Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:58:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549068.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_SRR1549068 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549068.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:58:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549068.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,204,359
Mapped reads	8,849,167 / 86.72%
Unmapped reads	1,355,192 / 13.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	333,741 / 3.27%
Duplication rate	2.53%
Clipped reads	407,917 / 4%

2.2. ACGT Content

Number/percentage of A's	103,171,100 / 29.35%
Number/percentage of C's	72,469,818 / 20.62%
Number/percentage of T's	103,521,606 / 29.45%
Number/percentage of G's	72,343,762 / 20.58%
Number/percentage of N's	6,399 / 0%
GC Percentage	41.2%

2.3. Coverage

Mean	0.1136
Standard Deviation	1.0592

2.4. Mapping Quality

Mean Mapping Quality	44.17

2.5. Mismatches and indels

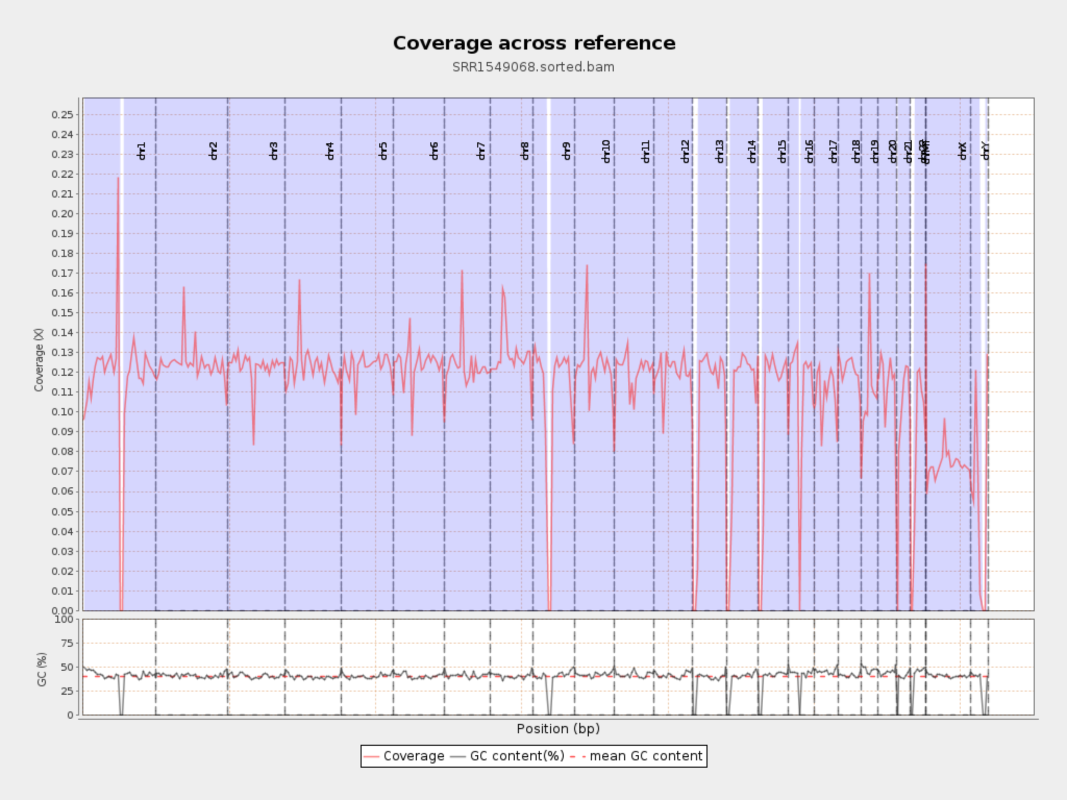
General error rate	0.31%
Mismatches	1,088,125
Insertions	8,702
Mapped reads with at least one insertion	0.1%
Deletions	29,085
Mapped reads with at least one deletion	0.33%
Homopolymer indels	44.57%

2.6. Chromosome stats

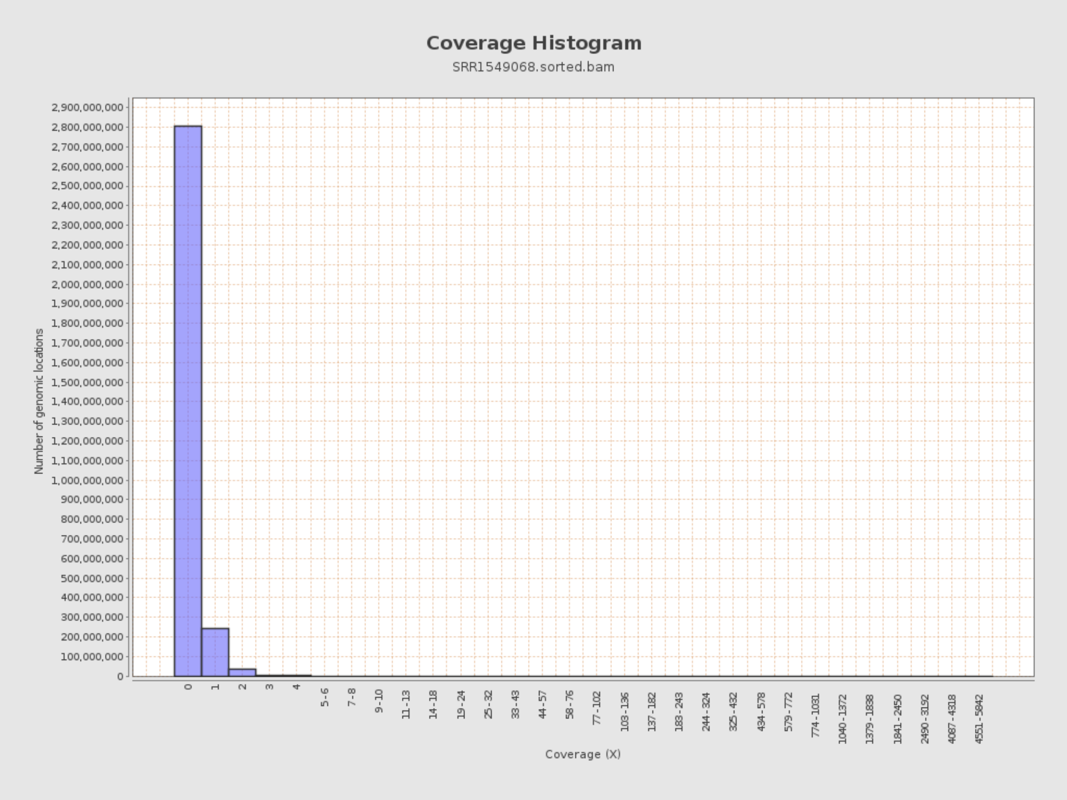
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28928711	0.1161	2.2543
chr2	243199373	30323870	0.1247	0.6448
chr3	198022430	24296569	0.1227	0.4113
chr4	191154276	23698088	0.124	0.4822
chr5	180915260	22208492	0.1228	0.4173
chr6	171115067	21242651	0.1241	0.4906
chr7	159138663	19632429	0.1234	0.8585
chr8	146364022	18802501	0.1285	2.8824

chr9	141213431	14952076	0.1059	0.5765
chr10	135534747	16799747	0.124	0.7157
chr11	135006516	16266635	0.1205	0.6037
chr12	133851895	16108843	0.1203	0.4258
chr13	115169878	11776467	0.1023	0.3638
chr14	107349540	10902977	0.1016	0.4335
chr15	102531392	10186327	0.0993	0.3602
chr16	90354753	9731506	0.1077	0.4467
chr17	81195210	8954905	0.1103	0.4286
chr18	78077248	9493893	0.1216	1.1863
chr19	59128983	6586123	0.1114	1.6357
chr20	63025520	7268023	0.1153	0.4151
chr21	48129895	4640766	0.0964	0.4627
chr22	51304566	4008780	0.0781	0.3546
chrMT	16571	2897	0.1748	0.4835
chrX	155270560	11437549	0.0737	0.4212
chrY	59373566	3299076	0.0556	0.6595

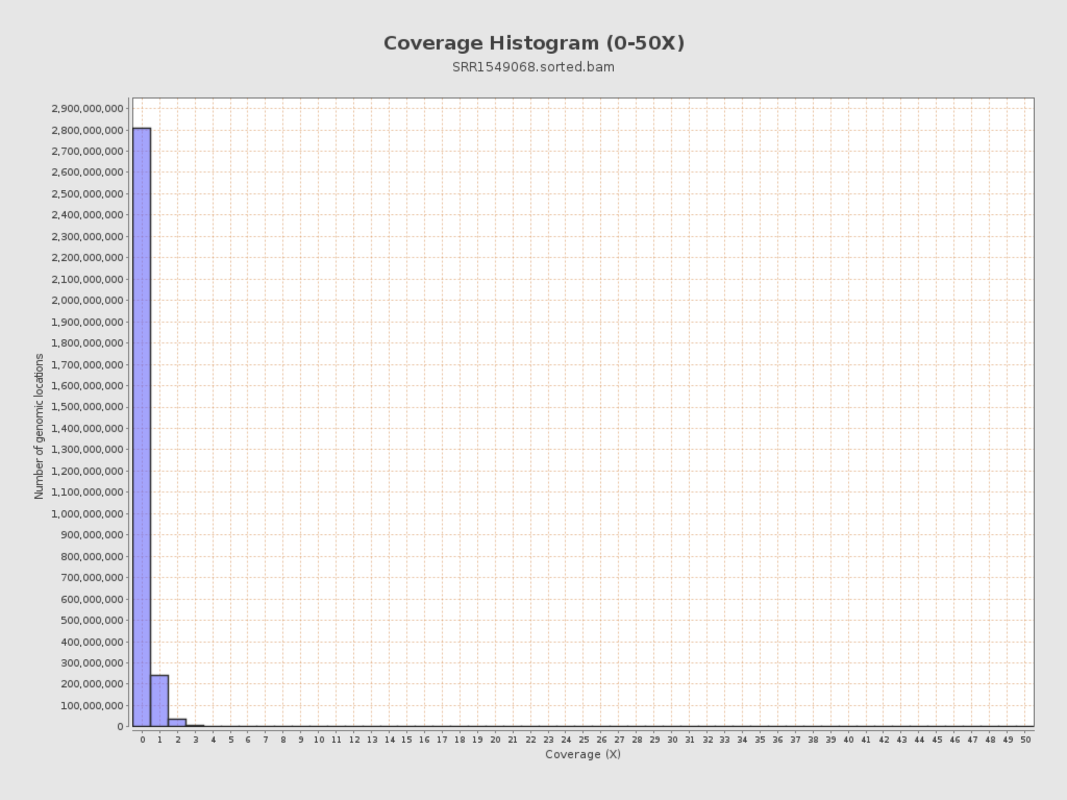
3. Results : Coverage across reference



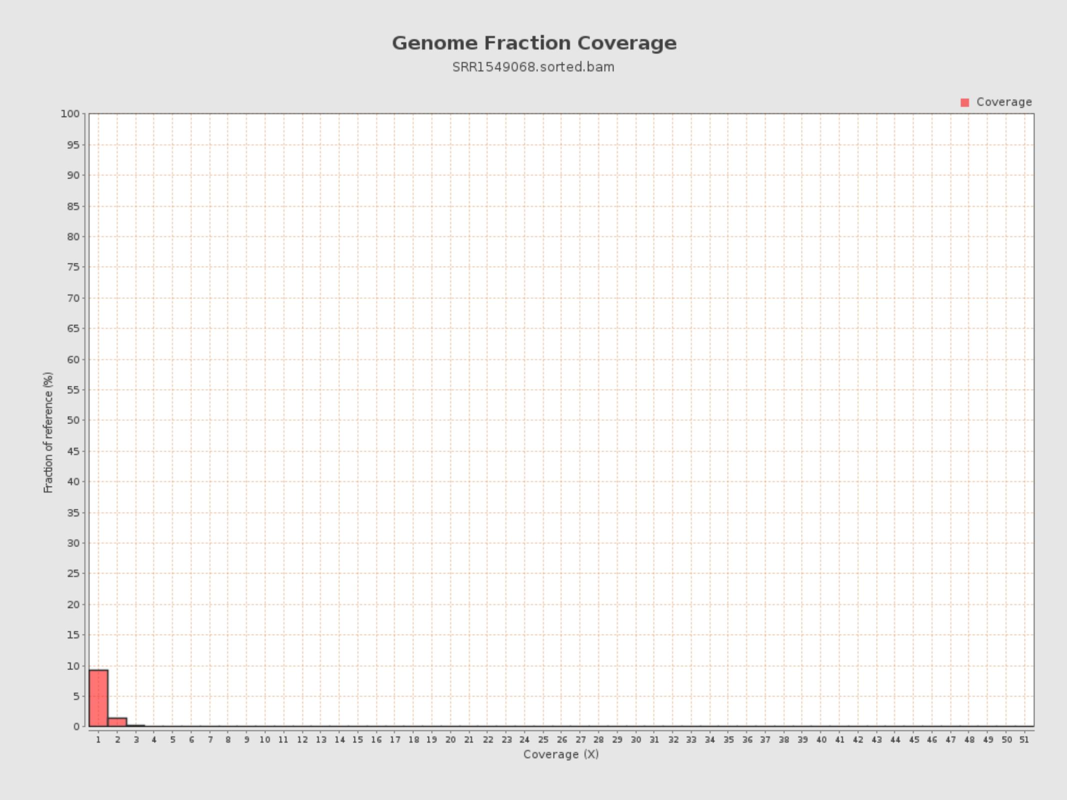
4. Results : Coverage Histogram



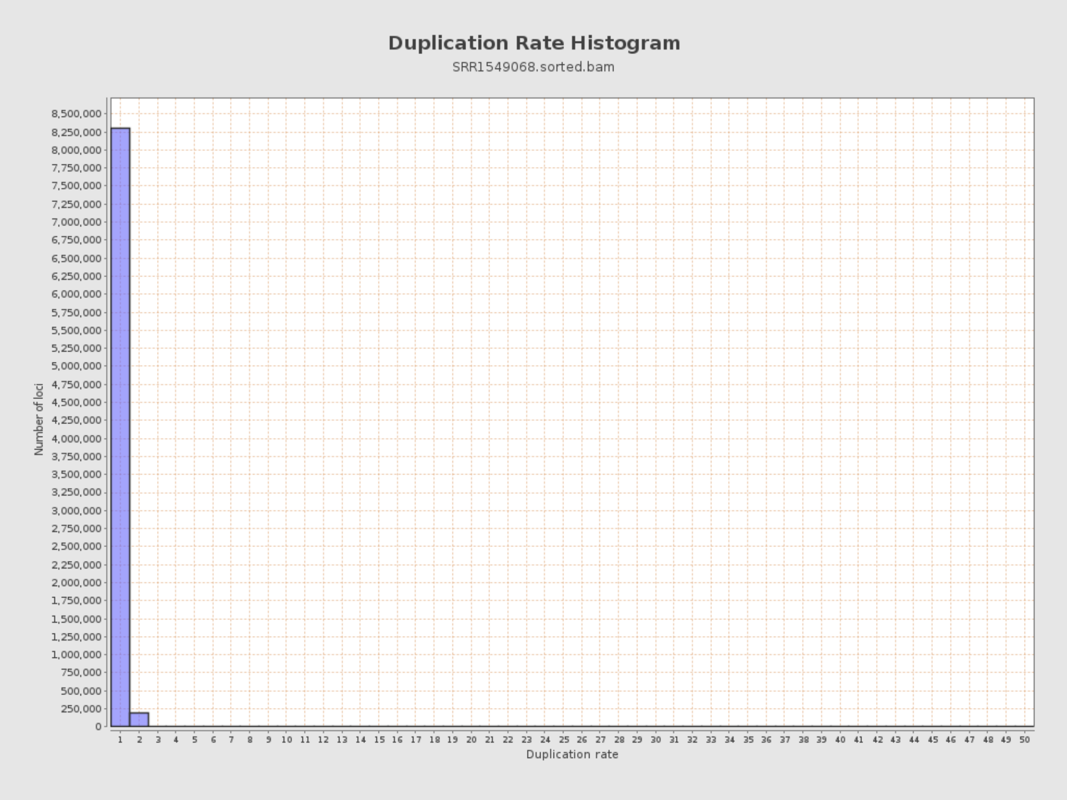
5. Results : Coverage Histogram (0-50X)



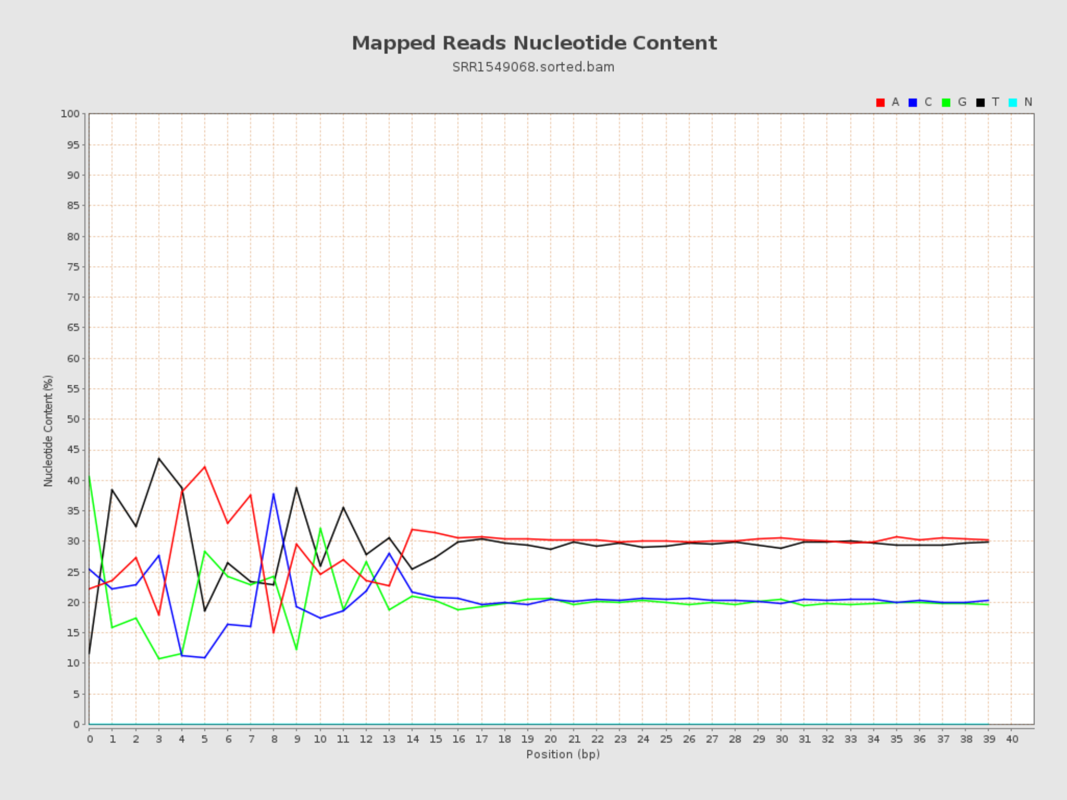
6. Results : Genome Fraction Coverage



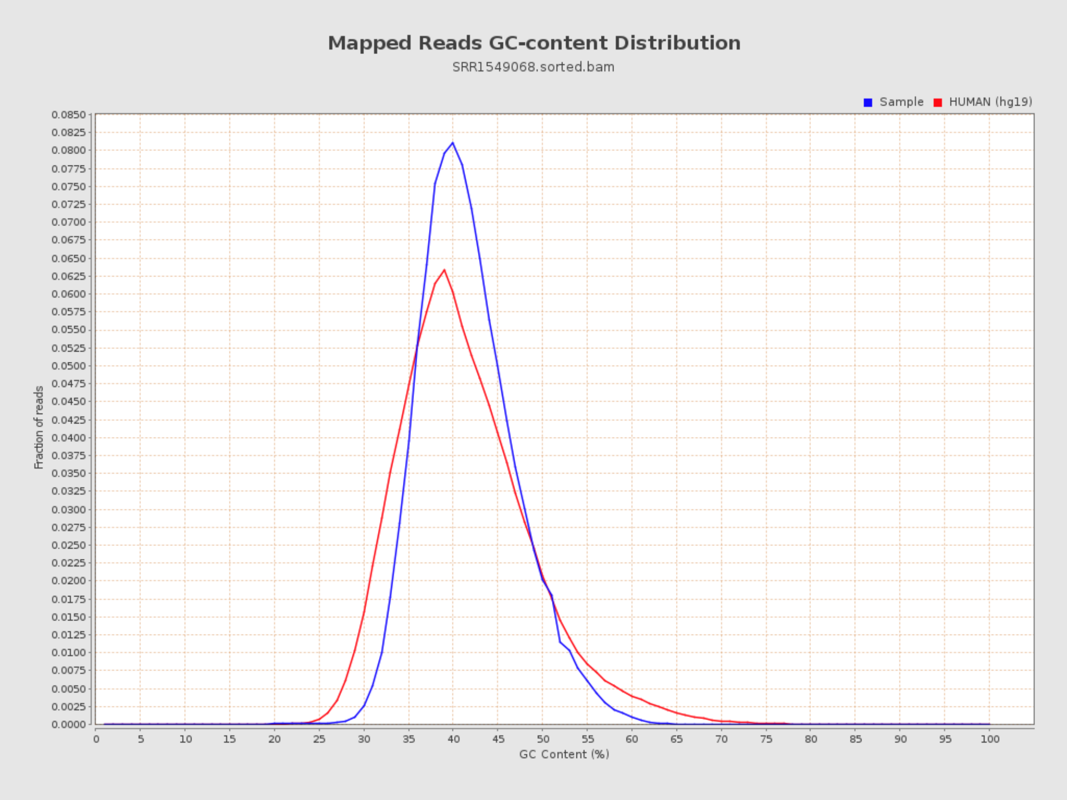
7. Results : Duplication Rate Histogram



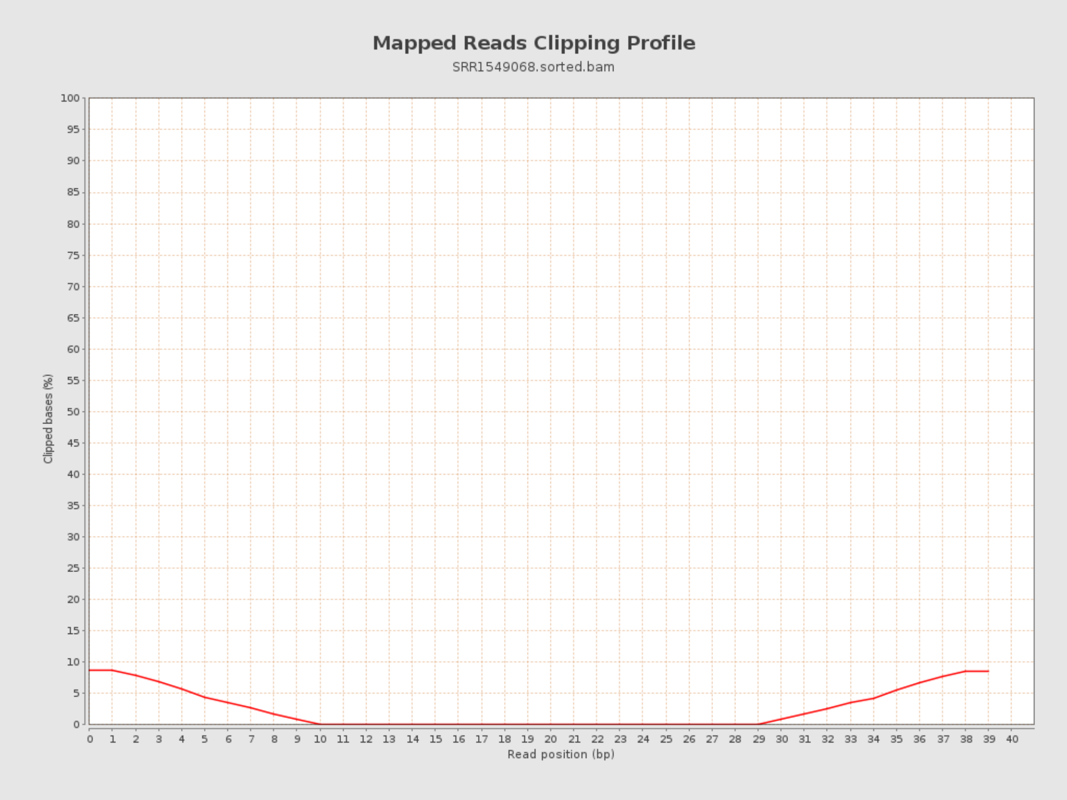
8. Results : Mapped Reads Nucleotide Content



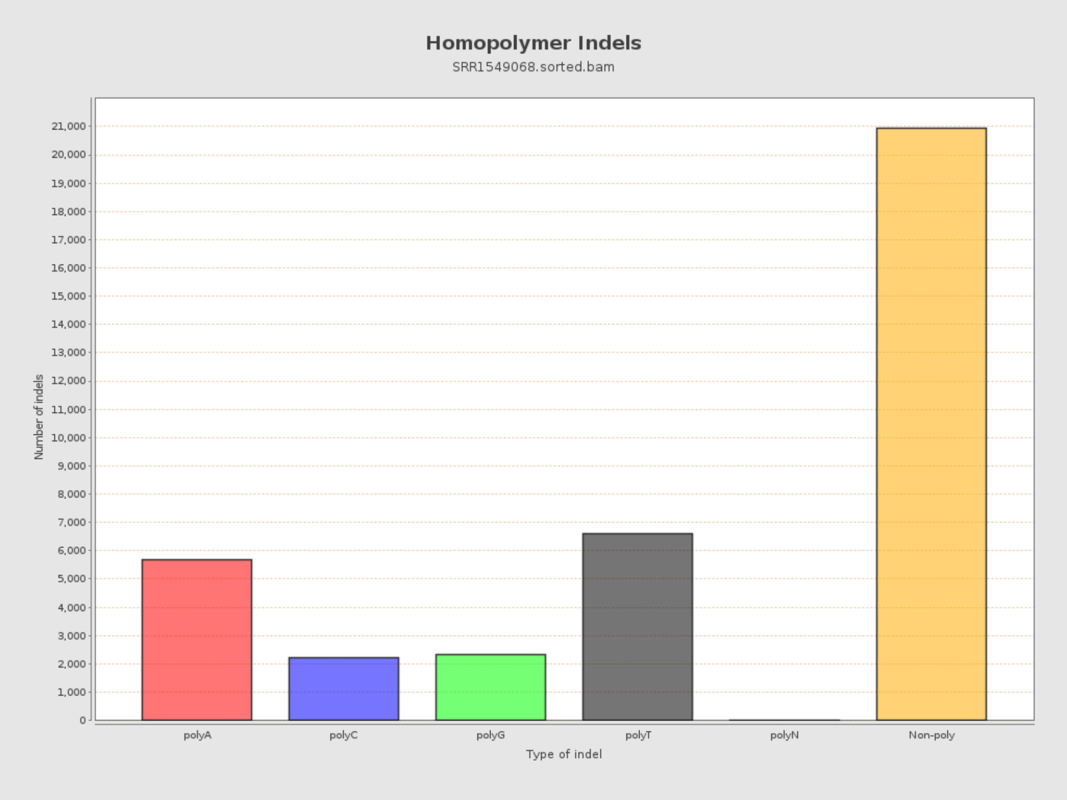
9. Results : Mapped Reads GC-content Distribution



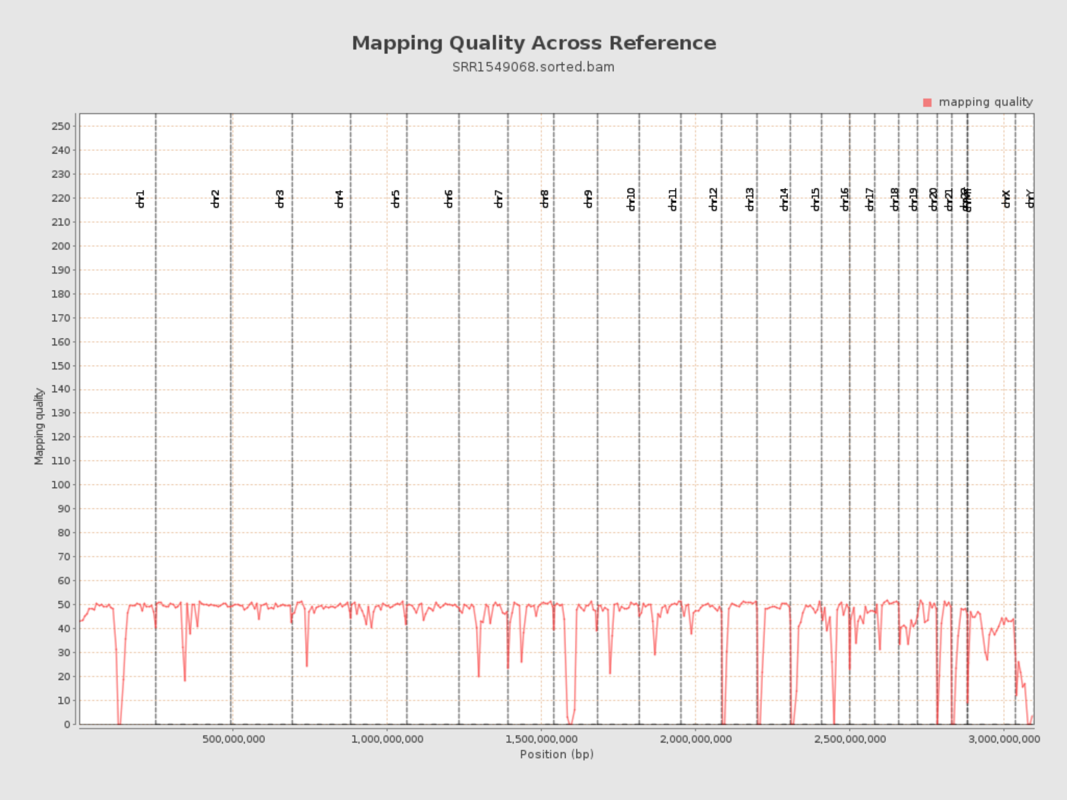
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram