Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 18:02:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234132.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_SRR6234132 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234132.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 18:02:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234132.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,778,767
Mapped reads	985,582 / 55.41%
Unmapped reads	793,185 / 44.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,993 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	99,217 / 5.58%
Duplication rate	8.49%
Clipped reads	613,474 / 34.49%

2.2. ACGT Content

Number/percentage of A's	16,547,186 / 26.91%
Number/percentage of C's	10,823,525 / 17.6%
Number/percentage of T's	20,104,764 / 32.7%
Number/percentage of G's	14,000,600 / 22.77%
Number/percentage of N's	10,604 / 0.02%
GC Percentage	40.37%

2.3. Coverage

Mean	0.0199

Standard Deviation	0.2339

2.4. Mapping Quality

Mean Mapping Quality	43.94

2.5. Mismatches and indels

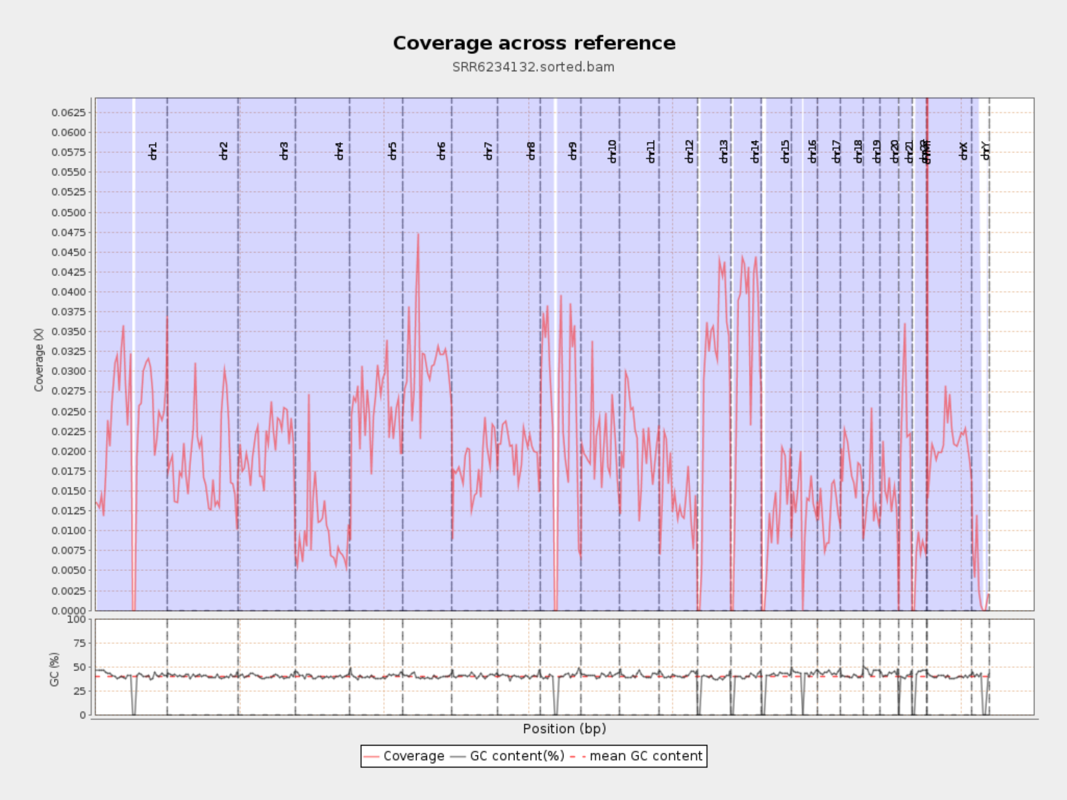
General error rate	0.94%
Mismatches	563,507
Insertions	5,439
Mapped reads with at least one insertion	0.54%
Deletions	25,299
Mapped reads with at least one deletion	2.53%
Homopolymer indels	44.24%

2.6. Chromosome stats

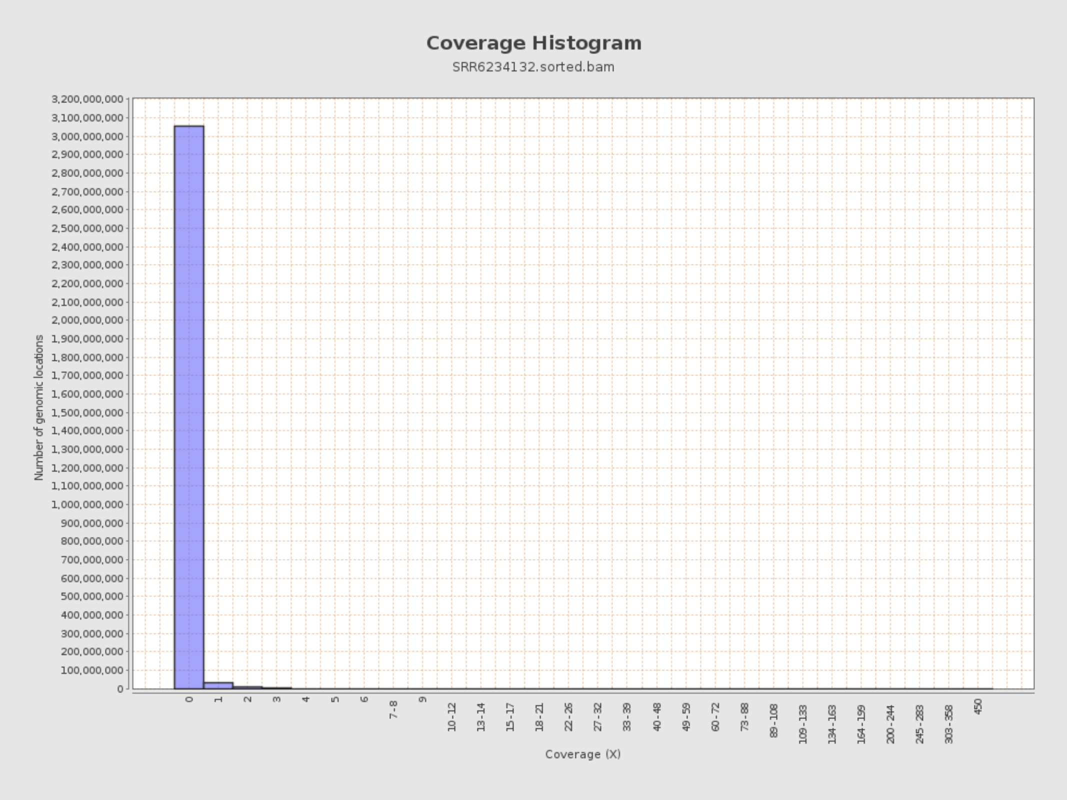
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5864247	0.0235	0.3334
chr2	243199373	4469723	0.0184	0.2823
chr3	198022430	4126375	0.0208	0.1962
chr4	191154276	1874356	0.0098	0.1518
chr5	180915260	4625531	0.0256	0.2181
chr6	171115067	5338682	0.0312	0.2689
chr7	159138663	2894010	0.0182	0.2051

chr8	146364022	2985811	0.0204	0.2849
chr9	141213431	3572652	0.0253	0.2412
chr10	135534747	2790890	0.0206	0.2365
chr11	135006516	2815327	0.0209	0.2185
chr12	133851895	1895402	0.0142	0.1623
chr13	115169878	3447875	0.0299	0.2464
chr14	107349540	3454249	0.0322	0.2545
chr15	102531392	1166569	0.0114	0.1463
chr16	90354753	1145798	0.0127	0.1735
chr17	81195210	976670	0.012	0.1536
chr18	78077248	1408851	0.018	0.3444
chr19	59128983	833555	0.0141	0.2164
chr20	63025520	929635	0.0148	0.1758
chr21	48129895	1043367	0.0217	0.2092
chr22	51304566	331557	0.0065	0.1048
chrMT	16571	41501	2.5044	2.7714
chrX	155270560	3292718	0.0212	0.2043
chrY	59373566	205115	0.0035	0.1019

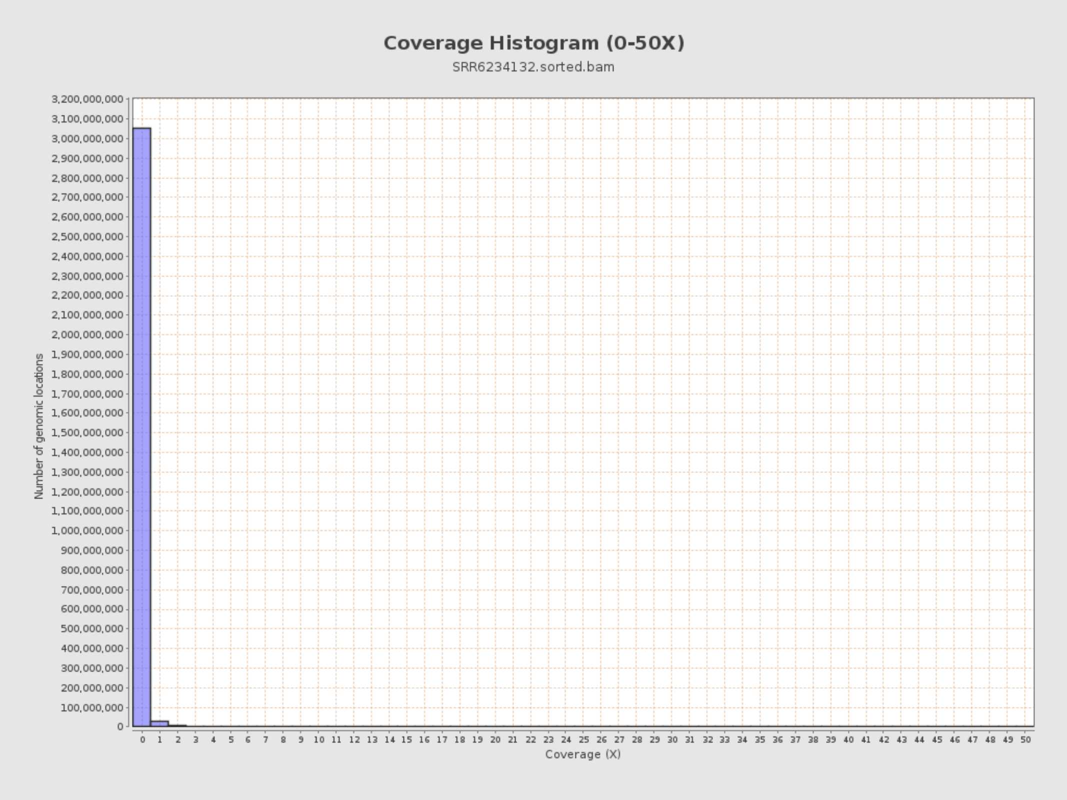
3. Results : Coverage across reference



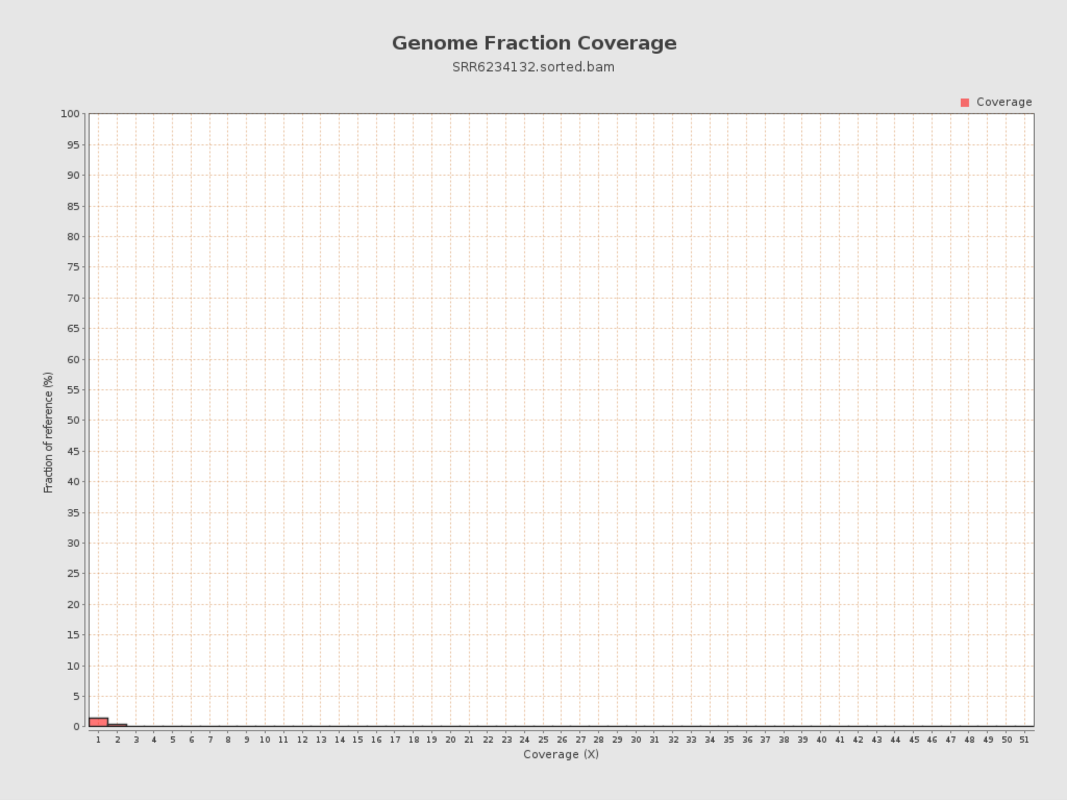
4. Results : Coverage Histogram



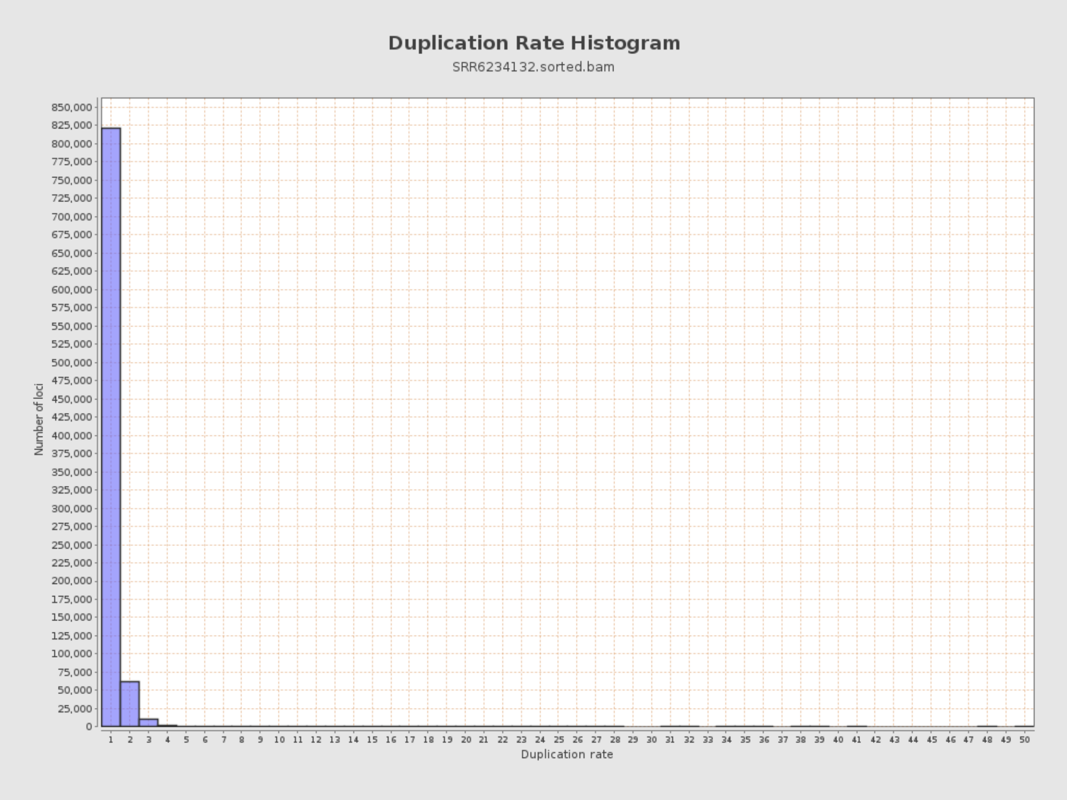
5. Results : Coverage Histogram (0-50X)



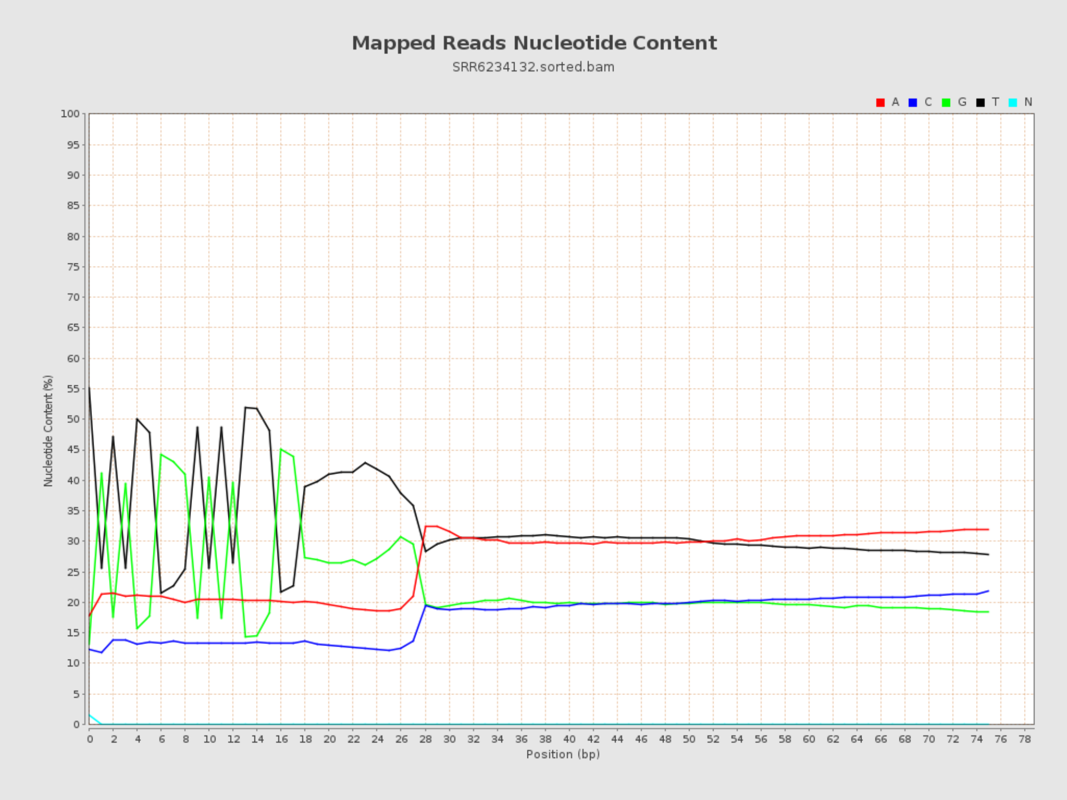
6. Results : Genome Fraction Coverage



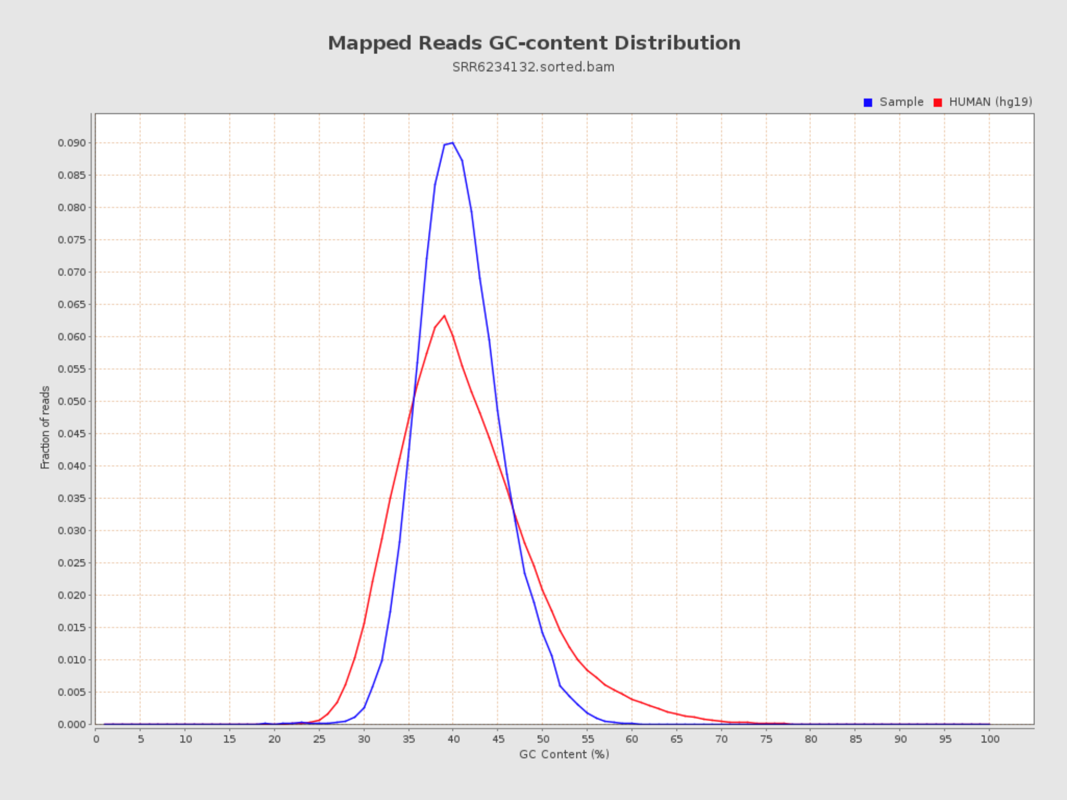
7. Results : Duplication Rate Histogram



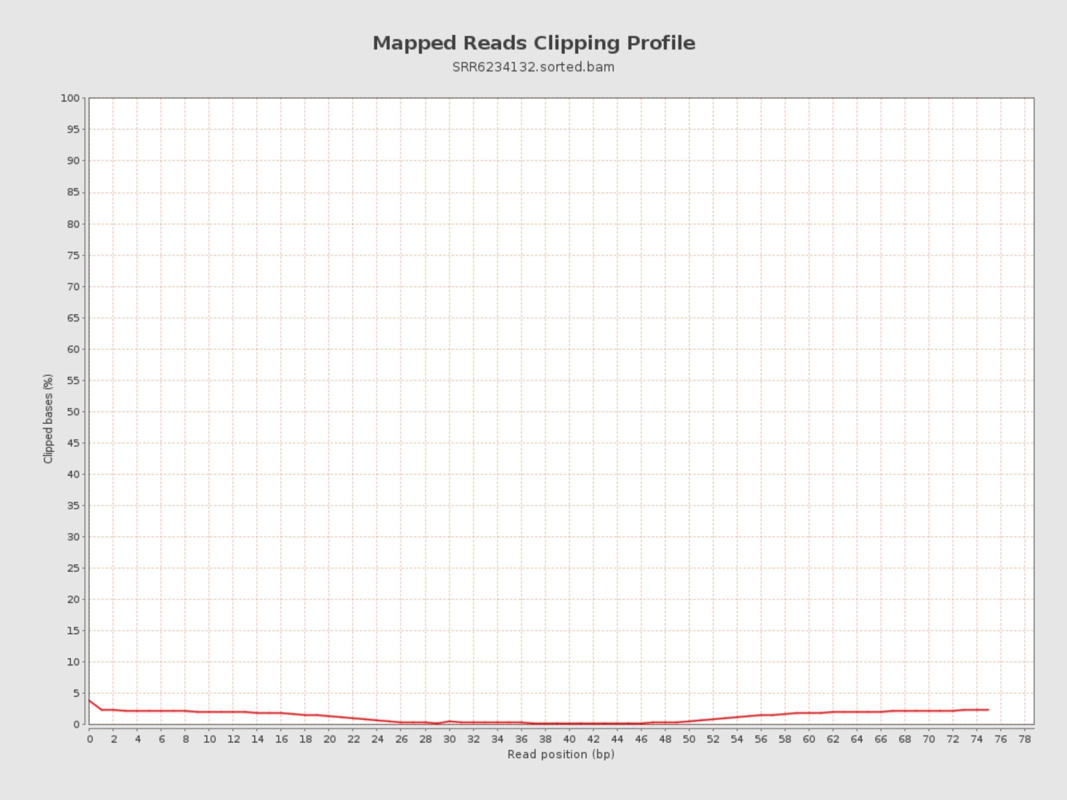
8. Results : Mapped Reads Nucleotide Content



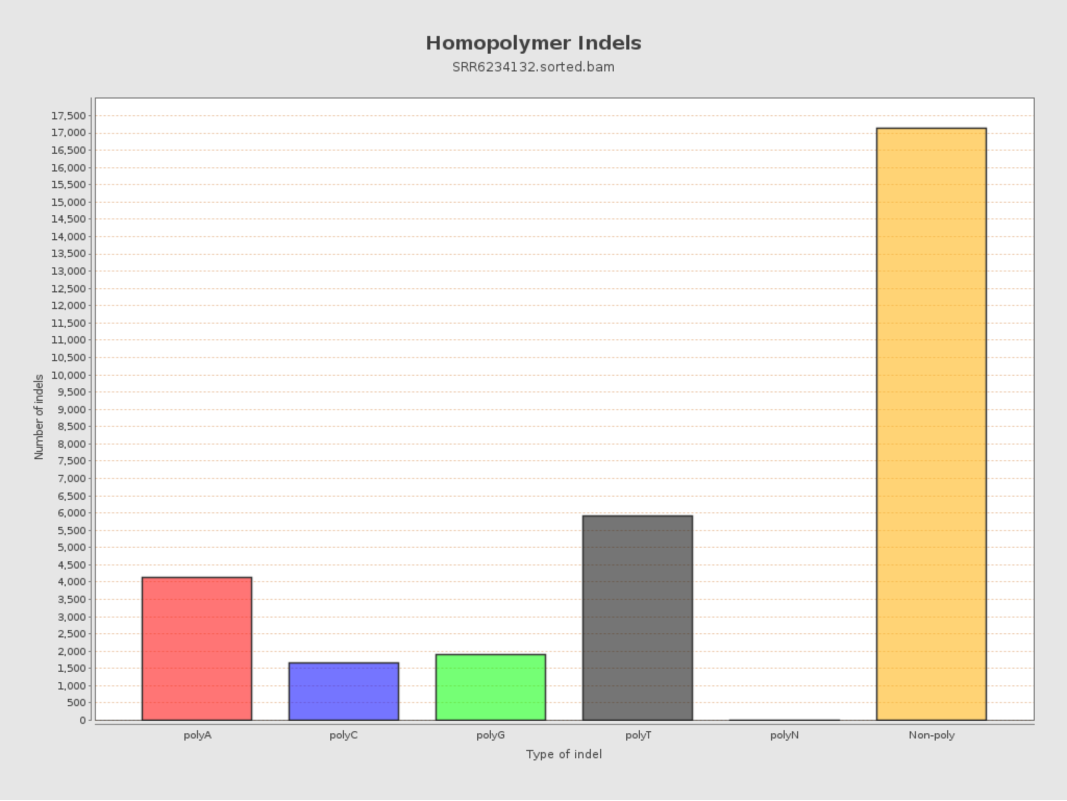
9. Results : Mapped Reads GC-content Distribution



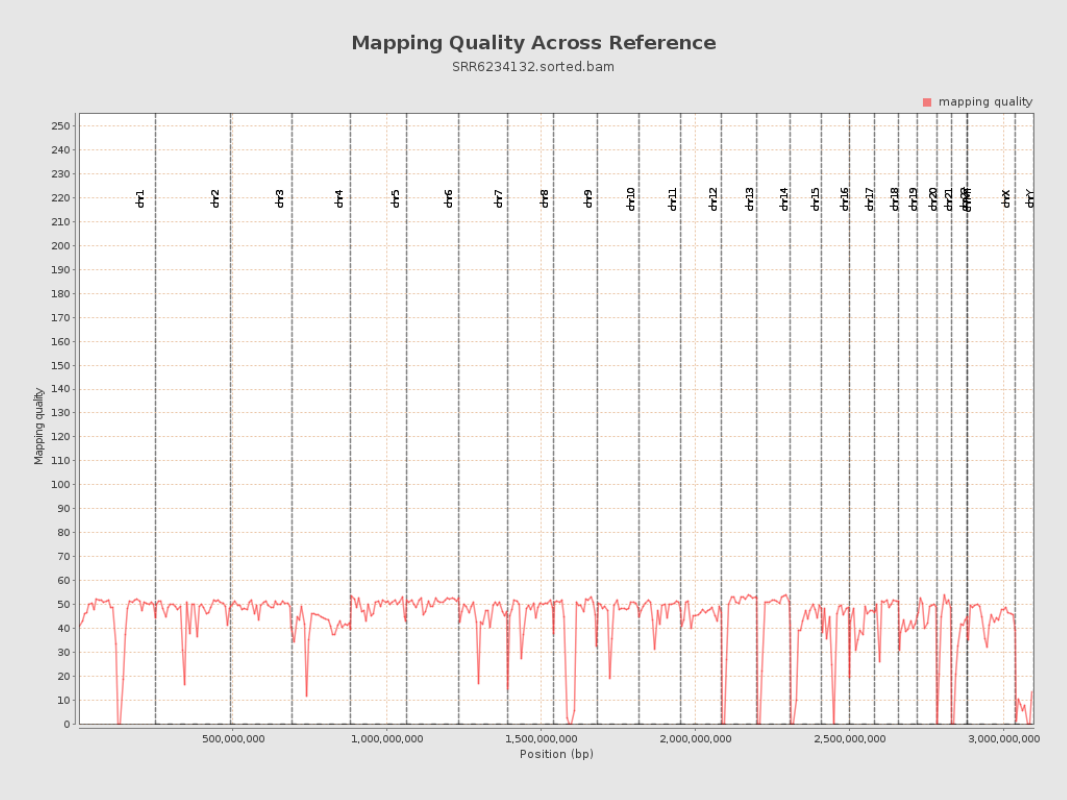
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram