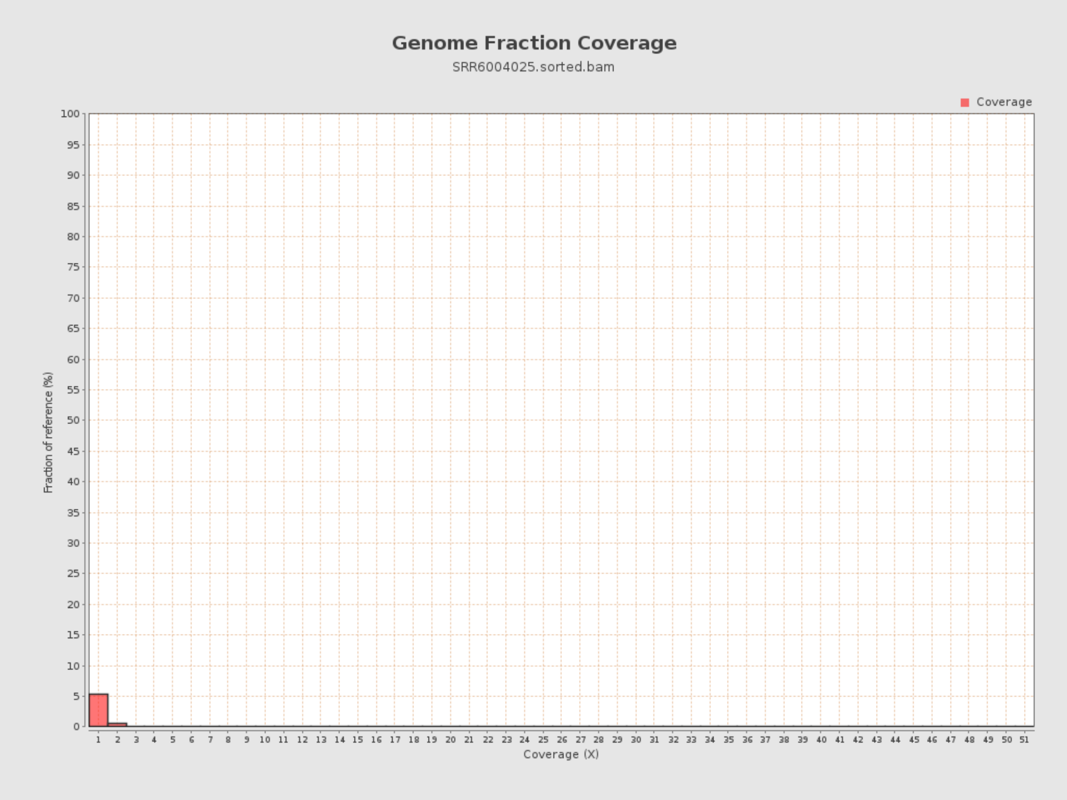
4. Results : Coverage Histogram



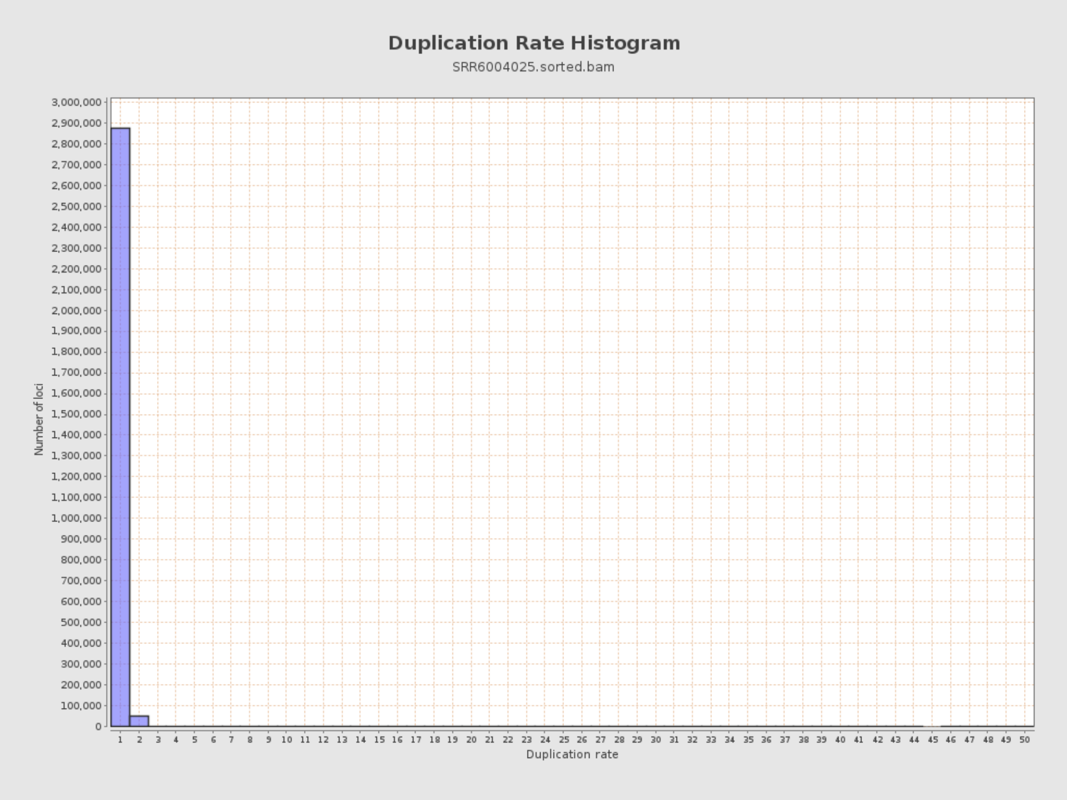
5. Results : Coverage Histogram (0-50X)



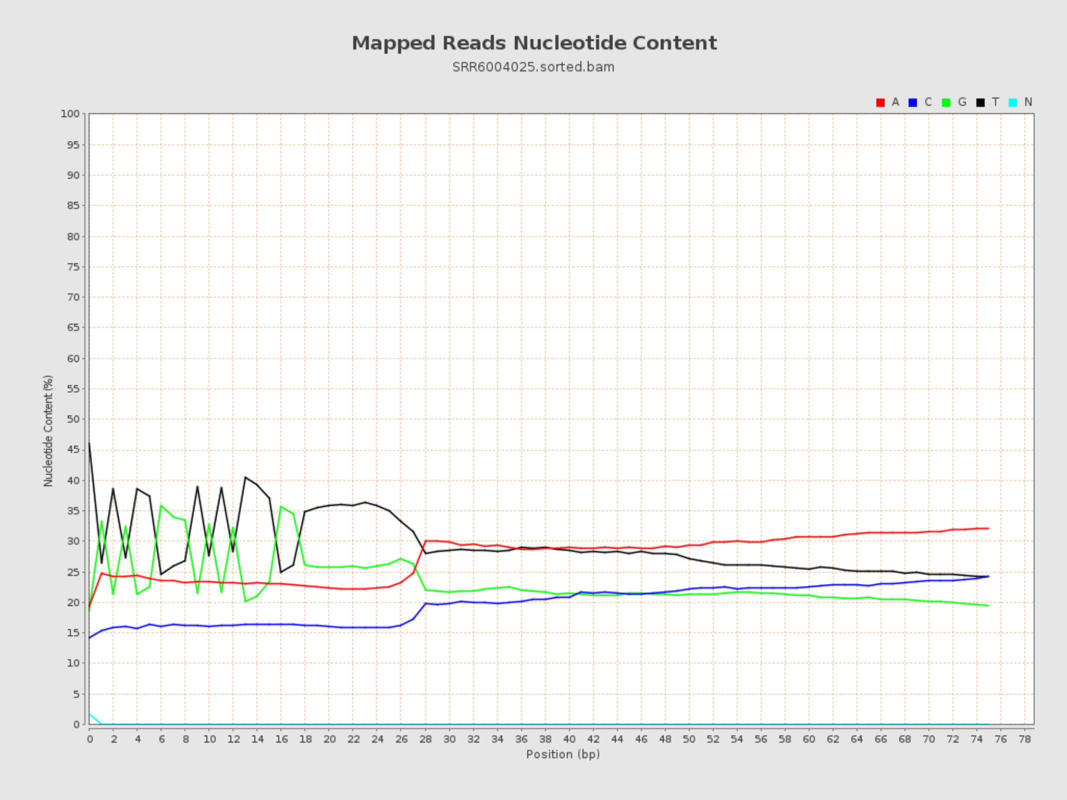
6. Results : Genome Fraction Coverage



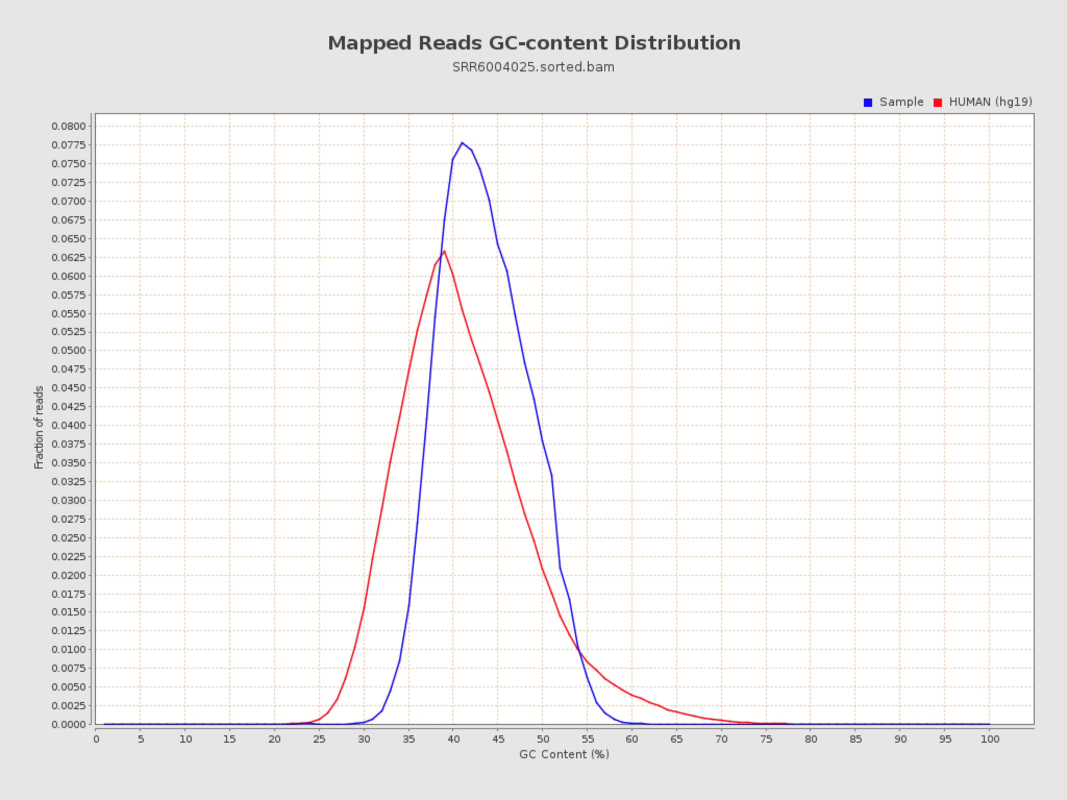
7. Results : Duplication Rate Histogram



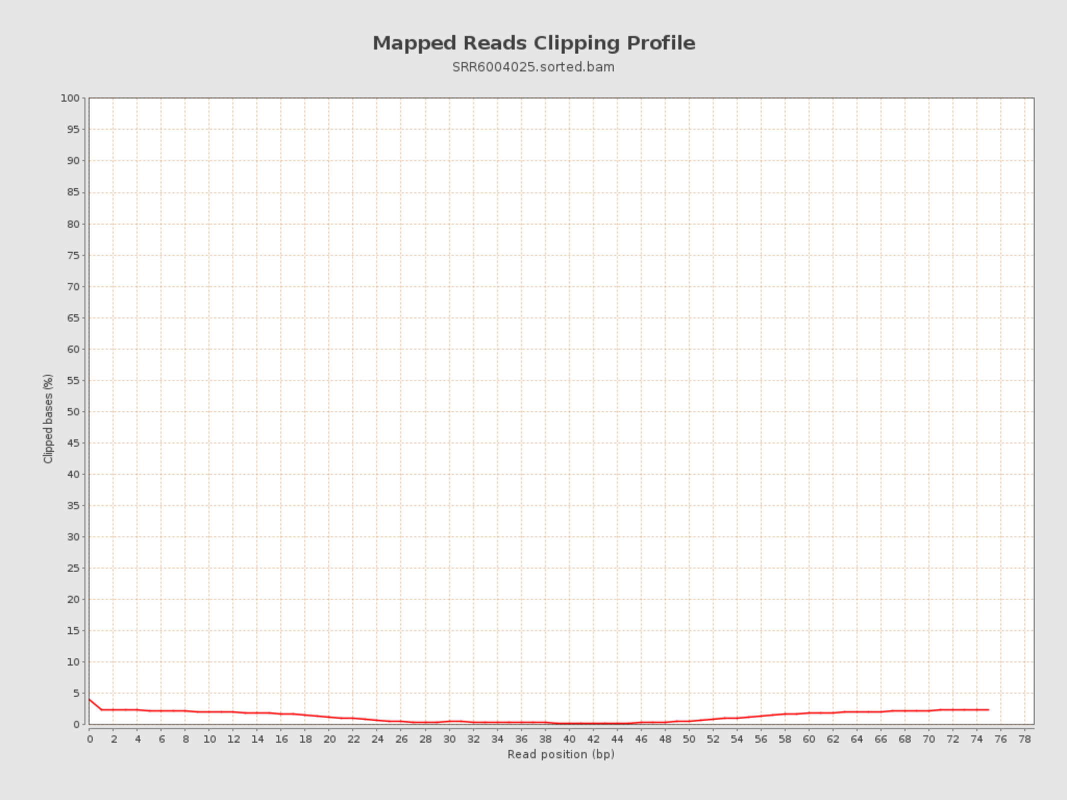
8. Results : Mapped Reads Nucleotide Content



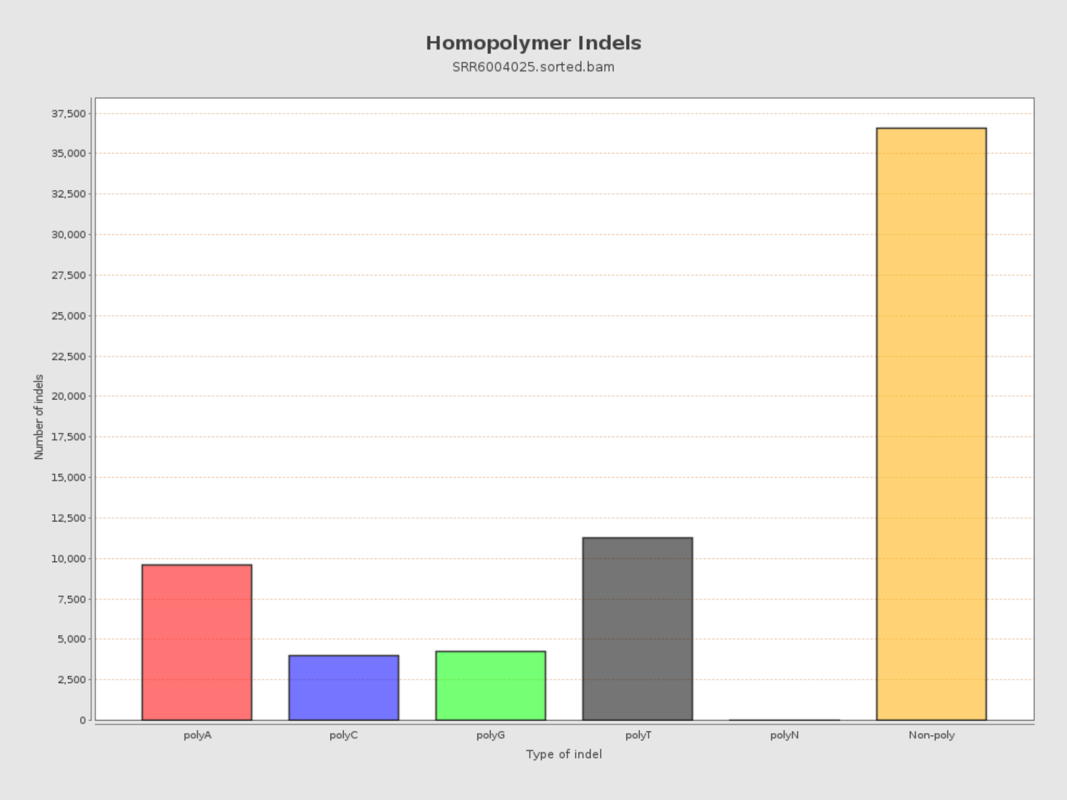
9. Results : Mapped Reads GC-content Distribution



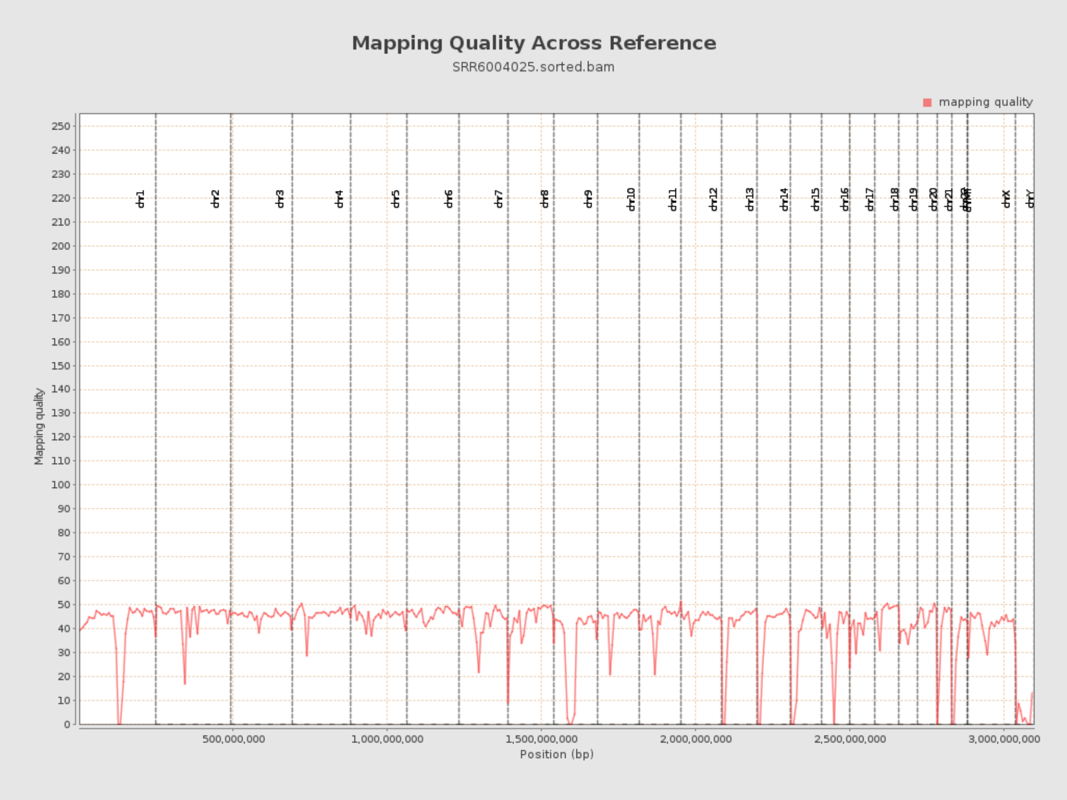
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram