Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 14:45:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082439.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_SRR3082439 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082439.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 14:45:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082439.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,139,269
Mapped reads	2,803,467 / 89.3%
Unmapped reads	335,802 / 10.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,185 / 0.93%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	112,401 / 3.58%
Duplication rate	3.21%
Clipped reads	1,189,399 / 37.89%

2.2. ACGT Content

Number/percentage of A's	53,649,091 / 28.29%
Number/percentage of C's	35,507,152 / 18.72%
Number/percentage of T's	59,396,993 / 31.32%
Number/percentage of G's	41,093,339 / 21.67%
Number/percentage of N's	4,071 / 0%
GC Percentage	40.39%

2.3. Coverage

Mean	0.0613

Standard Deviation	0.4302

2.4. Mapping Quality

Mean Mapping Quality	47

2.5. Mismatches and indels

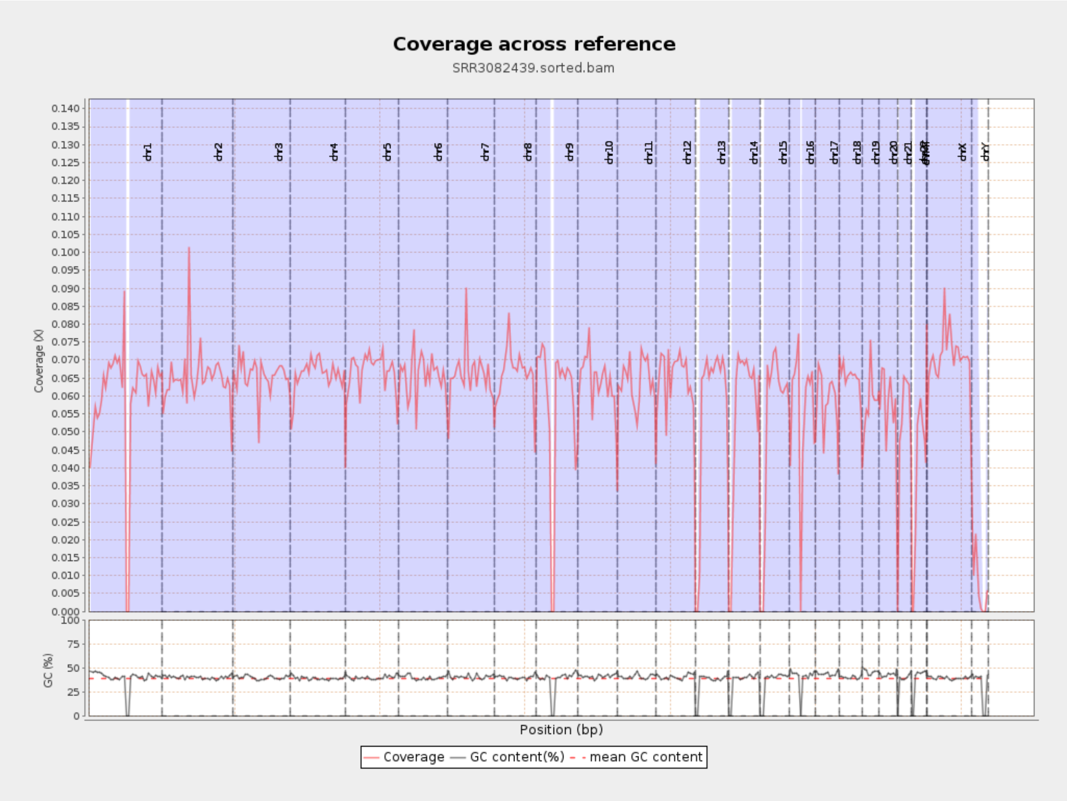
General error rate	0.83%
Mismatches	1,541,824
Insertions	14,660
Mapped reads with at least one insertion	0.52%
Deletions	40,653
Mapped reads with at least one deletion	1.44%
Homopolymer indels	47.58%

2.6. Chromosome stats

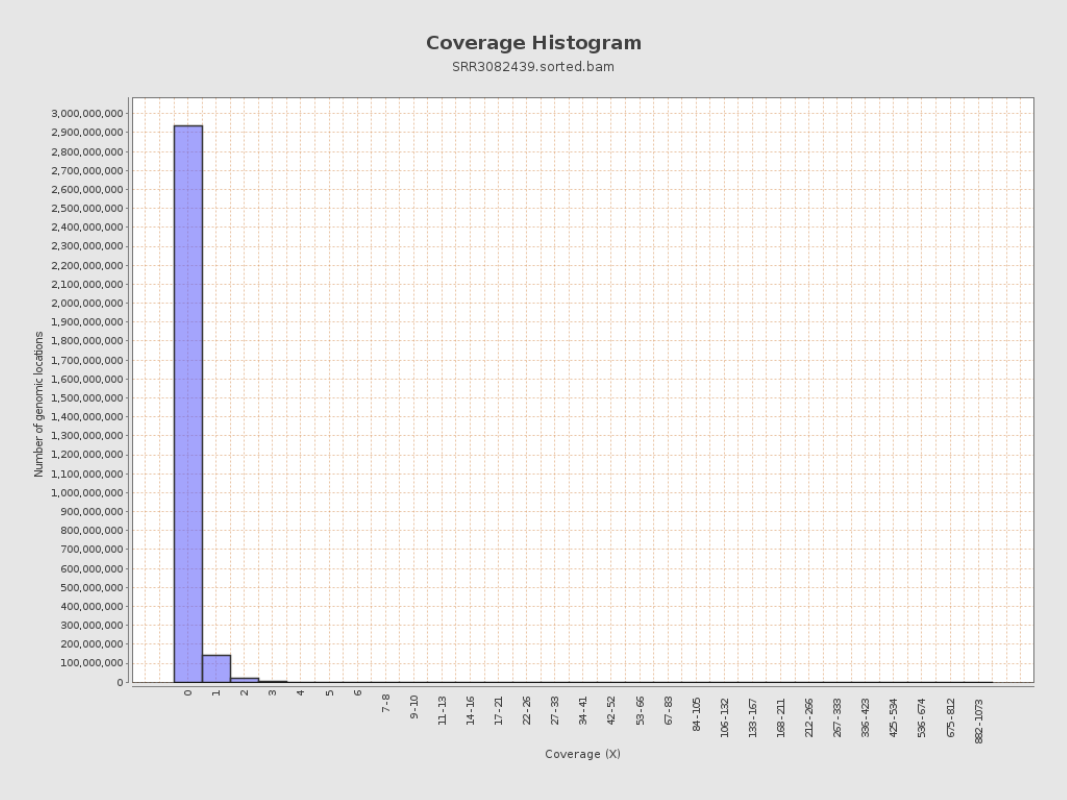
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14907683	0.0598	0.6862
chr2	243199373	15920444	0.0655	0.5464
chr3	198022430	13012900	0.0657	0.2905
chr4	191154276	12602299	0.0659	0.3002
chr5	180915260	12145683	0.0671	0.2958
chr6	171115067	11243615	0.0657	0.3426
chr7	159138663	10564754	0.0664	0.5216

chr8	146364022	9692820	0.0662	0.7196
chr9	141213431	8140895	0.0576	0.3984
chr10	135534747	8738952	0.0645	0.3841
chr11	135006516	8587042	0.0636	0.3749
chr12	133851895	8697709	0.065	0.2929
chr13	115169878	6392196	0.0555	0.2679
chr14	107349540	5864914	0.0546	0.2817
chr15	102531392	5434966	0.053	0.2671
chr16	90354753	5072527	0.0561	0.2914
chr17	81195210	4692188	0.0578	0.3011
chr18	78077248	5112918	0.0655	0.6734
chr19	59128983	3454550	0.0584	0.5323
chr20	63025520	3640447	0.0578	0.2786
chr21	48129895	2483096	0.0516	0.2712
chr22	51304566	1869433	0.0364	0.2153
chrMT	16571	1328	0.0801	0.2978
chrX	155270560	11006551	0.0709	0.337
chrY	59373566	436002	0.0073	0.1446

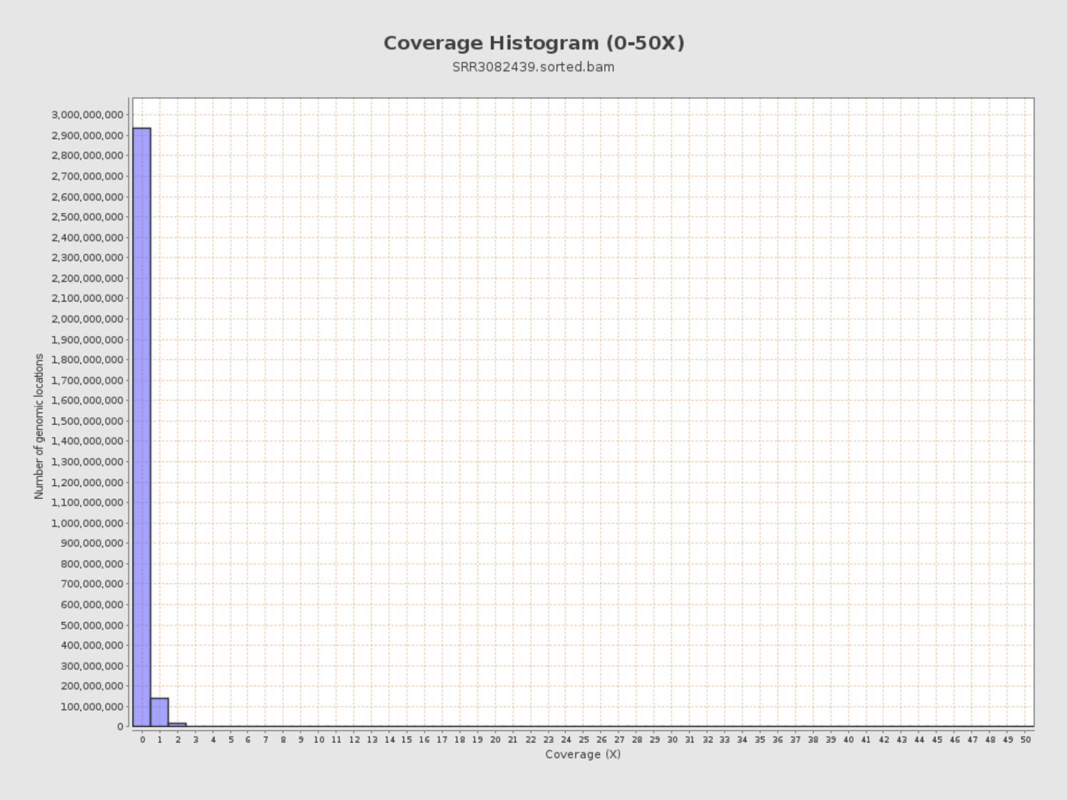
3. Results : Coverage across reference



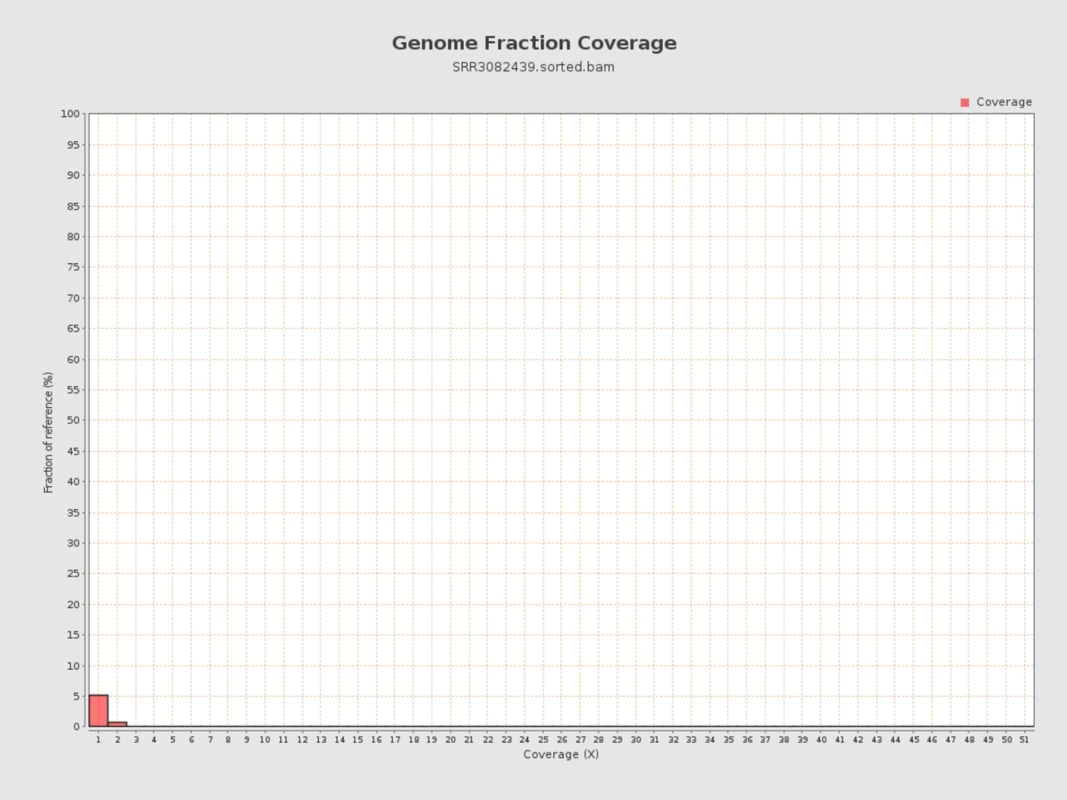
4. Results : Coverage Histogram



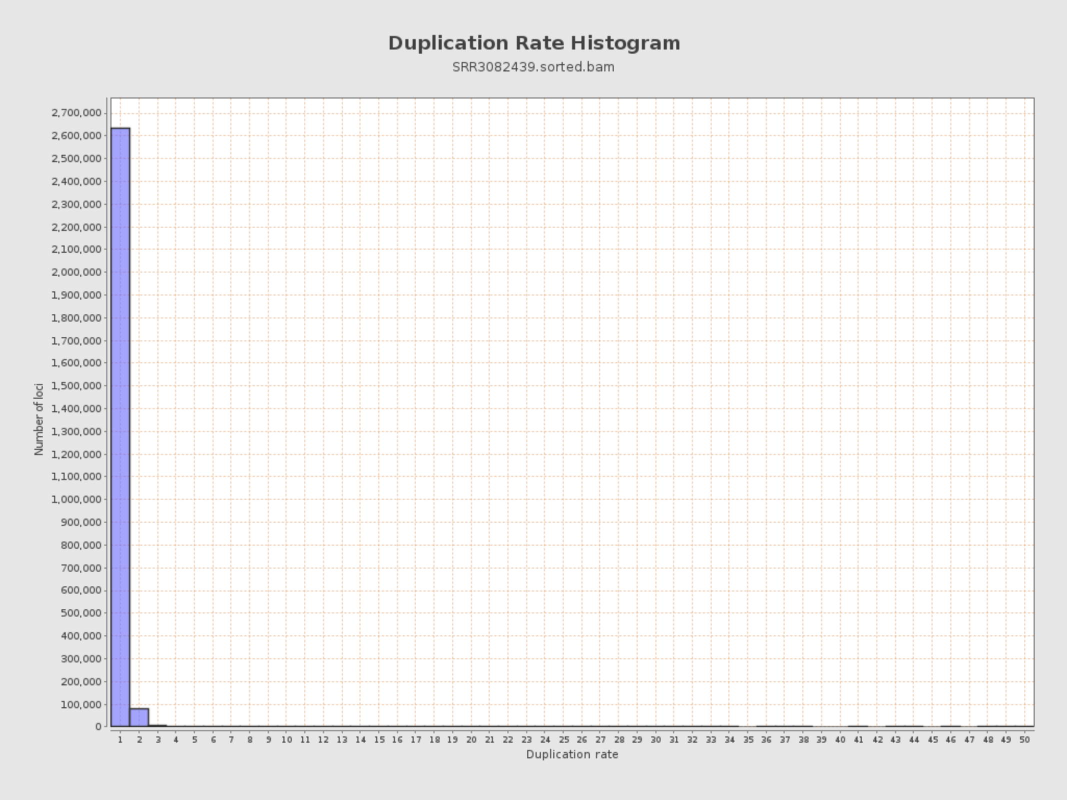
5. Results : Coverage Histogram (0-50X)



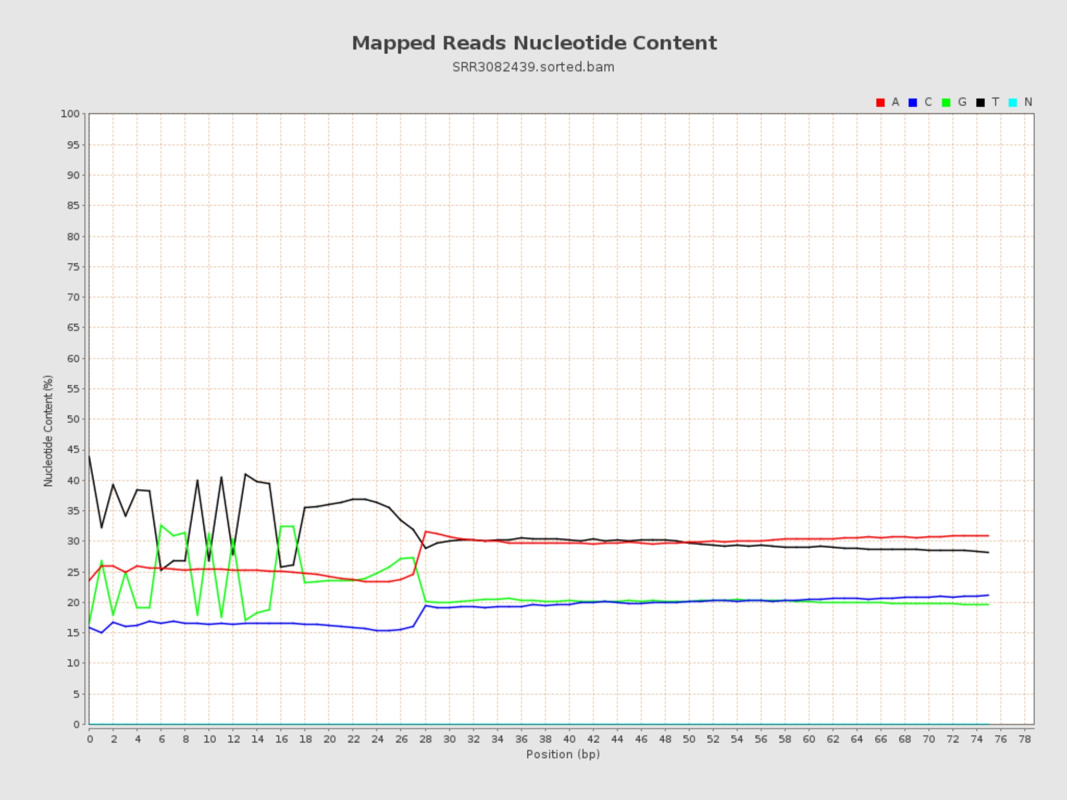
6. Results : Genome Fraction Coverage



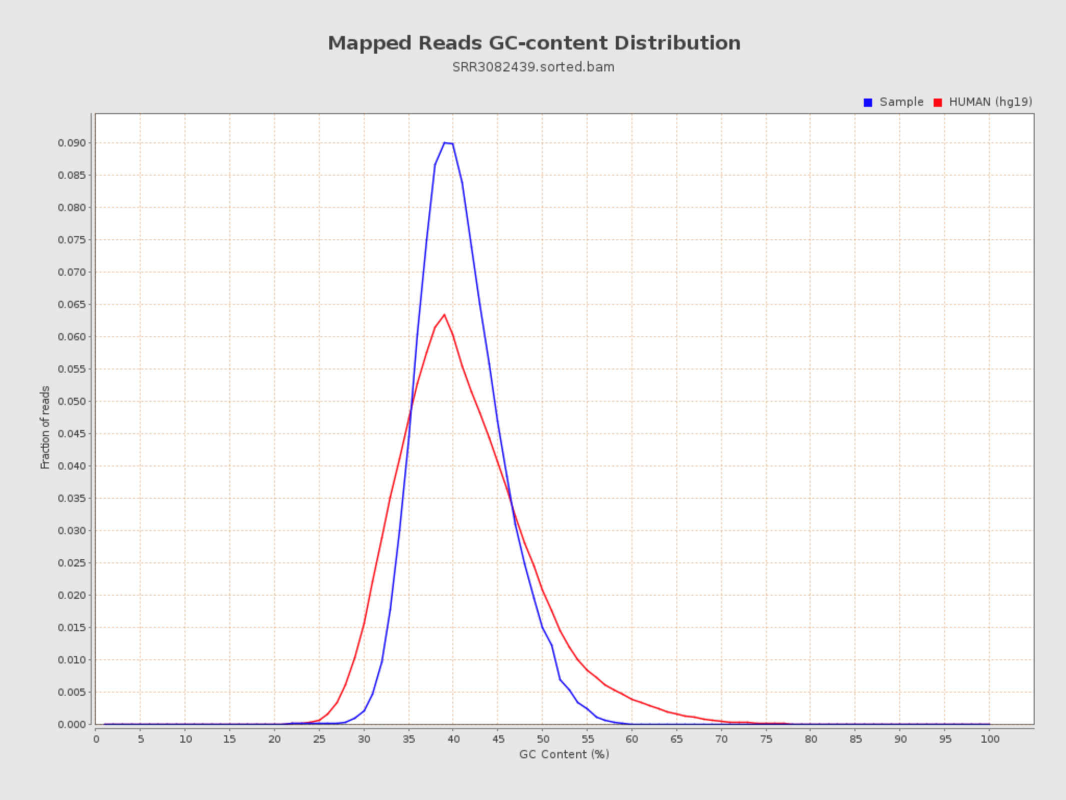
7. Results : Duplication Rate Histogram



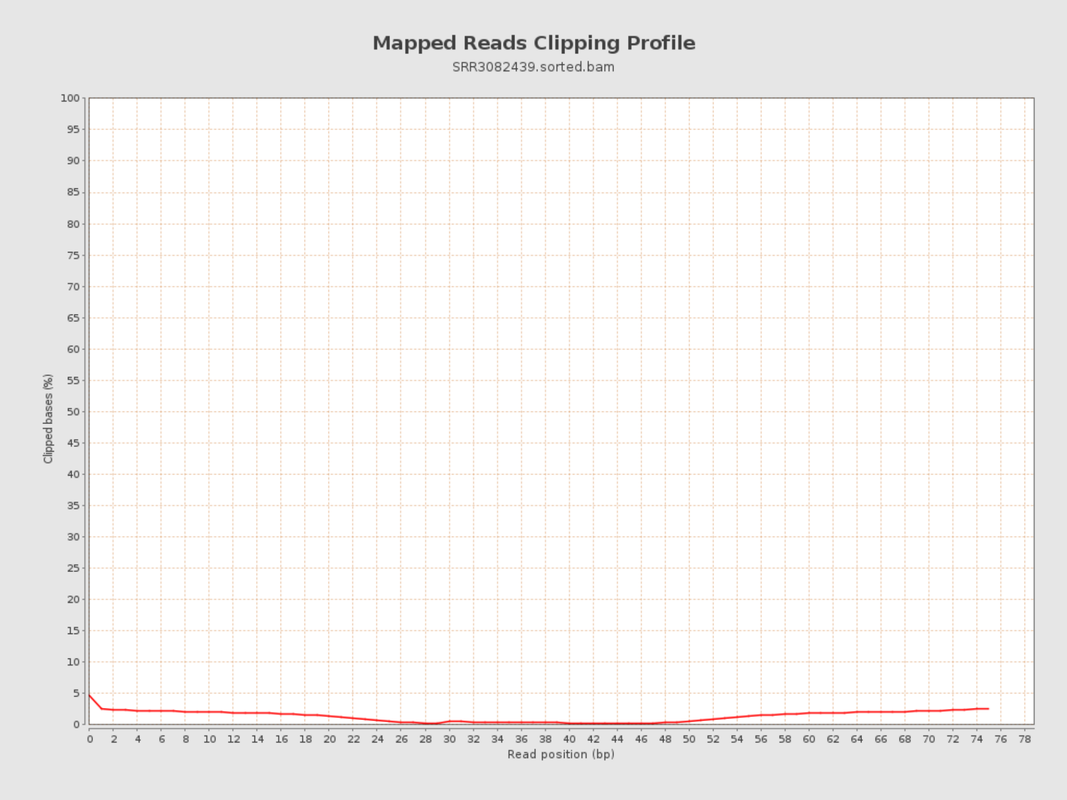
8. Results : Mapped Reads Nucleotide Content



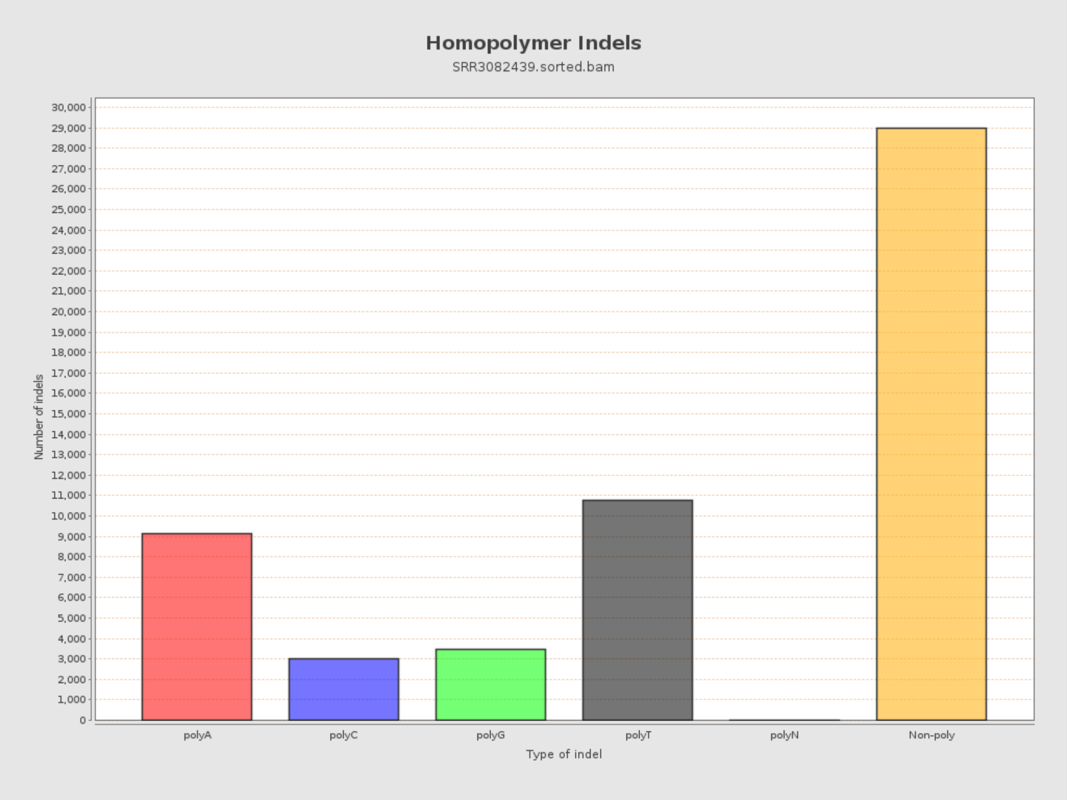
9. Results : Mapped Reads GC-content Distribution



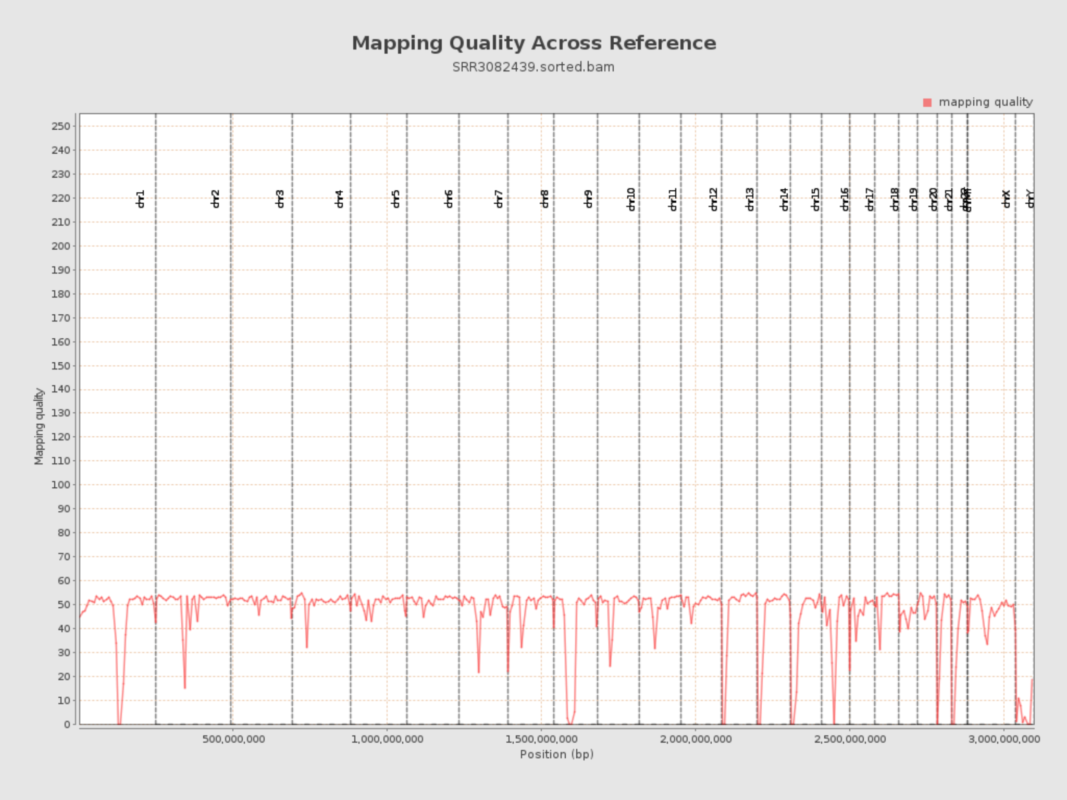
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram