

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/02/23 14:53:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR16328250.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_SRR16328250 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16328250_1.fastq.gz SRR16328250_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Feb 23 14:53:10 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR16328250.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	726,500,714
Mapped reads	712,689,196 / 98.1%
Unmapped reads	13,811,518 / 1.9%
Mapped paired reads	712,689,196 / 98.1%
Mapped reads, first in pair	358,720,128 / 49.38%
Mapped reads, second in pair	353,969,068 / 48.72%
Mapped reads, both in pair	704,547,030 / 96.98%
Mapped reads, singletons	8,142,166 / 1.12%
Secondary alignments	0
Supplementary alignments	31,298,934 / 4.31%
Read min/max/mean length	30 / 150 / 152.15
Duplicated reads (estimated)	279,823,787 / 38.52%
Duplication rate	31.81%
Clipped reads	461,918,603 / 63.58%

2.2. ACGT Content

Number/percentage of A's	28,338,120,307 / 28.8%
Number/percentage of C's	20,196,685,694 / 20.53%
Number/percentage of T's	28,076,083,564 / 28.54%
Number/percentage of G's	21,776,004,838 / 22.13%
Number/percentage of N's	1,777,541 / 0%

GC Percentage	42.66%
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2.3. Coverage

Mean	31.8088
Standard Deviation	1,659.1312

2.4. Mapping Quality

Mean Mapping Quality	53.58
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2.5. Insert size

Mean	185,359.9
Standard Deviation	4,172,750.26
P25/Median/P75	278 / 404 / 559

2.6. Mismatches and indels

General error rate	0.98%
Mismatches	916,558,053
Insertions	18,122,933
Mapped reads with at least one insertion	2.42%
Deletions	44,832,590
Mapped reads with at least one deletion	6.03%
Homopolymer indels	44.32%

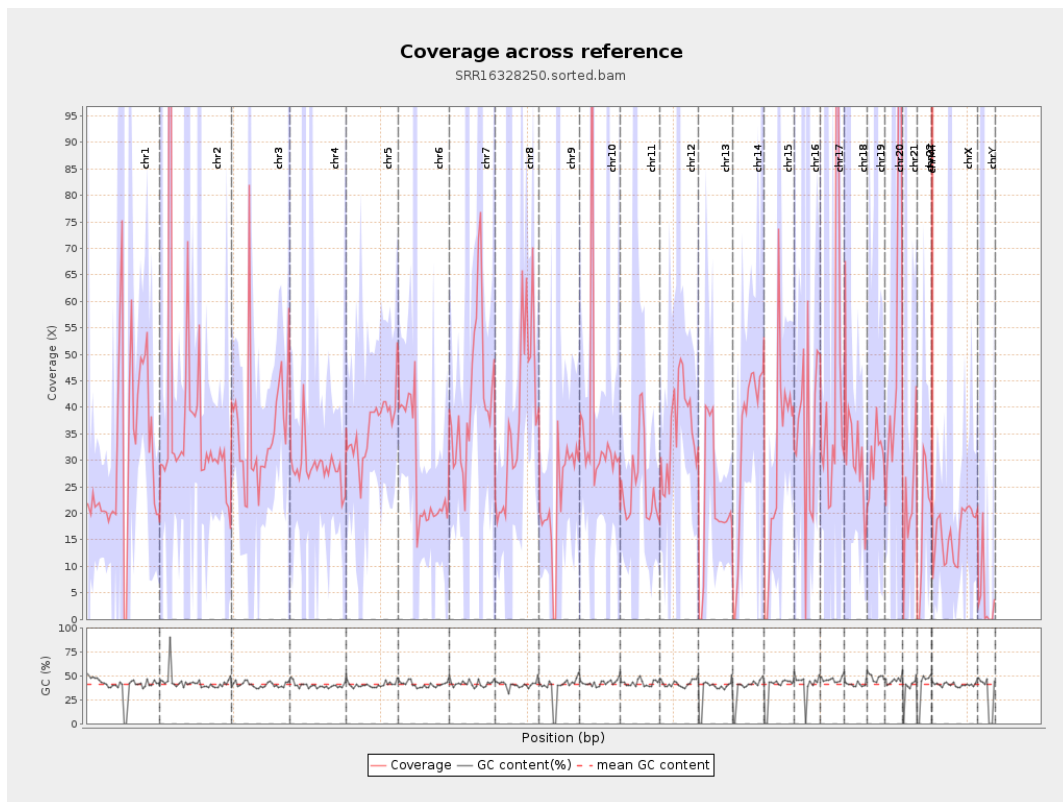
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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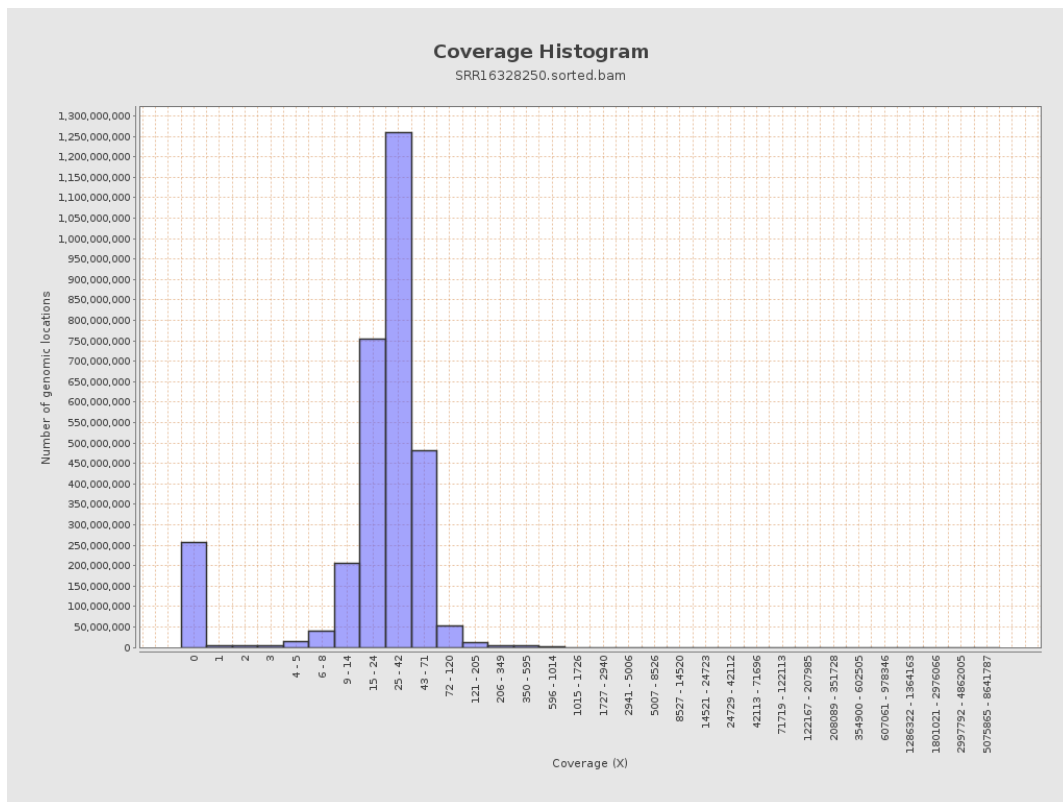
		bases	coverage	deviation
chr1	249250621	7723528636	30.987	785.4264
chr2	243199373	9246739225	38.0212	5,791.9961
chr3	198022430	7045408589	35.5788	42.0435
chr4	191154276	5480057543	28.6682	173.7486
chr5	180915260	6587148061	36.4101	21.1573
chr6	171115067	4664551206	27.2597	124.1451
chr7	159138663	6676809081	41.9559	210.2692
chr8	146364022	5543196036	37.8727	582.9918
chr9	141213431	3258056264	23.0719	337.4779
chr10	135534747	4888383172	36.0674	706.9055
chr11	135006516	3432401724	25.424	118.5056
chr12	133851895	4796165900	35.8319	68.2276
chr13	115169878	2478372216	21.5193	21.3365
chr14	107349540	3637151131	33.8814	45.7402
chr15	102531392	3097734818	30.2126	32.458
chr16	90354753	3306223292	36.5916	263.3441
chr17	81195210	3484788946	42.9187	143.1355
chr18	78077248	2427644228	31.0929	334.7606
chr19	59128983	1830414151	30.9563	439.9971
chr20	63025520	3429935509	54.4214	105.5773
chr21	48129895	1124557601	23.3651	81.9726
chr22	51304566	947907283	18.4761	24.1869
chrMT	16571	632967534	38,197.3046	6,135.5534
chrX	155270560	2491844721	16.0484	44.5704

chrY	59373566	238220096	4.0122	199.3391
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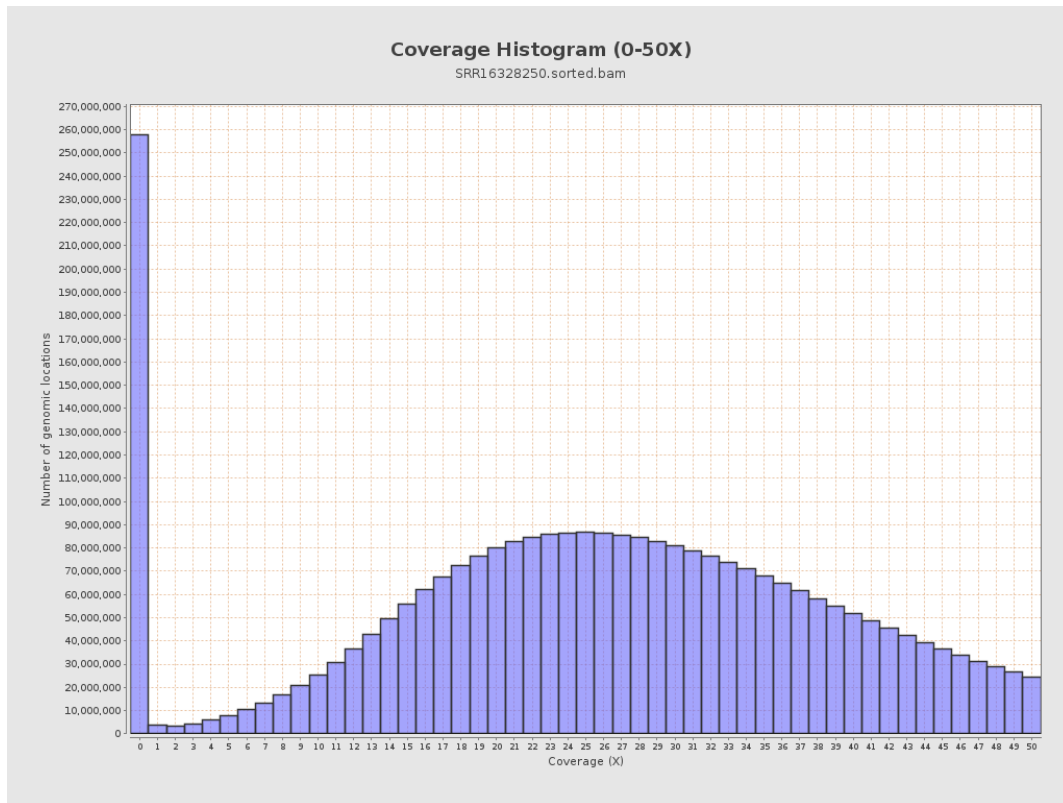
3. Results : Coverage across reference



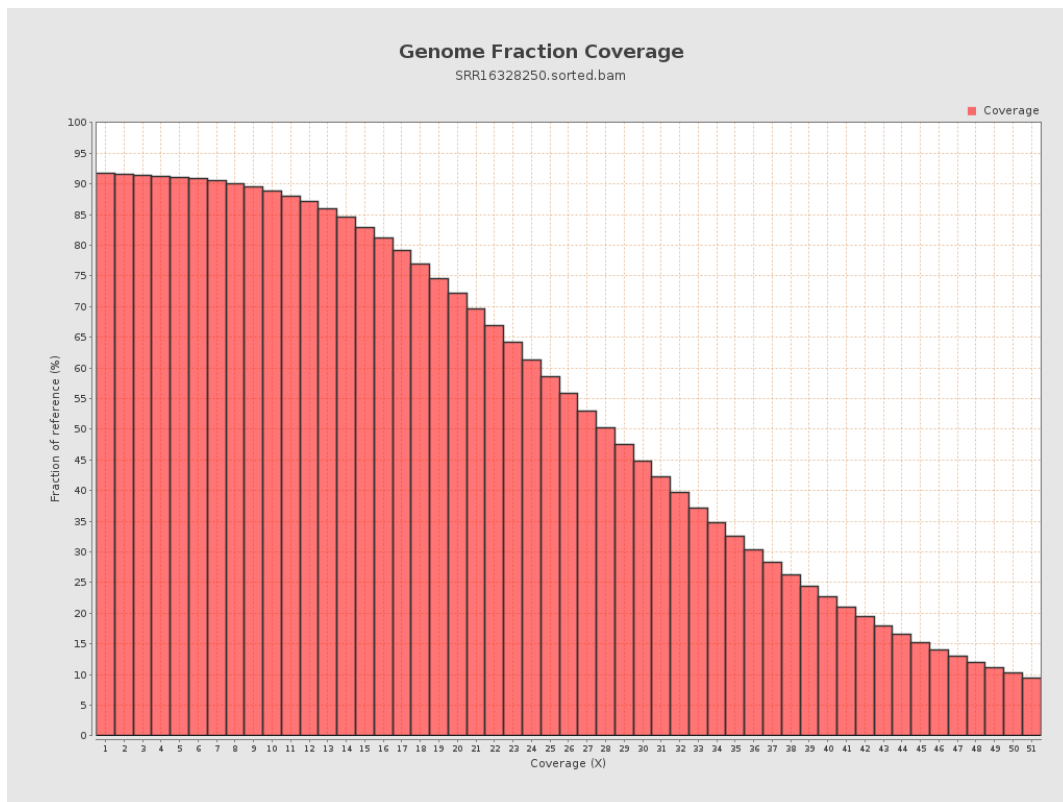
4. Results : Coverage Histogram



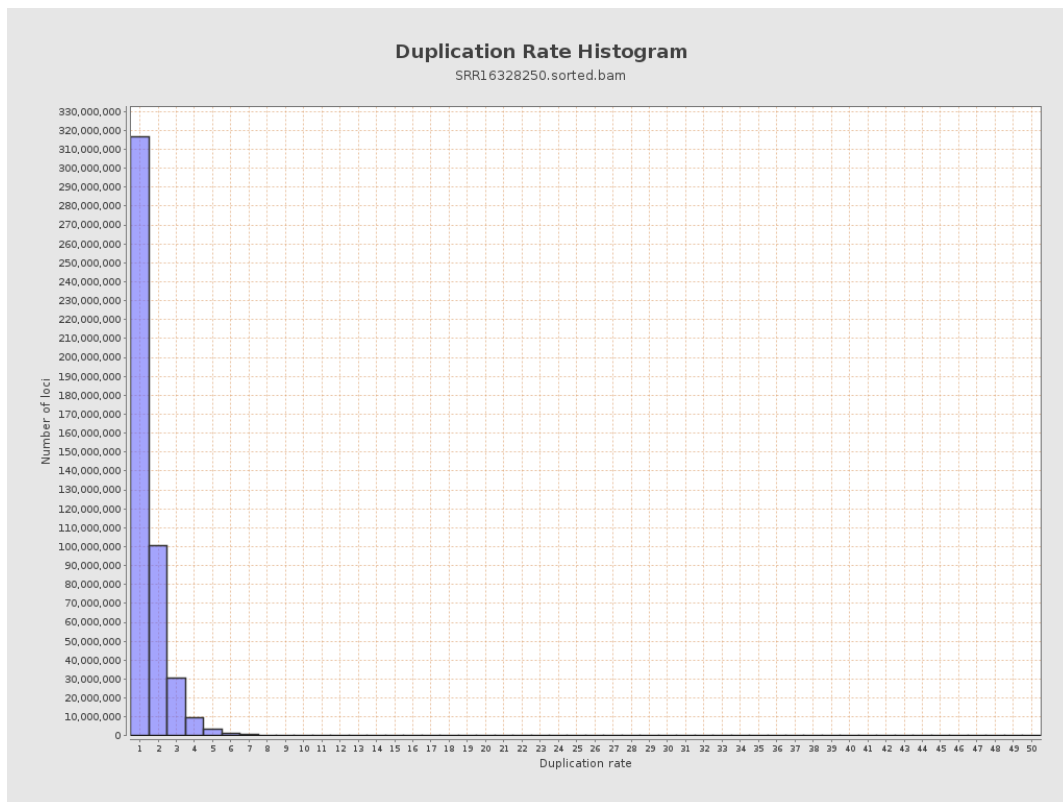
5. Results : Coverage Histogram (0-50X)



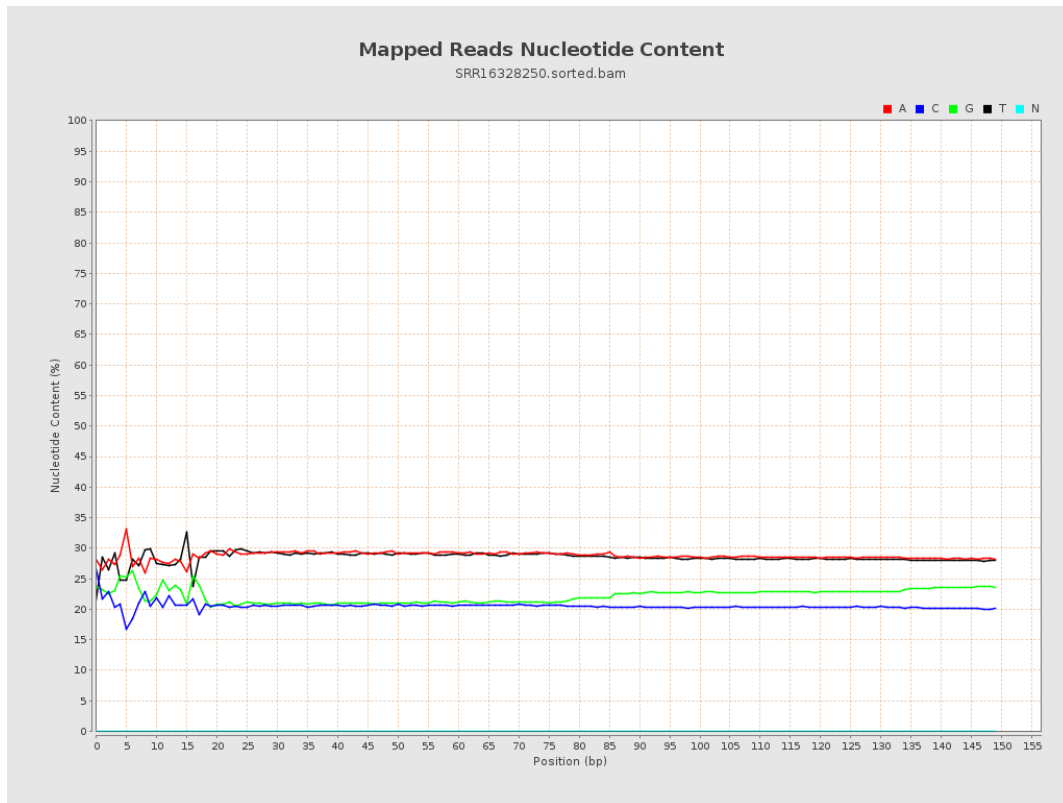
6. Results : Genome Fraction Coverage



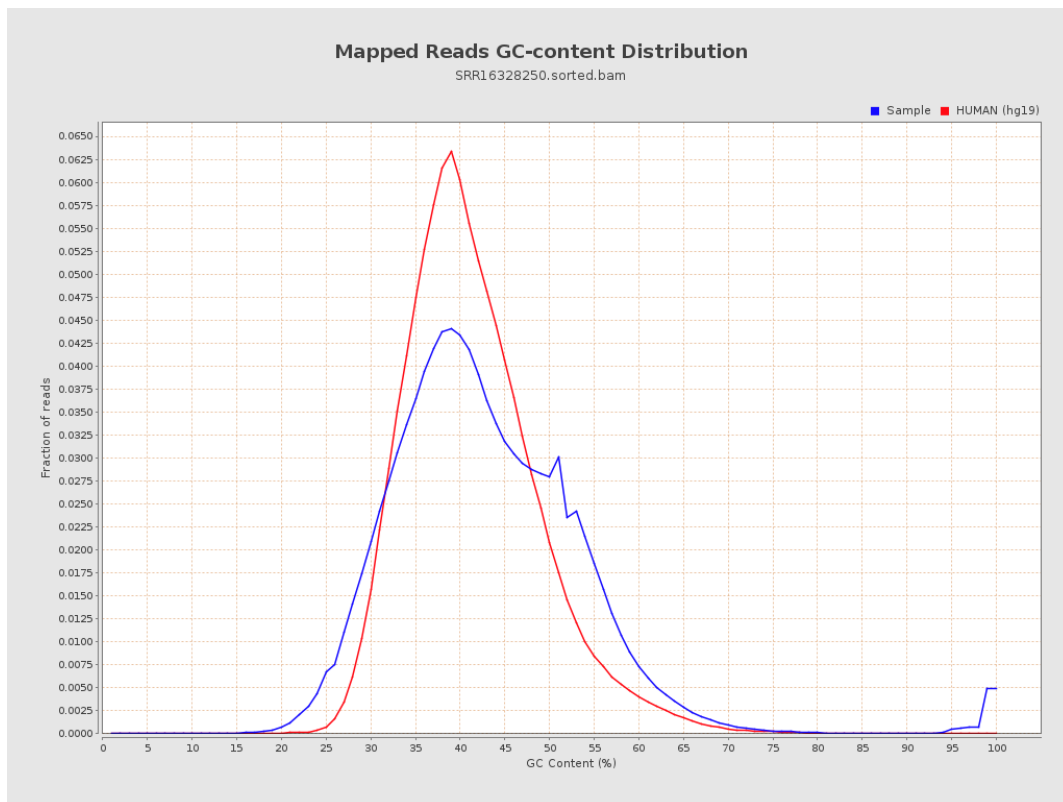
7. Results : Duplication Rate Histogram



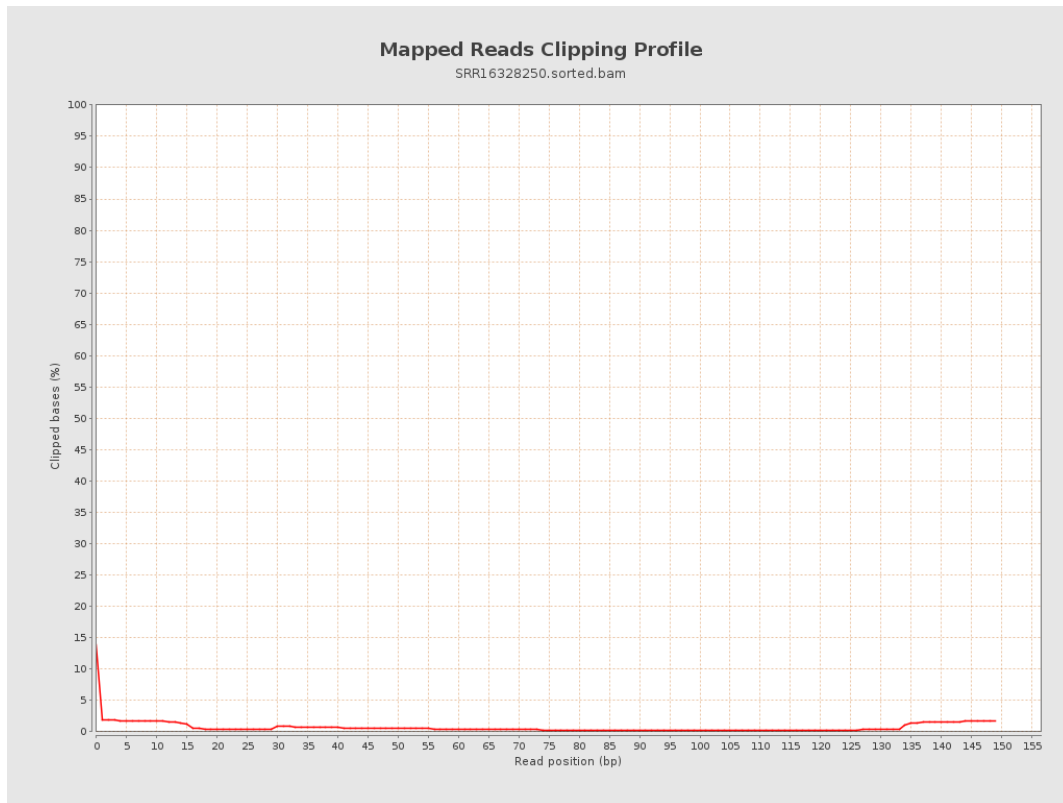
8. Results : Mapped Reads Nucleotide Content



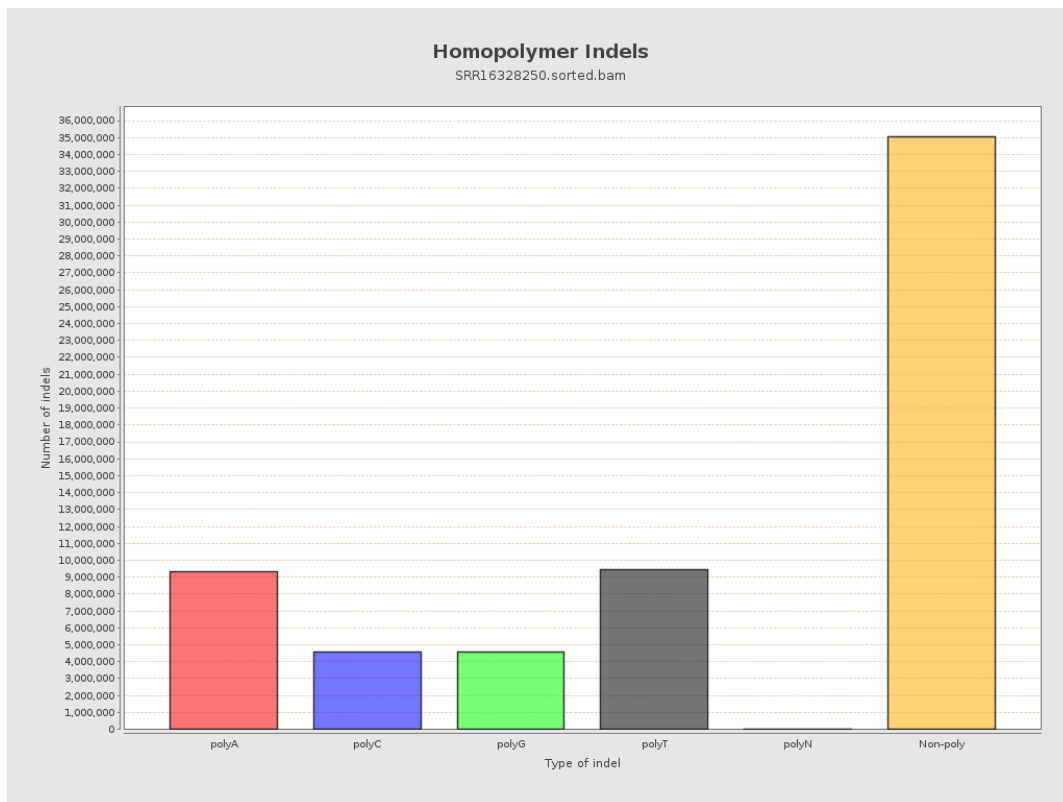
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



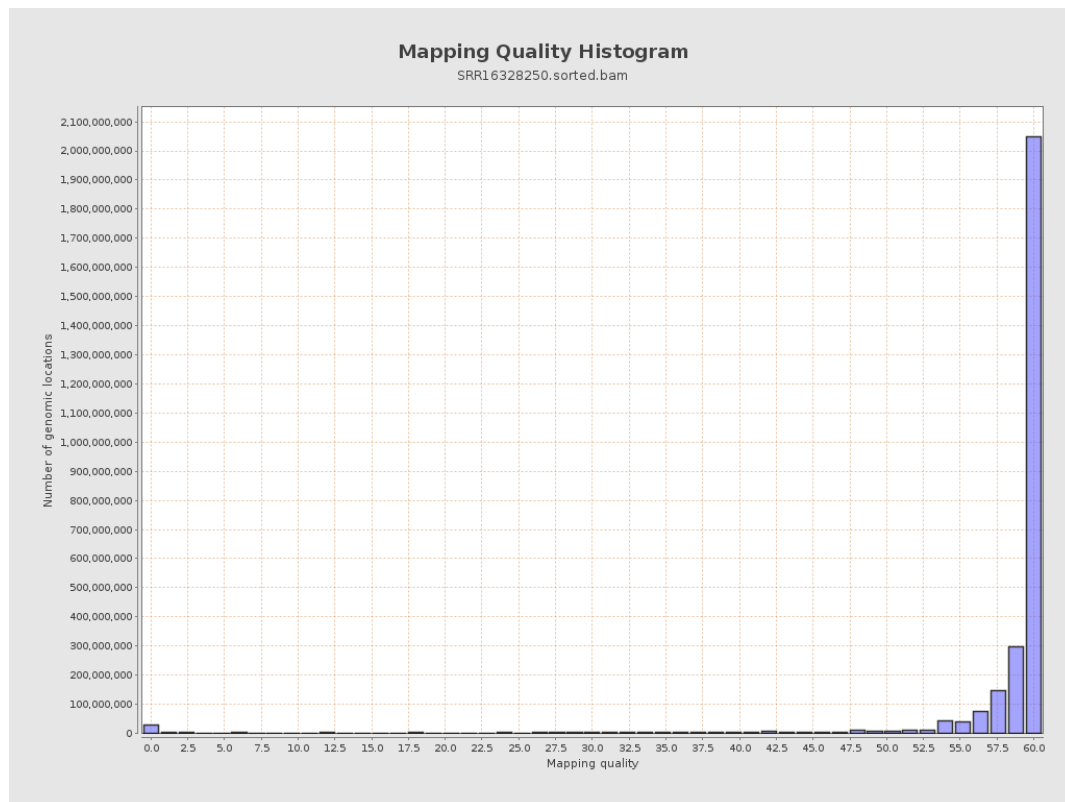
11. Results : Homopolymer Indels



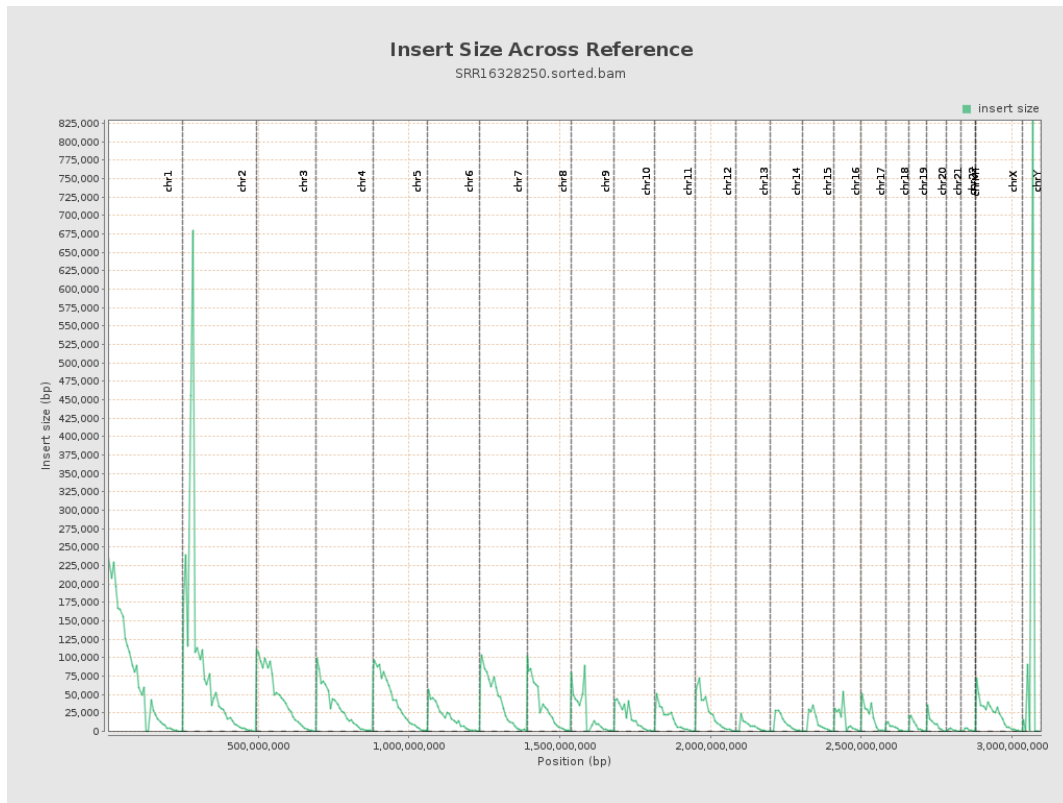
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

