Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 08:57:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716724.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_SRR9716724 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716724.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 08:57:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716724.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,460,750
Mapped reads	2,255,258 / 91.65%
Unmapped reads	205,492 / 8.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,971 / 0.49%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	89,500 / 3.64%
Duplication rate	2.91%
Clipped reads	2,261,967 / 91.92%

2.2. ACGT Content

Number/percentage of A's	33,575,633 / 25.62%
Number/percentage of C's	26,351,857 / 20.11%
Number/percentage of T's	40,156,154 / 30.65%
Number/percentage of G's	30,947,303 / 23.62%
Number/percentage of N's	1,666 / 0%
GC Percentage	43.73%

2.3. Coverage

Mean	0.0423

Standard Deviation	0.3505

2.4. Mapping Quality

Mean Mapping Quality	44.29

2.5. Mismatches and indels

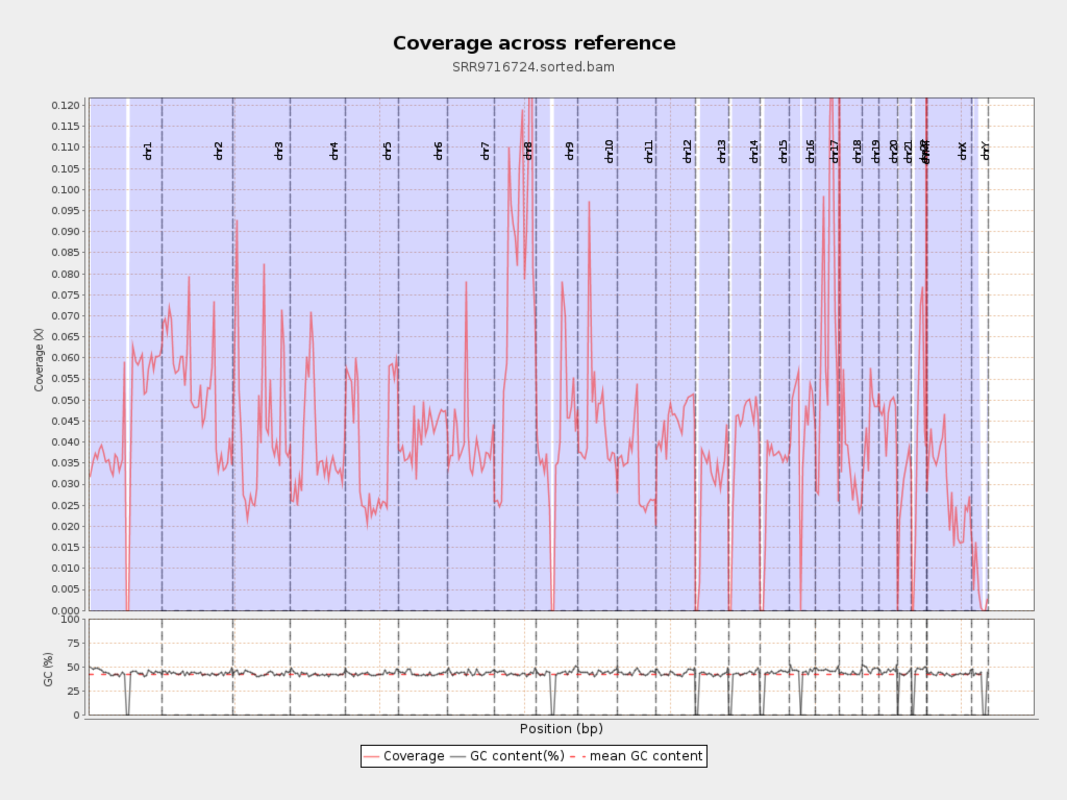
General error rate	0.5%
Mismatches	645,583
Insertions	8,520
Mapped reads with at least one insertion	0.38%
Deletions	23,298
Mapped reads with at least one deletion	1.03%
Homopolymer indels	42.75%

2.6. Chromosome stats

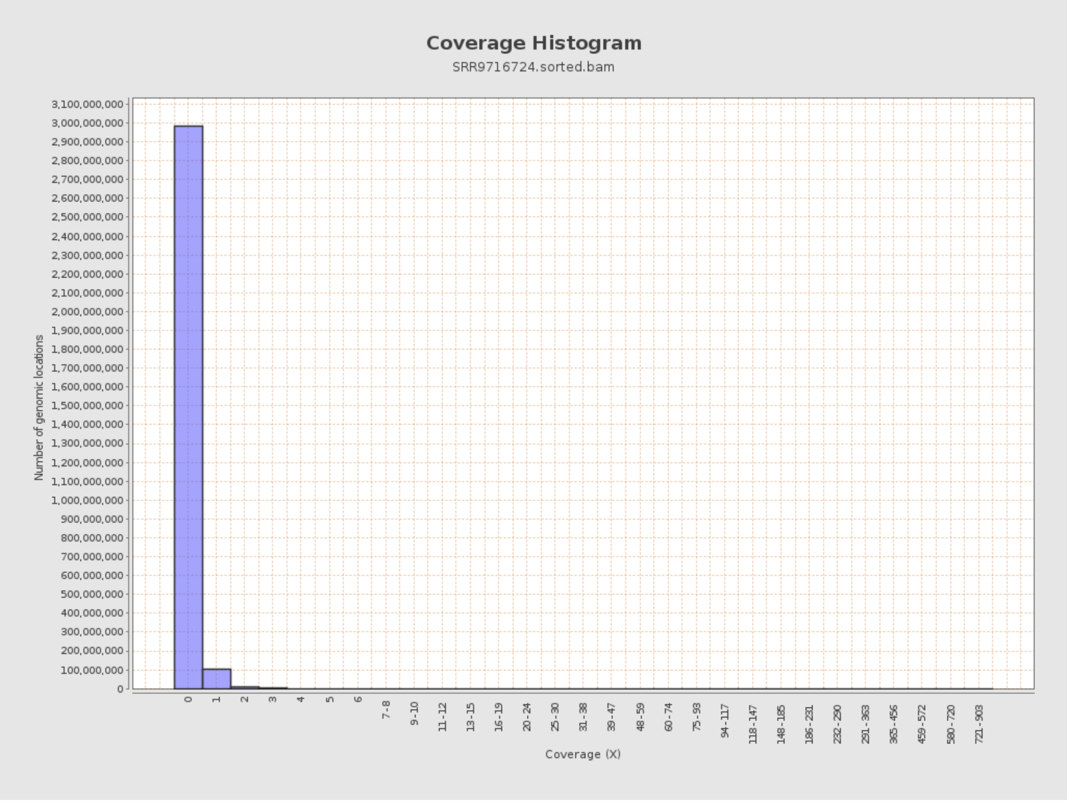
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10862460	0.0436	0.5687
chr2	243199373	12883046	0.053	0.4711
chr3	198022430	8640051	0.0436	0.237
chr4	191154276	7281996	0.0381	0.2471
chr5	180915260	6978769	0.0386	0.22
chr6	171115067	7222412	0.0422	0.2567
chr7	159138663	6343815	0.0399	0.5604

chr8	146364022	11643381	0.0796	0.4392
chr9	141213431	5493513	0.0389	0.2685
chr10	135534747	6129138	0.0452	0.4119
chr11	135006516	4427426	0.0328	0.2661
chr12	133851895	6054029	0.0452	0.2521
chr13	115169878	3357612	0.0292	0.1904
chr14	107349540	4256188	0.0396	0.2311
chr15	102531392	3115465	0.0304	0.2039
chr16	90354753	4022742	0.0445	0.2497
chr17	81195210	5559034	0.0685	0.3127
chr18	78077248	3001588	0.0384	0.4349
chr19	59128983	2656847	0.0449	0.4749
chr20	63025520	2925774	0.0464	0.2489
chr21	48129895	1353041	0.0281	0.2028
chr22	51304566	2025713	0.0395	0.2239
chrMT	16571	5308	0.3203	0.6311
chrX	155270560	4533355	0.0292	0.2216
chrY	59373566	296958	0.005	0.1279

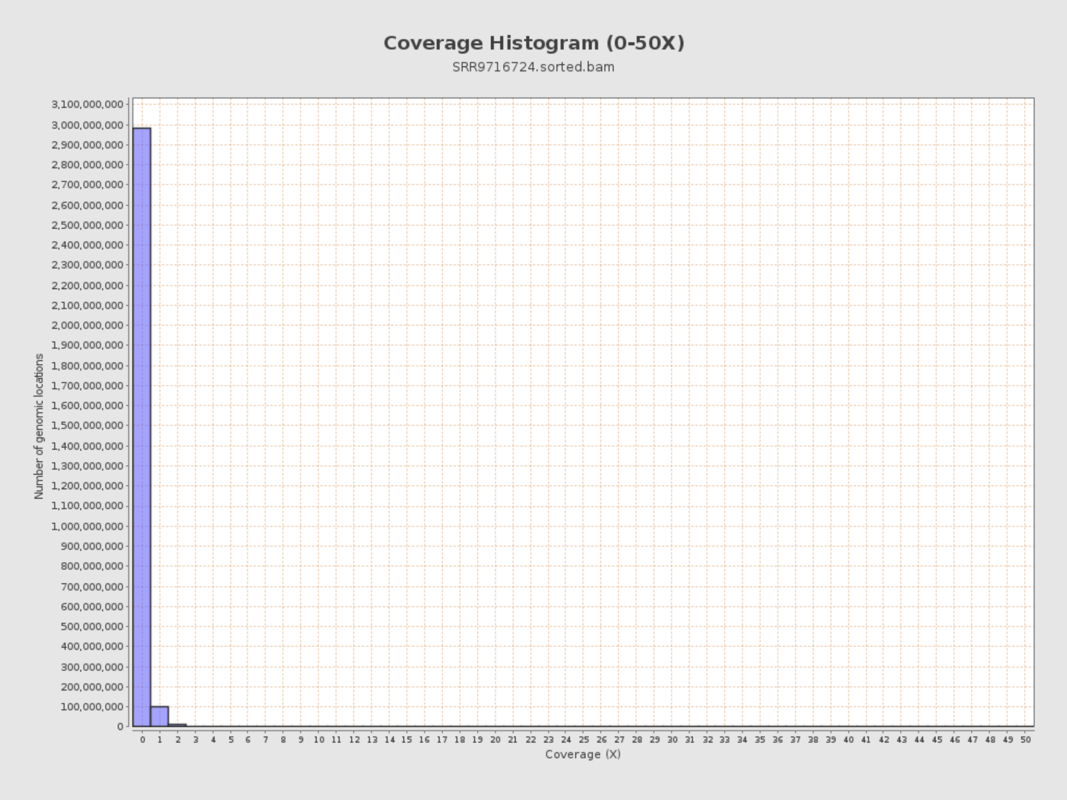
3. Results : Coverage across reference



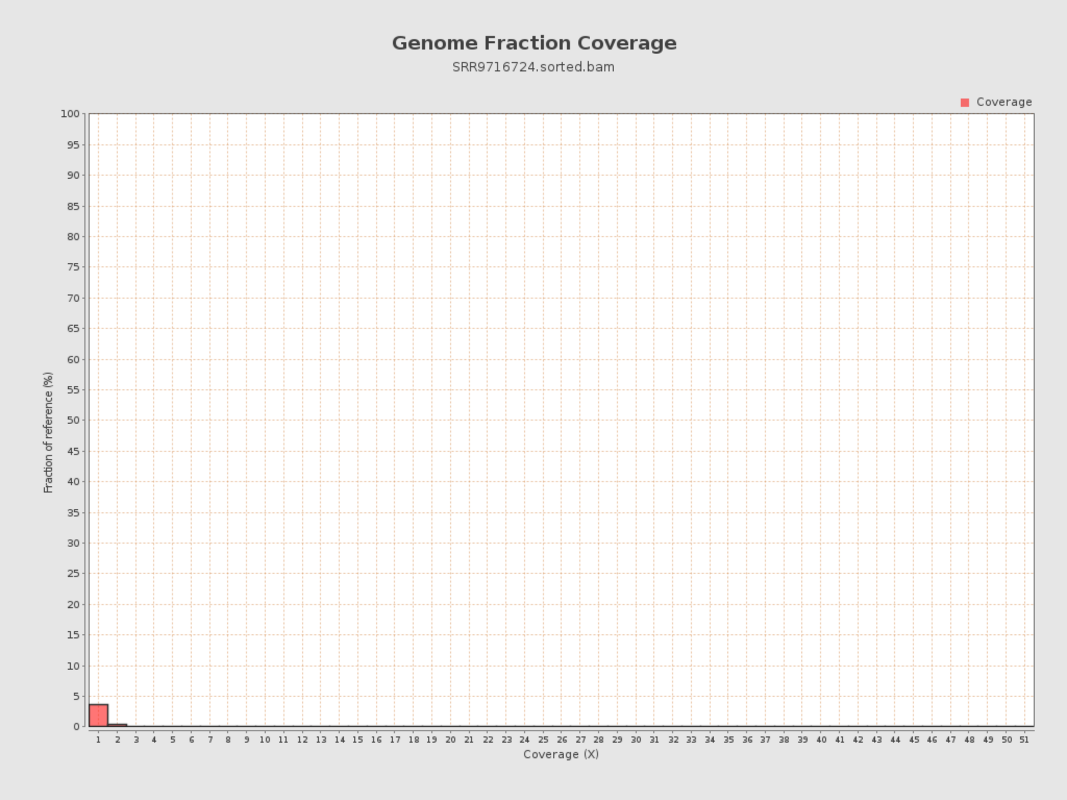
4. Results : Coverage Histogram



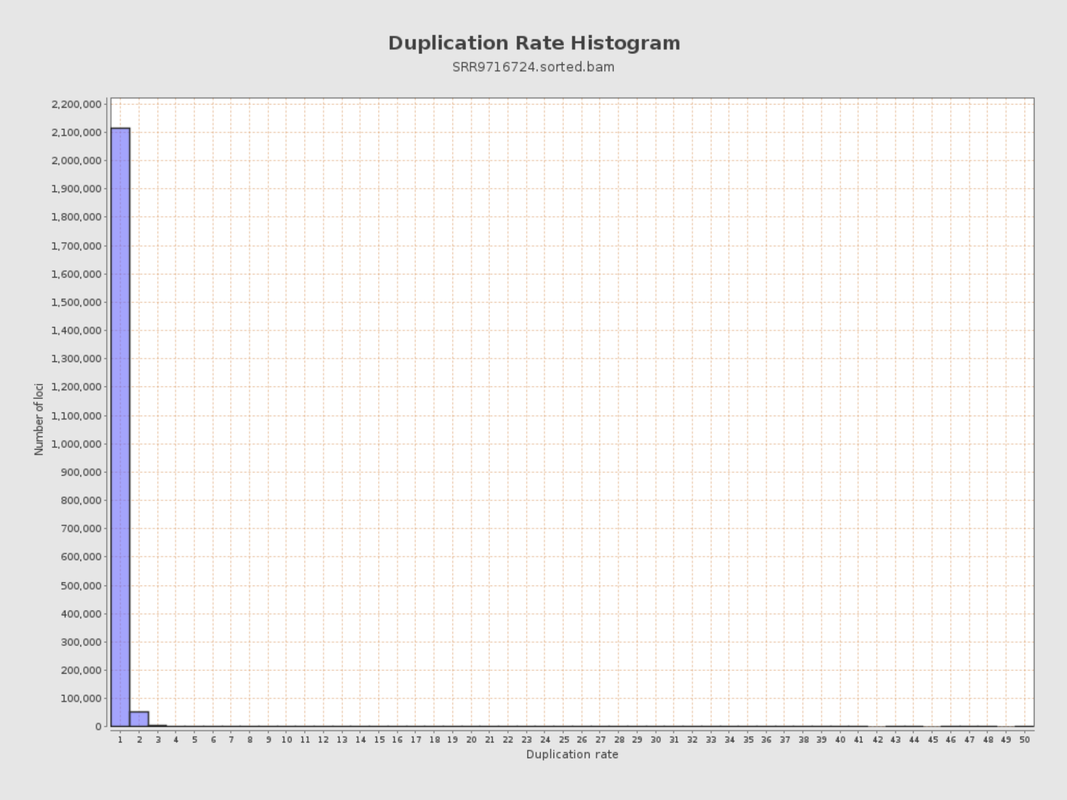
5. Results : Coverage Histogram (0-50X)



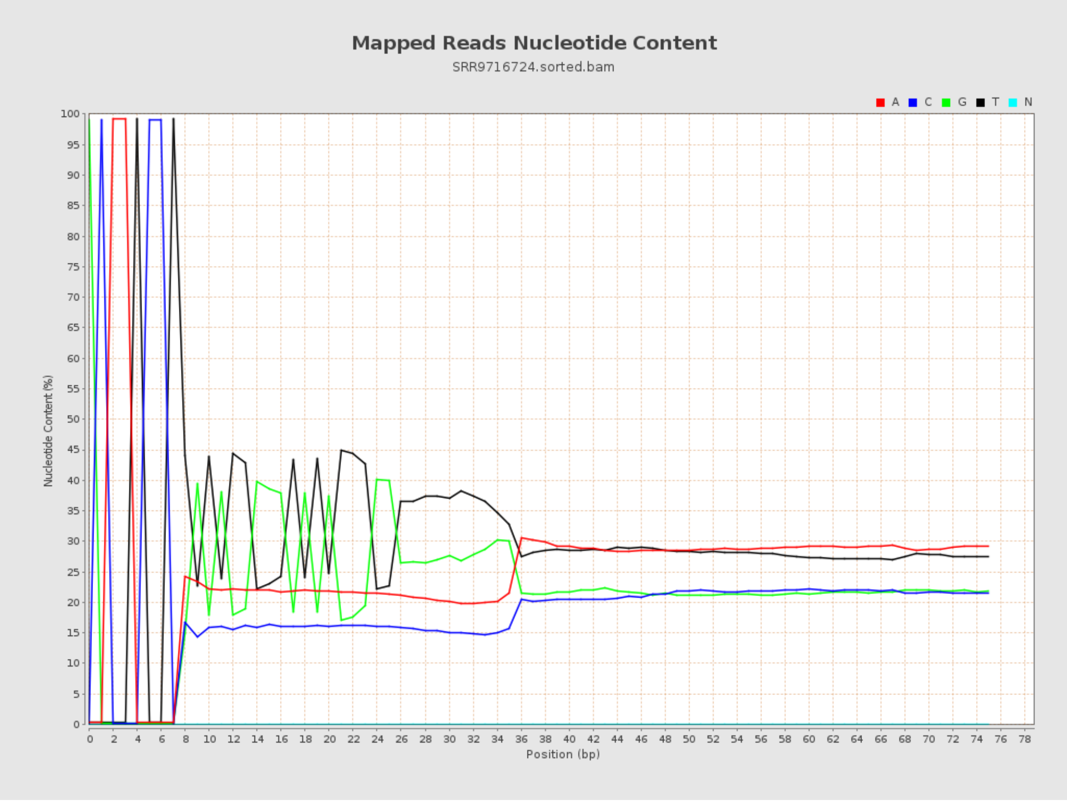
6. Results : Genome Fraction Coverage



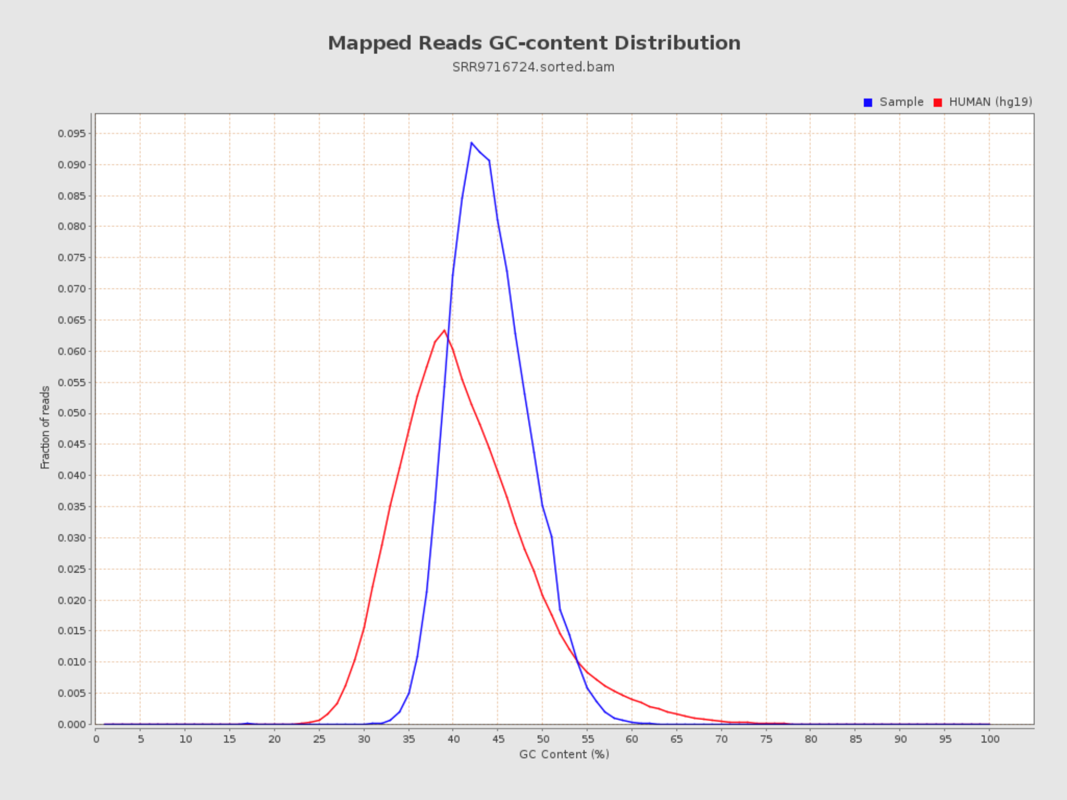
7. Results : Duplication Rate Histogram



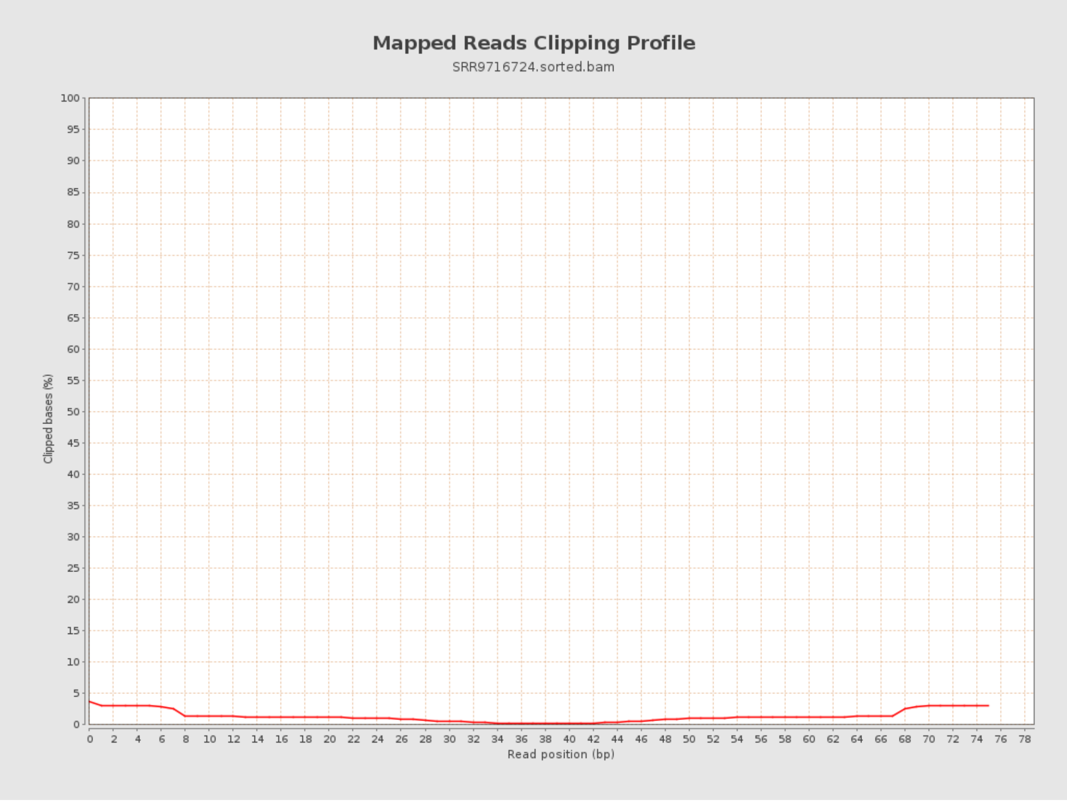
8. Results : Mapped Reads Nucleotide Content



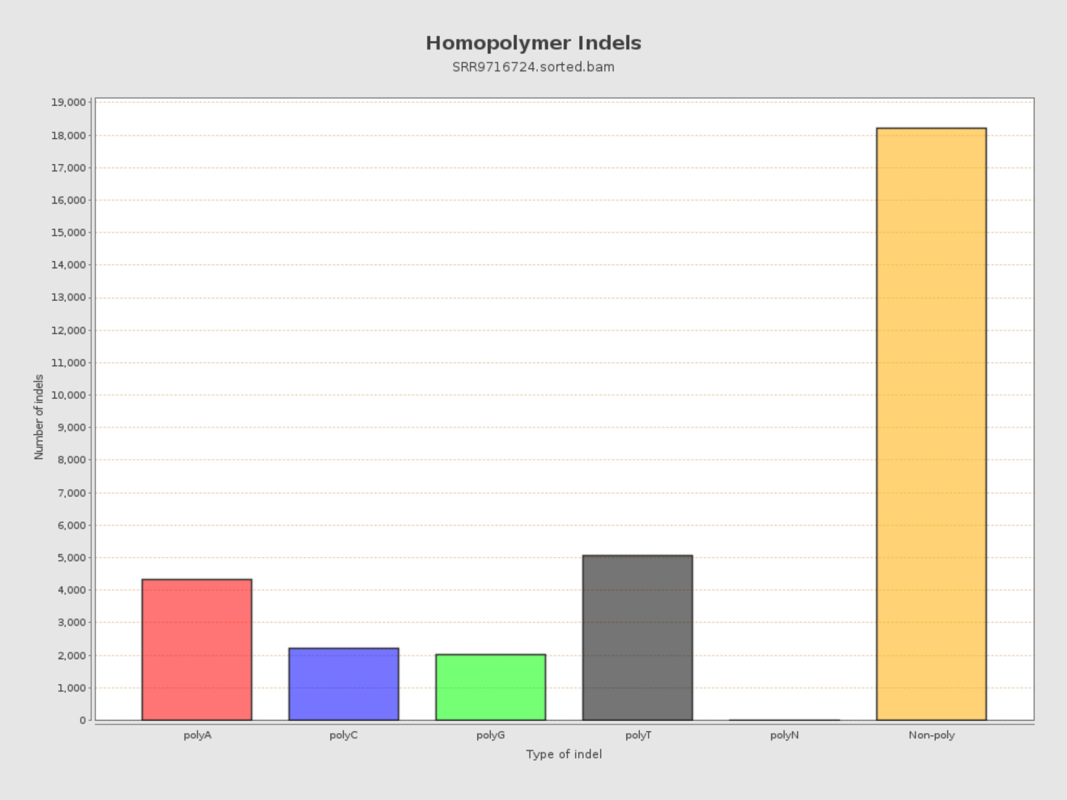
9. Results : Mapped Reads GC-content Distribution



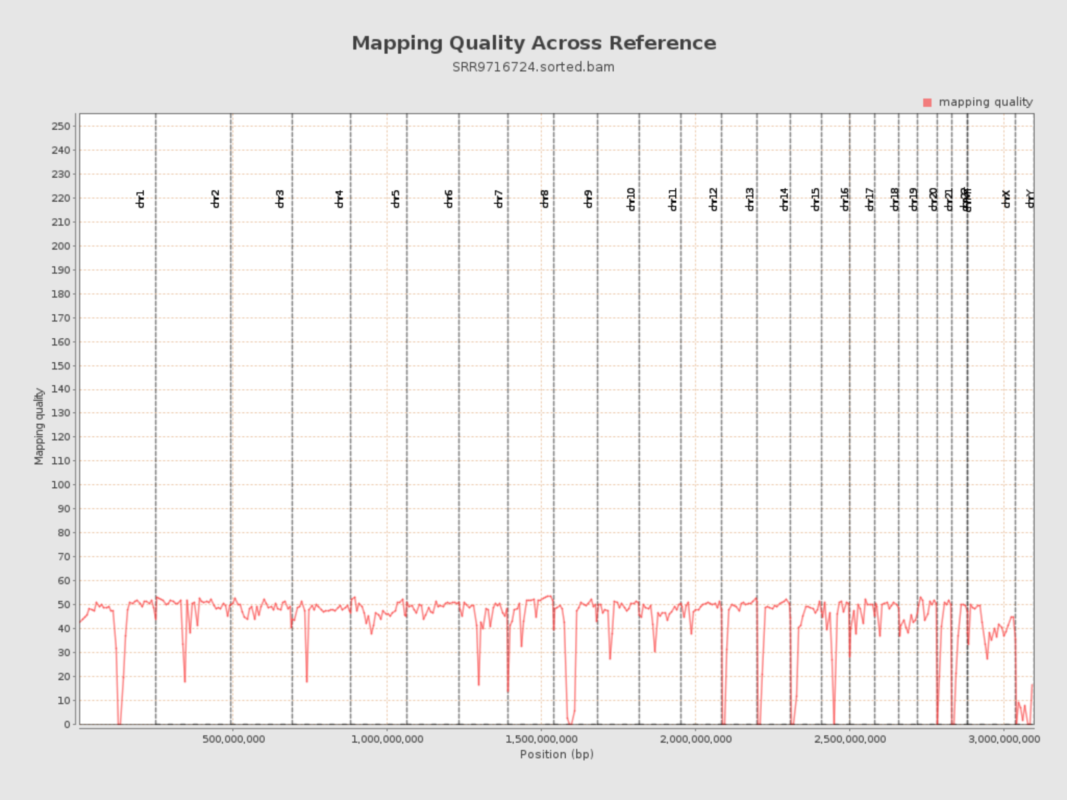
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram