

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:05:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173877.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_SRR10173877 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173877_1.fastq.gz SRR10173877_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:05:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173877.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,989,262
Mapped reads	1,942,224 / 97.64%
Unmapped reads	47,038 / 2.36%
Mapped paired reads	1,942,224 / 97.64%
Mapped reads, first in pair	972,880 / 48.91%
Mapped reads, second in pair	969,344 / 48.73%
Mapped reads, both in pair	1,912,134 / 96.12%
Mapped reads, singletons	30,090 / 1.51%
Secondary alignments	0
Supplementary alignments	177,317 / 8.91%
Read min/max/mean length	30 / 133 / 127.83
Duplicated reads (estimated)	1,460,908 / 73.44%
Duplication rate	63.76%
Clipped reads	715,042 / 35.95%

2.2. ACGT Content

Number/percentage of A's	69,593,191 / 30.18%
Number/percentage of C's	44,904,677 / 19.48%
Number/percentage of T's	69,450,602 / 30.12%
Number/percentage of G's	46,609,431 / 20.22%
Number/percentage of N's	3,214 / 0%

GC Percentage	39.69%
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2.3. Coverage

Mean	0.0745
Standard Deviation	1.1981

2.4. Mapping Quality

Mean Mapping Quality	53.22
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2.5. Insert size

Mean	992,475.28
Standard Deviation	9,661,702.67
P25/Median/P75	146 / 199 / 278

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	2,309,204
Insertions	25,038
Mapped reads with at least one insertion	1.24%
Deletions	55,375
Mapped reads with at least one deletion	2.79%
Homopolymer indels	43.2%

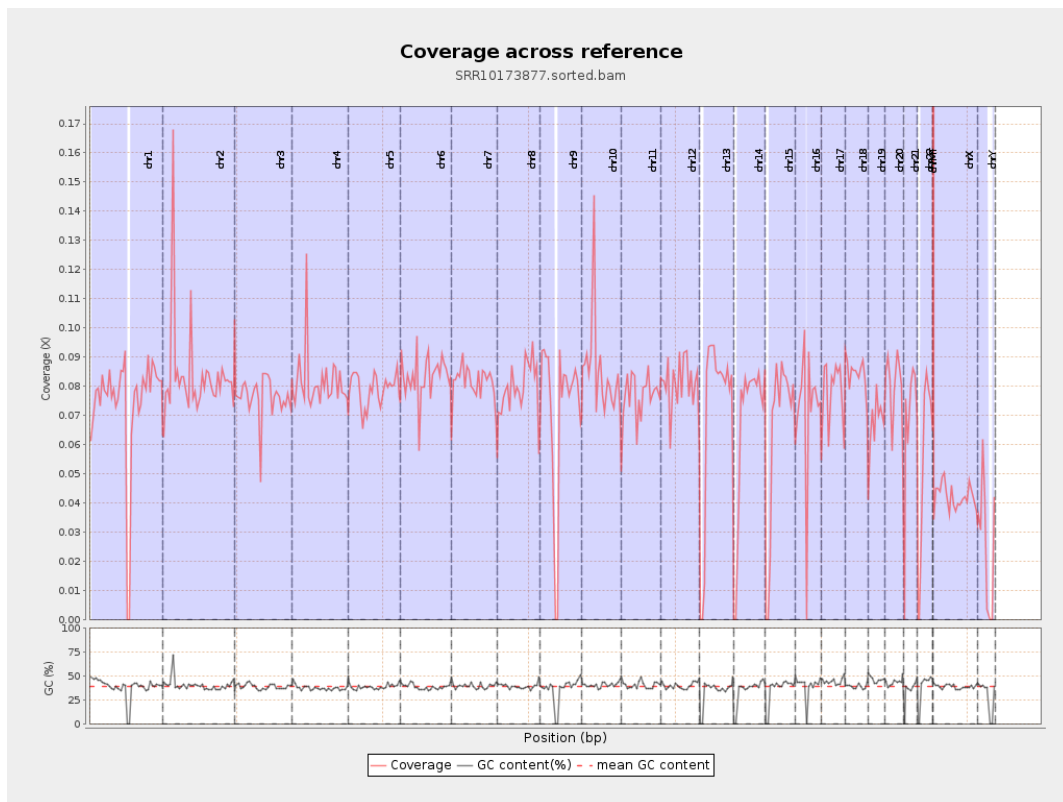
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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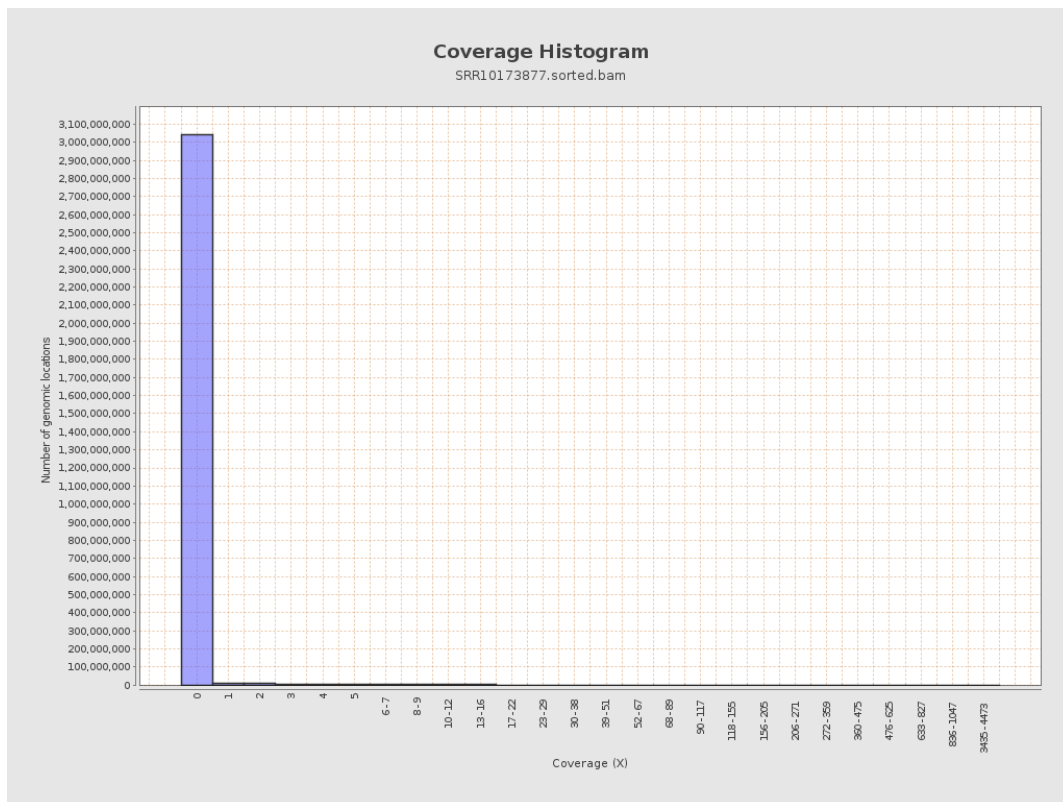
		bases	coverage	deviation
chr1	249250621	18480120	0.0741	0.8834
chr2	243199373	20249006	0.0833	3.1936
chr3	198022430	15177433	0.0766	0.7801
chr4	191154276	15582615	0.0815	0.8986
chr5	180915260	14266527	0.0789	0.7929
chr6	171115067	14276930	0.0834	0.8356
chr7	159138663	12923043	0.0812	0.8718
chr8	146364022	11635533	0.0795	0.9102
chr9	141213431	10244005	0.0725	0.8937
chr10	135534747	11517156	0.085	1.0485
chr11	135006516	10345100	0.0766	0.7798
chr12	133851895	10834963	0.0809	0.7955
chr13	115169878	8226139	0.0714	0.7554
chr14	107349540	7193553	0.067	0.7169
chr15	102531392	6545505	0.0638	0.6922
chr16	90354753	6447675	0.0714	0.7958
chr17	81195210	6383100	0.0786	0.7728
chr18	78077248	6594046	0.0845	1.0951
chr19	59128983	4035039	0.0682	0.8055
chr20	63025520	5068858	0.0804	0.7943
chr21	48129895	3331482	0.0692	0.8559
chr22	51304566	2804396	0.0547	0.6479
chrMT	16571	425919	25.7027	22.7791
chrX	155270560	6535640	0.0421	0.5742

chrY	59373566	1570970	0.0265	0.4905
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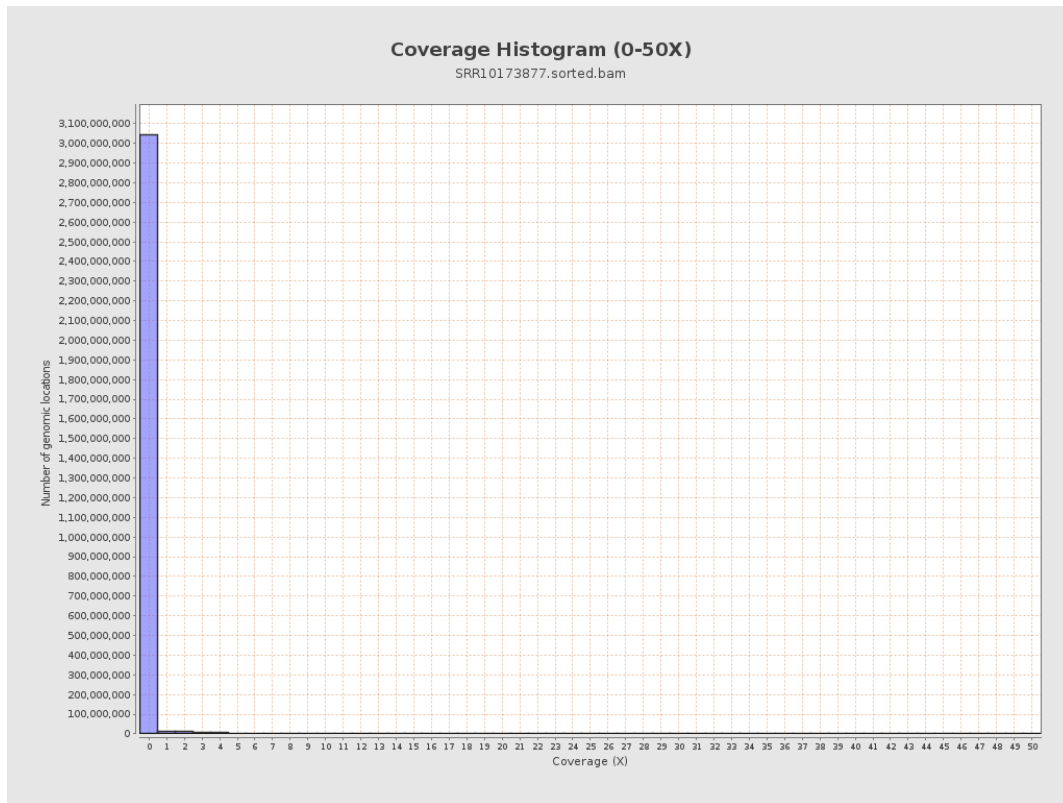
3. Results : Coverage across reference



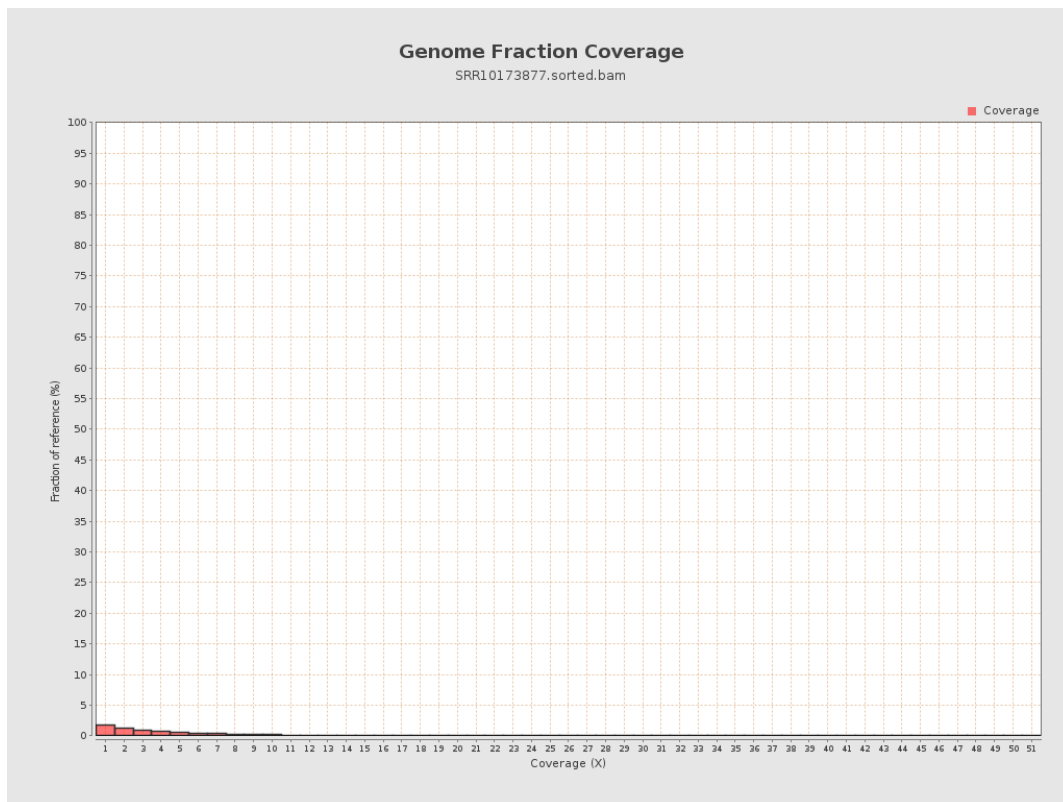
4. Results : Coverage Histogram



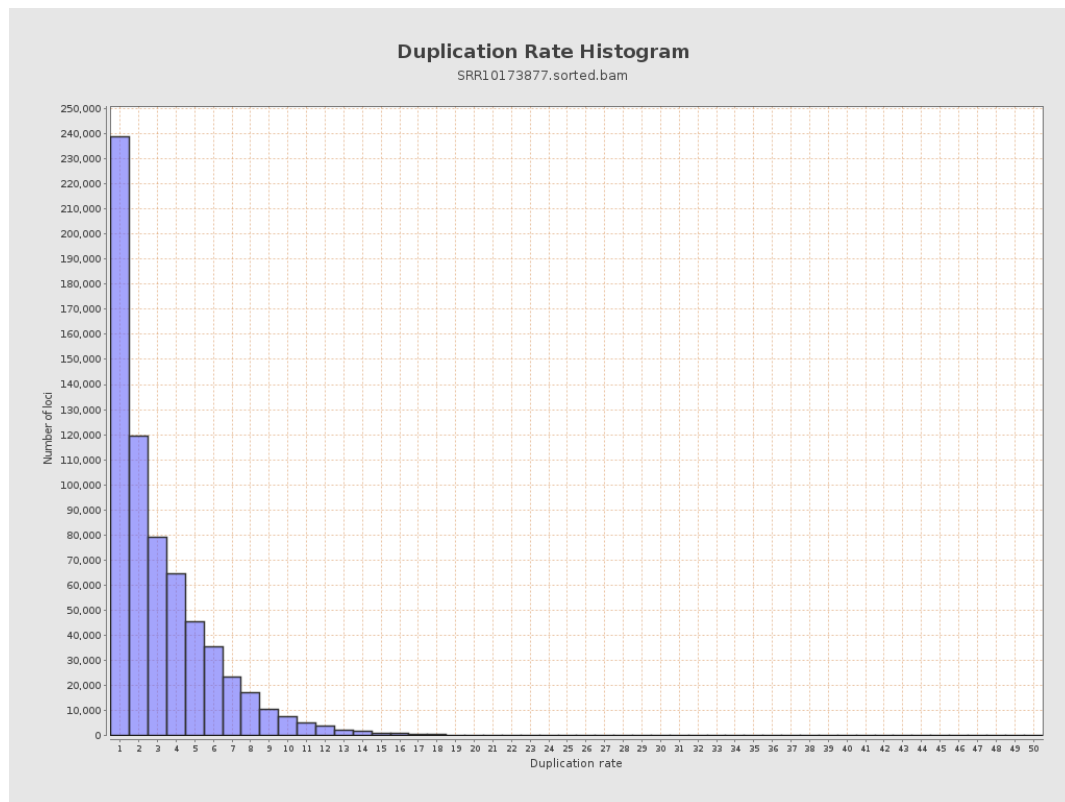
5. Results : Coverage Histogram (0-50X)



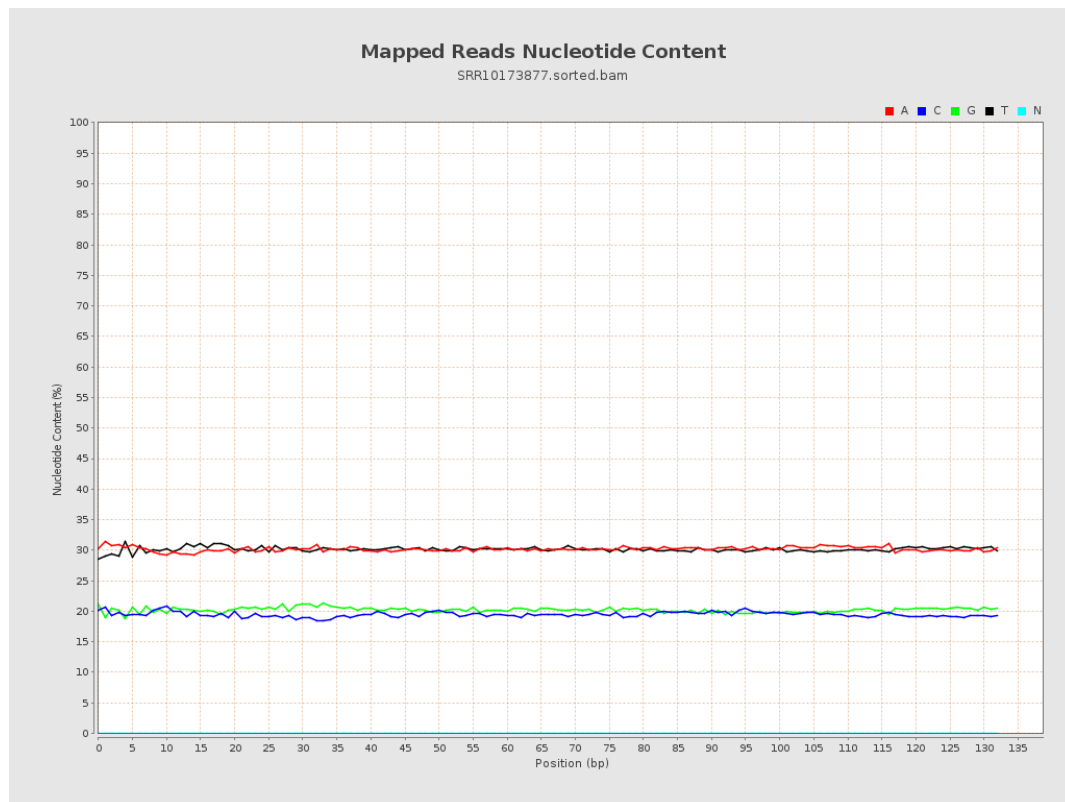
6. Results : Genome Fraction Coverage



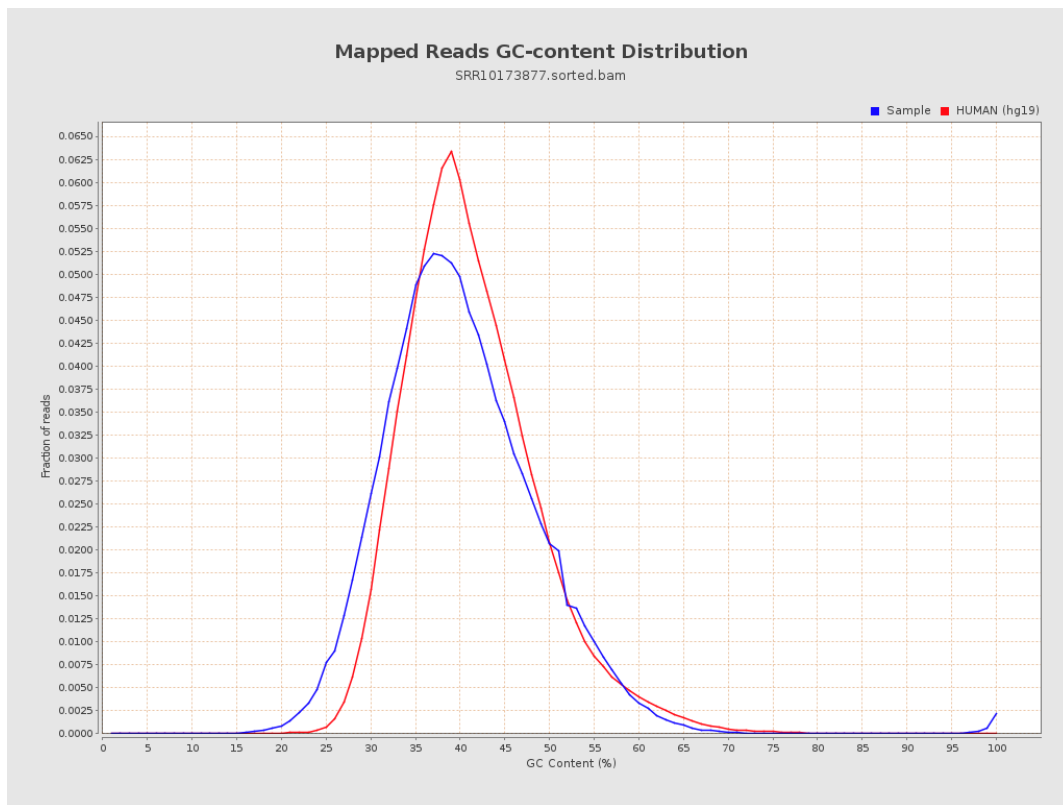
7. Results : Duplication Rate Histogram



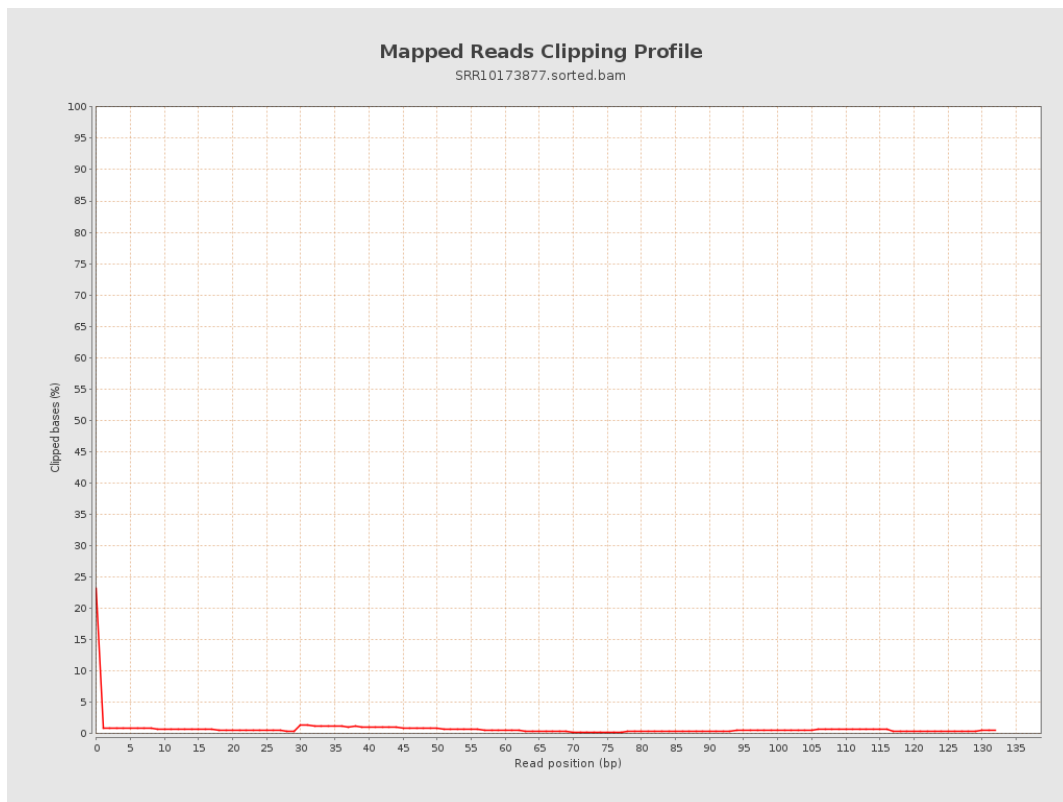
8. Results : Mapped Reads Nucleotide Content



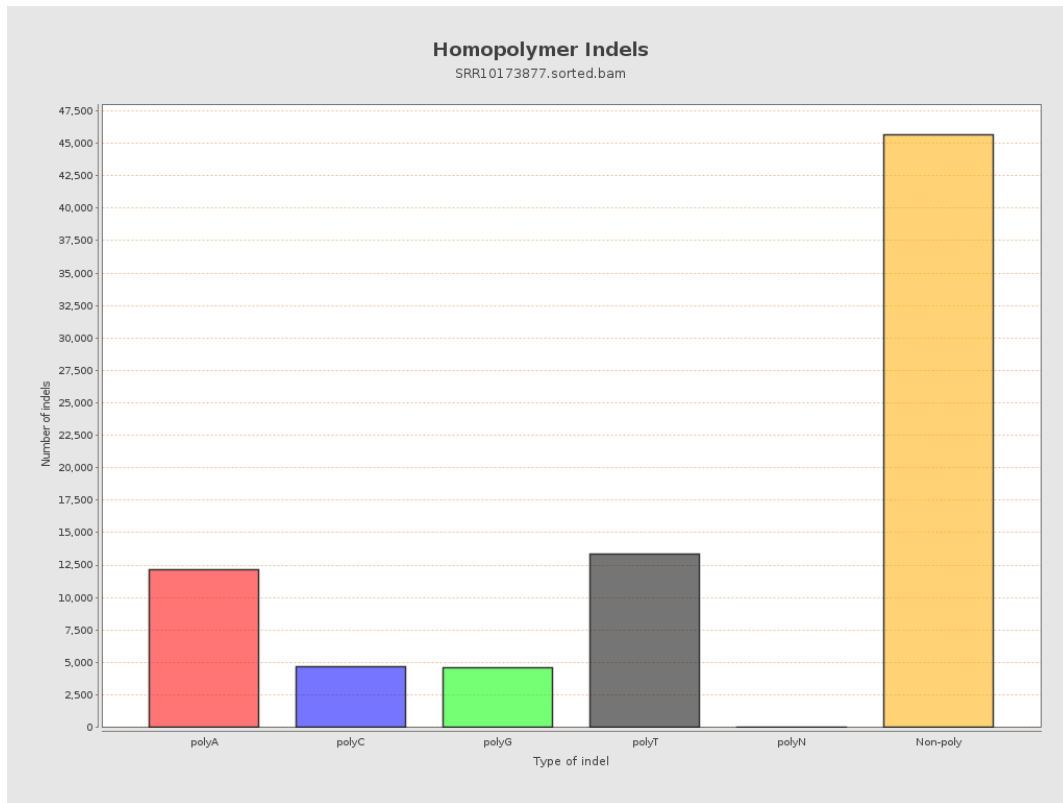
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



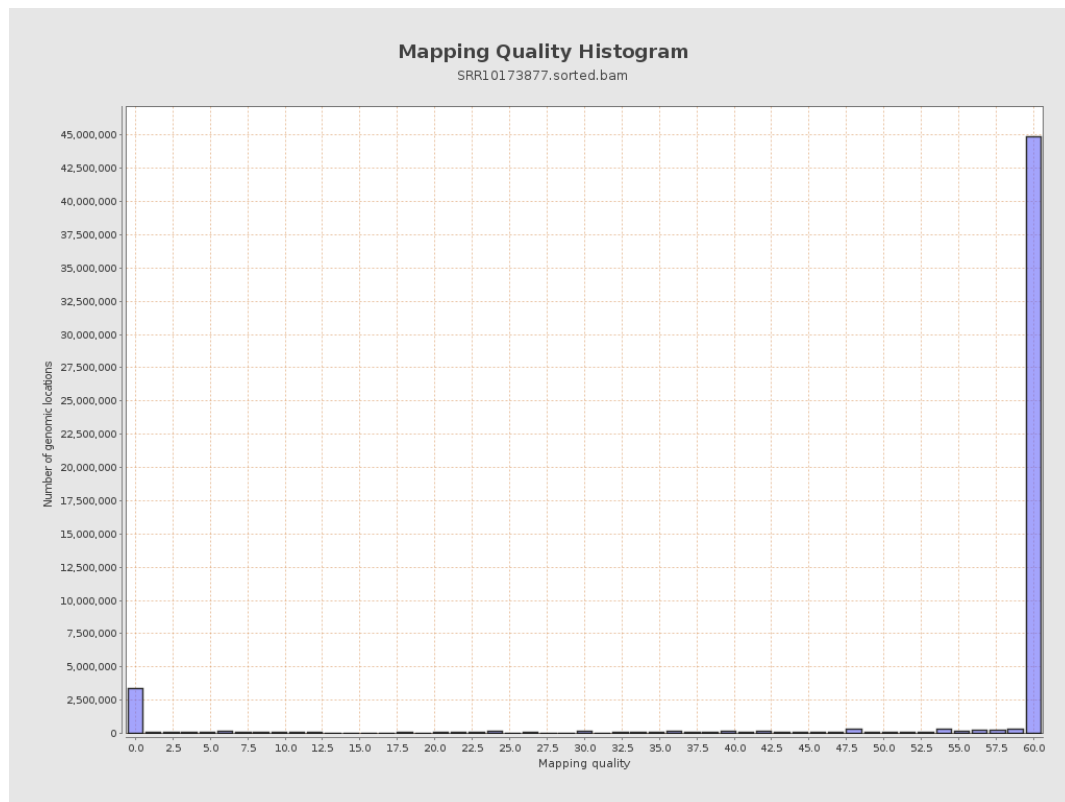
11. Results : Homopolymer Indels



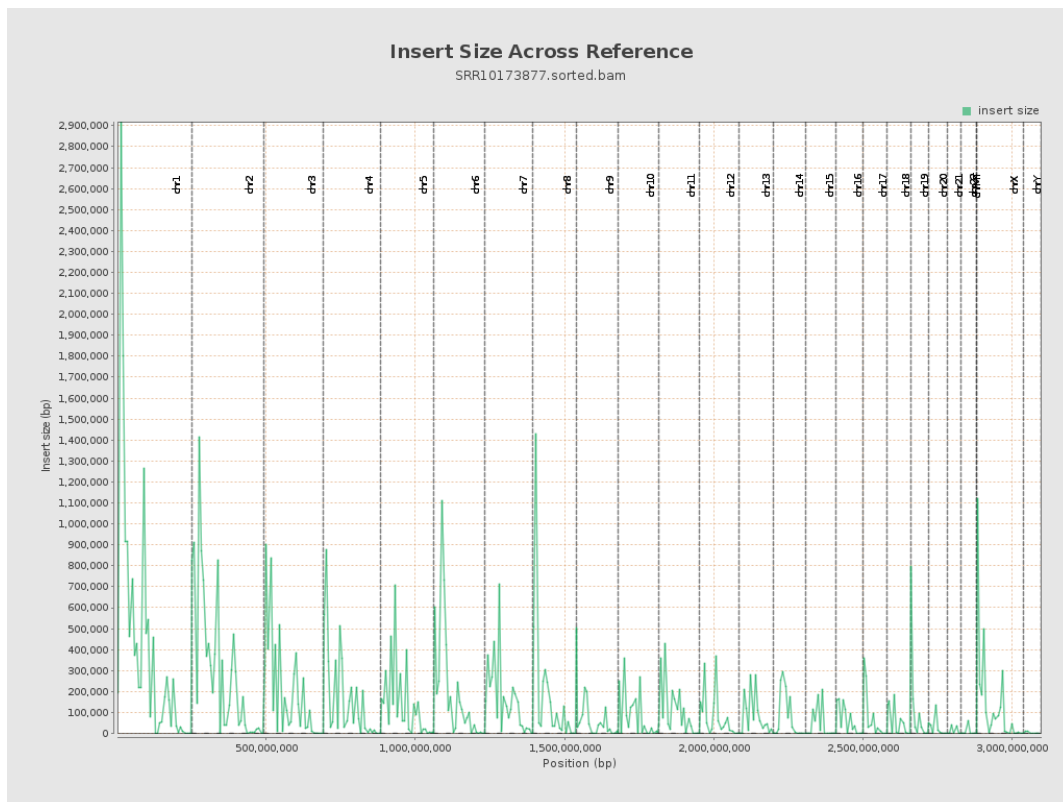
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

