Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:23:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549038.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_SRR1549038 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549038.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:23:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549038.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,369,374
Mapped reads	6,194,334 / 84.06%
Unmapped reads	1,175,040 / 15.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	294,439 / 4%
Duplication rate	4.1%
Clipped reads	392,916 / 5.33%

2.2. ACGT Content

Number/percentage of A's	69,882,645 / 28.46%
Number/percentage of C's	51,856,261 / 21.12%
Number/percentage of T's	71,137,829 / 28.97%
Number/percentage of G's	52,656,589 / 21.45%
Number/percentage of N's	205 / 0%
GC Percentage	42.57%

2.3. Coverage

Mean	0.0793
Standard Deviation	0.4968

2.4. Mapping Quality

Mean Mapping Quality	42.13

2.5. Mismatches and indels

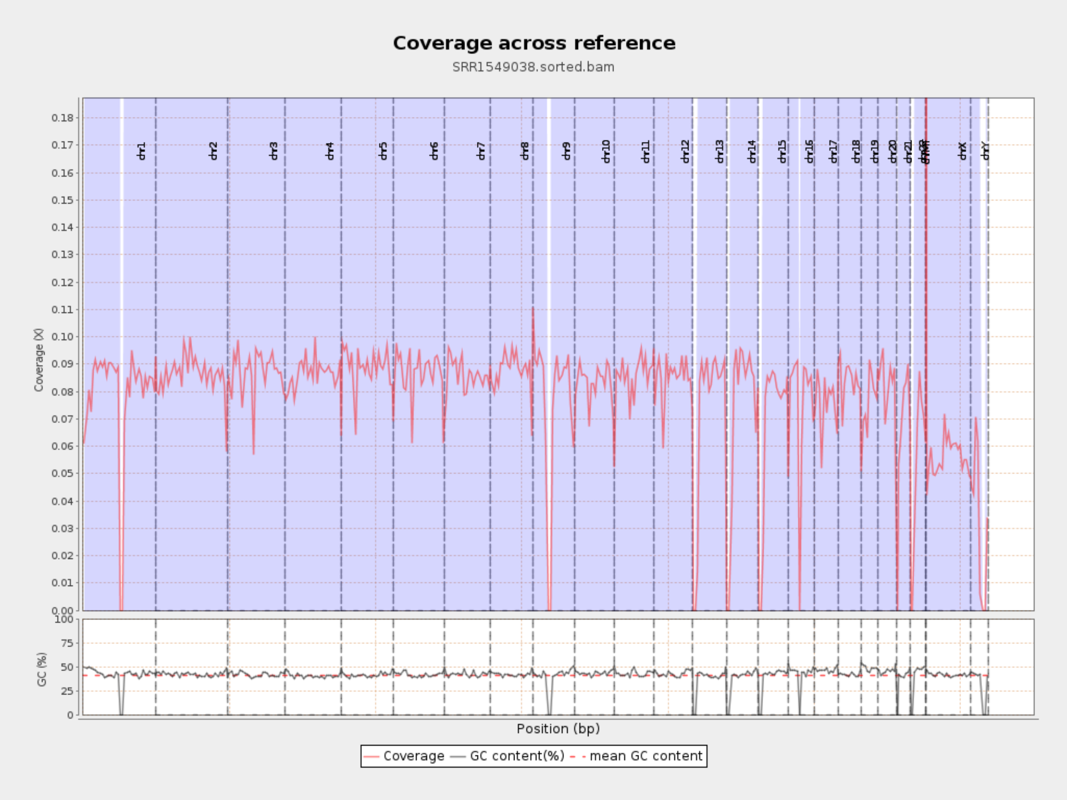
General error rate	0.25%
Mismatches	597,437
Insertions	6,508
Mapped reads with at least one insertion	0.11%
Deletions	16,853
Mapped reads with at least one deletion	0.27%
Homopolymer indels	42.32%

2.6. Chromosome stats

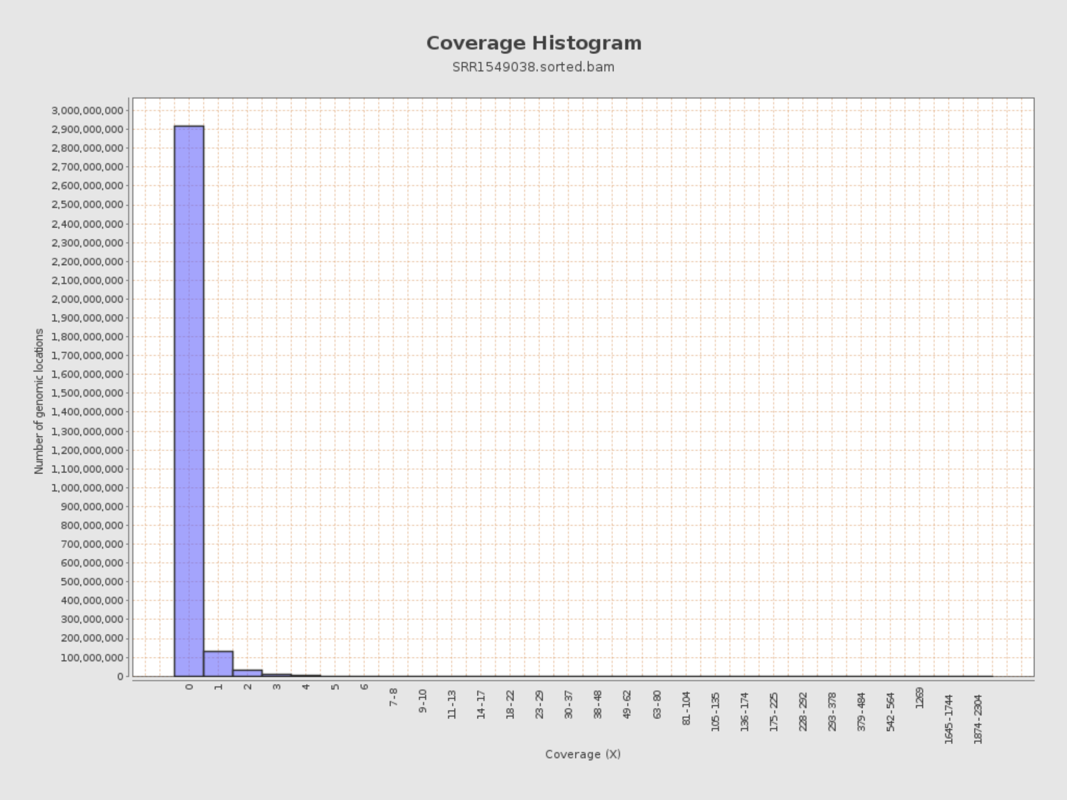
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19681075	0.079	0.5326
chr2	243199373	21044850	0.0865	0.4656
chr3	198022430	17225361	0.087	0.3951
chr4	191154276	16602989	0.0869	0.4011
chr5	180915260	16039234	0.0887	0.4004
chr6	171115067	14905149	0.0871	0.4126
chr7	159138663	13646813	0.0858	0.5332
chr8	146364022	12844587	0.0878	1.1922

chr9	141213431	10640000	0.0753	0.4389
chr10	135534747	11329241	0.0836	0.4275
chr11	135006516	11561270	0.0856	0.4352
chr12	133851895	11404322	0.0852	0.3952
chr13	115169878	8331701	0.0723	0.3631
chr14	107349540	7838755	0.073	0.3964
chr15	102531392	6779603	0.0661	0.3442
chr16	90354753	6673346	0.0739	0.3777
chr17	81195210	6182667	0.0761	0.3715
chr18	78077248	6565929	0.0841	0.6473
chr19	59128983	4520573	0.0765	0.5329
chr20	63025520	5227000	0.0829	0.4011
chr21	48129895	3201941	0.0665	0.3987
chr22	51304566	2696531	0.0526	0.4449
chrMT	16571	16931	1.0217	1.6827
chrX	155270560	8697672	0.056	0.3456
chrY	59373566	1898194	0.032	0.2703

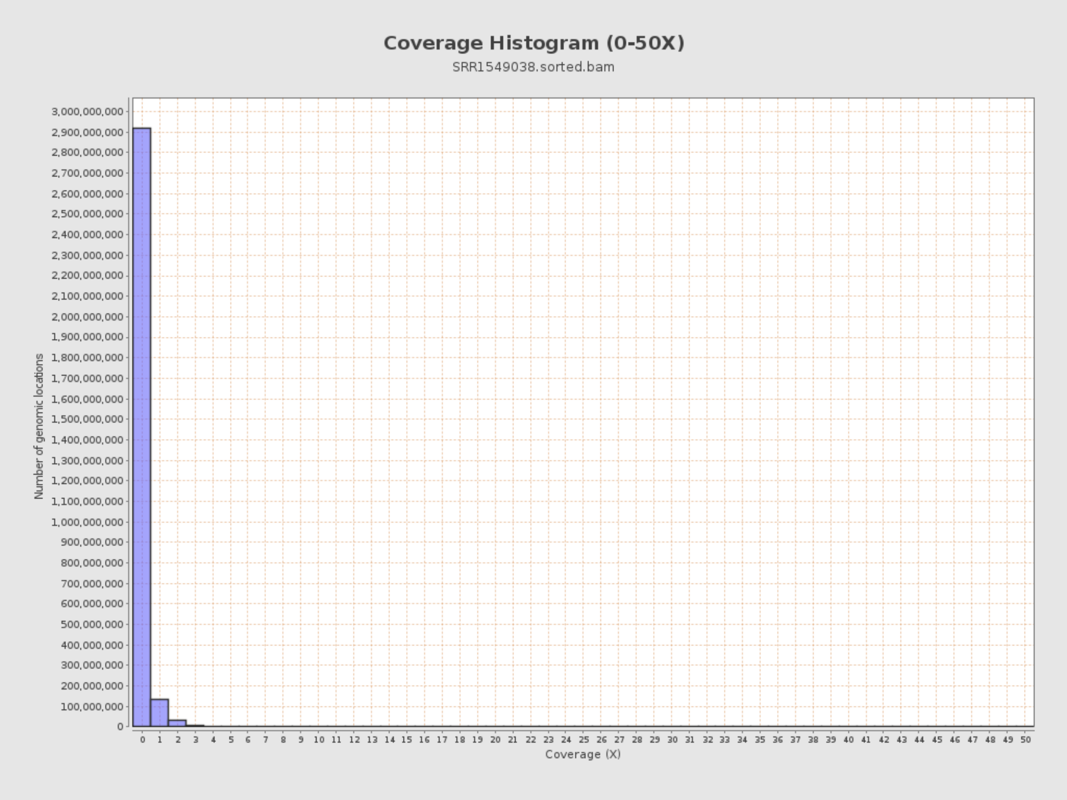
3. Results : Coverage across reference



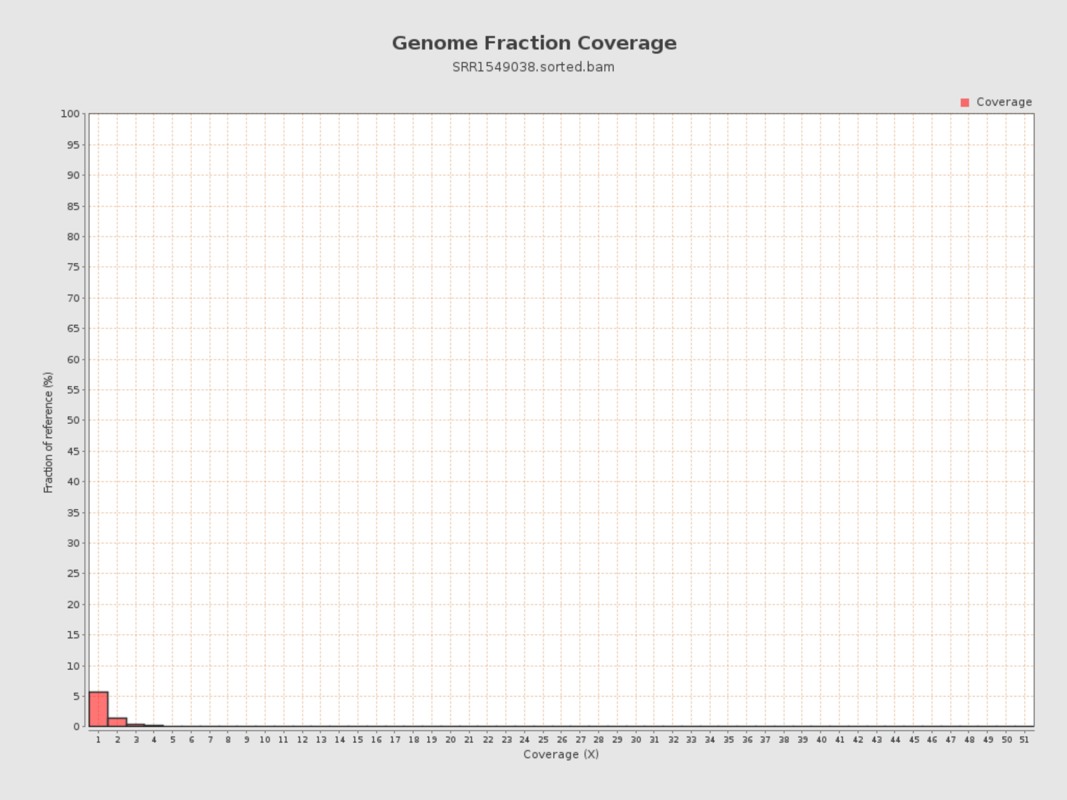
4. Results : Coverage Histogram



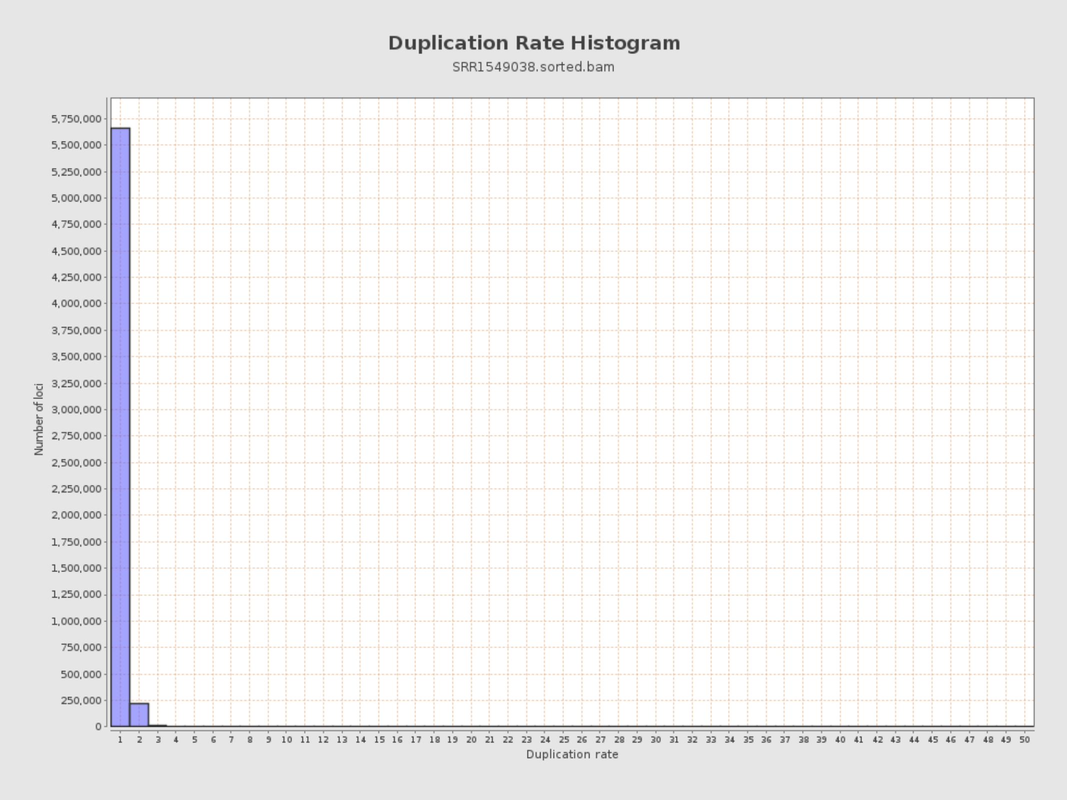
5. Results : Coverage Histogram (0-50X)



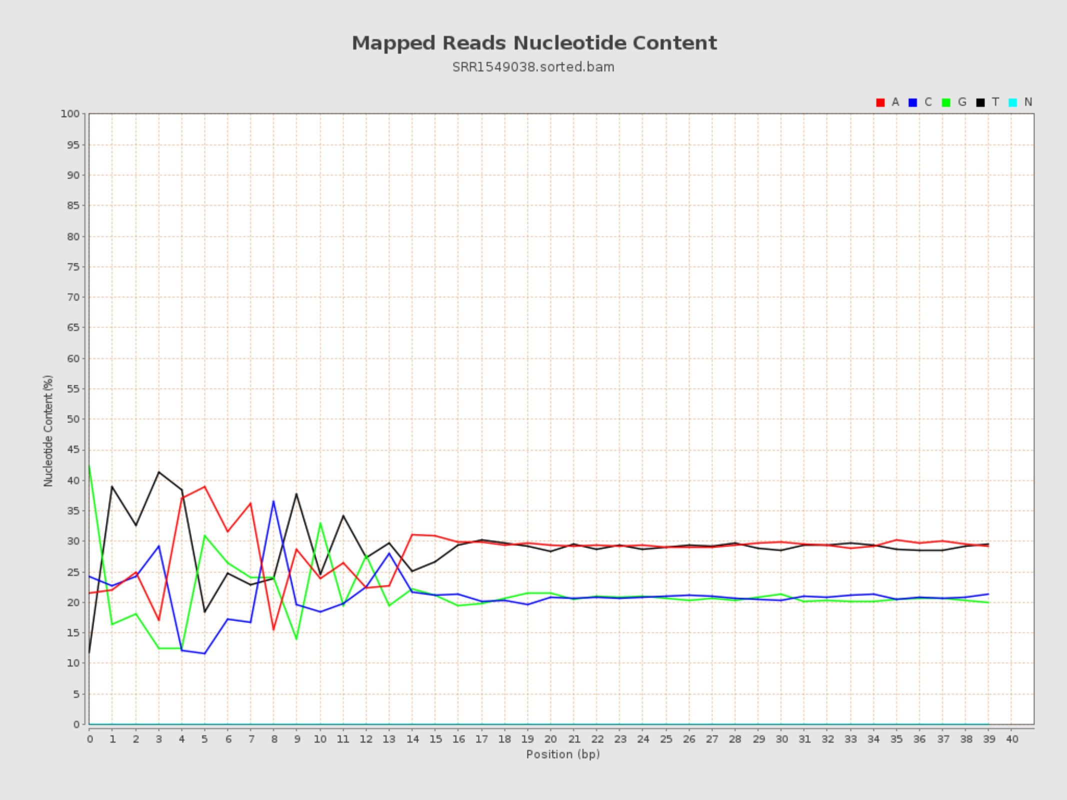
6. Results : Genome Fraction Coverage



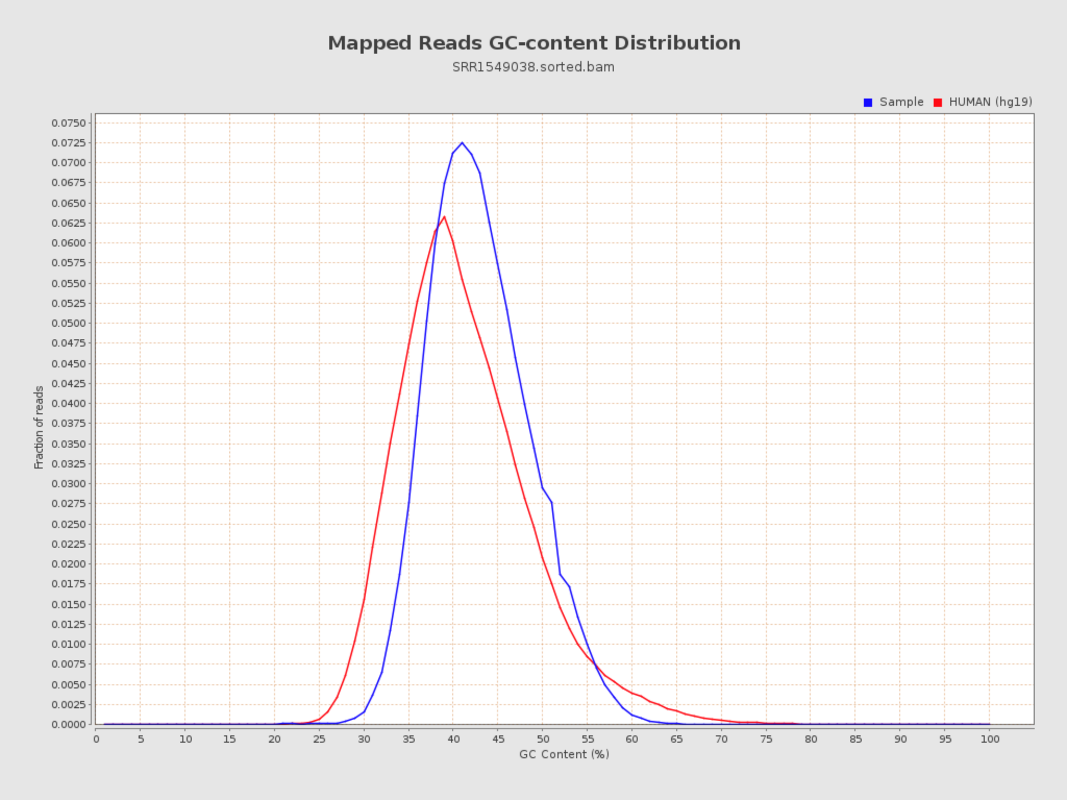
7. Results : Duplication Rate Histogram



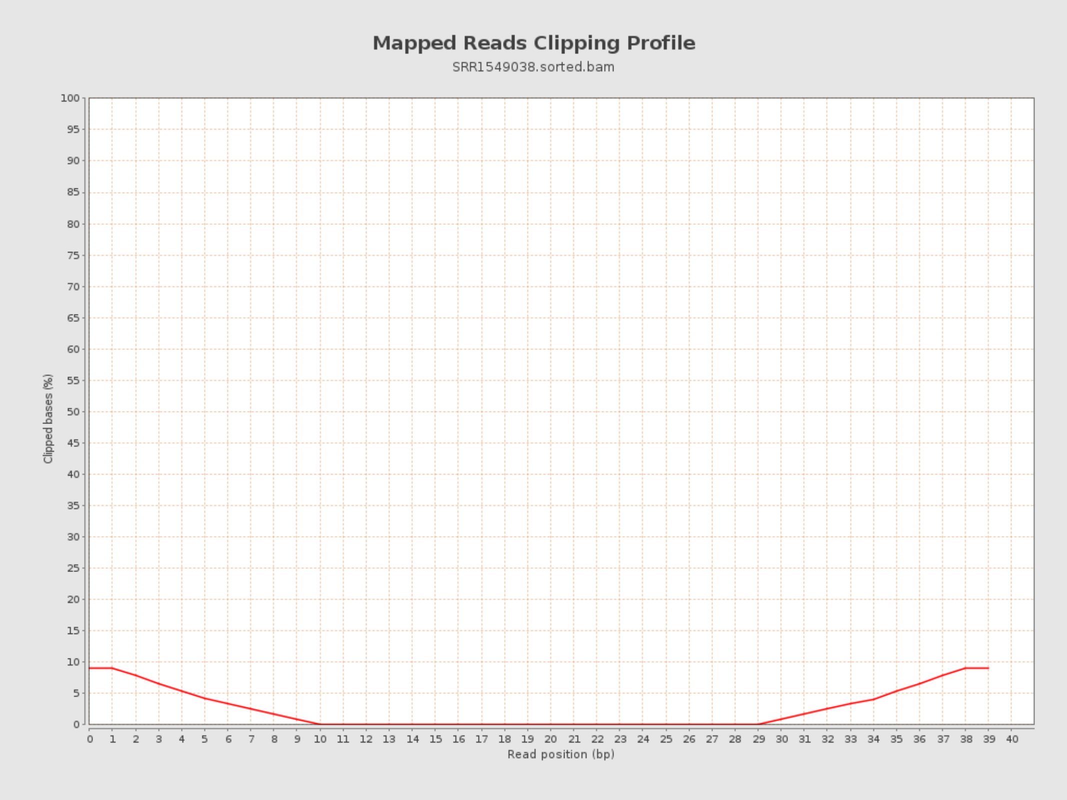
8. Results : Mapped Reads Nucleotide Content



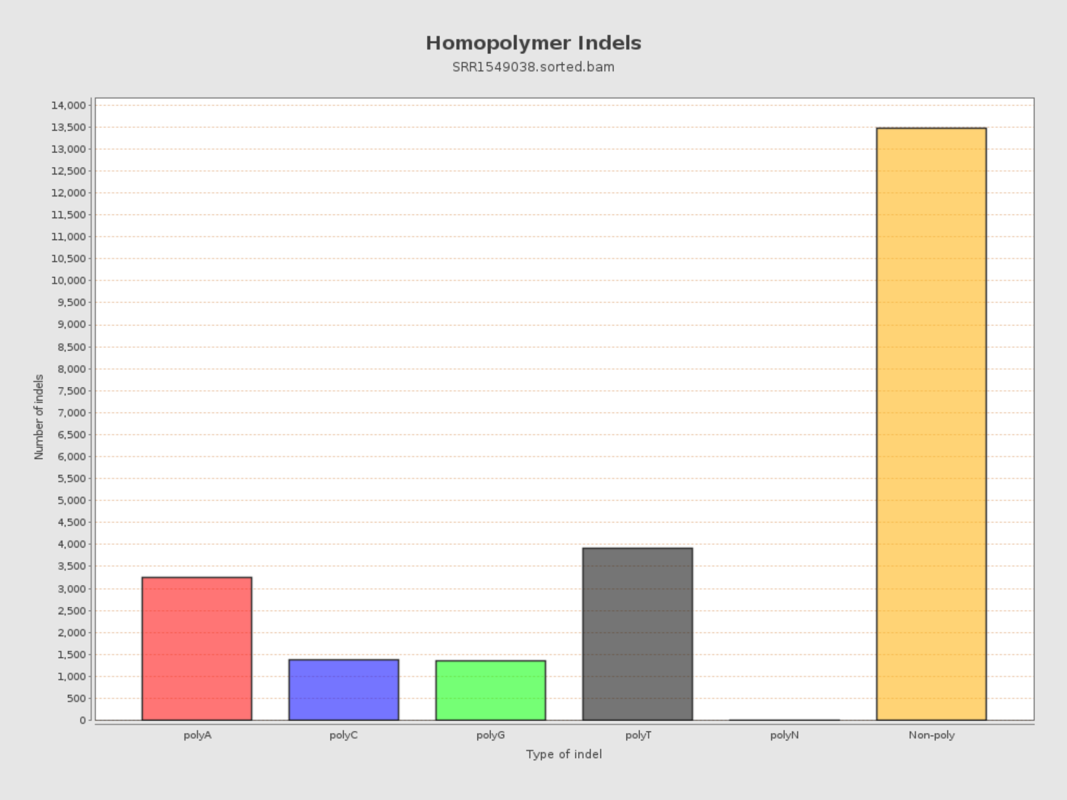
9. Results : Mapped Reads GC-content Distribution



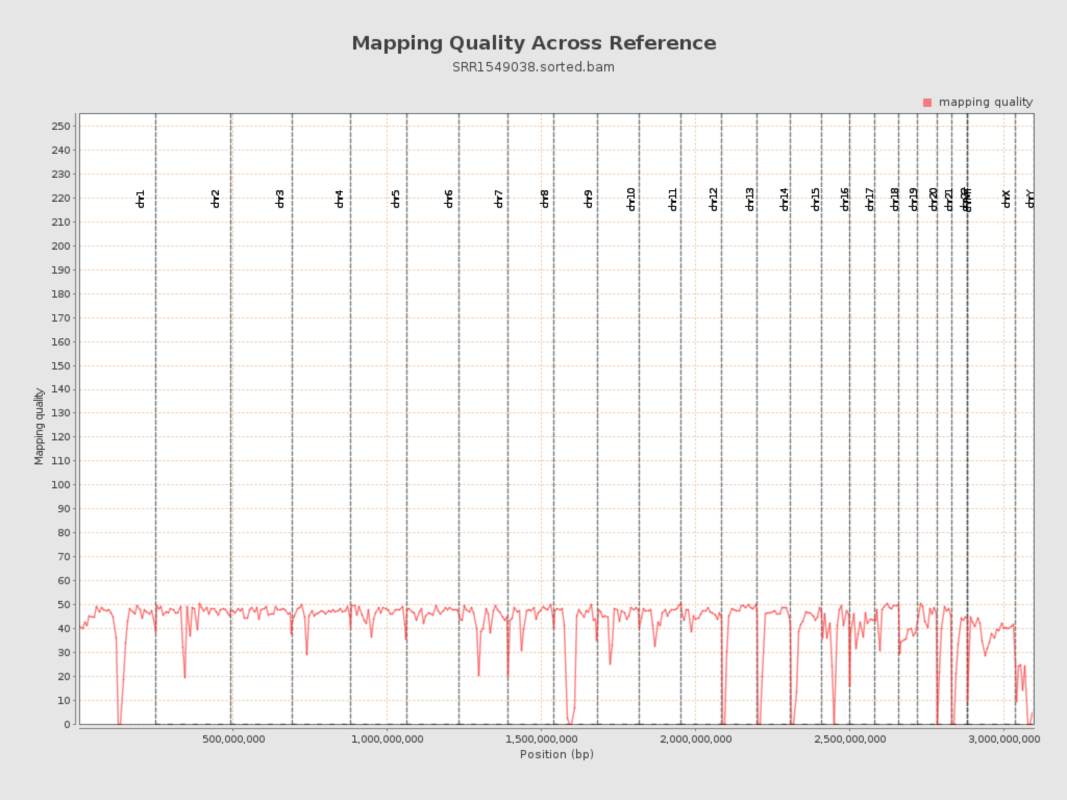
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram