Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 06:07:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3212163.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_SRR3212163 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3212163.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 06:07:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3212163.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,403,785
Mapped reads	3,890,188 / 88.34%
Unmapped reads	513,597 / 11.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,544 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	185,663 / 4.22%
Duplication rate	3.31%
Clipped reads	1,625,582 / 36.91%

2.2. ACGT Content

Number/percentage of A's	72,189,780 / 27.56%
Number/percentage of C's	47,634,944 / 18.19%
Number/percentage of T's	83,821,231 / 32%
Number/percentage of G's	58,191,307 / 22.22%
Number/percentage of N's	69,963 / 0.03%
GC Percentage	40.41%

2.3. Coverage

Mean	0.0846

Standard Deviation	0.7695

2.4. Mapping Quality

Mean Mapping Quality	45.72

2.5. Mismatches and indels

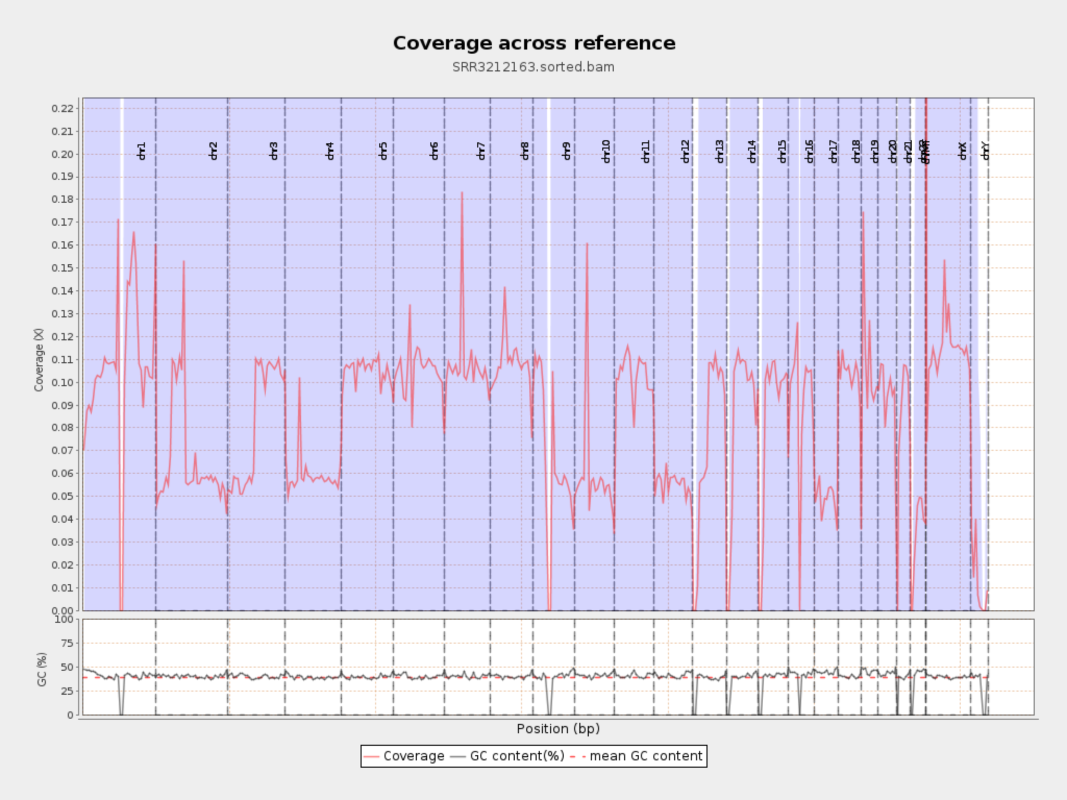
General error rate	0.87%
Mismatches	2,248,214
Insertions	21,990
Mapped reads with at least one insertion	0.56%
Deletions	70,335
Mapped reads with at least one deletion	1.79%
Homopolymer indels	49.85%

2.6. Chromosome stats

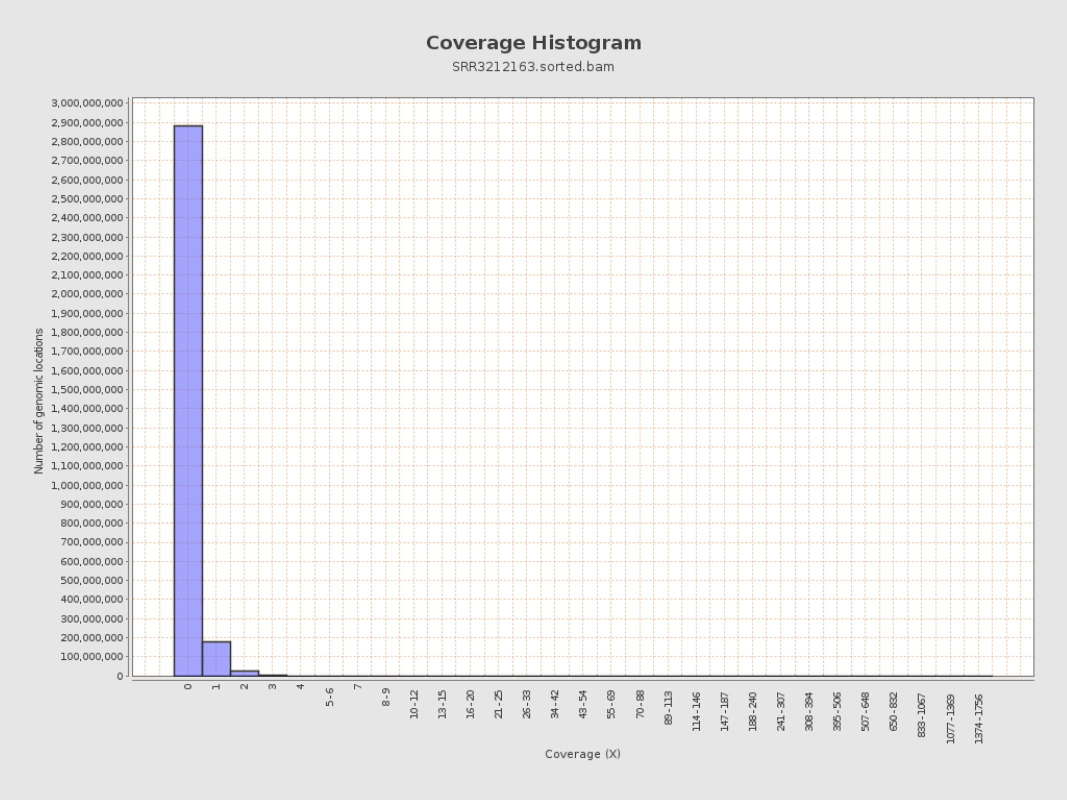
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26375356	0.1058	1.5805
chr2	243199373	16337457	0.0672	0.7639
chr3	198022430	16175247	0.0817	0.3527
chr4	191154276	11332176	0.0593	0.3561
chr5	180915260	18938003	0.1047	0.3852
chr6	171115067	18078277	0.1056	0.5341
chr7	159138663	17108588	0.1075	1.1829

chr8	146364022	15810124	0.108	0.9688
chr9	141213431	9354808	0.0662	0.674
chr10	135534747	8101974	0.0598	0.8534
chr11	135006516	13761221	0.1019	0.8128
chr12	133851895	7397958	0.0553	0.2978
chr13	115169878	8541851	0.0742	0.3156
chr14	107349540	9249983	0.0862	0.4028
chr15	102531392	8466794	0.0826	0.337
chr16	90354753	8151667	0.0902	0.4255
chr17	81195210	4008558	0.0494	0.4029
chr18	78077248	8171539	0.1047	1.1787
chr19	59128983	6423478	0.1086	1.1461
chr20	63025520	6005112	0.0953	0.3853
chr21	48129895	4008945	0.0833	0.4163
chr22	51304566	1673769	0.0326	0.2066
chrMT	16571	99411	5.9991	3.6523
chrX	155270560	17719011	0.1141	0.482
chrY	59373566	736219	0.0124	0.2982

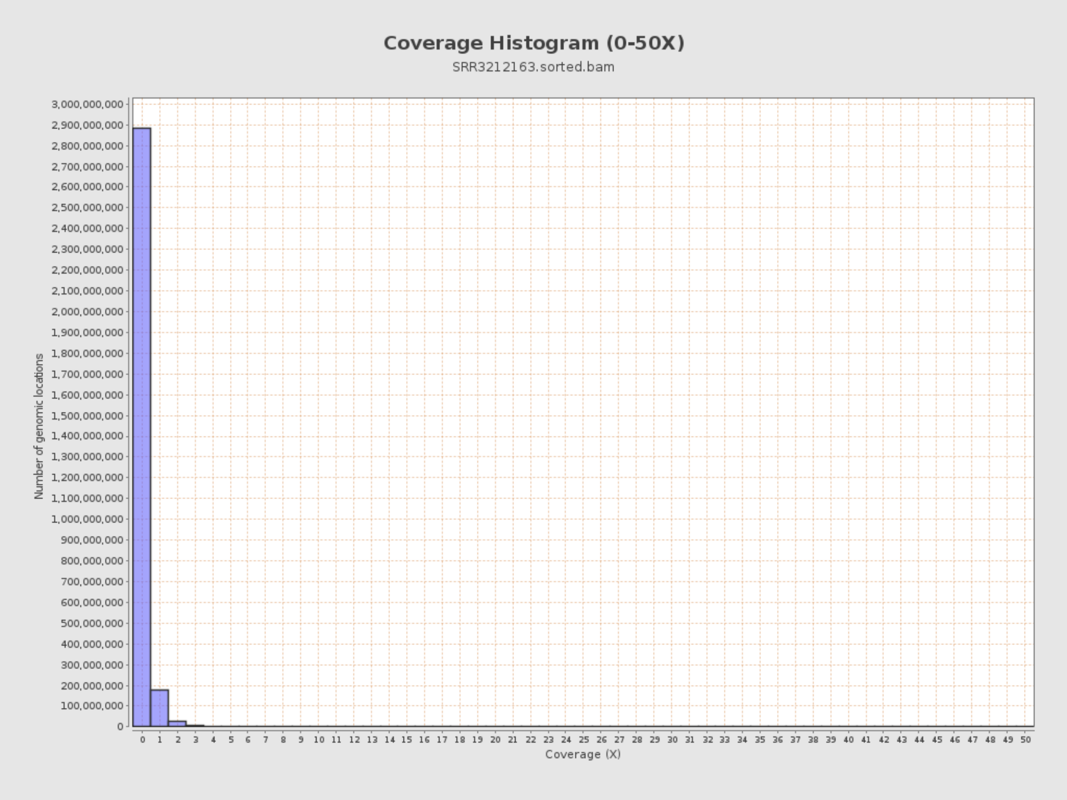
3. Results : Coverage across reference



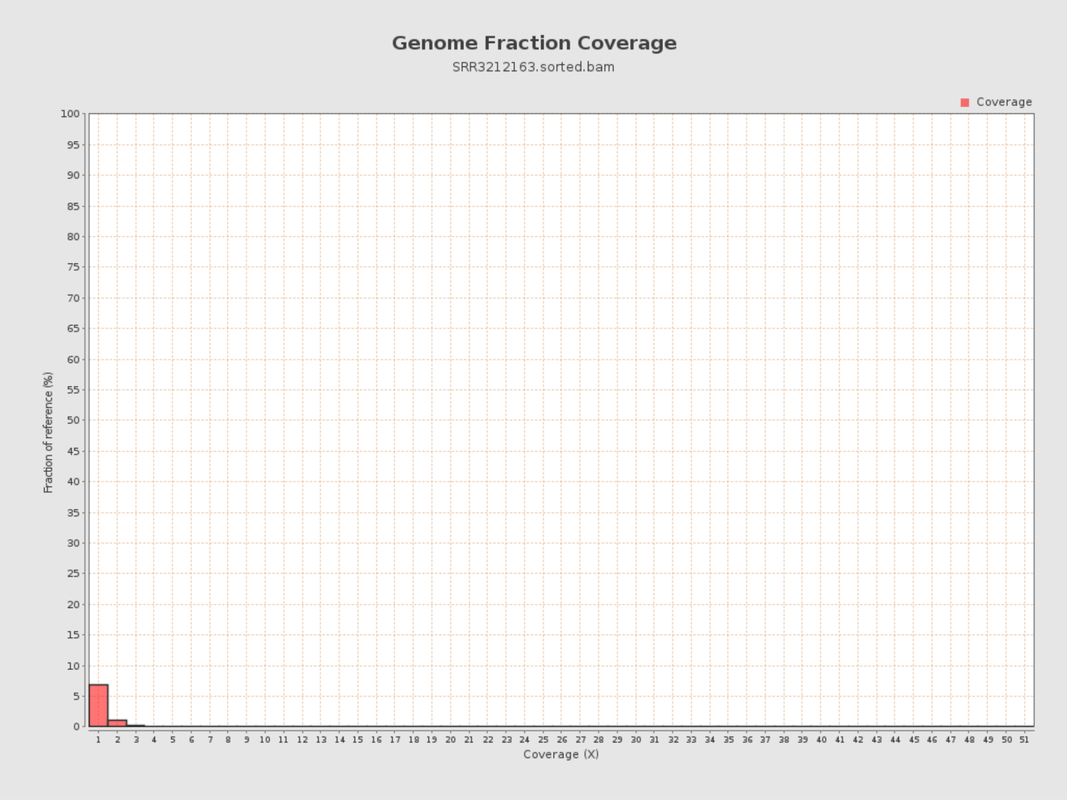
4. Results : Coverage Histogram



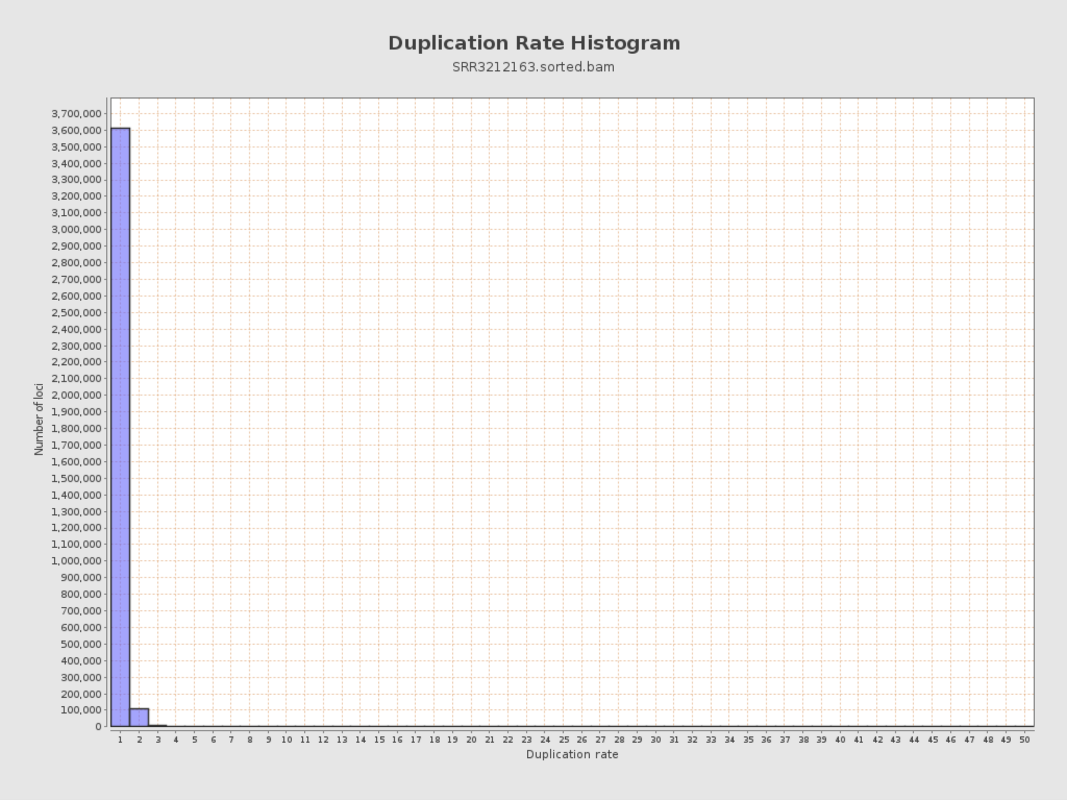
5. Results : Coverage Histogram (0-50X)



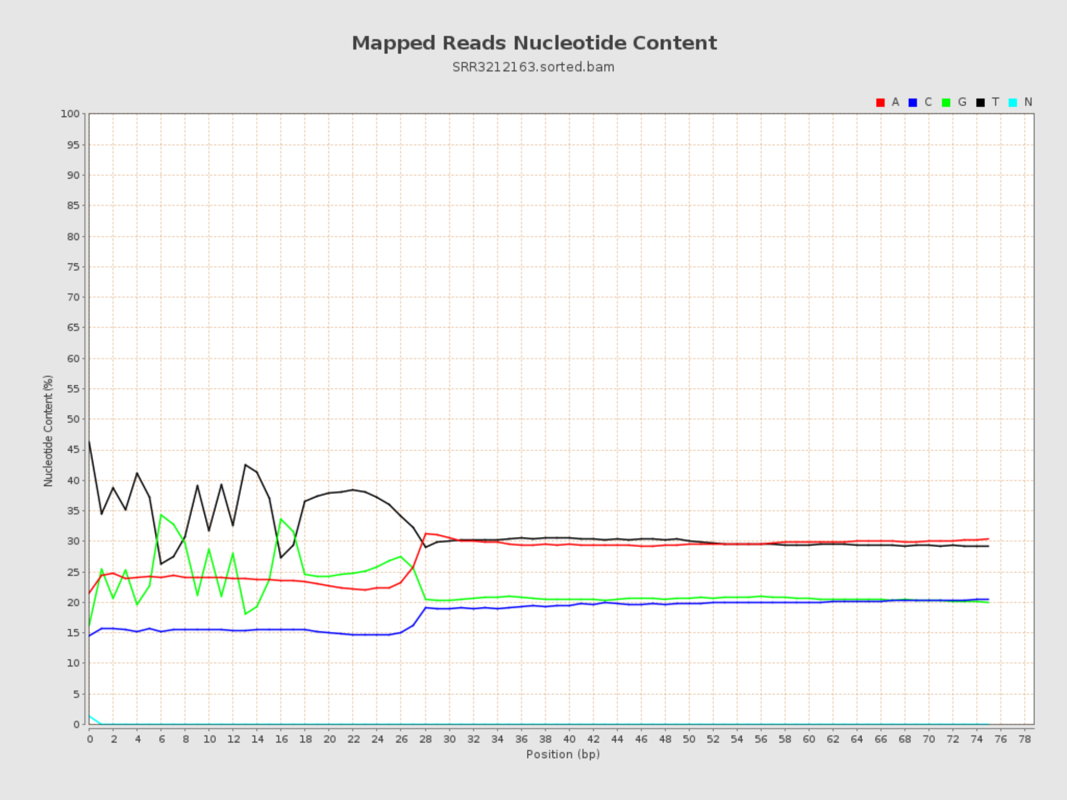
6. Results : Genome Fraction Coverage



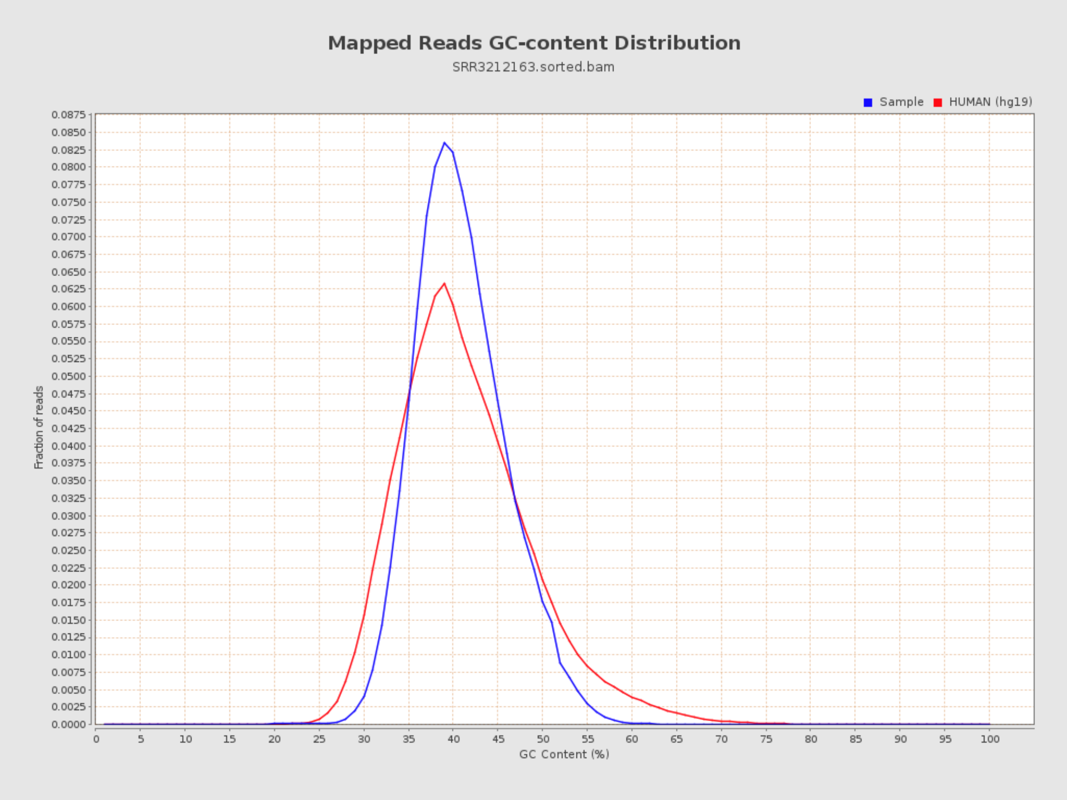
7. Results : Duplication Rate Histogram



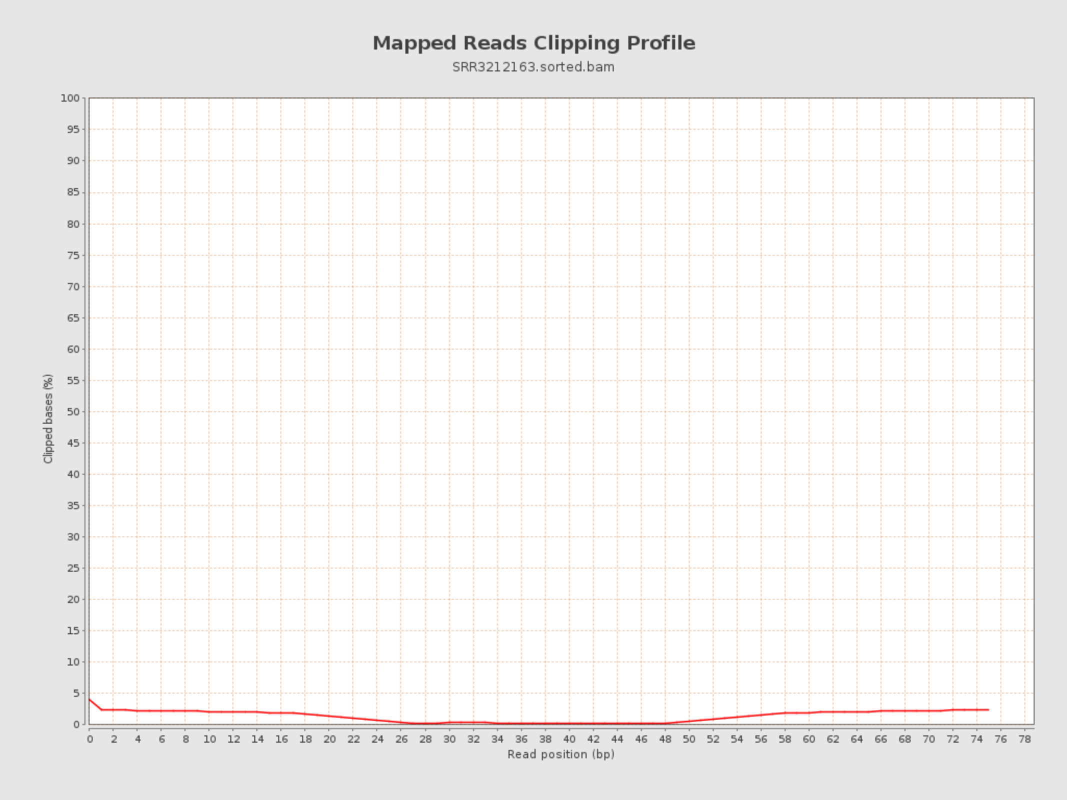
8. Results : Mapped Reads Nucleotide Content



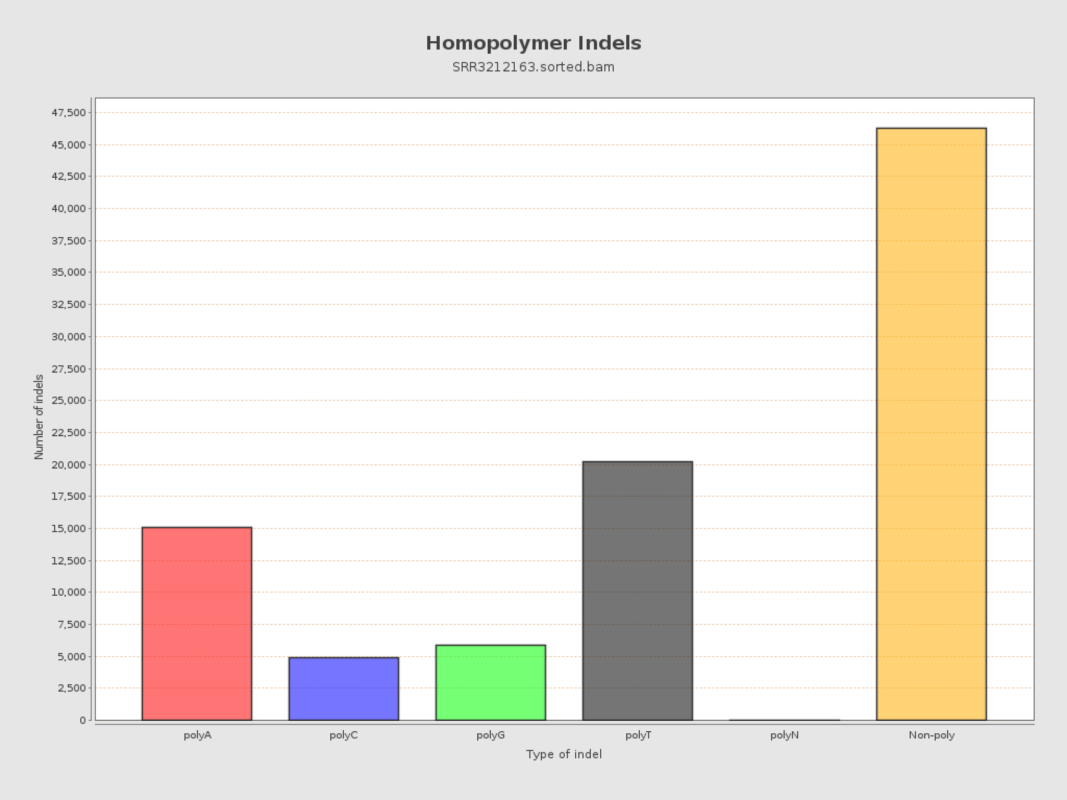
9. Results : Mapped Reads GC-content Distribution



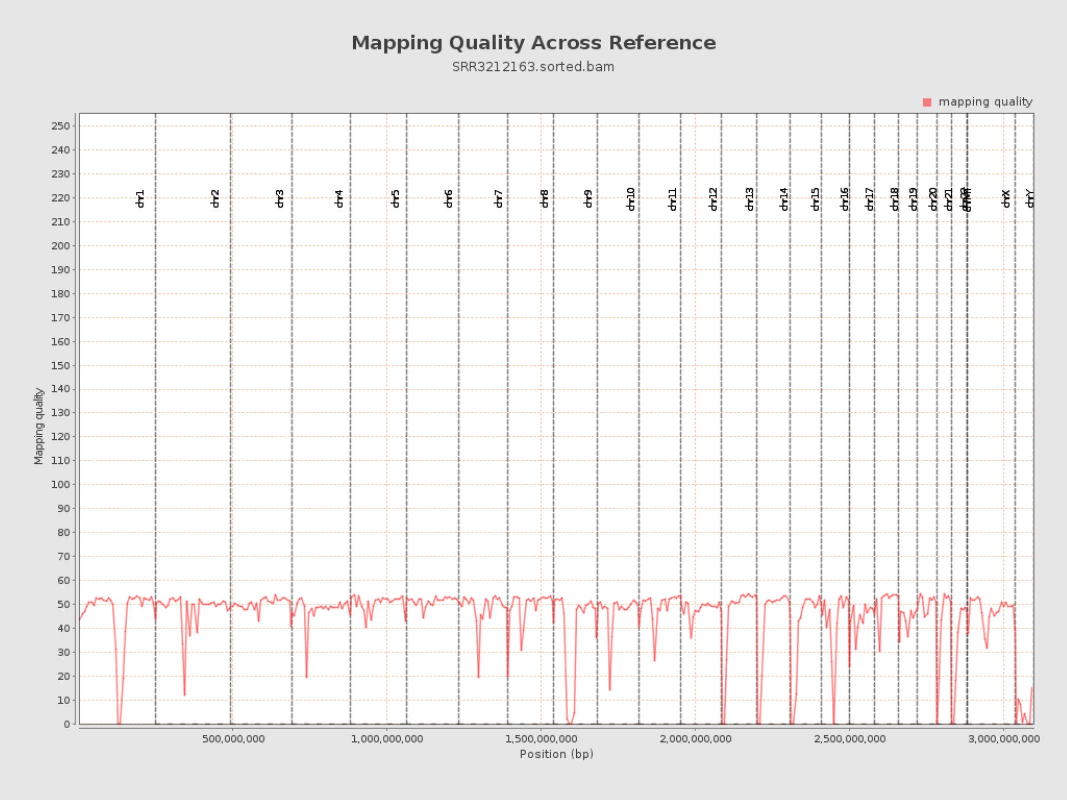
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram