Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:25:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549024.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_SRR1549024 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549024.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:25:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549024.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,379,615
Mapped reads	6,566,494 / 88.98%
Unmapped reads	813,121 / 11.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	267,421 / 3.62%
Duplication rate	2.85%
Clipped reads	527,655 / 7.15%

2.2. ACGT Content

Number/percentage of A's	73,042,336 / 28.13%
Number/percentage of C's	55,614,725 / 21.42%
Number/percentage of T's	74,443,798 / 28.67%
Number/percentage of G's	56,557,222 / 21.78%
Number/percentage of N's	2,740 / 0%
GC Percentage	43.2%

2.3. Coverage

Mean	0.0839
Standard Deviation	0.6447

2.4. Mapping Quality

Mean Mapping Quality	38.14

2.5. Mismatches and indels

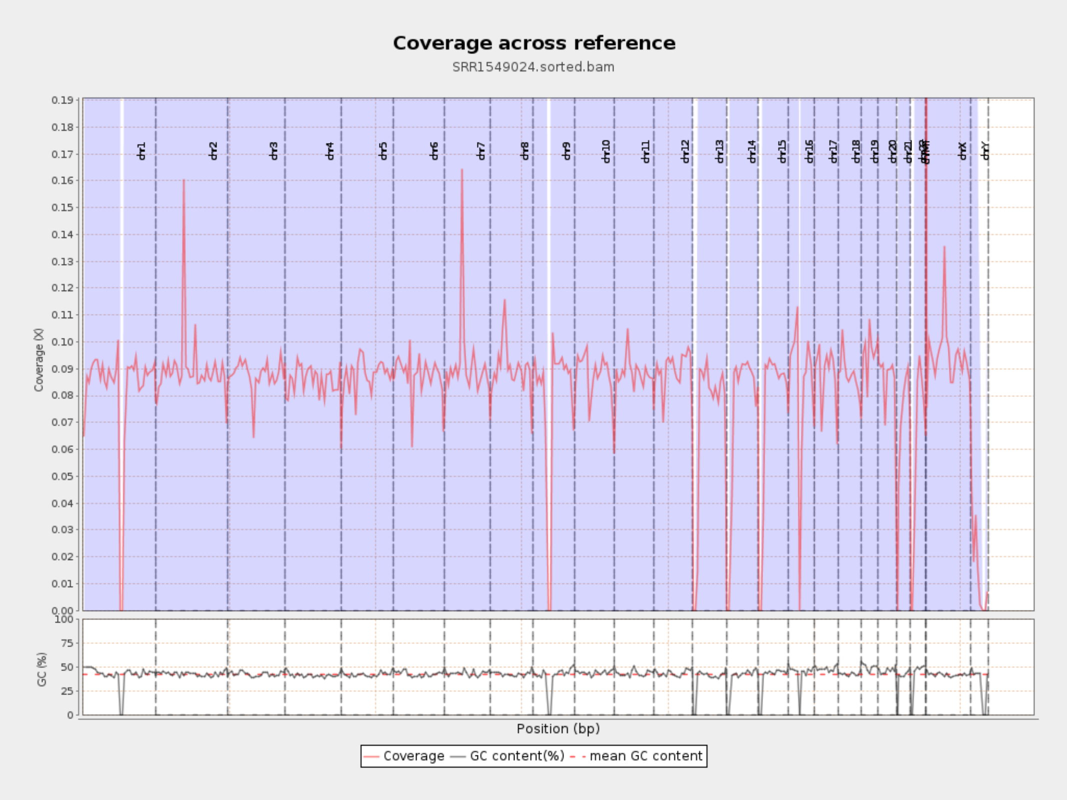
General error rate	0.31%
Mismatches	788,069
Insertions	8,681
Mapped reads with at least one insertion	0.13%
Deletions	18,842
Mapped reads with at least one deletion	0.29%
Homopolymer indels	39.66%

2.6. Chromosome stats

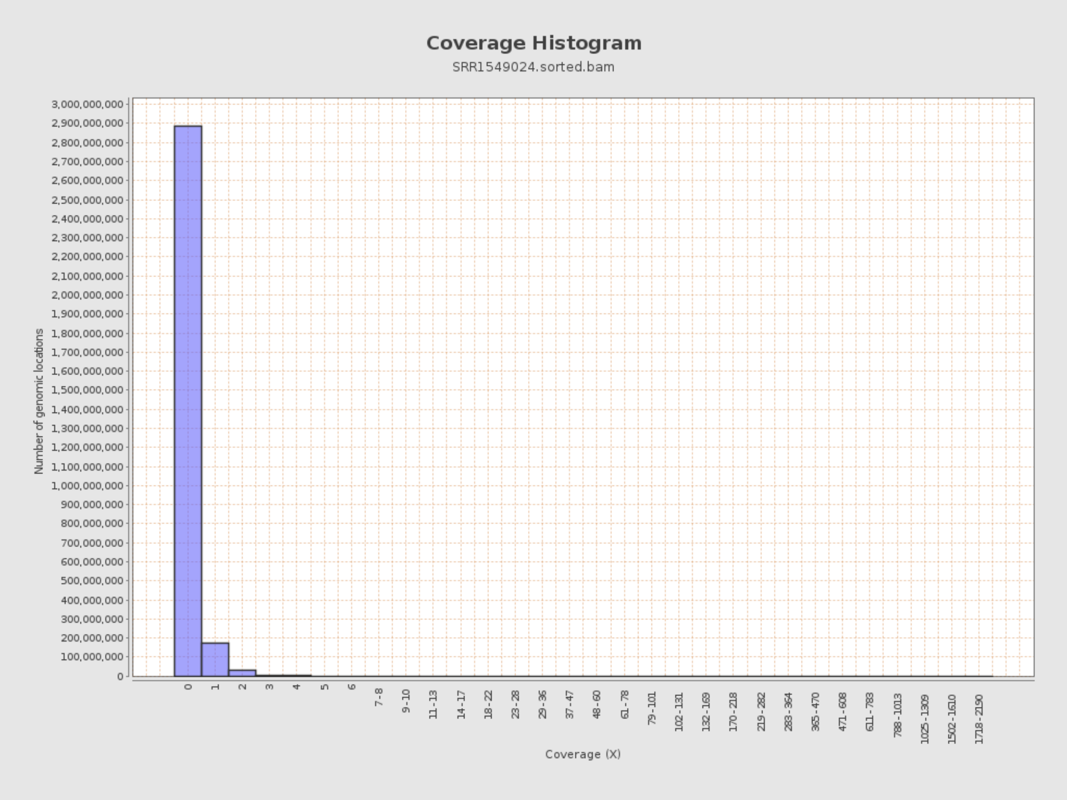
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20408950	0.0819	0.6144
chr2	243199373	21964714	0.0903	0.766
chr3	198022430	17373939	0.0877	0.3543
chr4	191154276	16428162	0.0859	0.3642
chr5	180915260	15852943	0.0876	0.3655
chr6	171115067	15017334	0.0878	0.4259
chr7	159138663	14639710	0.092	1.0388
chr8	146364022	13159014	0.0899	1.1773

chr9	141213431	11029148	0.0781	0.7931
chr10	135534747	11946000	0.0881	0.4653
chr11	135006516	11876831	0.088	0.8446
chr12	133851895	12041311	0.09	0.3794
chr13	115169878	8104760	0.0704	0.3143
chr14	107349540	7927560	0.0738	0.4614
chr15	102531392	7434717	0.0725	0.3245
chr16	90354753	7415248	0.0821	0.4511
chr17	81195210	7227046	0.089	0.4148
chr18	78077248	6907977	0.0885	1.4428
chr19	59128983	5630128	0.0952	0.753
chr20	63025520	5414676	0.0859	0.3672
chr21	48129895	3241195	0.0673	0.3968
chr22	51304566	3034444	0.0591	0.3454
chrMT	16571	19682	1.1877	2.9192
chrX	155270560	14748021	0.095	0.4947
chrY	59373566	841290	0.0142	0.1791

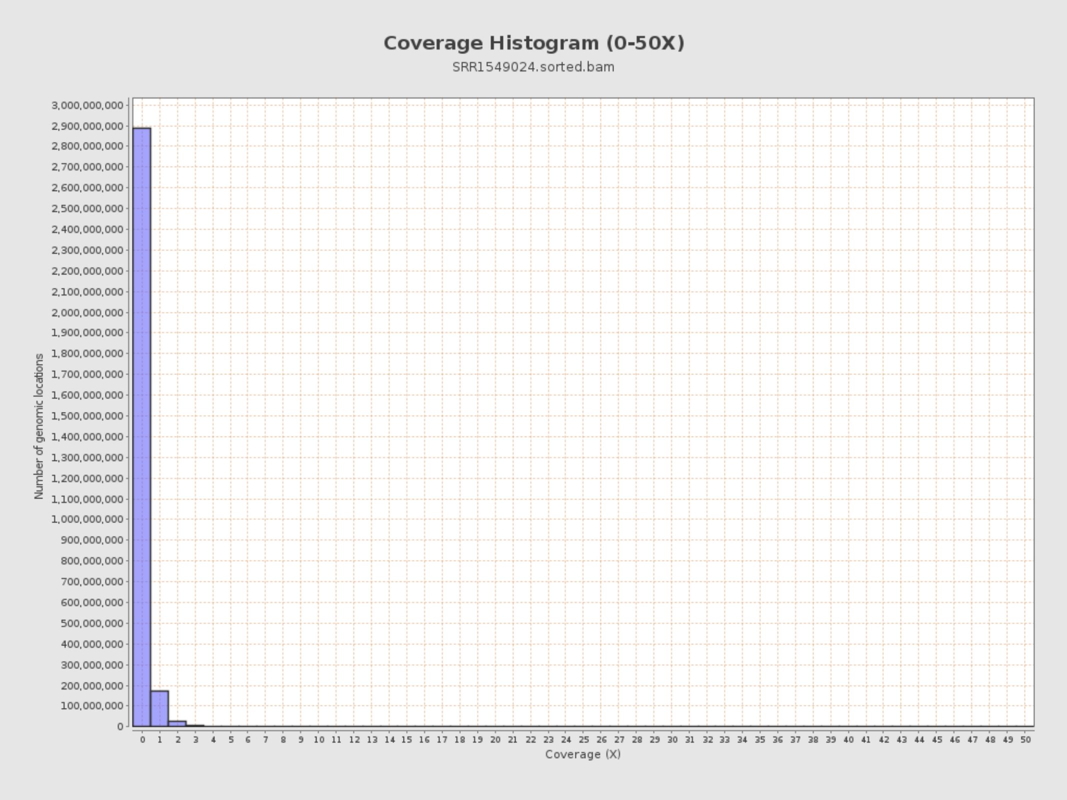
3. Results : Coverage across reference



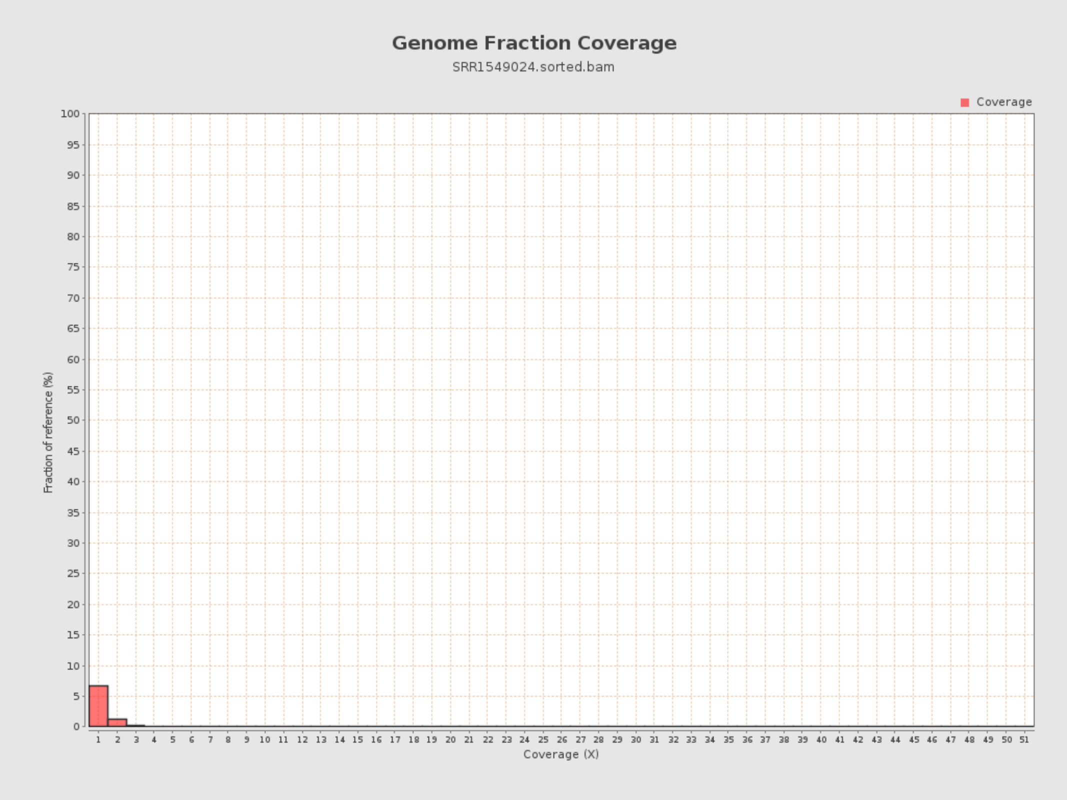
4. Results : Coverage Histogram



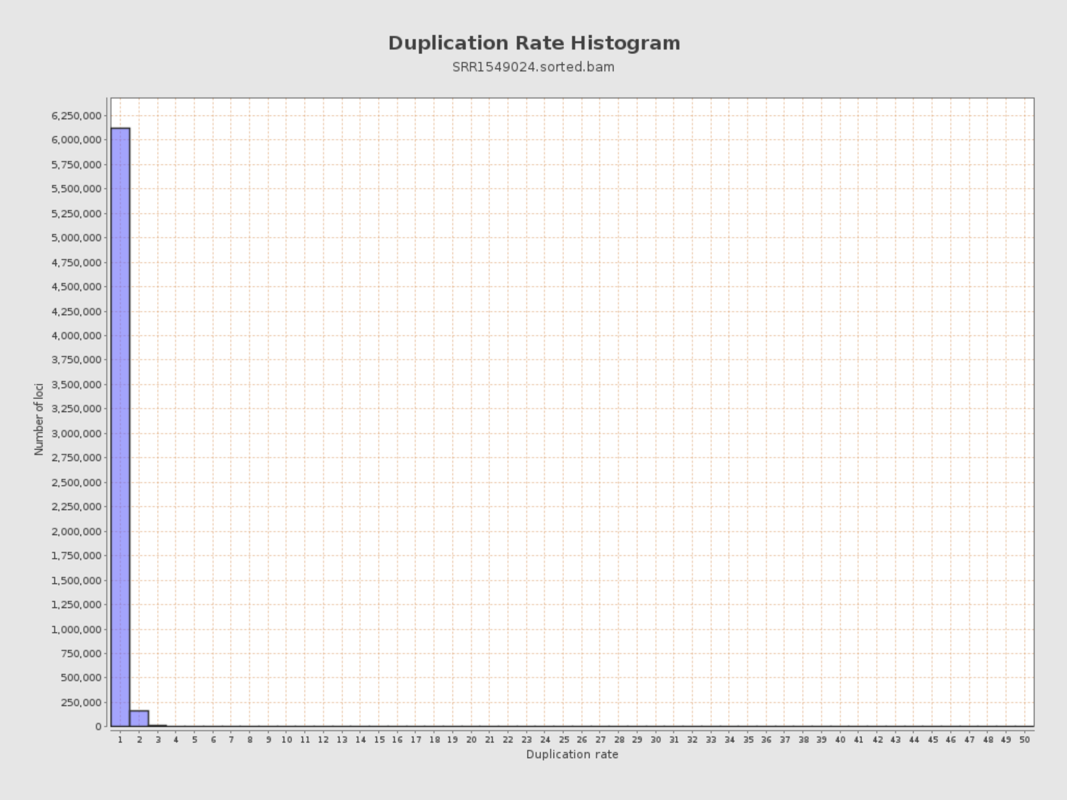
5. Results : Coverage Histogram (0-50X)



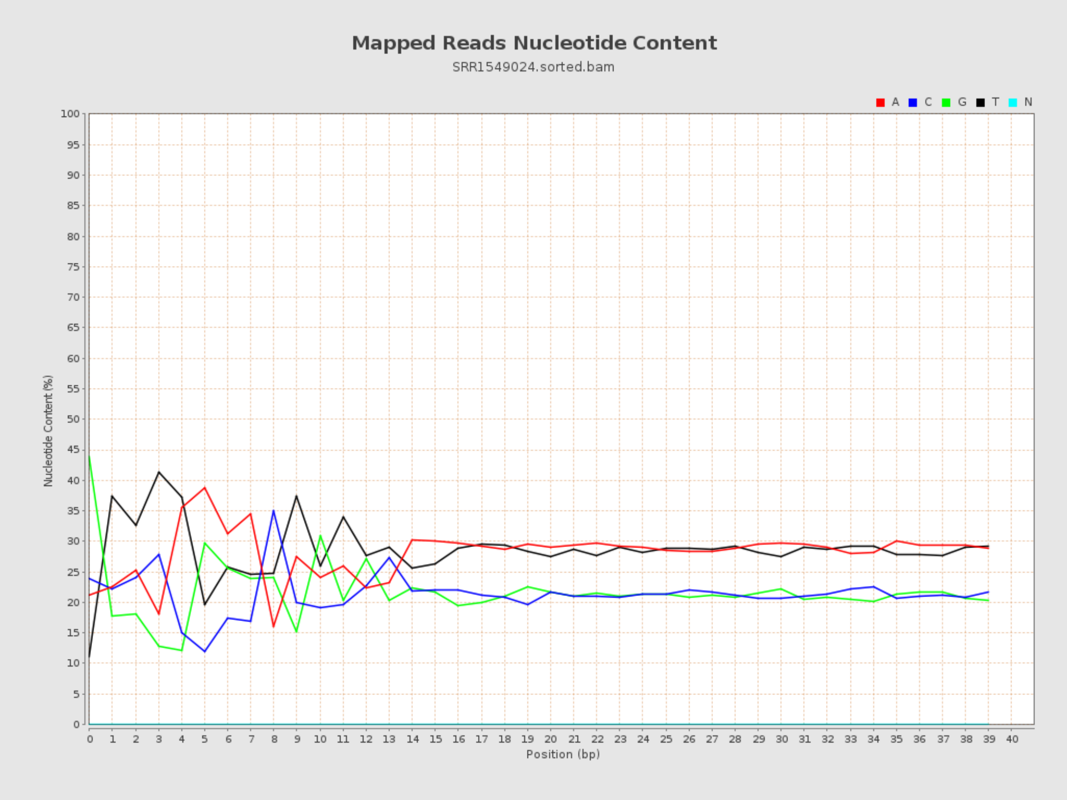
6. Results : Genome Fraction Coverage



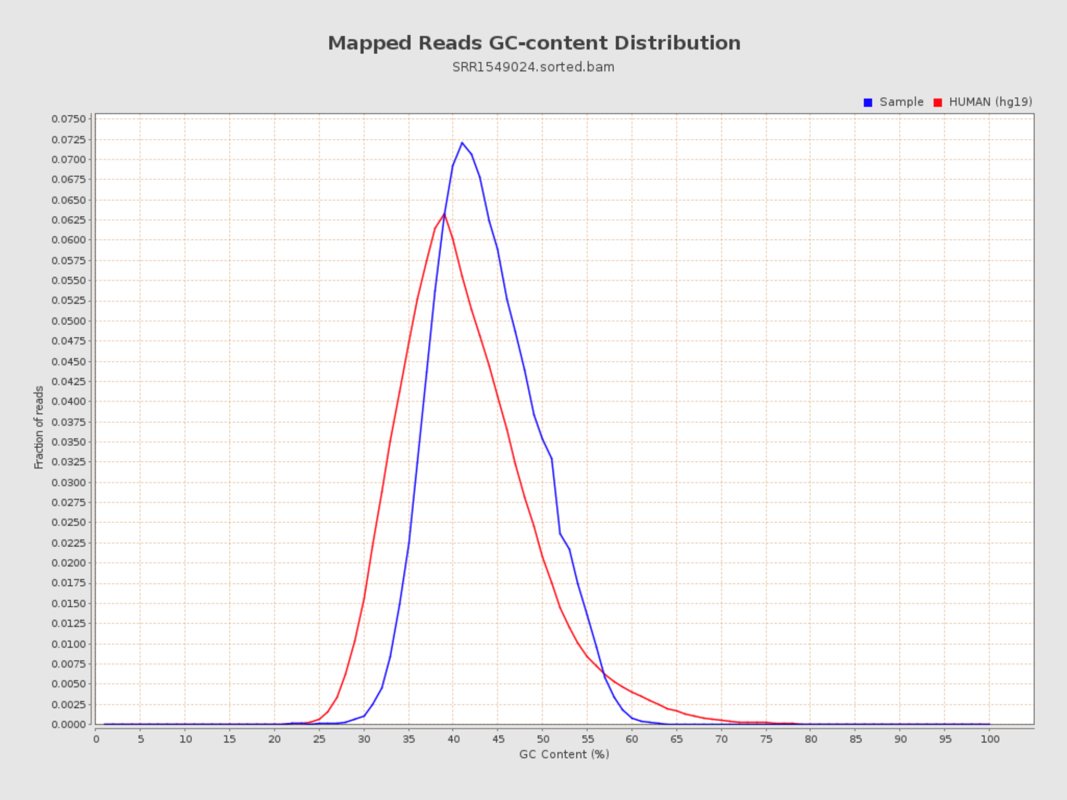
7. Results : Duplication Rate Histogram



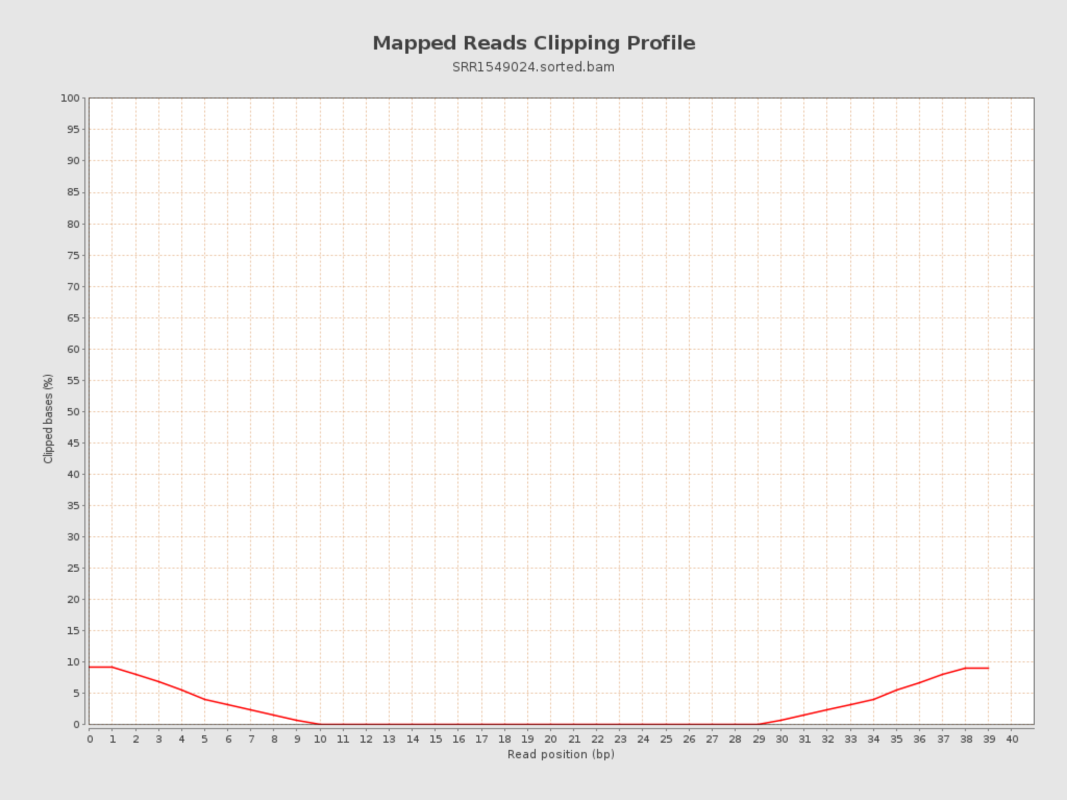
8. Results : Mapped Reads Nucleotide Content



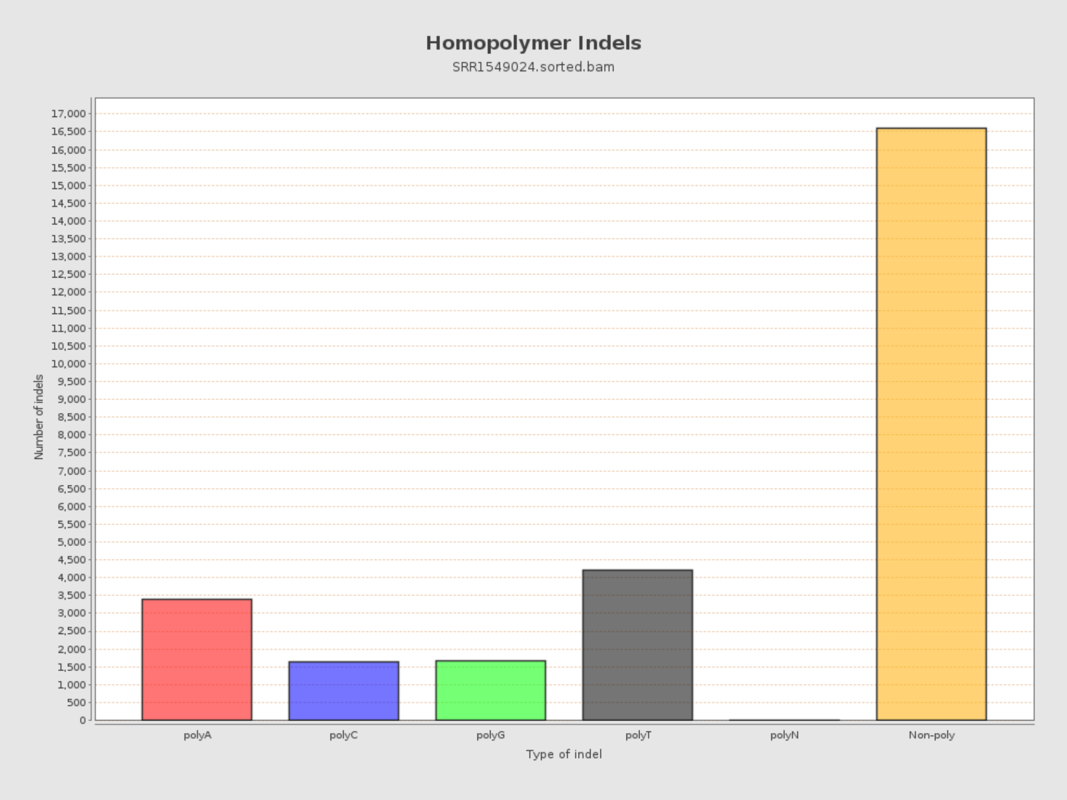
9. Results : Mapped Reads GC-content Distribution



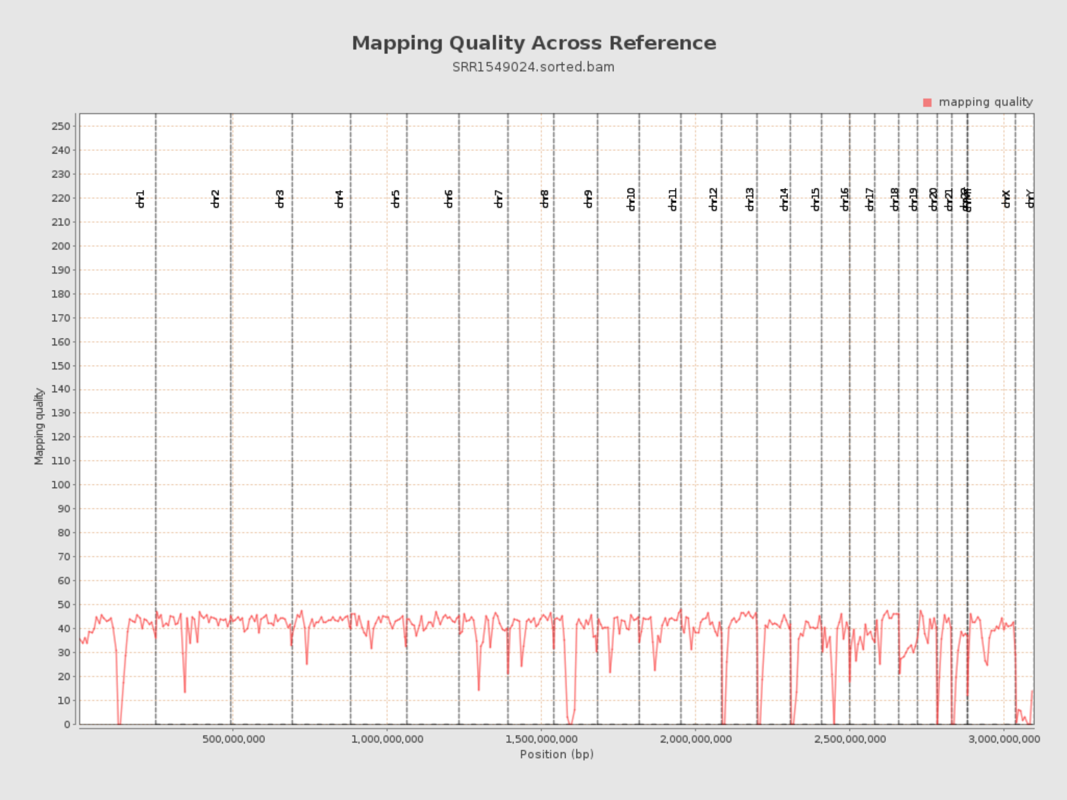
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram