

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 16:40:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618627.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_SRR618627 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618627_1.fastq.gz SRR618627_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 16:40:50 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618627.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	37,472,144
Mapped reads	36,179,437 / 96.55%
Unmapped reads	1,292,707 / 3.45%
Mapped paired reads	36,179,437 / 96.55%
Mapped reads, first in pair	18,271,117 / 48.76%
Mapped reads, second in pair	17,908,320 / 47.79%
Mapped reads, both in pair	35,571,384 / 94.93%
Mapped reads, singletons	608,053 / 1.62%
Secondary alignments	0
Supplementary alignments	120,945 / 0.32%
Read min/max/mean length	30 / 100 / 100.13
Duplicated reads (estimated)	16,597,654 / 44.29%
Duplication rate	34.49%
Clipped reads	8,802,387 / 23.49%

2.2. ACGT Content

Number/percentage of A's	929,376,194 / 27.48%
Number/percentage of C's	720,926,157 / 21.32%
Number/percentage of T's	945,594,682 / 27.96%
Number/percentage of G's	785,728,143 / 23.23%
Number/percentage of N's	120,011 / 0%

GC Percentage	44.55%
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2.3. Coverage

Mean	1.0932
Standard Deviation	4.3773

2.4. Mapping Quality

Mean Mapping Quality	52.19
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2.5. Insert size

Mean	73,796.71
Standard Deviation	2,727,471.17
P25/Median/P75	152 / 182 / 224

2.6. Mismatches and indels

General error rate	1.21%
Mismatches	40,145,876
Insertions	614,627
Mapped reads with at least one insertion	1.67%
Deletions	1,753,704
Mapped reads with at least one deletion	4.72%
Homopolymer indels	53.04%

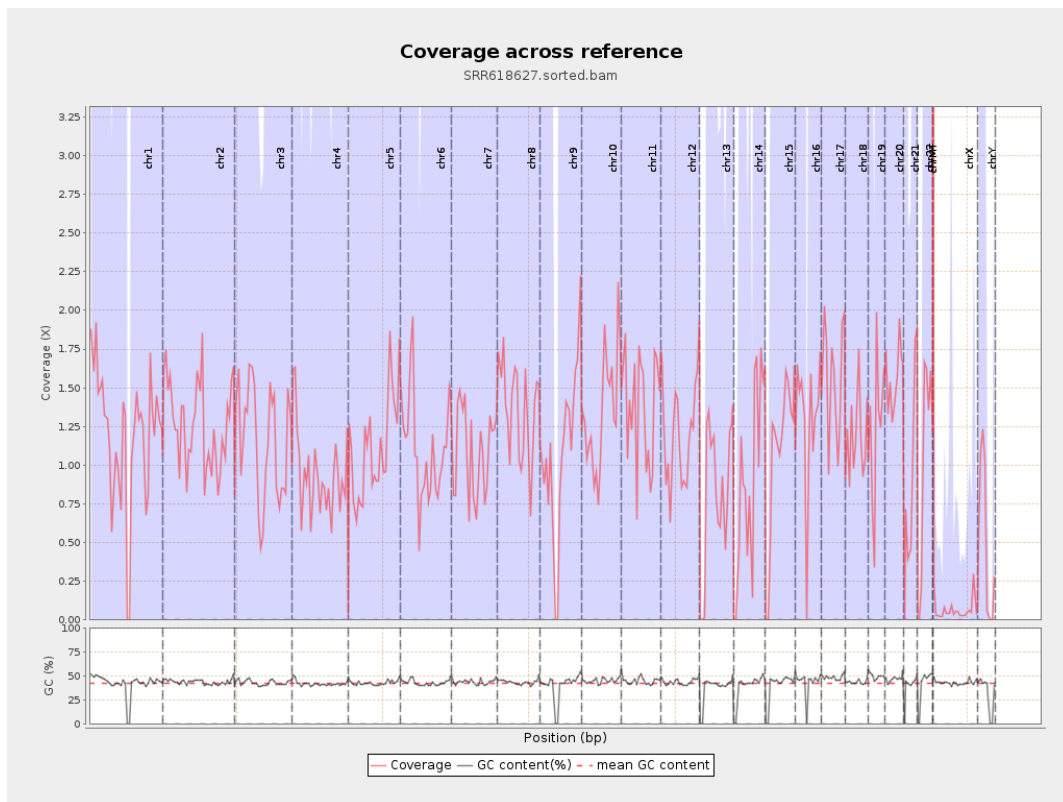
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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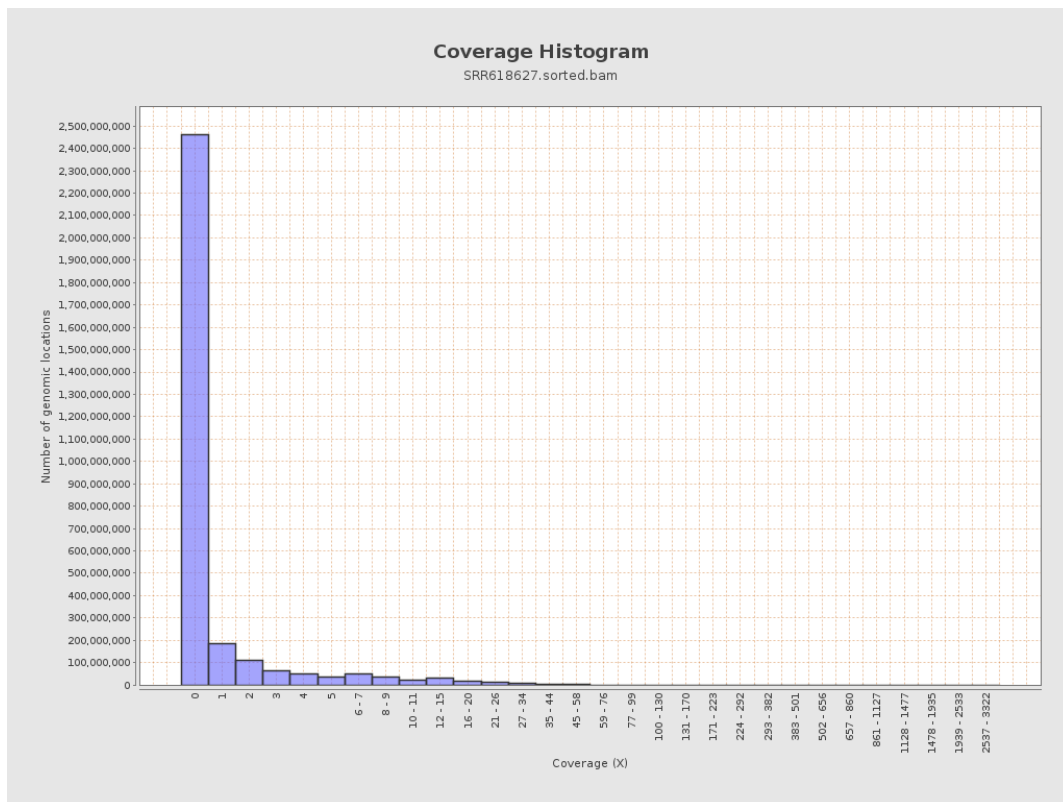
		bases	coverage	deviation
chr1	249250621	295219095	1.1844	5.4973
chr2	243199373	304686202	1.2528	5.0886
chr3	198022430	226298425	1.1428	3.8103
chr4	191154276	179299600	0.938	3.6402
chr5	180915260	202708324	1.1205	3.7687
chr6	171115067	188095798	1.0992	3.7757
chr7	159138663	172799997	1.0858	3.7528
chr8	146364022	196377769	1.3417	4.3227
chr9	141213431	151535536	1.0731	4.6399
chr10	135534747	180618499	1.3326	4.4228
chr11	135006516	185065724	1.3708	5.0541
chr12	133851895	160279256	1.1974	4.1949
chr13	115169878	92654105	0.8045	3.0759
chr14	107349540	96962809	0.9032	3.6341
chr15	102531392	109335776	1.0664	3.8329
chr16	90354753	115643608	1.2799	7.2125
chr17	81195210	126025055	1.5521	5.1102
chr18	78077248	91248691	1.1687	4.4903
chr19	59128983	72887018	1.2327	5.0109
chr20	63025520	98194490	1.558	4.7605
chr21	48129895	44050774	0.9152	5.2306
chr22	51304566	52429317	1.0219	3.93
chrMT	16571	639524	38.593	37.0027
chrX	155270560	9646020	0.0621	1.0995

chrY	59373566	31433937	0.5294	3.3279
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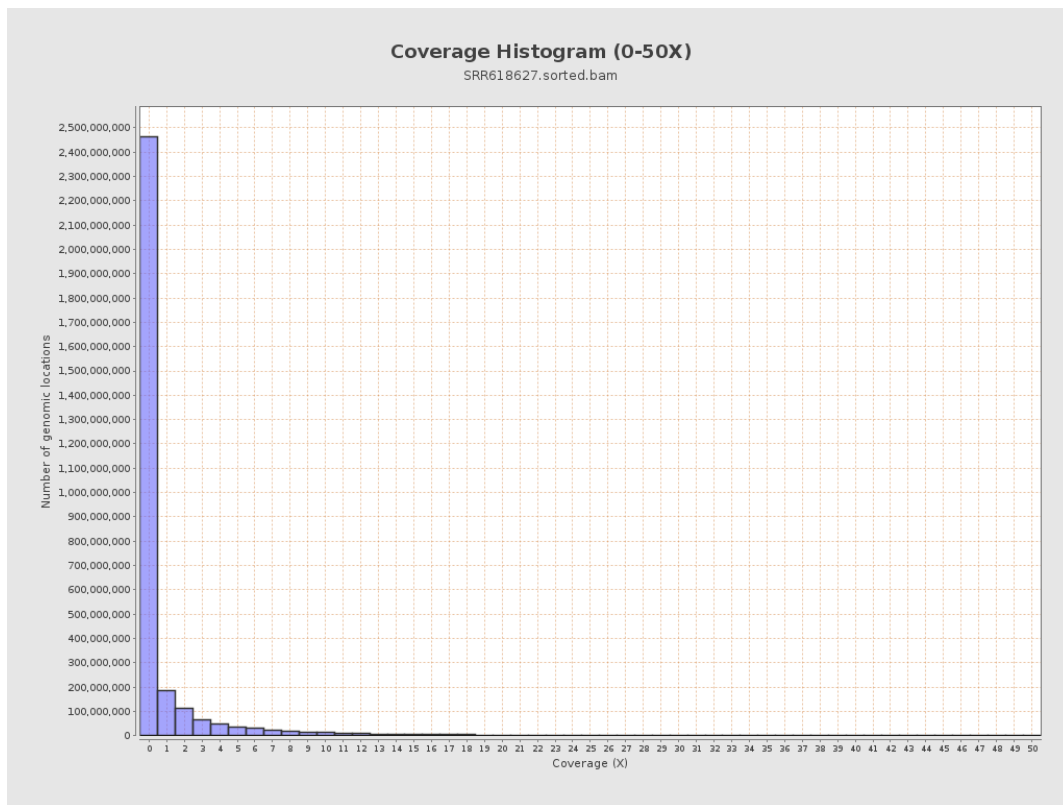
3. Results : Coverage across reference



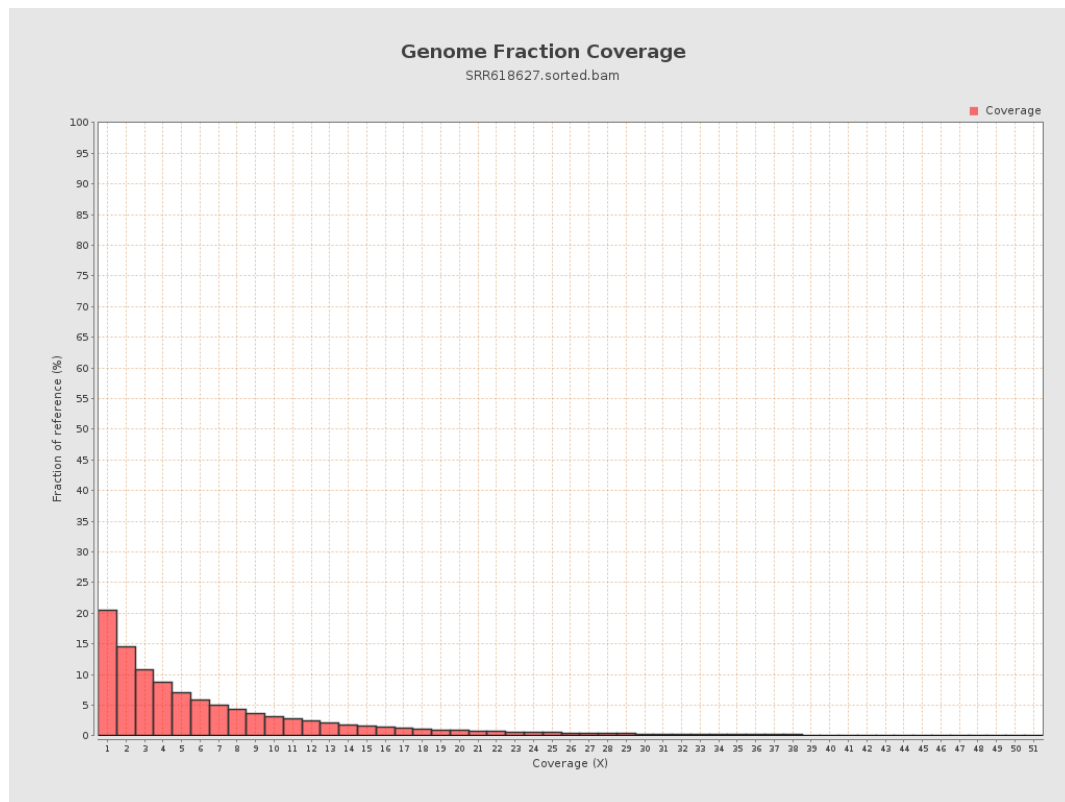
4. Results : Coverage Histogram



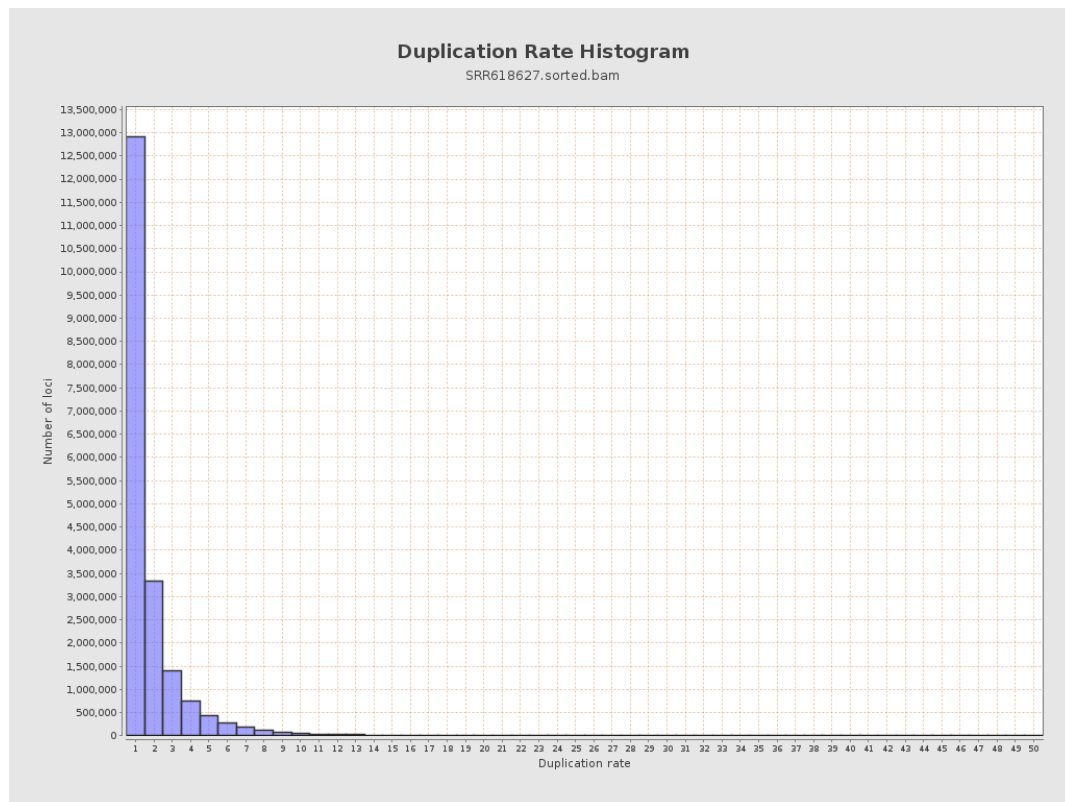
5. Results : Coverage Histogram (0-50X)



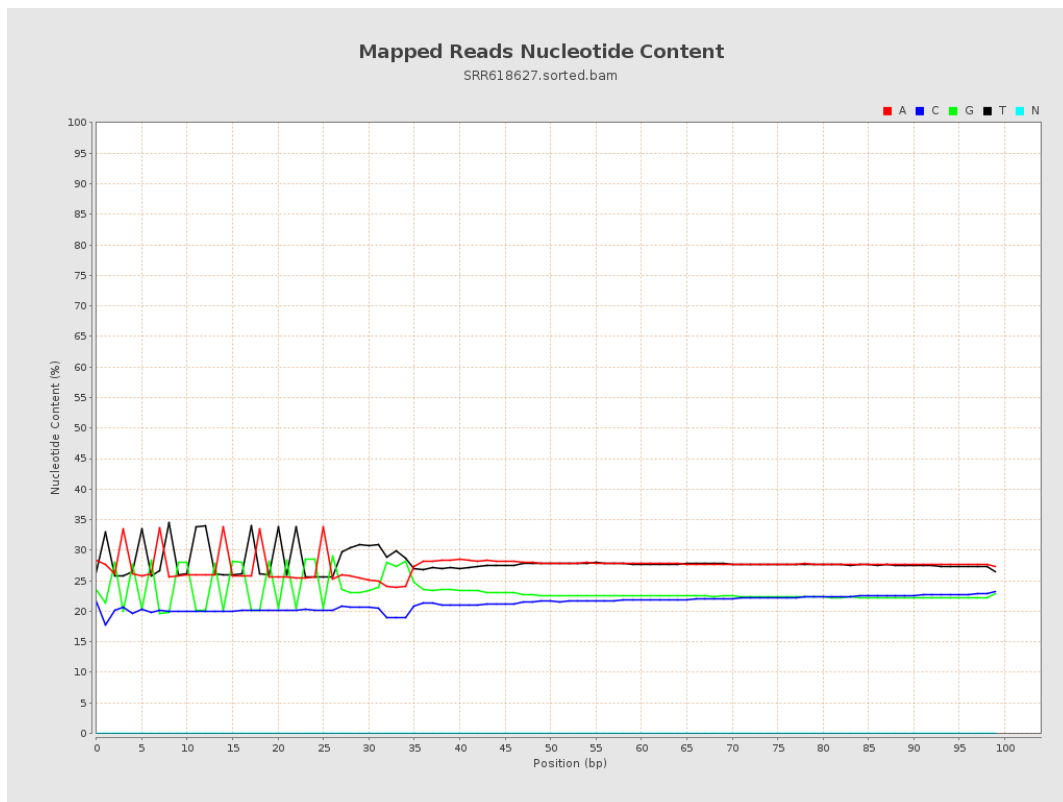
6. Results : Genome Fraction Coverage



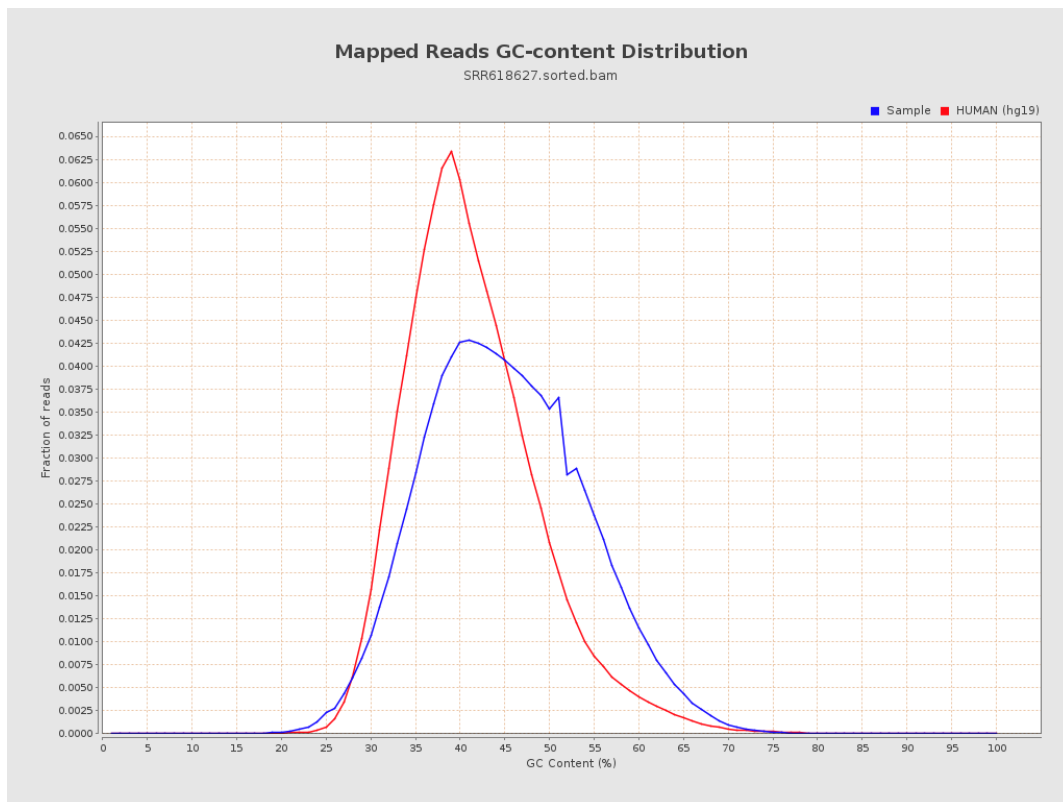
7. Results : Duplication Rate Histogram



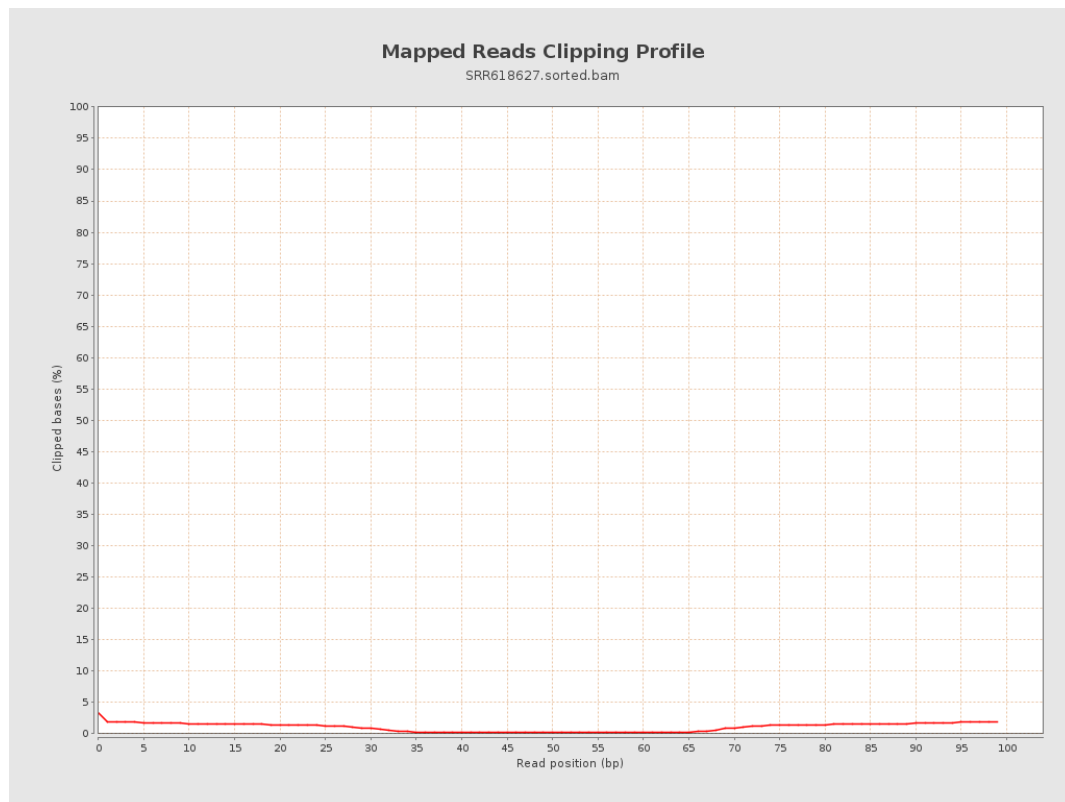
8. Results : Mapped Reads Nucleotide Content



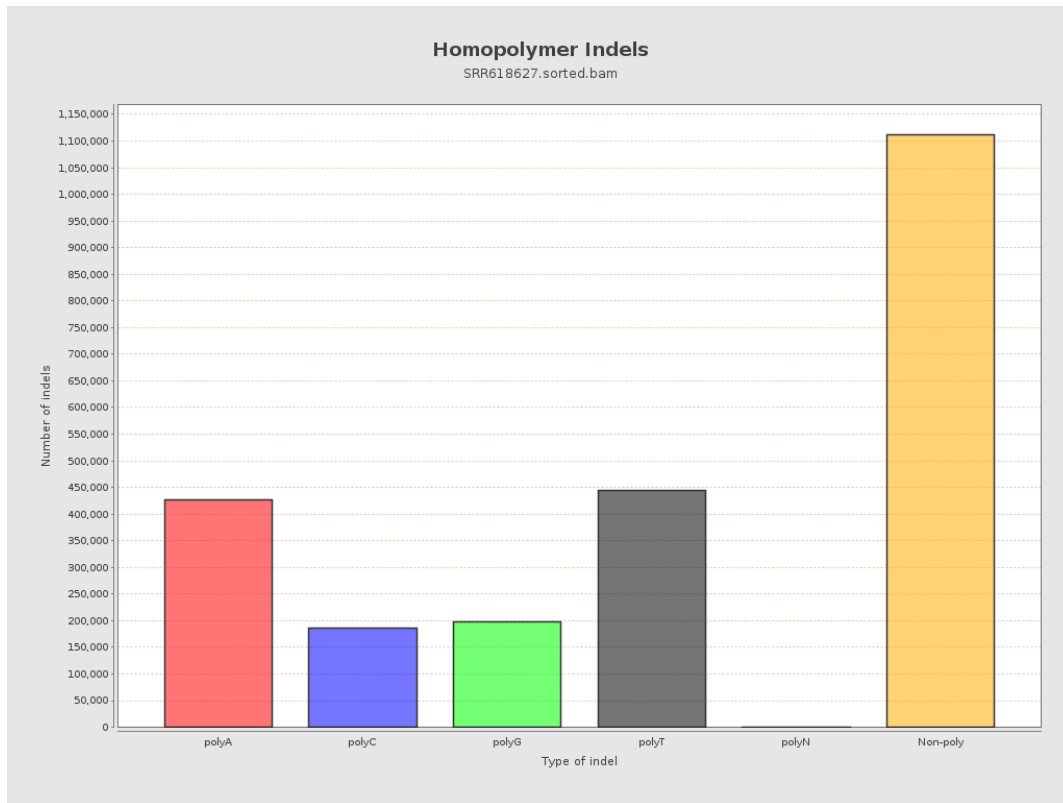
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



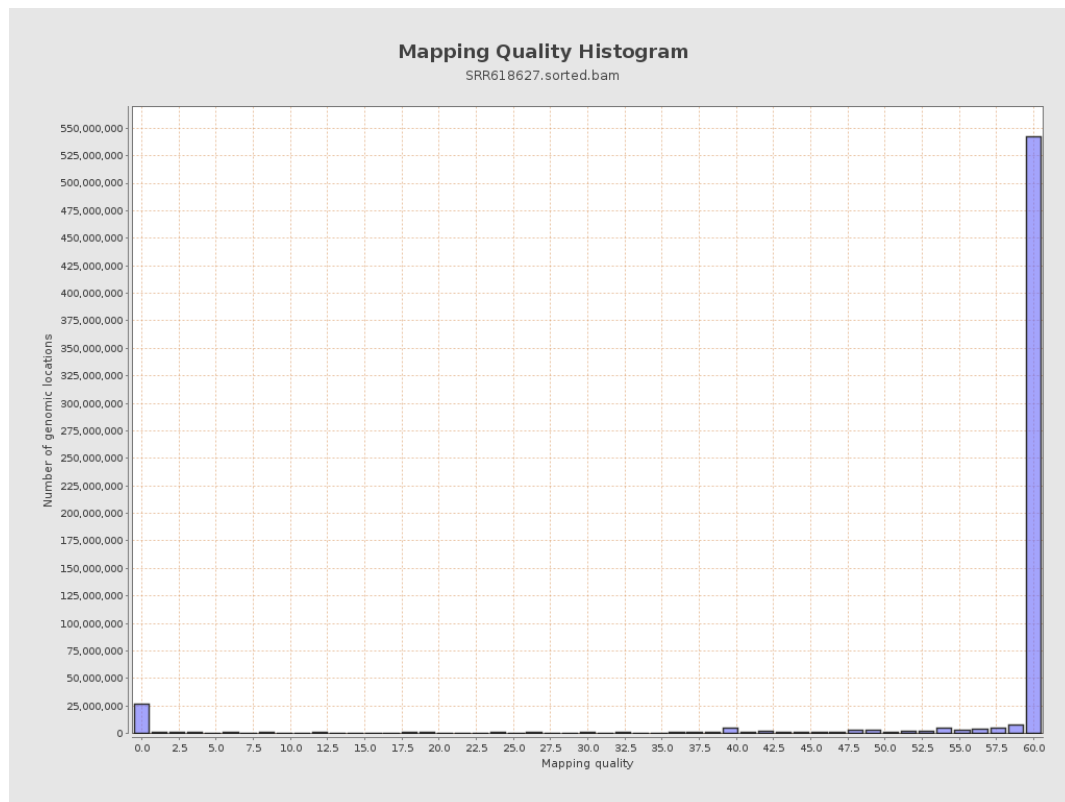
11. Results : Homopolymer Indels



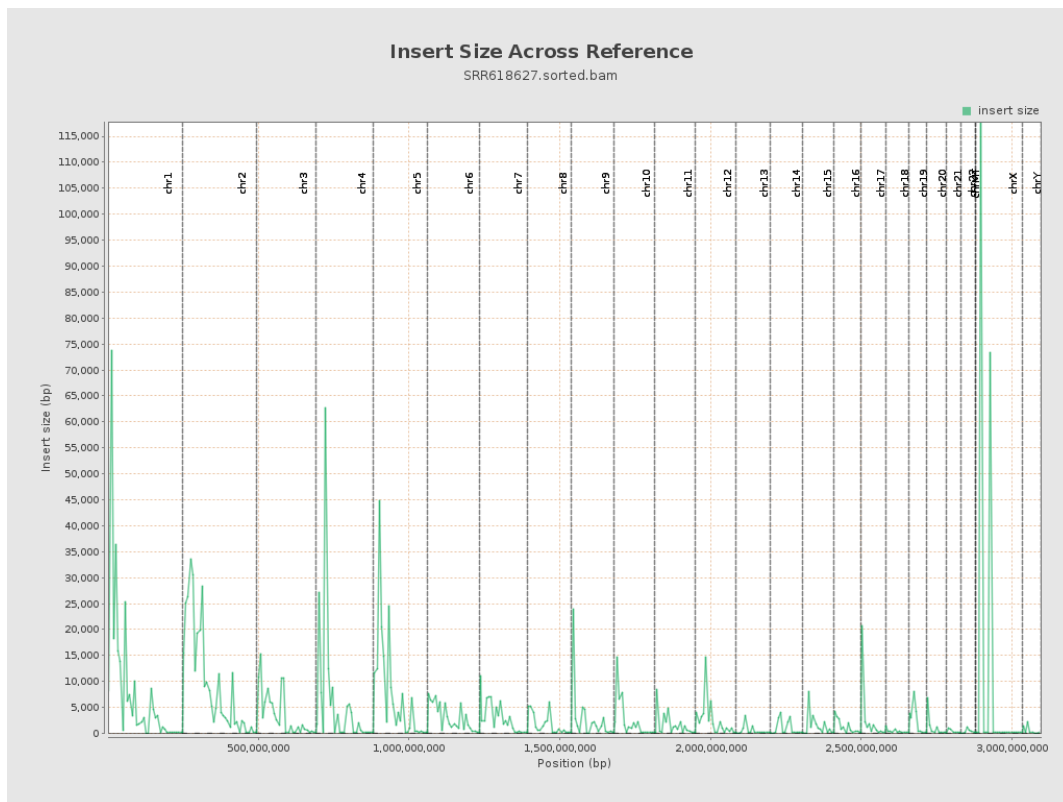
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

