

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 01:20:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618603.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_SRR618603 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618603_1.fastq.gz SRR618603_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 01:20:20 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618603.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	48,398,738
Mapped reads	44,151,328 / 91.22%
Unmapped reads	4,247,410 / 8.78%
Mapped paired reads	44,151,328 / 91.22%
Mapped reads, first in pair	22,633,324 / 46.76%
Mapped reads, second in pair	21,518,004 / 44.46%
Mapped reads, both in pair	42,116,676 / 87.02%
Mapped reads, singletons	2,034,652 / 4.2%
Secondary alignments	0
Supplementary alignments	95,576 / 0.2%
Read min/max/mean length	30 / 100 / 100.08
Duplicated reads (estimated)	14,784,134 / 30.55%
Duplication rate	27.55%
Clipped reads	9,814,814 / 20.28%

2.2. ACGT Content

Number/percentage of A's	1,105,123,140 / 26.61%
Number/percentage of C's	945,713,054 / 22.77%
Number/percentage of T's	1,114,370,931 / 26.83%
Number/percentage of G's	986,374,272 / 23.75%
Number/percentage of N's	1,255,459 / 0.03%

GC Percentage	46.52%
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2.3. Coverage

Mean	1.3424
Standard Deviation	6.2035

2.4. Mapping Quality

Mean Mapping Quality	52.3
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2.5. Insert size

Mean	66,800.16
Standard Deviation	2,636,089.65
P25/Median/P75	195 / 222 / 258

2.6. Mismatches and indels

General error rate	1.46%
Mismatches	59,492,008
Insertions	750,129
Mapped reads with at least one insertion	1.67%
Deletions	2,025,642
Mapped reads with at least one deletion	4.47%
Homopolymer indels	52.3%

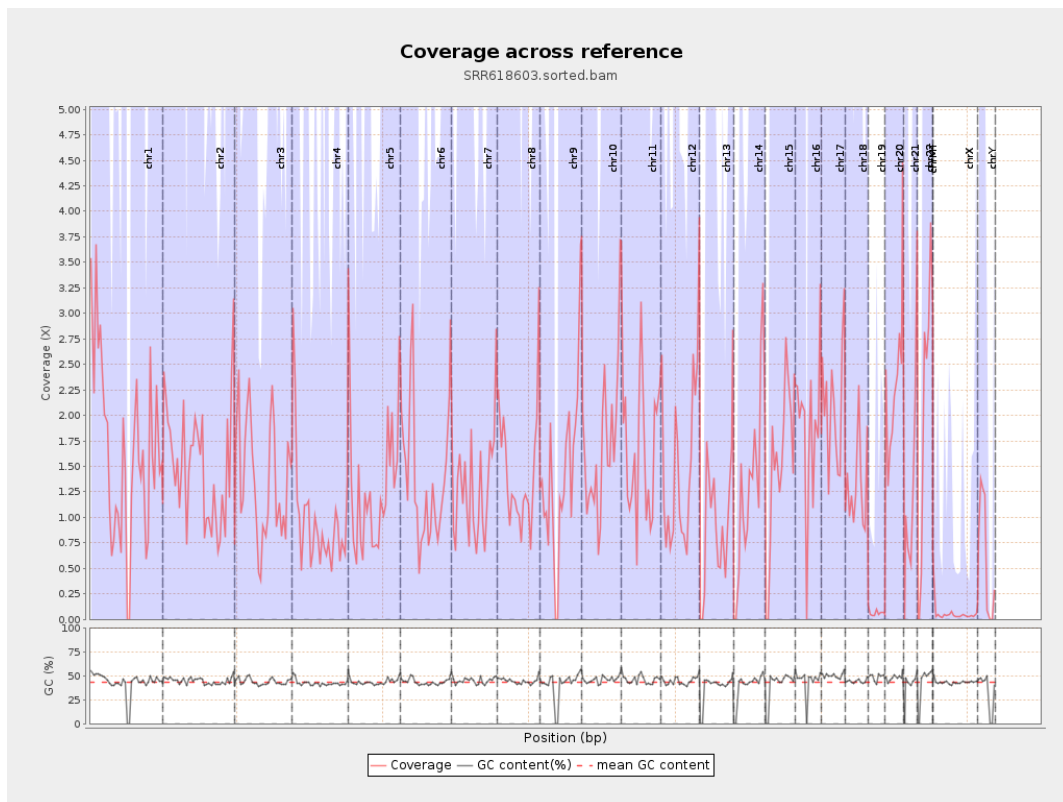
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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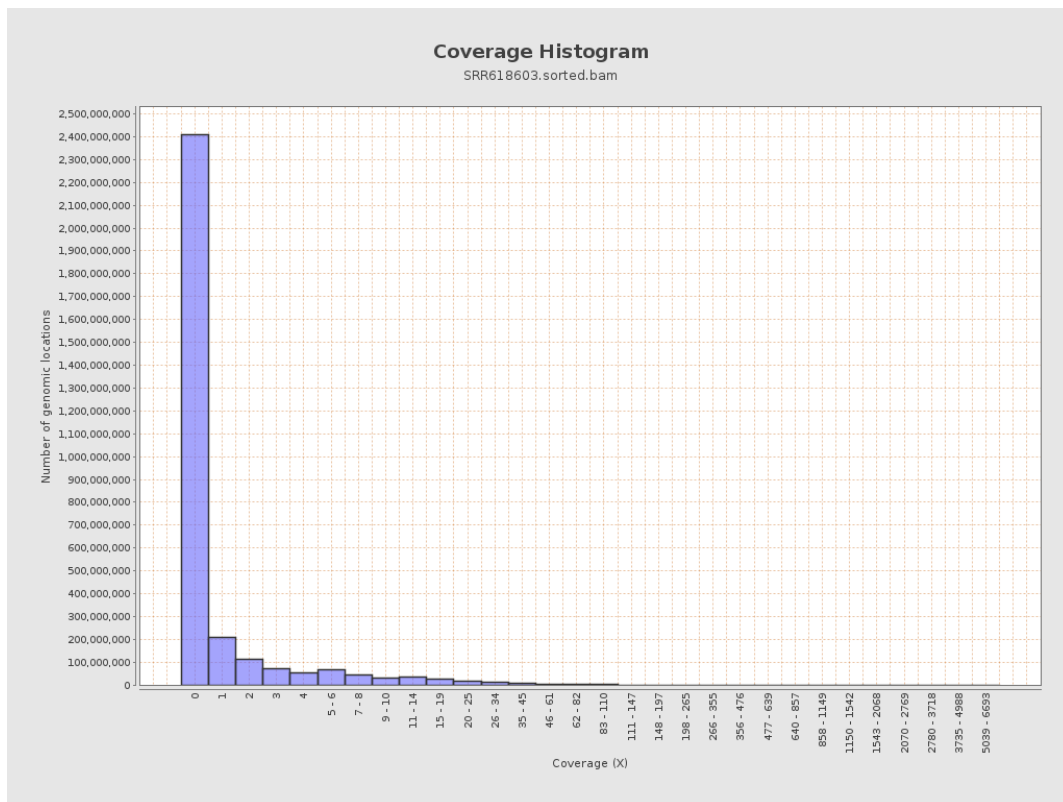
		bases	coverage	deviation
chr1	249250621	406663859	1.6315	6.863
chr2	243199373	363890702	1.4963	6.4136
chr3	198022430	269230214	1.3596	5.135
chr4	191154276	184032386	0.9627	5.4263
chr5	180915260	234945551	1.2986	6.2108
chr6	171115067	233946749	1.3672	5.3699
chr7	159138663	209044465	1.3136	5.4224
chr8	146364022	209101738	1.4286	5.8571
chr9	141213431	197590122	1.3992	6.7847
chr10	135534747	226074493	1.668	6.8153
chr11	135006516	226602430	1.6785	8.2768
chr12	133851895	197797661	1.4777	6.4506
chr13	115169878	106667649	0.9262	4.1692
chr14	107349540	140485242	1.3087	5.6212
chr15	102531392	154092372	1.5029	6.2963
chr16	90354753	170166635	1.8833	8.5855
chr17	81195210	167687950	2.0652	7.9791
chr18	78077248	100346885	1.2852	5.5988
chr19	59128983	3671023	0.0621	1.9713
chr20	63025520	142104356	2.2547	7.5442
chr21	48129895	62550157	1.2996	9.1722
chr22	51304566	103452433	2.0164	8.0584
chrMT	16571	11009	0.6644	3.2389
chrX	155270560	8277398	0.0533	1.732

chrY	59373566	37178244	0.6262	4.6274
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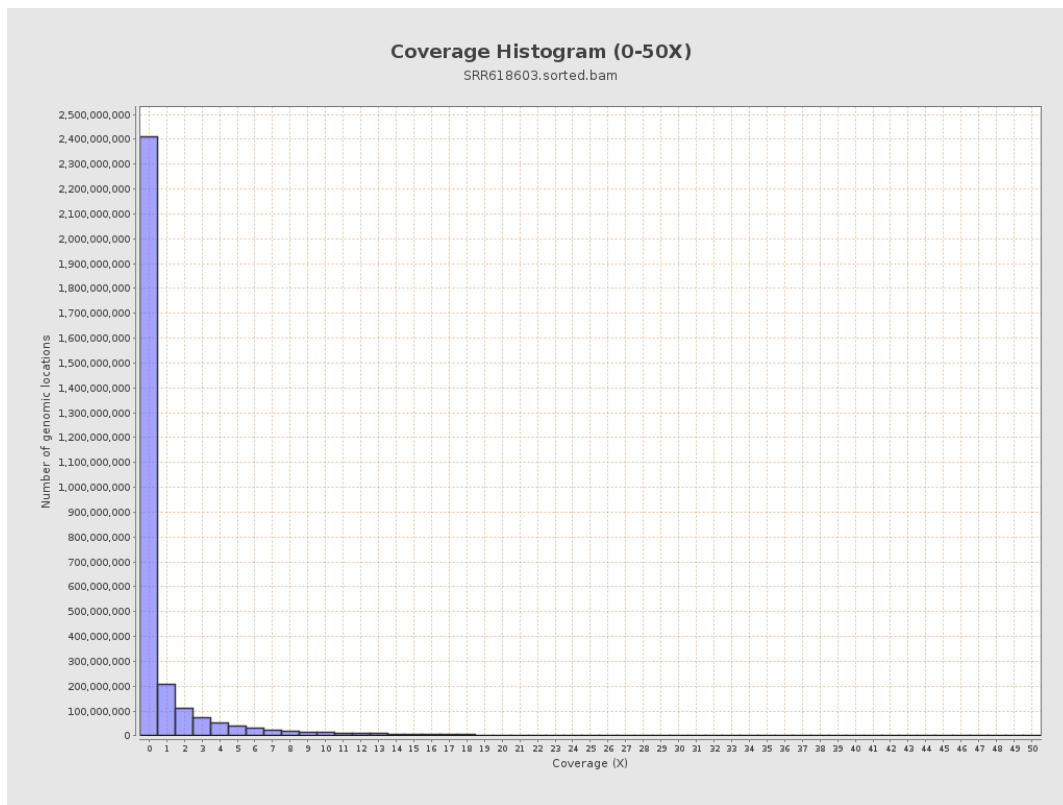
3. Results : Coverage across reference



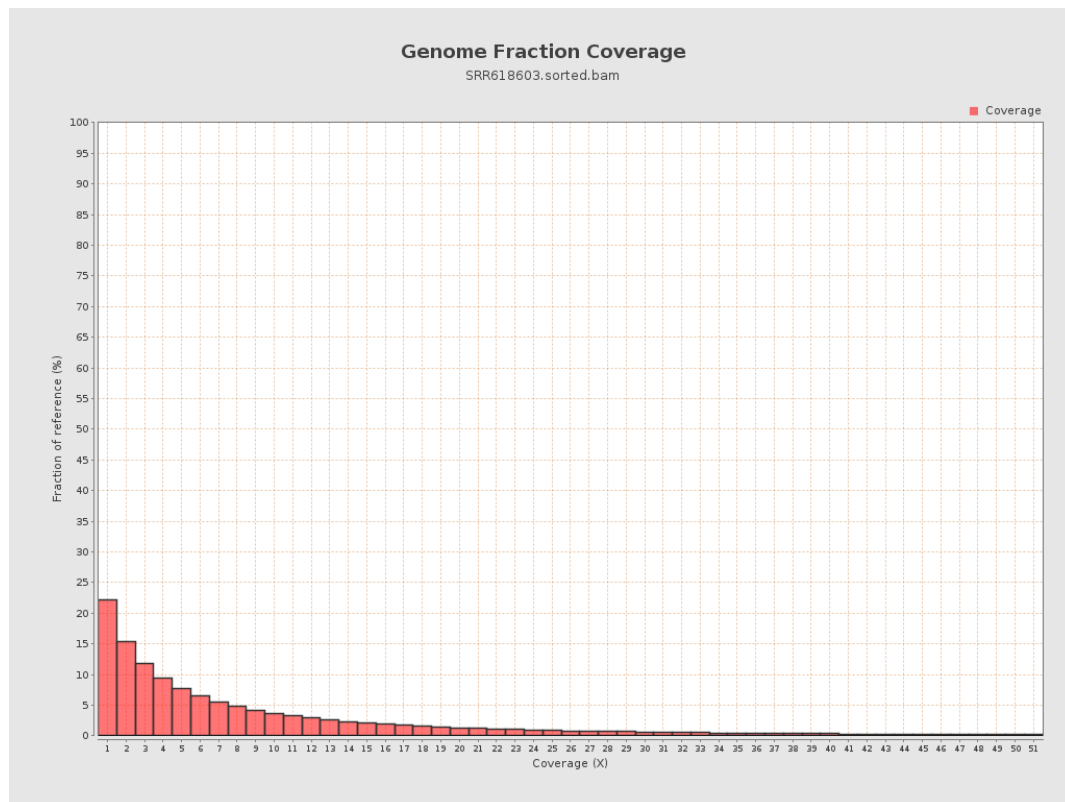
4. Results : Coverage Histogram



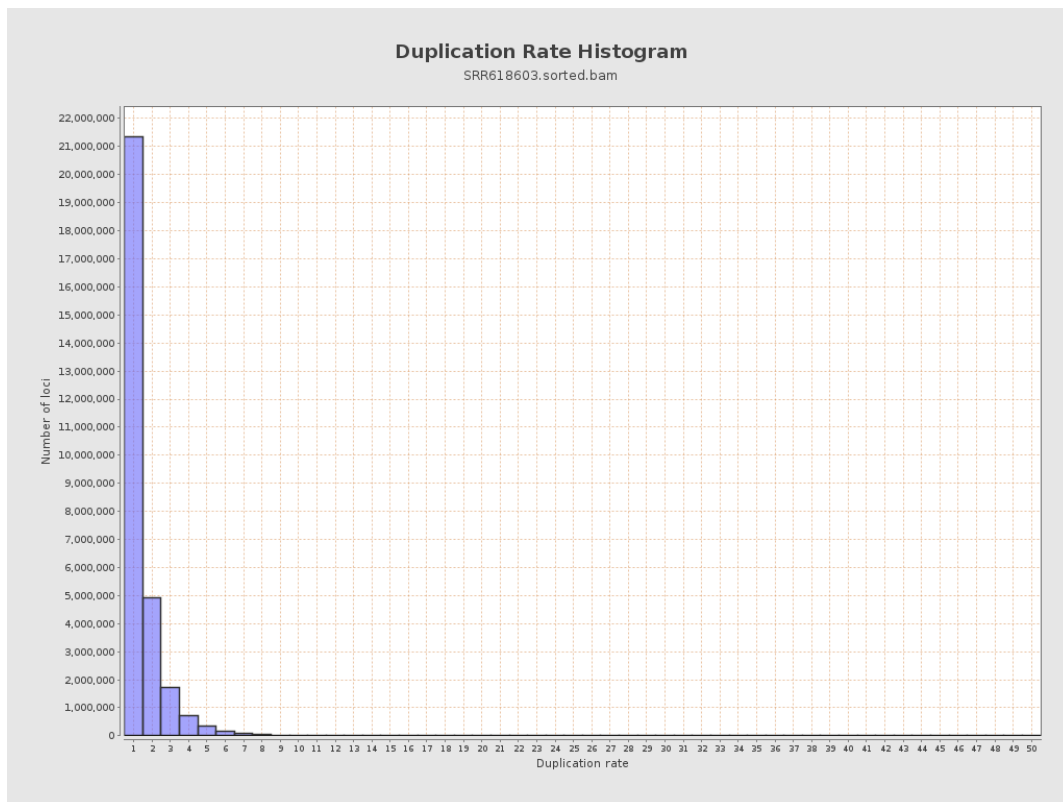
5. Results : Coverage Histogram (0-50X)



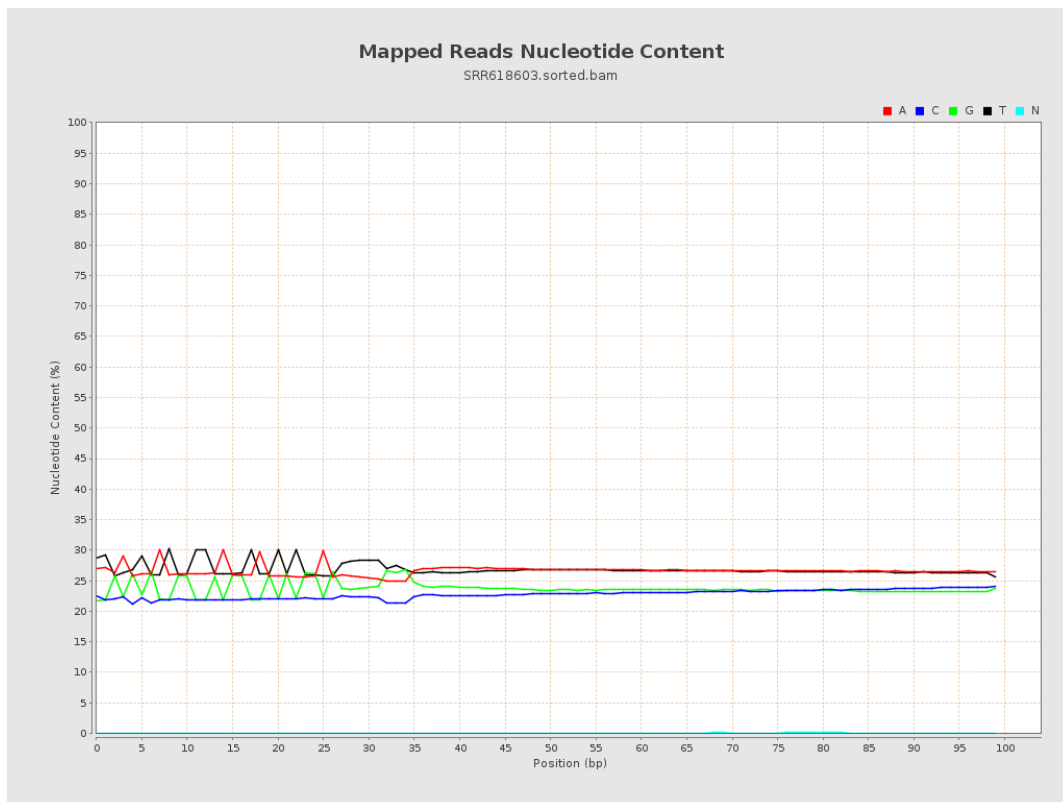
6. Results : Genome Fraction Coverage



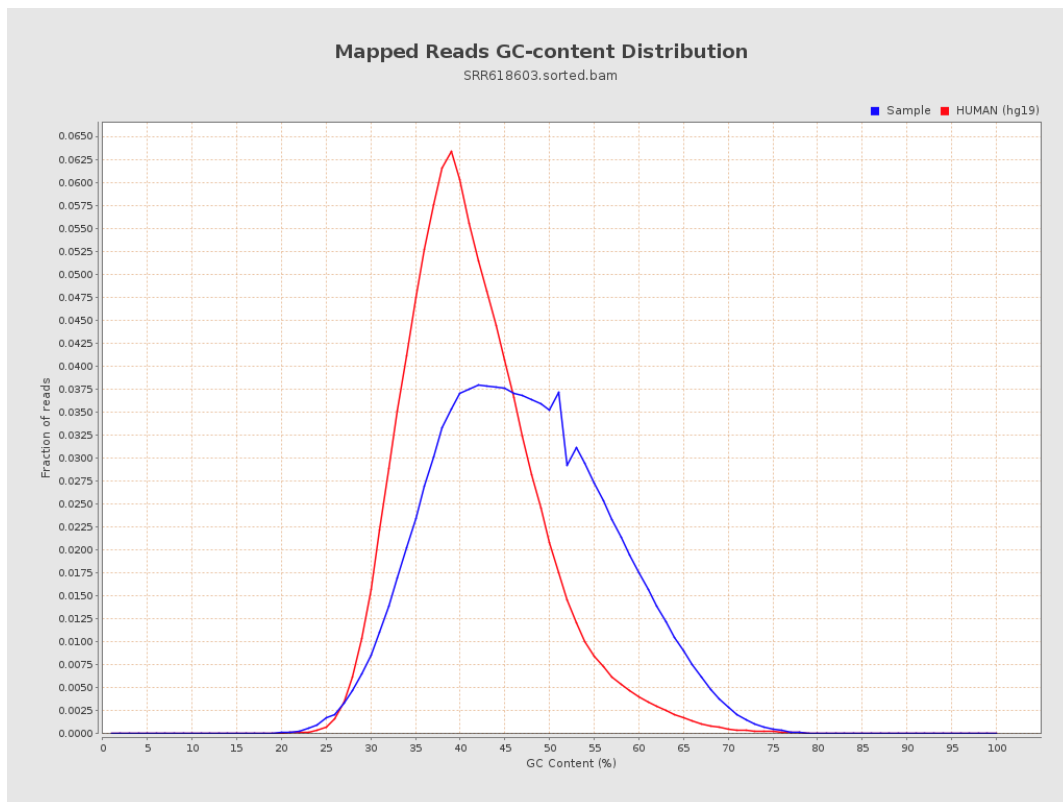
7. Results : Duplication Rate Histogram



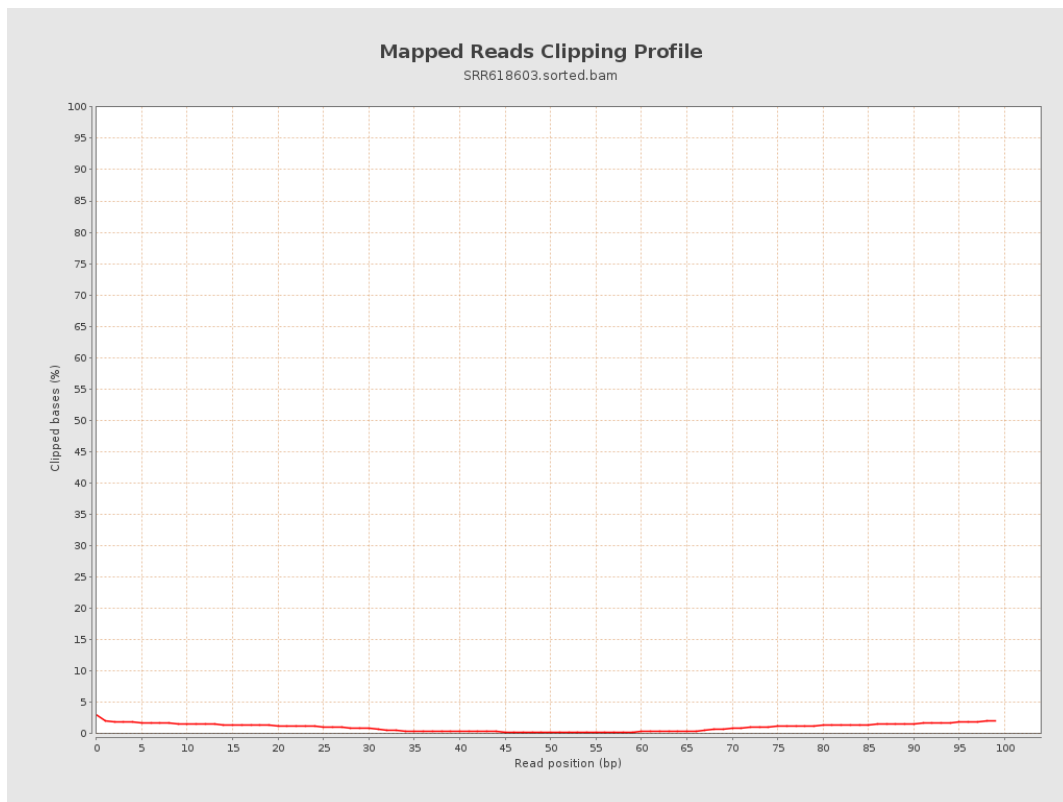
8. Results : Mapped Reads Nucleotide Content



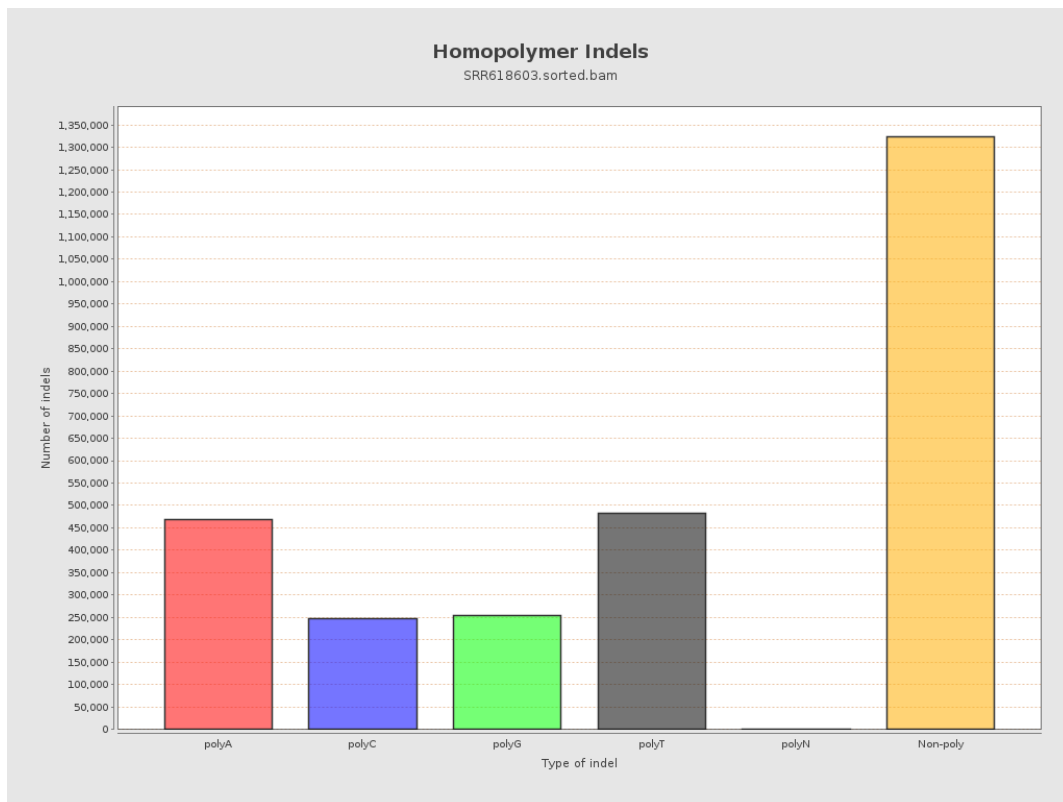
9. Results : Mapped Reads GC-content Distribution



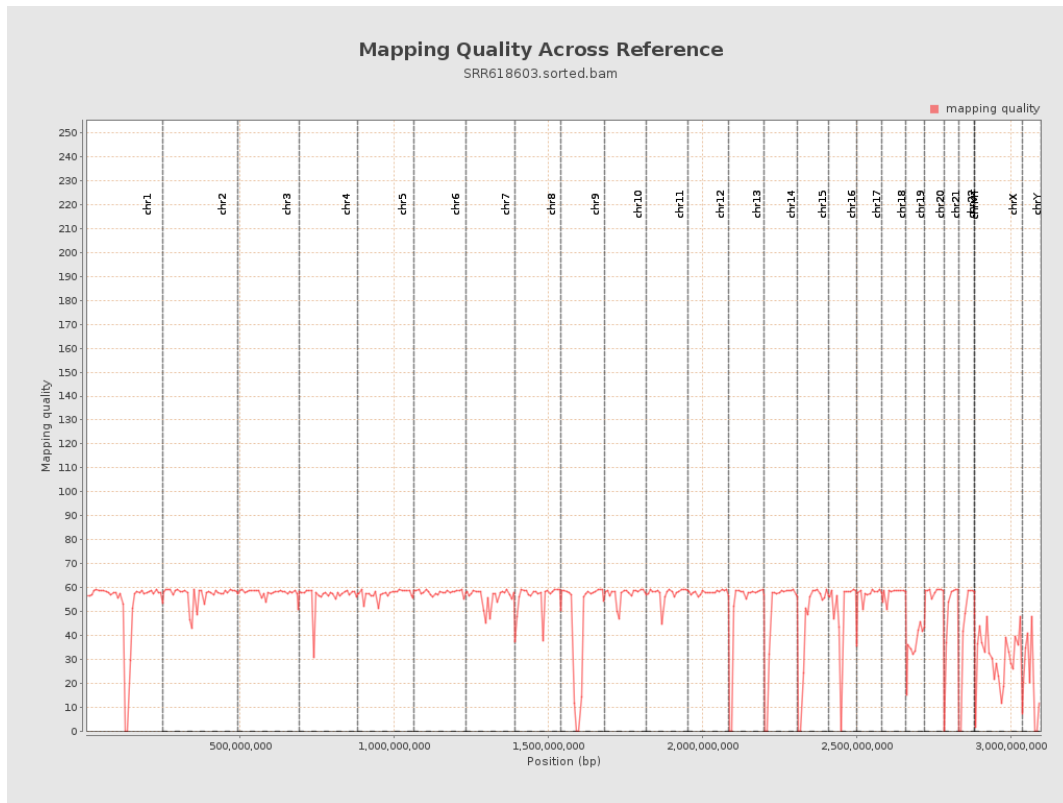
10. Results : Mapped Reads Clipping Profile



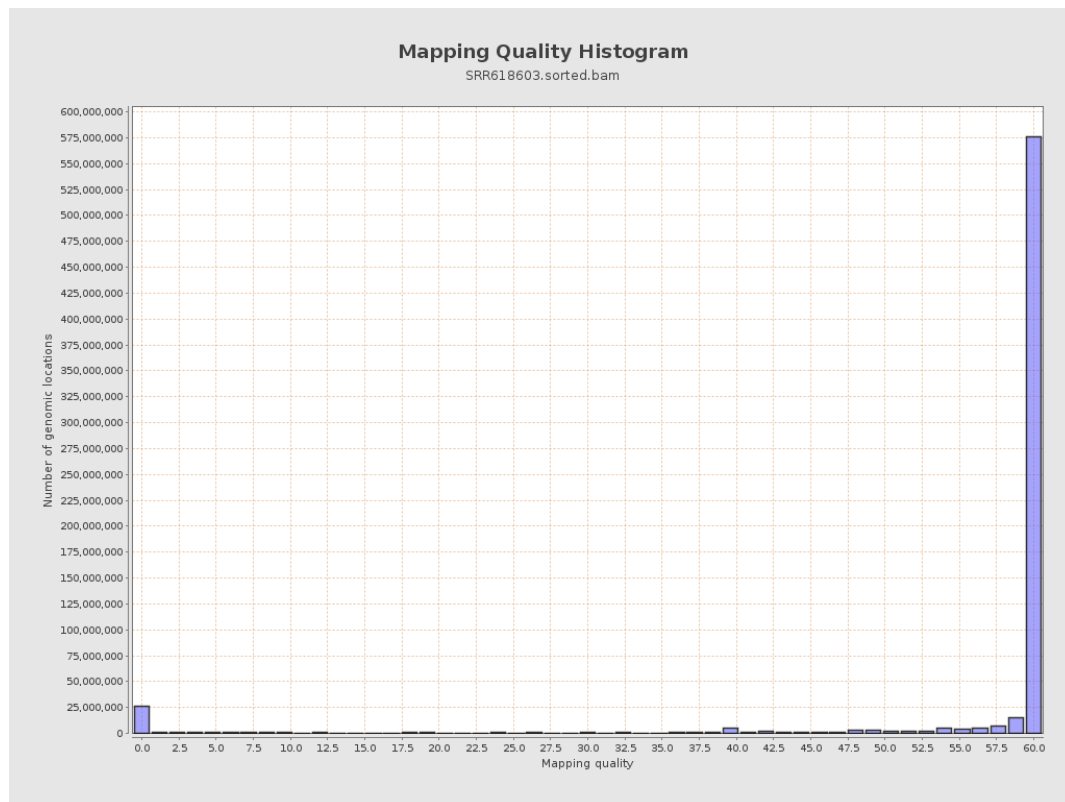
11. Results : Homopolymer Indels



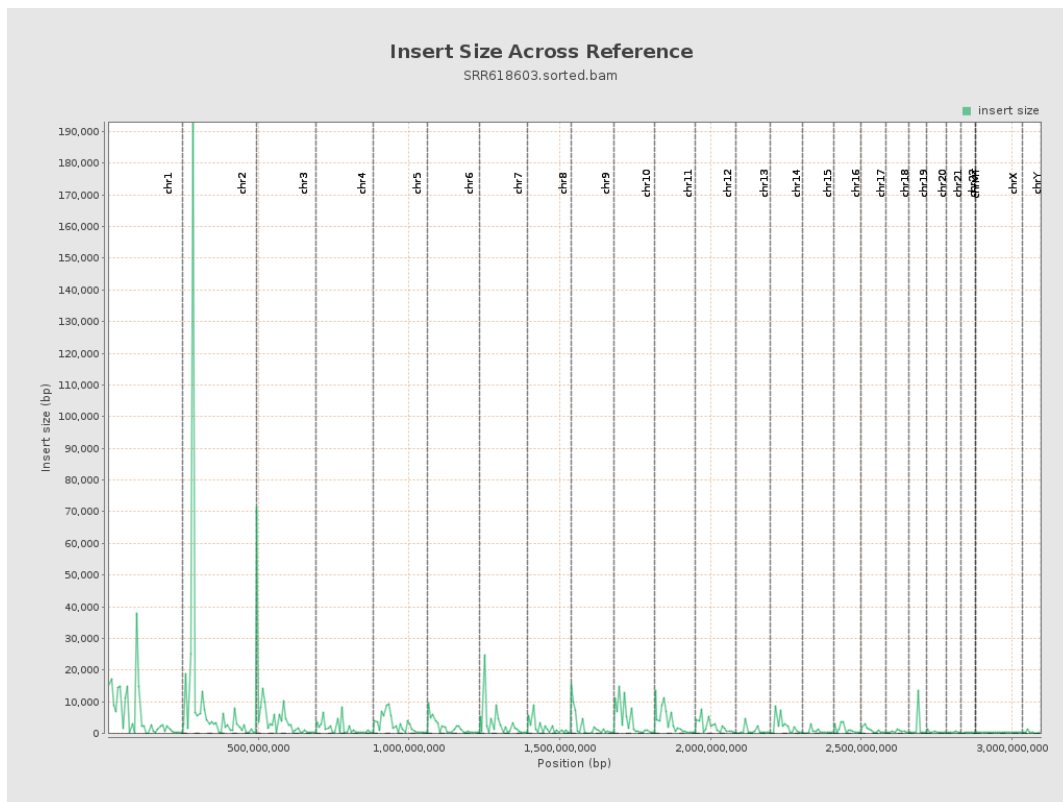
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

