

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/05 07:06:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174088.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_SRR10174088 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174088_1.fastq.gz SRR10174088_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Sep 05 07:06:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174088.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,279,740
Mapped reads	4,185,661 / 97.8%
Unmapped reads	94,079 / 2.2%
Mapped paired reads	4,185,661 / 97.8%
Mapped reads, first in pair	2,095,482 / 48.96%
Mapped reads, second in pair	2,090,179 / 48.84%
Mapped reads, both in pair	4,127,580 / 96.44%
Mapped reads, singletons	58,081 / 1.36%
Secondary alignments	0
Supplementary alignments	535,969 / 12.52%
Read min/max/mean length	30 / 133 / 124.98
Duplicated reads (estimated)	3,337,816 / 77.99%
Duplication rate	63.83%
Clipped reads	2,119,987 / 49.54%

2.2. ACGT Content

Number/percentage of A's	141,741,654 / 29.96%
Number/percentage of C's	93,627,368 / 19.79%
Number/percentage of T's	140,493,259 / 29.7%
Number/percentage of G's	97,183,211 / 20.54%
Number/percentage of N's	4,053 / 0%

GC Percentage	40.34%
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2.3. Coverage

Mean	0.1529
Standard Deviation	2.845

2.4. Mapping Quality

Mean Mapping Quality	52.67
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2.5. Insert size

Mean	1,176,744.72
Standard Deviation	10,096,198.84
P25/Median/P75	105 / 151 / 231

2.6. Mismatches and indels

General error rate	0.89%
Mismatches	4,056,901
Insertions	52,377
Mapped reads with at least one insertion	1.2%
Deletions	144,982
Mapped reads with at least one deletion	3.38%
Homopolymer indels	40.67%

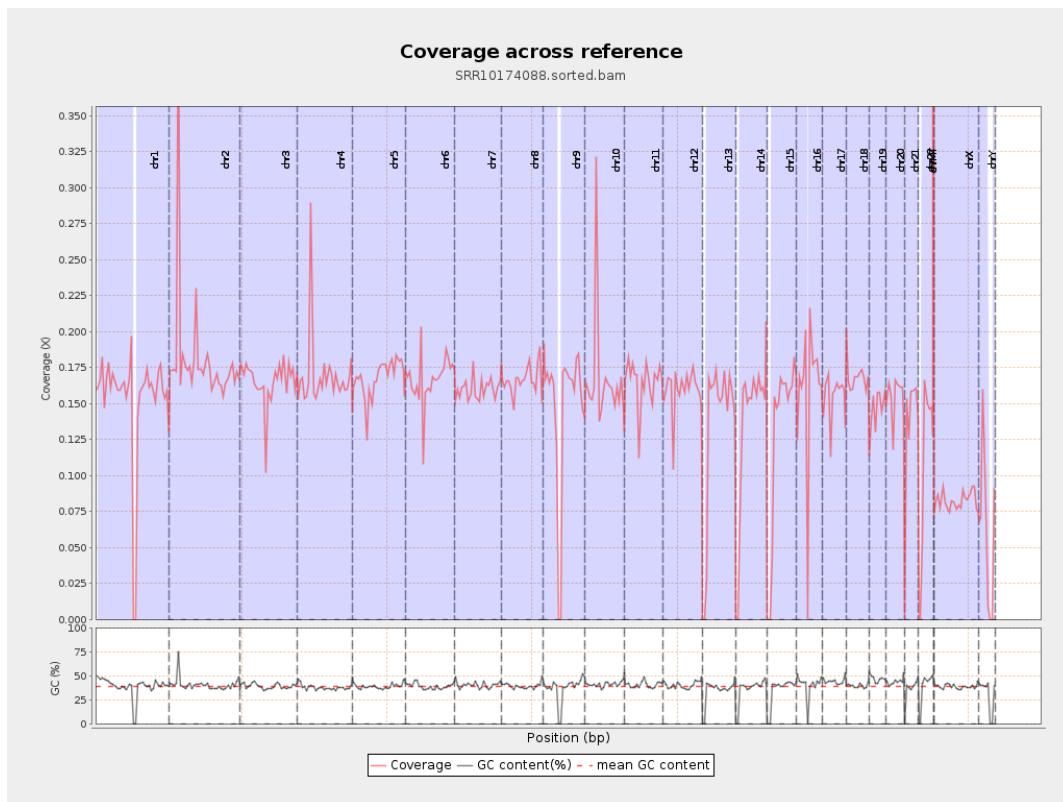
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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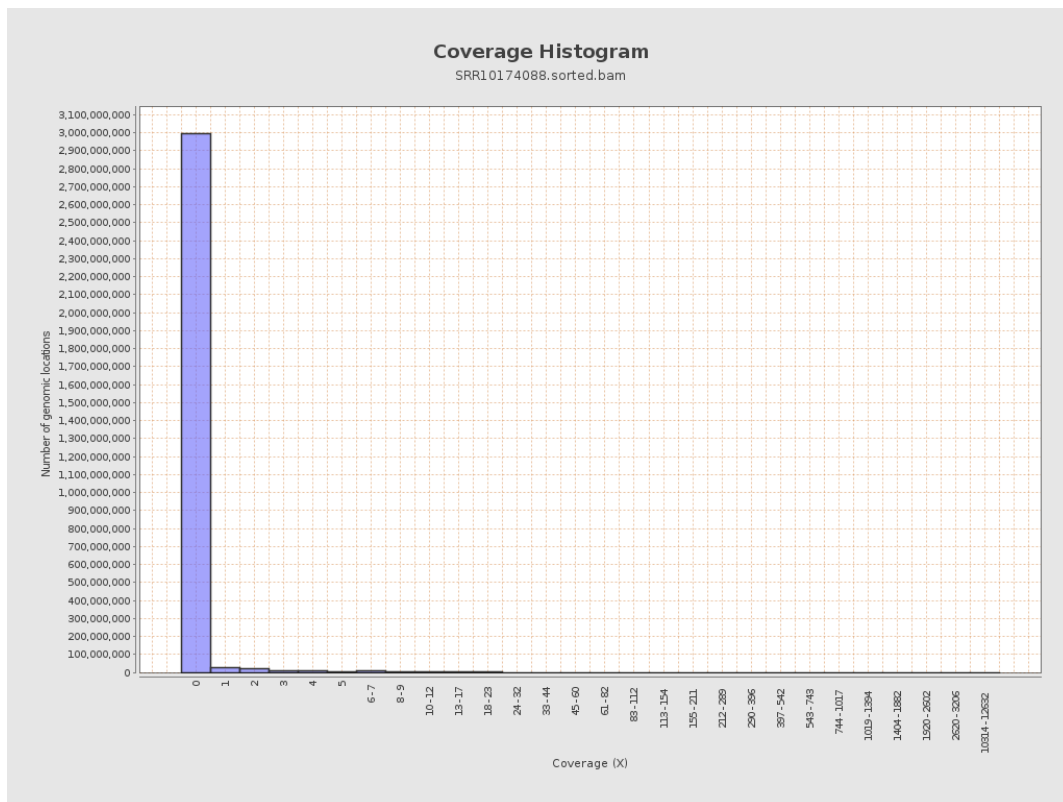
		bases	coverage	deviation
chr1	249250621	38252811	0.1535	1.7362
chr2	243199373	44055617	0.1812	8.9226
chr3	198022430	32783451	0.1656	1.2504
chr4	191154276	32273396	0.1688	1.5713
chr5	180915260	30380625	0.1679	1.256
chr6	171115067	28554756	0.1669	1.3697
chr7	159138663	25483070	0.1601	1.5099
chr8	146364022	24341508	0.1663	1.6956
chr9	141213431	20770404	0.1471	1.4436
chr10	135534747	22561211	0.1665	1.889
chr11	135006516	22223525	0.1646	1.2769
chr12	133851895	21354516	0.1595	1.2419
chr13	115169878	15387351	0.1336	1.1188
chr14	107349540	14292507	0.1331	1.1195
chr15	102531392	13243764	0.1292	1.1075
chr16	90354753	14443325	0.1599	1.4323
chr17	81195210	12501284	0.154	1.2074
chr18	78077248	13107792	0.1679	1.8139
chr19	59128983	8687266	0.1469	1.2853
chr20	63025520	9760450	0.1549	1.2298
chr21	48129895	6546007	0.136	1.433
chr22	51304566	5395580	0.1052	1.1473
chrMT	16571	677577	40.8893	34.8451
chrX	155270560	12791212	0.0824	0.8779

chrY	59373566	3524657	0.0594	1.11
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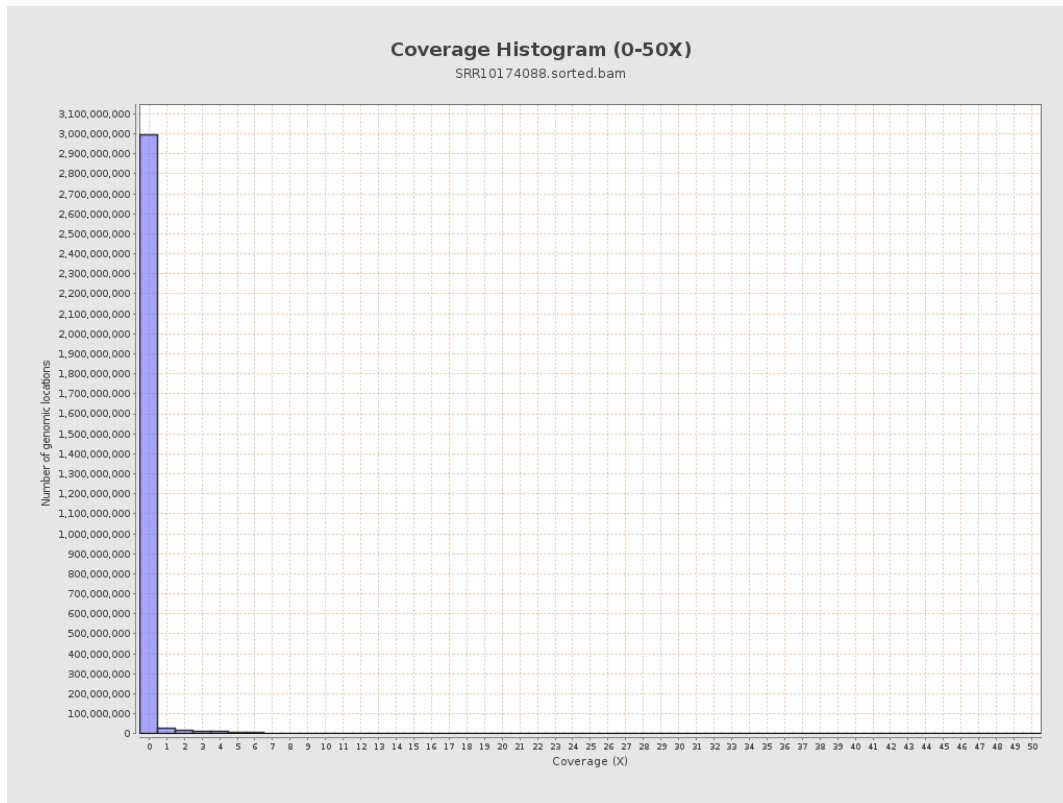
3. Results : Coverage across reference



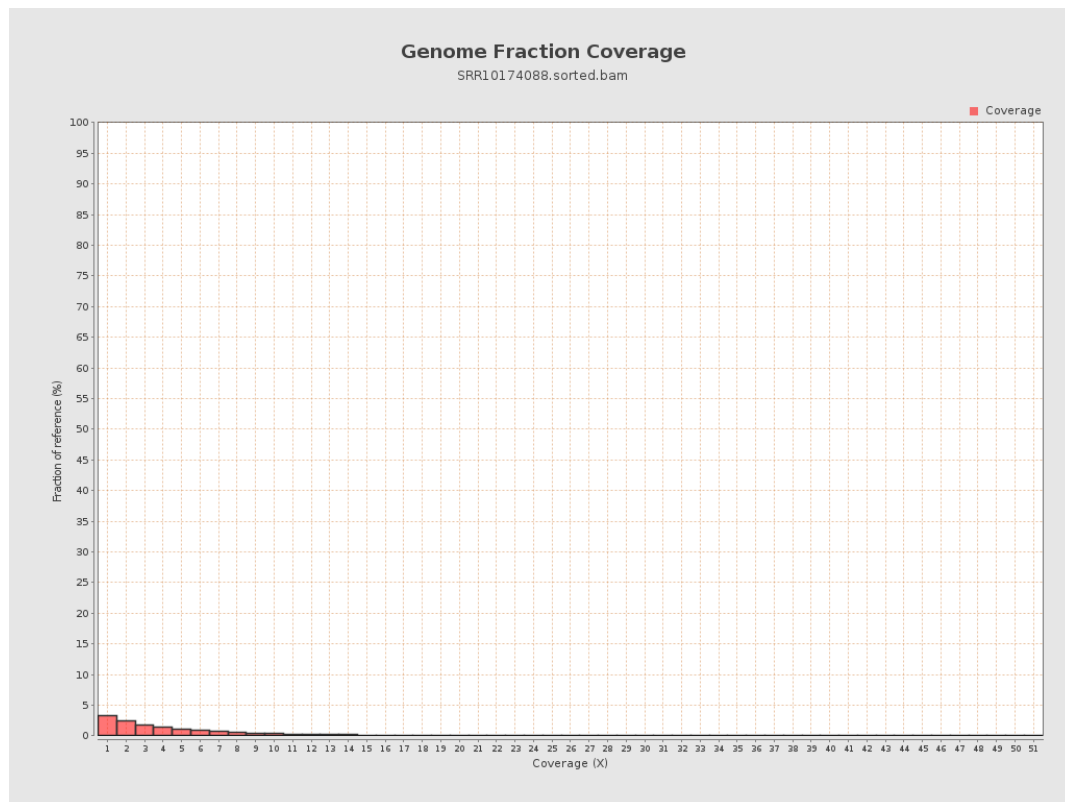
4. Results : Coverage Histogram



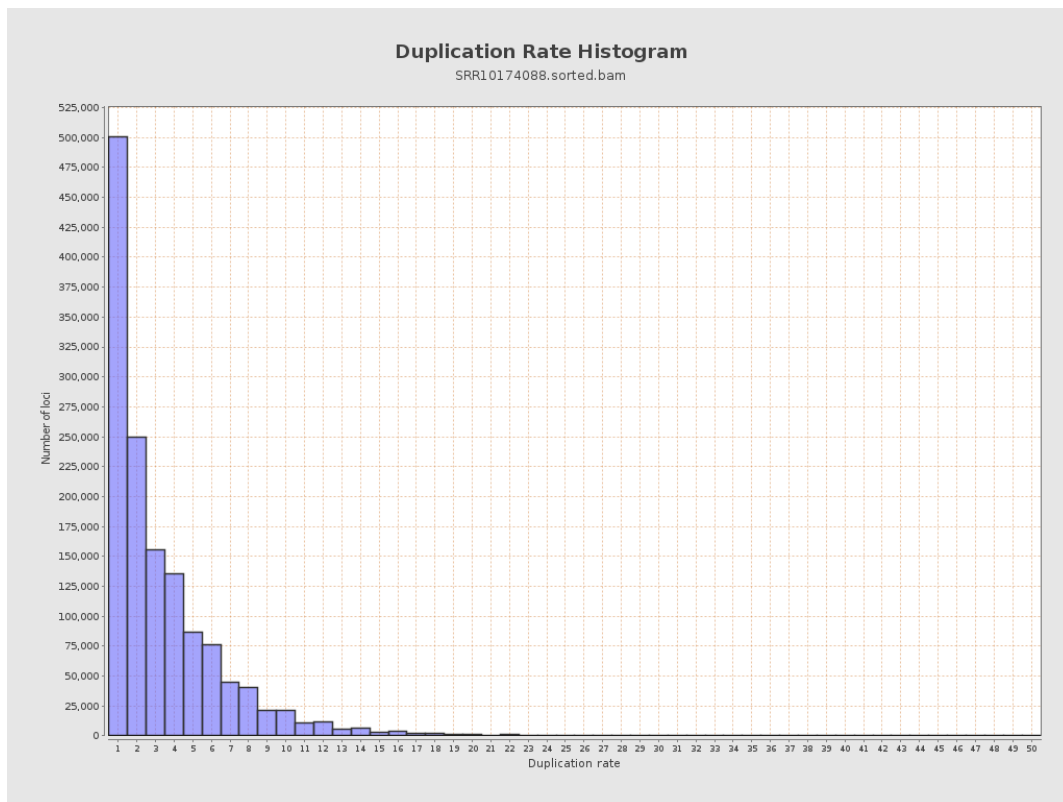
5. Results : Coverage Histogram (0-50X)



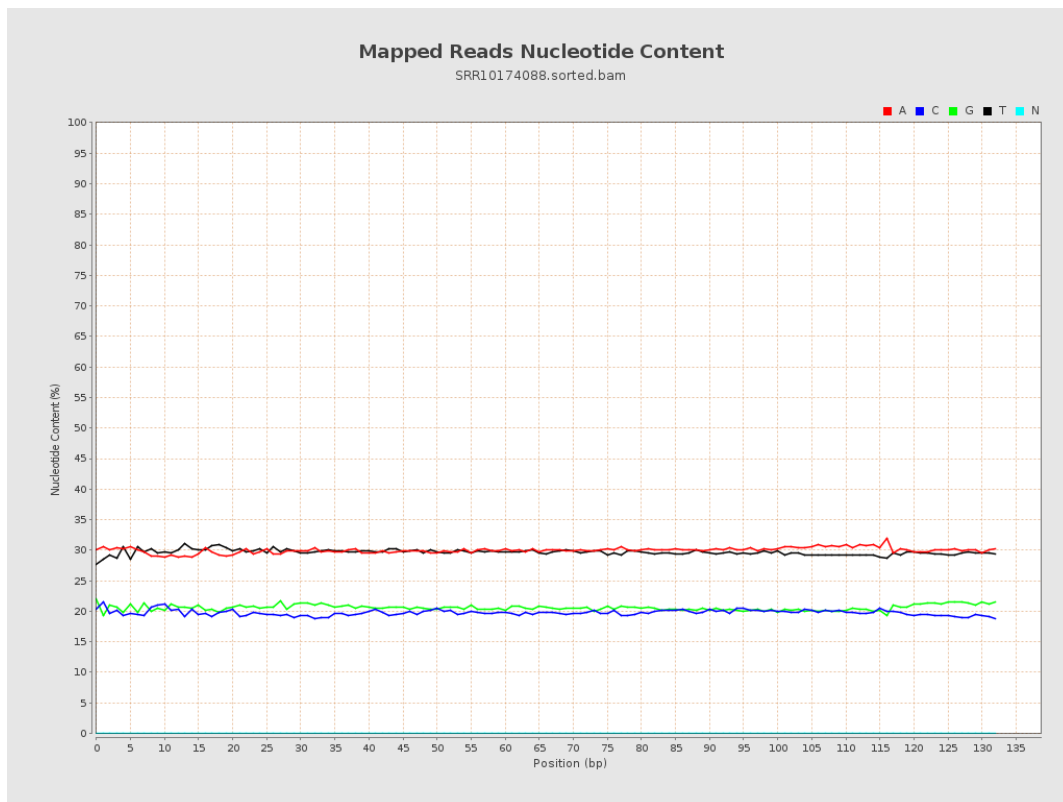
6. Results : Genome Fraction Coverage



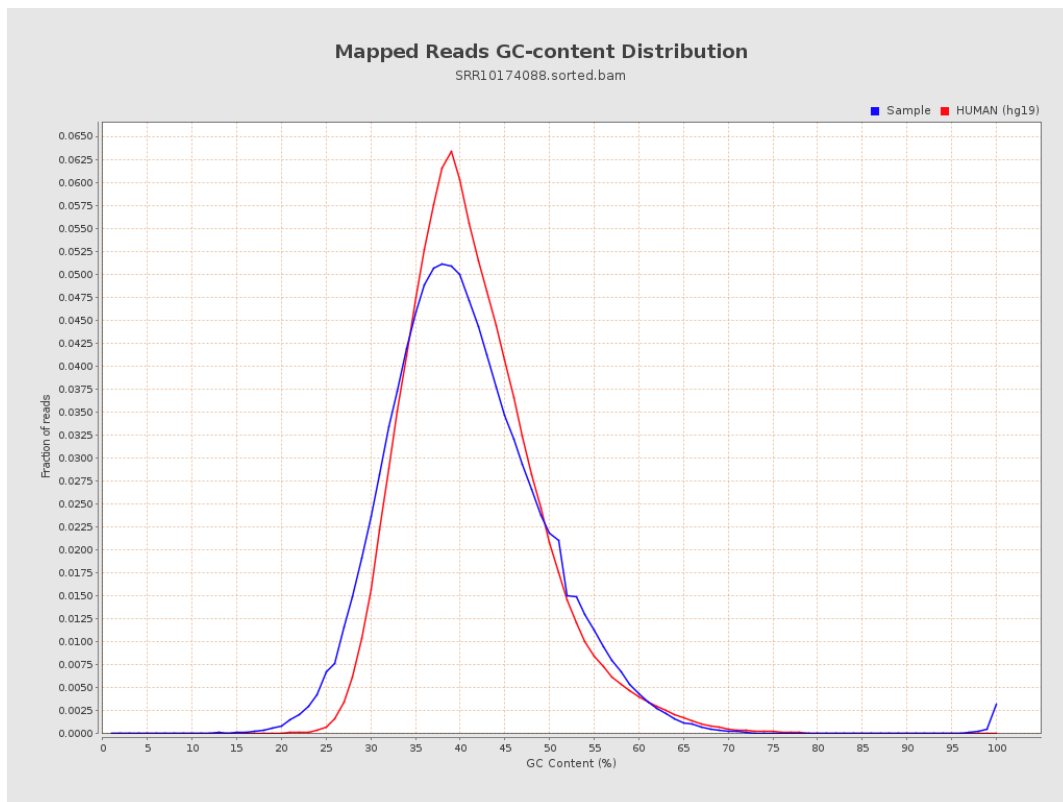
7. Results : Duplication Rate Histogram



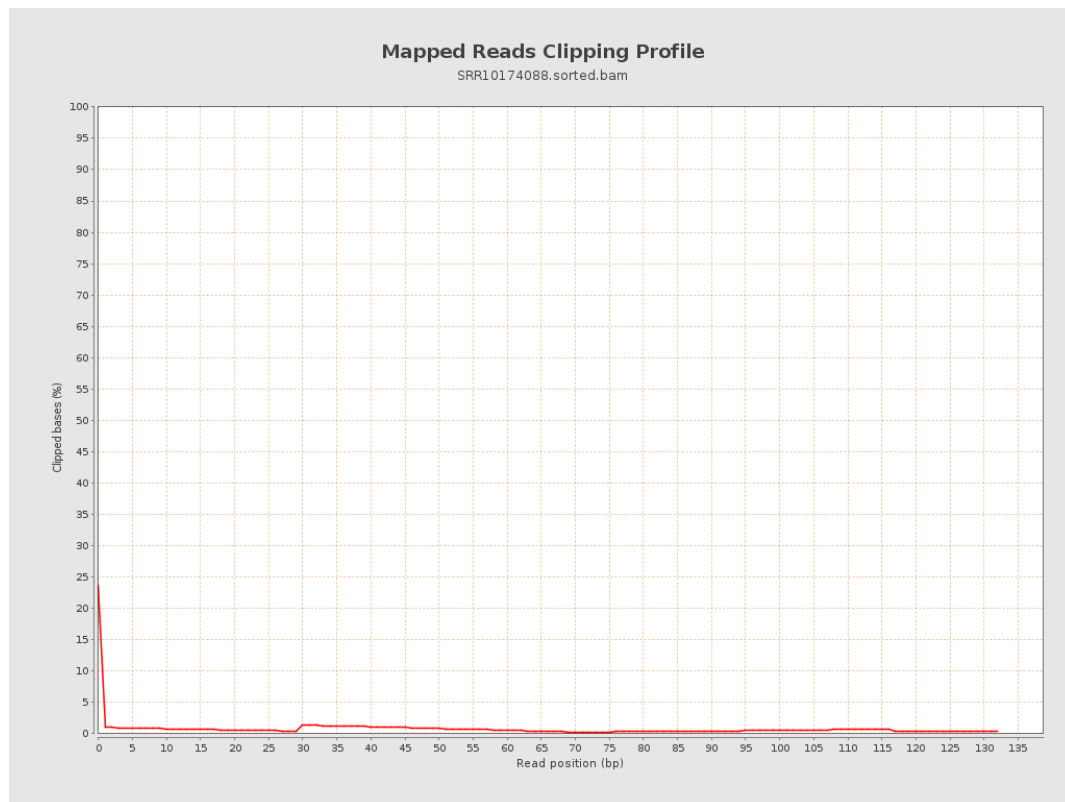
8. Results : Mapped Reads Nucleotide Content



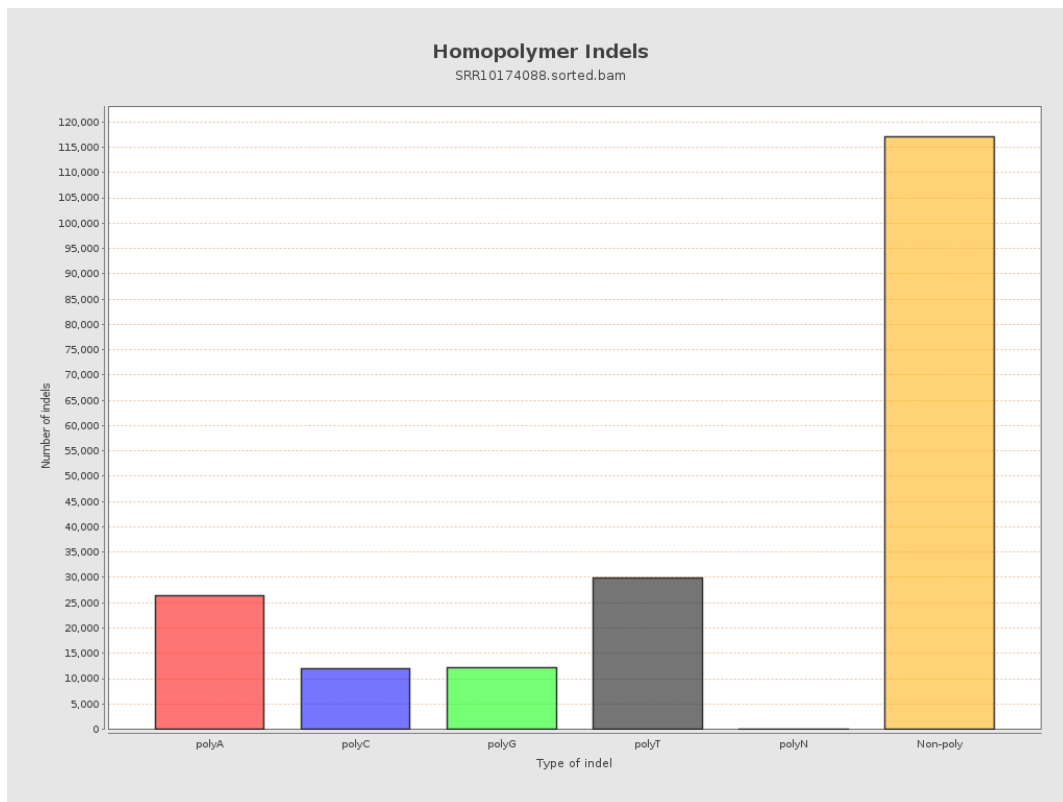
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



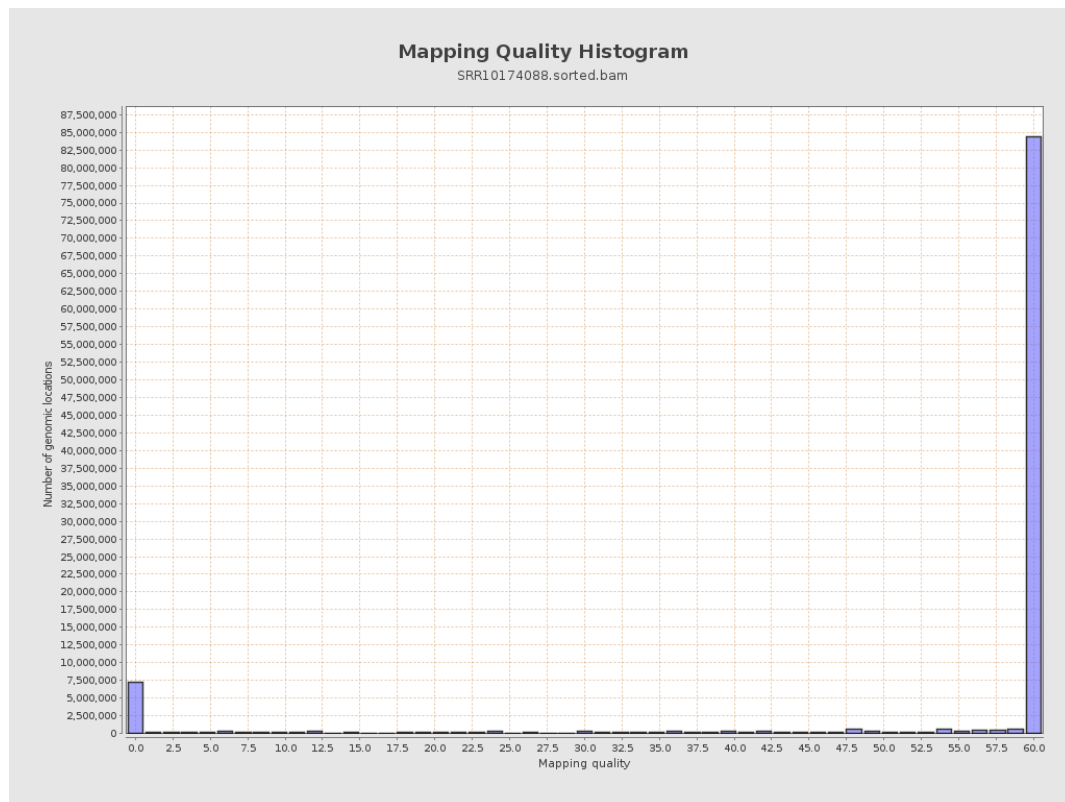
11. Results : Homopolymer Indels



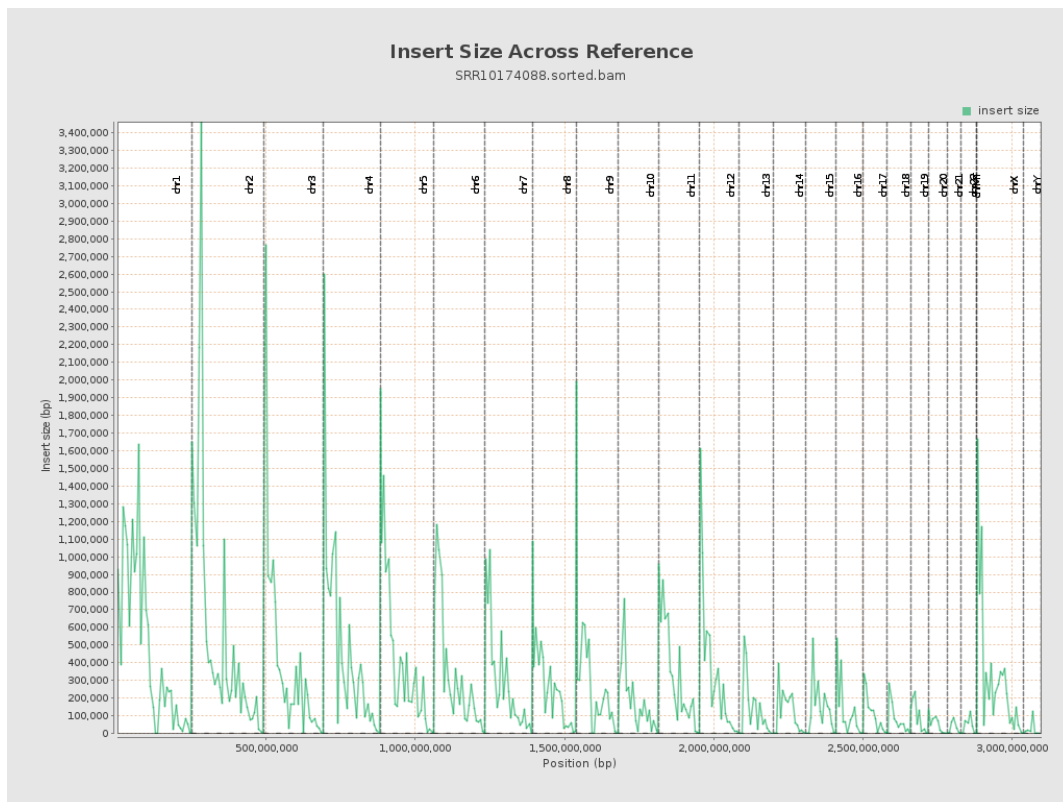
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

