Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 14:41:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234081.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_SRR6234081 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234081.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 14:41:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234081.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	912,840
Mapped reads	614,655 / 67.33%
Unmapped reads	298,185 / 32.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,758 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	16,154 / 1.77%
Duplication rate	2.06%
Clipped reads	309,062 / 33.86%

2.2. ACGT Content

Number/percentage of A's	11,285,142 / 28.31%
Number/percentage of C's	6,648,271 / 16.68%
Number/percentage of T's	12,964,502 / 32.53%
Number/percentage of G's	8,953,401 / 22.46%
Number/percentage of N's	7,572 / 0.02%
GC Percentage	39.14%

2.3. Coverage

Mean	0.0129

Standard Deviation	0.1592

2.4. Mapping Quality

Mean Mapping Quality	46.43

2.5. Mismatches and indels

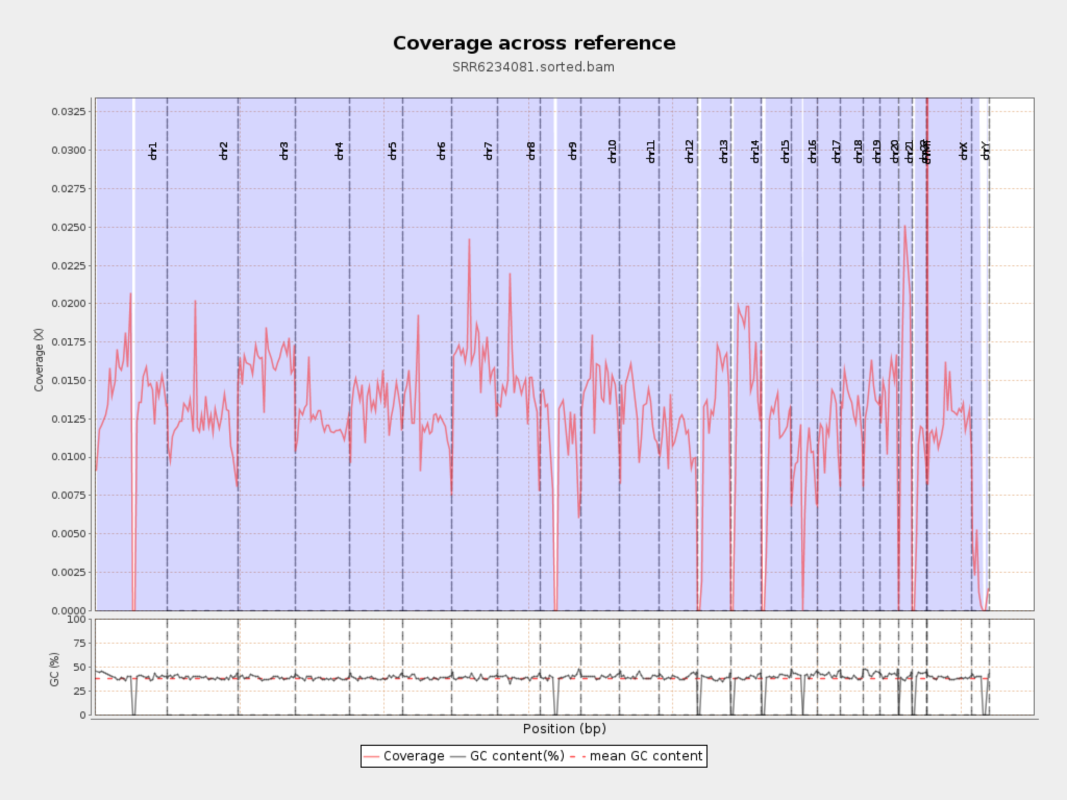
General error rate	0.96%
Mismatches	375,646
Insertions	3,375
Mapped reads with at least one insertion	0.54%
Deletions	11,974
Mapped reads with at least one deletion	1.92%
Homopolymer indels	47.43%

2.6. Chromosome stats

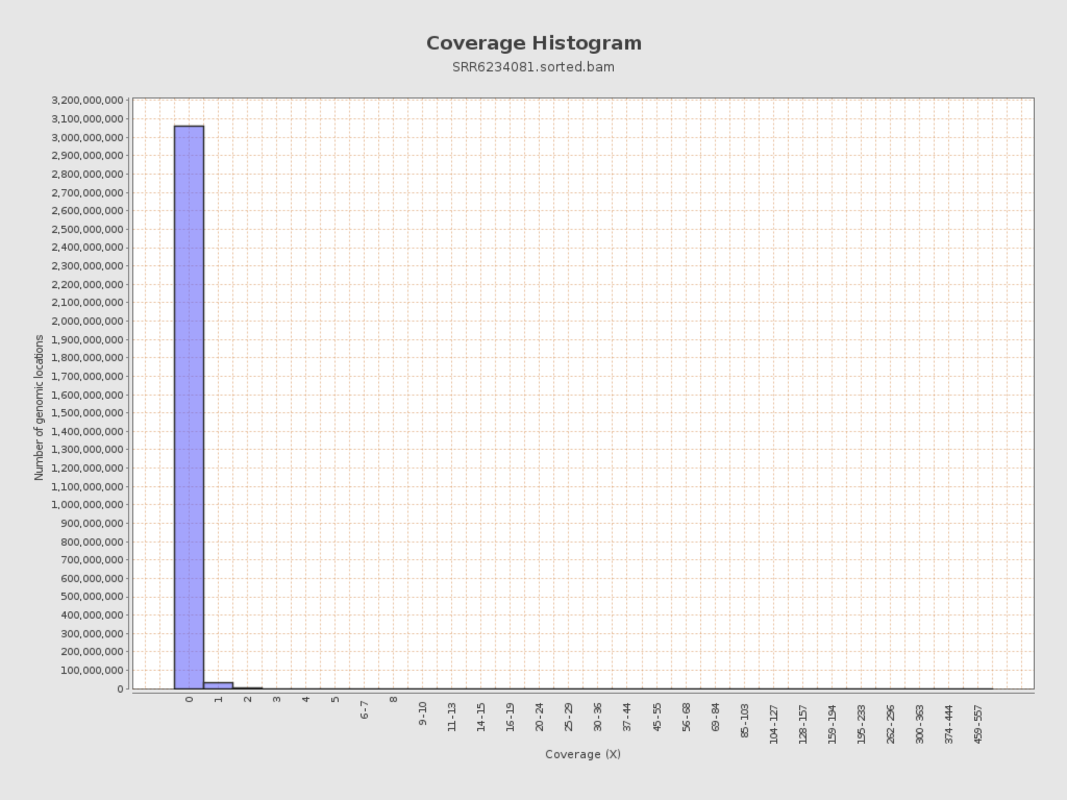
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3383951	0.0136	0.2113
chr2	243199373	2997132	0.0123	0.1554
chr3	198022430	3225392	0.0163	0.1351
chr4	191154276	2357551	0.0123	0.1198
chr5	180915260	2482929	0.0137	0.1237
chr6	171115067	2164999	0.0127	0.1274
chr7	159138663	2648416	0.0166	0.1901

chr8	146364022	2124996	0.0145	0.3564
chr9	141213431	1486967	0.0105	0.1285
chr10	135534747	1966464	0.0145	0.1384
chr11	135006516	1766024	0.0131	0.1383
chr12	133851895	1513270	0.0113	0.1134
chr13	115169878	1394244	0.0121	0.1168
chr14	107349540	1539005	0.0143	0.1277
chr15	102531392	1040329	0.0101	0.1076
chr16	90354753	779798	0.0086	0.1013
chr17	81195210	953179	0.0117	0.1175
chr18	78077248	1049497	0.0134	0.1985
chr19	59128983	817714	0.0138	0.1526
chr20	63025520	888065	0.0141	0.1263
chr21	48129895	844301	0.0175	0.1415
chr22	51304566	394566	0.0077	0.0925
chrMT	16571	23579	1.4229	1.399
chrX	155270560	1934187	0.0125	0.1215
chrY	59373566	102920	0.0017	0.051

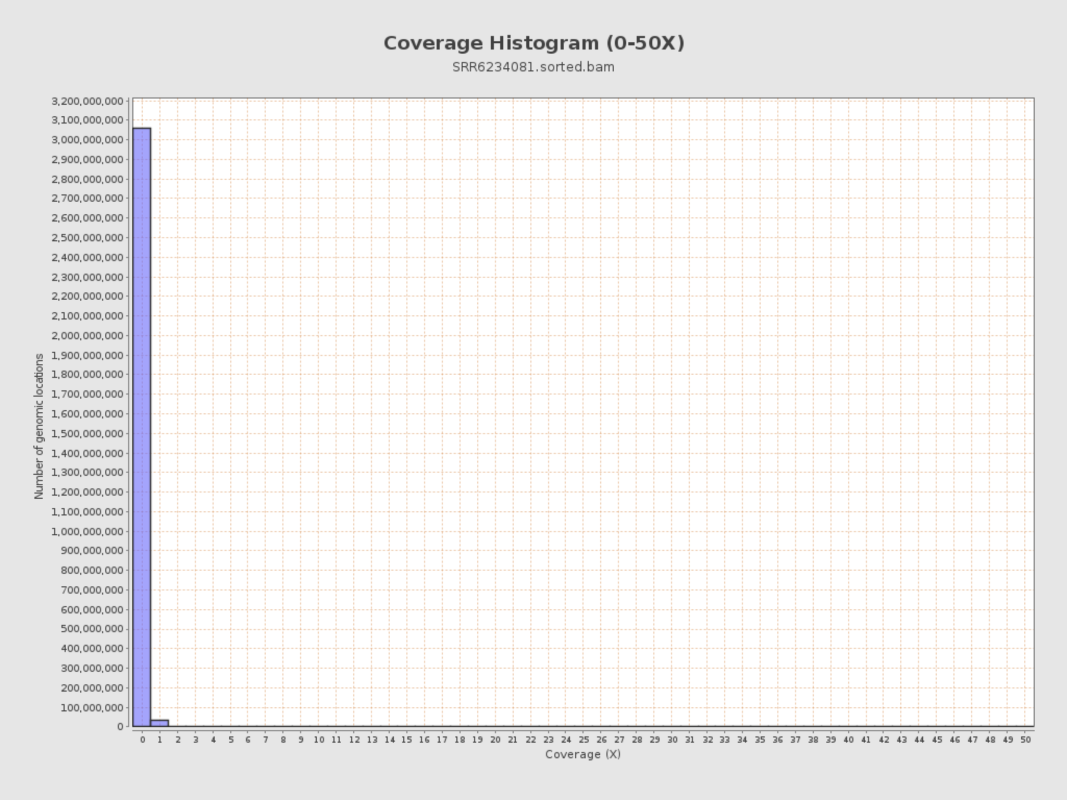
3. Results : Coverage across reference



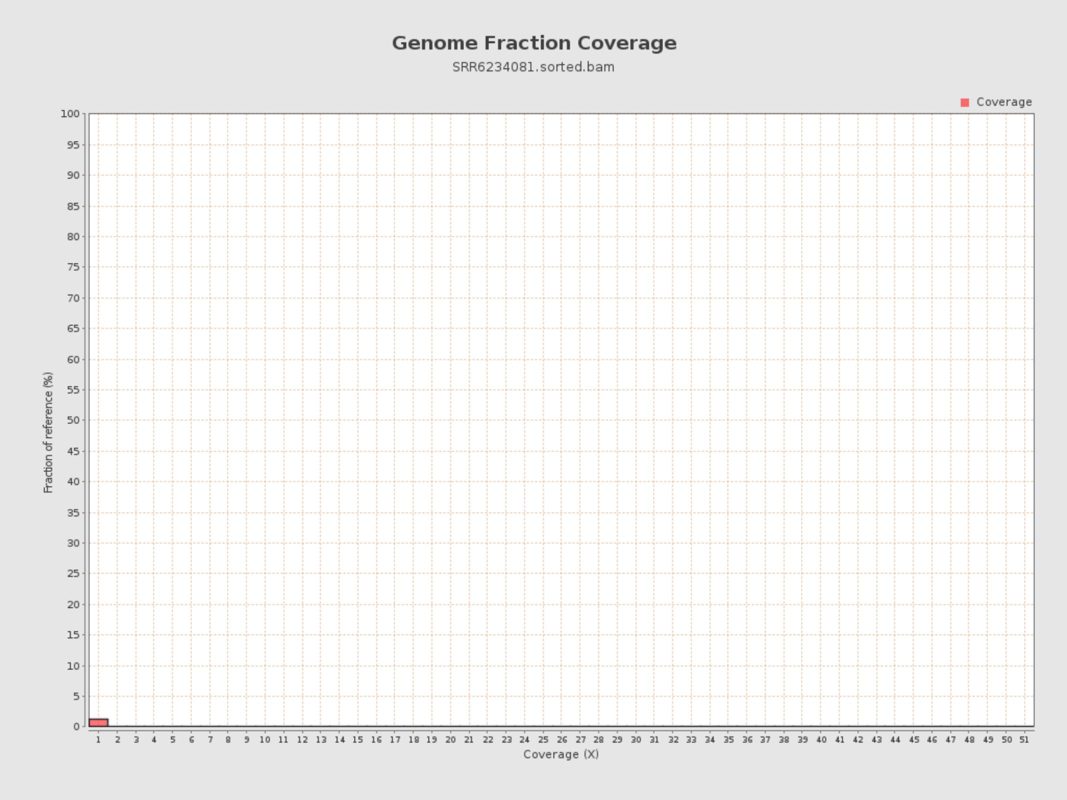
4. Results : Coverage Histogram



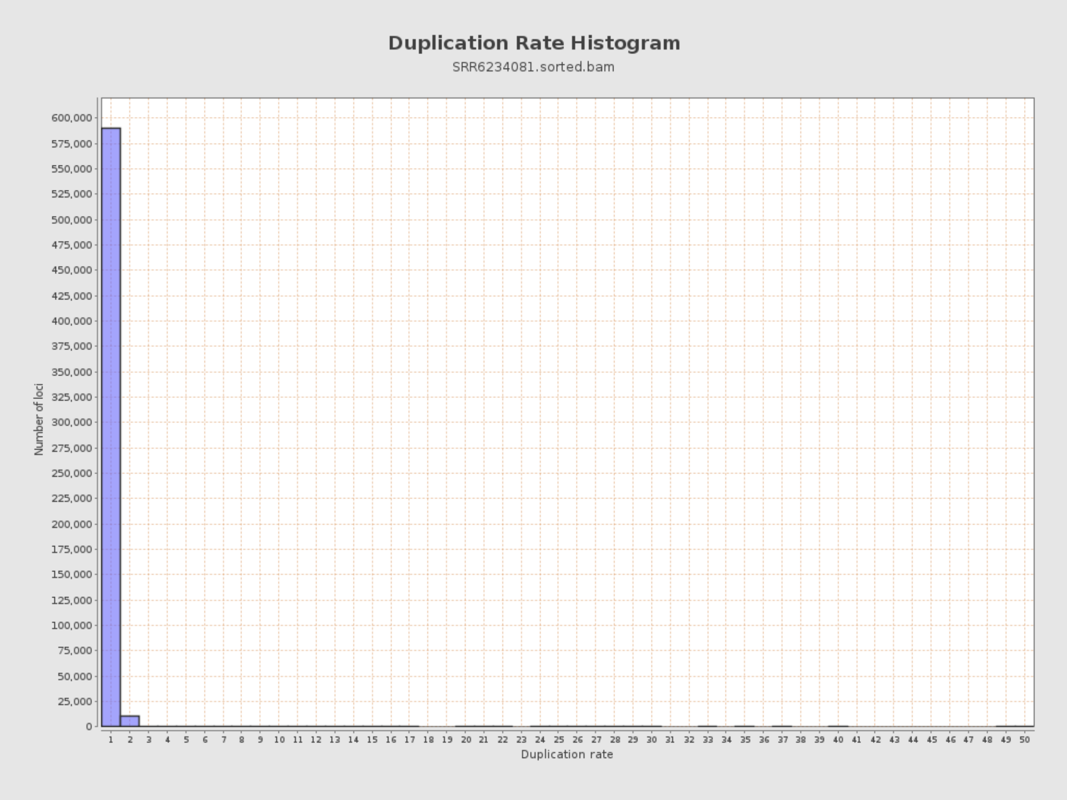
5. Results : Coverage Histogram (0-50X)



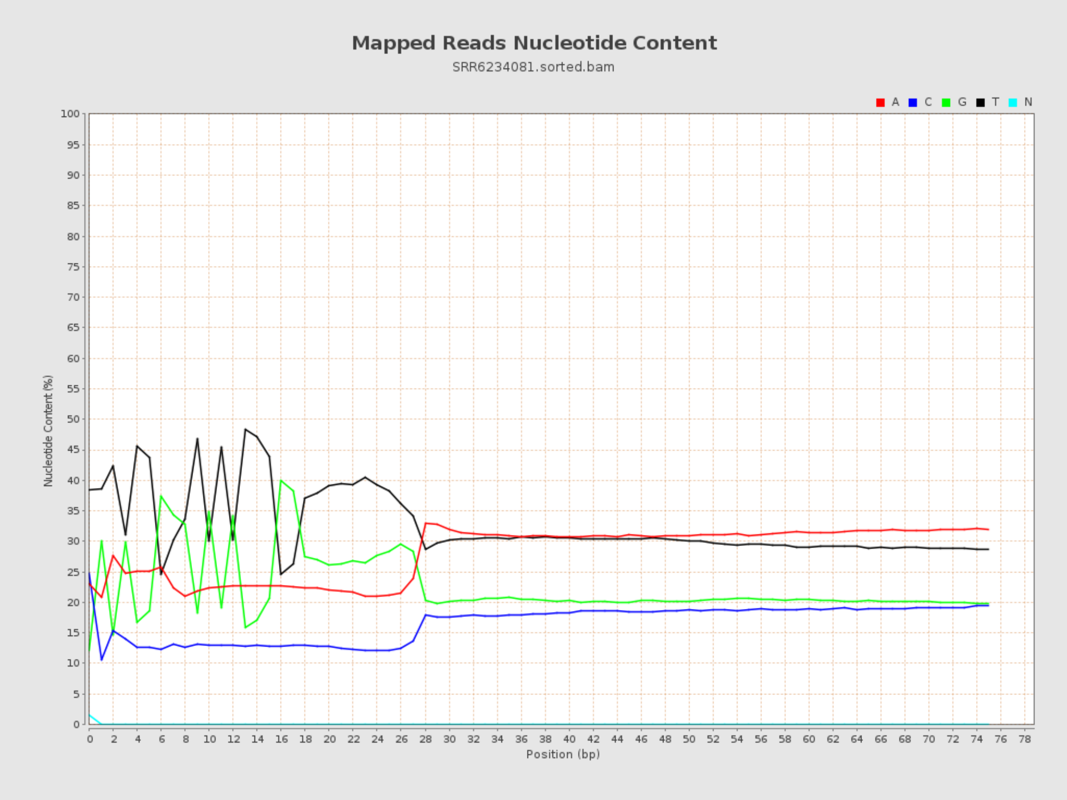
6. Results : Genome Fraction Coverage



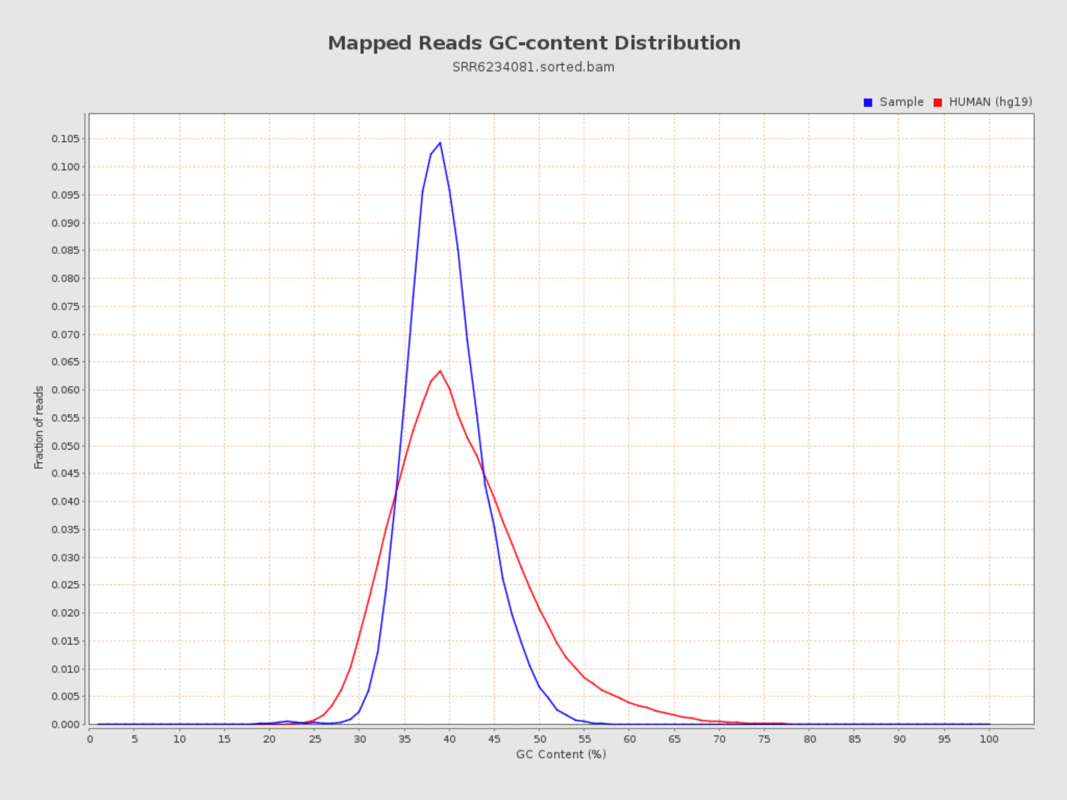
7. Results : Duplication Rate Histogram



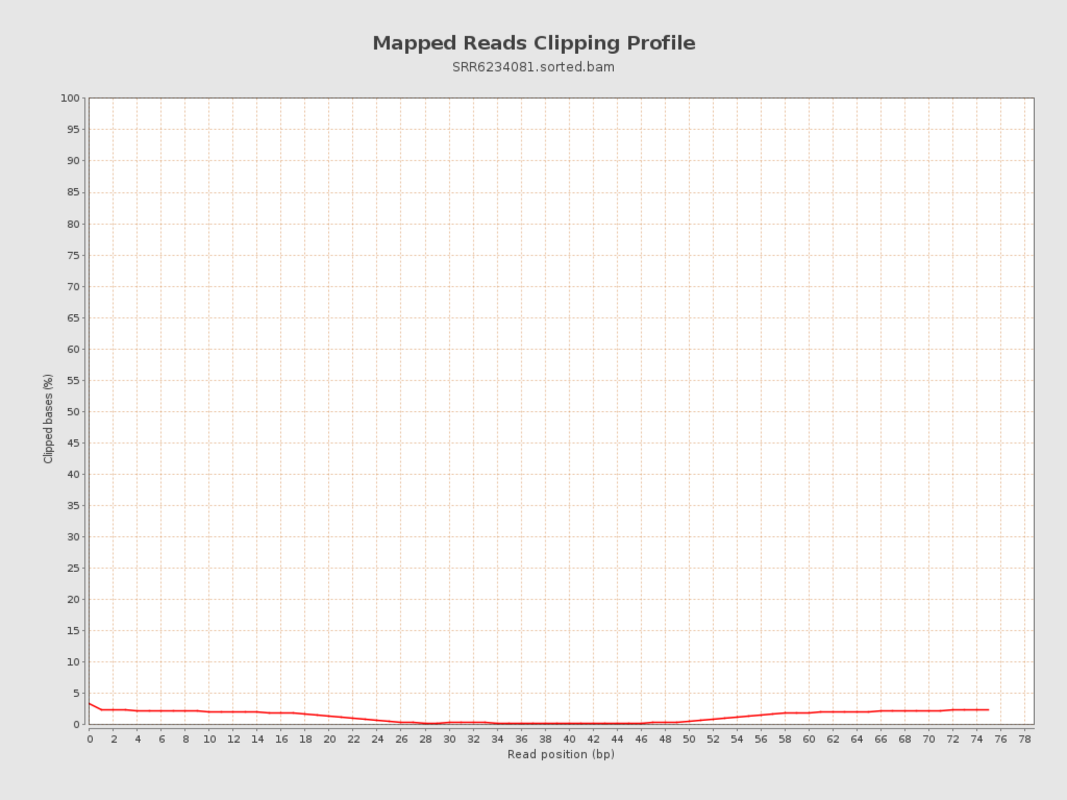
8. Results : Mapped Reads Nucleotide Content



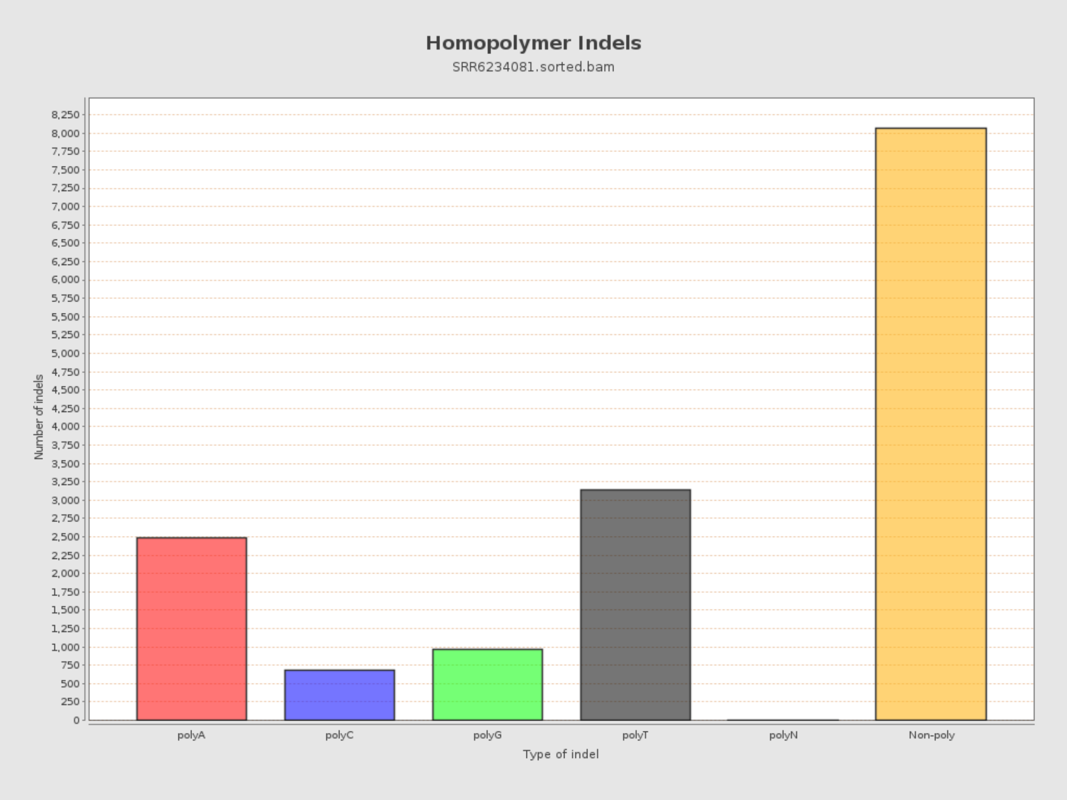
9. Results : Mapped Reads GC-content Distribution



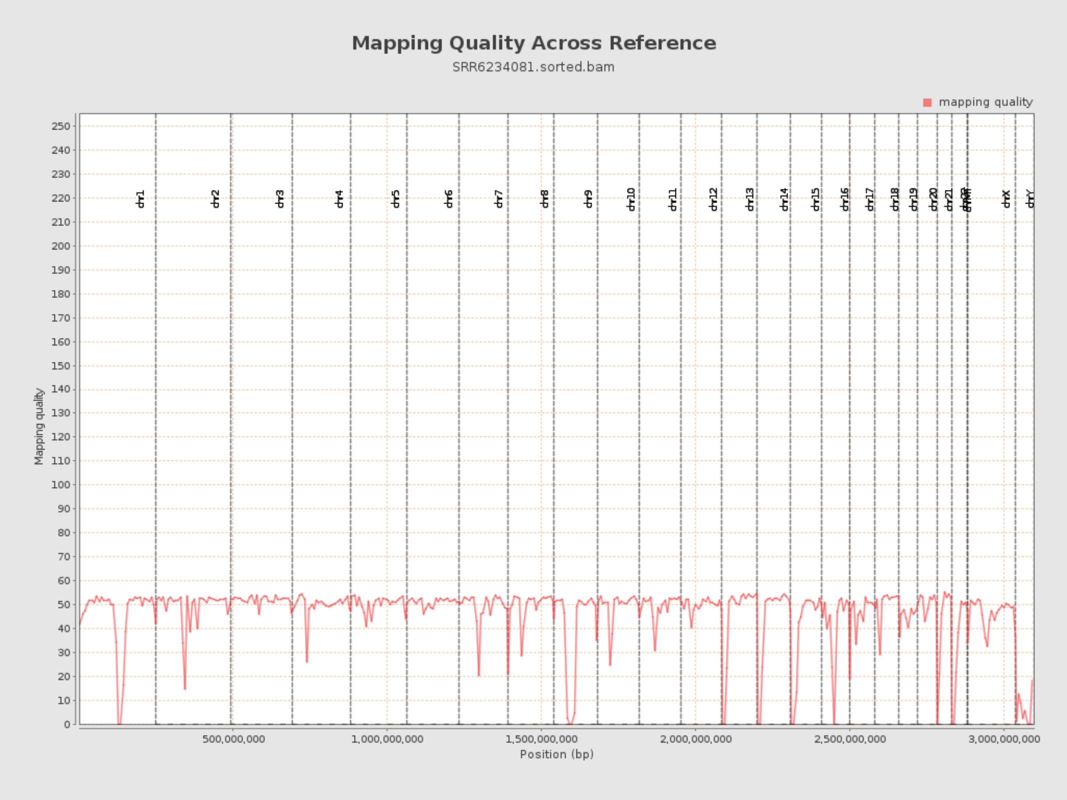
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram