Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 10:47:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716767.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_SRR9716767 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716767.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 10:47:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716767.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,297,960
Mapped reads	1,153,860 / 88.9%
Unmapped reads	144,100 / 11.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,140 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	24,670 / 1.9%
Duplication rate	1.47%
Clipped reads	1,157,388 / 89.17%

2.2. ACGT Content

Number/percentage of A's	16,433,920 / 24.92%
Number/percentage of C's	13,950,153 / 21.15%
Number/percentage of T's	19,625,315 / 29.76%
Number/percentage of G's	15,936,350 / 24.17%
Number/percentage of N's	539 / 0%
GC Percentage	45.32%

2.3. Coverage

Mean	0.0213

Standard Deviation	0.1939

2.4. Mapping Quality

Mean Mapping Quality	41.91

2.5. Mismatches and indels

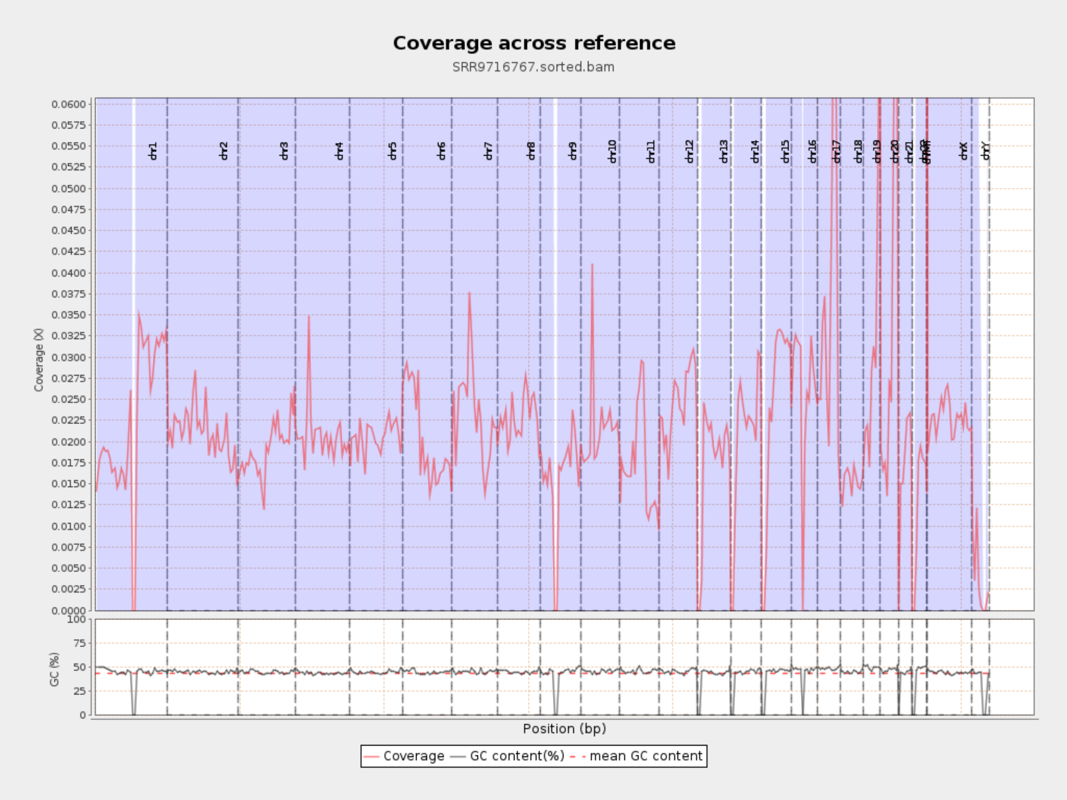
General error rate	0.52%
Mismatches	334,118
Insertions	4,583
Mapped reads with at least one insertion	0.4%
Deletions	12,147
Mapped reads with at least one deletion	1.05%
Homopolymer indels	41.98%

2.6. Chromosome stats

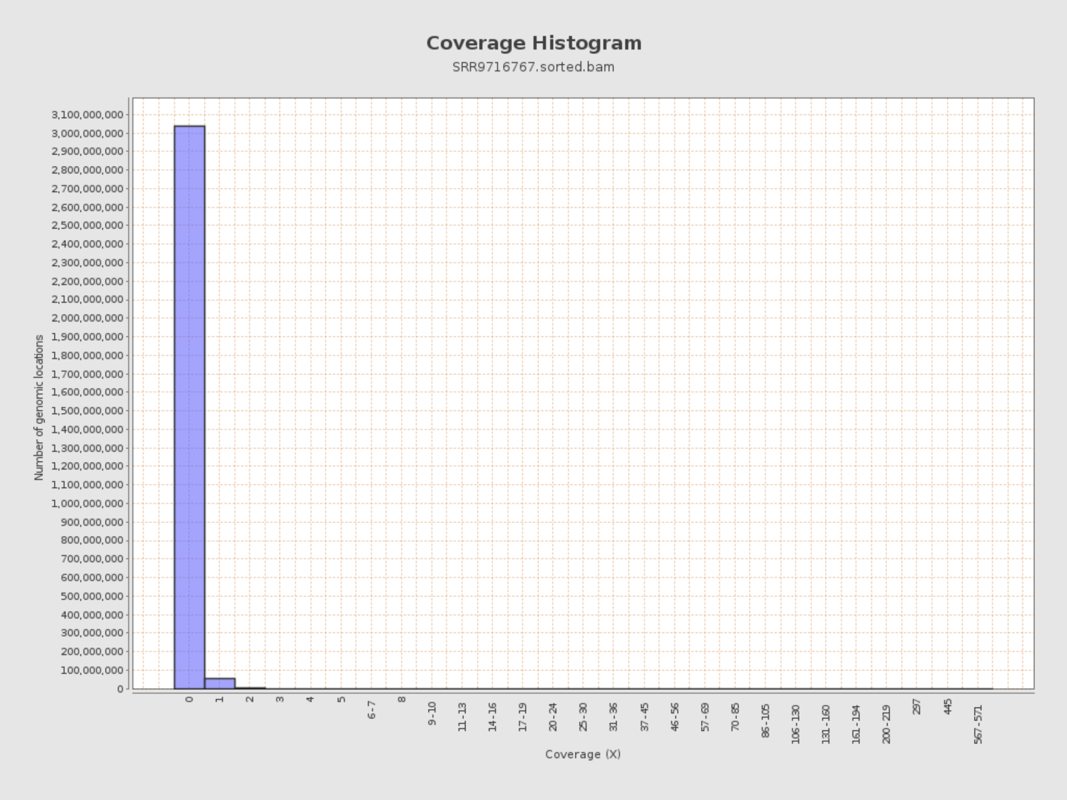
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5566809	0.0223	0.2302
chr2	243199373	5125561	0.0211	0.2795
chr3	198022430	3764902	0.019	0.1493
chr4	191154276	3977706	0.0208	0.1669
chr5	180915260	3743474	0.0207	0.1522
chr6	171115067	3495357	0.0204	0.175
chr7	159138663	3737015	0.0235	0.2642

chr8	146364022	3342341	0.0228	0.1809
chr9	141213431	2212761	0.0157	0.1505
chr10	135534747	2928068	0.0216	0.2295
chr11	135006516	2365864	0.0175	0.1677
chr12	133851895	3277621	0.0245	0.1679
chr13	115169878	1971538	0.0171	0.1393
chr14	107349540	2206874	0.0206	0.1572
chr15	102531392	2462017	0.024	0.1695
chr16	90354753	2322274	0.0257	0.1824
chr17	81195210	2996516	0.0369	0.2135
chr18	78077248	1186127	0.0152	0.2127
chr19	59128983	1880987	0.0318	0.241
chr20	63025520	2168525	0.0344	0.2066
chr21	48129895	834660	0.0173	0.1483
chr22	51304566	643294	0.0125	0.1202
chrMT	16571	4620	0.2788	0.5643
chrX	155270560	3539313	0.0228	0.1683
chrY	59373566	211661	0.0036	0.1078

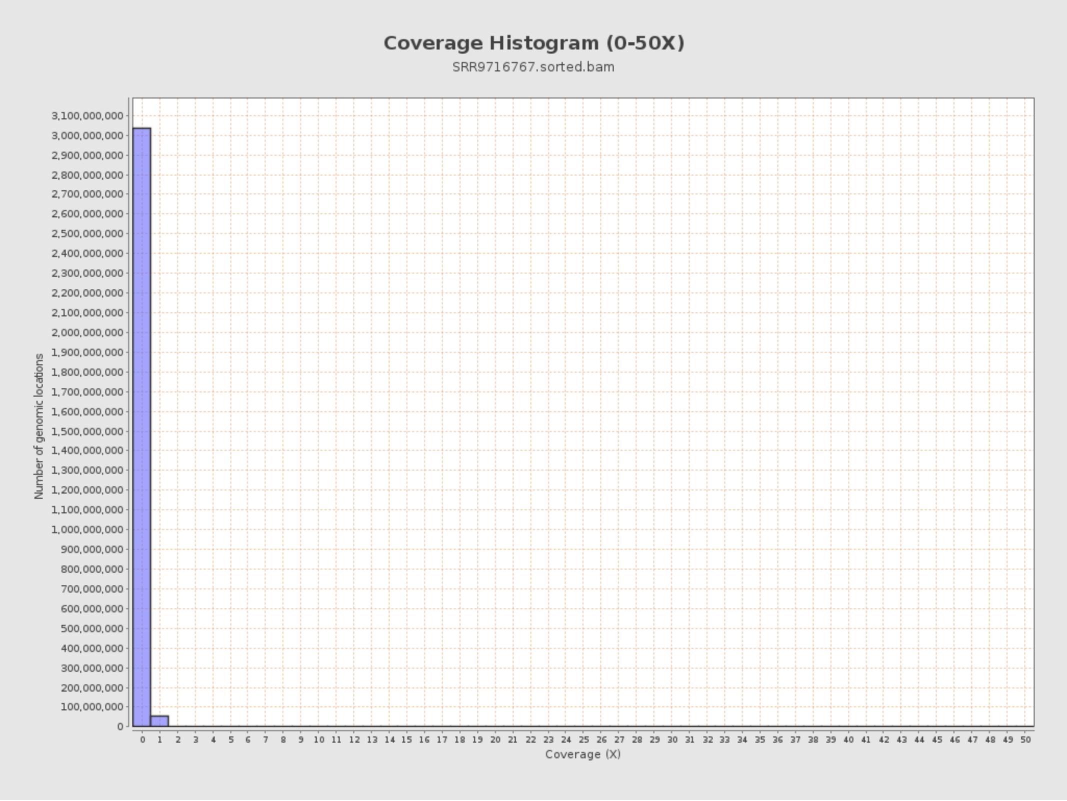
3. Results : Coverage across reference



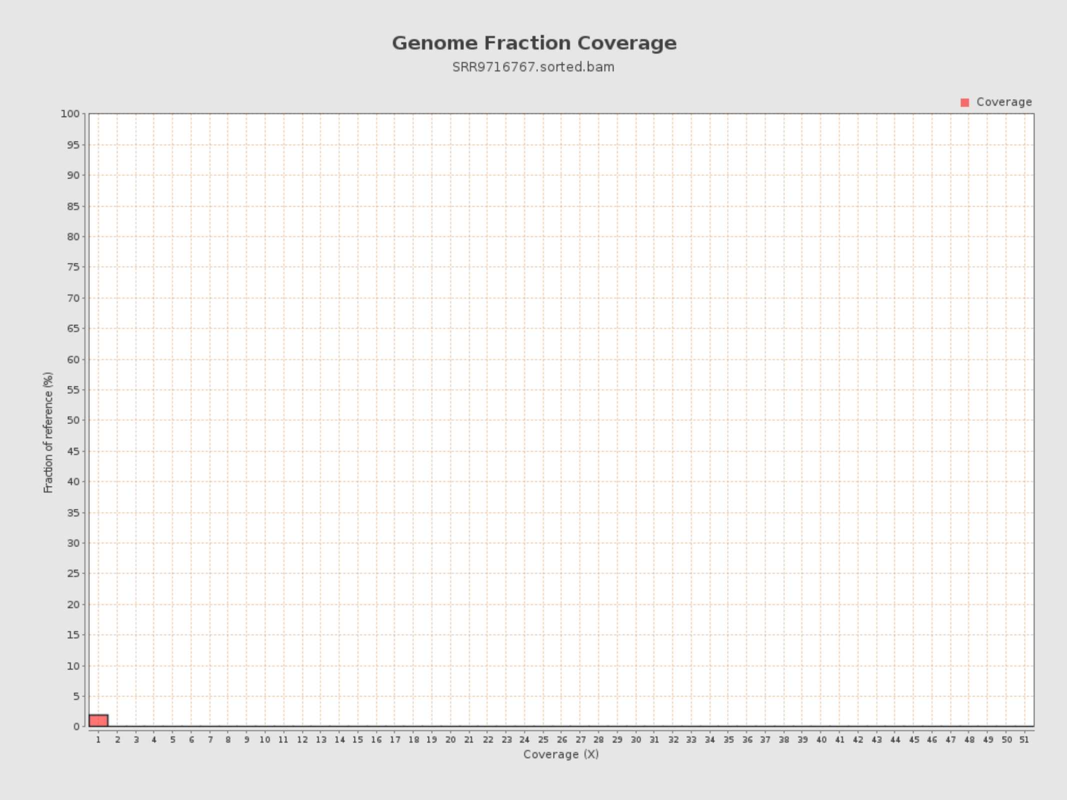
4. Results : Coverage Histogram



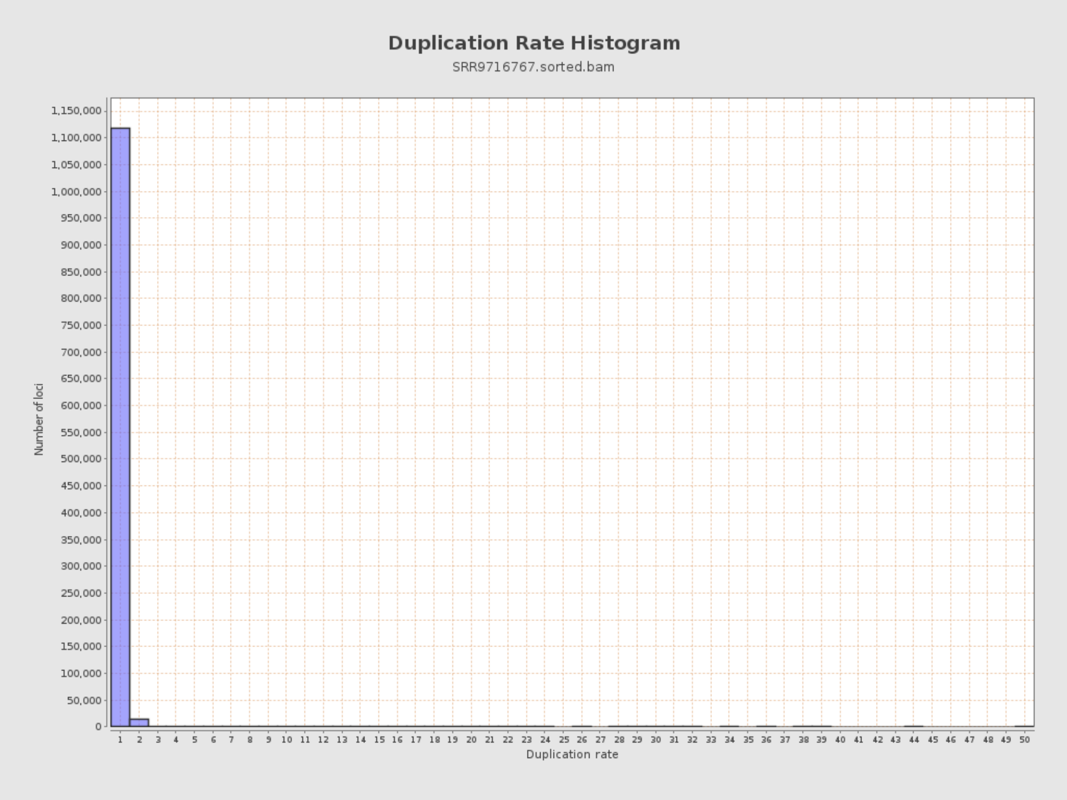
5. Results : Coverage Histogram (0-50X)



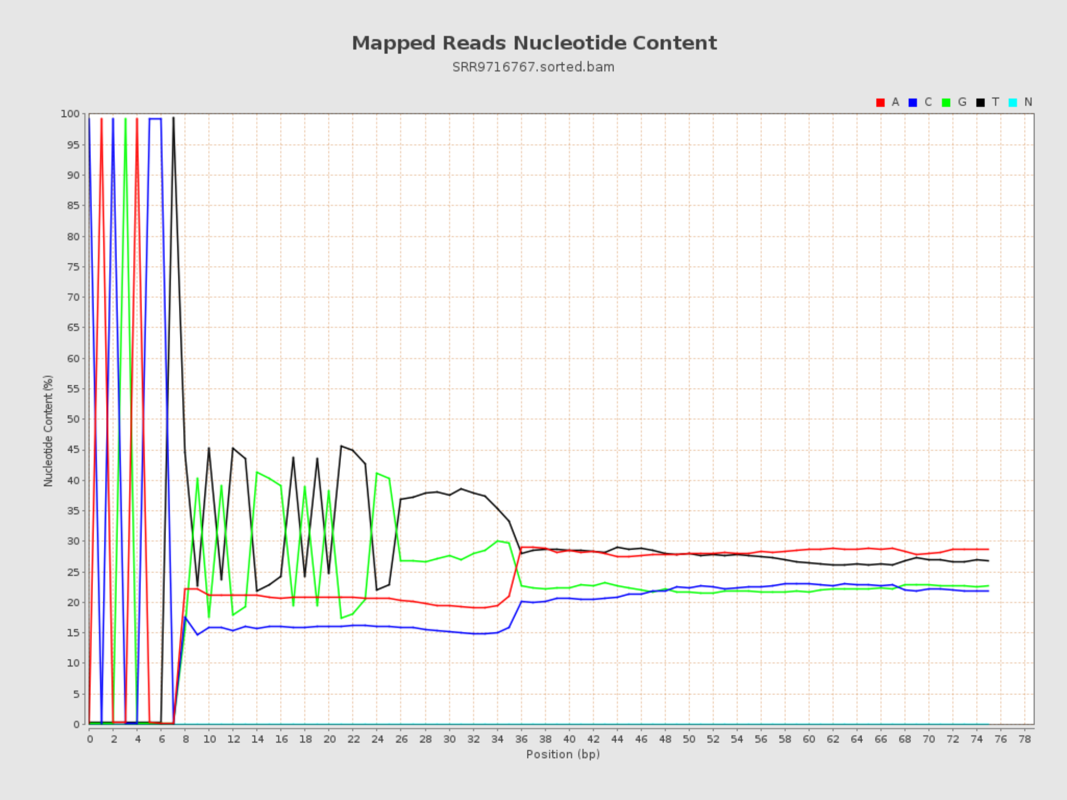
6. Results : Genome Fraction Coverage



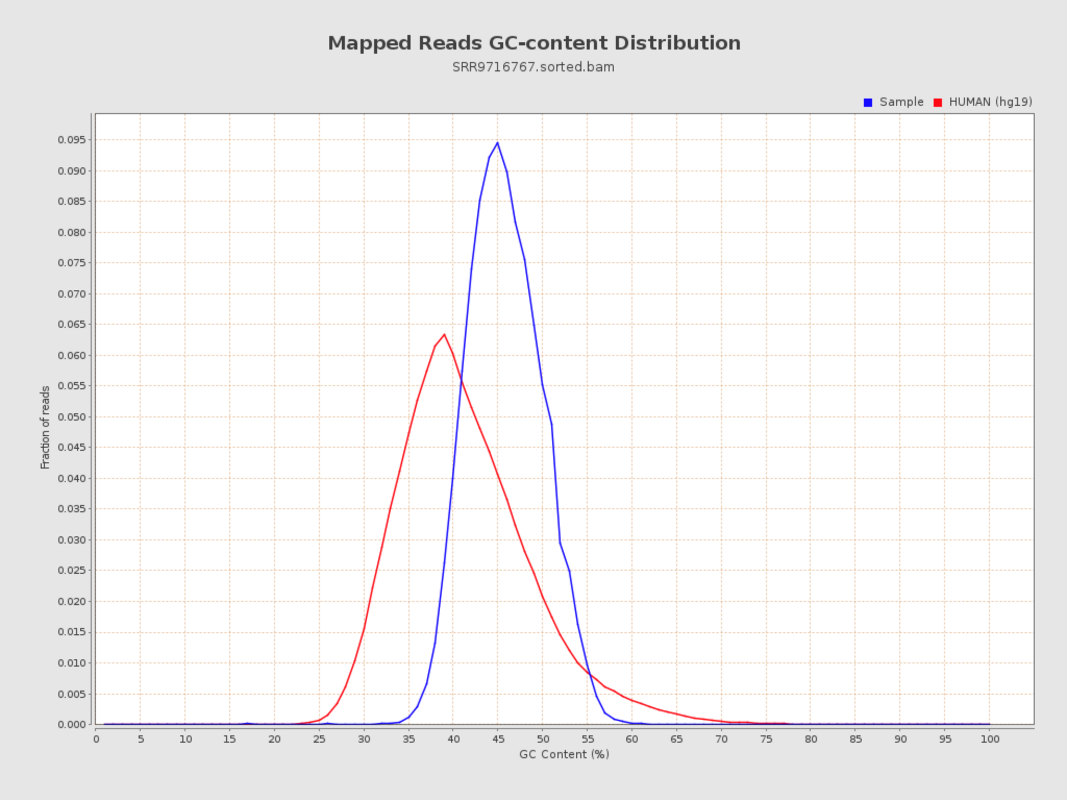
7. Results : Duplication Rate Histogram



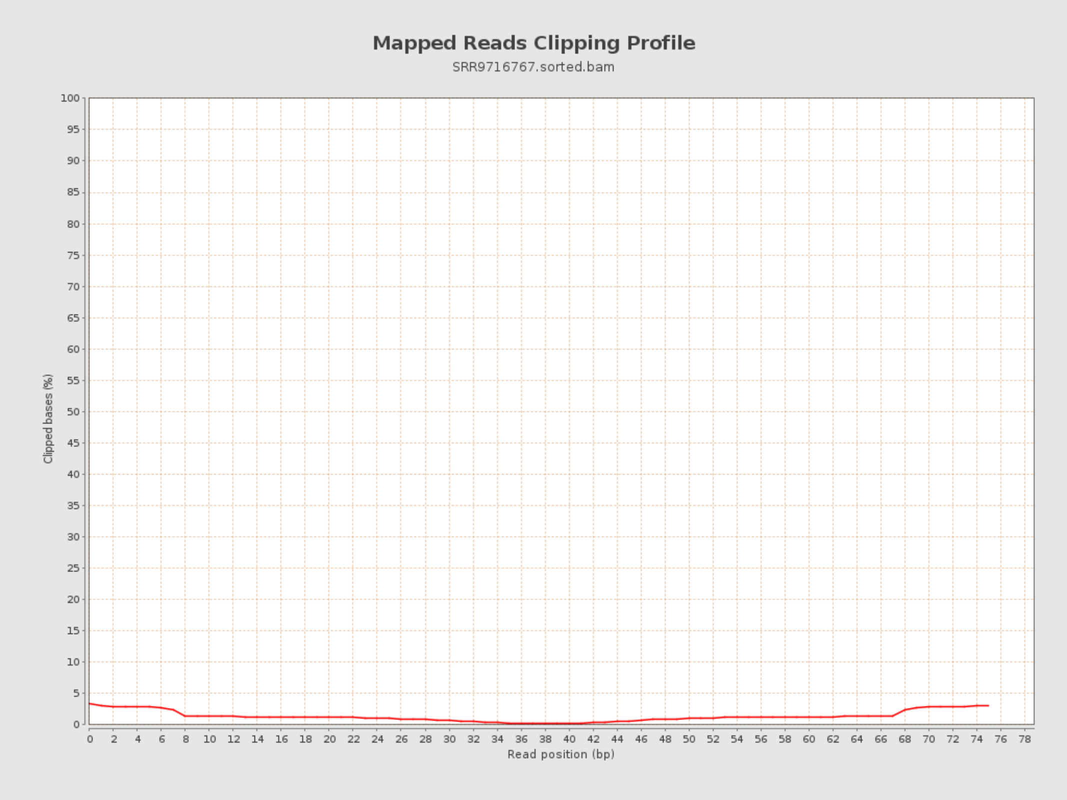
8. Results : Mapped Reads Nucleotide Content



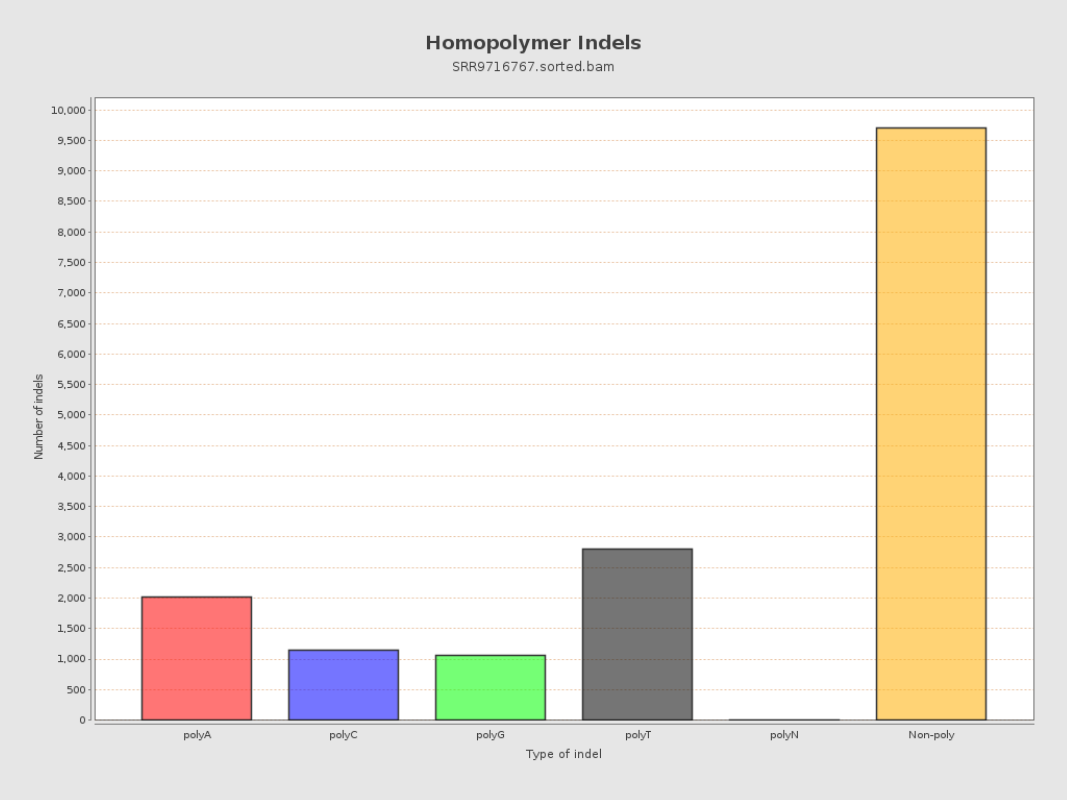
9. Results : Mapped Reads GC-content Distribution



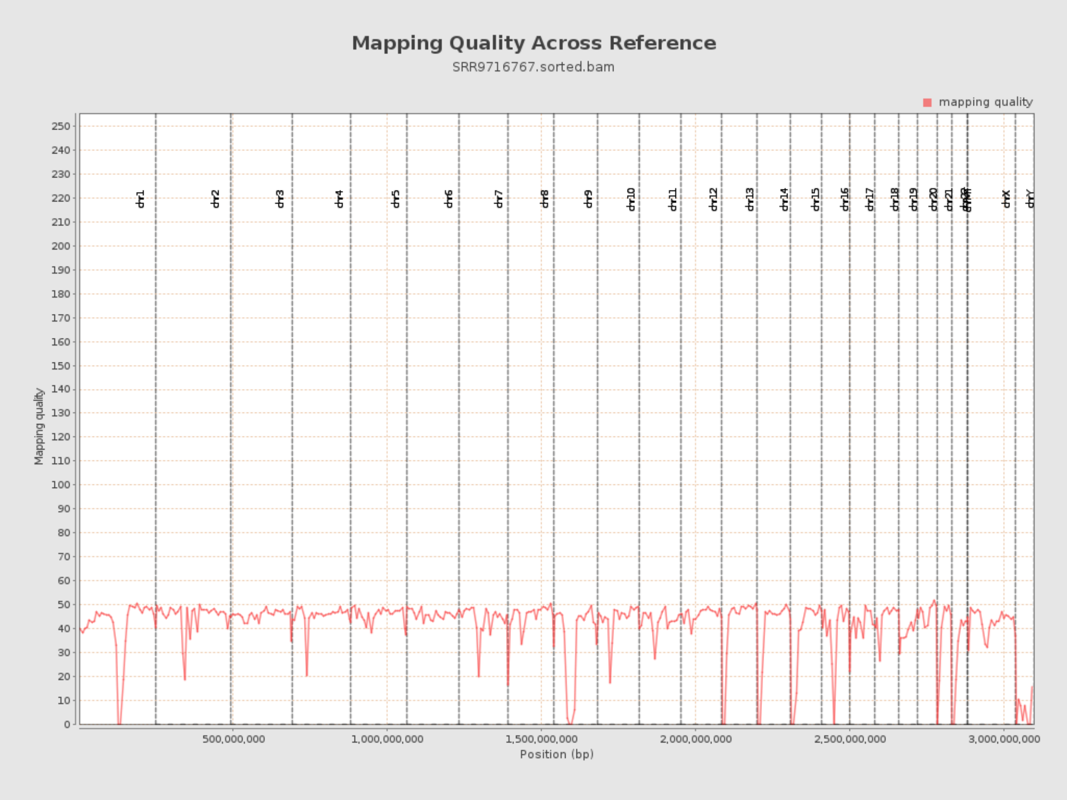
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram