Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 12:37:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234055.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_SRR6234055 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234055.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 12:37:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234055.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,069,439
Mapped reads	690,289 / 64.55%
Unmapped reads	379,150 / 35.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,179 / 0.76%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	83,575 / 7.81%
Duplication rate	9.74%
Clipped reads	388,006 / 36.28%

2.2. ACGT Content

Number/percentage of A's	12,079,444 / 27.46%
Number/percentage of C's	7,602,729 / 17.29%
Number/percentage of T's	14,636,909 / 33.28%
Number/percentage of G's	9,655,693 / 21.95%
Number/percentage of N's	8,612 / 0.02%
GC Percentage	39.24%

2.3. Coverage

Mean	0.0142

Standard Deviation	0.2357

2.4. Mapping Quality

Mean Mapping Quality	44.43

2.5. Mismatches and indels

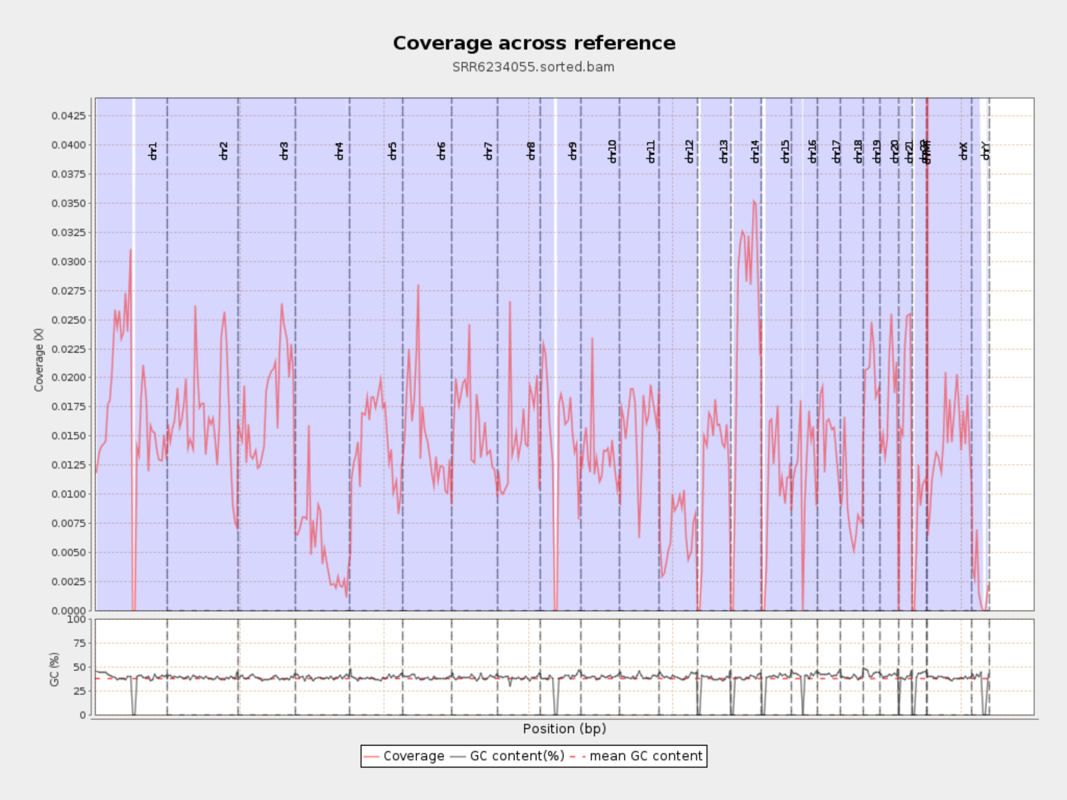
General error rate	0.88%
Mismatches	379,258
Insertions	3,783
Mapped reads with at least one insertion	0.54%
Deletions	18,283
Mapped reads with at least one deletion	2.61%
Homopolymer indels	43.07%

2.6. Chromosome stats

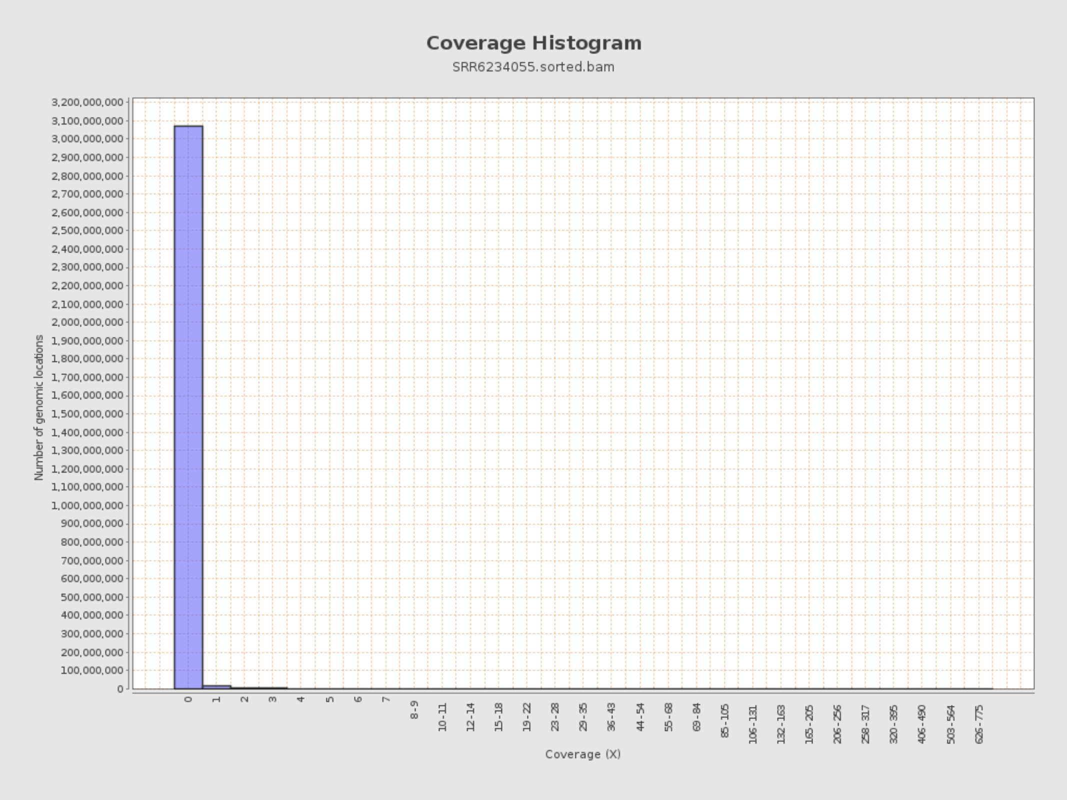
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4216302	0.0169	0.3574
chr2	243199373	4033091	0.0166	0.2415
chr3	198022430	3529908	0.0178	0.2032
chr4	191154276	1020474	0.0053	0.1103
chr5	180915260	2658406	0.0147	0.1837
chr6	171115067	2571459	0.015	0.1974
chr7	159138663	2549272	0.016	0.2189

chr8	146364022	2181626	0.0149	0.507
chr9	141213431	2100200	0.0149	0.1987
chr10	135534747	1814399	0.0134	0.1911
chr11	135006516	2153982	0.016	0.2171
chr12	133851895	905792	0.0068	0.1225
chr13	115169878	1471553	0.0128	0.1765
chr14	107349540	2697806	0.0251	0.2475
chr15	102531392	1081598	0.0105	0.1539
chr16	90354753	1082898	0.012	0.171
chr17	81195210	1233327	0.0152	0.1869
chr18	78077248	657801	0.0084	0.2592
chr19	59128983	1216891	0.0206	0.2472
chr20	63025520	1125405	0.0179	0.2072
chr21	48129895	892850	0.0186	0.2102
chr22	51304566	397736	0.0078	0.125
chrMT	16571	26102	1.5752	1.9873
chrX	155270560	2270662	0.0146	0.188
chrY	59373566	126067	0.0021	0.0679

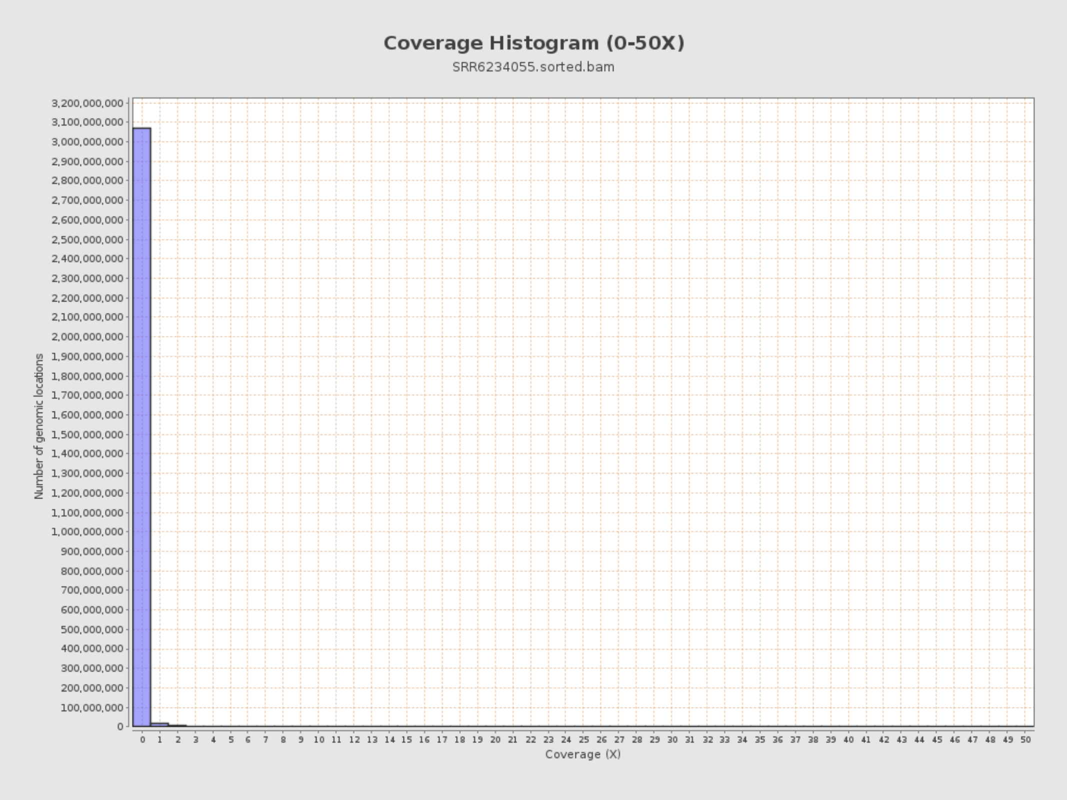
3. Results : Coverage across reference



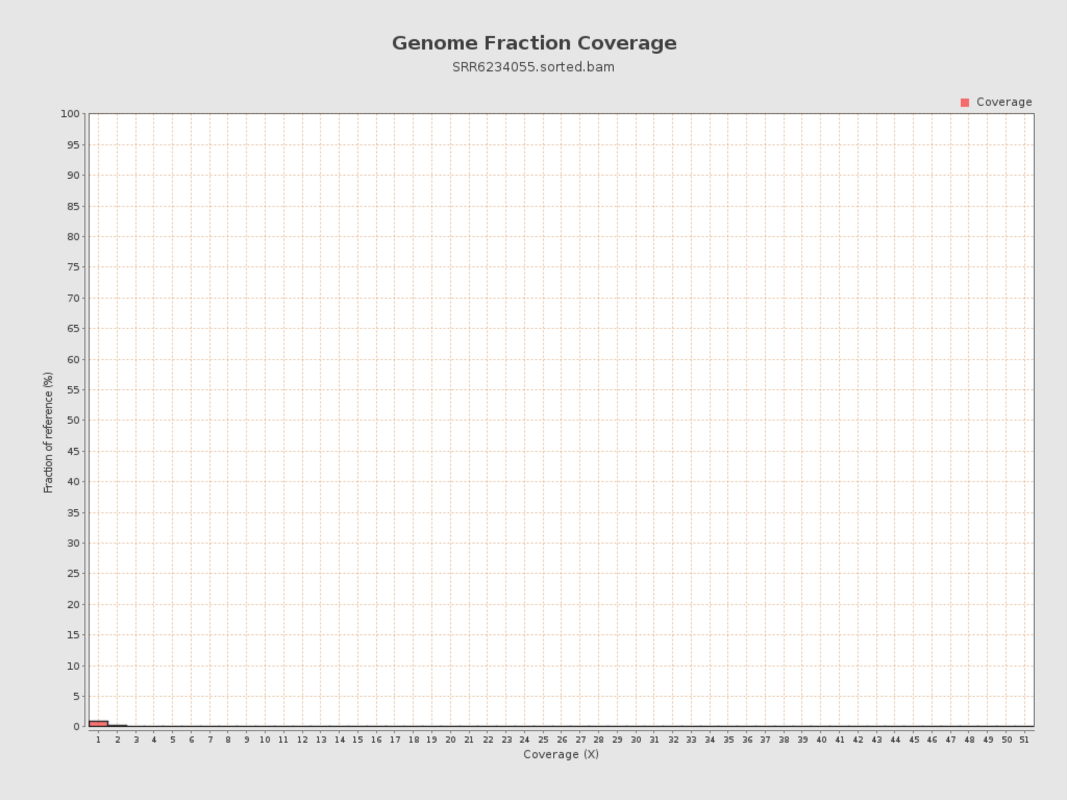
4. Results : Coverage Histogram



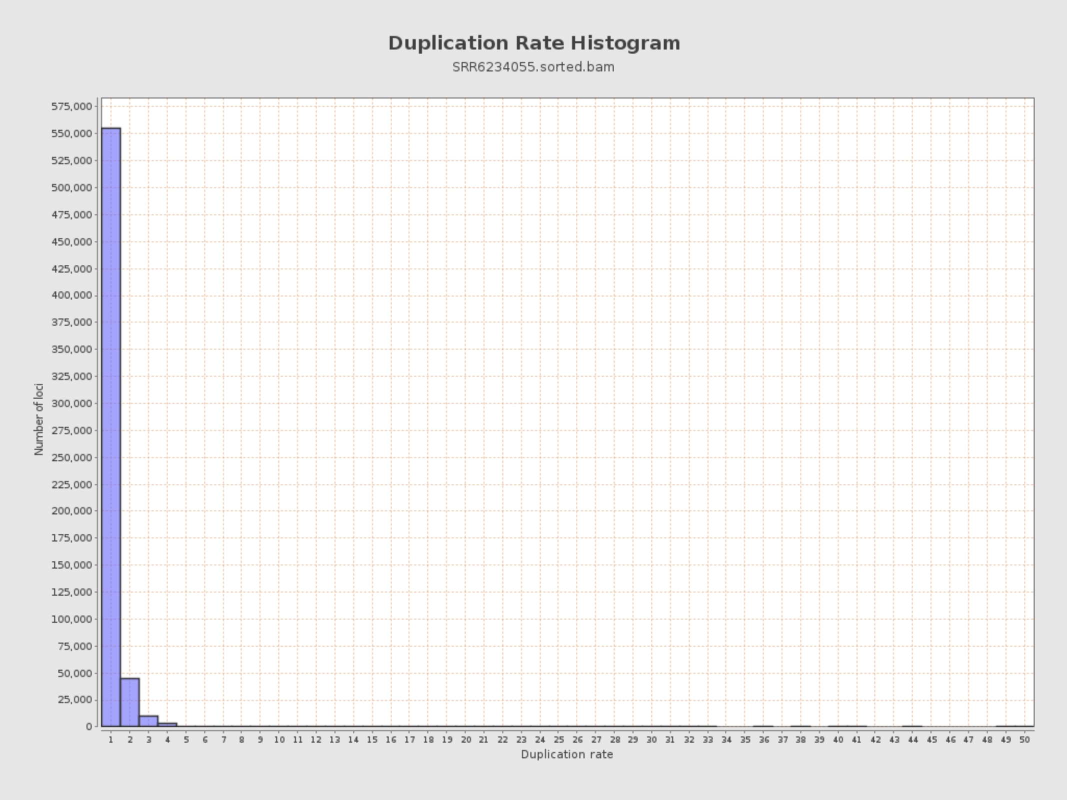
5. Results : Coverage Histogram (0-50X)



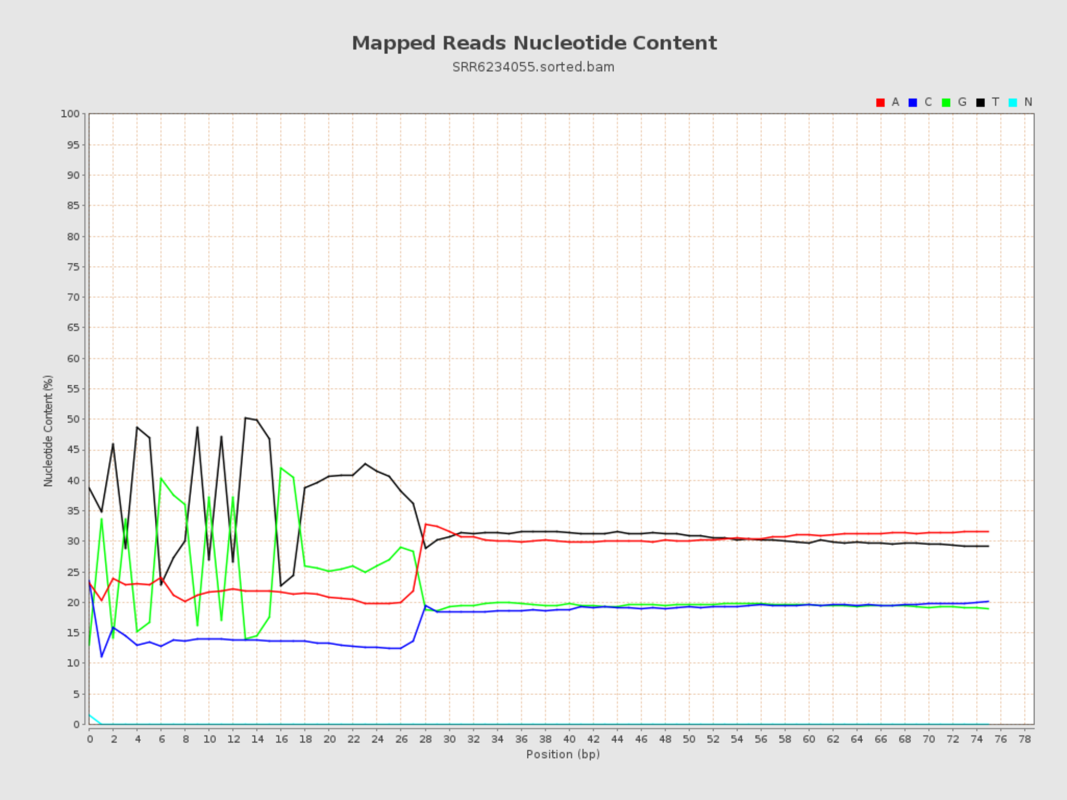
6. Results : Genome Fraction Coverage



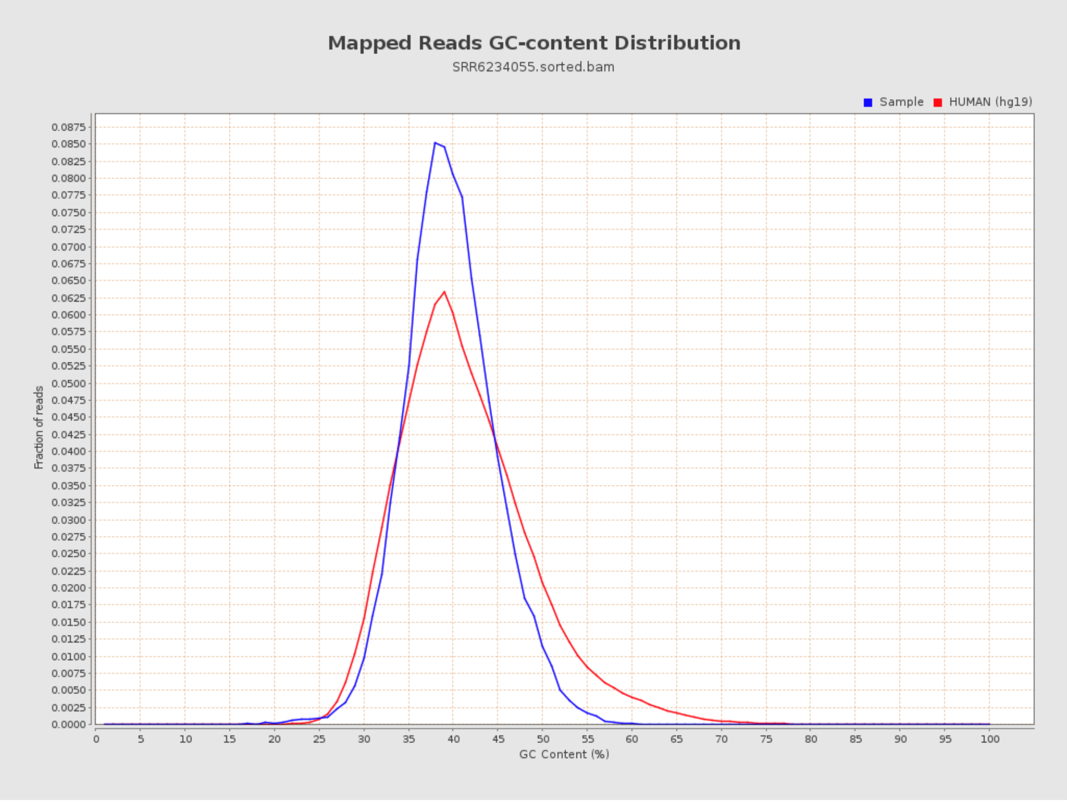
7. Results : Duplication Rate Histogram



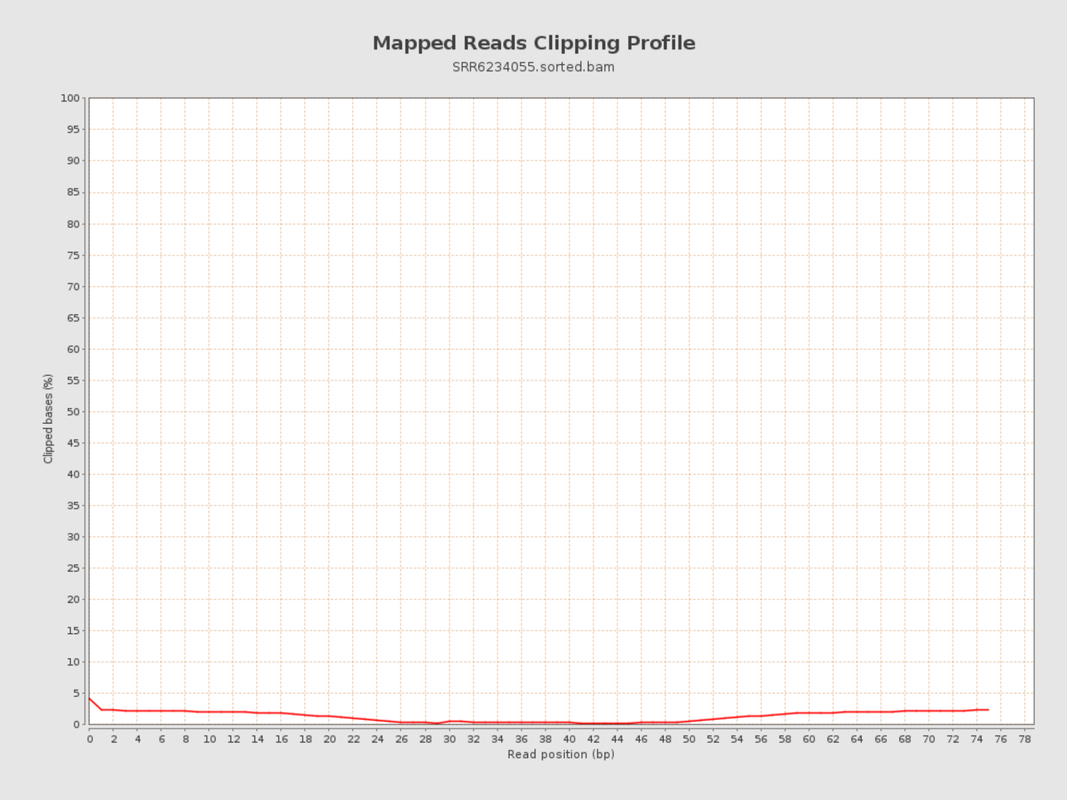
8. Results : Mapped Reads Nucleotide Content



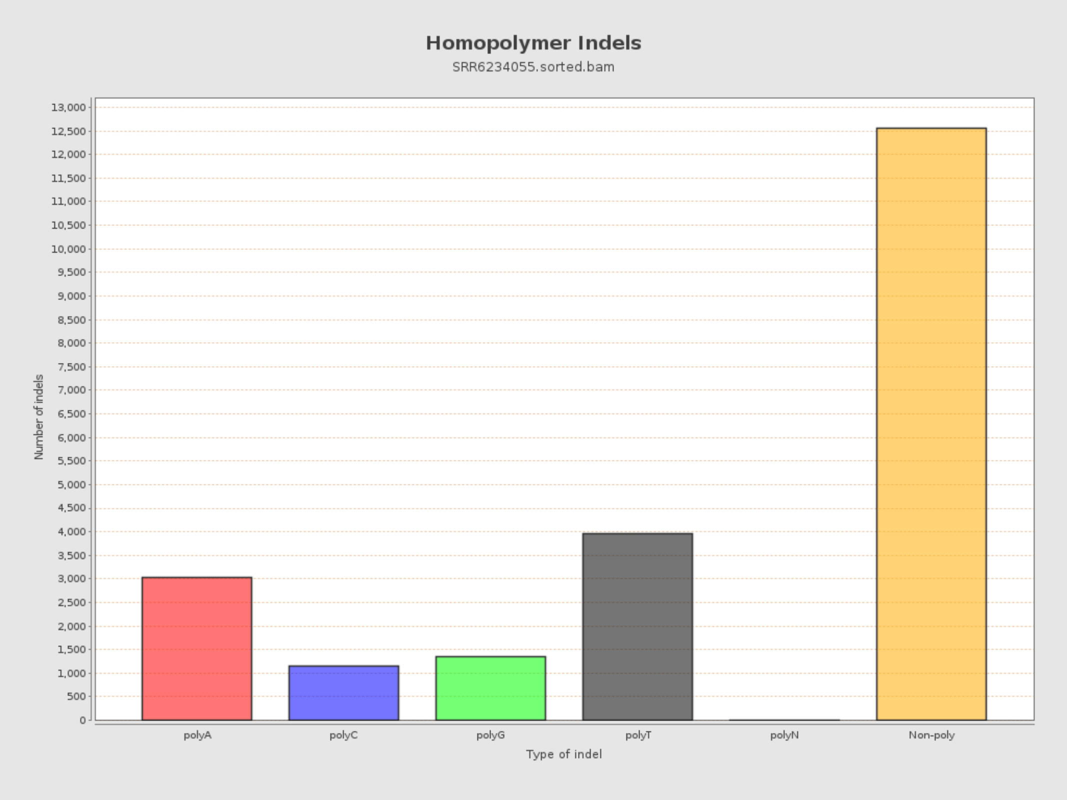
9. Results : Mapped Reads GC-content Distribution



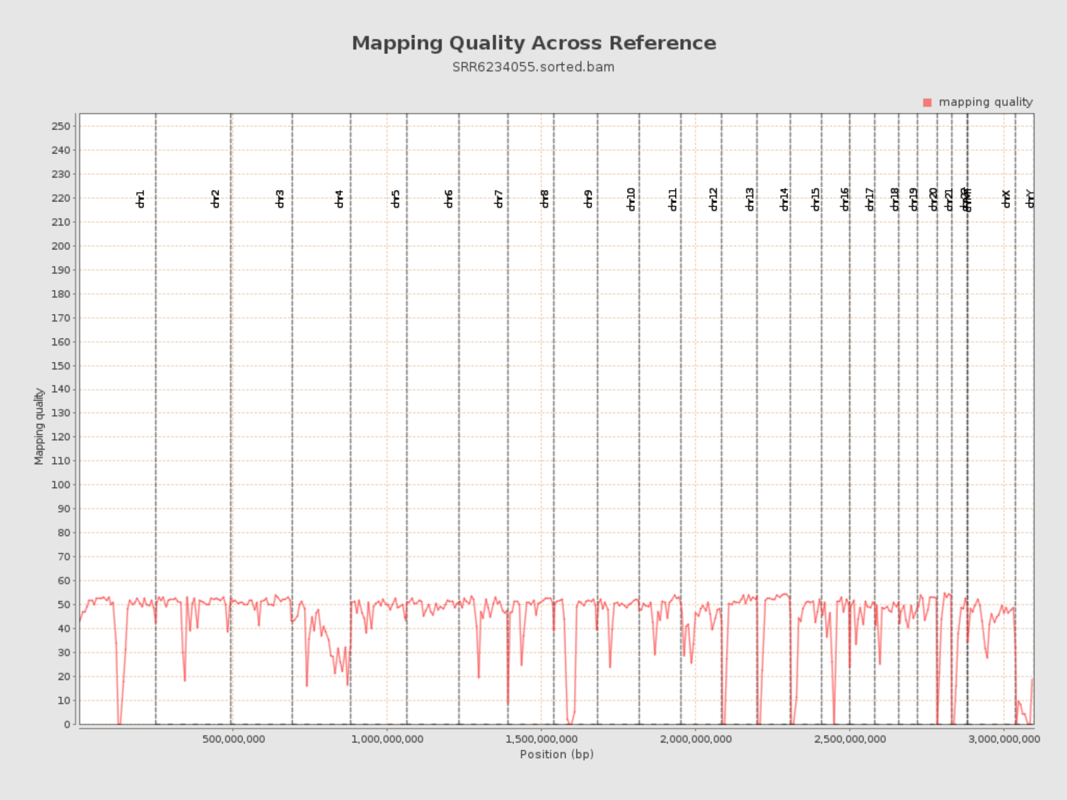
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram