Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 02:08:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080747.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_SRR3080747 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080747.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 02:08:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080747.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,309,022
Mapped reads	4,344,962 / 81.84%
Unmapped reads	964,060 / 18.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,901 / 0.56%
Read min/max/mean length	30 / 66 / 66.19
Duplicated reads (estimated)	601,512 / 11.33%
Duplication rate	10.81%
Clipped reads	651,546 / 12.27%

2.2. ACGT Content

Number/percentage of A's	81,657,150 / 29.46%
Number/percentage of C's	56,733,963 / 20.47%
Number/percentage of T's	77,803,696 / 28.07%
Number/percentage of G's	60,384,108 / 21.78%
Number/percentage of N's	626,834 / 0.23%
GC Percentage	42.25%

2.3. Coverage

Mean	0.0896

Standard Deviation	0.5342

2.4. Mapping Quality

Mean Mapping Quality	45.45

2.5. Mismatches and indels

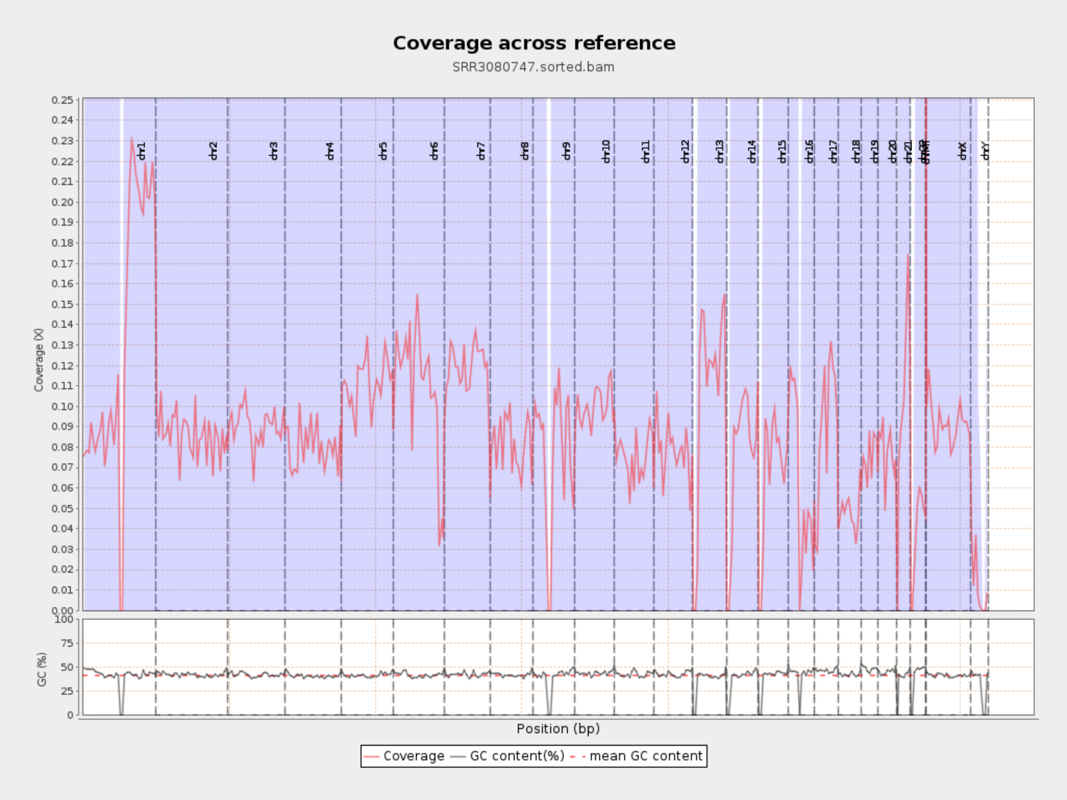
General error rate	1.01%
Mismatches	2,767,541
Insertions	18,280
Mapped reads with at least one insertion	0.42%
Deletions	45,001
Mapped reads with at least one deletion	1.03%
Homopolymer indels	44.18%

2.6. Chromosome stats

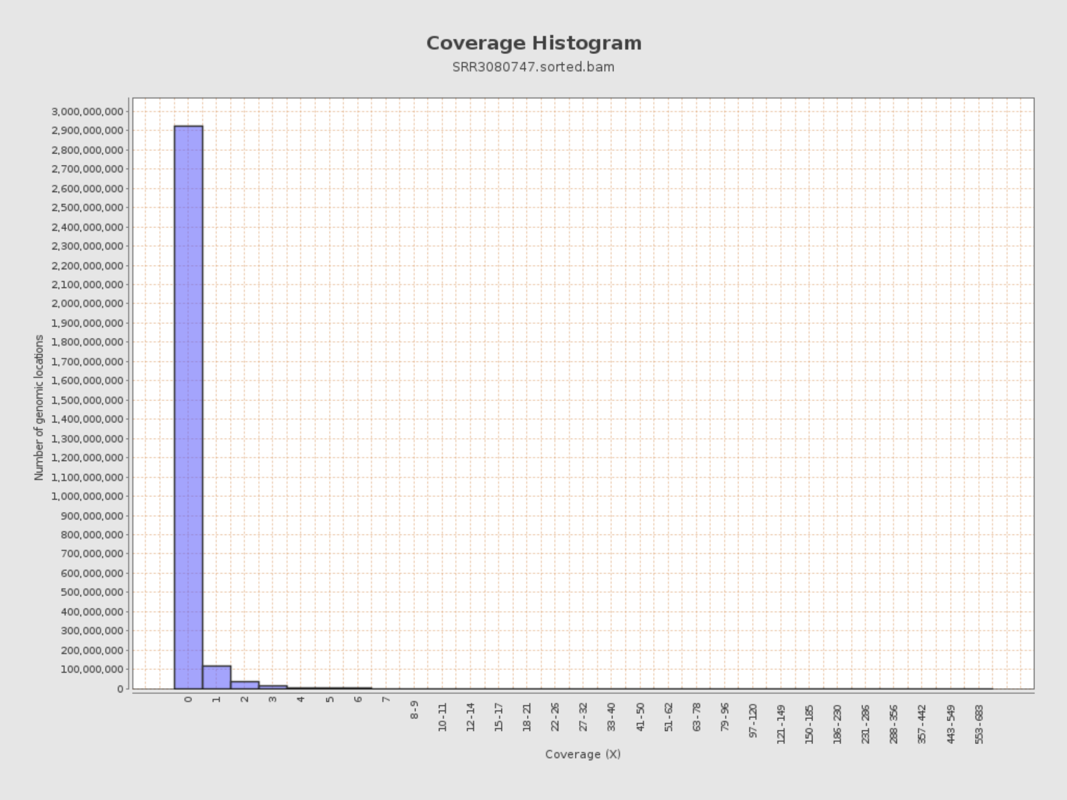
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	32795286	0.1316	0.7943
chr2	243199373	20922173	0.086	0.4919
chr3	198022430	17878273	0.0903	0.449
chr4	191154276	15405073	0.0806	0.4567
chr5	180915260	20113936	0.1112	0.4983
chr6	171115067	18991347	0.111	0.5738
chr7	159138663	18900053	0.1188	0.6896

chr8	146364022	11961075	0.0817	0.6105
chr9	141213431	10902606	0.0772	0.4713
chr10	135534747	13546630	0.0999	0.5386
chr11	135006516	10155886	0.0752	0.4785
chr12	133851895	10587916	0.0791	0.427
chr13	115169878	12432021	0.1079	0.5024
chr14	107349540	8072561	0.0752	0.4525
chr15	102531392	6761867	0.0659	0.3884
chr16	90354753	5560933	0.0615	0.3965
chr17	81195210	7388446	0.091	0.4733
chr18	78077248	3696076	0.0473	0.6407
chr19	59128983	4414511	0.0747	0.6477
chr20	63025520	4877826	0.0774	0.4315
chr21	48129895	5060297	0.1051	0.5784
chr22	51304566	1942922	0.0379	0.2963
chrMT	16571	6591	0.3977	0.9775
chrX	155270560	14202245	0.0915	0.4746
chrY	59373566	710583	0.012	0.2982

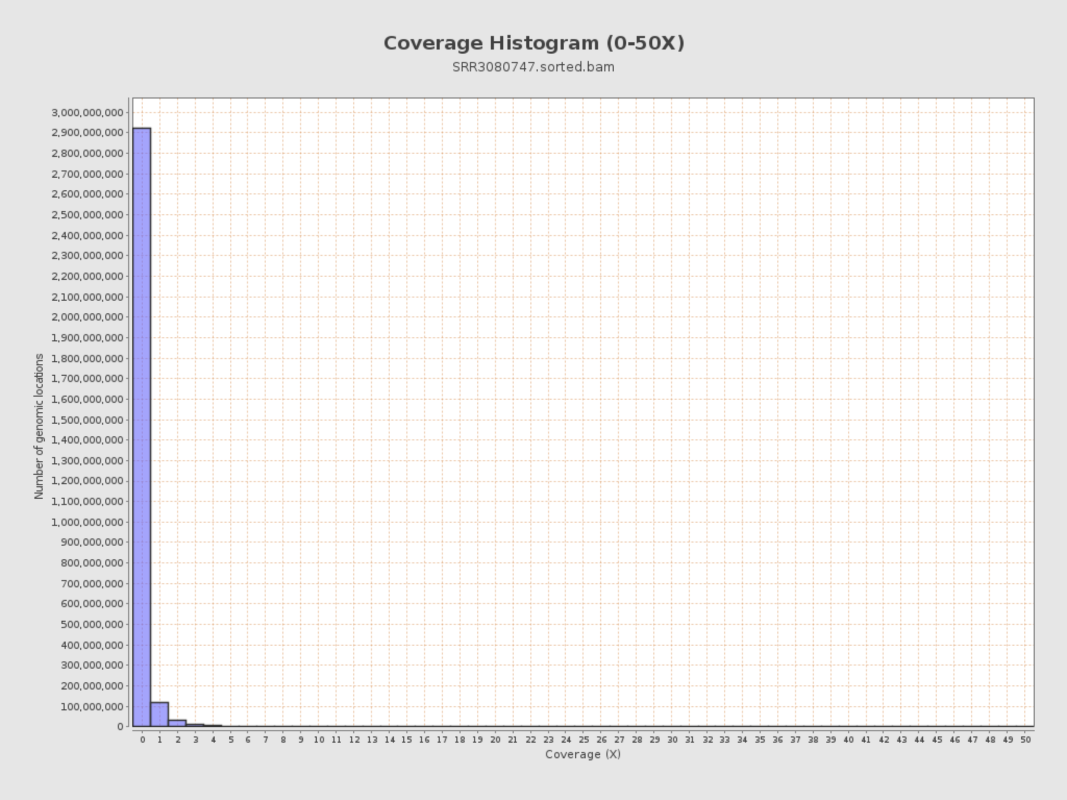
3. Results : Coverage across reference



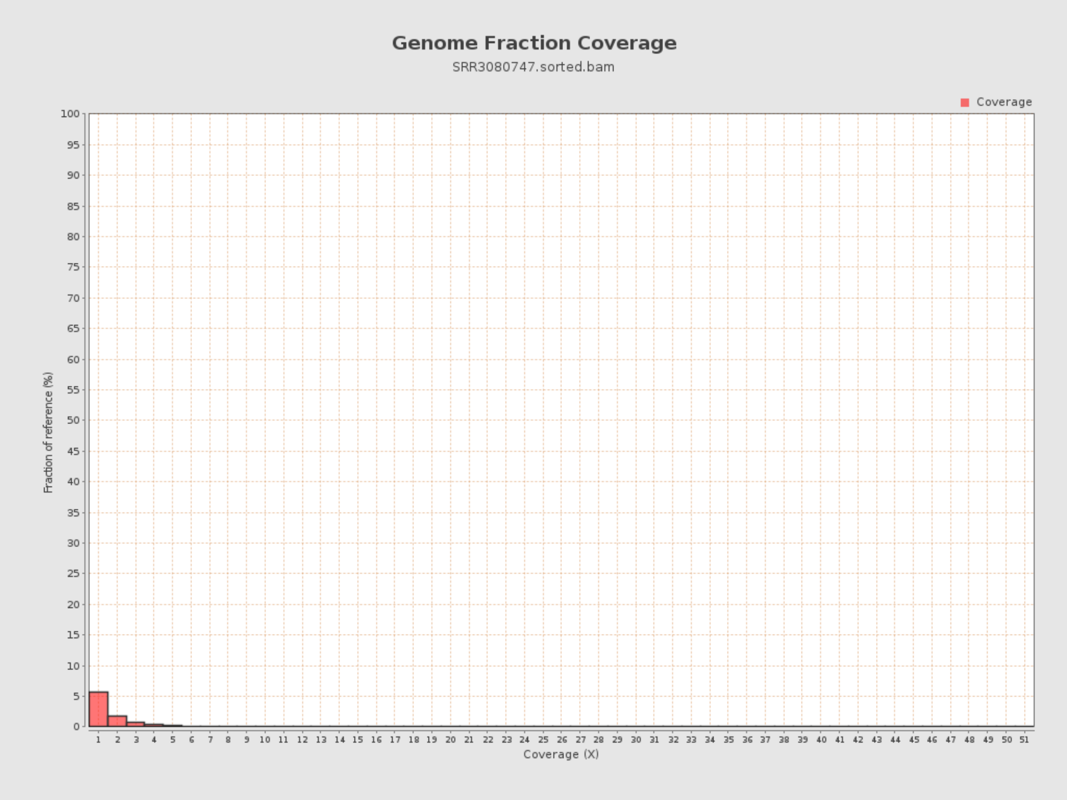
4. Results : Coverage Histogram



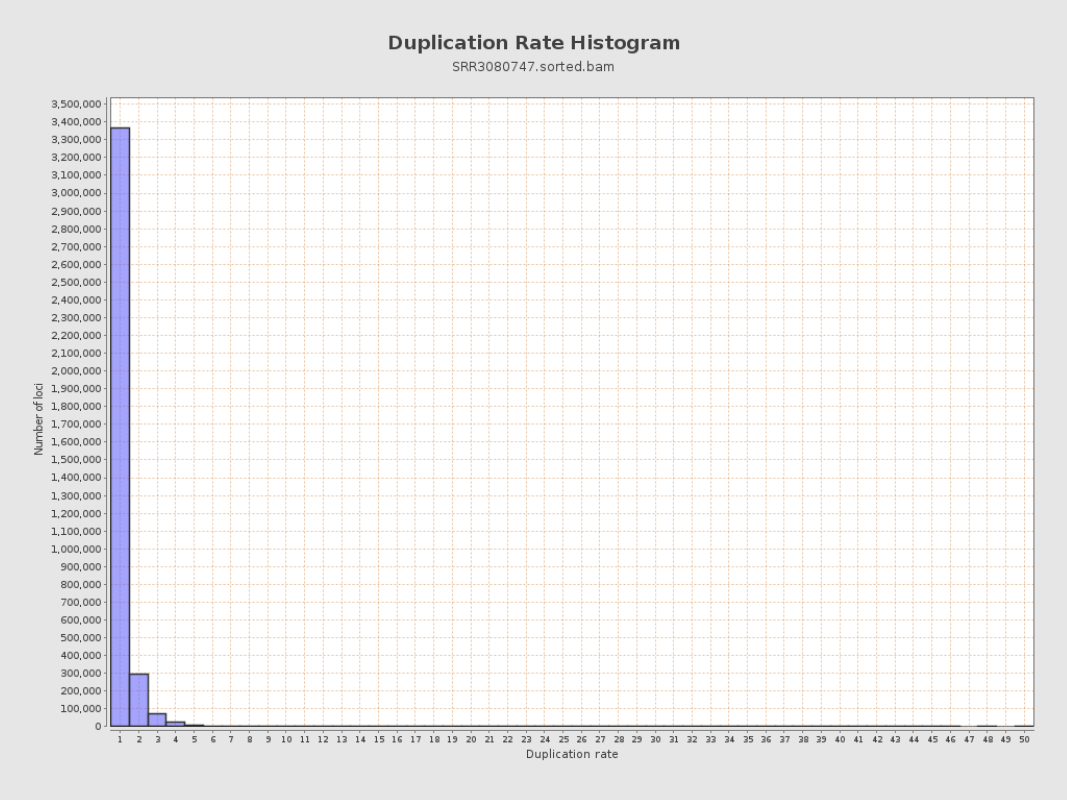
5. Results : Coverage Histogram (0-50X)



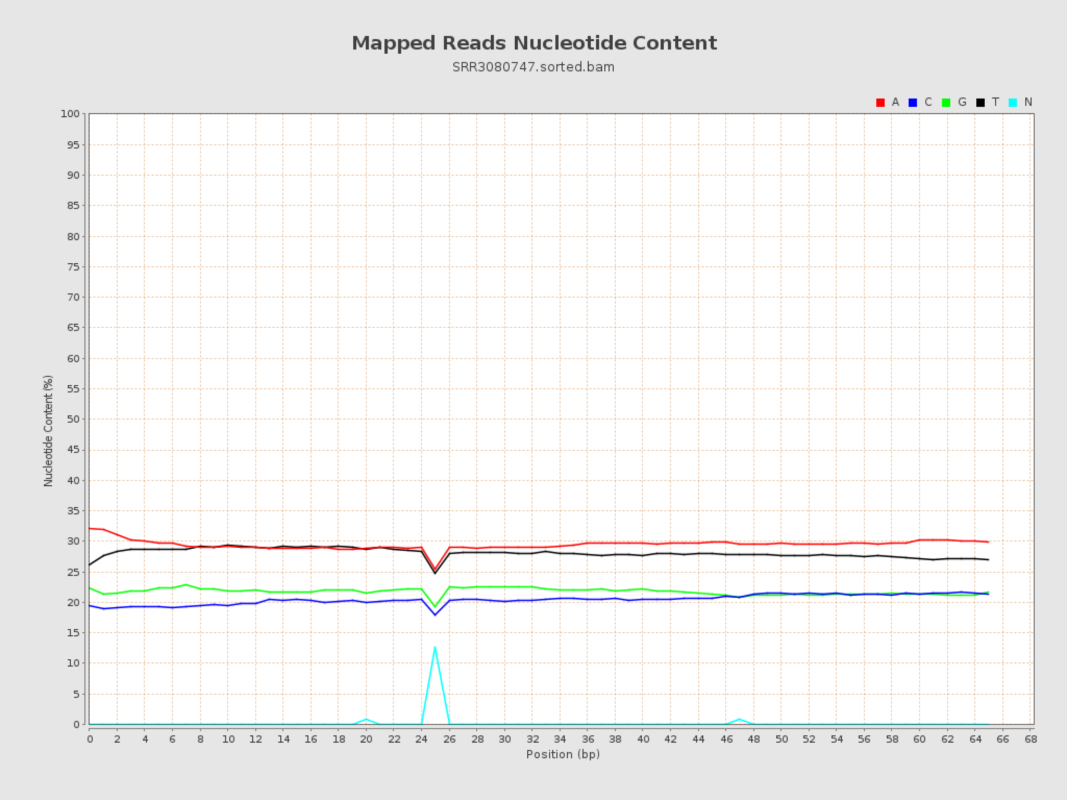
6. Results : Genome Fraction Coverage



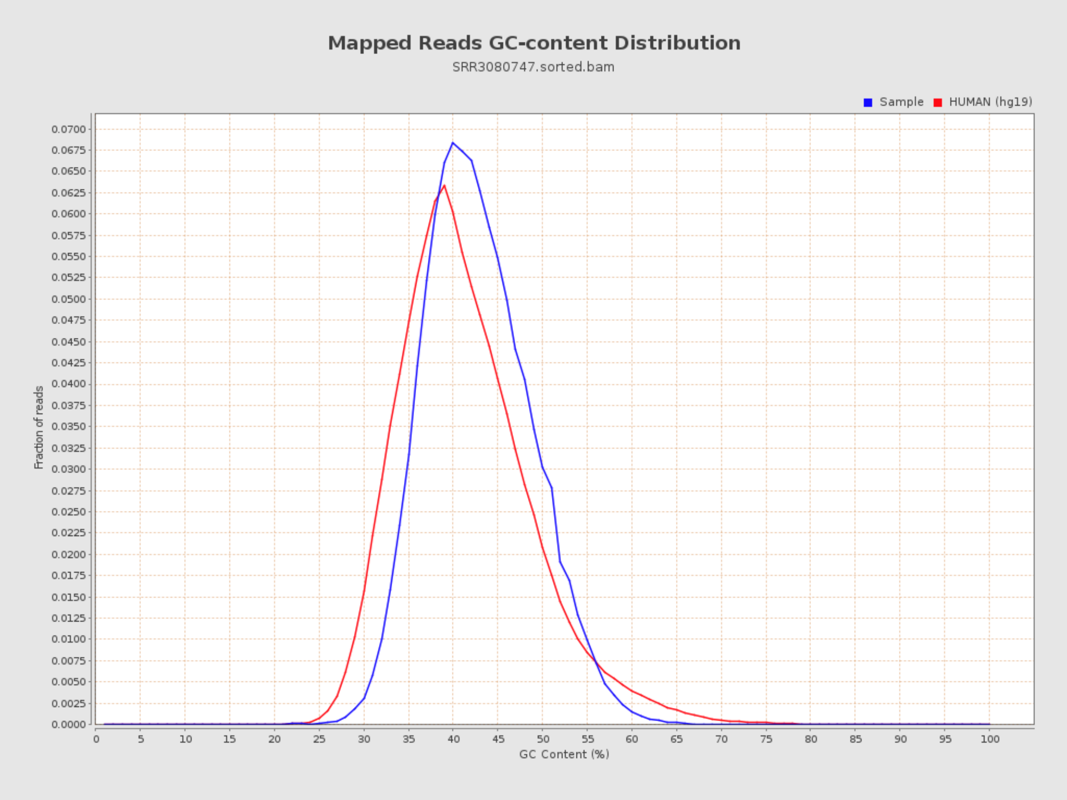
7. Results : Duplication Rate Histogram



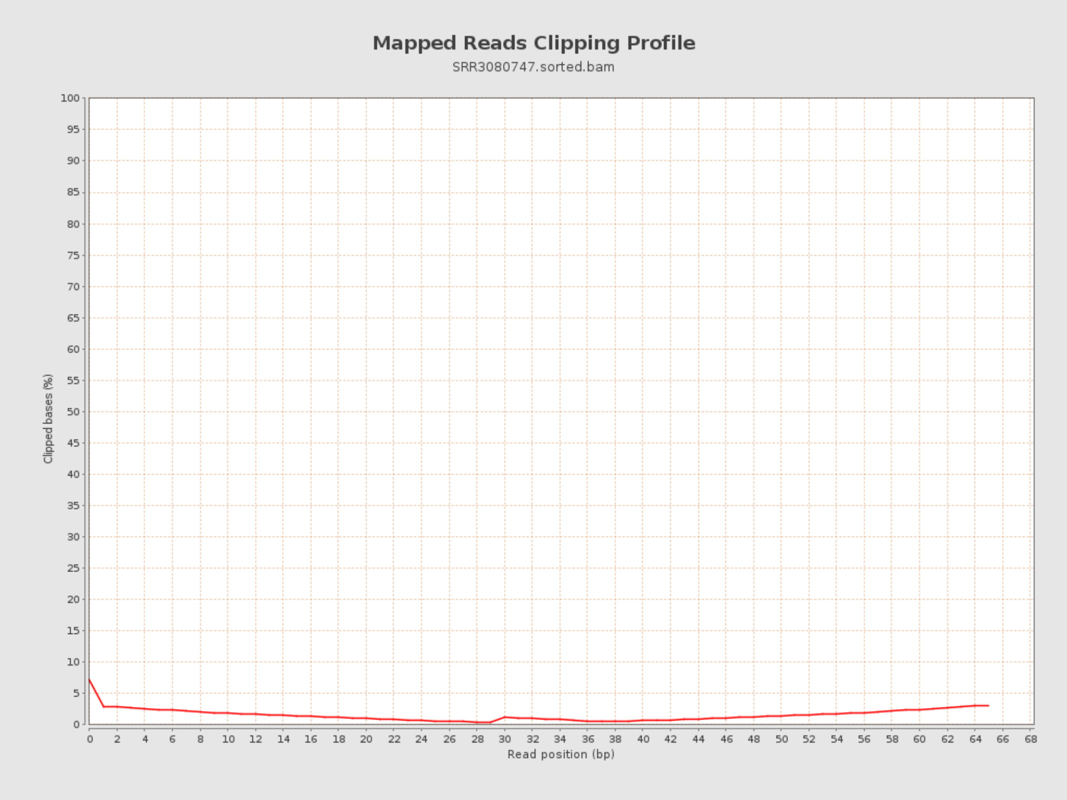
8. Results : Mapped Reads Nucleotide Content



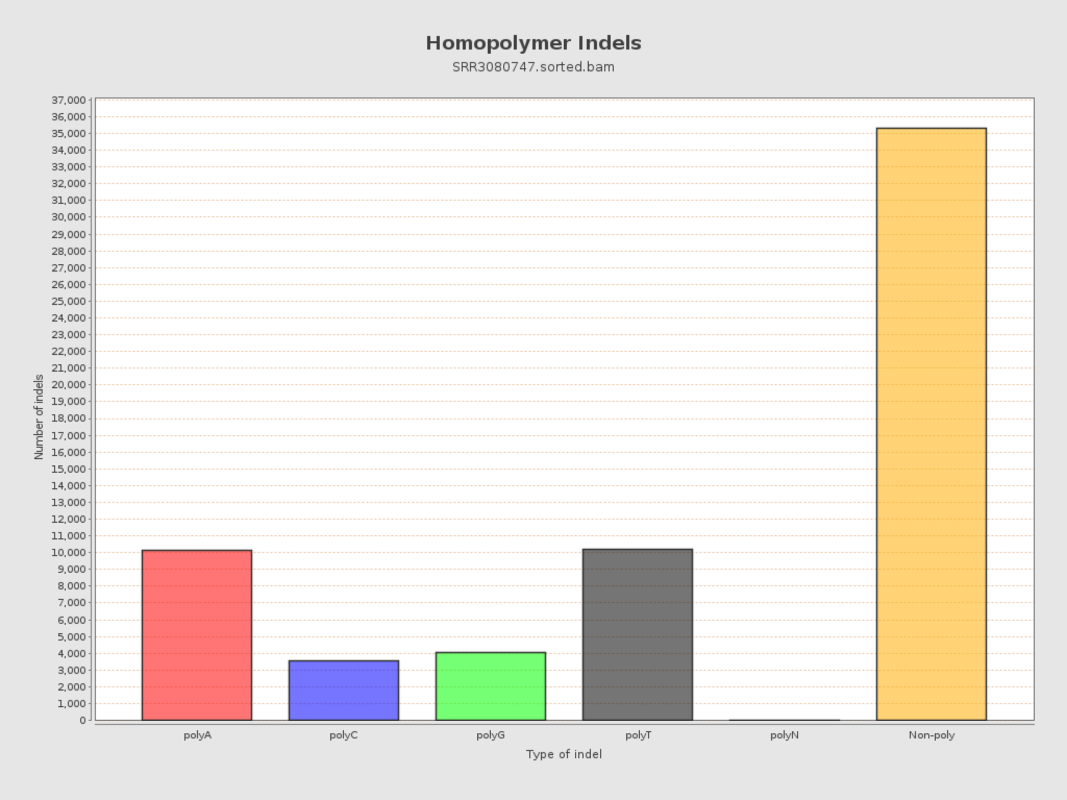
9. Results : Mapped Reads GC-content Distribution



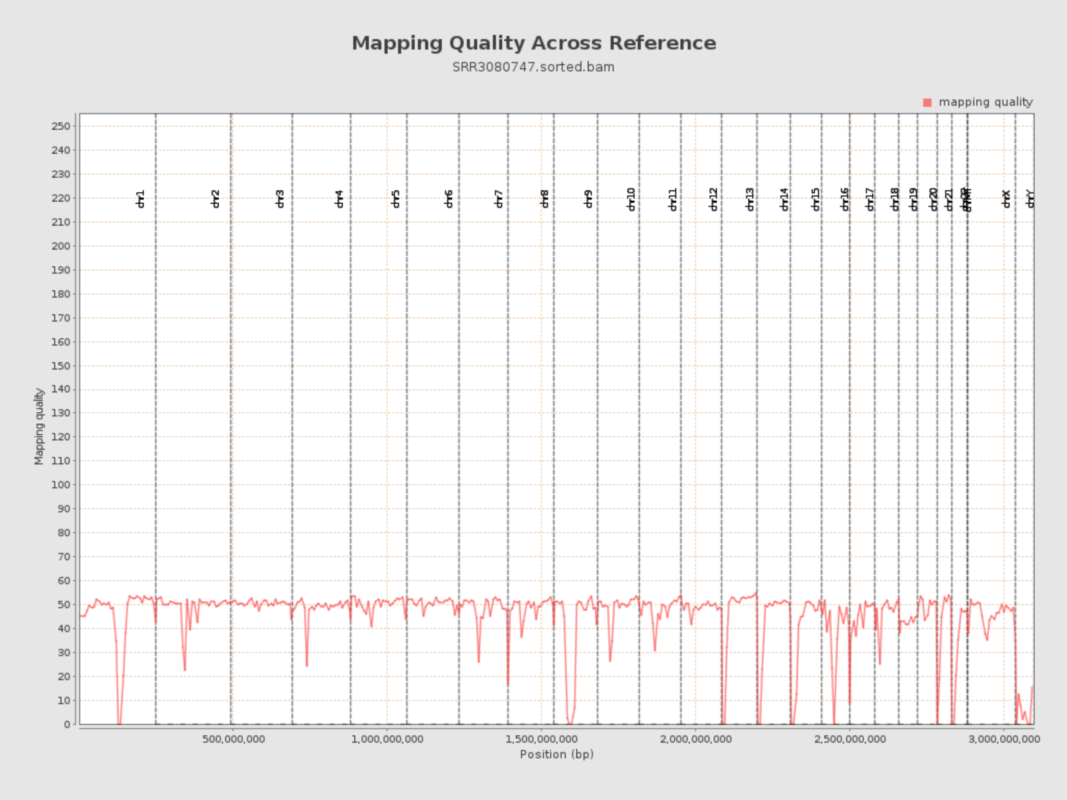
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram