Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 23:38:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716999.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_SRR9716999 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716999.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 23:38:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716999.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,446,318
Mapped reads	1,291,081 / 89.27%
Unmapped reads	155,237 / 10.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,309 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	43,332 / 3%
Duplication rate	2.48%
Clipped reads	1,295,180 / 89.55%

2.2. ACGT Content

Number/percentage of A's	19,545,676 / 26.33%
Number/percentage of C's	13,828,920 / 18.63%
Number/percentage of T's	23,629,659 / 31.83%
Number/percentage of G's	17,220,749 / 23.2%
Number/percentage of N's	1,190 / 0%
GC Percentage	41.83%

2.3. Coverage

Mean	0.024

Standard Deviation	0.2417

2.4. Mapping Quality

Mean Mapping Quality	44.08

2.5. Mismatches and indels

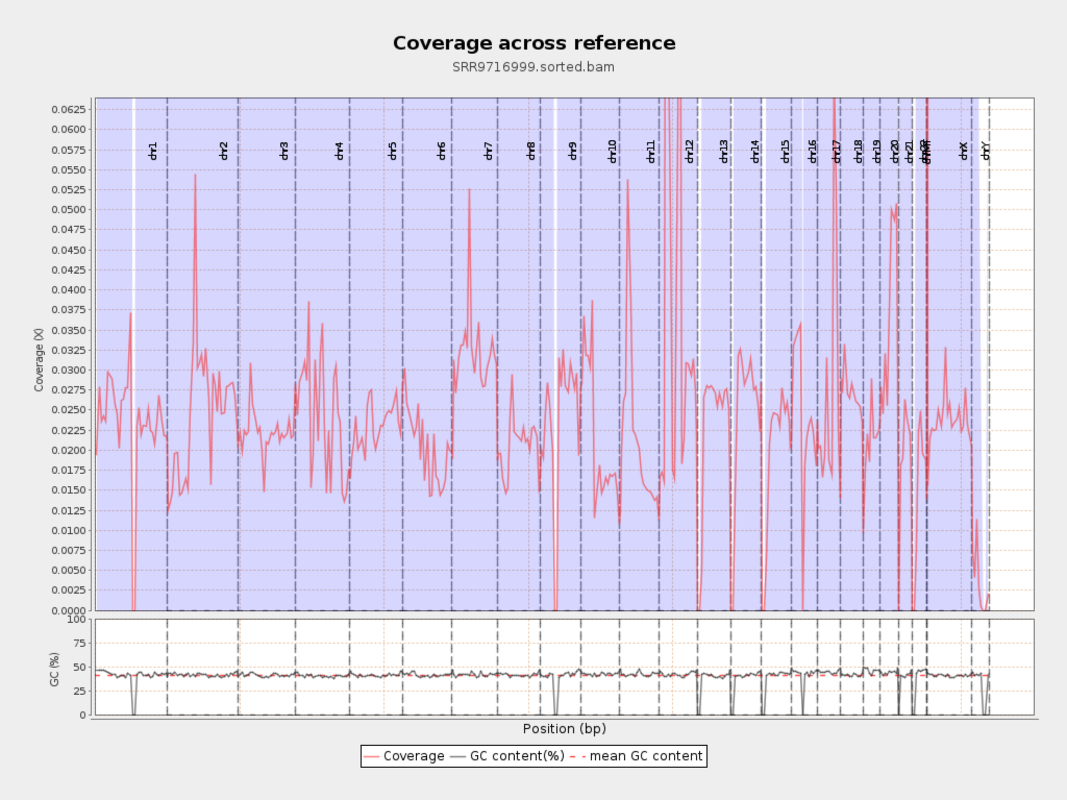
General error rate	0.55%
Mismatches	397,556
Insertions	4,600
Mapped reads with at least one insertion	0.36%
Deletions	11,920
Mapped reads with at least one deletion	0.92%
Homopolymer indels	42.23%

2.6. Chromosome stats

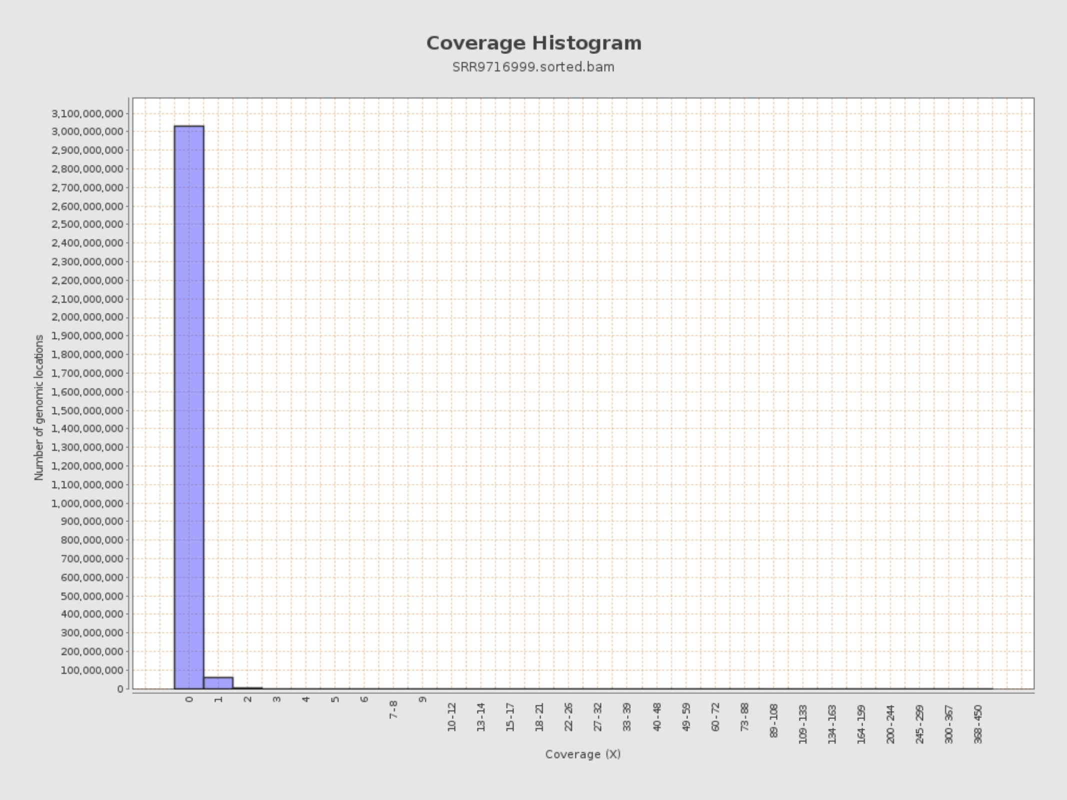
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5817103	0.0233	0.3798
chr2	243199373	6029895	0.0248	0.2767
chr3	198022430	4392906	0.0222	0.1594
chr4	191154276	4635620	0.0243	0.1792
chr5	180915260	4180814	0.0231	0.1645
chr6	171115067	3513284	0.0205	0.1684
chr7	159138663	5123185	0.0322	0.3625

chr8	146364022	3038913	0.0208	0.2278
chr9	141213431	3313251	0.0235	0.2502
chr10	135534747	2887018	0.0213	0.2351
chr11	135006516	2920931	0.0216	0.2089
chr12	133851895	5493317	0.041	0.2391
chr13	115169878	2574833	0.0224	0.1591
chr14	107349540	2589570	0.0241	0.1936
chr15	102531392	1988144	0.0194	0.1499
chr16	90354753	2159634	0.0239	0.1806
chr17	81195210	2279071	0.0281	0.1861
chr18	78077248	2125493	0.0272	0.4412
chr19	59128983	1260324	0.0213	0.3011
chr20	63025520	2338390	0.0371	0.2142
chr21	48129895	924792	0.0192	0.1643
chr22	51304566	749820	0.0146	0.1277
chrMT	16571	12019	0.7253	1.0064
chrX	155270560	3698295	0.0238	0.1933
chrY	59373566	199607	0.0034	0.0831

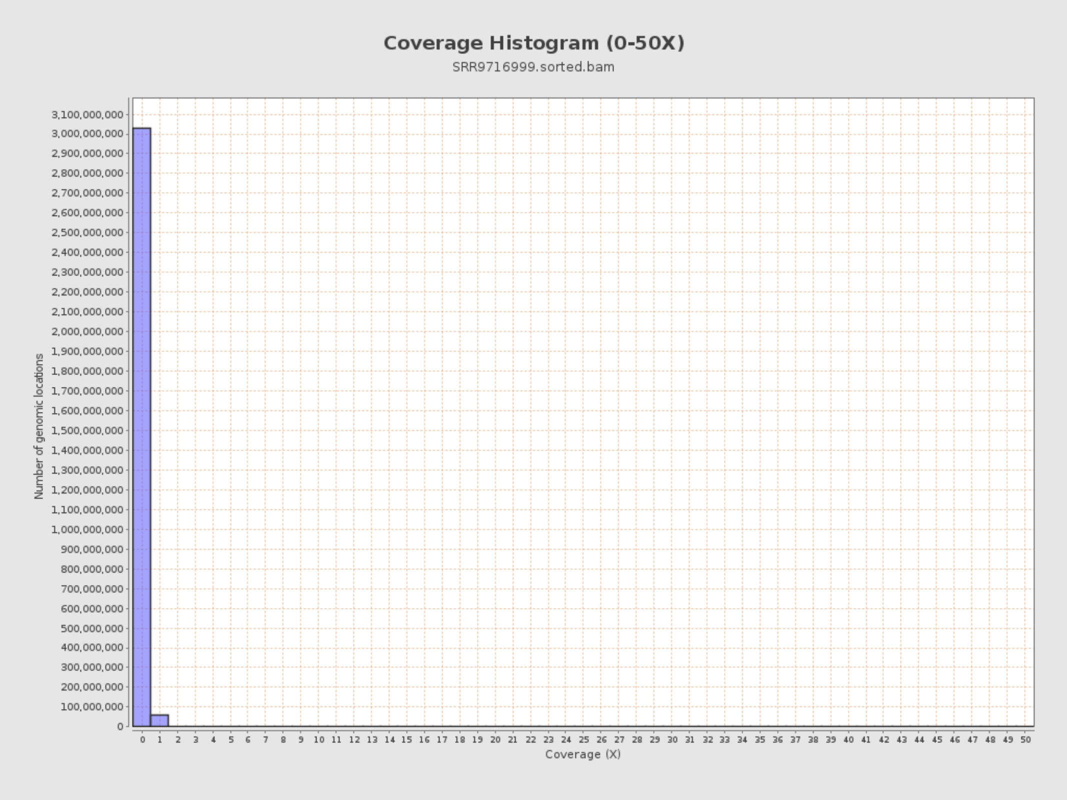
3. Results : Coverage across reference



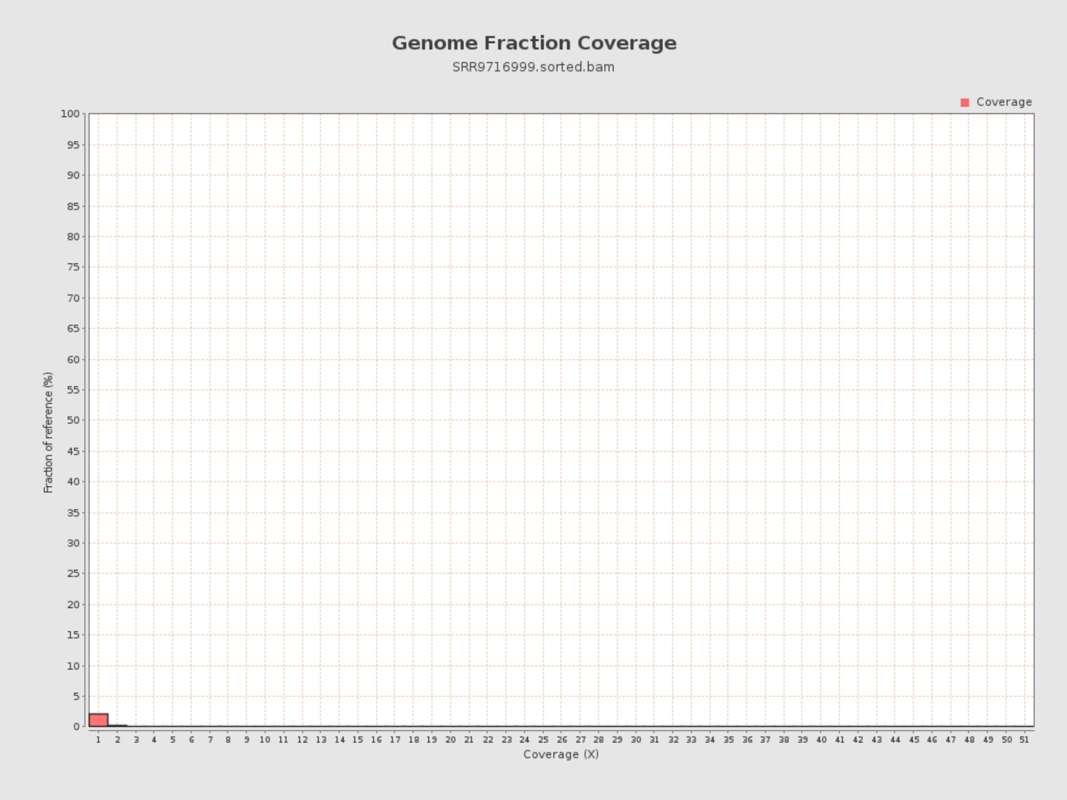
4. Results : Coverage Histogram



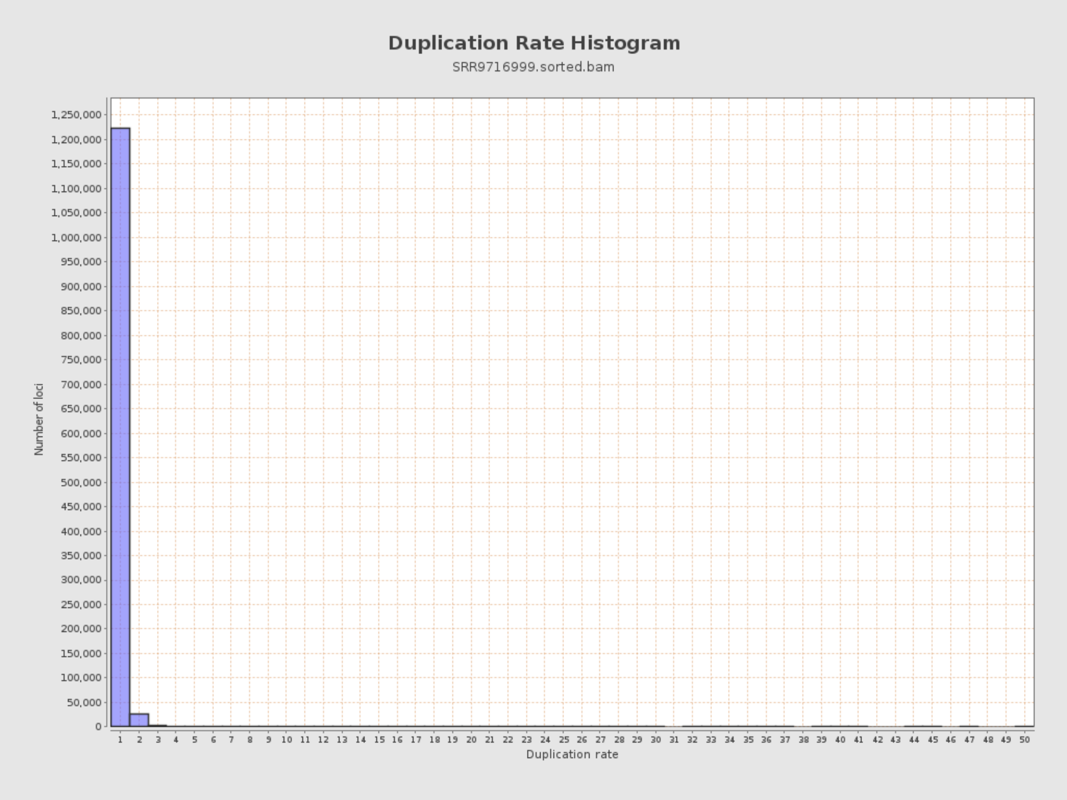
5. Results : Coverage Histogram (0-50X)



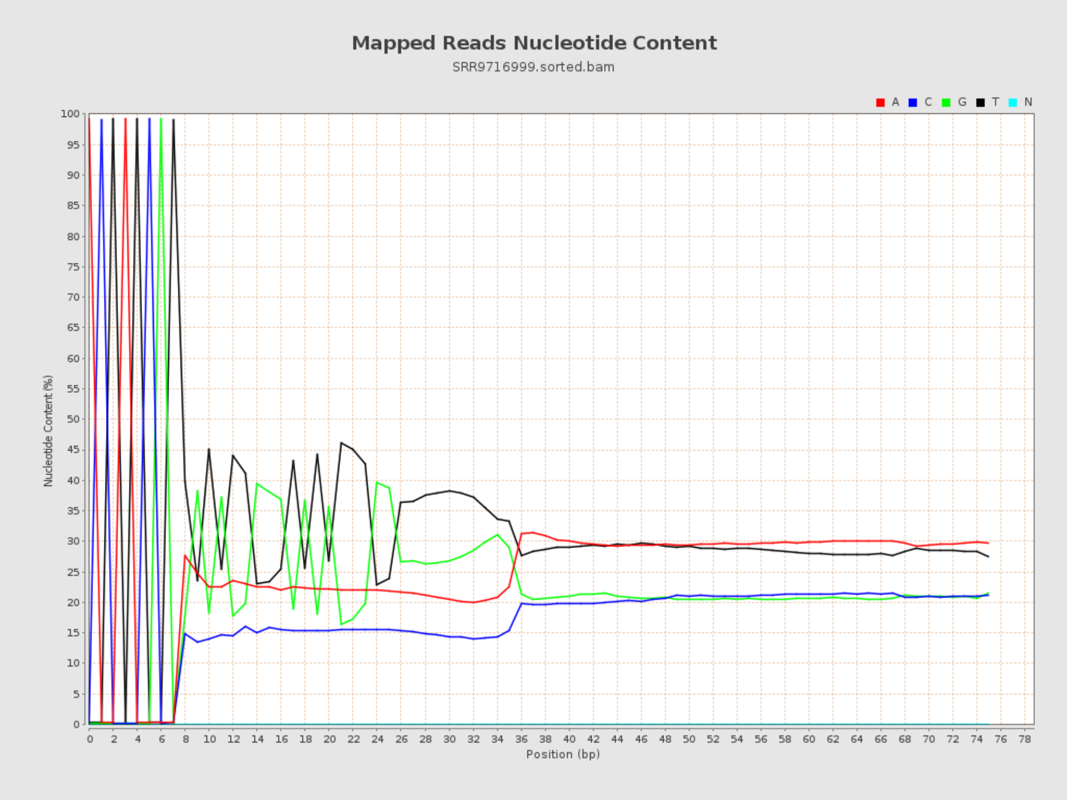
6. Results : Genome Fraction Coverage



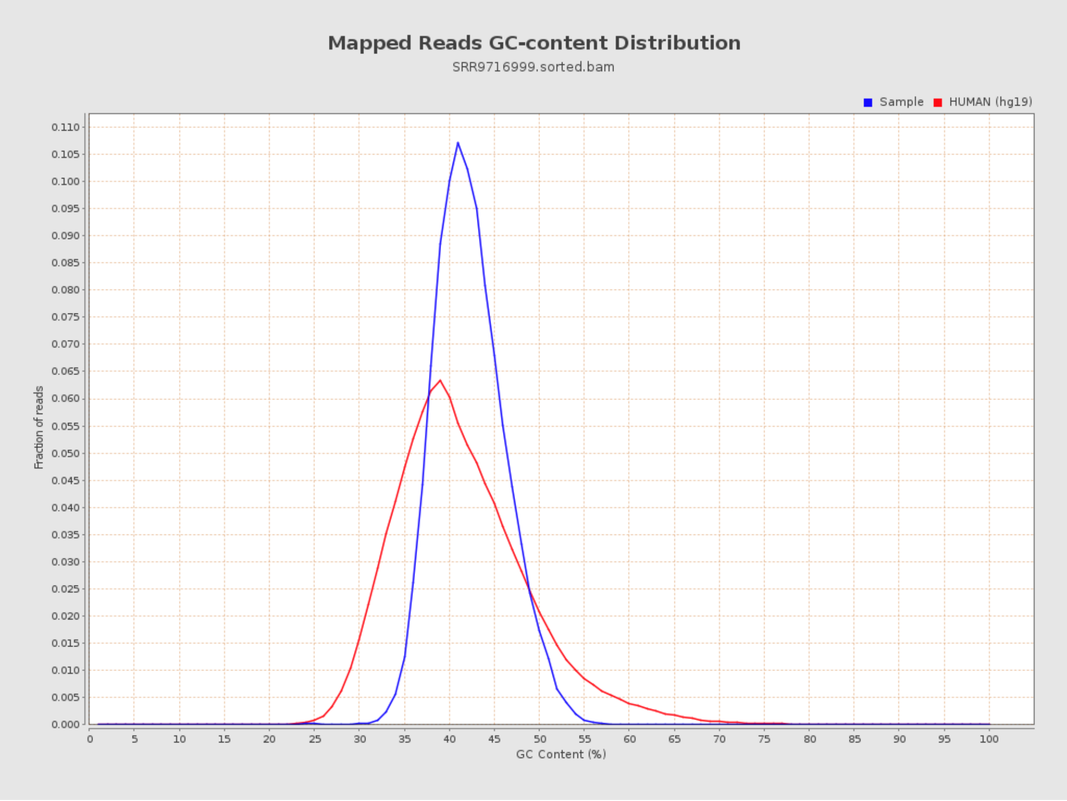
7. Results : Duplication Rate Histogram



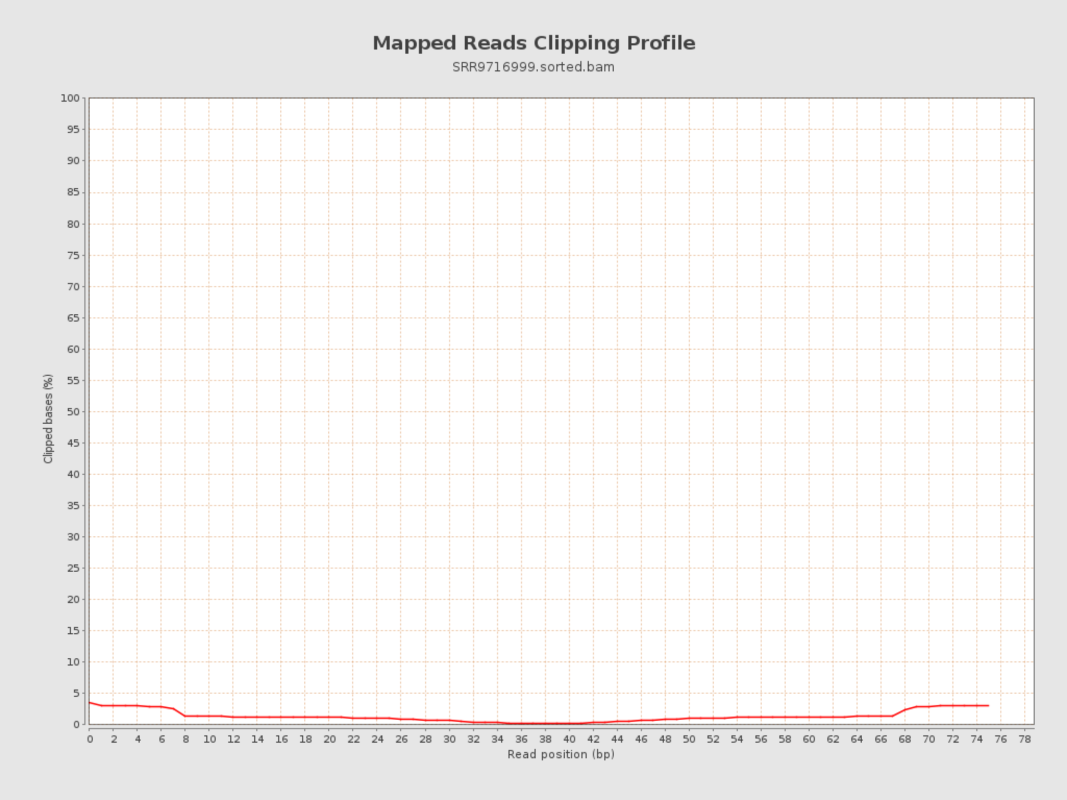
8. Results : Mapped Reads Nucleotide Content



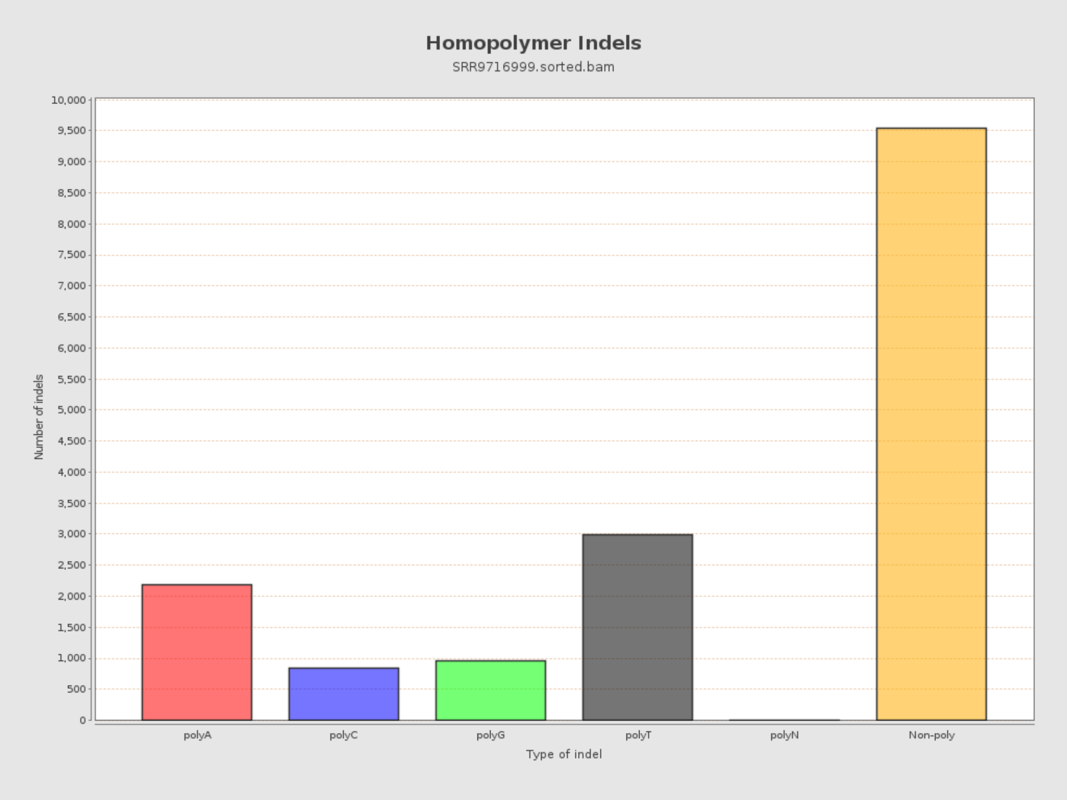
9. Results : Mapped Reads GC-content Distribution



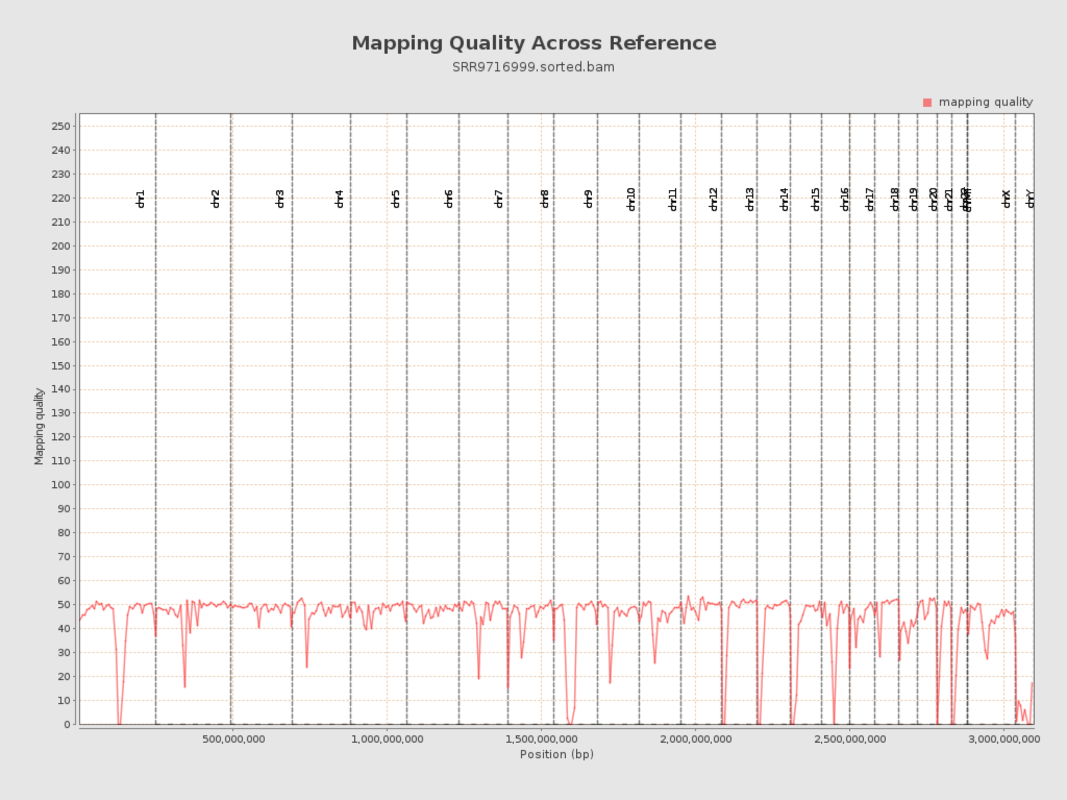
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram