

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 13:46:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618622.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_SRR618622 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618622_1.fastq.gz SRR618622_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 13:46:39 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618622.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,841,948
Mapped reads	30,295,170 / 92.25%
Unmapped reads	2,546,778 / 7.75%
Mapped paired reads	30,295,170 / 92.25%
Mapped reads, first in pair	15,419,899 / 46.95%
Mapped reads, second in pair	14,875,271 / 45.29%
Mapped reads, both in pair	29,356,292 / 89.39%
Mapped reads, singletons	938,878 / 2.86%
Secondary alignments	0
Supplementary alignments	67,329 / 0.21%
Read min/max/mean length	30 / 100 / 100.08
Duplicated reads (estimated)	11,869,412 / 36.14%
Duplication rate	31.51%
Clipped reads	5,534,029 / 16.85%

2.2. ACGT Content

Number/percentage of A's	769,268,198 / 26.64%
Number/percentage of C's	658,699,727 / 22.81%
Number/percentage of T's	772,833,100 / 26.76%
Number/percentage of G's	686,904,243 / 23.79%
Number/percentage of N's	108,973 / 0%

GC Percentage	46.6%
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2.3. Coverage

Mean	0.9334
Standard Deviation	4.6301

2.4. Mapping Quality

Mean Mapping Quality	53.91
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2.5. Insert size

Mean	65,419.81
Standard Deviation	2,596,426.92
P25/Median/P75	201 / 230 / 266

2.6. Mismatches and indels

General error rate	1.24%
Mismatches	35,149,497
Insertions	516,328
Mapped reads with at least one insertion	1.67%
Deletions	1,323,951
Mapped reads with at least one deletion	4.27%
Homopolymer indels	52.74%

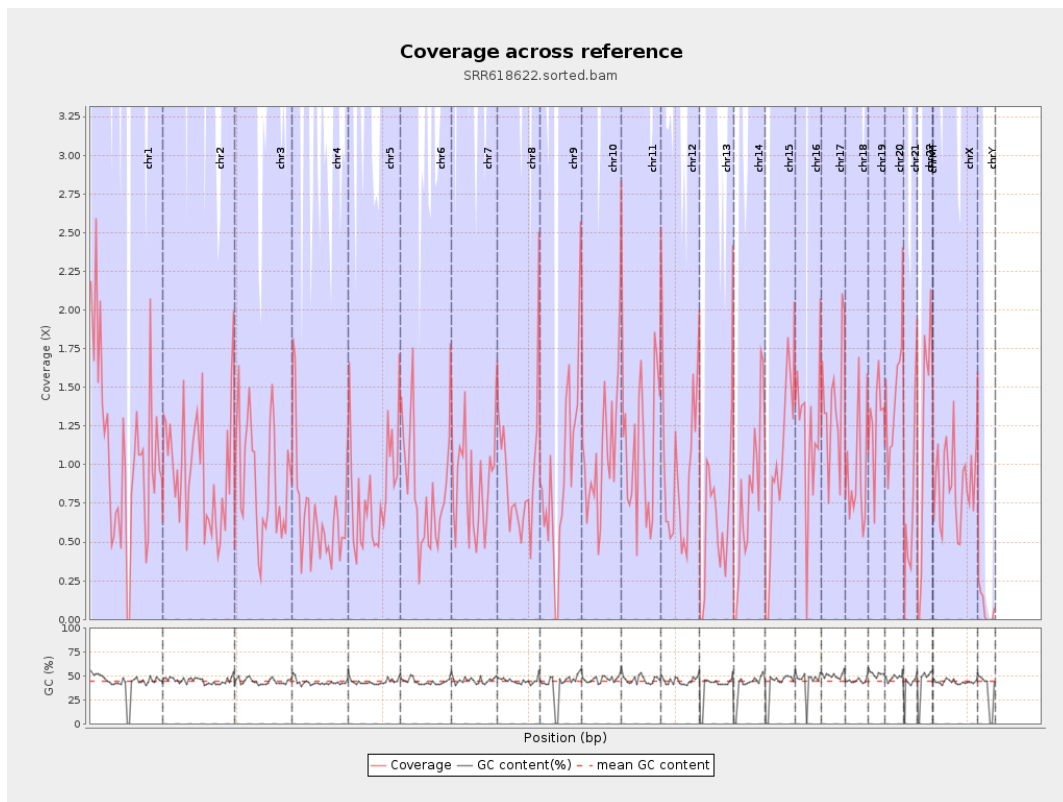
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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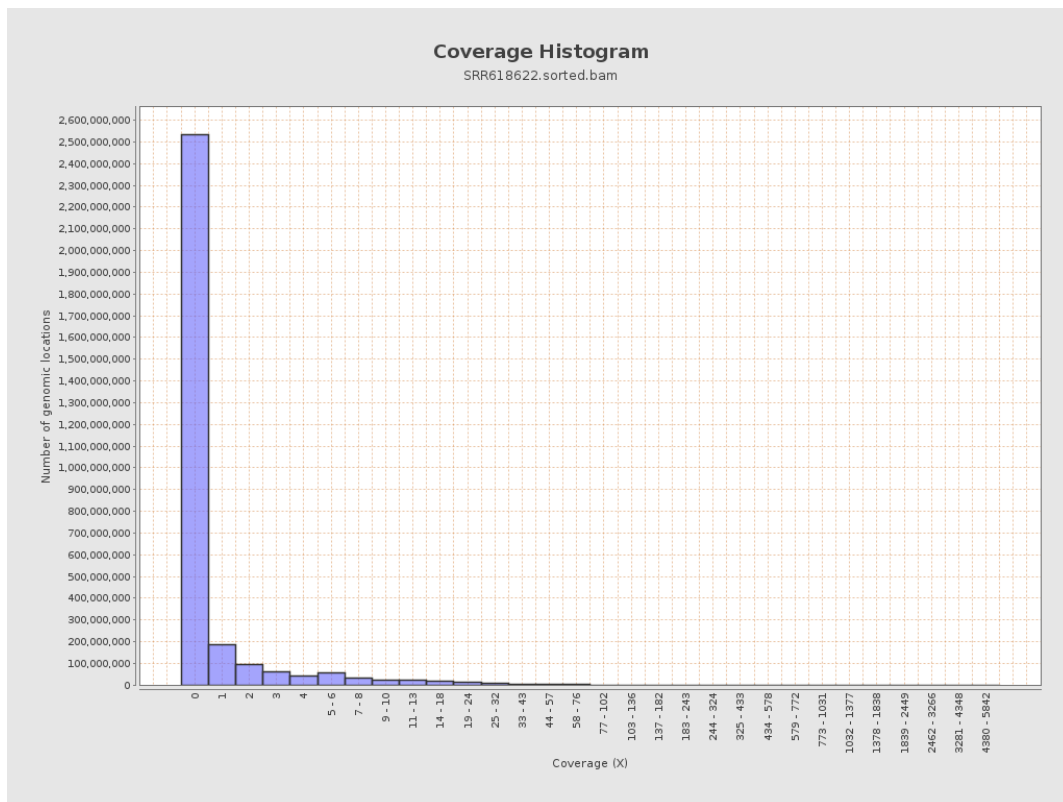
		bases	coverage	deviation
chr1	249250621	266797724	1.0704	5.2639
chr2	243199373	232857781	0.9575	5.4826
chr3	198022430	176597802	0.8918	3.7227
chr4	191154276	129684448	0.6784	3.7825
chr5	180915260	150408178	0.8314	3.6364
chr6	171115067	142059170	0.8302	3.5716
chr7	159138663	140347311	0.8819	4.2034
chr8	146364022	133899926	0.9148	4.0504
chr9	141213431	133407497	0.9447	4.713
chr10	135534747	142755661	1.0533	4.4238
chr11	135006516	152102818	1.1266	4.9406
chr12	133851895	129822369	0.9699	4.2182
chr13	115169878	74089649	0.6433	3.099
chr14	107349540	85269608	0.7943	3.6684
chr15	102531392	101012101	0.9852	4.298
chr16	90354753	108856069	1.2048	9.4594
chr17	81195210	112915031	1.3907	5.296
chr18	78077248	70836103	0.9073	3.9767
chr19	59128983	75916184	1.2839	5.4873
chr20	63025520	89806948	1.4249	5.2168
chr21	48129895	37519631	0.7795	6.1984
chr22	51304566	61027065	1.1895	5.1638
chrMT	16571	17451	1.0531	5.4295
chrX	155270560	137193879	0.8836	3.5801

chrY	59373566	4453058	0.075	2.9999
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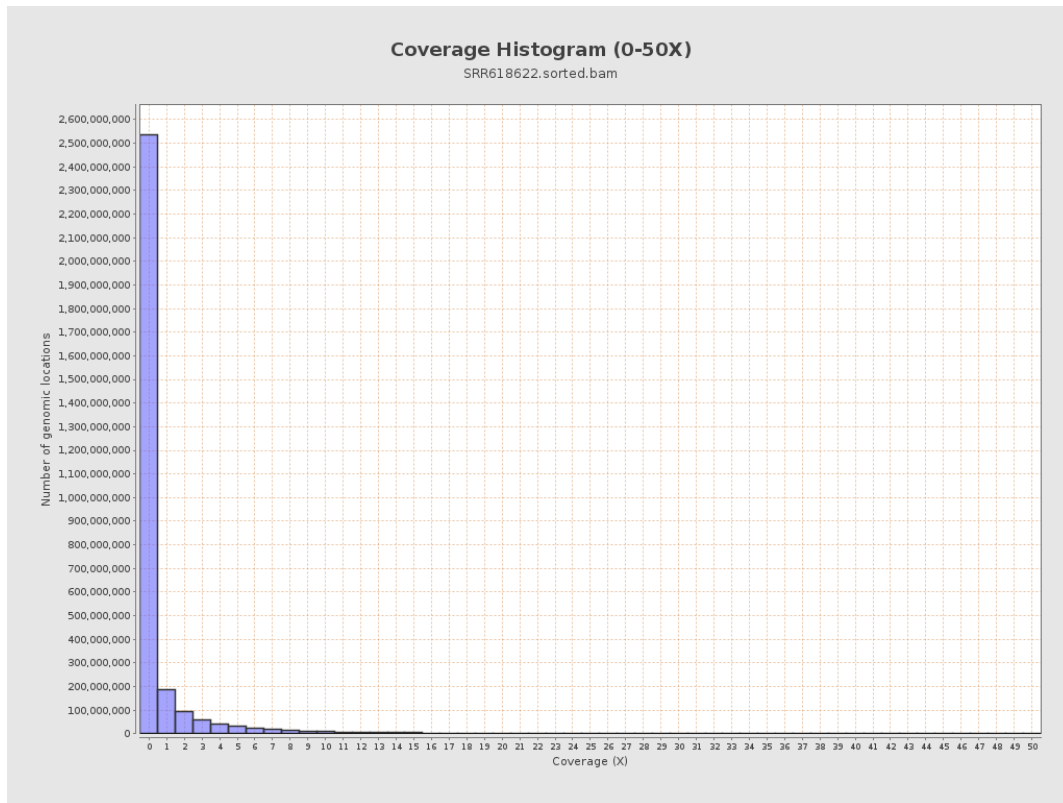
3. Results : Coverage across reference



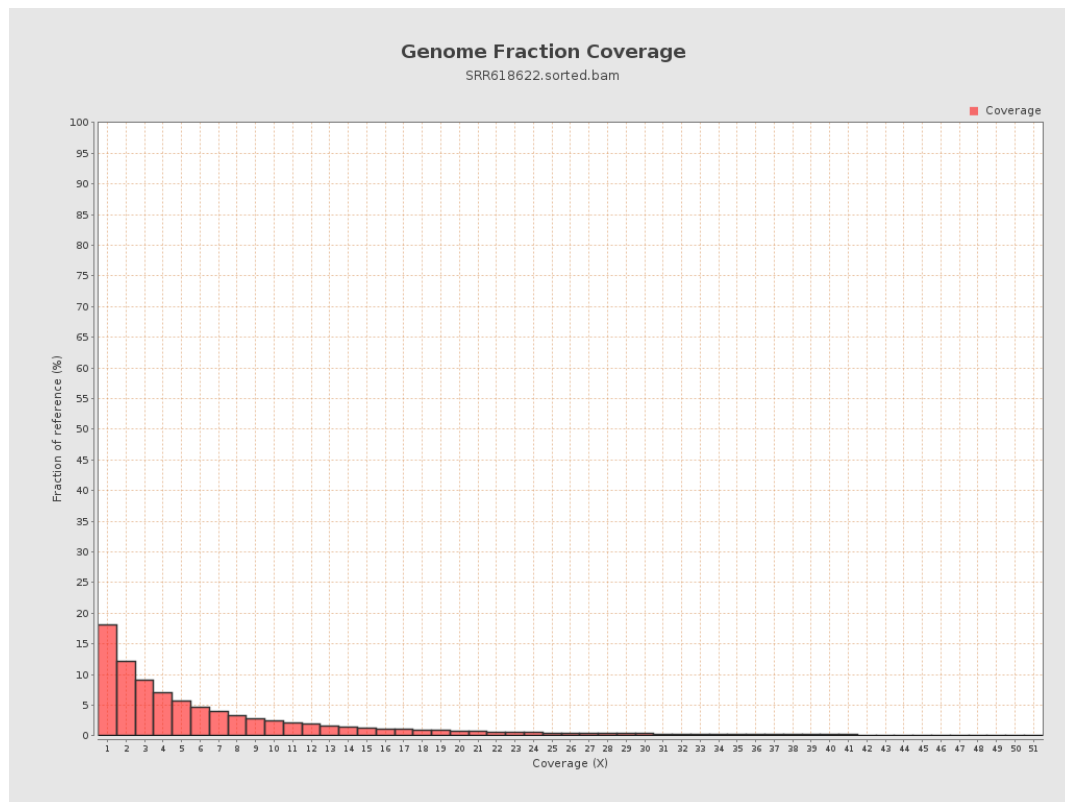
4. Results : Coverage Histogram



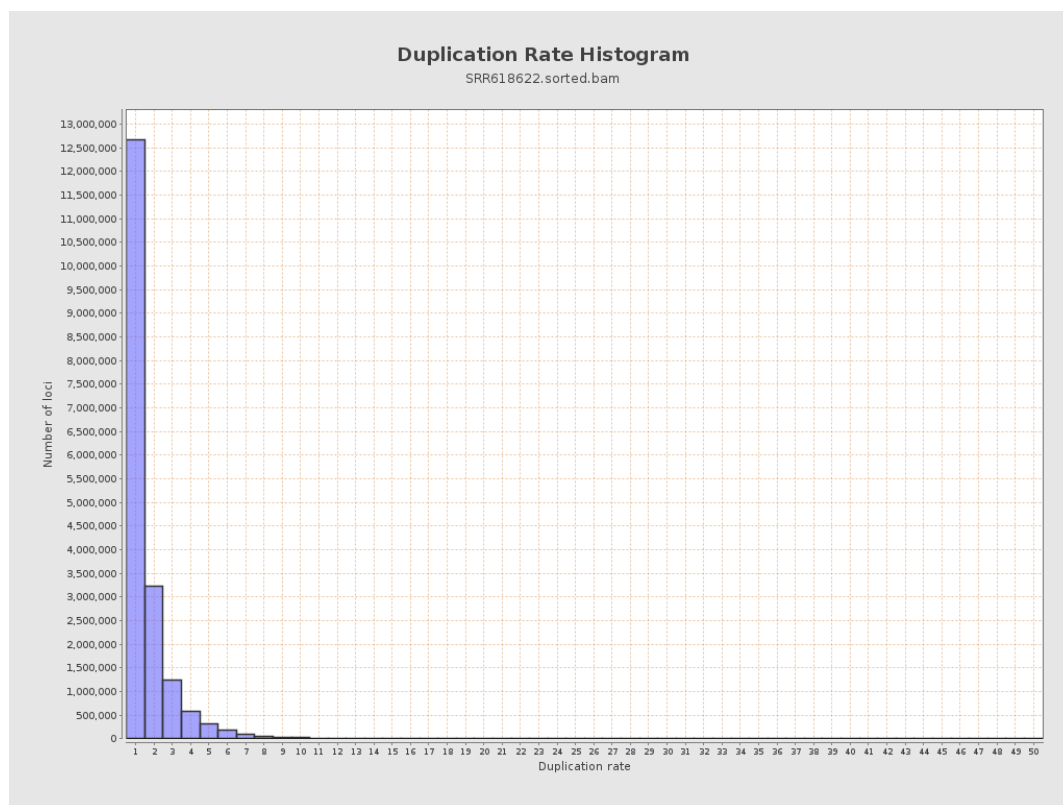
5. Results : Coverage Histogram (0-50X)



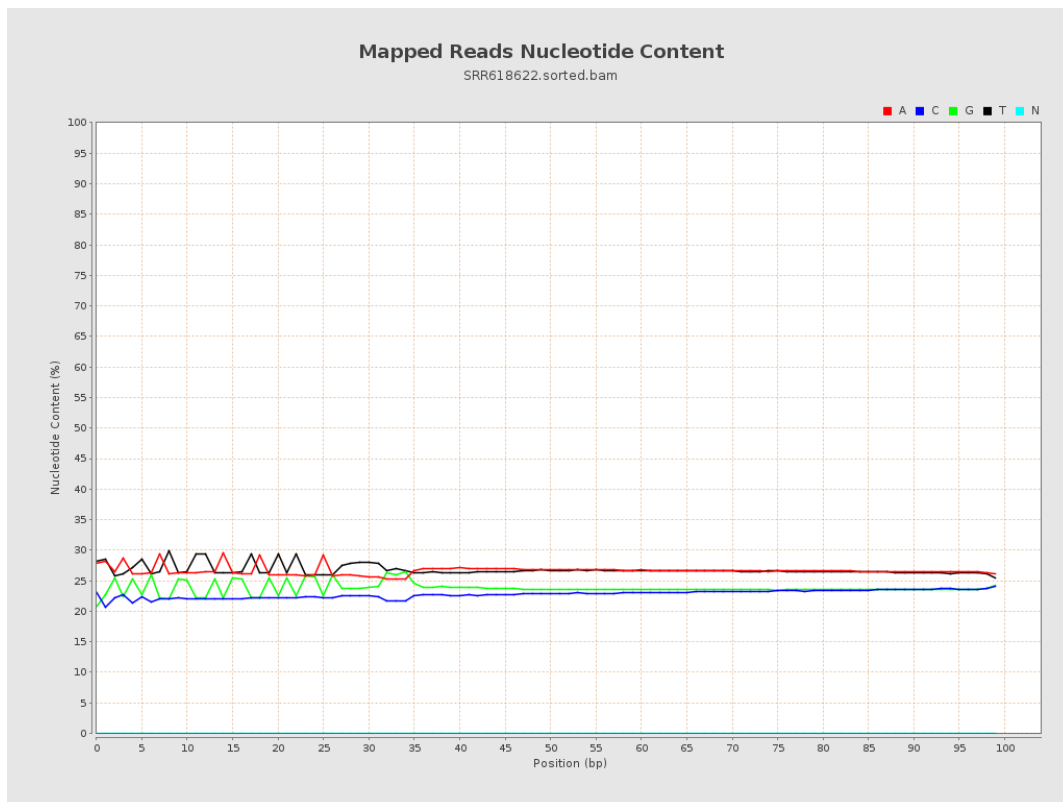
6. Results : Genome Fraction Coverage



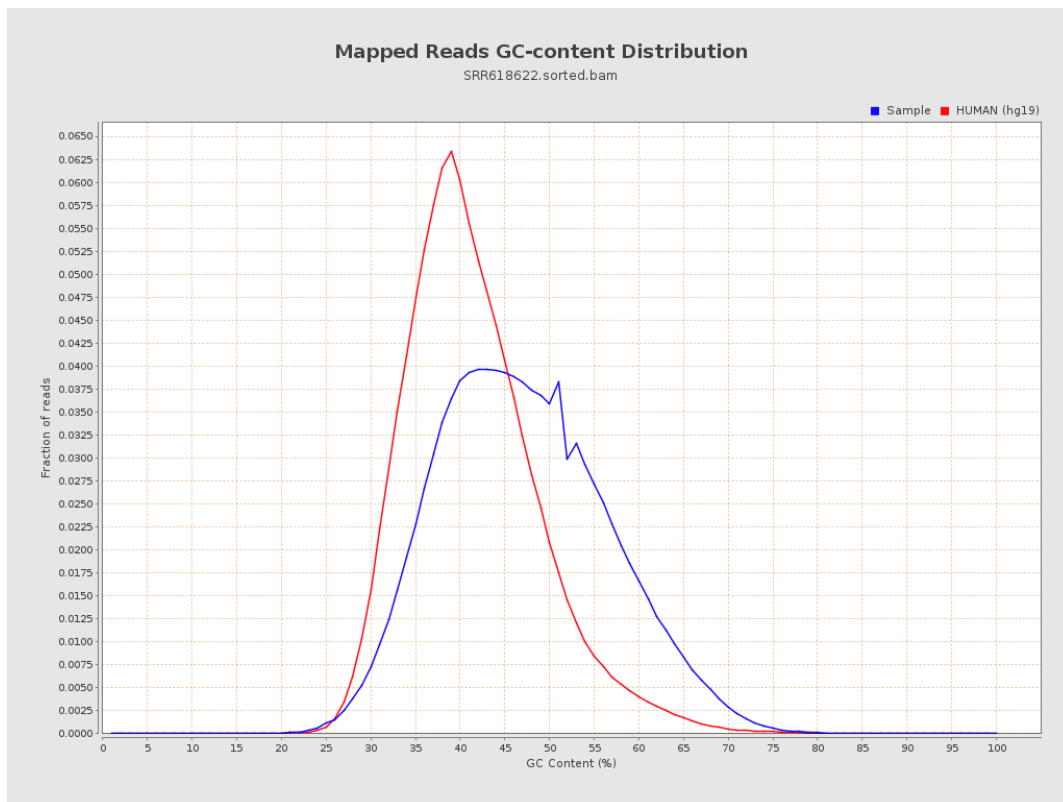
7. Results : Duplication Rate Histogram



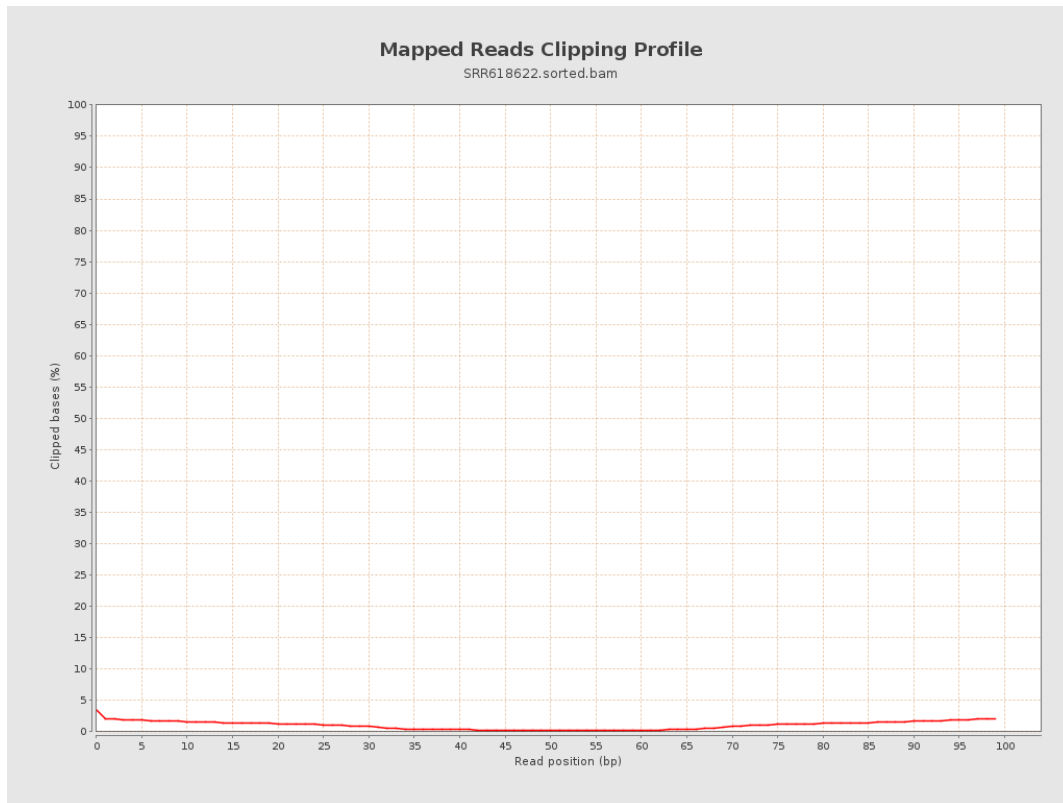
8. Results : Mapped Reads Nucleotide Content



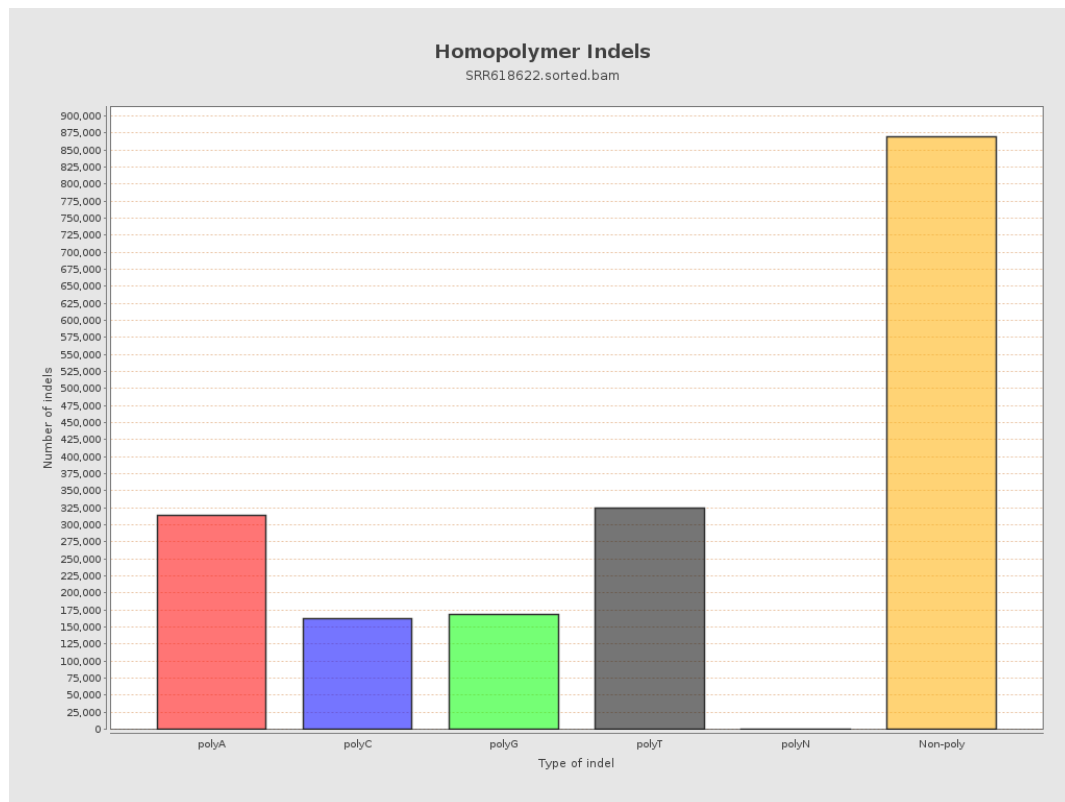
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



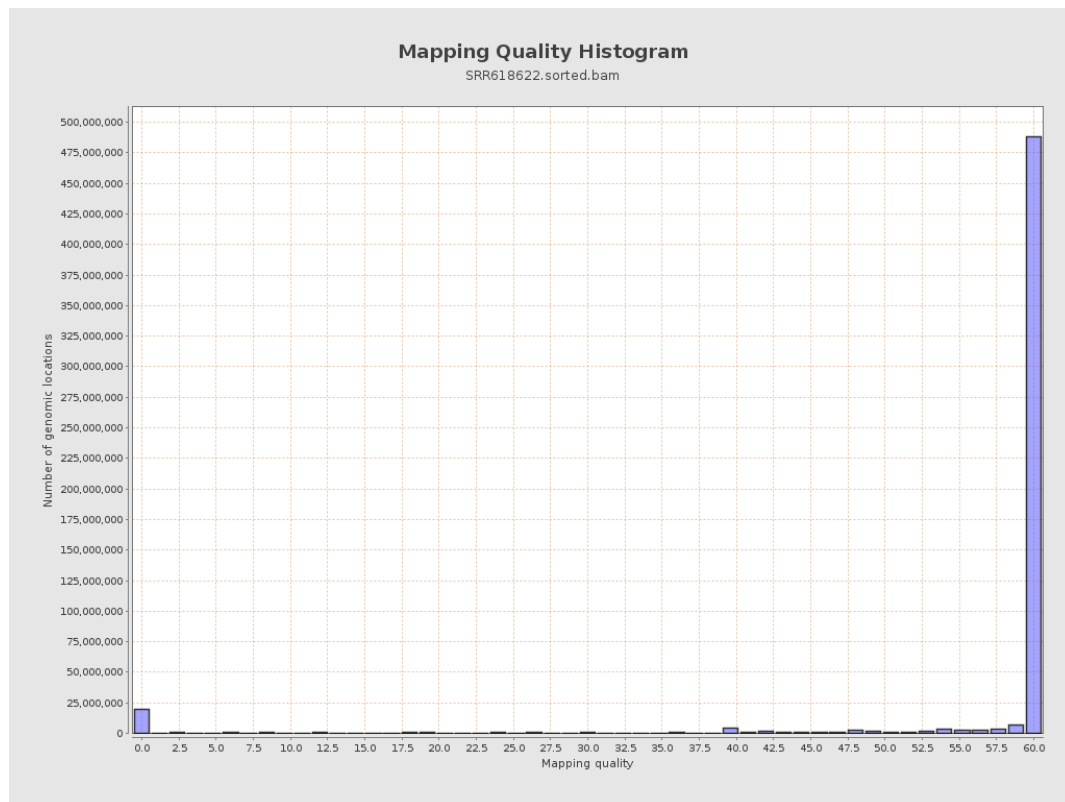
11. Results : Homopolymer Indels



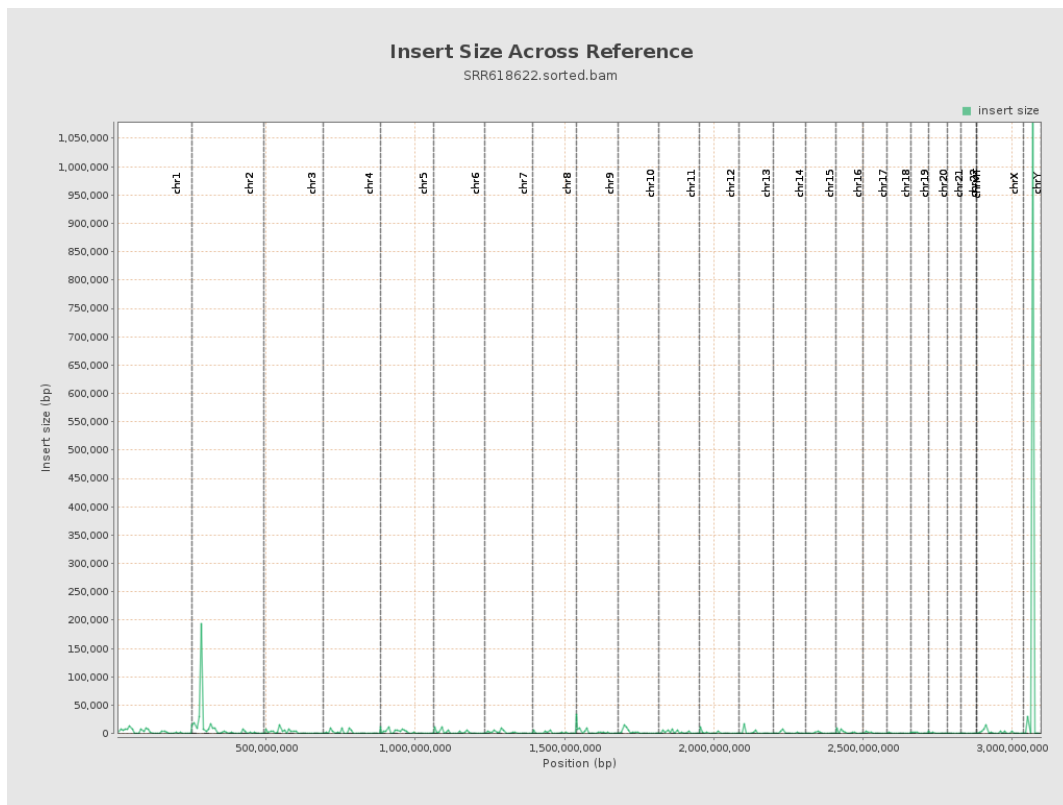
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

