Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 07:53:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716709.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_SRR9716709 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716709.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 07:53:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716709.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,838,927
Mapped reads	4,560,950 / 94.26%
Unmapped reads	277,977 / 5.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	89,183 / 1.84%
Read min/max/mean length	30 / 101 / 101.67
Duplicated reads (estimated)	456,457 / 9.43%
Duplication rate	7.52%
Clipped reads	4,640,365 / 95.9%

2.2. ACGT Content

Number/percentage of A's	91,064,167 / 25.63%
Number/percentage of C's	72,573,518 / 20.43%
Number/percentage of T's	106,620,547 / 30.01%
Number/percentage of G's	85,004,348 / 23.93%
Number/percentage of N's	14,656 / 0%
GC Percentage	44.35%

2.3. Coverage

Mean	0.1148

Standard Deviation	0.8513

2.4. Mapping Quality

Mean Mapping Quality	47.01

2.5. Mismatches and indels

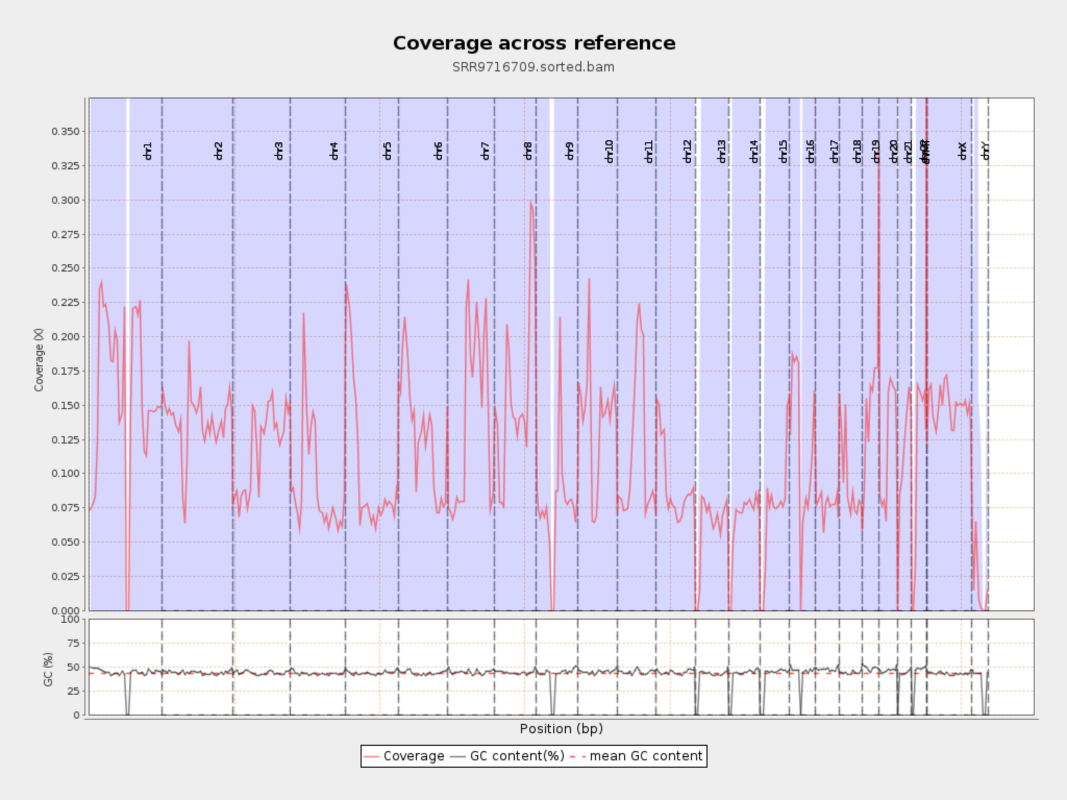
General error rate	0.66%
Mismatches	2,257,700
Insertions	30,012
Mapped reads with at least one insertion	0.65%
Deletions	66,288
Mapped reads with at least one deletion	1.43%
Homopolymer indels	37.85%

2.6. Chromosome stats

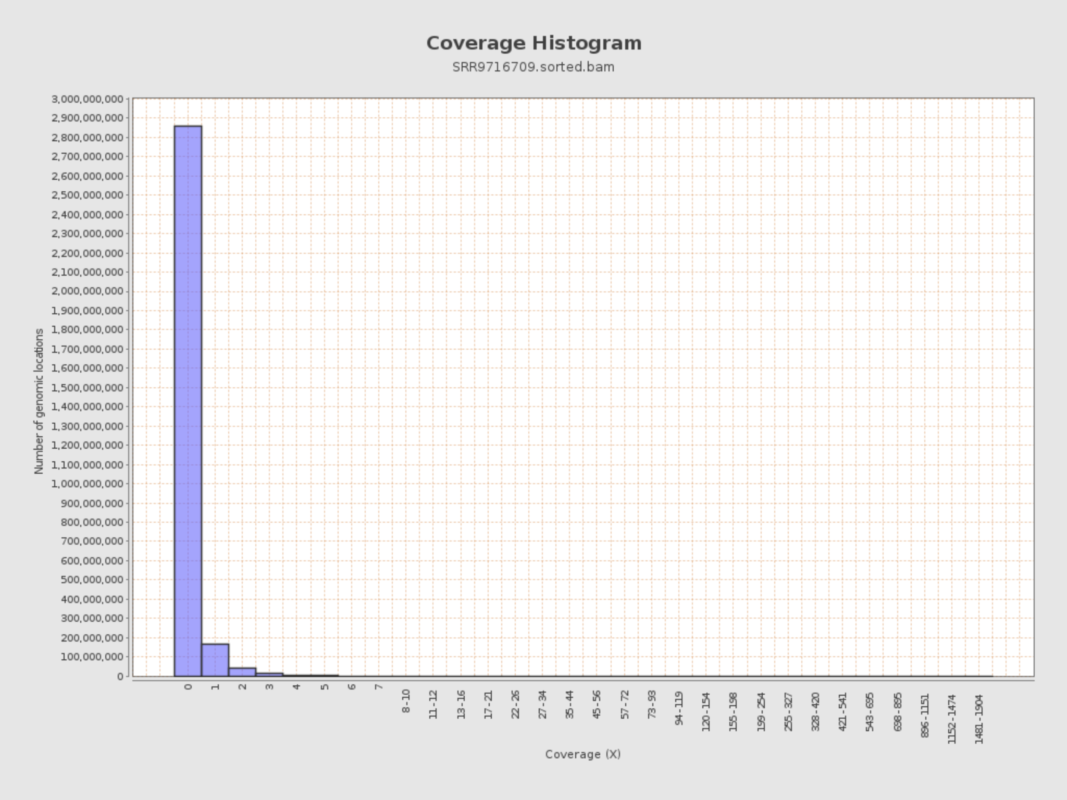
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	39302303	0.1577	1.7601
chr2	243199373	33572283	0.138	0.8791
chr3	198022430	23486799	0.1186	0.4945
chr4	191154276	17301858	0.0905	0.6961
chr5	180915260	18515511	0.1023	0.4624
chr6	171115067	22075241	0.129	0.5741
chr7	159138663	22402195	0.1408	1.2297

chr8	146364022	23424134	0.16	0.8936
chr9	141213431	10683209	0.0757	0.5728
chr10	135534747	18951303	0.1398	1.09
chr11	135006516	15720087	0.1164	0.7726
chr12	133851895	12336556	0.0922	0.4304
chr13	115169878	6873422	0.0597	0.3375
chr14	107349540	6967669	0.0649	0.4035
chr15	102531392	7355638	0.0717	0.3865
chr16	90354753	10908697	0.1207	0.556
chr17	81195210	6285021	0.0774	0.4818
chr18	78077248	7457518	0.0955	0.8875
chr19	59128983	8964218	0.1516	1.2354
chr20	63025520	7667032	0.1216	0.5503
chr21	48129895	5414080	0.1125	0.6312
chr22	51304566	5453017	0.1063	0.5128
chrMT	16571	8849	0.534	1.1317
chrX	155270560	23213316	0.1495	0.6105
chrY	59373566	1073918	0.0181	0.5774

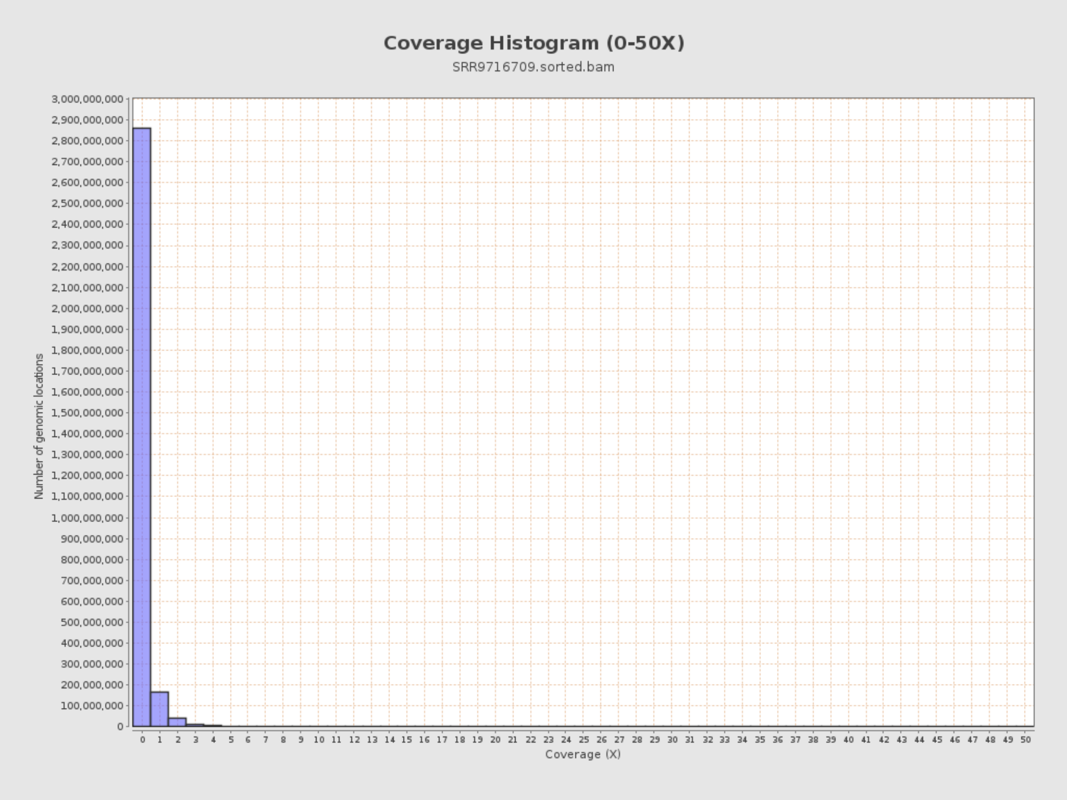
3. Results : Coverage across reference



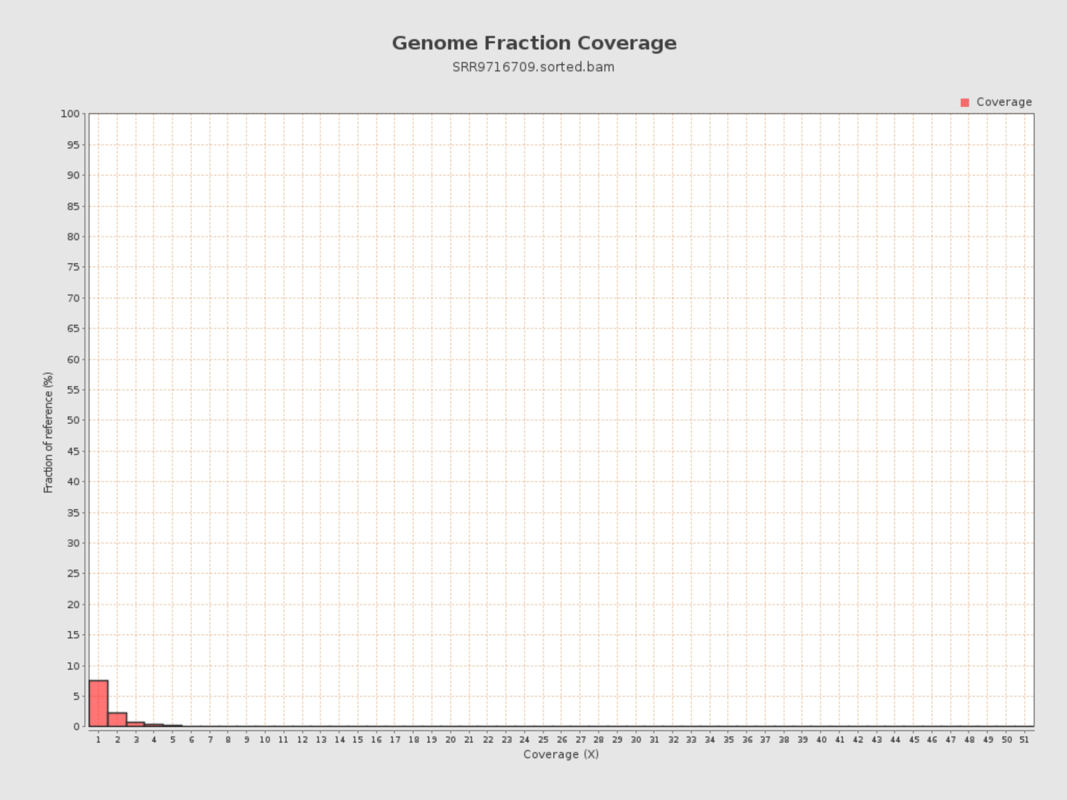
4. Results : Coverage Histogram



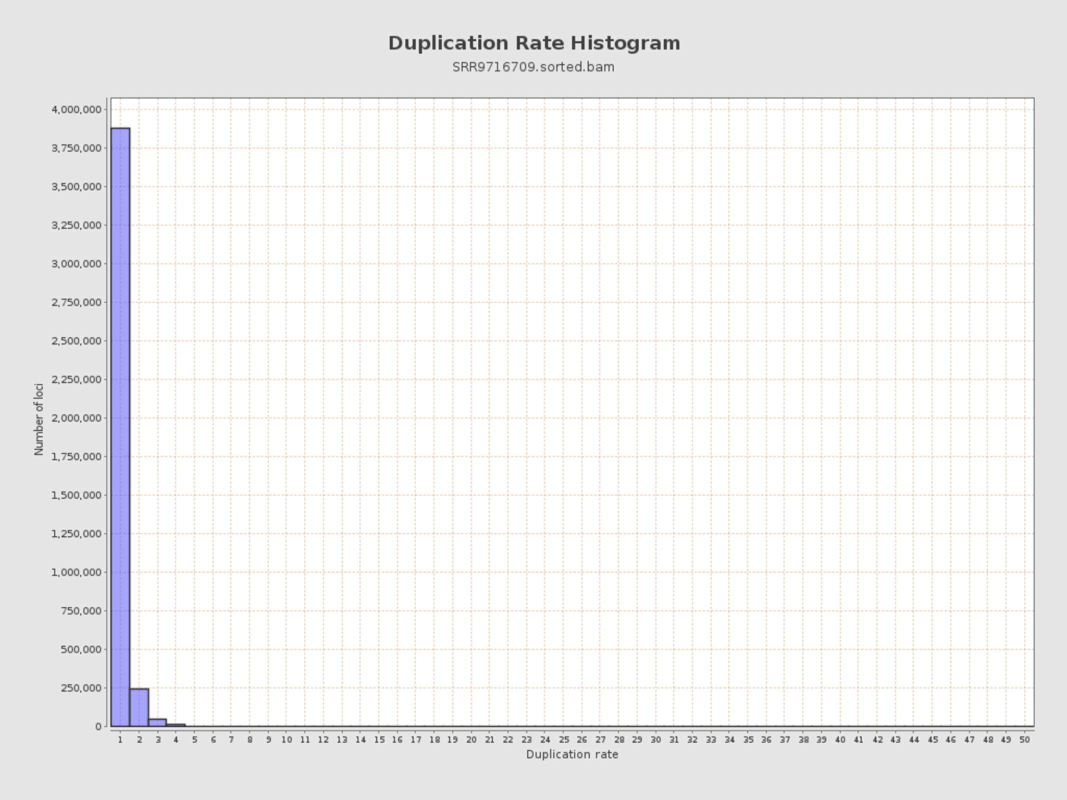
5. Results : Coverage Histogram (0-50X)



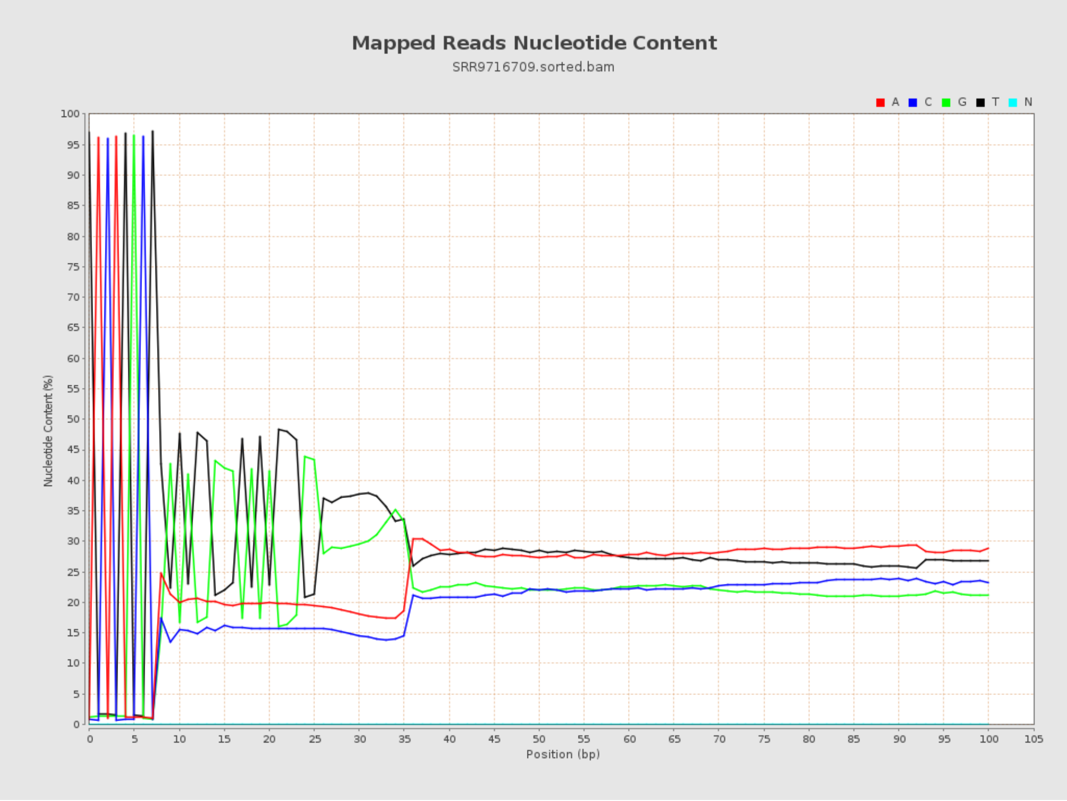
6. Results : Genome Fraction Coverage



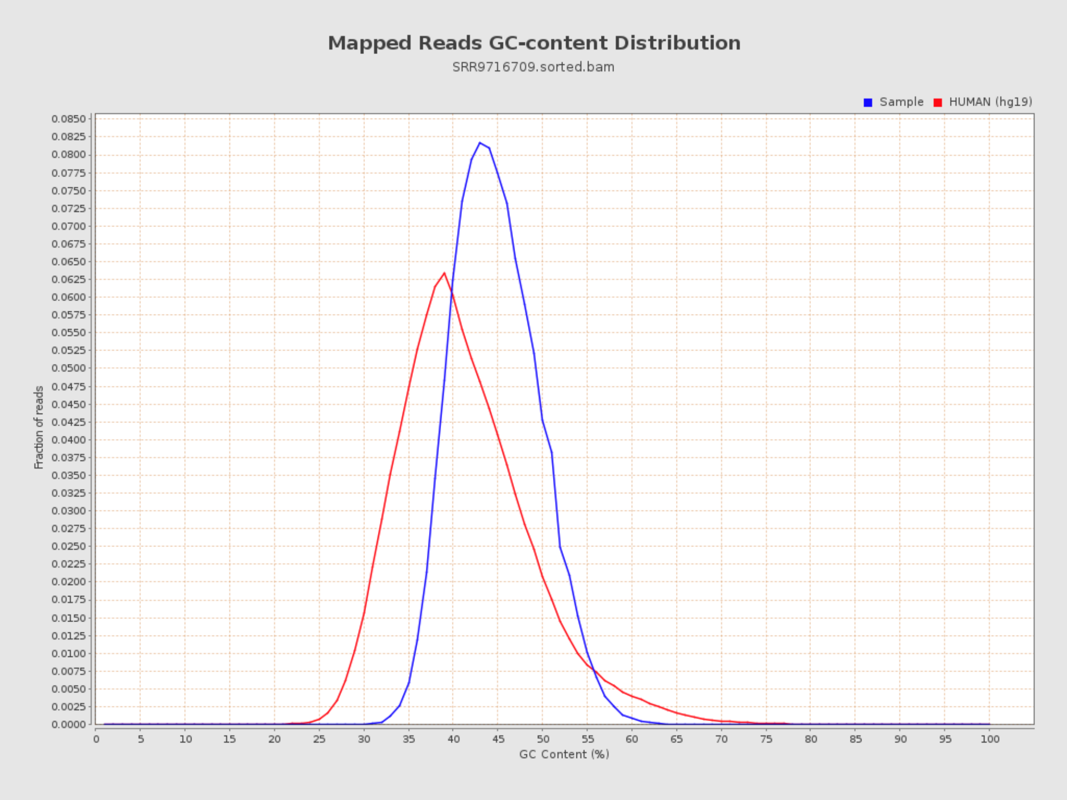
7. Results : Duplication Rate Histogram



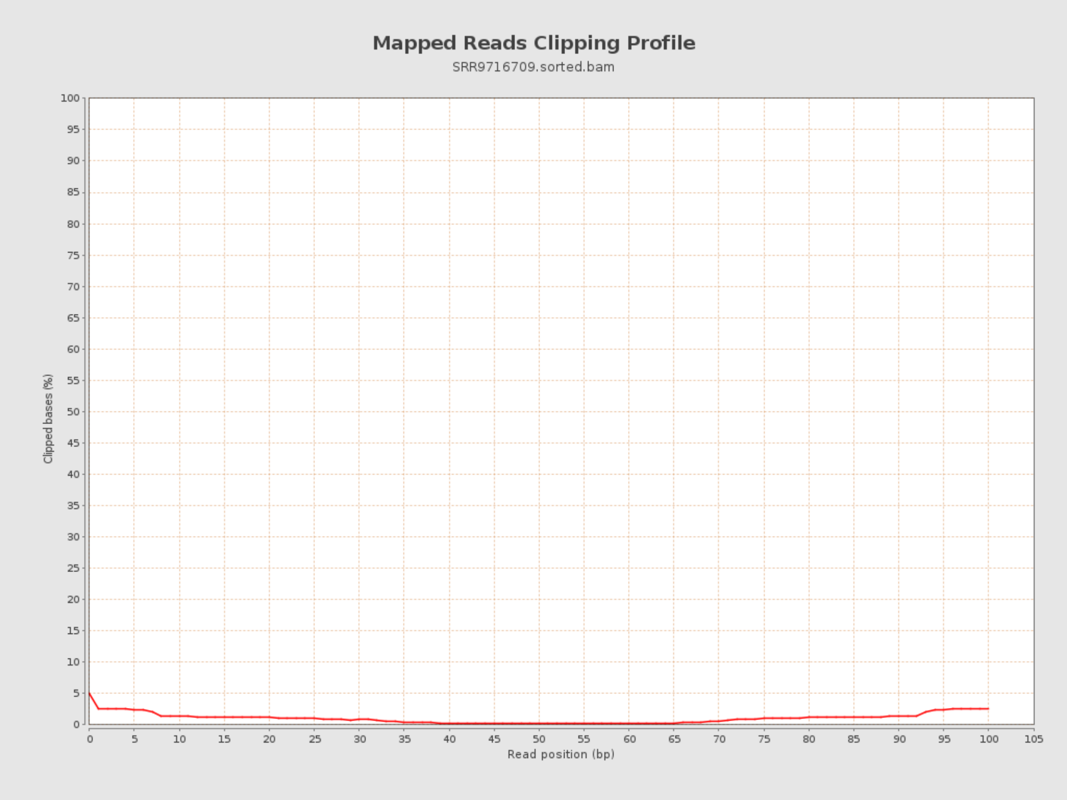
8. Results : Mapped Reads Nucleotide Content



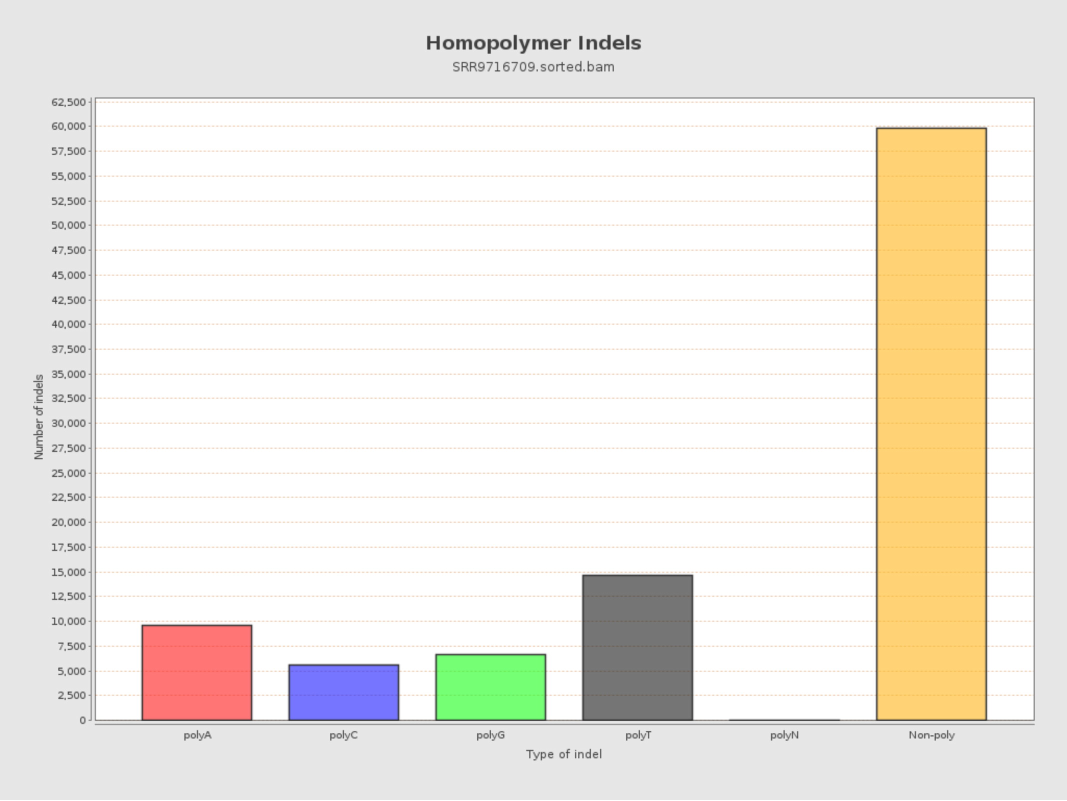
9. Results : Mapped Reads GC-content Distribution



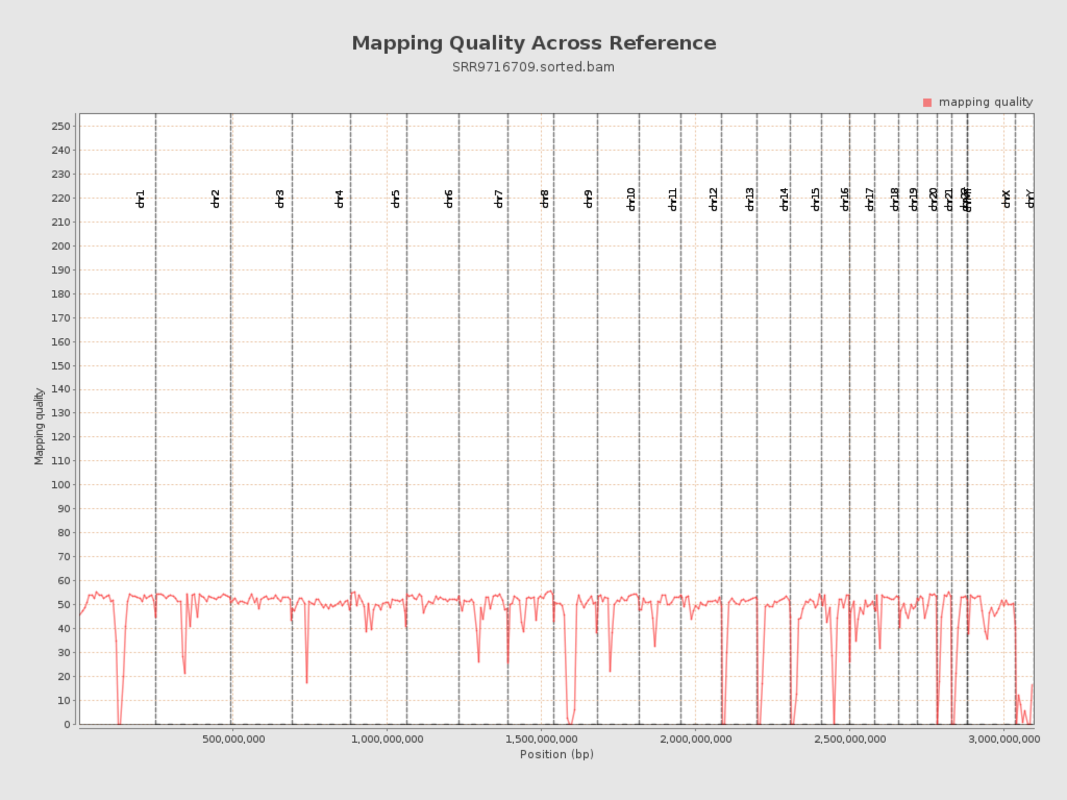
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram