Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:16:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549046.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_SRR1549046 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549046.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:16:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549046.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,832,202
Mapped reads	2,084,744 / 73.61%
Unmapped reads	747,458 / 26.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	56,433 / 1.99%
Duplication rate	2.27%
Clipped reads	149,411 / 5.28%

2.2. ACGT Content

Number/percentage of A's	23,501,558 / 28.48%
Number/percentage of C's	17,265,478 / 20.92%
Number/percentage of T's	24,246,813 / 29.38%
Number/percentage of G's	17,504,041 / 21.21%
Number/percentage of N's	642 / 0%
GC Percentage	42.14%

2.3. Coverage

Mean	0.0267
Standard Deviation	0.2338

2.4. Mapping Quality

Mean Mapping Quality	40.61

2.5. Mismatches and indels

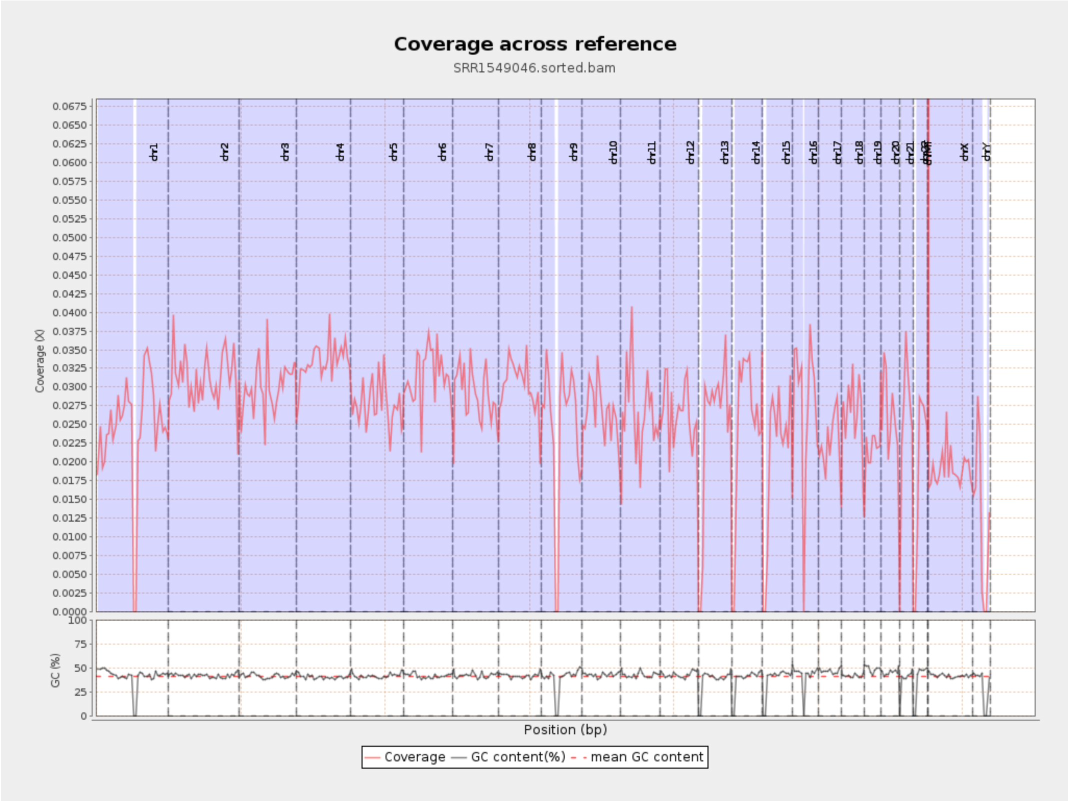
General error rate	0.24%
Mismatches	198,541
Insertions	2,347
Mapped reads with at least one insertion	0.11%
Deletions	5,866
Mapped reads with at least one deletion	0.28%
Homopolymer indels	41.85%

2.6. Chromosome stats

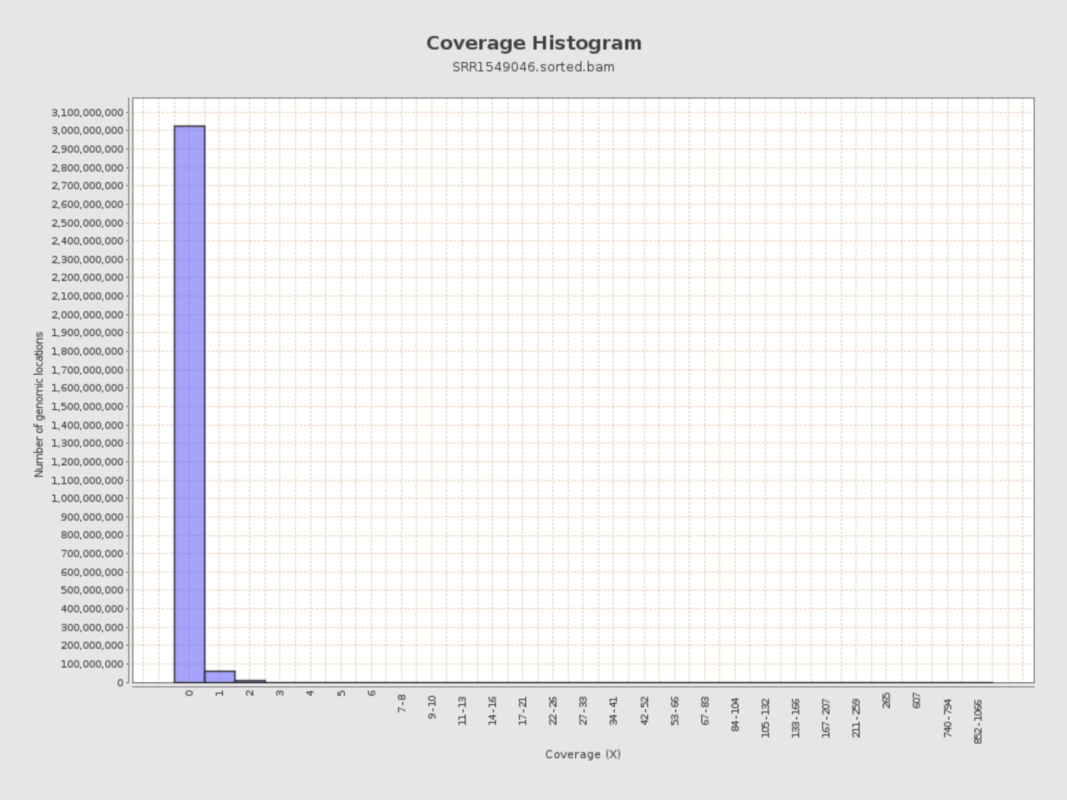
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6099747	0.0245	0.2292
chr2	243199373	7597396	0.0312	0.2274
chr3	198022430	5928079	0.0299	0.2022
chr4	191154276	6373002	0.0333	0.2102
chr5	180915260	4999592	0.0276	0.1879
chr6	171115067	5384013	0.0315	0.2057
chr7	159138663	4618192	0.029	0.241
chr8	146364022	4434441	0.0303	0.5554

chr9	141213431	3527002	0.025	0.2075
chr10	135534747	3587665	0.0265	0.1921
chr11	135006516	3577642	0.0265	0.1967
chr12	133851895	3525656	0.0263	0.1833
chr13	115169878	2811832	0.0244	0.1813
chr14	107349540	2673798	0.0249	0.1894
chr15	102531392	2145431	0.0209	0.1667
chr16	90354753	2457239	0.0272	0.1933
chr17	81195210	1826983	0.0225	0.1676
chr18	78077248	2108561	0.027	0.3132
chr19	59128983	1296463	0.0219	0.2275
chr20	63025520	1635525	0.026	0.1848
chr21	48129895	1243940	0.0258	0.2031
chr22	51304566	966221	0.0188	0.1918
chrMT	16571	11563	0.6978	1.0461
chrX	155270560	2957806	0.019	0.1635
chrY	59373566	738479	0.0124	0.1353

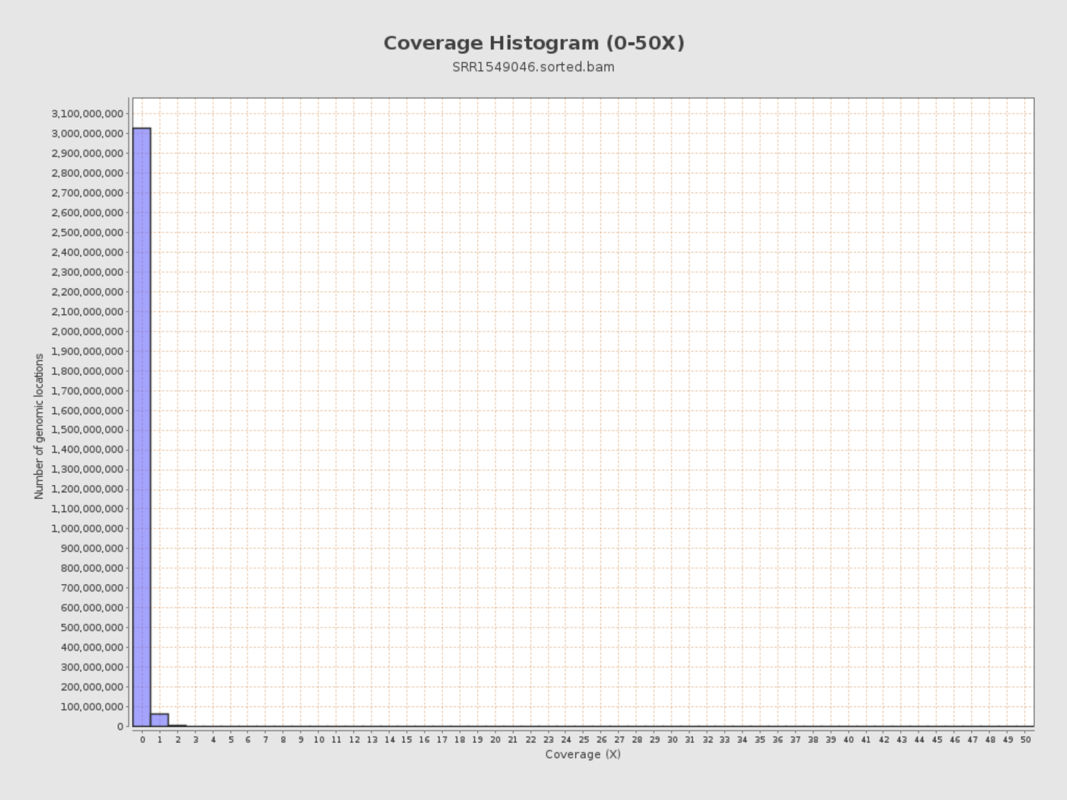
3. Results : Coverage across reference



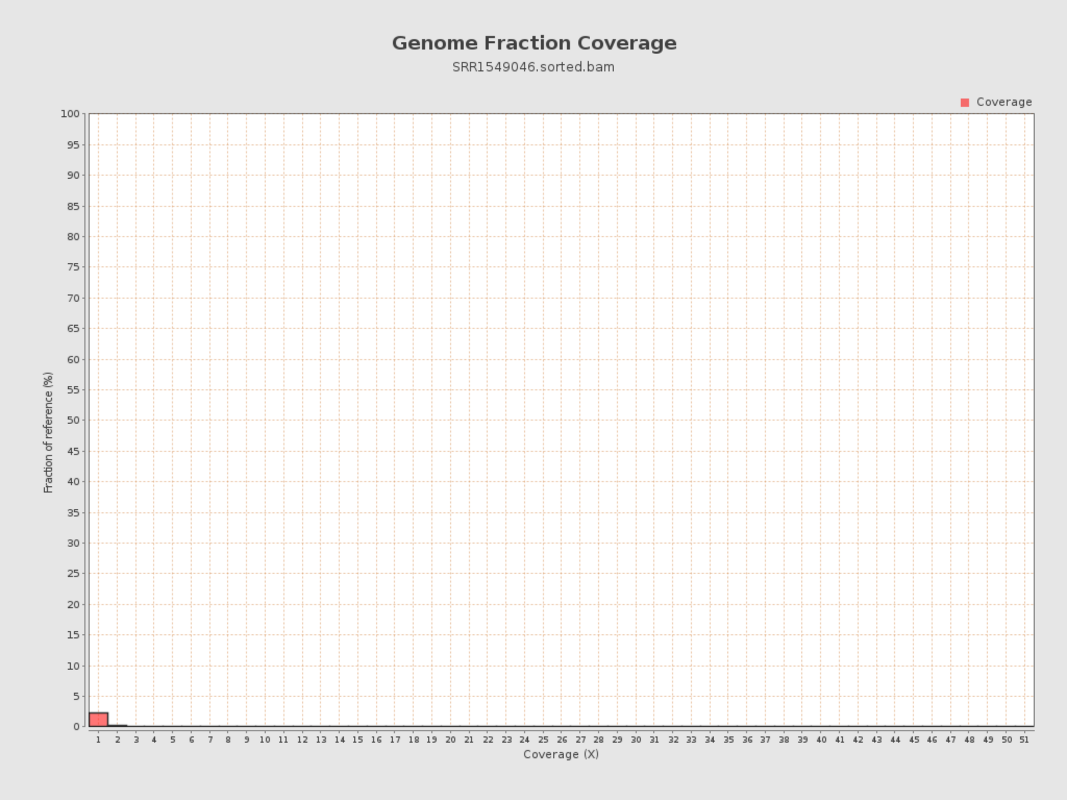
4. Results : Coverage Histogram



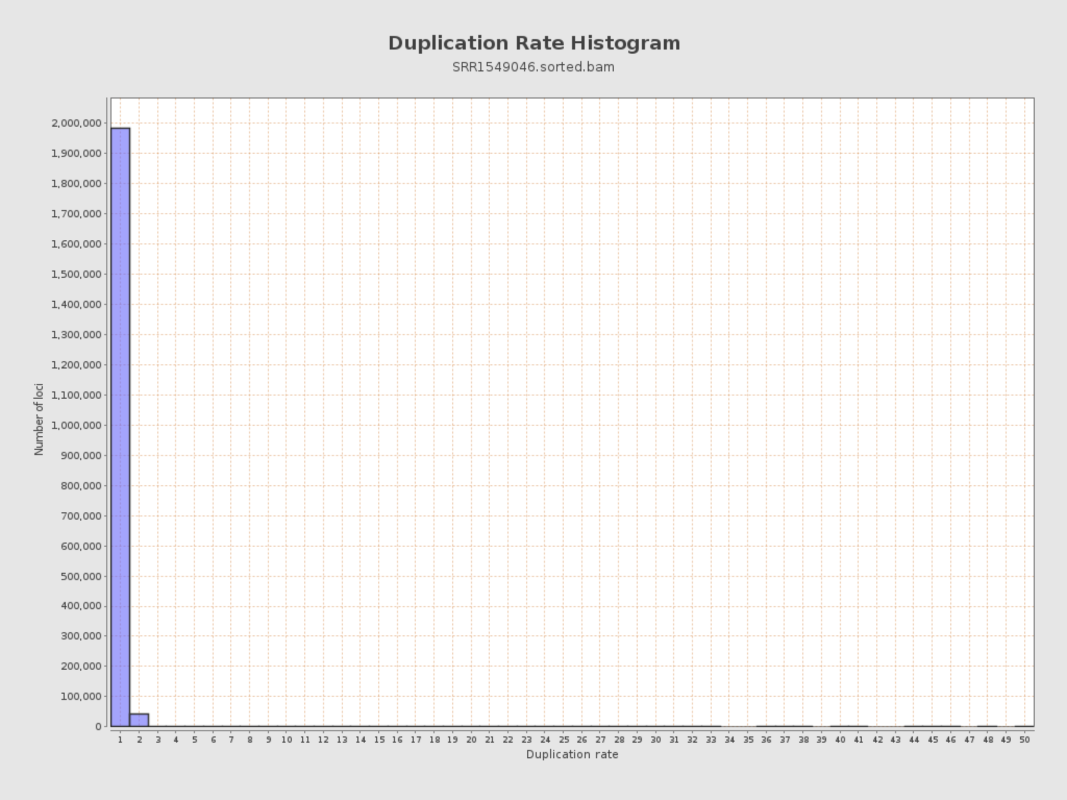
5. Results : Coverage Histogram (0-50X)



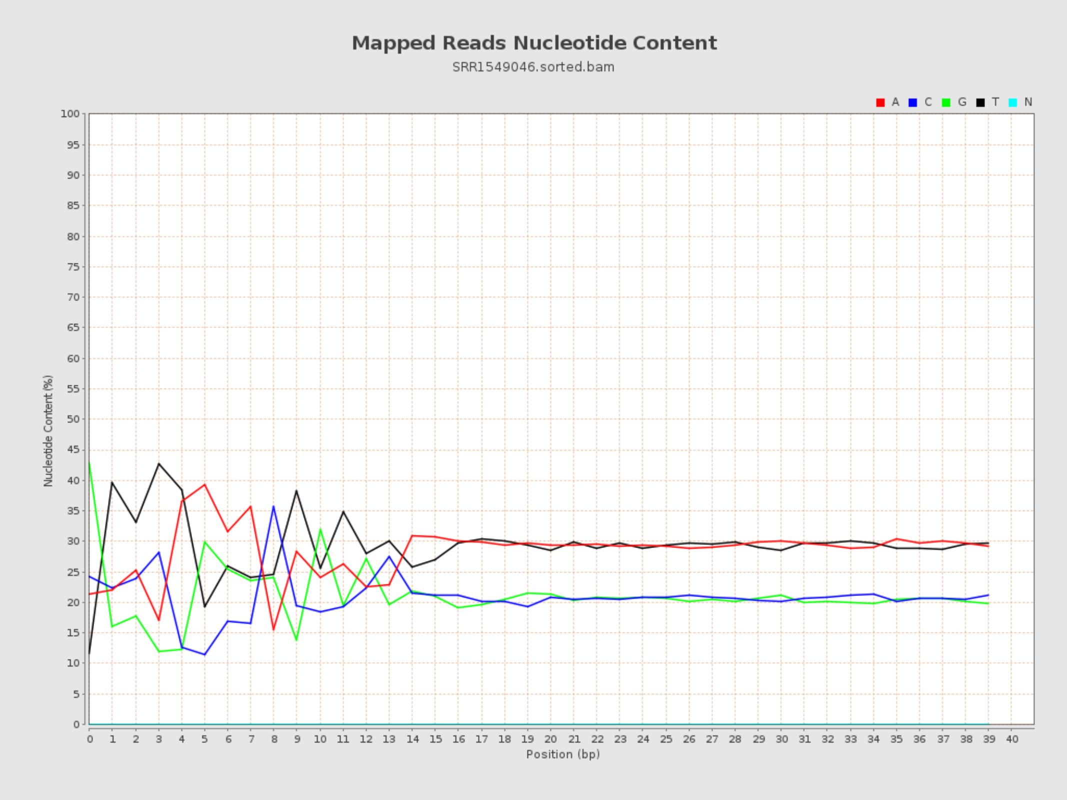
6. Results : Genome Fraction Coverage



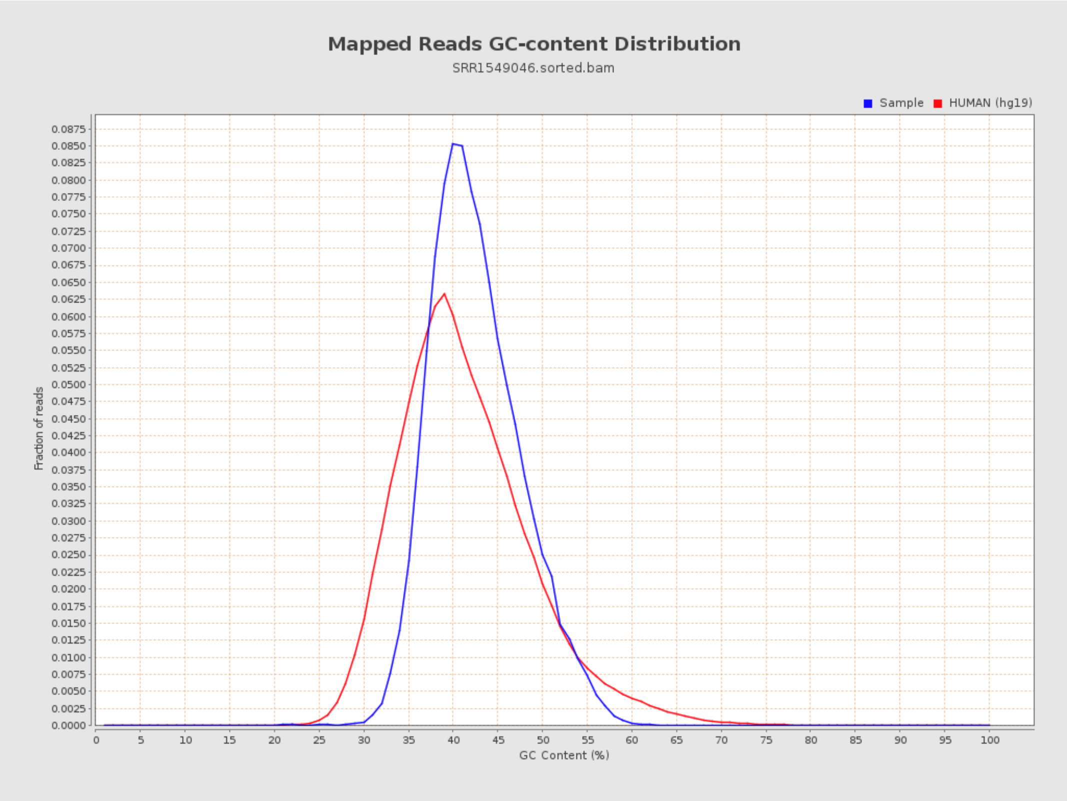
7. Results : Duplication Rate Histogram



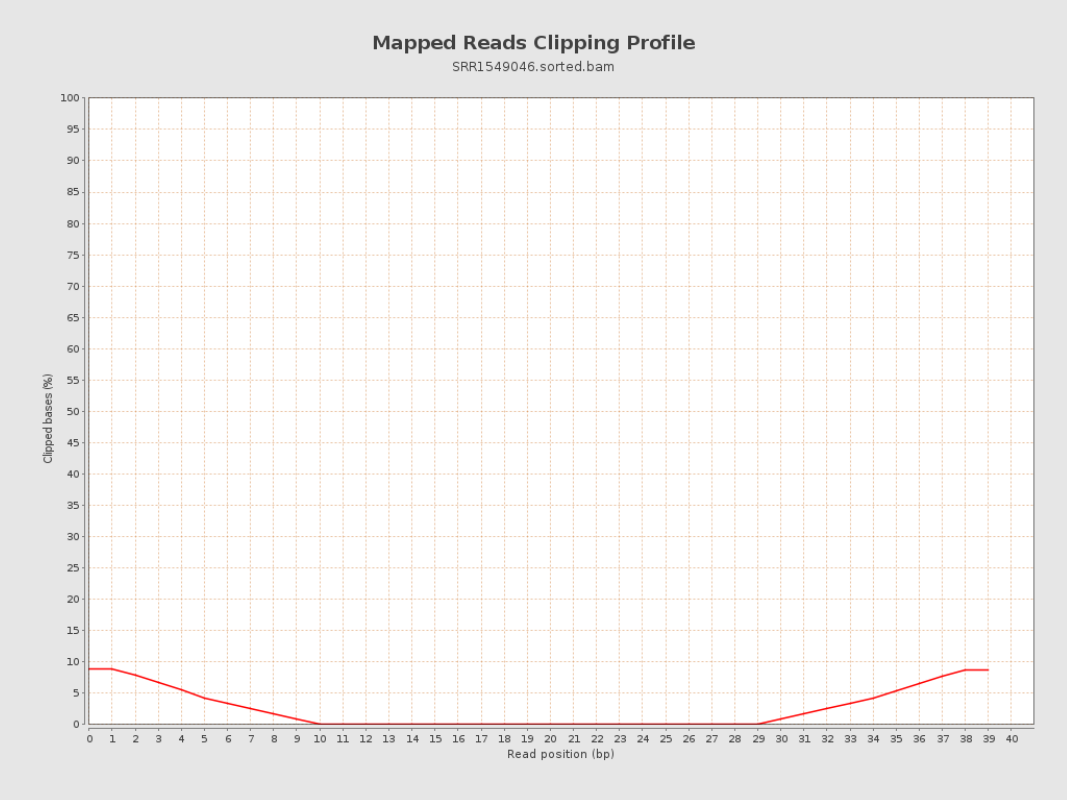
8. Results : Mapped Reads Nucleotide Content



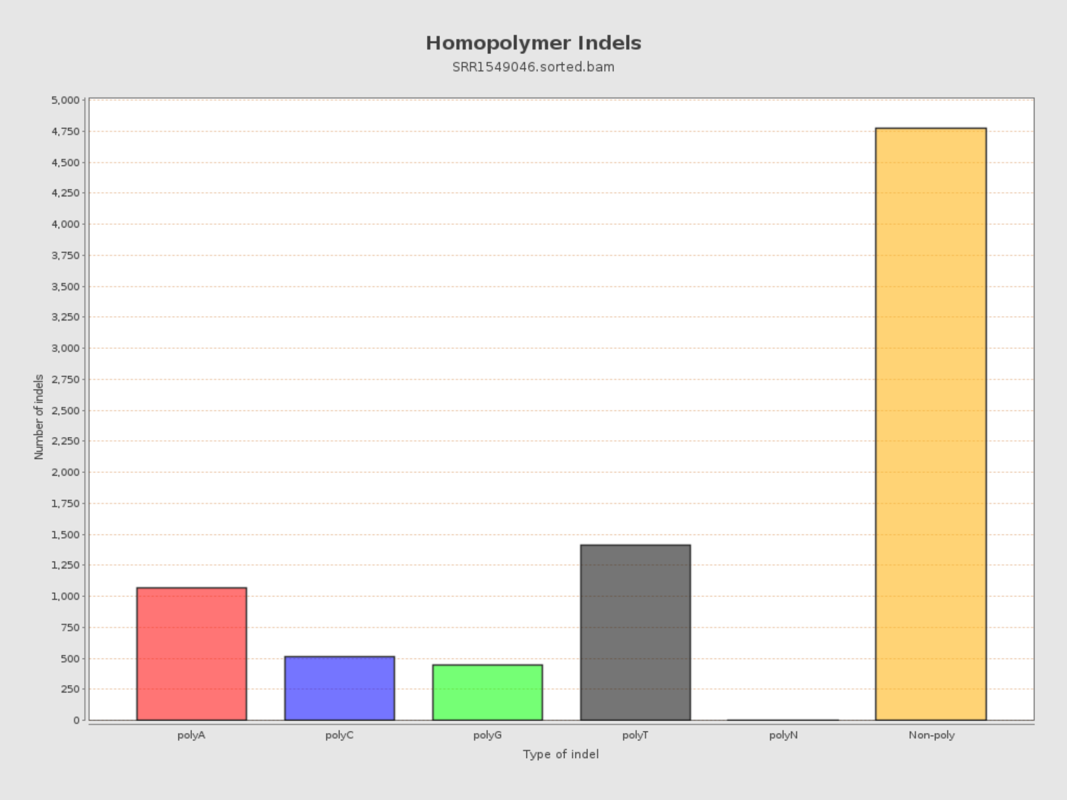
9. Results : Mapped Reads GC-content Distribution



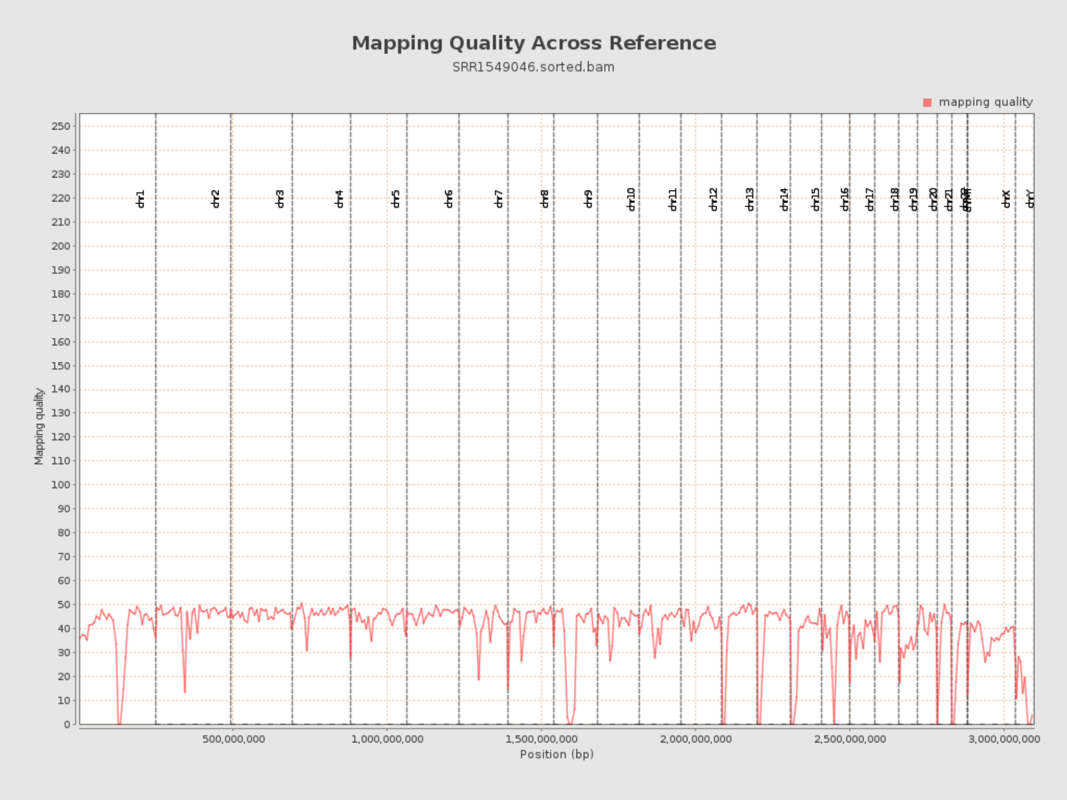
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram