Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:59:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549014.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_SRR1549014 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549014.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:59:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549014.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,017,269
Mapped reads	8,688,647 / 86.74%
Unmapped reads	1,328,622 / 13.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	449,043 / 4.48%
Duplication rate	4.15%
Clipped reads	633,828 / 6.33%

2.2. ACGT Content

Number/percentage of A's	100,941,326 / 29.35%
Number/percentage of C's	70,135,295 / 20.39%
Number/percentage of T's	102,150,177 / 29.7%
Number/percentage of G's	70,724,589 / 20.56%
Number/percentage of N's	13,336 / 0%
GC Percentage	40.95%

2.3. Coverage

Mean	0.1111
Standard Deviation	1.248

2.4. Mapping Quality

Mean Mapping Quality	43.66

2.5. Mismatches and indels

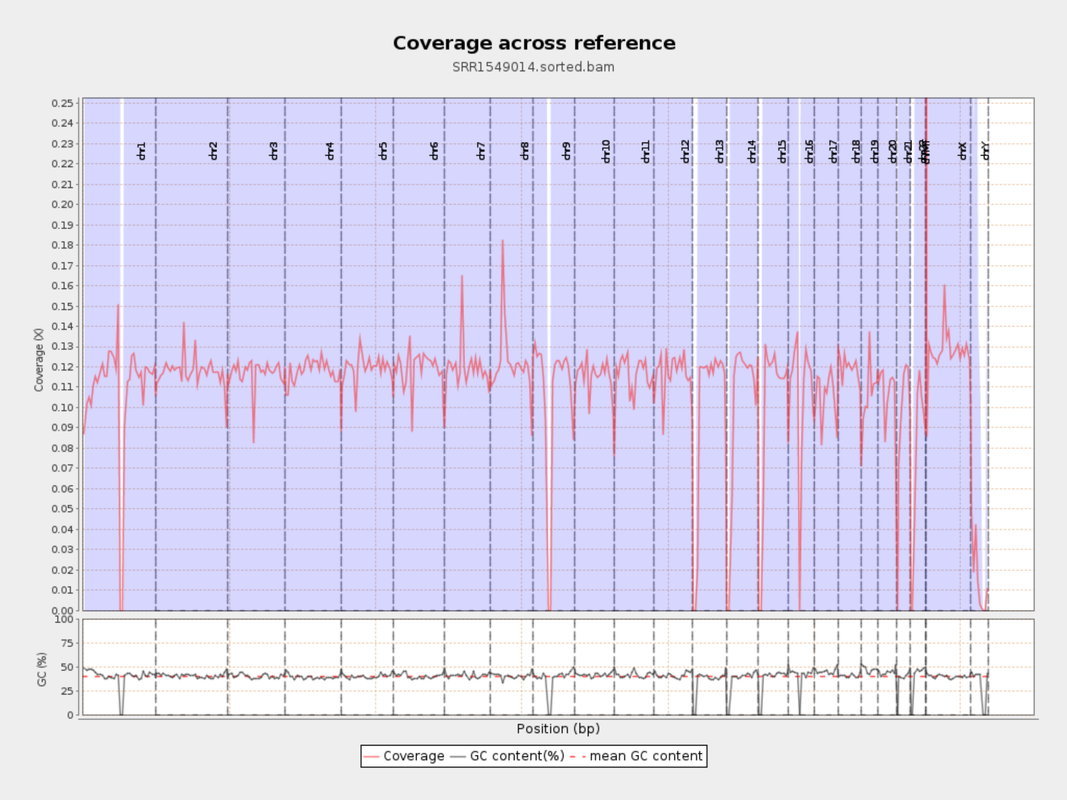
General error rate	0.25%
Mismatches	840,195
Insertions	10,399
Mapped reads with at least one insertion	0.12%
Deletions	28,460
Mapped reads with at least one deletion	0.33%
Homopolymer indels	42.75%

2.6. Chromosome stats

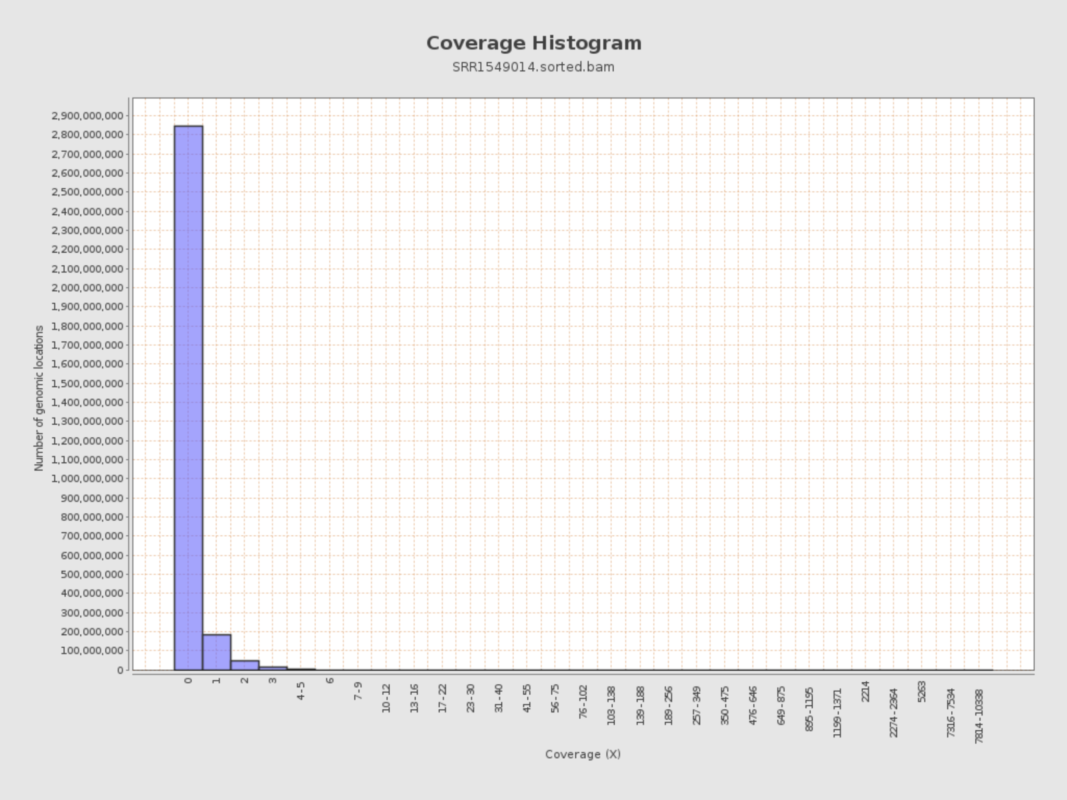
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27004118	0.1083	1.0918
chr2	243199373	28659398	0.1178	0.6043
chr3	198022430	23154371	0.1169	0.4495
chr4	191154276	22589008	0.1182	0.4666
chr5	180915260	21566473	0.1192	0.4597
chr6	171115067	20481313	0.1197	0.5067
chr7	159138663	19032653	0.1196	0.8592
chr8	146364022	17850646	0.122	5.0011

chr9	141213431	14786507	0.1047	0.5641
chr10	135534747	15730635	0.1161	0.551
chr11	135006516	15666440	0.116	0.7208
chr12	133851895	15691471	0.1172	0.4625
chr13	115169878	11477497	0.0997	0.4124
chr14	107349540	10716591	0.0998	0.4712
chr15	102531392	10038364	0.0979	0.4071
chr16	90354753	9397722	0.104	0.4523
chr17	81195210	8618153	0.1061	0.4684
chr18	78077248	9353552	0.1198	0.9865
chr19	59128983	6350212	0.1074	0.938
chr20	63025520	6786391	0.1077	0.4417
chr21	48129895	4522678	0.094	0.4448
chr22	51304566	3785461	0.0738	0.4237
chrMT	16571	19040	1.149	1.6238
chrX	155270560	19782979	0.1274	0.5646
chrY	59373566	940800	0.0158	0.2239

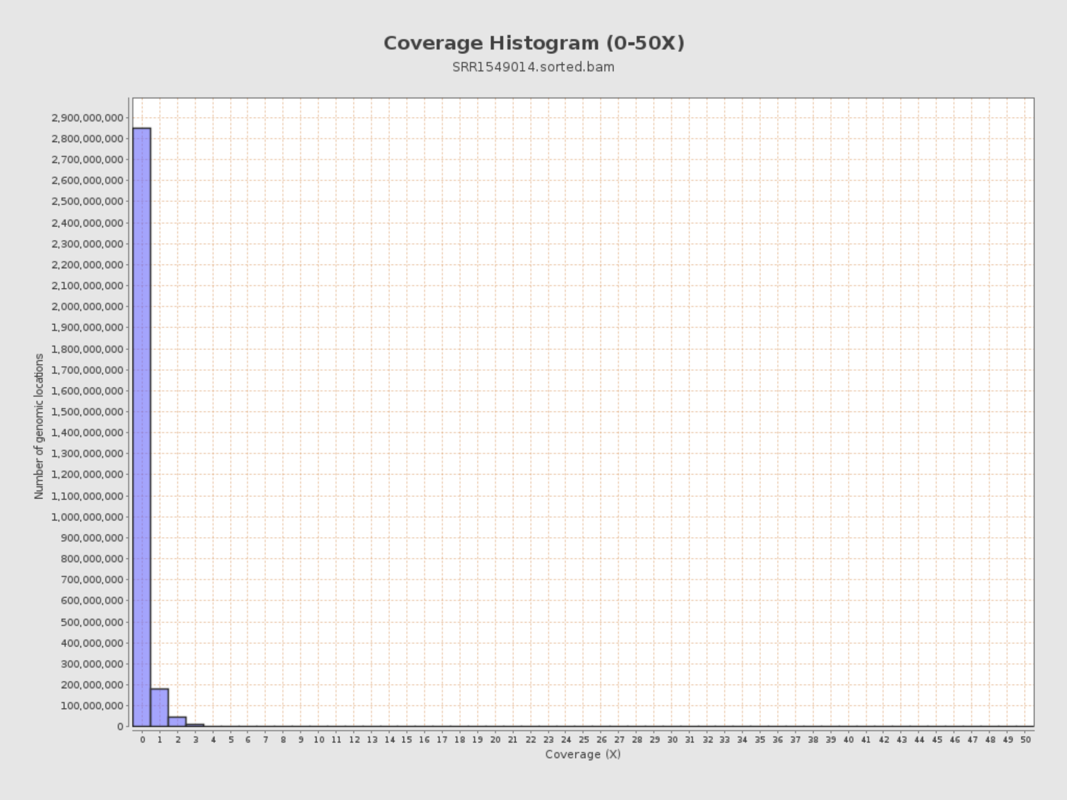
3. Results : Coverage across reference



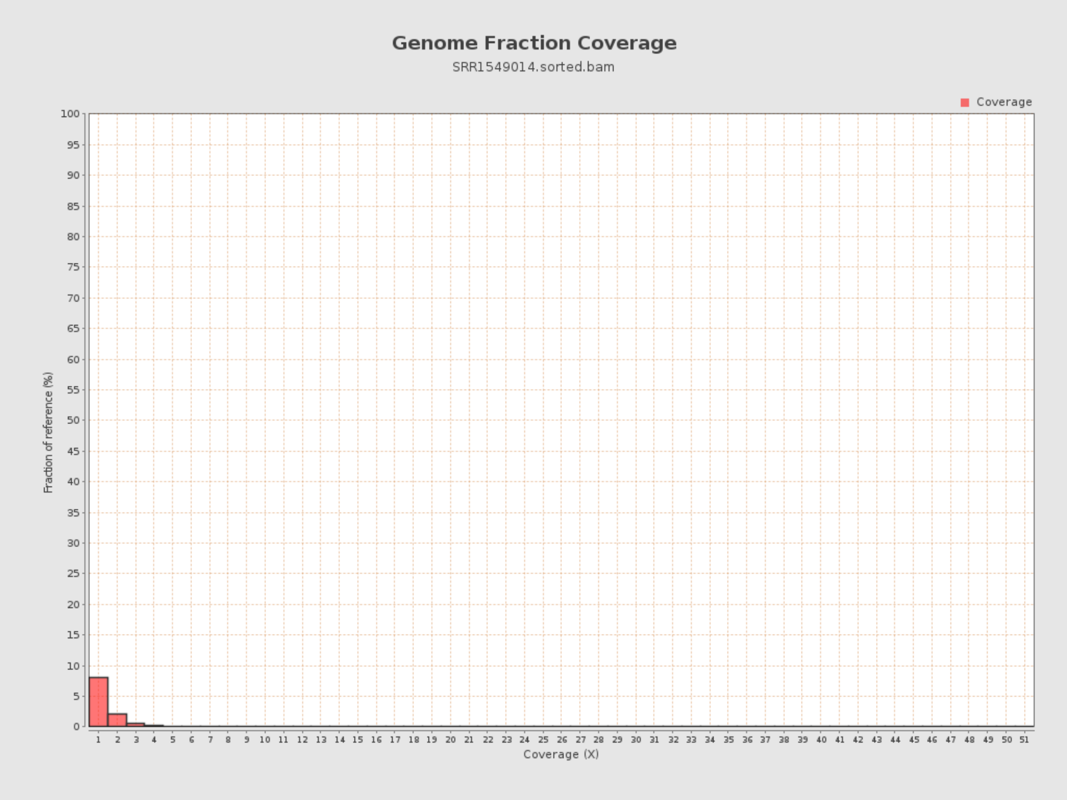
4. Results : Coverage Histogram



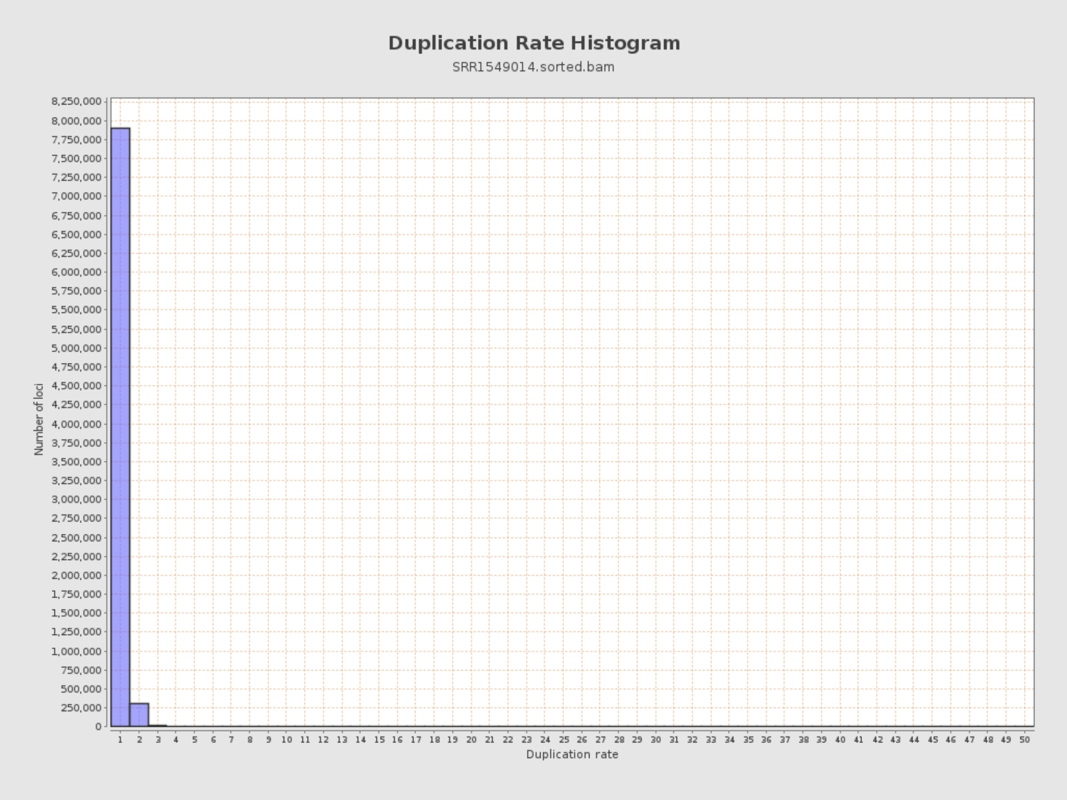
5. Results : Coverage Histogram (0-50X)



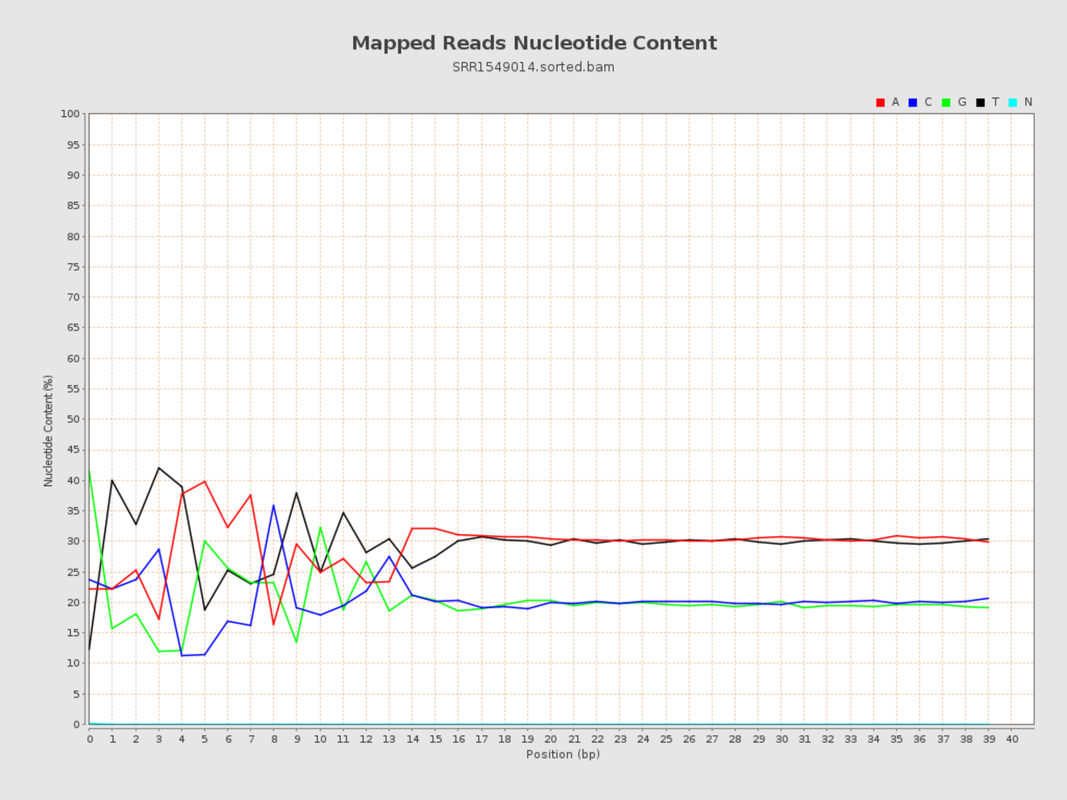
6. Results : Genome Fraction Coverage



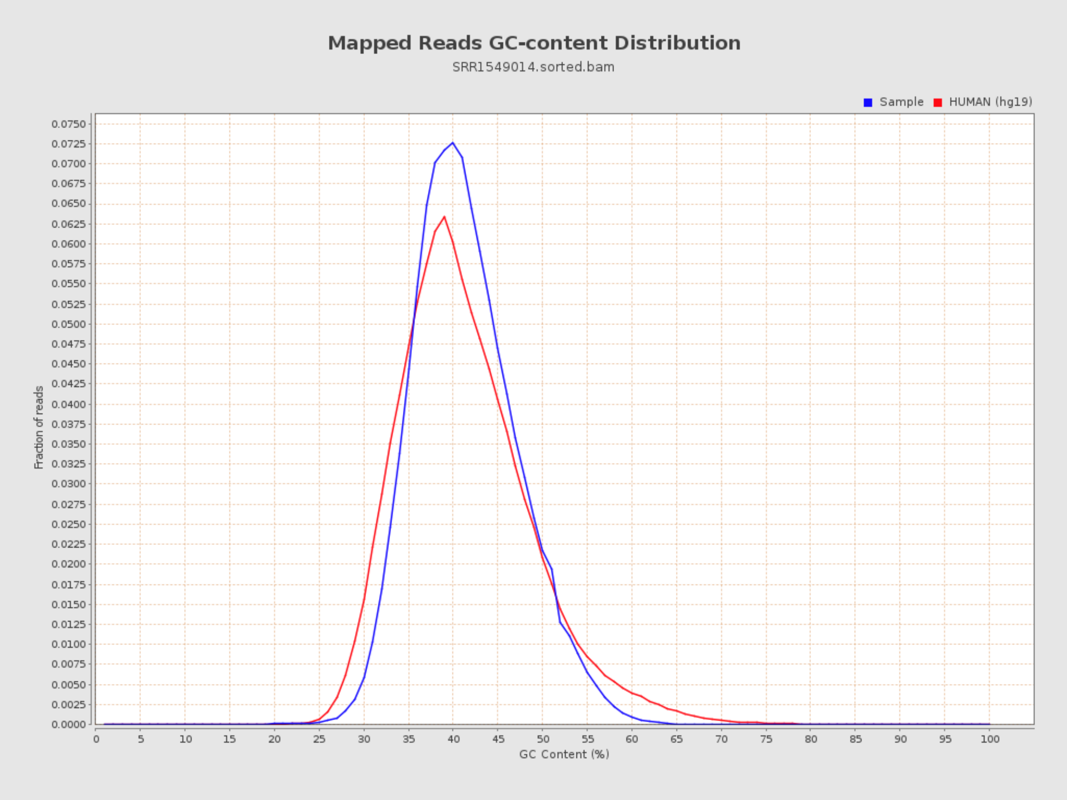
7. Results : Duplication Rate Histogram



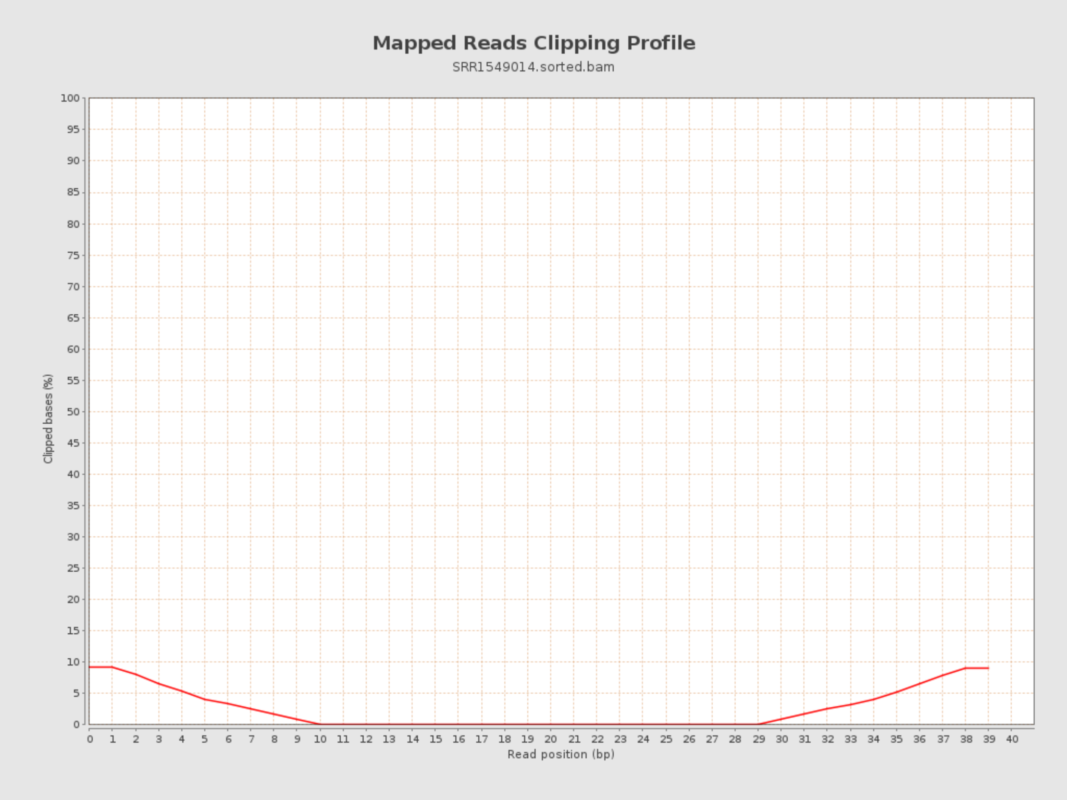
8. Results : Mapped Reads Nucleotide Content



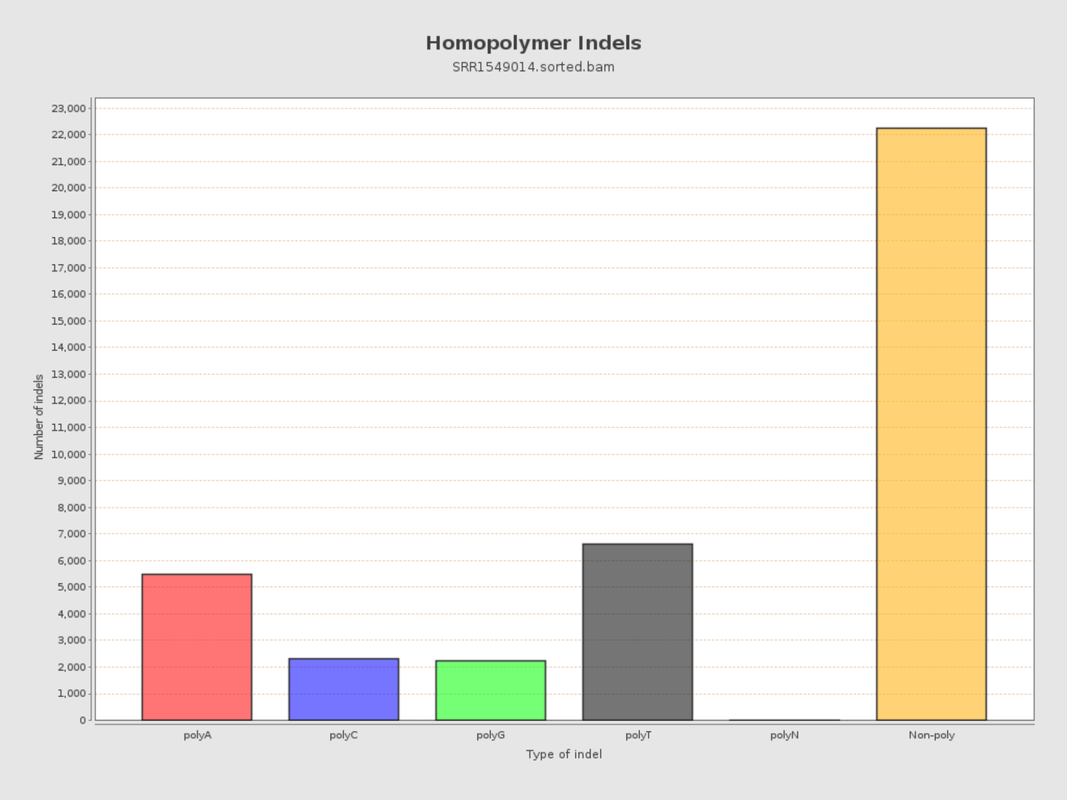
9. Results : Mapped Reads GC-content Distribution



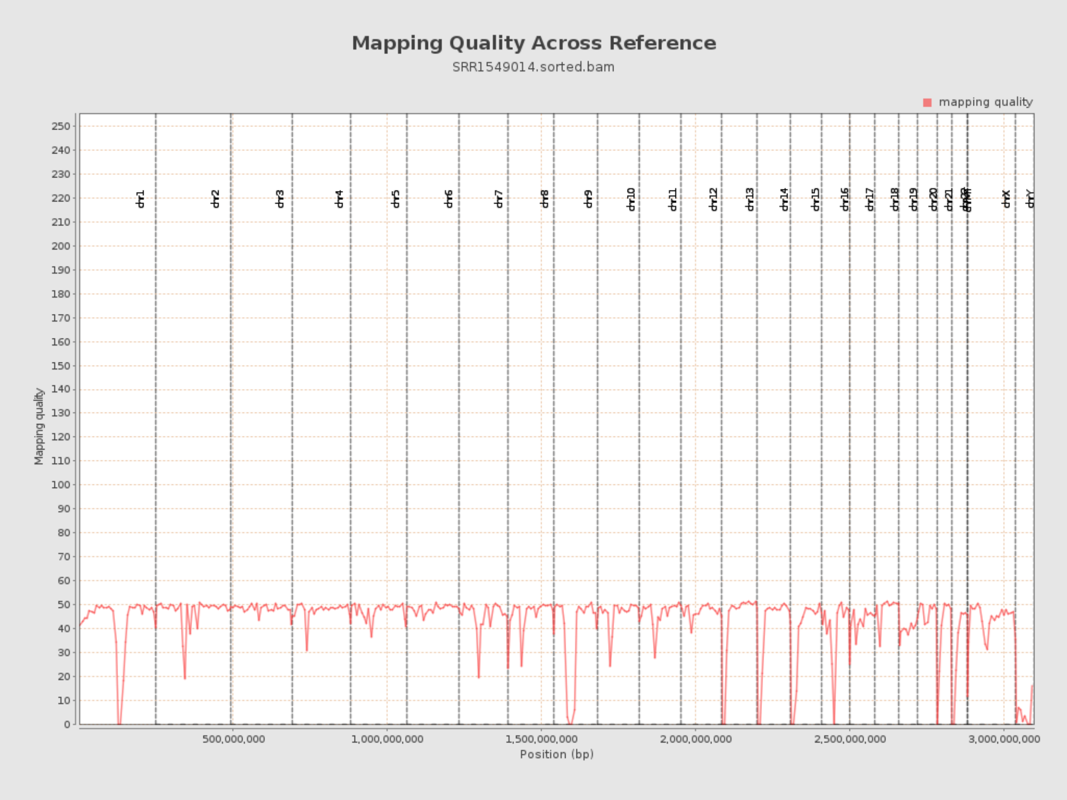
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram