Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 13:51:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084789.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_SRR3084789 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084789.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 13:51:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084789.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,357,537
Mapped reads	2,123,423 / 90.07%
Unmapped reads	234,114 / 9.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,295 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	90,739 / 3.85%
Duplication rate	3.28%
Clipped reads	903,756 / 38.33%

2.2. ACGT Content

Number/percentage of A's	39,750,995 / 27.8%
Number/percentage of C's	27,304,332 / 19.09%
Number/percentage of T's	44,262,647 / 30.95%
Number/percentage of G's	31,622,684 / 22.11%
Number/percentage of N's	57,262 / 0.04%
GC Percentage	41.21%

2.3. Coverage

Mean	0.0462

Standard Deviation	0.3835

2.4. Mapping Quality

Mean Mapping Quality	46.71

2.5. Mismatches and indels

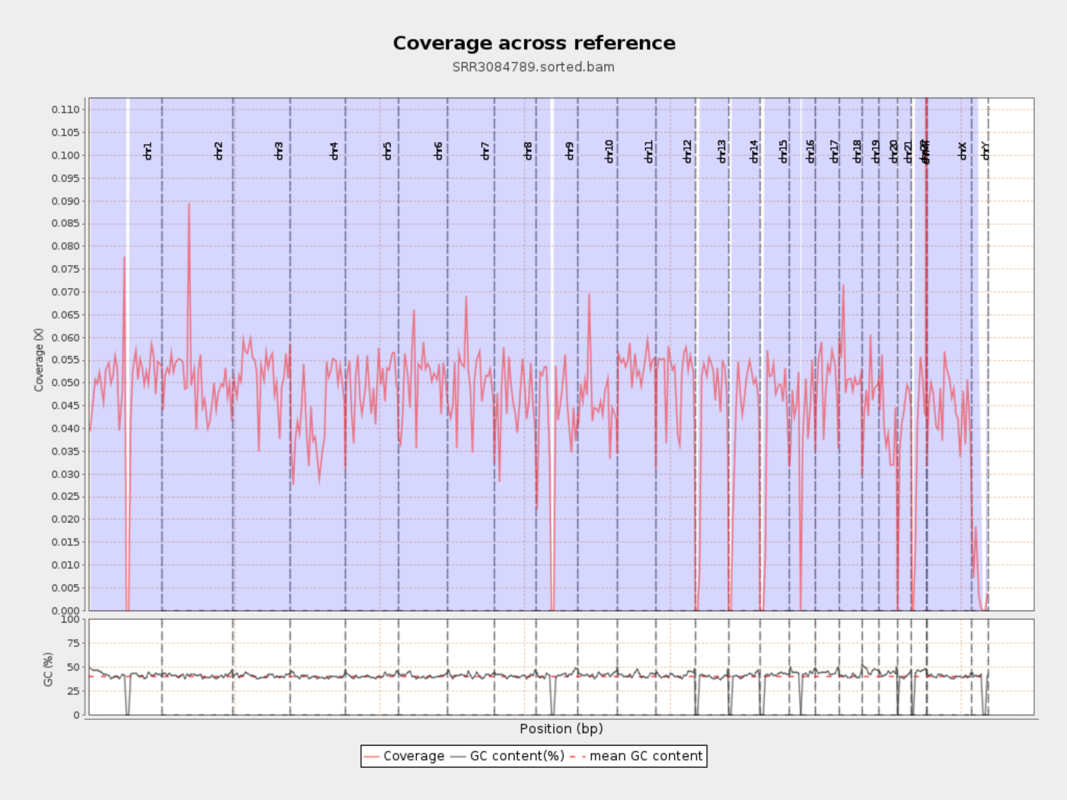
General error rate	0.89%
Mismatches	1,257,515
Insertions	11,068
Mapped reads with at least one insertion	0.52%
Deletions	35,997
Mapped reads with at least one deletion	1.68%
Homopolymer indels	46.7%

2.6. Chromosome stats

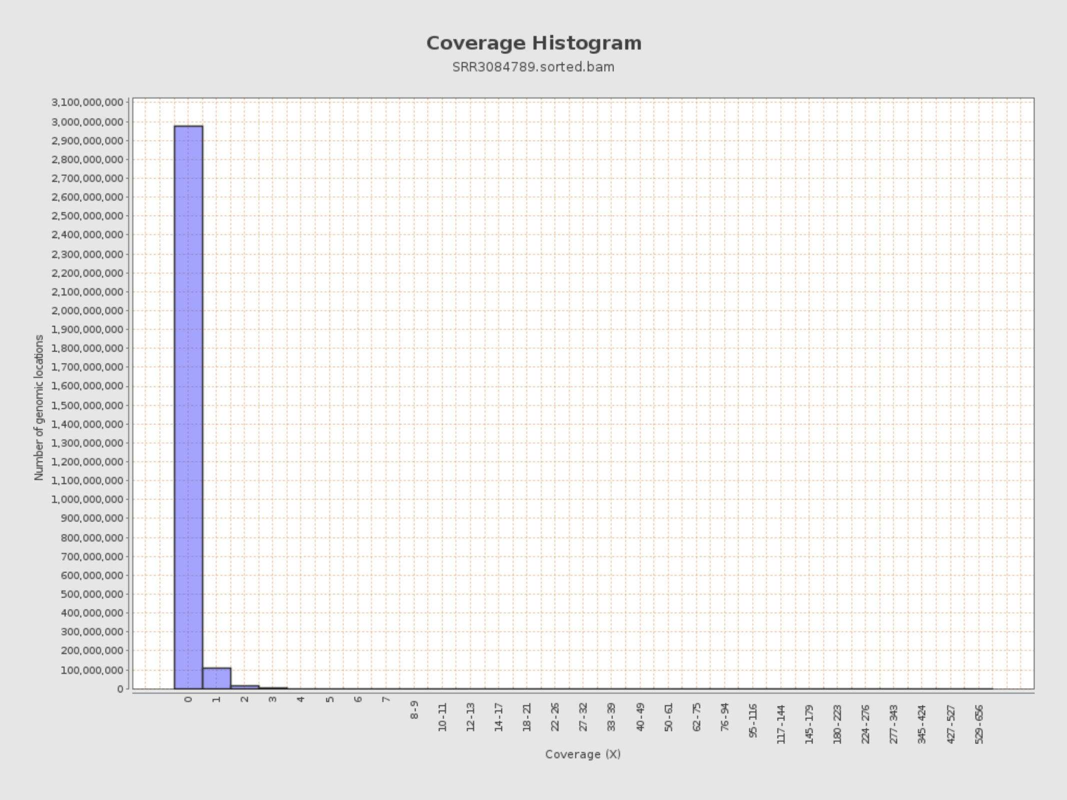
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12090187	0.0485	0.626
chr2	243199373	12337604	0.0507	0.4775
chr3	198022430	10292955	0.052	0.2579
chr4	191154276	8233376	0.0431	0.2552
chr5	180915260	8994356	0.0497	0.2551
chr6	171115067	8667695	0.0507	0.3224
chr7	159138663	7989057	0.0502	0.4678

chr8	146364022	6773247	0.0463	0.3746
chr9	141213431	5676038	0.0402	0.3603
chr10	135534747	6268349	0.0462	0.369
chr11	135006516	7262670	0.0538	0.38
chr12	133851895	6874231	0.0514	0.2614
chr13	115169878	4937982	0.0429	0.2363
chr14	107349540	4416618	0.0411	0.26
chr15	102531392	4084115	0.0398	0.2322
chr16	90354753	3736912	0.0414	0.2722
chr17	81195210	4067296	0.0501	0.2998
chr18	78077248	4148675	0.0531	0.8525
chr19	59128983	2823131	0.0477	0.5002
chr20	63025520	2523655	0.04	0.2449
chr21	48129895	1903276	0.0395	0.2422
chr22	51304566	1667750	0.0325	0.203
chrMT	16571	14619	0.8822	1.136
chrX	155270560	6948892	0.0448	0.2724
chrY	59373566	324082	0.0055	0.1319

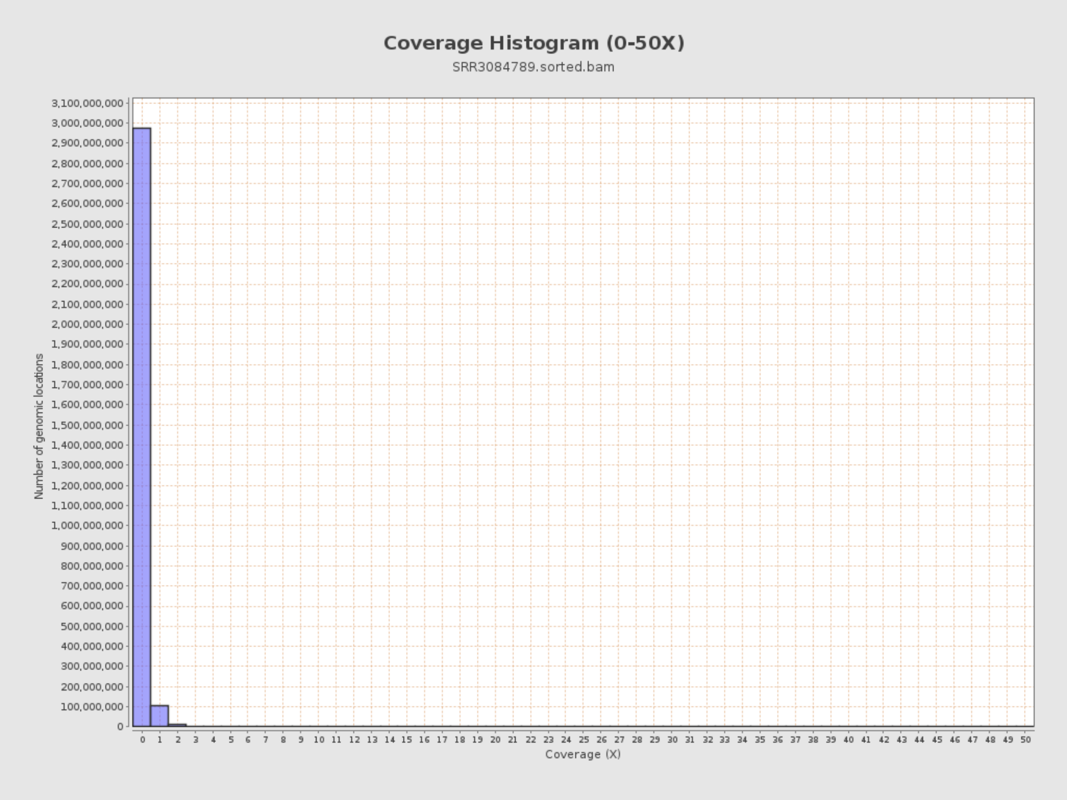
3. Results : Coverage across reference



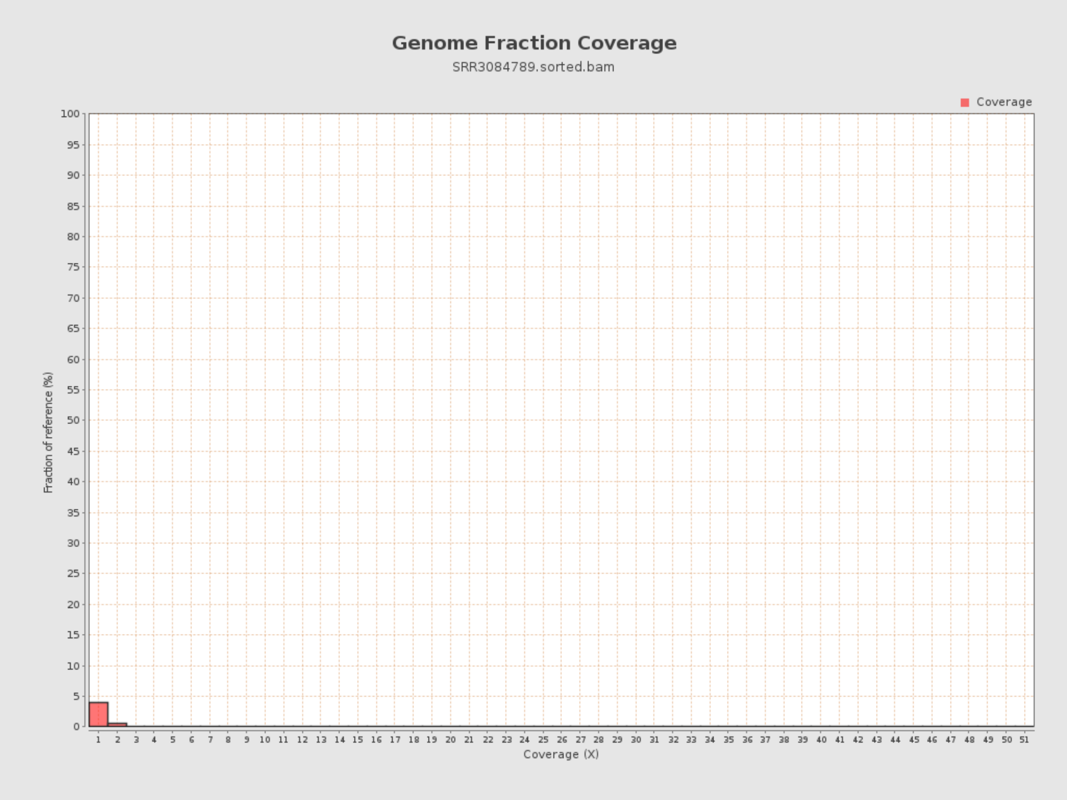
4. Results : Coverage Histogram



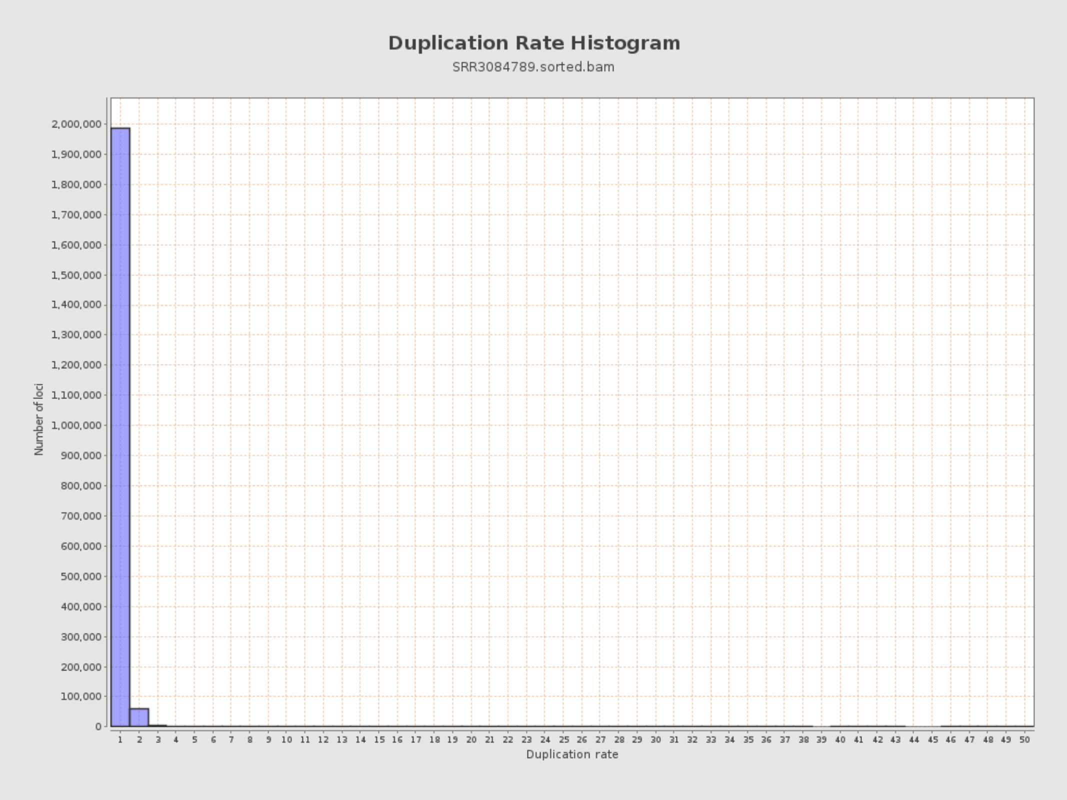
5. Results : Coverage Histogram (0-50X)



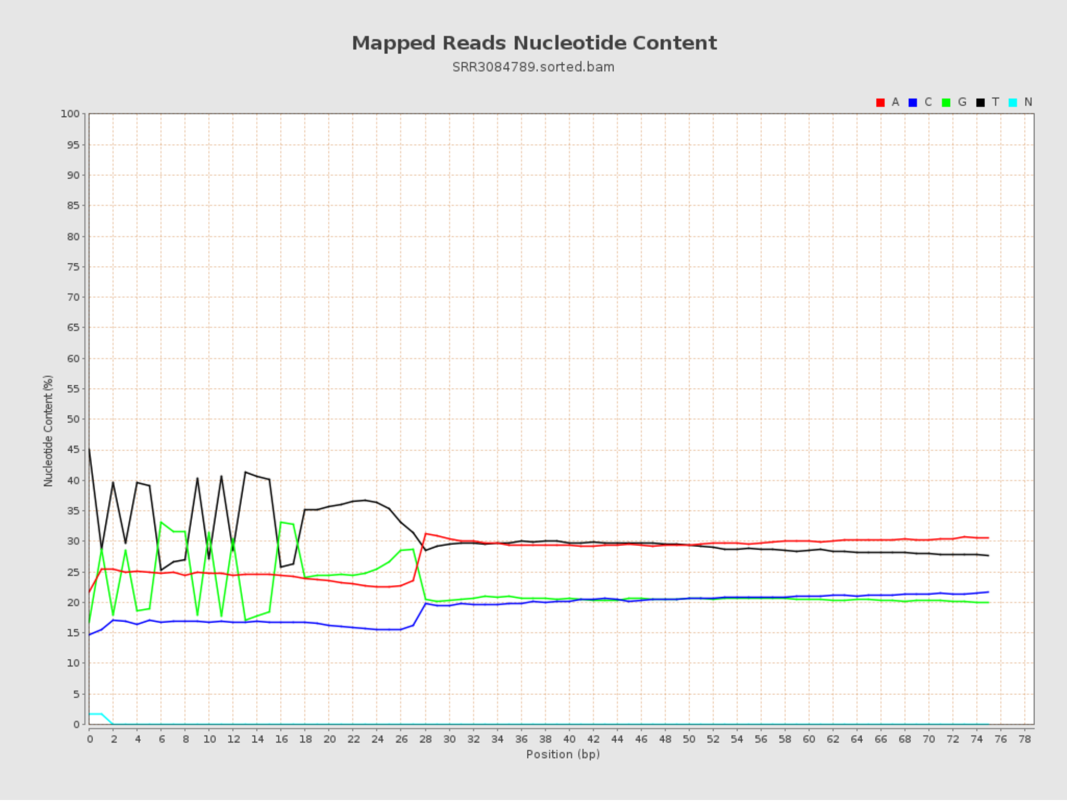
6. Results : Genome Fraction Coverage



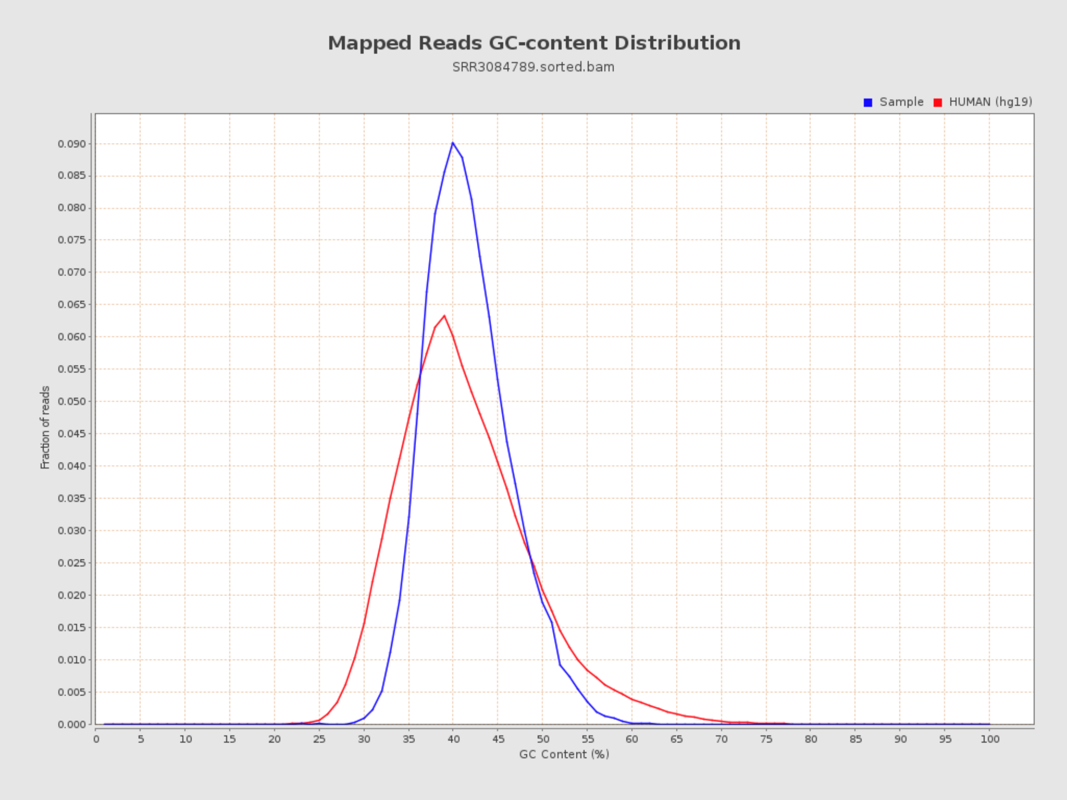
7. Results : Duplication Rate Histogram



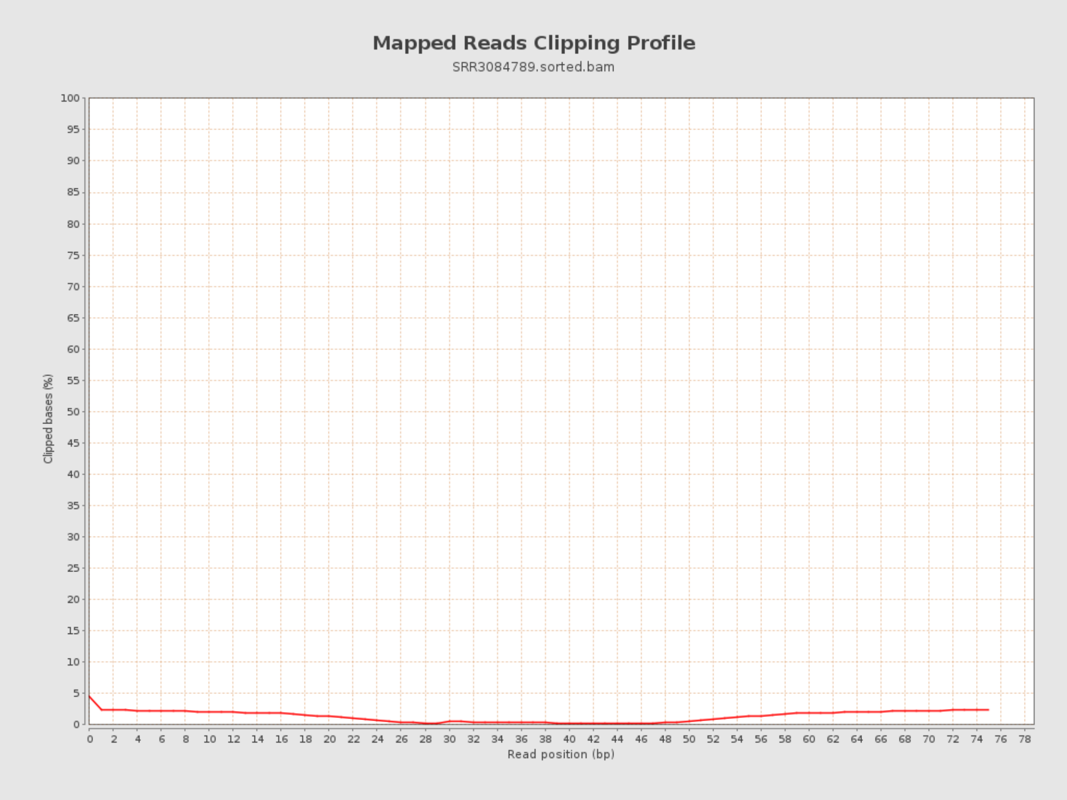
8. Results : Mapped Reads Nucleotide Content



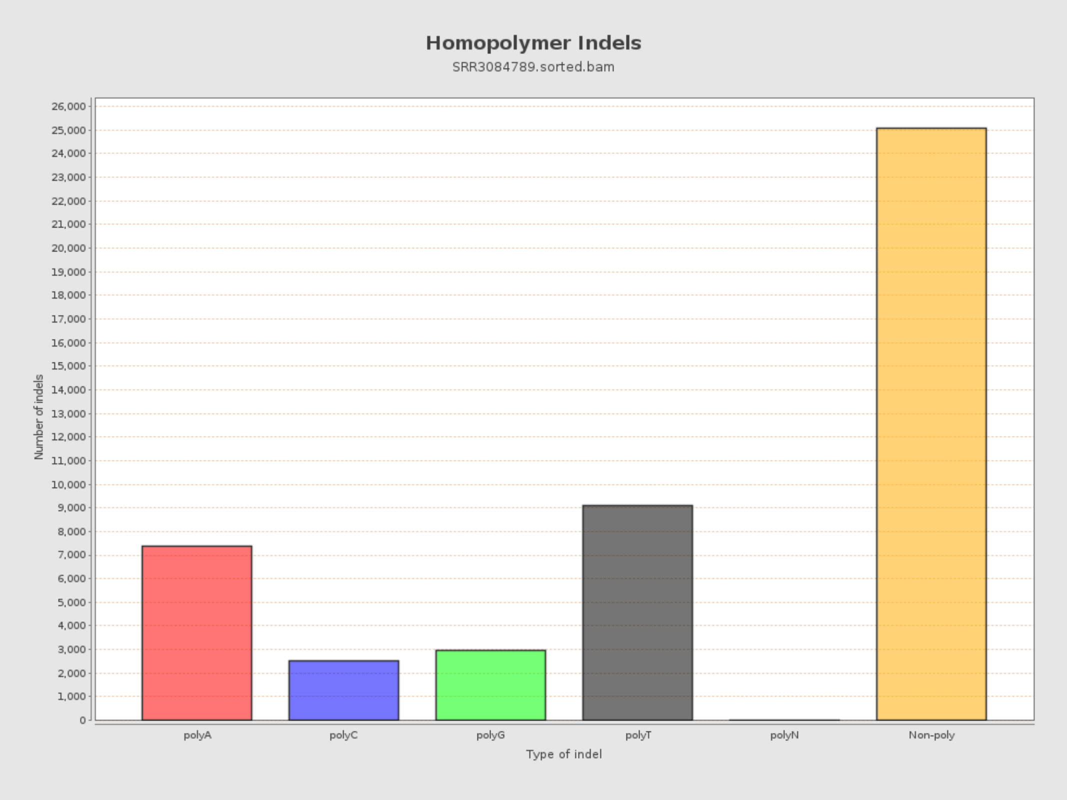
9. Results : Mapped Reads GC-content Distribution



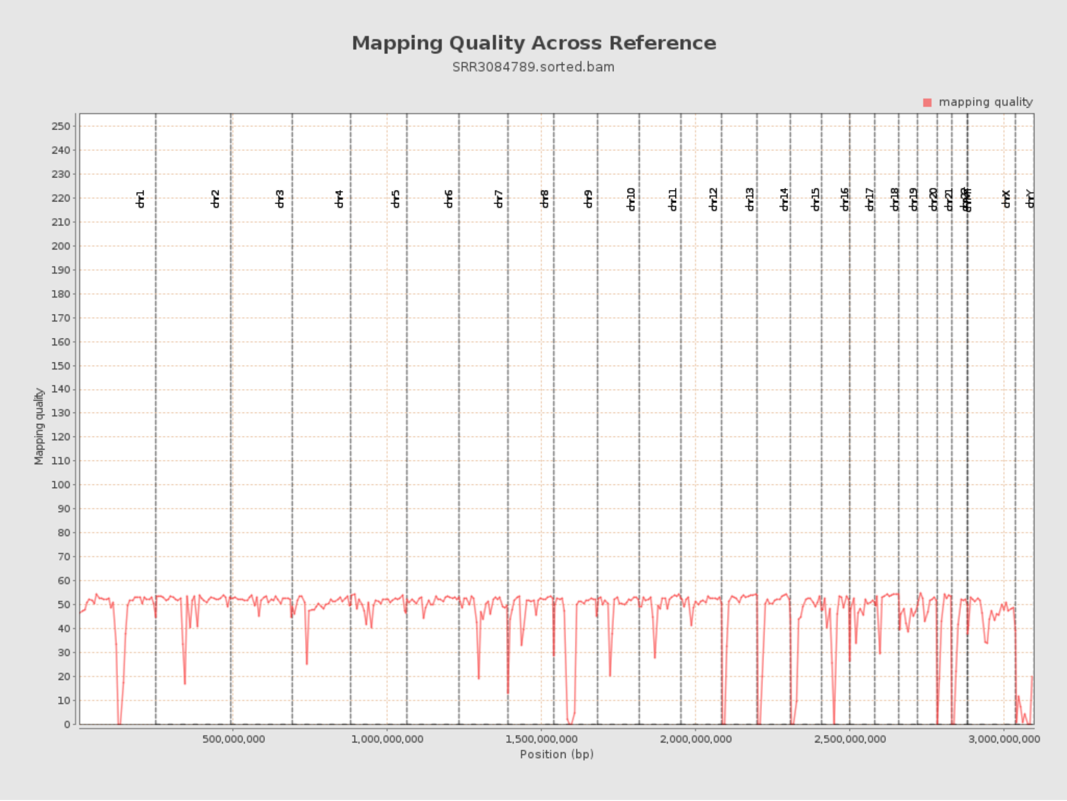
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram