

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 07:51:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618612.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_SRR618612 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618612_1.fastq.gz SRR618612_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 07:51:41 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618612.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	45,902,432
Mapped reads	42,965,428 / 93.6%
Unmapped reads	2,937,004 / 6.4%
Mapped paired reads	42,965,428 / 93.6%
Mapped reads, first in pair	21,975,555 / 47.87%
Mapped reads, second in pair	20,989,873 / 45.73%
Mapped reads, both in pair	41,229,356 / 89.82%
Mapped reads, singletons	1,736,072 / 3.78%
Secondary alignments	0
Supplementary alignments	289,000 / 0.63%
Read min/max/mean length	30 / 100 / 100.26
Duplicated reads (estimated)	16,025,817 / 34.91%
Duplication rate	29.22%
Clipped reads	10,997,228 / 23.96%

2.2. ACGT Content

Number/percentage of A's	1,085,757,010 / 27.09%
Number/percentage of C's	878,625,340 / 21.92%
Number/percentage of T's	1,106,462,047 / 27.61%
Number/percentage of G's	935,324,772 / 23.34%
Number/percentage of N's	1,824,506 / 0.05%

GC Percentage	45.26%
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2.3. Coverage

Mean	1.2956
Standard Deviation	5.5399

2.4. Mapping Quality

Mean Mapping Quality	51.88
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2.5. Insert size

Mean	150,371.32
Standard Deviation	3,884,857.46
P25/Median/P75	178 / 206 / 242

2.6. Mismatches and indels

General error rate	1.38%
Mismatches	54,065,850
Insertions	760,989
Mapped reads with at least one insertion	1.74%
Deletions	2,060,491
Mapped reads with at least one deletion	4.67%
Homopolymer indels	52.35%

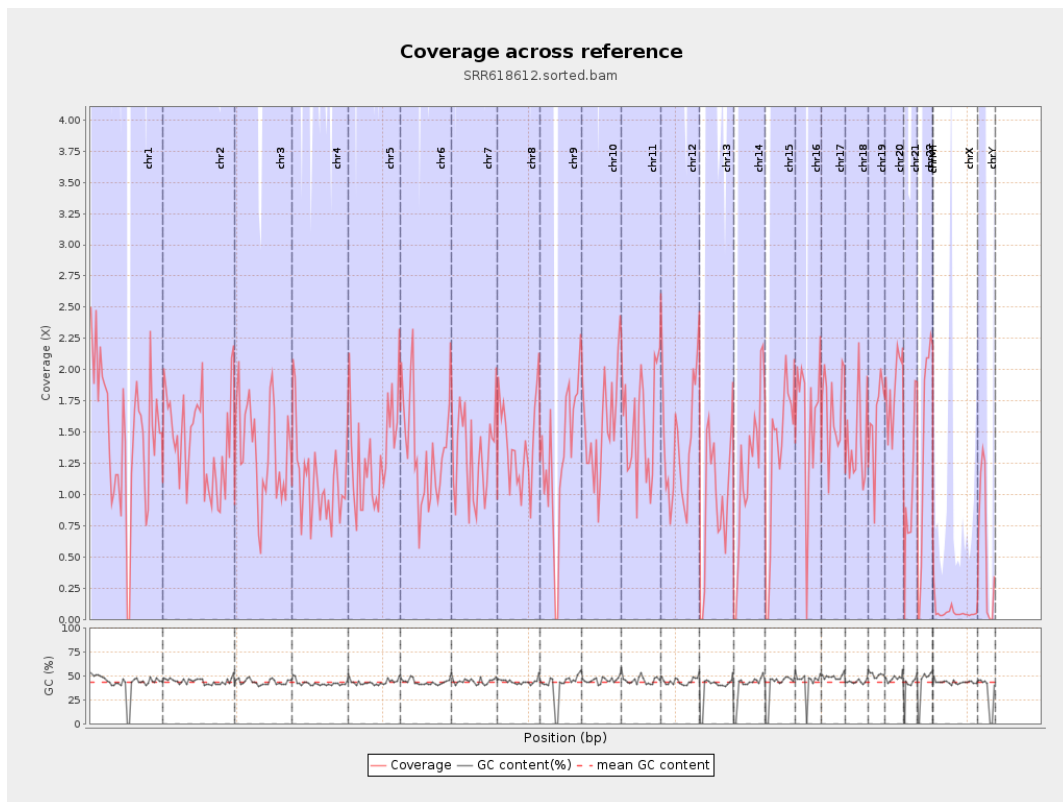
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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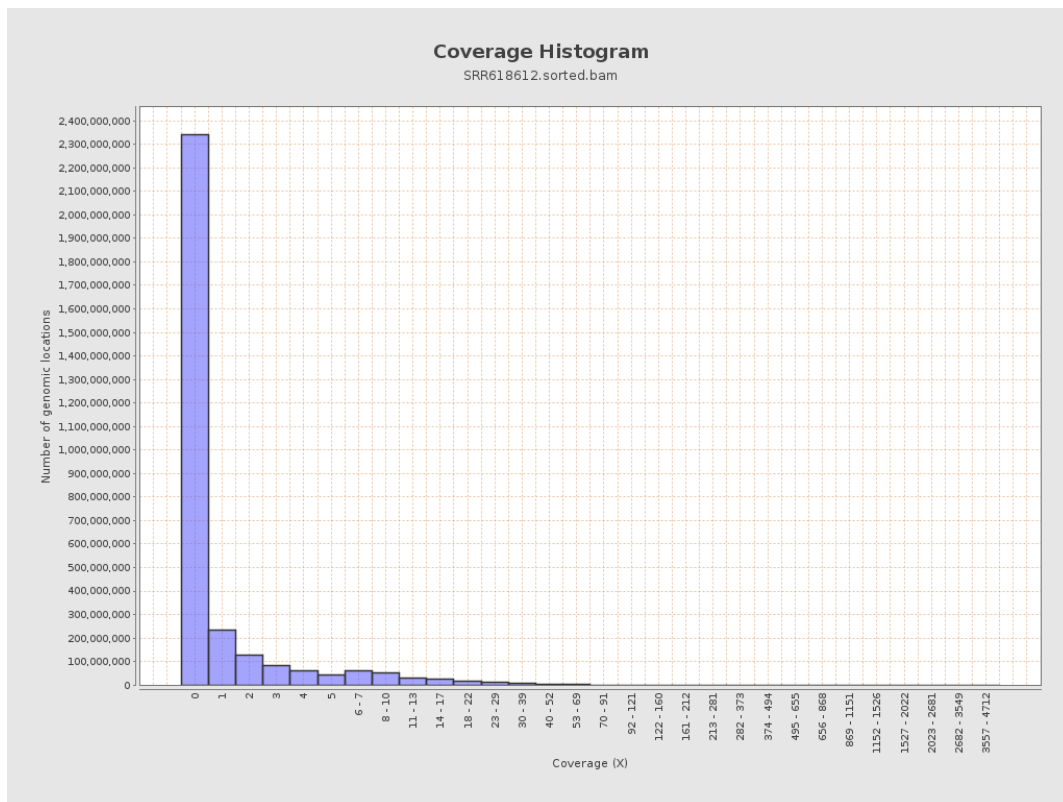
		bases	coverage	deviation
chr1	249250621	367100202	1.4728	7.3027
chr2	243199373	346819862	1.4261	6.3291
chr3	198022430	266413638	1.3454	5.1618
chr4	191154276	212011063	1.1091	4.5374
chr5	180915260	239606428	1.3244	4.6644
chr6	171115067	229172050	1.3393	4.64
chr7	159138663	210615425	1.3235	5.1061
chr8	146364022	205404491	1.4034	4.8829
chr9	141213431	183594155	1.3001	6.3435
chr10	135534747	208173922	1.5359	5.0496
chr11	135006516	211145409	1.564	5.9151
chr12	133851895	188565576	1.4088	5.1073
chr13	115169878	110593336	0.9603	3.6468
chr14	107349540	128671404	1.1986	4.6738
chr15	102531392	135108990	1.3177	4.9155
chr16	90354753	144284159	1.5969	9.0712
chr17	81195210	135625566	1.6704	5.7013
chr18	78077248	108536892	1.3901	6.5557
chr19	59128983	93966136	1.5892	7.0974
chr20	63025520	116327791	1.8457	5.6615
chr21	48129895	51097335	1.0617	6.6823
chr22	51304566	72652595	1.4161	5.6397
chrMT	16571	10999	0.6637	3.0114
chrX	155270560	8977048	0.0578	1.3646

chrY	59373566	36347607	0.6122	3.9564
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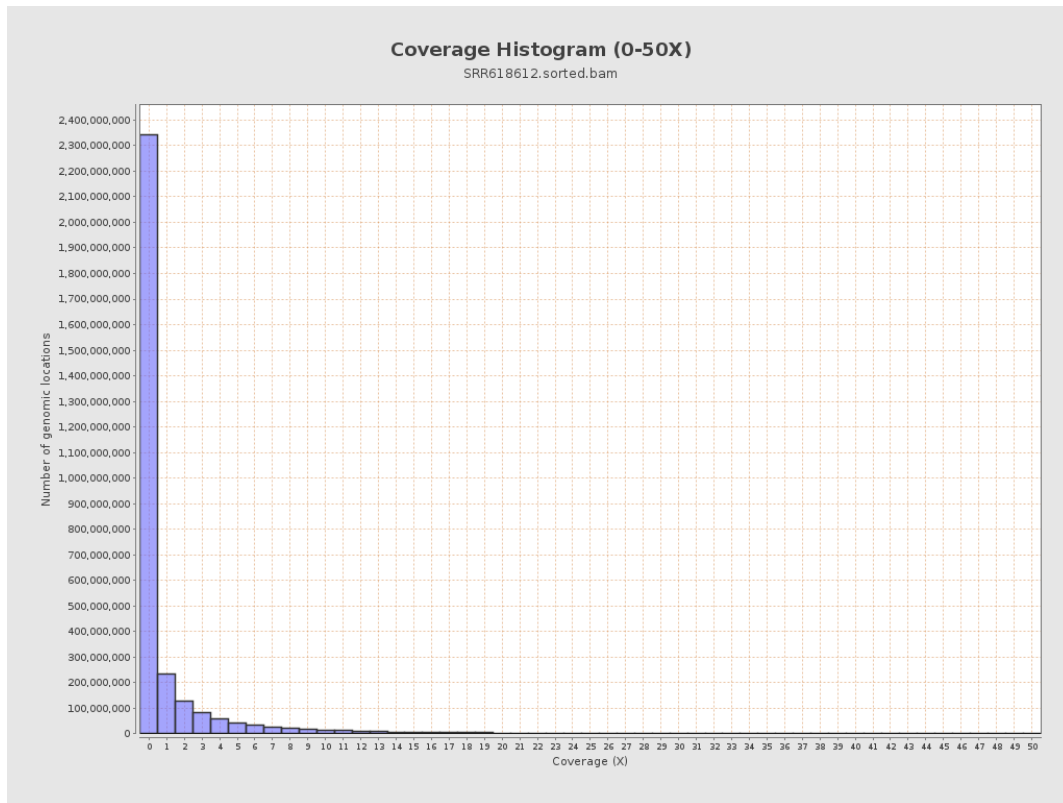
3. Results : Coverage across reference



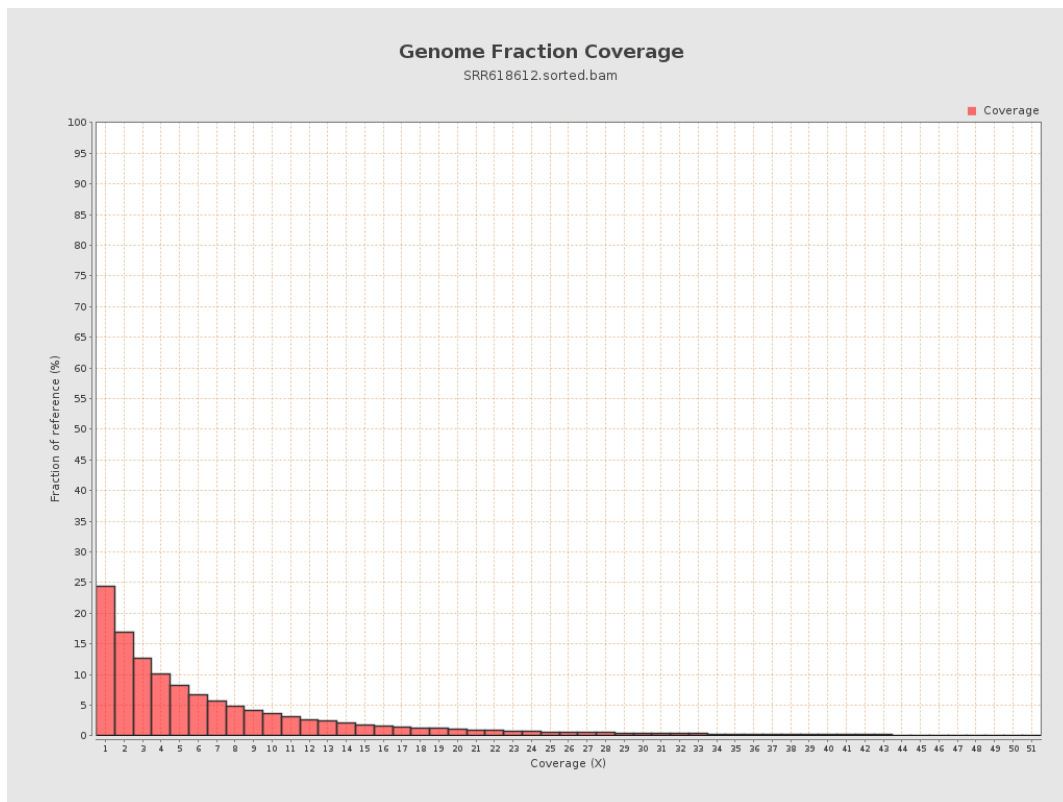
4. Results : Coverage Histogram



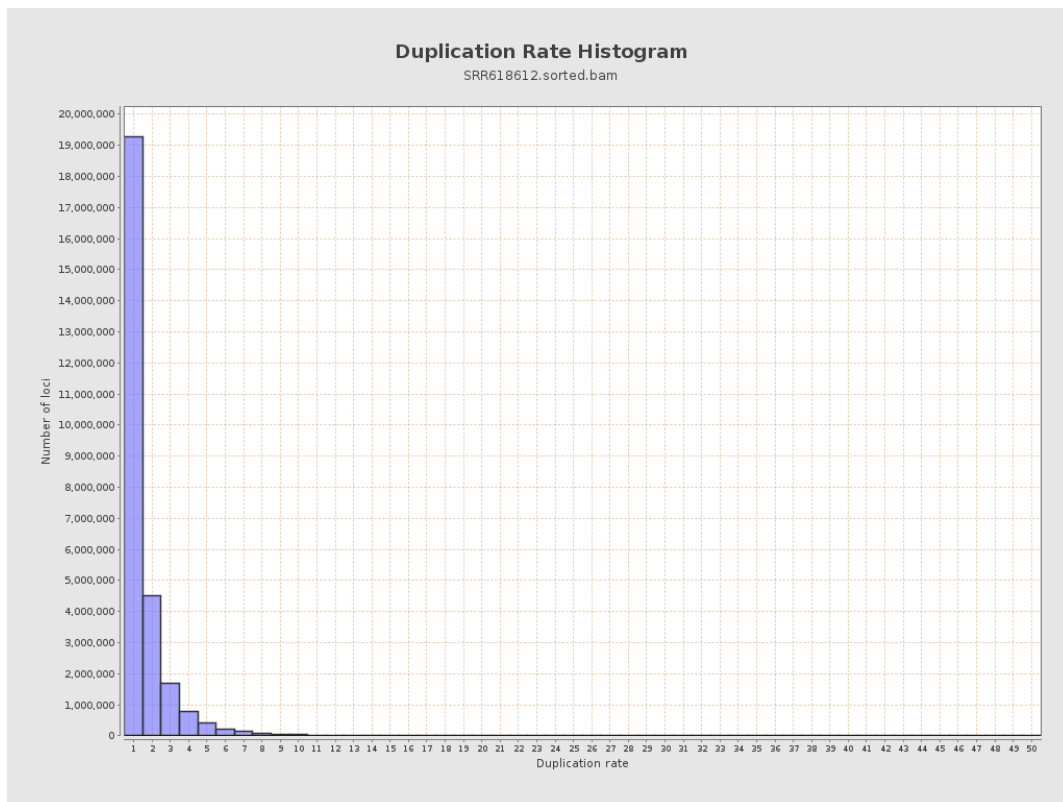
5. Results : Coverage Histogram (0-50X)



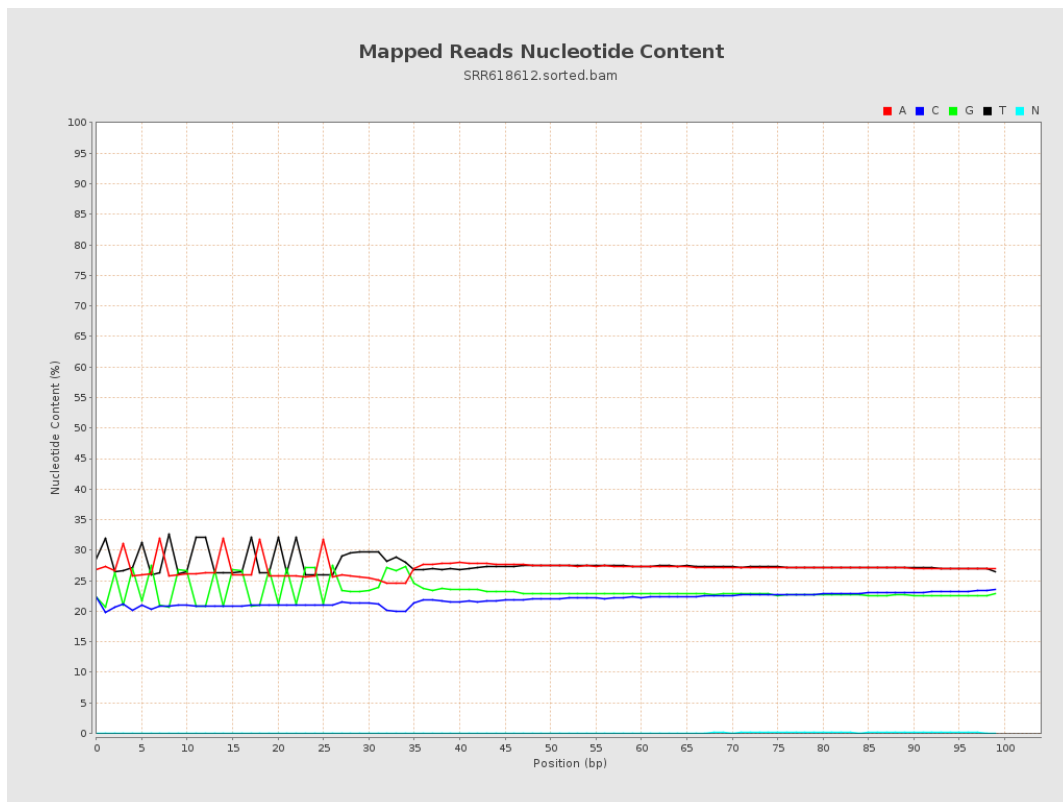
6. Results : Genome Fraction Coverage



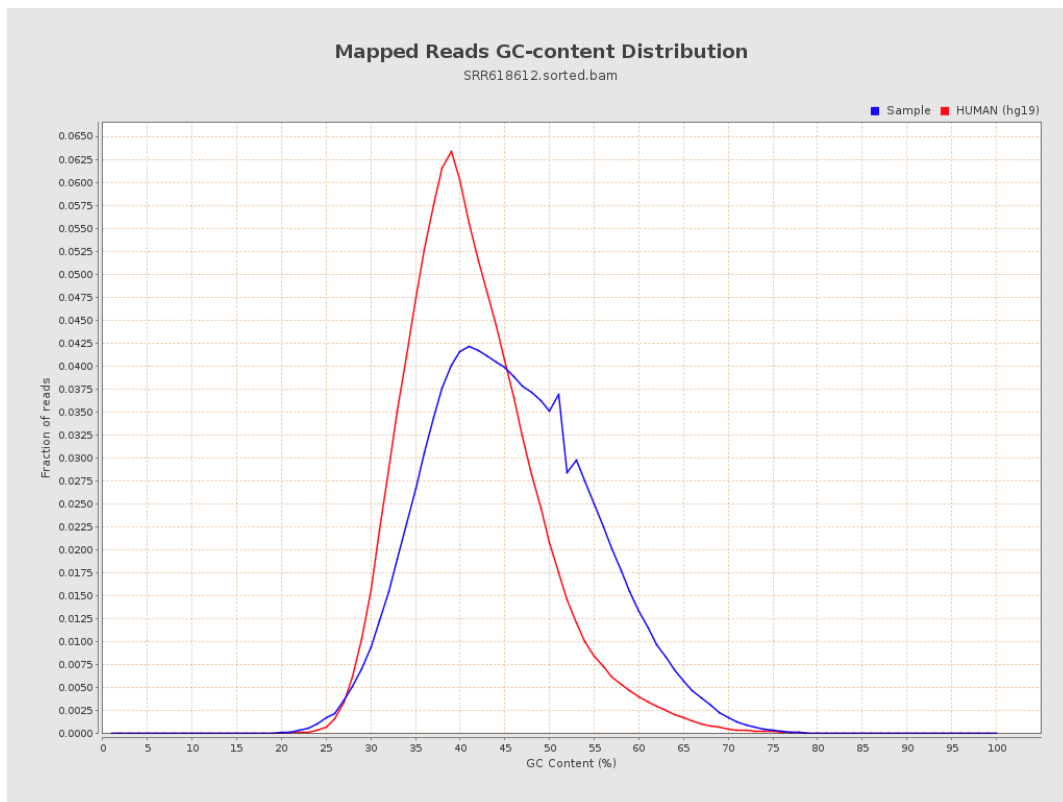
7. Results : Duplication Rate Histogram



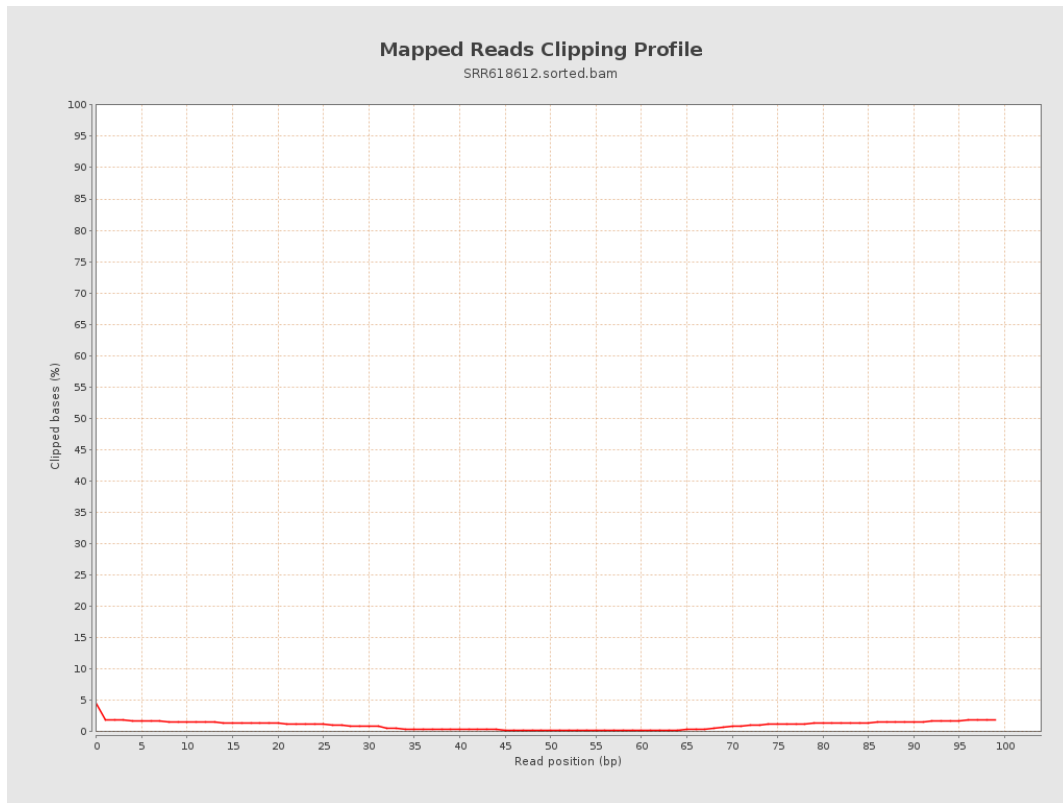
8. Results : Mapped Reads Nucleotide Content



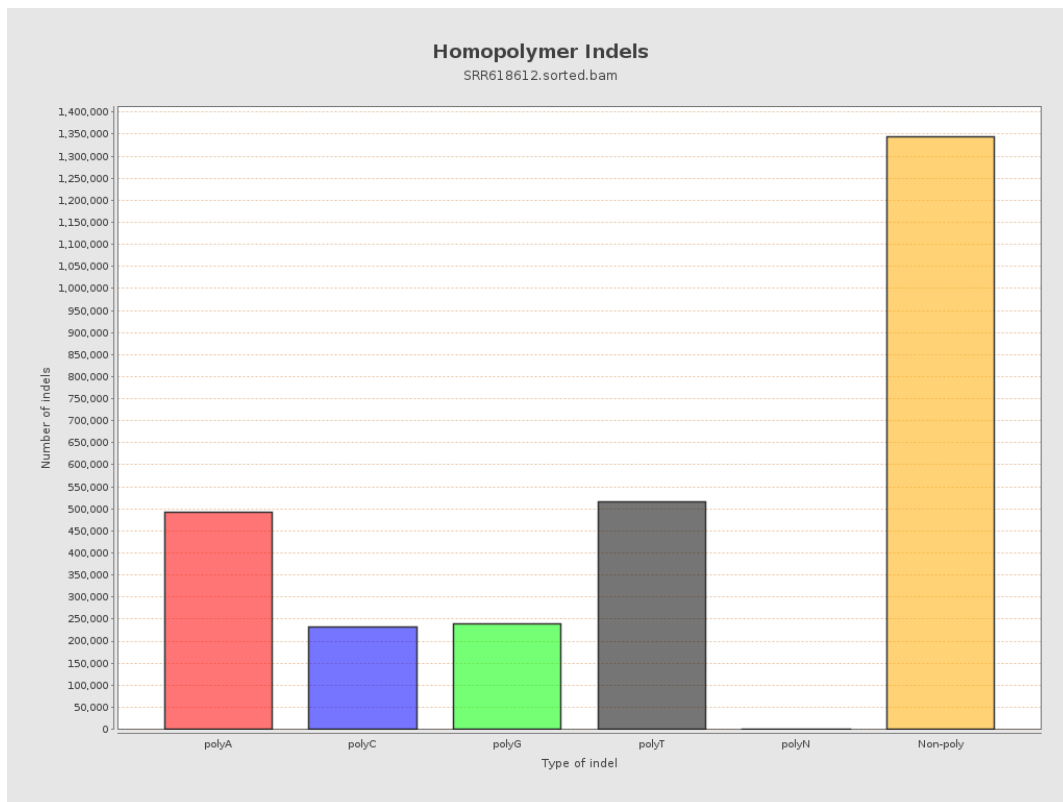
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



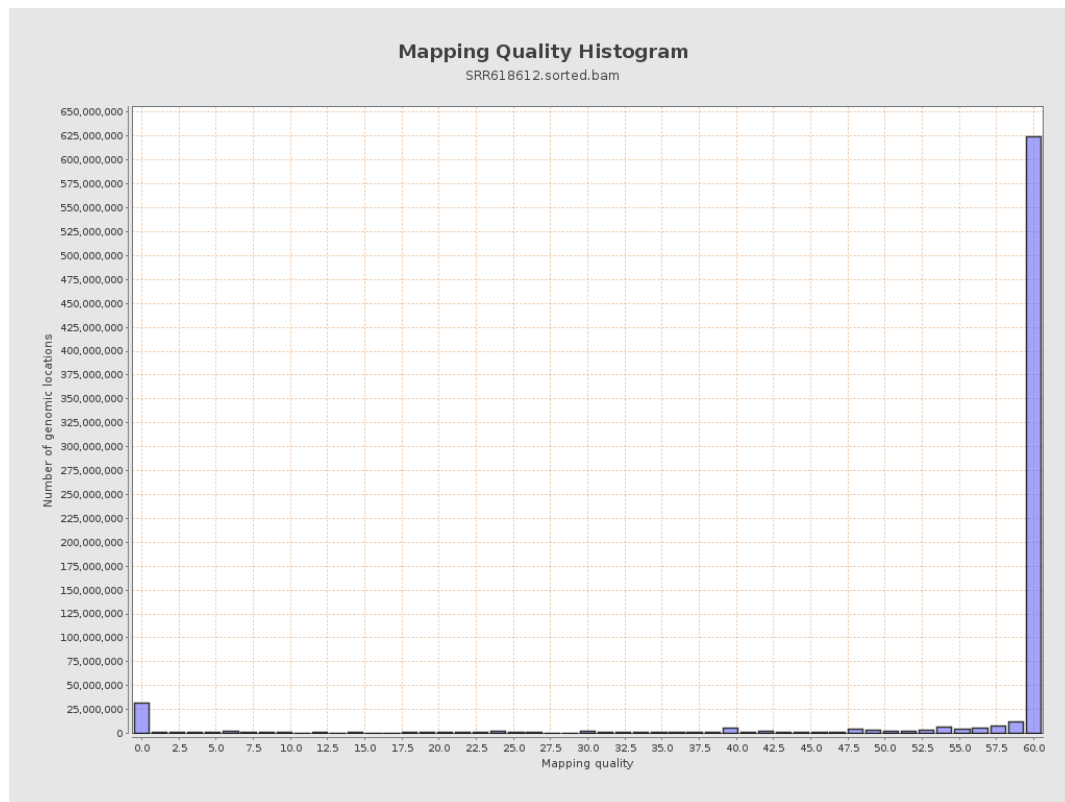
11. Results : Homopolymer Indels



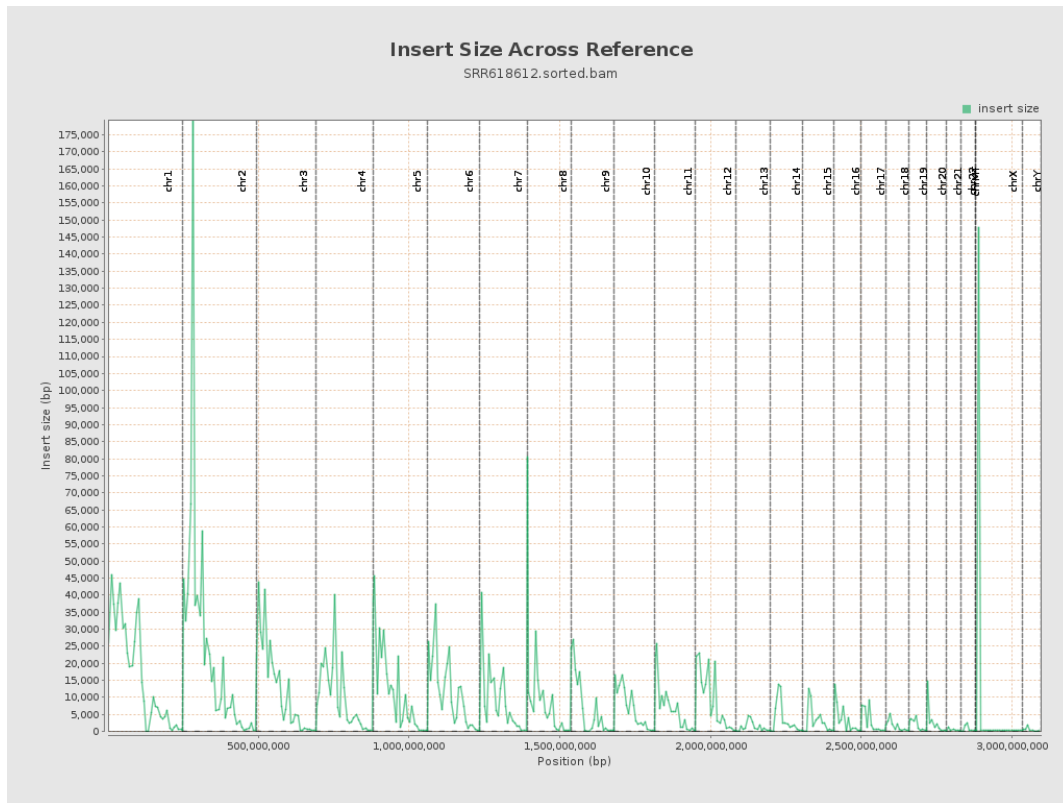
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

