Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:45:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549019.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_SRR1549019 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549019.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:45:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549019.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,289,140
Mapped reads	6,312,534 / 86.6%
Unmapped reads	976,606 / 13.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	239,666 / 3.29%
Duplication rate	2.85%
Clipped reads	433,167 / 5.94%

2.2. ACGT Content

Number/percentage of A's	74,361,275 / 29.74%
Number/percentage of C's	50,629,605 / 20.25%
Number/percentage of T's	74,286,704 / 29.71%
Number/percentage of G's	50,741,333 / 20.29%
Number/percentage of N's	2,607 / 0%
GC Percentage	40.54%

2.3. Coverage

Mean	0.0808
Standard Deviation	1.1182

2.4. Mapping Quality

Mean Mapping Quality	42.98

2.5. Mismatches and indels

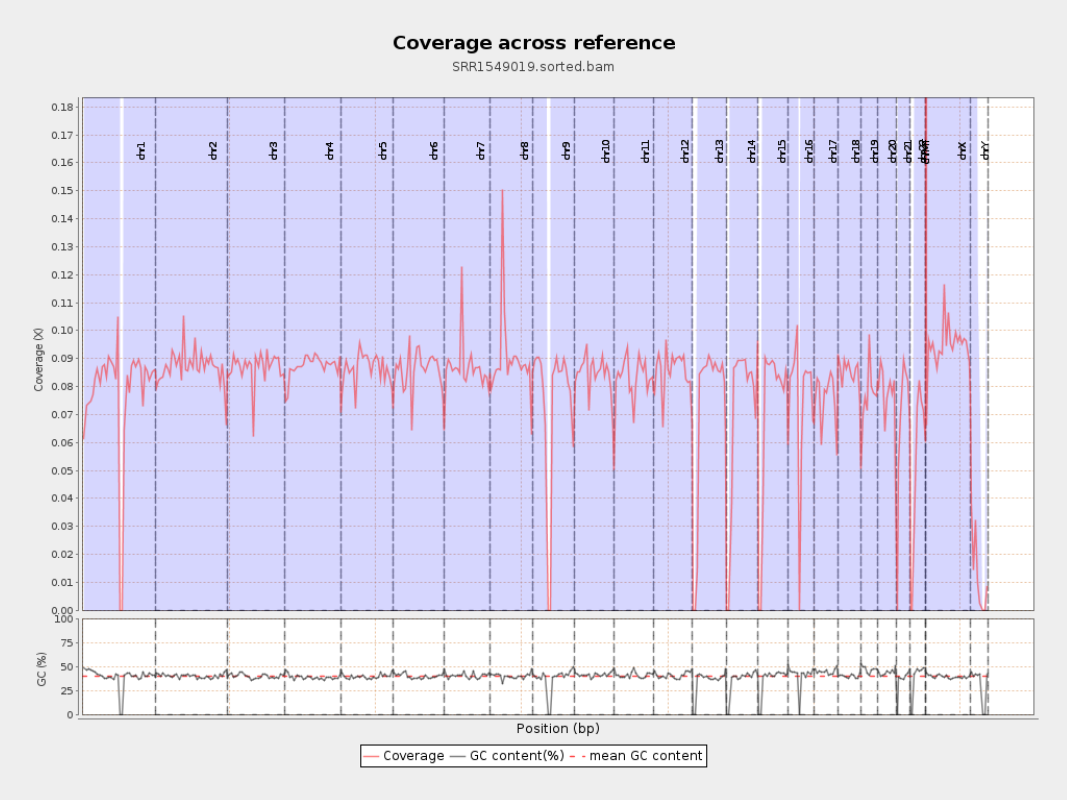
General error rate	0.27%
Mismatches	659,807
Insertions	7,536
Mapped reads with at least one insertion	0.12%
Deletions	20,773
Mapped reads with at least one deletion	0.33%
Homopolymer indels	42.88%

2.6. Chromosome stats

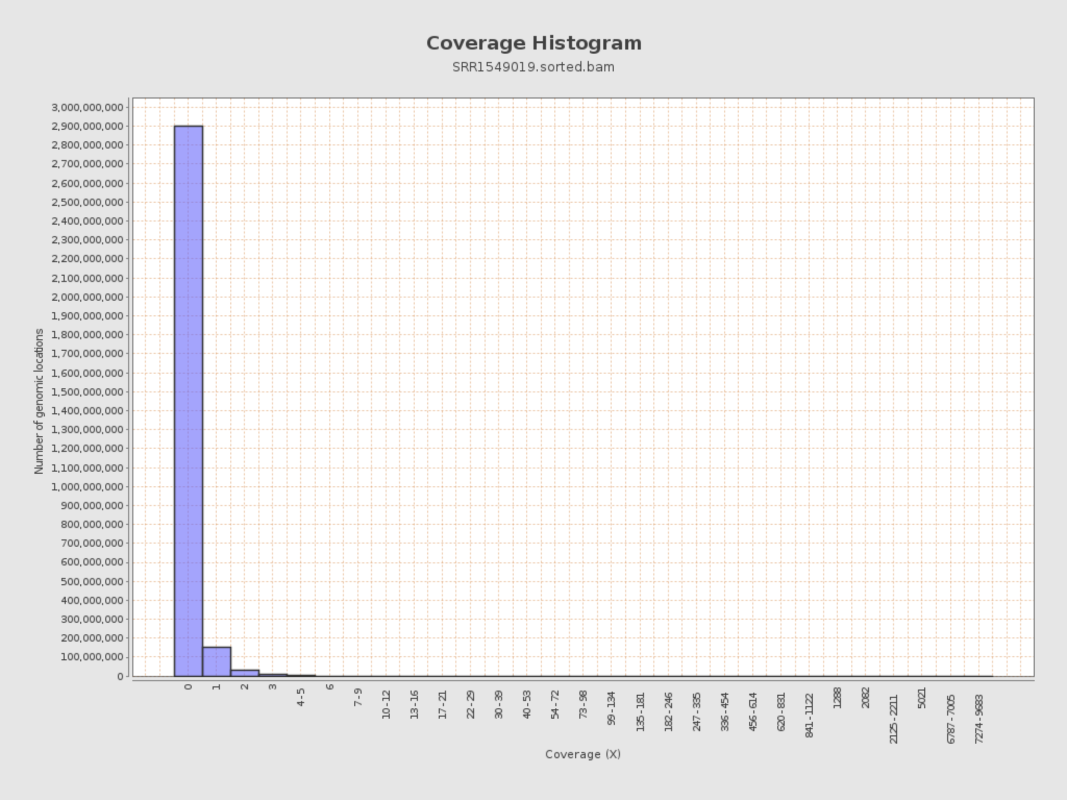
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19410322	0.0779	0.7942
chr2	243199373	21189917	0.0871	0.4711
chr3	198022430	17210201	0.0869	0.3627
chr4	191154276	16723680	0.0875	0.373
chr5	180915260	15580930	0.0861	0.3652
chr6	171115067	14760984	0.0863	0.3931
chr7	159138663	13803837	0.0867	0.6454
chr8	146364022	13183244	0.0901	4.6746

chr9	141213431	10459787	0.0741	0.4361
chr10	135534747	11498925	0.0848	0.4329
chr11	135006516	11211740	0.083	0.5421
chr12	133851895	11475172	0.0857	0.3688
chr13	115169878	8290828	0.072	0.3279
chr14	107349540	7616561	0.071	0.3716
chr15	102531392	7165252	0.0699	0.3219
chr16	90354753	6692179	0.0741	0.349
chr17	81195210	6223289	0.0766	0.362
chr18	78077248	6672338	0.0855	0.7365
chr19	59128983	4581715	0.0775	0.7008
chr20	63025520	4920026	0.0781	0.3521
chr21	48129895	3255920	0.0676	0.347
chr22	51304566	2667682	0.052	0.3064
chrMT	16571	33142	2	2.5942
chrX	155270560	14702619	0.0947	0.4389
chrY	59373566	718815	0.0121	0.1781

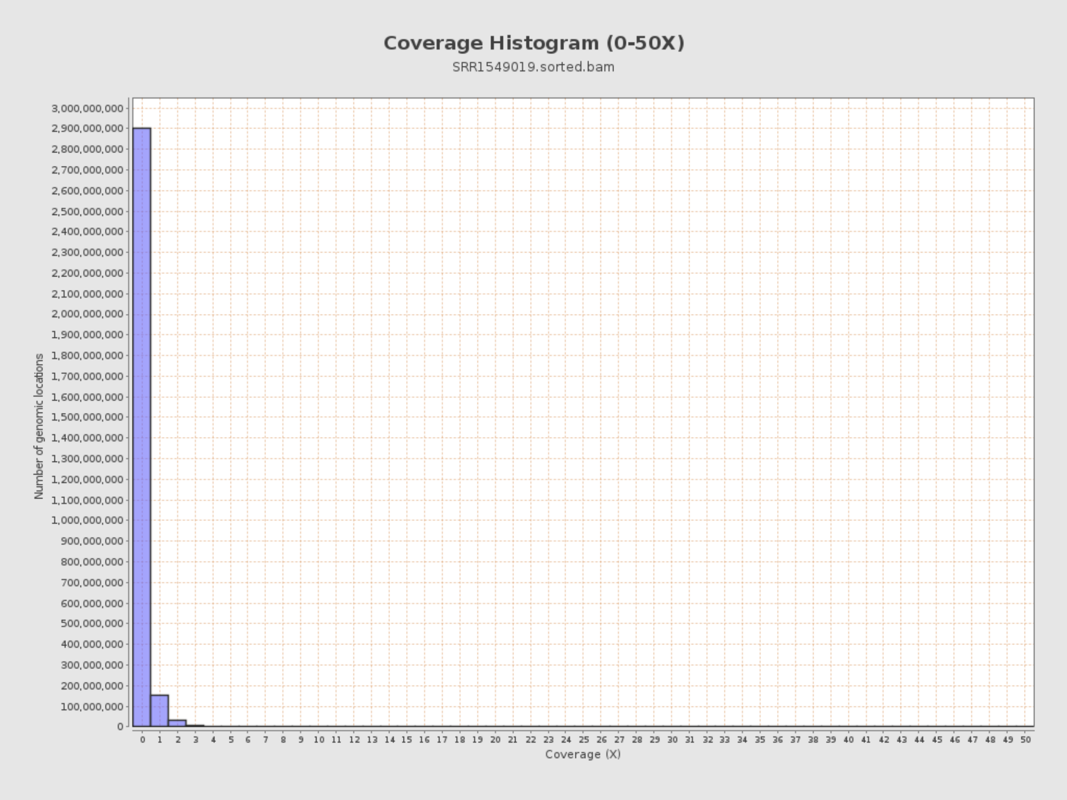
3. Results : Coverage across reference



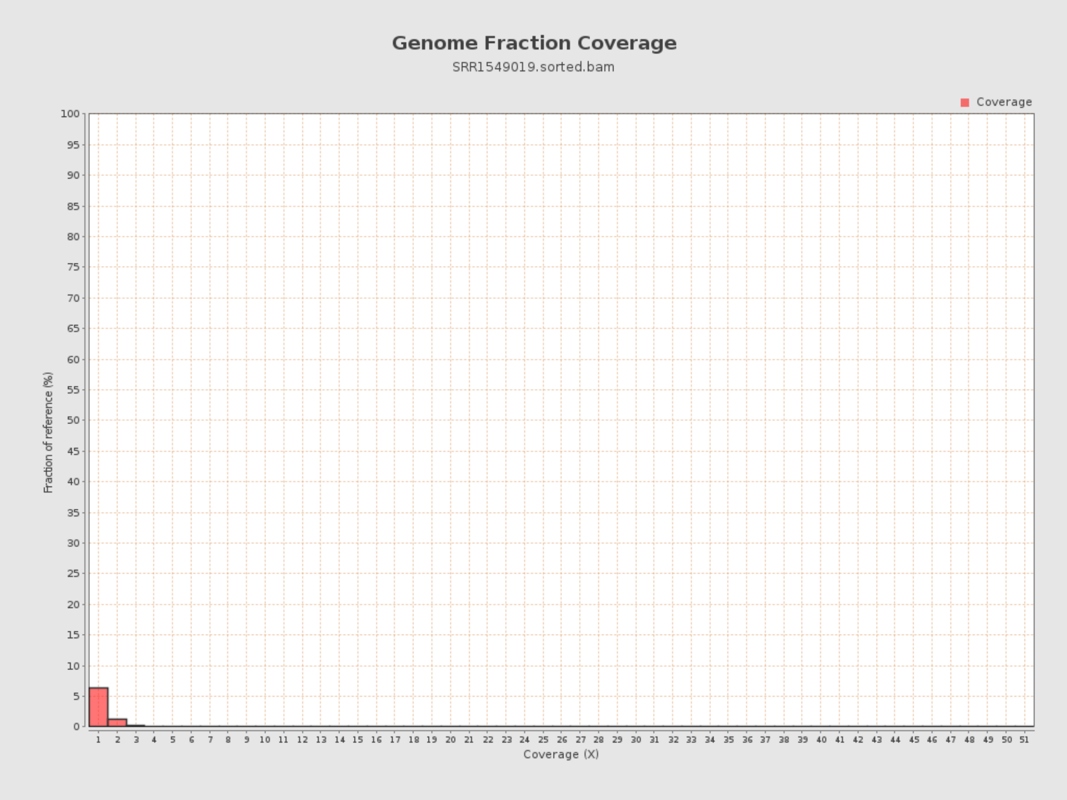
4. Results : Coverage Histogram



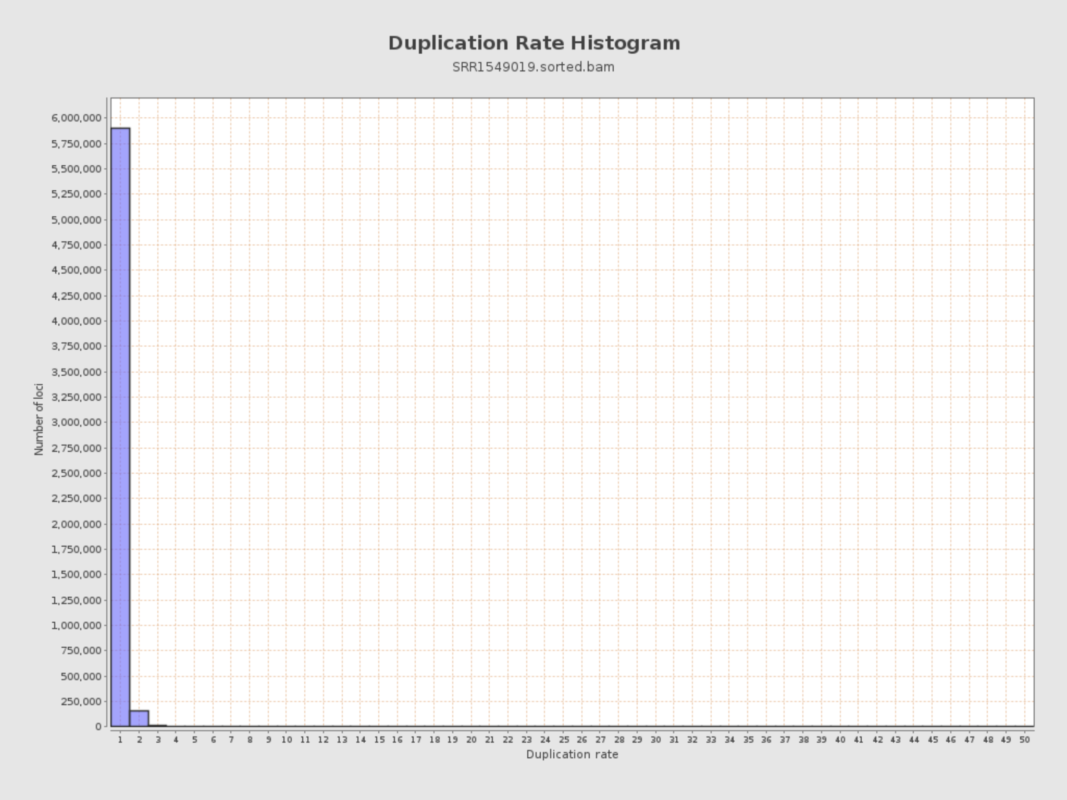
5. Results : Coverage Histogram (0-50X)



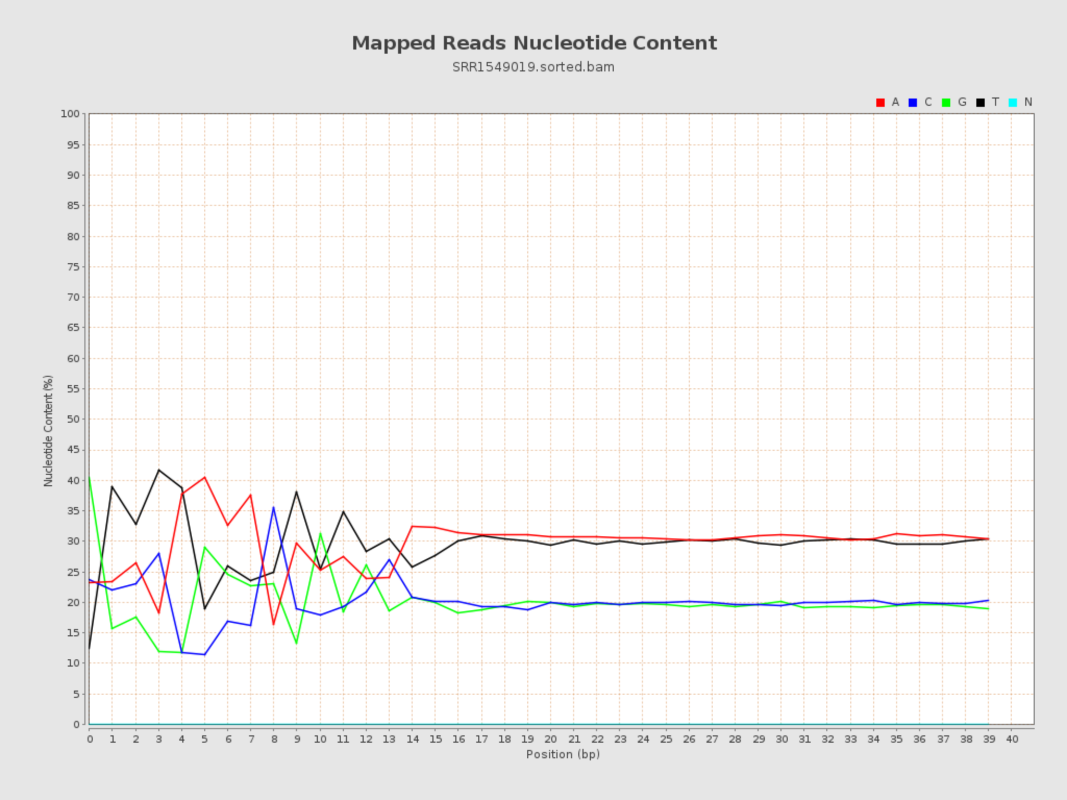
6. Results : Genome Fraction Coverage



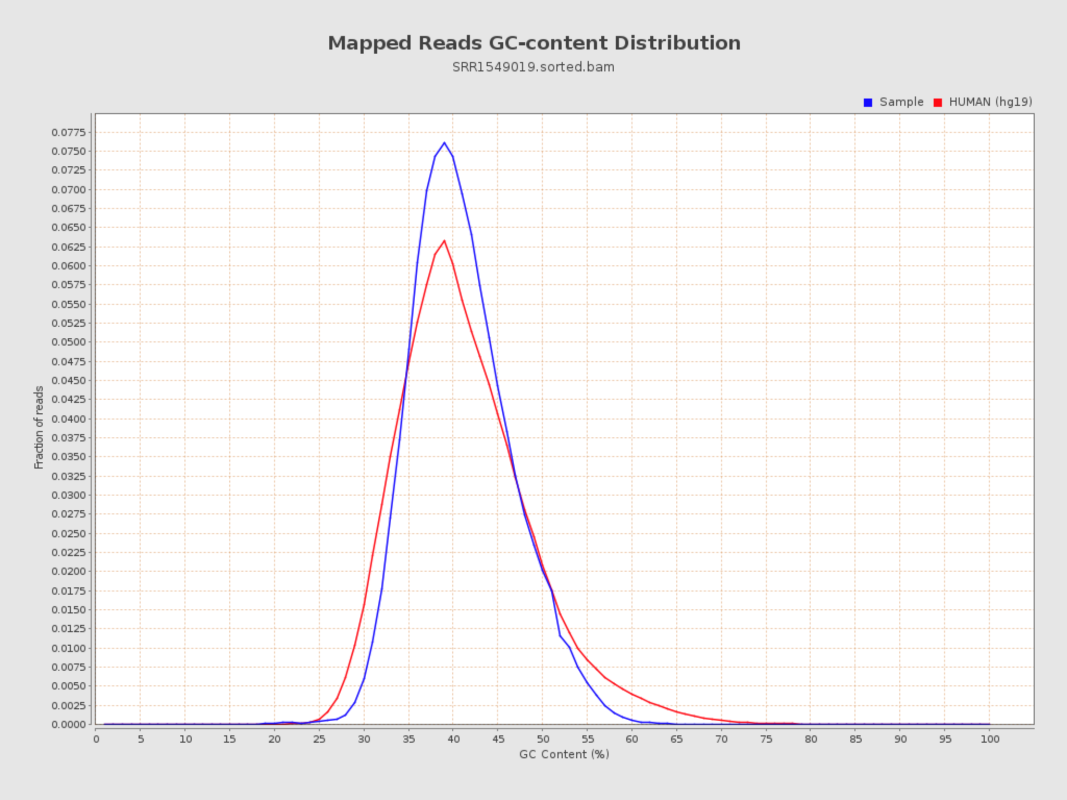
7. Results : Duplication Rate Histogram



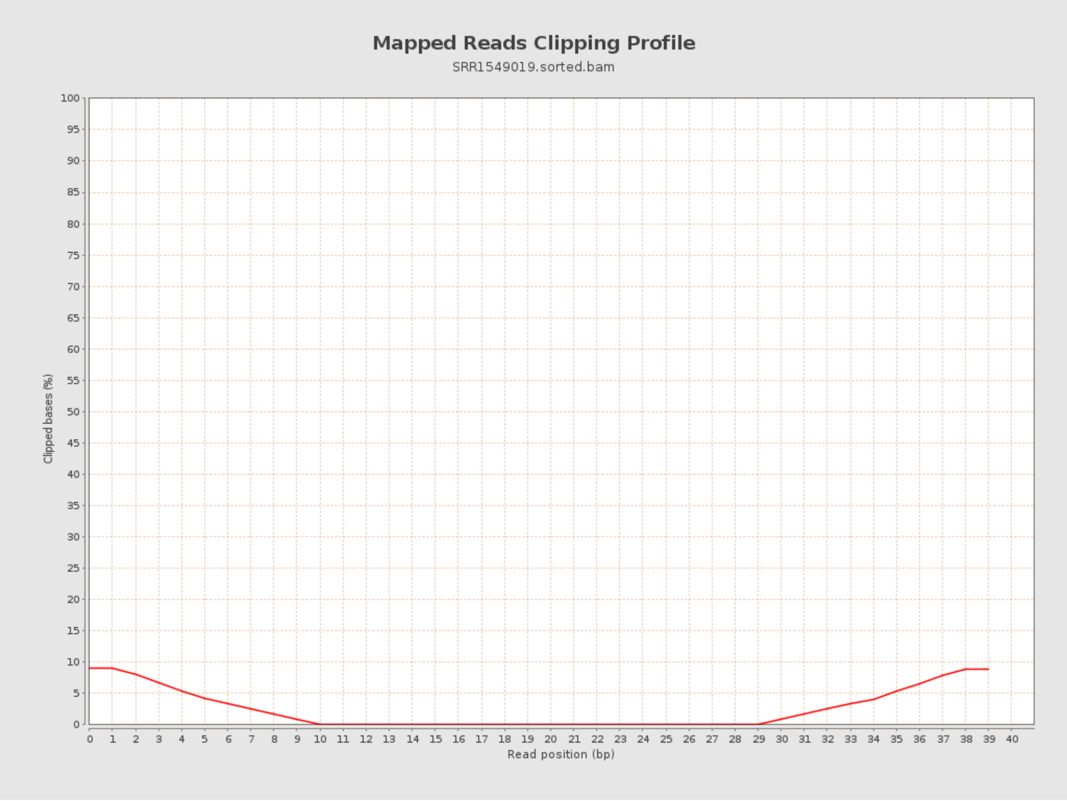
8. Results : Mapped Reads Nucleotide Content



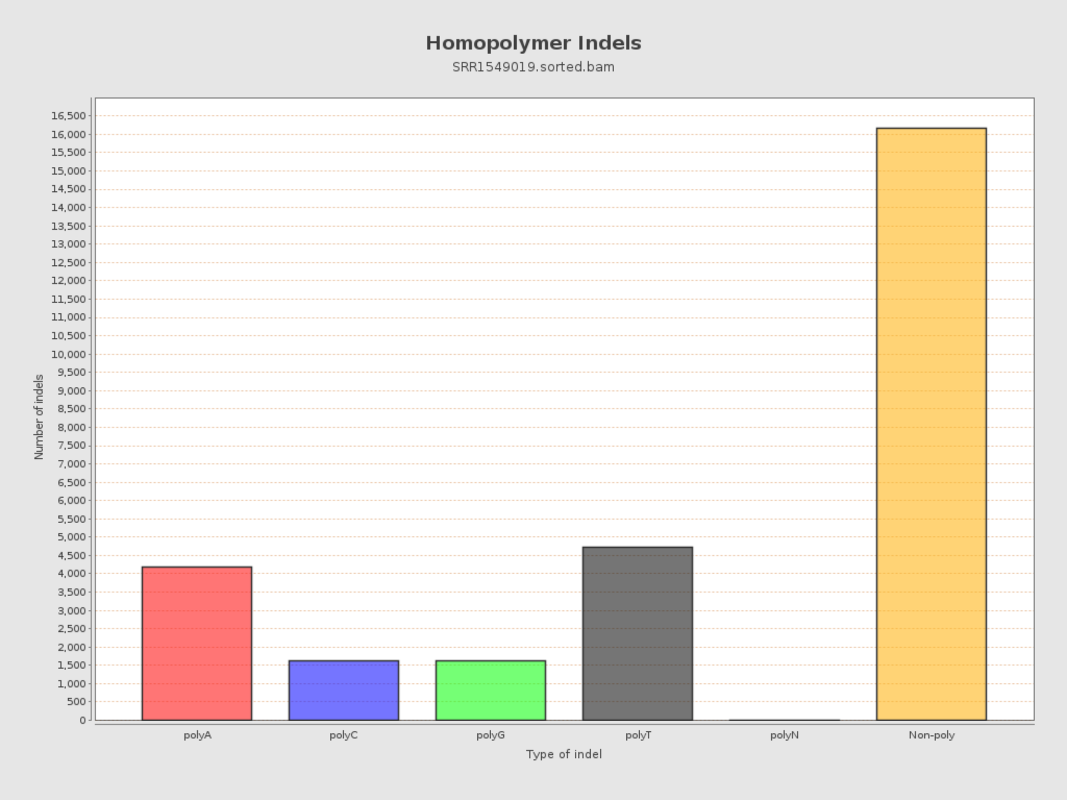
9. Results : Mapped Reads GC-content Distribution



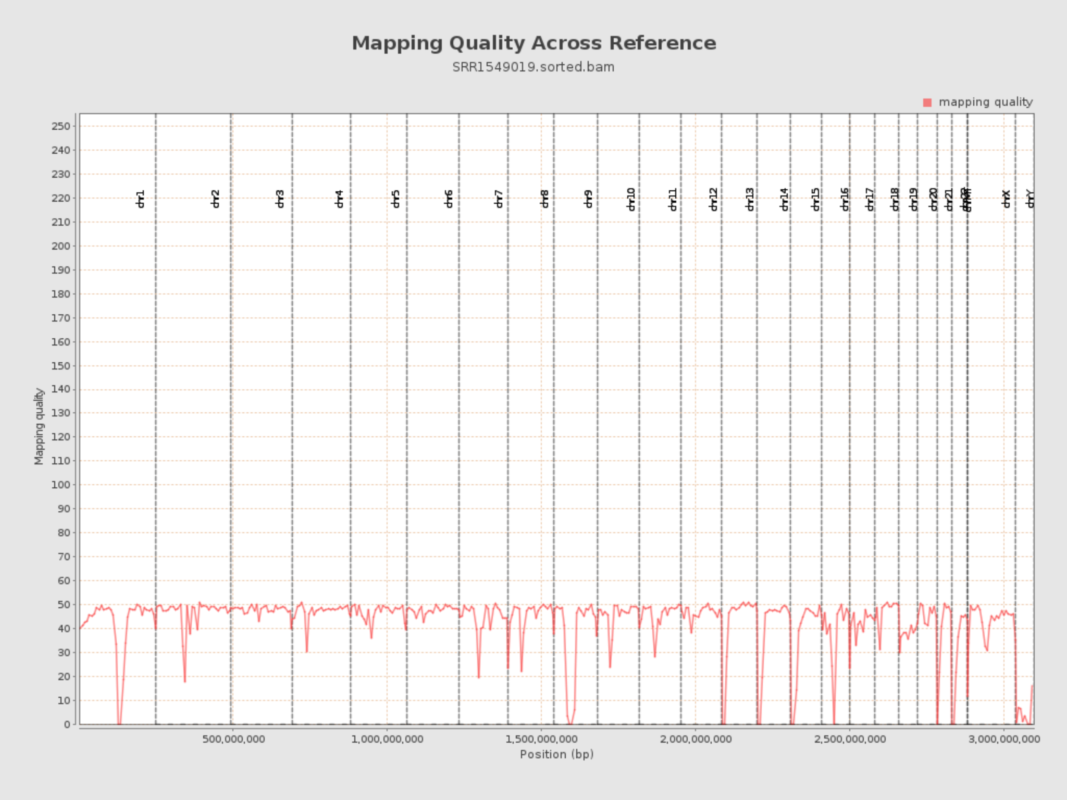
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram