

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 02:08:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173889.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_SRR10173889 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173889_1.fastq.gz SRR10173889_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 02:08:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173889.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,487,094
Mapped reads	6,329,460 / 97.57%
Unmapped reads	157,634 / 2.43%
Mapped paired reads	6,329,460 / 97.57%
Mapped reads, first in pair	3,168,996 / 48.85%
Mapped reads, second in pair	3,160,464 / 48.72%
Mapped reads, both in pair	6,225,812 / 95.97%
Mapped reads, singletons	103,648 / 1.6%
Secondary alignments	0
Supplementary alignments	658,991 / 10.16%
Read min/max/mean length	30 / 133 / 128.49
Duplicated reads (estimated)	5,157,360 / 79.5%
Duplication rate	66.79%
Clipped reads	2,561,563 / 39.49%

2.2. ACGT Content

Number/percentage of A's	222,213,706 / 29.58%
Number/percentage of C's	150,548,566 / 20.04%
Number/percentage of T's	221,985,551 / 29.55%
Number/percentage of G's	156,455,530 / 20.83%
Number/percentage of N's	8,377 / 0%

GC Percentage	40.87%
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2.3. Coverage

Mean	0.2428
Standard Deviation	3.2644

2.4. Mapping Quality

Mean Mapping Quality	52.7
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2.5. Insert size

Mean	1,001,464.51
Standard Deviation	9,024,482.11
P25/Median/P75	148 / 206 / 294

2.6. Mismatches and indels

General error rate	1.06%
Mismatches	7,796,642
Insertions	75,009
Mapped reads with at least one insertion	1.15%
Deletions	193,197
Mapped reads with at least one deletion	2.98%
Homopolymer indels	42.5%

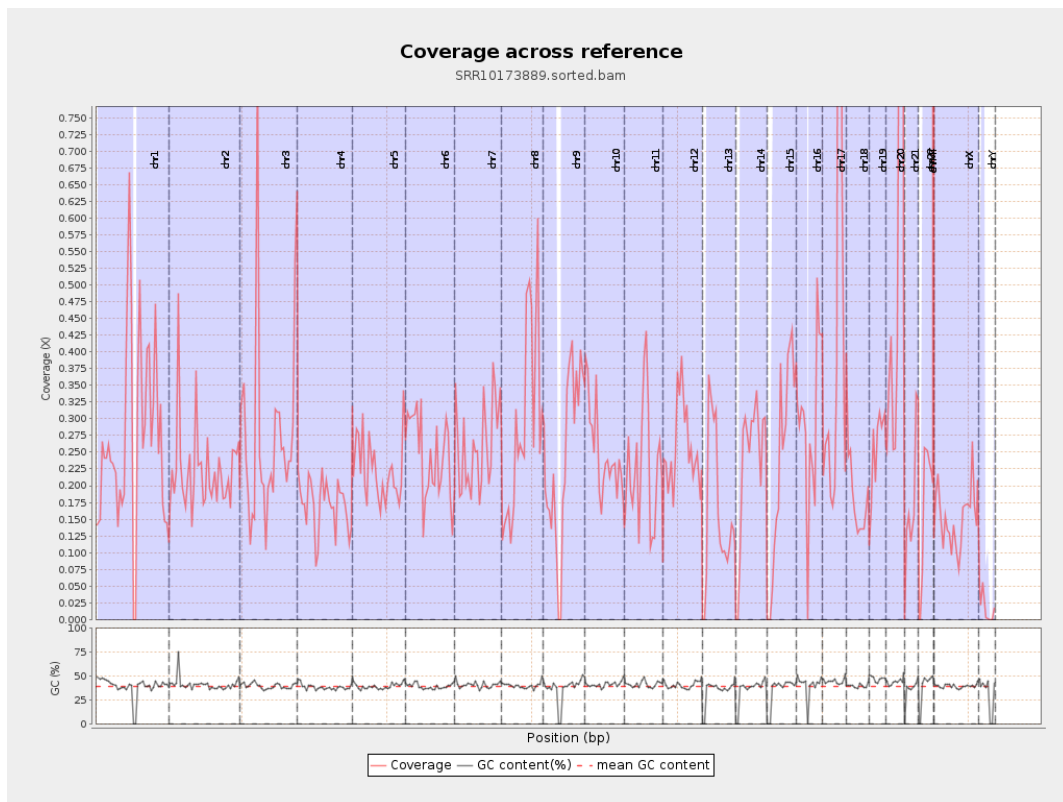
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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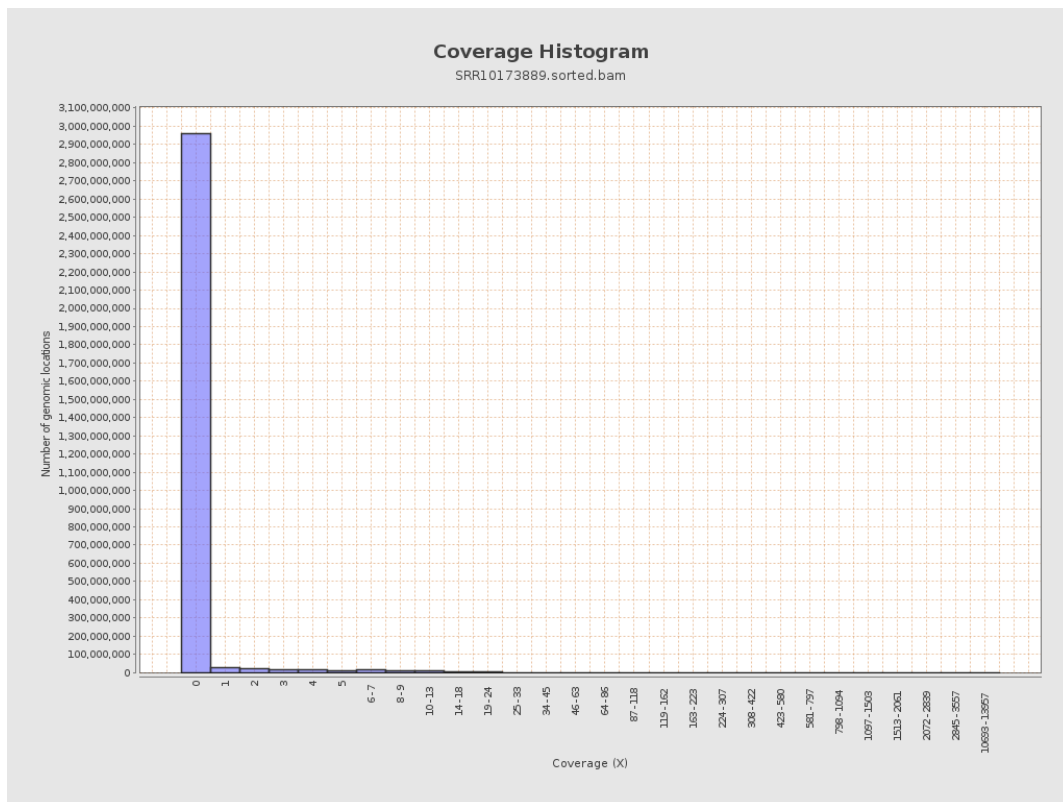
		bases	coverage	deviation
chr1	249250621	66299716	0.266	2.493
chr2	243199373	54327814	0.2234	9.7861
chr3	198022430	53296620	0.2691	1.625
chr4	191154276	32499854	0.17	1.3789
chr5	180915260	40547821	0.2241	1.4461
chr6	171115067	41791103	0.2442	1.8381
chr7	159138663	41078217	0.2581	2.0993
chr8	146364022	42320428	0.2891	1.8447
chr9	141213431	33637255	0.2382	1.9221
chr10	135534747	33801936	0.2494	2.3129
chr11	135006516	30694504	0.2274	1.5107
chr12	133851895	34471150	0.2575	1.5597
chr13	115169878	18286884	0.1588	1.2337
chr14	107349540	25176736	0.2345	1.4873
chr15	102531392	24277938	0.2368	1.4839
chr16	90354753	26667802	0.2951	1.8172
chr17	81195210	38528577	0.4745	2.47
chr18	78077248	14386853	0.1843	2.6683
chr19	59128983	15194576	0.257	1.9575
chr20	63025520	42117723	0.6683	2.8974
chr21	48129895	8587253	0.1784	1.308
chr22	51304566	8407634	0.1639	1.1723
chrMT	16571	813577	49.0964	42.4175
chrX	155270560	23464486	0.1511	1.1832

chrY	59373566	1001967	0.0169	0.5807
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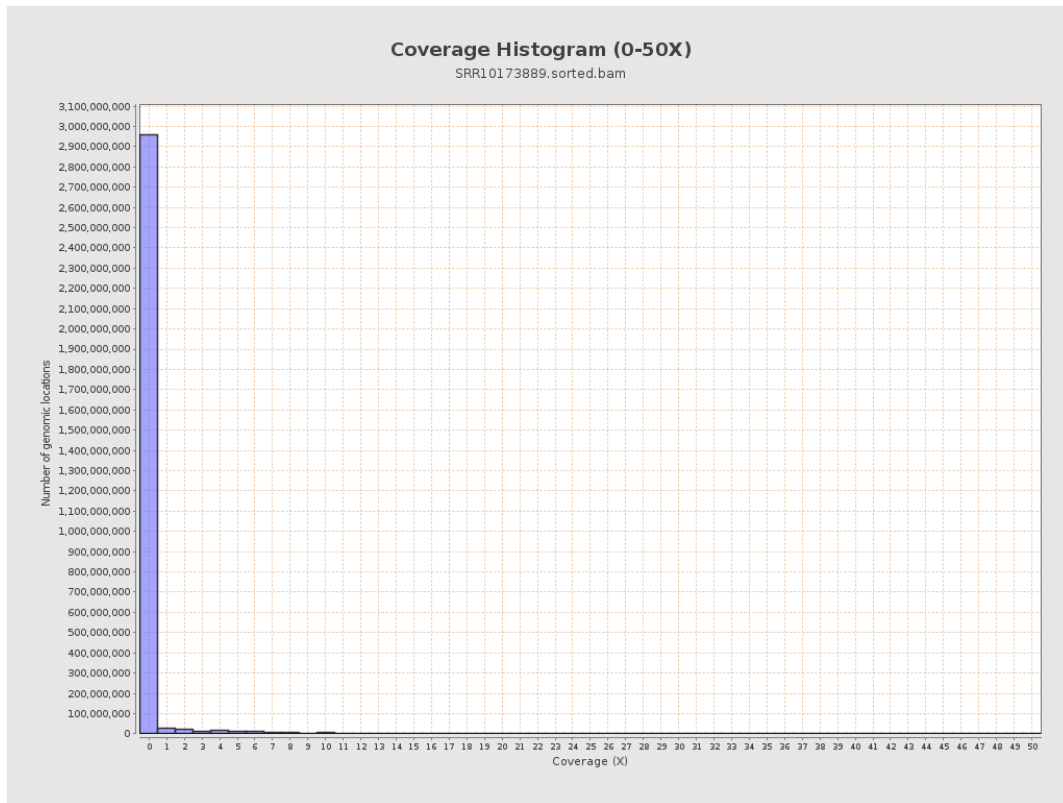
3. Results : Coverage across reference



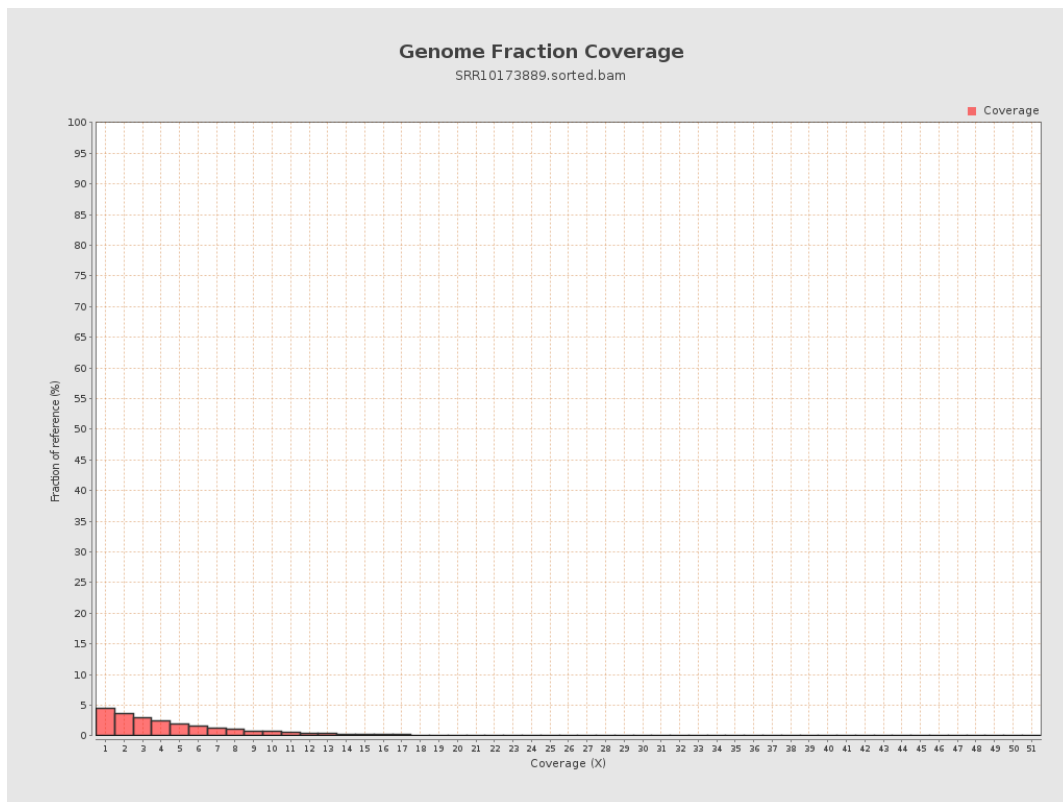
4. Results : Coverage Histogram



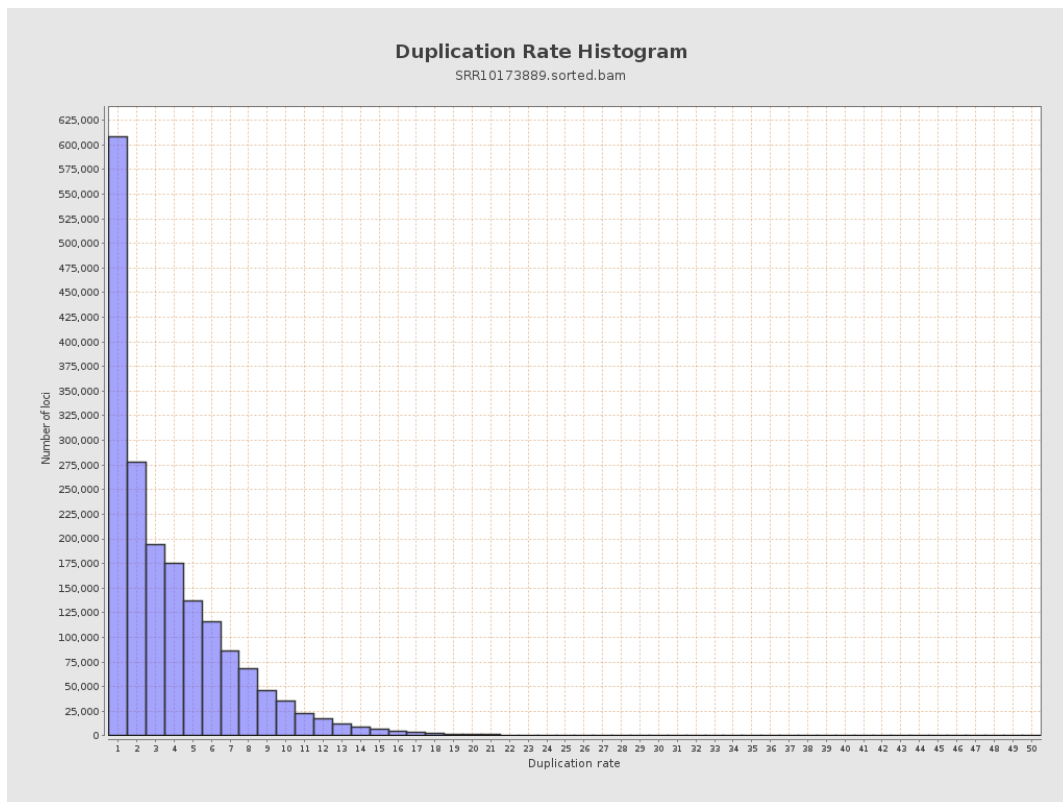
5. Results : Coverage Histogram (0-50X)



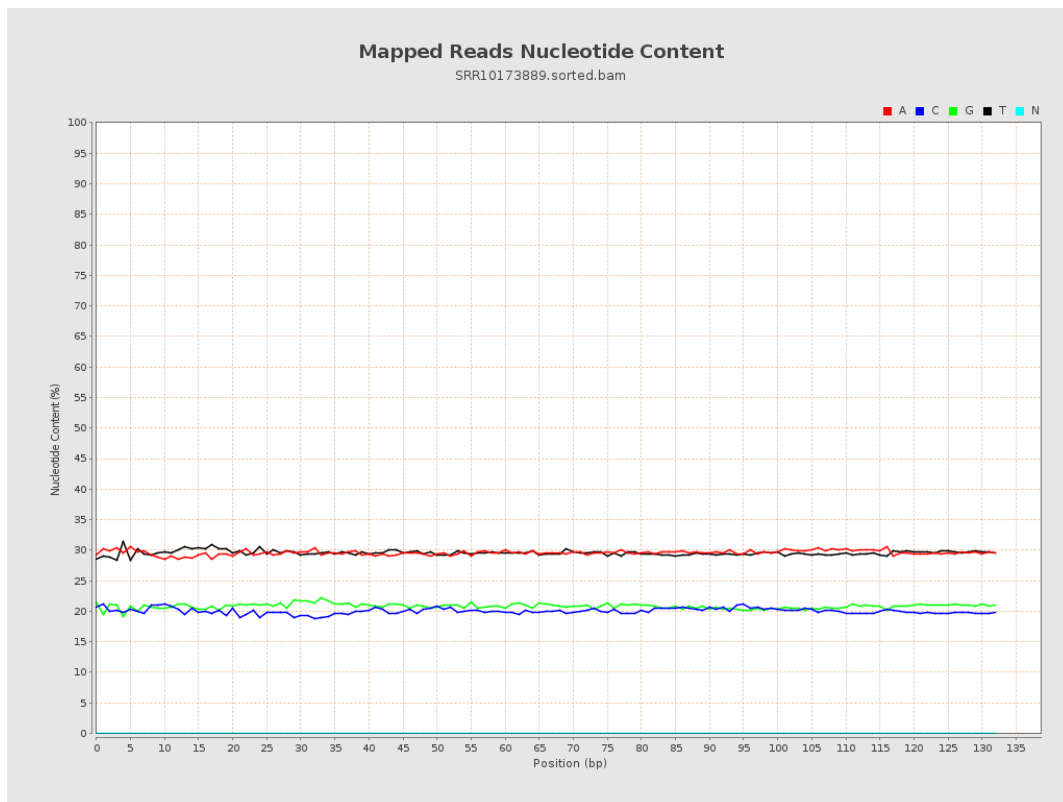
6. Results : Genome Fraction Coverage



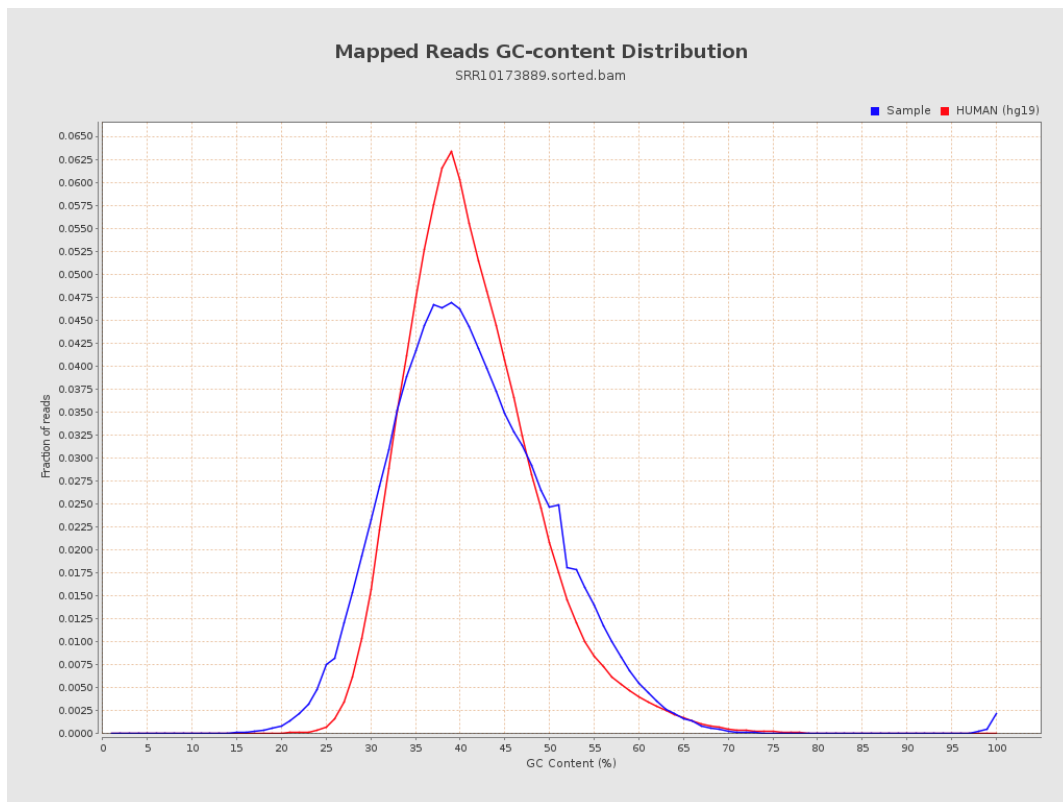
7. Results : Duplication Rate Histogram



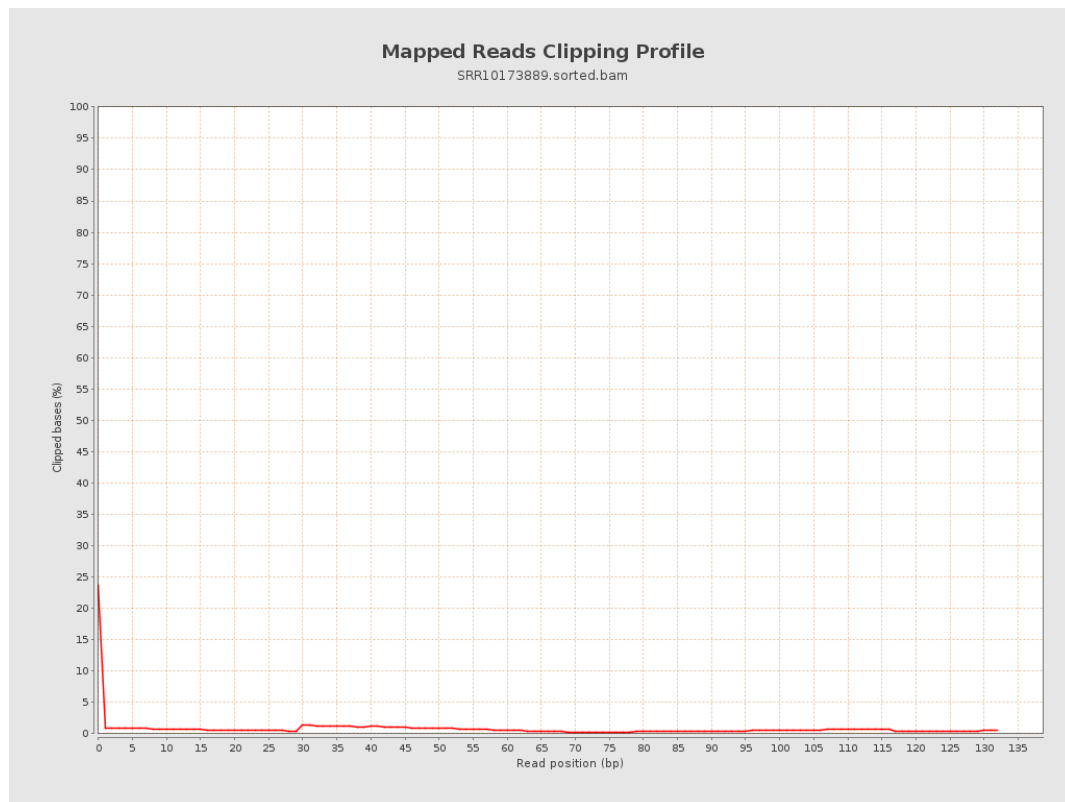
8. Results : Mapped Reads Nucleotide Content



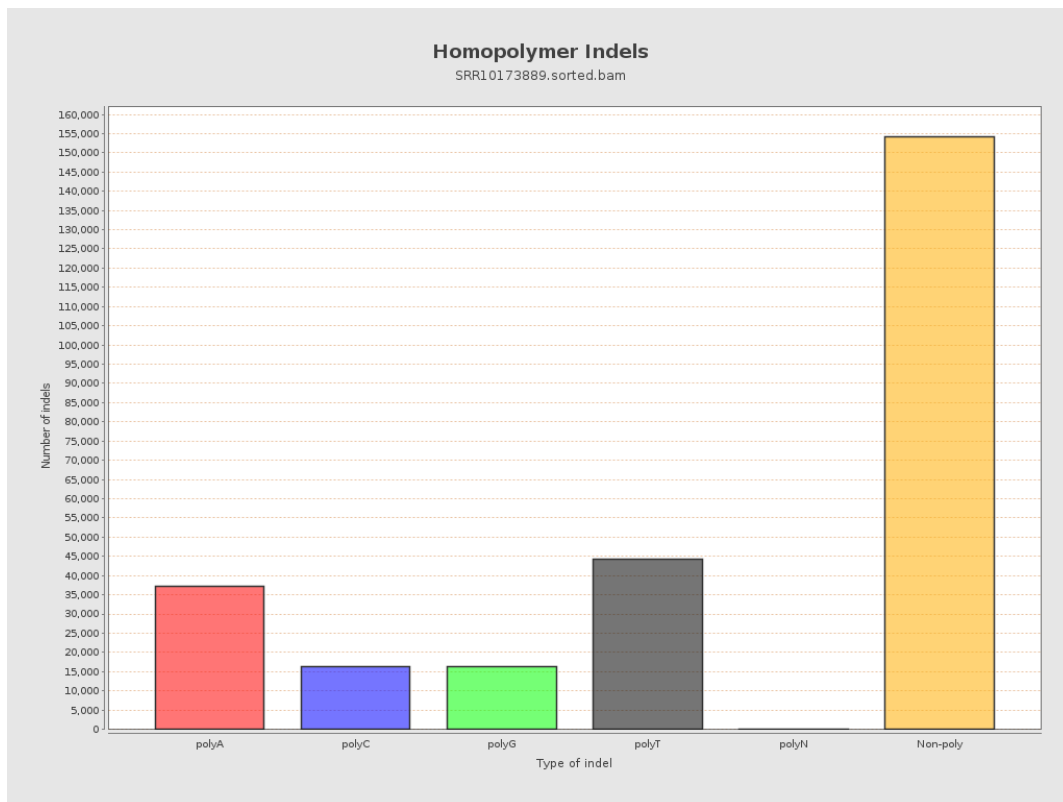
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



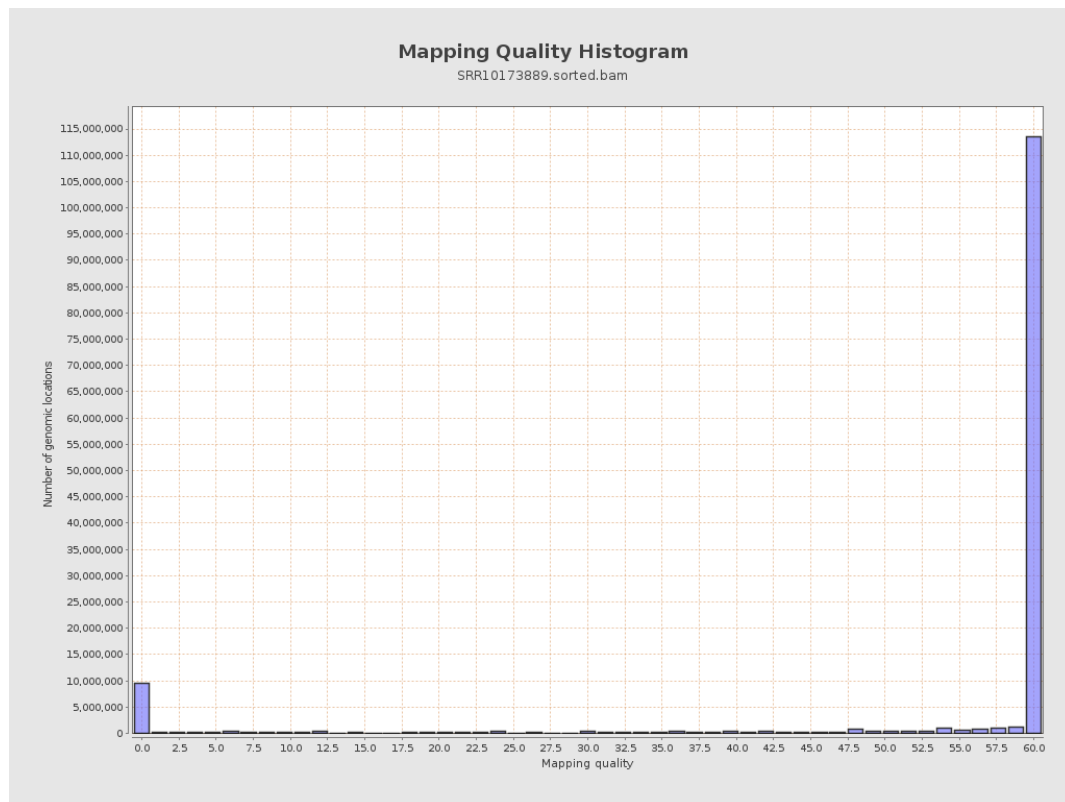
11. Results : Homopolymer Indels



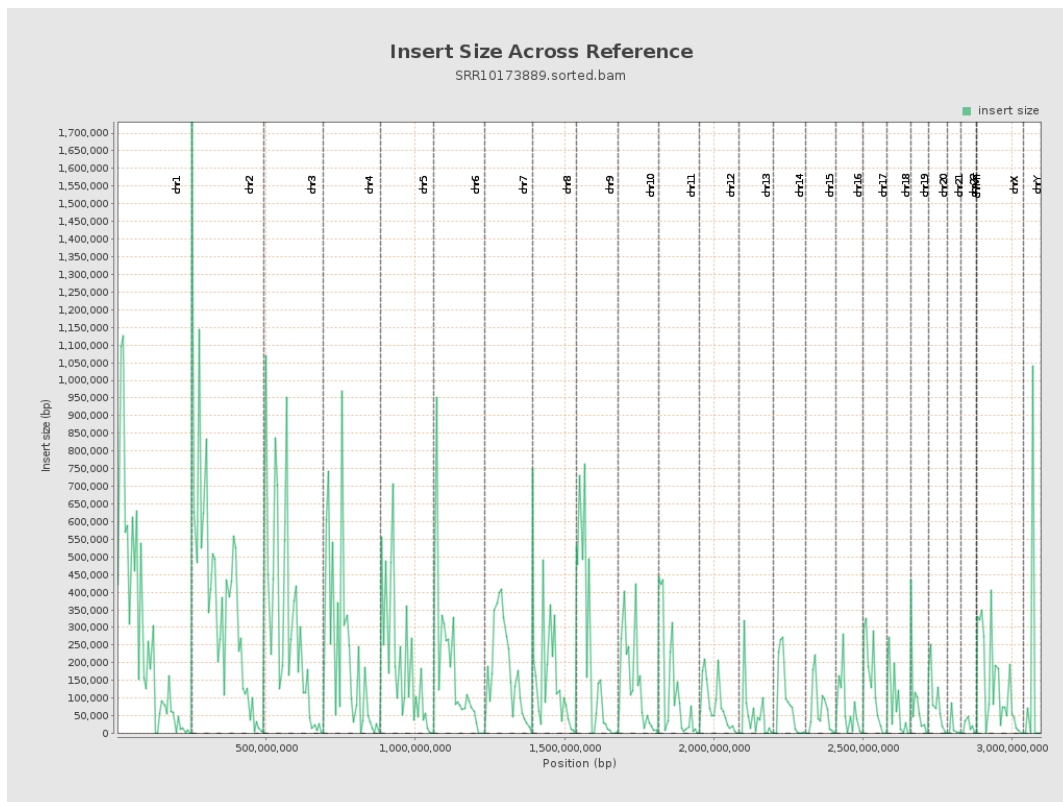
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

