

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/21 19:37:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617600.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_SRR8617600 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617600_1.fastq.gz SRR8617600_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 21 19:37:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617600.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	47,369,174
Mapped reads	46,431,485 / 98.02%
Unmapped reads	937,689 / 1.98%
Mapped paired reads	46,431,485 / 98.02%
Mapped reads, first in pair	23,461,735 / 49.53%
Mapped reads, second in pair	22,969,750 / 48.49%
Mapped reads, both in pair	45,812,488 / 96.71%
Mapped reads, singletons	618,997 / 1.31%
Secondary alignments	0
Supplementary alignments	757,913 / 1.6%
Read min/max/mean length	30 / 150 / 150.76
Duplicated reads (estimated)	13,659,724 / 28.84%
Duplication rate	22.08%
Clipped reads	22,711,150 / 47.94%

2.2. ACGT Content

Number/percentage of A's	1,804,123,167 / 28.92%
Number/percentage of C's	1,186,955,176 / 19.03%
Number/percentage of T's	1,860,226,448 / 29.82%
Number/percentage of G's	1,386,430,949 / 22.23%
Number/percentage of N's	255,757 / 0%

GC Percentage	41.25%
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2.3. Coverage

Mean	2.0164
Standard Deviation	19.6945

2.4. Mapping Quality

Mean Mapping Quality	53.68
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2.5. Insert size

Mean	107,816.54
Standard Deviation	3,157,814.83
P25/Median/P75	225 / 281 / 355

2.6. Mismatches and indels

General error rate	1.2%
Mismatches	71,849,099
Insertions	1,030,929
Mapped reads with at least one insertion	2.09%
Deletions	2,194,642
Mapped reads with at least one deletion	4.54%
Homopolymer indels	45.99%

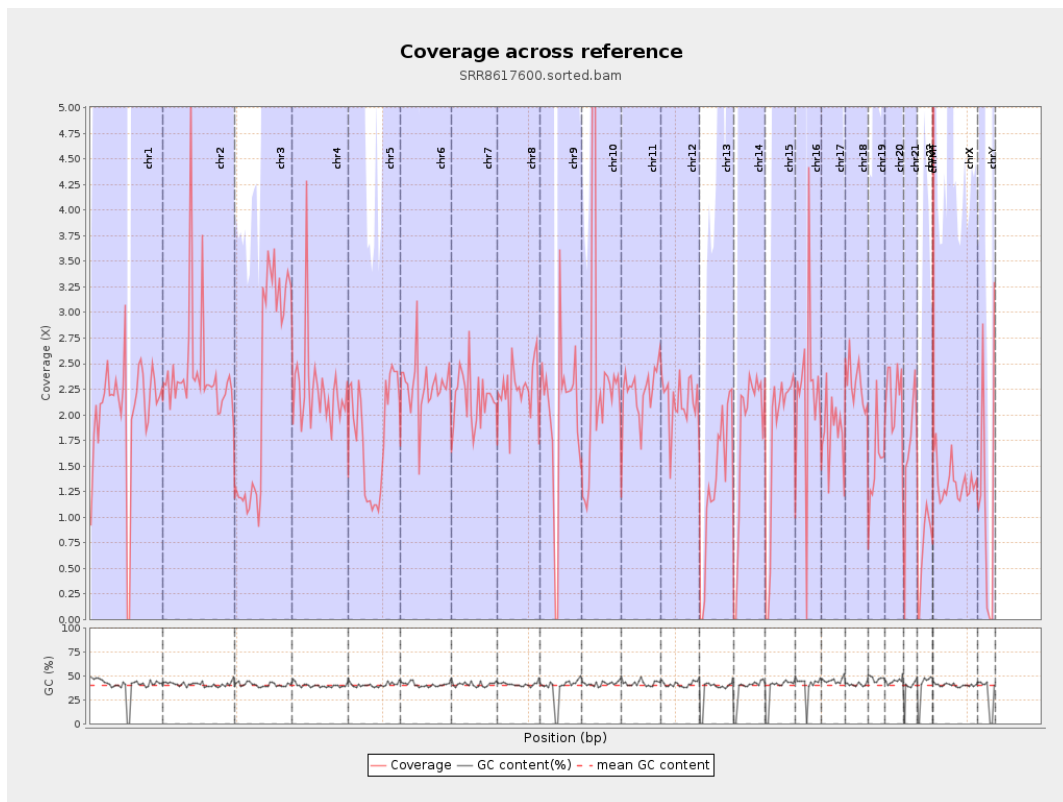
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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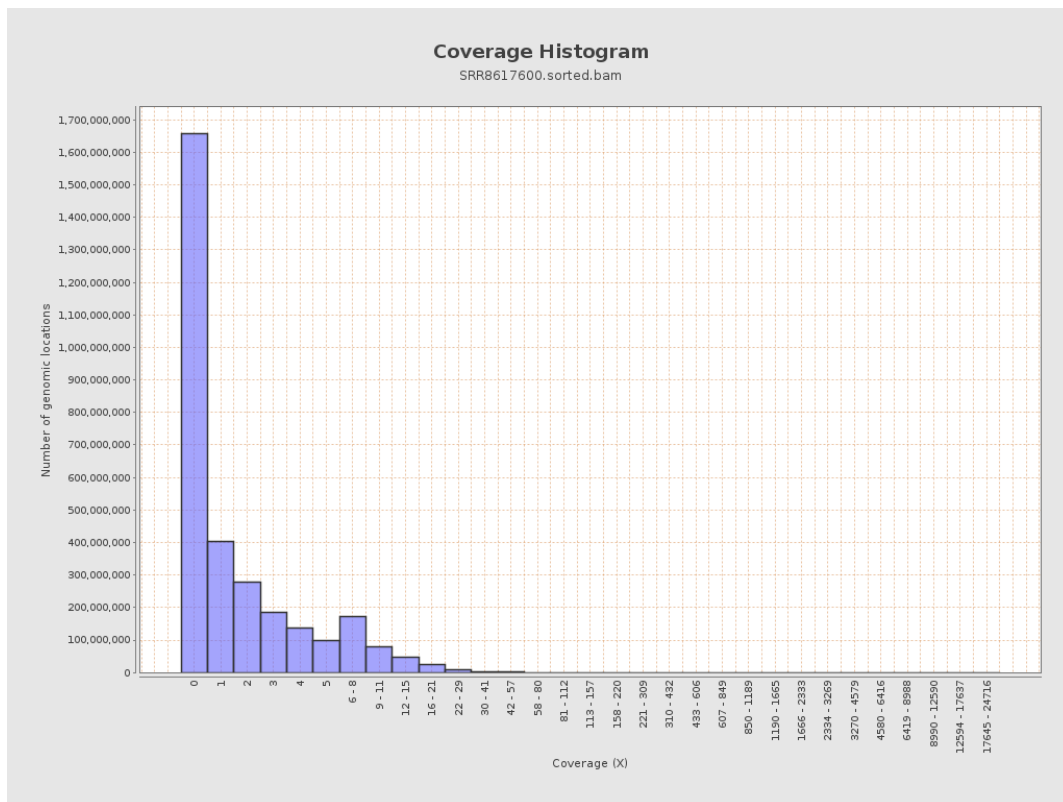
		bases	coverage	deviation
chr1	249250621	507339840	2.0355	18.0252
chr2	243199373	588708134	2.4207	22.7113
chr3	198022430	446084549	2.2527	4.2662
chr4	191154276	431165765	2.2556	17.5064
chr5	180915260	327385194	1.8096	3.8058
chr6	171115067	389959850	2.2789	11.0025
chr7	159138663	343043767	2.1556	20.2847
chr8	146364022	330048517	2.255	5.8572
chr9	141213431	283473497	2.0074	35.7433
chr10	135534747	320459603	2.3644	57.125
chr11	135006516	301133263	2.2305	10.8973
chr12	133851895	285543513	2.1333	7.1439
chr13	115169878	156266147	1.3568	2.9271
chr14	107349540	195581503	1.8219	4.0213
chr15	102531392	179911501	1.7547	4.4668
chr16	90354753	197883658	2.1901	20.3212
chr17	81195210	150811775	1.8574	20.7742
chr18	78077248	179305152	2.2965	24.5025
chr19	59128983	91105558	1.5408	10.8287
chr20	63025520	138392799	2.1958	6.2278
chr21	48129895	80816102	1.6791	9.1667
chr22	51304566	35844020	0.6987	2.6823
chrMT	16571	953703	57.5525	29.2121
chrX	155270560	207951694	1.3393	4.6611

chrY	59373566	73113064	1.2314	29.3348
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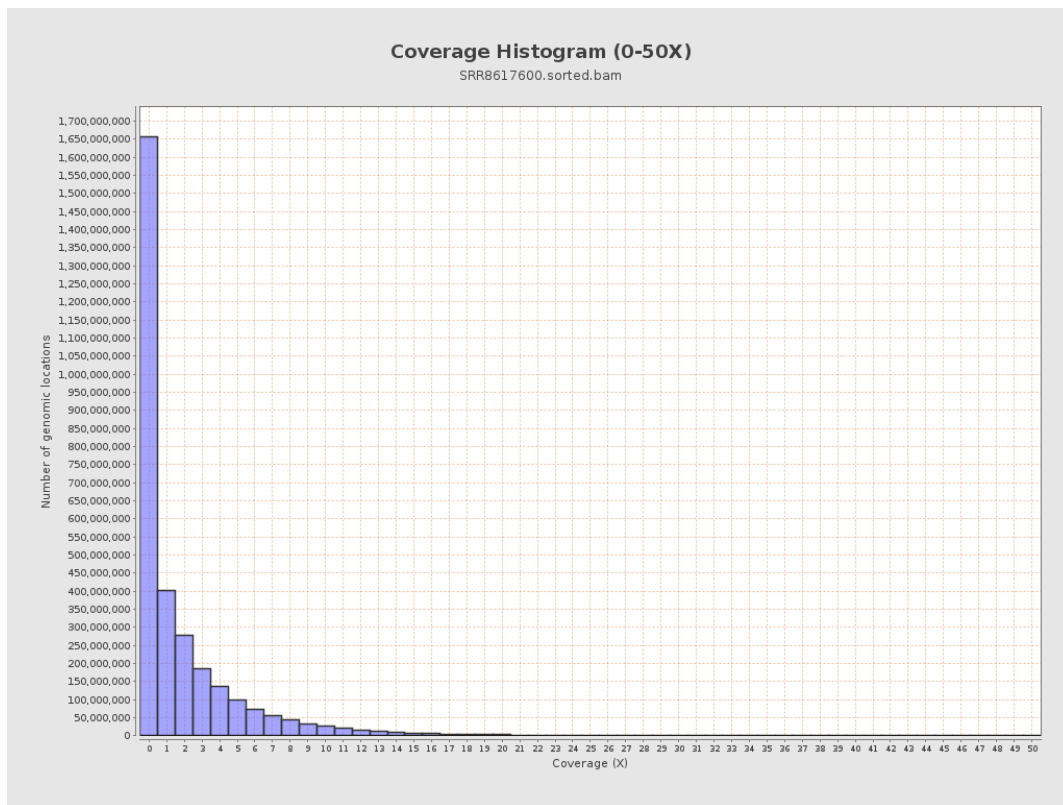
3. Results : Coverage across reference



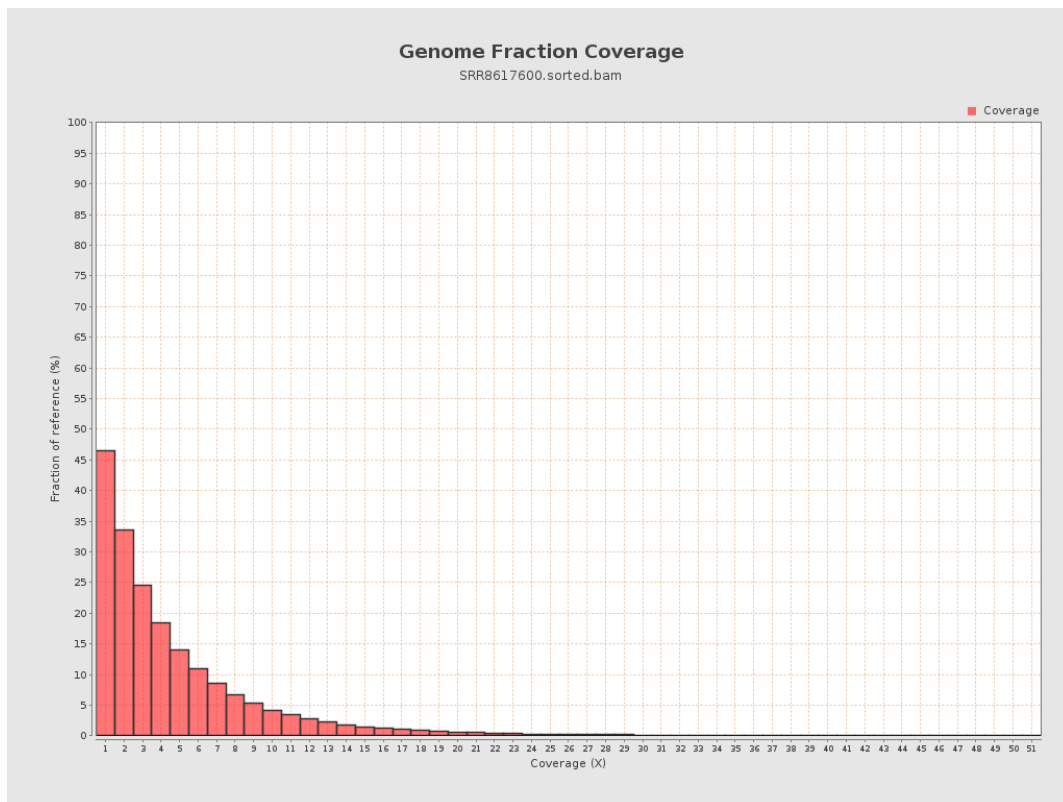
4. Results : Coverage Histogram



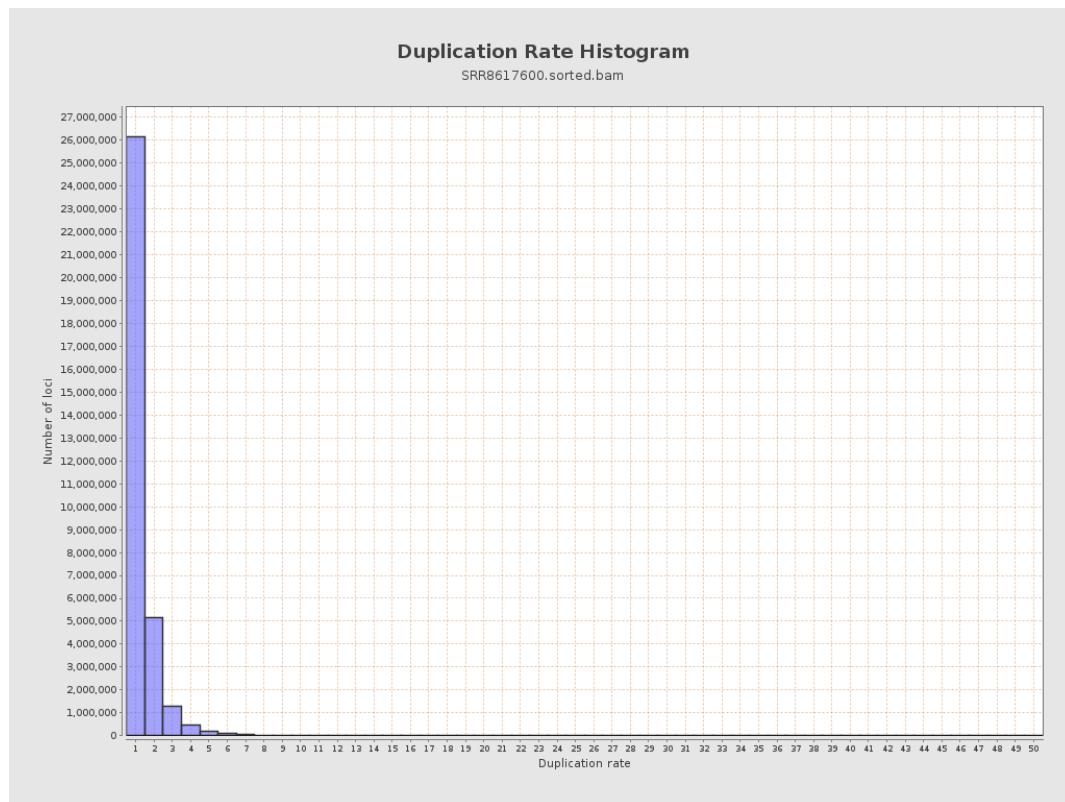
5. Results : Coverage Histogram (0-50X)



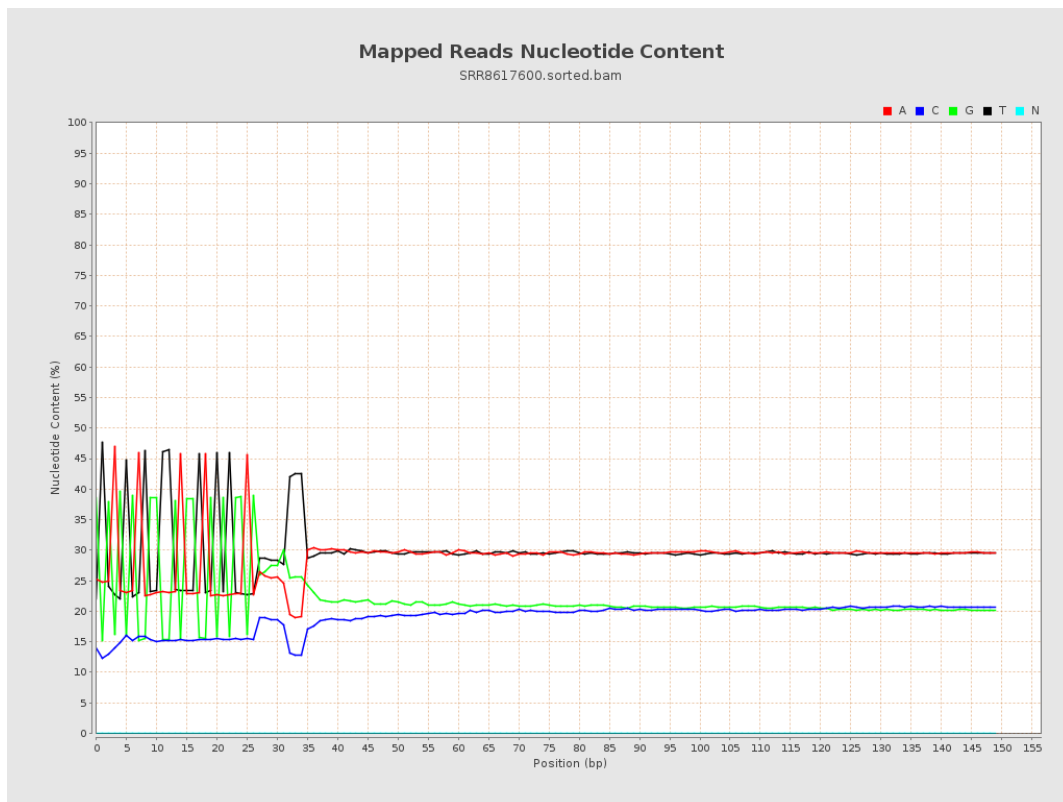
6. Results : Genome Fraction Coverage



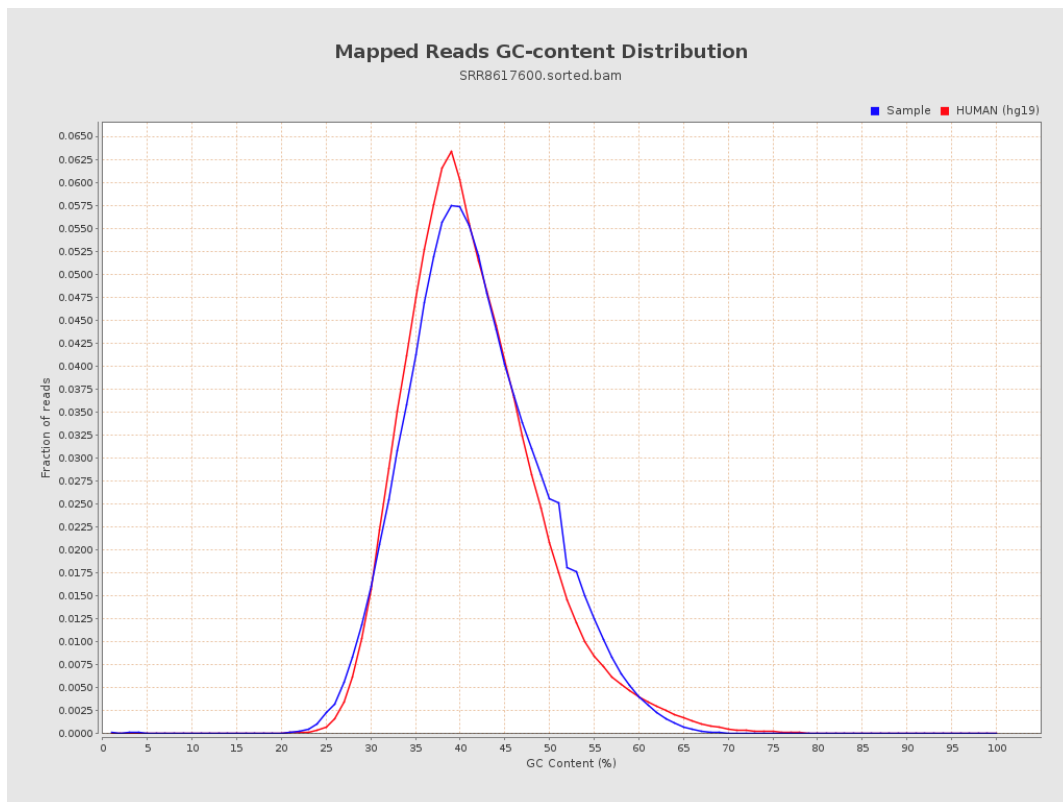
7. Results : Duplication Rate Histogram



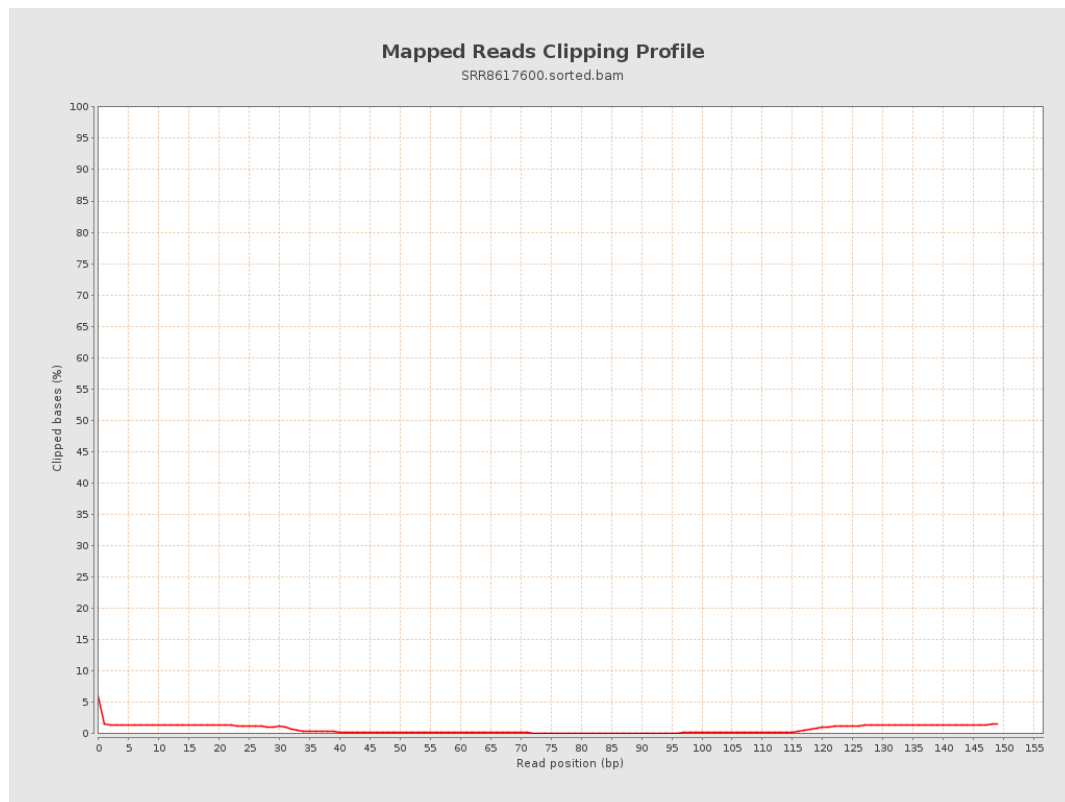
8. Results : Mapped Reads Nucleotide Content



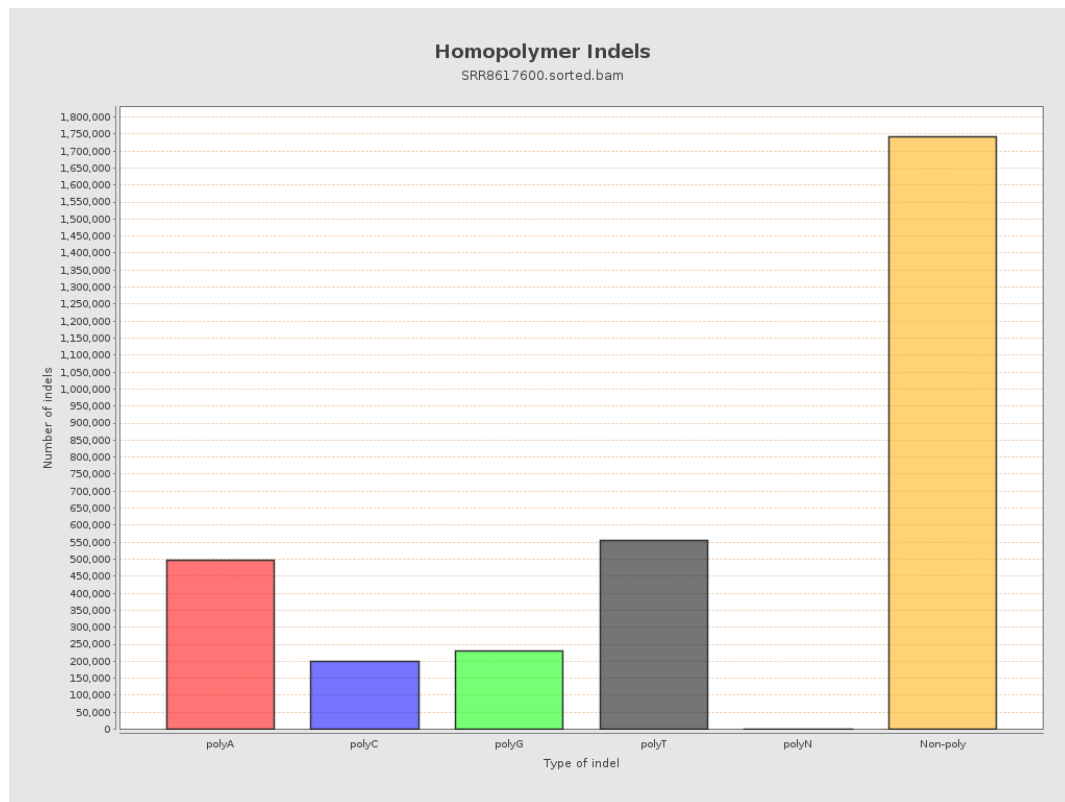
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



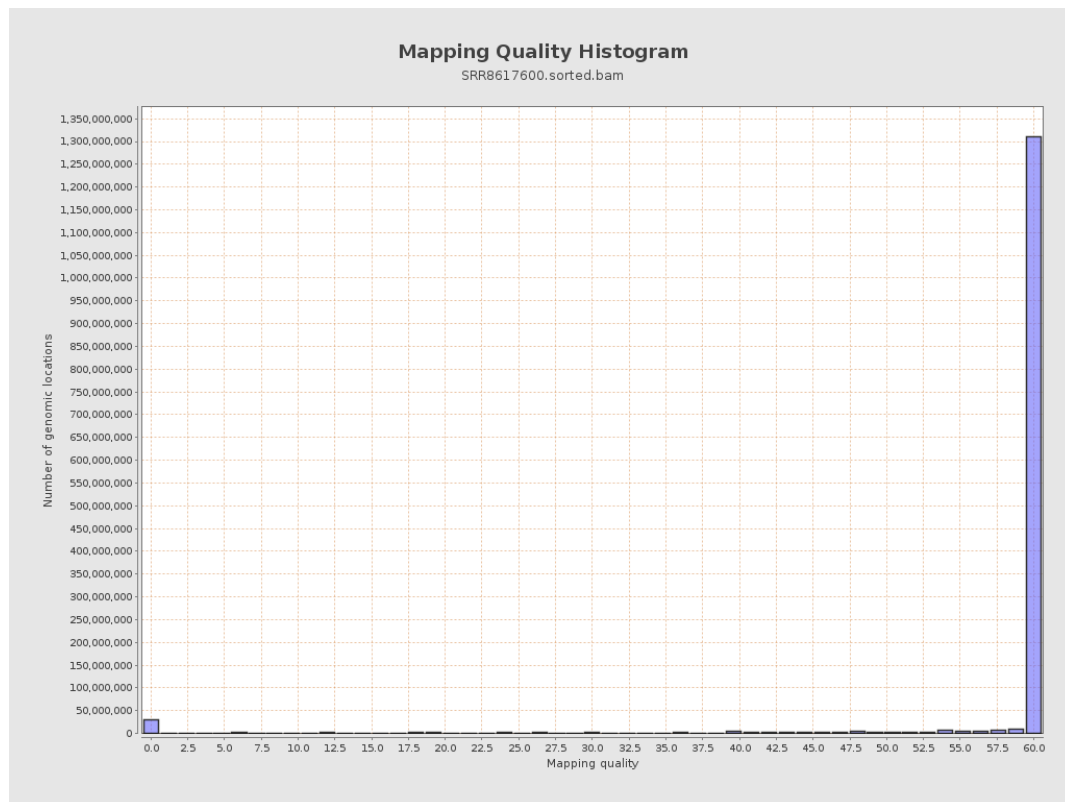
11. Results : Homopolymer Indels



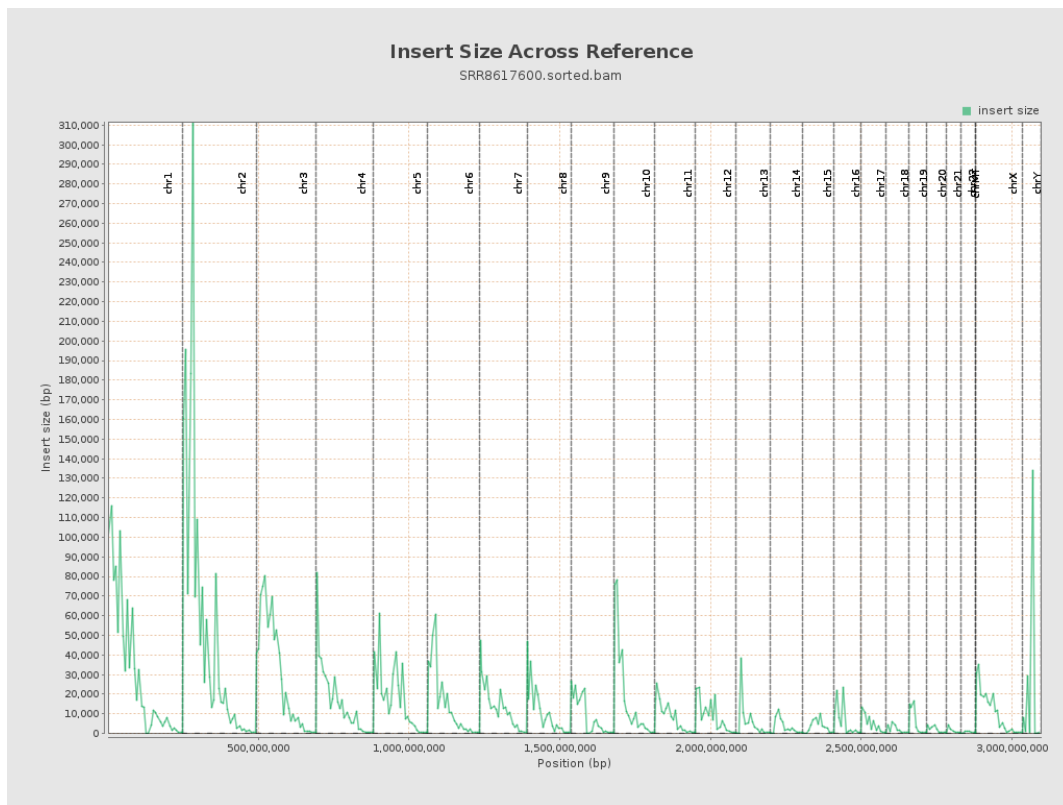
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

