

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/20 03:32:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618642.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_SRR618642 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618642_1.fastq.gz SRR618642_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 20 03:32:07 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618642.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	52,759,976
Mapped reads	47,213,665 / 89.49%
Unmapped reads	5,546,311 / 10.51%
Mapped paired reads	47,213,665 / 89.49%
Mapped reads, first in pair	25,273,709 / 47.9%
Mapped reads, second in pair	21,939,956 / 41.58%
Mapped reads, both in pair	43,264,284 / 82%
Mapped reads, singletons	3,949,381 / 7.49%
Secondary alignments	0
Supplementary alignments	288,336 / 0.55%
Read min/max/mean length	30 / 100 / 100.22
Duplicated reads (estimated)	9,848,828 / 18.67%
Duplication rate	17.64%
Clipped reads	12,192,450 / 23.11%

2.2. ACGT Content

Number/percentage of A's	1,212,186,362 / 27.51%
Number/percentage of C's	949,431,739 / 21.54%
Number/percentage of T's	1,245,288,192 / 28.26%
Number/percentage of G's	999,849,894 / 22.69%
Number/percentage of N's	234,741 / 0.01%

GC Percentage	44.23%
---------------	--------

2.3. Coverage

Mean	1.4246
Standard Deviation	6.1835

2.4. Mapping Quality

Mean Mapping Quality	53.05
----------------------	-------

2.5. Insert size

Mean	171,142.35
Standard Deviation	4,098,238.45
P25/Median/P75	196 / 223 / 253

2.6. Mismatches and indels

General error rate	1.43%
Mismatches	61,855,013
Insertions	841,428
Mapped reads with at least one insertion	1.75%
Deletions	2,260,829
Mapped reads with at least one deletion	4.67%
Homopolymer indels	52.32%

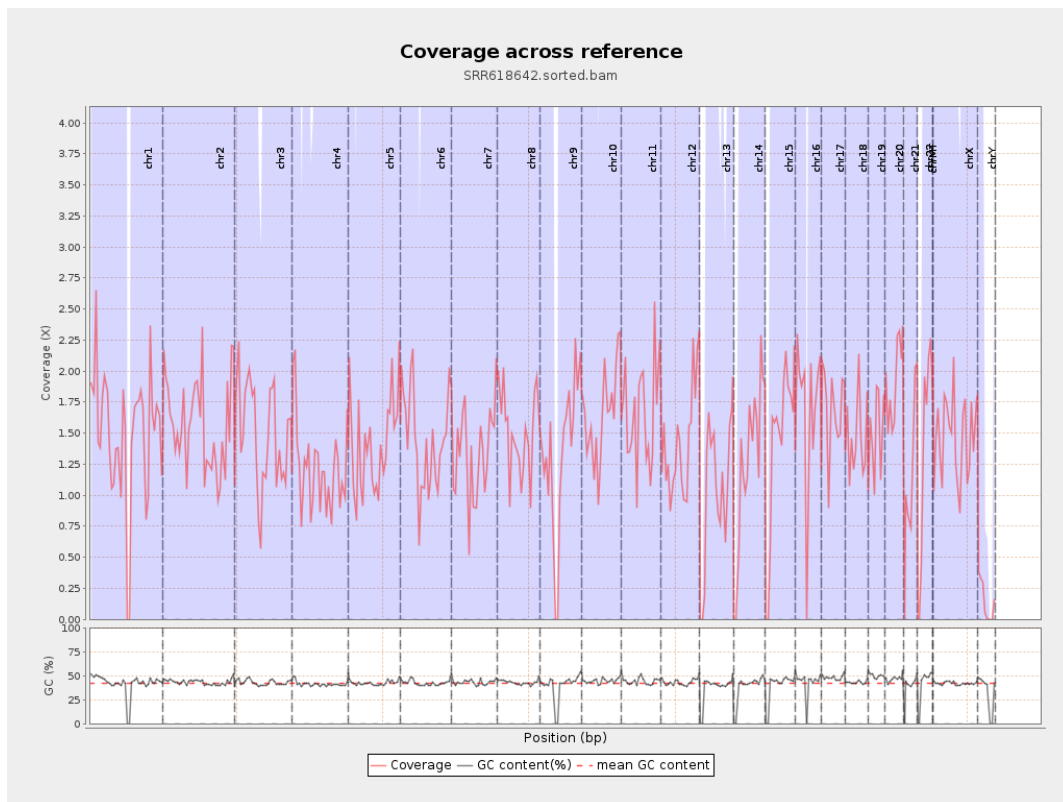
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

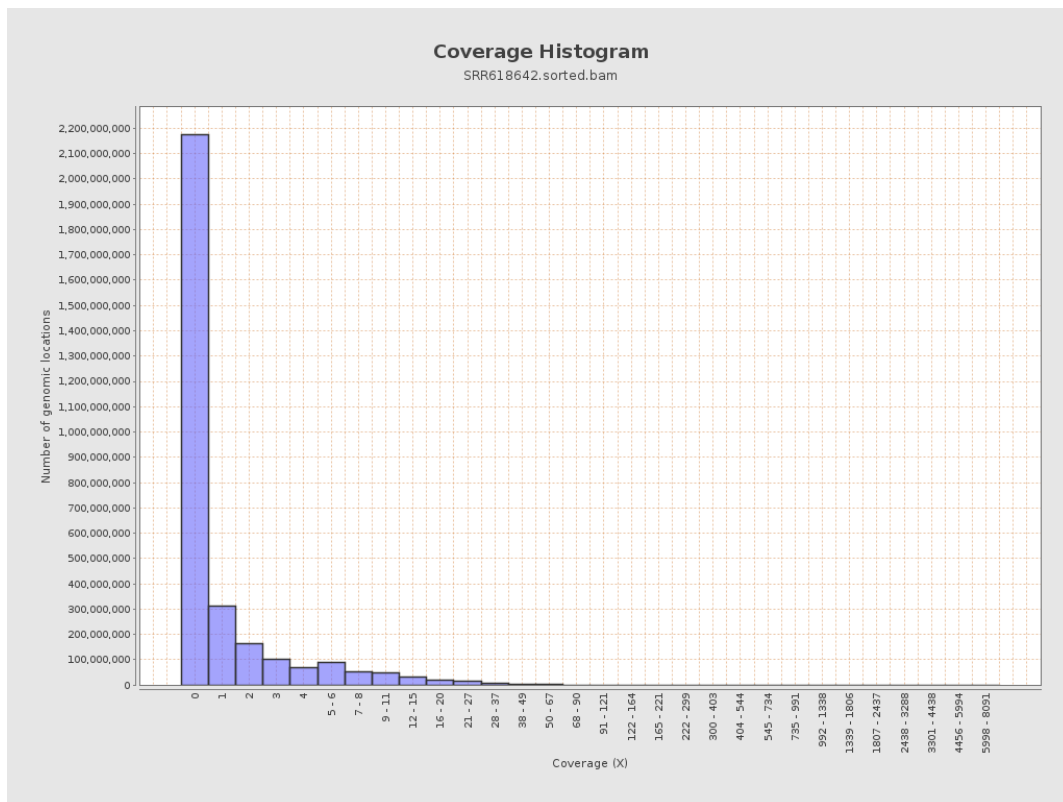
		bases	coverage	deviation
chr1	249250621	369519018	1.4825	6.5342
chr2	243199373	380089009	1.5629	8.1545
chr3	198022430	293912684	1.4842	5.0855
chr4	191154276	232014921	1.2138	4.9576
chr5	180915260	257316765	1.4223	5.3647
chr6	171115067	245967138	1.4374	4.8462
chr7	159138663	214902309	1.3504	4.9313
chr8	146364022	219196638	1.4976	5.1872
chr9	141213431	188214372	1.3328	6.2133
chr10	135534747	222631091	1.6426	5.6759
chr11	135006516	223820276	1.6578	6.7064
chr12	133851895	189753385	1.4176	5.1718
chr13	115169878	119174957	1.0348	4.2155
chr14	107349540	135892050	1.2659	4.8139
chr15	102531392	143962155	1.4041	5.3793
chr16	90354753	151066658	1.6719	13.7209
chr17	81195210	138164164	1.7016	5.8723
chr18	78077248	113166580	1.4494	6.0296
chr19	59128983	89106360	1.507	7.024
chr20	63025520	120036248	1.9046	6.1122
chr21	48129895	56513174	1.1742	7.4807
chr22	51304566	69433756	1.3534	5.8314
chrMT	16571	35640	2.1507	7.1281
chrX	155270560	227546618	1.4655	4.7062

chrY	59373566	8703915	0.1466	5.4296
------	----------	---------	--------	--------

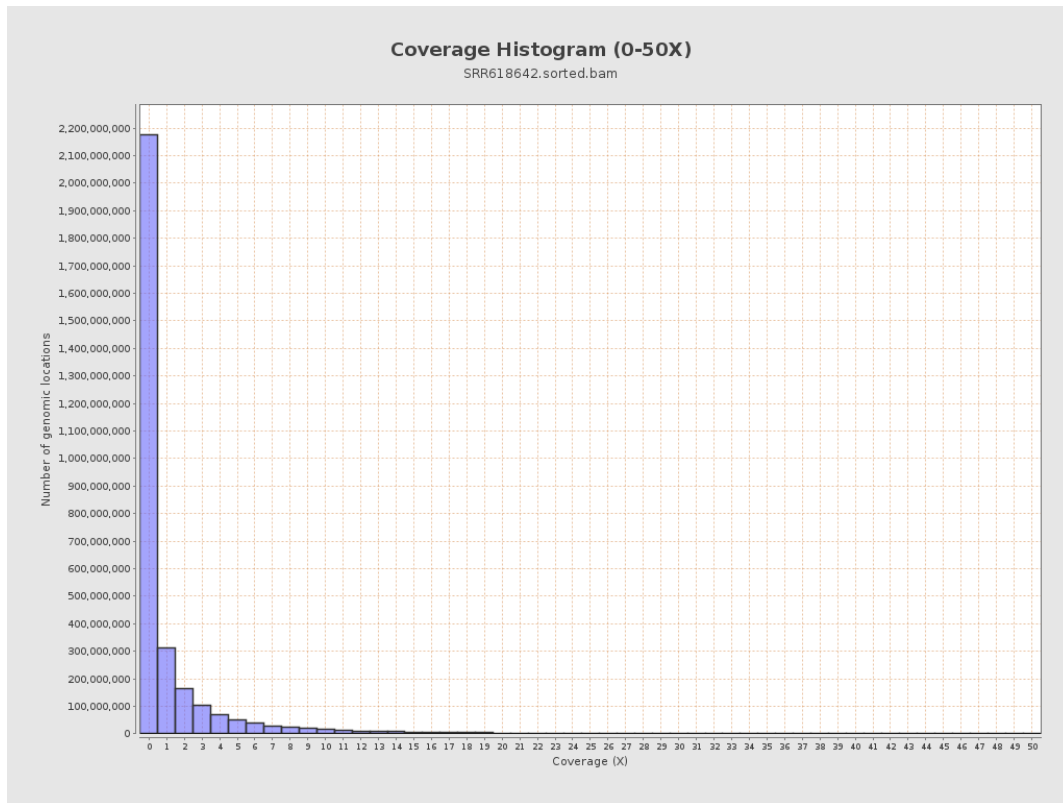
3. Results : Coverage across reference



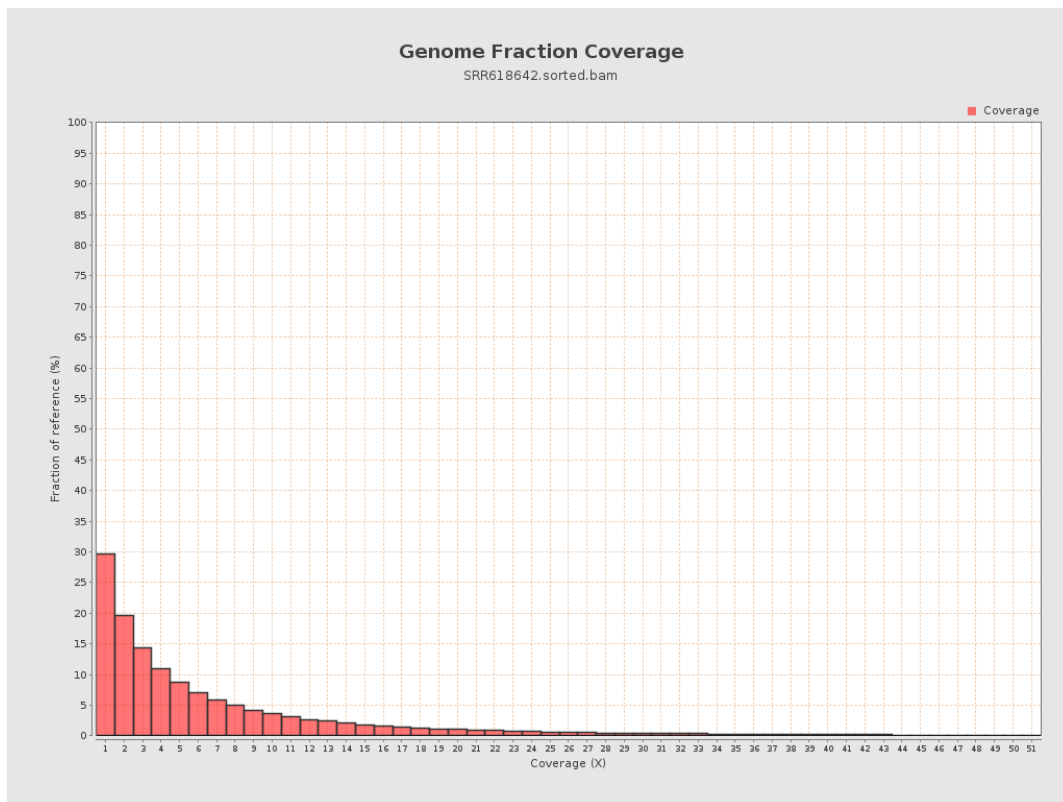
4. Results : Coverage Histogram



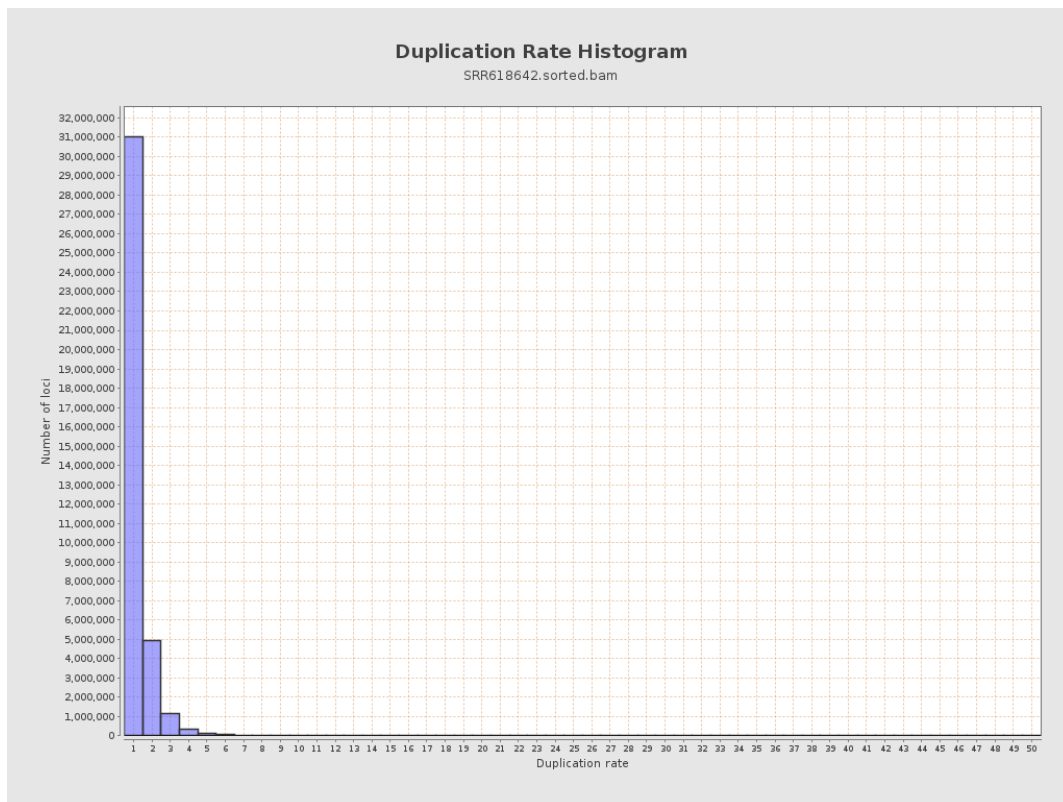
5. Results : Coverage Histogram (0-50X)



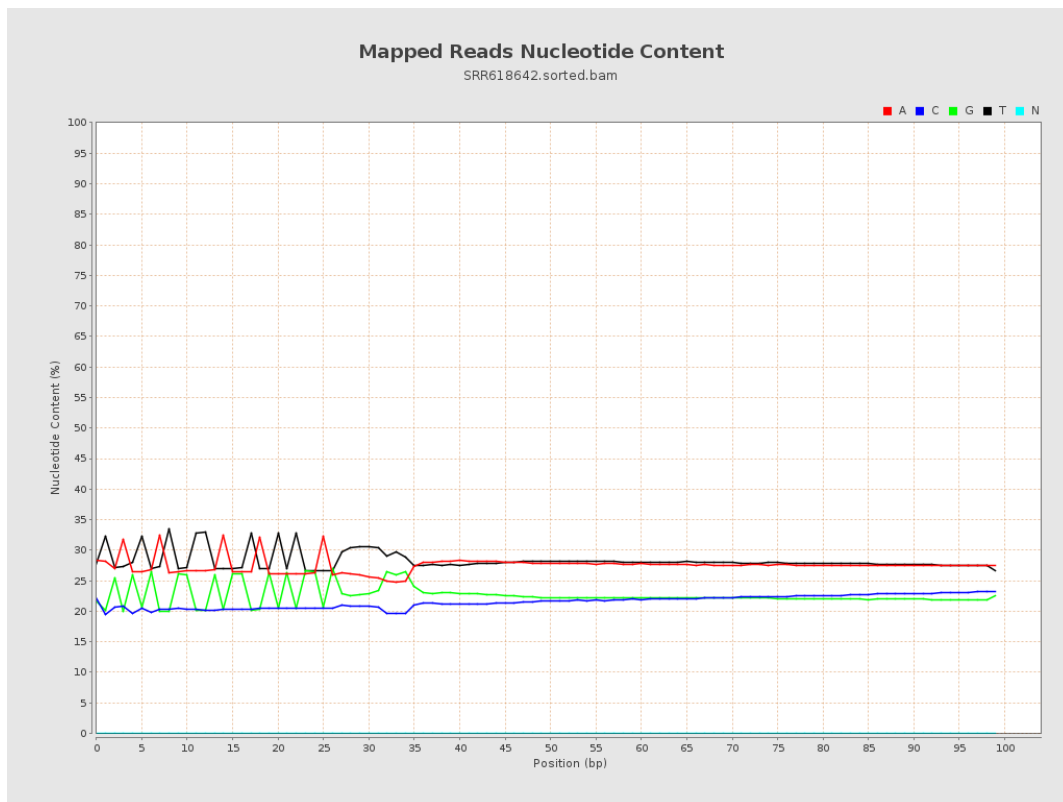
6. Results : Genome Fraction Coverage



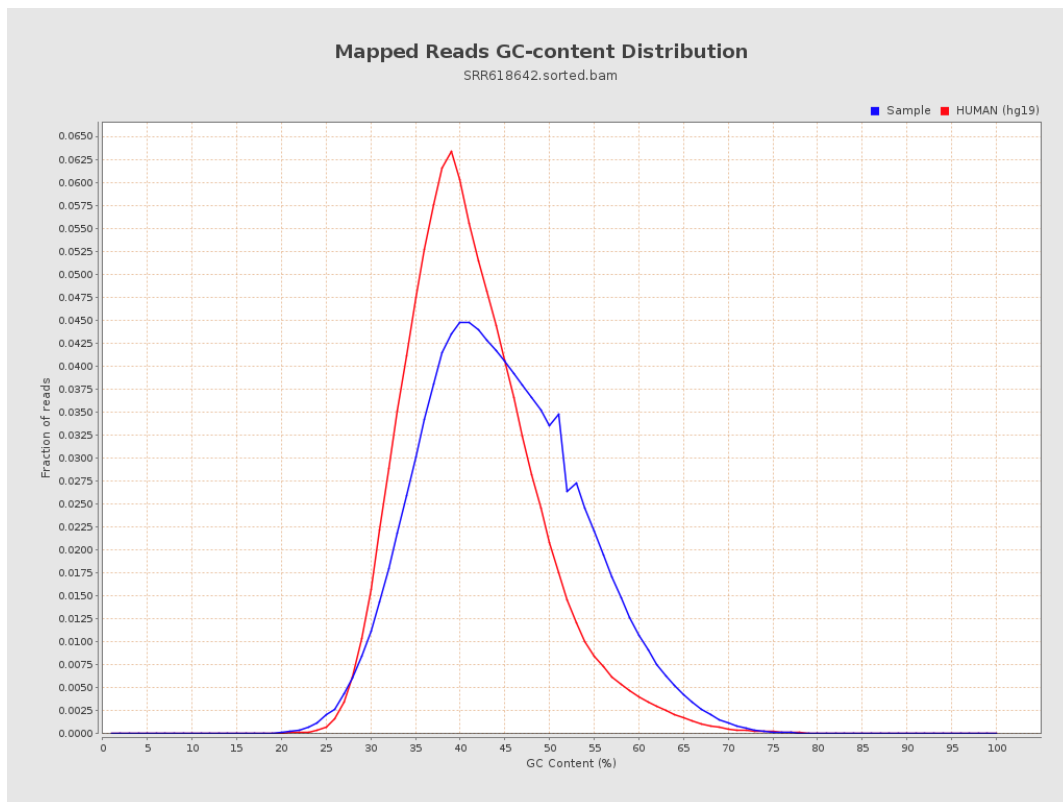
7. Results : Duplication Rate Histogram



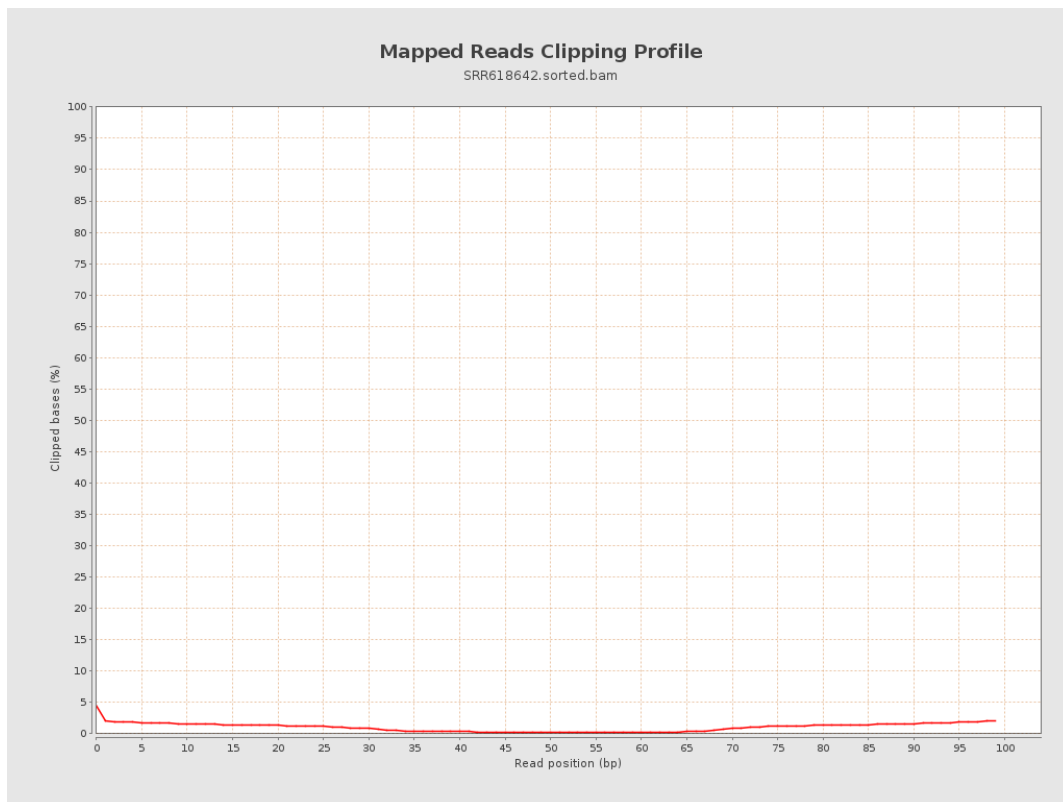
8. Results : Mapped Reads Nucleotide Content



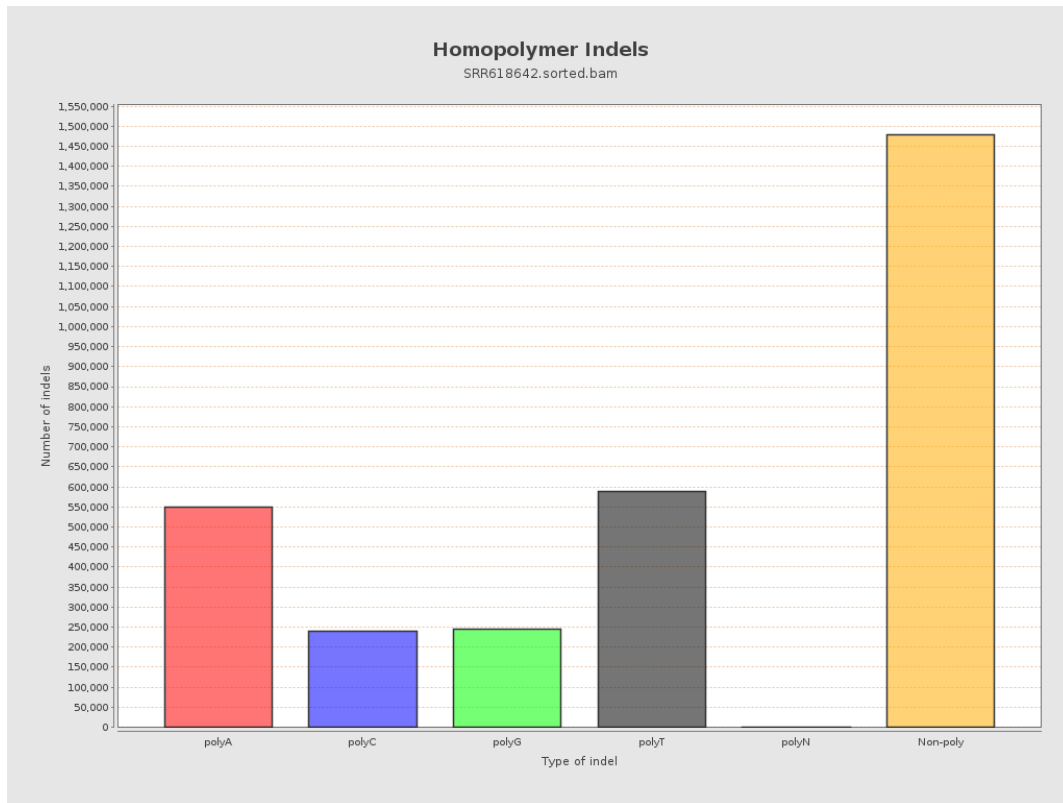
9. Results : Mapped Reads GC-content Distribution



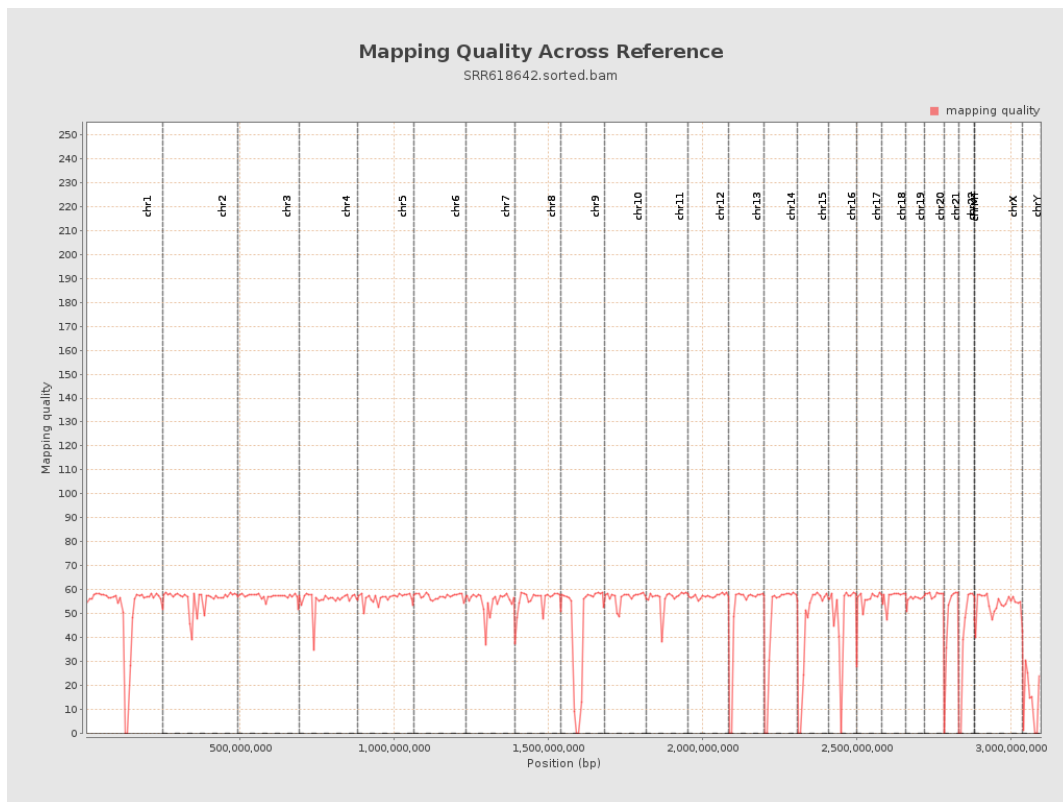
10. Results : Mapped Reads Clipping Profile



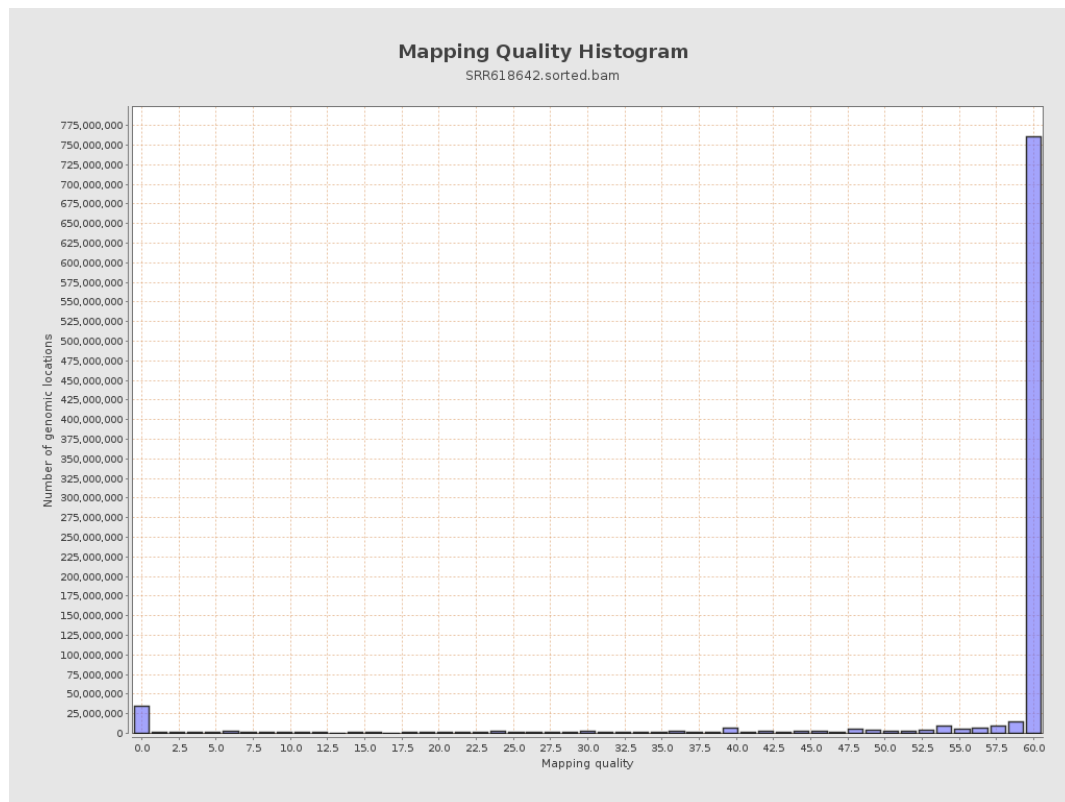
11. Results : Homopolymer Indels



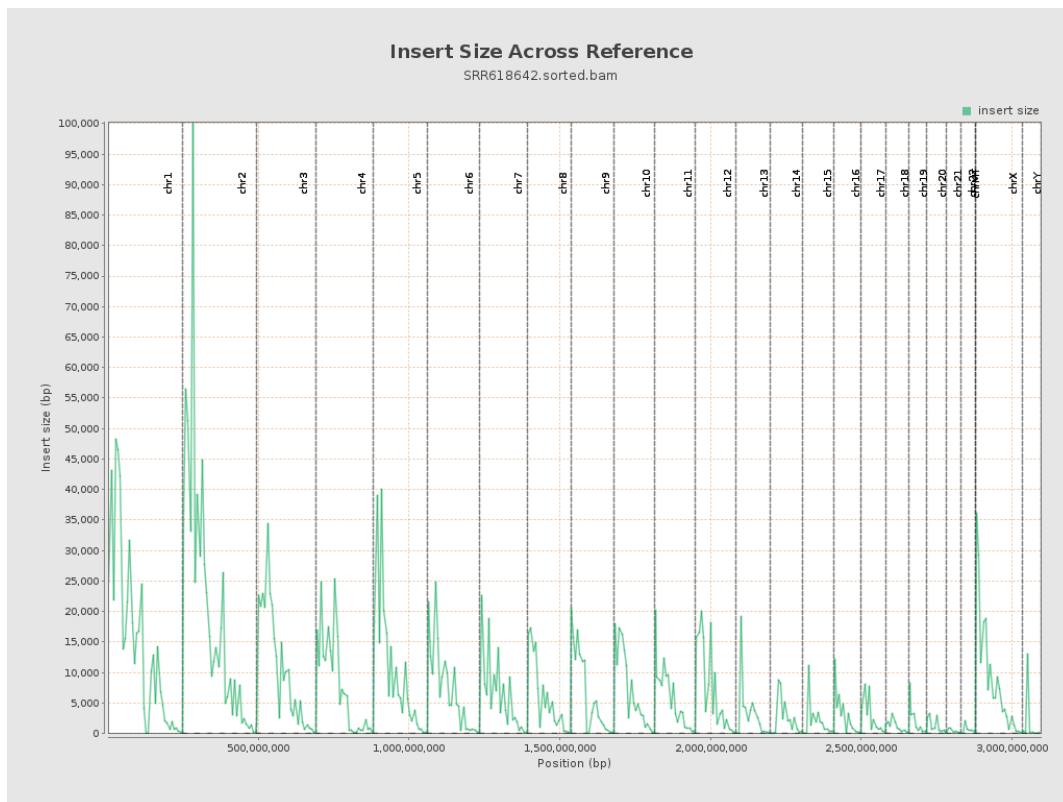
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

