Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 01:57:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080746.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_SRR3080746 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080746.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 01:57:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080746.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,354,729
Mapped reads	4,710,757 / 74.13%
Unmapped reads	1,643,972 / 25.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,388 / 0.42%
Read min/max/mean length	30 / 66 / 66.14
Duplicated reads (estimated)	480,498 / 7.56%
Duplication rate	7.91%
Clipped reads	738,243 / 11.62%

2.2. ACGT Content

Number/percentage of A's	93,045,506 / 31.02%
Number/percentage of C's	60,900,880 / 20.3%
Number/percentage of T's	76,574,161 / 25.53%
Number/percentage of G's	68,737,193 / 22.92%
Number/percentage of N's	678,877 / 0.23%
GC Percentage	43.22%

2.3. Coverage

Mean	0.0969

Standard Deviation	0.6066

2.4. Mapping Quality

Mean Mapping Quality	44.64

2.5. Mismatches and indels

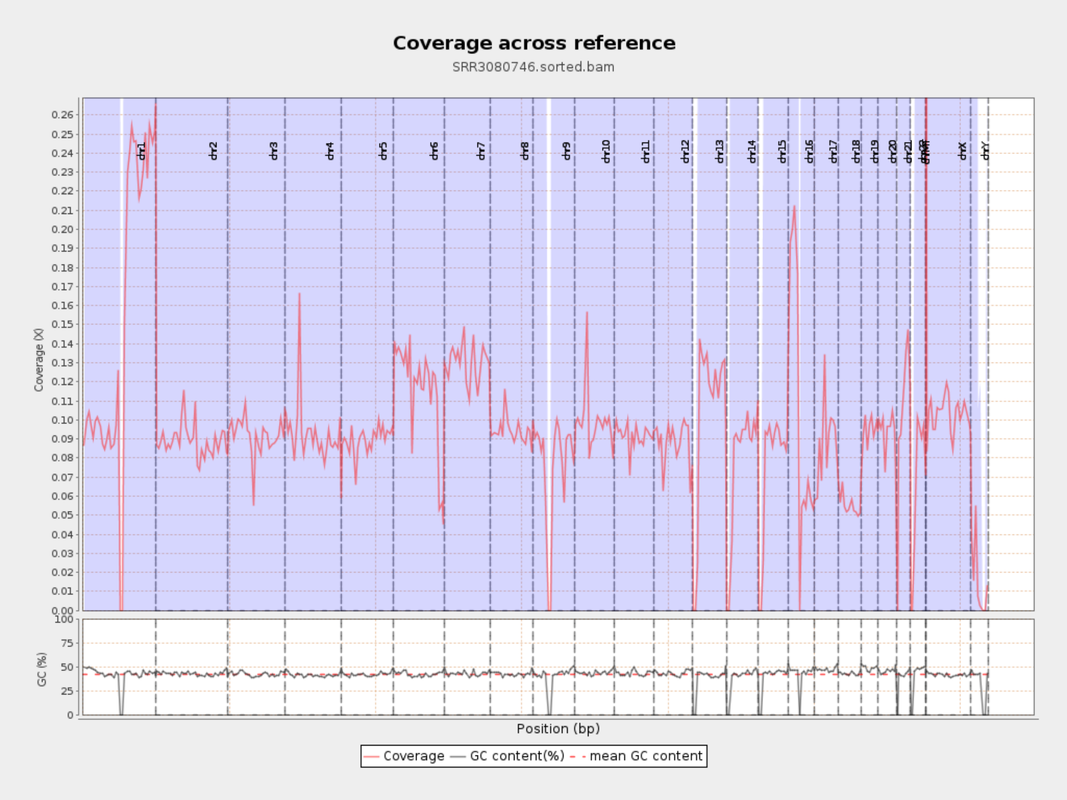
General error rate	1.01%
Mismatches	3,000,884
Insertions	21,765
Mapped reads with at least one insertion	0.46%
Deletions	51,797
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.7%

2.6. Chromosome stats

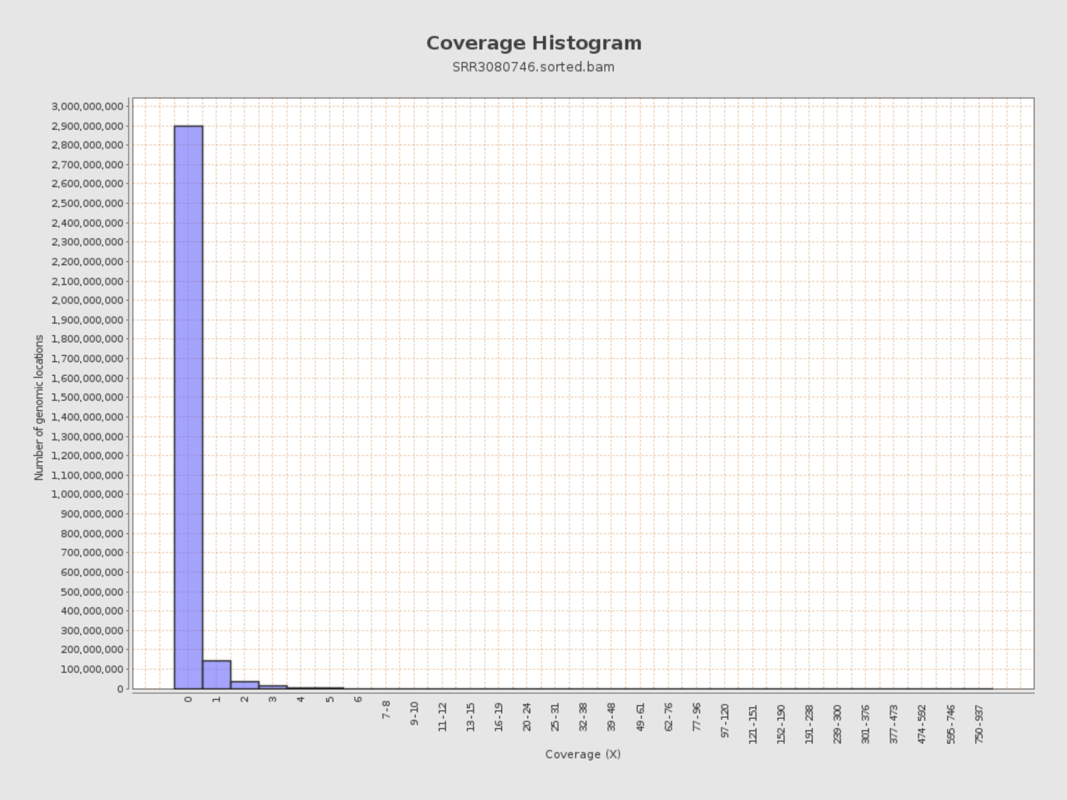
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	37539956	0.1506	0.8964
chr2	243199373	21727130	0.0893	0.5858
chr3	198022430	18125189	0.0915	0.4316
chr4	191154276	17846106	0.0934	0.5432
chr5	180915260	16174924	0.0894	0.4229
chr6	171115067	19973492	0.1167	0.6326
chr7	159138663	20763047	0.1305	0.9351

chr8	146364022	13740978	0.0939	0.7601
chr9	141213431	10688937	0.0757	0.4687
chr10	135534747	13431632	0.0991	0.7071
chr11	135006516	12364481	0.0916	0.5555
chr12	133851895	11865226	0.0886	0.4356
chr13	115169878	12069380	0.1048	0.4673
chr14	107349540	8350440	0.0778	0.4589
chr15	102531392	7549834	0.0736	0.3888
chr16	90354753	9402164	0.1041	0.5264
chr17	81195210	7091019	0.0873	0.4453
chr18	78077248	4331712	0.0555	0.7341
chr19	59128983	5576635	0.0943	0.7949
chr20	63025520	5938475	0.0942	0.4586
chr21	48129895	5095540	0.1059	0.592
chr22	51304566	3377343	0.0658	0.3743
chrMT	16571	35247	2.127	2.3421
chrX	155270560	16049047	0.1034	0.4876
chrY	59373566	926453	0.0156	0.4432

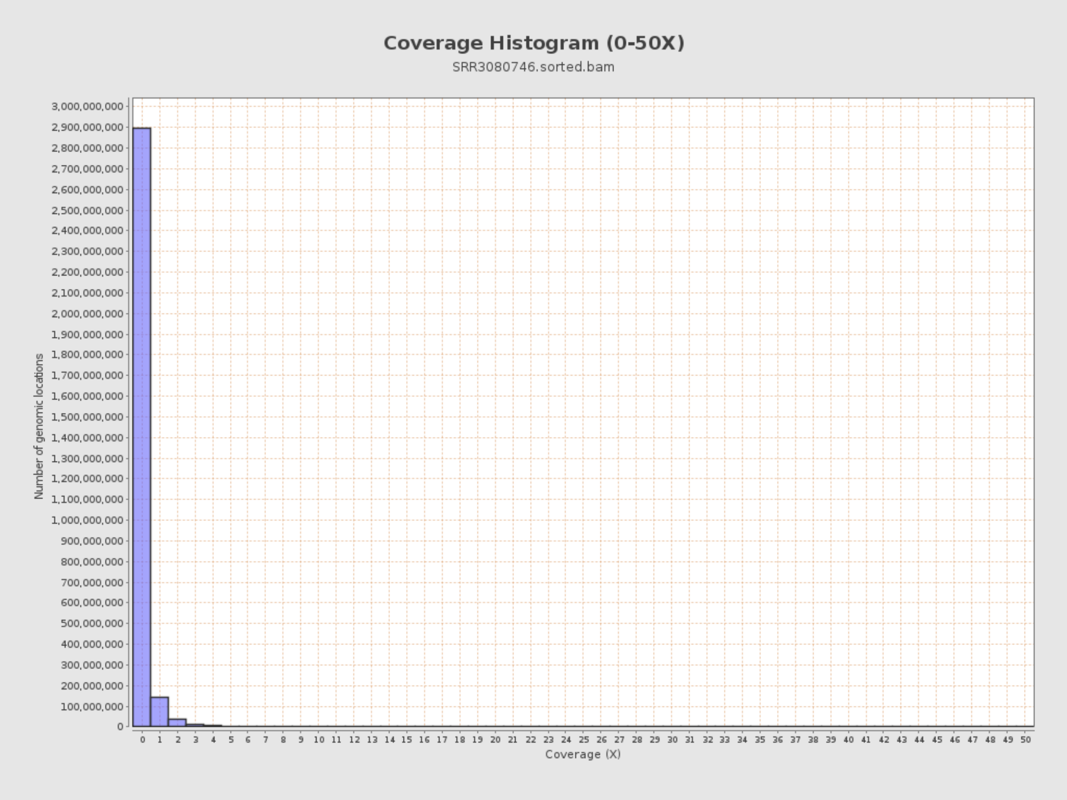
3. Results : Coverage across reference



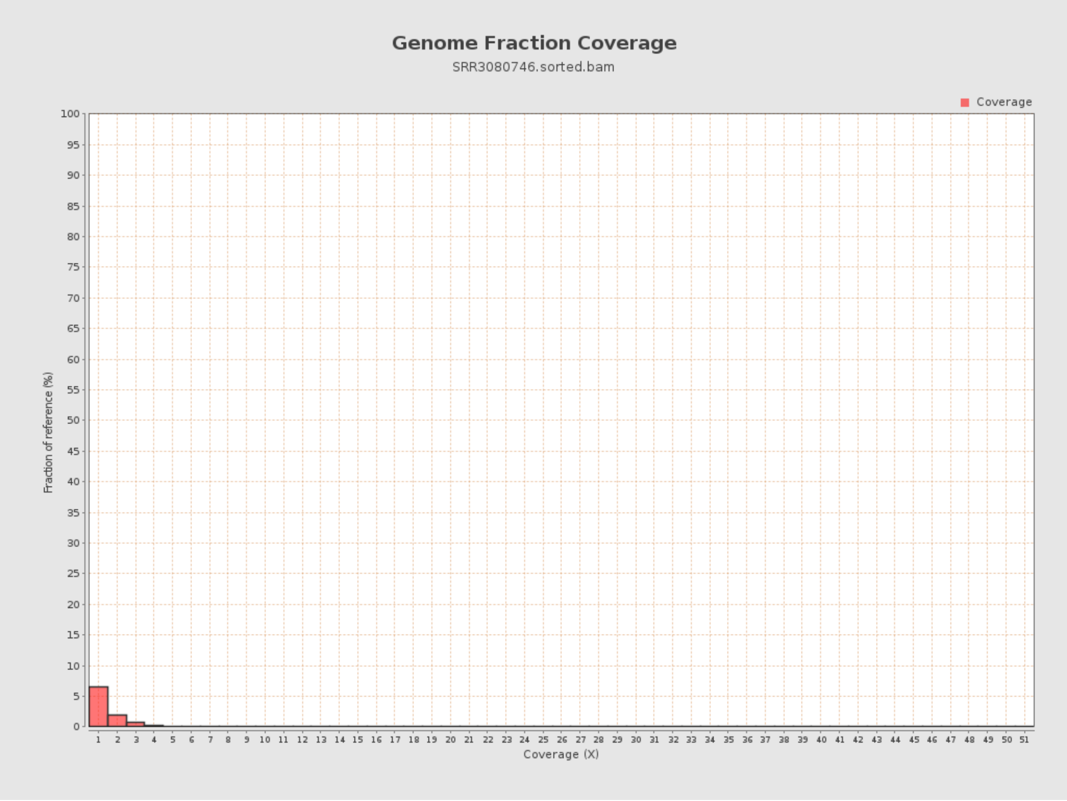
4. Results : Coverage Histogram



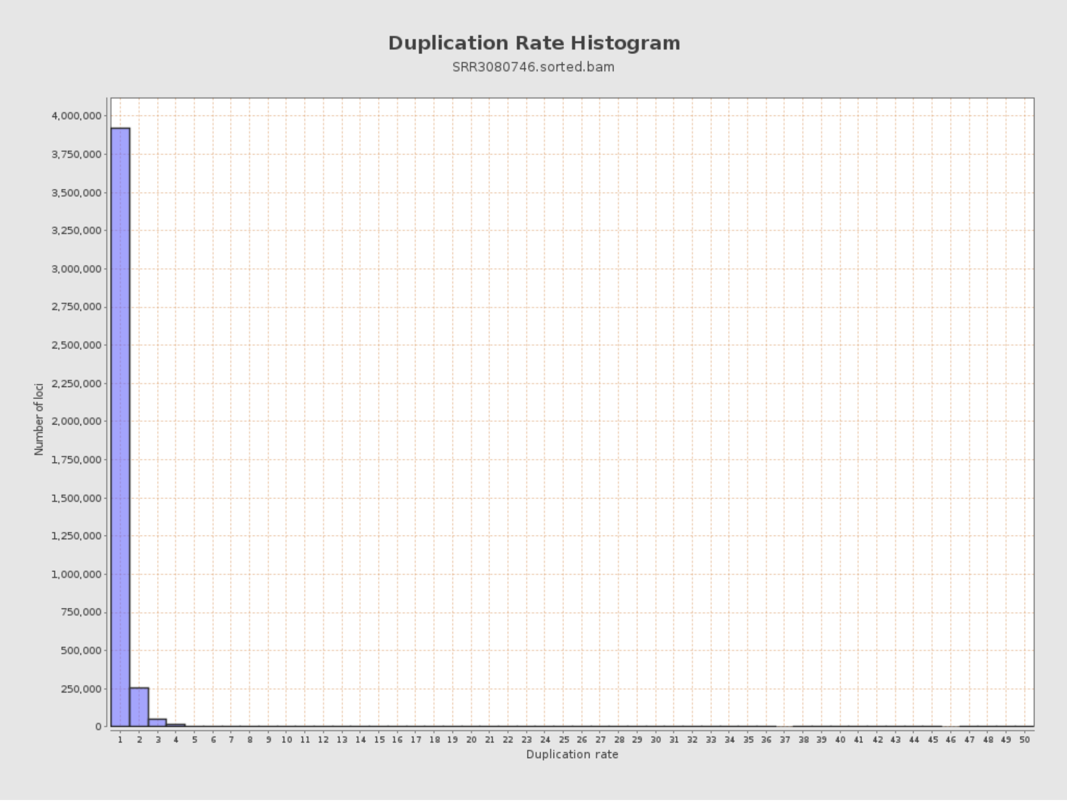
5. Results : Coverage Histogram (0-50X)



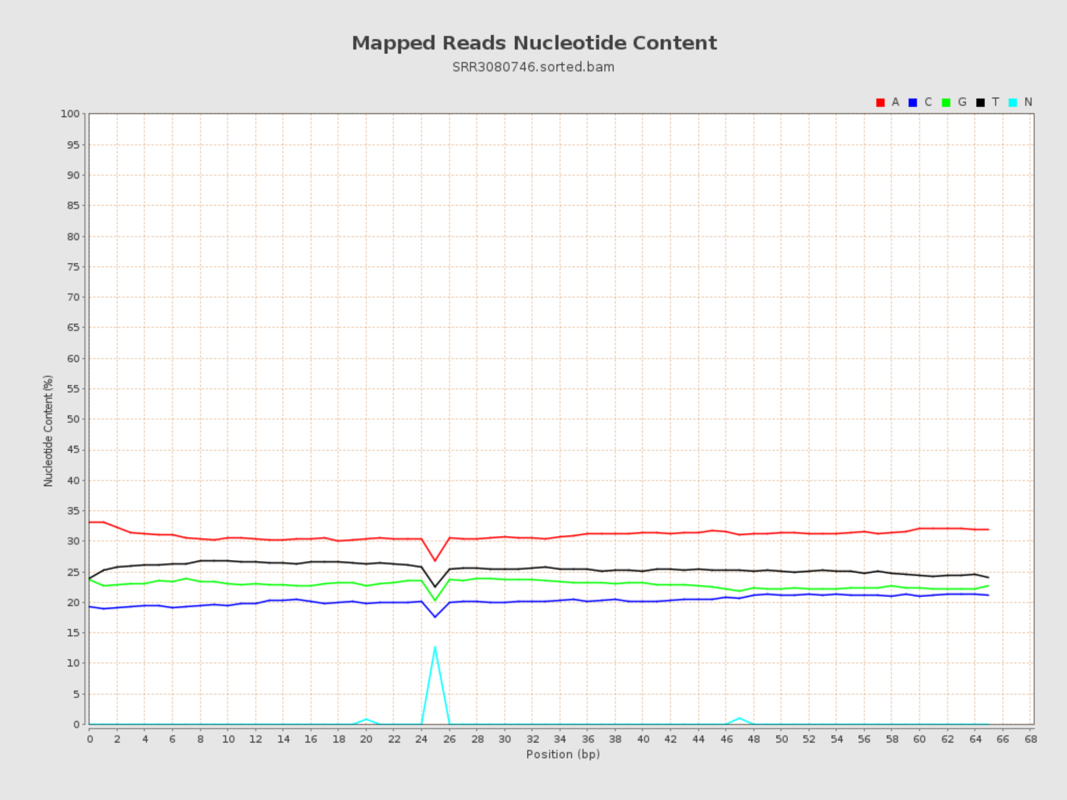
6. Results : Genome Fraction Coverage



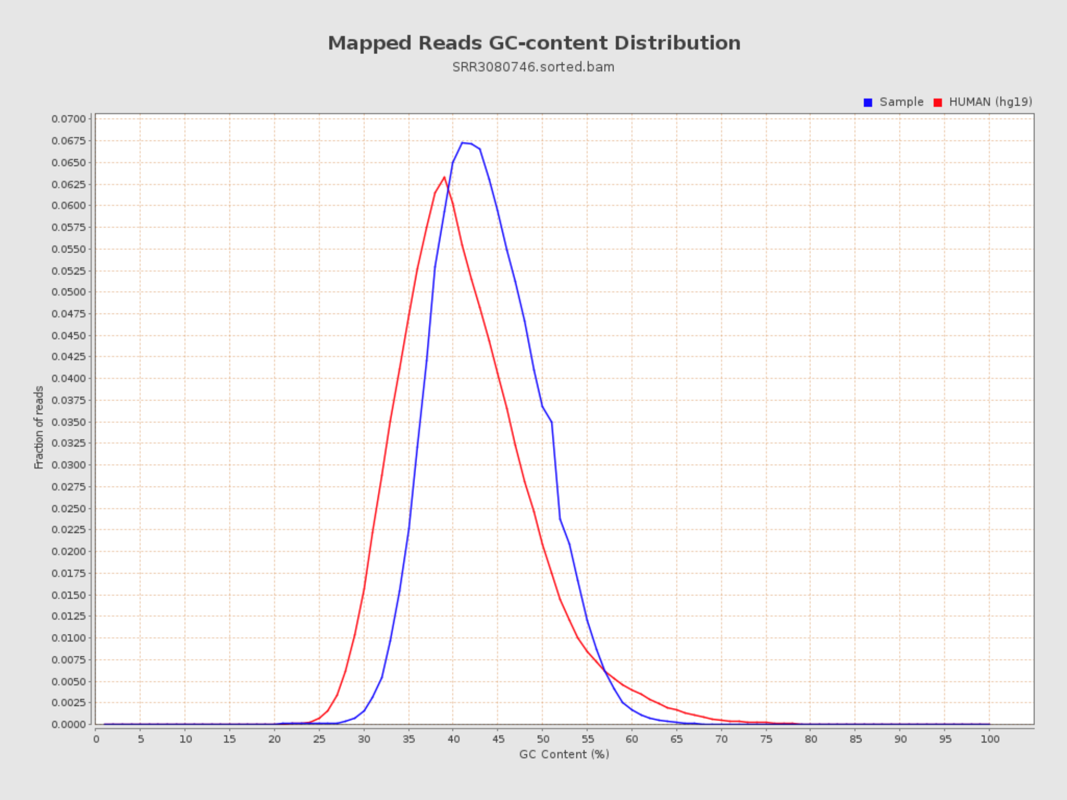
7. Results : Duplication Rate Histogram



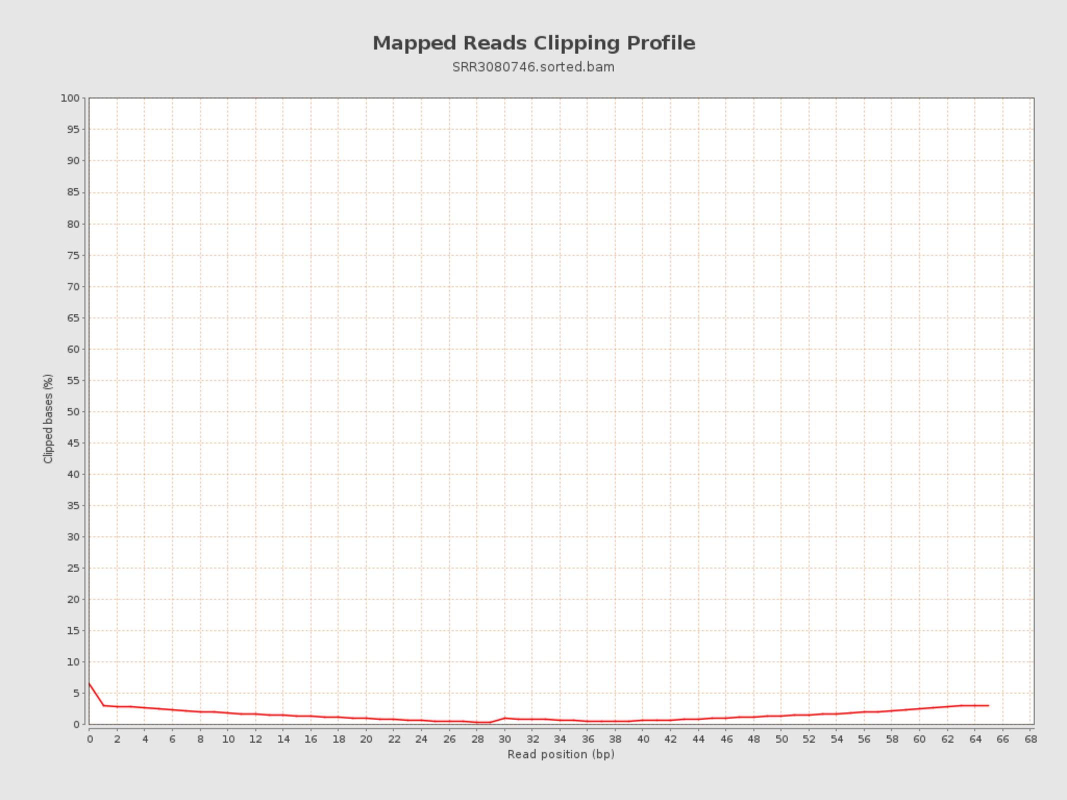
8. Results : Mapped Reads Nucleotide Content



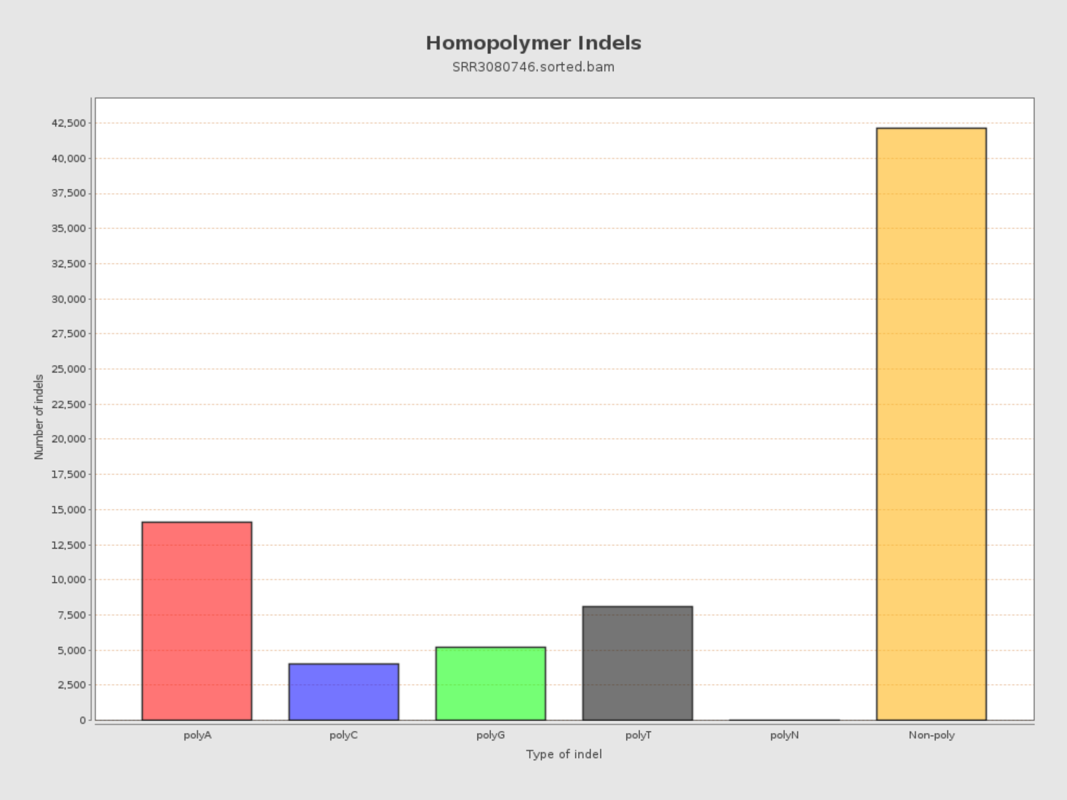
9. Results : Mapped Reads GC-content Distribution



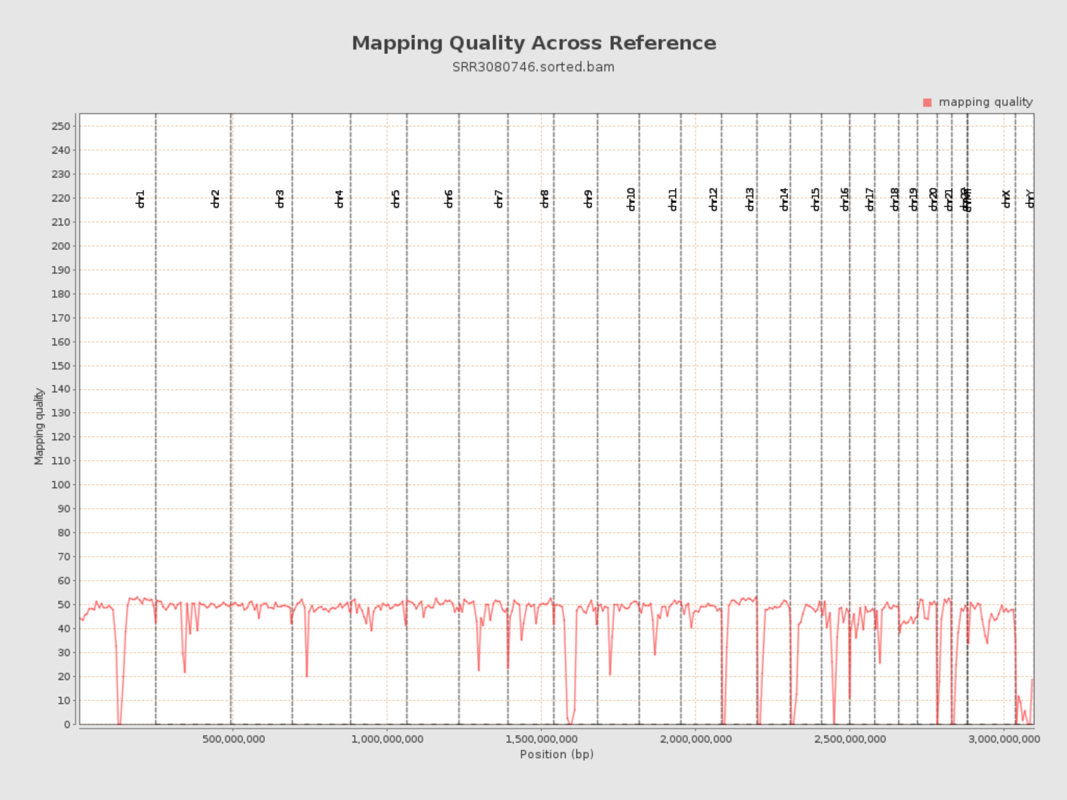
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram