Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 16:28:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716886.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_SRR9716886 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716886.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 16:28:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716886.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,766,050
Mapped reads	1,244,456 / 70.47%
Unmapped reads	521,594 / 29.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,544 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	41,213 / 2.33%
Duplication rate	2.5%
Clipped reads	1,247,248 / 70.62%

2.2. ACGT Content

Number/percentage of A's	18,271,683 / 25.51%
Number/percentage of C's	13,252,628 / 18.5%
Number/percentage of T's	23,217,057 / 32.41%
Number/percentage of G's	16,887,234 / 23.58%
Number/percentage of N's	2,030 / 0%
GC Percentage	42.08%

2.3. Coverage

Mean	0.0231

Standard Deviation	0.2267

2.4. Mapping Quality

Mean Mapping Quality	44.6

2.5. Mismatches and indels

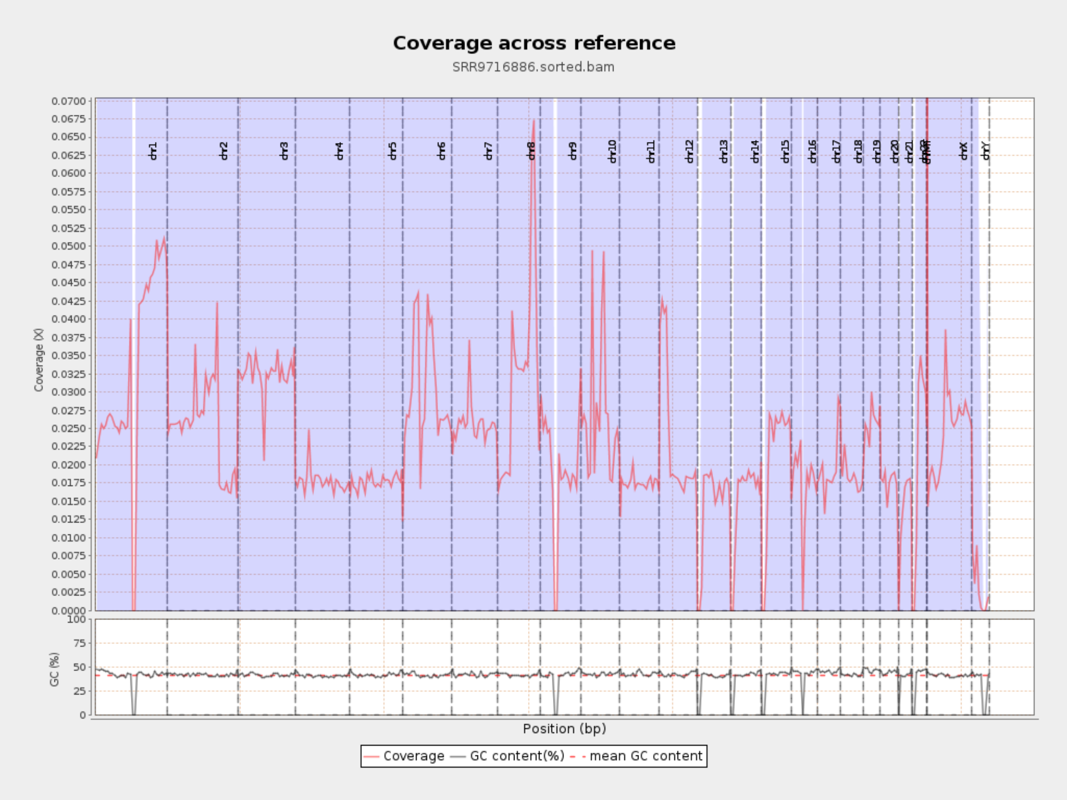
General error rate	0.51%
Mismatches	353,827
Insertions	4,575
Mapped reads with at least one insertion	0.37%
Deletions	13,090
Mapped reads with at least one deletion	1.04%
Homopolymer indels	43.28%

2.6. Chromosome stats

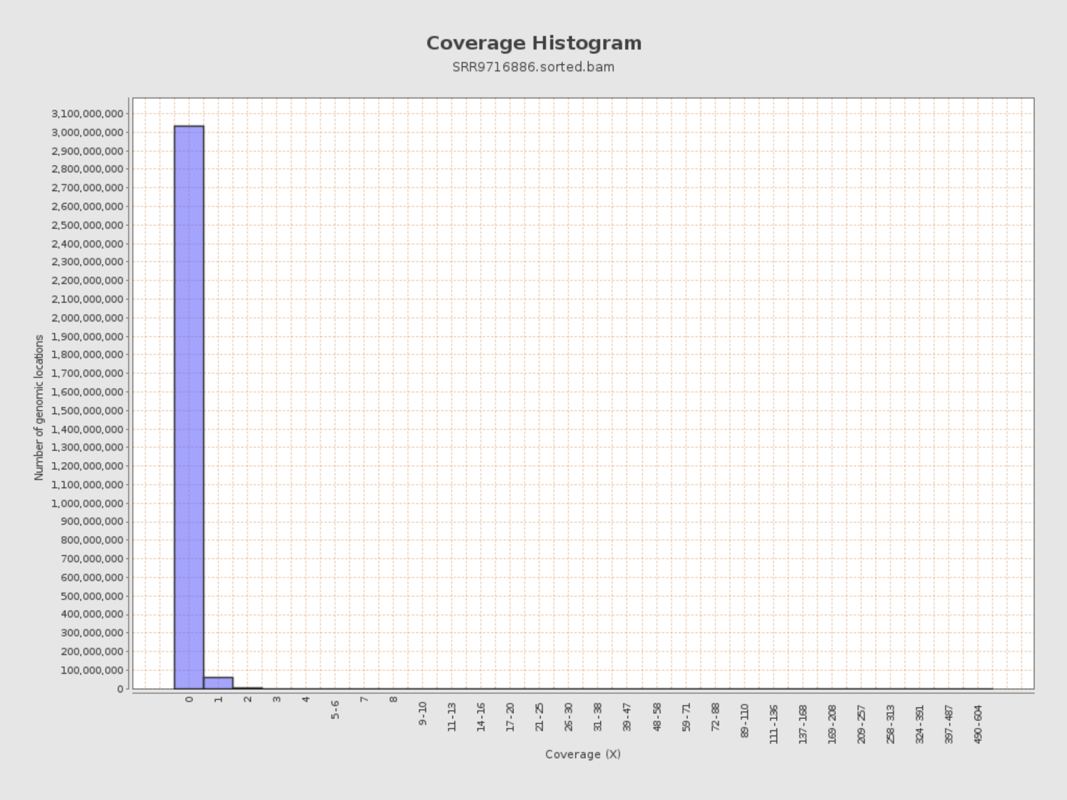
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8170127	0.0328	0.3881
chr2	243199373	6155070	0.0253	0.3015
chr3	198022430	6427754	0.0325	0.1949
chr4	191154276	3400362	0.0178	0.1496
chr5	180915260	3209180	0.0177	0.1455
chr6	171115067	5163192	0.0302	0.2412
chr7	159138663	4096762	0.0257	0.2728

chr8	146364022	4760765	0.0325	0.2151
chr9	141213431	2672408	0.0189	0.1931
chr10	135534747	3684258	0.0272	0.2459
chr11	135006516	2365904	0.0175	0.1877
chr12	133851895	3180267	0.0238	0.1686
chr13	115169878	1663877	0.0144	0.1296
chr14	107349540	1608494	0.015	0.1423
chr15	102531392	2135691	0.0208	0.156
chr16	90354753	1535589	0.017	0.1566
chr17	81195210	1583113	0.0195	0.1541
chr18	78077248	1428316	0.0183	0.3196
chr19	59128983	1517793	0.0257	0.2852
chr20	63025520	1097296	0.0174	0.1427
chr21	48129895	673321	0.014	0.1382
chr22	51304566	1114317	0.0217	0.1599
chrMT	16571	4527	0.2732	0.5405
chrX	155270560	3827728	0.0247	0.1925
chrY	59373566	175065	0.0029	0.0748

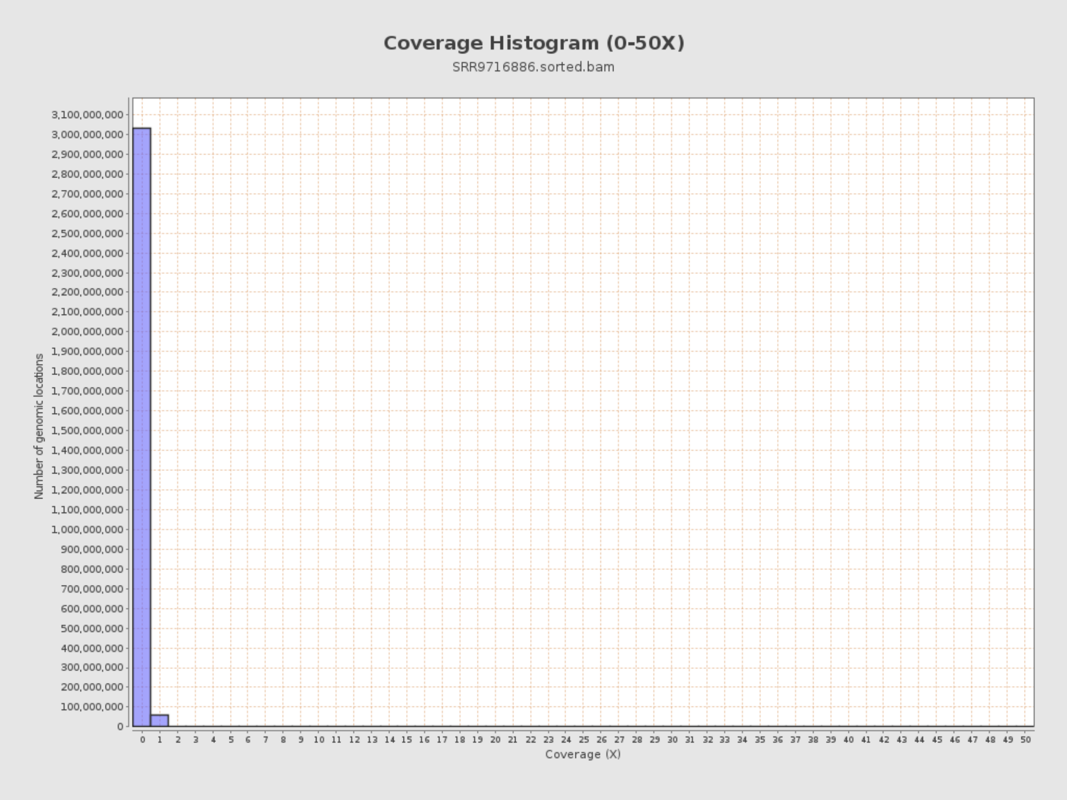
3. Results : Coverage across reference



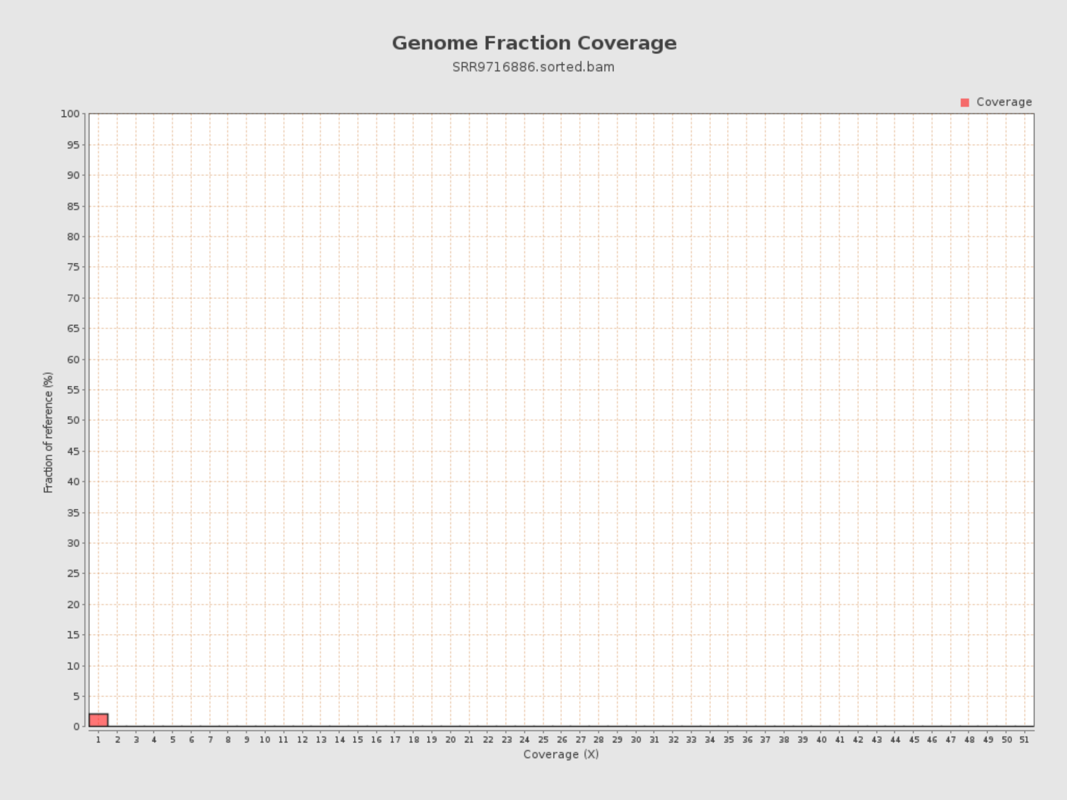
4. Results : Coverage Histogram



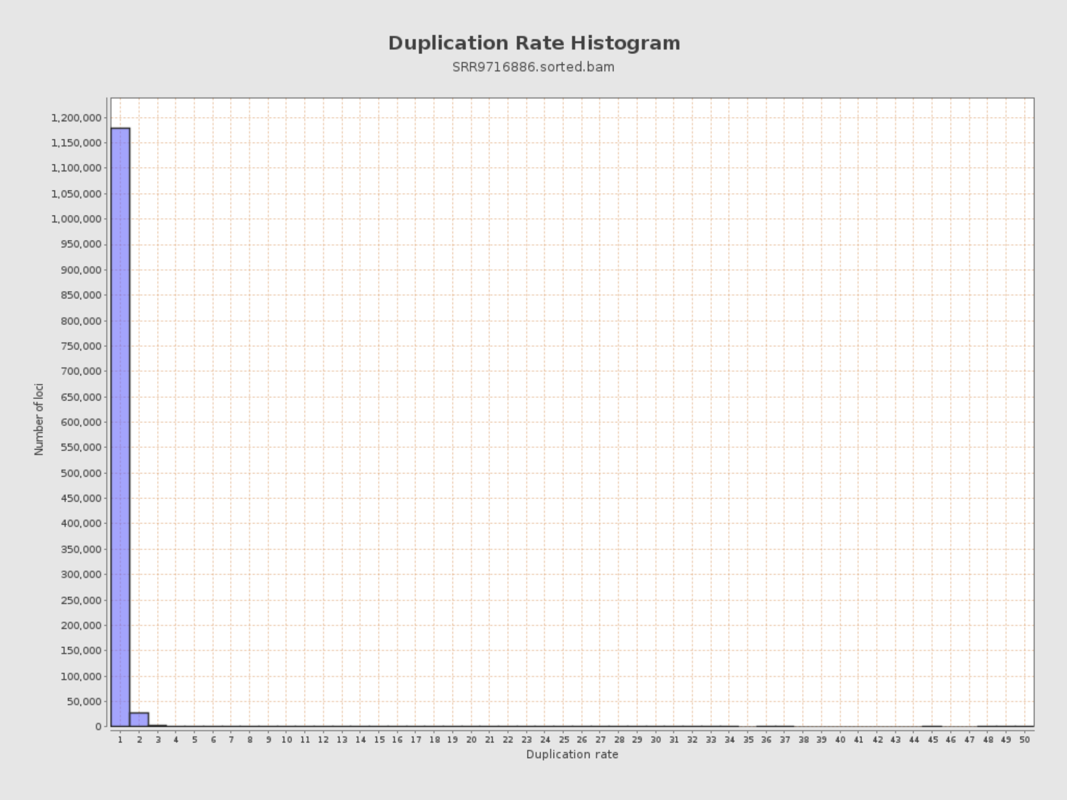
5. Results : Coverage Histogram (0-50X)



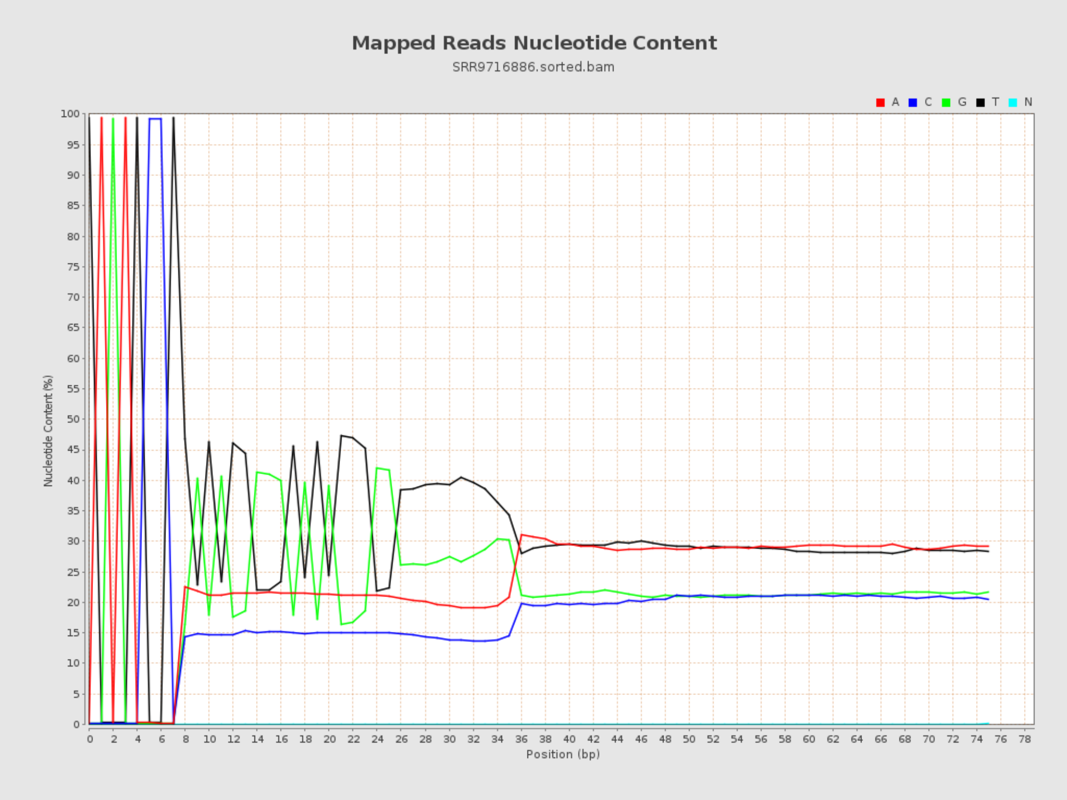
6. Results : Genome Fraction Coverage



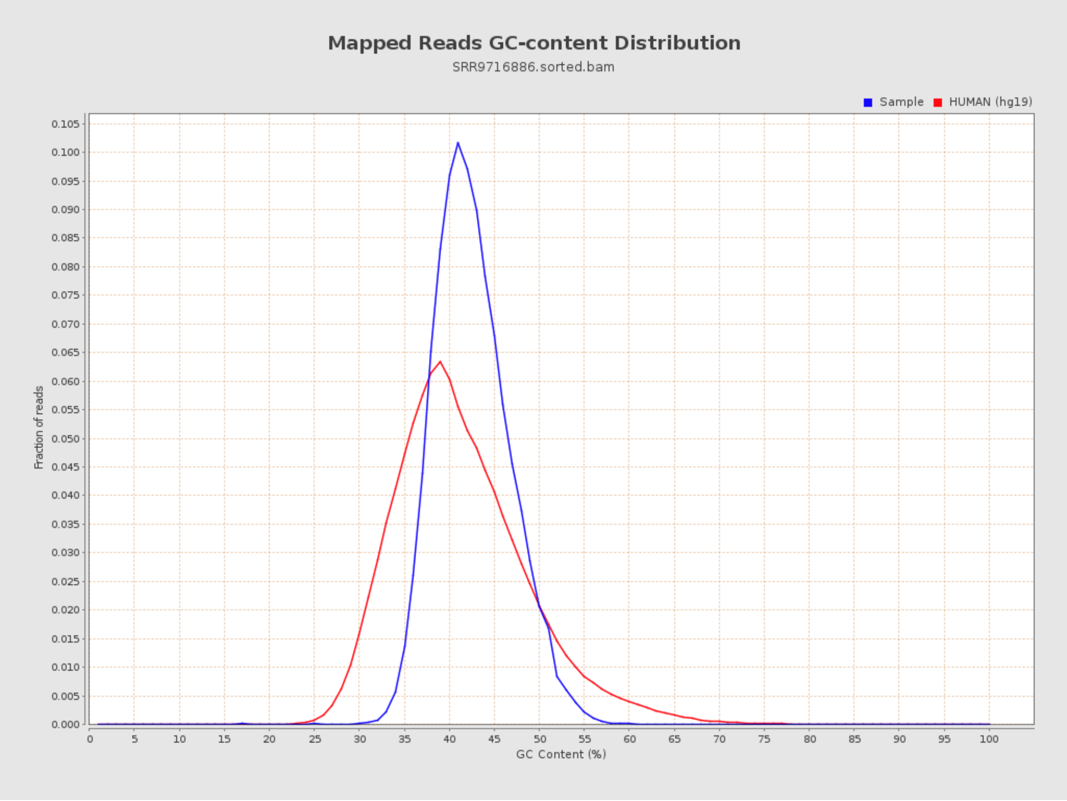
7. Results : Duplication Rate Histogram



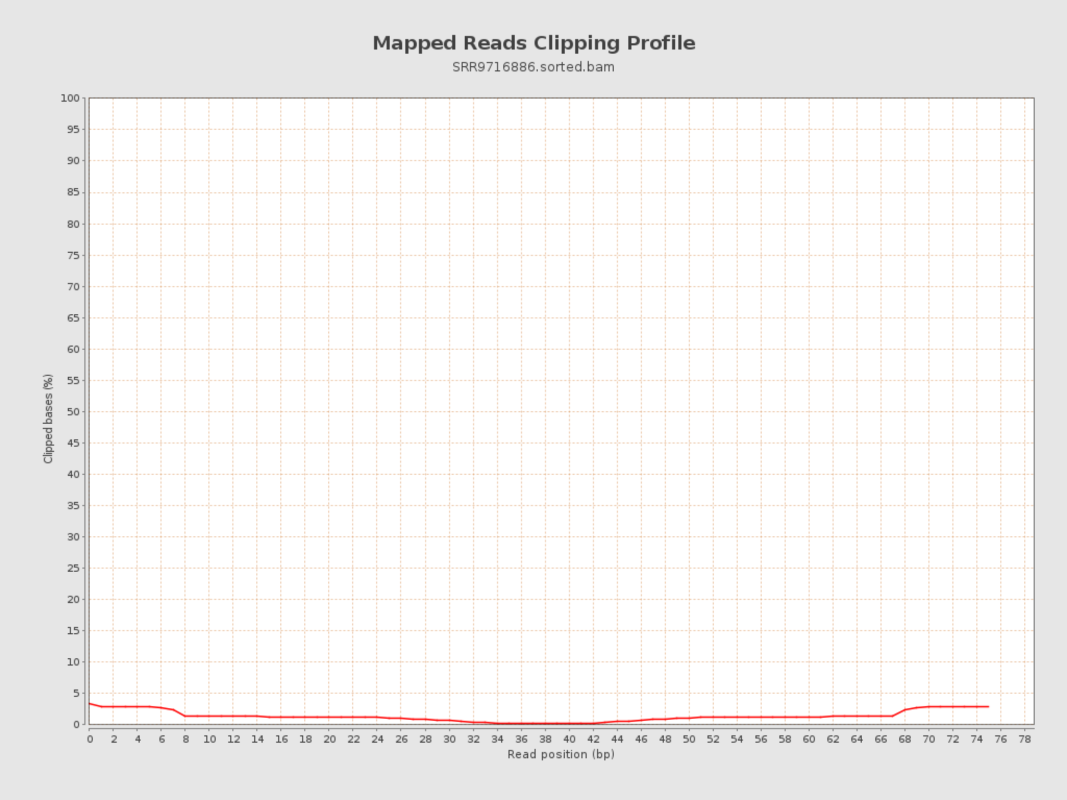
8. Results : Mapped Reads Nucleotide Content



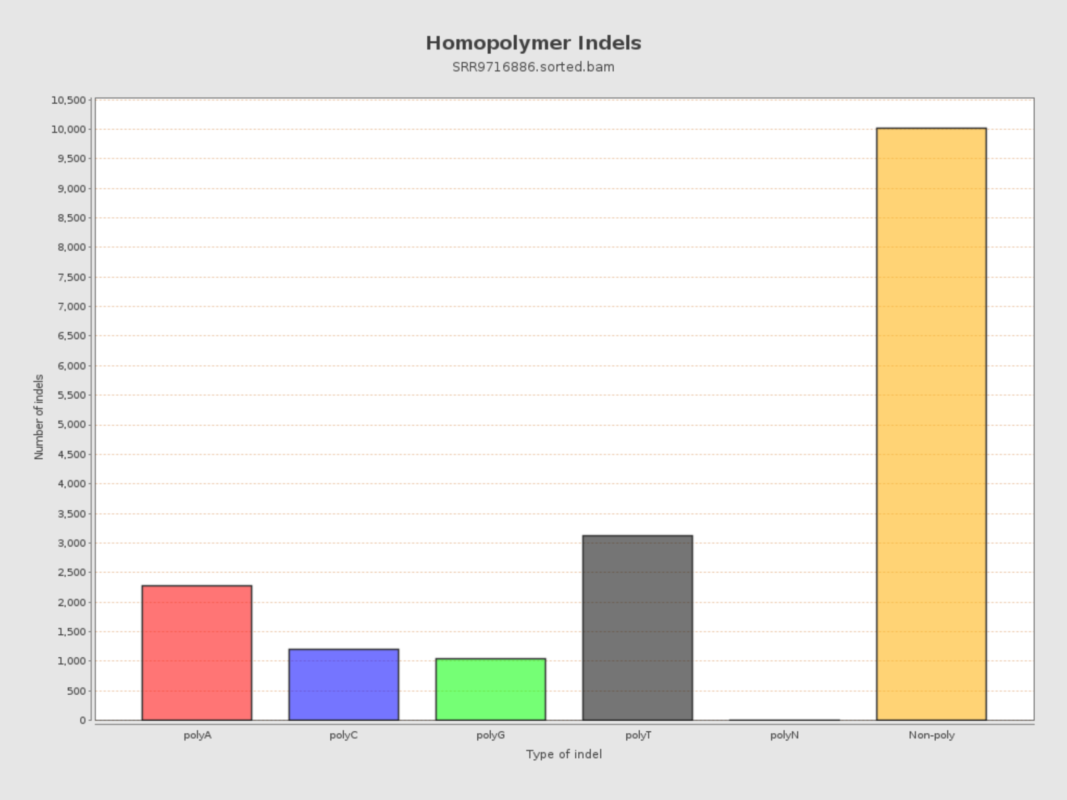
9. Results : Mapped Reads GC-content Distribution



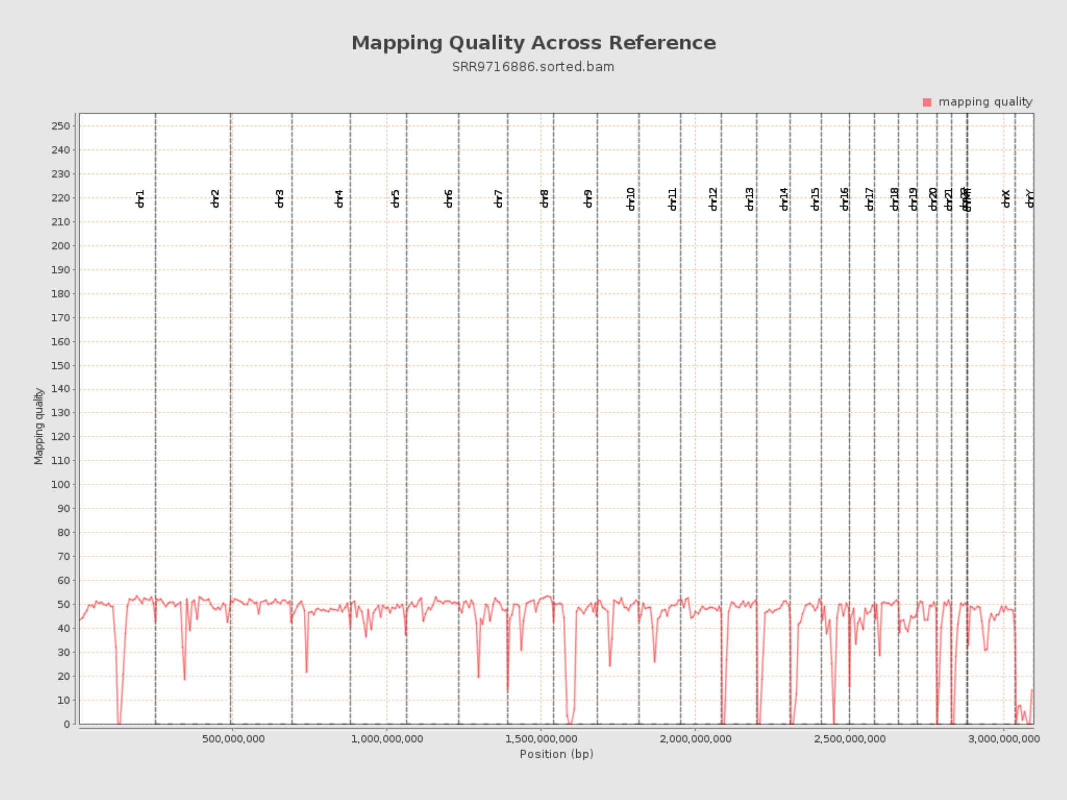
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram