Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 13:26:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082322.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_SRR3082322 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082322.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 13:26:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082322.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,006,277
Mapped reads	2,709,124 / 90.12%
Unmapped reads	297,153 / 9.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,858 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	116,837 / 3.89%
Duplication rate	3.23%
Clipped reads	1,146,926 / 38.15%

2.2. ACGT Content

Number/percentage of A's	52,141,030 / 28.44%
Number/percentage of C's	33,949,963 / 18.52%
Number/percentage of T's	57,656,050 / 31.45%
Number/percentage of G's	39,585,324 / 21.59%
Number/percentage of N's	3,847 / 0%
GC Percentage	40.11%

2.3. Coverage

Mean	0.0592

Standard Deviation	0.5207

2.4. Mapping Quality

Mean Mapping Quality	46.87

2.5. Mismatches and indels

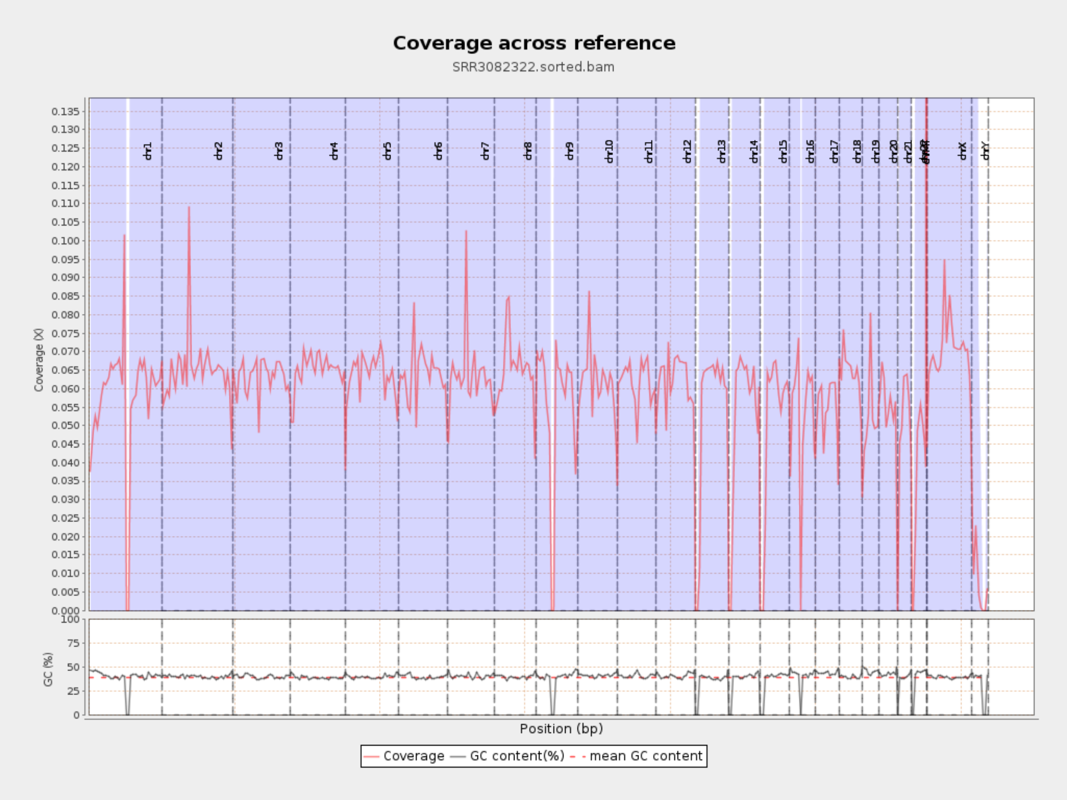
General error rate	0.85%
Mismatches	1,531,091
Insertions	14,596
Mapped reads with at least one insertion	0.53%
Deletions	40,170
Mapped reads with at least one deletion	1.47%
Homopolymer indels	47.76%

2.6. Chromosome stats

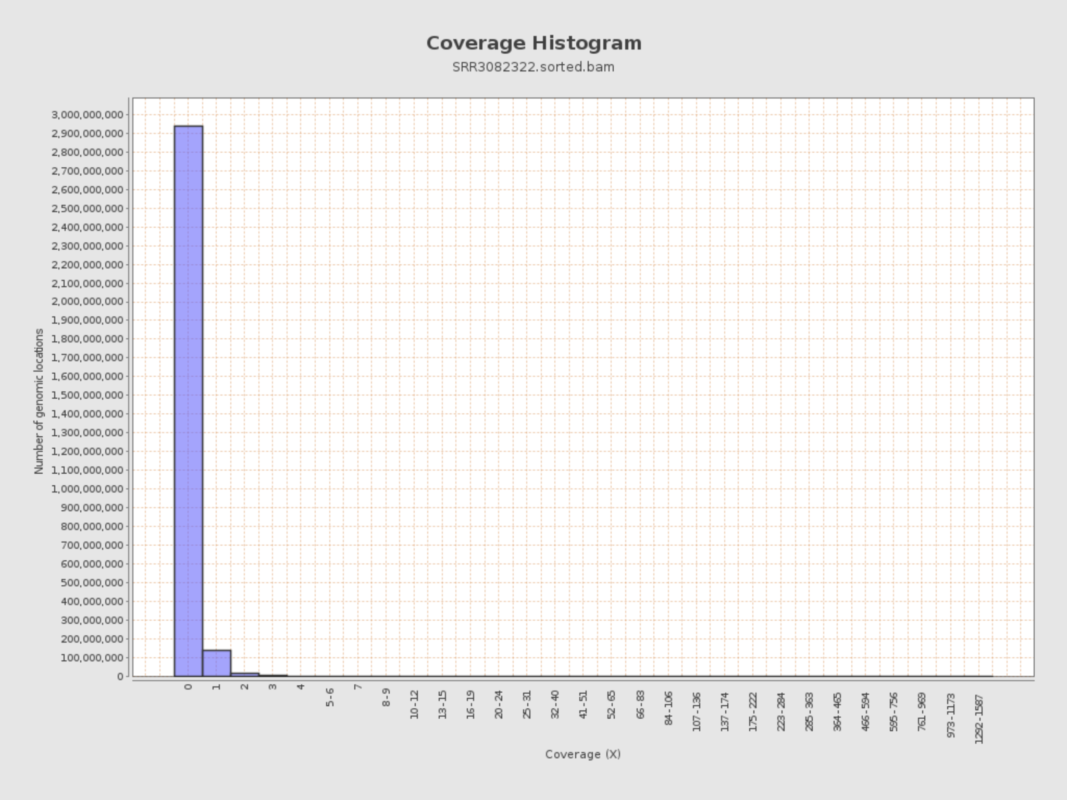
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14394627	0.0578	0.9473
chr2	243199373	15851713	0.0652	0.6005
chr3	198022430	12543814	0.0633	0.2839
chr4	191154276	12422045	0.065	0.3016
chr5	180915260	11592890	0.0641	0.2888
chr6	171115067	10935150	0.0639	0.3541
chr7	159138663	10200040	0.0641	0.6768

chr8	146364022	9473620	0.0647	0.9896
chr9	141213431	7729920	0.0547	0.4416
chr10	135534747	8437243	0.0623	0.4279
chr11	135006516	8276541	0.0613	0.4121
chr12	133851895	8324413	0.0622	0.2894
chr13	115169878	6106288	0.053	0.2592
chr14	107349540	5588550	0.0521	0.2792
chr15	102531392	5127859	0.05	0.2608
chr16	90354753	4799050	0.0531	0.2914
chr17	81195210	4394748	0.0541	0.3008
chr18	78077248	5070385	0.0649	0.8472
chr19	59128983	3102173	0.0525	0.7135
chr20	63025520	3509816	0.0557	0.2747
chr21	48129895	2365147	0.0491	0.2685
chr22	51304566	1782105	0.0347	0.2068
chrMT	16571	12308	0.7427	1.046
chrX	155270560	10921807	0.0703	0.3465
chrY	59373566	438427	0.0074	0.1632

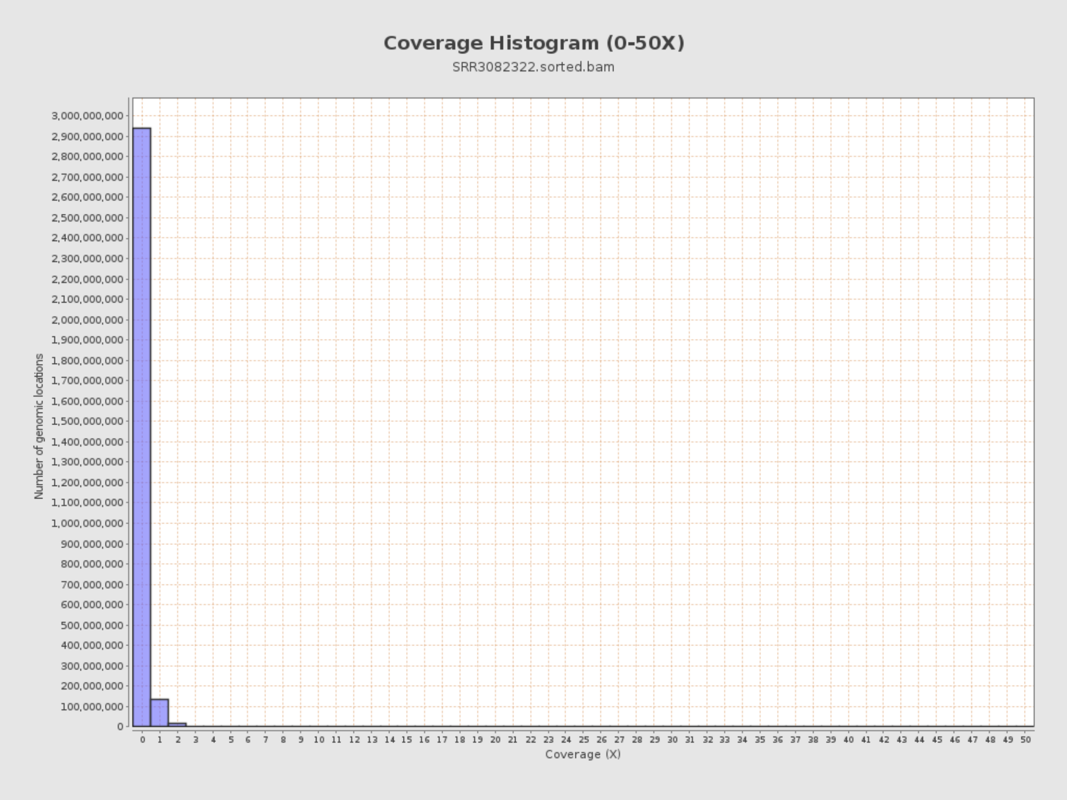
3. Results : Coverage across reference



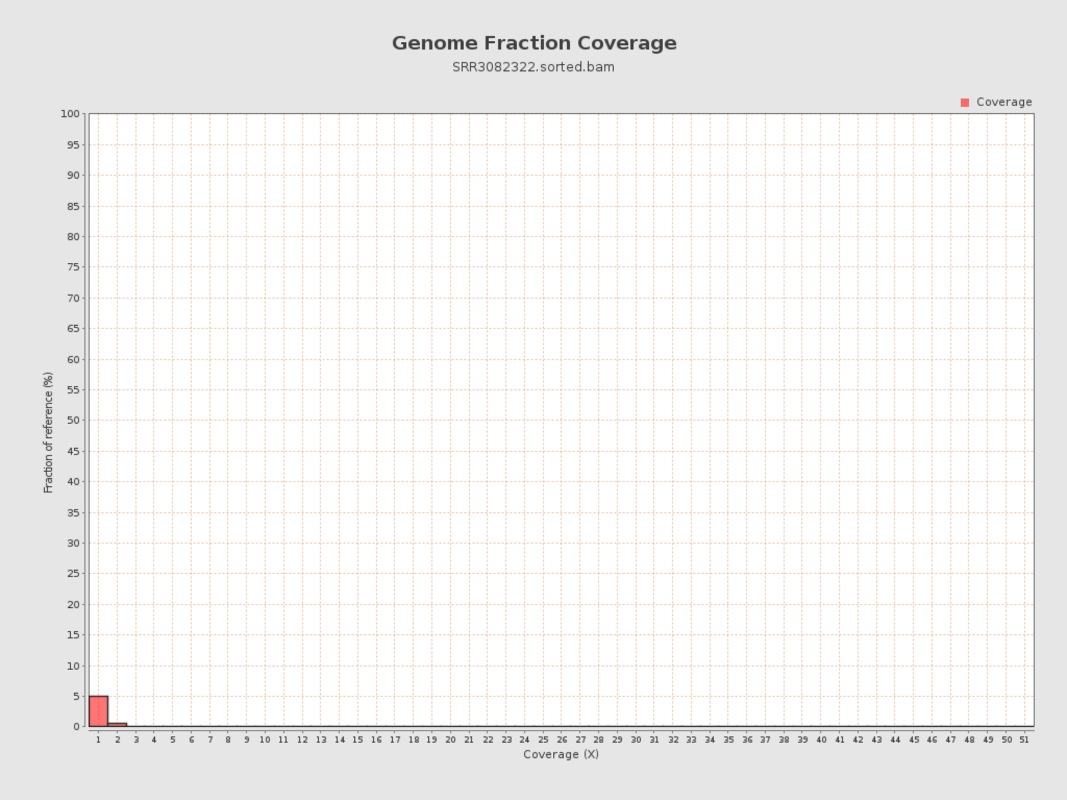
4. Results : Coverage Histogram



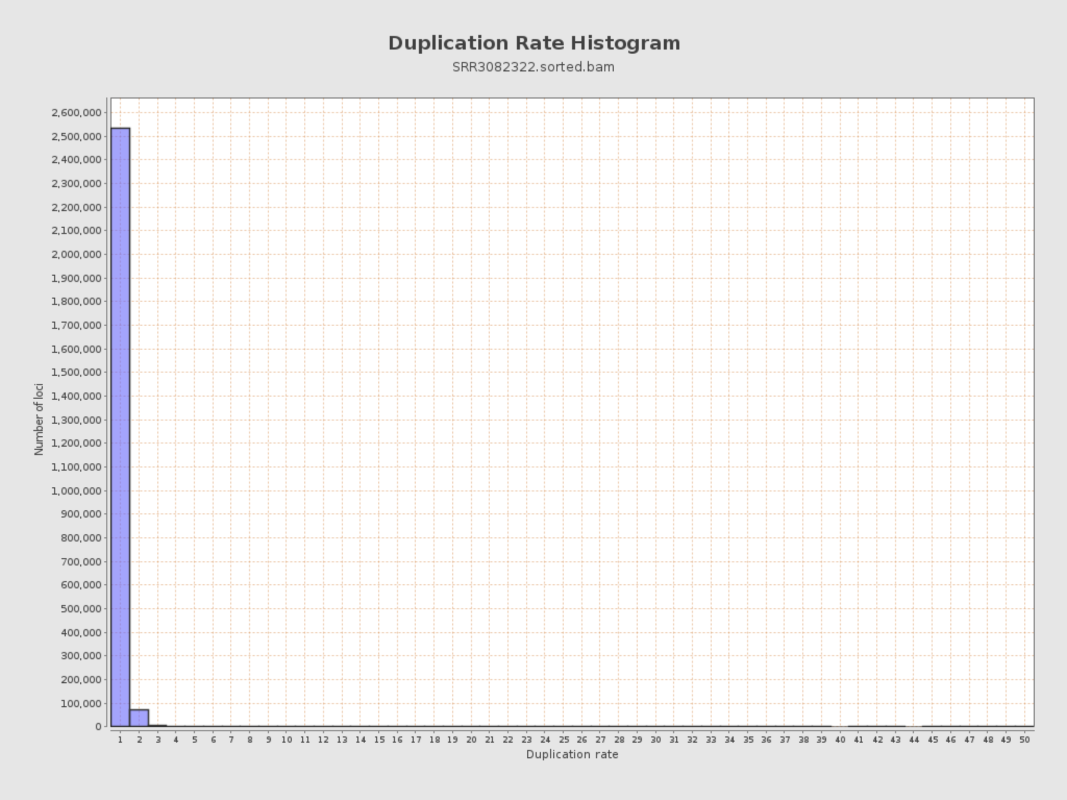
5. Results : Coverage Histogram (0-50X)



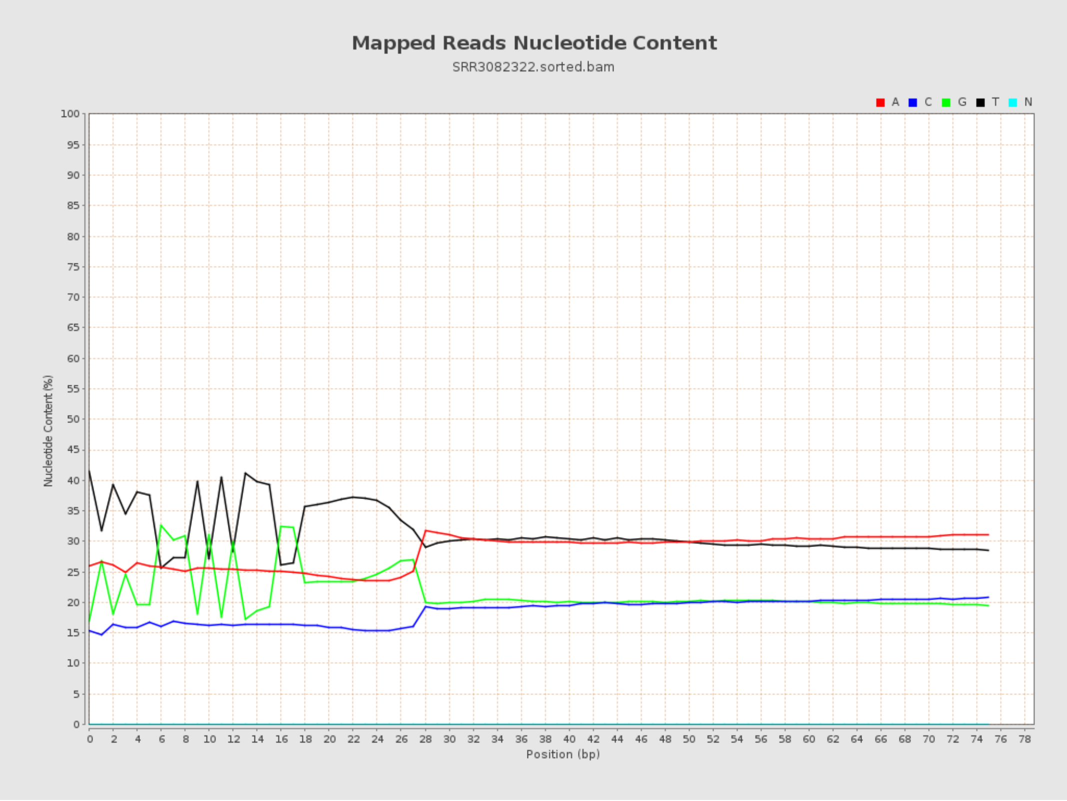
6. Results : Genome Fraction Coverage



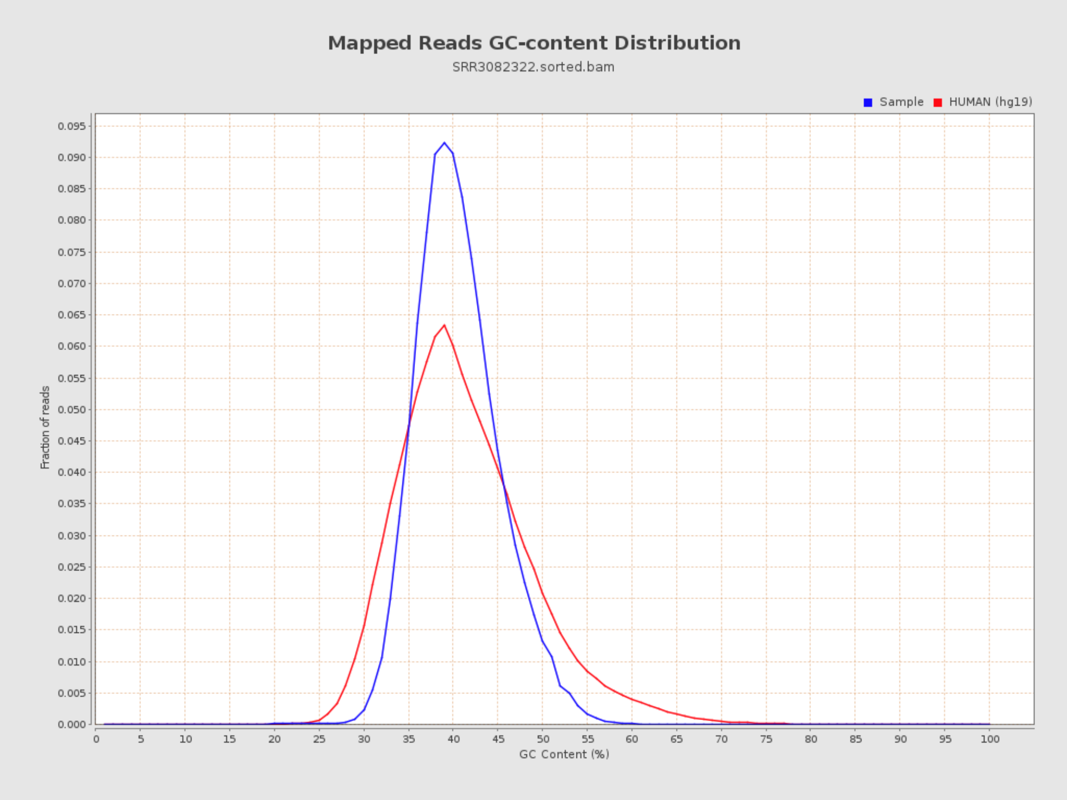
7. Results : Duplication Rate Histogram



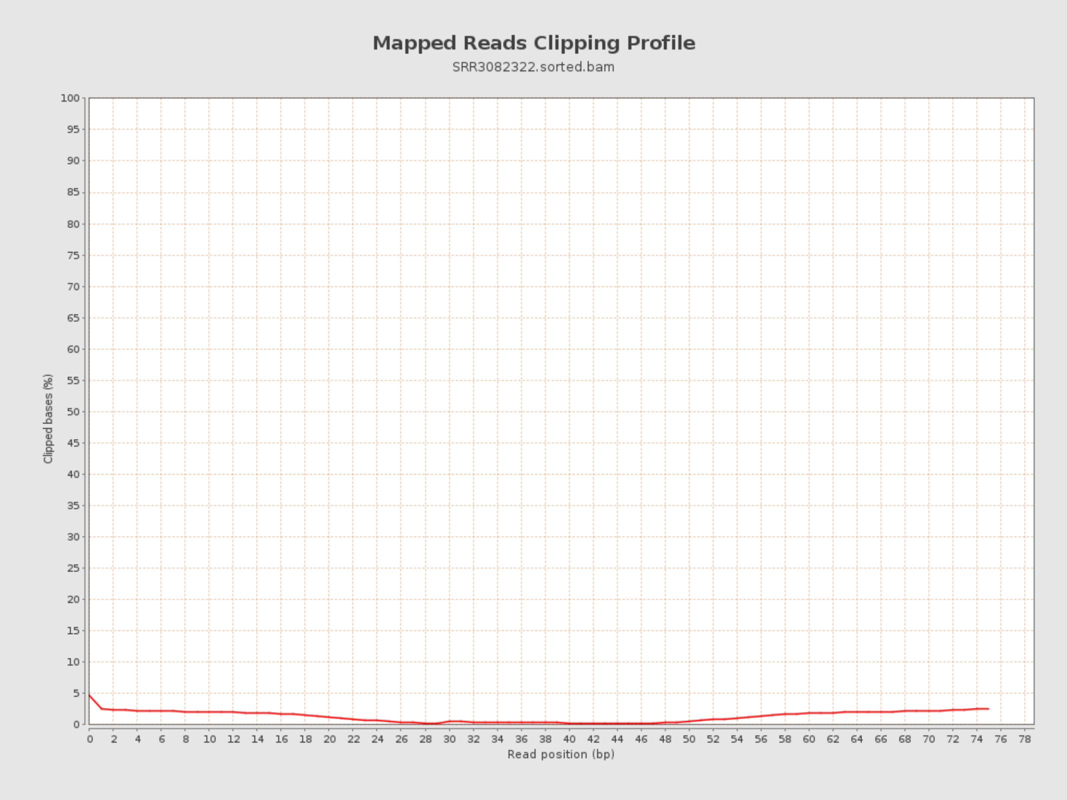
8. Results : Mapped Reads Nucleotide Content



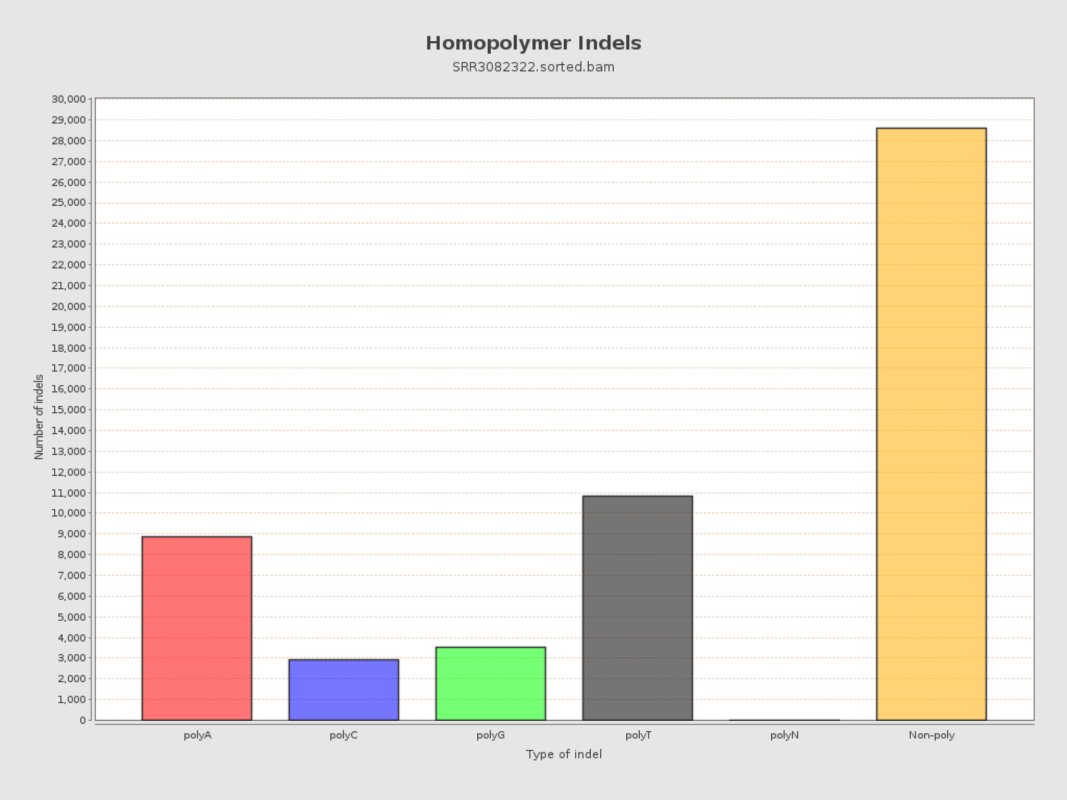
9. Results : Mapped Reads GC-content Distribution



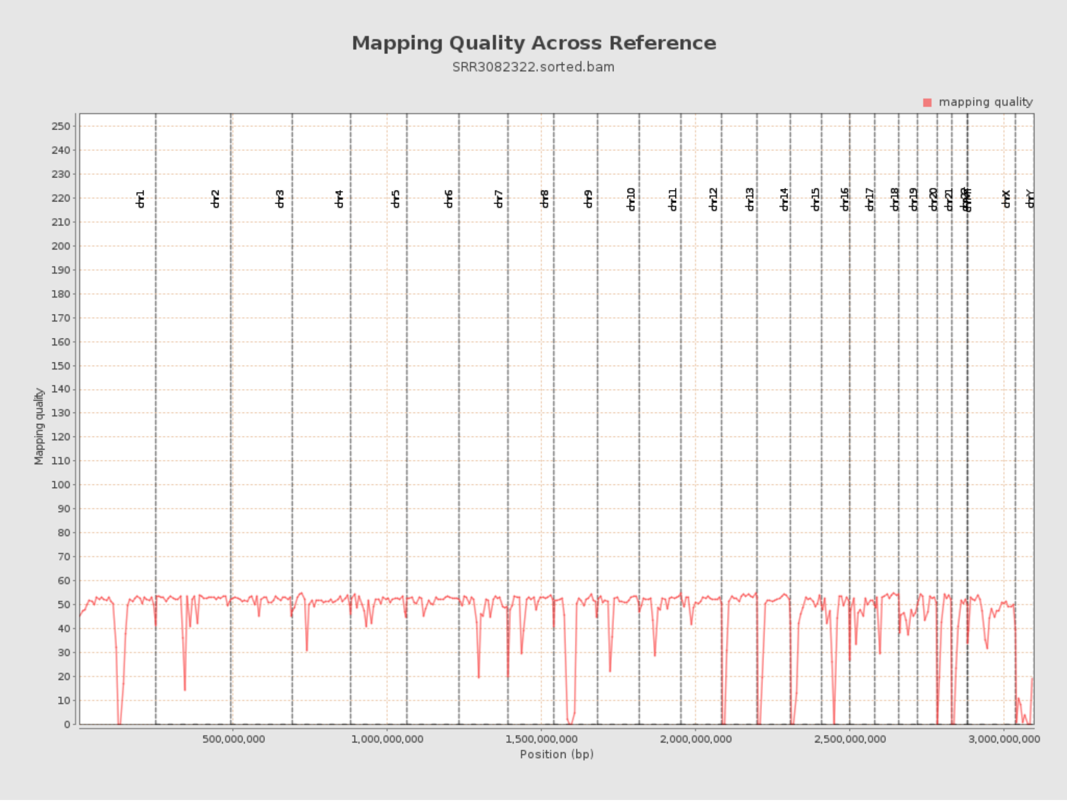
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram