Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 18:35:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234147.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_SRR6234147 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234147.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 18:35:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234147.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,333,316
Mapped reads	251,524 / 18.86%
Unmapped reads	1,081,792 / 81.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,474 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	33,152 / 2.49%
Duplication rate	9.01%
Clipped reads	143,335 / 10.75%

2.2. ACGT Content

Number/percentage of A's	4,282,605 / 27.44%
Number/percentage of C's	2,749,440 / 17.62%
Number/percentage of T's	5,094,423 / 32.64%
Number/percentage of G's	3,473,595 / 22.26%
Number/percentage of N's	6,353 / 0.04%
GC Percentage	39.87%

2.3. Coverage

Mean	0.005

Standard Deviation	0.1525

2.4. Mapping Quality

Mean Mapping Quality	42.16

2.5. Mismatches and indels

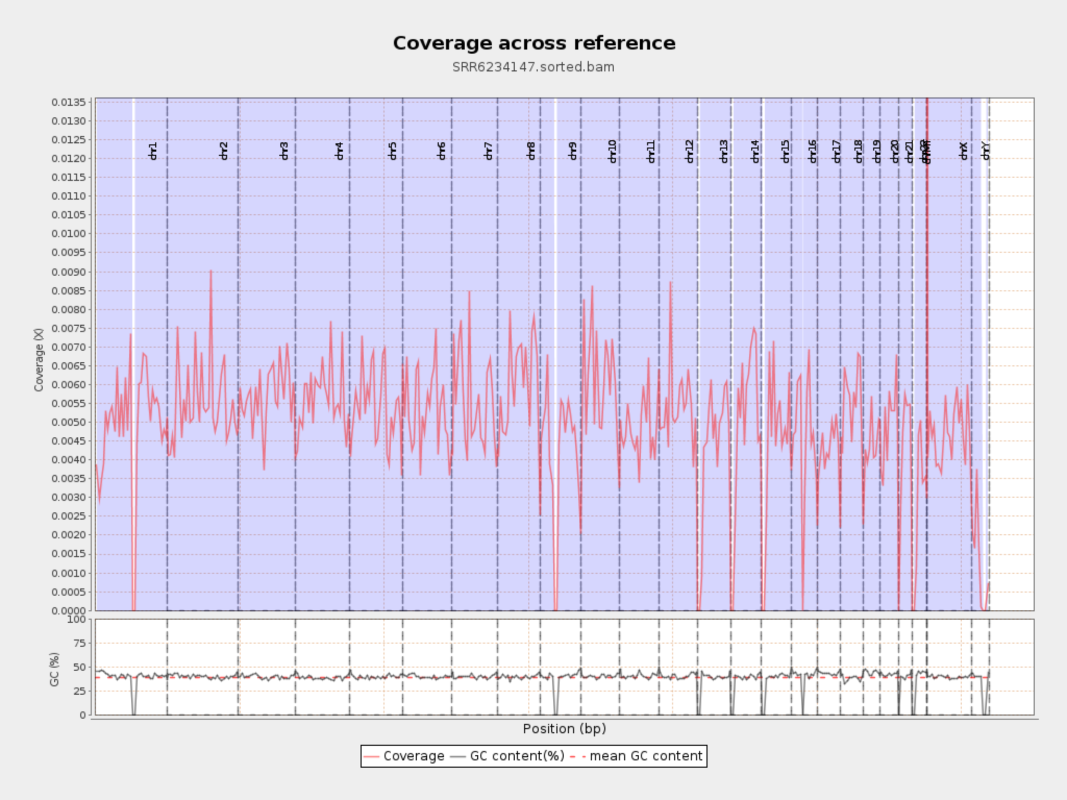
General error rate	1.02%
Mismatches	153,972
Insertions	2,086
Mapped reads with at least one insertion	0.81%
Deletions	4,735
Mapped reads with at least one deletion	1.85%
Homopolymer indels	39.61%

2.6. Chromosome stats

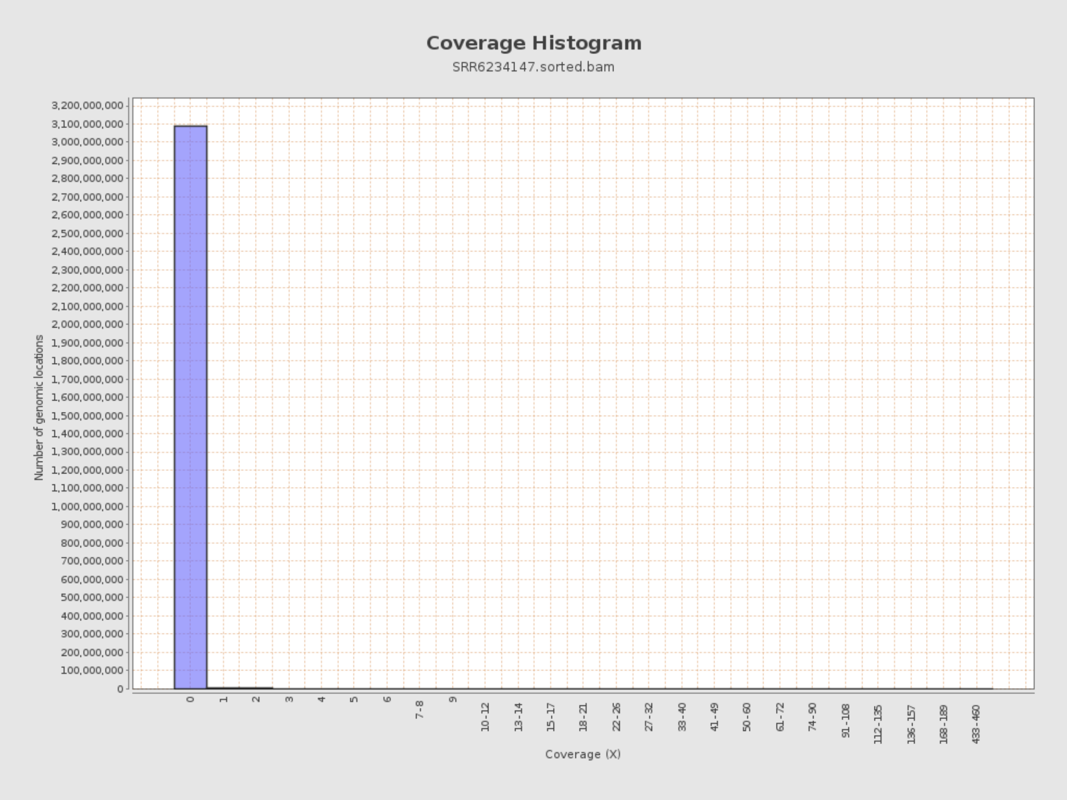
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1221070	0.0049	0.1296
chr2	243199373	1339960	0.0055	0.2852
chr3	198022430	1134406	0.0057	0.1291
chr4	191154276	1071195	0.0056	0.1339
chr5	180915260	986784	0.0055	0.1301
chr6	171115067	916267	0.0054	0.1256
chr7	159138663	882032	0.0055	0.1364

chr8	146364022	882944	0.006	0.1728
chr9	141213431	600528	0.0043	0.1103
chr10	135534747	825464	0.0061	0.1419
chr11	135006516	647251	0.0048	0.1181
chr12	133851895	722572	0.0054	0.1279
chr13	115169878	485997	0.0042	0.1246
chr14	107349540	526191	0.0049	0.1361
chr15	102531392	447334	0.0044	0.1855
chr16	90354753	409731	0.0045	0.121
chr17	81195210	345900	0.0043	0.1109
chr18	78077248	434652	0.0056	0.2523
chr19	59128983	260578	0.0044	0.1126
chr20	63025520	313752	0.005	0.12
chr21	48129895	204243	0.0042	0.1098
chr22	51304566	144174	0.0028	0.0886
chrMT	16571	7228	0.4362	1.0119
chrX	155270560	732243	0.0047	0.1213
chrY	59373566	72191	0.0012	0.0528

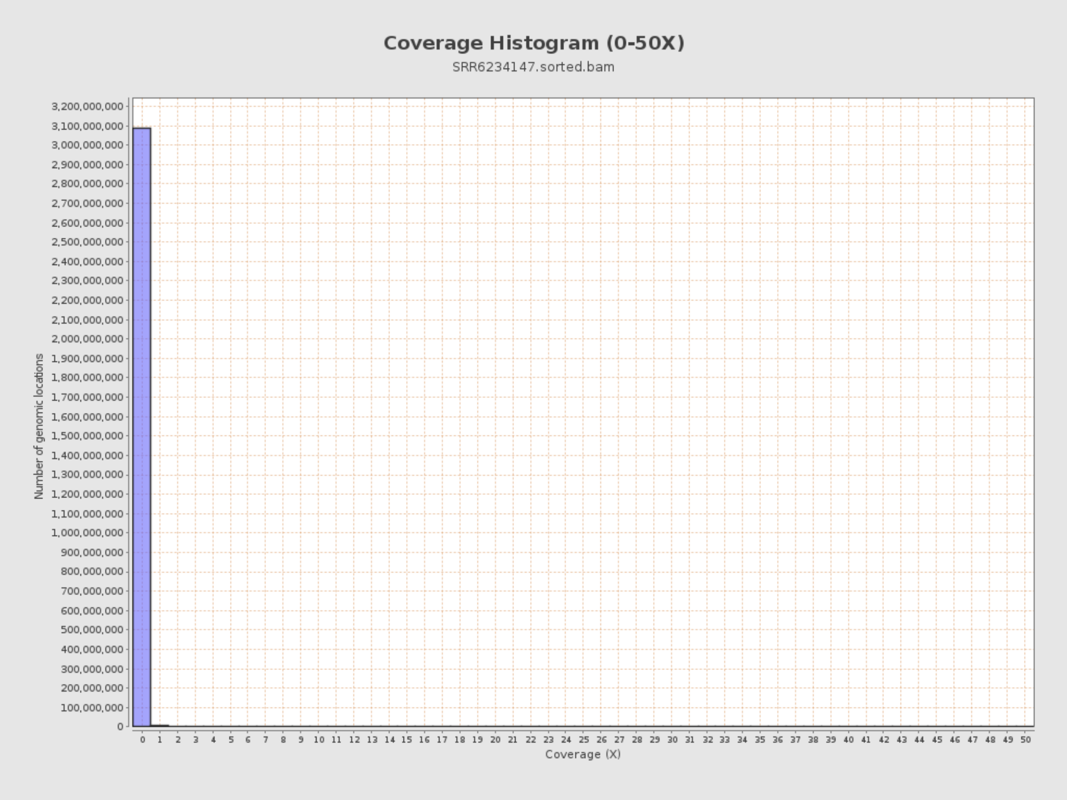
3. Results : Coverage across reference



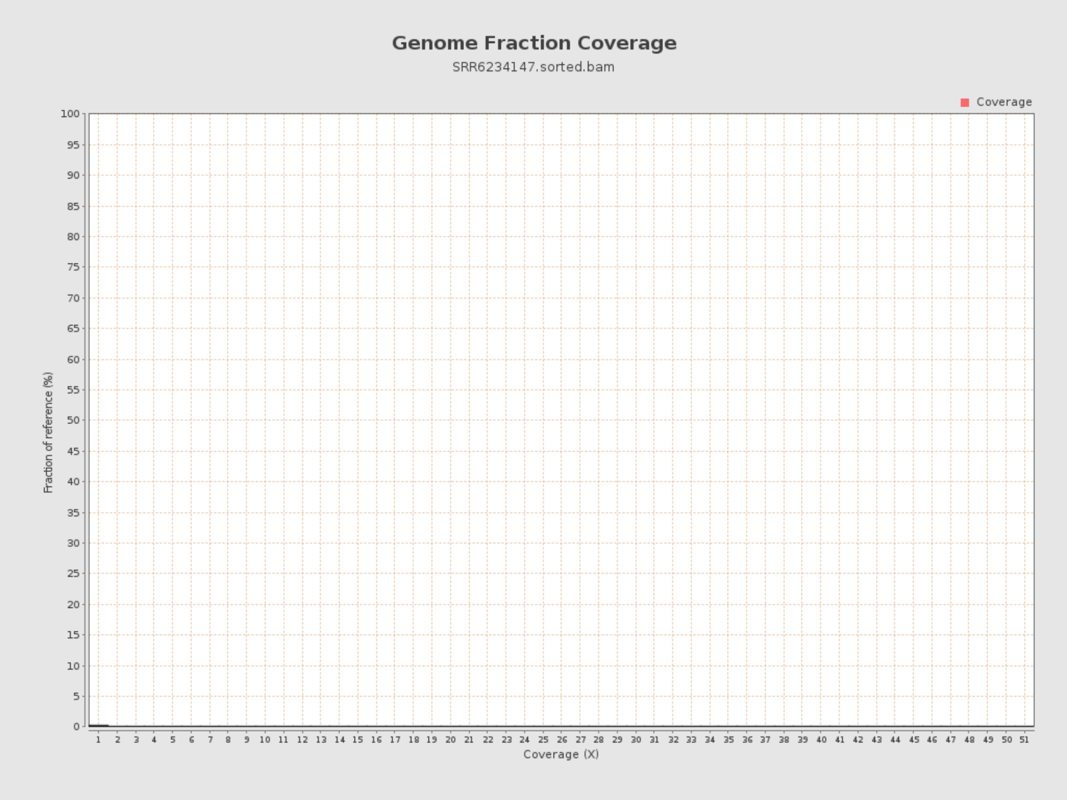
4. Results : Coverage Histogram



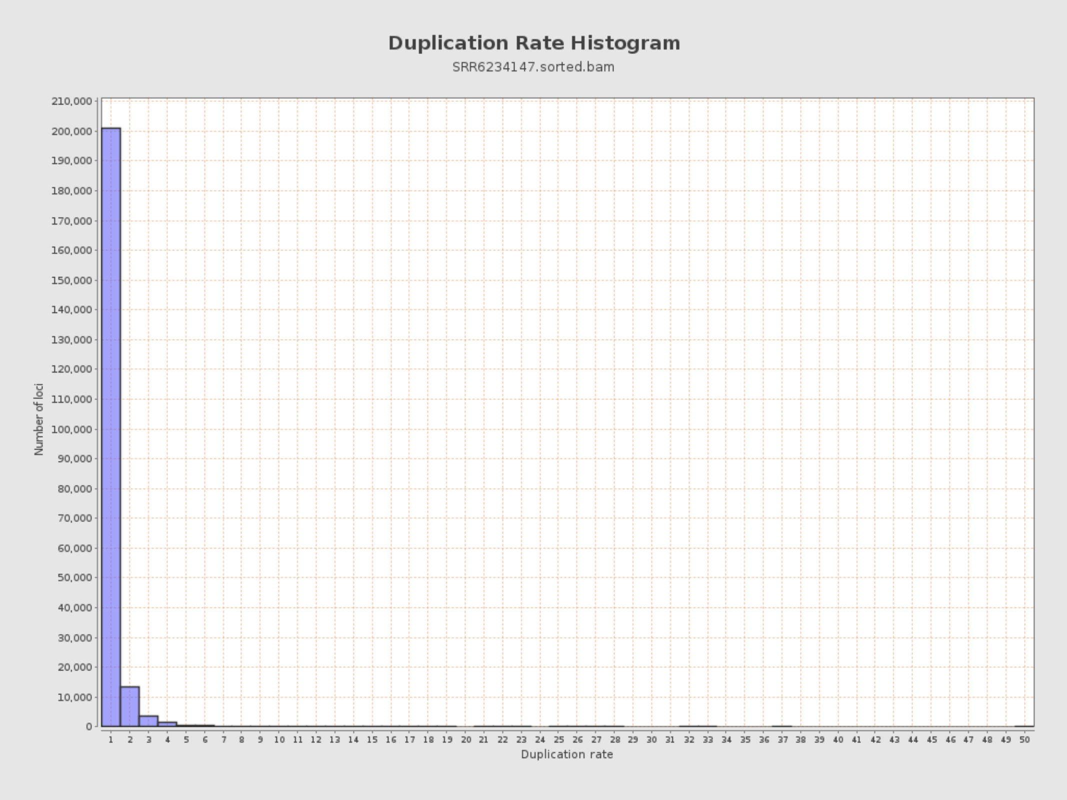
5. Results : Coverage Histogram (0-50X)



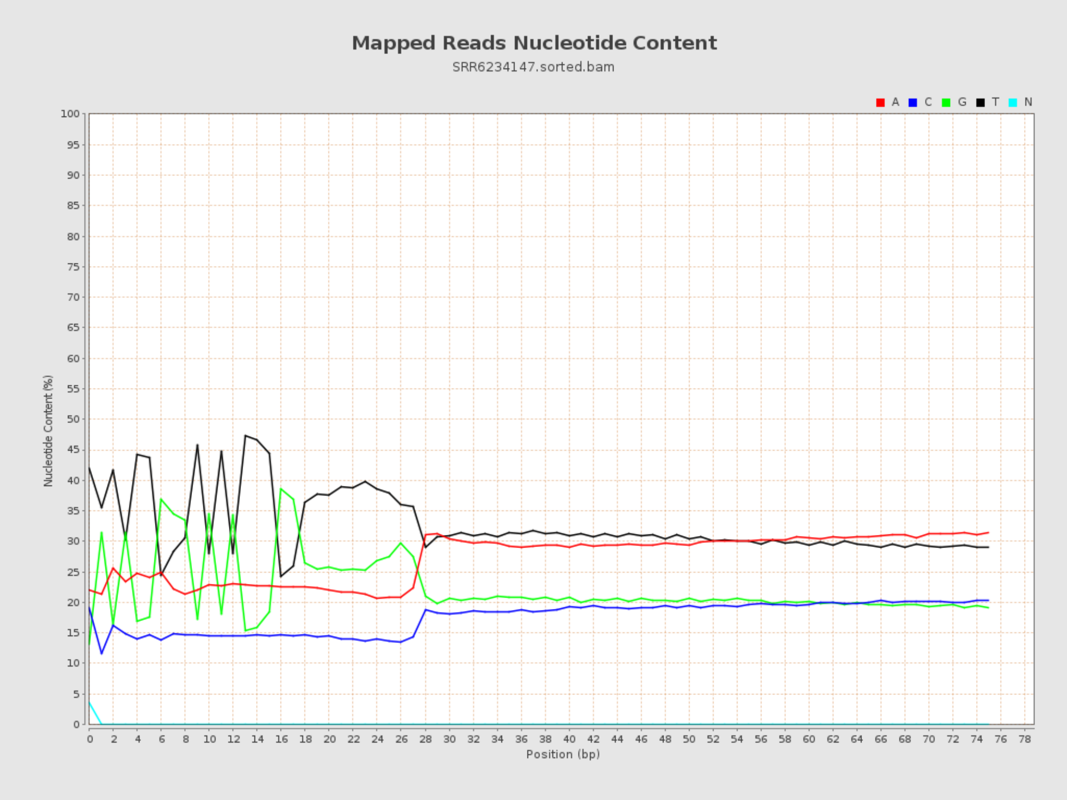
6. Results : Genome Fraction Coverage



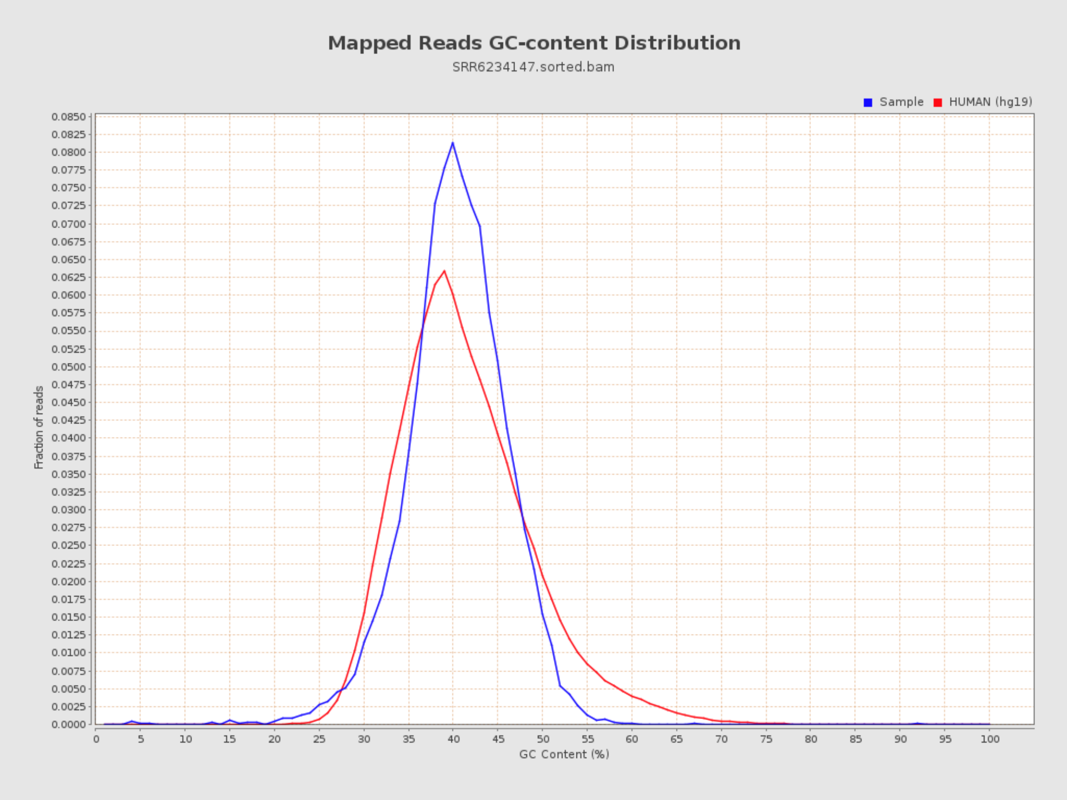
7. Results : Duplication Rate Histogram



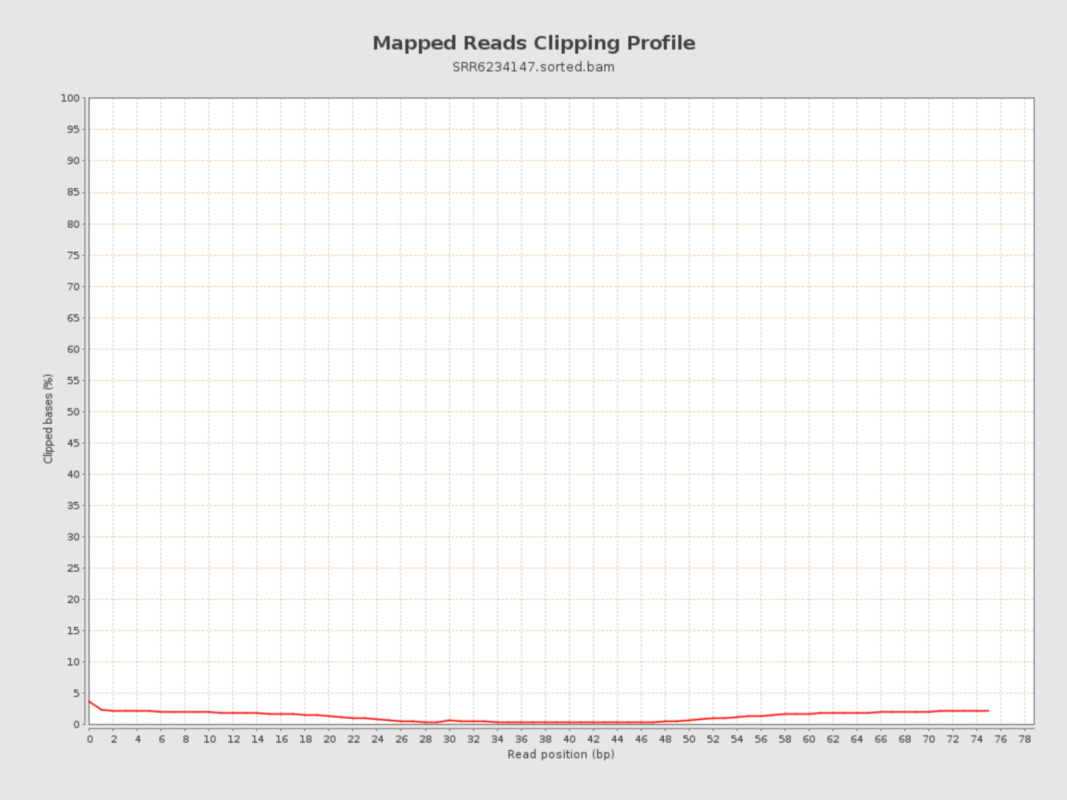
8. Results : Mapped Reads Nucleotide Content



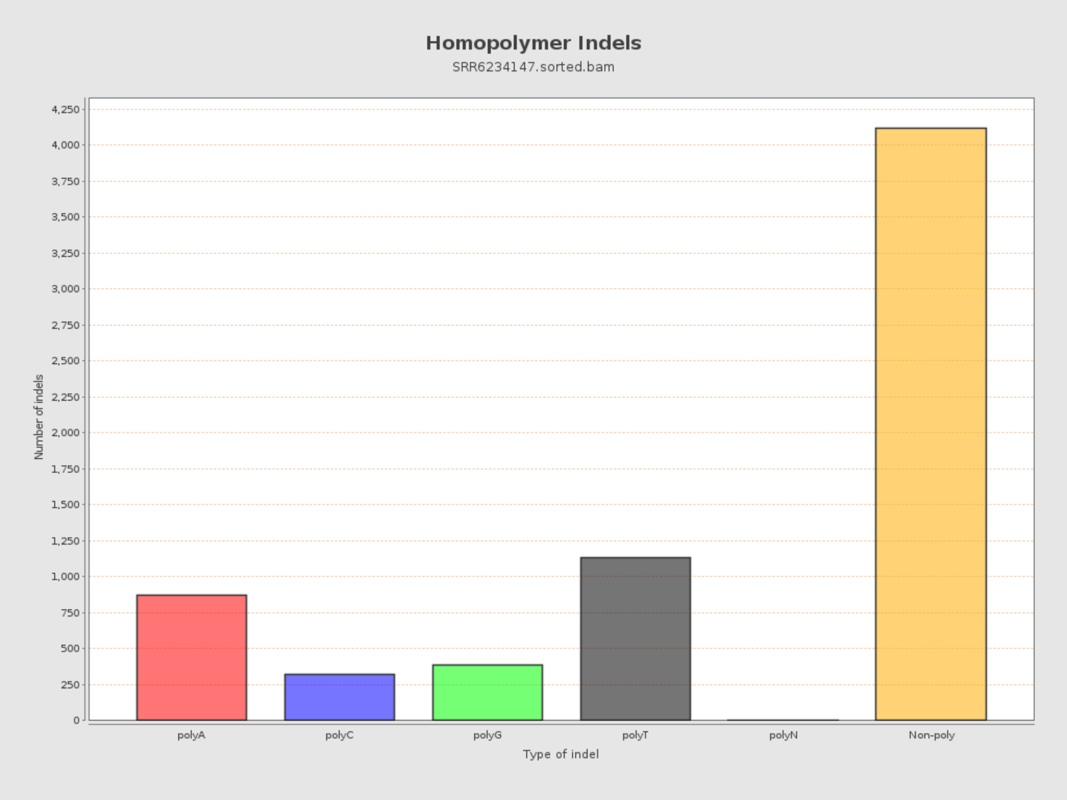
9. Results : Mapped Reads GC-content Distribution



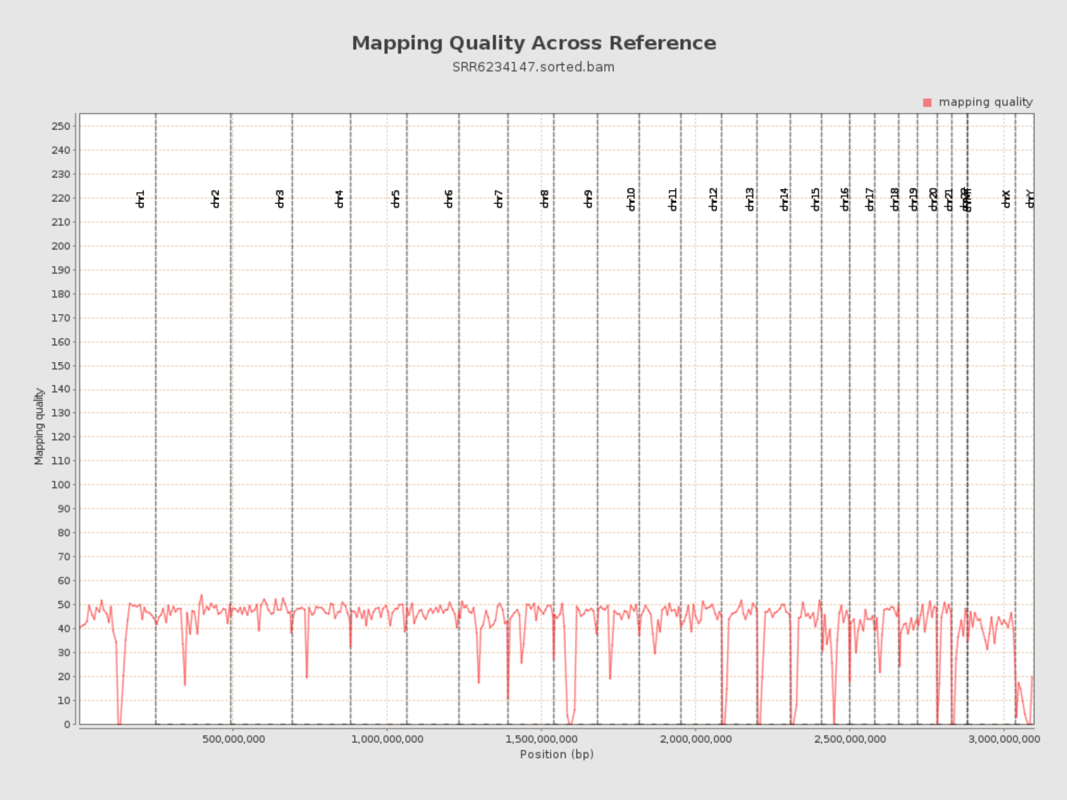
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram