Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 09:31:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716736.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_SRR9716736 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716736.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 09:31:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716736.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,719,933
Mapped reads	1,550,464 / 90.15%
Unmapped reads	169,469 / 9.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,237 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	43,245 / 2.51%
Duplication rate	1.92%
Clipped reads	1,553,083 / 90.3%

2.2. ACGT Content

Number/percentage of A's	21,815,153 / 24.36%
Number/percentage of C's	17,880,009 / 19.97%
Number/percentage of T's	28,904,141 / 32.28%
Number/percentage of G's	20,952,391 / 23.4%
Number/percentage of N's	1,101 / 0%
GC Percentage	43.36%

2.3. Coverage

Mean	0.0289

Standard Deviation	0.2732

2.4. Mapping Quality

Mean Mapping Quality	44.05

2.5. Mismatches and indels

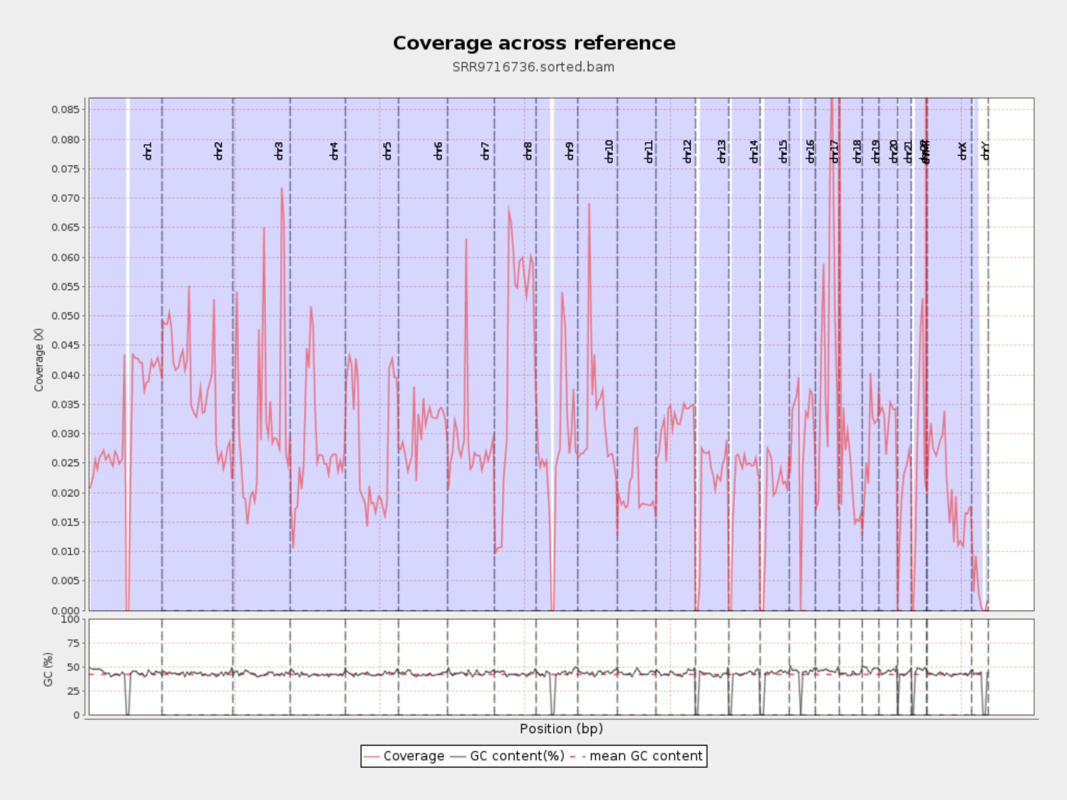
General error rate	0.51%
Mismatches	441,986
Insertions	6,680
Mapped reads with at least one insertion	0.43%
Deletions	15,761
Mapped reads with at least one deletion	1.01%
Homopolymer indels	40.43%

2.6. Chromosome stats

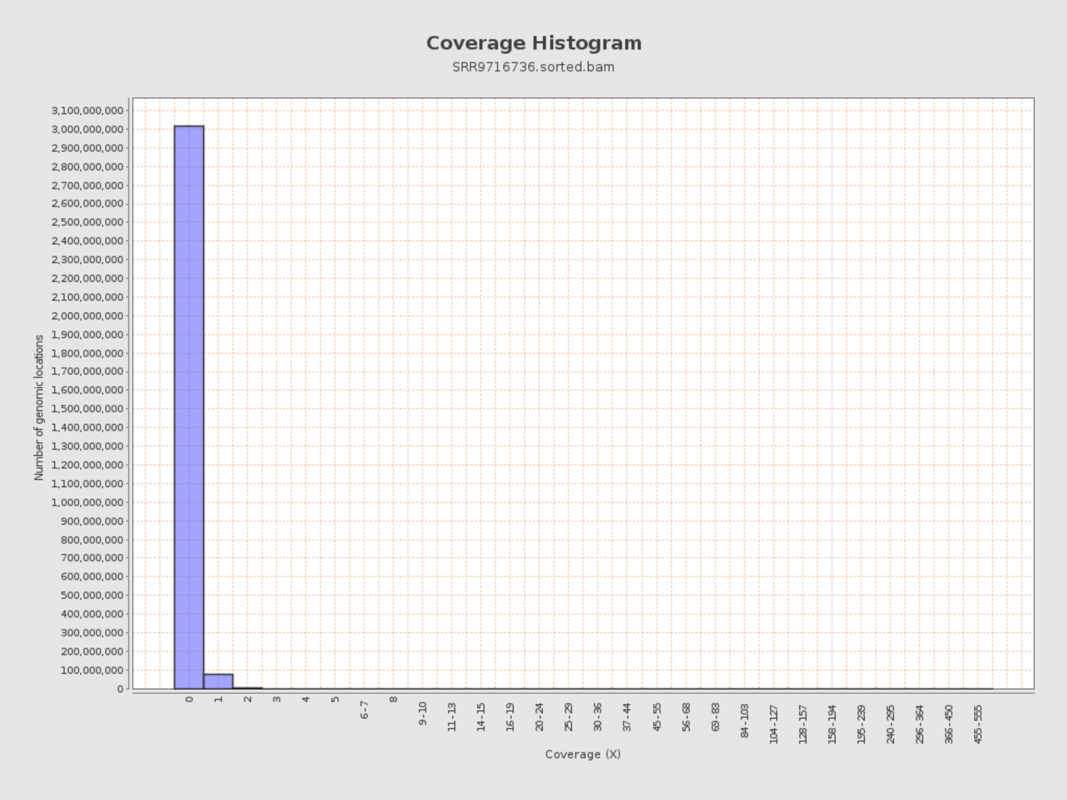
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7678979	0.0308	0.4376
chr2	243199373	9248247	0.038	0.3269
chr3	198022430	6420219	0.0324	0.2004
chr4	191154276	5226463	0.0273	0.1875
chr5	180915260	5069152	0.028	0.1803
chr6	171115067	5254419	0.0307	0.2038
chr7	159138663	4537653	0.0285	0.522

chr8	146364022	6504776	0.0444	0.2876
chr9	141213431	3753989	0.0266	0.2051
chr10	135534747	4436173	0.0327	0.3346
chr11	135006516	2686718	0.0199	0.1881
chr12	133851895	4275651	0.0319	0.2056
chr13	115169878	2397206	0.0208	0.1542
chr14	107349540	2287966	0.0213	0.1649
chr15	102531392	1936235	0.0189	0.1563
chr16	90354753	2757815	0.0305	0.1979
chr17	81195210	3581666	0.0441	0.234
chr18	78077248	2005914	0.0257	0.3103
chr19	59128983	1685345	0.0285	0.3647
chr20	63025520	2037143	0.0323	0.1985
chr21	48129895	946309	0.0197	0.1548
chr22	51304566	1315537	0.0256	0.173
chrMT	16571	42376	2.5572	2.0332
chrX	155270560	3306588	0.0213	0.1827
chrY	59373566	184830	0.0031	0.0816

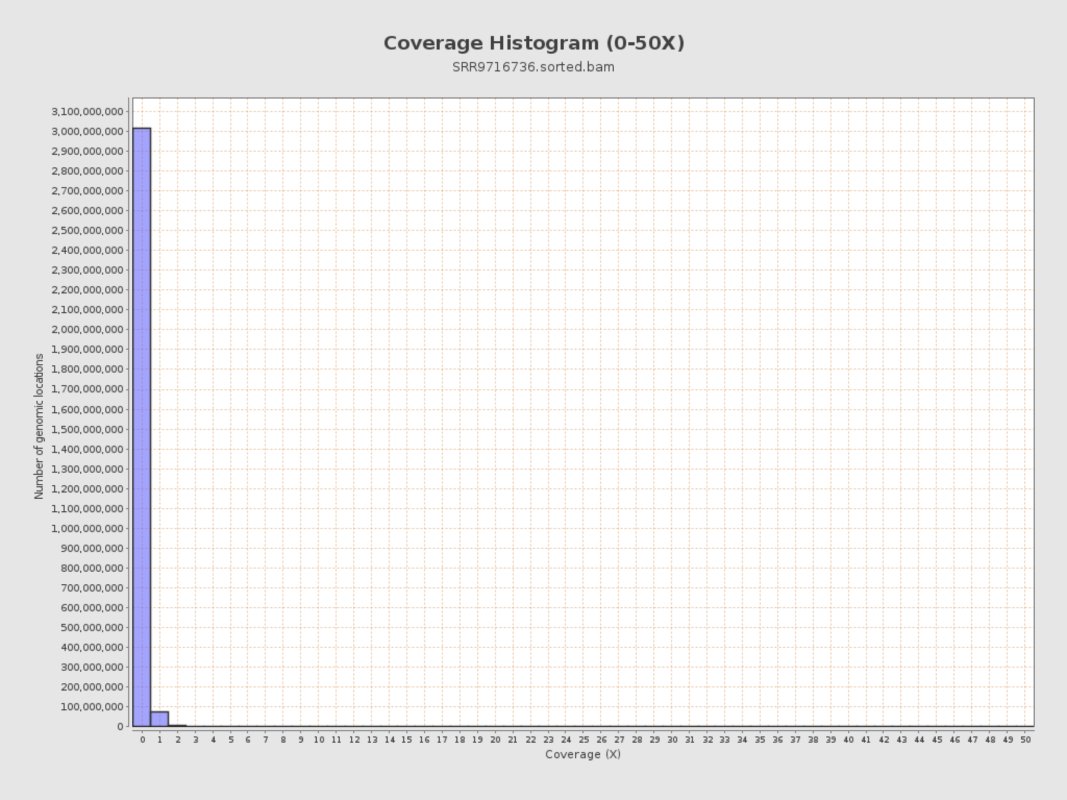
3. Results : Coverage across reference



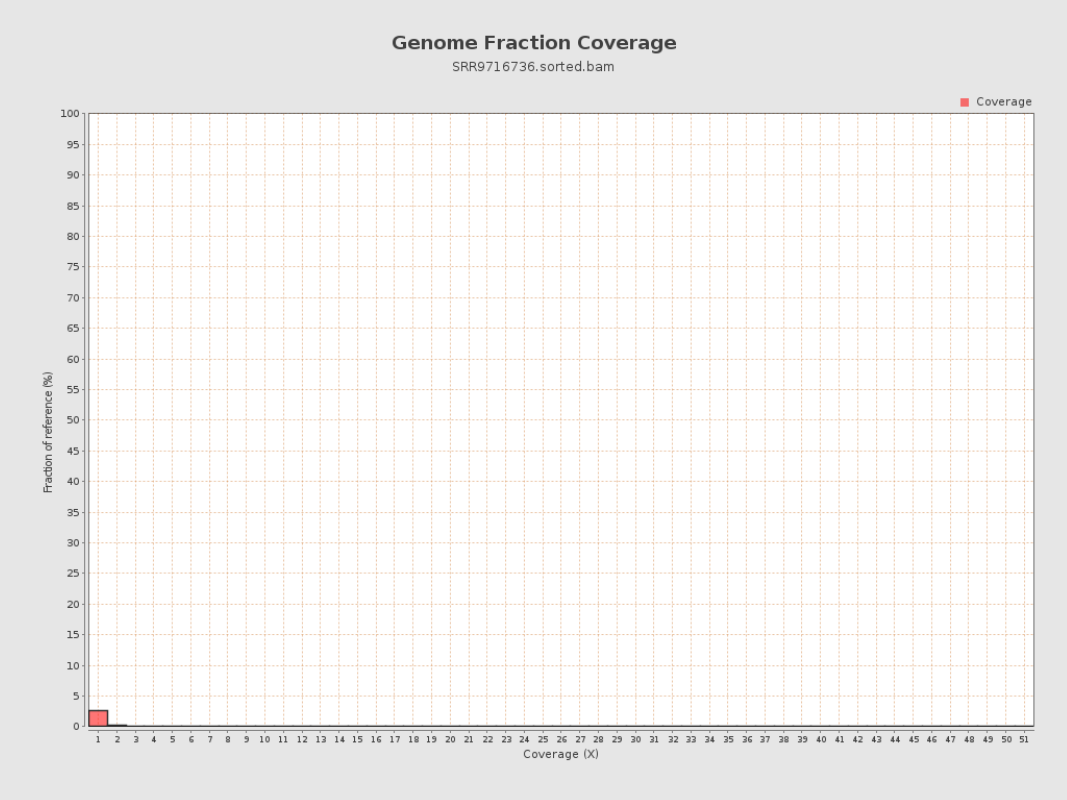
4. Results : Coverage Histogram



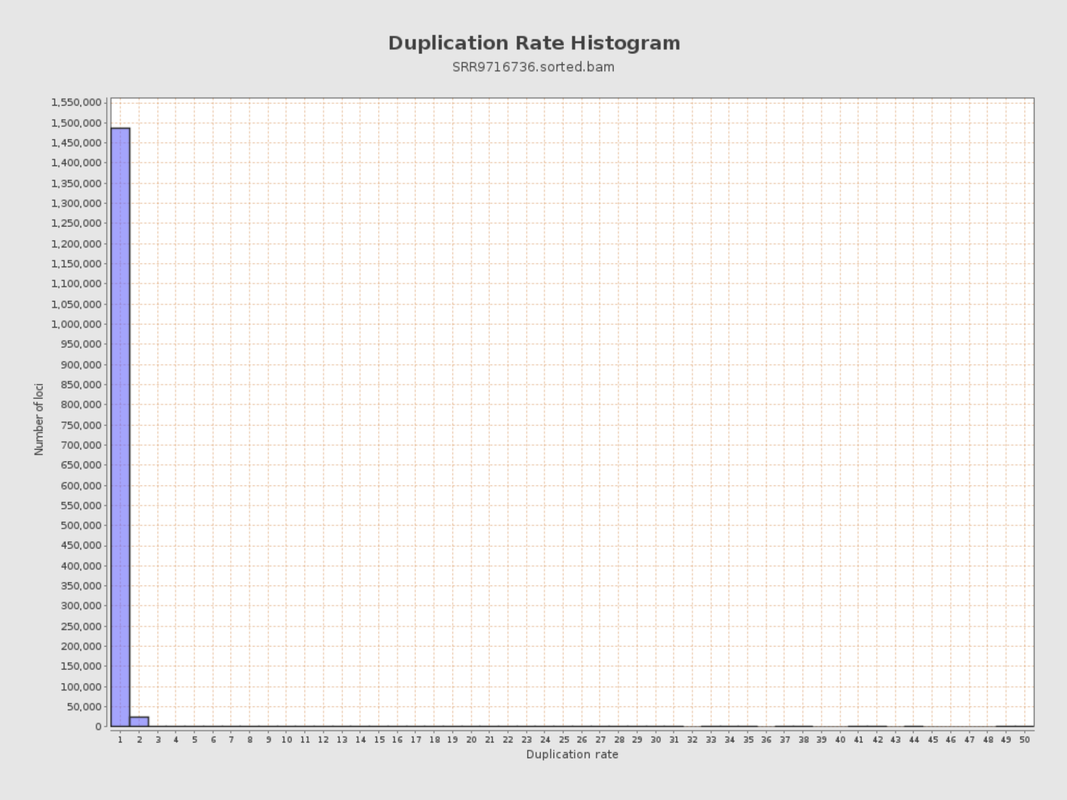
5. Results : Coverage Histogram (0-50X)



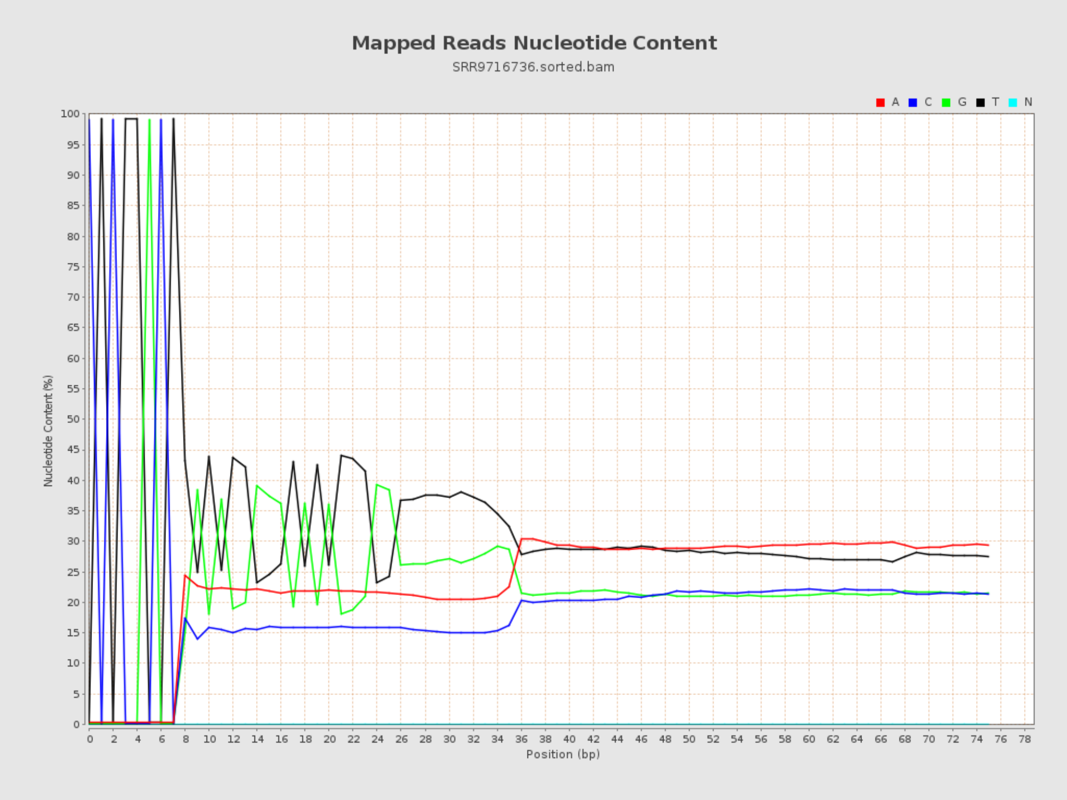
6. Results : Genome Fraction Coverage



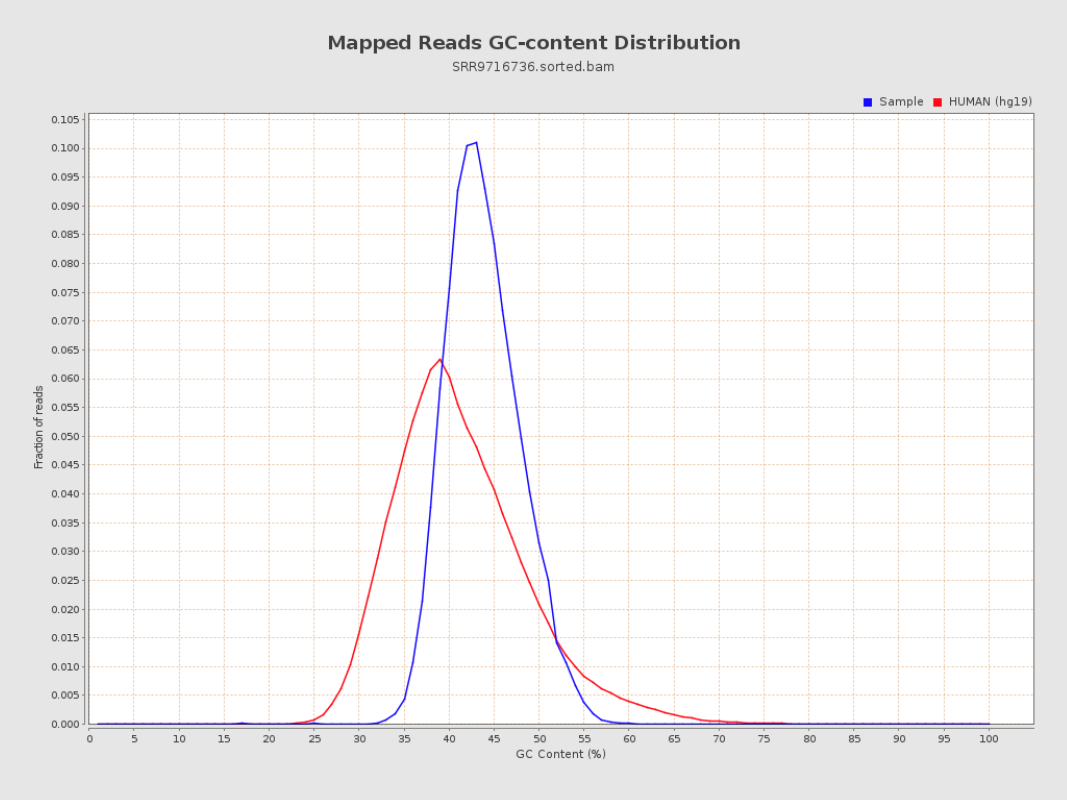
7. Results : Duplication Rate Histogram



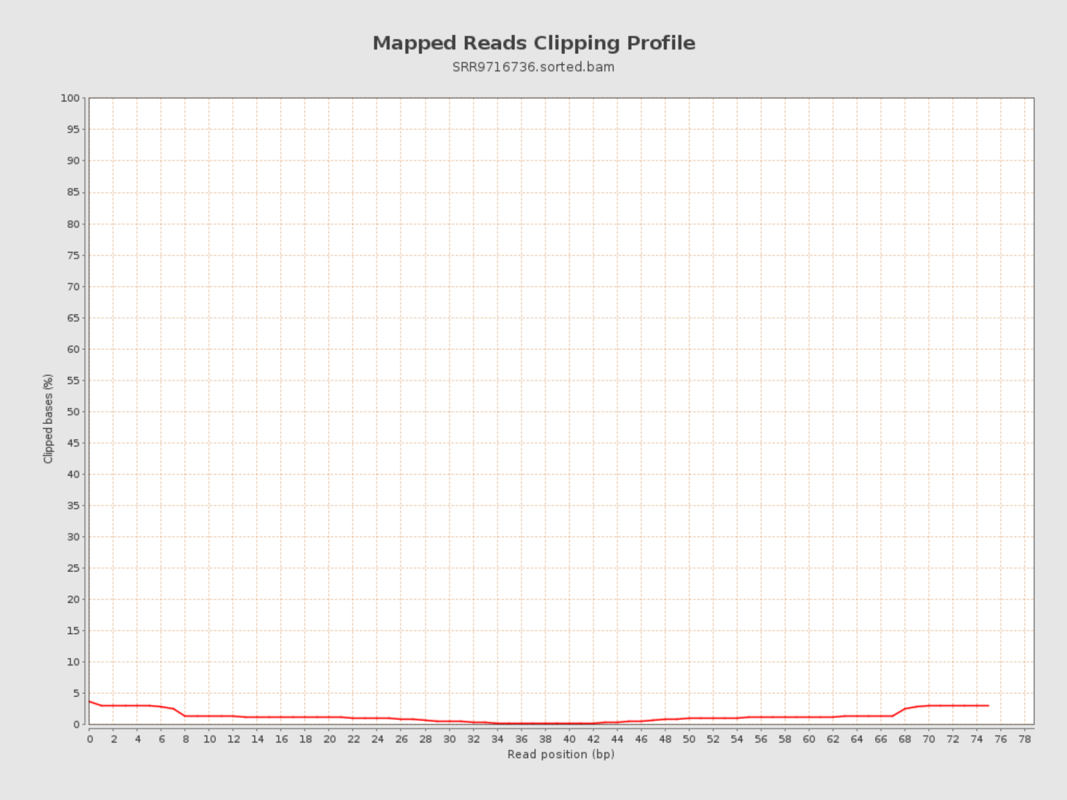
8. Results : Mapped Reads Nucleotide Content



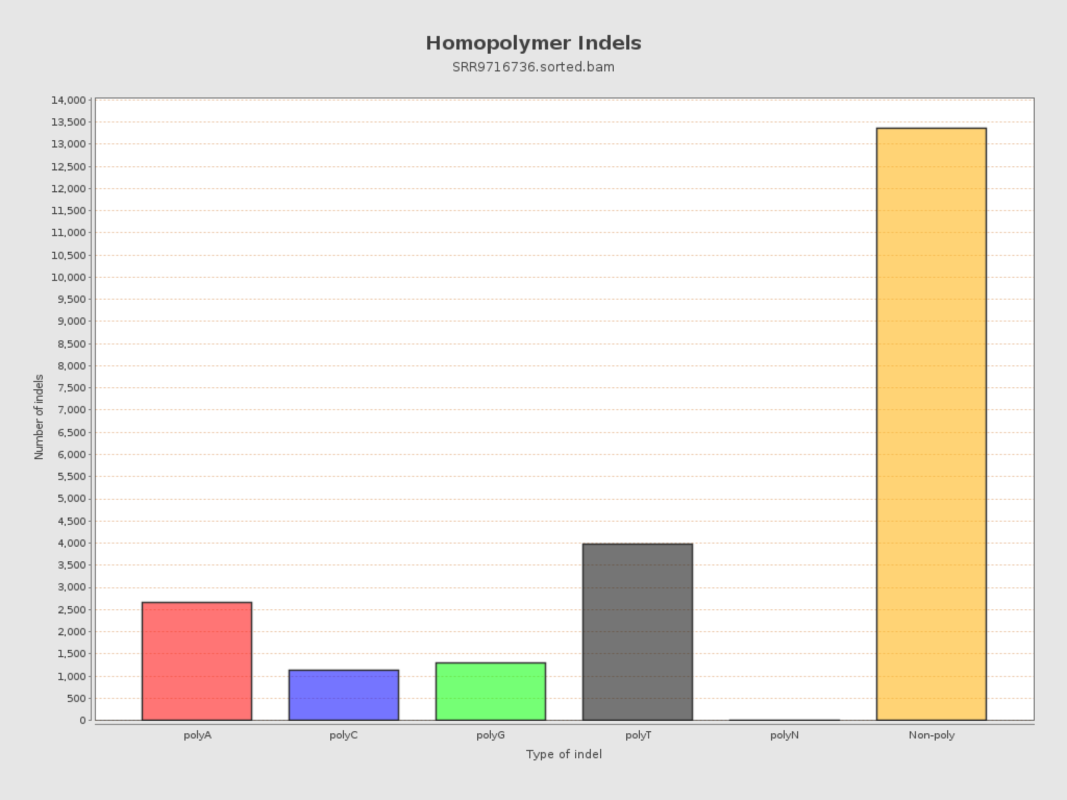
9. Results : Mapped Reads GC-content Distribution



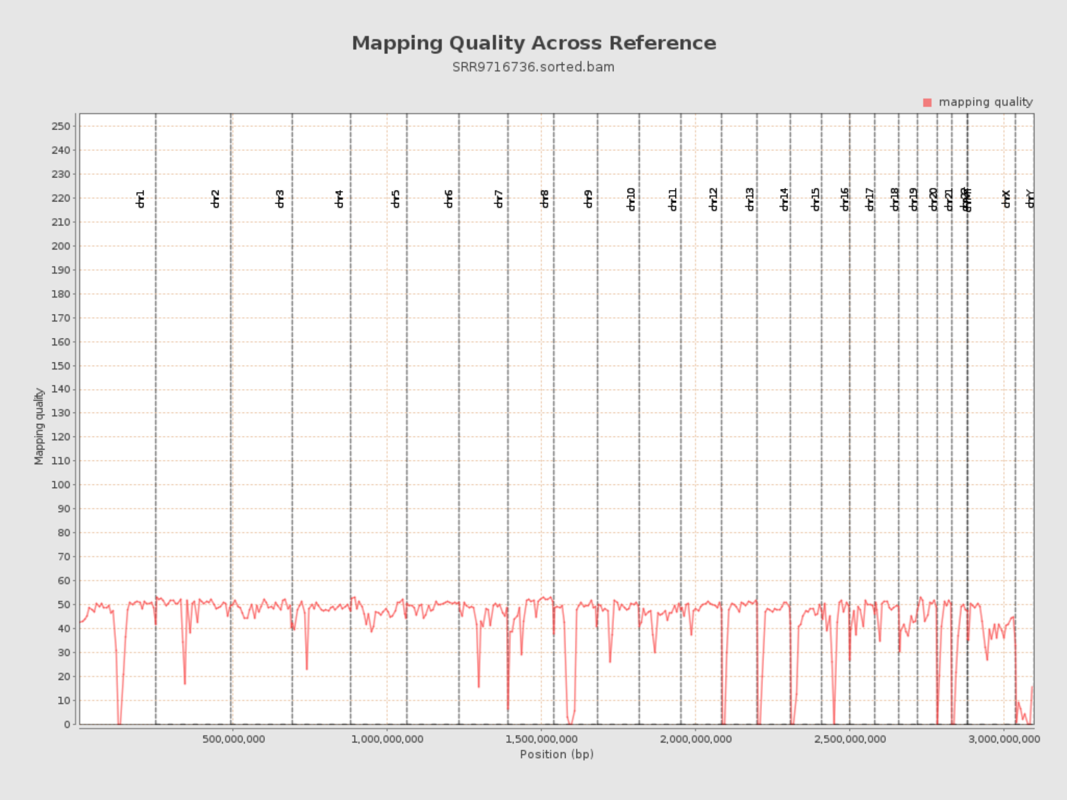
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram