Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 05:52:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3212162.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_SRR3212162 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3212162.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 05:52:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3212162.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,937,852
Mapped reads	4,249,965 / 86.07%
Unmapped reads	687,887 / 13.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,485 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	260,899 / 5.28%
Duplication rate	4.67%
Clipped reads	1,715,557 / 34.74%

2.2. ACGT Content

Number/percentage of A's	79,676,550 / 27.77%
Number/percentage of C's	51,938,972 / 18.1%
Number/percentage of T's	92,481,962 / 32.24%
Number/percentage of G's	62,724,353 / 21.86%
Number/percentage of N's	72,376 / 0.03%
GC Percentage	39.97%

2.3. Coverage

Mean	0.0927

Standard Deviation	0.7769

2.4. Mapping Quality

Mean Mapping Quality	47.2

2.5. Mismatches and indels

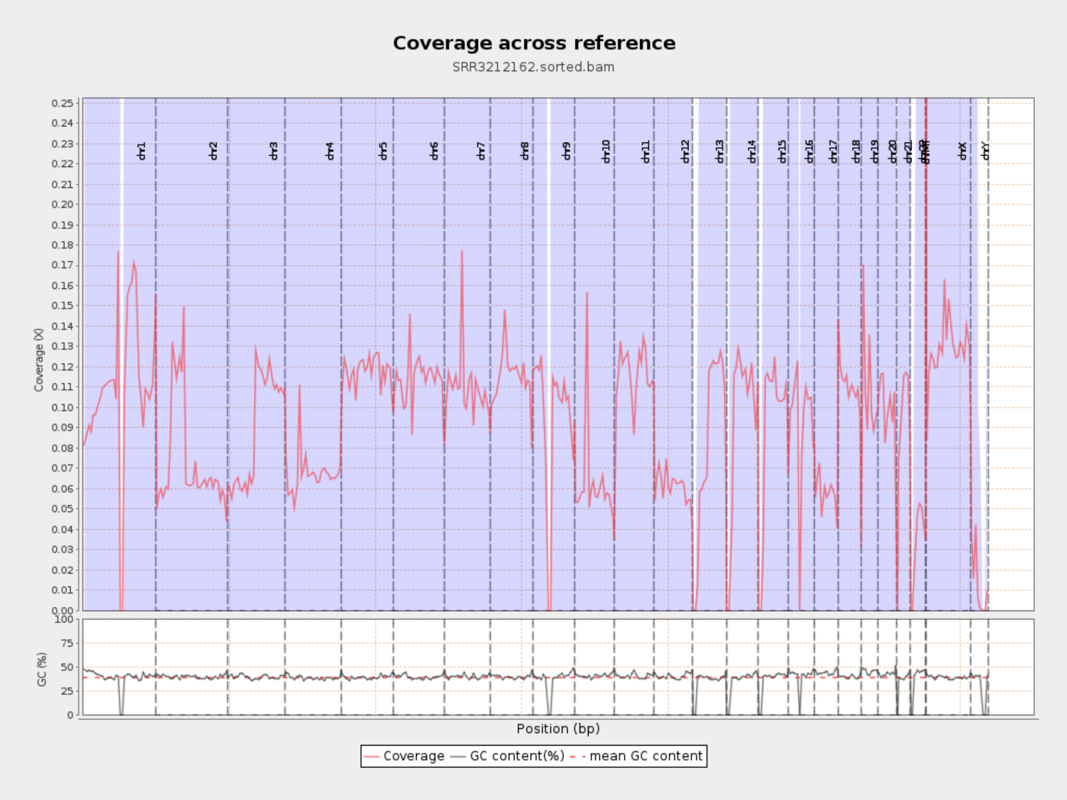
General error rate	0.87%
Mismatches	2,460,666
Insertions	23,899
Mapped reads with at least one insertion	0.56%
Deletions	78,599
Mapped reads with at least one deletion	1.83%
Homopolymer indels	49.73%

2.6. Chromosome stats

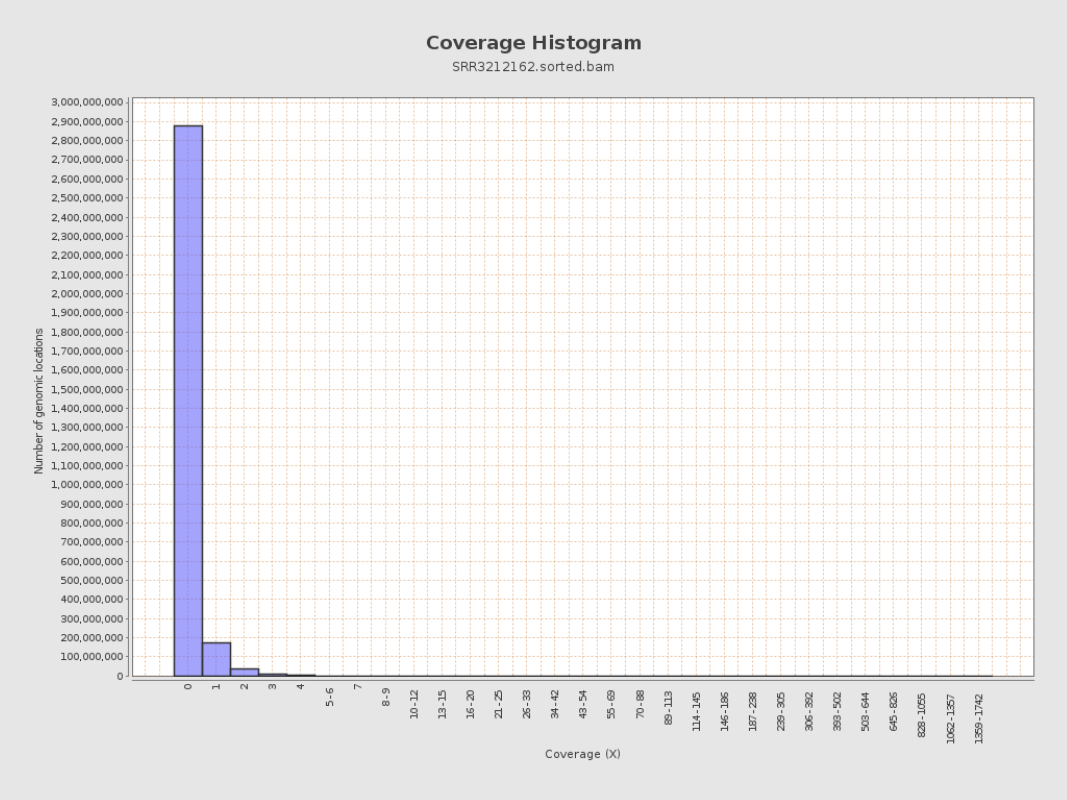
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27327898	0.1096	1.5959
chr2	243199373	18003804	0.074	0.7273
chr3	198022430	17656895	0.0892	0.3848
chr4	191154276	12876953	0.0674	0.4069
chr5	180915260	21245903	0.1174	0.4334
chr6	171115067	19628179	0.1147	0.5684
chr7	159138663	17491638	0.1099	1.1177

chr8	146364022	16844932	0.1151	1.0583
chr9	141213431	13362307	0.0946	0.6673
chr10	135534747	8471083	0.0625	0.8009
chr11	135006516	15598477	0.1155	0.787
chr12	133851895	8216449	0.0614	0.3242
chr13	115169878	9627154	0.0836	0.358
chr14	107349540	10167804	0.0947	0.4176
chr15	102531392	9124205	0.089	0.3699
chr16	90354753	8187895	0.0906	0.4289
chr17	81195210	4733159	0.0583	0.4235
chr18	78077248	8721925	0.1117	1.2038
chr19	59128983	6370255	0.1077	1.1561
chr20	63025520	6347342	0.1007	0.4097
chr21	48129895	4401246	0.0914	0.4639
chr22	51304566	1728491	0.0337	0.2211
chrMT	16571	69349	4.185	2.7812
chrX	155270560	20041499	0.1291	0.5198
chrY	59373566	783028	0.0132	0.3211

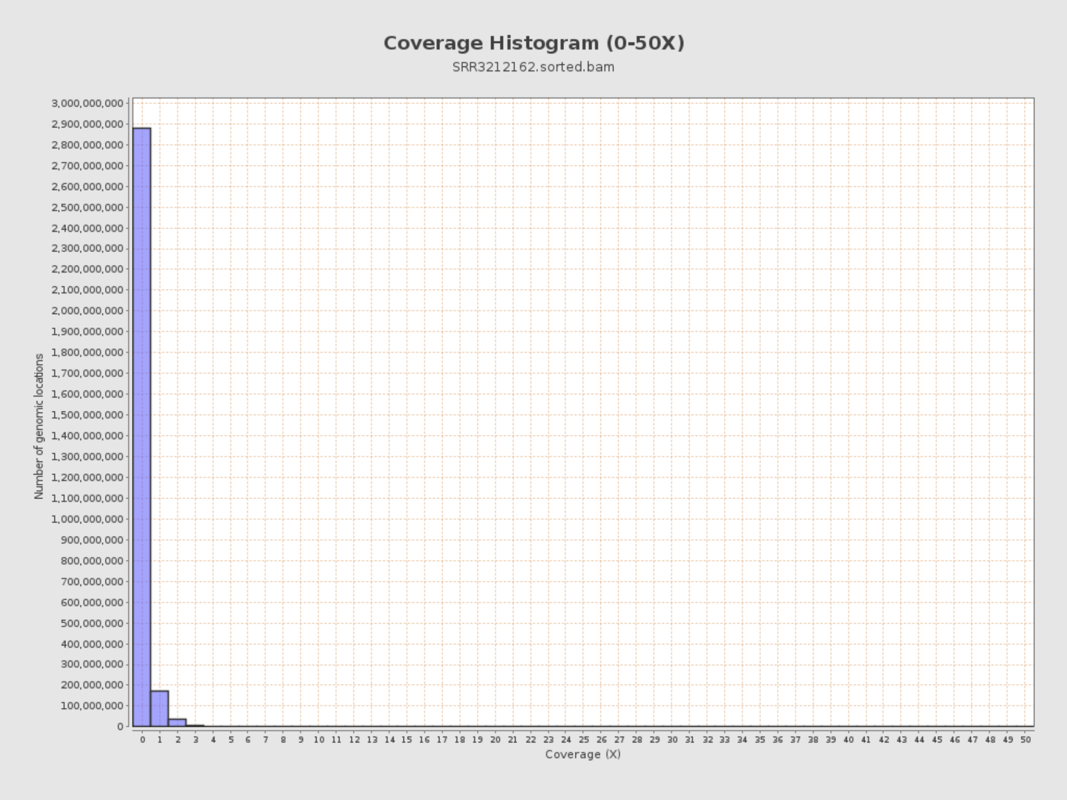
3. Results : Coverage across reference



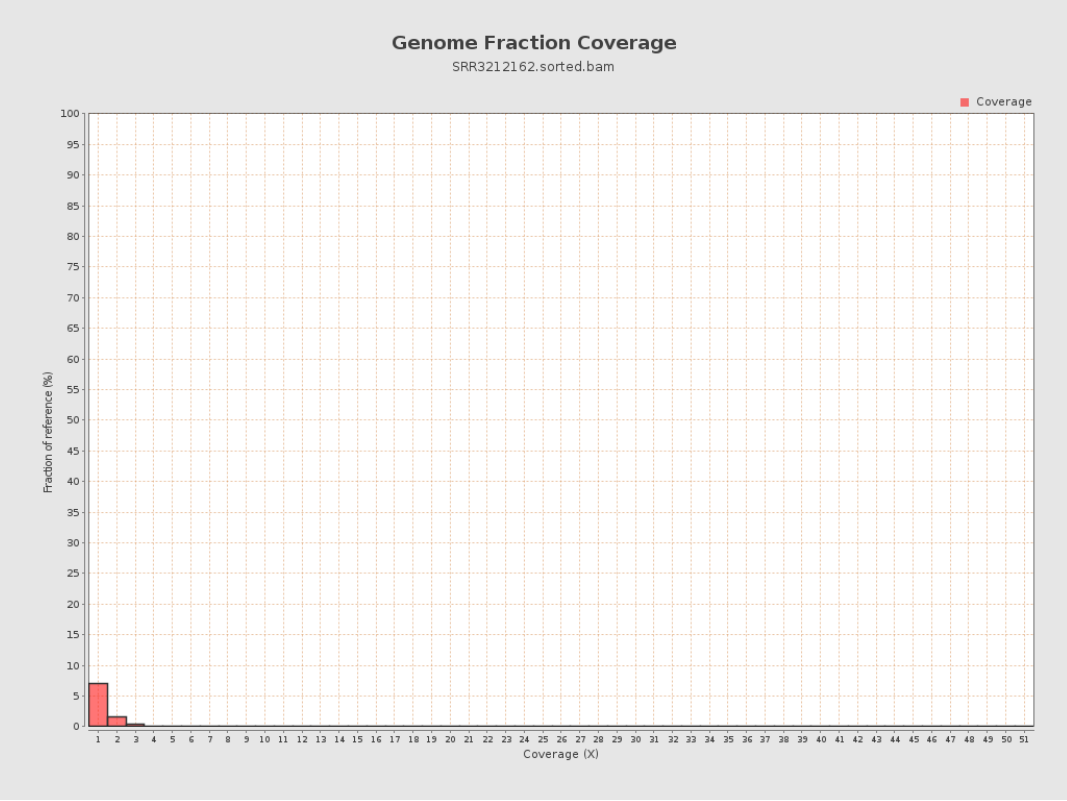
4. Results : Coverage Histogram



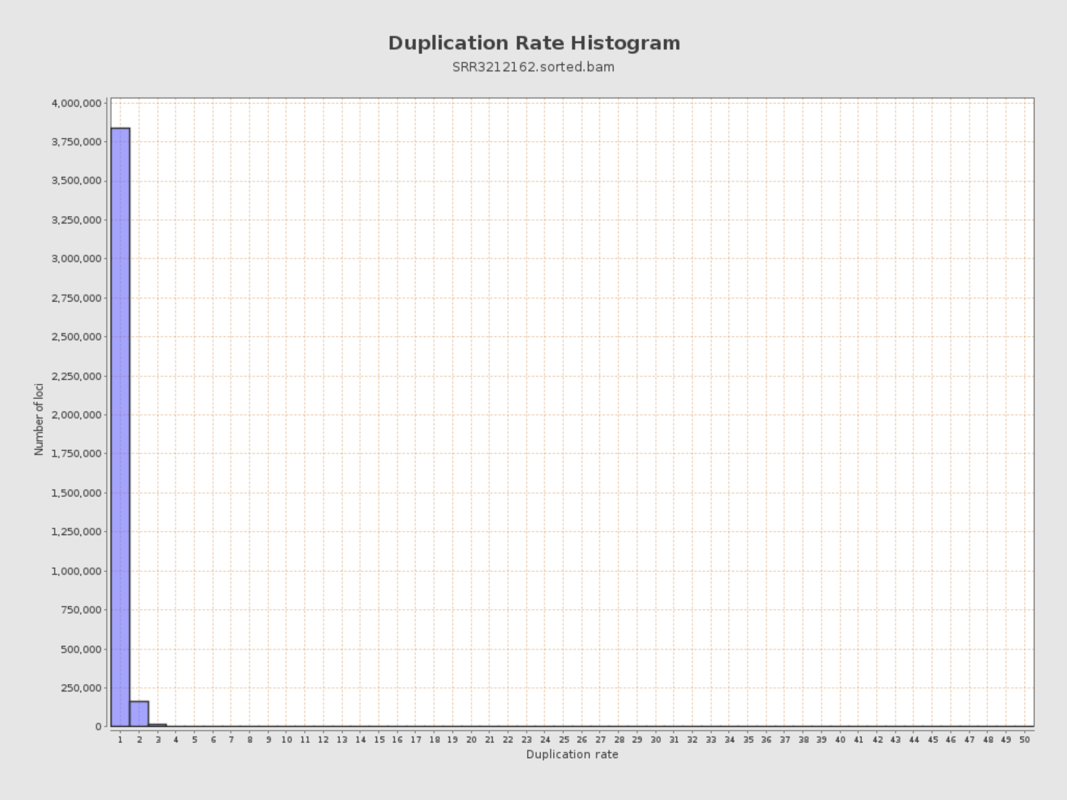
5. Results : Coverage Histogram (0-50X)



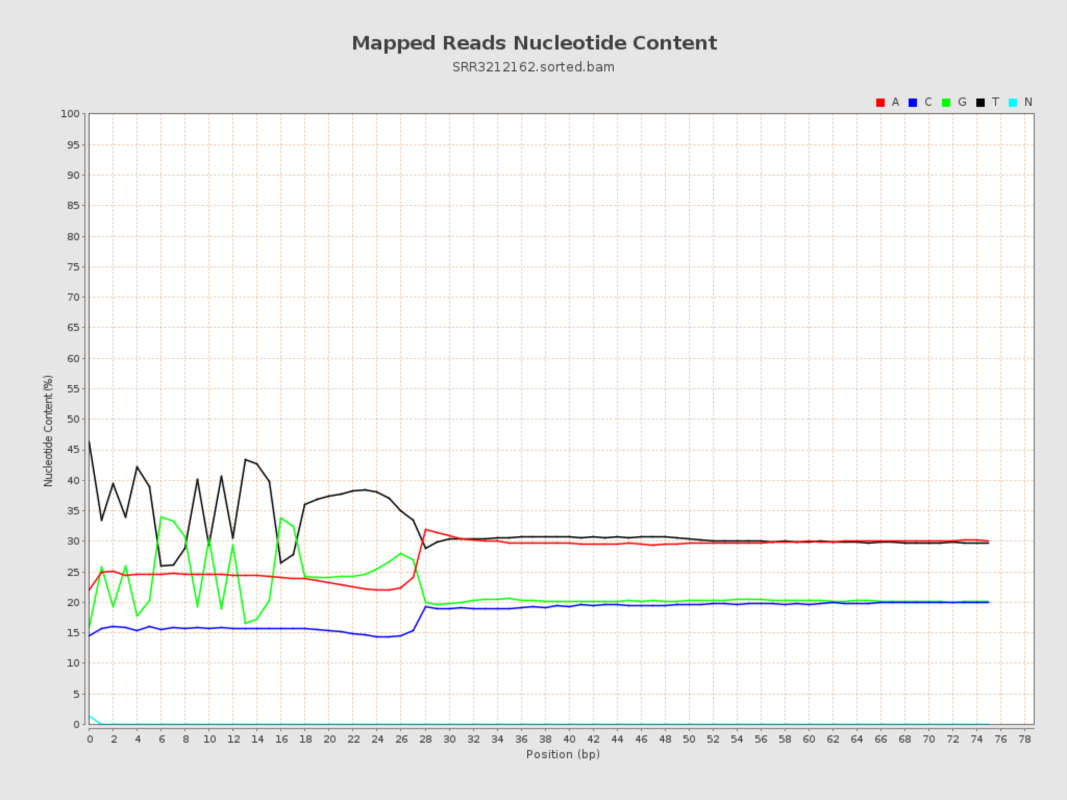
6. Results : Genome Fraction Coverage



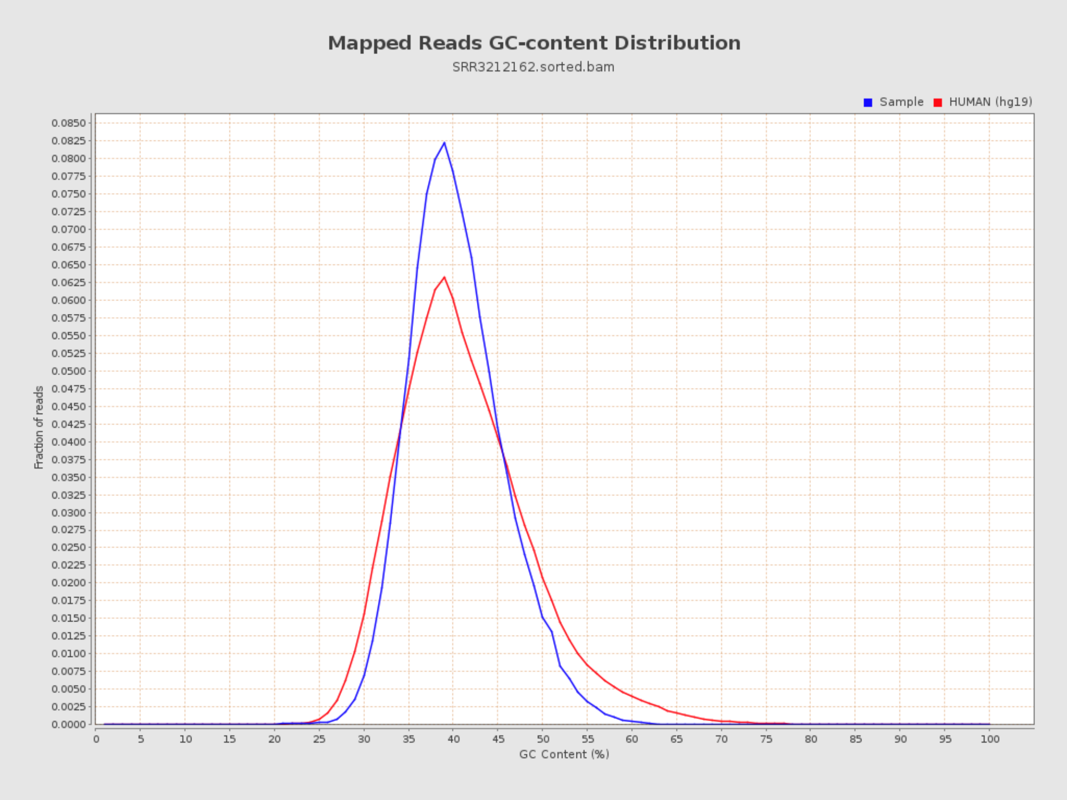
7. Results : Duplication Rate Histogram



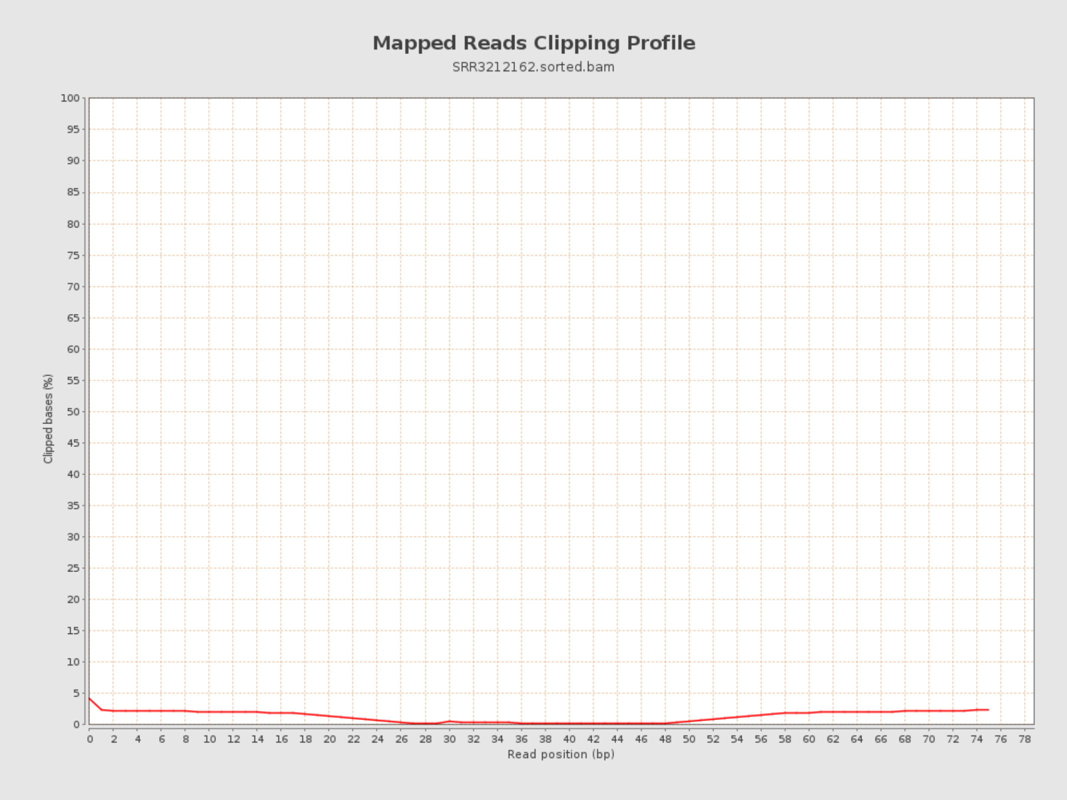
8. Results : Mapped Reads Nucleotide Content



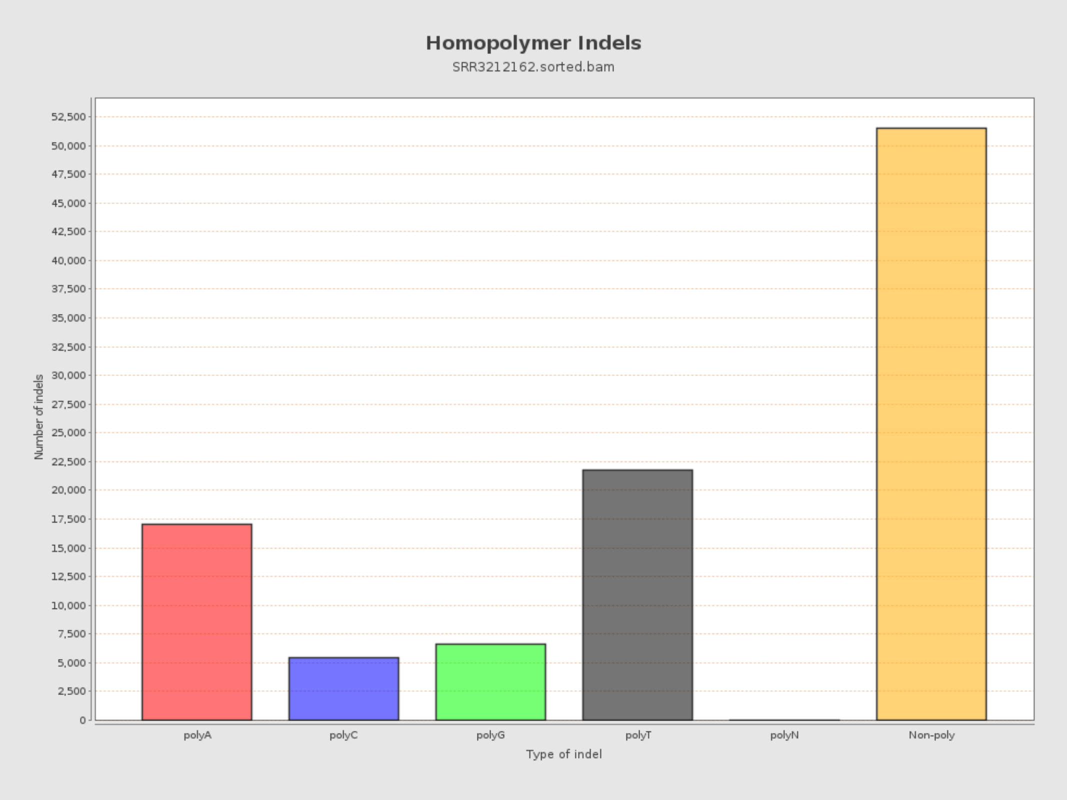
9. Results : Mapped Reads GC-content Distribution



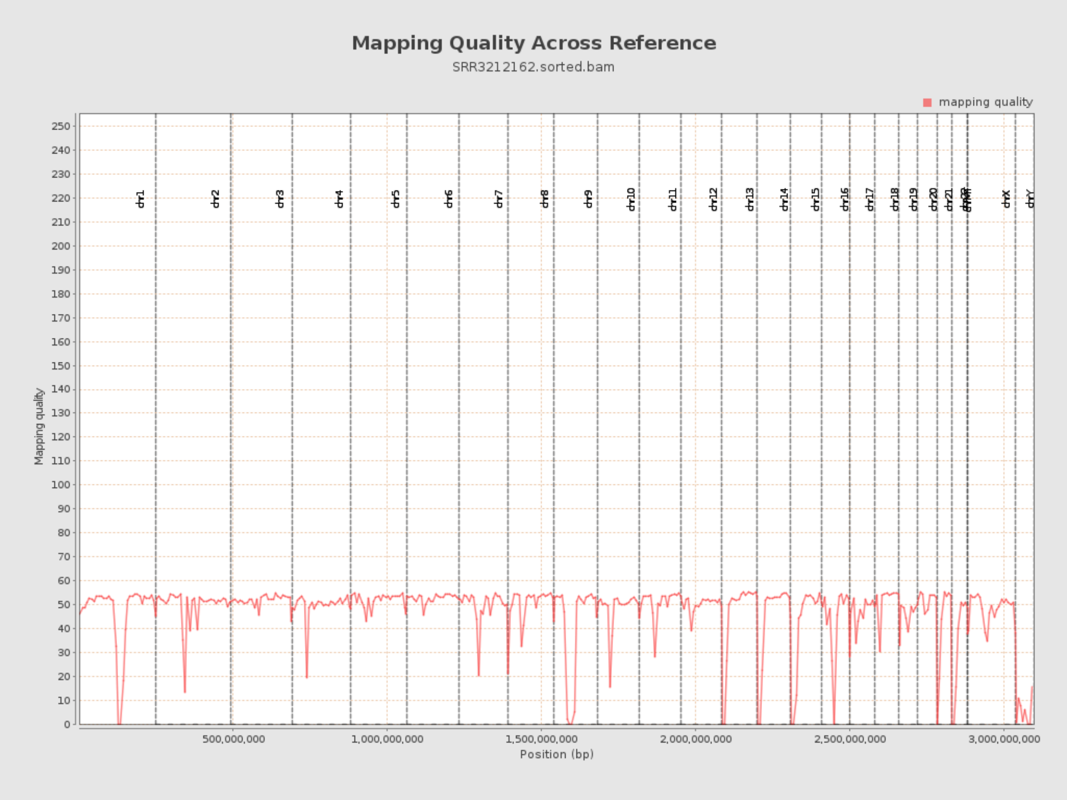
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram