

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 17:43:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618629.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_SRR618629 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618629_1.fastq.gz SRR618629_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 17:43:31 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618629.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	30,993,522
Mapped reads	28,990,835 / 93.54%
Unmapped reads	2,002,687 / 6.46%
Mapped paired reads	28,990,835 / 93.54%
Mapped reads, first in pair	14,761,137 / 47.63%
Mapped reads, second in pair	14,229,698 / 45.91%
Mapped reads, both in pair	28,017,398 / 90.4%
Mapped reads, singletons	973,437 / 3.14%
Secondary alignments	0
Supplementary alignments	142,019 / 0.46%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	13,454,086 / 43.41%
Duplication rate	34.37%
Clipped reads	7,210,471 / 23.26%

2.2. ACGT Content

Number/percentage of A's	738,330,644 / 27.29%
Number/percentage of C's	587,856,281 / 21.73%
Number/percentage of T's	749,954,306 / 27.72%
Number/percentage of G's	627,500,506 / 23.19%
Number/percentage of N's	1,882,728 / 0.07%

GC Percentage	44.92%
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2.3. Coverage

Mean	0.8746
Standard Deviation	4.5506

2.4. Mapping Quality

Mean Mapping Quality	53.54
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2.5. Insert size

Mean	109,126.72
Standard Deviation	3,289,396.38
P25/Median/P75	188 / 218 / 256

2.6. Mismatches and indels

General error rate	1.38%
Mismatches	36,602,876
Insertions	512,927
Mapped reads with at least one insertion	1.73%
Deletions	1,318,878
Mapped reads with at least one deletion	4.44%
Homopolymer indels	51.85%

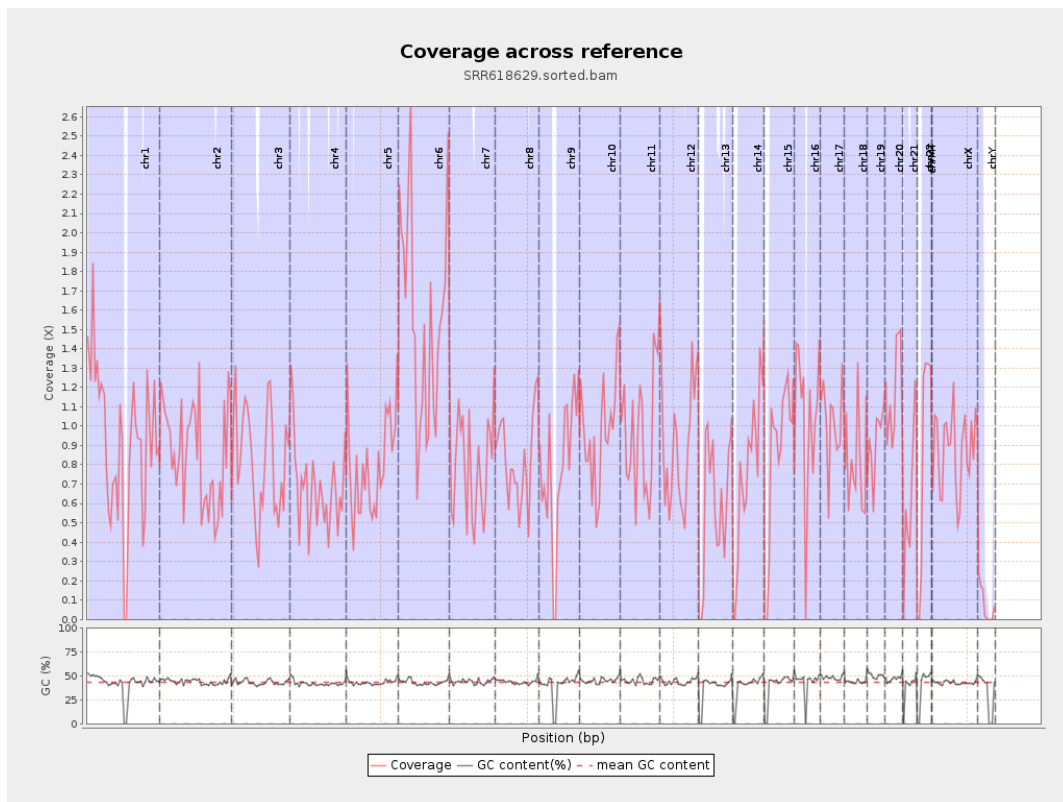
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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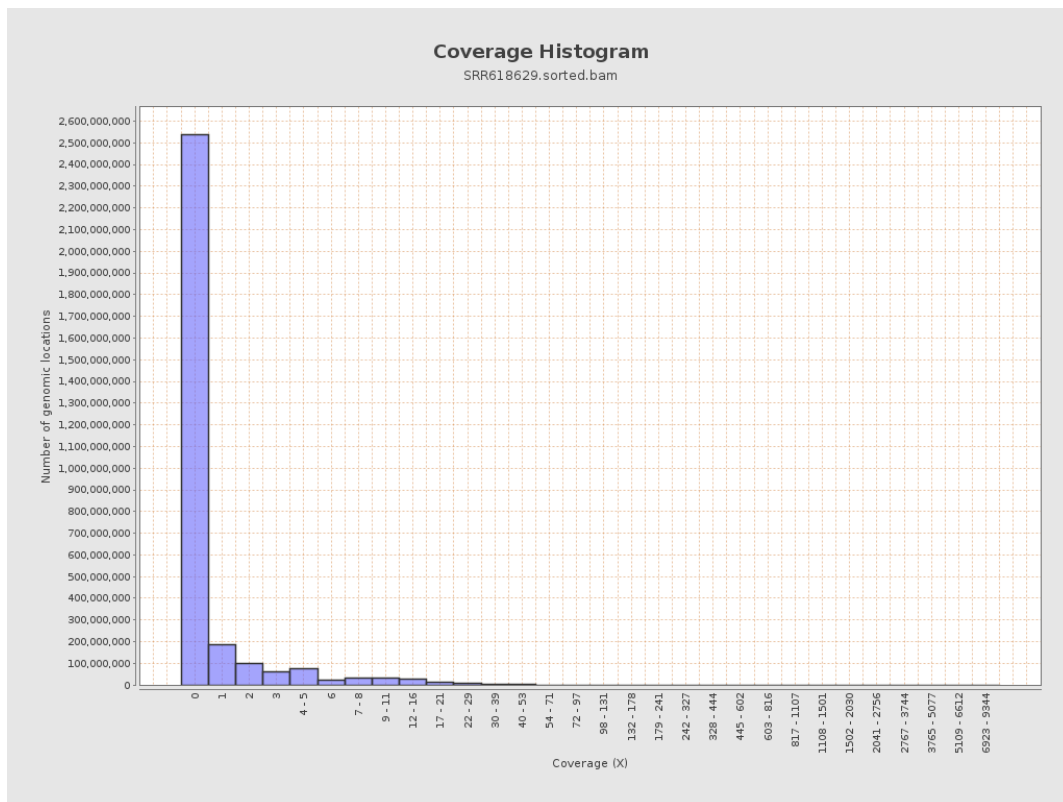
		bases	coverage	deviation
chr1	249250621	229120107	0.9192	7.1476
chr2	243199373	208502169	0.8573	5.2372
chr3	198022430	163887432	0.8276	3.2748
chr4	191154276	129682489	0.6784	3.1129
chr5	180915260	145710024	0.8054	3.3003
chr6	171115067	267716913	1.5645	5.345
chr7	159138663	127361597	0.8003	3.4936
chr8	146364022	121581797	0.8307	3.3979
chr9	141213431	111781838	0.7916	4.1238
chr10	135534747	132419896	0.977	3.7478
chr11	135006516	130718501	0.9682	4.1387
chr12	133851895	120606779	0.901	3.9748
chr13	115169878	67624006	0.5872	2.7536
chr14	107349540	80849629	0.7531	3.2542
chr15	102531392	86383457	0.8425	3.3762
chr16	90354753	93116235	1.0306	10.3554
chr17	81195210	82672342	1.0182	4.0405
chr18	78077248	63776667	0.8168	3.8376
chr19	59128983	54387502	0.9198	3.9814
chr20	63025520	74234863	1.1779	4.186
chr21	48129895	31799297	0.6607	4.555
chr22	51304566	44183538	0.8612	3.7532
chrMT	16571	15170	0.9155	3.3608
chrX	155270560	134810910	0.8682	3.3045

chrY	59373566	4430299	0.0746	3.0249
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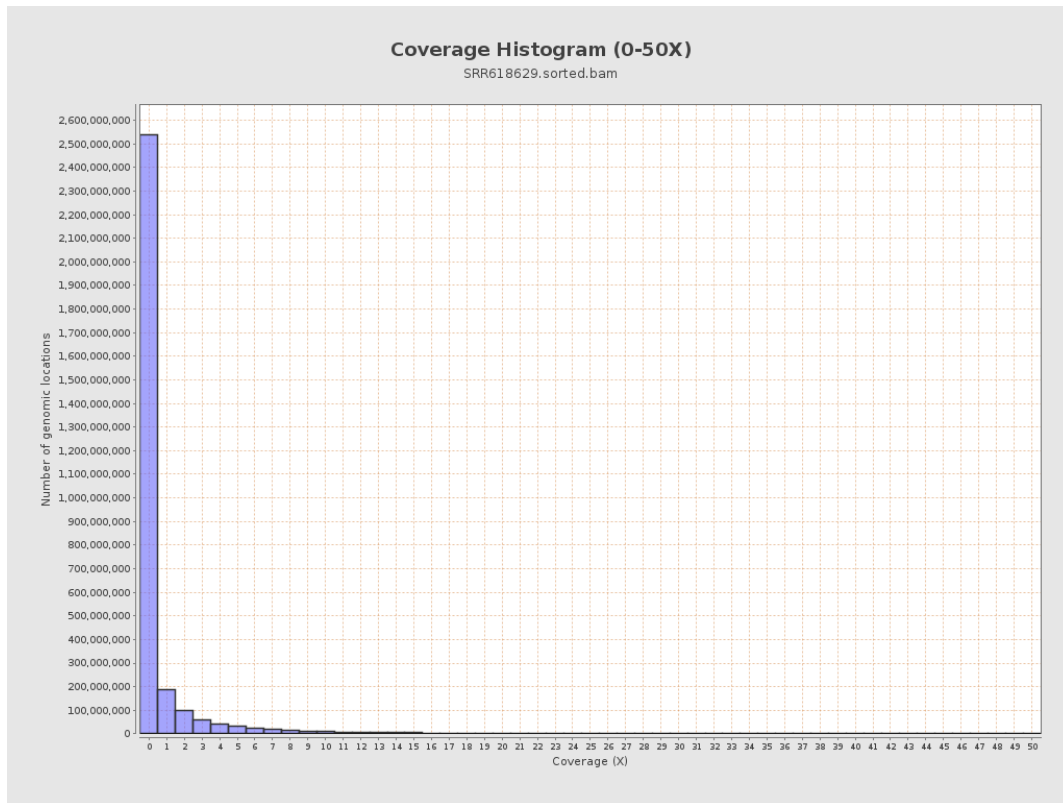
3. Results : Coverage across reference



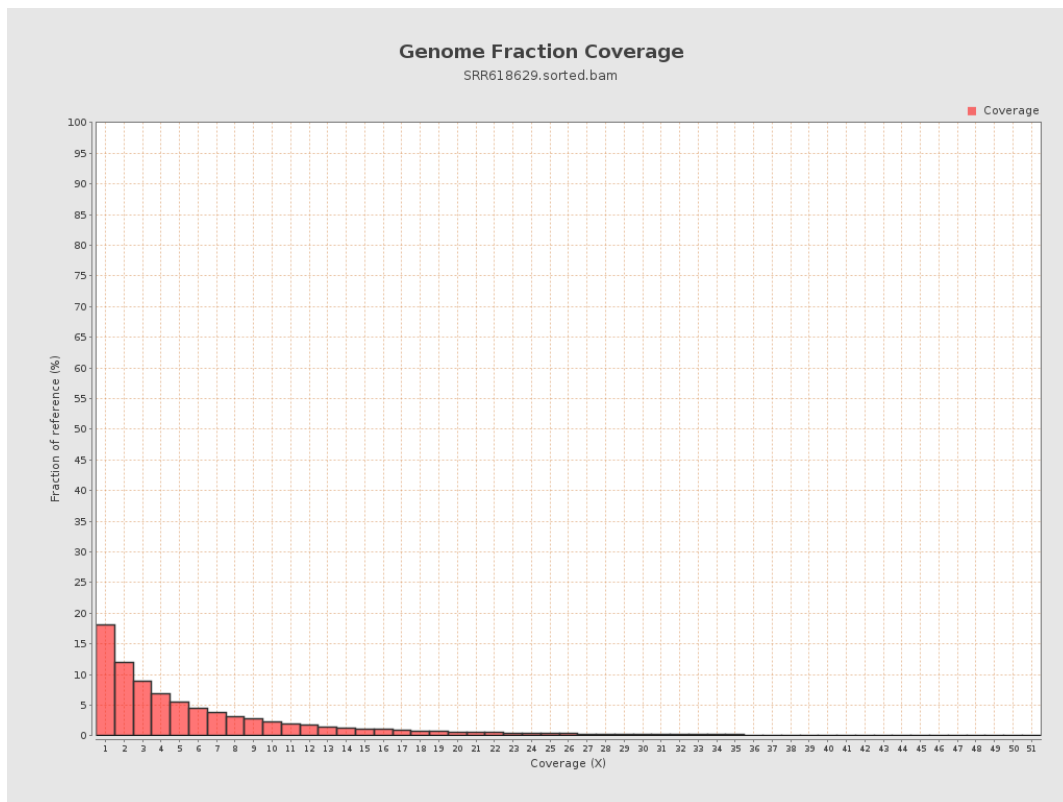
4. Results : Coverage Histogram



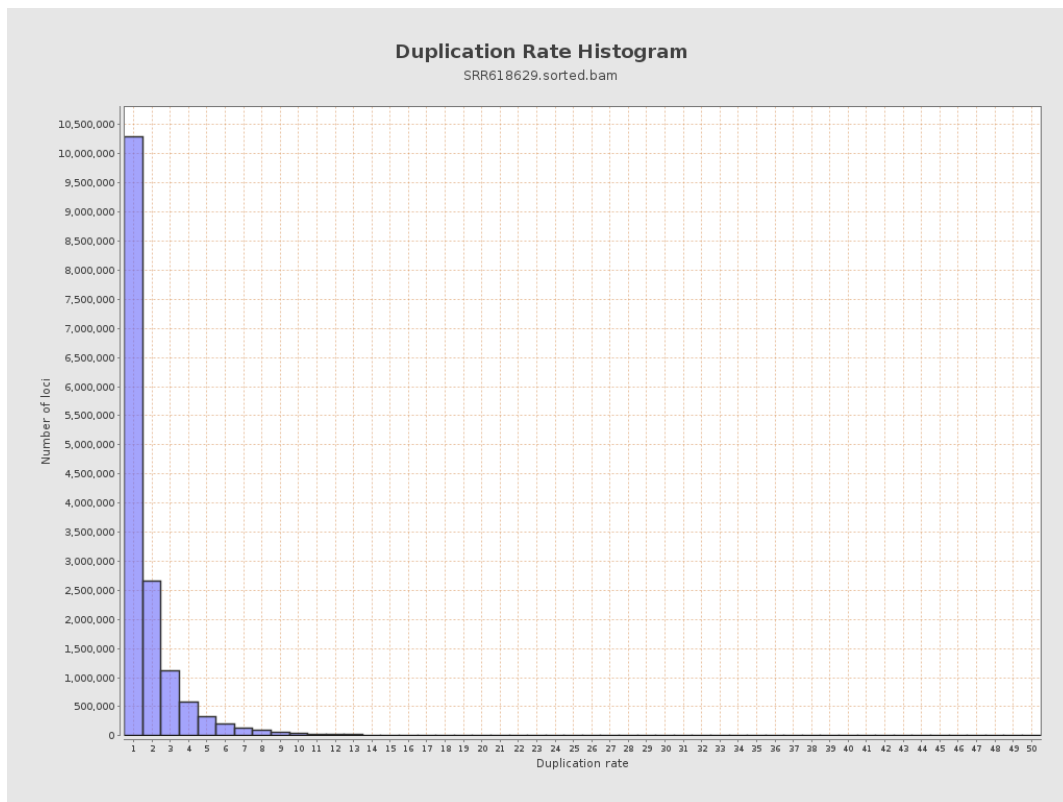
5. Results : Coverage Histogram (0-50X)



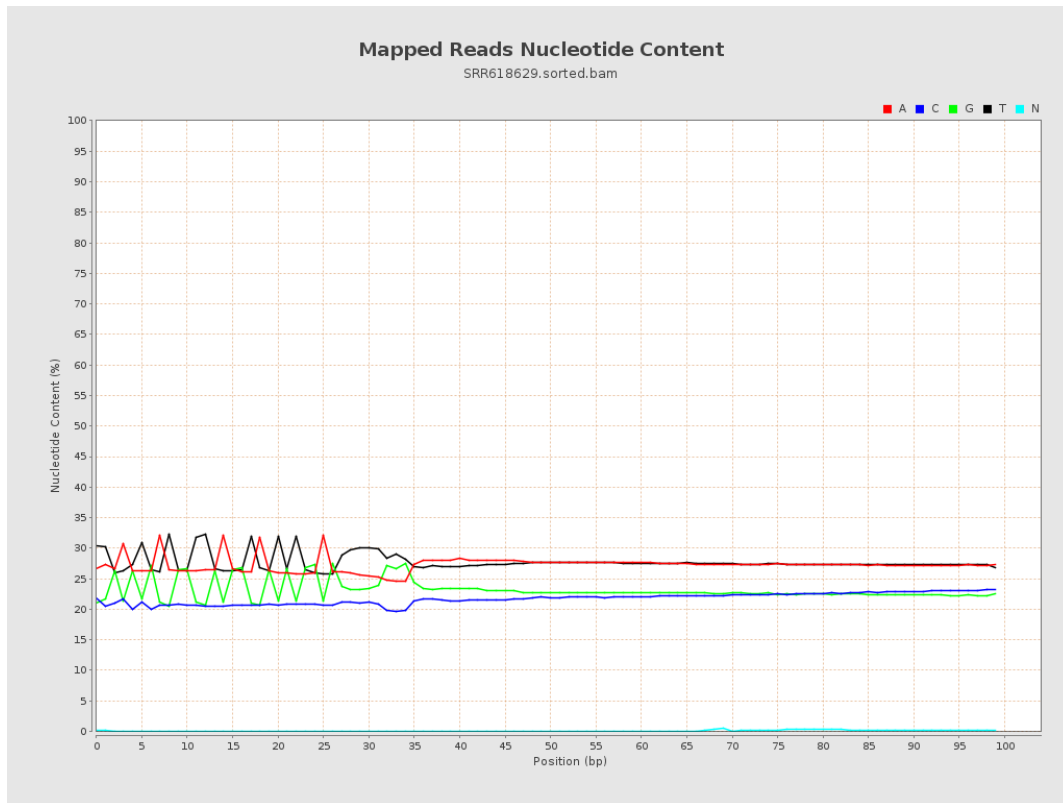
6. Results : Genome Fraction Coverage



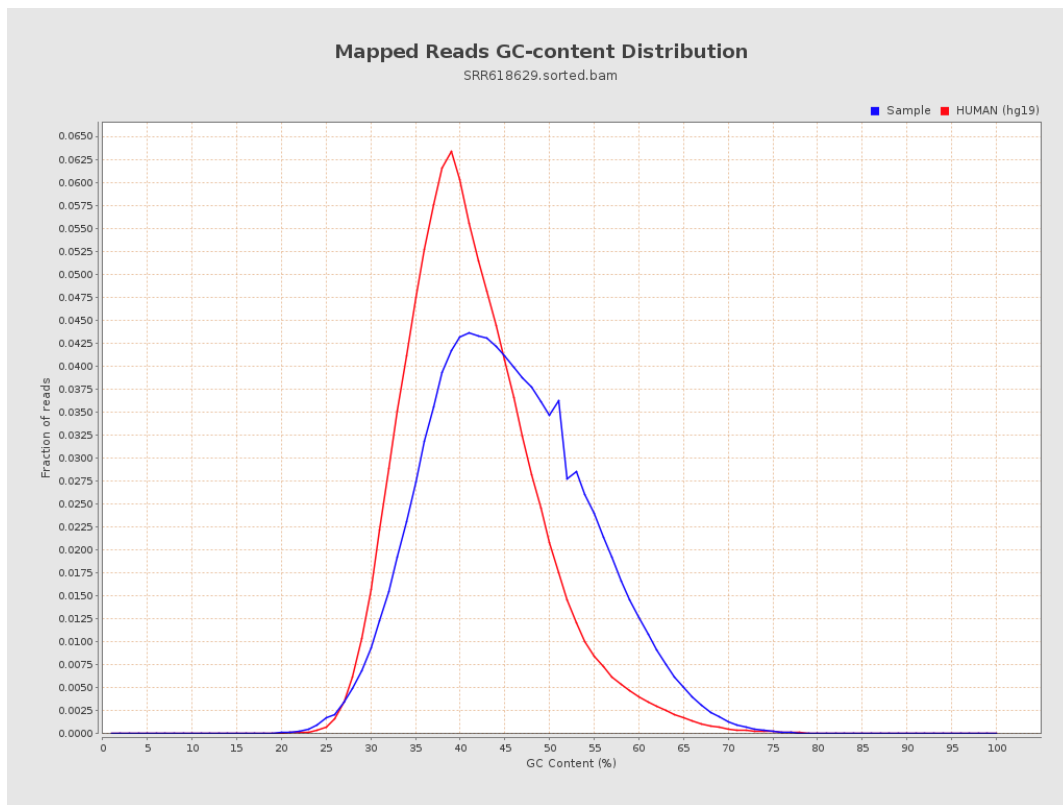
7. Results : Duplication Rate Histogram



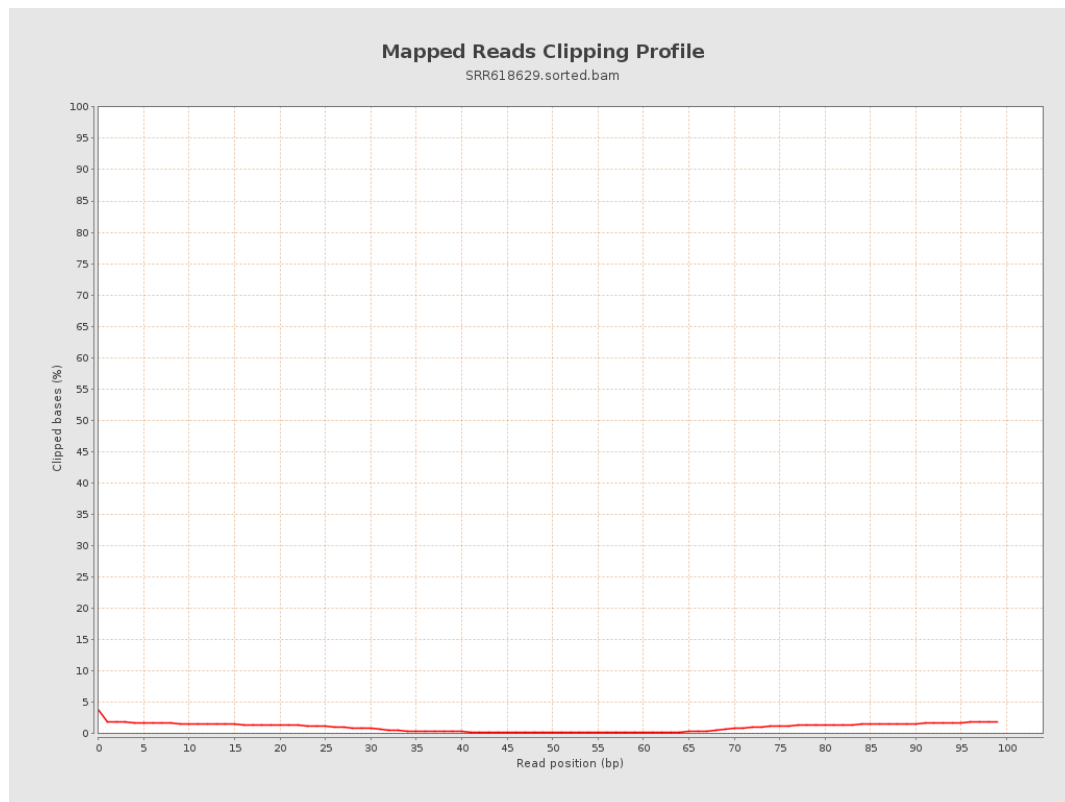
8. Results : Mapped Reads Nucleotide Content



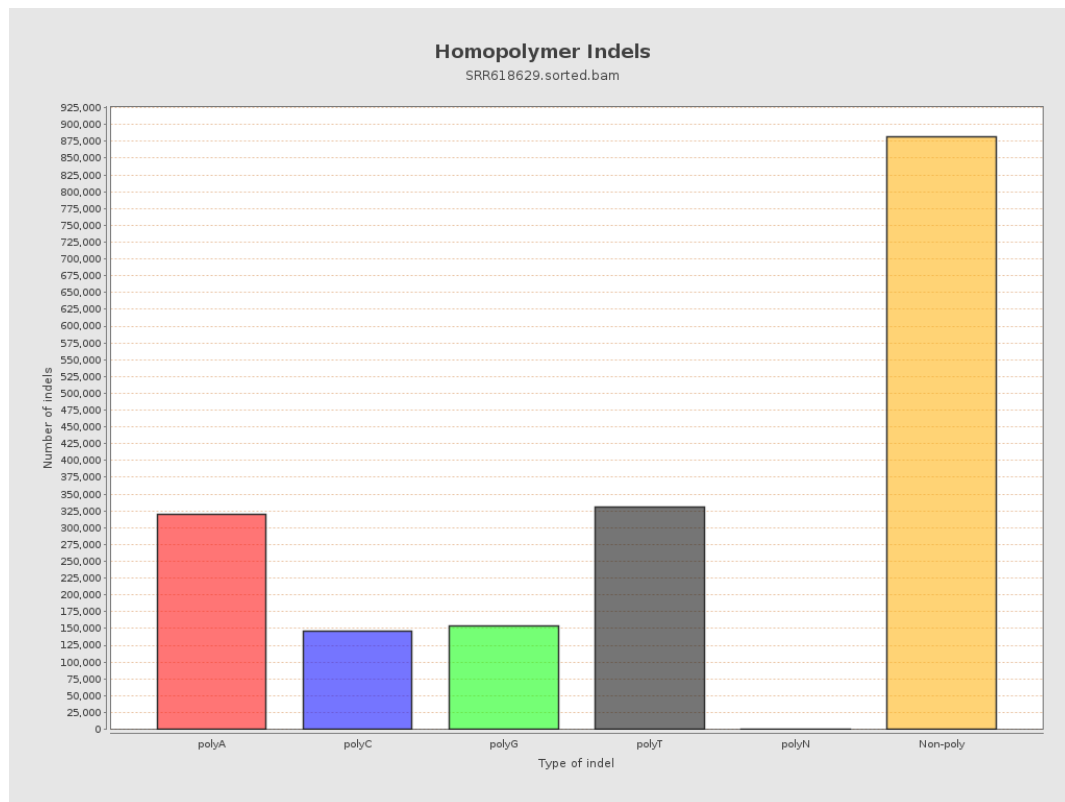
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



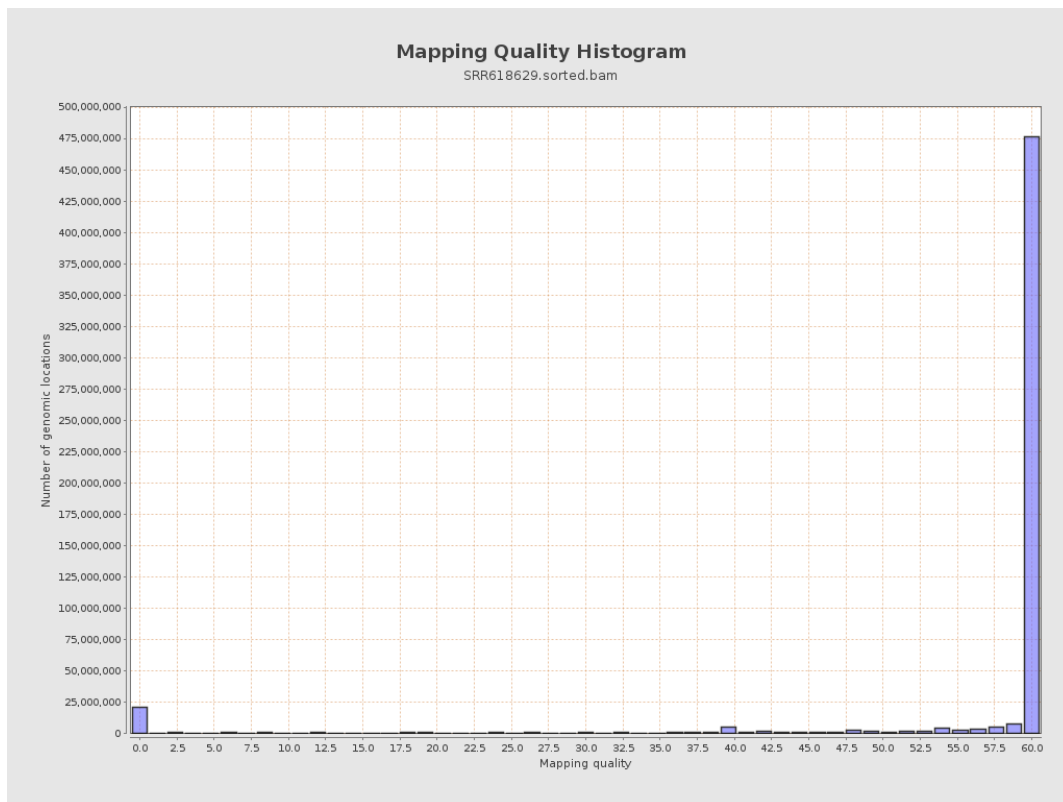
11. Results : Homopolymer Indels



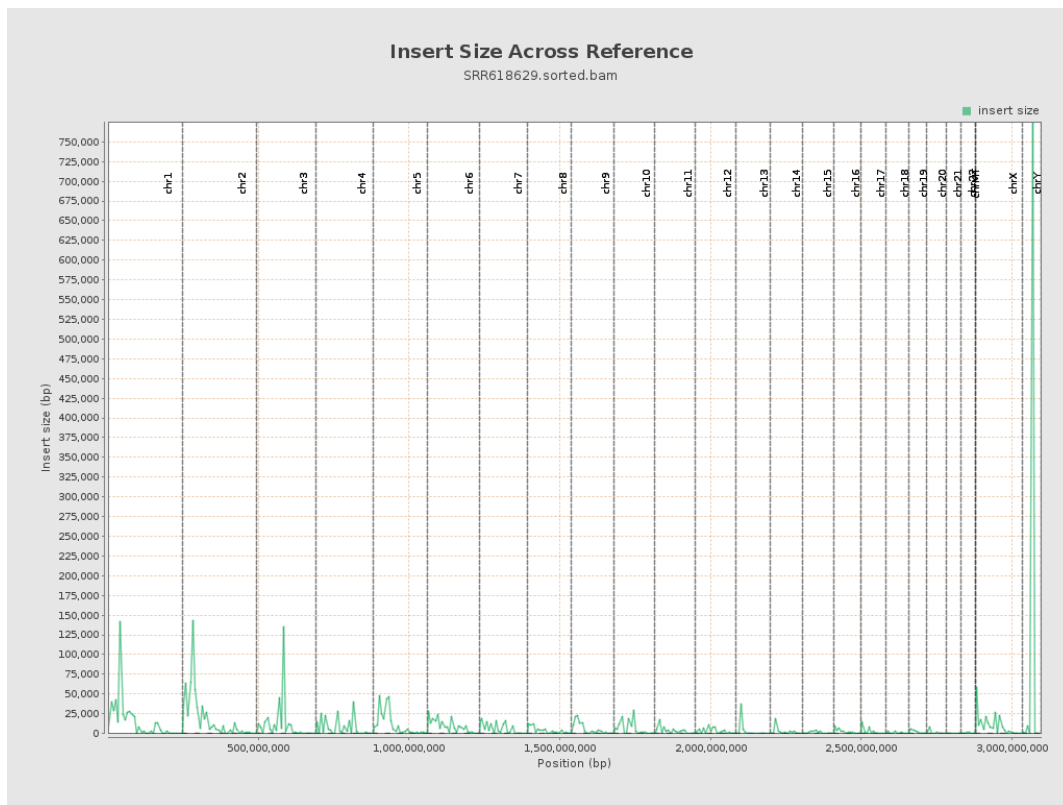
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

