Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 23:21:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080721.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_SRR3080721 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080721.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 23:21:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080721.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,764,217
Mapped reads	2,566,964 / 92.86%
Unmapped reads	197,253 / 7.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,862 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	108,704 / 3.93%
Duplication rate	3.42%
Clipped reads	780,995 / 28.25%

2.2. ACGT Content

Number/percentage of A's	52,433,194 / 29.21%
Number/percentage of C's	33,169,161 / 18.48%
Number/percentage of T's	57,146,159 / 31.84%
Number/percentage of G's	36,741,018 / 20.47%
Number/percentage of N's	2,660 / 0%
GC Percentage	38.95%

2.3. Coverage

Mean	0.058

Standard Deviation	0.4936

2.4. Mapping Quality

Mean Mapping Quality	47.01

2.5. Mismatches and indels

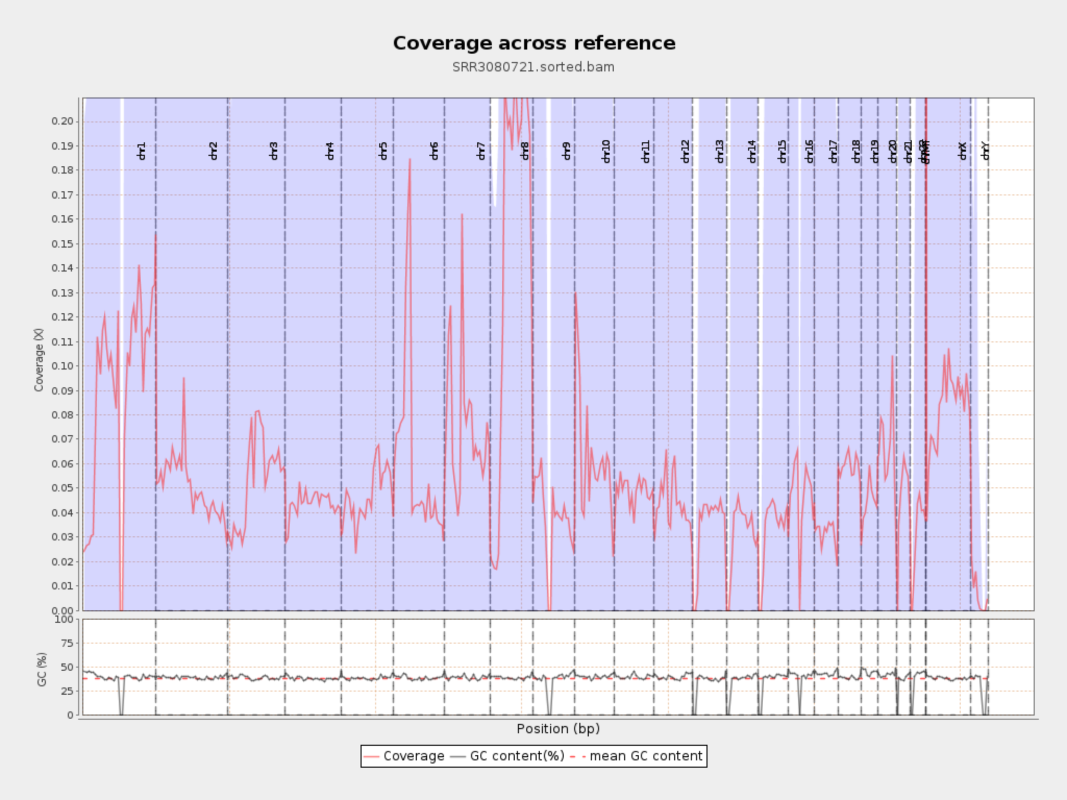
General error rate	0.81%
Mismatches	1,437,399
Insertions	13,476
Mapped reads with at least one insertion	0.52%
Deletions	38,801
Mapped reads with at least one deletion	1.5%
Homopolymer indels	48.45%

2.6. Chromosome stats

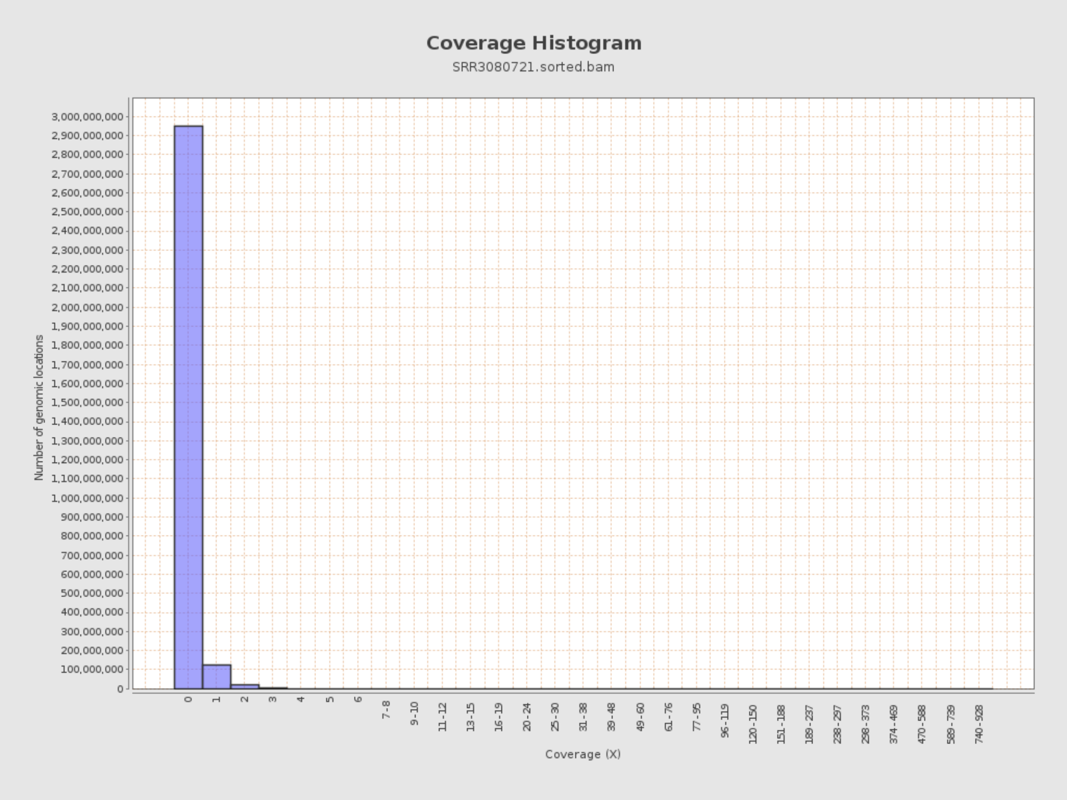
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22368883	0.0897	0.7717
chr2	243199373	12391157	0.051	0.4271
chr3	198022430	10638957	0.0537	0.2719
chr4	191154276	8360936	0.0437	0.2493
chr5	180915260	8434639	0.0466	0.2474
chr6	171115067	10901147	0.0637	0.4182
chr7	159138663	11996272	0.0754	1.2855

chr8	146364022	22008949	0.1504	0.7325
chr9	141213431	5382017	0.0381	0.3183
chr10	135534747	8705029	0.0642	0.449
chr11	135006516	6578106	0.0487	0.2886
chr12	133851895	5871279	0.0439	0.2404
chr13	115169878	3929135	0.0341	0.2101
chr14	107349540	3394154	0.0316	0.2124
chr15	102531392	3286099	0.032	0.2044
chr16	90354753	4132897	0.0457	0.2736
chr17	81195210	2597003	0.032	0.212
chr18	78077248	4639800	0.0594	0.5144
chr19	59128983	2695210	0.0456	0.457
chr20	63025520	4287820	0.068	0.3034
chr21	48129895	2192496	0.0456	0.253
chr22	51304566	1551110	0.0302	0.1967
chrMT	16571	16352	0.9868	1.1292
chrX	155270560	12818741	0.0826	0.3579
chrY	59373566	383661	0.0065	0.1273

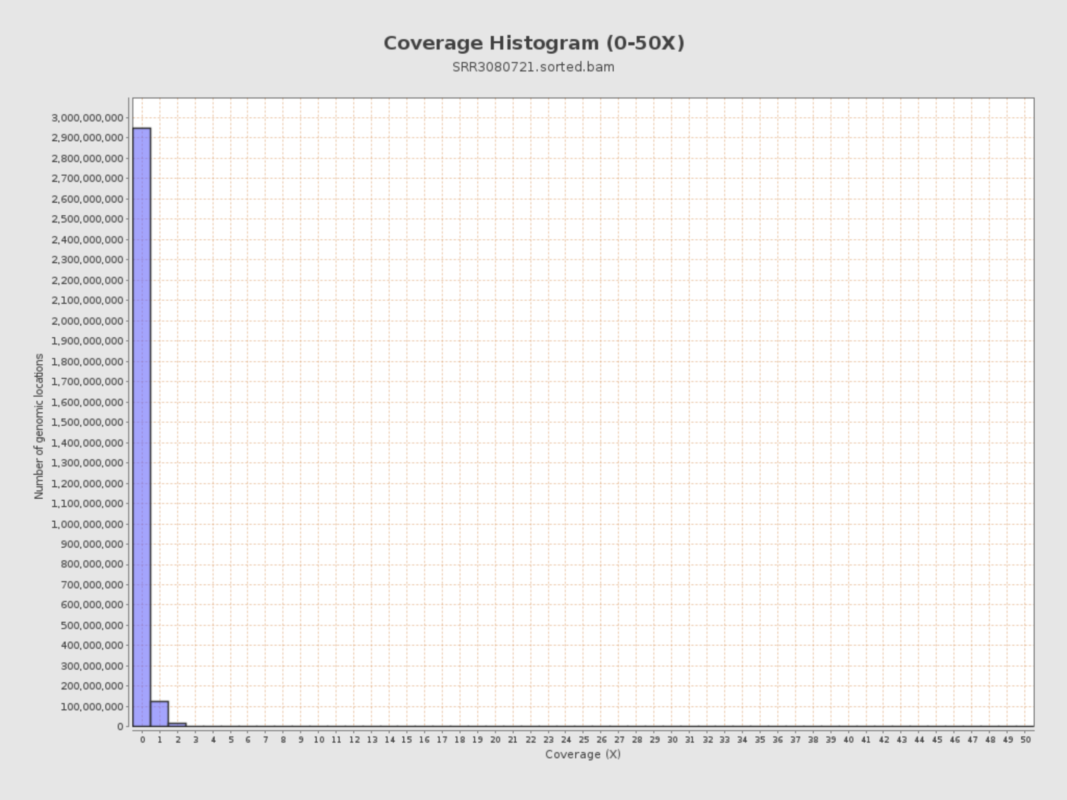
3. Results : Coverage across reference



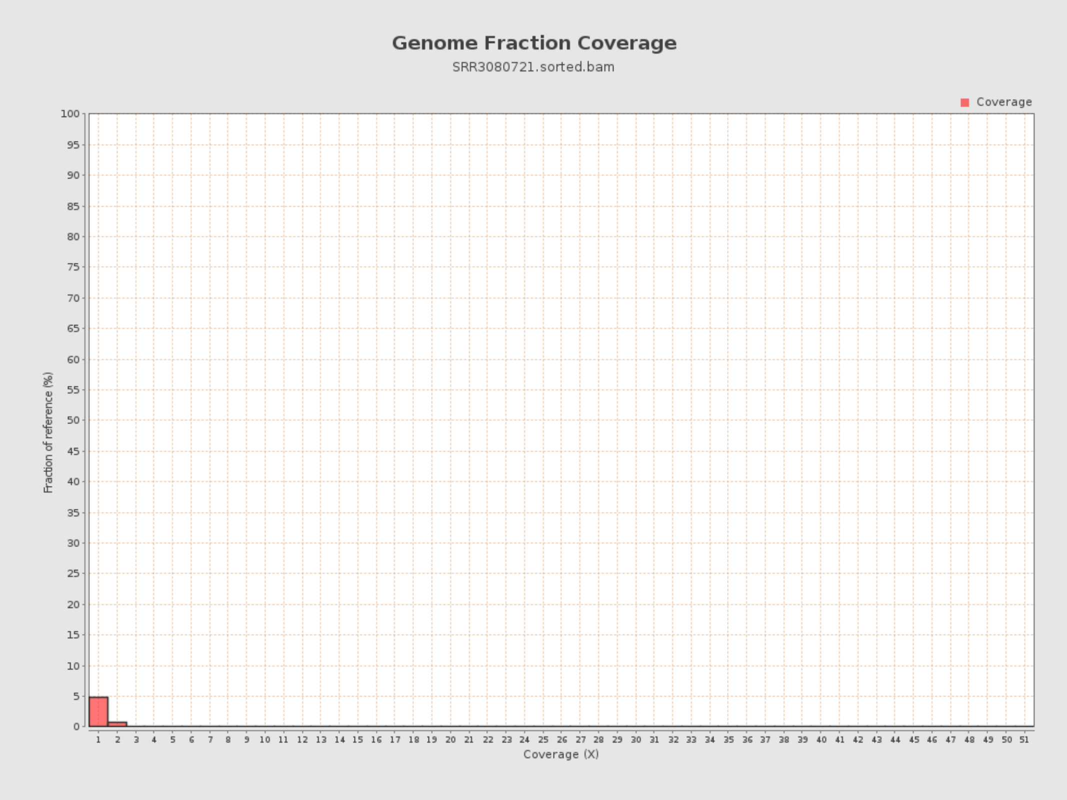
4. Results : Coverage Histogram



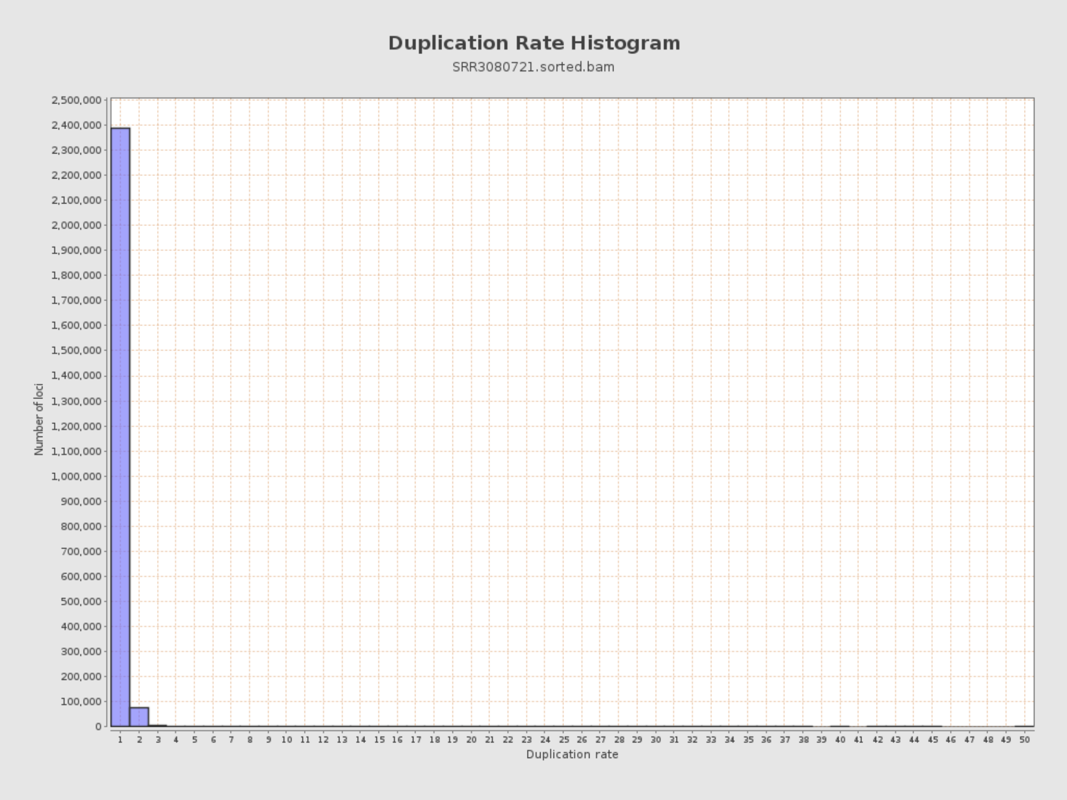
5. Results : Coverage Histogram (0-50X)



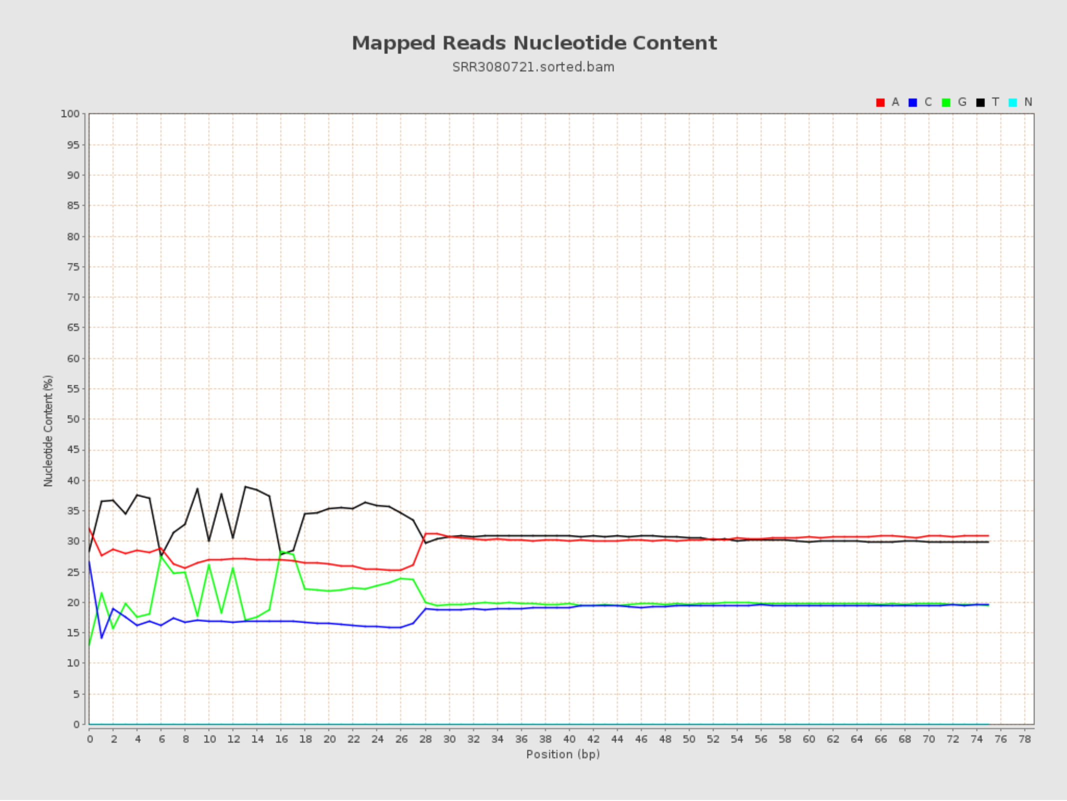
6. Results : Genome Fraction Coverage



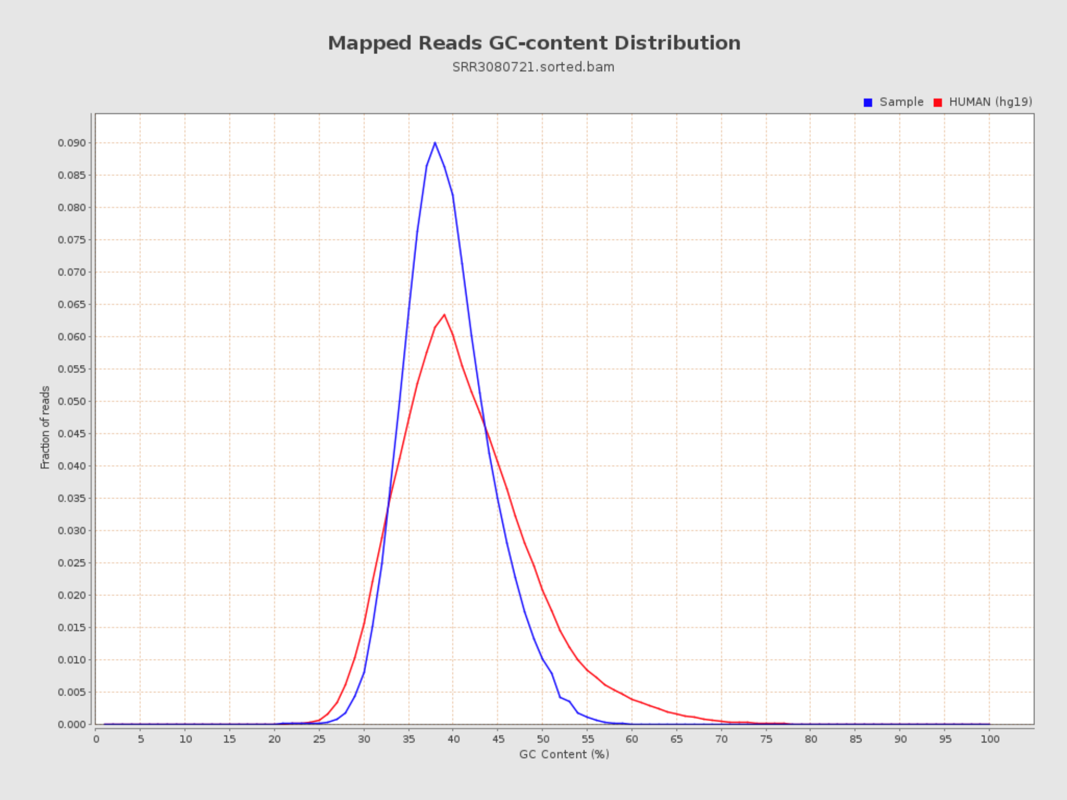
7. Results : Duplication Rate Histogram



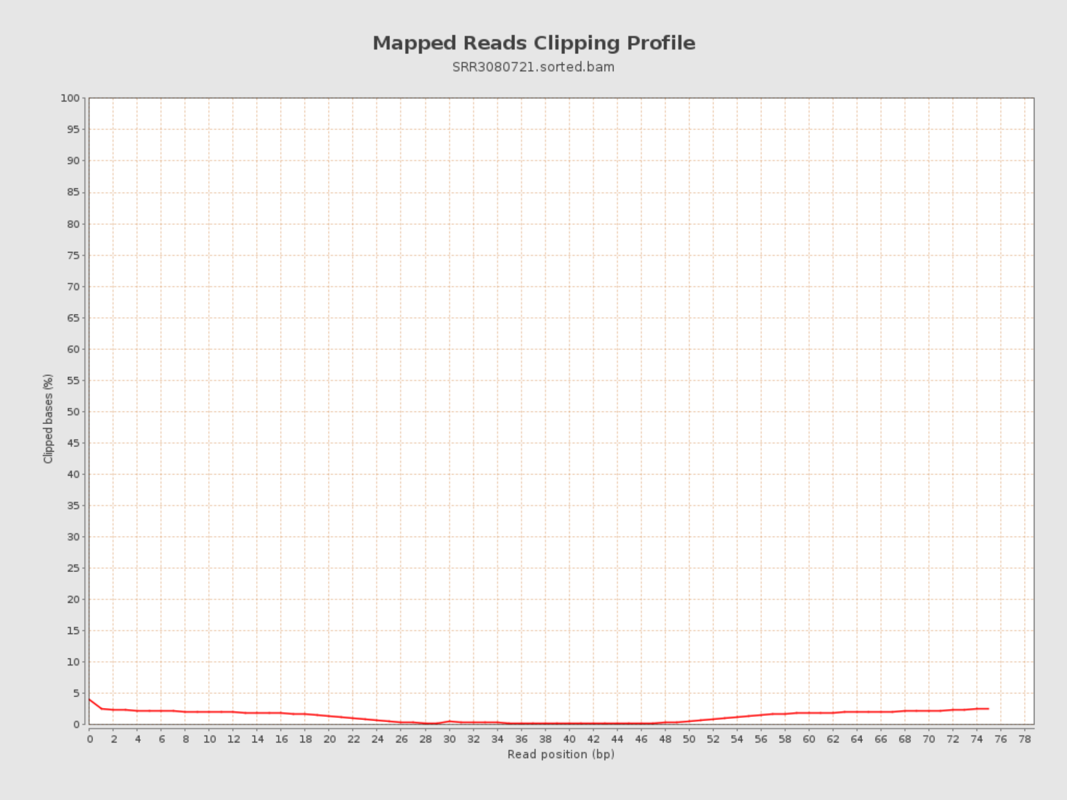
8. Results : Mapped Reads Nucleotide Content



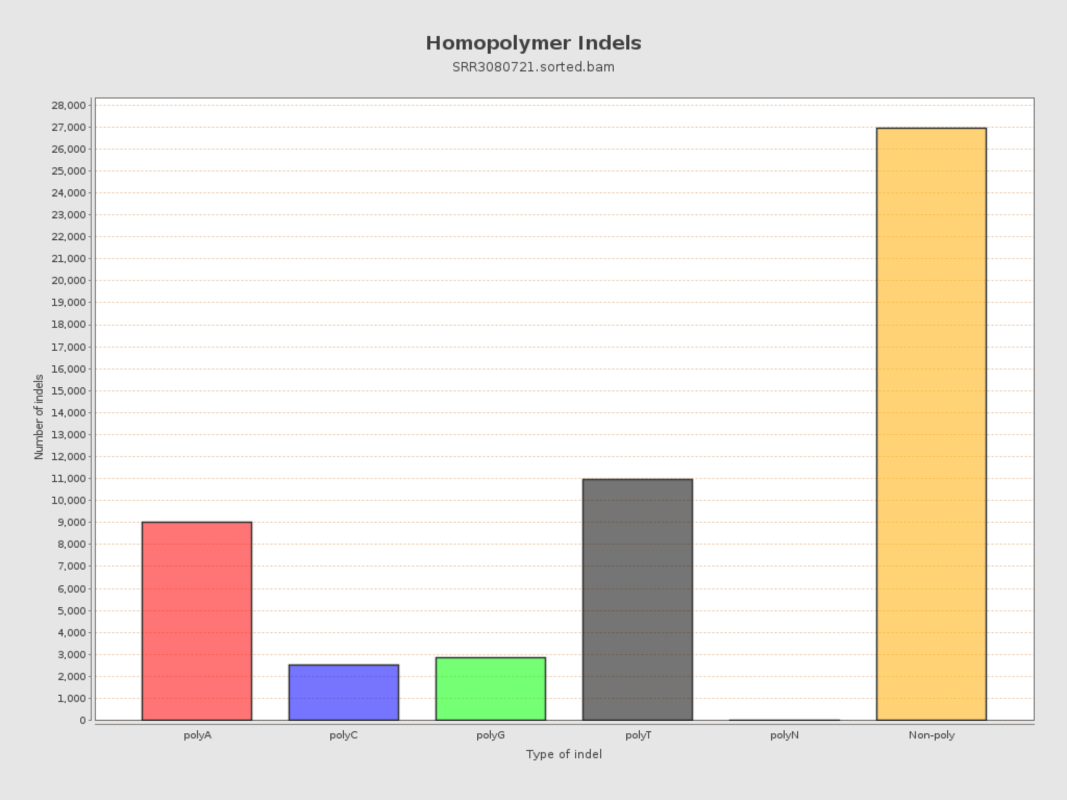
9. Results : Mapped Reads GC-content Distribution



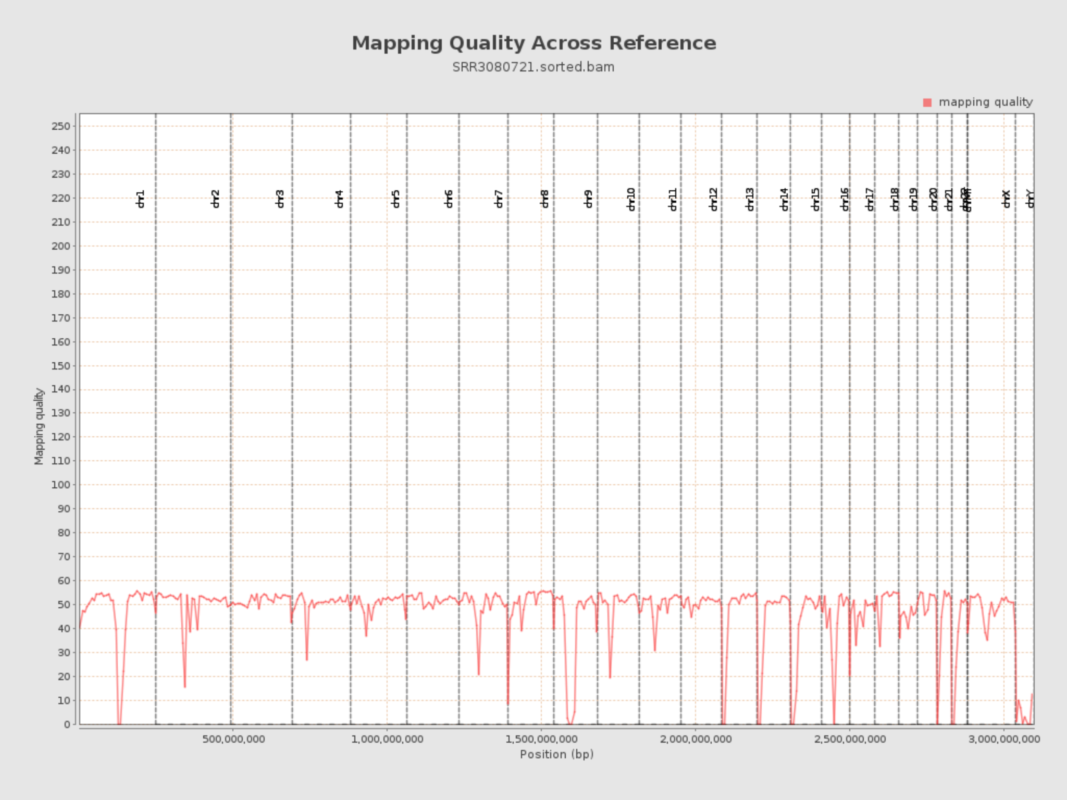
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram