

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 17:27:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173988.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_SRR10173988 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173988_1.fastq.gz SRR10173988_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 17:27:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173988.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,664,012
Mapped reads	10,439,499 / 97.89%
Unmapped reads	224,513 / 2.11%
Mapped paired reads	10,439,499 / 97.89%
Mapped reads, first in pair	5,221,154 / 48.96%
Mapped reads, second in pair	5,218,345 / 48.93%
Mapped reads, both in pair	10,292,716 / 96.52%
Mapped reads, singletons	146,783 / 1.38%
Secondary alignments	0
Supplementary alignments	1,422,973 / 13.34%
Read min/max/mean length	30 / 133 / 125.62
Duplicated reads (estimated)	8,412,499 / 78.89%
Duplication rate	64.59%
Clipped reads	5,380,346 / 50.45%

2.2. ACGT Content

Number/percentage of A's	353,331,151 / 29.84%
Number/percentage of C's	235,536,906 / 19.9%
Number/percentage of T's	350,471,938 / 29.6%
Number/percentage of G's	244,548,482 / 20.66%
Number/percentage of N's	9,326 / 0%

GC Percentage	40.55%
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2.3. Coverage

Mean	0.3827
Standard Deviation	6.4255

2.4. Mapping Quality

Mean Mapping Quality	52.58
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2.5. Insert size

Mean	1,084,367.29
Standard Deviation	9,594,124.83
P25/Median/P75	105 / 153 / 235

2.6. Mismatches and indels

General error rate	0.86%
Mismatches	9,806,942
Insertions	131,223
Mapped reads with at least one insertion	1.21%
Deletions	333,138
Mapped reads with at least one deletion	3.11%
Homopolymer indels	41.34%

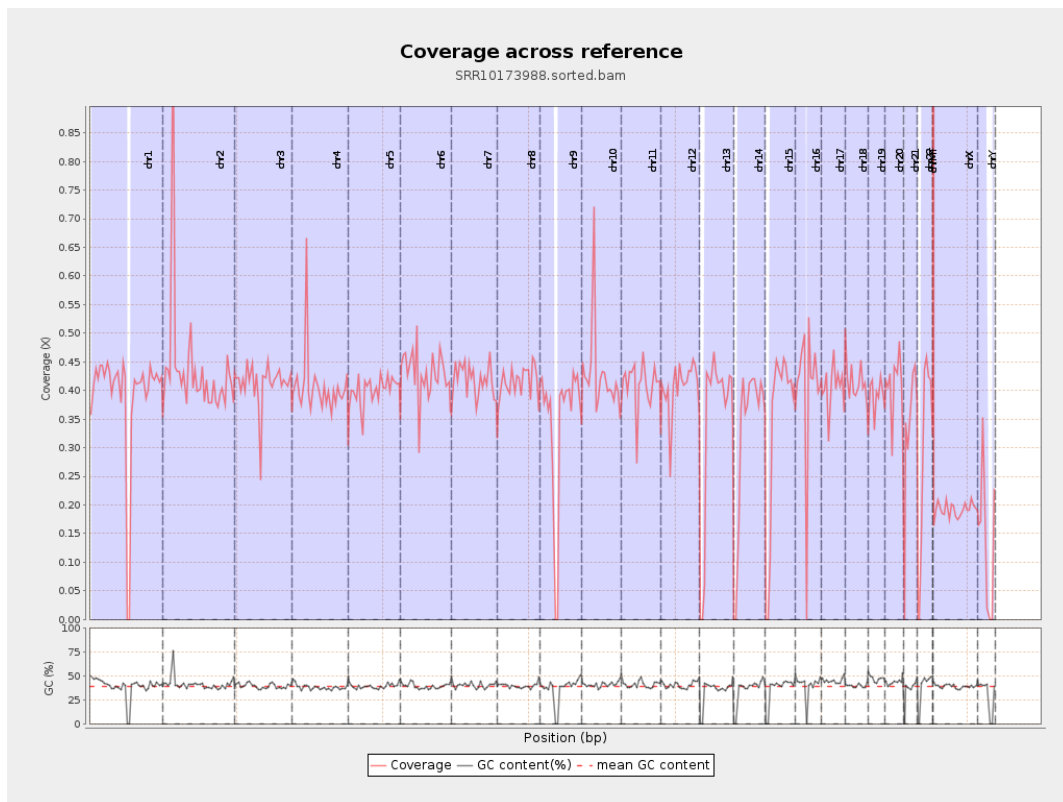
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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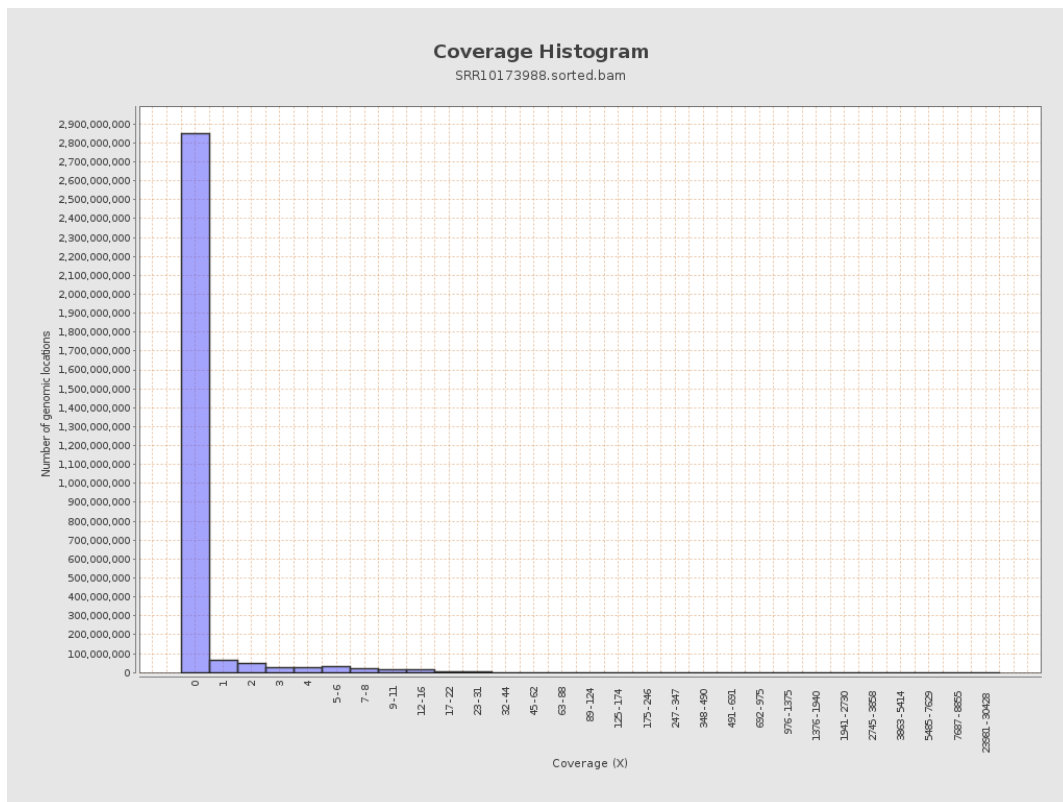
		bases	coverage	deviation
chr1	249250621	97570963	0.3915	2.8918
chr2	243199373	105834216	0.4352	21.2222
chr3	198022430	81535512	0.4117	1.9728
chr4	191154276	77787774	0.4069	2.836
chr5	180915260	72264969	0.3994	1.9234
chr6	171115067	73505214	0.4296	2.3318
chr7	159138663	66400187	0.4172	2.7722
chr8	146364022	60791474	0.4153	3.5498
chr9	141213431	48736639	0.3451	2.6099
chr10	135534747	57724211	0.4259	3.7538
chr11	135006516	55301759	0.4096	2.0547
chr12	133851895	54693752	0.4086	2.0687
chr13	115169878	40007974	0.3474	1.8148
chr14	107349540	35410820	0.3299	1.7822
chr15	102531392	34733829	0.3388	1.8699
chr16	90354753	36351931	0.4023	2.6326
chr17	81195210	33042251	0.4069	2.1389
chr18	78077248	32375254	0.4147	3.5499
chr19	59128983	23014122	0.3892	2.4855
chr20	63025520	25822680	0.4097	2.0811
chr21	48129895	16496968	0.3428	2.574
chr22	51304566	15149716	0.2953	2.219
chrMT	16571	1969140	118.8305	98.2813
chrX	155270560	29797934	0.1919	1.3469

chrY	59373566	8387538	0.1413	2.0412
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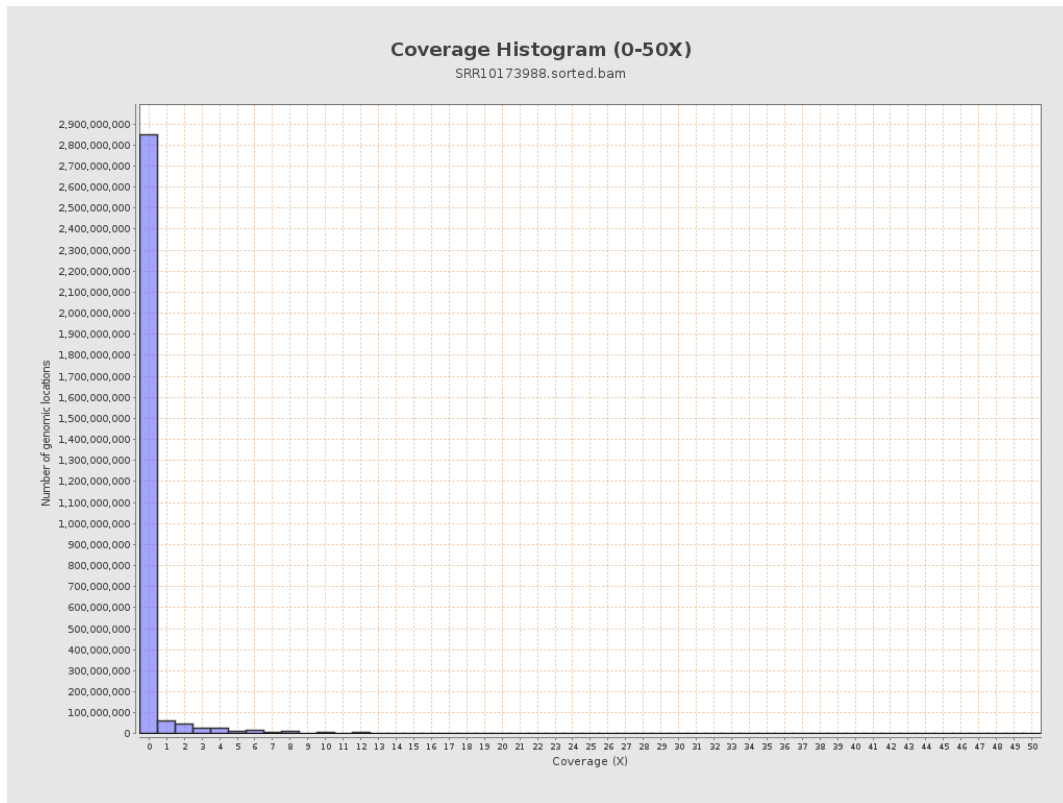
3. Results : Coverage across reference



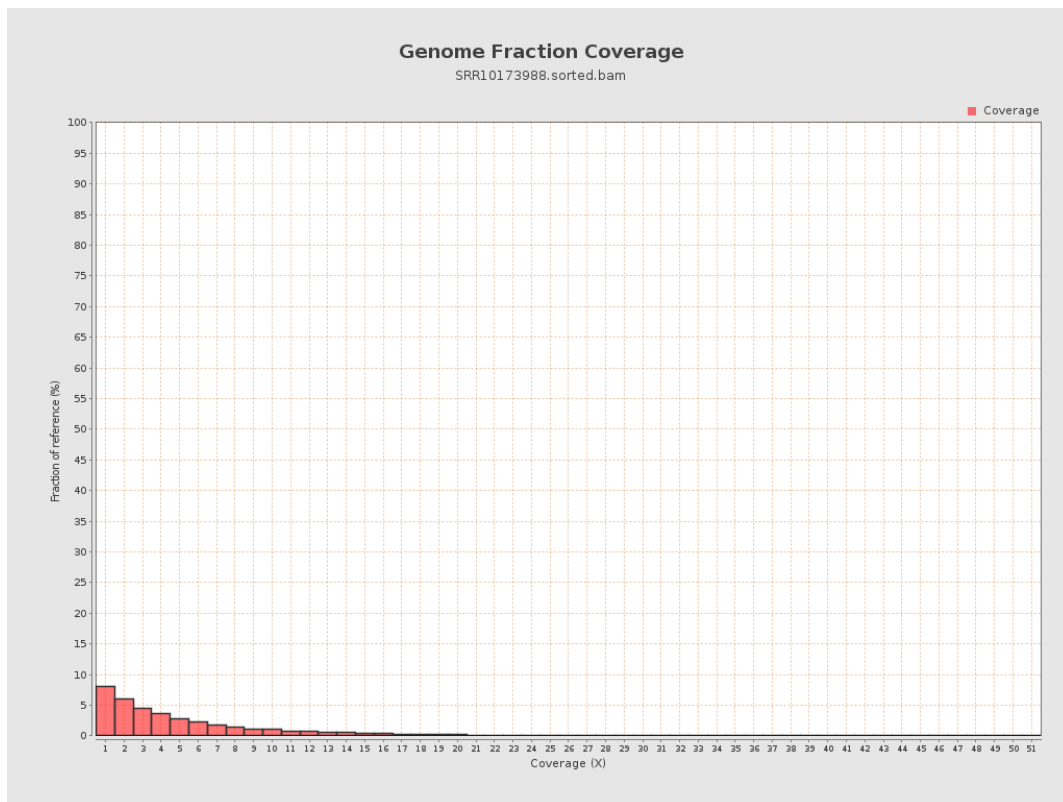
4. Results : Coverage Histogram



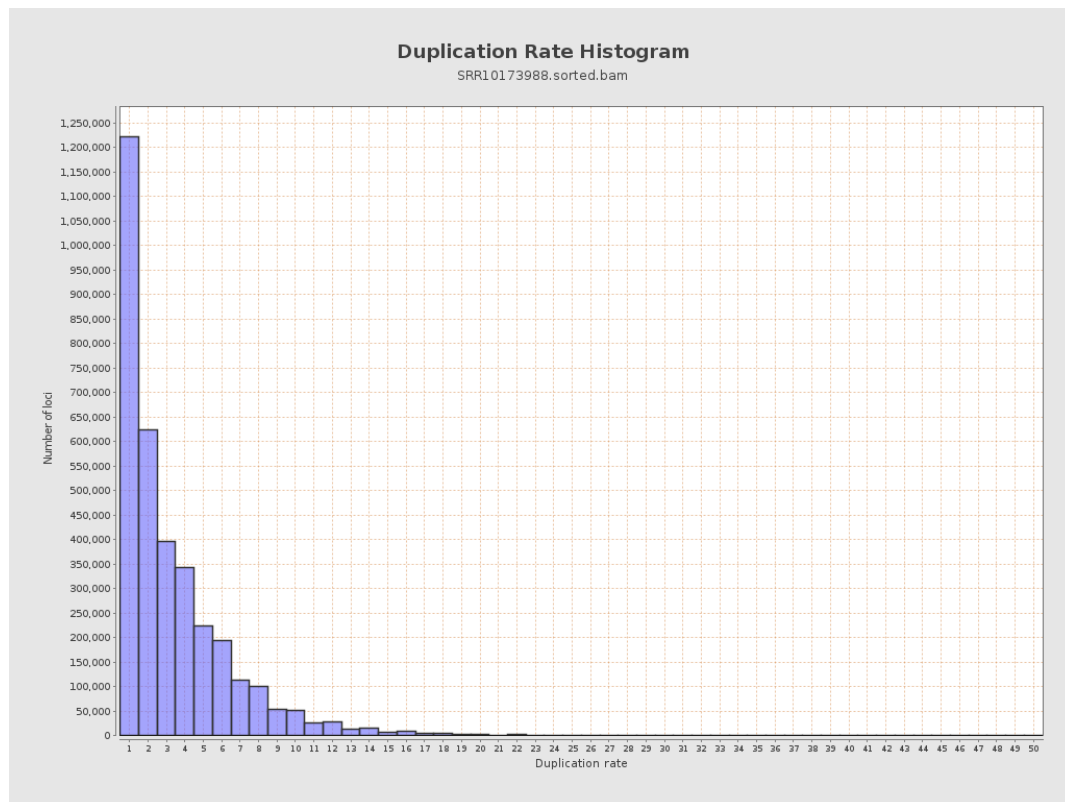
5. Results : Coverage Histogram (0-50X)



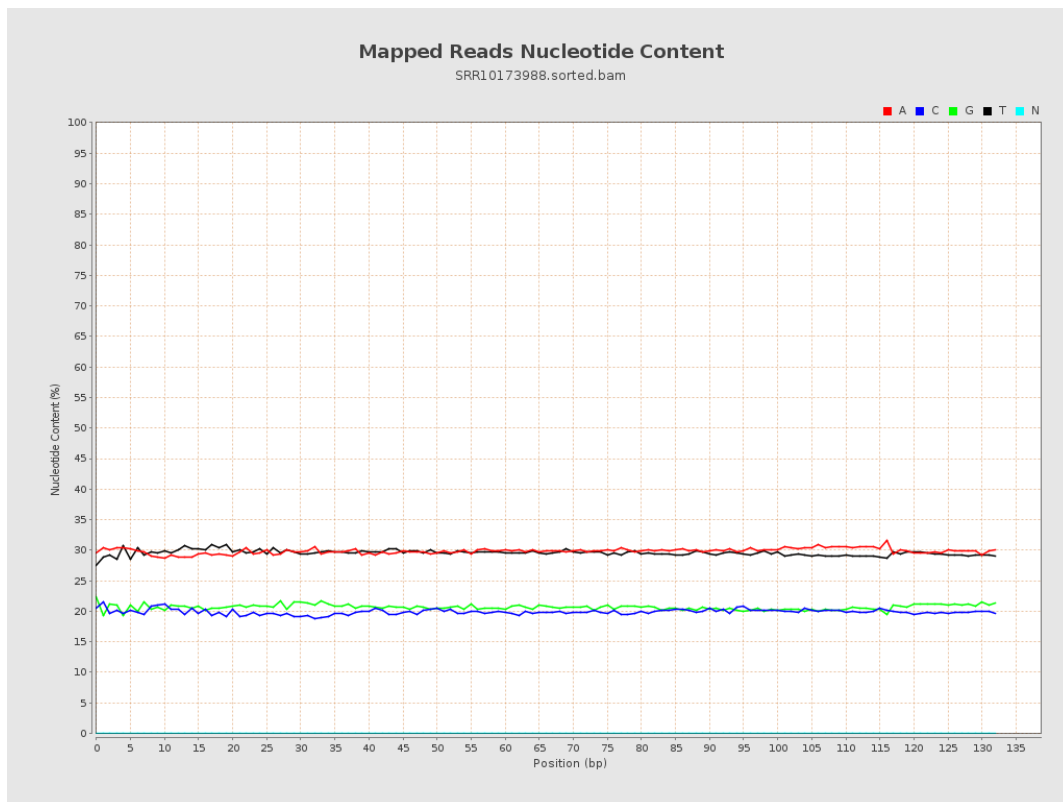
6. Results : Genome Fraction Coverage



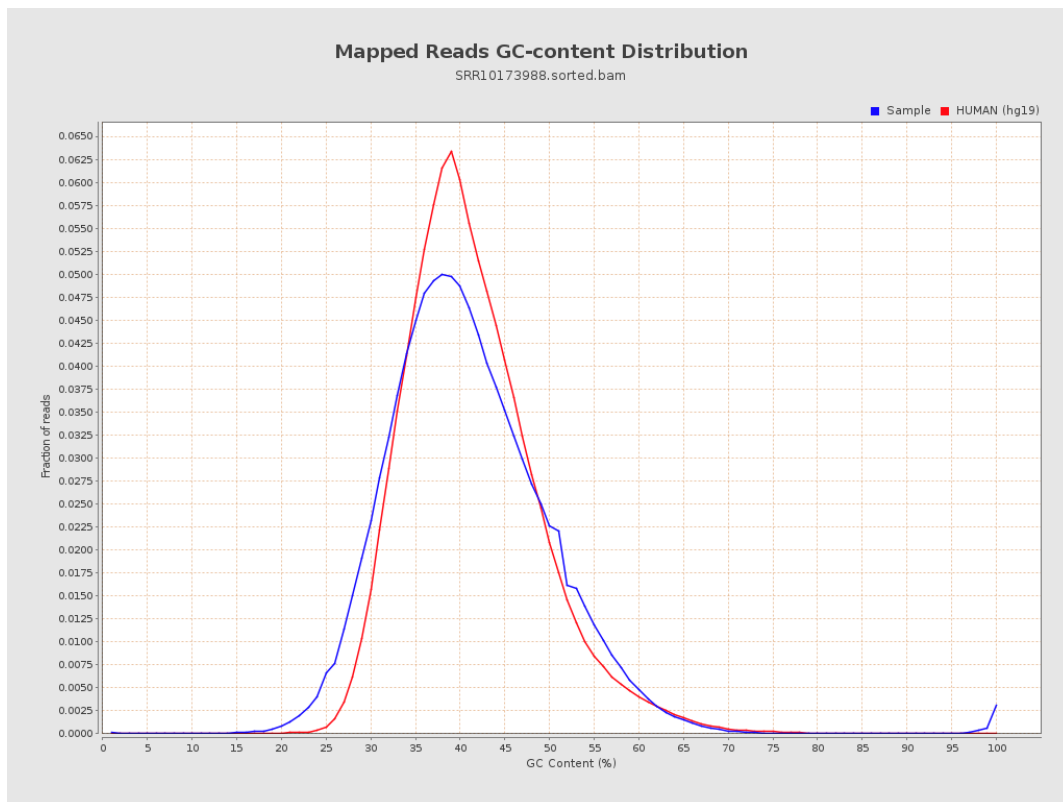
7. Results : Duplication Rate Histogram



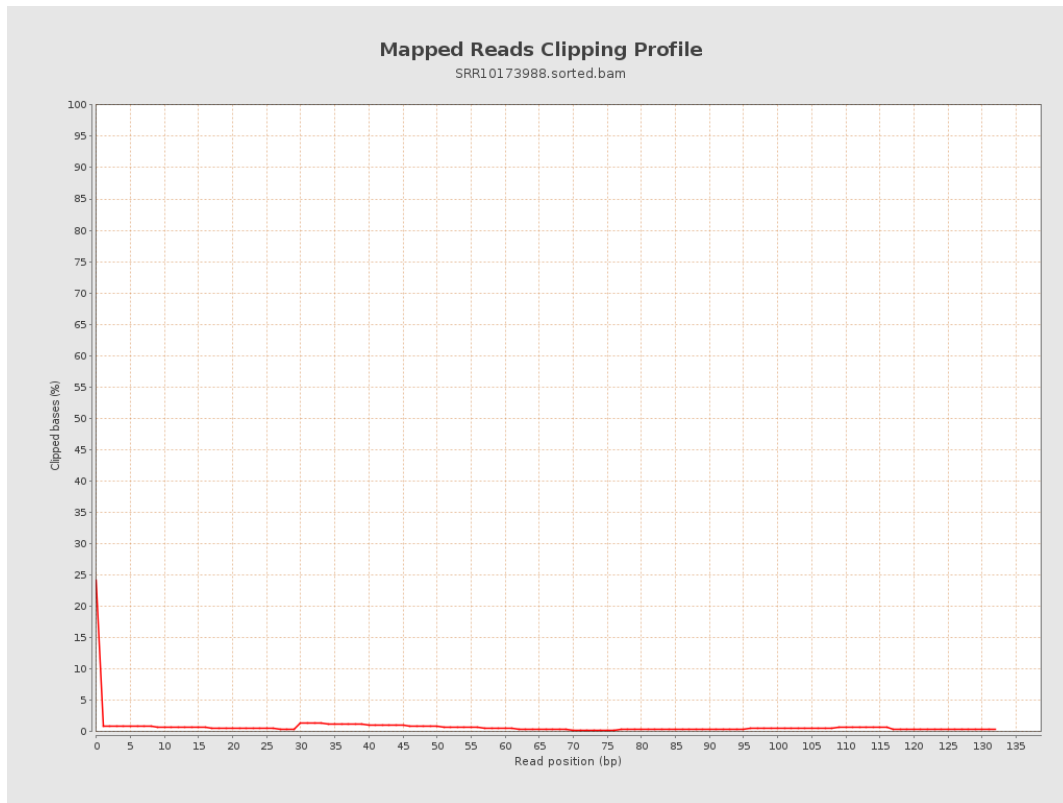
8. Results : Mapped Reads Nucleotide Content



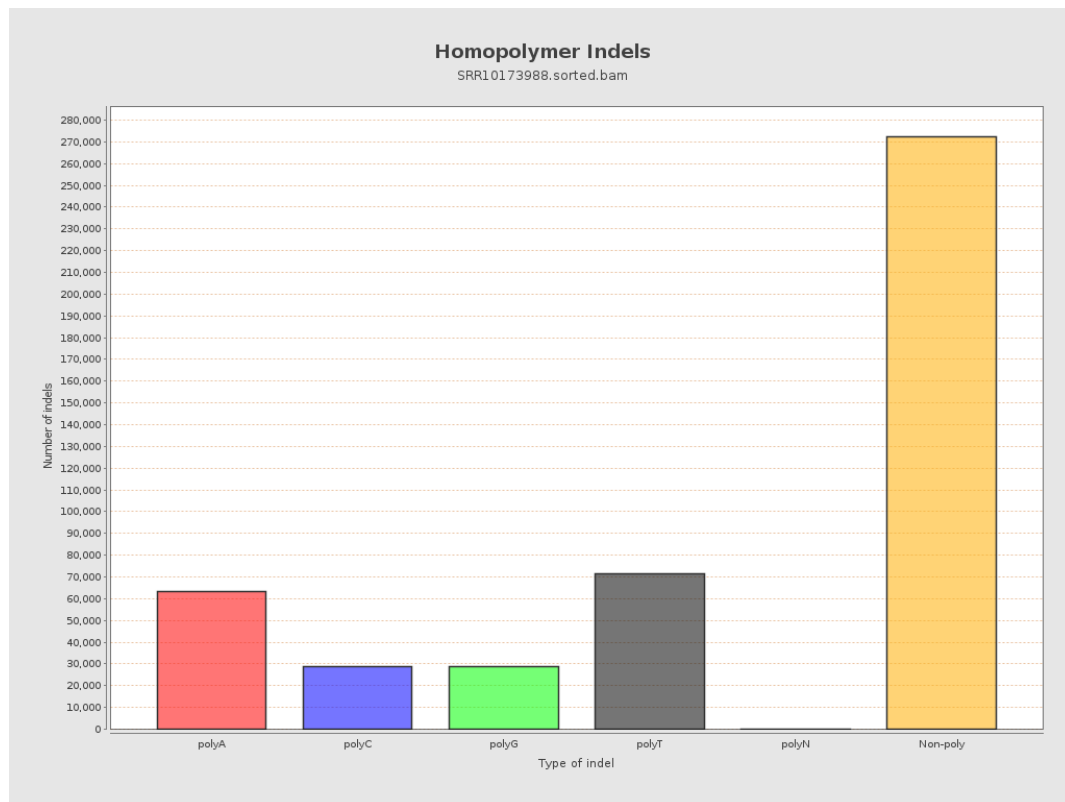
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



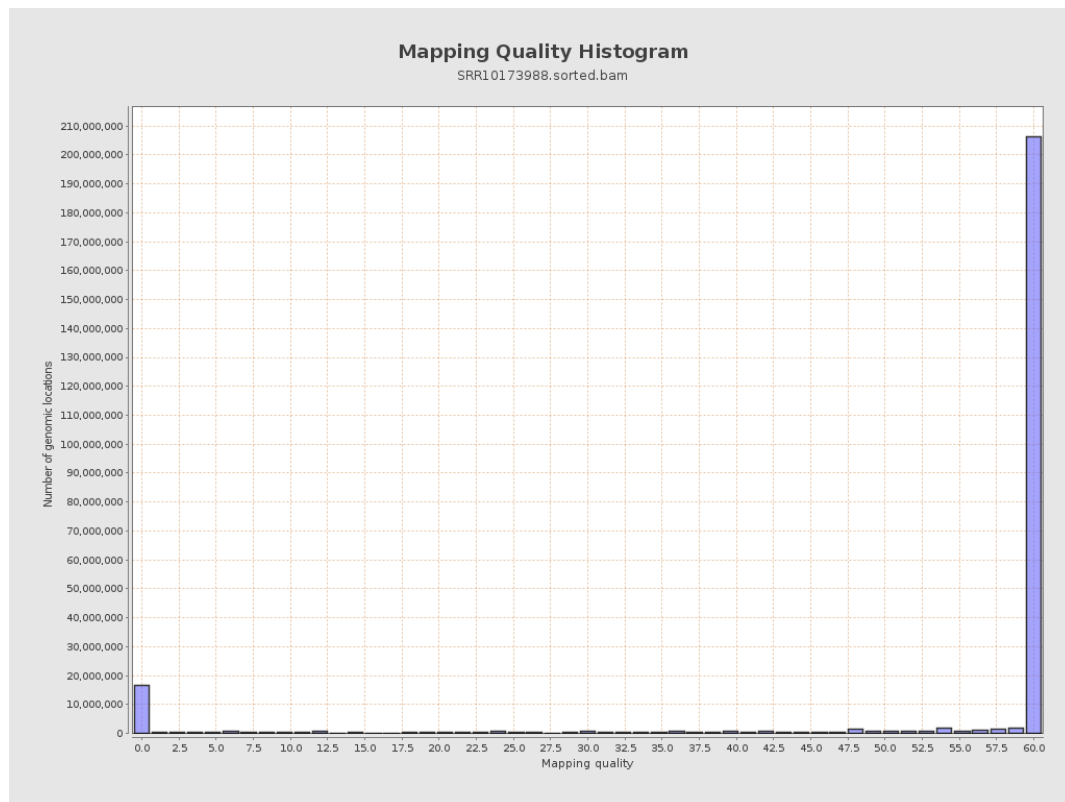
11. Results : Homopolymer Indels



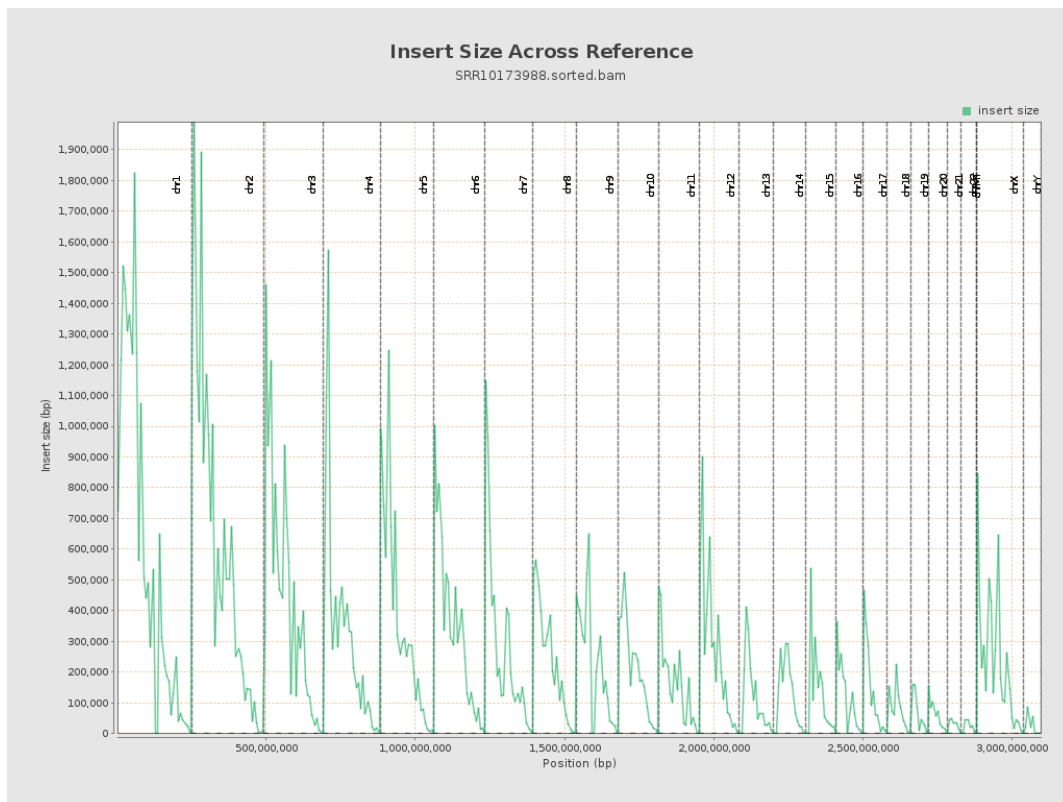
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

