Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 15:49:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082511.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_SRR3082511 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082511.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 15:49:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082511.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,057,101
Mapped reads	1,874,003 / 91.1%
Unmapped reads	183,098 / 8.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,162 / 0.79%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	74,933 / 3.64%
Duplication rate	3.08%
Clipped reads	771,351 / 37.5%

2.2. ACGT Content

Number/percentage of A's	35,984,740 / 28.28%
Number/percentage of C's	23,727,195 / 18.65%
Number/percentage of T's	39,896,738 / 31.36%
Number/percentage of G's	27,619,074 / 21.71%
Number/percentage of N's	2,672 / 0%
GC Percentage	40.36%

2.3. Coverage

Mean	0.0411

Standard Deviation	0.3688

2.4. Mapping Quality

Mean Mapping Quality	47.07

2.5. Mismatches and indels

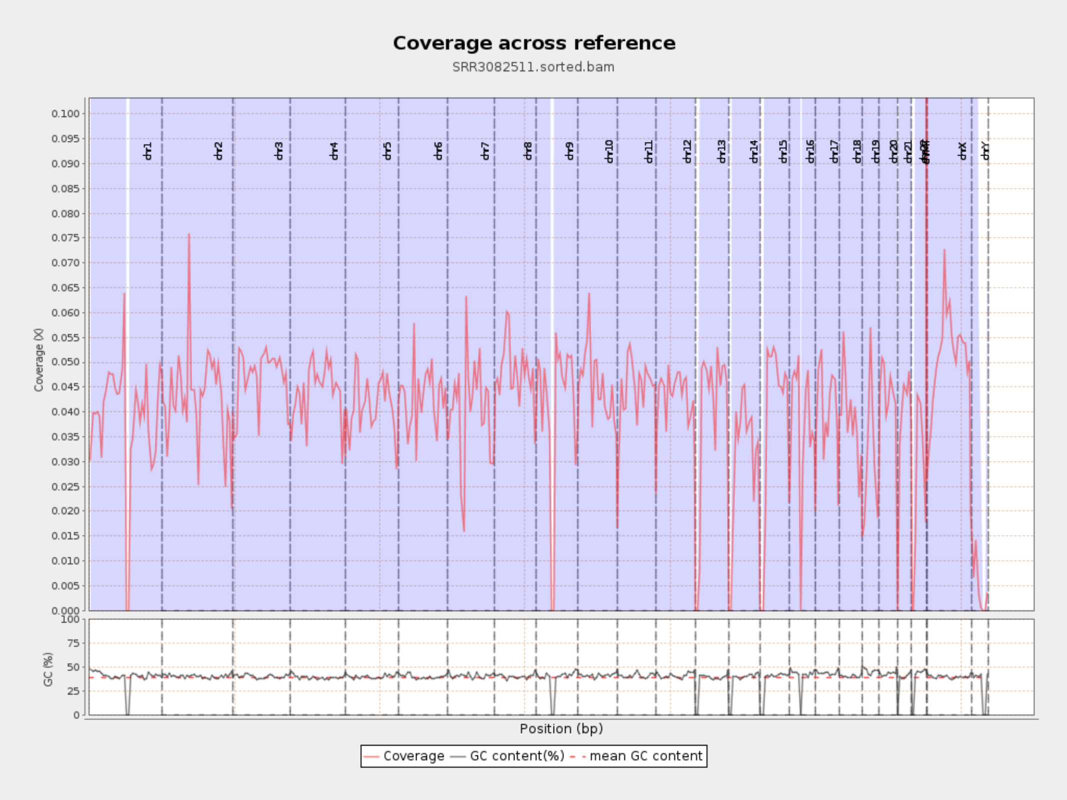
General error rate	0.86%
Mismatches	1,071,462
Insertions	10,193
Mapped reads with at least one insertion	0.54%
Deletions	32,834
Mapped reads with at least one deletion	1.73%
Homopolymer indels	47.28%

2.6. Chromosome stats

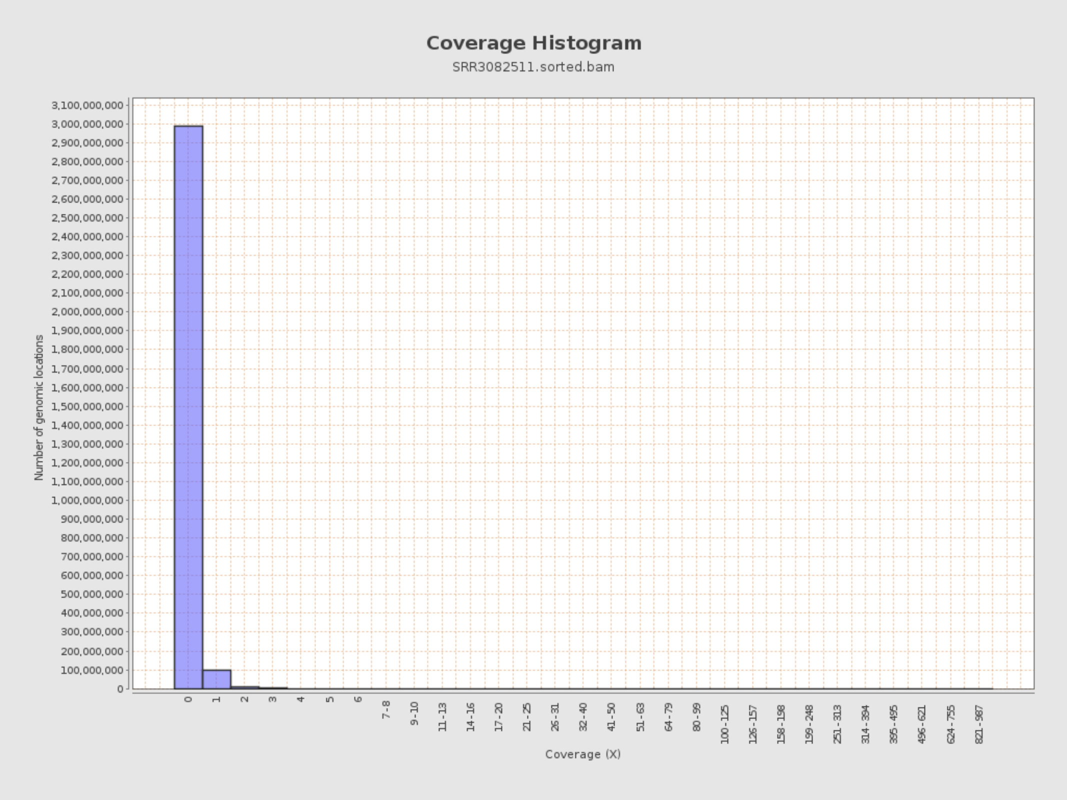
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9627938	0.0386	0.6131
chr2	243199373	10439665	0.0429	0.4271
chr3	198022430	9331104	0.0471	0.2411
chr4	191154276	8465833	0.0443	0.2445
chr5	180915260	7484398	0.0414	0.2275
chr6	171115067	7368800	0.0431	0.2837
chr7	159138663	6507530	0.0409	0.3757

chr8	146364022	7028655	0.048	0.6433
chr9	141213431	5811252	0.0412	0.356
chr10	135534747	6202024	0.0458	0.3261
chr11	135006516	5970938	0.0442	0.4139
chr12	133851895	5816790	0.0435	0.2358
chr13	115169878	4450882	0.0386	0.2184
chr14	107349540	3282790	0.0306	0.2167
chr15	102531392	3977920	0.0388	0.2235
chr16	90354753	3384916	0.0375	0.2334
chr17	81195210	3289008	0.0405	0.28
chr18	78077248	3049696	0.0391	0.6374
chr19	59128983	1849024	0.0313	0.4164
chr20	63025520	2752642	0.0437	0.2408
chr21	48129895	1818890	0.0378	0.2314
chr22	51304566	1253582	0.0244	0.1717
chrMT	16571	5087	0.307	0.6169
chrX	155270560	7834626	0.0505	0.294
chrY	59373566	279090	0.0047	0.1089

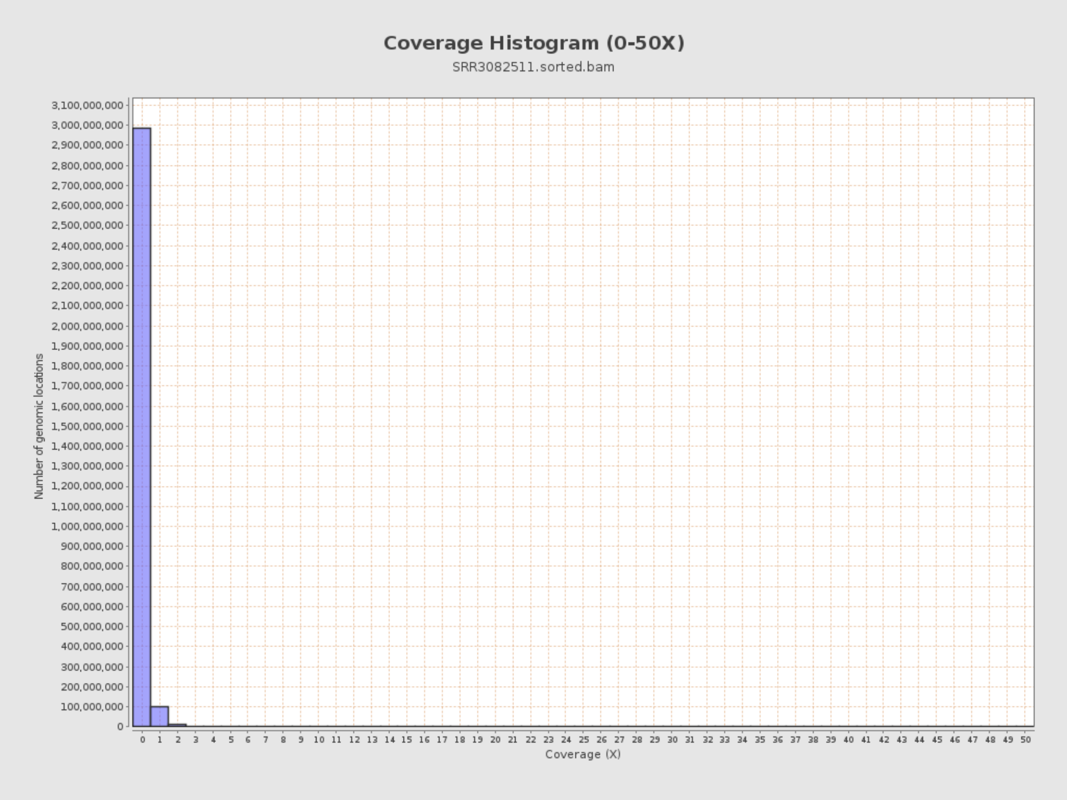
3. Results : Coverage across reference



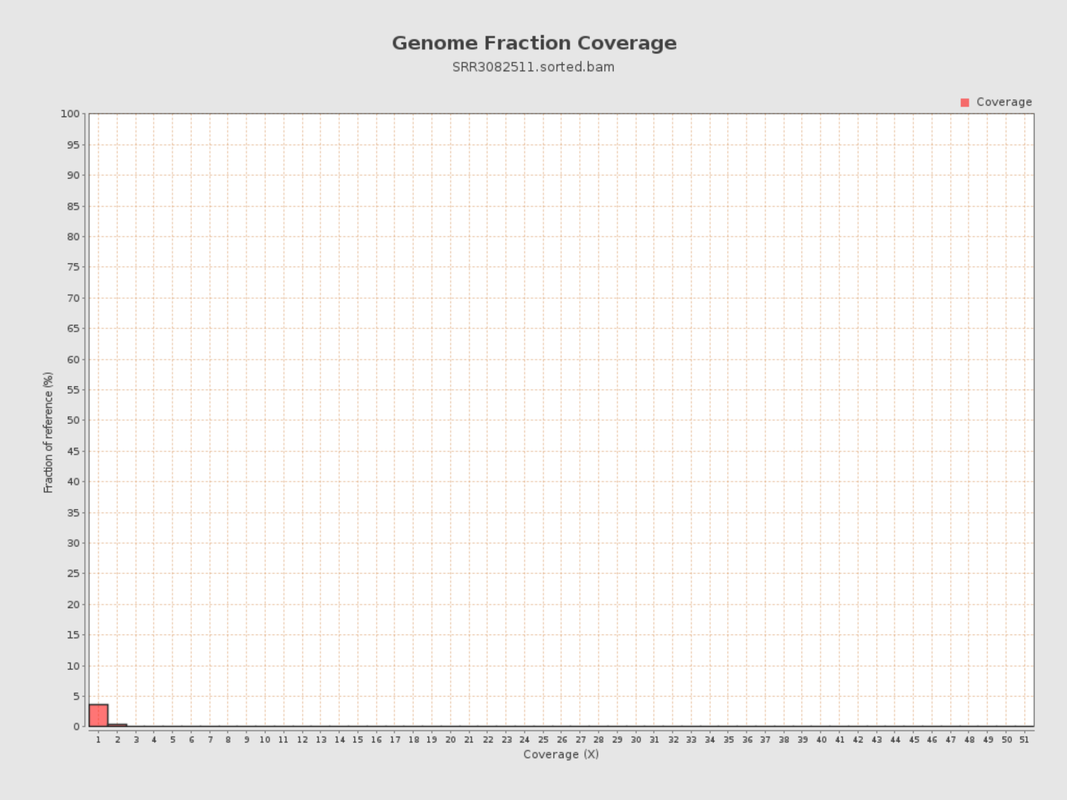
4. Results : Coverage Histogram



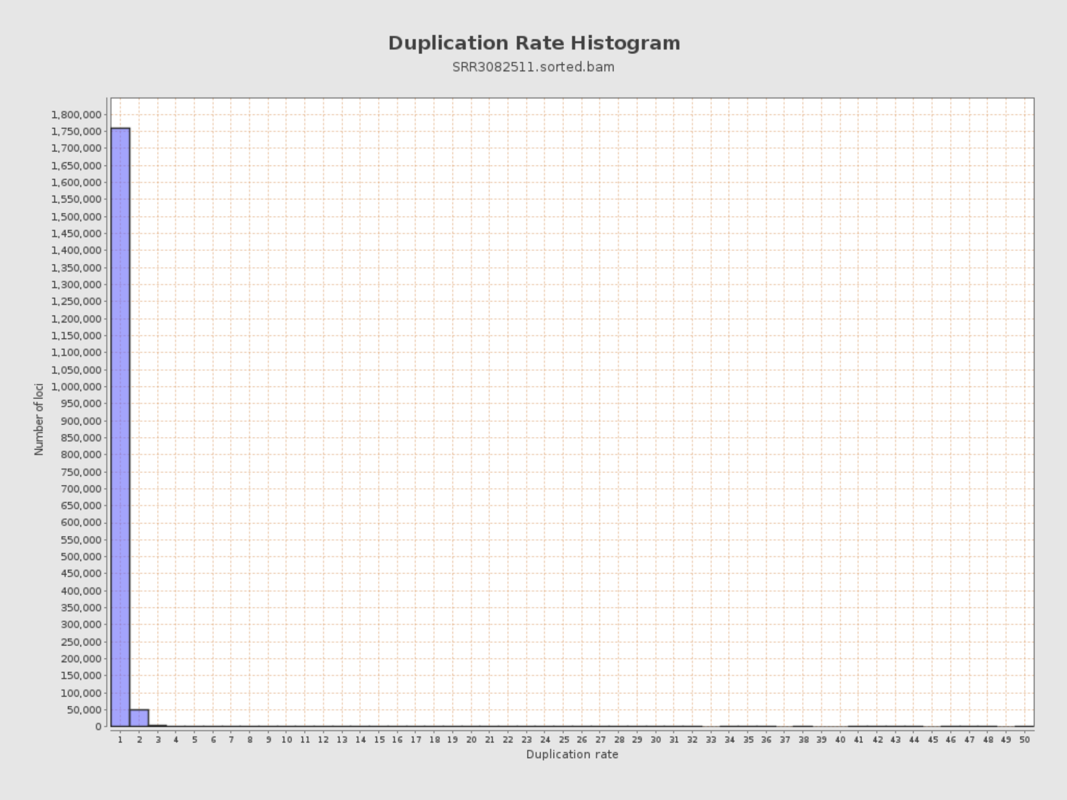
5. Results : Coverage Histogram (0-50X)



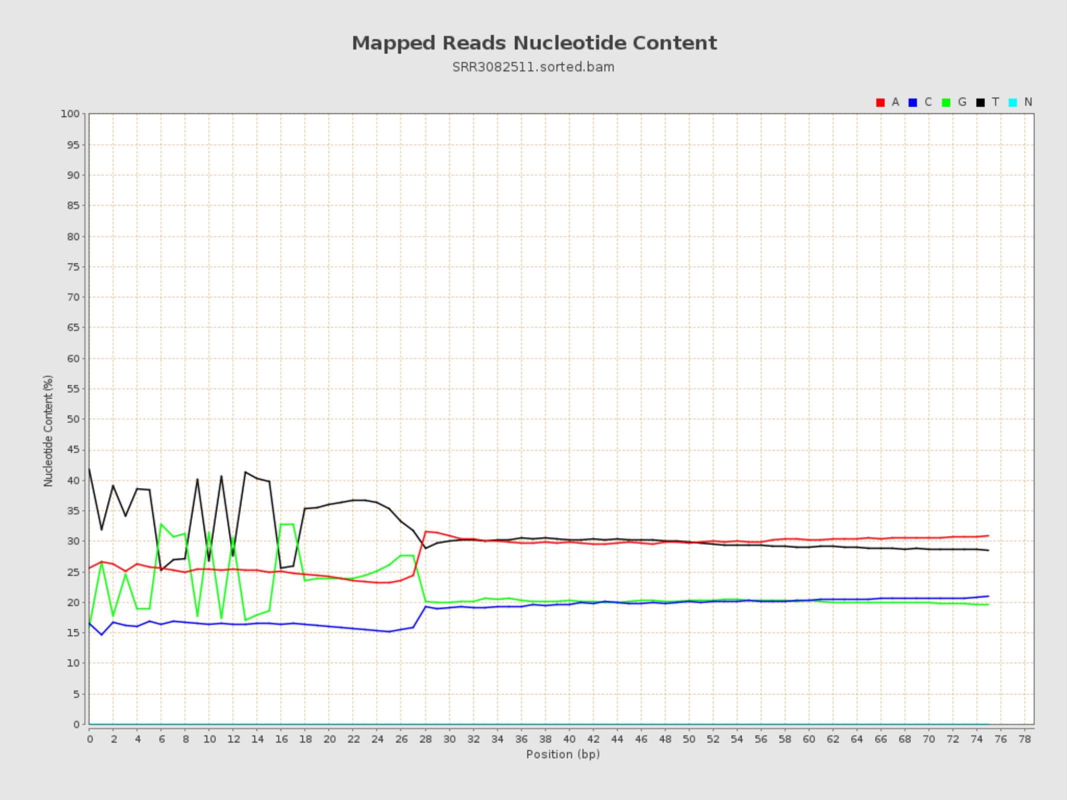
6. Results : Genome Fraction Coverage



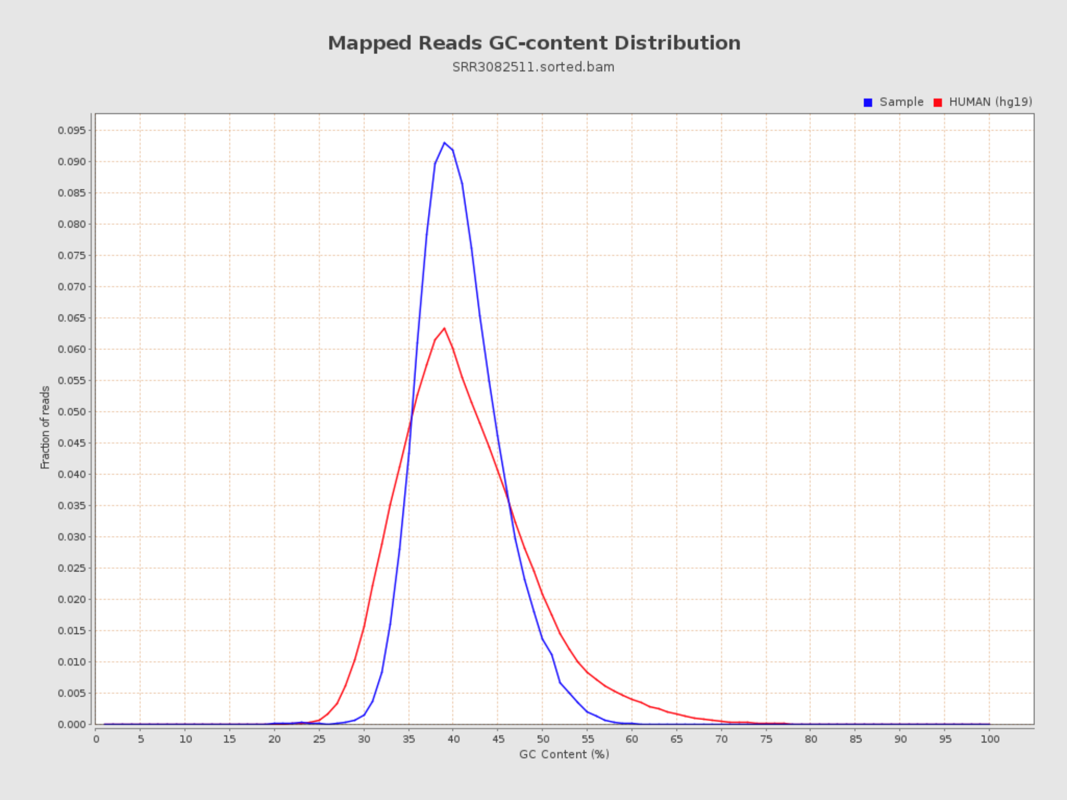
7. Results : Duplication Rate Histogram



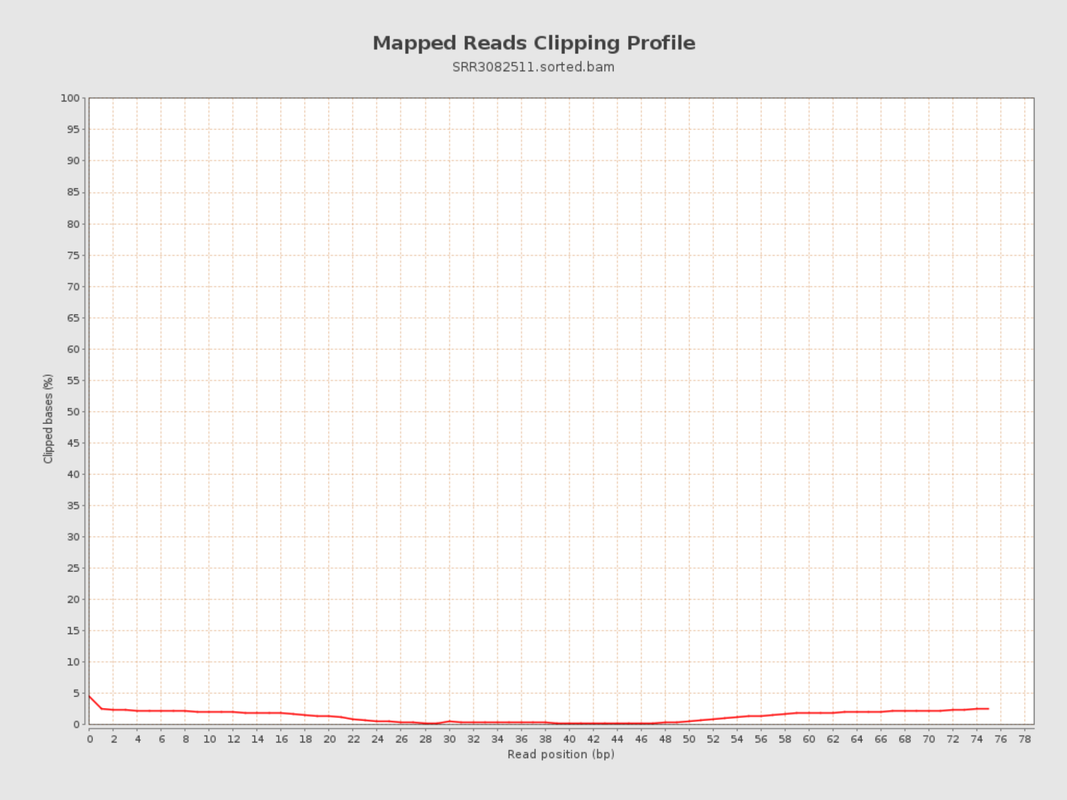
8. Results : Mapped Reads Nucleotide Content



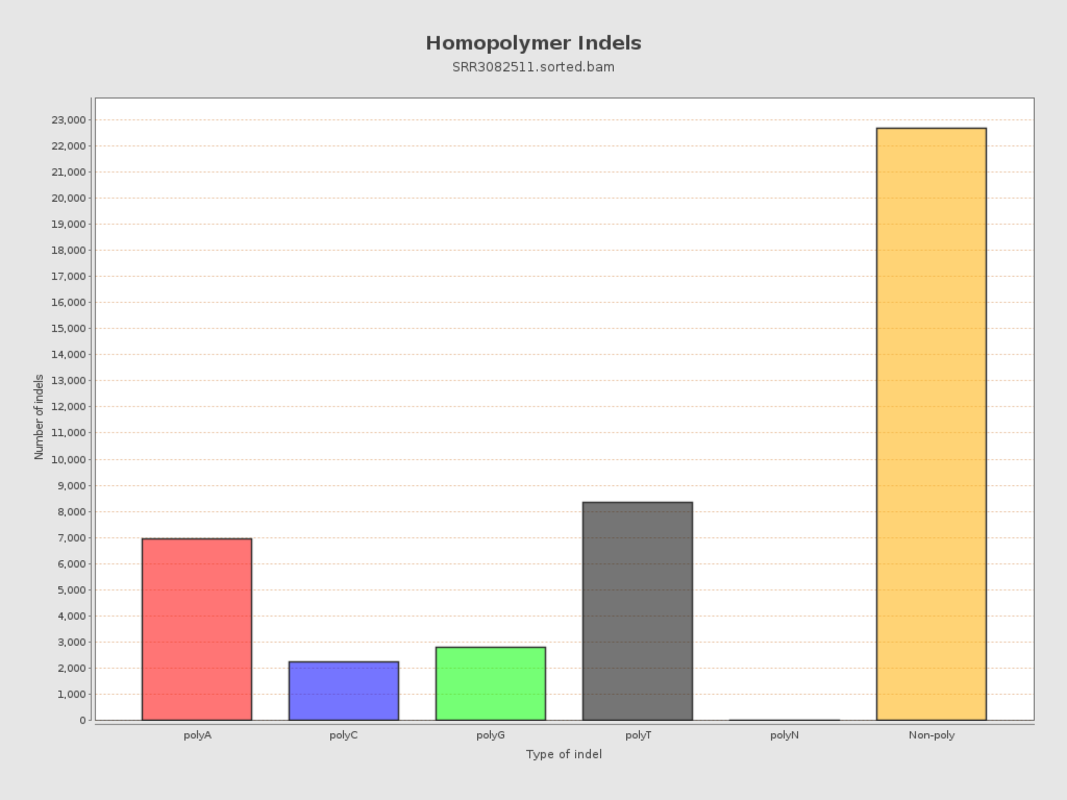
9. Results : Mapped Reads GC-content Distribution



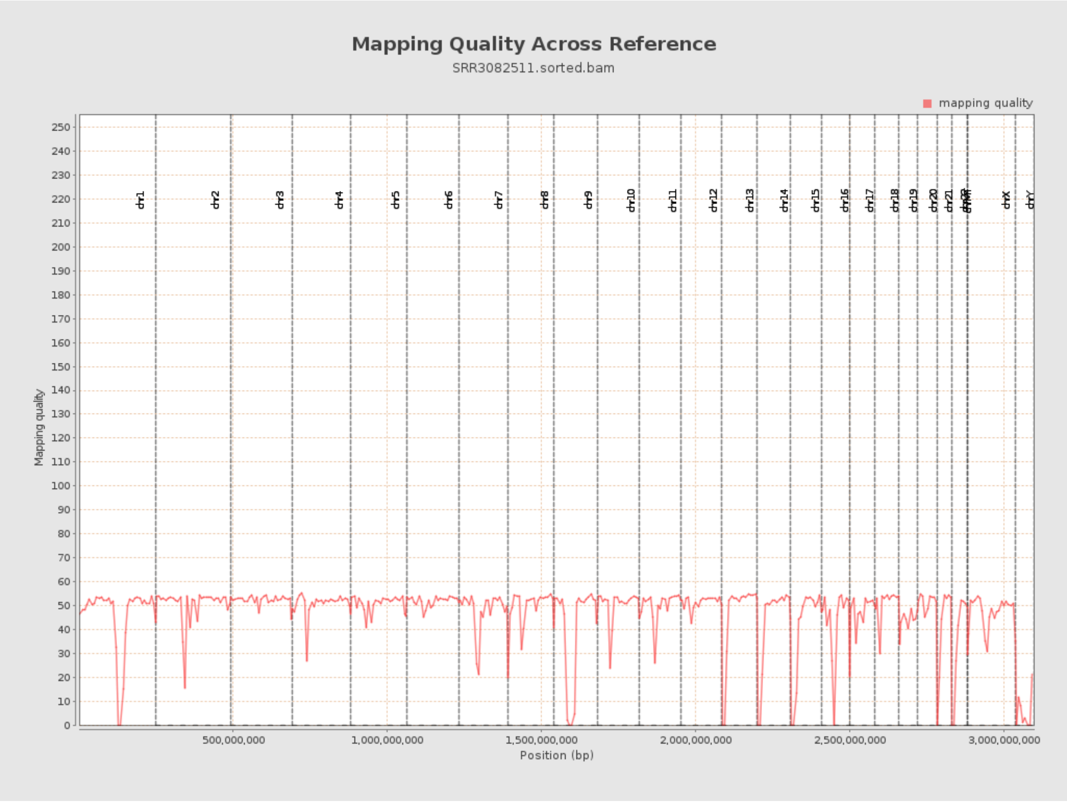
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram