Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 22:11:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549086.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_SRR1549086 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549086.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 22:10:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549086.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,328,873
Mapped reads	6,451,991 / 88.04%
Unmapped reads	876,882 / 11.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	197,174 / 2.69%
Duplication rate	1.82%
Clipped reads	333,829 / 4.55%

2.2. ACGT Content

Number/percentage of A's	77,651,682 / 30.32%
Number/percentage of C's	50,460,700 / 19.7%
Number/percentage of T's	78,578,442 / 30.68%
Number/percentage of G's	49,371,891 / 19.28%
Number/percentage of N's	63,698 / 0.02%
GC Percentage	38.98%

2.3. Coverage

Mean	0.0827
Standard Deviation	0.7264

2.4. Mapping Quality

Mean Mapping Quality	44.07

2.5. Mismatches and indels

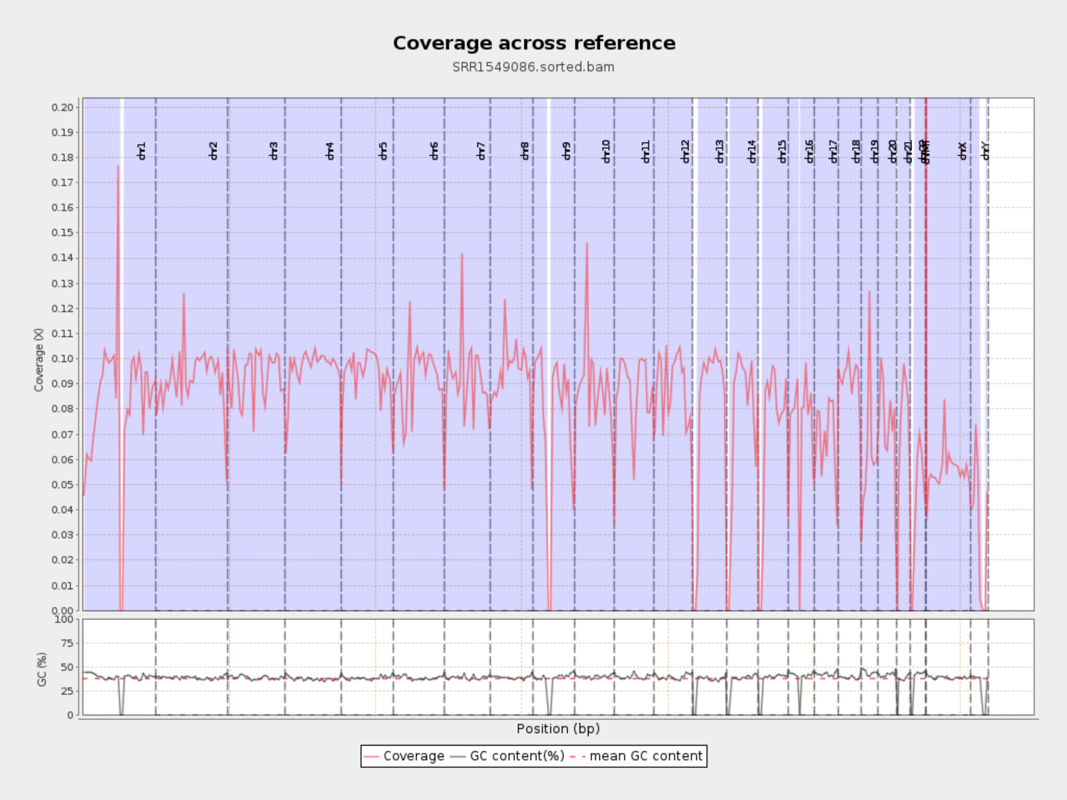
General error rate	0.41%
Mismatches	1,046,170
Insertions	6,581
Mapped reads with at least one insertion	0.1%
Deletions	20,231
Mapped reads with at least one deletion	0.31%
Homopolymer indels	45.81%

2.6. Chromosome stats

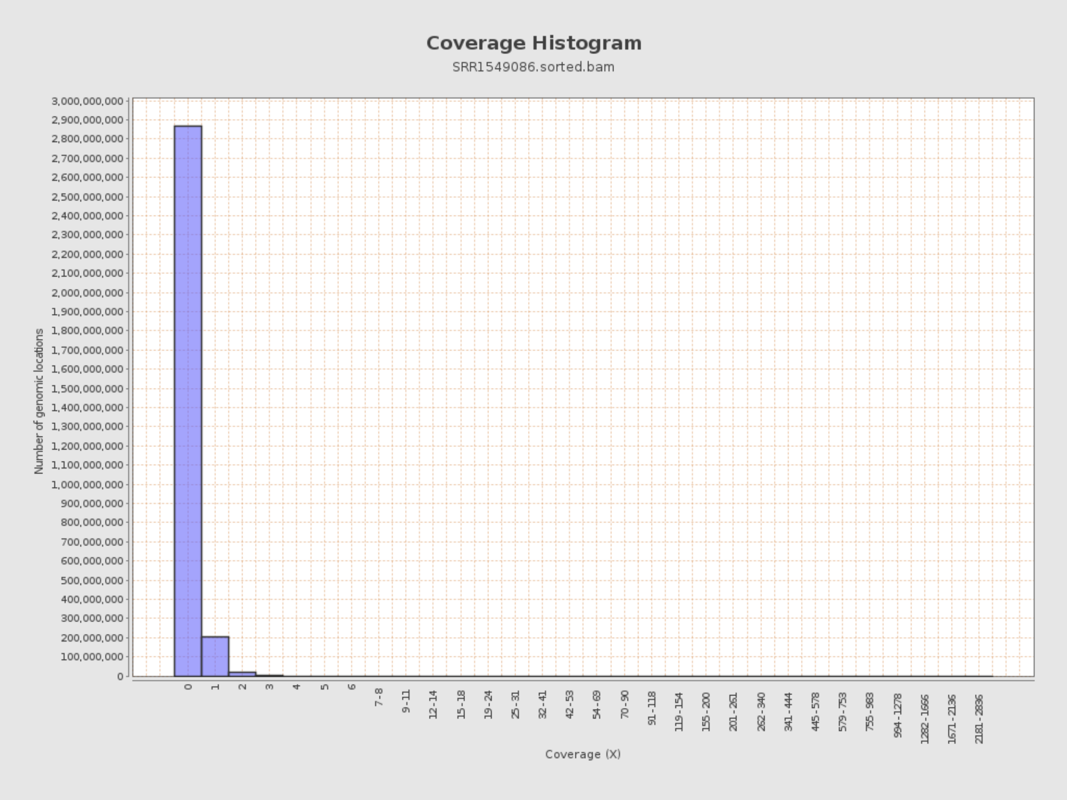
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20564284	0.0825	1.885
chr2	243199373	22513873	0.0926	0.5139
chr3	198022430	18522875	0.0935	0.3423
chr4	191154276	18459753	0.0966	0.342
chr5	180915260	16933084	0.0936	0.3469
chr6	171115067	15928723	0.0931	0.4459
chr7	159138663	14554181	0.0915	0.7317
chr8	146364022	13784382	0.0942	0.4983

chr9	141213431	10863867	0.0769	0.5034
chr10	135534747	12101189	0.0893	0.6633
chr11	135006516	11777791	0.0872	0.5487
chr12	133851895	11808252	0.0882	0.3504
chr13	115169878	9125685	0.0792	0.2996
chr14	107349540	8021905	0.0747	0.3755
chr15	102531392	7112425	0.0694	0.2841
chr16	90354753	6442015	0.0713	0.3942
chr17	81195210	5609663	0.0691	0.3396
chr18	78077248	7276642	0.0932	1.0678
chr19	59128983	3800295	0.0643	1.4316
chr20	63025520	4826395	0.0766	0.3158
chr21	48129895	3346561	0.0695	0.3424
chr22	51304566	2179458	0.0425	0.2751
chrMT	16571	7918	0.4778	0.8705
chrX	155270560	8632077	0.0556	0.3576
chrY	59373566	1958387	0.033	0.278

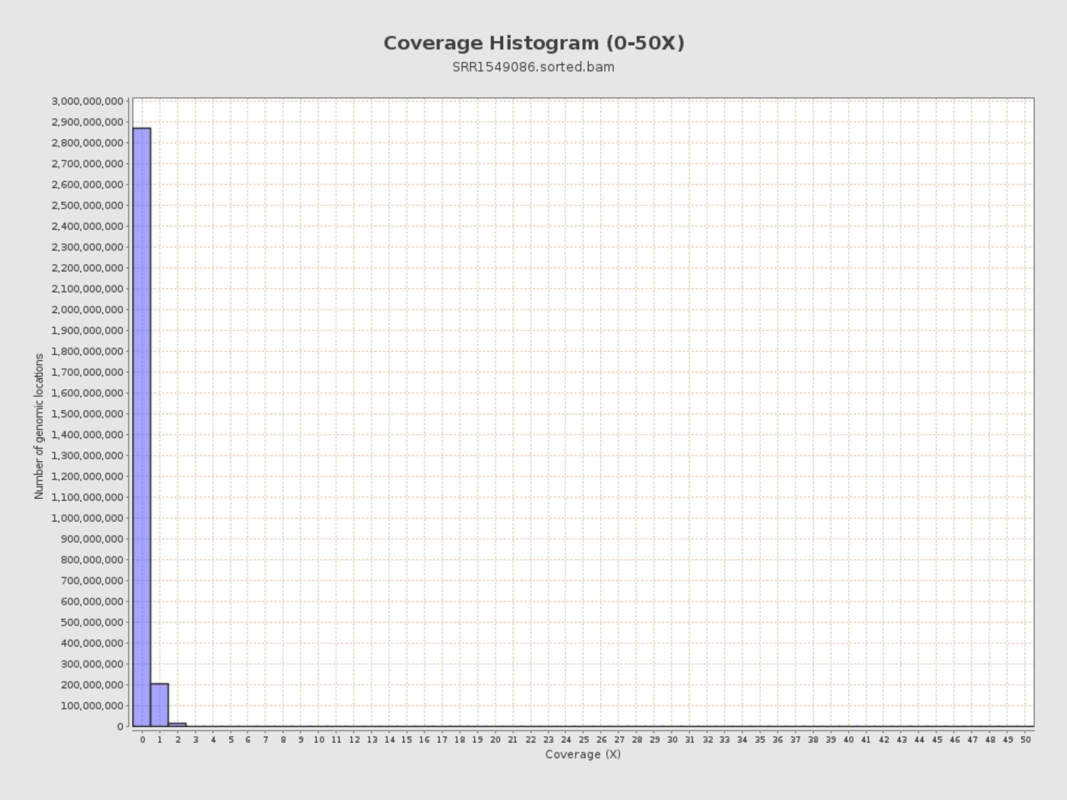
3. Results : Coverage across reference



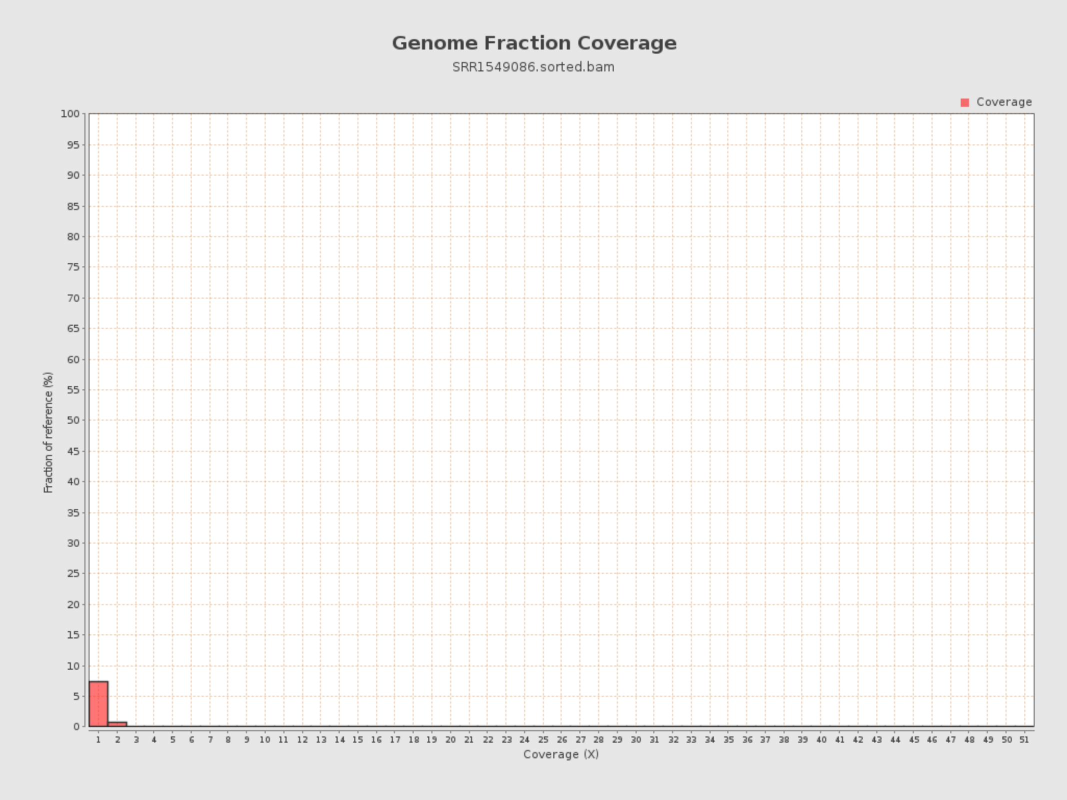
4. Results : Coverage Histogram



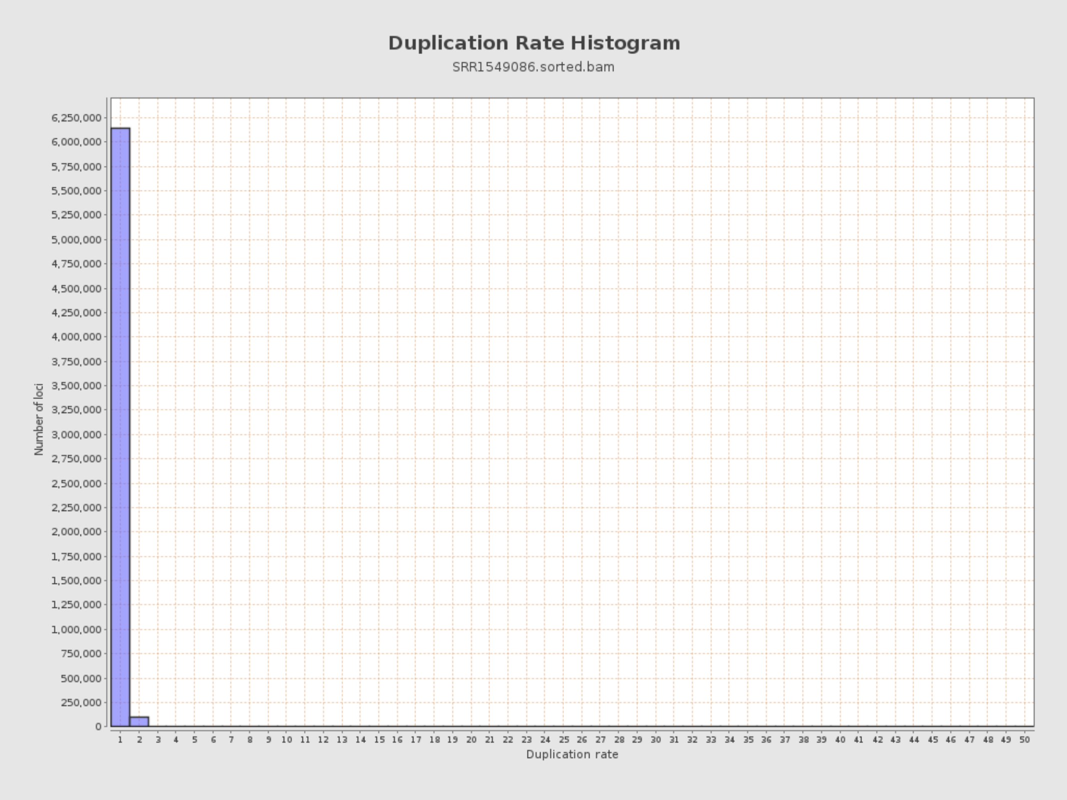
5. Results : Coverage Histogram (0-50X)



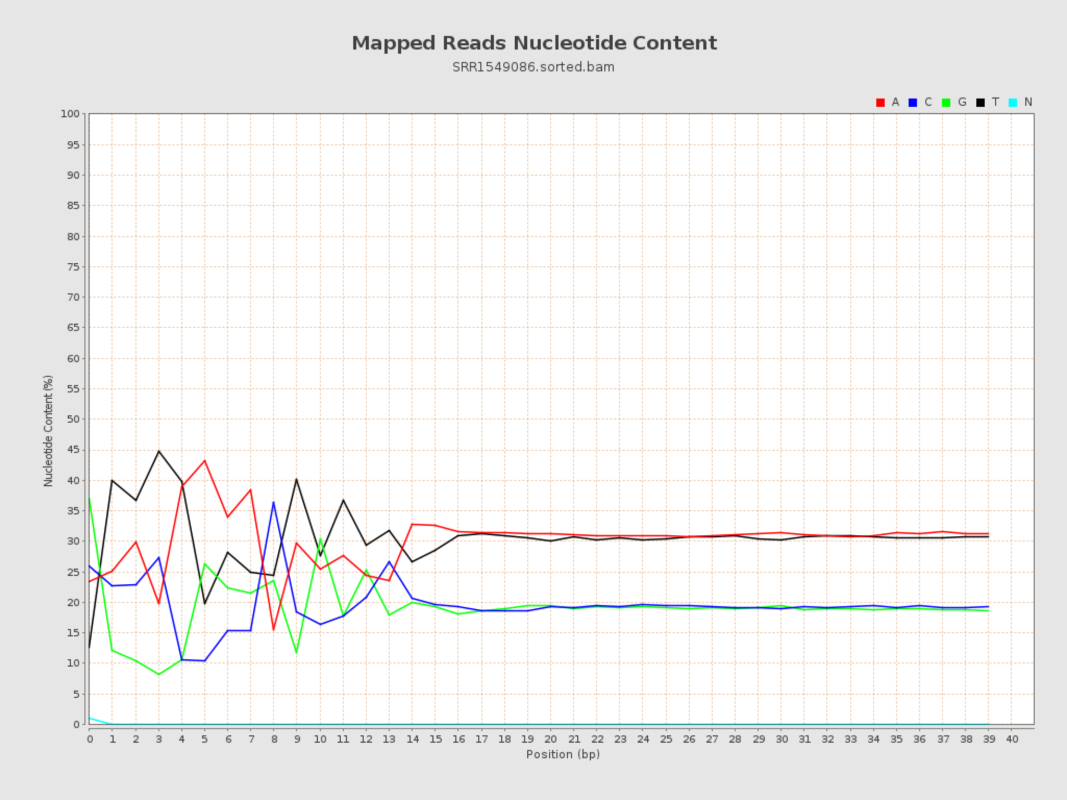
6. Results : Genome Fraction Coverage



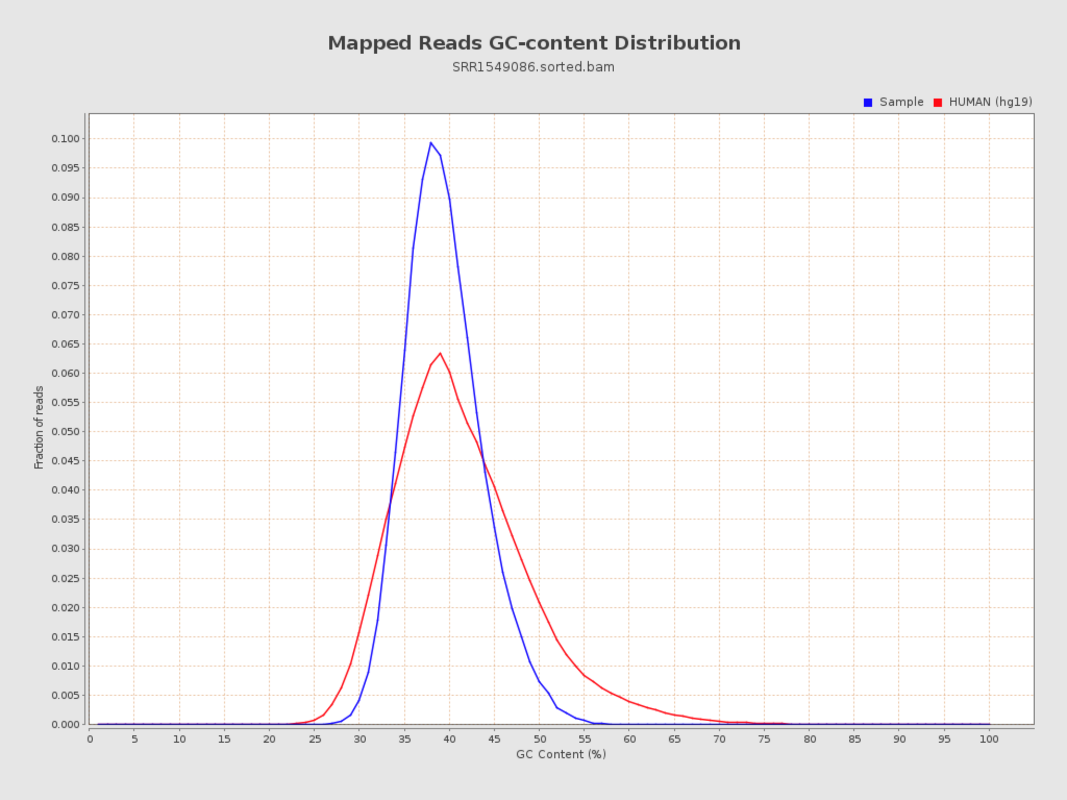
7. Results : Duplication Rate Histogram



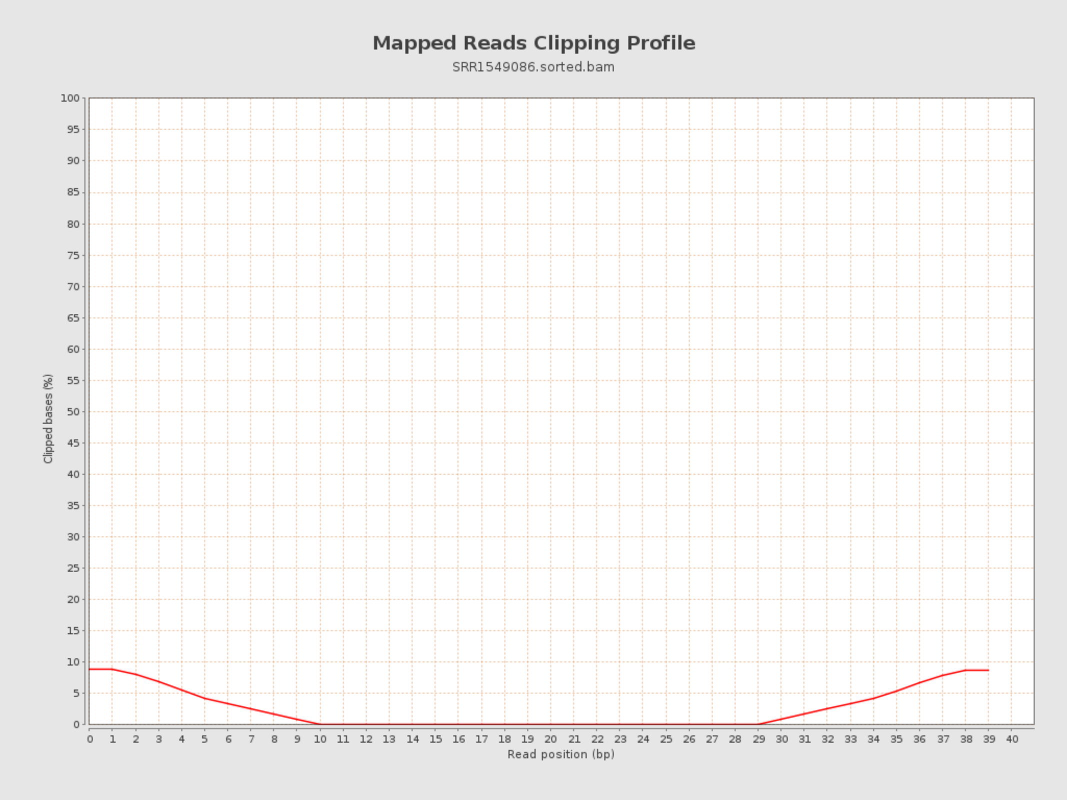
8. Results : Mapped Reads Nucleotide Content



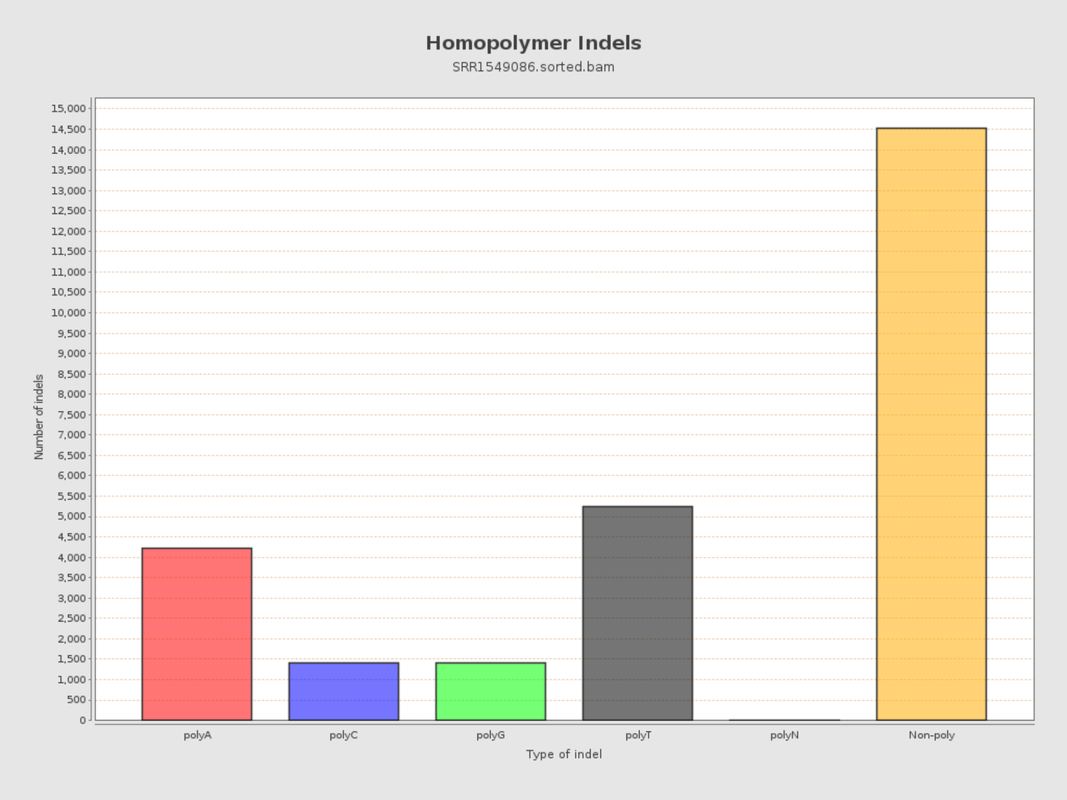
9. Results : Mapped Reads GC-content Distribution



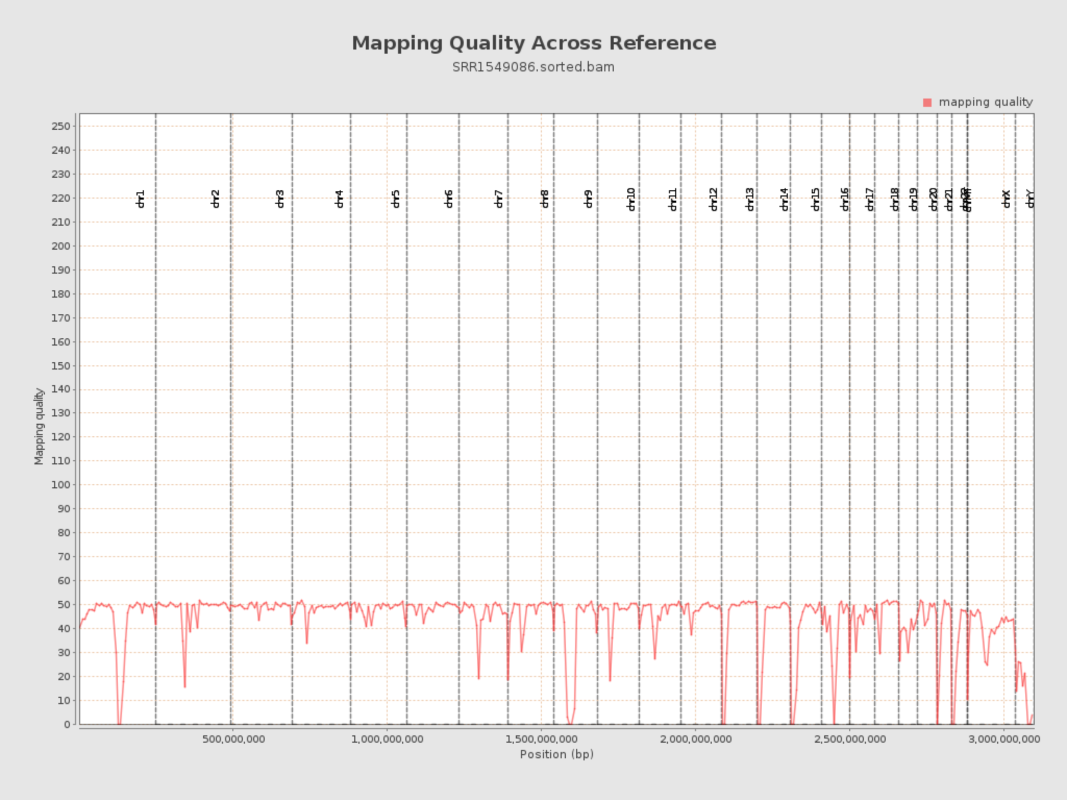
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram