Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 02:13:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085121.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_SRR3085121 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085121.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 02:13:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085121.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,424,947
Mapped reads	2,198,520 / 90.66%
Unmapped reads	226,427 / 9.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,923 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	78,767 / 3.25%
Duplication rate	2.67%
Clipped reads	905,377 / 37.34%

2.2. ACGT Content

Number/percentage of A's	42,440,334 / 28.44%
Number/percentage of C's	27,818,580 / 18.64%
Number/percentage of T's	46,626,986 / 31.25%
Number/percentage of G's	32,288,221 / 21.64%
Number/percentage of N's	27,521 / 0.02%
GC Percentage	40.29%

2.3. Coverage

Mean	0.0482

Standard Deviation	0.4211

2.4. Mapping Quality

Mean Mapping Quality	46.14

2.5. Mismatches and indels

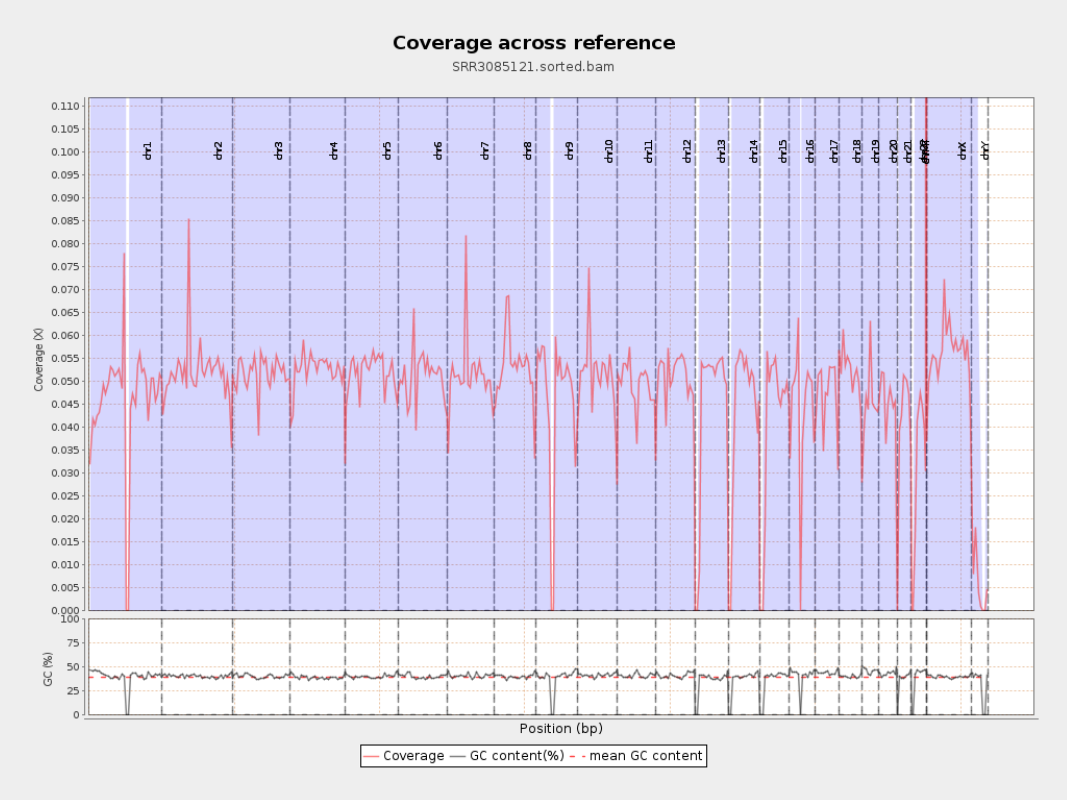
General error rate	0.91%
Mismatches	1,329,313
Insertions	11,973
Mapped reads with at least one insertion	0.54%
Deletions	32,699
Mapped reads with at least one deletion	1.47%
Homopolymer indels	47.3%

2.6. Chromosome stats

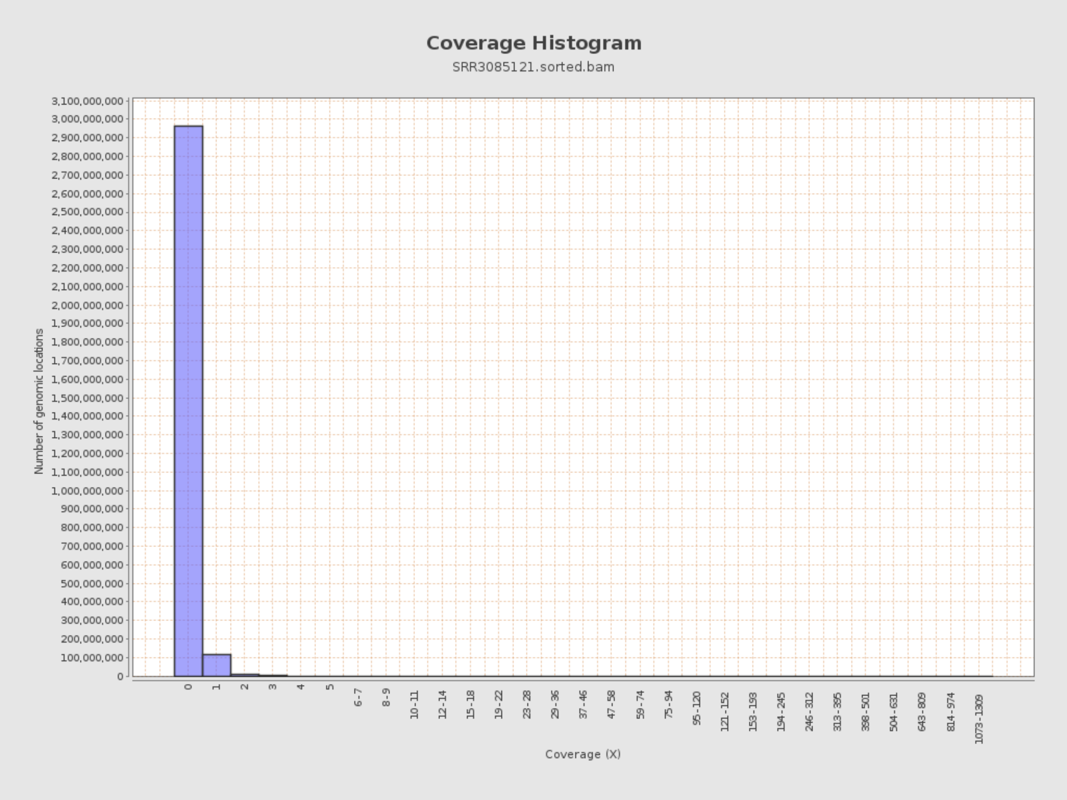
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11449108	0.0459	0.7133
chr2	243199373	12672935	0.0521	0.4584
chr3	198022430	10244988	0.0517	0.2507
chr4	191154276	10052335	0.0526	0.2615
chr5	180915260	9413786	0.052	0.2519
chr6	171115067	8741753	0.0511	0.2978
chr7	159138663	8224252	0.0517	0.5334

chr8	146364022	7739316	0.0529	0.8244
chr9	141213431	6410003	0.0454	0.3798
chr10	135534747	7043596	0.052	0.3793
chr11	135006516	6626559	0.0491	0.3387
chr12	133851895	6821845	0.051	0.2535
chr13	115169878	5043180	0.0438	0.2323
chr14	107349540	4604402	0.0429	0.249
chr15	102531392	4187650	0.0408	0.2268
chr16	90354753	3968977	0.0439	0.2619
chr17	81195210	3793169	0.0467	0.2612
chr18	78077248	4103030	0.0526	0.718
chr19	59128983	2699613	0.0457	0.5402
chr20	63025520	2842629	0.0451	0.2391
chr21	48129895	1957171	0.0407	0.236
chr22	51304566	1522315	0.0297	0.1883
chrMT	16571	9205	0.5555	0.7969
chrX	155270560	8720903	0.0562	0.2935
chrY	59373566	362468	0.0061	0.1291

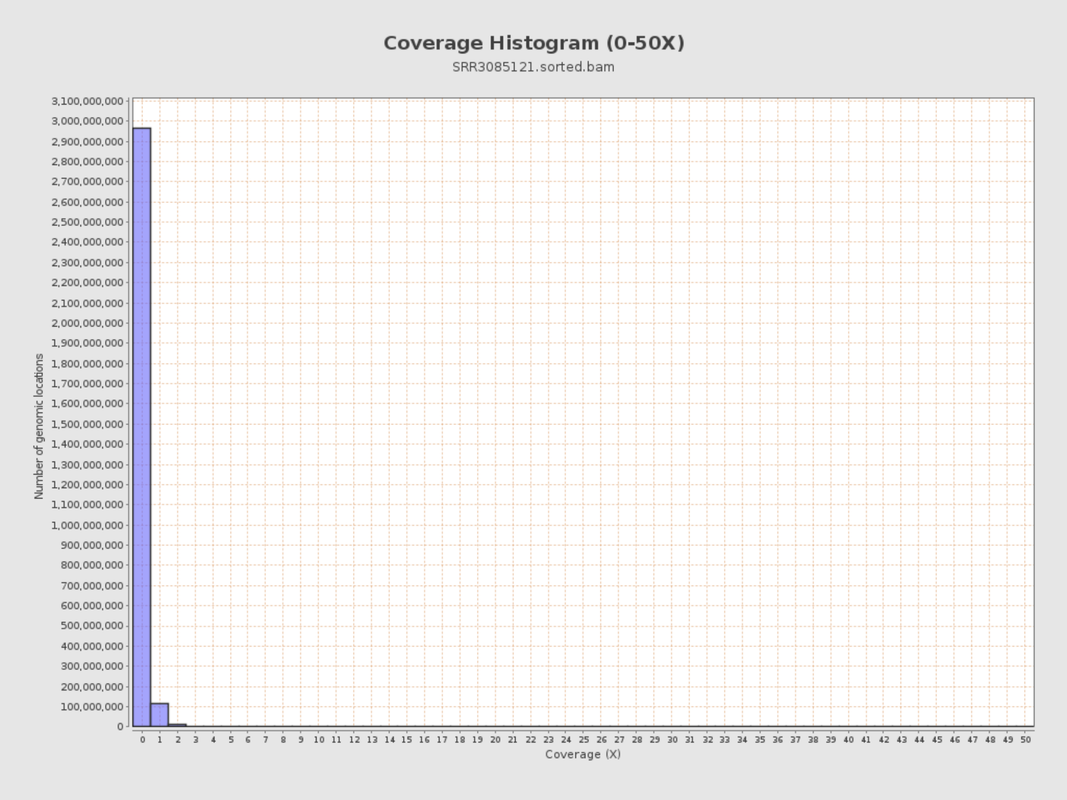
3. Results : Coverage across reference



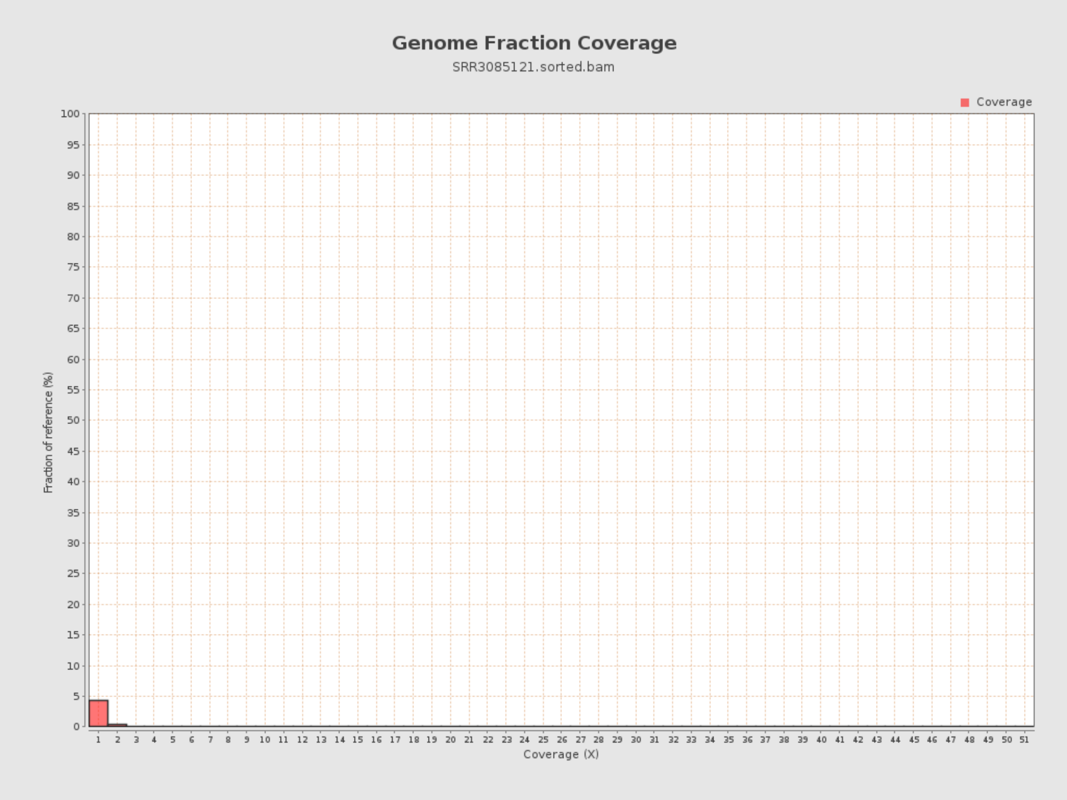
4. Results : Coverage Histogram



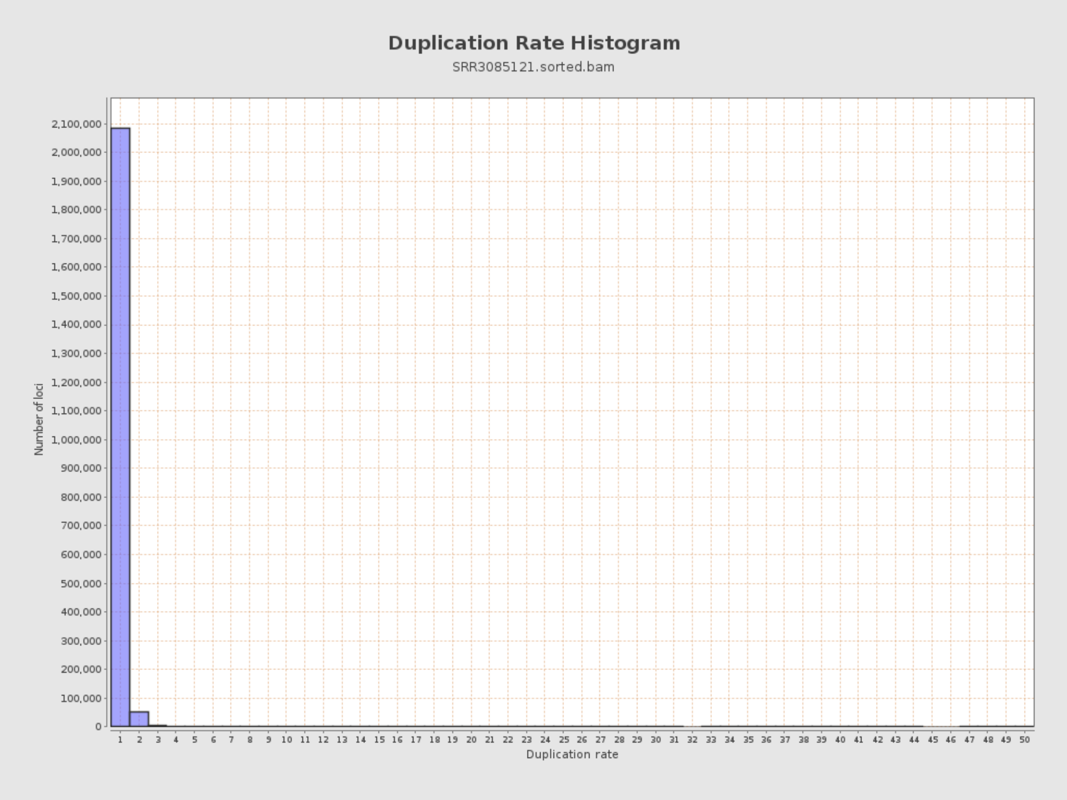
5. Results : Coverage Histogram (0-50X)



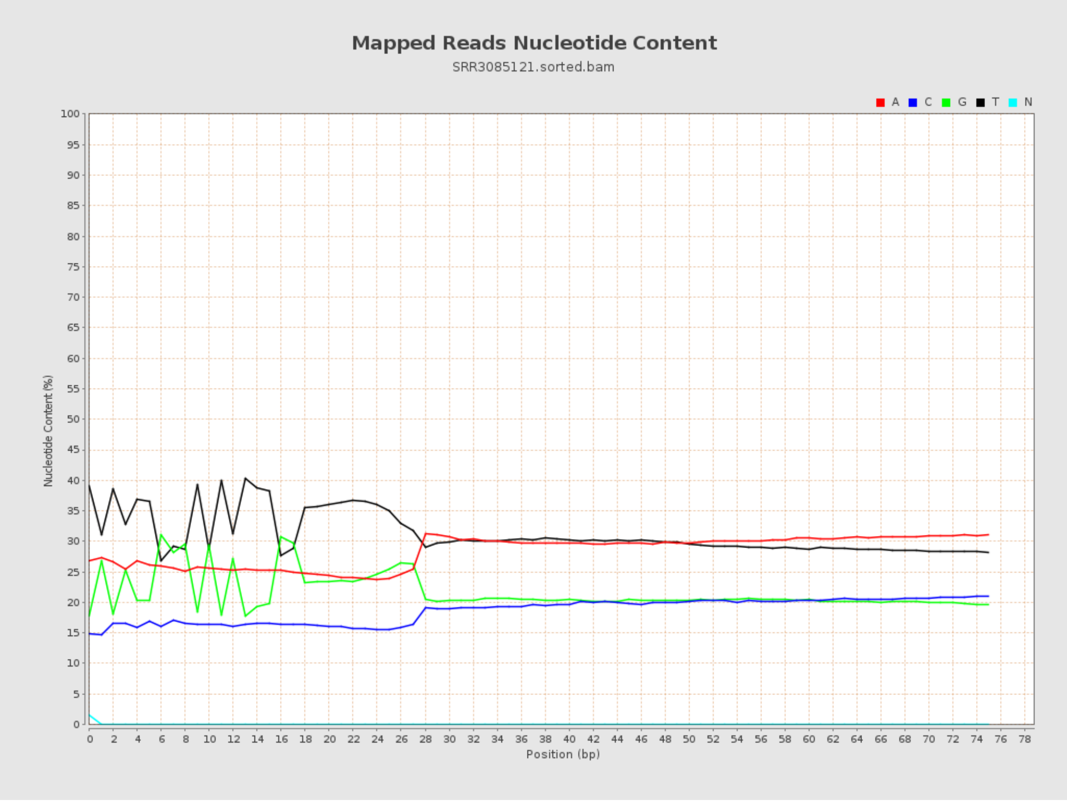
6. Results : Genome Fraction Coverage



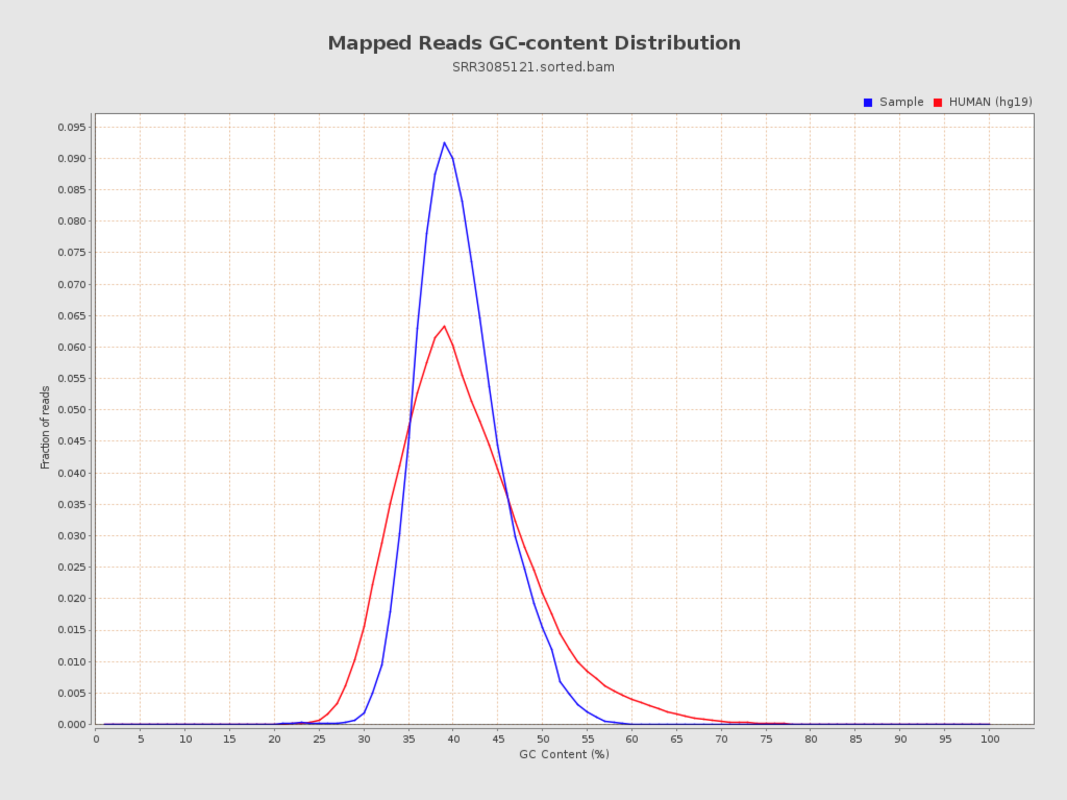
7. Results : Duplication Rate Histogram



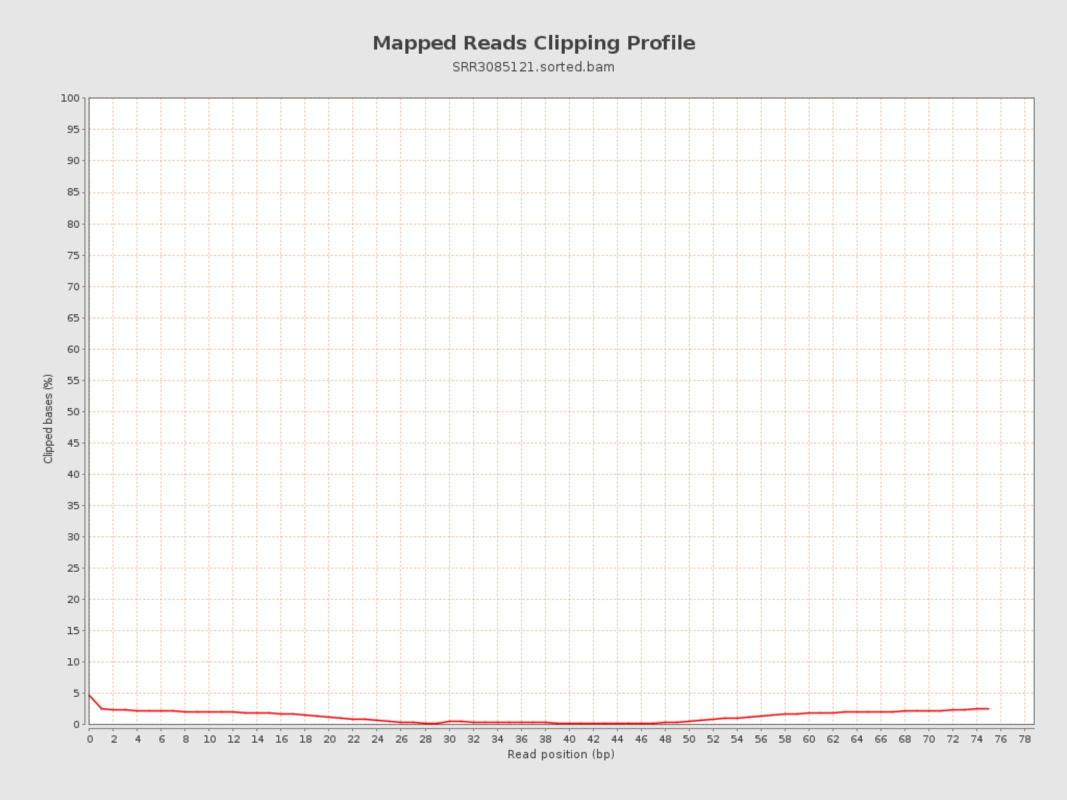
8. Results : Mapped Reads Nucleotide Content



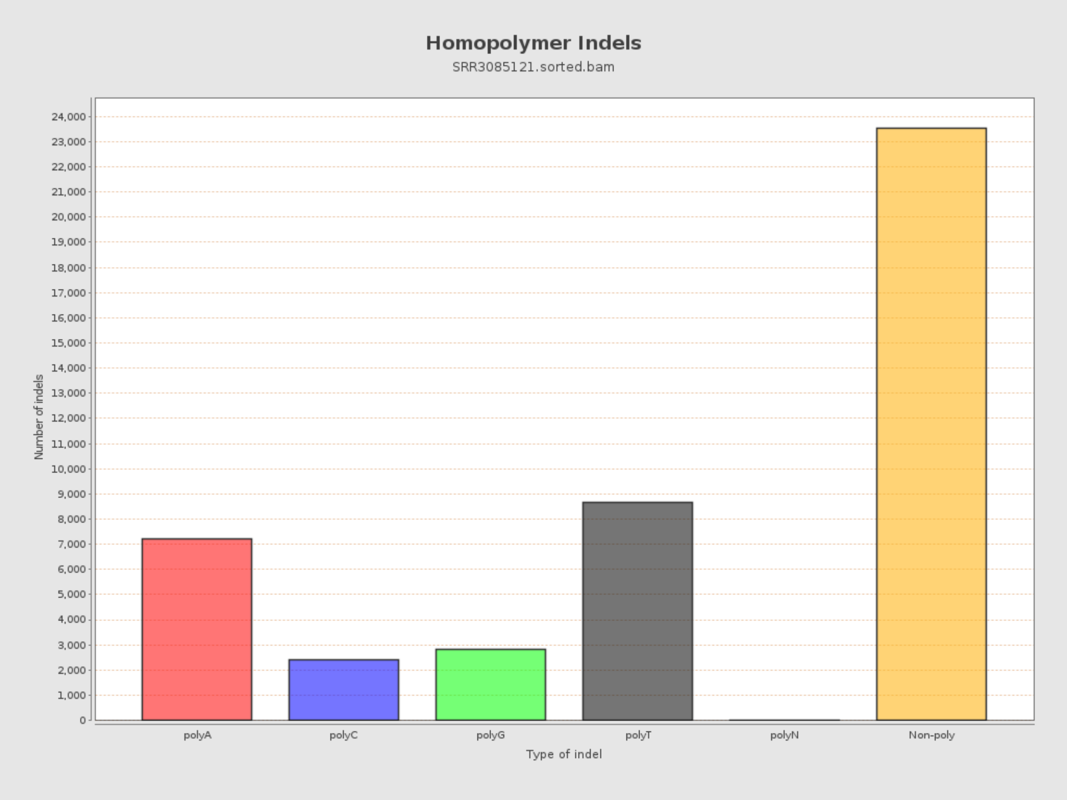
9. Results : Mapped Reads GC-content Distribution



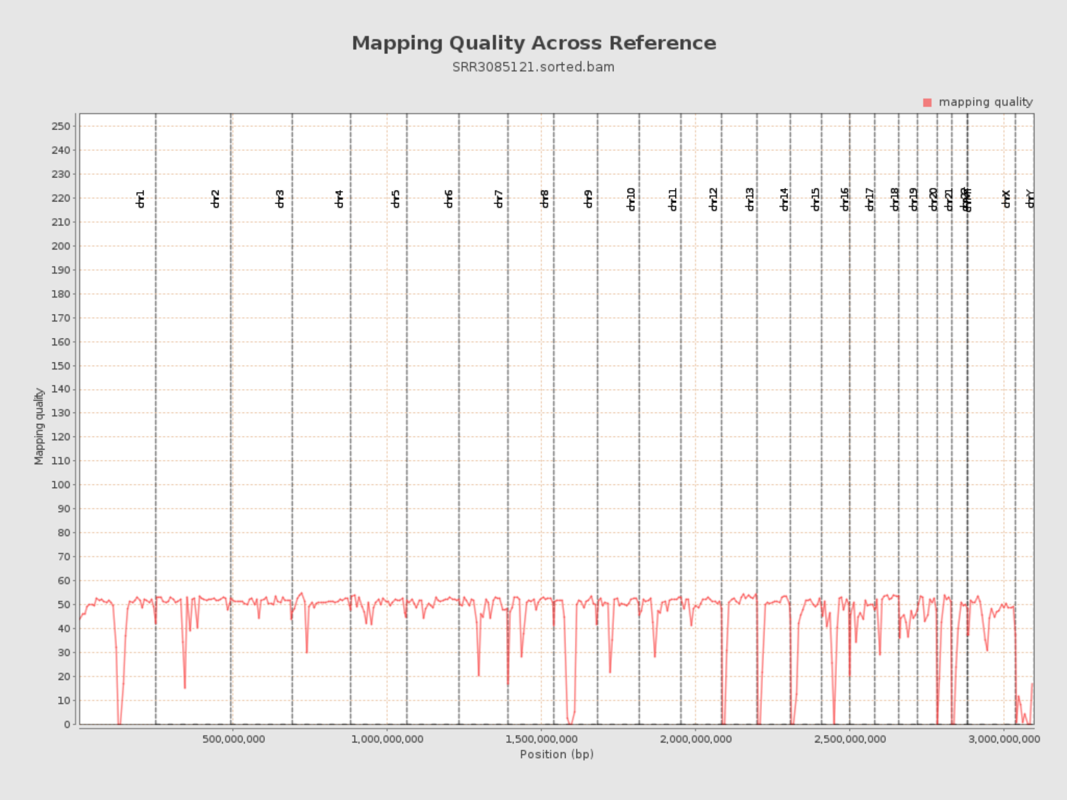
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram