

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 20:08:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618632.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_SRR618632 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618632_1.fastq.gz SRR618632_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 20:08:55 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618632.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	151,321,526
Mapped reads	145,706,591 / 96.29%
Unmapped reads	5,614,935 / 3.71%
Mapped paired reads	145,706,591 / 96.29%
Mapped reads, first in pair	73,375,396 / 48.49%
Mapped reads, second in pair	72,331,195 / 47.8%
Mapped reads, both in pair	142,740,870 / 94.33%
Mapped reads, singletons	2,965,721 / 1.96%
Secondary alignments	0
Supplementary alignments	239,638 / 0.16%
Read min/max/mean length	30 / 100 / 100.06
Duplicated reads (estimated)	59,722,771 / 39.47%
Duplication rate	33.74%
Clipped reads	28,224,825 / 18.65%

2.2. ACGT Content

Number/percentage of A's	3,652,203,200 / 26.42%
Number/percentage of C's	3,184,844,926 / 23.04%
Number/percentage of T's	3,673,707,830 / 26.58%
Number/percentage of G's	3,307,017,348 / 23.92%
Number/percentage of N's	5,925,244 / 0.04%

GC Percentage	46.96%
---------------	--------

2.3. Coverage

Mean	4.4684
Standard Deviation	18.5625

2.4. Mapping Quality

Mean Mapping Quality	52.32
----------------------	-------

2.5. Insert size

Mean	30,402.54
Standard Deviation	1,746,117.13
P25/Median/P75	184 / 214 / 251

2.6. Mismatches and indels

General error rate	1.39%
Mismatches	188,268,907
Insertions	2,555,219
Mapped reads with at least one insertion	1.72%
Deletions	6,456,701
Mapped reads with at least one deletion	4.32%
Homopolymer indels	51.64%

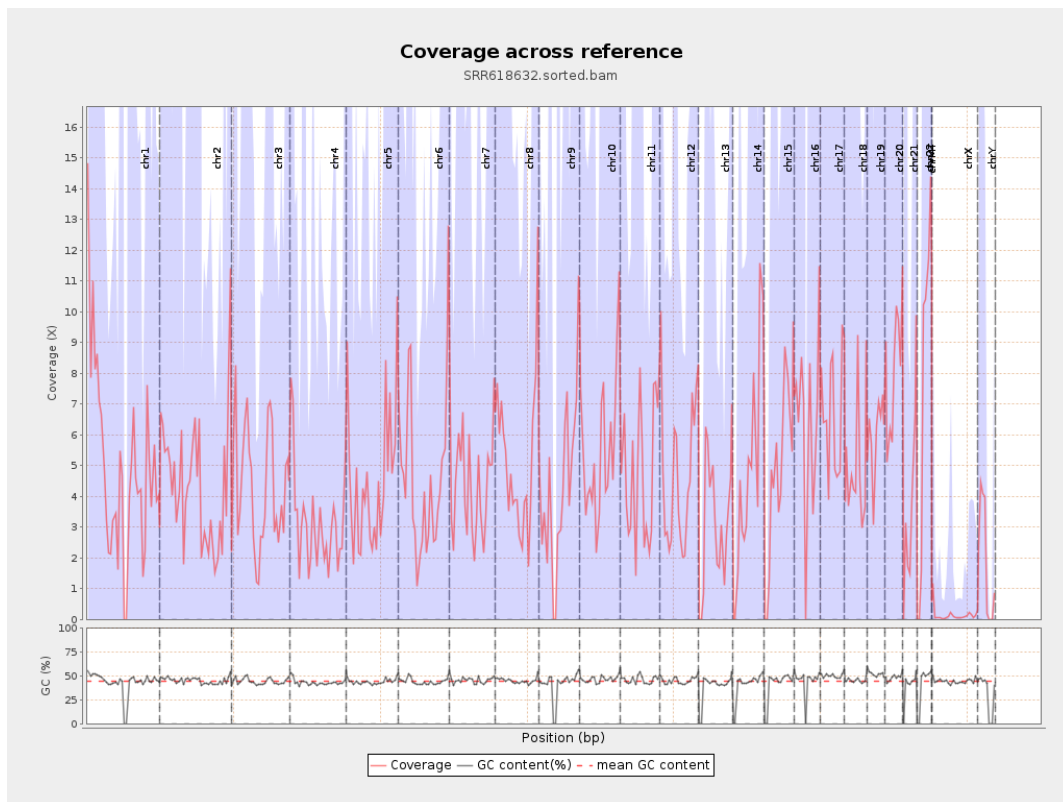
2.7. Chromosome stats

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

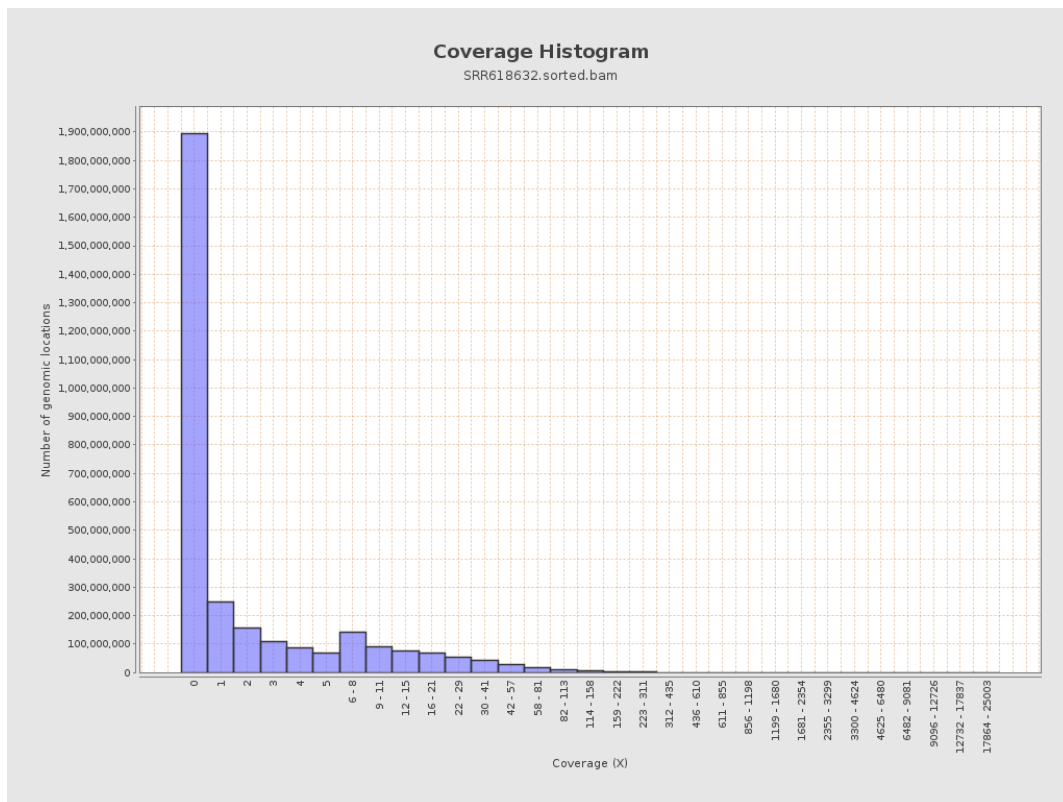
		bases	coverage	deviation
chr1	249250621	1224865137	4.9142	19.2531
chr2	243199373	1055929371	4.3418	22.6936
chr3	198022430	861559079	4.3508	13.495
chr4	191154276	589060752	3.0816	14.5664
chr5	180915260	827900249	4.5762	14.3823
chr6	171115067	770052828	4.5002	14.6938
chr7	159138663	706870683	4.4419	13.5205
chr8	146364022	745327576	5.0923	16.2131
chr9	141213431	614731151	4.3532	16.8704
chr10	135534747	744640956	5.4941	16.3312
chr11	135006516	643837766	4.7689	15.9901
chr12	133851895	617364719	4.6123	14.7314
chr13	115169878	355977013	3.0909	11.3606
chr14	107349540	506077087	4.7143	16.2479
chr15	102531392	482904584	4.7098	15.4808
chr16	90354753	574625993	6.3597	46.9206
chr17	81195210	544447489	6.7054	20.1362
chr18	78077248	388710211	4.9785	17.9416
chr19	59128983	357996069	6.0545	19.7727
chr20	63025520	504639890	8.0069	22.497
chr21	48129895	179957591	3.739	31.2767
chr22	51304566	397321878	7.7444	25.4903
chrMT	16571	9354	0.5645	3.1923
chrX	155270560	20591973	0.1326	3.0189

chrY	59373566	117314788	1.9759	19.4915
------	----------	-----------	--------	---------

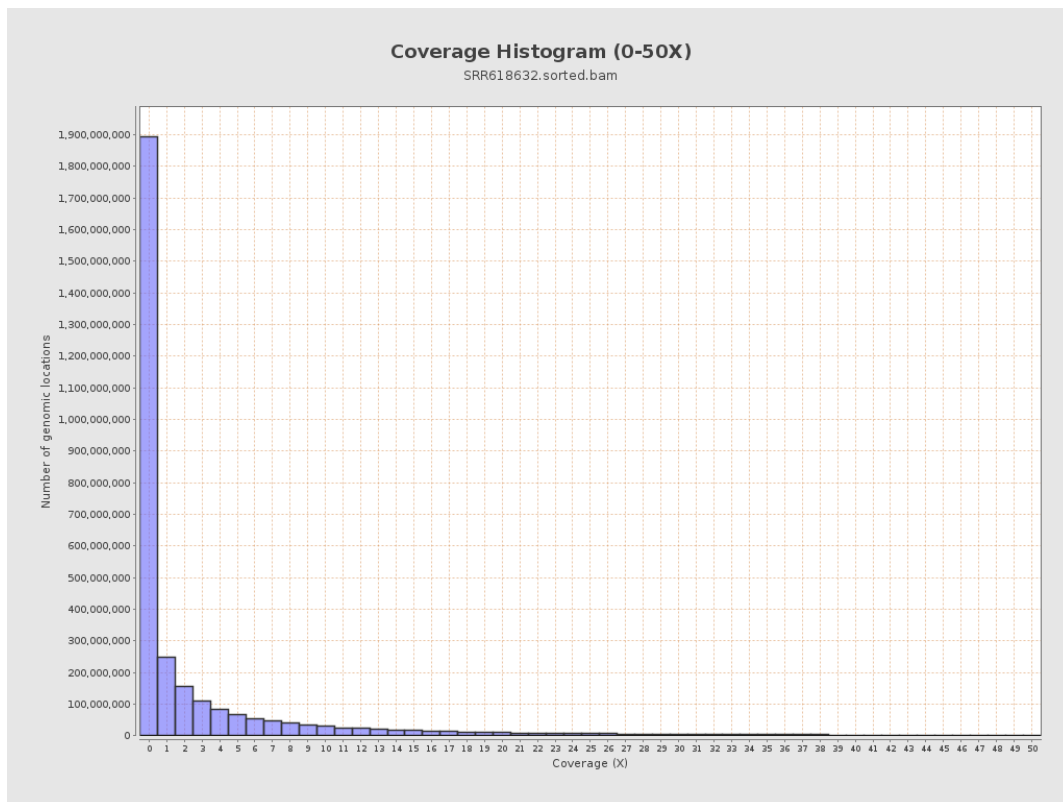
3. Results : Coverage across reference



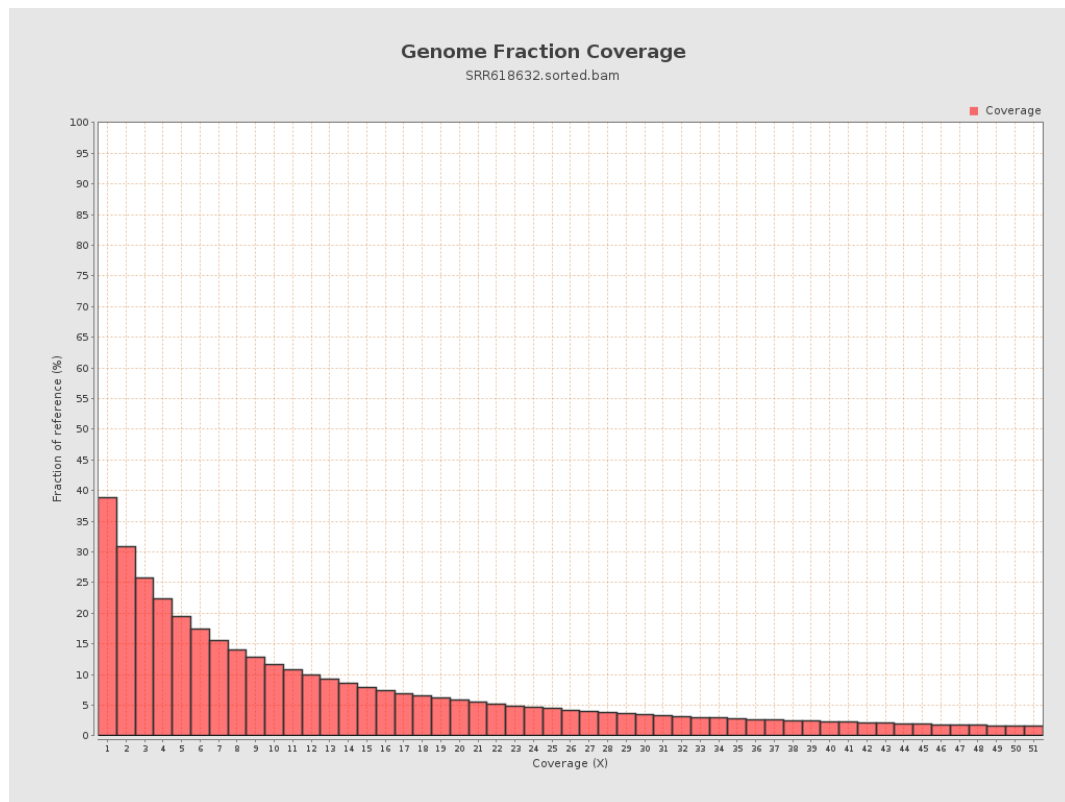
4. Results : Coverage Histogram



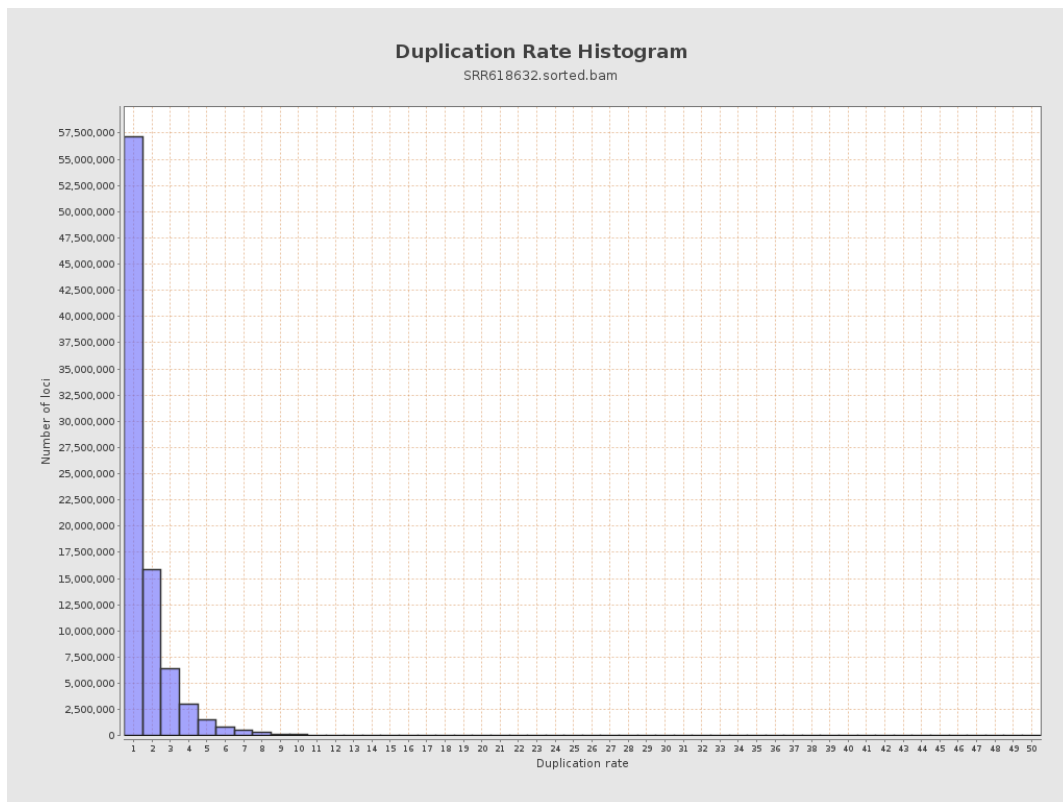
5. Results : Coverage Histogram (0-50X)



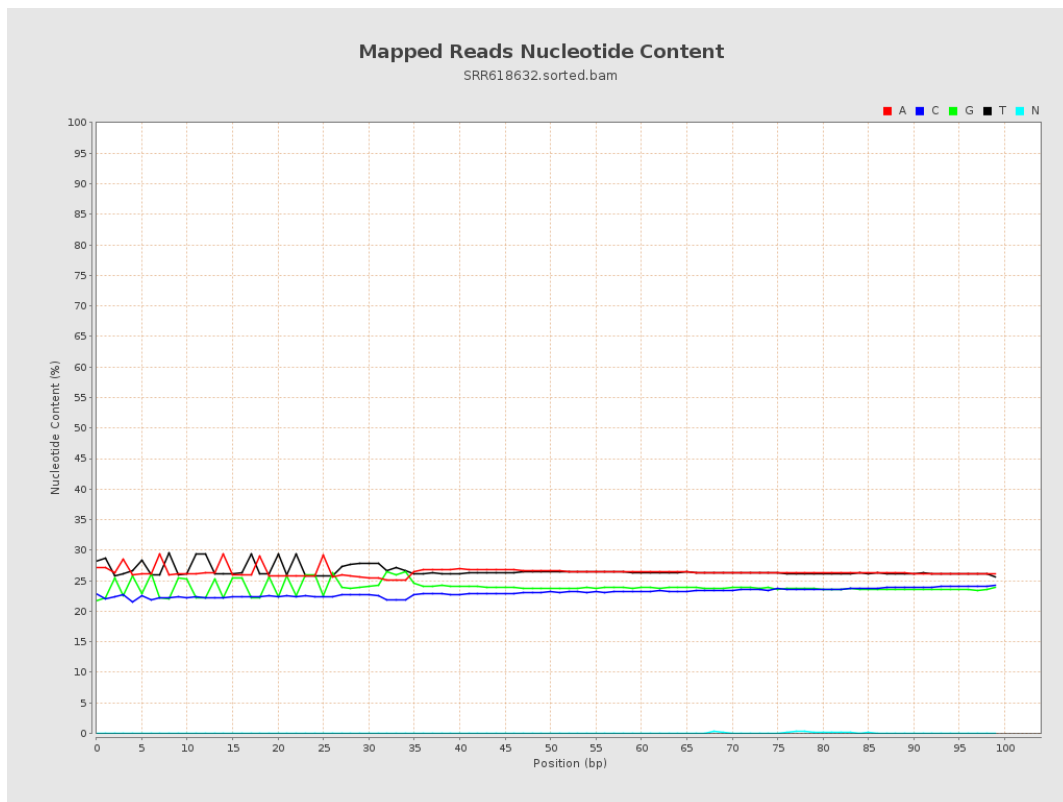
6. Results : Genome Fraction Coverage



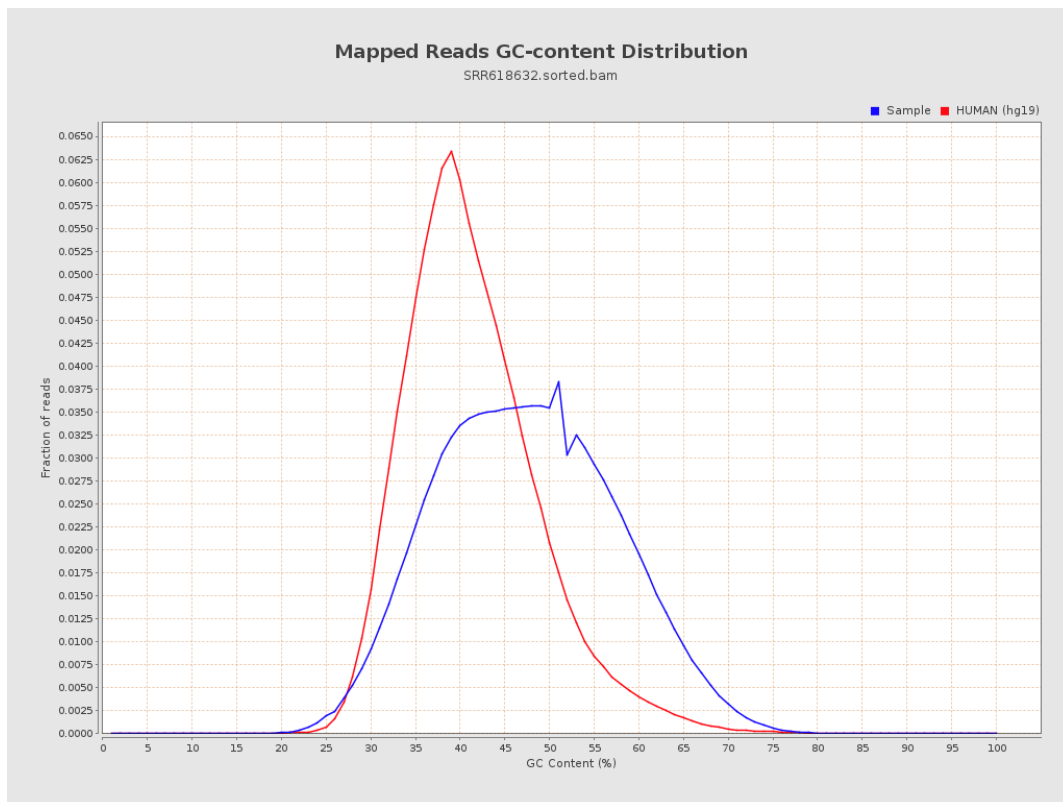
7. Results : Duplication Rate Histogram



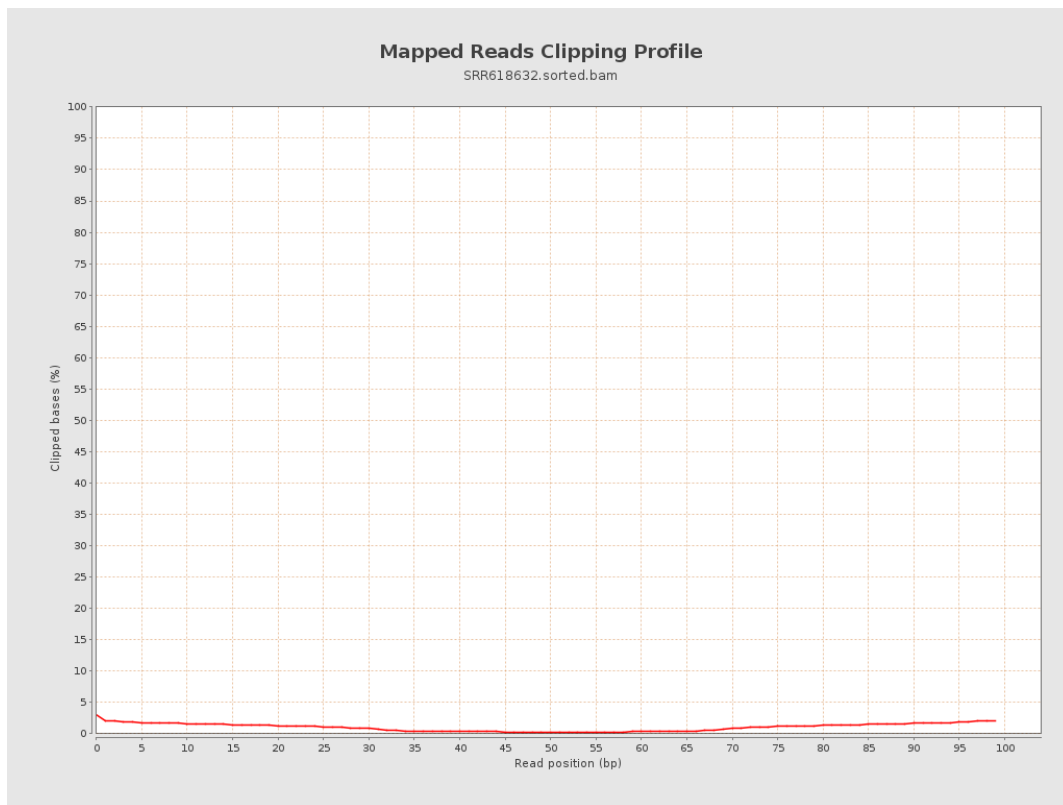
8. Results : Mapped Reads Nucleotide Content



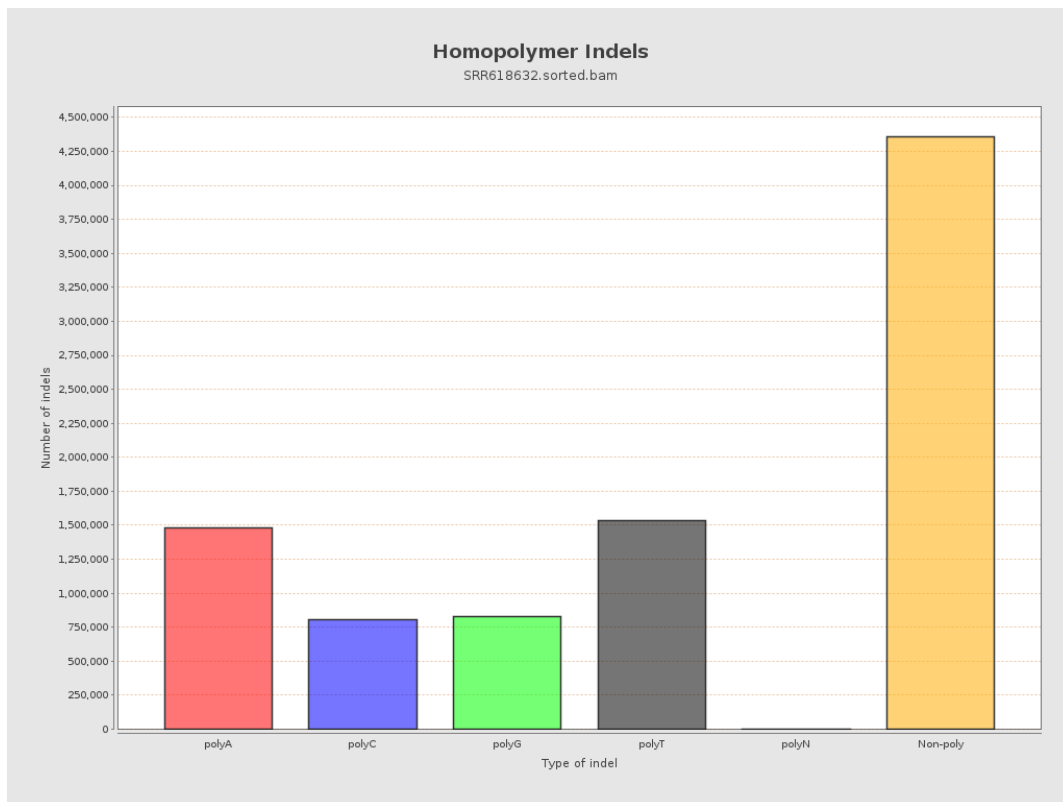
9. Results : Mapped Reads GC-content Distribution



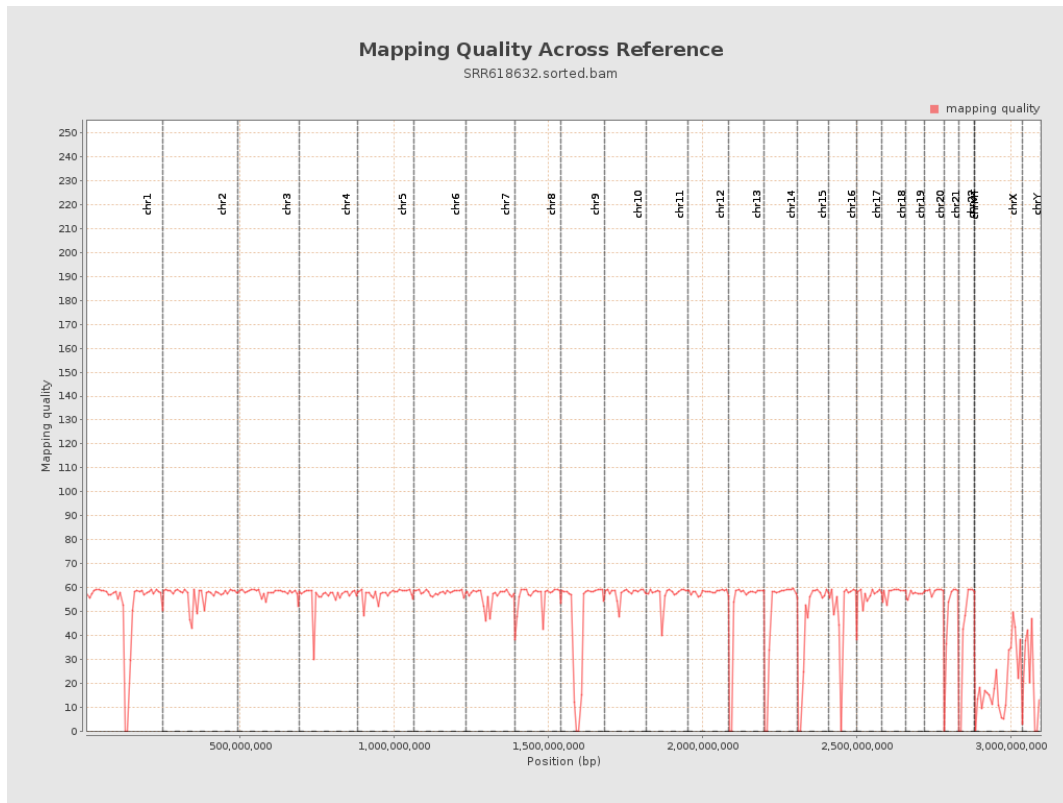
10. Results : Mapped Reads Clipping Profile



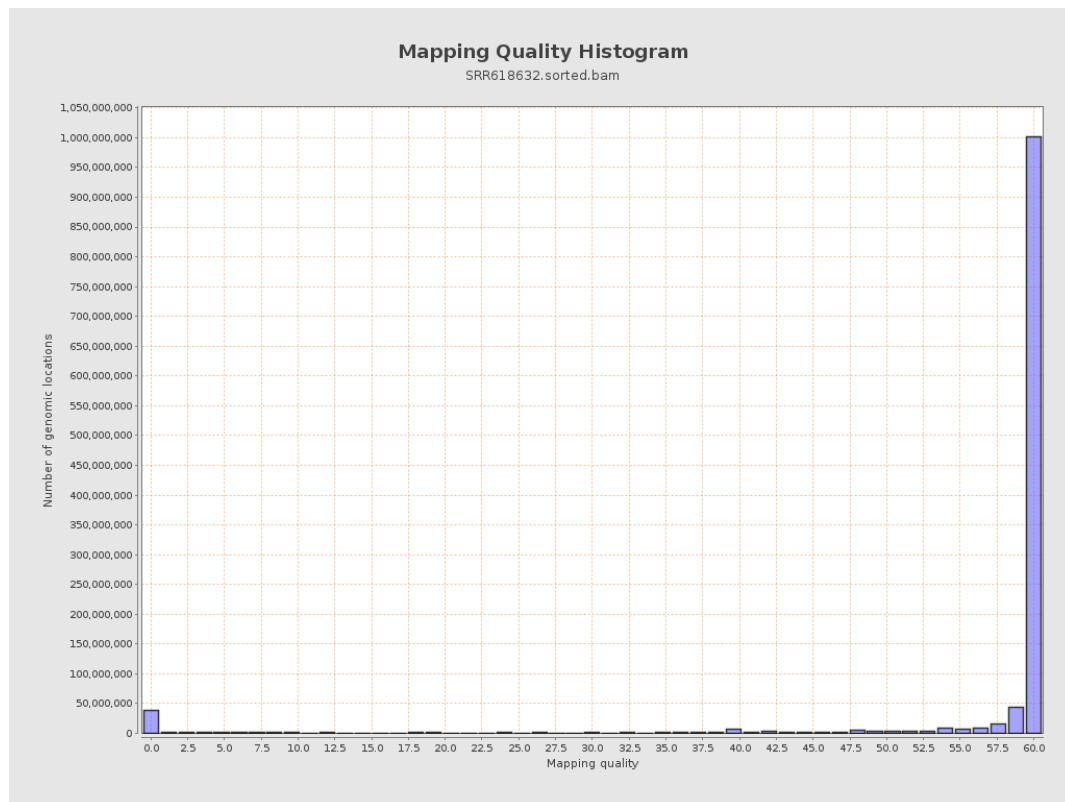
11. Results : Homopolymer Indels



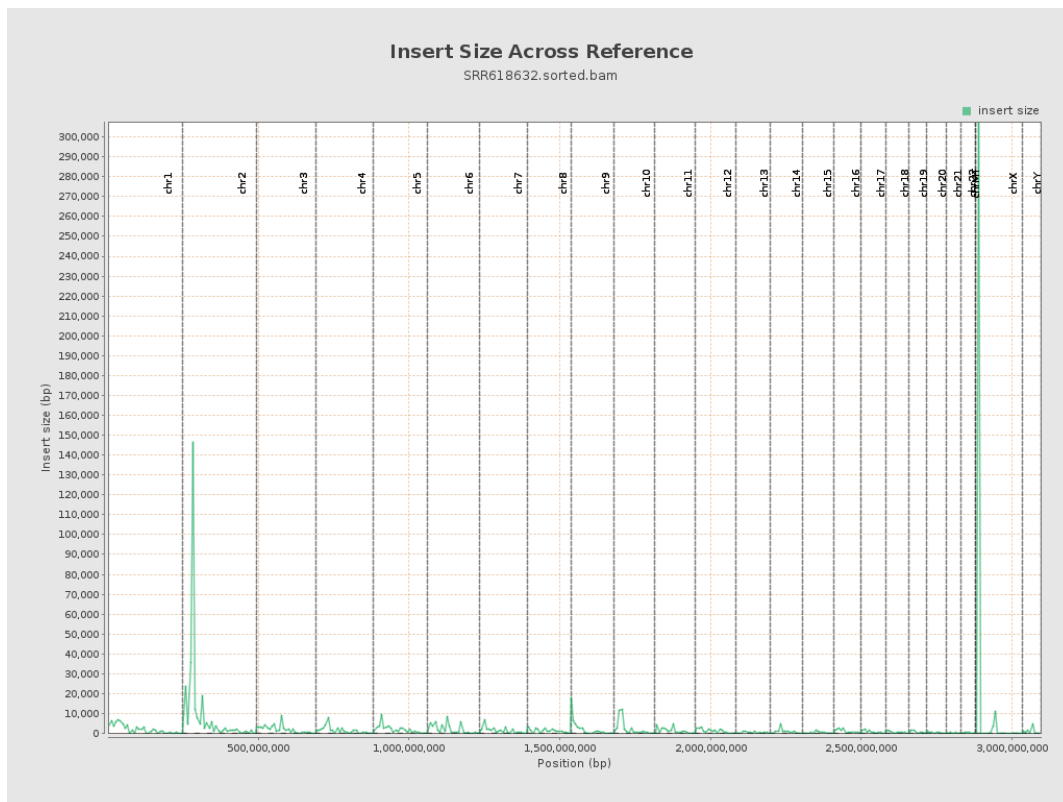
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

