Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 18:07:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234134.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_SRR6234134 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234134.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 18:07:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234134.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,501,087
Mapped reads	717,044 / 47.77%
Unmapped reads	784,043 / 52.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,498 / 0.17%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	53,259 / 3.55%
Duplication rate	5.84%
Clipped reads	533,942 / 35.57%

2.2. ACGT Content

Number/percentage of A's	10,986,372 / 26.19%
Number/percentage of C's	6,410,700 / 15.28%
Number/percentage of T's	14,136,556 / 33.7%
Number/percentage of G's	10,410,837 / 24.82%
Number/percentage of N's	6,200 / 0.01%
GC Percentage	40.1%

2.3. Coverage

Mean	0.0136

Standard Deviation	0.1712

2.4. Mapping Quality

Mean Mapping Quality	43.99

2.5. Mismatches and indels

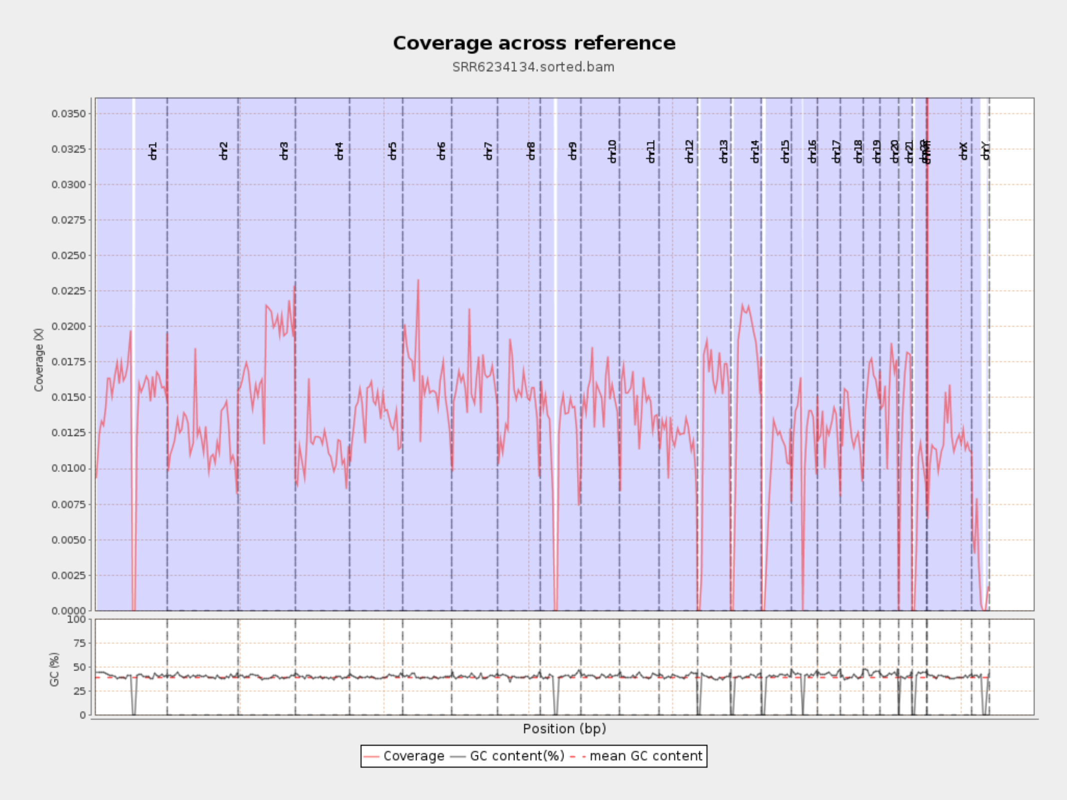
General error rate	1.13%
Mismatches	467,763
Insertions	3,700
Mapped reads with at least one insertion	0.51%
Deletions	16,955
Mapped reads with at least one deletion	2.33%
Homopolymer indels	48.05%

2.6. Chromosome stats

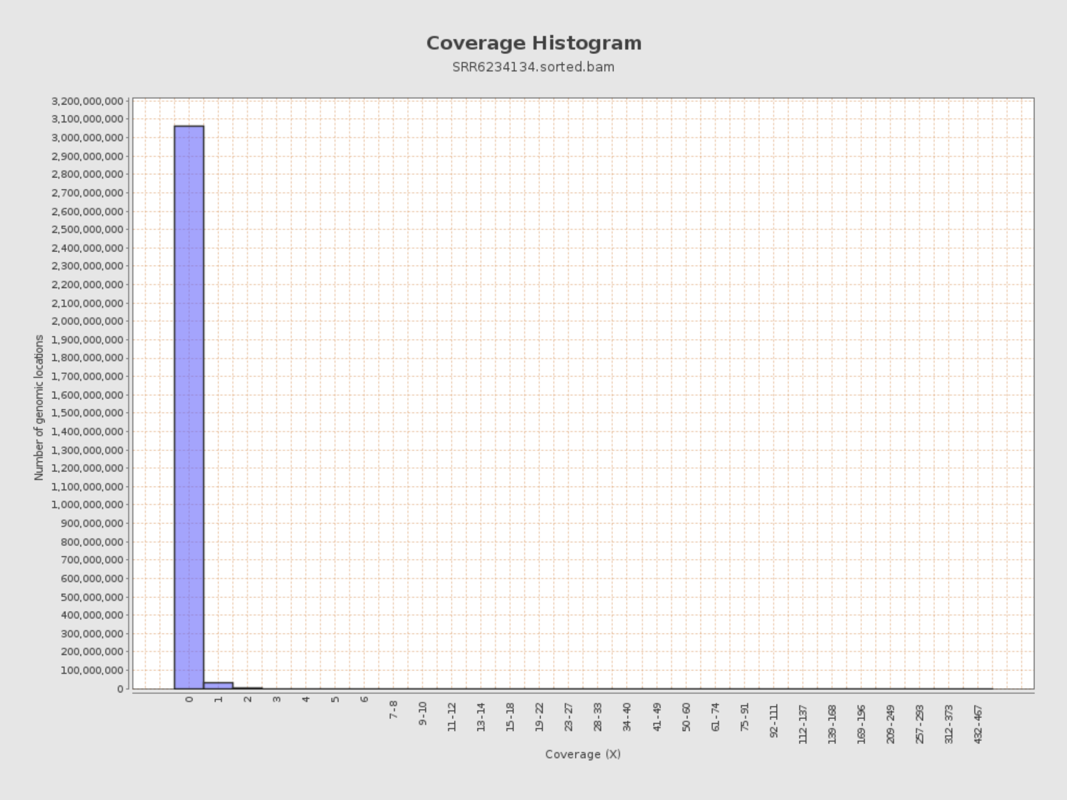
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3637136	0.0146	0.1924
chr2	243199373	2962133	0.0122	0.1668
chr3	198022430	3590265	0.0181	0.1664
chr4	191154276	2153480	0.0113	0.1316
chr5	180915260	2520474	0.0139	0.1431
chr6	171115067	2795341	0.0163	0.1745
chr7	159138663	2554944	0.0161	0.1948

chr8	146364022	2119840	0.0145	0.3014
chr9	141213431	1684932	0.0119	0.1571
chr10	135534747	2043171	0.0151	0.1645
chr11	135006516	1974960	0.0146	0.1871
chr12	133851895	1621302	0.0121	0.1305
chr13	115169878	1617903	0.014	0.1464
chr14	107349540	1745492	0.0163	0.156
chr15	102531392	947938	0.0092	0.1166
chr16	90354753	1062200	0.0118	0.1332
chr17	81195210	1007322	0.0124	0.1345
chr18	78077248	990574	0.0127	0.2748
chr19	59128983	936995	0.0158	0.1633
chr20	63025520	953625	0.0151	0.1607
chr21	48129895	662578	0.0138	0.1415
chr22	51304566	372783	0.0073	0.1005
chrMT	16571	31357	1.8923	2.4356
chrX	155270560	1834565	0.0118	0.1382
chrY	59373566	159251	0.0027	0.065

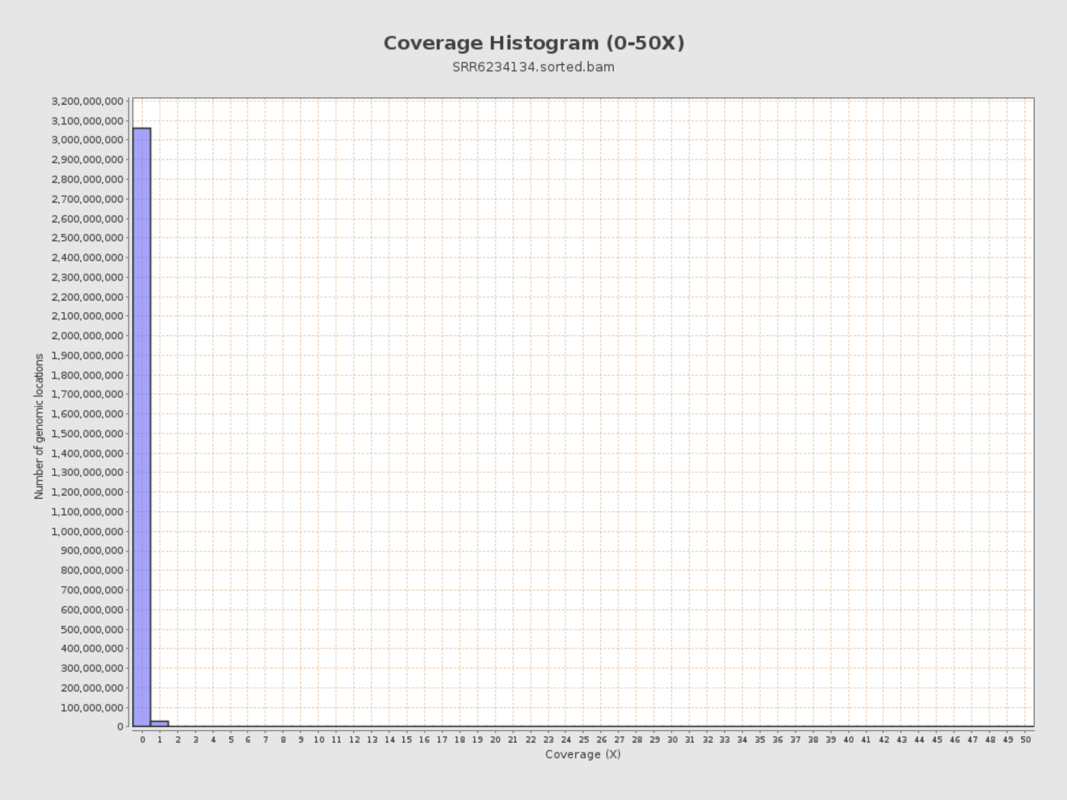
3. Results : Coverage across reference



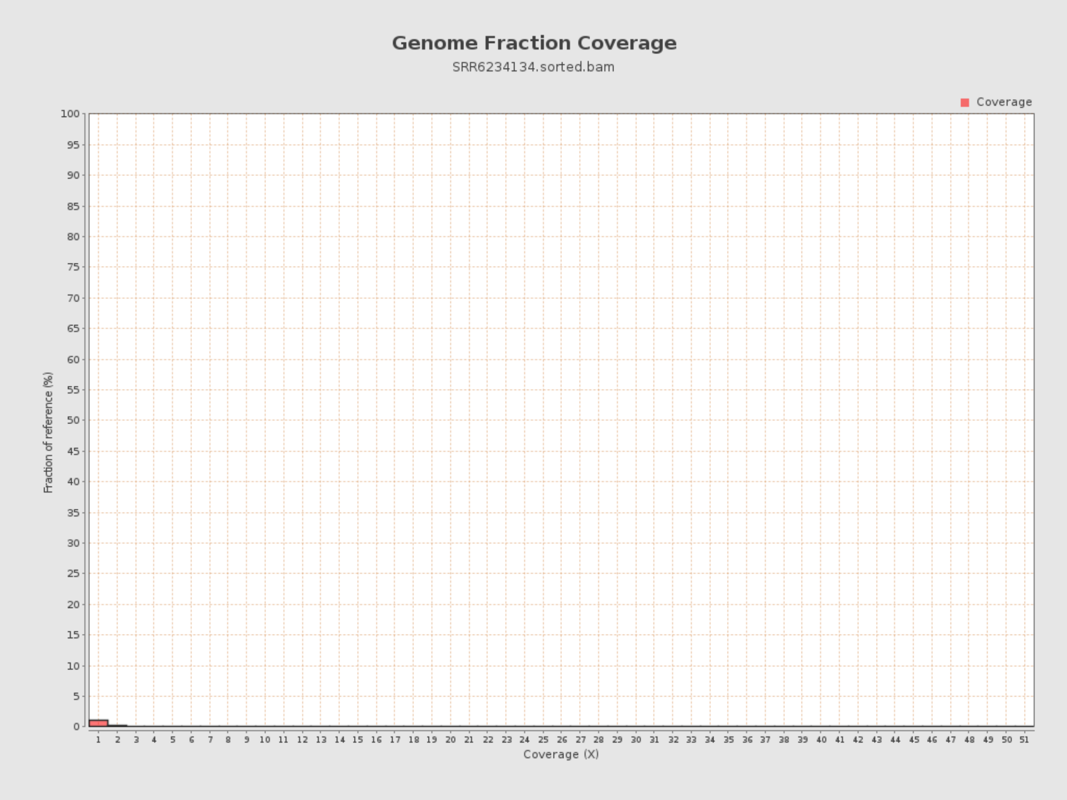
4. Results : Coverage Histogram



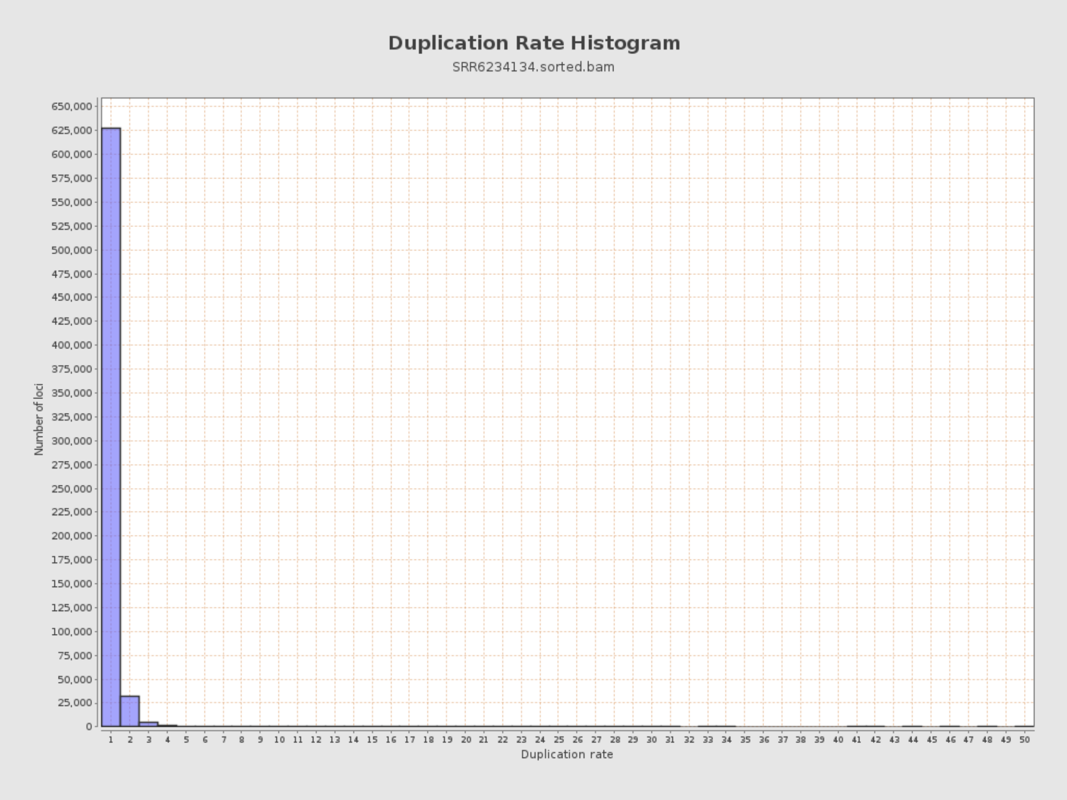
5. Results : Coverage Histogram (0-50X)



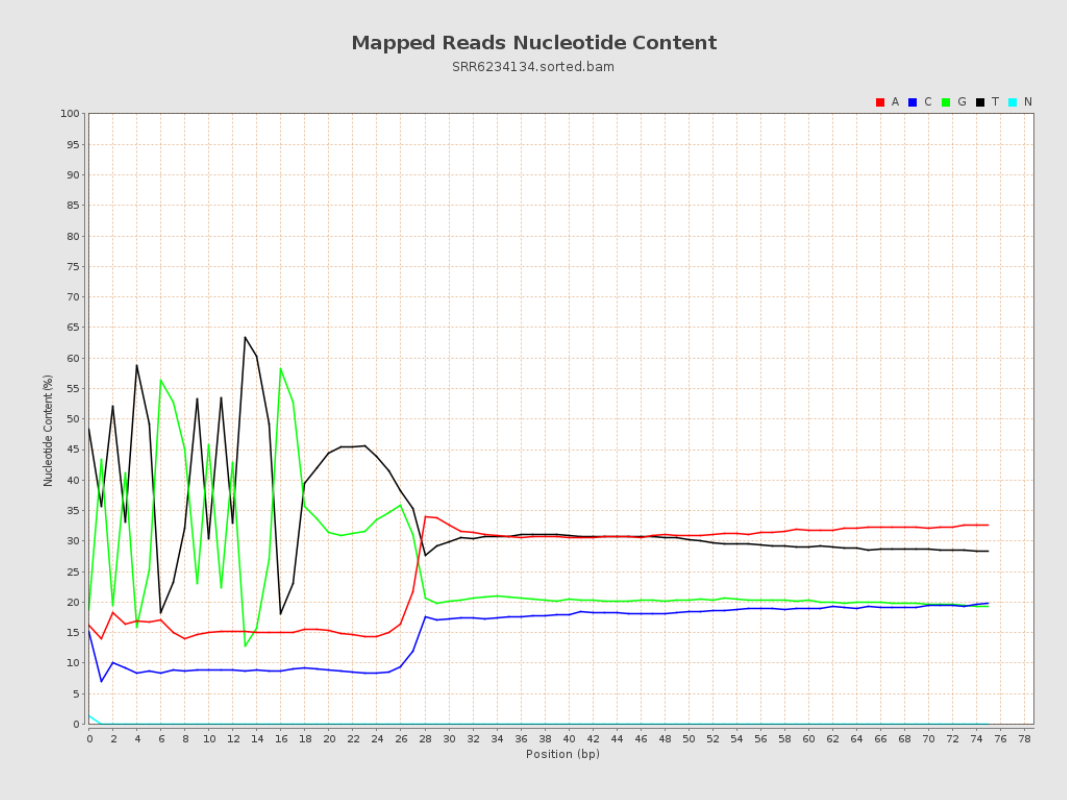
6. Results : Genome Fraction Coverage



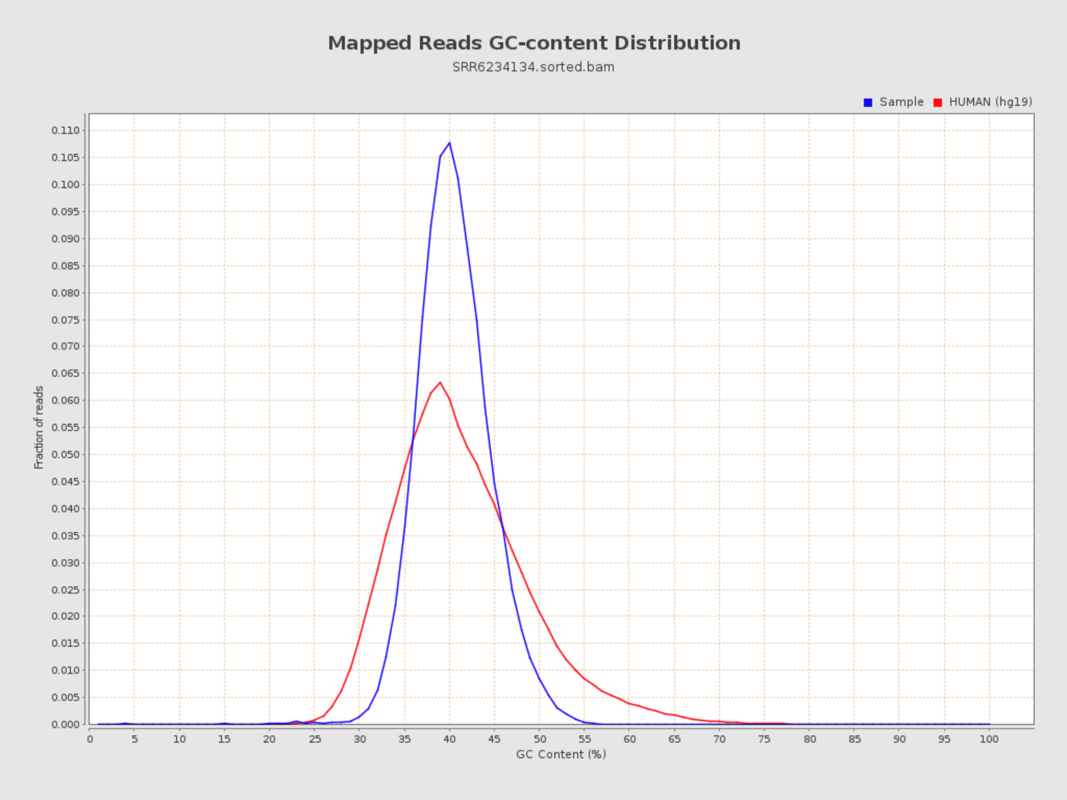
7. Results : Duplication Rate Histogram



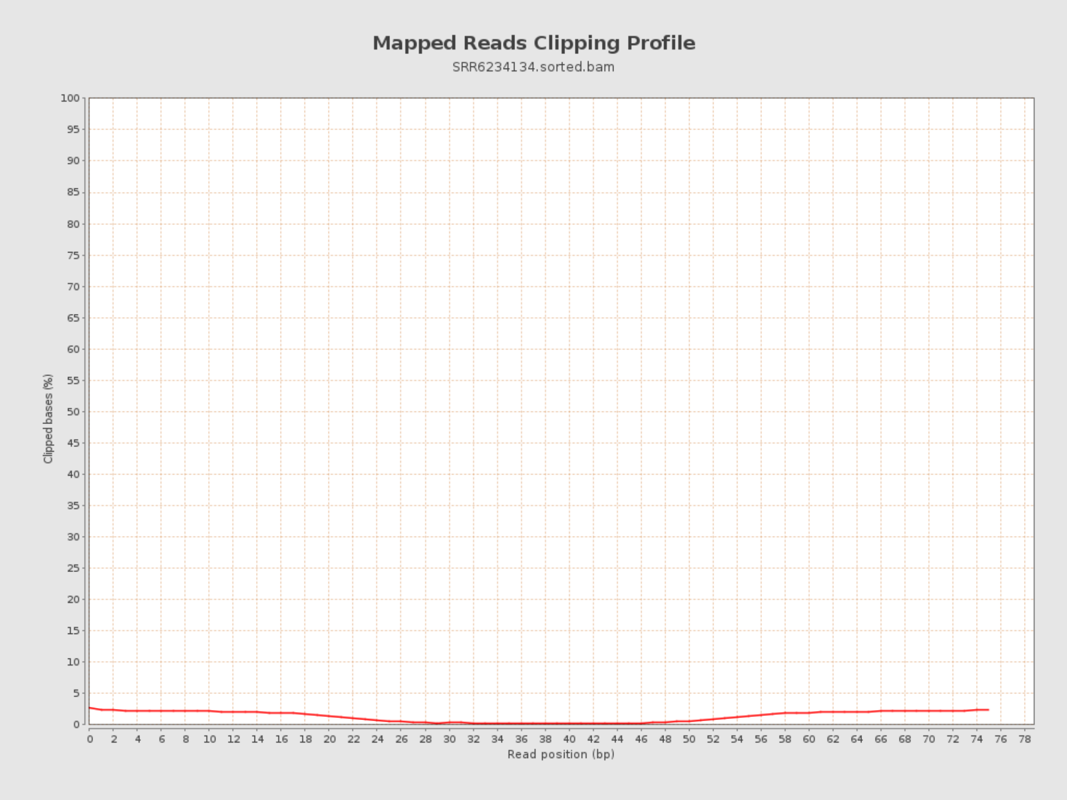
8. Results : Mapped Reads Nucleotide Content



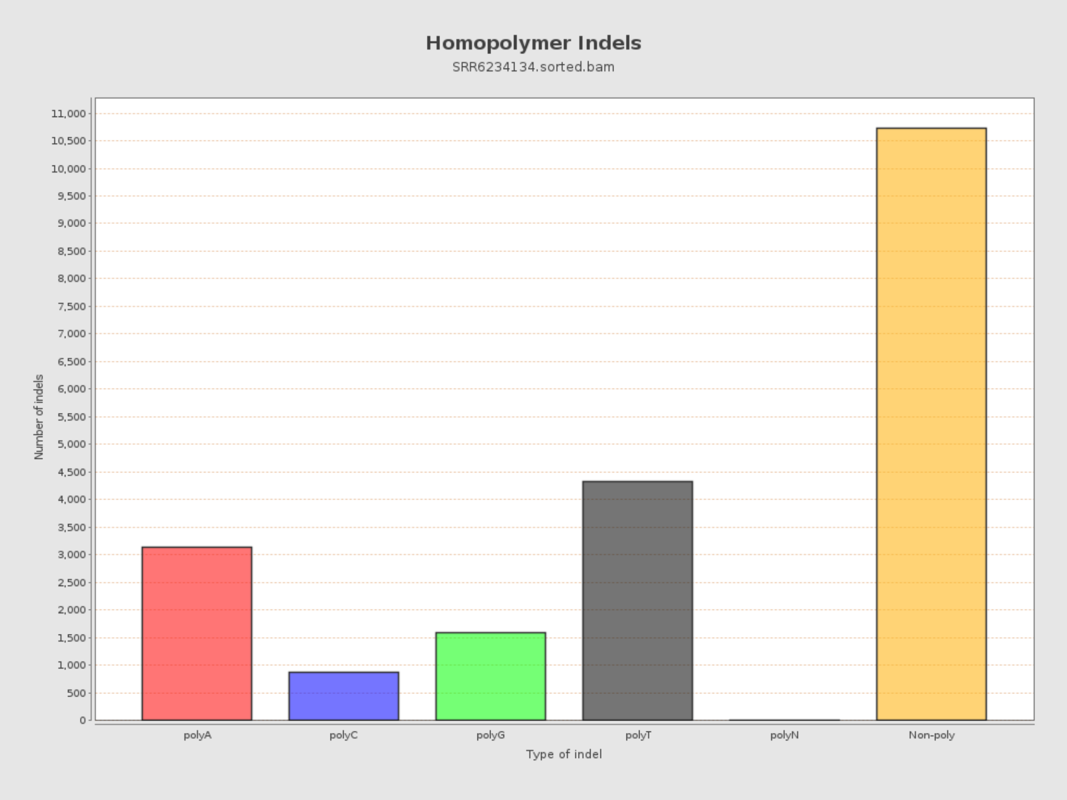
9. Results : Mapped Reads GC-content Distribution



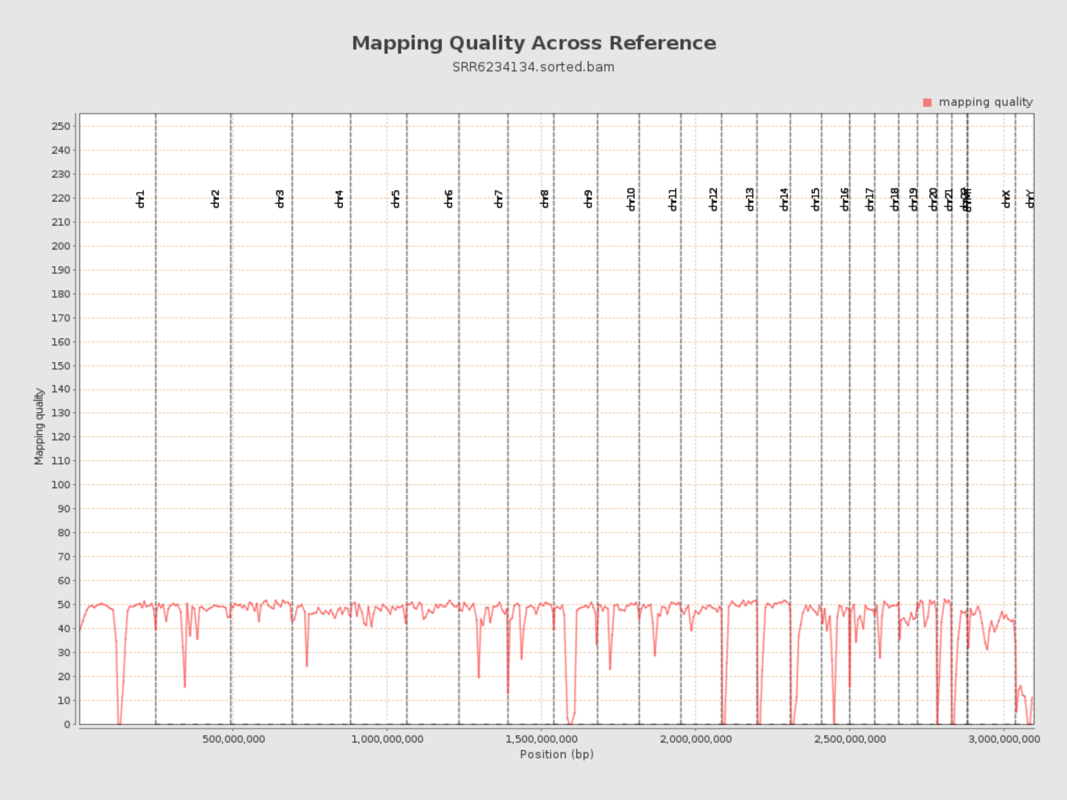
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram