Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 14:21:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082422.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_SRR3082422 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082422.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 14:21:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082422.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,112,561
Mapped reads	2,757,139 / 88.58%
Unmapped reads	355,422 / 11.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,713 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	121,170 / 3.89%
Duplication rate	3.33%
Clipped reads	1,207,837 / 38.81%

2.2. ACGT Content

Number/percentage of A's	51,882,849 / 27.98%
Number/percentage of C's	34,432,422 / 18.57%
Number/percentage of T's	58,328,051 / 31.46%
Number/percentage of G's	40,784,974 / 21.99%
Number/percentage of N's	3,815 / 0%
GC Percentage	40.56%

2.3. Coverage

Mean	0.0599

Standard Deviation	0.5012

2.4. Mapping Quality

Mean Mapping Quality	46.43

2.5. Mismatches and indels

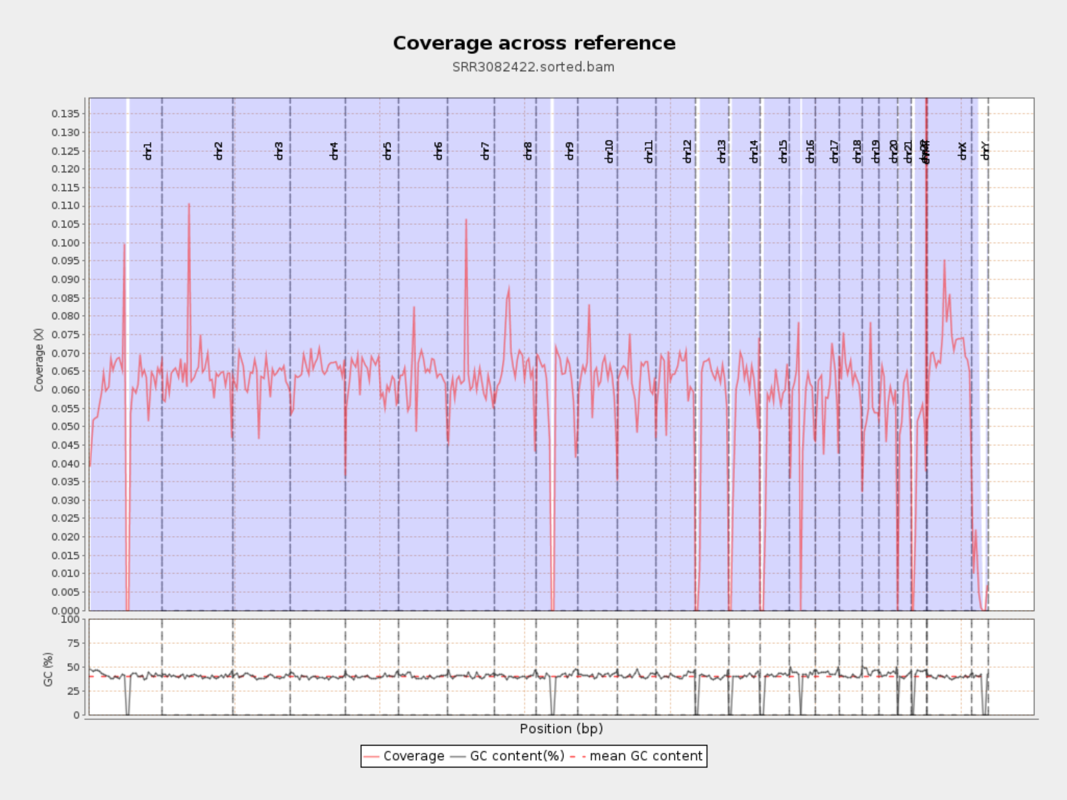
General error rate	0.85%
Mismatches	1,553,306
Insertions	14,817
Mapped reads with at least one insertion	0.53%
Deletions	40,725
Mapped reads with at least one deletion	1.46%
Homopolymer indels	47.79%

2.6. Chromosome stats

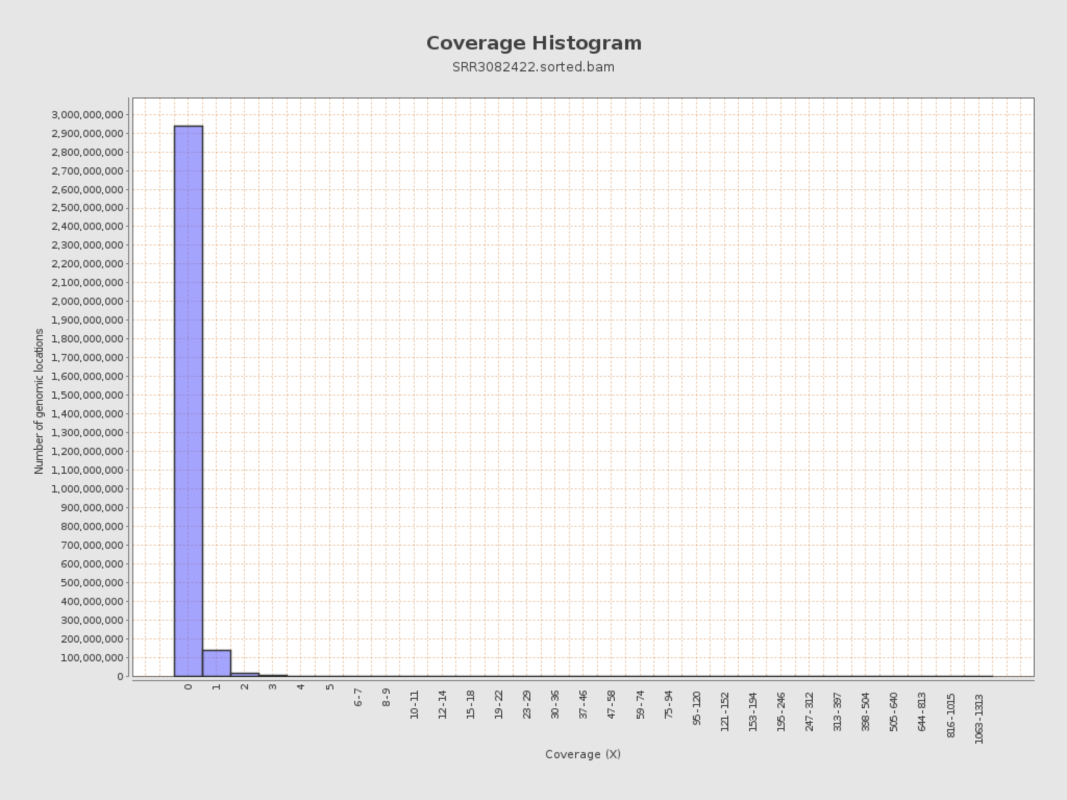
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14568201	0.0584	0.8764
chr2	243199373	15846060	0.0652	0.6339
chr3	198022430	12586771	0.0636	0.2847
chr4	191154276	12521182	0.0655	0.3015
chr5	180915260	11450129	0.0633	0.2883
chr6	171115067	10985122	0.0642	0.3662
chr7	159138663	10043643	0.0631	0.6874

chr8	146364022	9757186	0.0667	0.8578
chr9	141213431	7969808	0.0564	0.4385
chr10	135534747	8681976	0.0641	0.4118
chr11	135006516	8466962	0.0627	0.4198
chr12	133851895	8485541	0.0634	0.2922
chr13	115169878	6150690	0.0534	0.2627
chr14	107349540	5629157	0.0524	0.2775
chr15	102531392	4995727	0.0487	0.2594
chr16	90354753	4862140	0.0538	0.2936
chr17	81195210	4740370	0.0584	0.3081
chr18	78077248	5065824	0.0649	0.8154
chr19	59128983	3265961	0.0552	0.6781
chr20	63025520	3601142	0.0571	0.277
chr21	48129895	2409378	0.0501	0.2718
chr22	51304566	1861381	0.0363	0.2138
chrMT	16571	8950	0.5401	0.7866
chrX	155270560	11088967	0.0714	0.3466
chrY	59373566	455103	0.0077	0.1547

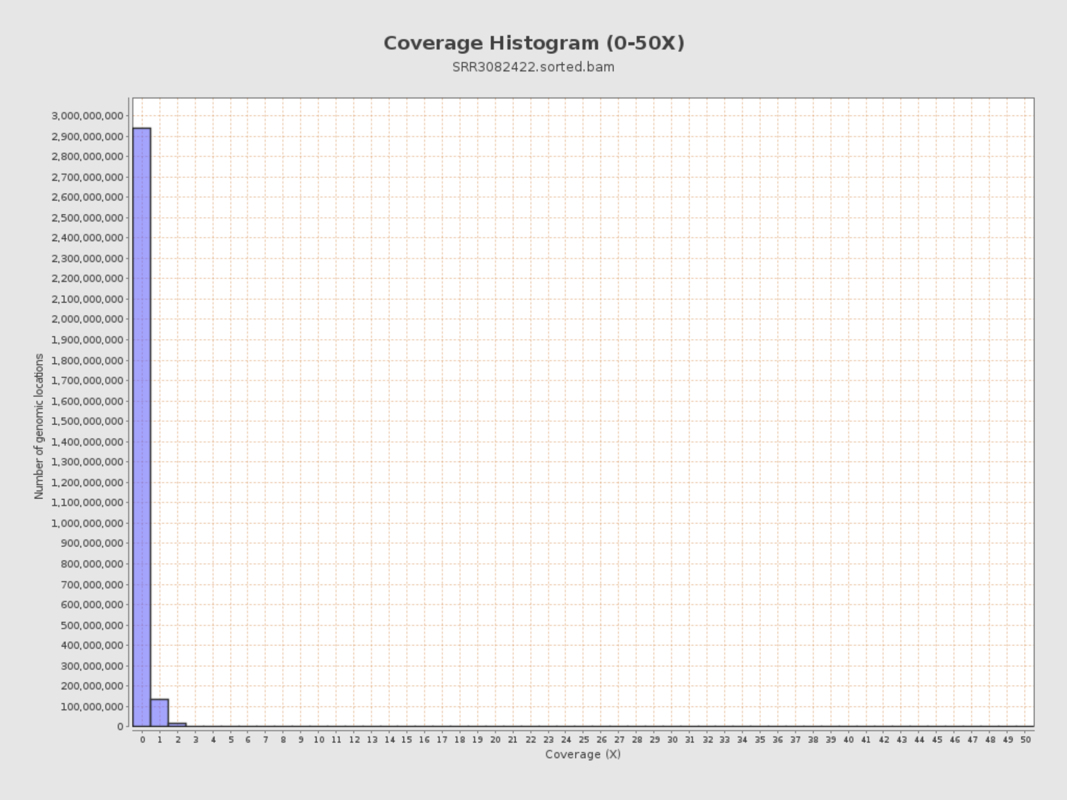
3. Results : Coverage across reference



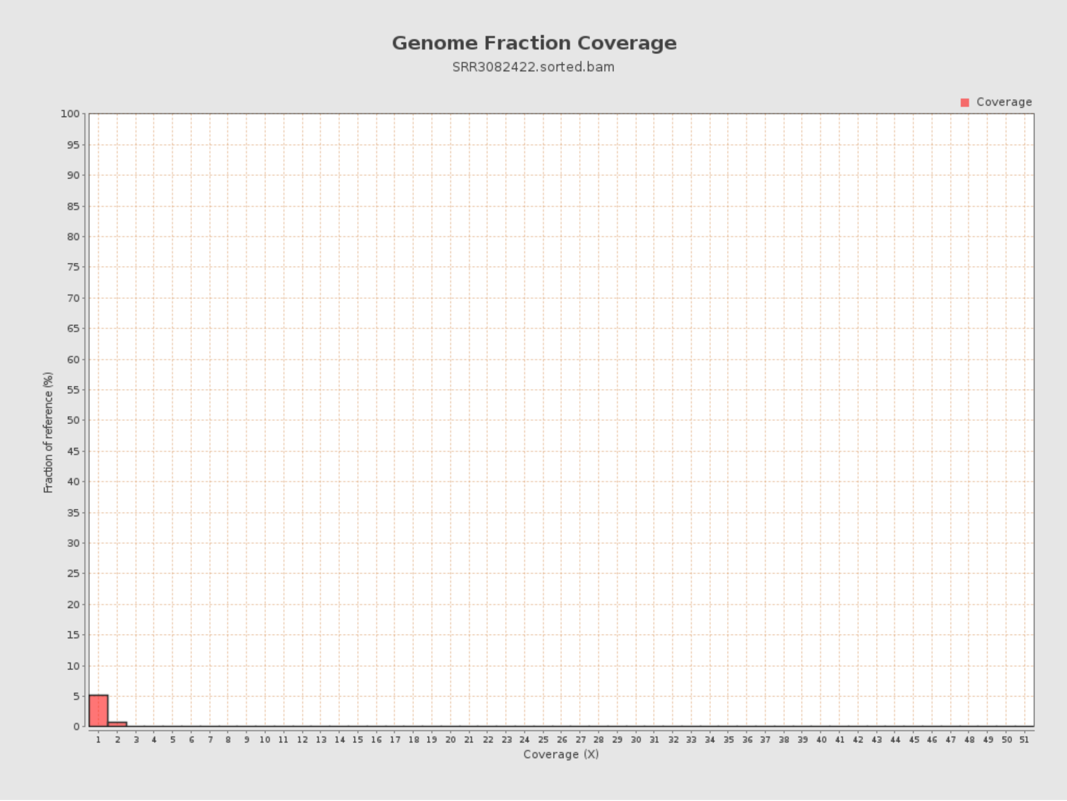
4. Results : Coverage Histogram



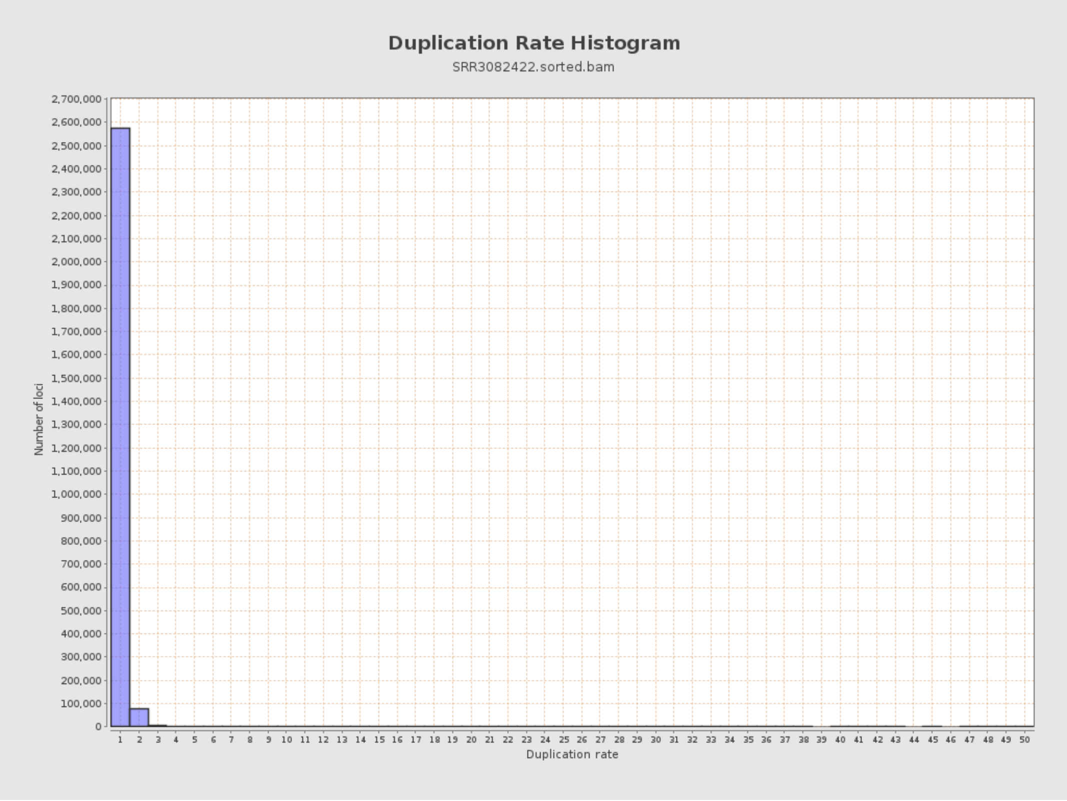
5. Results : Coverage Histogram (0-50X)



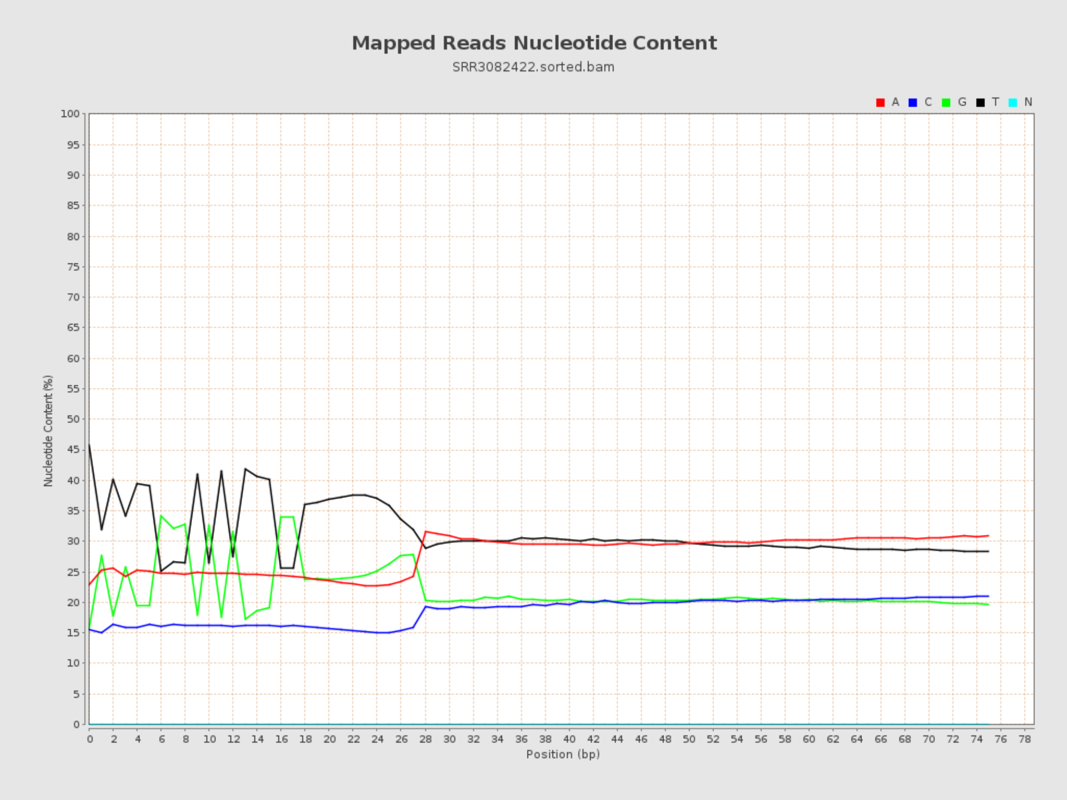
6. Results : Genome Fraction Coverage



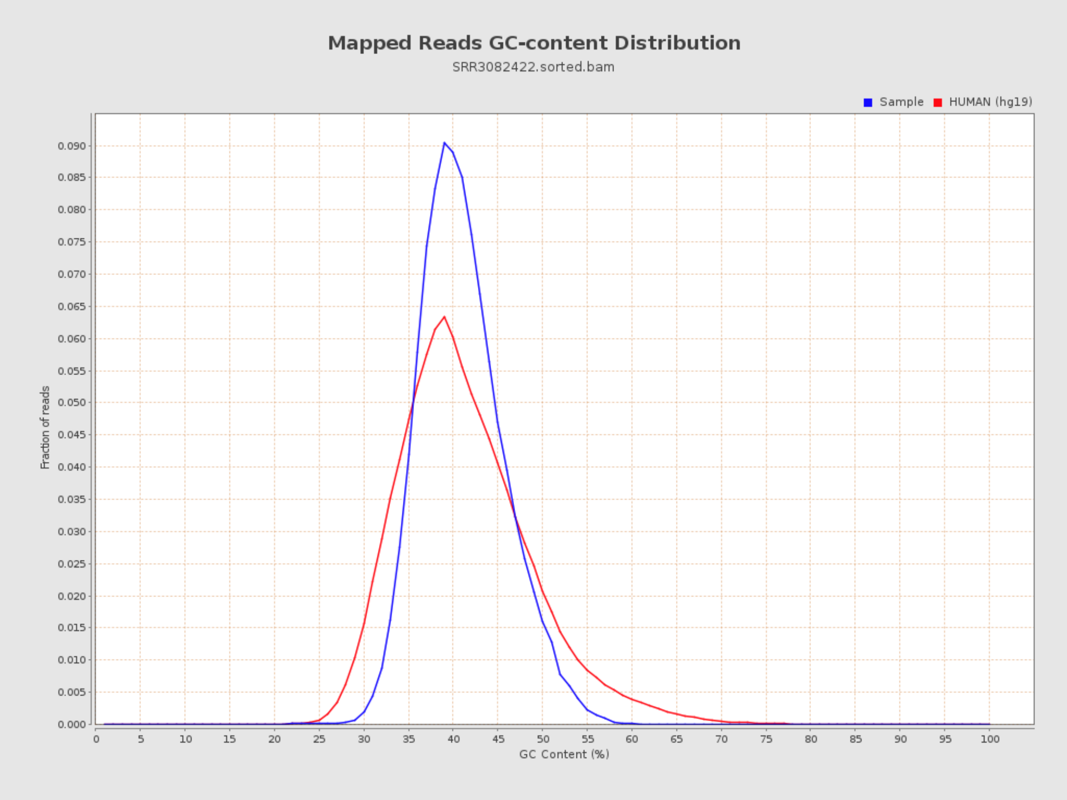
7. Results : Duplication Rate Histogram



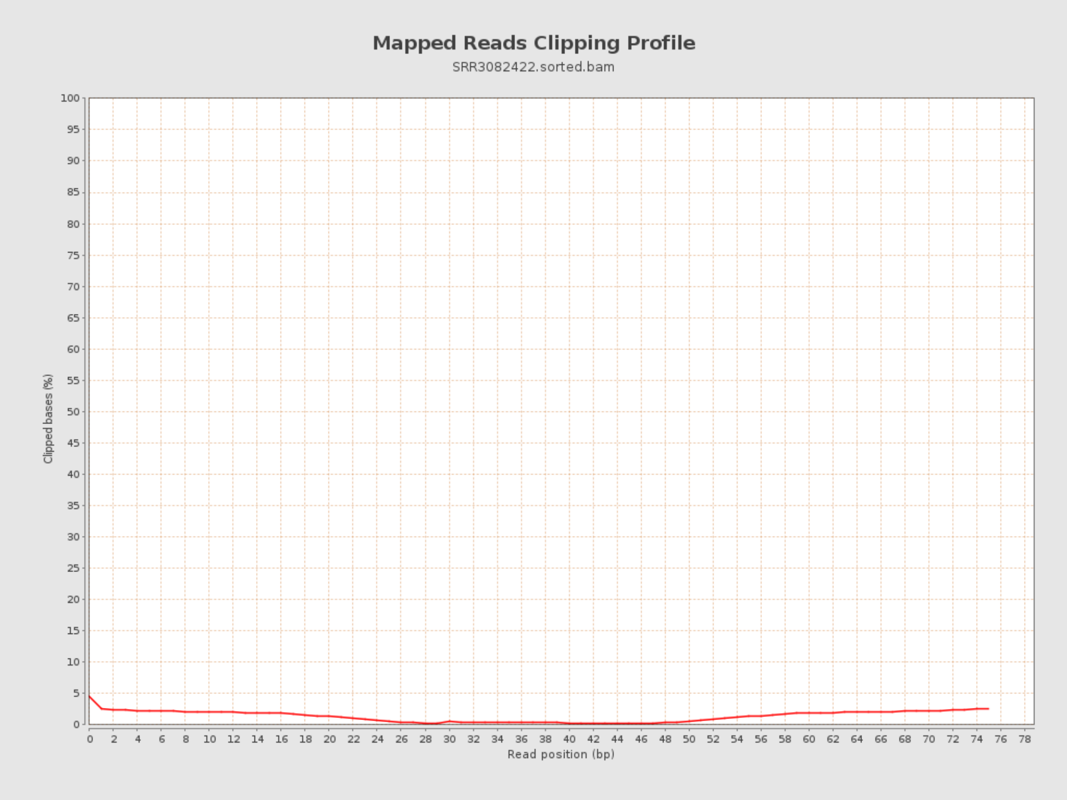
8. Results : Mapped Reads Nucleotide Content



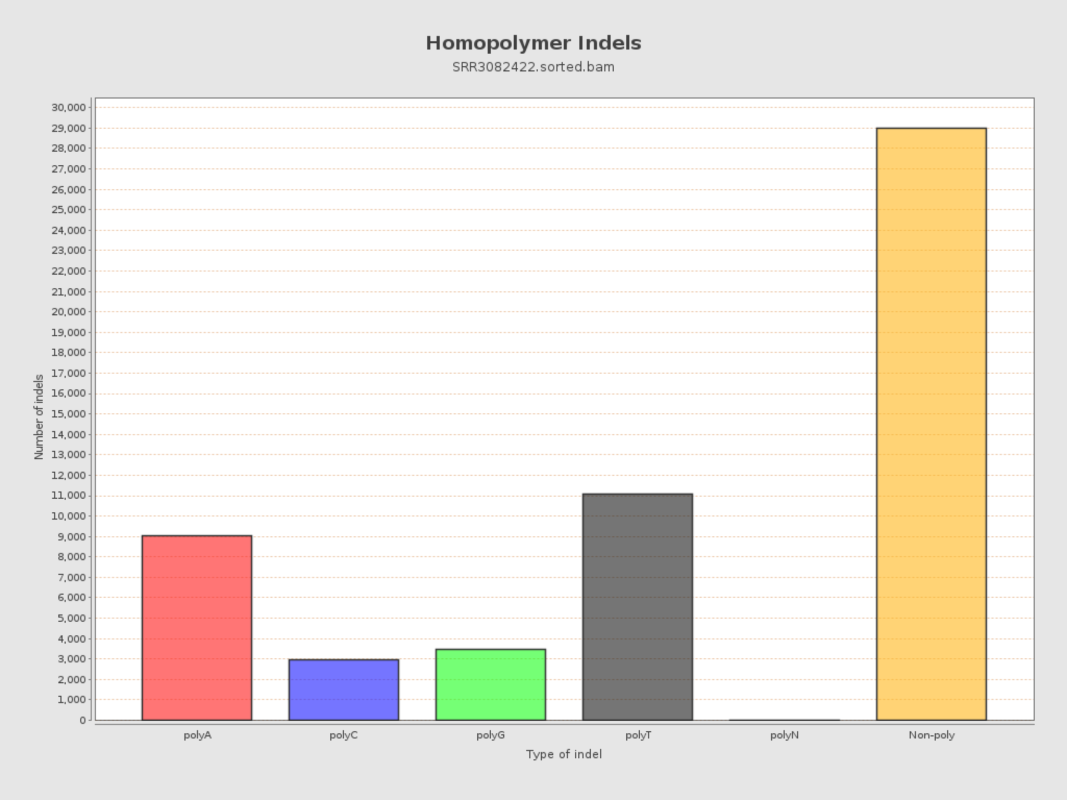
9. Results : Mapped Reads GC-content Distribution



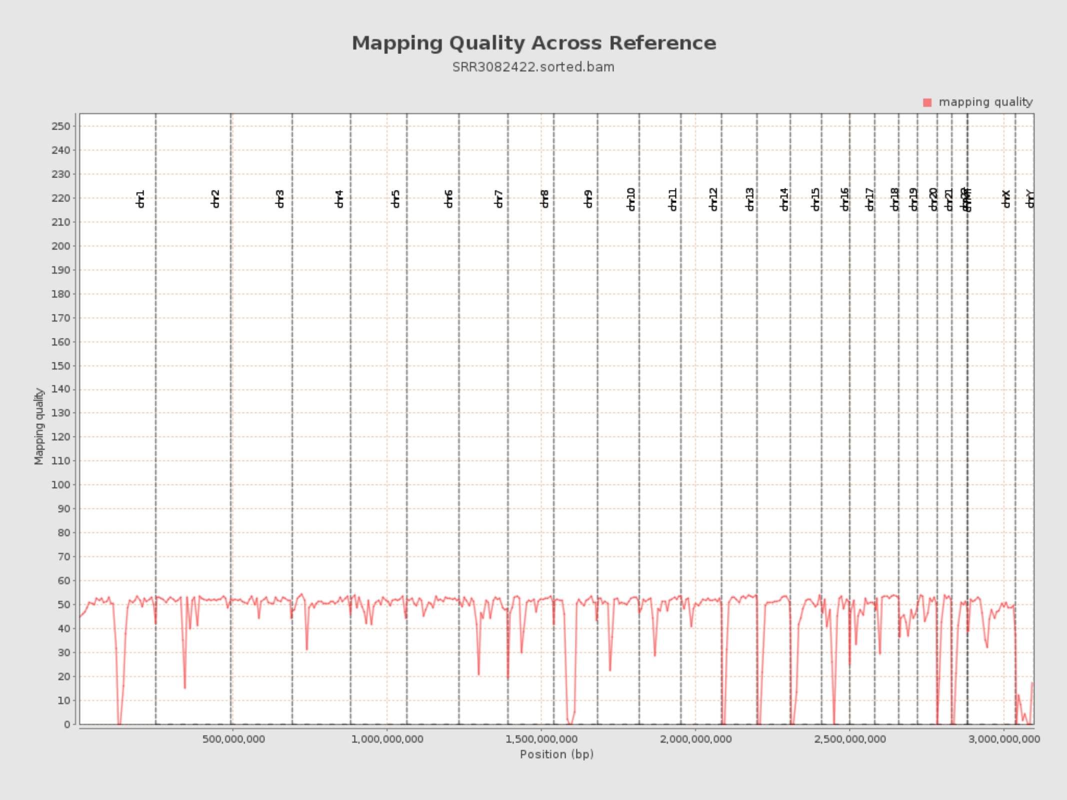
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram