Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 09:52:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548936.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_SRR1548936 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548936.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 09:52:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548936.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,905,395
Mapped reads	6,916,073 / 87.49%
Unmapped reads	989,322 / 12.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	356,870 / 4.51%
Duplication rate	2.82%
Clipped reads	704,243 / 8.91%

2.2. ACGT Content

Number/percentage of A's	77,679,604 / 28.48%
Number/percentage of C's	58,718,625 / 21.53%
Number/percentage of T's	78,102,152 / 28.64%
Number/percentage of G's	58,238,055 / 21.35%
Number/percentage of N's	2,289 / 0%
GC Percentage	42.88%

2.3. Coverage

Mean	0.0881
Standard Deviation	1.1373

2.4. Mapping Quality

Mean Mapping Quality	33.35

2.5. Mismatches and indels

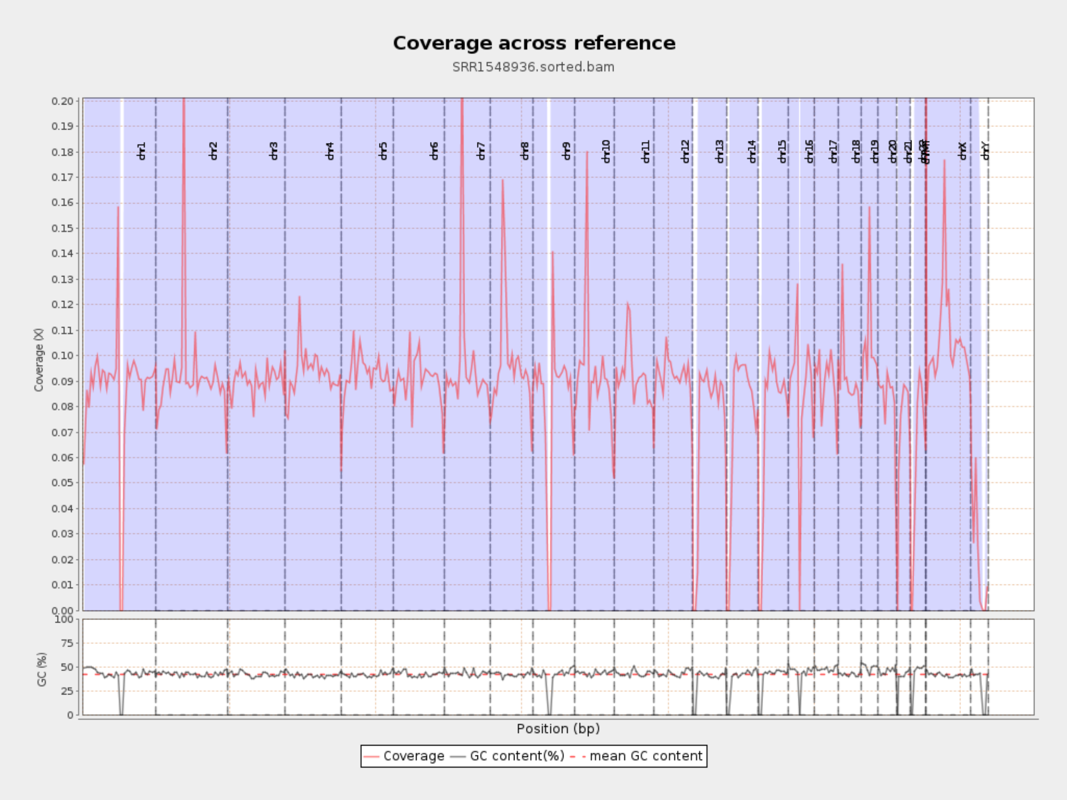
General error rate	0.39%
Mismatches	1,057,219
Insertions	11,285
Mapped reads with at least one insertion	0.16%
Deletions	22,121
Mapped reads with at least one deletion	0.32%
Homopolymer indels	36.43%

2.6. Chromosome stats

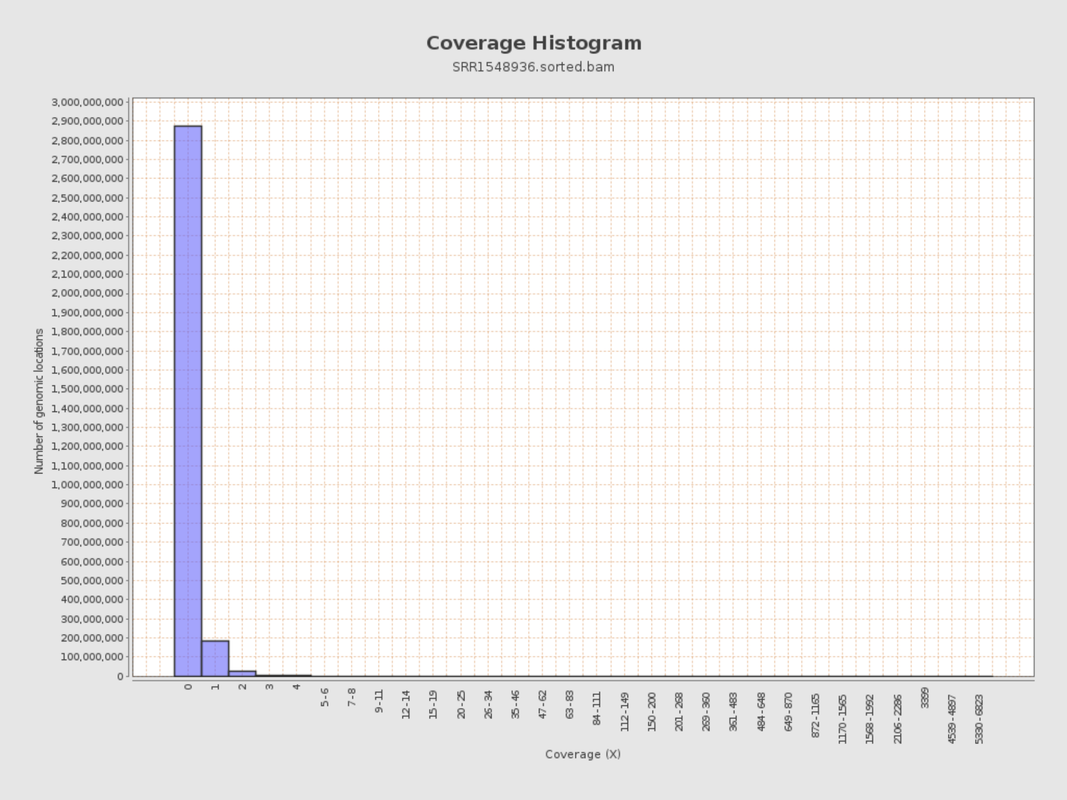
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21500203	0.0863	1.5394
chr2	243199373	22699789	0.0933	1.0143
chr3	198022430	17872793	0.0903	0.3672
chr4	191154276	17856588	0.0934	0.4144
chr5	180915260	16712129	0.0924	0.4029
chr6	171115067	15542353	0.0908	0.4357
chr7	159138663	15498429	0.0974	1.4253
chr8	146364022	14279887	0.0976	3.3495

chr9	141213431	11537089	0.0817	1.0875
chr10	135534747	12635199	0.0932	0.7917
chr11	135006516	12387454	0.0918	0.8917
chr12	133851895	12377207	0.0925	0.4278
chr13	115169878	8390248	0.0729	0.3111
chr14	107349540	8182877	0.0762	0.5609
chr15	102531392	7543071	0.0736	0.3316
chr16	90354753	7563061	0.0837	0.5197
chr17	81195210	7371566	0.0908	0.432
chr18	78077248	7168620	0.0918	2.0861
chr19	59128983	6212706	0.1051	1.6269
chr20	63025520	5292220	0.084	0.4053
chr21	48129895	3355252	0.0697	0.4835
chr22	51304566	3012285	0.0587	0.3539
chrMT	16571	6279	0.3789	0.7095
chrX	155270560	16523839	0.1064	0.658
chrY	59373566	1247523	0.021	0.2801

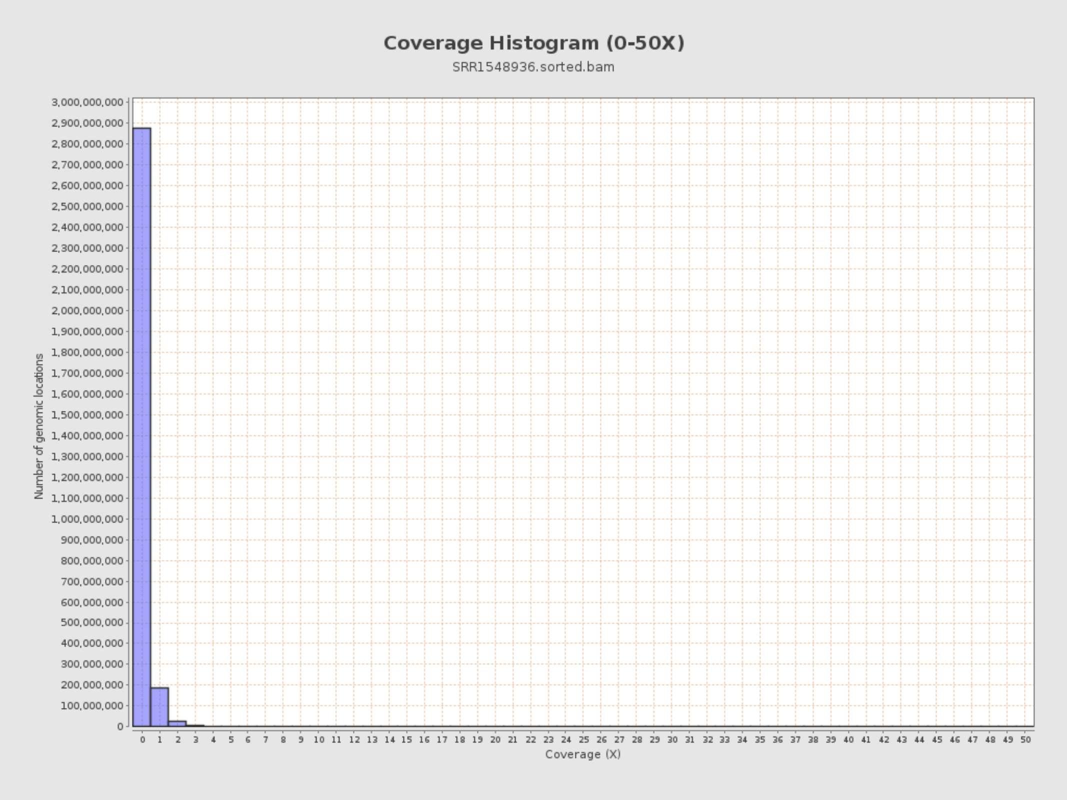
3. Results : Coverage across reference



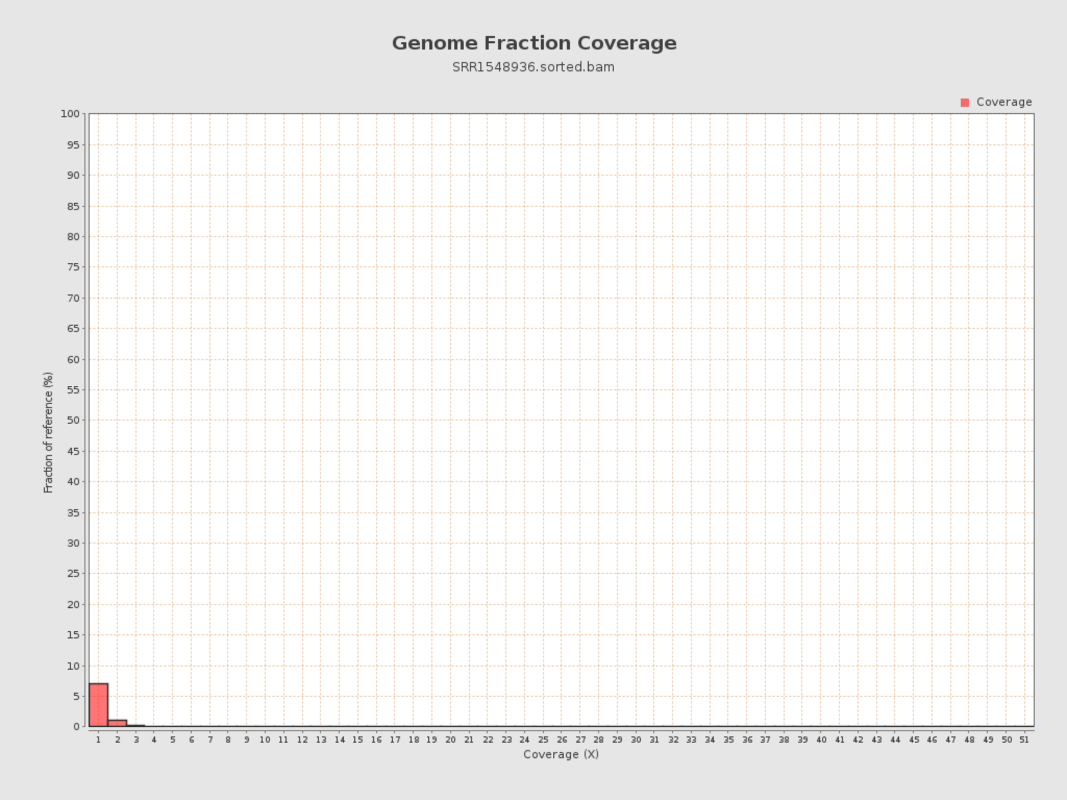
4. Results : Coverage Histogram



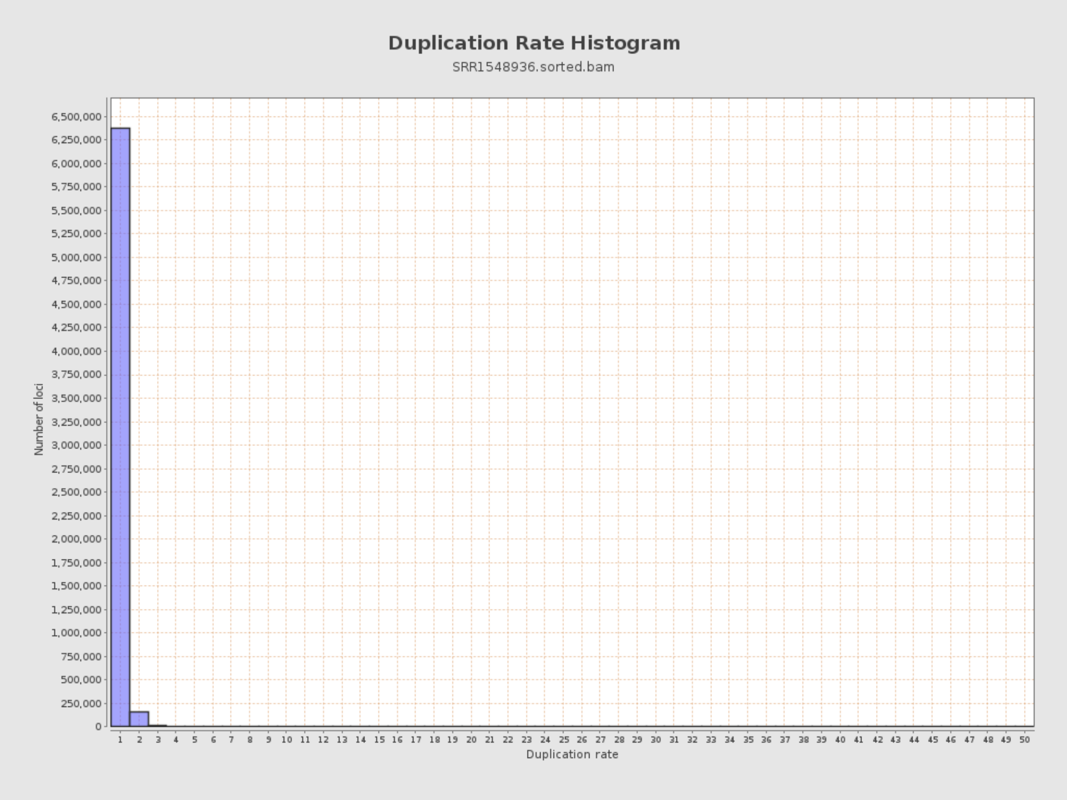
5. Results : Coverage Histogram (0-50X)



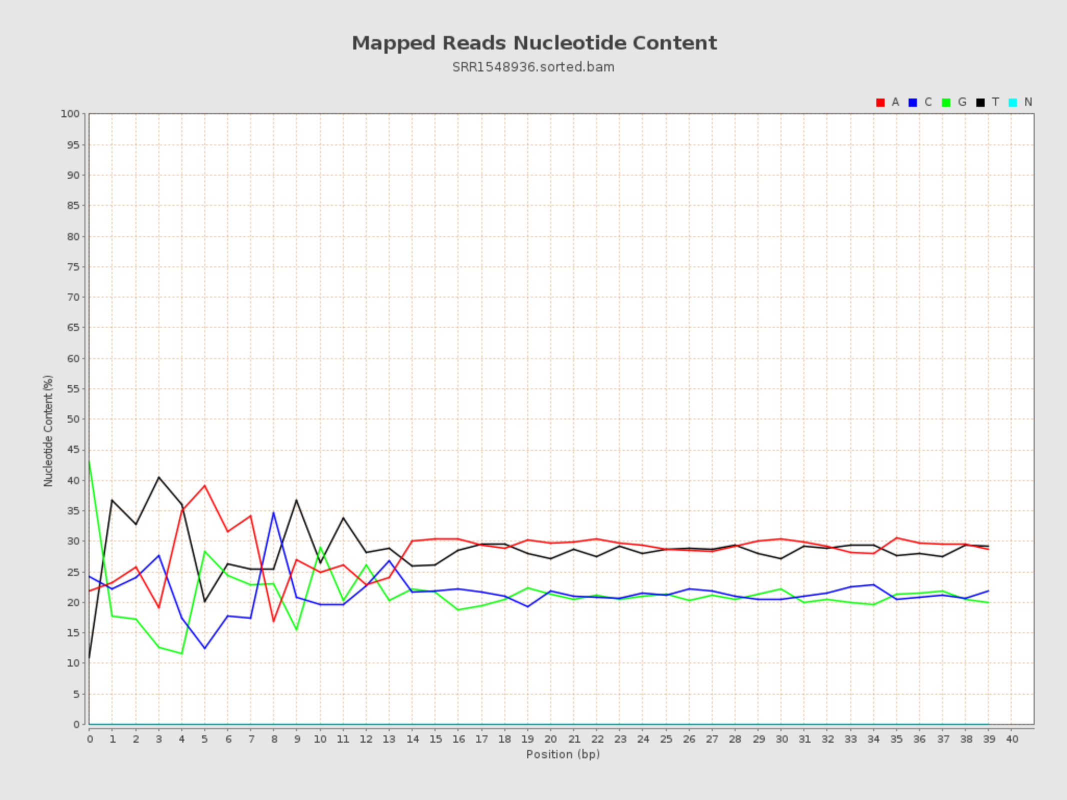
6. Results : Genome Fraction Coverage



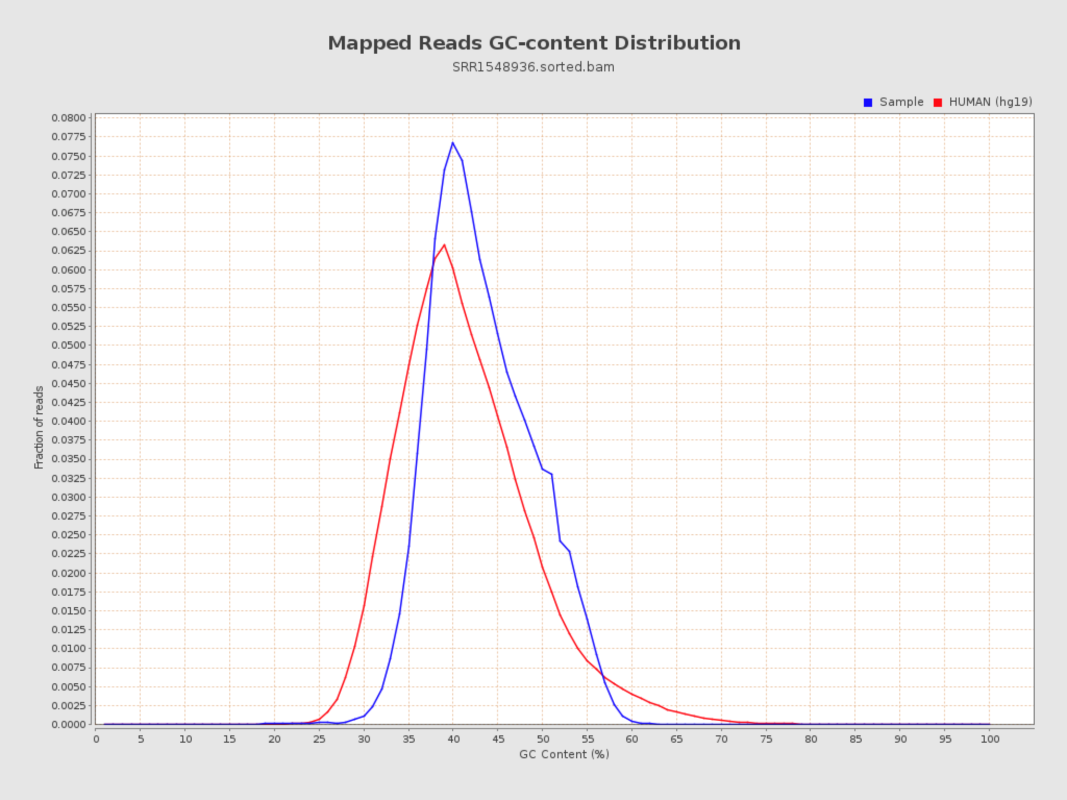
7. Results : Duplication Rate Histogram



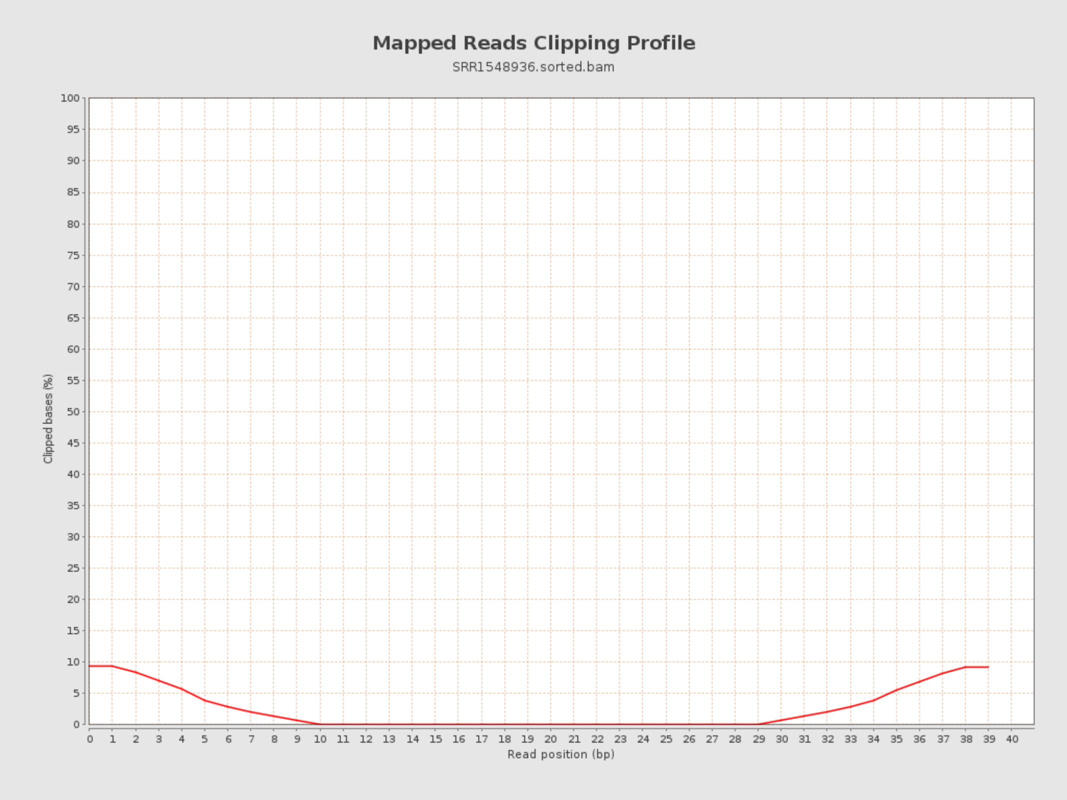
8. Results : Mapped Reads Nucleotide Content



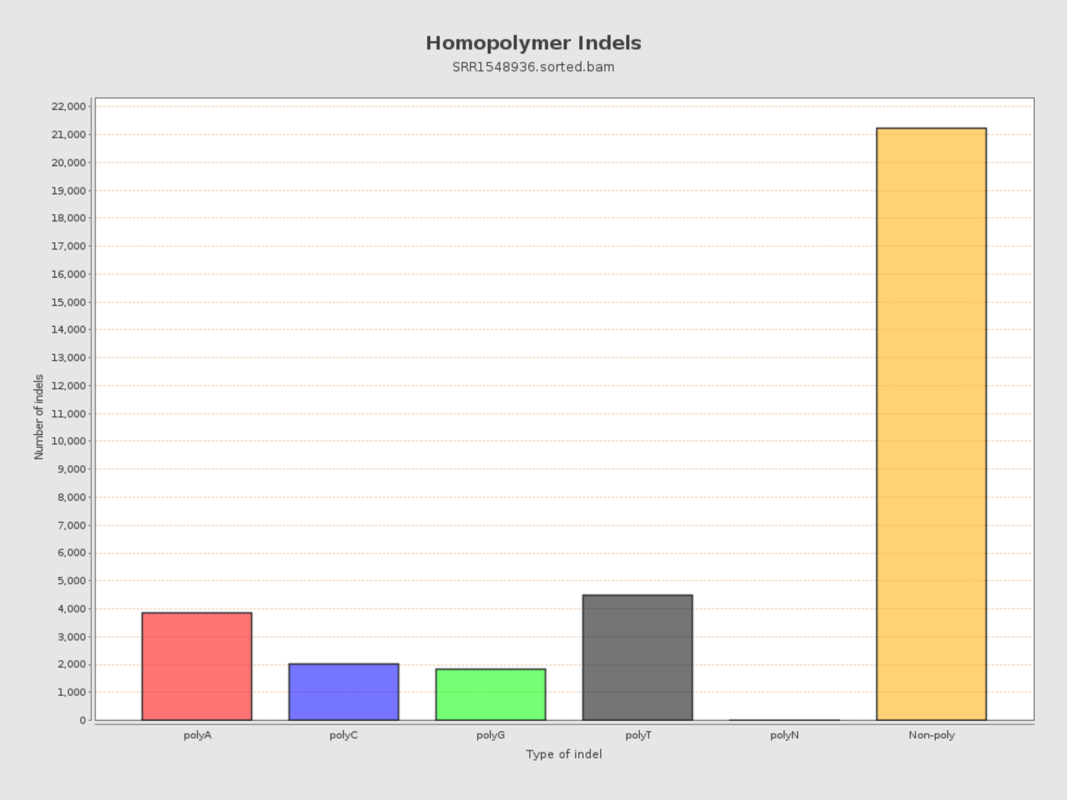
9. Results : Mapped Reads GC-content Distribution



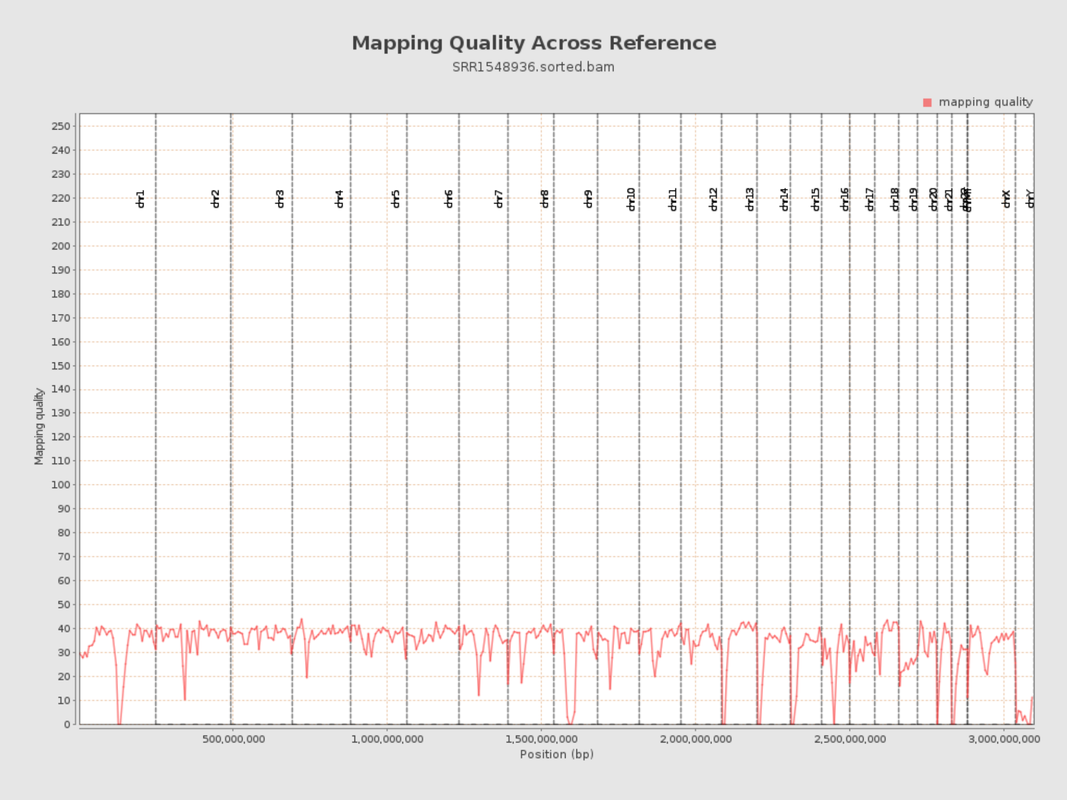
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram