

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/02/20 07:03:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR16328244.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_SRR16328244 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16328244_1.fastq.gz SRR16328244_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Feb 20 07:03:26 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR16328244.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,032,170,794
Mapped reads	1,014,283,850 / 98.27%
Unmapped reads	17,886,944 / 1.73%
Mapped paired reads	1,014,283,850 / 98.27%
Mapped reads, first in pair	508,593,780 / 49.27%
Mapped reads, second in pair	505,690,070 / 48.99%
Mapped reads, both in pair	1,007,168,312 / 97.58%
Mapped reads, singletons	7,115,538 / 0.69%
Secondary alignments	0
Supplementary alignments	44,943,857 / 4.35%
Read min/max/mean length	30 / 150 / 152.18
Duplicated reads (estimated)	391,238,973 / 37.9%
Duplication rate	33.71%
Clipped reads	654,128,486 / 63.37%

2.2. ACGT Content

Number/percentage of A's	40,394,942,663 / 28.58%
Number/percentage of C's	29,888,362,582 / 21.15%
Number/percentage of T's	39,964,883,828 / 28.28%
Number/percentage of G's	31,072,683,864 / 21.99%
Number/percentage of N's	2,624,229 / 0%

GC Percentage	43.14%
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2.3. Coverage

Mean	45.7214
Standard Deviation	925.6419

2.4. Mapping Quality

Mean Mapping Quality	53.75
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2.5. Insert size

Mean	169,141.93
Standard Deviation	3,993,354.45
P25/Median/P75	199 / 274 / 405

2.6. Mismatches and indels

General error rate	0.89%
Mismatches	1,198,894,398
Insertions	20,872,132
Mapped reads with at least one insertion	1.95%
Deletions	91,153,462
Mapped reads with at least one deletion	8.57%
Homopolymer indels	48.45%

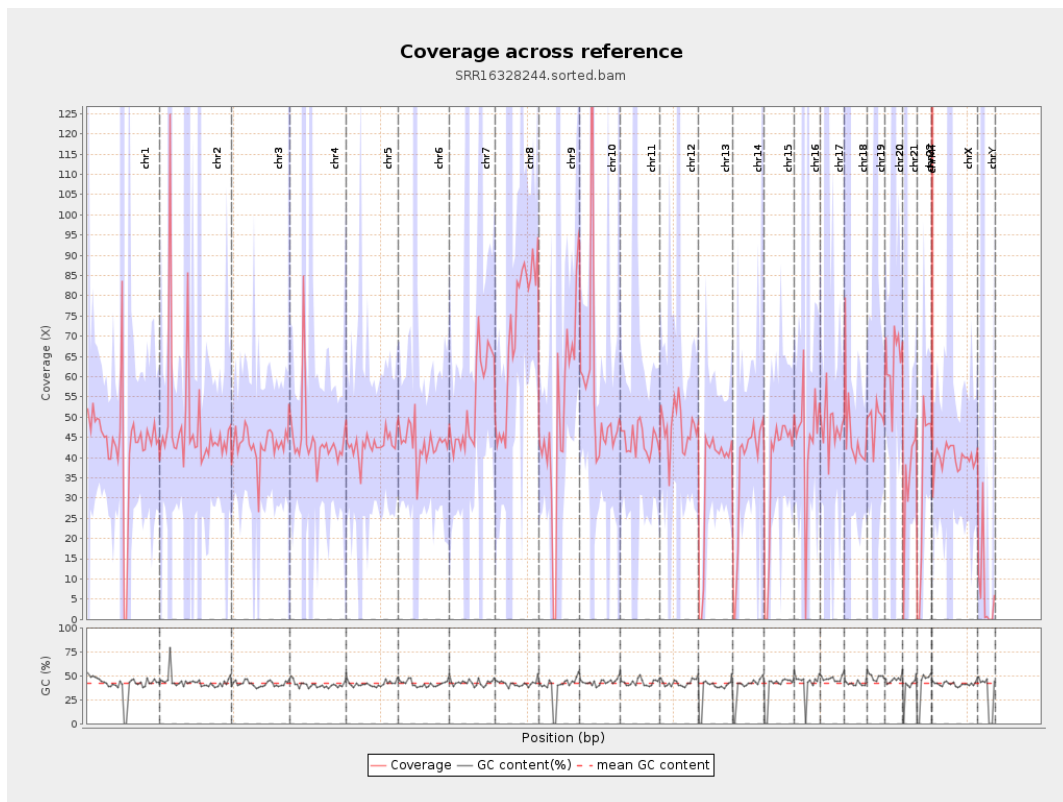
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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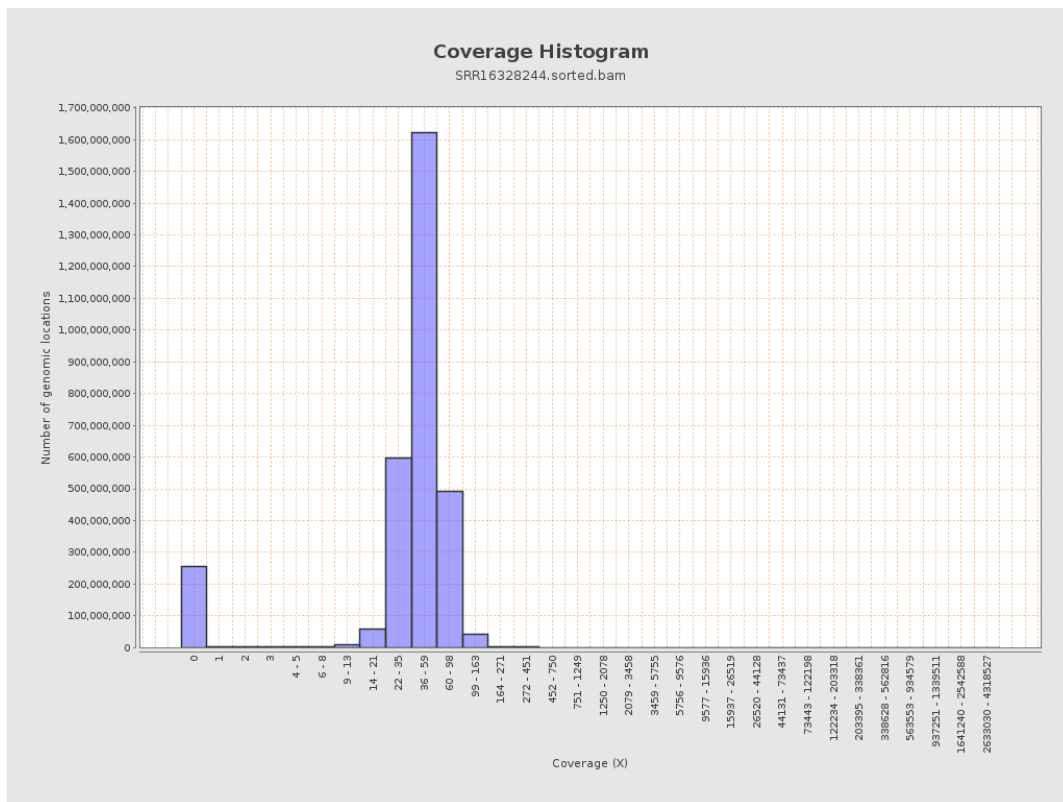
		bases	coverage	deviation
chr1	249250621	10888980515	43.6869	944.8558
chr2	243199373	11690416415	48.0693	2,945.4032
chr3	198022430	8574873294	43.3025	41.1982
chr4	191154276	8445001507	44.179	385.2183
chr5	180915260	7820790168	43.229	27.7874
chr6	171115067	7439567870	43.477	136.2128
chr7	159138663	8555620140	53.762	223.8058
chr8	146364022	10411719808	71.1358	669.482
chr9	141213431	7121731408	50.4324	526.4035
chr10	135534747	7607142932	56.1269	869.4869
chr11	135006516	5998092337	44.4282	186.277
chr12	133851895	6354316271	47.4727	65.9537
chr13	115169878	4065753855	35.3022	23.2379
chr14	107349540	3942179363	36.7228	45.4668
chr15	102531392	3746481805	36.5399	27.2133
chr16	90354753	4080452980	45.1604	88.1405
chr17	81195210	3865477837	47.6072	170.0225
chr18	78077248	3469707141	44.4394	530.6383
chr19	59128983	2928222812	49.5226	526.1351
chr20	63025520	4030703118	63.9535	113.0219
chr21	48129895	1723727322	35.8141	170.0389
chr22	51304566	1753901049	34.1861	32.1698
chrMT	16571	442271539	26,689.49	4,122.9081
chrX	155270560	6166217745	39.7127	83.9872

chrY	59373566	416016867	7.0068	414.0646
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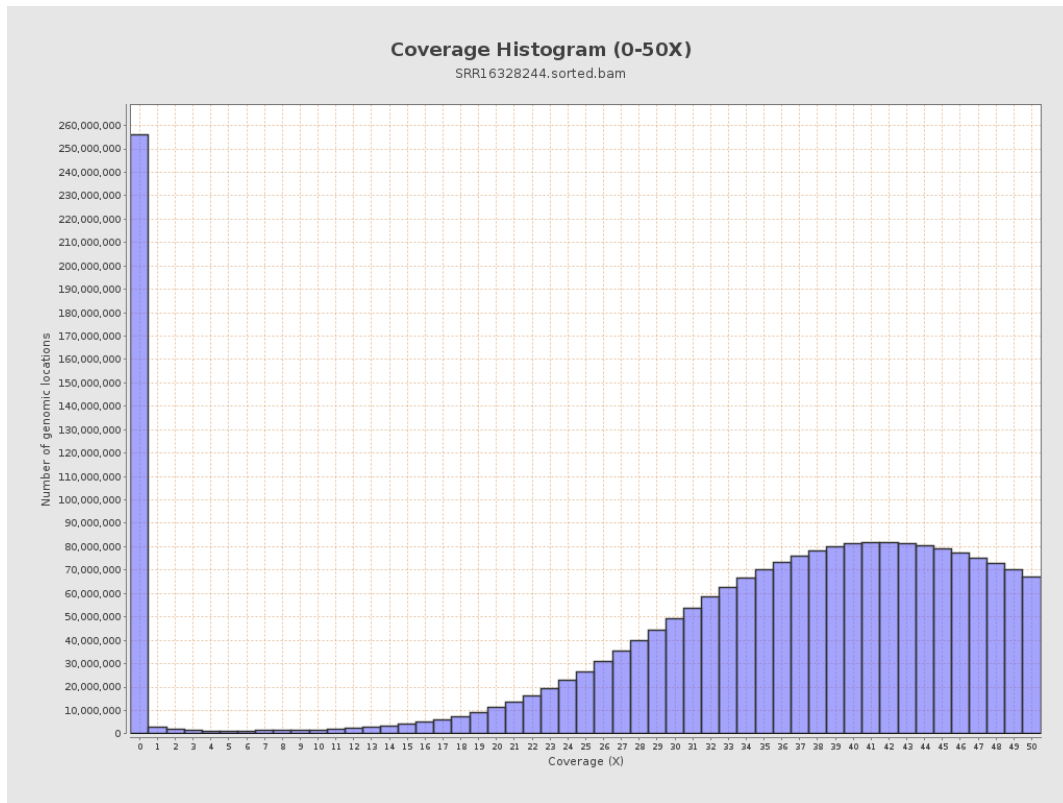
3. Results : Coverage across reference



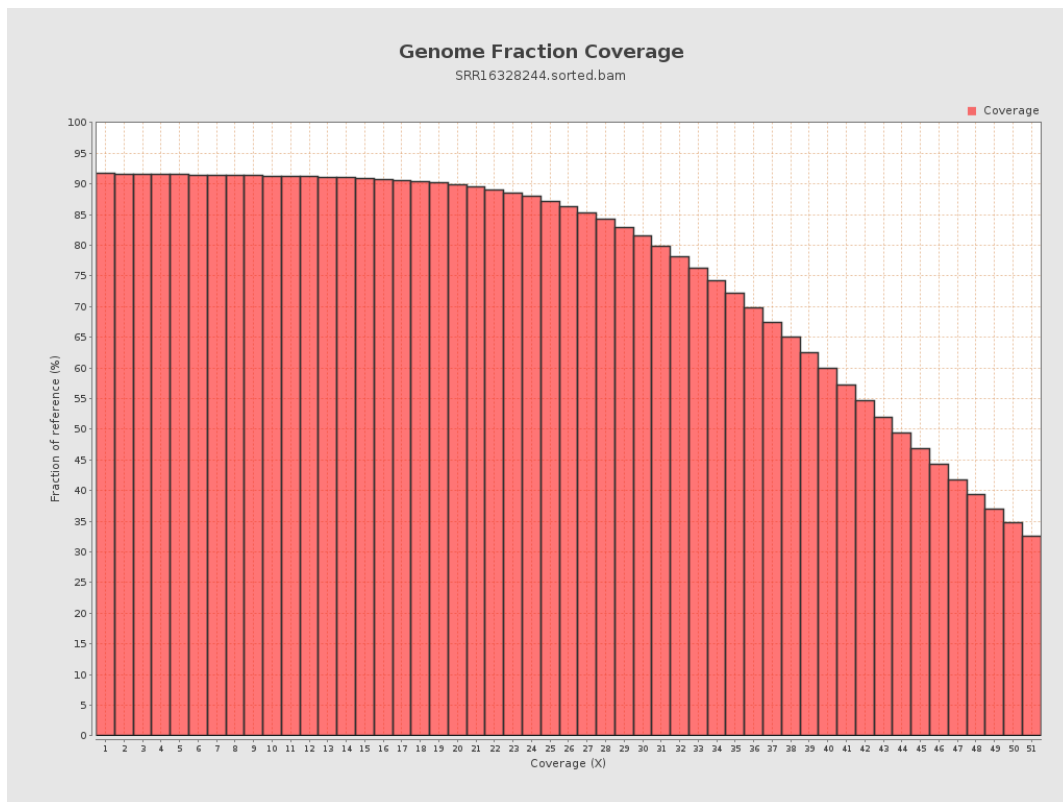
4. Results : Coverage Histogram



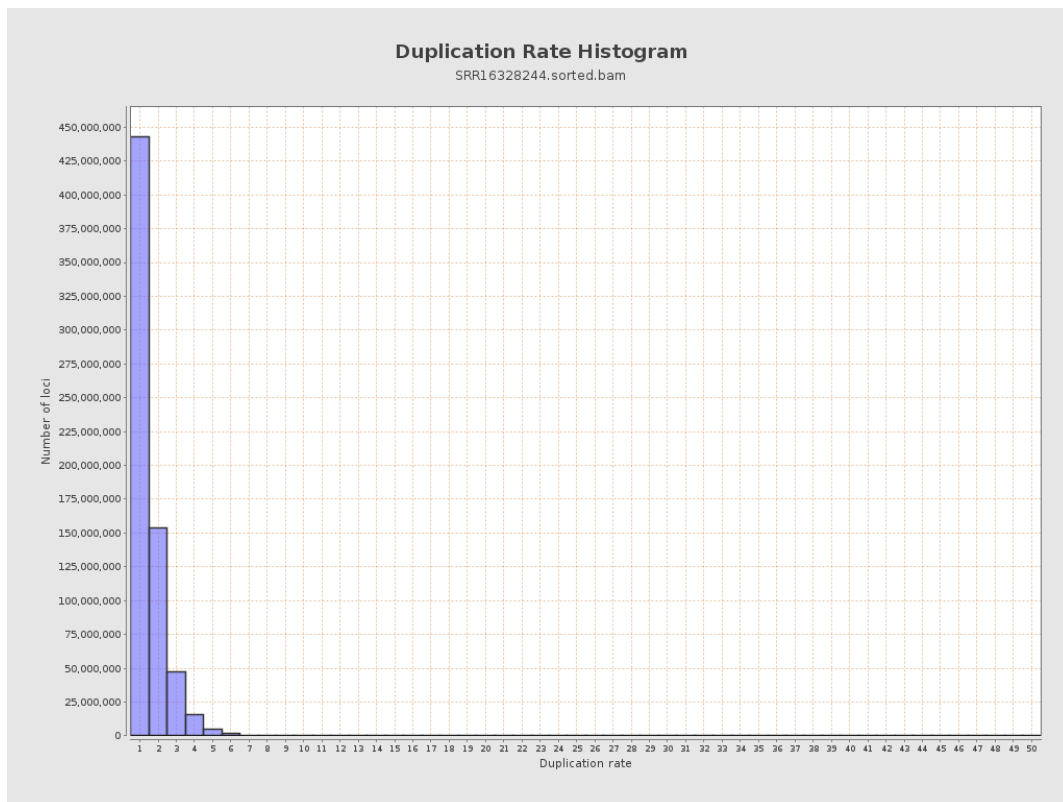
5. Results : Coverage Histogram (0-50X)



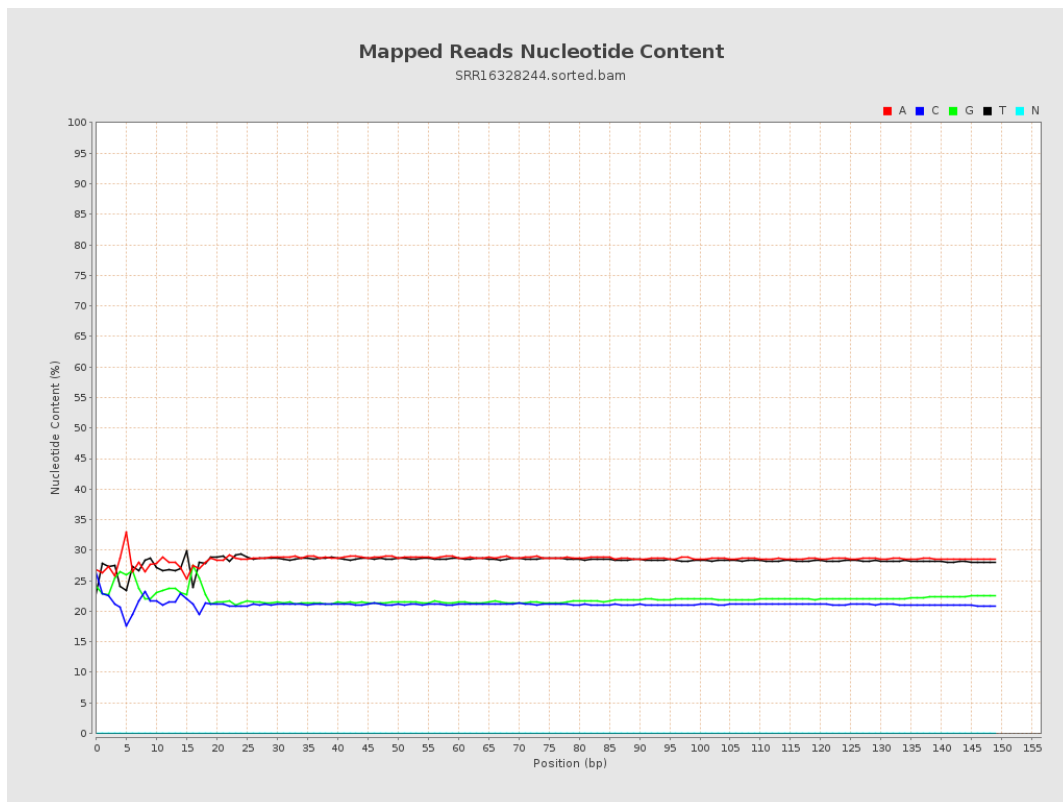
6. Results : Genome Fraction Coverage



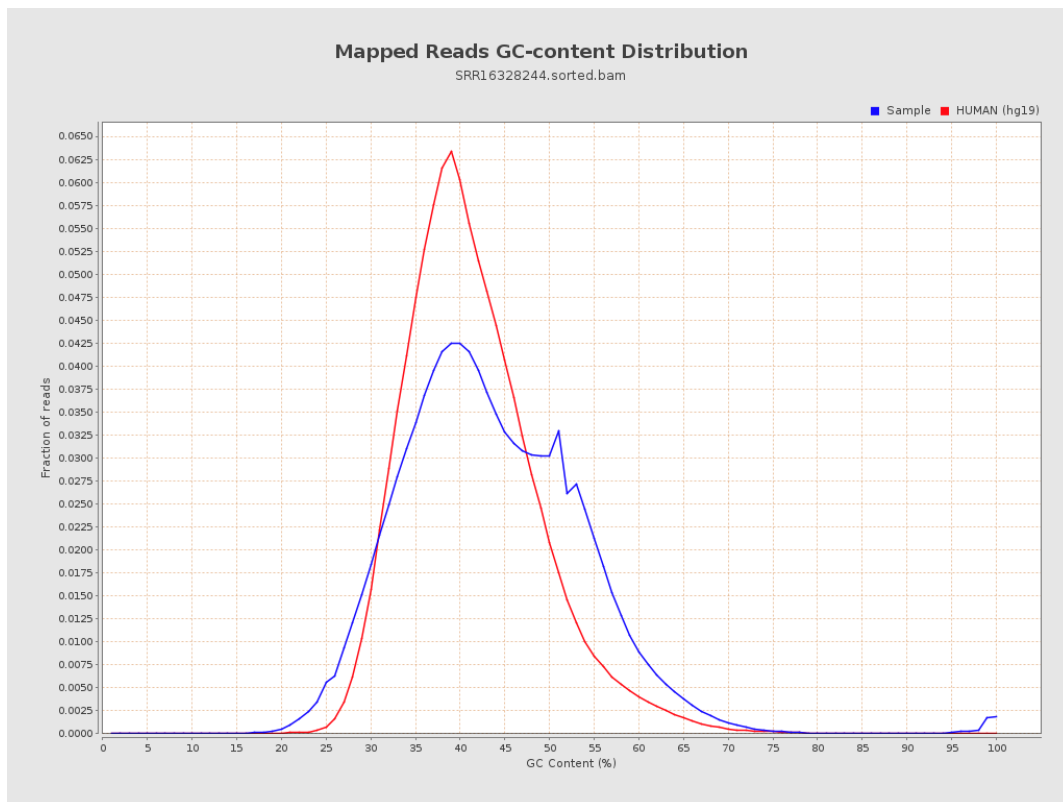
7. Results : Duplication Rate Histogram



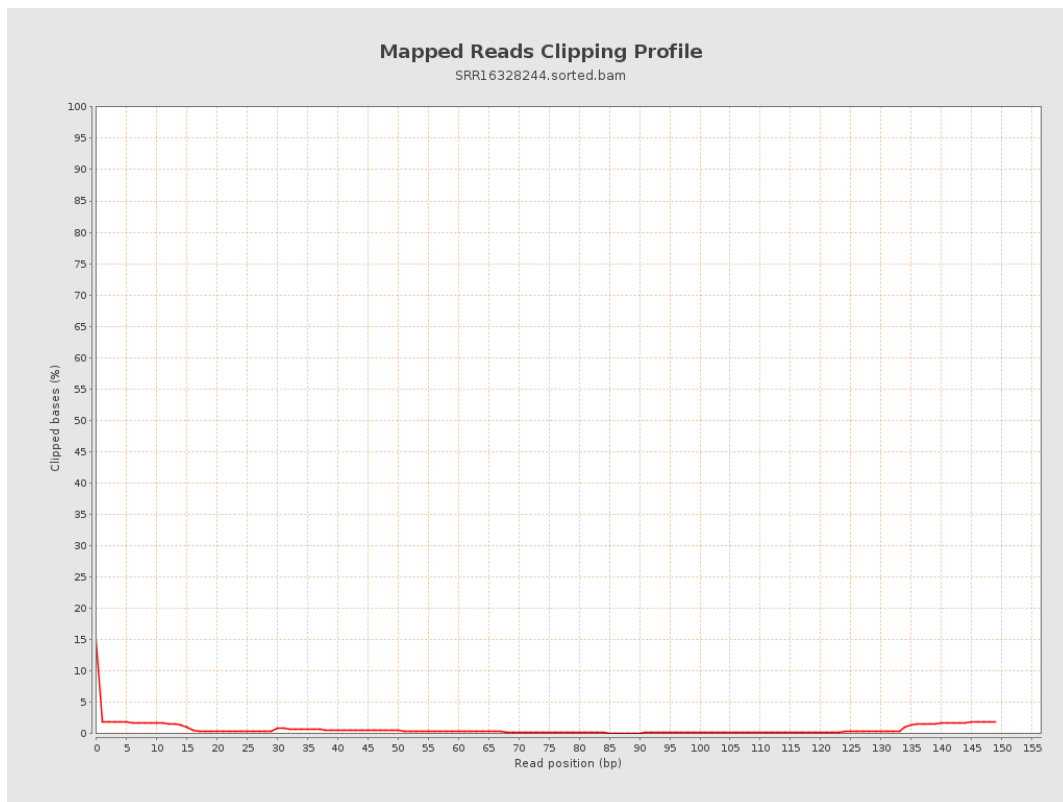
8. Results : Mapped Reads Nucleotide Content



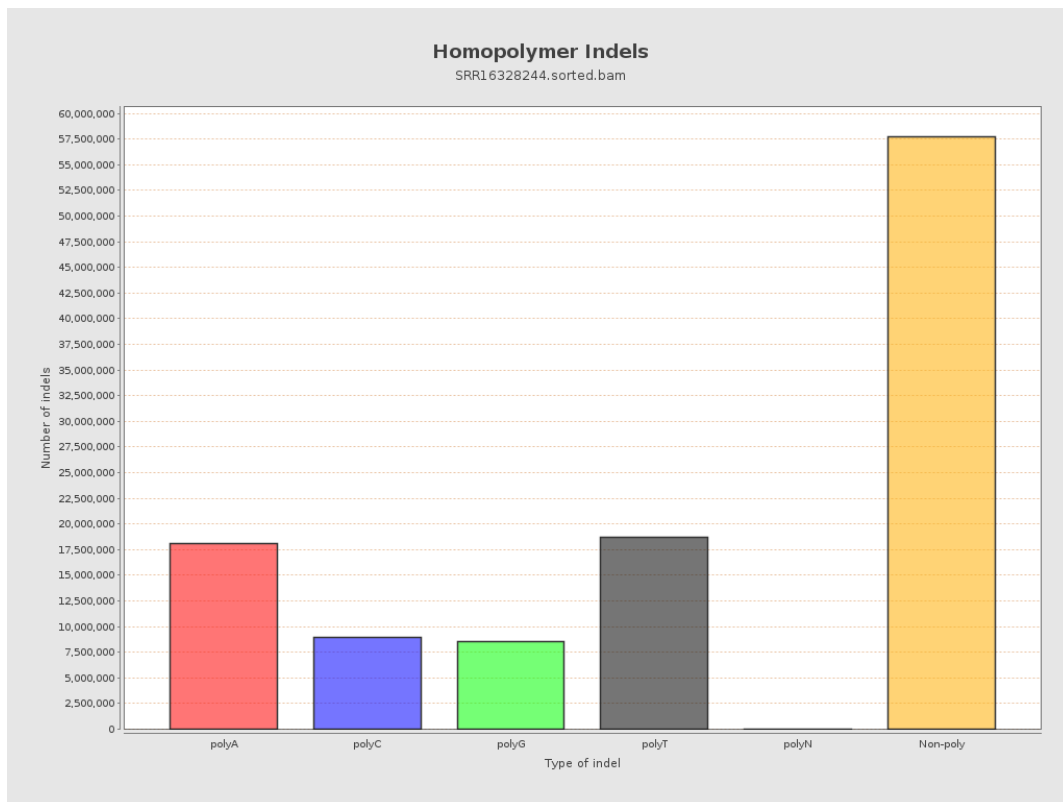
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



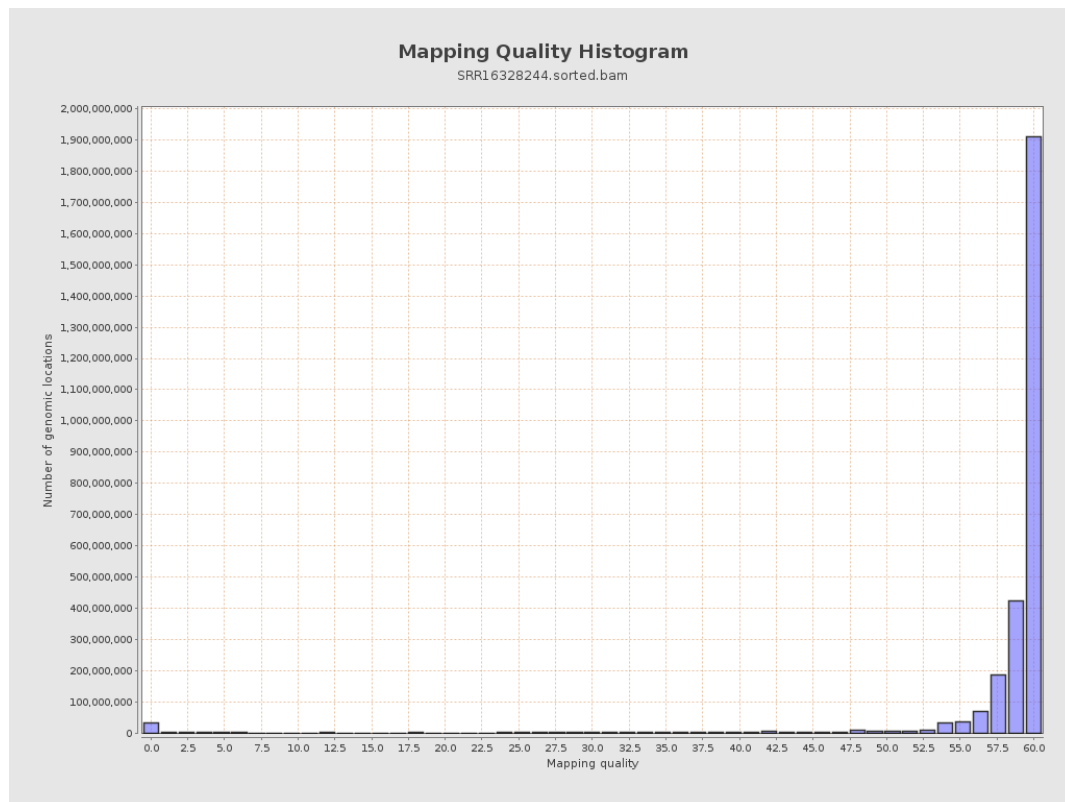
11. Results : Homopolymer Indels



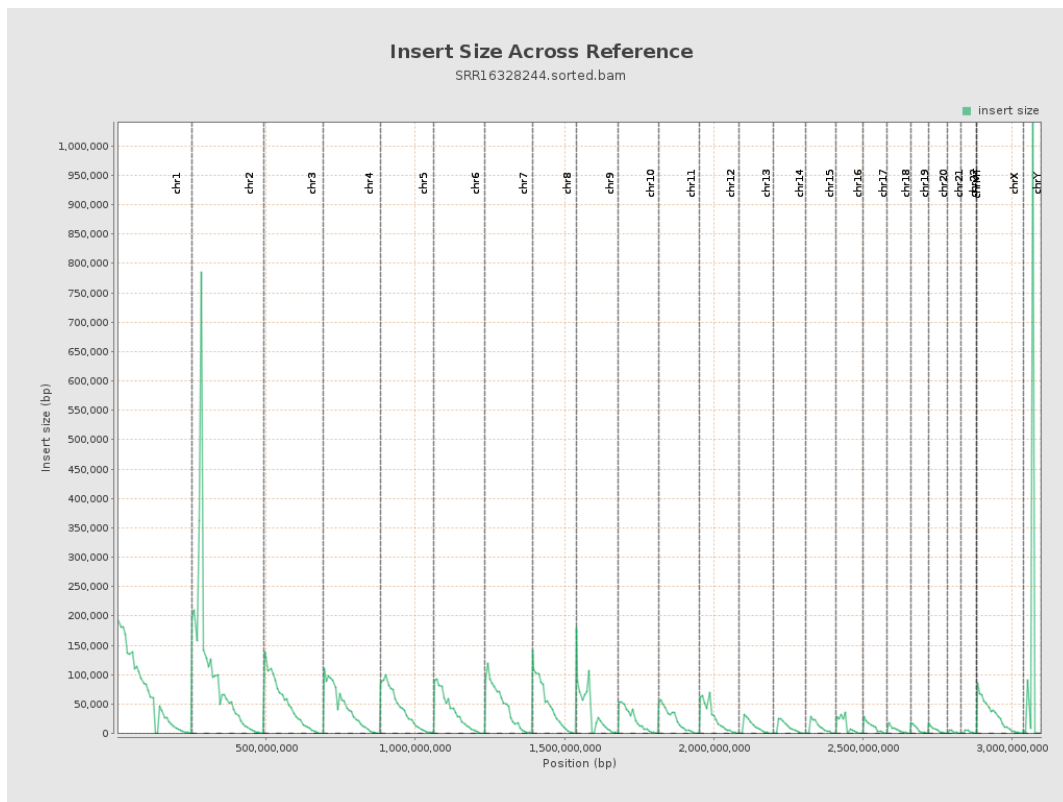
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

