Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 02:25:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085125.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_SRR3085125 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085125.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 02:25:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085125.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,380,220
Mapped reads	2,140,436 / 89.93%
Unmapped reads	239,784 / 10.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,998 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	83,165 / 3.49%
Duplication rate	2.9%
Clipped reads	943,559 / 39.64%

2.2. ACGT Content

Number/percentage of A's	40,385,815 / 28.13%
Number/percentage of C's	26,719,612 / 18.61%
Number/percentage of T's	44,900,451 / 31.27%
Number/percentage of G's	31,554,713 / 21.98%
Number/percentage of N's	27,338 / 0.02%
GC Percentage	40.58%

2.3. Coverage

Mean	0.0464

Standard Deviation	0.4094

2.4. Mapping Quality

Mean Mapping Quality	45.77

2.5. Mismatches and indels

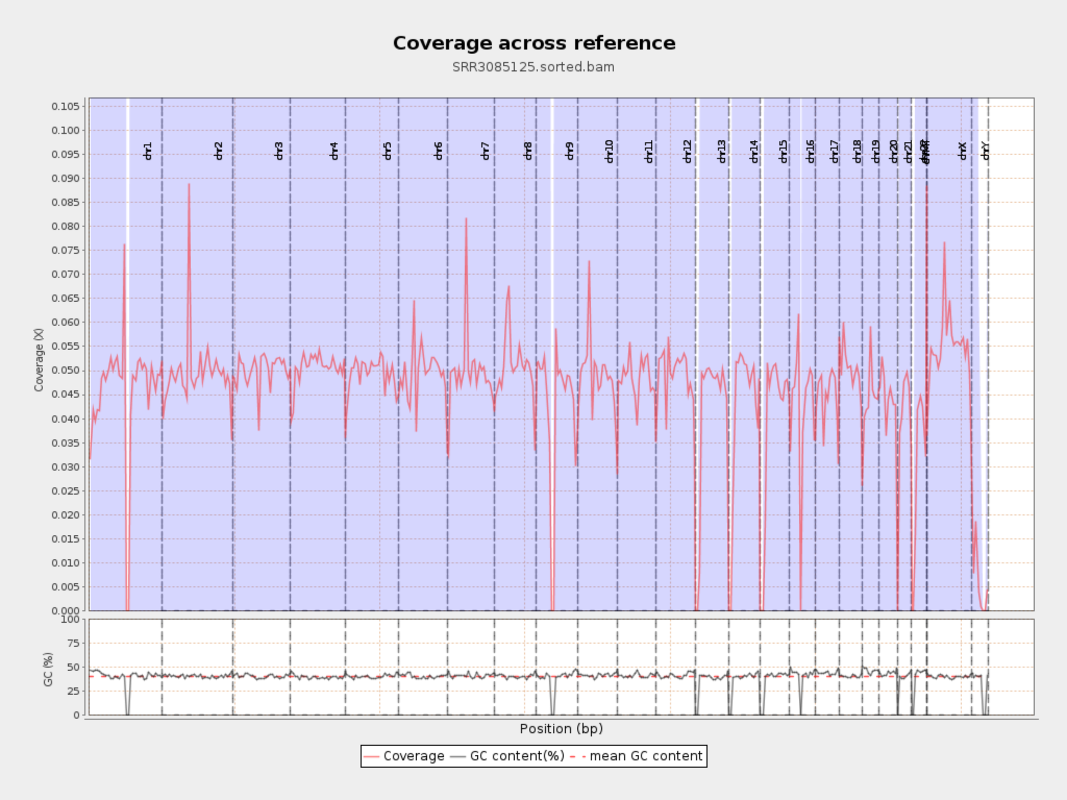
General error rate	0.9%
Mismatches	1,278,911
Insertions	11,472
Mapped reads with at least one insertion	0.53%
Deletions	31,908
Mapped reads with at least one deletion	1.48%
Homopolymer indels	46.65%

2.6. Chromosome stats

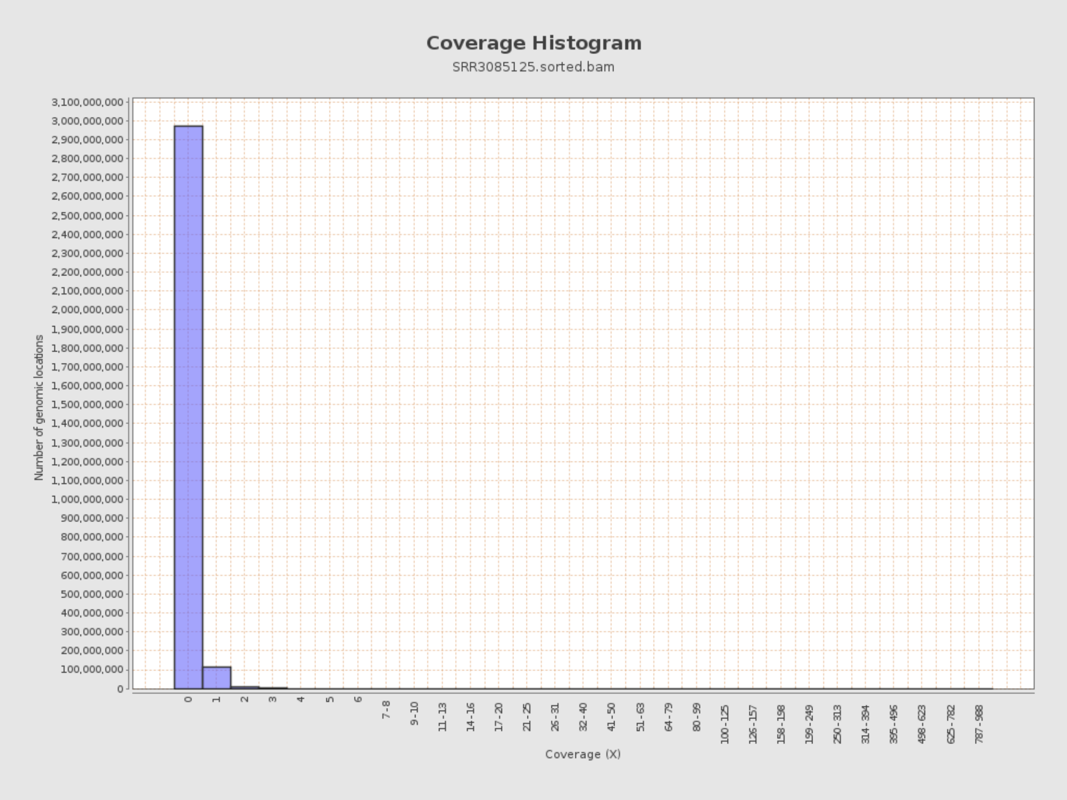
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11329218	0.0455	0.718
chr2	243199373	12081890	0.0497	0.5002
chr3	198022430	9921937	0.0501	0.2467
chr4	191154276	9663093	0.0506	0.2563
chr5	180915260	8944863	0.0494	0.2464
chr6	171115067	8460946	0.0494	0.303
chr7	159138663	7980847	0.0502	0.5391

chr8	146364022	7419122	0.0507	0.6552
chr9	141213431	5957226	0.0422	0.3757
chr10	135534747	6694576	0.0494	0.3644
chr11	135006516	6510417	0.0482	0.3513
chr12	133851895	6590910	0.0492	0.251
chr13	115169878	4617564	0.0401	0.2206
chr14	107349540	4413175	0.0411	0.2433
chr15	102531392	3990097	0.0389	0.2238
chr16	90354753	3834741	0.0424	0.2612
chr17	81195210	3593877	0.0443	0.2614
chr18	78077248	3969489	0.0508	0.6938
chr19	59128983	2633605	0.0445	0.533
chr20	63025520	2775659	0.044	0.2395
chr21	48129895	1882358	0.0391	0.2338
chr22	51304566	1463609	0.0285	0.1846
chrMT	16571	1469	0.0886	0.2953
chrX	155270560	8542839	0.055	0.2977
chrY	59373566	366422	0.0062	0.132

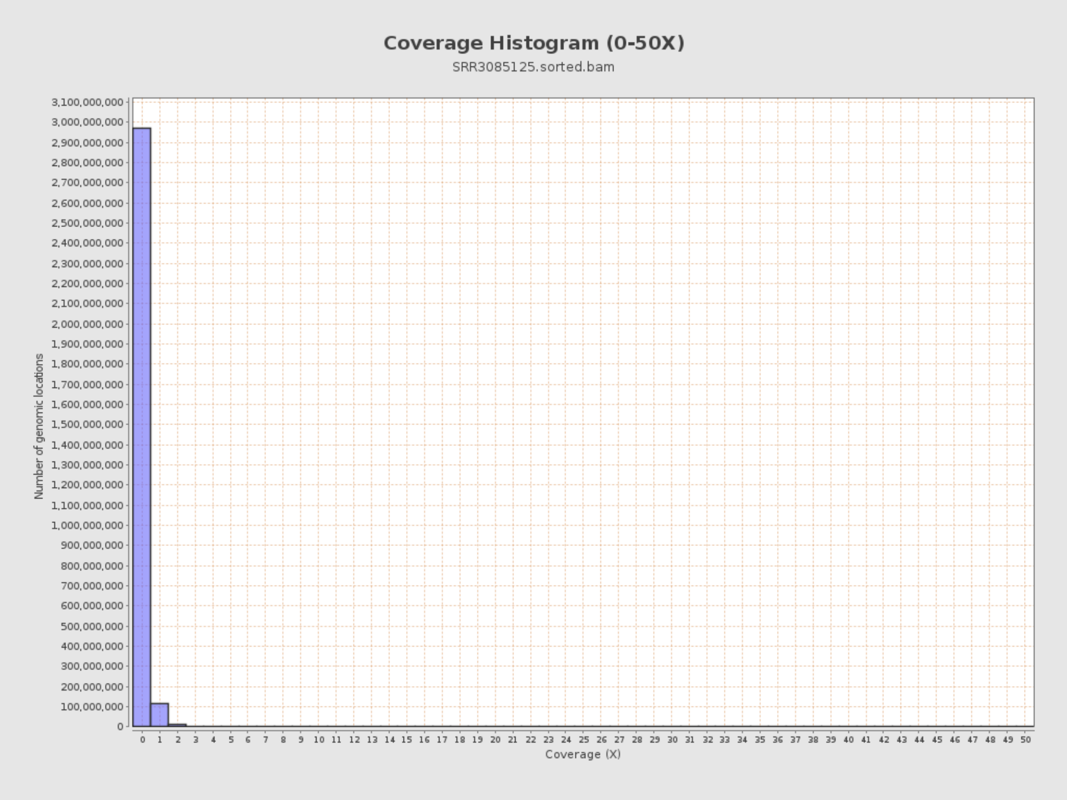
3. Results : Coverage across reference



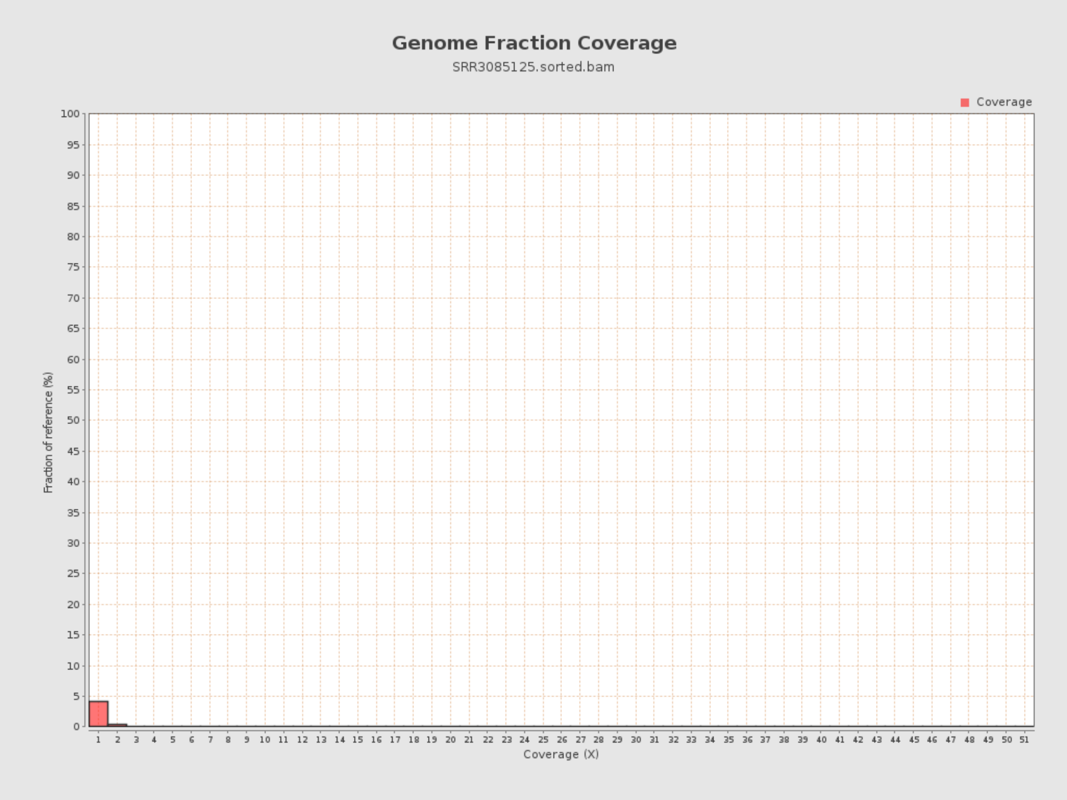
4. Results : Coverage Histogram



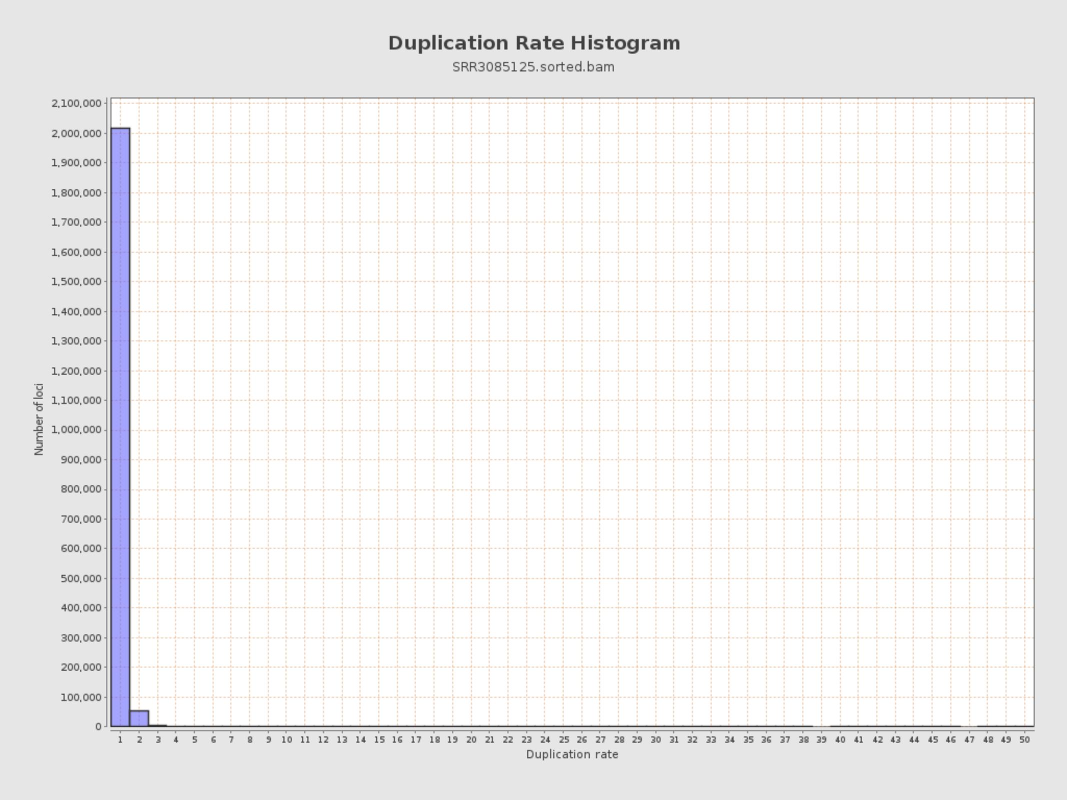
5. Results : Coverage Histogram (0-50X)



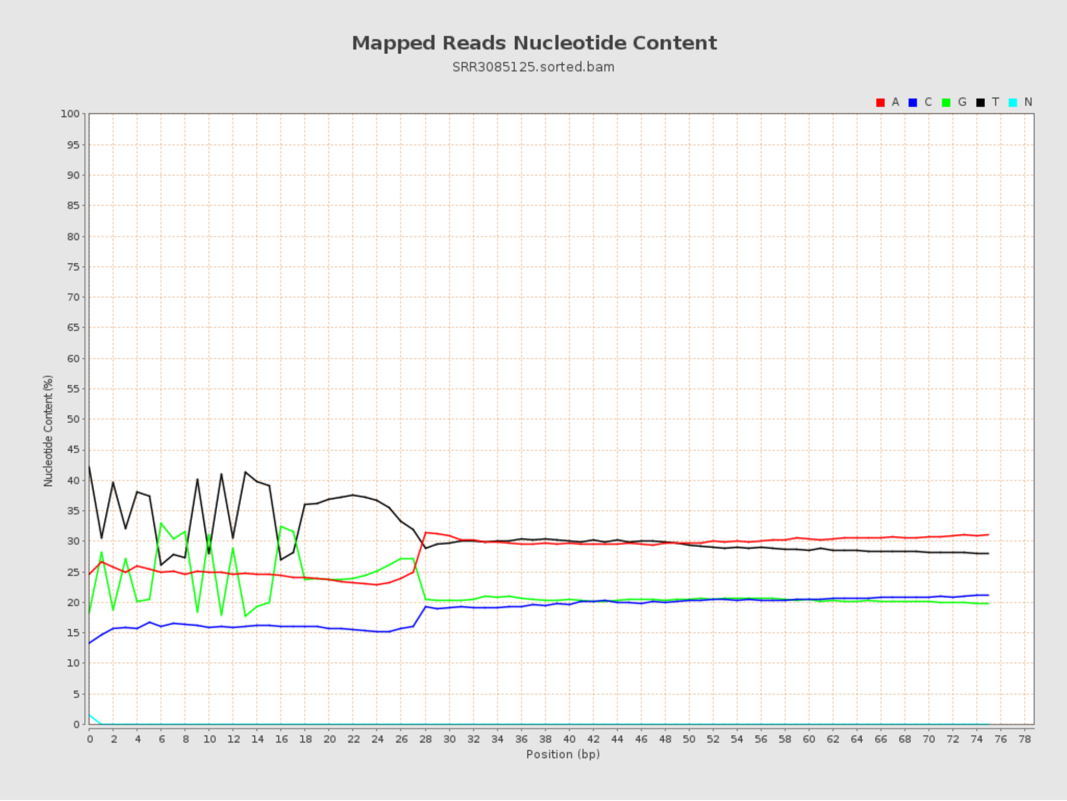
6. Results : Genome Fraction Coverage



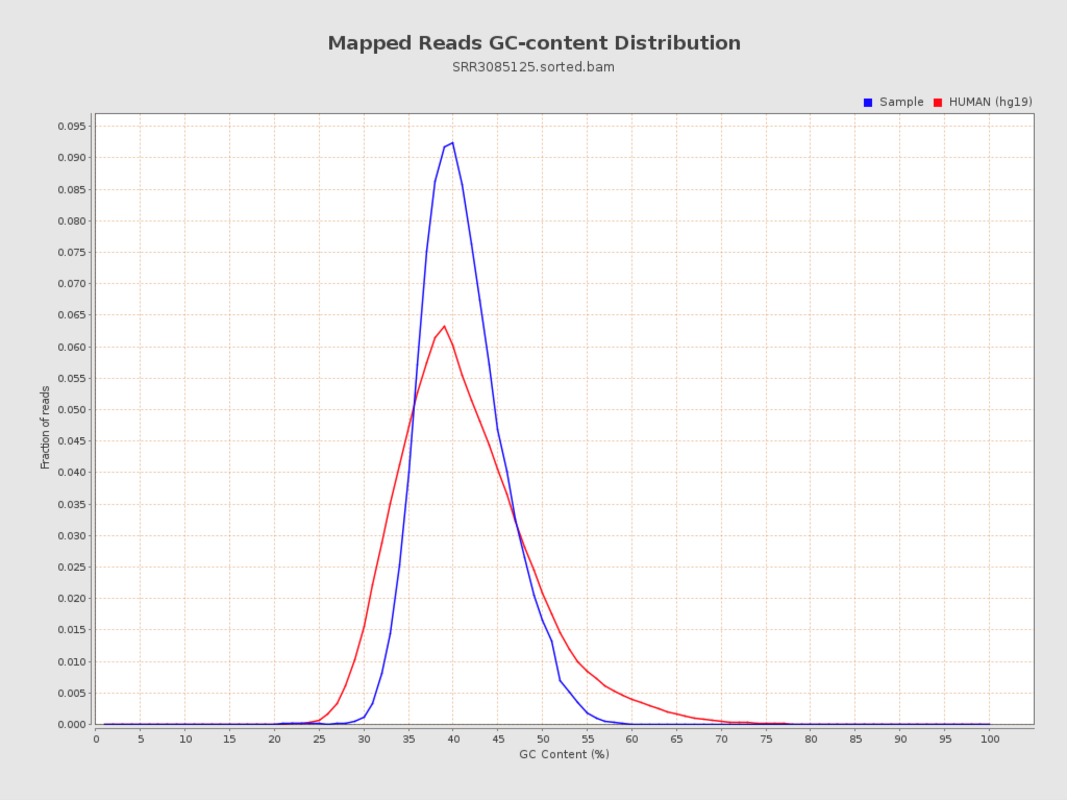
7. Results : Duplication Rate Histogram



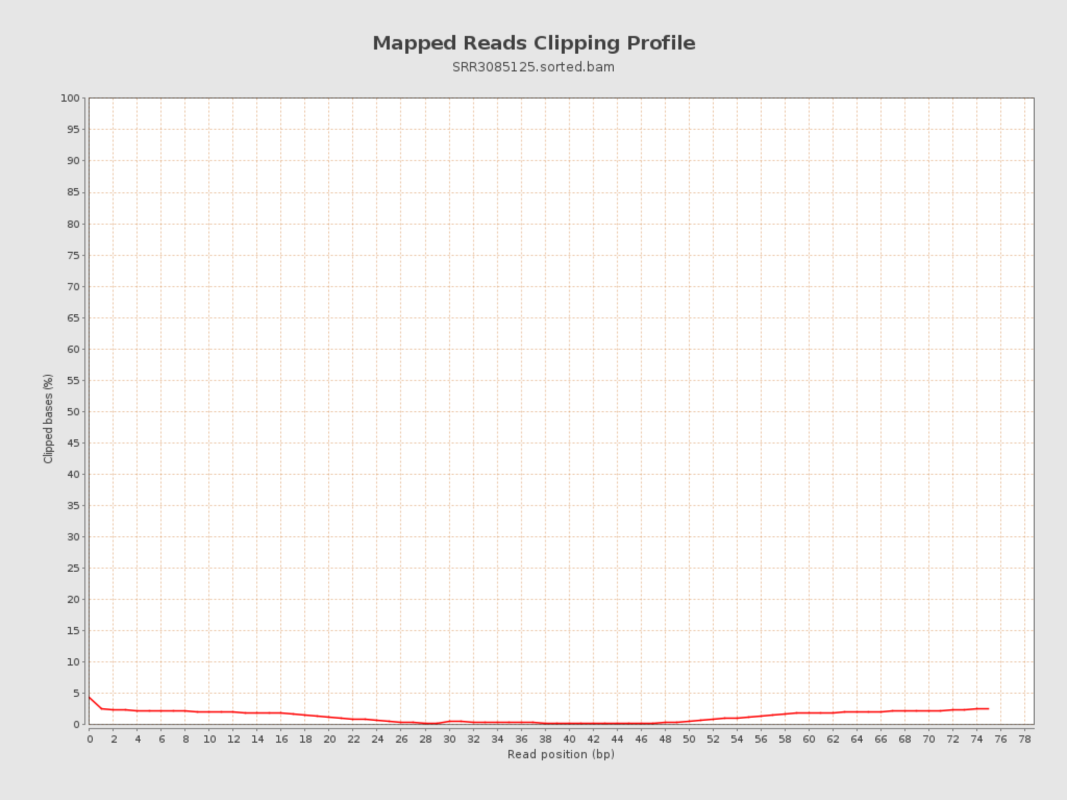
8. Results : Mapped Reads Nucleotide Content



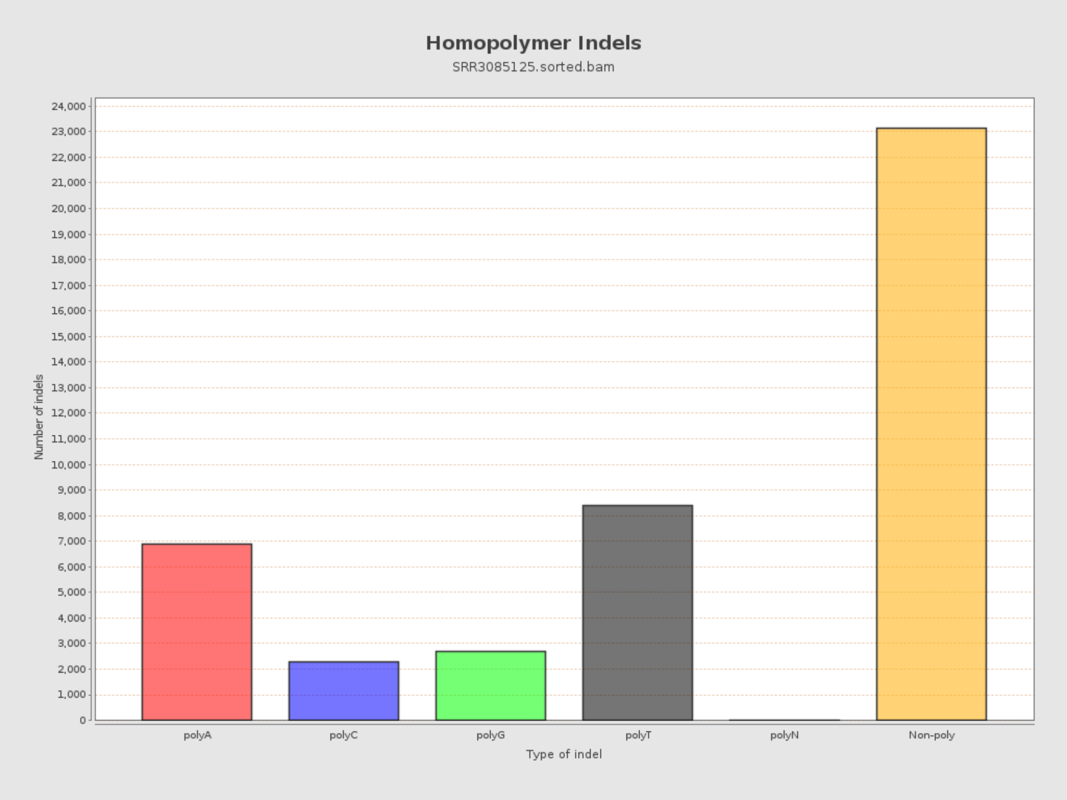
9. Results : Mapped Reads GC-content Distribution



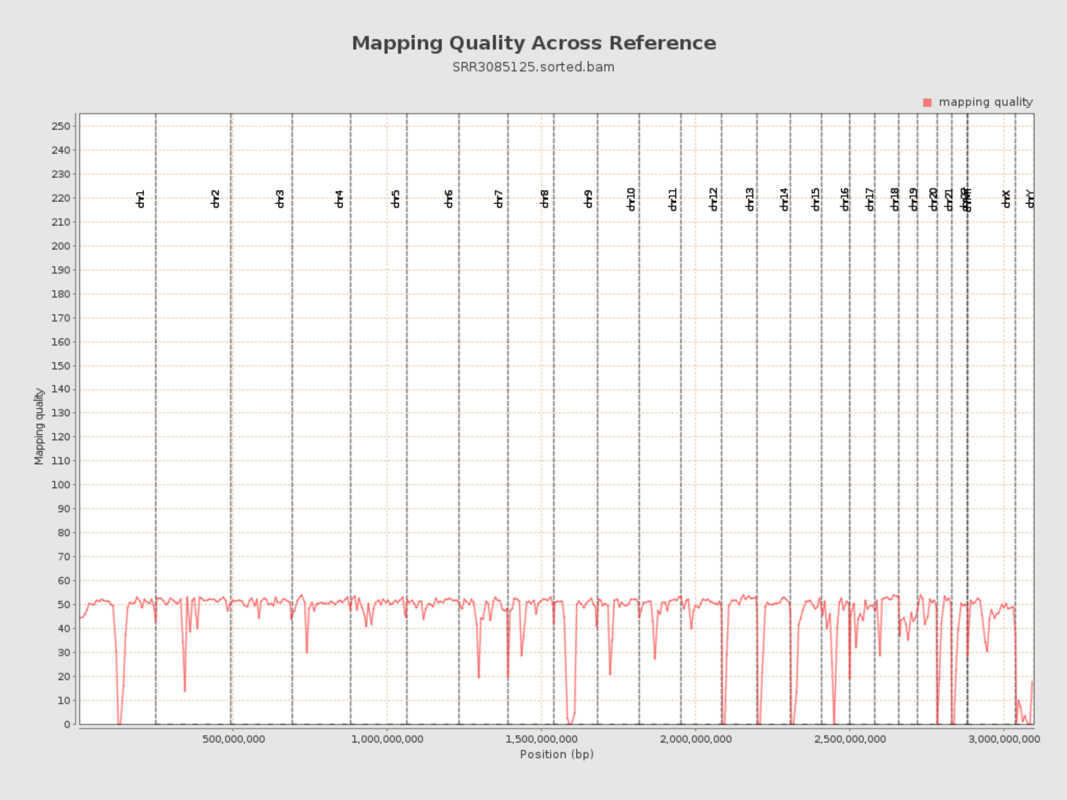
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram