Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 22:26:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085024.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_SRR3085024 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085024.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 22:26:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085024.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,394,457
Mapped reads	2,176,881 / 90.91%
Unmapped reads	217,576 / 9.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,142 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	88,172 / 3.68%
Duplication rate	3.41%
Clipped reads	977,303 / 40.82%

2.2. ACGT Content

Number/percentage of A's	40,899,266 / 28.08%
Number/percentage of C's	28,292,736 / 19.42%
Number/percentage of T's	44,629,083 / 30.64%
Number/percentage of G's	31,836,169 / 21.85%
Number/percentage of N's	16,120 / 0.01%
GC Percentage	41.28%

2.3. Coverage

Mean	0.0471

Standard Deviation	0.3371

2.4. Mapping Quality

Mean Mapping Quality	46.14

2.5. Mismatches and indels

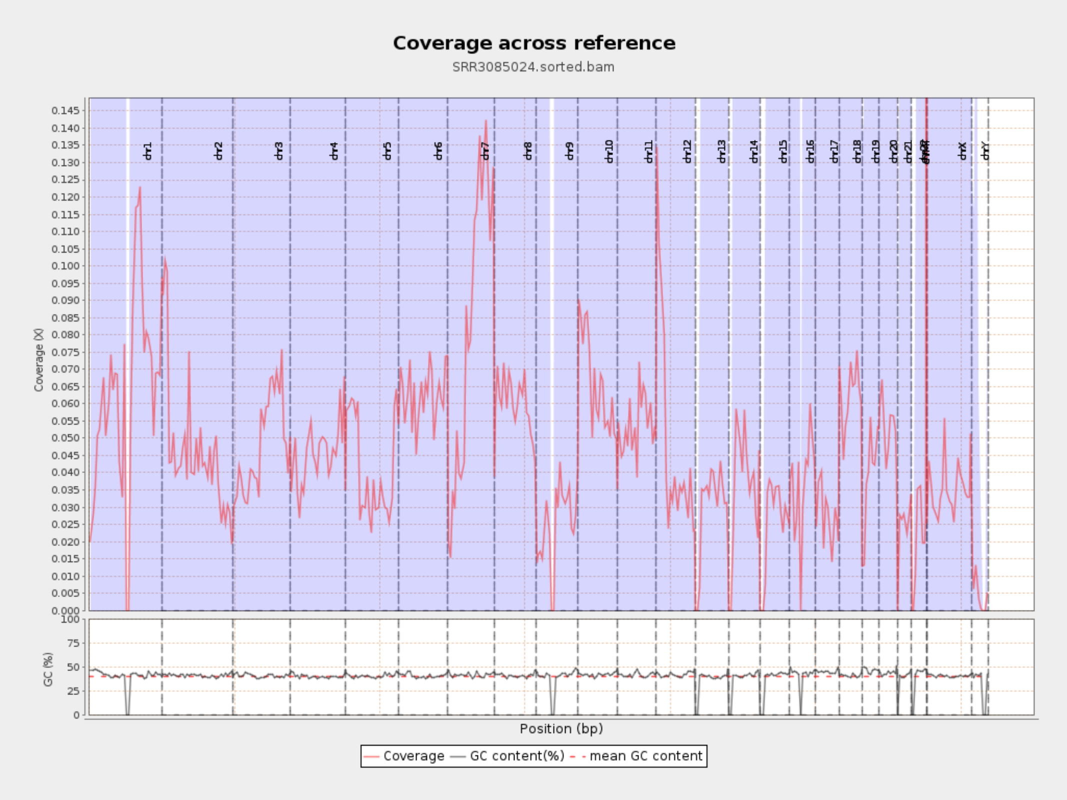
General error rate	0.87%
Mismatches	1,252,549
Insertions	9,820
Mapped reads with at least one insertion	0.45%
Deletions	30,123
Mapped reads with at least one deletion	1.37%
Homopolymer indels	47.22%

2.6. Chromosome stats

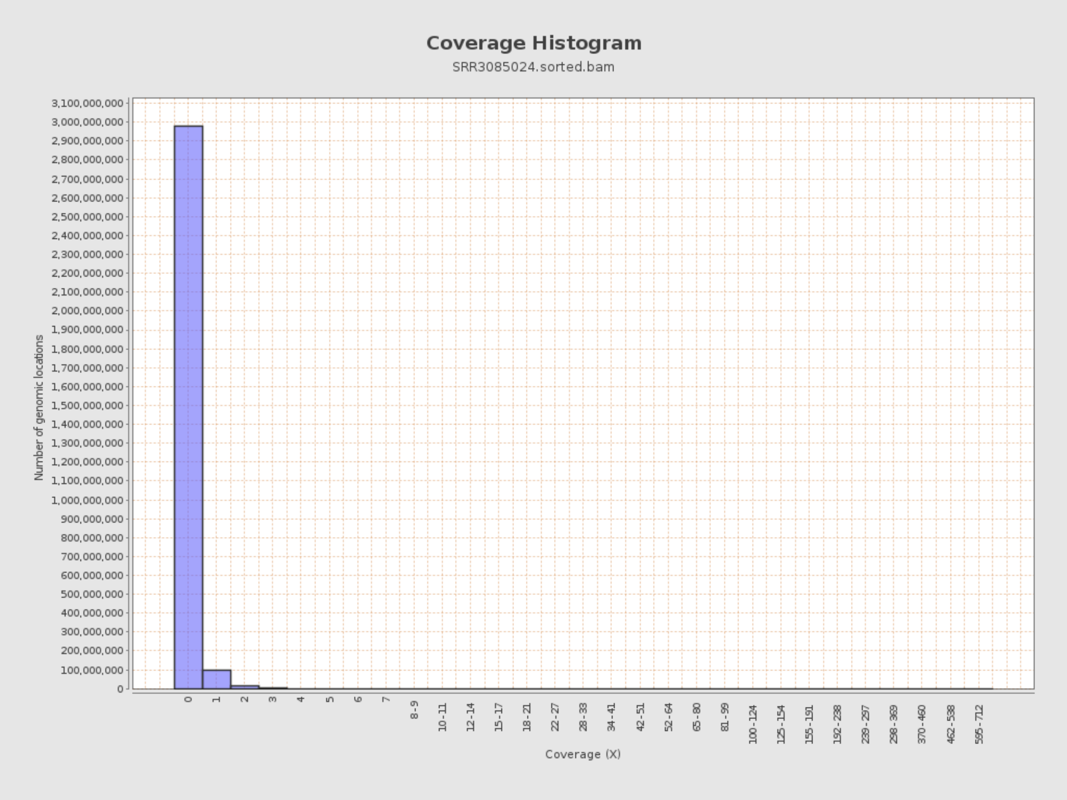
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15766141	0.0633	0.5017
chr2	243199373	11316870	0.0465	0.3816
chr3	198022430	9491007	0.0479	0.2602
chr4	191154276	8747101	0.0458	0.2558
chr5	180915260	7447049	0.0412	0.2411
chr6	171115067	10706164	0.0626	0.3385
chr7	159138663	13312932	0.0837	0.4592

chr8	146364022	8830757	0.0603	0.5189
chr9	141213431	3473663	0.0246	0.2529
chr10	135534747	9014044	0.0665	0.4063
chr11	135006516	7252497	0.0537	0.3682
chr12	133851895	6521779	0.0487	0.2667
chr13	115169878	3408267	0.0296	0.2019
chr14	107349540	3798731	0.0354	0.2284
chr15	102531392	2615437	0.0255	0.192
chr16	90354753	3319158	0.0367	0.2334
chr17	81195210	2208680	0.0272	0.22
chr18	78077248	4877544	0.0625	0.4614
chr19	59128983	2348601	0.0397	0.3442
chr20	63025520	3363904	0.0534	0.2759
chr21	48129895	1187877	0.0247	0.1953
chr22	51304566	990126	0.0193	0.1614
chrMT	16571	12394	0.7479	1.1482
chrX	155270560	5435946	0.035	0.2468
chrY	59373566	279086	0.0047	0.0984

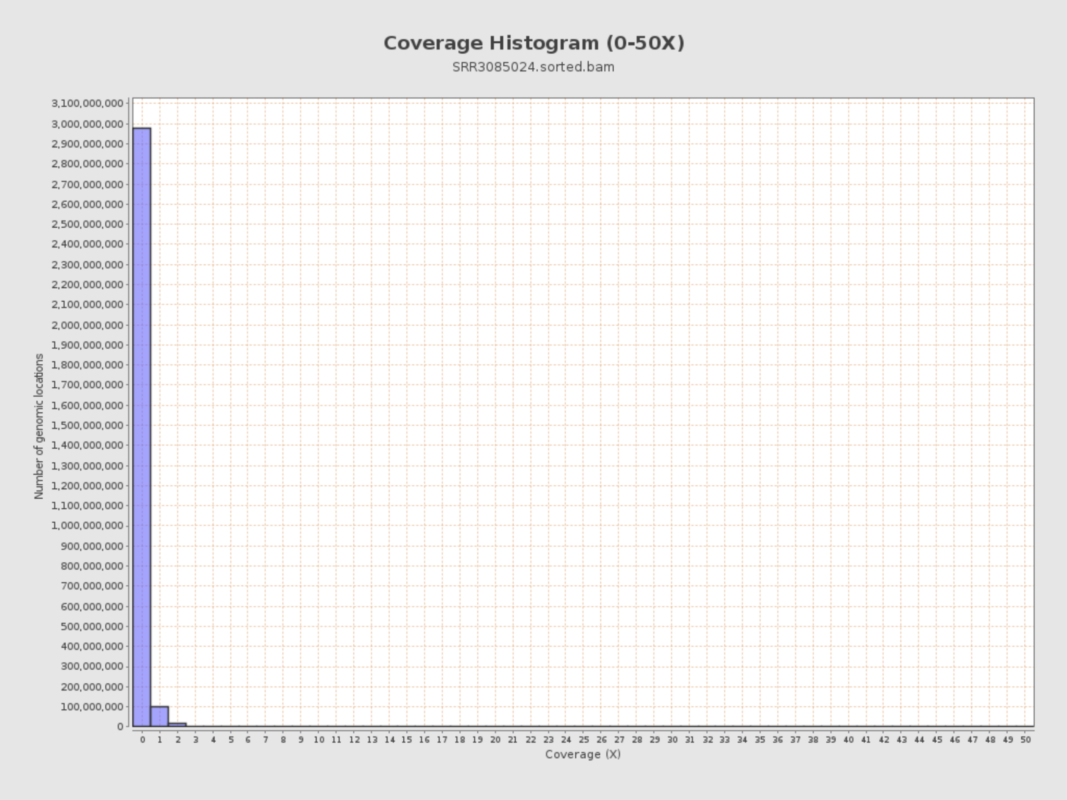
3. Results : Coverage across reference



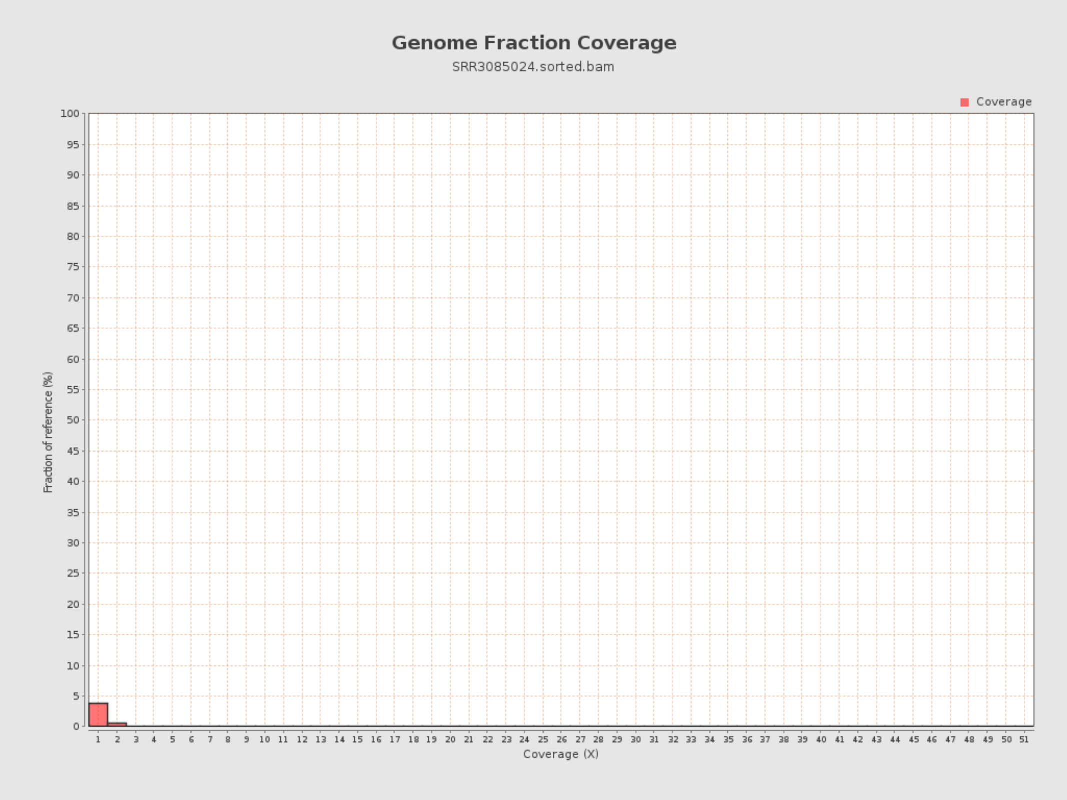
4. Results : Coverage Histogram



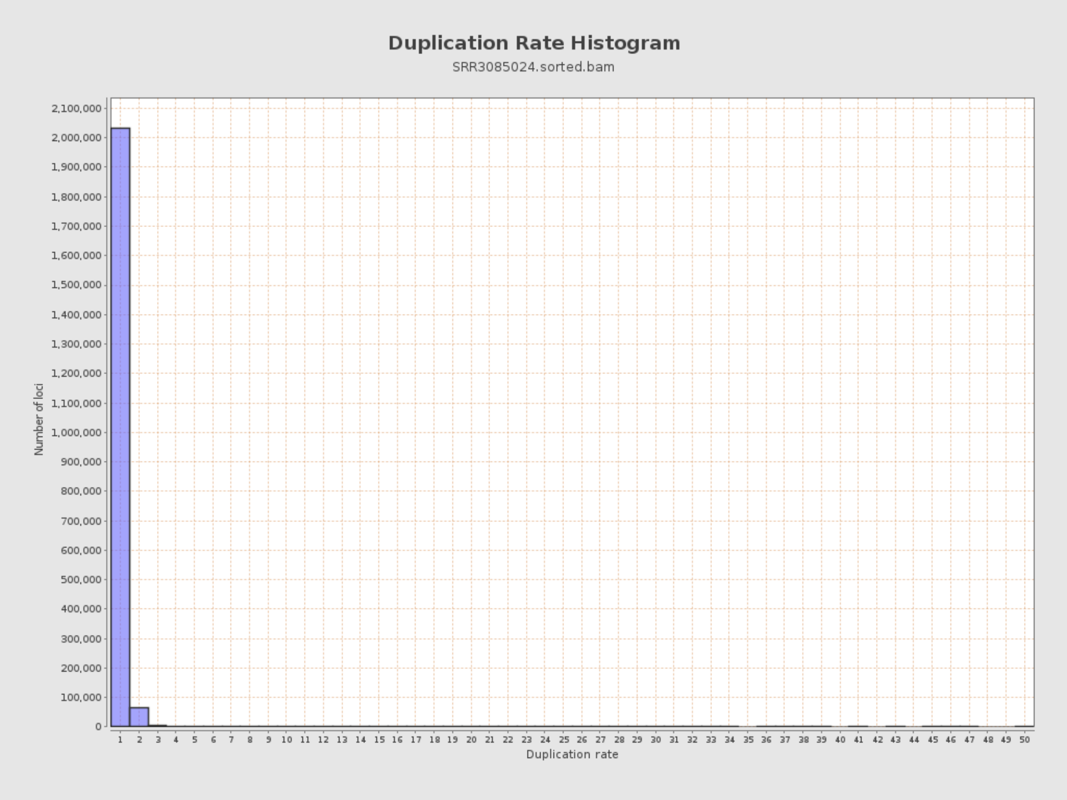
5. Results : Coverage Histogram (0-50X)



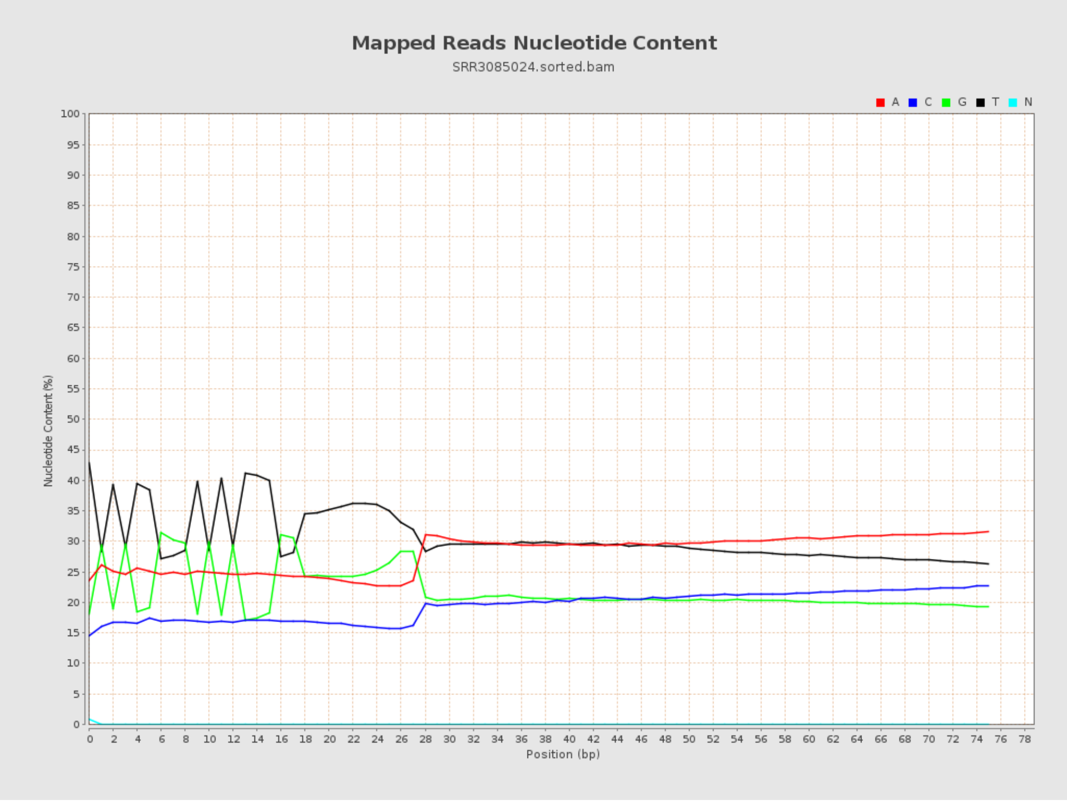
6. Results : Genome Fraction Coverage



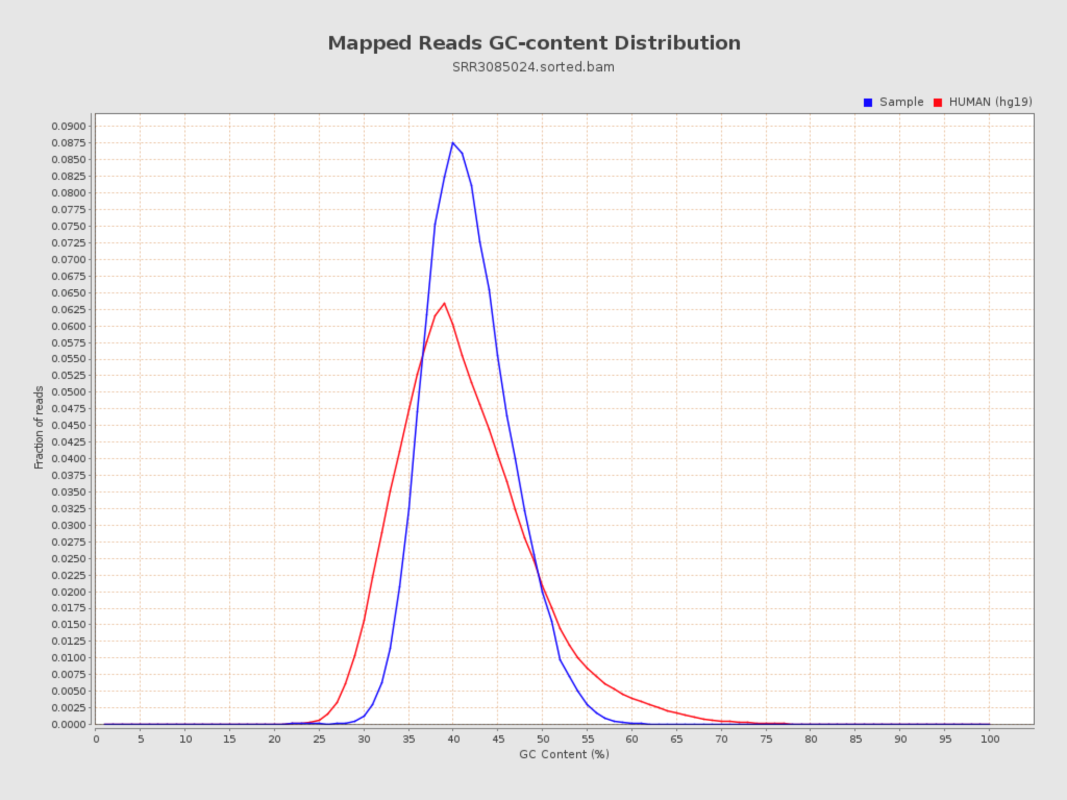
7. Results : Duplication Rate Histogram



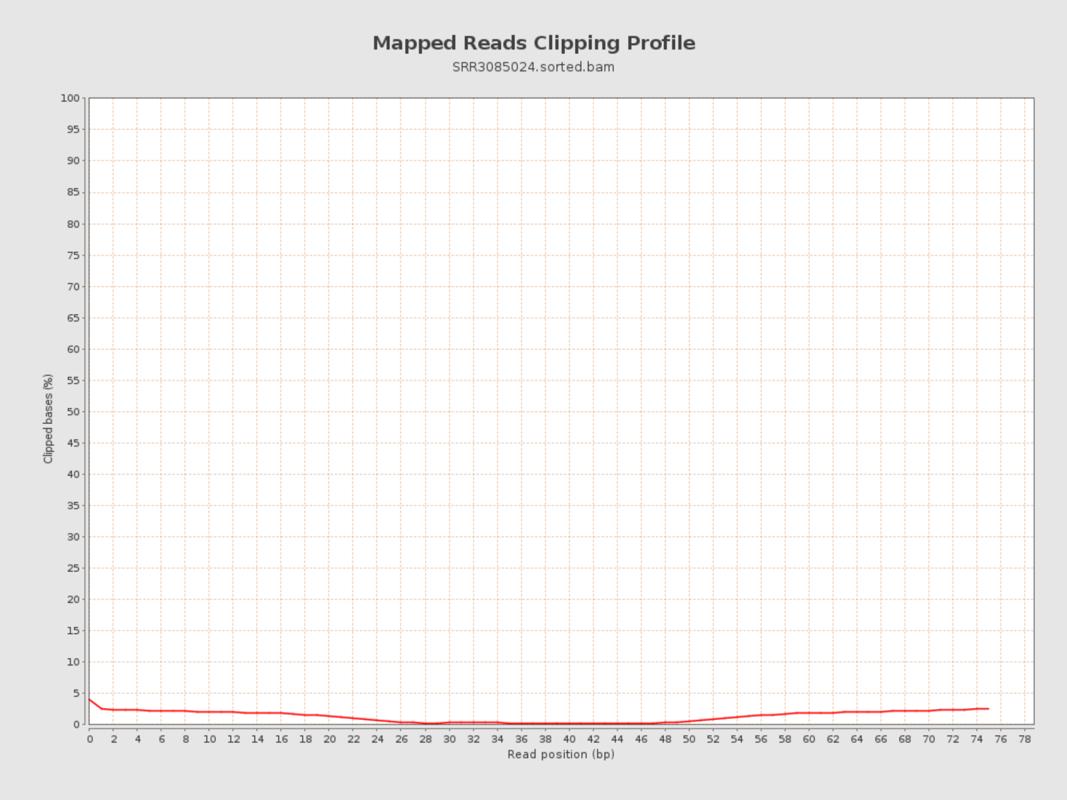
8. Results : Mapped Reads Nucleotide Content



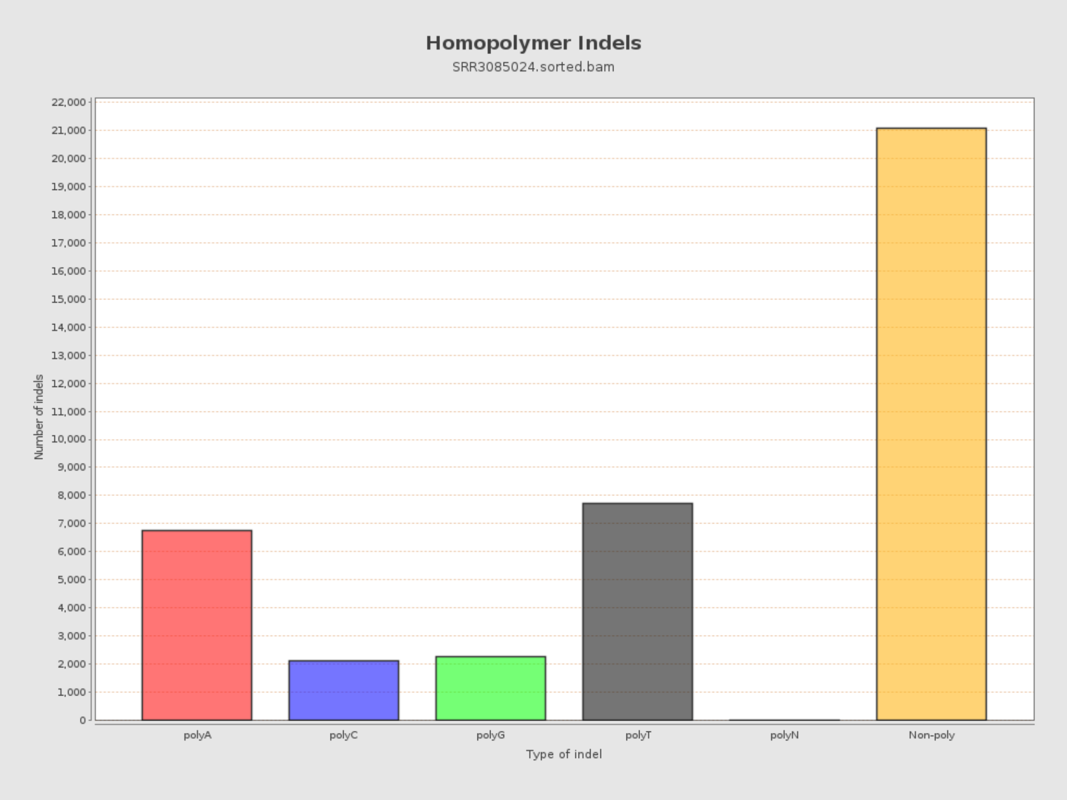
9. Results : Mapped Reads GC-content Distribution



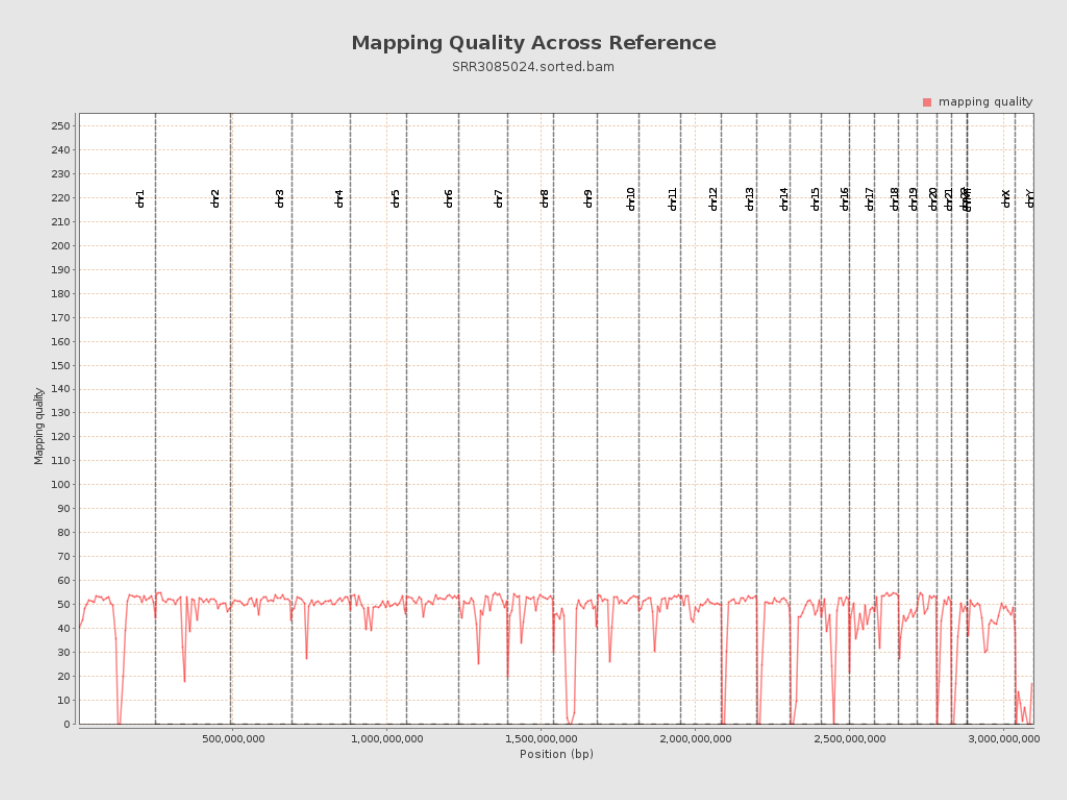
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram