

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 05:07:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617360.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_SRR617360 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617360_1.fastq.gz SRR617360_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 05:07:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617360.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,586,377 / 95.58%
Unmapped reads	1,413,623 / 4.42%
Mapped paired reads	30,586,377 / 95.58%
Mapped reads, first in pair	15,376,429 / 48.05%
Mapped reads, second in pair	15,209,948 / 47.53%
Mapped reads, both in pair	30,075,602 / 93.99%
Mapped reads, singletons	510,775 / 1.6%
Secondary alignments	0
Supplementary alignments	67,570 / 0.21%
Read min/max/mean length	30 / 100 / 100.09
Duplicated reads (estimated)	1,583,917 / 4.95%
Duplication rate	1.48%
Clipped reads	2,212,597 / 6.91%

2.2. ACGT Content

Number/percentage of A's	908,272,072 / 30.19%
Number/percentage of C's	599,189,081 / 19.92%
Number/percentage of T's	897,343,420 / 29.83%
Number/percentage of G's	602,279,237 / 20.02%
Number/percentage of N's	1,295,037 / 0.04%

GC Percentage	39.94%
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2.3. Coverage

Mean	0.9721
Standard Deviation	9.8662

2.4. Mapping Quality

Mean Mapping Quality	53.51
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2.5. Insert size

Mean	56,773.67
Standard Deviation	2,268,129.84
P25/Median/P75	173 / 215 / 280

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	30,164,808
Insertions	303,232
Mapped reads with at least one insertion	0.96%
Deletions	370,554
Mapped reads with at least one deletion	1.17%
Homopolymer indels	41.27%

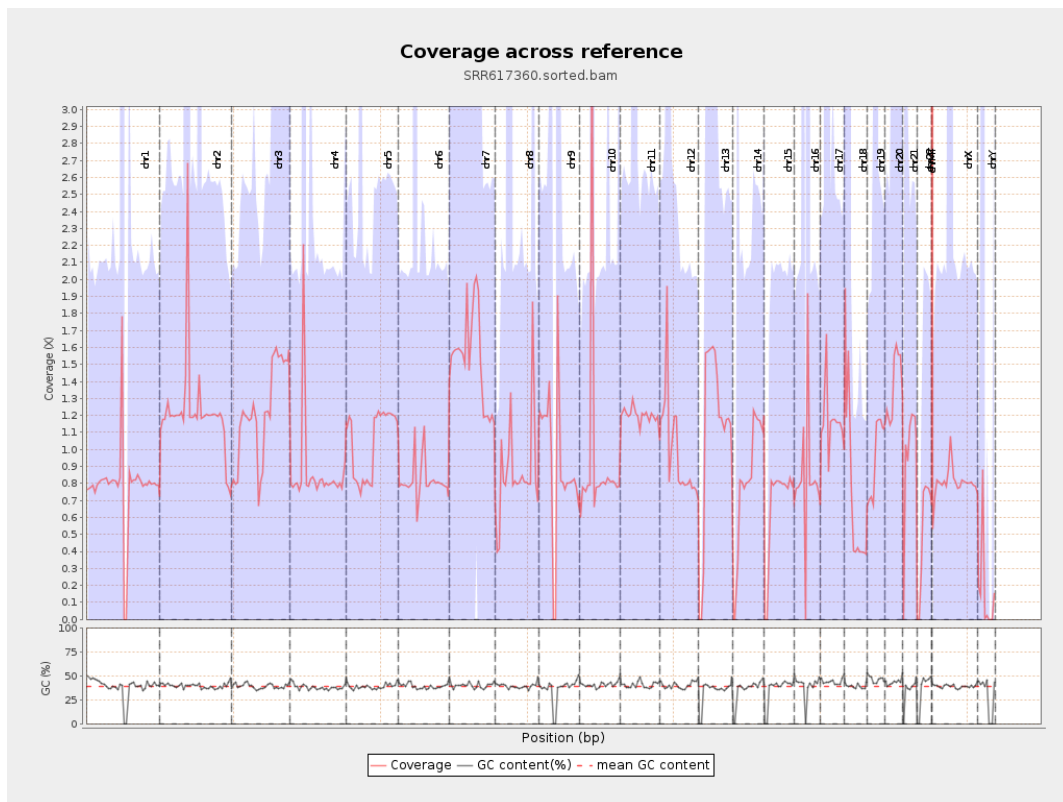
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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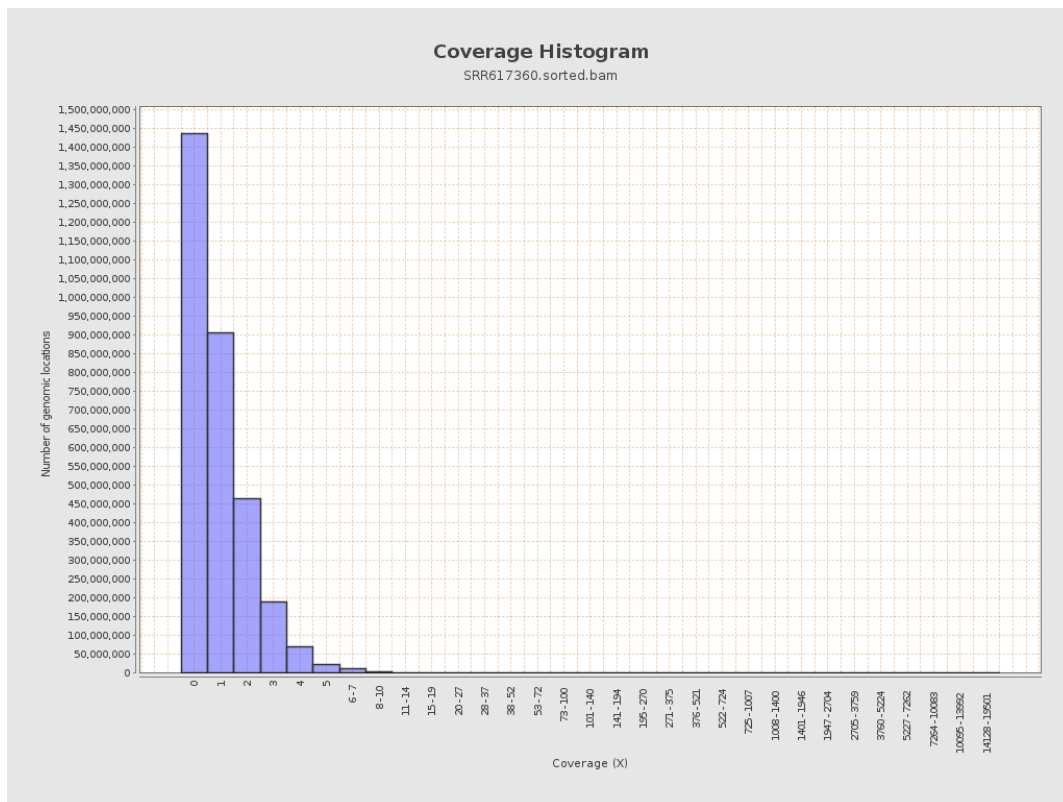
		bases	coverage	deviation
chr1	249250621	195697808	0.7851	20.1009
chr2	243199373	296805441	1.2204	8.9008
chr3	198022430	239318294	1.2085	1.4763
chr4	191154276	164328783	0.8597	9.7011
chr5	180915260	188121634	1.0398	1.4735
chr6	171115067	140864446	0.8232	3.7072
chr7	159138663	243954499	1.533	10.8521
chr8	146364022	126332530	0.8631	7.7713
chr9	141213431	126978848	0.8992	15.1508
chr10	135534747	126524031	0.9335	19.9608
chr11	135006516	161733574	1.198	5.5509
chr12	133851895	132589791	0.9906	1.3499
chr13	115169878	130613441	1.1341	1.2976
chr14	107349540	86942013	0.8099	1.3944
chr15	102531392	67817746	0.6614	0.9826
chr16	90354753	75864094	0.8396	7.8796
chr17	81195210	94577887	1.1648	7.1246
chr18	78077248	54668175	0.7002	15.6022
chr19	59128983	56425925	0.9543	9.6611
chr20	63025520	86968702	1.3799	2.4381
chr21	48129895	47870934	0.9946	3.2531
chr22	51304566	27124800	0.5287	0.9277
chrMT	16571	2085922	125.8779	20.9889
chrX	155270560	124754609	0.8035	3.0314

chrY	59373566	10311429	0.1737	8.439
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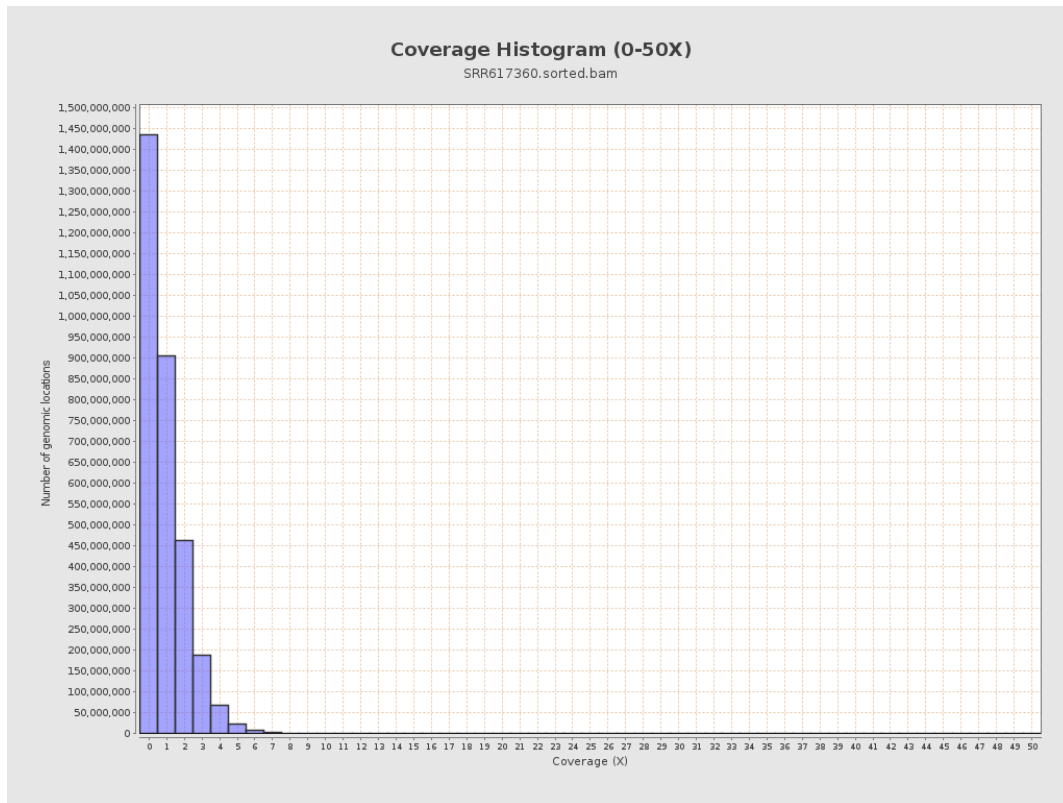
3. Results : Coverage across reference



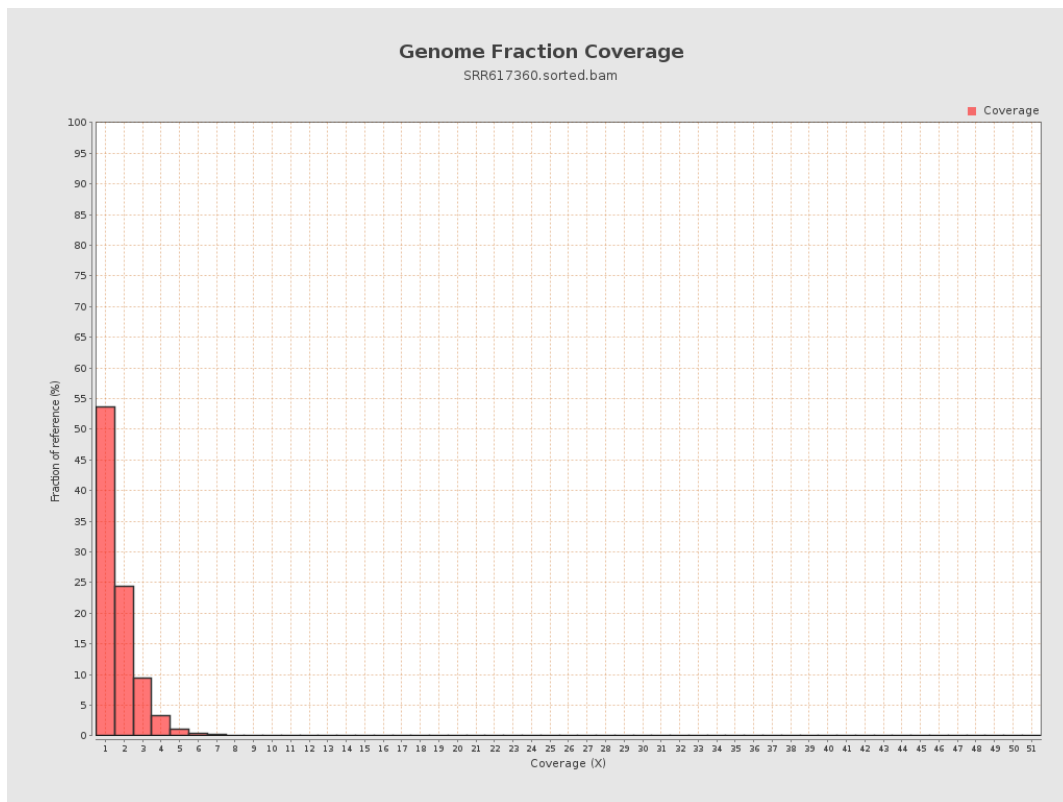
4. Results : Coverage Histogram



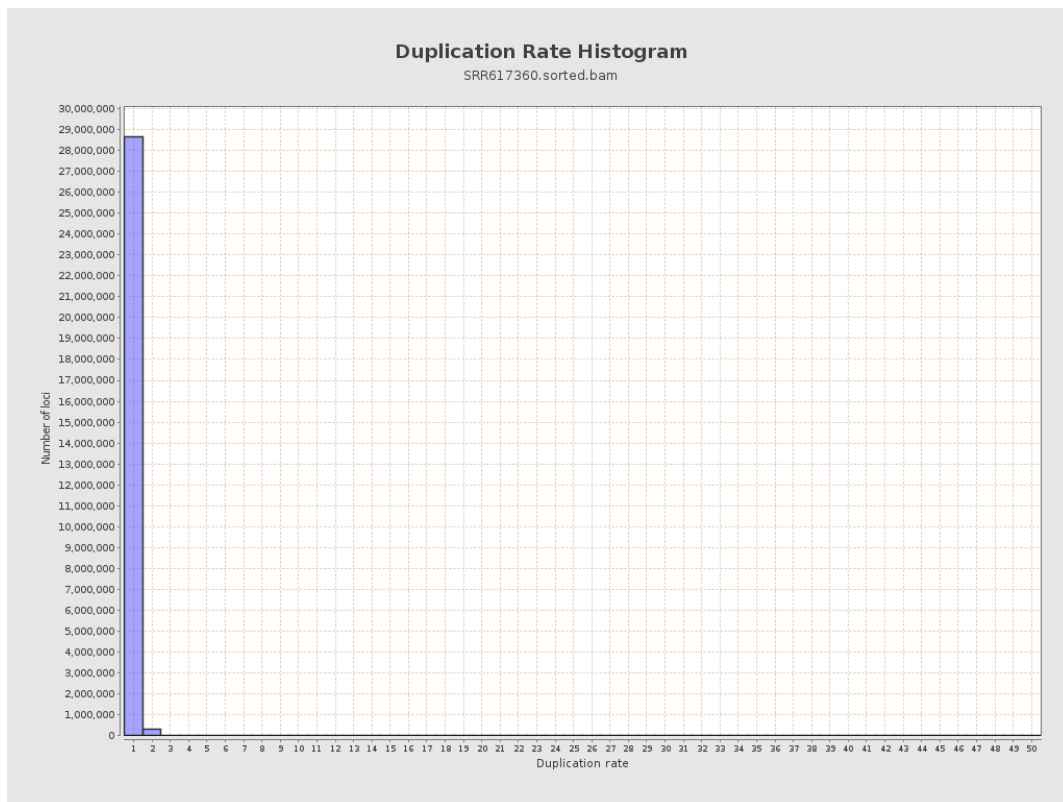
5. Results : Coverage Histogram (0-50X)



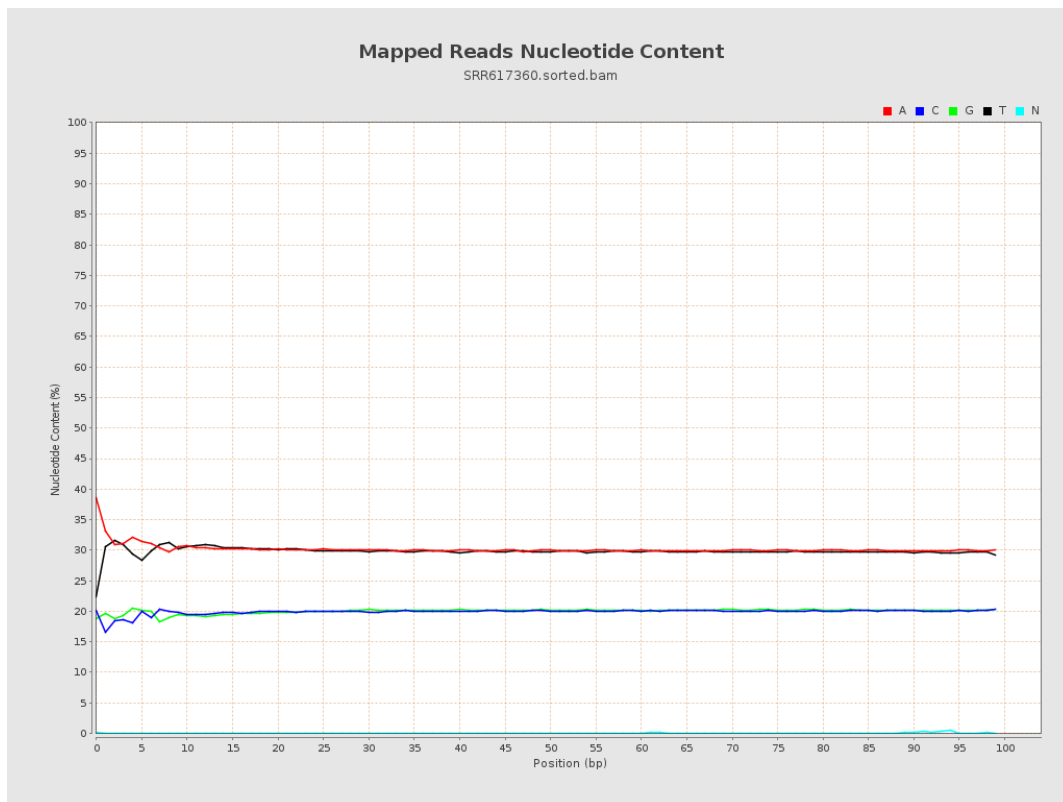
6. Results : Genome Fraction Coverage



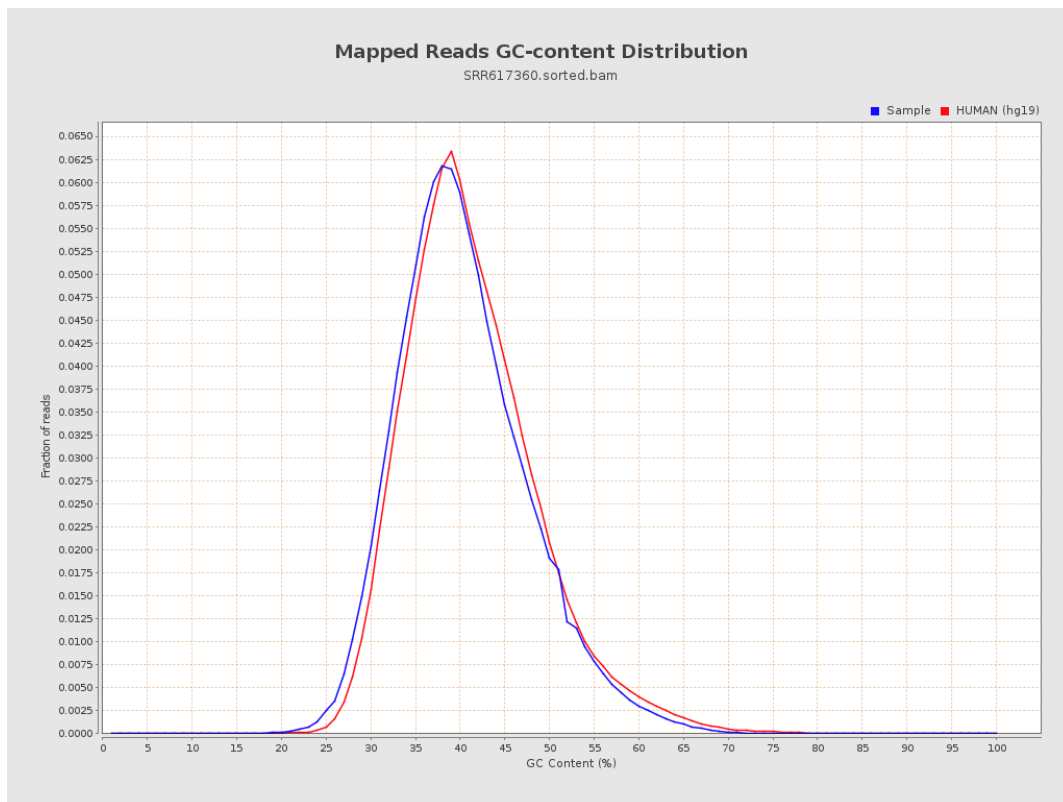
7. Results : Duplication Rate Histogram



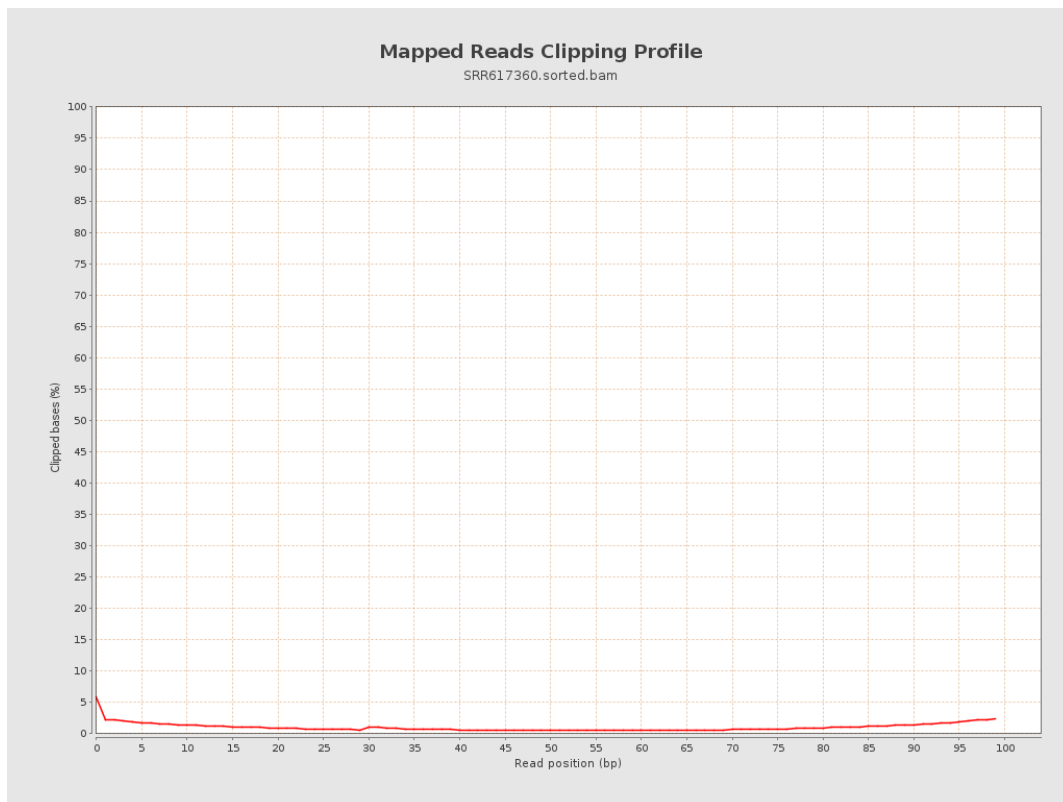
8. Results : Mapped Reads Nucleotide Content



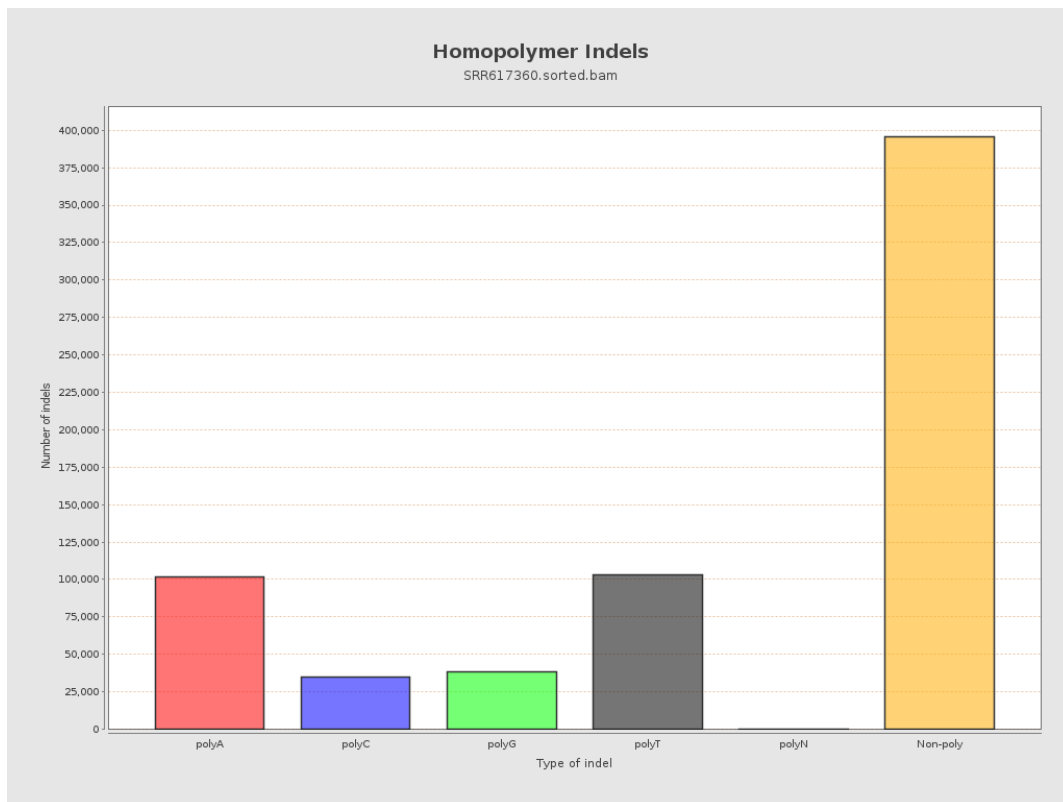
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



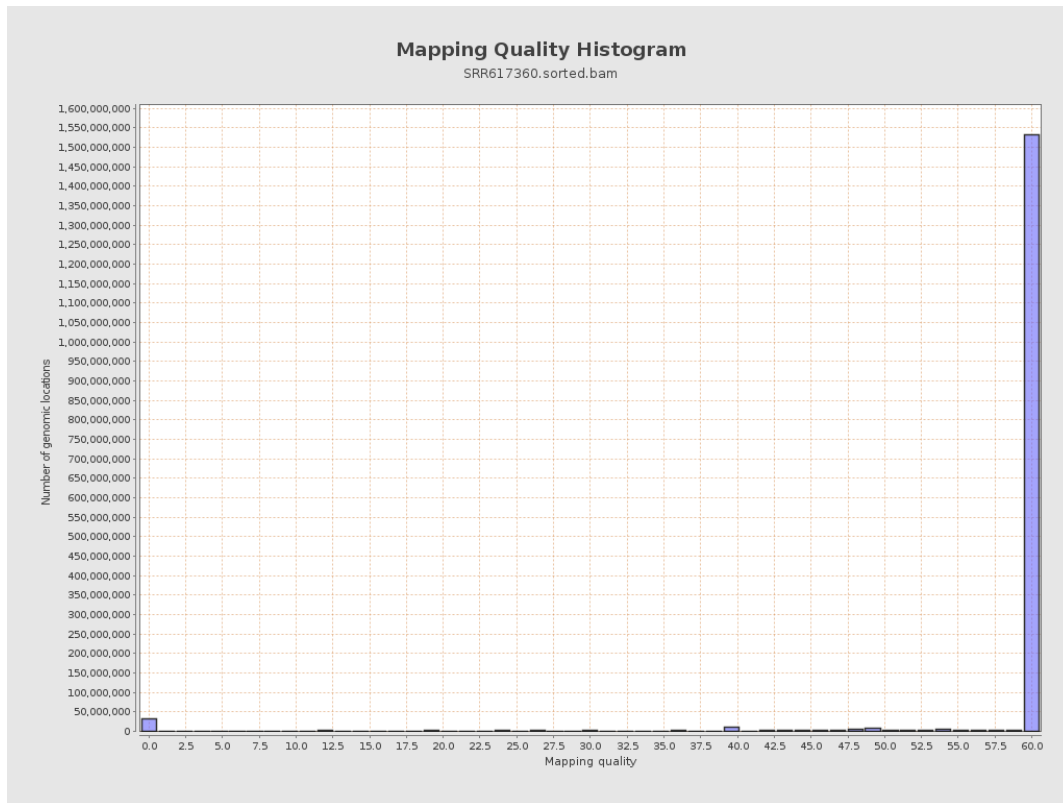
11. Results : Homopolymer Indels



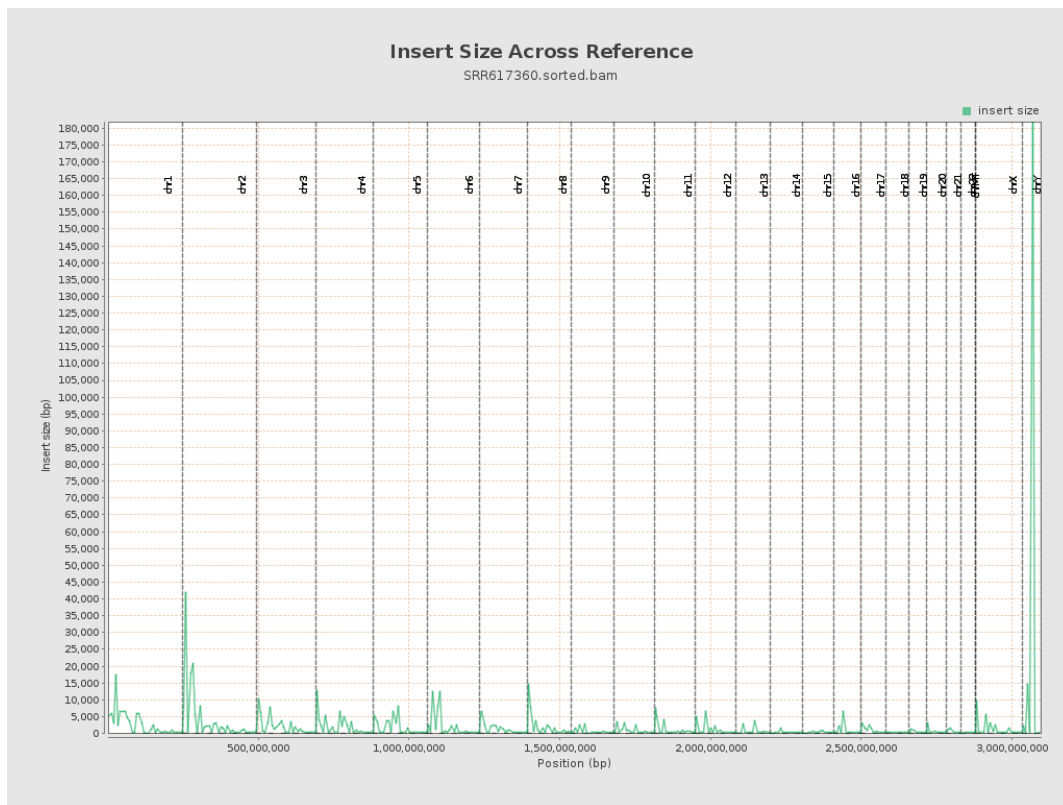
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

