

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/02/19 16:30:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR16328243.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_SRR16328243 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16328243_1.fastq.gz SRR16328243_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Feb 19 16:30:50 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR16328243.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	41,713,784
Mapped reads	39,231,856 / 94.05%
Unmapped reads	2,481,928 / 5.95%
Mapped paired reads	39,231,856 / 94.05%
Mapped reads, first in pair	19,659,581 / 47.13%
Mapped reads, second in pair	19,572,275 / 46.92%
Mapped reads, both in pair	38,330,562 / 91.89%
Mapped reads, singletons	901,294 / 2.16%
Secondary alignments	0
Supplementary alignments	445,260 / 1.07%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	3,117,439 / 7.47%
Duplication rate	4.39%
Clipped reads	22,807,309 / 54.68%

2.2. ACGT Content

Number/percentage of A's	776,639,630 / 29.41%
Number/percentage of C's	537,805,522 / 20.36%
Number/percentage of T's	768,916,598 / 29.12%
Number/percentage of G's	557,433,224 / 21.11%
Number/percentage of N's	88,999 / 0%

GC Percentage	41.47%
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2.3. Coverage

Mean	0.8535
Standard Deviation	9.4878

2.4. Mapping Quality

Mean Mapping Quality	51.71
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2.5. Insert size

Mean	166,725.51
Standard Deviation	3,909,777.09
P25/Median/P75	256 / 348 / 462

2.6. Mismatches and indels

General error rate	0.94%
Mismatches	24,320,400
Insertions	260,343
Mapped reads with at least one insertion	0.66%
Deletions	1,027,197
Mapped reads with at least one deletion	2.58%
Homopolymer indels	44.64%

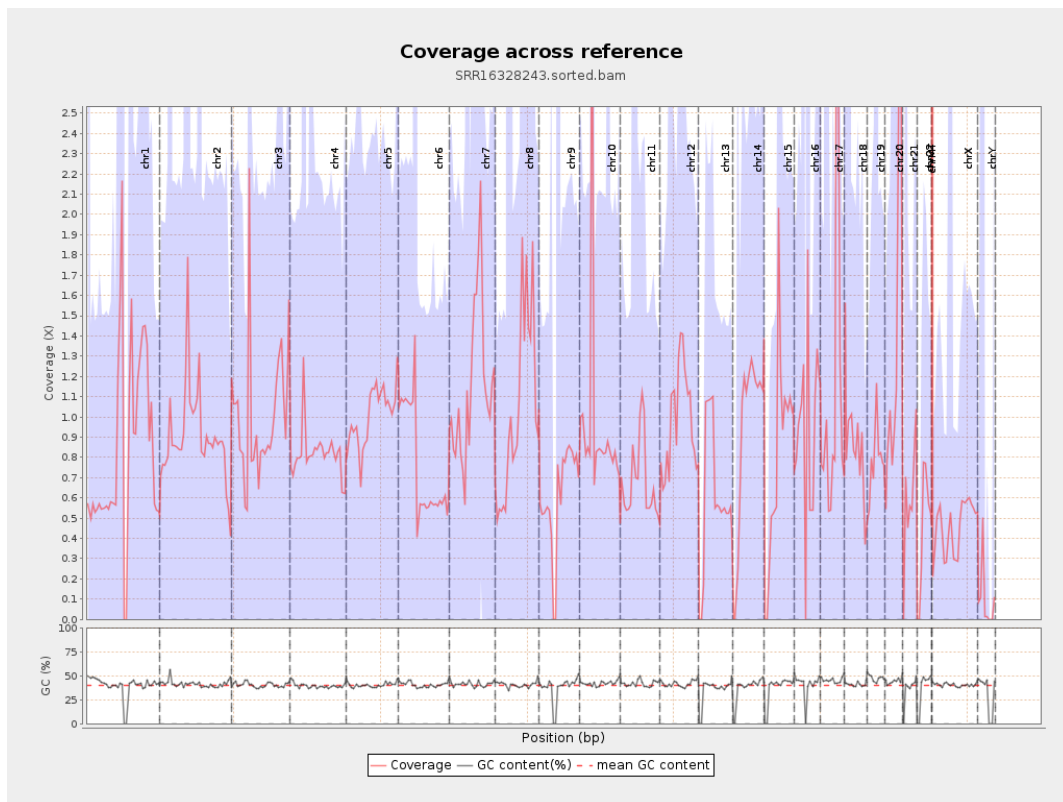
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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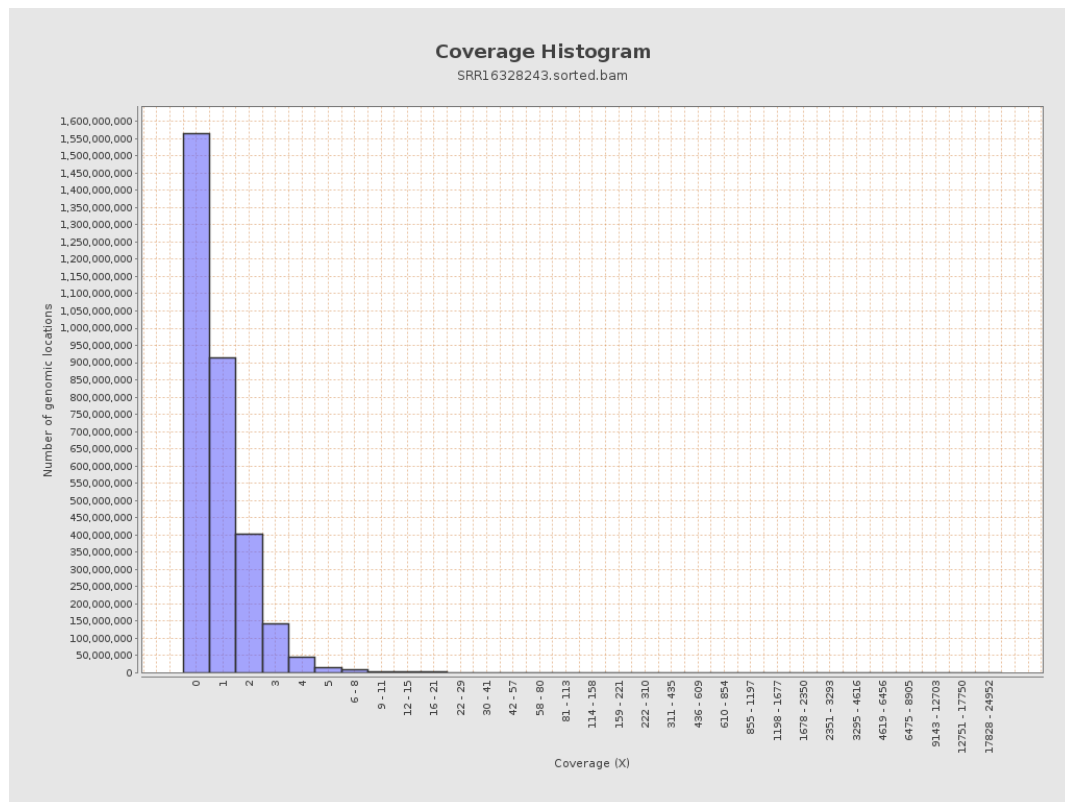
		bases	coverage	deviation
chr1	249250621	210571198	0.8448	21.7244
chr2	243199373	221324941	0.9101	14.1819
chr3	198022430	195824163	0.9889	1.5666
chr4	191154276	156121786	0.8167	3.0158
chr5	180915260	182507616	1.0088	1.1866
chr6	171115067	128596135	0.7515	3.766
chr7	159138663	182997471	1.1499	5.943
chr8	146364022	152115475	1.0393	12.6932
chr9	141213431	85650429	0.6065	3.9358
chr10	135534747	132127456	0.9749	16.7059
chr11	135006516	92334964	0.6839	2.7558
chr12	133851895	131478596	0.9823	1.2578
chr13	115169878	69474939	0.6032	0.9383
chr14	107349540	98988844	0.9221	1.4297
chr15	102531392	82569608	0.8053	1.2595
chr16	90354753	86156865	0.9535	7.6331
chr17	81195210	89552946	1.1029	3.2543
chr18	78077248	64919466	0.8315	7.5819
chr19	59128983	46385521	0.7845	12.4327
chr20	63025520	88185195	1.3992	2.837
chr21	48129895	29784990	0.6188	1.8153
chr22	51304566	23333835	0.4548	0.9202
chrMT	16571	15065012	909.1191	194.8399
chrX	155270560	69980738	0.4507	1.3988

chrY	59373566	6220214	0.1048	4.2611
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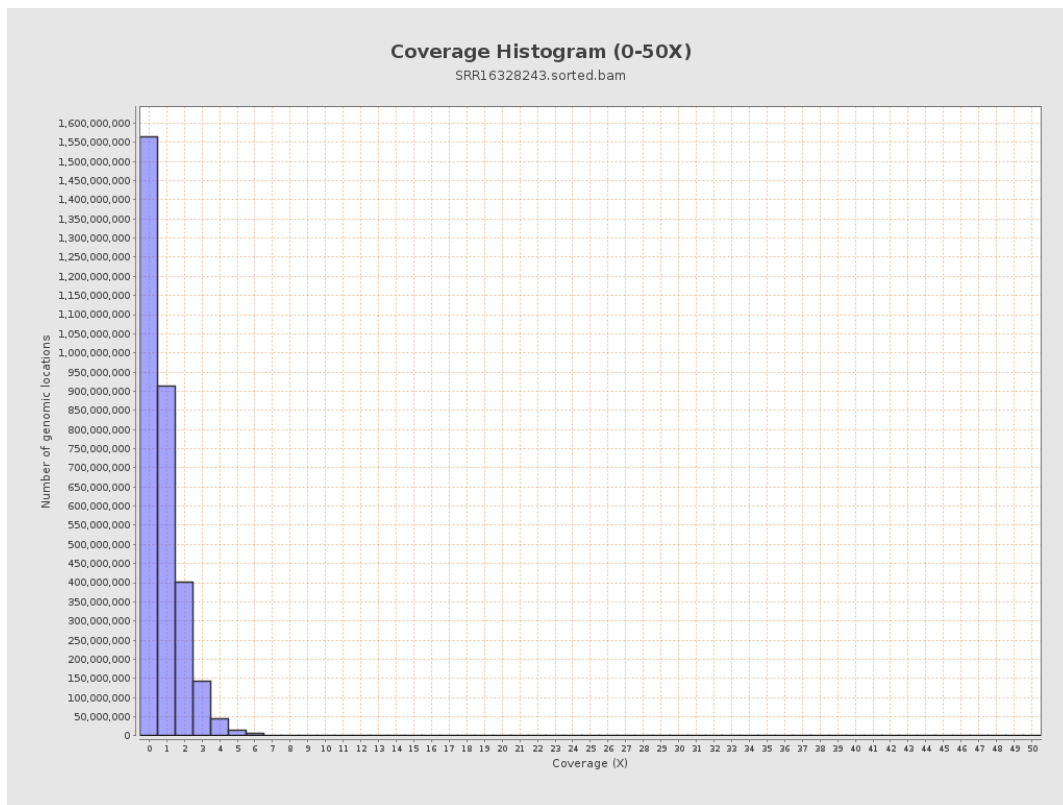
3. Results : Coverage across reference



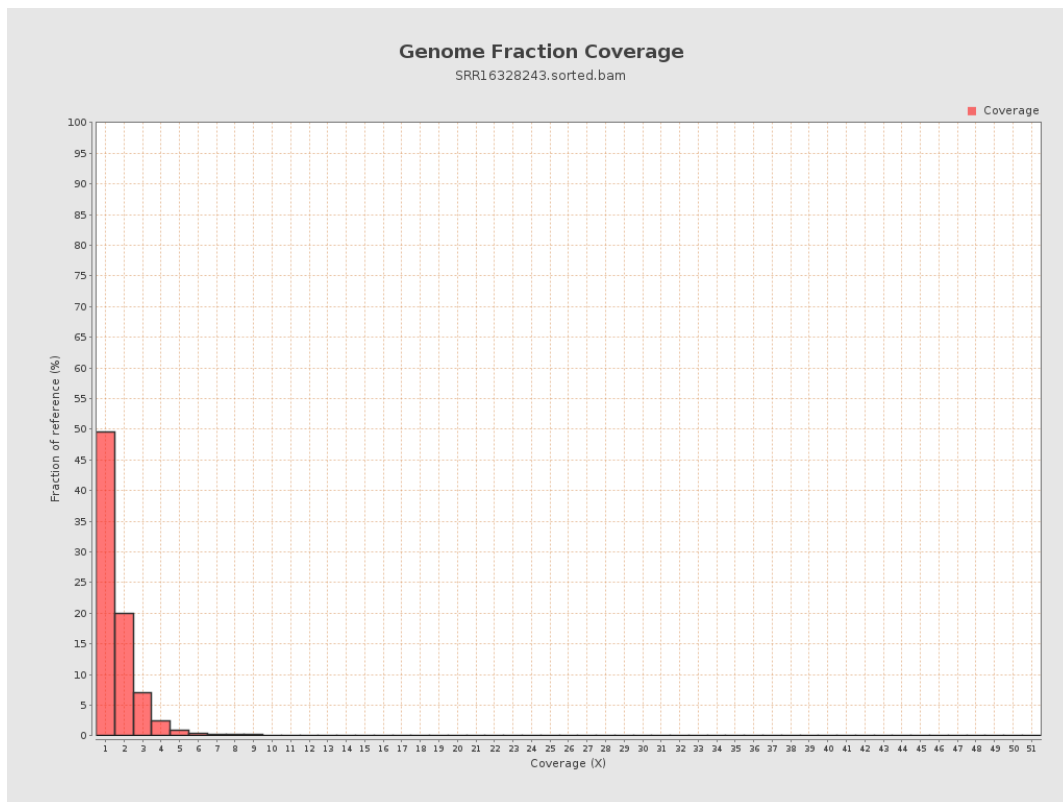
4. Results : Coverage Histogram



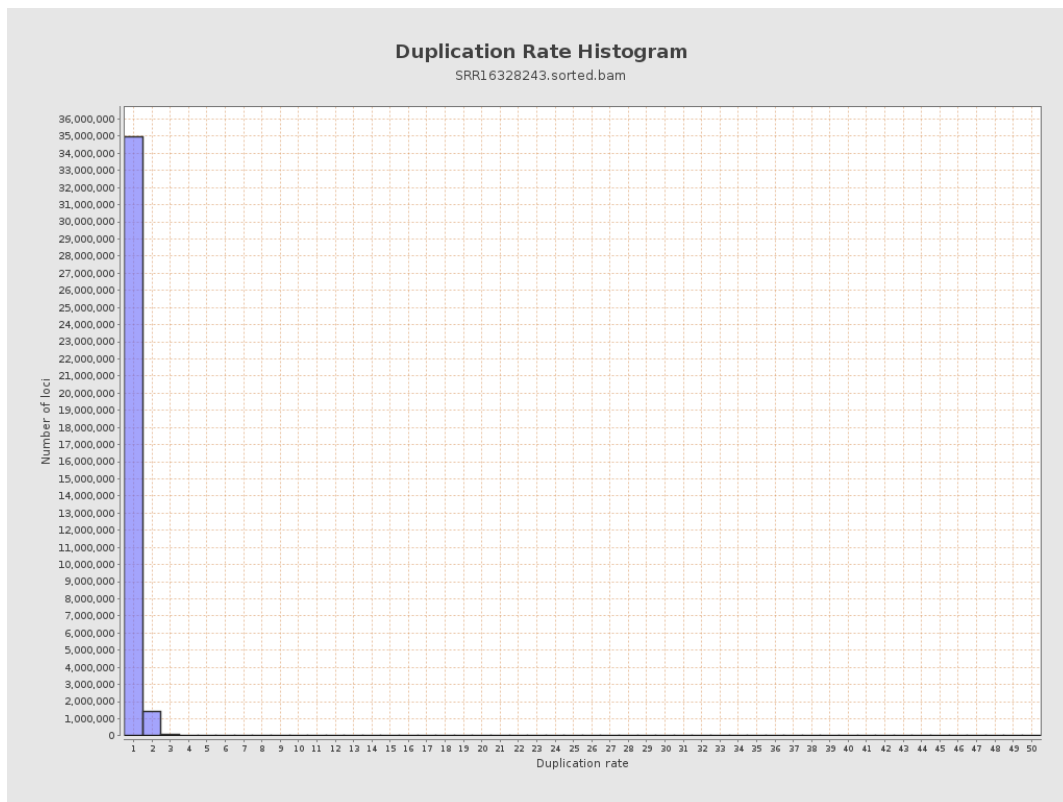
5. Results : Coverage Histogram (0-50X)



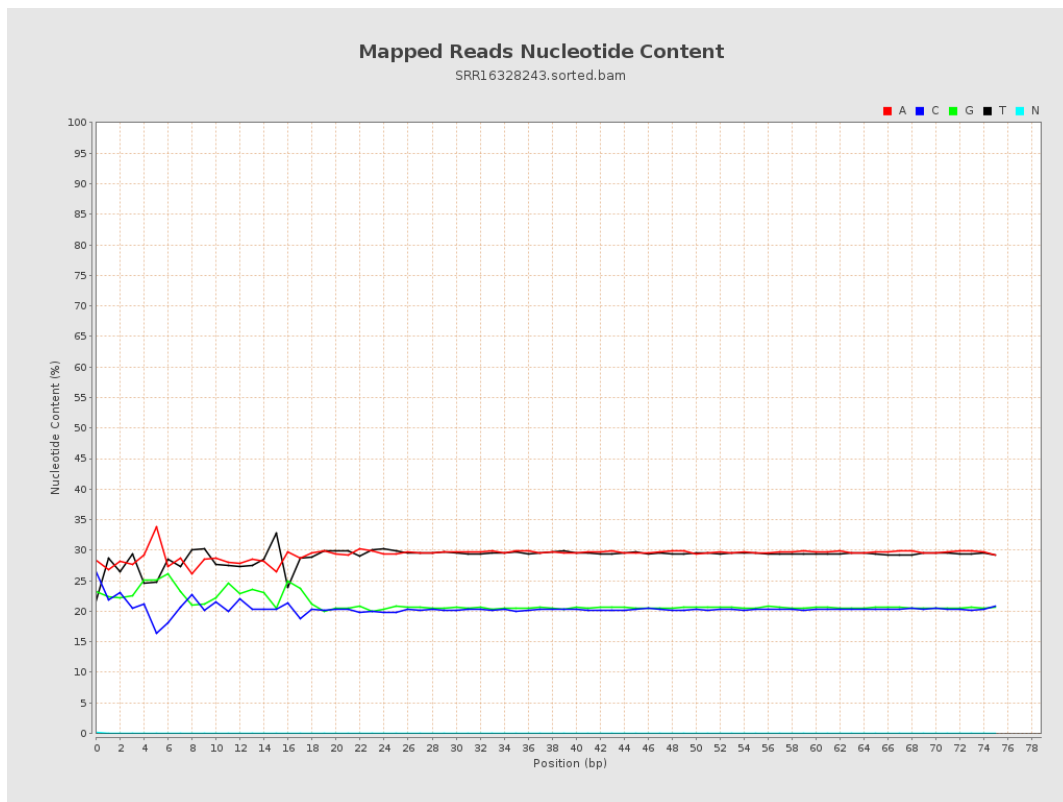
6. Results : Genome Fraction Coverage



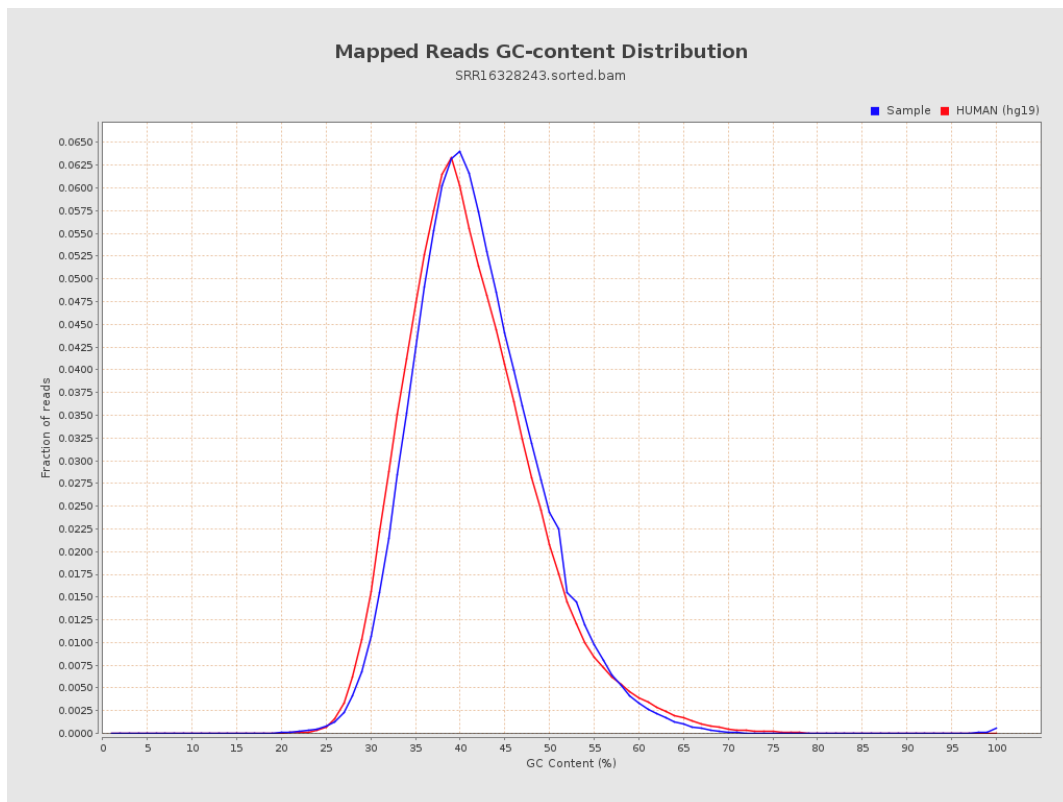
7. Results : Duplication Rate Histogram



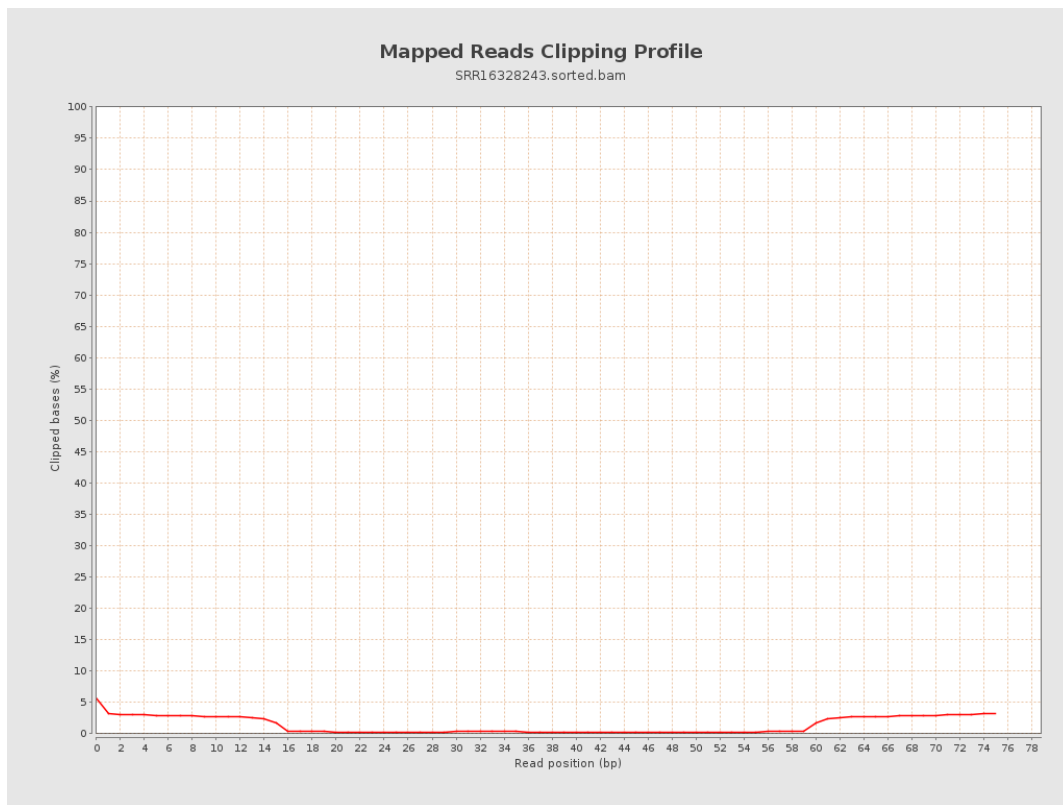
8. Results : Mapped Reads Nucleotide Content



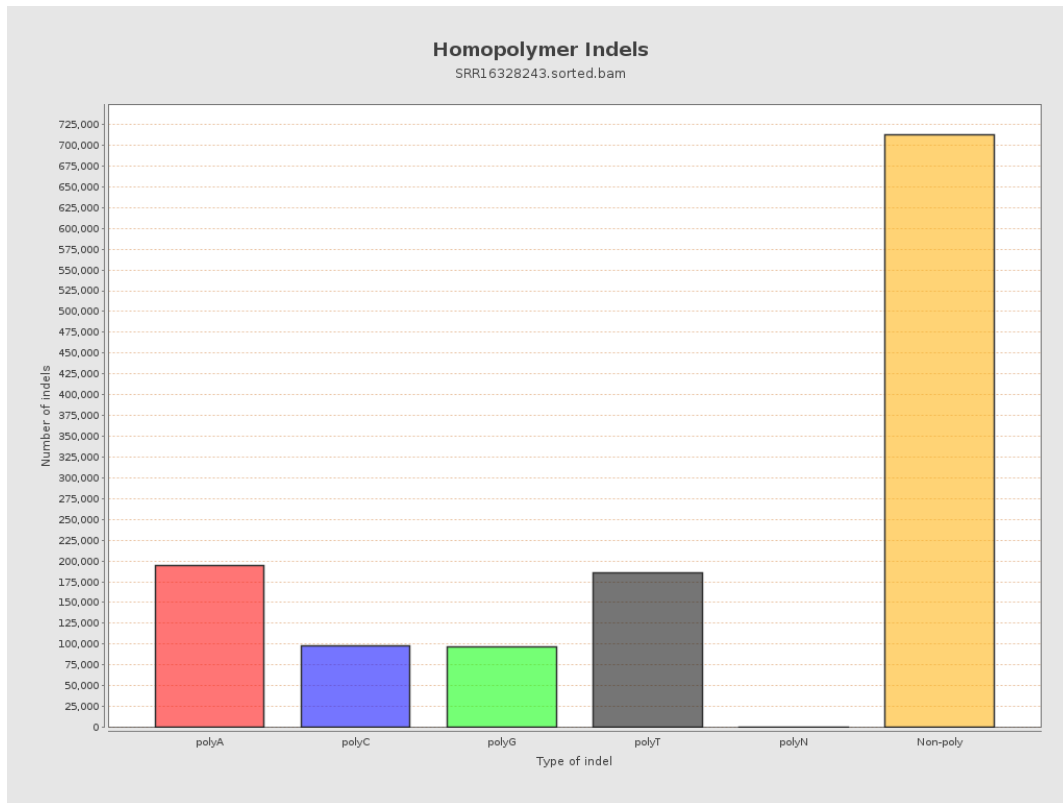
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



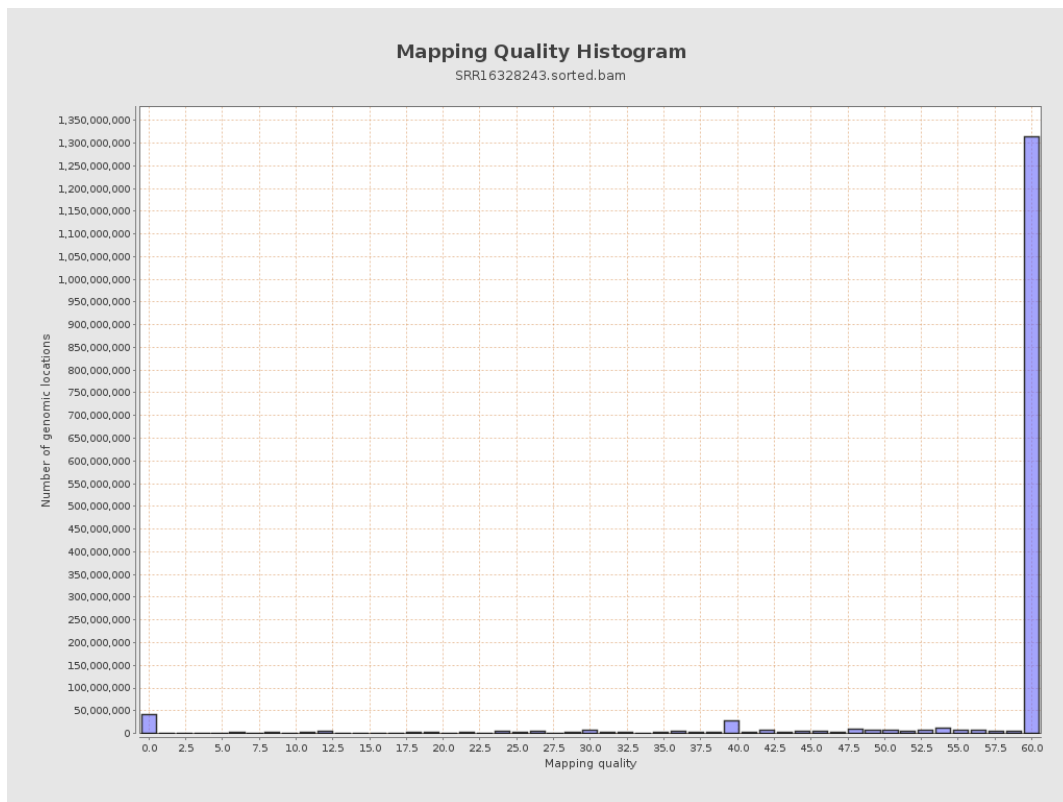
11. Results : Homopolymer Indels



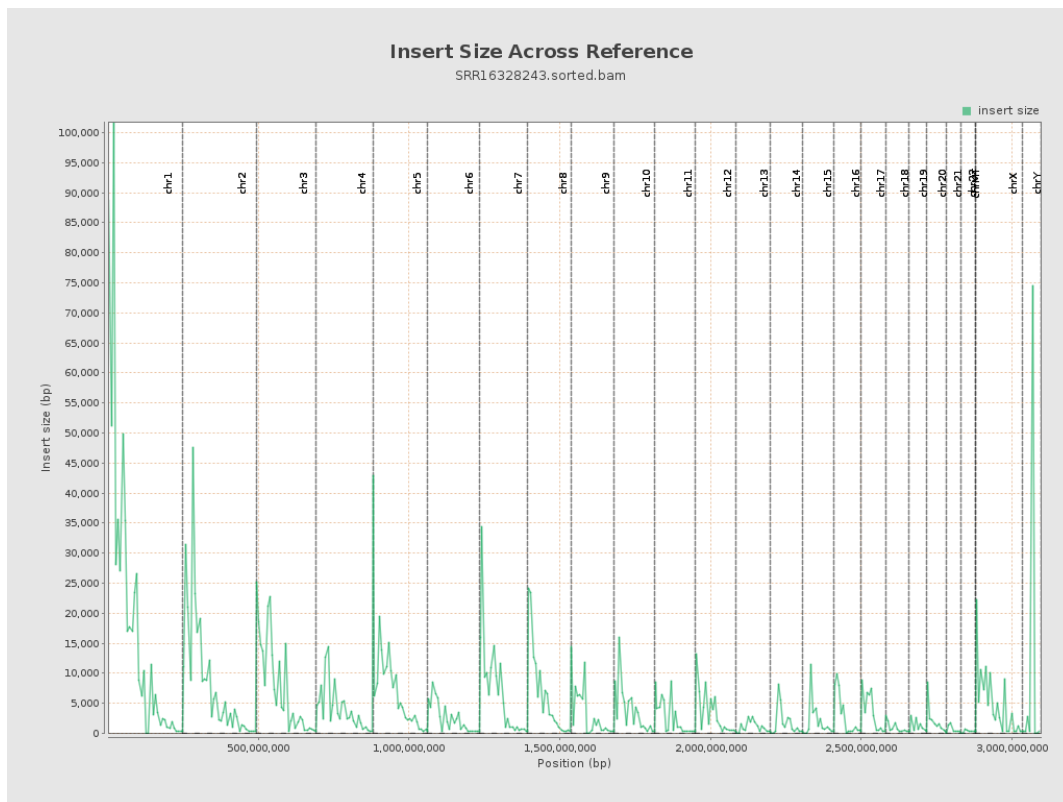
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

