Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 15:53:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082512.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_SRR3082512 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082512.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 15:53:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082512.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,819,107
Mapped reads	2,542,321 / 90.18%
Unmapped reads	276,786 / 9.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,152 / 1.07%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	176,248 / 6.25%
Duplication rate	5.45%
Clipped reads	1,092,402 / 38.75%

2.2. ACGT Content

Number/percentage of A's	49,238,842 / 28.57%
Number/percentage of C's	32,707,276 / 18.98%
Number/percentage of T's	53,459,464 / 31.02%
Number/percentage of G's	36,913,550 / 21.42%
Number/percentage of N's	3,469 / 0%
GC Percentage	40.4%

2.3. Coverage

Mean	0.0557

Standard Deviation	0.5309

2.4. Mapping Quality

Mean Mapping Quality	46.84

2.5. Mismatches and indels

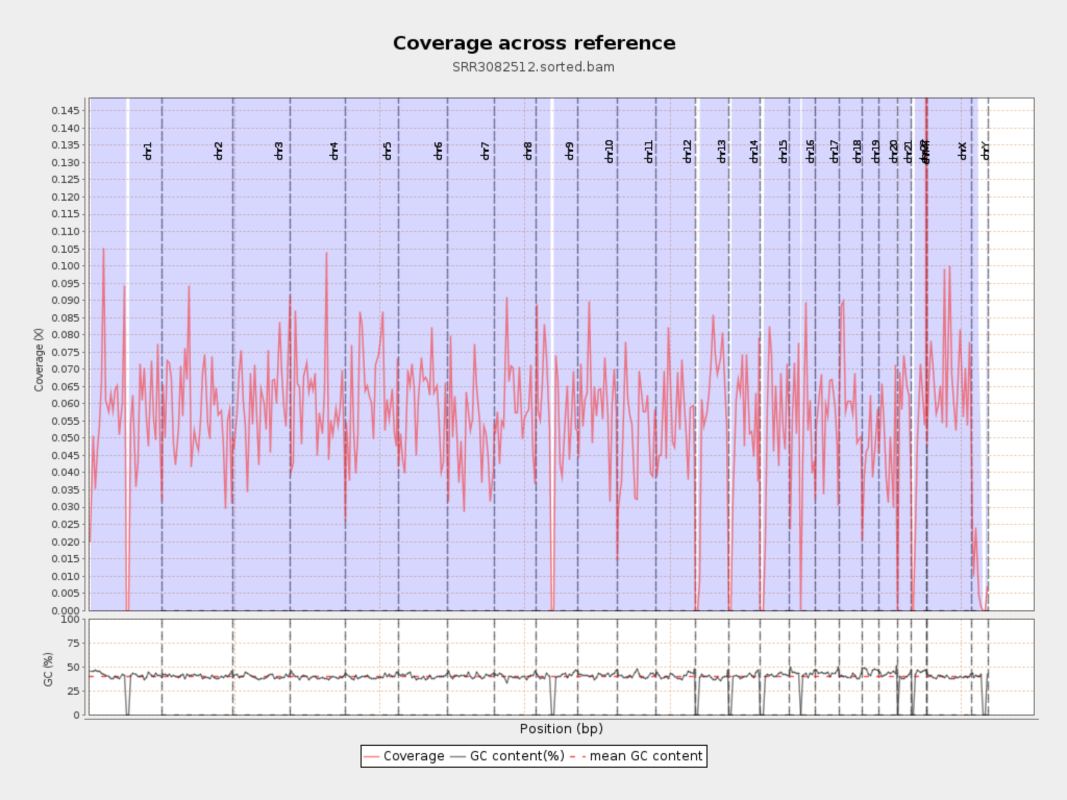
General error rate	0.85%
Mismatches	1,446,818
Insertions	14,087
Mapped reads with at least one insertion	0.55%
Deletions	39,934
Mapped reads with at least one deletion	1.55%
Homopolymer indels	47.23%

2.6. Chromosome stats

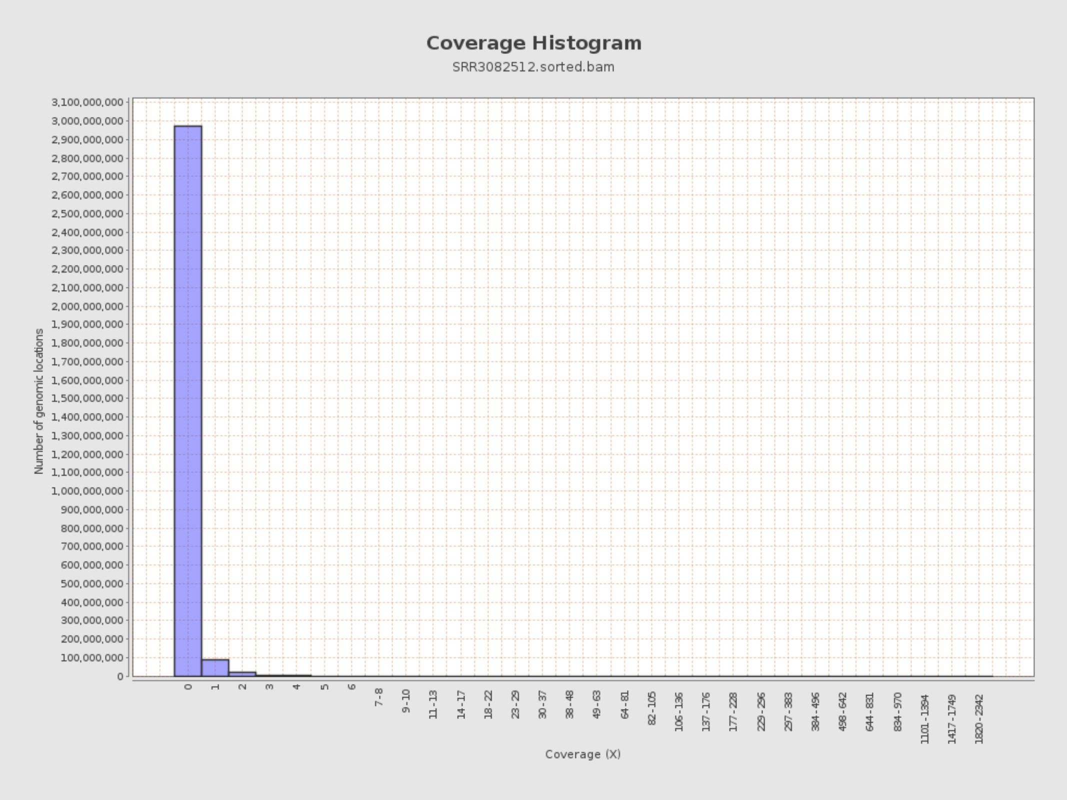
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13691979	0.0549	0.6475
chr2	243199373	14226692	0.0585	0.5326
chr3	198022430	12070301	0.061	0.3302
chr4	191154276	11593224	0.0606	0.3468
chr5	180915260	11235678	0.0621	0.3357
chr6	171115067	10139817	0.0593	0.3642
chr7	159138663	8209144	0.0516	0.3875

chr8	146364022	8643722	0.0591	1.431
chr9	141213431	7515324	0.0532	0.4748
chr10	135534747	8207098	0.0606	0.4001
chr11	135006516	6949600	0.0515	0.4184
chr12	133851895	7463960	0.0558	0.32
chr13	115169878	6397370	0.0555	0.3162
chr14	107349540	5253310	0.0489	0.3368
chr15	102531392	5012177	0.0489	0.2997
chr16	90354753	4658312	0.0516	0.3362
chr17	81195210	4533764	0.0558	0.3279
chr18	78077248	4962500	0.0636	1.0827
chr19	59128983	2771342	0.0469	0.4614
chr20	63025520	3021229	0.0479	0.3191
chr21	48129895	2716434	0.0564	0.3565
chr22	51304566	2131076	0.0415	0.2656
chrMT	16571	68463	4.1315	3.5803
chrX	155270560	10440231	0.0672	0.3825
chrY	59373566	474420	0.008	0.1573

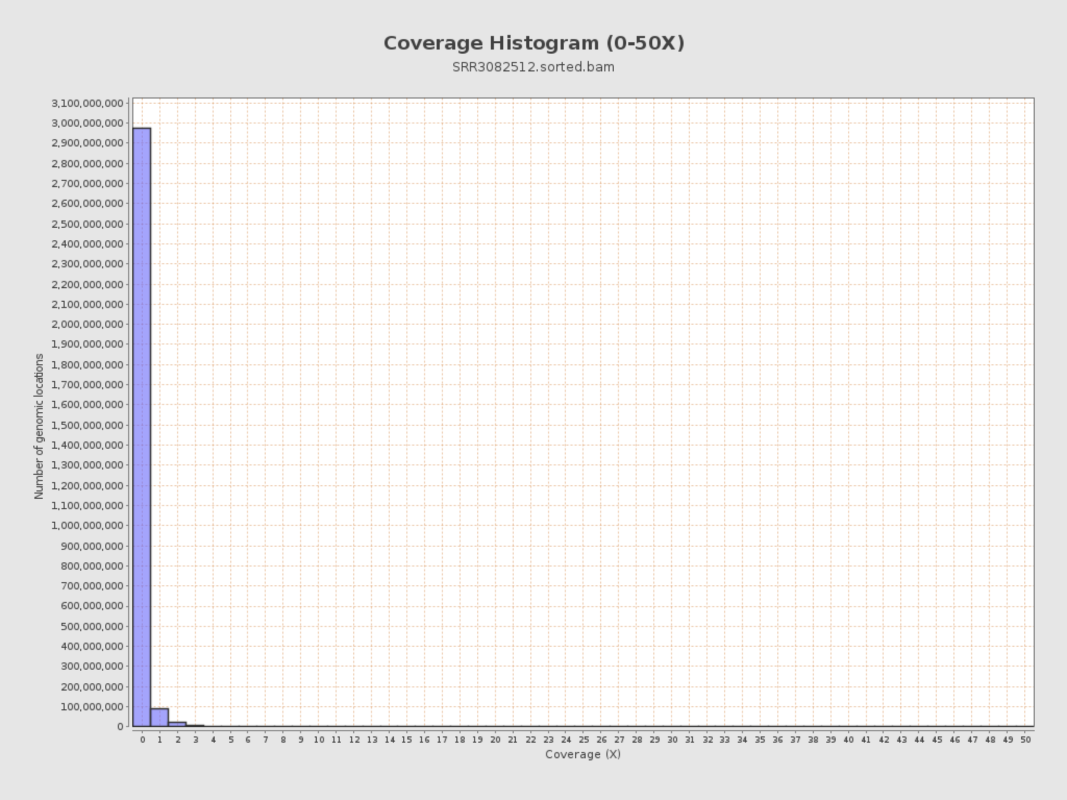
3. Results : Coverage across reference



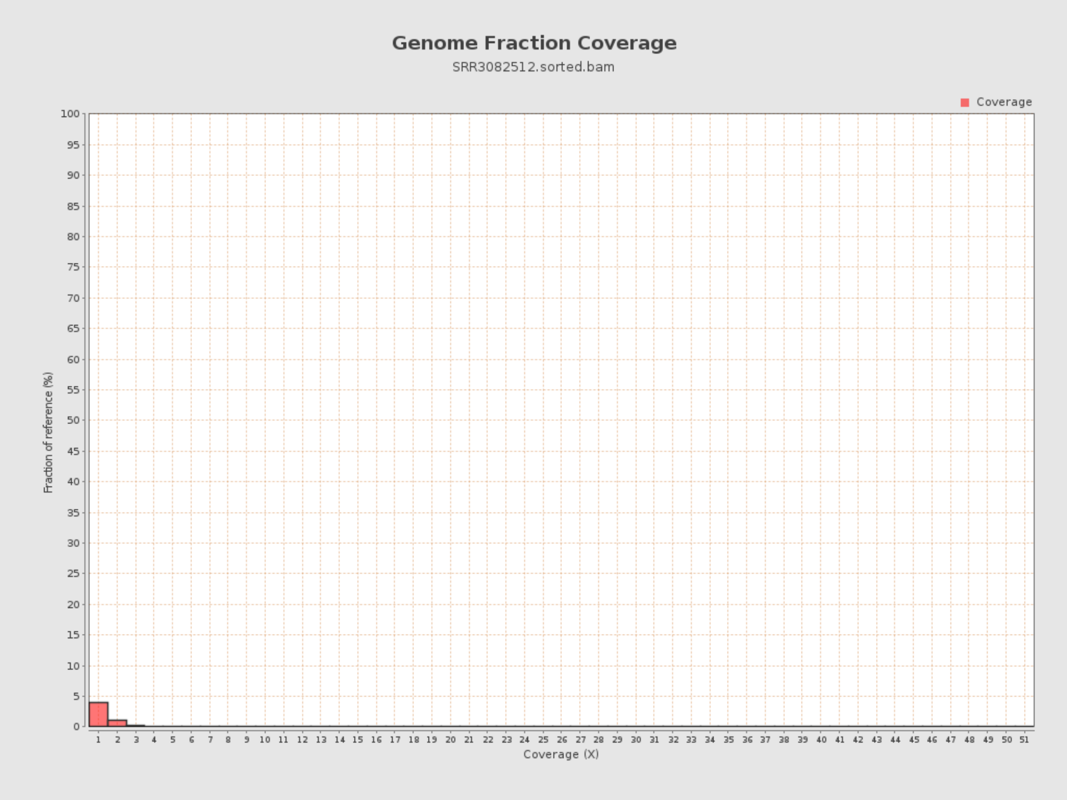
4. Results : Coverage Histogram



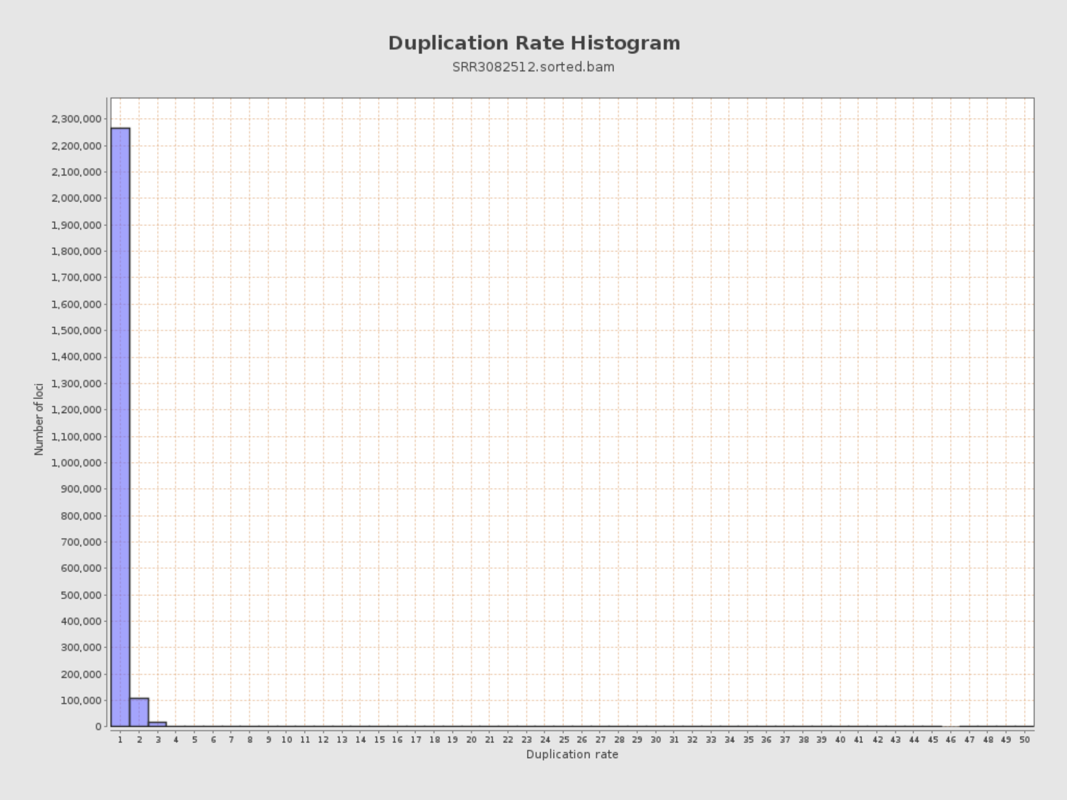
5. Results : Coverage Histogram (0-50X)



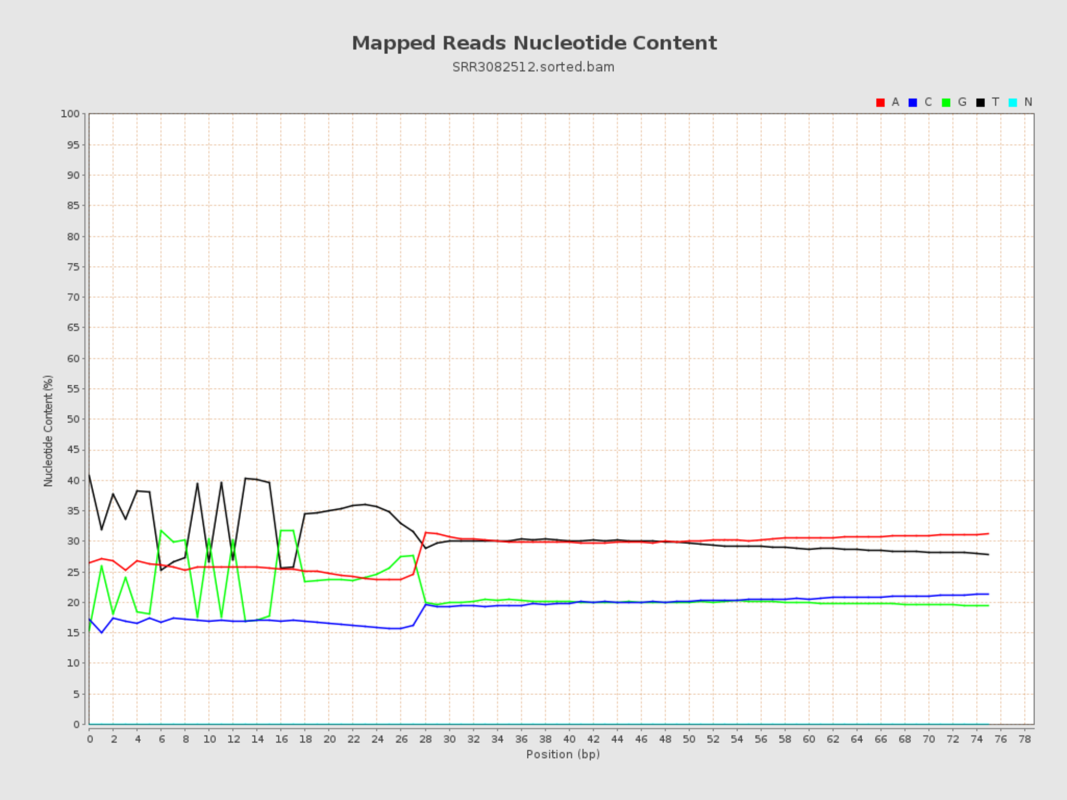
6. Results : Genome Fraction Coverage



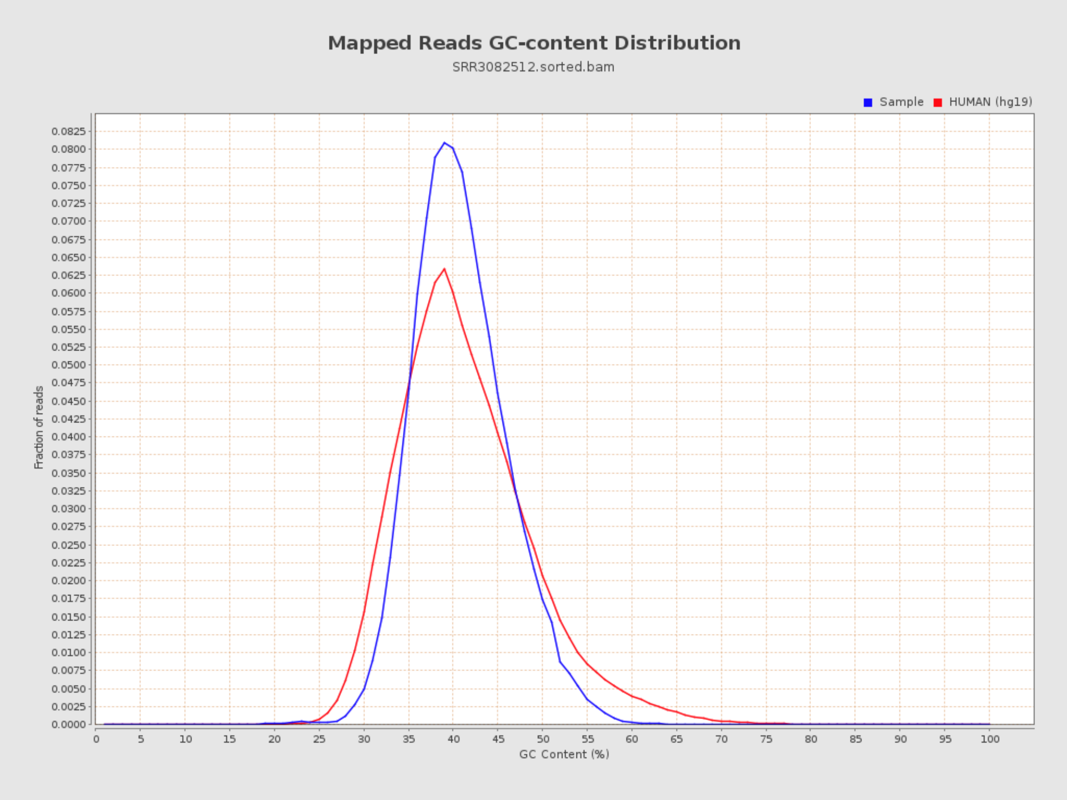
7. Results : Duplication Rate Histogram



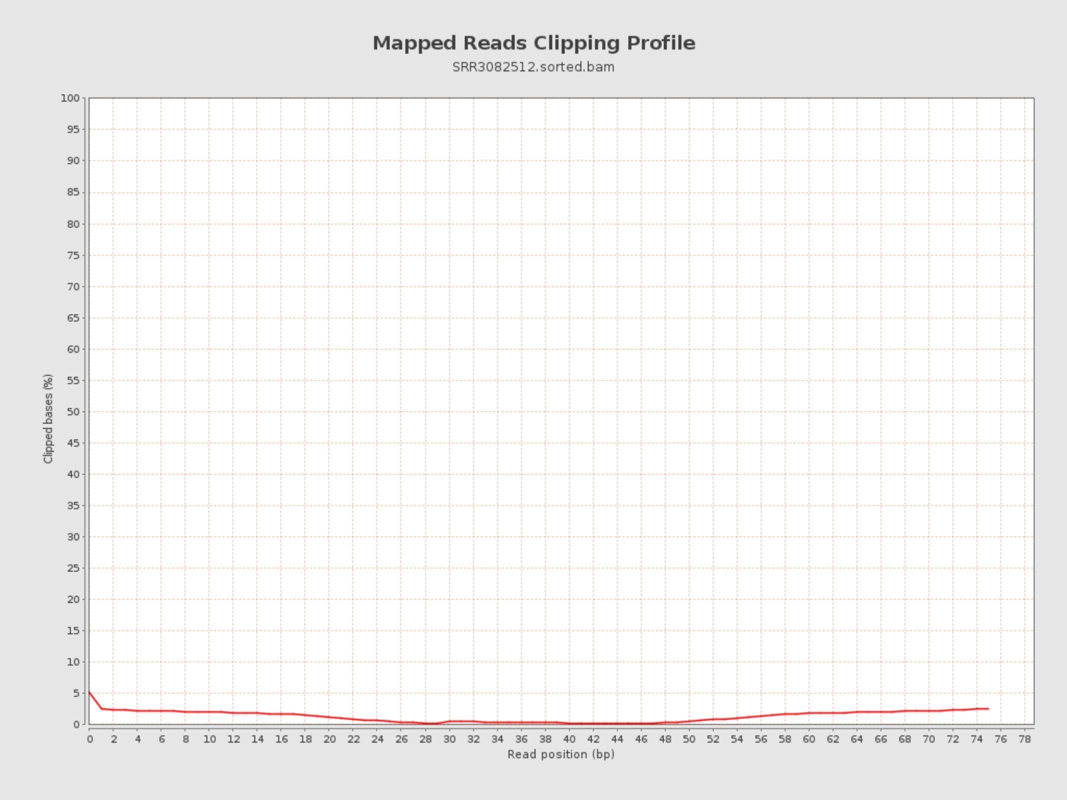
8. Results : Mapped Reads Nucleotide Content



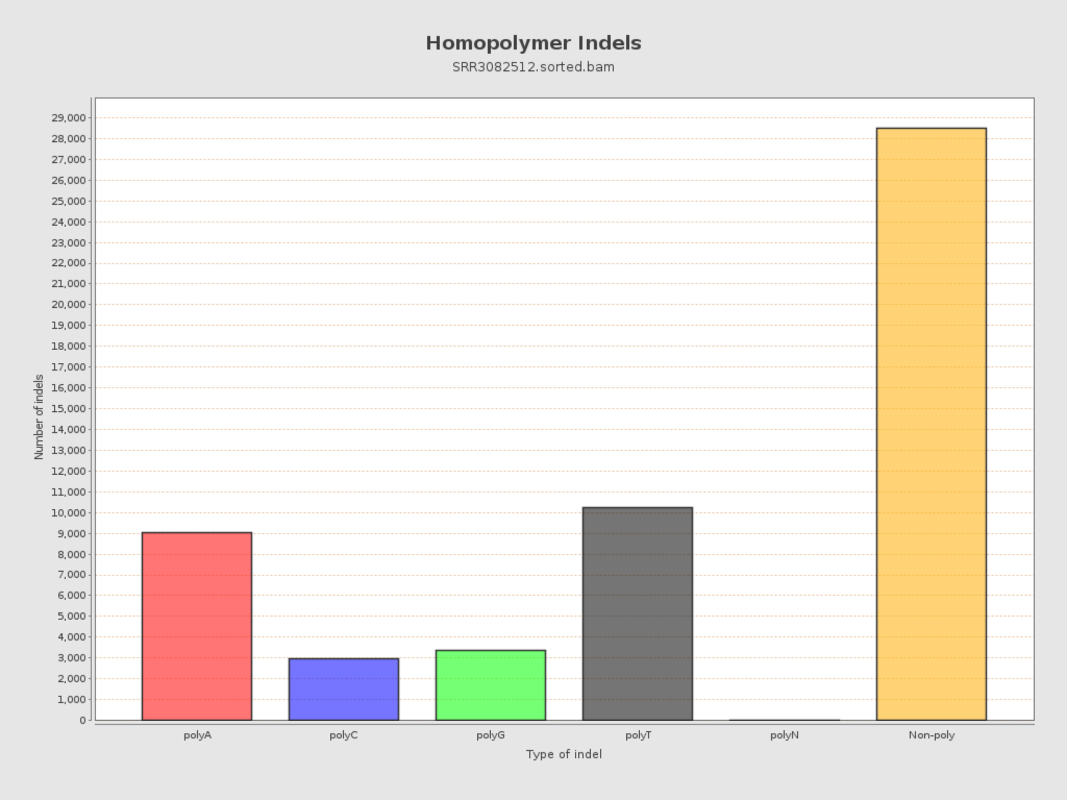
9. Results : Mapped Reads GC-content Distribution



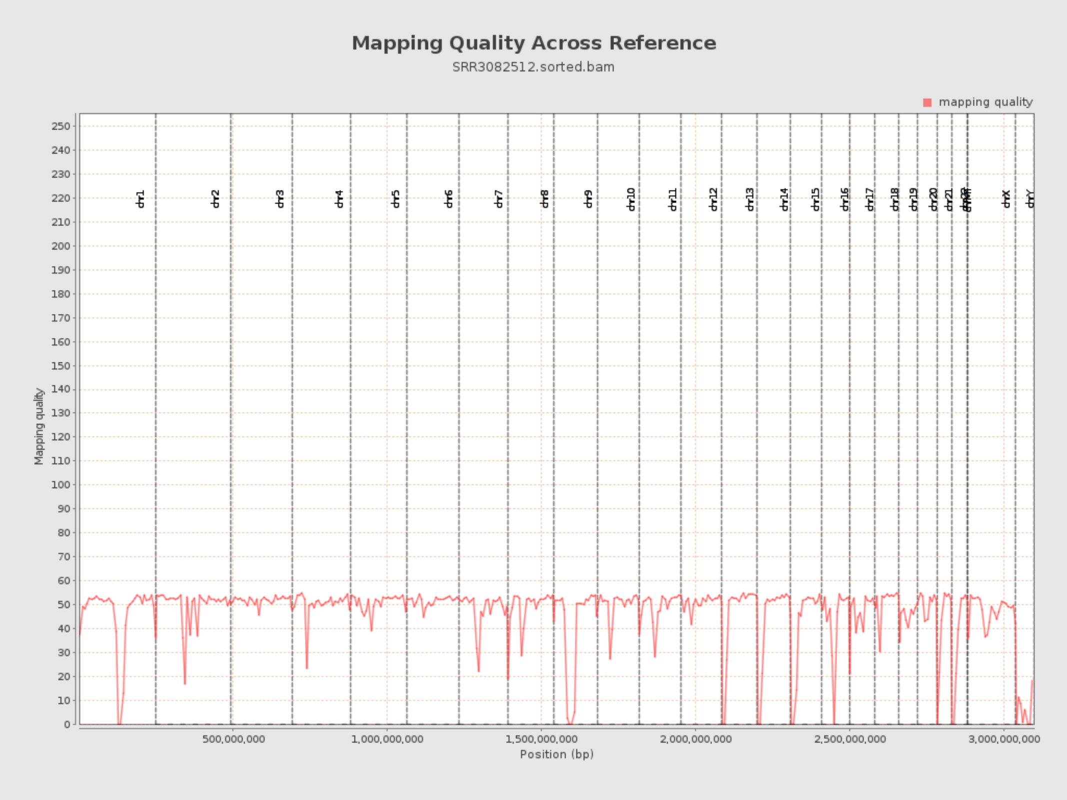
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram