

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 14:50:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173969.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_SRR10173969 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173969_1.fastq.gz SRR10173969_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 14:50:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173969.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,259,002
Mapped reads	7,109,943 / 97.95%
Unmapped reads	149,059 / 2.05%
Mapped paired reads	7,109,943 / 97.95%
Mapped reads, first in pair	3,553,282 / 48.95%
Mapped reads, second in pair	3,556,661 / 49%
Mapped reads, both in pair	7,014,212 / 96.63%
Mapped reads, singletons	95,731 / 1.32%
Secondary alignments	0
Supplementary alignments	928,227 / 12.79%
Read min/max/mean length	30 / 133 / 125.46
Duplicated reads (estimated)	5,797,703 / 79.87%
Duplication rate	65.7%
Clipped reads	3,521,738 / 48.52%

2.2. ACGT Content

Number/percentage of A's	241,083,064 / 29.82%
Number/percentage of C's	160,981,402 / 19.91%
Number/percentage of T's	239,173,304 / 29.59%
Number/percentage of G's	167,170,950 / 20.68%
Number/percentage of N's	6,266 / 0%

GC Percentage	40.59%
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2.3. Coverage

Mean	0.2613
Standard Deviation	4.6234

2.4. Mapping Quality

Mean Mapping Quality	52.54
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2.5. Insert size

Mean	940,335.65
Standard Deviation	8,757,814.2
P25/Median/P75	107 / 156 / 242

2.6. Mismatches and indels

General error rate	0.87%
Mismatches	6,759,677
Insertions	89,827
Mapped reads with at least one insertion	1.22%
Deletions	227,194
Mapped reads with at least one deletion	3.11%
Homopolymer indels	41.7%

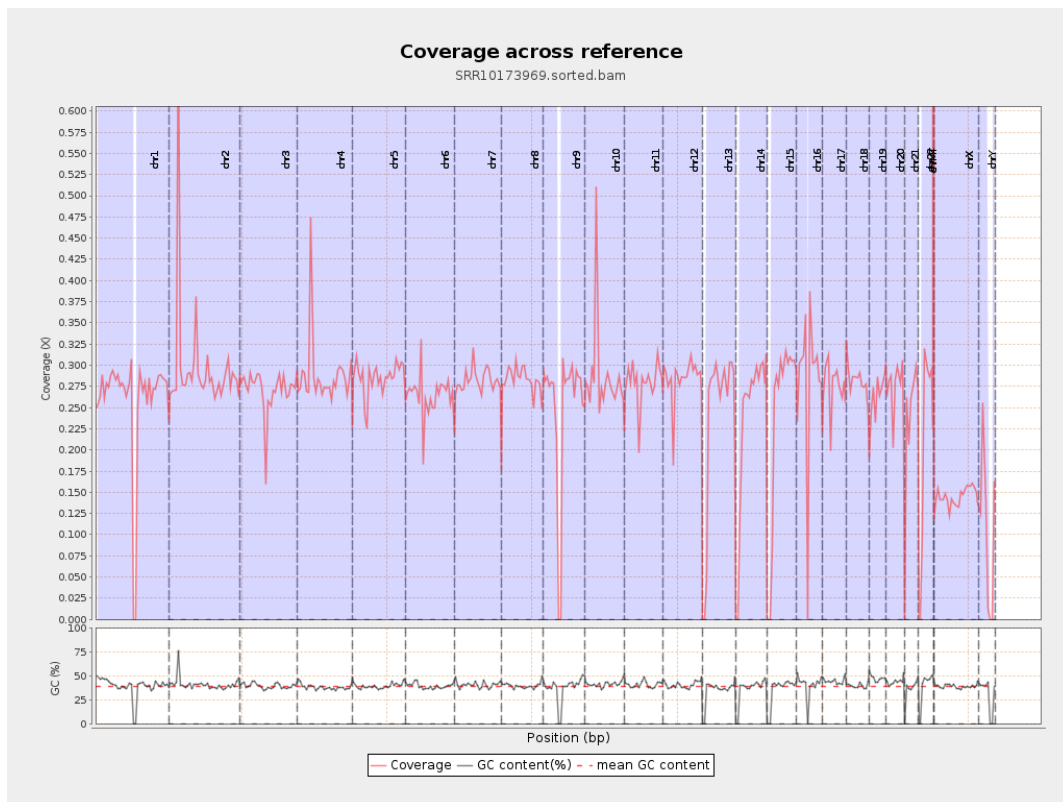
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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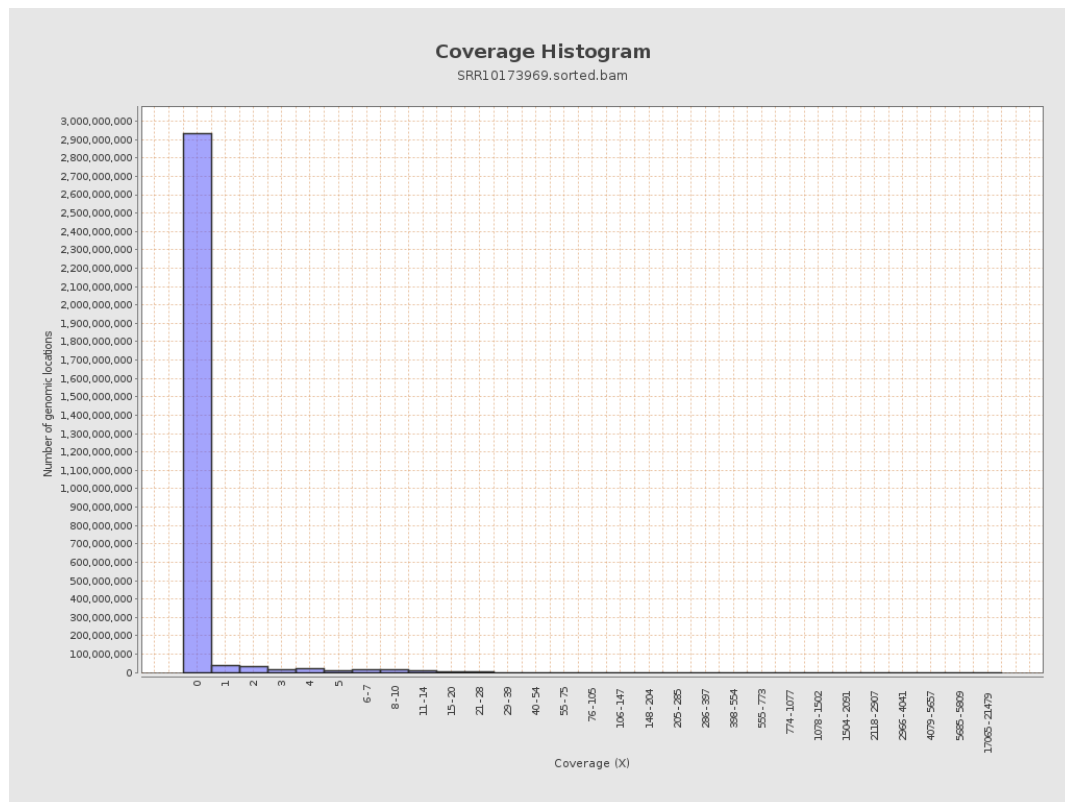
		bases	coverage	deviation
chr1	249250621	64619499	0.2593	2.1807
chr2	243199373	72531571	0.2982	14.9942
chr3	198022430	53606543	0.2707	1.617
chr4	191154276	54919628	0.2873	2.2722
chr5	180915260	51582407	0.2851	1.6729
chr6	171115067	45105567	0.2636	1.7926
chr7	159138663	44937862	0.2824	2.1796
chr8	146364022	41403975	0.2829	2.9256
chr9	141213431	34978931	0.2477	2.1282
chr10	135534747	38851607	0.2867	2.7448
chr11	135006516	37714505	0.2794	1.7045
chr12	133851895	38038111	0.2842	1.7349
chr13	115169878	27307332	0.2371	1.5226
chr14	107349540	25096725	0.2338	1.5343
chr15	102531392	24509182	0.239	1.5765
chr16	90354753	25564893	0.2829	2.1489
chr17	81195210	22351415	0.2753	1.846
chr18	78077248	22022400	0.2821	2.7303
chr19	59128983	15634344	0.2644	1.9911
chr20	63025520	17178404	0.2726	1.731
chr21	48129895	11466279	0.2382	2.0871
chr22	51304566	10489767	0.2045	1.8395
chrMT	16571	536997	32.4058	31.4712
chrX	155270560	22456472	0.1446	1.19

chrY	59373566	6059054	0.102	1.6872
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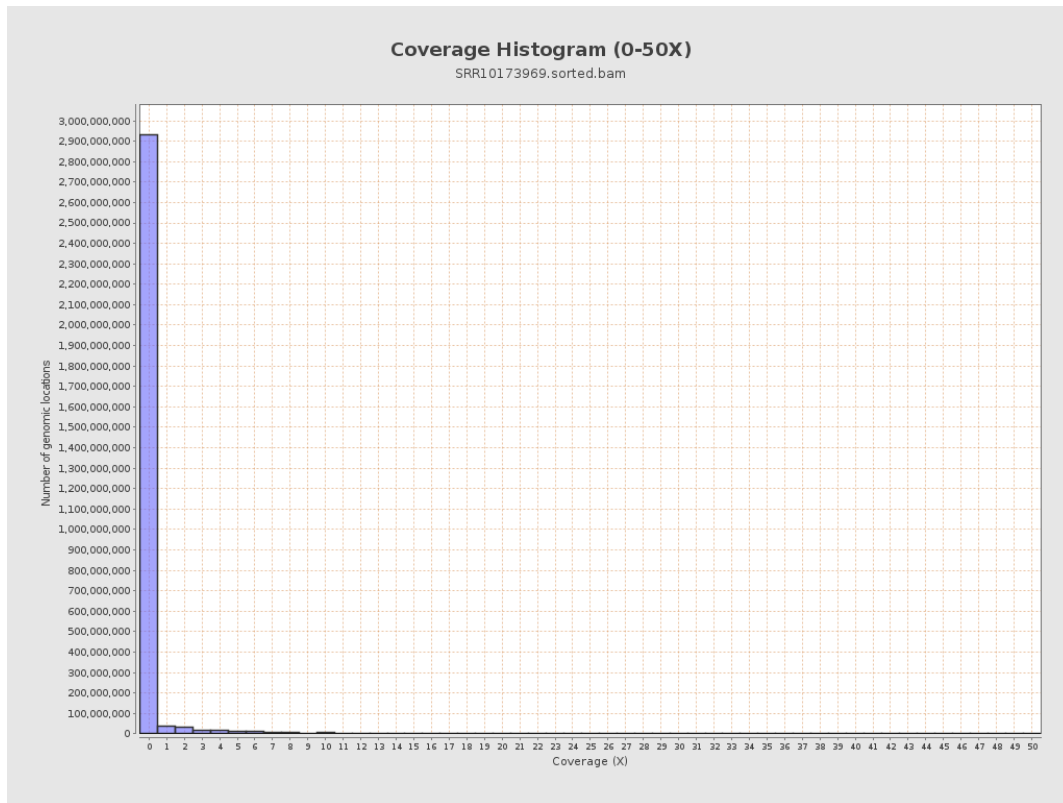
3. Results : Coverage across reference



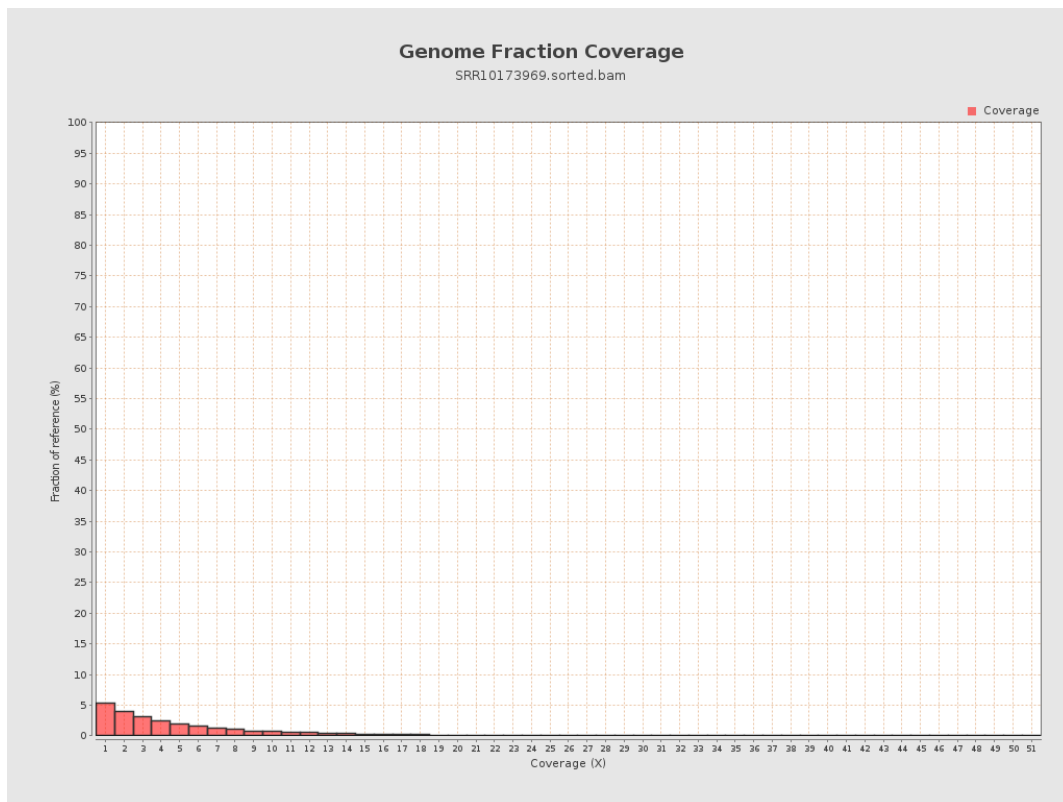
4. Results : Coverage Histogram



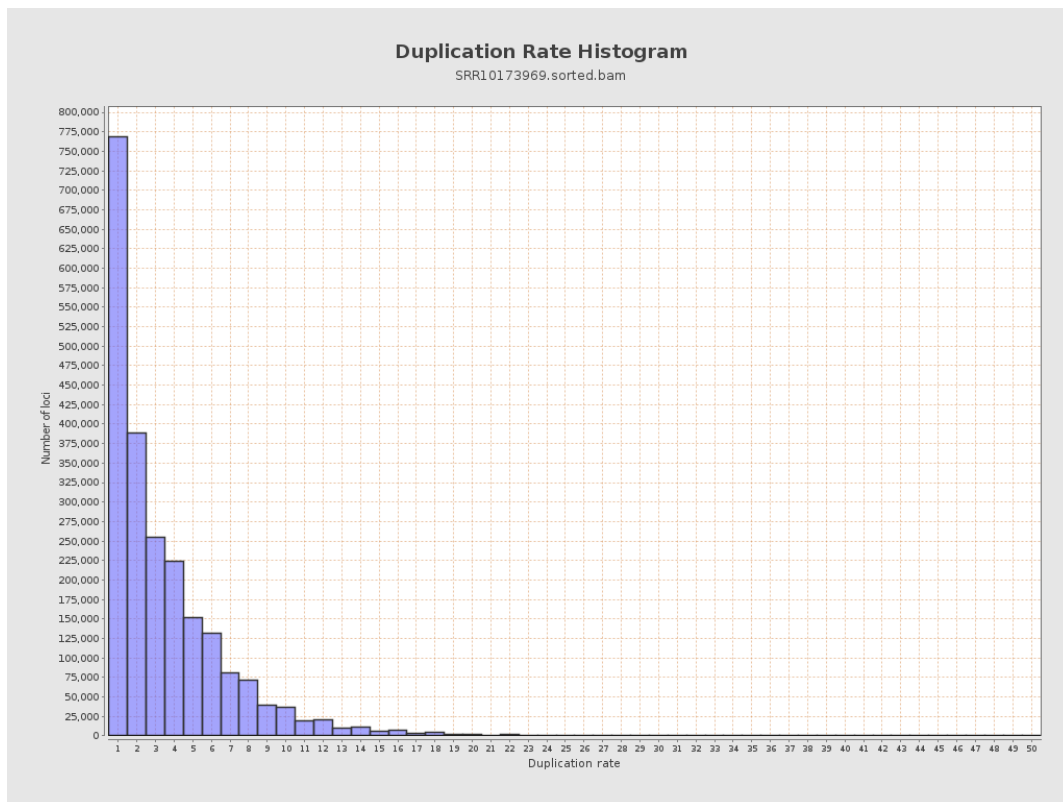
5. Results : Coverage Histogram (0-50X)



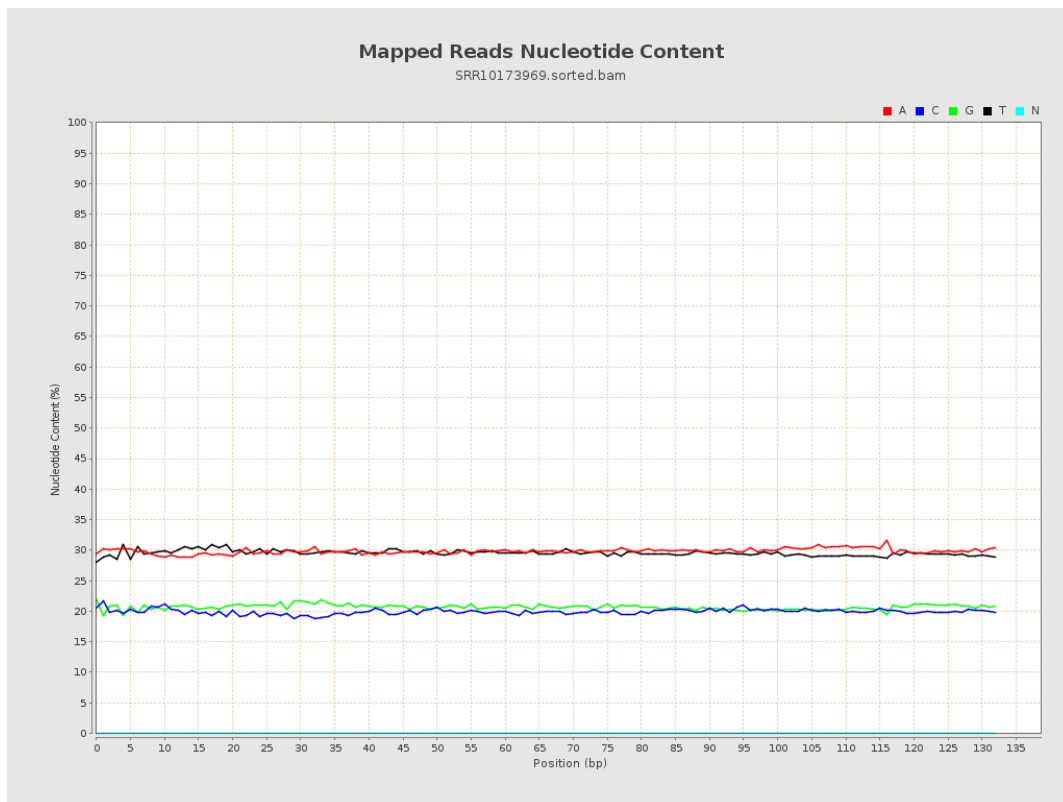
6. Results : Genome Fraction Coverage



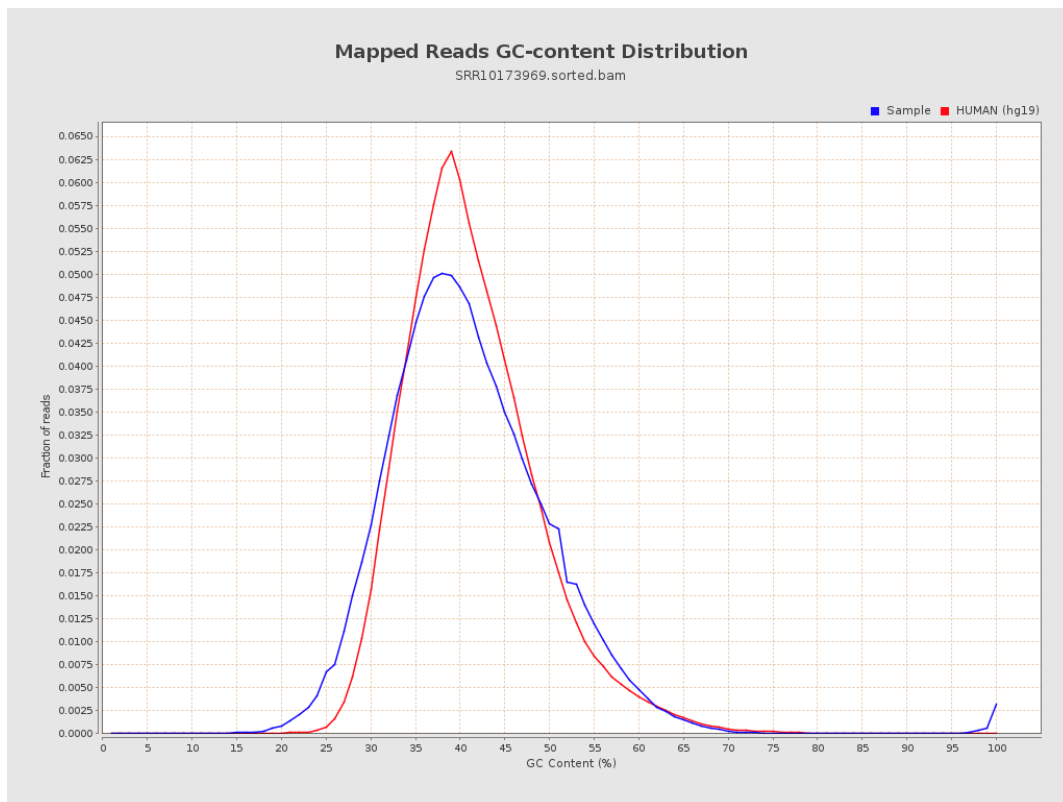
7. Results : Duplication Rate Histogram



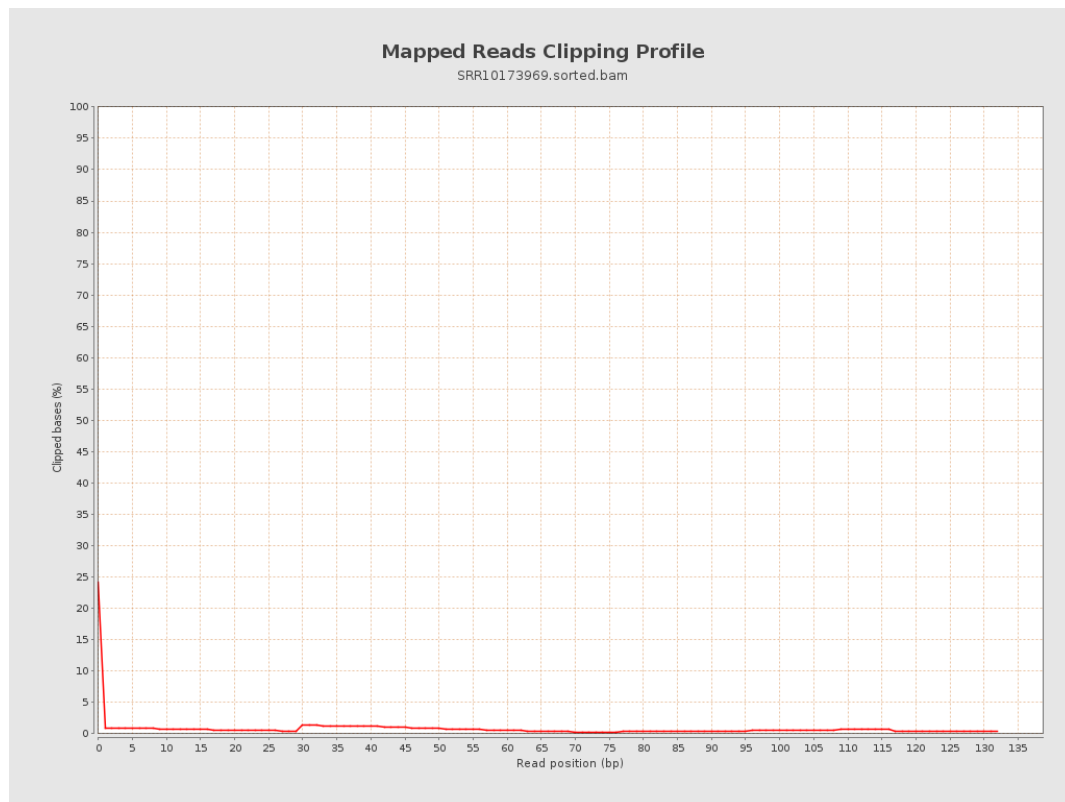
8. Results : Mapped Reads Nucleotide Content



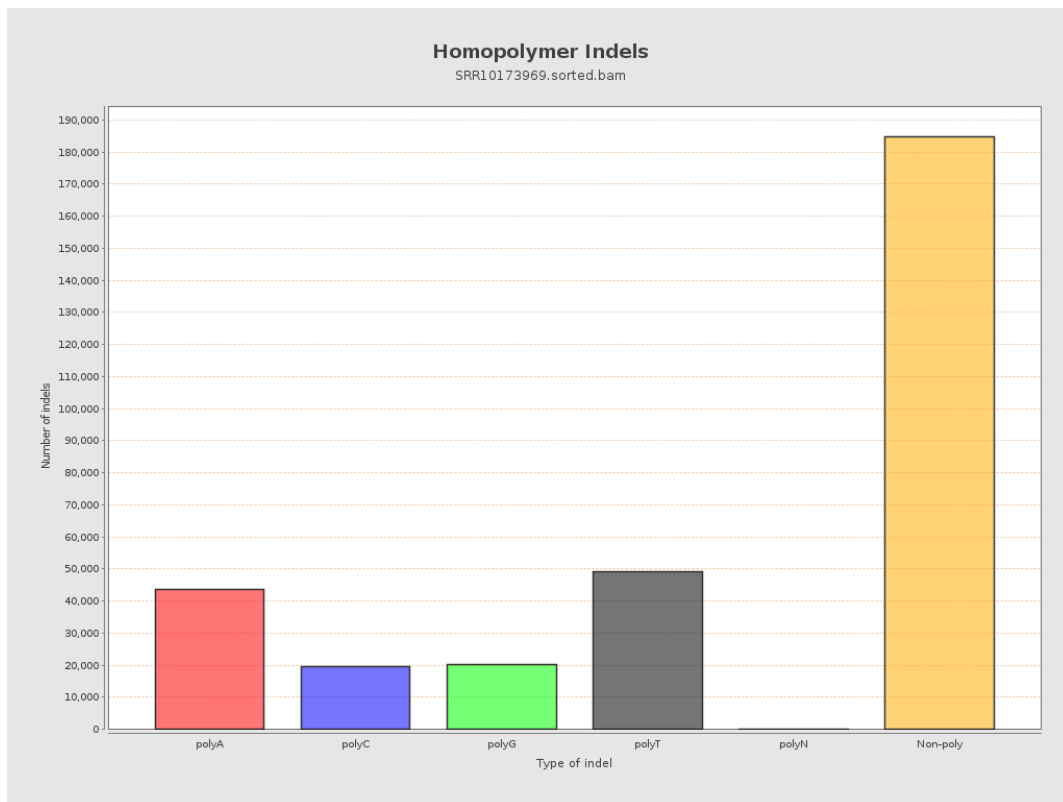
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



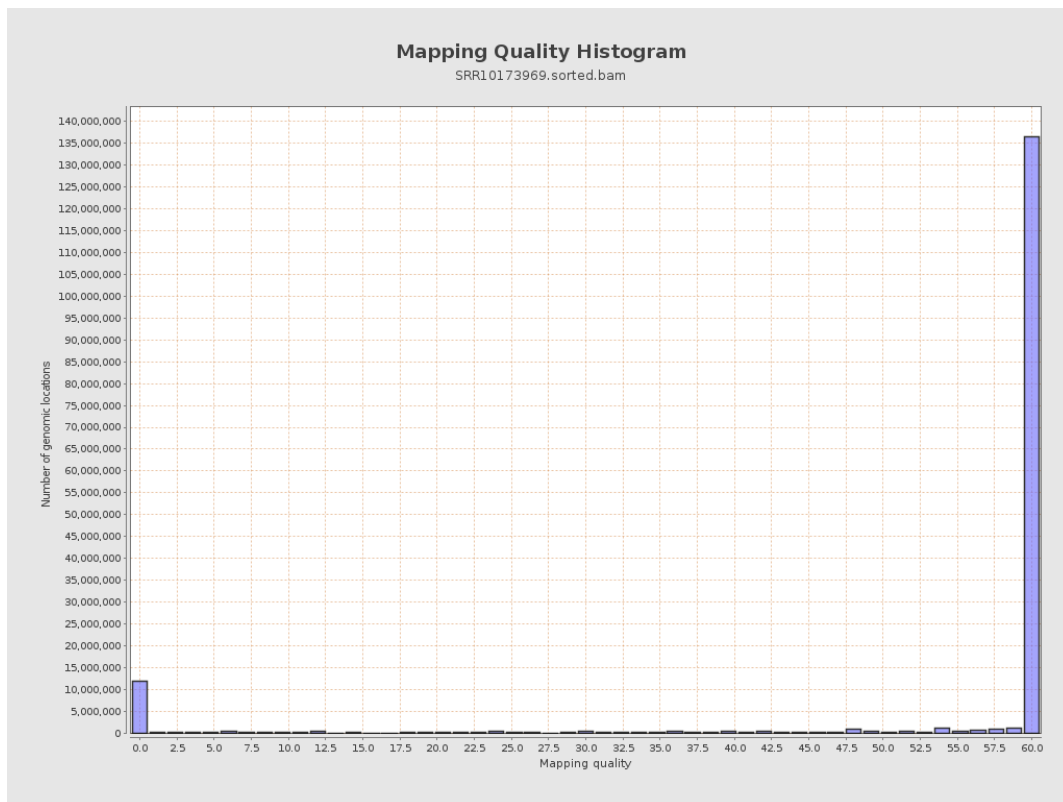
11. Results : Homopolymer Indels



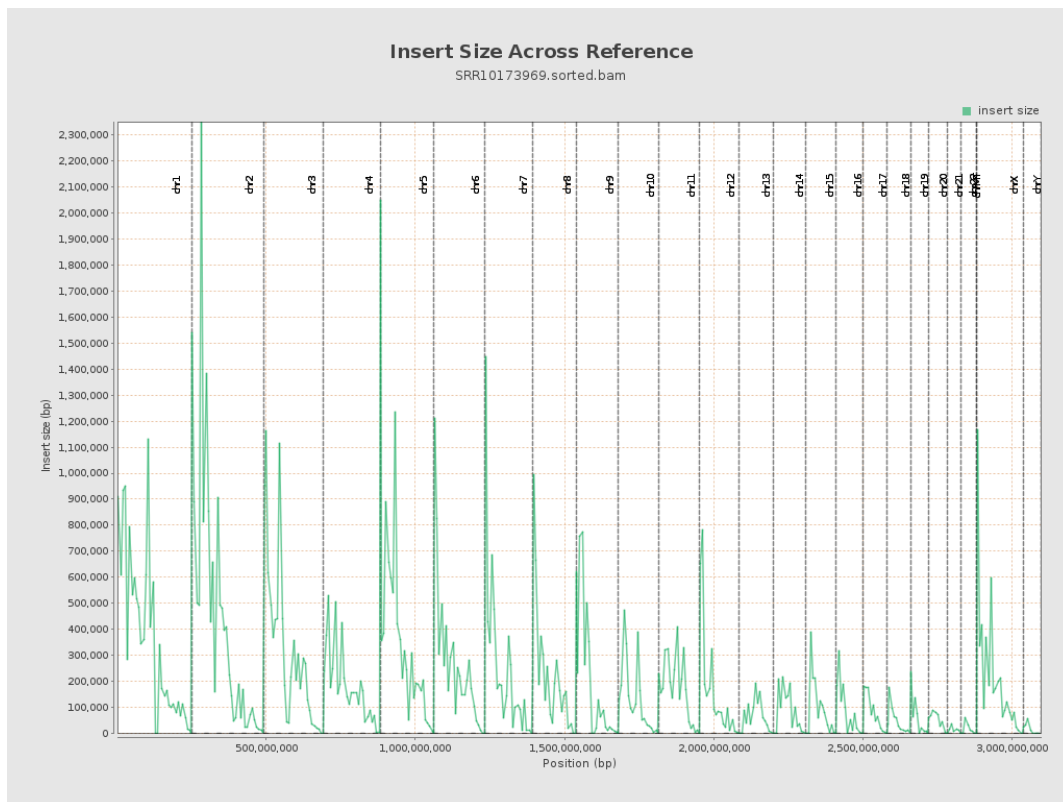
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

