Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 11:25:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234034.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_SRR6234034 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234034.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 11:25:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234034.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,873,701
Mapped reads	1,468,421 / 78.37%
Unmapped reads	405,280 / 21.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,253 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	66,044 / 3.52%
Duplication rate	3.7%
Clipped reads	668,702 / 35.69%

2.2. ACGT Content

Number/percentage of A's	26,832,153 / 27.61%
Number/percentage of C's	18,079,000 / 18.6%
Number/percentage of T's	30,812,127 / 31.7%
Number/percentage of G's	21,436,967 / 22.06%
Number/percentage of N's	25,764 / 0.03%
GC Percentage	40.66%

2.3. Coverage

Mean	0.0314

Standard Deviation	0.2788

2.4. Mapping Quality

Mean Mapping Quality	45.48

2.5. Mismatches and indels

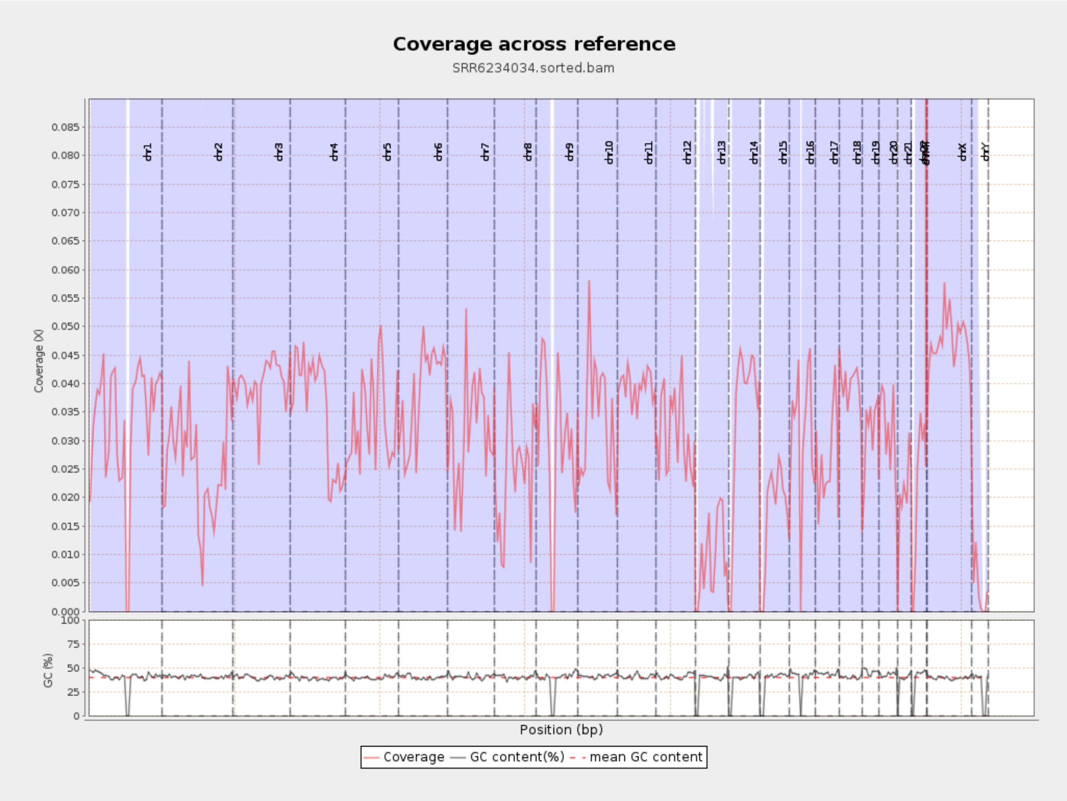
General error rate	0.77%
Mismatches	737,720
Insertions	7,121
Mapped reads with at least one insertion	0.48%
Deletions	30,699
Mapped reads with at least one deletion	2.06%
Homopolymer indels	45.34%

2.6. Chromosome stats

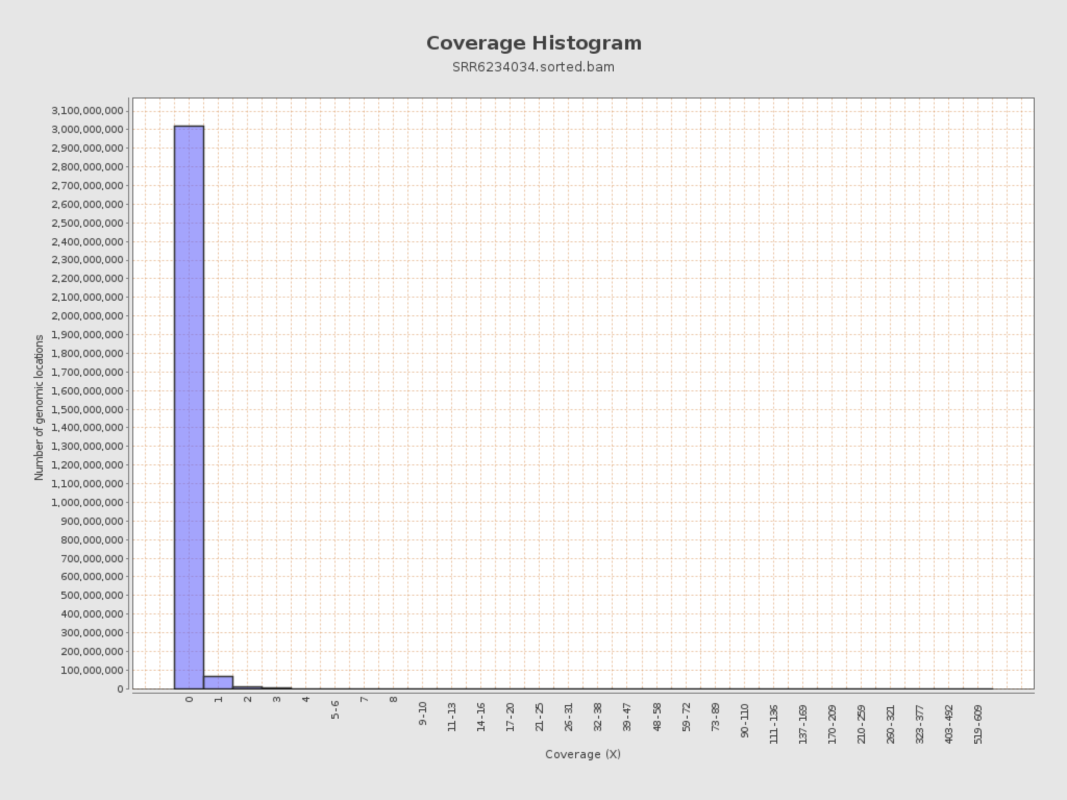
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8402947	0.0337	0.324
chr2	243199373	6285825	0.0258	0.3589
chr3	198022430	7970342	0.0402	0.2391
chr4	191154276	6781489	0.0355	0.2303
chr5	180915260	6092634	0.0337	0.2184
chr6	171115067	6571159	0.0384	0.2664
chr7	159138663	5073193	0.0319	0.4134

chr8	146364022	3570270	0.0244	0.3813
chr9	141213431	4191918	0.0297	0.2476
chr10	135534747	4550701	0.0336	0.3081
chr11	135006516	5289644	0.0392	0.2979
chr12	133851895	4193267	0.0313	0.2127
chr13	115169878	1074016	0.0093	0.1173
chr14	107349540	3699351	0.0345	0.2302
chr15	102531392	1792357	0.0175	0.1572
chr16	90354753	2861595	0.0317	0.2243
chr17	81195210	2157855	0.0266	0.2109
chr18	78077248	3121922	0.04	0.3774
chr19	59128983	1846821	0.0312	0.2991
chr20	63025520	2009862	0.0319	0.2176
chr21	48129895	990558	0.0206	0.1785
chr22	51304566	1068983	0.0208	0.1712
chrMT	16571	33693	2.0333	2.4244
chrX	155270560	7341865	0.0473	0.273
chrY	59373566	267218	0.0045	0.094

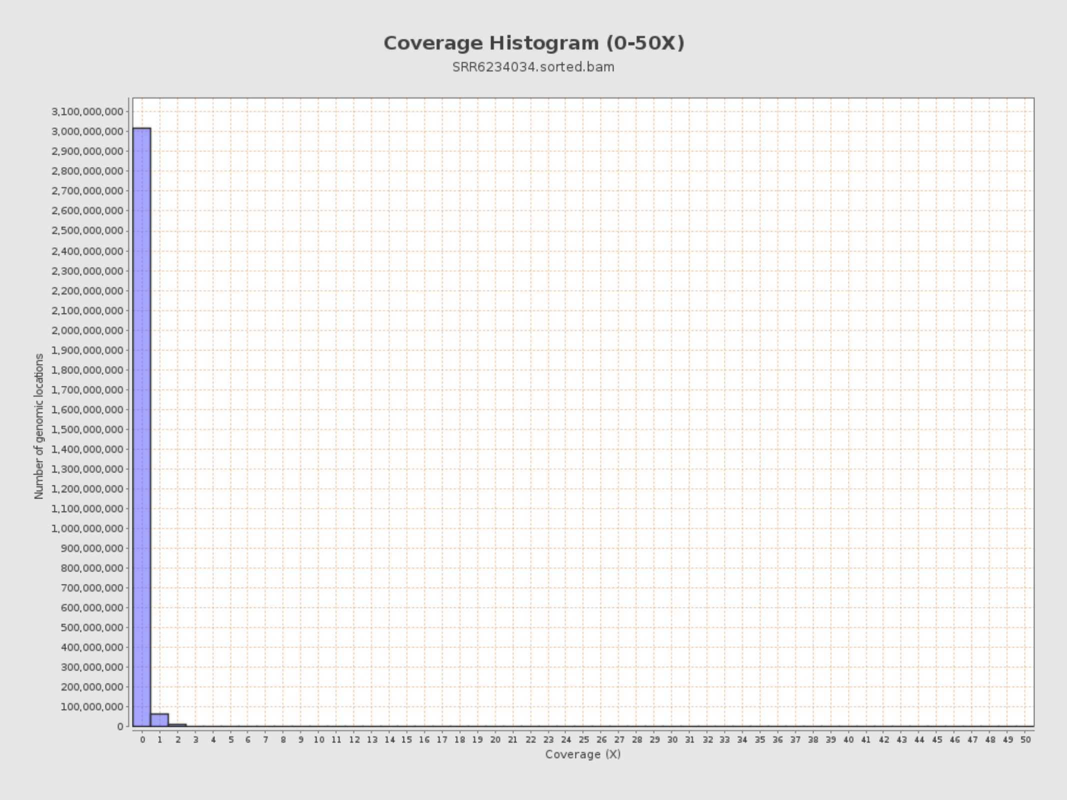
3. Results : Coverage across reference



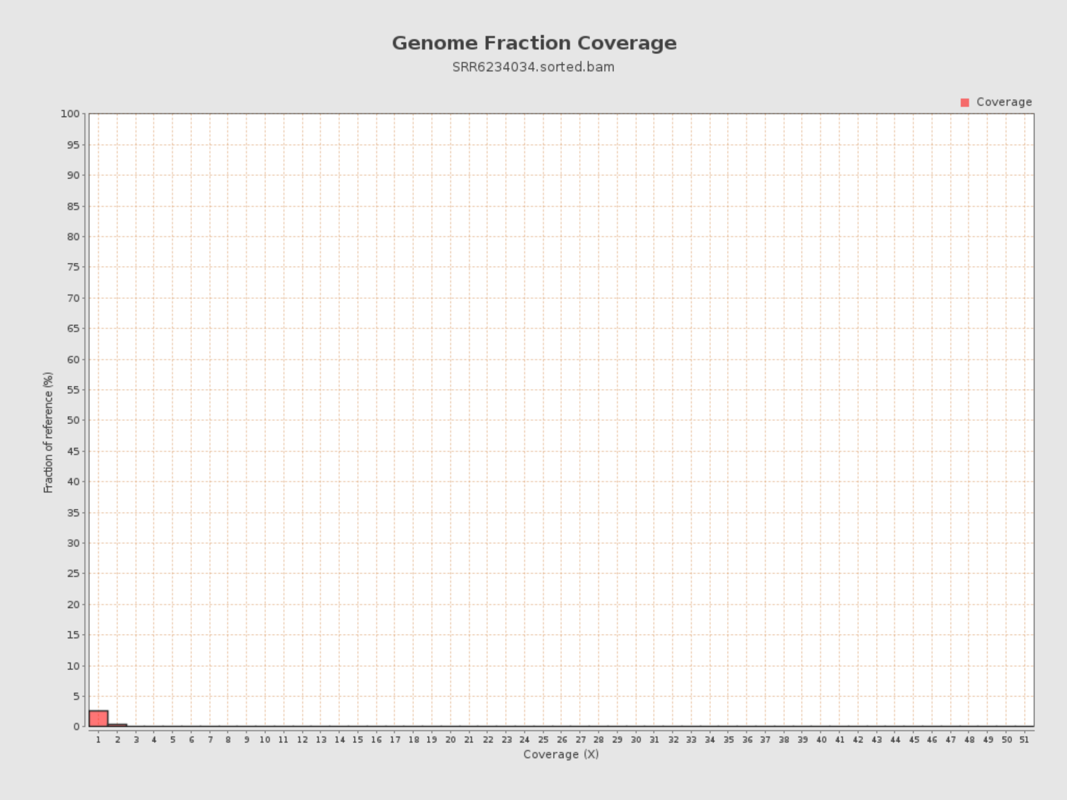
4. Results : Coverage Histogram



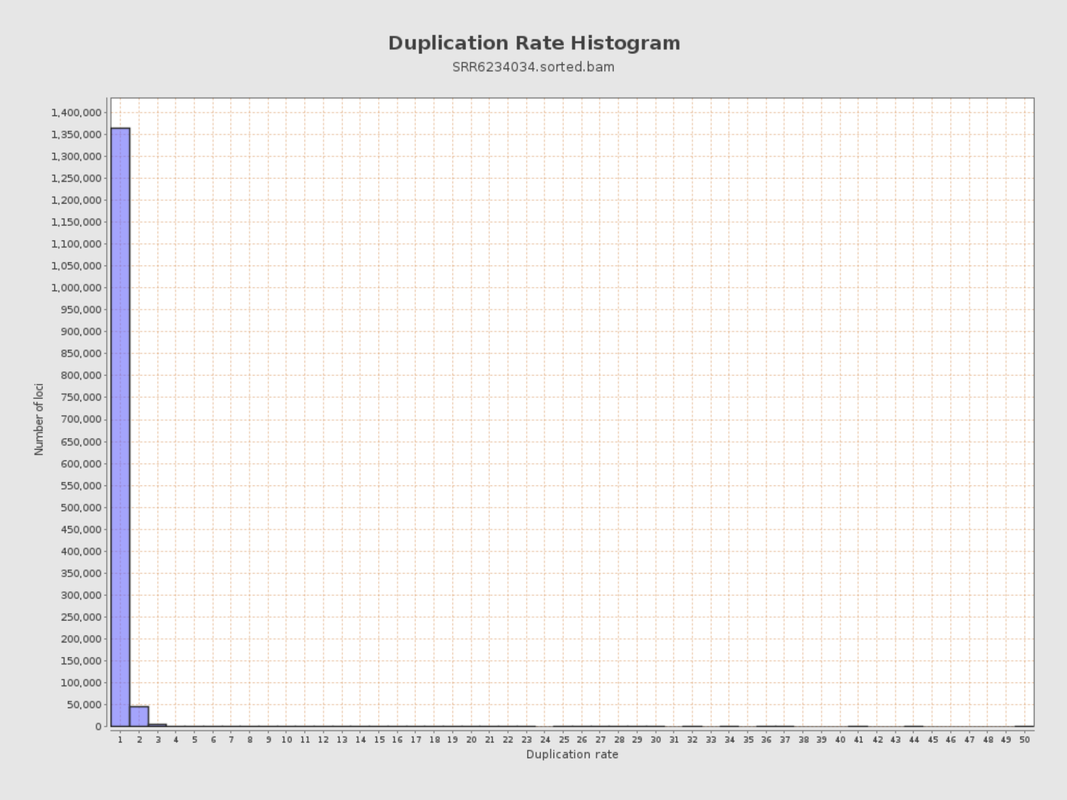
5. Results : Coverage Histogram (0-50X)



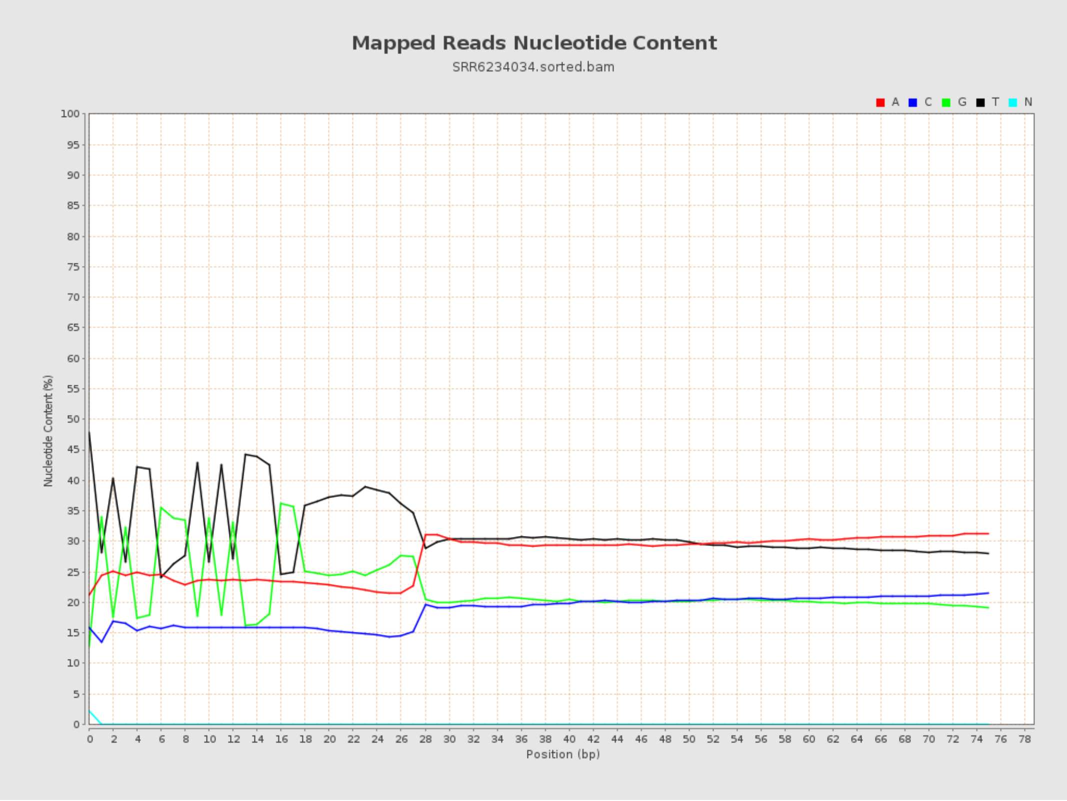
6. Results : Genome Fraction Coverage



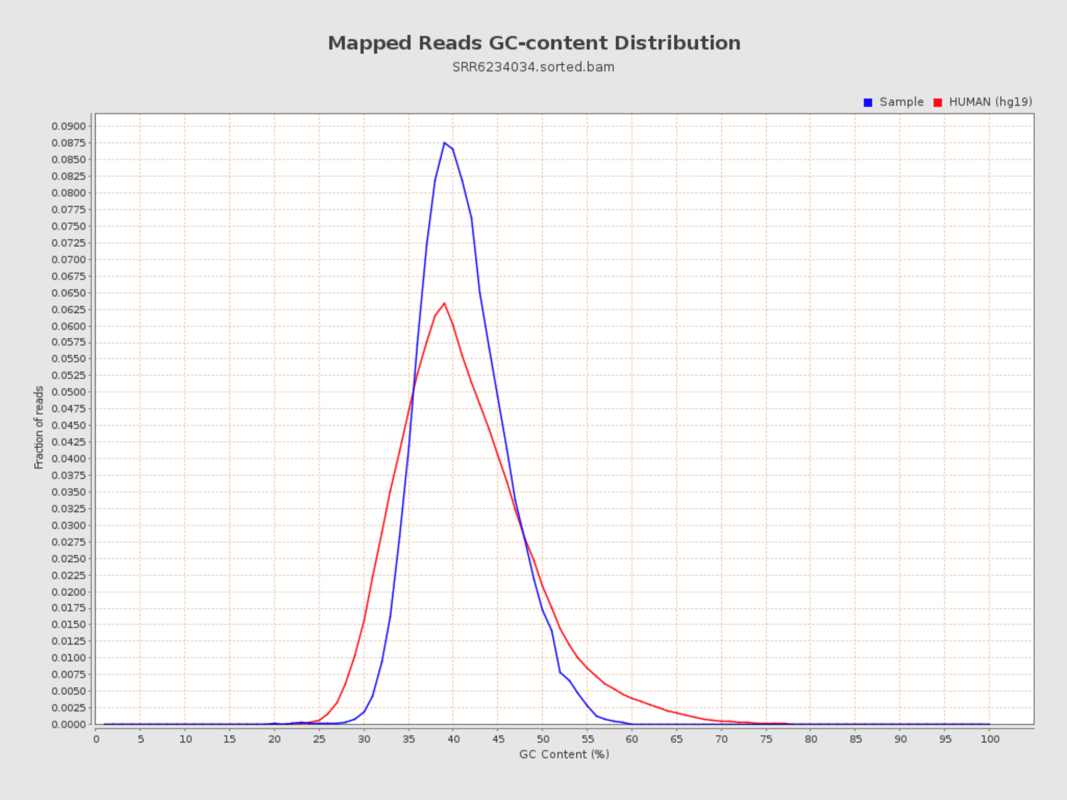
7. Results : Duplication Rate Histogram



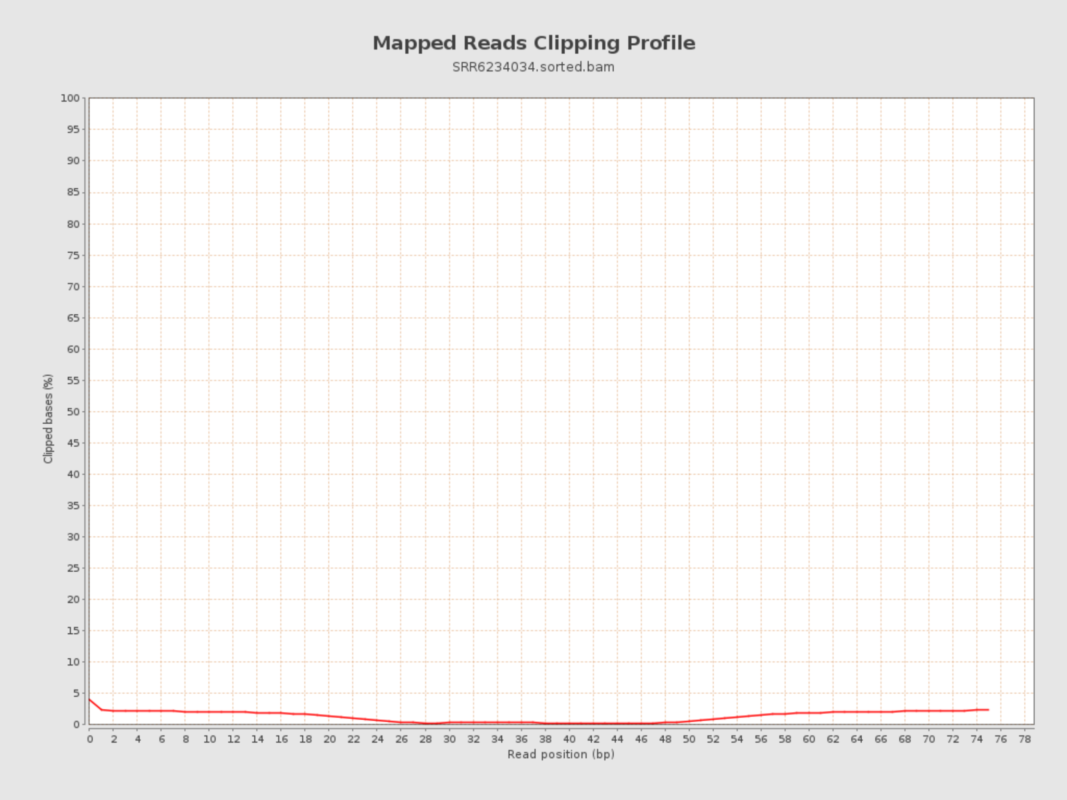
8. Results : Mapped Reads Nucleotide Content



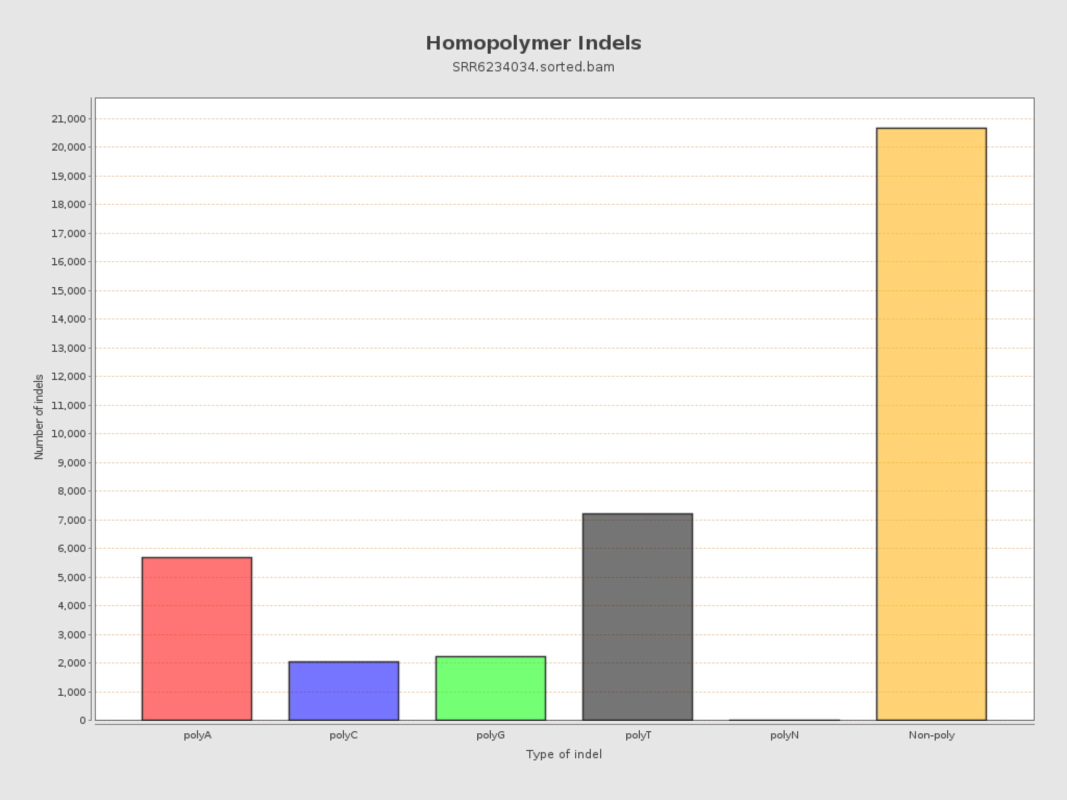
9. Results : Mapped Reads GC-content Distribution



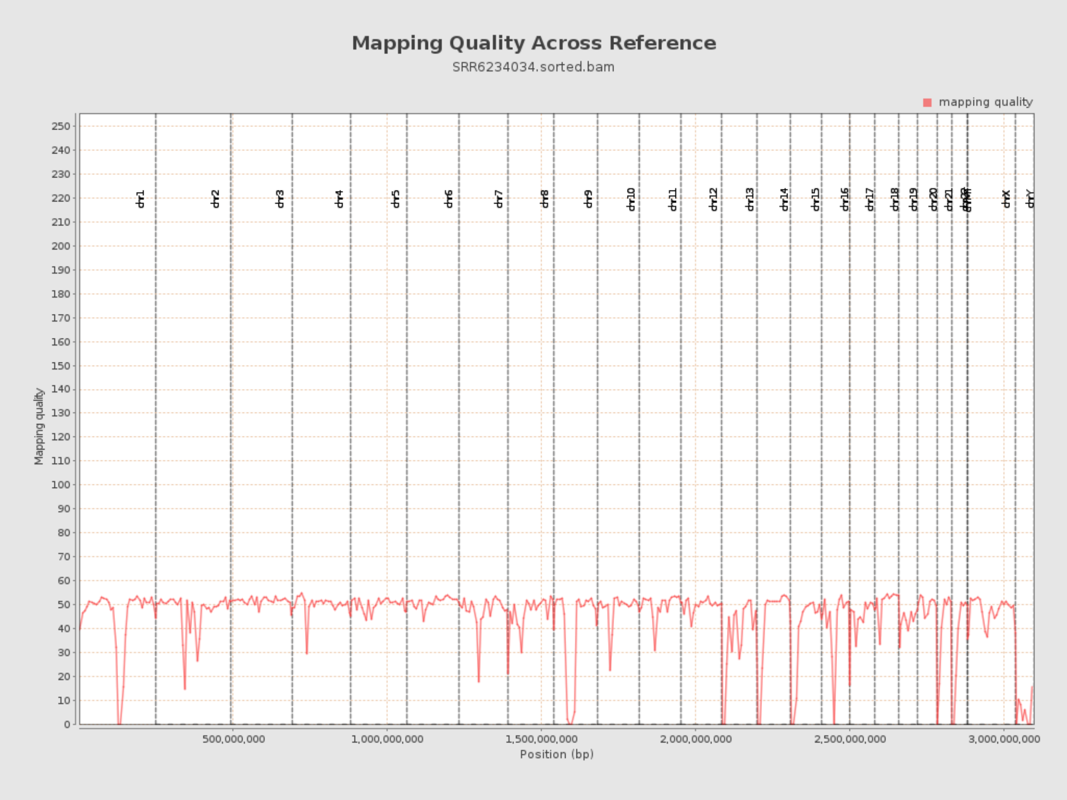
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram