Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 22:37:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085027.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_SRR3085027 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085027.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 22:37:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085027.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,882,462
Mapped reads	2,612,471 / 90.63%
Unmapped reads	269,991 / 9.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,848 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	113,595 / 3.94%
Duplication rate	3.09%
Clipped reads	1,213,810 / 42.11%

2.2. ACGT Content

Number/percentage of A's	48,844,944 / 28.19%
Number/percentage of C's	31,738,639 / 18.31%
Number/percentage of T's	54,458,154 / 31.42%
Number/percentage of G's	38,231,878 / 22.06%
Number/percentage of N's	24,329 / 0.01%
GC Percentage	40.38%

2.3. Coverage

Mean	0.056

Standard Deviation	0.5394

2.4. Mapping Quality

Mean Mapping Quality	45.41

2.5. Mismatches and indels

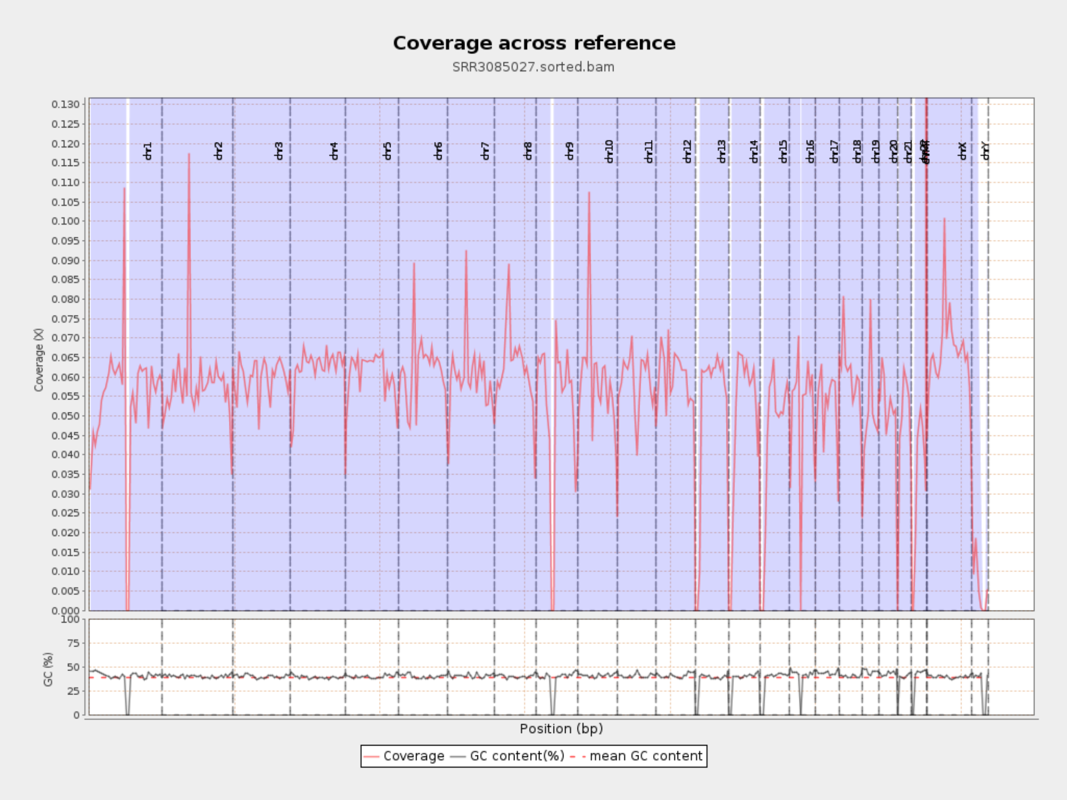
General error rate	0.84%
Mismatches	1,431,348
Insertions	13,450
Mapped reads with at least one insertion	0.51%
Deletions	37,387
Mapped reads with at least one deletion	1.42%
Homopolymer indels	47.63%

2.6. Chromosome stats

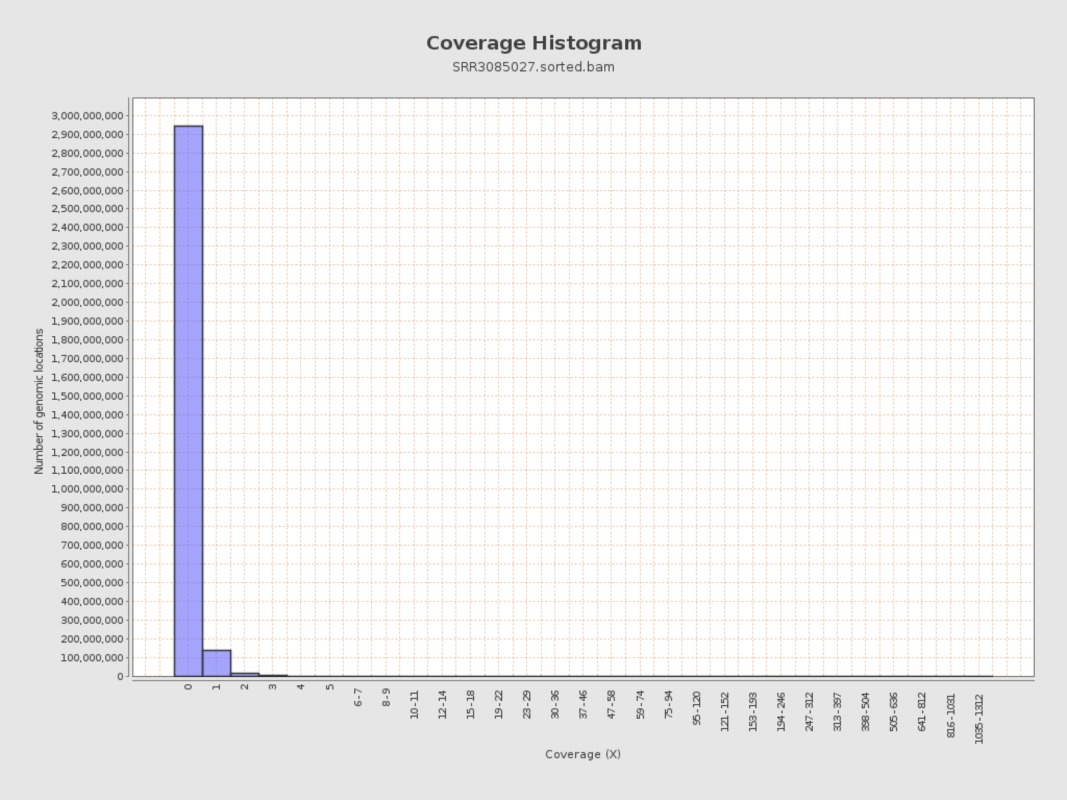
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13492478	0.0541	1.0972
chr2	243199373	14273762	0.0587	0.5996
chr3	198022430	11867567	0.0599	0.2756
chr4	191154276	11941322	0.0625	0.2864
chr5	180915260	11050484	0.0611	0.2771
chr6	171115067	10564395	0.0617	0.4101
chr7	159138663	9614924	0.0604	0.4989

chr8	146364022	9108252	0.0622	0.8023
chr9	141213431	7348612	0.052	0.4862
chr10	135534747	8104841	0.0598	0.5624
chr11	135006516	7872294	0.0583	0.5018
chr12	133851895	7995183	0.0597	0.286
chr13	115169878	5831871	0.0506	0.2465
chr14	107349540	5260115	0.049	0.2986
chr15	102531392	4500418	0.0439	0.2401
chr16	90354753	4603914	0.051	0.3224
chr17	81195210	4210638	0.0519	0.3421
chr18	78077248	4782226	0.0612	1.0077
chr19	59128983	3002427	0.0508	0.7379
chr20	63025520	3288701	0.0522	0.2746
chr21	48129895	2253527	0.0468	0.2673
chr22	51304566	1602717	0.0312	0.1933
chrMT	16571	39196	2.3653	2.0481
chrX	155270560	10352324	0.0667	0.3639
chrY	59373566	395552	0.0067	0.1243

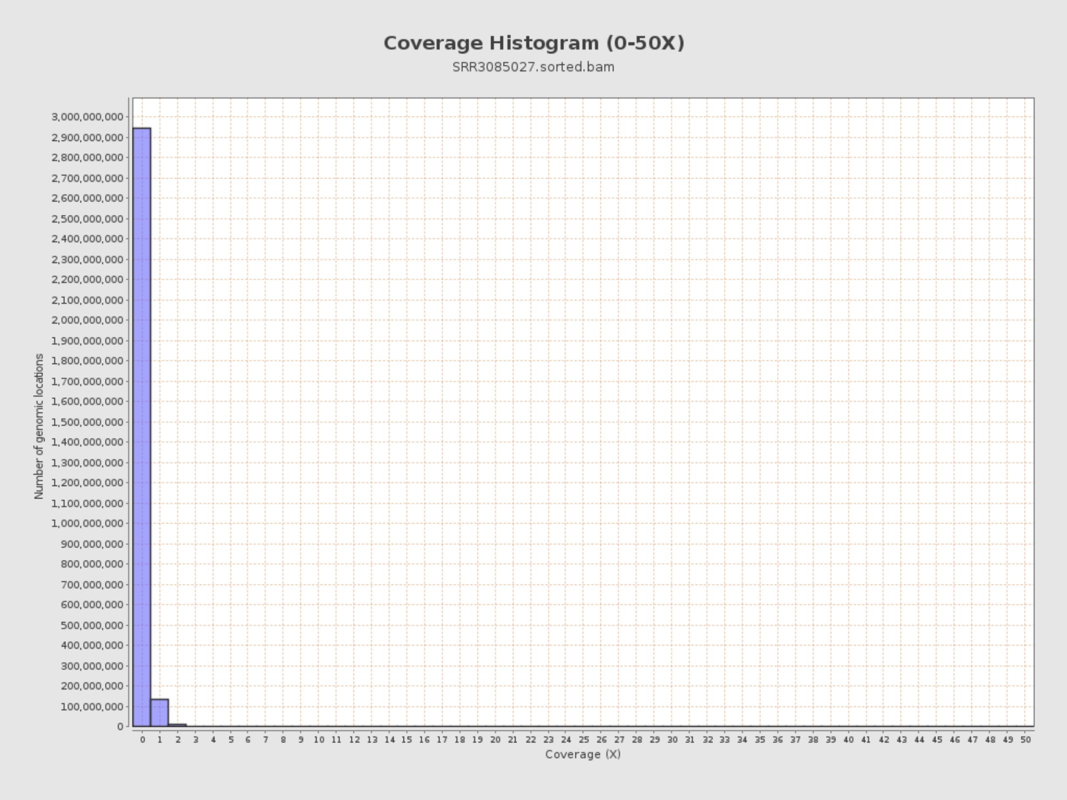
3. Results : Coverage across reference



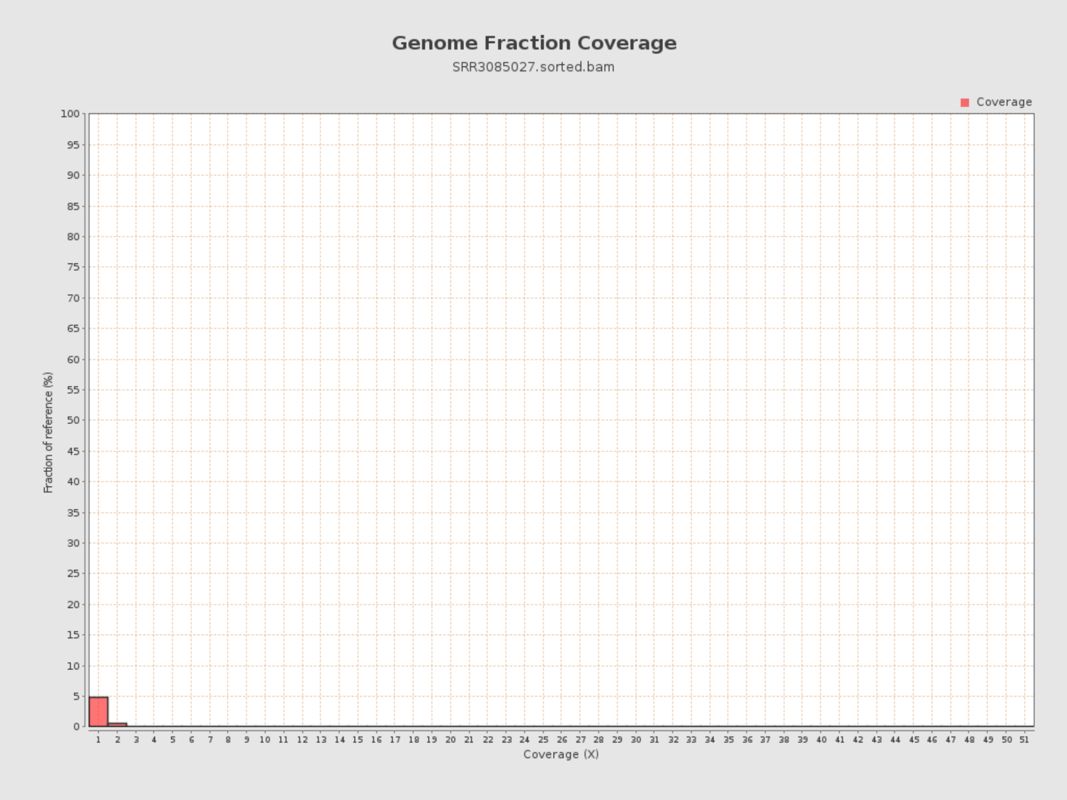
4. Results : Coverage Histogram



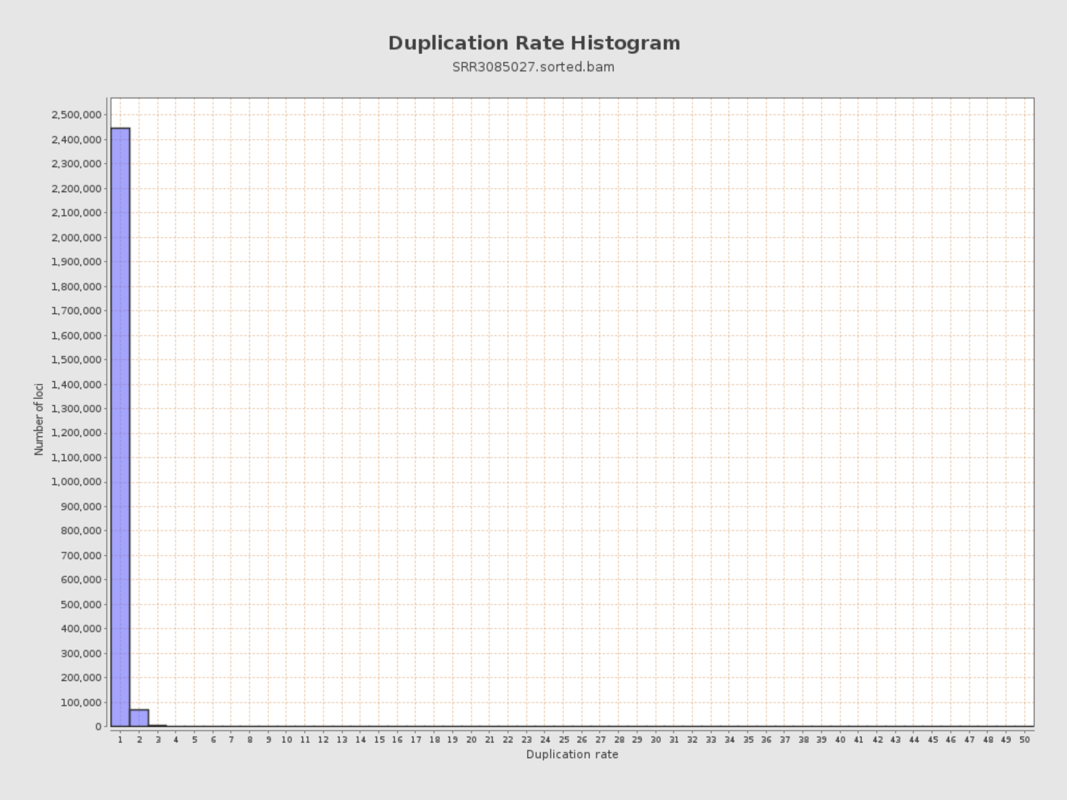
5. Results : Coverage Histogram (0-50X)



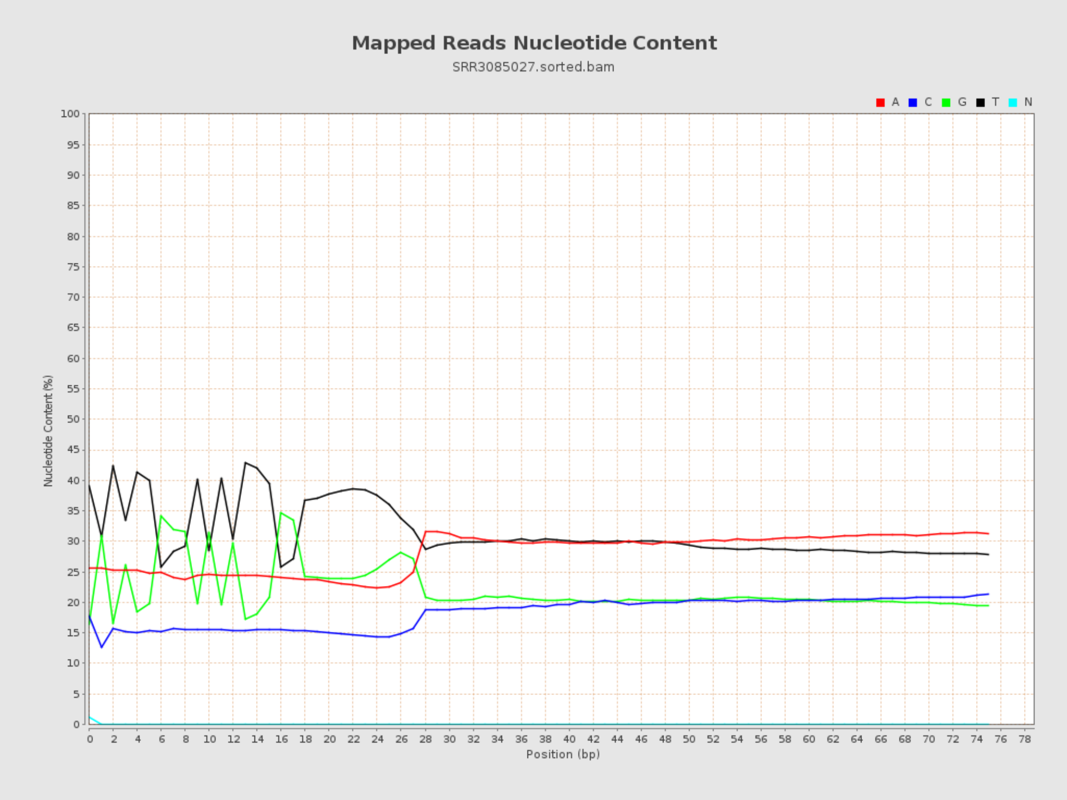
6. Results : Genome Fraction Coverage



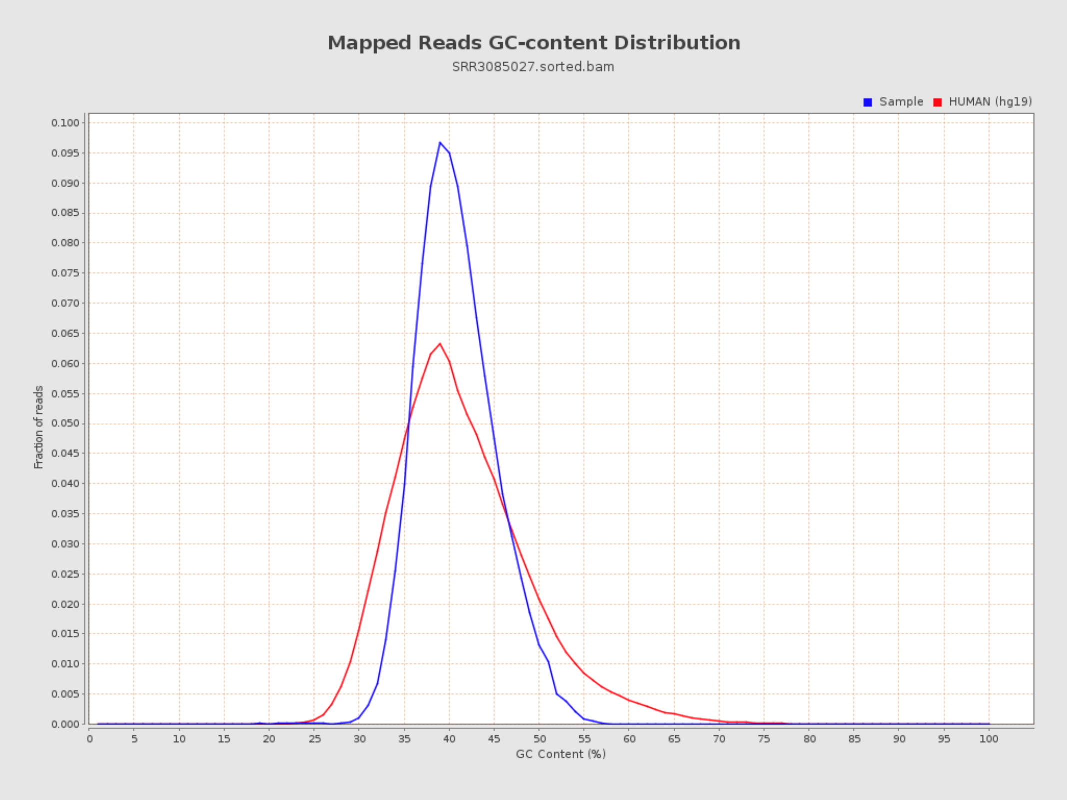
7. Results : Duplication Rate Histogram



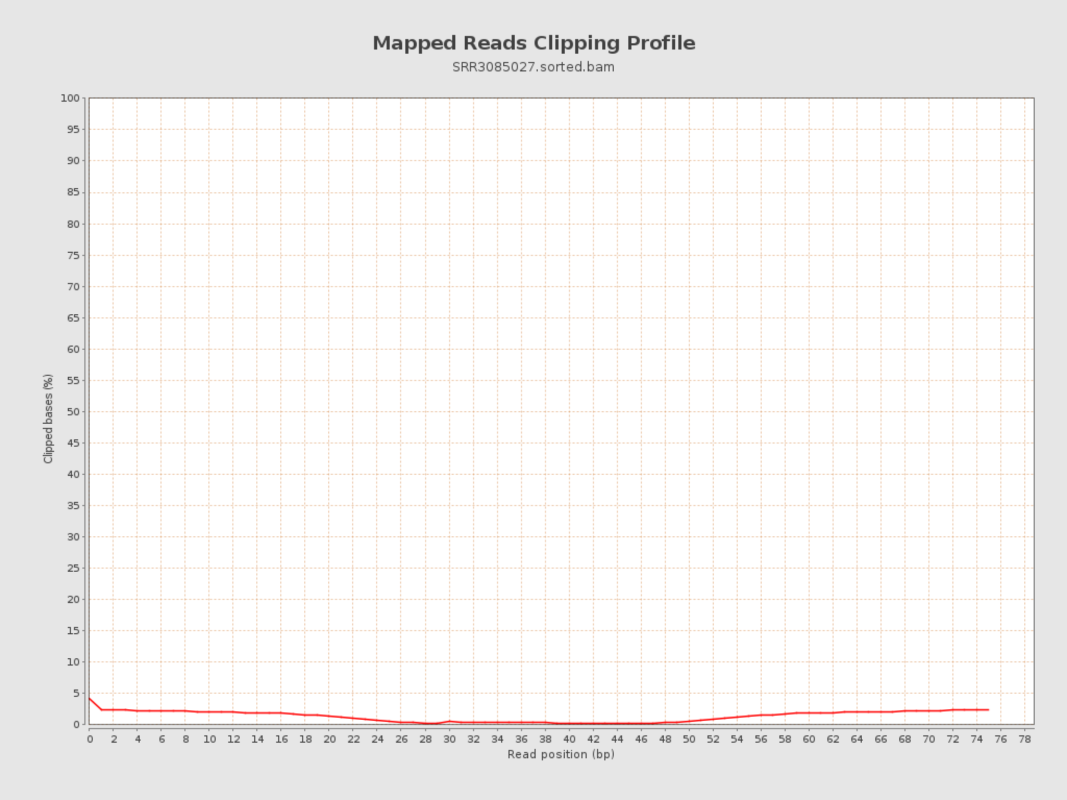
8. Results : Mapped Reads Nucleotide Content



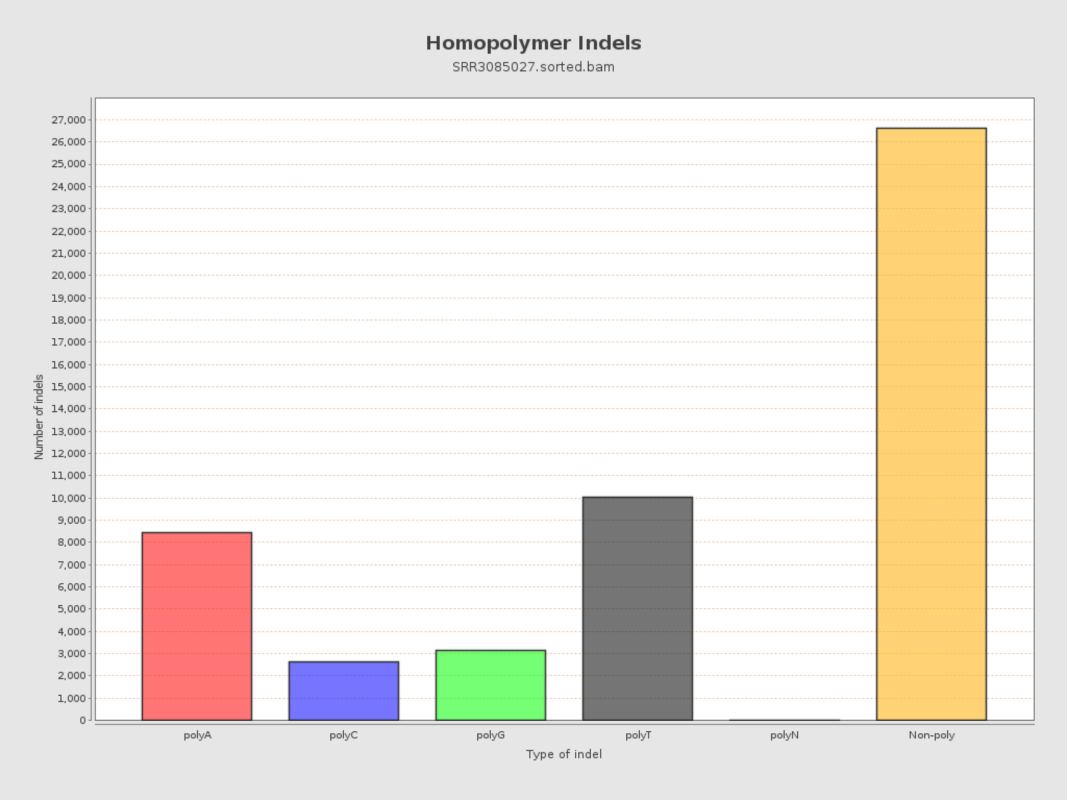
9. Results : Mapped Reads GC-content Distribution



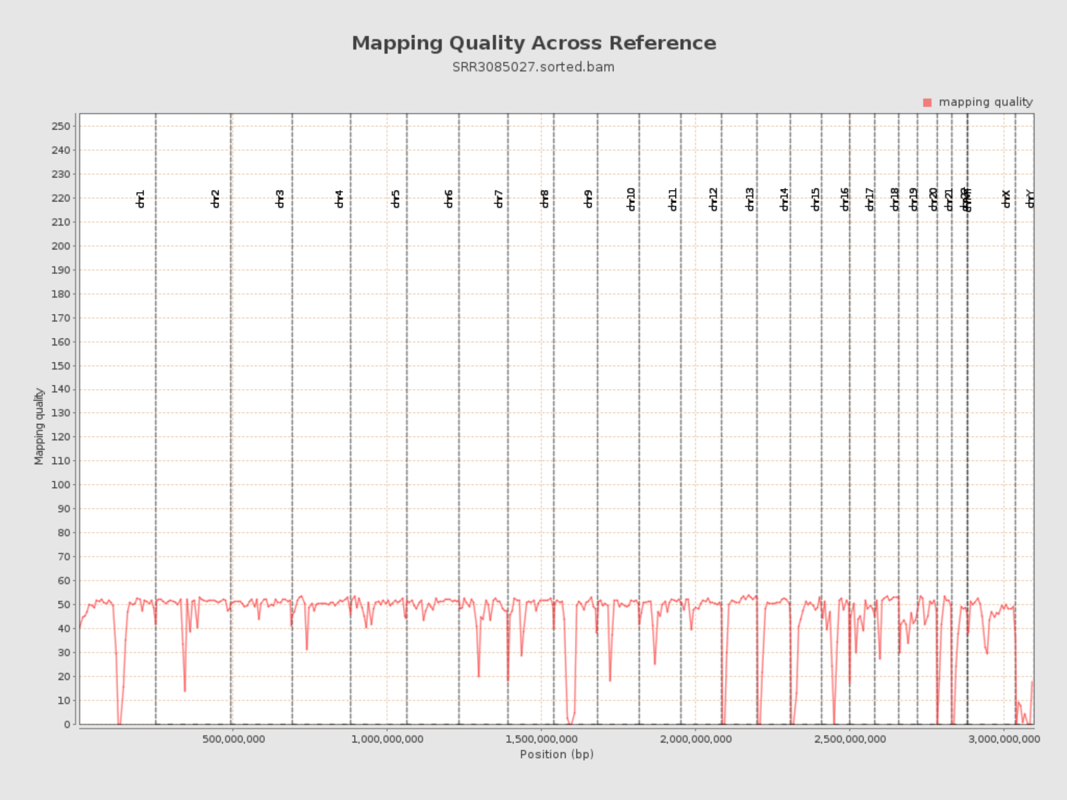
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram