Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:52:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549013.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_SRR1549013 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549013.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:52:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549013.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,306,390
Mapped reads	4,631,988 / 87.29%
Unmapped reads	674,402 / 12.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	150,074 / 2.83%
Duplication rate	2.01%
Clipped reads	435,564 / 8.21%

2.2. ACGT Content

Number/percentage of A's	52,918,993 / 28.94%
Number/percentage of C's	38,516,060 / 21.06%
Number/percentage of T's	53,277,548 / 29.13%
Number/percentage of G's	38,147,429 / 20.86%
Number/percentage of N's	6,234 / 0%
GC Percentage	41.92%

2.3. Coverage

Mean	0.0591
Standard Deviation	0.7279

2.4. Mapping Quality

Mean Mapping Quality	38.32

2.5. Mismatches and indels

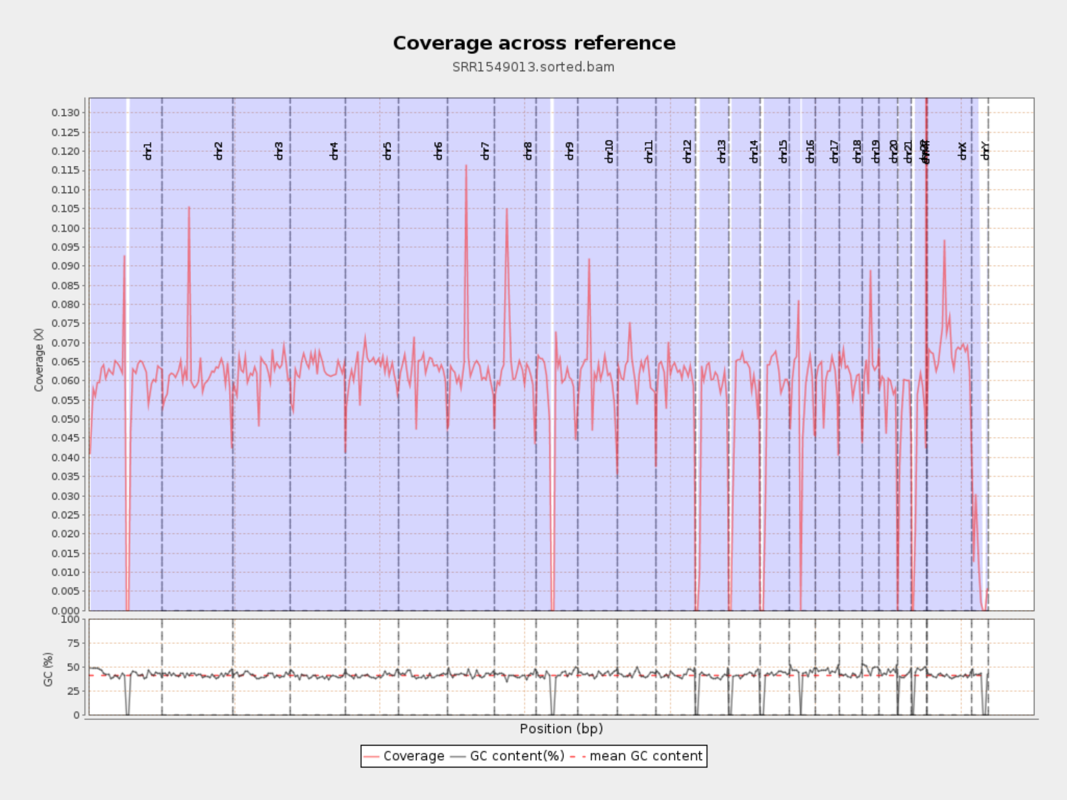
General error rate	0.32%
Mismatches	577,633
Insertions	6,776
Mapped reads with at least one insertion	0.15%
Deletions	16,158
Mapped reads with at least one deletion	0.35%
Homopolymer indels	39.5%

2.6. Chromosome stats

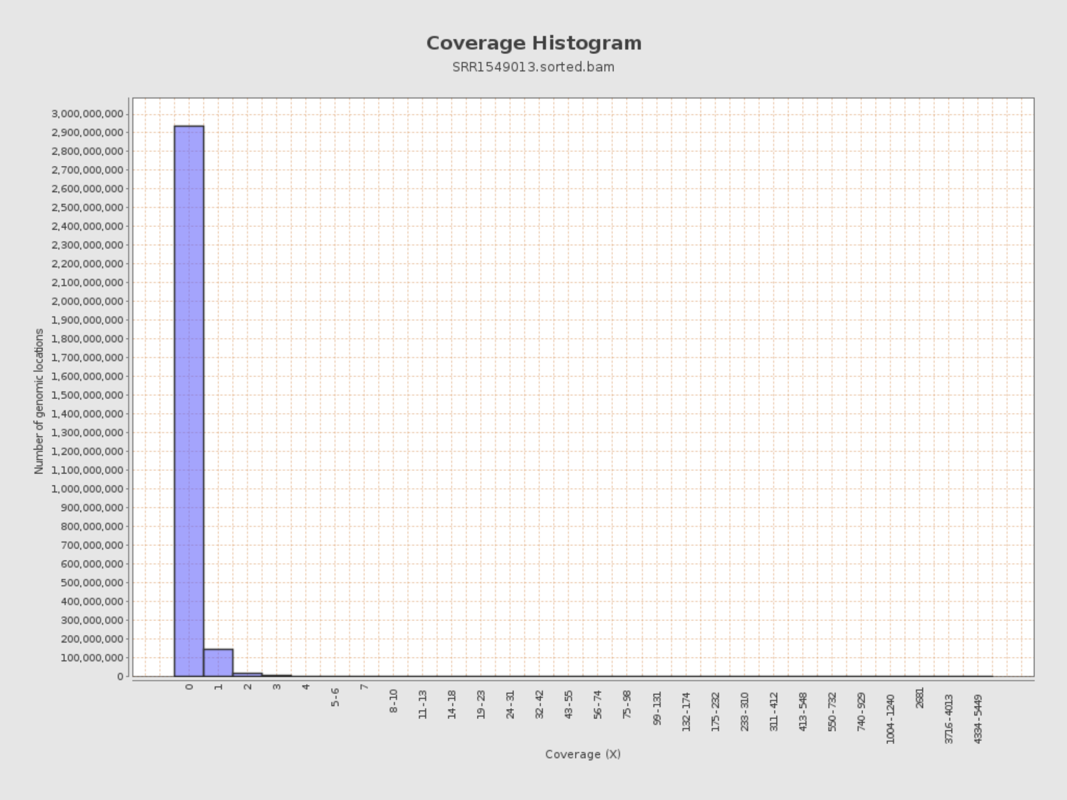
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14431217	0.0579	0.8564
chr2	243199373	15078428	0.062	0.4509
chr3	198022430	12372261	0.0625	0.2817
chr4	191154276	12025683	0.0629	0.2901
chr5	180915260	11405550	0.063	0.2895
chr6	171115067	10757970	0.0629	0.3088
chr7	159138663	10233613	0.0643	0.6242
chr8	146364022	9398377	0.0642	2.6401

chr9	141213431	7733377	0.0548	0.4407
chr10	135534747	8427873	0.0622	0.4117
chr11	135006516	8360785	0.0619	0.4535
chr12	133851895	8286387	0.0619	0.2949
chr13	115169878	5814818	0.0505	0.2472
chr14	107349540	5591170	0.0521	0.324
chr15	102531392	5231528	0.051	0.2526
chr16	90354753	5011767	0.0555	0.3017
chr17	81195210	4847539	0.0597	0.2997
chr18	78077248	4815694	0.0617	0.8189
chr19	59128983	3860149	0.0653	0.8574
chr20	63025520	3560789	0.0565	0.2816
chr21	48129895	2314862	0.0481	0.2849
chr22	51304566	2025285	0.0395	0.2731
chrMT	16571	9358	0.5647	0.9337
chrX	155270560	10655084	0.0686	0.3764
chrY	59373566	637734	0.0107	0.156

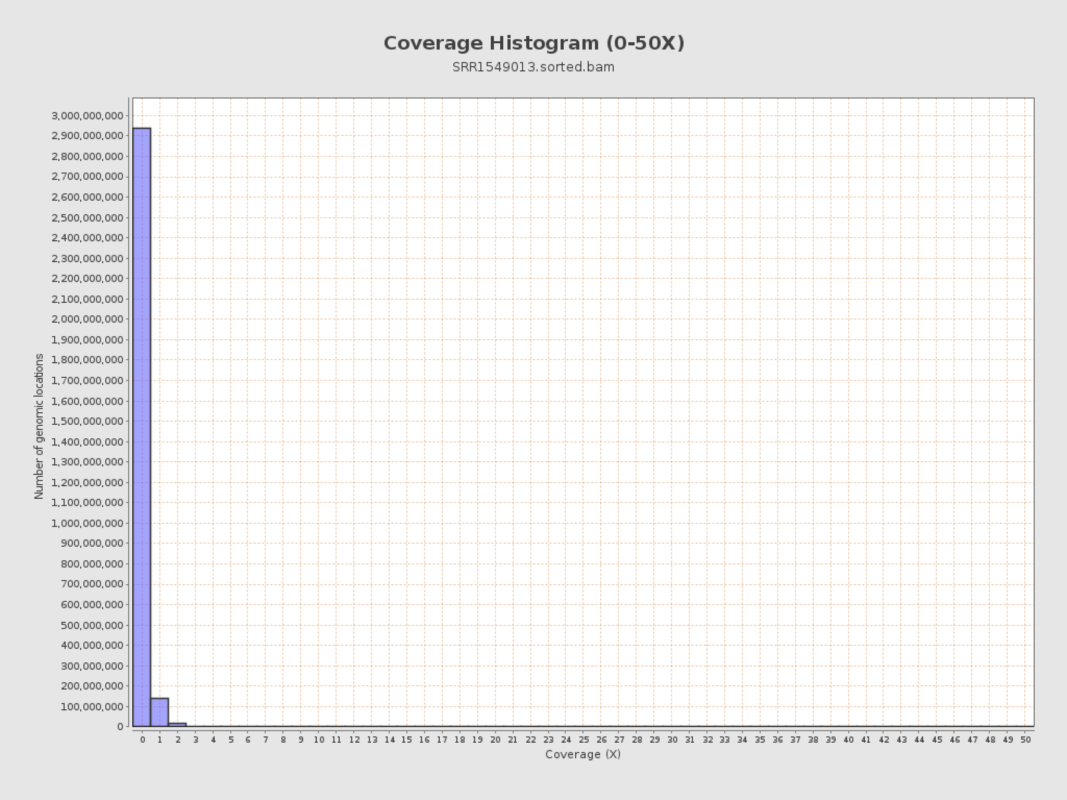
3. Results : Coverage across reference



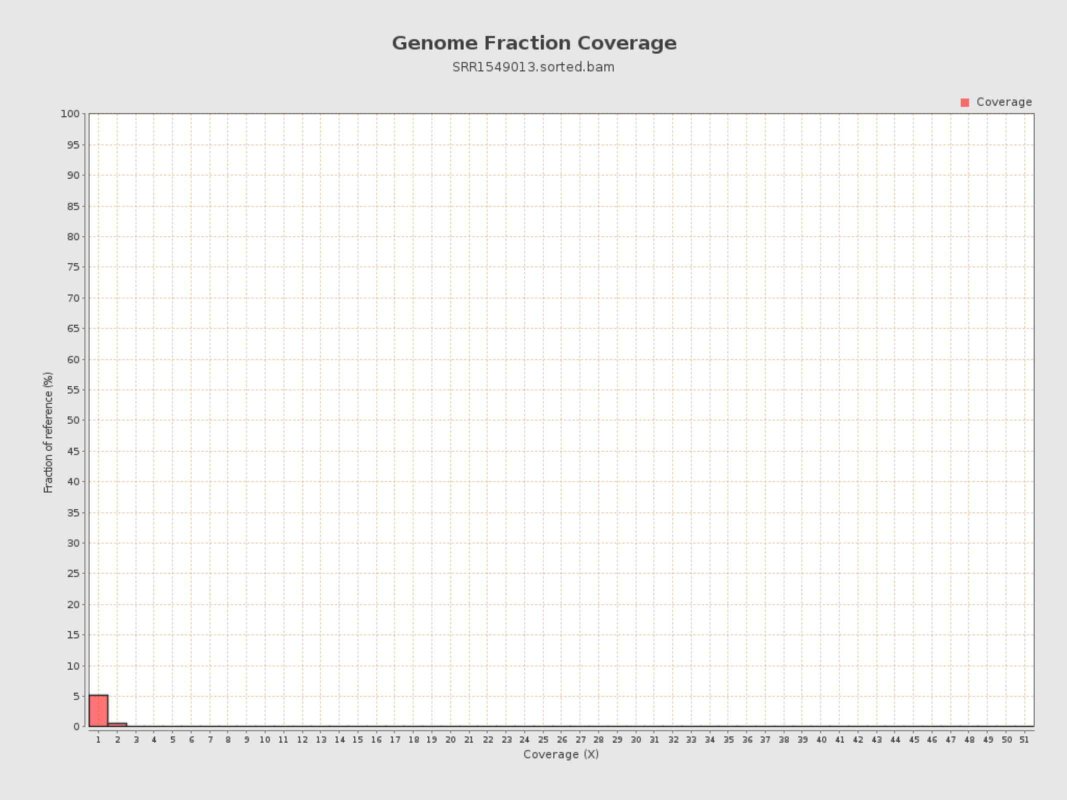
4. Results : Coverage Histogram



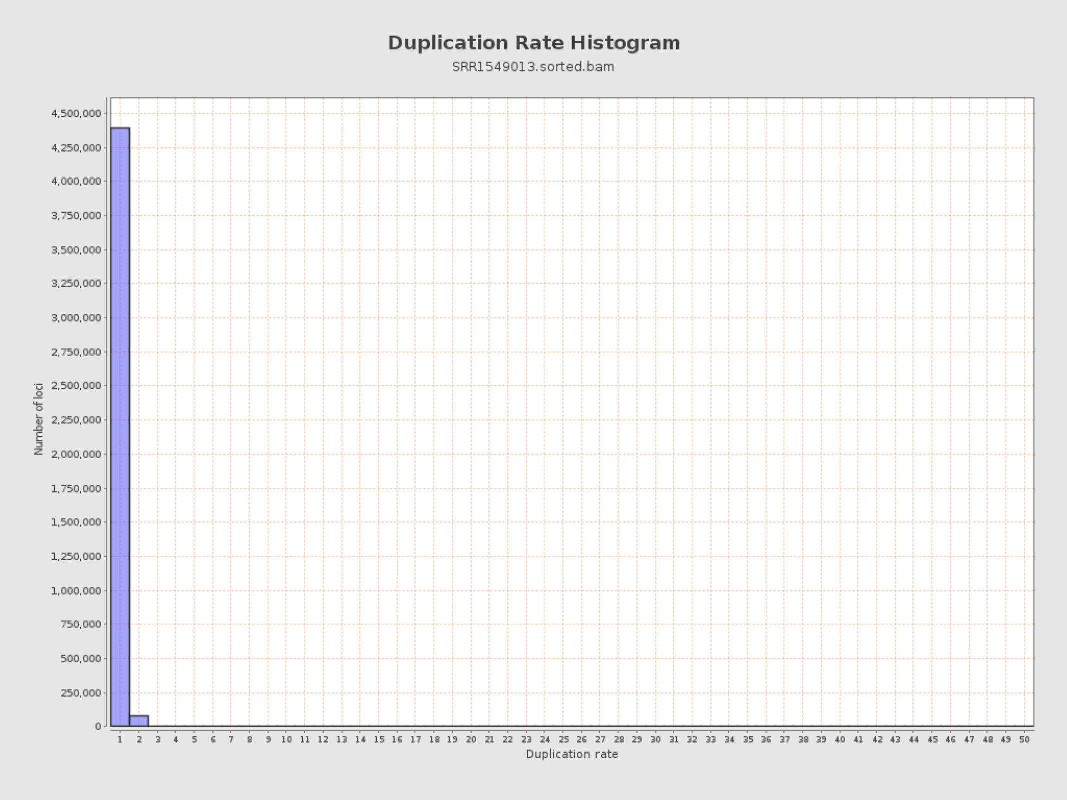
5. Results : Coverage Histogram (0-50X)



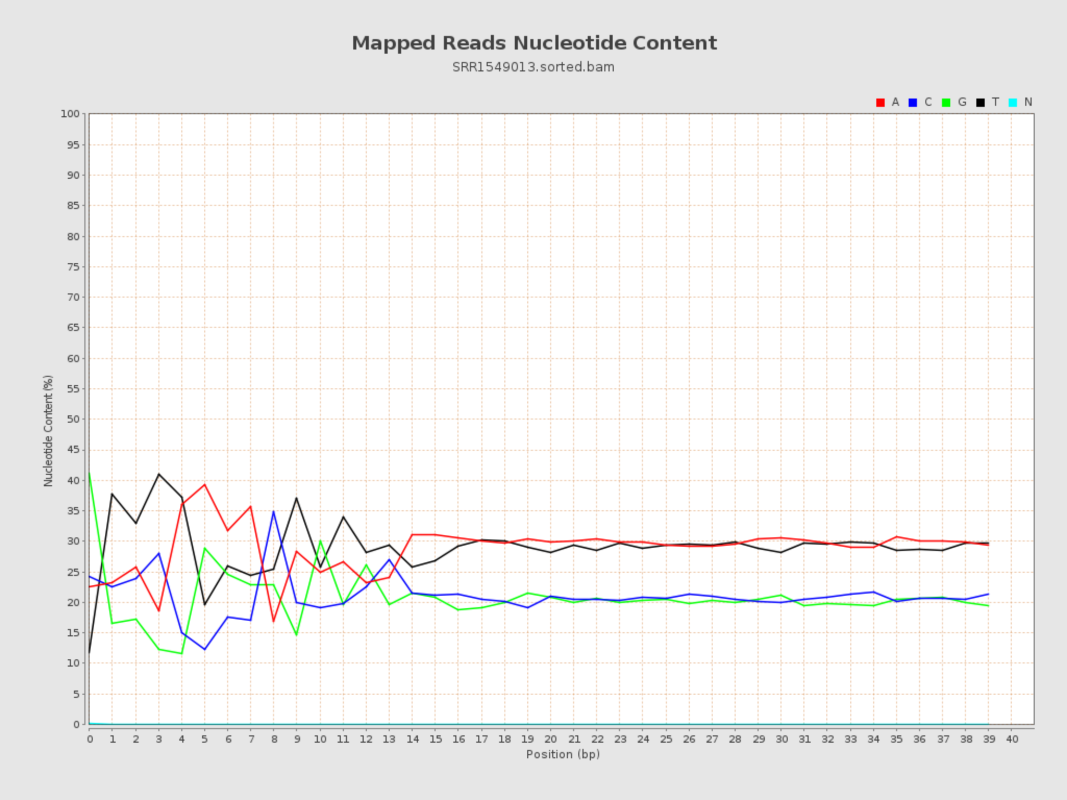
6. Results : Genome Fraction Coverage



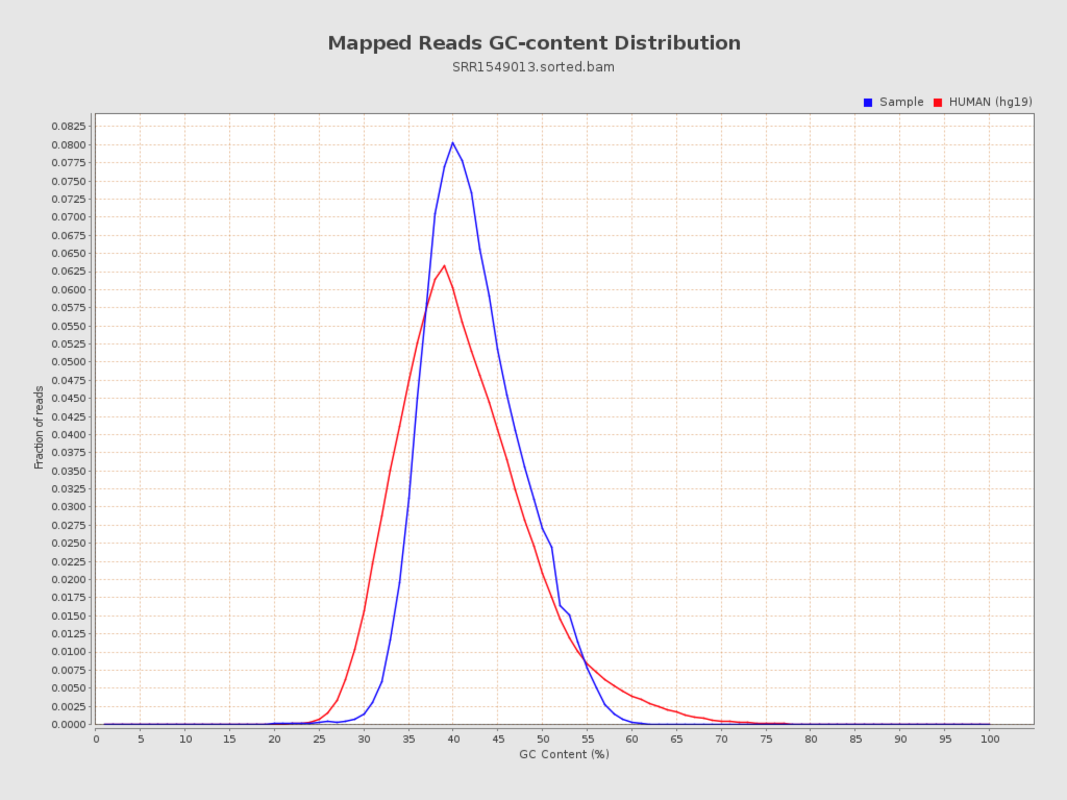
7. Results : Duplication Rate Histogram



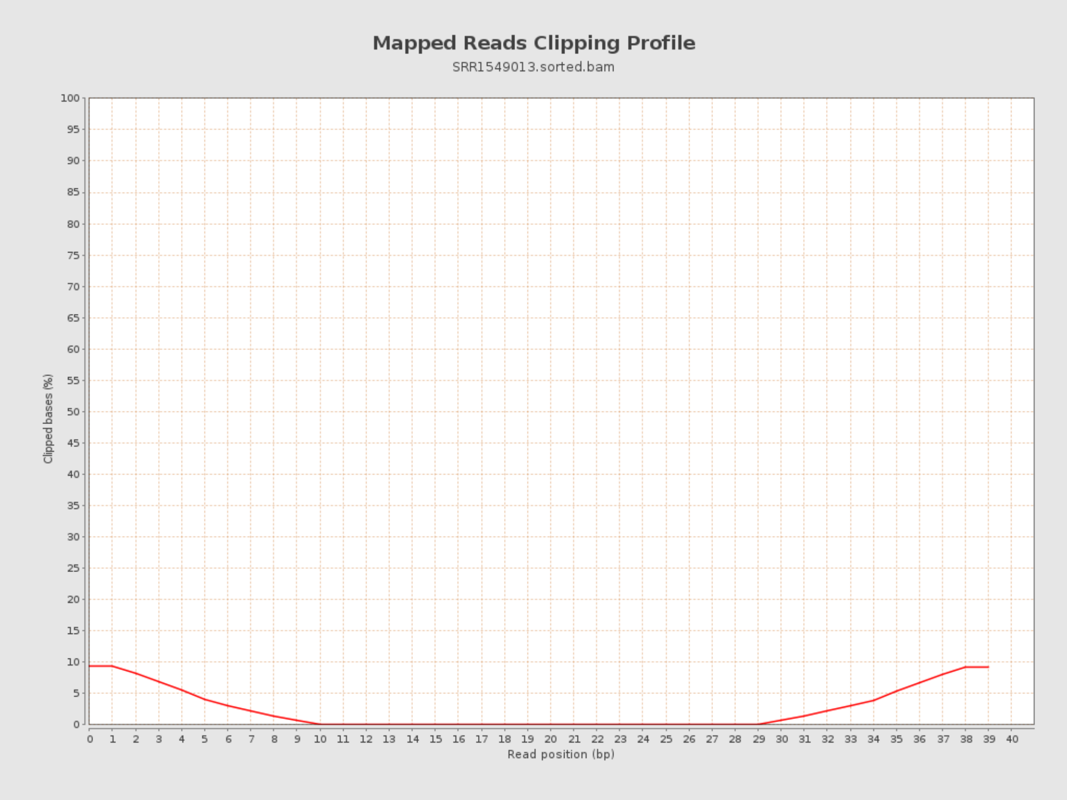
8. Results : Mapped Reads Nucleotide Content



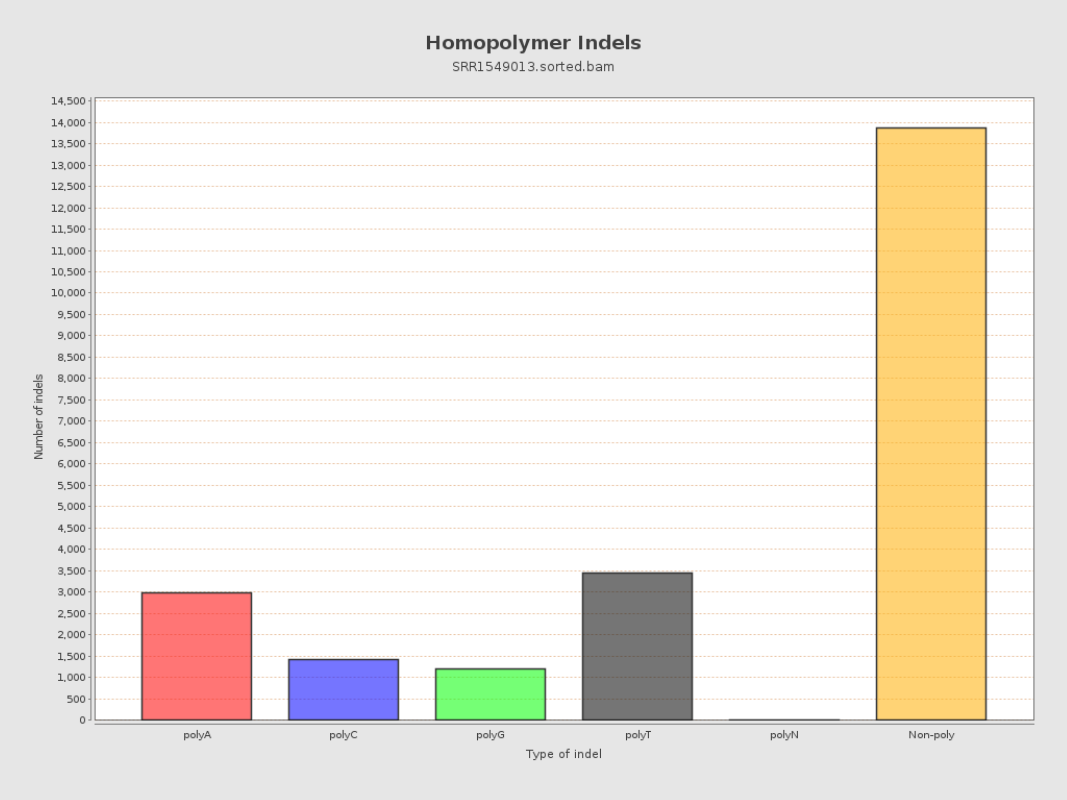
9. Results : Mapped Reads GC-content Distribution



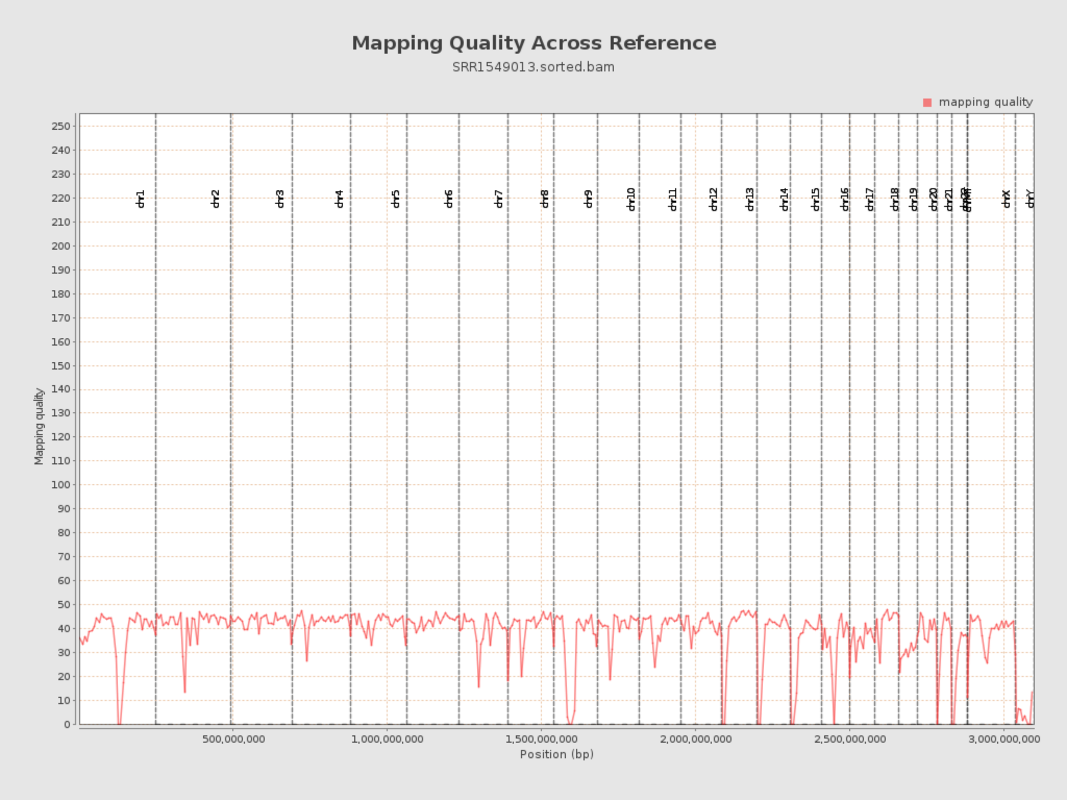
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram