Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 21:40:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174017.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_SRR10174017 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174017_1.fastq.gz SRR10174017_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 21:40:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174017.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,125,814
Mapped reads	3,041,051 / 97.29%
Unmapped reads	84,763 / 2.71%
Mapped paired reads	3,041,051 / 97.29%
Mapped reads, first in pair	1,522,848 / 48.72%
Mapped reads, second in pair	1,518,203 / 48.57%
Mapped reads, both in pair	2,983,618 / 95.45%
Mapped reads, singletons	57,433 / 1.84%
Secondary alignments	0
Supplementary alignments	312,390 / 9.99%
Read min/max/mean length	30 / 133 / 128.38
Duplicated reads (estimated)	2,336,942 / 74.76%
Duplication rate	63.83%
Clipped reads	1,315,004 / 42.07%

2.2. ACGT Content

Number/percentage of A's	107,950,318 / 30.14%
Number/percentage of C's	69,806,635 / 19.49%
Number/percentage of T's	107,876,101 / 30.12%
Number/percentage of G's	72,468,969 / 20.24%
Number/percentage of N's	4,172 / 0%

GC Percentage	39.73%

2.3. Coverage

Mean	0.1157
Standard Deviation	1.8527

2.4. Mapping Quality

Mean Mapping Quality	52.49

2.5. Insert size

Mean	986,177.3
Standard Deviation	9,250,216.3
P25/Median/P75	145 / 203 / 296

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	3,725,129
Insertions	38,806
Mapped reads with at least one insertion	1.23%
Deletions	87,170
Mapped reads with at least one deletion	2.79%
Homopolymer indels	42.9%

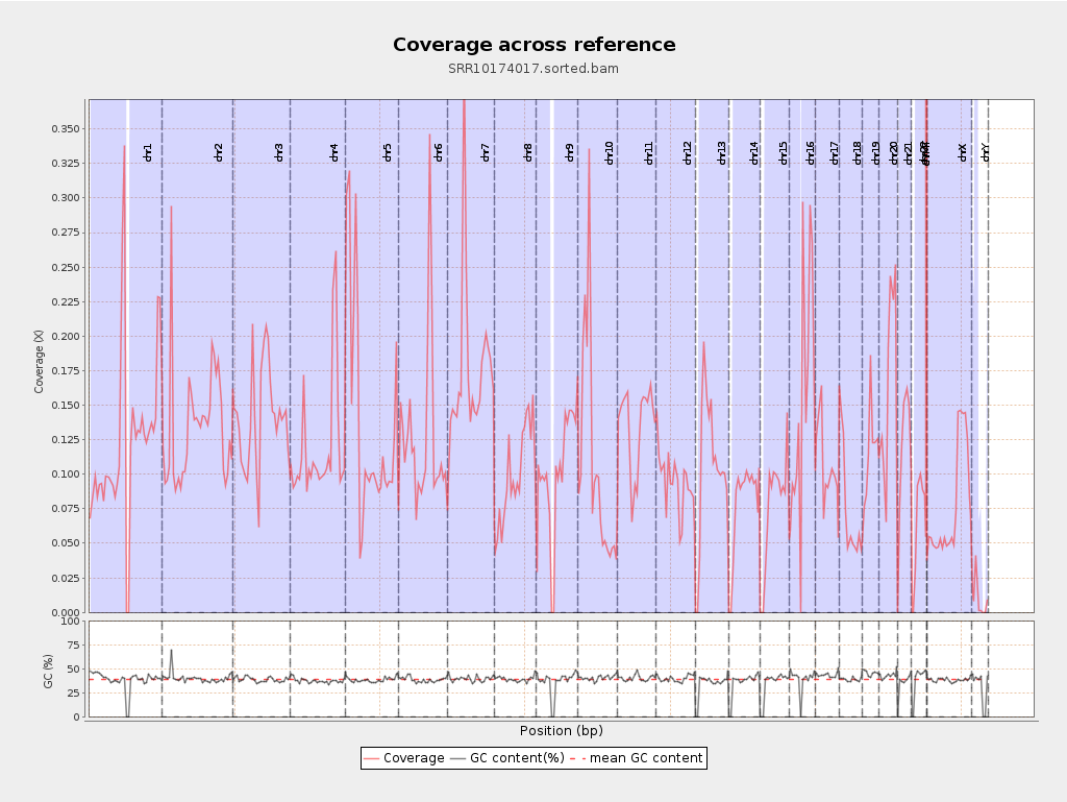
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

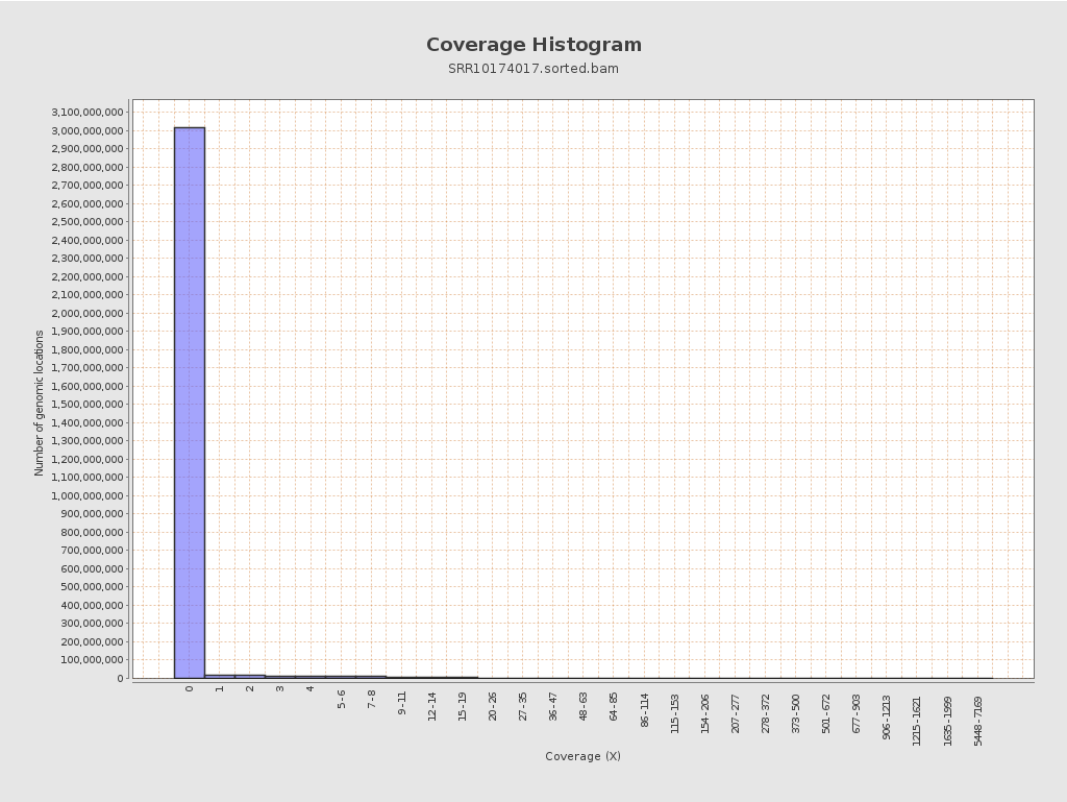
		bases	coverage	deviation
chr1	249250621	30659492	0.123	1.5874
chr2	243199373	32564143	0.1339	5.0686
chr3	198022430	27977705	0.1413	1.0723
chr4	191154276	22373013	0.117	1.1504
chr5	180915260	25035224	0.1384	1.0605
chr6	171115067	21746414	0.1271	1.0455
chr7	159138663	27976822	0.1758	1.987
chr8	146364022	14627312	0.0999	1.044
chr9	141213431	14353374	0.1016	1.0444
chr10	135534747	14393489	0.1062	1.9224
chr11	135006516	18162732	0.1345	1.0629
chr12	133851895	12570950	0.0939	0.8716
chr13	115169878	12149231	0.1055	0.934
chr14	107349540	8249482	0.0768	0.7882
chr15	102531392	7795786	0.076	0.7697
chr16	90354753	13870110	0.1535	1.5081
chr17	81195210	8488080	0.1045	0.9652
chr18	78077248	5819842	0.0745	1.2524
chr19	59128983	6835540	0.1156	1.632
chr20	63025520	10376062	0.1646	1.1458
chr21	48129895	5641677	0.1172	1.0058
chr22	51304566	3185038	0.0621	0.6692
chrMT	16571	1131248	68.2667	56.5506
chrX	155270560	11788390	0.0759	0.7781

chrY	59373566	549277	0.0093	0.4463

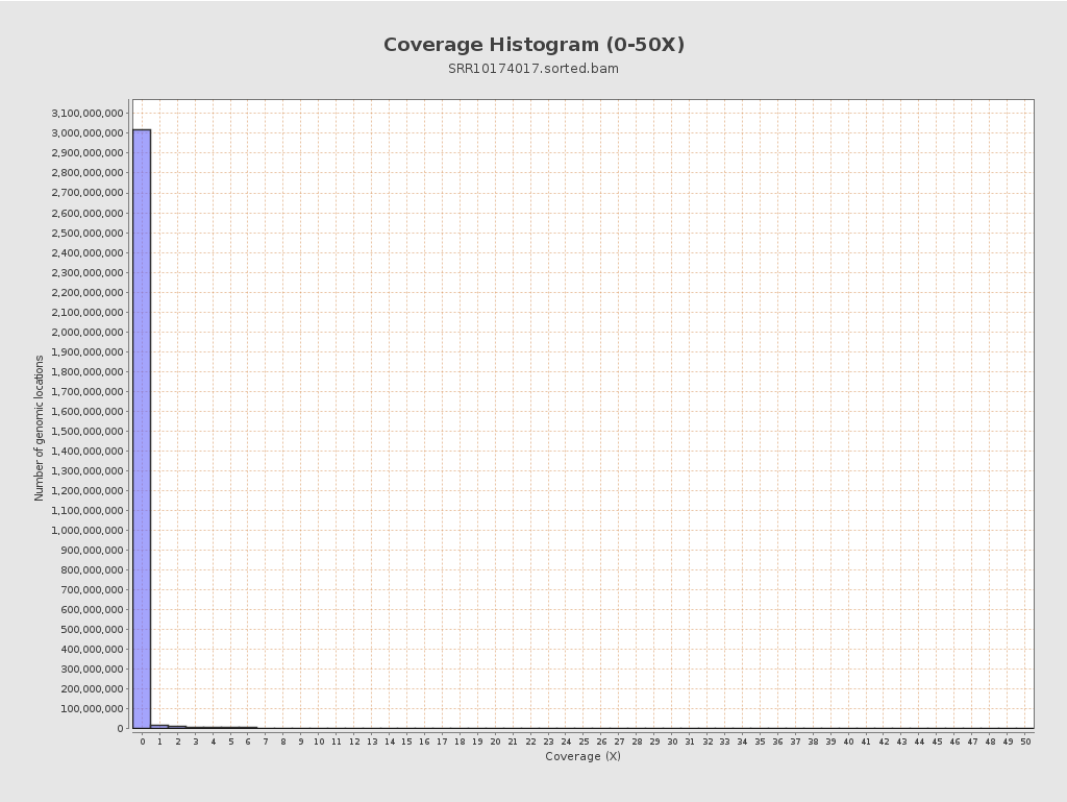
3. Results : Coverage across reference



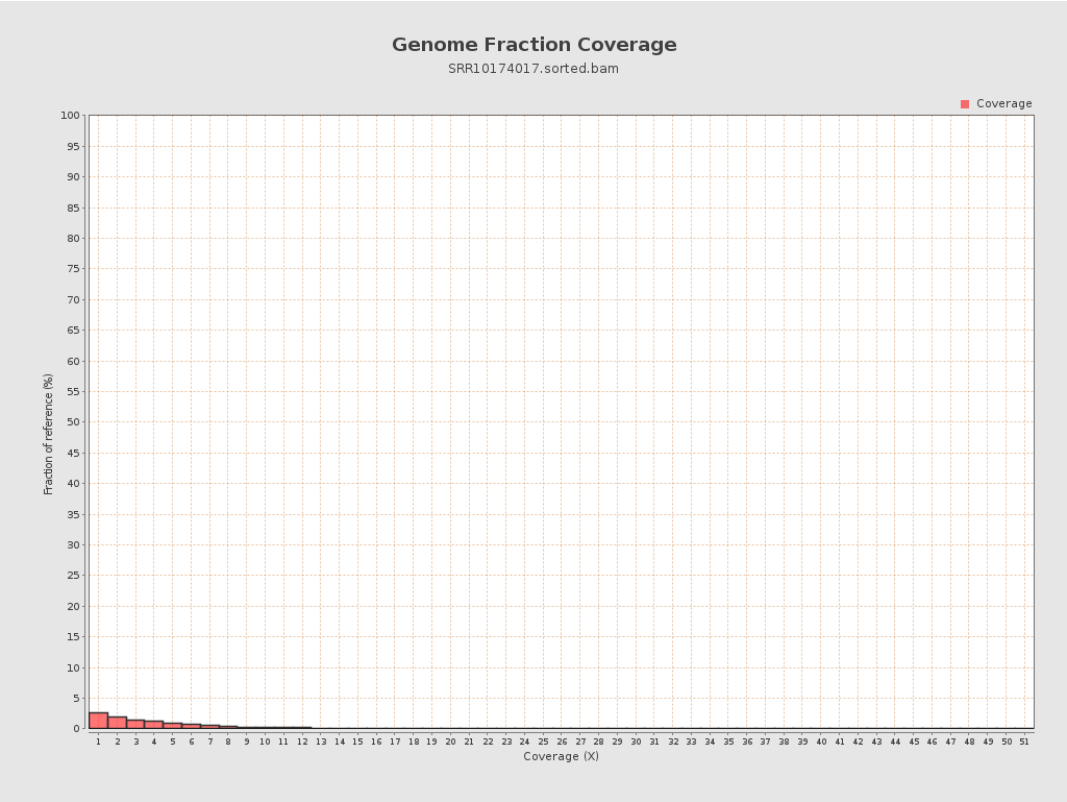
4. Results : Coverage Histogram



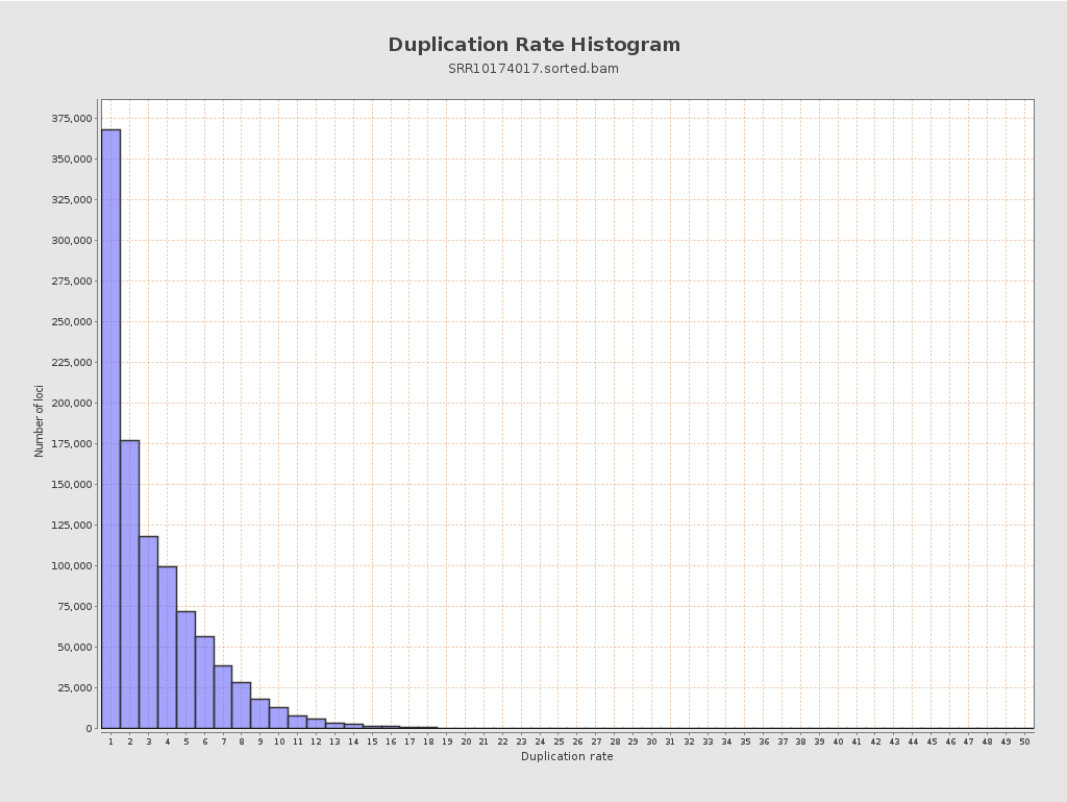
5. Results : Coverage Histogram (0-50X)



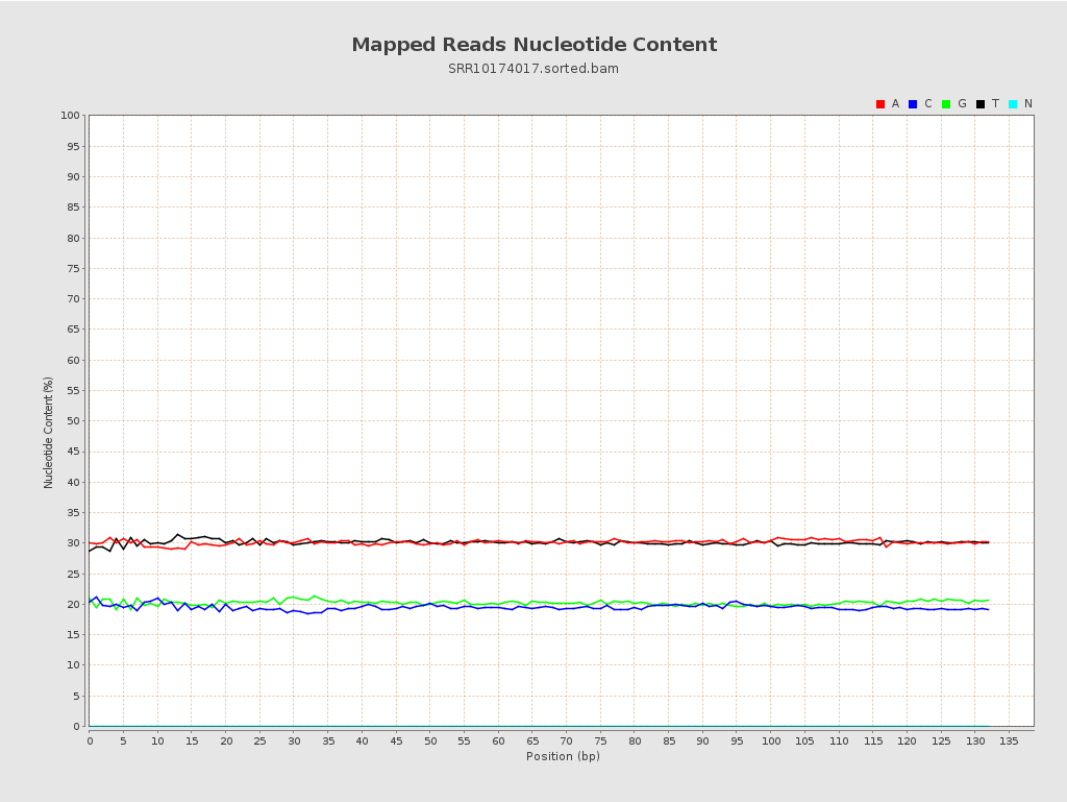
6. Results : Genome Fraction Coverage



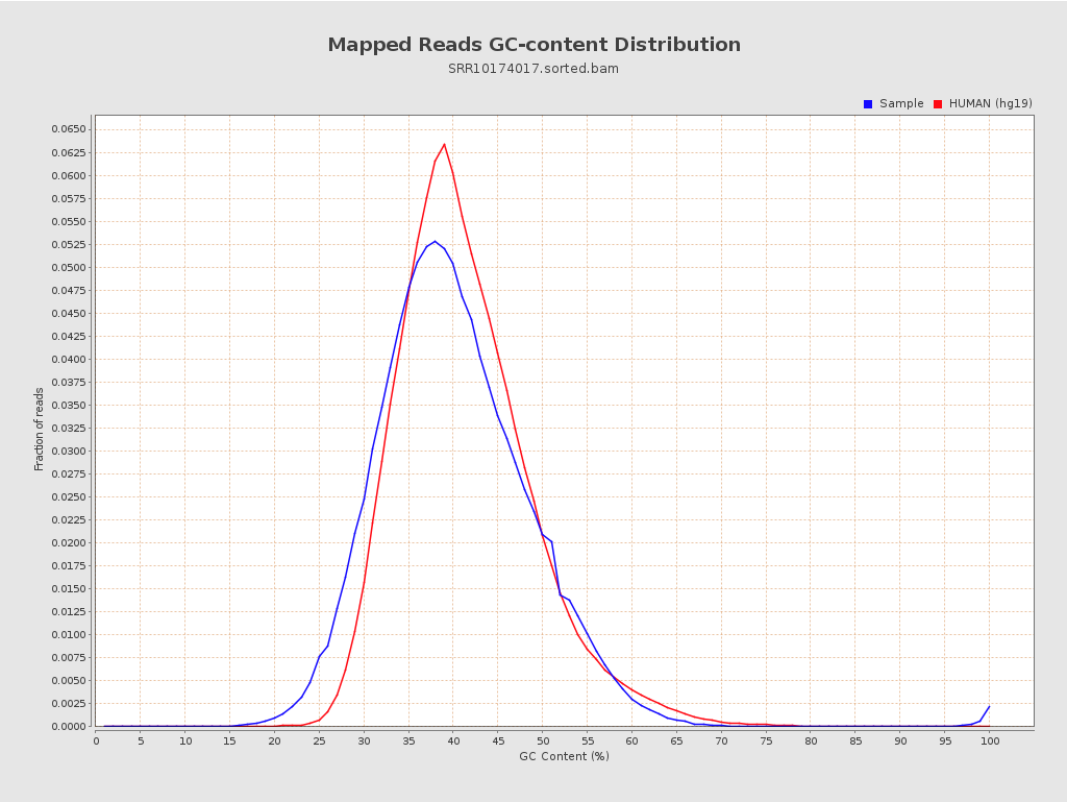
7. Results : Duplication Rate Histogram



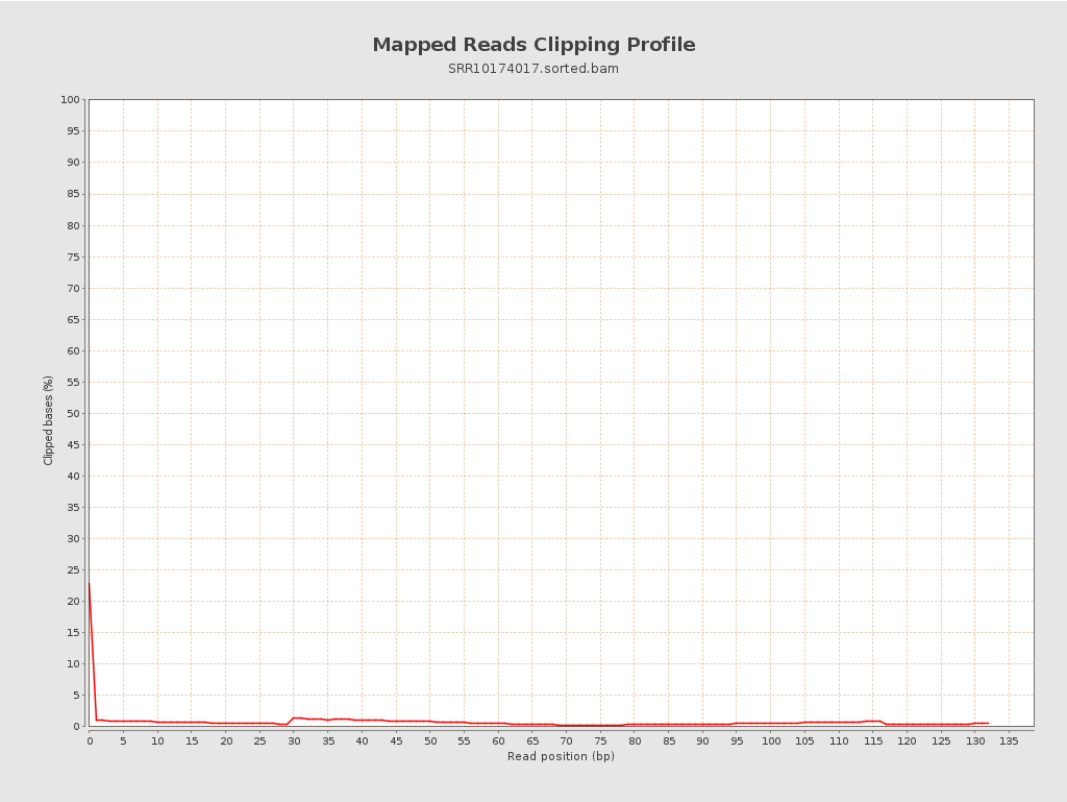
8. Results : Mapped Reads Nucleotide Content



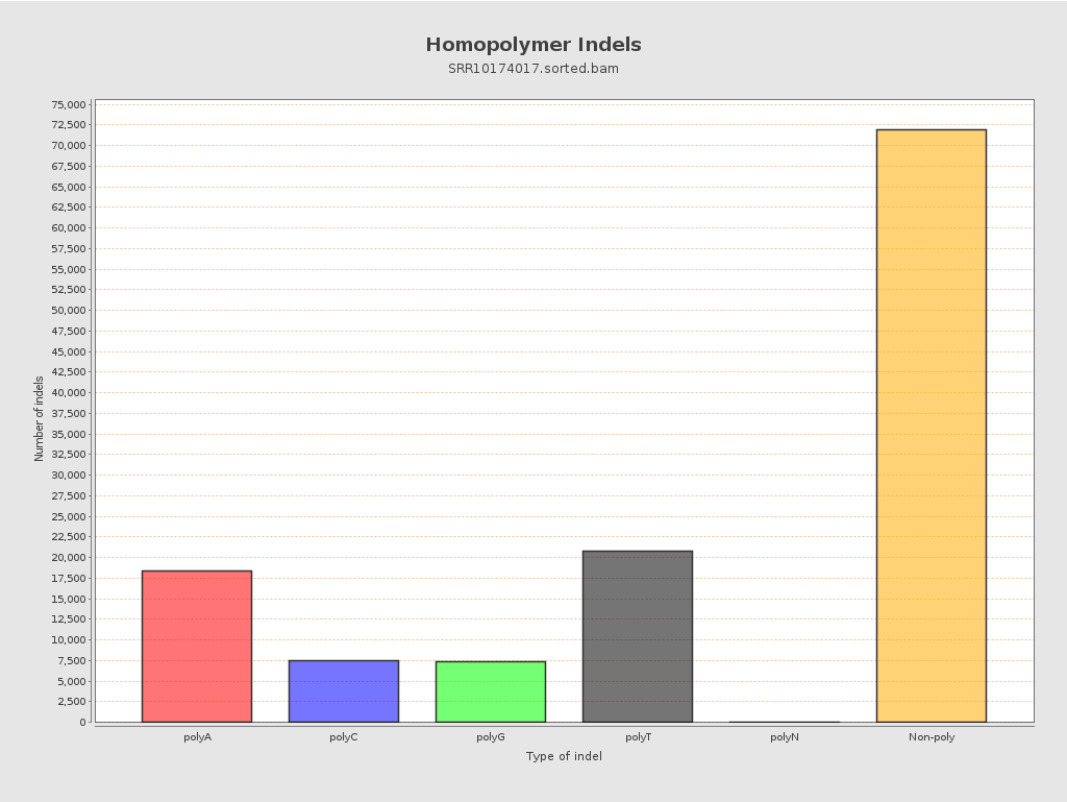
9. Results : Mapped Reads GC-content Distribution



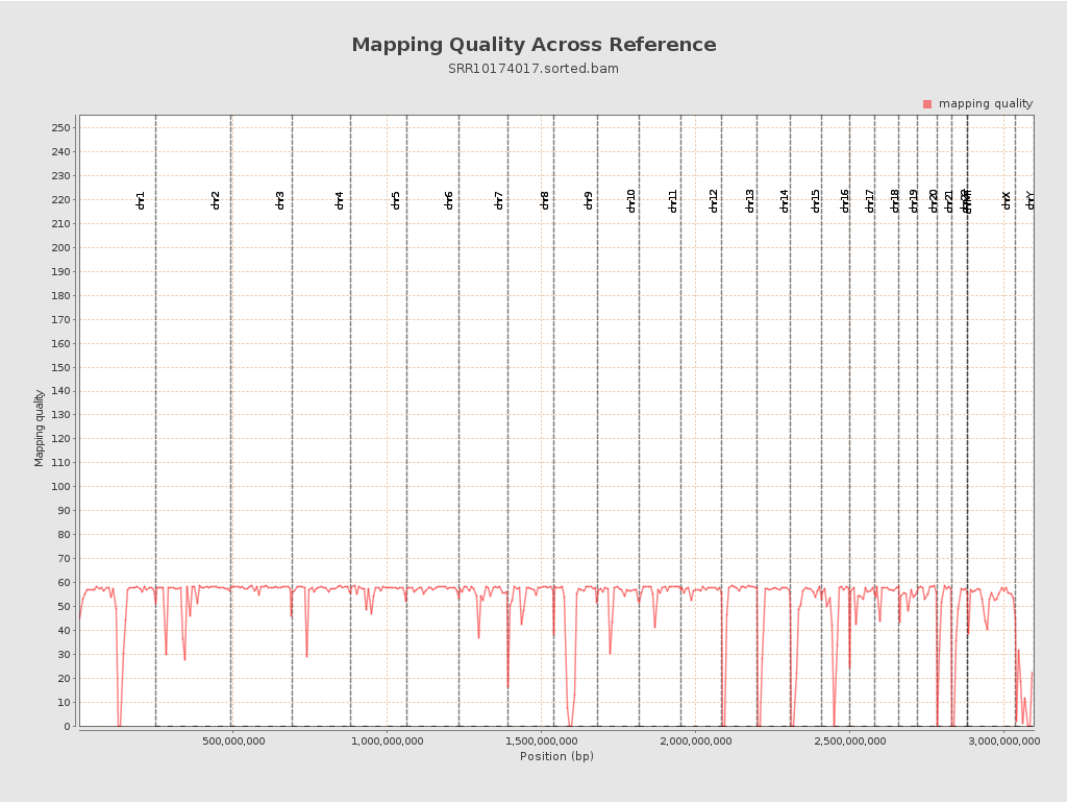
10. Results : Mapped Reads Clipping Profile



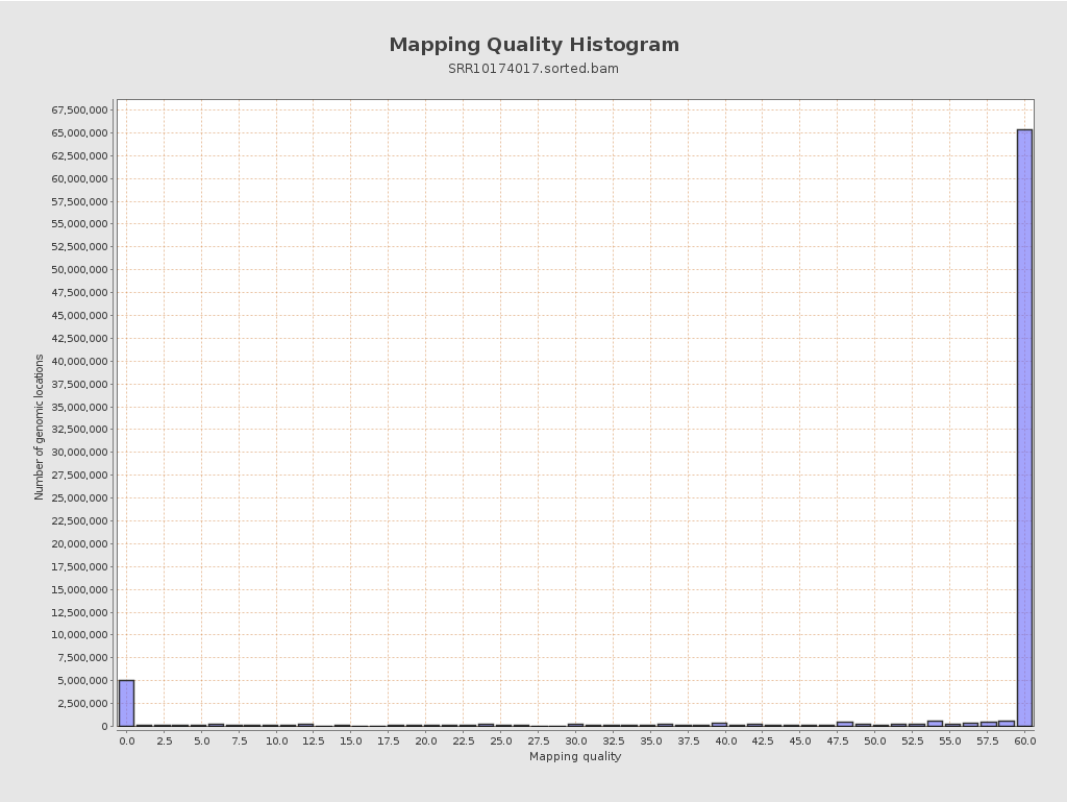
11. Results : Homopolymer Indels



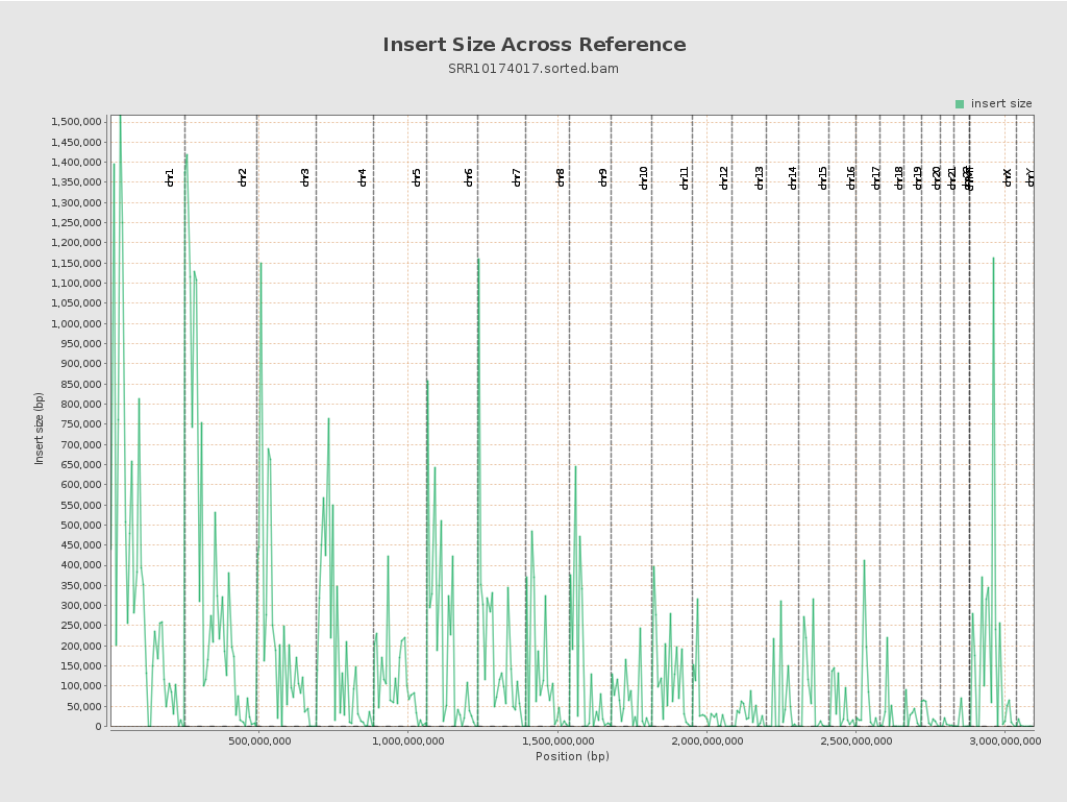
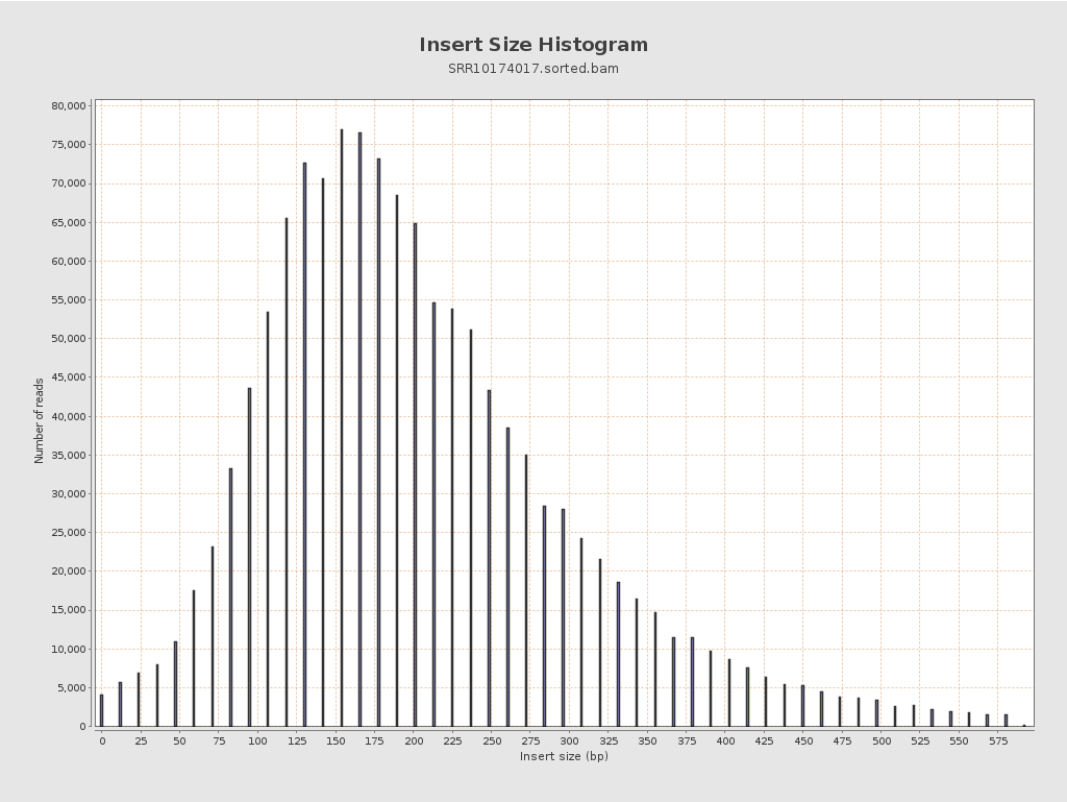
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram