Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 23:54:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549091.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_SRR1549091 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549091.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 23:54:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549091.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,410,499
Mapped reads	8,272,349 / 87.91%
Unmapped reads	1,138,150 / 12.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	354,241 / 3.76%
Duplication rate	2.38%
Clipped reads	456,318 / 4.85%

2.2. ACGT Content

Number/percentage of A's	98,925,279 / 30.14%
Number/percentage of C's	65,233,557 / 19.87%
Number/percentage of T's	100,132,032 / 30.51%
Number/percentage of G's	63,851,305 / 19.45%
Number/percentage of N's	81,032 / 0.02%
GC Percentage	39.33%

2.3. Coverage

Mean	0.106
Standard Deviation	1.2602

2.4. Mapping Quality

Mean Mapping Quality	41.8

2.5. Mismatches and indels

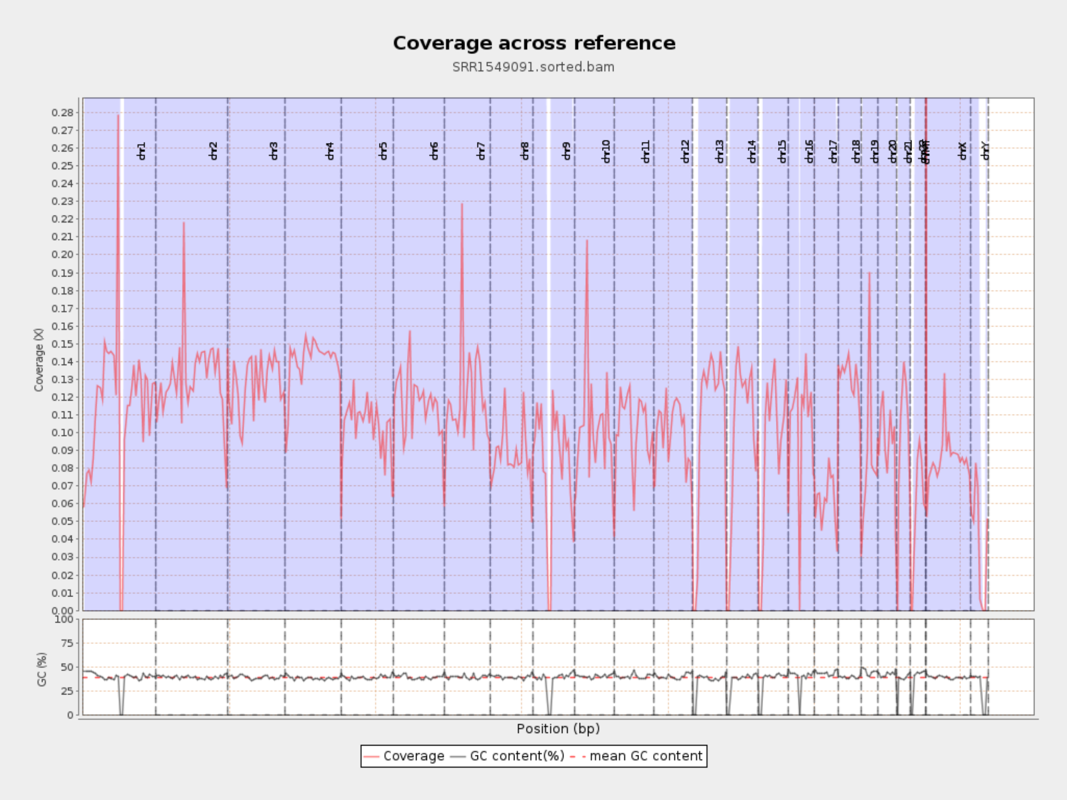
General error rate	0.42%
Mismatches	1,378,708
Insertions	8,407
Mapped reads with at least one insertion	0.1%
Deletions	25,848
Mapped reads with at least one deletion	0.31%
Homopolymer indels	44.16%

2.6. Chromosome stats

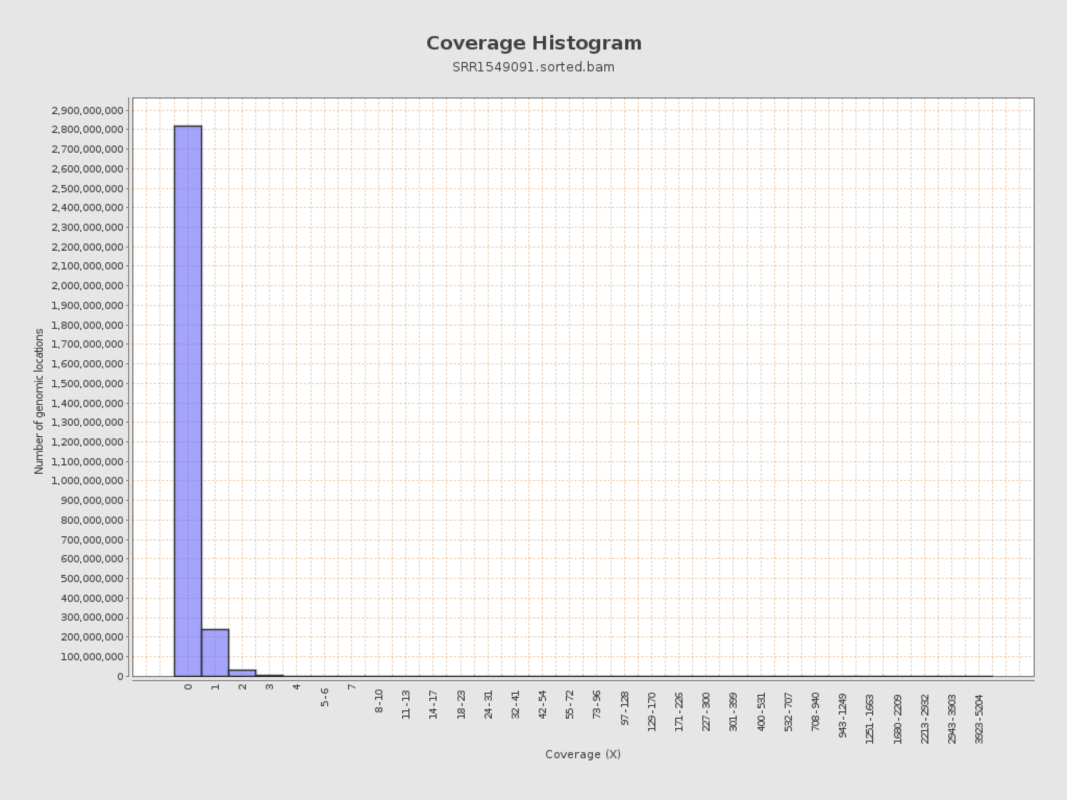
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28635701	0.1149	3.4323
chr2	243199373	31846453	0.1309	0.8638
chr3	198022430	25392006	0.1282	0.4244
chr4	191154276	26845767	0.1404	0.4408
chr5	180915260	18717482	0.1035	0.4013
chr6	171115067	20159735	0.1178	0.5506
chr7	159138663	19098064	0.12	1.3277
chr8	146364022	12800250	0.0875	1.1119

chr9	141213431	11728533	0.0831	0.8151
chr10	135534747	13979205	0.1031	0.9917
chr11	135006516	13910400	0.103	0.7824
chr12	133851895	13378638	0.1	0.4296
chr13	115169878	12308076	0.1069	0.3606
chr14	107349540	10904686	0.1016	0.4687
chr15	102531392	9427244	0.0919	0.3435
chr16	90354753	9323828	0.1032	0.5437
chr17	81195210	5081906	0.0626	0.3288
chr18	78077248	10262666	0.1314	1.7481
chr19	59128983	5207833	0.0881	2.7623
chr20	63025520	6153755	0.0976	0.3959
chr21	48129895	4601209	0.0956	0.4482
chr22	51304566	2919356	0.0569	0.3482
chrMT	16571	9489	0.5726	1.0335
chrX	155270560	13259459	0.0854	0.5065
chrY	59373566	2303726	0.0388	0.3172

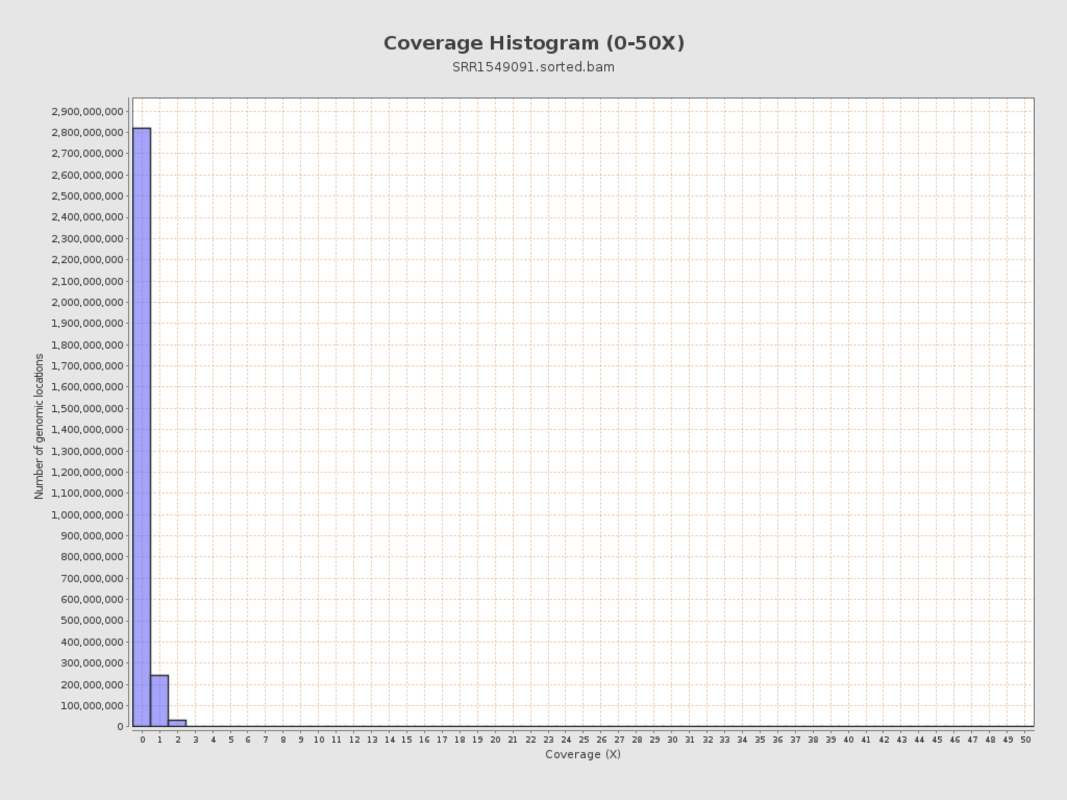
3. Results : Coverage across reference



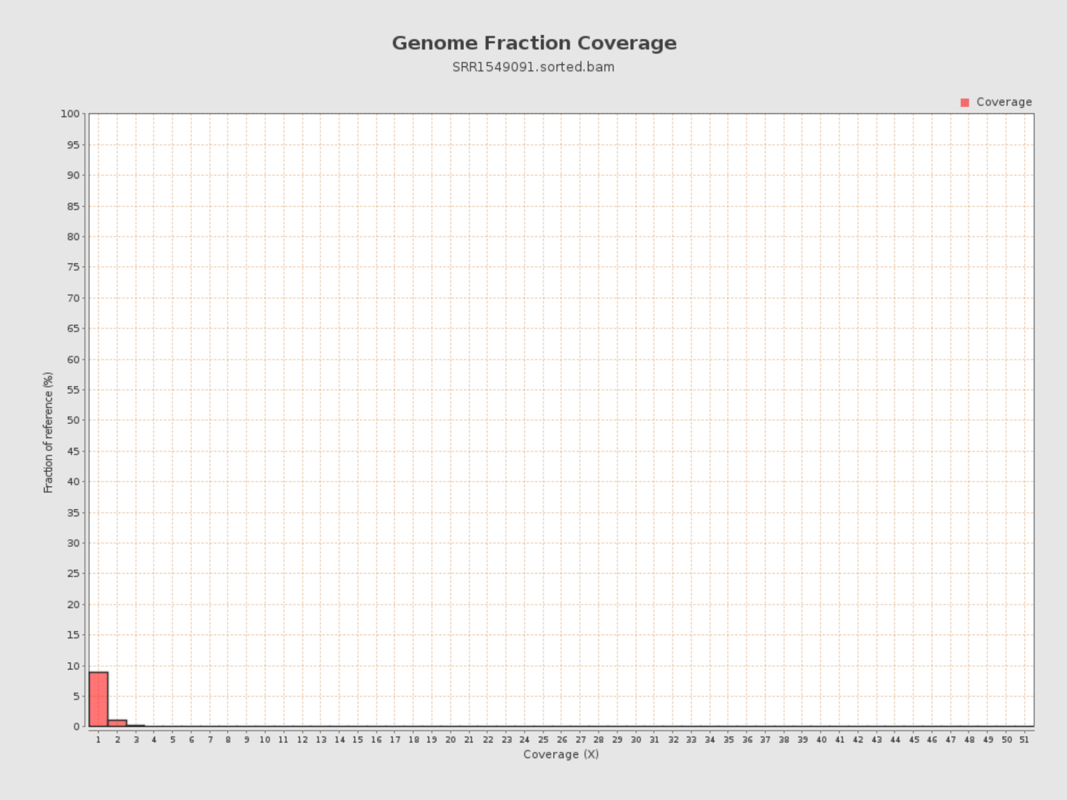
4. Results : Coverage Histogram



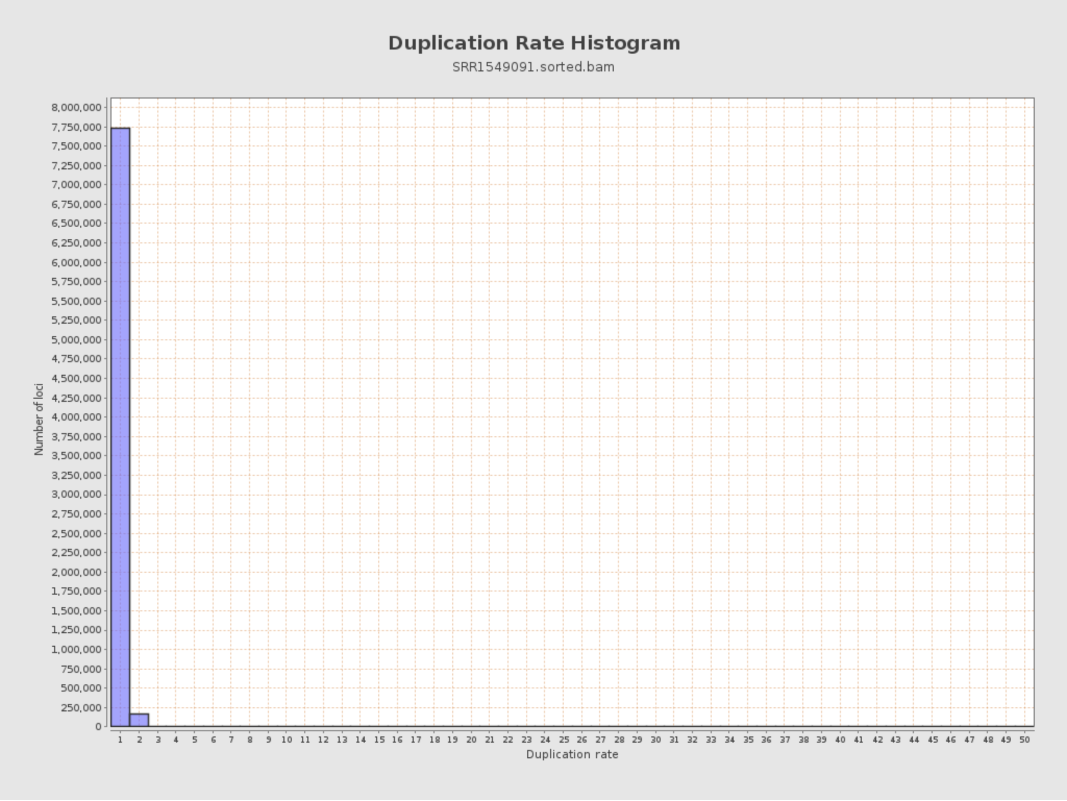
5. Results : Coverage Histogram (0-50X)



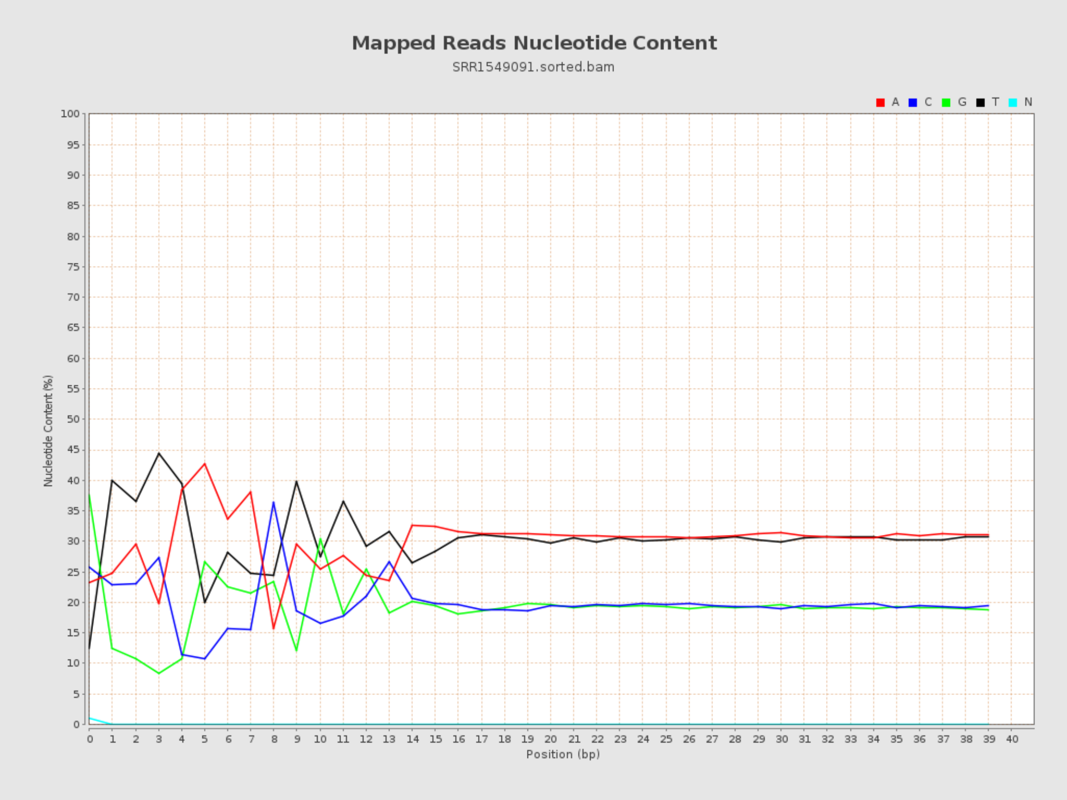
6. Results : Genome Fraction Coverage



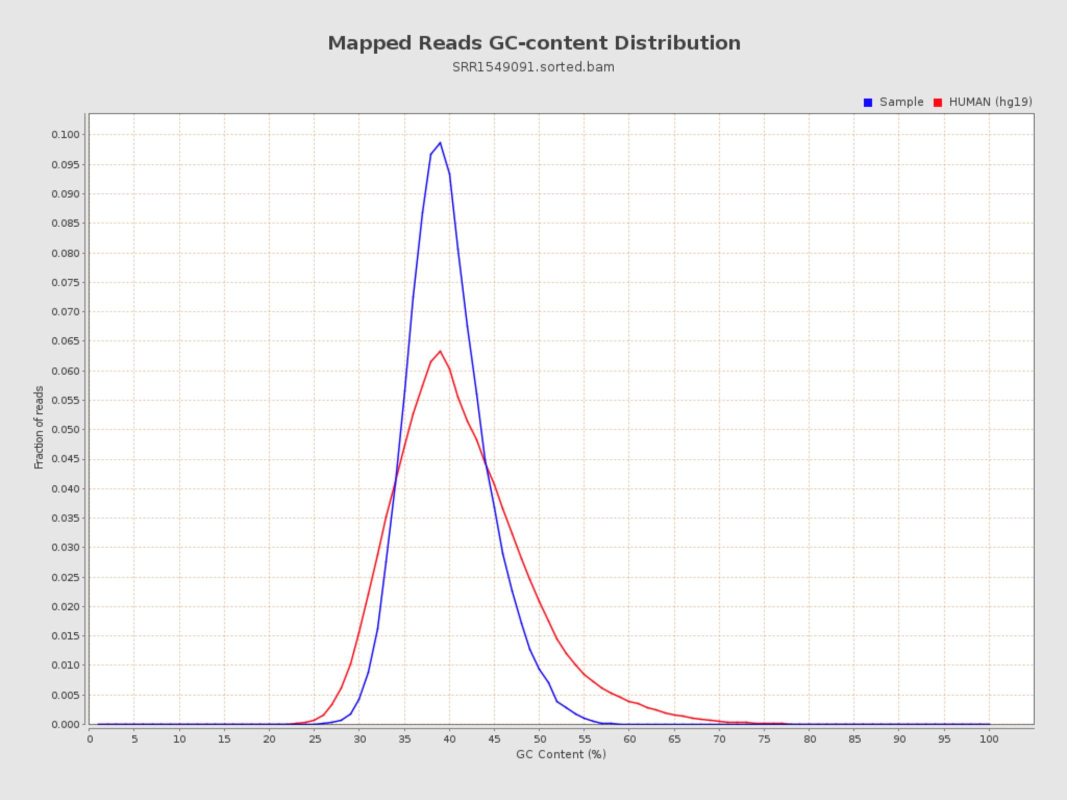
7. Results : Duplication Rate Histogram



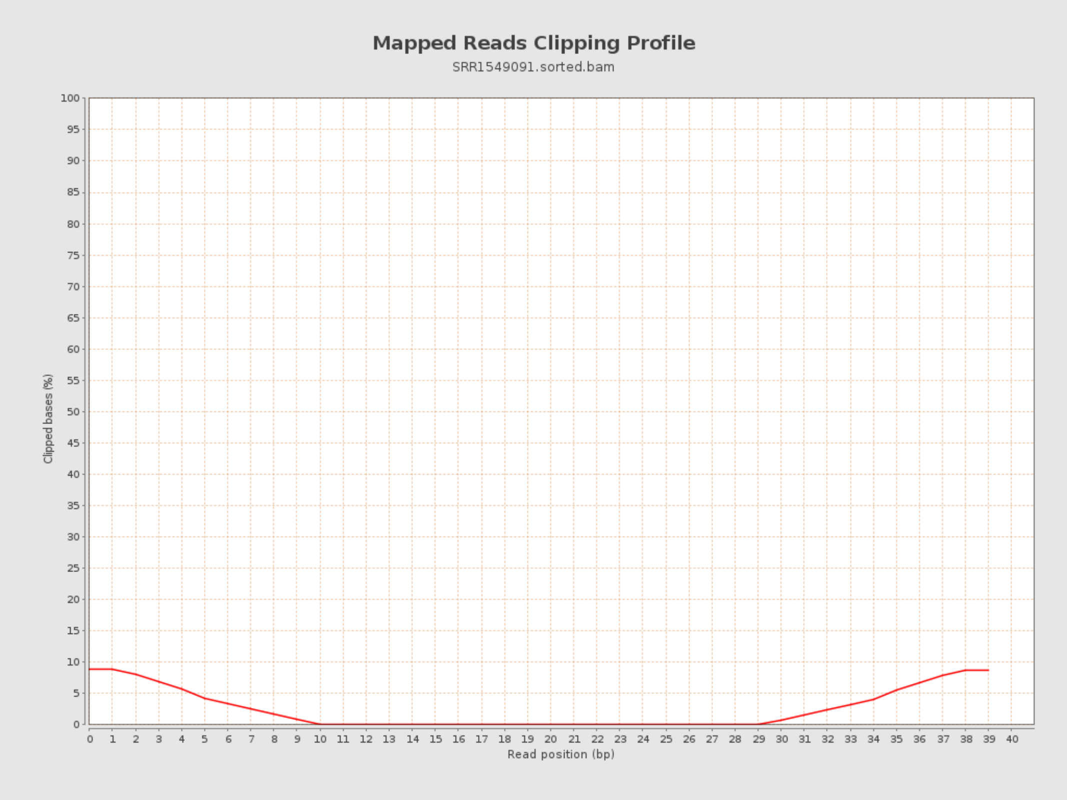
8. Results : Mapped Reads Nucleotide Content



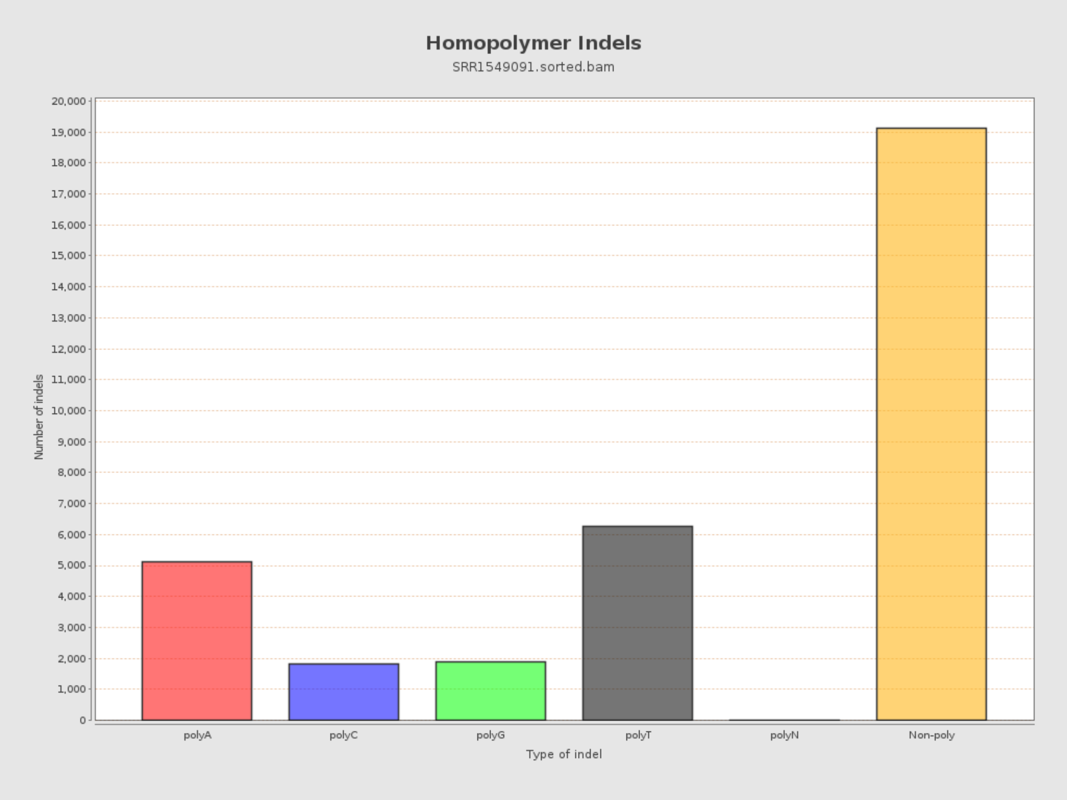
9. Results : Mapped Reads GC-content Distribution



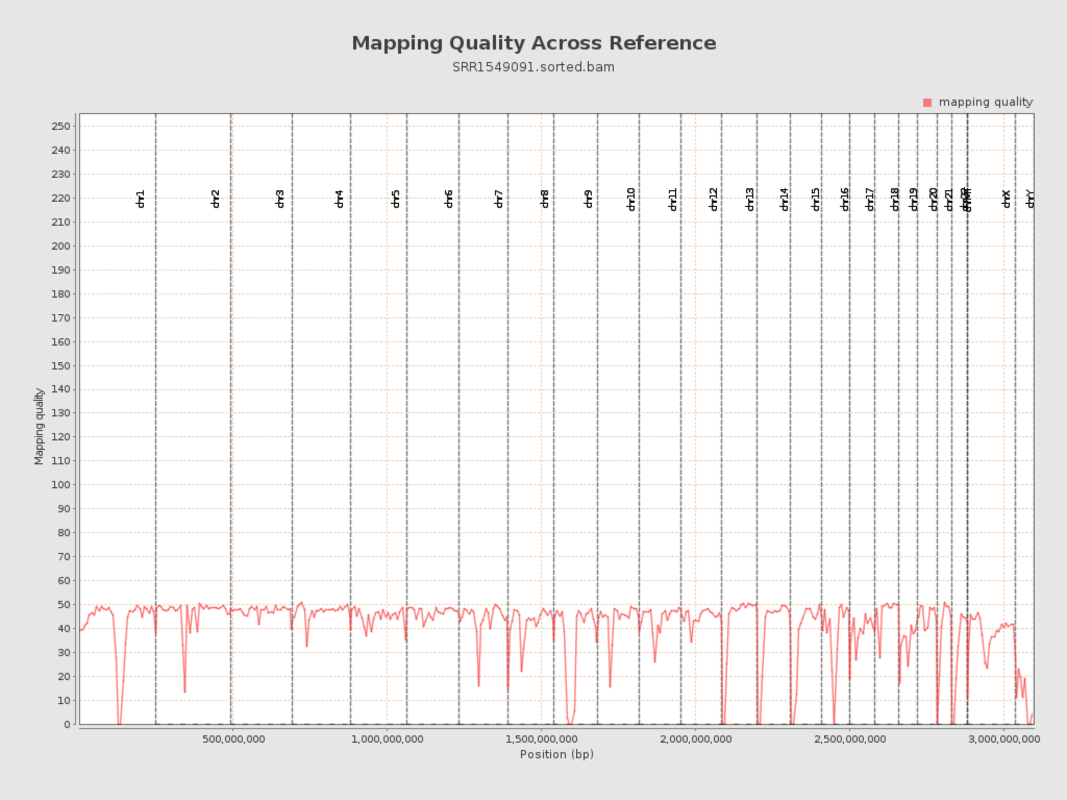
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram