

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/24 08:07:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617704.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_SRR8617704 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617704_1.fastq.gz SRR8617704_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 24 08:07:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617704.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	53,893,928
Mapped reads	53,030,430 / 98.4%
Unmapped reads	863,498 / 1.6%
Mapped paired reads	53,030,430 / 98.4%
Mapped reads, first in pair	26,797,710 / 49.72%
Mapped reads, second in pair	26,232,720 / 48.67%
Mapped reads, both in pair	52,395,224 / 97.22%
Mapped reads, singletons	635,206 / 1.18%
Secondary alignments	0
Supplementary alignments	973,007 / 1.81%
Read min/max/mean length	30 / 150 / 150.85
Duplicated reads (estimated)	20,407,939 / 37.87%
Duplication rate	28.44%
Clipped reads	28,666,886 / 53.19%

2.2. ACGT Content

Number/percentage of A's	2,037,329,072 / 28.87%
Number/percentage of C's	1,334,688,118 / 18.91%
Number/percentage of T's	2,116,618,267 / 29.99%
Number/percentage of G's	1,568,630,432 / 22.23%
Number/percentage of N's	299,582 / 0%

GC Percentage	41.14%
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2.3. Coverage

Mean	2.2815
Standard Deviation	22.4232

2.4. Mapping Quality

Mean Mapping Quality	53.66
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2.5. Insert size

Mean	107,826.4
Standard Deviation	3,148,400.38
P25/Median/P75	212 / 267 / 335

2.6. Mismatches and indels

General error rate	1.14%
Mismatches	77,748,132
Insertions	1,181,974
Mapped reads with at least one insertion	2.1%
Deletions	2,765,432
Mapped reads with at least one deletion	5.01%
Homopolymer indels	46.55%

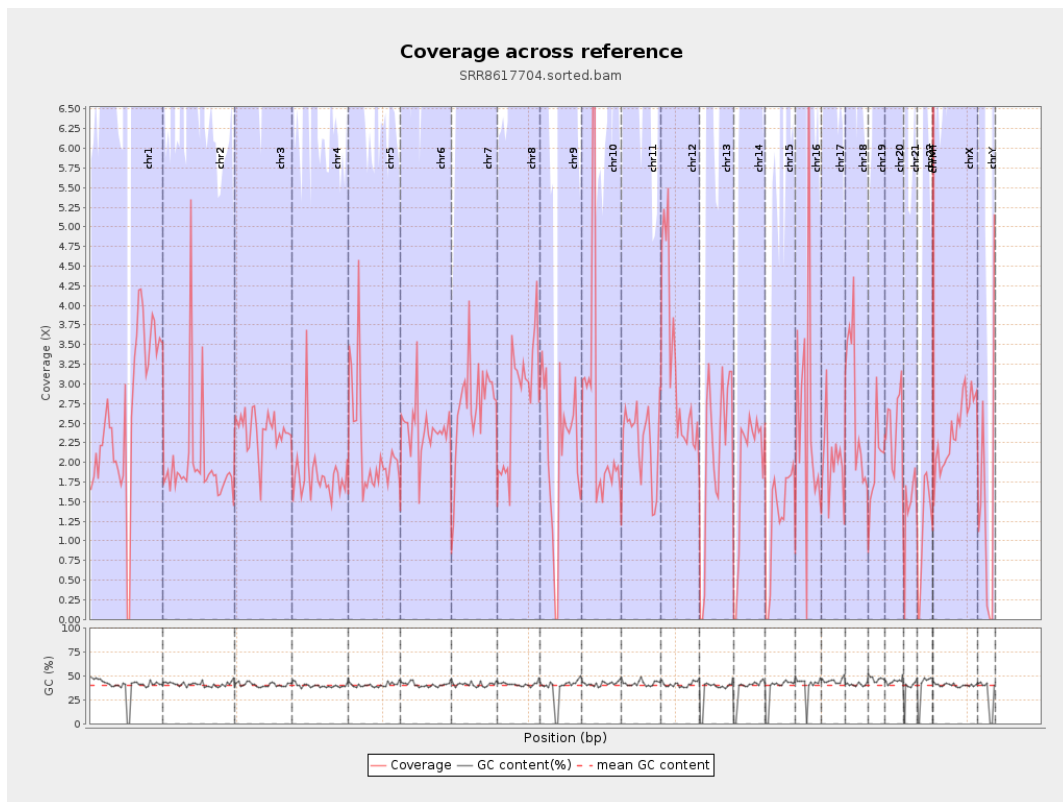
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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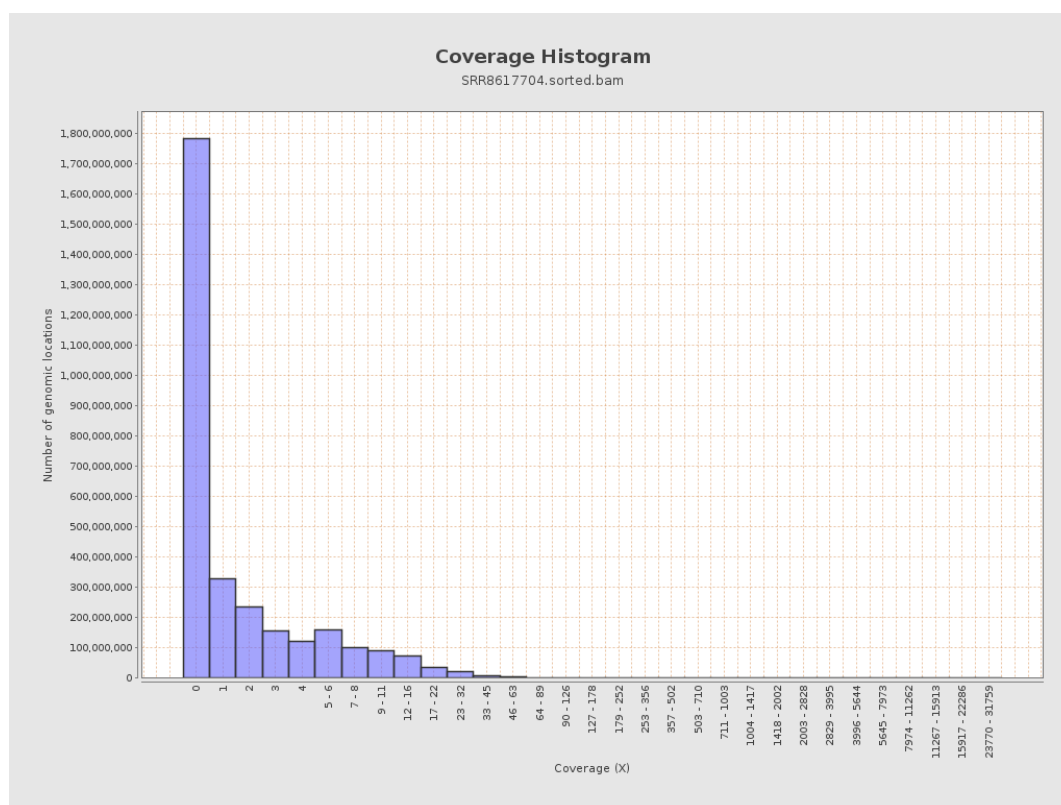
		bases	coverage	deviation
chr1	249250621	659095644	2.6443	20.8115
chr2	243199373	481104834	1.9782	25.8386
chr3	198022430	474669324	2.397	4.8691
chr4	191154276	355246448	1.8584	14.1082
chr5	180915260	394786194	2.1822	4.9933
chr6	171115067	415049776	2.4256	14.4971
chr7	159138663	432194094	2.7158	33.7892
chr8	146364022	409958279	2.8009	8.1035
chr9	141213431	302945642	2.1453	33.4366
chr10	135534747	344759900	2.5437	61.4674
chr11	135006516	304095153	2.2524	21.1338
chr12	133851895	423828115	3.1664	13.4964
chr13	115169878	245787290	2.1341	4.6526
chr14	107349540	208236813	1.9398	4.7436
chr15	102531392	132853195	1.2957	5.2358
chr16	90354753	227248126	2.5151	29.2091
chr17	81195210	167144367	2.0585	18.7509
chr18	78077248	212776116	2.7252	29.7203
chr19	59128983	119112364	2.0144	13.2207
chr20	63025520	156872841	2.489	6.3839
chr21	48129895	69446972	1.4429	7.4086
chr22	51304566	59805219	1.1657	4.1368
chrMT	16571	974142	58.786	31.988
chrX	155270560	373065498	2.4027	7.029

chrY	59373566	91725153	1.5449	29.0176
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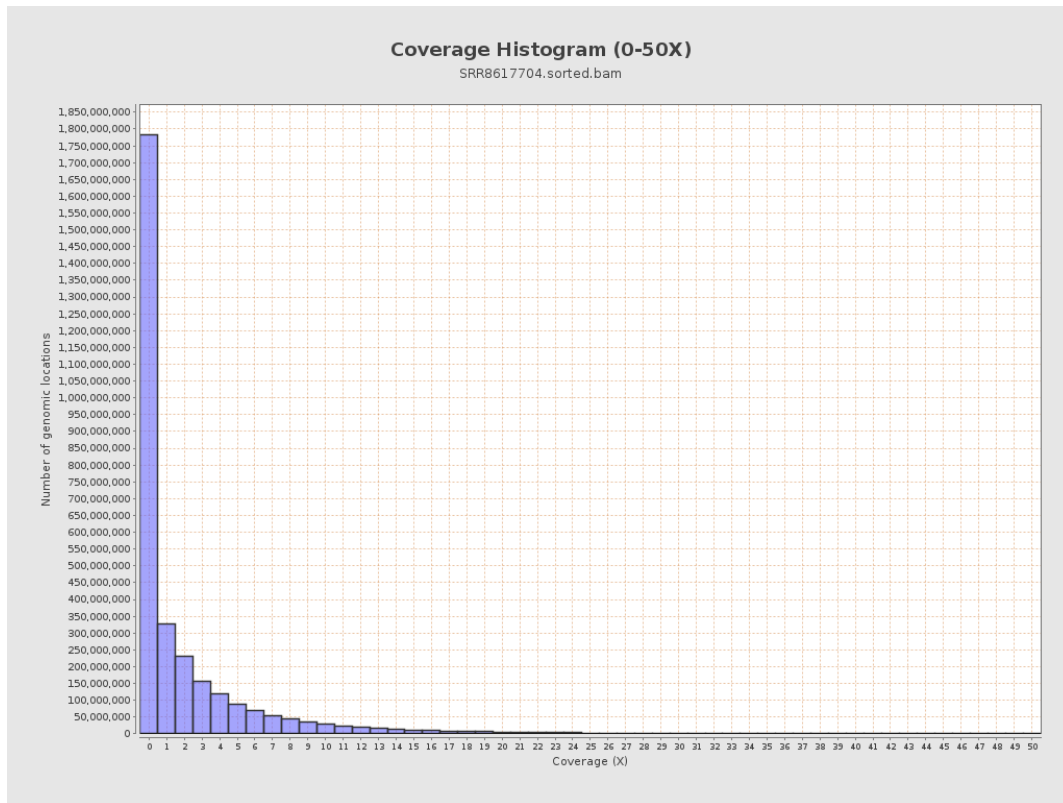
3. Results : Coverage across reference



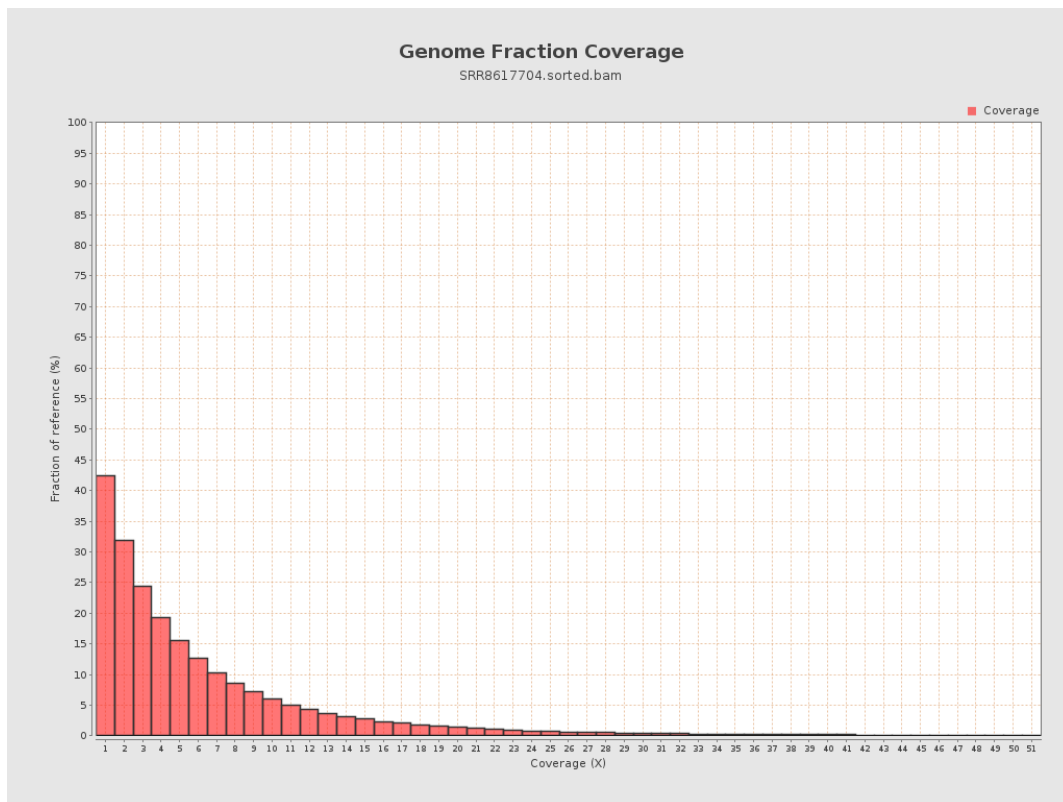
4. Results : Coverage Histogram



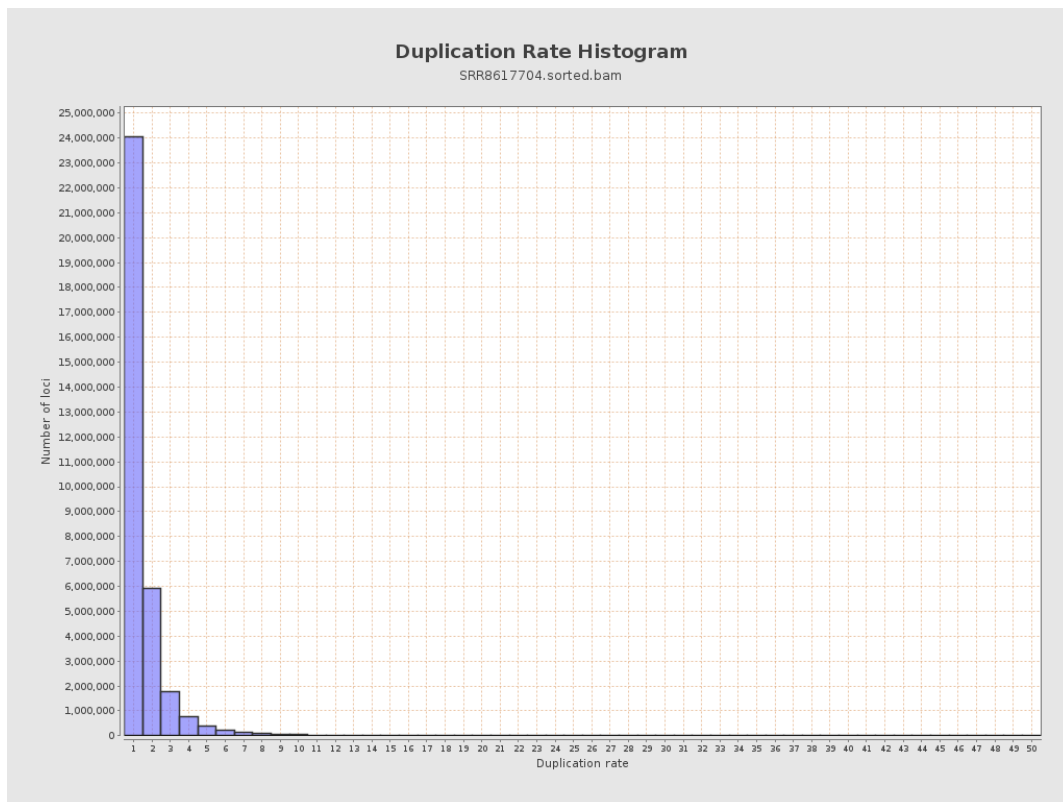
5. Results : Coverage Histogram (0-50X)



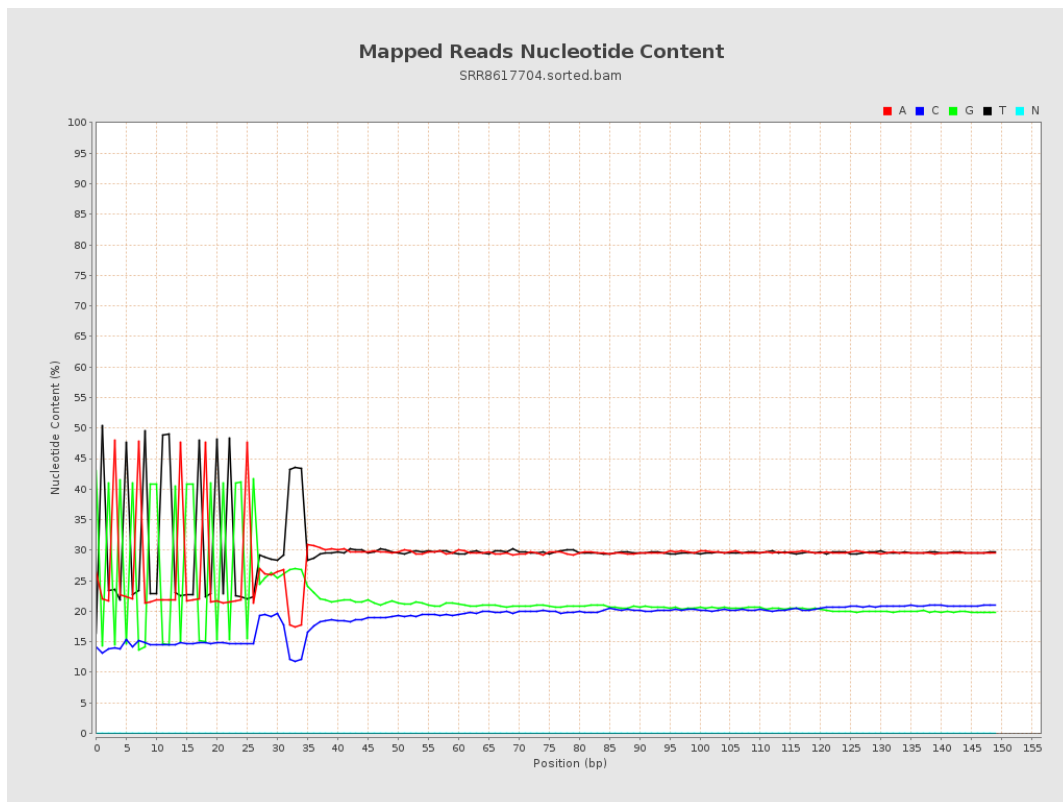
6. Results : Genome Fraction Coverage



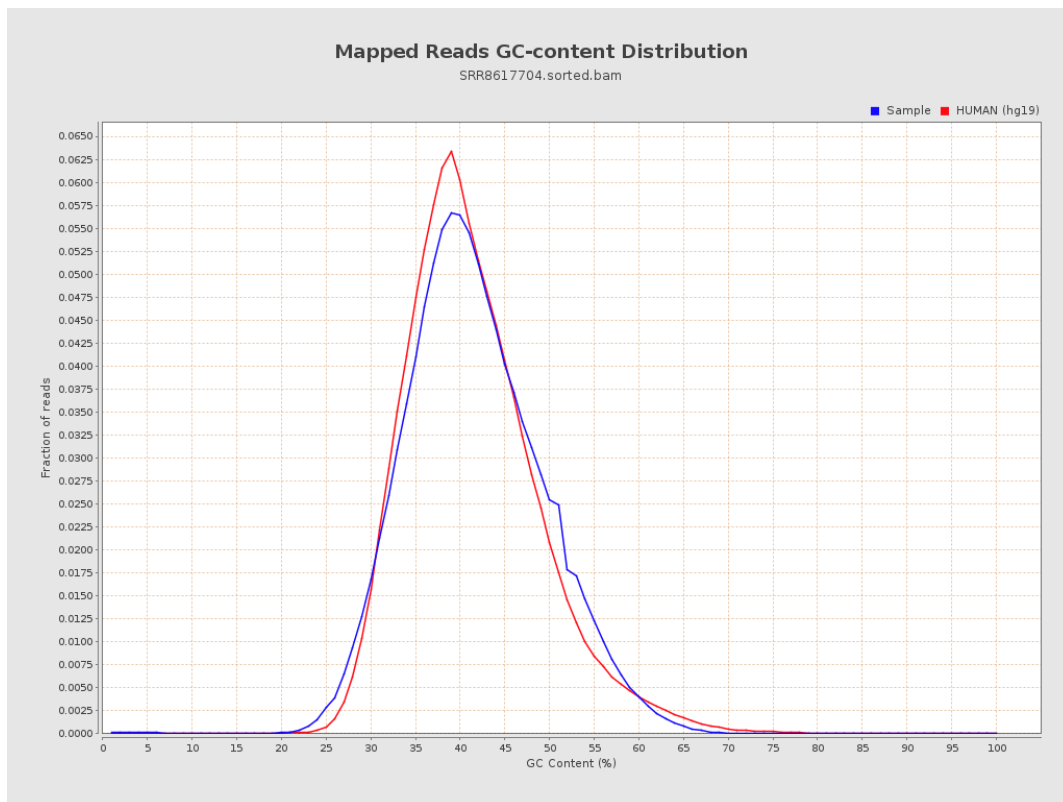
7. Results : Duplication Rate Histogram



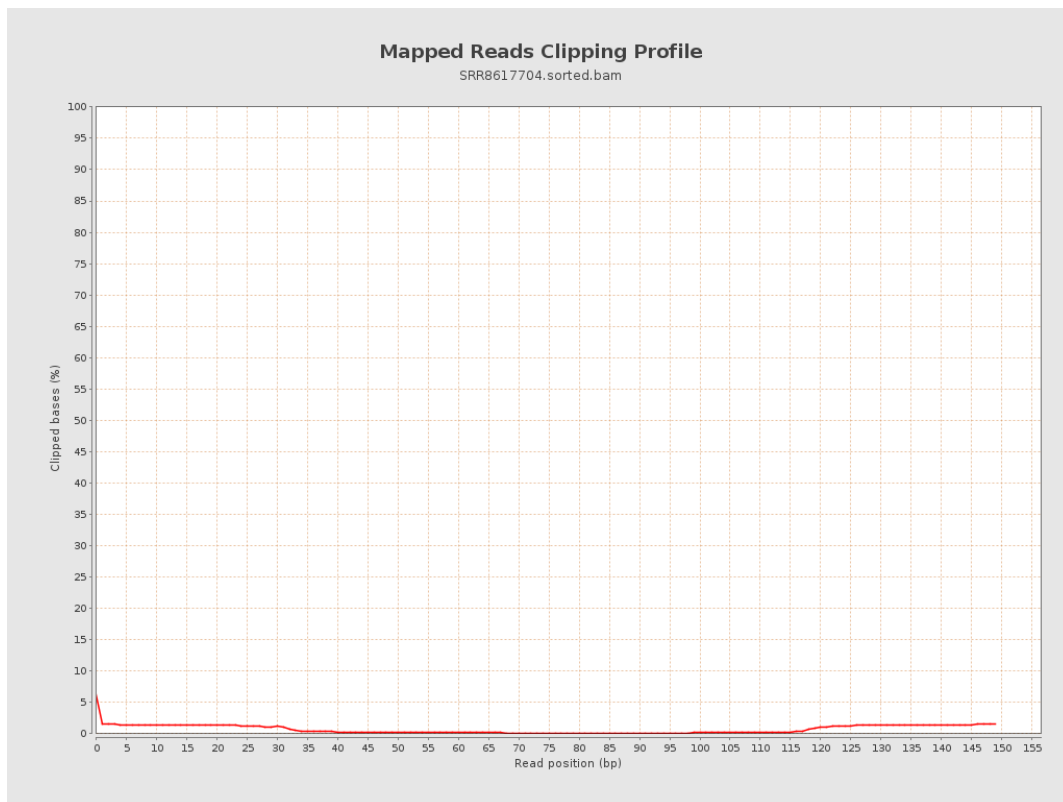
8. Results : Mapped Reads Nucleotide Content



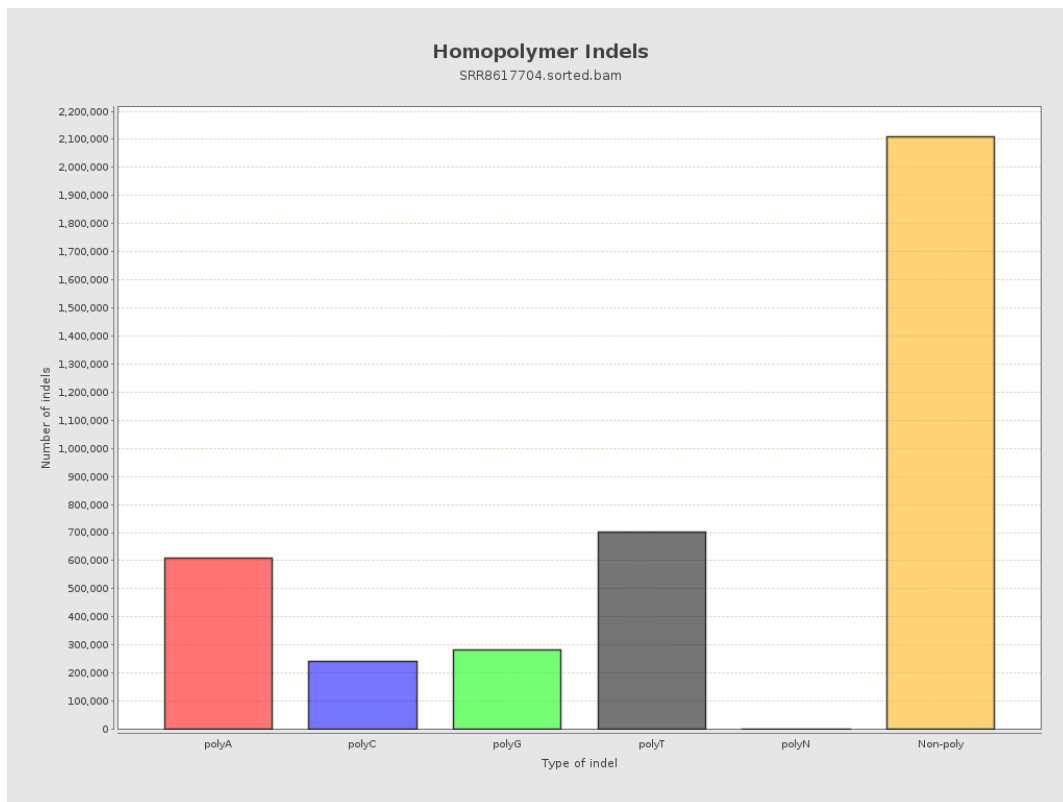
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



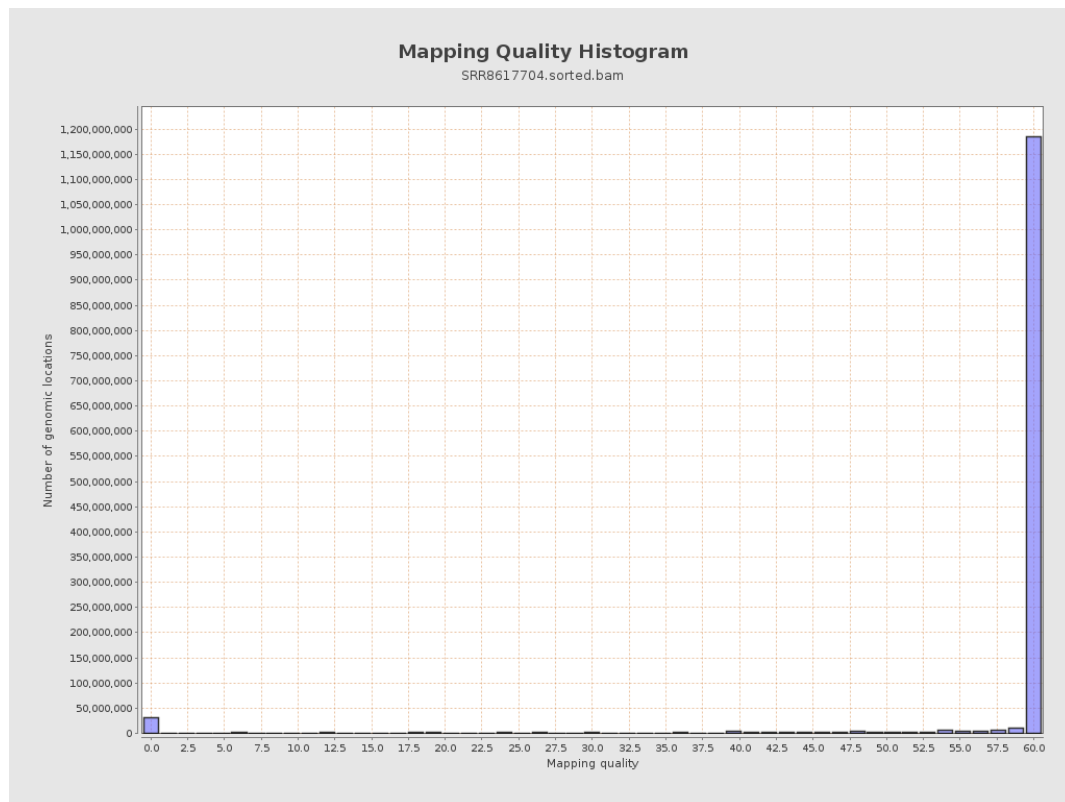
11. Results : Homopolymer Indels



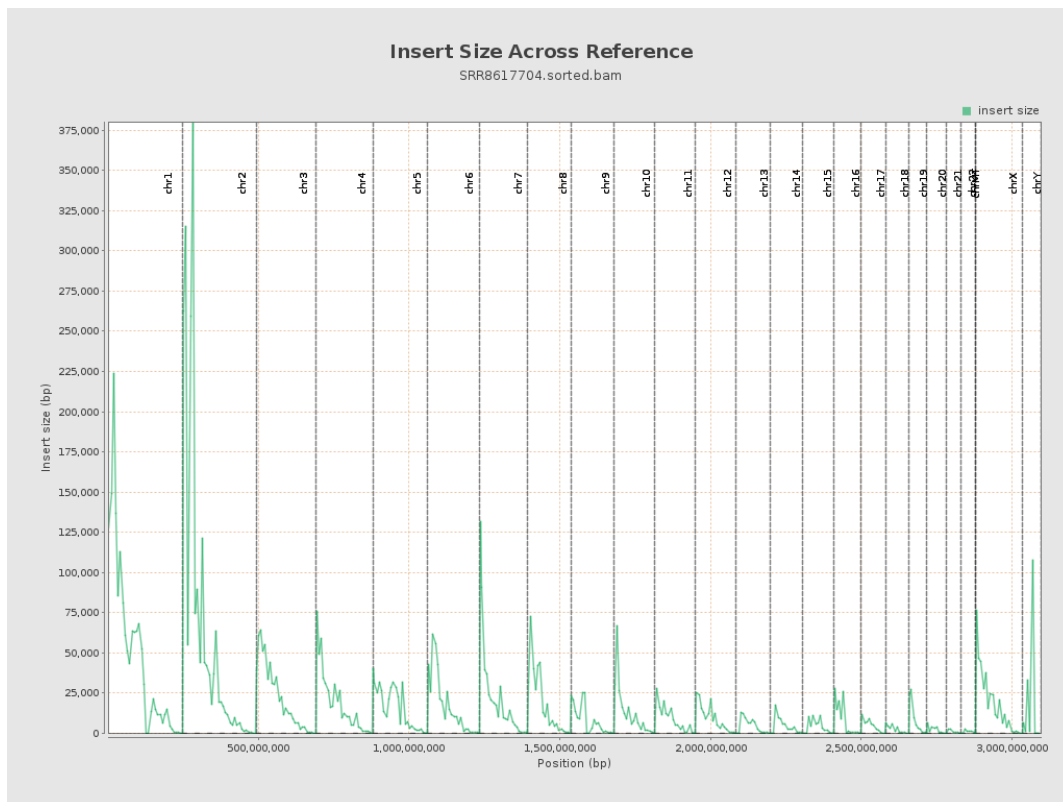
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

