

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/23 23:58:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617698.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_SRR8617698 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617698_1.fastq.gz SRR8617698_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 23 23:58:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617698.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	43,081,624
Mapped reads	42,322,187 / 98.24%
Unmapped reads	759,437 / 1.76%
Mapped paired reads	42,322,187 / 98.24%
Mapped reads, first in pair	21,340,962 / 49.54%
Mapped reads, second in pair	20,981,225 / 48.7%
Mapped reads, both in pair	41,843,678 / 97.13%
Mapped reads, singletons	478,509 / 1.11%
Secondary alignments	0
Supplementary alignments	1,636,752 / 3.8%
Read min/max/mean length	30 / 150 / 151.88
Duplicated reads (estimated)	13,342,832 / 30.97%
Duplication rate	23.4%
Clipped reads	25,227,222 / 58.56%

2.2. ACGT Content

Number/percentage of A's	1,611,963,814 / 28.73%
Number/percentage of C's	1,070,489,202 / 19.08%
Number/percentage of T's	1,663,602,093 / 29.65%
Number/percentage of G's	1,263,982,486 / 22.53%
Number/percentage of N's	214,031 / 0%

GC Percentage	41.61%
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2.3. Coverage

Mean	1.8136
Standard Deviation	14.8945

2.4. Mapping Quality

Mean Mapping Quality	53.14
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2.5. Insert size

Mean	270,608.32
Standard Deviation	5,088,590.7
P25/Median/P75	207 / 259 / 323

2.6. Mismatches and indels

General error rate	1.14%
Mismatches	61,360,465
Insertions	972,611
Mapped reads with at least one insertion	2.17%
Deletions	2,194,310
Mapped reads with at least one deletion	4.98%
Homopolymer indels	46.44%

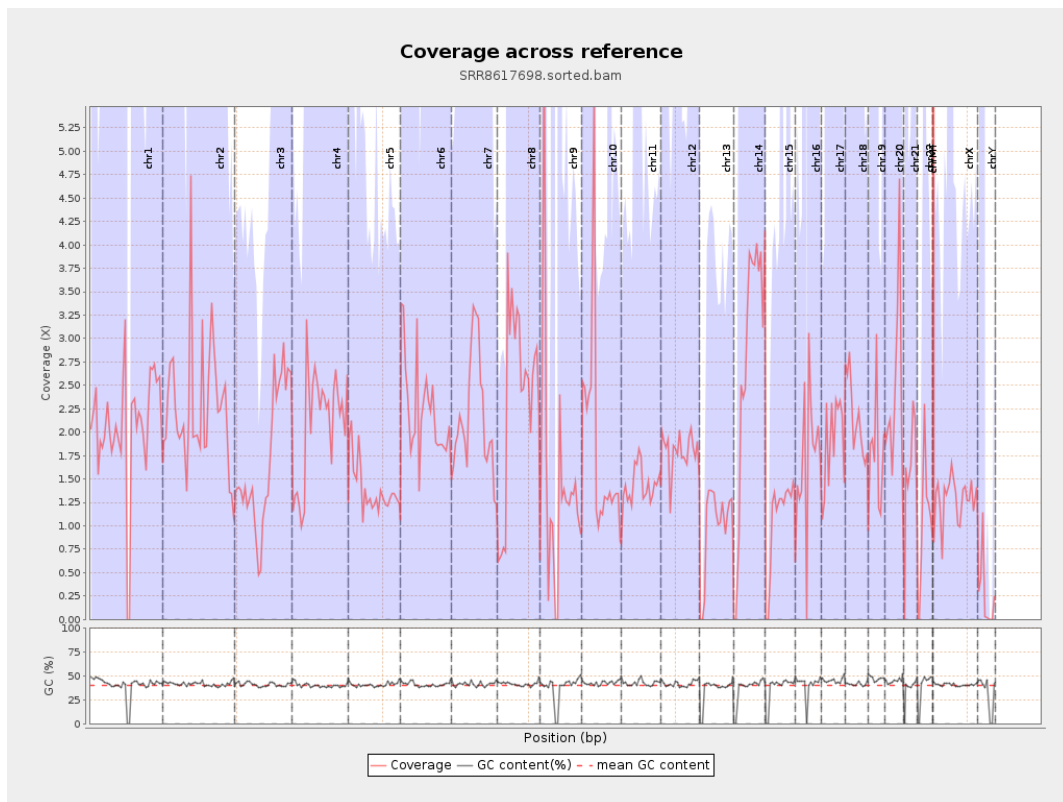
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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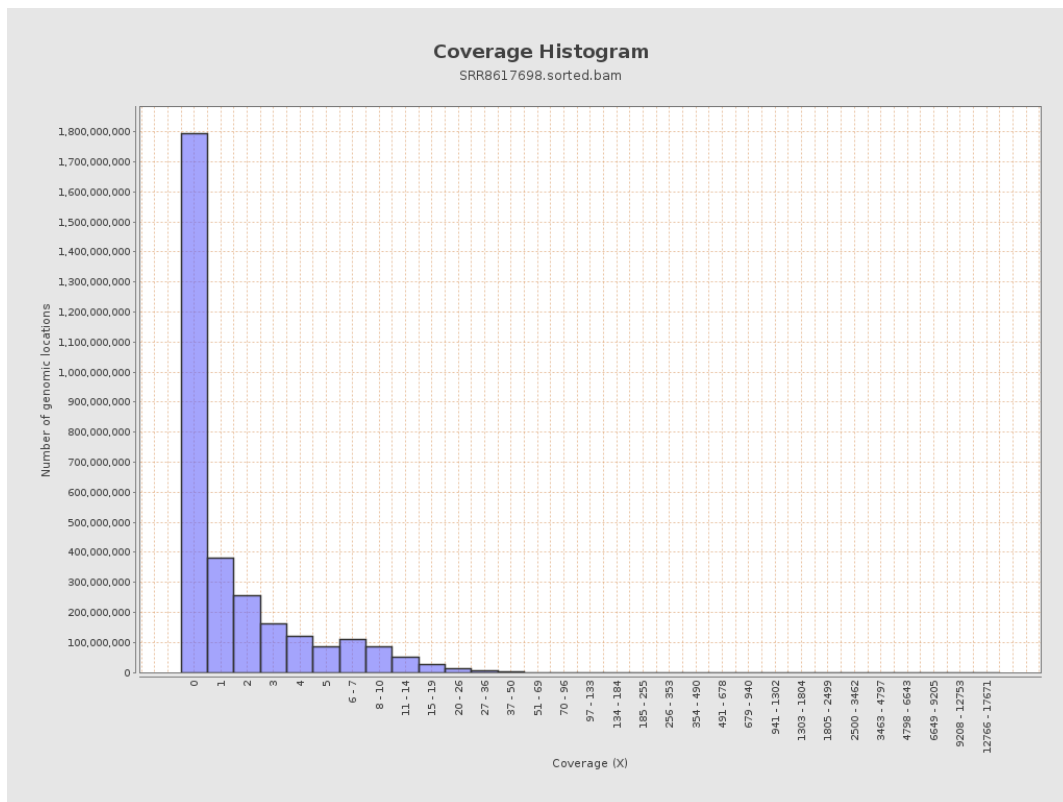
		bases	coverage	deviation
chr1	249250621	510826834	2.0495	17.4258
chr2	243199373	546972885	2.2491	21.4854
chr3	198022430	333706936	1.6852	3.5312
chr4	191154276	403118892	2.1089	11.8905
chr5	180915260	251824962	1.3919	3.3109
chr6	171115067	380296573	2.2225	13.2277
chr7	159138663	341303137	2.1447	17.1105
chr8	146364022	350070559	2.3918	7.2764
chr9	141213431	207365662	1.4685	28.6747
chr10	135534747	244834978	1.8064	29.0239
chr11	135006516	193721743	1.4349	10.4306
chr12	133851895	241692724	1.8057	8.3822
chr13	115169878	114747204	0.9963	2.4311
chr14	107349540	296601500	2.763	5.2949
chr15	102531392	109061666	1.0637	4.2896
chr16	90354753	153786262	1.702	14.7887
chr17	81195210	154796208	1.9065	17.7983
chr18	78077248	167480282	2.1451	24.7035
chr19	59128983	105814203	1.7895	8.8853
chr20	63025520	153958082	2.4428	5.6145
chr21	48129895	75903603	1.5771	6.3392
chr22	51304566	52978252	1.0326	3.1853
chrMT	16571	8317744	501.9458	241.2427
chrX	155270560	199236027	1.2832	4.7457

chrY	59373566	16047784	0.2703	13.933
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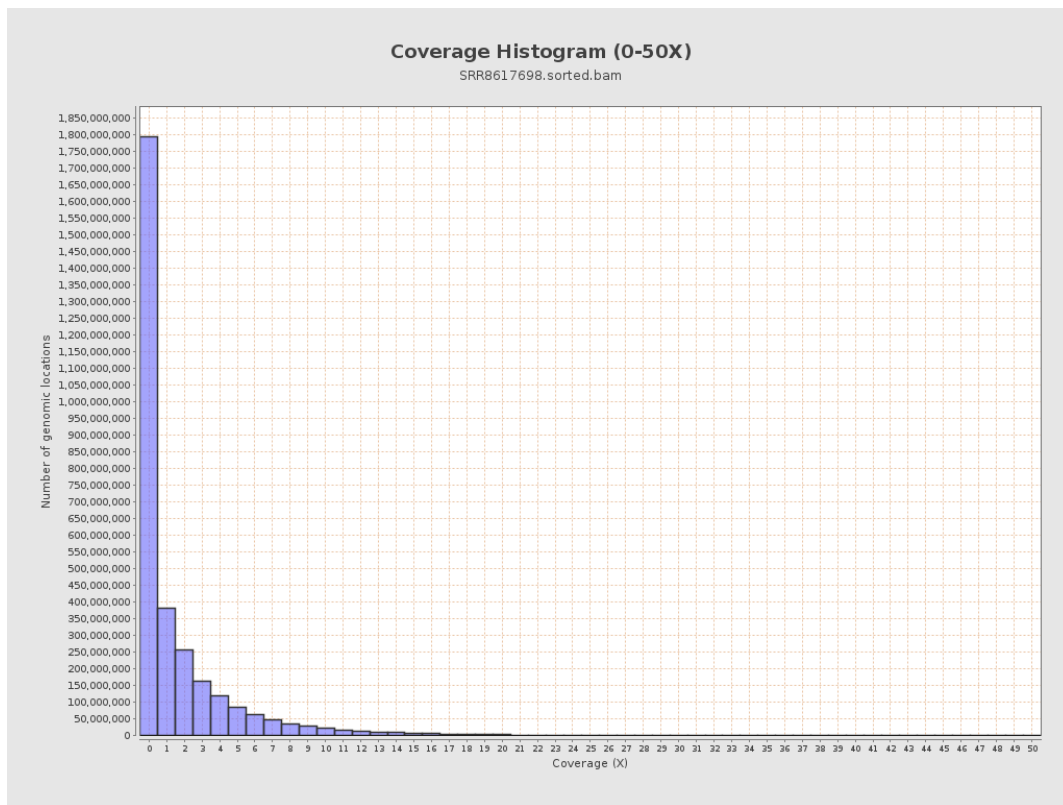
3. Results : Coverage across reference



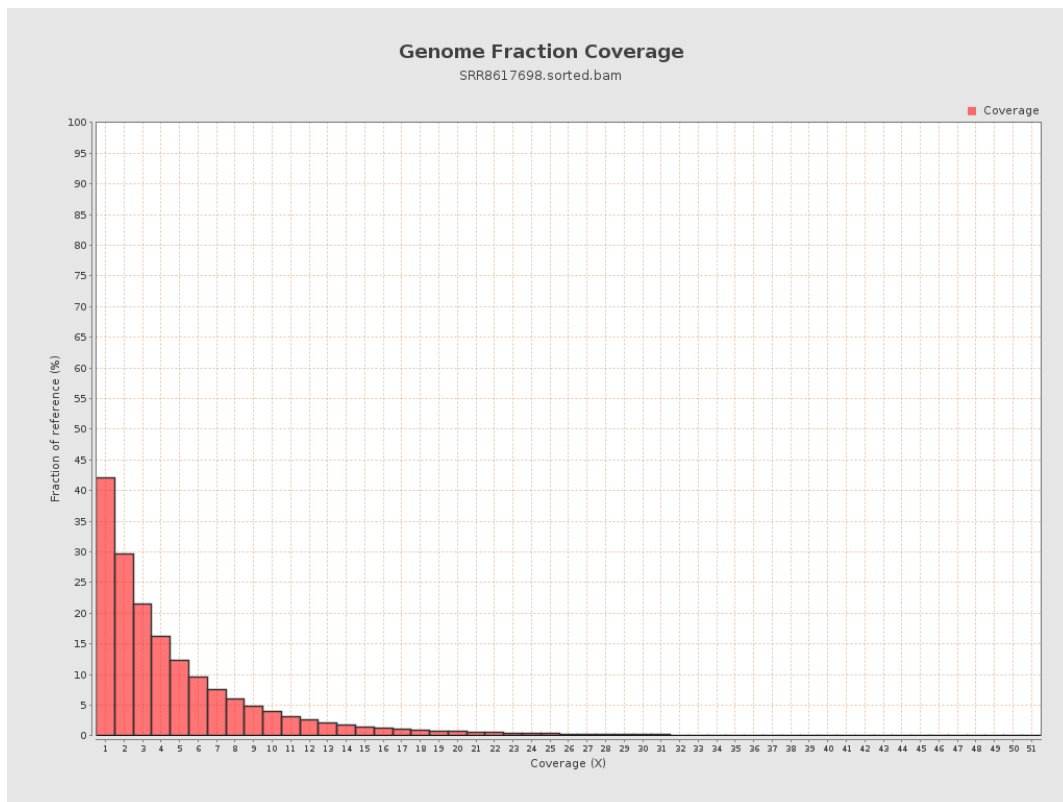
4. Results : Coverage Histogram



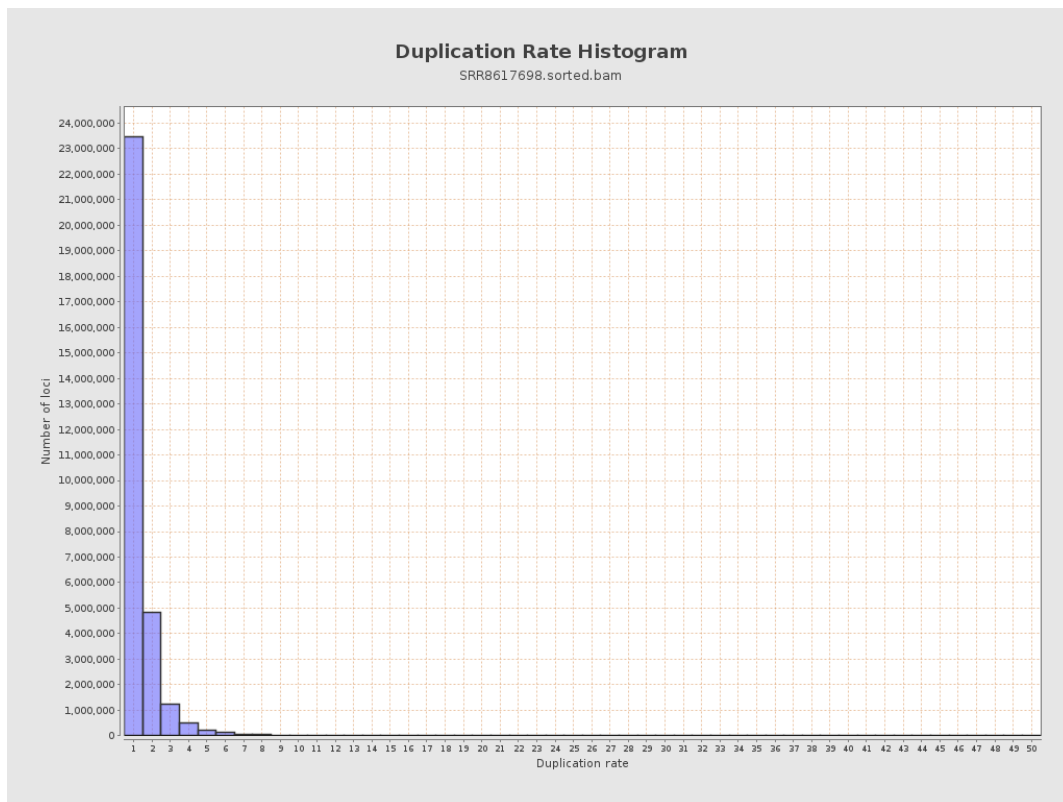
5. Results : Coverage Histogram (0-50X)



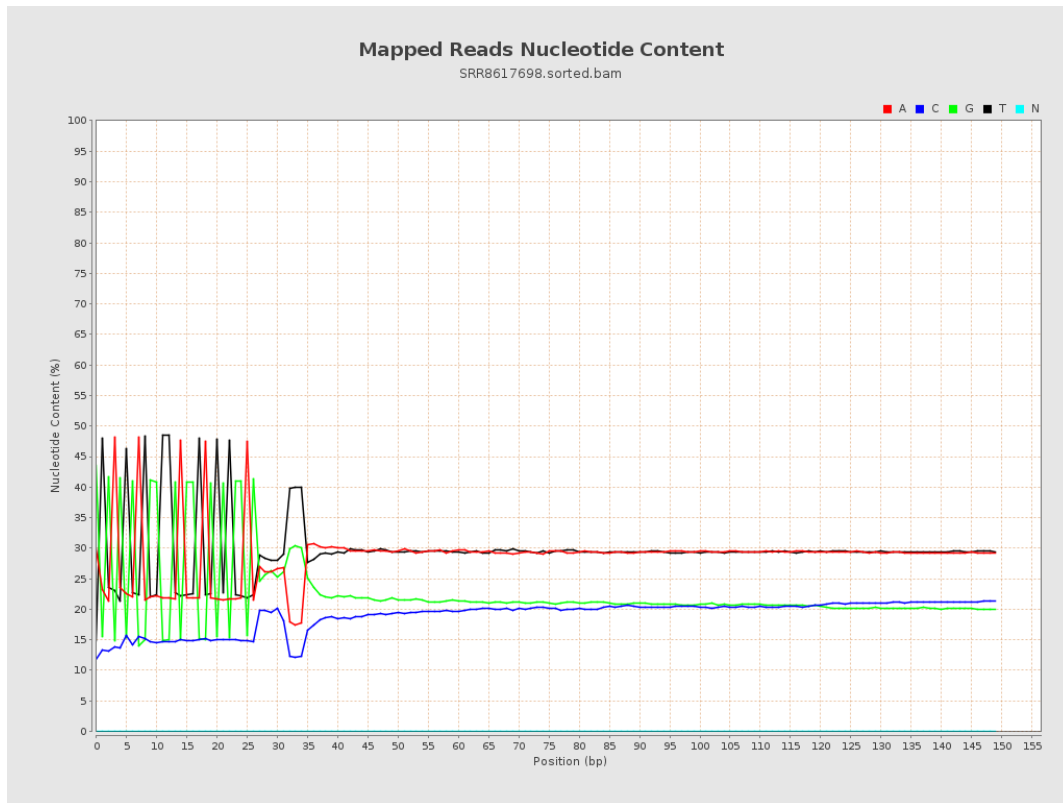
6. Results : Genome Fraction Coverage



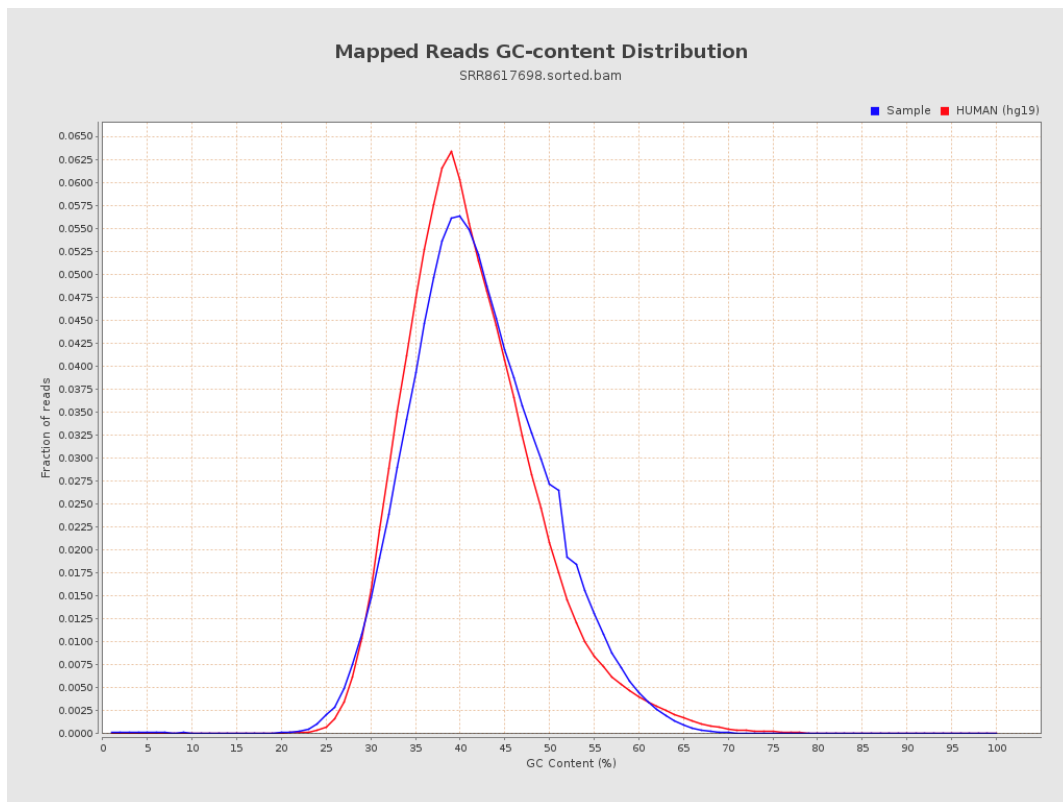
7. Results : Duplication Rate Histogram



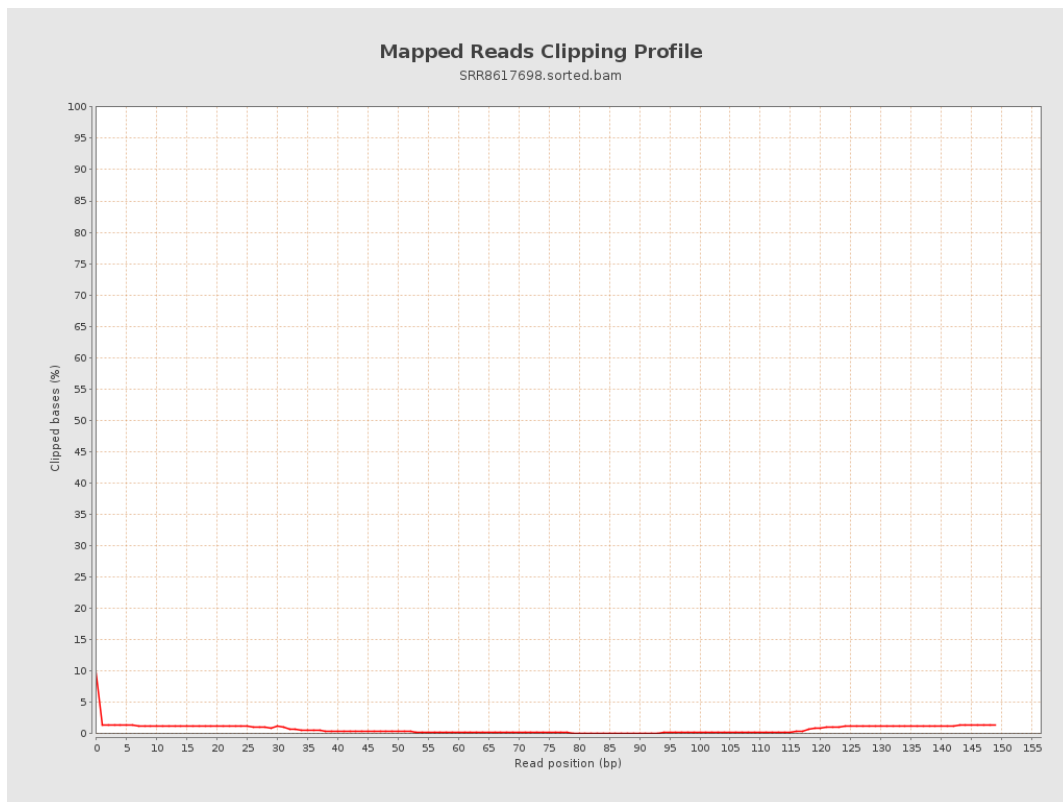
8. Results : Mapped Reads Nucleotide Content



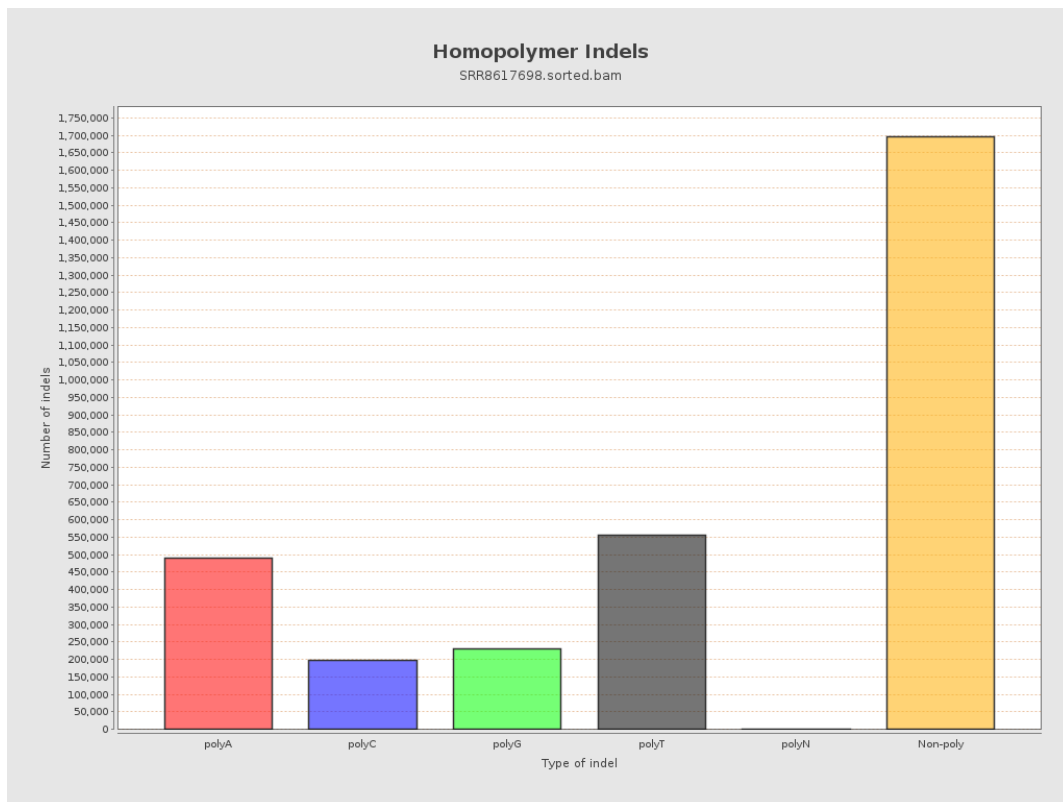
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



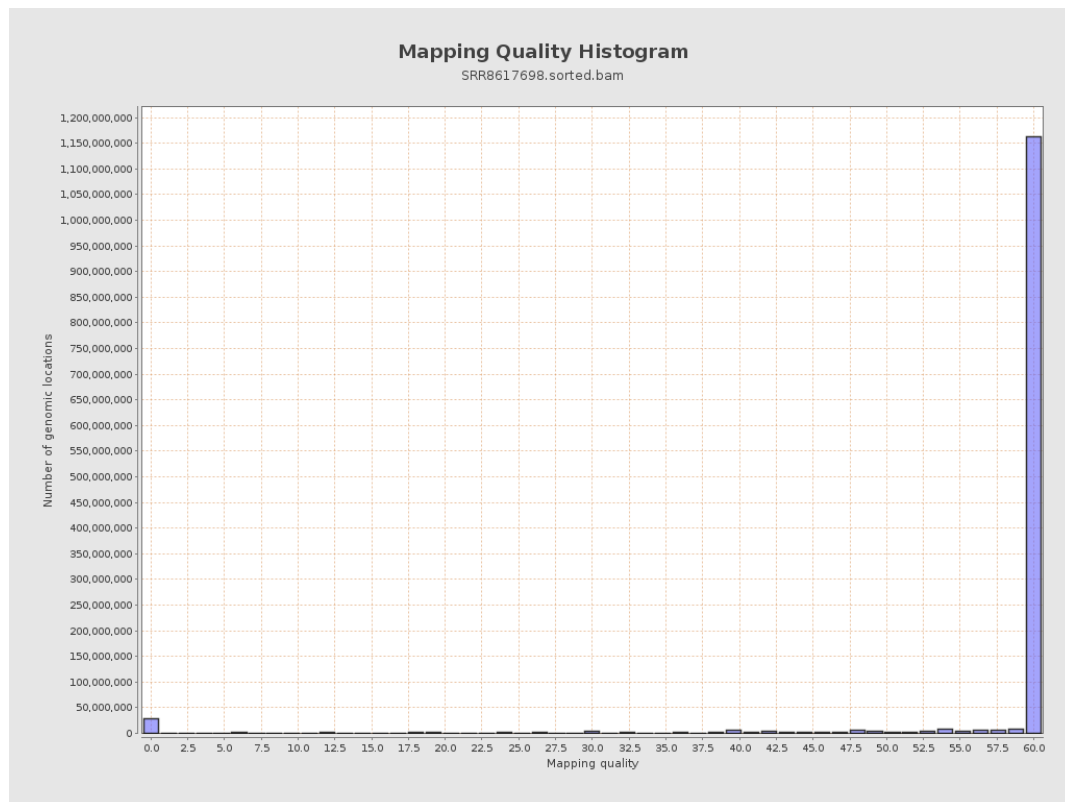
11. Results : Homopolymer Indels



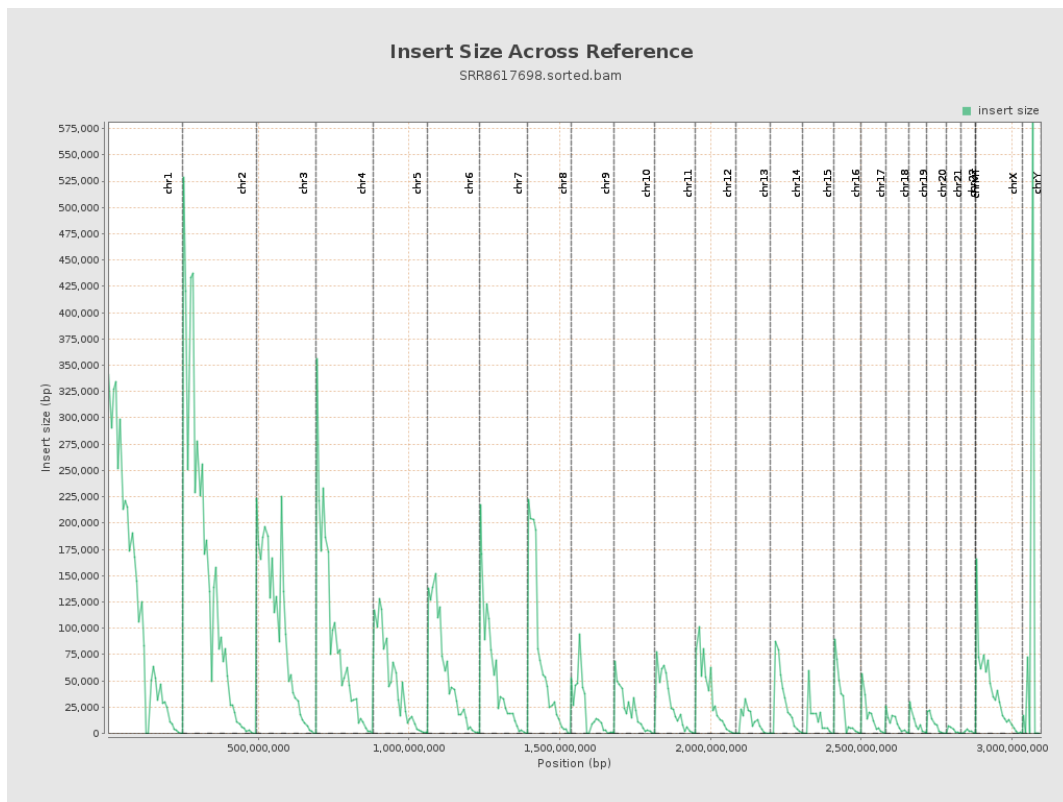
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

