Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:22:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080970.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_SRR3080970 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080970.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:22:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080970.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,840,001
Mapped reads	6,089,285 / 89.02%
Unmapped reads	750,716 / 10.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	70,676 / 1.03%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	465,397 / 6.8%
Duplication rate	5.89%
Clipped reads	2,591,889 / 37.89%

2.2. ACGT Content

Number/percentage of A's	116,468,273 / 28.31%
Number/percentage of C's	73,744,662 / 17.92%
Number/percentage of T's	132,457,695 / 32.19%
Number/percentage of G's	87,962,618 / 21.38%
Number/percentage of N's	824,560 / 0.2%
GC Percentage	39.3%

2.3. Coverage

Mean	0.133

Standard Deviation	0.9208

2.4. Mapping Quality

Mean Mapping Quality	46.84

2.5. Mismatches and indels

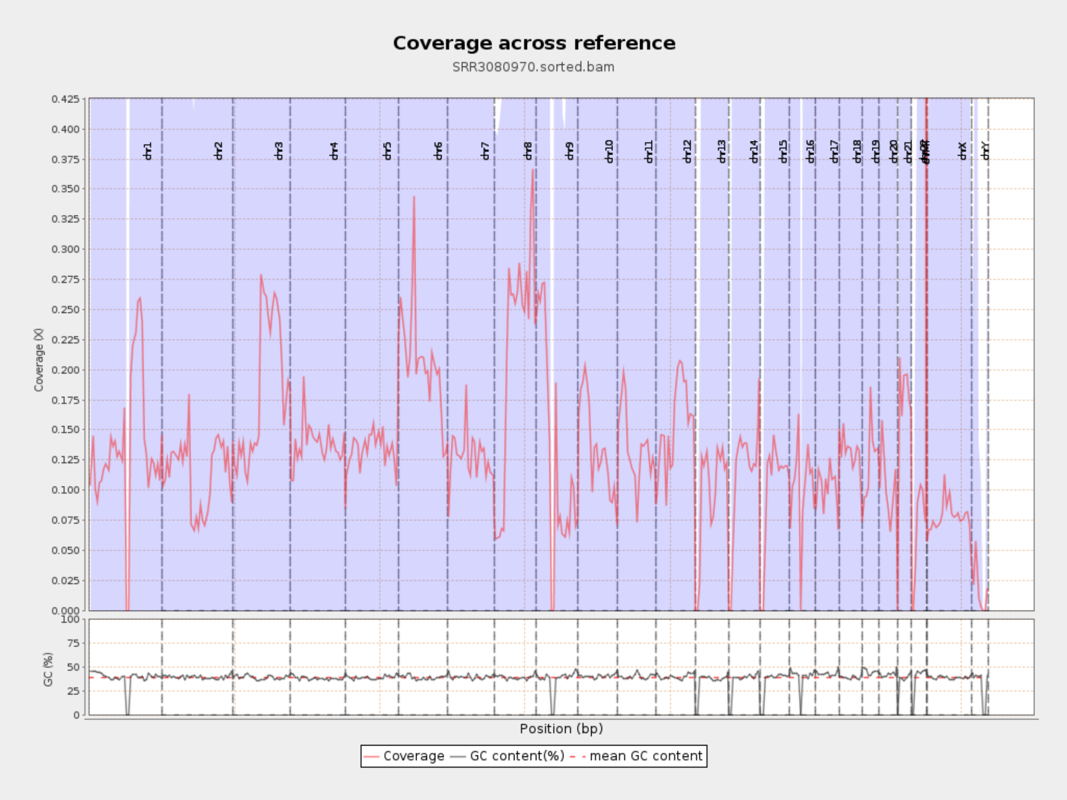
General error rate	1.02%
Mismatches	4,155,123
Insertions	33,186
Mapped reads with at least one insertion	0.54%
Deletions	92,527
Mapped reads with at least one deletion	1.5%
Homopolymer indels	48.74%

2.6. Chromosome stats

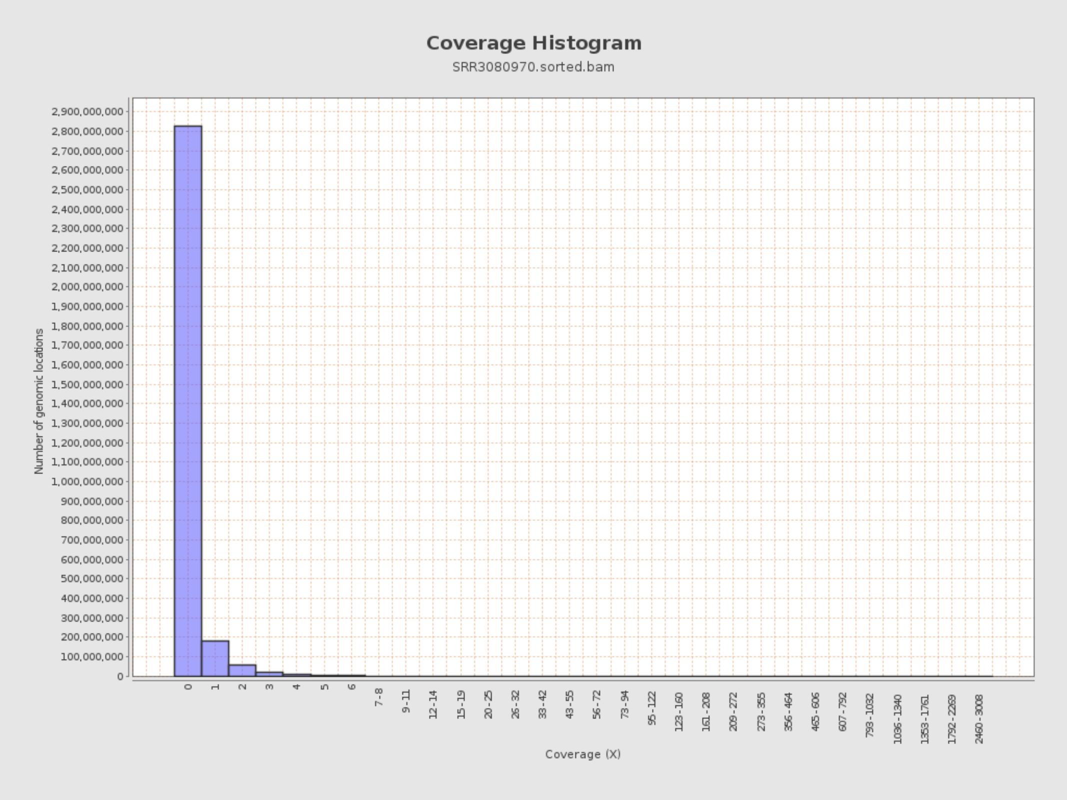
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	33945752	0.1362	1.3195
chr2	243199373	27795100	0.1143	0.8544
chr3	198022430	36156403	0.1826	0.6078
chr4	191154276	26390225	0.1381	0.5831
chr5	180915260	24271659	0.1342	0.518
chr6	171115067	35604367	0.2081	1.0316
chr7	159138663	20476805	0.1287	1.0801

chr8	146364022	31606725	0.2159	1.9655
chr9	141213431	18206671	0.1289	0.9916
chr10	135534747	18697549	0.138	0.7512
chr11	135006516	18073995	0.1339	0.7664
chr12	133851895	20653197	0.1543	0.5841
chr13	115169878	10929129	0.0949	0.4342
chr14	107349540	11836643	0.1103	0.6435
chr15	102531392	10369167	0.1011	0.4489
chr16	90354753	9291311	0.1028	0.5904
chr17	81195210	8265773	0.1018	0.499
chr18	78077248	10276716	0.1316	1.7823
chr19	59128983	7320718	0.1238	1.0421
chr20	63025520	6621121	0.1051	0.5016
chr21	48129895	8084204	0.168	0.7212
chr22	51304566	3297986	0.0643	0.351
chrMT	16571	343787	20.7463	10.8649
chrX	155270560	12097267	0.0779	0.4743
chrY	59373566	998431	0.0168	0.332

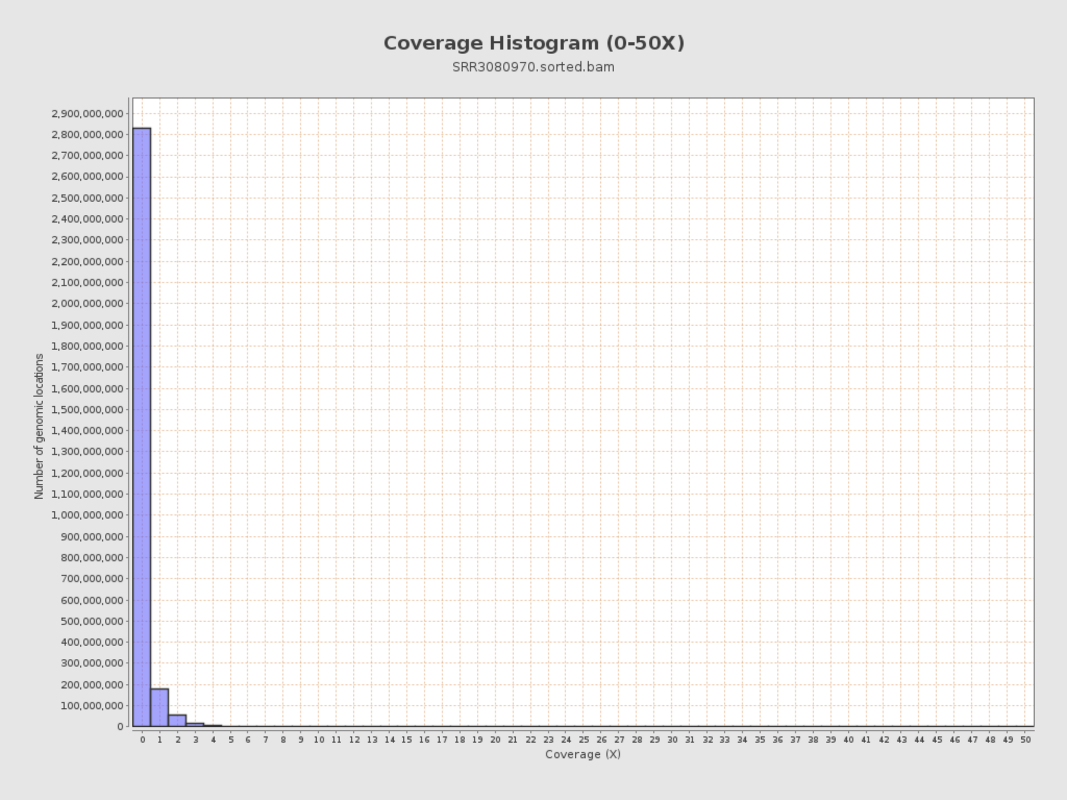
3. Results : Coverage across reference



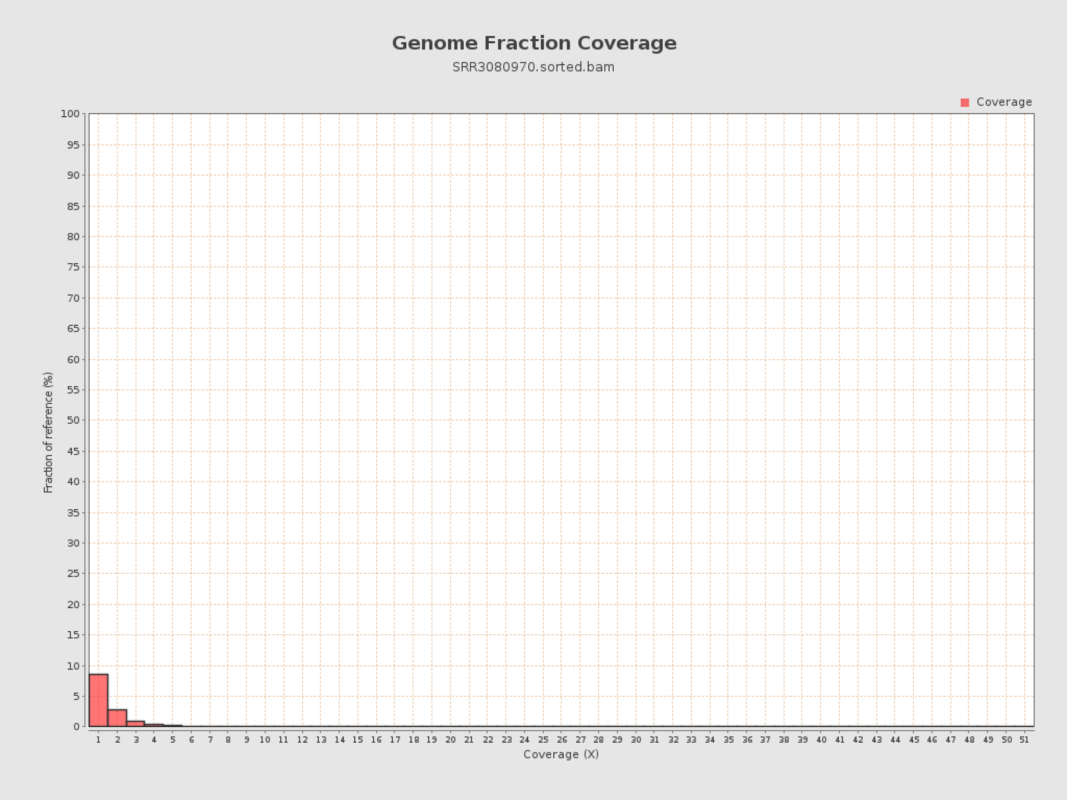
4. Results : Coverage Histogram



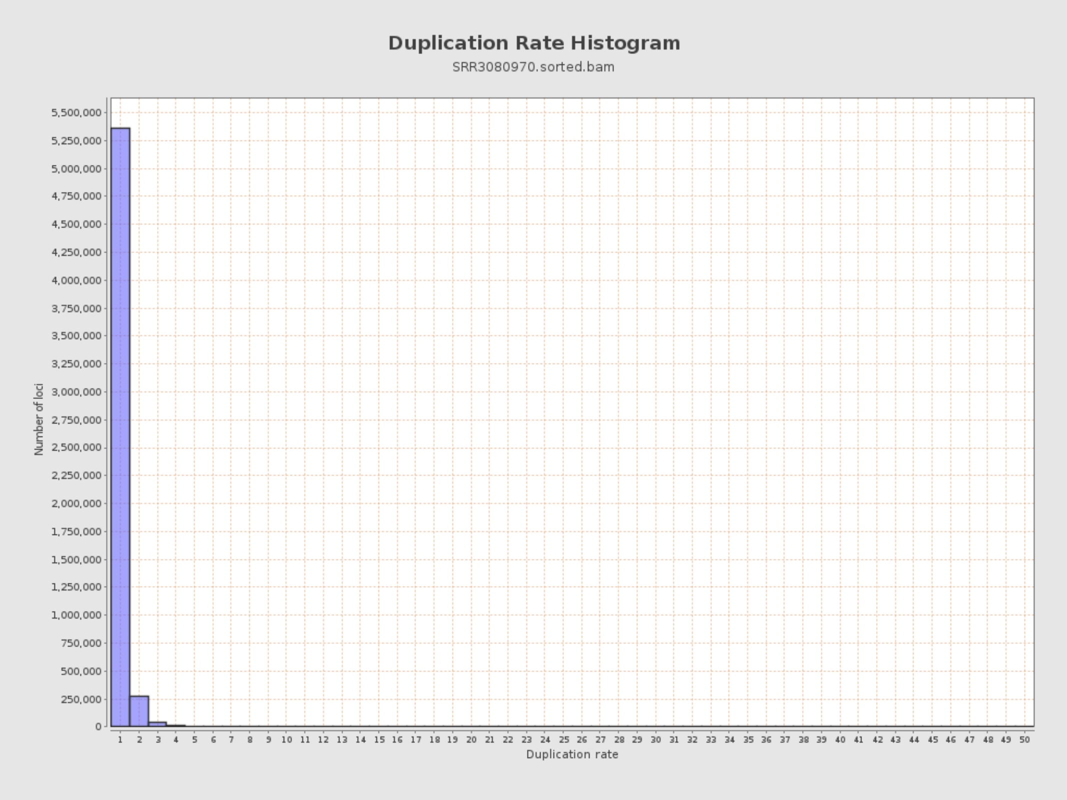
5. Results : Coverage Histogram (0-50X)



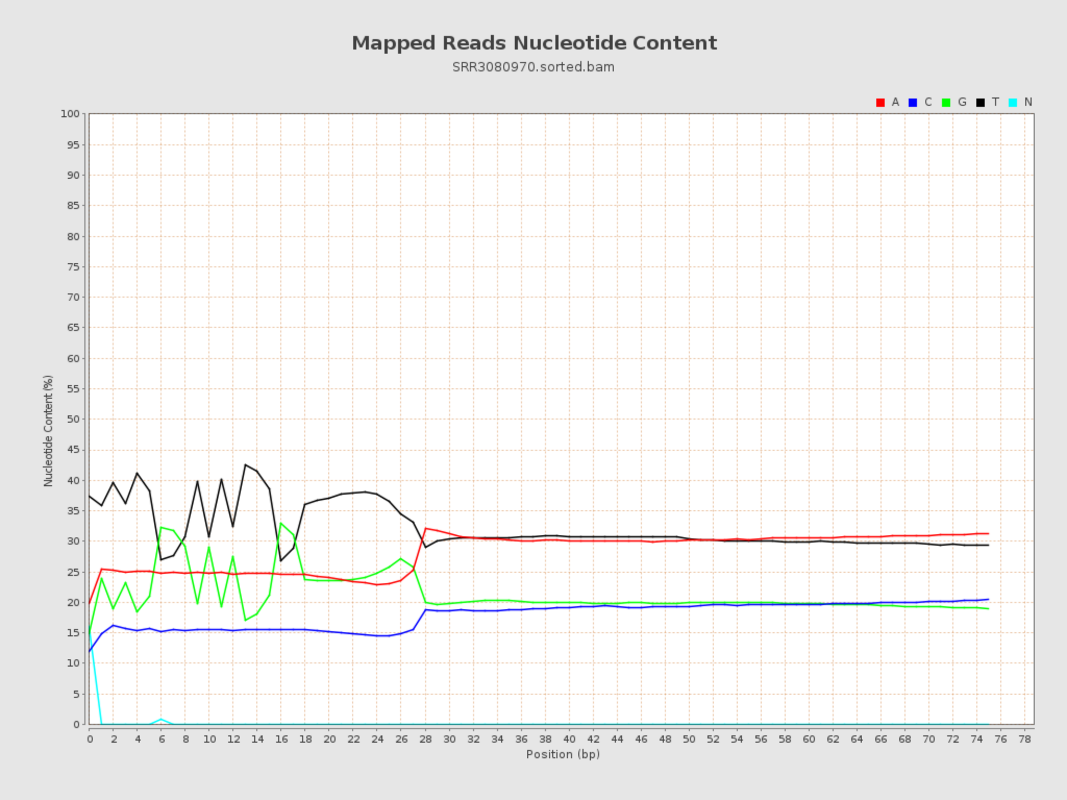
6. Results : Genome Fraction Coverage



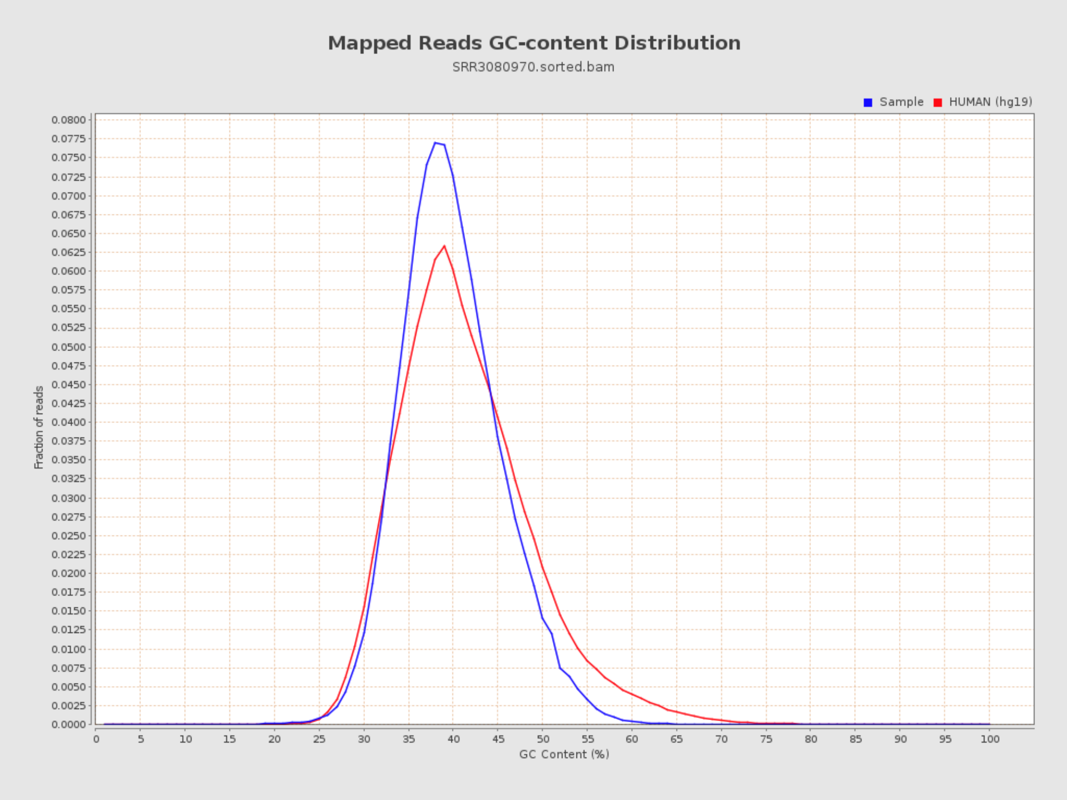
7. Results : Duplication Rate Histogram



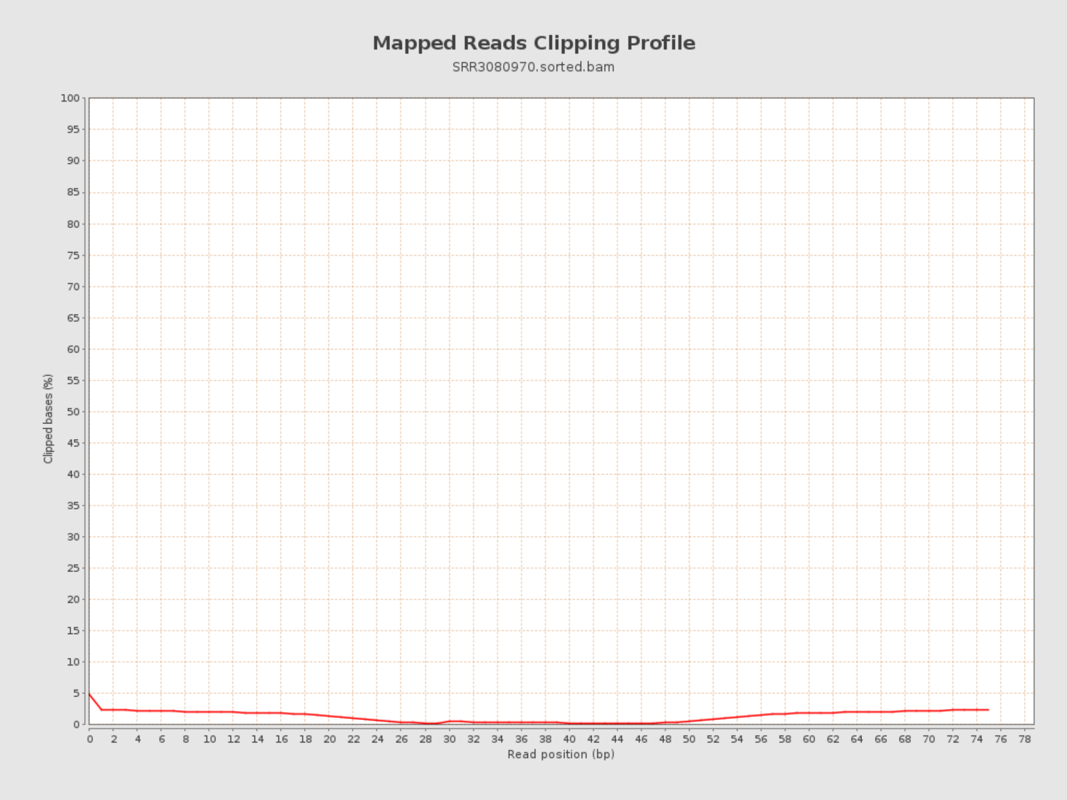
8. Results : Mapped Reads Nucleotide Content



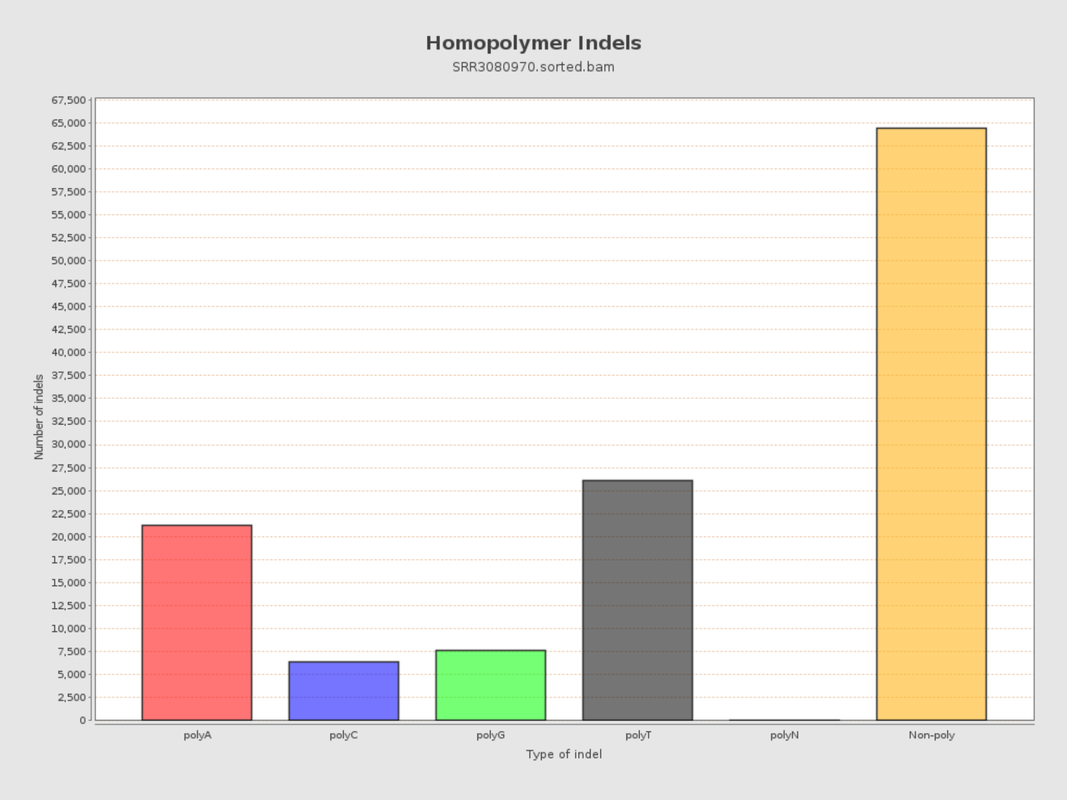
9. Results : Mapped Reads GC-content Distribution



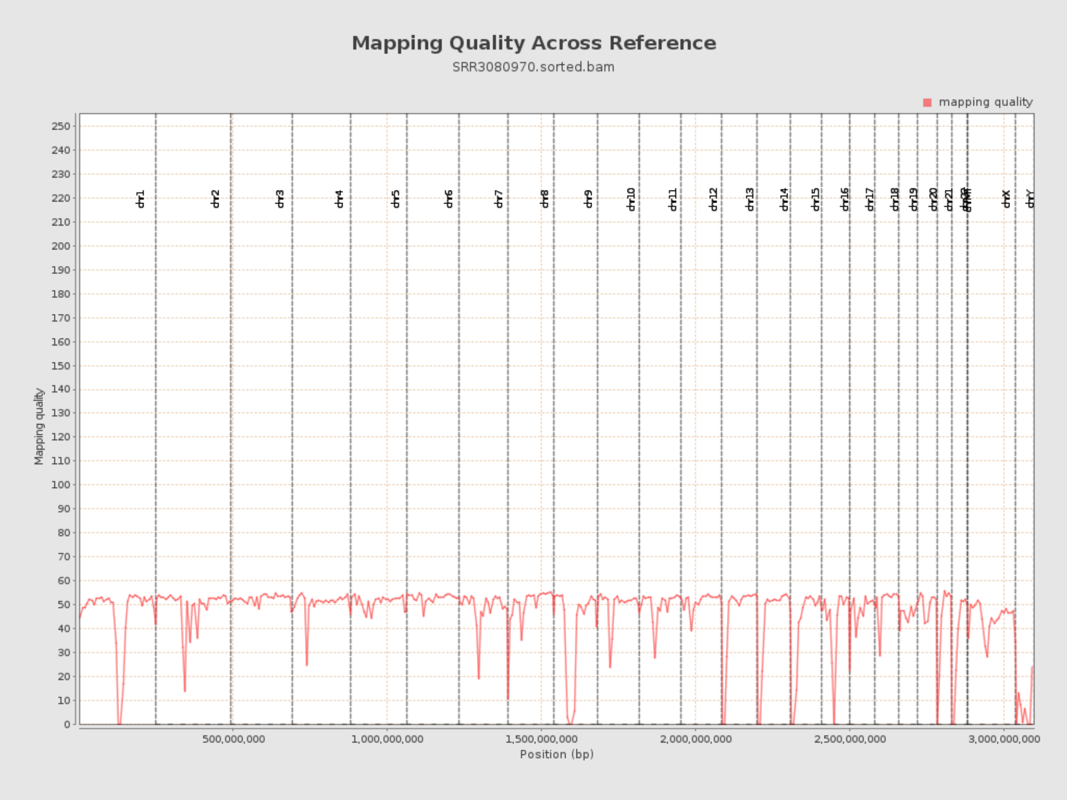
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram