Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:15:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549063.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_SRR1549063 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549063.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:15:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549063.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,826,109
Mapped reads	8,464,213 / 86.14%
Unmapped reads	1,361,896 / 13.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	468,165 / 4.76%
Duplication rate	4.14%
Clipped reads	339,282 / 3.45%

2.2. ACGT Content

Number/percentage of A's	96,763,245 / 28.75%
Number/percentage of C's	71,383,203 / 21.21%
Number/percentage of T's	97,088,952 / 28.85%
Number/percentage of G's	71,281,338 / 21.18%
Number/percentage of N's	6,210 / 0%
GC Percentage	42.39%

2.3. Coverage

Mean	0.1087
Standard Deviation	1.1746

2.4. Mapping Quality

Mean Mapping Quality	44.58

2.5. Mismatches and indels

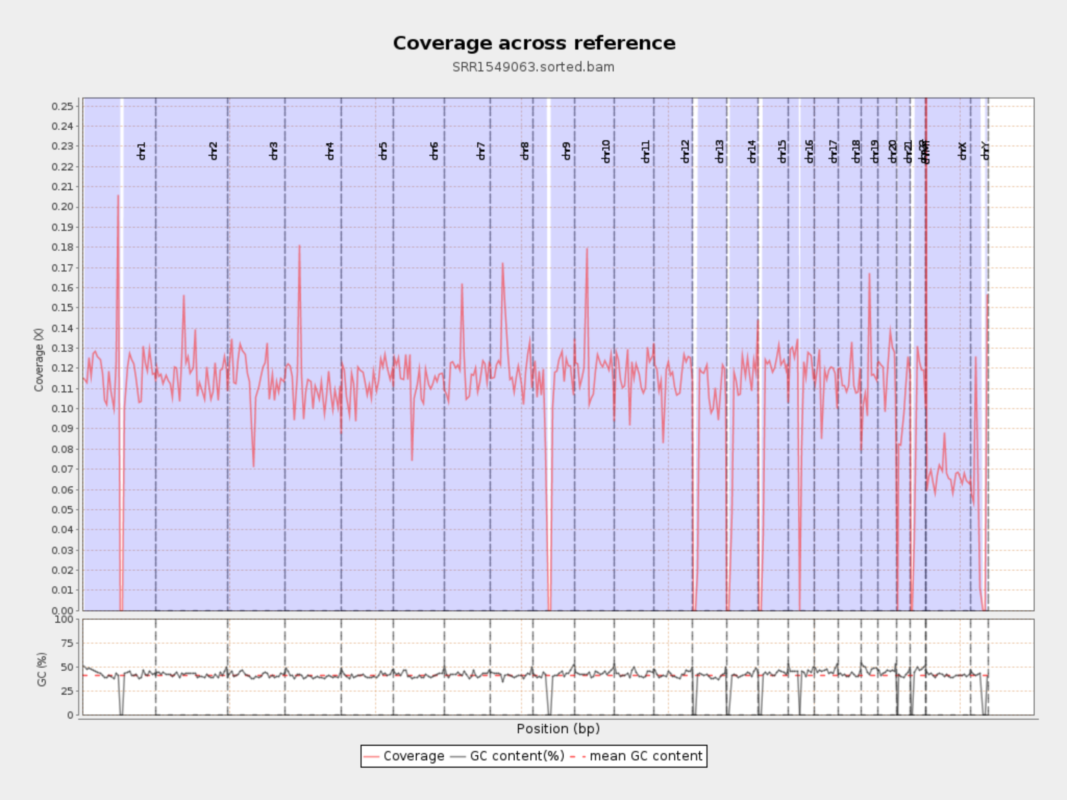
General error rate	0.31%
Mismatches	1,019,502
Insertions	7,694
Mapped reads with at least one insertion	0.09%
Deletions	25,696
Mapped reads with at least one deletion	0.3%
Homopolymer indels	44.56%

2.6. Chromosome stats

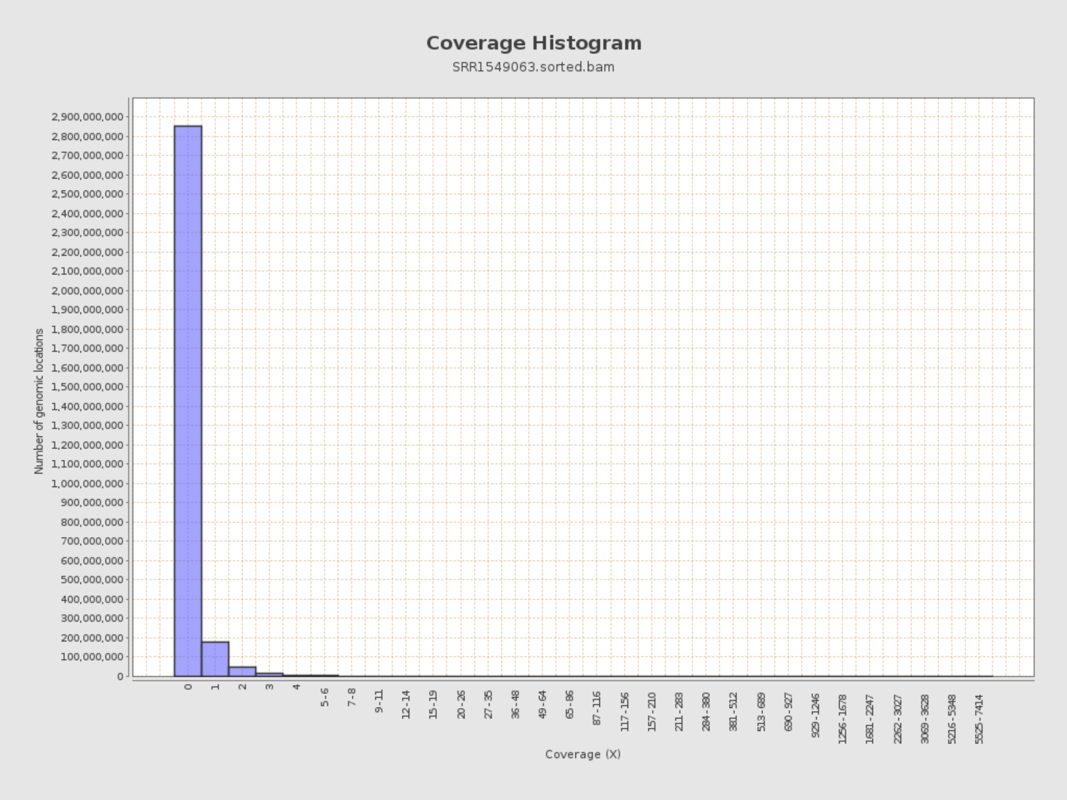
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28124651	0.1128	2.2639
chr2	243199373	28541389	0.1174	0.6652
chr3	198022430	22714464	0.1147	0.4443
chr4	191154276	21468416	0.1123	0.5409
chr5	180915260	20686529	0.1143	0.4555
chr6	171115067	19469598	0.1138	0.4774
chr7	159138663	18838211	0.1184	0.8739
chr8	146364022	17942828	0.1226	3.6368

chr9	141213431	14439471	0.1023	0.586
chr10	135534747	16427433	0.1212	0.7883
chr11	135006516	15800233	0.117	0.6256
chr12	133851895	15502644	0.1158	0.4598
chr13	115169878	10696181	0.0929	0.3907
chr14	107349540	10433414	0.0972	0.4561
chr15	102531392	10171897	0.0992	0.4058
chr16	90354753	9915460	0.1097	0.4983
chr17	81195210	9343142	0.1151	0.4845
chr18	78077248	8924311	0.1143	1.1712
chr19	59128983	6841716	0.1157	1.5187
chr20	63025520	7645806	0.1213	0.4887
chr21	48129895	4446009	0.0924	0.5138
chr22	51304566	4287480	0.0836	0.4027
chrMT	16571	10871	0.656	1.1996
chrX	155270560	10338954	0.0666	0.4246
chrY	59373566	3544453	0.0597	0.7868

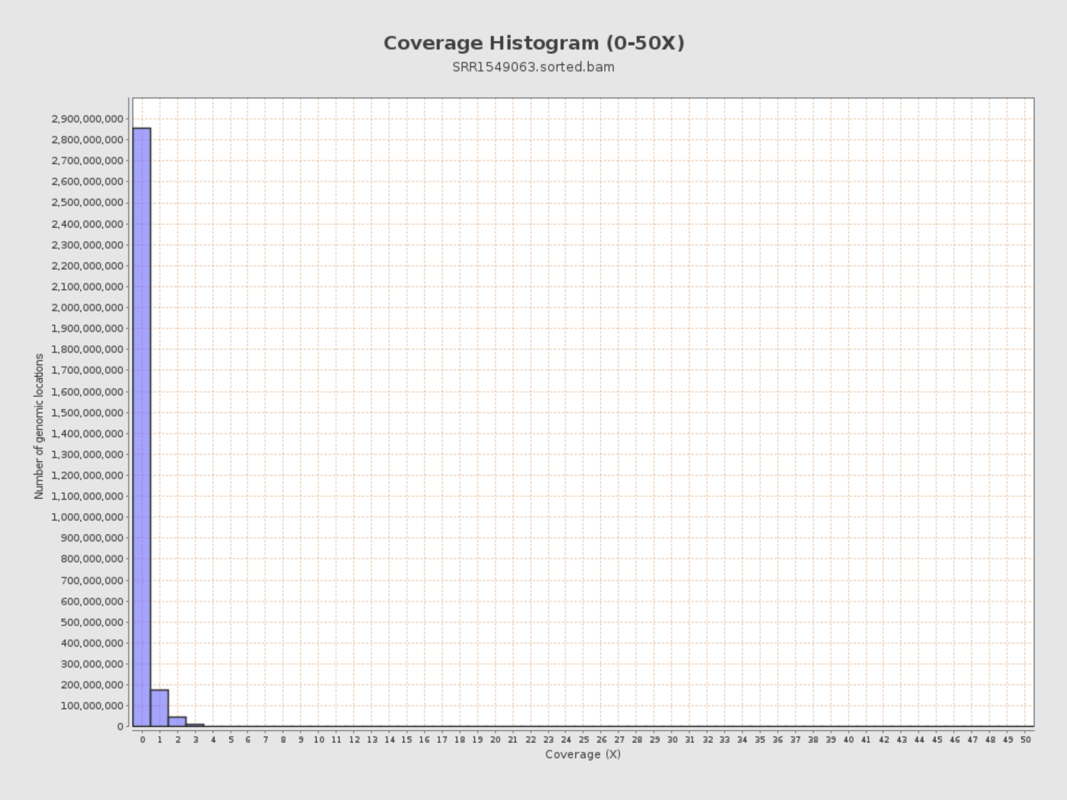
3. Results : Coverage across reference



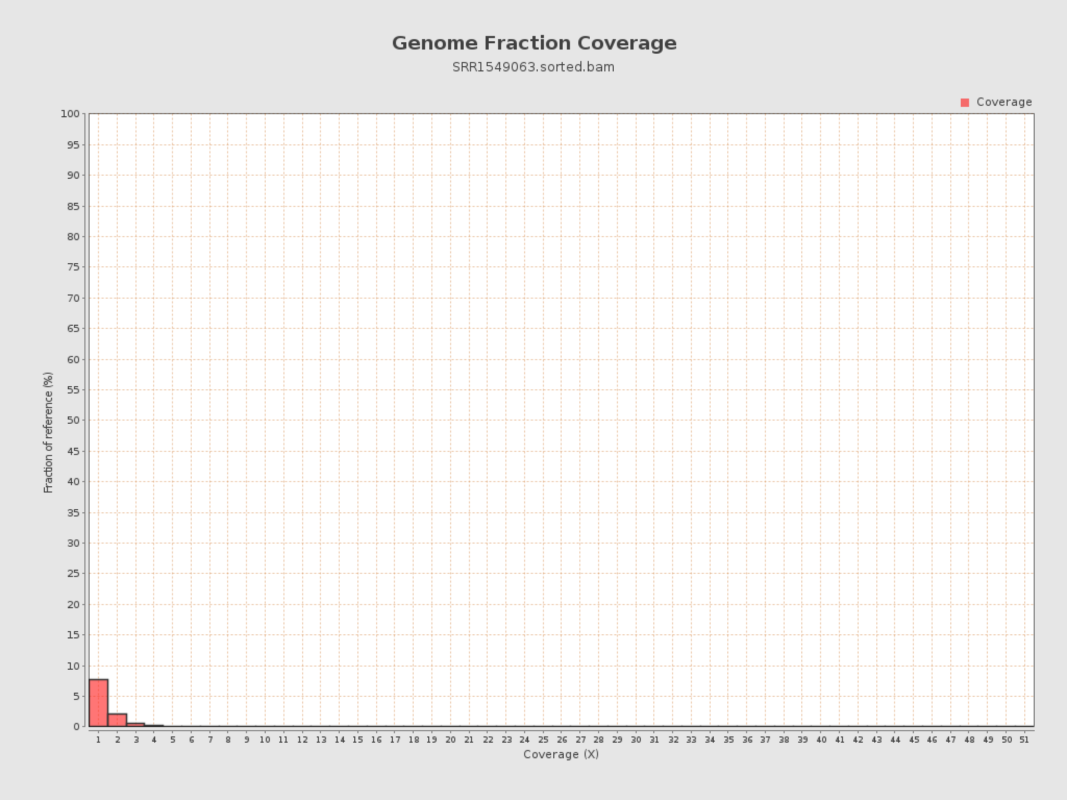
4. Results : Coverage Histogram



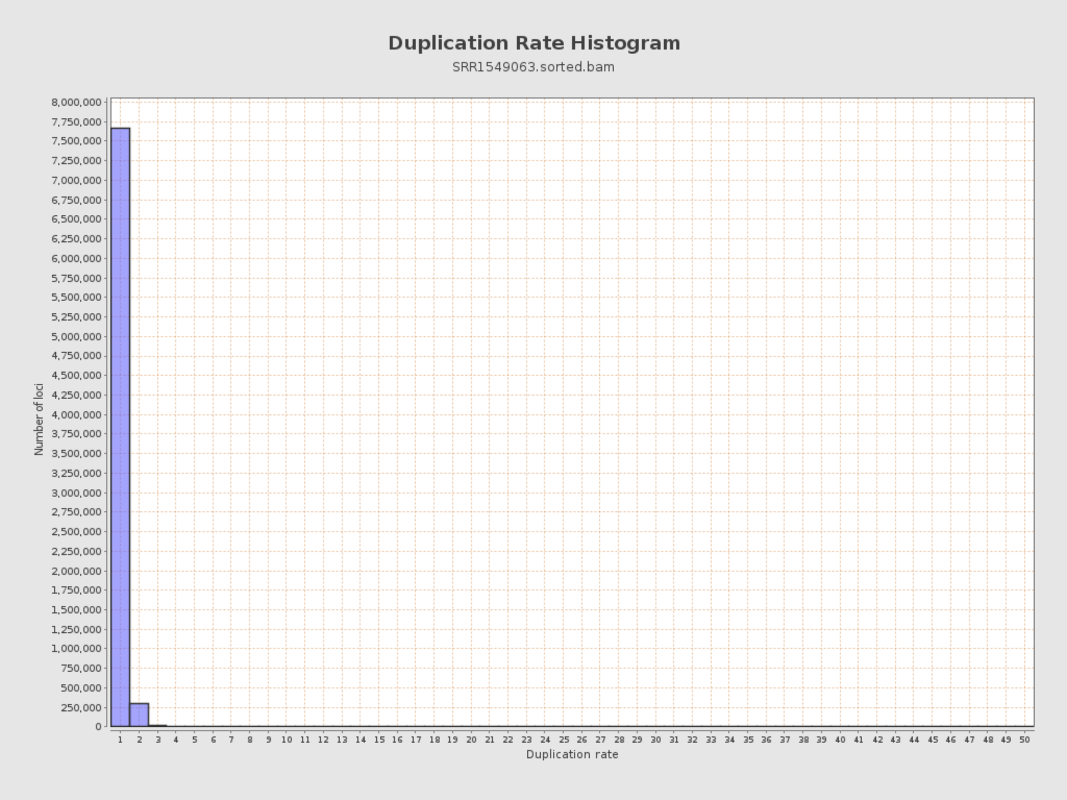
5. Results : Coverage Histogram (0-50X)



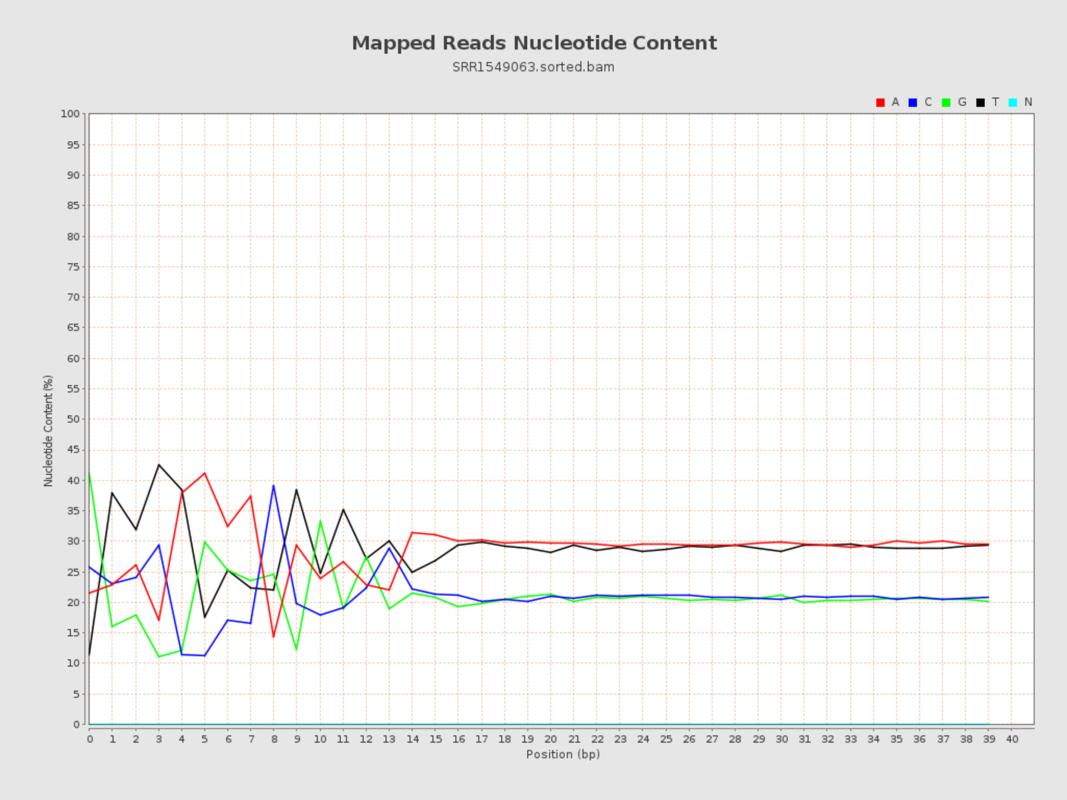
6. Results : Genome Fraction Coverage



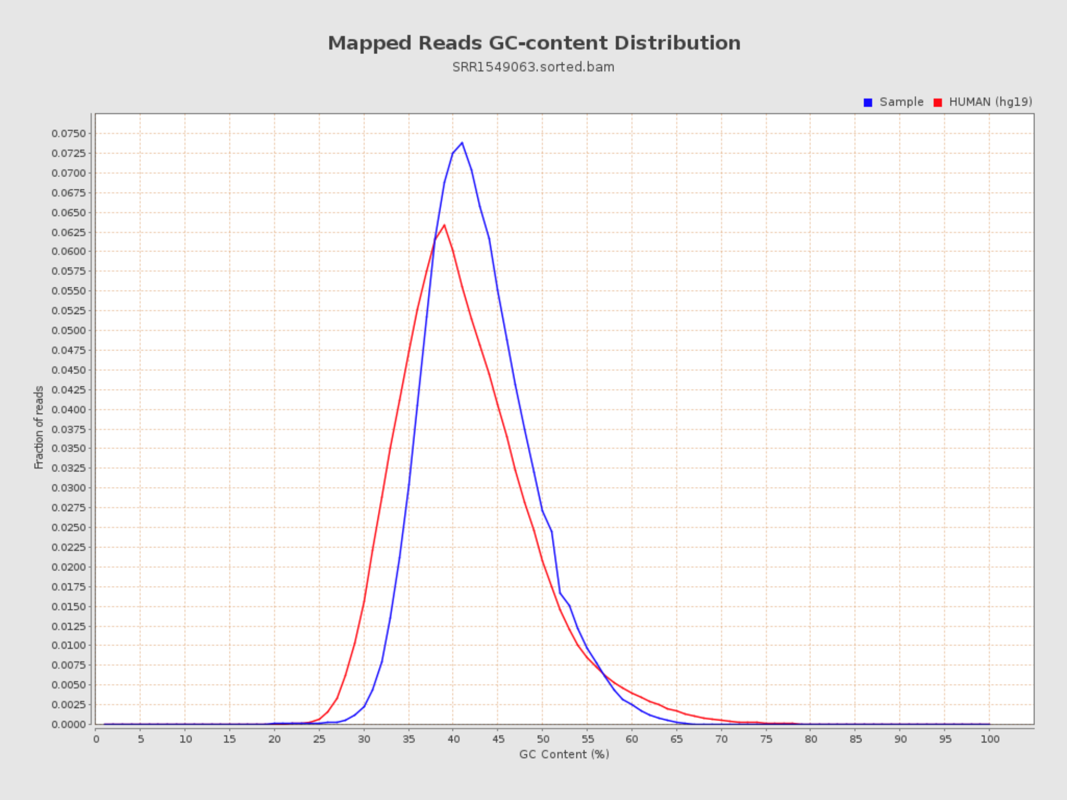
7. Results : Duplication Rate Histogram



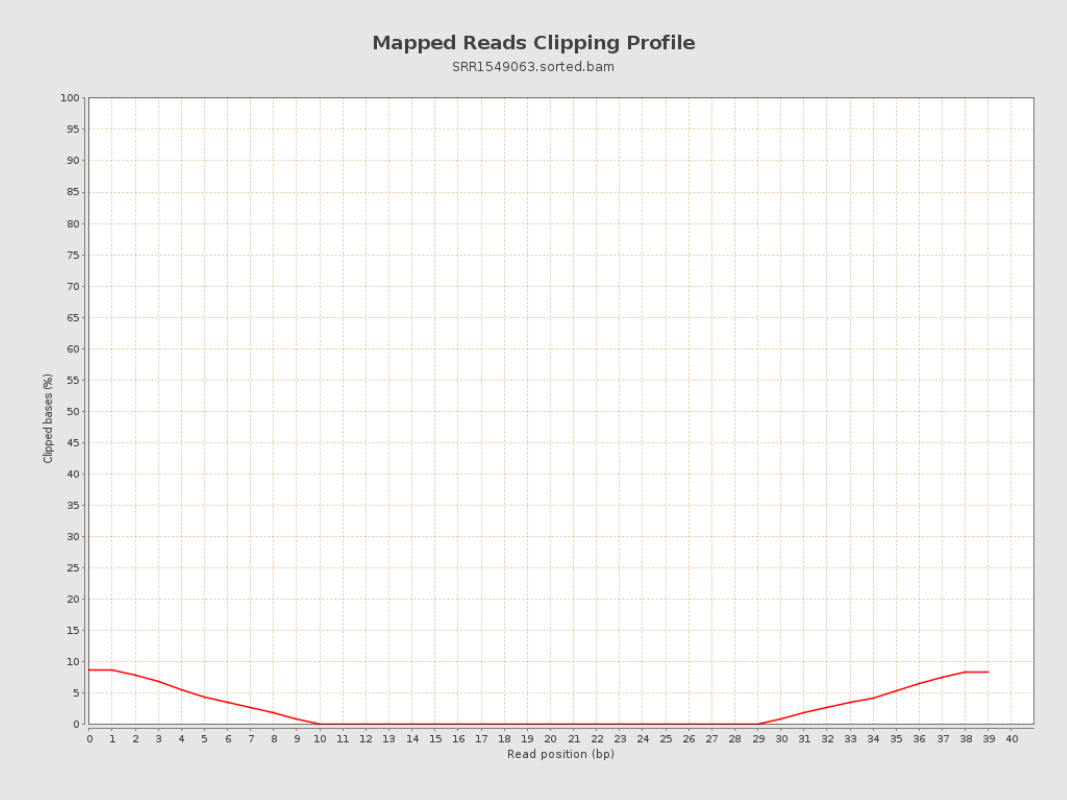
8. Results : Mapped Reads Nucleotide Content



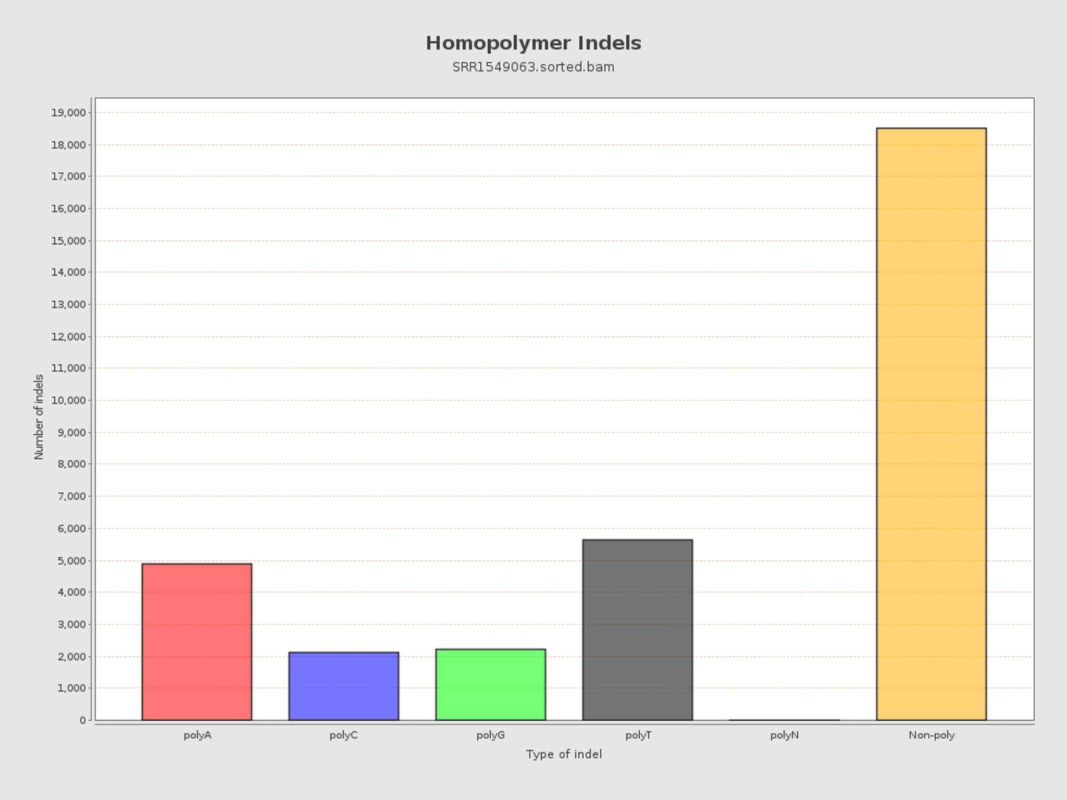
9. Results : Mapped Reads GC-content Distribution



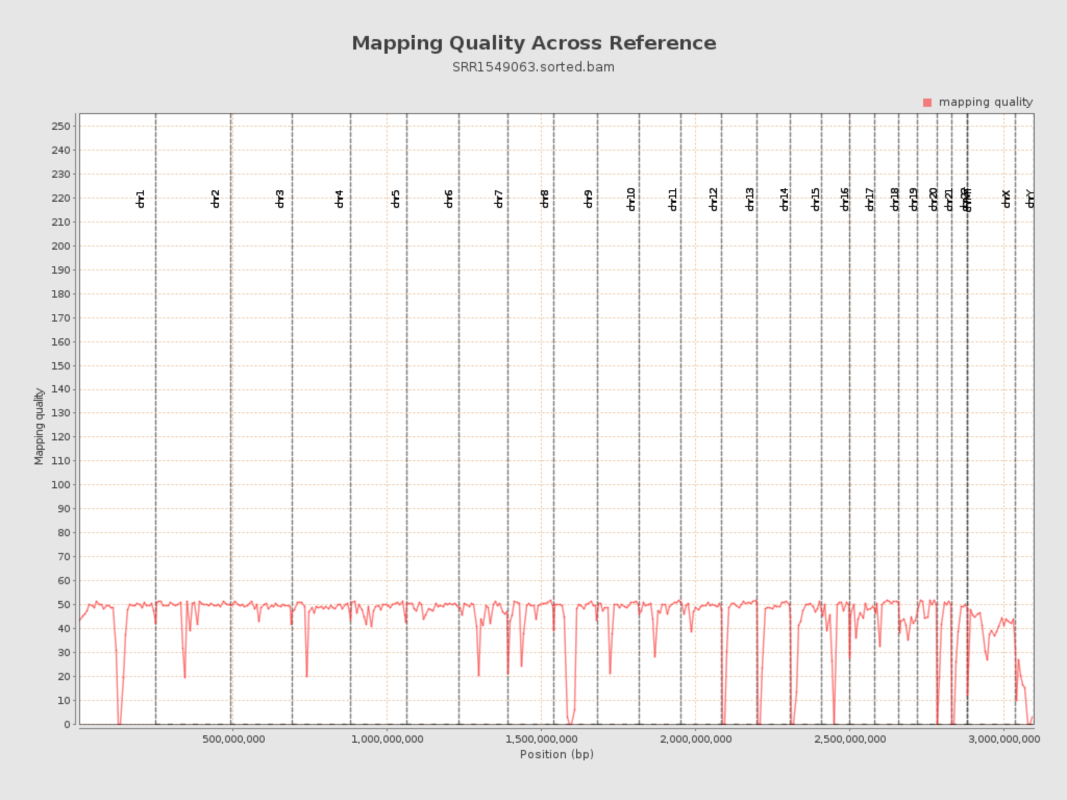
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram