Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 13:49:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082327.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_SRR3082327 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082327.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 13:49:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082327.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,870,678
Mapped reads	2,499,293 / 87.06%
Unmapped reads	371,385 / 12.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,357 / 0.64%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	105,323 / 3.67%
Duplication rate	3.27%
Clipped reads	1,213,285 / 42.26%

2.2. ACGT Content

Number/percentage of A's	45,410,752 / 27.51%
Number/percentage of C's	30,684,297 / 18.59%
Number/percentage of T's	51,591,327 / 31.26%
Number/percentage of G's	37,365,475 / 22.64%
Number/percentage of N's	3,335 / 0%
GC Percentage	41.23%

2.3. Coverage

Mean	0.0533

Standard Deviation	0.4283

2.4. Mapping Quality

Mean Mapping Quality	44.98

2.5. Mismatches and indels

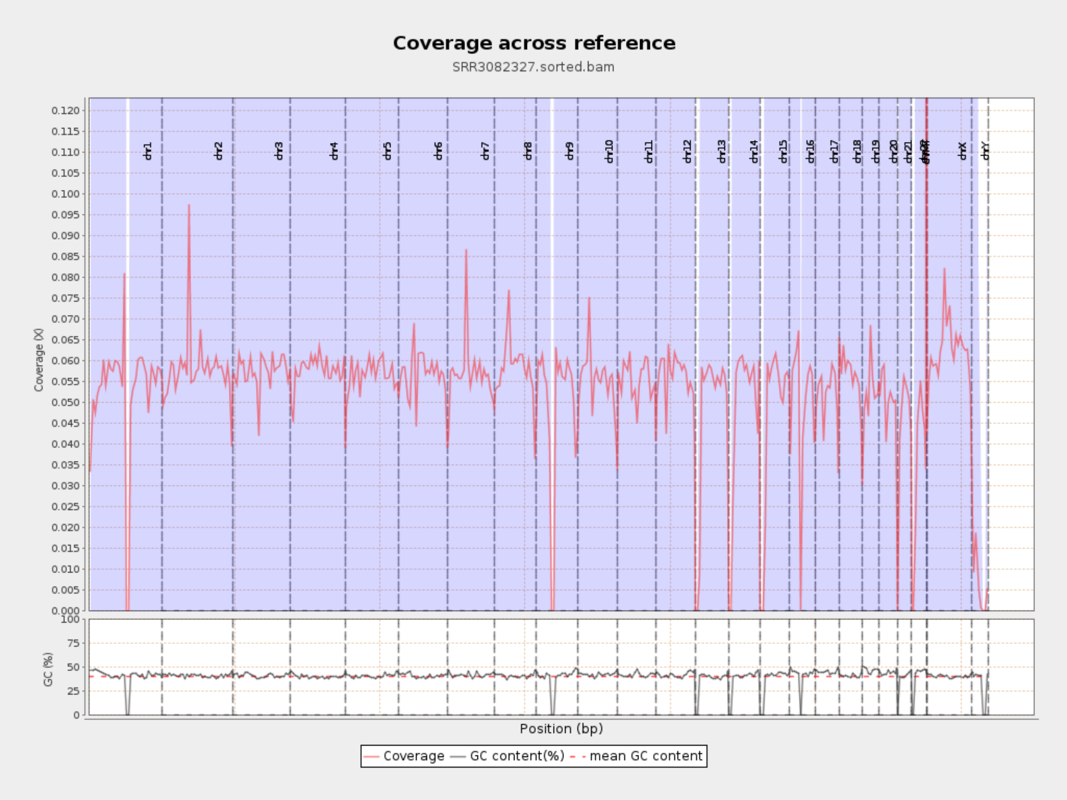
General error rate	0.86%
Mismatches	1,391,930
Insertions	12,990
Mapped reads with at least one insertion	0.52%
Deletions	35,999
Mapped reads with at least one deletion	1.43%
Homopolymer indels	46.88%

2.6. Chromosome stats

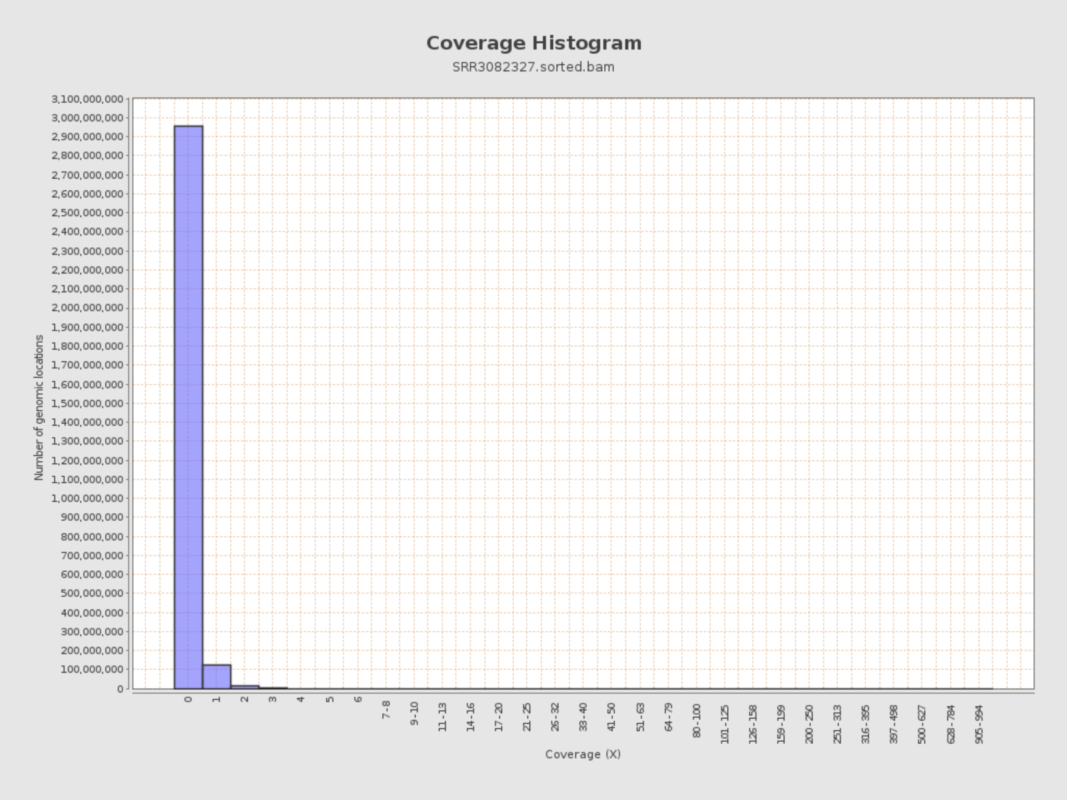
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13097986	0.0525	0.6952
chr2	243199373	14130308	0.0581	0.5958
chr3	198022430	11371769	0.0574	0.2689
chr4	191154276	11012602	0.0576	0.2803
chr5	180915260	10281837	0.0568	0.2697
chr6	171115067	9693016	0.0566	0.3298
chr7	159138663	9144077	0.0575	0.5547

chr8	146364022	8506984	0.0581	0.6522
chr9	141213431	6944829	0.0492	0.4022
chr10	135534747	7571695	0.0559	0.3874
chr11	135006516	7437345	0.0551	0.3586
chr12	133851895	7535242	0.0563	0.273
chr13	115169878	5351642	0.0465	0.2424
chr14	107349540	5043181	0.047	0.2666
chr15	102531392	4693323	0.0458	0.2582
chr16	90354753	4474606	0.0495	0.2762
chr17	81195210	4171971	0.0514	0.2807
chr18	78077248	4456352	0.0571	0.7128
chr19	59128983	3095790	0.0524	0.5396
chr20	63025520	3169989	0.0503	0.2608
chr21	48129895	2143155	0.0445	0.253
chr22	51304566	1688180	0.0329	0.2036
chrMT	16571	9348	0.5641	0.8381
chrX	155270560	9683316	0.0624	0.3206
chrY	59373566	403723	0.0068	0.1311

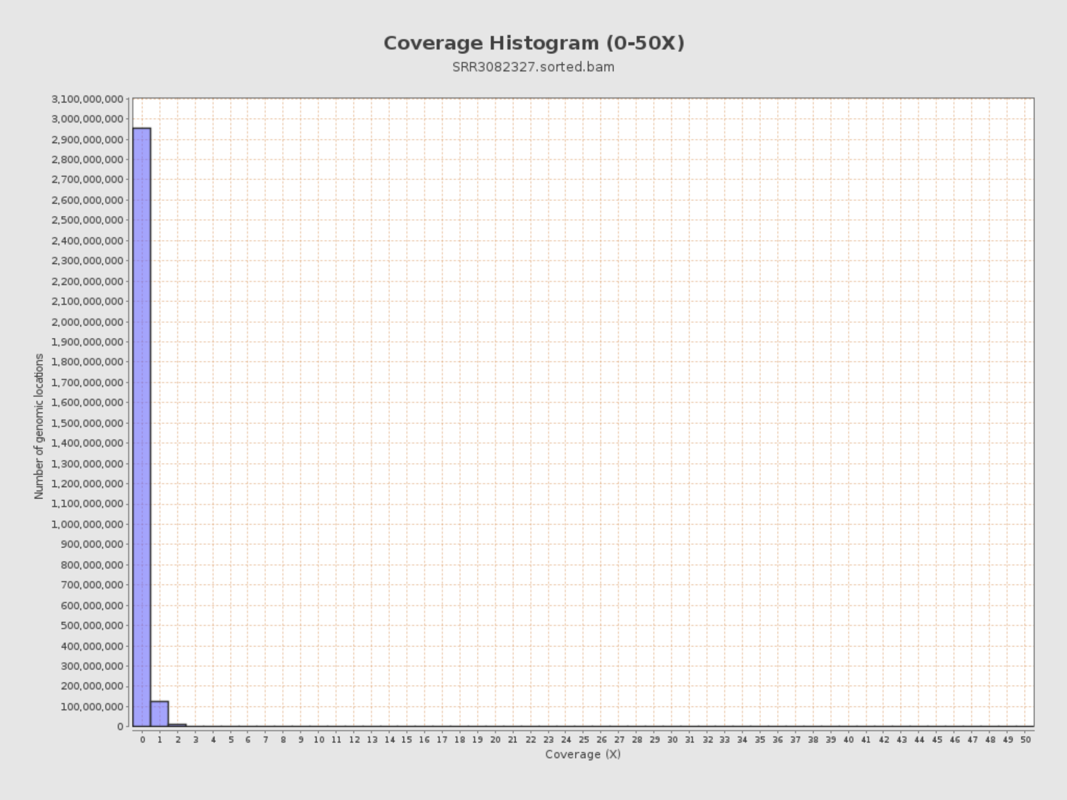
3. Results : Coverage across reference



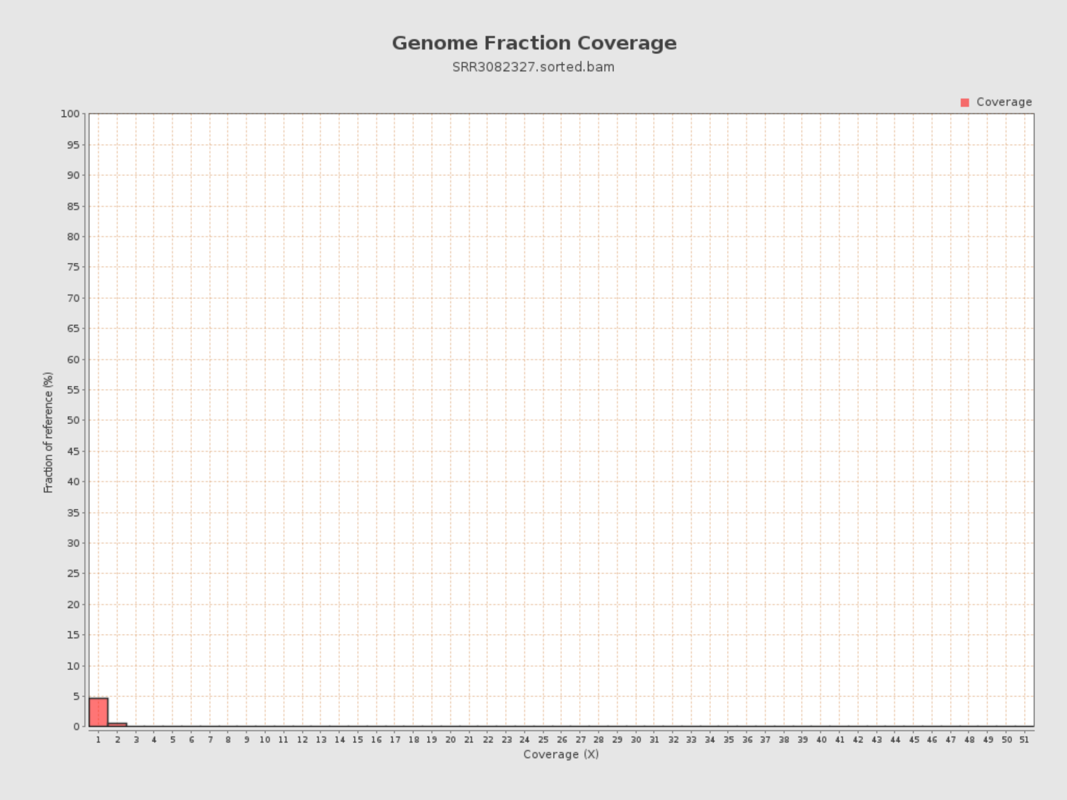
4. Results : Coverage Histogram



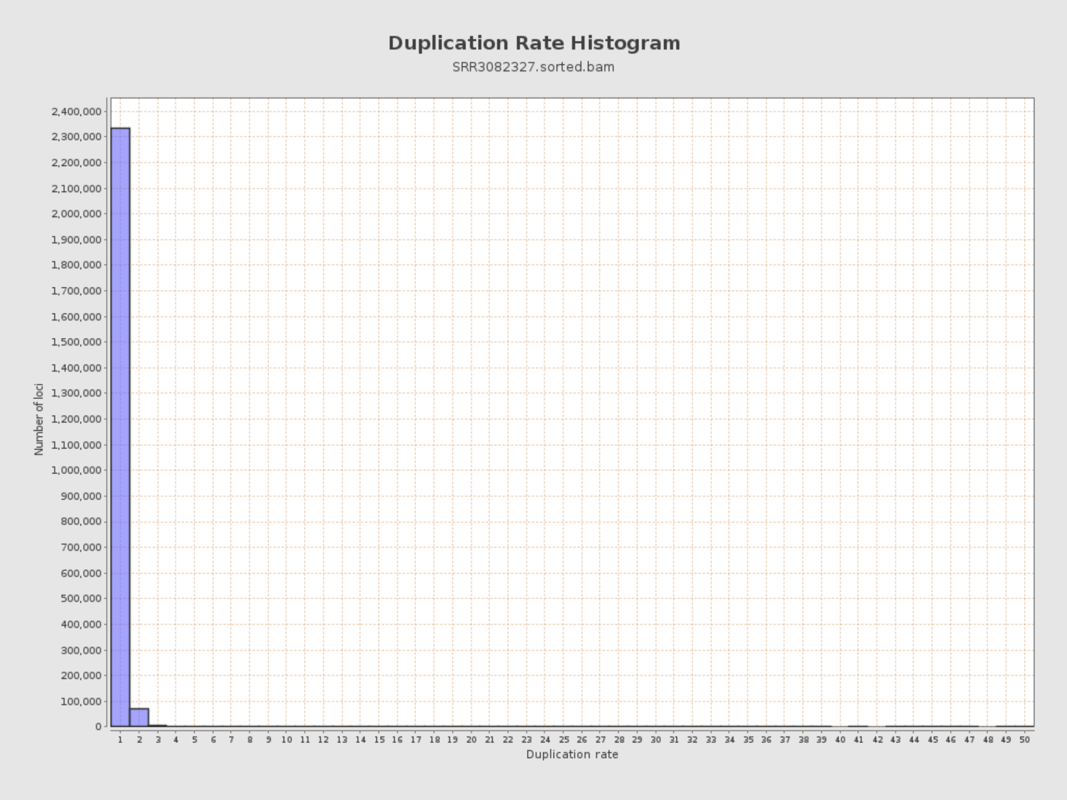
5. Results : Coverage Histogram (0-50X)



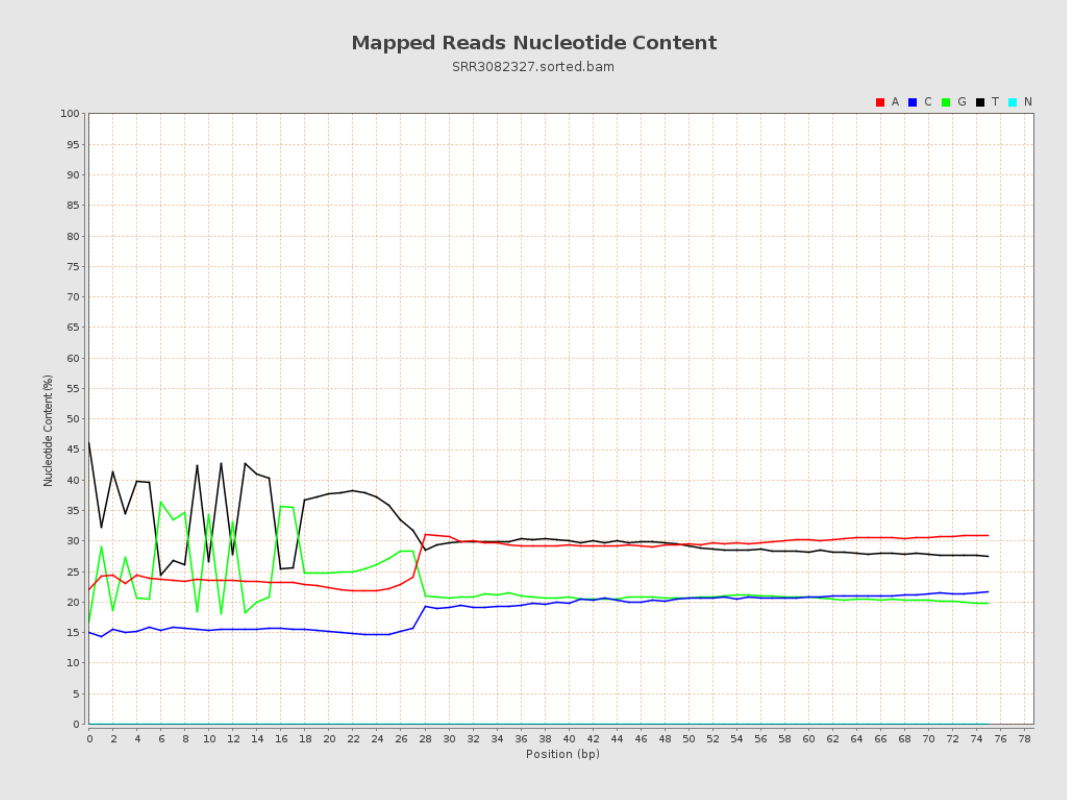
6. Results : Genome Fraction Coverage



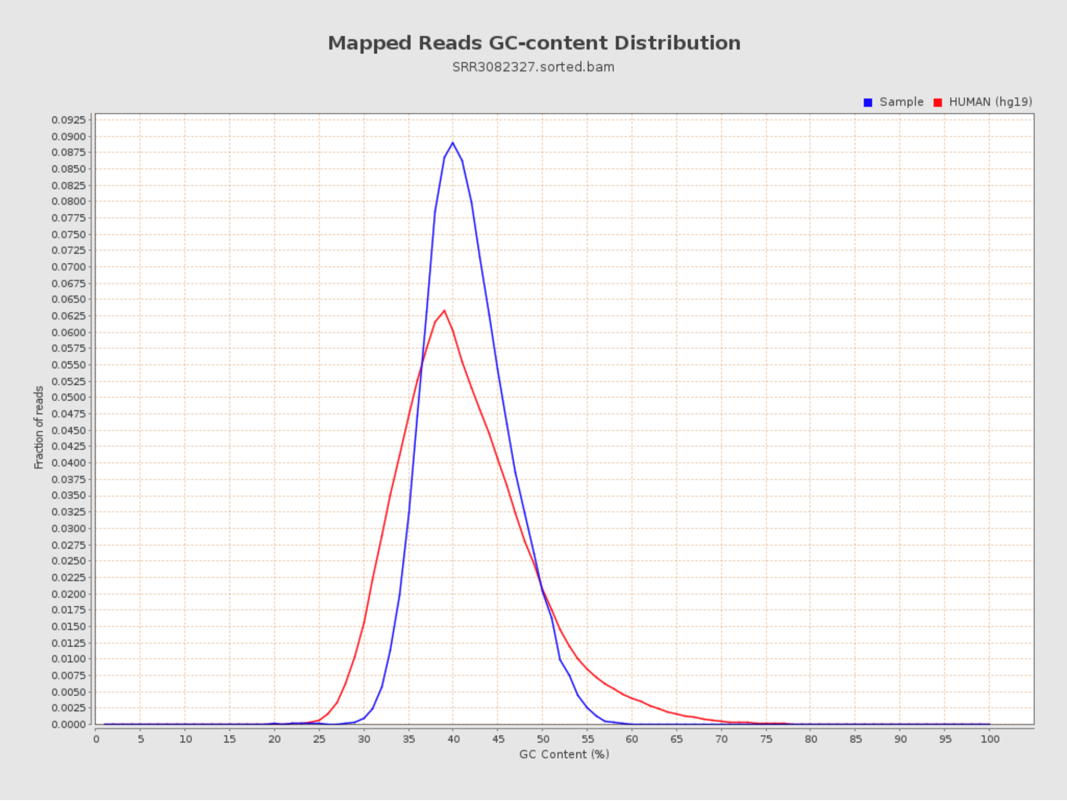
7. Results : Duplication Rate Histogram



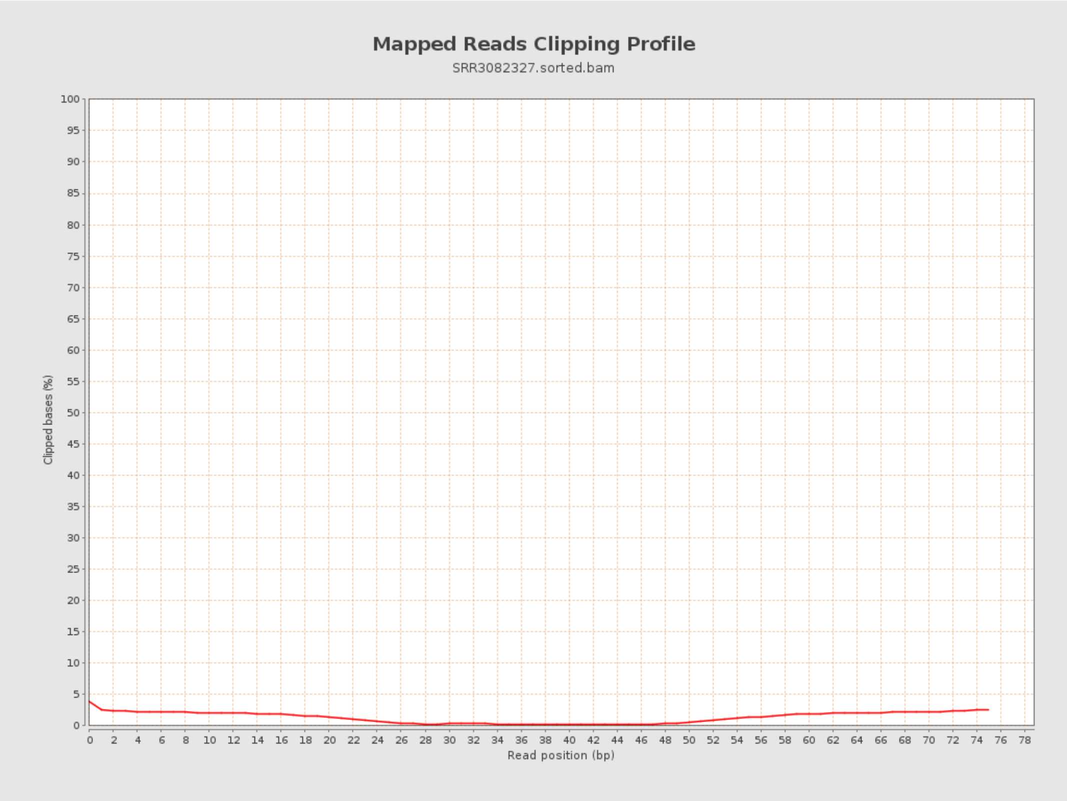
8. Results : Mapped Reads Nucleotide Content



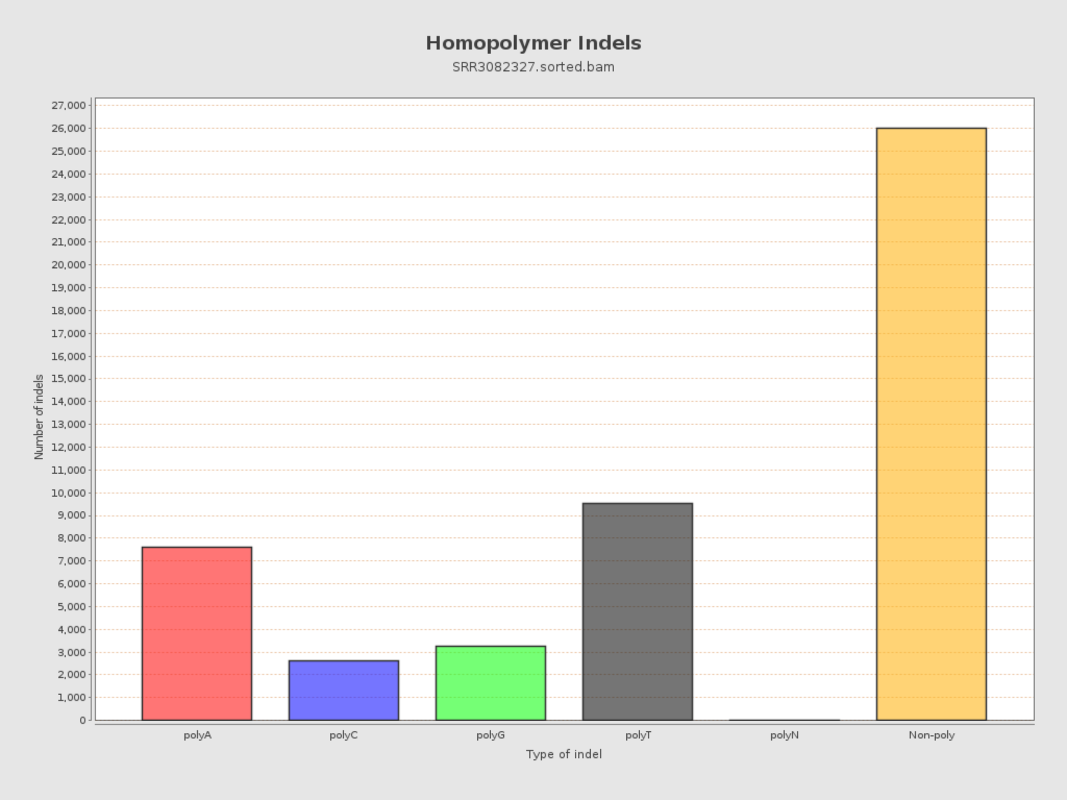
9. Results : Mapped Reads GC-content Distribution



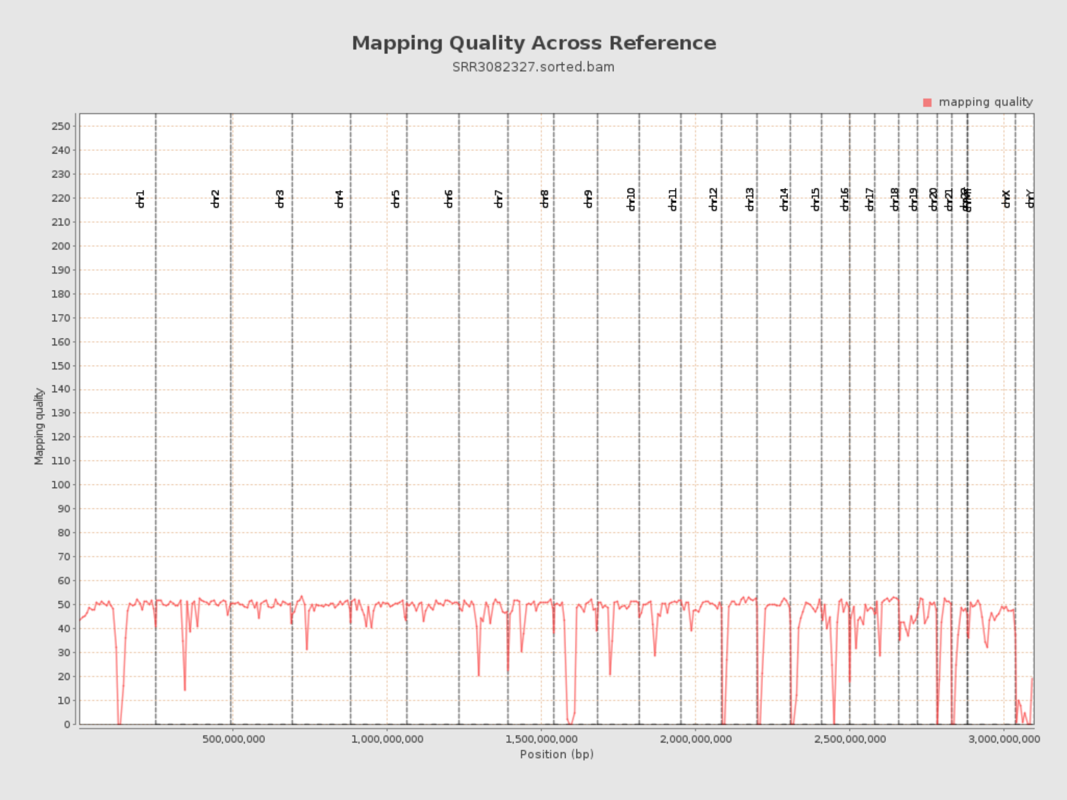
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram