

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 12:22:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173955.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_SRR10173955 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173955_1.fastq.gz SRR10173955_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 12:22:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173955.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,893,586
Mapped reads	3,793,813 / 97.44%
Unmapped reads	99,773 / 2.56%
Mapped paired reads	3,793,813 / 97.44%
Mapped reads, first in pair	1,901,834 / 48.85%
Mapped reads, second in pair	1,891,979 / 48.59%
Mapped reads, both in pair	3,727,430 / 95.73%
Mapped reads, singletons	66,383 / 1.7%
Secondary alignments	0
Supplementary alignments	499,600 / 12.83%
Read min/max/mean length	30 / 133 / 125.73
Duplicated reads (estimated)	3,023,102 / 77.64%
Duplication rate	64.86%
Clipped reads	1,983,851 / 50.95%

2.2. ACGT Content

Number/percentage of A's	126,760,091 / 29.59%
Number/percentage of C's	86,096,274 / 20.09%
Number/percentage of T's	125,676,518 / 29.33%
Number/percentage of G's	89,917,406 / 20.99%
Number/percentage of N's	3,436 / 0%

GC Percentage	41.08%
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2.3. Coverage

Mean	0.1385
Standard Deviation	2.7633

2.4. Mapping Quality

Mean Mapping Quality	52.36
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2.5. Insert size

Mean	1,111,734.62
Standard Deviation	9,733,645.1
P25/Median/P75	107 / 159 / 253

2.6. Mismatches and indels

General error rate	0.92%
Mismatches	3,813,580
Insertions	49,130
Mapped reads with at least one insertion	1.24%
Deletions	129,927
Mapped reads with at least one deletion	3.34%
Homopolymer indels	40.64%

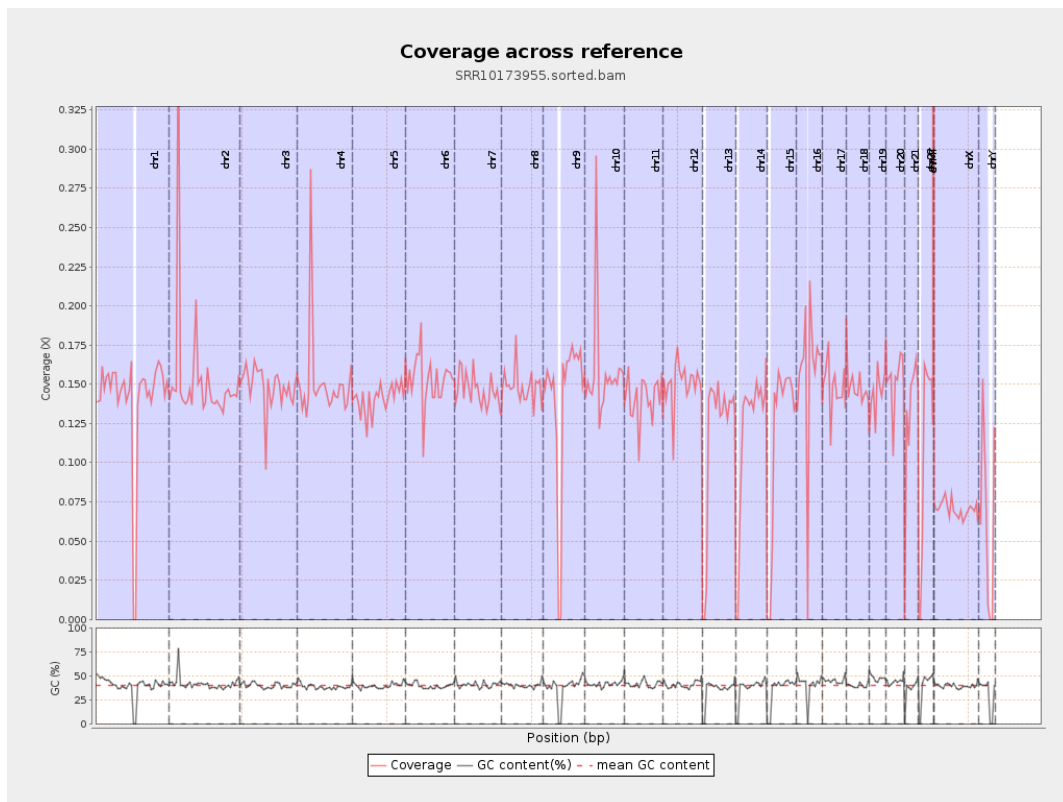
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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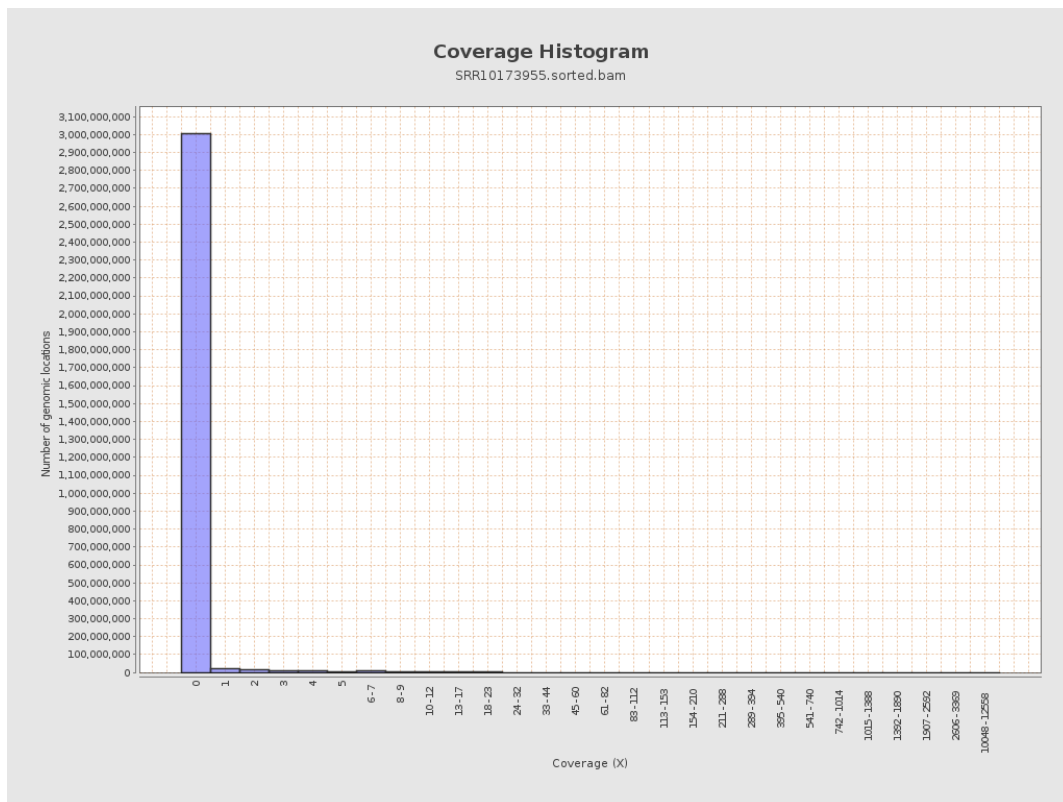
		bases	coverage	deviation
chr1	249250621	35015207	0.1405	1.3389
chr2	243199373	37435842	0.1539	8.792
chr3	198022430	29397604	0.1485	1.1372
chr4	191154276	28696438	0.1501	1.559
chr5	180915260	25485020	0.1409	1.11
chr6	171115067	26240817	0.1534	1.2806
chr7	159138663	23356963	0.1468	1.4361
chr8	146364022	21745712	0.1486	1.5895
chr9	141213431	19803501	0.1402	1.3854
chr10	135534747	21259286	0.1569	1.7726
chr11	135006516	19019981	0.1409	1.1246
chr12	133851895	20161200	0.1506	1.173
chr13	115169878	13361262	0.116	1.0055
chr14	107349540	12686469	0.1182	1.0246
chr15	102531392	12211500	0.1191	1.0416
chr16	90354753	14151120	0.1566	1.3981
chr17	81195210	12007705	0.1479	1.1992
chr18	78077248	11571647	0.1482	1.7529
chr19	59128983	8612784	0.1457	1.2655
chr20	63025520	9562087	0.1517	1.2369
chr21	48129895	6259392	0.1301	1.3166
chr22	51304566	5482824	0.1069	1.0761
chrMT	16571	632680	38.18	34.6396
chrX	155270560	10947170	0.0705	0.7849

chrY	59373566	3664531	0.0617	1.084
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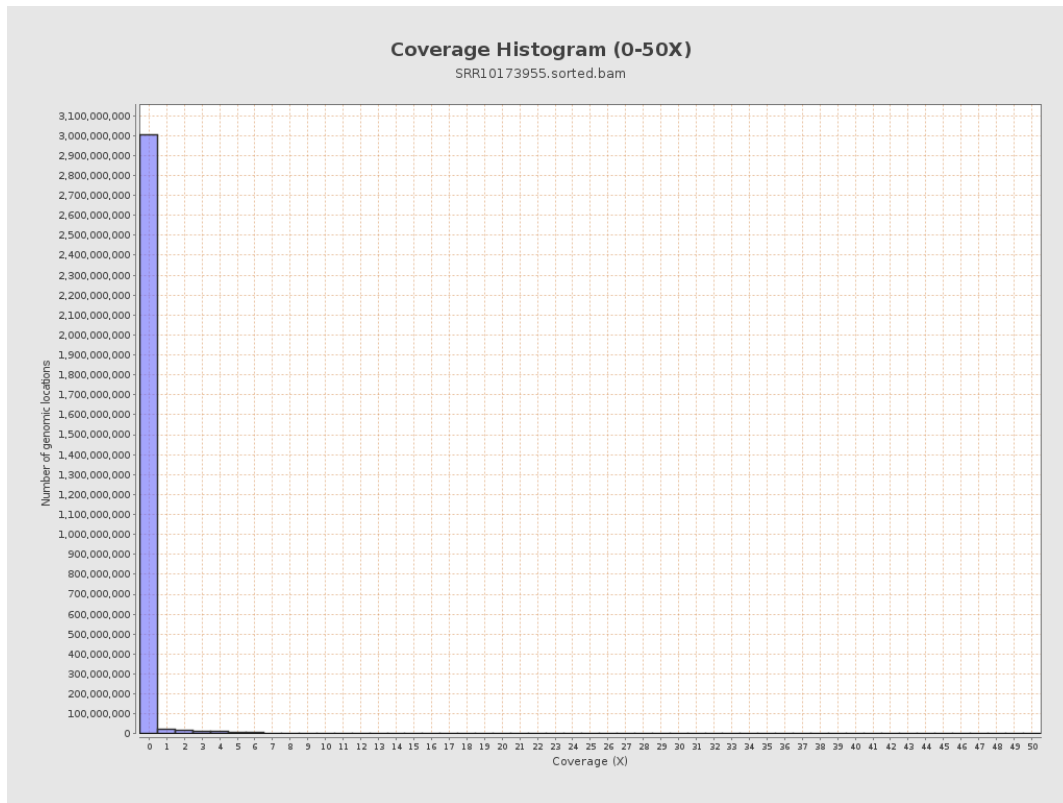
3. Results : Coverage across reference



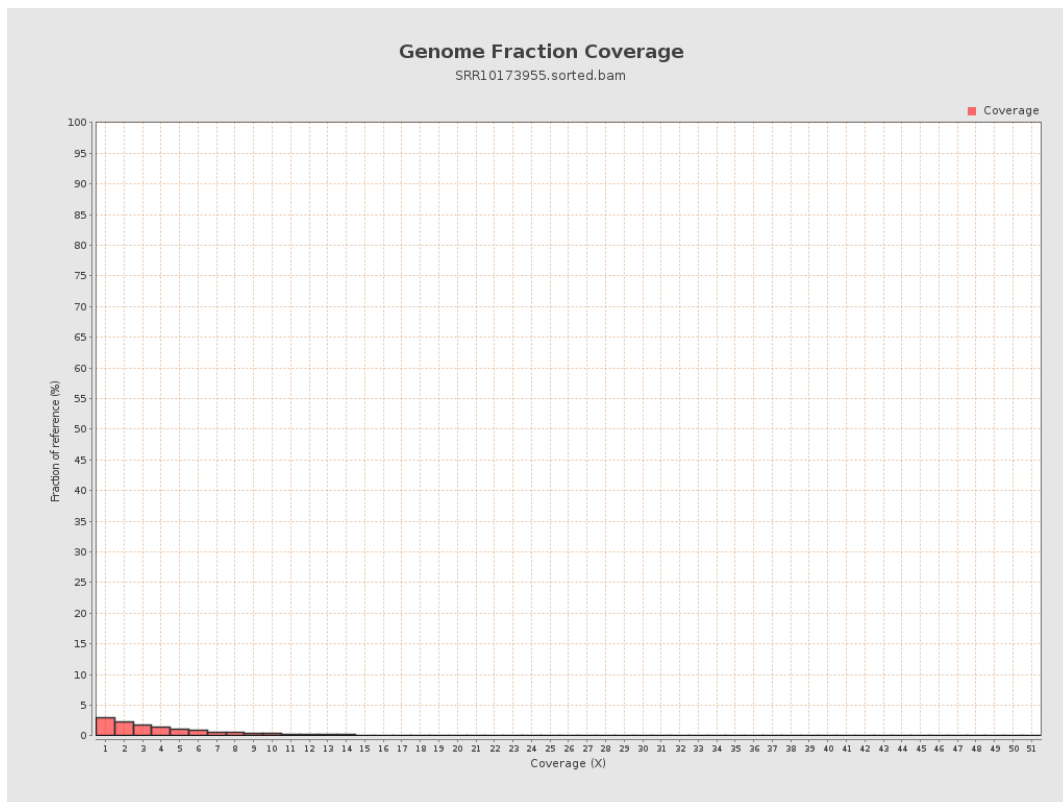
4. Results : Coverage Histogram



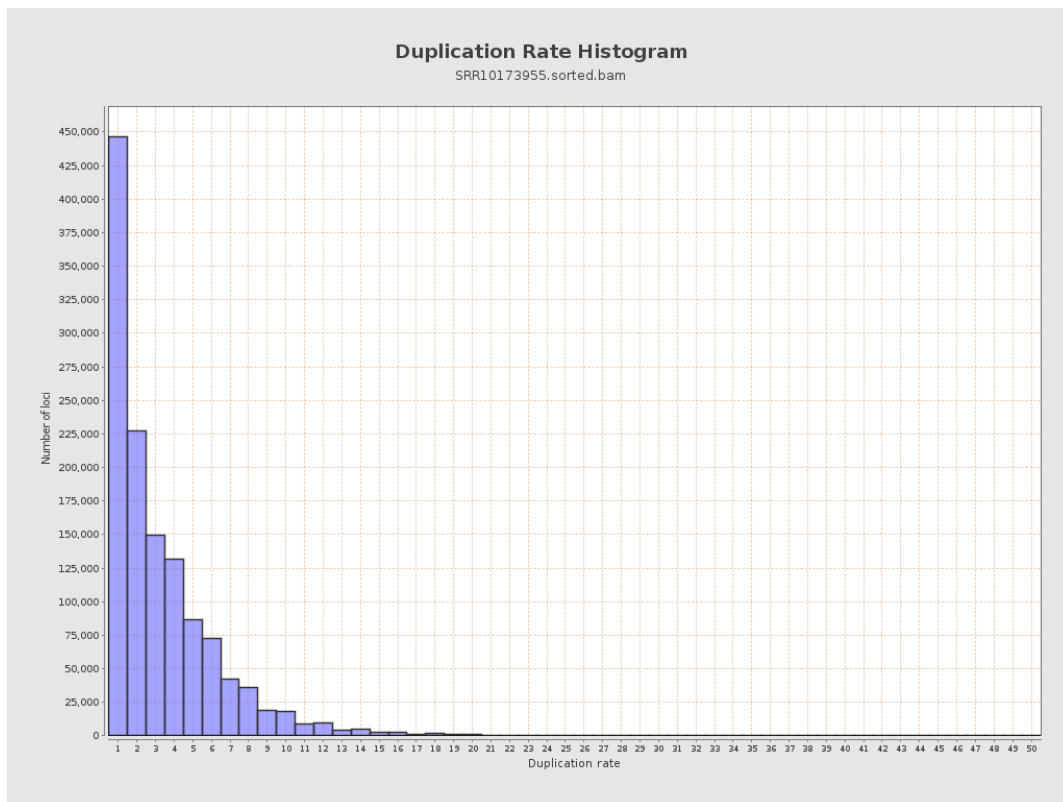
5. Results : Coverage Histogram (0-50X)



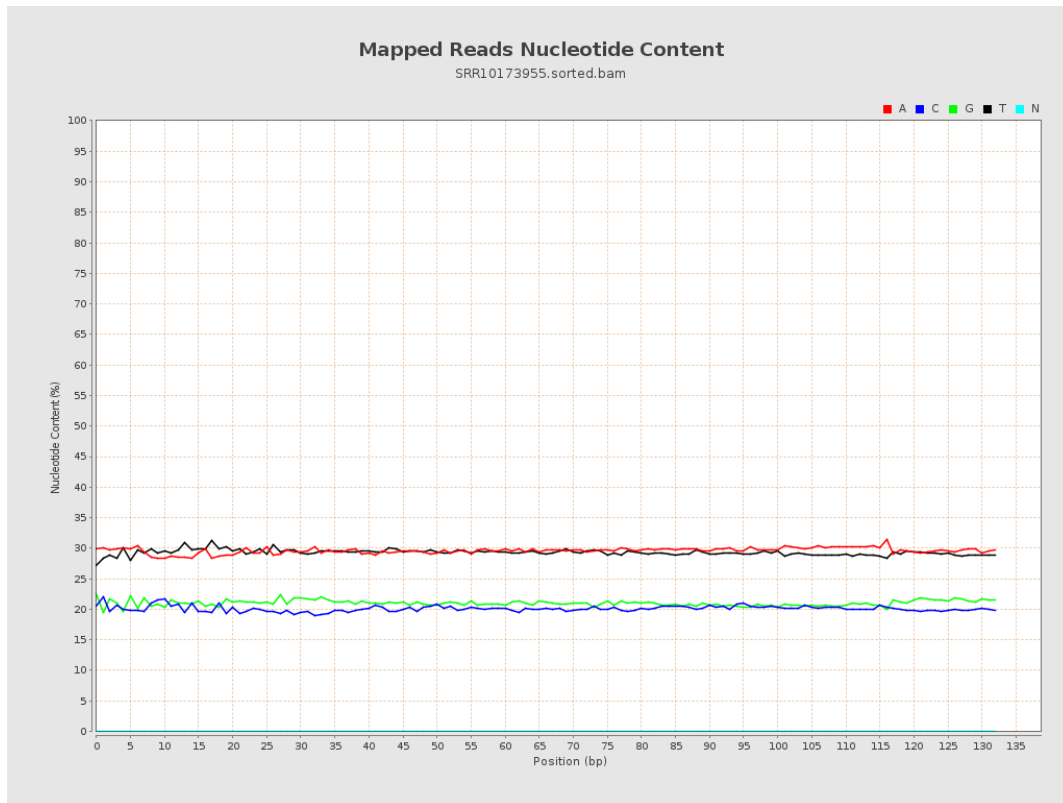
6. Results : Genome Fraction Coverage



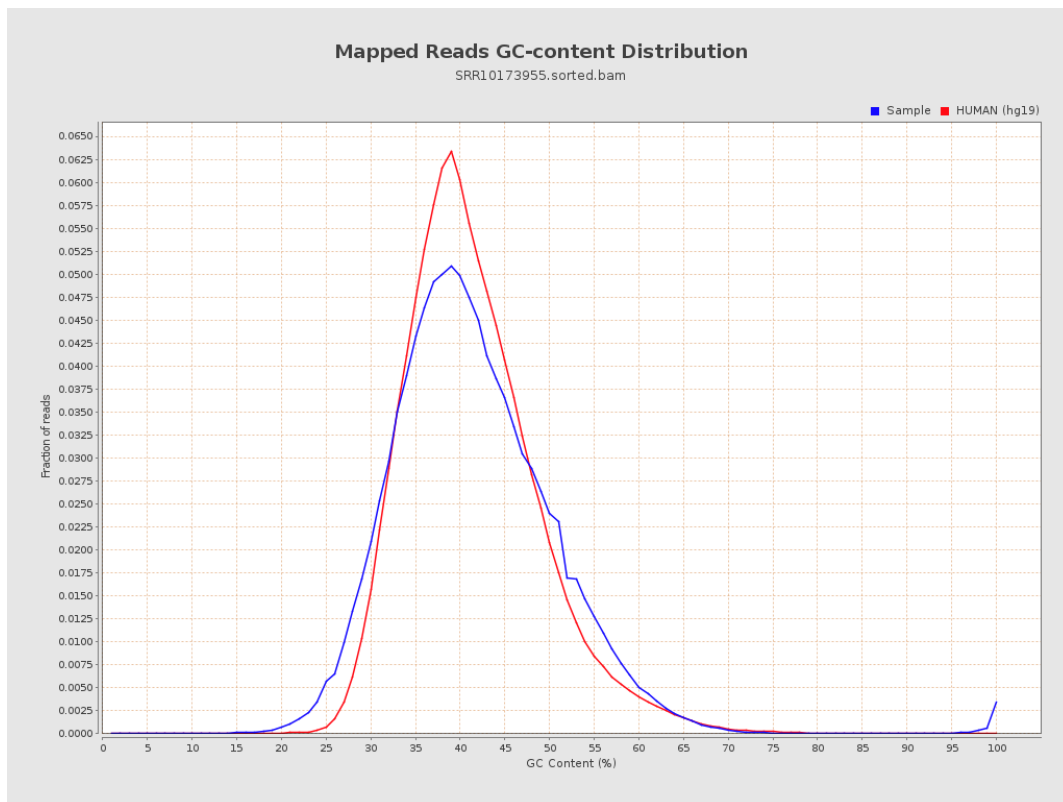
7. Results : Duplication Rate Histogram



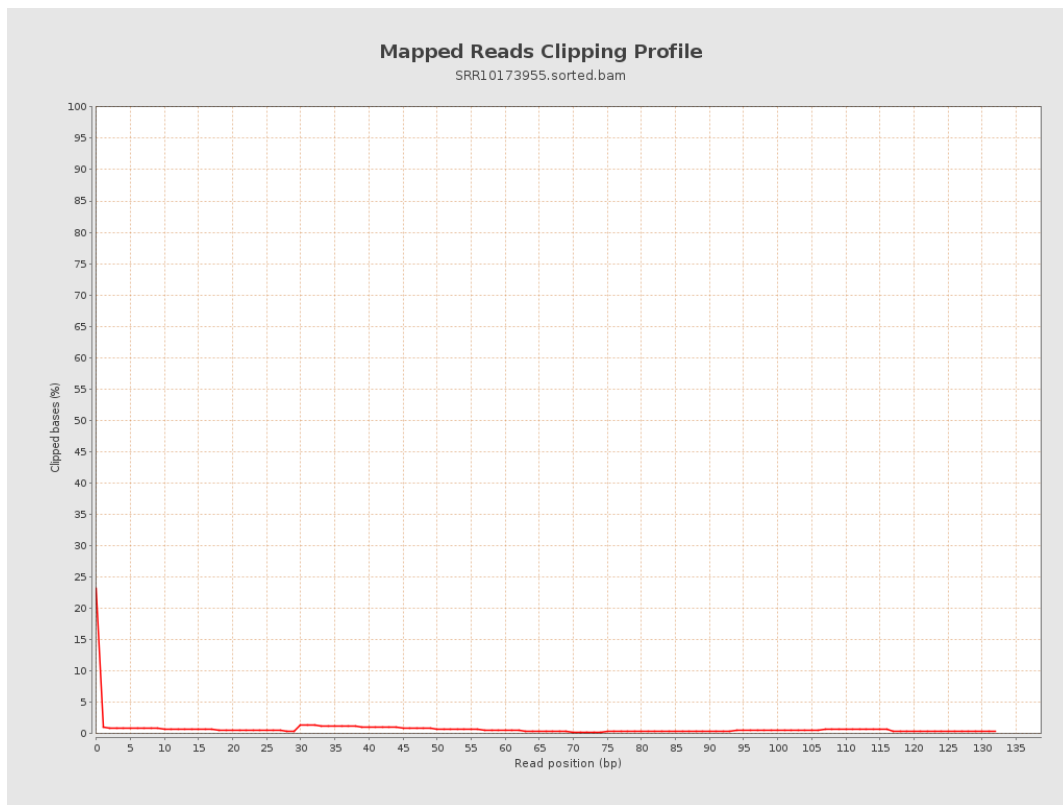
8. Results : Mapped Reads Nucleotide Content



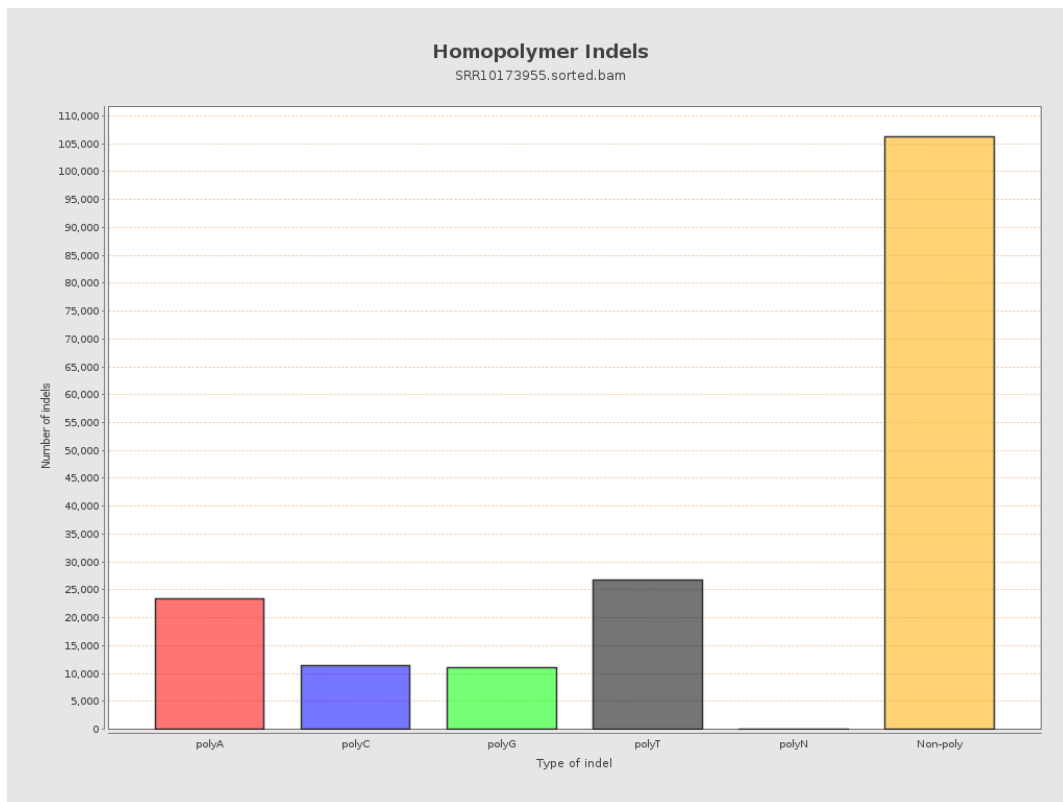
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



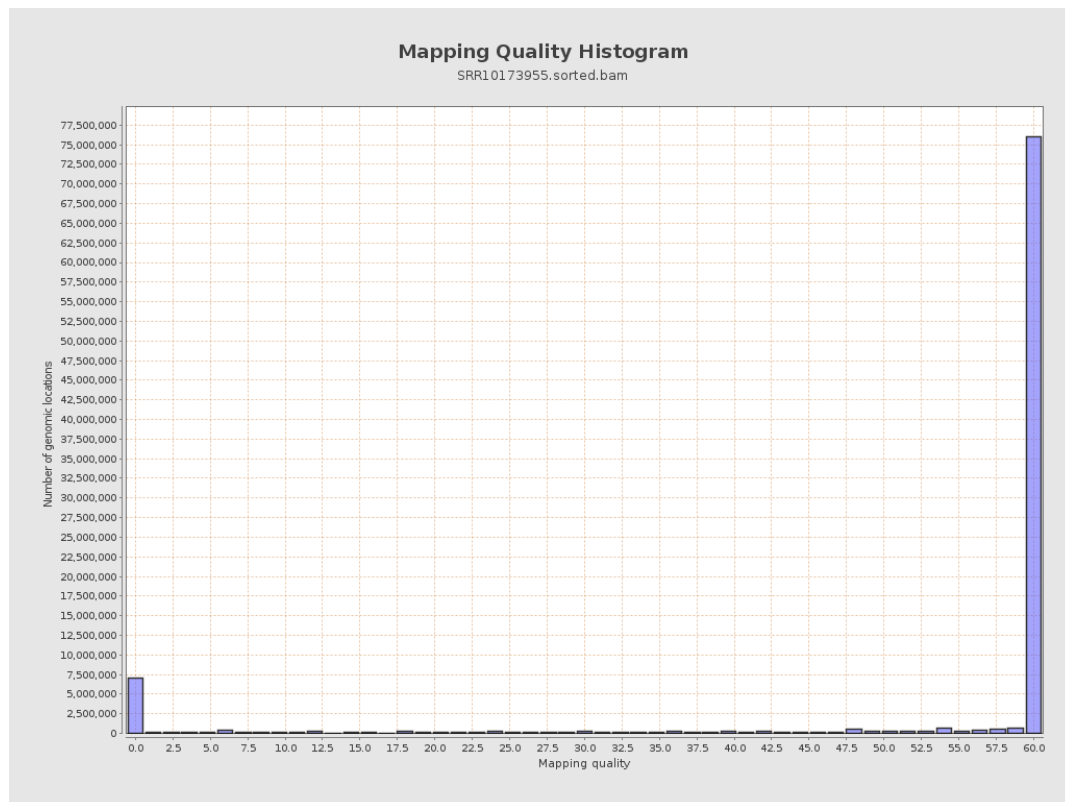
11. Results : Homopolymer Indels



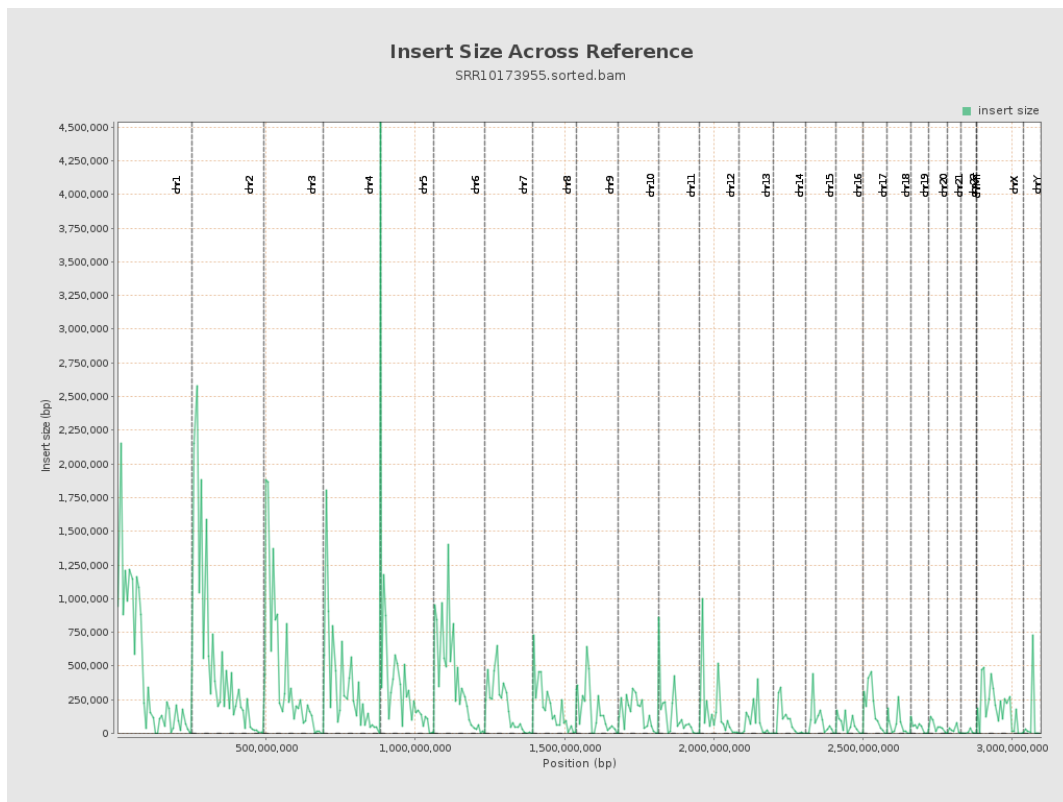
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

