

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/02/21 07:23:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR16328246.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_SRR16328246 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16328246_1.fastq.gz SRR16328246_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Feb 21 07:23:35 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR16328246.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	603,411,566
Mapped reads	590,043,456 / 97.78%
Unmapped reads	13,368,110 / 2.22%
Mapped paired reads	590,043,456 / 97.78%
Mapped reads, first in pair	297,072,535 / 49.23%
Mapped reads, second in pair	292,970,921 / 48.55%
Mapped reads, both in pair	582,393,082 / 96.52%
Mapped reads, singletons	7,650,374 / 1.27%
Secondary alignments	0
Supplementary alignments	31,178,808 / 5.17%
Read min/max/mean length	30 / 150 / 152.57
Duplicated reads (estimated)	340,823,639 / 56.48%
Duplication rate	45.94%
Clipped reads	378,000,323 / 62.64%

2.2. ACGT Content

Number/percentage of A's	23,032,286,543 / 28.2%
Number/percentage of C's	17,259,661,795 / 21.13%
Number/percentage of T's	22,865,434,139 / 27.99%
Number/percentage of G's	18,528,141,481 / 22.68%
Number/percentage of N's	1,468,967 / 0%

GC Percentage	43.81%
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2.3. Coverage

Mean	26.4495
Standard Deviation	1,002.5069

2.4. Mapping Quality

Mean Mapping Quality	52.92
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2.5. Insert size

Mean	412,613.29
Standard Deviation	6,656,853.61
P25/Median/P75	253 / 375 / 542

2.6. Mismatches and indels

General error rate	1.27%
Mismatches	967,145,563
Insertions	20,708,719
Mapped reads with at least one insertion	3.18%
Deletions	66,421,809
Mapped reads with at least one deletion	10.57%
Homopolymer indels	47.65%

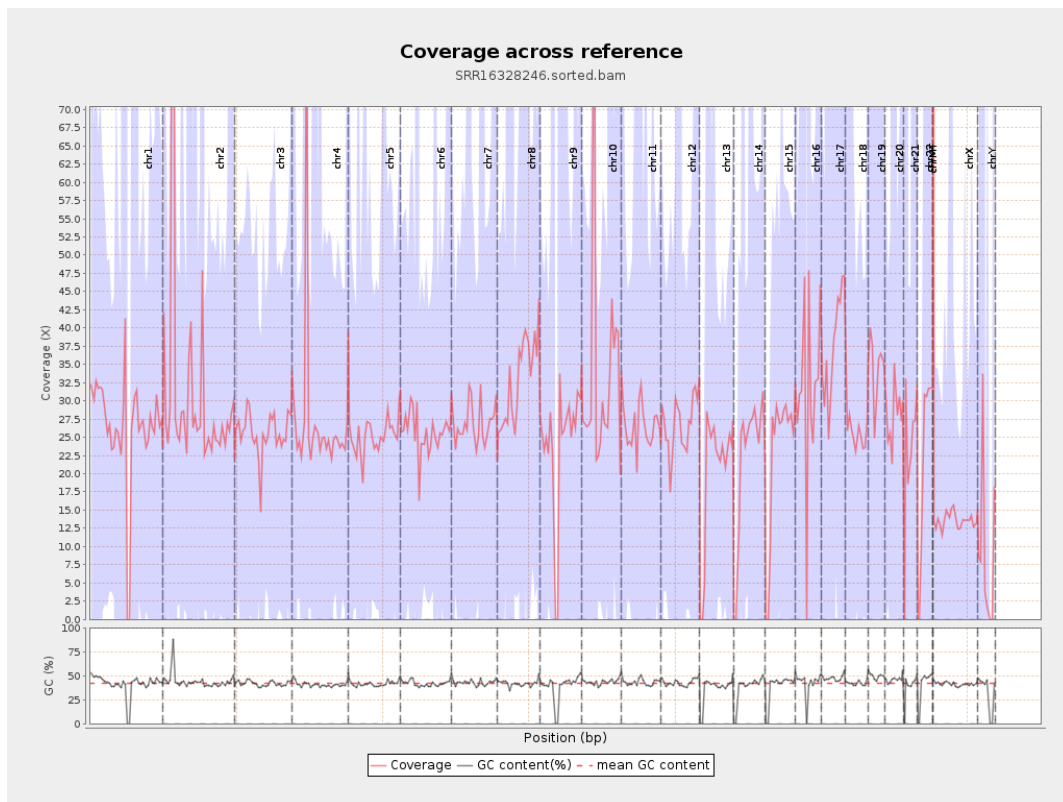
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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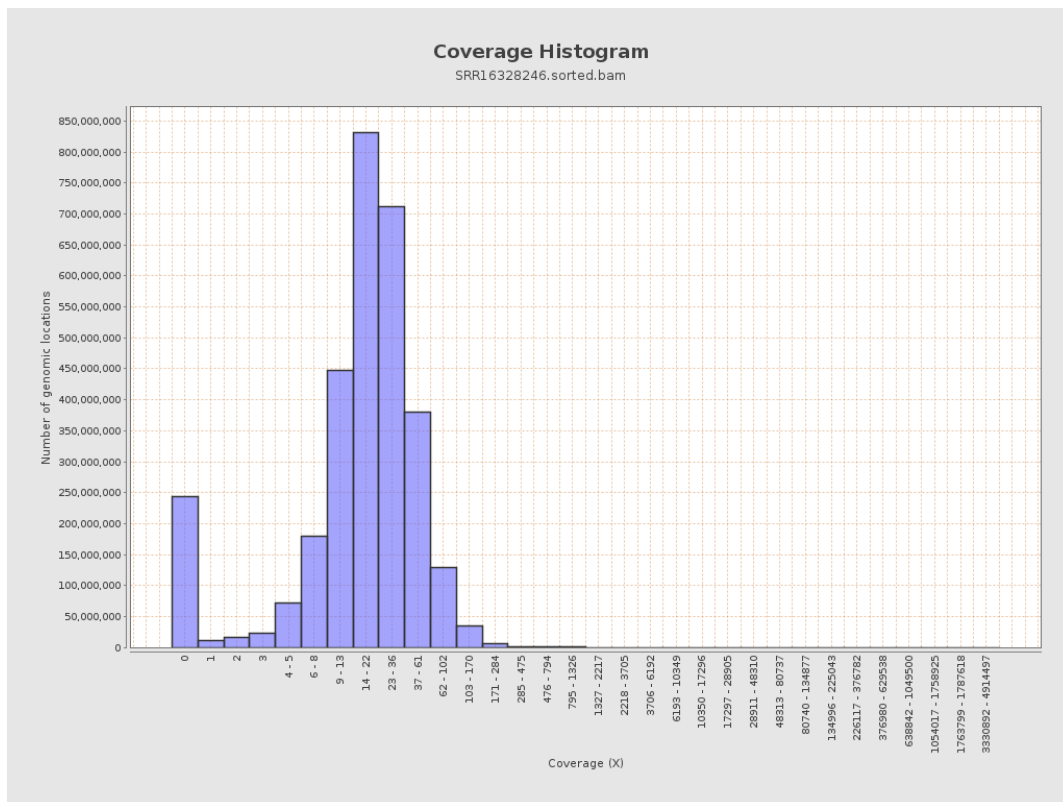
		bases	coverage	deviation
chr1	249250621	6564524350	26.337	398.4598
chr2	243199373	7526810694	30.9491	3,443.5593
chr3	198022430	5059037451	25.5478	35.9777
chr4	191154276	5220905272	27.3125	481.8794
chr5	180915260	4573996165	25.2825	39.239
chr6	171115067	4374861470	25.5668	75.6284
chr7	159138663	4302694177	27.0374	160.9814
chr8	146364022	4837318353	33.0499	407.0387
chr9	141213431	3388736583	23.9973	254.2933
chr10	135534747	4525907319	33.393	525.4775
chr11	135006516	3576682441	26.4927	86.1199
chr12	133851895	3604062578	26.9257	100.9141
chr13	115169878	2349631141	20.4014	52.9937
chr14	107349540	2404386403	22.3977	55.266
chr15	102531392	2286758168	22.303	30.9988
chr16	90354753	2863171494	31.6881	258.1731
chr17	81195210	3048818110	37.5492	128.6159
chr18	78077248	2032209161	26.0282	212.674
chr19	59128983	2029332823	34.3204	305.807
chr20	63025520	1756084417	27.8631	134.5758
chr21	48129895	1151475780	23.9243	232.2626
chr22	51304566	1108948949	21.615	44.8748
chrMT	16571	629957621	38,015.6672	20,827.5031
chrX	155270560	2111244359	13.5972	37.9454

chrY	59373566	552014655	9.2973	452.9028
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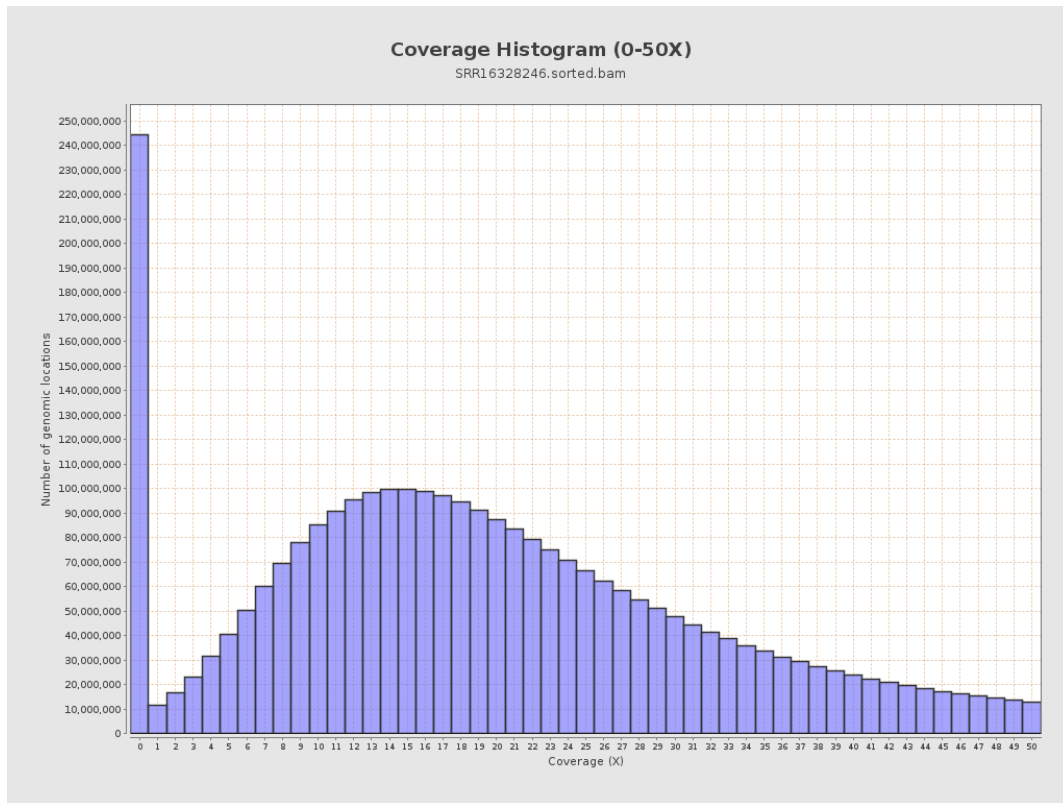
3. Results : Coverage across reference



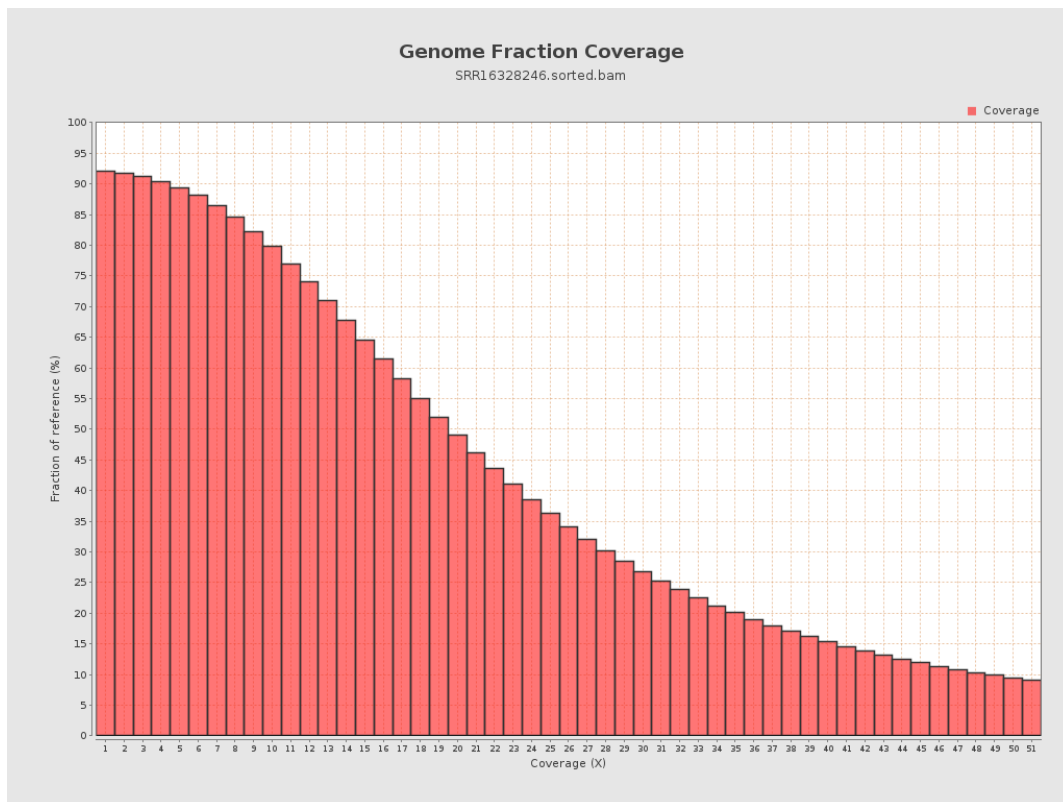
4. Results : Coverage Histogram



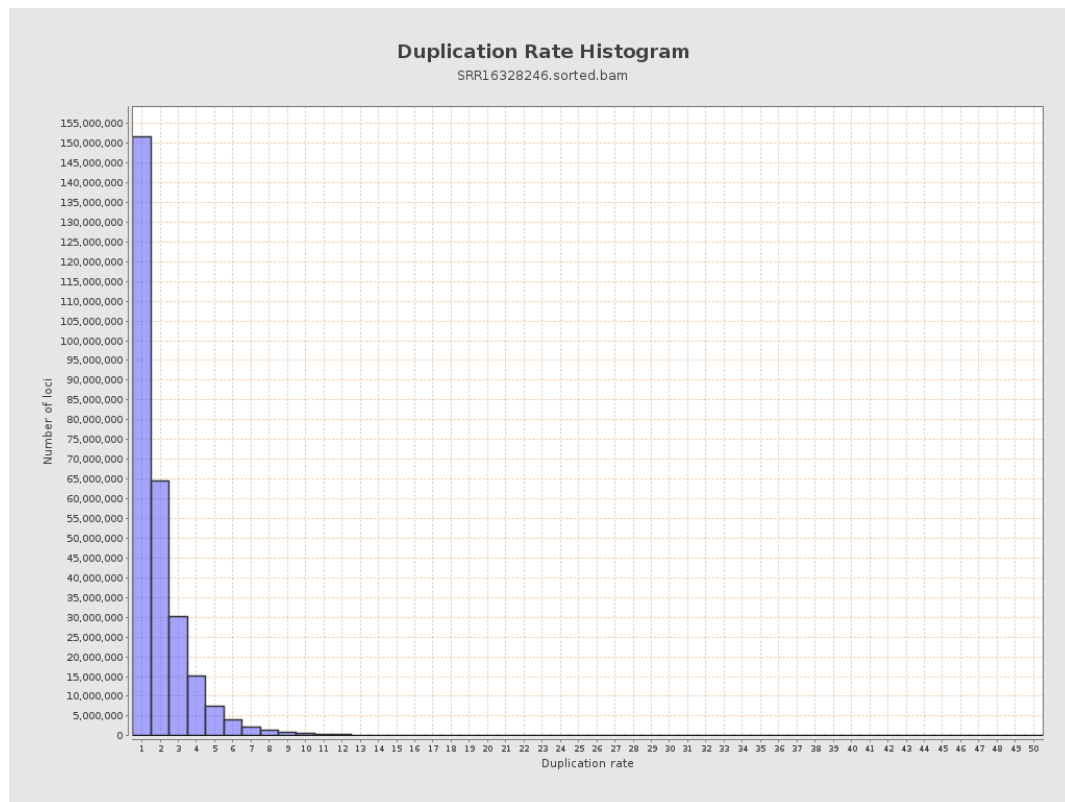
5. Results : Coverage Histogram (0-50X)



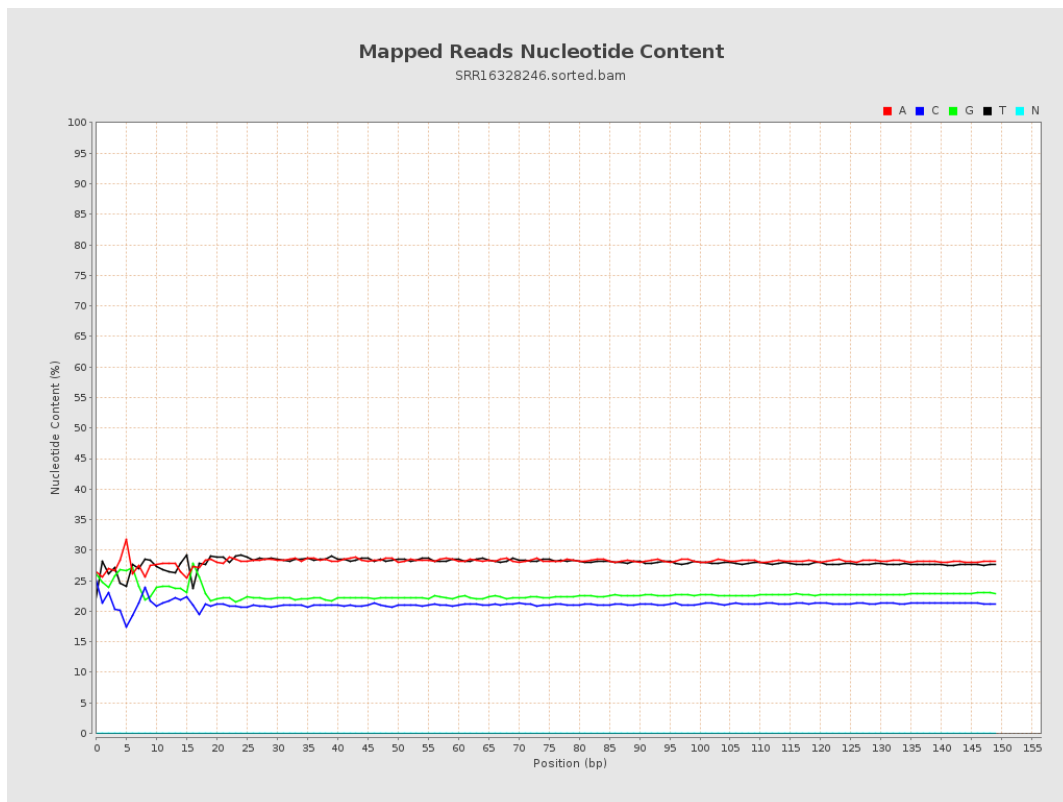
6. Results : Genome Fraction Coverage



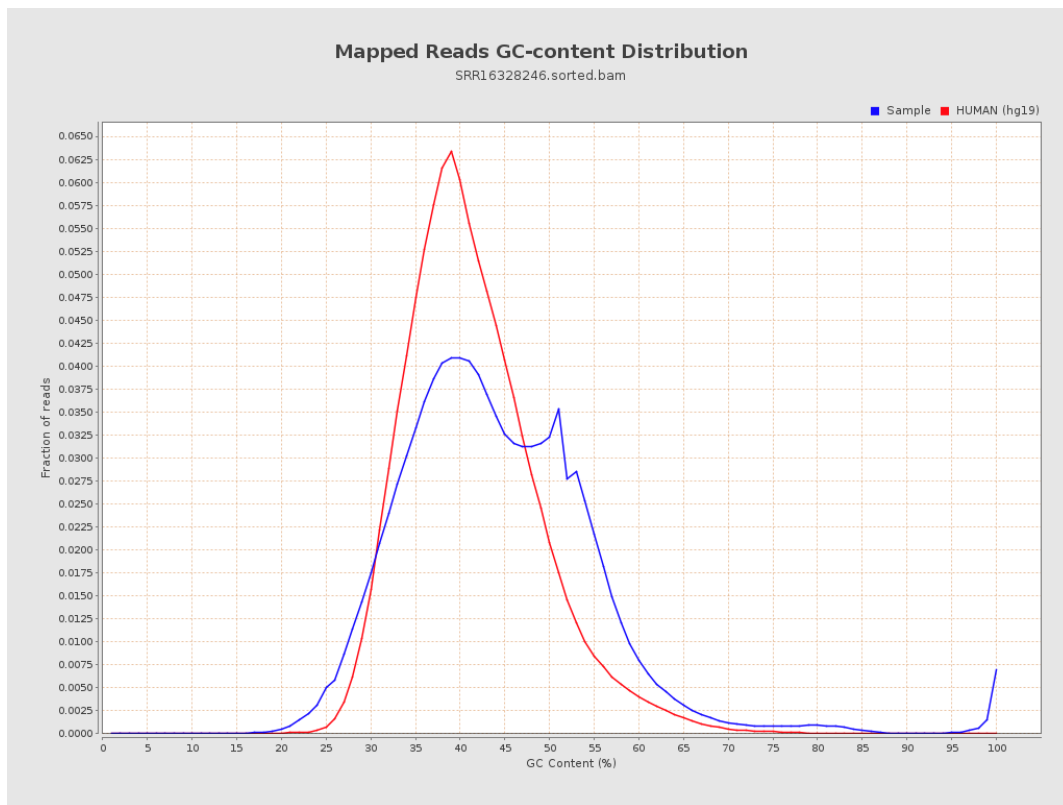
7. Results : Duplication Rate Histogram



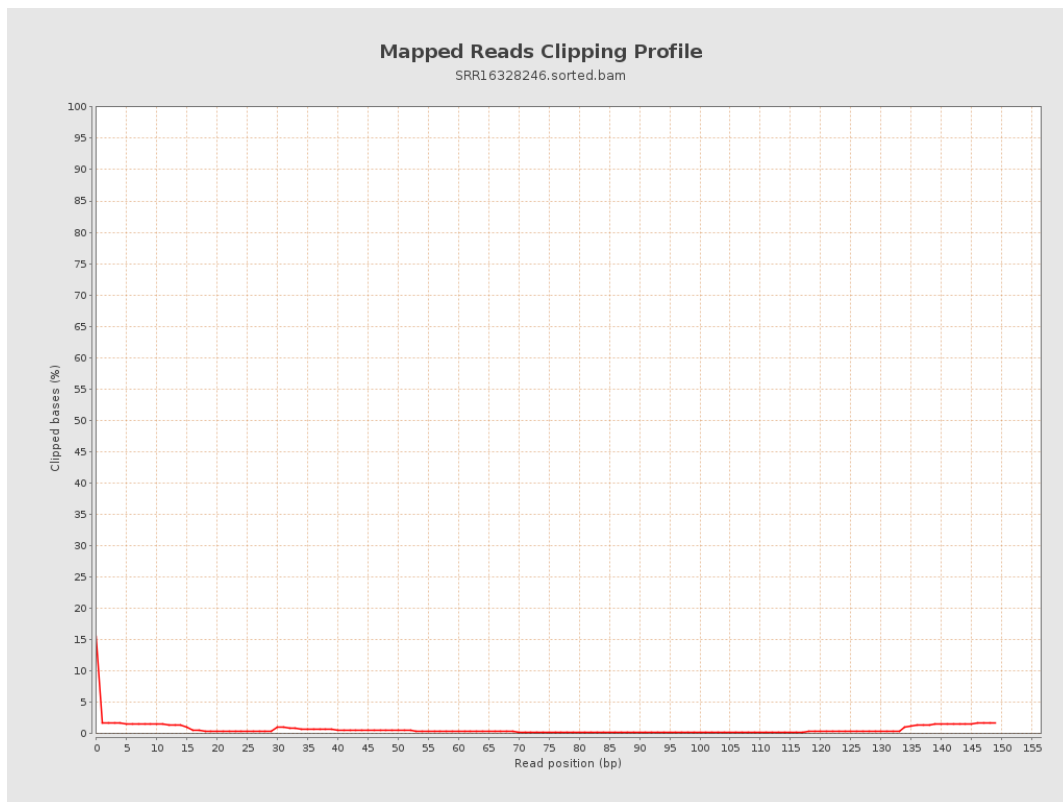
8. Results : Mapped Reads Nucleotide Content



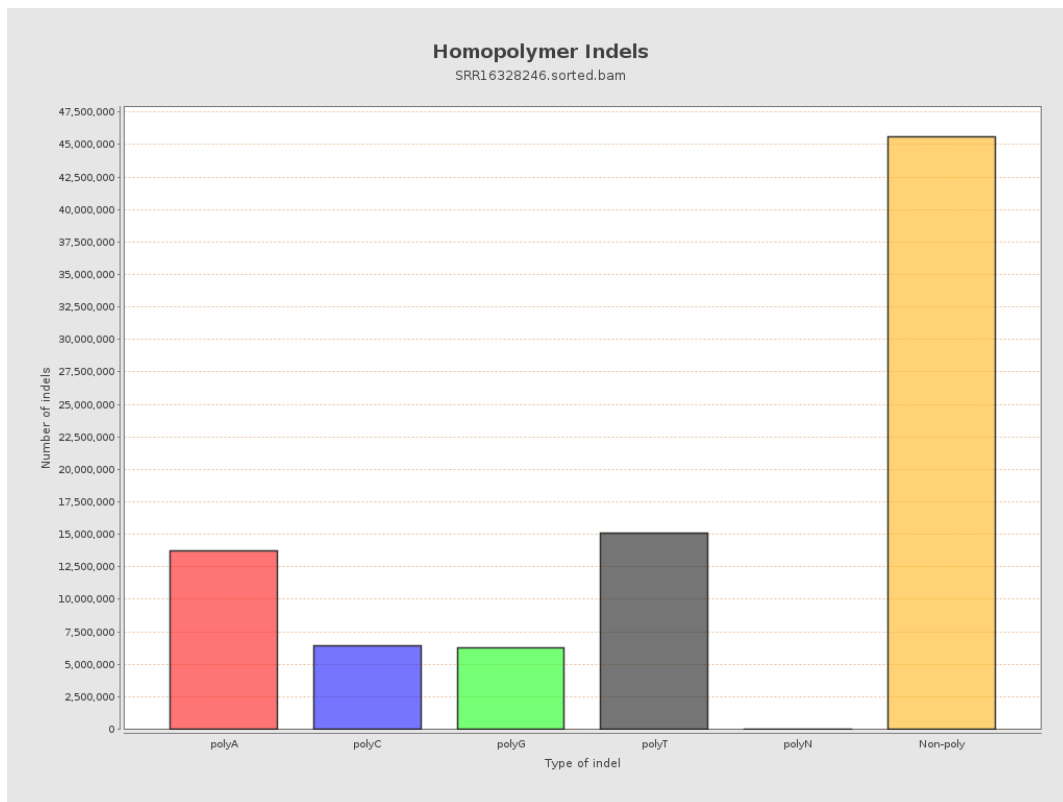
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



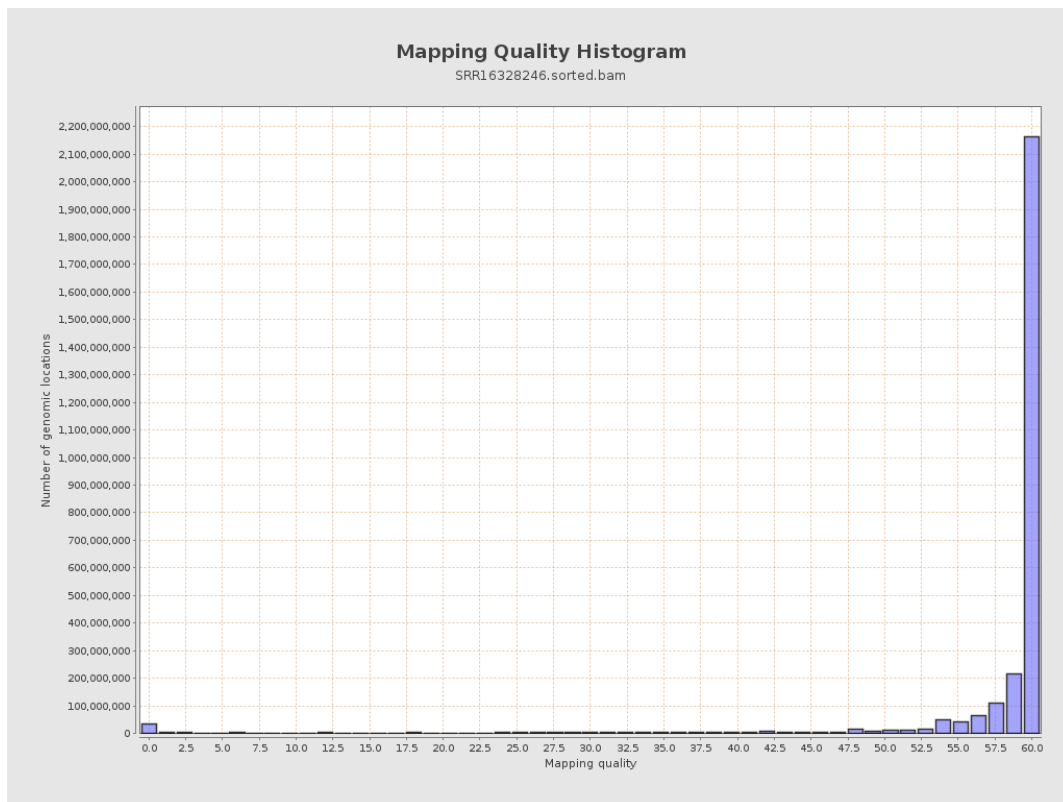
11. Results : Homopolymer Indels



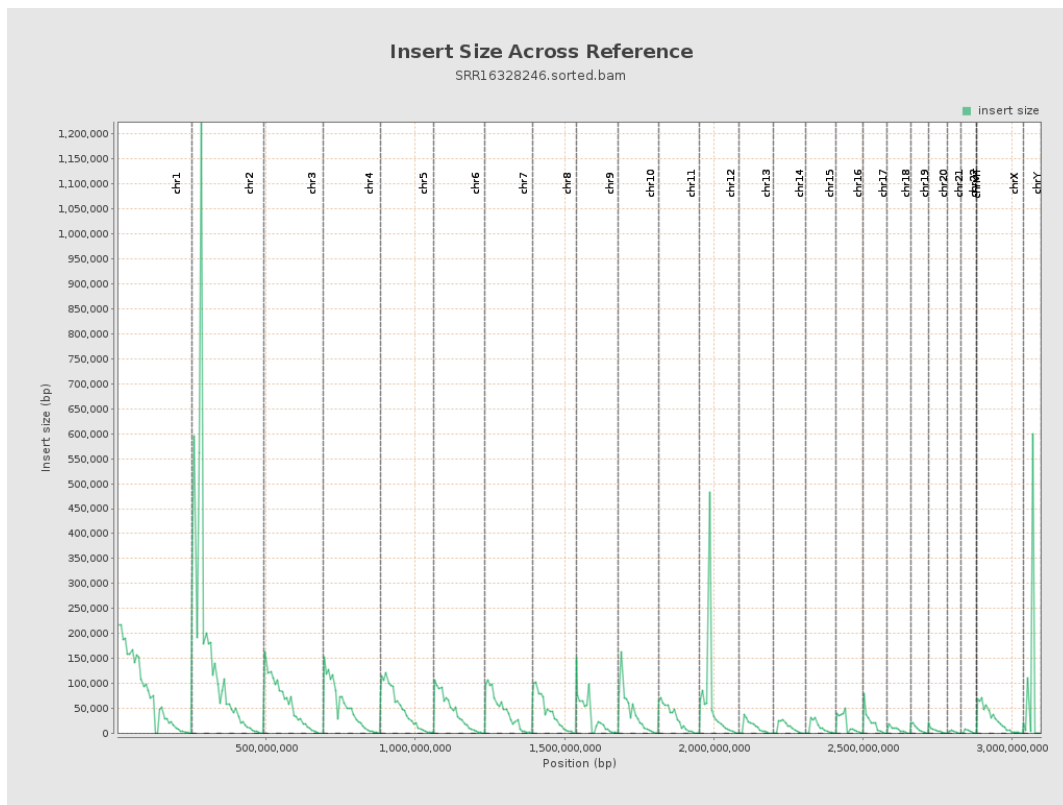
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

