

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 10:40:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617366.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_SRR617366 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617366_1.fastq.gz SRR617366_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 10:40:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617366.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,139,374 / 94.19%
Unmapped reads	1,860,626 / 5.81%
Mapped paired reads	30,139,374 / 94.19%
Mapped reads, first in pair	15,180,843 / 47.44%
Mapped reads, second in pair	14,958,531 / 46.75%
Mapped reads, both in pair	29,538,672 / 92.31%
Mapped reads, singletons	600,702 / 1.88%
Secondary alignments	0
Supplementary alignments	95,816 / 0.3%
Read min/max/mean length	30 / 100 / 100.12
Duplicated reads (estimated)	1,603,034 / 5.01%
Duplication rate	1.52%
Clipped reads	2,583,497 / 8.07%

2.2. ACGT Content

Number/percentage of A's	894,444,981 / 30.31%
Number/percentage of C's	585,434,672 / 19.84%
Number/percentage of T's	882,588,423 / 29.91%
Number/percentage of G's	587,220,201 / 19.9%
Number/percentage of N's	1,146,775 / 0.04%

GC Percentage	39.74%
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2.3. Coverage

Mean	0.9535
Standard Deviation	9.7907

2.4. Mapping Quality

Mean Mapping Quality	53.39
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2.5. Insert size

Mean	64,337.29
Standard Deviation	2,425,571.62
P25/Median/P75	171 / 211 / 273

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	30,994,228
Insertions	300,979
Mapped reads with at least one insertion	0.97%
Deletions	362,218
Mapped reads with at least one deletion	1.16%
Homopolymer indels	41.24%

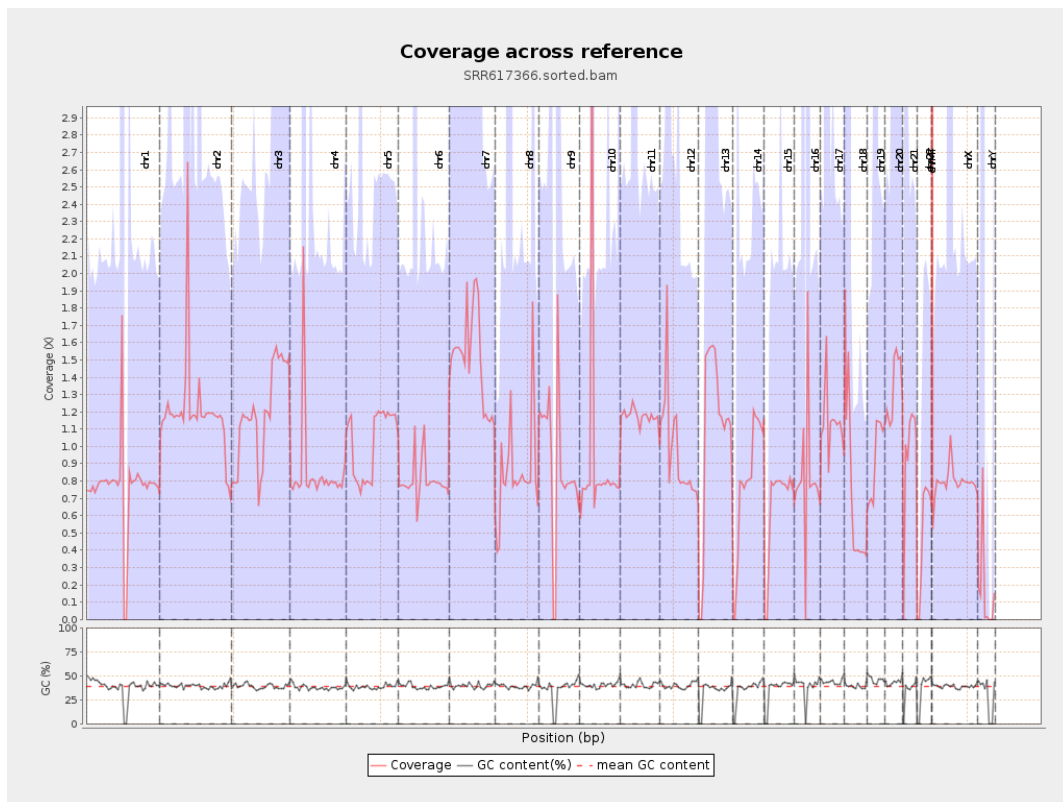
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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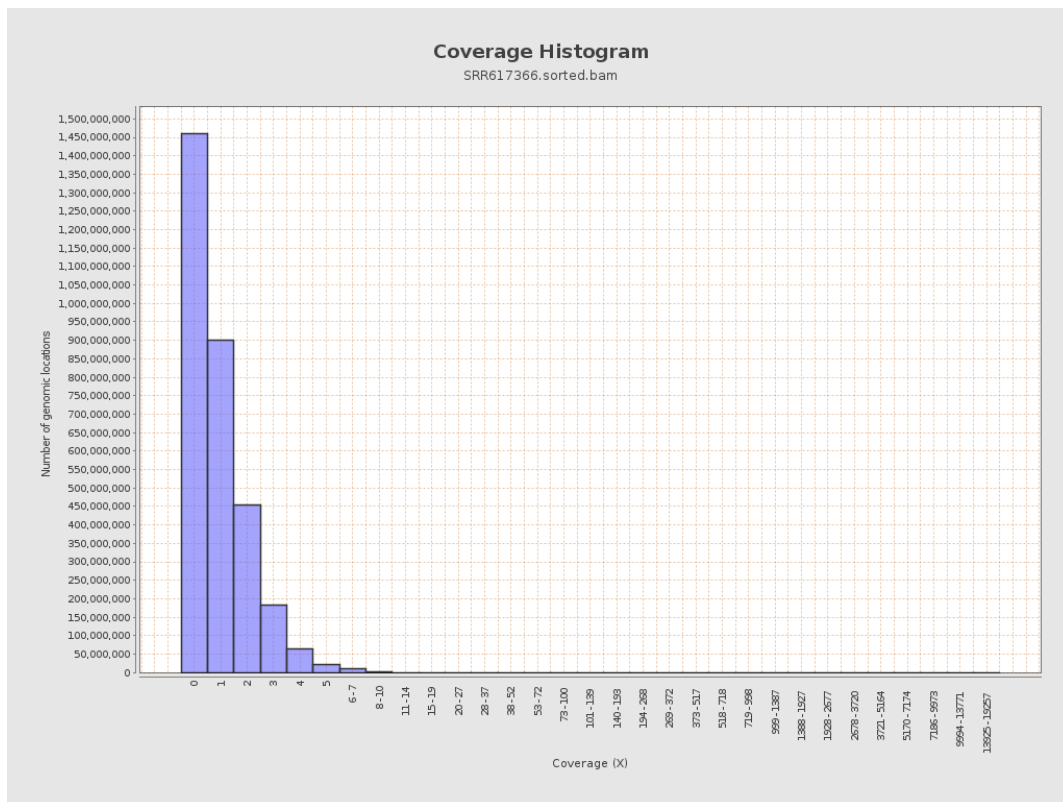
		bases	coverage	deviation
chr1	249250621	191632236	0.7688	19.8435
chr2	243199373	291614469	1.1991	8.904
chr3	198022430	234785097	1.1856	1.4719
chr4	191154276	161522752	0.845	9.342
chr5	180915260	185207850	1.0237	1.4756
chr6	171115067	138251193	0.8079	3.6125
chr7	159138663	239641504	1.5059	10.8444
chr8	146364022	124196497	0.8485	7.7189
chr9	141213431	124197634	0.8795	14.9898
chr10	135534747	124254216	0.9168	20.1675
chr11	135006516	158288936	1.1725	5.5425
chr12	133851895	130028099	0.9714	1.4541
chr13	115169878	128501197	1.1158	1.3296
chr14	107349540	85294891	0.7946	1.3918
chr15	102531392	66480005	0.6484	1.1444
chr16	90354753	74152089	0.8207	7.8963
chr17	81195210	92092534	1.1342	7.0916
chr18	78077248	53411536	0.6841	15.2741
chr19	59128983	54903038	0.9285	9.5242
chr20	63025520	84828086	1.3459	2.5083
chr21	48129895	47089165	0.9784	3.2348
chr22	51304566	26208726	0.5108	0.9289
chrMT	16571	2000560	120.7266	19.7189
chrX	155270560	122925360	0.7917	2.9911

chrY	59373566	10199744	0.1718	8.4698
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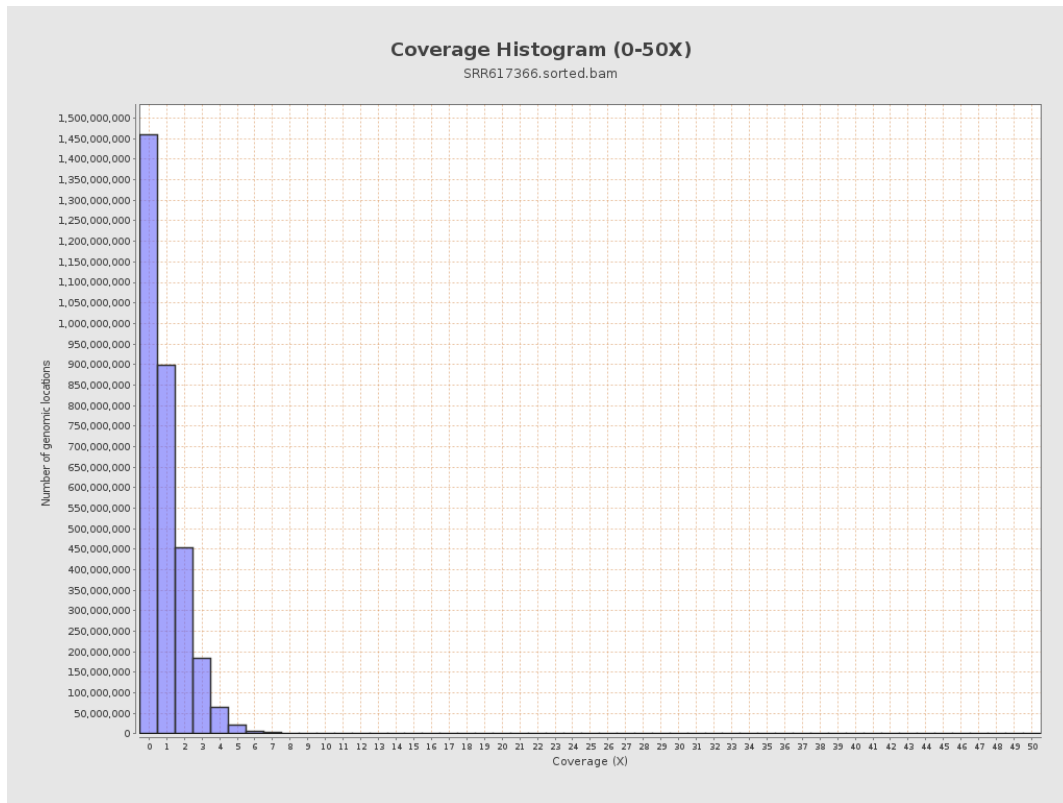
3. Results : Coverage across reference



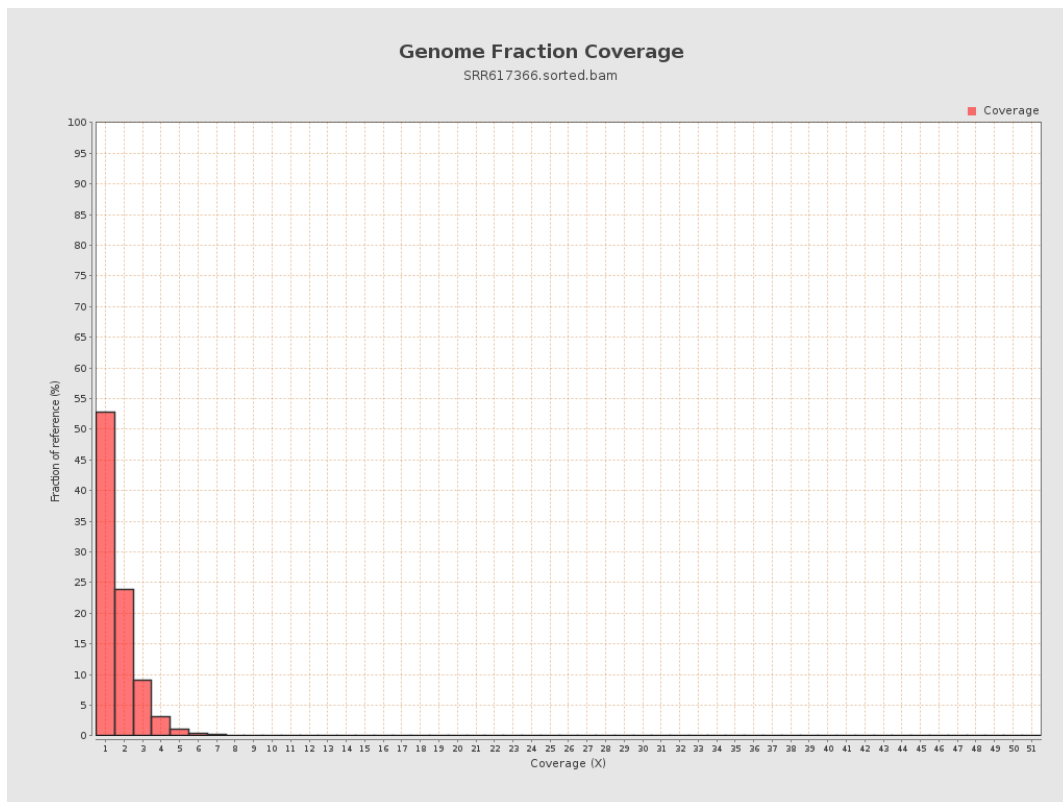
4. Results : Coverage Histogram



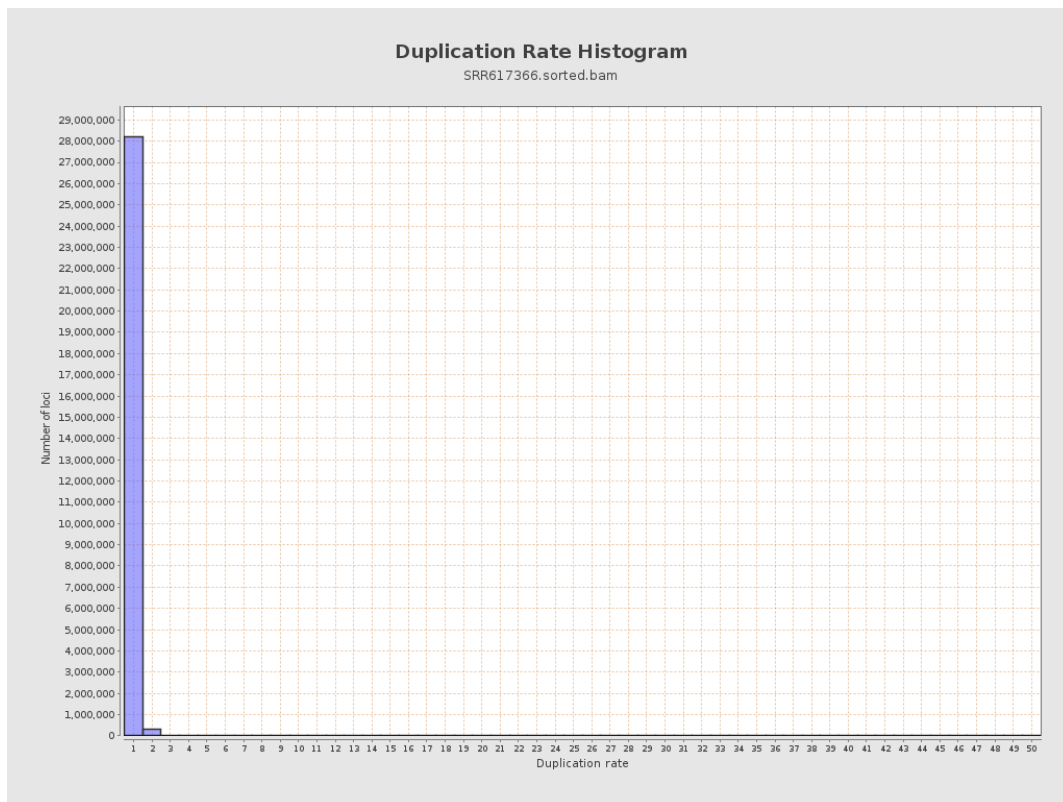
5. Results : Coverage Histogram (0-50X)



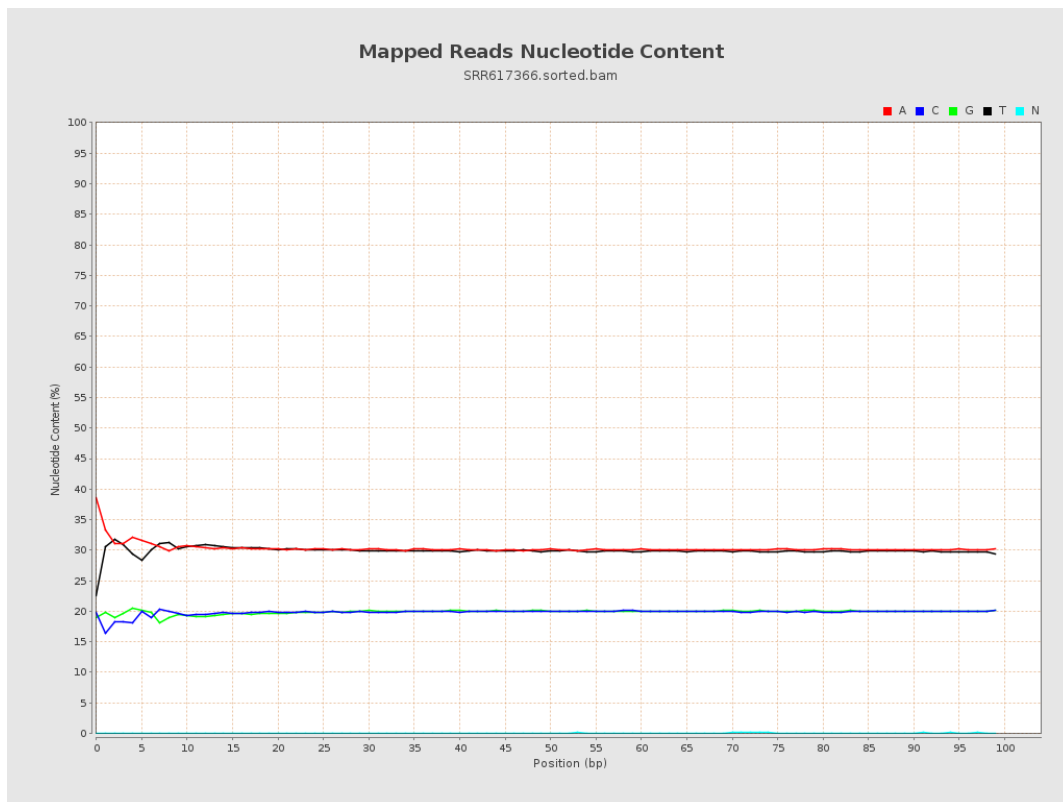
6. Results : Genome Fraction Coverage



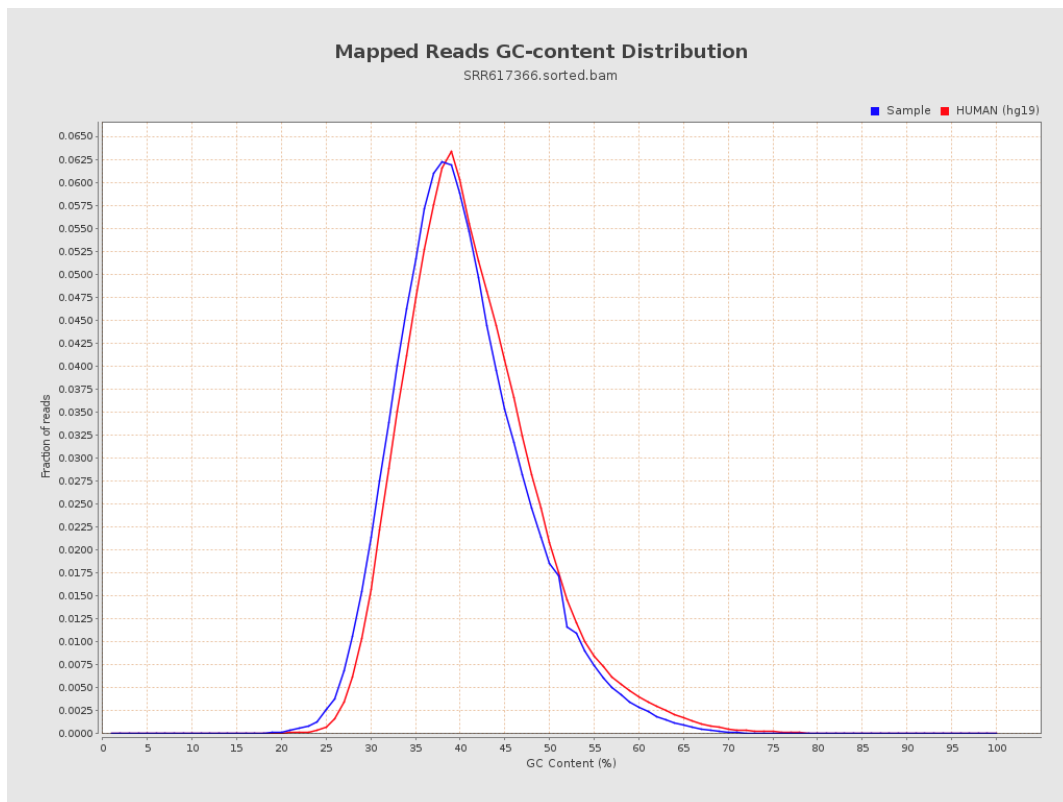
7. Results : Duplication Rate Histogram



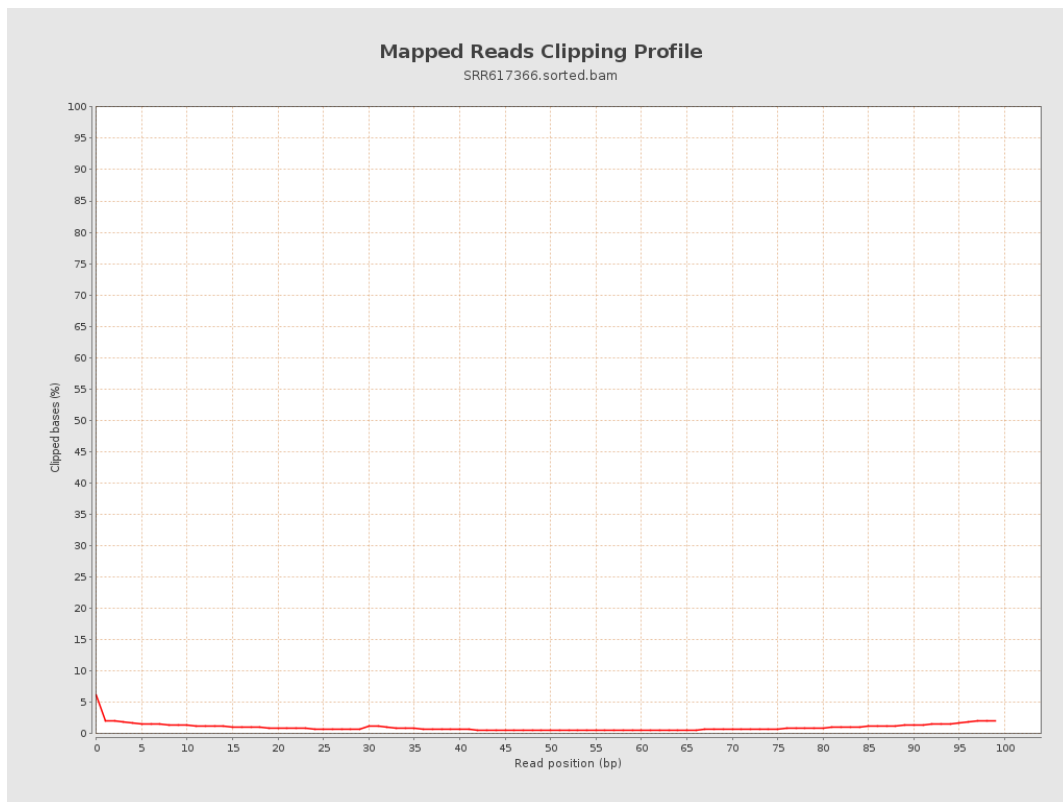
8. Results : Mapped Reads Nucleotide Content



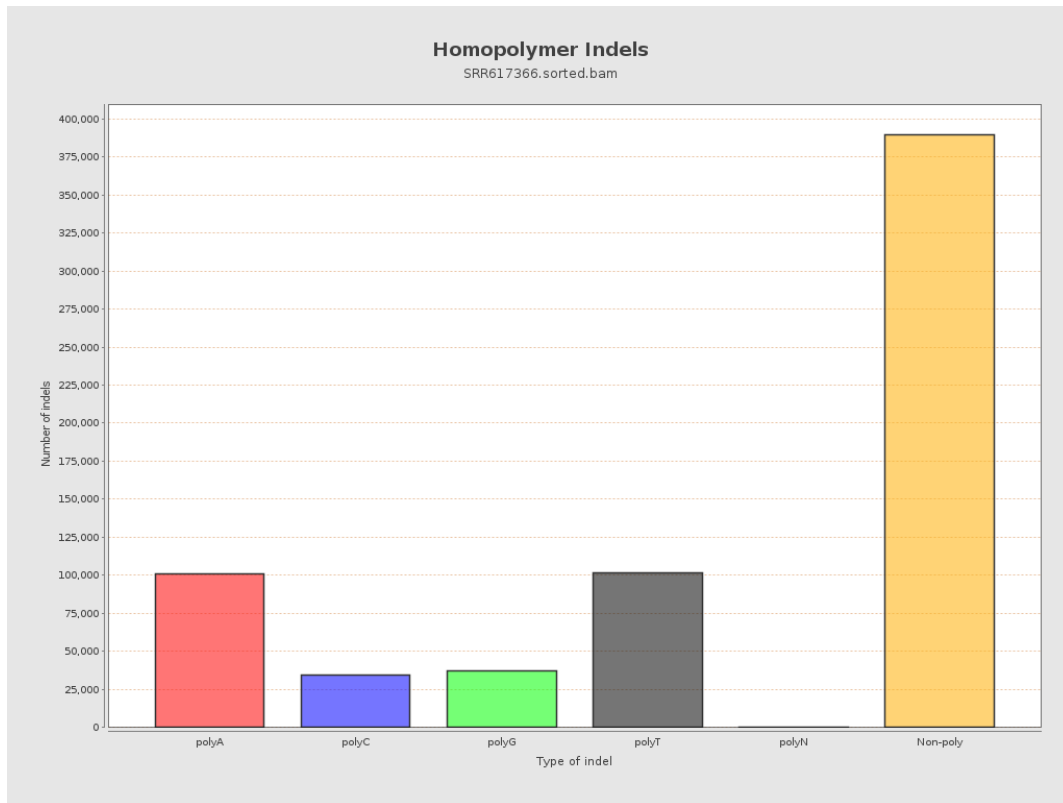
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



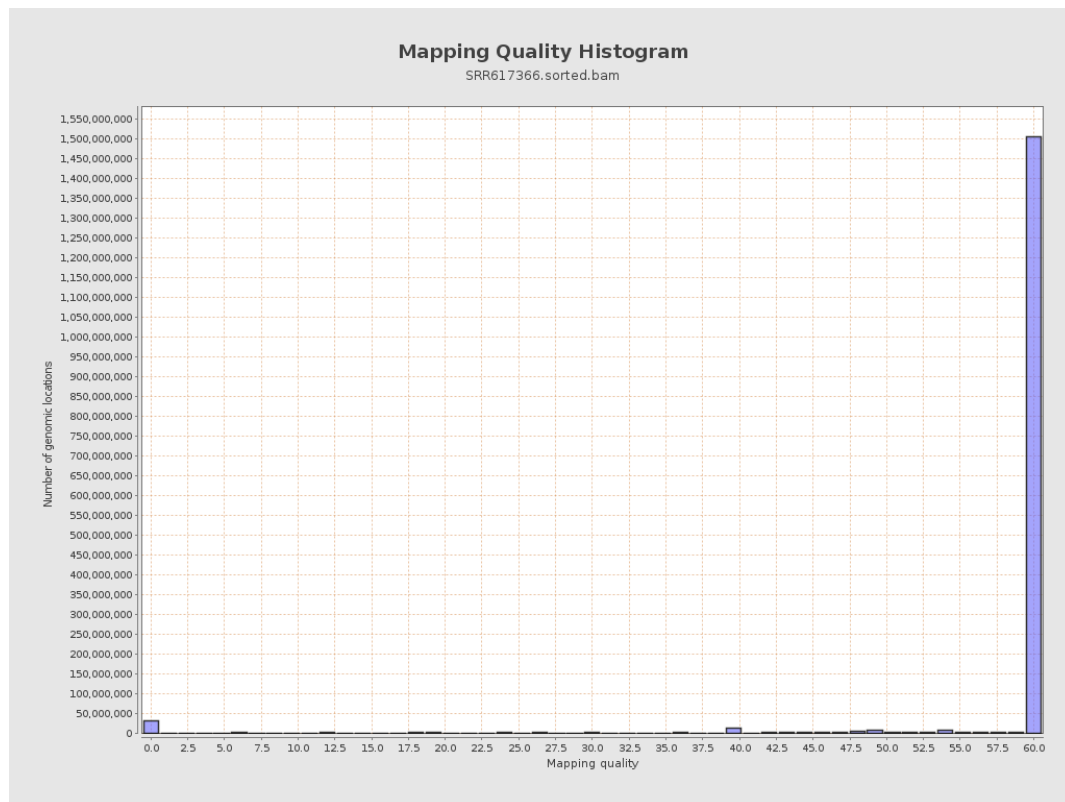
11. Results : Homopolymer Indels



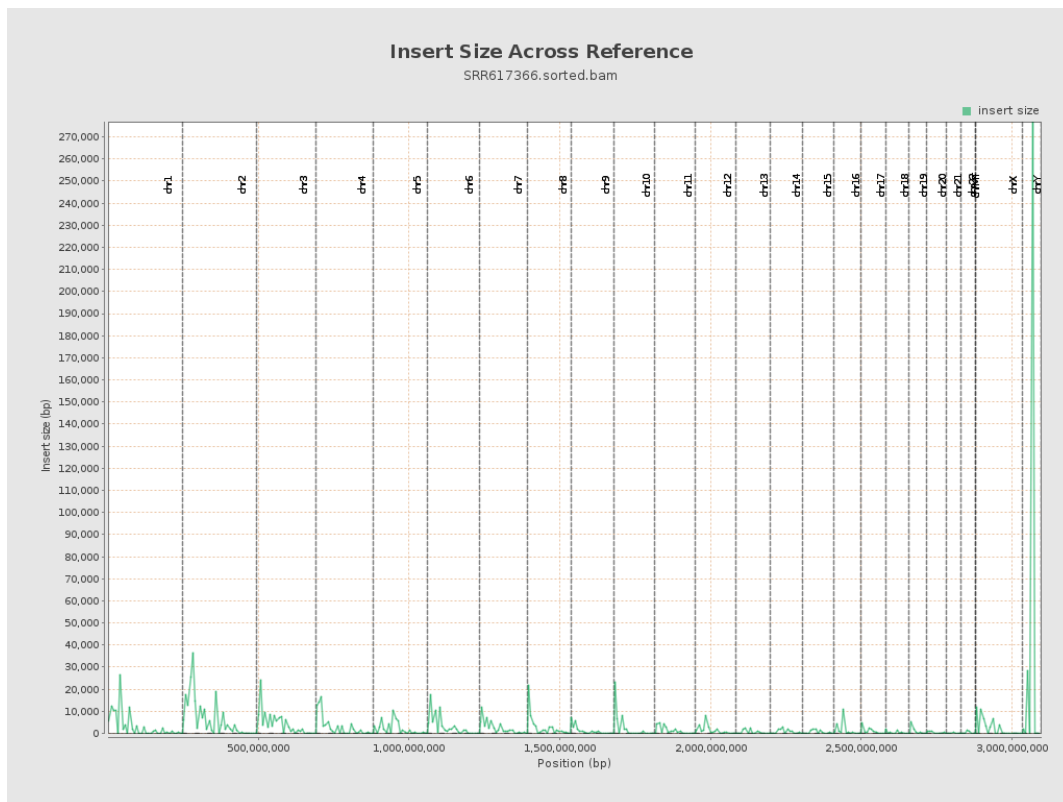
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

