Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 12:48:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716799.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_SRR9716799 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716799.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 12:48:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716799.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,061,637
Mapped reads	899,857 / 84.76%
Unmapped reads	161,780 / 15.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,030 / 0.1%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	73,825 / 6.95%
Duplication rate	7.06%
Clipped reads	900,248 / 84.8%

2.2. ACGT Content

Number/percentage of A's	10,613,849 / 22.01%
Number/percentage of C's	8,757,831 / 18.16%
Number/percentage of T's	14,901,675 / 30.89%
Number/percentage of G's	13,959,559 / 28.94%
Number/percentage of N's	757 / 0%
GC Percentage	47.1%

2.3. Coverage

Mean	0.0156

Standard Deviation	0.1621

2.4. Mapping Quality

Mean Mapping Quality	43.37

2.5. Mismatches and indels

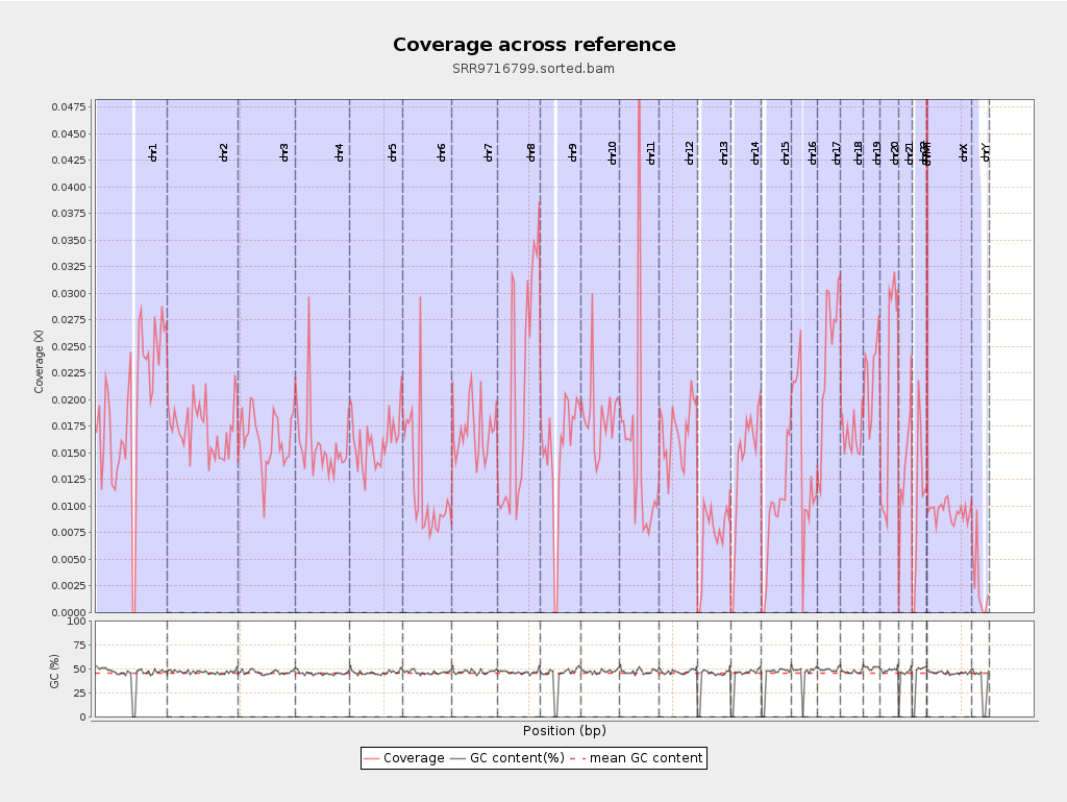
General error rate	0.63%
Mismatches	299,275
Insertions	2,606
Mapped reads with at least one insertion	0.29%
Deletions	7,392
Mapped reads with at least one deletion	0.82%
Homopolymer indels	40.88%

2.6. Chromosome stats

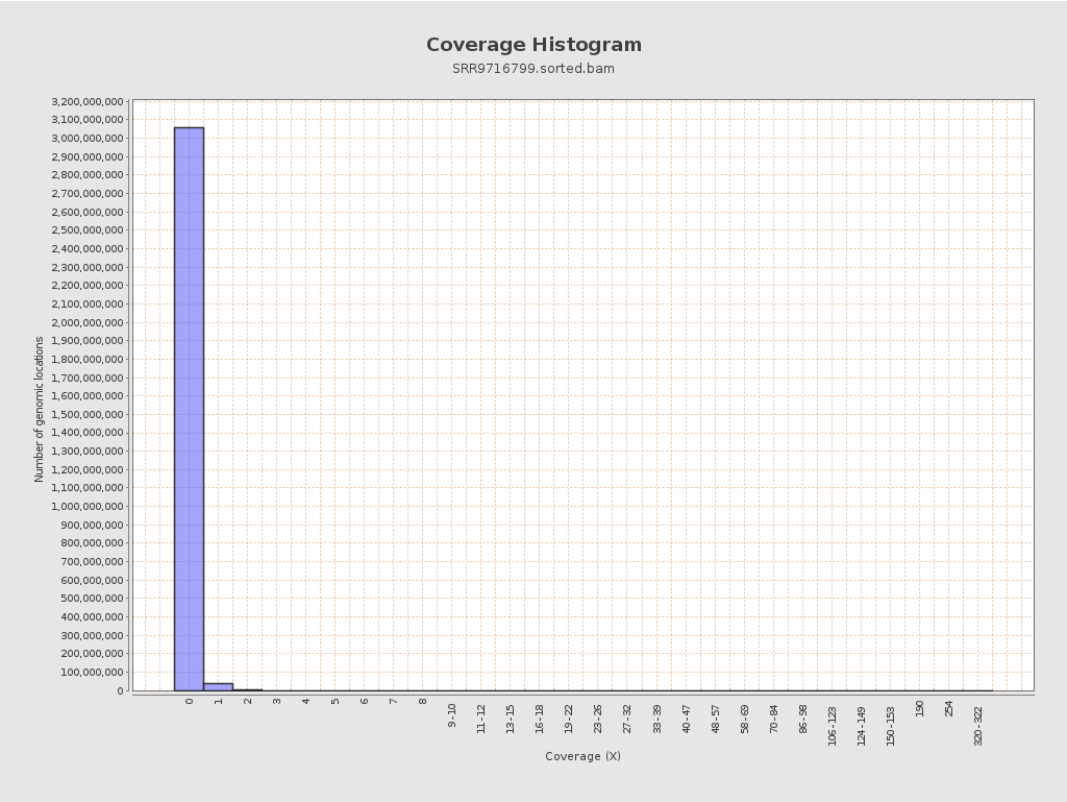
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4789744	0.0192	0.1921
chr2	243199373	4200766	0.0173	0.212
chr3	198022430	3239388	0.0164	0.15
chr4	191154276	3045131	0.0159	0.1554
chr5	180915260	2906512	0.0161	0.146
chr6	171115067	2028169	0.0119	0.1389
chr7	159138663	2726247	0.0171	0.1752

chr8	146364022	3022500	0.0207	0.1744
chr9	141213431	2131064	0.0151	0.1529
chr10	135534747	2514387	0.0186	0.1898
chr11	135006516	2078923	0.0154	0.1573
chr12	133851895	2267686	0.0169	0.1521
chr13	115169878	826203	0.0072	0.0994
chr14	107349540	1502597	0.014	0.1393
chr15	102531392	951006	0.0093	0.114
chr16	90354753	1299136	0.0144	0.1509
chr17	81195210	1956158	0.0241	0.1896
chr18	78077248	1296449	0.0166	0.1755
chr19	59128983	1323459	0.0224	0.2157
chr20	63025520	1295290	0.0206	0.1748
chr21	48129895	662861	0.0138	0.1478
chr22	51304566	555229	0.0108	0.1233
chrMT	16571	4057	0.2448	0.6173
chrX	155270560	1473135	0.0095	0.1161
chrY	59373566	150377	0.0025	0.0828

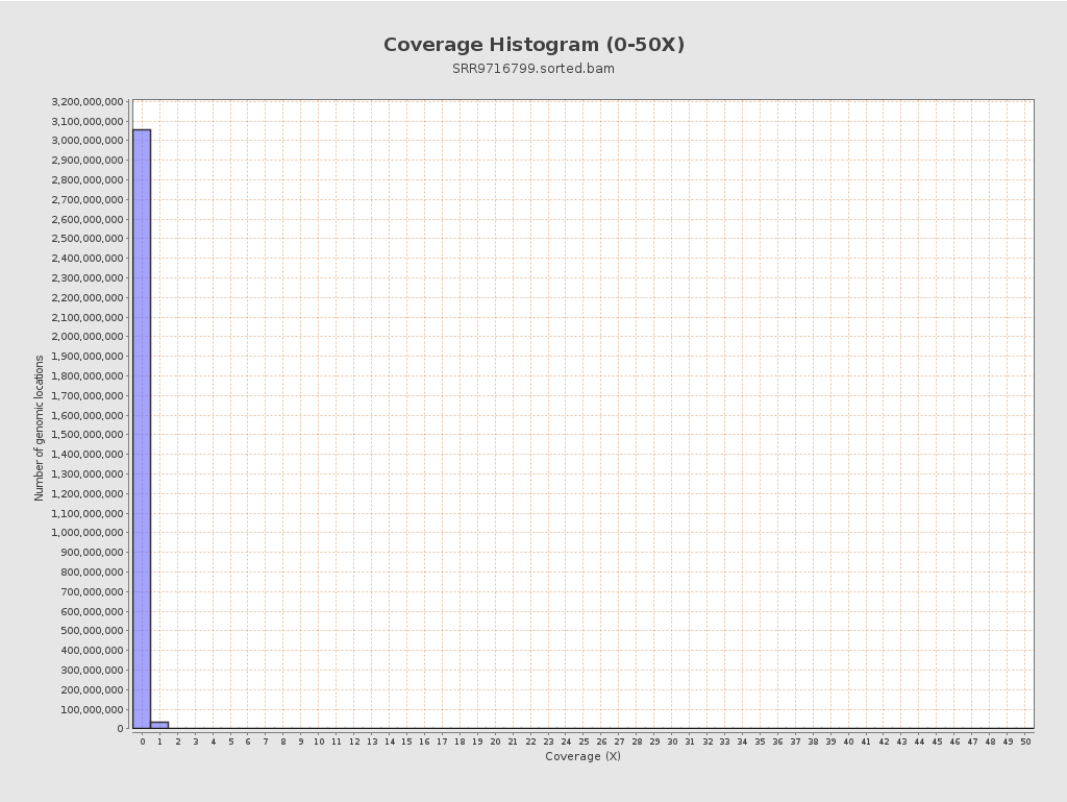
3. Results : Coverage across reference



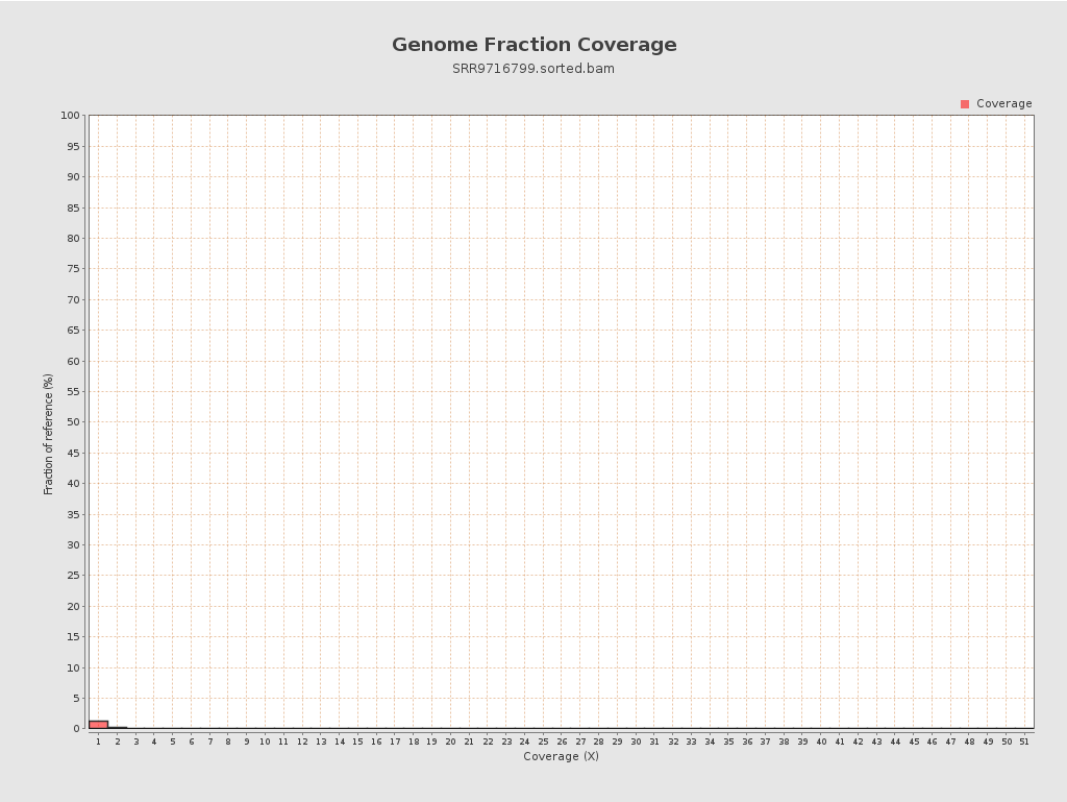
4. Results : Coverage Histogram



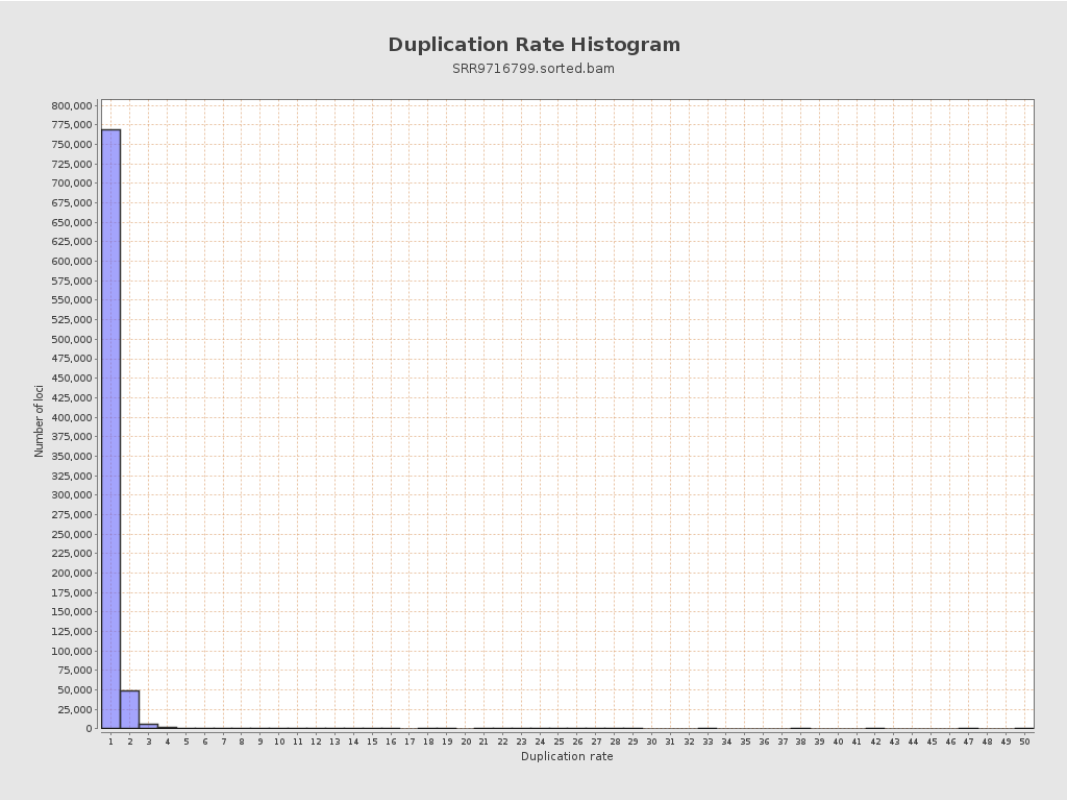
5. Results : Coverage Histogram (0-50X)



