

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/18 20:13:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618596.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_SRR618596 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618596_1.fastq.gz SRR618596_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Jan 18 20:13:42 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618596.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	42,047,662
Mapped reads	40,444,066 / 96.19%
Unmapped reads	1,603,596 / 3.81%
Mapped paired reads	40,444,066 / 96.19%
Mapped reads, first in pair	20,419,705 / 48.56%
Mapped reads, second in pair	20,024,361 / 47.62%
Mapped reads, both in pair	39,708,710 / 94.44%
Mapped reads, singletons	735,356 / 1.75%
Secondary alignments	0
Supplementary alignments	49,761 / 0.12%
Read min/max/mean length	30 / 100 / 100.05
Duplicated reads (estimated)	6,083,674 / 14.47%
Duplication rate	13.45%
Clipped reads	6,951,943 / 16.53%

2.2. ACGT Content

Number/percentage of A's	1,038,569,565 / 26.84%
Number/percentage of C's	879,436,905 / 22.72%
Number/percentage of T's	1,042,245,692 / 26.93%
Number/percentage of G's	909,571,420 / 23.5%
Number/percentage of N's	173,538 / 0%

GC Percentage	46.23%
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2.3. Coverage

Mean	1.2509
Standard Deviation	5.2568

2.4. Mapping Quality

Mean Mapping Quality	53.87
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2.5. Insert size

Mean	25,842.12
Standard Deviation	1,607,722.32
P25/Median/P75	188 / 216 / 252

2.6. Mismatches and indels

General error rate	1.32%
Mismatches	49,995,891
Insertions	687,701
Mapped reads with at least one insertion	1.67%
Deletions	1,787,312
Mapped reads with at least one deletion	4.32%
Homopolymer indels	52.3%

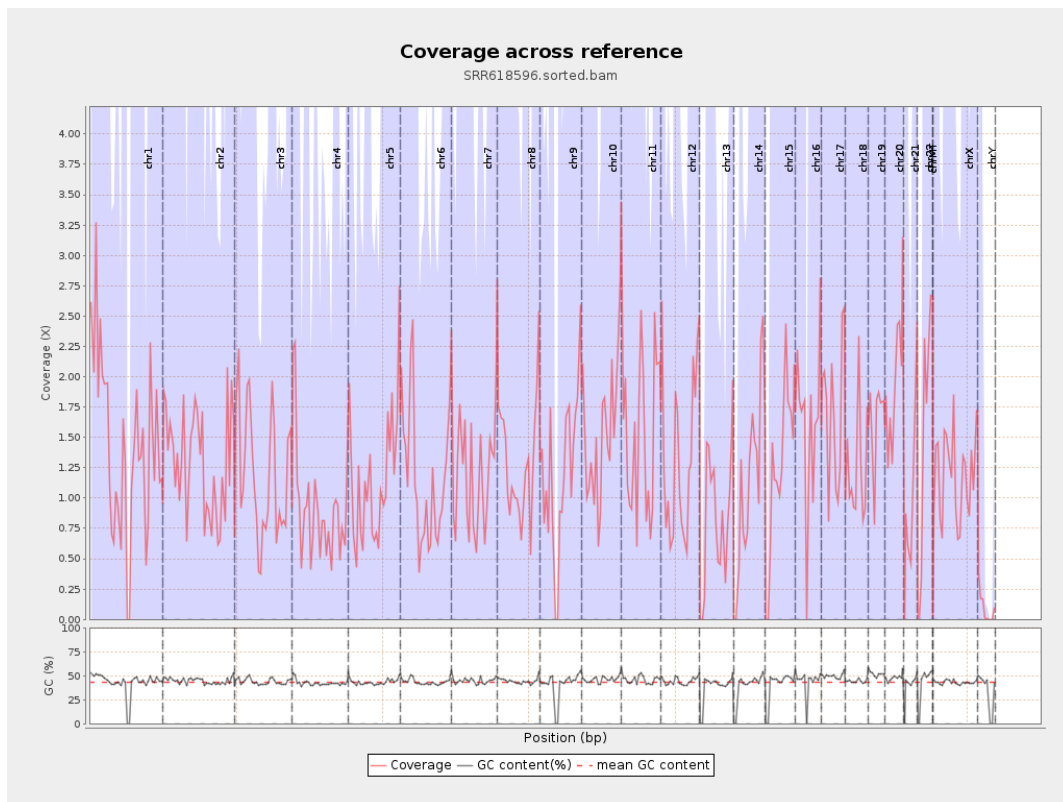
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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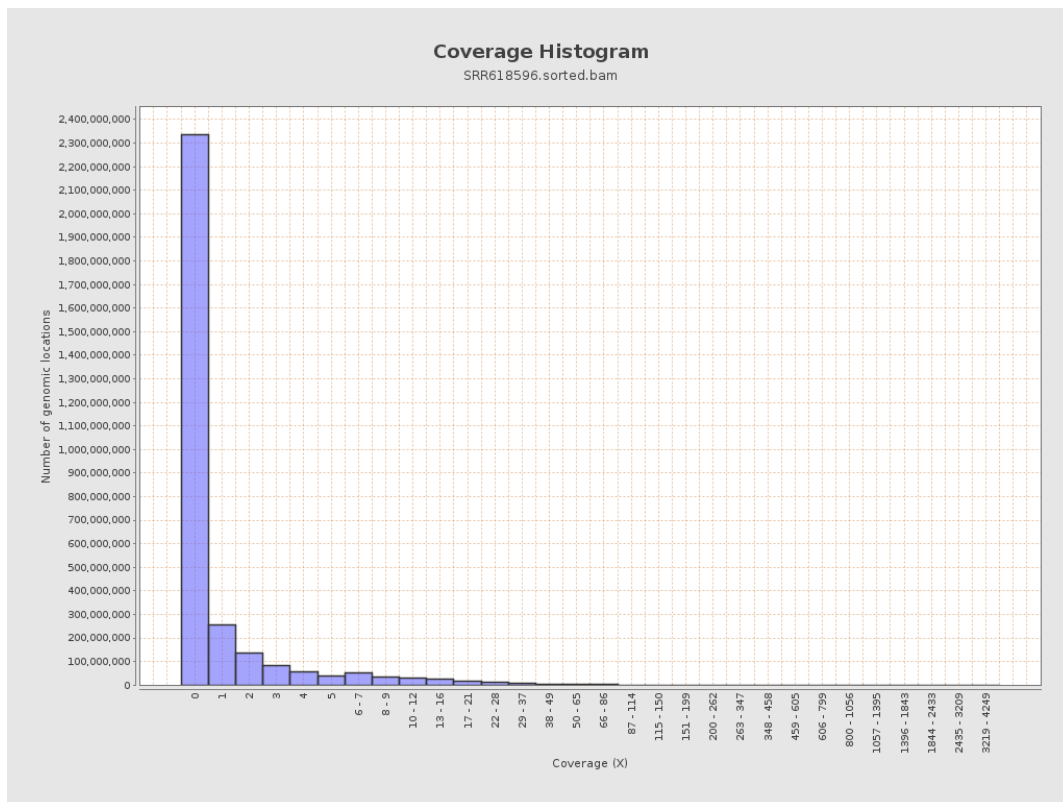
		bases	coverage	deviation
chr1	249250621	351454222	1.41	6.2113
chr2	243199373	314555707	1.2934	5.4839
chr3	198022430	233370188	1.1785	4.2821
chr4	191154276	173526745	0.9078	4.4605
chr5	180915260	210832307	1.1654	4.1652
chr6	171115067	197176811	1.1523	4.3813
chr7	159138663	191182394	1.2014	4.4039
chr8	146364022	186512656	1.2743	4.649
chr9	141213431	169160889	1.1979	5.7544
chr10	135534747	205487265	1.5161	5.511
chr11	135006516	207476493	1.5368	5.8219
chr12	133851895	178316452	1.3322	4.8266
chr13	115169878	94184183	0.8178	3.4369
chr14	107349540	120803768	1.1253	4.6128
chr15	102531392	128251549	1.2509	4.8573
chr16	90354753	145401826	1.6092	8.7974
chr17	81195210	136005009	1.675	6.0847
chr18	78077248	95079193	1.2178	5.6739
chr19	59128983	95140643	1.609	6.3546
chr20	63025520	120640559	1.9142	6.248
chr21	48129895	49572471	1.03	8.3927
chr22	51304566	77745357	1.5154	6.1127
chrMT	16571	249	0.015	0.1384
chrX	155270560	185160530	1.1925	4.0973

chrY	59373566	5417074	0.0912	2.7786
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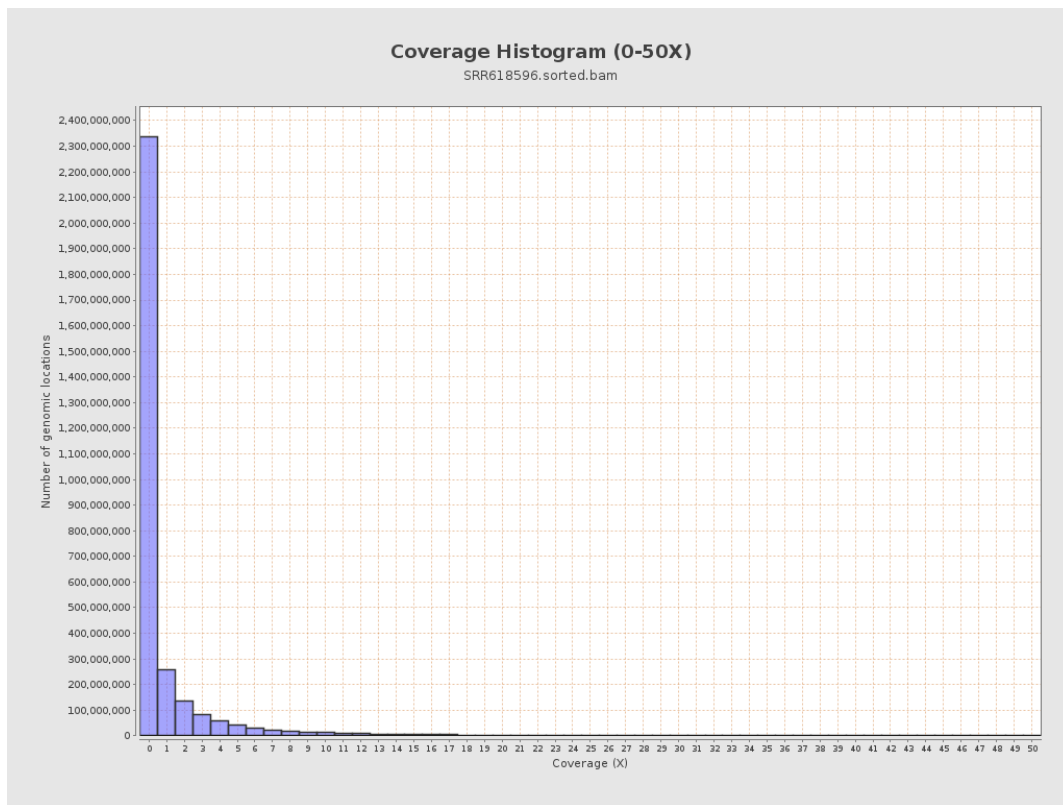
3. Results : Coverage across reference



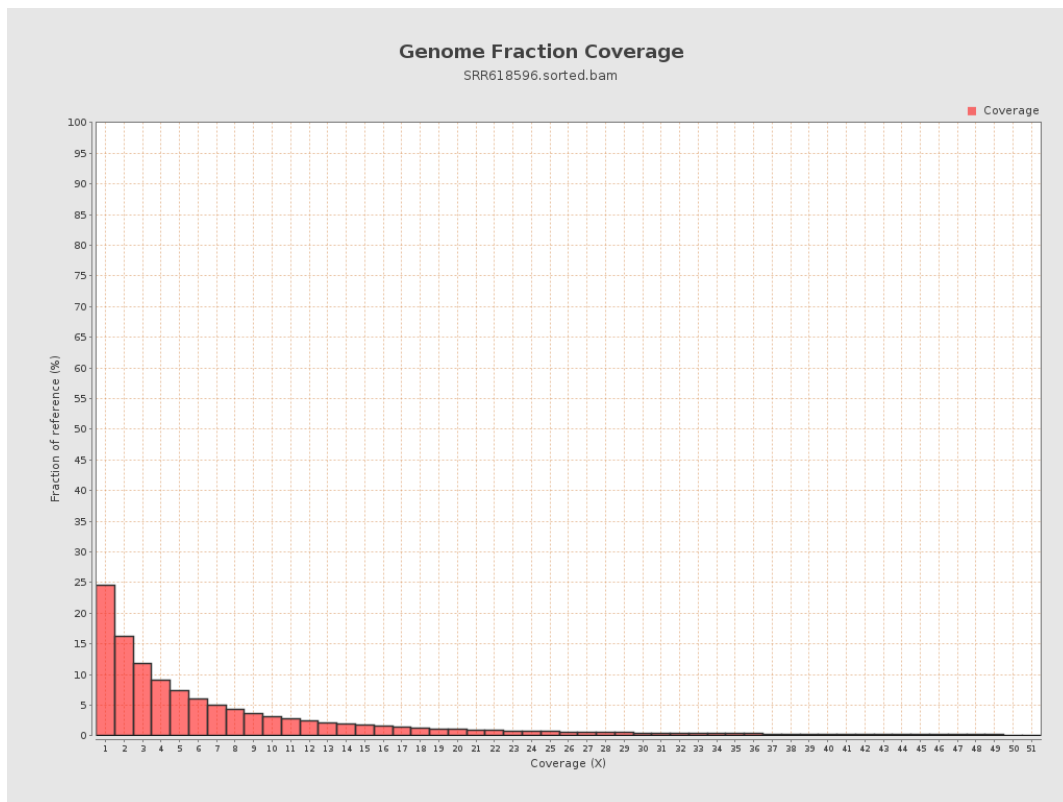
4. Results : Coverage Histogram



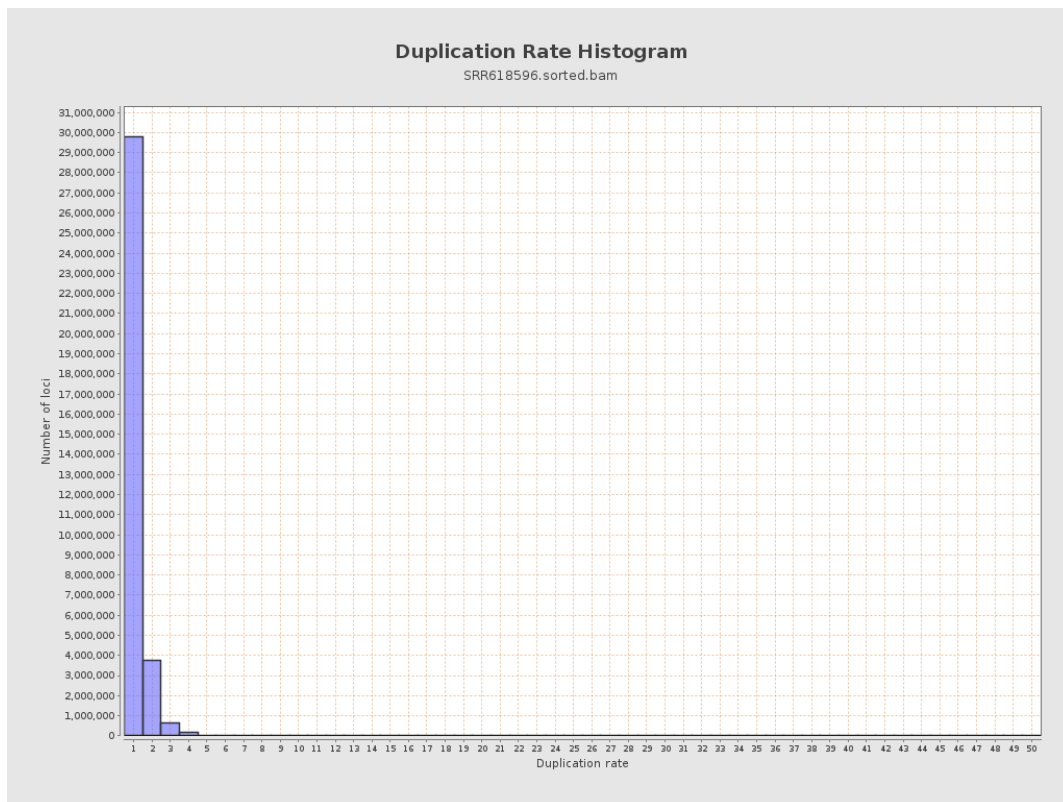
5. Results : Coverage Histogram (0-50X)



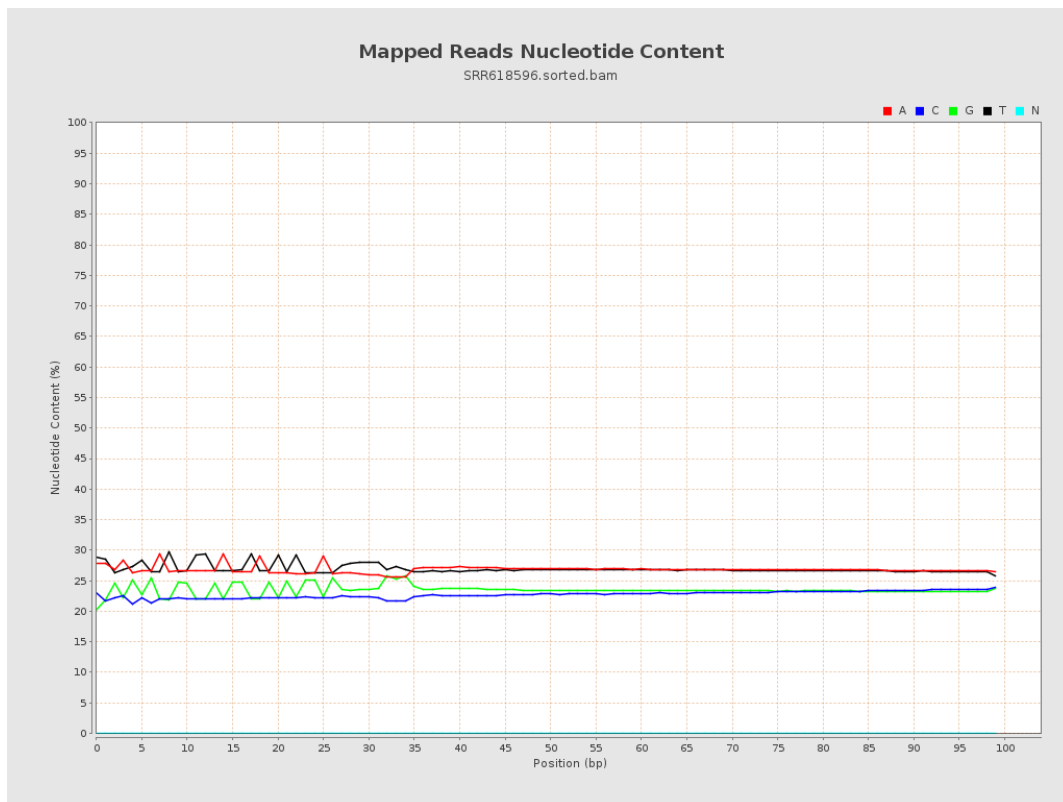
6. Results : Genome Fraction Coverage



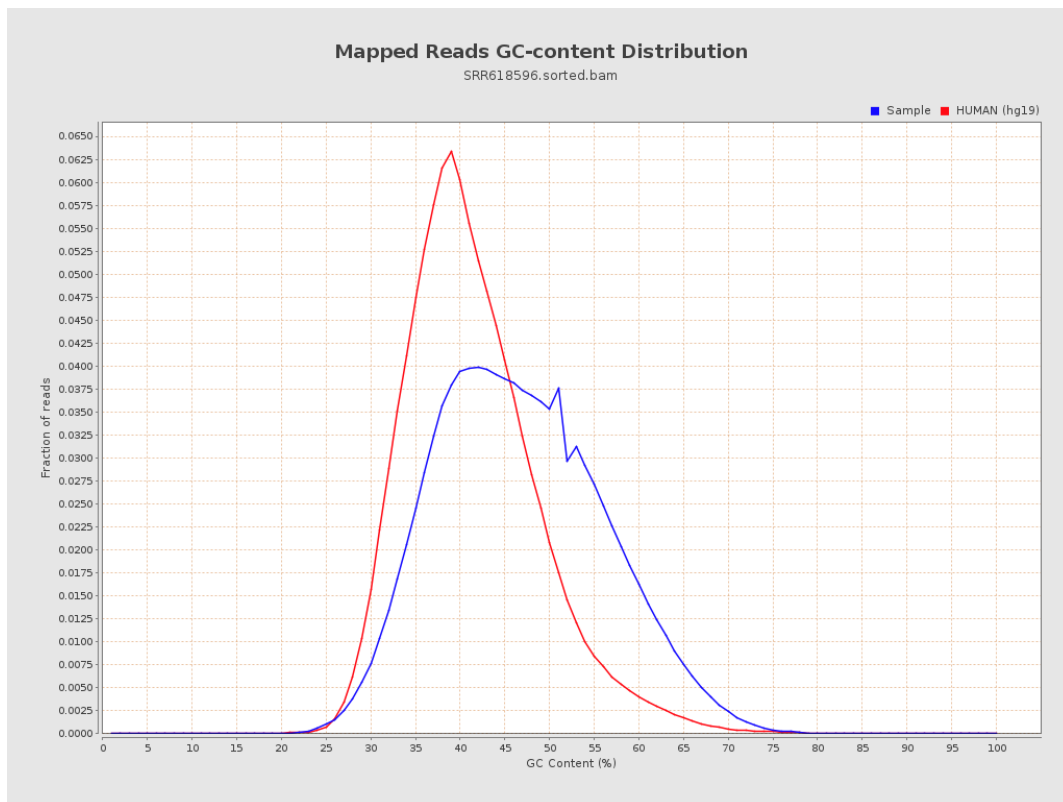
7. Results : Duplication Rate Histogram



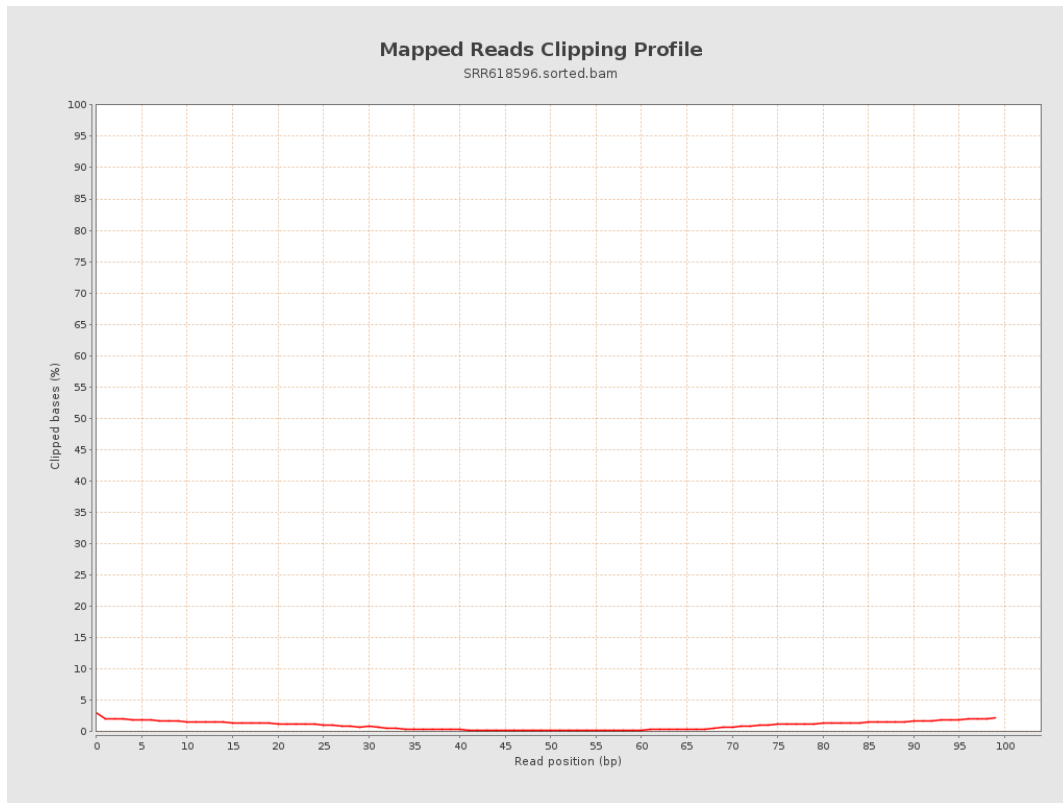
8. Results : Mapped Reads Nucleotide Content



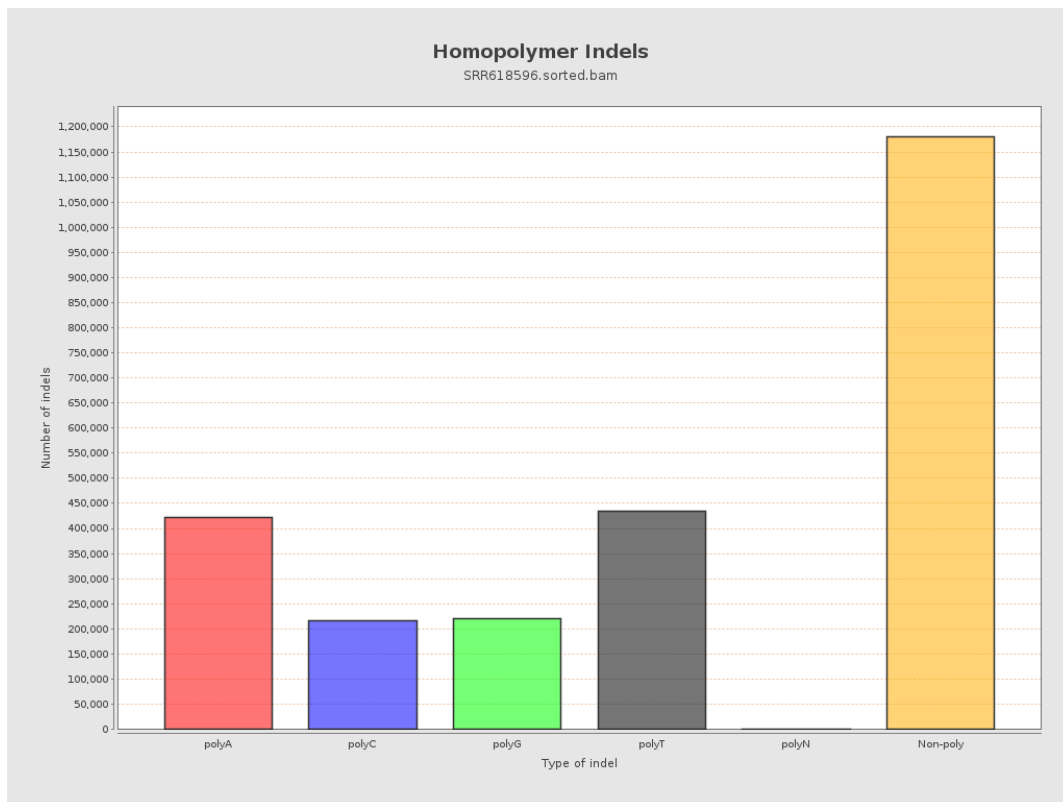
9. Results : Mapped Reads GC-content Distribution



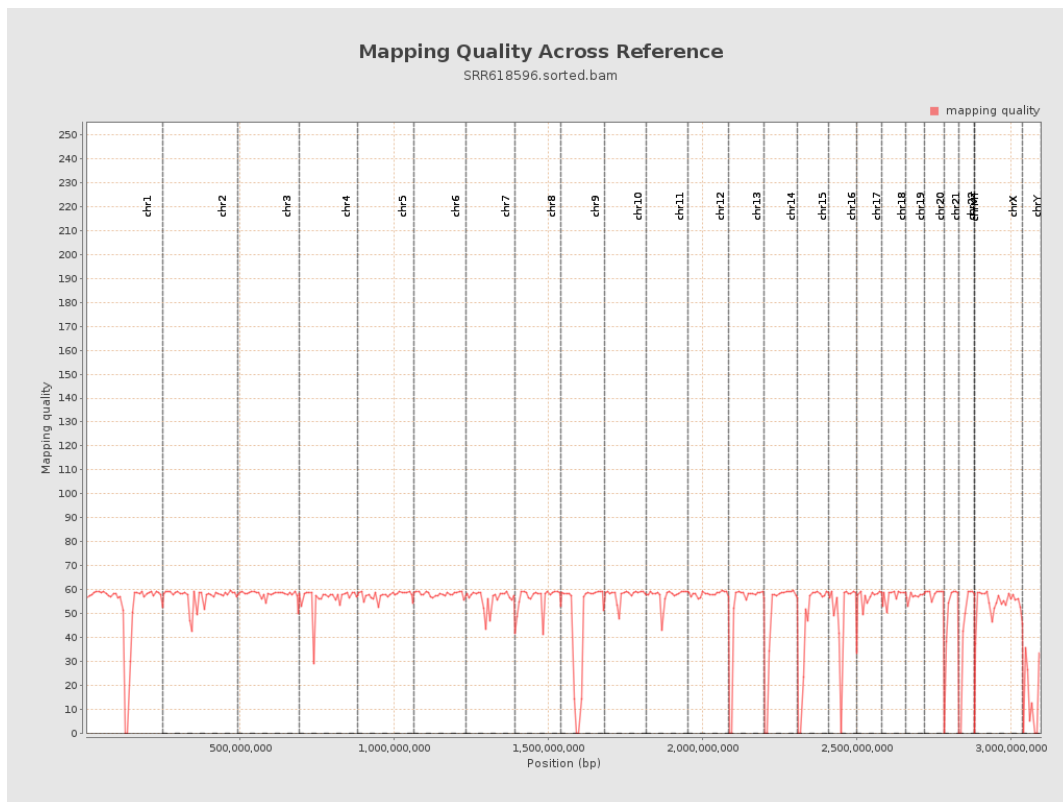
10. Results : Mapped Reads Clipping Profile



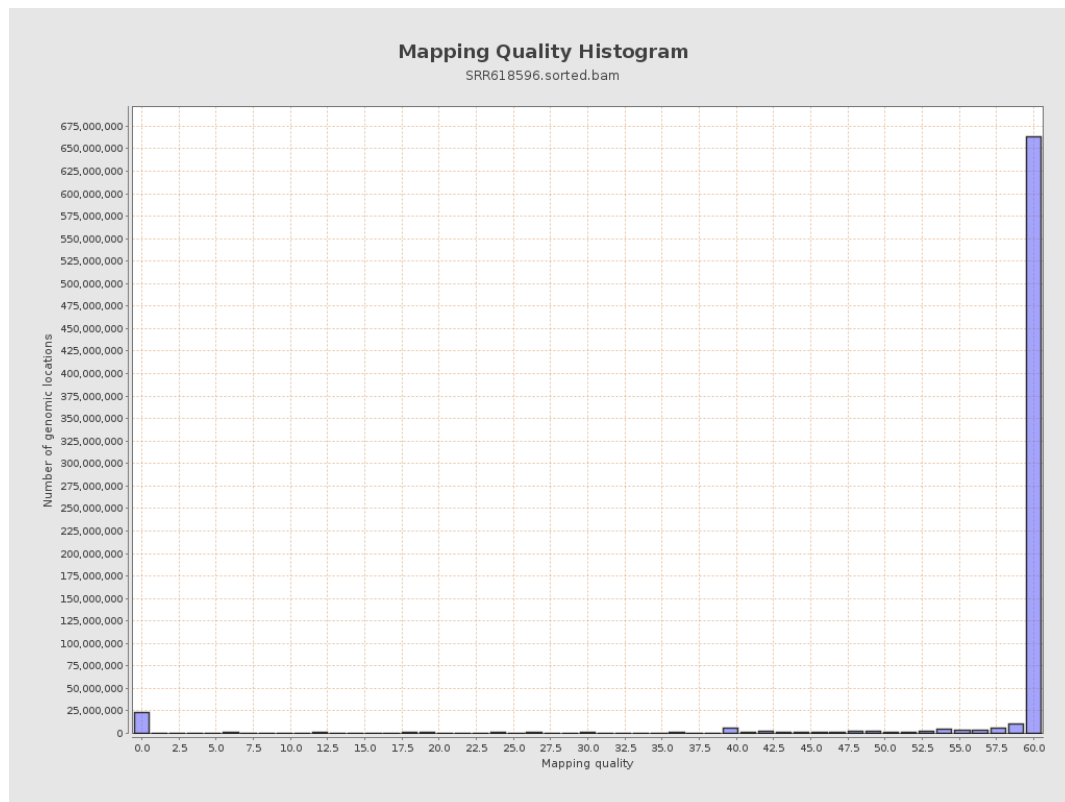
11. Results : Homopolymer Indels



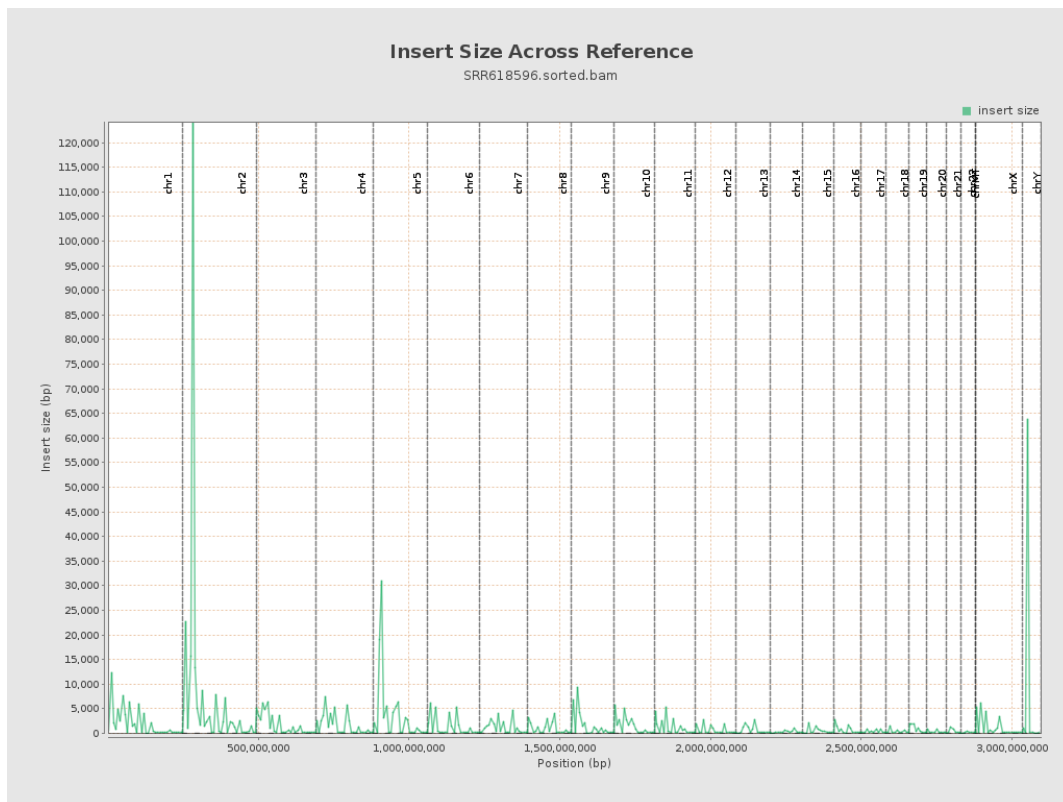
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

