Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 16:25:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716885.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_SRR9716885 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716885.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 16:25:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716885.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	851,275
Mapped reads	743,523 / 87.34%
Unmapped reads	107,752 / 12.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,262 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	16,821 / 1.98%
Duplication rate	1.68%
Clipped reads	744,002 / 87.4%

2.2. ACGT Content

Number/percentage of A's	11,221,433 / 26%
Number/percentage of C's	8,433,327 / 19.54%
Number/percentage of T's	13,485,197 / 31.24%
Number/percentage of G's	10,023,248 / 23.22%
Number/percentage of N's	1,117 / 0%
GC Percentage	42.76%

2.3. Coverage

Mean	0.0139

Standard Deviation	0.1582

2.4. Mapping Quality

Mean Mapping Quality	44.81

2.5. Mismatches and indels

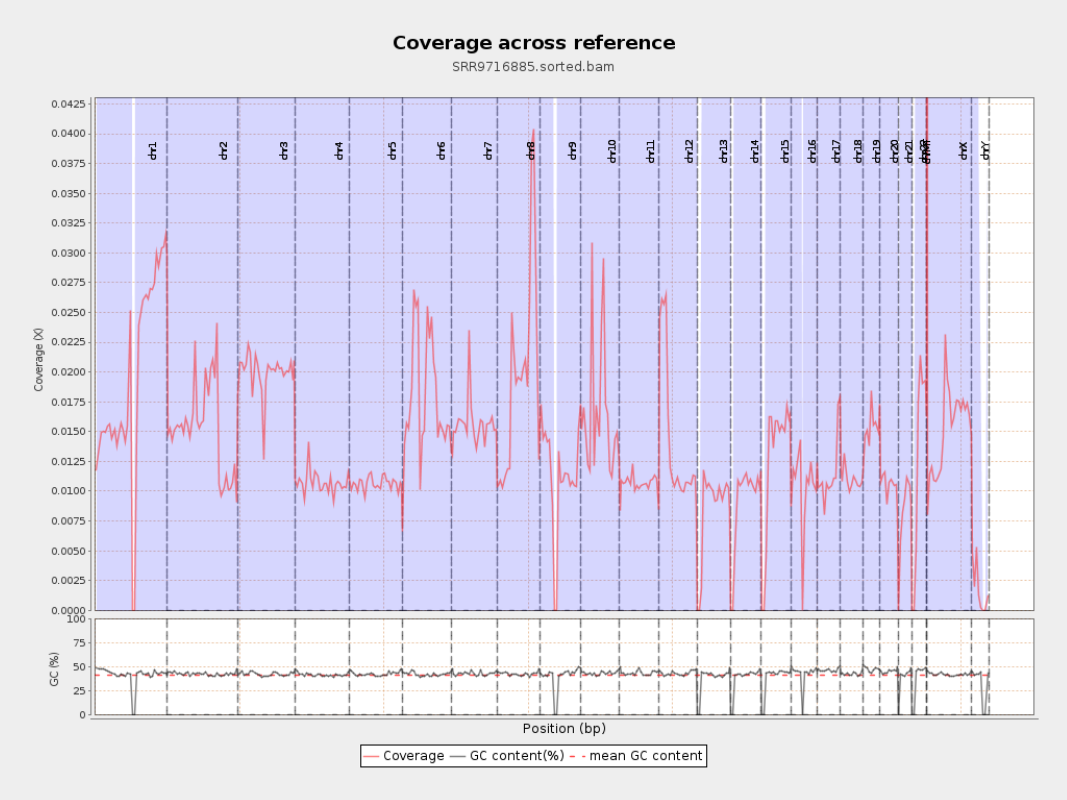
General error rate	0.51%
Mismatches	212,312
Insertions	3,420
Mapped reads with at least one insertion	0.46%
Deletions	8,045
Mapped reads with at least one deletion	1.07%
Homopolymer indels	41.68%

2.6. Chromosome stats

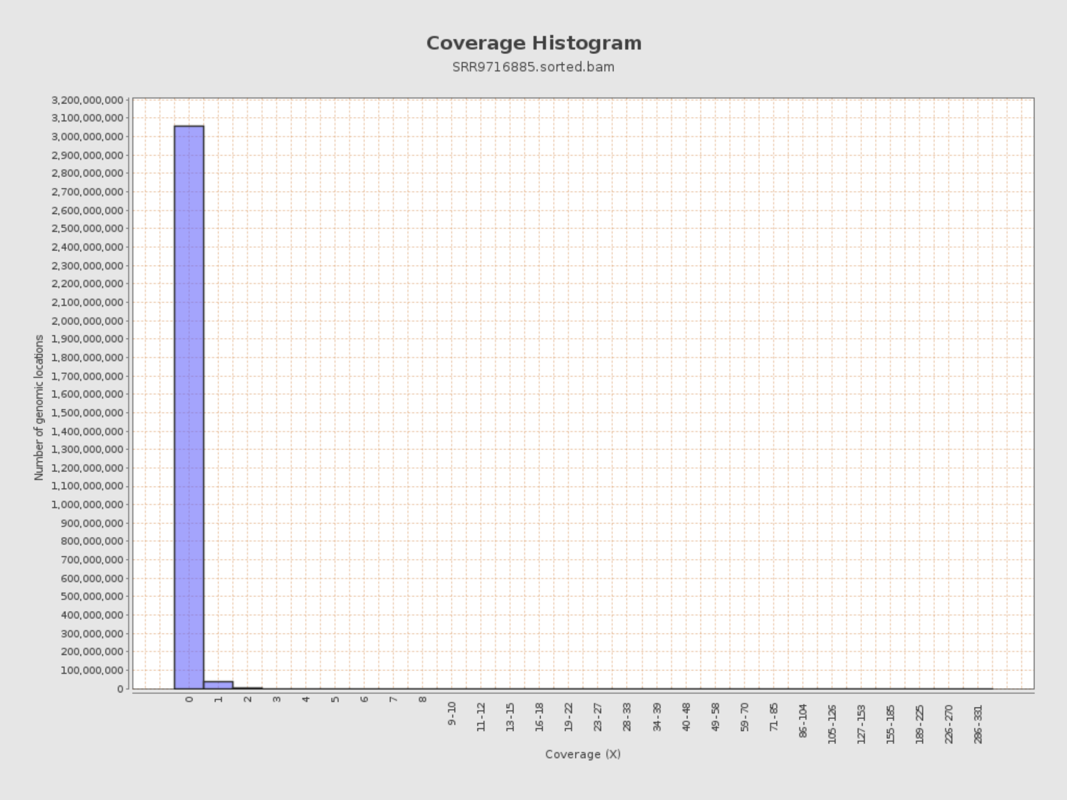
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4849444	0.0195	0.2754
chr2	243199373	3717194	0.0153	0.1896
chr3	198022430	3949741	0.0199	0.1485
chr4	191154276	2046546	0.0107	0.1108
chr5	180915260	1926081	0.0106	0.109
chr6	171115067	3063714	0.0179	0.1646
chr7	159138663	2493835	0.0157	0.1906

chr8	146364022	2870827	0.0196	0.1569
chr9	141213431	1573089	0.0111	0.1321
chr10	135534747	2255607	0.0166	0.1701
chr11	135006516	1448212	0.0107	0.1251
chr12	133851895	1935170	0.0145	0.1272
chr13	115169878	975598	0.0085	0.0967
chr14	107349540	963620	0.009	0.1042
chr15	102531392	1294565	0.0126	0.1177
chr16	90354753	918791	0.0102	0.1129
chr17	81195210	924774	0.0114	0.1134
chr18	78077248	855119	0.011	0.1991
chr19	59128983	907887	0.0154	0.19
chr20	63025520	663804	0.0105	0.1083
chr21	48129895	392525	0.0082	0.0987
chr22	51304566	671298	0.0131	0.1195
chrMT	16571	7859	0.4743	0.7182
chrX	155270560	2369621	0.0153	0.1389
chrY	59373566	102059	0.0017	0.0517

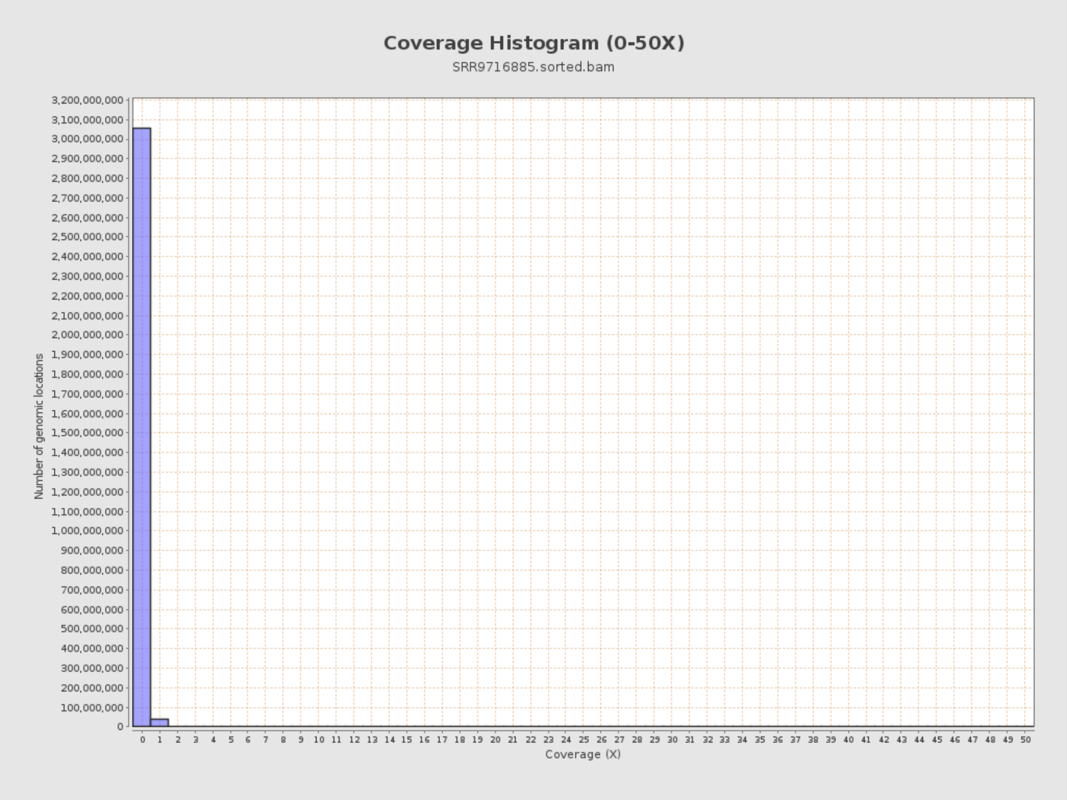
3. Results : Coverage across reference



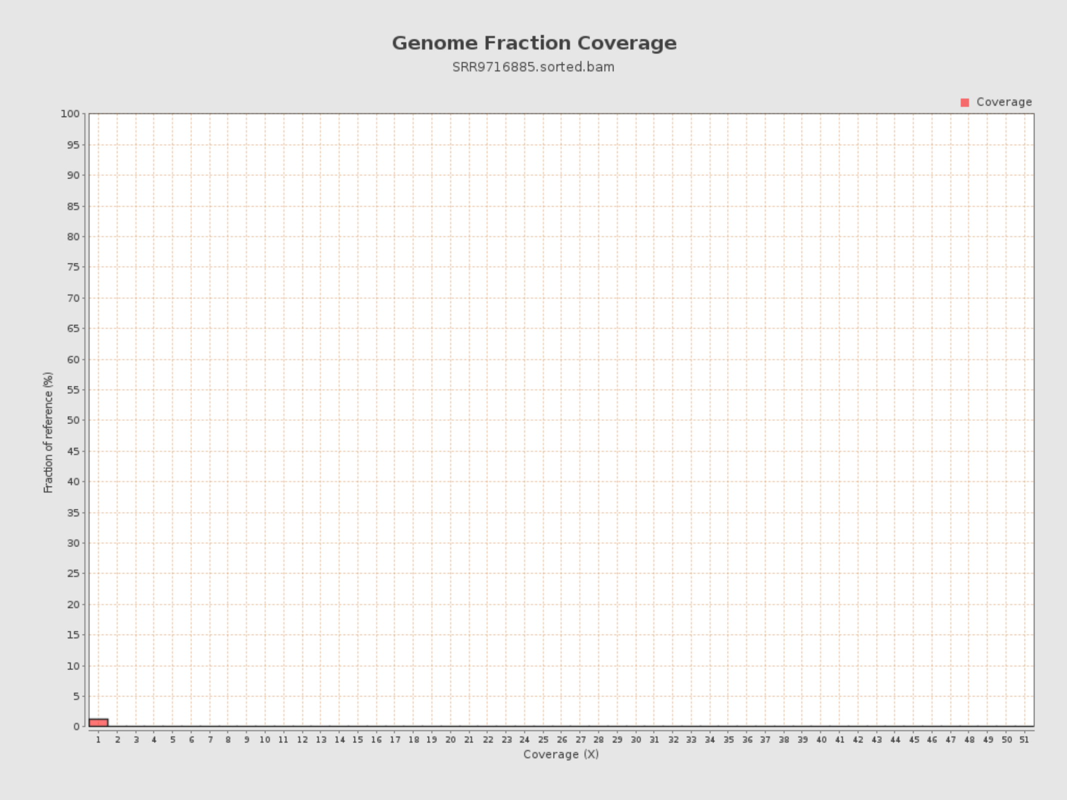
4. Results : Coverage Histogram



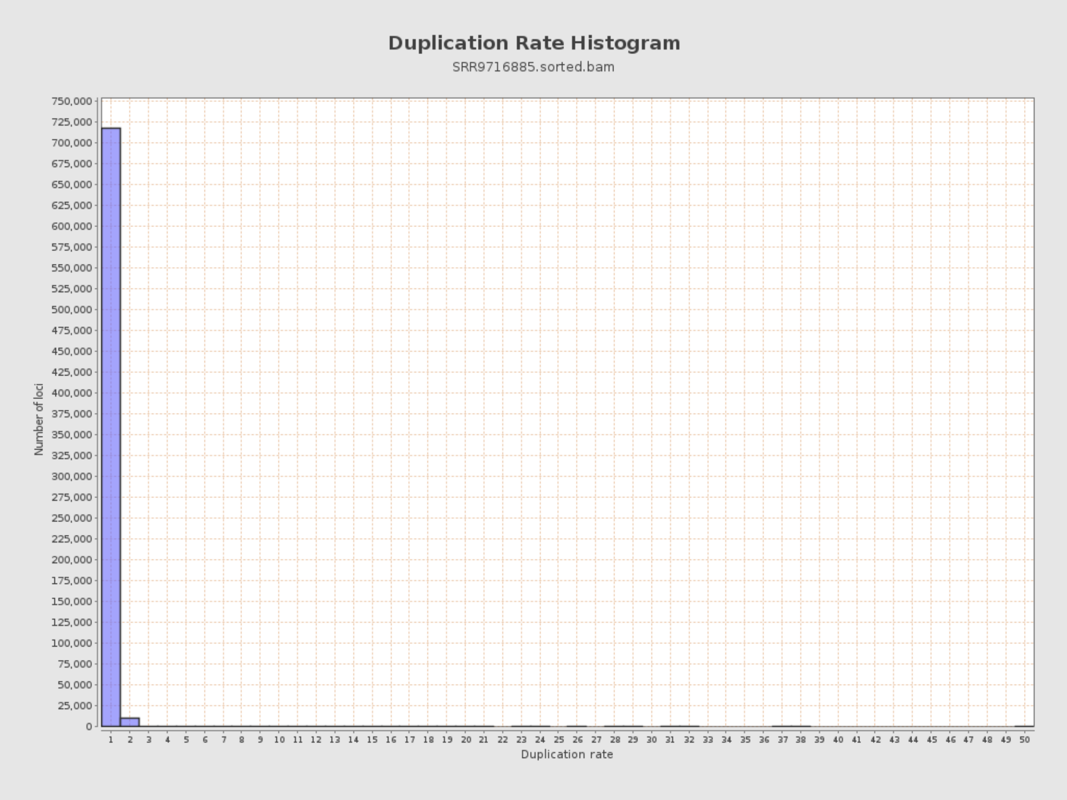
5. Results : Coverage Histogram (0-50X)



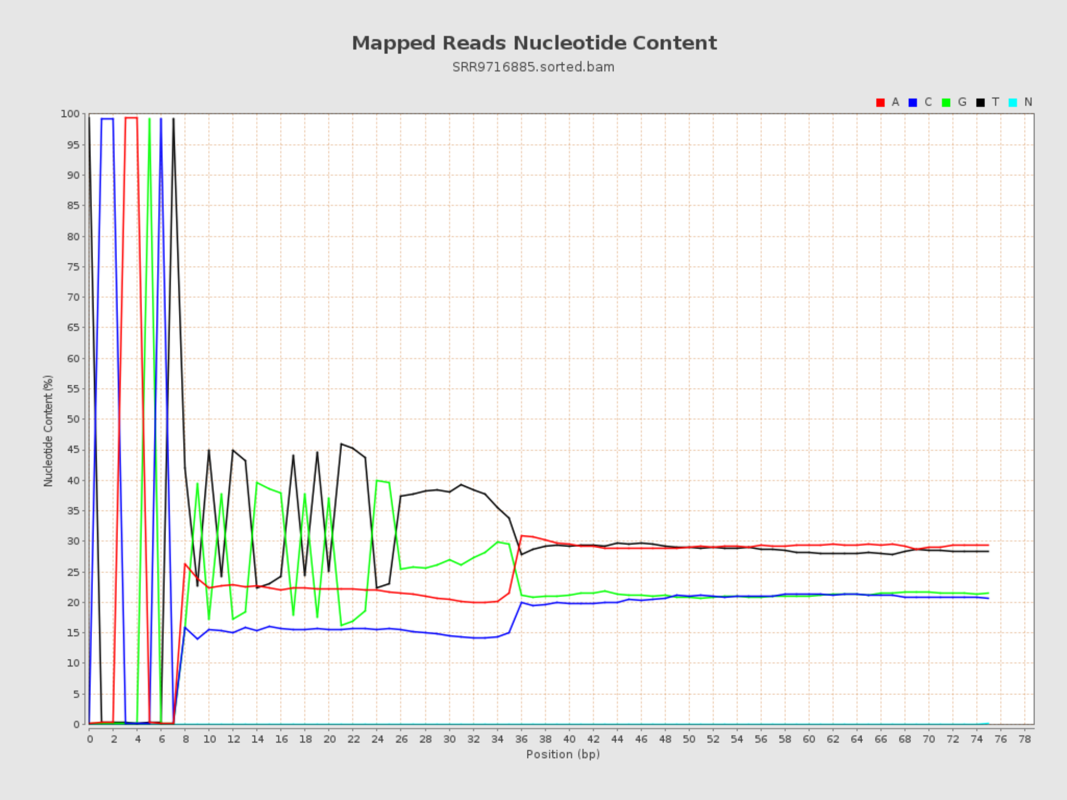
6. Results : Genome Fraction Coverage



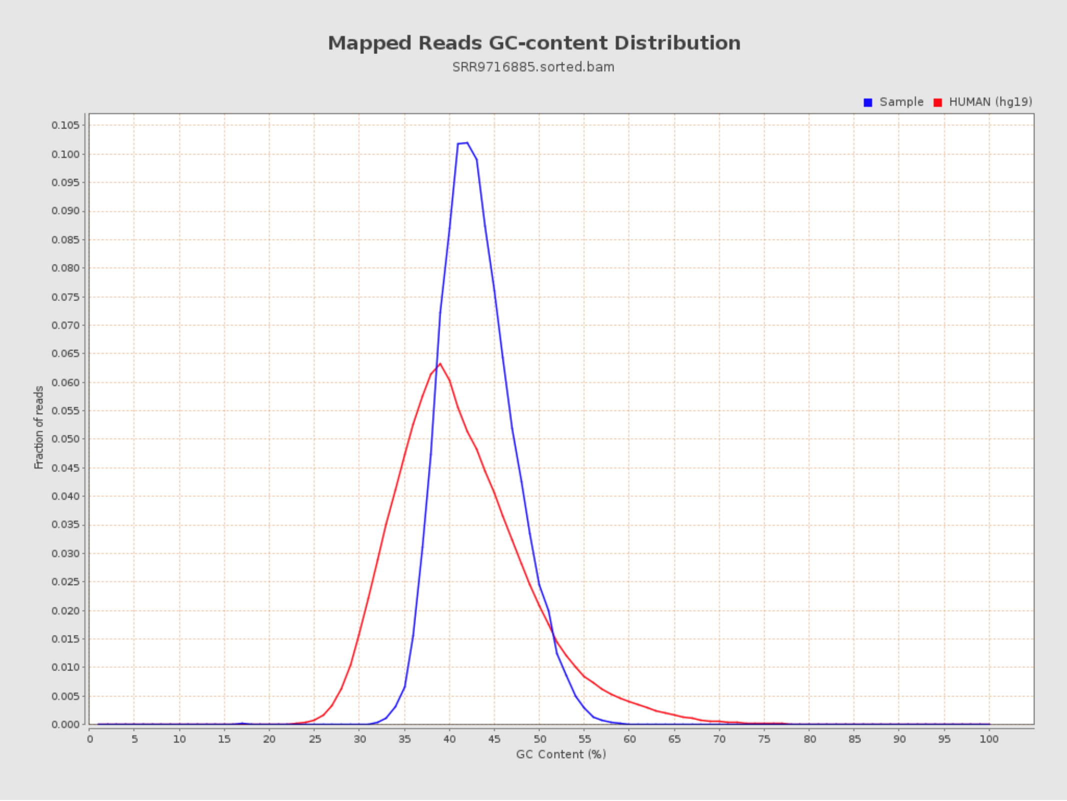
7. Results : Duplication Rate Histogram



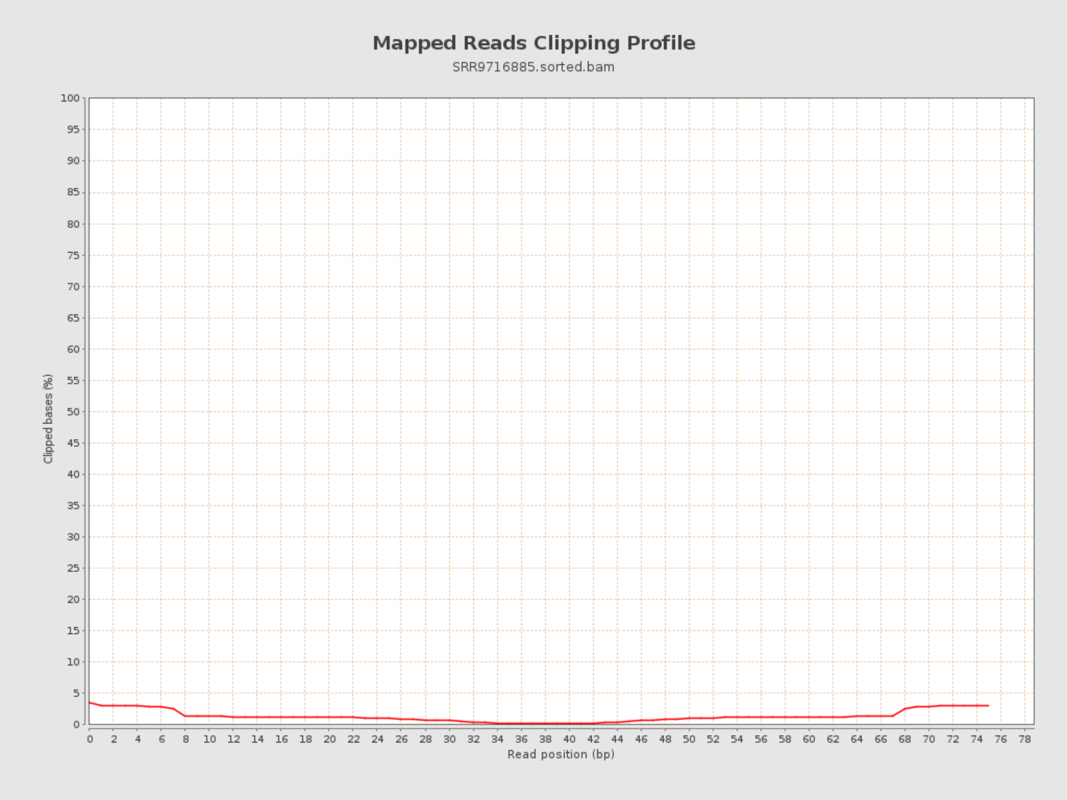
8. Results : Mapped Reads Nucleotide Content



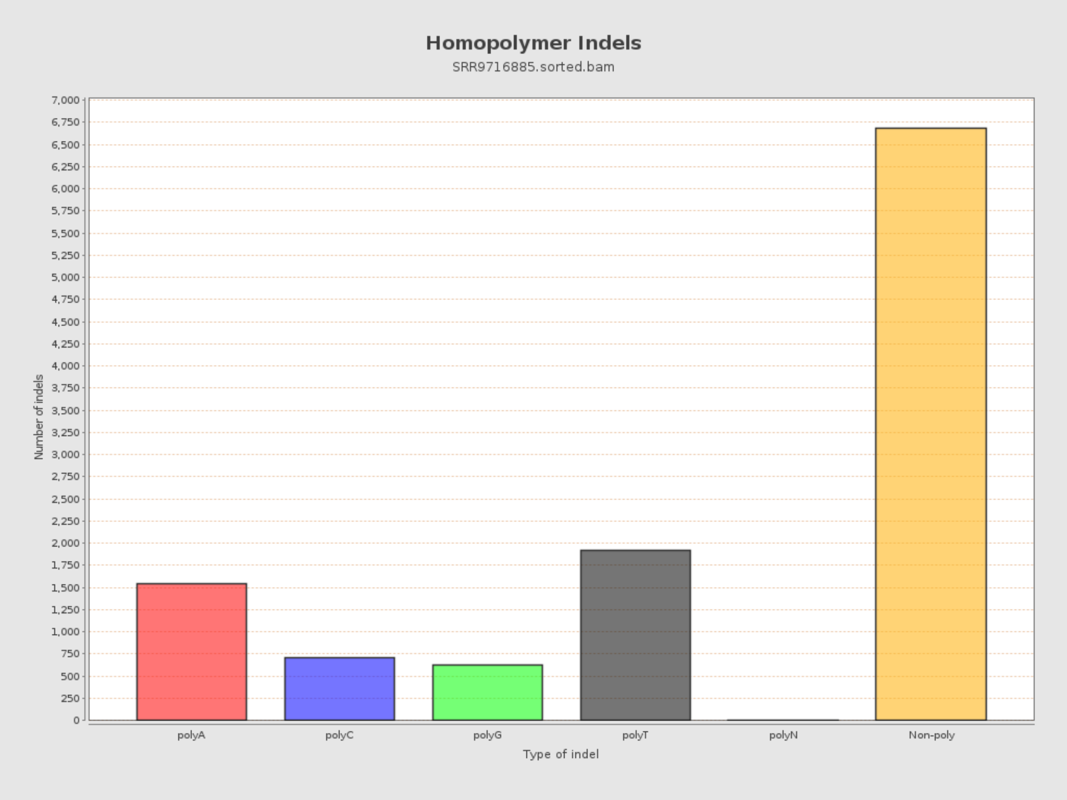
9. Results : Mapped Reads GC-content Distribution



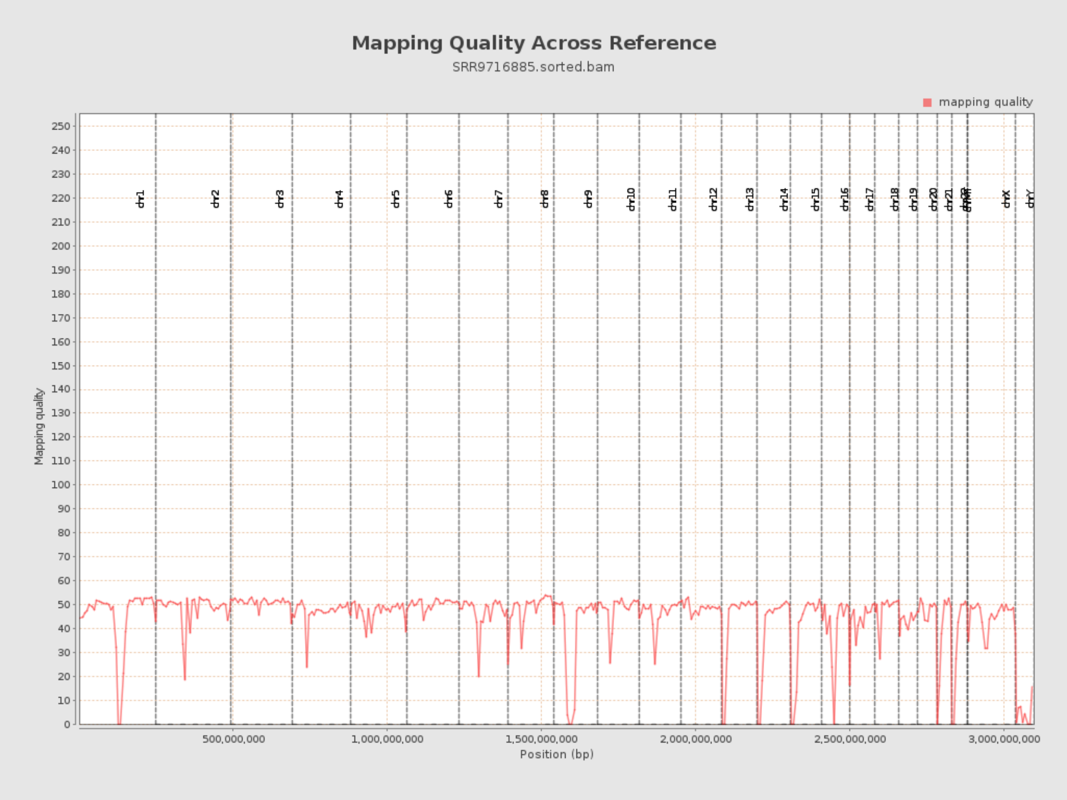
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram