Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 16:22:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971300.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_SRR2971300 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971300.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 16:22:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971300.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,550,443
Mapped reads	8,989,661 / 85.21%
Unmapped reads	1,560,782 / 14.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	742,270 / 7.04%
Duplication rate	6.51%
Clipped reads	916,260 / 8.68%

2.2. ACGT Content

Number/percentage of A's	100,598,595 / 28.41%
Number/percentage of C's	73,722,016 / 20.82%
Number/percentage of T's	103,902,879 / 29.34%
Number/percentage of G's	75,899,811 / 21.43%
Number/percentage of N's	2,717 / 0%
GC Percentage	42.25%

2.3. Coverage

Mean	0.1144
Standard Deviation	1.1106

2.4. Mapping Quality

Mean Mapping Quality	36.27

2.5. Mismatches and indels

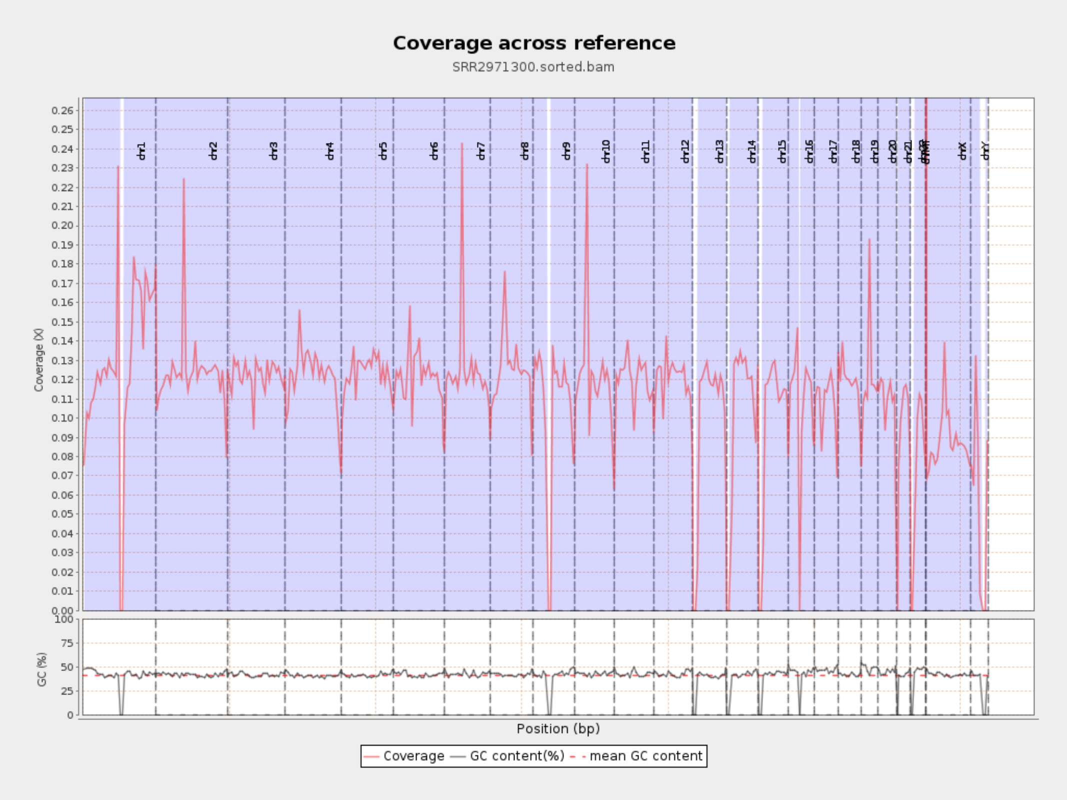
General error rate	0.33%
Mismatches	1,163,998
Insertions	13,034
Mapped reads with at least one insertion	0.14%
Deletions	28,040
Mapped reads with at least one deletion	0.31%
Homopolymer indels	39.18%

2.6. Chromosome stats

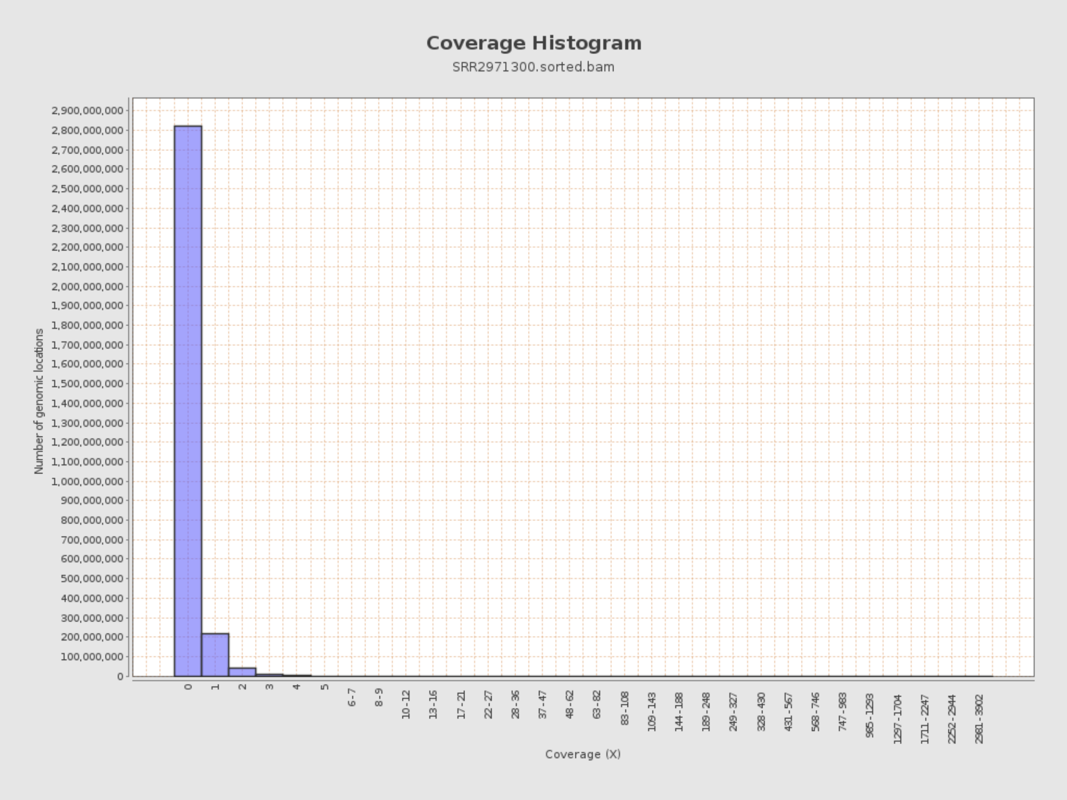
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	32052770	0.1286	2.5395
chr2	243199373	30181400	0.1241	0.916
chr3	198022430	24208626	0.1223	0.4393
chr4	191154276	23417507	0.1225	0.4941
chr5	180915260	22254210	0.123	0.4771
chr6	171115067	20958645	0.1225	0.581
chr7	159138663	19969434	0.1255	1.4193
chr8	146364022	18306827	0.1251	1.6444

chr9	141213431	14855843	0.1052	0.9157
chr10	135534747	16639777	0.1228	0.9923
chr11	135006516	16197202	0.12	0.7576
chr12	133851895	16151617	0.1207	0.4828
chr13	115169878	11335386	0.0984	0.3771
chr14	107349540	10890121	0.1014	0.5285
chr15	102531392	9733276	0.0949	0.3799
chr16	90354753	9486115	0.105	0.5083
chr17	81195210	8870785	0.1093	0.4624
chr18	78077248	9390644	0.1203	1.7931
chr19	59128983	7233235	0.1223	2.2258
chr20	63025520	6891703	0.1093	0.4698
chr21	48129895	4402739	0.0915	0.5079
chr22	51304566	3631265	0.0708	0.4033
chrMT	16571	57642	3.4785	3.6517
chrX	155270560	13672614	0.0881	0.5603
chrY	59373566	3371543	0.0568	0.5137

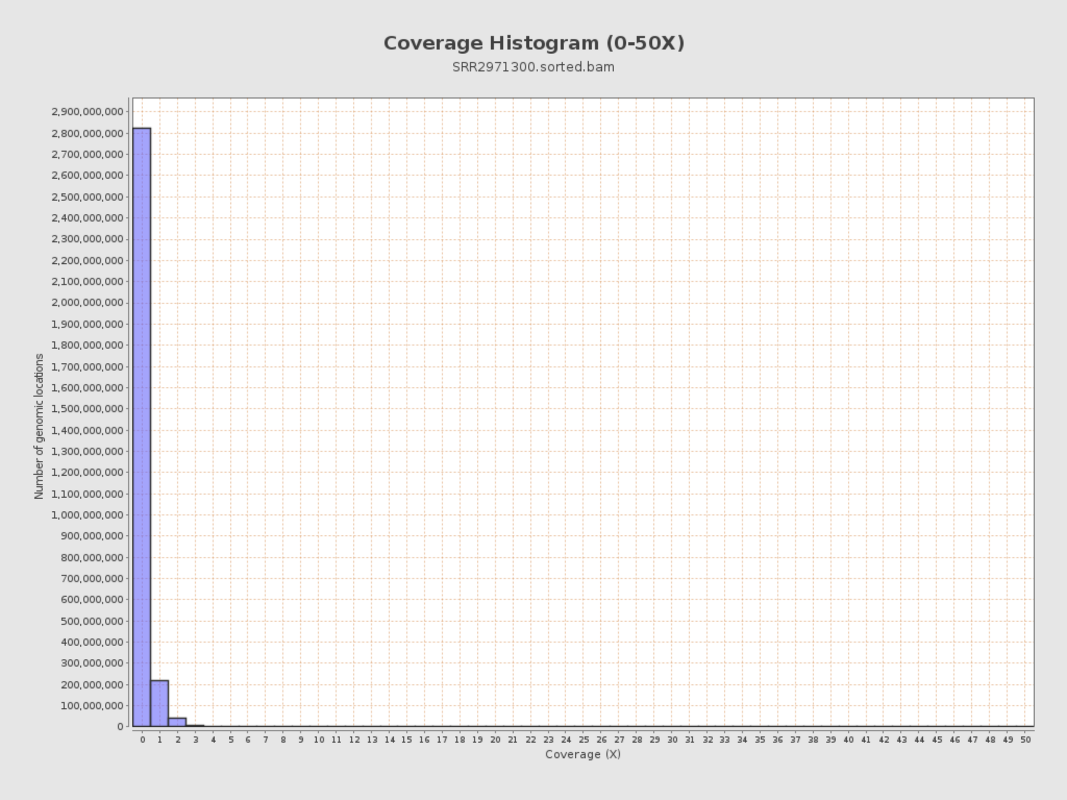
3. Results : Coverage across reference



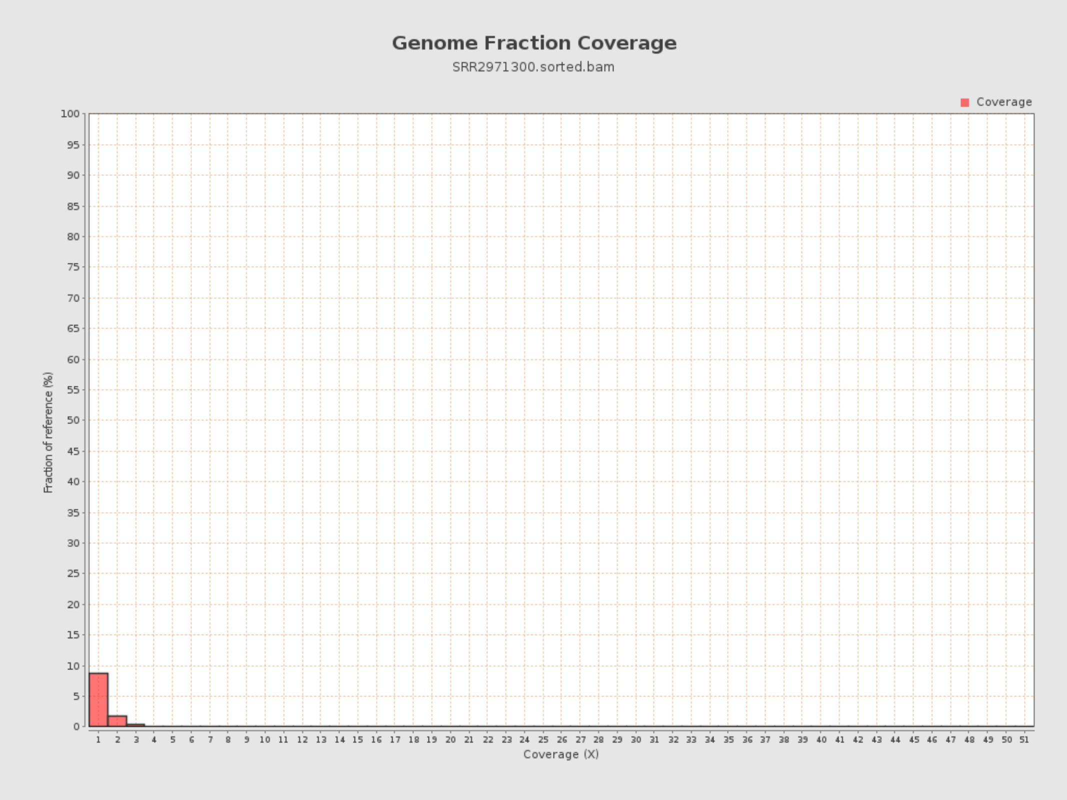
4. Results : Coverage Histogram



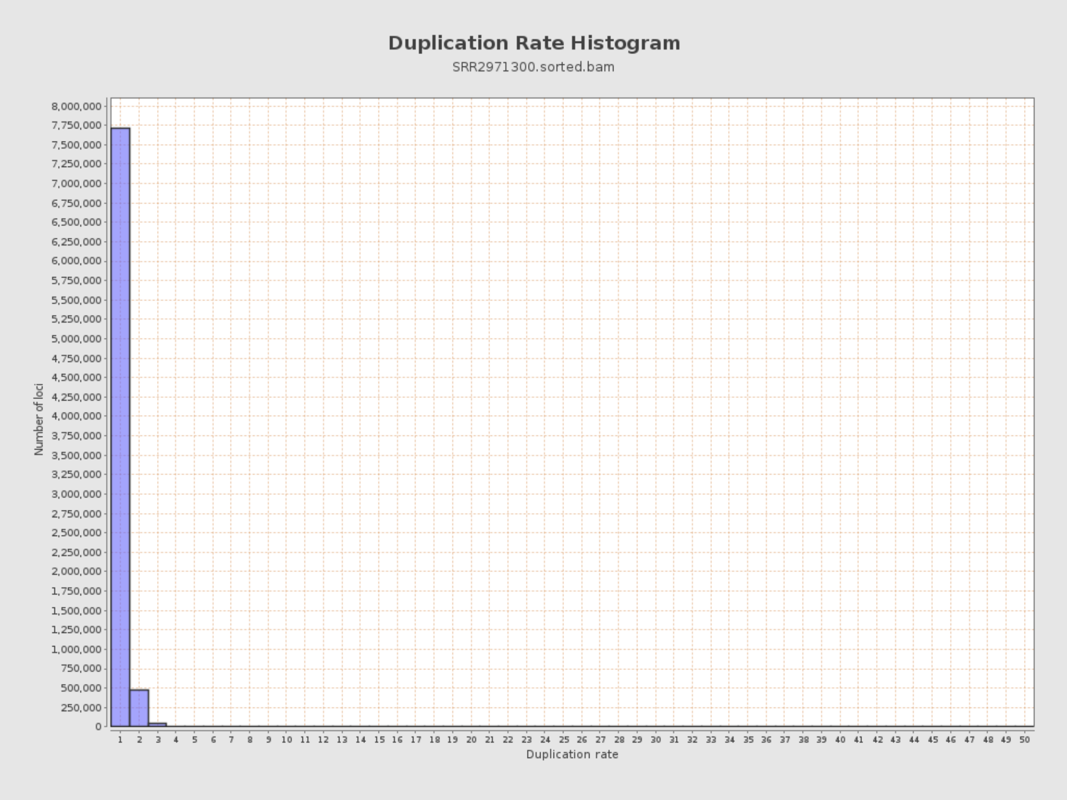
5. Results : Coverage Histogram (0-50X)



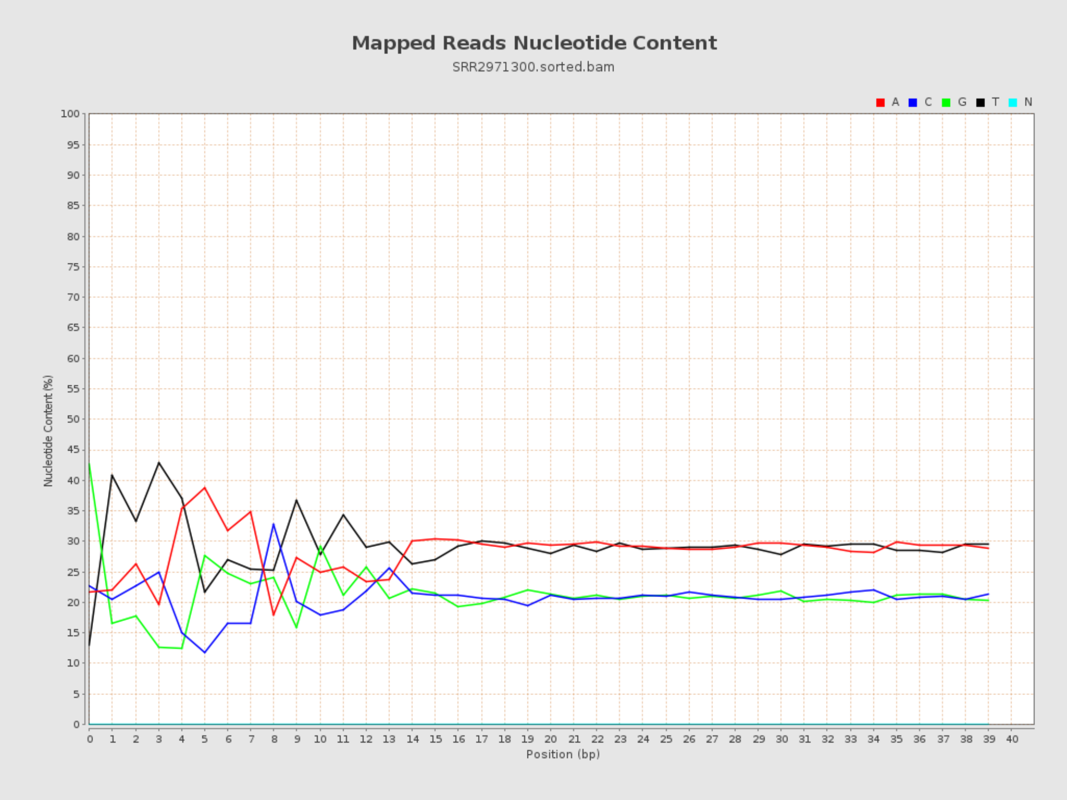
6. Results : Genome Fraction Coverage



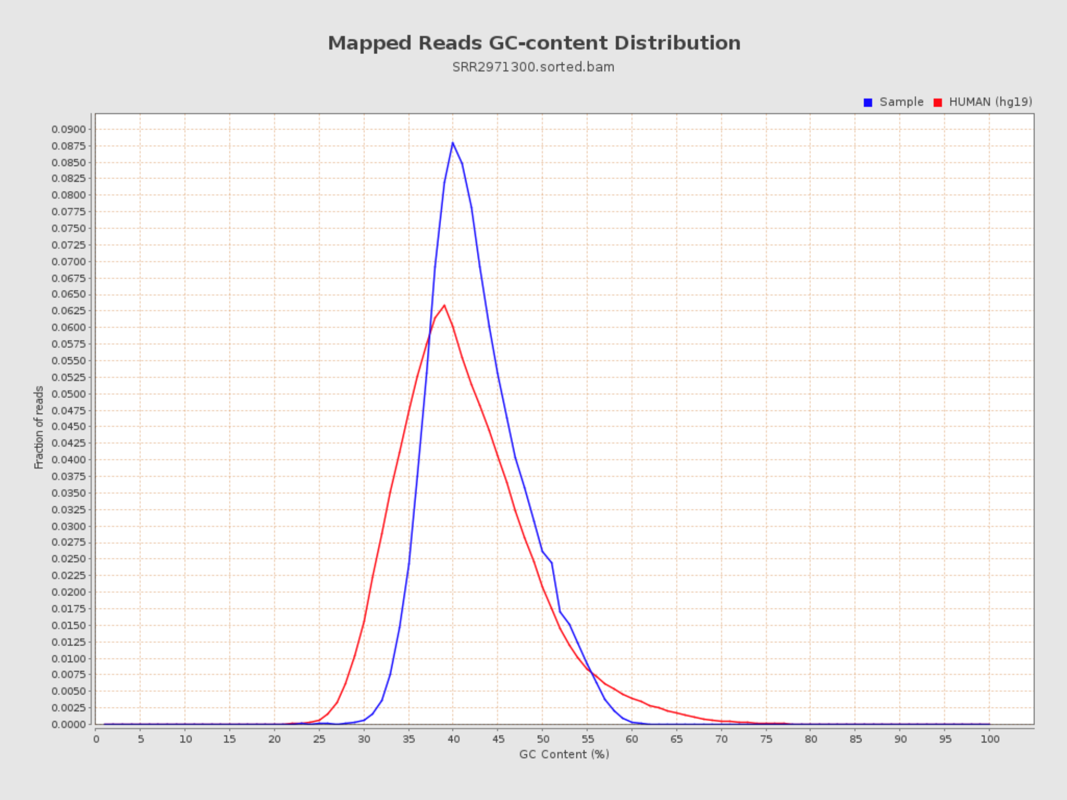
7. Results : Duplication Rate Histogram



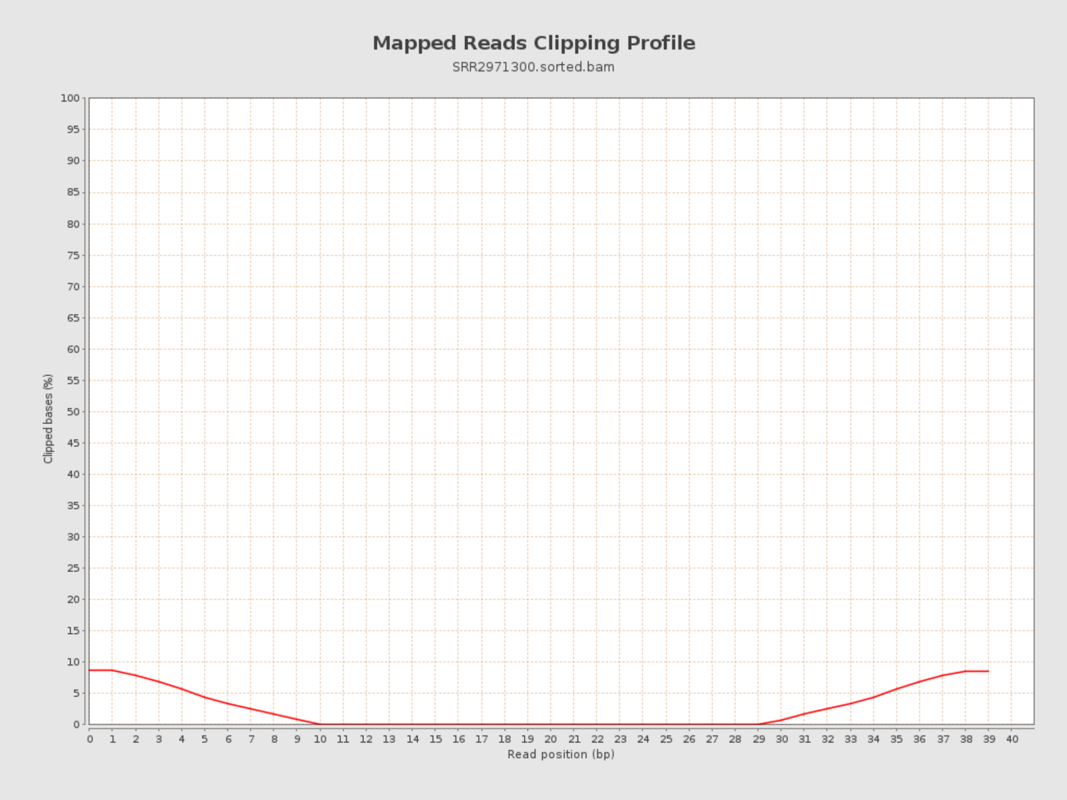
8. Results : Mapped Reads Nucleotide Content



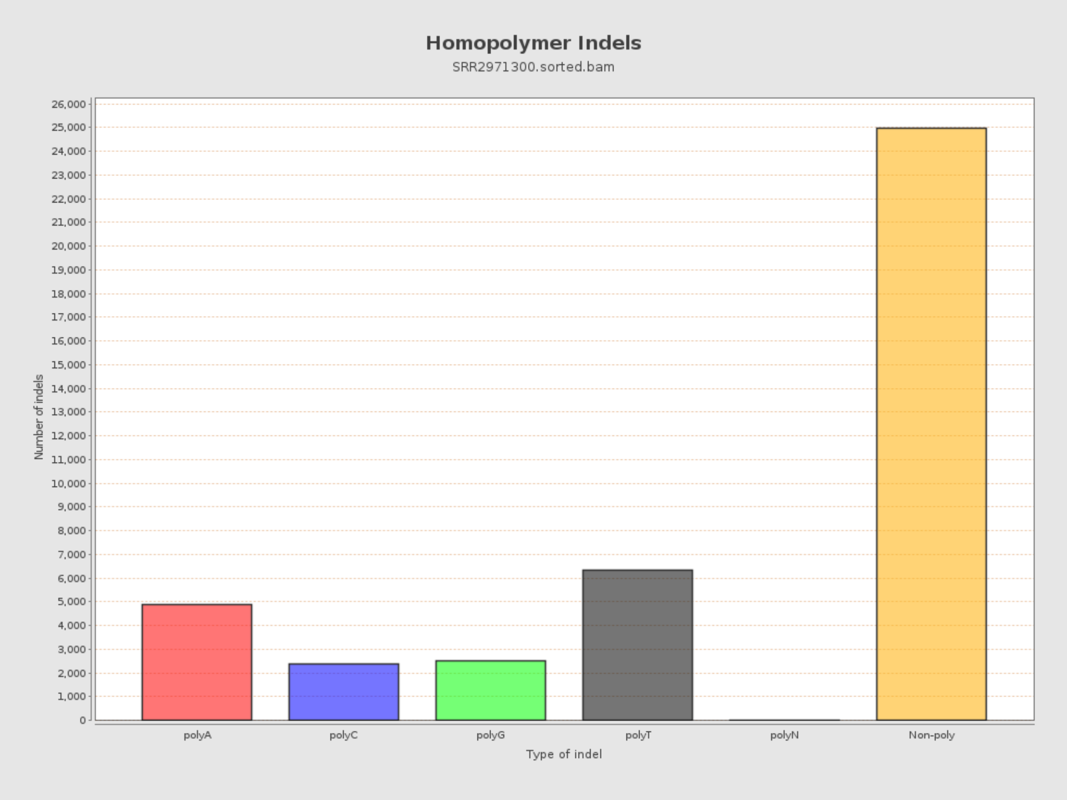
9. Results : Mapped Reads GC-content Distribution



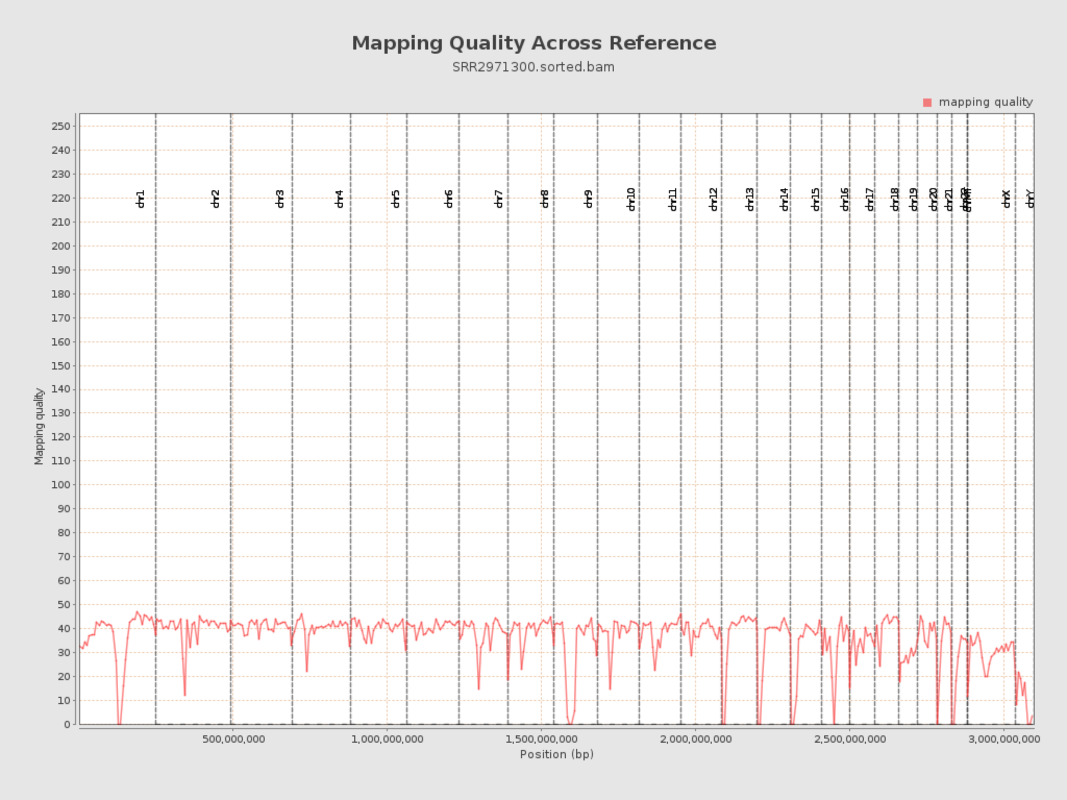
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram