Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 22:21:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080717.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_SRR3080717 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080717.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 22:20:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080717.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,098,090
Mapped reads	1,883,667 / 89.78%
Unmapped reads	214,423 / 10.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,883 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	99,603 / 4.75%
Duplication rate	4.47%
Clipped reads	794,769 / 37.88%

2.2. ACGT Content

Number/percentage of A's	35,117,987 / 27.78%
Number/percentage of C's	23,266,969 / 18.4%
Number/percentage of T's	40,345,018 / 31.91%
Number/percentage of G's	27,698,416 / 21.91%
Number/percentage of N's	1,828 / 0%
GC Percentage	40.31%

2.3. Coverage

Mean	0.0409

Standard Deviation	0.3608

2.4. Mapping Quality

Mean Mapping Quality	46.06

2.5. Mismatches and indels

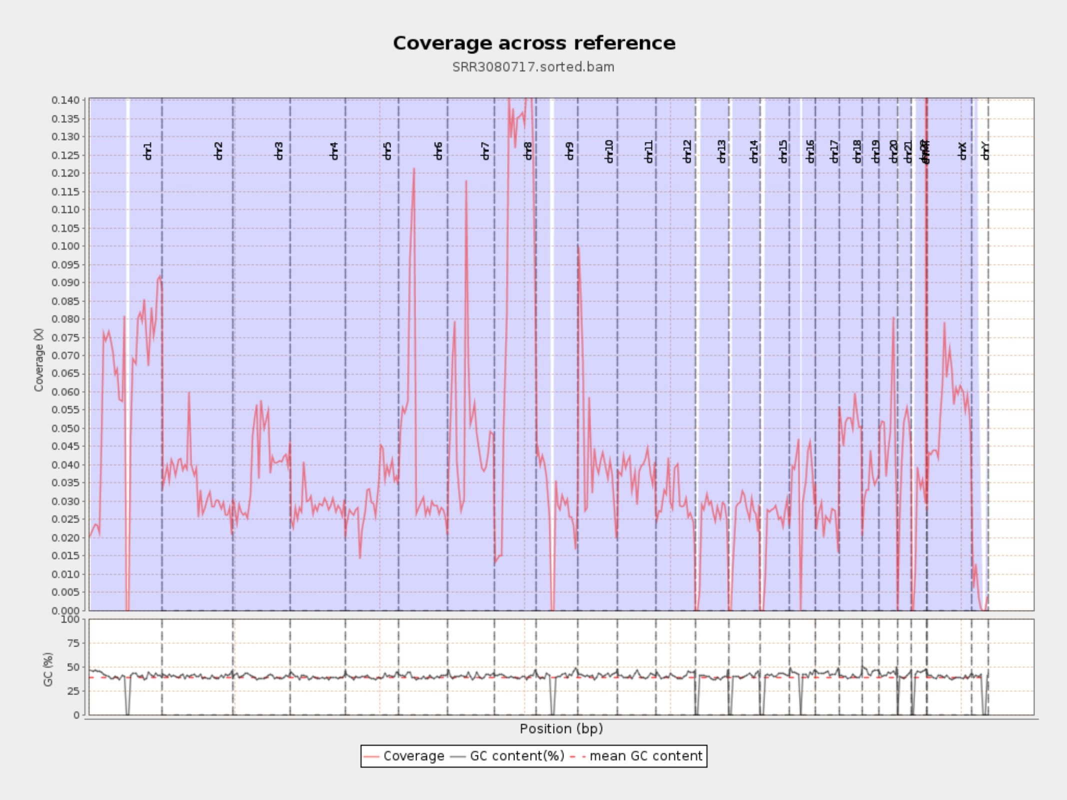
General error rate	0.83%
Mismatches	1,027,034
Insertions	8,988
Mapped reads with at least one insertion	0.47%
Deletions	26,077
Mapped reads with at least one deletion	1.37%
Homopolymer indels	48.06%

2.6. Chromosome stats

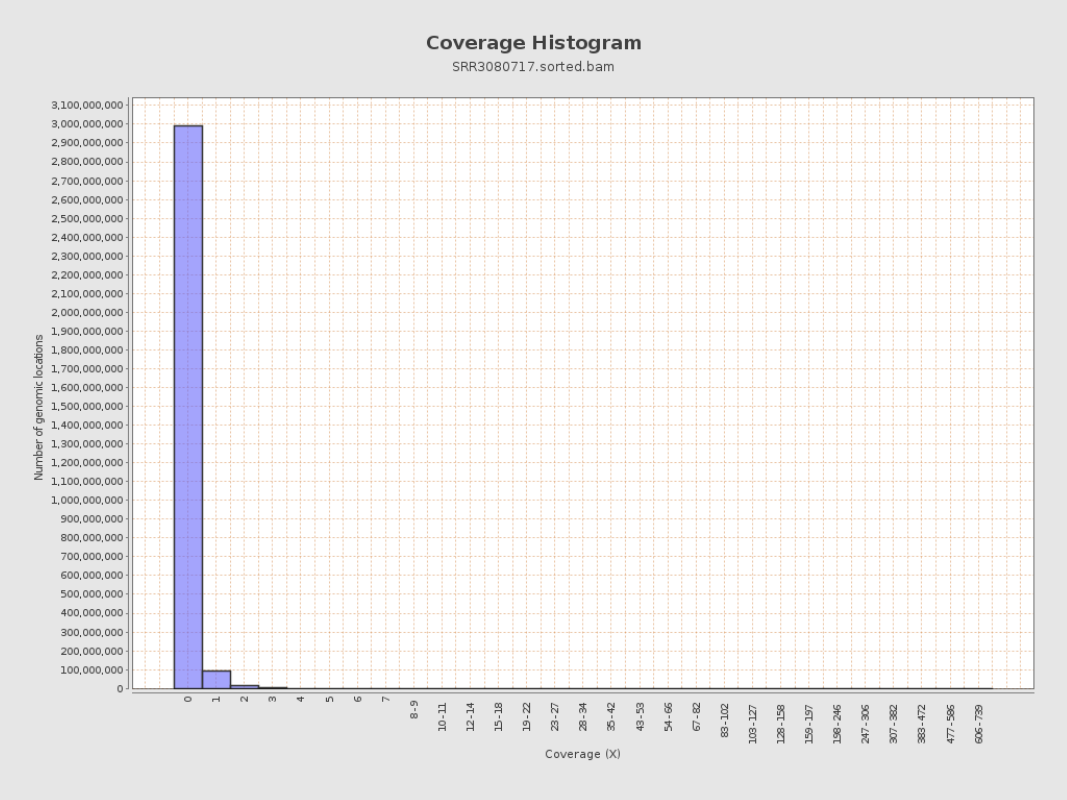
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15097407	0.0606	0.5048
chr2	243199373	8361842	0.0344	0.3308
chr3	198022430	7873528	0.0398	0.2263
chr4	191154276	5489566	0.0287	0.2009
chr5	180915260	5719100	0.0316	0.2015
chr6	171115067	7510728	0.0439	0.3317
chr7	159138663	8136819	0.0511	0.9323

chr8	146364022	14823664	0.1013	0.4739
chr9	141213431	3972618	0.0281	0.2489
chr10	135534747	6130726	0.0452	0.3292
chr11	135006516	5169539	0.0383	0.2468
chr12	133851895	4040393	0.0302	0.1996
chr13	115169878	2679104	0.0233	0.1732
chr14	107349540	2538727	0.0236	0.1806
chr15	102531392	2234608	0.0218	0.1679
chr16	90354753	3177496	0.0352	0.2252
chr17	81195210	1991339	0.0245	0.1875
chr18	78077248	4068150	0.0521	0.3801
chr19	59128983	2065013	0.0349	0.3366
chr20	63025520	3123087	0.0496	0.2585
chr21	48129895	1959018	0.0407	0.2378
chr22	51304566	1226825	0.0239	0.1732
chrMT	16571	168780	10.1853	5.6566
chrX	155270560	8628117	0.0556	0.2891
chrY	59373566	290082	0.0049	0.103

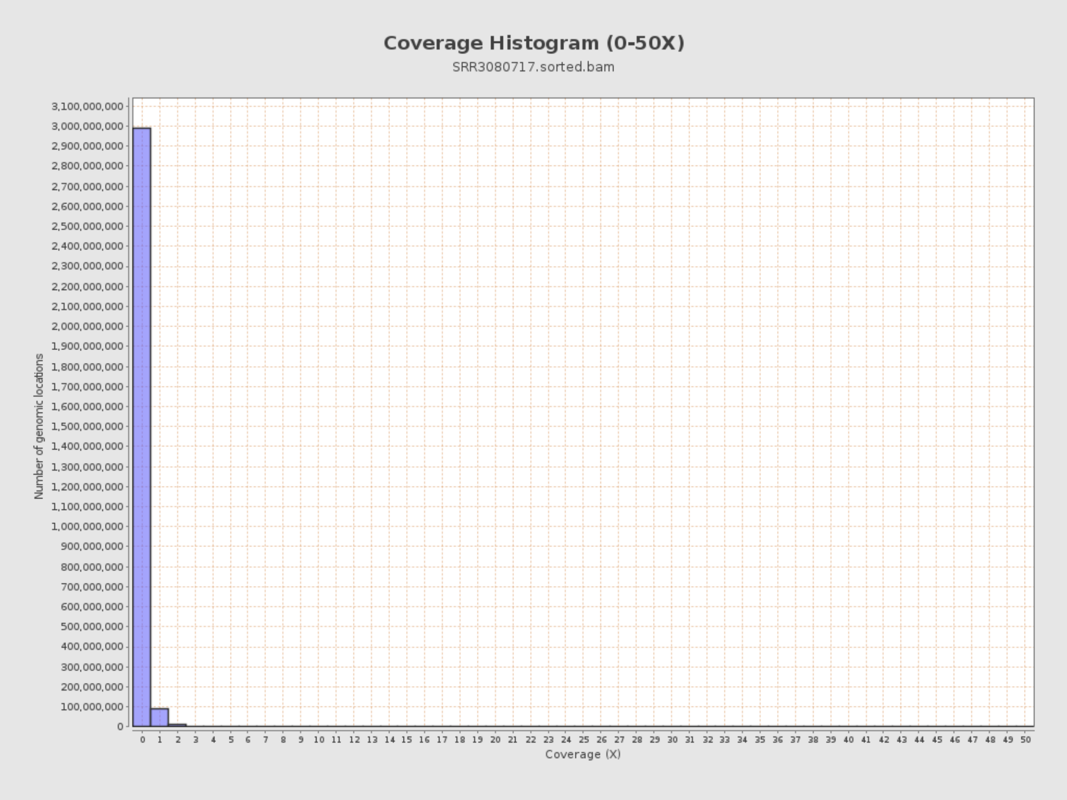
3. Results : Coverage across reference



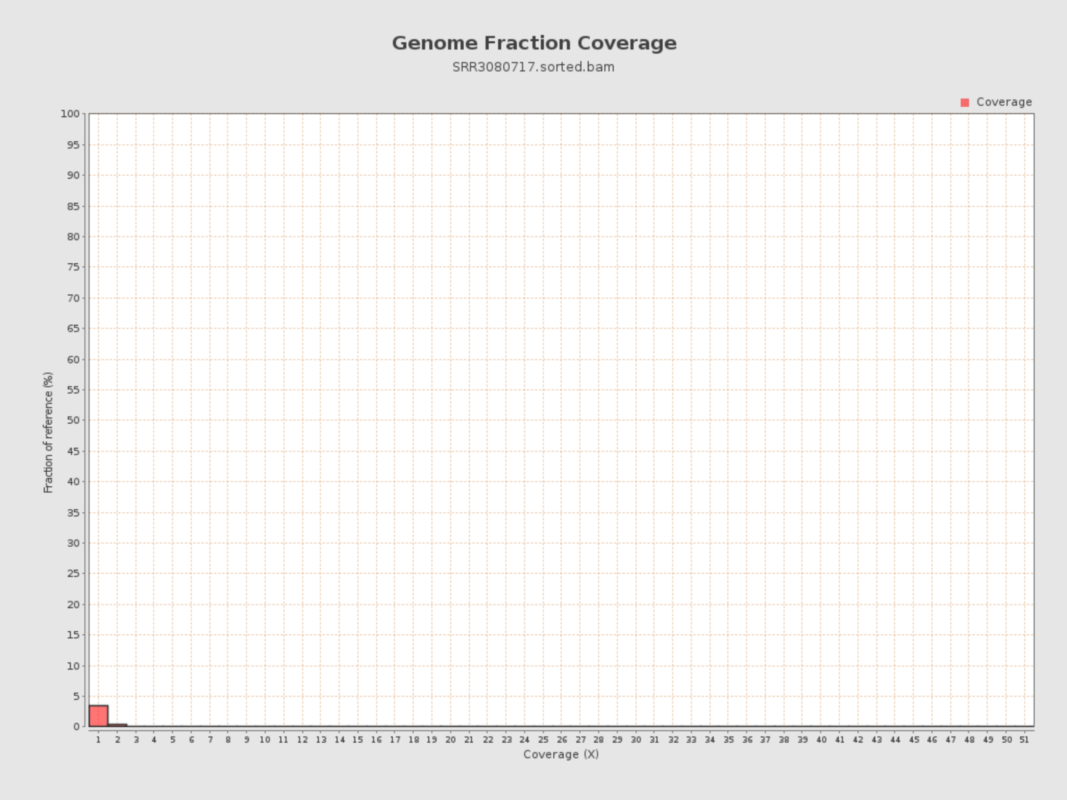
4. Results : Coverage Histogram



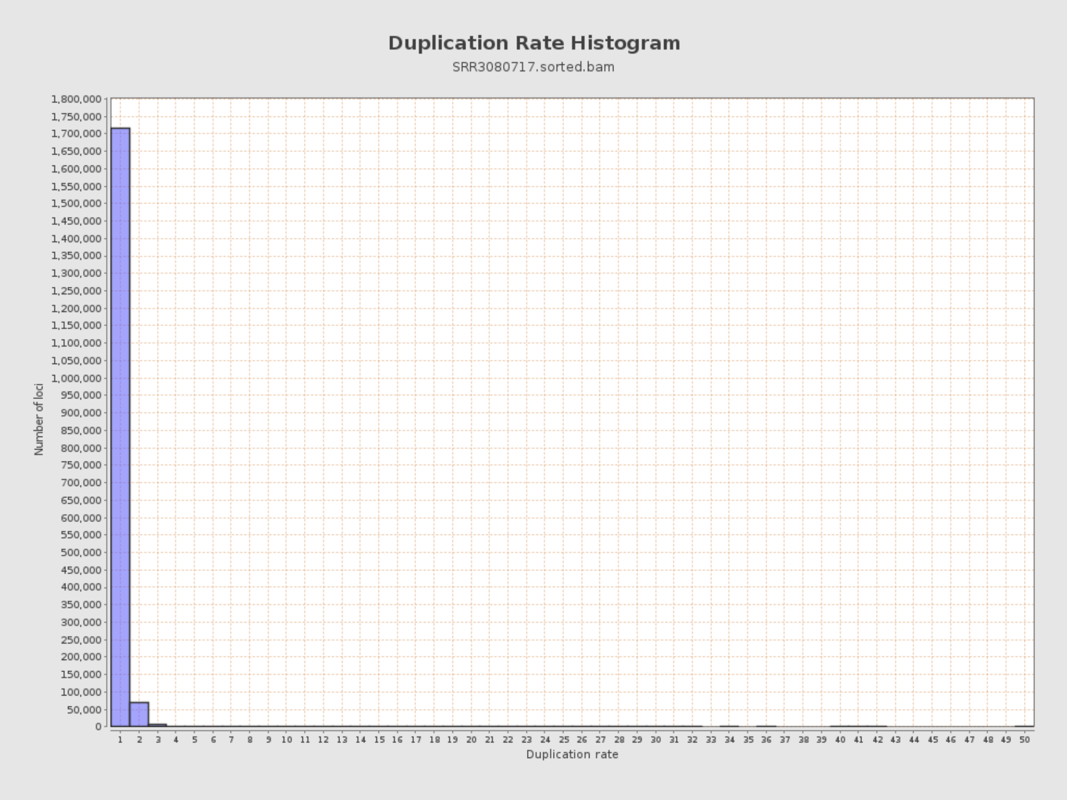
5. Results : Coverage Histogram (0-50X)



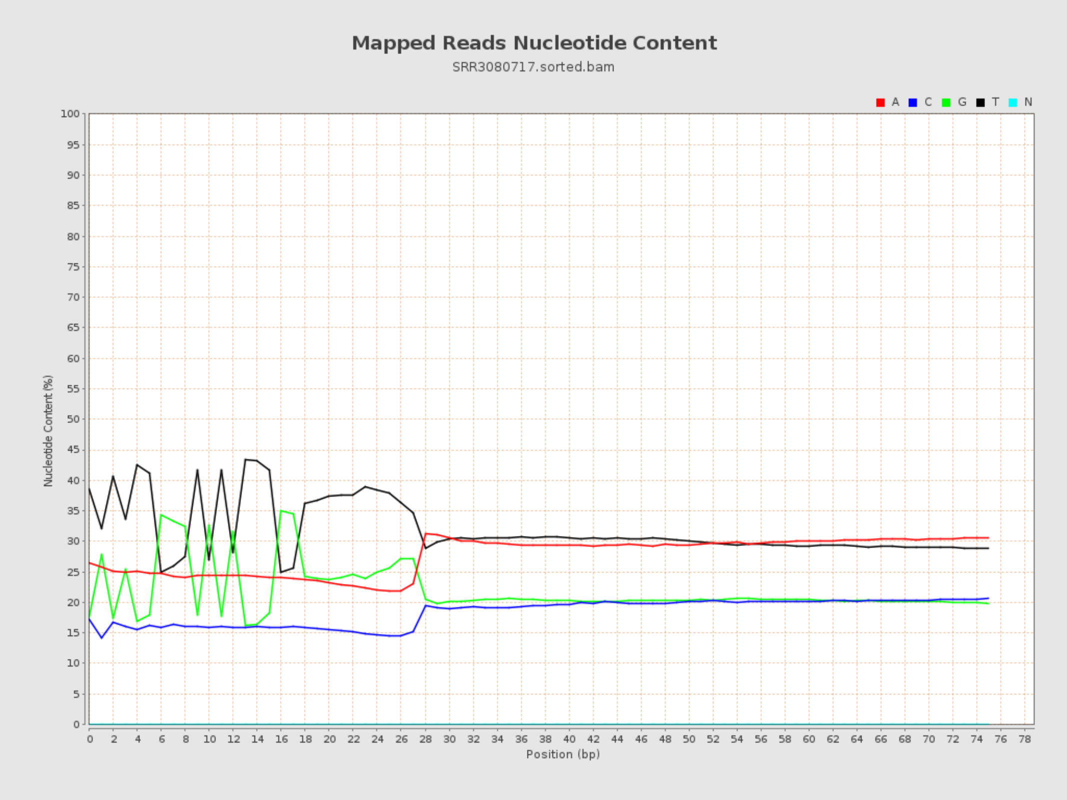
6. Results : Genome Fraction Coverage



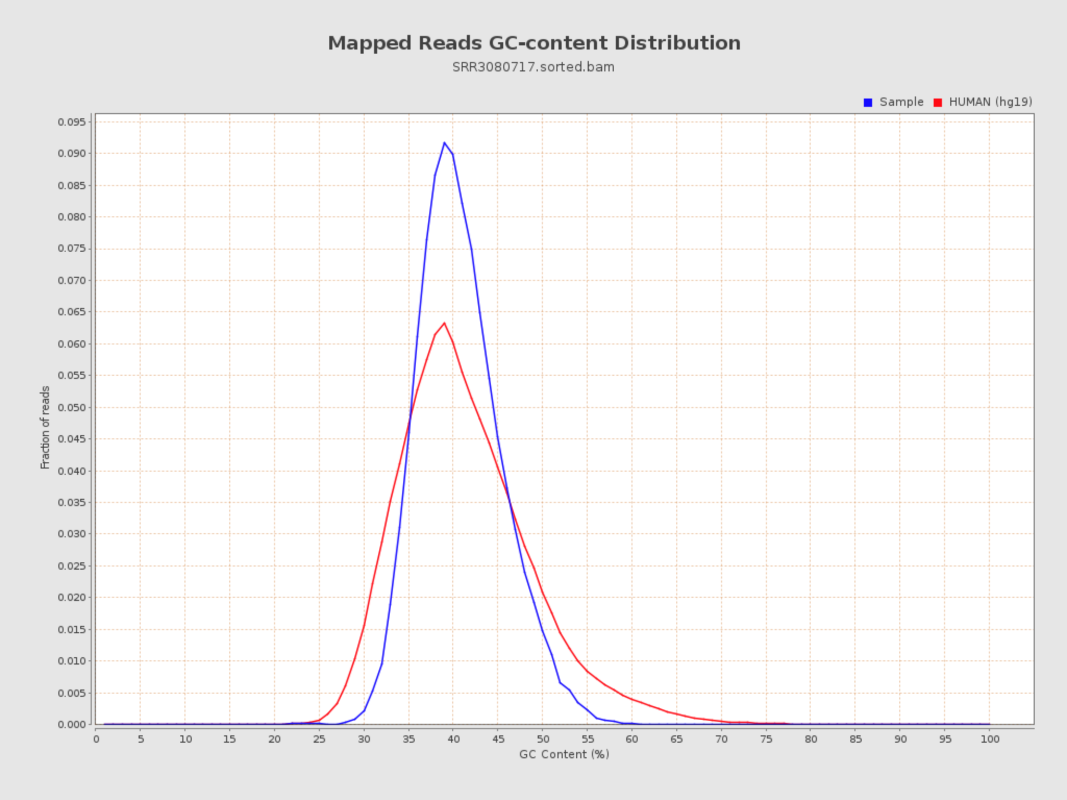
7. Results : Duplication Rate Histogram



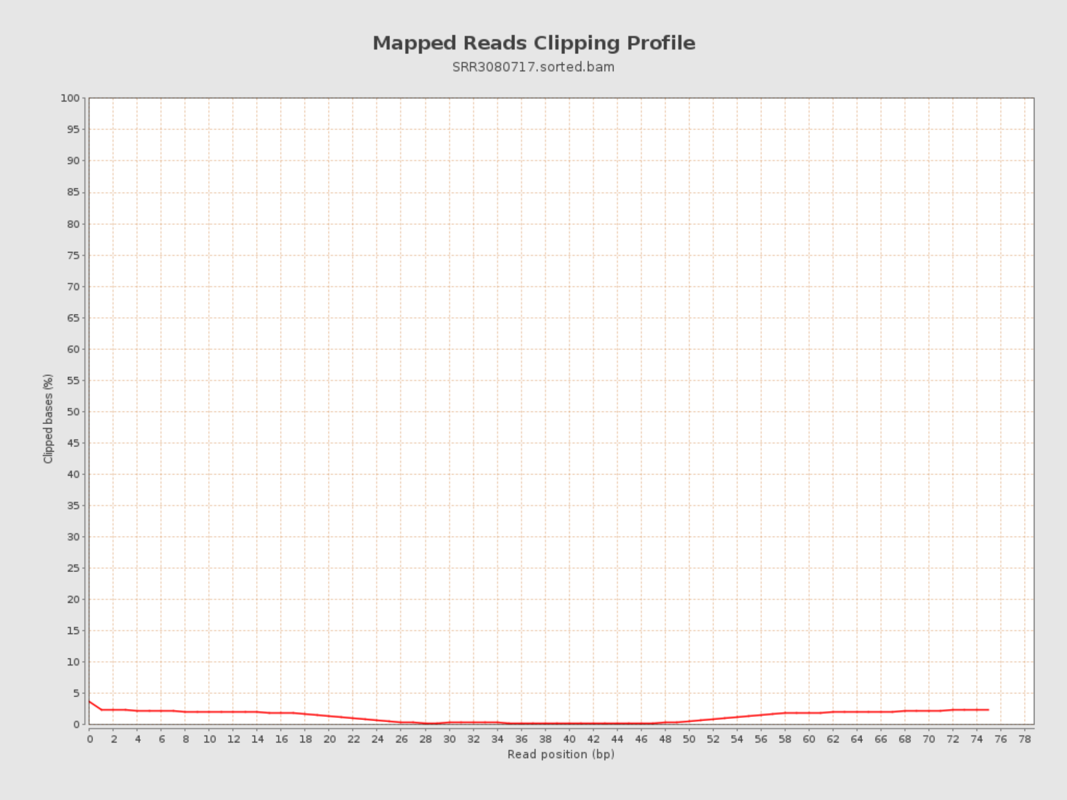
8. Results : Mapped Reads Nucleotide Content



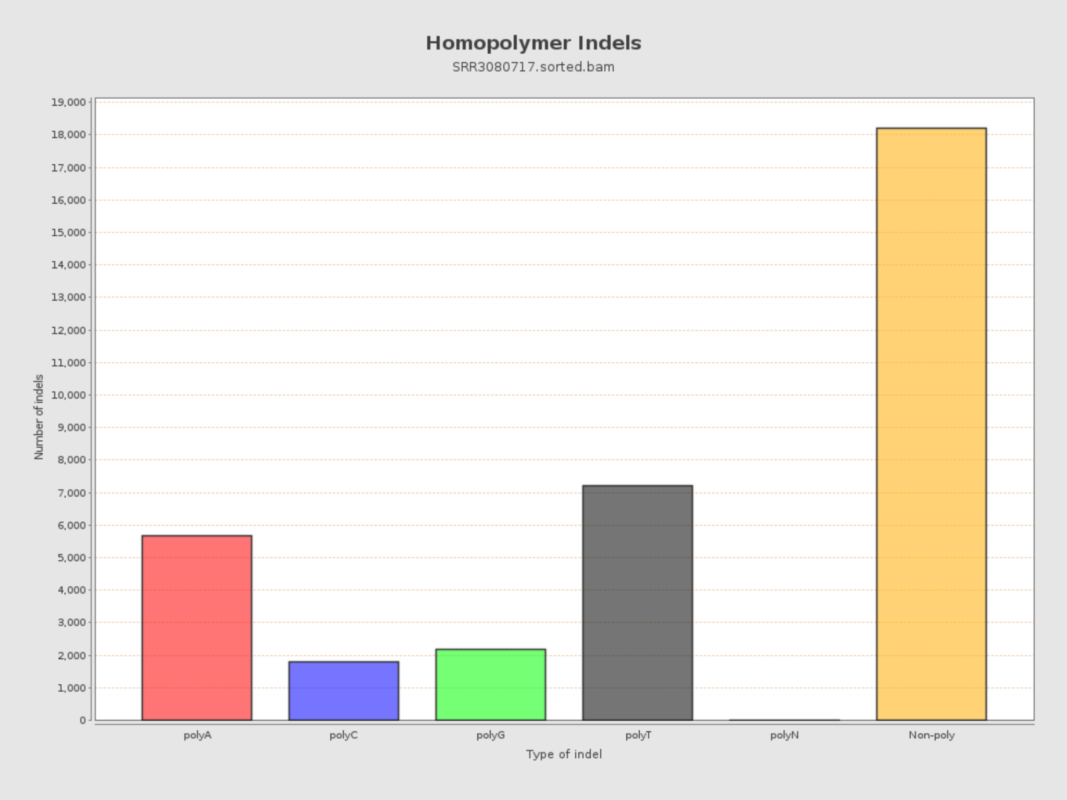
9. Results : Mapped Reads GC-content Distribution



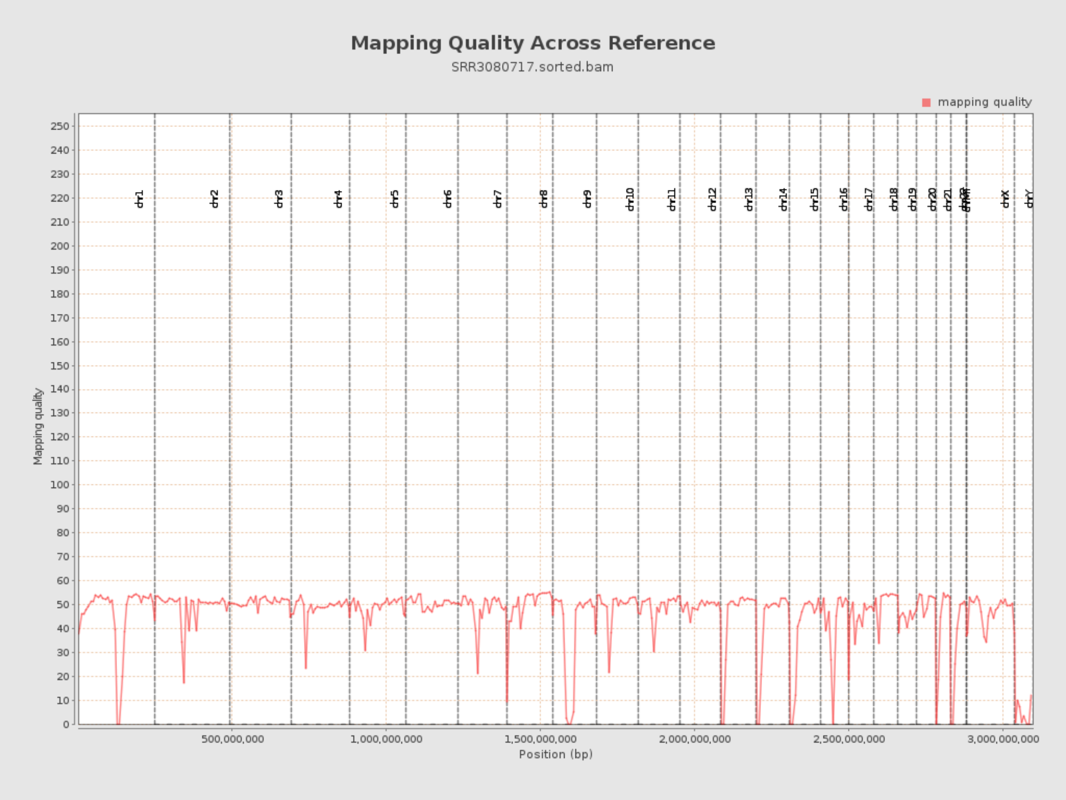
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram