Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 18:54:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617376.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_SRR617376 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617376_1.fastq.gz SRR617376_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 18:54:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617376.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	27,985,361 / 87.45%
Unmapped reads	4,014,639 / 12.55%
Mapped paired reads	27,985,361 / 87.45%
Mapped reads, first in pair	14,380,099 / 44.94%
Mapped reads, second in pair	13,605,262 / 42.52%
Mapped reads, both in pair	26,846,328 / 83.89%
Mapped reads, singletons	1,139,033 / 3.56%
Secondary alignments	0
Supplementary alignments	60,814 / 0.19%
Read min/max/mean length	30 / 100 / 100.08
Duplicated reads (estimated)	1,368,461 / 4.28%
Duplication rate	1.44%
Clipped reads	3,155,953 / 9.86%

2.2. ACGT Content

Number/percentage of A's	829,707,019 / 30.44%
Number/percentage of C's	538,087,803 / 19.74%
Number/percentage of T's	815,370,610 / 29.91%
Number/percentage of G's	541,100,228 / 19.85%
Number/percentage of N's	1,556,781 / 0.06%

GC Percentage	39.59%

2.3. Coverage

Mean	0.8808
Standard Deviation	8.6269

2.4. Mapping Quality

Mean Mapping Quality	53.16

2.5. Insert size

Mean	49,007.79
Standard Deviation	2,106,810.83
P25/Median/P75	169 / 208 / 267

2.6. Mismatches and indels

General error rate	1.8%
Mismatches	48,338,823
Insertions	275,266
Mapped reads with at least one insertion	0.95%
Deletions	326,274
Mapped reads with at least one deletion	1.13%
Homopolymer indels	40.37%

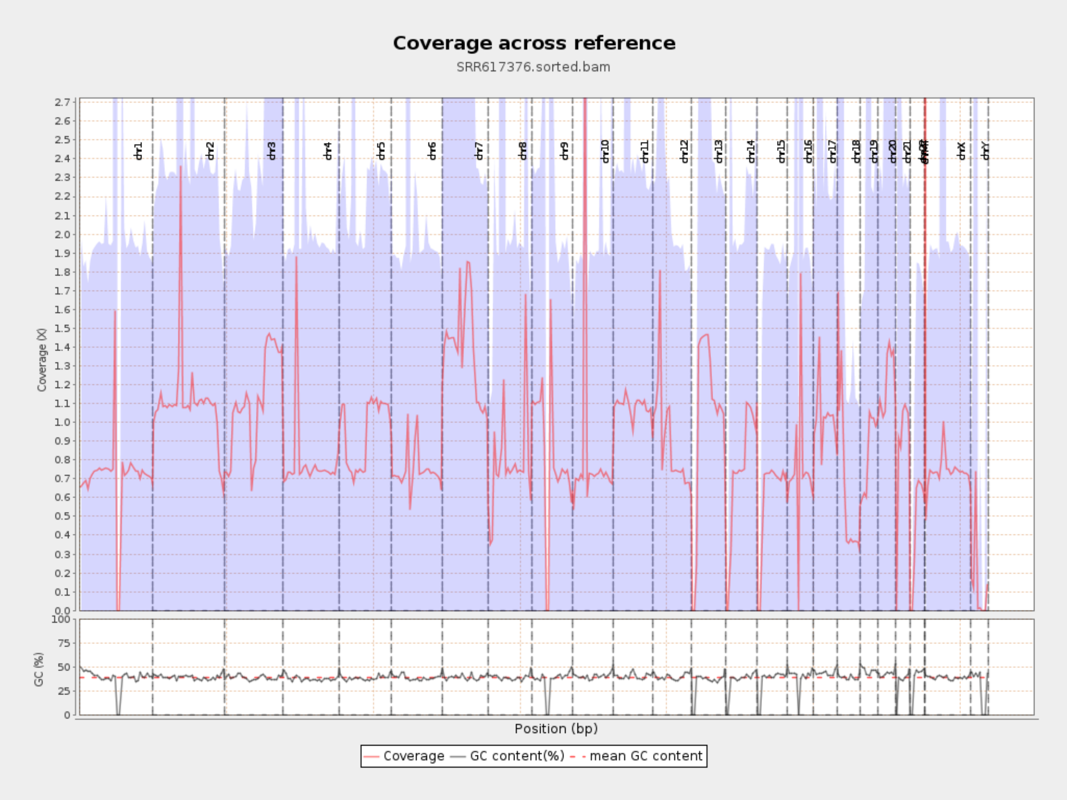
2.7. Chromosome stats

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

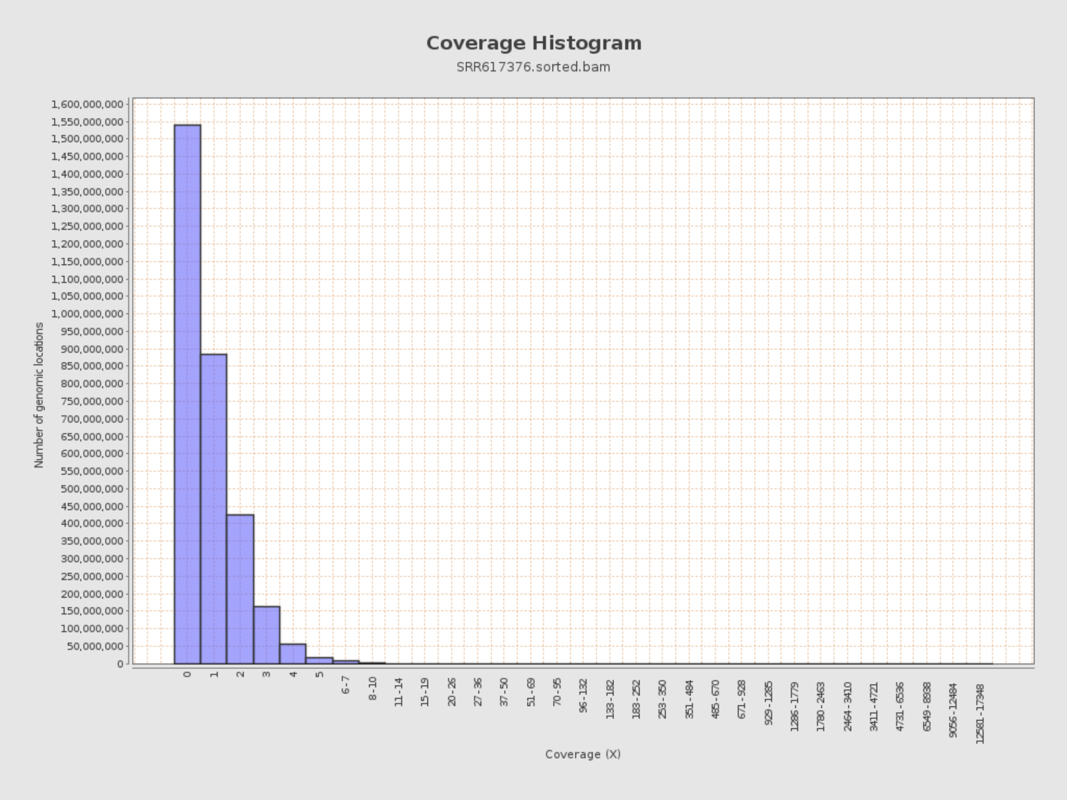
		bases	coverage	deviation
chr1	249250621	177109954	0.7106	17.7306
chr2	243199373	269564593	1.1084	7.6355
chr3	198022430	218843546	1.1051	1.4271
chr4	191154276	150223698	0.7859	7.4791
chr5	180915260	172172495	0.9517	1.3782
chr6	171115067	128517461	0.7511	3.3682
chr7	159138663	221973731	1.3948	10.078
chr8	146364022	115042606	0.786	6.6671
chr9	141213431	114346453	0.8097	12.4947
chr10	135534747	114213262	0.8427	18.1453
chr11	135006516	146085051	1.0821	4.8556
chr12	133851895	120604040	0.901	1.2652
chr13	115169878	120159589	1.0433	1.2397
chr14	107349540	78792487	0.734	1.2968
chr15	102531392	61018173	0.5951	0.9301
chr16	90354753	67901491	0.7515	7.5437
chr17	81195210	82873030	1.0207	6.1756
chr18	78077248	48837405	0.6255	13.159
chr19	59128983	49319750	0.8341	8.7256
chr20	63025520	77058643	1.2227	2.181
chr21	48129895	43218209	0.8979	2.8424
chr22	51304566	23540850	0.4588	0.8546
chrMT	16571	1804329	108.8847	22.9579
chrX	155270560	114571519	0.7379	2.7368

chrY	59373566	8803351	0.1483	6.8454

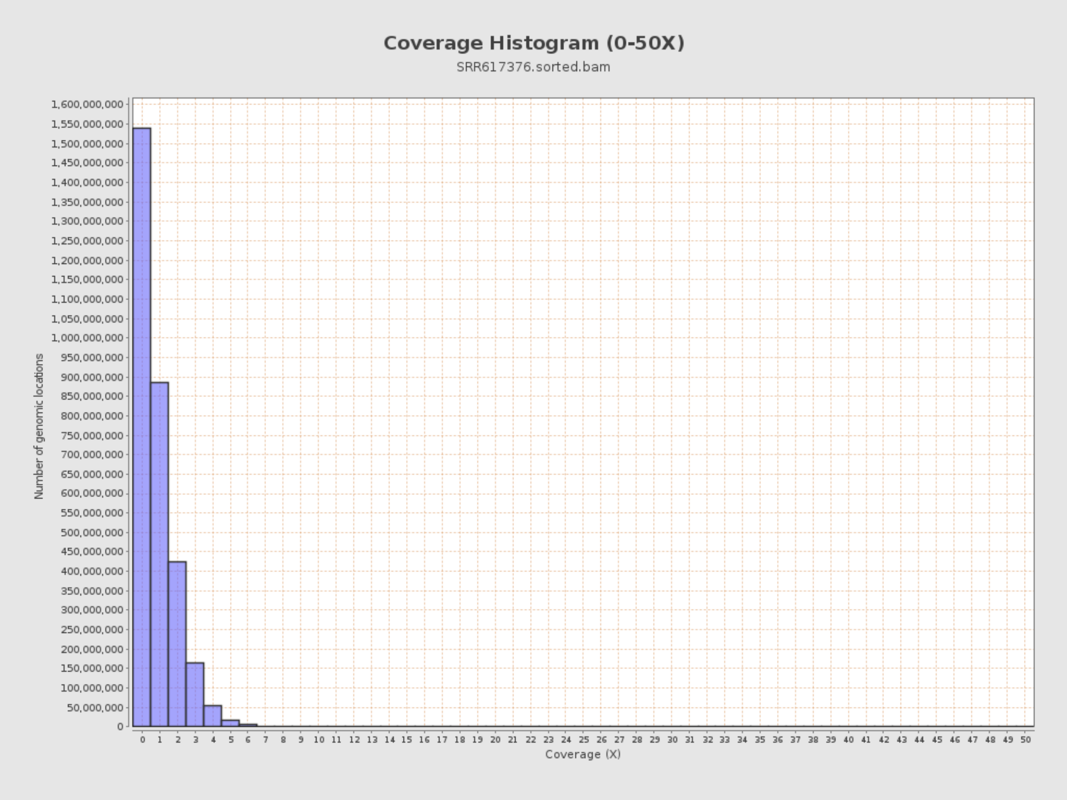
3. Results : Coverage across reference



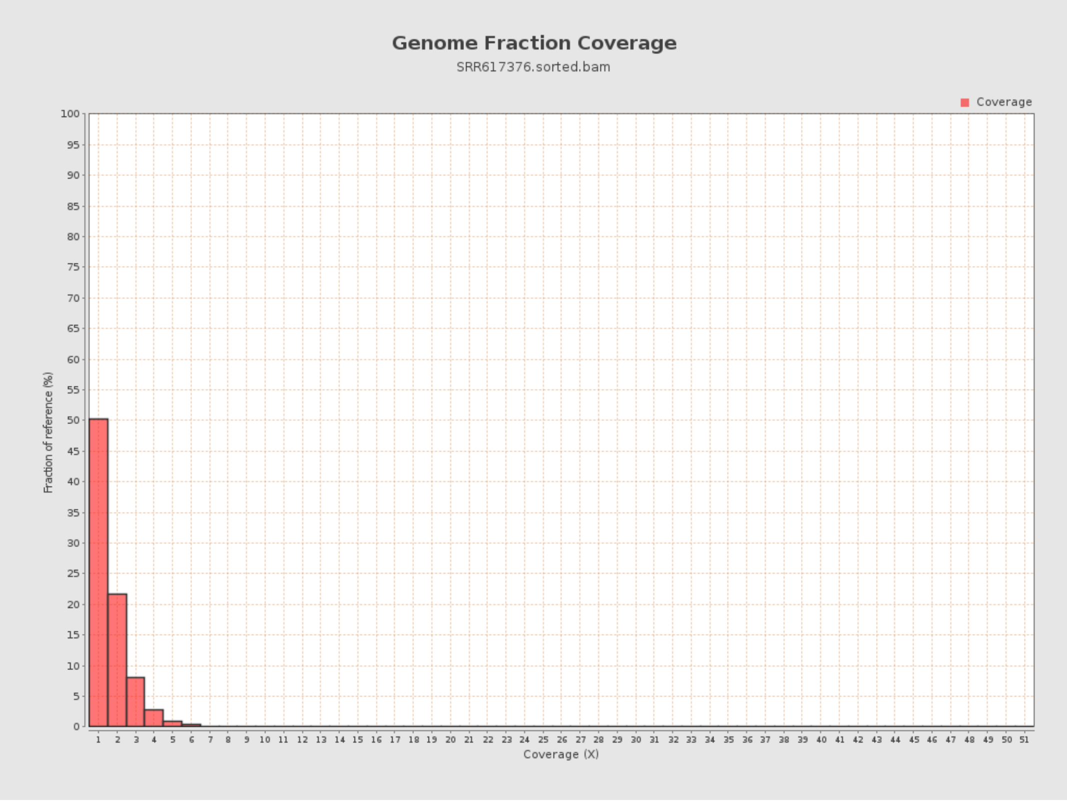
4. Results : Coverage Histogram



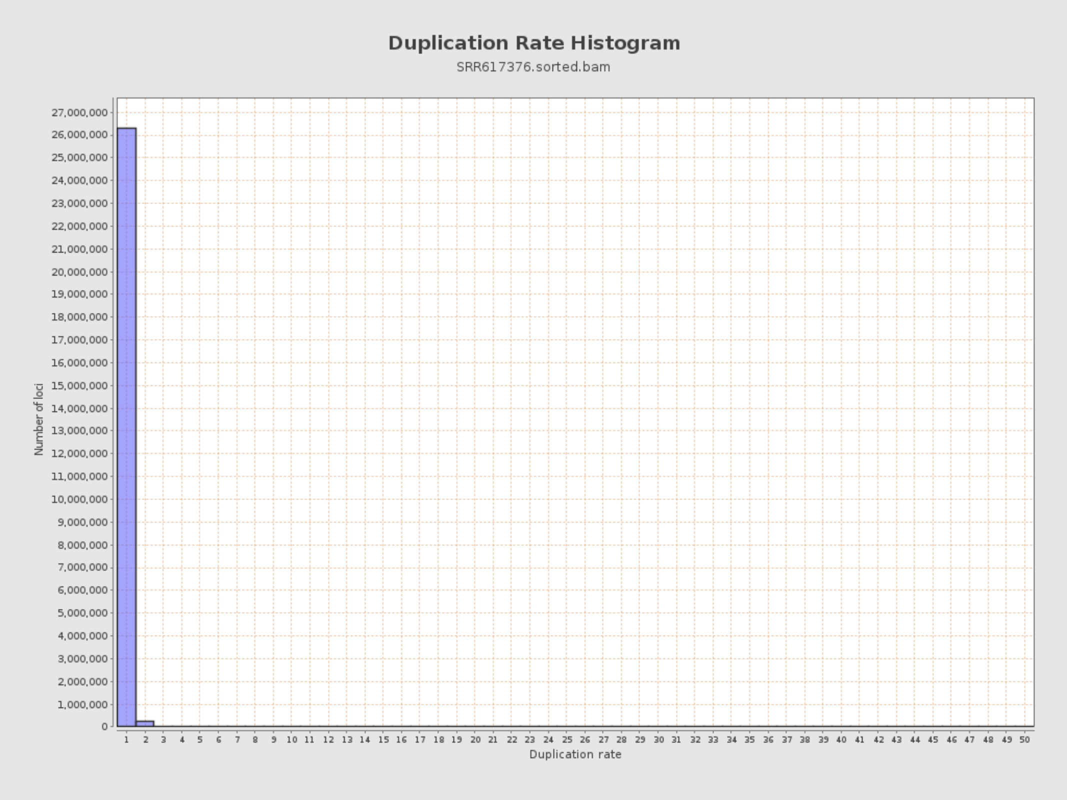
5. Results : Coverage Histogram (0-50X)



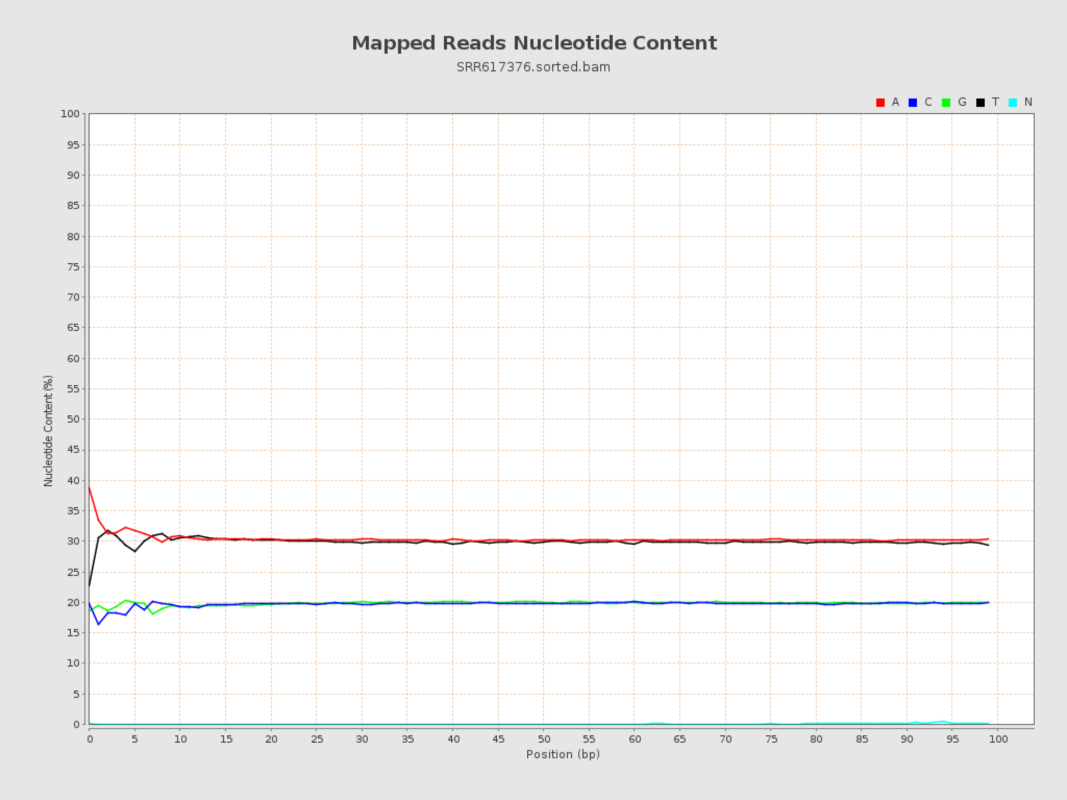
6. Results : Genome Fraction Coverage



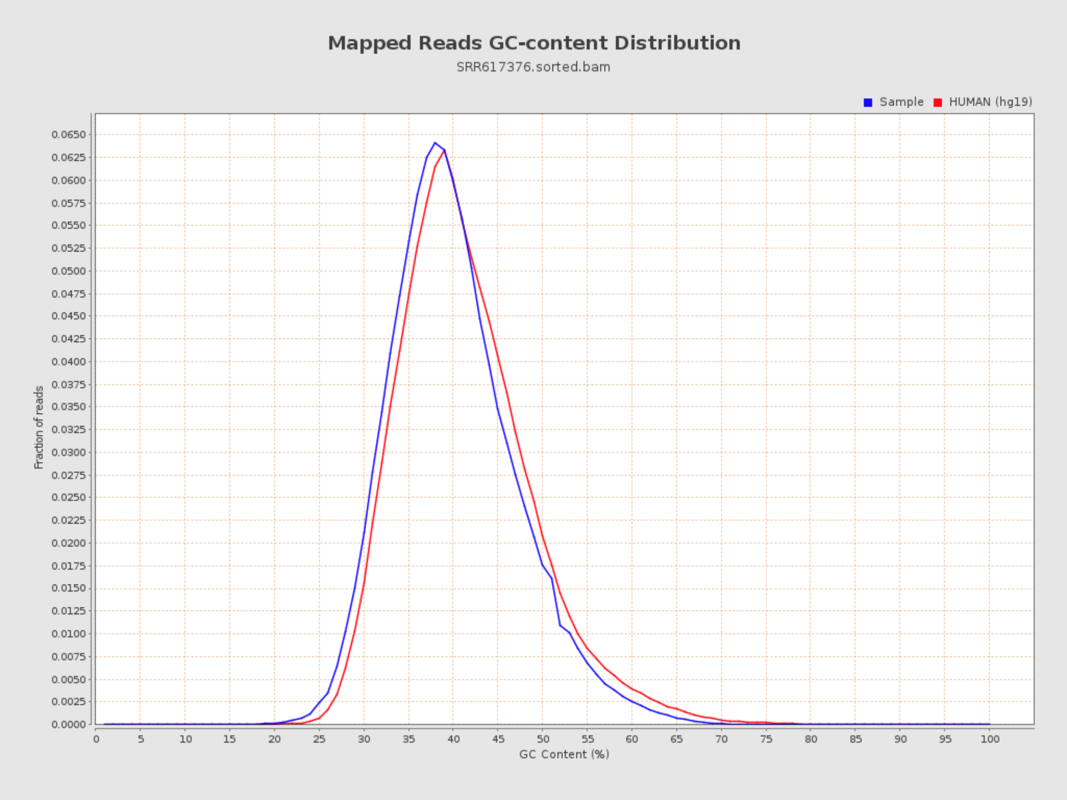
7. Results : Duplication Rate Histogram



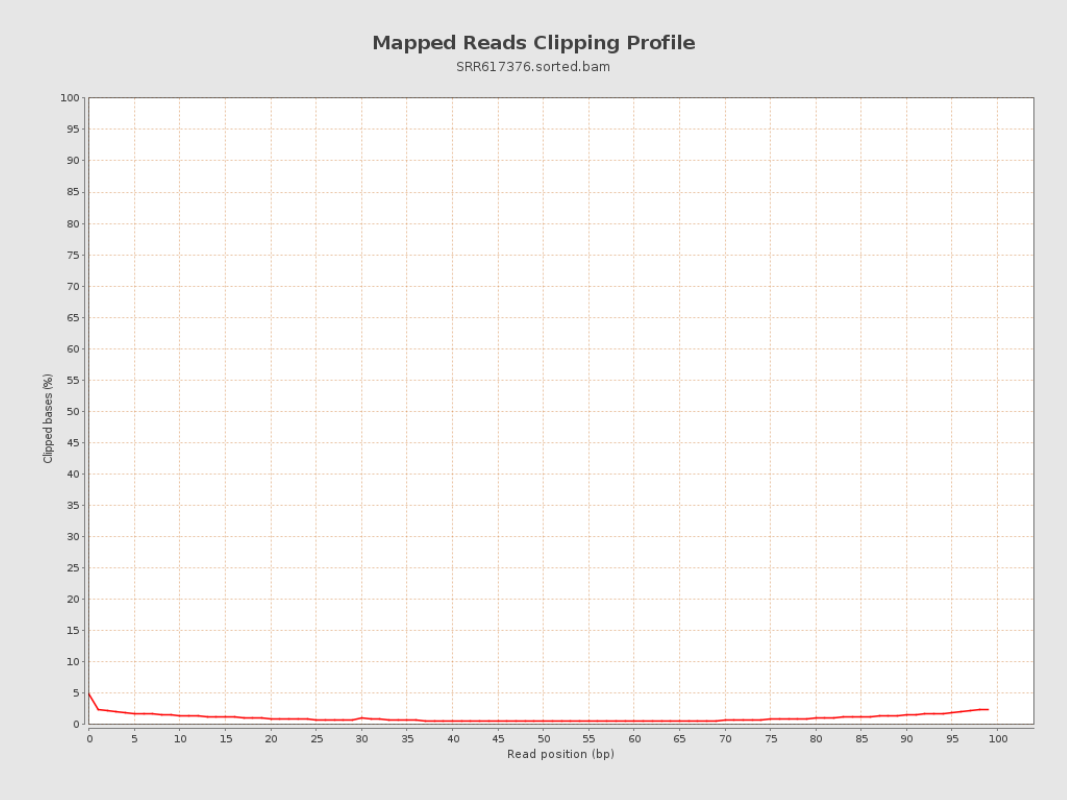
8. Results : Mapped Reads Nucleotide Content



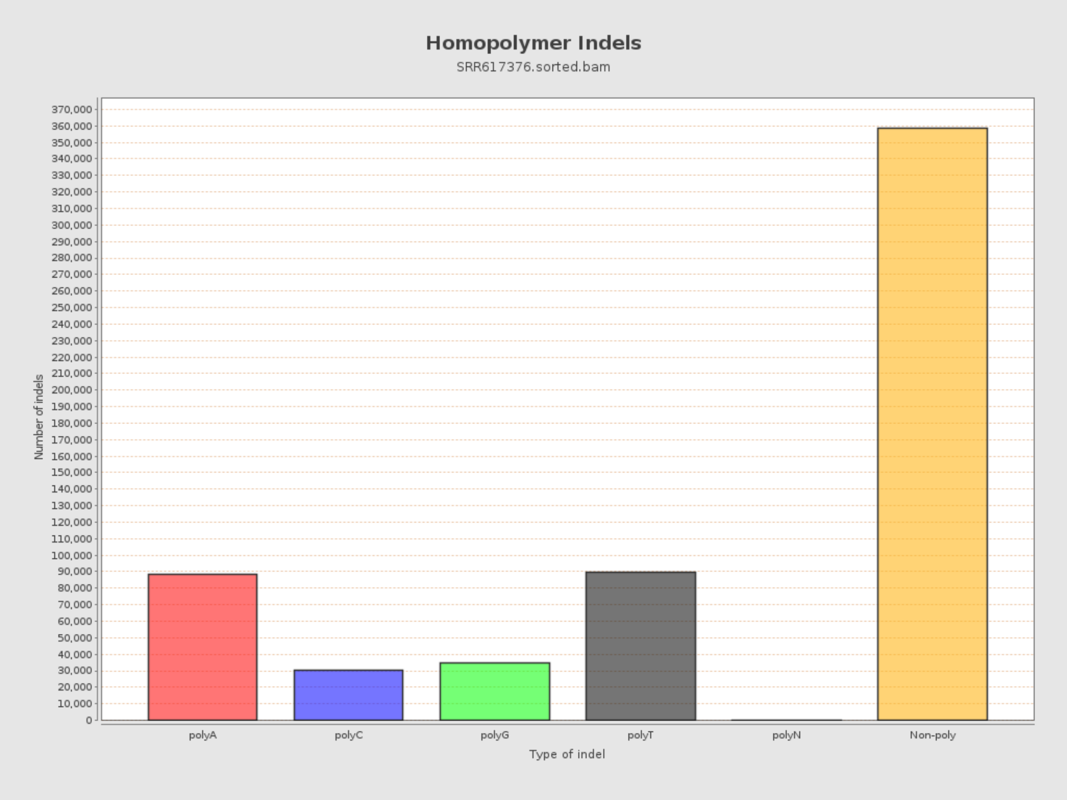
9. Results : Mapped Reads GC-content Distribution



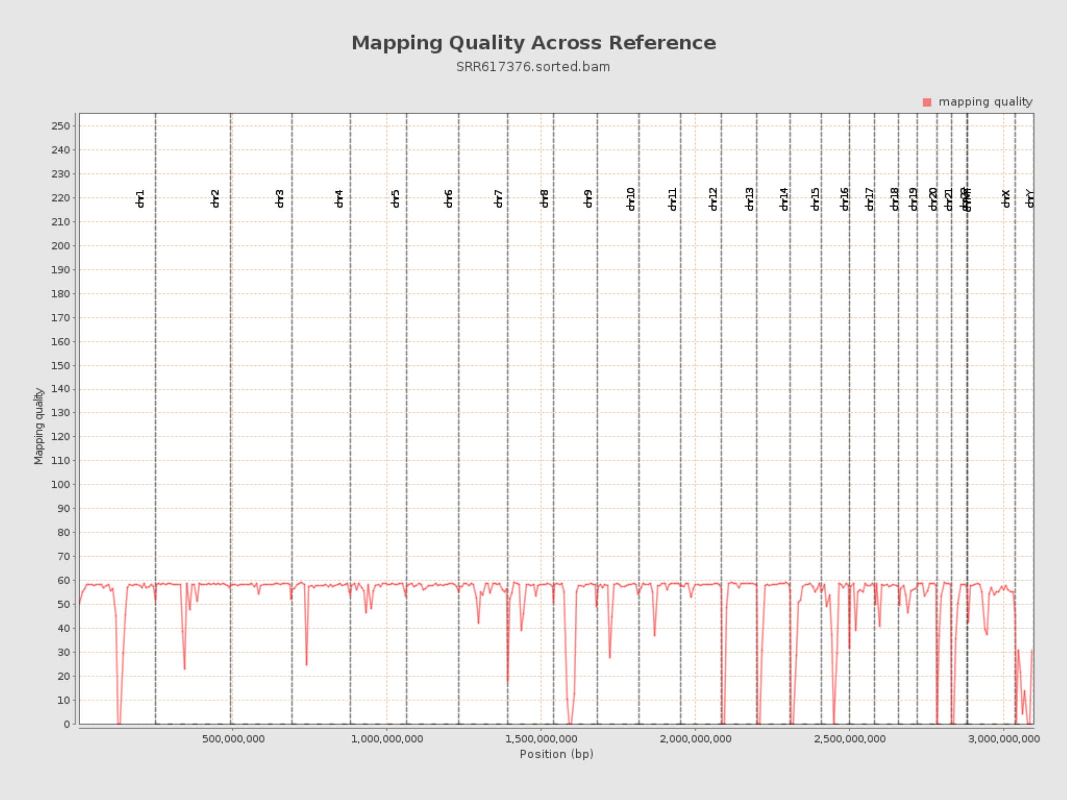
10. Results : Mapped Reads Clipping Profile



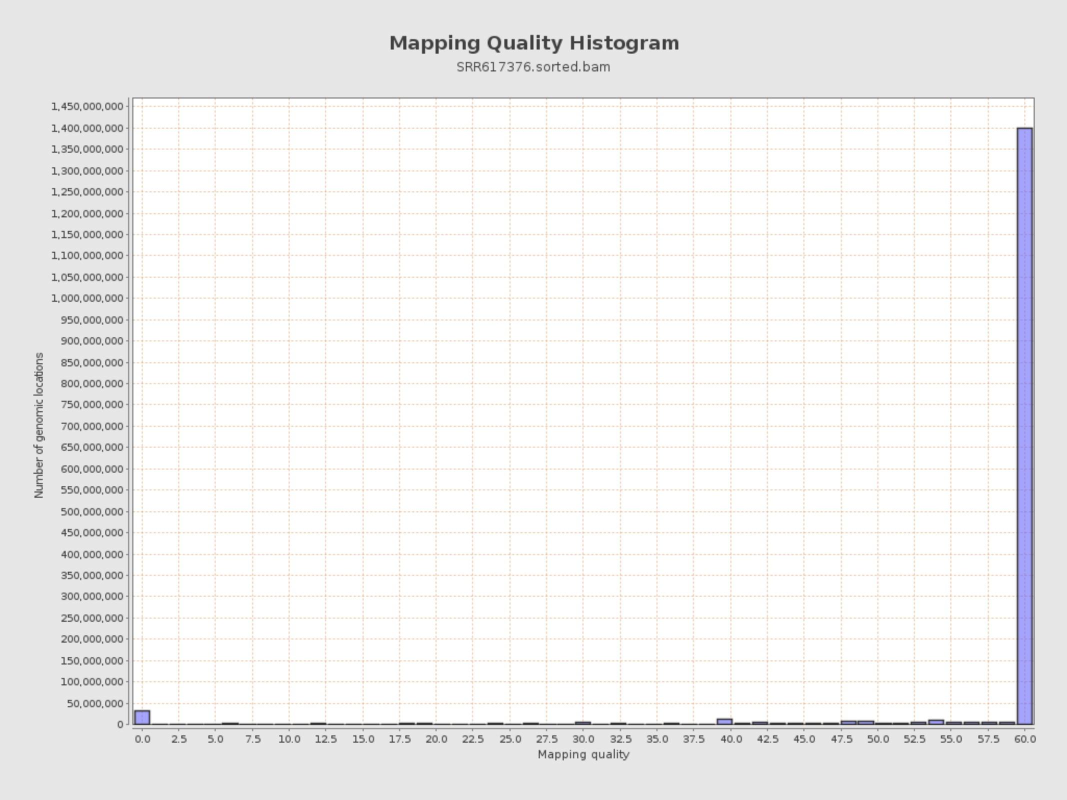
11. Results : Homopolymer Indels



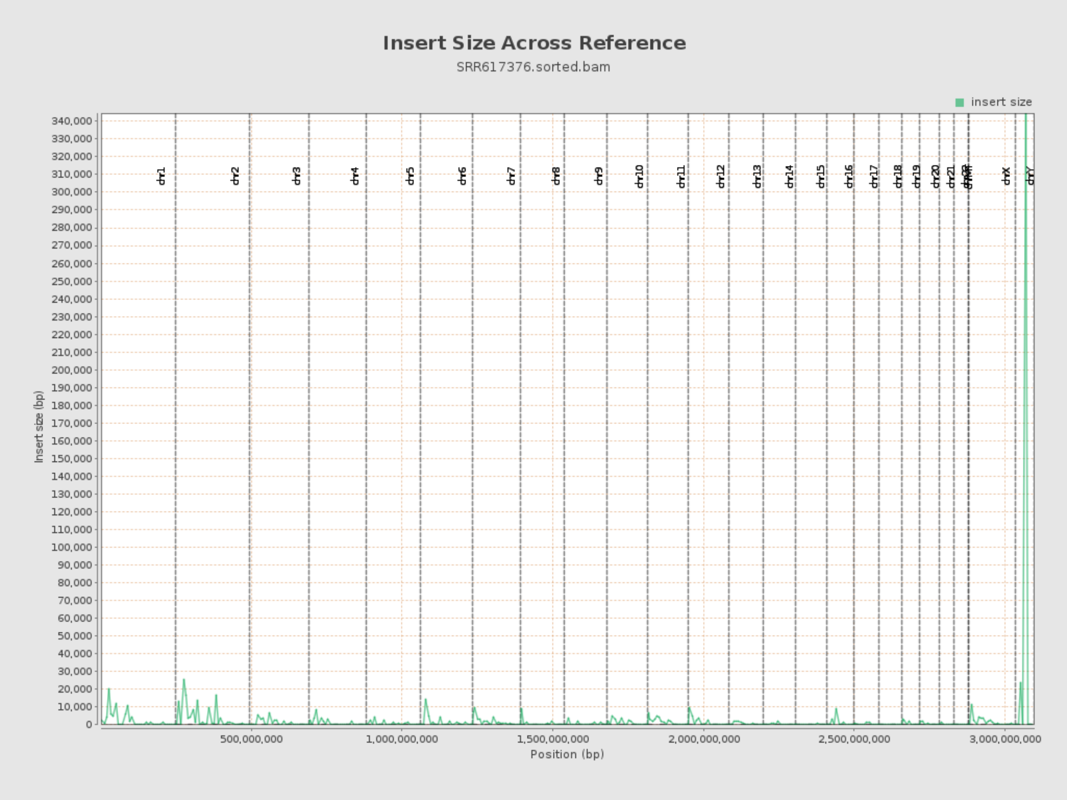
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram