Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:05:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080917.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_SRR3080917 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080917.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:05:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080917.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,006,797
Mapped reads	4,516,593 / 90.21%
Unmapped reads	490,204 / 9.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	56,342 / 1.13%
Read min/max/mean length	30 / 76 / 76.4
Duplicated reads (estimated)	245,763 / 4.91%
Duplication rate	4.18%
Clipped reads	1,565,227 / 31.26%

2.2. ACGT Content

Number/percentage of A's	89,696,743 / 28.75%
Number/percentage of C's	56,381,526 / 18.07%
Number/percentage of T's	98,609,763 / 31.61%
Number/percentage of G's	65,754,863 / 21.08%
Number/percentage of N's	1,512,395 / 0.48%
GC Percentage	39.15%

2.3. Coverage

Mean	0.1008

Standard Deviation	0.707

2.4. Mapping Quality

Mean Mapping Quality	47.7

2.5. Mismatches and indels

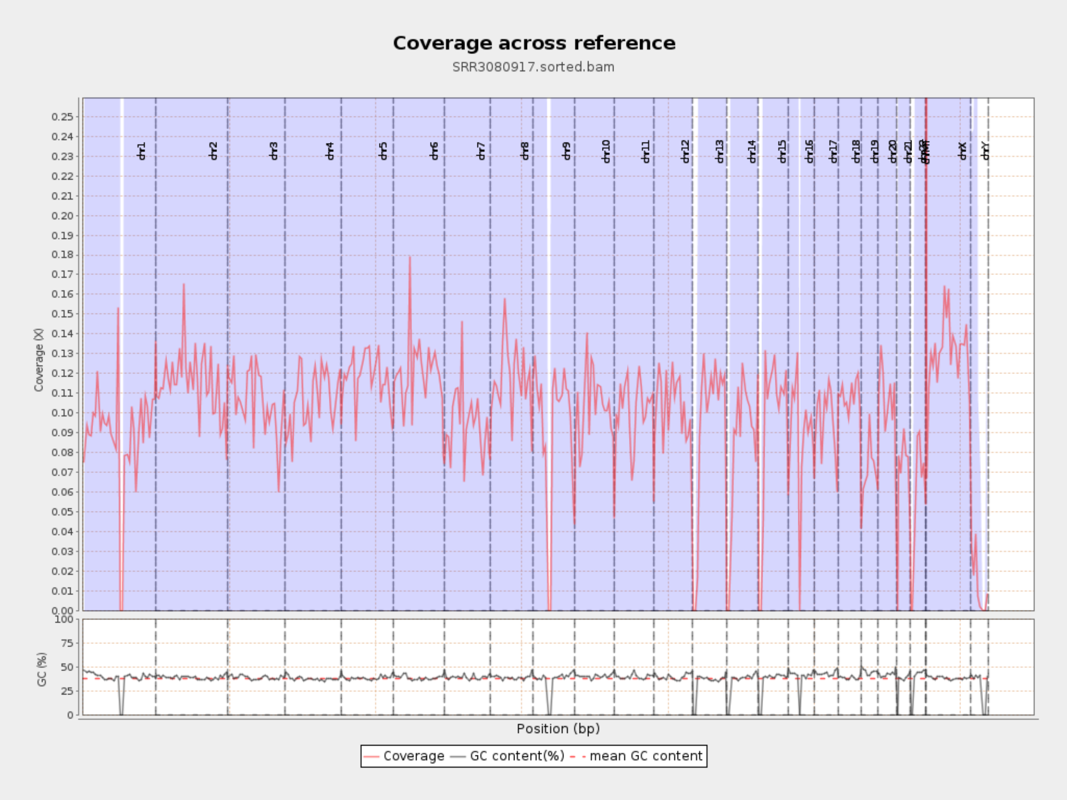
General error rate	1.16%
Mismatches	3,565,651
Insertions	23,697
Mapped reads with at least one insertion	0.52%
Deletions	70,090
Mapped reads with at least one deletion	1.54%
Homopolymer indels	49.65%

2.6. Chromosome stats

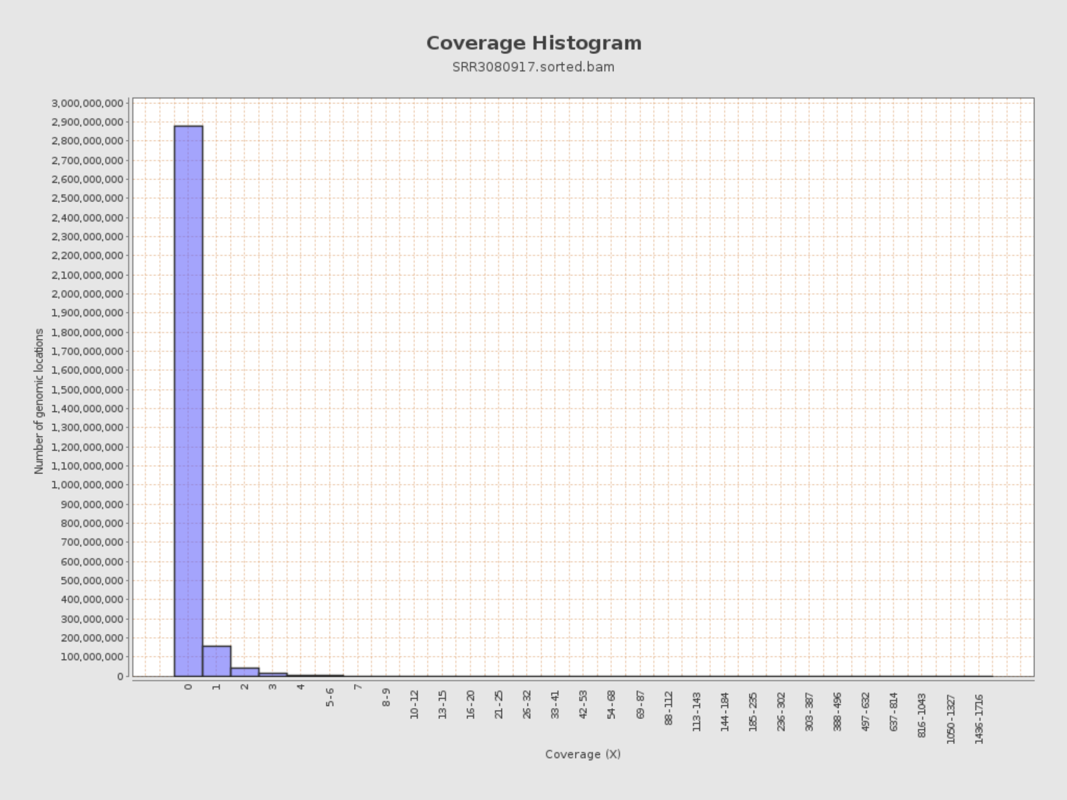
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22178430	0.089	1.2112
chr2	243199373	28096410	0.1155	0.7141
chr3	198022430	20950857	0.1058	0.4363
chr4	191154276	20440965	0.1069	0.4733
chr5	180915260	21340534	0.118	0.4632
chr6	171115067	20720599	0.1211	0.7303
chr7	159138663	15045832	0.0945	0.9212

chr8	146364022	17153915	0.1172	1.1583
chr9	141213431	13122721	0.0929	0.6254
chr10	135534747	14055530	0.1037	0.6822
chr11	135006516	13600718	0.1007	0.6308
chr12	133851895	13786518	0.103	0.4355
chr13	115169878	10775696	0.0936	0.4115
chr14	107349540	8900864	0.0829	0.4039
chr15	102531392	9605700	0.0937	0.4105
chr16	90354753	7852662	0.0869	0.435
chr17	81195210	7904355	0.0974	0.5179
chr18	78077248	8509505	0.109	1.1551
chr19	59128983	4220915	0.0714	0.8743
chr20	63025520	6805221	0.108	0.4578
chr21	48129895	3266127	0.0679	0.3926
chr22	51304566	2845702	0.0555	0.3091
chrMT	16571	44597	2.6913	2.2325
chrX	155270560	20112600	0.1295	0.5385
chrY	59373566	734674	0.0124	0.2527

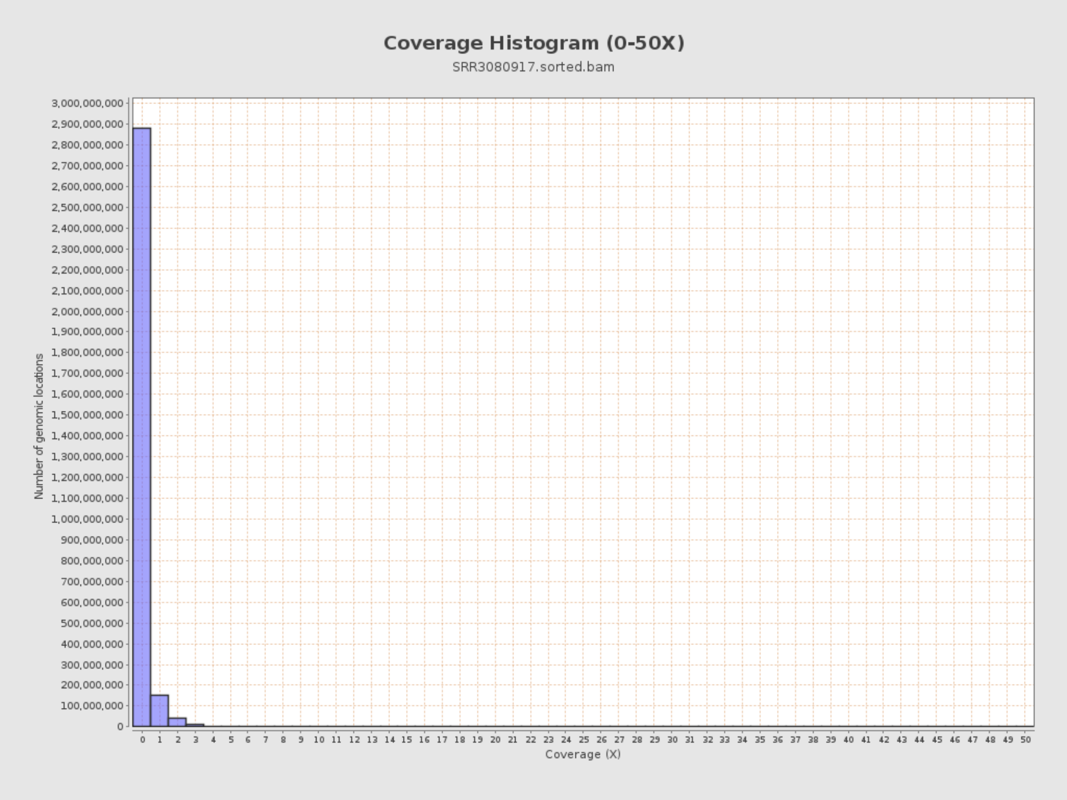
3. Results : Coverage across reference



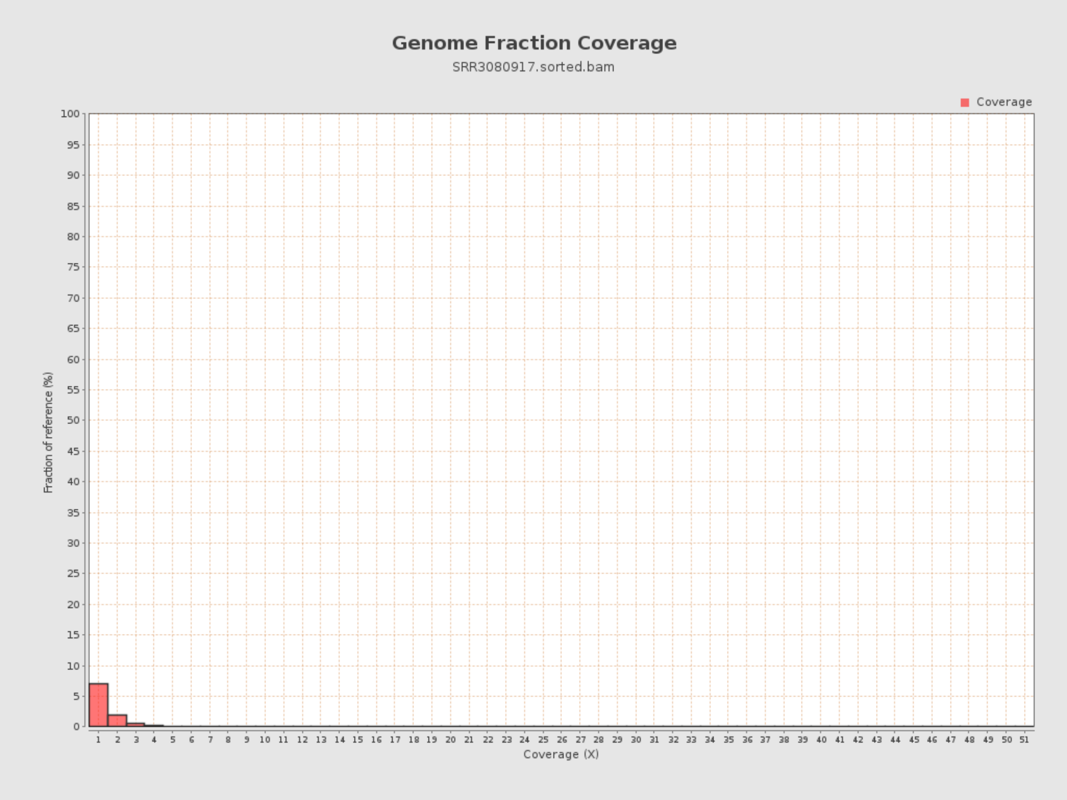
4. Results : Coverage Histogram



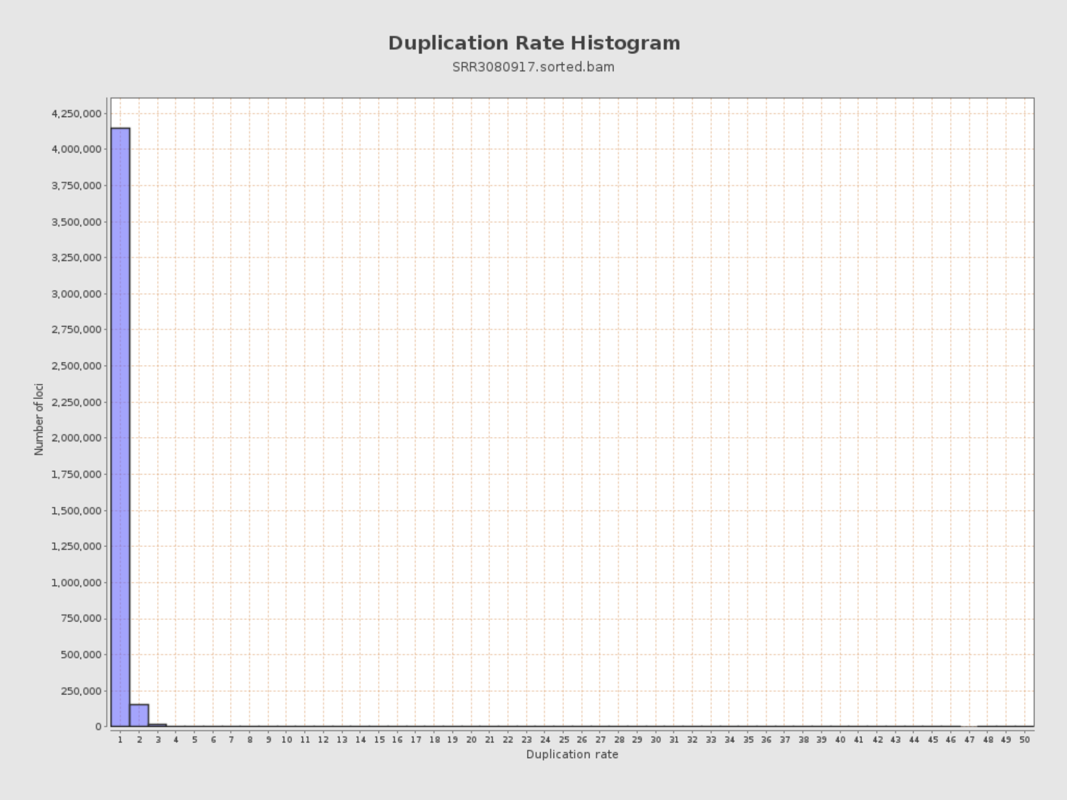
5. Results : Coverage Histogram (0-50X)



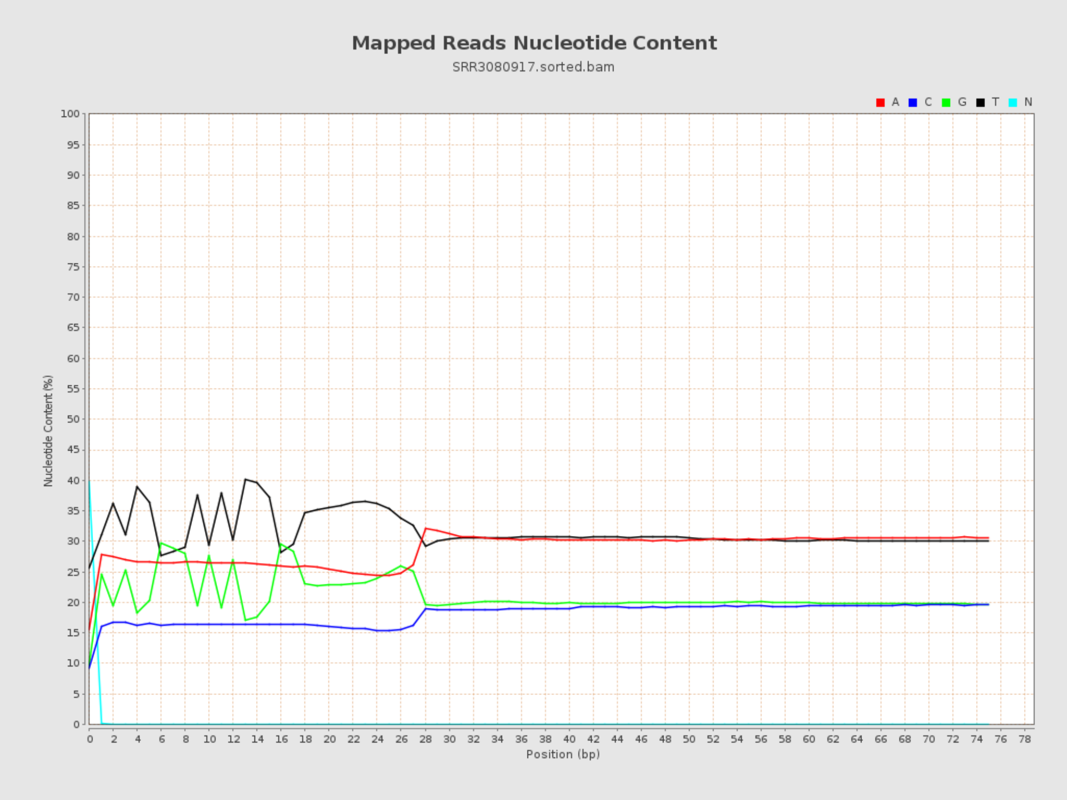
6. Results : Genome Fraction Coverage



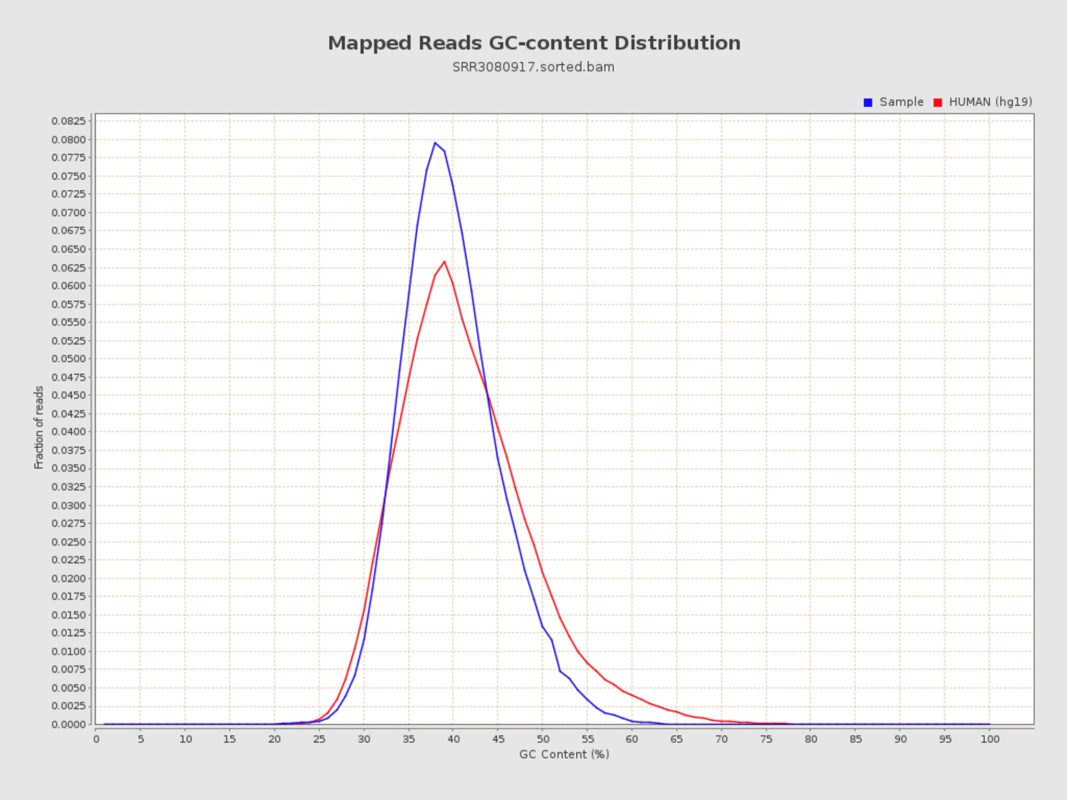
7. Results : Duplication Rate Histogram



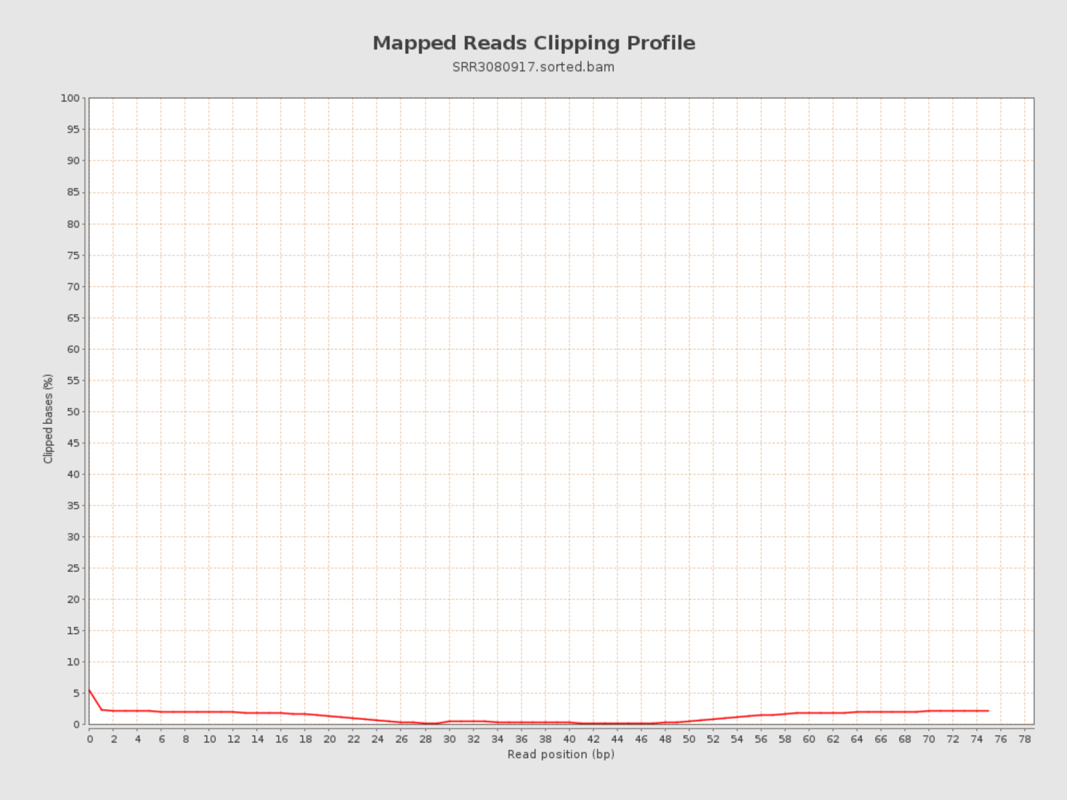
8. Results : Mapped Reads Nucleotide Content



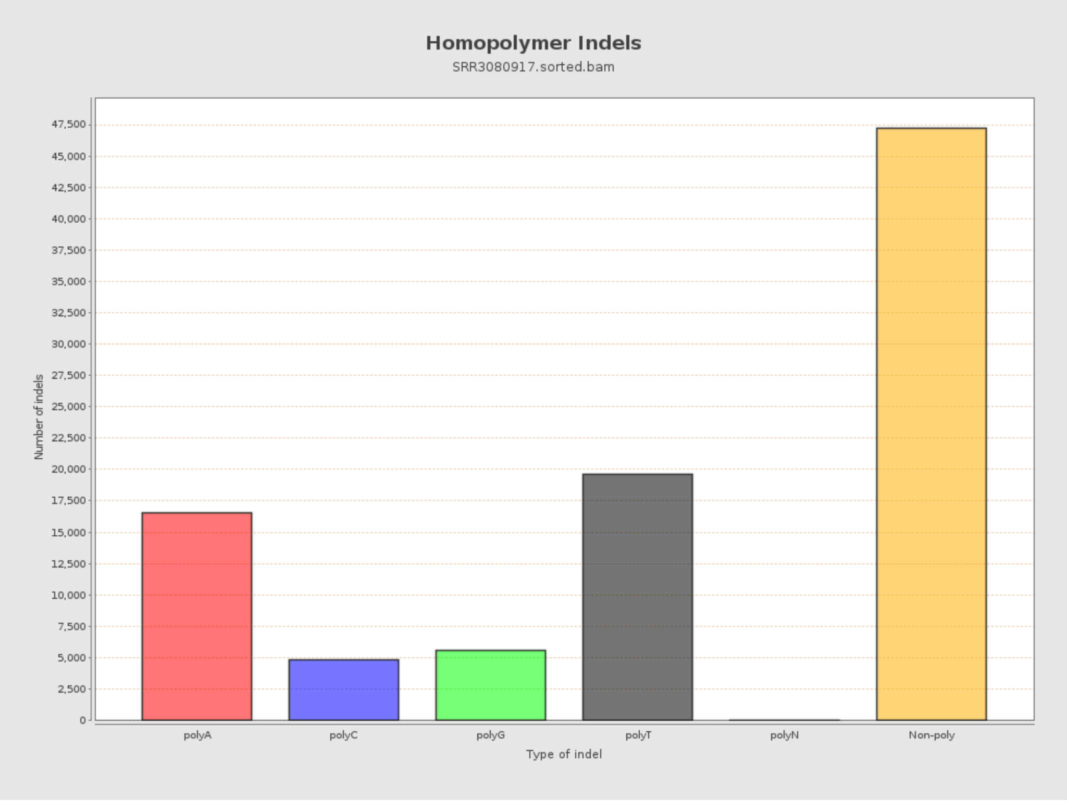
9. Results : Mapped Reads GC-content Distribution



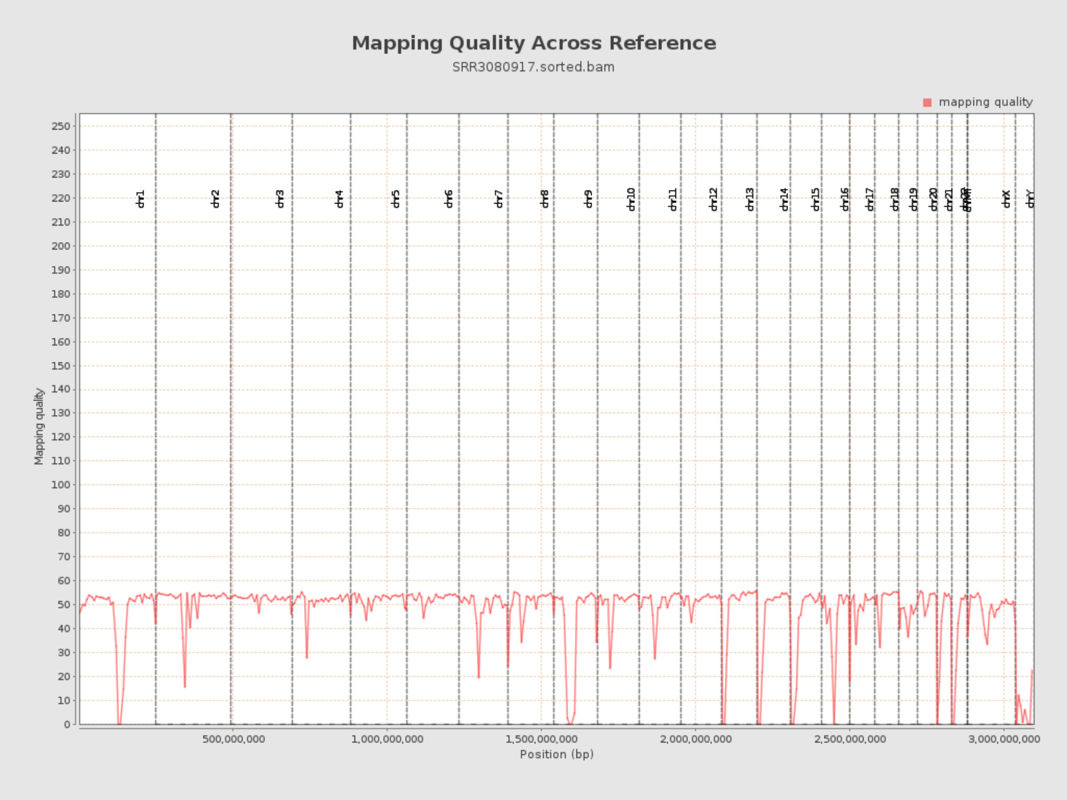
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram