

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 05:31:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618581.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_SRR618581 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618581_1.fastq.gz SRR618581_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 05:31:16 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618581.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	57,109,194
Mapped reads	53,649,451 / 93.94%
Unmapped reads	3,459,743 / 6.06%
Mapped paired reads	53,649,451 / 93.94%
Mapped reads, first in pair	27,157,674 / 47.55%
Mapped reads, second in pair	26,491,777 / 46.39%
Mapped reads, both in pair	52,515,410 / 91.96%
Mapped reads, singletons	1,134,041 / 1.99%
Secondary alignments	0
Supplementary alignments	81,975 / 0.14%
Read min/max/mean length	30 / 100 / 100.06
Duplicated reads (estimated)	11,497,489 / 20.13%
Duplication rate	18.79%
Clipped reads	9,915,846 / 17.36%

2.2. ACGT Content

Number/percentage of A's	1,373,356,499 / 26.89%
Number/percentage of C's	1,149,314,206 / 22.5%
Number/percentage of T's	1,379,750,866 / 27.01%
Number/percentage of G's	1,205,205,476 / 23.6%
Number/percentage of N's	231,596 / 0%

GC Percentage	46.1%
---------------	-------

2.3. Coverage

Mean	1.6511
Standard Deviation	7.1707

2.4. Mapping Quality

Mean Mapping Quality	54
----------------------	----

2.5. Insert size

Mean	29,669.71
Standard Deviation	1,691,205.88
P25/Median/P75	188 / 218 / 257

2.6. Mismatches and indels

General error rate	1.29%
Mismatches	64,553,130
Insertions	917,819
Mapped reads with at least one insertion	1.68%
Deletions	2,368,386
Mapped reads with at least one deletion	4.31%
Homopolymer indels	52.08%

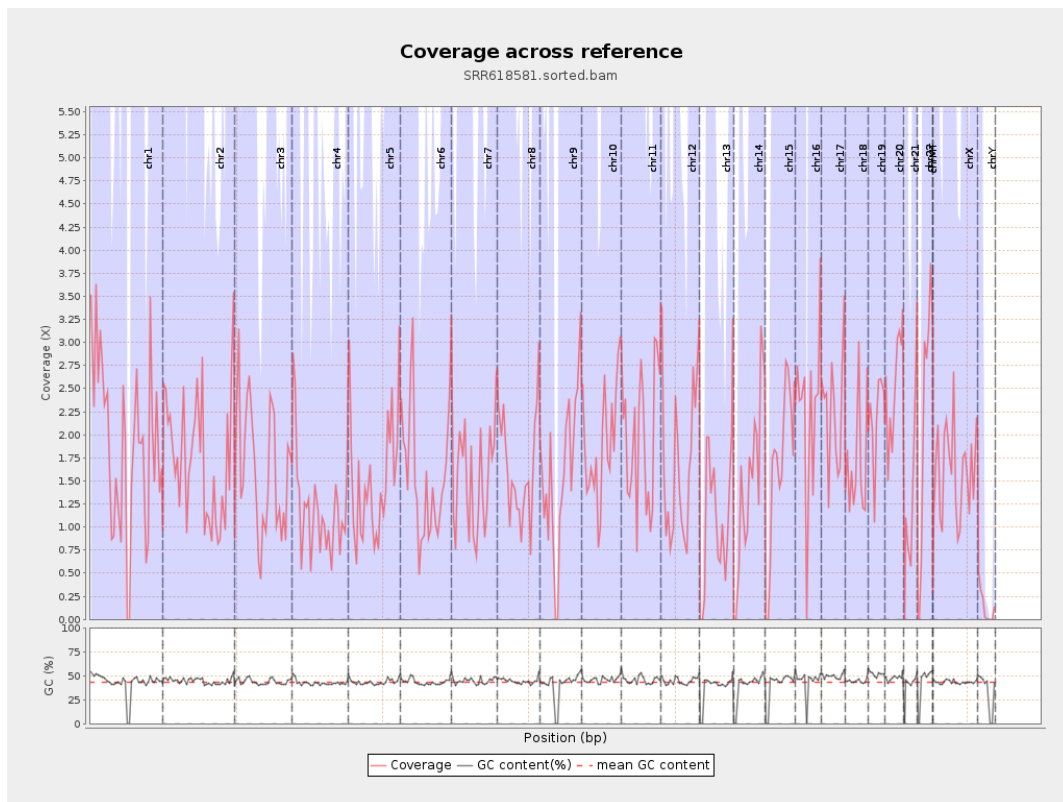
2.7. Chromosome stats

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

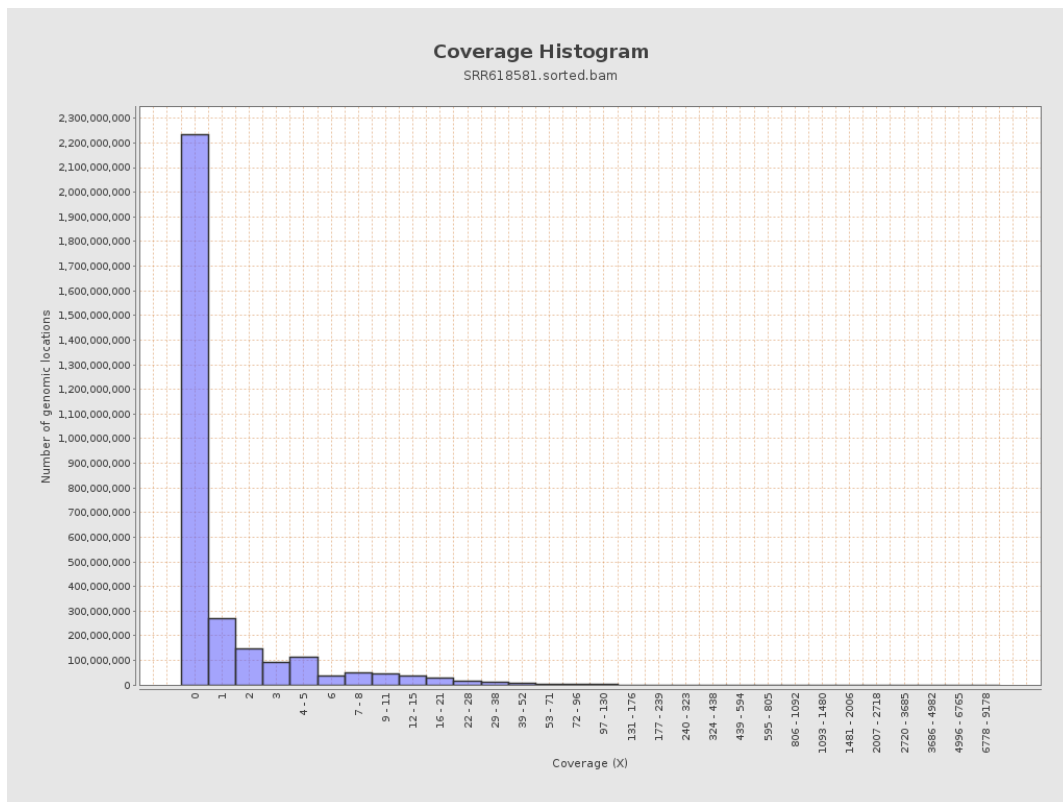
		bases	coverage	deviation
chr1	249250621	468323727	1.8789	7.9316
chr2	243199373	421364126	1.7326	8.7302
chr3	198022430	316721005	1.5994	5.5946
chr4	191154276	227310729	1.1891	5.1966
chr5	180915260	276990290	1.531	5.4707
chr6	171115067	262381889	1.5334	5.5189
chr7	159138663	247804932	1.5572	5.6326
chr8	146364022	238255633	1.6278	6.4196
chr9	141213431	220890682	1.5642	6.5109
chr10	135534747	256183957	1.8902	6.5458
chr11	135006516	264309056	1.9578	7.0098
chr12	133851895	227132547	1.6969	6.3289
chr13	115169878	126187508	1.0957	4.4705
chr14	107349540	156952888	1.4621	5.7634
chr15	102531392	168007859	1.6386	6.3648
chr16	90354753	202142749	2.2372	17.4902
chr17	81195210	180870529	2.2276	7.6309
chr18	78077248	127914814	1.6383	6.2662
chr19	59128983	128431091	2.172	8.1265
chr20	63025520	157048394	2.4918	8.0241
chr21	48129895	66594764	1.3836	9.0383
chr22	51304566	110667991	2.1571	8.3132
chrMT	16571	4719	0.2848	0.9167
chrX	155270560	250480677	1.6132	5.5364

chrY	59373566	8191545	0.138	5.8816
------	----------	---------	-------	--------

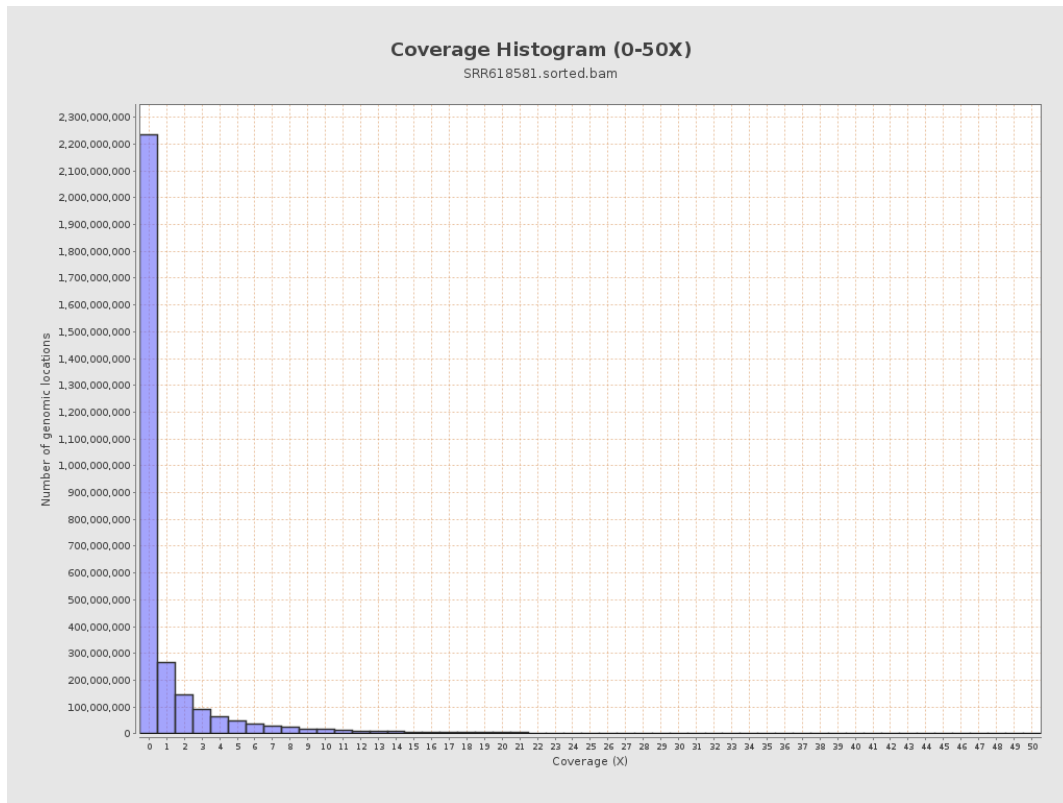
3. Results : Coverage across reference



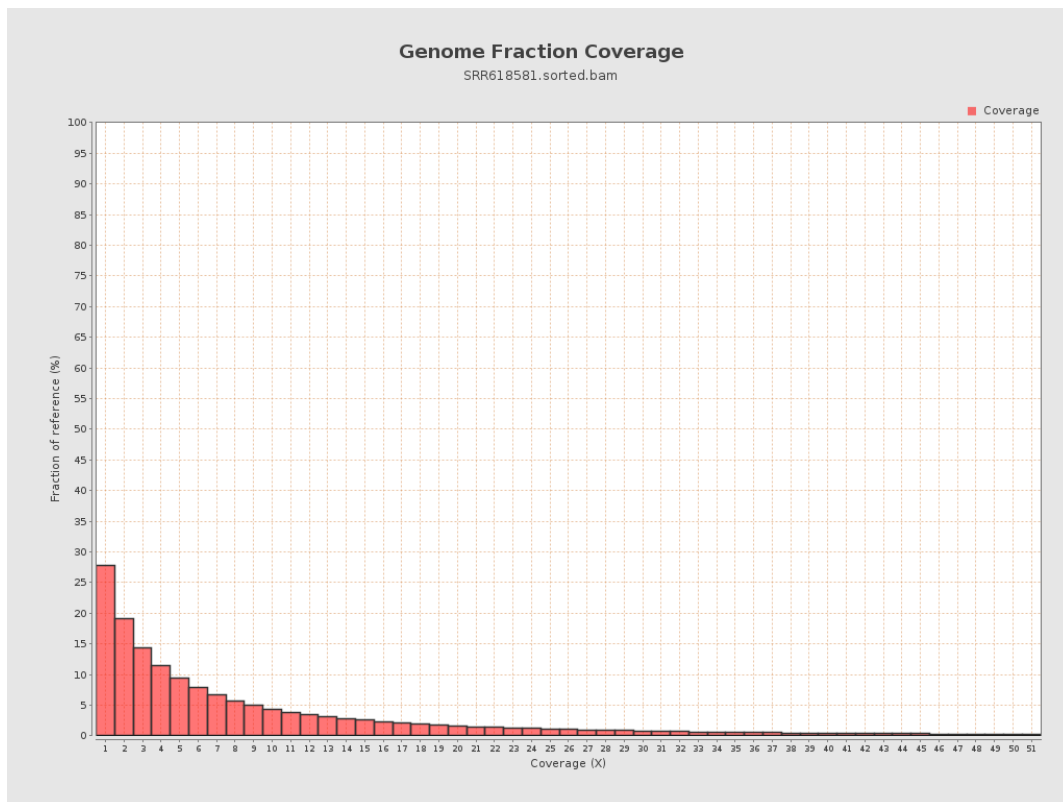
4. Results : Coverage Histogram



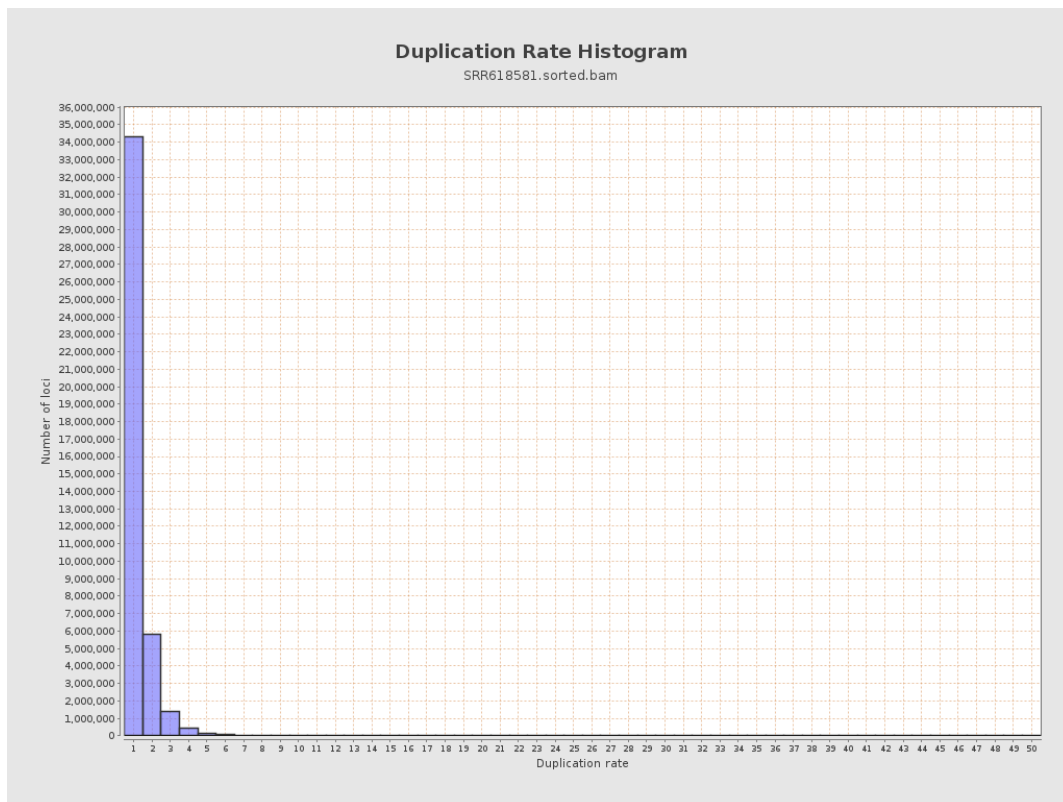
5. Results : Coverage Histogram (0-50X)



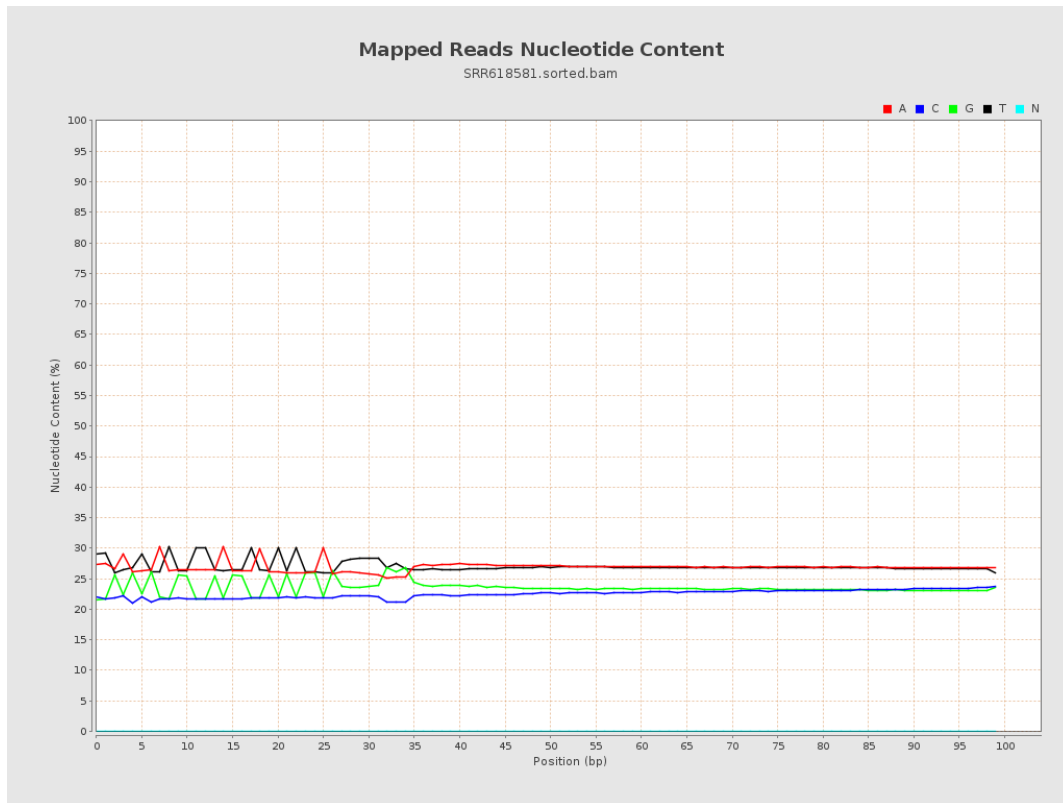
6. Results : Genome Fraction Coverage



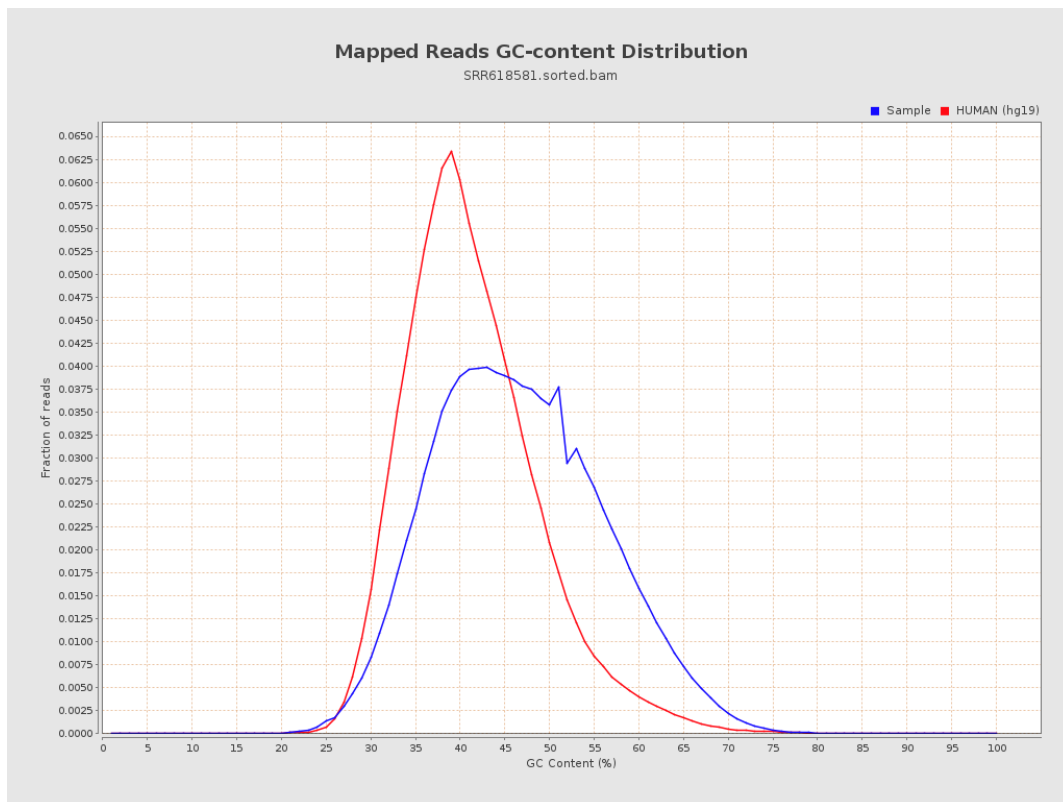
7. Results : Duplication Rate Histogram



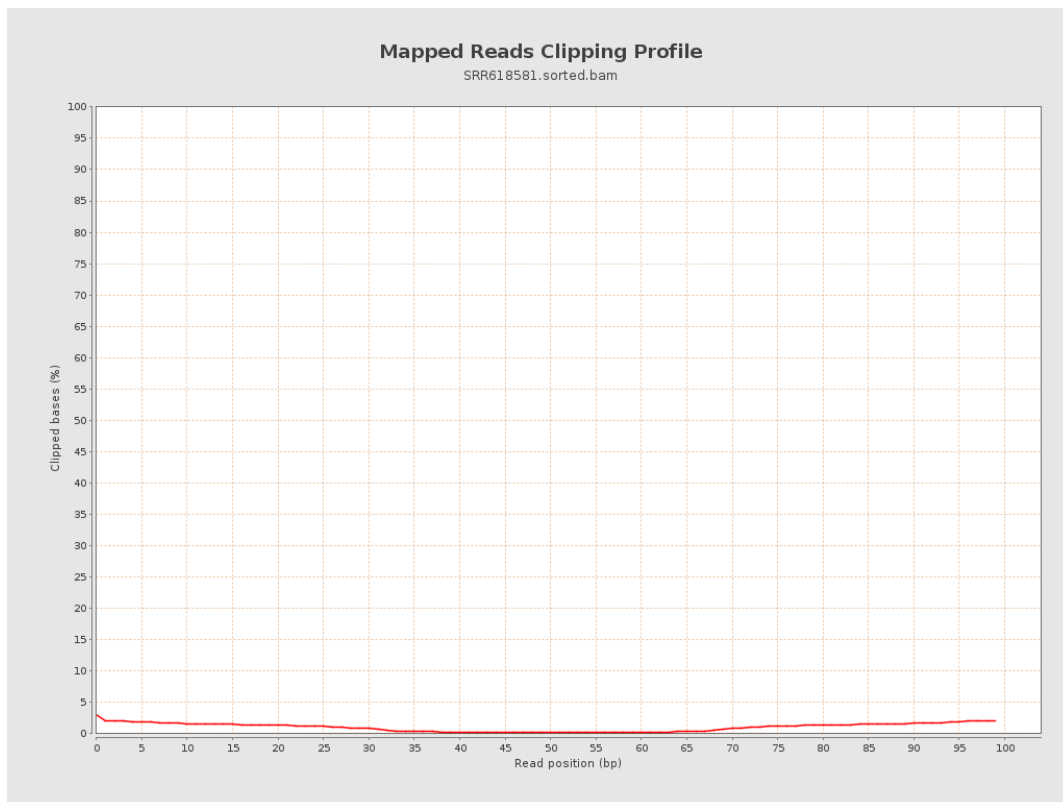
8. Results : Mapped Reads Nucleotide Content



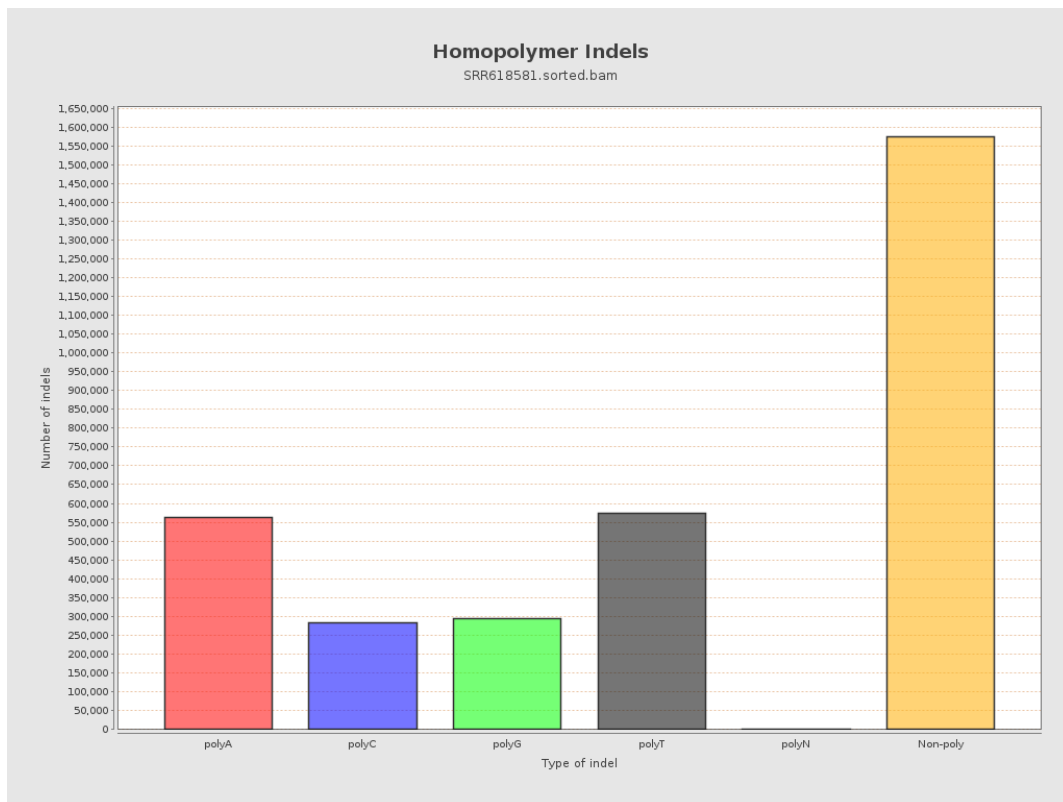
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



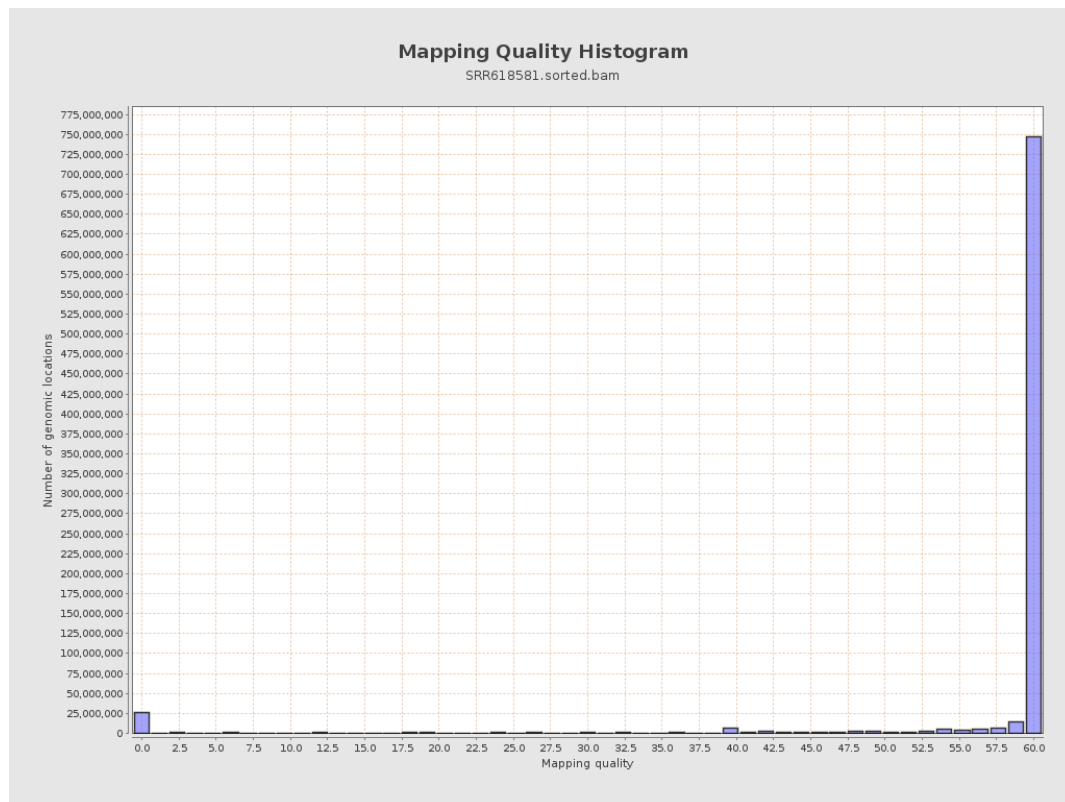
11. Results : Homopolymer Indels



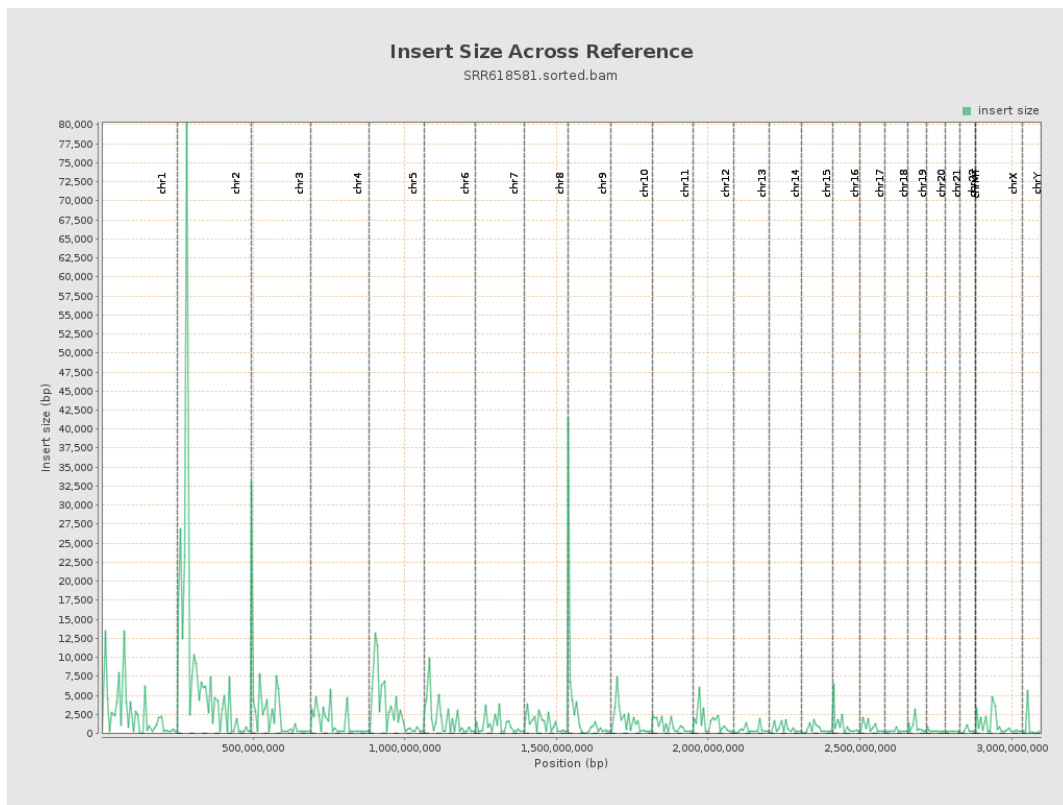
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

