

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 14:36:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046436.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_SRR2046436 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046436_1.fastq.gz SRR2046436_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 14:36:38 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046436.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,540,400
Mapped reads	9,483,508 / 99.4%
Unmapped reads	56,892 / 0.6%
Mapped paired reads	9,483,508 / 99.4%
Mapped reads, first in pair	4,744,765 / 49.73%
Mapped reads, second in pair	4,738,743 / 49.67%
Mapped reads, both in pair	9,447,170 / 99.02%
Mapped reads, singletons	36,338 / 0.38%
Secondary alignments	0
Supplementary alignments	72,534 / 0.76%
Read min/max/mean length	30 / 100 / 100.31
Duplicated reads (estimated)	8,291,951 / 86.91%
Duplication rate	31.45%
Clipped reads	2,680,137 / 28.09%

2.2. ACGT Content

Number/percentage of A's	272,126,254 / 30.15%
Number/percentage of C's	180,219,766 / 19.97%
Number/percentage of T's	270,431,430 / 29.97%
Number/percentage of G's	179,575,526 / 19.9%
Number/percentage of N's	81,887 / 0.01%

GC Percentage	39.87%
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2.3. Coverage

Mean	0.2916
Standard Deviation	76.8234

2.4. Mapping Quality

Mean Mapping Quality	50.53
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2.5. Insert size

Mean	15,780.56
Standard Deviation	1,372,815.98
P25/Median/P75	98 / 123 / 152

2.6. Mismatches and indels

General error rate	0.36%
Mismatches	3,160,183
Insertions	56,784
Mapped reads with at least one insertion	0.59%
Deletions	72,410
Mapped reads with at least one deletion	0.75%
Homopolymer indels	47.35%

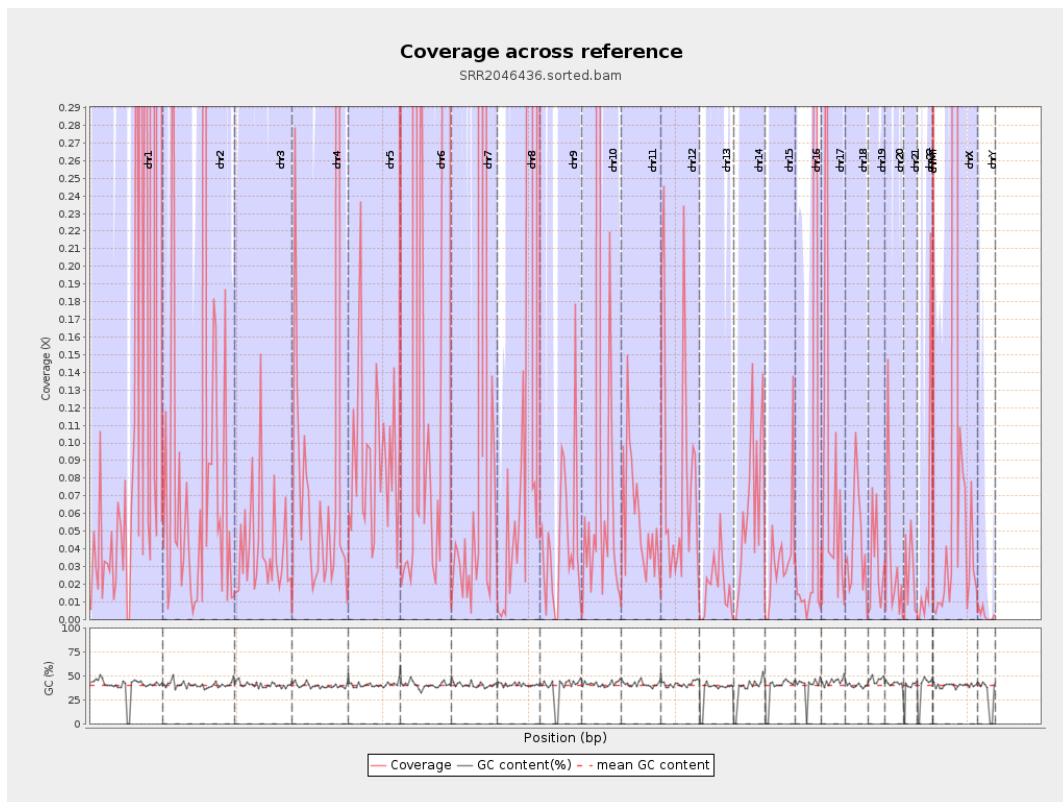
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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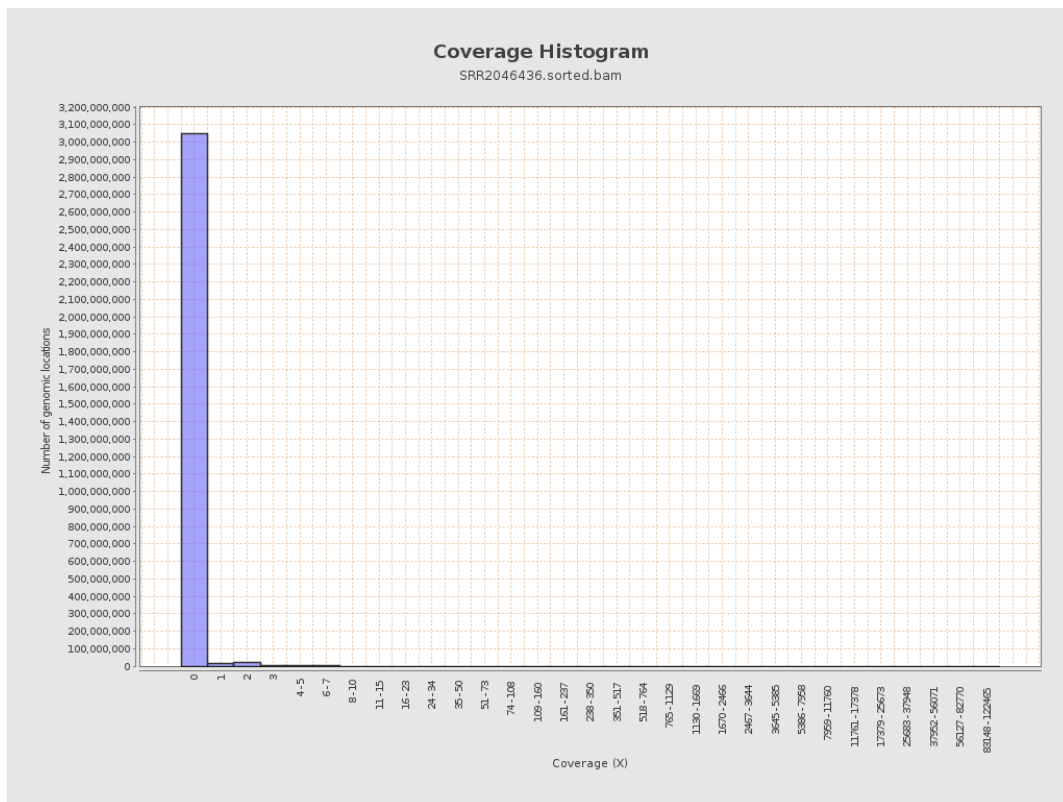
		bases	coverage	deviation
chr1	249250621	127542628	0.5117	89.2027
chr2	243199373	26701931	0.1098	12.6491
chr3	198022430	7990388	0.0404	2.5927
chr4	191154276	32813764	0.1717	41.6726
chr5	180915260	18489319	0.1022	5.2606
chr6	171115067	168060343	0.9821	130.0636
chr7	159138663	123707791	0.7774	127.673
chr8	146364022	229108633	1.5653	242.6233
chr9	141213431	6341890	0.0449	2.3331
chr10	135534747	27907443	0.2059	51.7398
chr11	135006516	7674577	0.0568	1.8804
chr12	133851895	10792684	0.0806	9.0538
chr13	115169878	2179969	0.0189	1.125
chr14	107349540	6663275	0.0621	5.5482
chr15	102531392	3653158	0.0356	2.2028
chr16	90354753	7634062	0.0845	10.2097
chr17	81195210	7439329	0.0916	8.5431
chr18	78077248	3374492	0.0432	1.0893
chr19	59128983	1955424	0.0331	1.5243
chr20	63025520	2081209	0.033	2.3145
chr21	48129895	1200266	0.0249	1.9509
chr22	51304566	2033106	0.0396	4.1203
chrMT	16571	330862	19.9663	8.7232
chrX	155270560	76818199	0.4947	95.2505

chrY	59373566	155041	0.0026	0.1279
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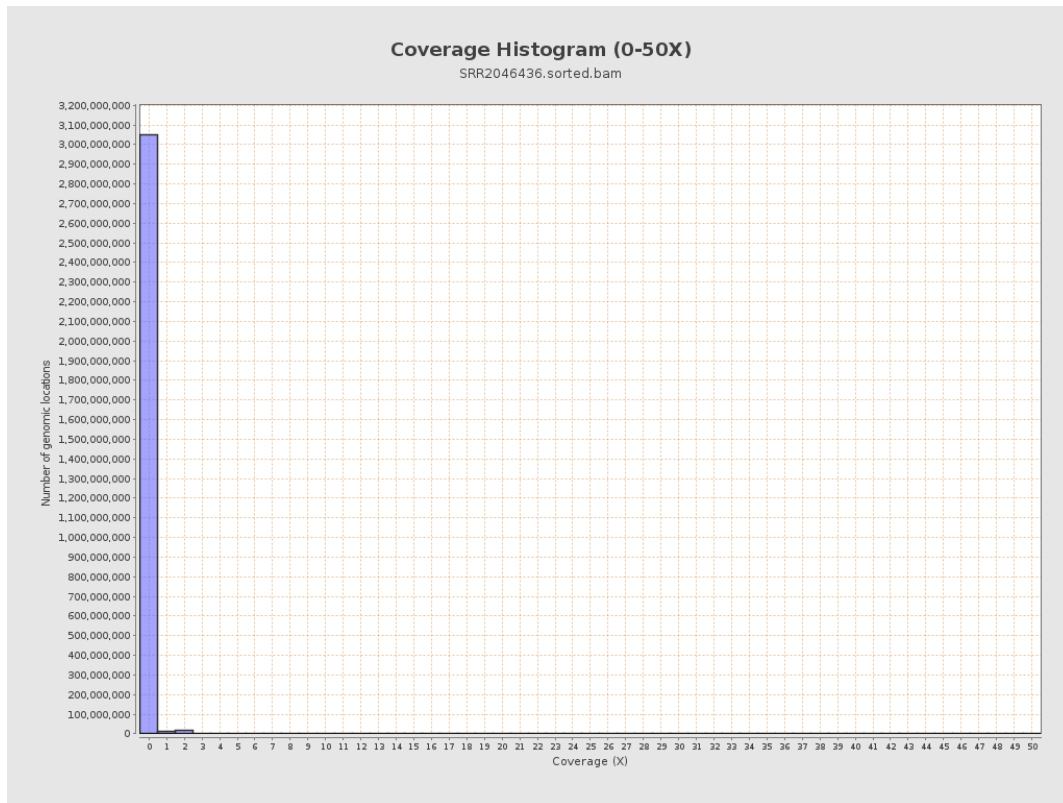
3. Results : Coverage across reference



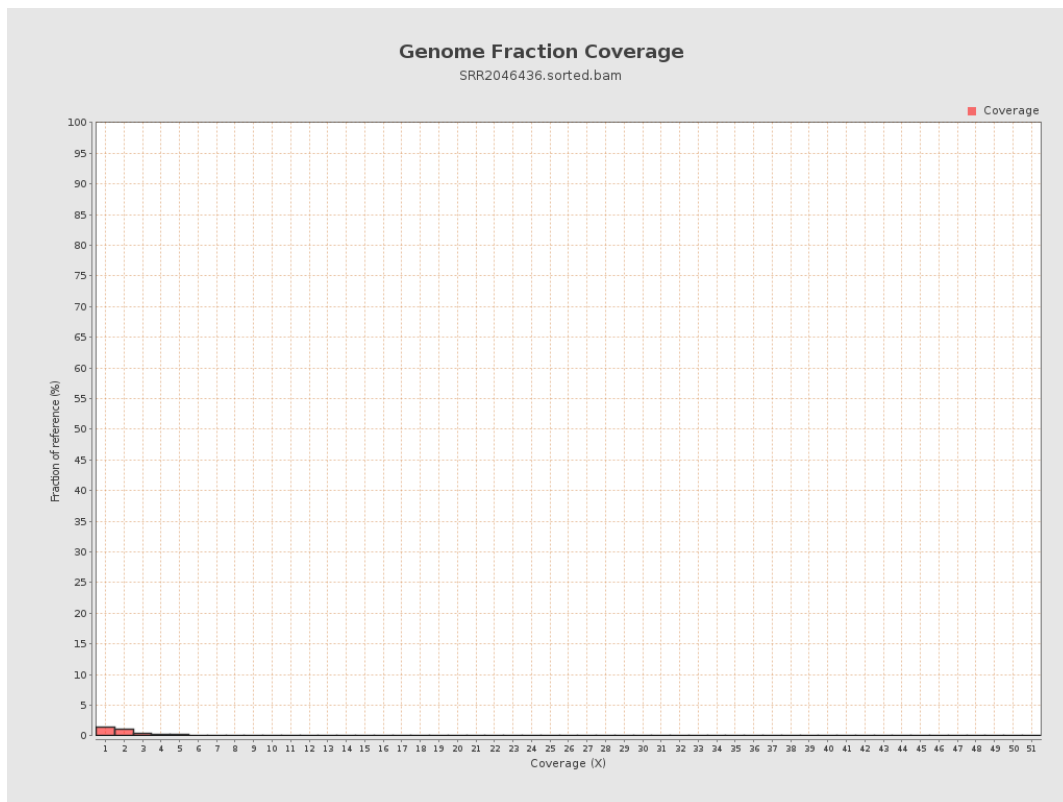
4. Results : Coverage Histogram



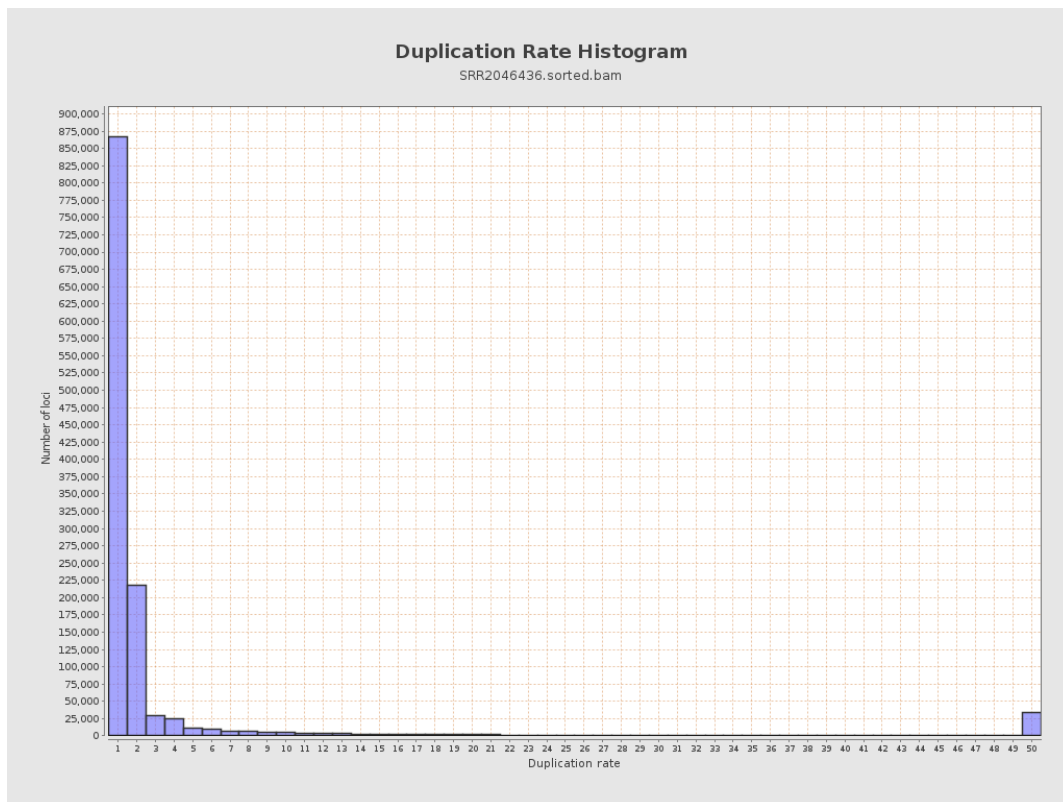
5. Results : Coverage Histogram (0-50X)



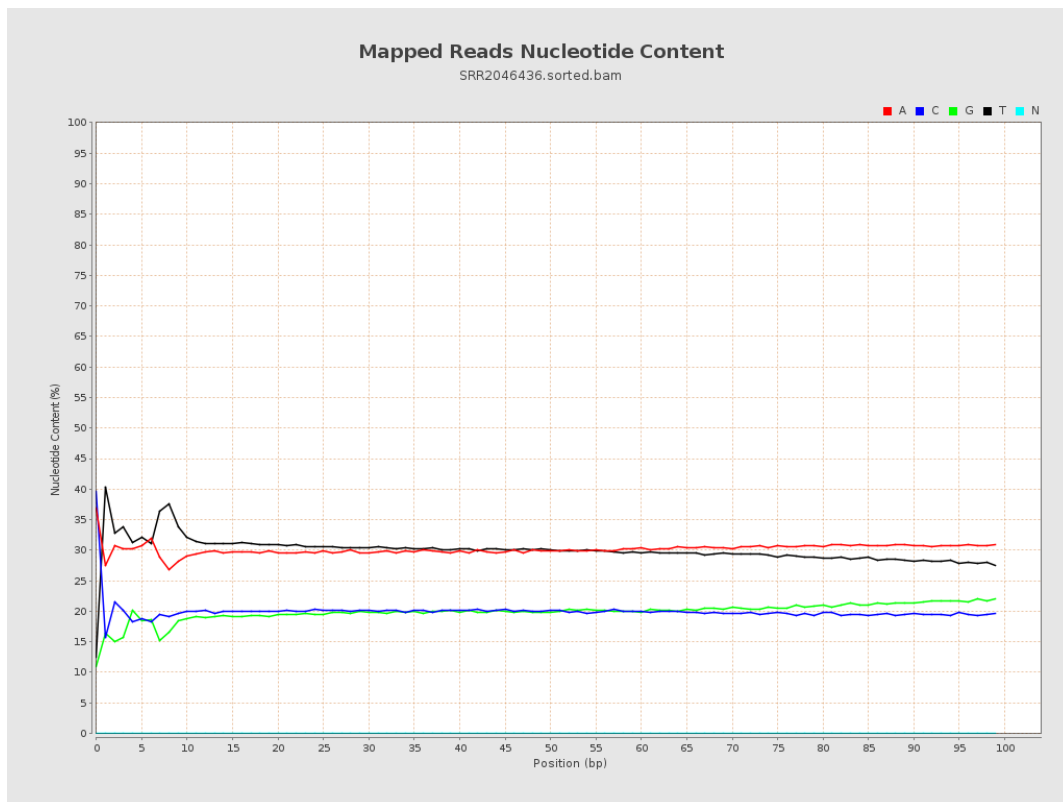
6. Results : Genome Fraction Coverage



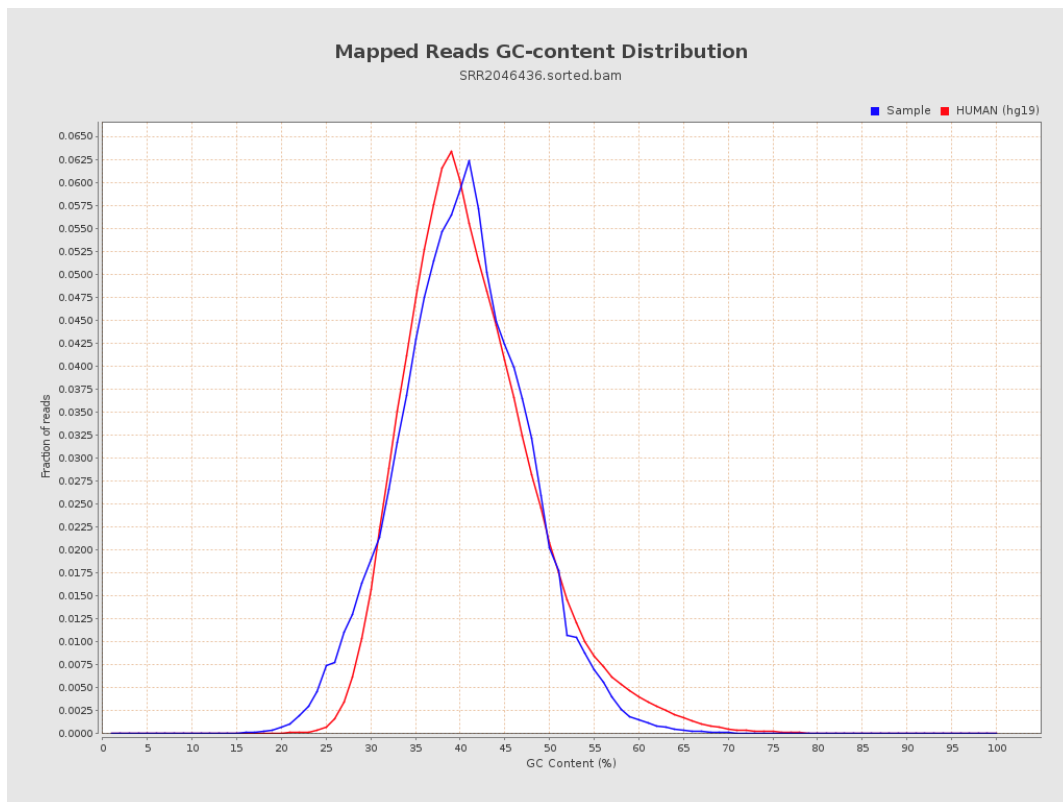
7. Results : Duplication Rate Histogram



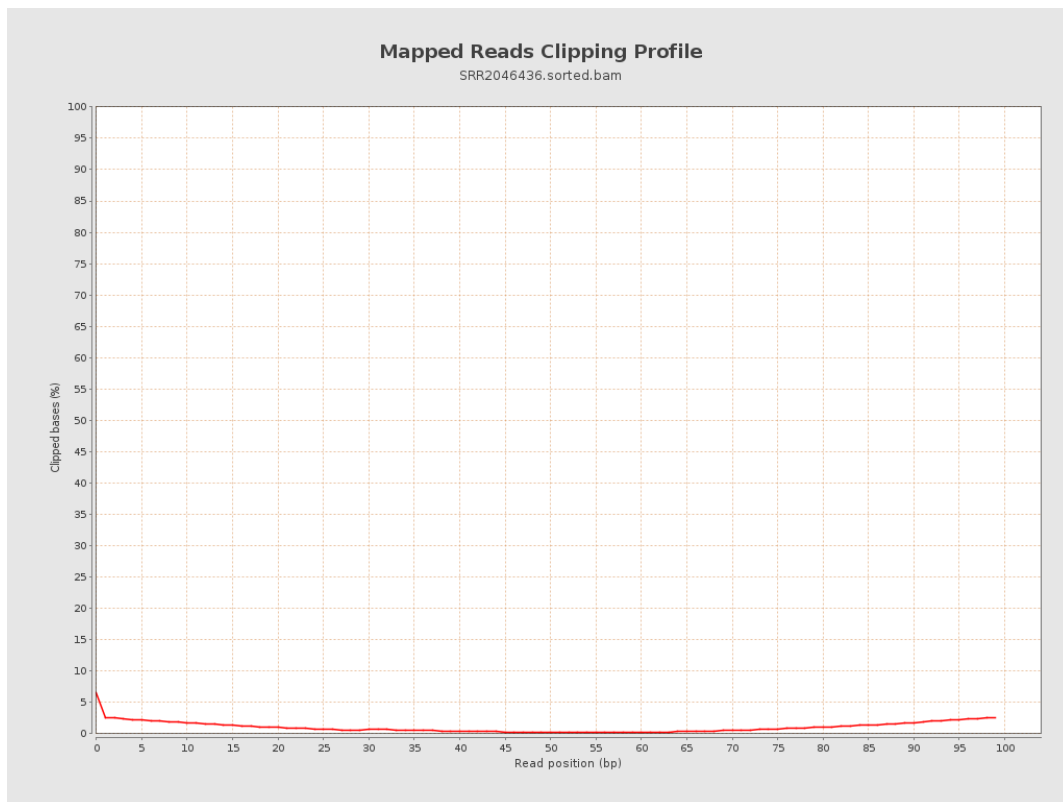
8. Results : Mapped Reads Nucleotide Content



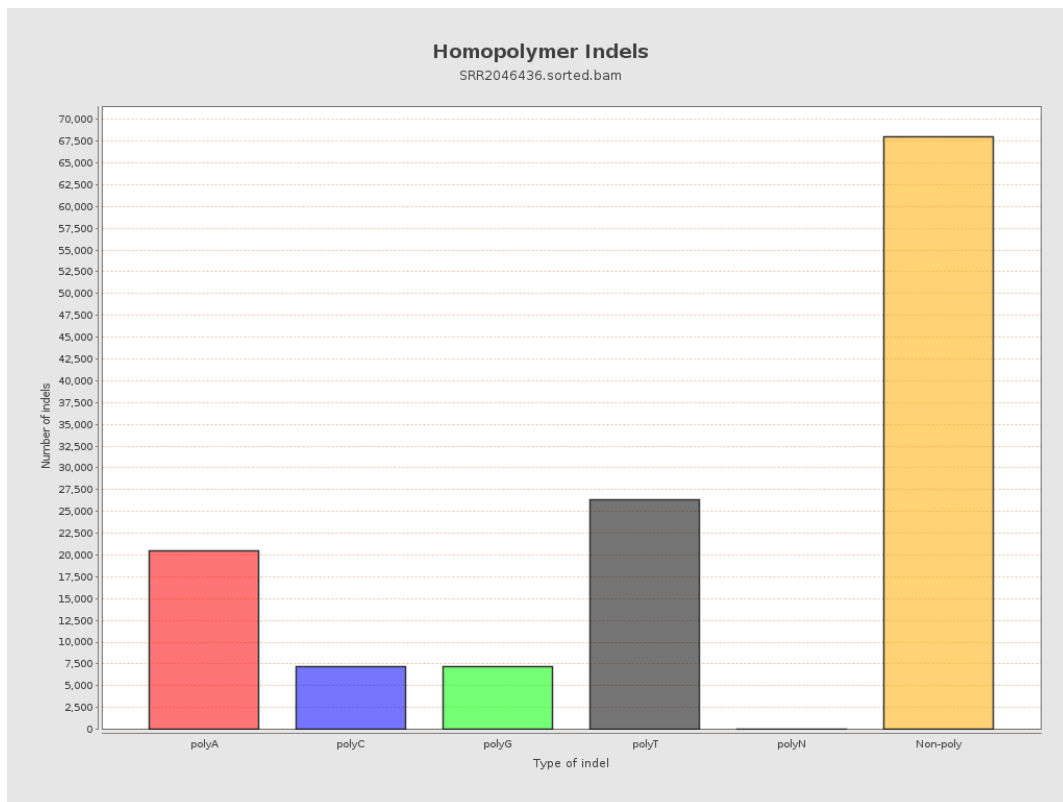
9. Results : Mapped Reads GC-content Distribution



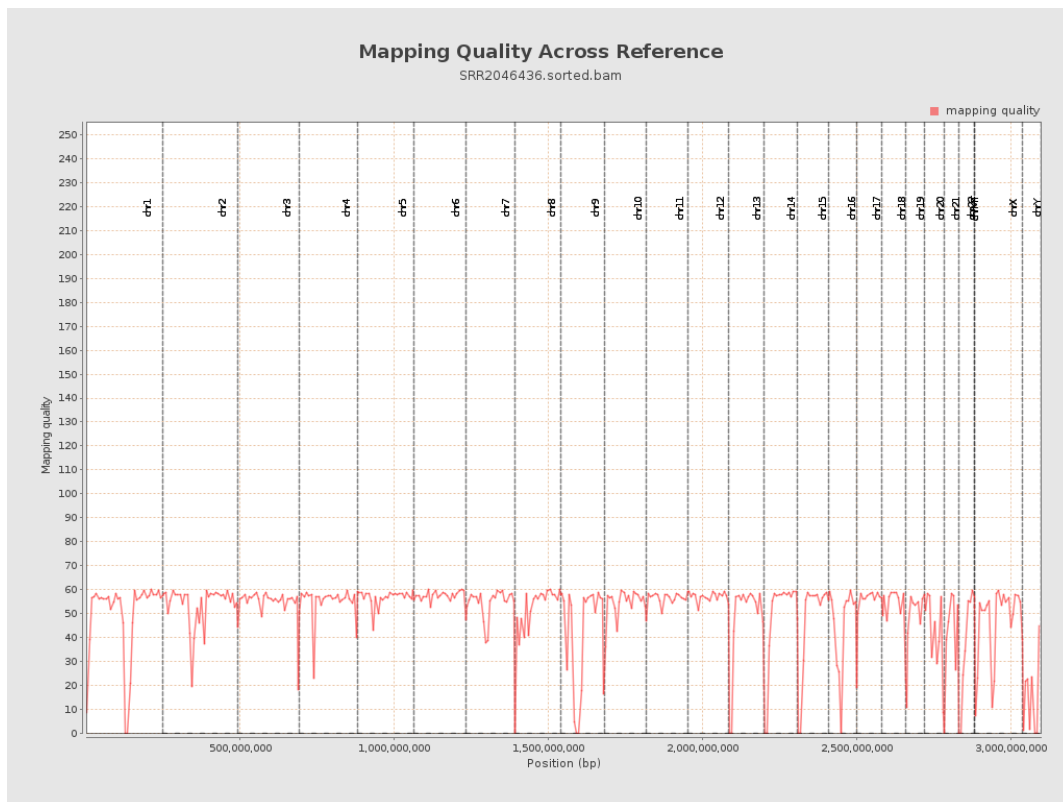
10. Results : Mapped Reads Clipping Profile



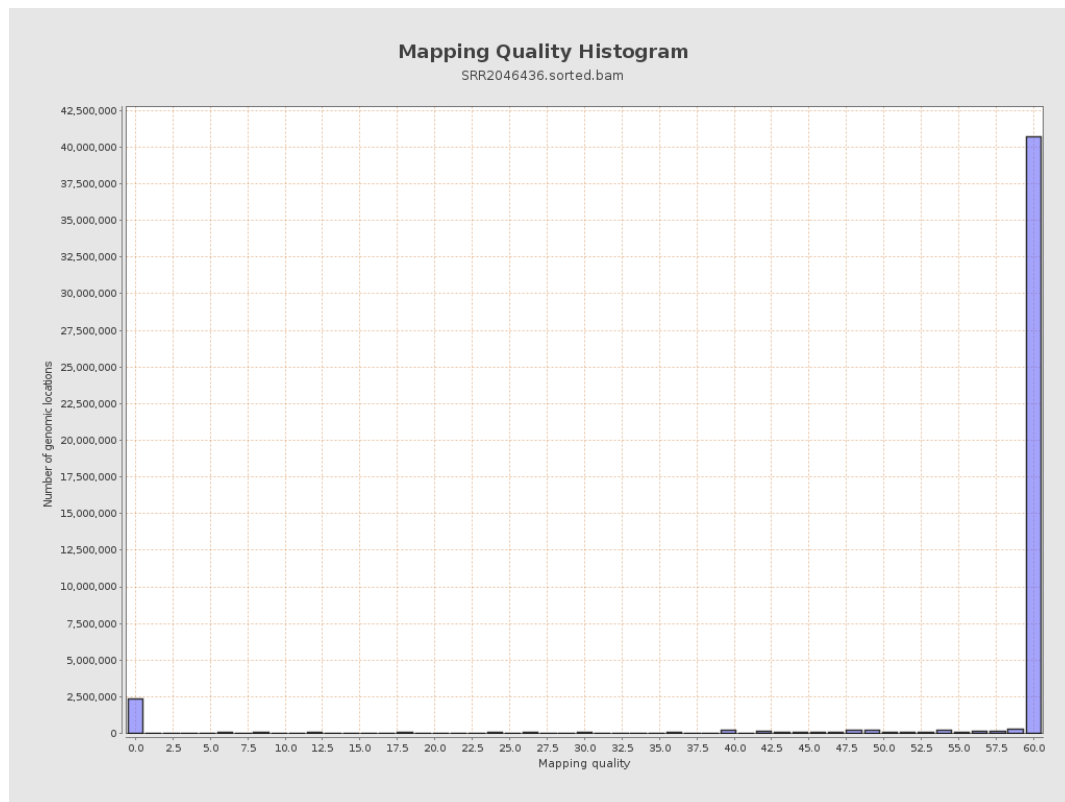
11. Results : Homopolymer Indels



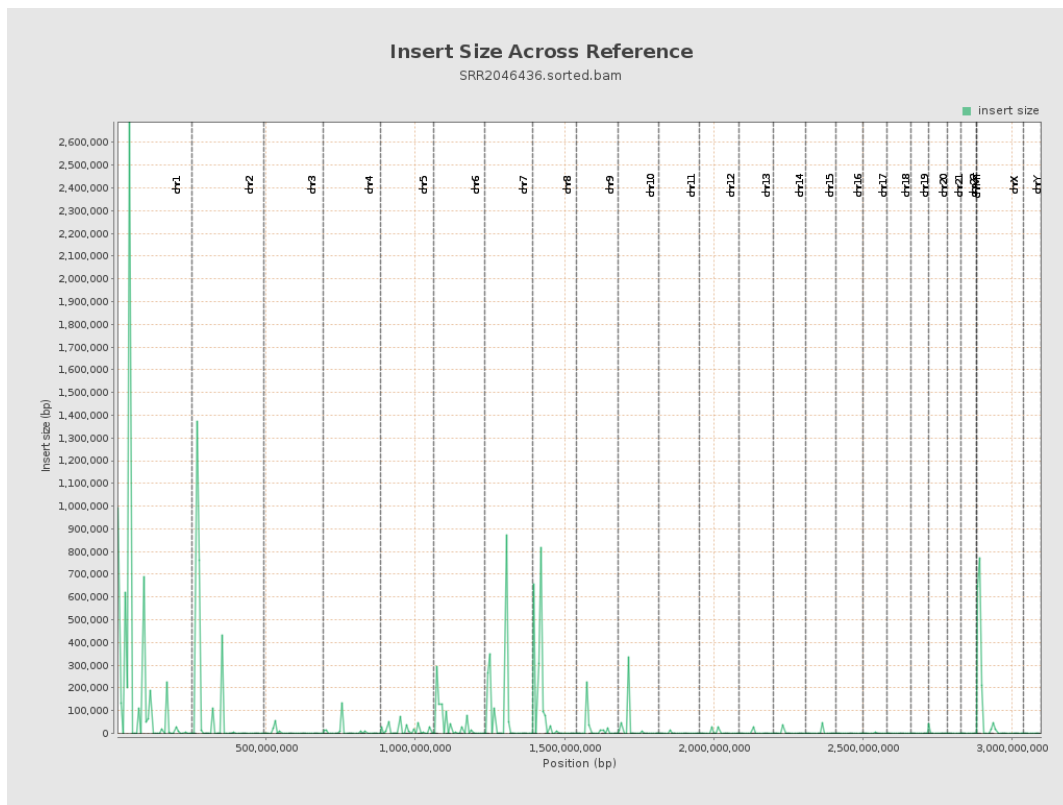
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

