Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 04:37:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549120.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_SRR1549120 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549120.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 04:37:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549120.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,599,972
Mapped reads	7,207,143 / 57.2%
Unmapped reads	5,392,829 / 42.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	442,165 / 3.51%
Duplication rate	4.77%
Clipped reads	380,903 / 3.02%

2.2. ACGT Content

Number/percentage of A's	84,557,701 / 29.57%
Number/percentage of C's	58,410,011 / 20.42%
Number/percentage of T's	84,656,681 / 29.6%
Number/percentage of G's	58,350,661 / 20.4%
Number/percentage of N's	11,285 / 0%
GC Percentage	40.83%

2.3. Coverage

Mean	0.0924
Standard Deviation	1.4337

2.4. Mapping Quality

Mean Mapping Quality	44.04

2.5. Mismatches and indels

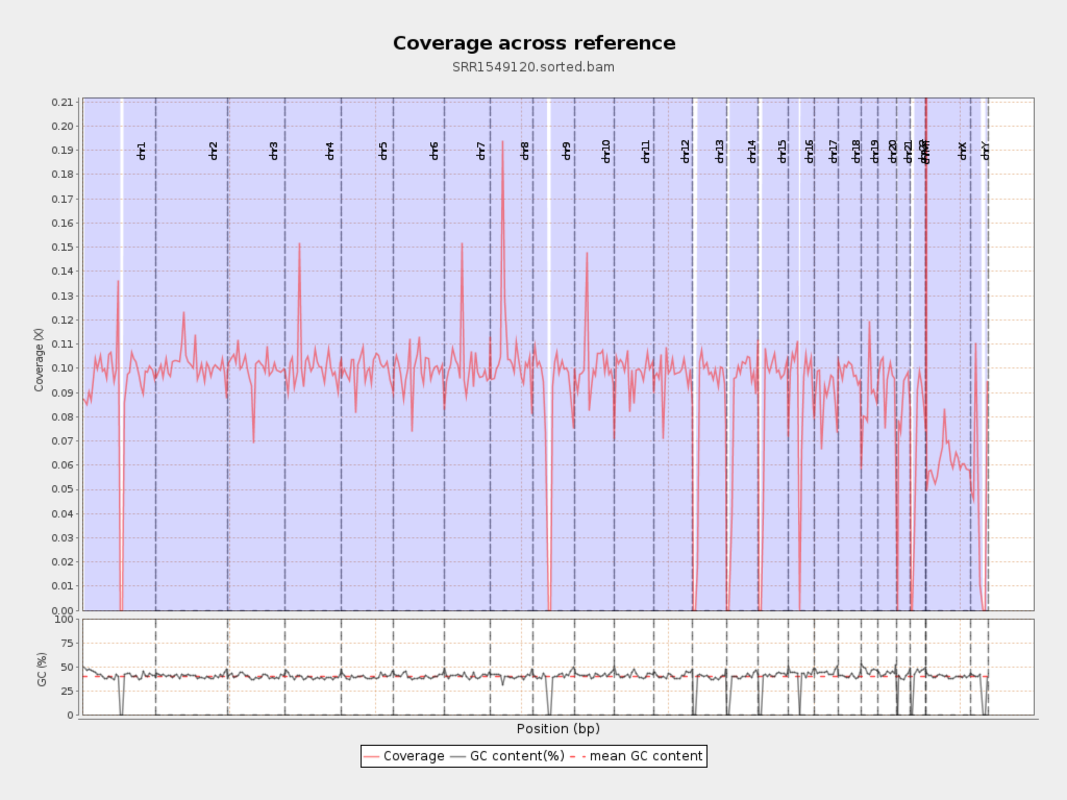
General error rate	0.32%
Mismatches	919,715
Insertions	7,267
Mapped reads with at least one insertion	0.1%
Deletions	23,626
Mapped reads with at least one deletion	0.33%
Homopolymer indels	44.58%

2.6. Chromosome stats

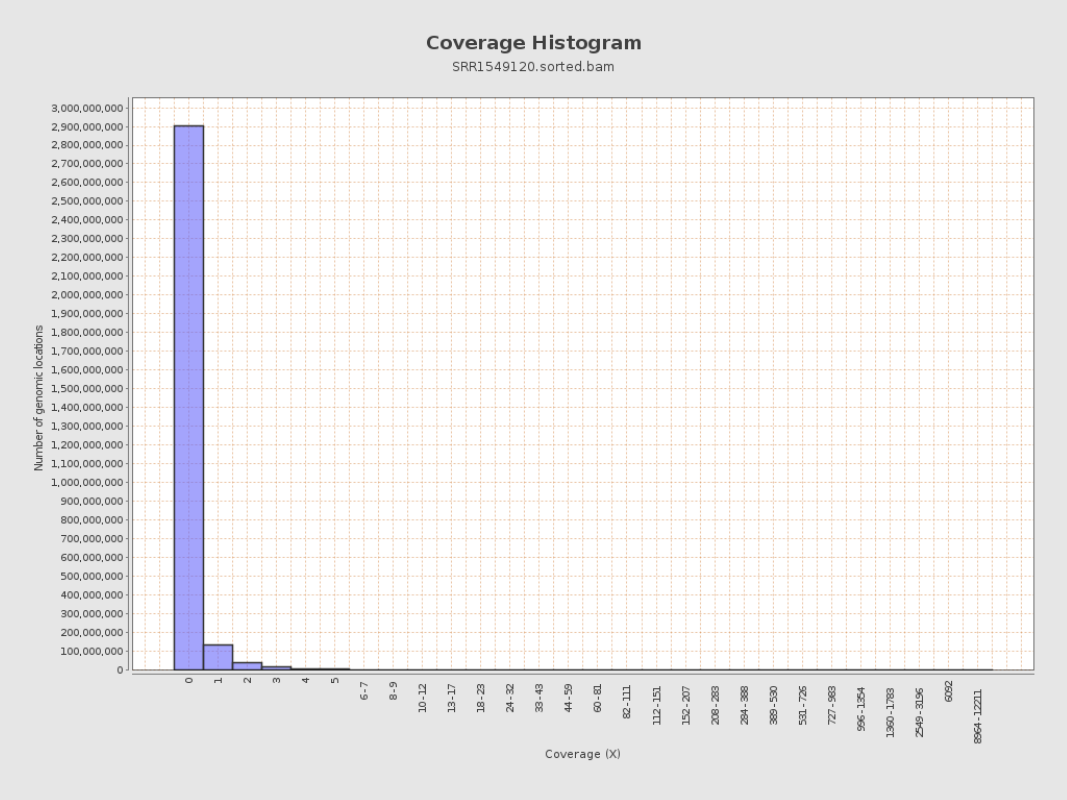
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23045779	0.0925	1.1793
chr2	243199373	24689227	0.1015	0.5988
chr3	198022430	19794136	0.1	0.4418
chr4	191154276	19421244	0.1016	0.5232
chr5	180915260	17970833	0.0993	0.4466
chr6	171115067	17000332	0.0994	0.459
chr7	159138663	16033687	0.1008	0.854
chr8	146364022	15593070	0.1065	5.955

chr9	141213431	12172211	0.0862	0.5288
chr10	135534747	13664643	0.1008	0.6709
chr11	135006516	13320947	0.0987	0.5585
chr12	133851895	13076106	0.0977	0.4461
chr13	115169878	9507048	0.0825	0.4012
chr14	107349540	8818555	0.0821	0.4726
chr15	102531392	8428424	0.0822	0.3943
chr16	90354753	7918011	0.0876	0.4444
chr17	81195210	7283232	0.0897	0.4355
chr18	78077248	7702543	0.0987	0.9629
chr19	59128983	5198547	0.0879	0.9341
chr20	63025520	5981524	0.0949	0.4592
chr21	48129895	3832039	0.0796	0.483
chr22	51304566	3230992	0.063	0.3552
chrMT	16571	86523	5.2214	6.6644
chrX	155270560	9508312	0.0612	0.3902
chrY	59373566	2738501	0.0461	0.5557

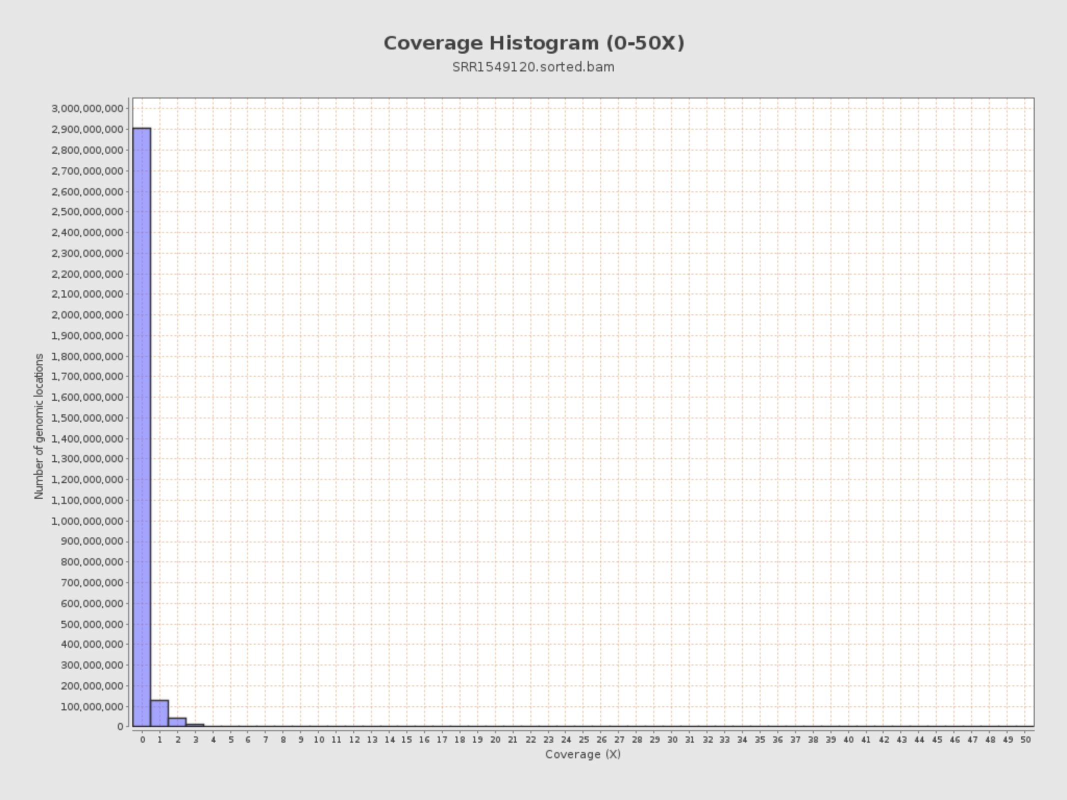
3. Results : Coverage across reference



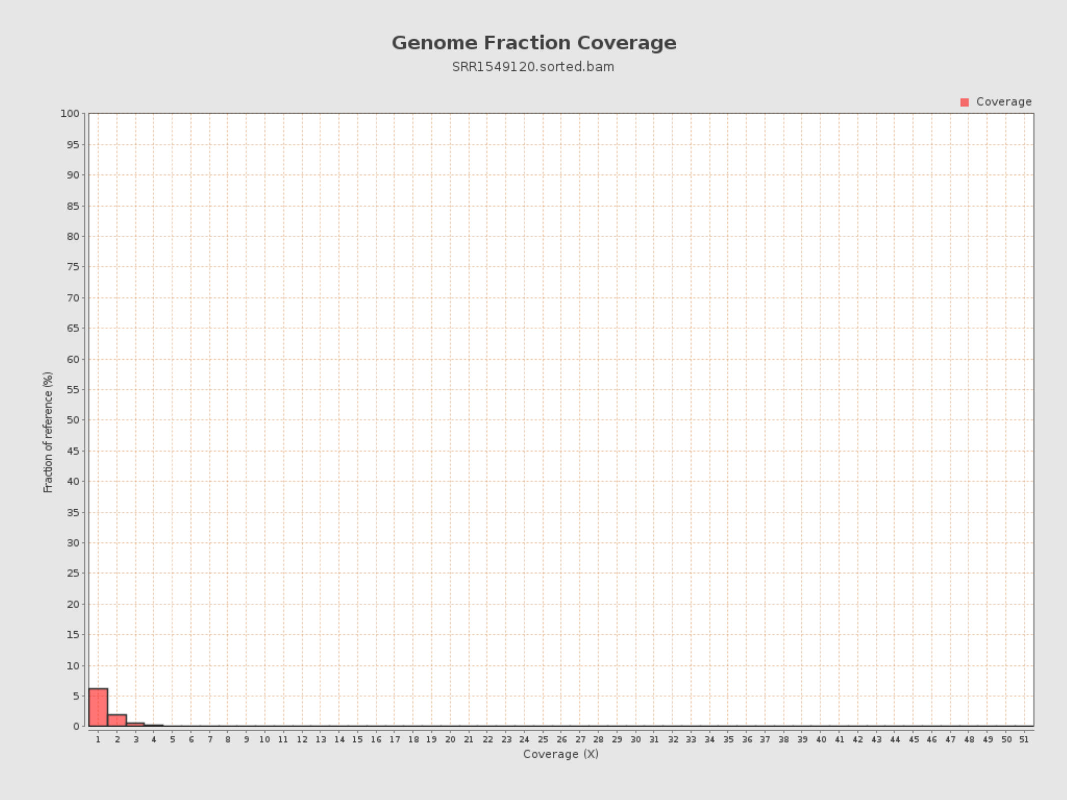
4. Results : Coverage Histogram



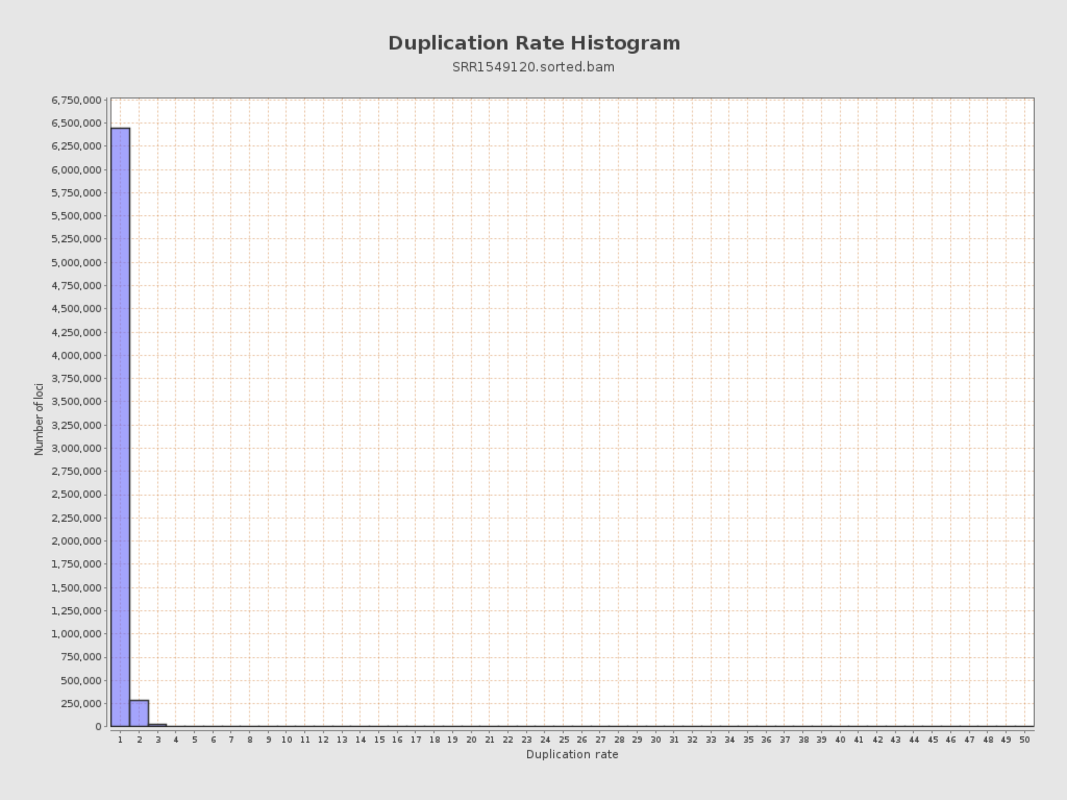
5. Results : Coverage Histogram (0-50X)



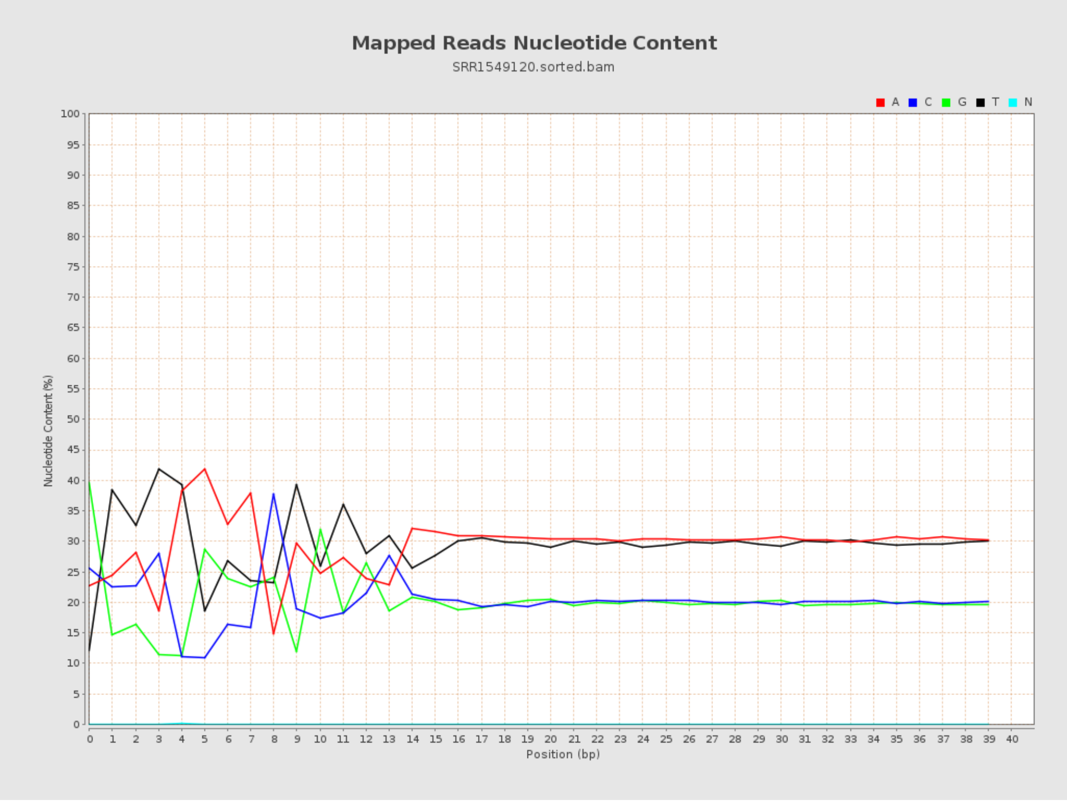
6. Results : Genome Fraction Coverage



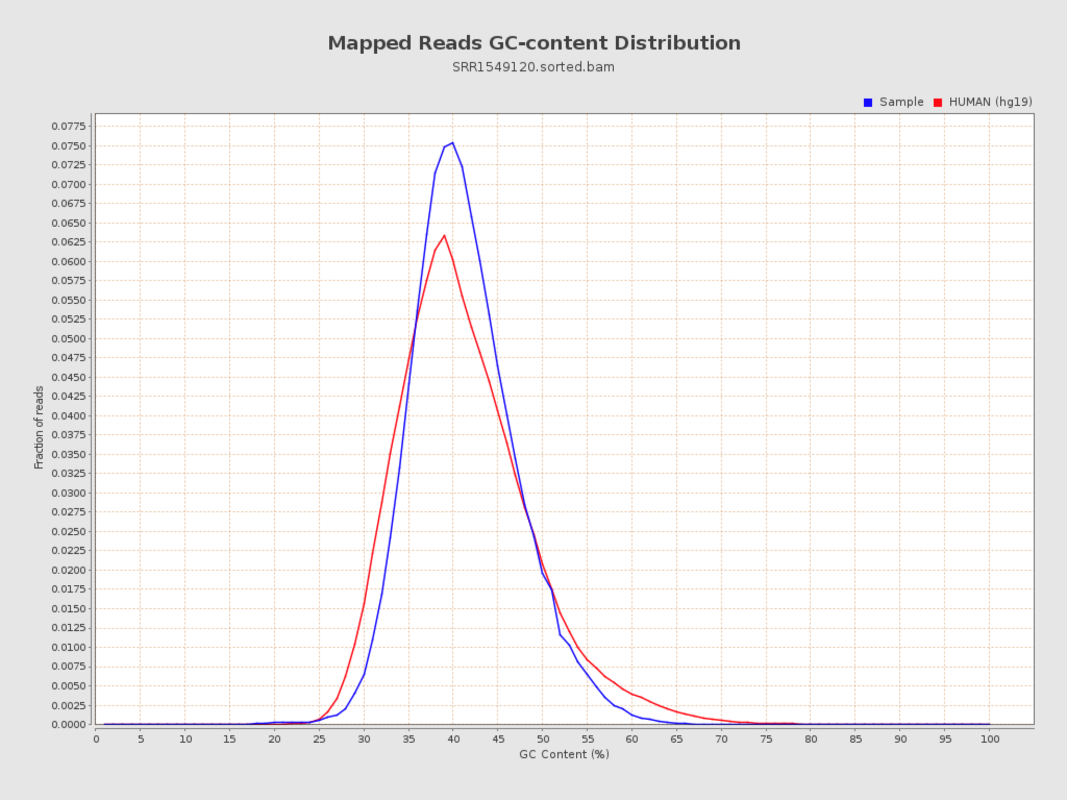
7. Results : Duplication Rate Histogram



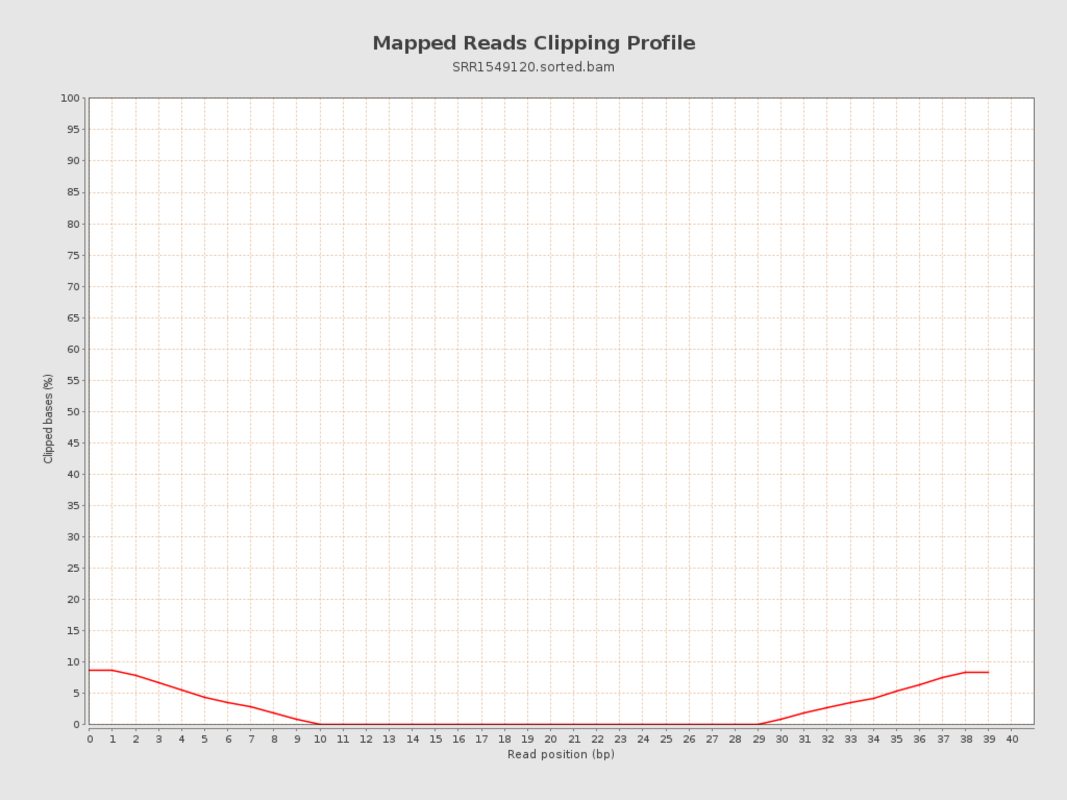
8. Results : Mapped Reads Nucleotide Content



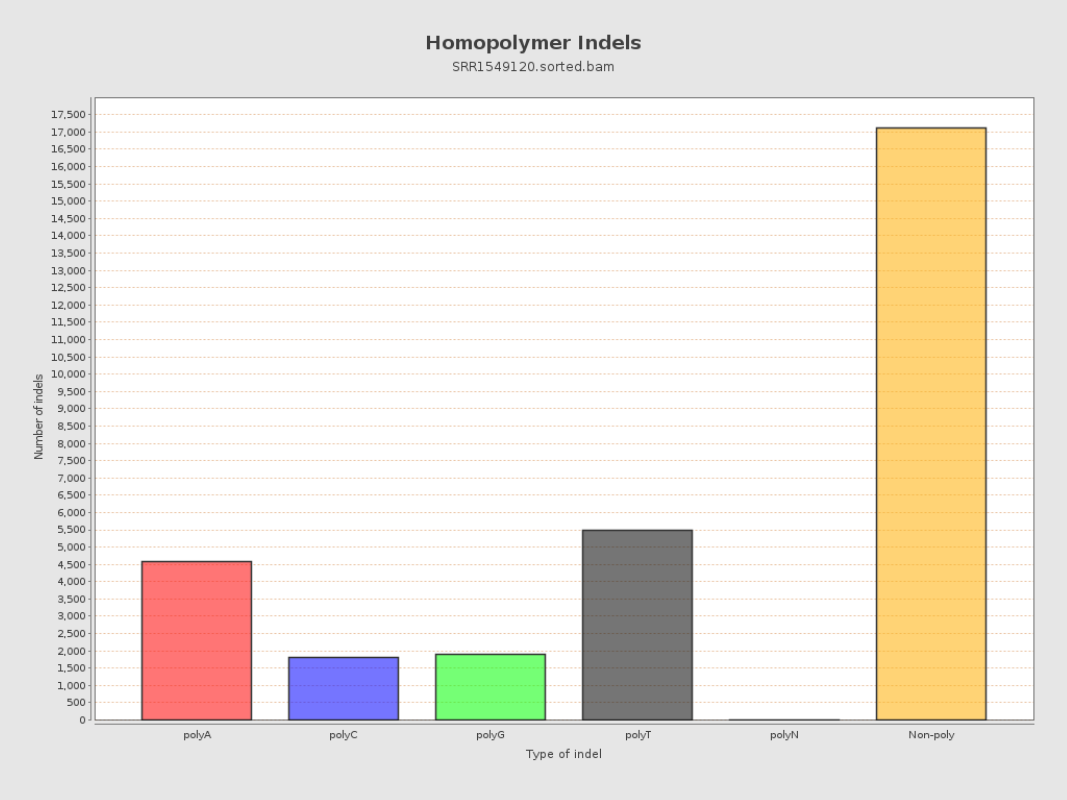
9. Results : Mapped Reads GC-content Distribution



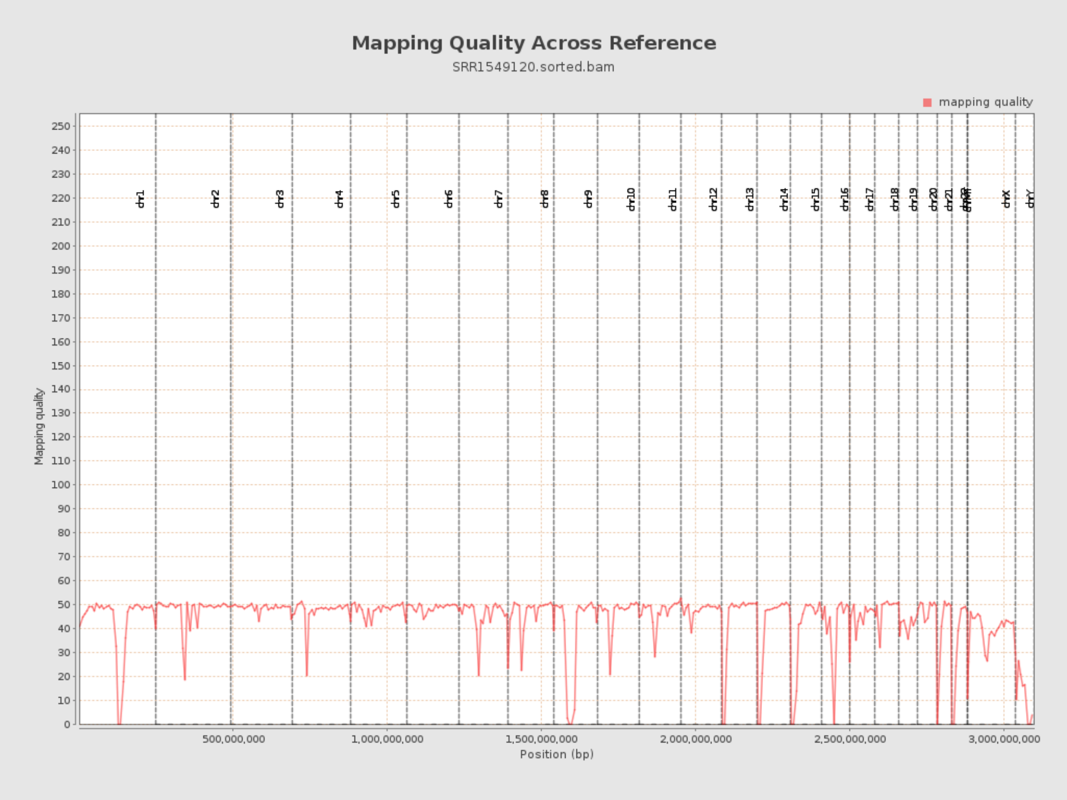
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram