Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 06:55:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716699.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_SRR9716699 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716699.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 06:55:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716699.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,615,561
Mapped reads	1,428,466 / 88.42%
Unmapped reads	187,095 / 11.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,742 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	33,881 / 2.1%
Duplication rate	1.66%
Clipped reads	1,430,200 / 88.53%

2.2. ACGT Content

Number/percentage of A's	20,384,938 / 25.09%
Number/percentage of C's	16,405,492 / 20.19%
Number/percentage of T's	24,964,240 / 30.72%
Number/percentage of G's	19,502,572 / 24%
Number/percentage of N's	562 / 0%
GC Percentage	44.19%

2.3. Coverage

Mean	0.0263

Standard Deviation	0.2246

2.4. Mapping Quality

Mean Mapping Quality	42.09

2.5. Mismatches and indels

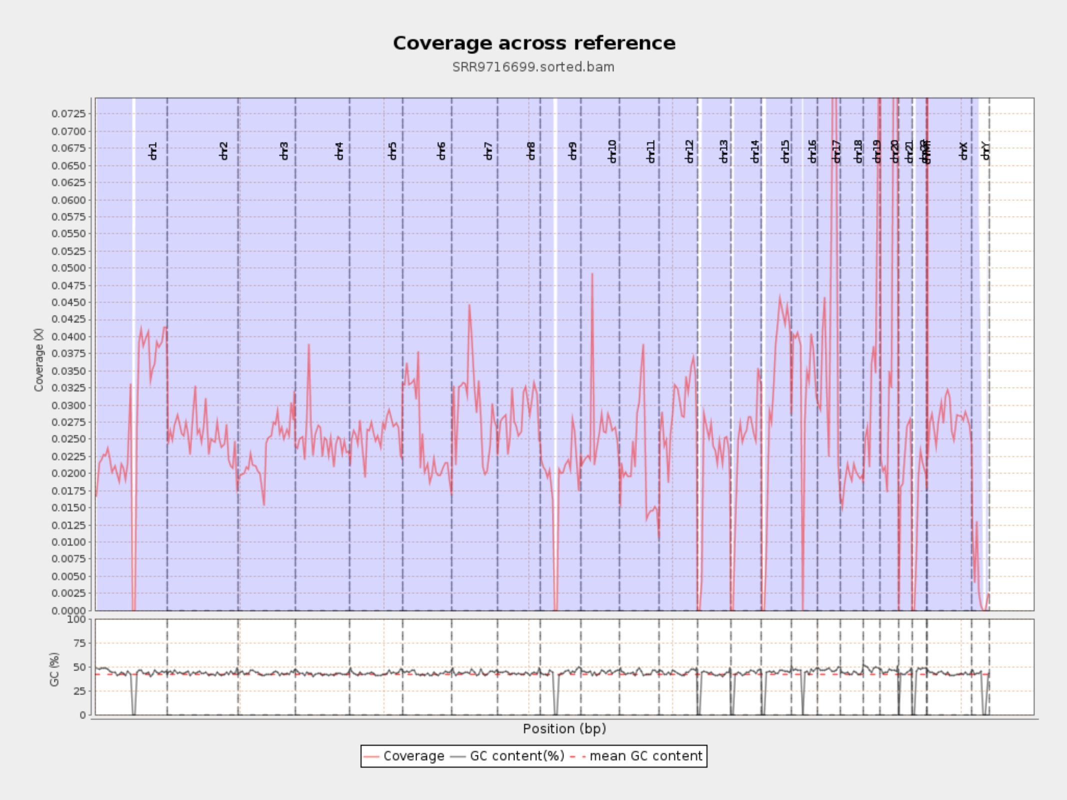
General error rate	0.53%
Mismatches	419,236
Insertions	5,758
Mapped reads with at least one insertion	0.4%
Deletions	15,204
Mapped reads with at least one deletion	1.06%
Homopolymer indels	41.39%

2.6. Chromosome stats

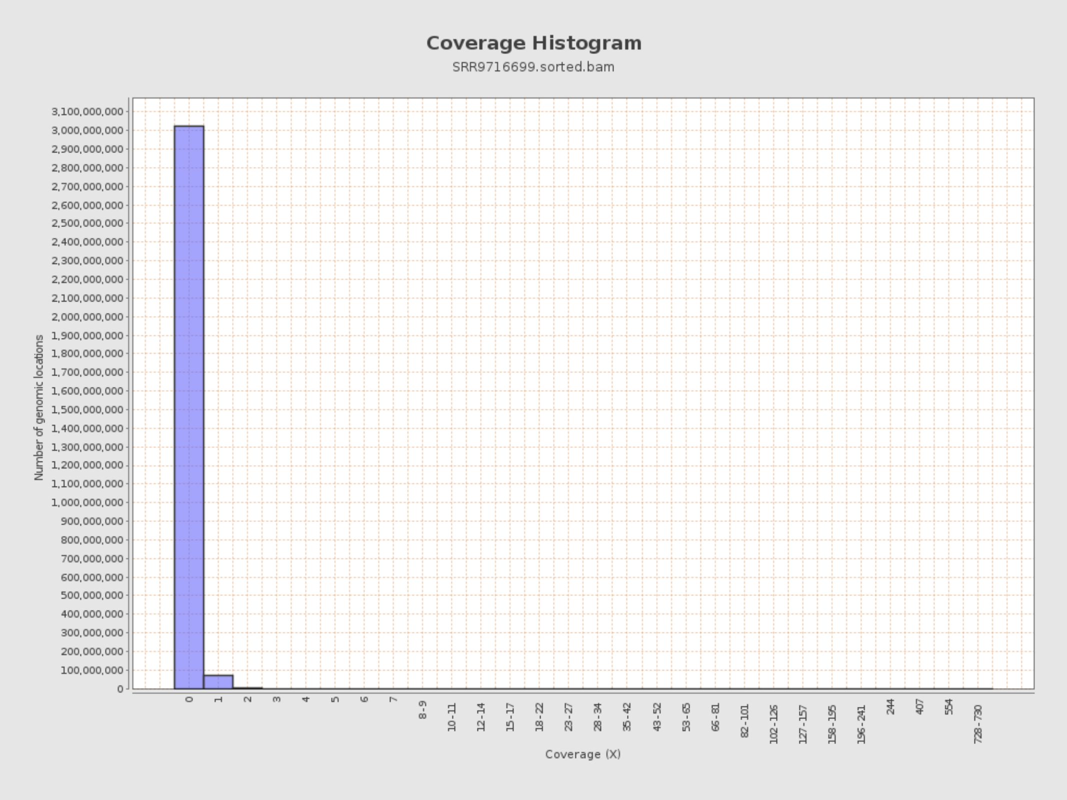
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6861483	0.0275	0.2686
chr2	243199373	6211889	0.0255	0.3423
chr3	198022430	4653665	0.0235	0.1698
chr4	191154276	4793923	0.0251	0.1827
chr5	180915260	4685236	0.0259	0.1728
chr6	171115067	4331922	0.0253	0.2018
chr7	159138663	4744708	0.0298	0.3051

chr8	146364022	4164695	0.0285	0.2157
chr9	141213431	2662425	0.0189	0.1686
chr10	135534747	3529361	0.026	0.2739
chr11	135006516	2885549	0.0214	0.1926
chr12	133851895	3954527	0.0295	0.1856
chr13	115169878	2373885	0.0206	0.1539
chr14	107349540	2481315	0.0231	0.1675
chr15	102531392	3186248	0.0311	0.1951
chr16	90354753	2982239	0.033	0.2065
chr17	81195210	3679236	0.0453	0.24
chr18	78077248	1506021	0.0193	0.2405
chr19	59128983	2340553	0.0396	0.2818
chr20	63025520	2936710	0.0466	0.2469
chr21	48129895	996593	0.0207	0.1641
chr22	51304566	749150	0.0146	0.131
chrMT	16571	5627	0.3396	0.6815
chrX	155270560	4327541	0.0279	0.1906
chrY	59373566	237246	0.004	0.1069

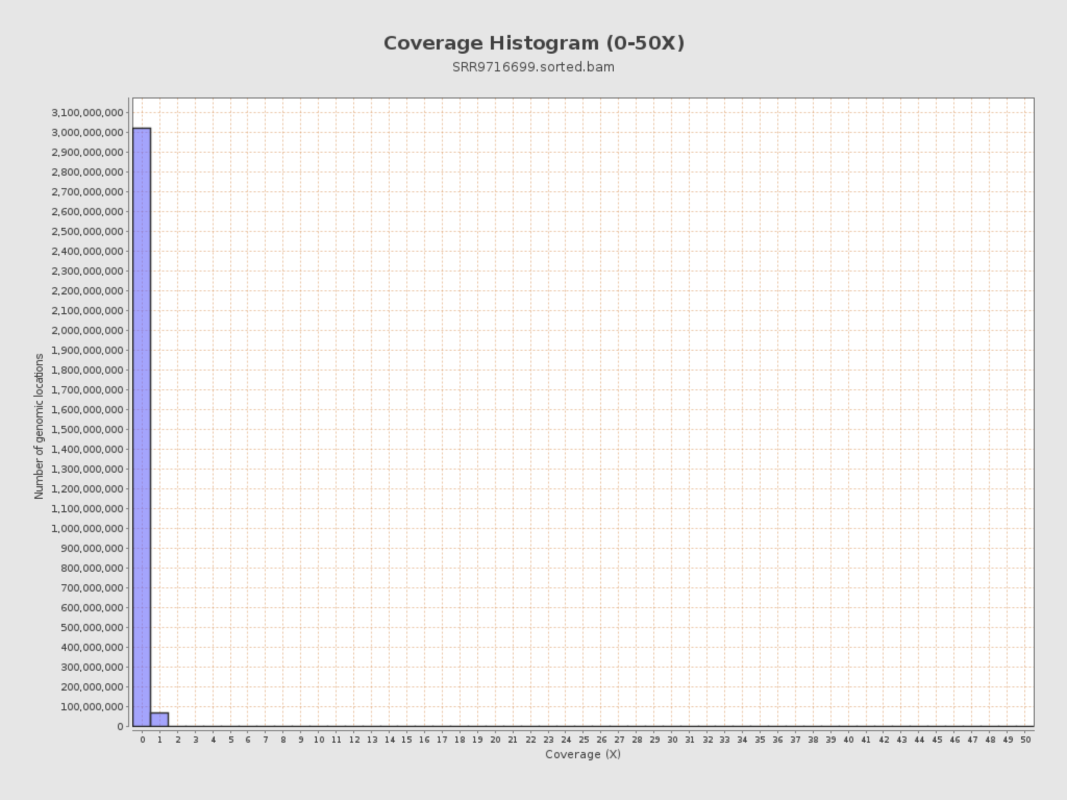
3. Results : Coverage across reference



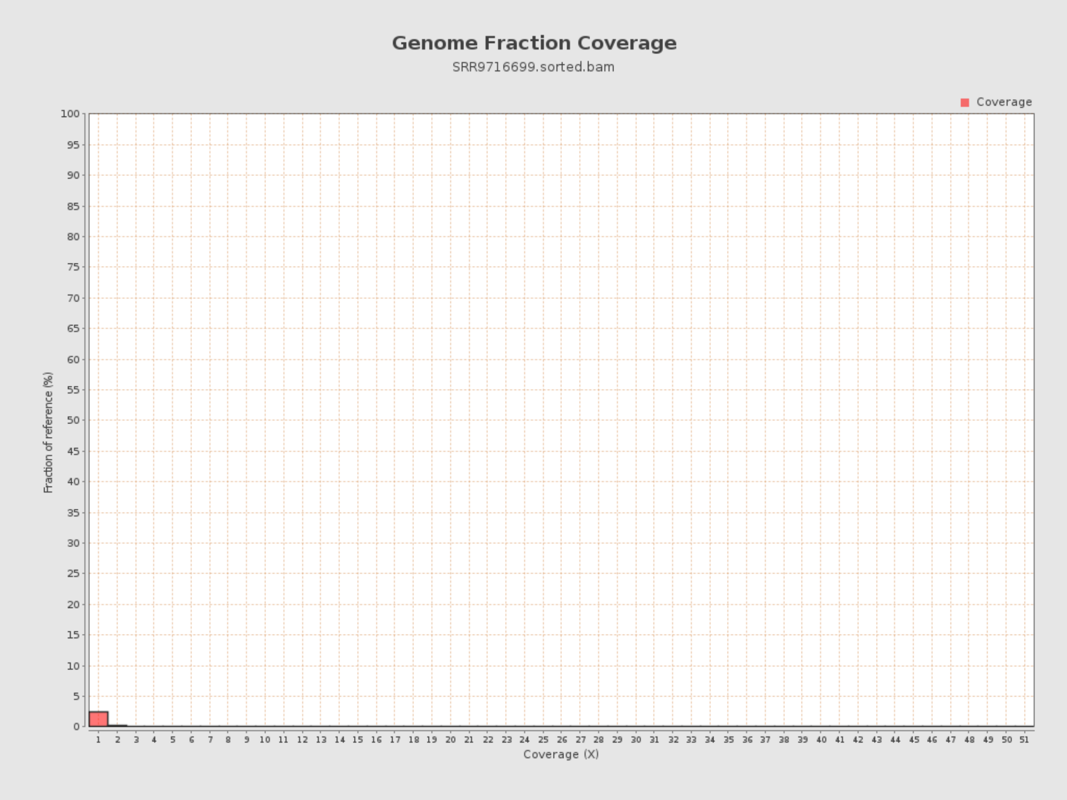
4. Results : Coverage Histogram



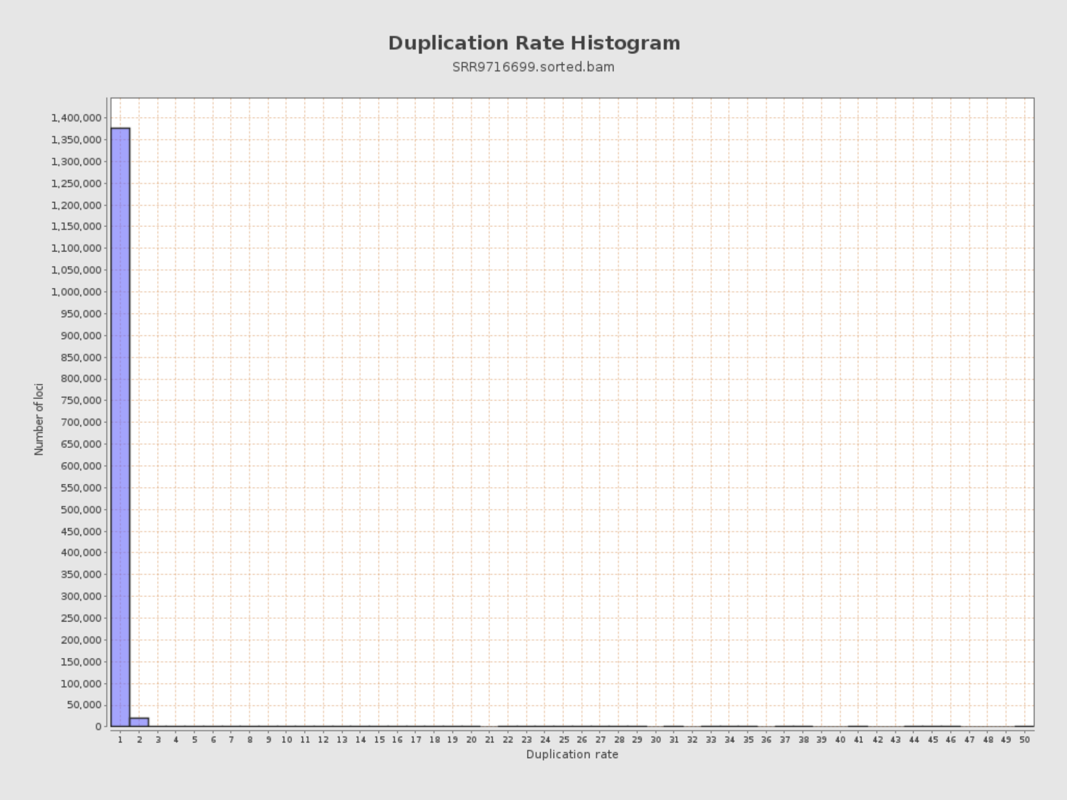
5. Results : Coverage Histogram (0-50X)



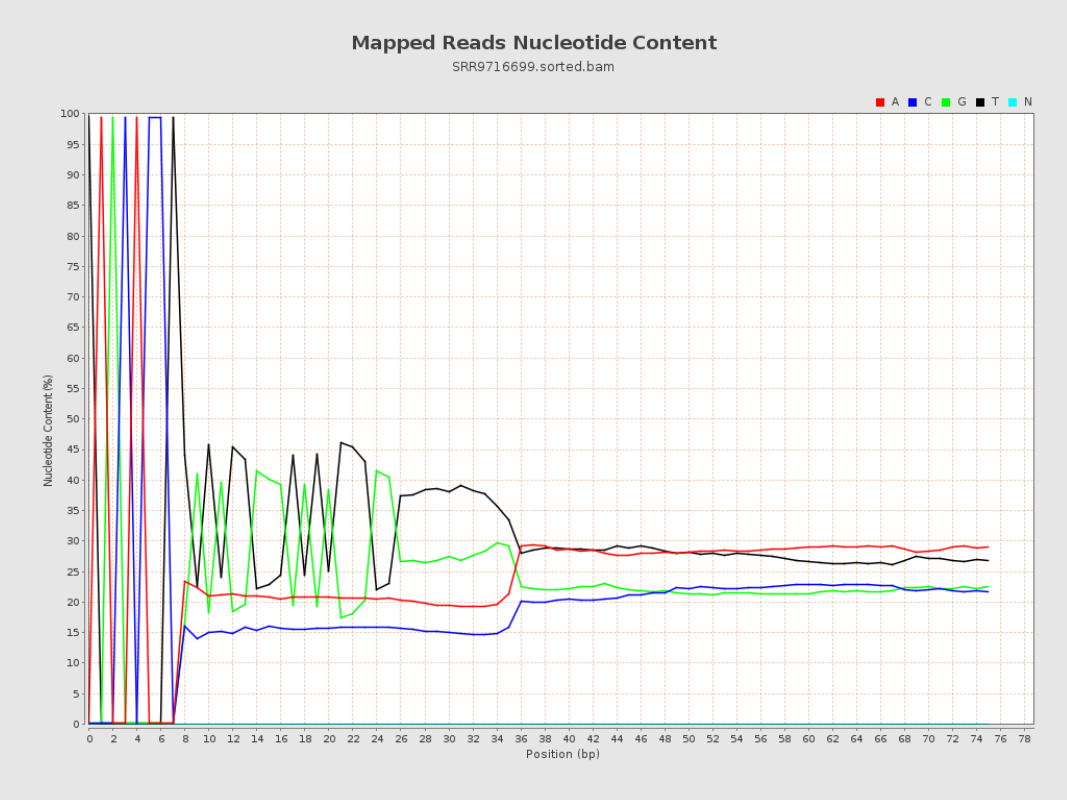
6. Results : Genome Fraction Coverage



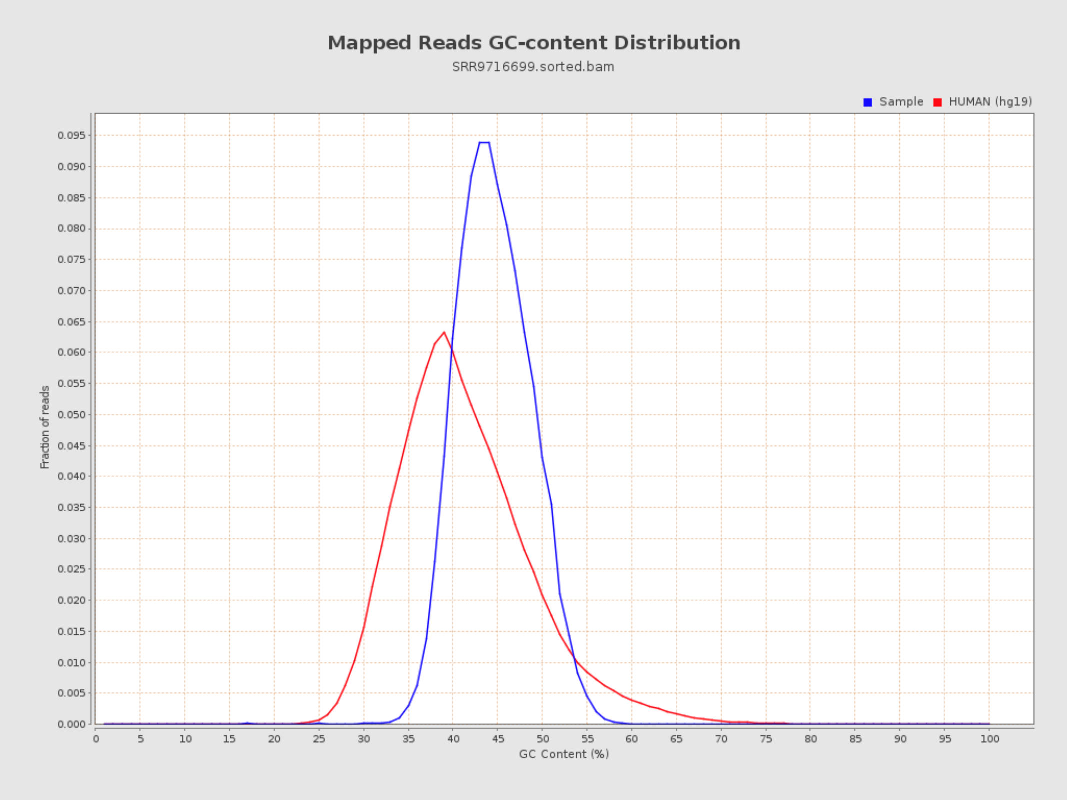
7. Results : Duplication Rate Histogram



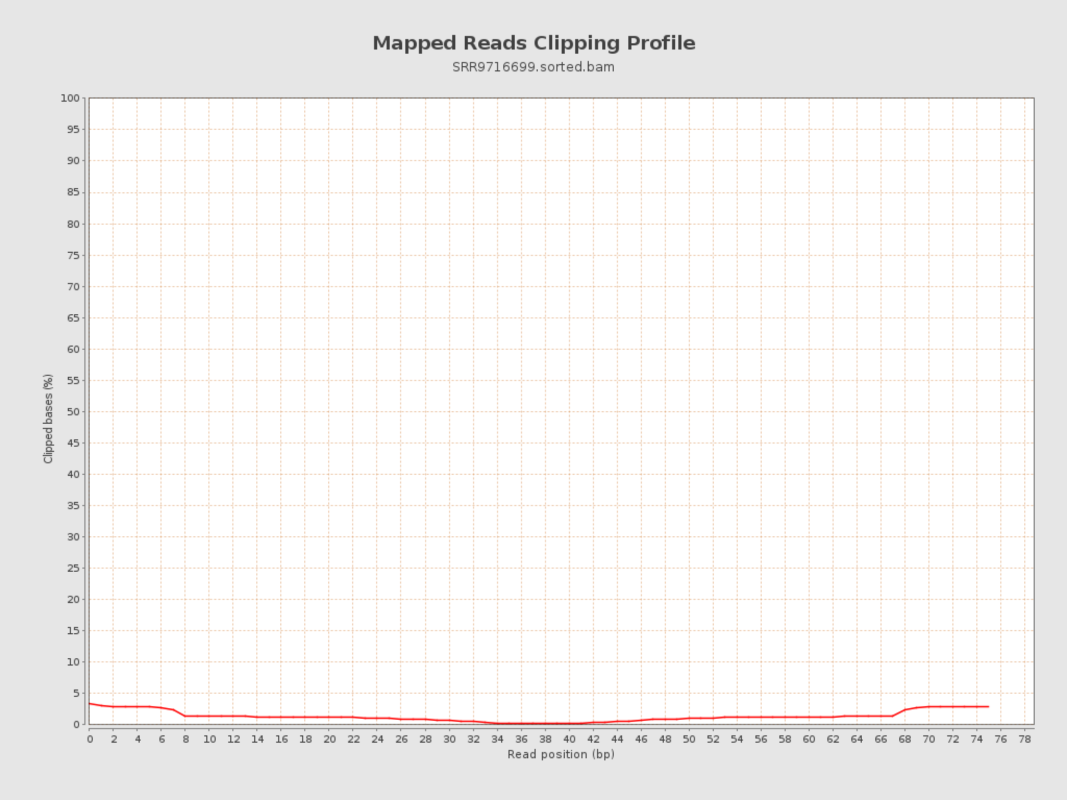
8. Results : Mapped Reads Nucleotide Content



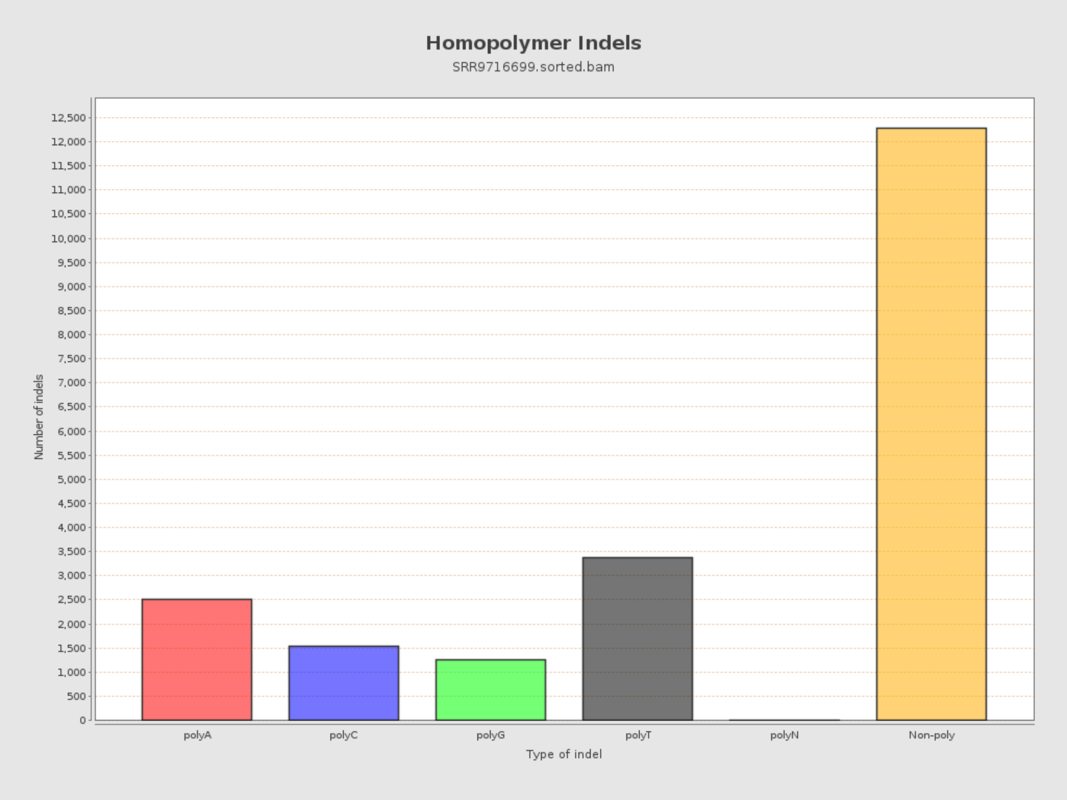
9. Results : Mapped Reads GC-content Distribution



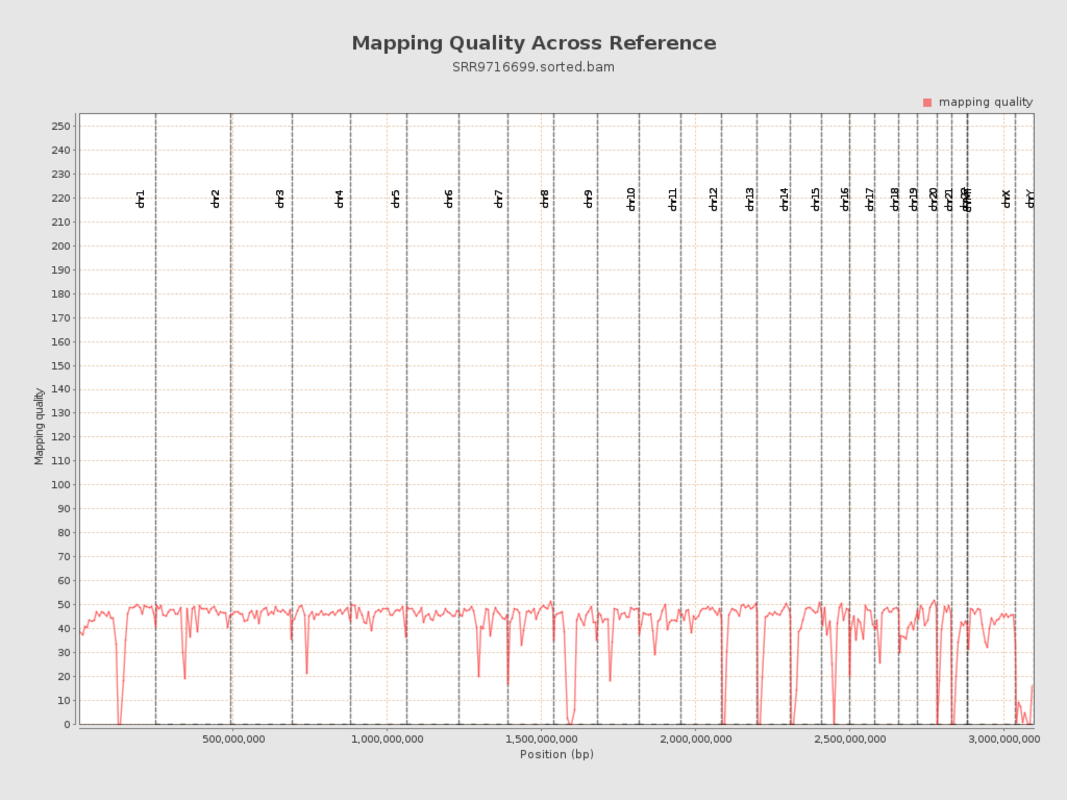
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram