

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 17:41:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173989.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_SRR10173989 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173989_1.fastq.gz SRR10173989_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 17:41:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173989.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,949,354
Mapped reads	10,710,453 / 97.82%
Unmapped reads	238,901 / 2.18%
Mapped paired reads	10,710,453 / 97.82%
Mapped reads, first in pair	5,360,264 / 48.96%
Mapped reads, second in pair	5,350,189 / 48.86%
Mapped reads, both in pair	10,561,932 / 96.46%
Mapped reads, singletons	148,521 / 1.36%
Secondary alignments	0
Supplementary alignments	1,401,179 / 12.8%
Read min/max/mean length	30 / 133 / 125.16
Duplicated reads (estimated)	8,611,658 / 78.65%
Duplication rate	65.03%
Clipped reads	5,363,618 / 48.99%

2.2. ACGT Content

Number/percentage of A's	364,204,005 / 30.02%
Number/percentage of C's	239,528,676 / 19.74%
Number/percentage of T's	360,991,366 / 29.76%
Number/percentage of G's	248,404,540 / 20.48%
Number/percentage of N's	9,057 / 0%

GC Percentage	40.22%
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2.3. Coverage

Mean	0.3922
Standard Deviation	6.5874

2.4. Mapping Quality

Mean Mapping Quality	52.59
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2.5. Insert size

Mean	972,070.44
Standard Deviation	9,149,246.28
P25/Median/P75	105 / 153 / 234

2.6. Mismatches and indels

General error rate	0.89%
Mismatches	10,461,661
Insertions	132,939
Mapped reads with at least one insertion	1.2%
Deletions	358,912
Mapped reads with at least one deletion	3.27%
Homopolymer indels	40.9%

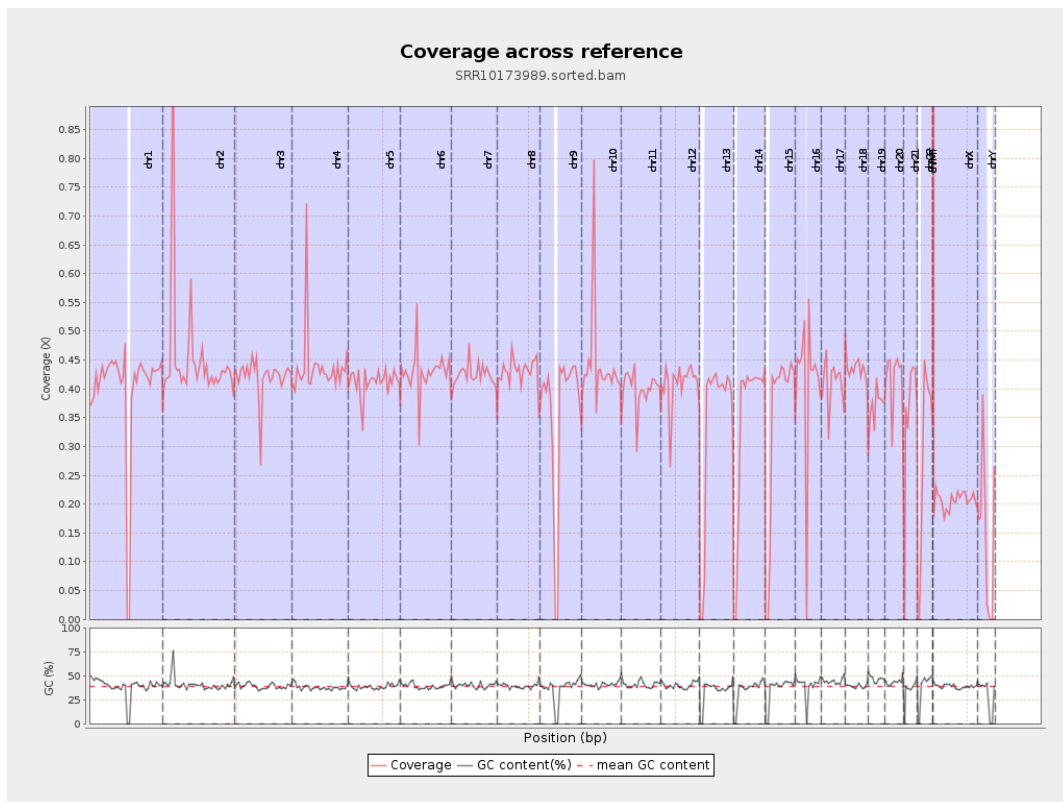
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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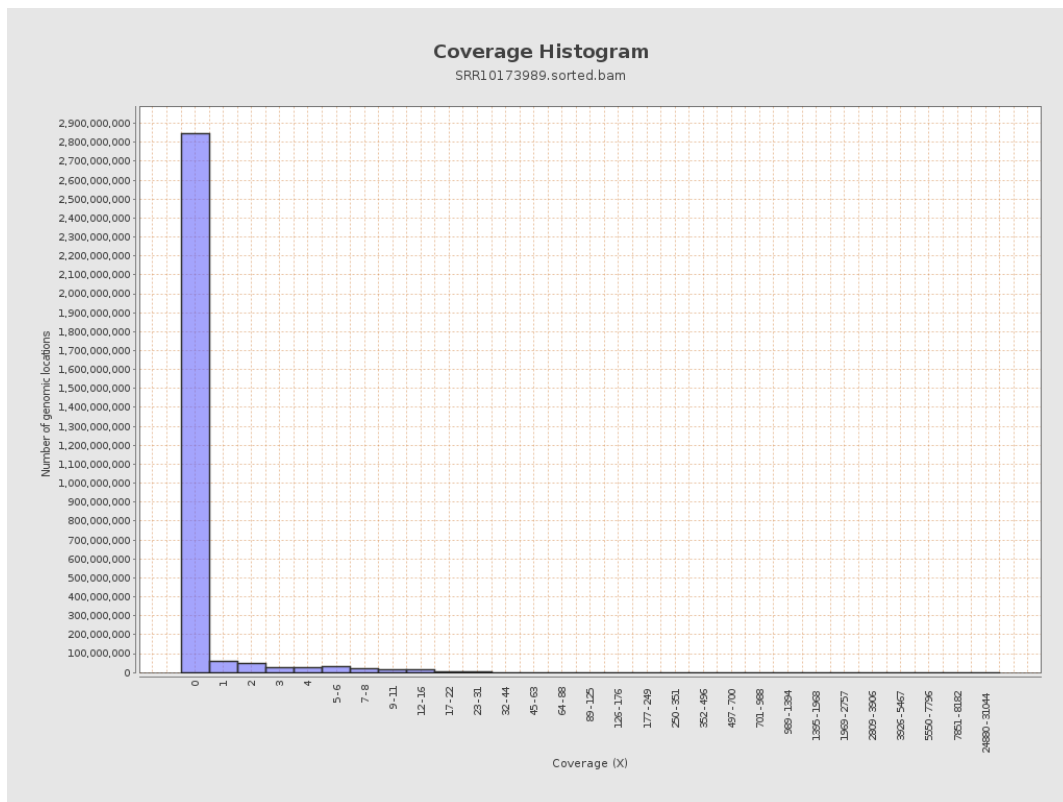
		bases	coverage	deviation
chr1	249250621	99539200	0.3994	3.0488
chr2	243199373	109988505	0.4523	21.6777
chr3	198022430	83268909	0.4205	1.9873
chr4	191154276	83801230	0.4384	3.0493
chr5	180915260	74442902	0.4115	1.9472
chr6	171115067	73600017	0.4301	2.5636
chr7	159138663	67432138	0.4237	2.9998
chr8	146364022	62971029	0.4302	3.5798
chr9	141213431	51267109	0.363	2.9285
chr10	135534747	59808194	0.4413	3.9744
chr11	135006516	53963647	0.3997	2.0486
chr12	133851895	54867098	0.4099	2.095
chr13	115169878	39249734	0.3408	1.7836
chr14	107349540	37347312	0.3479	1.846
chr15	102531392	35025348	0.3416	1.8693
chr16	90354753	37036270	0.4099	2.8196
chr17	81195210	33399247	0.4113	2.2813
chr18	78077248	33965581	0.435	3.9563
chr19	59128983	21913270	0.3706	2.3616
chr20	63025520	26441501	0.4195	2.0988
chr21	48129895	17284738	0.3591	2.7537
chr22	51304566	14565248	0.2839	2.1993
chrMT	16571	1459888	88.099	68.0615
chrX	155270560	32073658	0.2066	1.4088

chrY	59373566	9265219	0.156	2.4251
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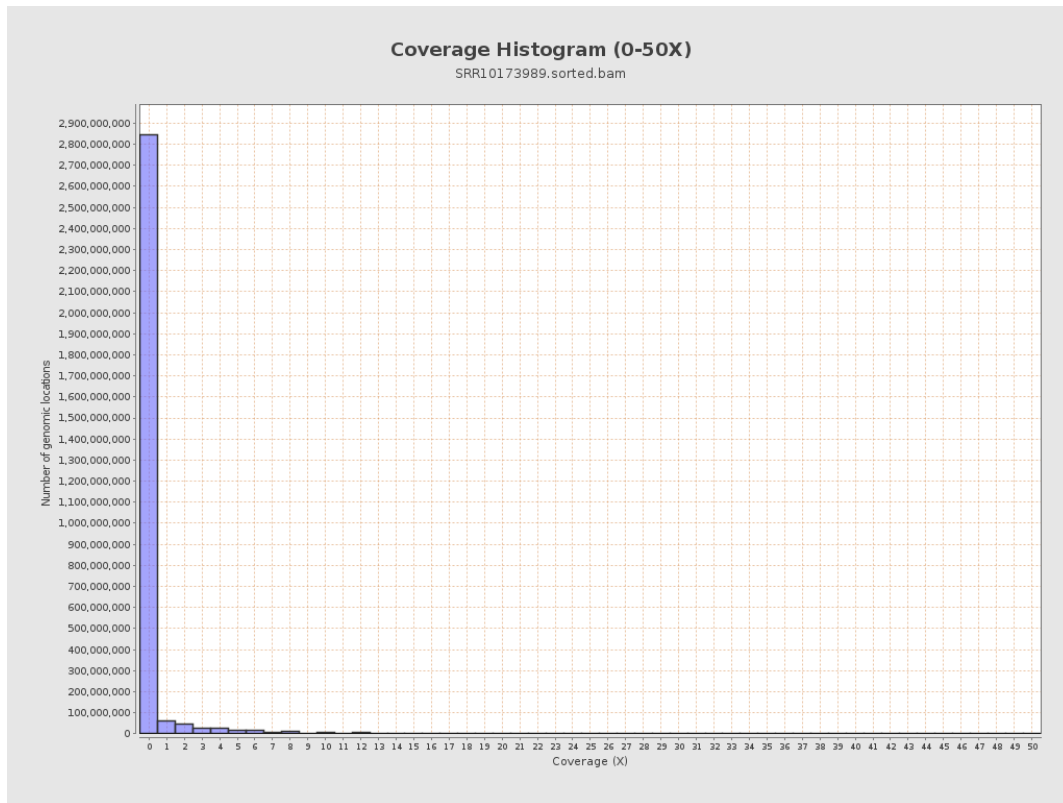
3. Results : Coverage across reference



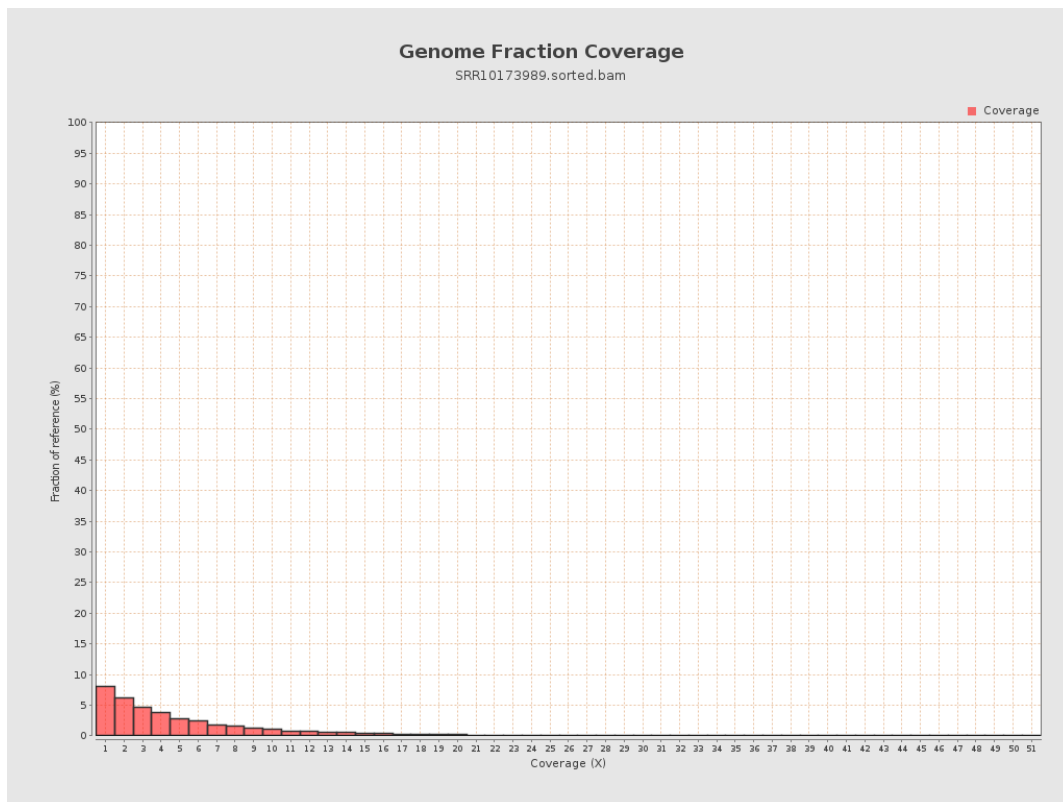
4. Results : Coverage Histogram



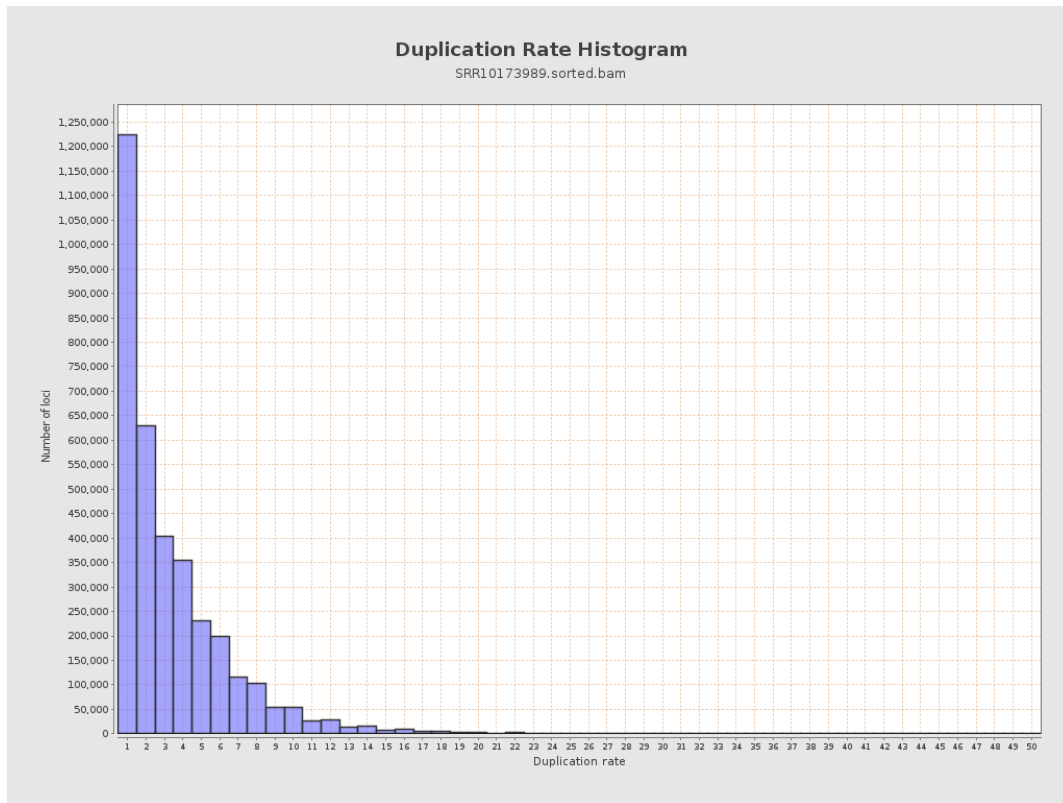
5. Results : Coverage Histogram (0-50X)



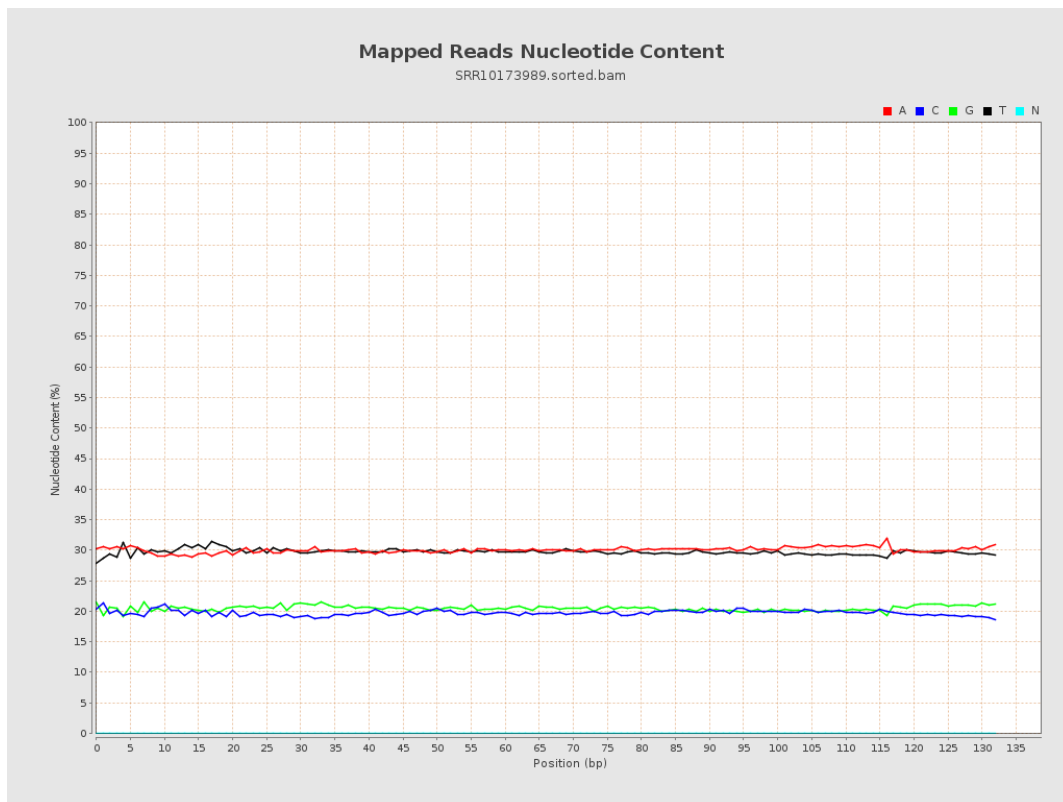
6. Results : Genome Fraction Coverage



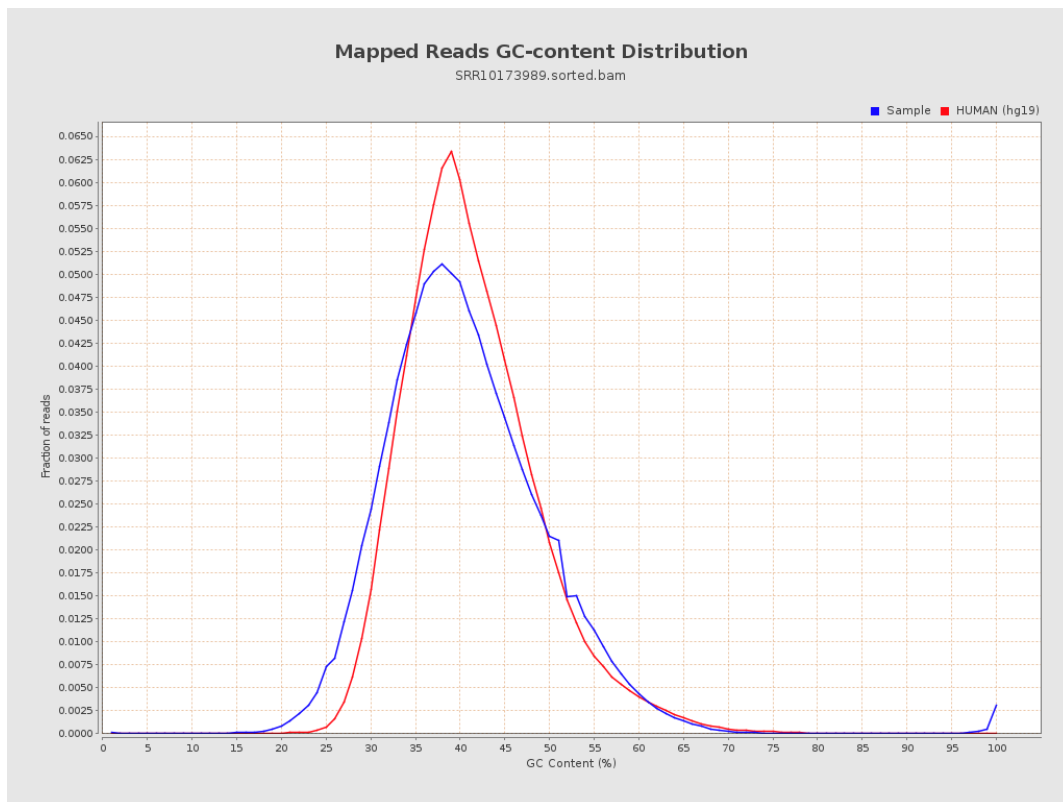
7. Results : Duplication Rate Histogram



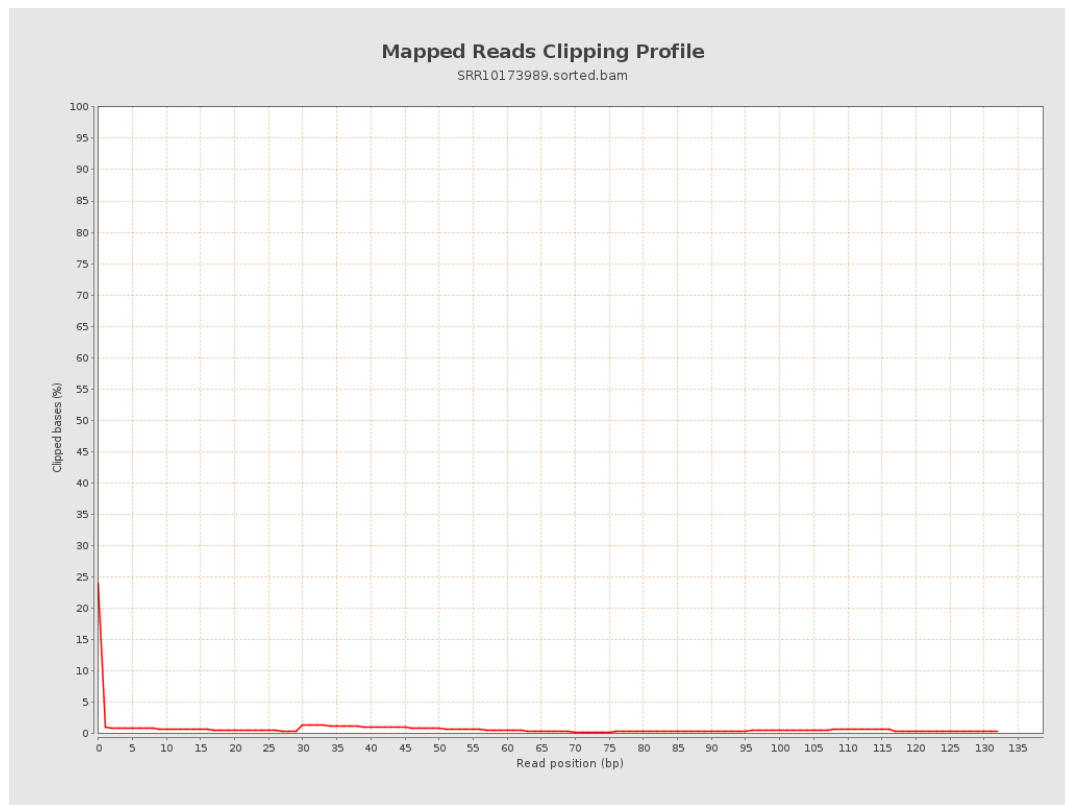
8. Results : Mapped Reads Nucleotide Content



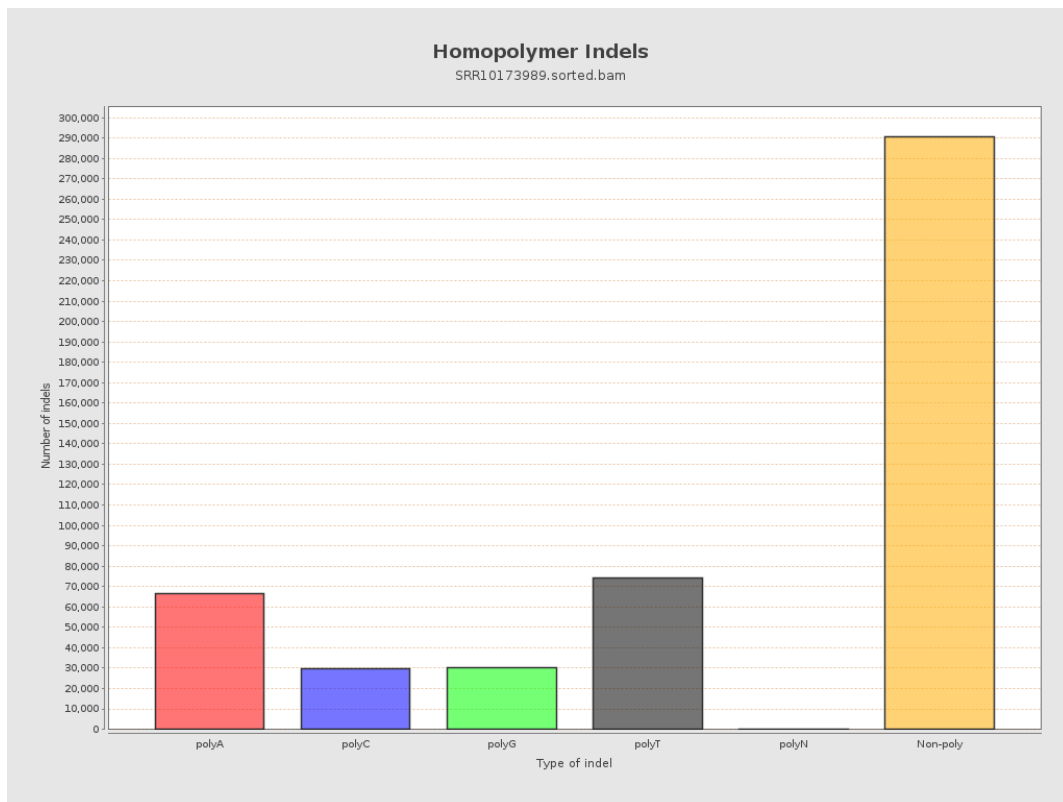
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



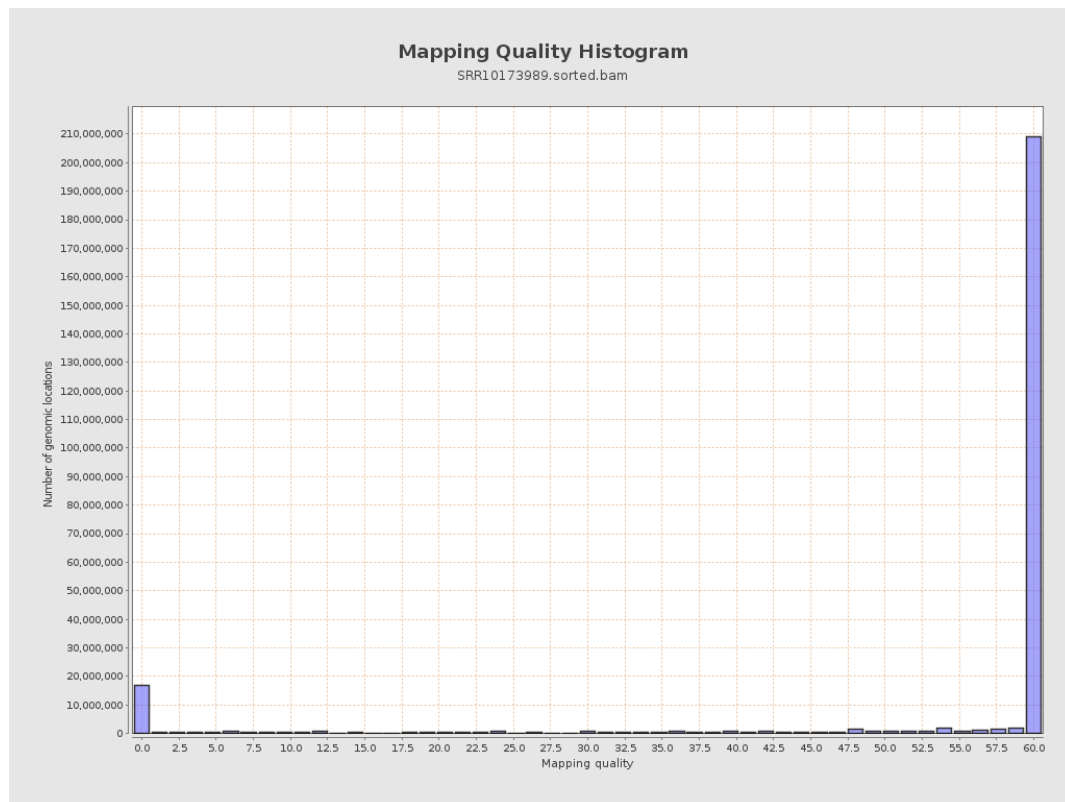
11. Results : Homopolymer Indels



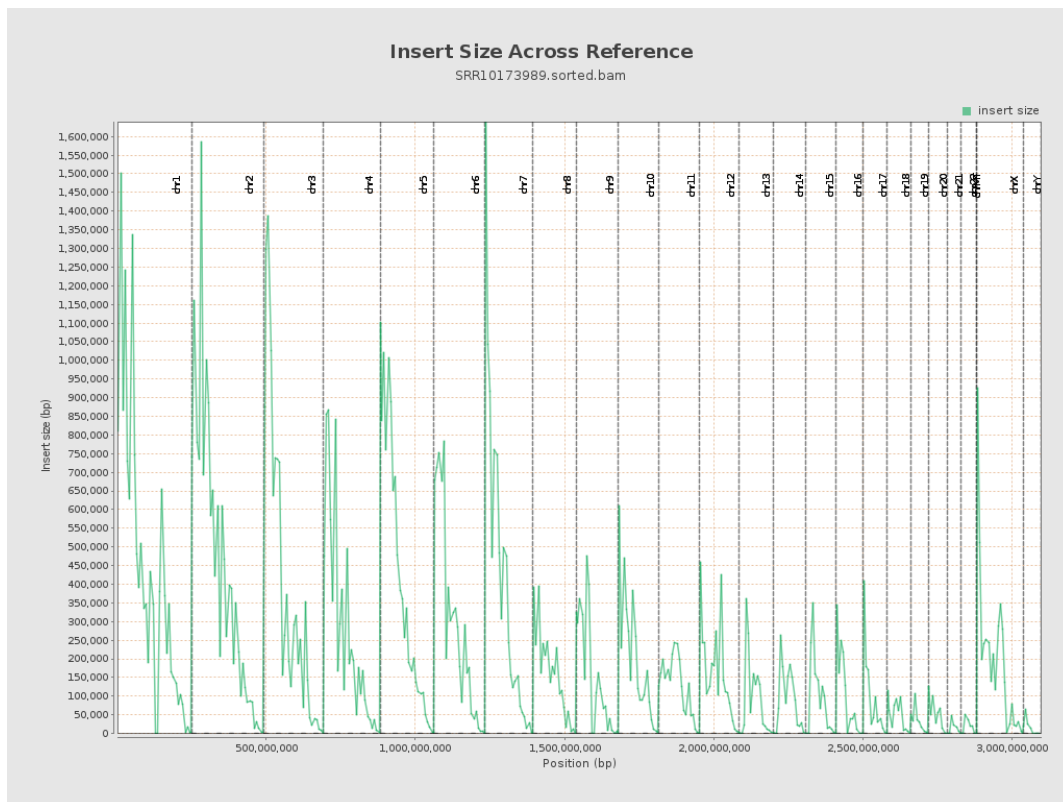
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

