Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 02:39:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548923.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_SRR1548923 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548923.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 02:39:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548923.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,952,109
Mapped reads	6,915,348 / 86.96%
Unmapped reads	1,036,761 / 13.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	230,633 / 2.9%
Duplication rate	2.38%
Clipped reads	468,565 / 5.89%

2.2. ACGT Content

Number/percentage of A's	80,836,064 / 29.51%
Number/percentage of C's	56,112,750 / 20.48%
Number/percentage of T's	81,131,520 / 29.61%
Number/percentage of G's	55,887,532 / 20.4%
Number/percentage of N's	2,352 / 0%
GC Percentage	40.88%

2.3. Coverage

Mean	0.0885
Standard Deviation	1.0541

2.4. Mapping Quality

Mean Mapping Quality	43.25

2.5. Mismatches and indels

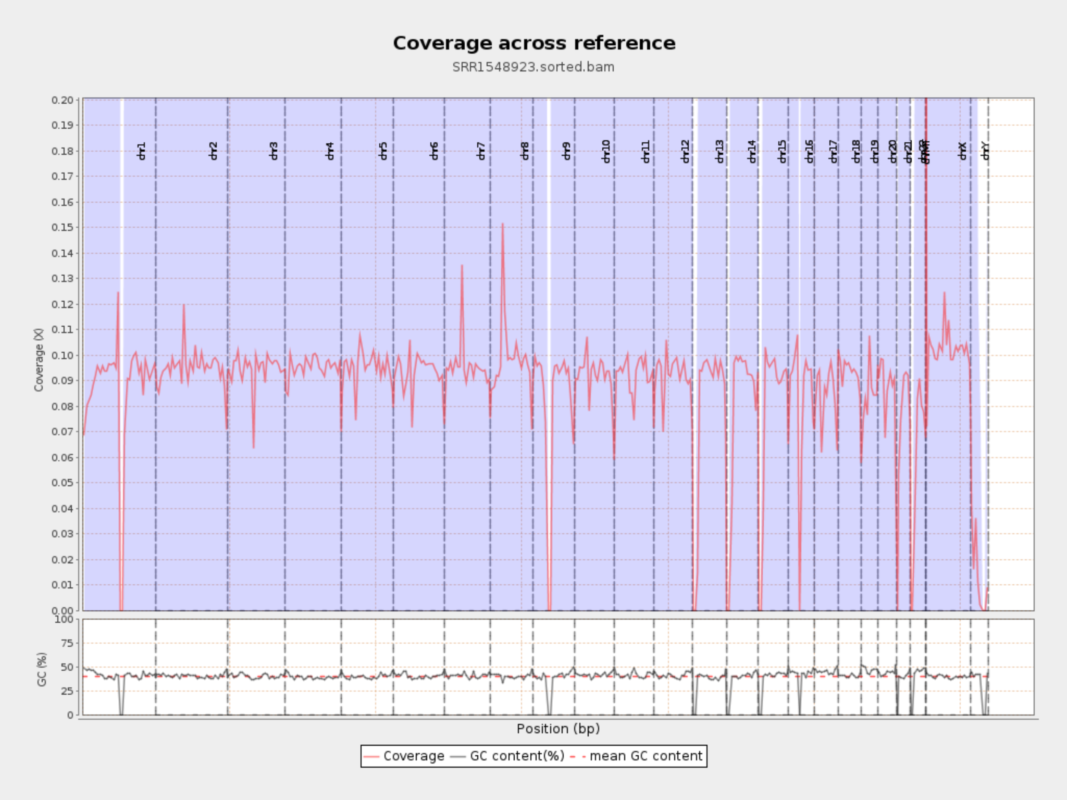
General error rate	0.26%
Mismatches	715,288
Insertions	8,293
Mapped reads with at least one insertion	0.12%
Deletions	22,243
Mapped reads with at least one deletion	0.32%
Homopolymer indels	42.06%

2.6. Chromosome stats

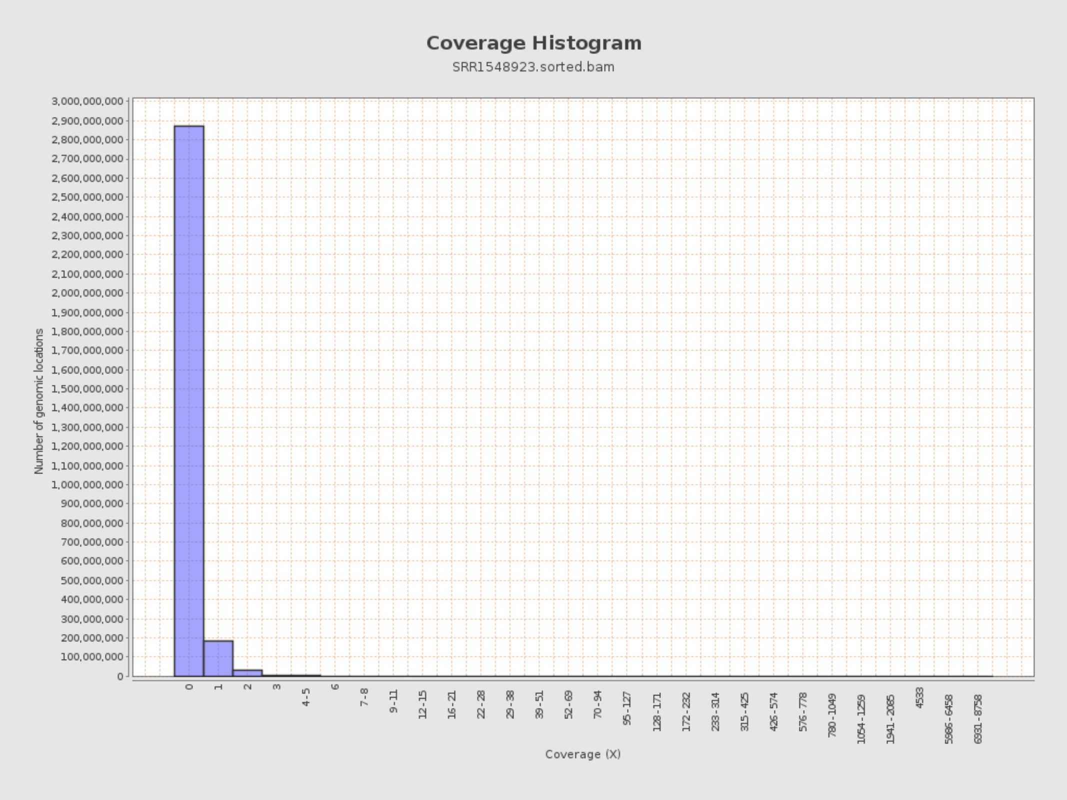
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21621558	0.0867	0.9804
chr2	243199373	23114002	0.095	0.4915
chr3	198022430	18740896	0.0946	0.3647
chr4	191154276	18259526	0.0955	0.3754
chr5	180915260	17153103	0.0948	0.3701
chr6	171115067	16051274	0.0938	0.3994
chr7	159138663	15230603	0.0957	0.7125
chr8	146364022	14461003	0.0988	4.2383

chr9	141213431	11435862	0.081	0.4533
chr10	135534747	12555080	0.0926	0.4588
chr11	135006516	12412246	0.0919	0.5597
chr12	133851895	12399337	0.0926	0.3697
chr13	115169878	9027095	0.0784	0.3264
chr14	107349540	8419684	0.0784	0.3784
chr15	102531392	7913949	0.0772	0.324
chr16	90354753	7367532	0.0815	0.3644
chr17	81195210	6905318	0.085	0.3778
chr18	78077248	7338352	0.094	0.8191
chr19	59128983	4996445	0.0845	0.8256
chr20	63025520	5510734	0.0874	0.3614
chr21	48129895	3502070	0.0728	0.3464
chr22	51304566	2937959	0.0573	0.3204
chrMT	16571	12252	0.7394	1.1416
chrX	155270560	15847582	0.1021	0.4454
chrY	59373566	786335	0.0132	0.1942

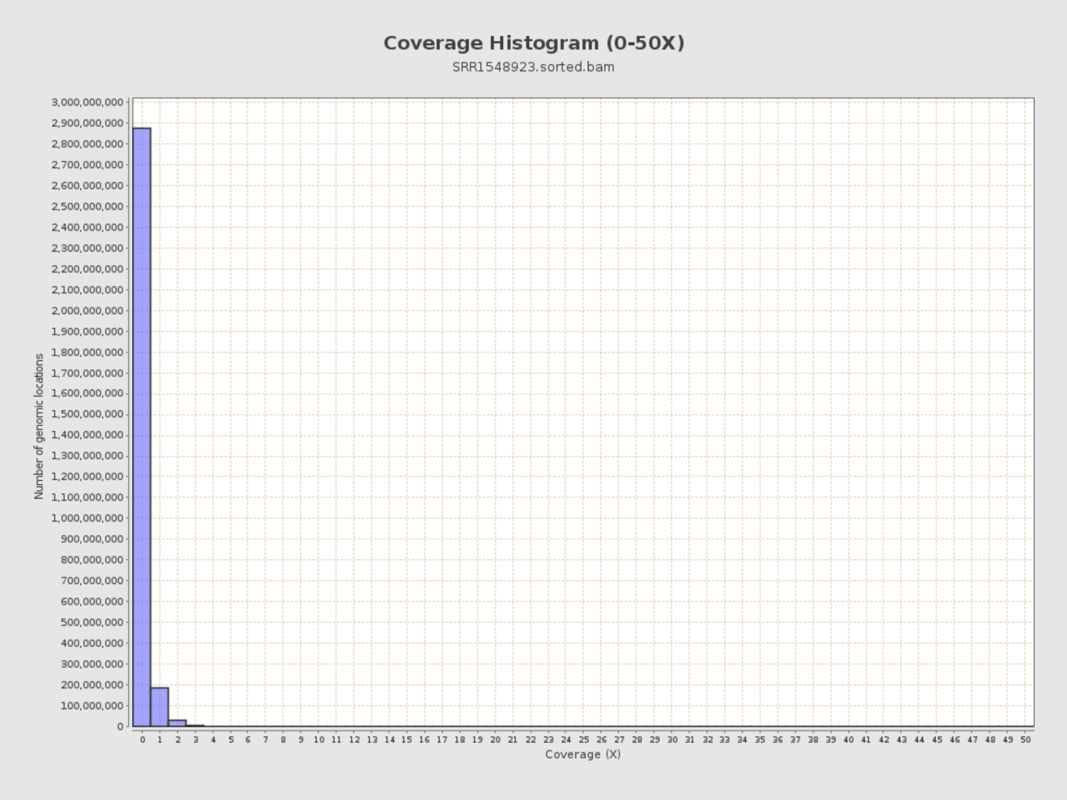
3. Results : Coverage across reference



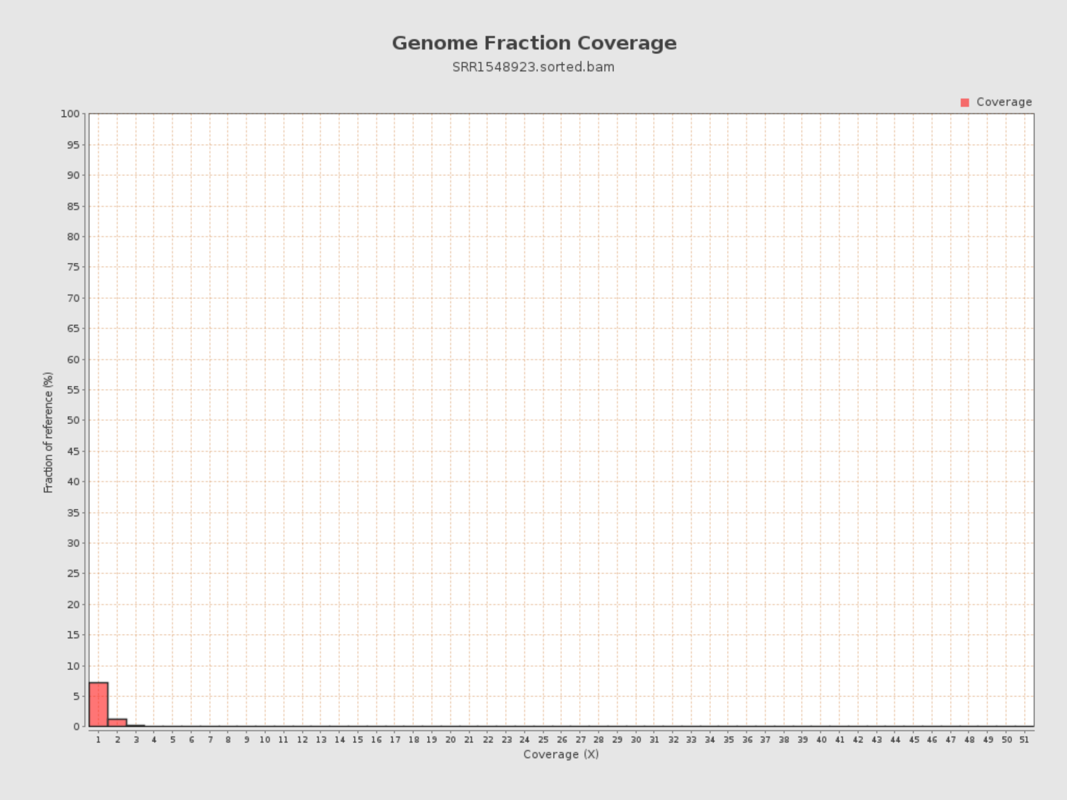
4. Results : Coverage Histogram



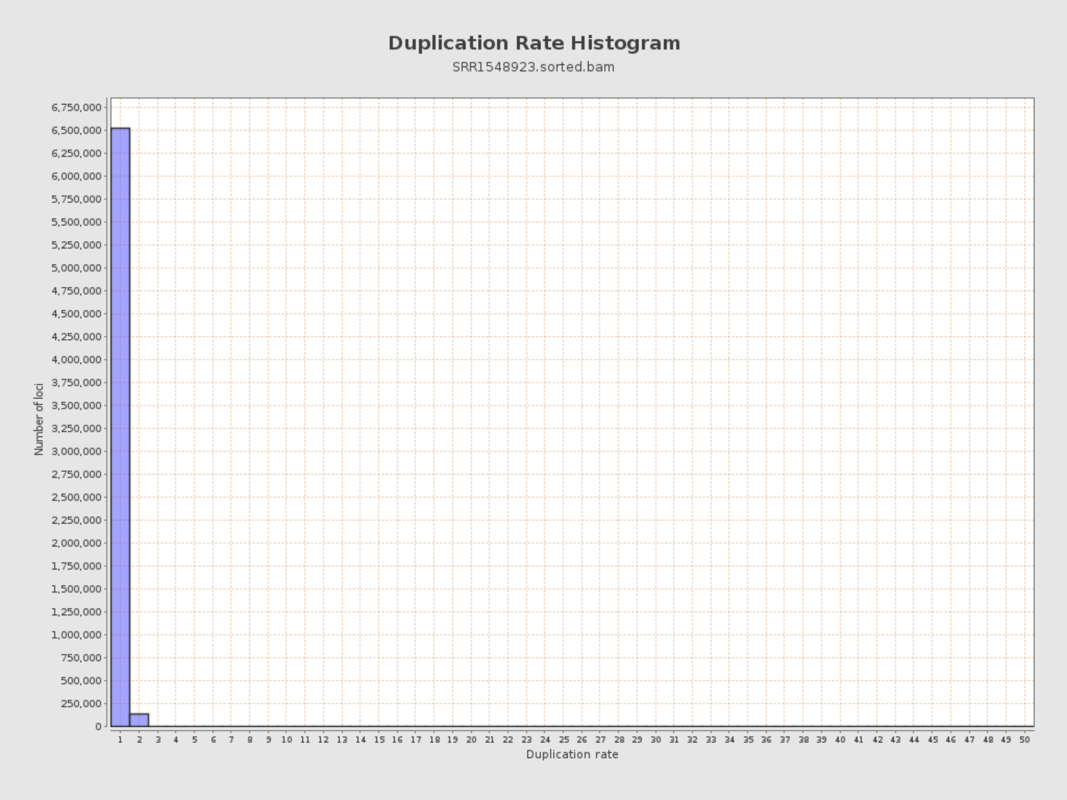
5. Results : Coverage Histogram (0-50X)



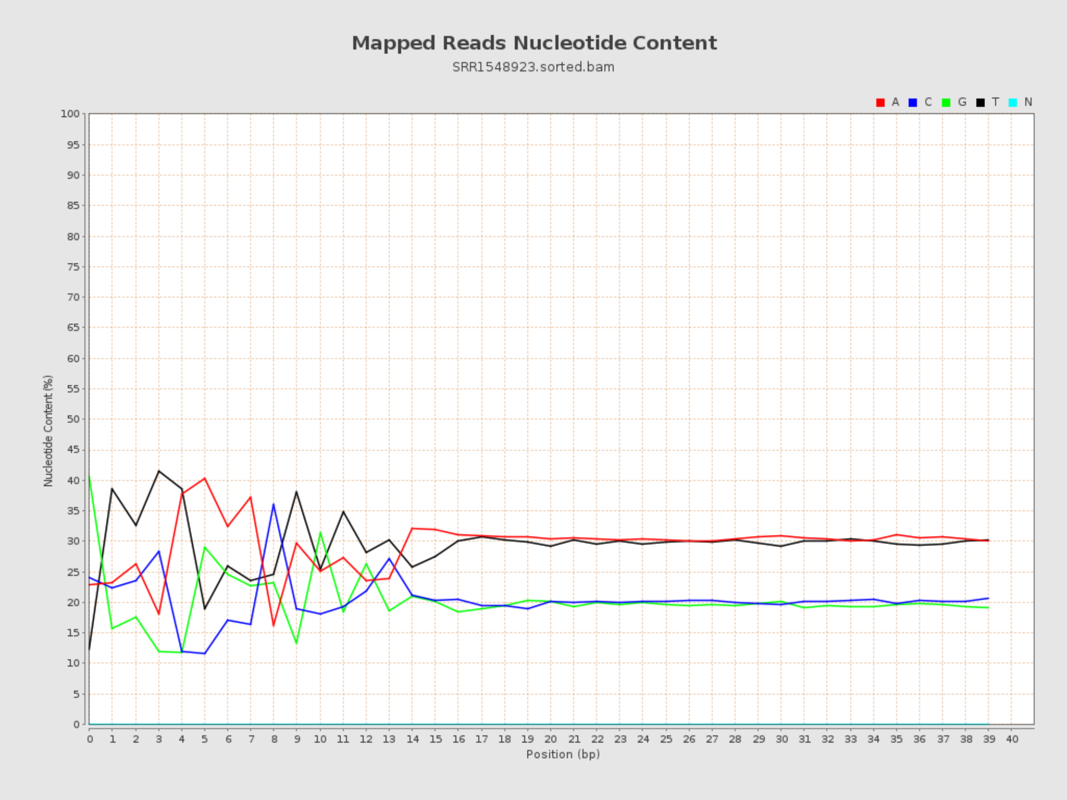
6. Results : Genome Fraction Coverage



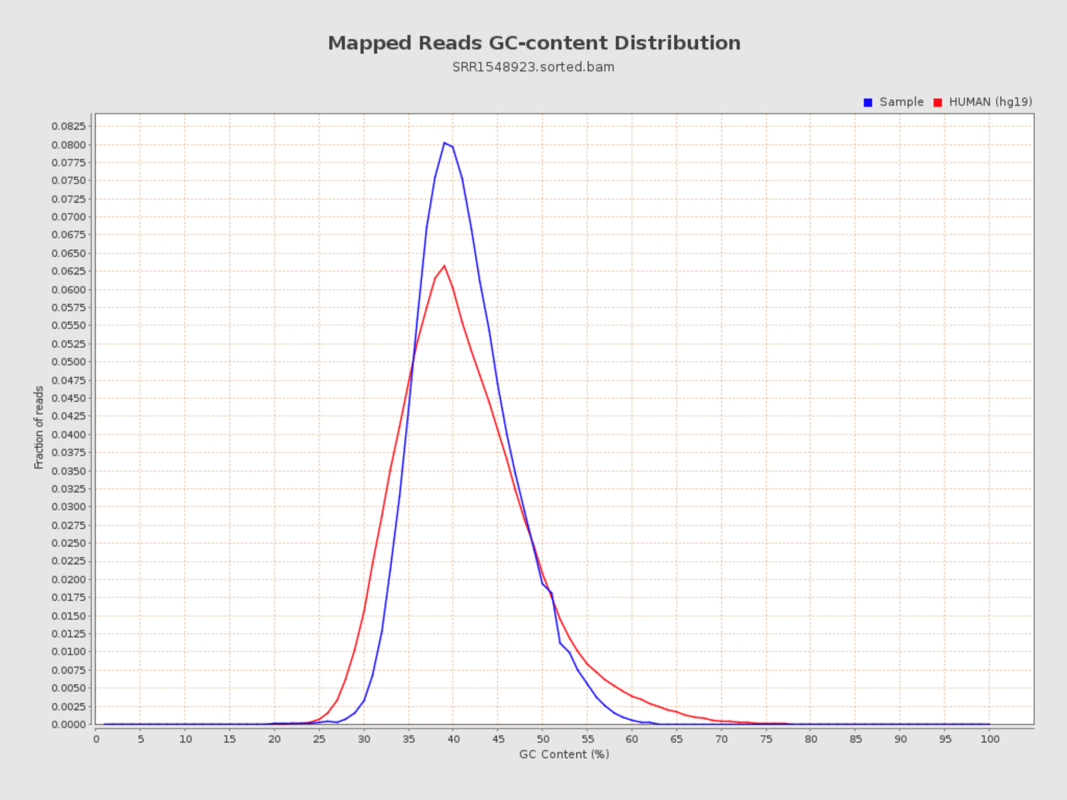
7. Results : Duplication Rate Histogram



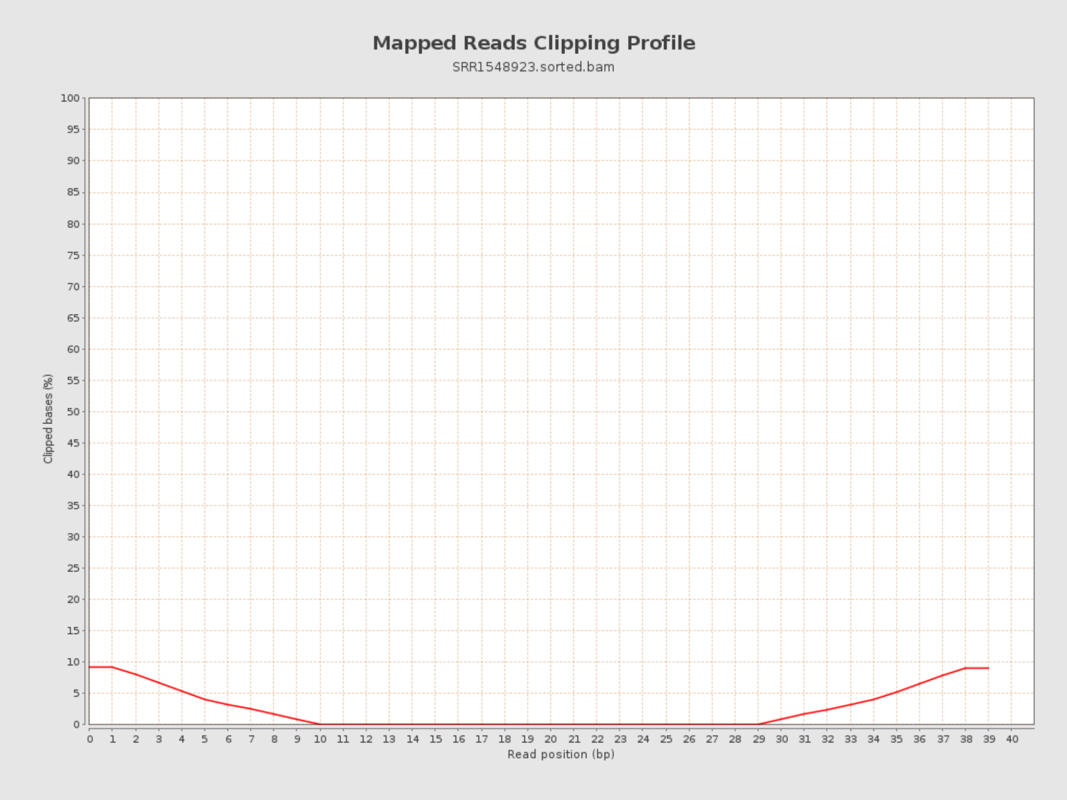
8. Results : Mapped Reads Nucleotide Content



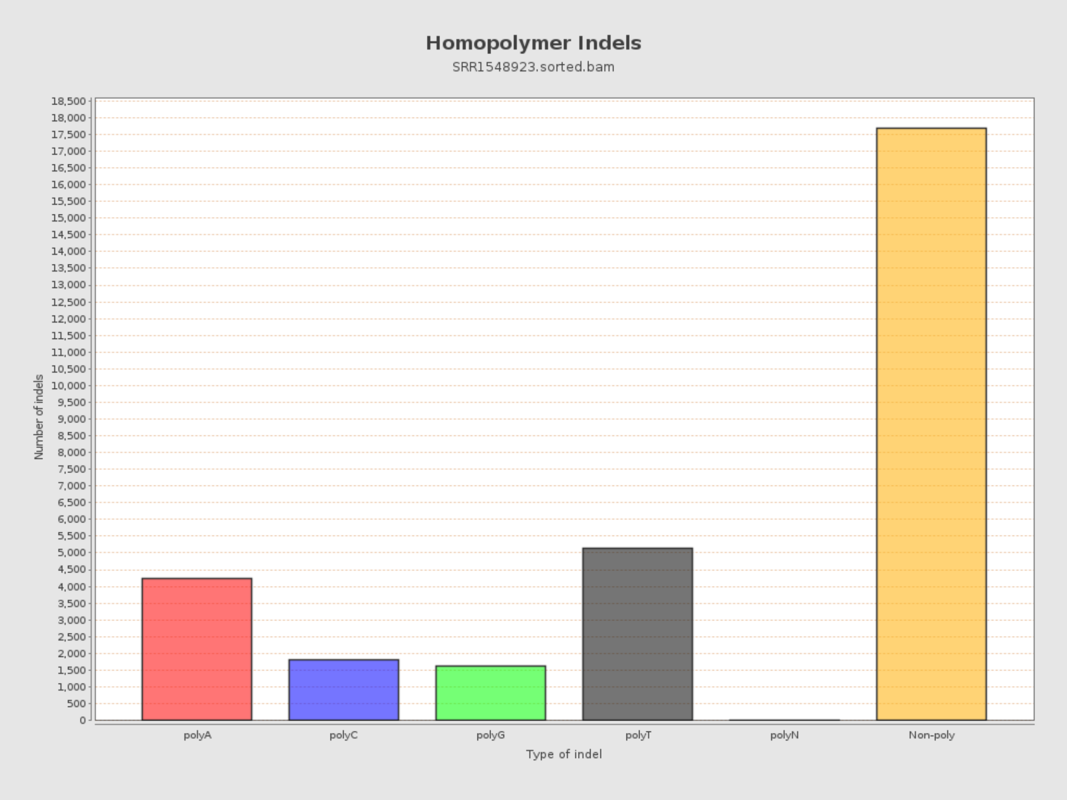
9. Results : Mapped Reads GC-content Distribution



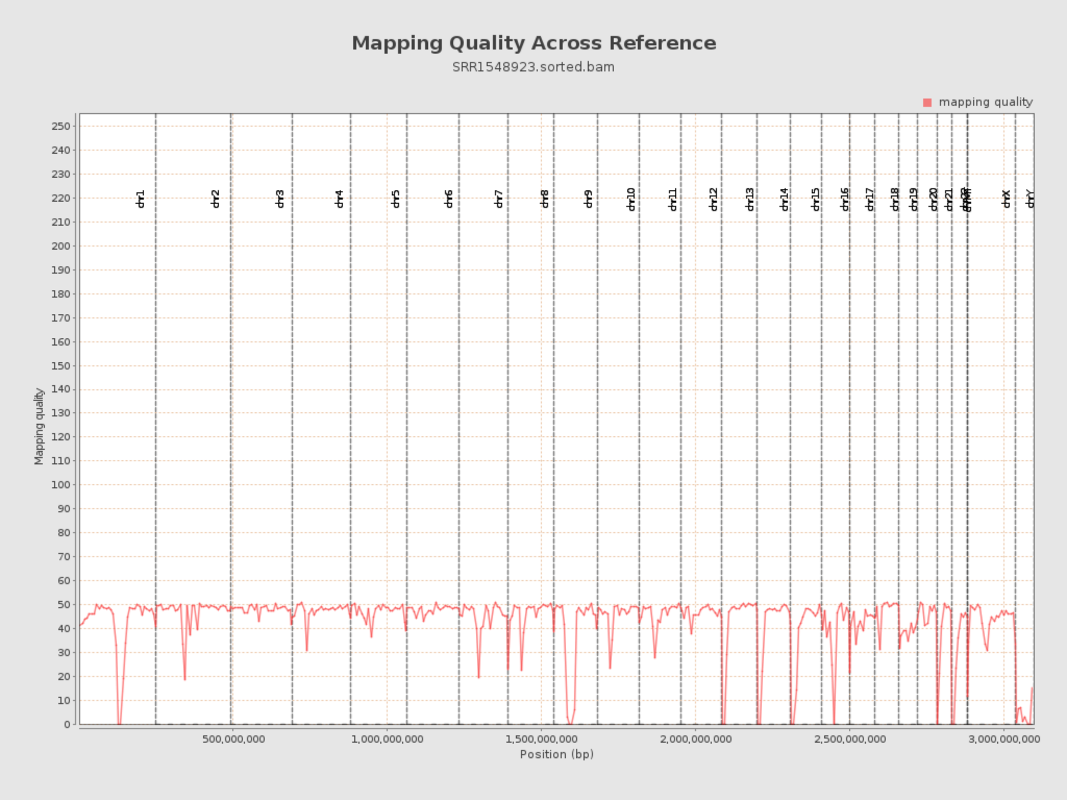
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram