

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 21:11:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046537.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_SRR2046537 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046537_1.fastq.gz SRR2046537_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 21:11:38 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046537.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,321,080
Mapped reads	5,237,727 / 98.43%
Unmapped reads	83,353 / 1.57%
Mapped paired reads	5,237,727 / 98.43%
Mapped reads, first in pair	2,651,101 / 49.82%
Mapped reads, second in pair	2,586,626 / 48.61%
Mapped reads, both in pair	5,165,270 / 97.07%
Mapped reads, singletons	72,457 / 1.36%
Secondary alignments	0
Supplementary alignments	31,842 / 0.6%
Read min/max/mean length	30 / 100 / 100.24
Duplicated reads (estimated)	3,619,098 / 68.01%
Duplication rate	23.2%
Clipped reads	1,055,809 / 19.84%

2.2. ACGT Content

Number/percentage of A's	147,739,430 / 29.23%
Number/percentage of C's	105,393,940 / 20.85%
Number/percentage of T's	147,001,451 / 29.08%
Number/percentage of G's	105,248,372 / 20.82%
Number/percentage of N's	44,896 / 0.01%

GC Percentage	41.68%
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2.3. Coverage

Mean	0.1633
Standard Deviation	48.5704

2.4. Mapping Quality

Mean Mapping Quality	51.78
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2.5. Insert size

Mean	34,610.8
Standard Deviation	1,861,617.01
P25/Median/P75	108 / 135 / 167

2.6. Mismatches and indels

General error rate	0.42%
Mismatches	1,991,295
Insertions	55,599
Mapped reads with at least one insertion	1.04%
Deletions	70,097
Mapped reads with at least one deletion	1.28%
Homopolymer indels	51.38%

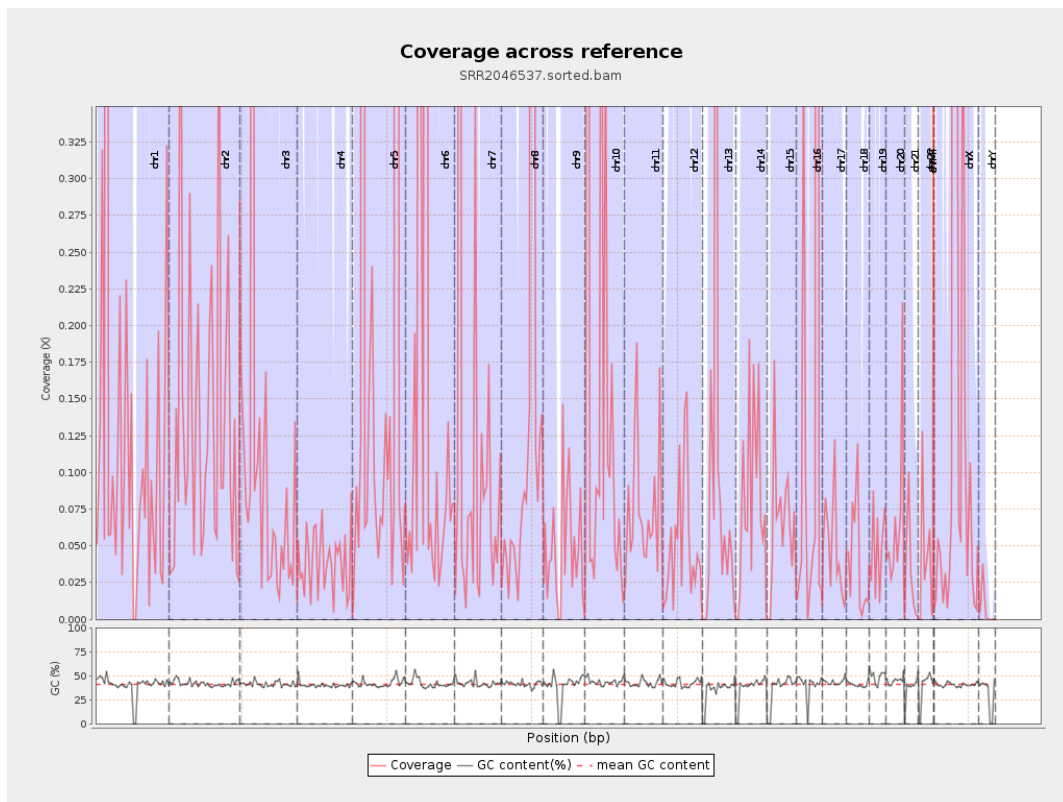
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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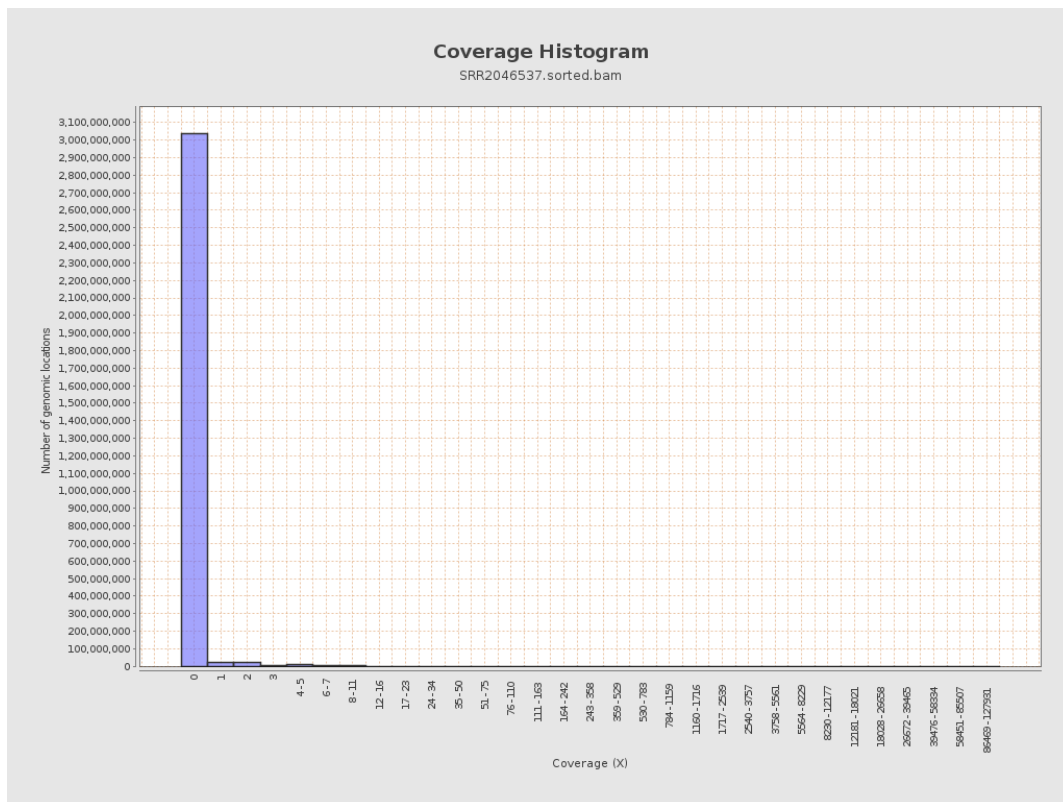
		bases	coverage	deviation
chr1	249250621	39052171	0.1567	17.579
chr2	243199373	33748393	0.1388	9.4193
chr3	198022430	24398032	0.1232	8.9108
chr4	191154276	7567977	0.0396	1.4521
chr5	180915260	76724082	0.4241	75.5564
chr6	171115067	36836205	0.2153	35.2786
chr7	159138663	19531330	0.1227	36.8356
chr8	146364022	125461785	0.8572	185.4513
chr9	141213431	6945068	0.0492	2.8864
chr10	135534747	23840200	0.1759	24.6235
chr11	135006516	10081870	0.0747	3.9849
chr12	133851895	6943359	0.0519	2.1742
chr13	115169878	11411687	0.0991	19.153
chr14	107349540	8682213	0.0809	3.8051
chr15	102531392	6597592	0.0643	2.7867
chr16	90354753	22861719	0.253	65.2033
chr17	81195210	3982835	0.0491	1.5448
chr18	78077248	3031734	0.0388	1.0212
chr19	59128983	2828529	0.0478	1.4739
chr20	63025520	4218473	0.0669	1.2294
chr21	48129895	1577429	0.0328	3.7831
chr22	51304566	2053269	0.04	5.1782
chrMT	16571	391855	23.647	9.7997
chrX	155270560	26491487	0.1706	33.5847

chrY	59373566	396975	0.0067	1.4054
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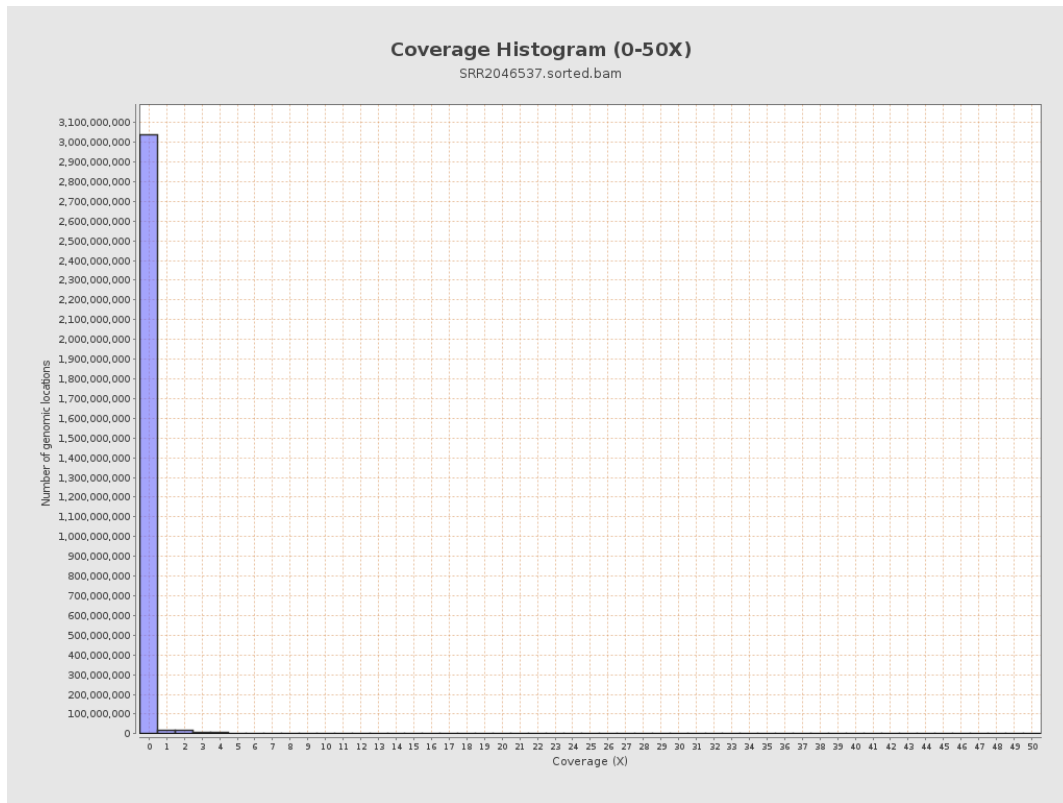
3. Results : Coverage across reference



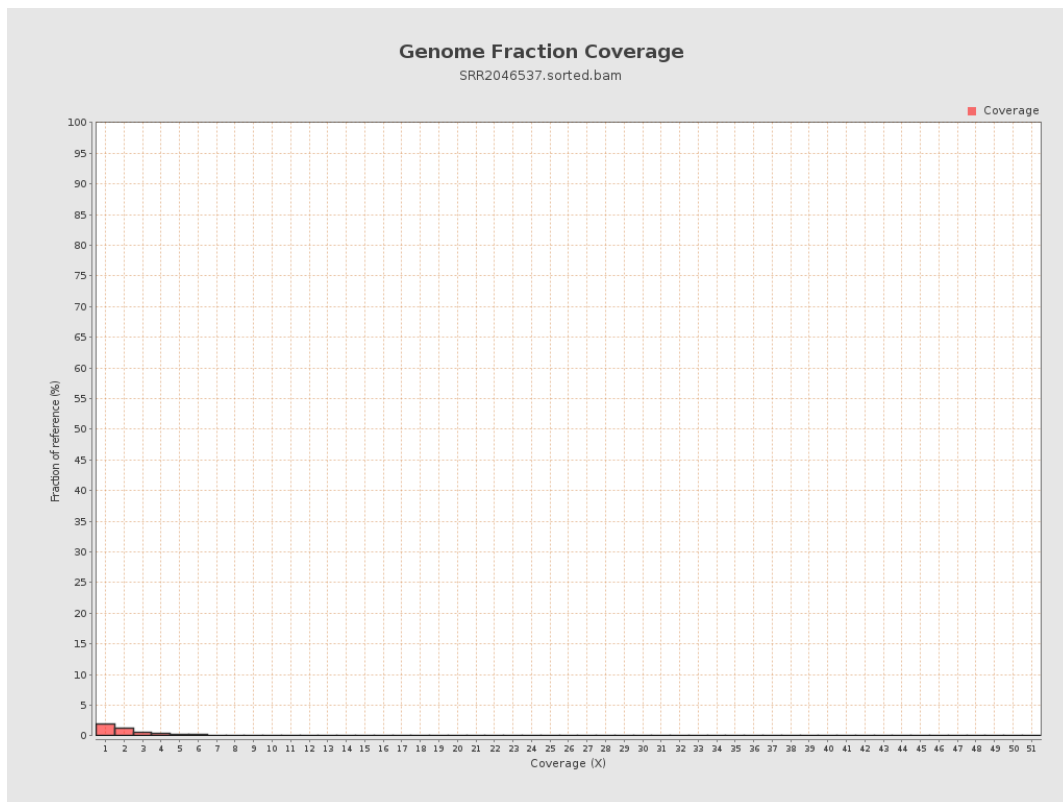
4. Results : Coverage Histogram



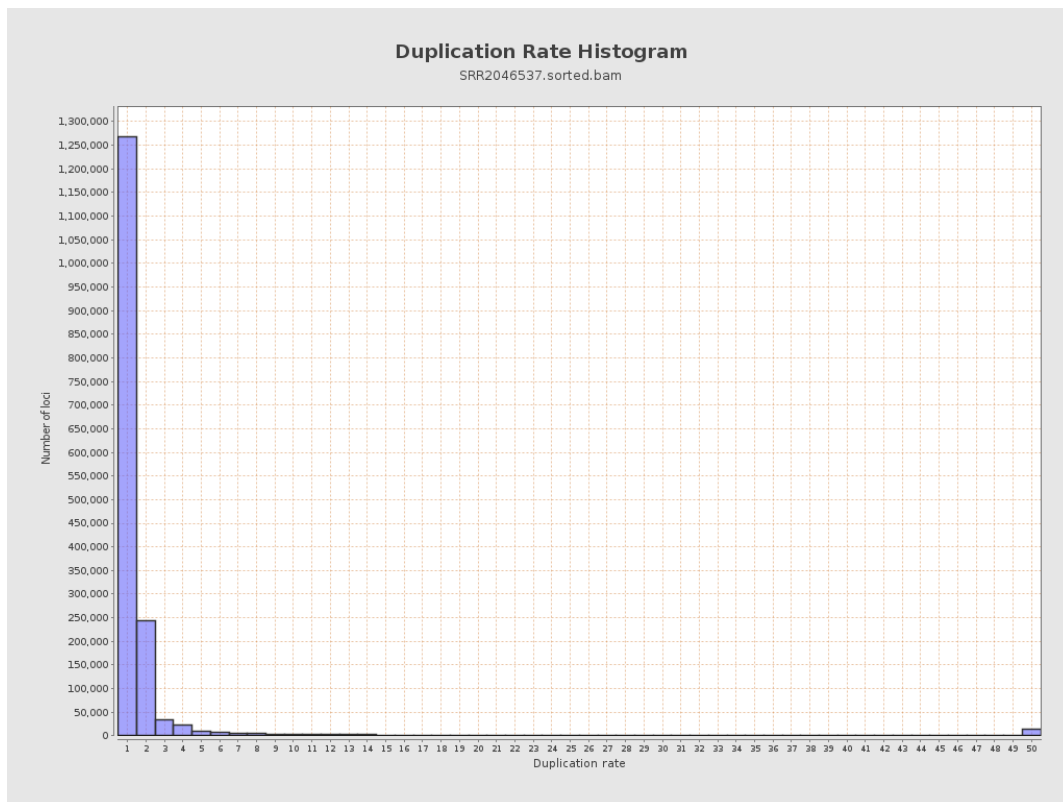
5. Results : Coverage Histogram (0-50X)



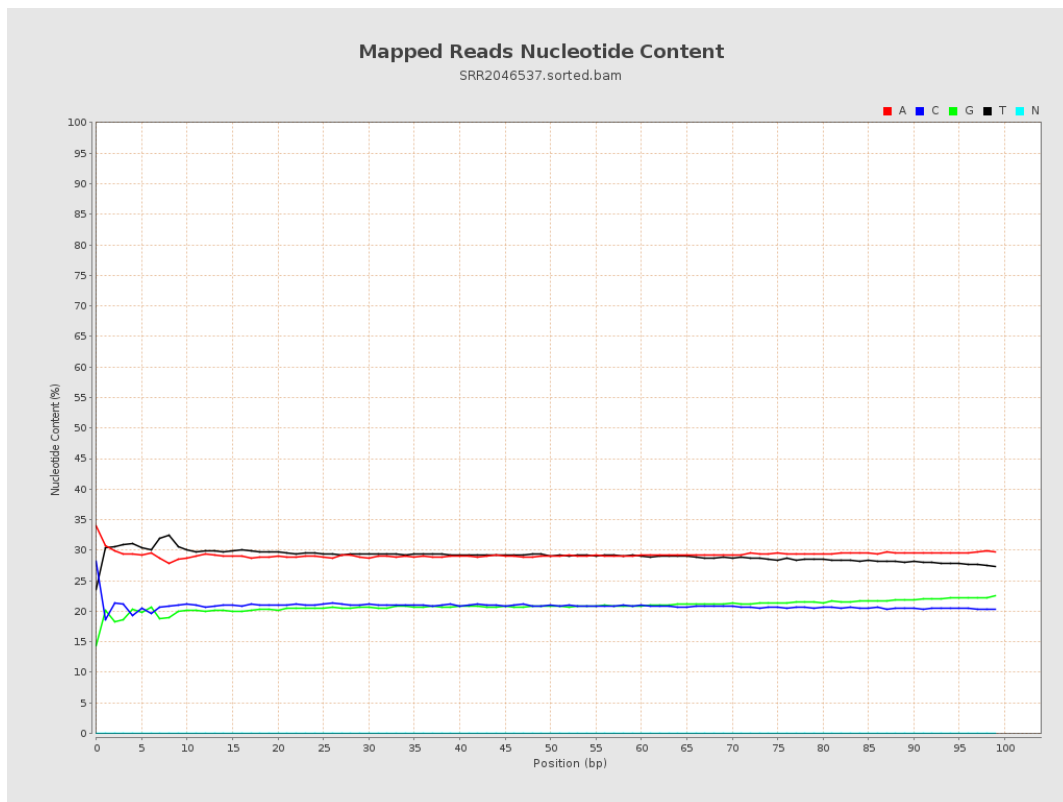
6. Results : Genome Fraction Coverage



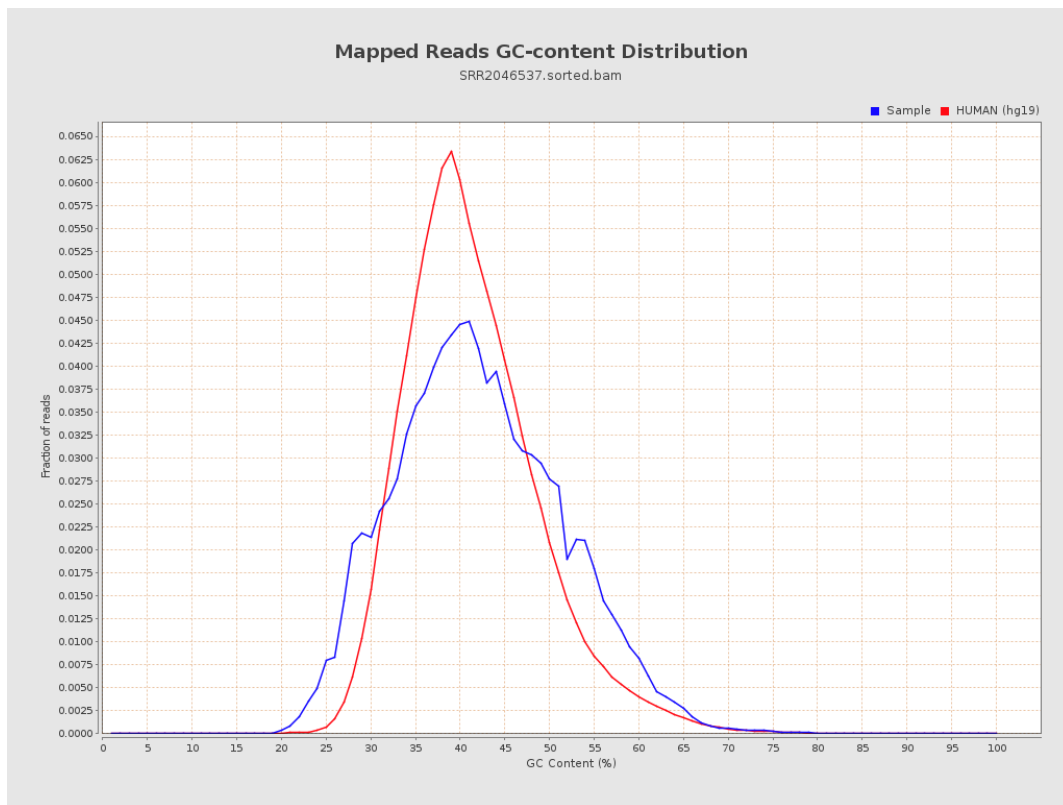
7. Results : Duplication Rate Histogram



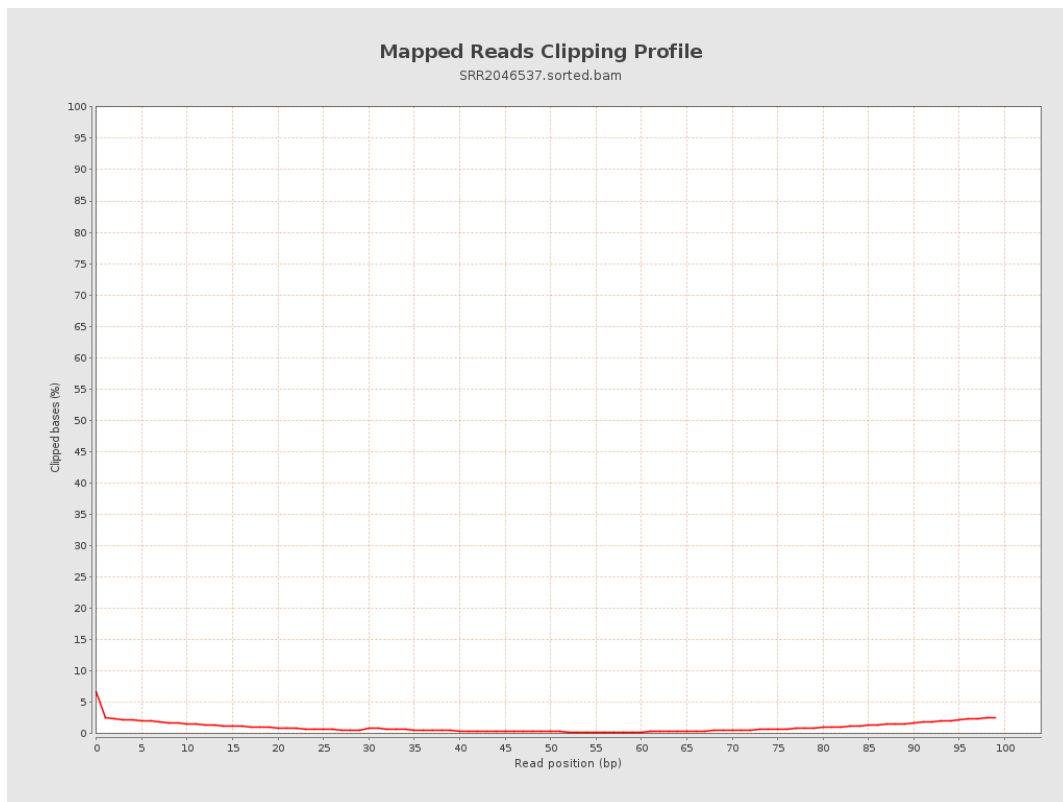
8. Results : Mapped Reads Nucleotide Content



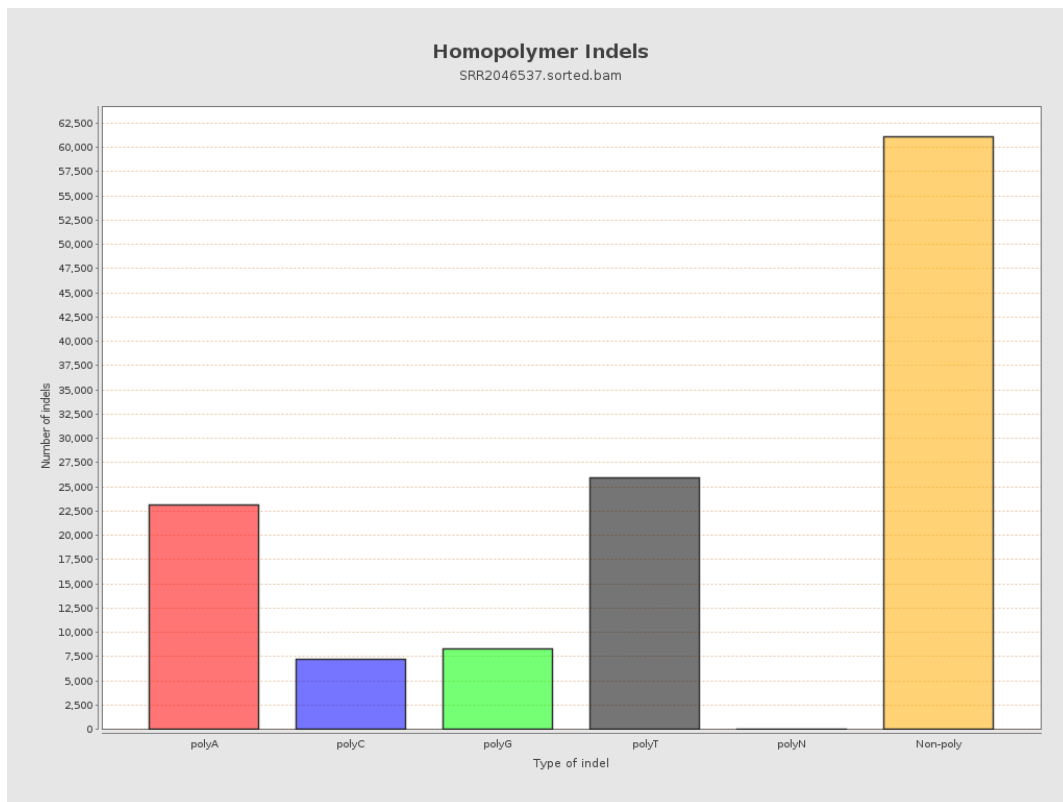
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



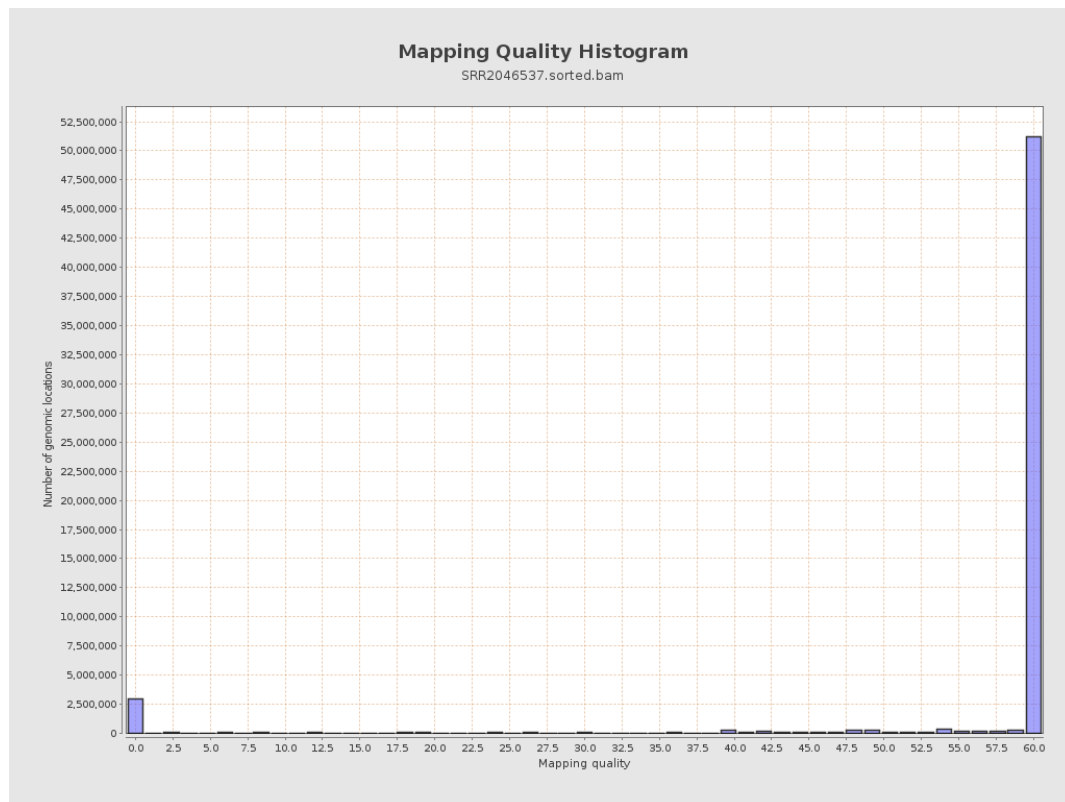
11. Results : Homopolymer Indels



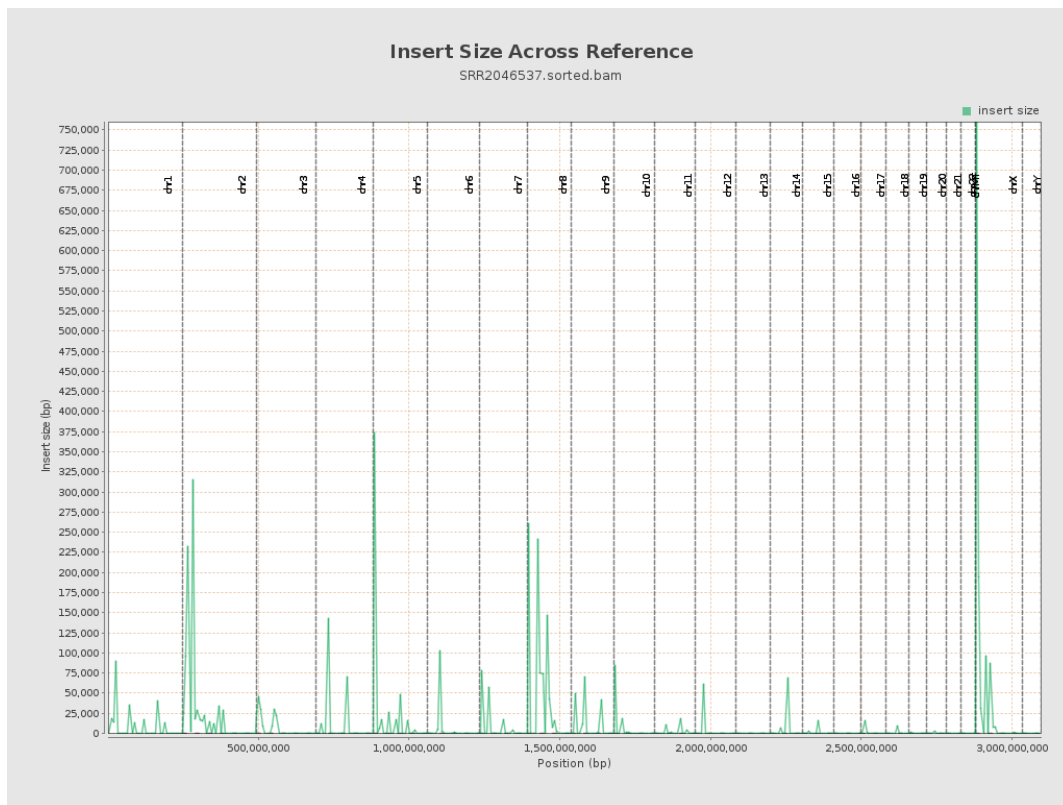
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

