Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 14:49:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971292.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_SRR2971292 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971292.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 14:49:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971292.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,430,343
Mapped reads	8,997,264 / 86.26%
Unmapped reads	1,433,079 / 13.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	590,790 / 5.66%
Duplication rate	5.45%
Clipped reads	645,392 / 6.19%

2.2. ACGT Content

Number/percentage of A's	102,684,201 / 28.85%
Number/percentage of C's	73,295,627 / 20.59%
Number/percentage of T's	104,470,733 / 29.35%
Number/percentage of G's	75,481,969 / 21.21%
Number/percentage of N's	5,803 / 0%
GC Percentage	41.8%

2.3. Coverage

Mean	0.115
Standard Deviation	0.8491

2.4. Mapping Quality

Mean Mapping Quality	42.79

2.5. Mismatches and indels

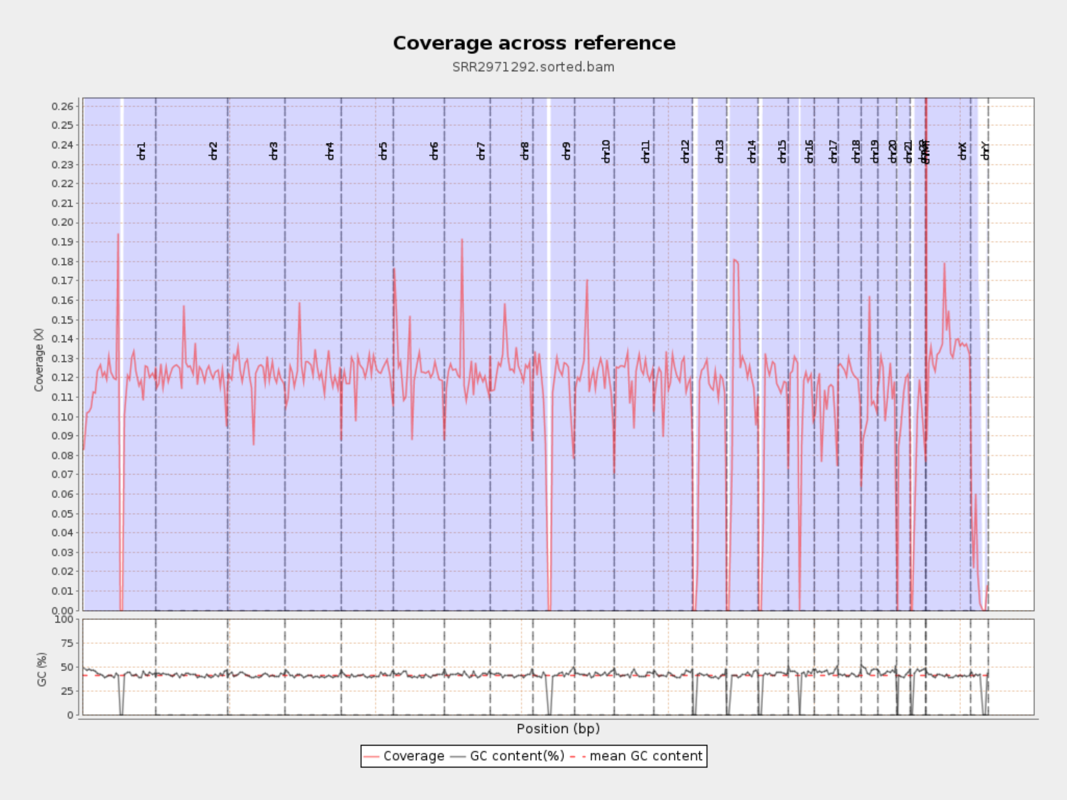
General error rate	0.25%
Mismatches	879,483
Insertions	9,147
Mapped reads with at least one insertion	0.1%
Deletions	24,183
Mapped reads with at least one deletion	0.27%
Homopolymer indels	41.88%

2.6. Chromosome stats

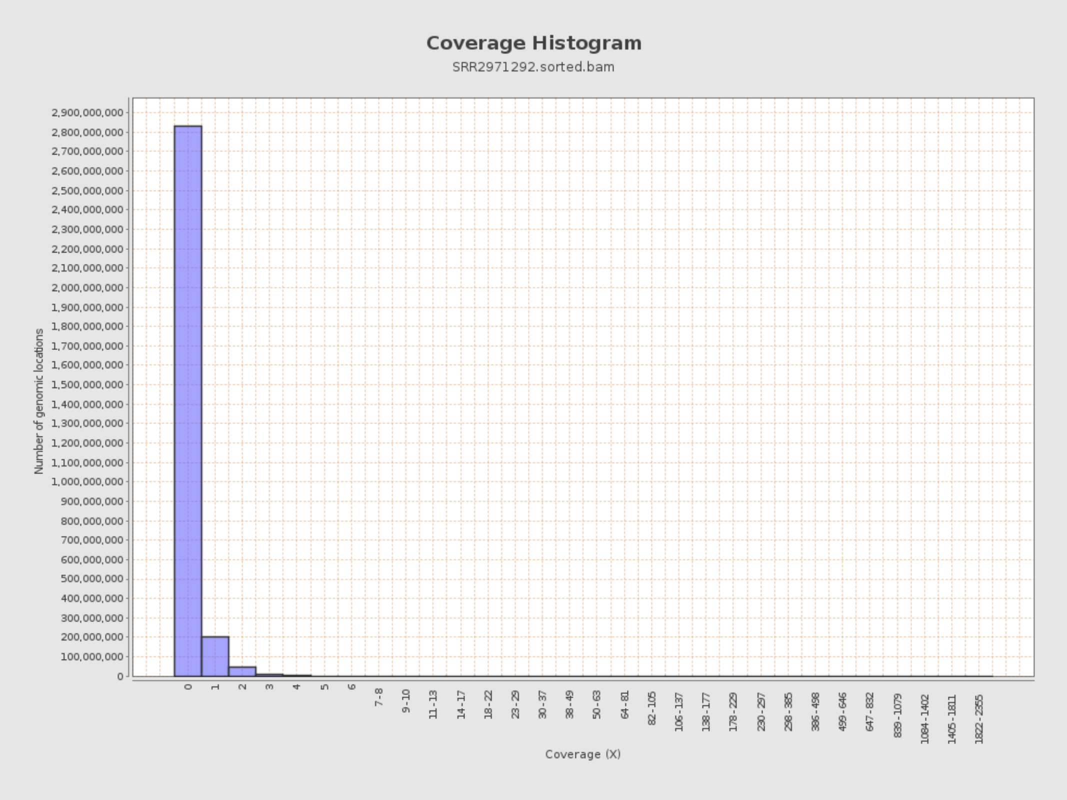
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28088560	0.1127	1.8209
chr2	243199373	29924080	0.123	0.6595
chr3	198022430	24136170	0.1219	0.45
chr4	191154276	23572787	0.1233	0.5055
chr5	180915260	22147820	0.1224	0.4566
chr6	171115067	21379686	0.1249	0.556
chr7	159138663	19424568	0.1221	1.0821
chr8	146364022	18241444	0.1246	1.2586

chr9	141213431	14748402	0.1044	0.6279
chr10	135534747	16640053	0.1228	0.7229
chr11	135006516	16337704	0.121	0.6824
chr12	133851895	15963871	0.1193	0.468
chr13	115169878	11370687	0.0987	0.3976
chr14	107349540	12276624	0.1144	0.504
chr15	102531392	10044975	0.098	0.4017
chr16	90354753	9441633	0.1045	0.4706
chr17	81195210	8624054	0.1062	0.4858
chr18	78077248	9569729	0.1226	1.4389
chr19	59128983	6294607	0.1065	1.5049
chr20	63025520	7205107	0.1143	0.4604
chr21	48129895	4573132	0.095	0.4765
chr22	51304566	3713294	0.0724	0.3385
chrMT	16571	56378	3.4022	3.8359
chrX	155270560	21031100	0.1354	0.5653
chrY	59373566	1164263	0.0196	0.3069

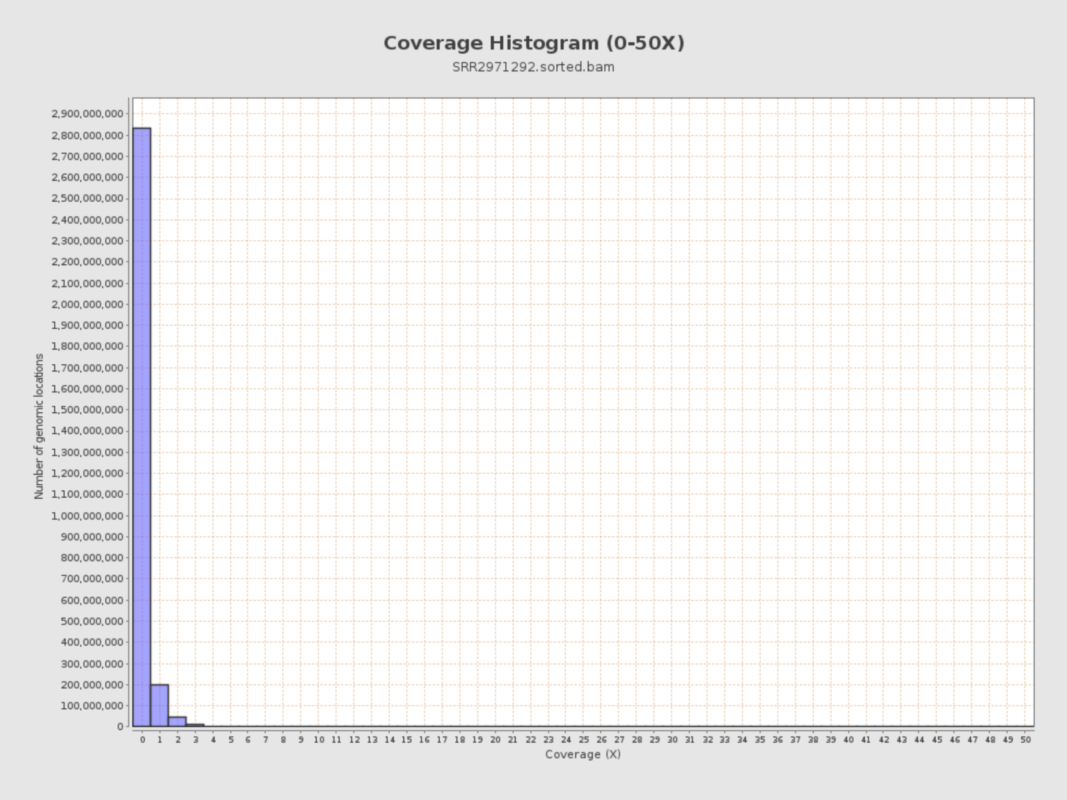
3. Results : Coverage across reference



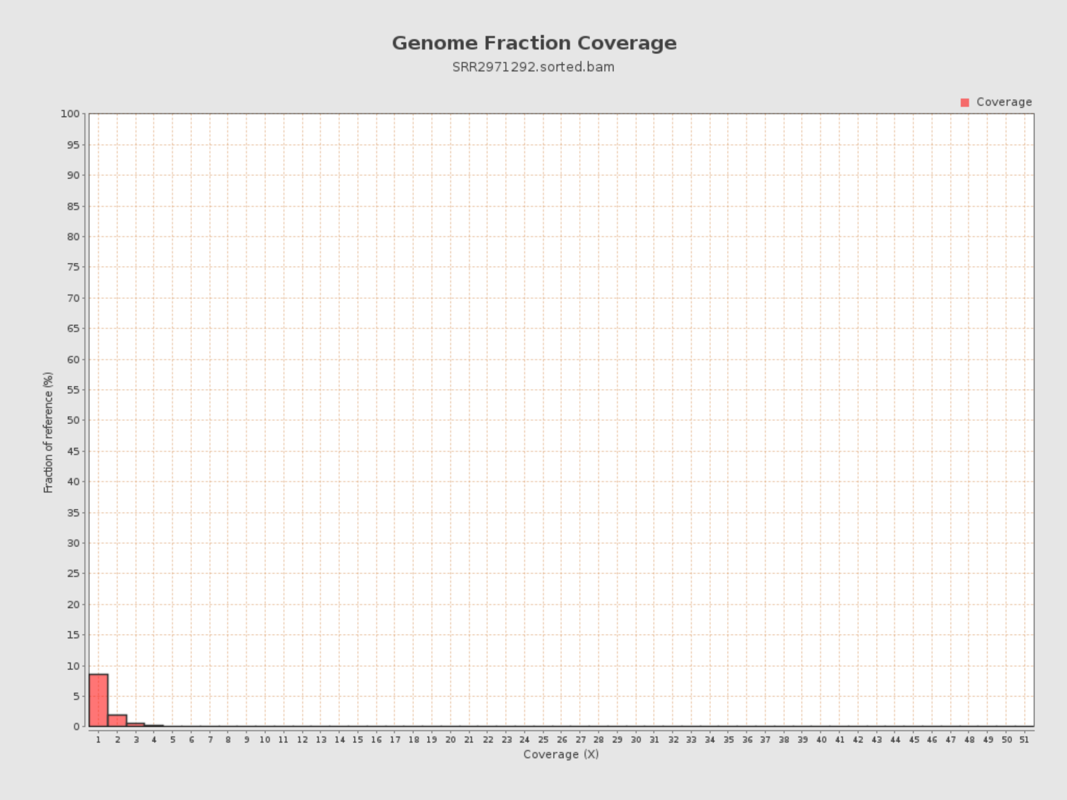
4. Results : Coverage Histogram



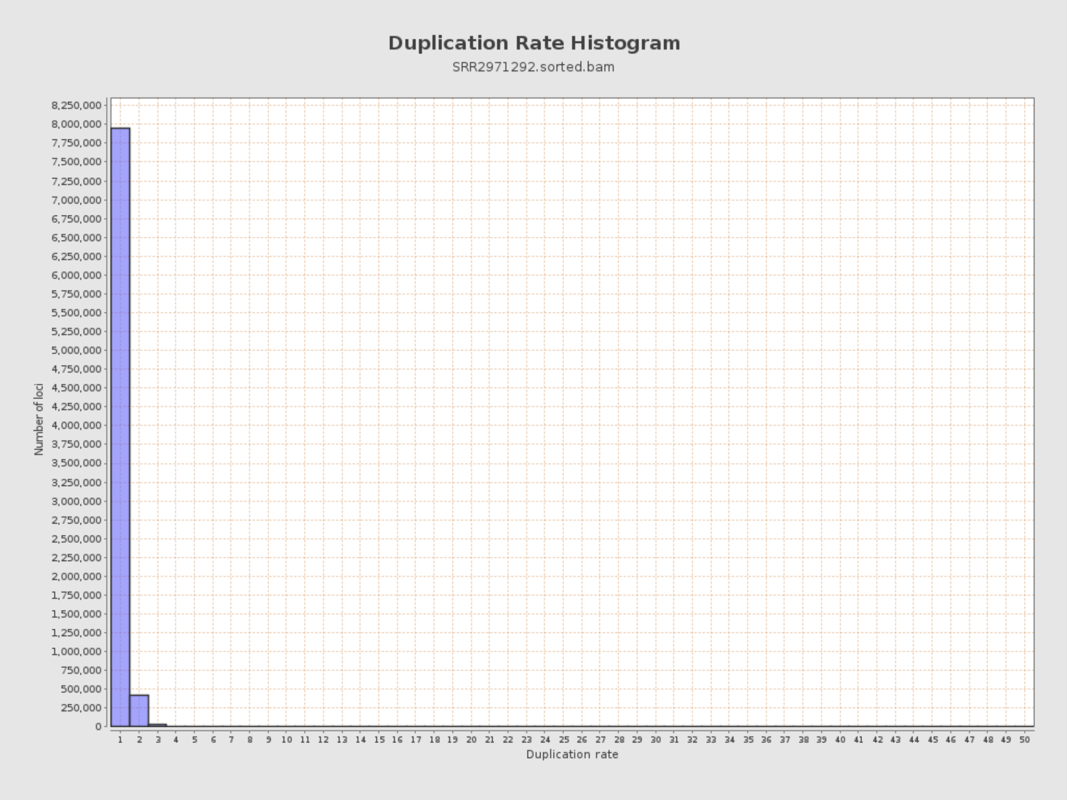
5. Results : Coverage Histogram (0-50X)



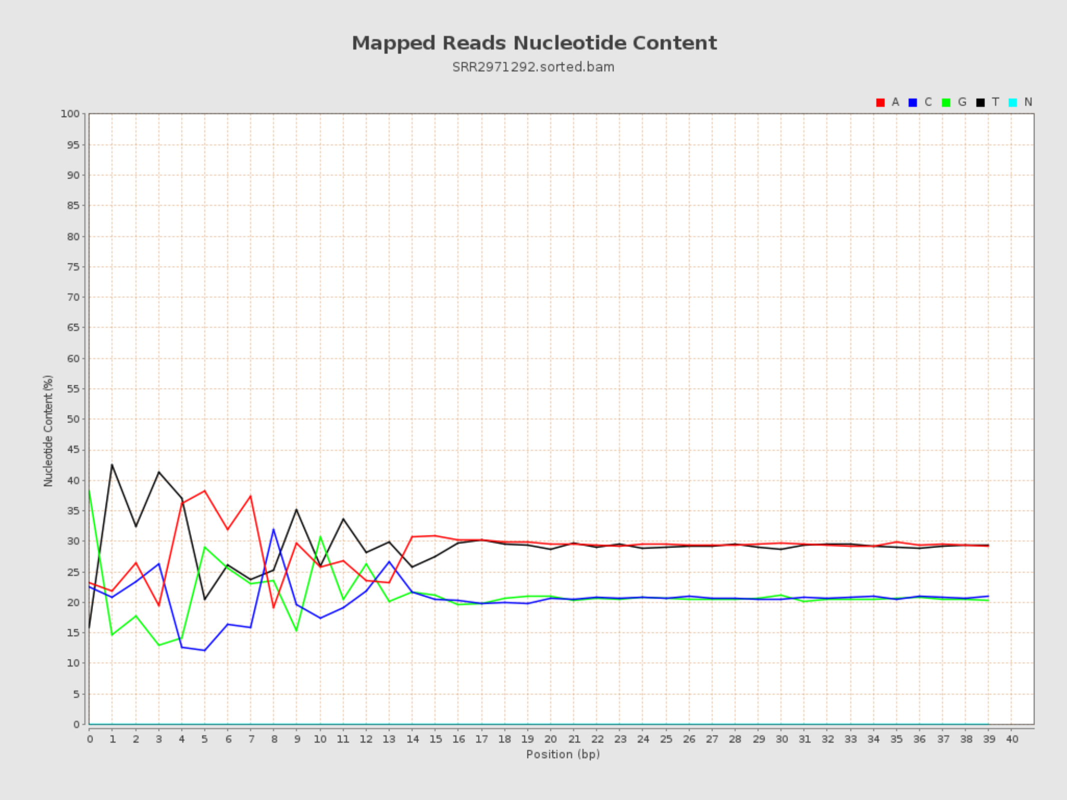
6. Results : Genome Fraction Coverage



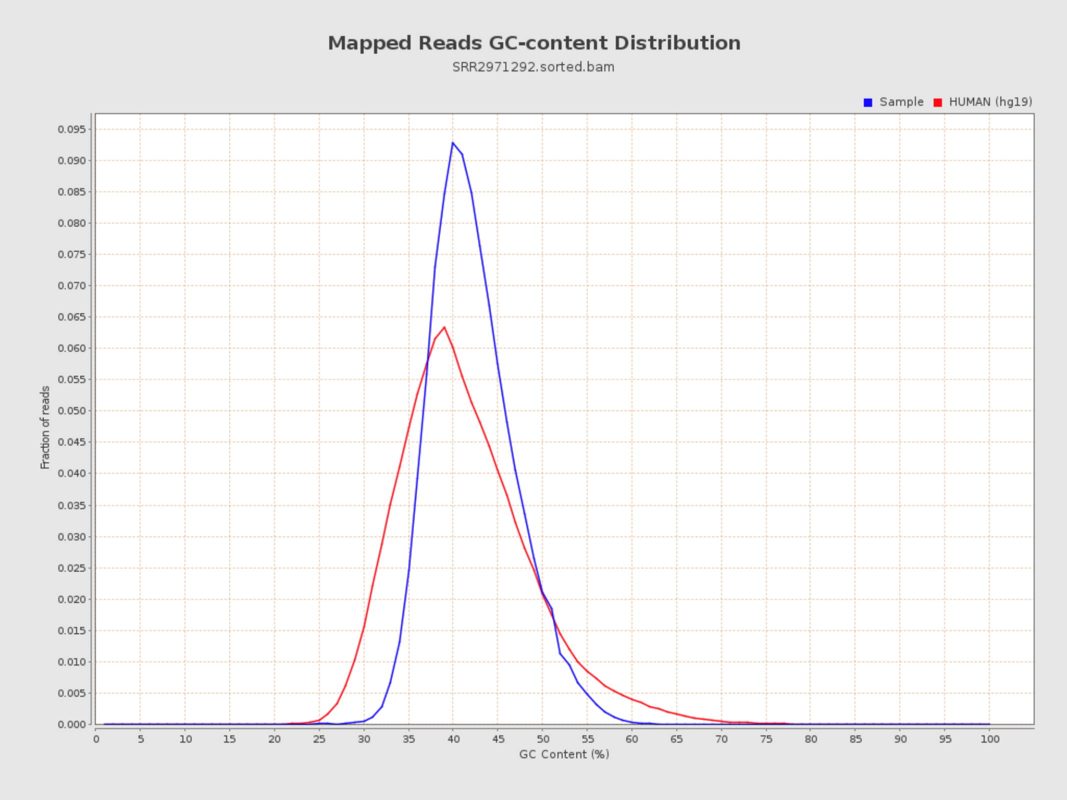
7. Results : Duplication Rate Histogram



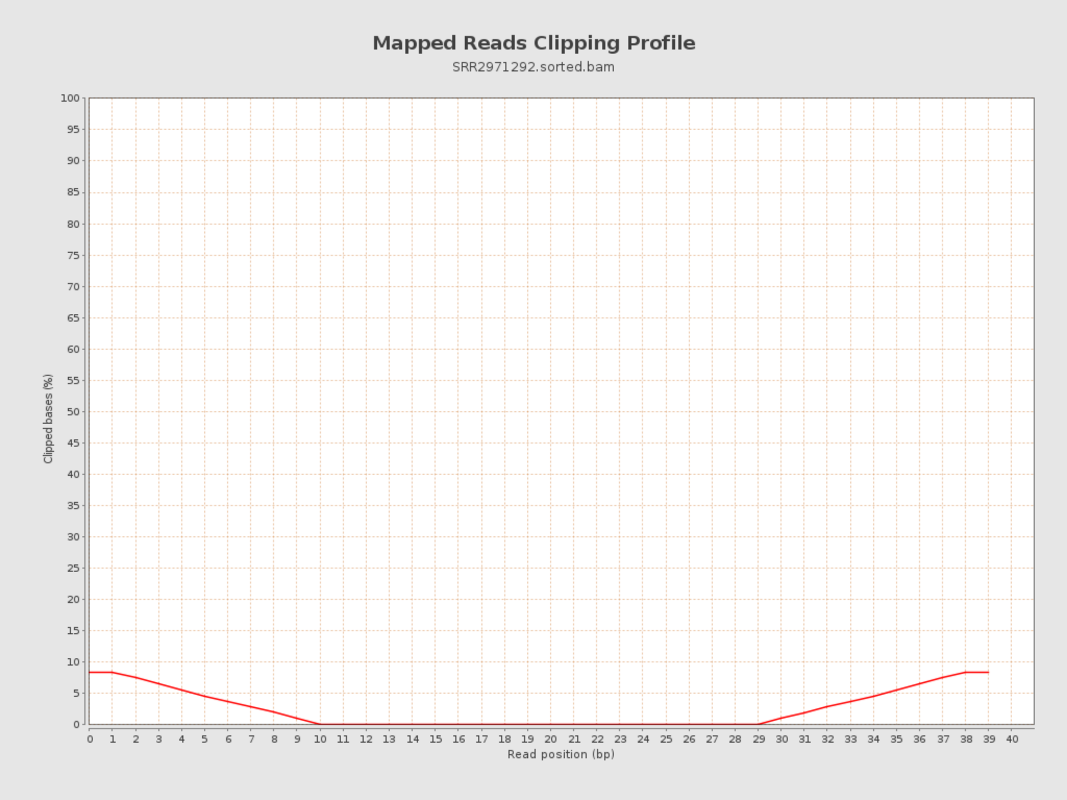
8. Results : Mapped Reads Nucleotide Content



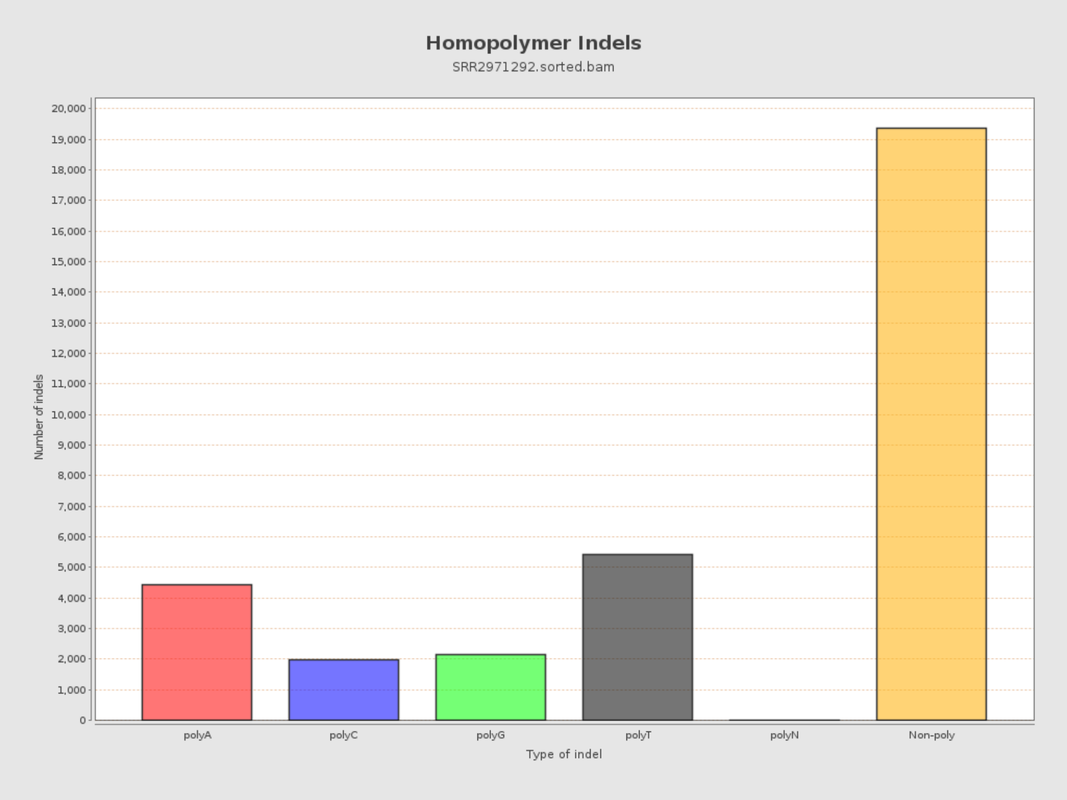
9. Results : Mapped Reads GC-content Distribution



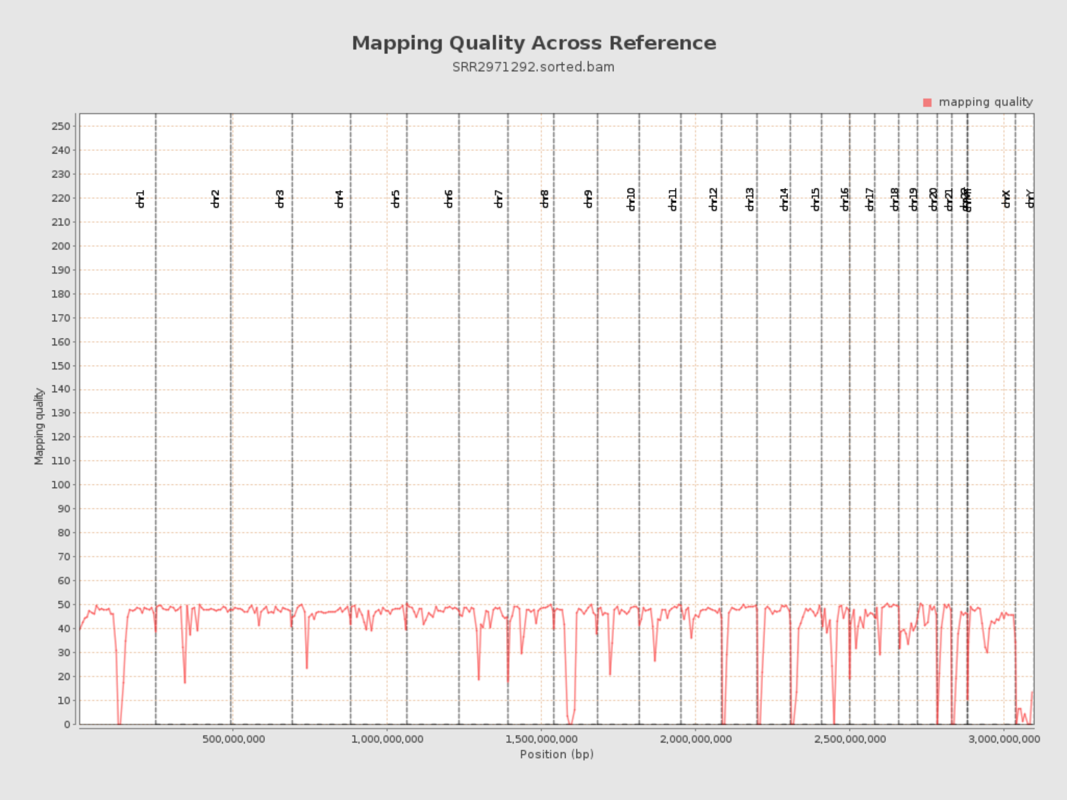
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram