

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 02:44:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618578.sorted.bam -c -nw 400 -hm 3
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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_SRR618578 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618578_1.fastq.gz SRR618578_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 02:44:55 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618578.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	63,651,058
Mapped reads	58,957,362 / 92.63%
Unmapped reads	4,693,696 / 7.37%
Mapped paired reads	58,957,362 / 92.63%
Mapped reads, first in pair	29,740,319 / 46.72%
Mapped reads, second in pair	29,217,043 / 45.9%
Mapped reads, both in pair	57,856,318 / 90.9%
Mapped reads, singletons	1,101,044 / 1.73%
Secondary alignments	0
Supplementary alignments	143,433 / 0.23%
Read min/max/mean length	30 / 100 / 100.09
Duplicated reads (estimated)	11,518,019 / 18.1%
Duplication rate	16.83%
Clipped reads	12,351,125 / 19.4%

2.2. ACGT Content

Number/percentage of A's	1,504,102,112 / 27.02%
Number/percentage of C's	1,232,802,768 / 22.14%
Number/percentage of T's	1,522,116,908 / 27.34%
Number/percentage of G's	1,307,975,439 / 23.49%
Number/percentage of N's	164,088 / 0%

GC Percentage	45.64%
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2.3. Coverage

Mean	1.7996
Standard Deviation	7.5036

2.4. Mapping Quality

Mean Mapping Quality	52.53
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2.5. Insert size

Mean	45,322.66
Standard Deviation	2,113,936.09
P25/Median/P75	170 / 199 / 236

2.6. Mismatches and indels

General error rate	1.29%
Mismatches	70,186,774
Insertions	1,000,543
Mapped reads with at least one insertion	1.67%
Deletions	2,804,520
Mapped reads with at least one deletion	4.64%
Homopolymer indels	52.69%

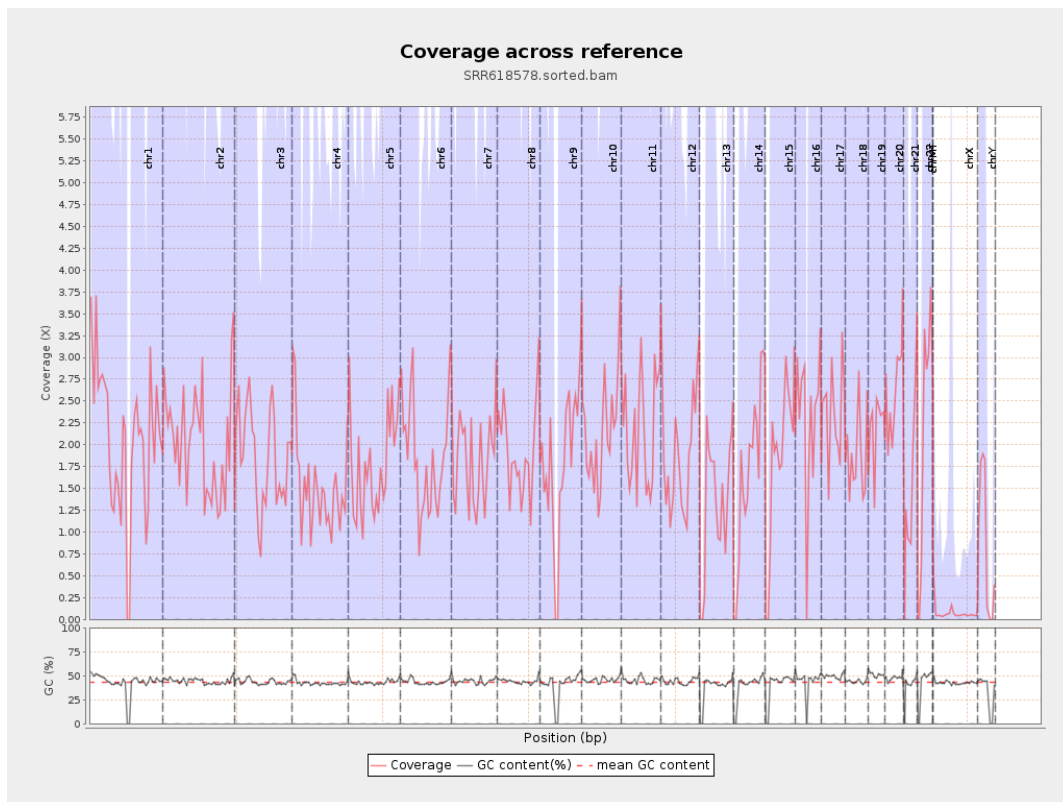
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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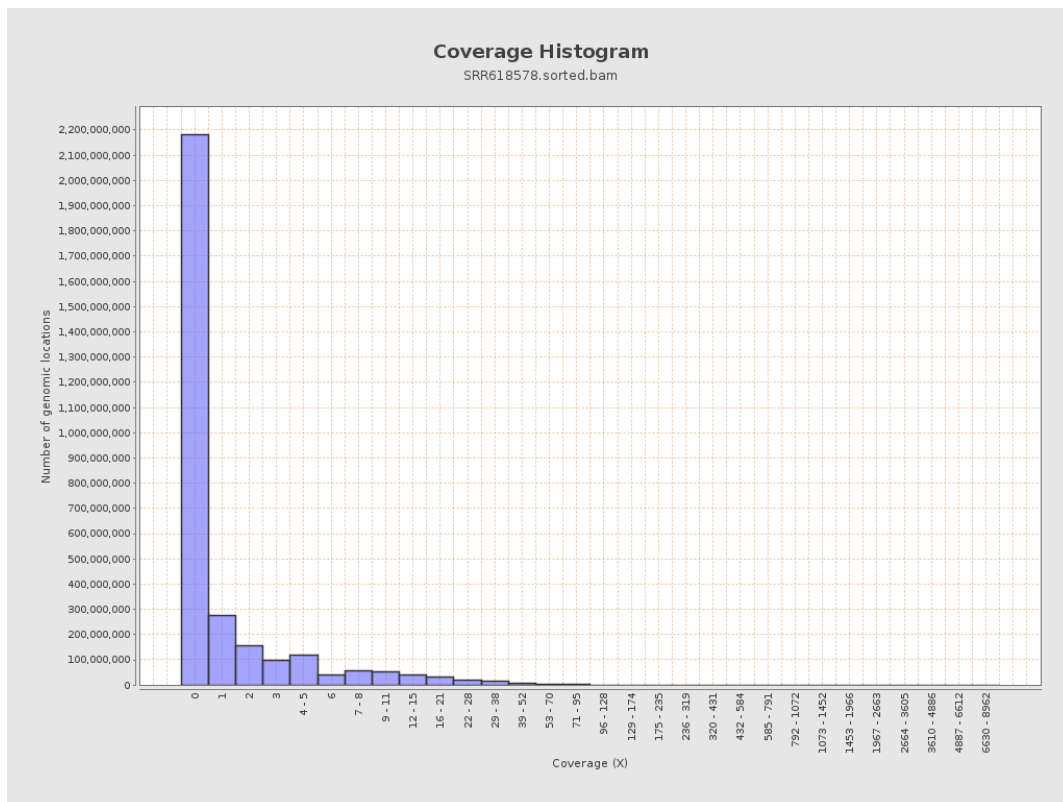
		bases	coverage	deviation
chr1	249250621	509865657	2.0456	9.2308
chr2	243199373	490412648	2.0165	9.1936
chr3	198022430	366835037	1.8525	5.7004
chr4	191154276	288510429	1.5093	5.6199
chr5	180915260	324023142	1.791	5.5919
chr6	171115067	316125215	1.8474	6.2359
chr7	159138663	292971302	1.841	5.95
chr8	146364022	283275461	1.9354	6.1272
chr9	141213431	251969410	1.7843	7.5233
chr10	135534747	289567667	2.1365	6.715
chr11	135006516	292803634	2.1688	8.7946
chr12	133851895	254058089	1.8981	6.1468
chr13	115169878	152964372	1.3282	4.8909
chr14	107349540	181082901	1.6869	5.8949
chr15	102531392	187603712	1.8297	6.2317
chr16	90354753	206394234	2.2843	17.4252
chr17	81195210	192639744	2.3726	8.0089
chr18	78077248	144696225	1.8532	7.0618
chr19	59128983	129592422	2.1917	8.2552
chr20	63025520	163764859	2.5984	7.809
chr21	48129895	76999269	1.5998	9.1343
chr22	51304566	111186383	2.1672	8.1092
chrMT	16571	13806	0.8331	2.51
chrX	155270560	11068435	0.0713	1.8334

chrY	59373566	52575164	0.8855	7.6506
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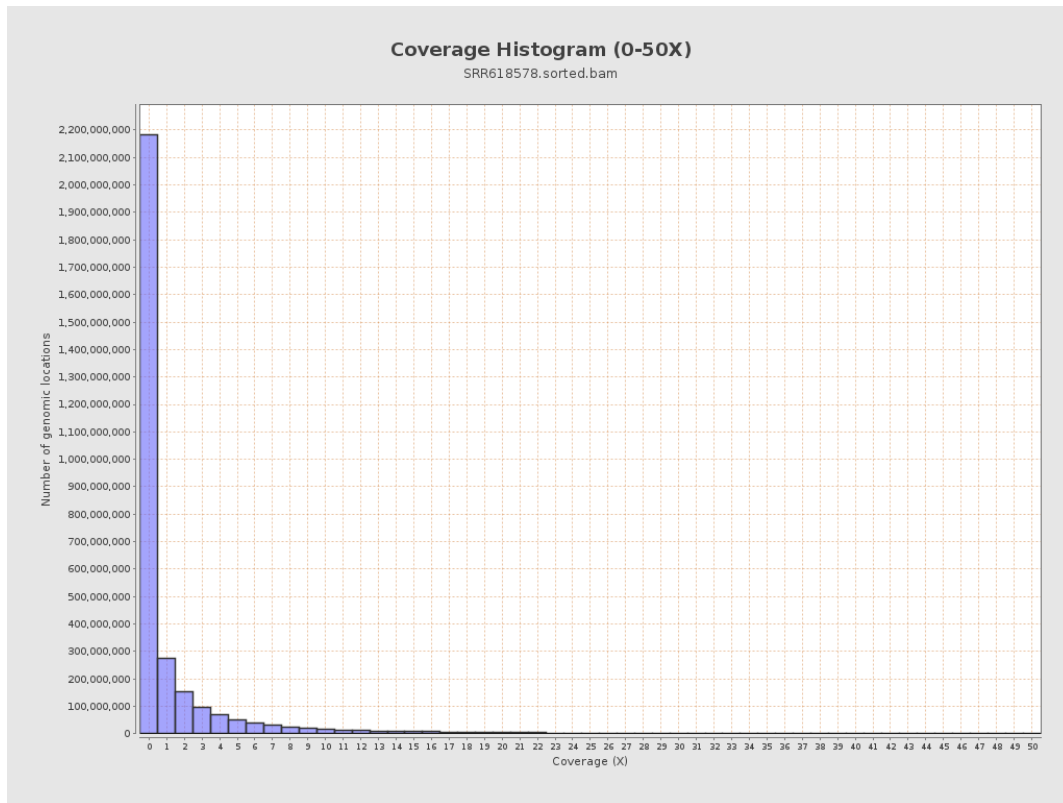
3. Results : Coverage across reference



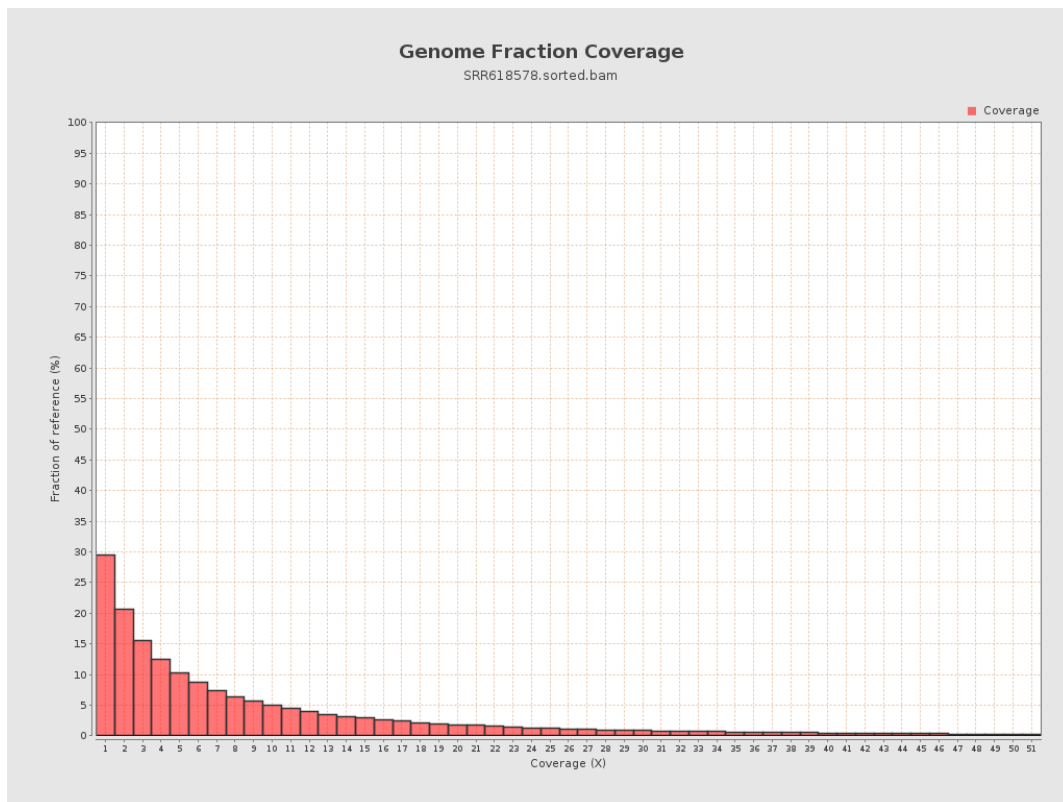
4. Results : Coverage Histogram



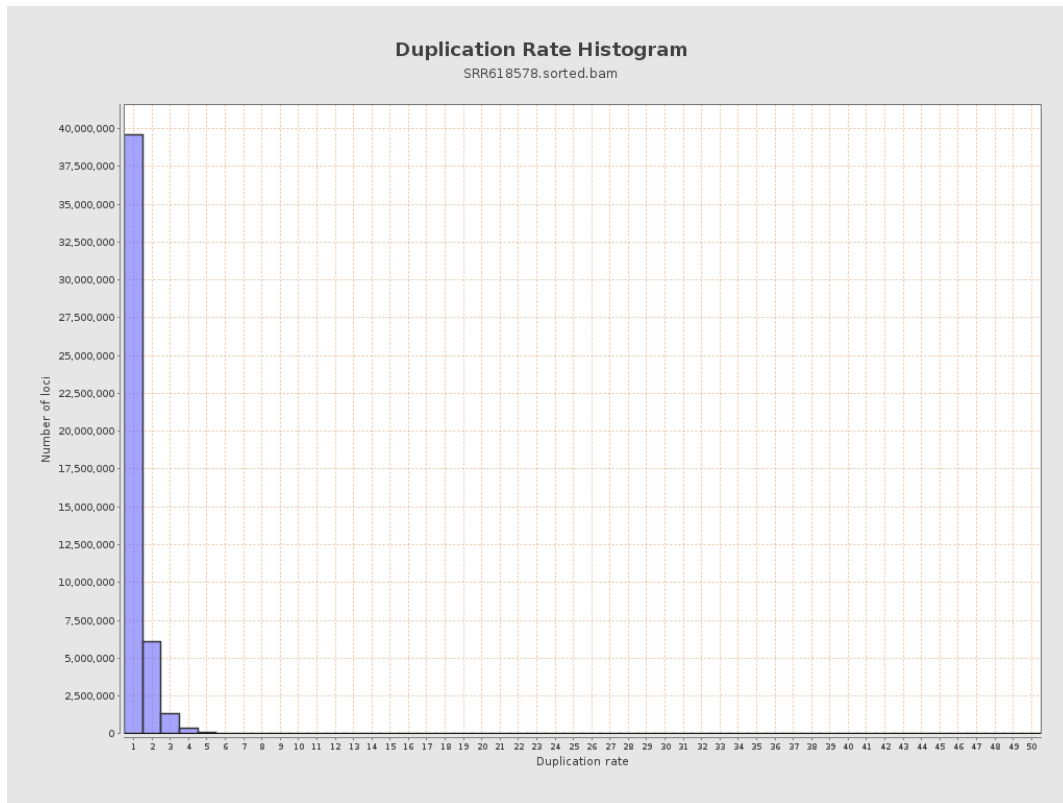
5. Results : Coverage Histogram (0-50X)



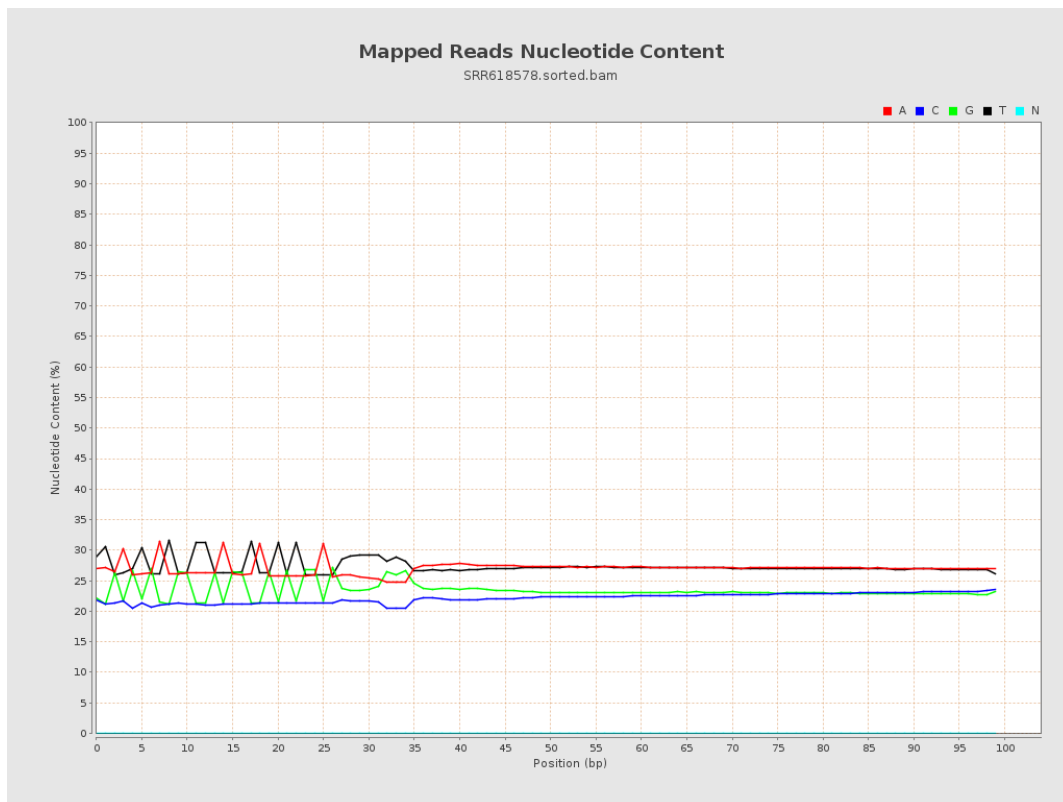
6. Results : Genome Fraction Coverage



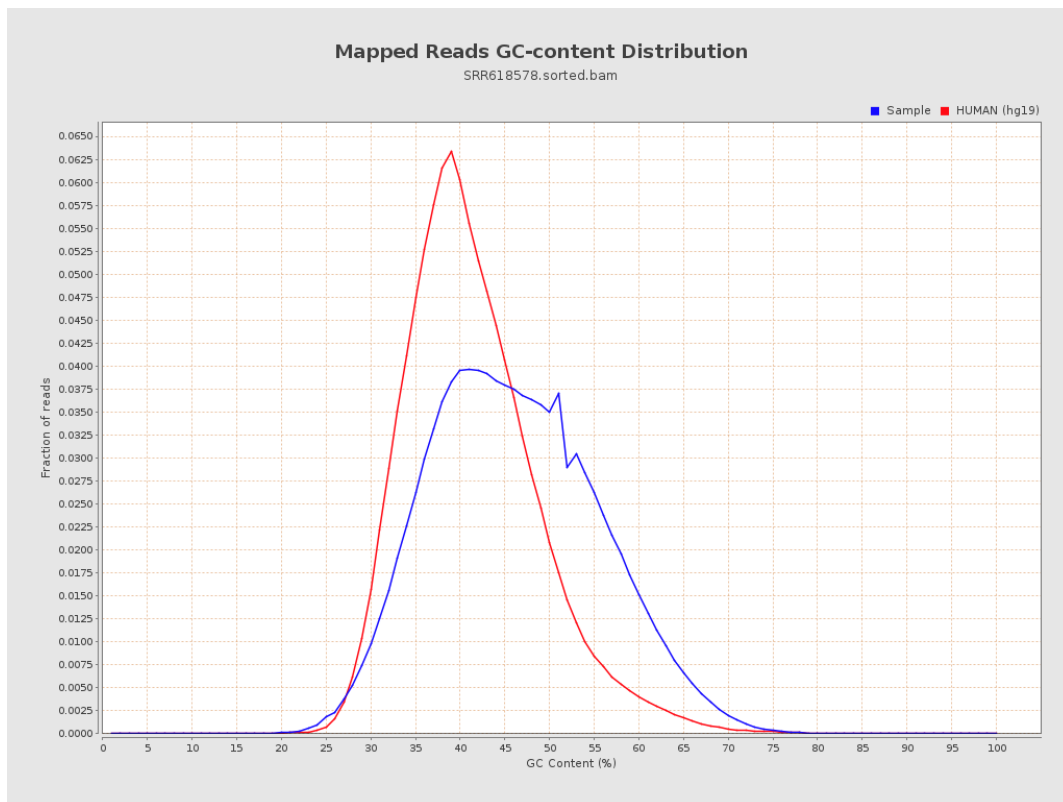
7. Results : Duplication Rate Histogram



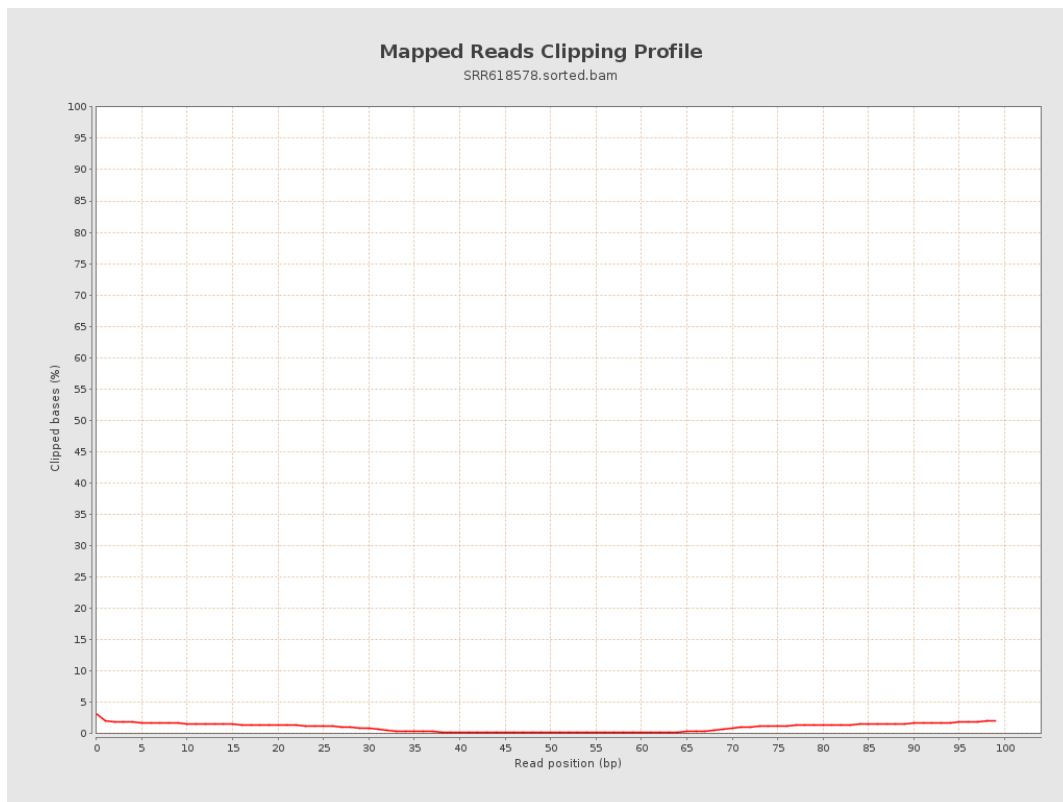
8. Results : Mapped Reads Nucleotide Content



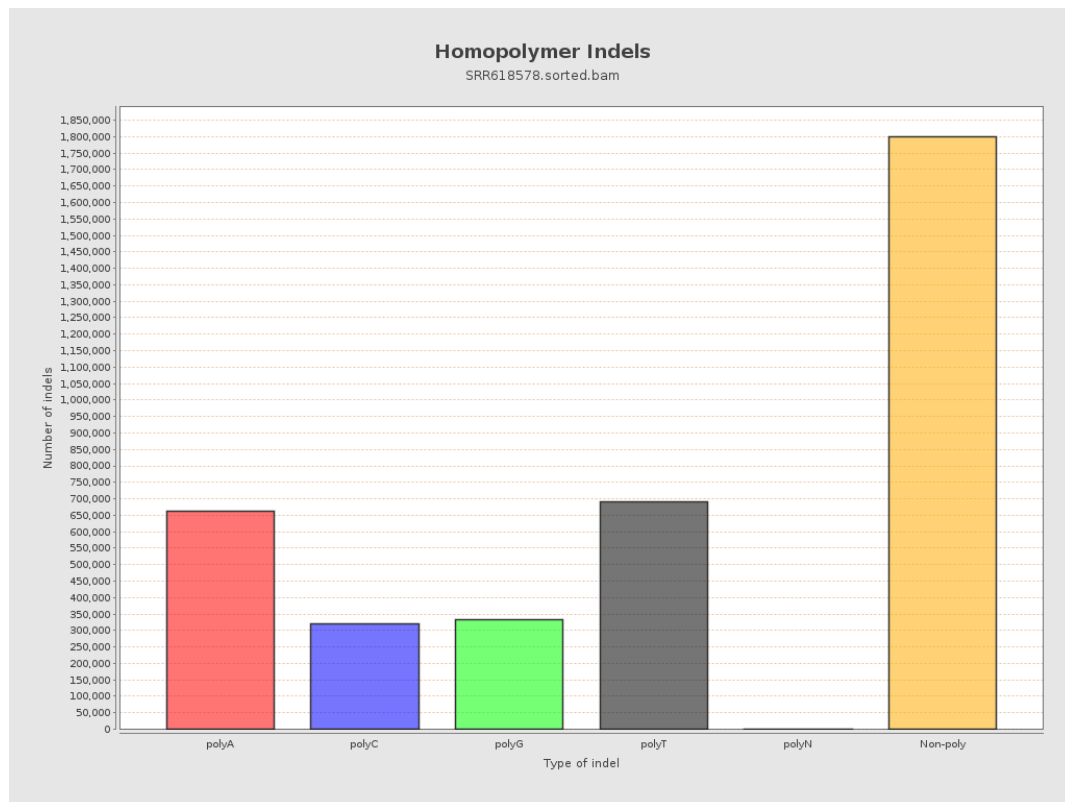
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



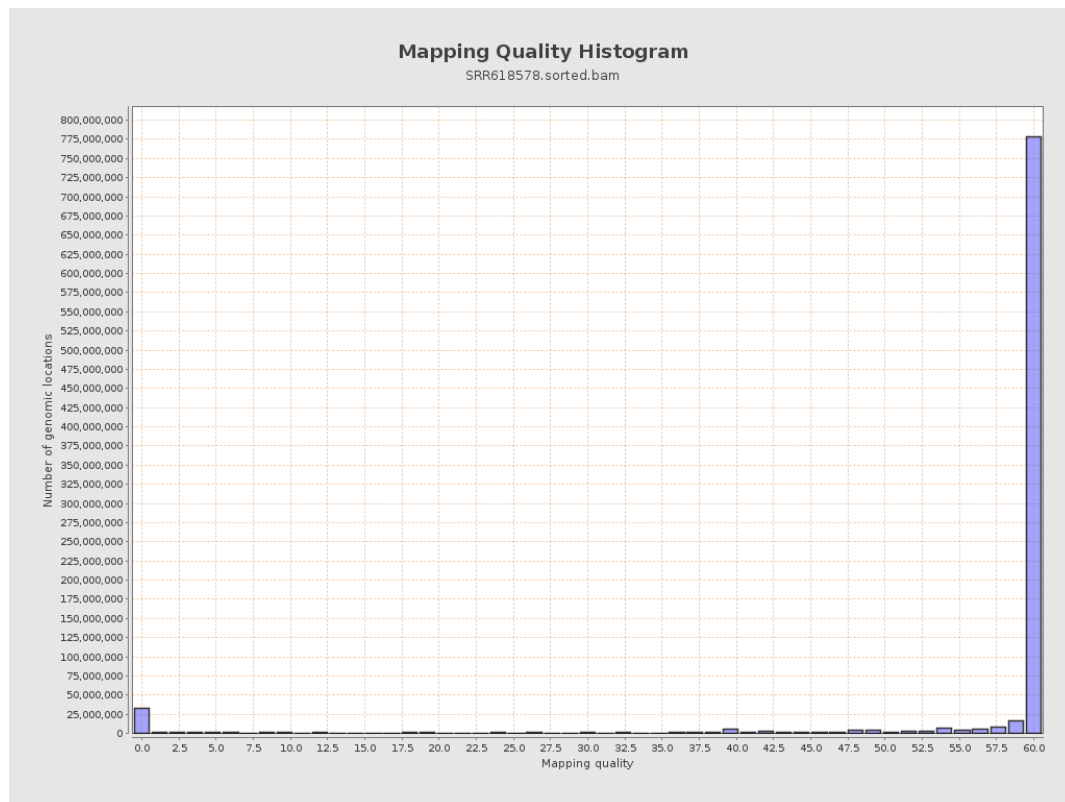
11. Results : Homopolymer Indels



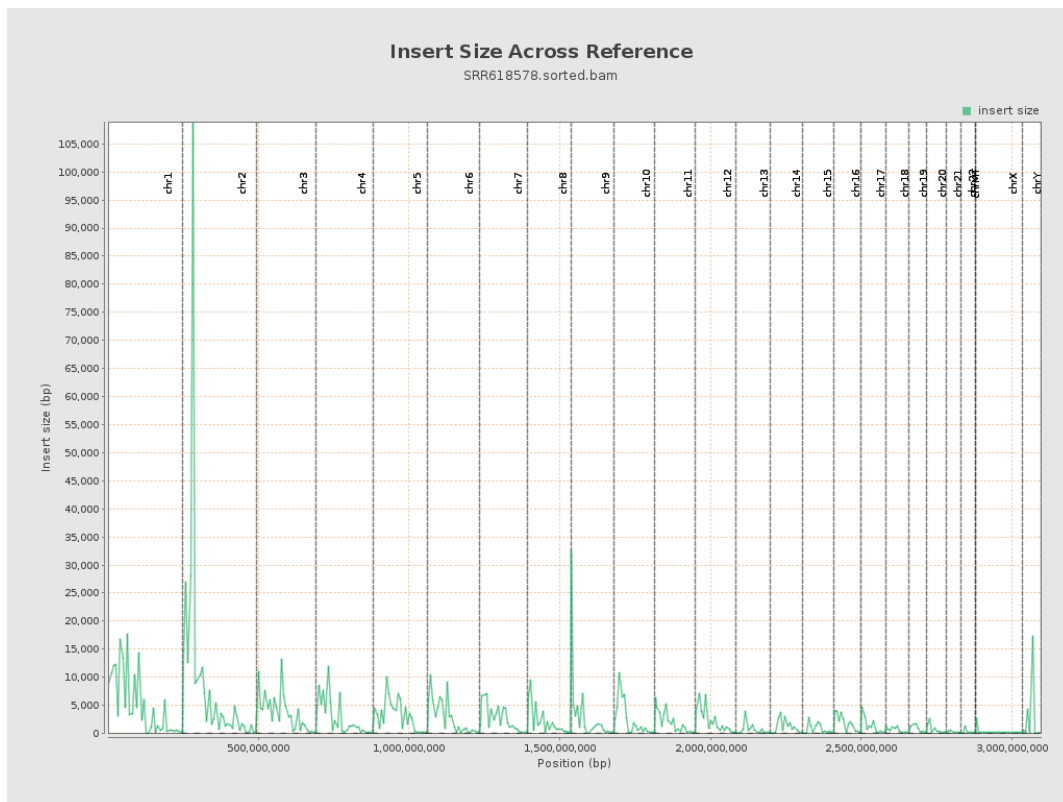
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

