Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 23:07:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716585.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_SRR9716585 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716585.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 23:07:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716585.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,972,199
Mapped reads	950,018 / 48.17%
Unmapped reads	1,022,181 / 51.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,322 / 0.17%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	18,297 / 0.93%
Duplication rate	1.32%
Clipped reads	952,976 / 48.32%

2.2. ACGT Content

Number/percentage of A's	12,868,548 / 24.1%
Number/percentage of C's	10,838,092 / 20.3%
Number/percentage of T's	16,315,077 / 30.56%
Number/percentage of G's	13,368,449 / 25.04%
Number/percentage of N's	471 / 0%
GC Percentage	45.34%

2.3. Coverage

Mean	0.0173

Standard Deviation	0.1704

2.4. Mapping Quality

Mean Mapping Quality	41.1

2.5. Mismatches and indels

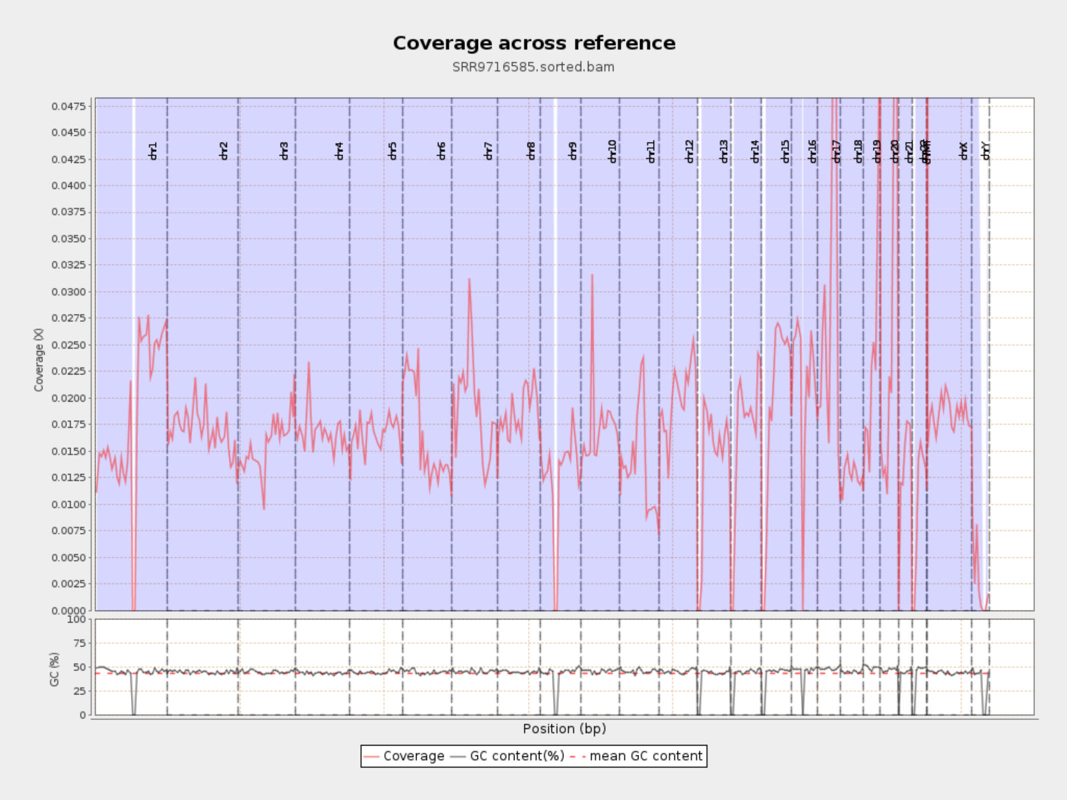
General error rate	0.53%
Mismatches	279,845
Insertions	3,178
Mapped reads with at least one insertion	0.33%
Deletions	9,800
Mapped reads with at least one deletion	1.03%
Homopolymer indels	40.35%

2.6. Chromosome stats

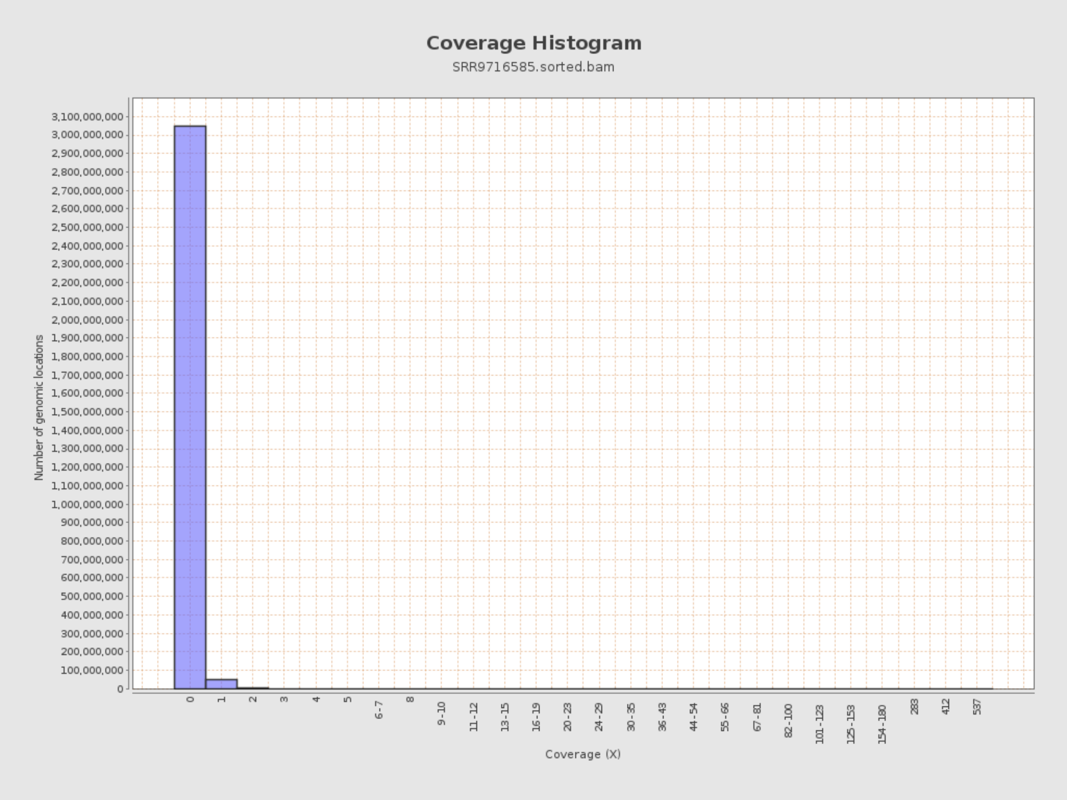
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4505170	0.0181	0.1981
chr2	243199373	4140448	0.017	0.2544
chr3	198022430	3075131	0.0155	0.1347
chr4	191154276	3215551	0.0168	0.1413
chr5	180915260	3045232	0.0168	0.1368
chr6	171115067	2843447	0.0166	0.1551
chr7	159138663	3058095	0.0192	0.2197

chr8	146364022	2735520	0.0187	0.1611
chr9	141213431	1784108	0.0126	0.1339
chr10	135534747	2344711	0.0173	0.1959
chr11	135006516	1878299	0.0139	0.147
chr12	133851895	2671307	0.02	0.1524
chr13	115169878	1601074	0.0139	0.1258
chr14	107349540	1779267	0.0166	0.1409
chr15	102531392	1974368	0.0193	0.1512
chr16	90354753	1904543	0.0211	0.1625
chr17	81195210	2436365	0.03	0.1905
chr18	78077248	992863	0.0127	0.1846
chr19	59128983	1467158	0.0248	0.2048
chr20	63025520	1738128	0.0276	0.1816
chr21	48129895	648488	0.0135	0.1316
chr22	51304566	516645	0.0101	0.1062
chrMT	16571	18065	1.0902	1.1775
chrX	155270560	2875581	0.0185	0.1511
chrY	59373566	156650	0.0026	0.0777

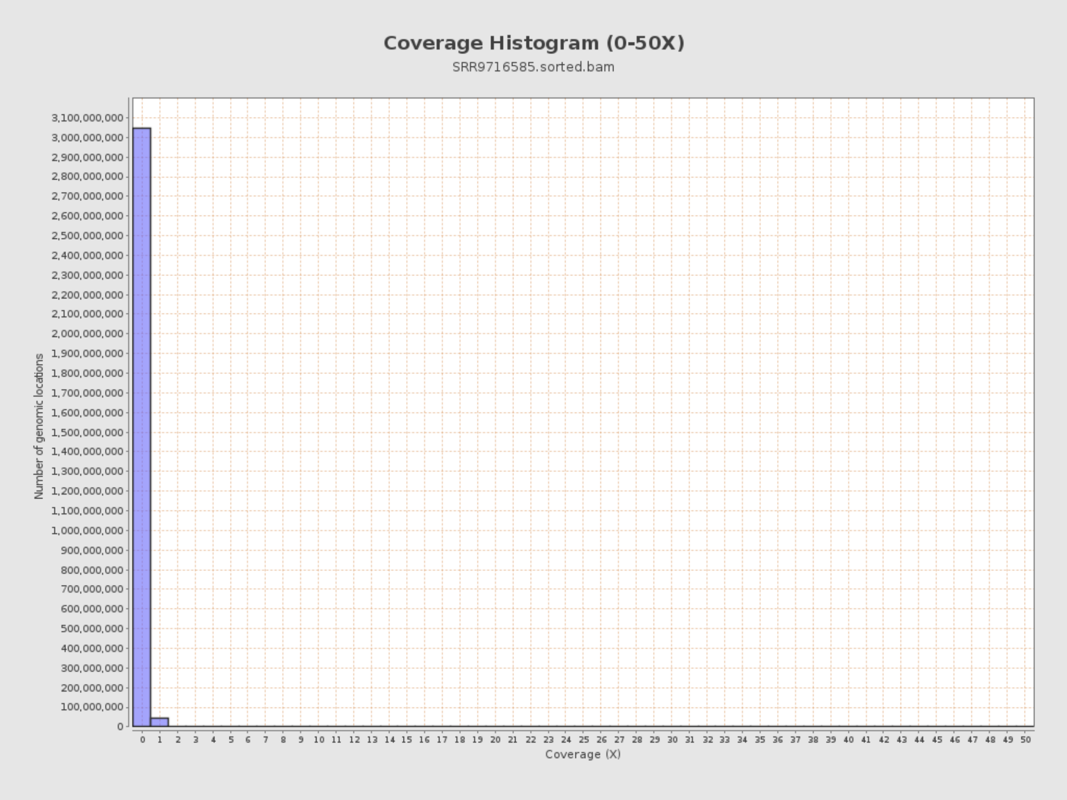
3. Results : Coverage across reference



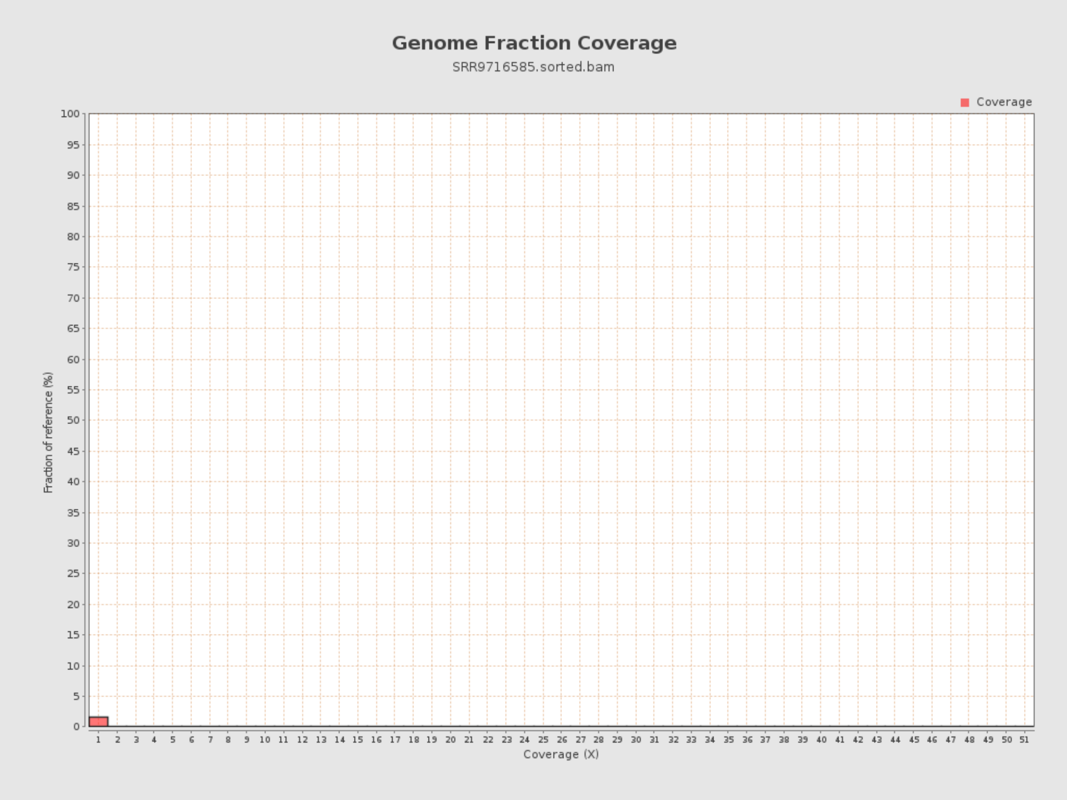
4. Results : Coverage Histogram



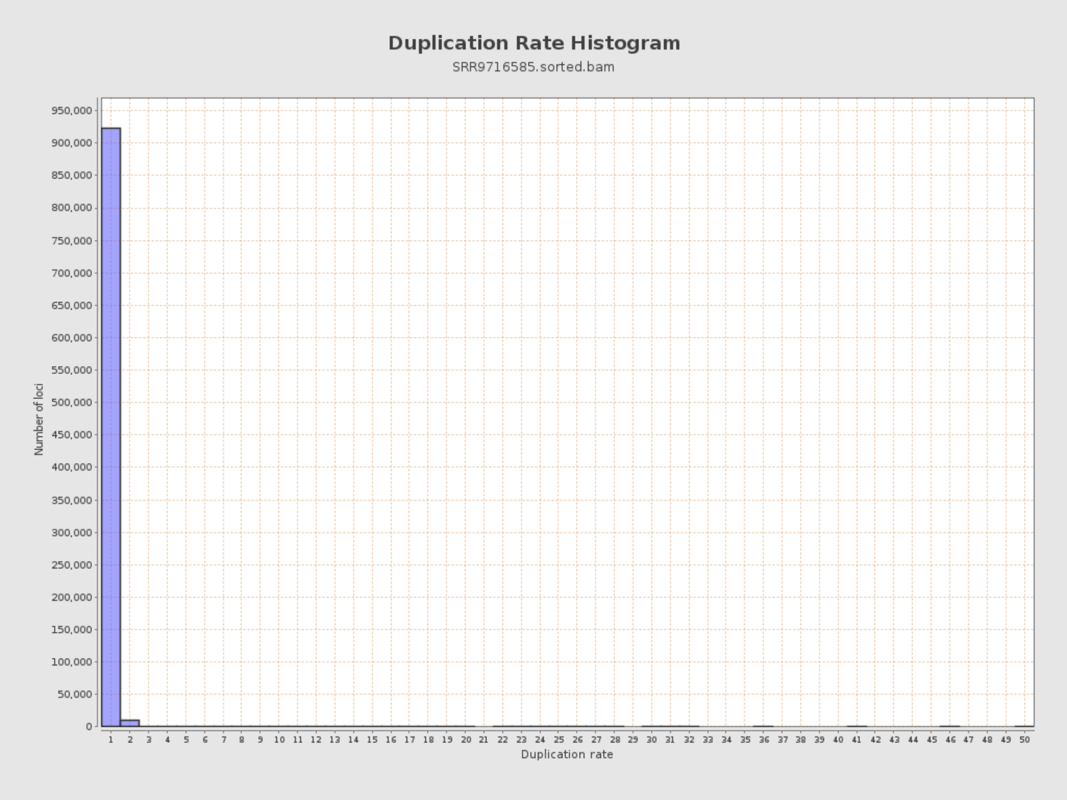
5. Results : Coverage Histogram (0-50X)



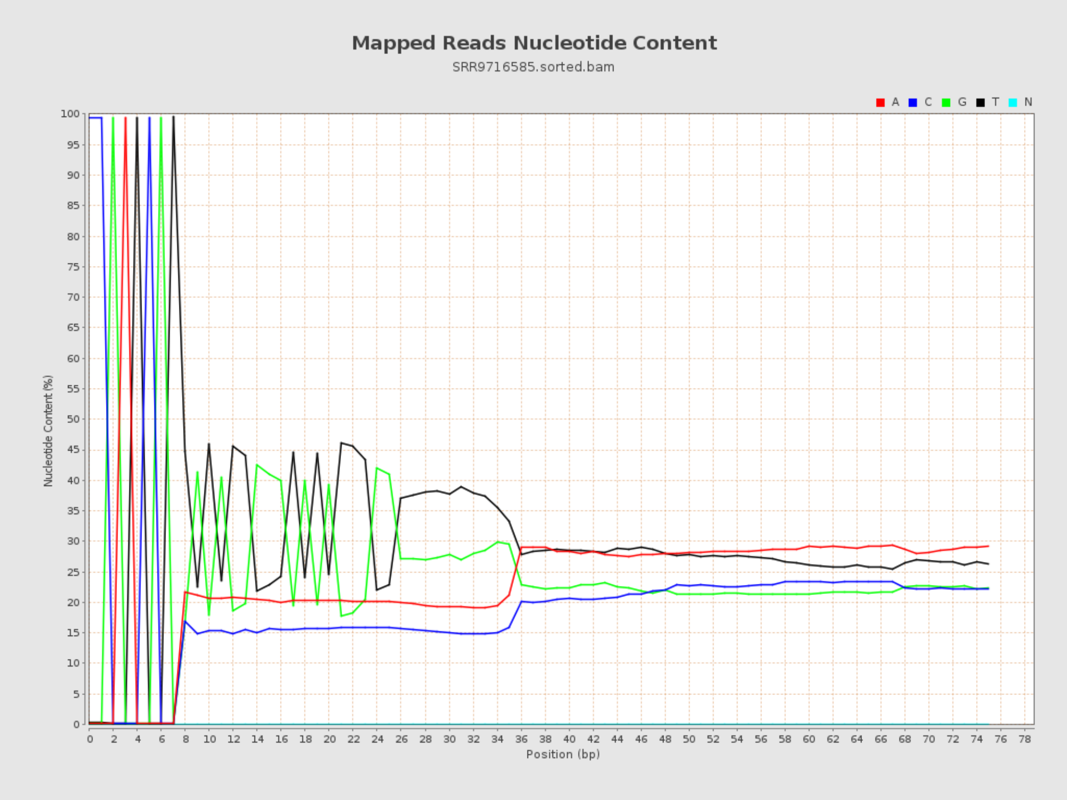
6. Results : Genome Fraction Coverage



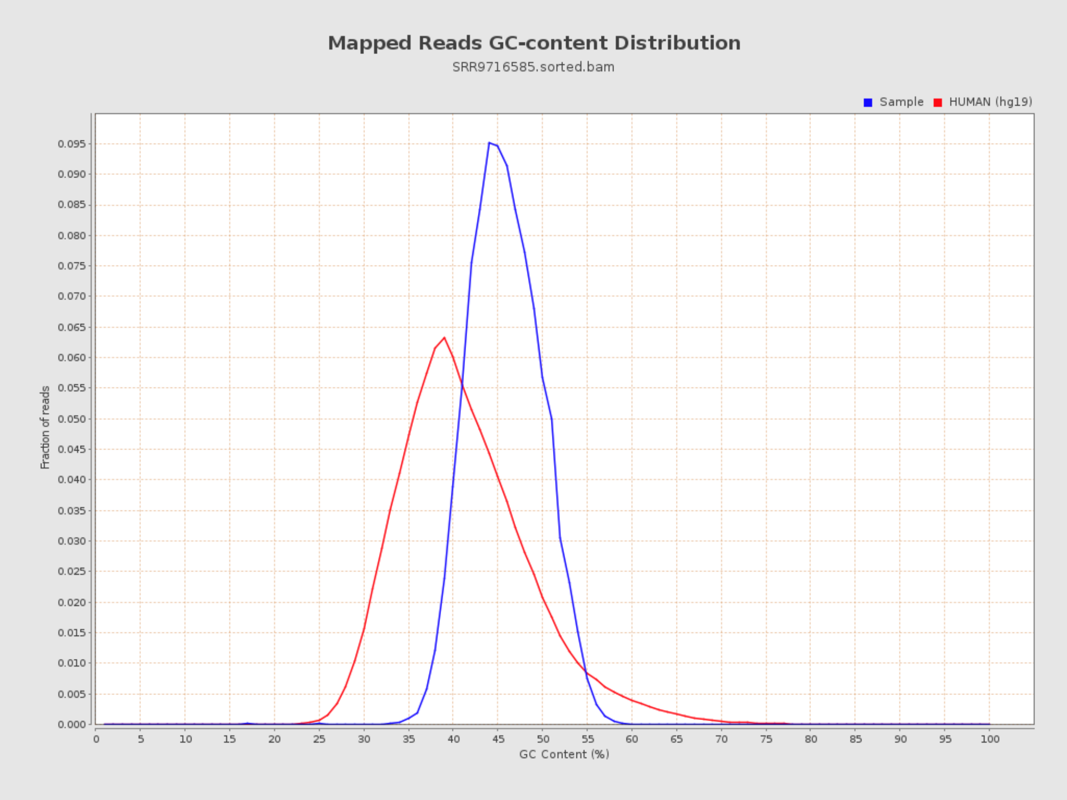
7. Results : Duplication Rate Histogram



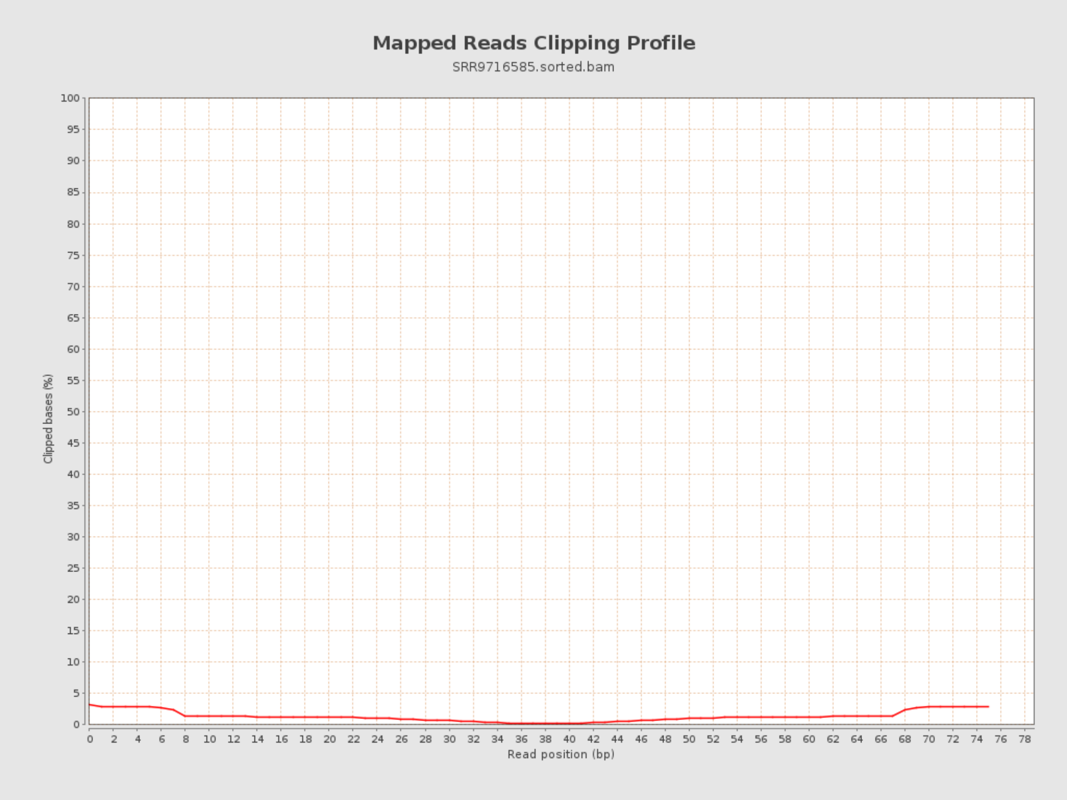
8. Results : Mapped Reads Nucleotide Content



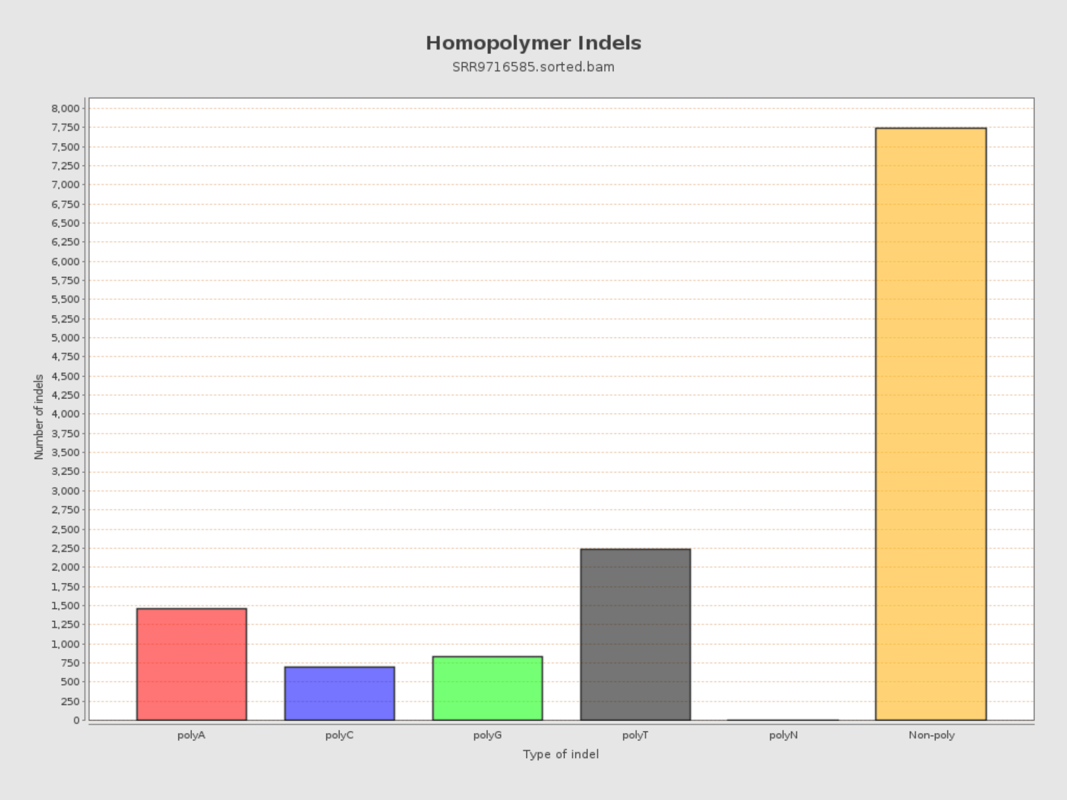
9. Results : Mapped Reads GC-content Distribution



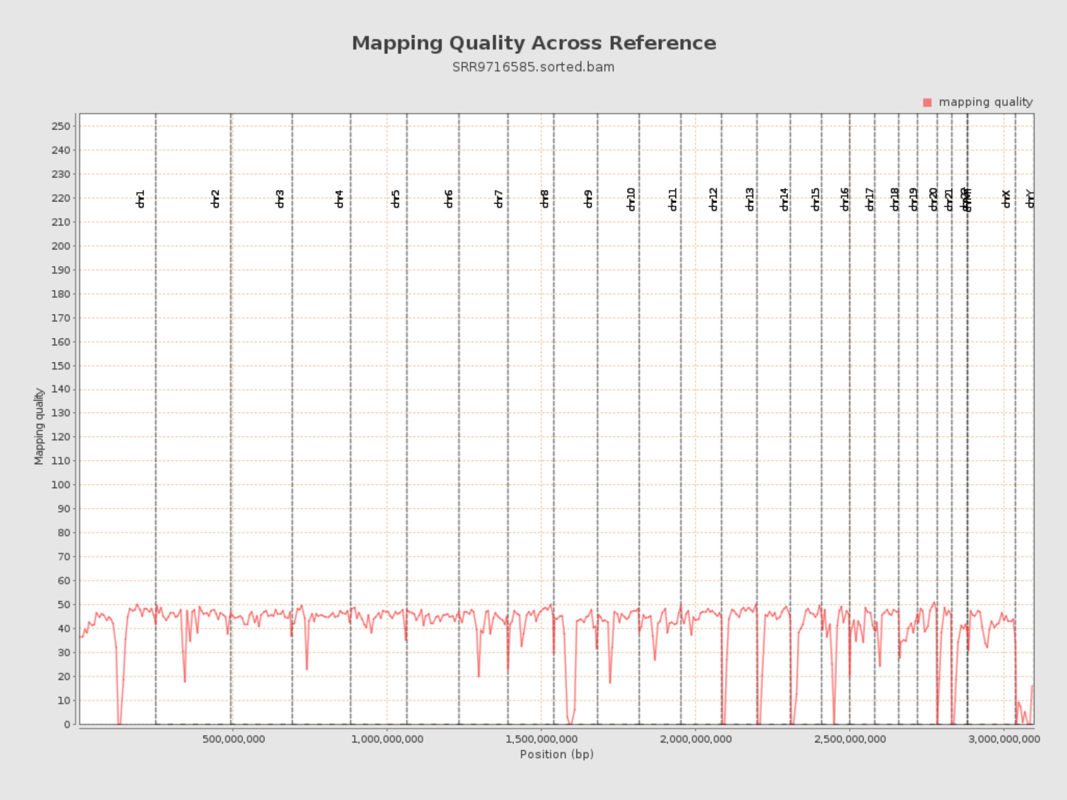
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram