Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 07:55:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549138.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_SRR1549138 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549138.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 07:55:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549138.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,062,297
Mapped reads	11,191,859 / 85.68%
Unmapped reads	1,870,438 / 14.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	819,656 / 6.27%
Duplication rate	5.95%
Clipped reads	647,425 / 4.96%

2.2. ACGT Content

Number/percentage of A's	129,008,332 / 29.07%
Number/percentage of C's	91,599,327 / 20.64%
Number/percentage of T's	130,839,574 / 29.49%
Number/percentage of G's	92,200,528 / 20.78%
Number/percentage of N's	98,229 / 0.02%
GC Percentage	41.42%

2.3. Coverage

Mean	0.1434
Standard Deviation	1.0579

2.4. Mapping Quality

Mean Mapping Quality	42.73

2.5. Mismatches and indels

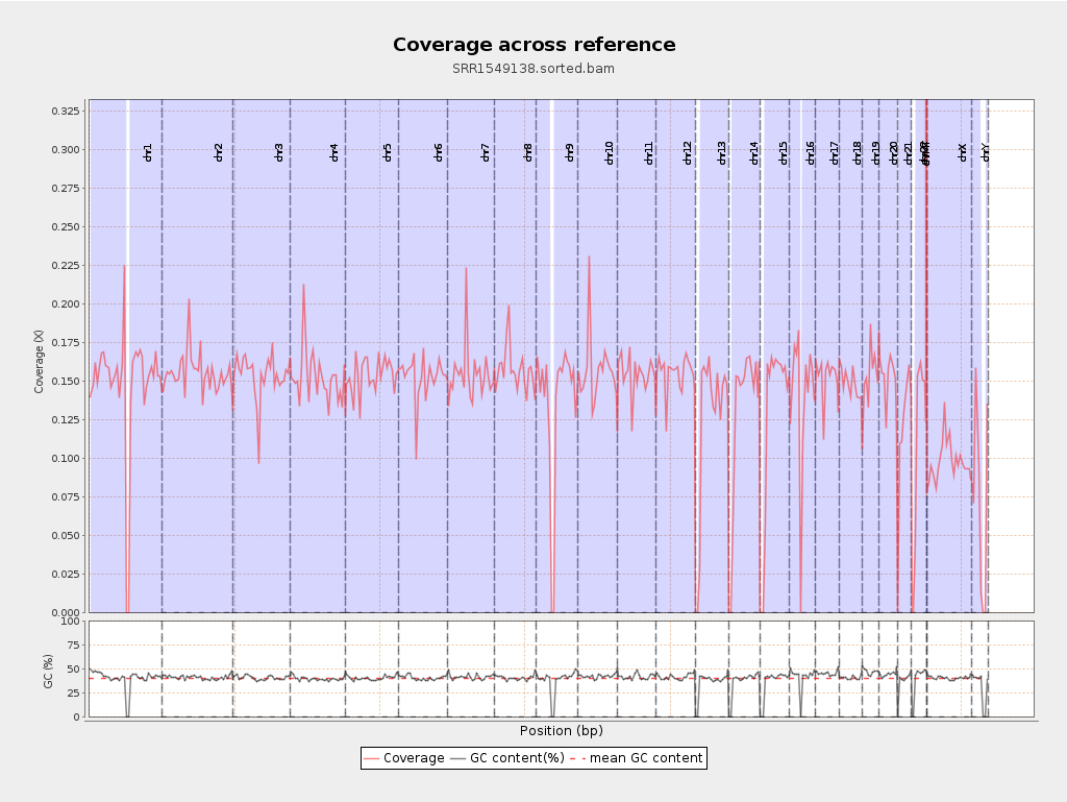
General error rate	0.33%
Mismatches	1,436,754
Insertions	11,657
Mapped reads with at least one insertion	0.1%
Deletions	33,485
Mapped reads with at least one deletion	0.3%
Homopolymer indels	44.53%

2.6. Chromosome stats

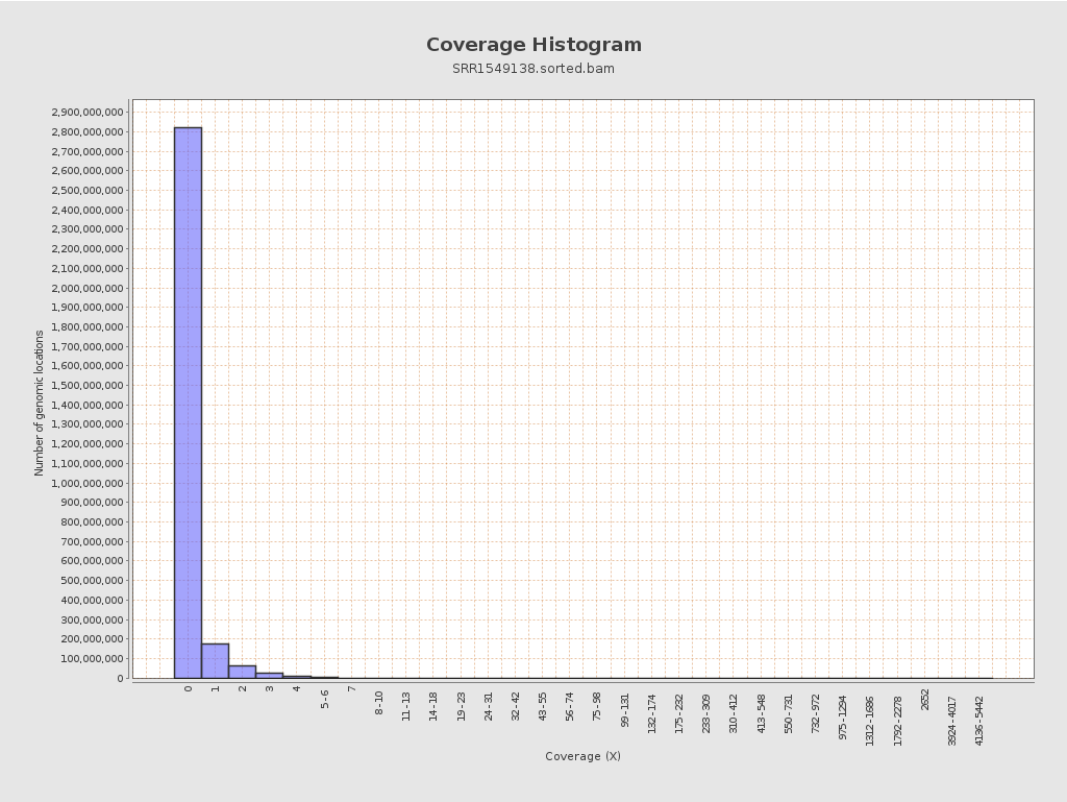
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	36867781	0.1479	1.7476
chr2	243199373	37807827	0.1555	0.8403
chr3	198022430	30298529	0.153	0.5771
chr4	191154276	29002802	0.1517	0.6851
chr5	180915260	27727035	0.1533	0.5901
chr6	171115067	26156691	0.1529	0.6251
chr7	159138663	24580163	0.1545	1.1881
chr8	146364022	22935053	0.1567	2.734

chr9	141213431	18905393	0.1339	0.7422
chr10	135534747	21198164	0.1564	0.9523
chr11	135006516	20752912	0.1537	0.7342
chr12	133851895	20786303	0.1553	0.6059
chr13	115169878	14182570	0.1231	0.5145
chr14	107349540	13674782	0.1274	0.6946
chr15	102531392	13144658	0.1282	0.522
chr16	90354753	12638801	0.1399	0.6094
chr17	81195210	12303551	0.1515	0.6143
chr18	78077248	11623894	0.1489	1.485
chr19	59128983	9139447	0.1546	1.3987
chr20	63025520	9519929	0.151	0.6358
chr21	48129895	5790349	0.1203	0.6546
chr22	51304566	5356641	0.1044	0.4904
chrMT	16571	137366	8.2895	9.5196
chrX	155270560	15175486	0.0977	0.5555
chrY	59373566	4082090	0.0688	0.7379

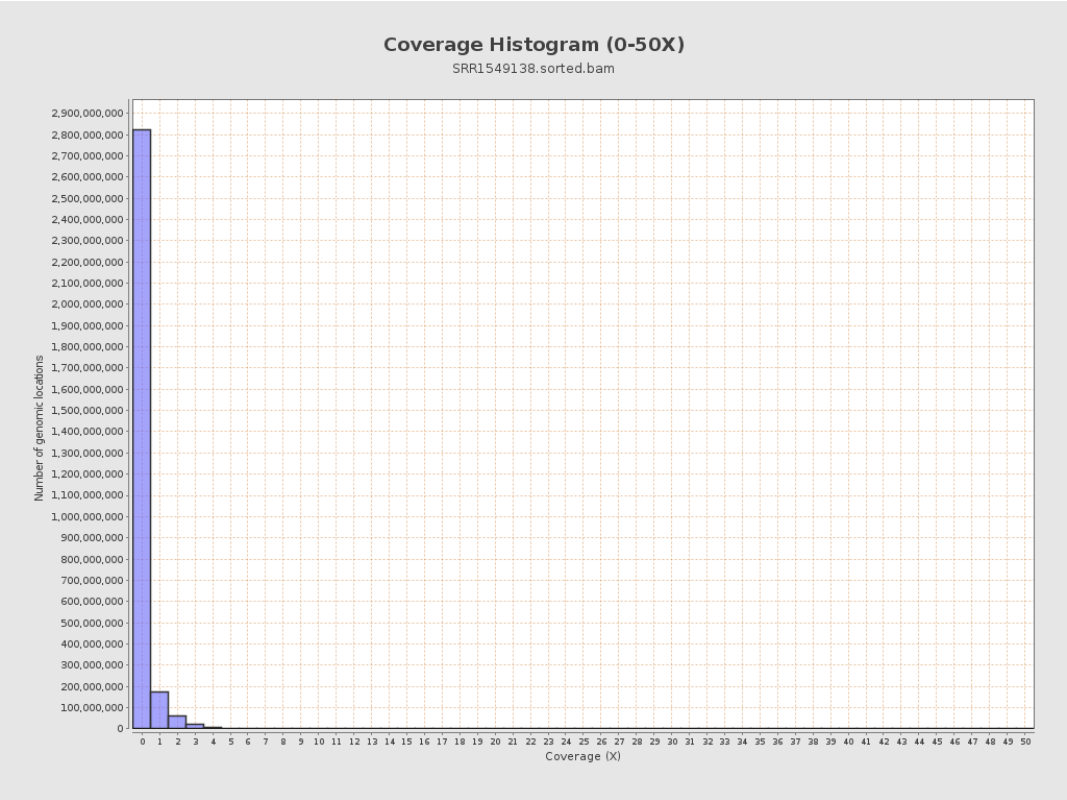
3. Results : Coverage across reference



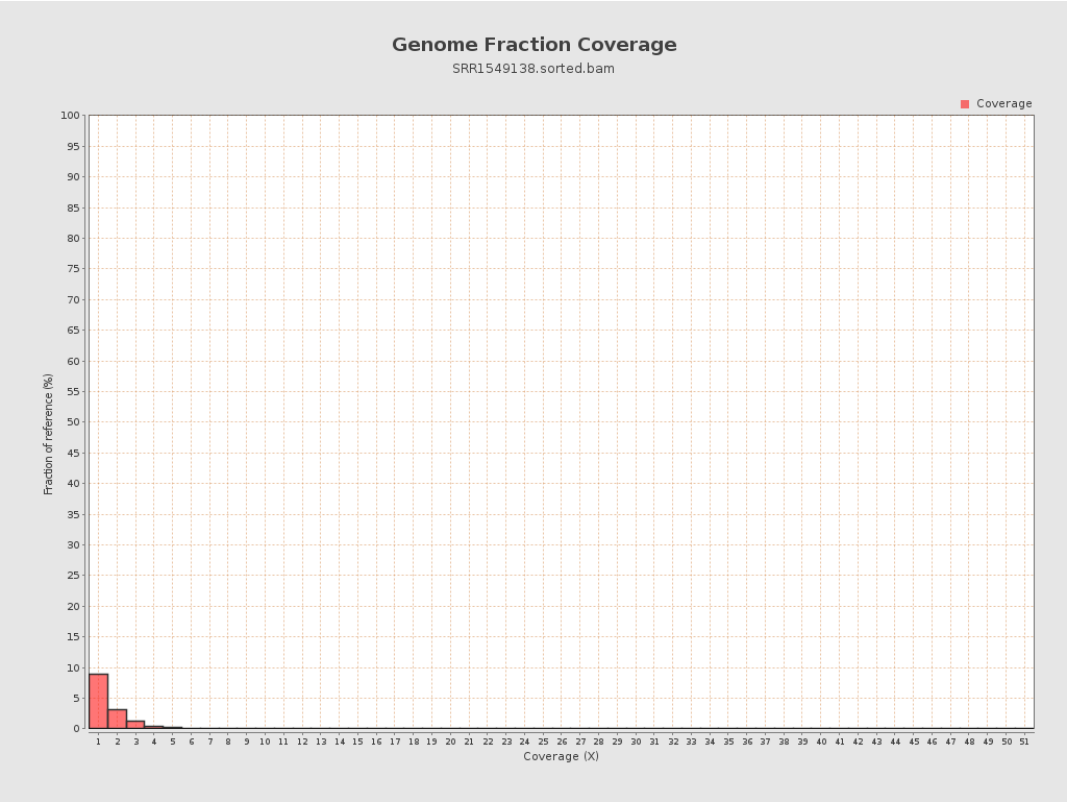
4. Results : Coverage Histogram



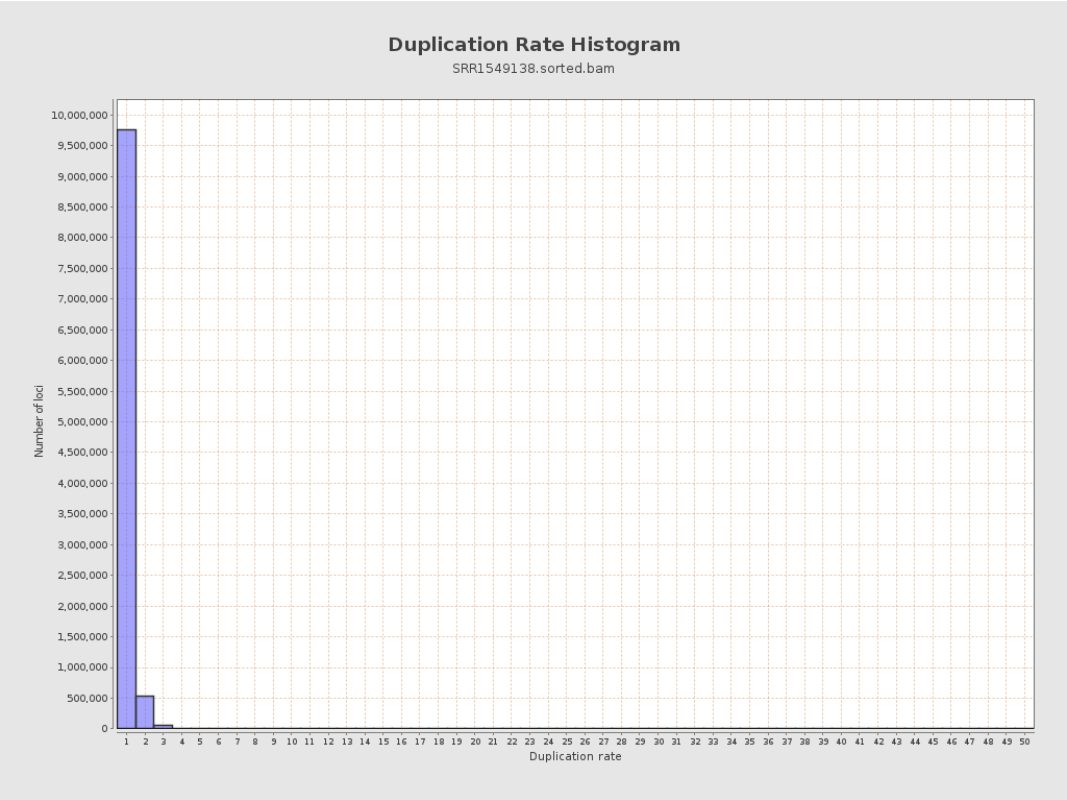
5. Results : Coverage Histogram (0-50X)



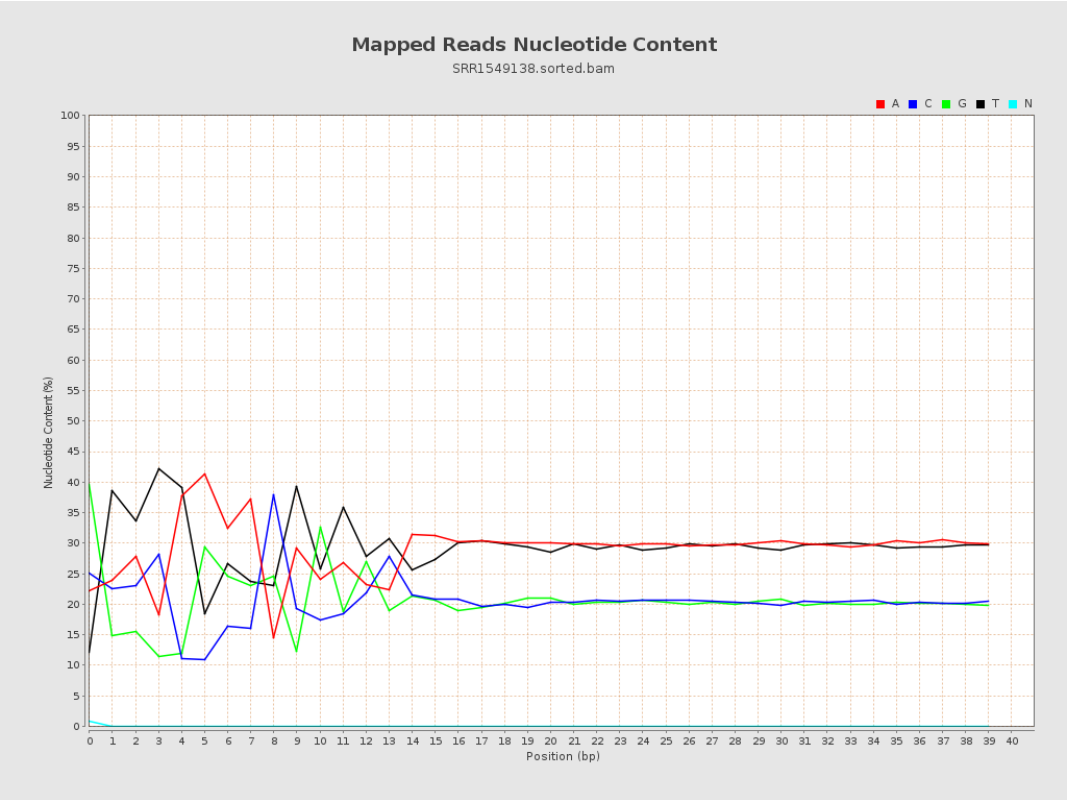
6. Results : Genome Fraction Coverage



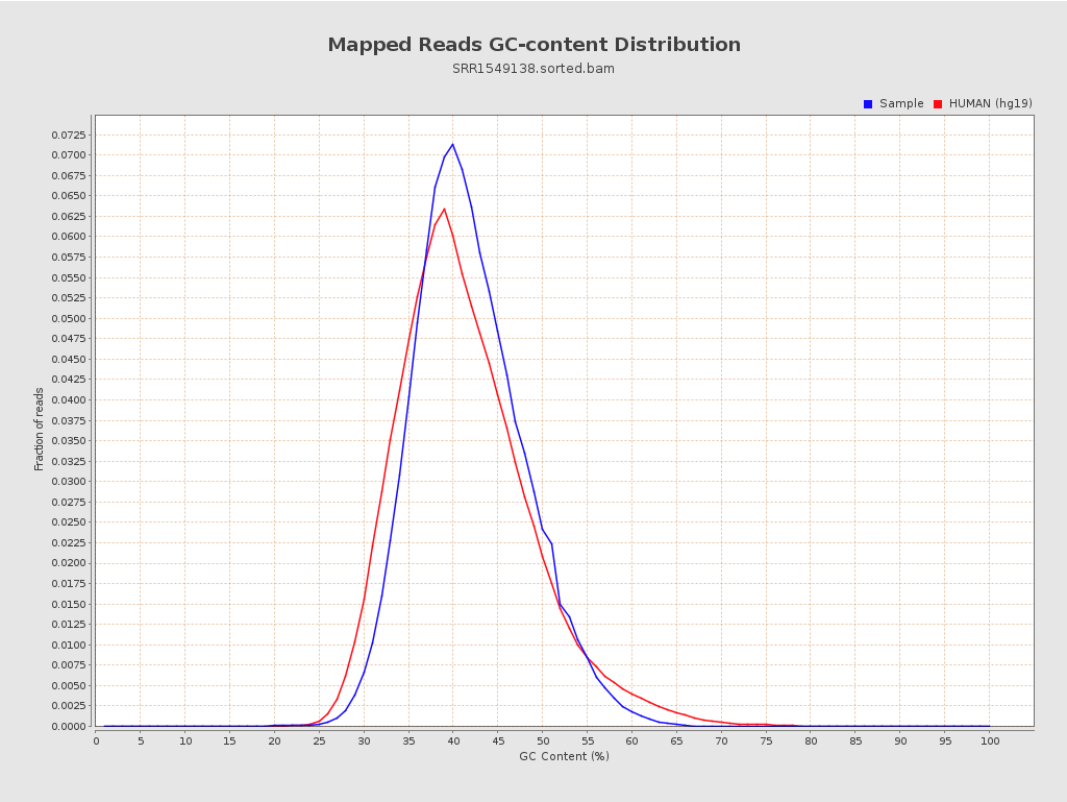
7. Results : Duplication Rate Histogram



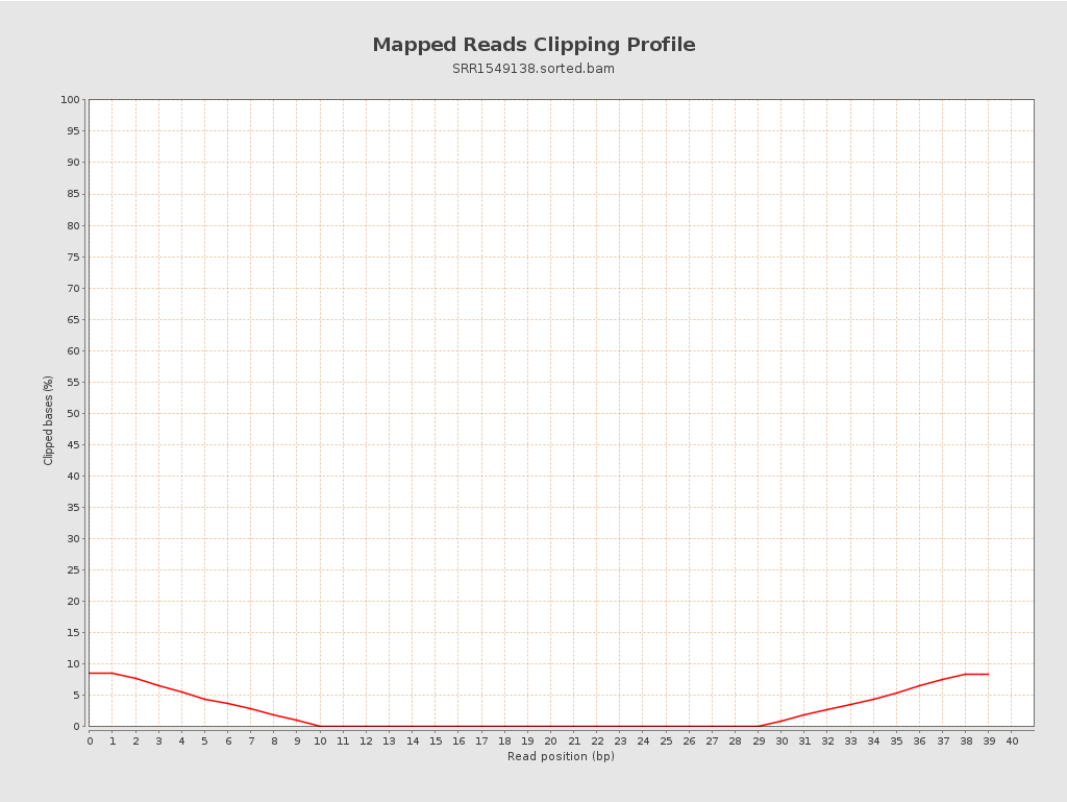
8. Results : Mapped Reads Nucleotide Content



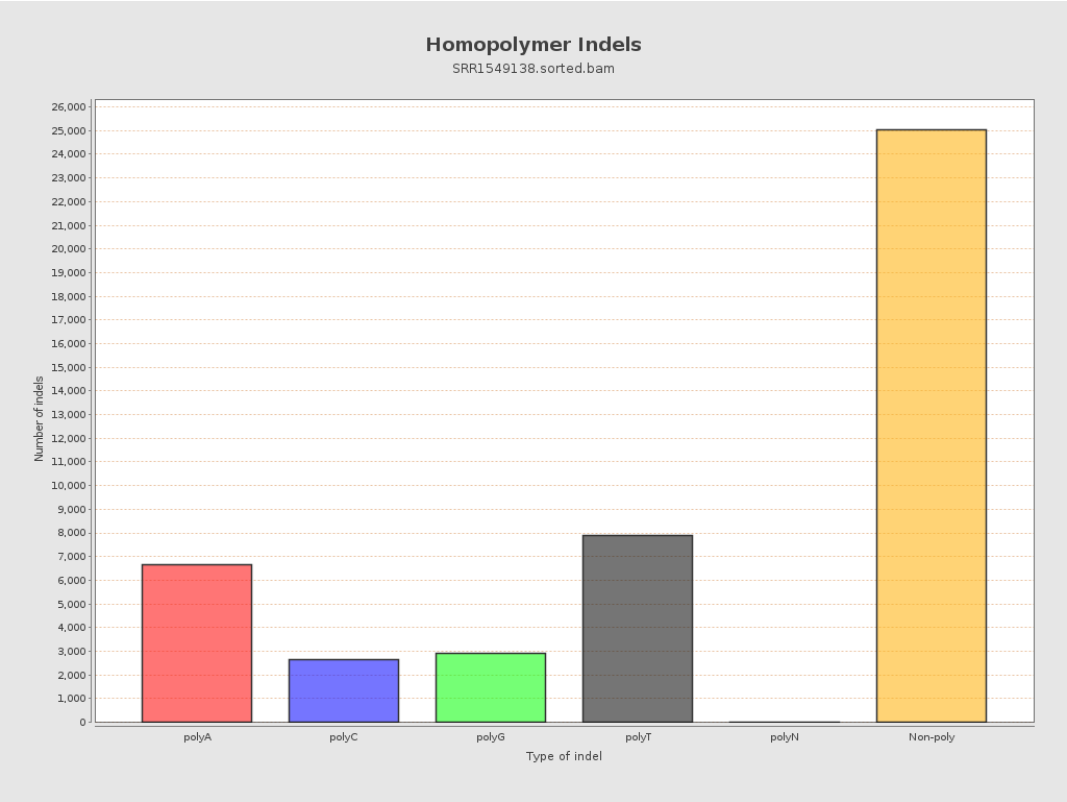
9. Results : Mapped Reads GC-content Distribution



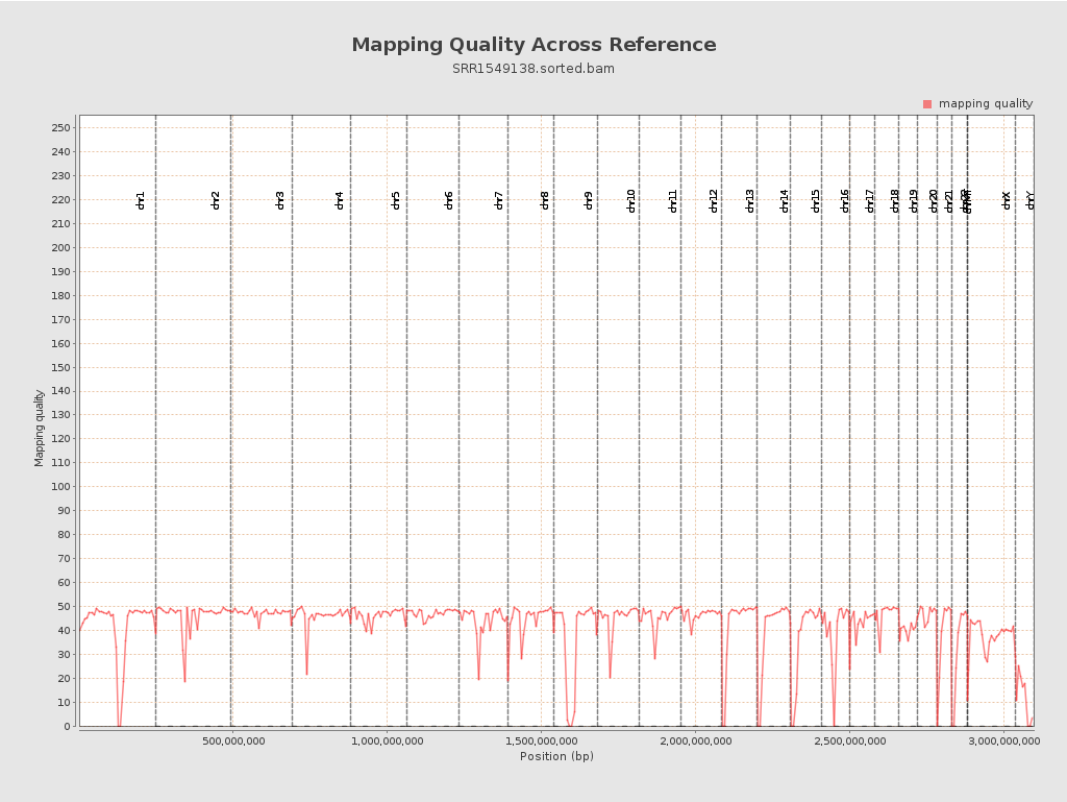
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram