Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 02:19:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085123.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_SRR3085123 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085123.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 02:19:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085123.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,401,855
Mapped reads	2,169,633 / 90.33%
Unmapped reads	232,222 / 9.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,804 / 0.87%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	91,742 / 3.82%
Duplication rate	3.23%
Clipped reads	869,902 / 36.22%

2.2. ACGT Content

Number/percentage of A's	41,531,142 / 28.17%
Number/percentage of C's	27,482,868 / 18.64%
Number/percentage of T's	46,398,976 / 31.47%
Number/percentage of G's	32,004,464 / 21.71%
Number/percentage of N's	23,445 / 0.02%
GC Percentage	40.35%

2.3. Coverage

Mean	0.0476

Standard Deviation	0.4204

2.4. Mapping Quality

Mean Mapping Quality	47.26

2.5. Mismatches and indels

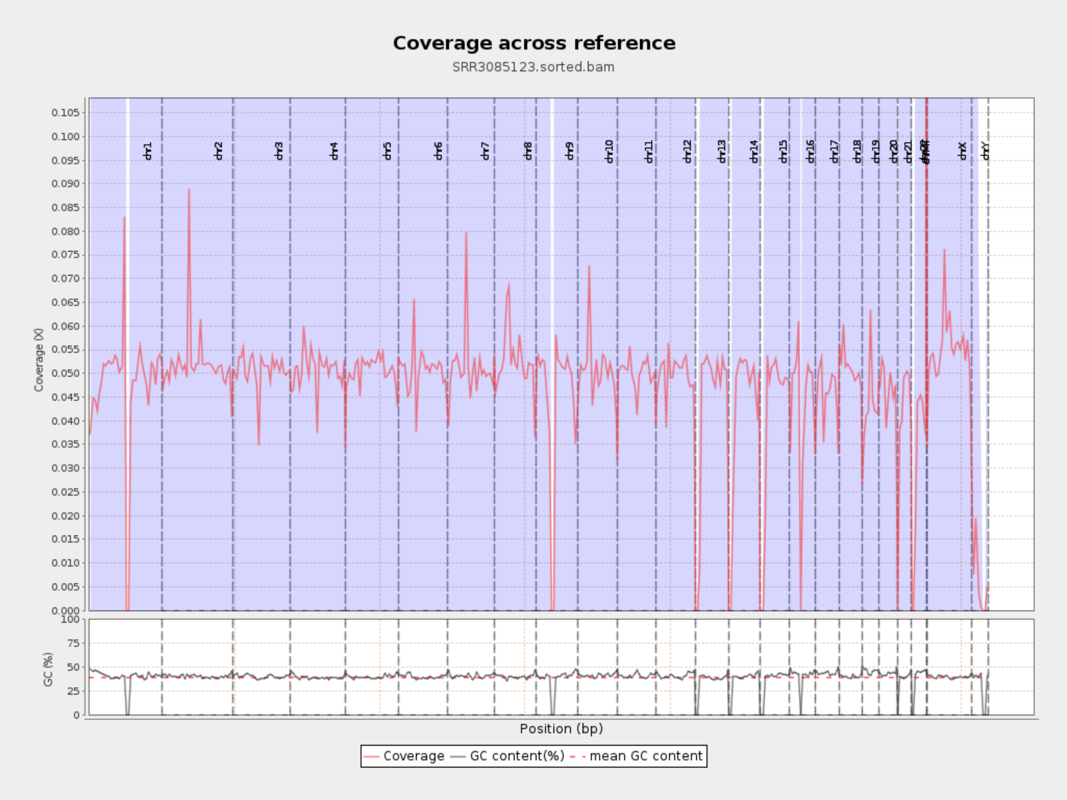
General error rate	0.93%
Mismatches	1,344,283
Insertions	11,627
Mapped reads with at least one insertion	0.53%
Deletions	38,893
Mapped reads with at least one deletion	1.77%
Homopolymer indels	46.61%

2.6. Chromosome stats

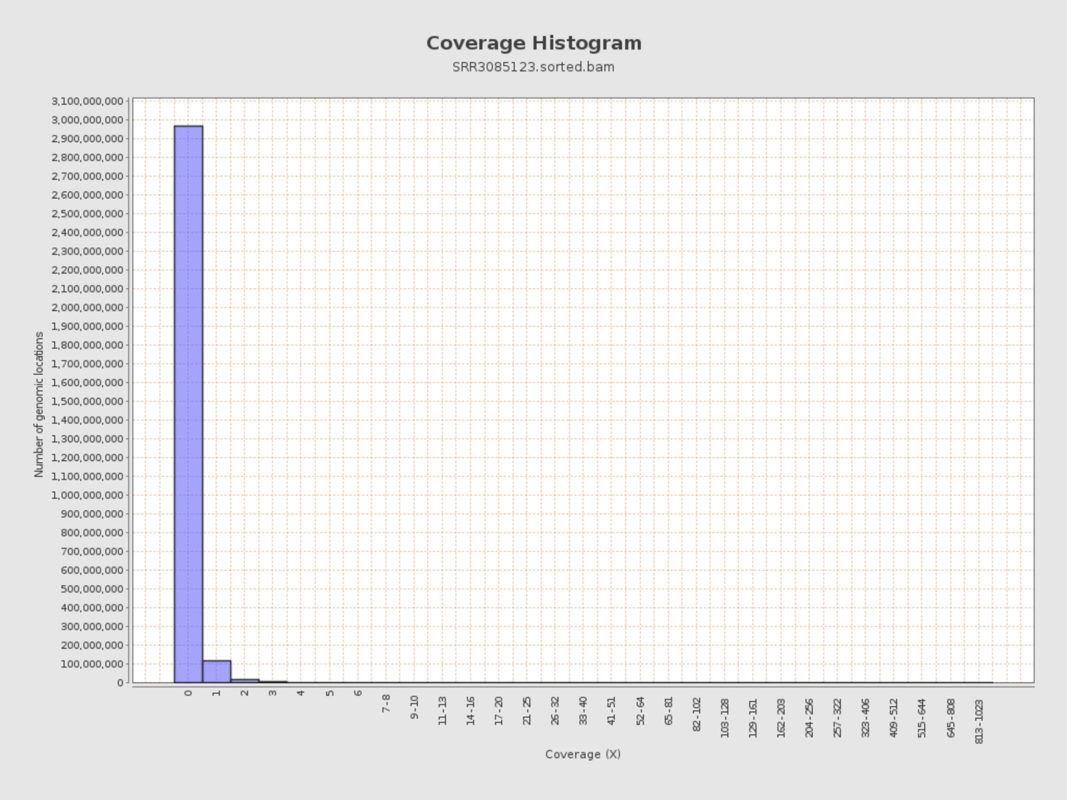
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11806109	0.0474	0.7923
chr2	243199373	12699999	0.0522	0.4617
chr3	198022430	10043505	0.0507	0.2495
chr4	191154276	9694913	0.0507	0.2688
chr5	180915260	9180807	0.0507	0.2523
chr6	171115067	8686477	0.0508	0.3049
chr7	159138663	8180087	0.0514	0.5344

chr8	146364022	7663883	0.0524	0.6761
chr9	141213431	6245511	0.0442	0.3623
chr10	135534747	6908903	0.051	0.3709
chr11	135006516	6728115	0.0498	0.3746
chr12	133851895	6653792	0.0497	0.2522
chr13	115169878	4868163	0.0423	0.2292
chr14	107349540	4449770	0.0415	0.2421
chr15	102531392	4164765	0.0406	0.2251
chr16	90354753	3929261	0.0435	0.2559
chr17	81195210	3680837	0.0453	0.2707
chr18	78077248	4023504	0.0515	0.6634
chr19	59128983	2592902	0.0439	0.5865
chr20	63025520	2908431	0.0461	0.2464
chr21	48129895	1951133	0.0405	0.2436
chr22	51304566	1526682	0.0298	0.1894
chrMT	16571	7560	0.4562	0.7255
chrX	155270560	8539603	0.055	0.3003
chrY	59373566	369668	0.0062	0.1537

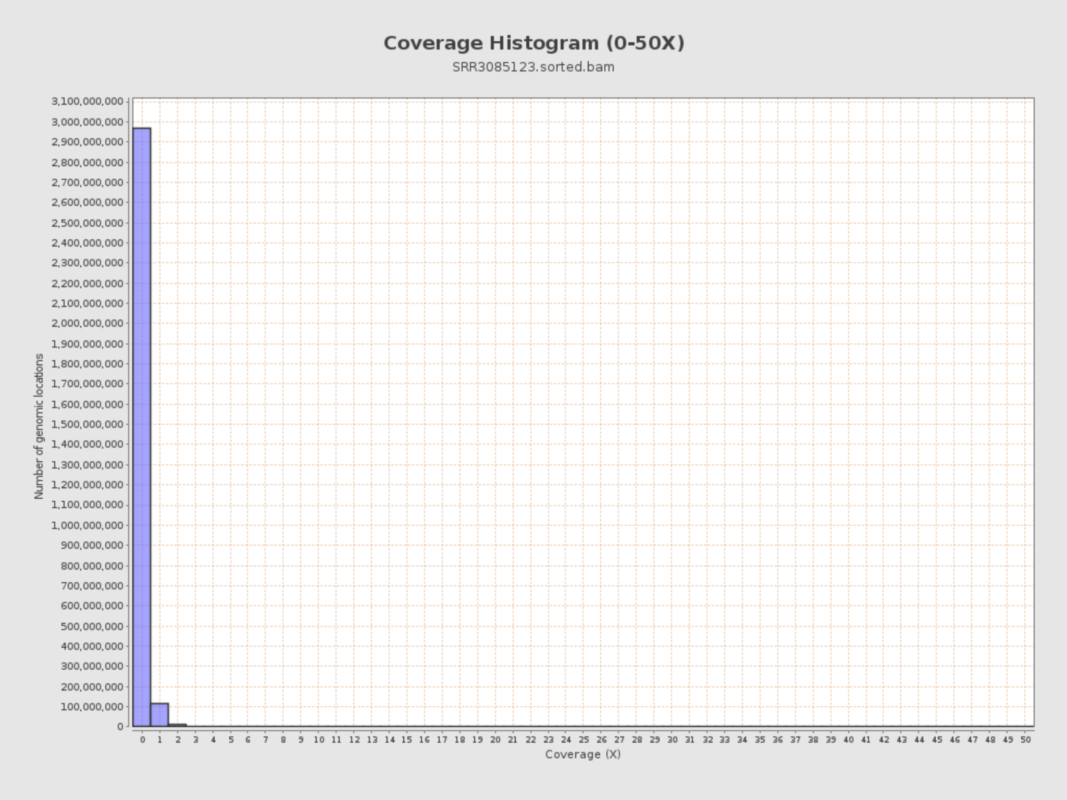
3. Results : Coverage across reference



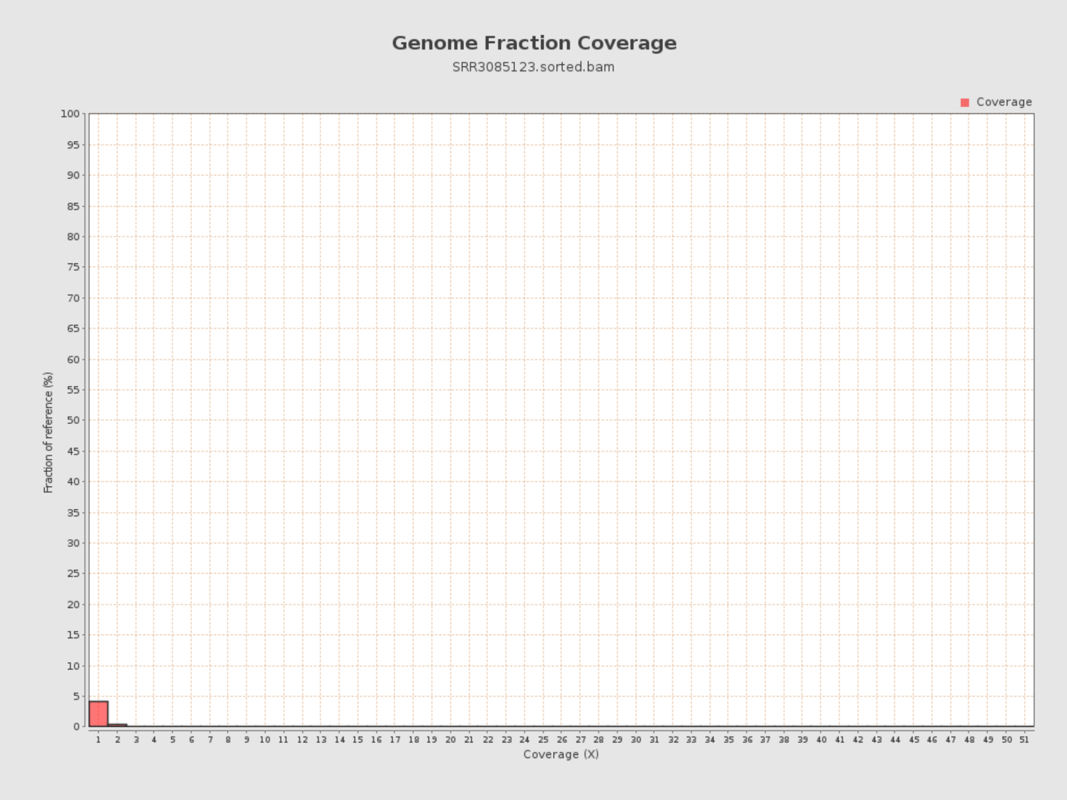
4. Results : Coverage Histogram



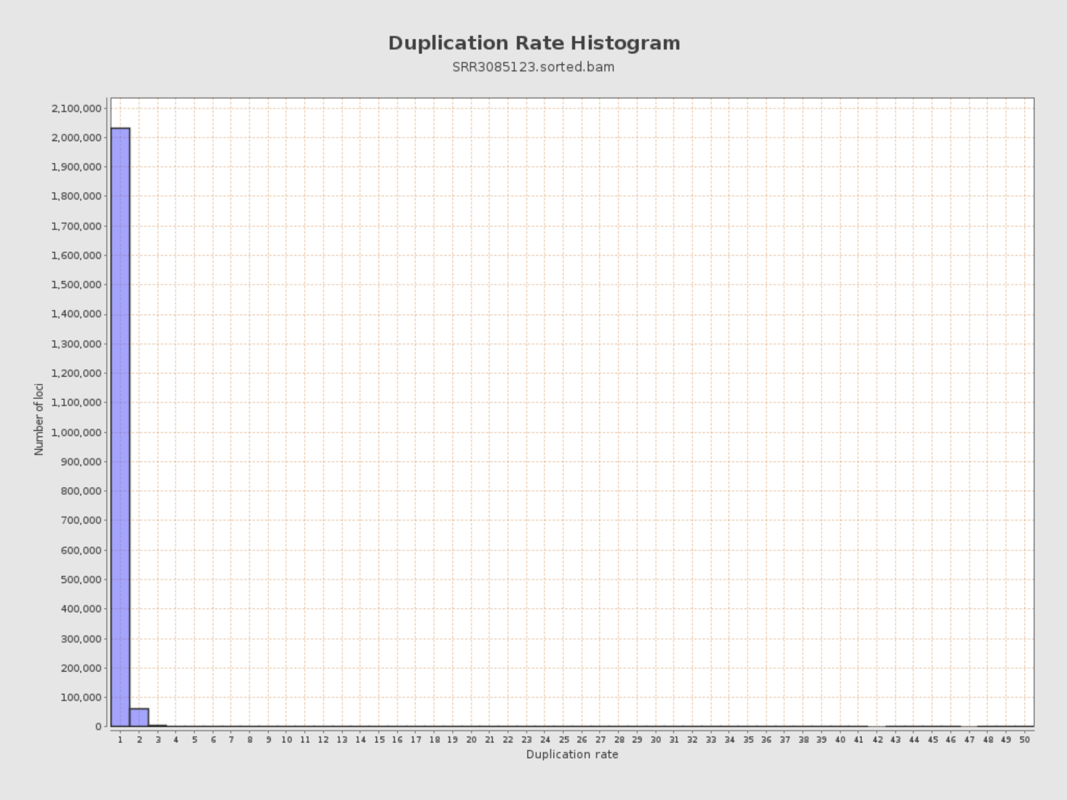
5. Results : Coverage Histogram (0-50X)



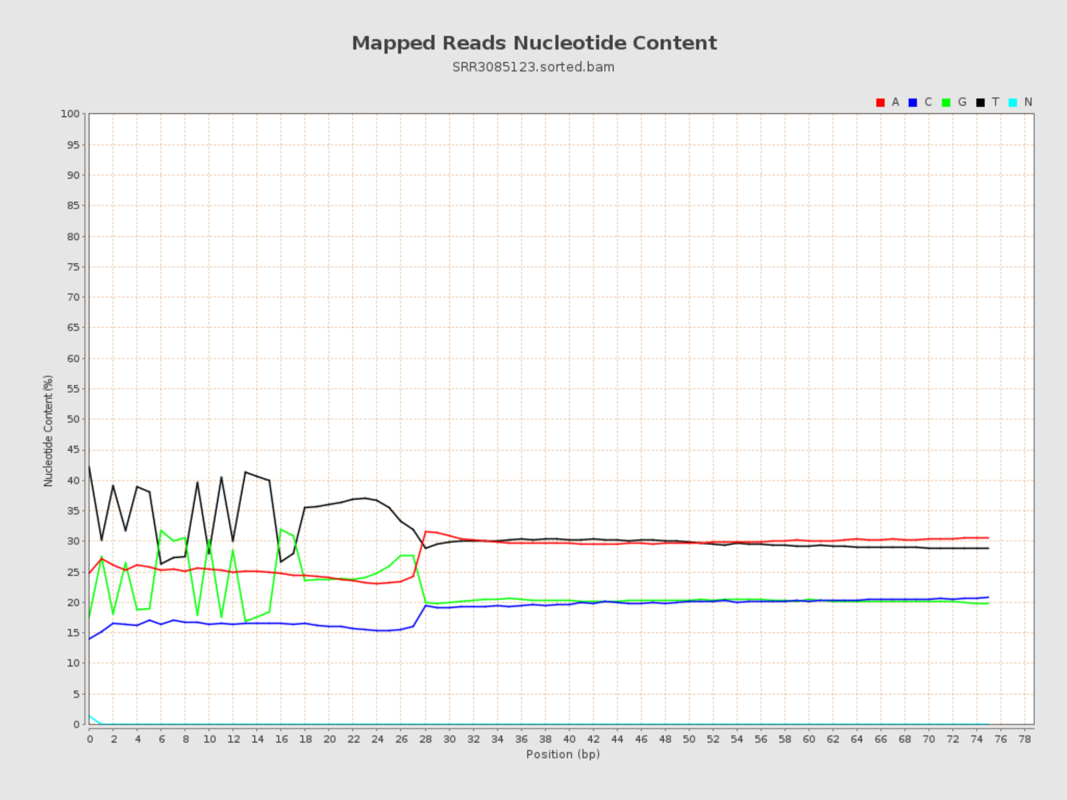
6. Results : Genome Fraction Coverage



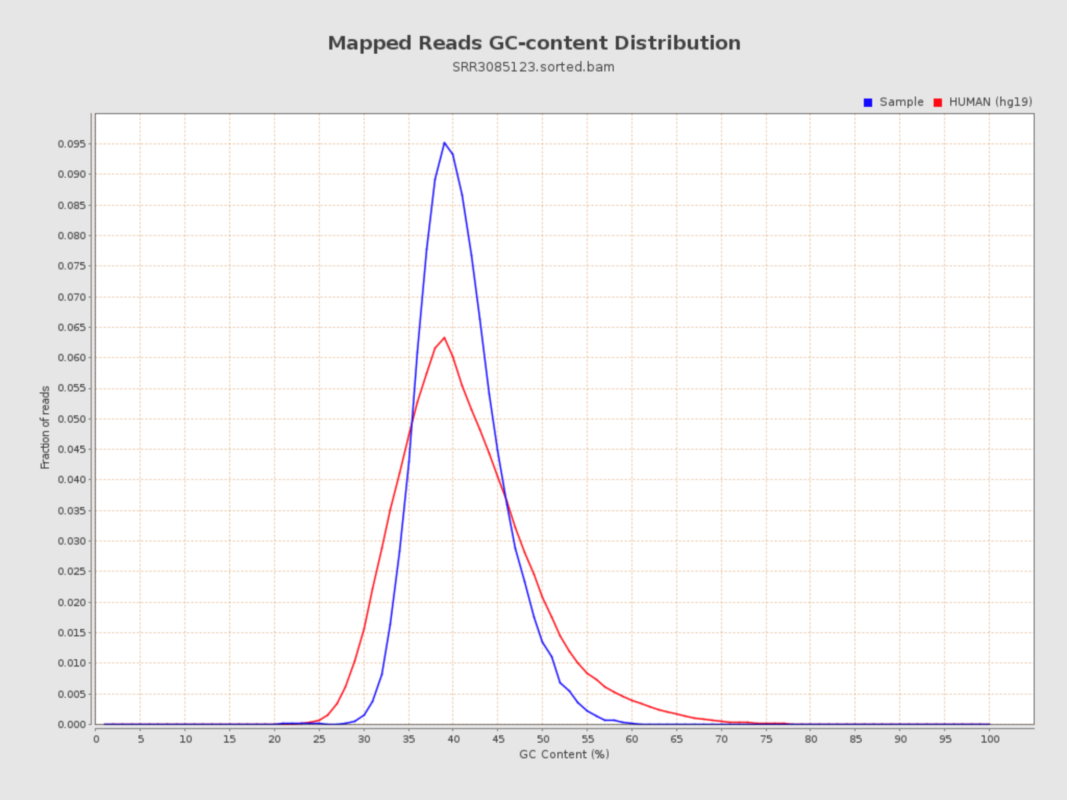
7. Results : Duplication Rate Histogram



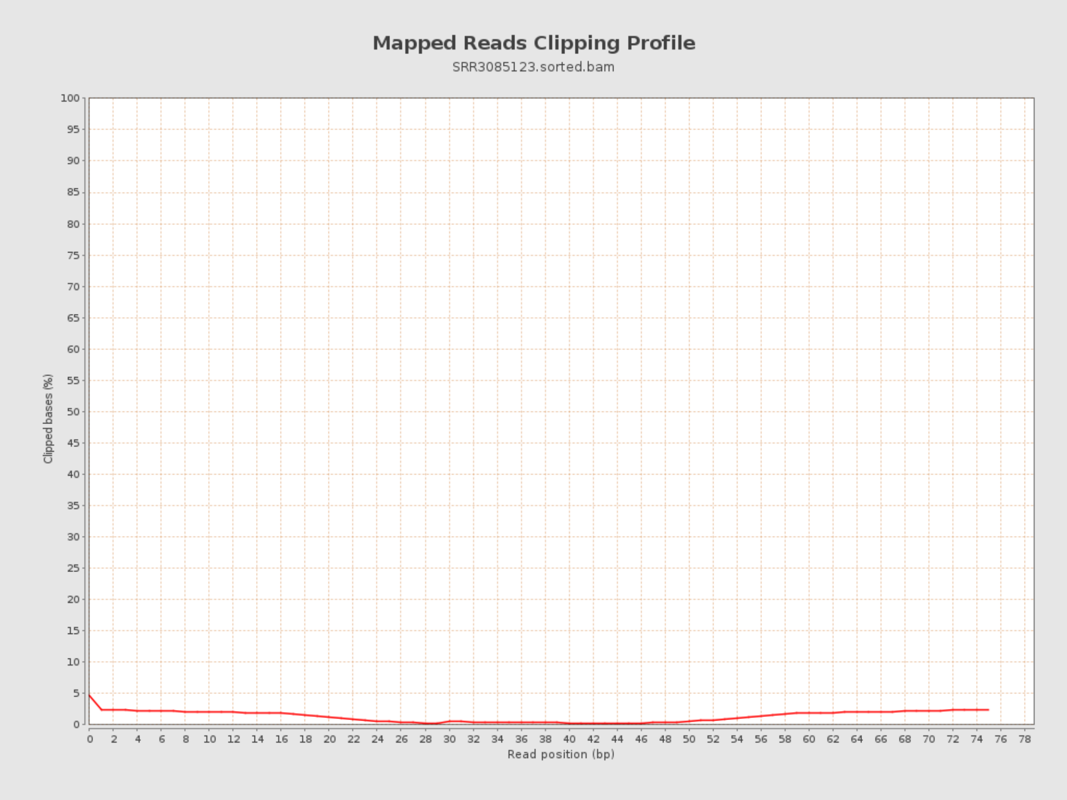
8. Results : Mapped Reads Nucleotide Content



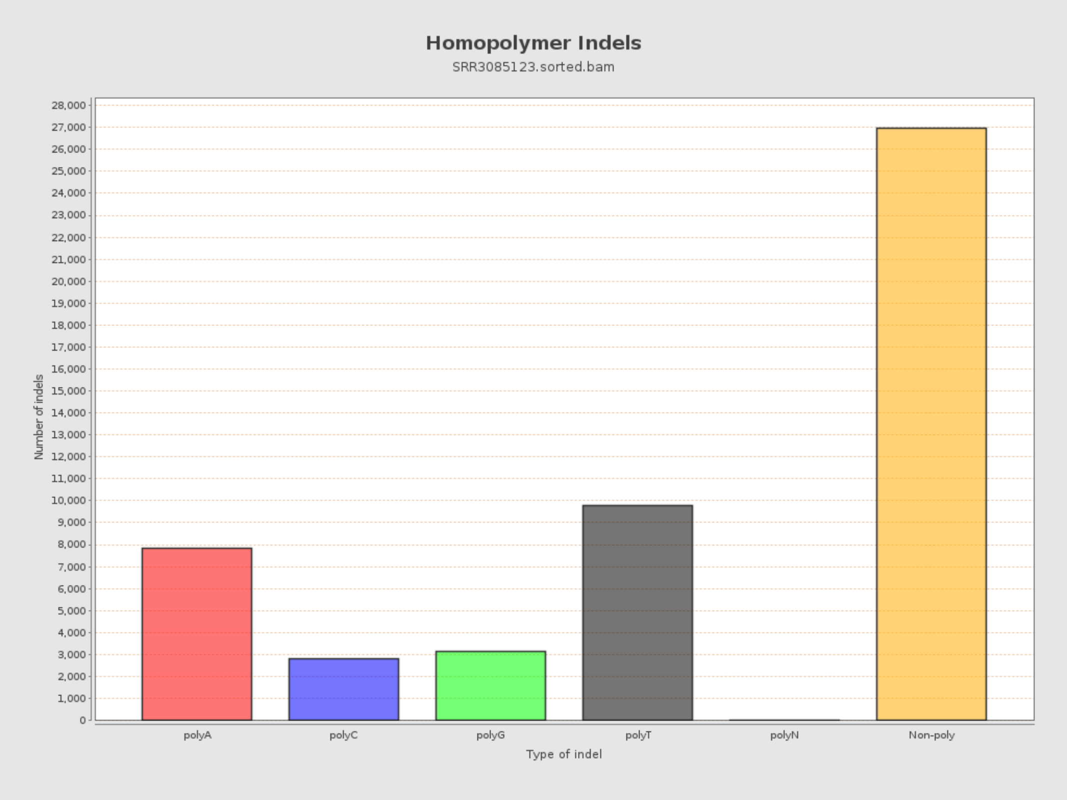
9. Results : Mapped Reads GC-content Distribution



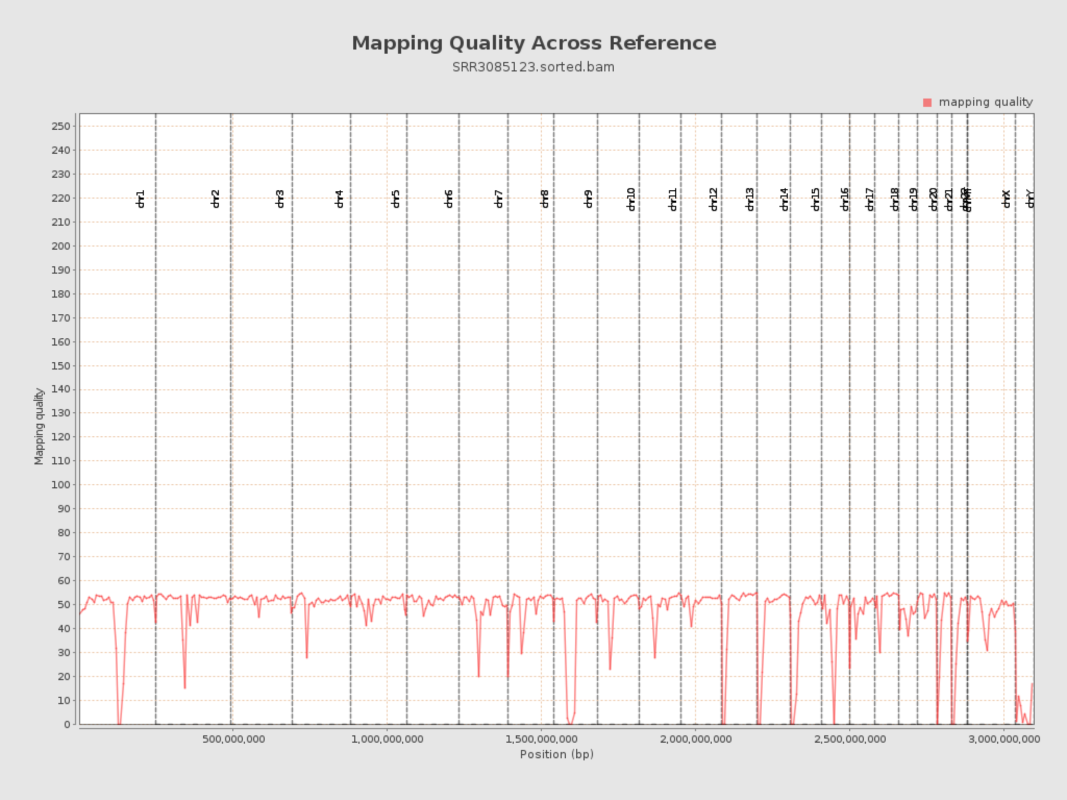
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram