

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 02:00:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173888.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_SRR10173888 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173888_1.fastq.gz SRR10173888_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 02:00:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173888.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,278,166
Mapped reads	2,219,075 / 97.41%
Unmapped reads	59,091 / 2.59%
Mapped paired reads	2,219,075 / 97.41%
Mapped reads, first in pair	1,111,746 / 48.8%
Mapped reads, second in pair	1,107,329 / 48.61%
Mapped reads, both in pair	2,179,914 / 95.69%
Mapped reads, singletons	39,161 / 1.72%
Secondary alignments	0
Supplementary alignments	225,955 / 9.92%
Read min/max/mean length	30 / 133 / 128.39
Duplicated reads (estimated)	1,780,570 / 78.16%
Duplication rate	65.41%
Clipped reads	884,907 / 38.84%

2.2. ACGT Content

Number/percentage of A's	79,355,871 / 30.19%
Number/percentage of C's	51,201,877 / 19.48%
Number/percentage of T's	79,186,381 / 30.13%
Number/percentage of G's	53,087,536 / 20.2%
Number/percentage of N's	2,949 / 0%

GC Percentage	39.68%
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2.3. Coverage

Mean	0.085
Standard Deviation	1.3852

2.4. Mapping Quality

Mean Mapping Quality	52.83
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2.5. Insert size

Mean	1,189,302.75
Standard Deviation	9,974,636.18
P25/Median/P75	149 / 209 / 300

2.6. Mismatches and indels

General error rate	1.12%
Mismatches	2,852,693
Insertions	30,020
Mapped reads with at least one insertion	1.31%
Deletions	61,433
Mapped reads with at least one deletion	2.7%
Homopolymer indels	43.39%

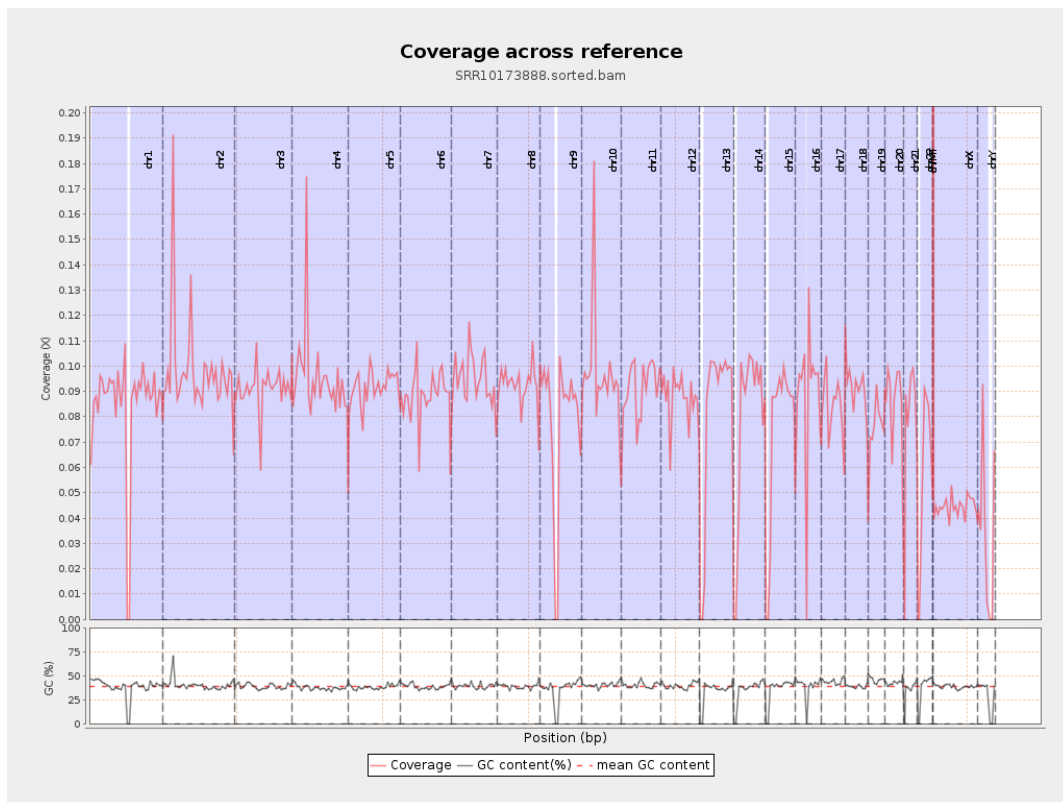
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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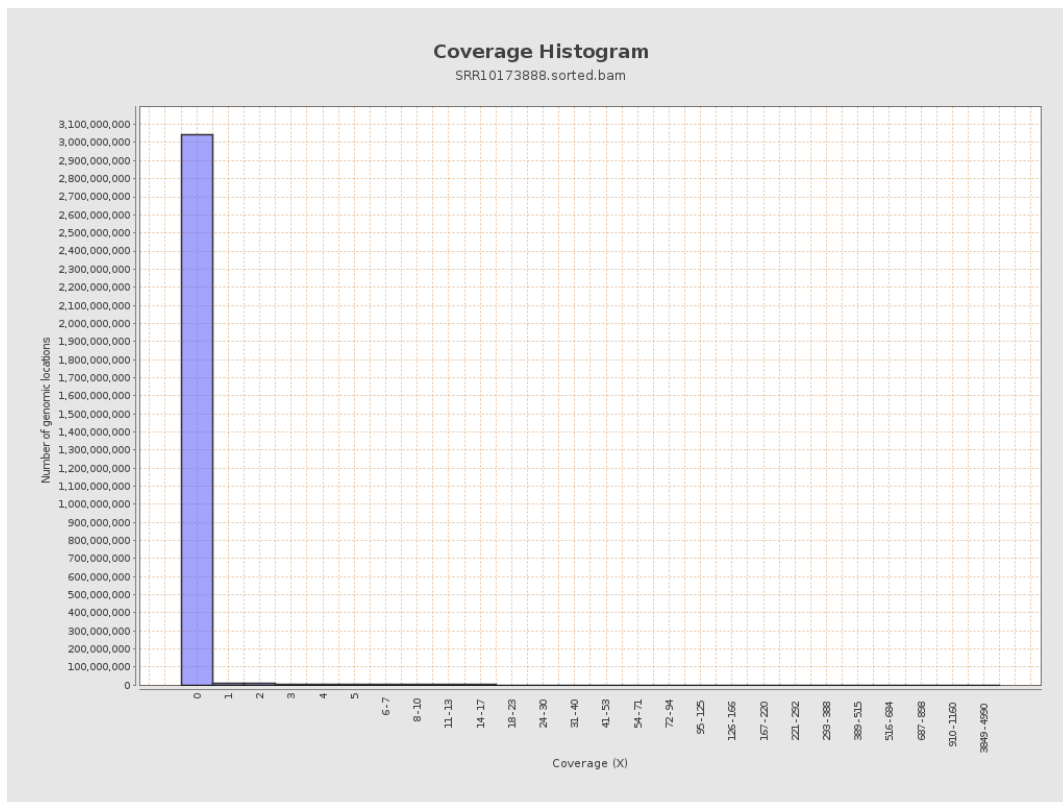
		bases	coverage	deviation
chr1	249250621	21021897	0.0843	1.1003
chr2	243199373	23824447	0.098	3.5805
chr3	198022430	18024669	0.091	0.9097
chr4	191154276	18252049	0.0955	1.124
chr5	180915260	16544788	0.0915	0.9151
chr6	171115067	15161622	0.0886	0.9398
chr7	159138663	15058006	0.0946	1.1214
chr8	146364022	13522876	0.0924	1.2297
chr9	141213431	11093253	0.0786	1.1091
chr10	135534747	13178738	0.0972	1.2304
chr11	135006516	12312604	0.0912	0.9165
chr12	133851895	11724839	0.0876	0.886
chr13	115169878	9321767	0.0809	0.8602
chr14	107349540	8571994	0.0799	0.8491
chr15	102531392	7471203	0.0729	0.8152
chr16	90354753	7834341	0.0867	1.0017
chr17	81195210	6895870	0.0849	0.8914
chr18	78077248	7180563	0.092	1.2777
chr19	59128983	4552656	0.077	0.9453
chr20	63025520	5461079	0.0866	0.9034
chr21	48129895	3805790	0.0791	0.9952
chr22	51304566	2939278	0.0573	0.7394
chrMT	16571	251213	15.1598	15.697
chrX	155270560	6899744	0.0444	0.6314

chrY	59373566	2084794	0.0351	0.7102
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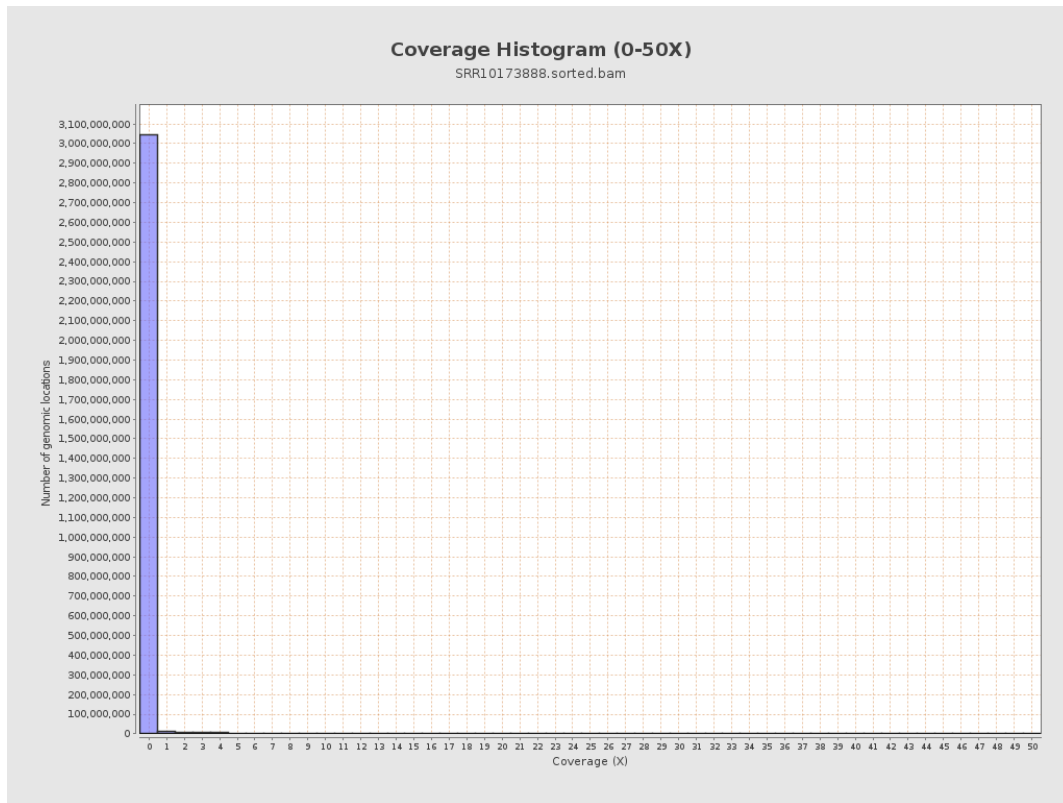
3. Results : Coverage across reference



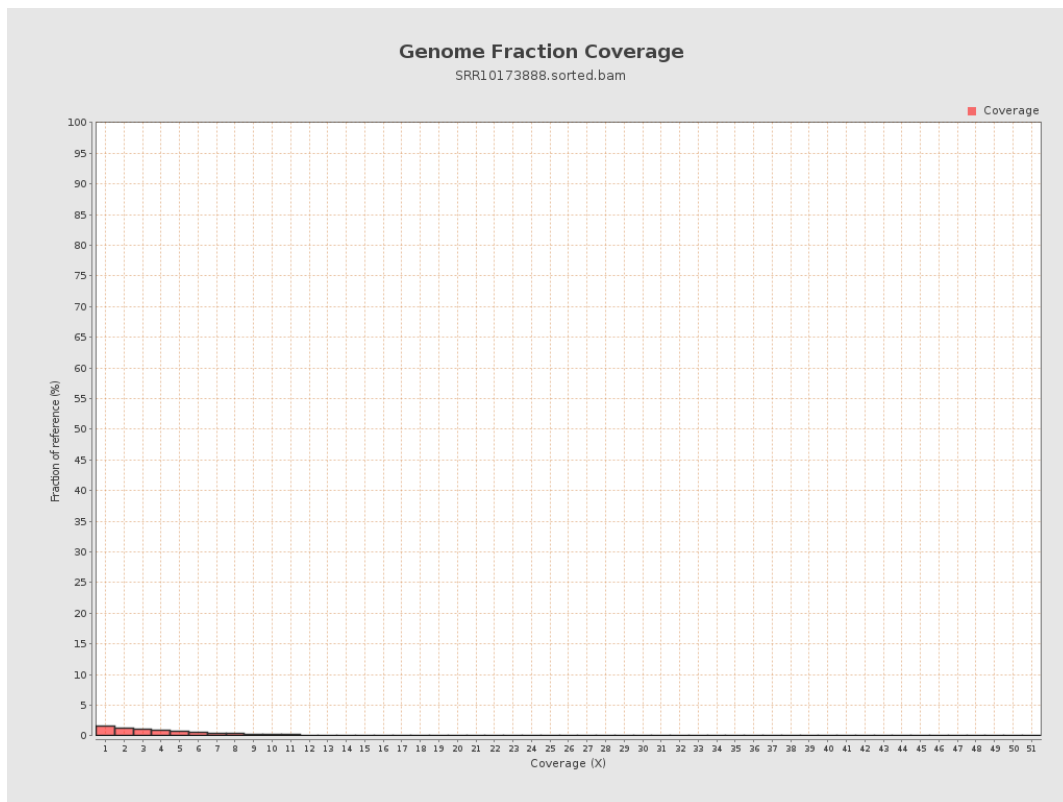
4. Results : Coverage Histogram



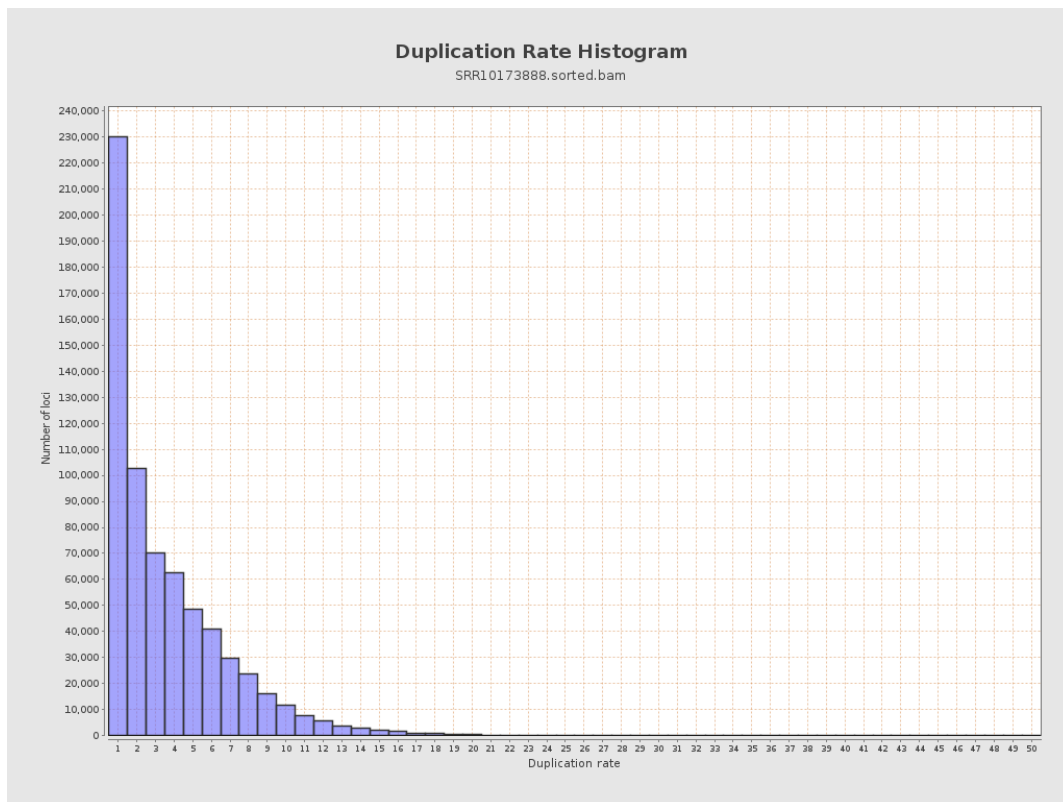
5. Results : Coverage Histogram (0-50X)



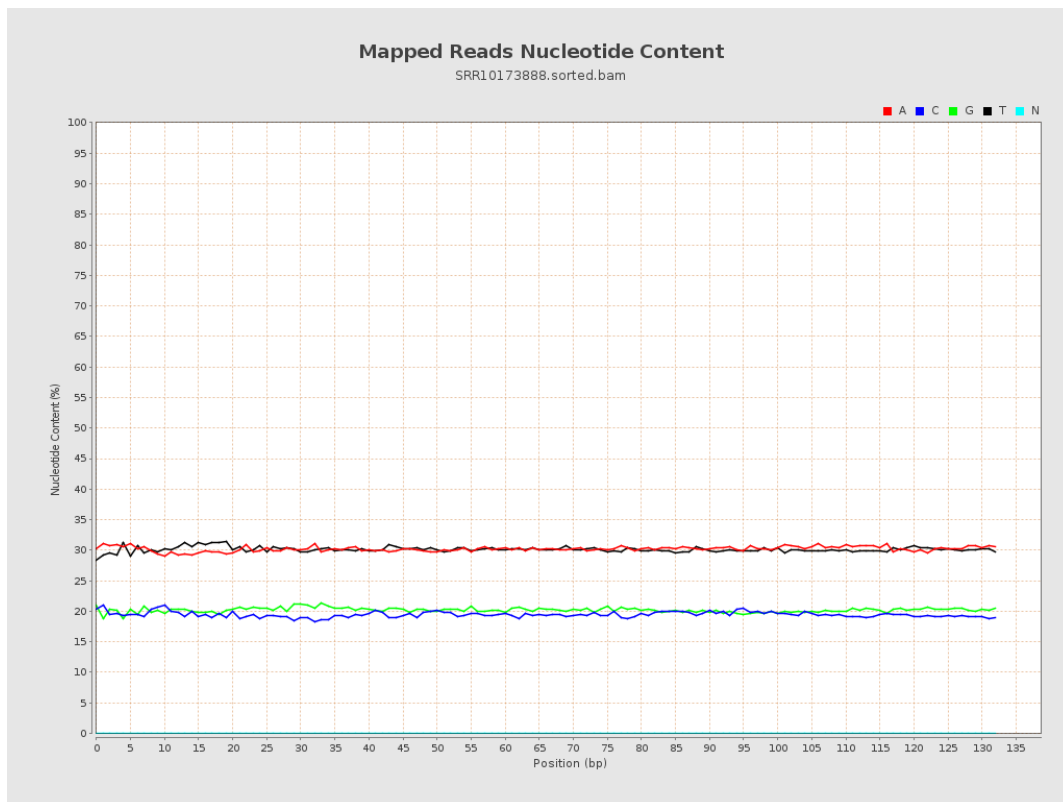
6. Results : Genome Fraction Coverage



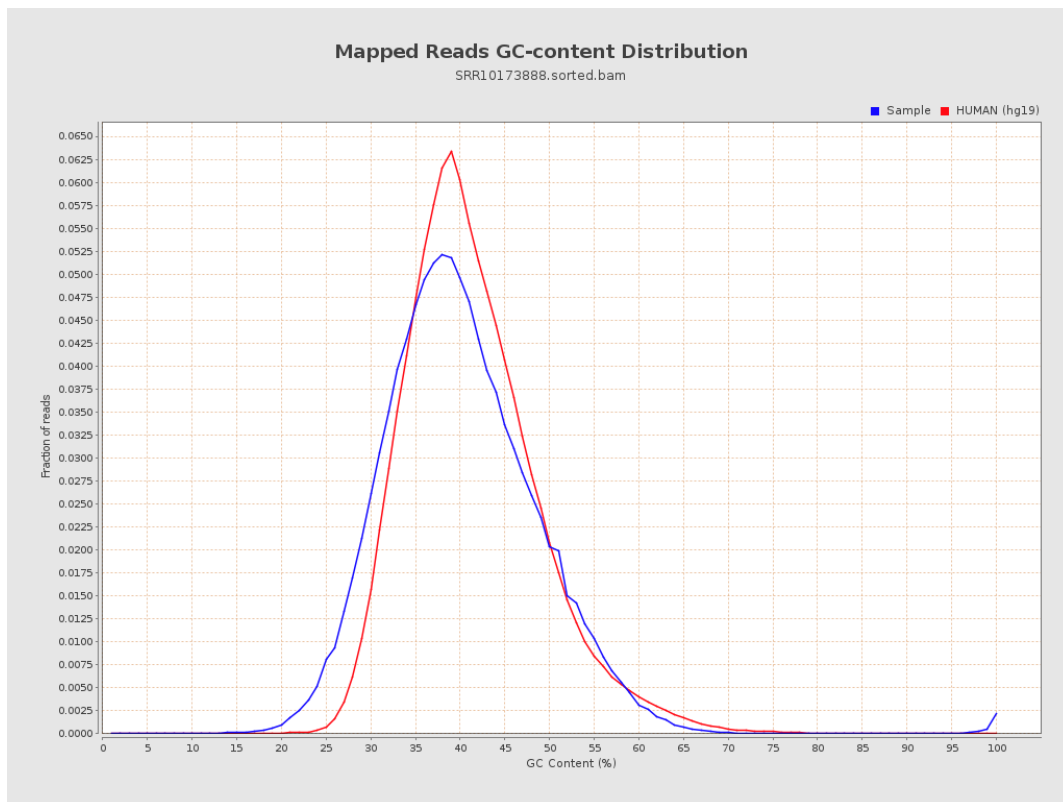
7. Results : Duplication Rate Histogram



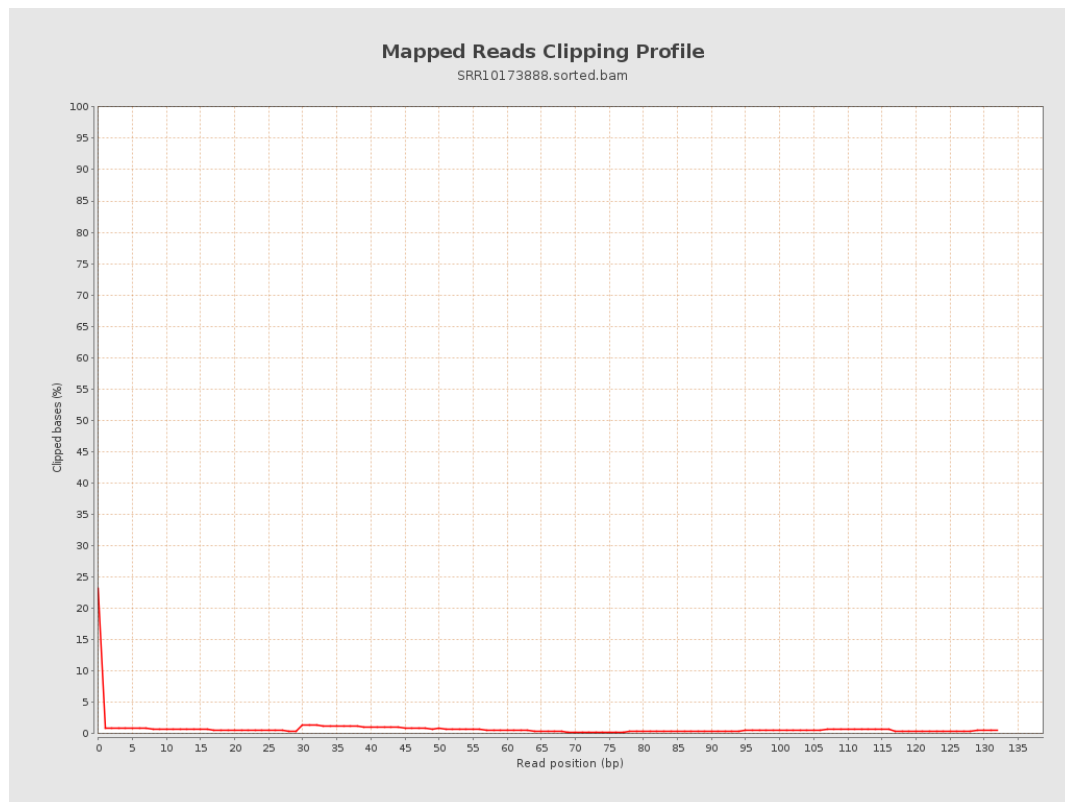
8. Results : Mapped Reads Nucleotide Content



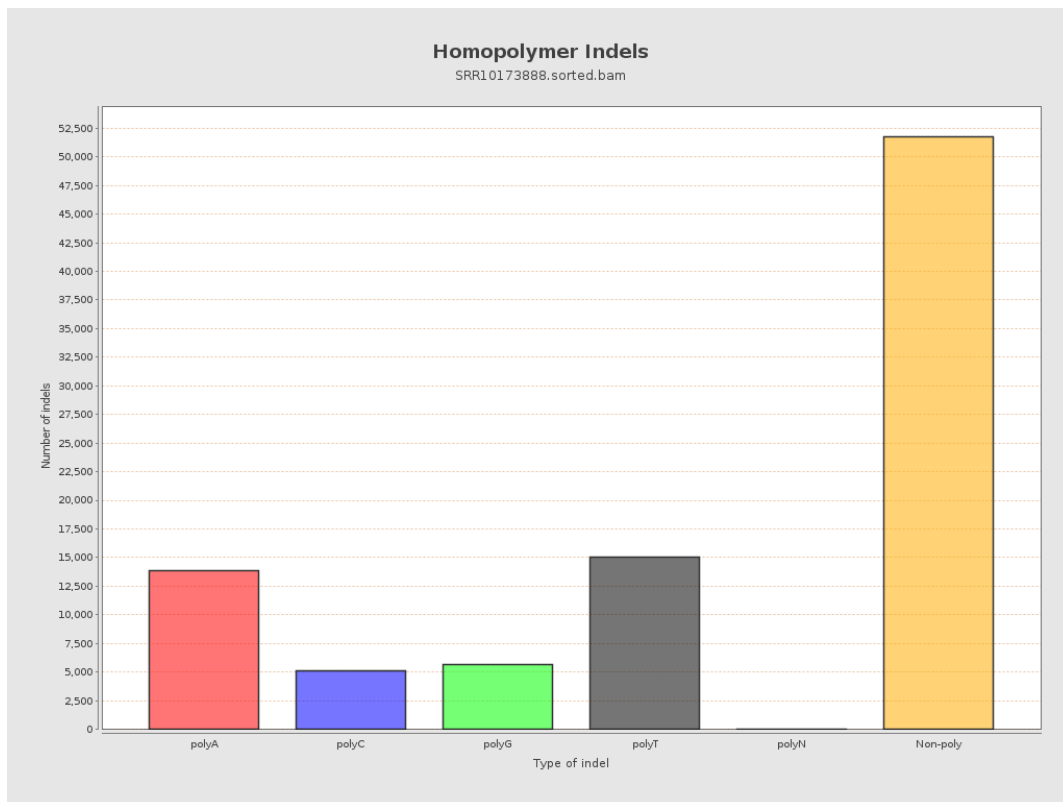
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



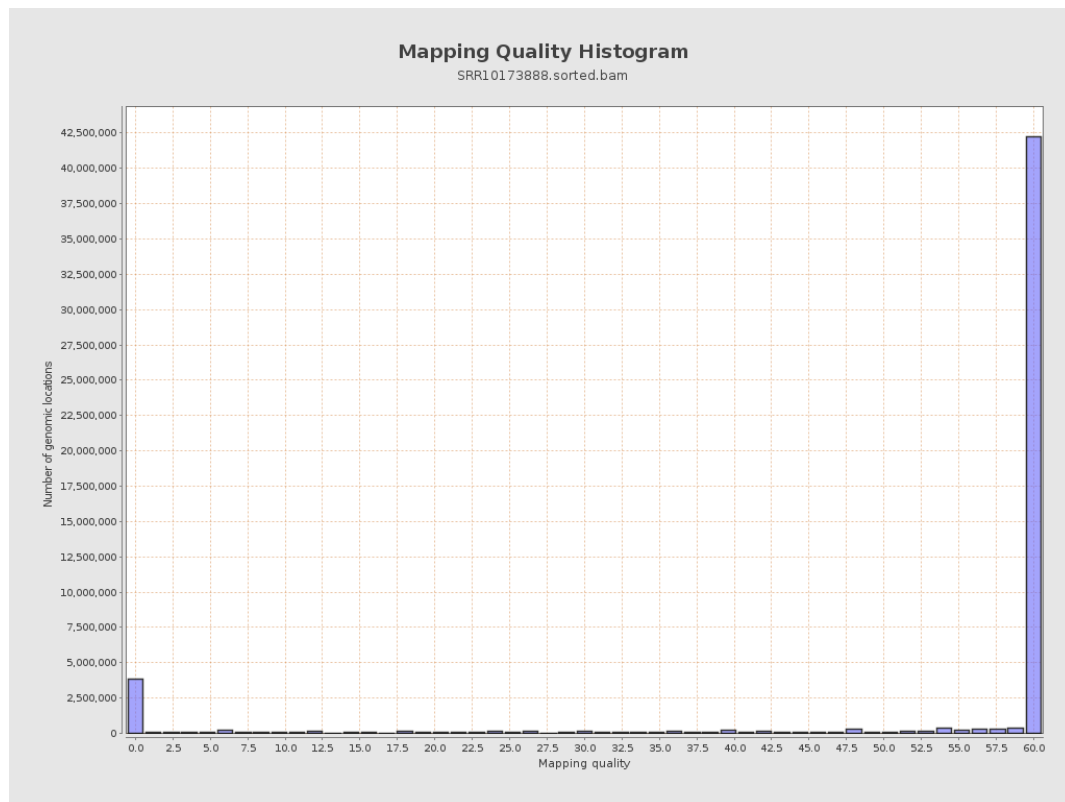
11. Results : Homopolymer Indels



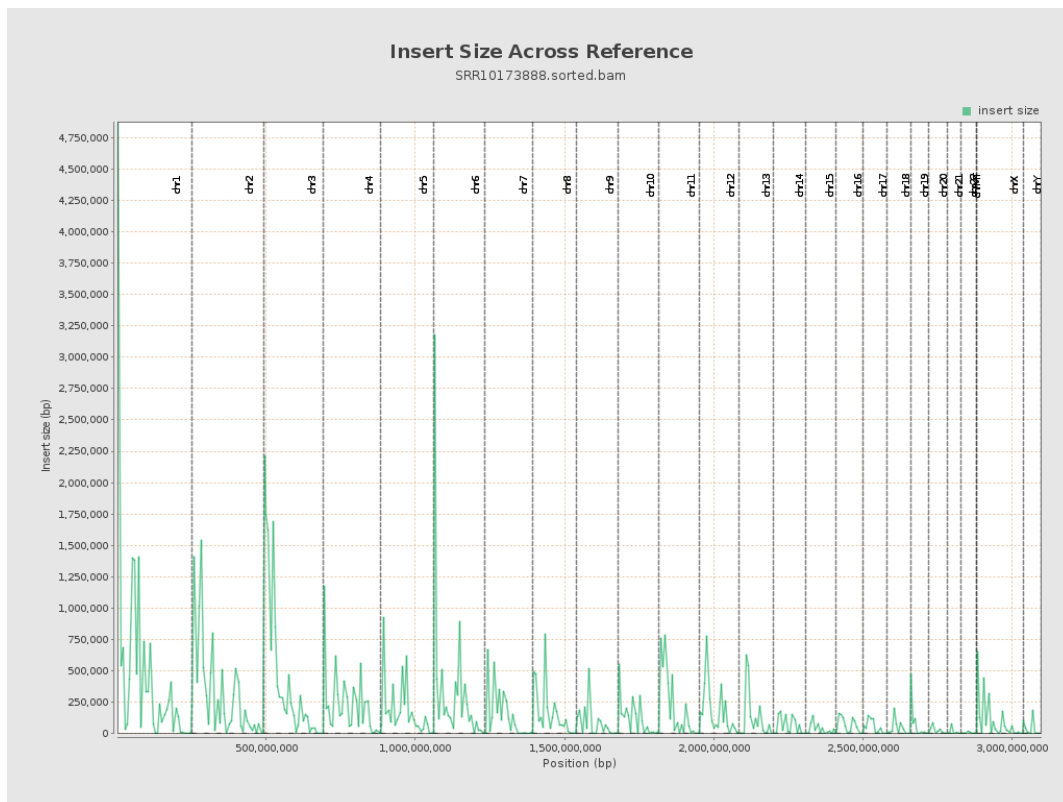
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

