Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 12:24:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716789.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_SRR9716789 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716789.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 12:24:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716789.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	547,360
Mapped reads	460,263 / 84.09%
Unmapped reads	87,097 / 15.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,802 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	10,010 / 1.83%
Duplication rate	1.74%
Clipped reads	460,829 / 84.19%

2.2. ACGT Content

Number/percentage of A's	6,924,403 / 25.83%
Number/percentage of C's	5,266,980 / 19.65%
Number/percentage of T's	8,349,021 / 31.15%
Number/percentage of G's	6,261,909 / 23.36%
Number/percentage of N's	796 / 0%
GC Percentage	43.01%

2.3. Coverage

Mean	0.0087

Standard Deviation	0.1124

2.4. Mapping Quality

Mean Mapping Quality	45.42

2.5. Mismatches and indels

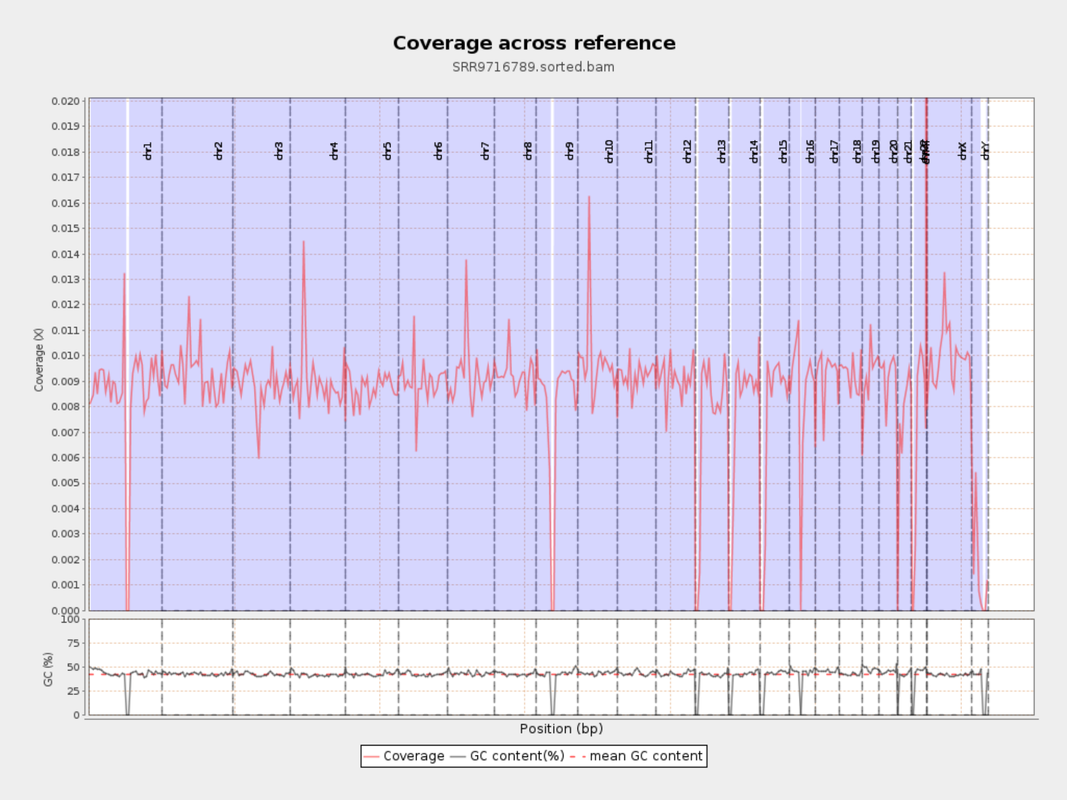
General error rate	0.52%
Mismatches	134,796
Insertions	2,194
Mapped reads with at least one insertion	0.47%
Deletions	4,956
Mapped reads with at least one deletion	1.07%
Homopolymer indels	41.78%

2.6. Chromosome stats

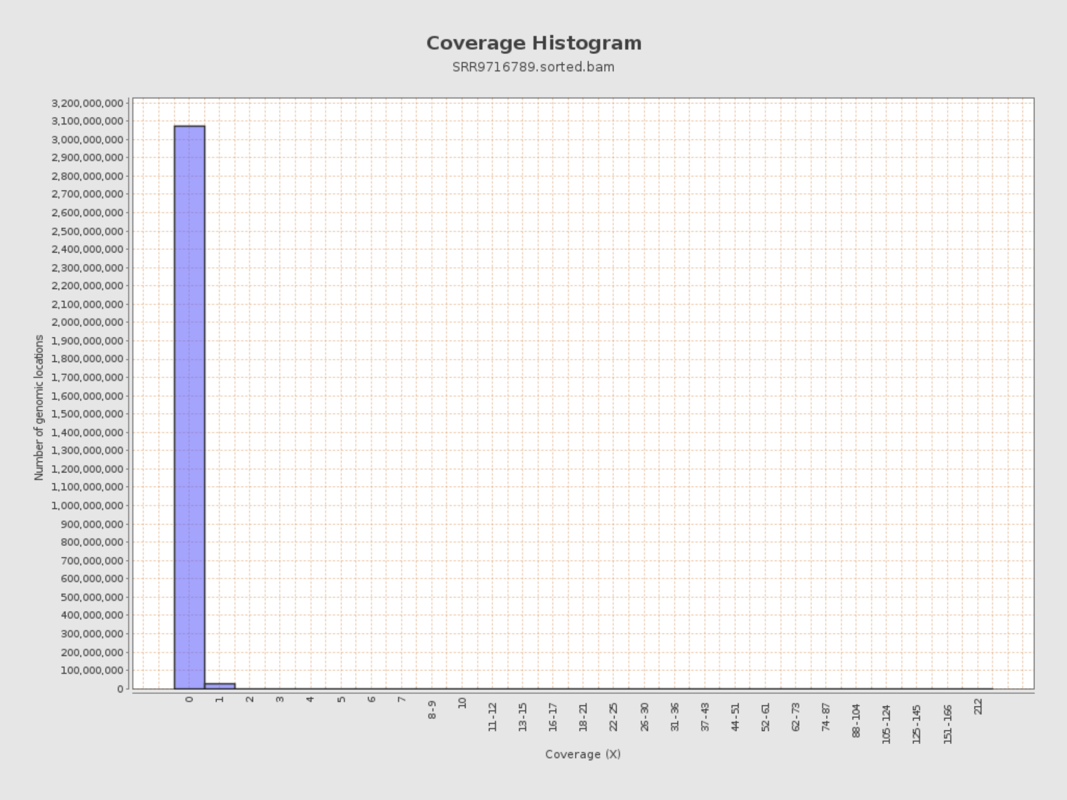
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2123292	0.0085	0.1586
chr2	243199373	2269587	0.0093	0.1344
chr3	198022430	1750670	0.0088	0.0979
chr4	191154276	1716055	0.009	0.1023
chr5	180915260	1582117	0.0087	0.0975
chr6	171115067	1542224	0.009	0.1058
chr7	159138663	1469876	0.0092	0.1213

chr8	146364022	1349335	0.0092	0.1184
chr9	141213431	1100512	0.0078	0.0999
chr10	135534747	1328454	0.0098	0.1184
chr11	135006516	1245198	0.0092	0.1096
chr12	133851895	1217923	0.0091	0.0994
chr13	115169878	842999	0.0073	0.089
chr14	107349540	803175	0.0075	0.0913
chr15	102531392	756150	0.0074	0.0897
chr16	90354753	778743	0.0086	0.0994
chr17	81195210	753159	0.0093	0.1022
chr18	78077248	723734	0.0093	0.138
chr19	59128983	552718	0.0093	0.1299
chr20	63025520	580620	0.0092	0.1002
chr21	48129895	351741	0.0073	0.0922
chr22	51304566	332233	0.0065	0.0839
chrMT	16571	1909	0.1152	0.3631
chrX	155270560	1548562	0.01	0.1077
chrY	59373566	90051	0.0015	0.056

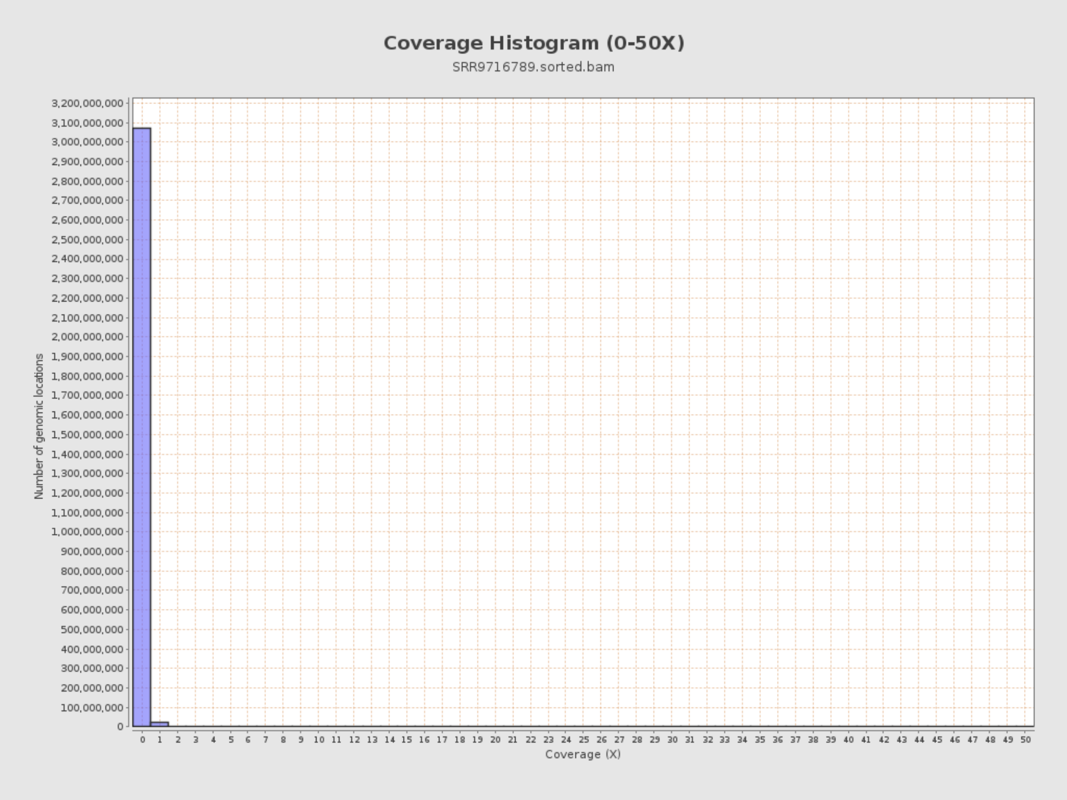
3. Results : Coverage across reference



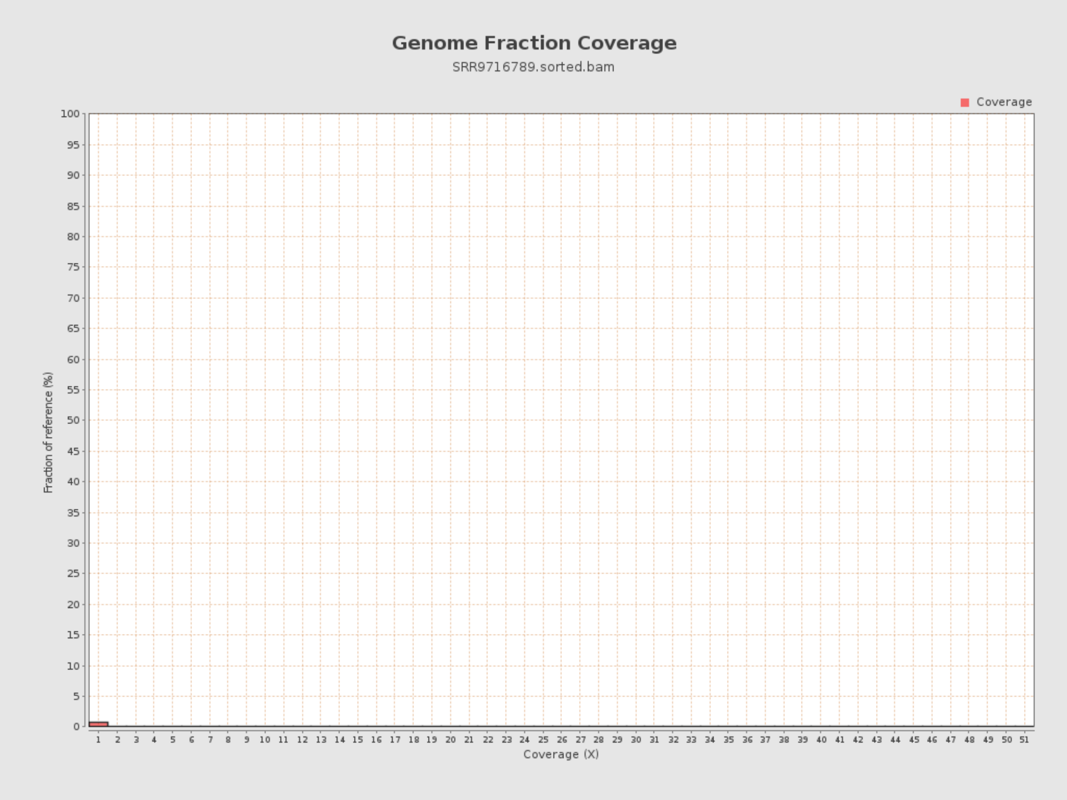
4. Results : Coverage Histogram



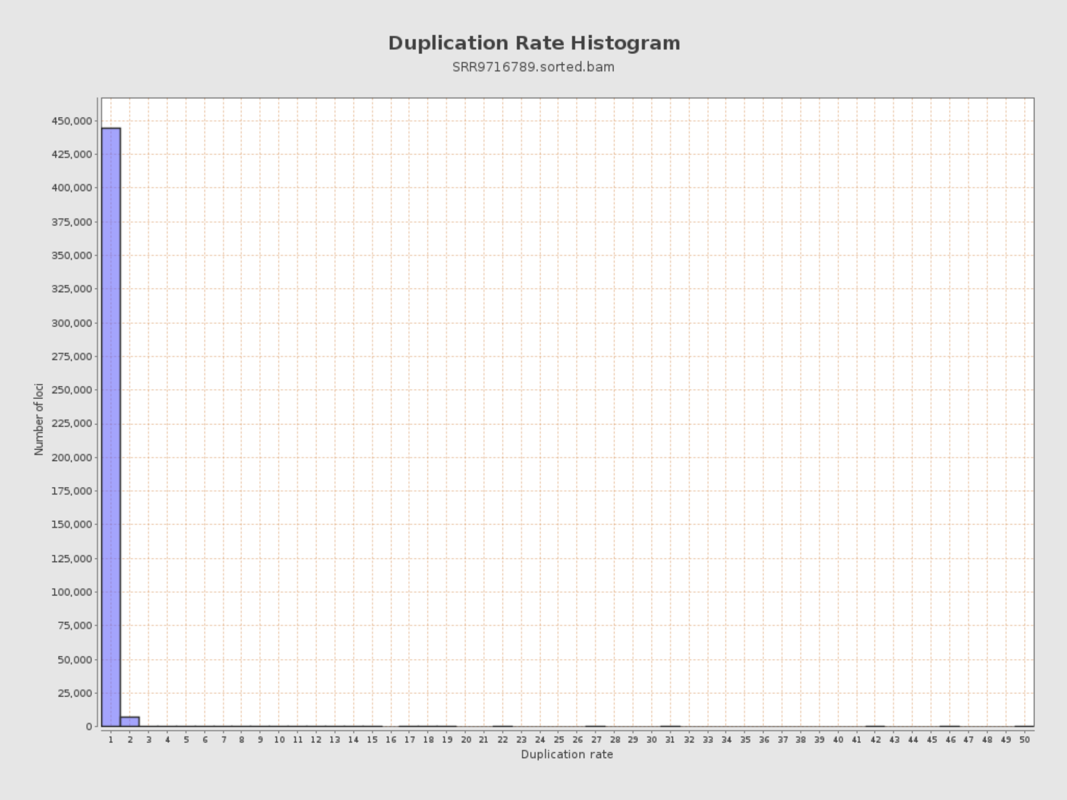
5. Results : Coverage Histogram (0-50X)



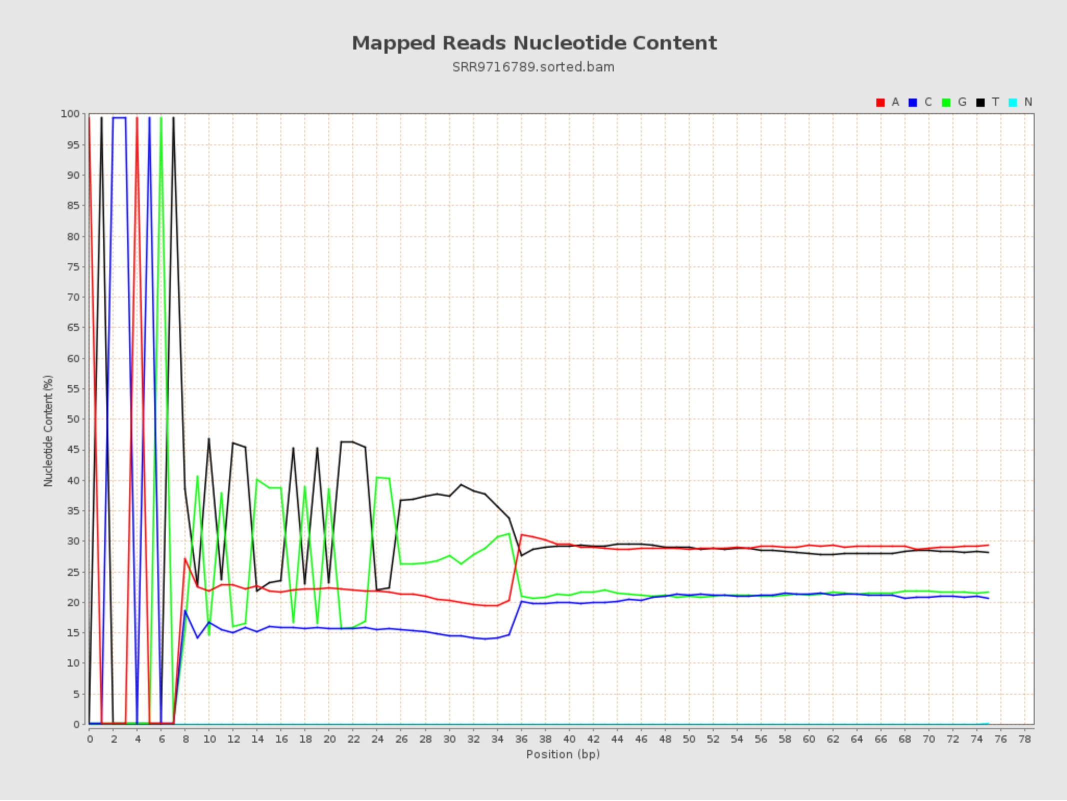
6. Results : Genome Fraction Coverage



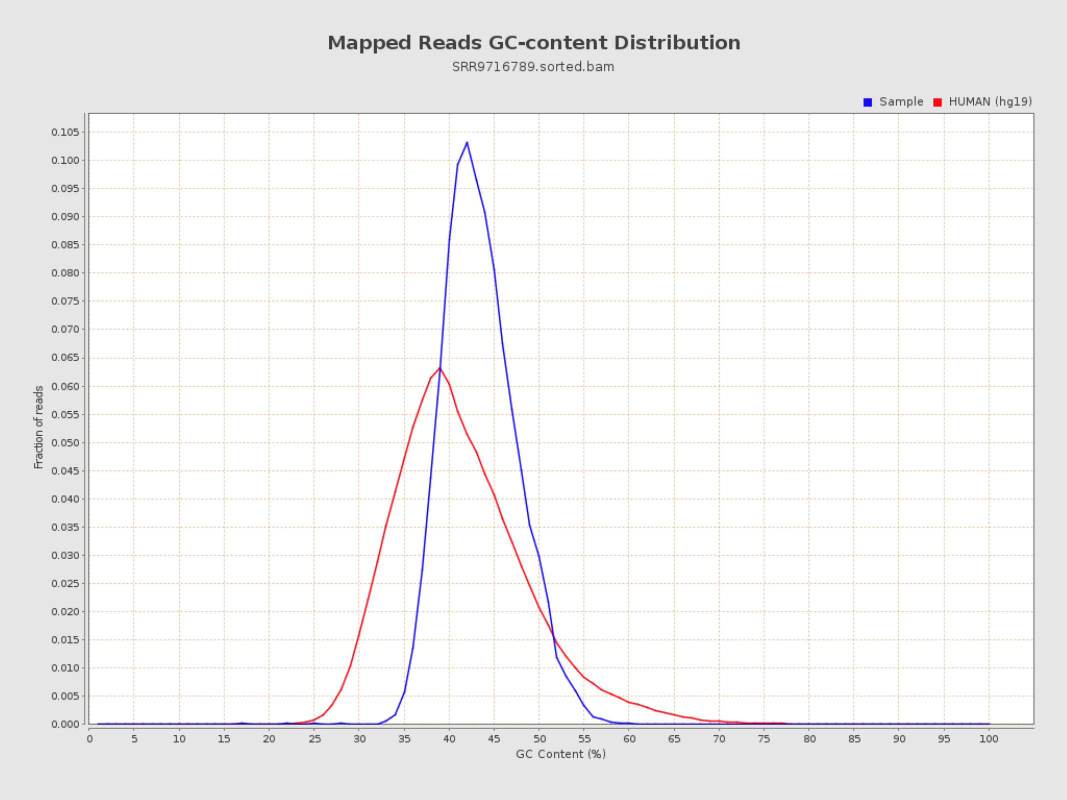
7. Results : Duplication Rate Histogram



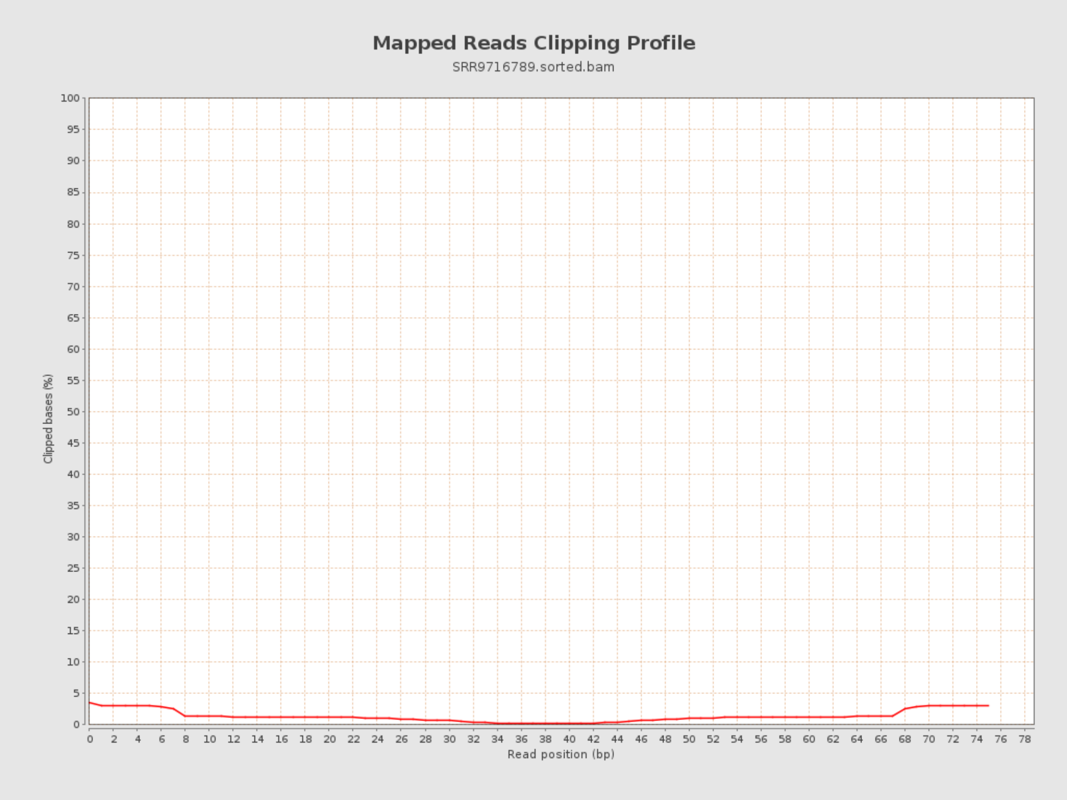
8. Results : Mapped Reads Nucleotide Content



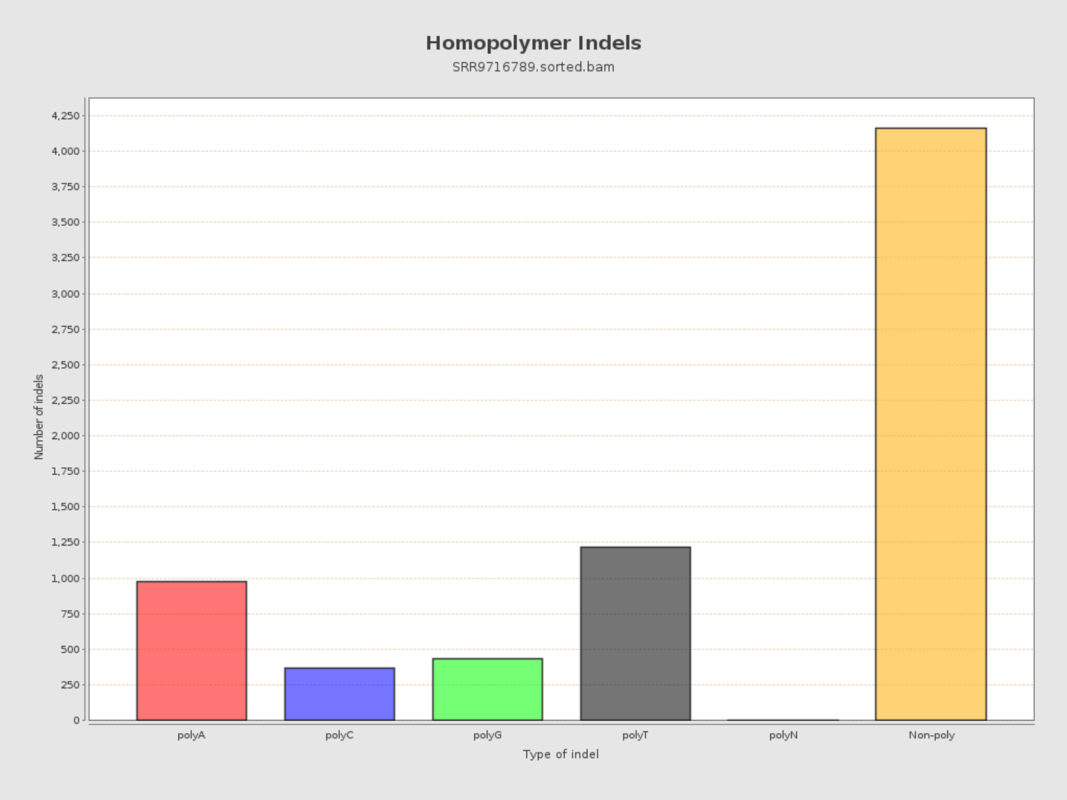
9. Results : Mapped Reads GC-content Distribution



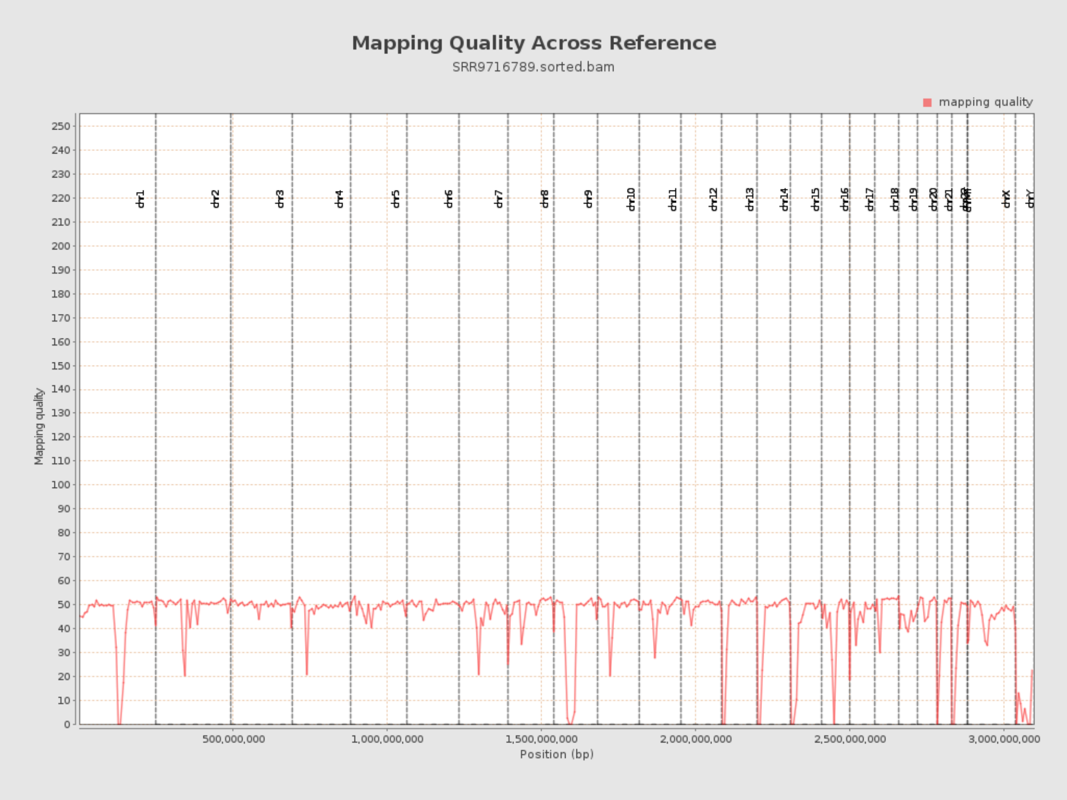
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram