

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 06:02:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173913.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_SRR10173913 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173913_1.fastq.gz SRR10173913_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 06:02:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173913.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,593,744
Mapped reads	5,459,676 / 97.6%
Unmapped reads	134,068 / 2.4%
Mapped paired reads	5,459,676 / 97.6%
Mapped reads, first in pair	2,732,115 / 48.84%
Mapped reads, second in pair	2,727,561 / 48.76%
Mapped reads, both in pair	5,369,078 / 95.98%
Mapped reads, singletons	90,598 / 1.62%
Secondary alignments	0
Supplementary alignments	574,251 / 10.27%
Read min/max/mean length	30 / 133 / 128.54
Duplicated reads (estimated)	4,376,731 / 78.24%
Duplication rate	66.06%
Clipped reads	2,182,707 / 39.02%

2.2. ACGT Content

Number/percentage of A's	194,998,893 / 30.1%
Number/percentage of C's	126,548,092 / 19.53%
Number/percentage of T's	194,812,419 / 30.07%
Number/percentage of G's	131,501,793 / 20.3%
Number/percentage of N's	7,733 / 0%

GC Percentage	39.83%
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2.3. Coverage

Mean	0.2094
Standard Deviation	2.9853

2.4. Mapping Quality

Mean Mapping Quality	52.73
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2.5. Insert size

Mean	1,018,366.58
Standard Deviation	9,119,547.75
P25/Median/P75	146 / 203 / 289

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	6,591,687
Insertions	66,662
Mapped reads with at least one insertion	1.18%
Deletions	164,168
Mapped reads with at least one deletion	2.94%
Homopolymer indels	42.38%

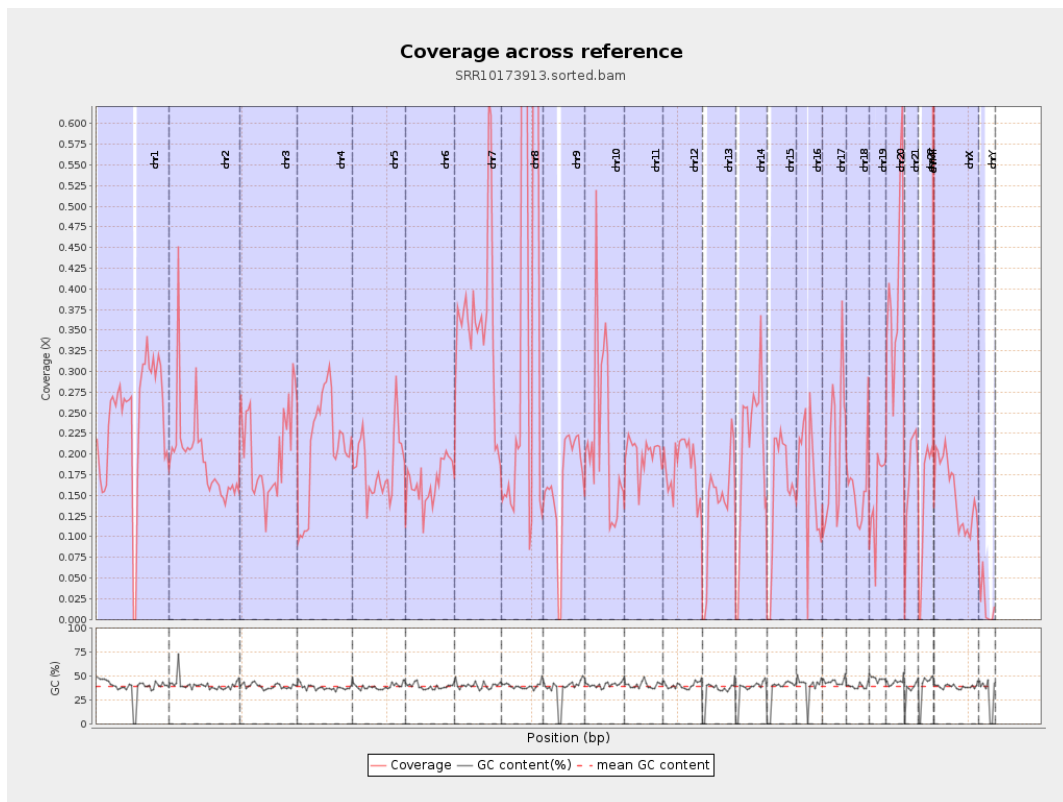
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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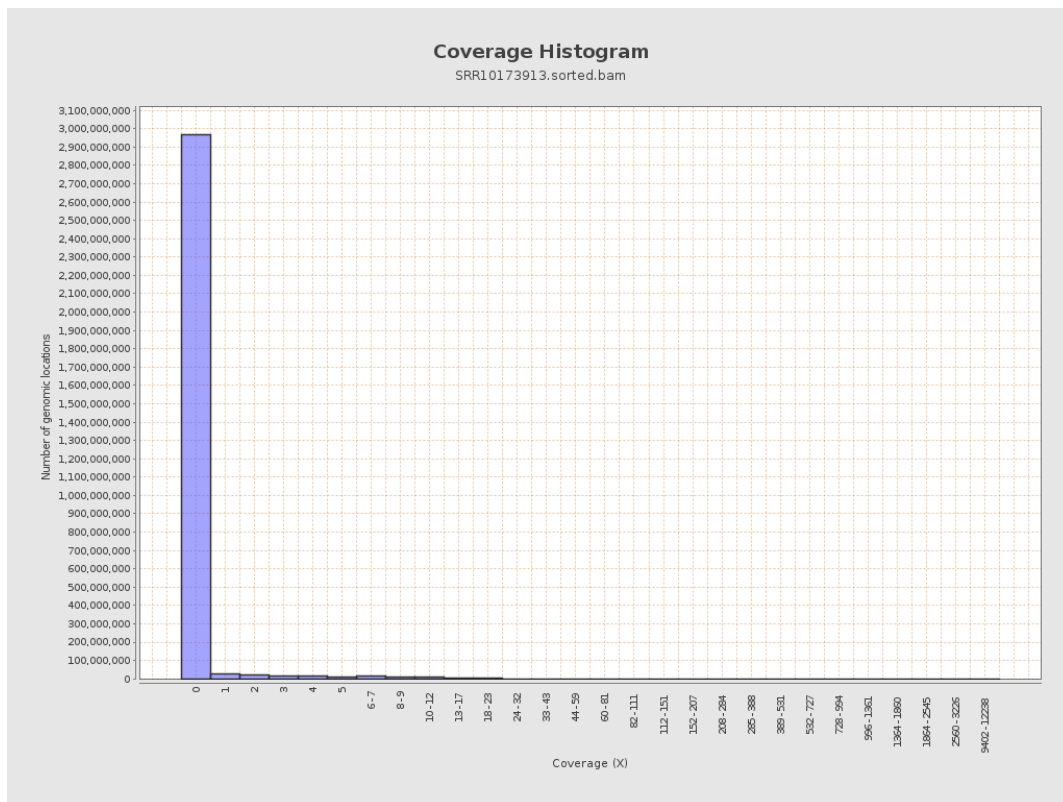
		bases	coverage	deviation
chr1	249250621	59836111	0.2401	1.7978
chr2	243199373	47384604	0.1948	8.6057
chr3	198022430	40297009	0.2035	1.3565
chr4	191154276	39400464	0.2061	1.61
chr5	180915260	33605328	0.1858	1.2909
chr6	171115067	28387169	0.1659	1.2915
chr7	159138663	57533915	0.3615	3.2074
chr8	146364022	62690969	0.4283	2.2918
chr9	141213431	23337309	0.1653	1.4306
chr10	135534747	29945774	0.2209	3.8355
chr11	135006516	26954250	0.1997	1.3526
chr12	133851895	24839484	0.1856	1.2849
chr13	115169878	16046317	0.1393	1.1141
chr14	107349540	22235269	0.2071	1.3607
chr15	102531392	15909172	0.1552	1.1632
chr16	90354753	15223046	0.1685	1.581
chr17	81195210	16722057	0.2059	1.5013
chr18	78077248	12249998	0.1569	1.9576
chr19	59128983	8829823	0.1493	1.4036
chr20	63025520	25166758	0.3993	1.9028
chr21	48129895	8288863	0.1722	1.2952
chr22	51304566	7218830	0.1407	1.0739
chrMT	16571	1500146	90.5284	75.2678
chrX	155270560	23565740	0.1518	1.1707

chrY	59373566	1085334	0.0183	0.7699
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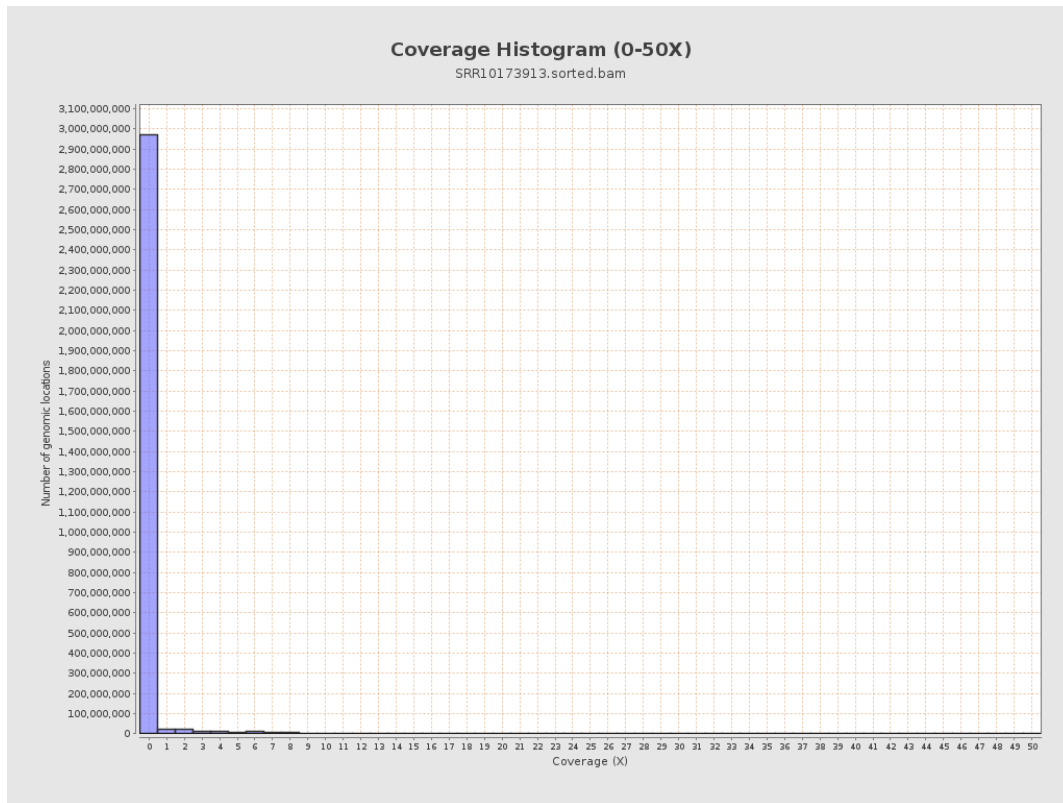
3. Results : Coverage across reference



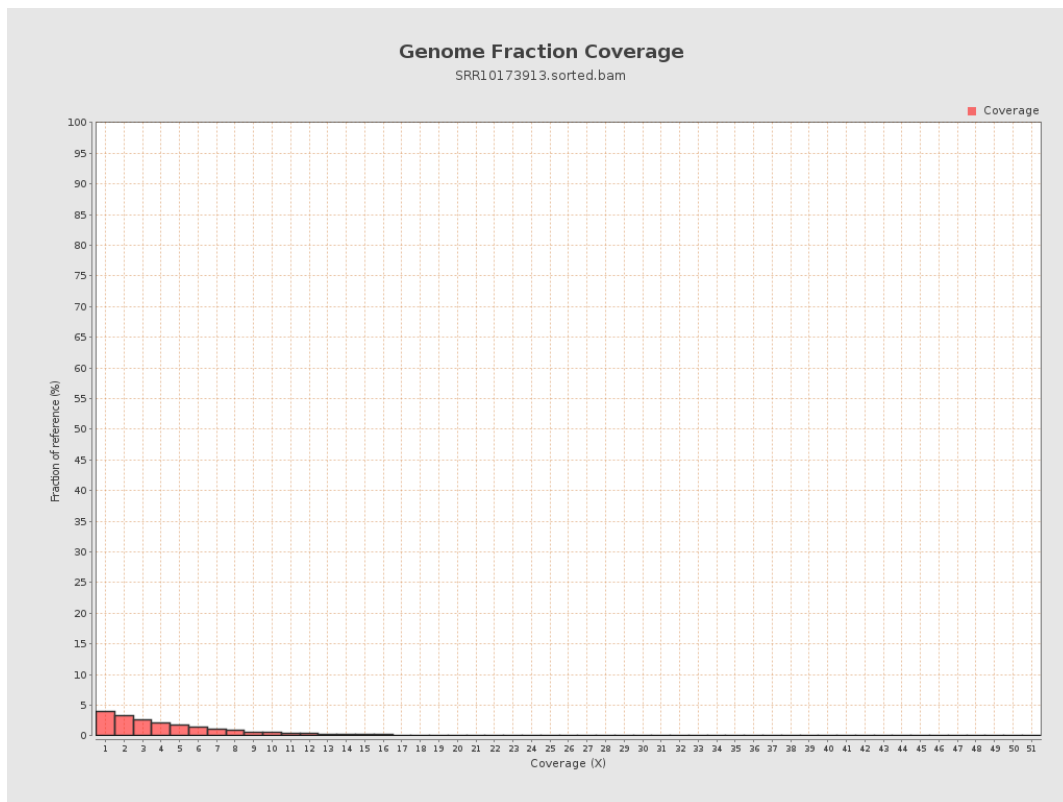
4. Results : Coverage Histogram



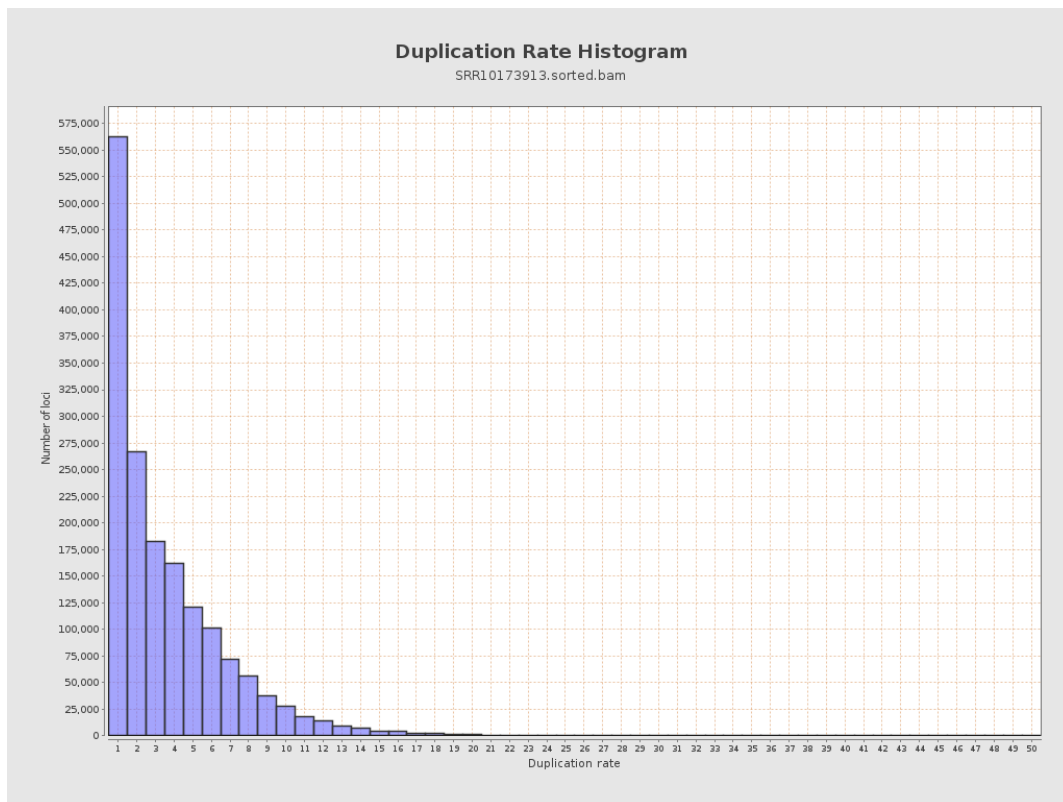
5. Results : Coverage Histogram (0-50X)



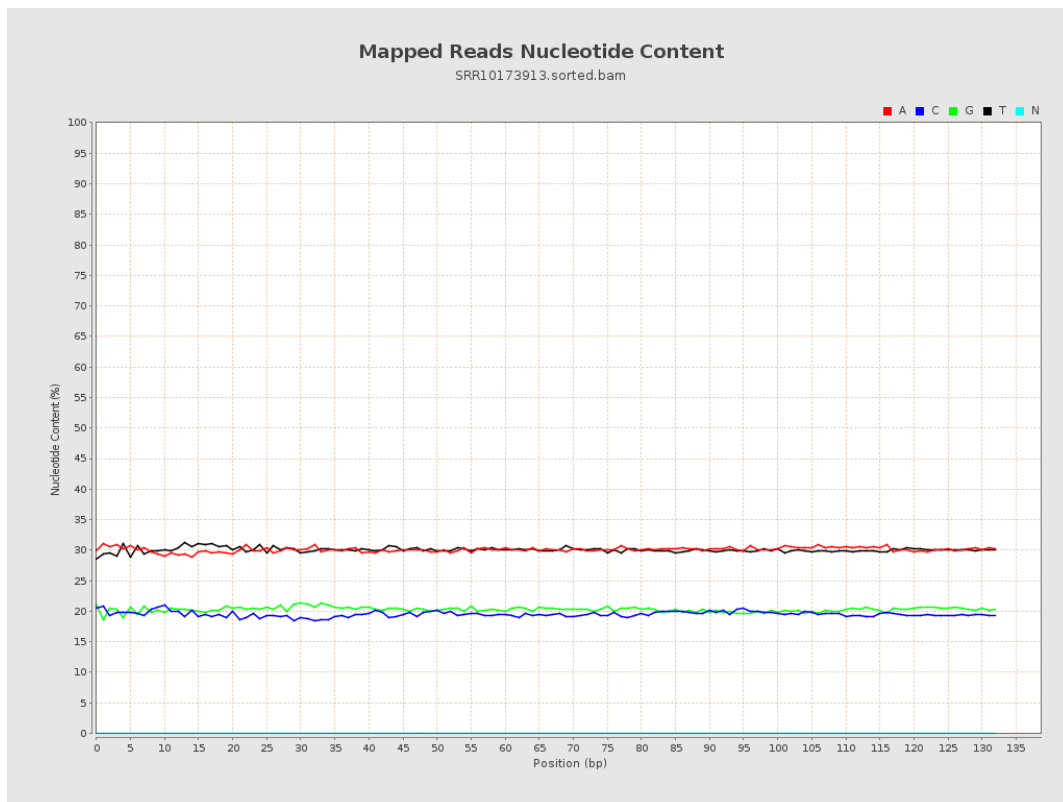
6. Results : Genome Fraction Coverage



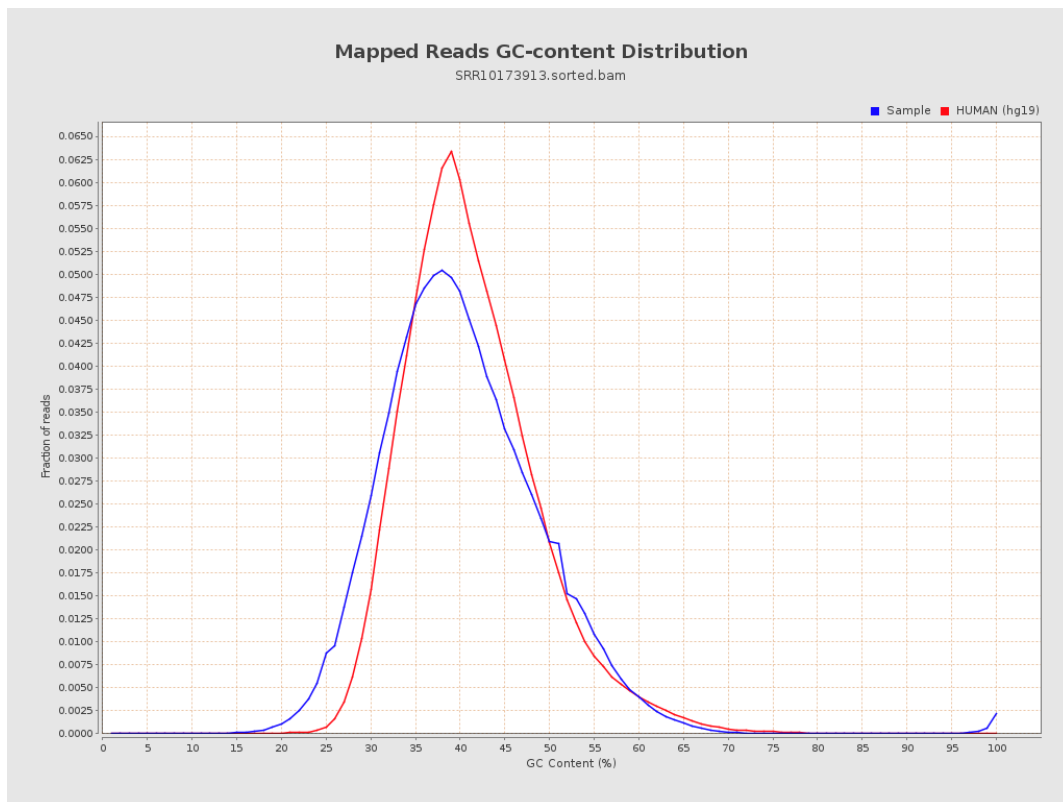
7. Results : Duplication Rate Histogram



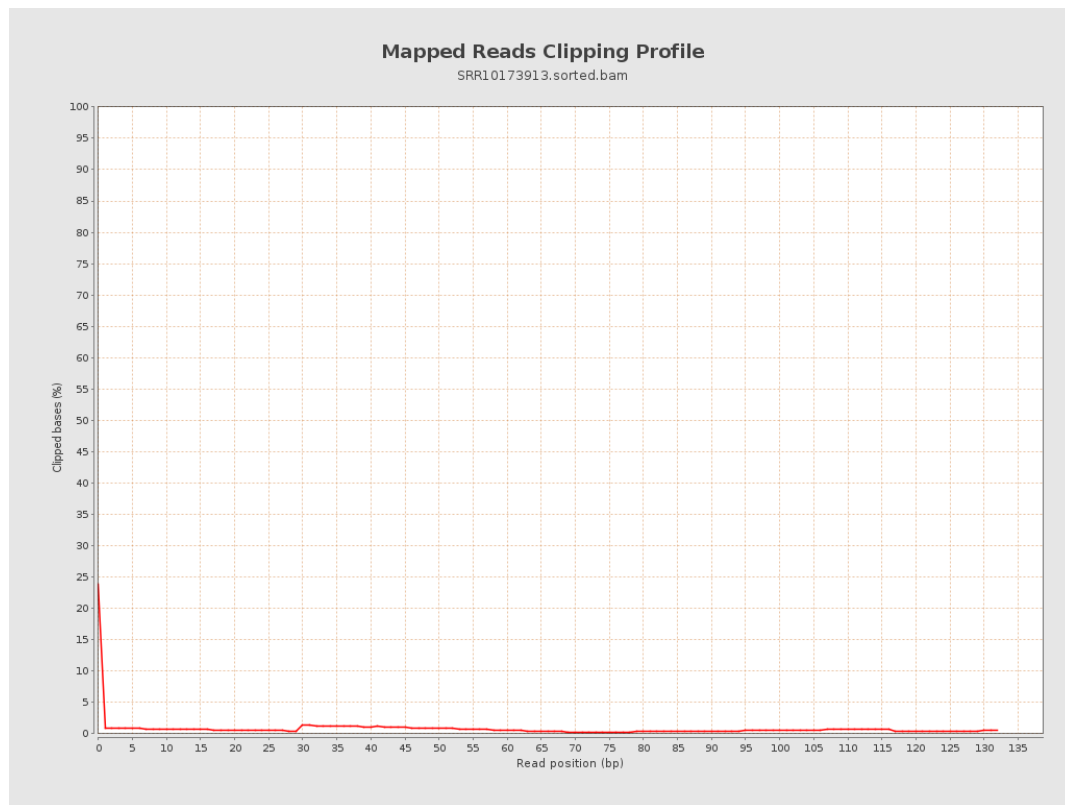
8. Results : Mapped Reads Nucleotide Content



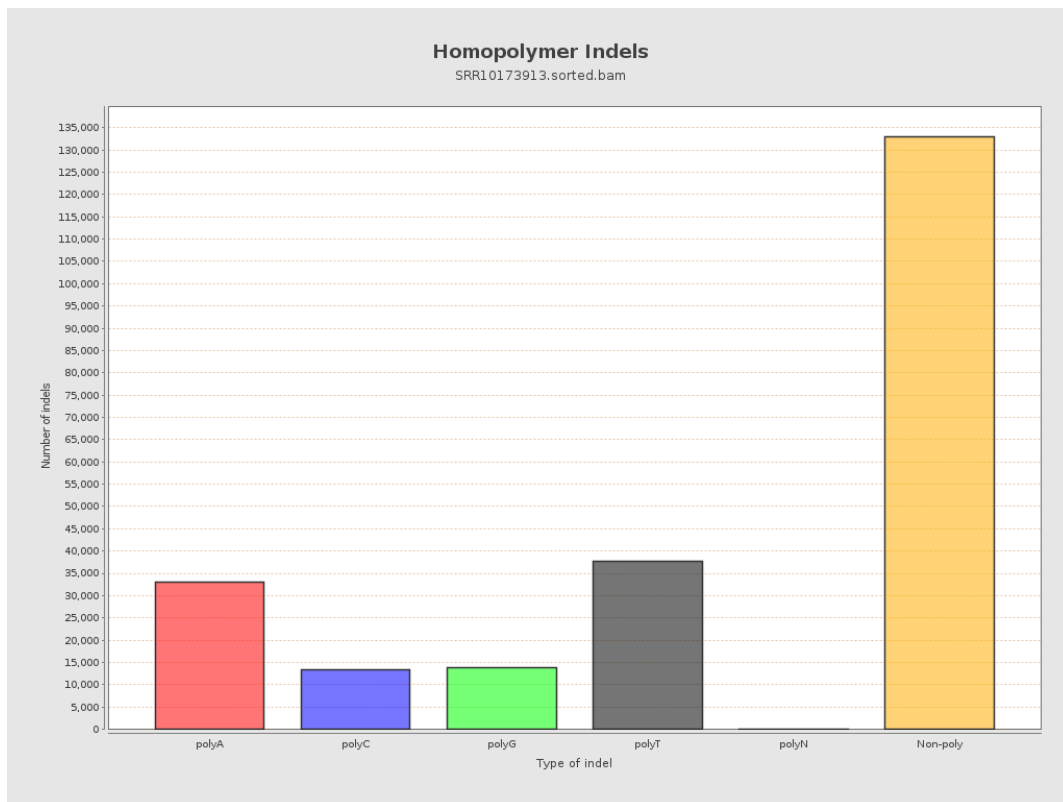
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



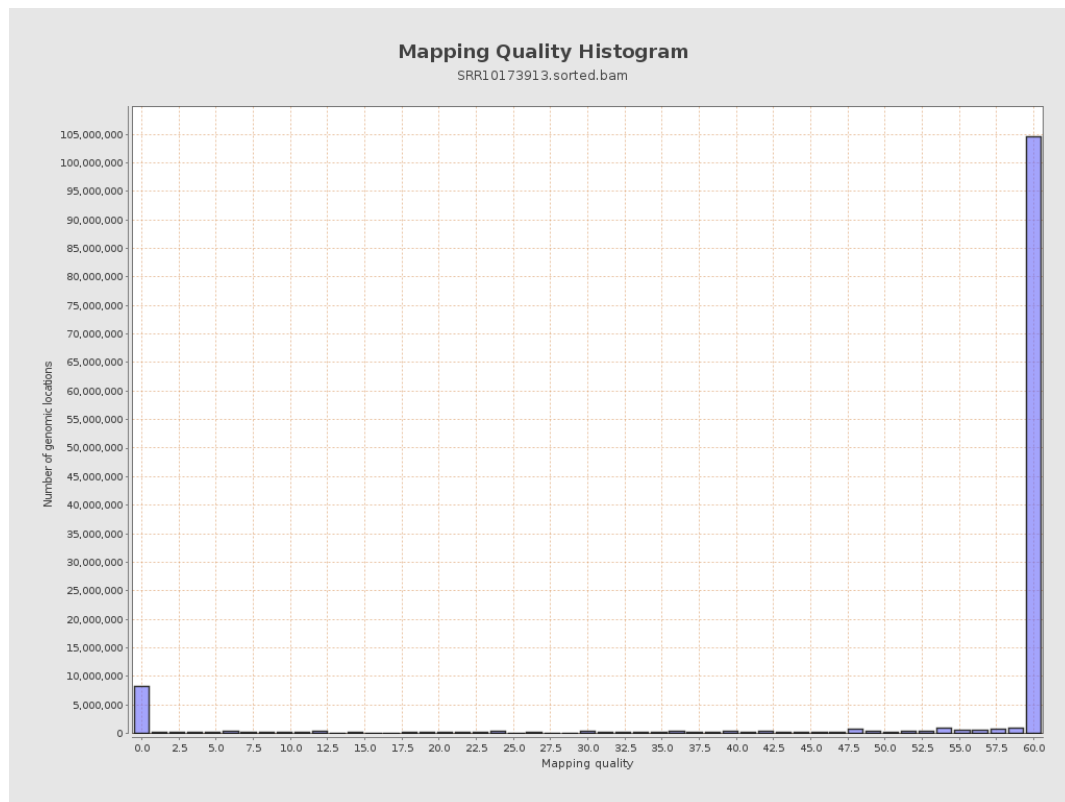
11. Results : Homopolymer Indels



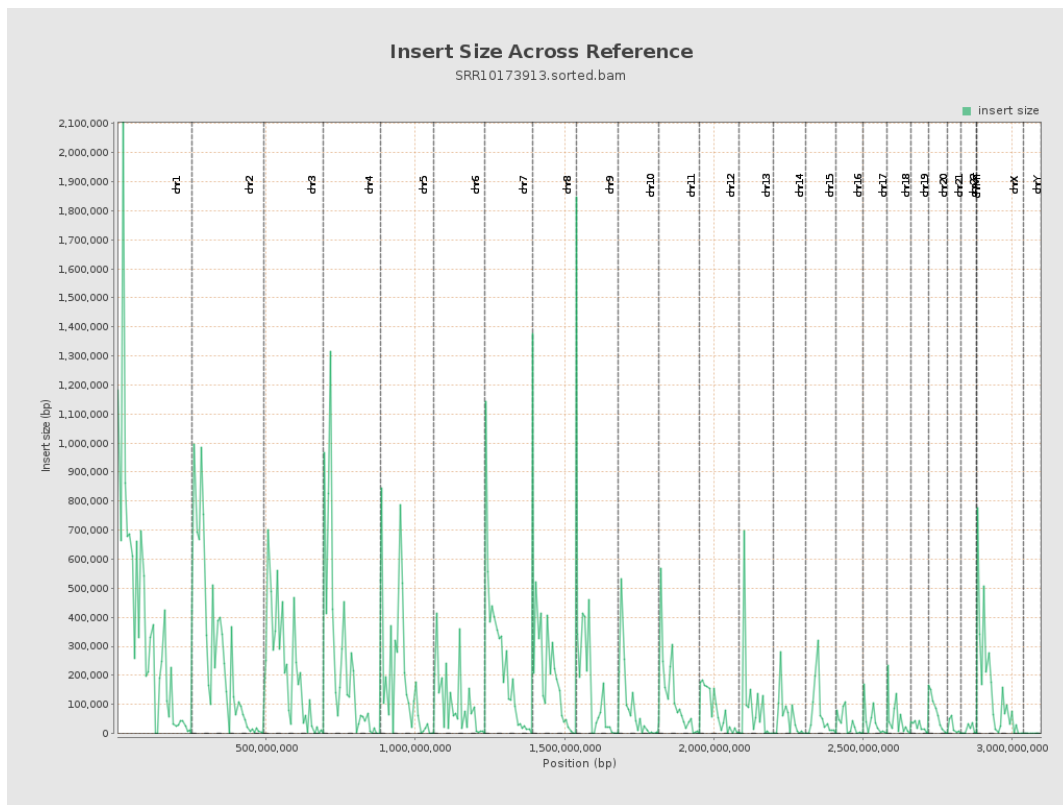
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

