

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:33:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173882.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_SRR10173882 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173882_1.fastq.gz SRR10173882_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:33:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173882.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,178,126
Mapped reads	2,126,751 / 97.64%
Unmapped reads	51,375 / 2.36%
Mapped paired reads	2,126,751 / 97.64%
Mapped reads, first in pair	1,065,335 / 48.91%
Mapped reads, second in pair	1,061,416 / 48.73%
Mapped reads, both in pair	2,094,896 / 96.18%
Mapped reads, singletons	31,855 / 1.46%
Secondary alignments	0
Supplementary alignments	200,975 / 9.23%
Read min/max/mean length	30 / 133 / 127.91
Duplicated reads (estimated)	1,623,491 / 74.54%
Duplication rate	63.86%
Clipped reads	803,684 / 36.9%

2.2. ACGT Content

Number/percentage of A's	76,751,604 / 30.43%
Number/percentage of C's	48,578,476 / 19.26%
Number/percentage of T's	76,545,343 / 30.35%
Number/percentage of G's	50,316,654 / 19.95%
Number/percentage of N's	3,333 / 0%

GC Percentage	39.21%
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2.3. Coverage

Mean	0.0815
Standard Deviation	1.3063

2.4. Mapping Quality

Mean Mapping Quality	53.18
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2.5. Insert size

Mean	889,645
Standard Deviation	8,743,086.45
P25/Median/P75	143 / 195 / 270

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	2,517,652
Insertions	28,027
Mapped reads with at least one insertion	1.27%
Deletions	59,857
Mapped reads with at least one deletion	2.74%
Homopolymer indels	42.62%

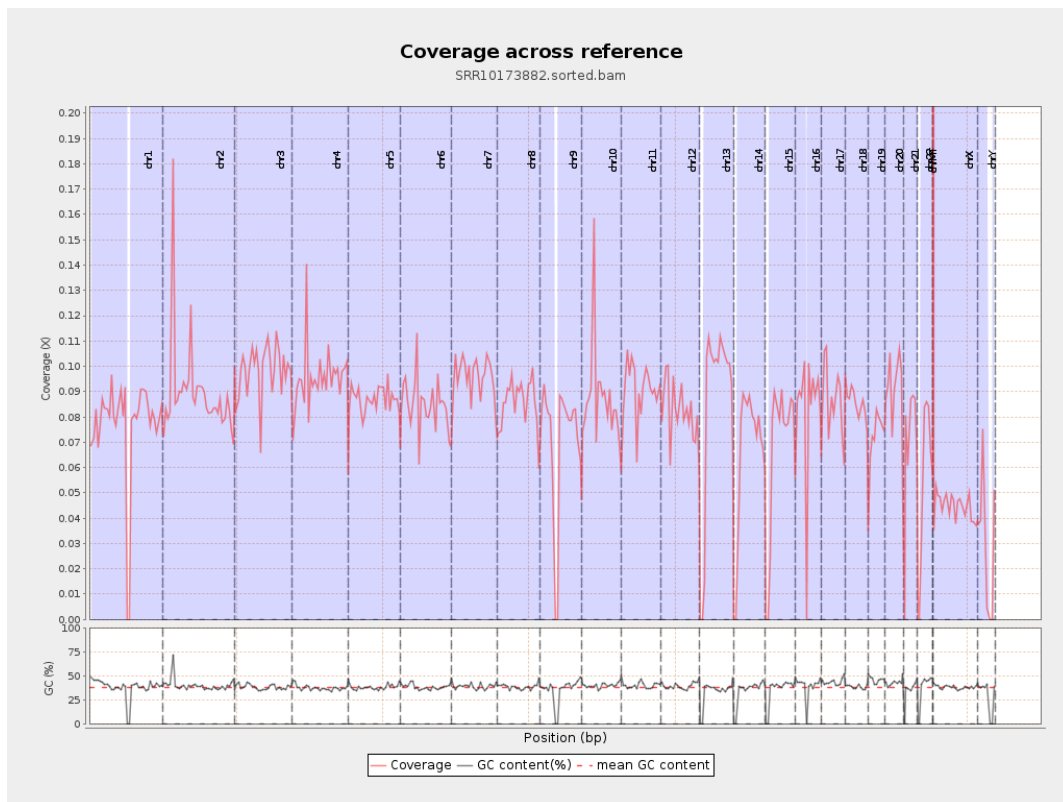
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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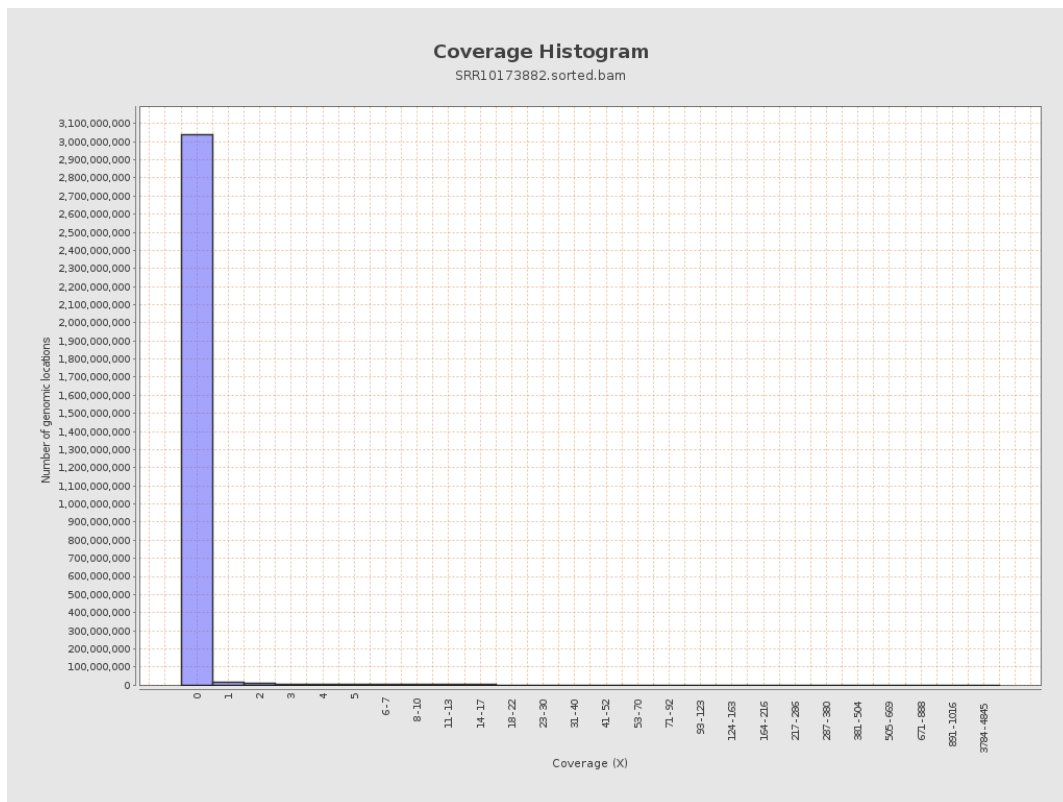
		bases	coverage	deviation
chr1	249250621	19128285	0.0767	0.9622
chr2	243199373	21724579	0.0893	3.4653
chr3	198022430	19464673	0.0983	0.9177
chr4	191154276	18229198	0.0954	1.0074
chr5	180915260	15677851	0.0867	0.8556
chr6	171115067	14575781	0.0852	0.8818
chr7	159138663	15136578	0.0951	1.0319
chr8	146364022	12598160	0.0861	1.0626
chr9	141213431	10032303	0.071	0.9153
chr10	135534747	11845238	0.0874	1.1432
chr11	135006516	12260770	0.0908	0.8787
chr12	133851895	11060403	0.0826	0.8294
chr13	115169878	9897952	0.0859	0.8632
chr14	107349540	7213109	0.0672	0.7427
chr15	102531392	6826299	0.0666	0.7319
chr16	90354753	7372582	0.0816	0.8821
chr17	81195210	7082821	0.0872	0.9107
chr18	78077248	6709219	0.0859	1.1328
chr19	59128983	4315661	0.073	0.8058
chr20	63025520	5808570	0.0922	0.8657
chr21	48129895	3434553	0.0714	0.8857
chr22	51304566	2820455	0.055	0.6848
chrMT	16571	378385	22.8342	20.8524
chrX	155270560	6928262	0.0446	0.6051

chrY	59373566	1819476	0.0306	0.5871
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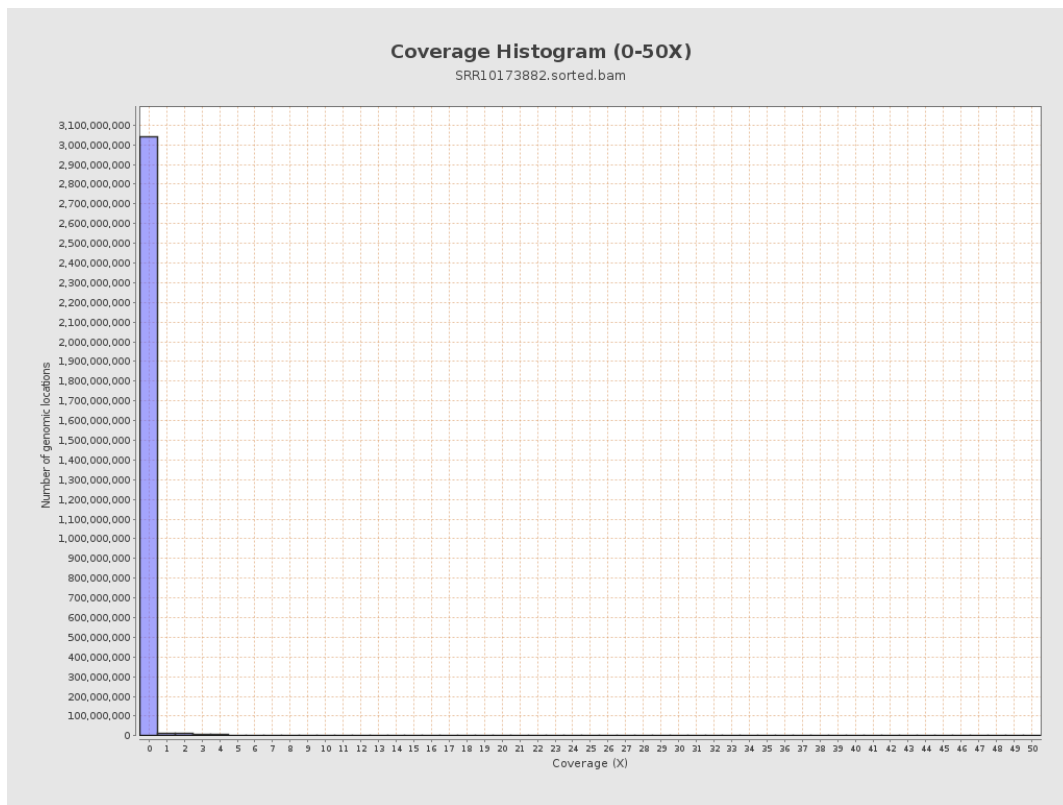
3. Results : Coverage across reference



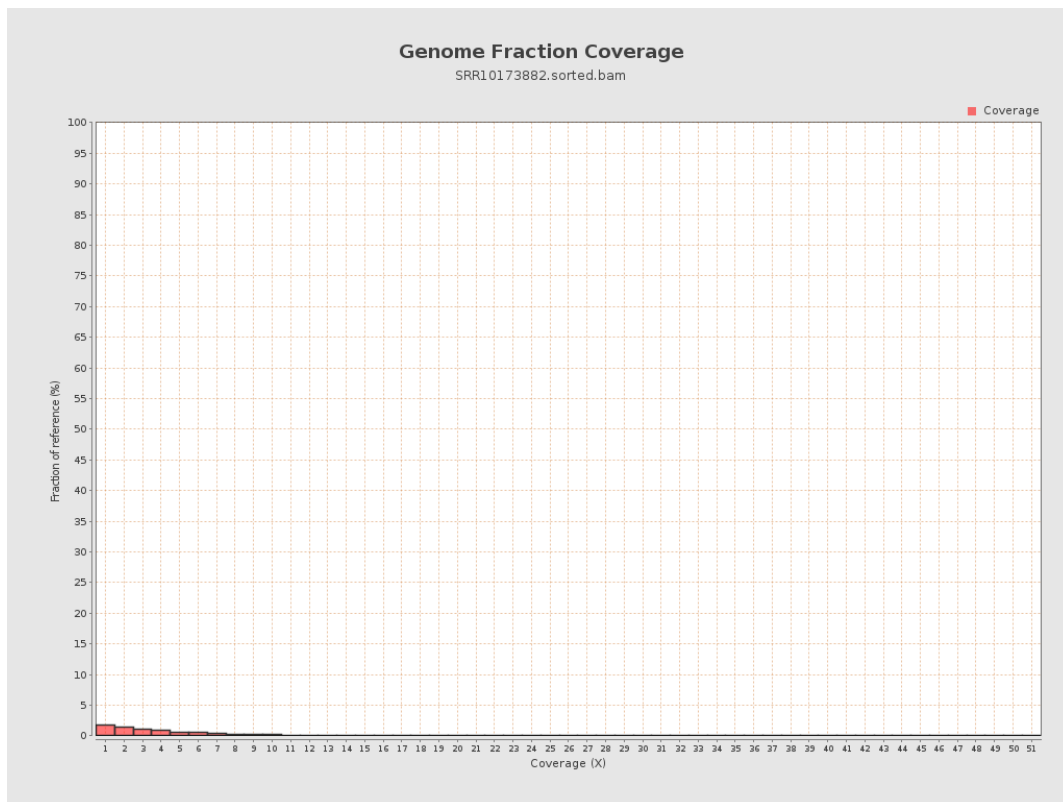
4. Results : Coverage Histogram



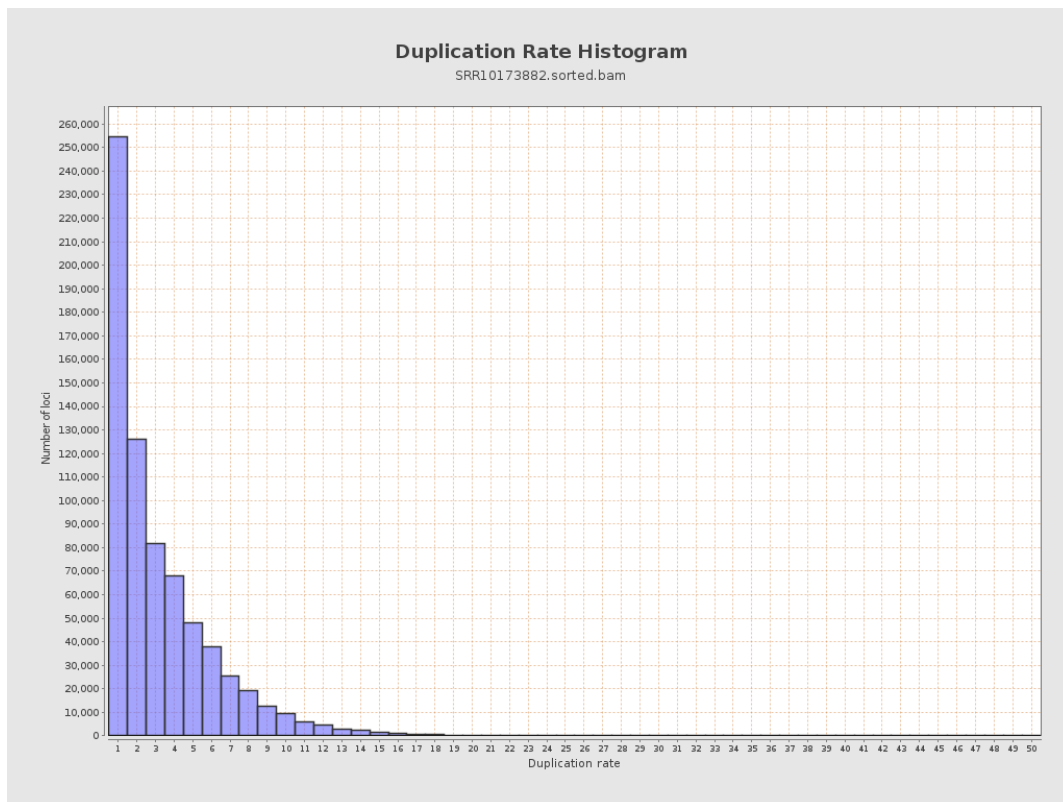
5. Results : Coverage Histogram (0-50X)



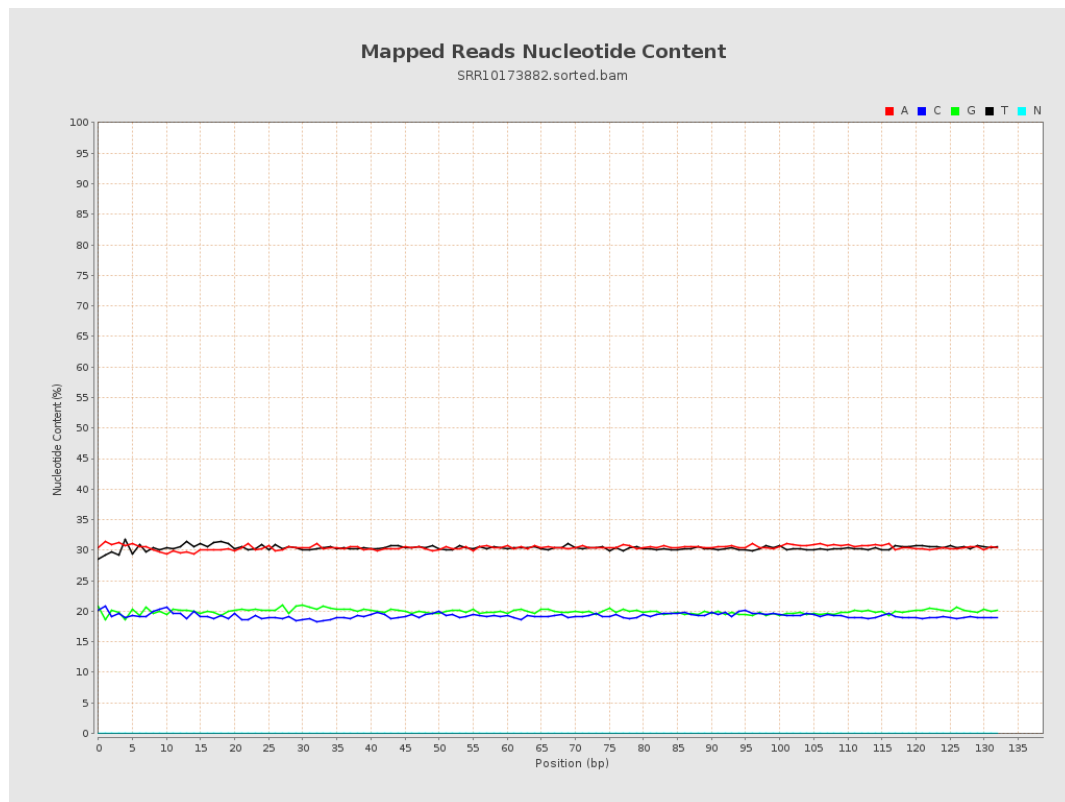
6. Results : Genome Fraction Coverage



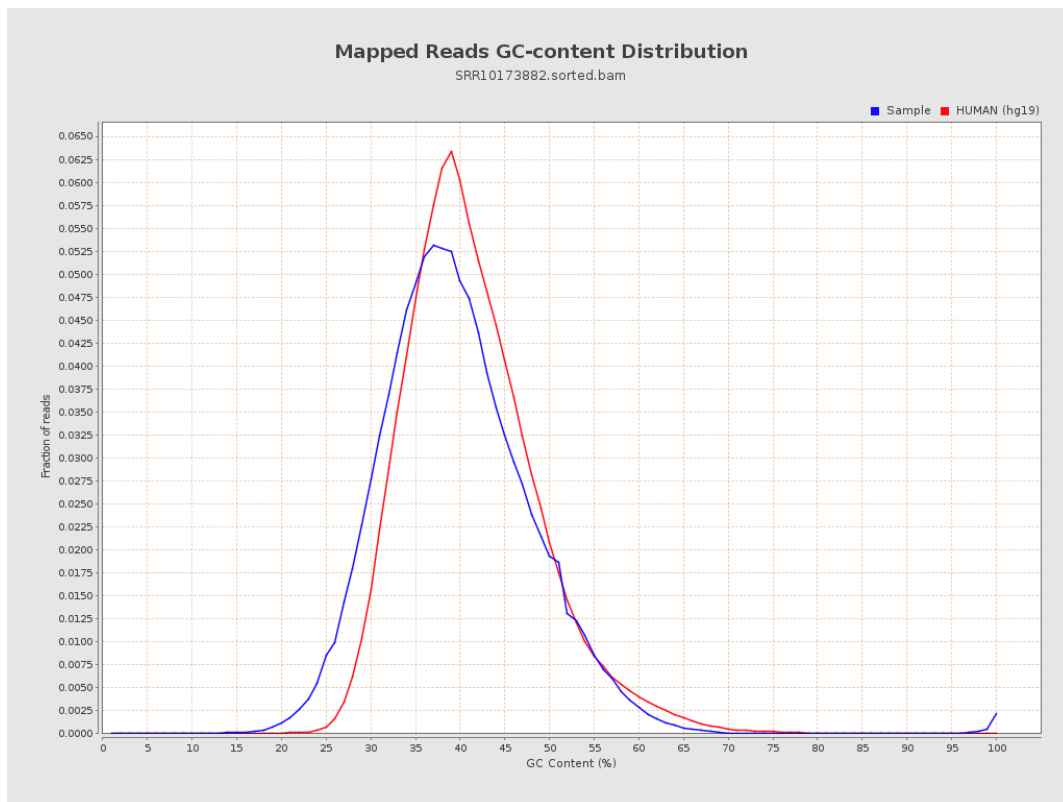
7. Results : Duplication Rate Histogram



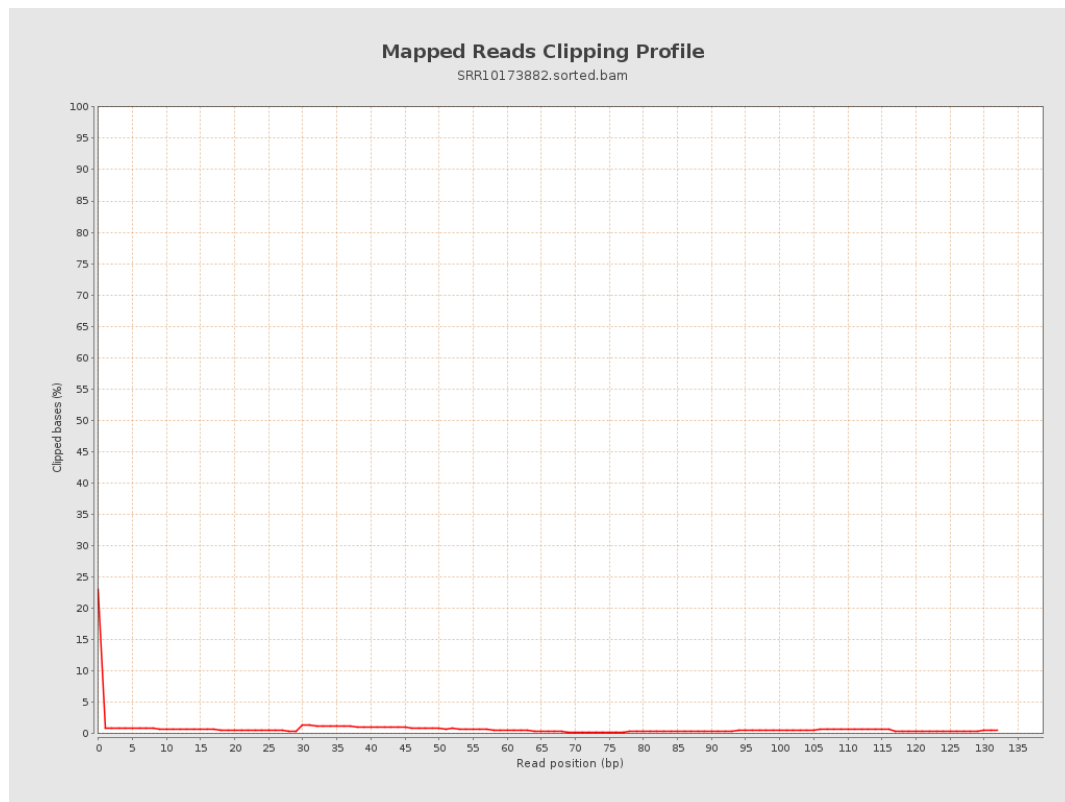
8. Results : Mapped Reads Nucleotide Content



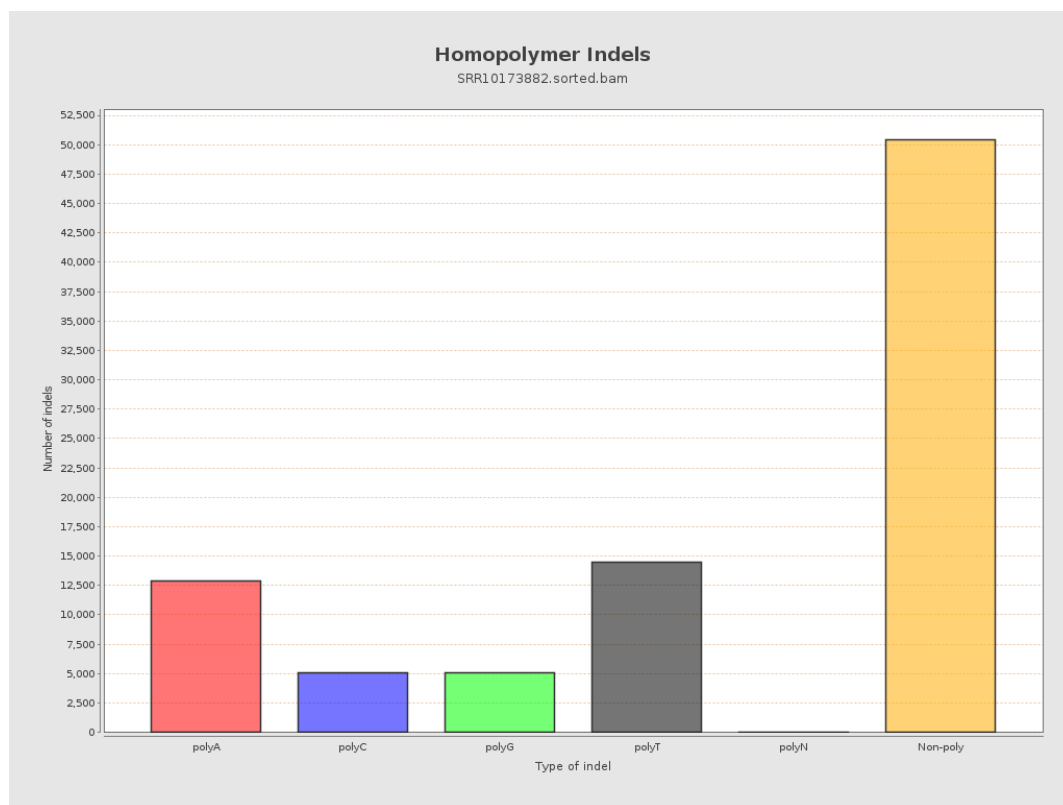
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



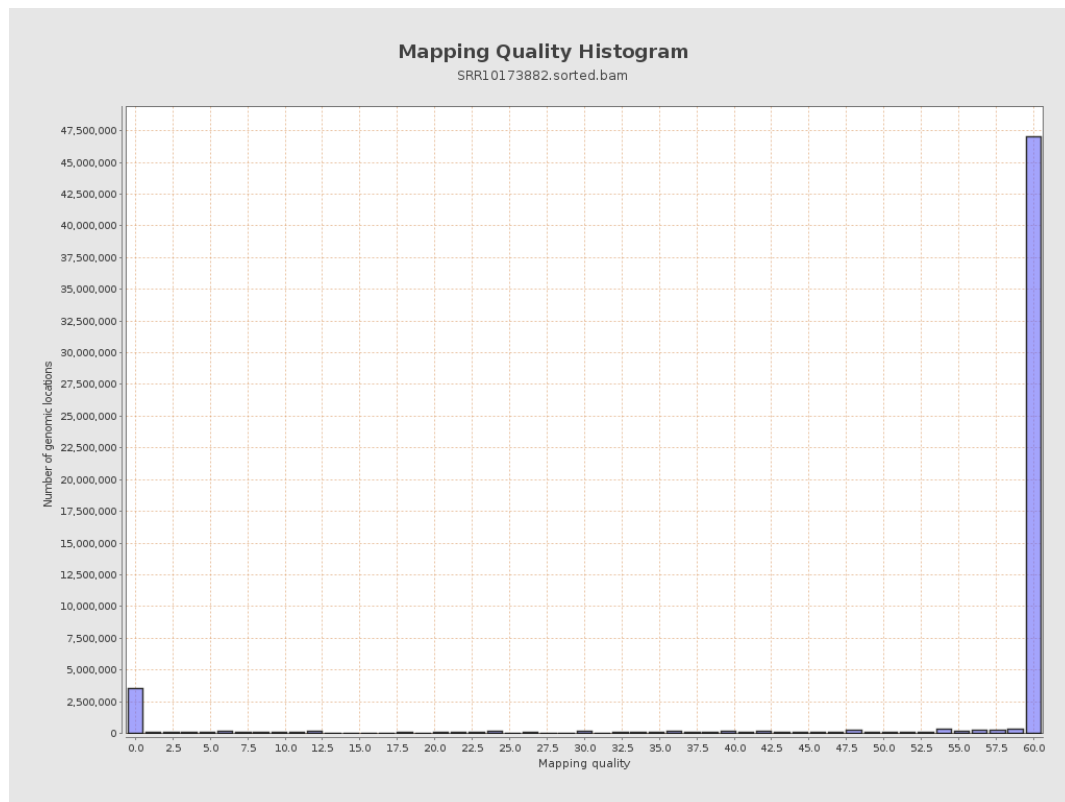
11. Results : Homopolymer Indels



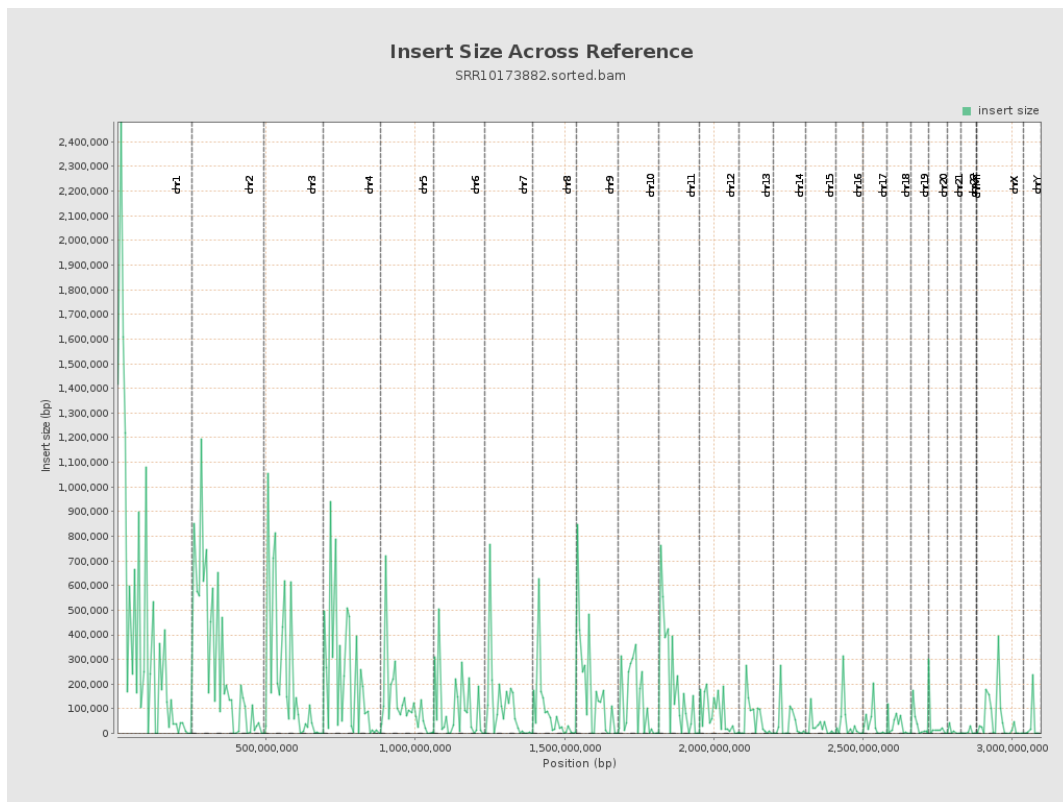
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