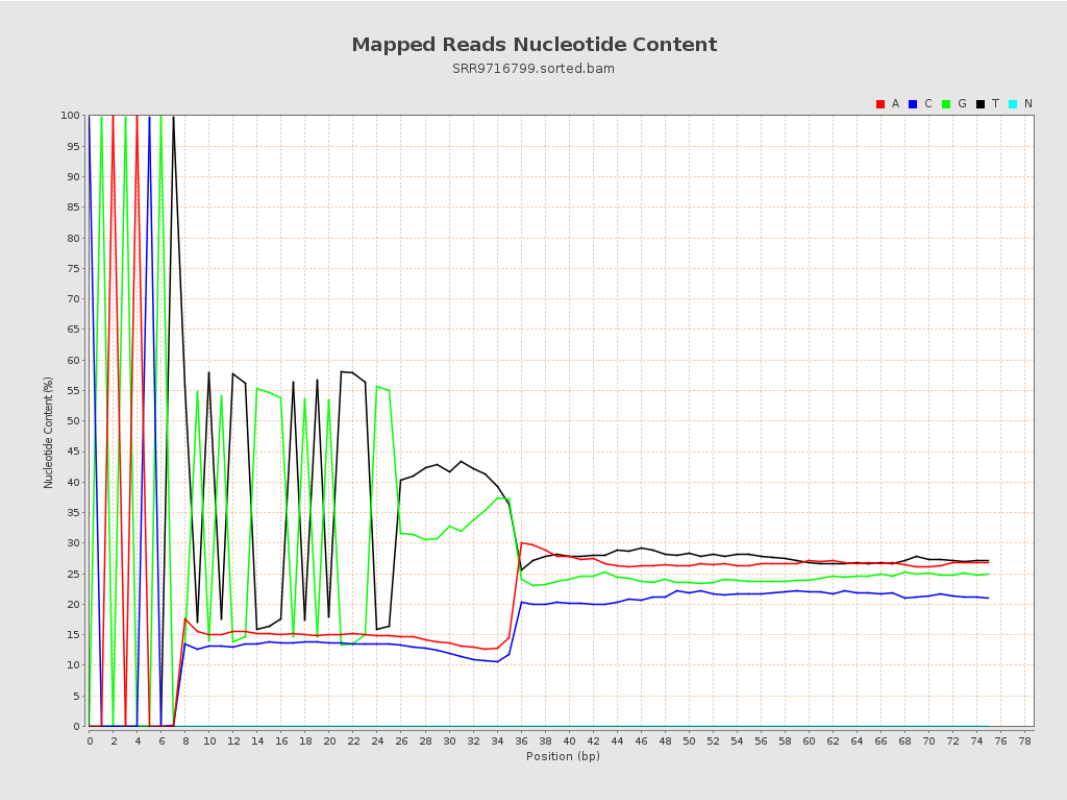
6. Results : Genome Fraction Coverage



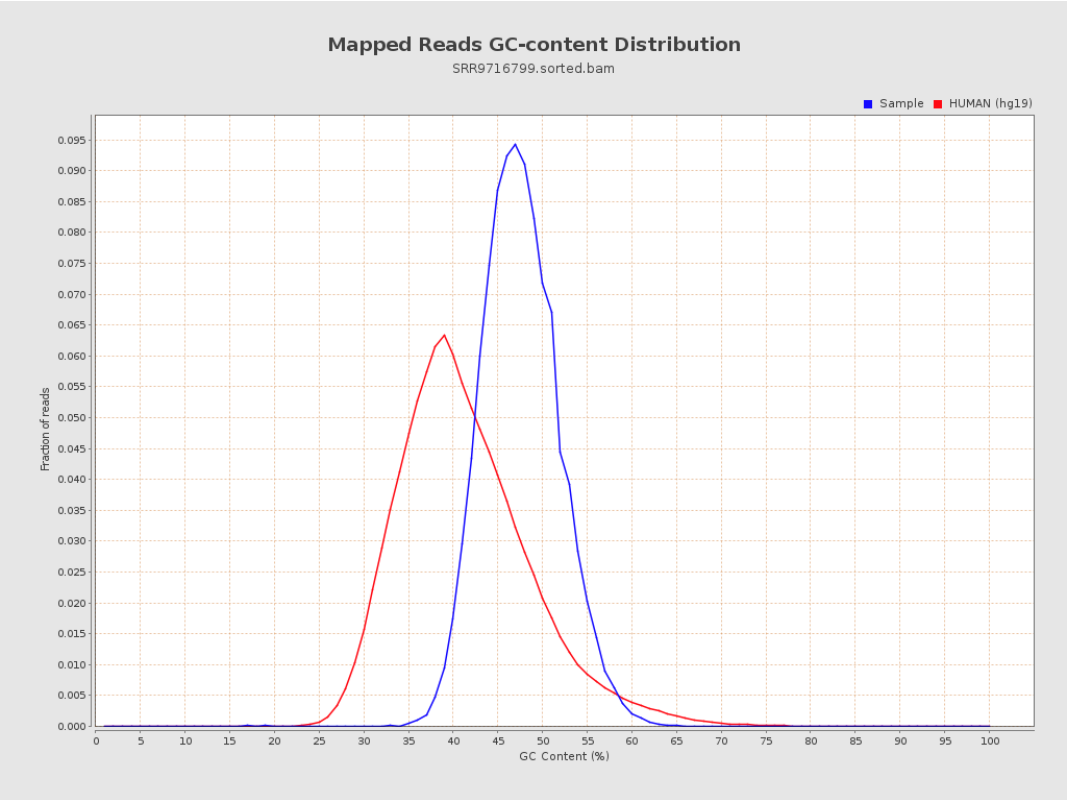
7. Results : Duplication Rate Histogram



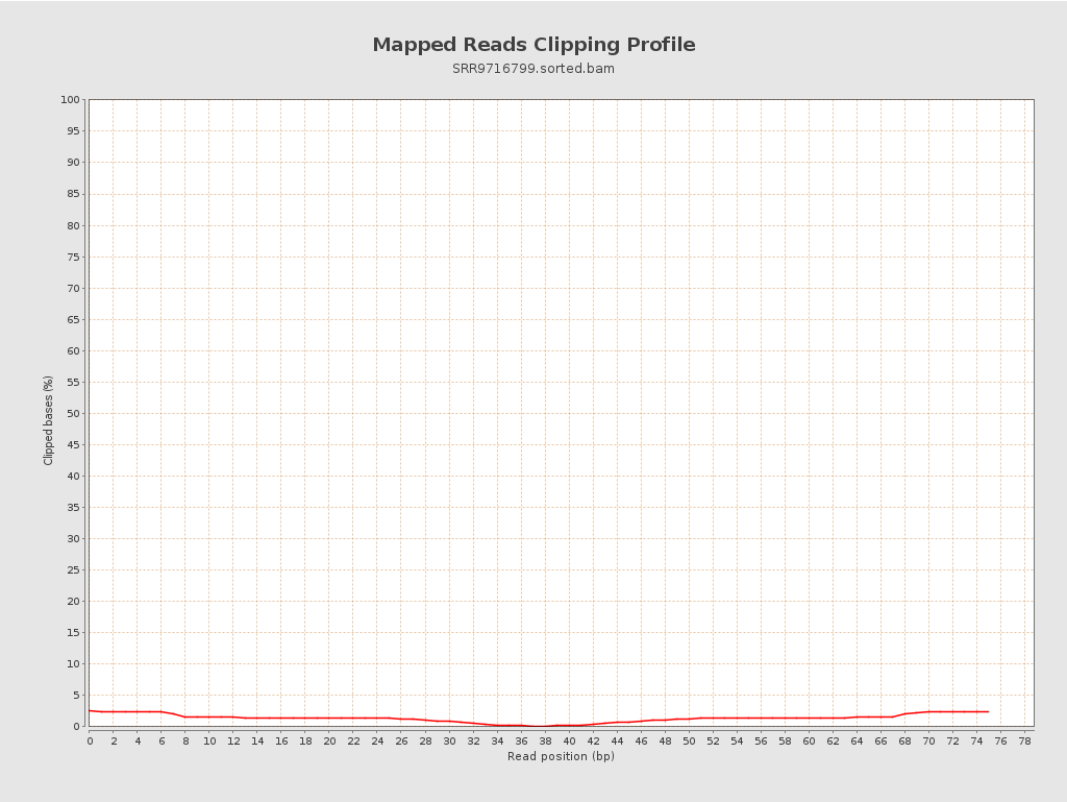
8. Results : Mapped Reads Nucleotide Content



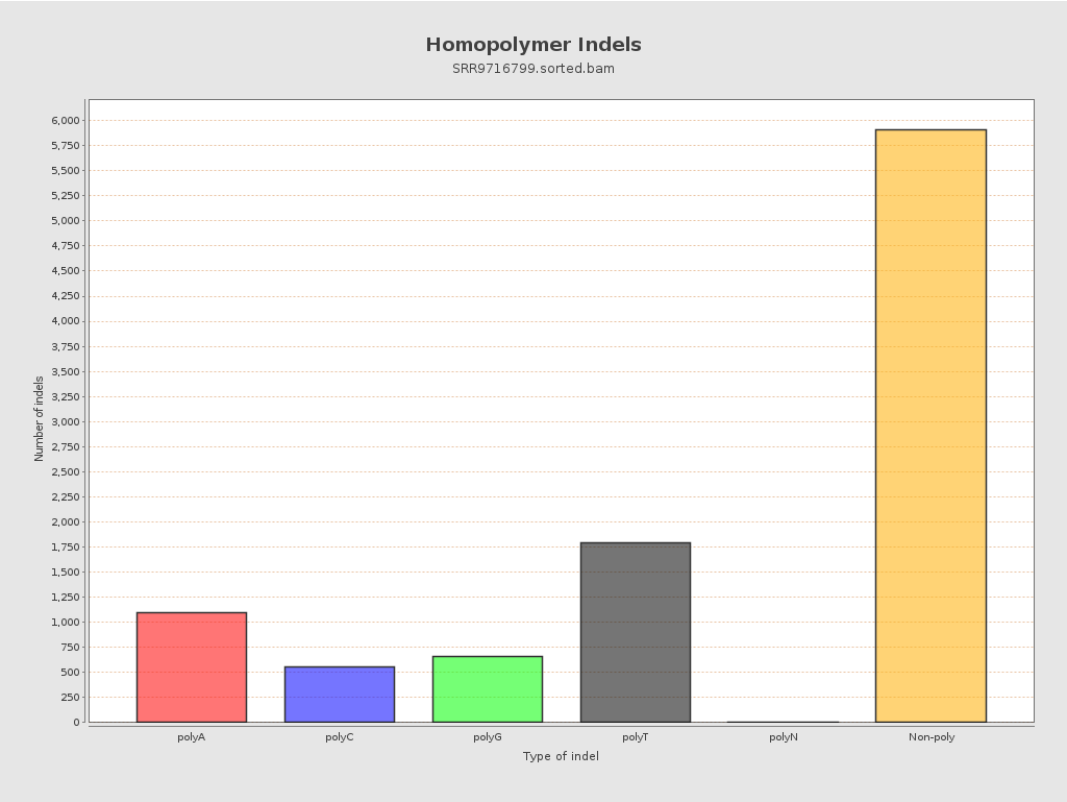
9. Results : Mapped Reads GC-content Distribution



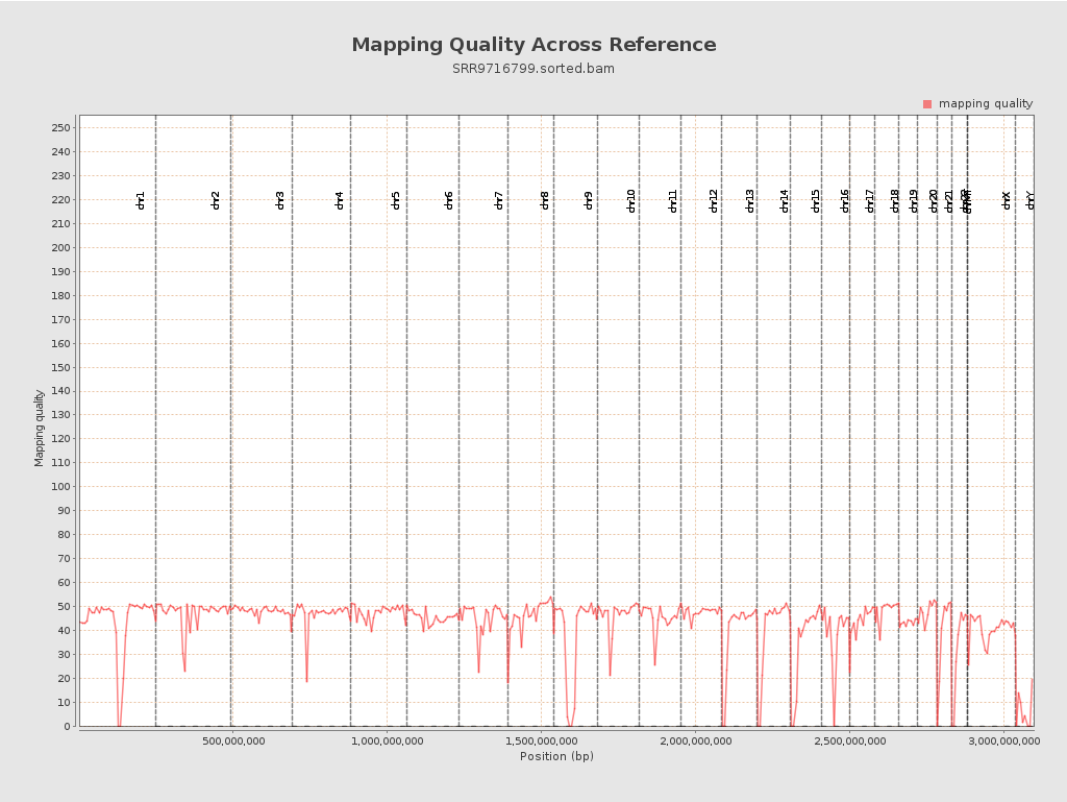
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram