Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 21:28:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716560.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_SRR9716560 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716560.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 21:28:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716560.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	24,975,509
Mapped reads	24,407,764 / 97.73%
Unmapped reads	567,745 / 2.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,969 / 0.08%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	1,405,763 / 5.63%
Duplication rate	1.72%
Clipped reads	24,293,709 / 97.27%

2.2. ACGT Content

Number/percentage of A's	465,368,576 / 28.07%
Number/percentage of C's	357,354,868 / 21.56%
Number/percentage of T's	484,062,111 / 29.2%
Number/percentage of G's	350,747,420 / 21.16%
Number/percentage of N's	83,064 / 0.01%
GC Percentage	42.72%

2.3. Coverage

Mean	0.5356

Standard Deviation	5.6579

2.4. Mapping Quality

Mean Mapping Quality	48.74

2.5. Mismatches and indels

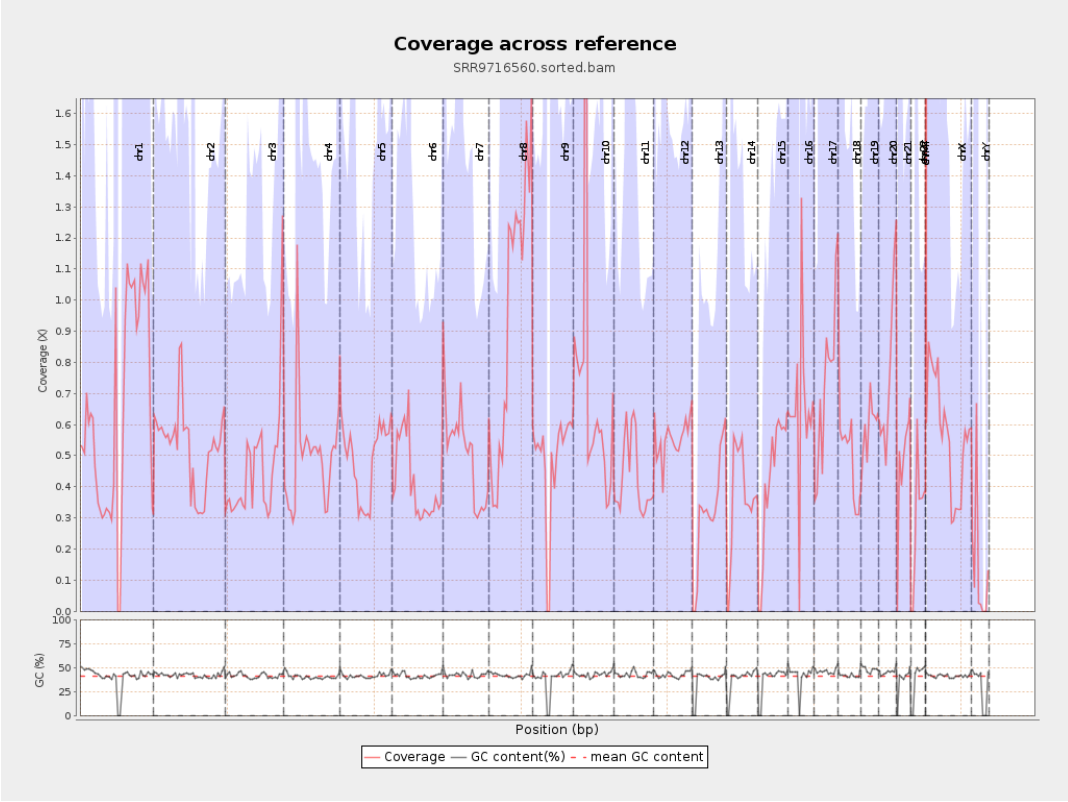
General error rate	0.32%
Mismatches	5,031,691
Insertions	139,166
Mapped reads with at least one insertion	0.57%
Deletions	133,420
Mapped reads with at least one deletion	0.54%
Homopolymer indels	35.62%

2.6. Chromosome stats

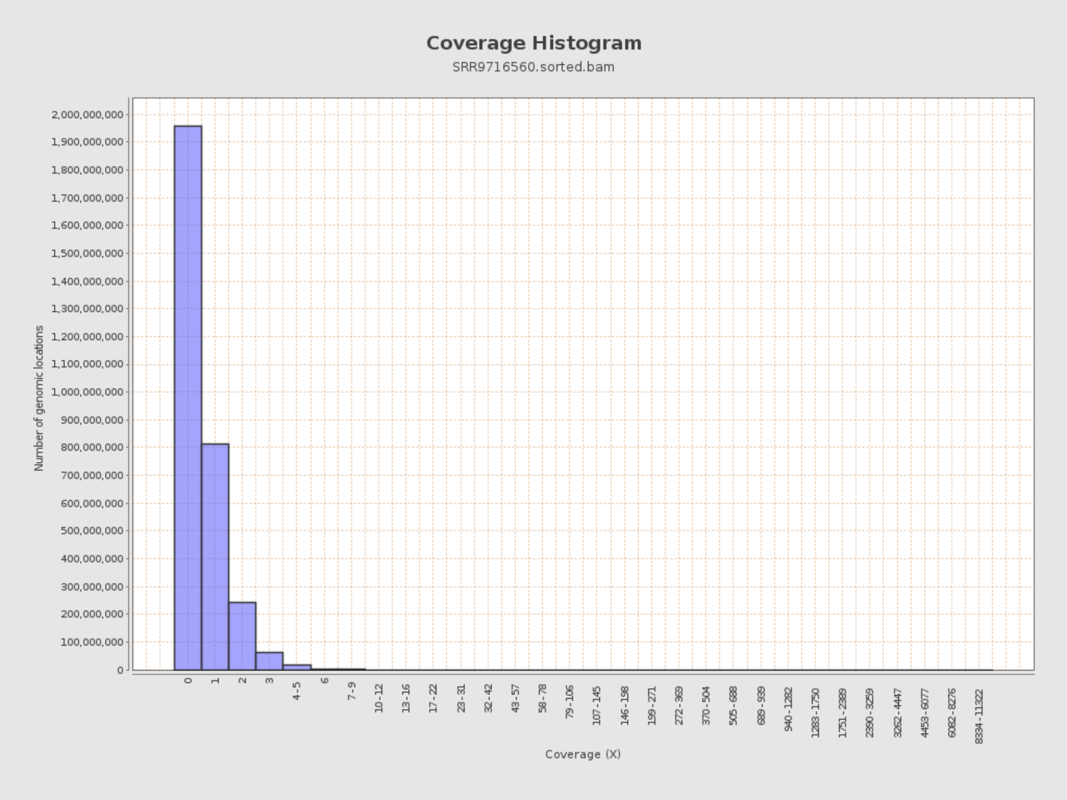
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	160793908	0.6451	10.1861
chr2	243199373	129118037	0.5309	4.06
chr3	198022430	89461133	0.4518	2.7824
chr4	191154276	93569527	0.4895	3.8515
chr5	180915260	88905360	0.4914	0.9461
chr6	171115067	70925973	0.4145	2.0992
chr7	159138663	80502018	0.5059	3.5295

chr8	146364022	139815356	0.9553	2.0544
chr9	141213431	68226600	0.4831	3.2728
chr10	135534747	97769879	0.7214	17.0424
chr11	135006516	58561532	0.4338	1.9257
chr12	133851895	73989834	0.5528	0.9813
chr13	115169878	37436653	0.3251	0.7047
chr14	107349540	39003627	0.3633	0.8656
chr15	102531392	43043951	0.4198	0.7306
chr16	90354753	59387334	0.6573	5.4219
chr17	81195210	59387061	0.7314	1.9074
chr18	78077248	38786021	0.4968	5.1454
chr19	59128983	34959394	0.5912	7.0669
chr20	63025520	47622730	0.7556	1.5463
chr21	48129895	23430283	0.4868	3.5769
chr22	51304566	15634613	0.3047	0.8955
chrMT	16571	11060470	667.4594	202.3838
chrX	155270560	88122477	0.5675	1.3643
chrY	59373566	8385375	0.1412	6.4342

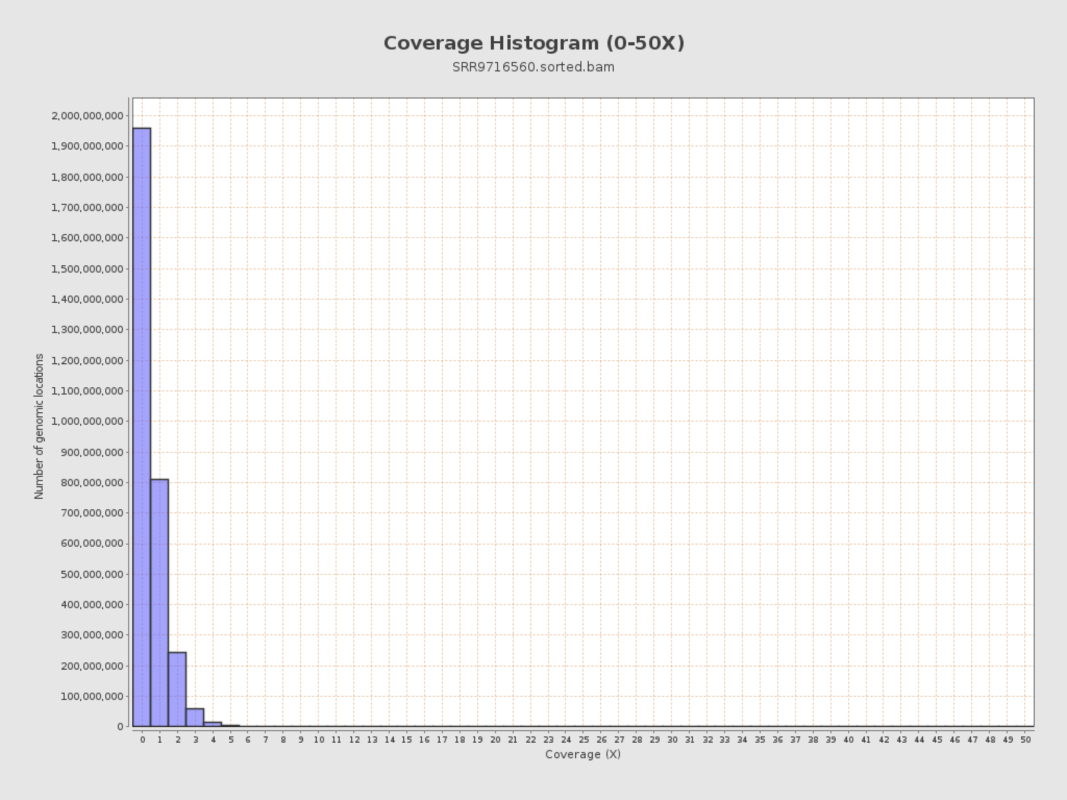
3. Results : Coverage across reference



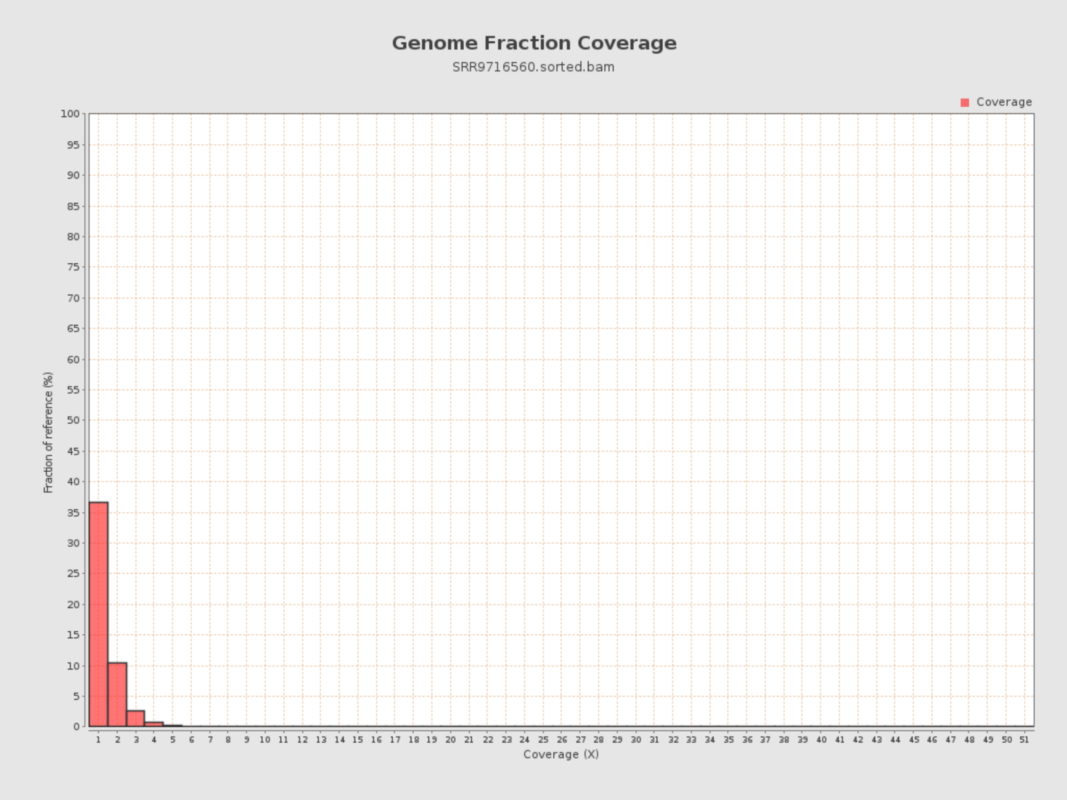
4. Results : Coverage Histogram



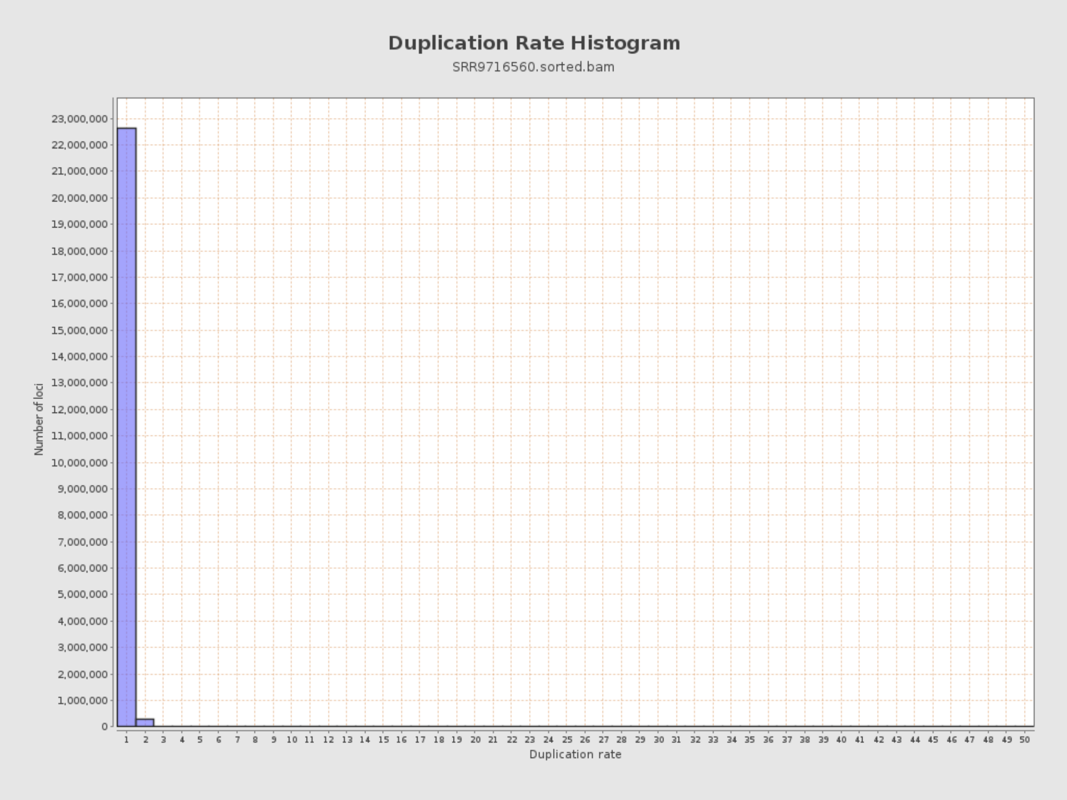
5. Results : Coverage Histogram (0-50X)



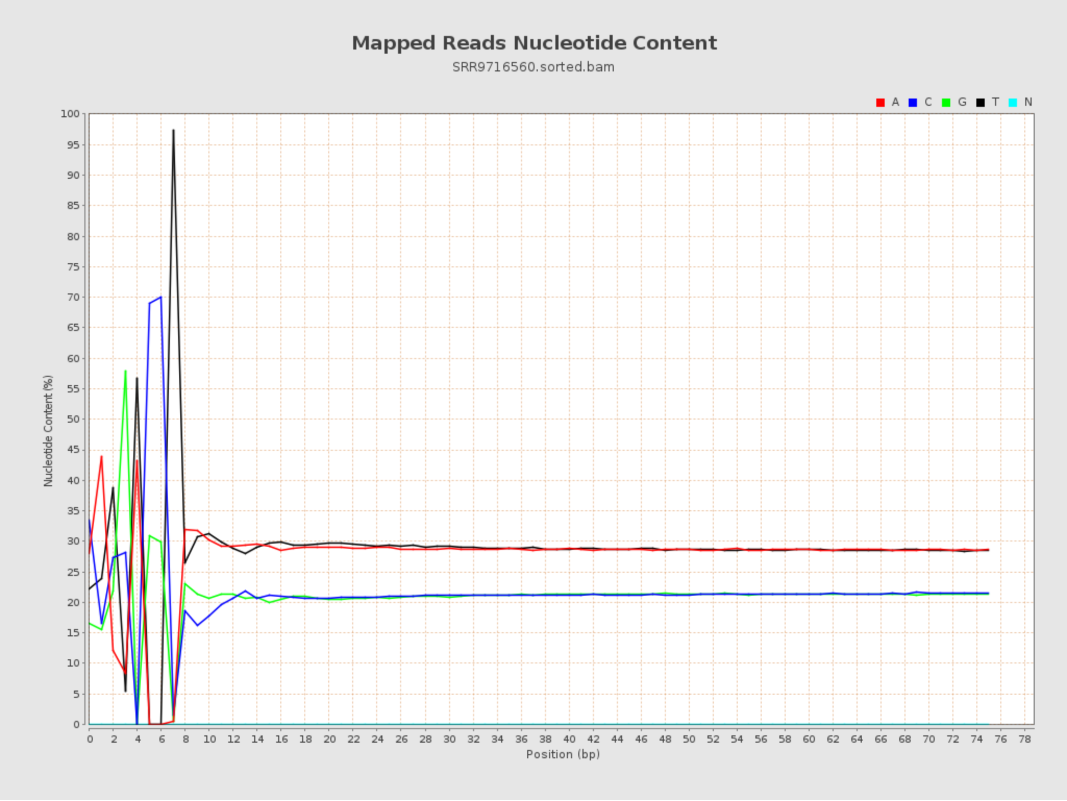
6. Results : Genome Fraction Coverage



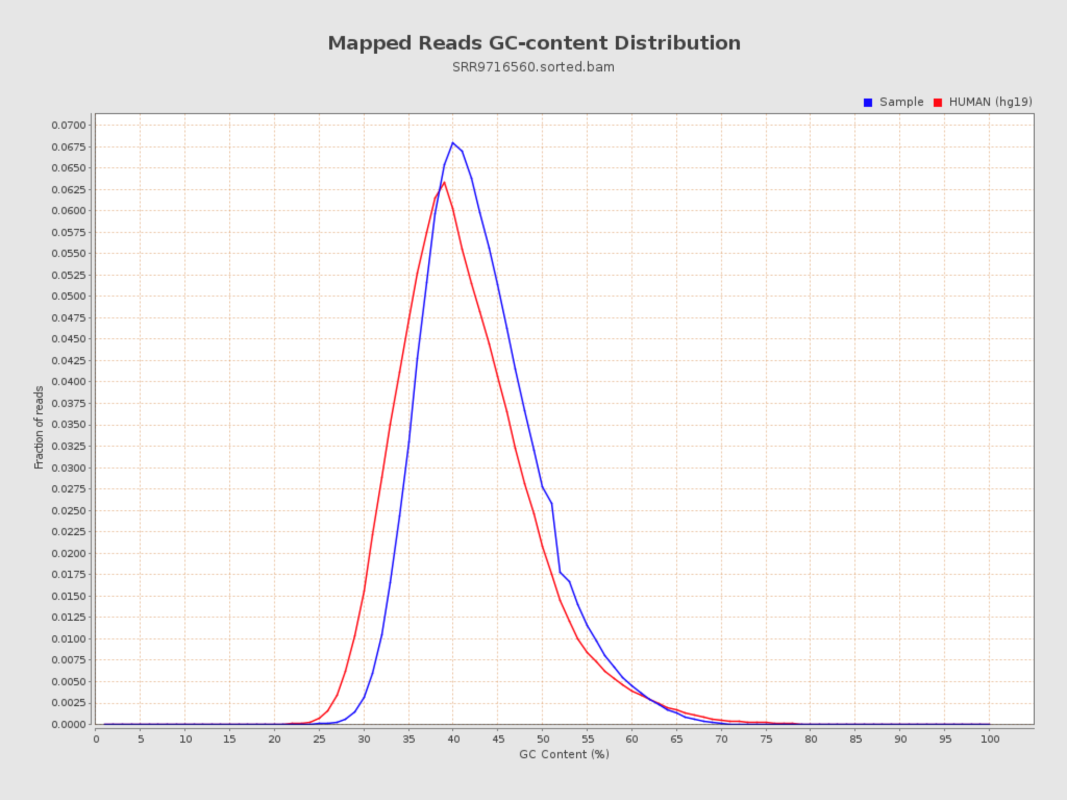
7. Results : Duplication Rate Histogram



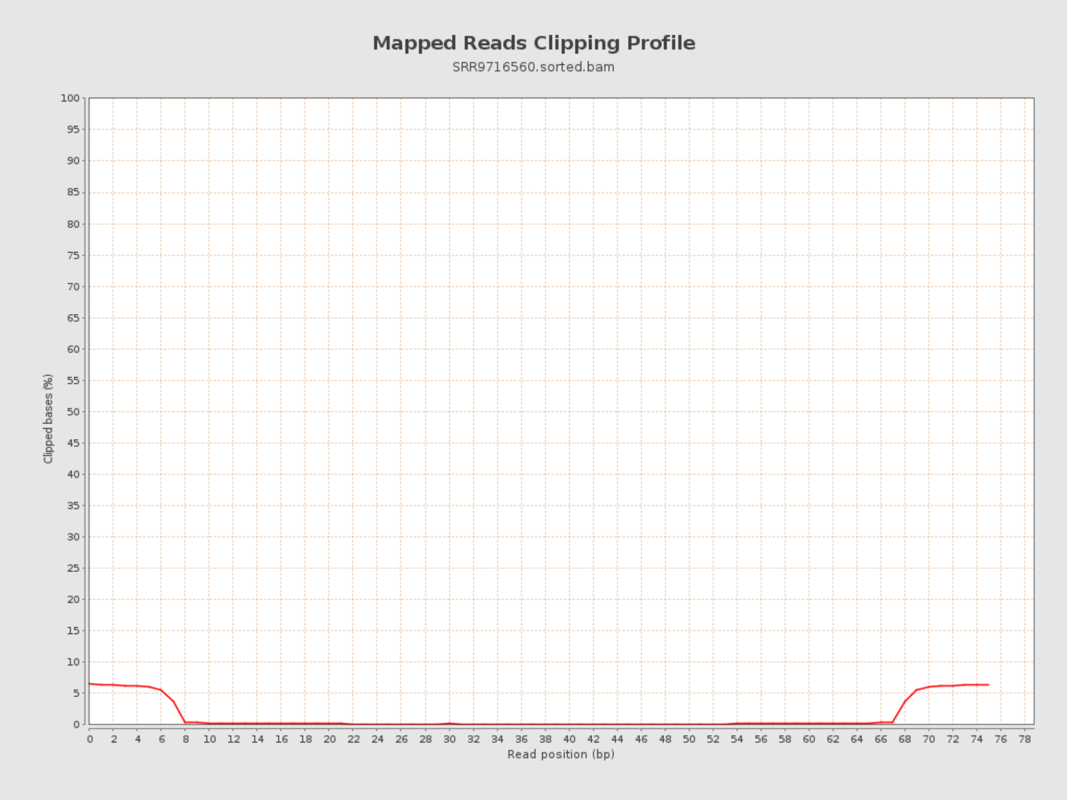
8. Results : Mapped Reads Nucleotide Content



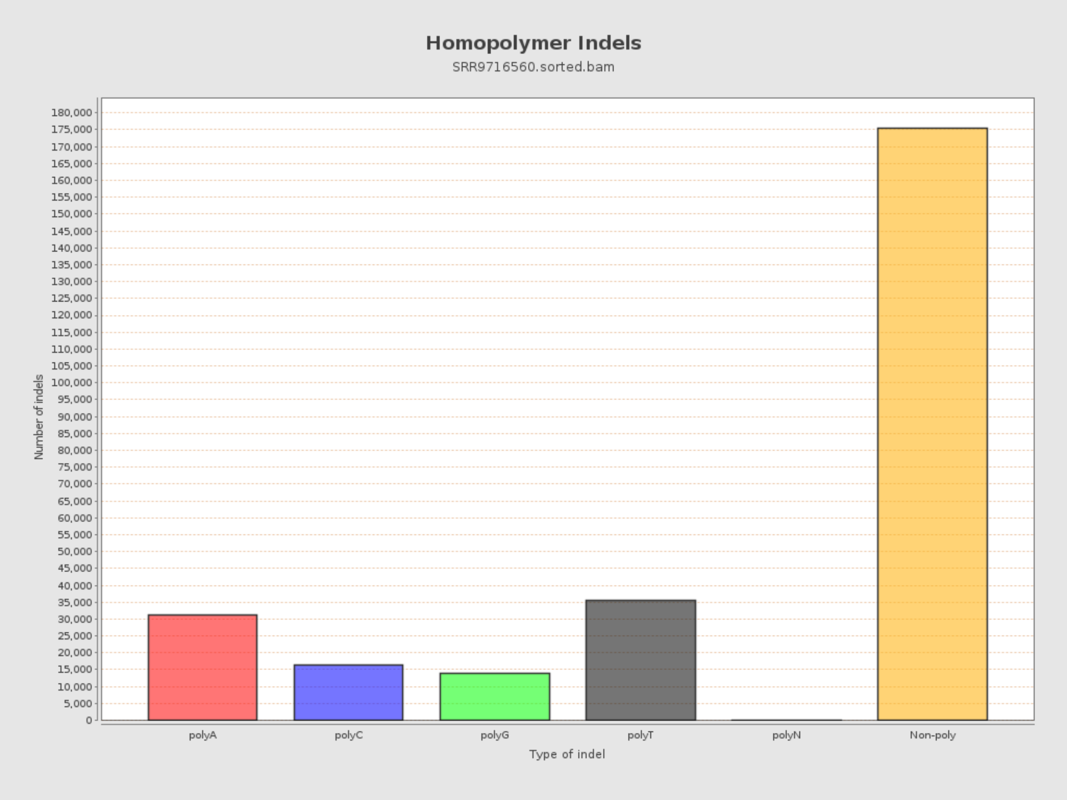
9. Results : Mapped Reads GC-content Distribution



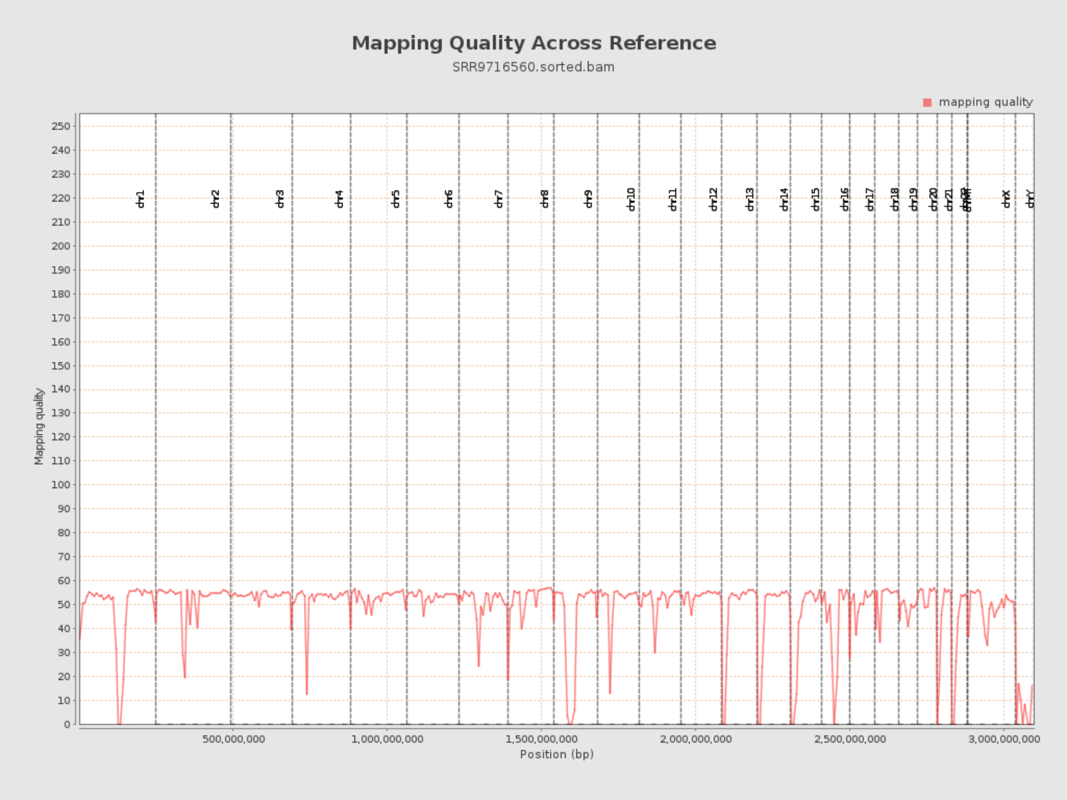
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram