

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 08:29:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618613.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_SRR618613 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618613_1.fastq.gz SRR618613_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 08:29:17 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618613.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	35,278,780
Mapped reads	33,237,447 / 94.21%
Unmapped reads	2,041,333 / 5.79%
Mapped paired reads	33,237,447 / 94.21%
Mapped reads, first in pair	16,763,503 / 47.52%
Mapped reads, second in pair	16,473,944 / 46.7%
Mapped reads, both in pair	32,626,106 / 92.48%
Mapped reads, singletons	611,341 / 1.73%
Secondary alignments	0
Supplementary alignments	63,753 / 0.18%
Read min/max/mean length	30 / 100 / 100.07
Duplicated reads (estimated)	7,877,000 / 22.33%
Duplication rate	20.87%
Clipped reads	5,830,542 / 16.53%

2.2. ACGT Content

Number/percentage of A's	855,454,182 / 26.98%
Number/percentage of C's	705,887,860 / 22.26%
Number/percentage of T's	861,683,550 / 27.17%
Number/percentage of G's	747,791,306 / 23.58%
Number/percentage of N's	254,324 / 0.01%

GC Percentage	45.84%
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2.3. Coverage

Mean	1.0251
Standard Deviation	4.6485

2.4. Mapping Quality

Mean Mapping Quality	52.52
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2.5. Insert size

Mean	38,611.31
Standard Deviation	1,961,234.8
P25/Median/P75	184 / 212 / 249

2.6. Mismatches and indels

General error rate	1.15%
Mismatches	35,645,763
Insertions	554,572
Mapped reads with at least one insertion	1.64%
Deletions	1,579,559
Mapped reads with at least one deletion	4.63%
Homopolymer indels	53.3%

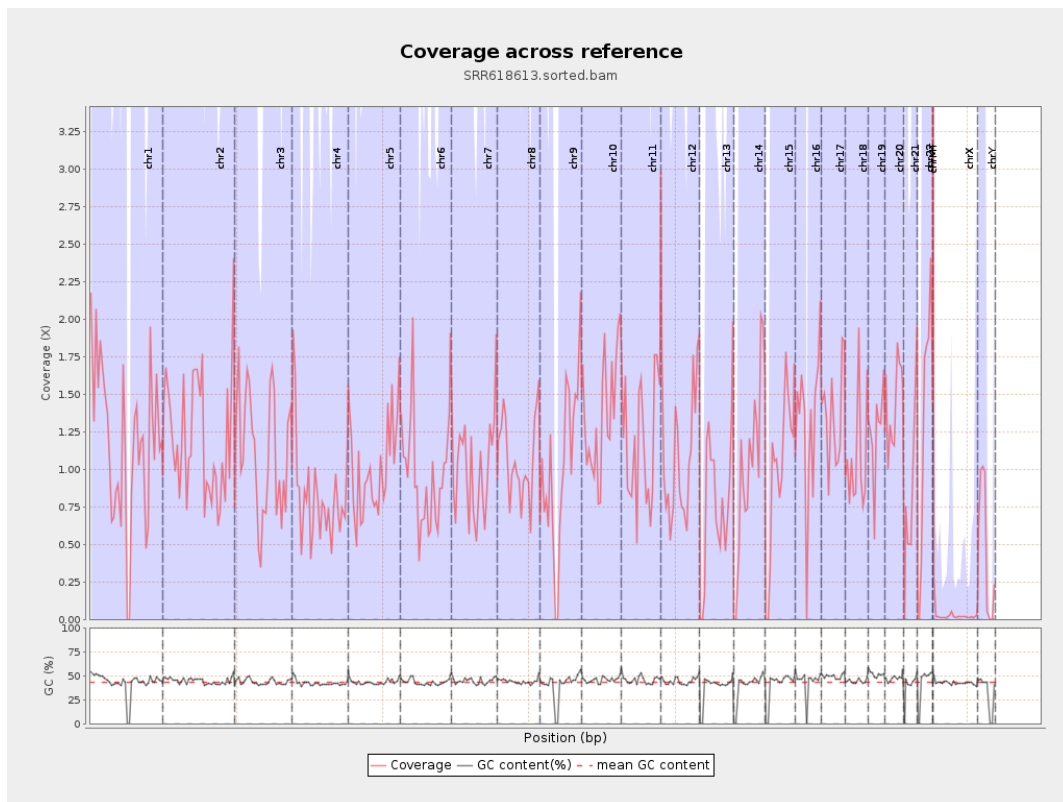
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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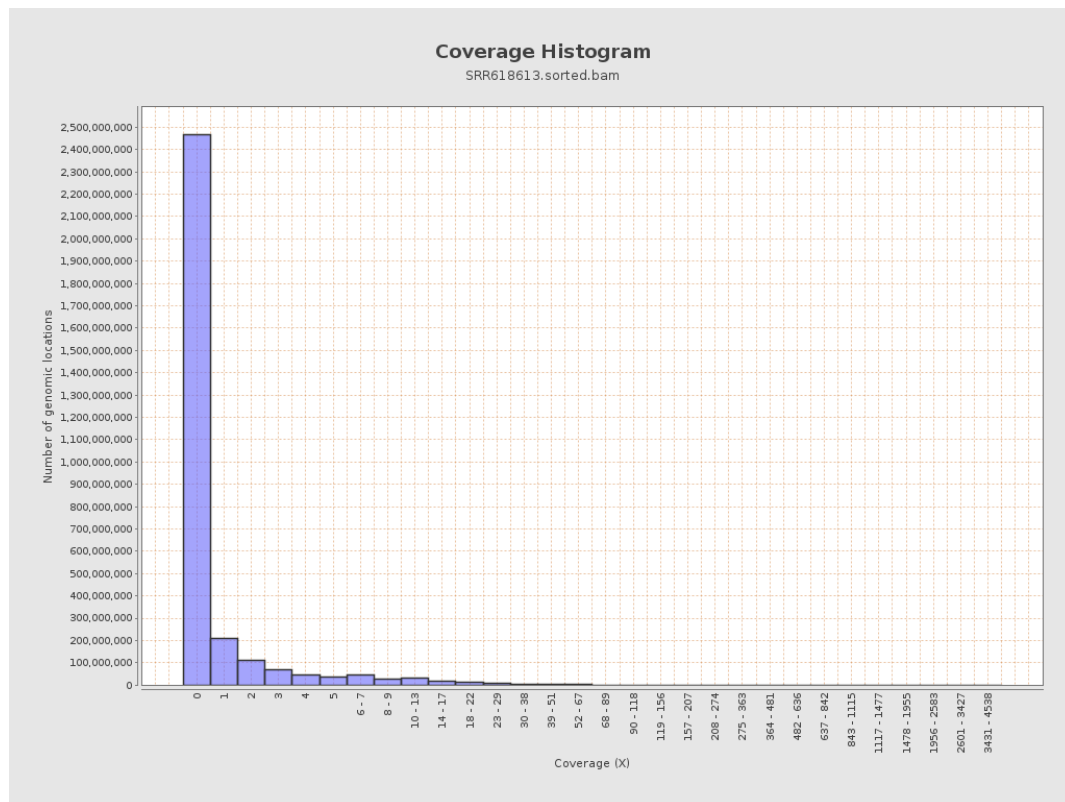
		bases	coverage	deviation
chr1	249250621	292309911	1.1728	4.974
chr2	243199373	292146407	1.2013	5.5188
chr3	198022430	218368251	1.1027	4.0996
chr4	191154276	156197711	0.8171	3.5703
chr5	180915260	183622724	1.015	3.8338
chr6	171115067	164299971	0.9602	3.7419
chr7	159138663	162283971	1.0198	4.0266
chr8	146364022	156647120	1.0703	3.9291
chr9	141213431	143505383	1.0162	4.4825
chr10	135534747	183472862	1.3537	5.5208
chr11	135006516	159347717	1.1803	5.5935
chr12	133851895	146309872	1.0931	4.2978
chr13	115169878	87467660	0.7595	3.1789
chr14	107349540	109518798	1.0202	4.3251
chr15	102531392	102183690	0.9966	4.2997
chr16	90354753	117748849	1.3032	8.8818
chr17	81195210	108853320	1.3406	5.2221
chr18	78077248	81709915	1.0465	4.3426
chr19	59128983	73577676	1.2444	5.4606
chr20	63025520	90633407	1.438	5.0619
chr21	48129895	43044877	0.8943	5.8548
chr22	51304566	66583247	1.2978	5.8168
chrMT	16571	144757	8.7356	37.246
chrX	155270560	4617555	0.0297	0.933

chrY	59373566	28648499	0.4825	3.9728
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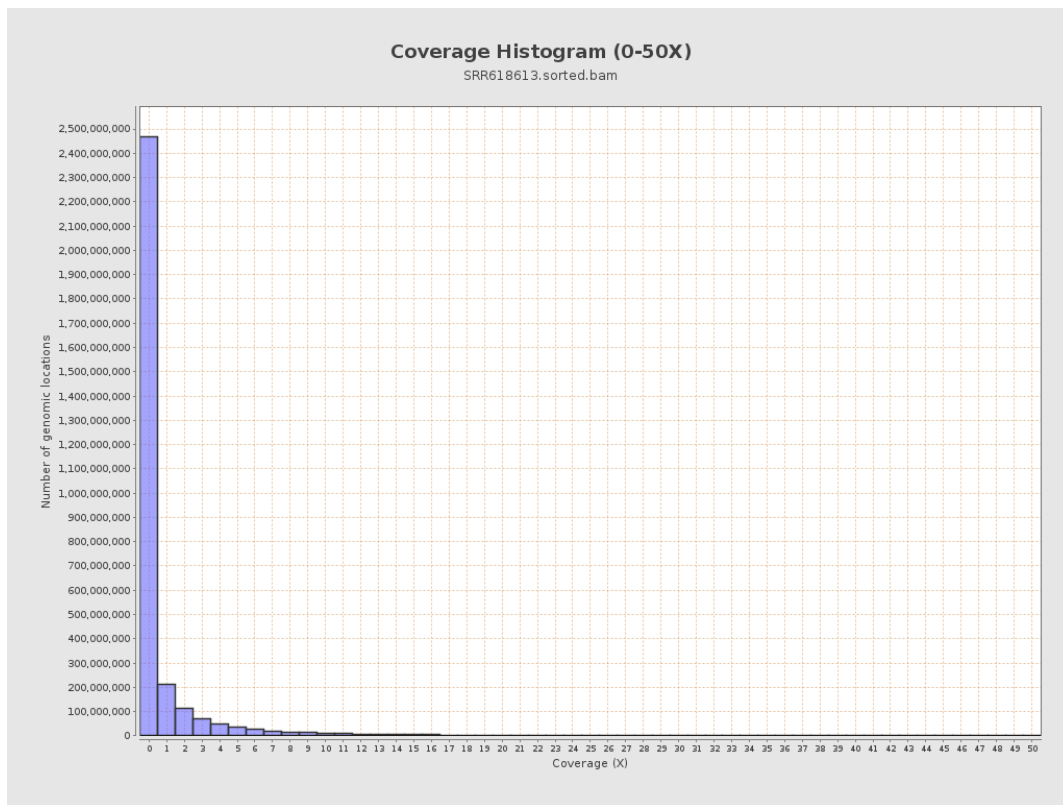
3. Results : Coverage across reference



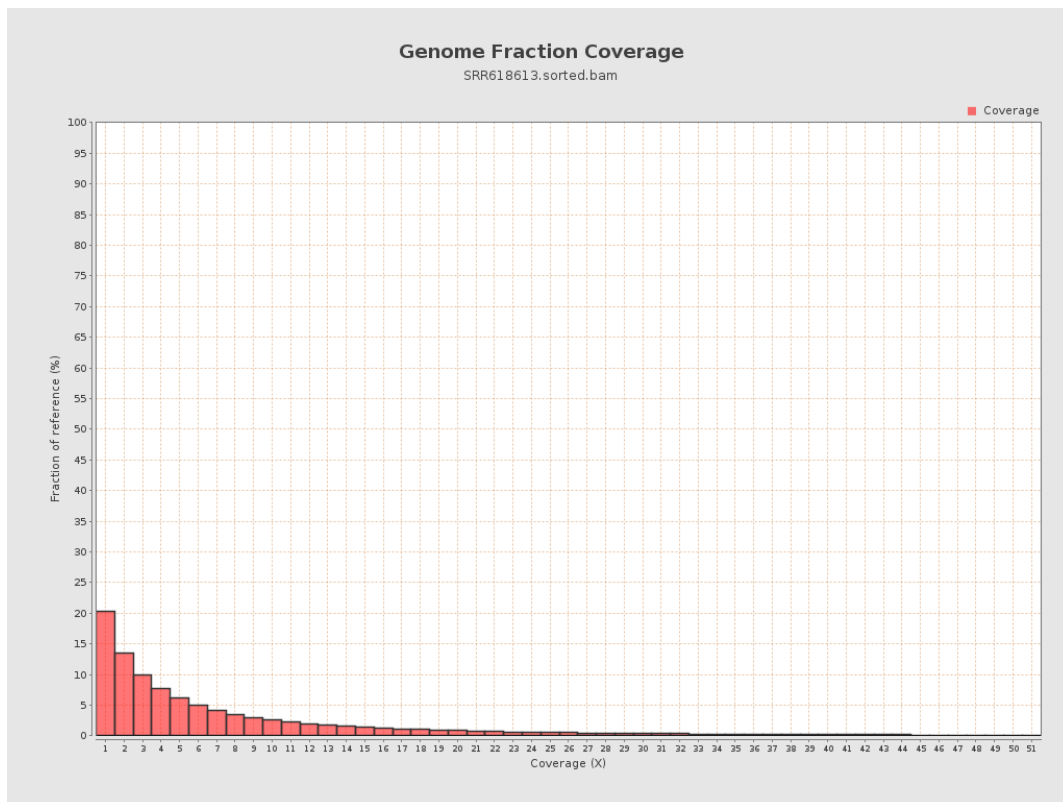
4. Results : Coverage Histogram



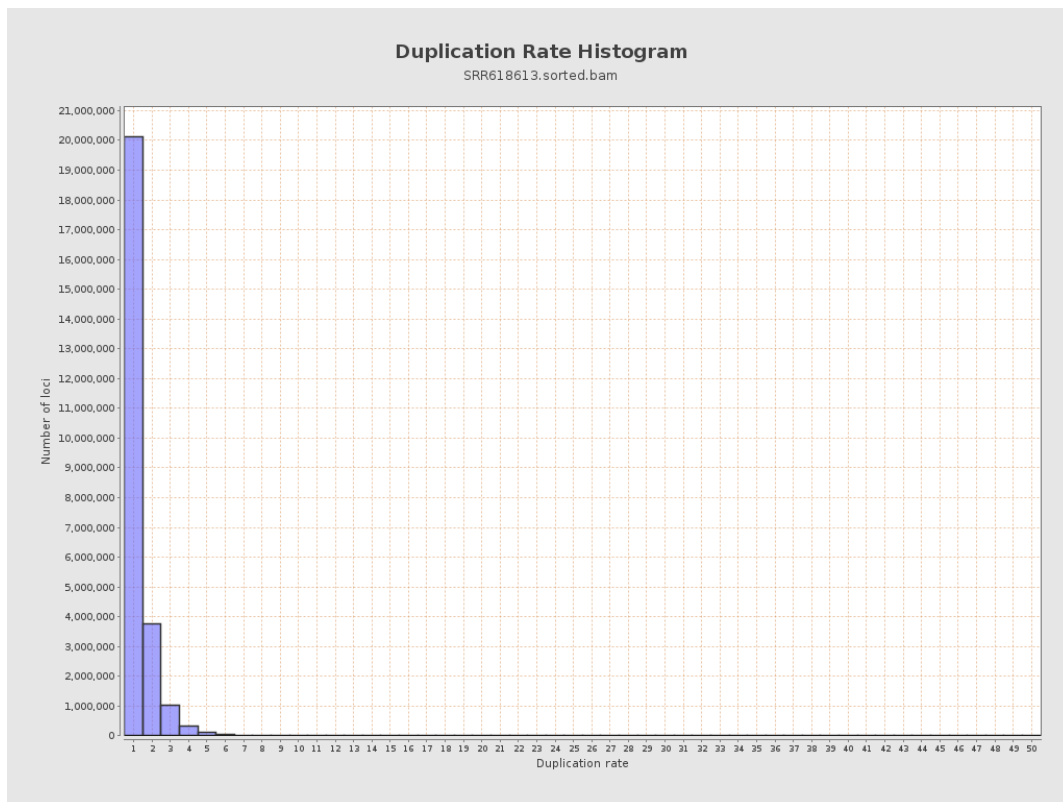
5. Results : Coverage Histogram (0-50X)



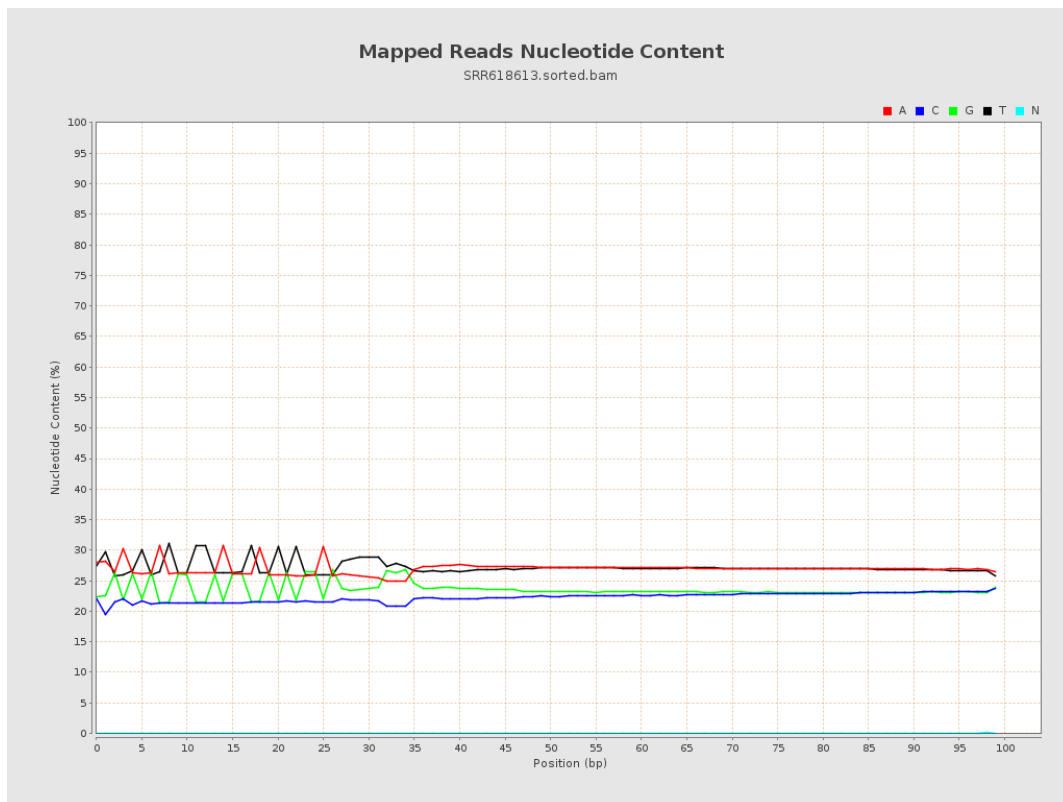
6. Results : Genome Fraction Coverage



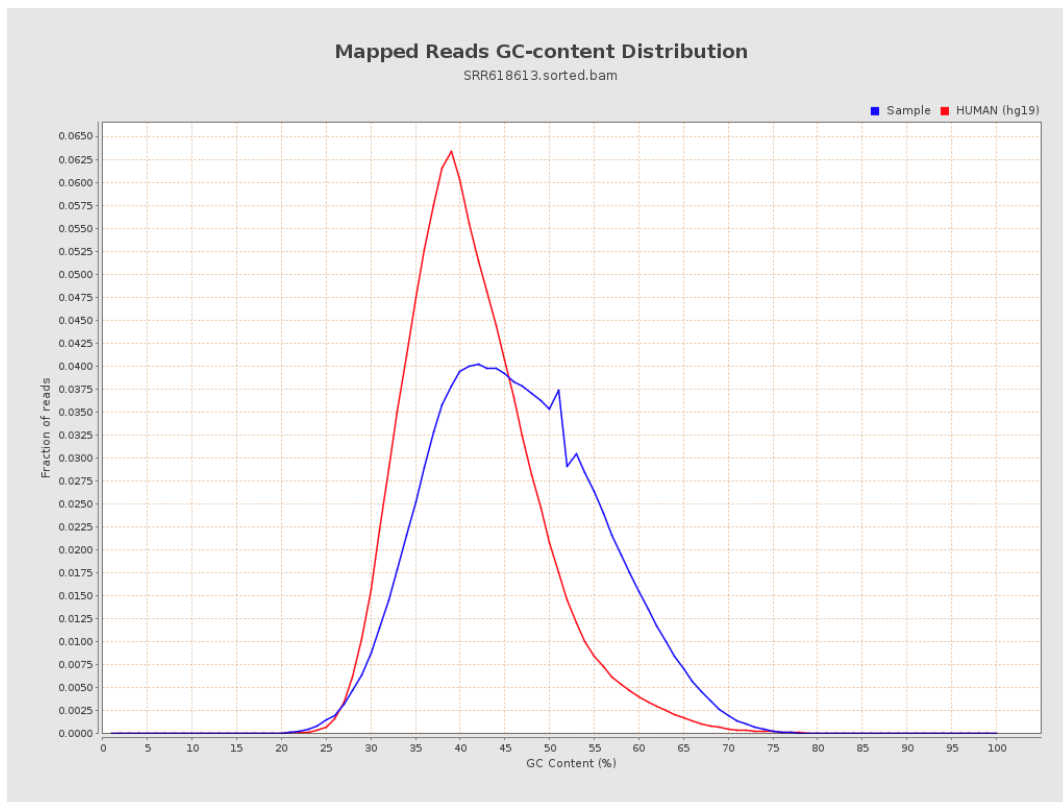
7. Results : Duplication Rate Histogram



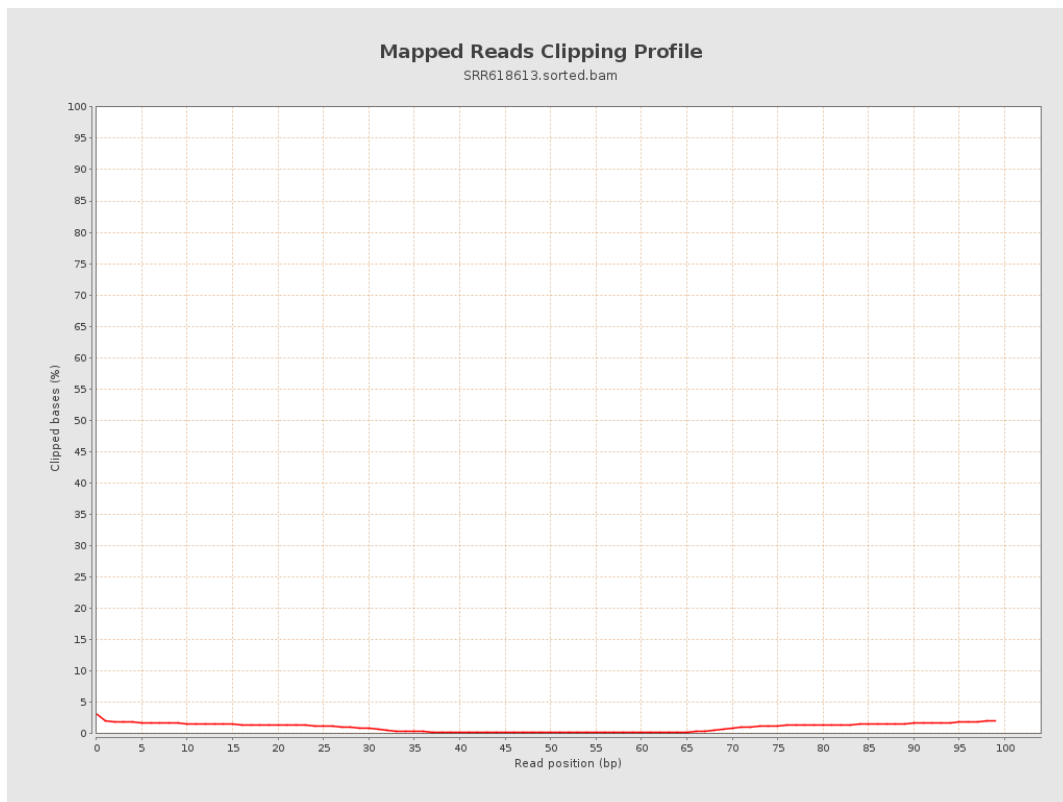
8. Results : Mapped Reads Nucleotide Content



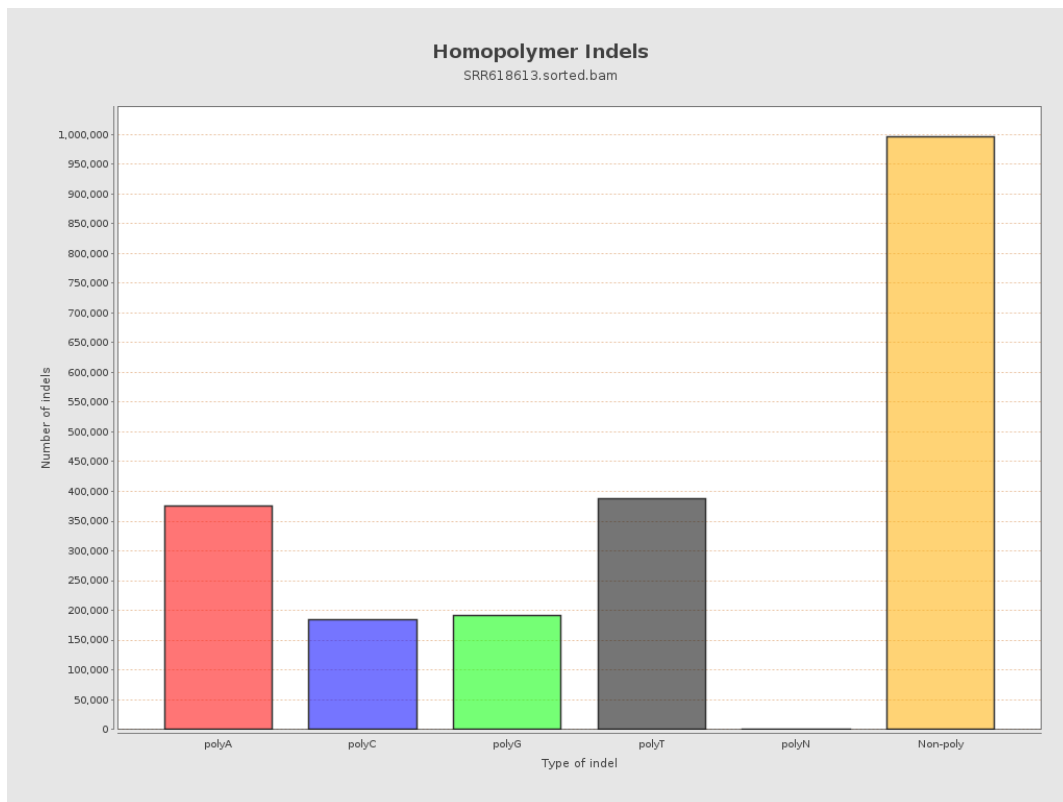
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



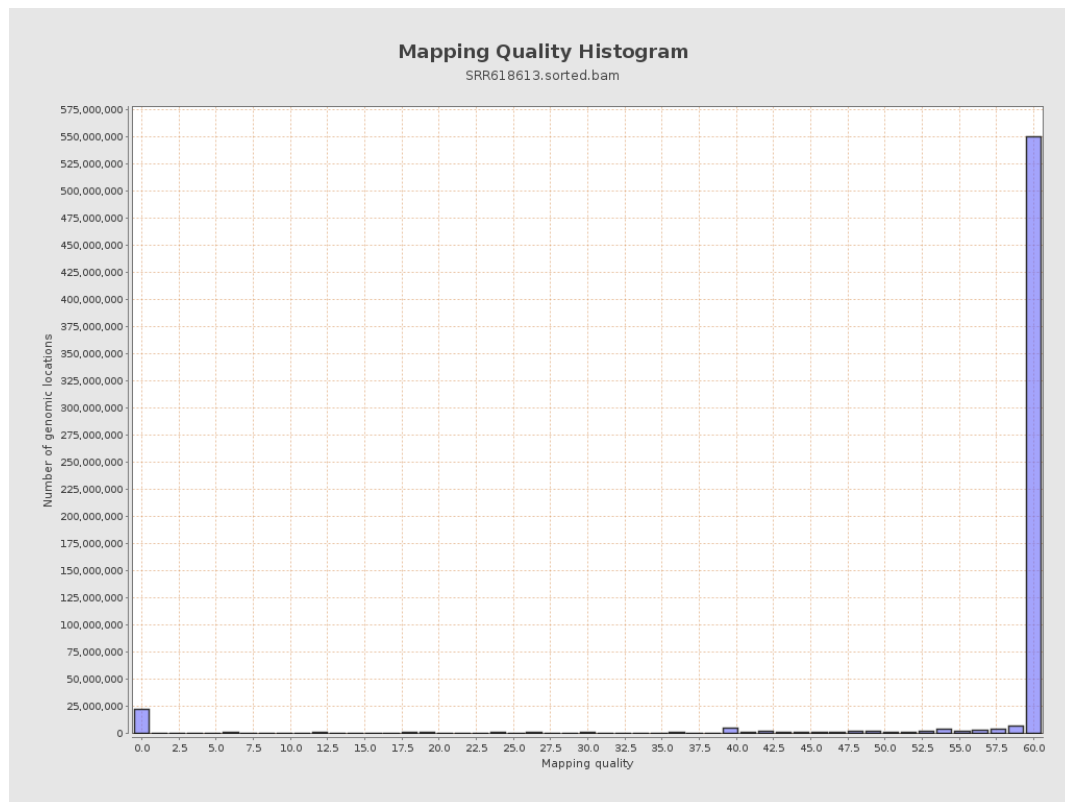
11. Results : Homopolymer Indels



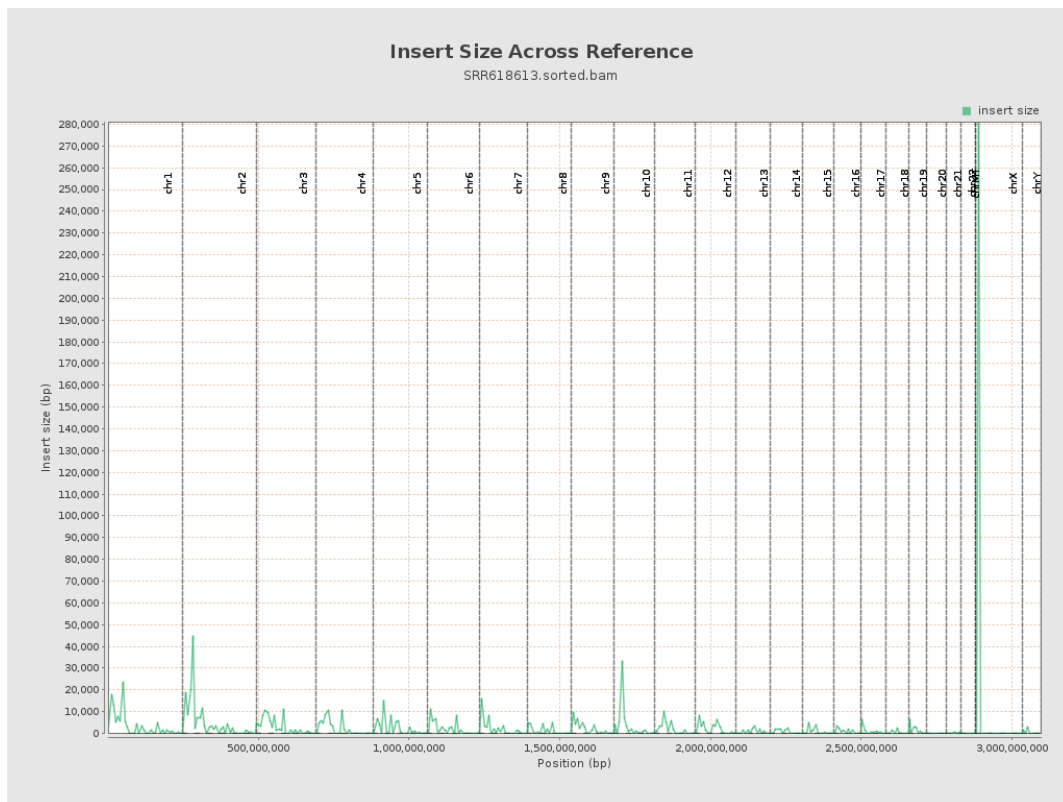
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

