

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 13:14:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618621.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_SRR618621 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618621_1.fastq.gz SRR618621_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 13:14:05 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618621.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	40,893,424
Mapped reads	37,426,212 / 91.52%
Unmapped reads	3,467,212 / 8.48%
Mapped paired reads	37,426,212 / 91.52%
Mapped reads, first in pair	19,062,780 / 46.62%
Mapped reads, second in pair	18,363,432 / 44.91%
Mapped reads, both in pair	35,868,388 / 87.71%
Mapped reads, singletons	1,557,824 / 3.81%
Secondary alignments	0
Supplementary alignments	96,682 / 0.24%
Read min/max/mean length	30 / 100 / 100.09
Duplicated reads (estimated)	22,759,794 / 55.66%
Duplication rate	42.8%
Clipped reads	8,873,323 / 21.7%

2.2. ACGT Content

Number/percentage of A's	870,166,972 / 24.83%
Number/percentage of C's	860,543,507 / 24.55%
Number/percentage of T's	880,825,624 / 25.13%
Number/percentage of G's	890,327,163 / 25.4%
Number/percentage of N's	2,867,145 / 0.08%

GC Percentage	49.96%
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2.3. Coverage

Mean	1.1328
Standard Deviation	6.7044

2.4. Mapping Quality

Mean Mapping Quality	52.73
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2.5. Insert size

Mean	76,513.32
Standard Deviation	2,840,106.39
P25/Median/P75	172 / 201 / 239

2.6. Mismatches and indels

General error rate	1.51%
Mismatches	52,038,531
Insertions	646,001
Mapped reads with at least one insertion	1.7%
Deletions	1,553,041
Mapped reads with at least one deletion	4.06%
Homopolymer indels	51.65%

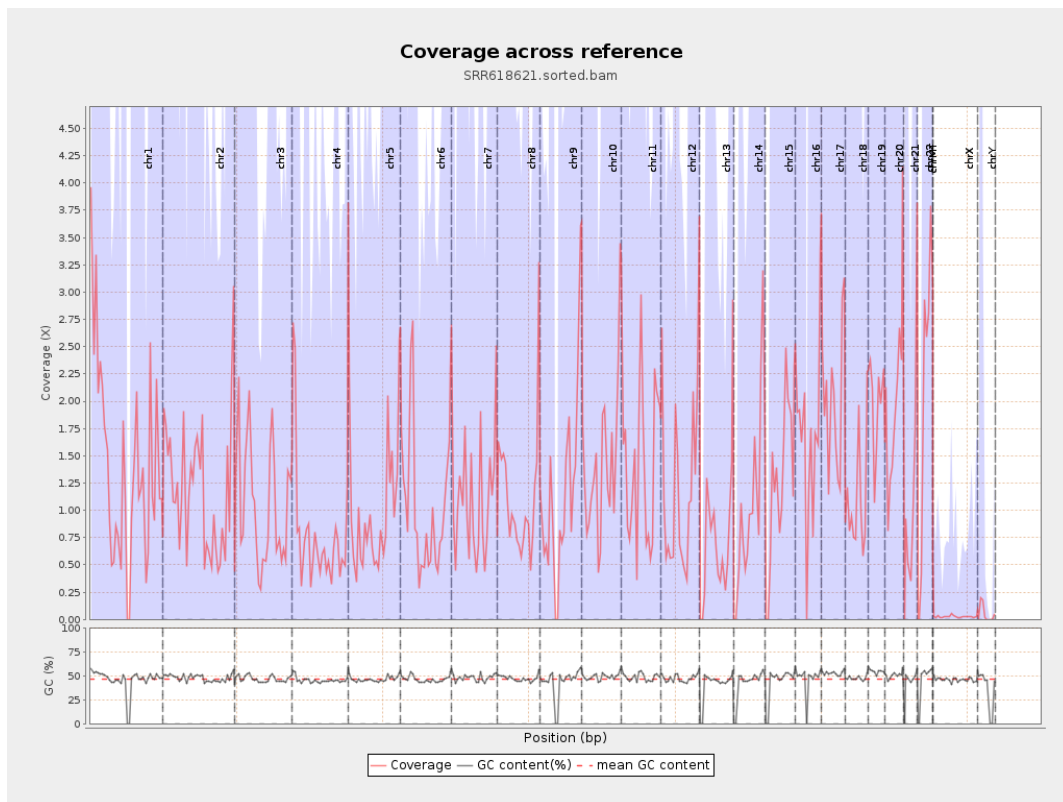
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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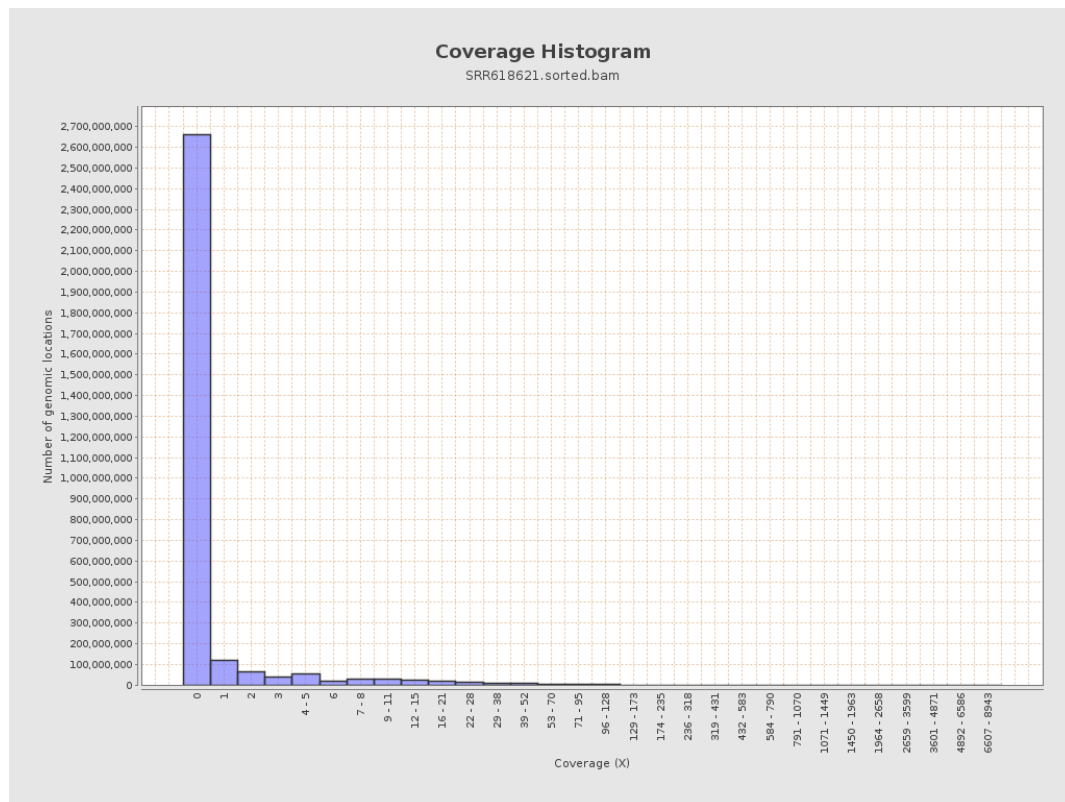
		bases	coverage	deviation
chr1	249250621	347576635	1.3945	7.518
chr2	243199373	286265545	1.1771	7.1167
chr3	198022430	207419503	1.0475	5.5526
chr4	191154276	146267685	0.7652	5.2832
chr5	180915260	184107949	1.0176	5.2998
chr6	171115067	175218290	1.024	5.3178
chr7	159138663	180392565	1.1336	5.9644
chr8	146364022	162309517	1.1089	5.5893
chr9	141213431	159874108	1.1321	6.7622
chr10	135534747	187978697	1.3869	8.9517
chr11	135006516	192684156	1.4272	6.9562
chr12	133851895	159791576	1.1938	6.2913
chr13	115169878	79949081	0.6942	4.1497
chr14	107349540	113025803	1.0529	5.9951
chr15	102531392	127508234	1.2436	6.3143
chr16	90354753	152361959	1.6863	12.6323
chr17	81195210	159917251	1.9695	8.3759
chr18	78077248	82242862	1.0534	5.7438
chr19	59128983	115538925	1.954	9.3008
chr20	63025520	121916367	1.9344	8.0932
chr21	48129895	53653315	1.1148	9.3692
chr22	51304566	103242092	2.0123	9.1807
chrMT	16571	9286	0.5604	2.3927
chrX	155270560	4098882	0.0264	0.9296

chrY	59373566	3542086	0.0597	3.8886
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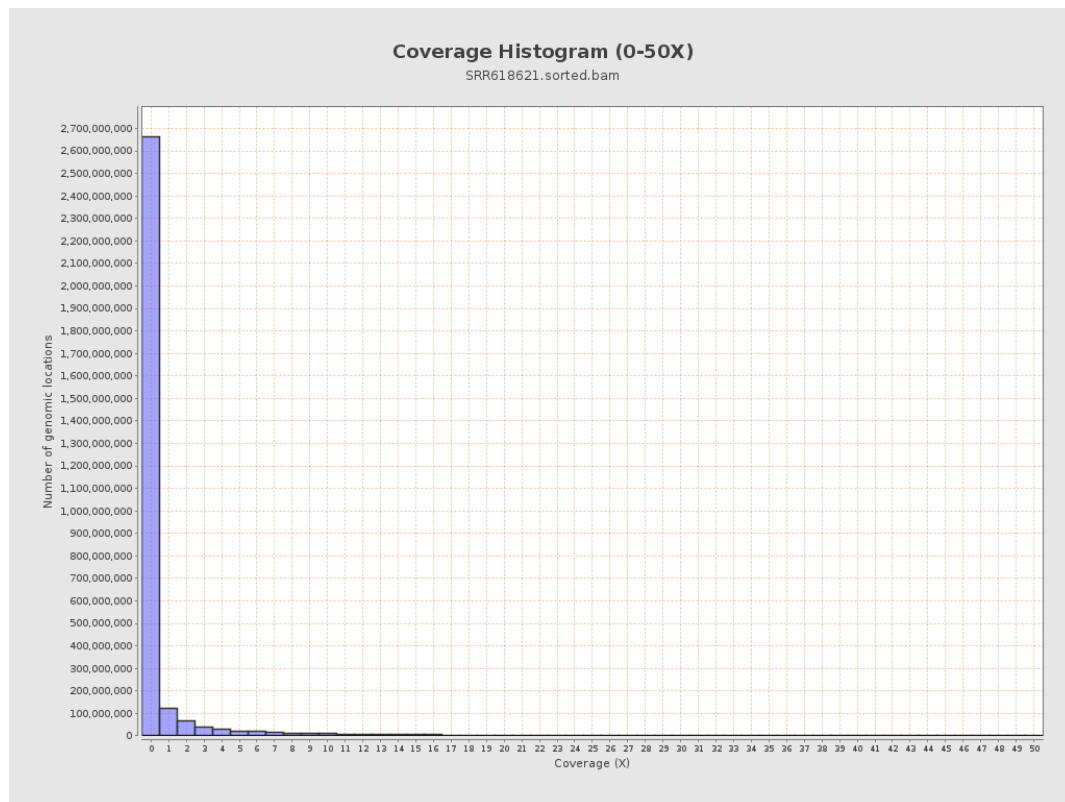
3. Results : Coverage across reference



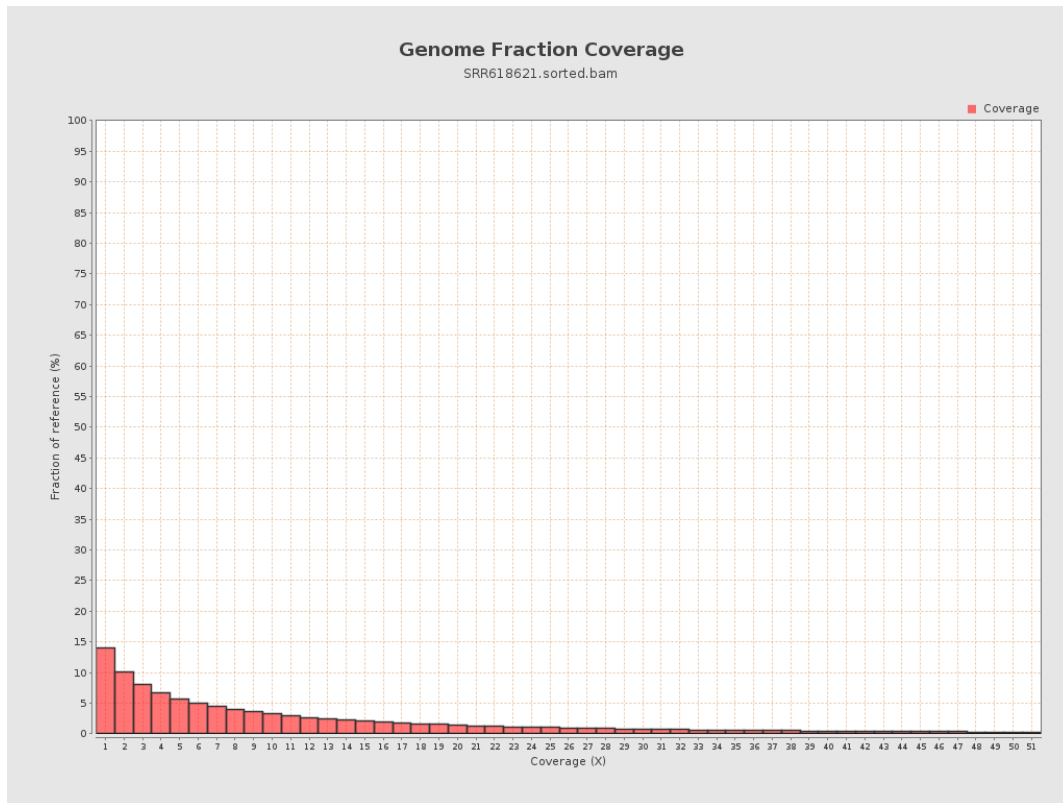
4. Results : Coverage Histogram



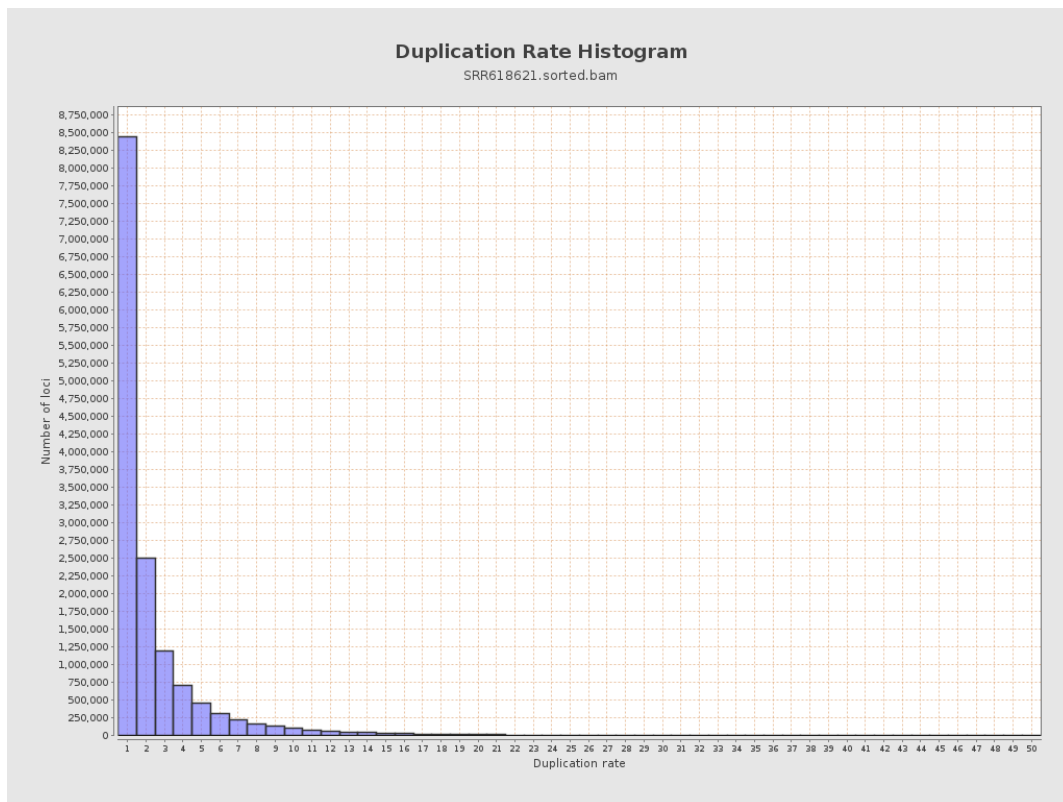
5. Results : Coverage Histogram (0-50X)



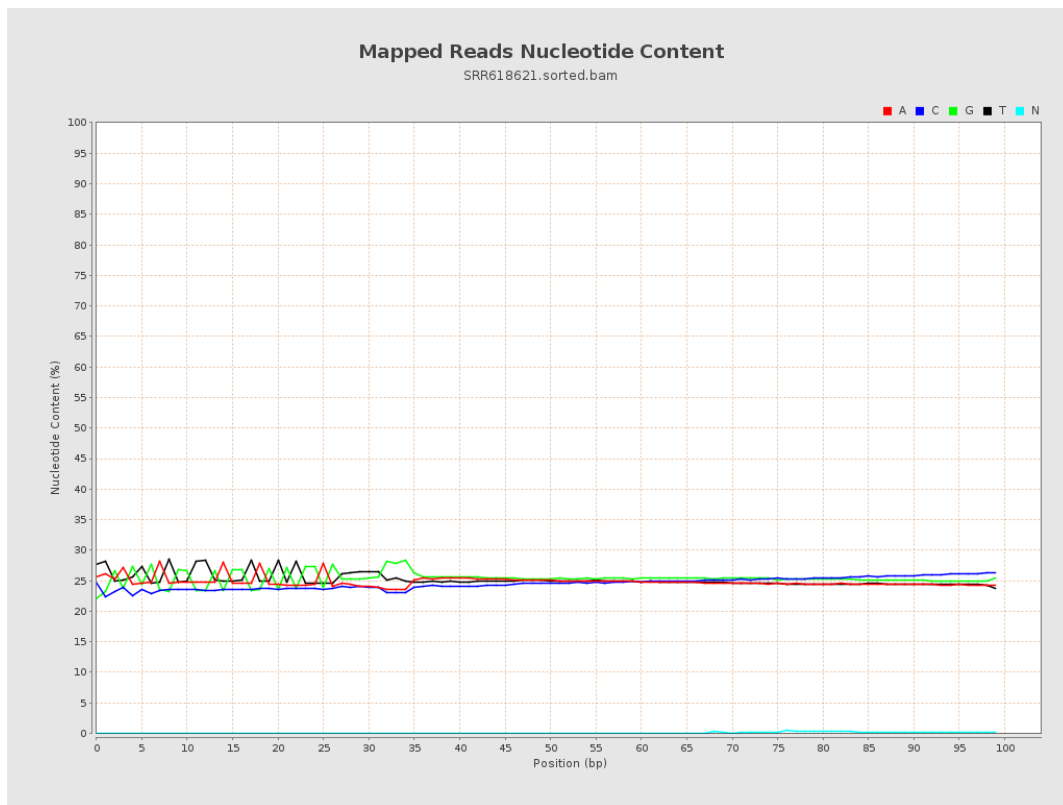
6. Results : Genome Fraction Coverage



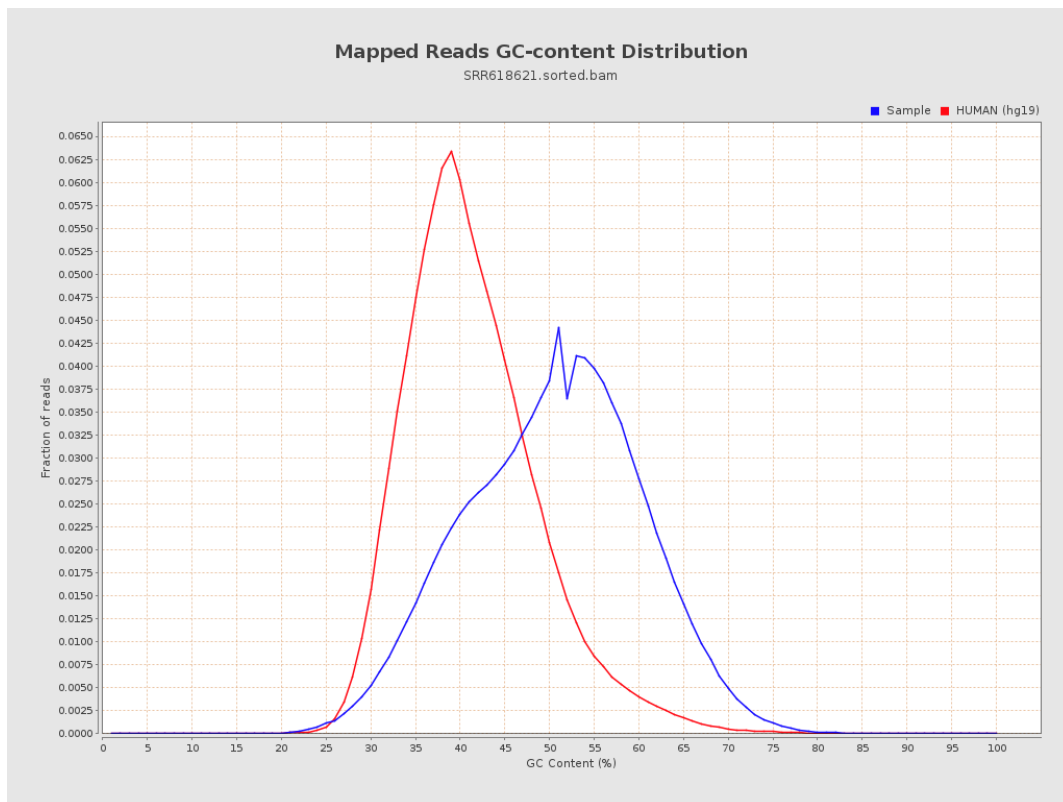
7. Results : Duplication Rate Histogram



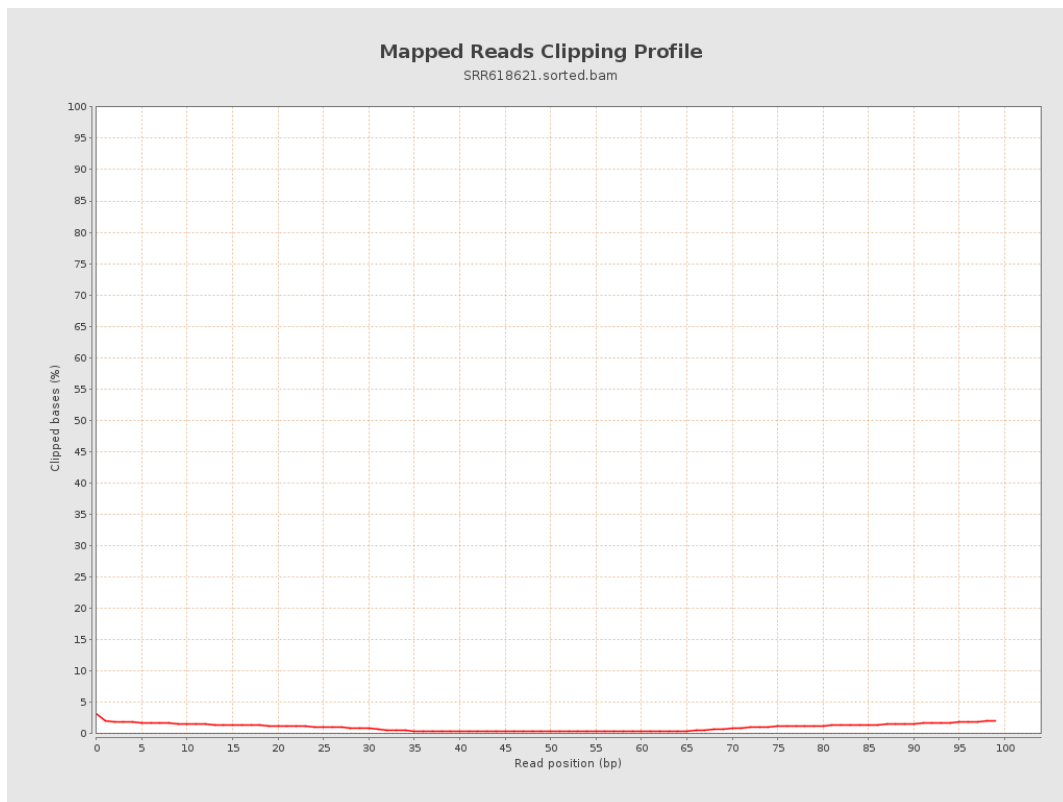
8. Results : Mapped Reads Nucleotide Content



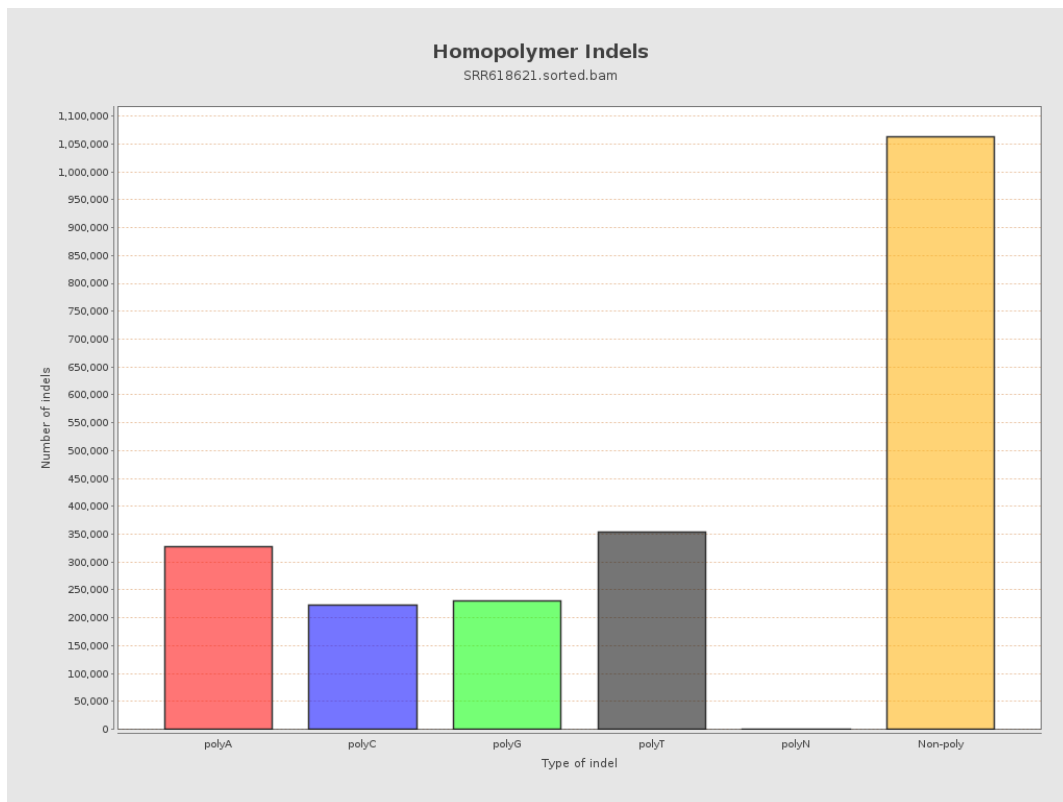
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



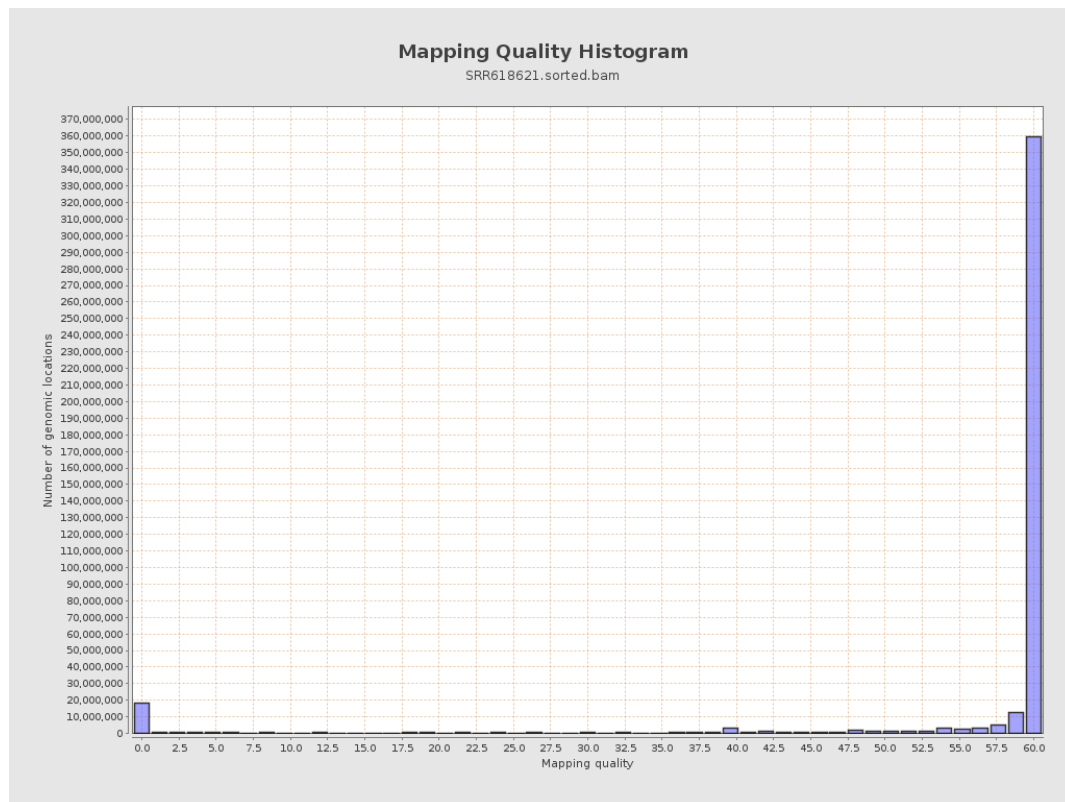
11. Results : Homopolymer Indels



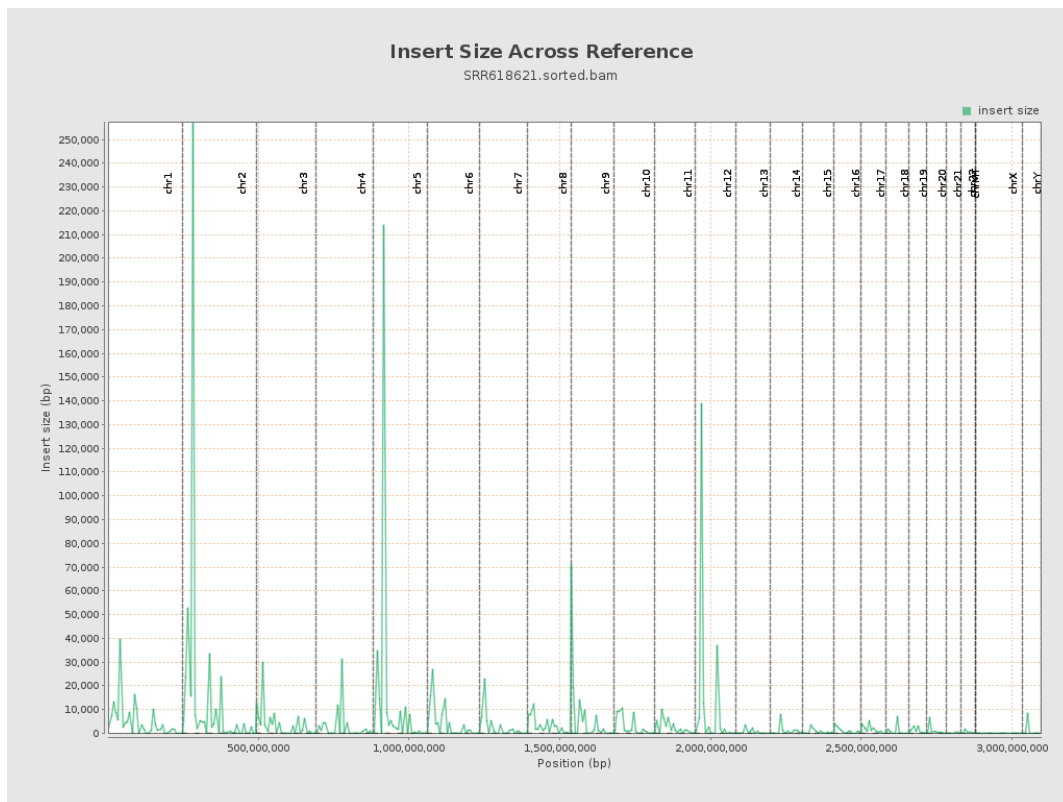
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

