

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/02/23 01:56:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR16328249.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_SRR16328249 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16328249_1.fastq.gz SRR16328249_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Feb 23 01:56:23 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR16328249.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	427,706,482
Mapped reads	403,596,223 / 94.36%
Unmapped reads	24,110,259 / 5.64%
Mapped paired reads	403,596,223 / 94.36%
Mapped reads, first in pair	203,067,335 / 47.48%
Mapped reads, second in pair	200,528,888 / 46.88%
Mapped reads, both in pair	400,026,962 / 93.53%
Mapped reads, singletons	3,569,261 / 0.83%
Secondary alignments	0
Supplementary alignments	17,915,701 / 4.19%
Read min/max/mean length	30 / 150 / 152.09
Duplicated reads (estimated)	152,122,475 / 35.57%
Duplication rate	32.66%
Clipped reads	268,139,538 / 62.69%

2.2. ACGT Content

Number/percentage of A's	16,117,849,412 / 28.86%
Number/percentage of C's	11,776,472,250 / 21.09%
Number/percentage of T's	16,000,460,839 / 28.65%
Number/percentage of G's	11,942,273,132 / 21.39%
Number/percentage of N's	4,199,393 / 0.01%

GC Percentage	42.48%
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2.3. Coverage

Mean	18.0538
Standard Deviation	191.0049

2.4. Mapping Quality

Mean Mapping Quality	53.77
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2.5. Insert size

Mean	153,528.81
Standard Deviation	3,803,003.45
P25/Median/P75	179 / 238 / 335

2.6. Mismatches and indels

General error rate	0.93%
Mismatches	495,315,073
Insertions	9,717,076
Mapped reads with at least one insertion	2.28%
Deletions	26,635,925
Mapped reads with at least one deletion	6.33%
Homopolymer indels	44.6%

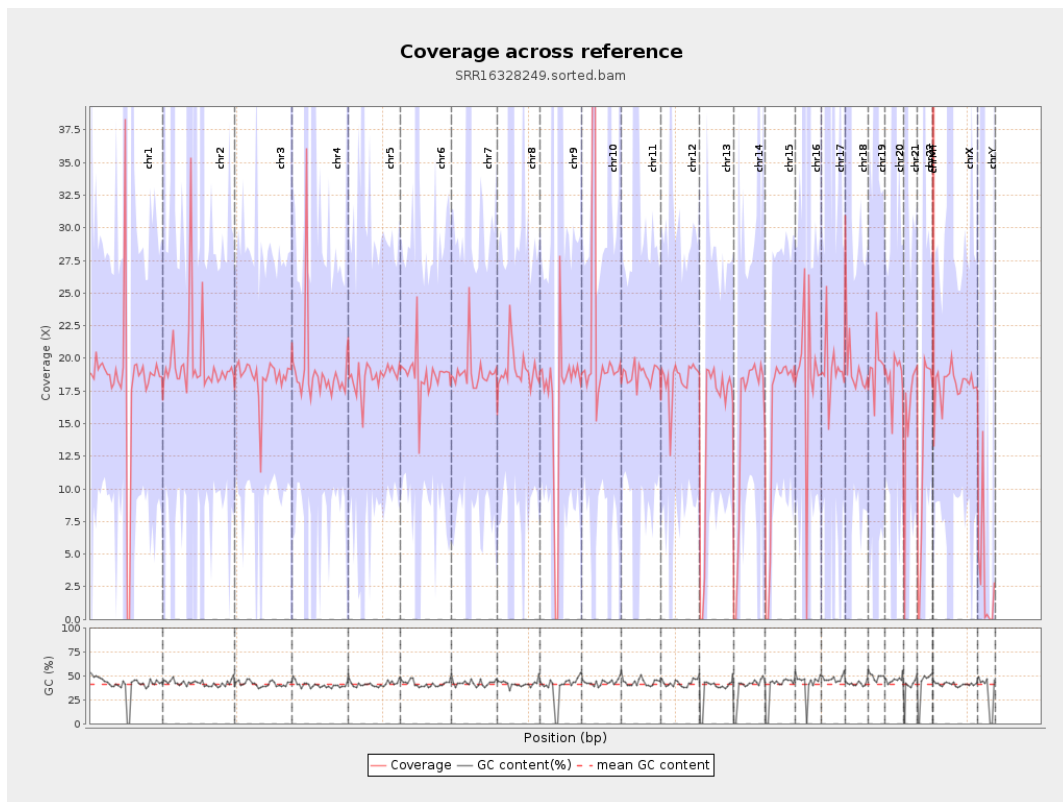
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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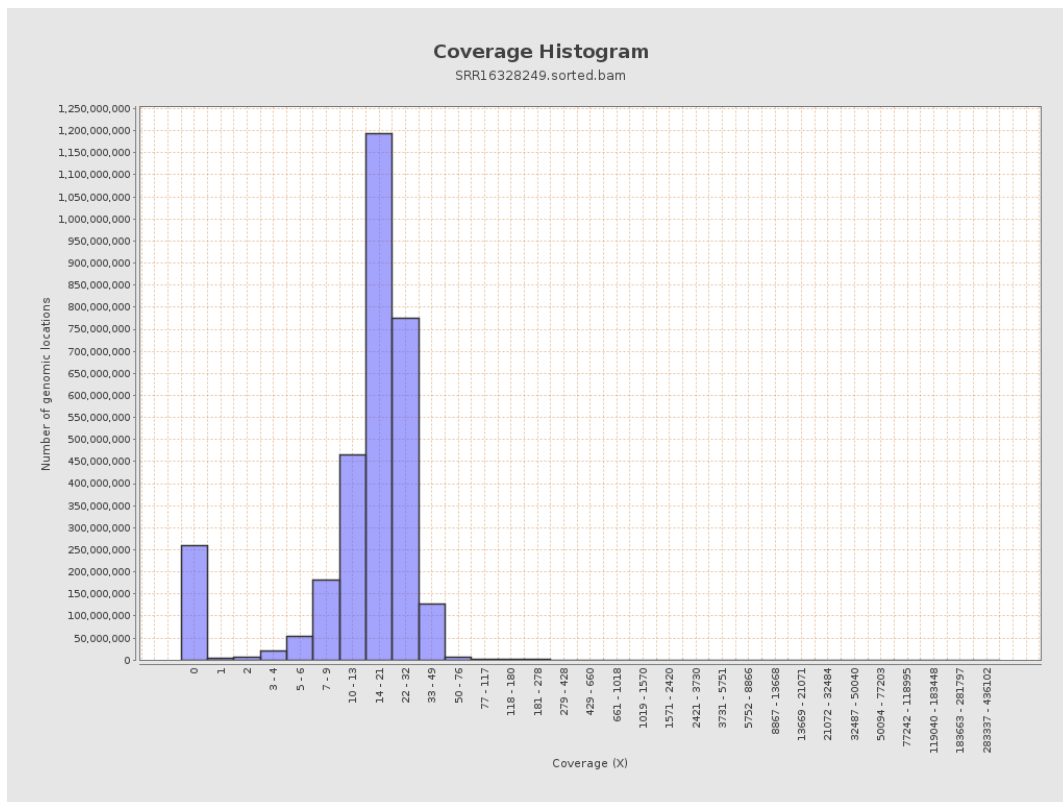
		bases	coverage	deviation
chr1	249250621	4543543277	18.2288	436.3666
chr2	243199373	4791666675	19.7026	151.4344
chr3	198022430	3672229991	18.5445	20.4178
chr4	191154276	3639025999	19.0371	150.9702
chr5	180915260	3360243192	18.5736	14.8663
chr6	171115067	3205653019	18.7339	74.845
chr7	159138663	3015678859	18.95	155.9403
chr8	146364022	2803973114	19.1575	277.4158
chr9	141213431	2397948267	16.981	197.6758
chr10	135534747	2906325890	21.4434	406.2972
chr11	135006516	2533500459	18.7658	70.958
chr12	133851895	2467370241	18.4336	12.5667
chr13	115169878	1741041039	15.1172	11.2462
chr14	107349540	1660953655	15.4724	16.5313
chr15	102531392	1549270107	15.1102	11.1209
chr16	90354753	1682439083	18.6204	83.7724
chr17	81195210	1565692311	19.2831	89.9931
chr18	78077248	1508690842	19.3231	192.5305
chr19	59128983	1148007999	19.4153	242.042
chr20	63025520	1169006256	18.5481	42.6587
chr21	48129895	764229793	15.8785	68.7773
chr22	51304566	685884865	13.3689	17.1281
chrMT	16571	103448562	6,242.7471	998.4811
chrX	155270560	2790344489	17.9709	38.8945

chrY	59373566	183014333	3.0824	172.1421
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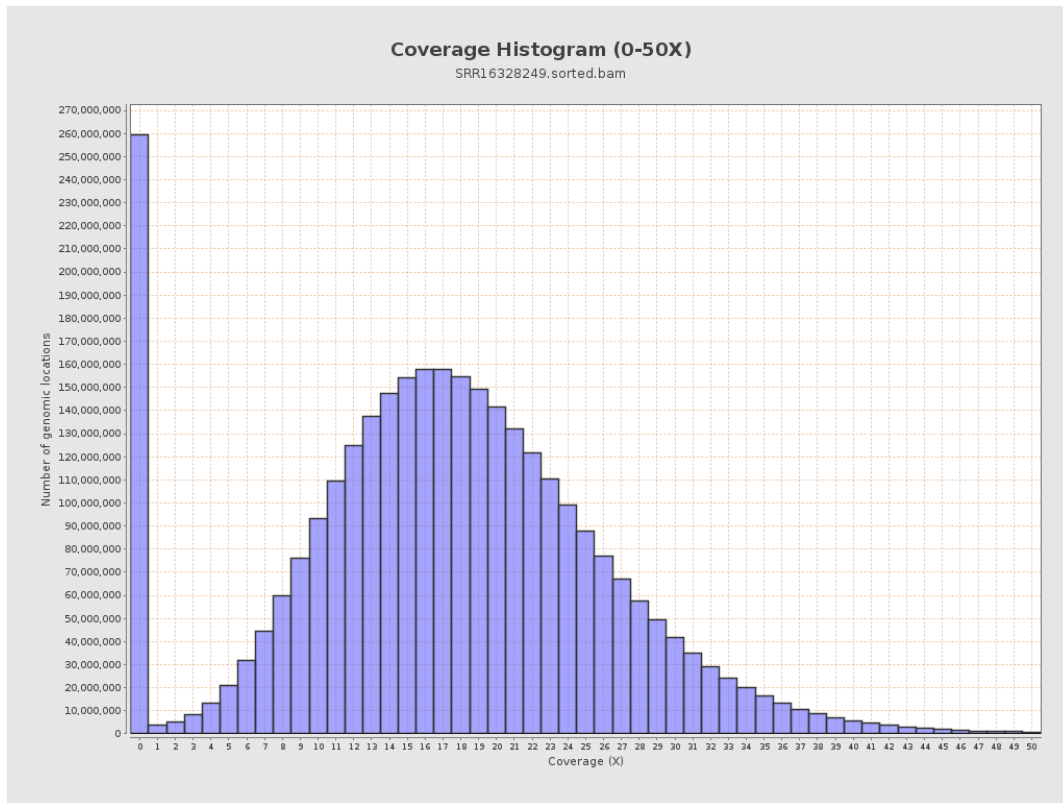
3. Results : Coverage across reference



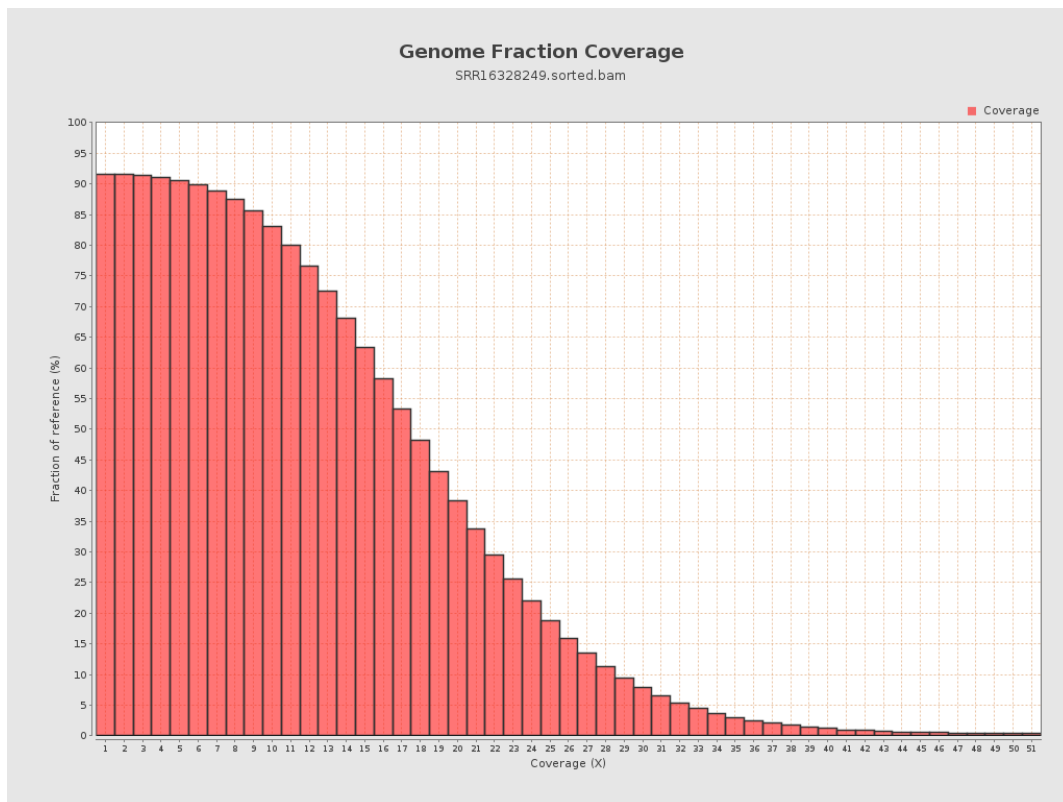
4. Results : Coverage Histogram



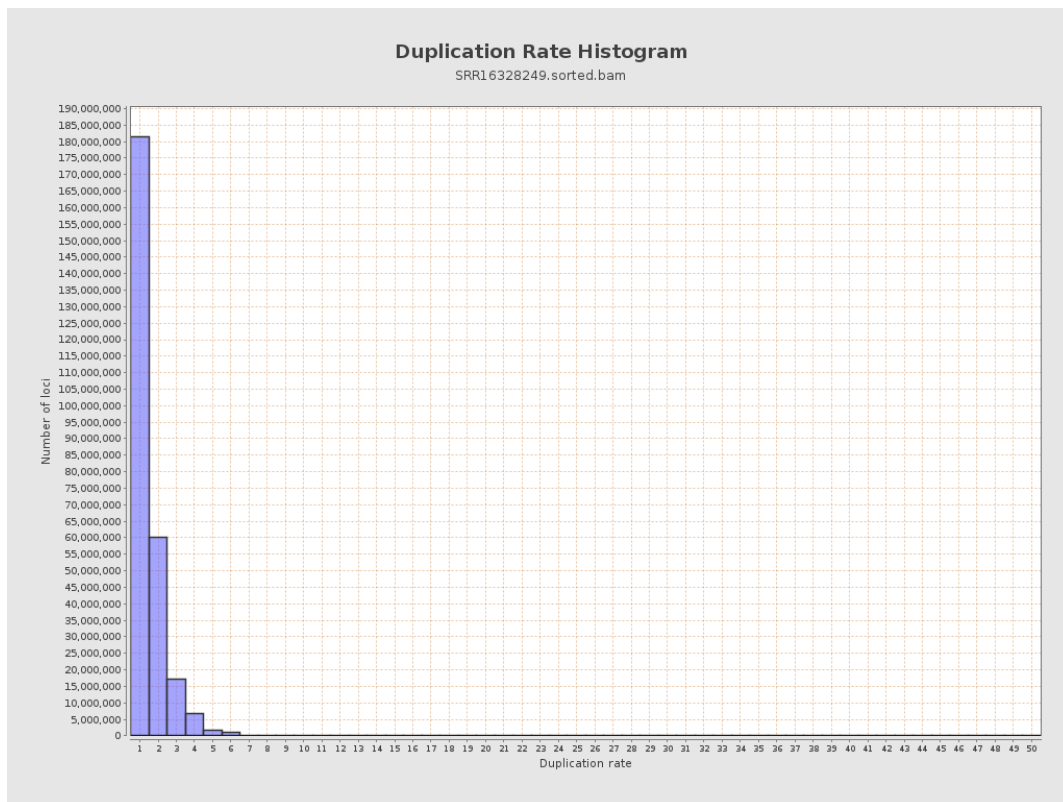
5. Results : Coverage Histogram (0-50X)



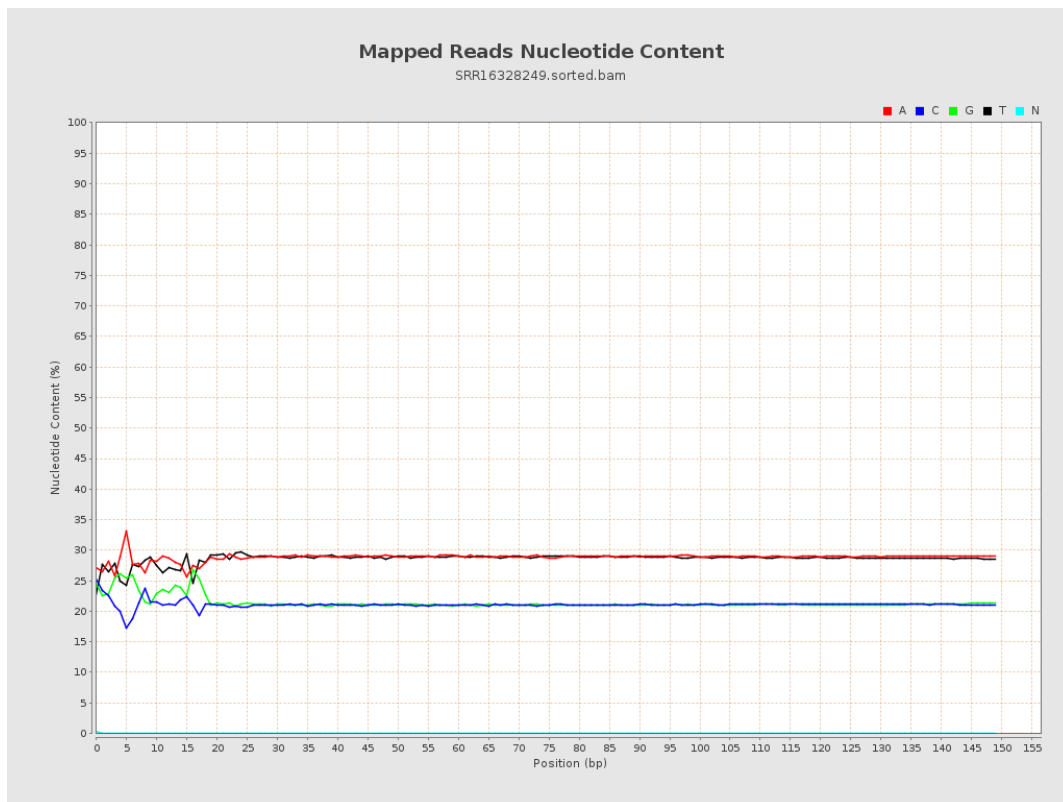
6. Results : Genome Fraction Coverage



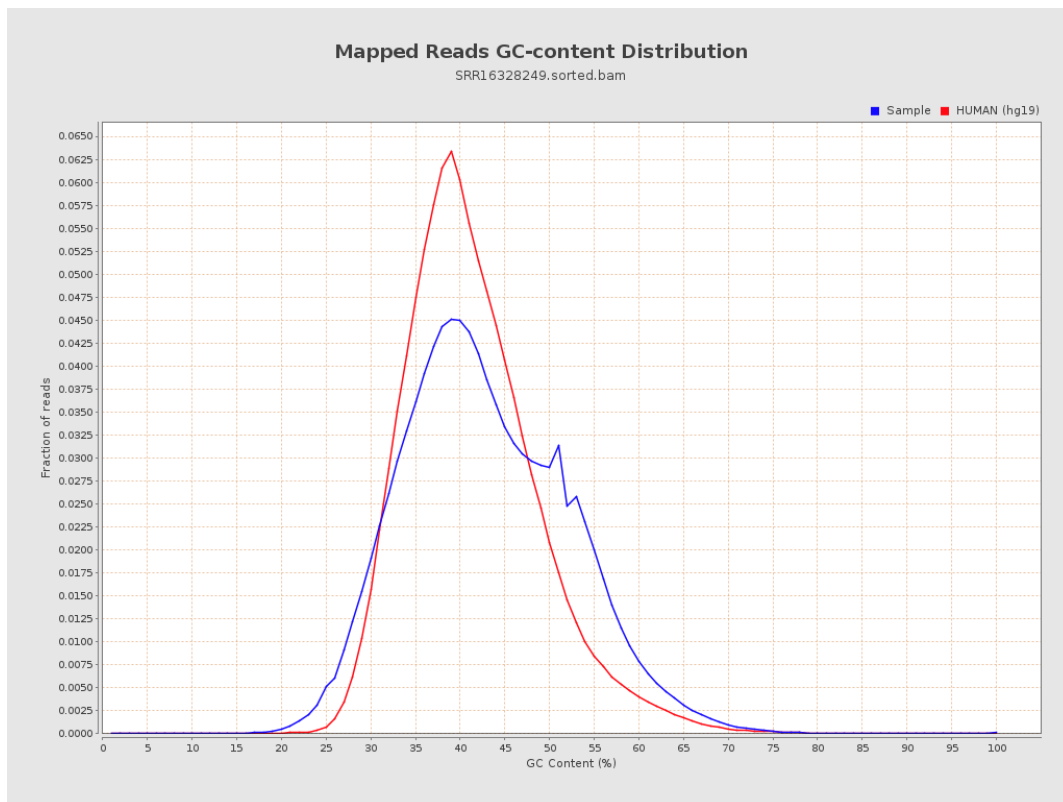
7. Results : Duplication Rate Histogram



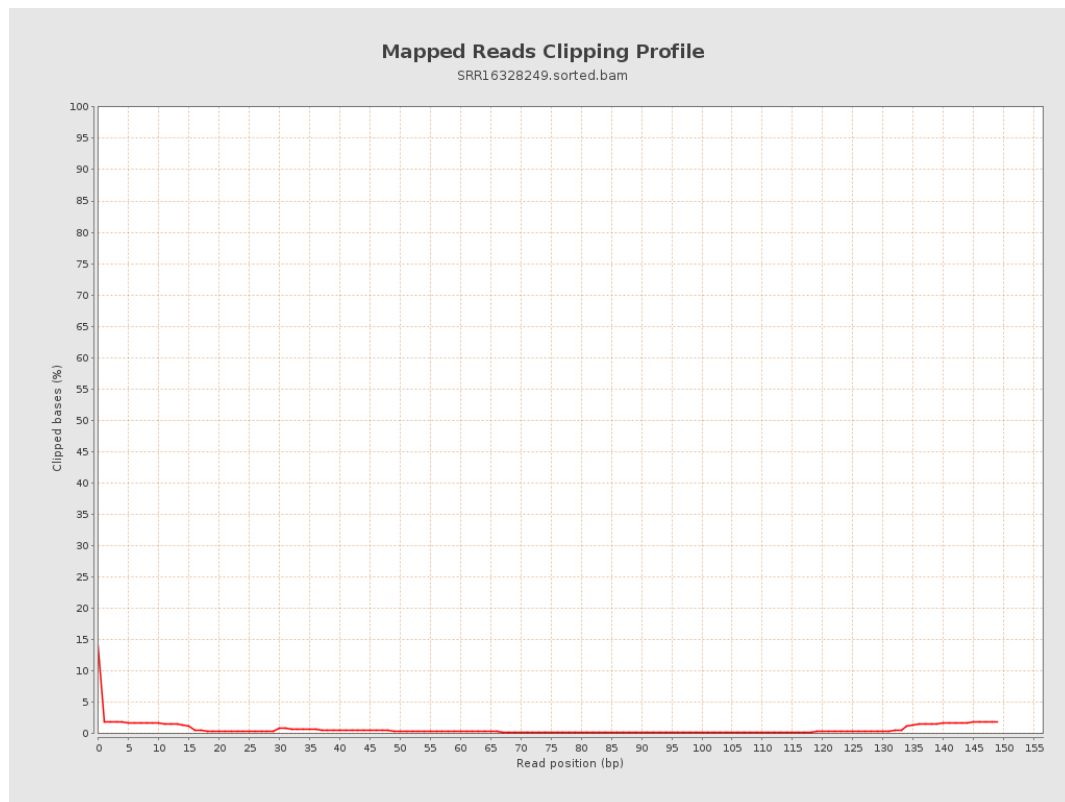
8. Results : Mapped Reads Nucleotide Content



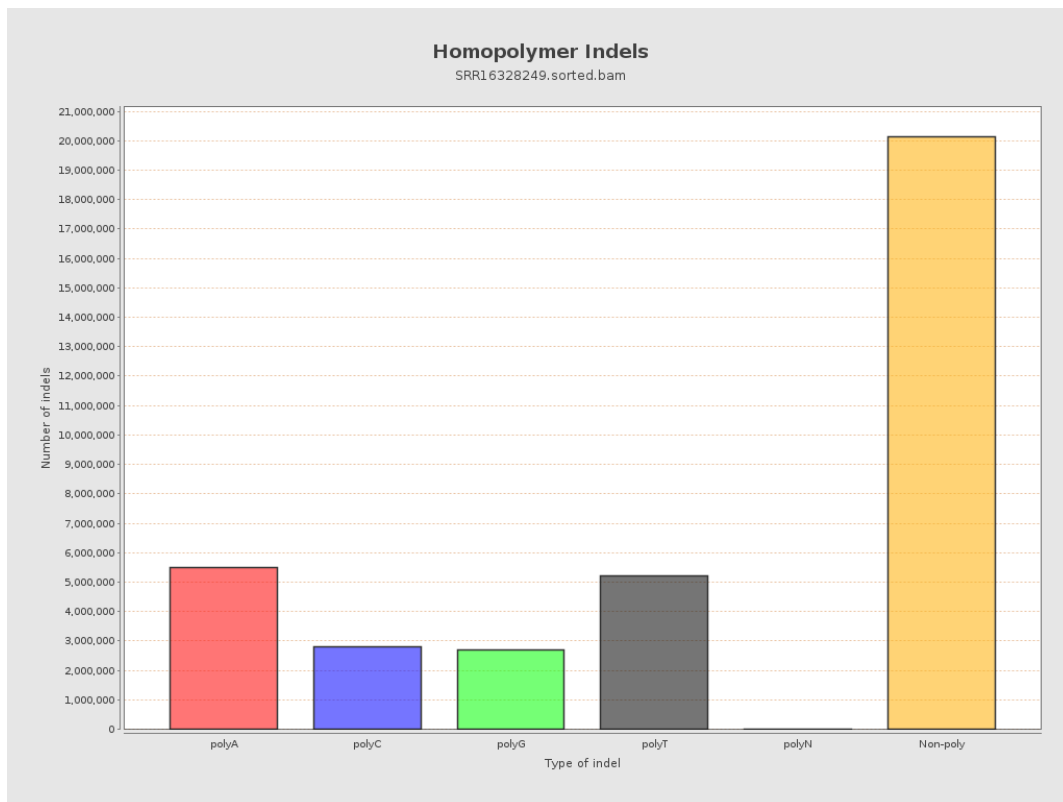
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



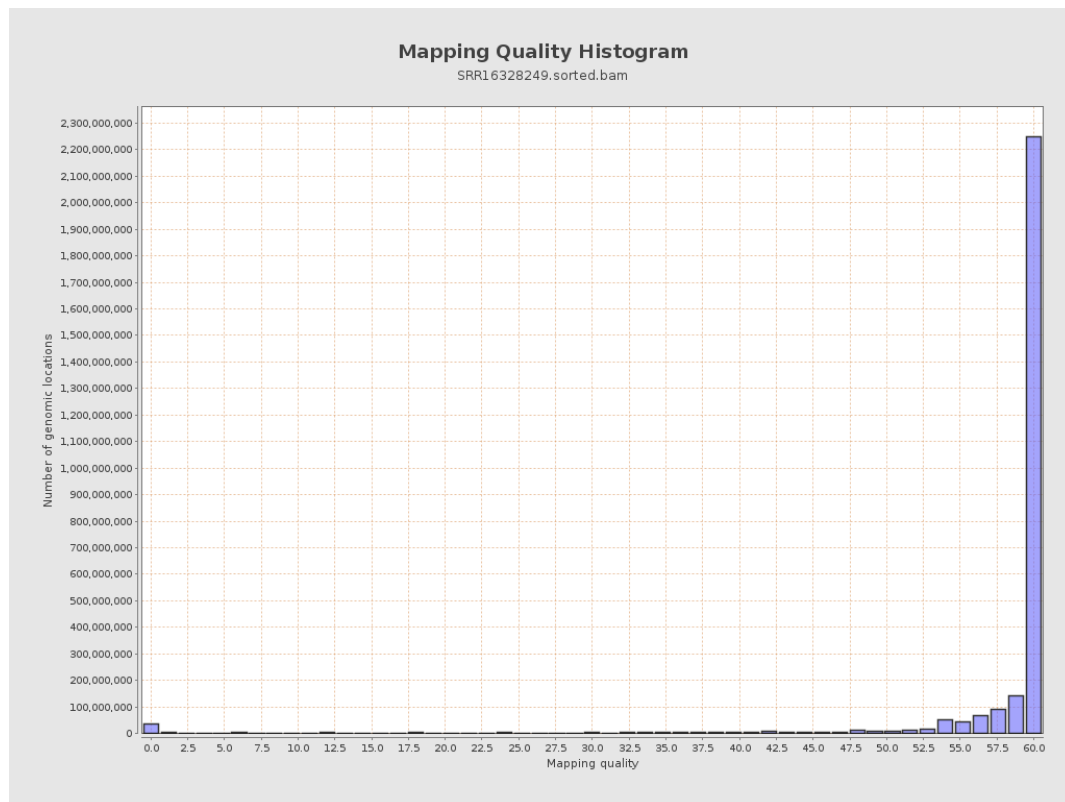
11. Results : Homopolymer Indels



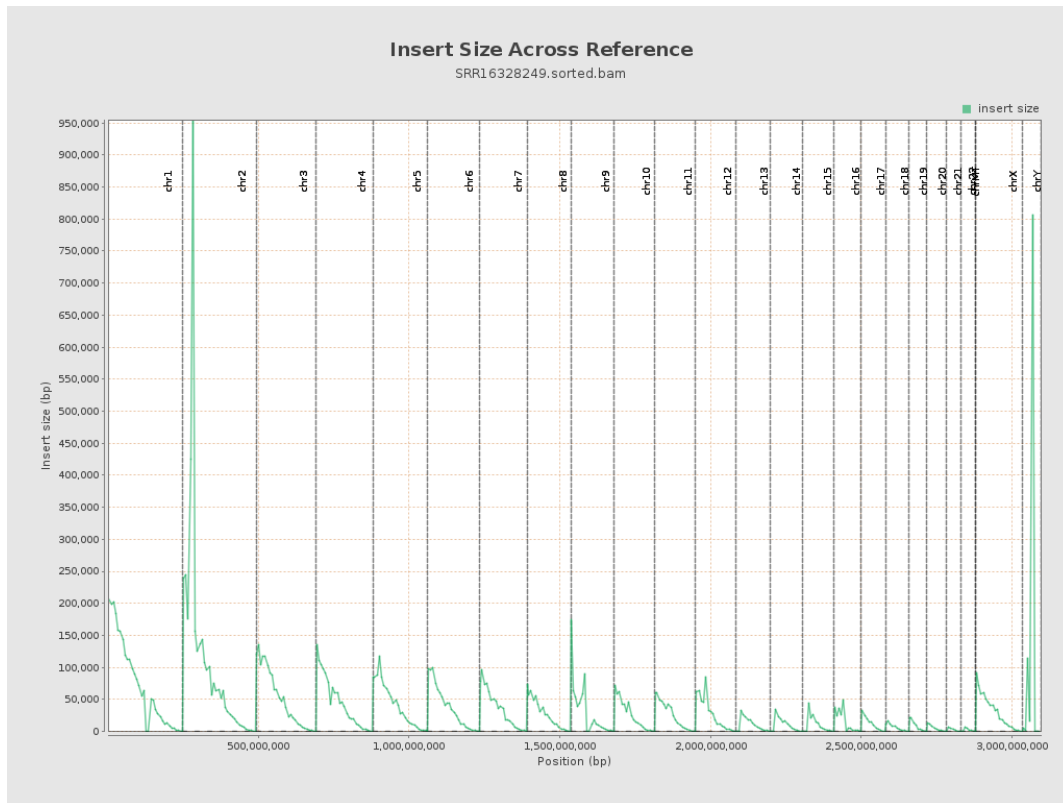
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

