

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 07:39:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716707.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_SRR9716707 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716707.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 07:39:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716707.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,933,922
Mapped reads	4,695,569 / 95.17%
Unmapped reads	238,353 / 4.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	109,415 / 2.22%
Read min/max/mean length	30 / 101 / 101.81
Duplicated reads (estimated)	419,731 / 8.51%
Duplication rate	6.71%
Clipped reads	4,803,221 / 97.35%

2.2. ACGT Content

Number/percentage of A's	90,651,041 / 24.81%
Number/percentage of C's	77,532,393 / 21.22%
Number/percentage of T's	106,474,370 / 29.14%
Number/percentage of G's	90,776,100 / 24.84%
Number/percentage of N's	15,140 / 0%
GC Percentage	46.06%

2.3. Coverage

Mean	0.1181

Standard Deviation	0.7468
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2.4. Mapping Quality

Mean Mapping Quality	46.94
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2.5. Mismatches and indels

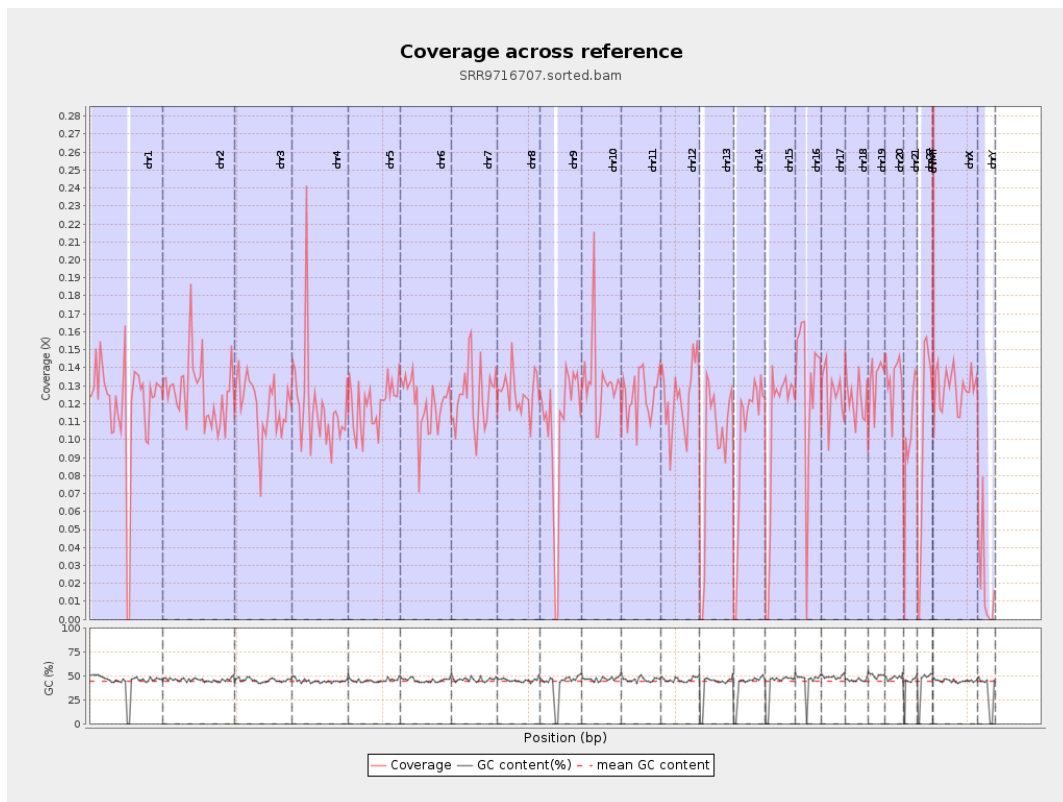
General error rate	0.64%
Mismatches	2,262,796
Insertions	28,380
Mapped reads with at least one insertion	0.59%
Deletions	64,431
Mapped reads with at least one deletion	1.35%
Homopolymer indels	38.93%

2.6. Chromosome stats

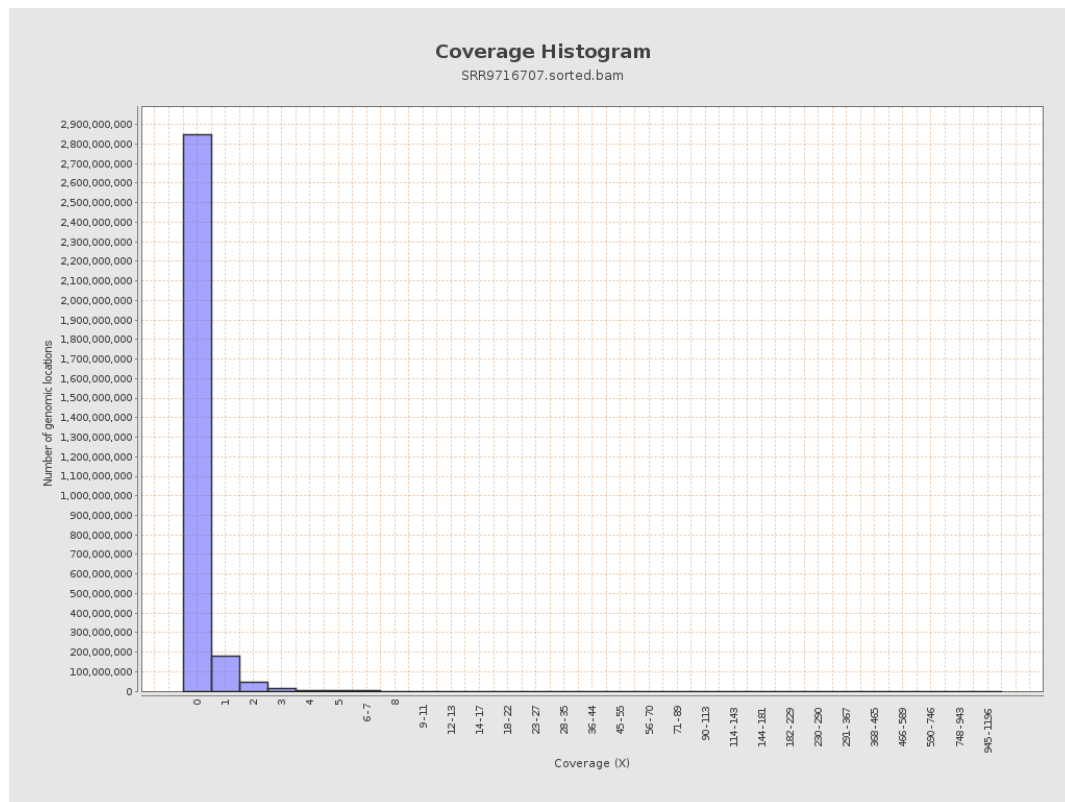
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	29646514	0.1189	1.1162
chr2	243199373	30811199	0.1267	0.8807
chr3	198022430	23466597	0.1185	0.4791
chr4	191154276	22729397	0.1189	0.7858
chr5	180915260	21701148	0.12	0.4847
chr6	171115067	20464790	0.1196	0.524
chr7	159138663	19804374	0.1244	0.9397

chr8	146364022	18457503	0.1261	0.7852
chr9	141213431	15125089	0.1071	0.6628
chr10	135534747	17868781	0.1318	1.0649
chr11	135006516	16780207	0.1243	0.7674
chr12	133851895	16692589	0.1247	0.5076
chr13	115169878	10982159	0.0954	0.434
chr14	107349540	10976640	0.1023	0.5332
chr15	102531392	10752270	0.1049	0.4578
chr16	90354753	11758329	0.1301	0.5735
chr17	81195210	10307026	0.1269	0.61
chr18	78077248	9579001	0.1227	1.139
chr19	59128983	7869246	0.1331	0.8403
chr20	63025520	8388342	0.1331	0.568
chr21	48129895	4967748	0.1032	0.6696
chr22	51304566	5237627	0.1021	0.4701
chrMT	16571	39842	2.4043	2.4057
chrX	155270560	19974617	0.1286	0.5765
chrY	59373566	1203696	0.0203	0.7255

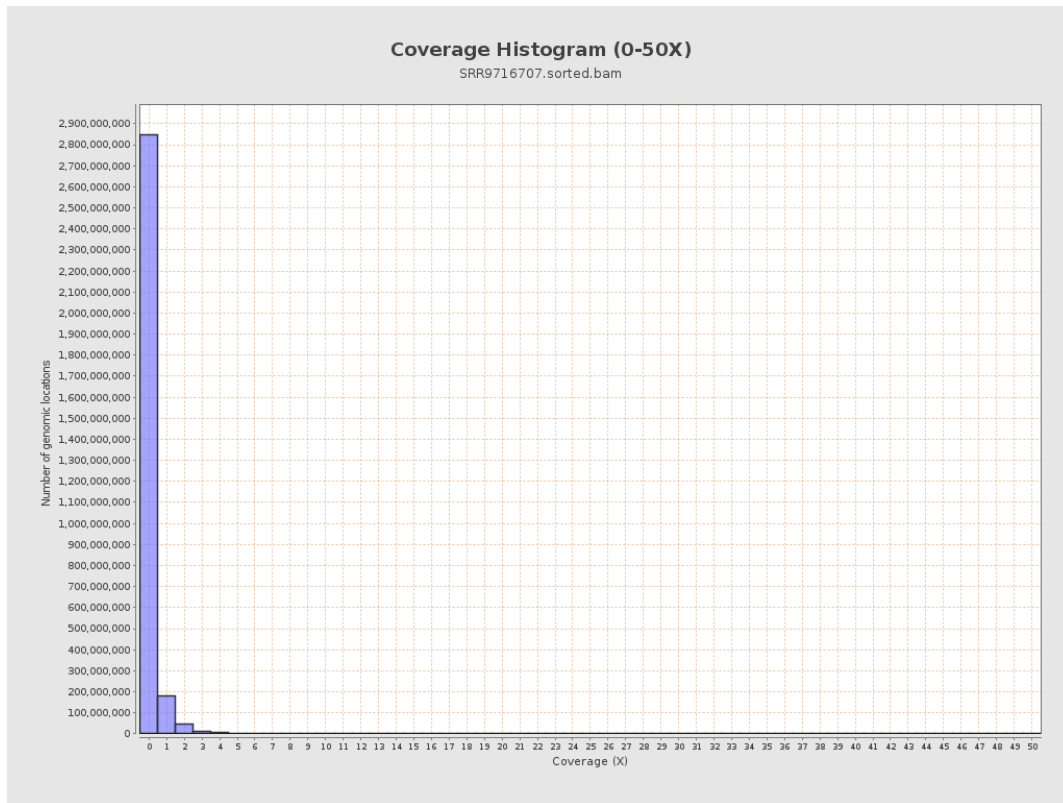
3. Results : Coverage across reference



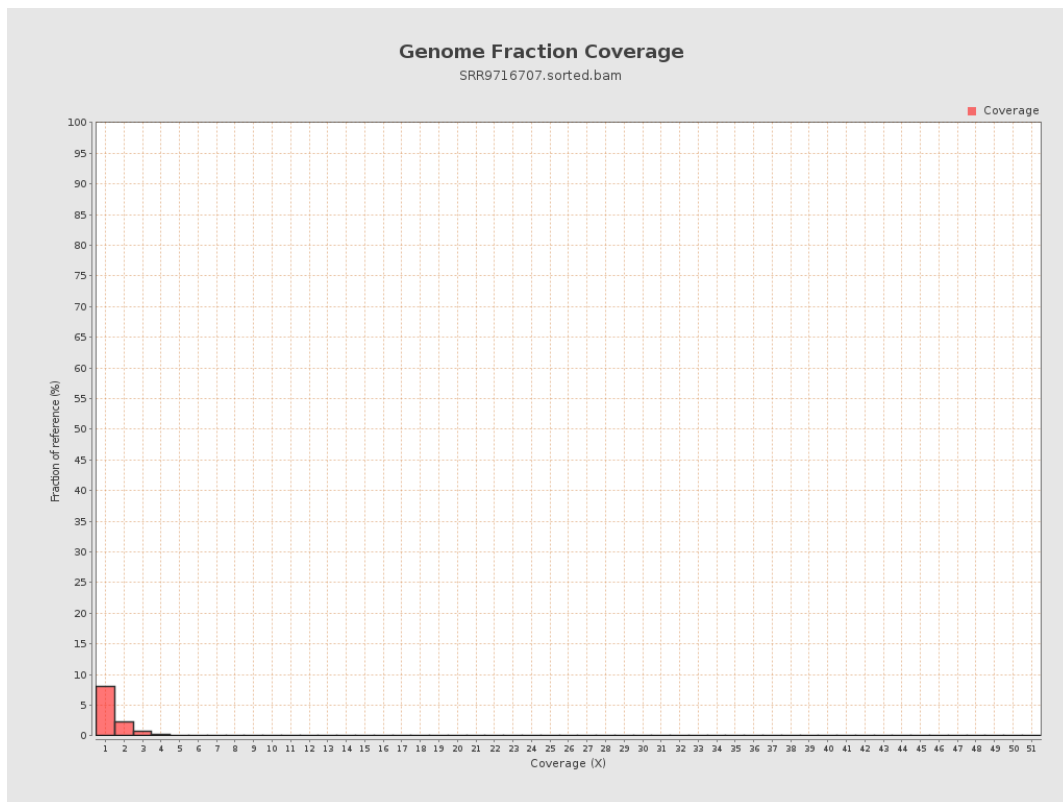
4. Results : Coverage Histogram



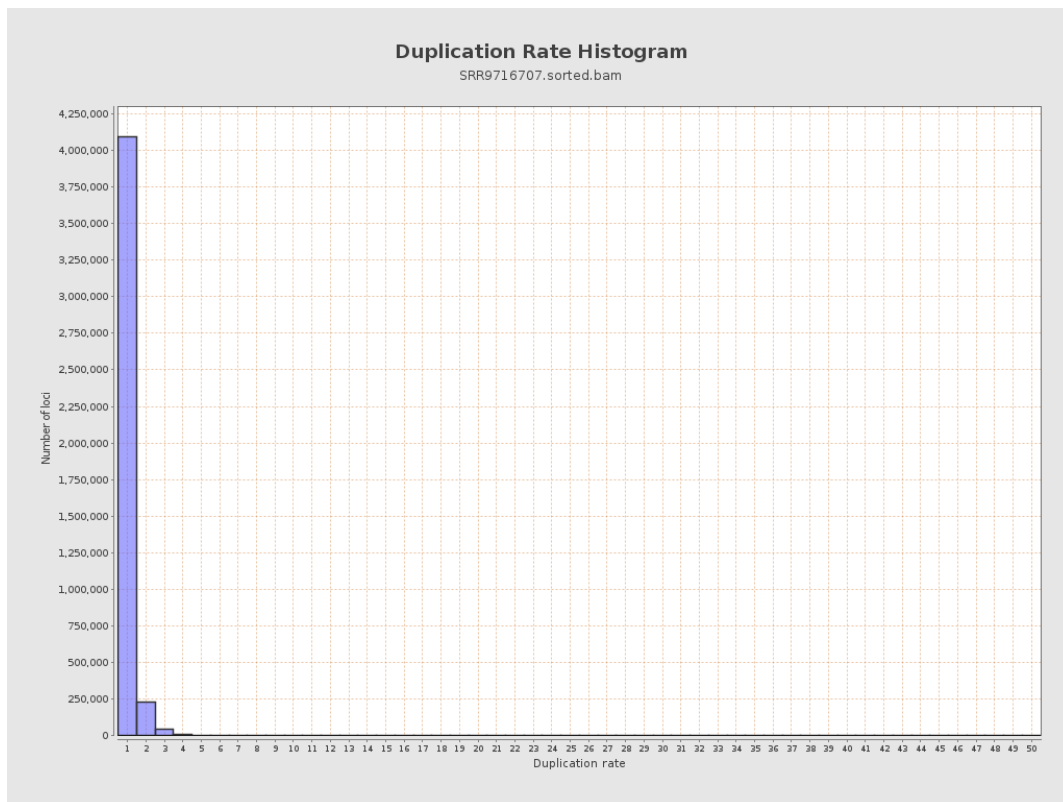
5. Results : Coverage Histogram (0-50X)



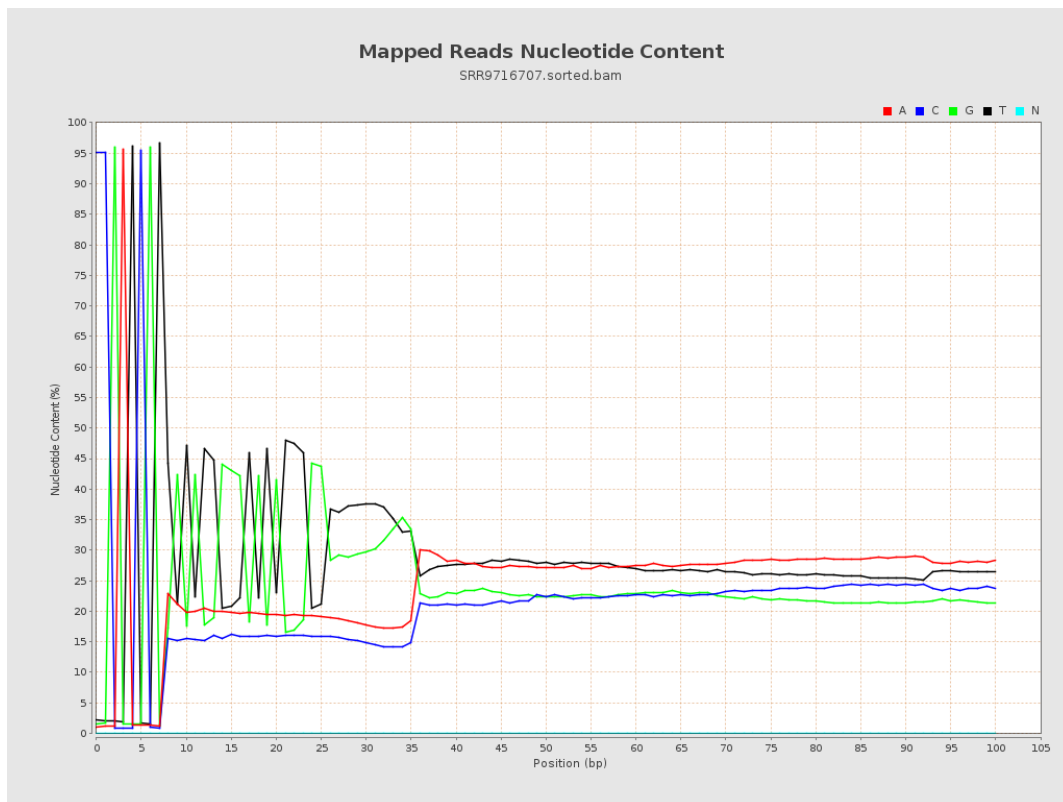
6. Results : Genome Fraction Coverage



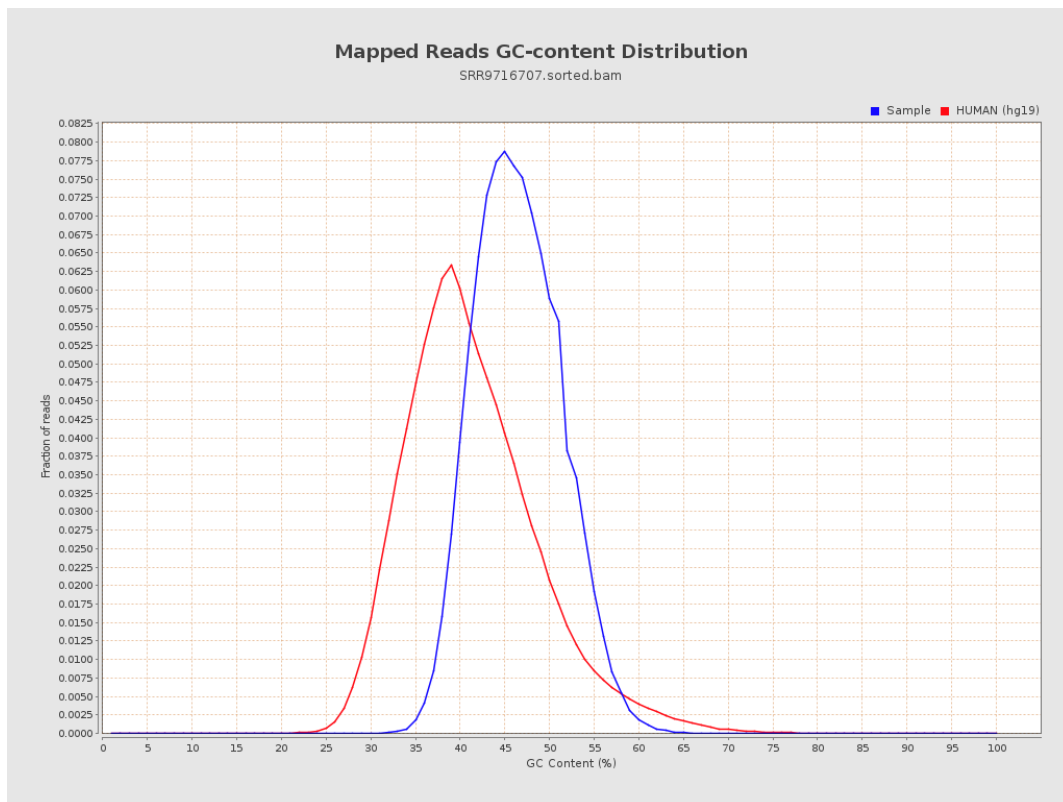
7. Results : Duplication Rate Histogram



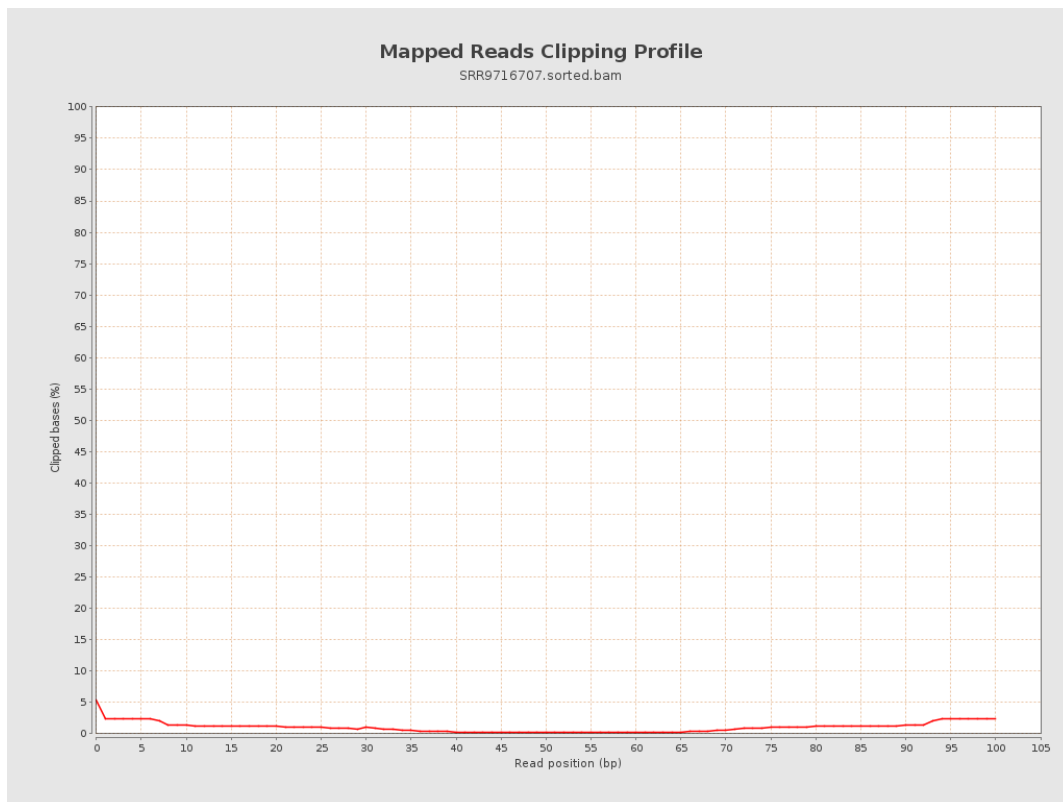
8. Results : Mapped Reads Nucleotide Content



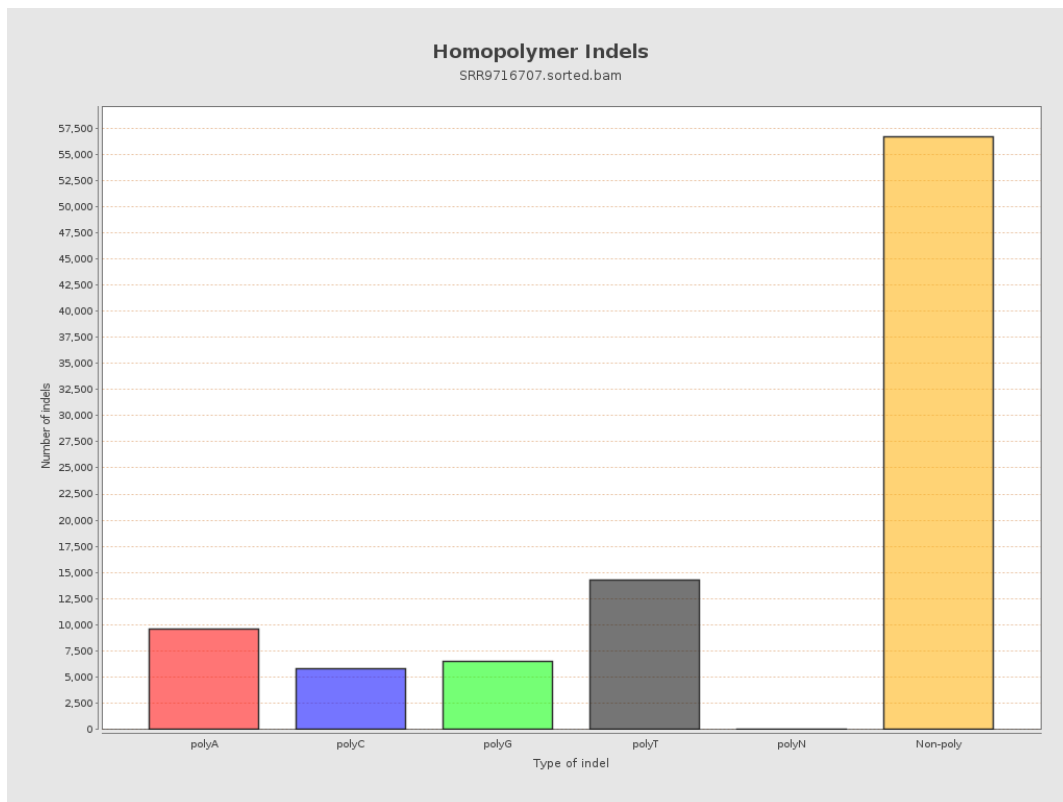
9. Results : Mapped Reads GC-content Distribution



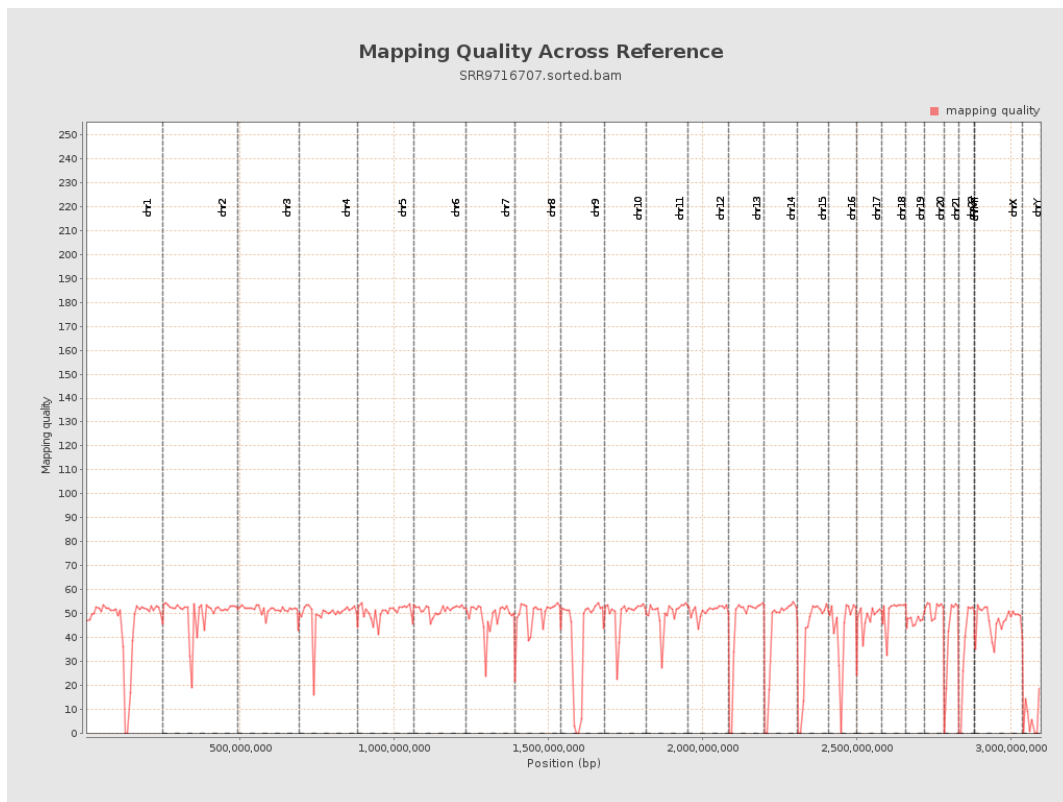
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

