Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 15:03:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234091.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_SRR6234091 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234091.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 15:03:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234091.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,576,018
Mapped reads	959,072 / 60.85%
Unmapped reads	616,946 / 39.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,433 / 0.85%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	71,431 / 4.53%
Duplication rate	6.32%
Clipped reads	558,134 / 35.41%

2.2. ACGT Content

Number/percentage of A's	16,299,329 / 26.82%
Number/percentage of C's	11,305,072 / 18.61%
Number/percentage of T's	19,228,021 / 31.64%
Number/percentage of G's	13,919,184 / 22.91%
Number/percentage of N's	10,379 / 0.02%
GC Percentage	41.51%

2.3. Coverage

Mean	0.0196

Standard Deviation	0.212

2.4. Mapping Quality

Mean Mapping Quality	43.31

2.5. Mismatches and indels

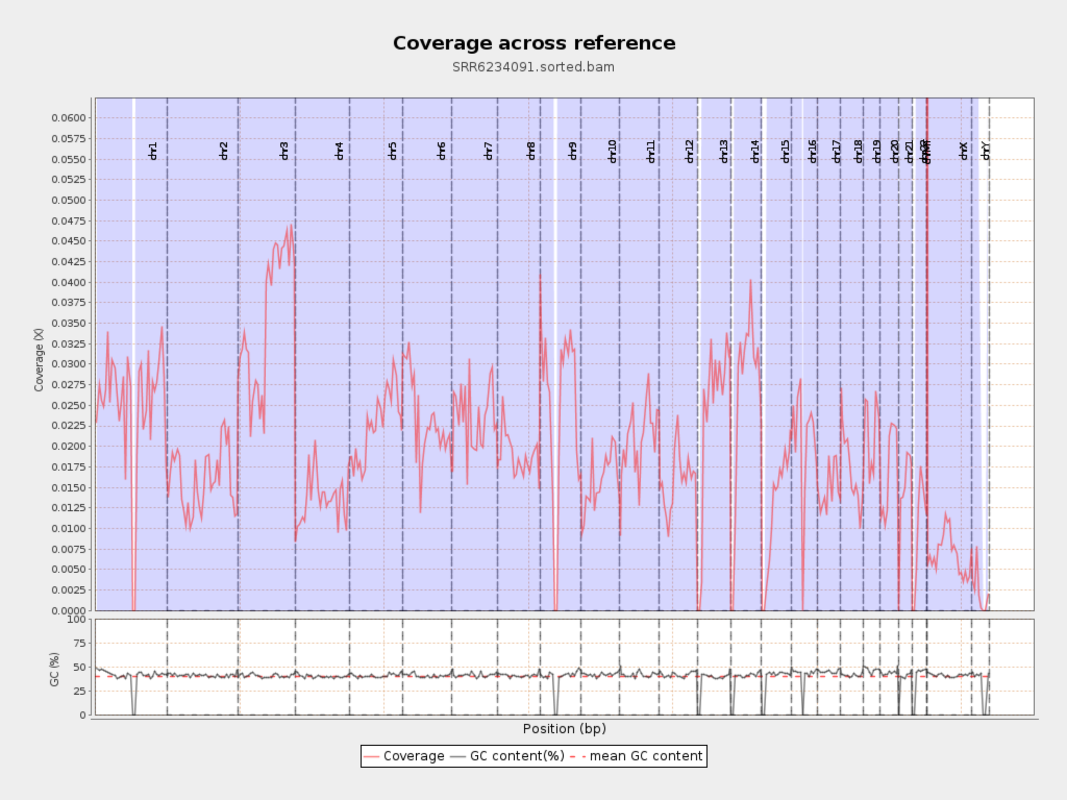
General error rate	0.87%
Mismatches	522,821
Insertions	4,621
Mapped reads with at least one insertion	0.48%
Deletions	25,867
Mapped reads with at least one deletion	2.65%
Homopolymer indels	42.27%

2.6. Chromosome stats

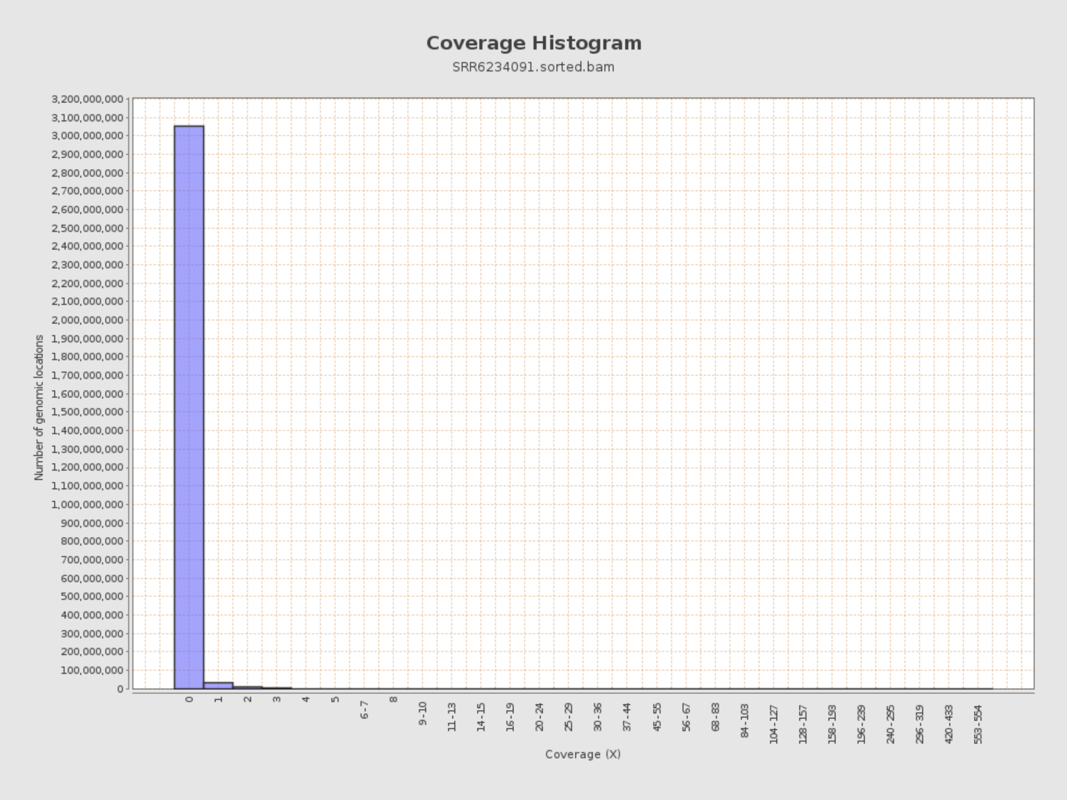
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6180128	0.0248	0.2792
chr2	243199373	3851637	0.0158	0.2807
chr3	198022430	7106015	0.0359	0.246
chr4	191154276	2601785	0.0136	0.1512
chr5	180915260	4105080	0.0227	0.1949
chr6	171115067	3974149	0.0232	0.2108
chr7	159138663	3753087	0.0236	0.2514

chr8	146364022	2756329	0.0188	0.2464
chr9	141213431	3480672	0.0246	0.2126
chr10	135534747	2132712	0.0157	0.1849
chr11	135006516	2820350	0.0209	0.2042
chr12	133851895	2086756	0.0156	0.1629
chr13	115169878	2752719	0.0239	0.2004
chr14	107349540	2807015	0.0261	0.2105
chr15	102531392	1253599	0.0122	0.1433
chr16	90354753	1840554	0.0204	0.1861
chr17	81195210	1202549	0.0148	0.1619
chr18	78077248	1330490	0.017	0.2277
chr19	59128983	1258353	0.0213	0.2323
chr20	63025520	1071690	0.017	0.1773
chr21	48129895	711997	0.0148	0.1573
chr22	51304566	514726	0.01	0.1271
chrMT	16571	26817	1.6183	2.1233
chrX	155270560	1057334	0.0068	0.1141
chrY	59373566	130550	0.0022	0.0642

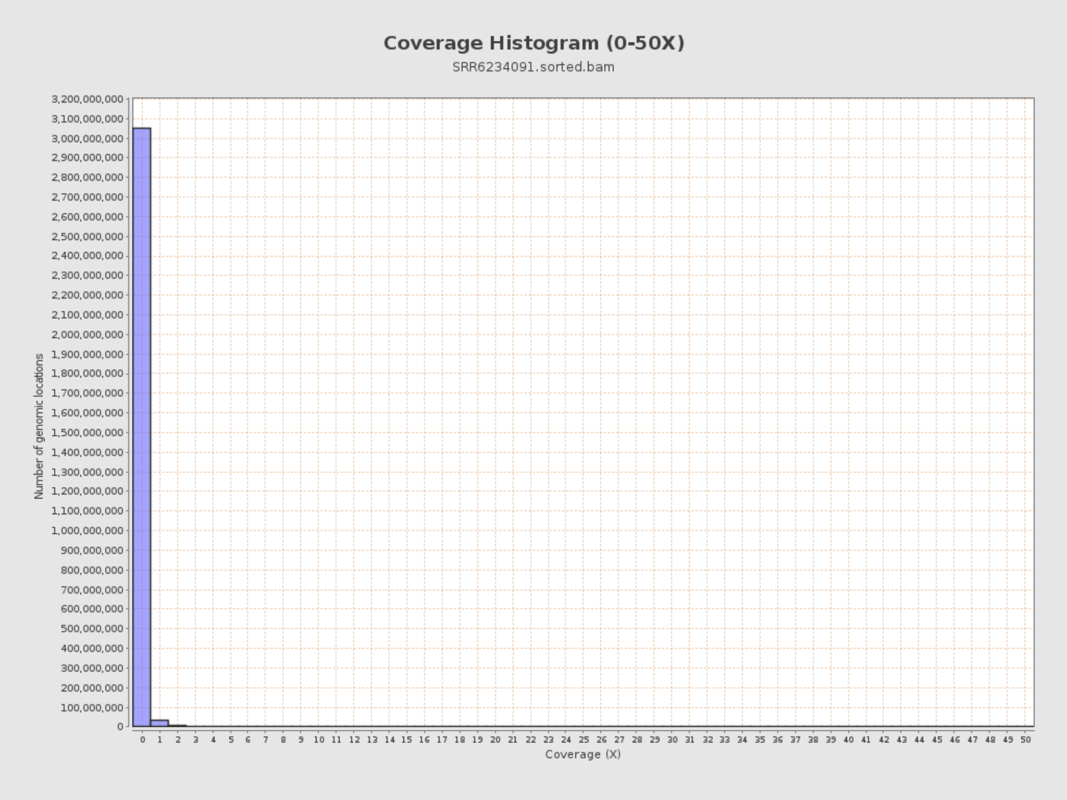
3. Results : Coverage across reference



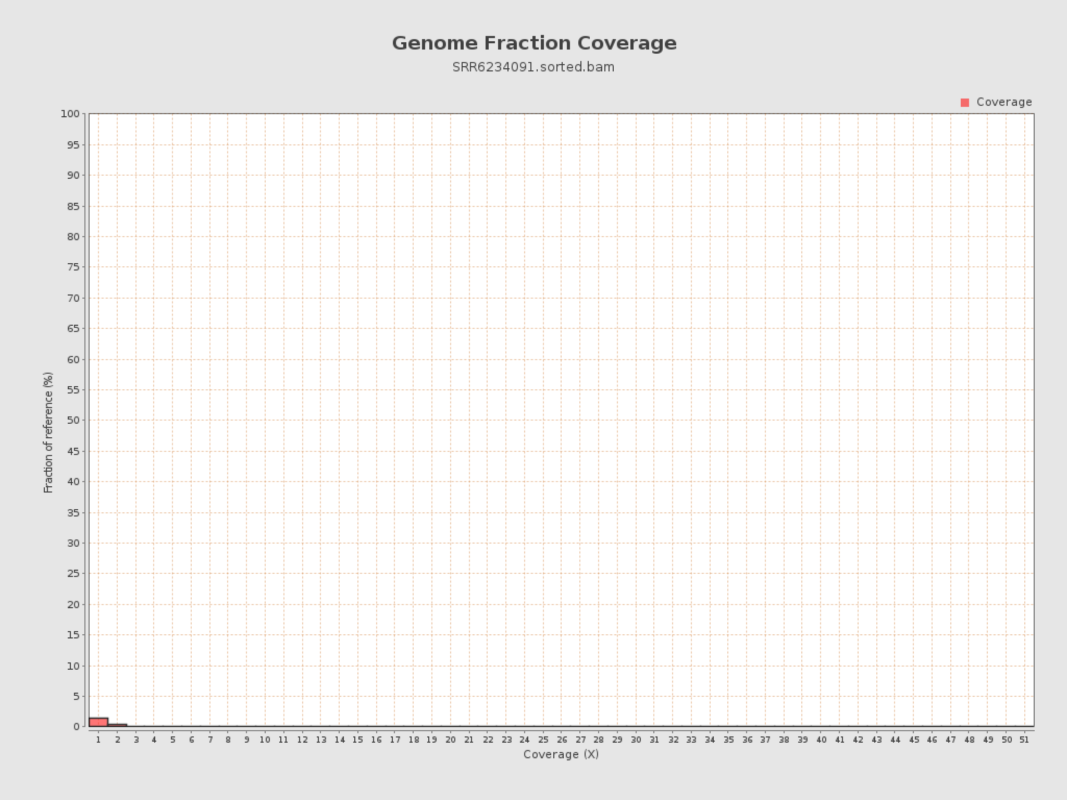
4. Results : Coverage Histogram



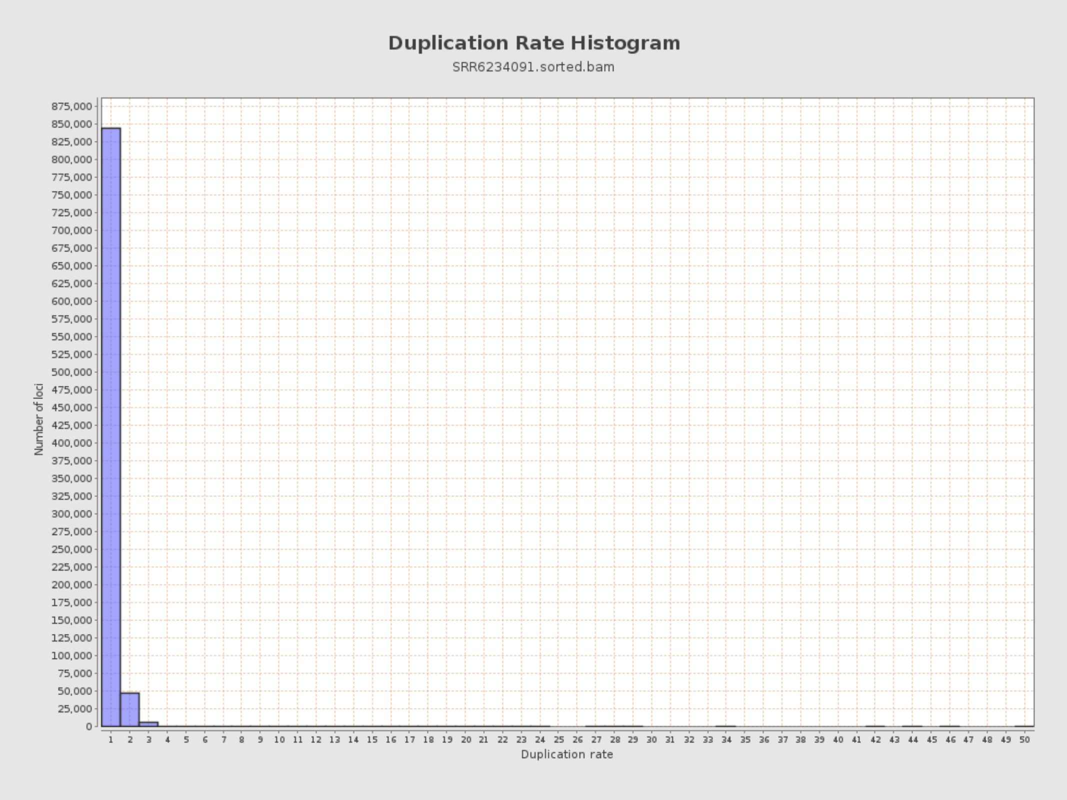
5. Results : Coverage Histogram (0-50X)



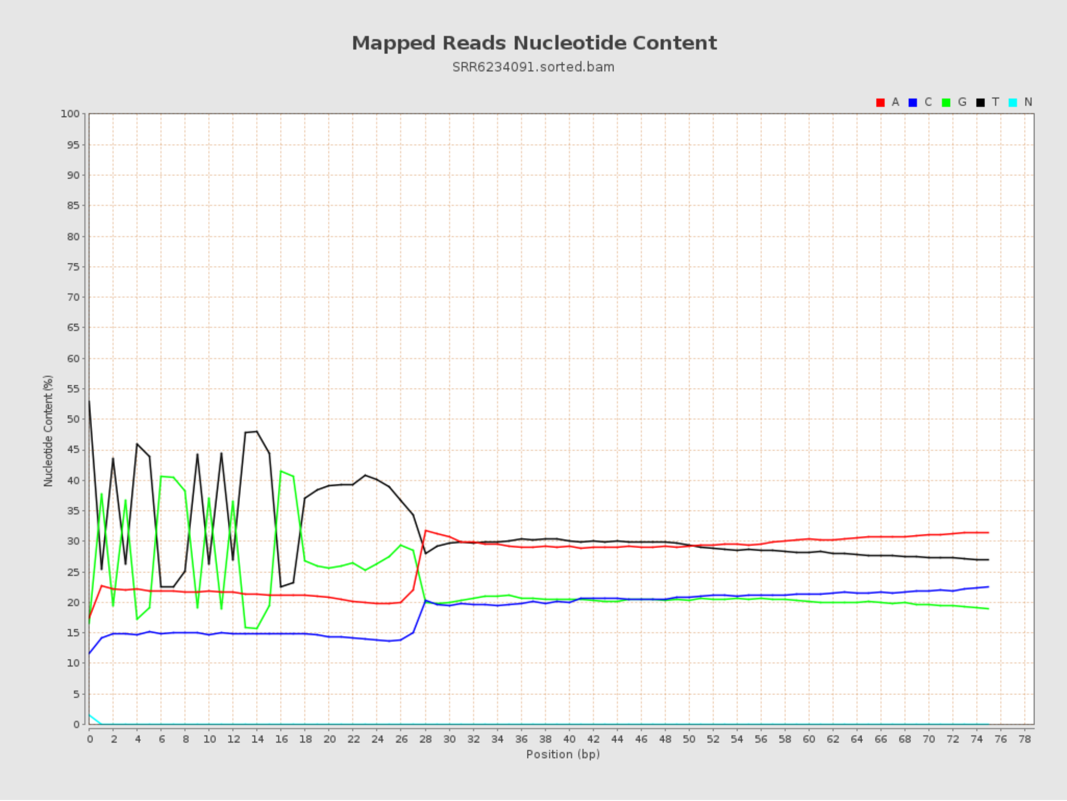
6. Results : Genome Fraction Coverage



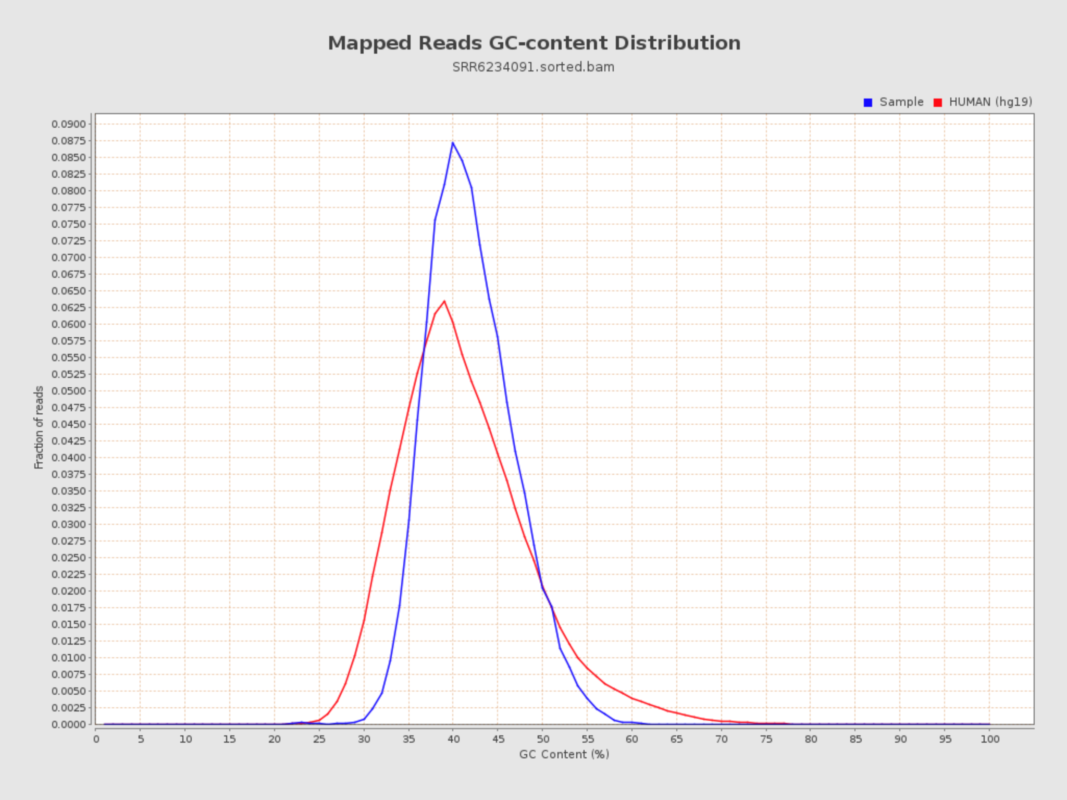
7. Results : Duplication Rate Histogram



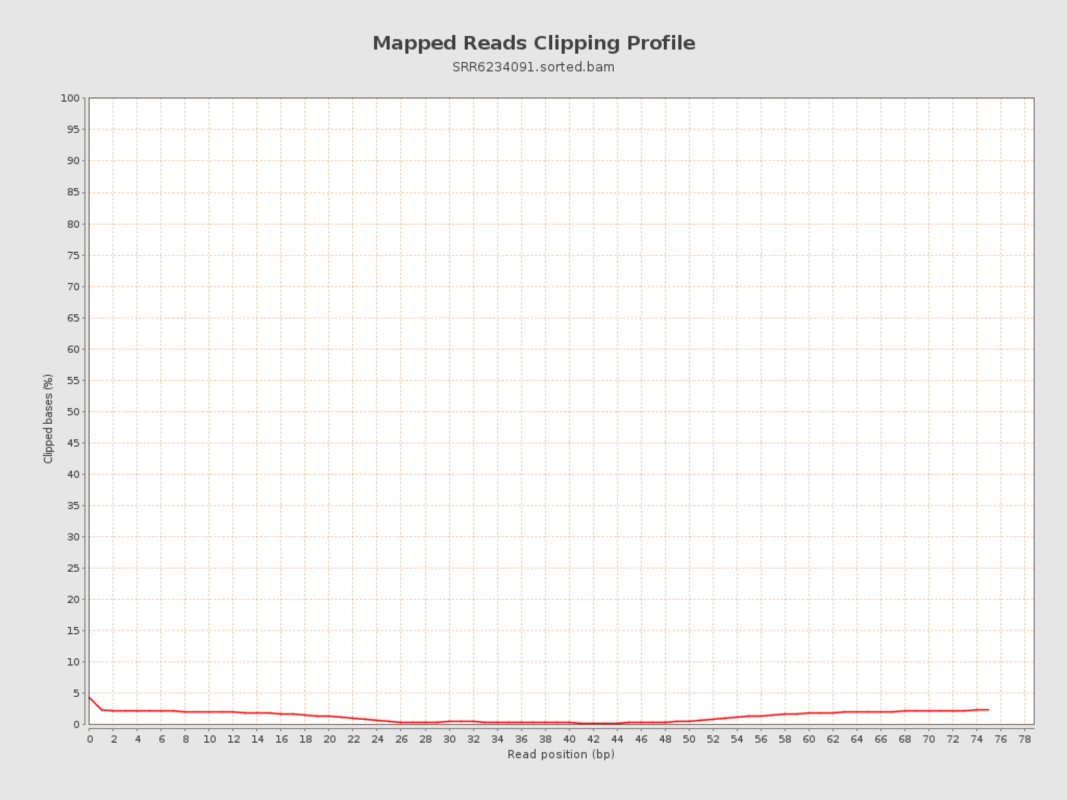
8. Results : Mapped Reads Nucleotide Content



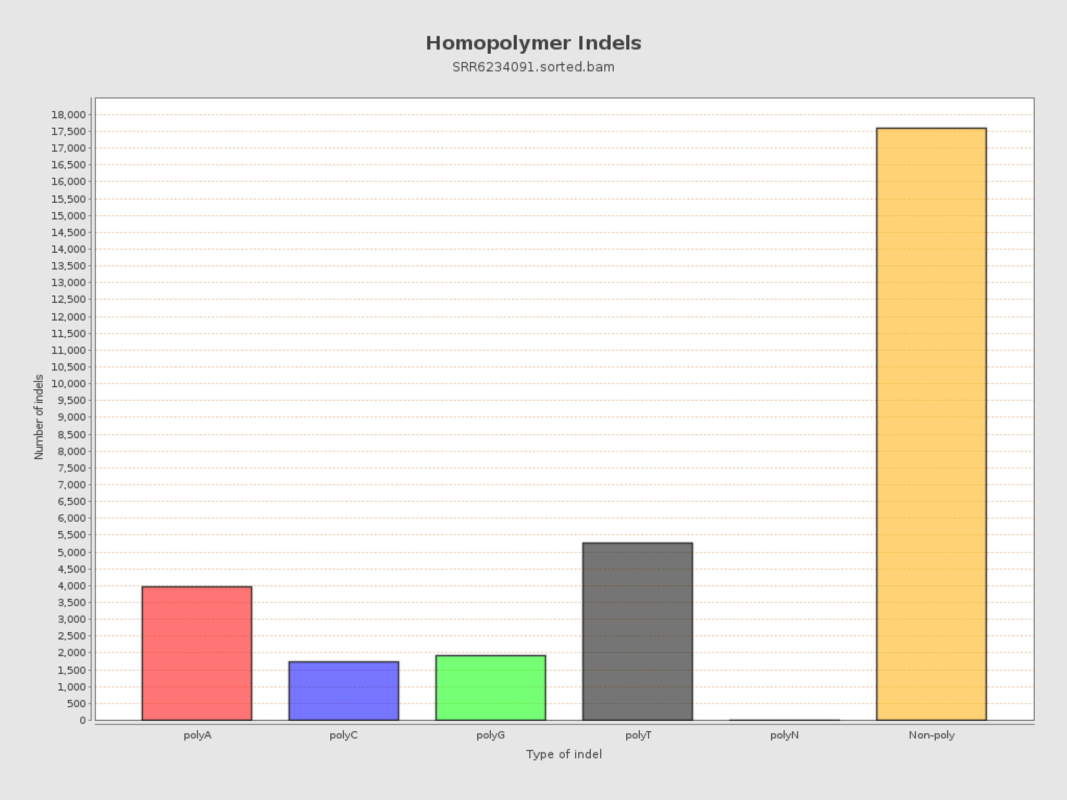
9. Results : Mapped Reads GC-content Distribution



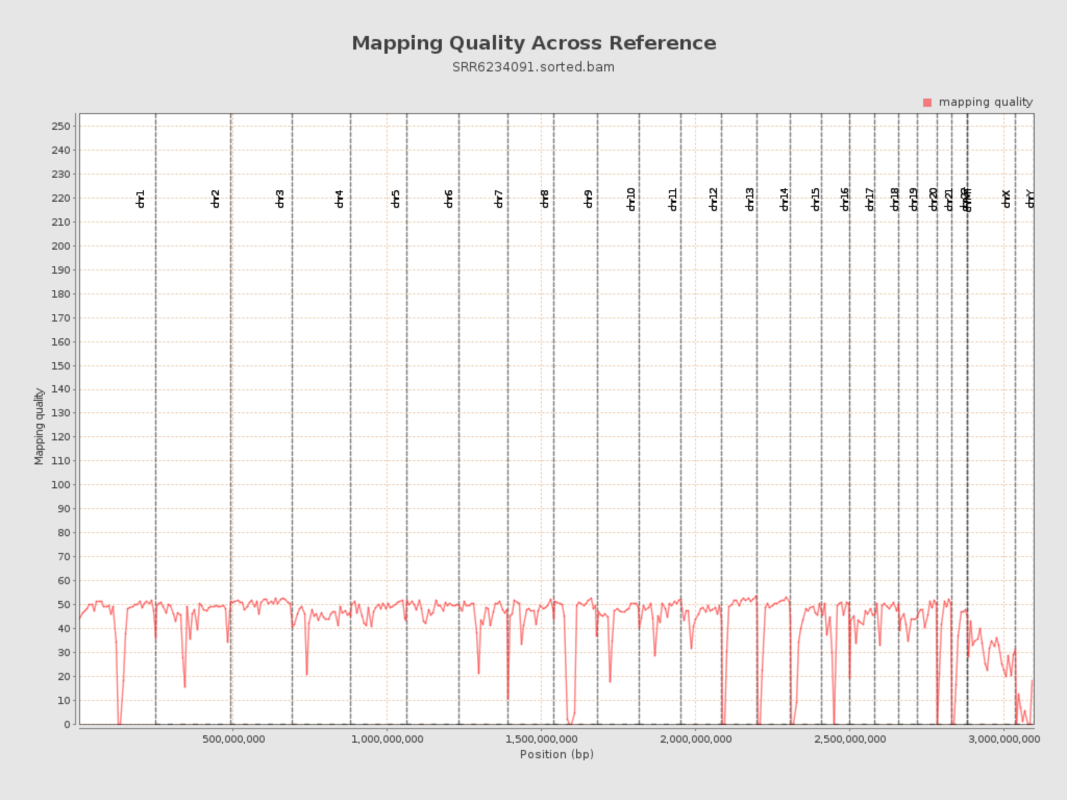
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram