

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/02/22 13:04:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR16328248.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_SRR16328248 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR16328248_1.fastq.gz SRR16328248_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Feb 22 13:04:21 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR16328248.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,548,702,256
Mapped reads	1,513,342,751 / 97.72%
Unmapped reads	35,359,505 / 2.28%
Mapped paired reads	1,513,342,751 / 97.72%
Mapped reads, first in pair	758,334,603 / 48.97%
Mapped reads, second in pair	755,008,148 / 48.75%
Mapped reads, both in pair	1,503,384,000 / 97.07%
Mapped reads, singletons	9,958,751 / 0.64%
Secondary alignments	0
Supplementary alignments	65,843,635 / 4.25%
Read min/max/mean length	30 / 150 / 152.13
Duplicated reads (estimated)	669,623,579 / 43.24%
Duplication rate	39.31%
Clipped reads	978,484,195 / 63.18%

2.2. ACGT Content

Number/percentage of A's	60,390,390,135 / 28.7%
Number/percentage of C's	44,199,269,064 / 21.01%
Number/percentage of T's	59,700,605,133 / 28.38%
Number/percentage of G's	46,097,619,455 / 21.91%
Number/percentage of N's	3,909,115 / 0%

GC Percentage	42.92%
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2.3. Coverage

Mean	68.0202
Standard Deviation	1,524.4578

2.4. Mapping Quality

Mean Mapping Quality	53.79
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2.5. Insert size

Mean	166,476.04
Standard Deviation	3,998,599.96
P25/Median/P75	194 / 265 / 386

2.6. Mismatches and indels

General error rate	0.82%
Mismatches	1,627,191,472
Insertions	37,498,061
Mapped reads with at least one insertion	2.36%
Deletions	98,990,504
Mapped reads with at least one deletion	6.28%
Homopolymer indels	44.72%

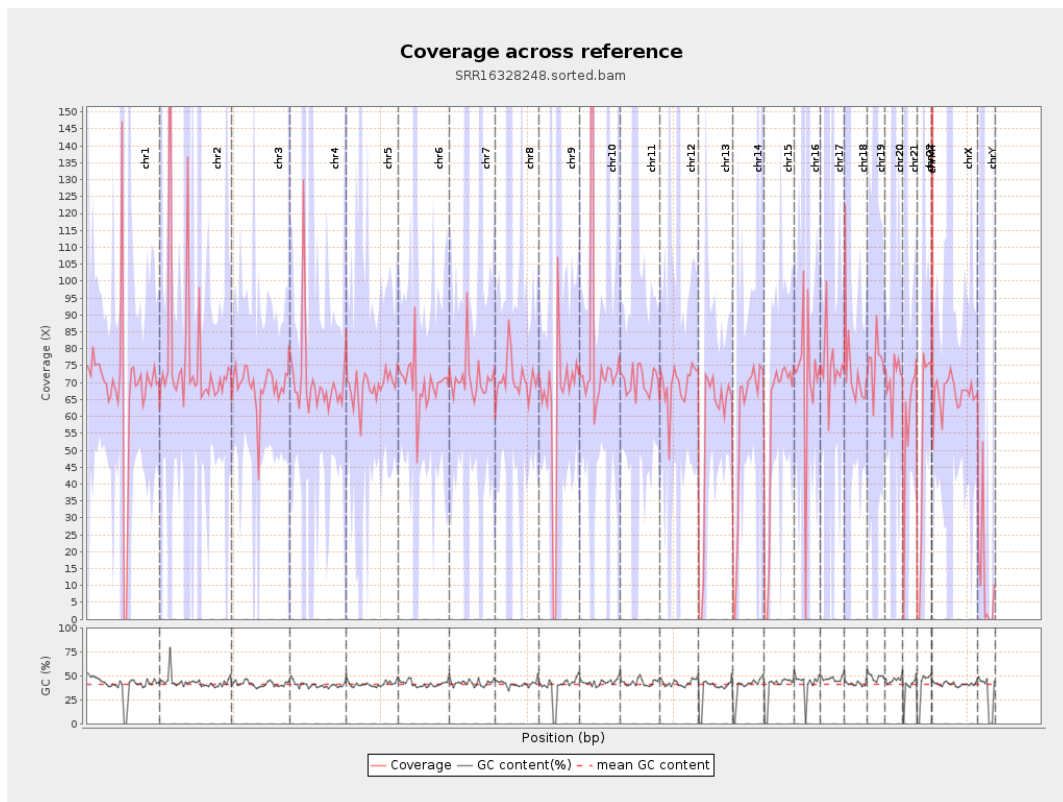
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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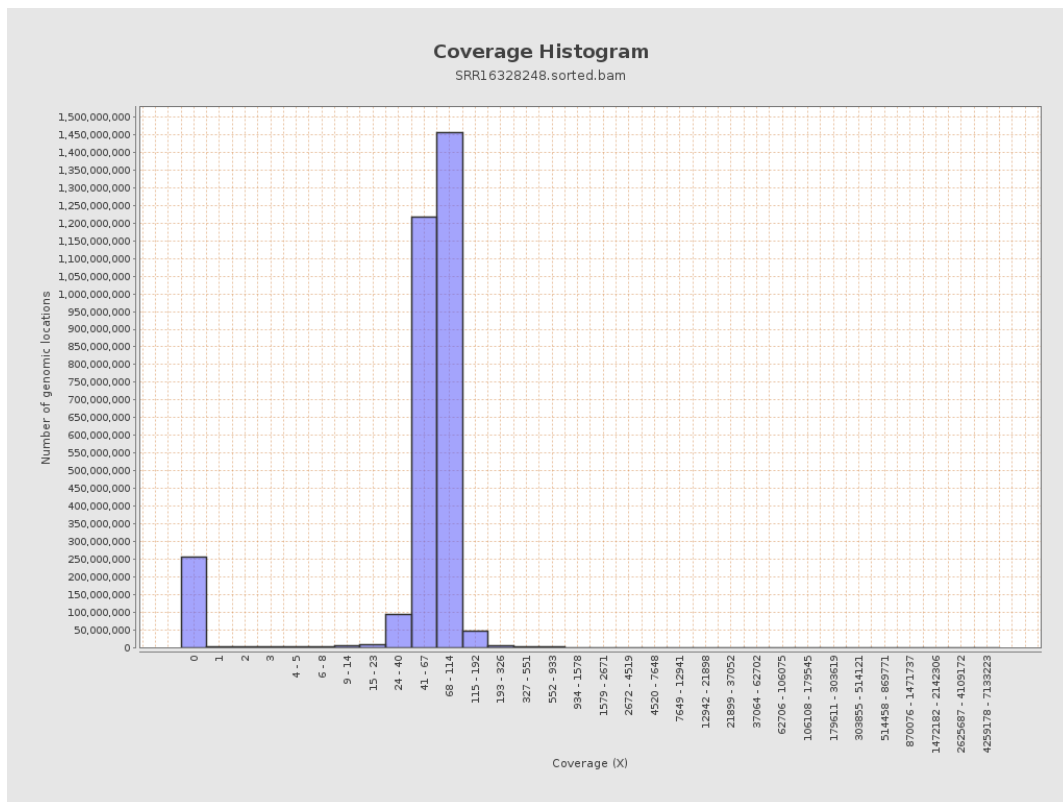
		bases	coverage	deviation
chr1	249250621	17131706966	68.7329	1,705.2596
chr2	243199373	18824197938	77.4023	4,810.9258
chr3	198022430	13658807400	68.9761	69.0967
chr4	191154276	13407731486	70.1409	559.07
chr5	180915260	12479645324	68.9806	52.1115
chr6	171115067	11924448822	69.6867	288.9981
chr7	159138663	11326100651	71.1713	610.2335
chr8	146364022	10447593852	71.3809	973.3759
chr9	141213431	9043853050	64.0439	803.2961
chr10	135534747	10940039758	80.7176	1,514.3997
chr11	135006516	9518653211	70.5051	269.3495
chr12	133851895	9264110660	69.2117	104.073
chr13	115169878	6445103013	55.9617	38.9407
chr14	107349540	6226999994	58.0068	73.1994
chr15	102531392	5861969734	57.1724	41.8901
chr16	90354753	6441489973	71.2911	302.1018
chr17	81195210	6065050211	74.6971	343.5641
chr18	78077248	5653226399	72.4056	763.5228
chr19	59128983	4513729065	76.337	928.1151
chr20	63025520	4463456465	70.8198	155.8888
chr21	48129895	2862703356	59.4787	241.9056
chr22	51304566	2691677474	52.4647	61.9861
chrMT	16571	380042065	22,934.166	3,111.3624
chrX	155270560	10325418534	66.4995	144.0825

chrY	59373566	671894313	11.3164	607.8494
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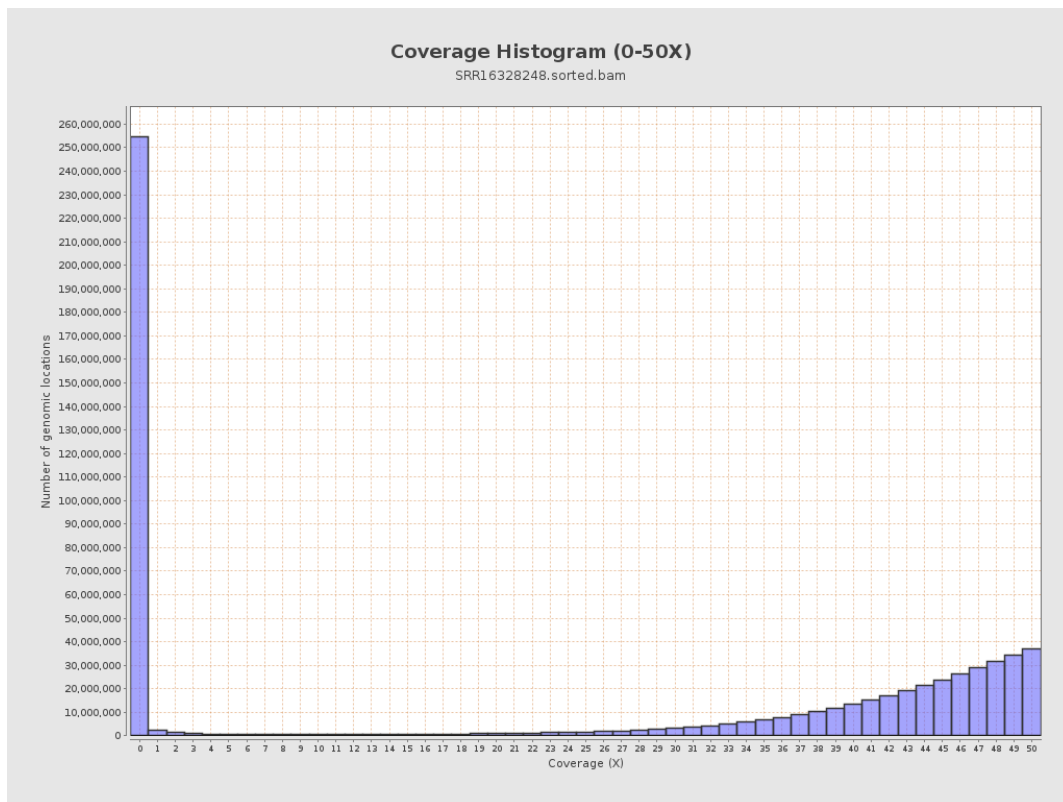
3. Results : Coverage across reference



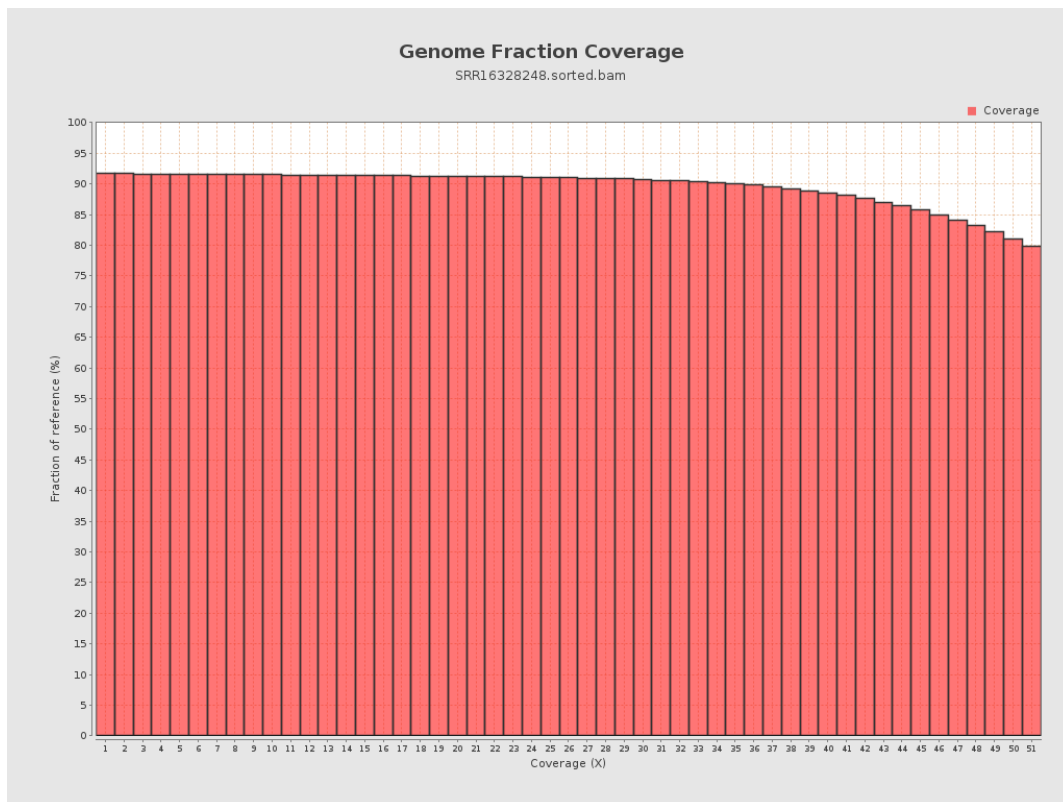
4. Results : Coverage Histogram



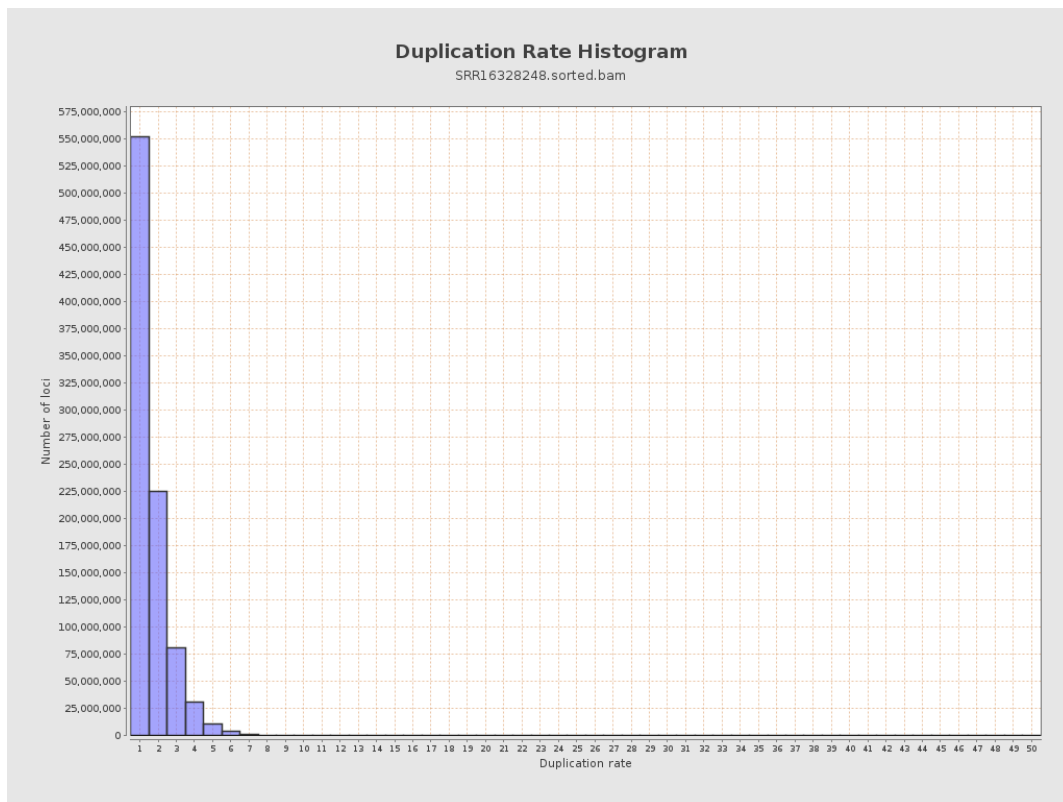
5. Results : Coverage Histogram (0-50X)



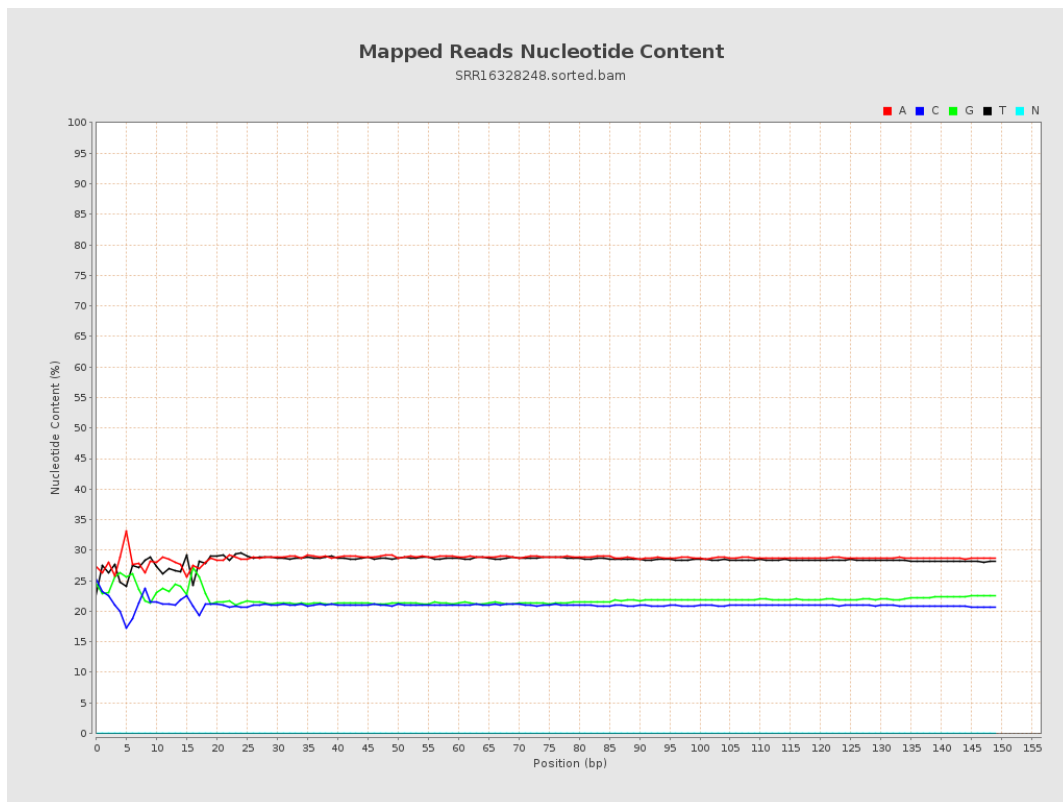
6. Results : Genome Fraction Coverage



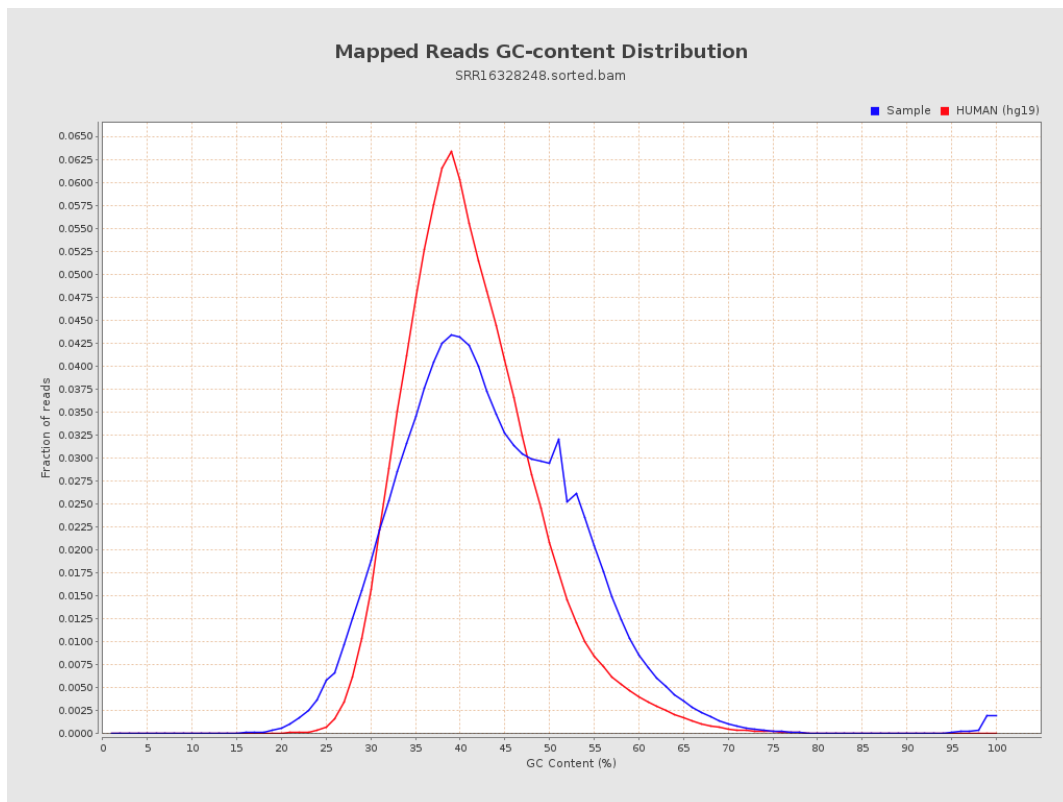
7. Results : Duplication Rate Histogram



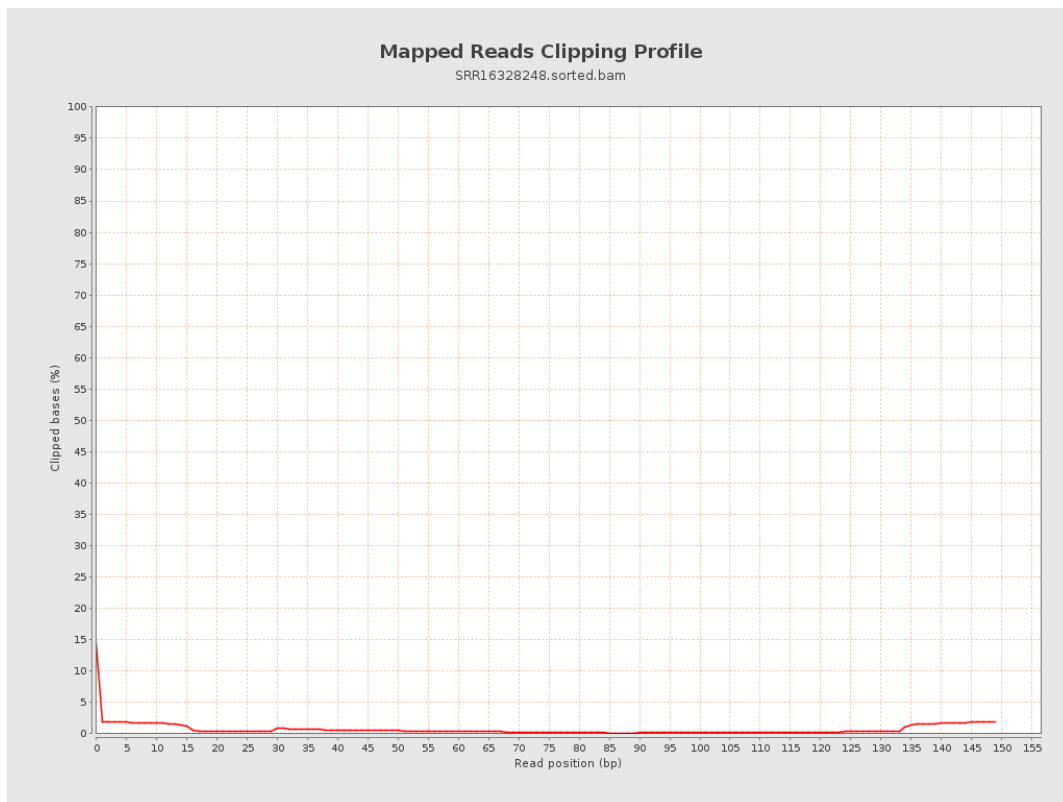
8. Results : Mapped Reads Nucleotide Content



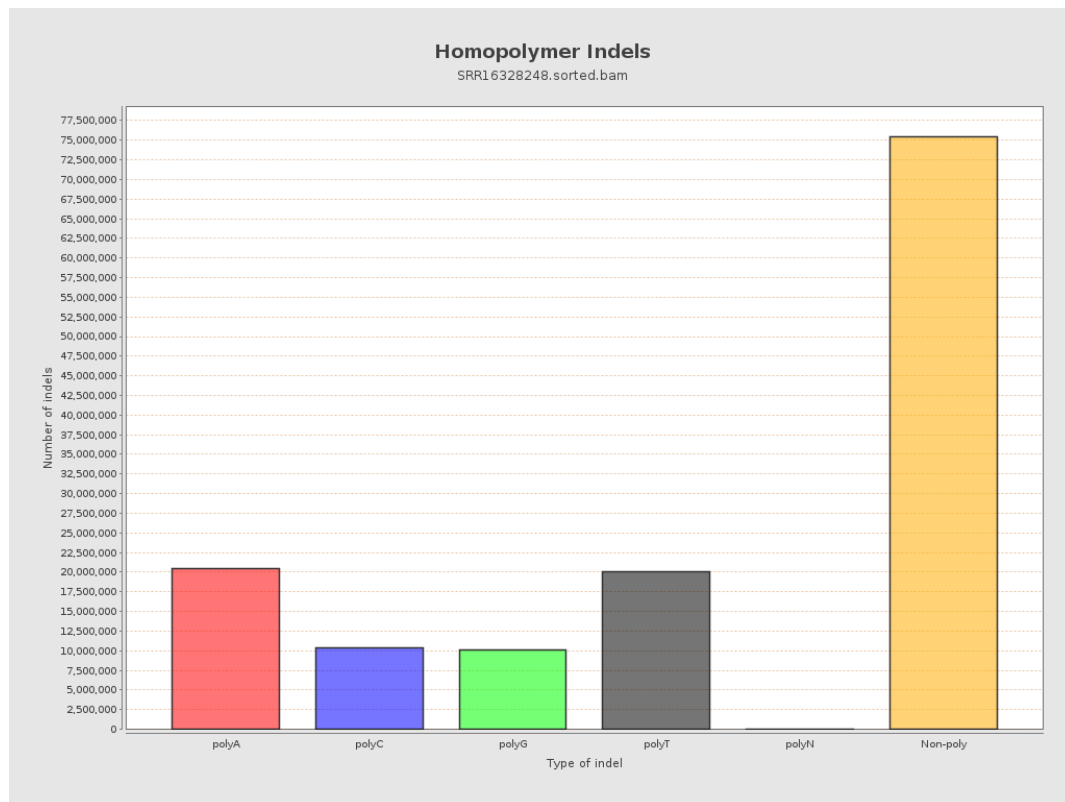
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



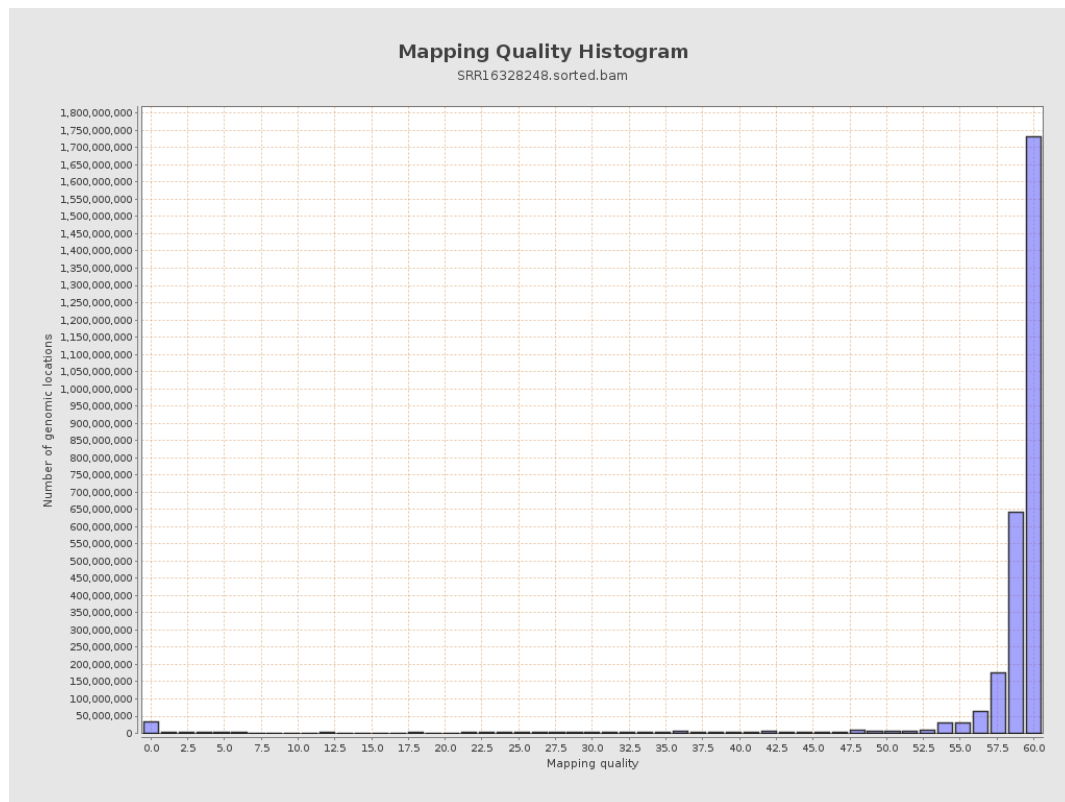
11. Results : Homopolymer Indels



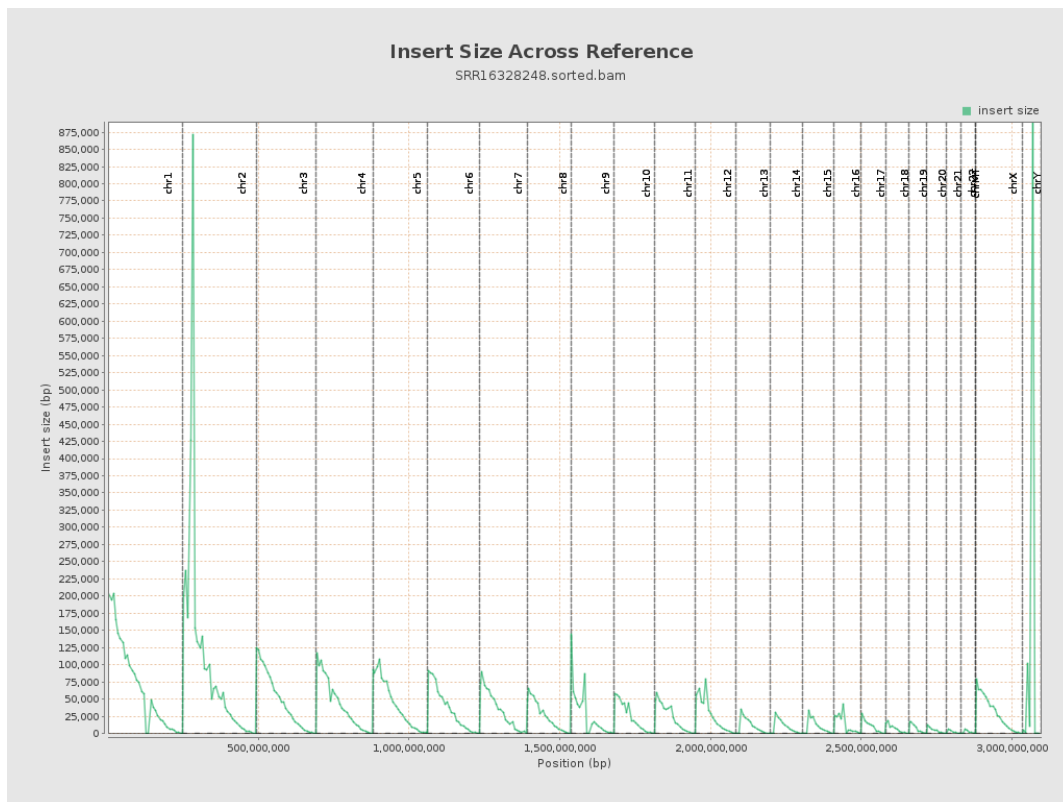
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

