Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 06:34:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3212164.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_SRR3212164 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3212164.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 06:34:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3212164.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,462,974
Mapped reads	3,924,340 / 87.93%
Unmapped reads	538,634 / 12.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,017 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	172,579 / 3.87%
Duplication rate	3.13%
Clipped reads	1,493,169 / 33.46%

2.2. ACGT Content

Number/percentage of A's	74,774,861 / 27.9%
Number/percentage of C's	49,386,524 / 18.43%
Number/percentage of T's	85,215,548 / 31.8%
Number/percentage of G's	58,532,922 / 21.84%
Number/percentage of N's	72,196 / 0.03%
GC Percentage	40.27%

2.3. Coverage

Mean	0.0866

Standard Deviation	0.7203

2.4. Mapping Quality

Mean Mapping Quality	46.37

2.5. Mismatches and indels

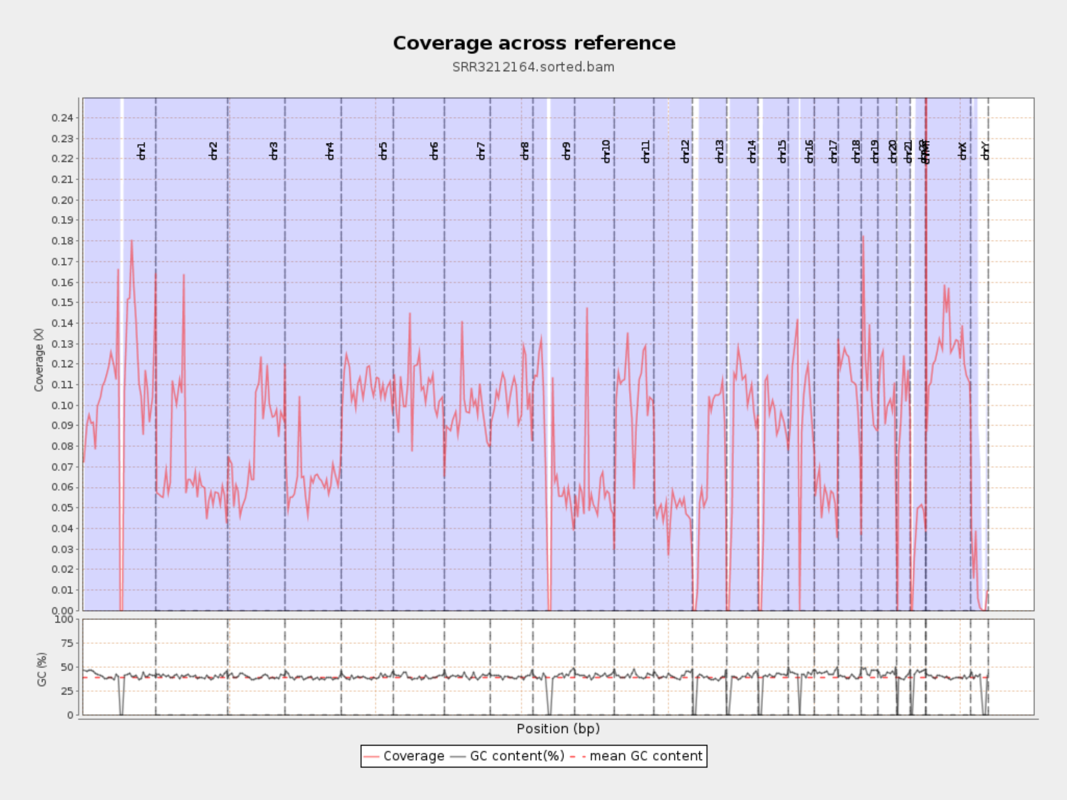
General error rate	0.89%
Mismatches	2,344,762
Insertions	22,527
Mapped reads with at least one insertion	0.57%
Deletions	71,557
Mapped reads with at least one deletion	1.8%
Homopolymer indels	49.34%

2.6. Chromosome stats

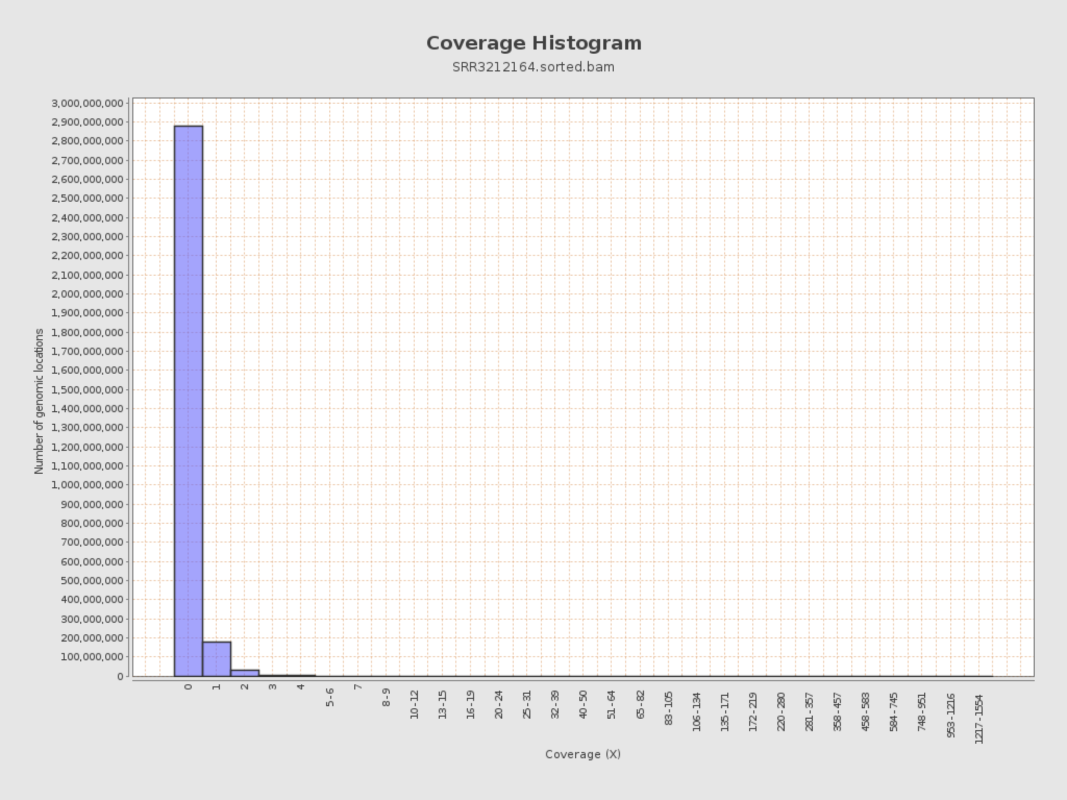
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26986123	0.1083	1.4594
chr2	243199373	16822328	0.0692	0.7699
chr3	198022430	16204864	0.0818	0.3475
chr4	191154276	12117033	0.0634	0.3478
chr5	180915260	19769653	0.1093	0.3958
chr6	171115067	18347835	0.1072	0.5191
chr7	159138663	15270711	0.096	0.7778

chr8	146364022	15403379	0.1052	1.0074
chr9	141213431	10098608	0.0715	0.6865
chr10	135534747	8068414	0.0595	0.7595
chr11	135006516	14273267	0.1057	0.7982
chr12	133851895	6430580	0.048	0.2806
chr13	115169878	8261726	0.0717	0.3125
chr14	107349540	9805638	0.0913	0.4147
chr15	102531392	8020539	0.0782	0.3282
chr16	90354753	8811231	0.0975	0.4365
chr17	81195210	4521538	0.0557	0.4125
chr18	78077248	8935037	0.1144	1.2021
chr19	59128983	6732026	0.1139	1.1169
chr20	63025520	6637003	0.1053	0.411
chr21	48129895	4425821	0.092	0.4313
chr22	51304566	1827713	0.0356	0.2174
chrMT	16571	8894	0.5367	0.8664
chrX	155270560	19573844	0.1261	0.4882
chrY	59373566	748400	0.0126	0.2641

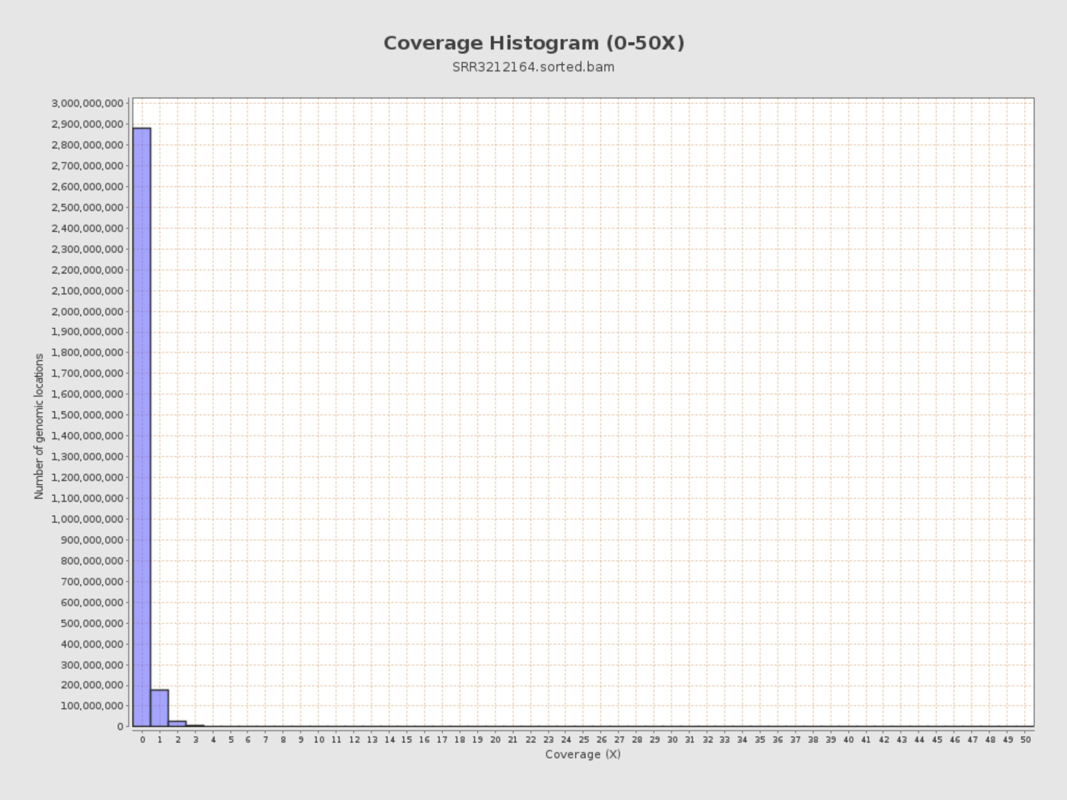
3. Results : Coverage across reference



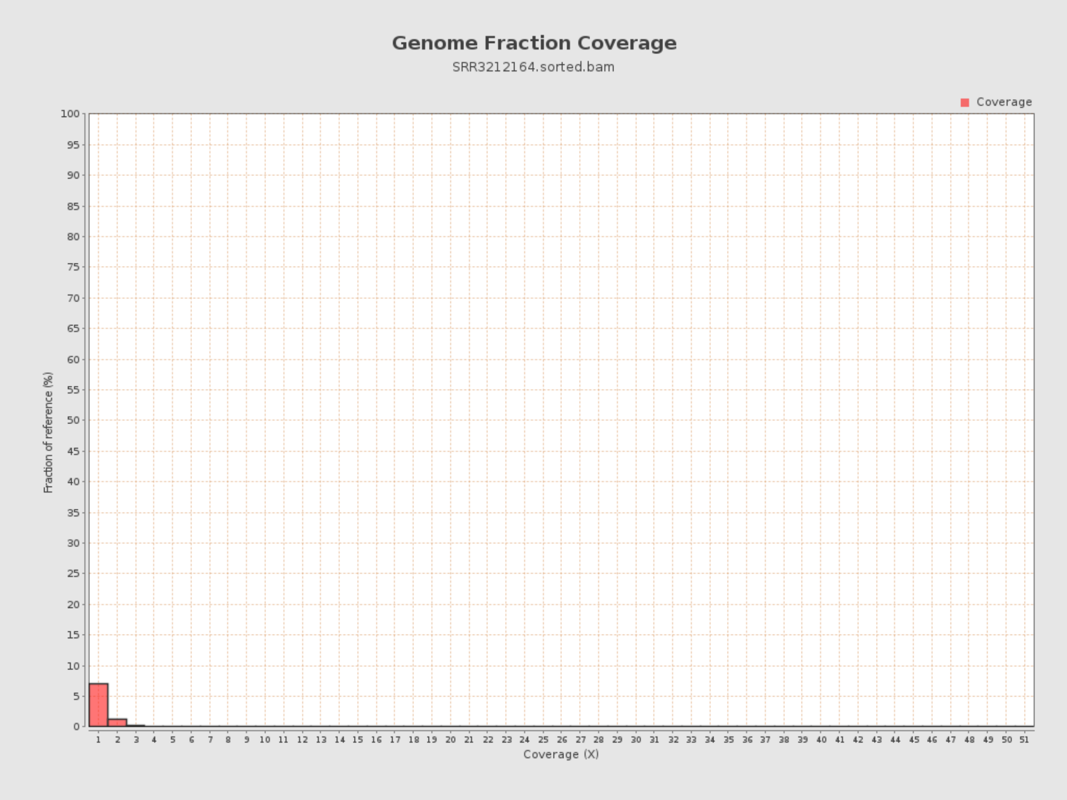
4. Results : Coverage Histogram



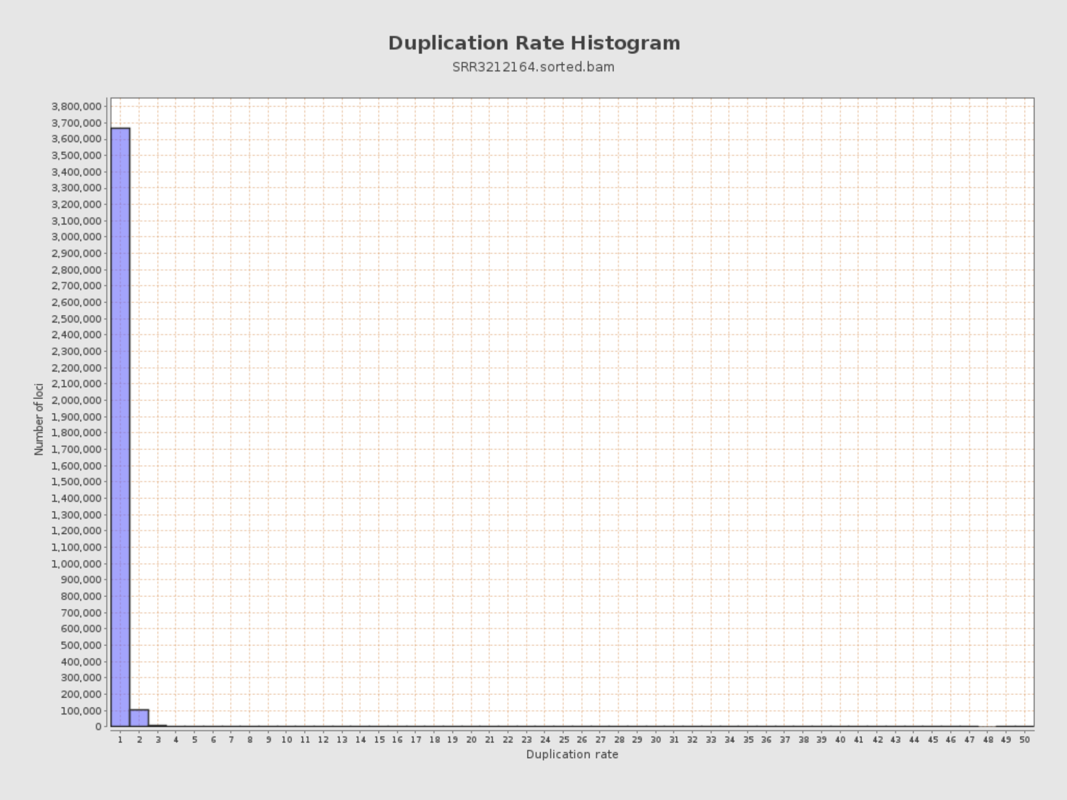
5. Results : Coverage Histogram (0-50X)



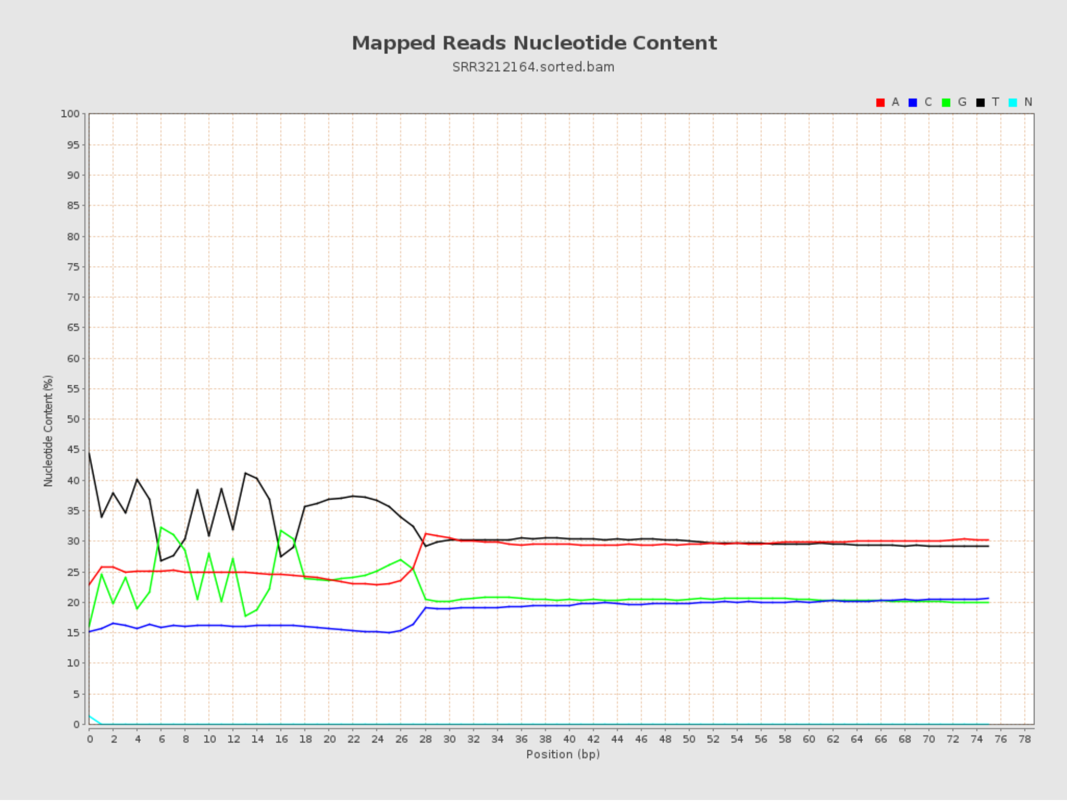
6. Results : Genome Fraction Coverage



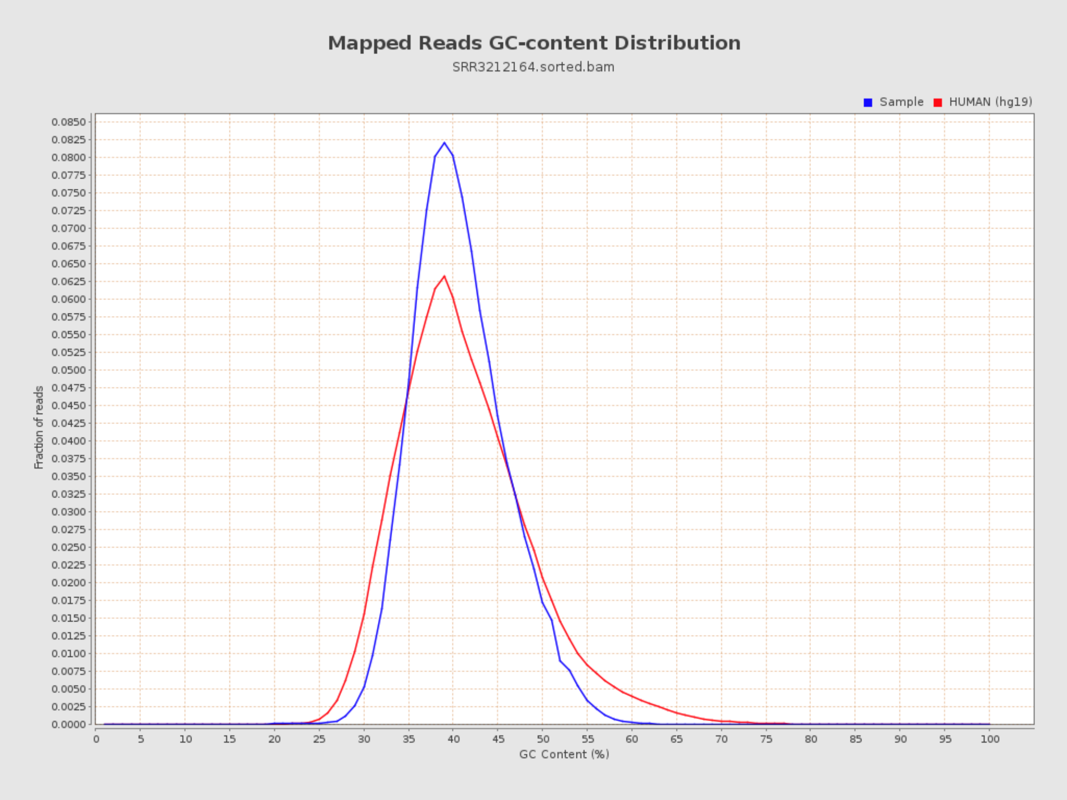
7. Results : Duplication Rate Histogram



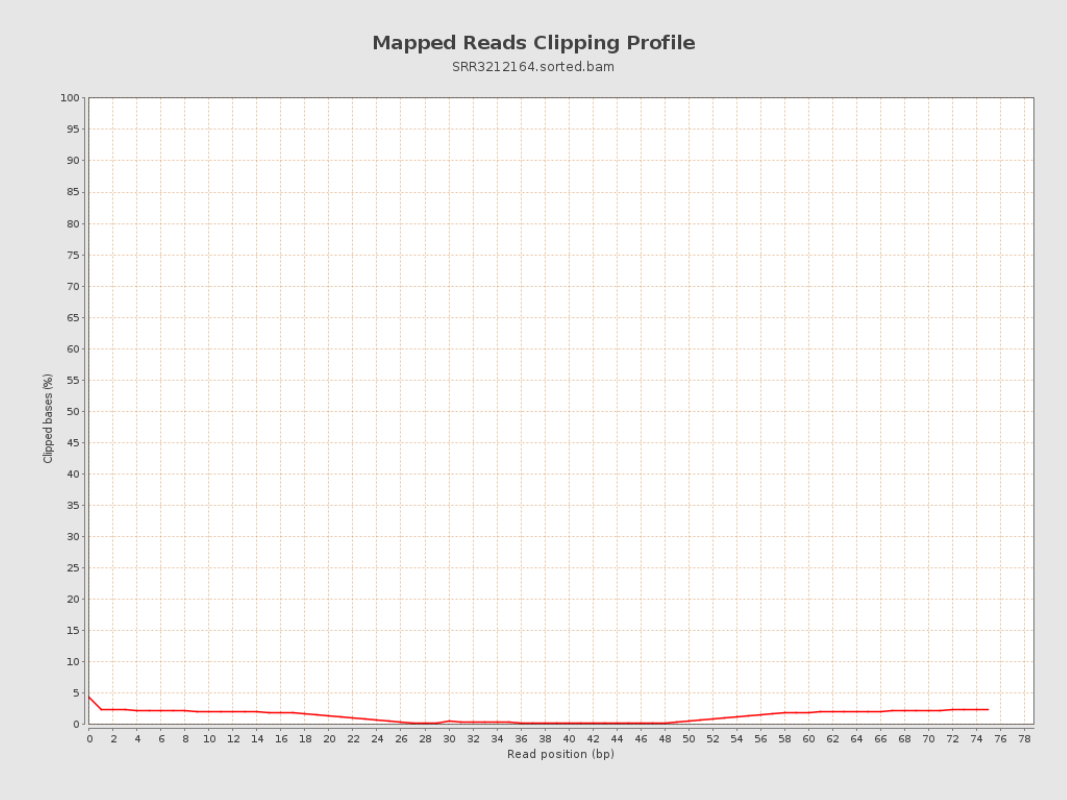
8. Results : Mapped Reads Nucleotide Content



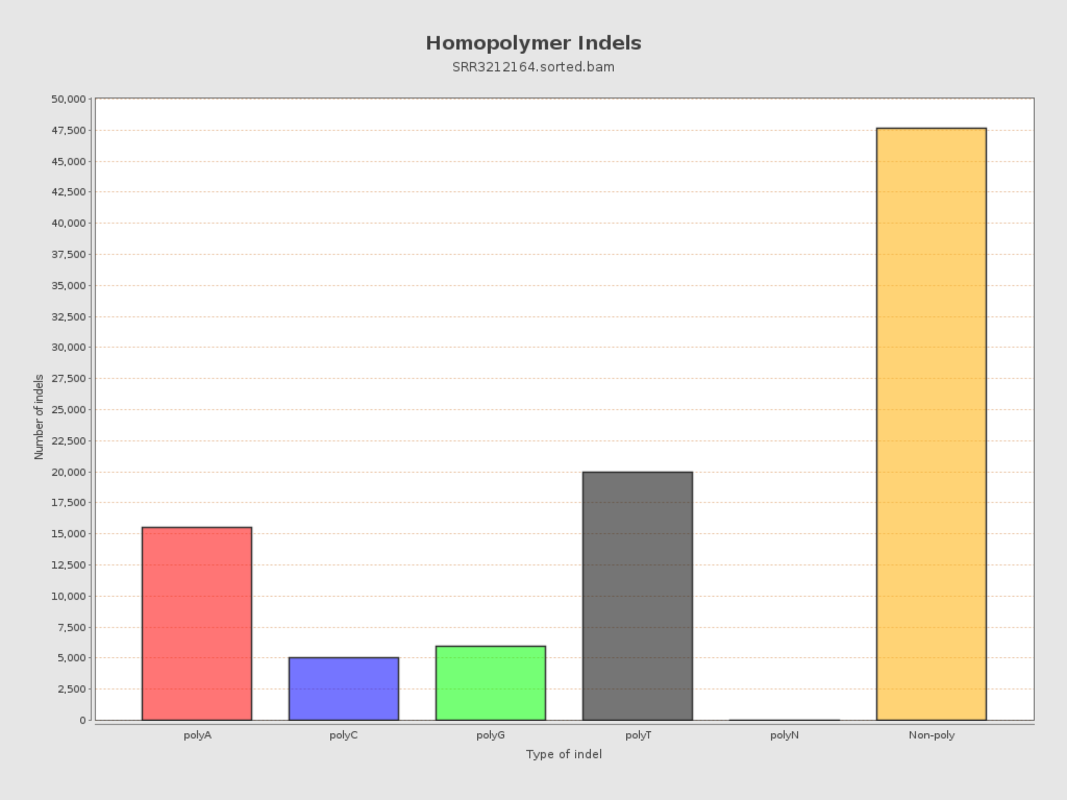
9. Results : Mapped Reads GC-content Distribution



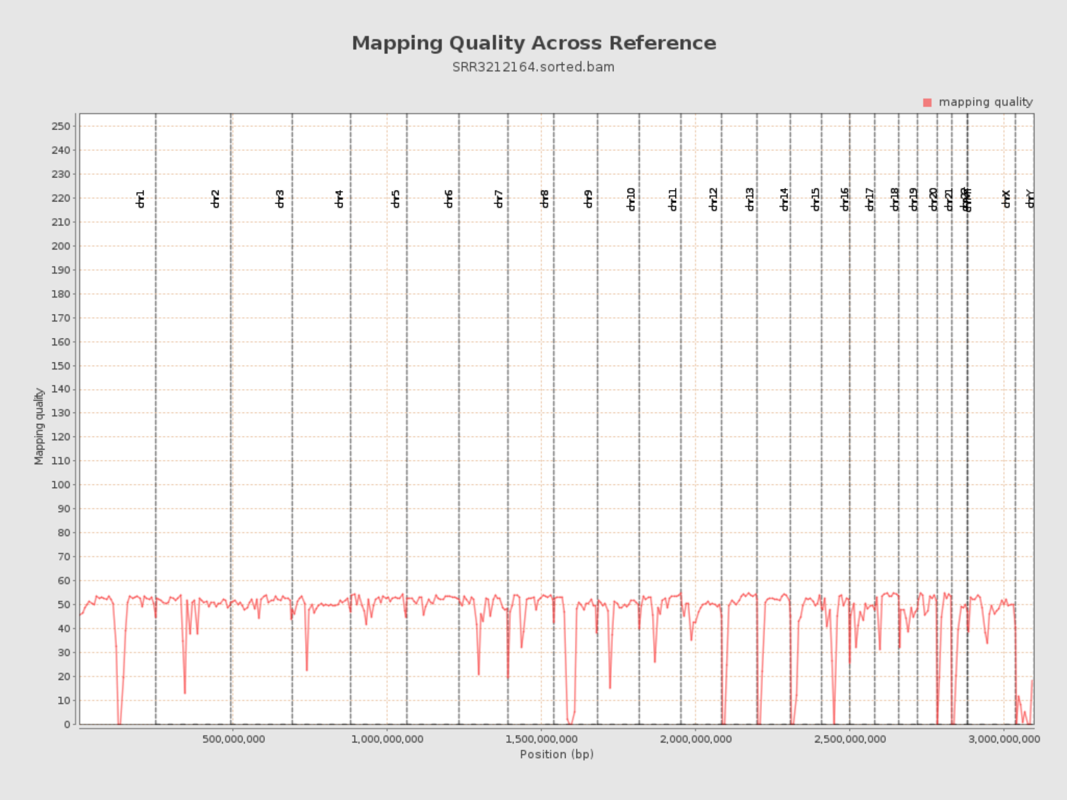
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram