Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 18:01:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617375.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_SRR617375 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617375_1.fastq.gz SRR617375_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 18:01:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617375.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,004,283 / 93.76%
Unmapped reads	1,995,717 / 6.24%
Mapped paired reads	30,004,283 / 93.76%
Mapped reads, first in pair	15,077,610 / 47.12%
Mapped reads, second in pair	14,926,673 / 46.65%
Mapped reads, both in pair	29,446,224 / 92.02%
Mapped reads, singletons	558,059 / 1.74%
Secondary alignments	0
Supplementary alignments	65,868 / 0.21%
Read min/max/mean length	30 / 100 / 100.08
Duplicated reads (estimated)	1,548,930 / 4.84%
Duplication rate	1.47%
Clipped reads	2,608,944 / 8.15%

2.2. ACGT Content

Number/percentage of A's	892,483,060 / 30.35%
Number/percentage of C's	582,346,979 / 19.8%
Number/percentage of T's	879,245,274 / 29.9%
Number/percentage of G's	584,596,586 / 19.88%
Number/percentage of N's	2,176,810 / 0.07%

GC Percentage	39.68%

2.3. Coverage

Mean	0.9503
Standard Deviation	9.732

2.4. Mapping Quality

Mean Mapping Quality	53.45

2.5. Insert size

Mean	50,455.18
Standard Deviation	2,124,350.18
P25/Median/P75	171 / 211 / 272

2.6. Mismatches and indels

General error rate	1.19%
Mismatches	34,347,963
Insertions	293,363
Mapped reads with at least one insertion	0.95%
Deletions	356,239
Mapped reads with at least one deletion	1.15%
Homopolymer indels	41.05%

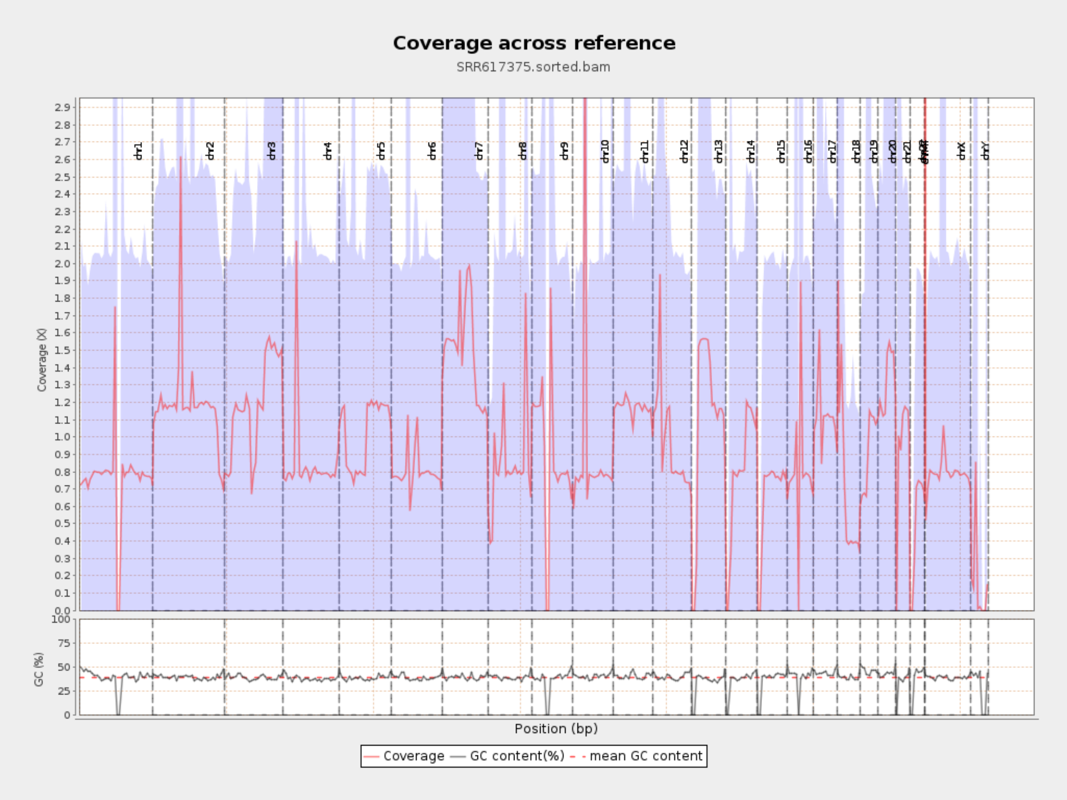
2.7. Chromosome stats

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

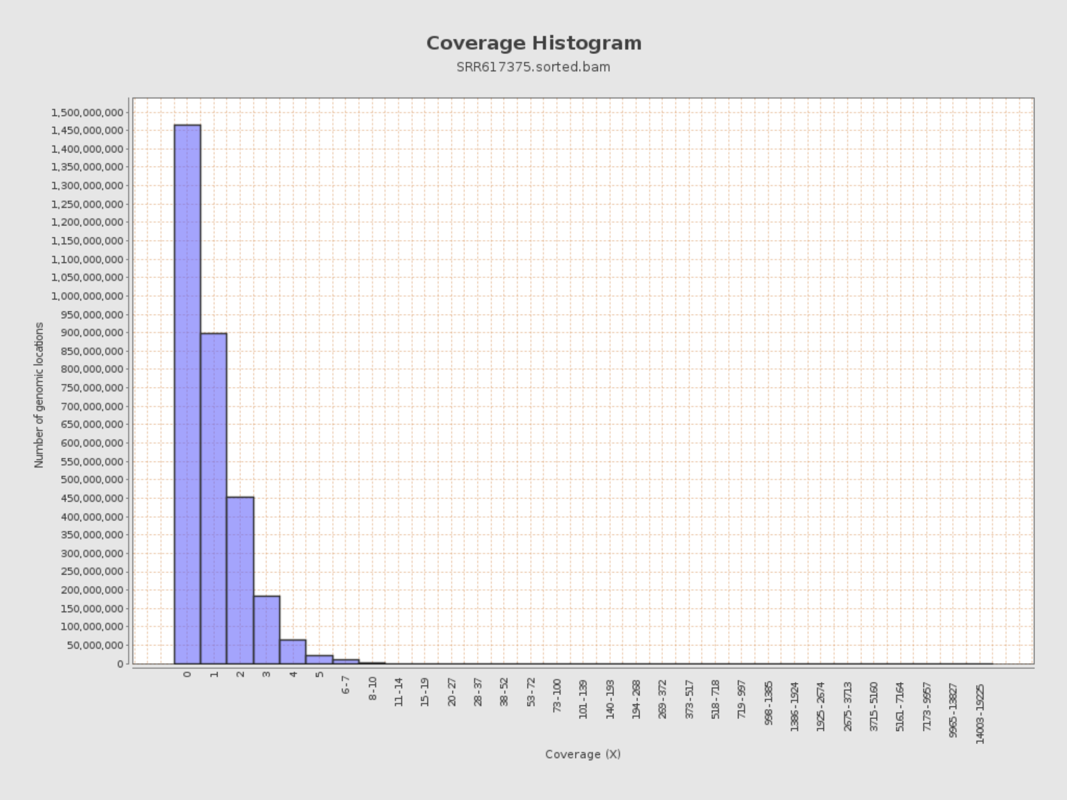
		bases	coverage	deviation
chr1	249250621	190610836	0.7647	19.7965
chr2	243199373	290469007	1.1944	8.7374
chr3	198022430	234266667	1.183	1.4906
chr4	191154276	161659387	0.8457	9.144
chr5	180915260	185238511	1.0239	1.4653
chr6	171115067	138173775	0.8075	3.7052
chr7	159138663	239479310	1.5048	10.8481
chr8	146364022	124094180	0.8478	7.5983
chr9	141213431	123913517	0.8775	14.8058
chr10	135534747	124052245	0.9153	20.1633
chr11	135006516	157687802	1.168	5.5266
chr12	133851895	129911941	0.9706	1.349
chr13	115169878	128871680	1.119	1.2922
chr14	107349540	85163614	0.7933	1.3867
chr15	102531392	65881352	0.6425	0.97
chr16	90354753	73616197	0.8147	7.8812
chr17	81195210	90679169	1.1168	7.1412
chr18	78077248	53084355	0.6799	15.1215
chr19	59128983	54026787	0.9137	9.5551
chr20	63025520	83803465	1.3297	2.3897
chr21	48129895	46767761	0.9717	3.189
chr22	51304566	25714433	0.5012	0.904
chrMT	16571	1995309	120.4097	21.2611
chrX	155270560	122556910	0.7893	2.9888

chrY	59373566	9986050	0.1682	8.1906

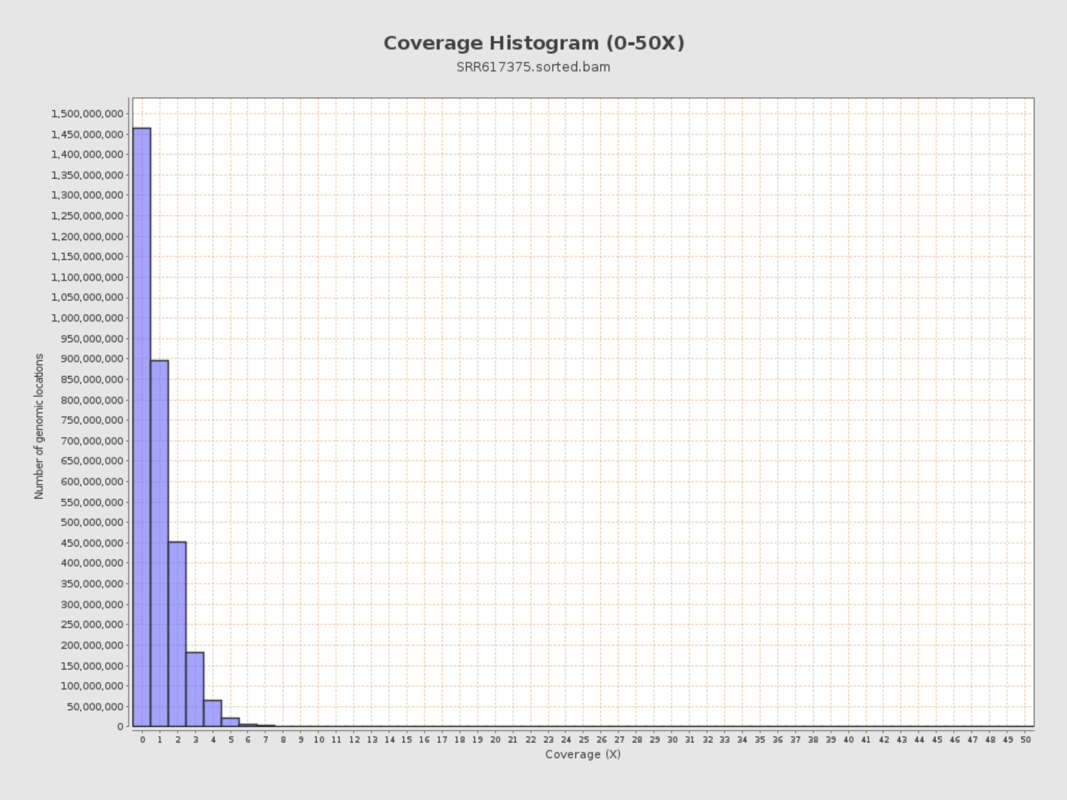
3. Results : Coverage across reference



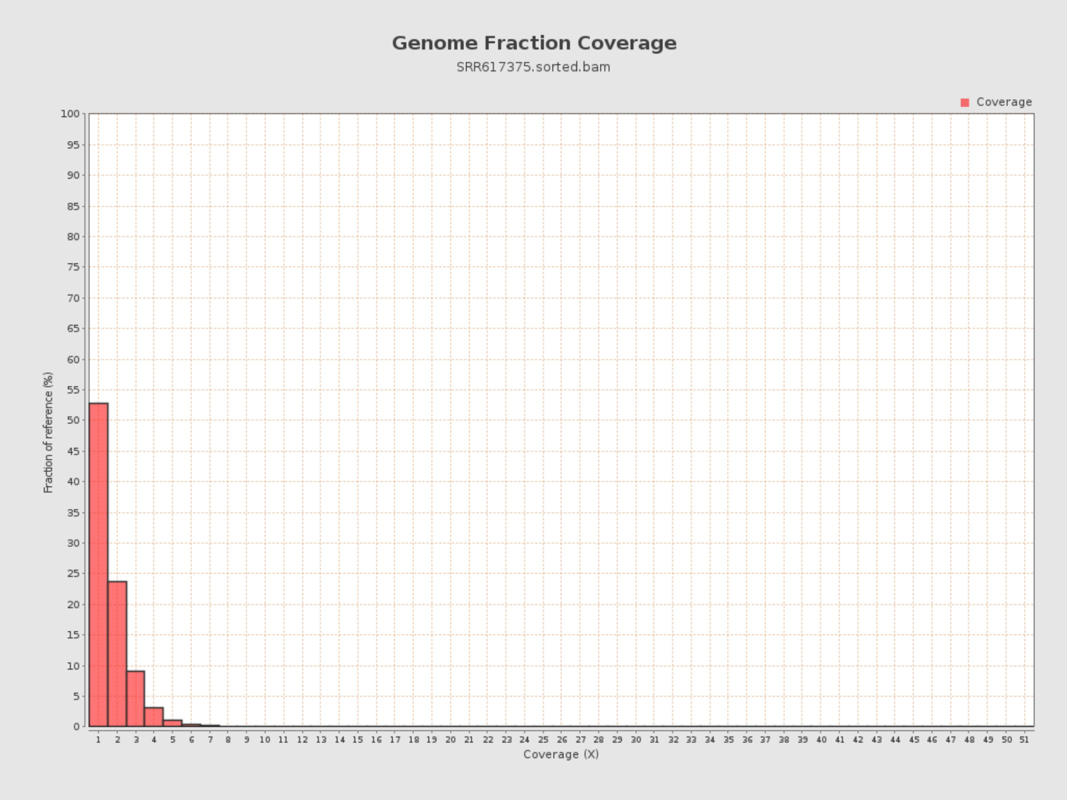
4. Results : Coverage Histogram



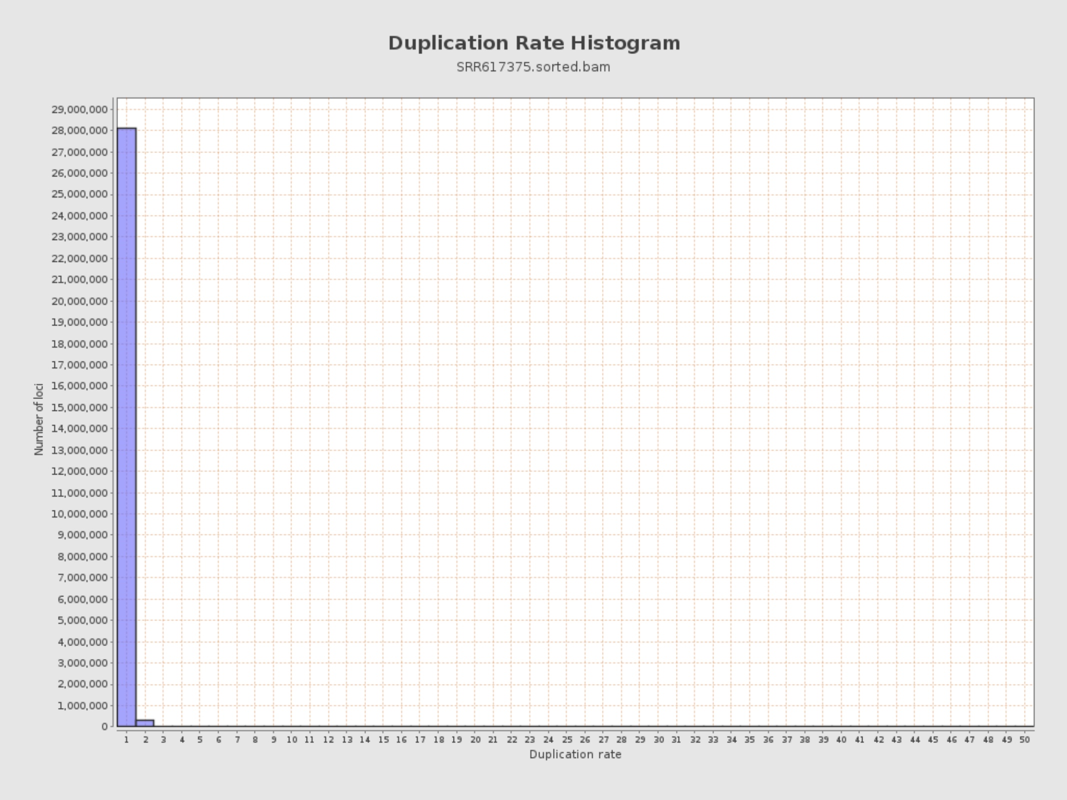
5. Results : Coverage Histogram (0-50X)



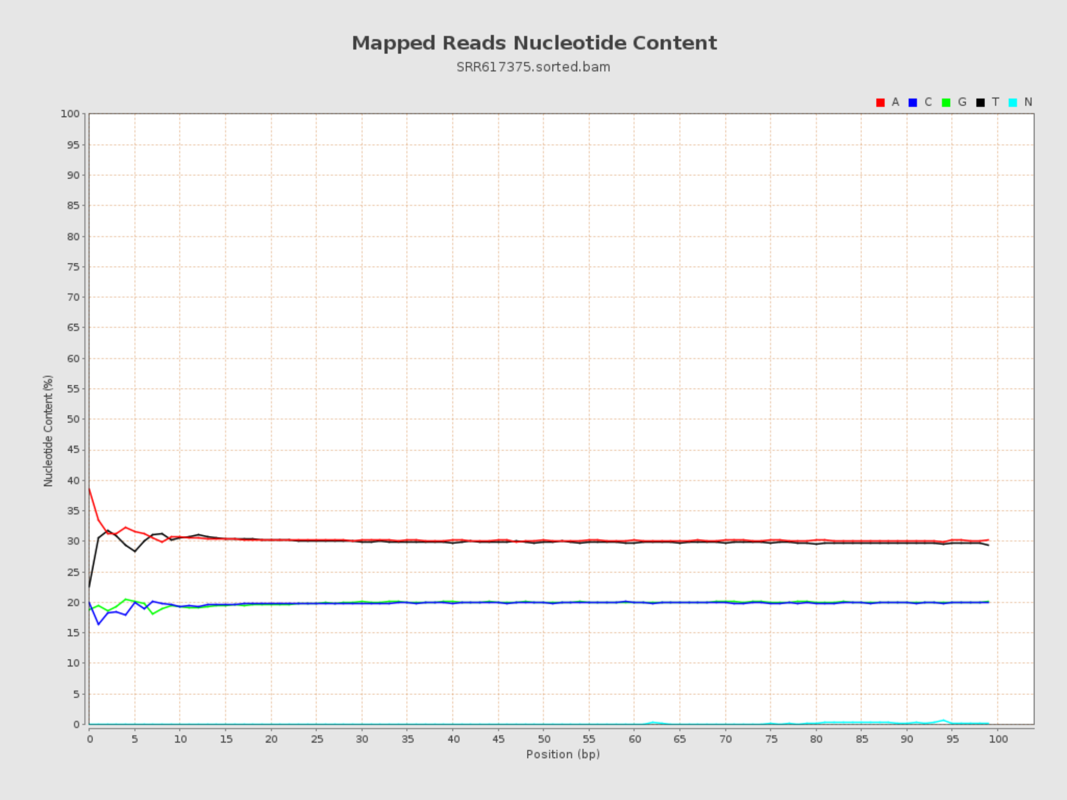
6. Results : Genome Fraction Coverage



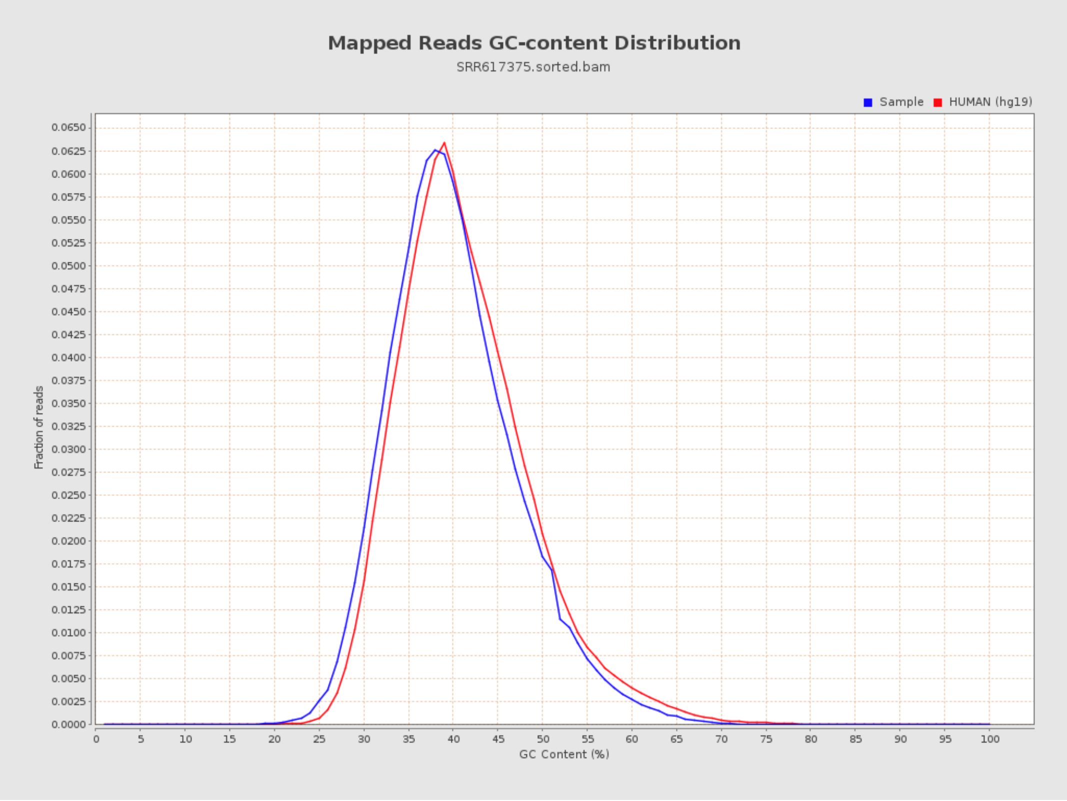
7. Results : Duplication Rate Histogram



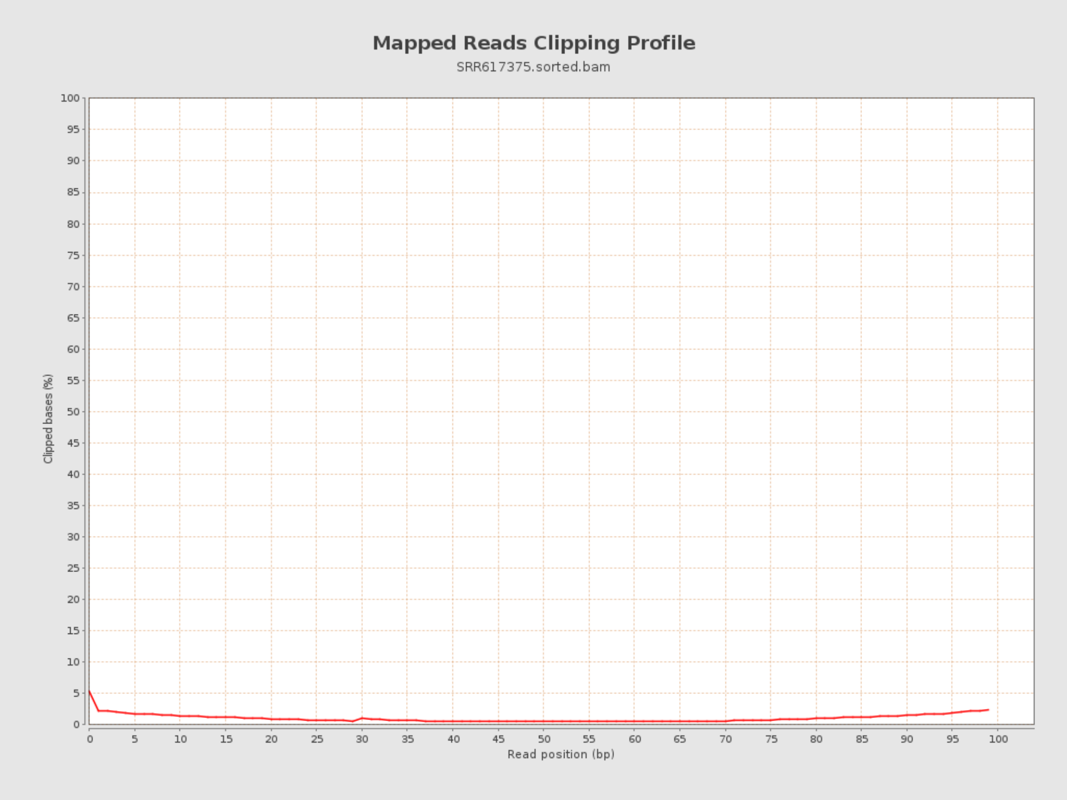
8. Results : Mapped Reads Nucleotide Content



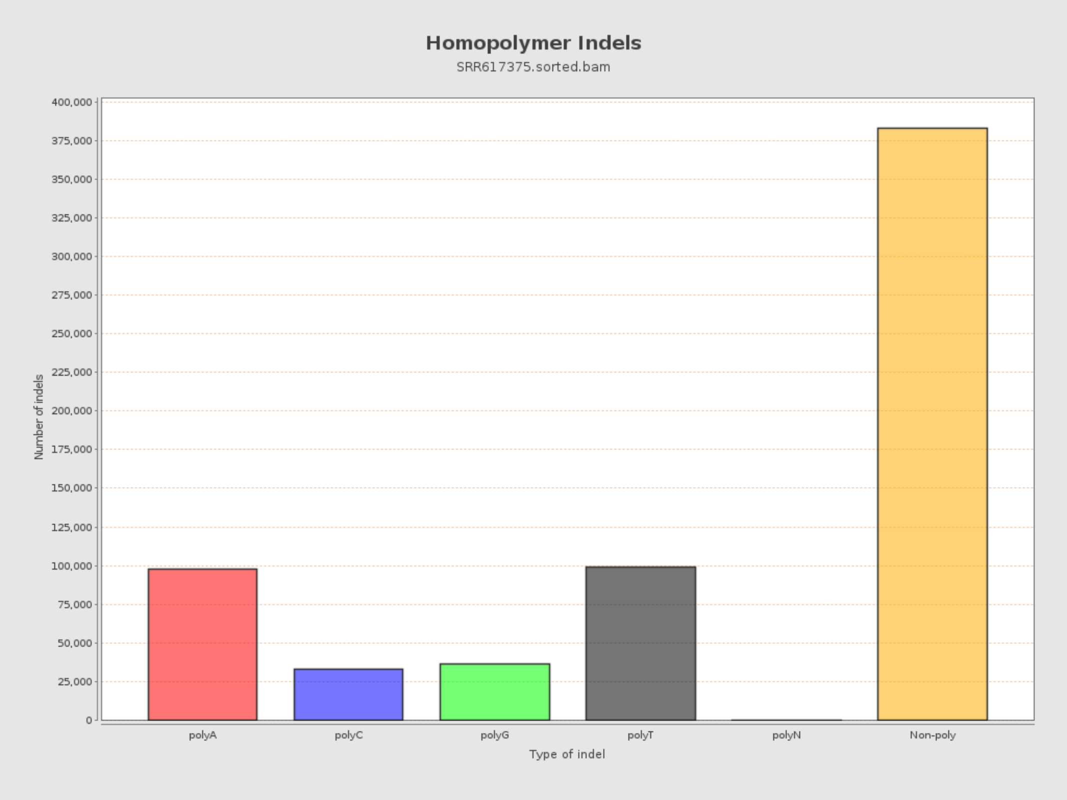
9. Results : Mapped Reads GC-content Distribution



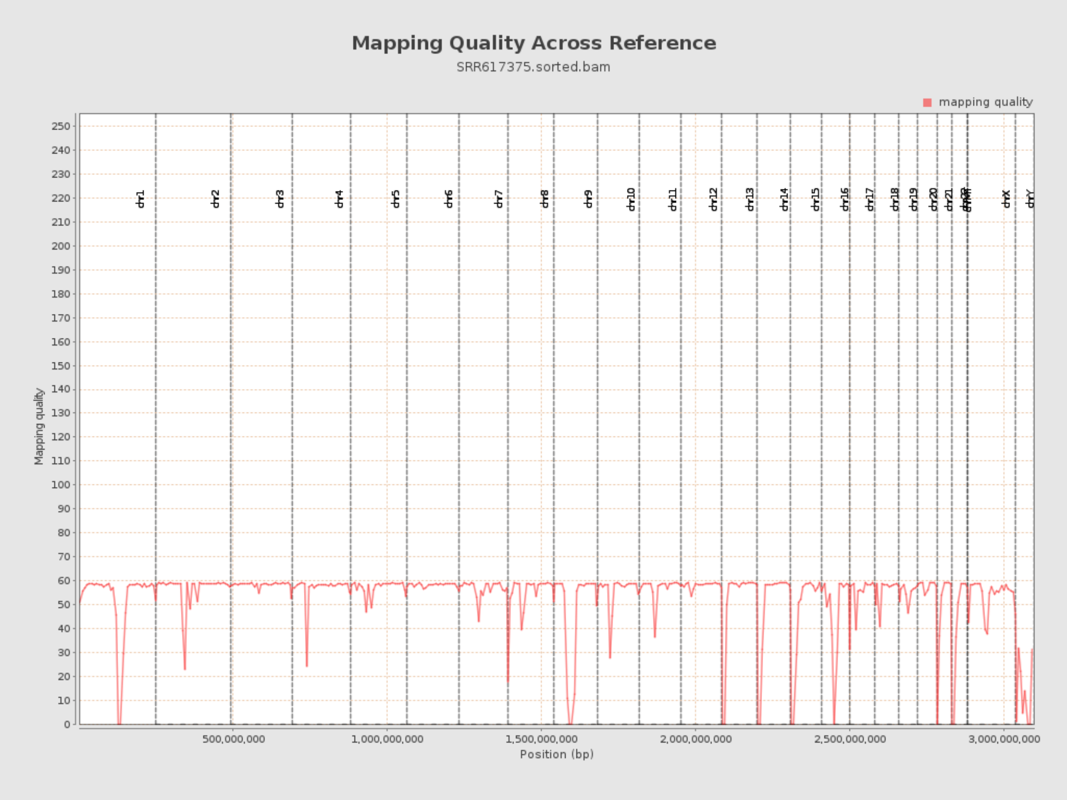
10. Results : Mapped Reads Clipping Profile



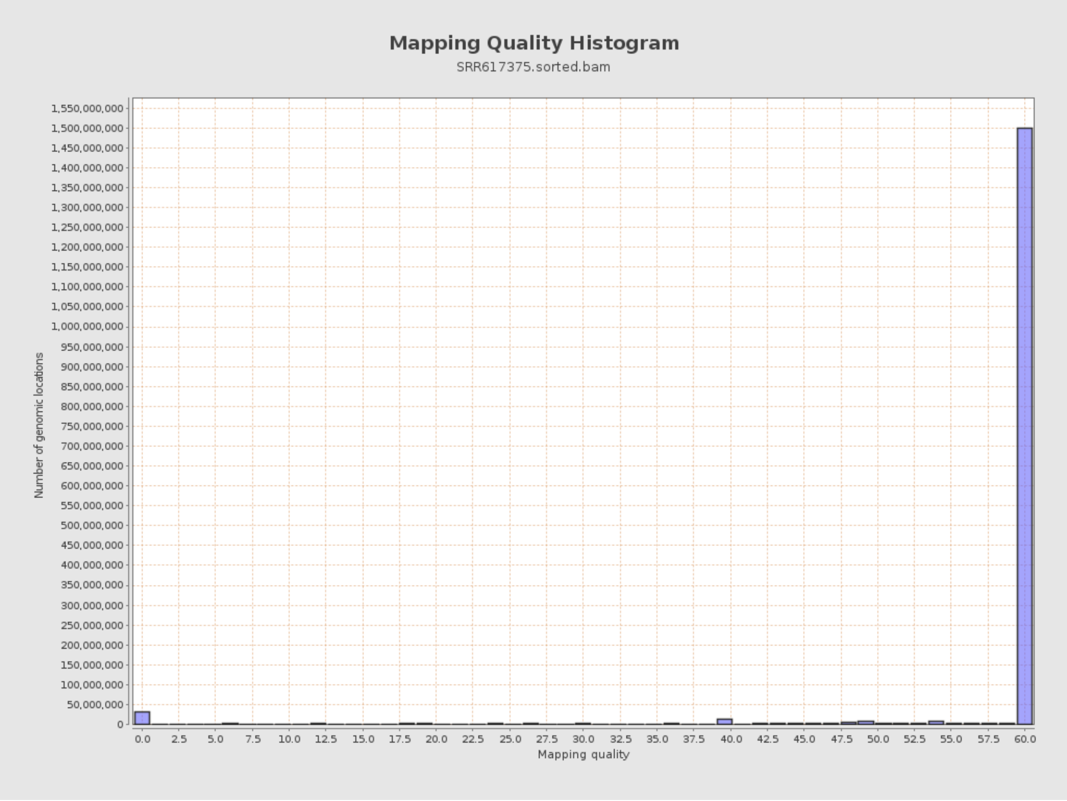
11. Results : Homopolymer Indels



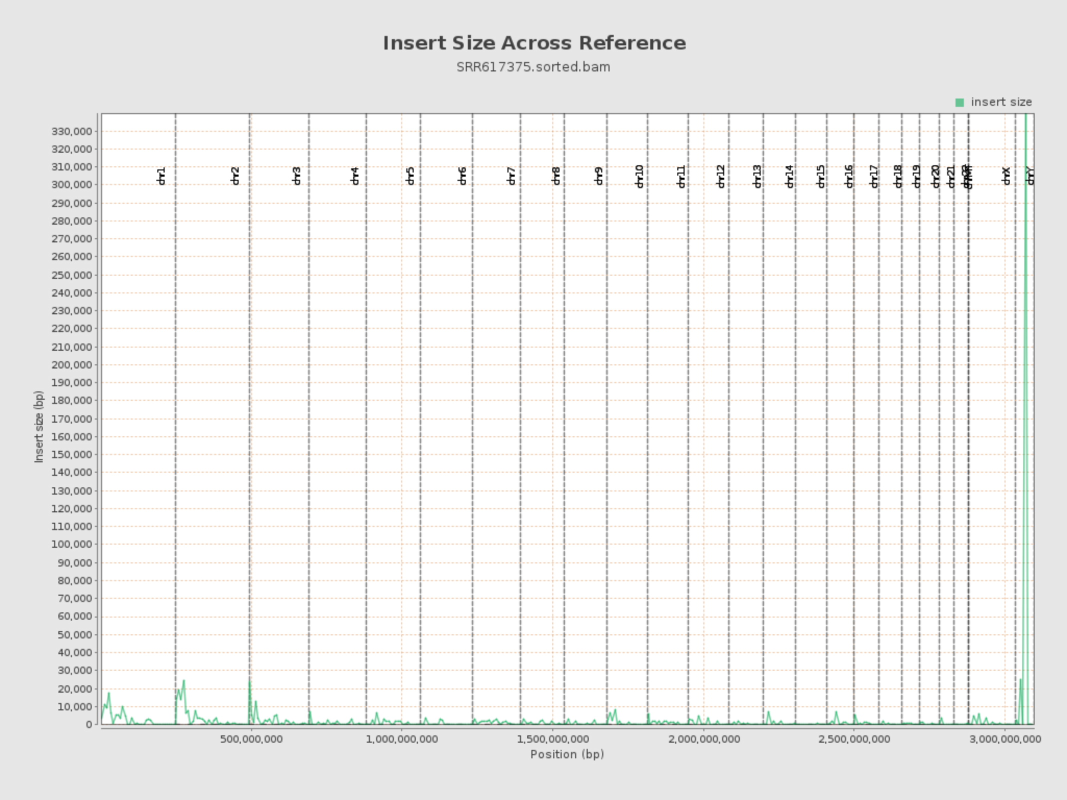
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram