Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 16:43:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234109.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_SRR6234109 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234109.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 16:43:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234109.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,405,543
Mapped reads	4,061,565 / 92.19%
Unmapped reads	343,978 / 7.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,219 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	406,883 / 9.24%
Duplication rate	8.13%
Clipped reads	2,147,120 / 48.74%

2.2. ACGT Content

Number/percentage of A's	68,819,293 / 26.27%
Number/percentage of C's	46,566,712 / 17.78%
Number/percentage of T's	85,859,198 / 32.78%
Number/percentage of G's	60,682,097 / 23.17%
Number/percentage of N's	25,107 / 0.01%
GC Percentage	40.94%

2.3. Coverage

Mean	0.0847

Standard Deviation	0.9976

2.4. Mapping Quality

Mean Mapping Quality	44.57

2.5. Mismatches and indels

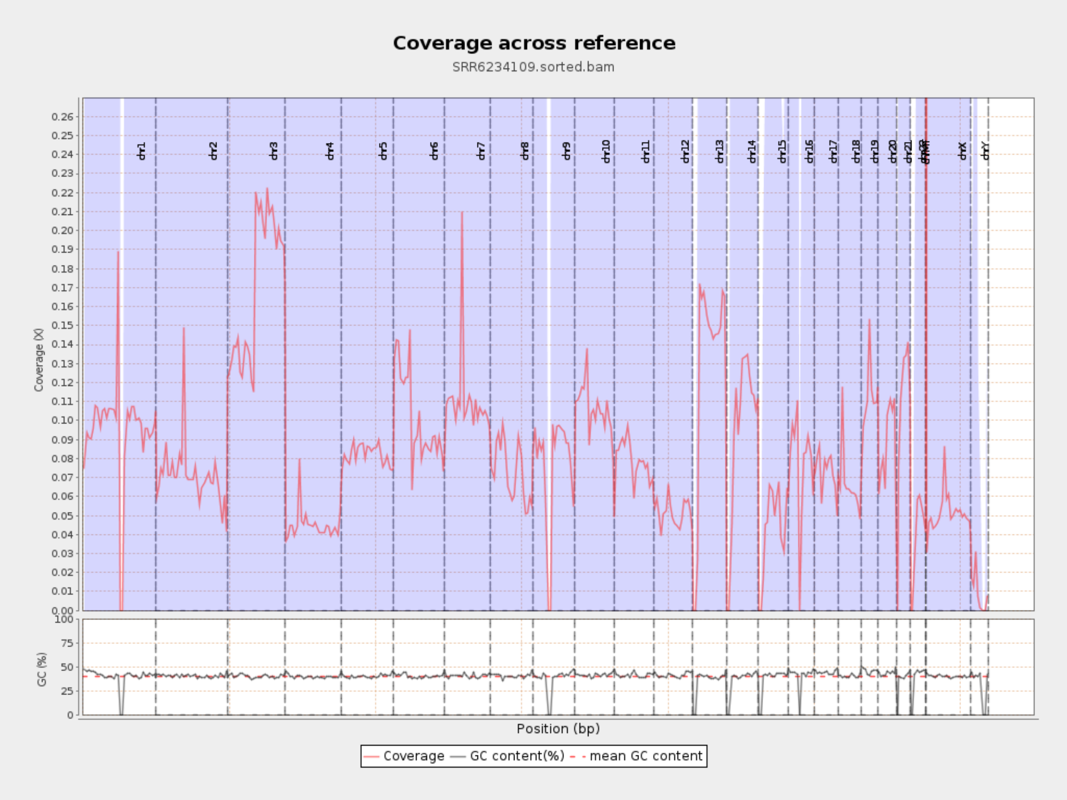
General error rate	0.58%
Mismatches	1,473,757
Insertions	17,746
Mapped reads with at least one insertion	0.43%
Deletions	61,309
Mapped reads with at least one deletion	1.49%
Homopolymer indels	44.68%

2.6. Chromosome stats

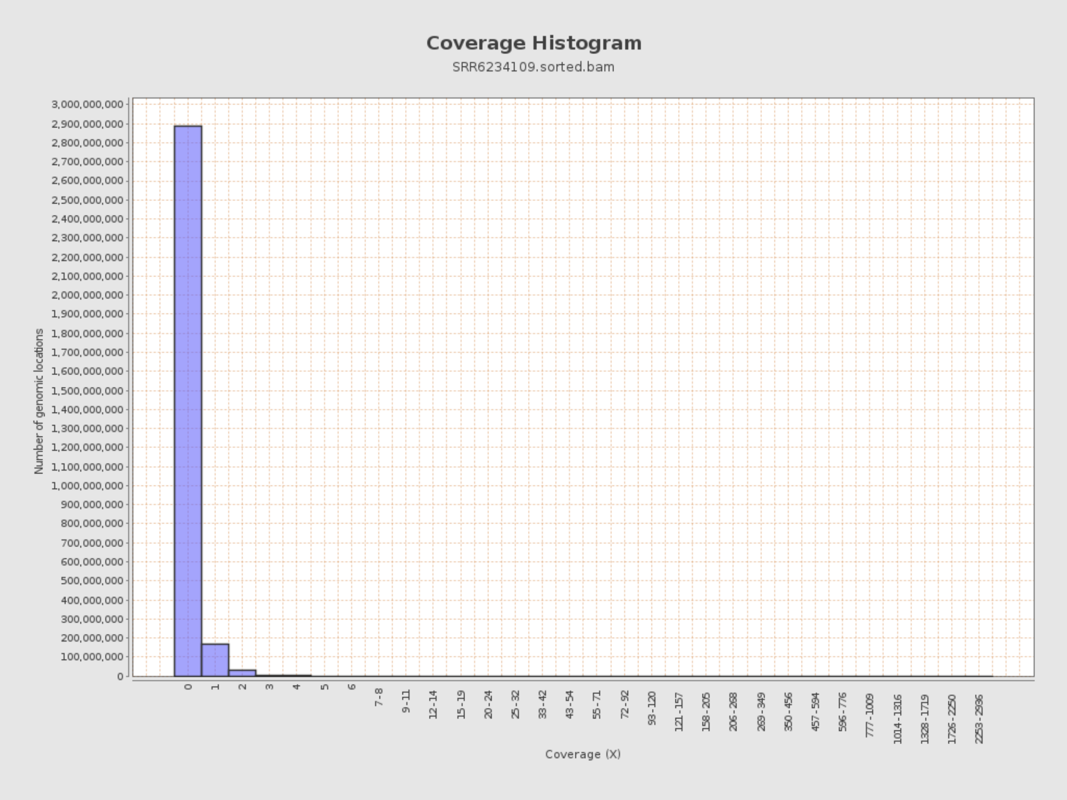
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23673407	0.095	2.1811
chr2	243199373	17306278	0.0712	1.4132
chr3	198022430	33499617	0.1692	0.5086
chr4	191154276	8609774	0.045	0.3198
chr5	180915260	14859908	0.0821	0.3632
chr6	171115067	17427113	0.1018	0.6188
chr7	159138663	17579078	0.1105	1.5328

chr8	146364022	10605001	0.0725	1.2413
chr9	141213431	10788284	0.0764	0.648
chr10	135534747	14410225	0.1063	0.6744
chr11	135006516	10655953	0.0789	0.6678
chr12	133851895	6929899	0.0518	0.3165
chr13	115169878	14926449	0.1296	0.4845
chr14	107349540	10288959	0.0958	0.4525
chr15	102531392	4353824	0.0425	0.3218
chr16	90354753	6776809	0.075	0.4785
chr17	81195210	5986280	0.0737	0.4091
chr18	78077248	5269569	0.0675	1.6714
chr19	59128983	6632249	0.1122	1.1799
chr20	63025520	5583217	0.0886	0.4535
chr21	48129895	5169038	0.1074	0.4268
chr22	51304566	1992948	0.0388	0.2295
chrMT	16571	211799	12.7813	8.6545
chrX	155270560	7962165	0.0513	0.4152
chrY	59373566	560183	0.0094	0.2091

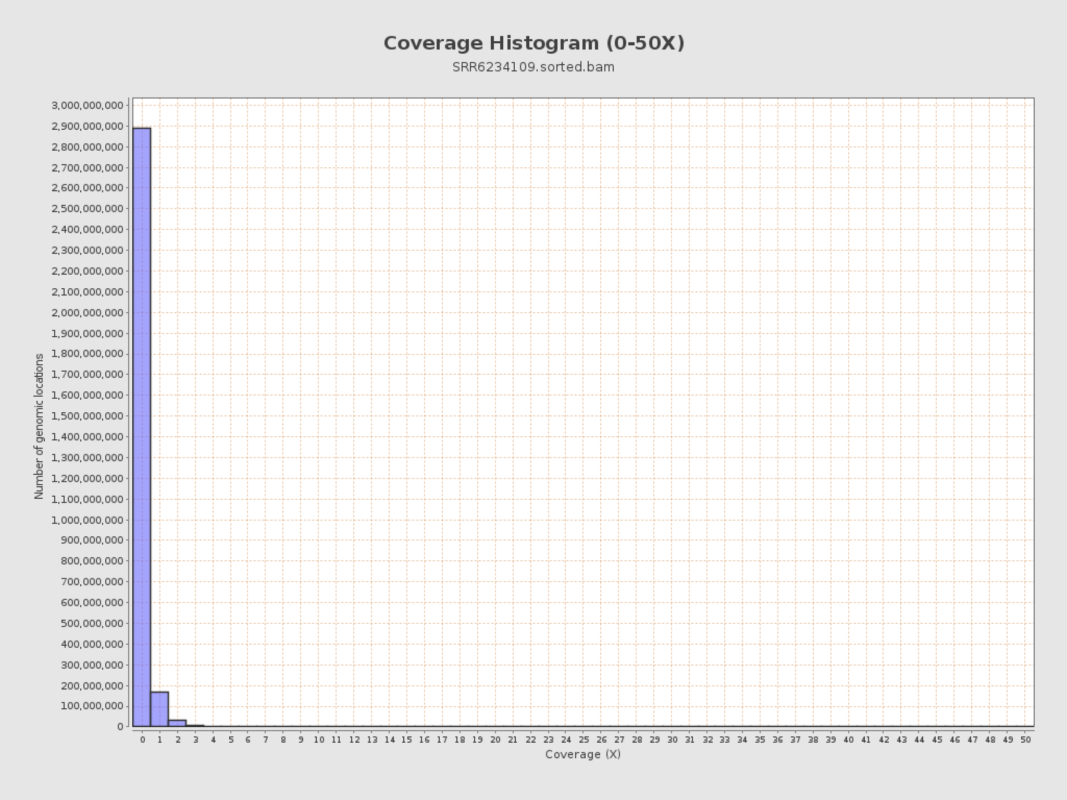
3. Results : Coverage across reference



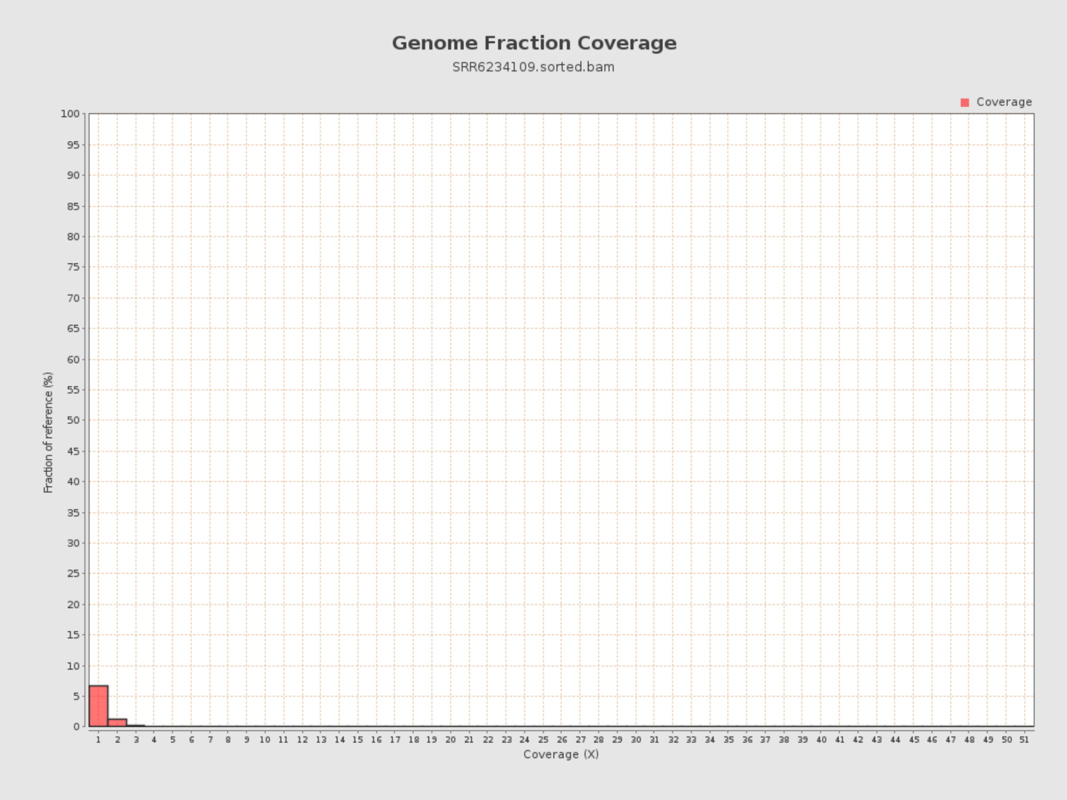
4. Results : Coverage Histogram



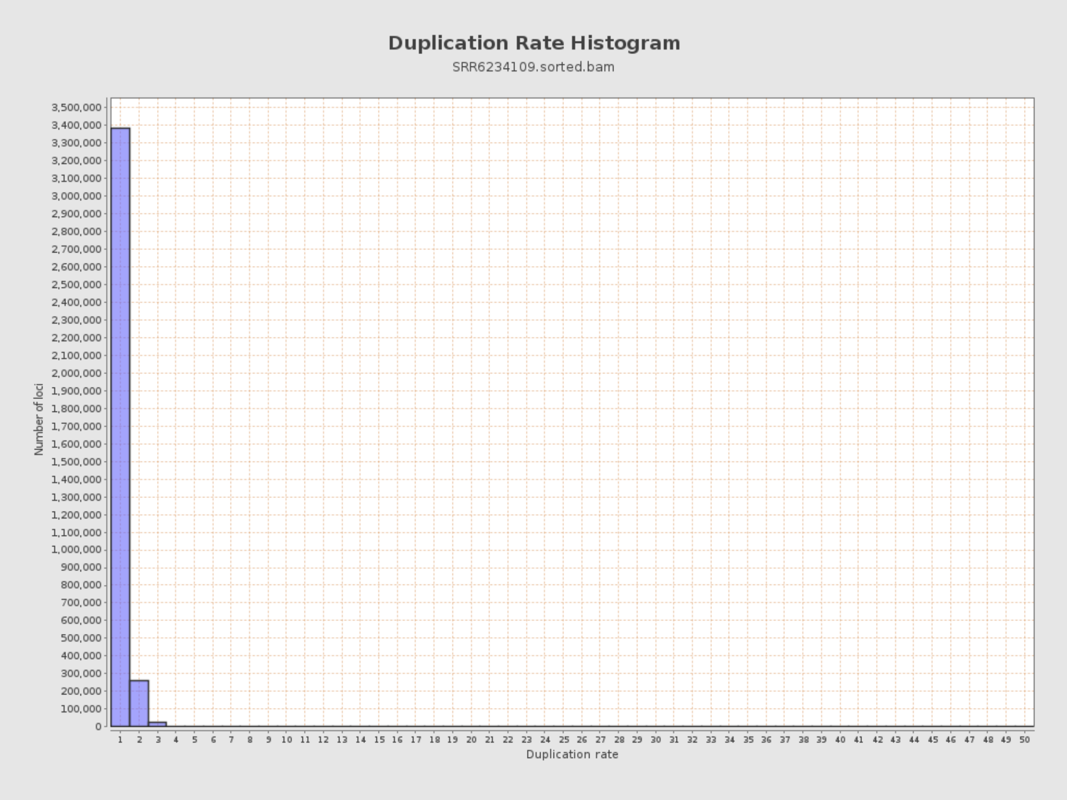
5. Results : Coverage Histogram (0-50X)



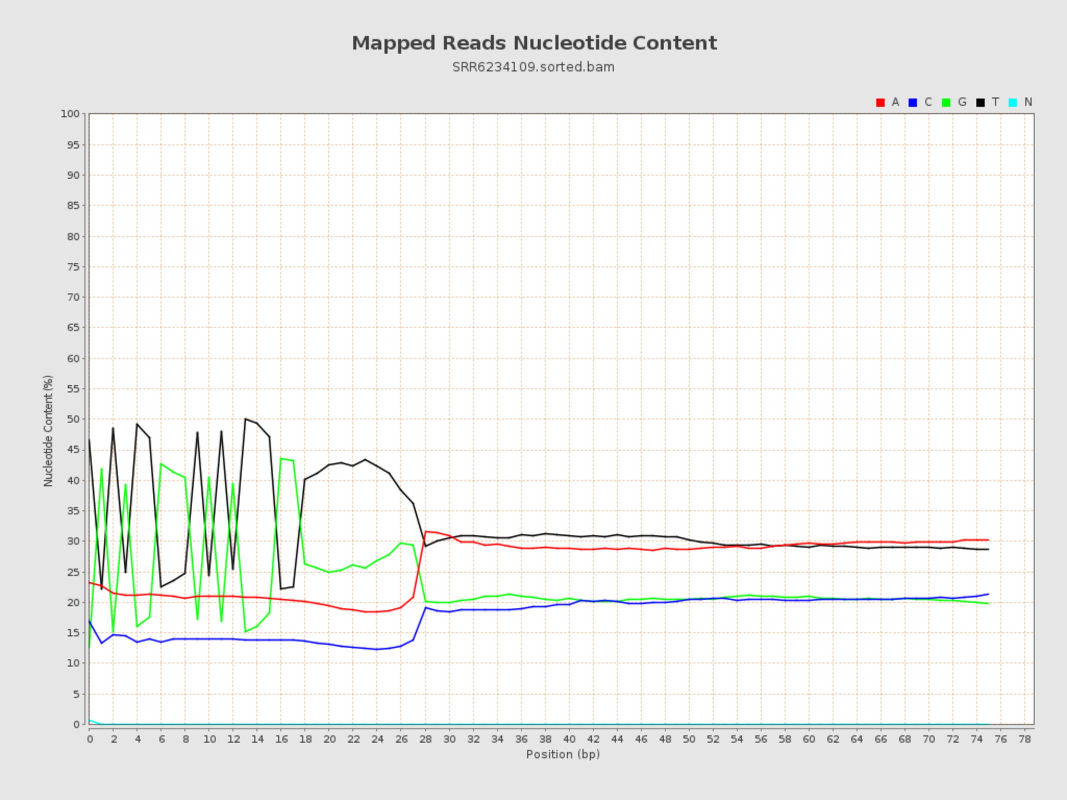
6. Results : Genome Fraction Coverage



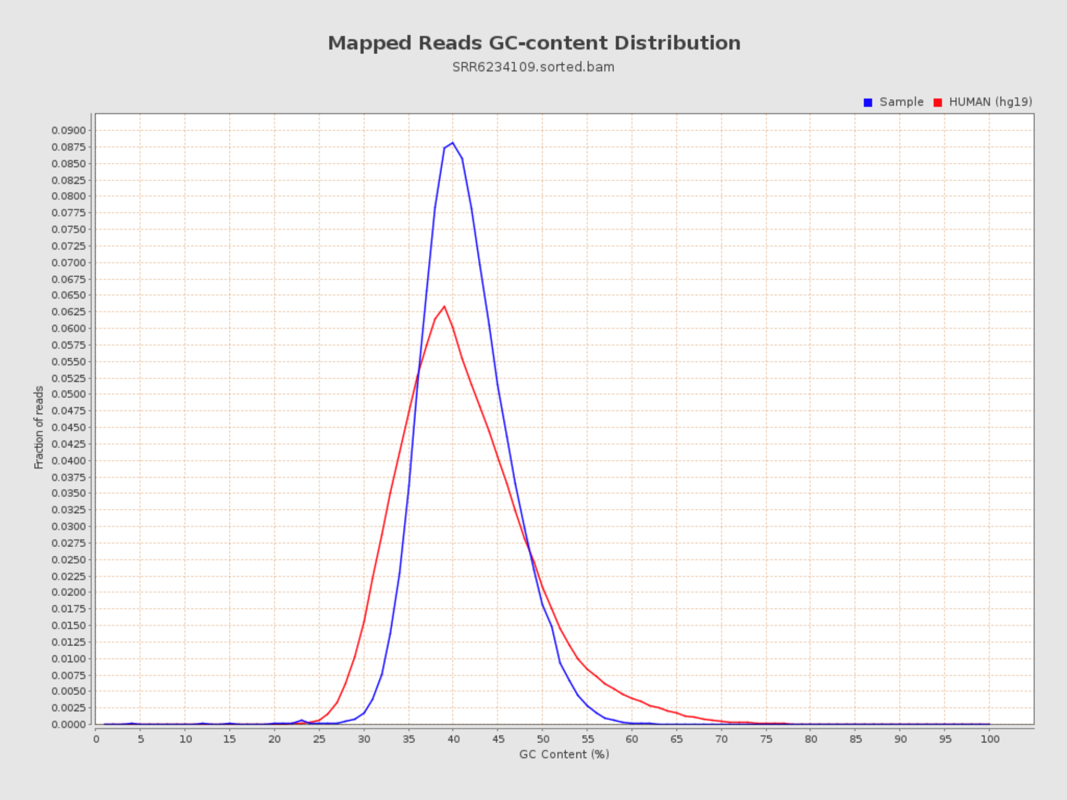
7. Results : Duplication Rate Histogram



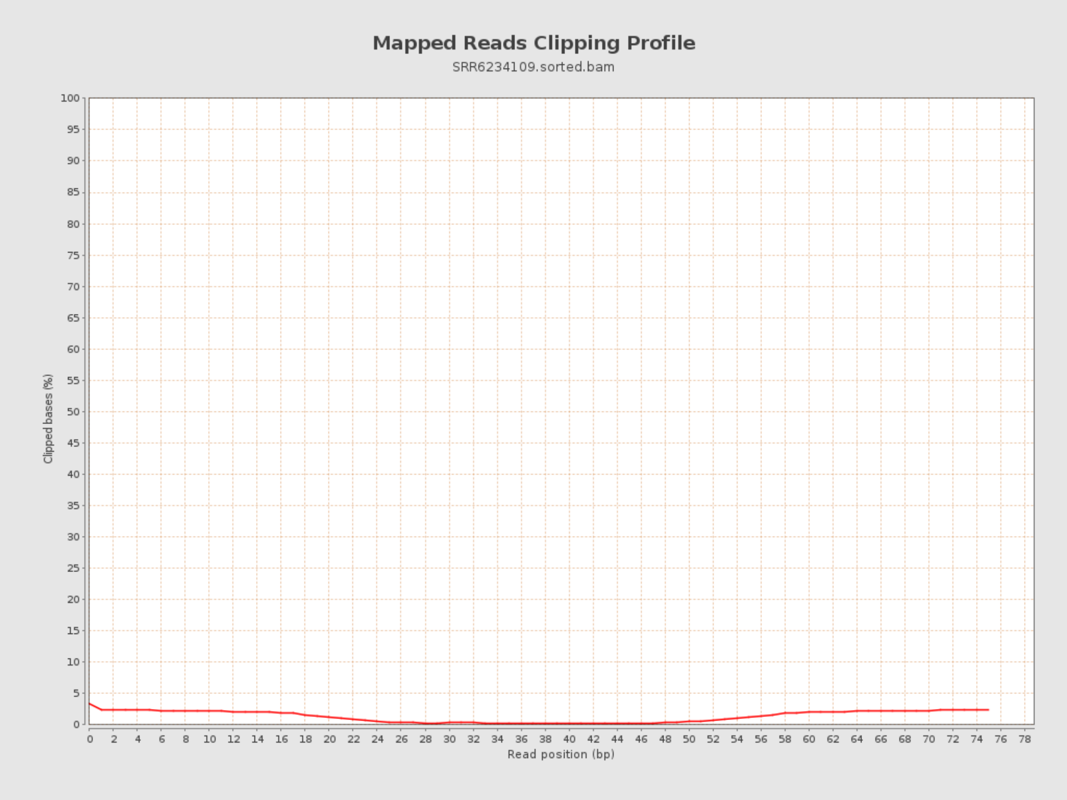
8. Results : Mapped Reads Nucleotide Content



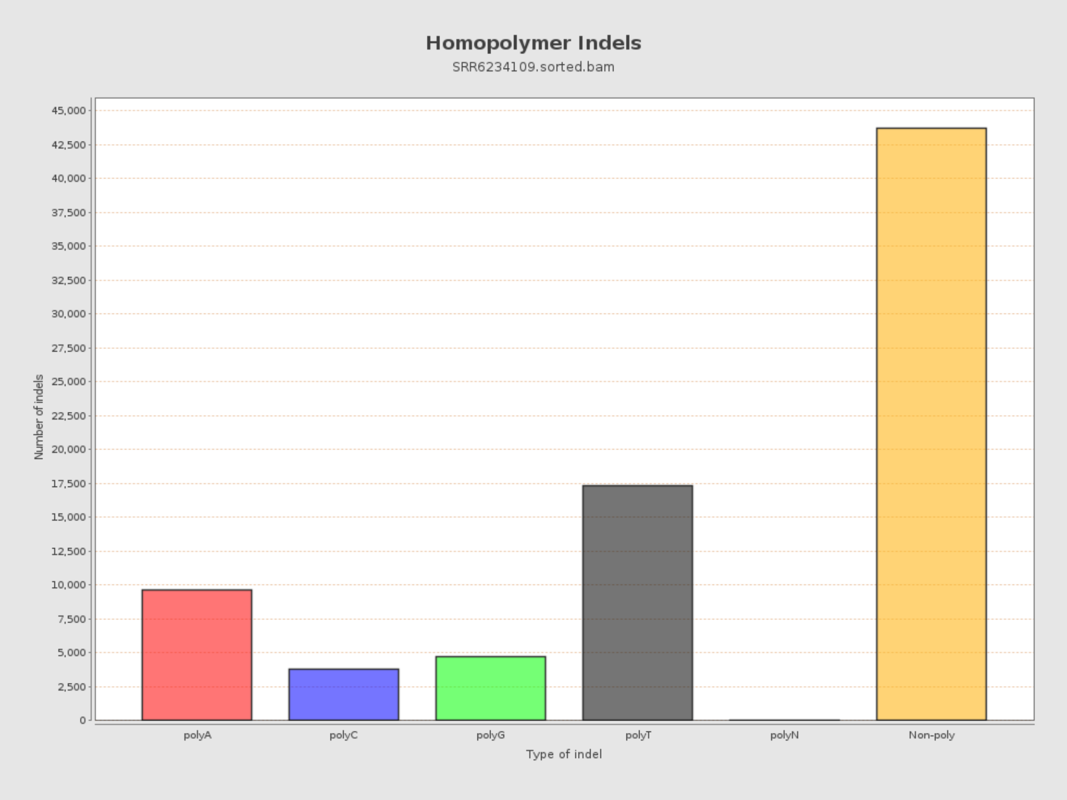
9. Results : Mapped Reads GC-content Distribution



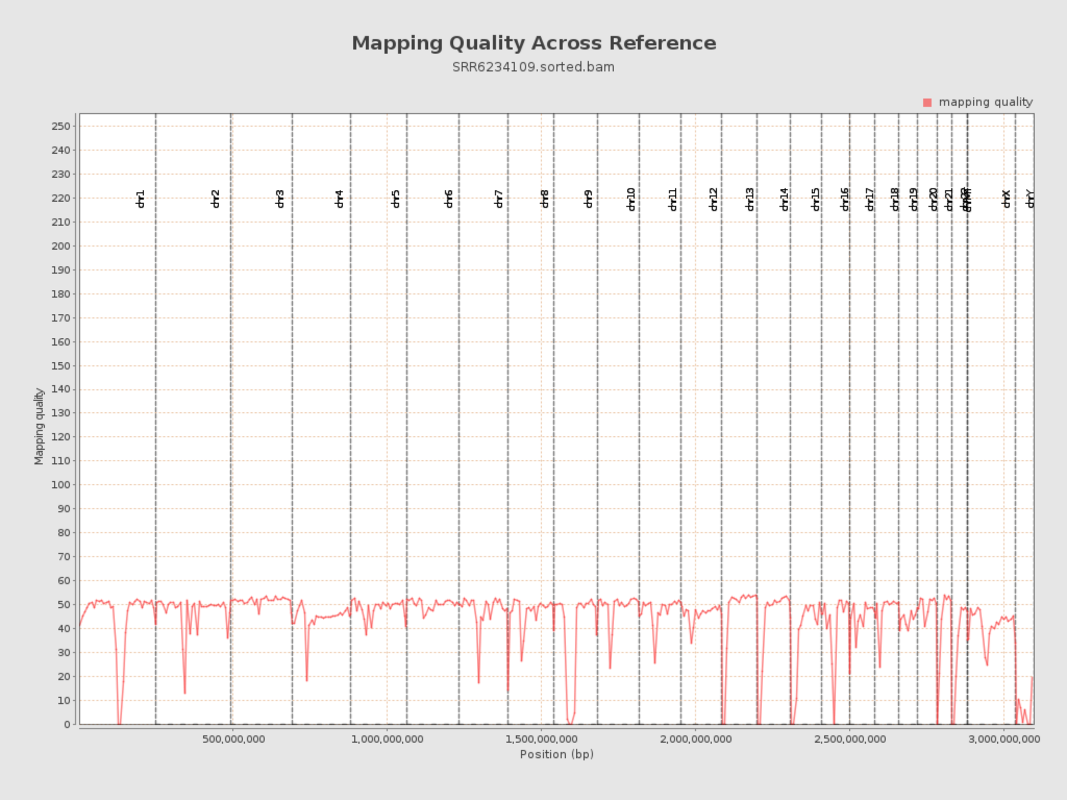
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram