Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 14:49:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234085.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_SRR6234085 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234085.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 14:49:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234085.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	727,688
Mapped reads	468,135 / 64.33%
Unmapped reads	259,553 / 35.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,174 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	15,089 / 2.07%
Duplication rate	2.71%
Clipped reads	310,472 / 42.67%

2.2. ACGT Content

Number/percentage of A's	7,617,727 / 26.53%
Number/percentage of C's	4,961,110 / 17.28%
Number/percentage of T's	9,158,106 / 31.89%
Number/percentage of G's	6,976,314 / 24.29%
Number/percentage of N's	5,076 / 0.02%
GC Percentage	41.57%

2.3. Coverage

Mean	0.0093

Standard Deviation	0.1218

2.4. Mapping Quality

Mean Mapping Quality	43.35

2.5. Mismatches and indels

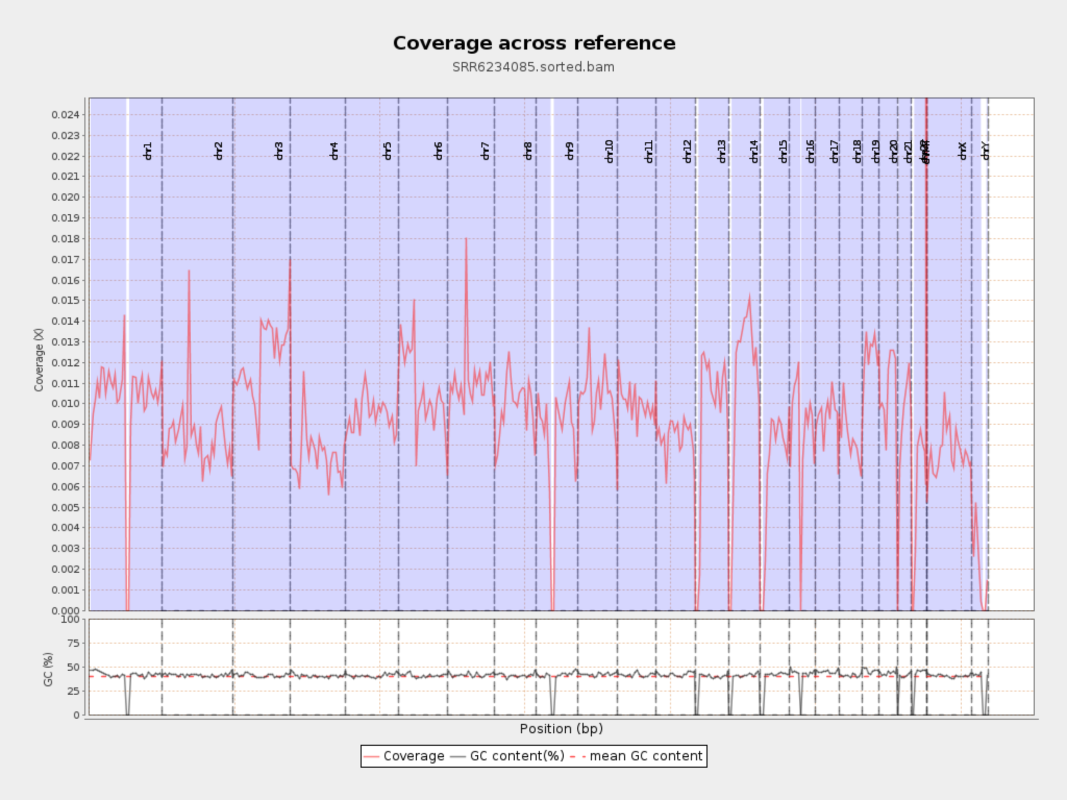
General error rate	1.01%
Mismatches	284,932
Insertions	2,466
Mapped reads with at least one insertion	0.52%
Deletions	11,911
Mapped reads with at least one deletion	2.51%
Homopolymer indels	46.53%

2.6. Chromosome stats

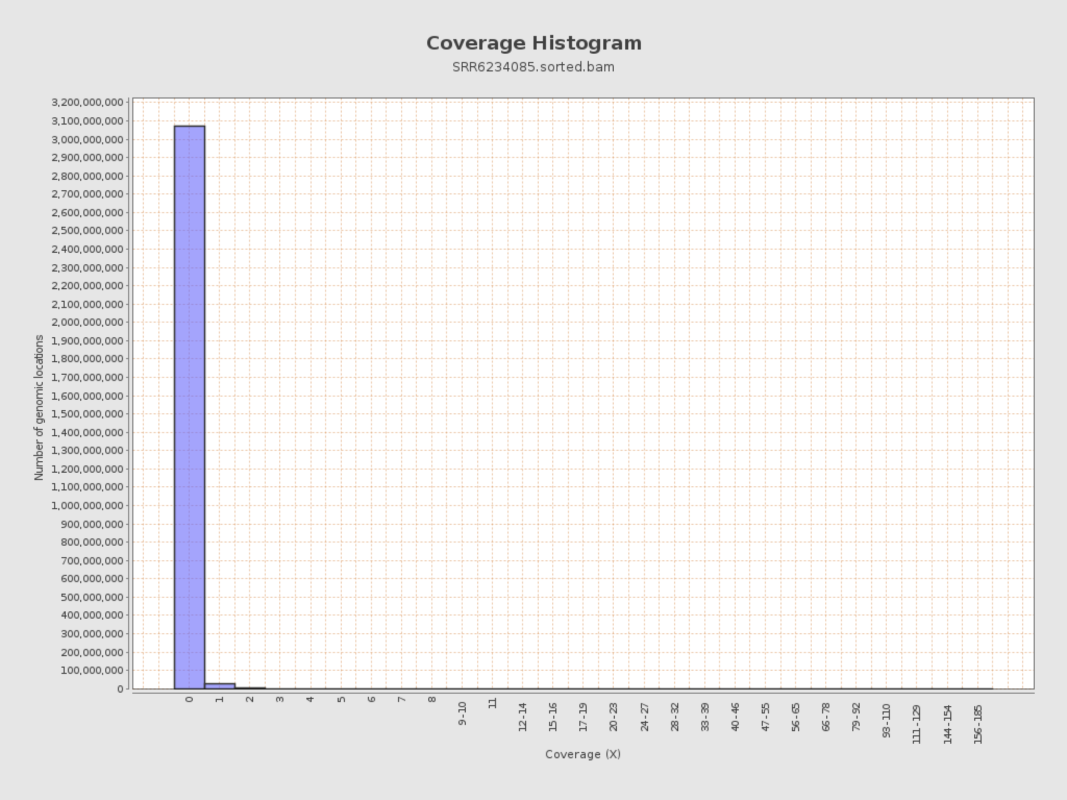
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2496430	0.01	0.1537
chr2	243199373	2053253	0.0084	0.1275
chr3	198022430	2381652	0.012	0.1188
chr4	191154276	1426149	0.0075	0.0963
chr5	180915260	1715107	0.0095	0.1064
chr6	171115067	1840442	0.0108	0.1207
chr7	159138663	1768806	0.0111	0.1658

chr8	146364022	1438491	0.0098	0.154
chr9	141213431	1157028	0.0082	0.1109
chr10	135534747	1420887	0.0105	0.1203
chr11	135006516	1344048	0.01	0.1319
chr12	133851895	1128719	0.0084	0.0992
chr13	115169878	1069421	0.0093	0.1068
chr14	107349540	1167824	0.0109	0.1159
chr15	102531392	689299	0.0067	0.0898
chr16	90354753	788002	0.0087	0.1037
chr17	81195210	762074	0.0094	0.1106
chr18	78077248	658233	0.0084	0.1493
chr19	59128983	734387	0.0124	0.1366
chr20	63025520	668437	0.0106	0.1146
chr21	48129895	422156	0.0088	0.1027
chr22	51304566	285053	0.0056	0.0797
chrMT	16571	21311	1.286	1.6051
chrX	155270560	1191158	0.0077	0.0984
chrY	59373566	111453	0.0019	0.0499

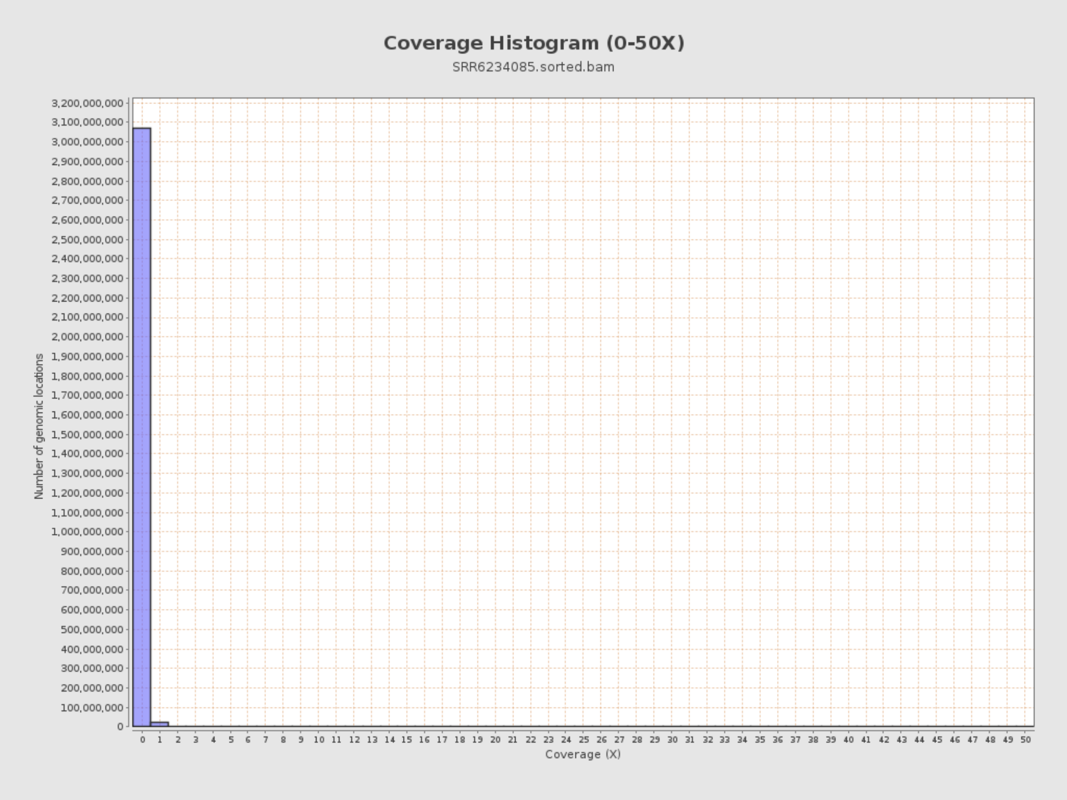
3. Results : Coverage across reference



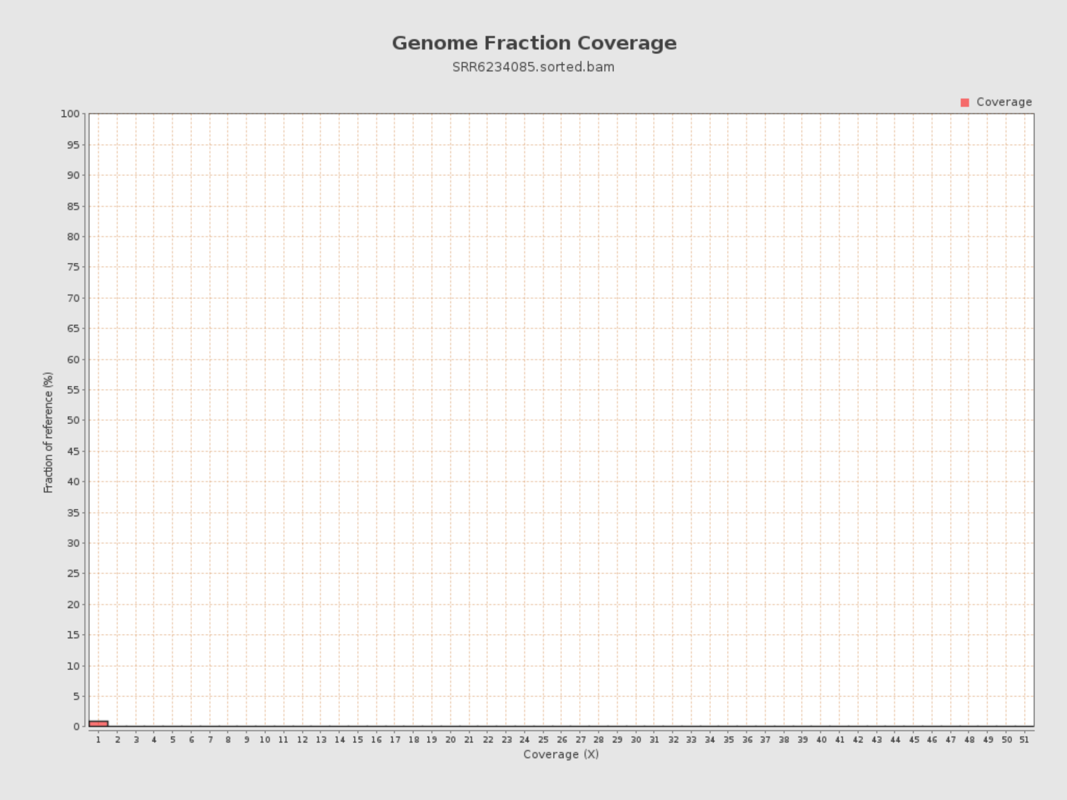
4. Results : Coverage Histogram



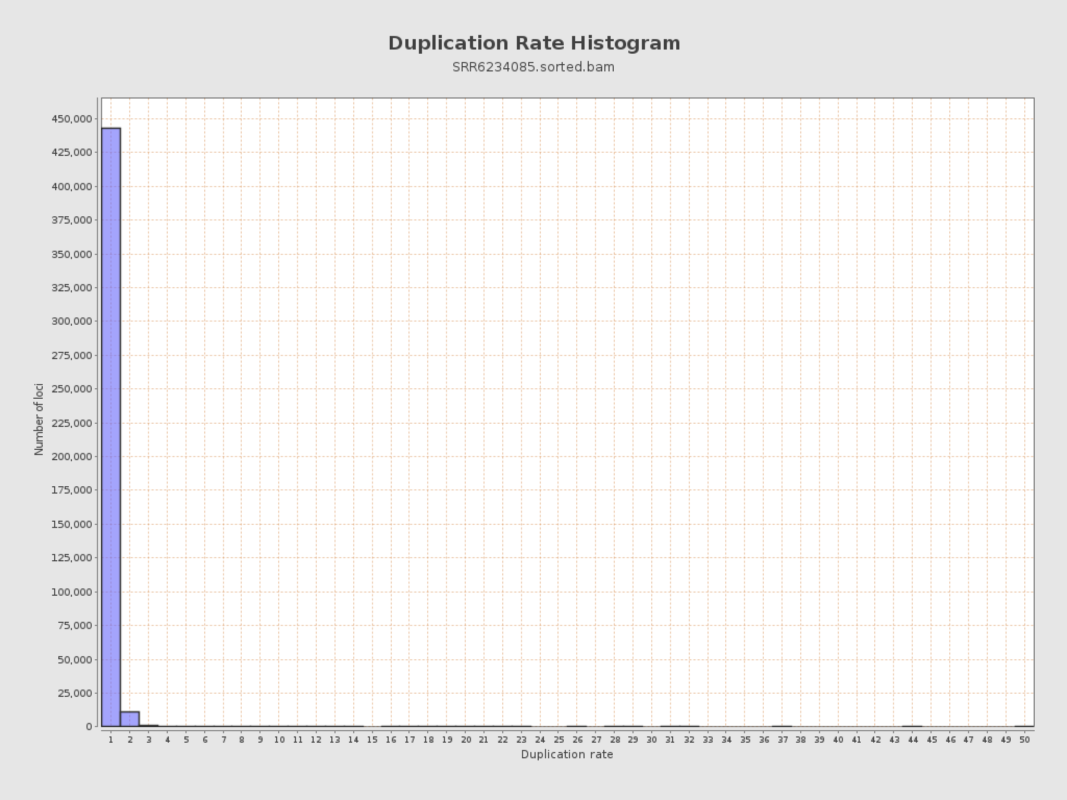
5. Results : Coverage Histogram (0-50X)



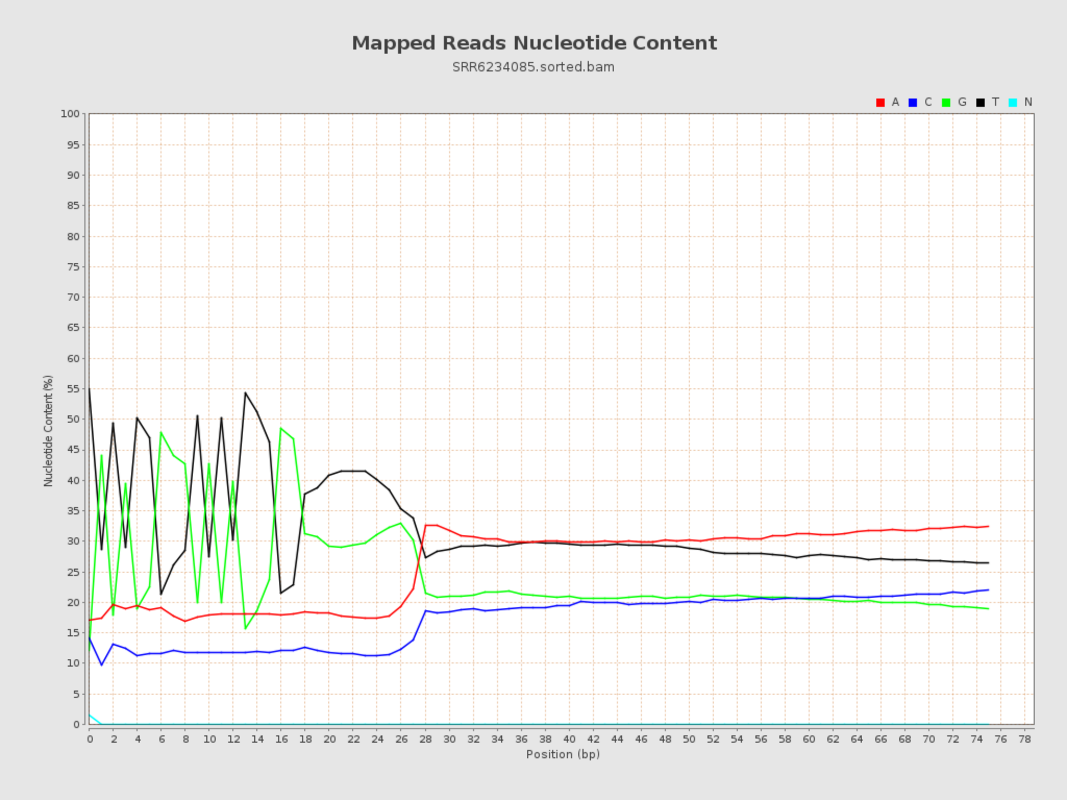
6. Results : Genome Fraction Coverage



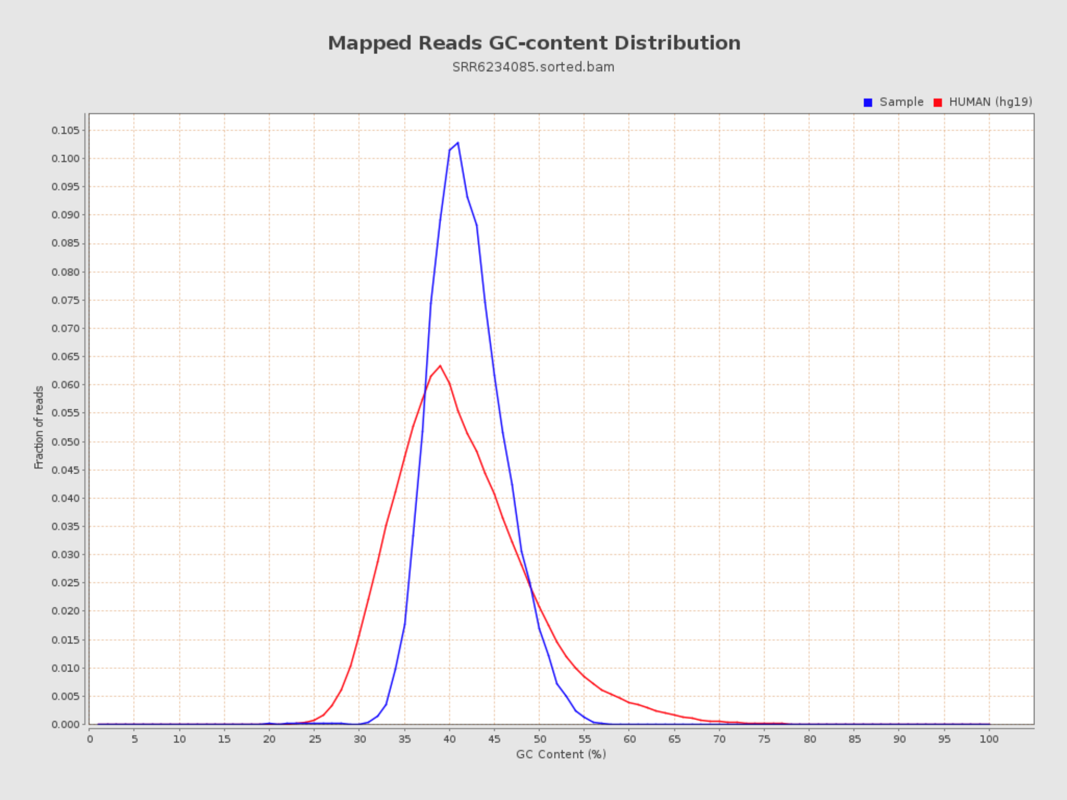
7. Results : Duplication Rate Histogram



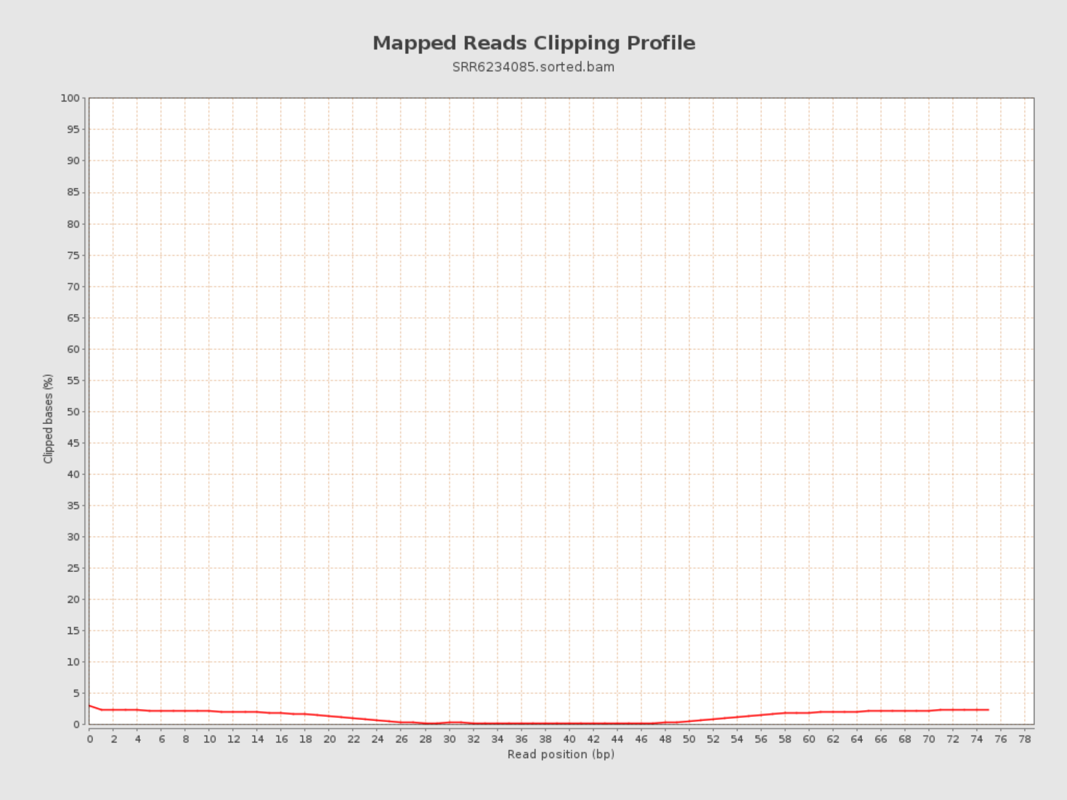
8. Results : Mapped Reads Nucleotide Content



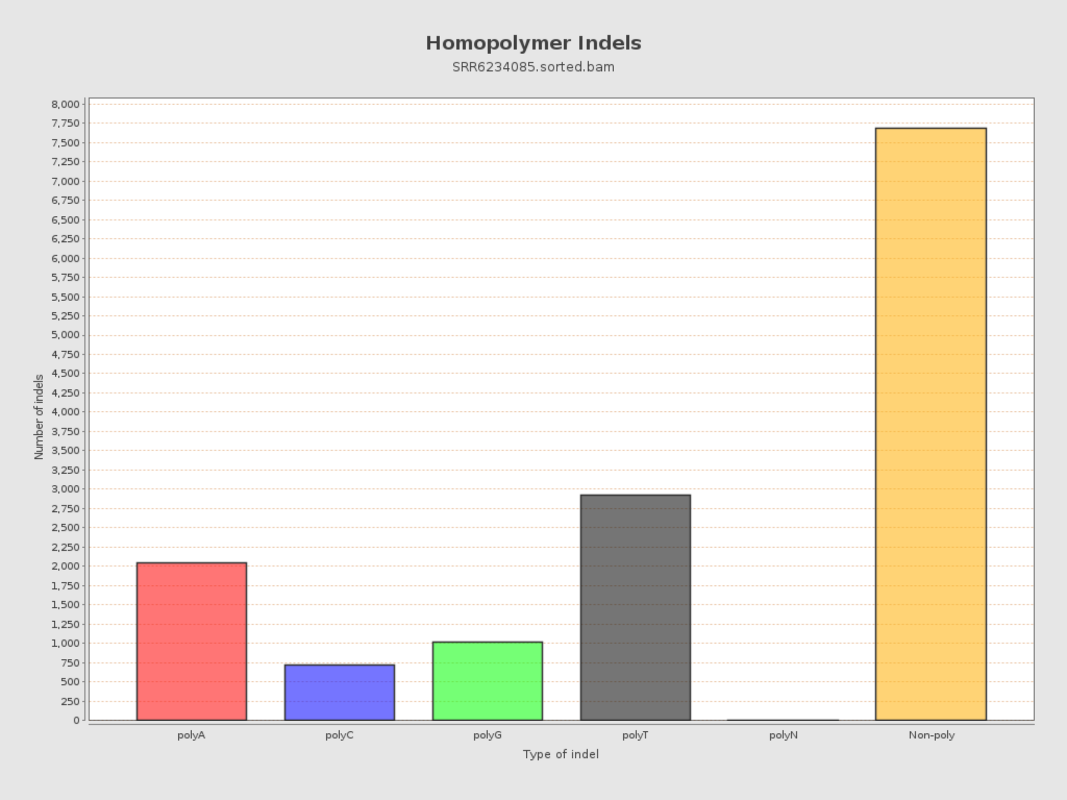
9. Results : Mapped Reads GC-content Distribution



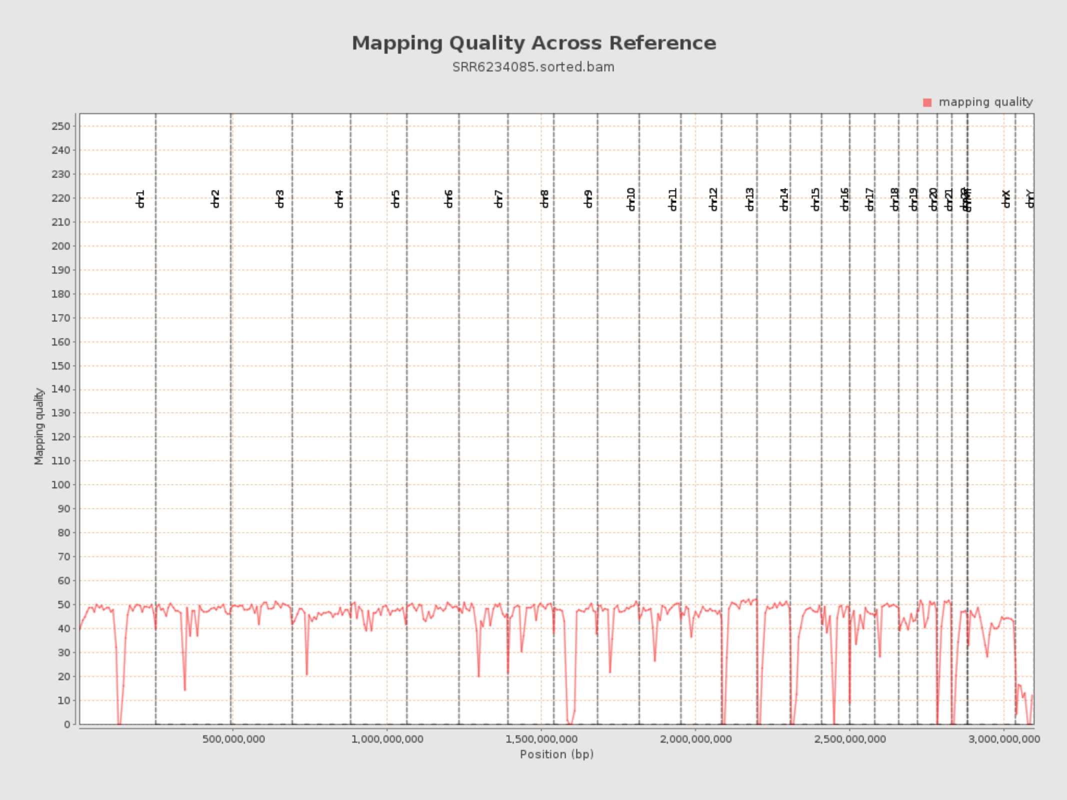
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram