Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 09:27:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084281.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_SRR3084281 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084281.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 09:27:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084281.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,194,431
Mapped reads	2,880,185 / 90.16%
Unmapped reads	314,246 / 9.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,923 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	114,941 / 3.6%
Duplication rate	3.36%
Clipped reads	1,539,163 / 48.18%

2.2. ACGT Content

Number/percentage of A's	52,614,354 / 28.07%
Number/percentage of C's	36,276,546 / 19.35%
Number/percentage of T's	57,196,901 / 30.51%
Number/percentage of G's	41,120,084 / 21.94%
Number/percentage of N's	236,933 / 0.13%
GC Percentage	41.29%

2.3. Coverage

Mean	0.0606

Standard Deviation	0.3742

2.4. Mapping Quality

Mean Mapping Quality	45.61

2.5. Mismatches and indels

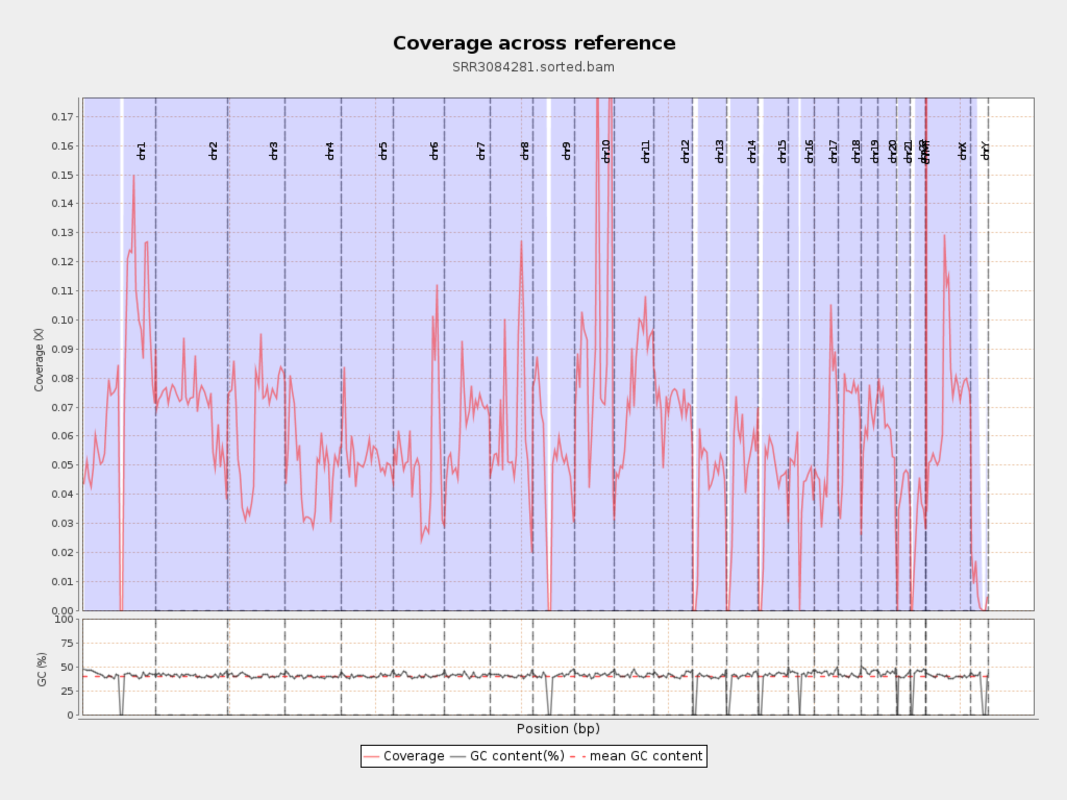
General error rate	1.04%
Mismatches	1,927,206
Insertions	13,722
Mapped reads with at least one insertion	0.47%
Deletions	36,701
Mapped reads with at least one deletion	1.26%
Homopolymer indels	45.96%

2.6. Chromosome stats

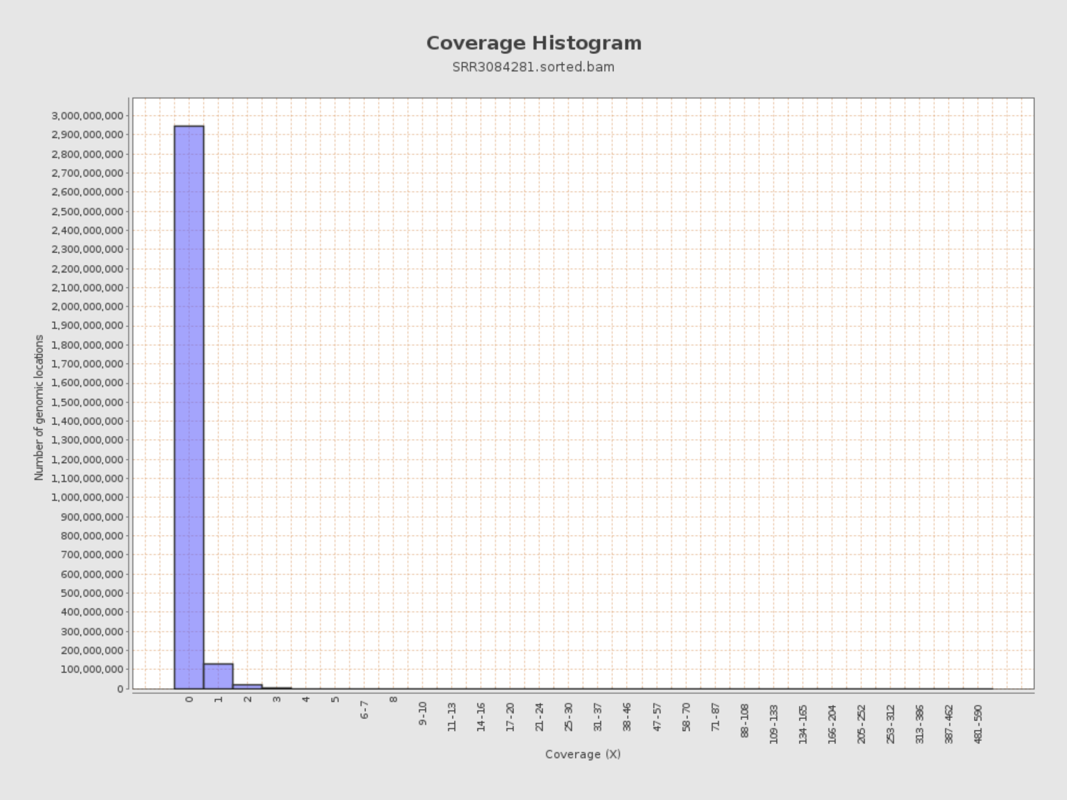
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19115731	0.0767	0.5529
chr2	243199373	17087321	0.0703	0.4436
chr3	198022430	13043523	0.0659	0.3053
chr4	191154276	9316706	0.0487	0.2707
chr5	180915260	9646607	0.0533	0.2717
chr6	171115067	9086391	0.0531	0.3103
chr7	159138663	10131035	0.0637	0.5575

chr8	146364022	9050713	0.0618	0.3565
chr9	141213431	7198349	0.051	0.3139
chr10	135534747	13160755	0.0971	0.5107
chr11	135006516	10357458	0.0767	0.3828
chr12	133851895	9497095	0.071	0.3165
chr13	115169878	4817717	0.0418	0.2419
chr14	107349540	5184983	0.0483	0.2783
chr15	102531392	4153575	0.0405	0.2462
chr16	90354753	3821460	0.0423	0.2616
chr17	81195210	4852717	0.0598	0.3066
chr18	78077248	5207813	0.0667	0.4845
chr19	59128983	3784125	0.064	0.4378
chr20	63025520	3974673	0.0631	0.3022
chr21	48129895	1847622	0.0384	0.2389
chr22	51304566	1360392	0.0265	0.1899
chrMT	16571	27235	1.6435	1.6913
chrX	155270560	11392940	0.0734	0.3562
chrY	59373566	387403	0.0065	0.1292

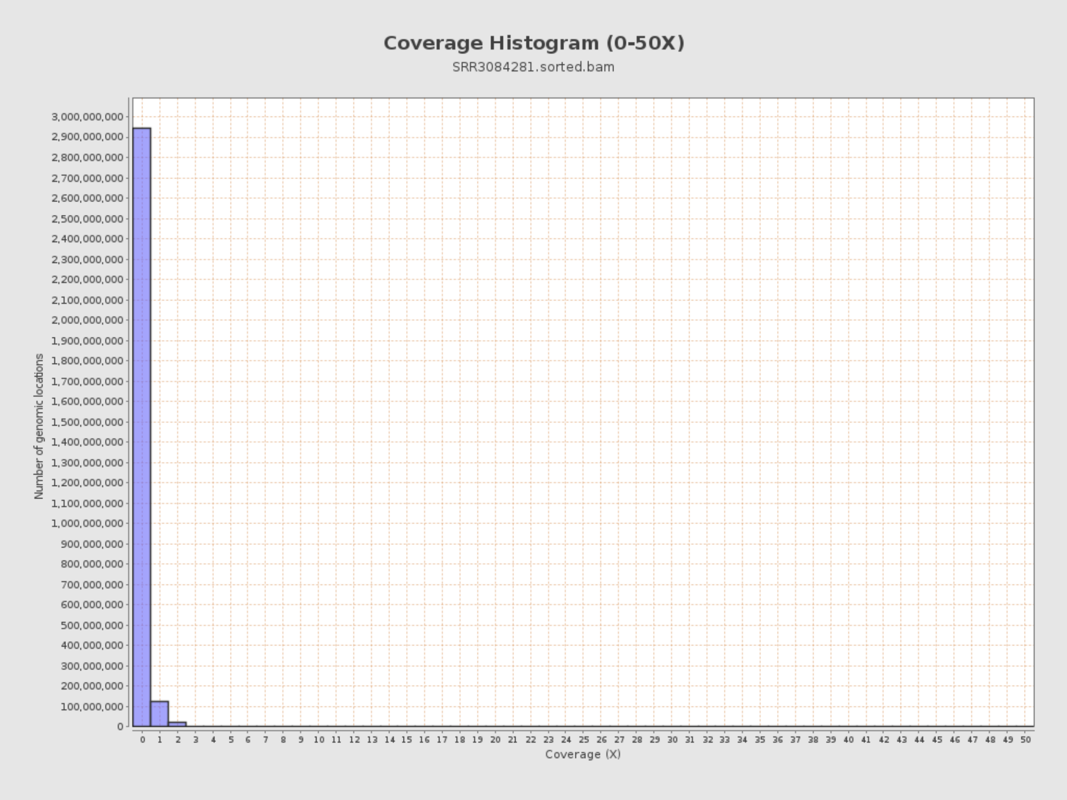
3. Results : Coverage across reference



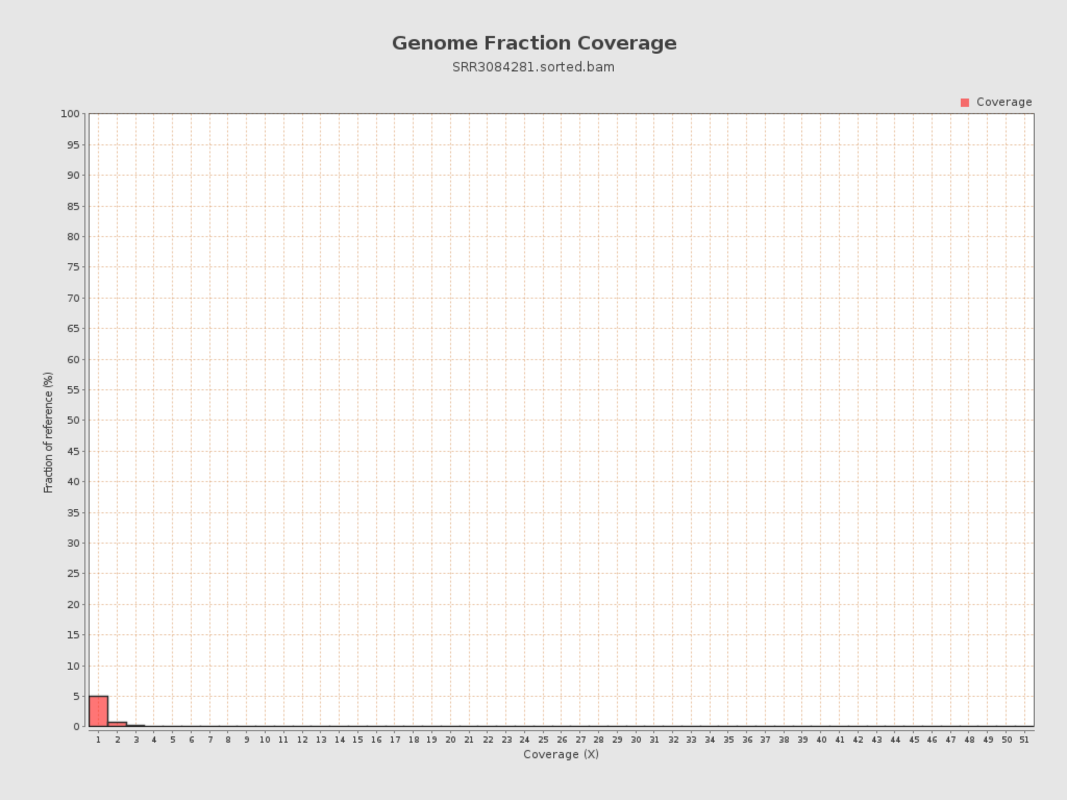
4. Results : Coverage Histogram



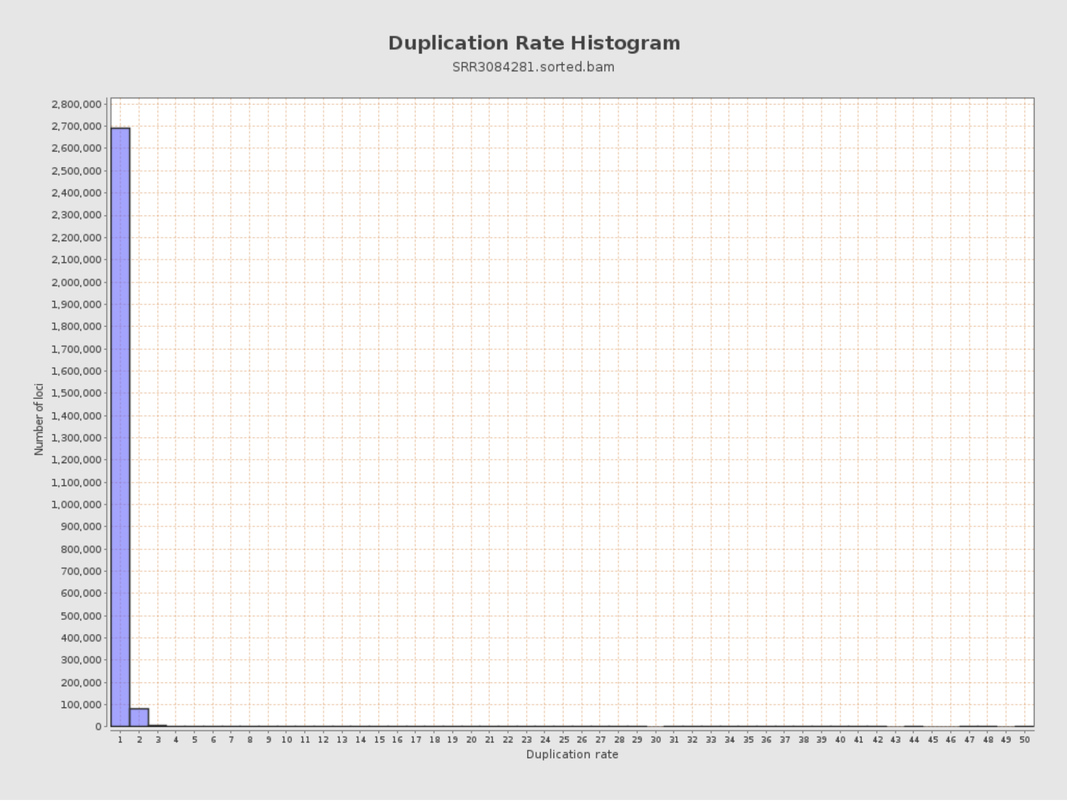
5. Results : Coverage Histogram (0-50X)



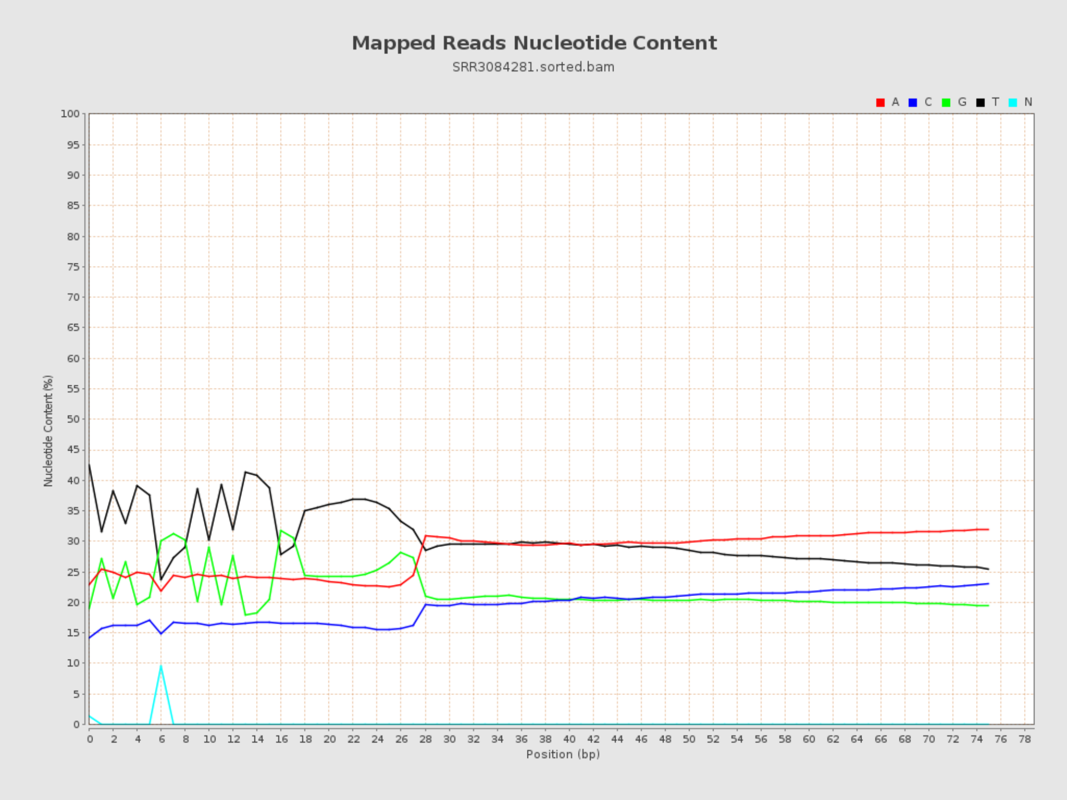
6. Results : Genome Fraction Coverage



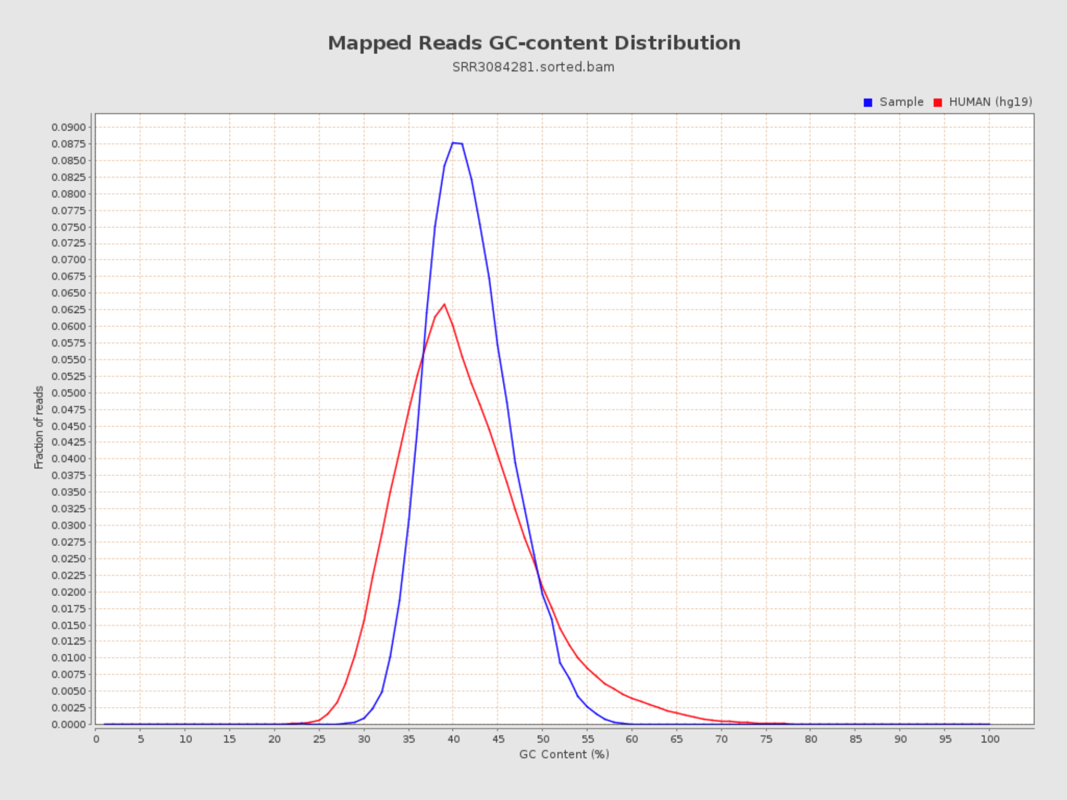
7. Results : Duplication Rate Histogram



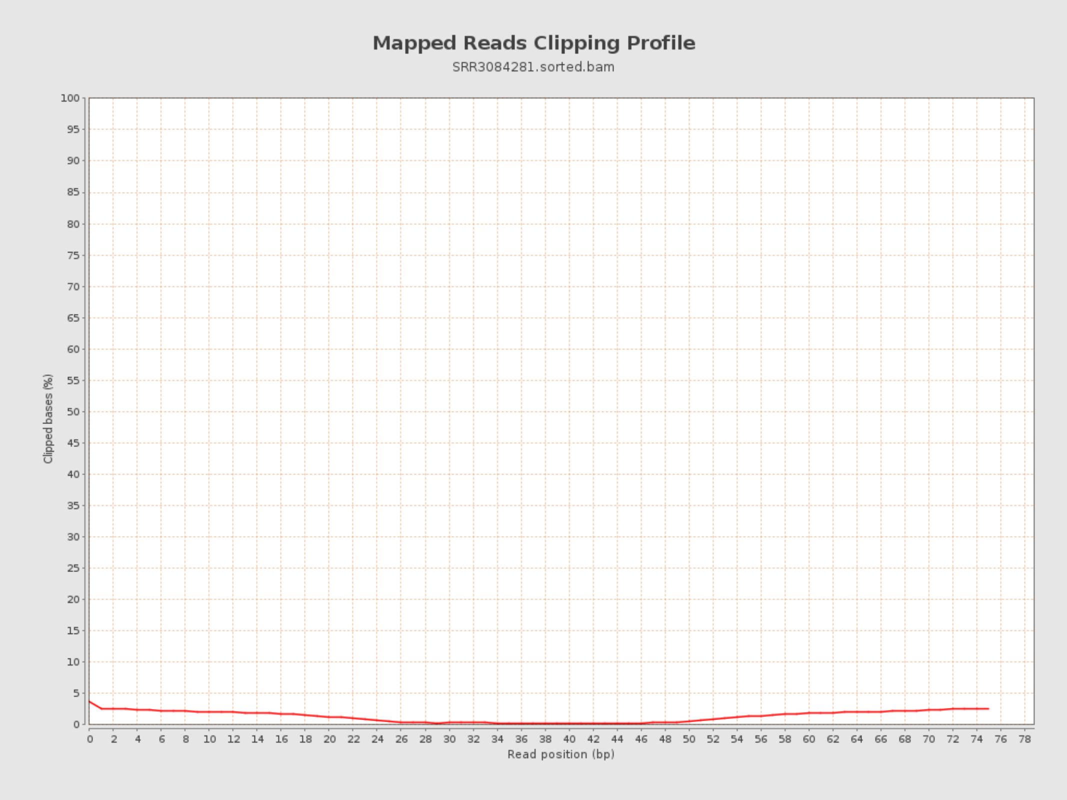
8. Results : Mapped Reads Nucleotide Content



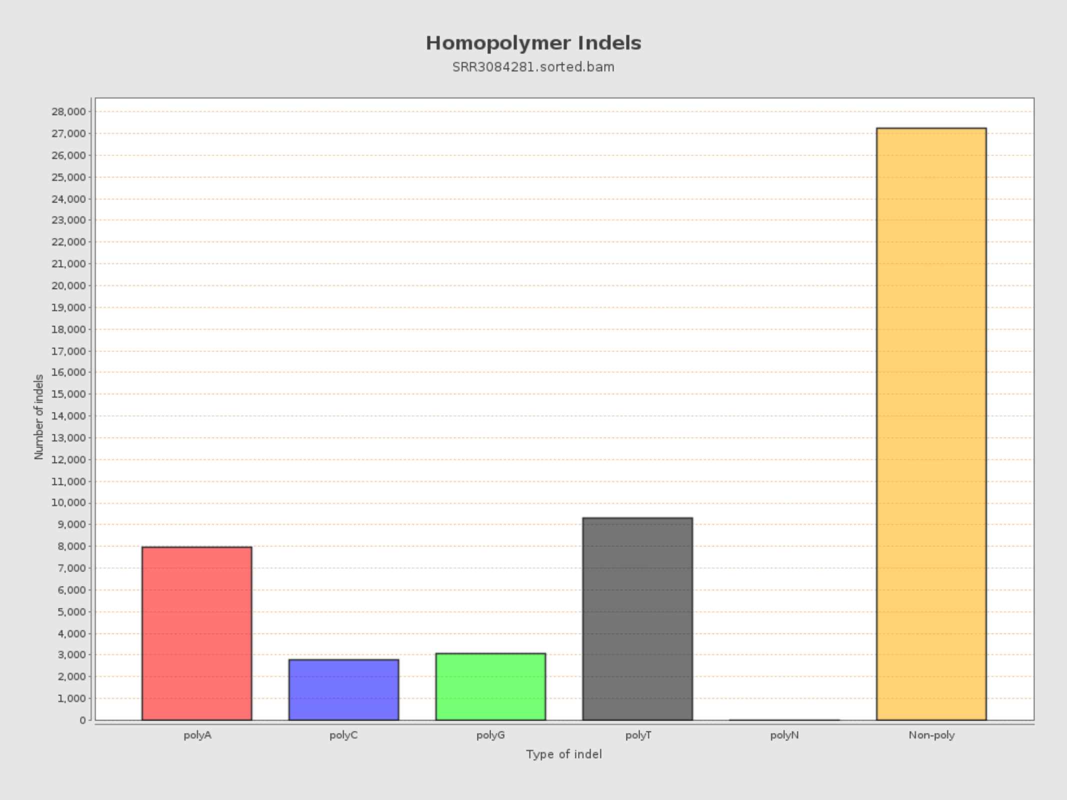
9. Results : Mapped Reads GC-content Distribution



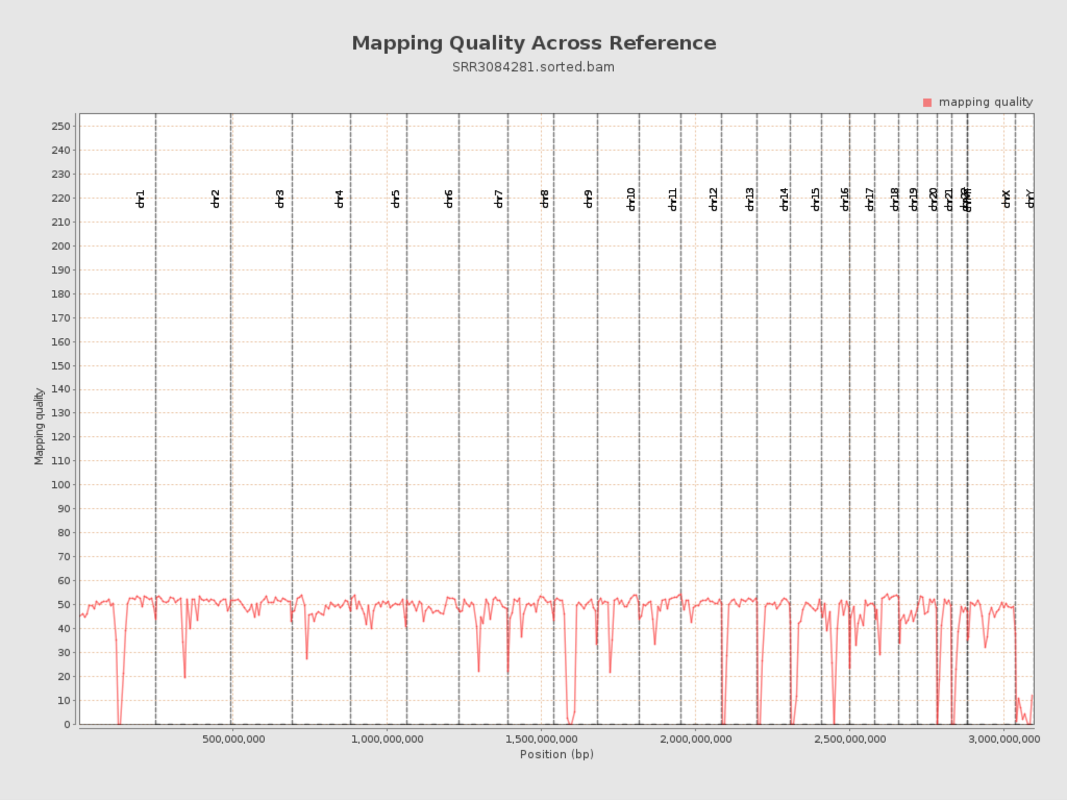
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram