Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 09:44:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716742.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_SRR9716742 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716742.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 09:44:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716742.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	702,876
Mapped reads	586,284 / 83.41%
Unmapped reads	116,592 / 16.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	751 / 0.11%
Read min/max/mean length	30 / 76 / 76.04
Duplicated reads (estimated)	28,142 / 4%
Duplication rate	4.3%
Clipped reads	586,787 / 83.48%

2.2. ACGT Content

Number/percentage of A's	7,015,469 / 22.02%
Number/percentage of C's	6,118,943 / 19.21%
Number/percentage of T's	10,125,396 / 31.78%
Number/percentage of G's	8,595,739 / 26.98%
Number/percentage of N's	639 / 0%
GC Percentage	46.19%

2.3. Coverage

Mean	0.0103

Standard Deviation	0.1205

2.4. Mapping Quality

Mean Mapping Quality	43.67

2.5. Mismatches and indels

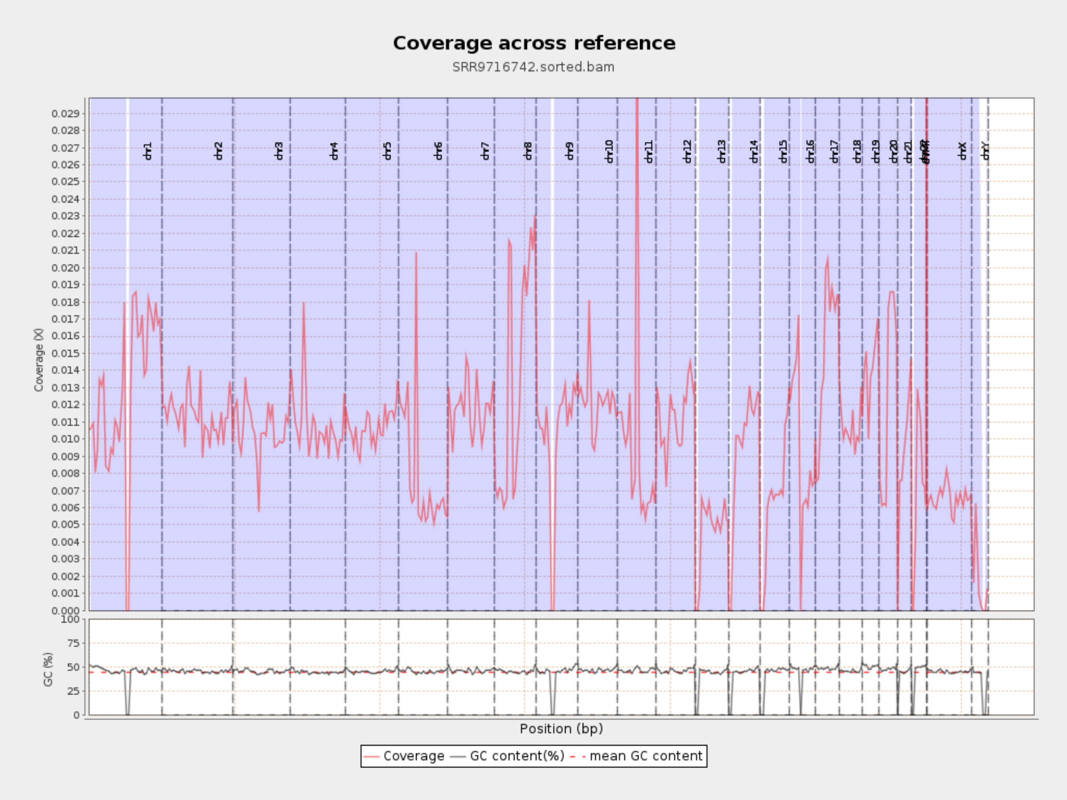
General error rate	0.65%
Mismatches	204,386
Insertions	1,674
Mapped reads with at least one insertion	0.28%
Deletions	4,922
Mapped reads with at least one deletion	0.83%
Homopolymer indels	42%

2.6. Chromosome stats

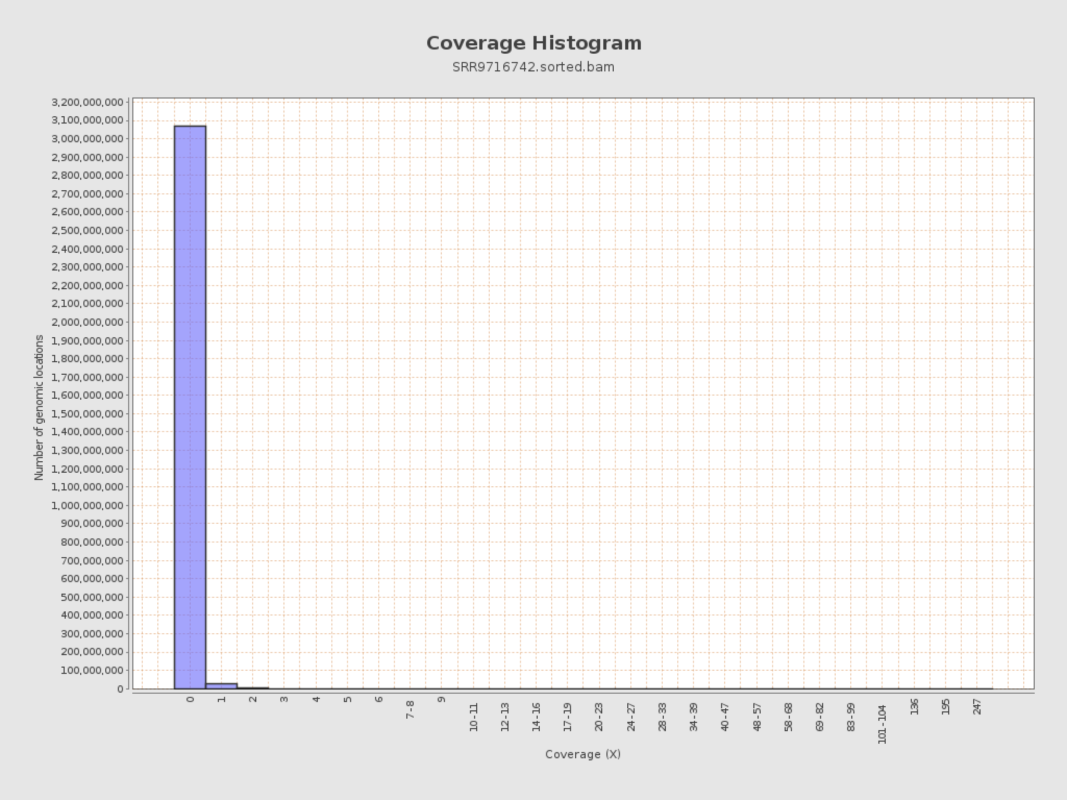
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3172011	0.0127	0.1444
chr2	243199373	2772632	0.0114	0.1558
chr3	198022430	2091121	0.0106	0.1114
chr4	191154276	2063892	0.0108	0.1165
chr5	180915260	1931571	0.0107	0.1117
chr6	171115067	1370274	0.008	0.1027
chr7	159138663	1873305	0.0118	0.1352

chr8	146364022	2009398	0.0137	0.1306
chr9	141213431	1417774	0.01	0.113
chr10	135534747	1655483	0.0122	0.1365
chr11	135006516	1346565	0.01	0.1205
chr12	133851895	1525355	0.0114	0.1163
chr13	115169878	534622	0.0046	0.074
chr14	107349540	996008	0.0093	0.106
chr15	102531392	635961	0.0062	0.085
chr16	90354753	846466	0.0094	0.1106
chr17	81195210	1267659	0.0156	0.1386
chr18	78077248	831274	0.0106	0.1304
chr19	59128983	831556	0.0141	0.1456
chr20	63025520	792996	0.0126	0.1242
chr21	48129895	444520	0.0092	0.1084
chr22	51304566	341457	0.0067	0.0895
chrMT	16571	1140	0.0688	0.3046
chrX	155270560	1016213	0.0065	0.0891
chrY	59373566	95410	0.0016	0.0568

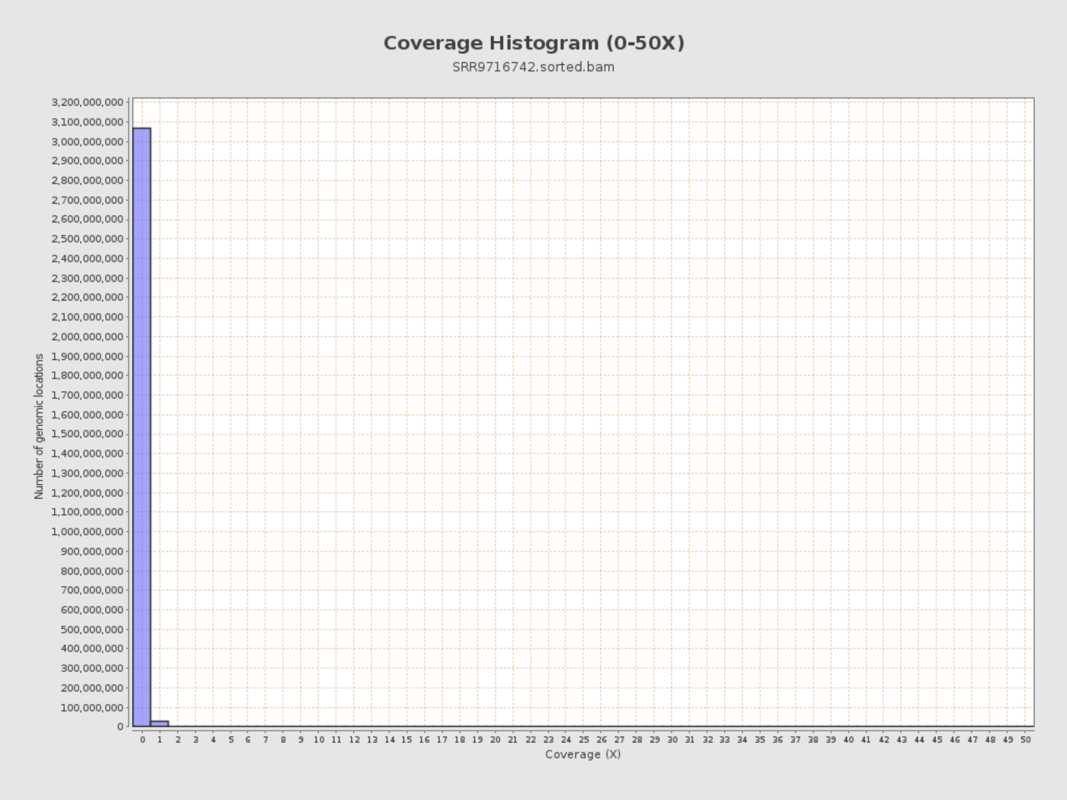
3. Results : Coverage across reference



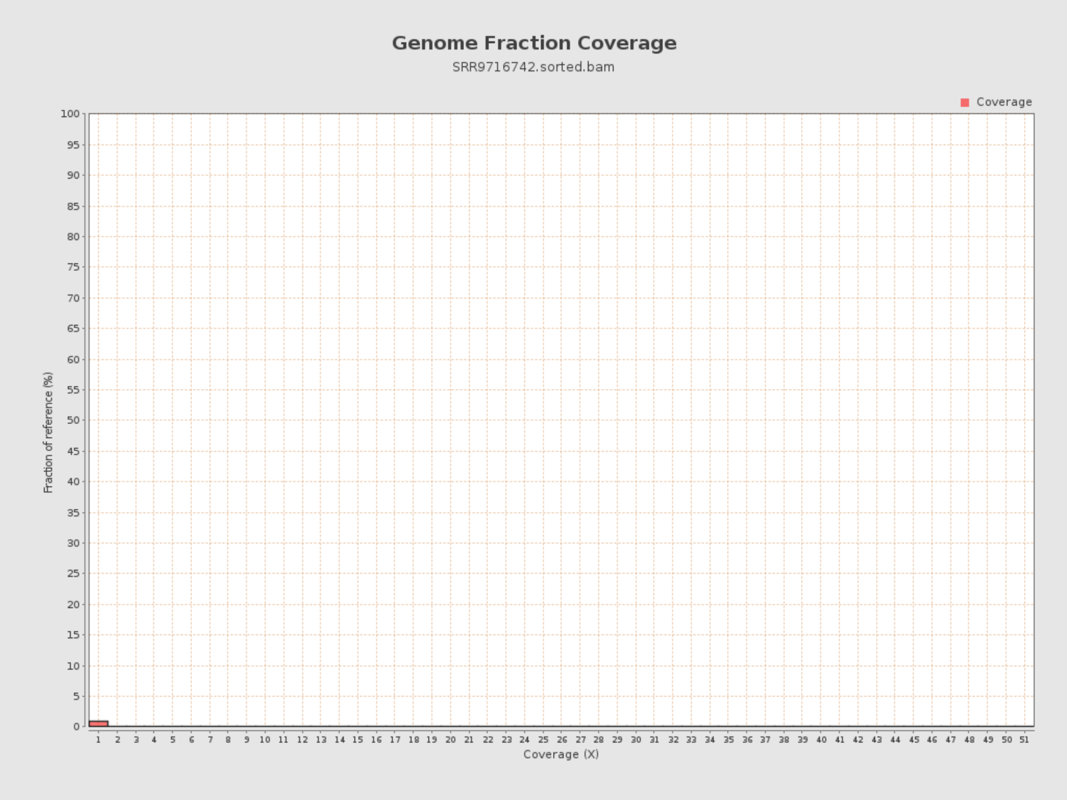
4. Results : Coverage Histogram



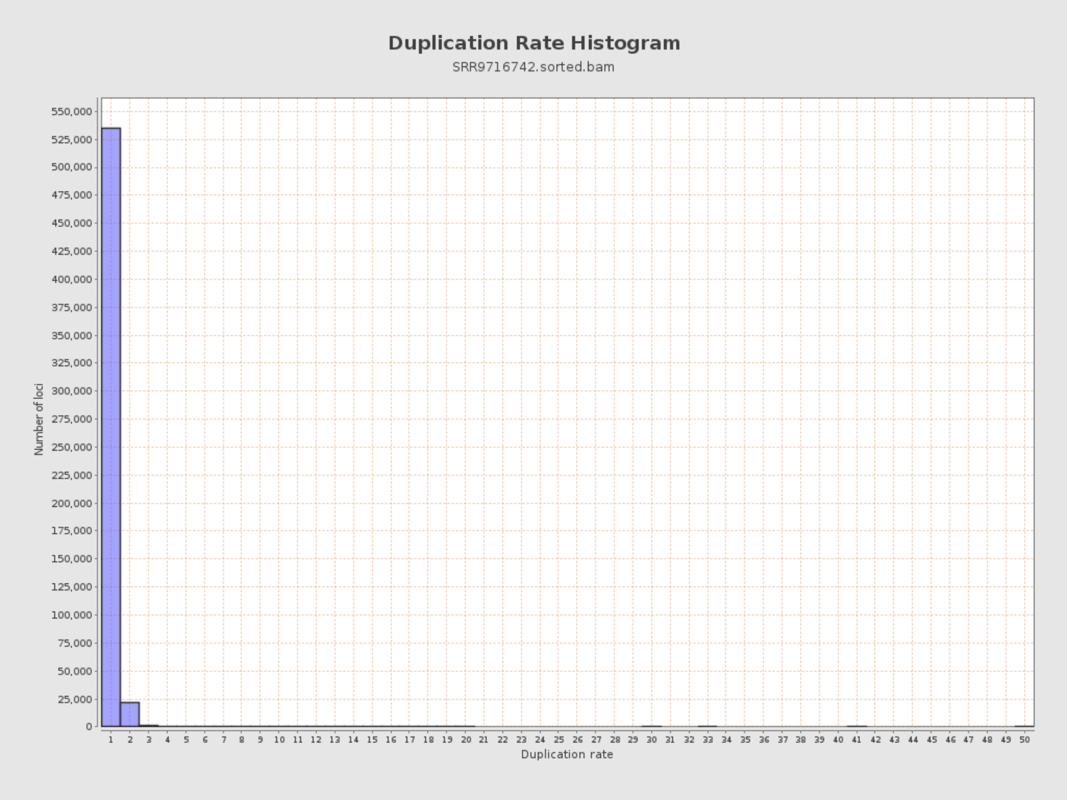
5. Results : Coverage Histogram (0-50X)



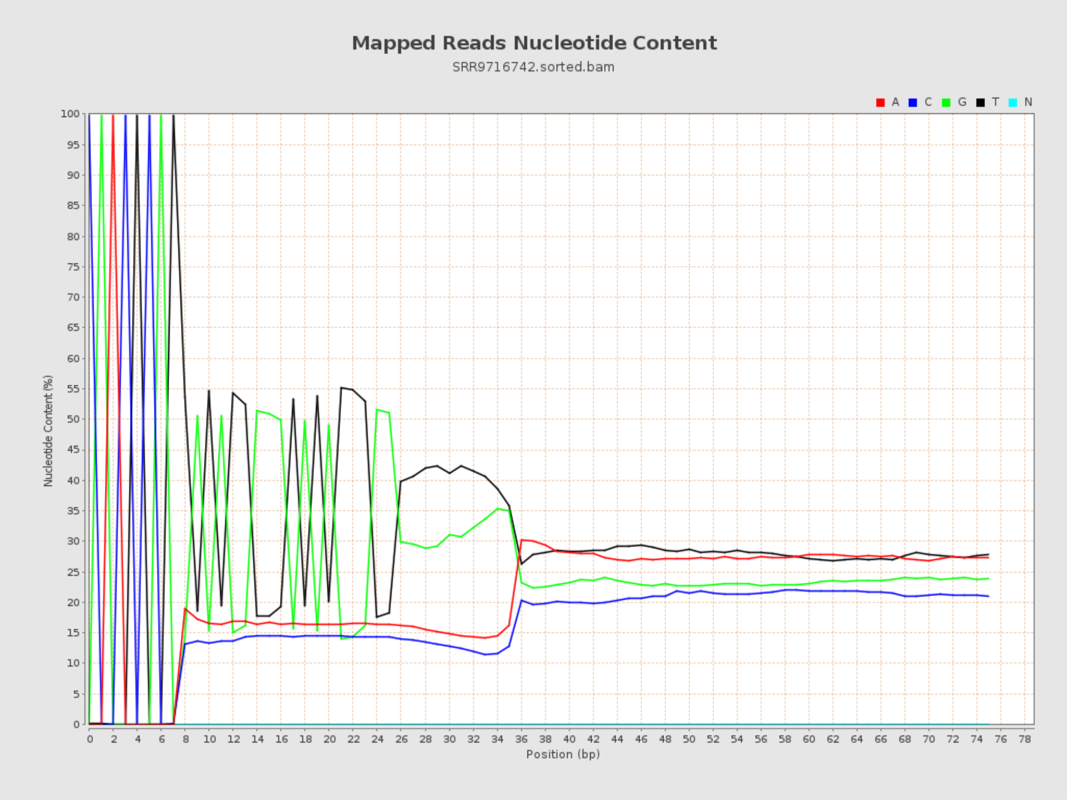
6. Results : Genome Fraction Coverage



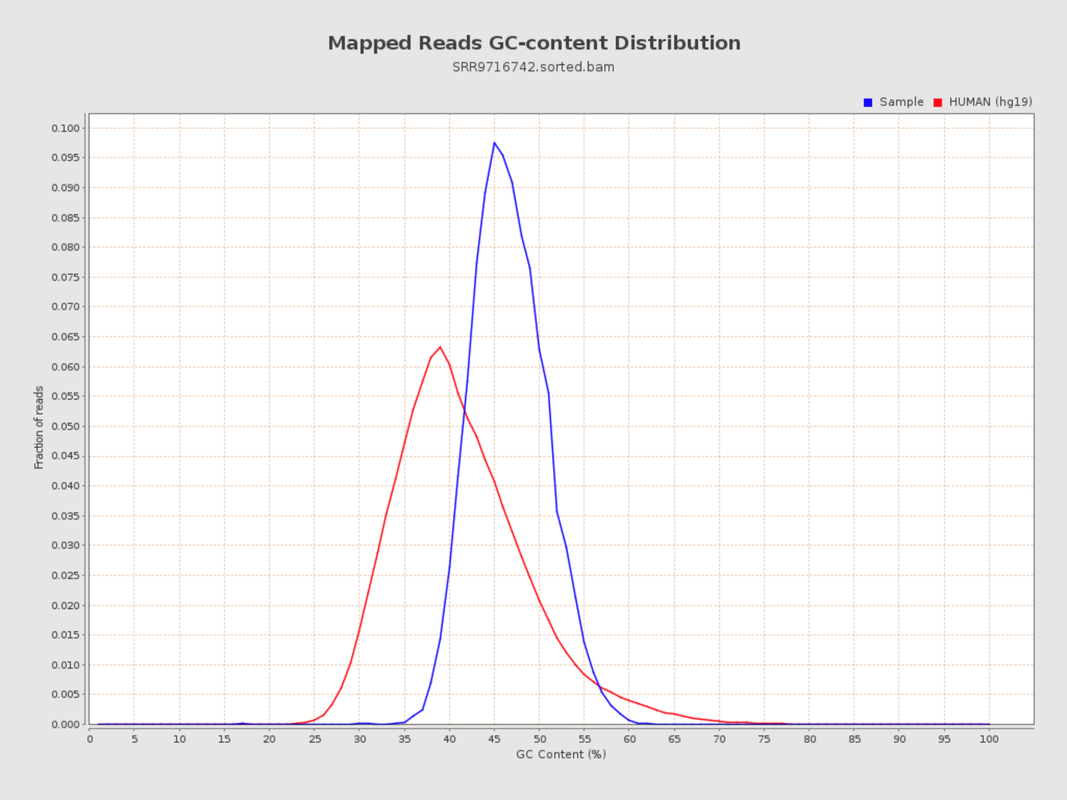
7. Results : Duplication Rate Histogram



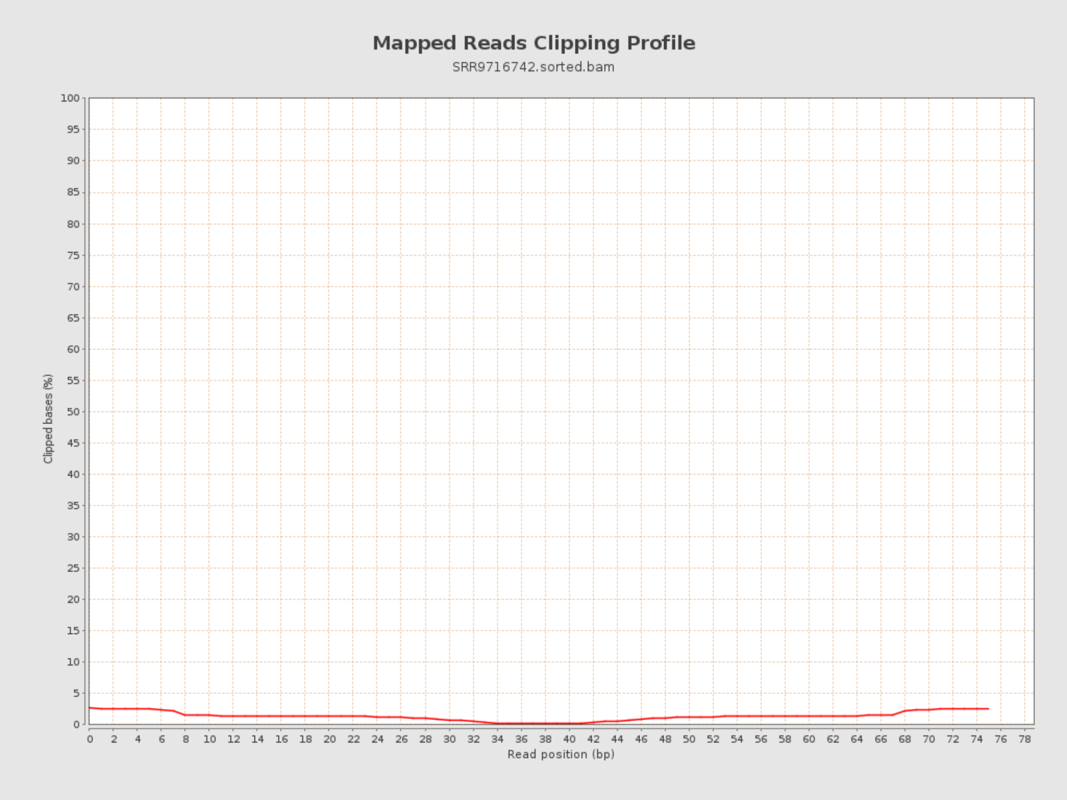
8. Results : Mapped Reads Nucleotide Content



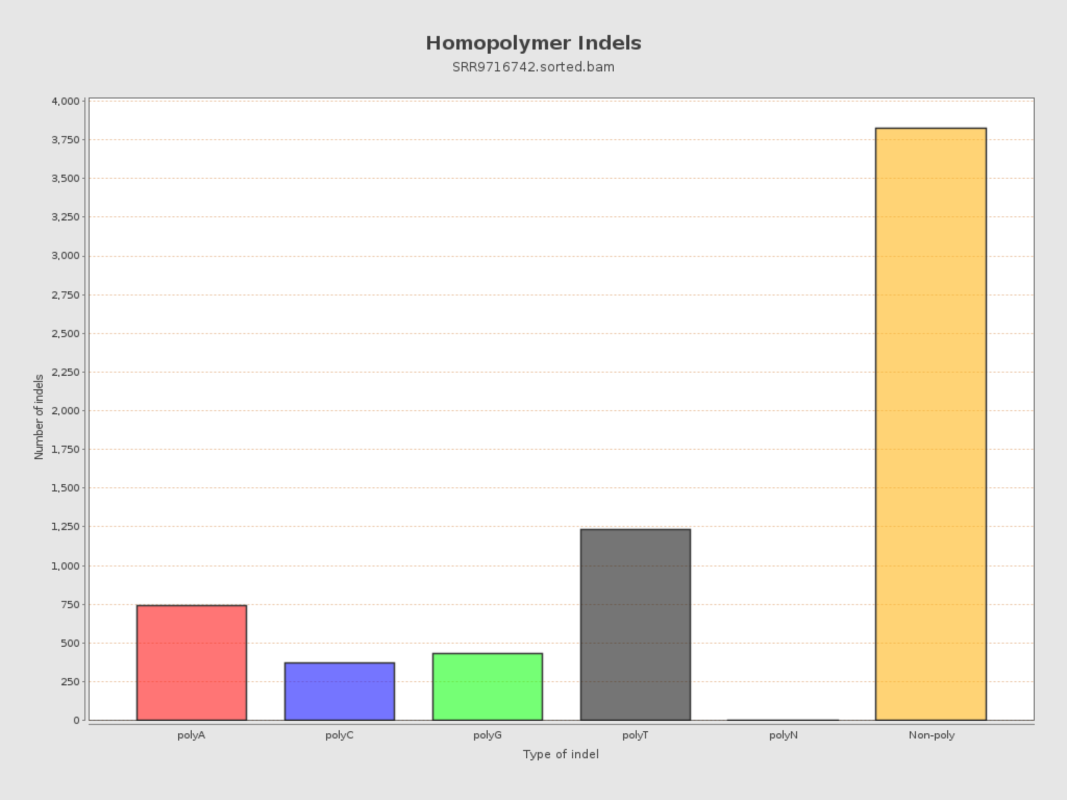
9. Results : Mapped Reads GC-content Distribution



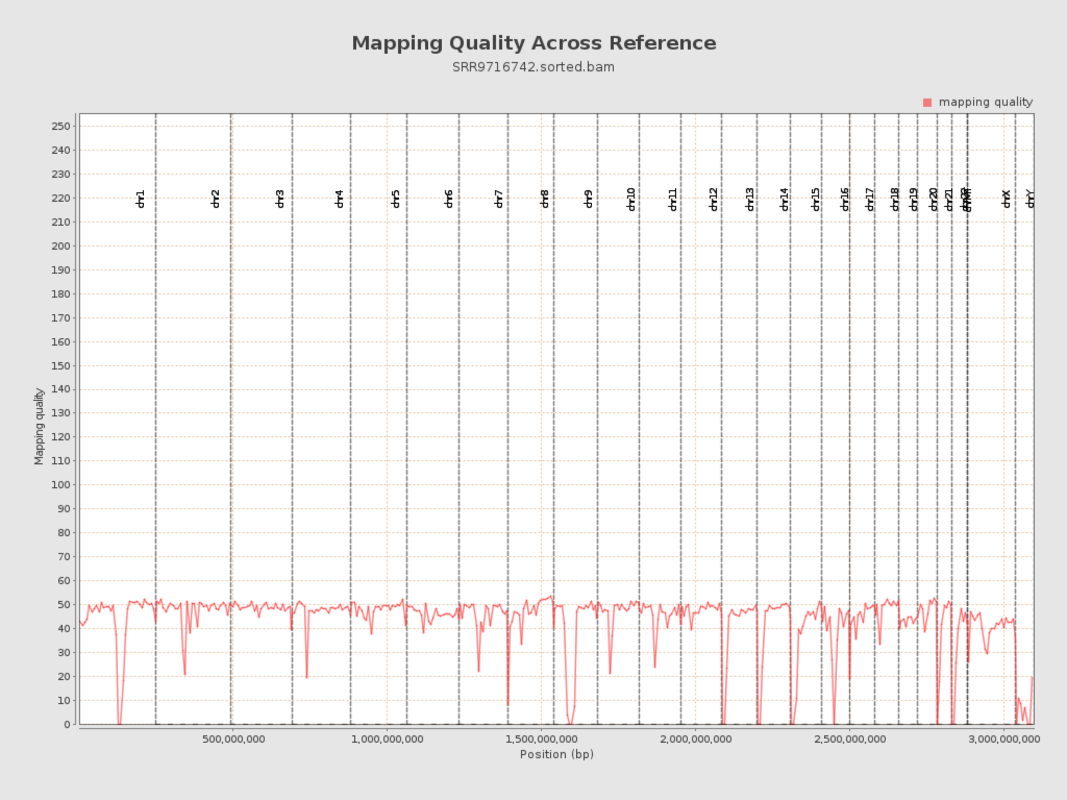
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram