Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:45:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549052.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_SRR1549052 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549052.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:45:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549052.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,940,125
Mapped reads	3,153,124 / 80.03%
Unmapped reads	787,001 / 19.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	111,229 / 2.82%
Duplication rate	2.3%
Clipped reads	281,437 / 7.14%

2.2. ACGT Content

Number/percentage of A's	34,375,844 / 27.61%
Number/percentage of C's	27,366,492 / 21.98%
Number/percentage of T's	35,285,492 / 28.34%
Number/percentage of G's	27,495,352 / 22.08%
Number/percentage of N's	1,039 / 0%
GC Percentage	44.06%

2.3. Coverage

Mean	0.0402
Standard Deviation	0.3976

2.4. Mapping Quality

Mean Mapping Quality	36.17

2.5. Mismatches and indels

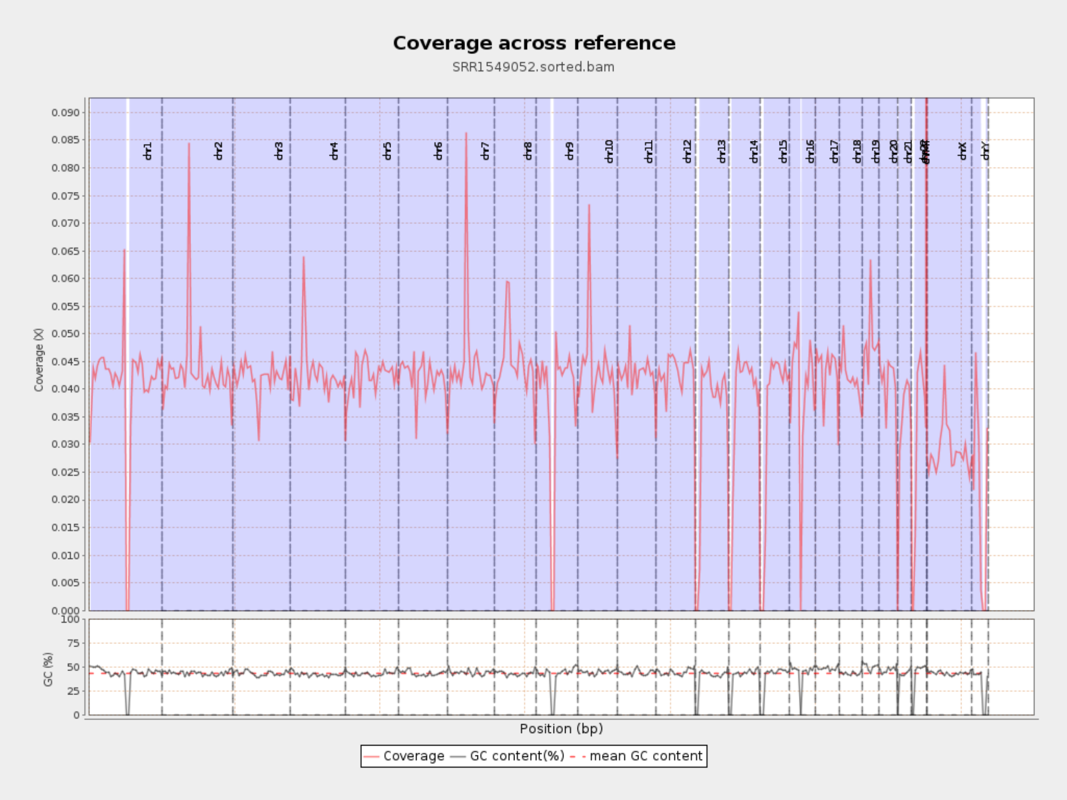
General error rate	0.31%
Mismatches	377,346
Insertions	4,350
Mapped reads with at least one insertion	0.14%
Deletions	8,530
Mapped reads with at least one deletion	0.27%
Homopolymer indels	38.62%

2.6. Chromosome stats

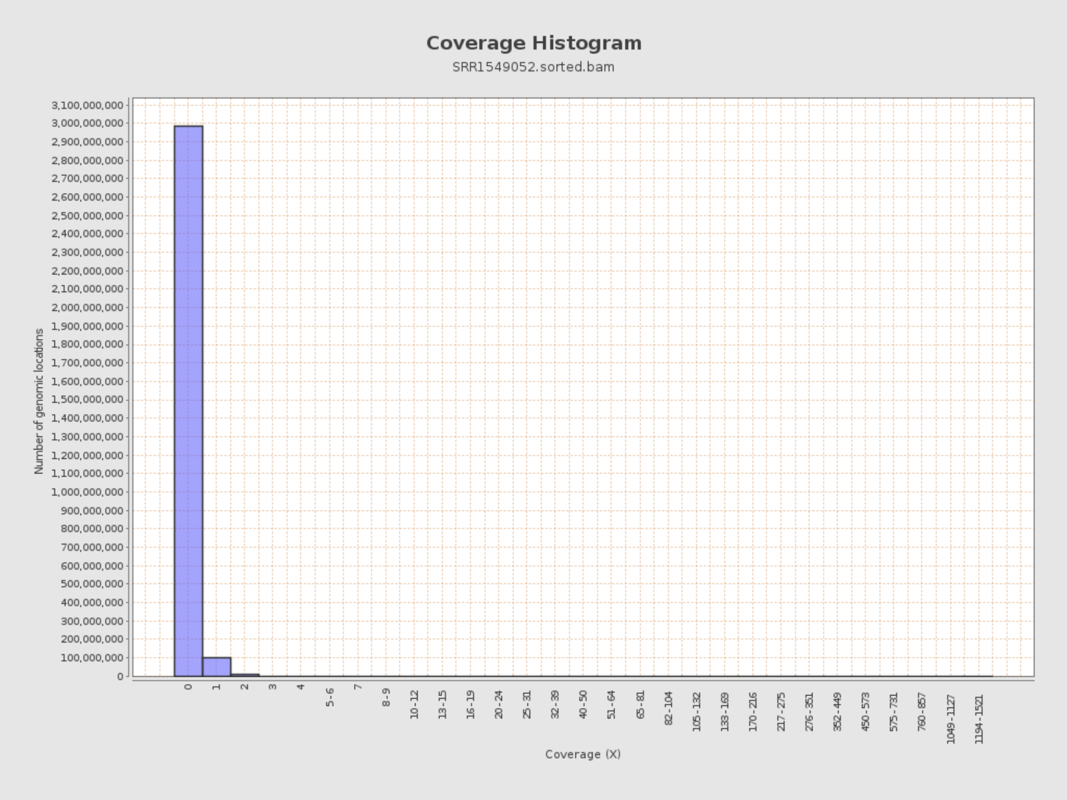
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10085261	0.0405	0.612
chr2	243199373	10590625	0.0435	0.4108
chr3	198022430	8361717	0.0422	0.2301
chr4	191154276	8134559	0.0426	0.2521
chr5	180915260	7683818	0.0425	0.2327
chr6	171115067	7222117	0.0422	0.2377
chr7	159138663	7154219	0.045	0.5292
chr8	146364022	6514174	0.0445	0.7986

chr9	141213431	5342076	0.0378	0.421
chr10	135534747	5934767	0.0438	0.3416
chr11	135006516	5767757	0.0427	0.2958
chr12	133851895	5775981	0.0432	0.2393
chr13	115169878	3933696	0.0342	0.2069
chr14	107349540	3853285	0.0359	0.2725
chr15	102531392	3555541	0.0347	0.2079
chr16	90354753	3583007	0.0397	0.2546
chr17	81195210	3498120	0.0431	0.2404
chr18	78077248	3312403	0.0424	0.7021
chr19	59128983	2851630	0.0482	0.6486
chr20	63025520	2586824	0.041	0.2368
chr21	48129895	1583367	0.0329	0.2635
chr22	51304566	1497884	0.0292	0.2609
chrMT	16571	7289	0.4399	0.8067
chrX	155270560	4512744	0.0291	0.251
chrY	59373566	1192183	0.0201	0.2319

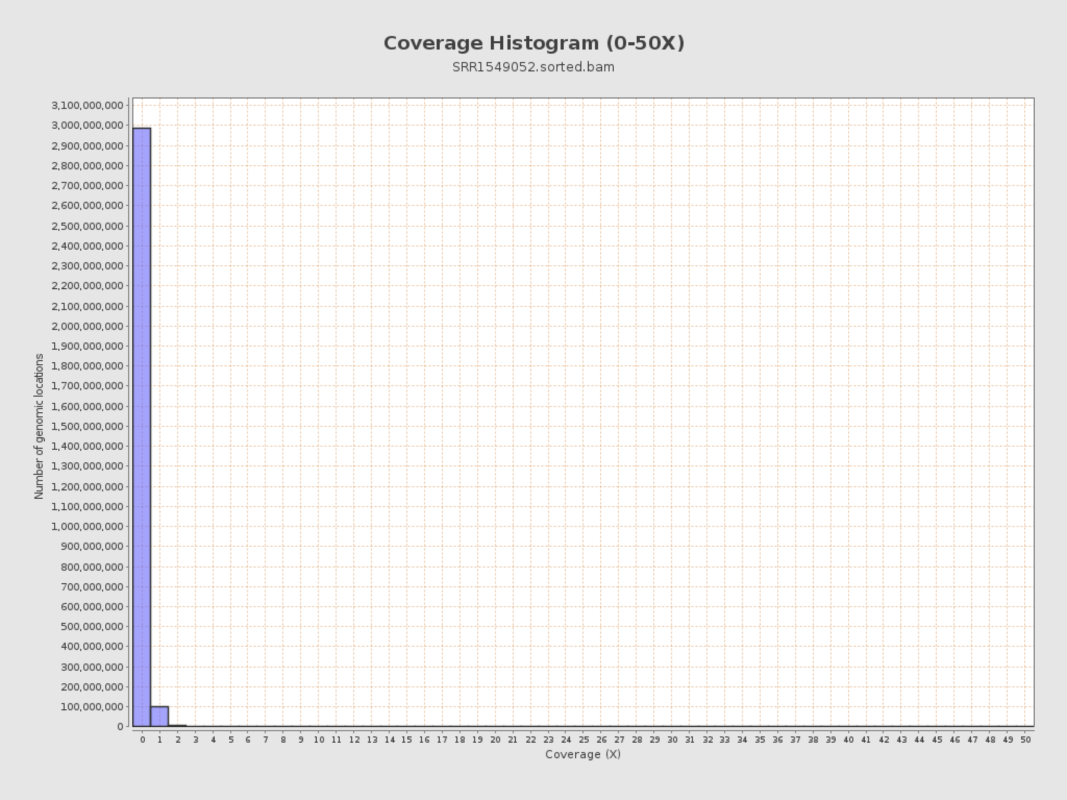
3. Results : Coverage across reference



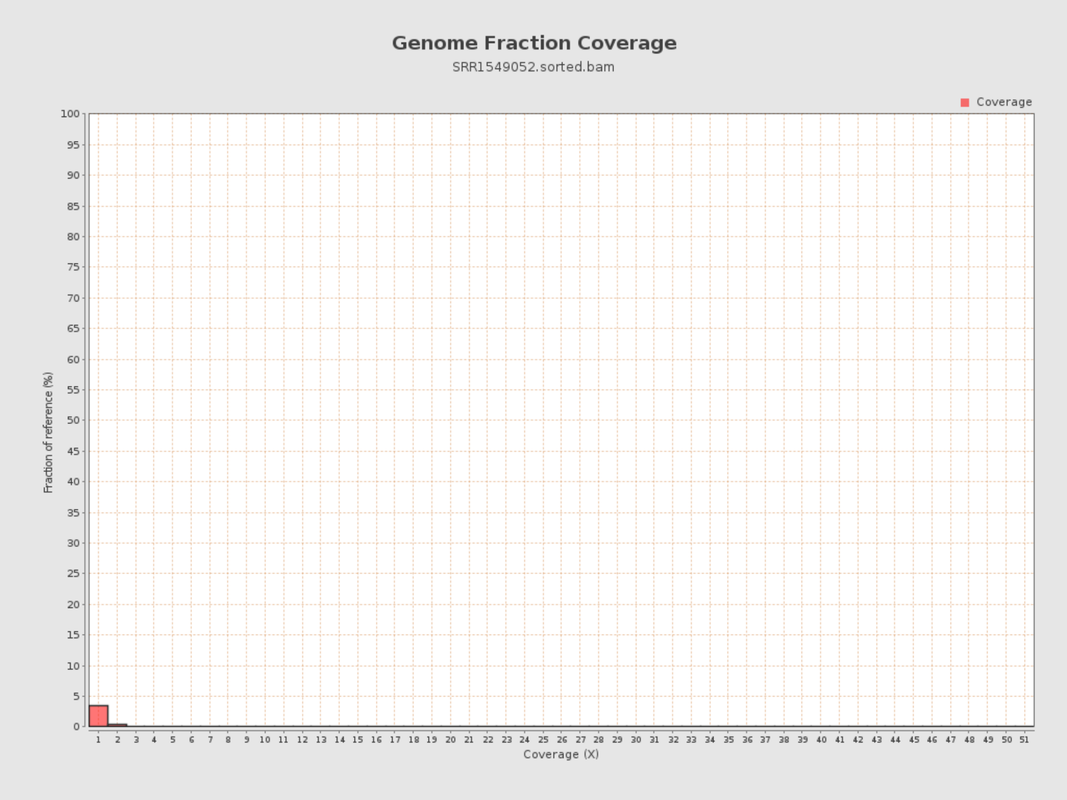
4. Results : Coverage Histogram



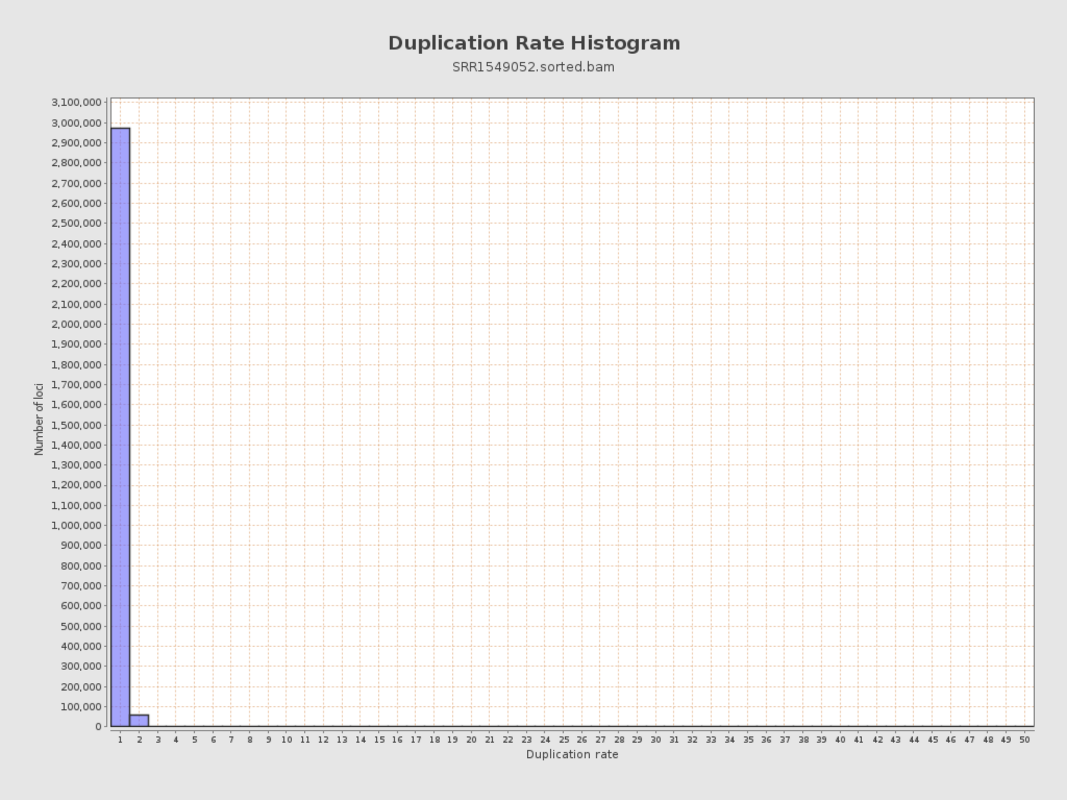
5. Results : Coverage Histogram (0-50X)



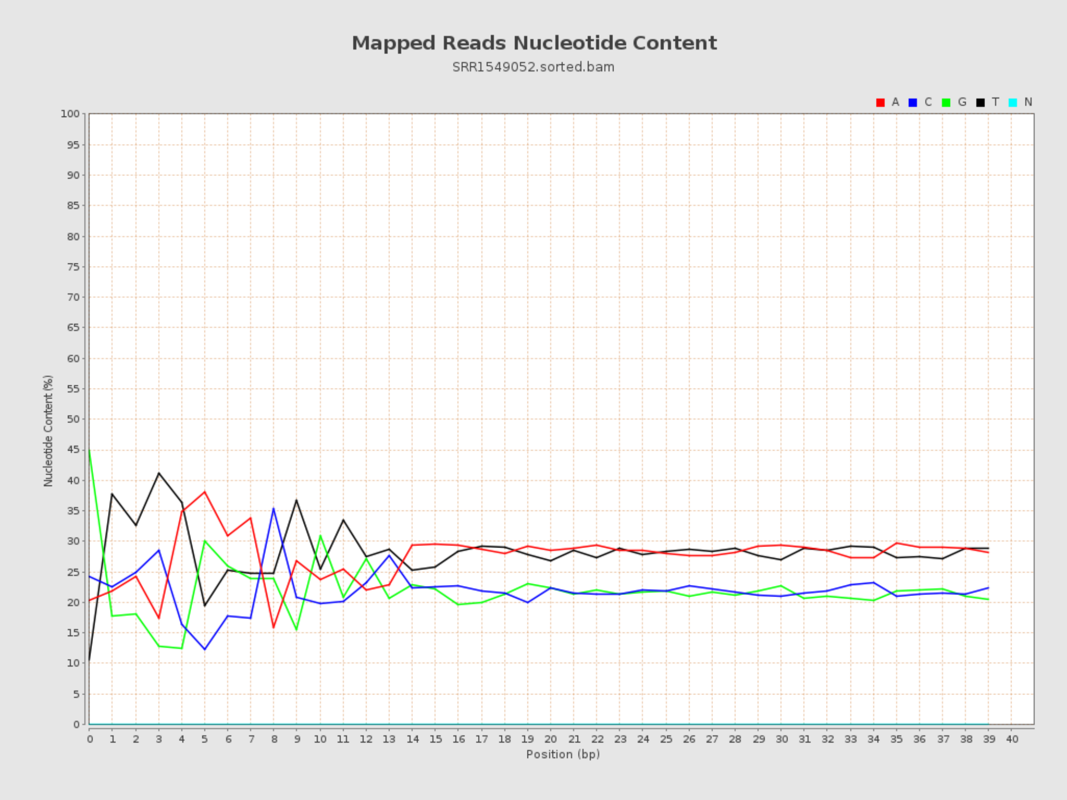
6. Results : Genome Fraction Coverage



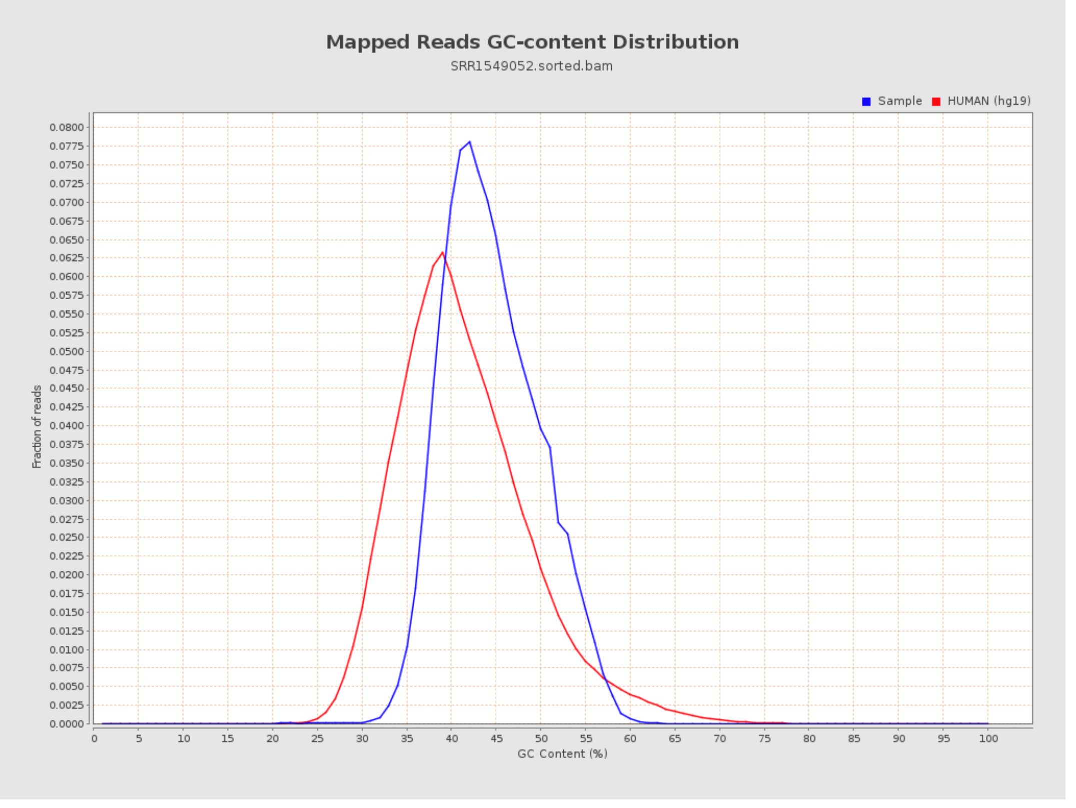
7. Results : Duplication Rate Histogram



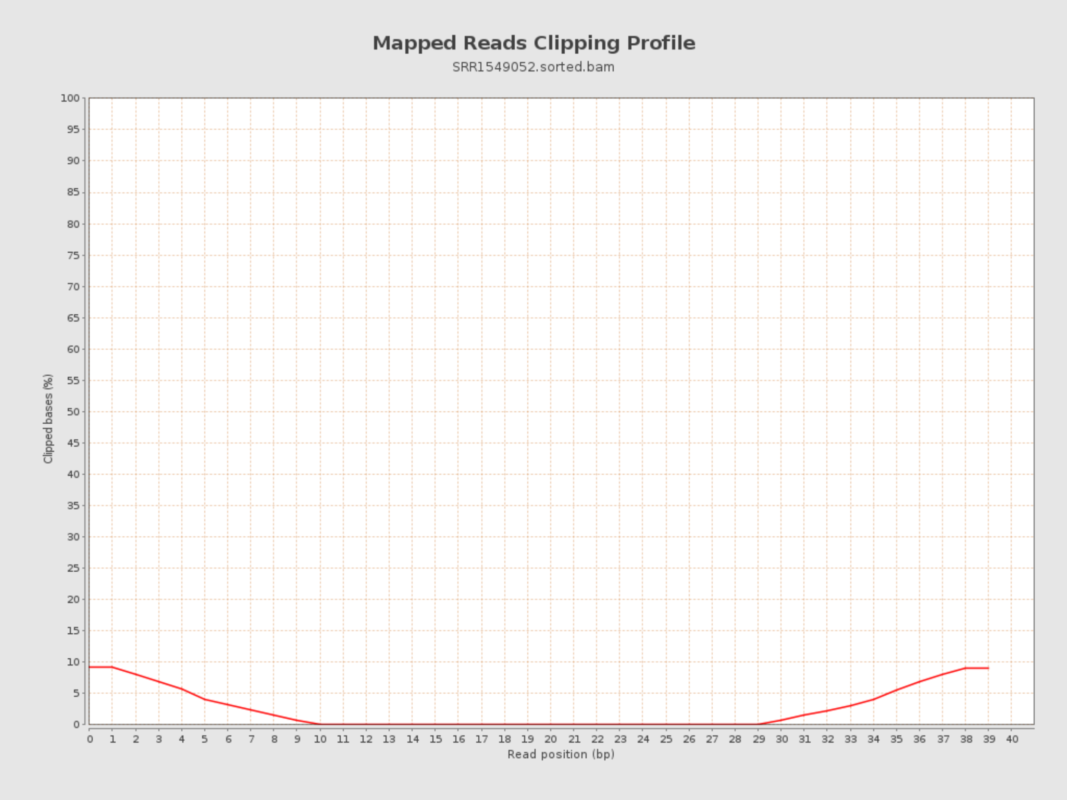
8. Results : Mapped Reads Nucleotide Content



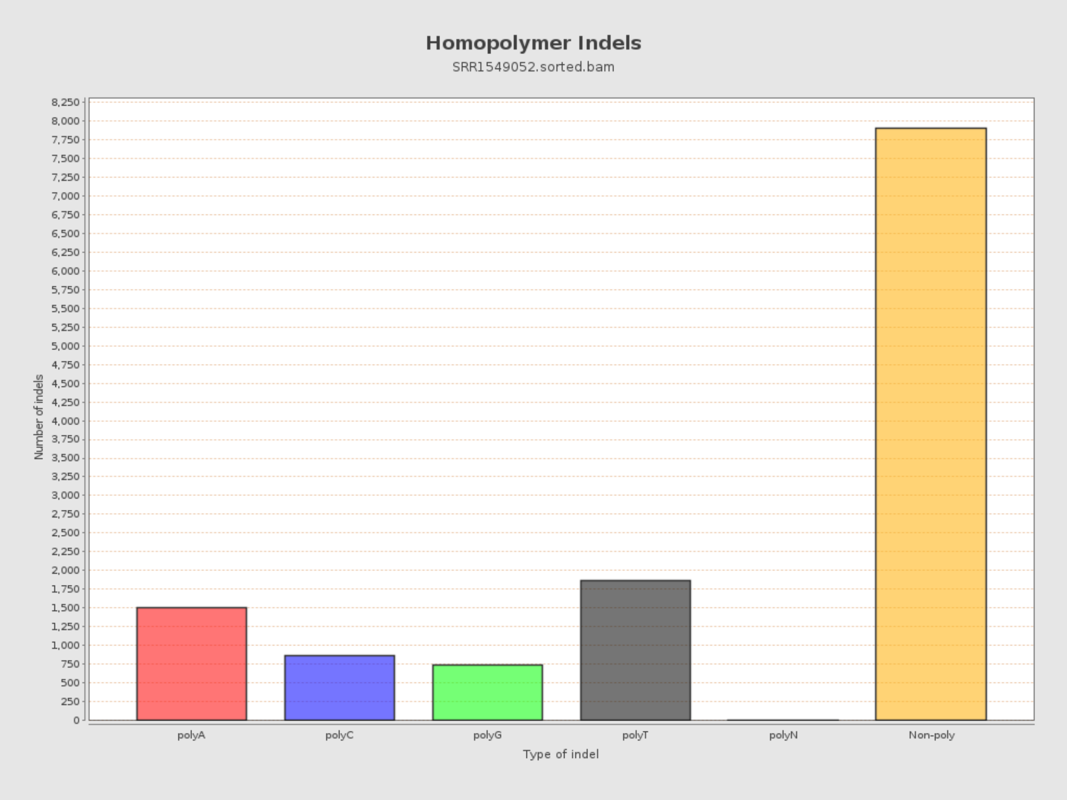
9. Results : Mapped Reads GC-content Distribution



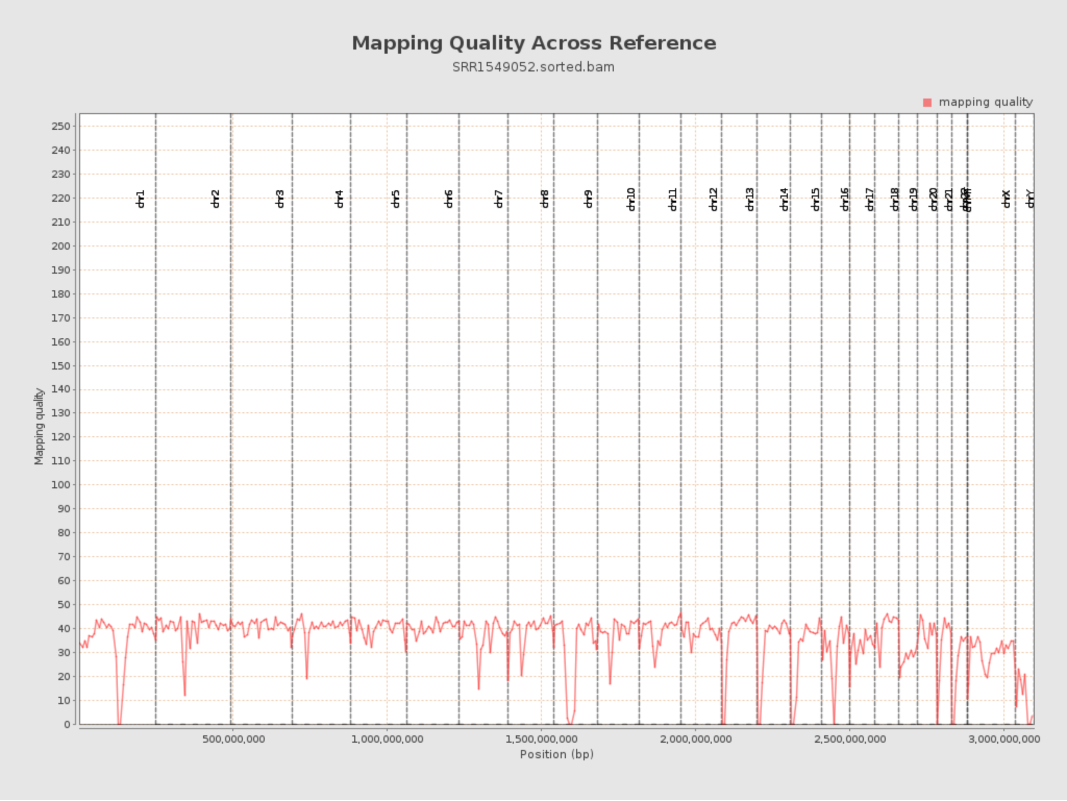
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram