

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/25 06:03:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617729.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_SRR8617729 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617729_1.fastq.gz SRR8617729_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 25 06:03:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617729.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	43,414,462
Mapped reads	42,782,181 / 98.54%
Unmapped reads	632,281 / 1.46%
Mapped paired reads	42,782,181 / 98.54%
Mapped reads, first in pair	21,542,926 / 49.62%
Mapped reads, second in pair	21,239,255 / 48.92%
Mapped reads, both in pair	42,400,204 / 97.66%
Mapped reads, singletons	381,977 / 0.88%
Secondary alignments	0
Supplementary alignments	1,034,428 / 2.38%
Read min/max/mean length	30 / 150 / 151.15
Duplicated reads (estimated)	20,281,758 / 46.72%
Duplication rate	27.05%
Clipped reads	23,667,250 / 54.51%

2.2. ACGT Content

Number/percentage of A's	1,624,980,891 / 28.54%
Number/percentage of C's	1,097,866,663 / 19.28%
Number/percentage of T's	1,685,763,015 / 29.6%
Number/percentage of G's	1,285,506,815 / 22.58%
Number/percentage of N's	223,802 / 0%

GC Percentage	41.86%
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2.3. Coverage

Mean	1.8408
Standard Deviation	34.3665

2.4. Mapping Quality

Mean Mapping Quality	53.32
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2.5. Insert size

Mean	234,707.62
Standard Deviation	5,191,189.21
P25/Median/P75	221 / 279 / 351

2.6. Mismatches and indels

General error rate	1.14%
Mismatches	62,671,840
Insertions	960,121
Mapped reads with at least one insertion	2.14%
Deletions	2,231,572
Mapped reads with at least one deletion	5.02%
Homopolymer indels	46.8%

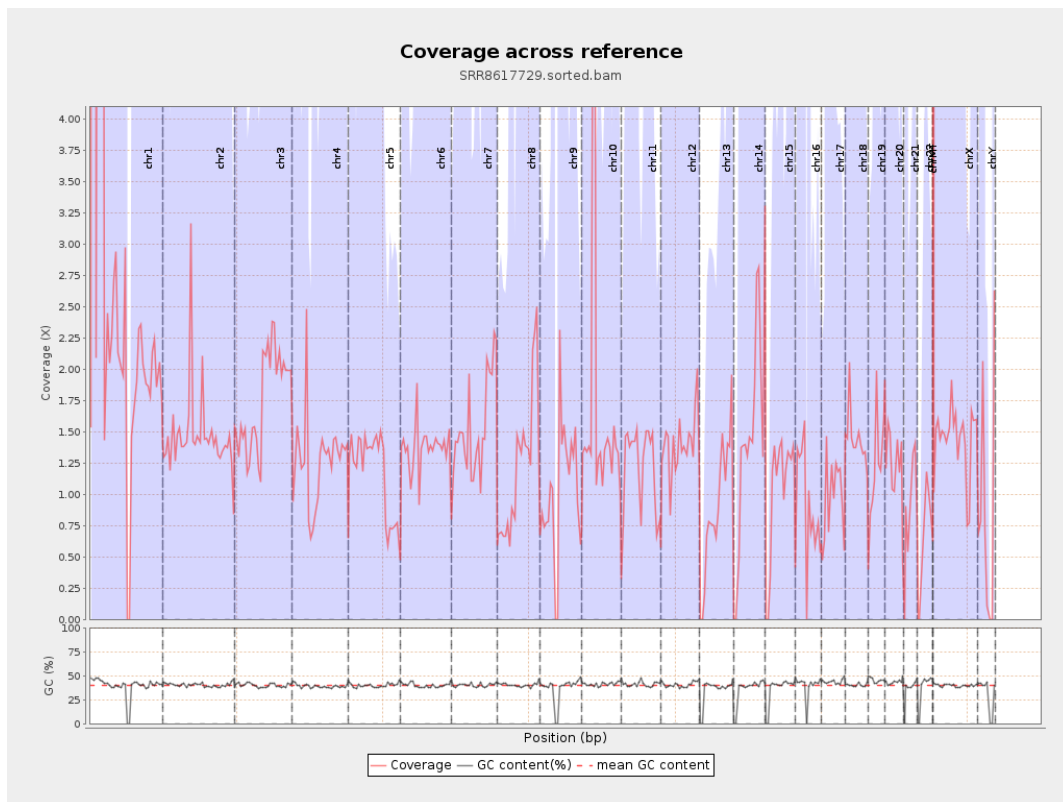
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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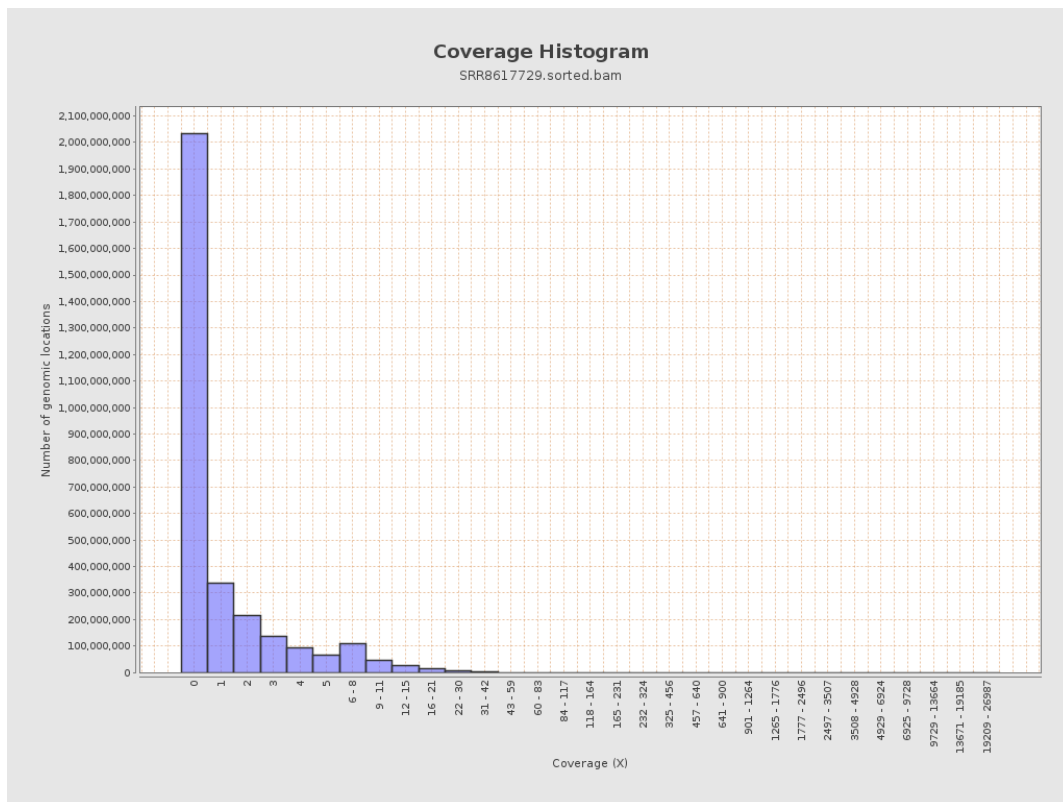
		bases	coverage	deviation
chr1	249250621	2009843487	8.0635	108.1314
chr2	243199373	358767342	1.4752	14.0295
chr3	198022430	346644281	1.7505	3.721
chr4	191154276	242648703	1.2694	10.3704
chr5	180915260	209817630	1.1598	3.0759
chr6	171115067	234678789	1.3715	6.8955
chr7	159138663	242562141	1.5242	14.6975
chr8	146364022	181965653	1.2432	3.6018
chr9	141213431	147450533	1.0442	24.215
chr10	135534747	226884231	1.674	55.5545
chr11	135006516	164239451	1.2165	8.8351
chr12	133851895	188425069	1.4077	8.5001
chr13	115169878	104191487	0.9047	2.3959
chr14	107349540	154688662	1.441	3.5037
chr15	102531392	104441036	1.0186	4.2681
chr16	90354753	79695716	0.882	6.7861
chr17	81195210	79836489	0.9833	12.2006
chr18	78077248	113357111	1.4519	20.9453
chr19	59128983	74170082	1.2544	8.9299
chr20	63025520	79300071	1.2582	4.1315
chr21	48129895	43994544	0.9141	5.7534
chr22	51304566	34033724	0.6634	2.342
chrMT	16571	1580921	95.4029	55.3337
chrX	155270560	223000428	1.4362	4.4696

chrY	59373566	52349731	0.8817	21.4271
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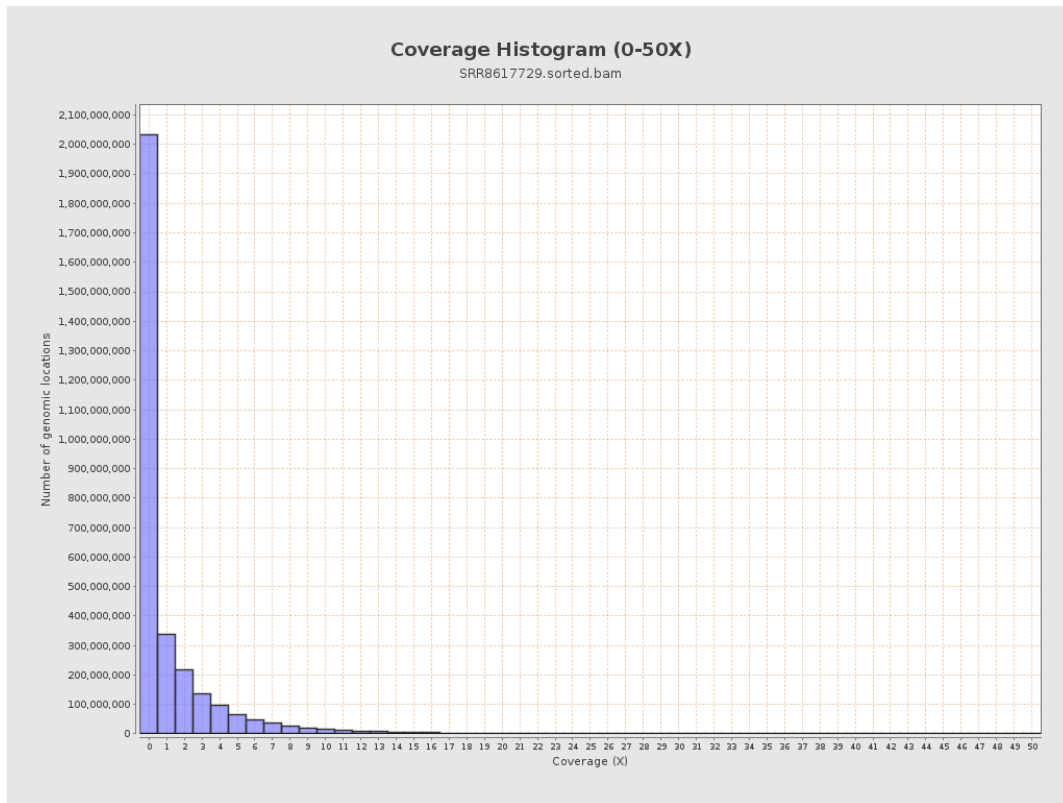
3. Results : Coverage across reference



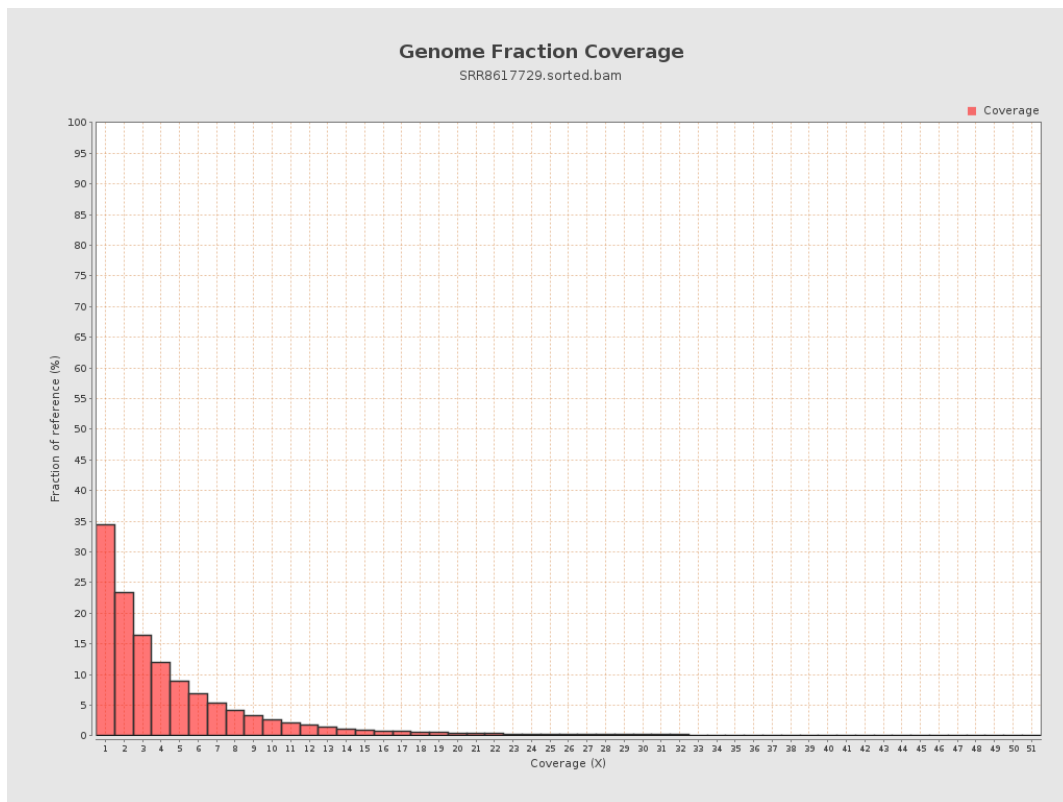
4. Results : Coverage Histogram



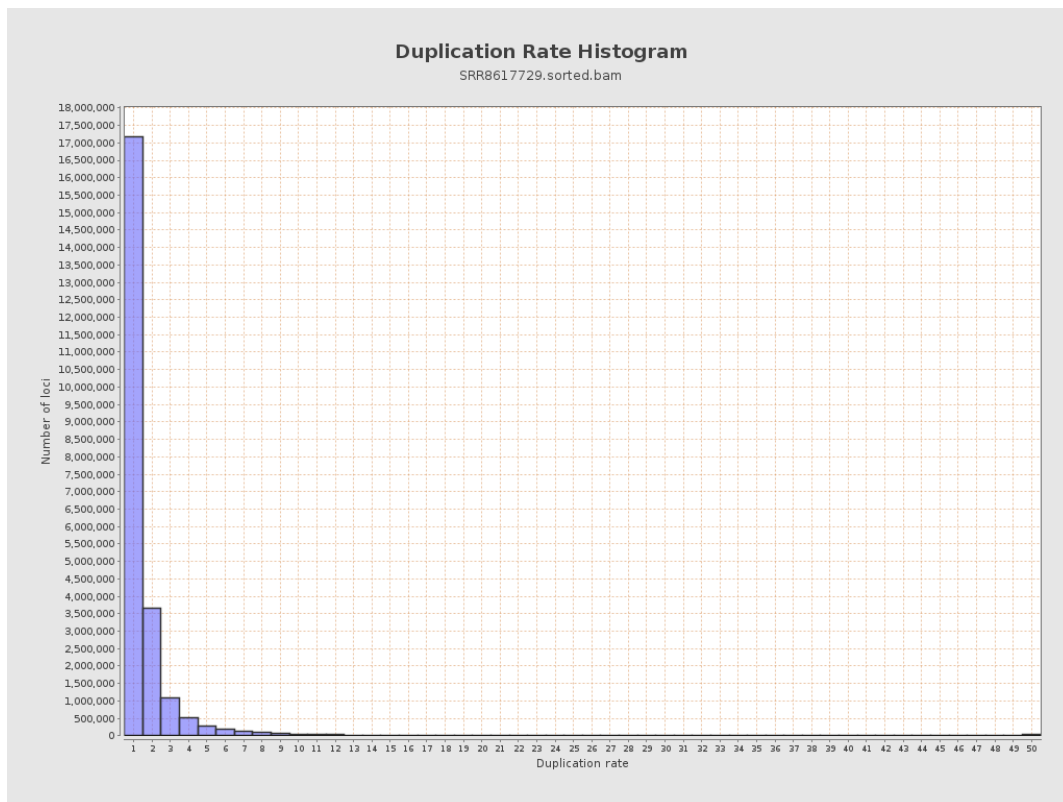
5. Results : Coverage Histogram (0-50X)



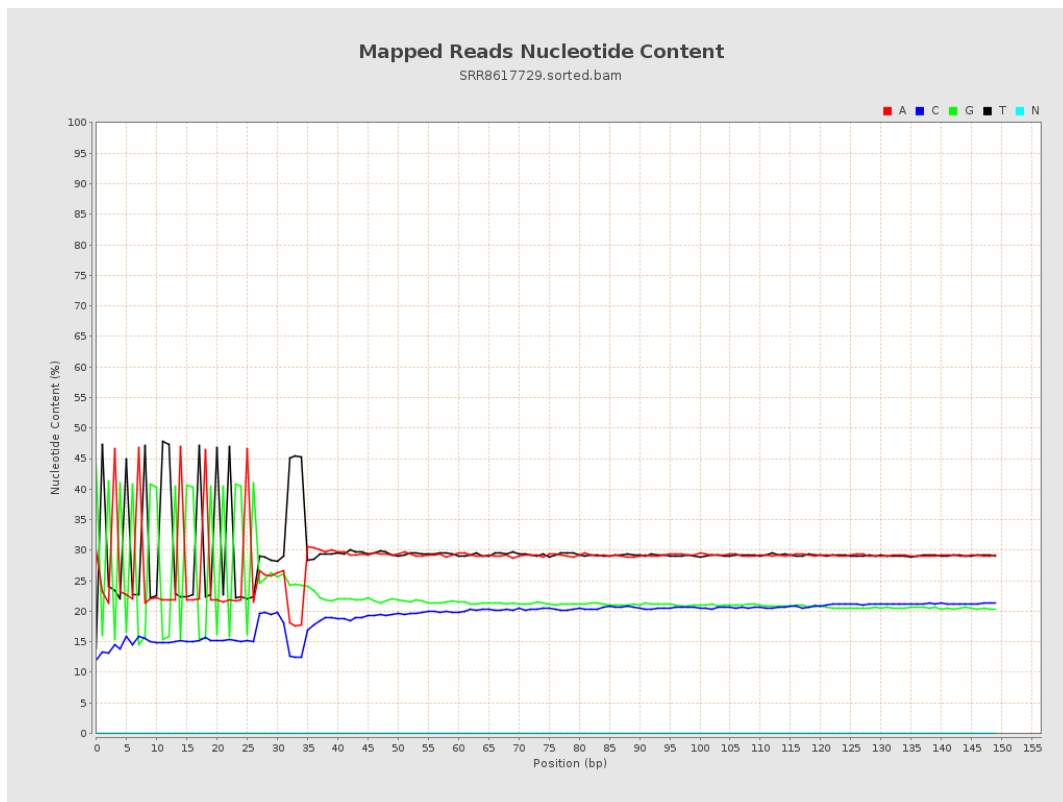
6. Results : Genome Fraction Coverage



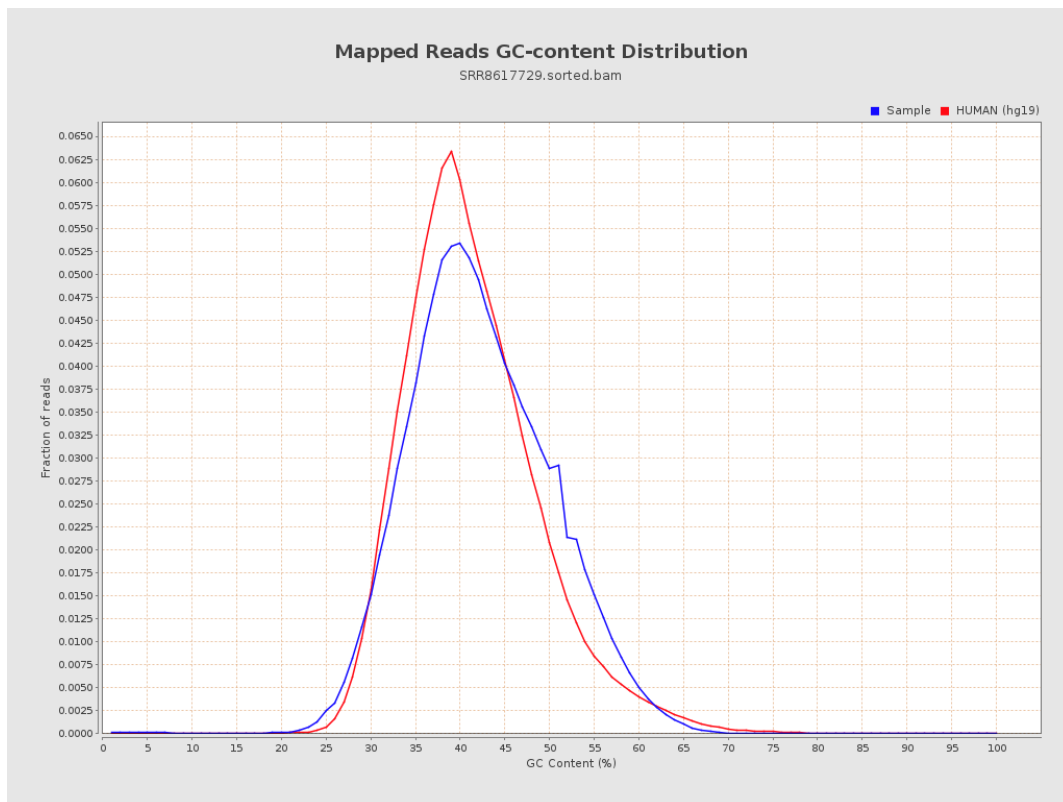
7. Results : Duplication Rate Histogram



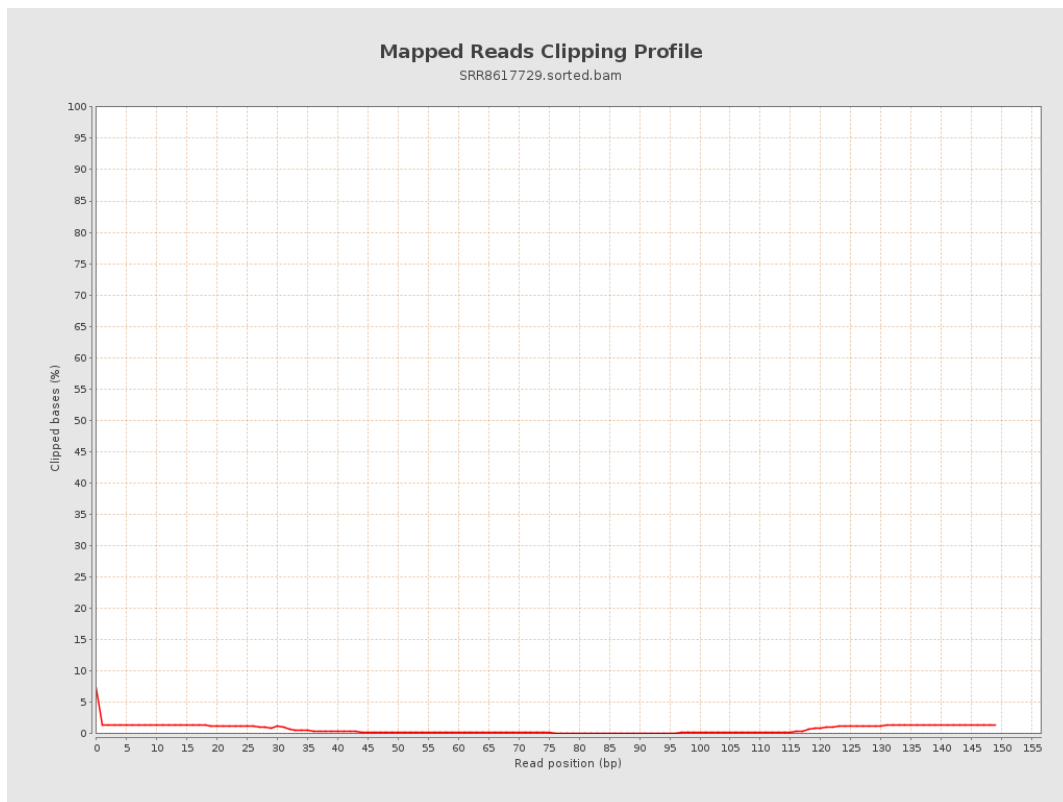
8. Results : Mapped Reads Nucleotide Content



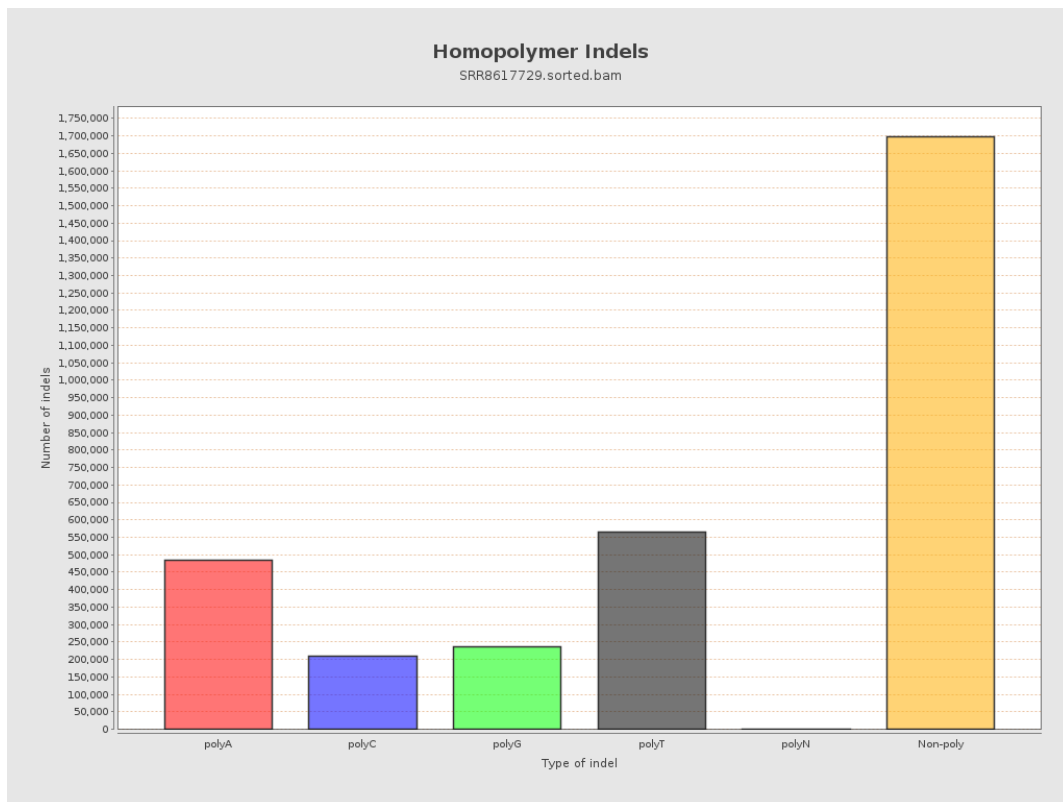
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



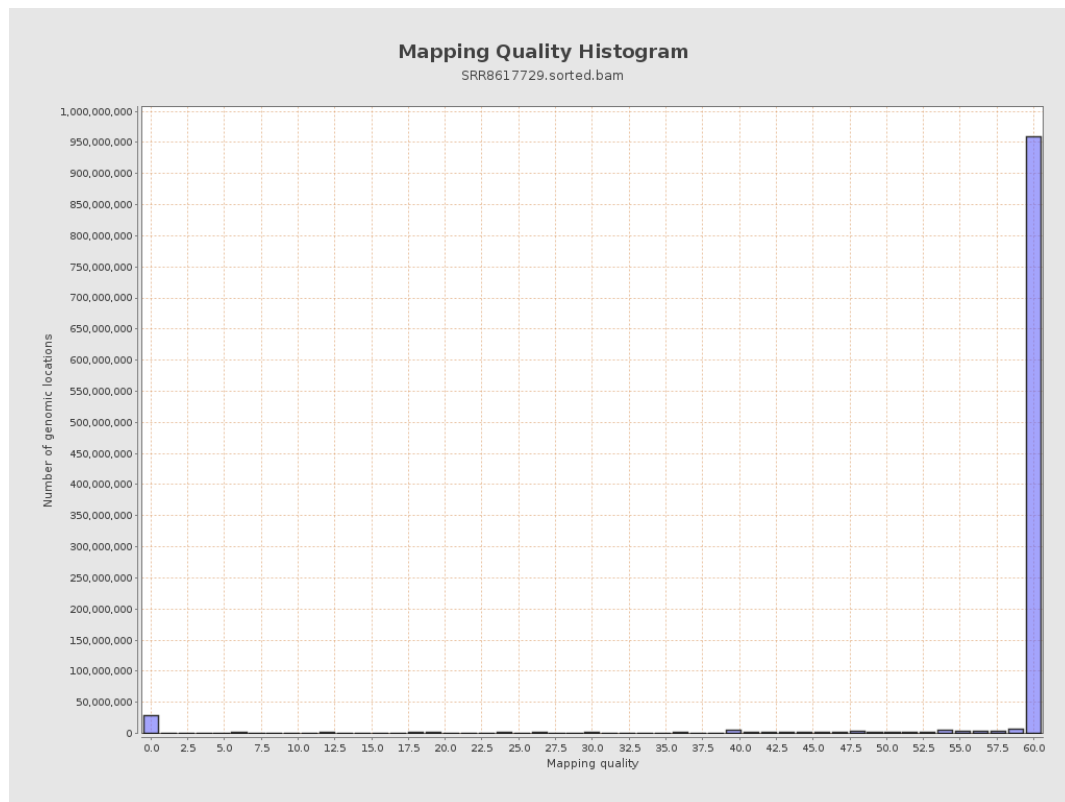
11. Results : Homopolymer Indels



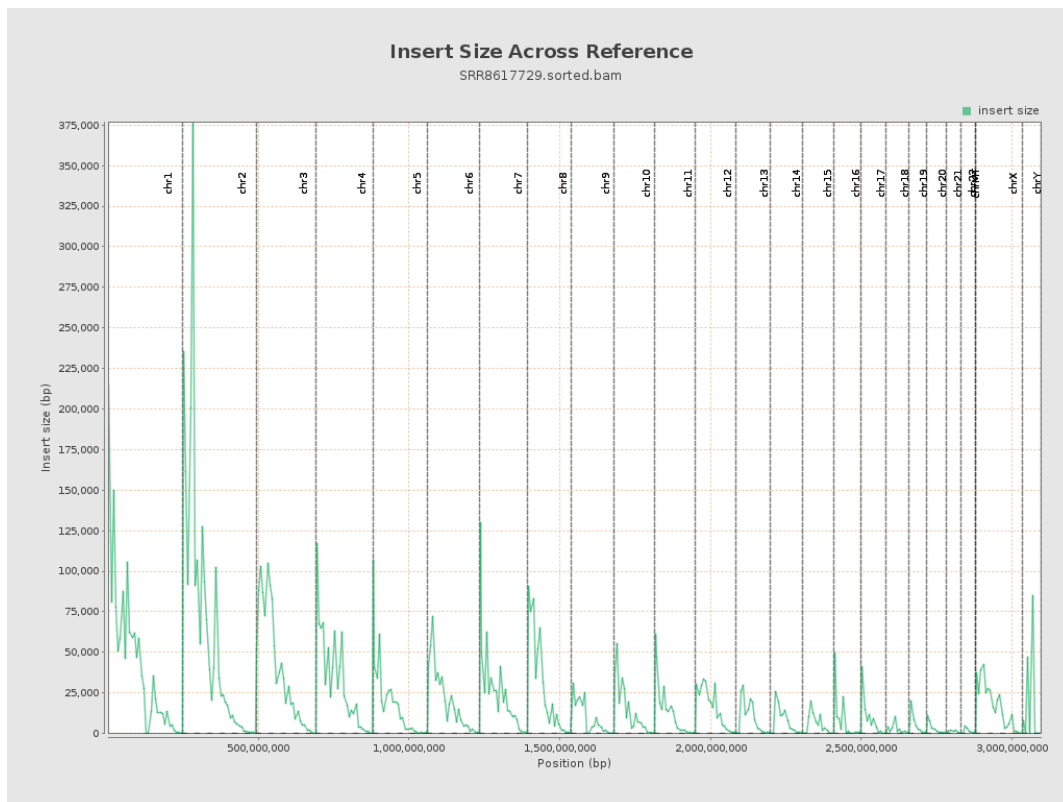
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

