Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 20:28:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549081.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_SRR1549081 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549081.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 20:28:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549081.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,625,940
Mapped reads	8,437,711 / 87.66%
Unmapped reads	1,188,229 / 12.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	304,348 / 3.16%
Duplication rate	2.34%
Clipped reads	434,787 / 4.52%

2.2. ACGT Content

Number/percentage of A's	100,084,774 / 29.88%
Number/percentage of C's	67,149,867 / 20.05%
Number/percentage of T's	101,721,677 / 30.37%
Number/percentage of G's	65,887,732 / 19.67%
Number/percentage of N's	85,625 / 0.03%
GC Percentage	39.72%

2.3. Coverage

Mean	0.1082
Standard Deviation	0.8585

2.4. Mapping Quality

Mean Mapping Quality	44.08

2.5. Mismatches and indels

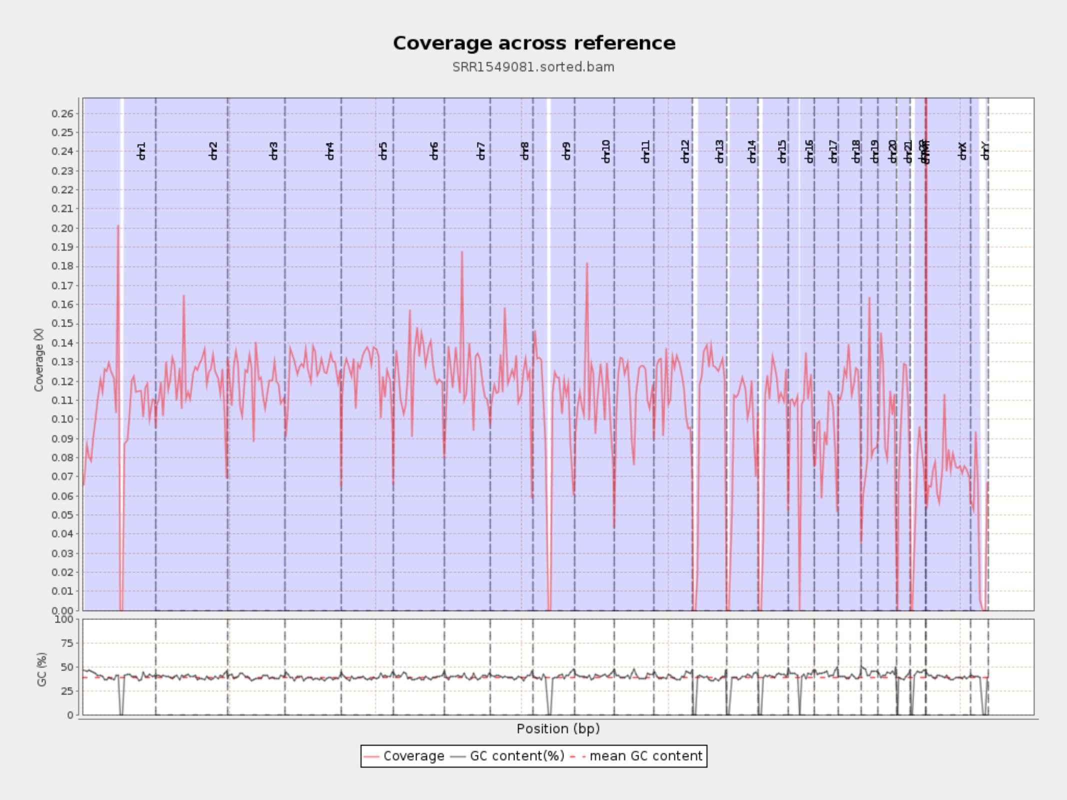
General error rate	0.4%
Mismatches	1,343,971
Insertions	8,030
Mapped reads with at least one insertion	0.1%
Deletions	24,108
Mapped reads with at least one deletion	0.29%
Homopolymer indels	45.96%

2.6. Chromosome stats

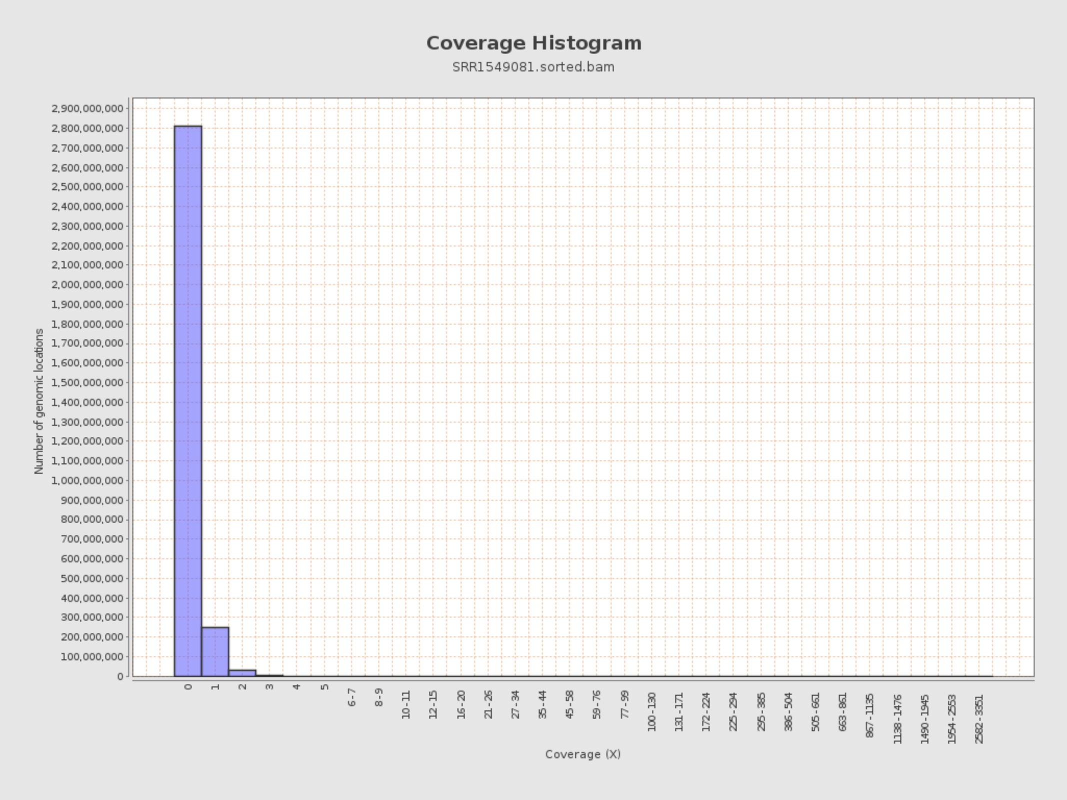
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25708704	0.1031	2.1286
chr2	243199373	29392657	0.1209	0.6377
chr3	198022430	23584190	0.1191	0.4024
chr4	191154276	24234292	0.1268	0.411
chr5	180915260	22397992	0.1238	0.4105
chr6	171115067	21600433	0.1262	0.5577
chr7	159138663	19527186	0.1227	1.0062
chr8	146364022	17514119	0.1197	0.6275

chr9	141213431	14309583	0.1013	0.62
chr10	135534747	15314513	0.113	0.7771
chr11	135006516	15468495	0.1146	0.6735
chr12	133851895	15556524	0.1162	0.4227
chr13	115169878	12214715	0.1061	0.359
chr14	107349540	9646723	0.0899	0.4868
chr15	102531392	9754485	0.0951	0.3439
chr16	90354753	8880038	0.0983	0.47
chr17	81195210	7385695	0.091	0.4157
chr18	78077248	9390255	0.1203	1.3861
chr19	59128983	5108652	0.0864	1.6779
chr20	63025520	6663105	0.1057	0.3942
chr21	48129895	4421745	0.0919	0.4087
chr22	51304566	2972850	0.0579	0.3263
chrMT	16571	22928	1.3836	1.7903
chrX	155270560	11389401	0.0734	0.4396
chrY	59373566	2500250	0.0421	0.3624

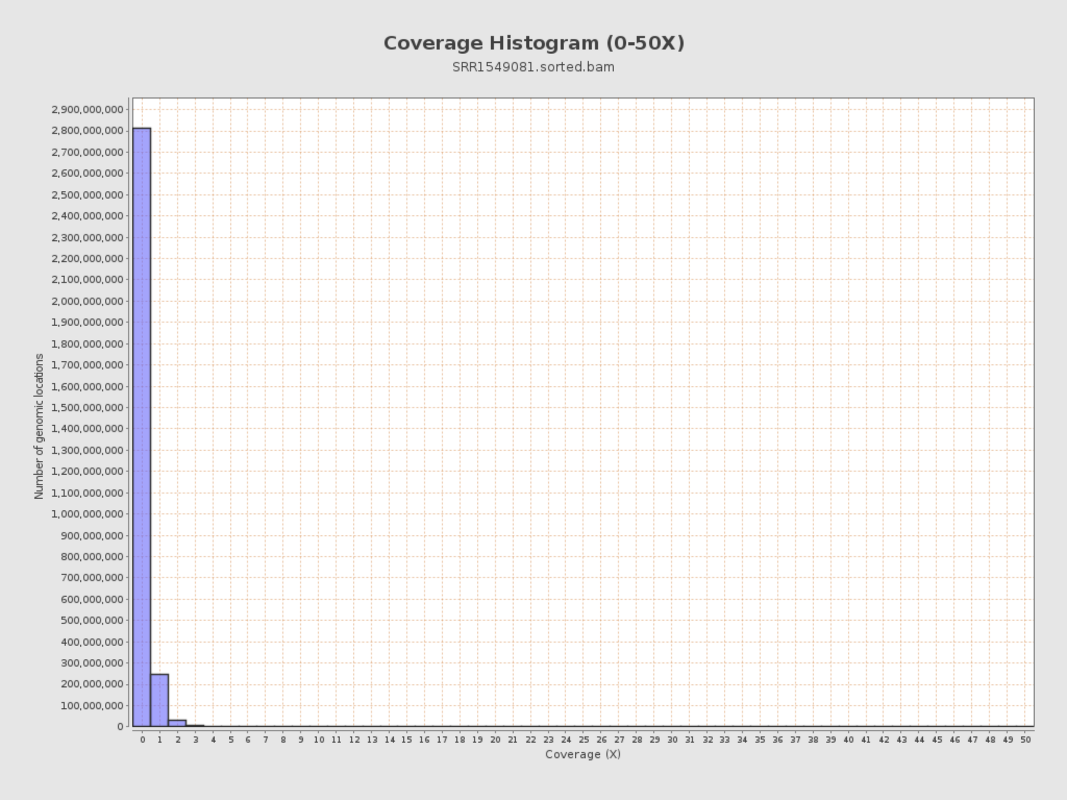
3. Results : Coverage across reference



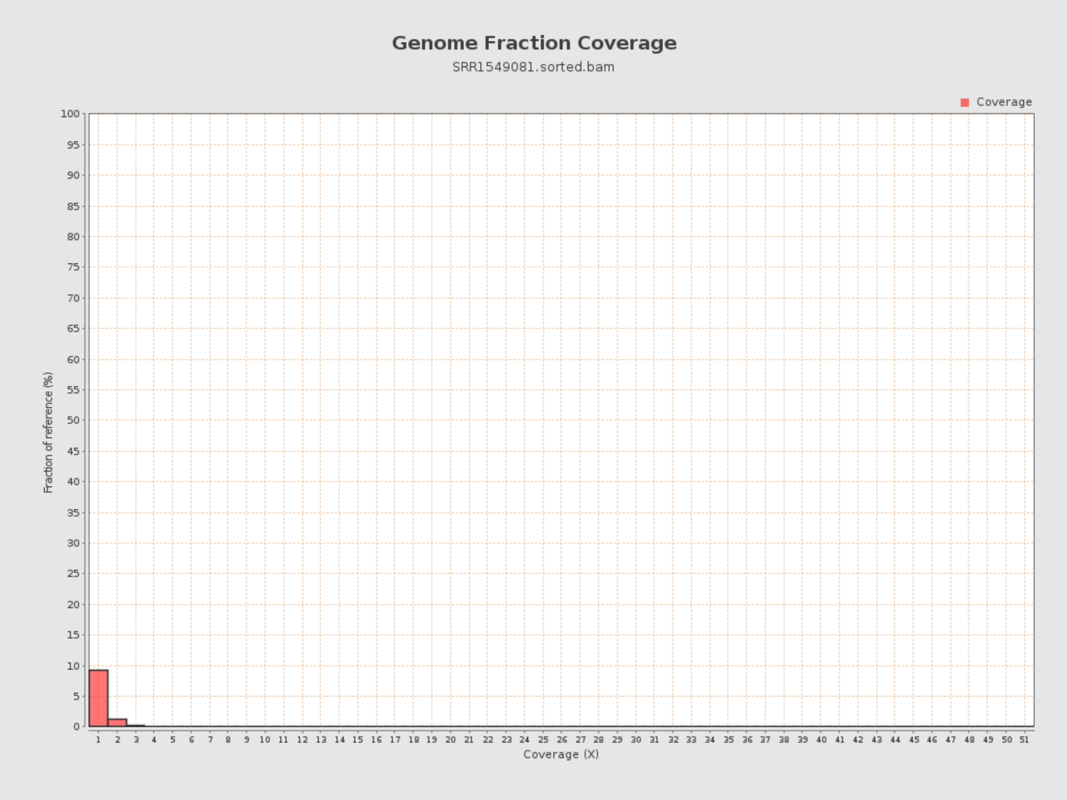
4. Results : Coverage Histogram



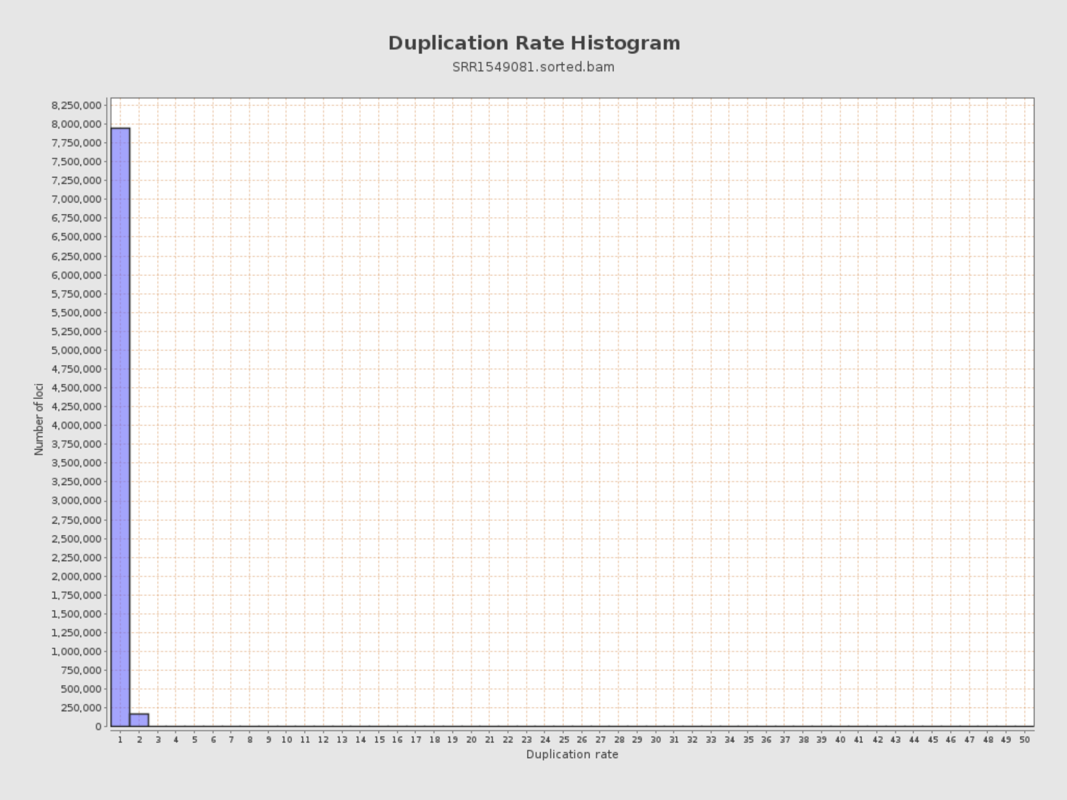
5. Results : Coverage Histogram (0-50X)



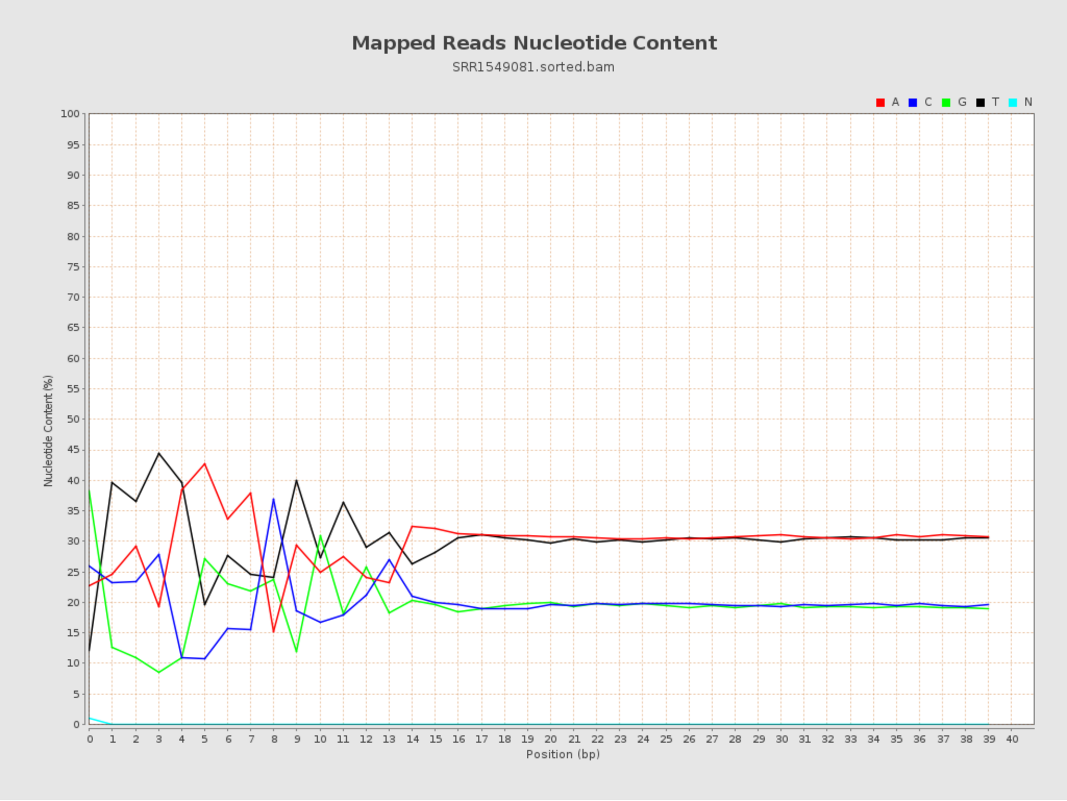
6. Results : Genome Fraction Coverage



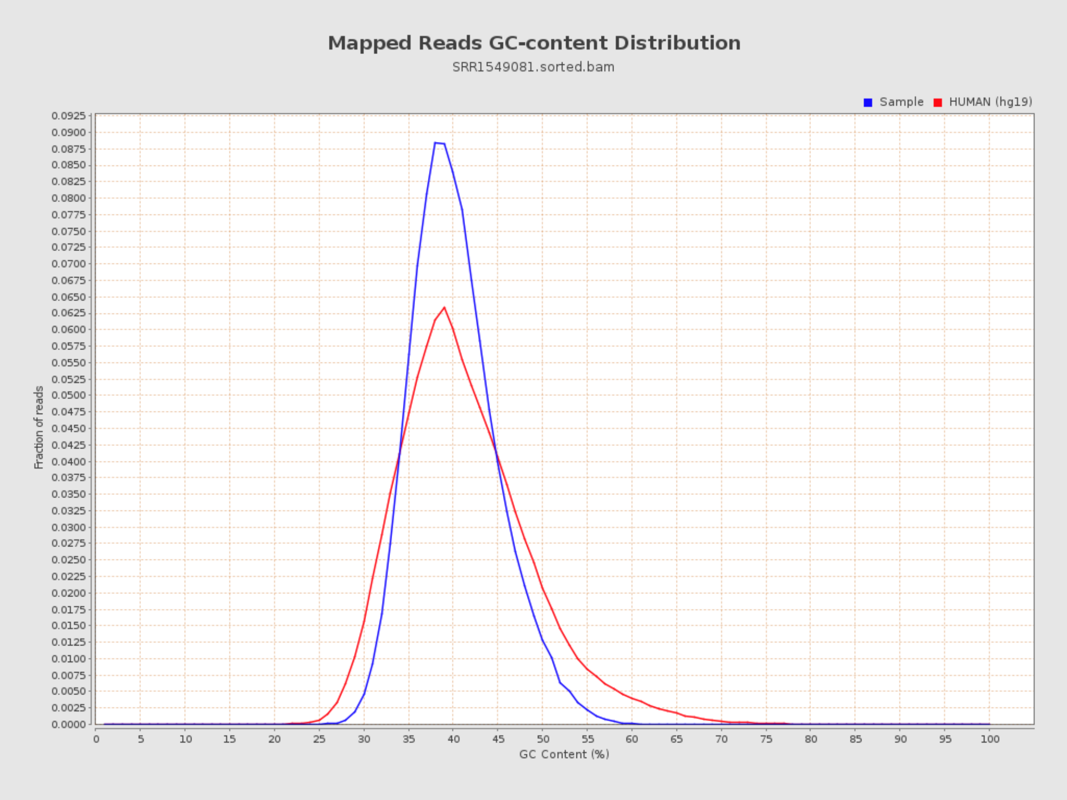
7. Results : Duplication Rate Histogram



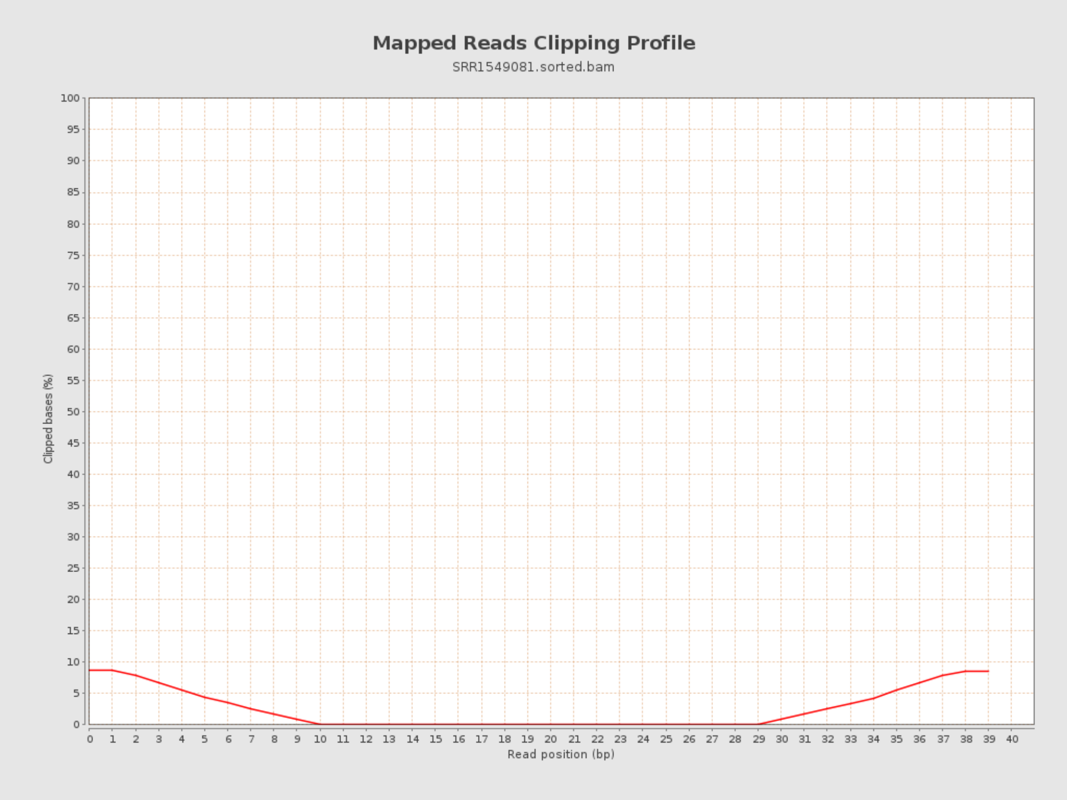
8. Results : Mapped Reads Nucleotide Content



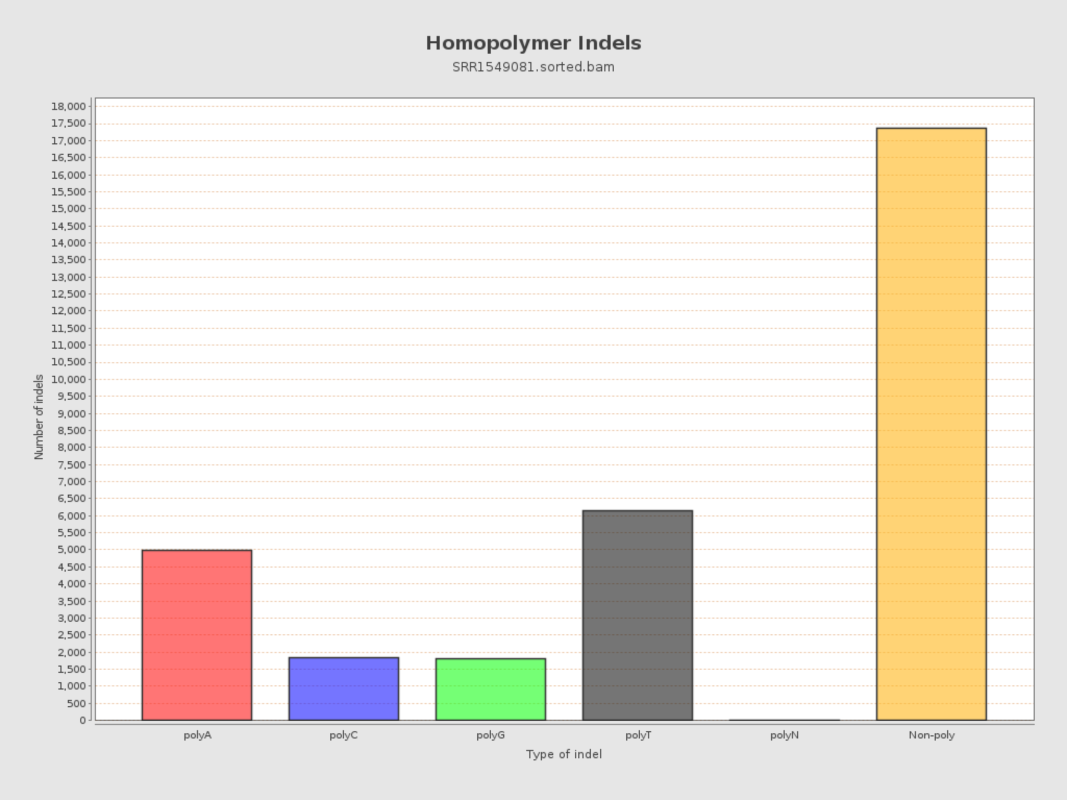
9. Results : Mapped Reads GC-content Distribution



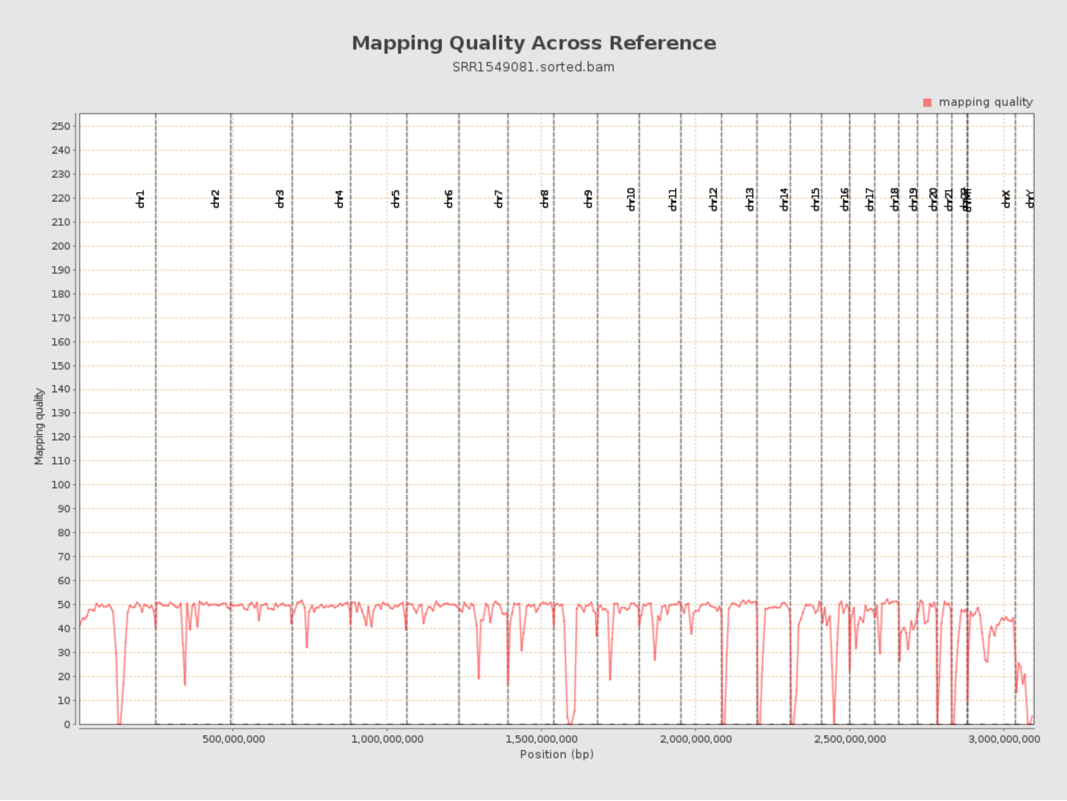
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram