Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 22:43:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716576.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_SRR9716576 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716576.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 22:43:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716576.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,461,341
Mapped reads	1,317,753 / 90.17%
Unmapped reads	143,588 / 9.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,335 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	42,036 / 2.88%
Duplication rate	2.32%
Clipped reads	1,320,998 / 90.4%

2.2. ACGT Content

Number/percentage of A's	20,027,299 / 26.3%
Number/percentage of C's	14,736,755 / 19.36%
Number/percentage of T's	22,788,796 / 29.93%
Number/percentage of G's	18,581,268 / 24.41%
Number/percentage of N's	912 / 0%
GC Percentage	43.76%

2.3. Coverage

Mean	0.0246

Standard Deviation	0.2415

2.4. Mapping Quality

Mean Mapping Quality	44.25

2.5. Mismatches and indels

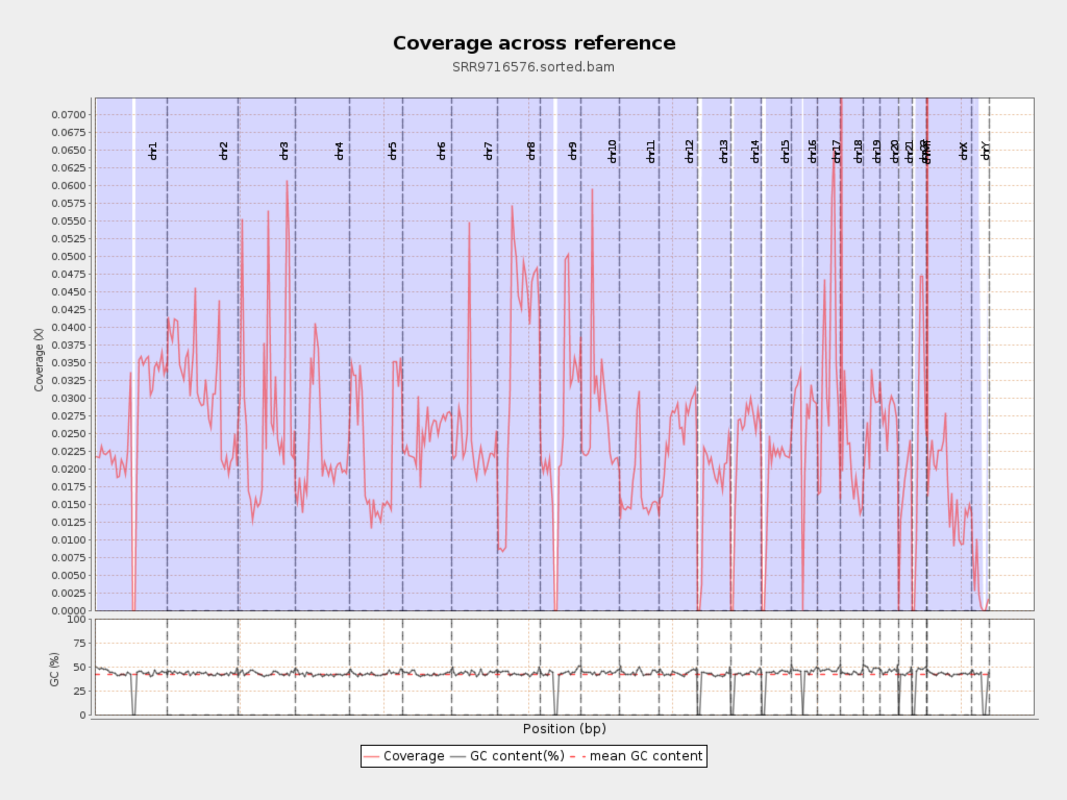
General error rate	0.52%
Mismatches	381,215
Insertions	6,248
Mapped reads with at least one insertion	0.47%
Deletions	14,283
Mapped reads with at least one deletion	1.08%
Homopolymer indels	40.68%

2.6. Chromosome stats

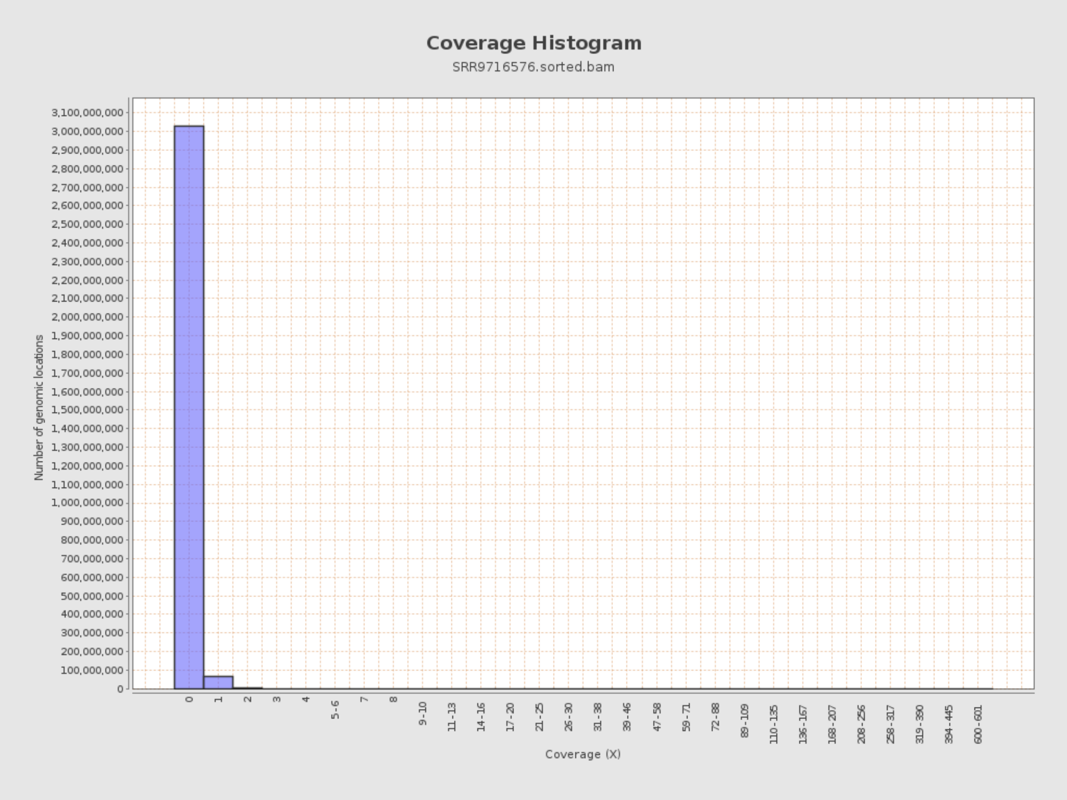
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6401153	0.0257	0.3463
chr2	243199373	7621434	0.0313	0.3159
chr3	198022430	5529780	0.0279	0.1847
chr4	191154276	4277583	0.0224	0.1736
chr5	180915260	4113258	0.0227	0.1619
chr6	171115067	4246477	0.0248	0.18
chr7	159138663	3828998	0.0241	0.4462

chr8	146364022	5391717	0.0368	0.2684
chr9	141213431	3538327	0.0251	0.1886
chr10	135534747	3731783	0.0275	0.3037
chr11	135006516	2291169	0.017	0.174
chr12	133851895	3414135	0.0255	0.1833
chr13	115169878	1992933	0.0173	0.1407
chr14	107349540	2451535	0.0228	0.1649
chr15	102531392	1862194	0.0182	0.147
chr16	90354753	2392957	0.0265	0.1811
chr17	81195210	2836435	0.0349	0.207
chr18	78077248	1856809	0.0238	0.2824
chr19	59128983	1613200	0.0273	0.2958
chr20	63025520	1733654	0.0275	0.1852
chr21	48129895	814089	0.0169	0.1493
chr22	51304566	1288317	0.0251	0.1713
chrMT	16571	104099	6.282	4.4016
chrX	155270560	2647642	0.0171	0.1563
chrY	59373566	177698	0.003	0.0874

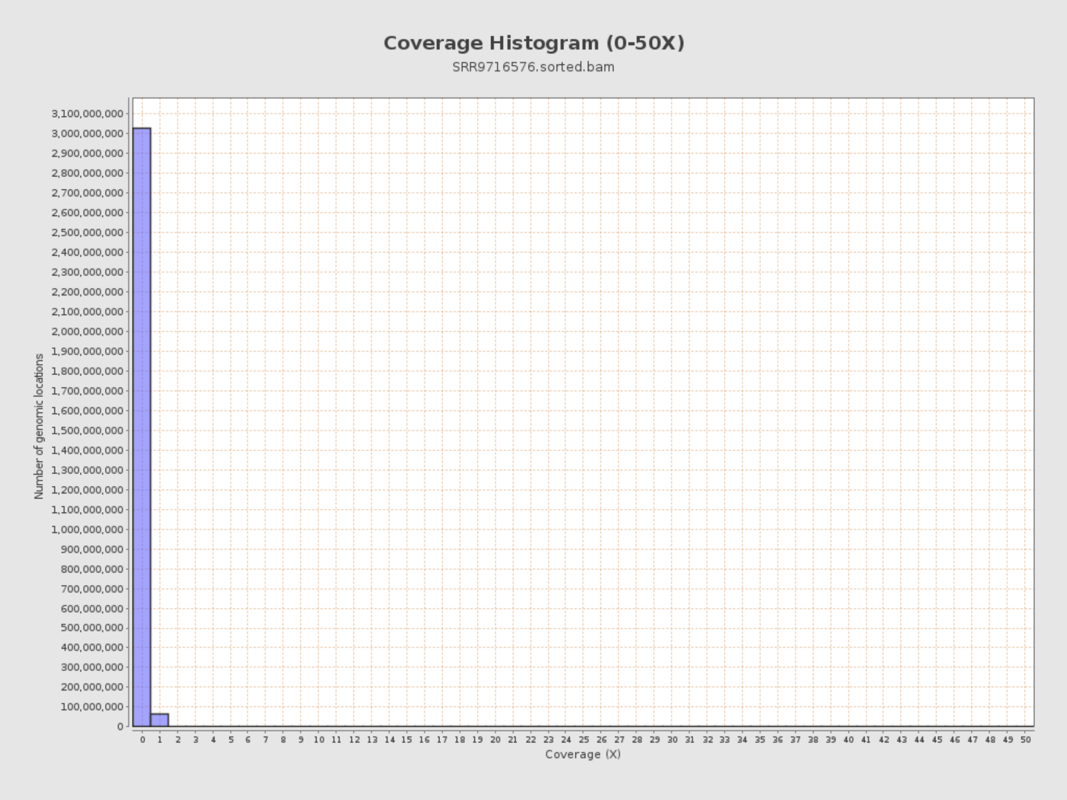
3. Results : Coverage across reference



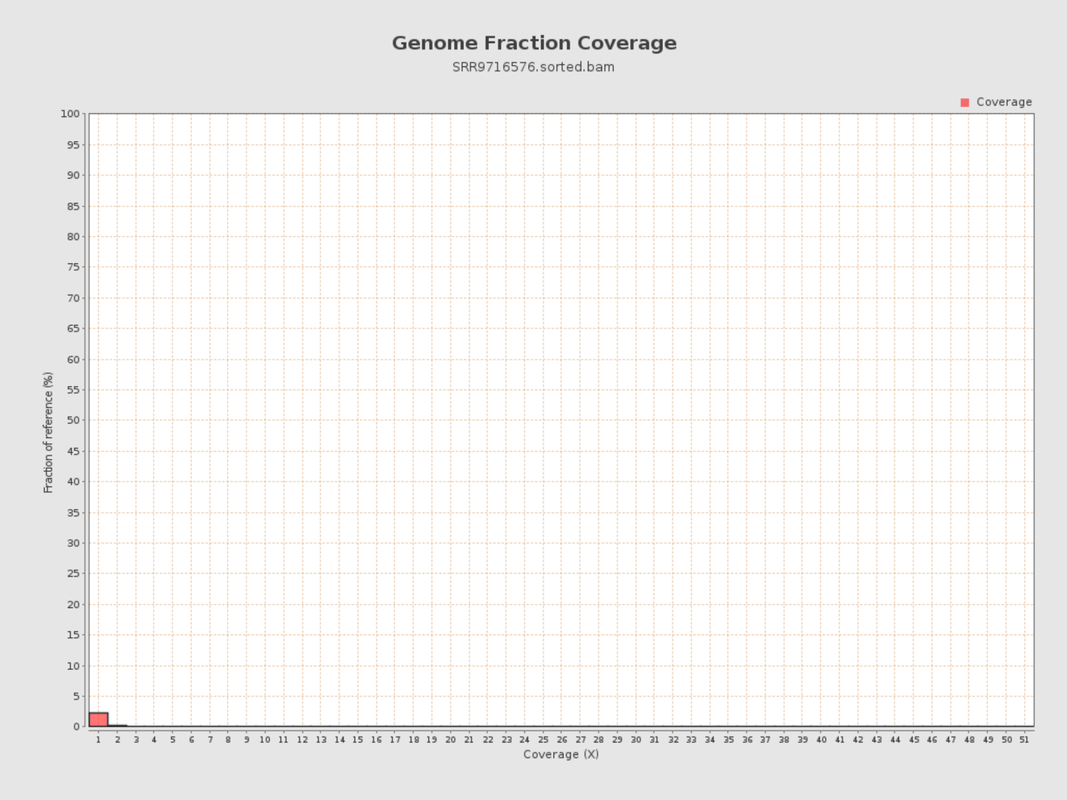
4. Results : Coverage Histogram



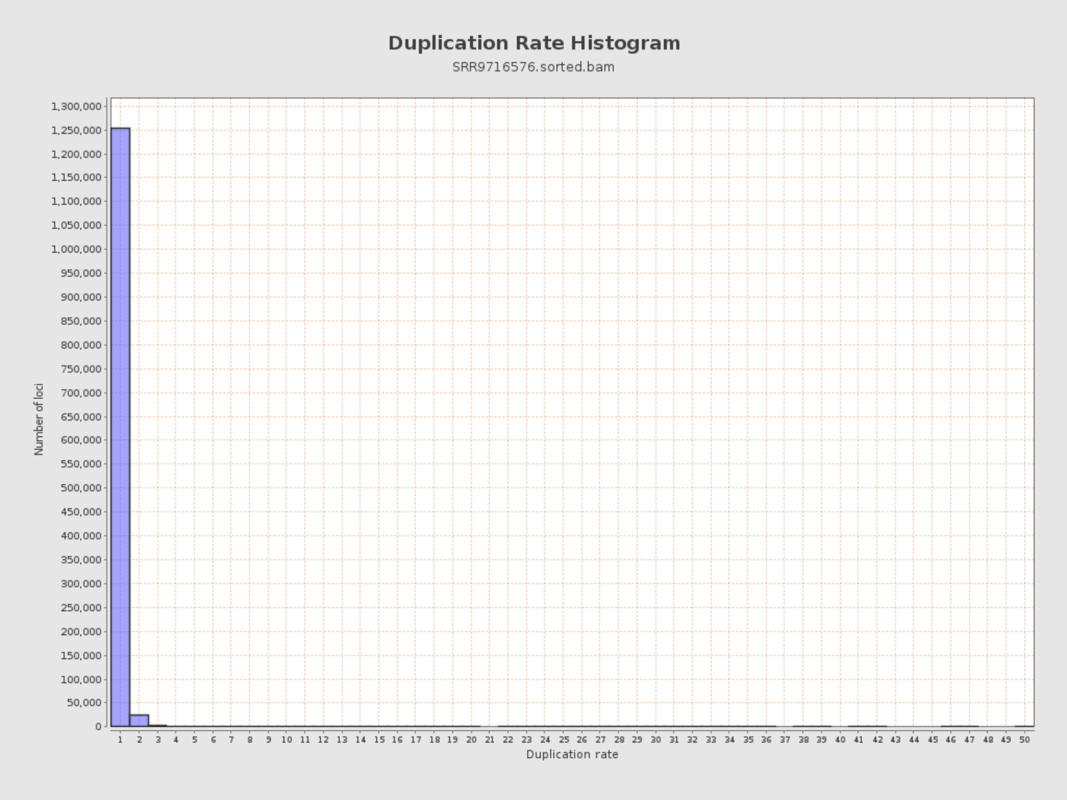
5. Results : Coverage Histogram (0-50X)



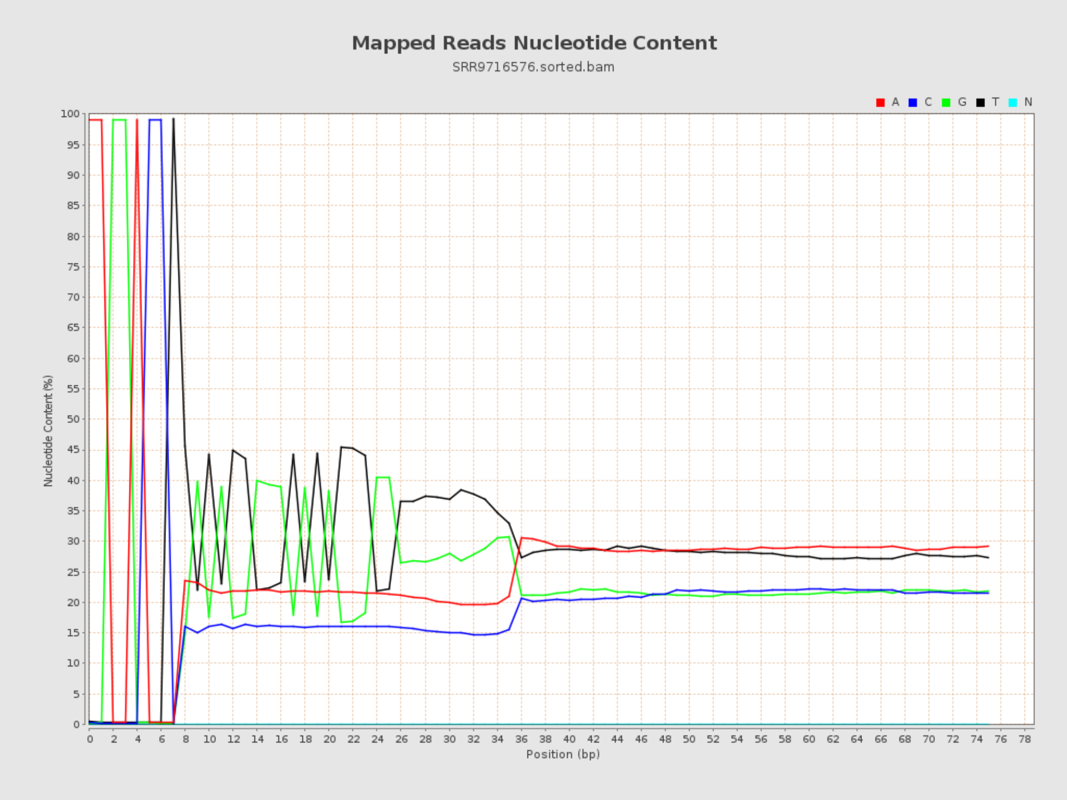
6. Results : Genome Fraction Coverage



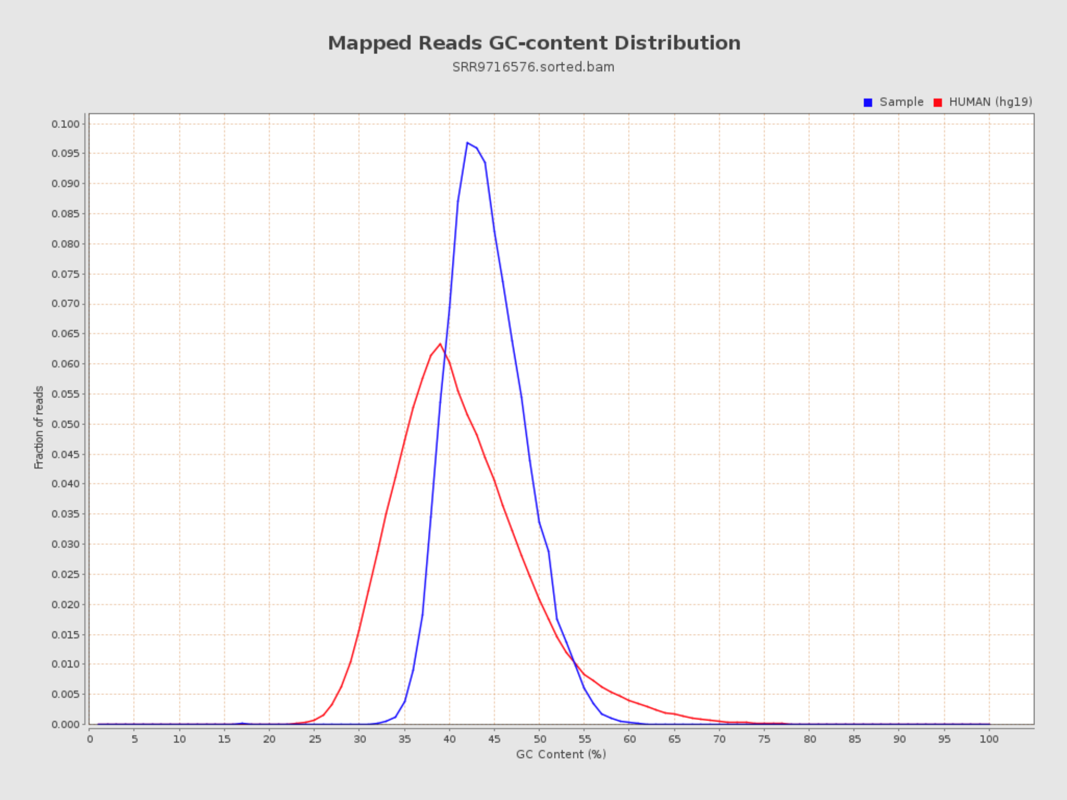
7. Results : Duplication Rate Histogram



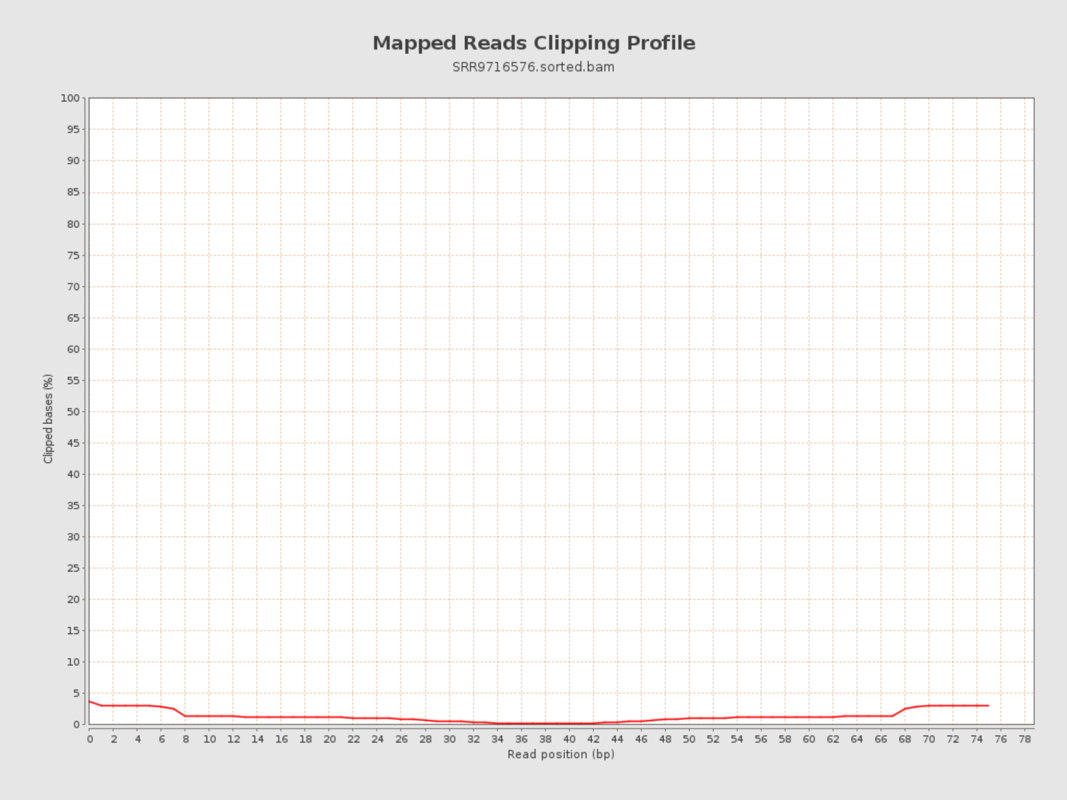
8. Results : Mapped Reads Nucleotide Content



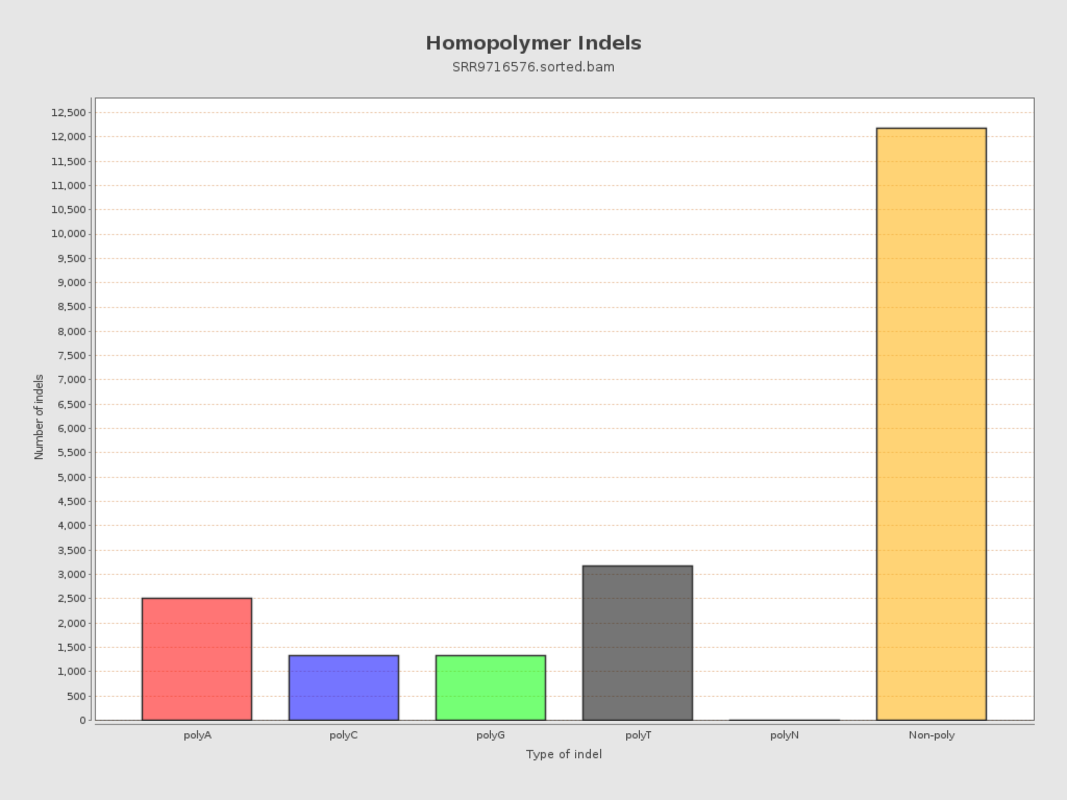
9. Results : Mapped Reads GC-content Distribution



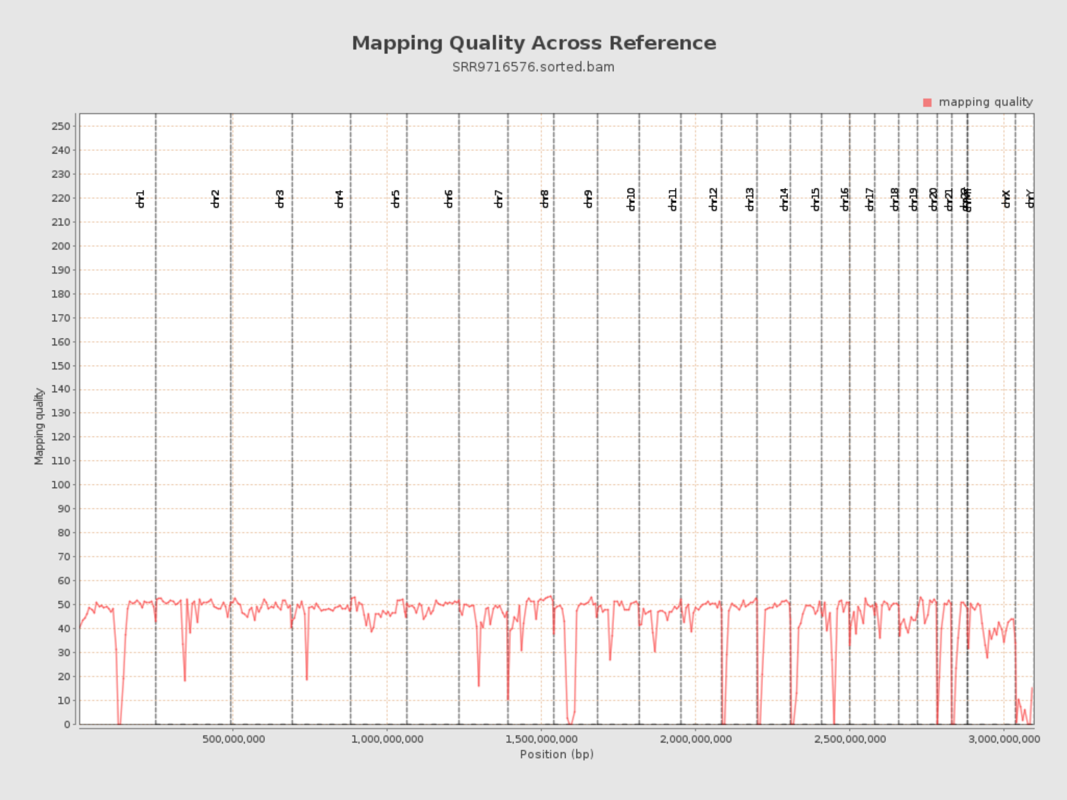
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram