

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 12:17:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173954.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_SRR10173954 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173954_1.fastq.gz SRR10173954_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 12:17:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173954.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,885,884
Mapped reads	2,820,391 / 97.73%
Unmapped reads	65,493 / 2.27%
Mapped paired reads	2,820,391 / 97.73%
Mapped reads, first in pair	1,410,678 / 48.88%
Mapped reads, second in pair	1,409,713 / 48.85%
Mapped reads, both in pair	2,779,200 / 96.3%
Mapped reads, singletons	41,191 / 1.43%
Secondary alignments	0
Supplementary alignments	362,614 / 12.57%
Read min/max/mean length	30 / 133 / 125.95
Duplicated reads (estimated)	2,250,170 / 77.97%
Duplication rate	64.93%
Clipped reads	1,441,935 / 49.97%

2.2. ACGT Content

Number/percentage of A's	95,365,888 / 29.71%
Number/percentage of C's	64,205,577 / 20%
Number/percentage of T's	94,547,543 / 29.46%
Number/percentage of G's	66,850,726 / 20.83%
Number/percentage of N's	2,362 / 0%

GC Percentage	40.83%
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2.3. Coverage

Mean	0.1037
Standard Deviation	2.0092

2.4. Mapping Quality

Mean Mapping Quality	52.61
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2.5. Insert size

Mean	1,090,651.59
Standard Deviation	9,964,332.11
P25/Median/P75	109 / 159 / 244

2.6. Mismatches and indels

General error rate	0.87%
Mismatches	2,714,878
Insertions	34,377
Mapped reads with at least one insertion	1.17%
Deletions	83,745
Mapped reads with at least one deletion	2.9%
Homopolymer indels	41.72%

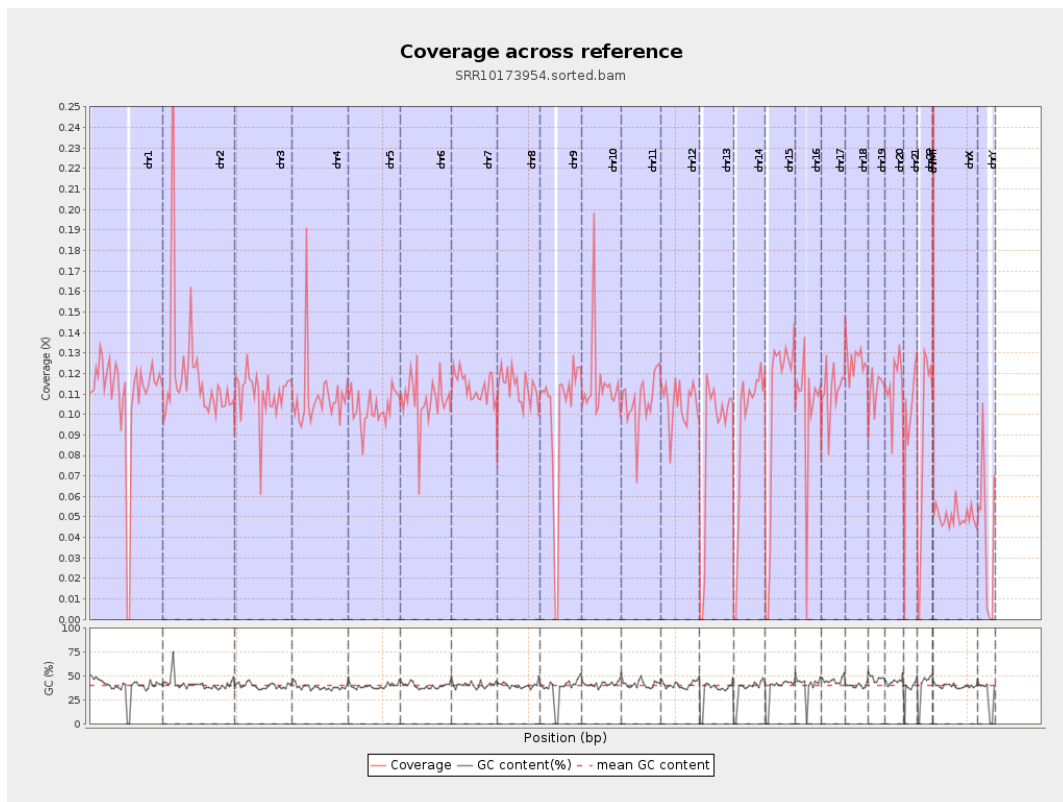
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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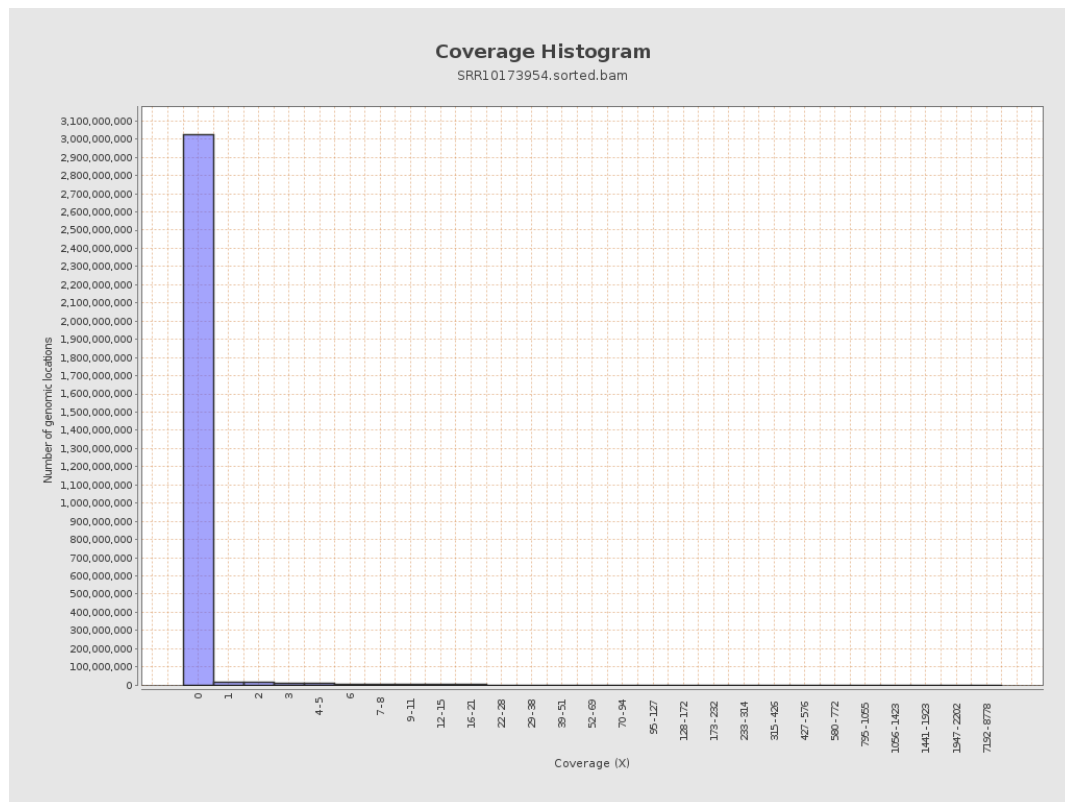
		bases	coverage	deviation
chr1	249250621	27187851	0.1091	1.0893
chr2	243199373	28841734	0.1186	6.2099
chr3	198022430	21755912	0.1099	0.9911
chr4	191154276	20781673	0.1087	1.1473
chr5	180915260	18668326	0.1032	0.9484
chr6	171115067	18313356	0.107	1.0293
chr7	159138663	18041865	0.1134	1.1428
chr8	146364022	16532536	0.113	1.2919
chr9	141213431	14075967	0.0997	1.0788
chr10	135534747	15526108	0.1146	1.2926
chr11	135006516	14377320	0.1065	0.9705
chr12	133851895	14171454	0.1059	0.9695
chr13	115169878	10176601	0.0884	0.8825
chr14	107349540	10059737	0.0937	0.9051
chr15	102531392	10524839	0.1026	0.9602
chr16	90354753	9301153	0.1029	0.9938
chr17	81195210	9087503	0.1119	0.977
chr18	78077248	9861009	0.1263	1.3392
chr19	59128983	6629608	0.1121	1.0233
chr20	63025520	7229556	0.1147	1.0171
chr21	48129895	4721746	0.0981	1.0595
chr22	51304566	4450390	0.0867	0.9707
chrMT	16571	483968	29.2057	26.2507
chrX	155270560	7799763	0.0502	0.6591

chrY	59373566	2572847	0.0433	0.7592
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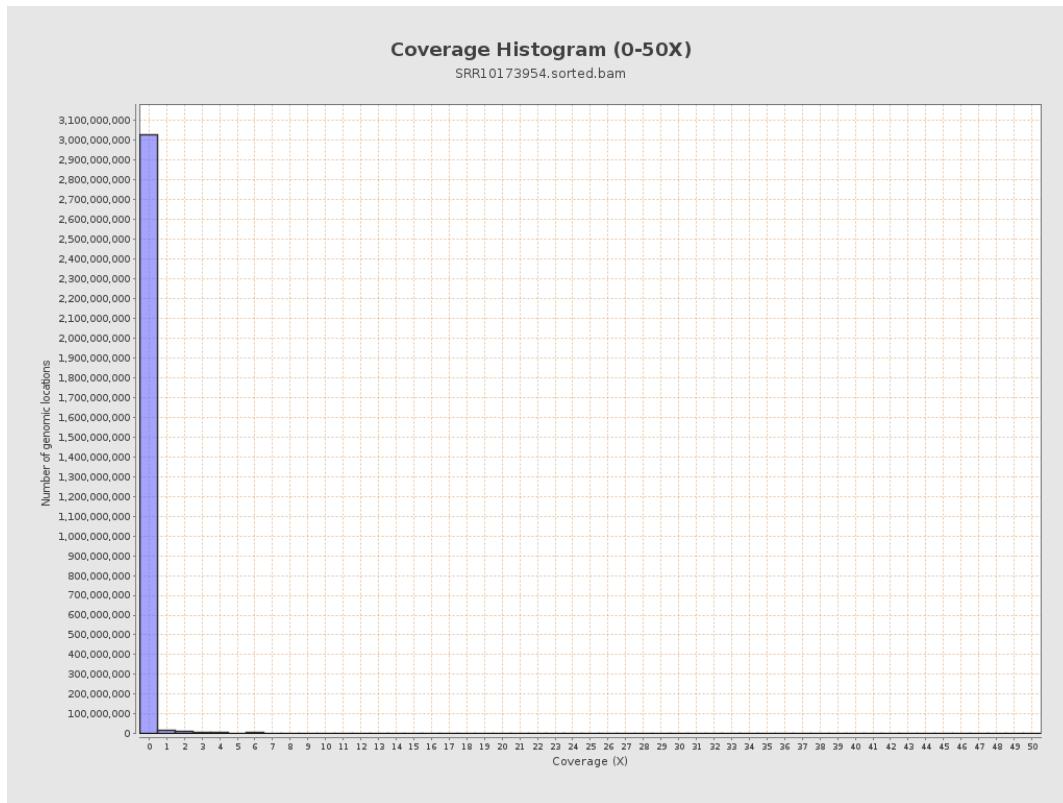
3. Results : Coverage across reference



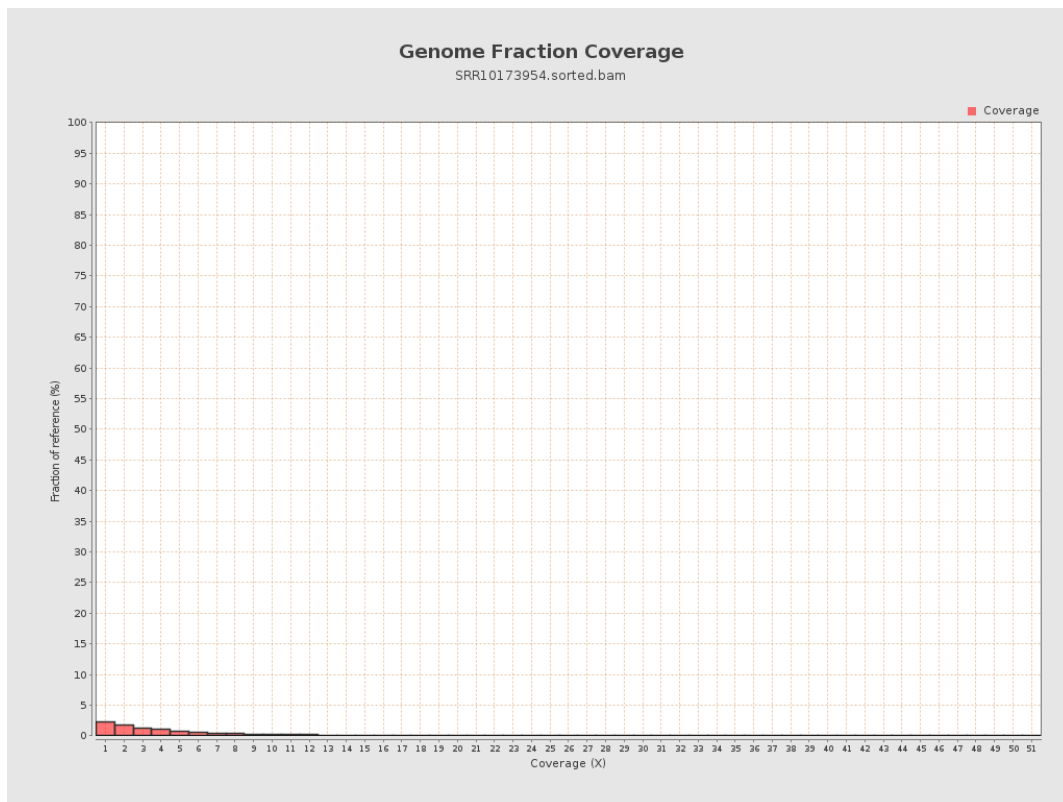
4. Results : Coverage Histogram



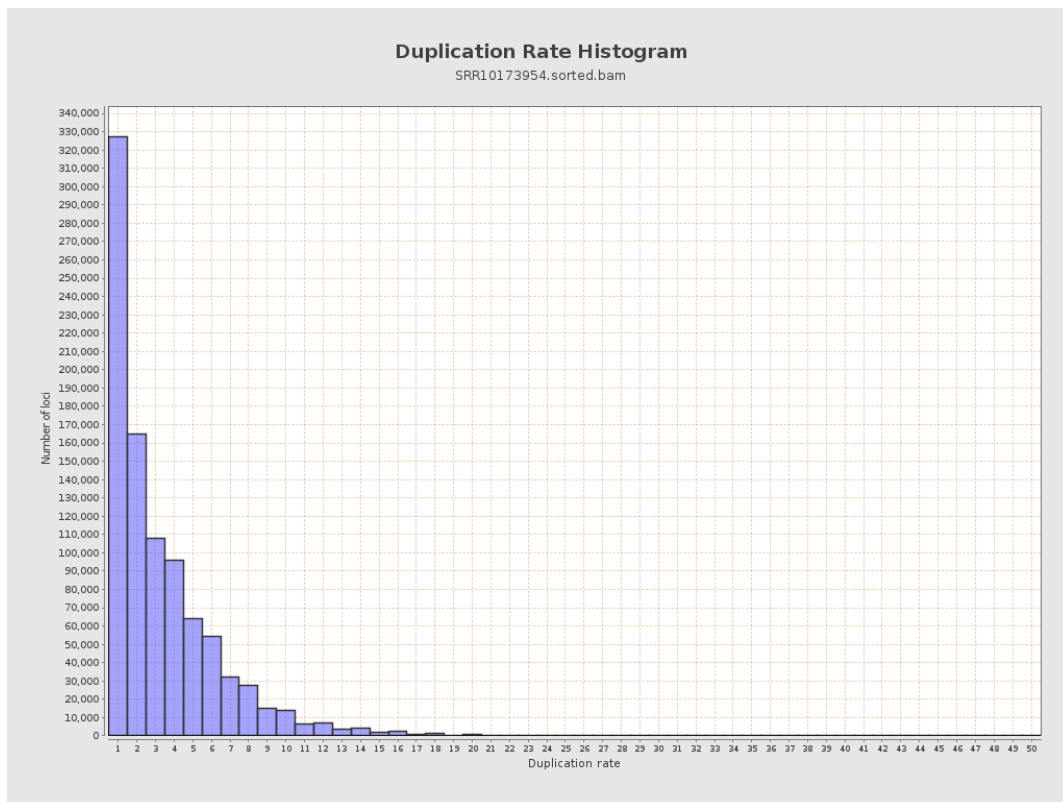
5. Results : Coverage Histogram (0-50X)



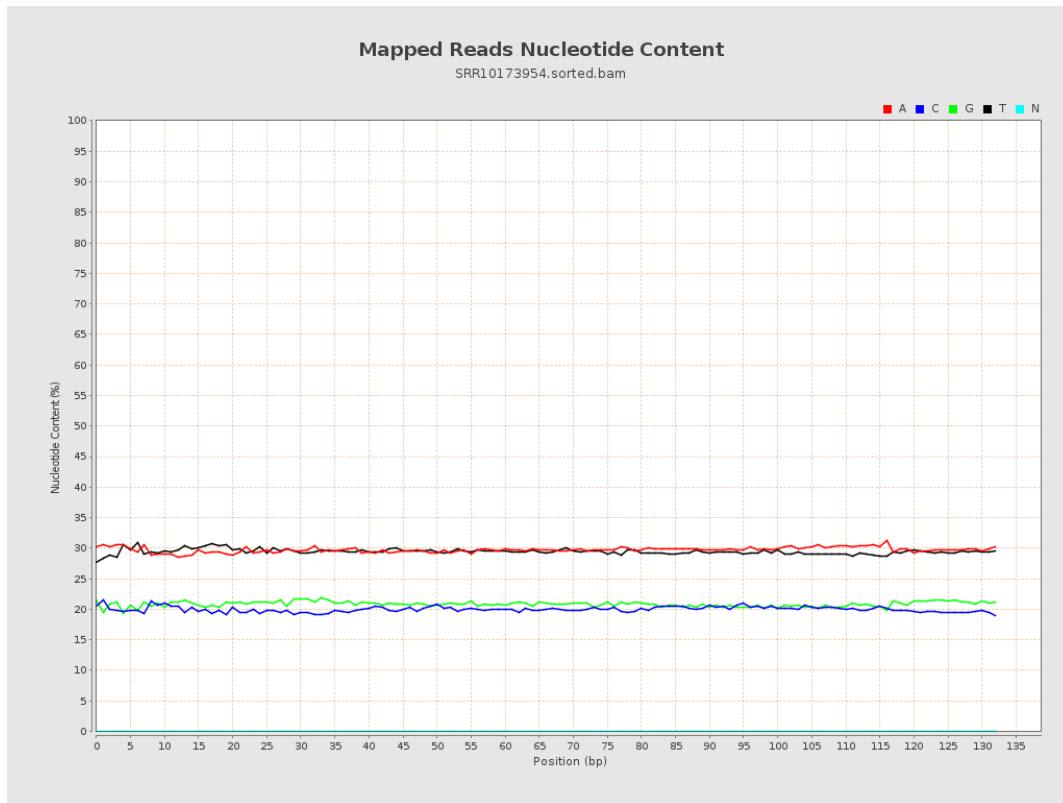
6. Results : Genome Fraction Coverage



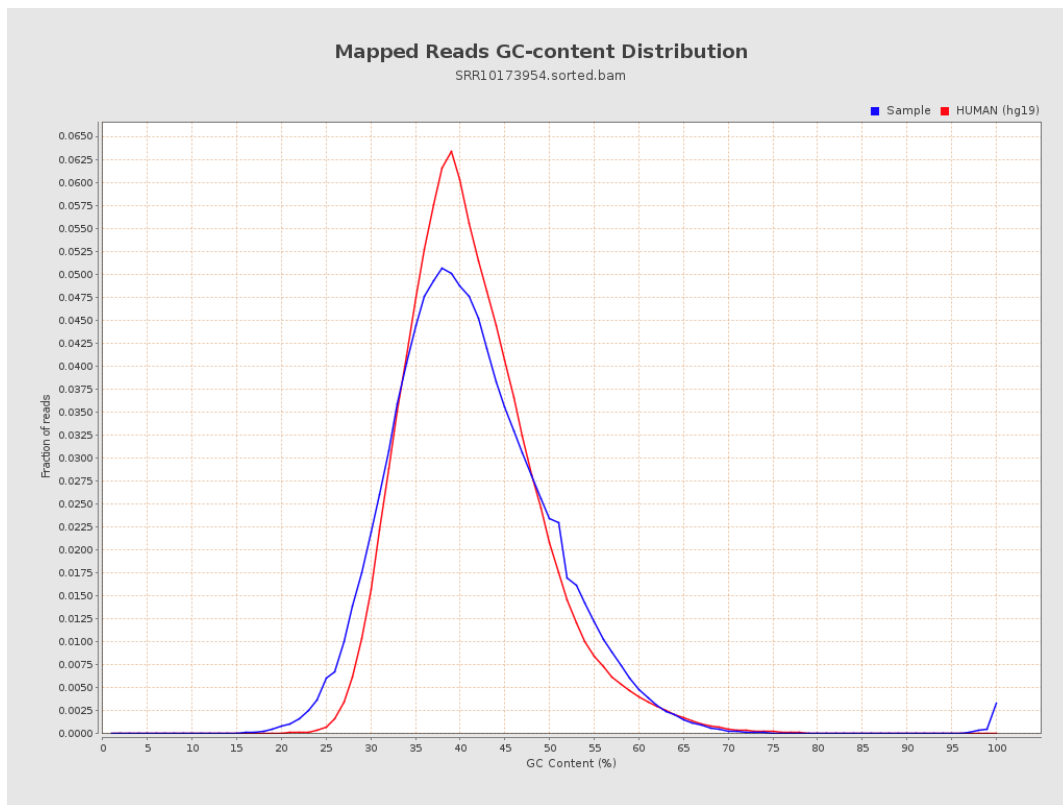
7. Results : Duplication Rate Histogram



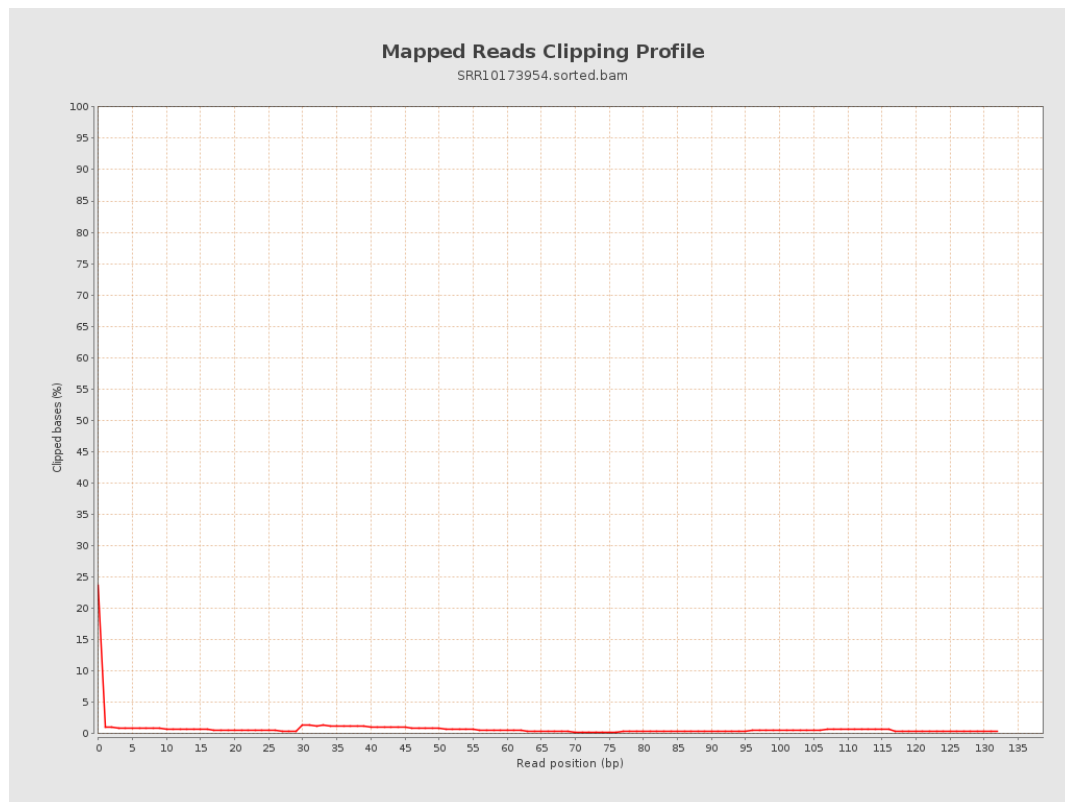
8. Results : Mapped Reads Nucleotide Content



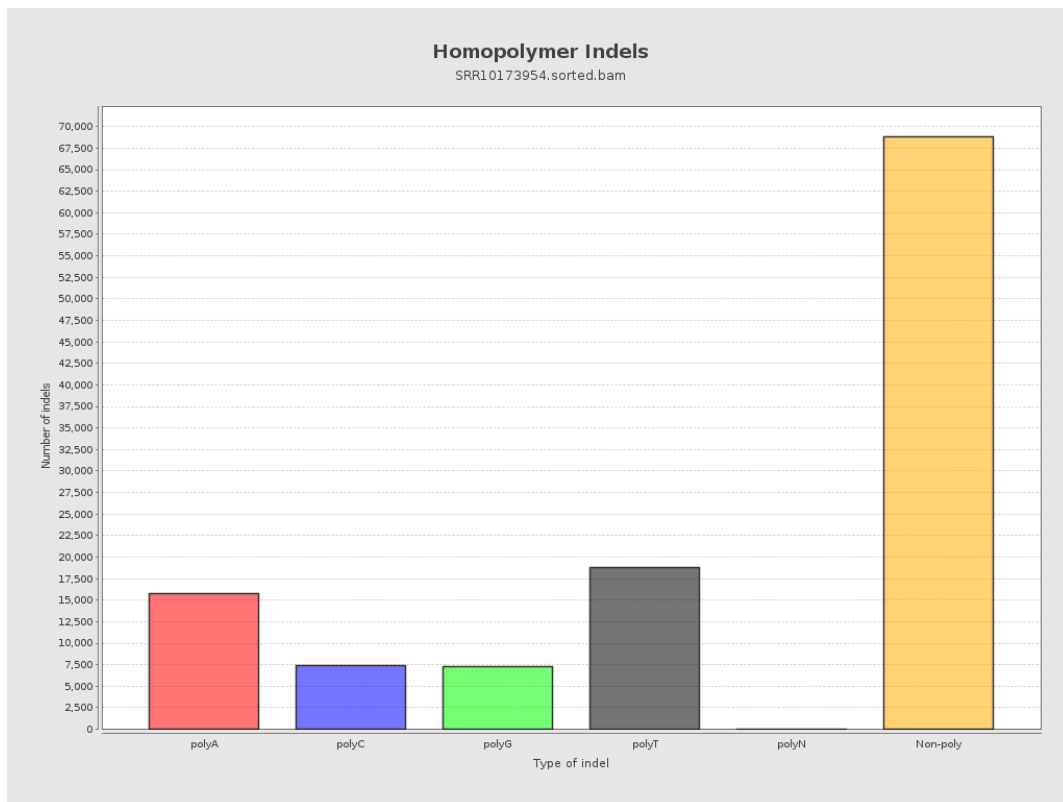
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



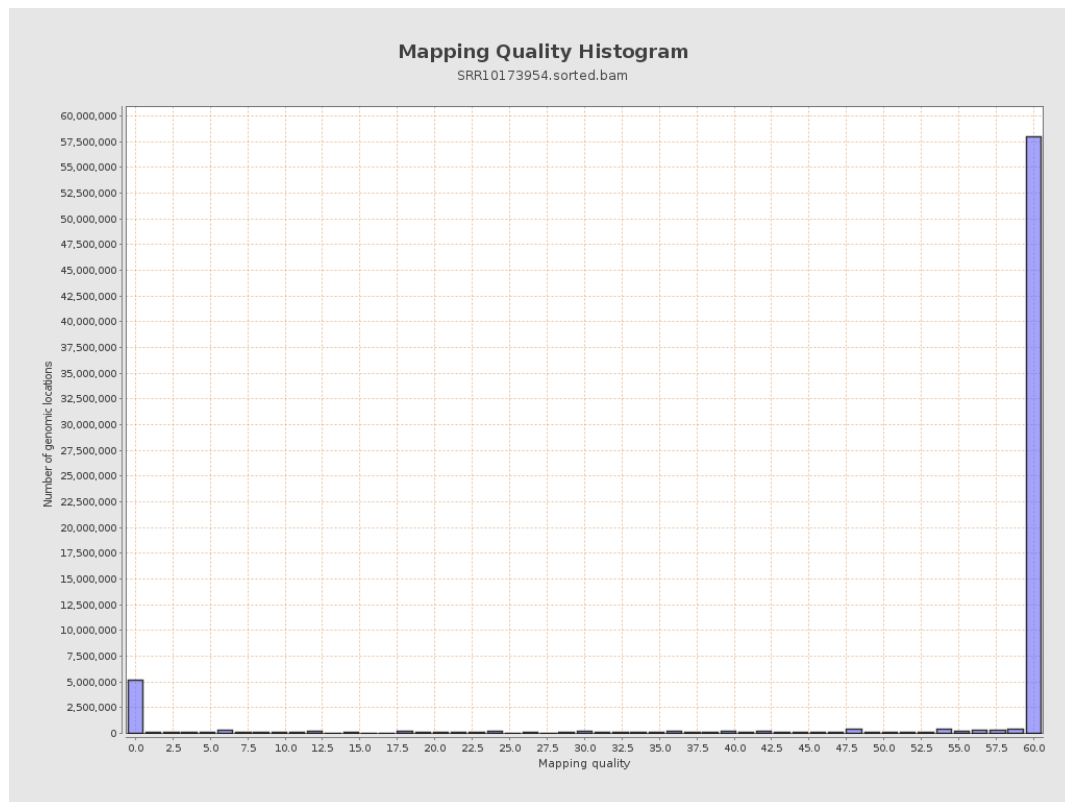
11. Results : Homopolymer Indels



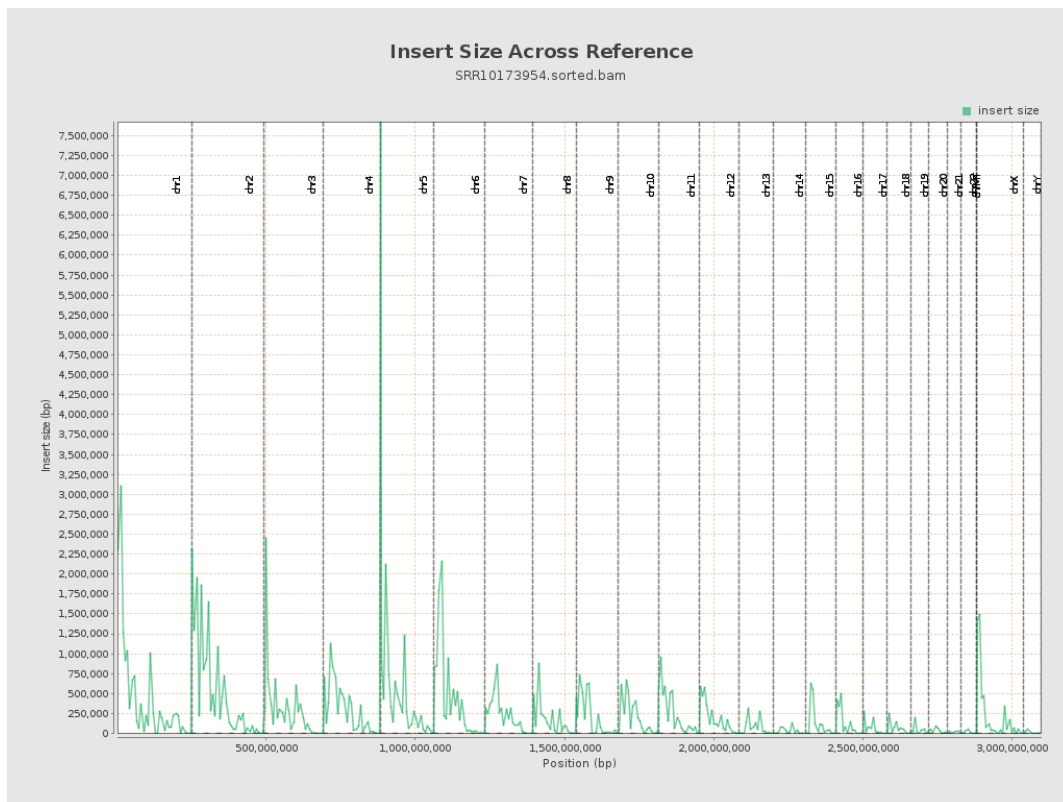
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

