Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 17:06:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082705.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_SRR3082705 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082705.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 17:06:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082705.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,877,889
Mapped reads	3,587,272 / 92.51%
Unmapped reads	290,617 / 7.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,331 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	164,099 / 4.23%
Duplication rate	3.12%
Clipped reads	1,714,684 / 44.22%

2.2. ACGT Content

Number/percentage of A's	64,905,438 / 27.33%
Number/percentage of C's	41,387,730 / 17.43%
Number/percentage of T's	78,286,699 / 32.97%
Number/percentage of G's	52,821,118 / 22.24%
Number/percentage of N's	63,083 / 0.03%
GC Percentage	39.67%

2.3. Coverage

Mean	0.0767

Standard Deviation	0.6786

2.4. Mapping Quality

Mean Mapping Quality	45.94

2.5. Mismatches and indels

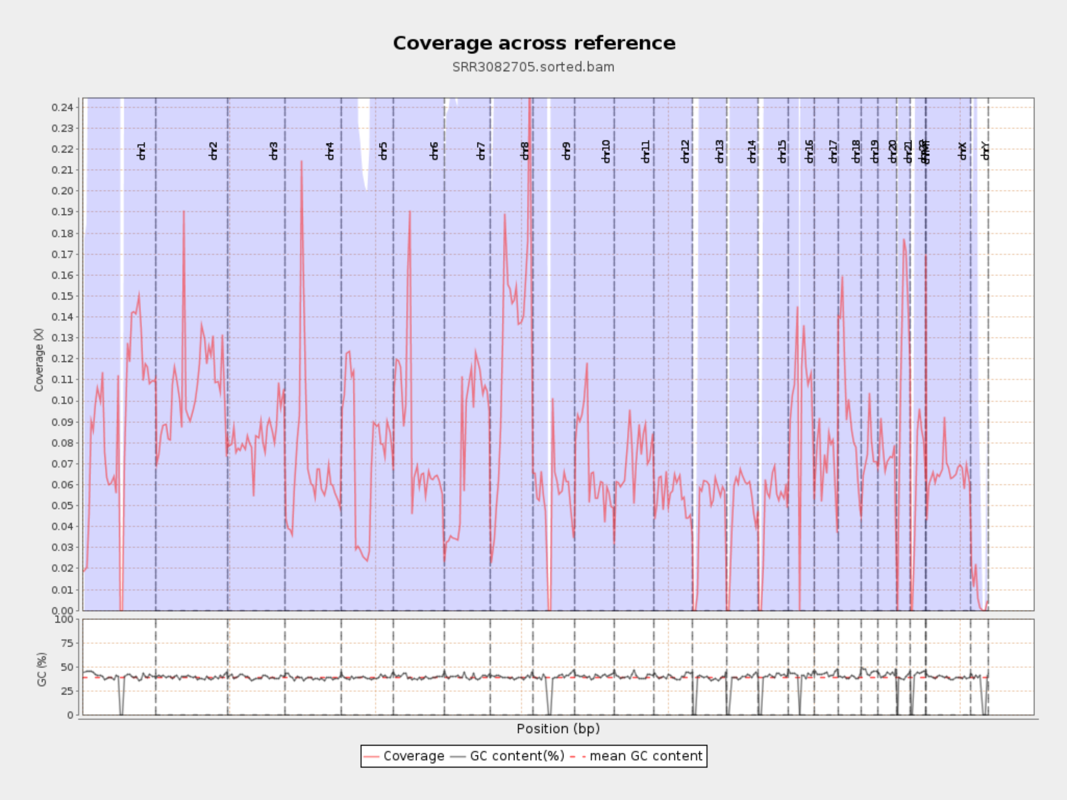
General error rate	0.95%
Mismatches	2,211,586
Insertions	21,889
Mapped reads with at least one insertion	0.6%
Deletions	57,384
Mapped reads with at least one deletion	1.58%
Homopolymer indels	48.46%

2.6. Chromosome stats

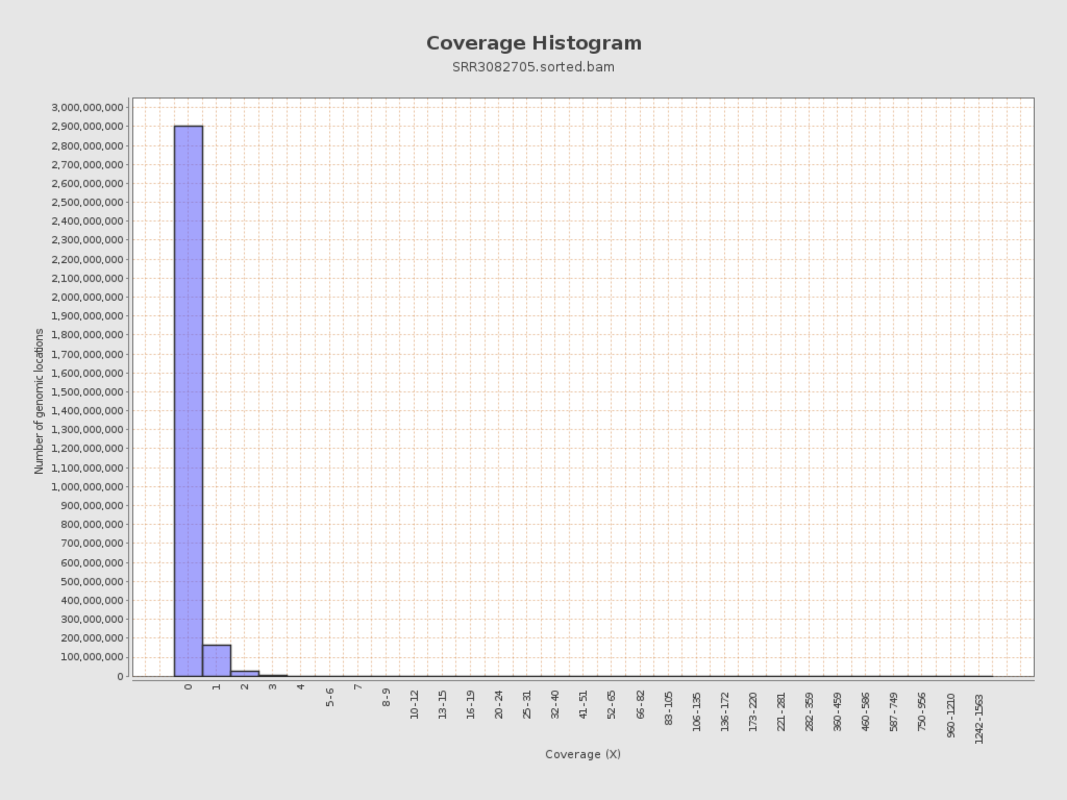
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22381880	0.0898	0.9614
chr2	243199373	25805853	0.1061	1.0434
chr3	198022430	16466785	0.0832	0.3475
chr4	191154276	13517226	0.0707	0.3372
chr5	180915260	13200438	0.073	0.329
chr6	171115067	14272371	0.0834	0.6263
chr7	159138663	12494263	0.0785	0.8915

chr8	146364022	19015577	0.1299	0.7763
chr9	141213431	7504339	0.0531	0.785
chr10	135534747	9414613	0.0695	0.552
chr11	135006516	9749559	0.0722	0.5938
chr12	133851895	7275510	0.0544	0.2973
chr13	115169878	5494478	0.0477	0.2508
chr14	107349540	5297646	0.0493	0.384
chr15	102531392	4839566	0.0472	0.2514
chr16	90354753	8907636	0.0986	0.4366
chr17	81195210	5821286	0.0717	0.4926
chr18	78077248	7818958	0.1001	1.7244
chr19	59128983	4407042	0.0745	0.8454
chr20	63025520	4650058	0.0738	0.3817
chr21	48129895	5594206	0.1162	0.4328
chr22	51304566	3041100	0.0593	0.2838
chrMT	16571	2814	0.1698	0.4674
chrX	155270560	10127773	0.0652	0.4337
chrY	59373566	455390	0.0077	0.1708

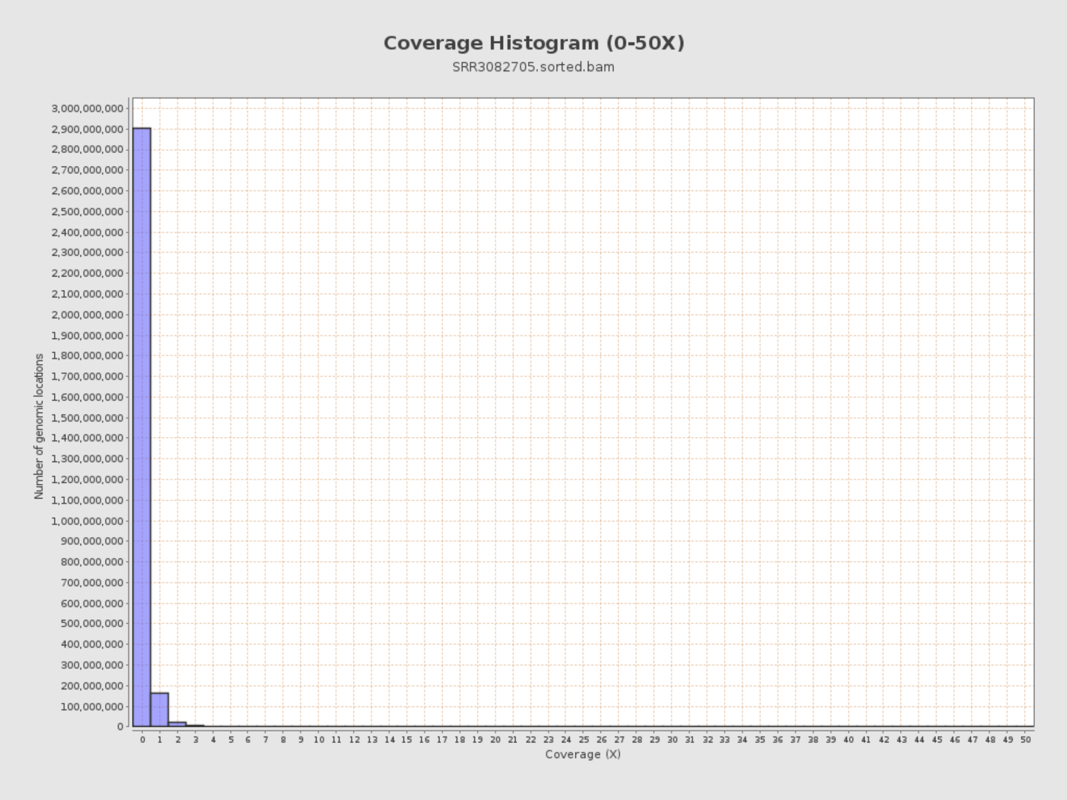
3. Results : Coverage across reference



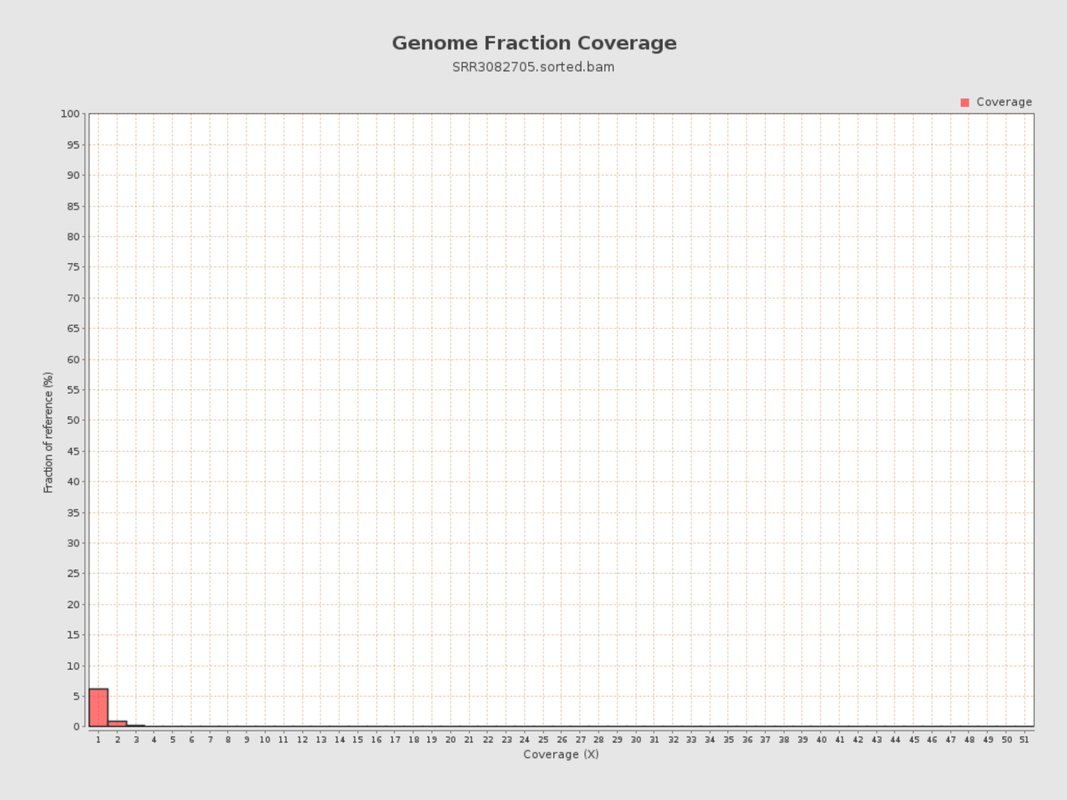
4. Results : Coverage Histogram



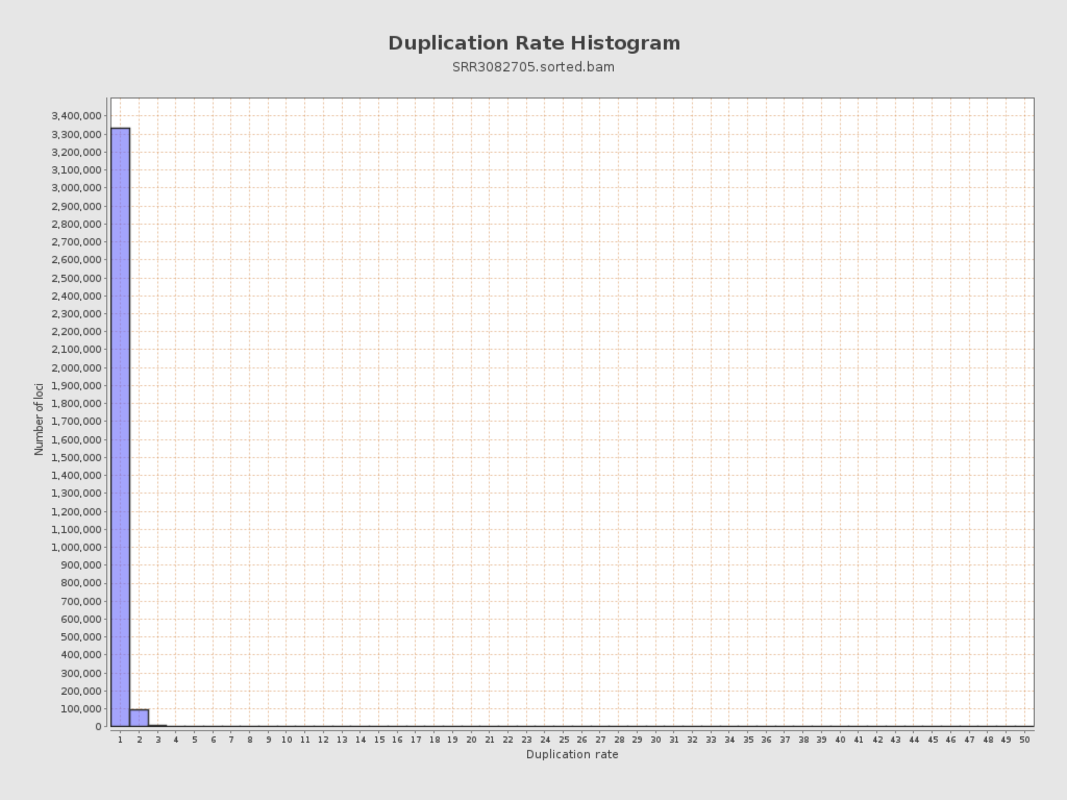
5. Results : Coverage Histogram (0-50X)



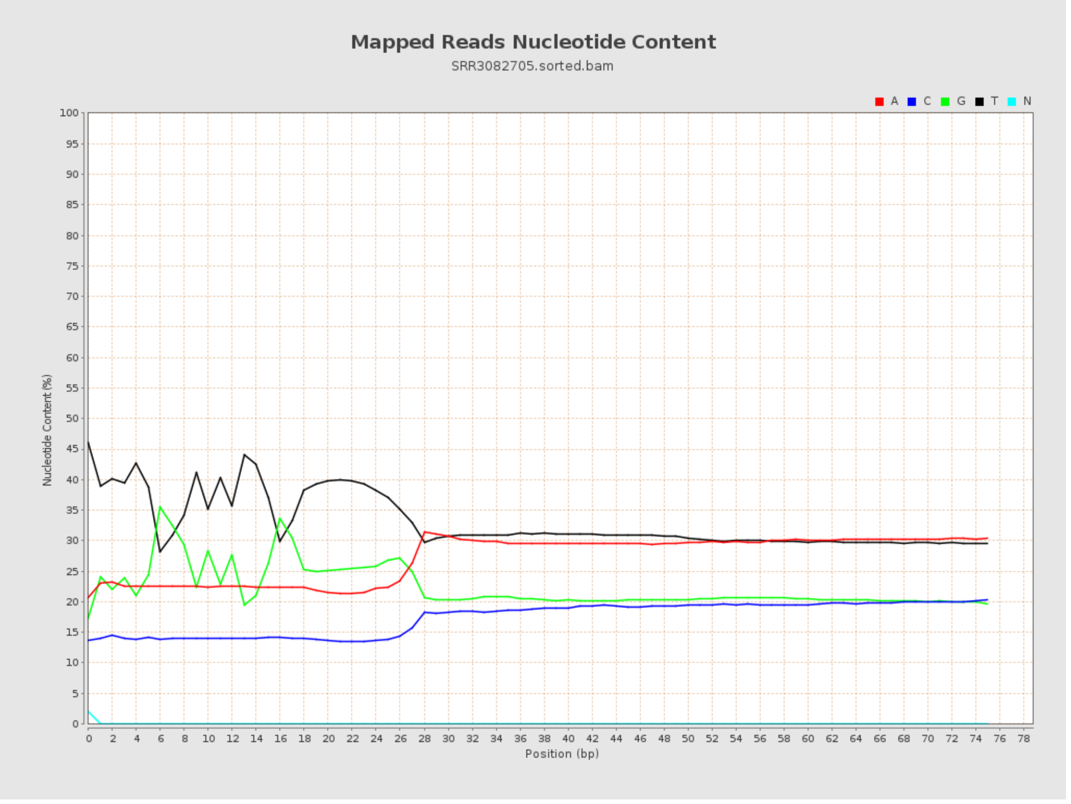
6. Results : Genome Fraction Coverage



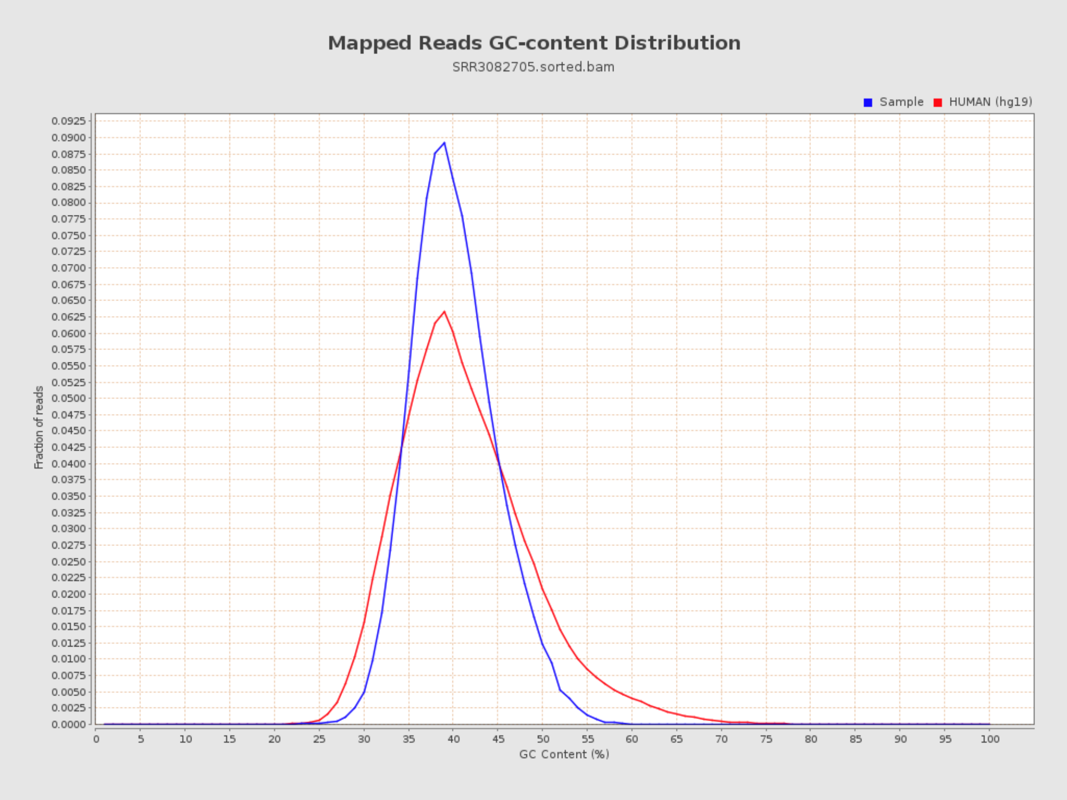
7. Results : Duplication Rate Histogram



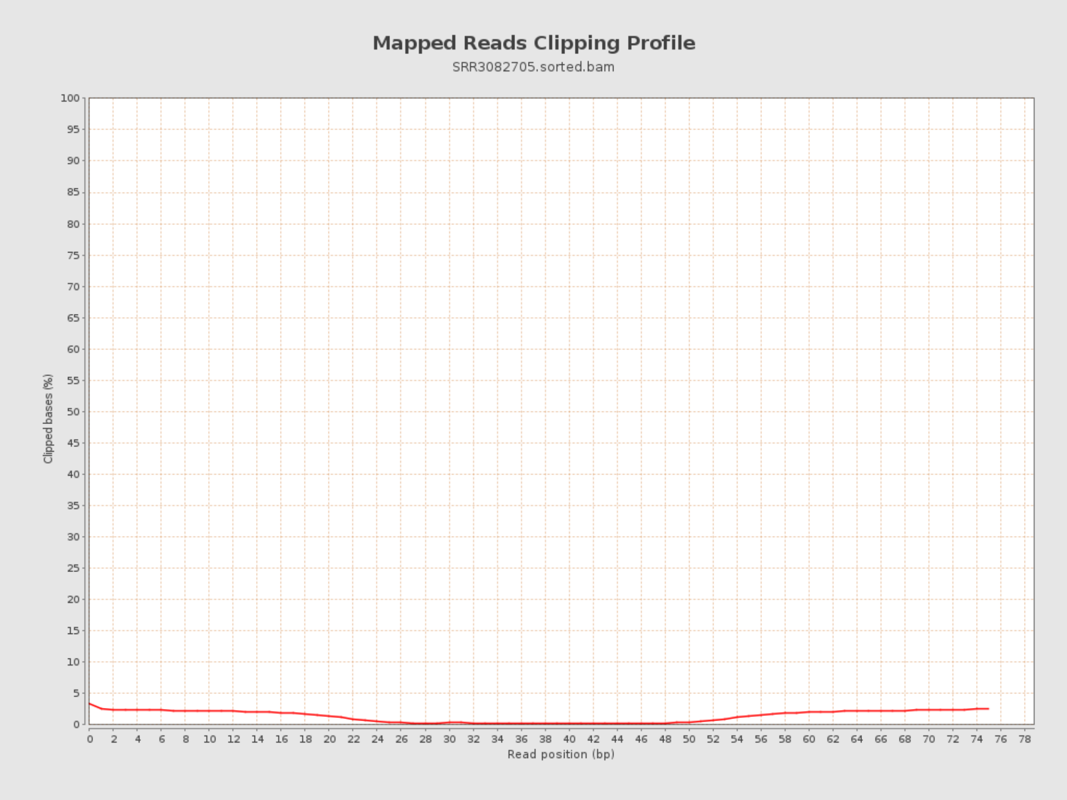
8. Results : Mapped Reads Nucleotide Content



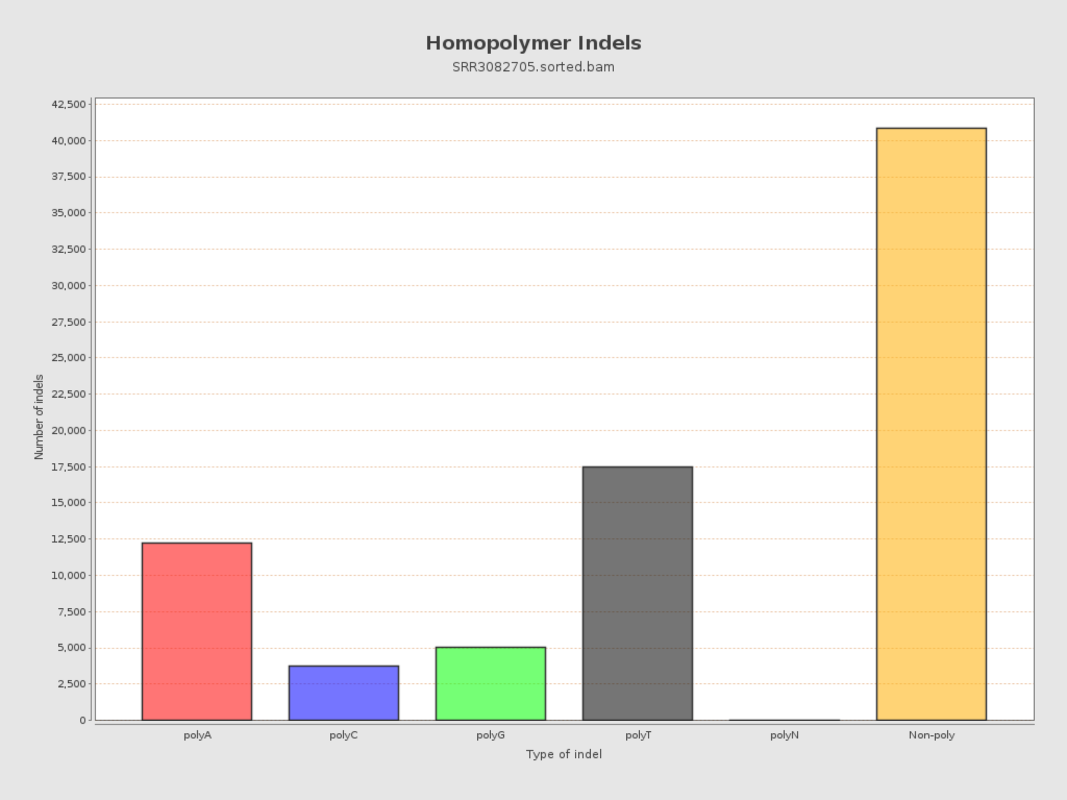
9. Results : Mapped Reads GC-content Distribution



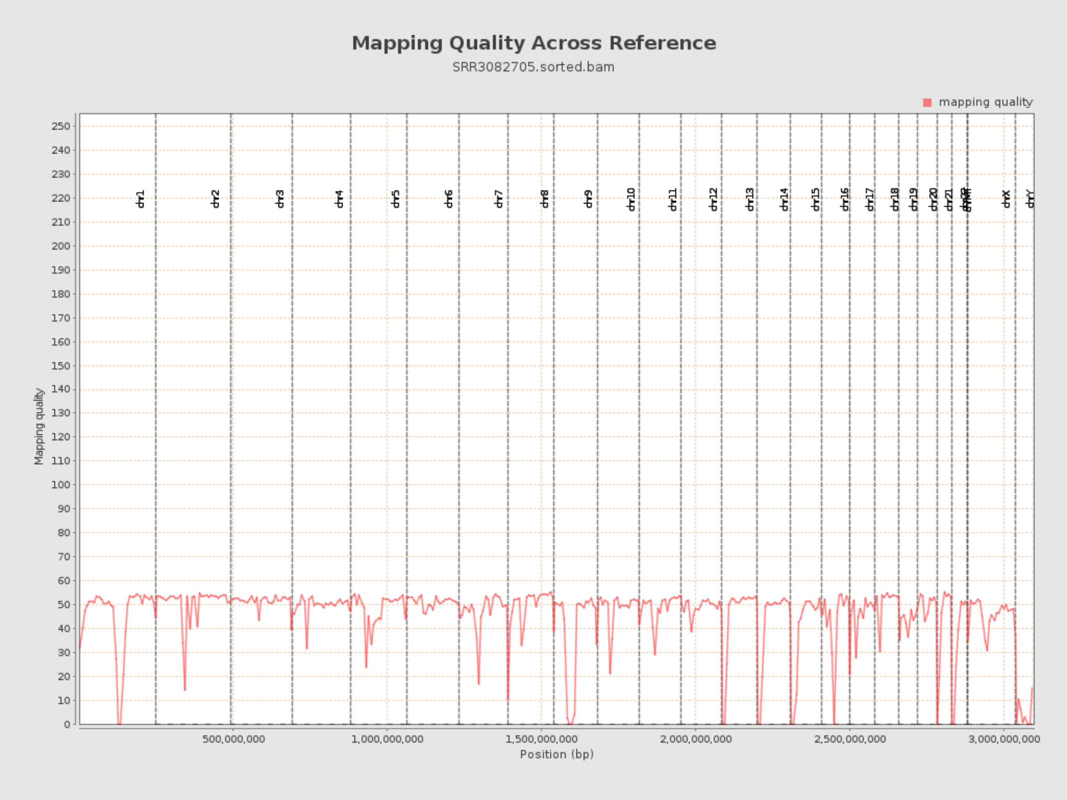
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram