Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 18:31:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716524.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_SRR9716524 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716524.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 18:31:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716524.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,855,305
Mapped reads	1,657,692 / 89.35%
Unmapped reads	197,613 / 10.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,414 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	46,040 / 2.48%
Duplication rate	2.11%
Clipped reads	1,660,378 / 89.49%

2.2. ACGT Content

Number/percentage of A's	22,970,998 / 24.4%
Number/percentage of C's	18,911,522 / 20.09%
Number/percentage of T's	30,312,462 / 32.2%
Number/percentage of G's	21,950,544 / 23.32%
Number/percentage of N's	2,066 / 0%
GC Percentage	43.4%

2.3. Coverage

Mean	0.0304

Standard Deviation	0.2366

2.4. Mapping Quality

Mean Mapping Quality	43.88

2.5. Mismatches and indels

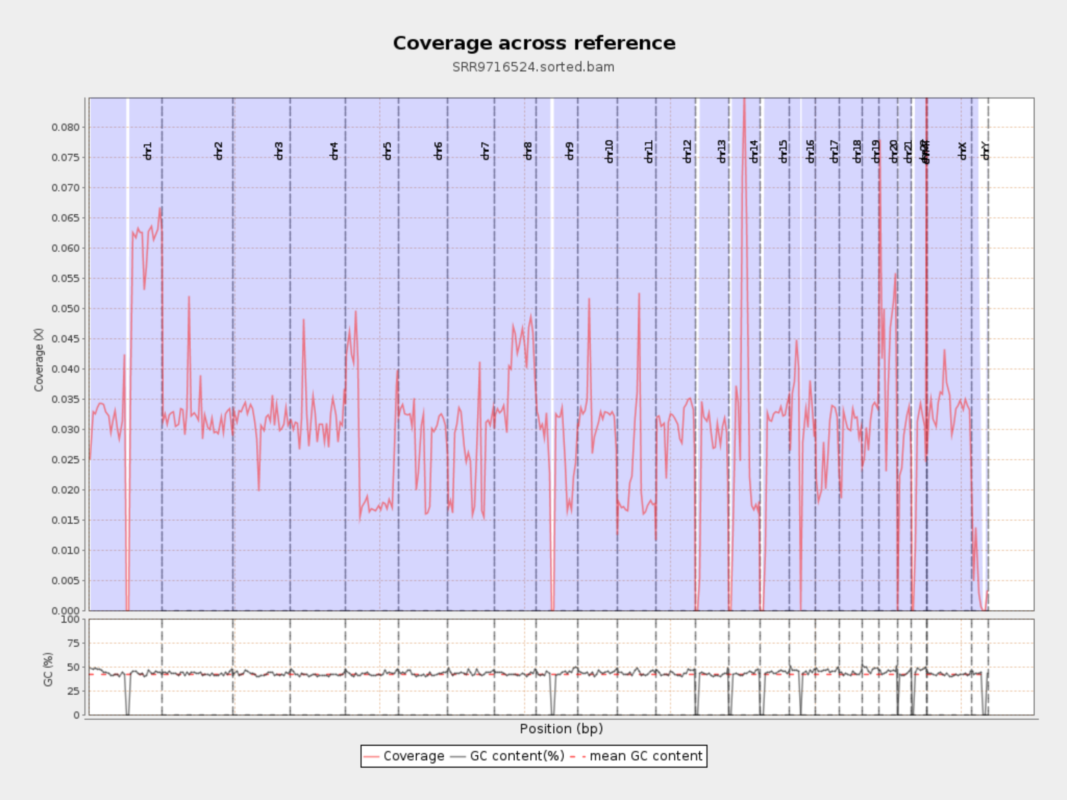
General error rate	0.51%
Mismatches	466,297
Insertions	5,584
Mapped reads with at least one insertion	0.34%
Deletions	14,733
Mapped reads with at least one deletion	0.88%
Homopolymer indels	40.97%

2.6. Chromosome stats

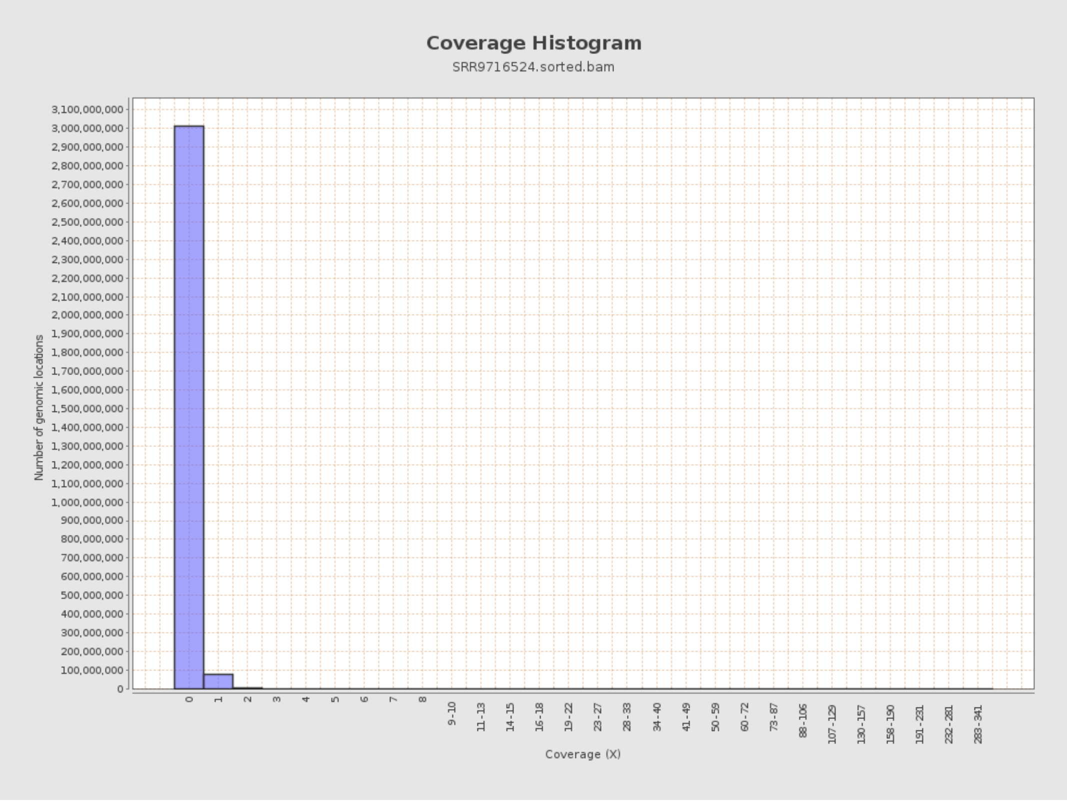
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10629110	0.0426	0.3393
chr2	243199373	7876938	0.0324	0.275
chr3	198022430	6250768	0.0316	0.1948
chr4	191154276	6049283	0.0316	0.2094
chr5	180915260	4643472	0.0257	0.177
chr6	171115067	4930503	0.0288	0.1957
chr7	159138663	4122740	0.0259	0.2071

chr8	146364022	5896713	0.0403	0.249
chr9	141213431	3392302	0.024	0.2446
chr10	135534747	4438700	0.0327	0.2696
chr11	135006516	2922908	0.0217	0.2161
chr12	133851895	4188183	0.0313	0.1955
chr13	115169878	2904794	0.0252	0.1715
chr14	107349540	3299903	0.0307	0.2057
chr15	102531392	2704679	0.0264	0.177
chr16	90354753	2860147	0.0317	0.2143
chr17	81195210	2146498	0.0264	0.185
chr18	78077248	2312145	0.0296	0.4261
chr19	59128983	1821265	0.0308	0.2788
chr20	63025520	2924556	0.0464	0.2416
chr21	48129895	1222347	0.0254	0.1946
chr22	51304566	1121369	0.0219	0.1609
chrMT	16571	2018	0.1218	0.3693
chrX	155270560	5243088	0.0338	0.2262
chrY	59373566	267790	0.0045	0.1065

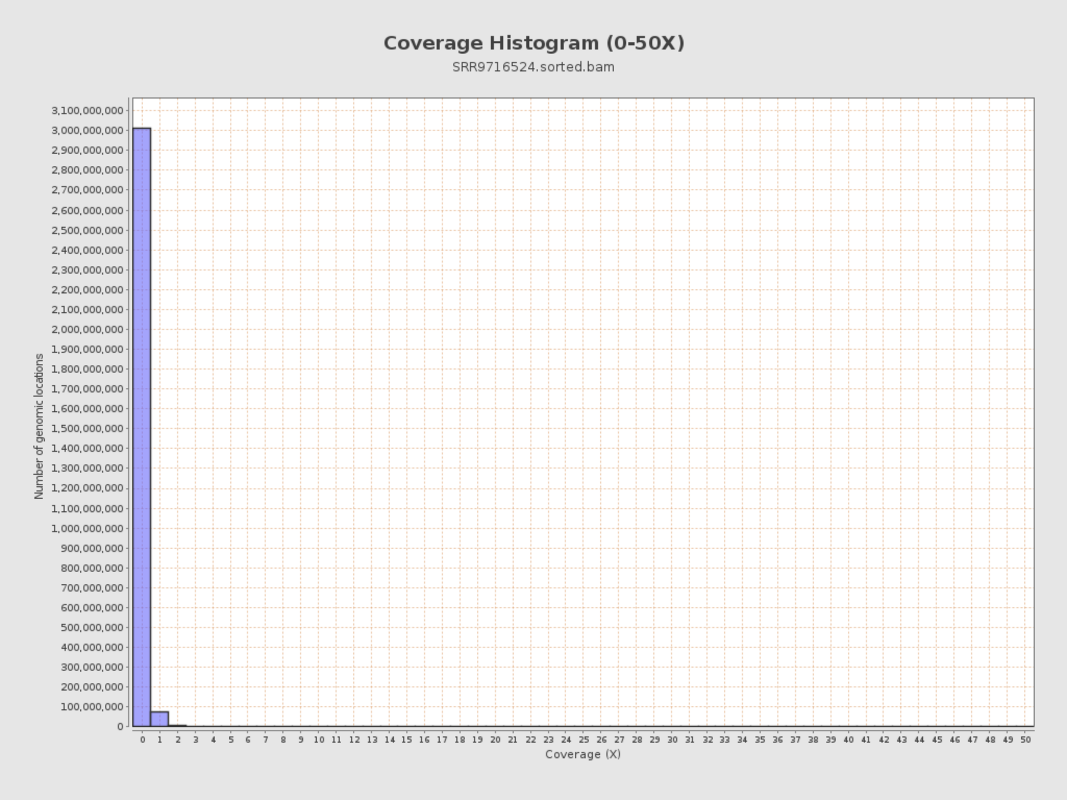
3. Results : Coverage across reference



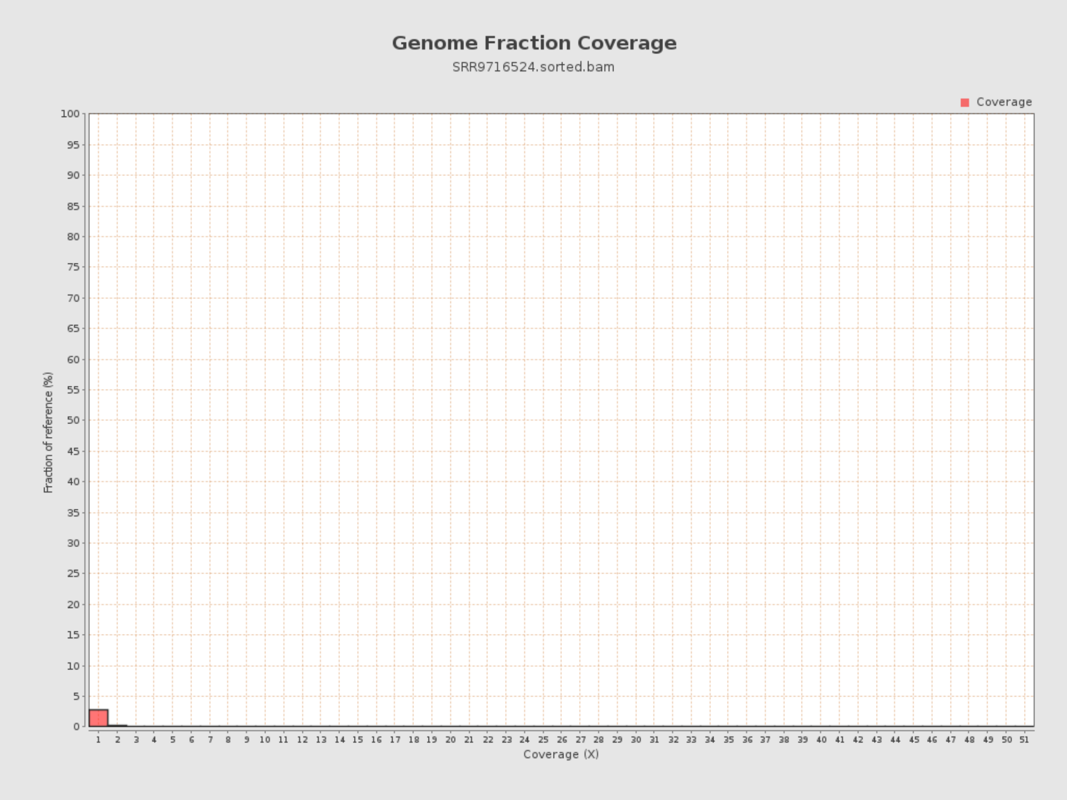
4. Results : Coverage Histogram



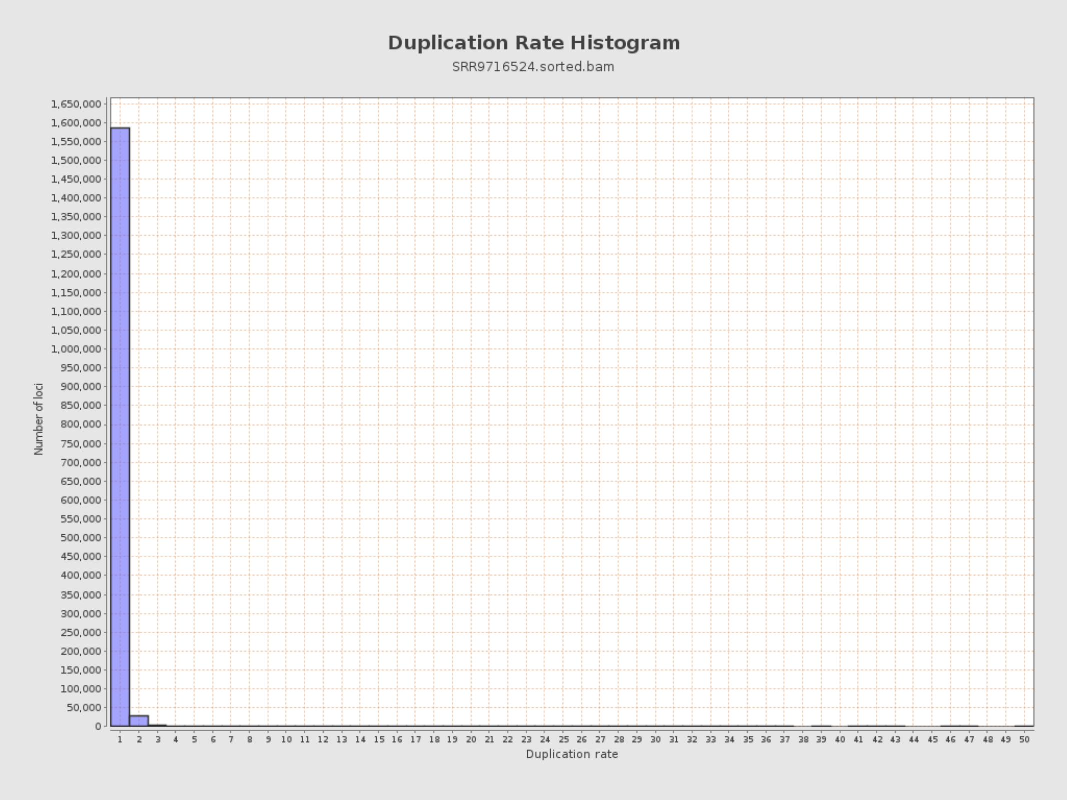
5. Results : Coverage Histogram (0-50X)



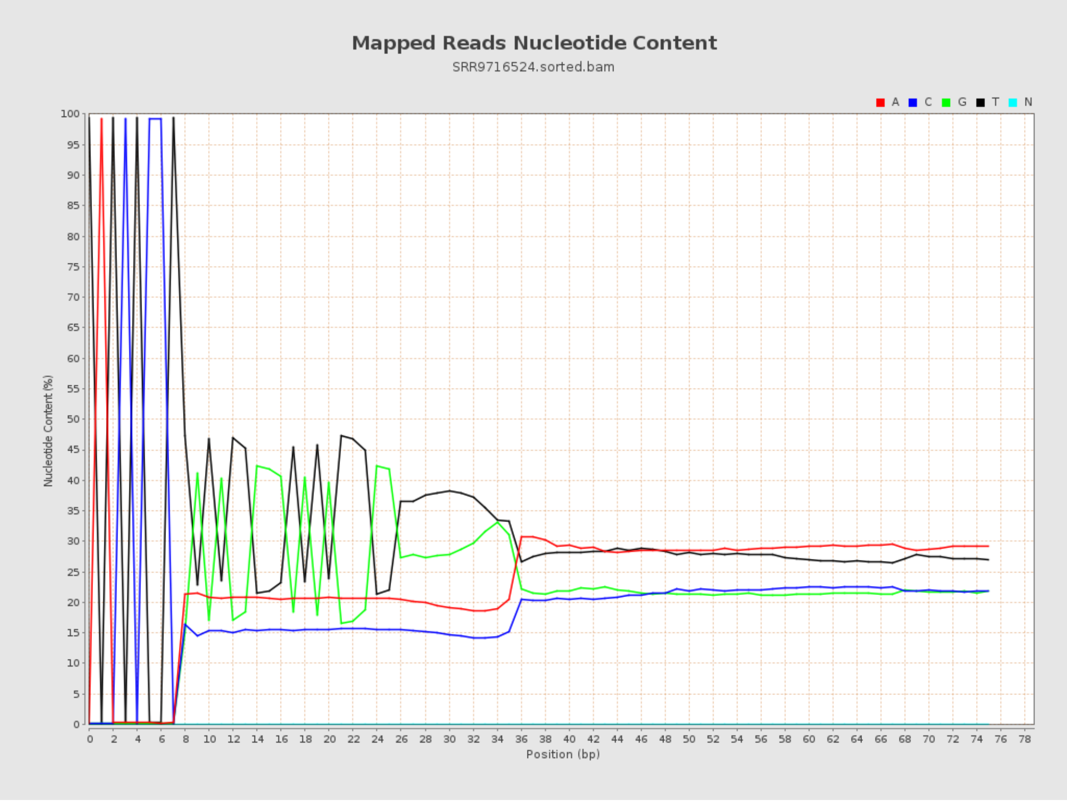
6. Results : Genome Fraction Coverage



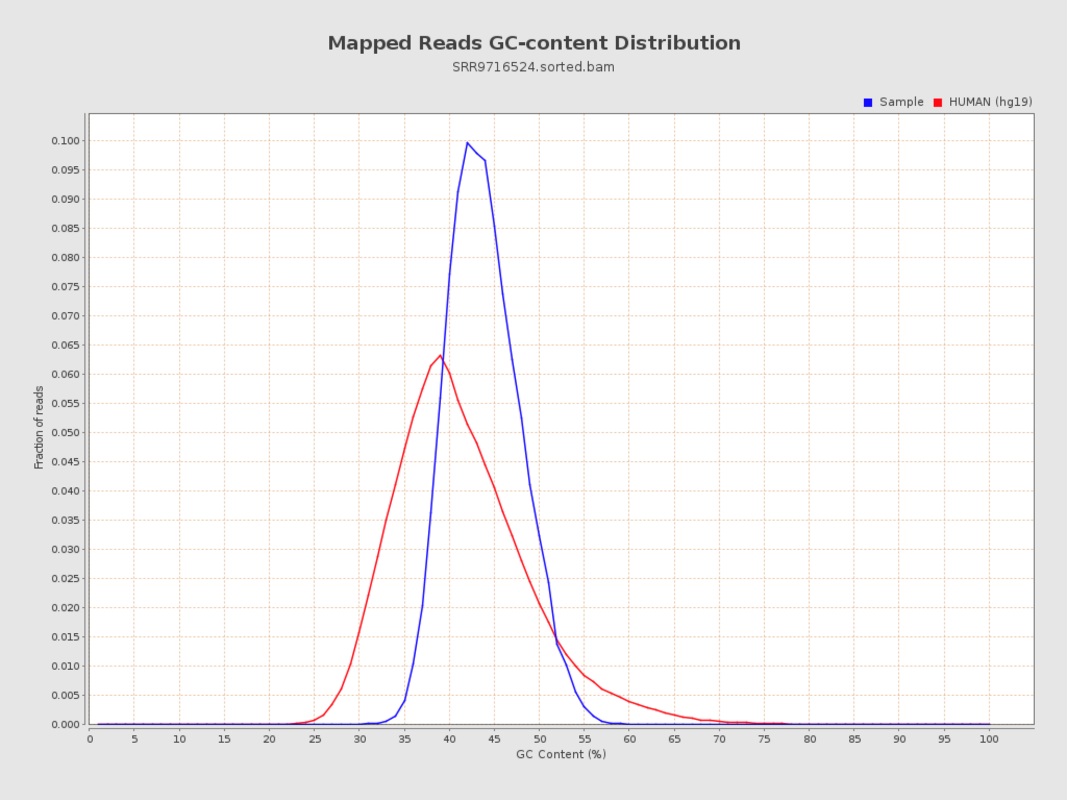
7. Results : Duplication Rate Histogram



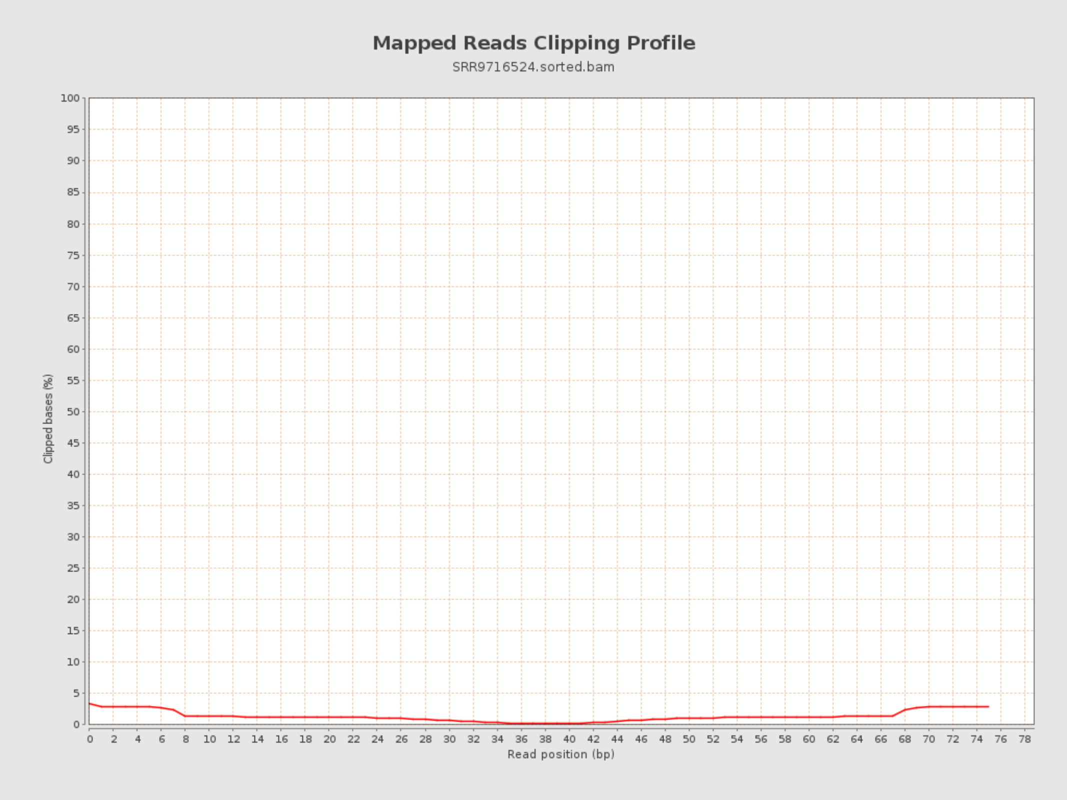
8. Results : Mapped Reads Nucleotide Content



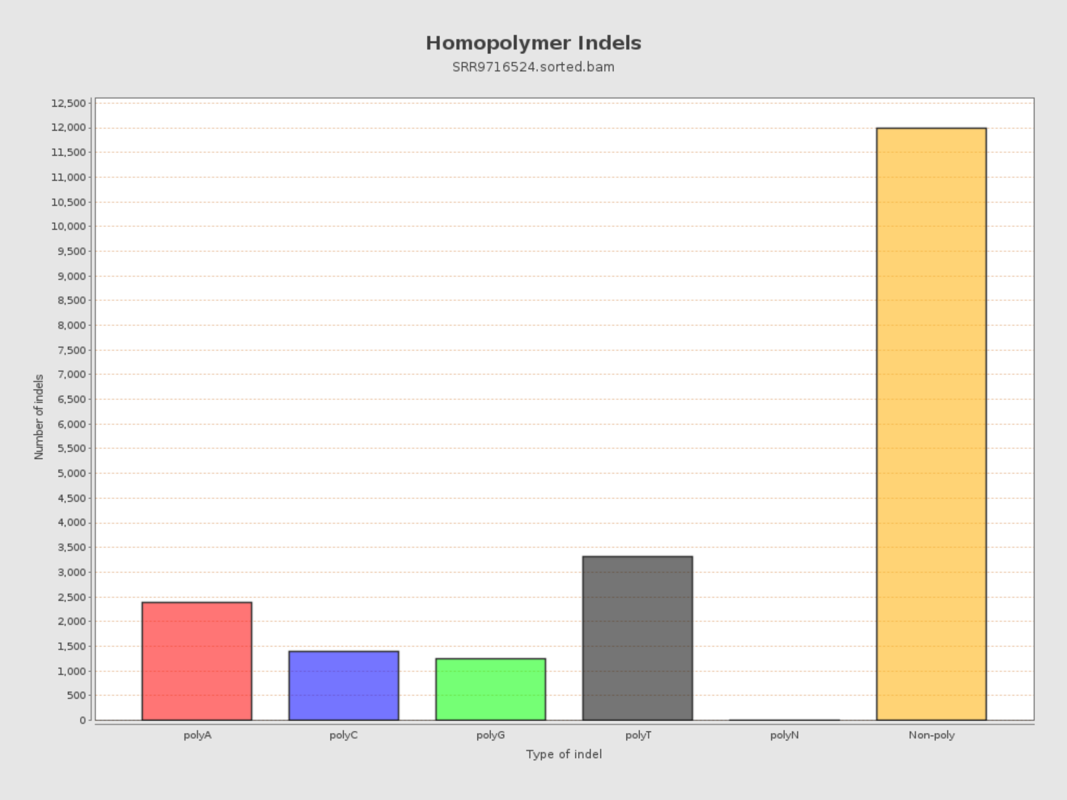
9. Results : Mapped Reads GC-content Distribution



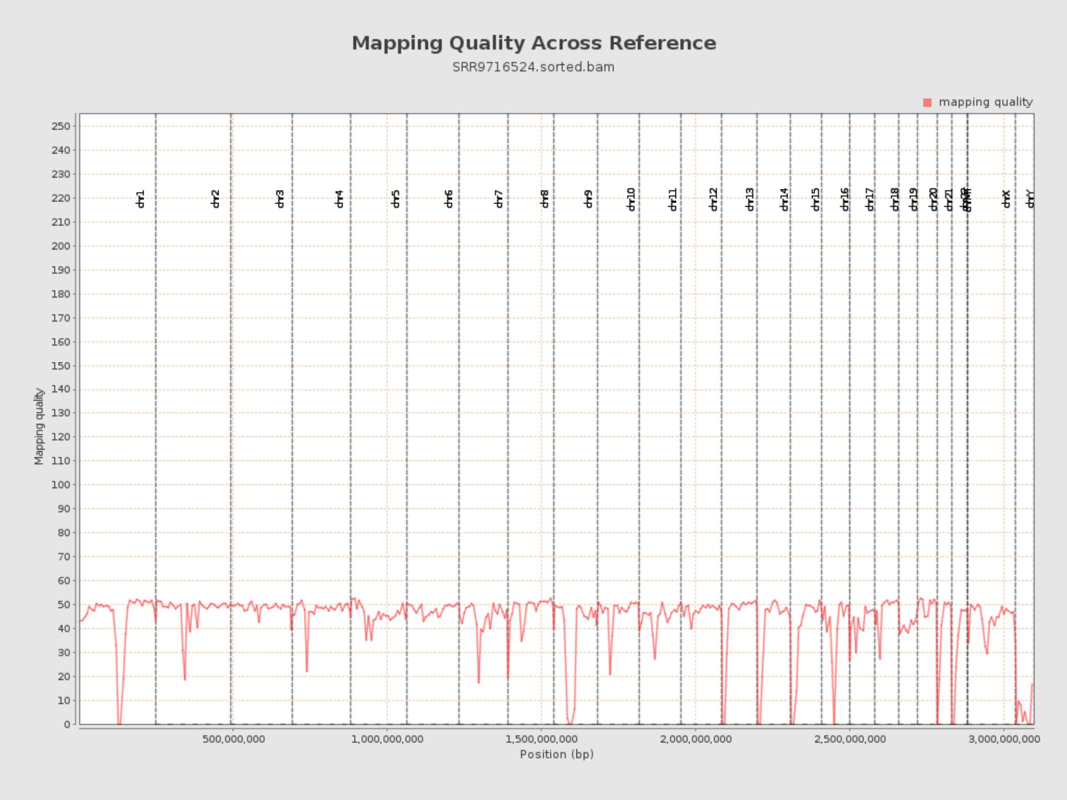
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram