Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 18:04:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234133.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_SRR6234133 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234133.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 18:04:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234133.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,921,880
Mapped reads	1,280,069 / 66.61%
Unmapped reads	641,811 / 33.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,282 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	74,727 / 3.89%
Duplication rate	4.76%
Clipped reads	869,354 / 45.23%

2.2. ACGT Content

Number/percentage of A's	20,275,875 / 25.97%
Number/percentage of C's	13,777,698 / 17.64%
Number/percentage of T's	24,776,186 / 31.73%
Number/percentage of G's	19,235,811 / 24.64%
Number/percentage of N's	17,608 / 0.02%
GC Percentage	42.28%

2.3. Coverage

Mean	0.0252

Standard Deviation	0.2565

2.4. Mapping Quality

Mean Mapping Quality	42.62

2.5. Mismatches and indels

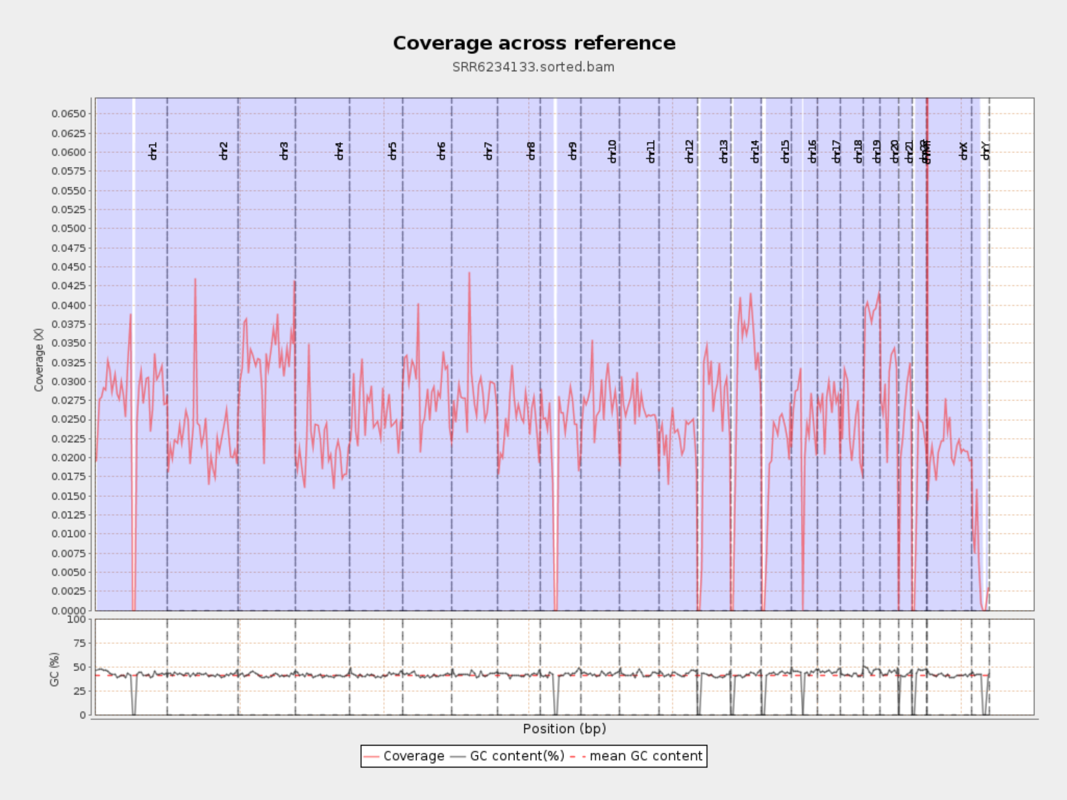
General error rate	0.94%
Mismatches	724,657
Insertions	6,634
Mapped reads with at least one insertion	0.51%
Deletions	30,047
Mapped reads with at least one deletion	2.31%
Homopolymer indels	47.12%

2.6. Chromosome stats

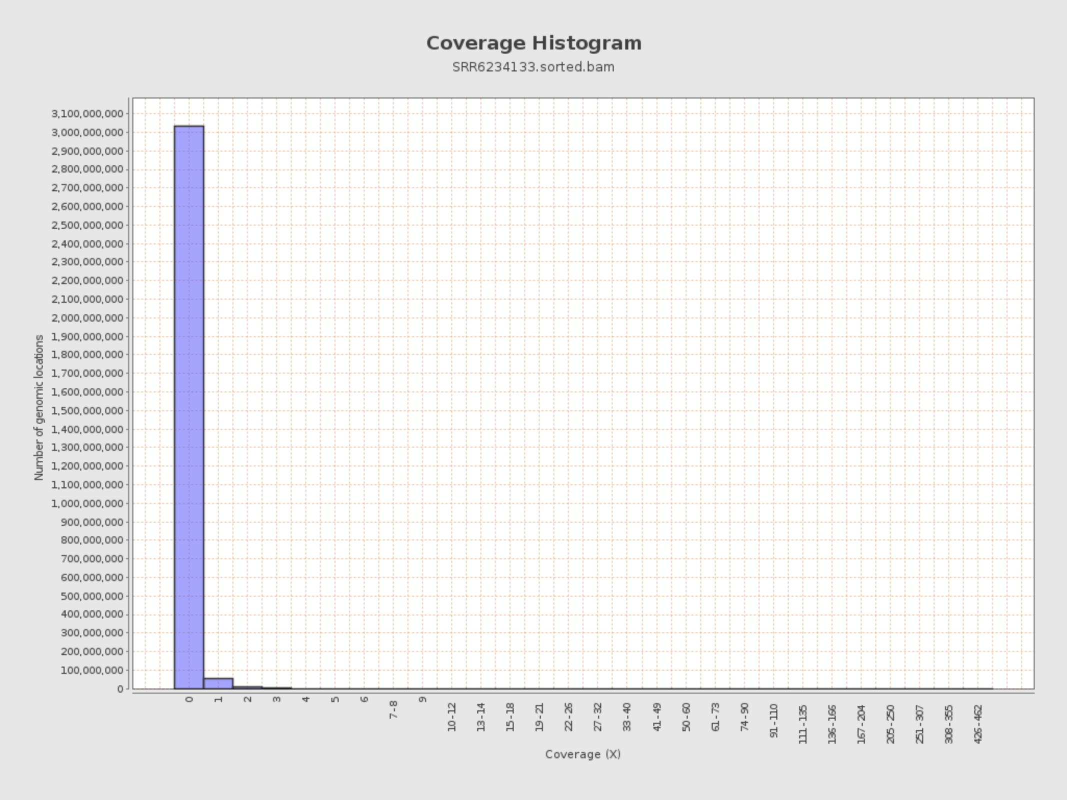
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6787170	0.0272	0.3938
chr2	243199373	5513657	0.0227	0.2913
chr3	198022430	6544290	0.033	0.2157
chr4	191154276	4040407	0.0211	0.1843
chr5	180915260	4649966	0.0257	0.193
chr6	171115067	5013771	0.0293	0.2446
chr7	159138663	4534210	0.0285	0.3603

chr8	146364022	3642833	0.0249	0.2924
chr9	141213431	3146695	0.0223	0.2444
chr10	135534747	3728750	0.0275	0.2314
chr11	135006516	3594905	0.0266	0.2642
chr12	133851895	3044039	0.0227	0.1813
chr13	115169878	2829158	0.0246	0.2007
chr14	107349540	3228859	0.0301	0.218
chr15	102531392	1895306	0.0185	0.1705
chr16	90354753	2104501	0.0233	0.1994
chr17	81195210	2179073	0.0268	0.2143
chr18	78077248	1904020	0.0244	0.3731
chr19	59128983	2300475	0.0389	0.3068
chr20	63025520	1807497	0.0287	0.2127
chr21	48129895	1142724	0.0237	0.1907
chr22	51304566	877310	0.0171	0.1543
chrMT	16571	44889	2.7089	3.3364
chrX	155270560	3266692	0.021	0.19
chrY	59373566	315083	0.0053	0.1032

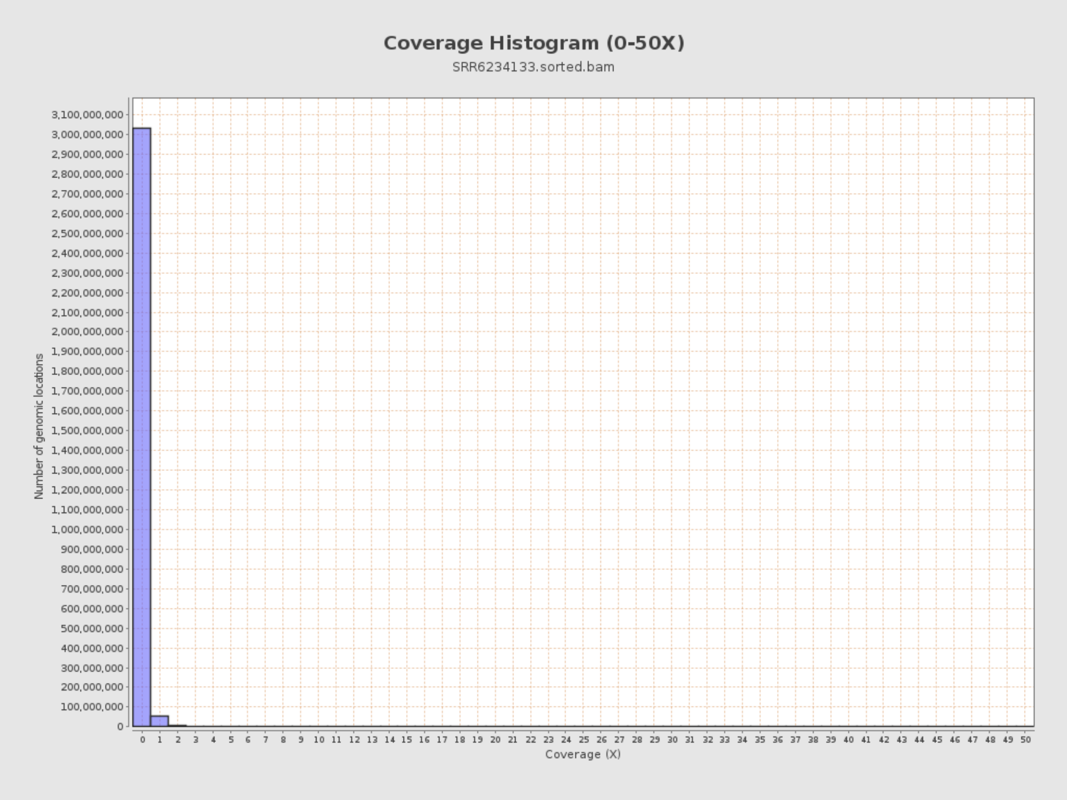
3. Results : Coverage across reference



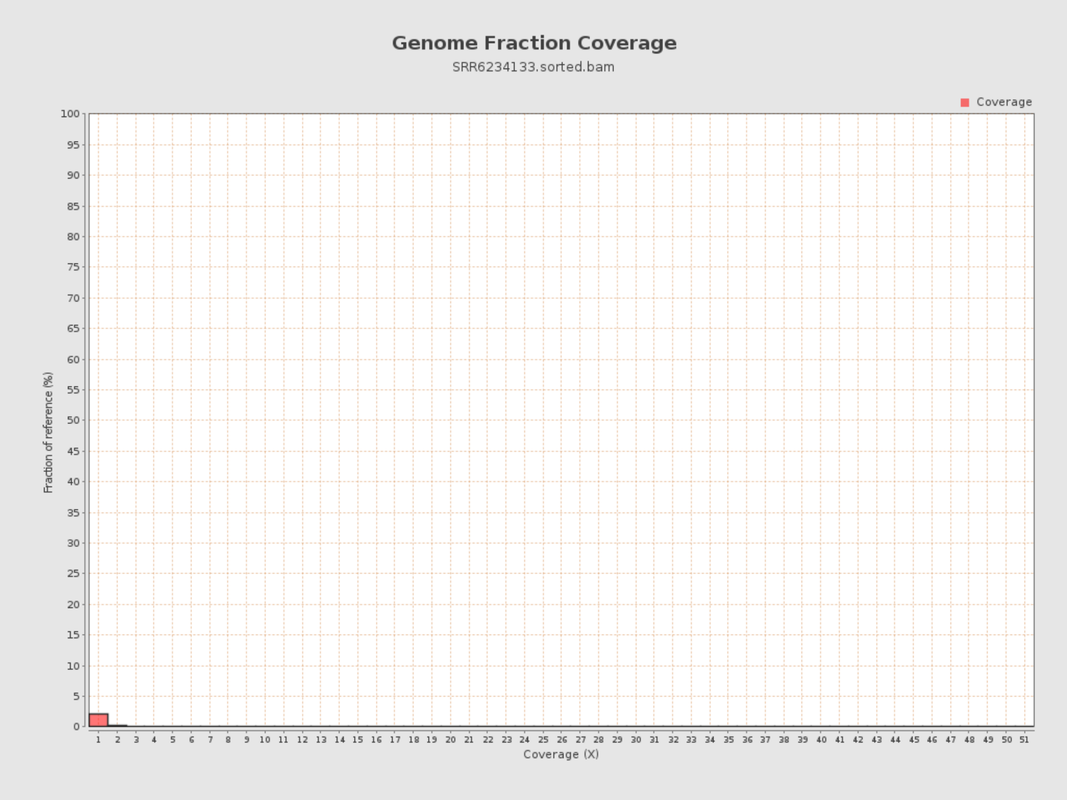
4. Results : Coverage Histogram



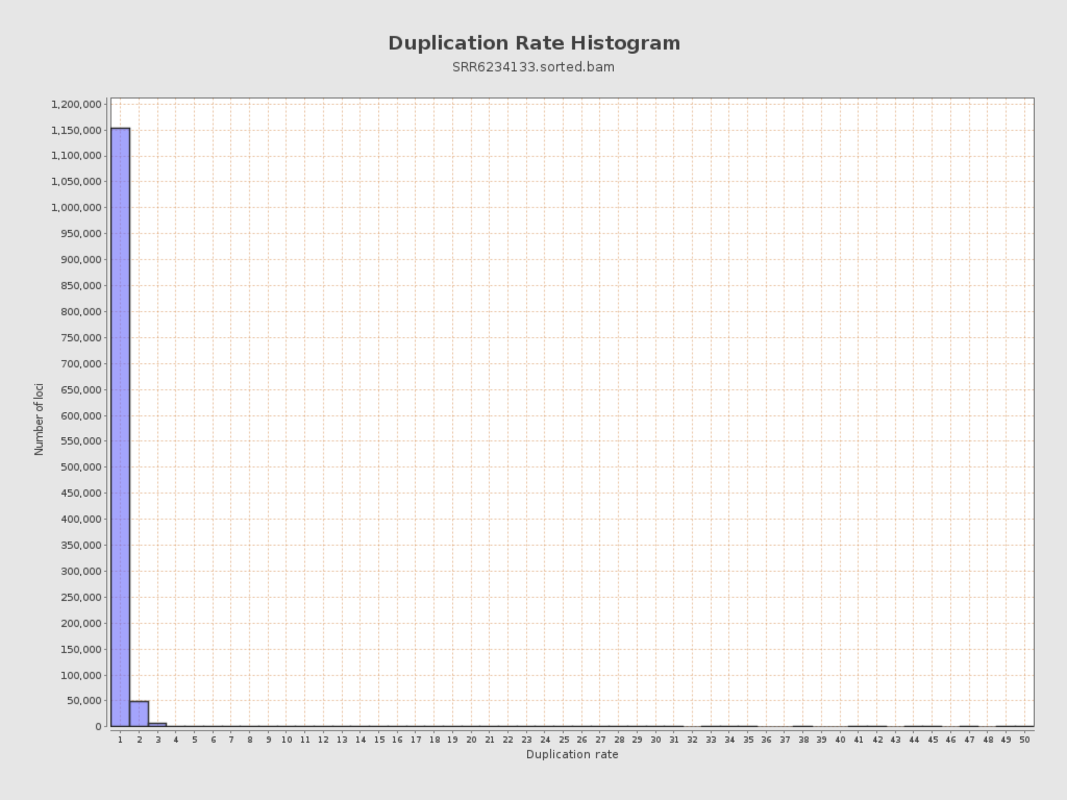
5. Results : Coverage Histogram (0-50X)



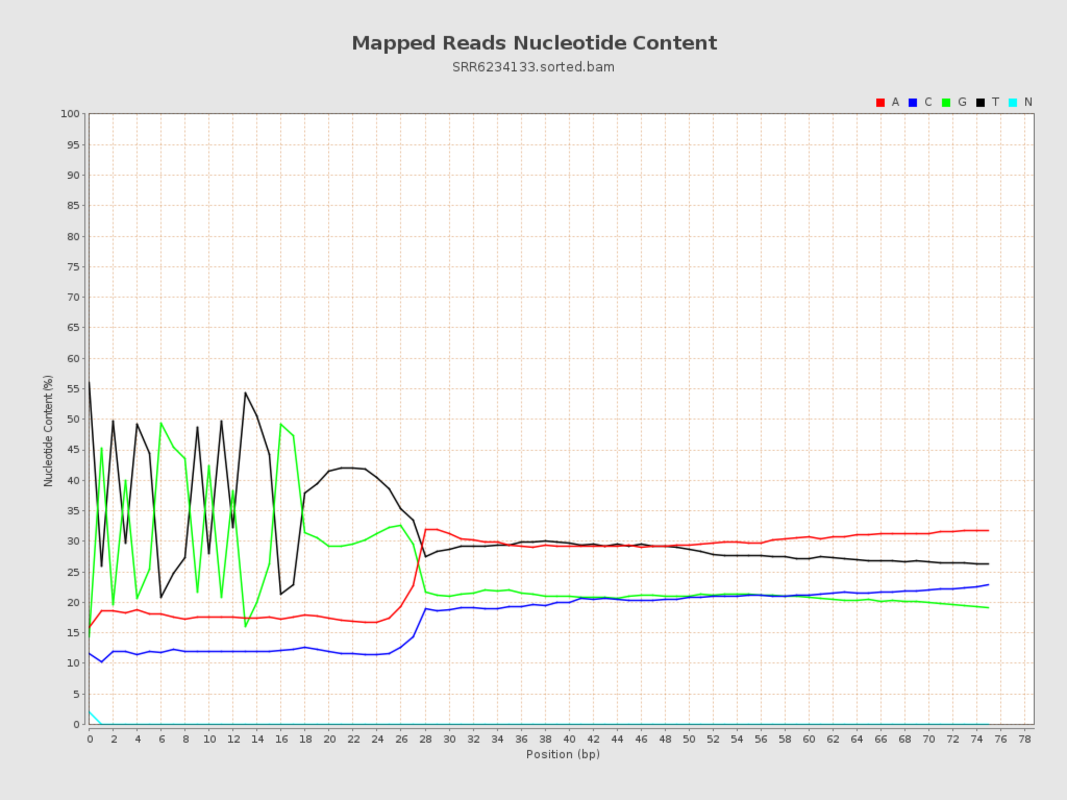
6. Results : Genome Fraction Coverage



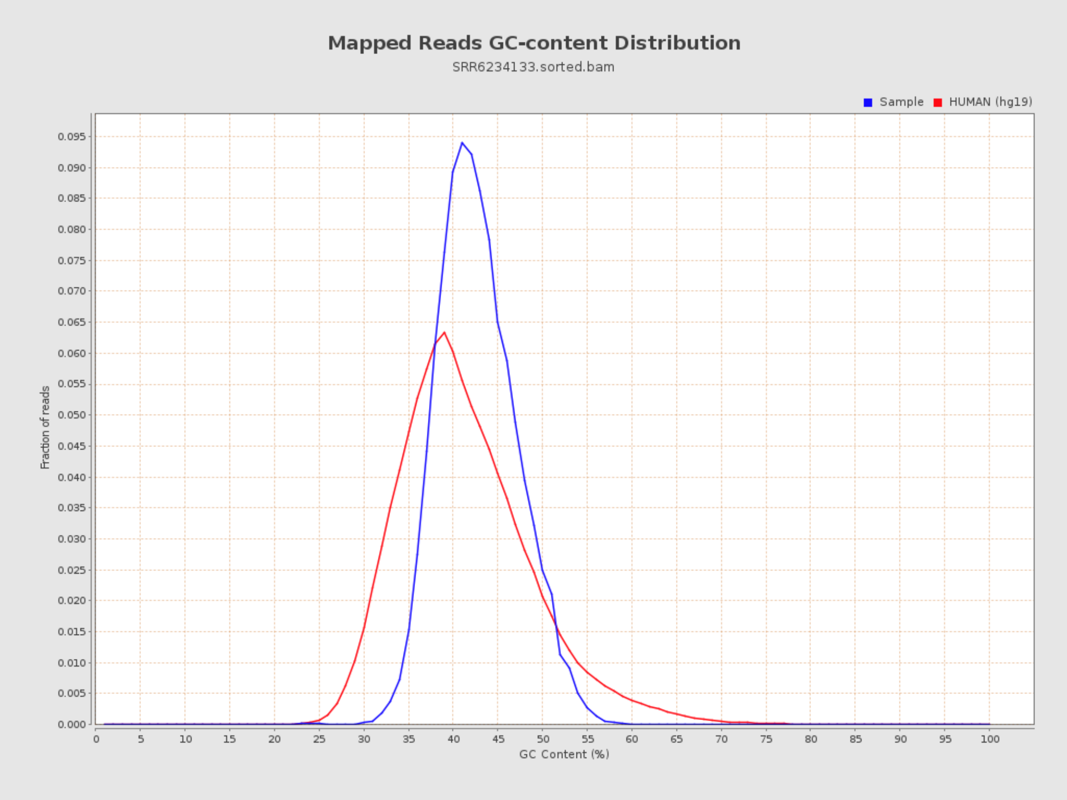
7. Results : Duplication Rate Histogram



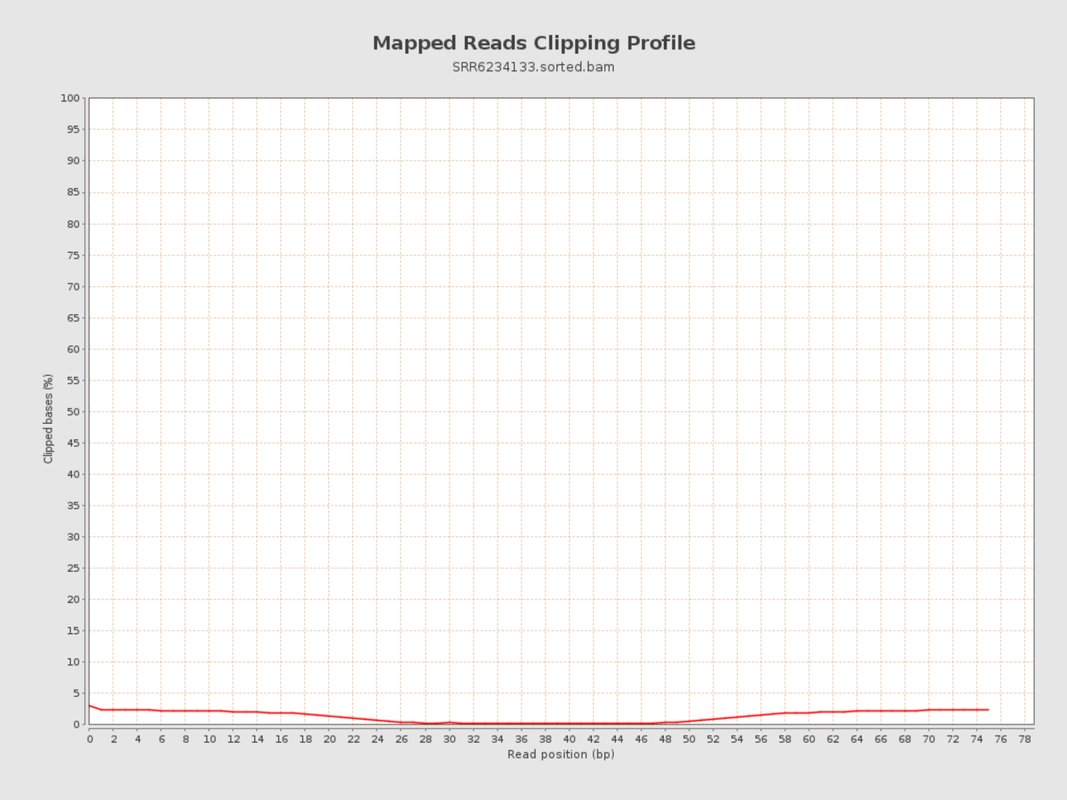
8. Results : Mapped Reads Nucleotide Content



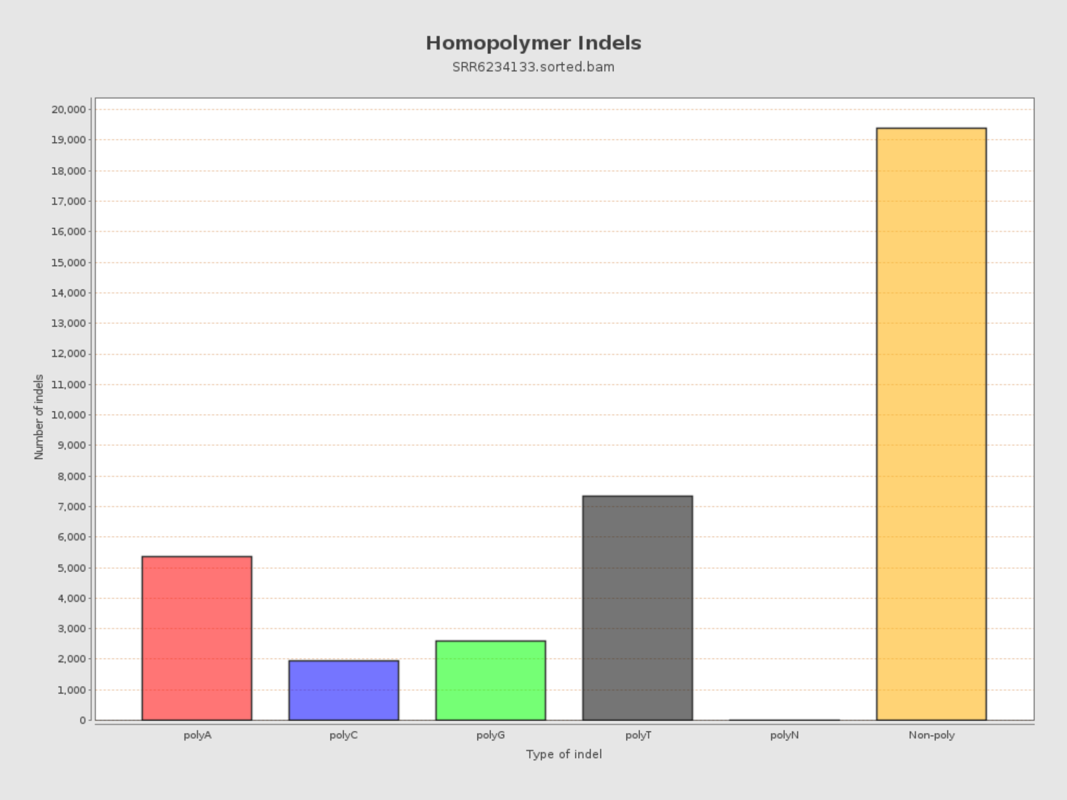
9. Results : Mapped Reads GC-content Distribution



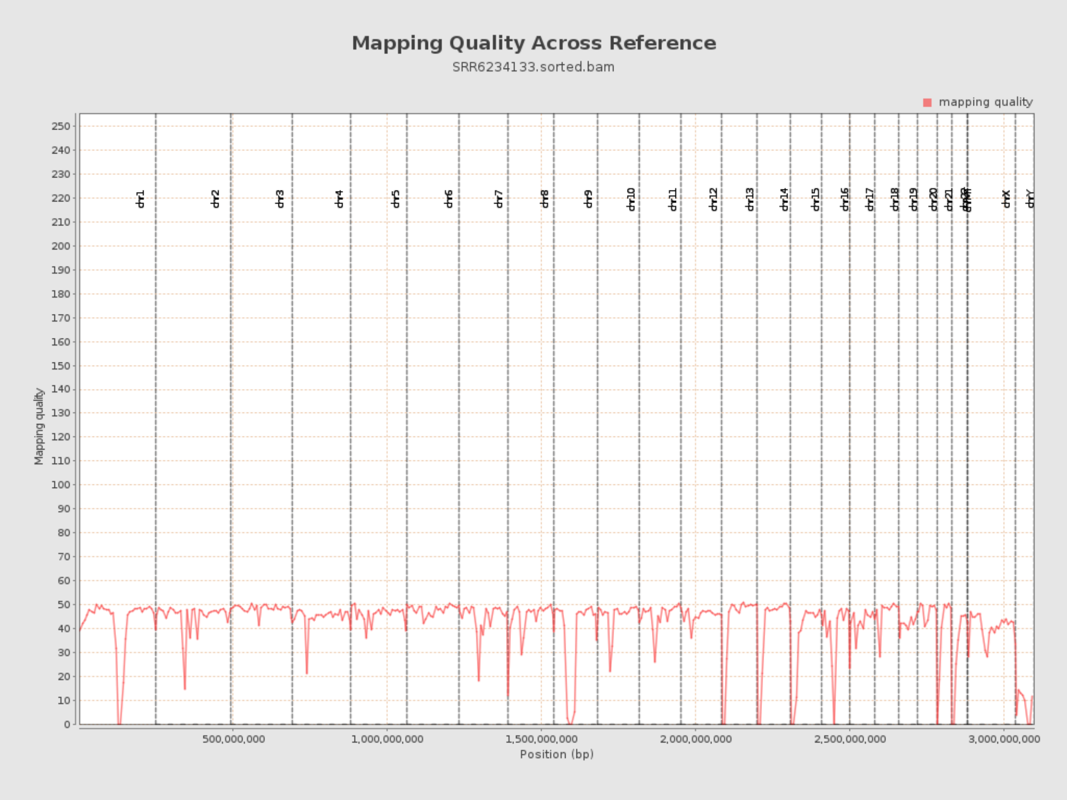
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram