

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 00:11:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173868.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_SRR10173868 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173868_1.fastq.gz SRR10173868_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 00:11:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173868.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,337,544
Mapped reads	5,185,170 / 97.15%
Unmapped reads	152,374 / 2.85%
Mapped paired reads	5,185,170 / 97.15%
Mapped reads, first in pair	2,596,652 / 48.65%
Mapped reads, second in pair	2,588,518 / 48.5%
Mapped reads, both in pair	5,086,748 / 95.3%
Mapped reads, singletons	98,422 / 1.84%
Secondary alignments	0
Supplementary alignments	516,415 / 9.68%
Read min/max/mean length	30 / 133 / 127.86
Duplicated reads (estimated)	3,930,729 / 73.64%
Duplication rate	64%
Clipped reads	2,219,262 / 41.58%

2.2. ACGT Content

Number/percentage of A's	183,632,136 / 30.16%
Number/percentage of C's	118,741,605 / 19.5%
Number/percentage of T's	183,388,239 / 30.12%
Number/percentage of G's	123,098,258 / 20.22%
Number/percentage of N's	7,254 / 0%

GC Percentage	39.72%
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2.3. Coverage

Mean	0.1968
Standard Deviation	2.9332

2.4. Mapping Quality

Mean Mapping Quality	52.76
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2.5. Insert size

Mean	702,136.15
Standard Deviation	7,789,121.24
P25/Median/P75	139 / 195 / 279

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	6,278,353
Insertions	62,285
Mapped reads with at least one insertion	1.16%
Deletions	145,922
Mapped reads with at least one deletion	2.75%
Homopolymer indels	42.51%

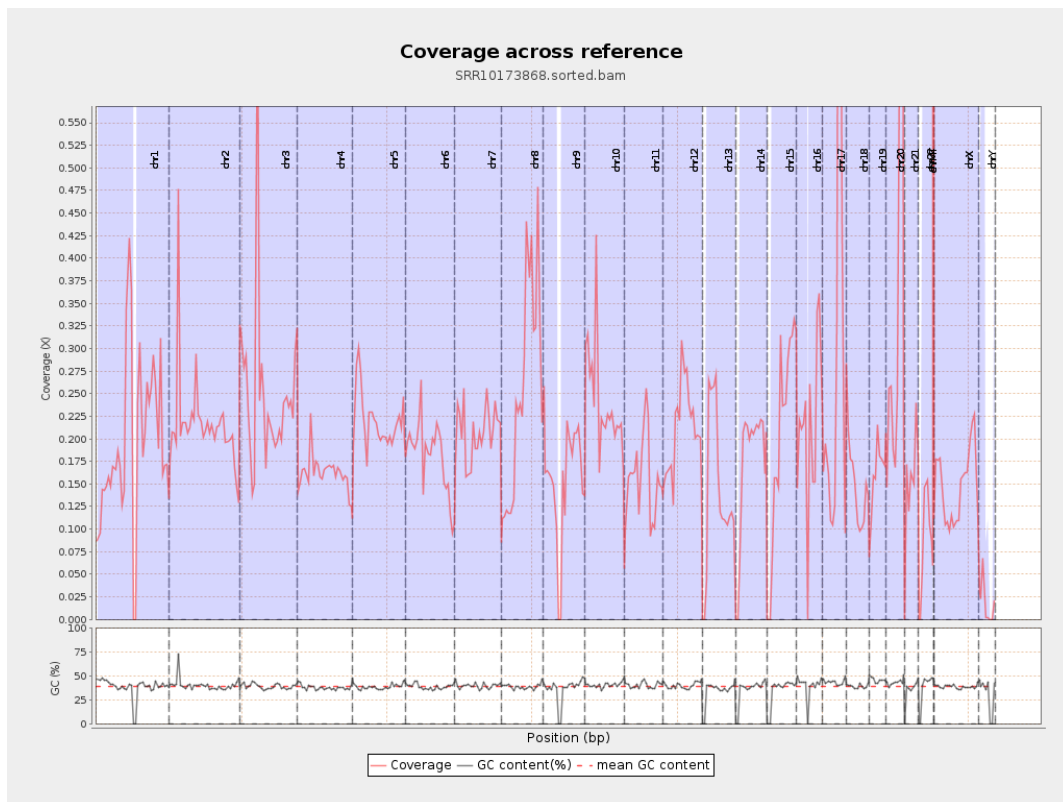
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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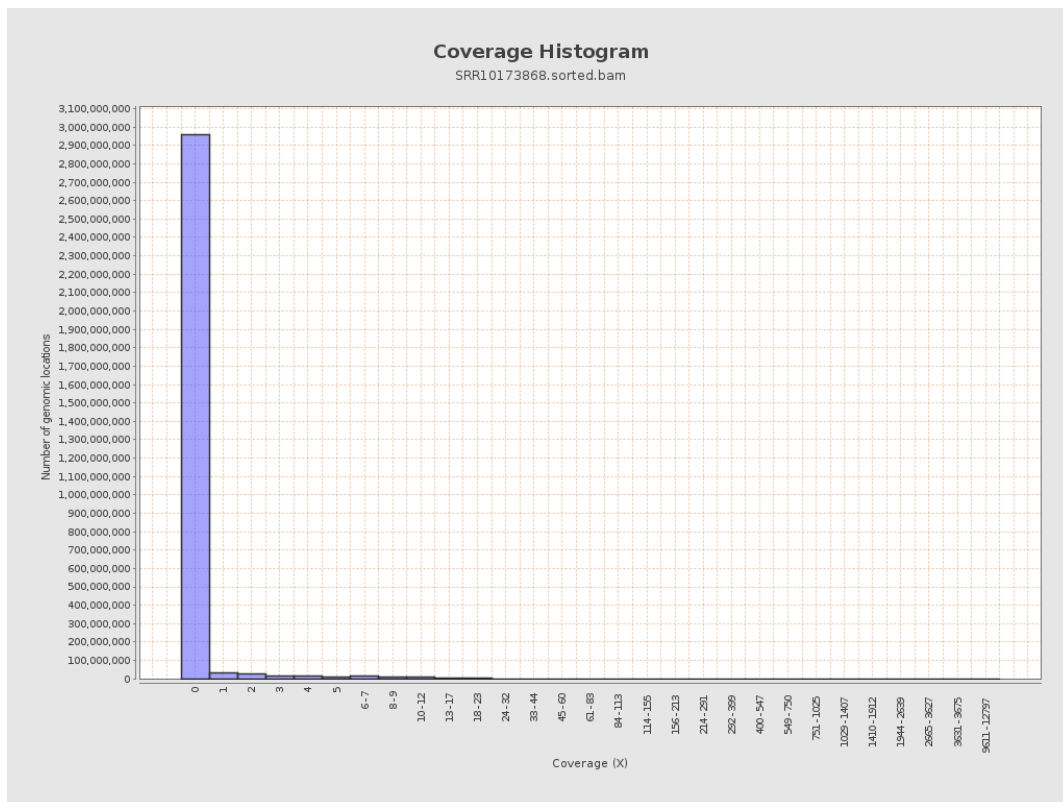
		bases	coverage	deviation
chr1	249250621	48731622	0.1955	2.1043
chr2	243199373	52637539	0.2164	8.944
chr3	198022430	49105530	0.248	1.4143
chr4	191154276	30957897	0.162	1.2862
chr5	180915260	39708723	0.2195	1.3101
chr6	171115067	31125252	0.1819	1.3935
chr7	159138663	33044944	0.2076	1.8431
chr8	146364022	37364472	0.2553	1.8277
chr9	141213431	21534370	0.1525	1.3844
chr10	135534747	32797721	0.242	2.6815
chr11	135006516	21130064	0.1565	1.1251
chr12	133851895	28369880	0.2119	1.2961
chr13	115169878	15939332	0.1384	1.0437
chr14	107349540	18446679	0.1718	1.1663
chr15	102531392	20792875	0.2028	1.2524
chr16	90354753	19611601	0.2171	1.6881
chr17	81195210	23904436	0.2944	1.6542
chr18	78077248	11599719	0.1486	2.106
chr19	59128983	9690722	0.1639	1.5327
chr20	63025520	25814591	0.4096	1.9679
chr21	48129895	7416124	0.1541	1.1443
chr22	51304566	4362055	0.085	0.7909
chrMT	16571	1045979	63.1211	46.1033
chrX	155270560	23039836	0.1484	1.0769

chrY	59373566	1049427	0.0177	0.6152
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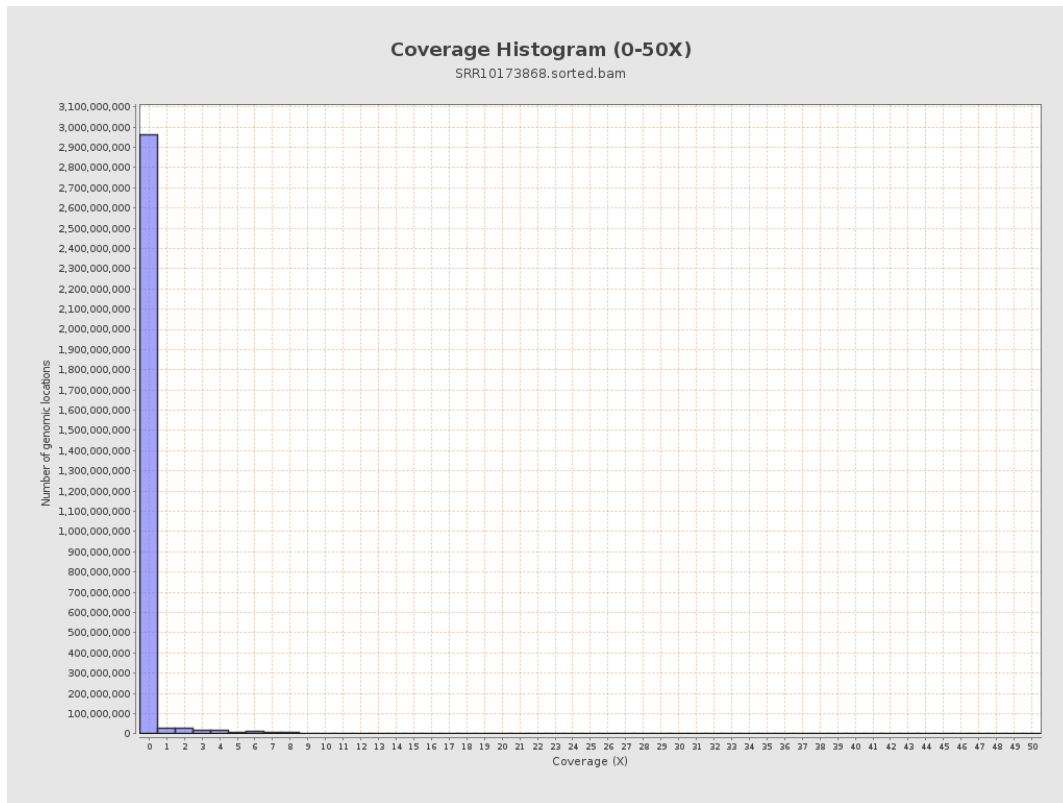
3. Results : Coverage across reference



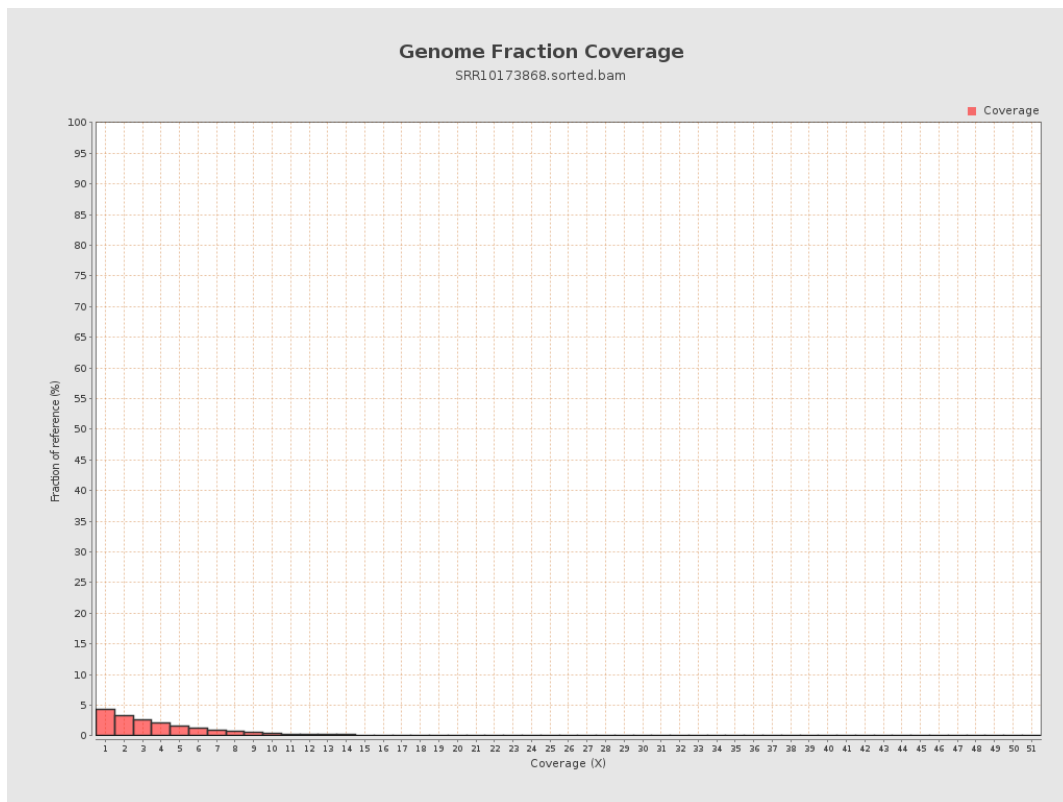
4. Results : Coverage Histogram



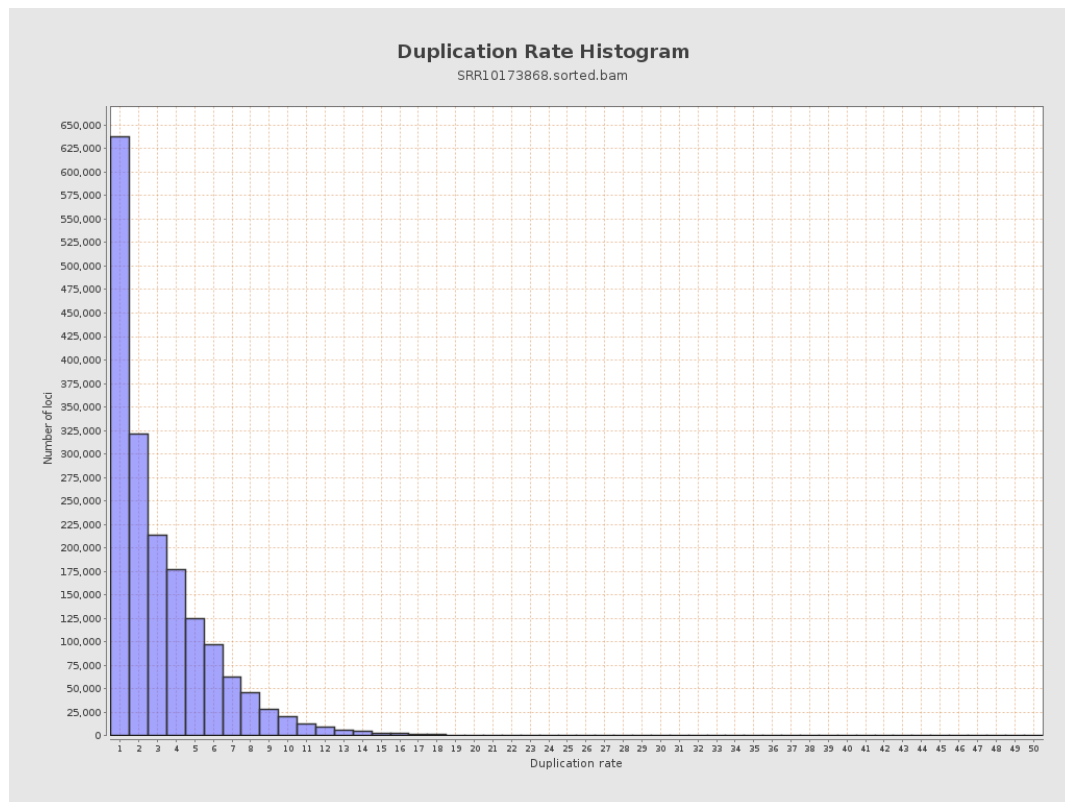
5. Results : Coverage Histogram (0-50X)



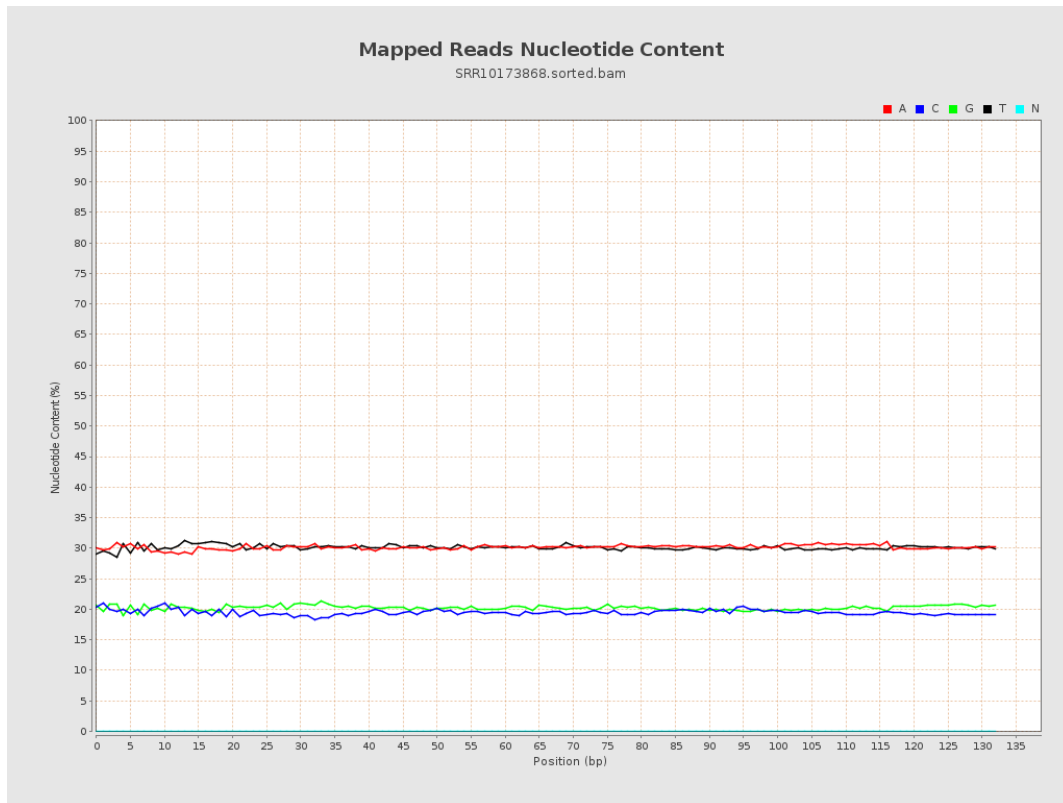
6. Results : Genome Fraction Coverage



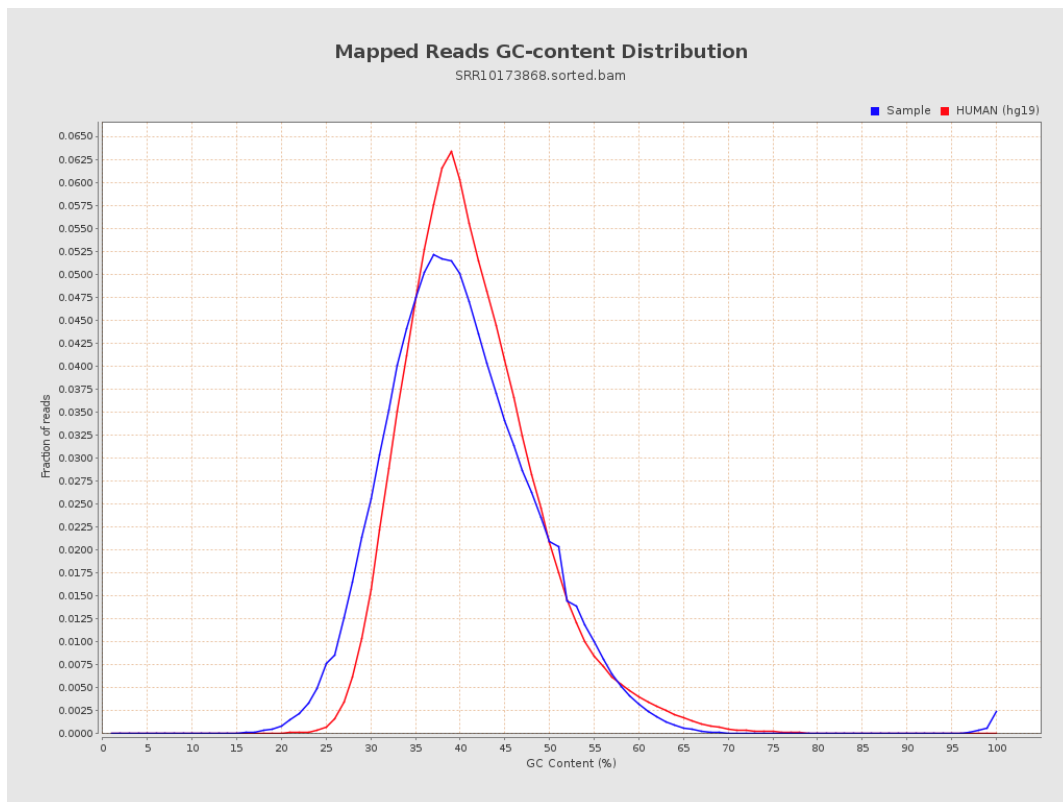
7. Results : Duplication Rate Histogram



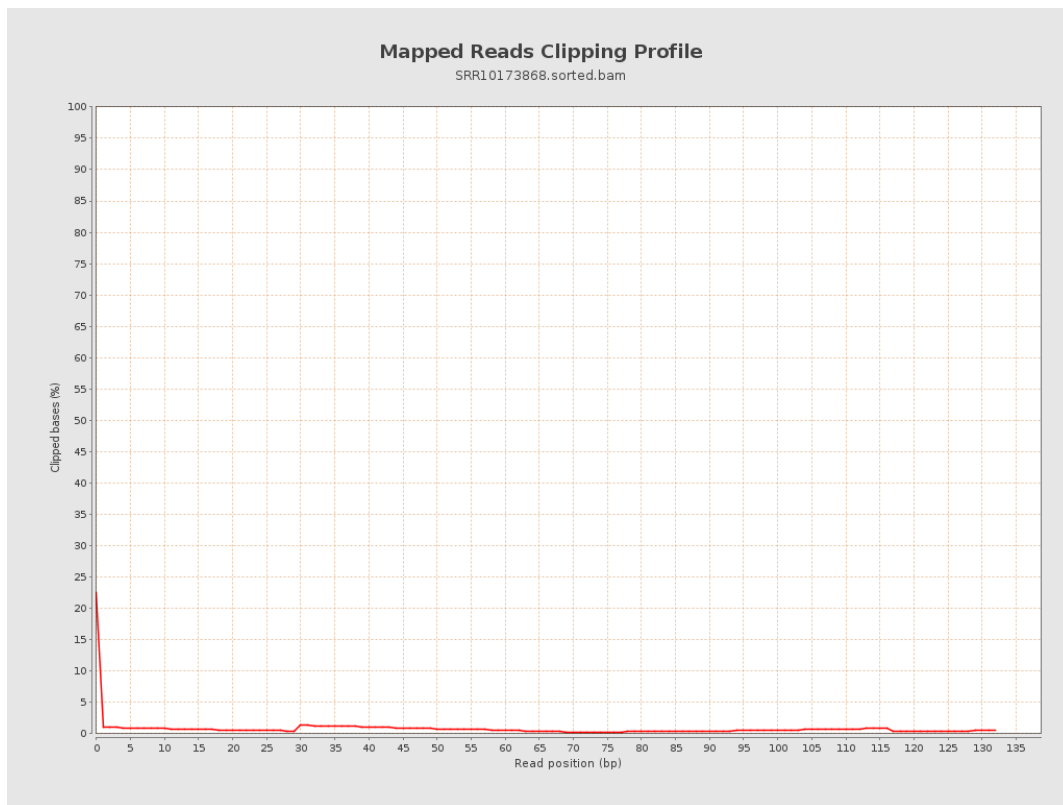
8. Results : Mapped Reads Nucleotide Content



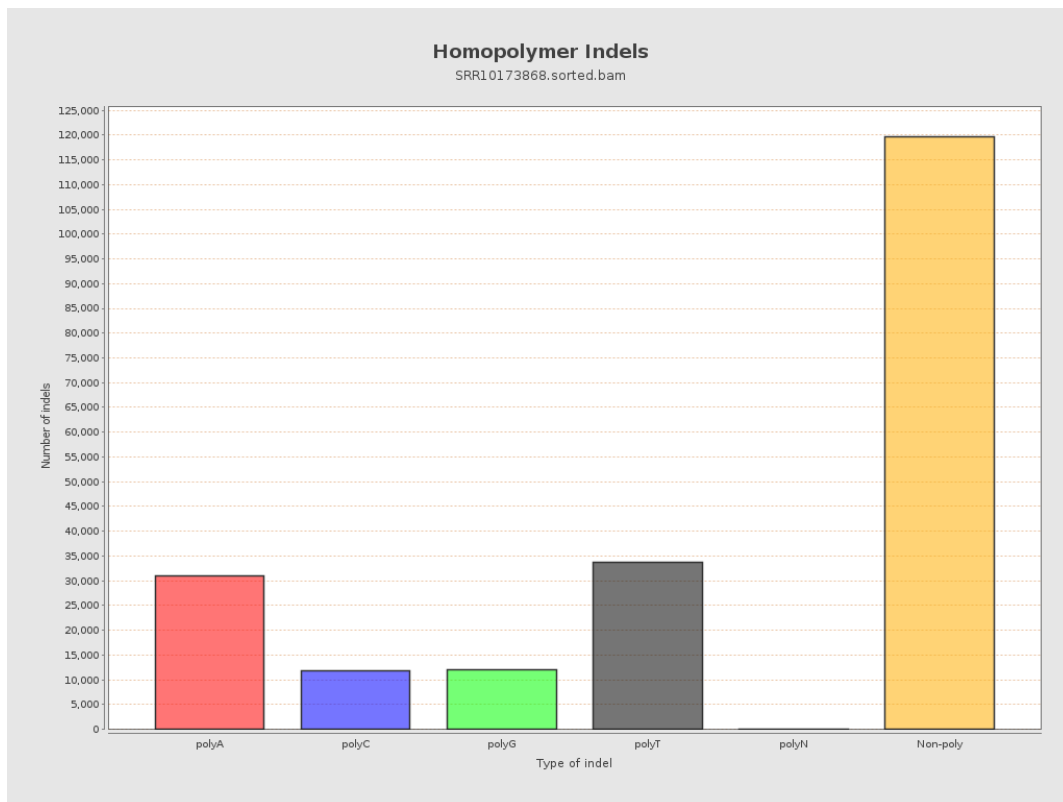
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



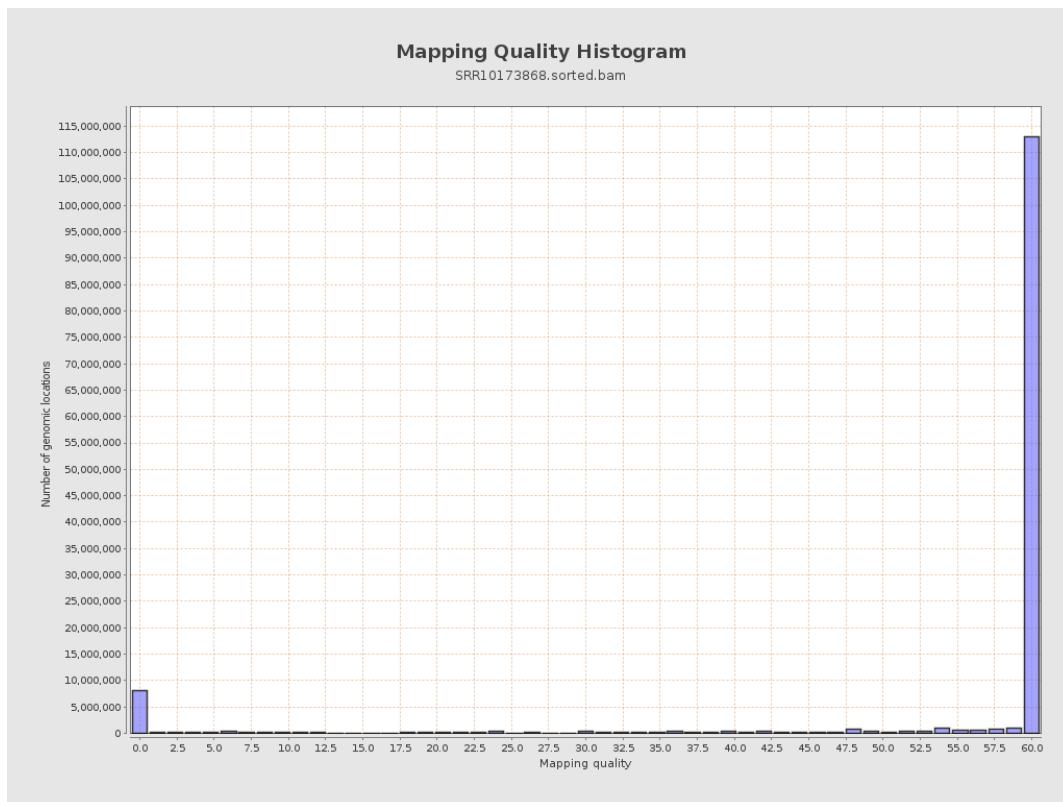
11. Results : Homopolymer Indels



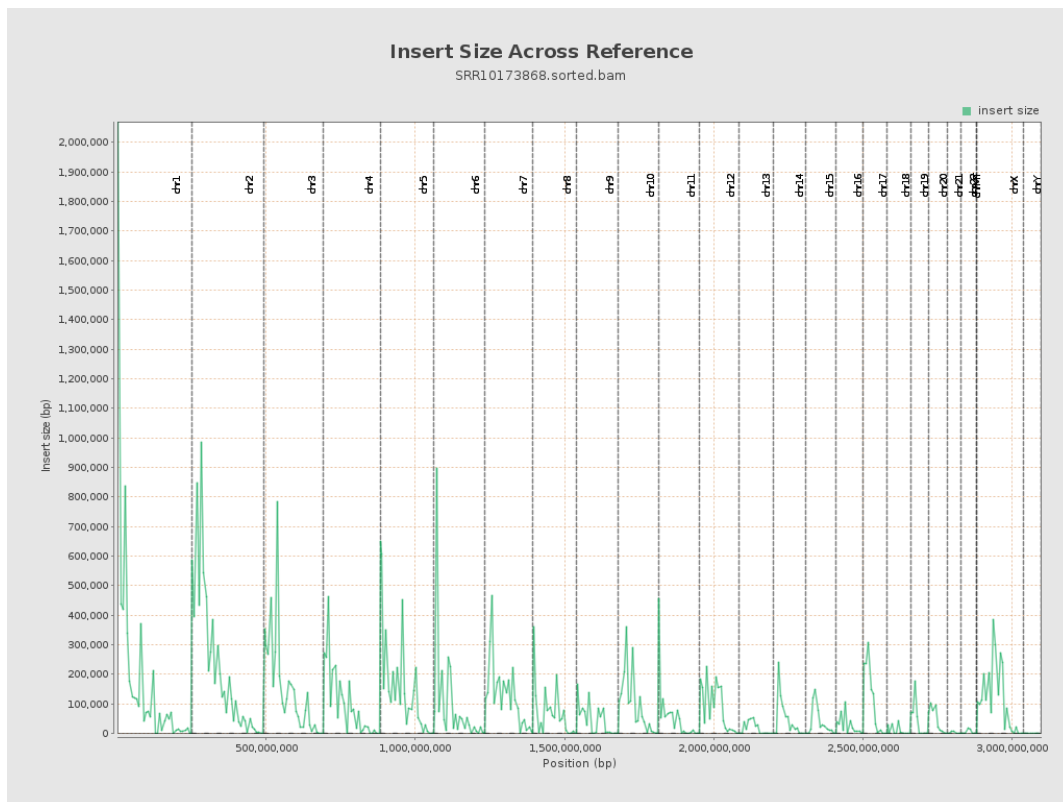
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

