

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/02/20 17:38:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR16328245.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_SRR16328245 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16328245_1.fastq.gz SRR16328245_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Feb 20 17:38:56 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR16328245.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	391,589,876
Mapped reads	372,185,300 / 95.04%
Unmapped reads	19,404,576 / 4.96%
Mapped paired reads	372,185,300 / 95.04%
Mapped reads, first in pair	187,443,820 / 47.87%
Mapped reads, second in pair	184,741,480 / 47.18%
Mapped reads, both in pair	368,607,222 / 94.13%
Mapped reads, singletons	3,578,078 / 0.91%
Secondary alignments	0
Supplementary alignments	16,906,520 / 4.32%
Read min/max/mean length	30 / 150 / 152.16
Duplicated reads (estimated)	138,321,815 / 35.32%
Duplication rate	32.4%
Clipped reads	247,083,005 / 63.1%

2.2. ACGT Content

Number/percentage of A's	14,833,282,953 / 28.75%
Number/percentage of C's	10,941,228,456 / 21.21%
Number/percentage of T's	14,734,263,154 / 28.56%
Number/percentage of G's	11,079,784,332 / 21.48%
Number/percentage of N's	3,910,862 / 0.01%

GC Percentage	42.68%
---------------	--------

2.3. Coverage

Mean	16.6911
Standard Deviation	156.9291

2.4. Mapping Quality

Mean Mapping Quality	53.73
----------------------	-------

2.5. Insert size

Mean	154,441.98
Standard Deviation	3,777,242.58
P25/Median/P75	182 / 244 / 347

2.6. Mismatches and indels

General error rate	1%
Mismatches	496,496,470
Insertions	7,646,819
Mapped reads with at least one insertion	1.94%
Deletions	33,479,818
Mapped reads with at least one deletion	8.57%
Homopolymer indels	48.25%

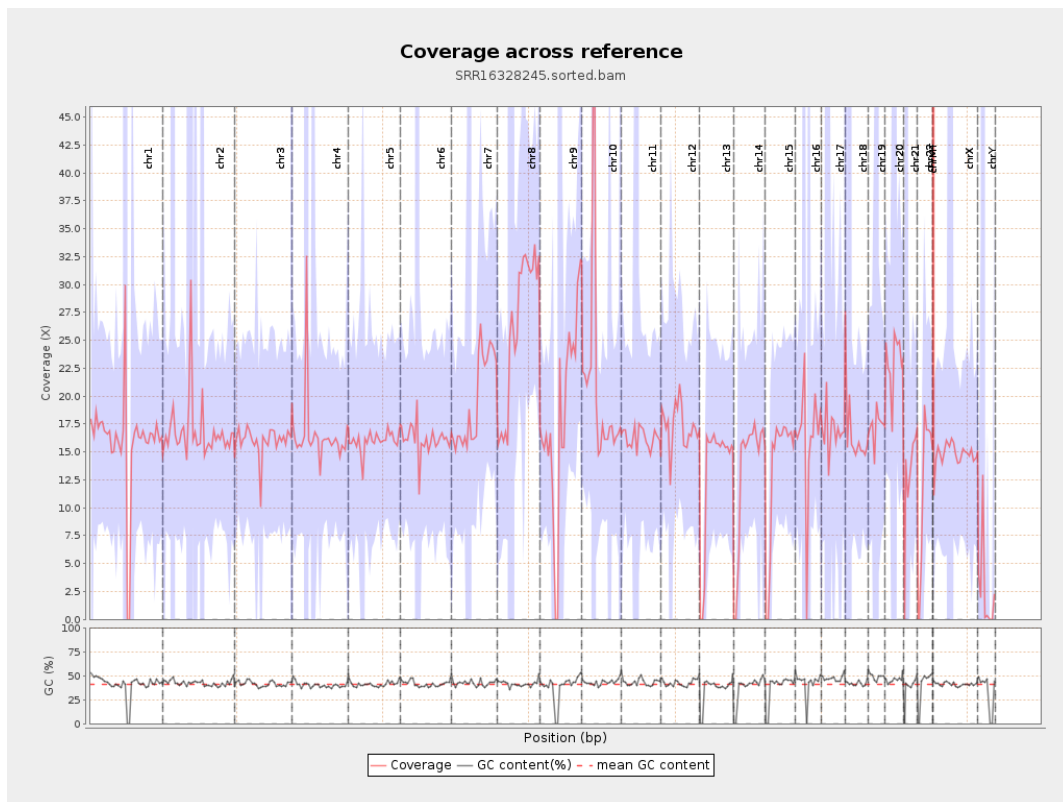
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

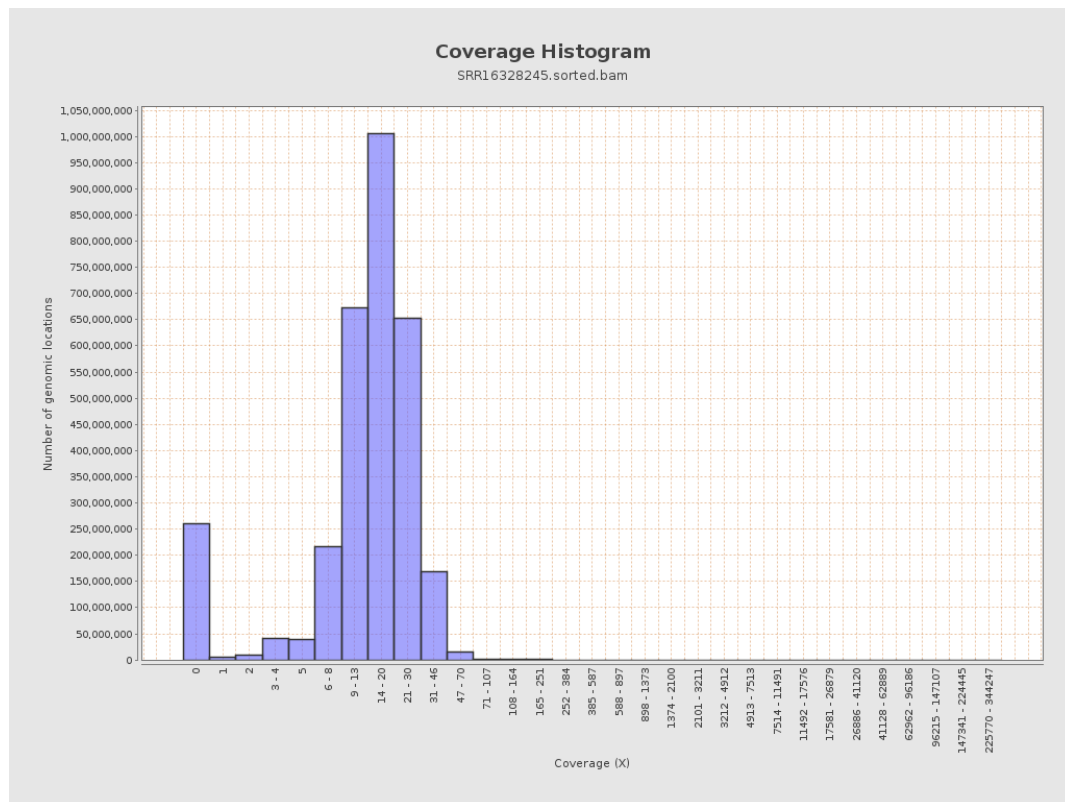
		bases	coverage	deviation
chr1	249250621	3968962322	15.9236	332.8601
chr2	243199373	4096241067	16.8431	134.2963
chr3	198022430	3171297539	16.0148	17.1848
chr4	191154276	3156821511	16.5145	144.1406
chr5	180915260	2896185055	16.0085	11.4613
chr6	171115067	2753803115	16.0933	48.407
chr7	159138663	3134792053	19.6985	78.6685
chr8	146364022	3848104037	26.2913	267.4157
chr9	141213431	2580215934	18.2717	177.6357
chr10	135534747	2780810673	20.5173	324.7655
chr11	135006516	2192138599	16.2373	67.027
chr12	133851895	2329005731	17.3999	11.3416
chr13	115169878	1515010811	13.1546	9.7101
chr14	107349540	1445260889	13.4631	13.5806
chr15	102531392	1361573238	13.2796	10.1469
chr16	90354753	1458724744	16.1444	33.9892
chr17	81195210	1369593610	16.8679	61.5739
chr18	78077248	1272700795	16.3005	181.1914
chr19	59128983	1023246709	17.3053	188.9143
chr20	63025520	1448973888	22.9903	42.3872
chr21	48129895	632164044	13.1345	67.218
chr22	51304566	613620766	11.9604	12.4184
chrMT	16571	167334066	10,098.0065	1,788.864
chrX	155270560	2297518610	14.7969	31.3805

chrY	59373566	156294148	2.6324	162.1732
------	----------	-----------	--------	----------

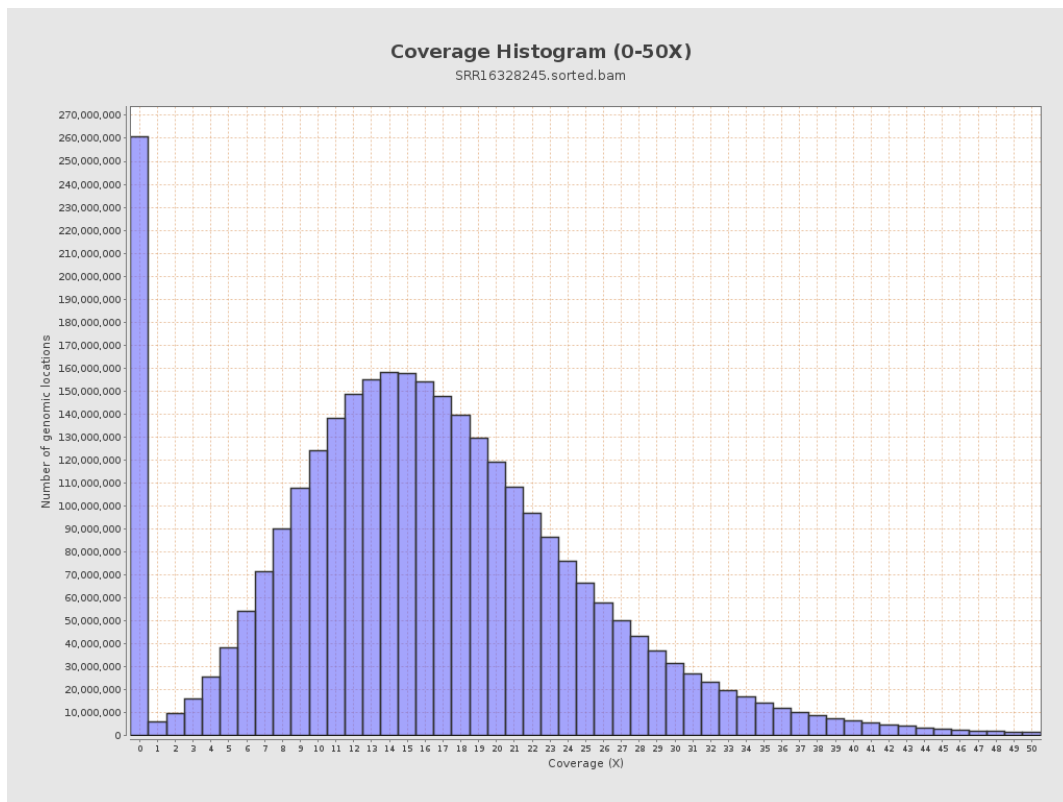
3. Results : Coverage across reference



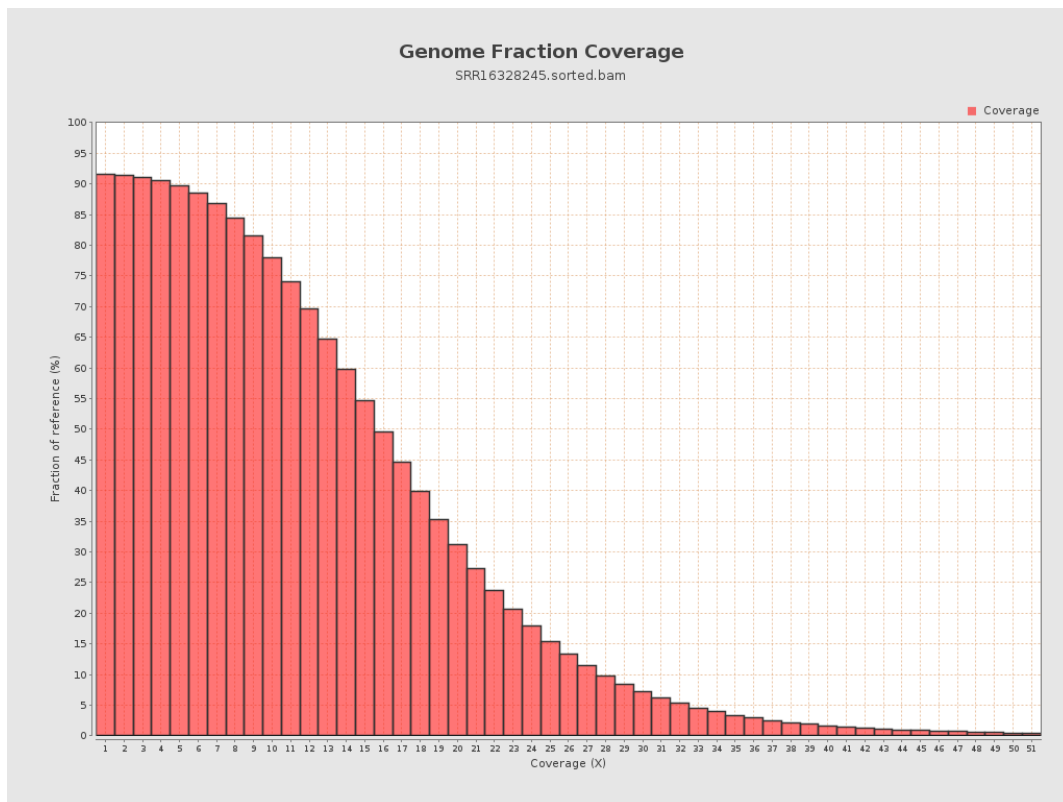
4. Results : Coverage Histogram



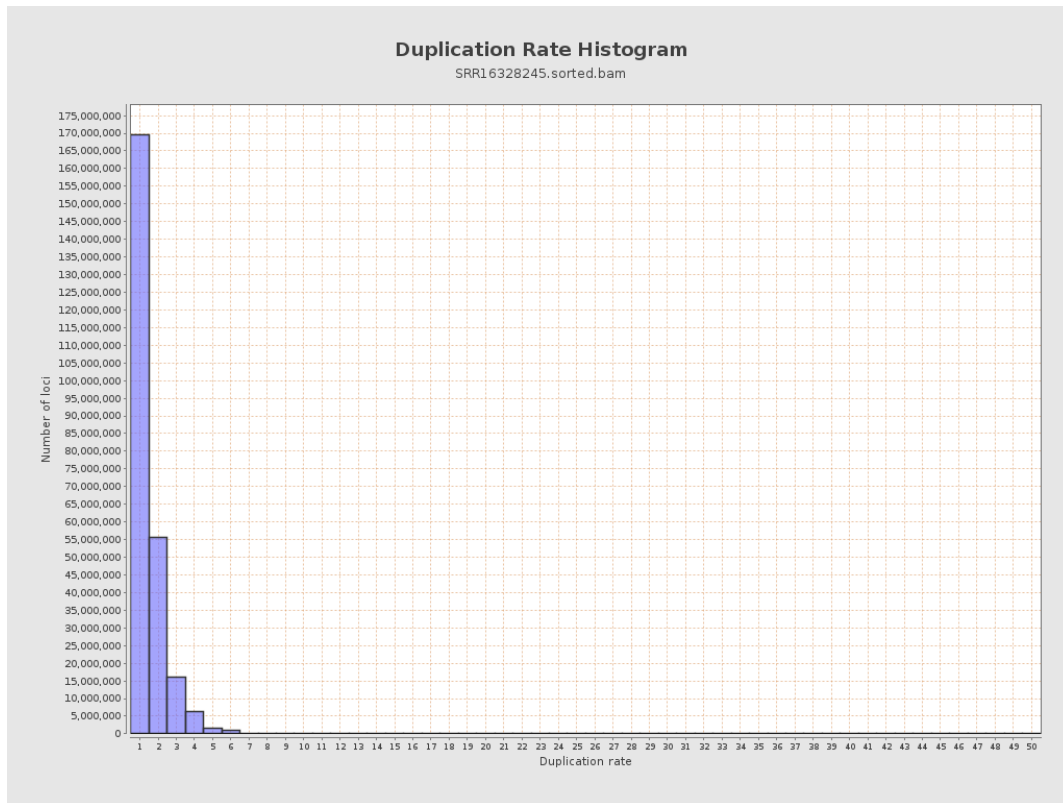
5. Results : Coverage Histogram (0-50X)



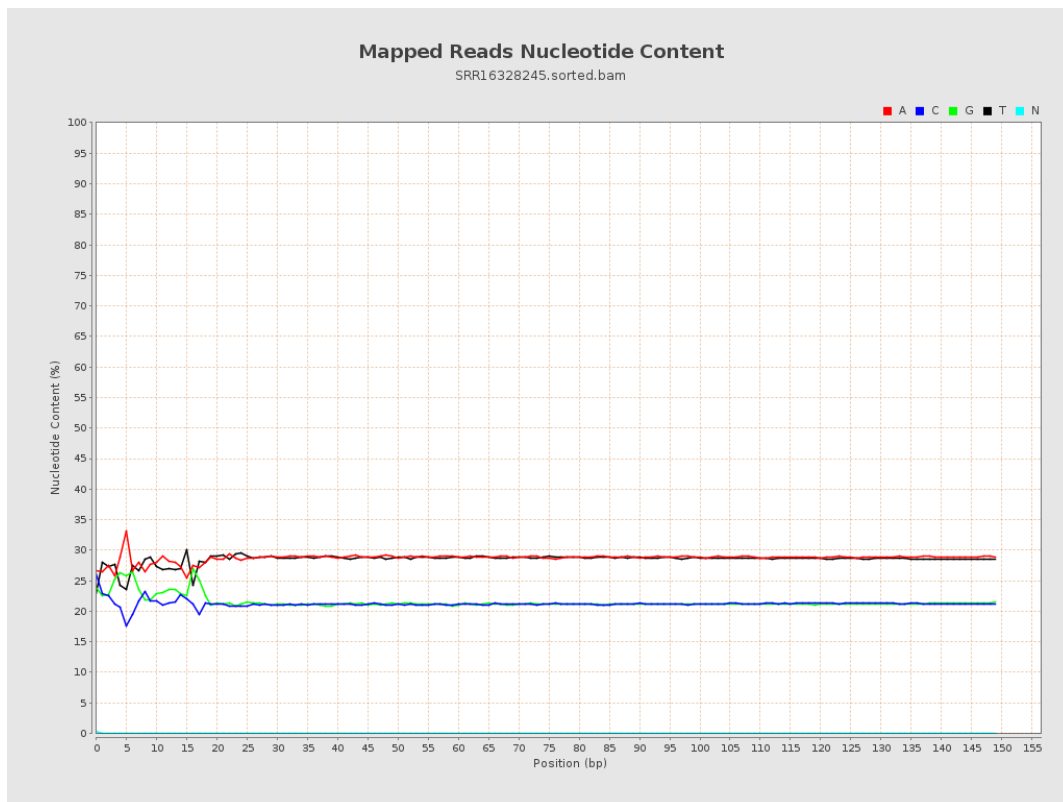
6. Results : Genome Fraction Coverage



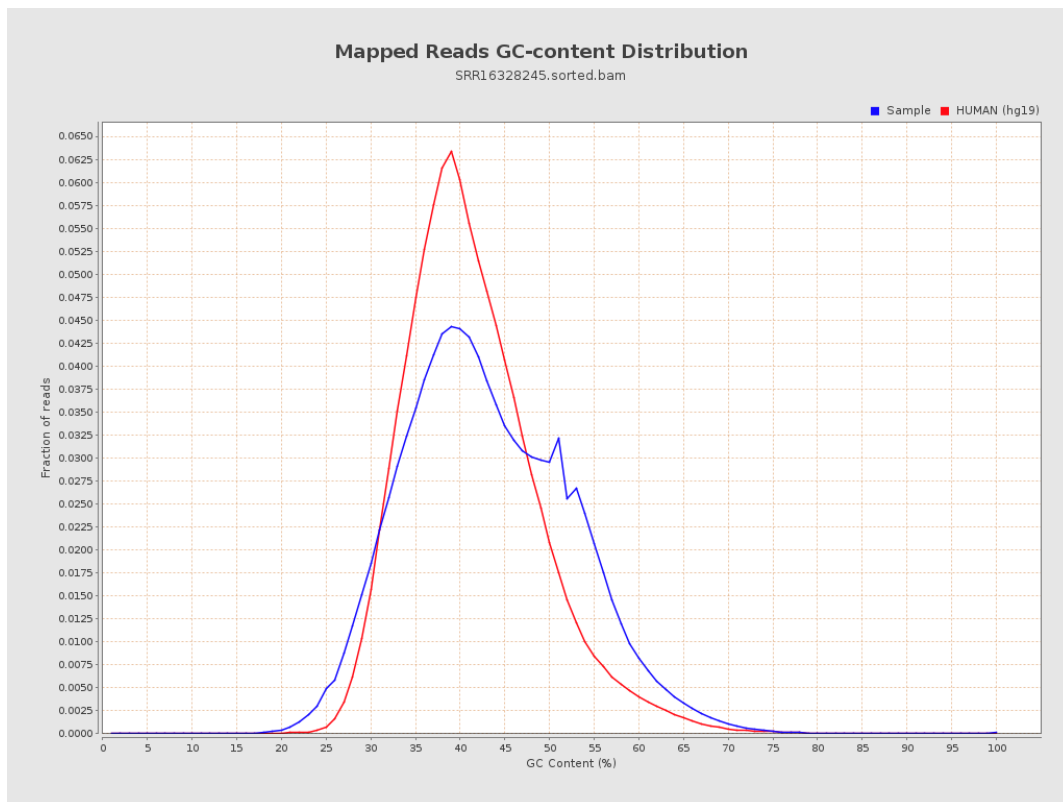
7. Results : Duplication Rate Histogram



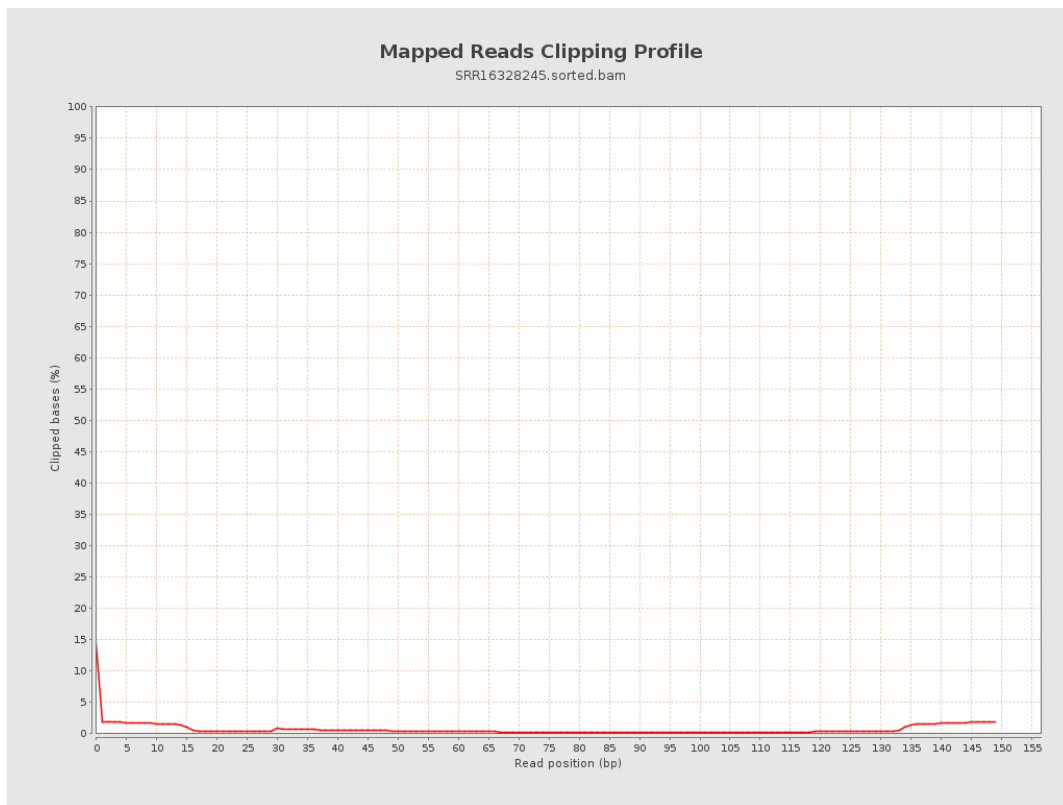
8. Results : Mapped Reads Nucleotide Content



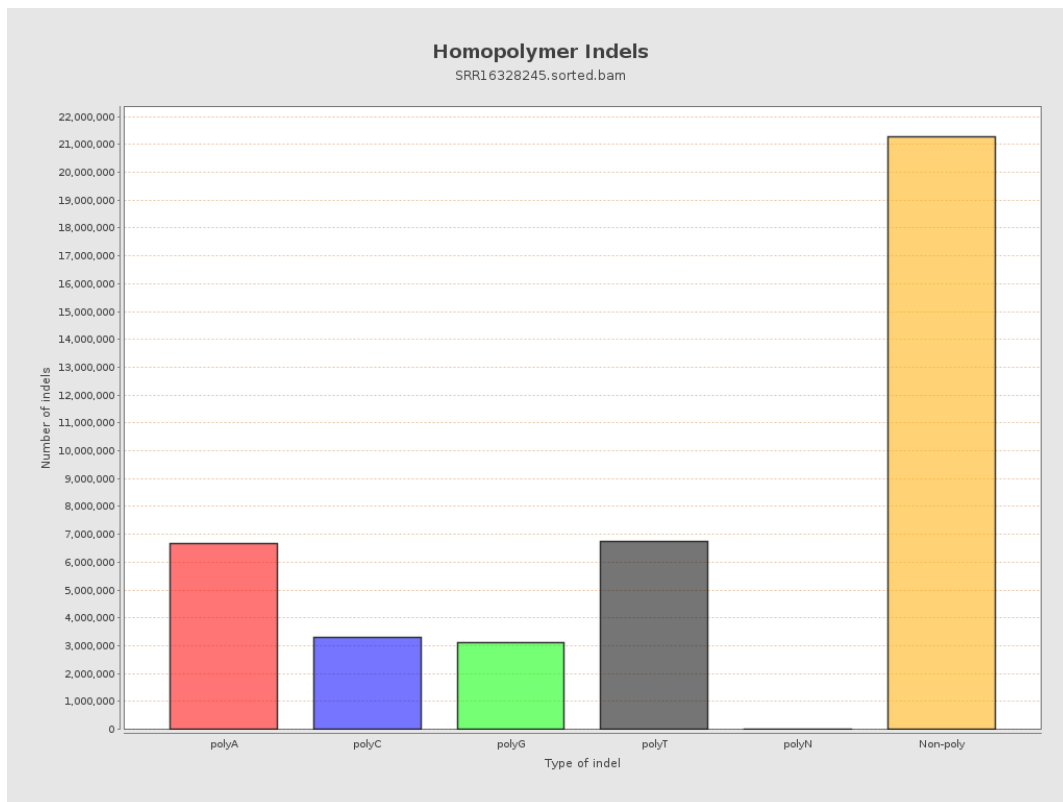
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



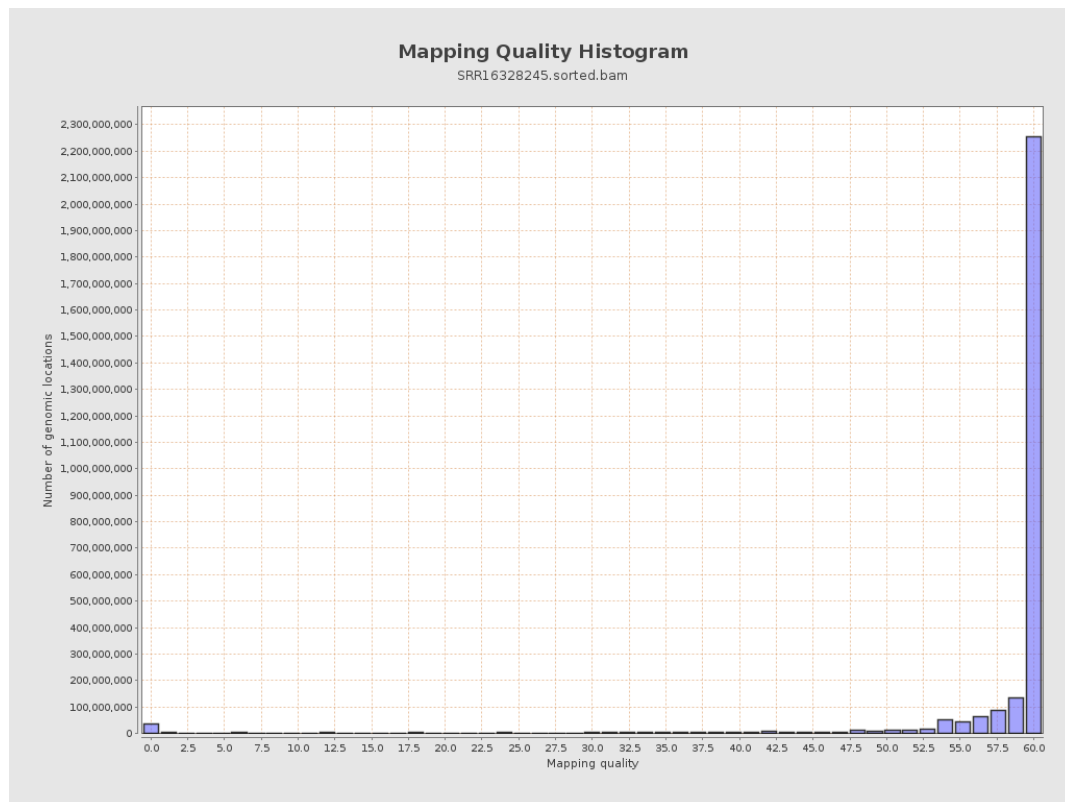
11. Results : Homopolymer Indels



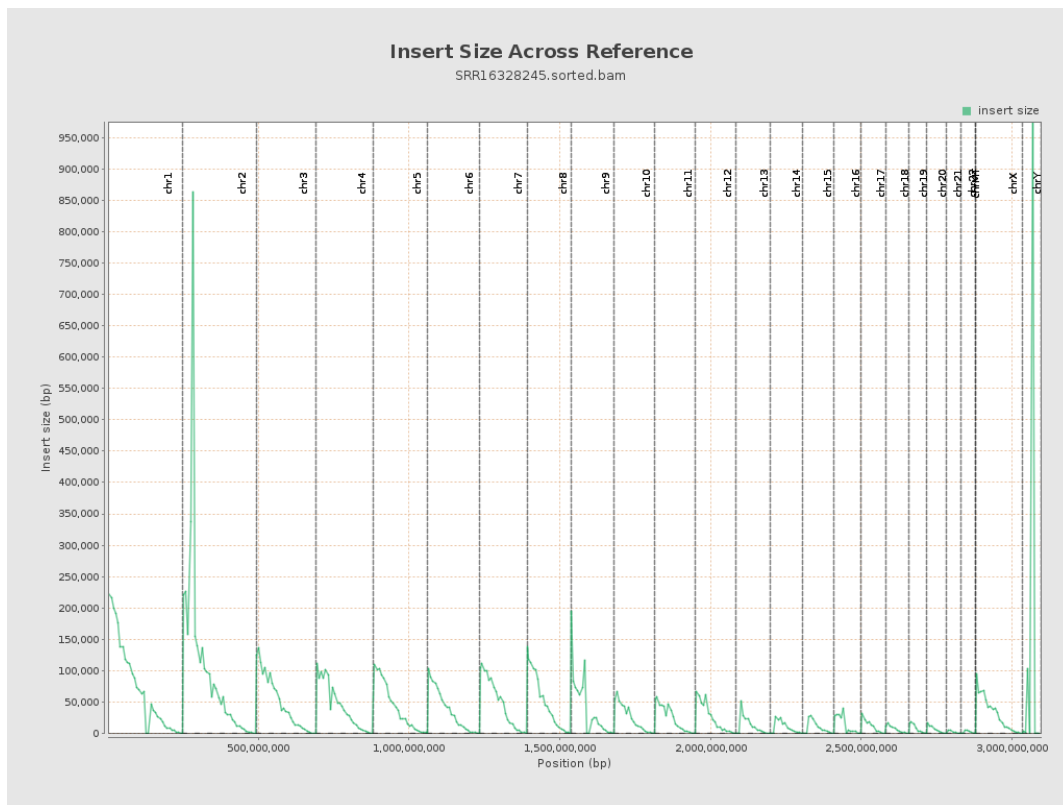
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

