

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 22:27:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046547.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_SRR2046547 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046547_1.fastq.gz SRR2046547_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 22:27:20 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046547.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,644,318
Mapped reads	9,606,031 / 99.6%
Unmapped reads	38,287 / 0.4%
Mapped paired reads	9,606,031 / 99.6%
Mapped reads, first in pair	4,811,837 / 49.89%
Mapped reads, second in pair	4,794,194 / 49.71%
Mapped reads, both in pair	9,578,908 / 99.32%
Mapped reads, singletons	27,123 / 0.28%
Secondary alignments	0
Supplementary alignments	42,016 / 0.44%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	8,157,014 / 84.58%
Duplication rate	23.84%
Clipped reads	783,167 / 8.12%

2.2. ACGT Content

Number/percentage of A's	253,747,565 / 26.74%
Number/percentage of C's	220,231,075 / 23.21%
Number/percentage of T's	255,160,596 / 26.89%
Number/percentage of G's	219,629,932 / 23.15%
Number/percentage of N's	82,369 / 0.01%

GC Percentage	46.36%
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2.3. Coverage

Mean	0.3066
Standard Deviation	72.2685

2.4. Mapping Quality

Mean Mapping Quality	49.07
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2.5. Insert size

Mean	14,862.35
Standard Deviation	1,296,667.6
P25/Median/P75	138 / 173 / 214

2.6. Mismatches and indels

General error rate	0.47%
Mismatches	4,304,773
Insertions	57,459
Mapped reads with at least one insertion	0.59%
Deletions	98,117
Mapped reads with at least one deletion	0.98%
Homopolymer indels	45.81%

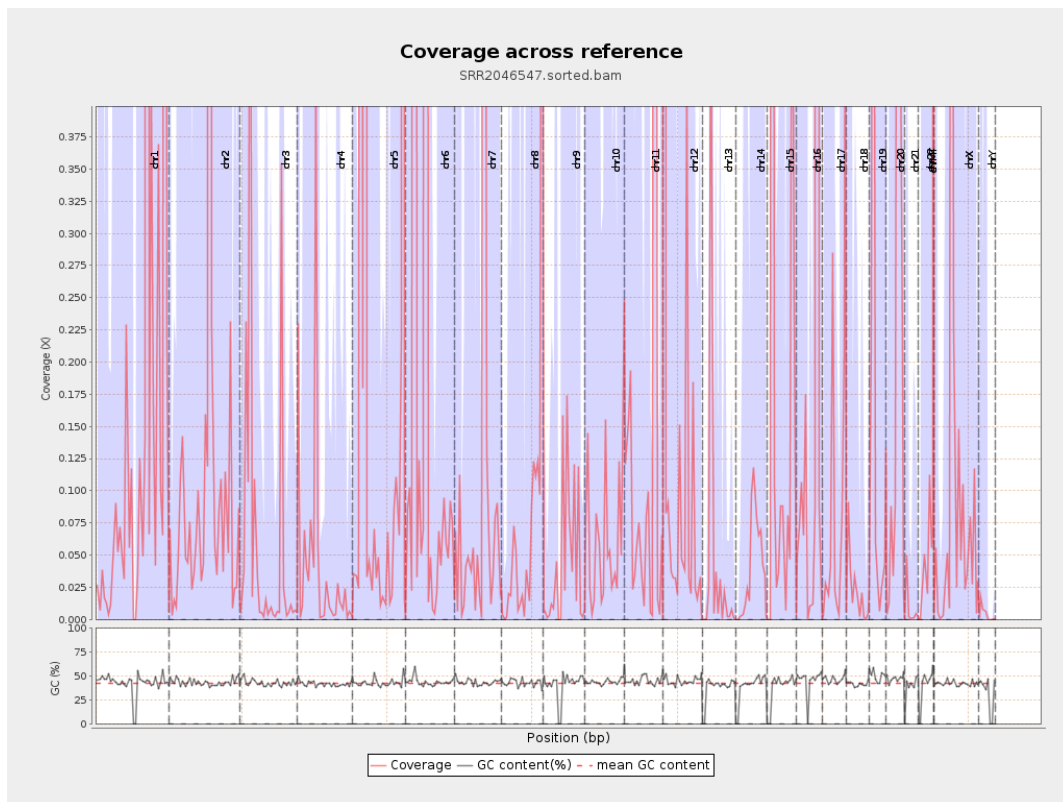
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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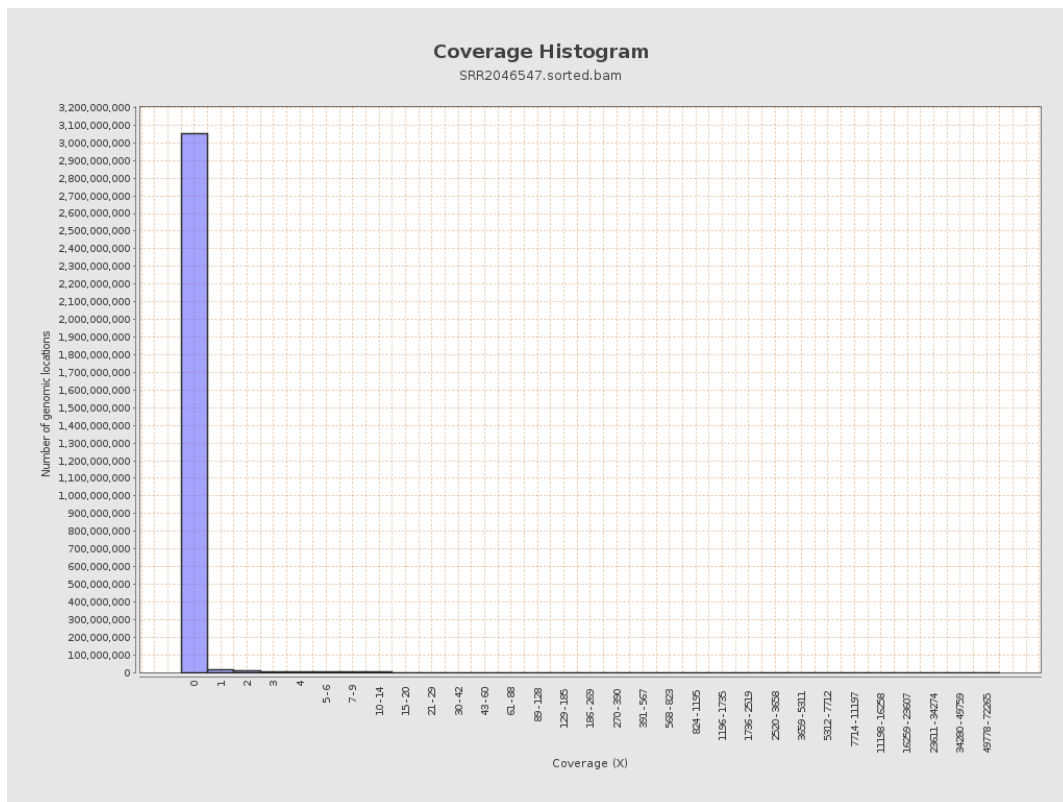
		bases	coverage	deviation
chr1	249250621	86045701	0.3452	84.5695
chr2	243199373	61415469	0.2525	66.1925
chr3	198022430	13353991	0.0674	7.089
chr4	191154276	8314980	0.0435	6.2102
chr5	180915260	237057192	1.3103	151.5365
chr6	171115067	85617626	0.5004	86.8536
chr7	159138663	19105572	0.1201	20.4244
chr8	146364022	12742993	0.0871	22.0773
chr9	141213431	6301822	0.0446	3.978
chr10	135534747	8179647	0.0604	2.4456
chr11	135006516	24611251	0.1823	33.0137
chr12	133851895	63368734	0.4734	88.2093
chr13	115169878	4971707	0.0432	14.9594
chr14	107349540	4339927	0.0404	2.2903
chr15	102531392	28396296	0.277	44.3699
chr16	90354753	229375705	2.5386	255.8906
chr17	81195210	7567933	0.0932	8.9544
chr18	78077248	1736464	0.0222	0.3884
chr19	59128983	10633923	0.1798	14.8013
chr20	63025520	13711024	0.2175	11.74
chr21	48129895	467465	0.0097	0.2432
chr22	51304566	2184861	0.0426	1.9026
chrMT	16571	297262	17.9387	7.77
chrX	155270560	19109721	0.1231	47.7566

chrY	59373566	258615	0.0044	0.4407
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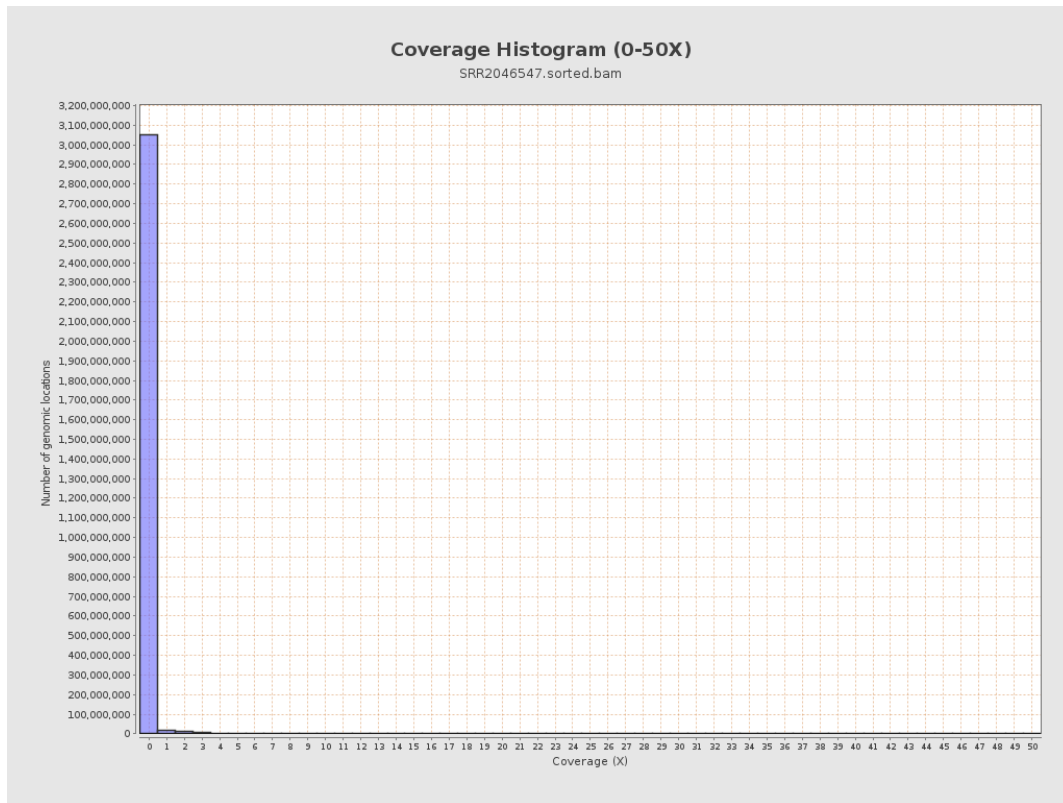
3. Results : Coverage across reference



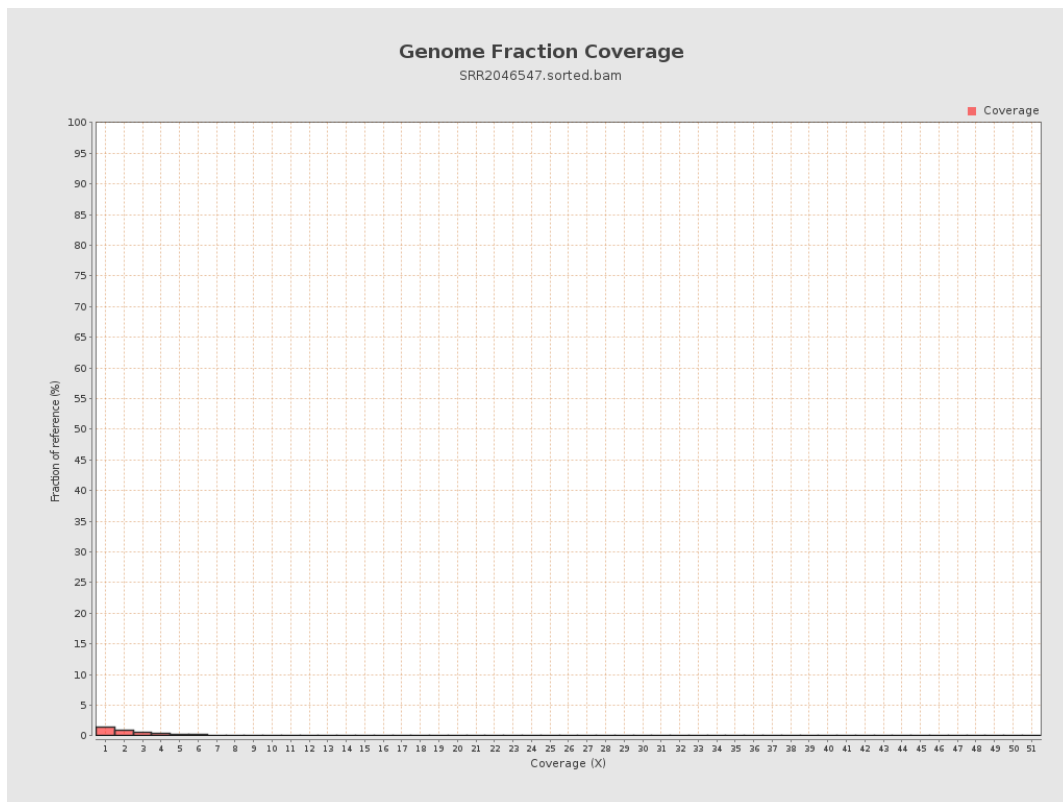
4. Results : Coverage Histogram



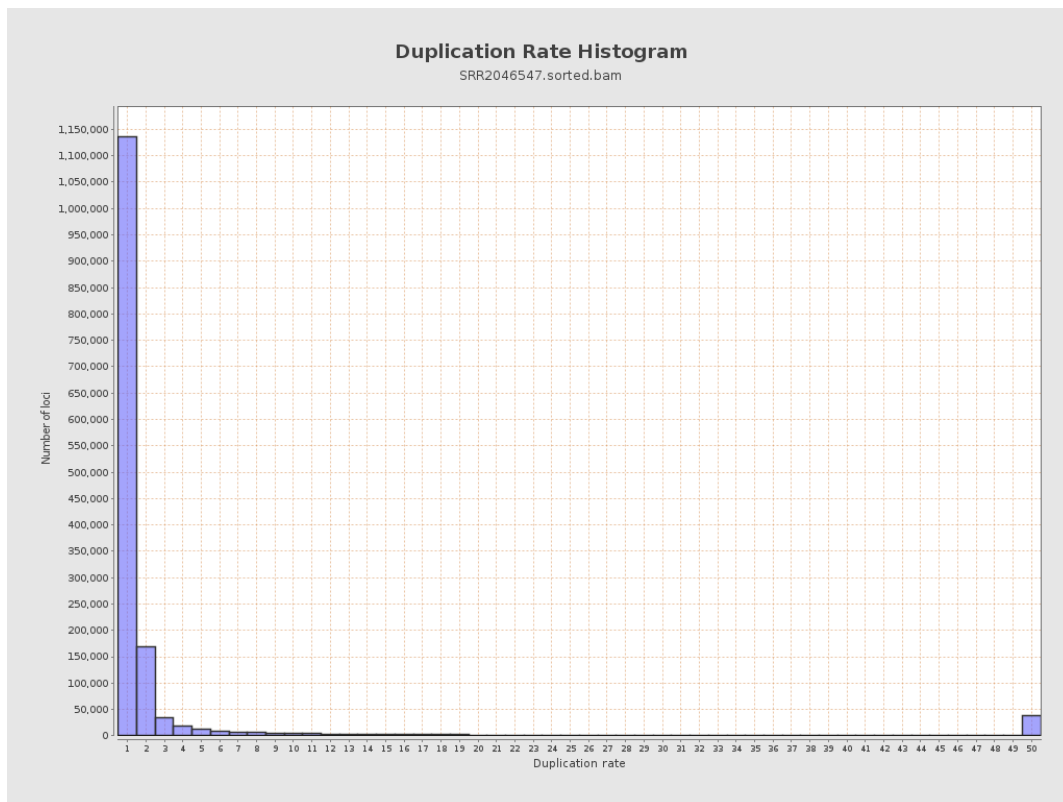
5. Results : Coverage Histogram (0-50X)



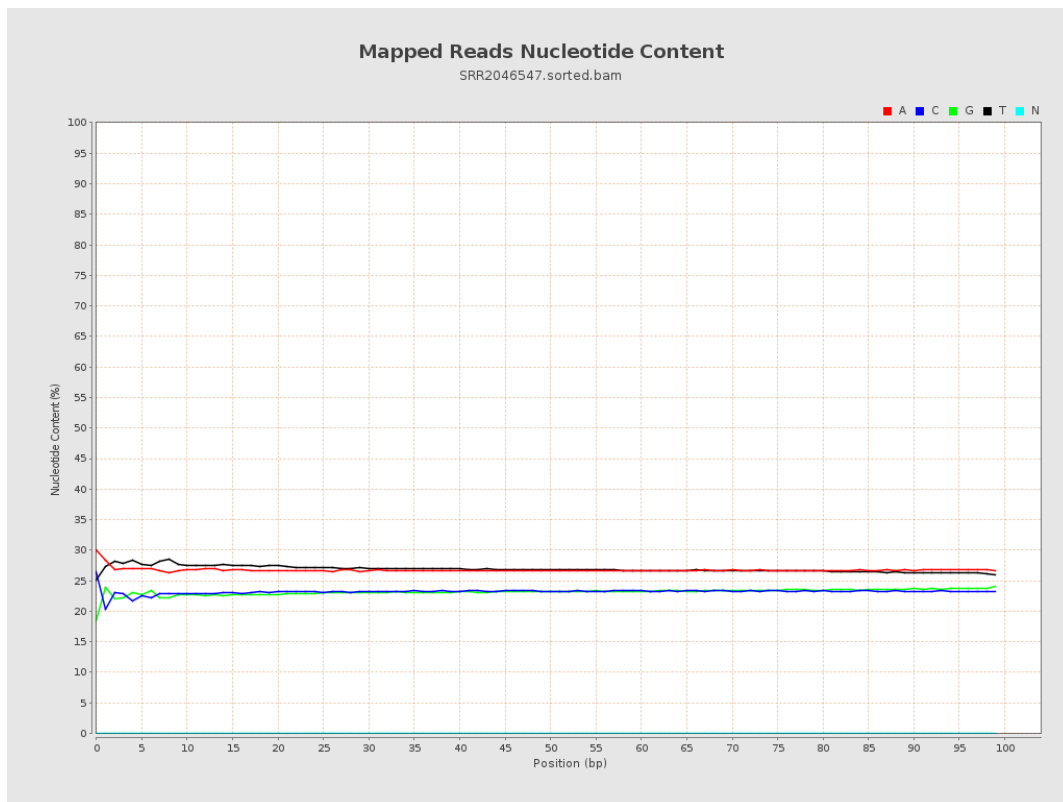
6. Results : Genome Fraction Coverage



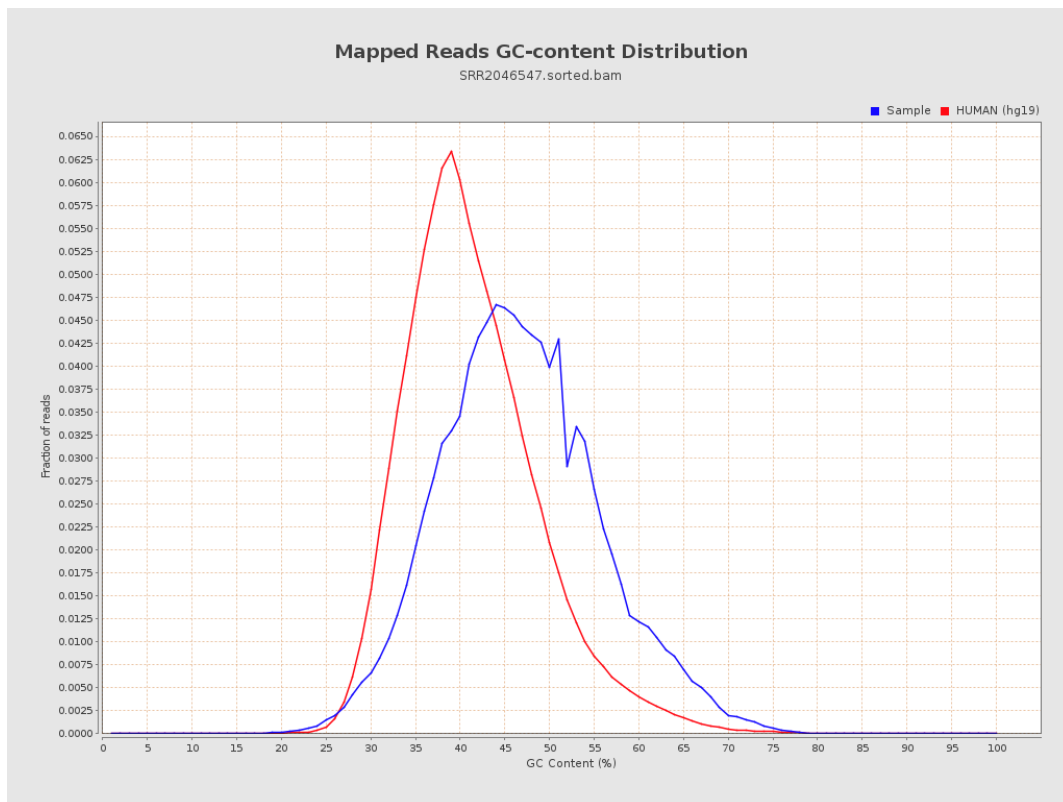
7. Results : Duplication Rate Histogram



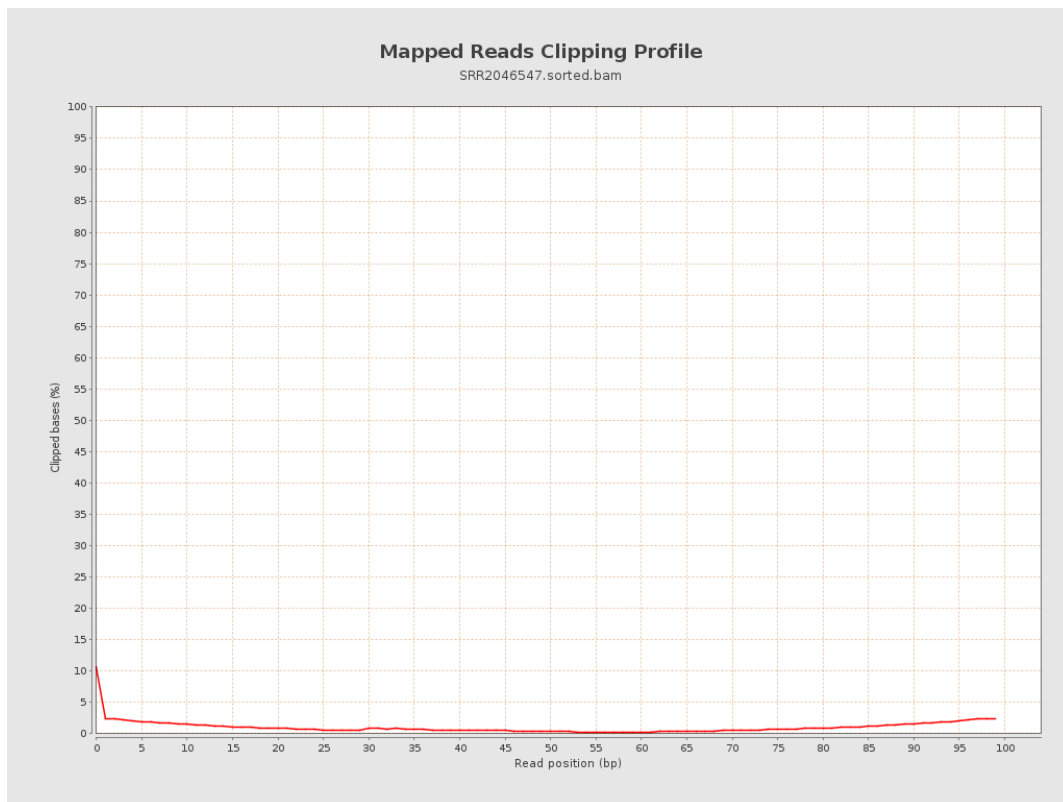
8. Results : Mapped Reads Nucleotide Content



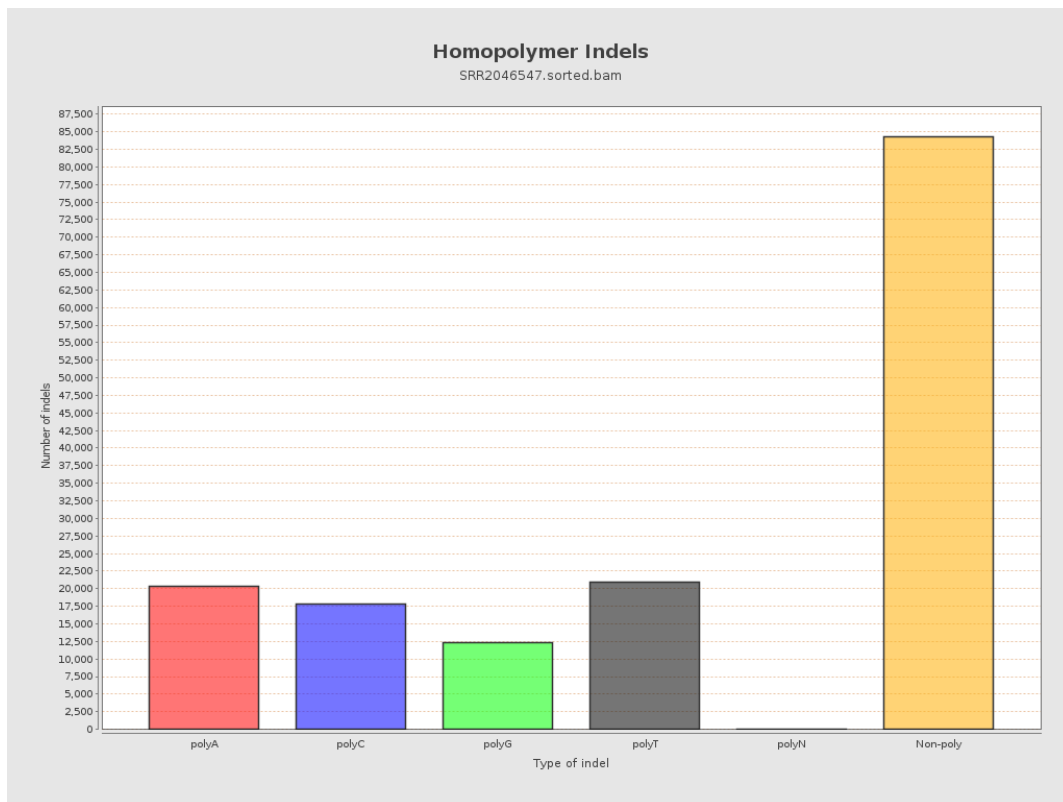
9. Results : Mapped Reads GC-content Distribution



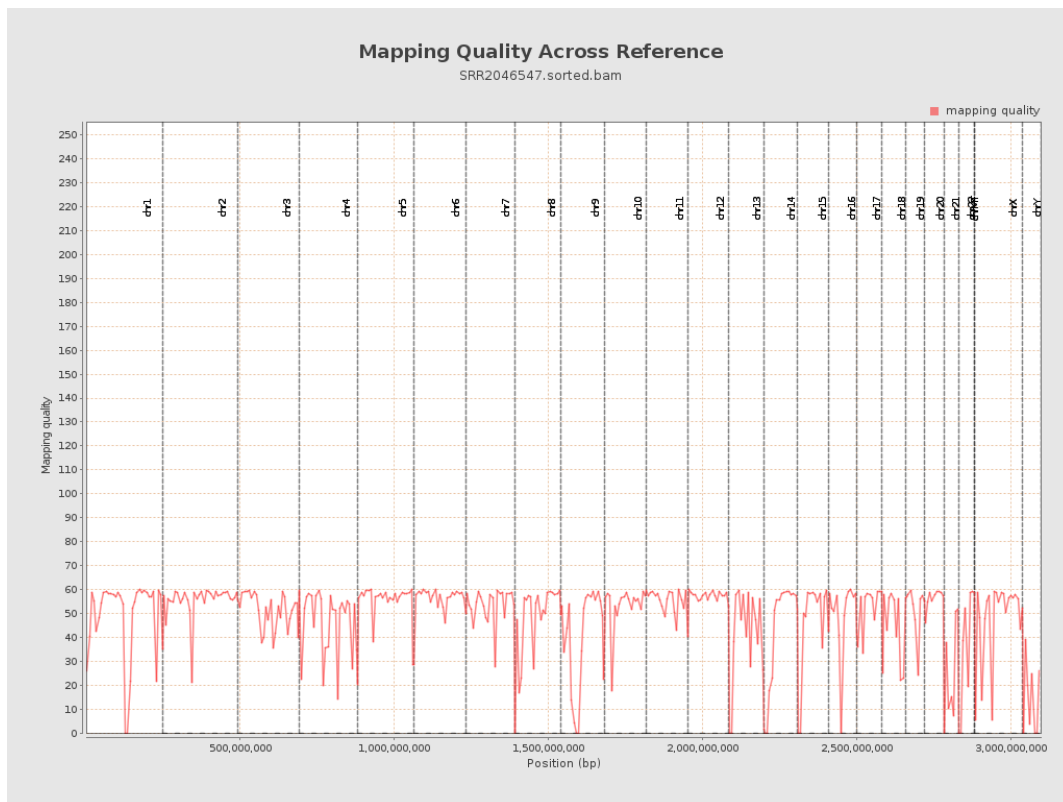
10. Results : Mapped Reads Clipping Profile



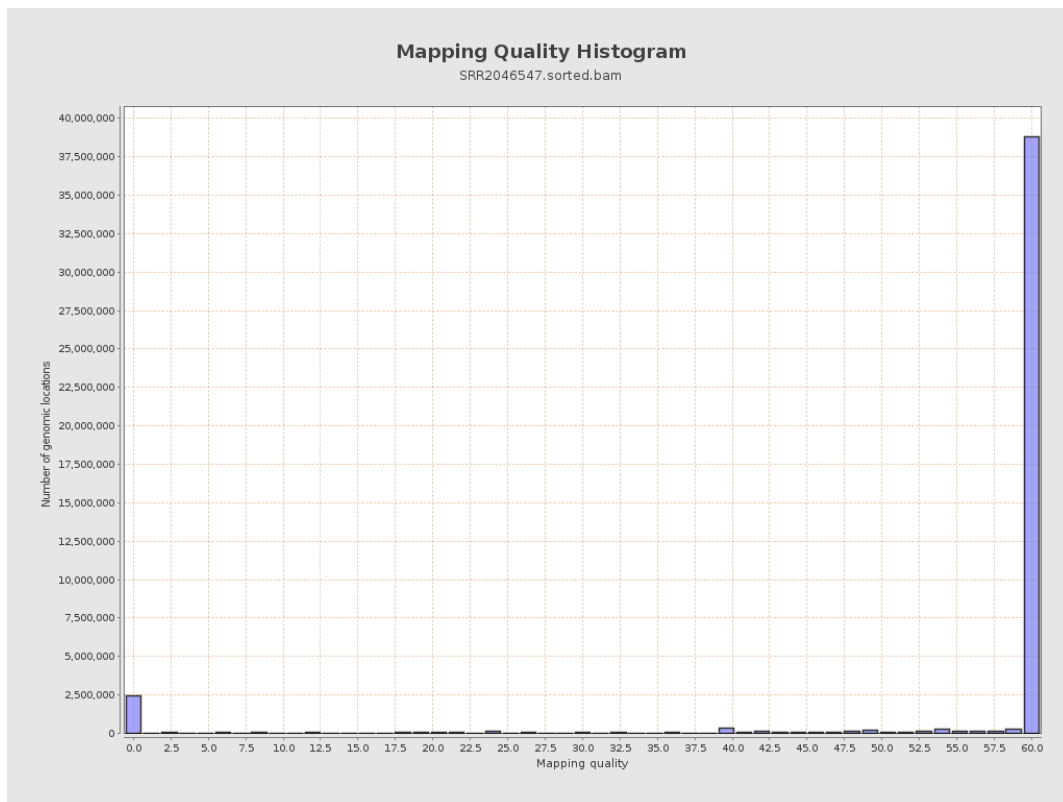
11. Results : Homopolymer Indels



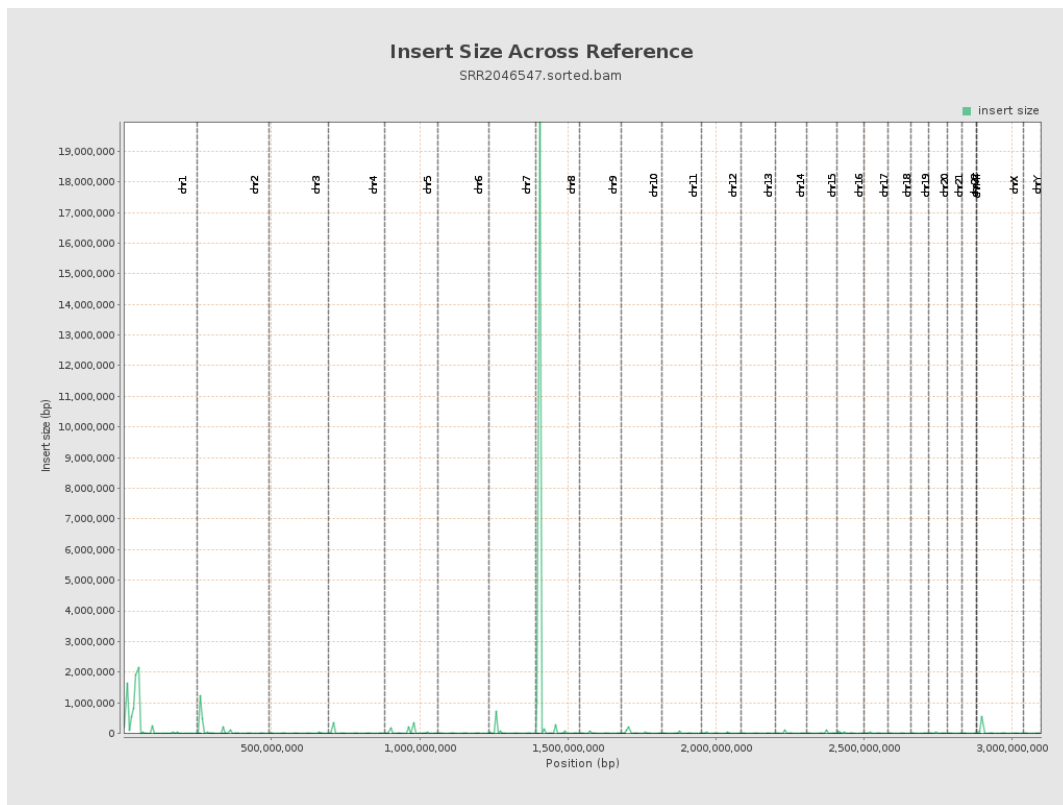
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

