

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 01:42:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472578.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_SRR3472578 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472578_1.fastq.gz SRR3472578_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 01:42:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472578.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,934,822
Mapped reads	9,057,969 / 91.17%
Unmapped reads	876,853 / 8.83%
Mapped paired reads	9,057,969 / 91.17%
Mapped reads, first in pair	4,569,012 / 45.99%
Mapped reads, second in pair	4,488,957 / 45.18%
Mapped reads, both in pair	8,847,090 / 89.05%
Mapped reads, singletons	210,879 / 2.12%
Secondary alignments	0
Supplementary alignments	275,026 / 2.77%
Read min/max/mean length	30 / 100 / 101.08
Duplicated reads (estimated)	1,486,247 / 14.96%
Duplication rate	14.05%
Clipped reads	6,962,300 / 70.08%

2.2. ACGT Content

Number/percentage of A's	189,247,135 / 25.75%
Number/percentage of C's	147,293,370 / 20.04%
Number/percentage of T's	218,390,955 / 29.71%
Number/percentage of G's	179,562,062 / 24.43%
Number/percentage of N's	495,694 / 0.07%

GC Percentage	44.47%
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2.3. Coverage

Mean	0.2375
Standard Deviation	2.4449

2.4. Mapping Quality

Mean Mapping Quality	50.46
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2.5. Insert size

Mean	215,029.68
Standard Deviation	4,453,188.53
P25/Median/P75	90 / 126 / 173

2.6. Mismatches and indels

General error rate	1.21%
Mismatches	8,743,030
Insertions	68,976
Mapped reads with at least one insertion	0.75%
Deletions	165,757
Mapped reads with at least one deletion	1.79%
Homopolymer indels	42.76%

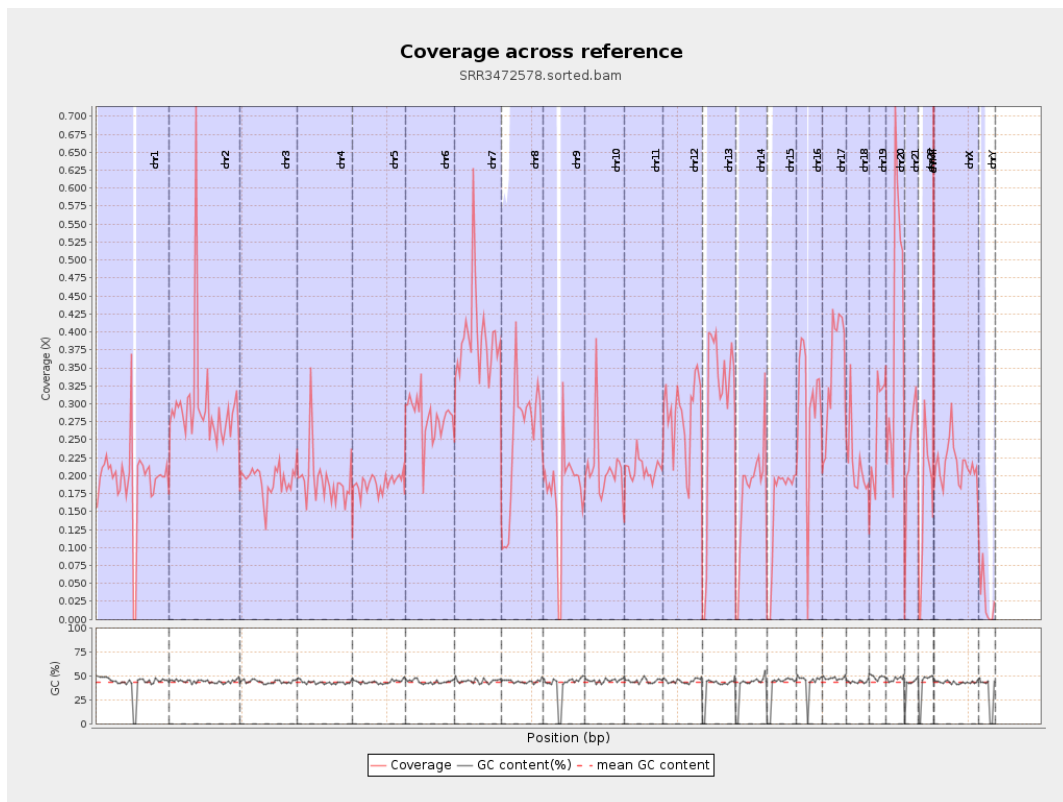
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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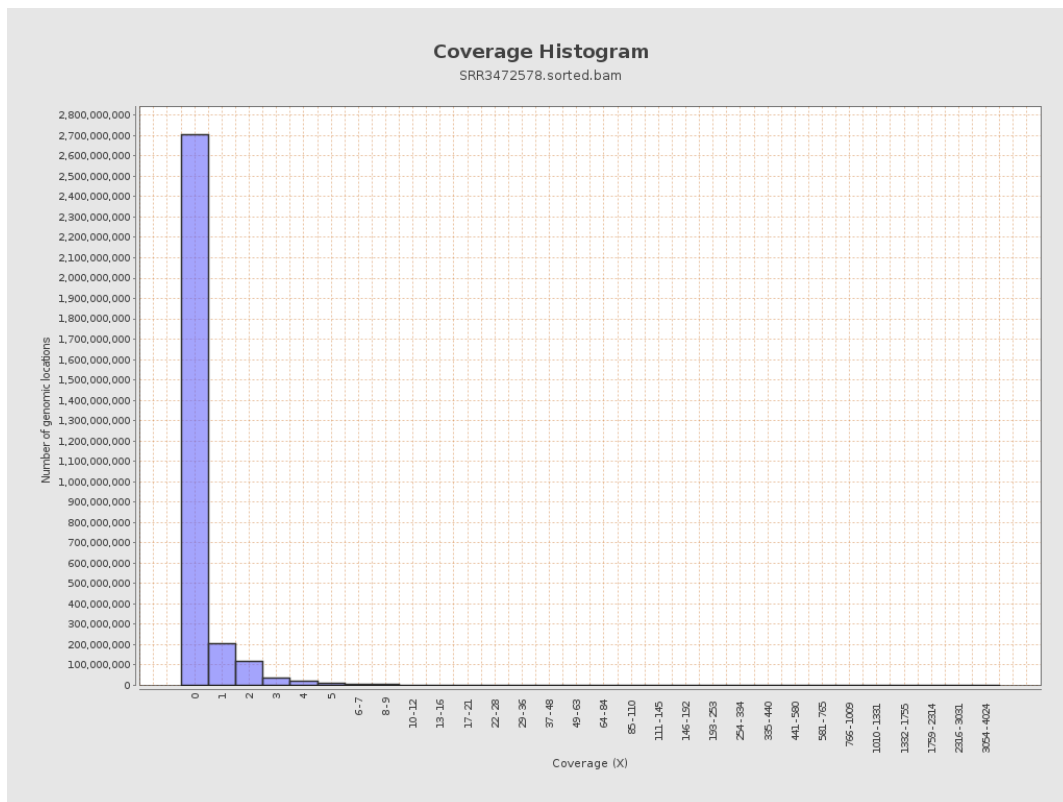
		bases	coverage	deviation
chr1	249250621	48112482	0.193	2.9615
chr2	243199373	72255432	0.2971	3.3755
chr3	198022430	38186940	0.1928	0.6776
chr4	191154276	36955949	0.1933	1.1575
chr5	180915260	34203315	0.1891	0.7225
chr6	171115067	48083226	0.281	1.2975
chr7	159138663	62718623	0.3941	4.5576
chr8	146364022	36435742	0.2489	2.0106
chr9	141213431	25195017	0.1784	2.5357
chr10	135534747	28549455	0.2106	2.1032
chr11	135006516	28032398	0.2076	1.8187
chr12	133851895	38112327	0.2847	0.8683
chr13	115169878	34101541	0.2961	0.8892
chr14	107349540	19168678	0.1786	6.1799
chr15	102531392	16200570	0.158	0.6219
chr16	90354753	27098372	0.2999	1.2381
chr17	81195210	28540299	0.3515	2.0317
chr18	78077248	16995477	0.2177	4.2994
chr19	59128983	15635940	0.2644	2.1014
chr20	63025520	26048140	0.4133	1.5238
chr21	48129895	11117205	0.231	0.9716
chr22	51304566	8310918	0.162	0.652
chrMT	16571	19192	1.1582	2.3259
chrX	155270560	33593466	0.2164	1.093

chrY	59373566	1627510	0.0274	0.8443
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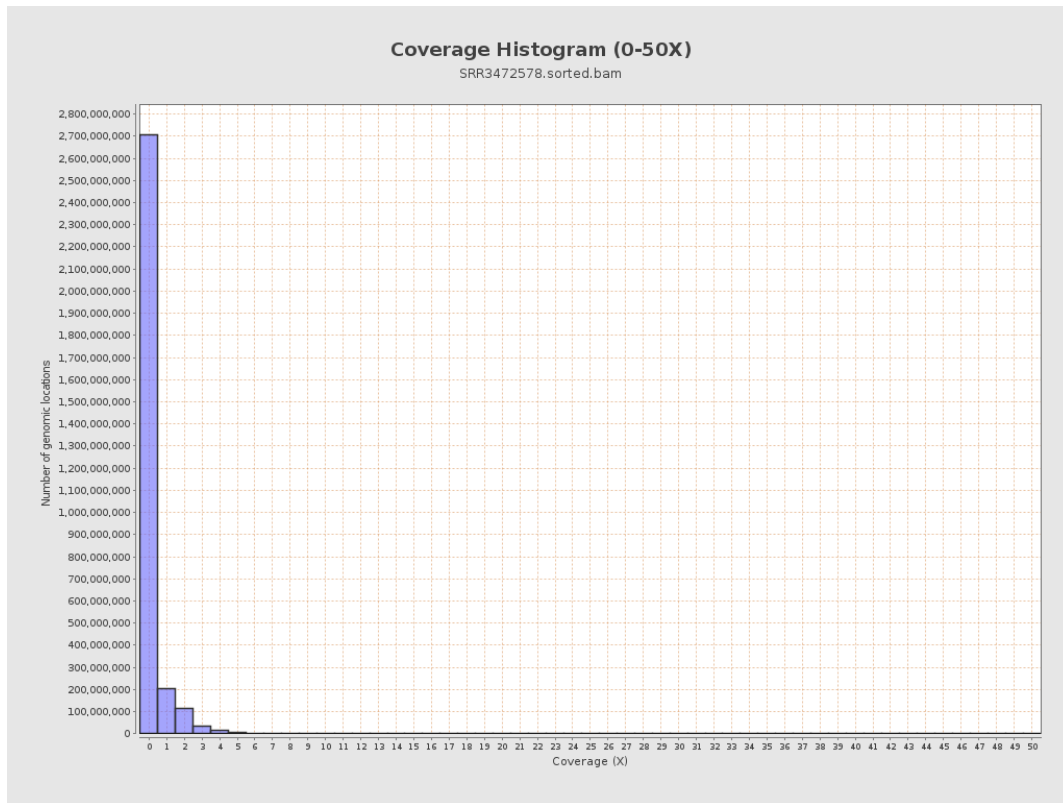
3. Results : Coverage across reference



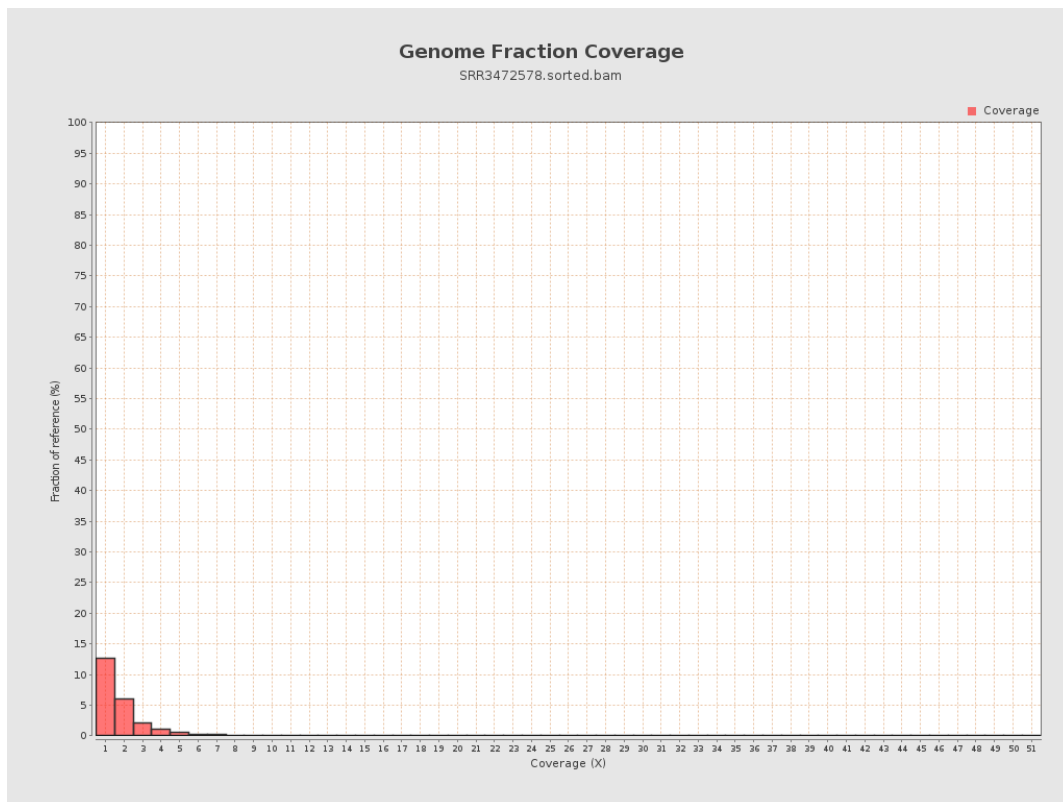
4. Results : Coverage Histogram



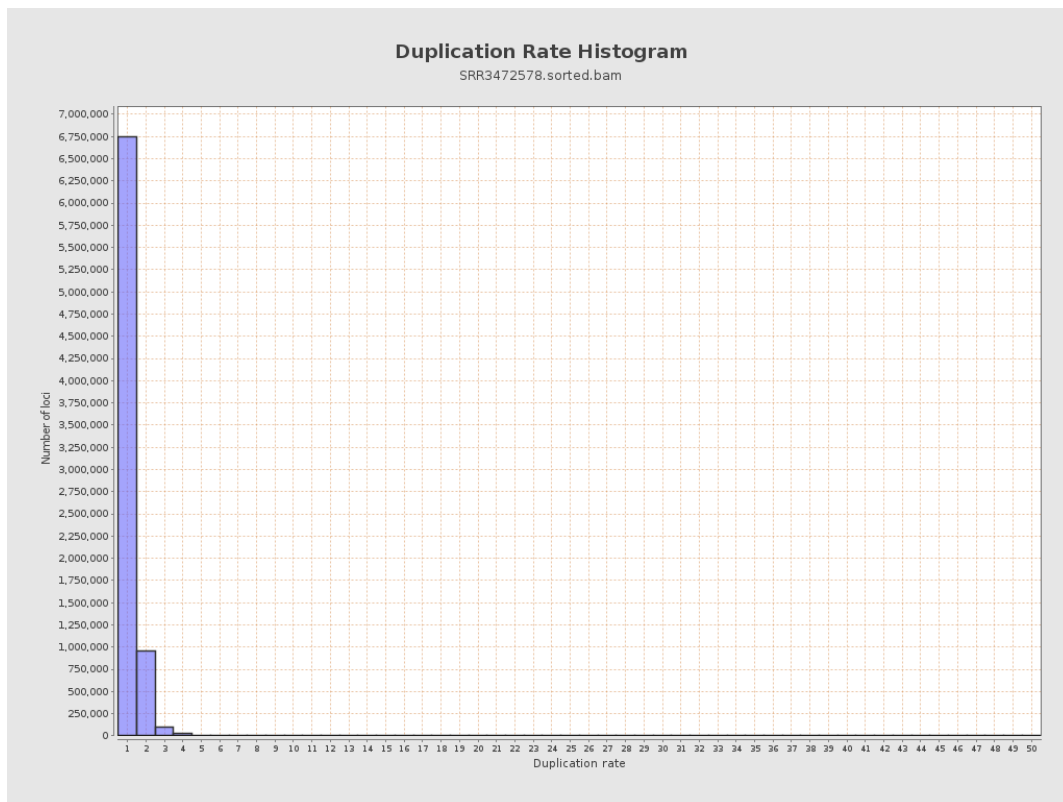
5. Results : Coverage Histogram (0-50X)



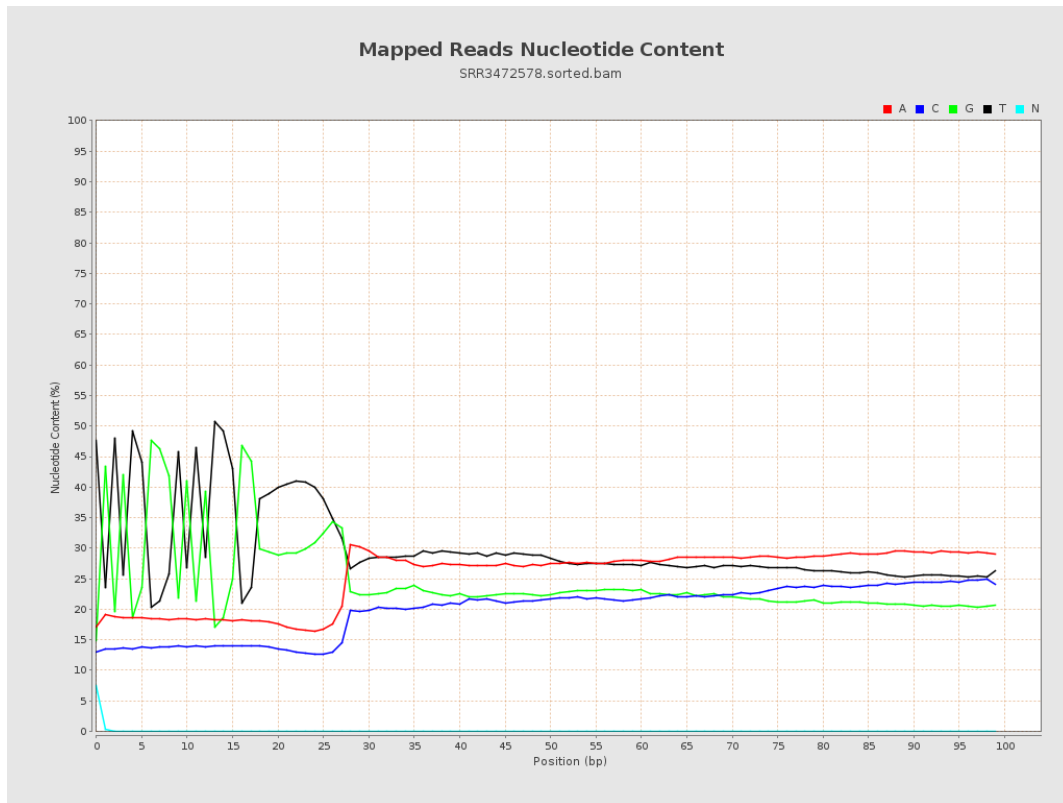
6. Results : Genome Fraction Coverage



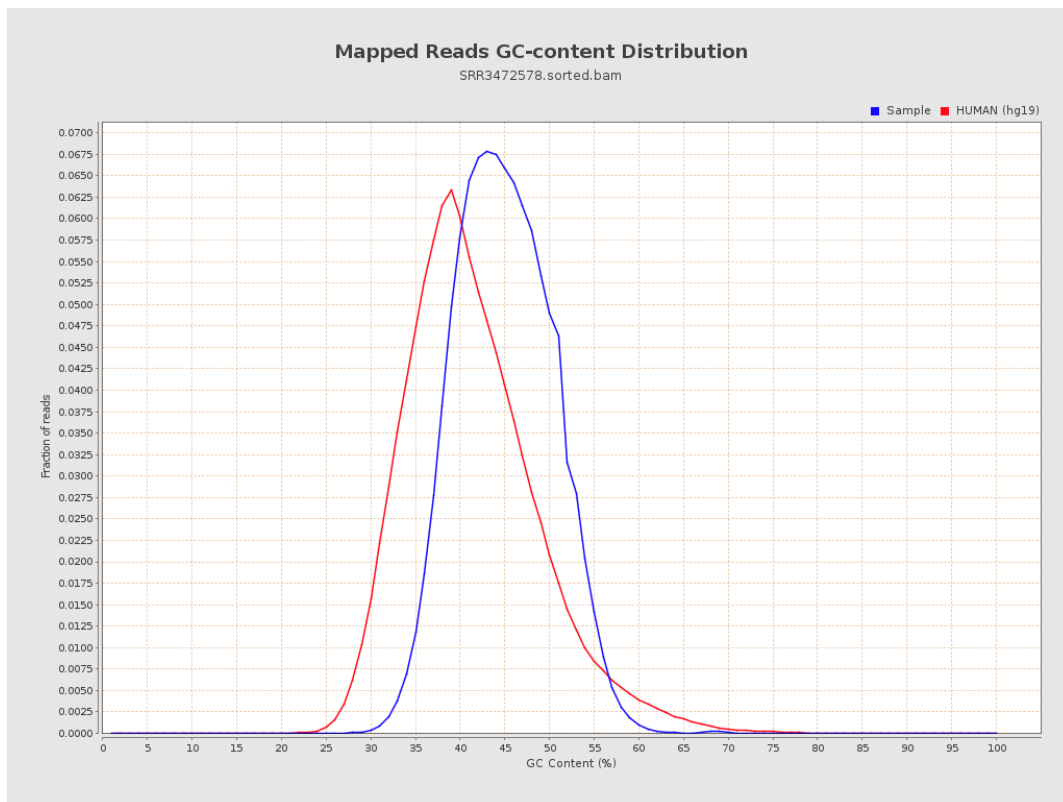
7. Results : Duplication Rate Histogram



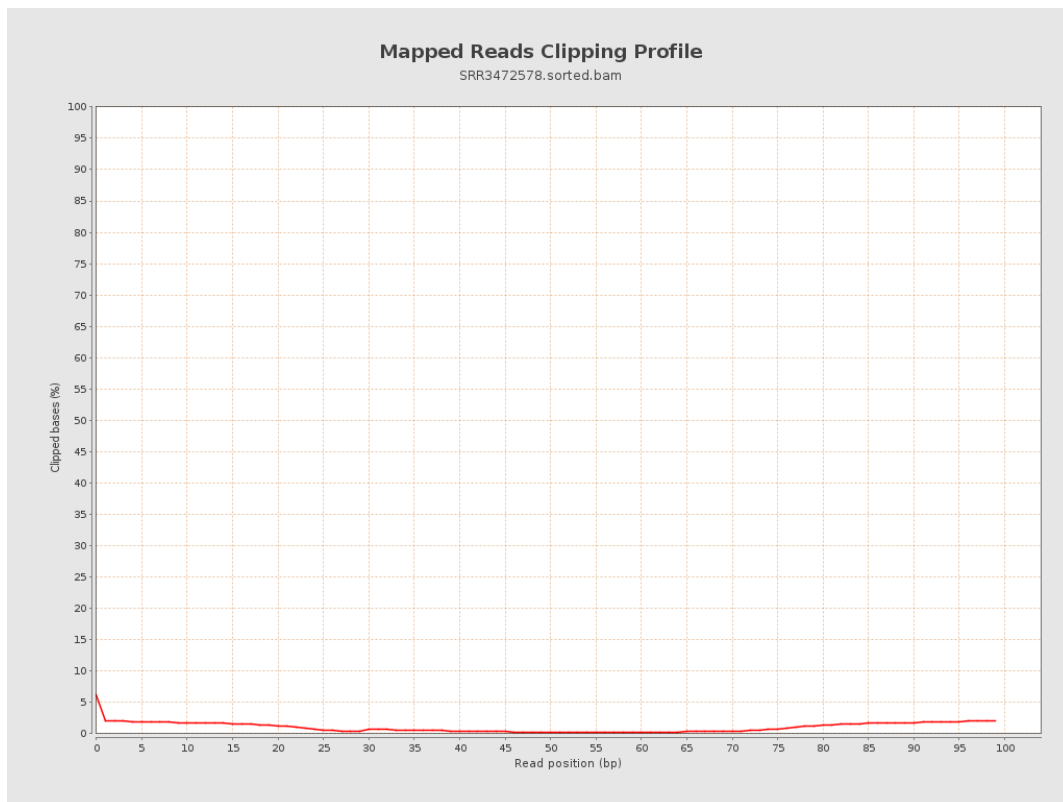
8. Results : Mapped Reads Nucleotide Content



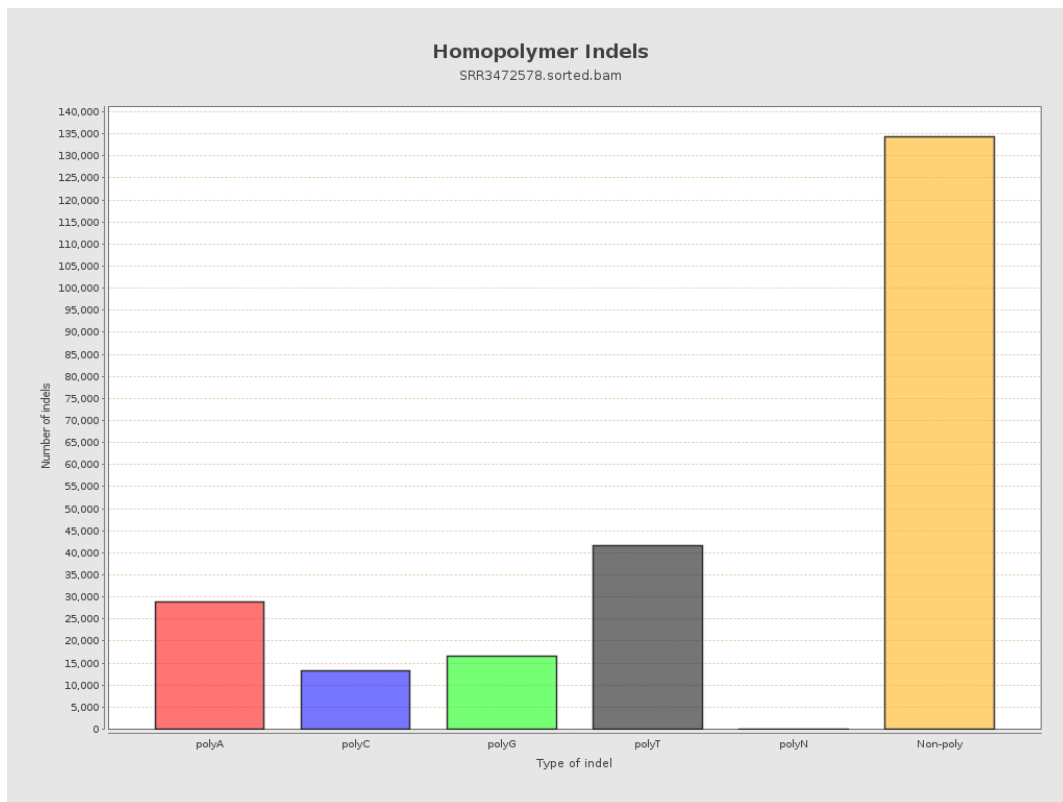
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



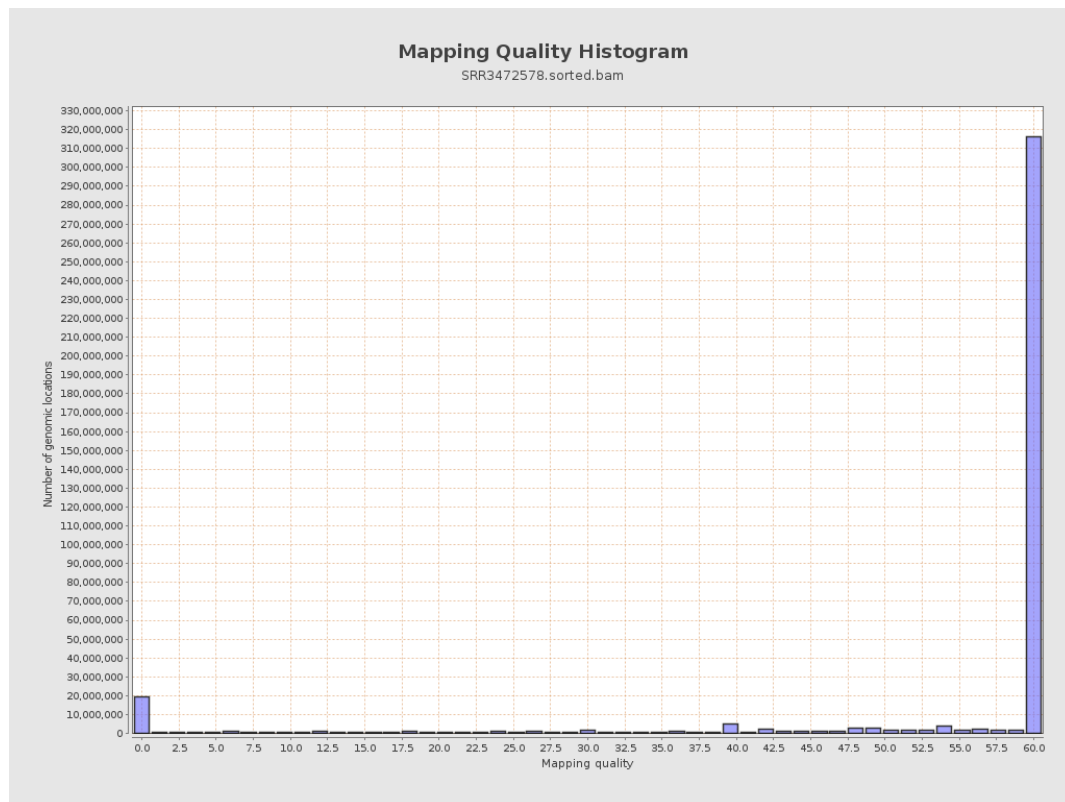
11. Results : Homopolymer Indels



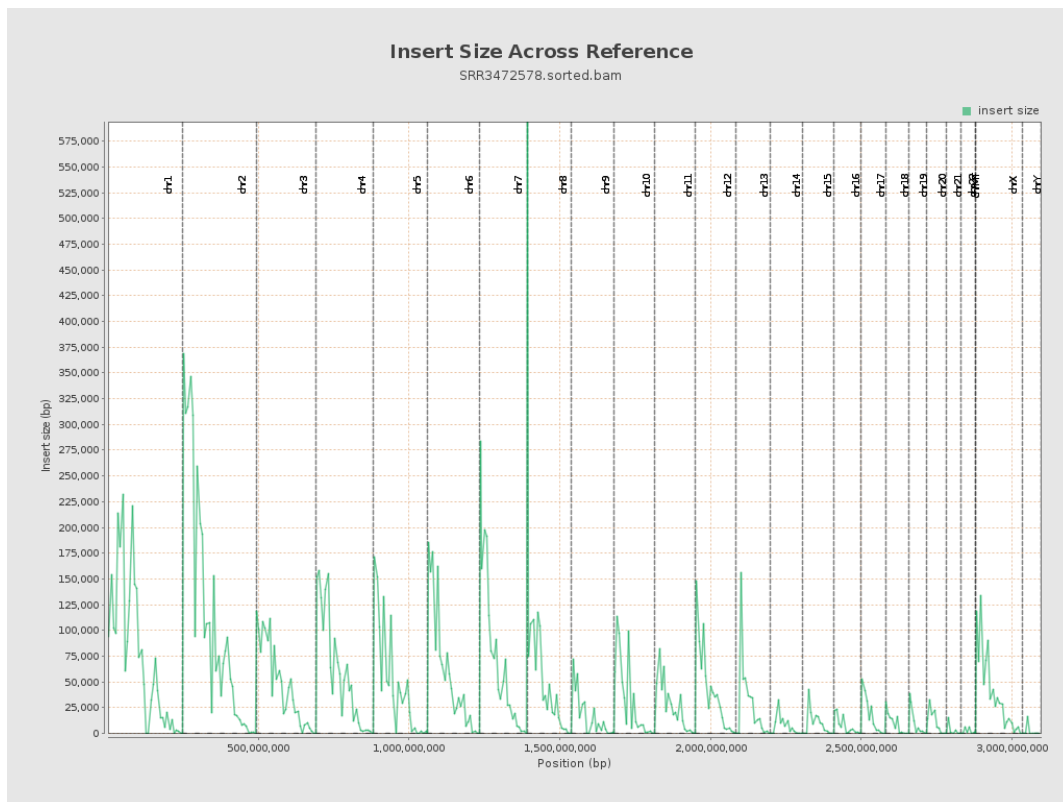
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

