

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 22:00:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046544.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_SRR2046544 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046544_1.fastq.gz SRR2046544_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 22:00:00 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046544.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,899,882
Mapped reads	6,761,763 / 98%
Unmapped reads	138,119 / 2%
Mapped paired reads	6,761,763 / 98%
Mapped reads, first in pair	3,428,513 / 49.69%
Mapped reads, second in pair	3,333,250 / 48.31%
Mapped reads, both in pair	6,645,786 / 96.32%
Mapped reads, singletons	115,977 / 1.68%
Secondary alignments	0
Supplementary alignments	42,993 / 0.62%
Read min/max/mean length	30 / 100 / 100.25
Duplicated reads (estimated)	5,429,844 / 78.69%
Duplication rate	45.27%
Clipped reads	3,901,995 / 56.55%

2.2. ACGT Content

Number/percentage of A's	173,166,382 / 29.39%
Number/percentage of C's	122,006,085 / 20.71%
Number/percentage of T's	167,070,291 / 28.36%
Number/percentage of G's	126,853,278 / 21.53%
Number/percentage of N's	52,611 / 0.01%

GC Percentage	42.24%
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2.3. Coverage

Mean	0.1904
Standard Deviation	29.1122

2.4. Mapping Quality

Mean Mapping Quality	49.63
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2.5. Insert size

Mean	26,532.15
Standard Deviation	1,589,926.95
P25/Median/P75	77 / 95 / 122

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	2,293,779
Insertions	35,738
Mapped reads with at least one insertion	0.52%
Deletions	48,799
Mapped reads with at least one deletion	0.71%
Homopolymer indels	45.88%

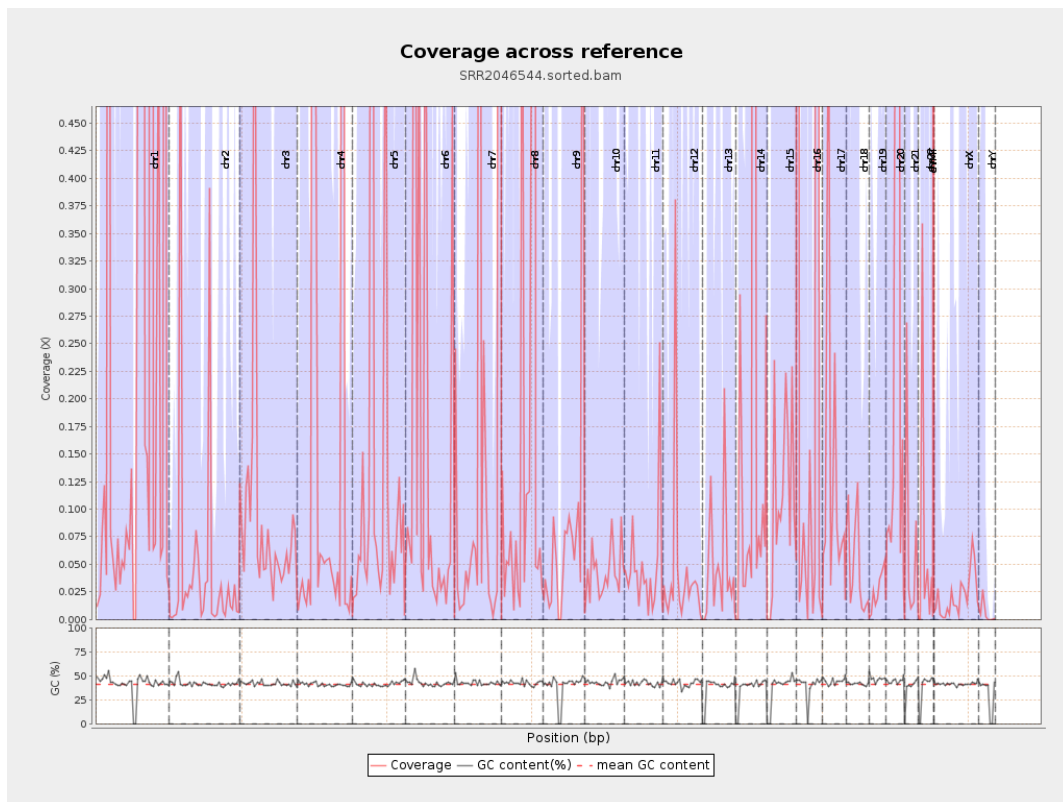
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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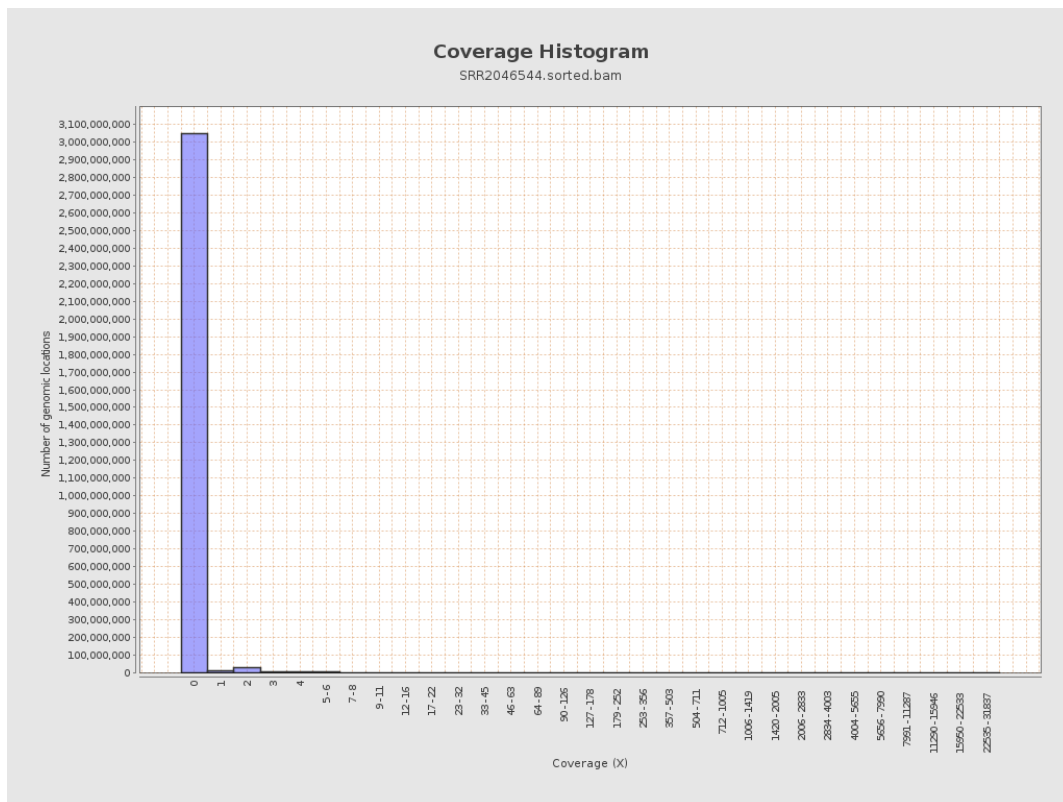
		bases	coverage	deviation
chr1	249250621	183611677	0.7367	80.6717
chr2	243199373	12538849	0.0516	8.4121
chr3	198022430	18757322	0.0947	7.8363
chr4	191154276	32243998	0.1687	22.1581
chr5	180915260	25764285	0.1424	14.8254
chr6	171115067	28162166	0.1646	14.4885
chr7	159138663	51384374	0.3229	36.4016
chr8	146364022	64325727	0.4395	38.6714
chr9	141213431	13554074	0.096	11.9259
chr10	135534747	5859715	0.0432	1.8341
chr11	135006516	6533503	0.0484	3.6329
chr12	133851895	6023252	0.045	8.3599
chr13	115169878	5240781	0.0455	3.4867
chr14	107349540	20657419	0.1924	23.7602
chr15	102531392	11041568	0.1077	6.7529
chr16	90354753	54775672	0.6062	47.5416
chr17	81195210	10900321	0.1342	9.1366
chr18	78077248	3610266	0.0462	1.1889
chr19	59128983	1552716	0.0263	0.4012
chr20	63025520	22134948	0.3512	29.1893
chr21	48129895	3209390	0.0667	7.8731
chr22	51304566	3617416	0.0705	10.9658
chrMT	16571	39467	2.3817	2.3321
chrX	155270560	3430205	0.0221	1.3312

chrY	59373566	304957	0.0051	1.6181
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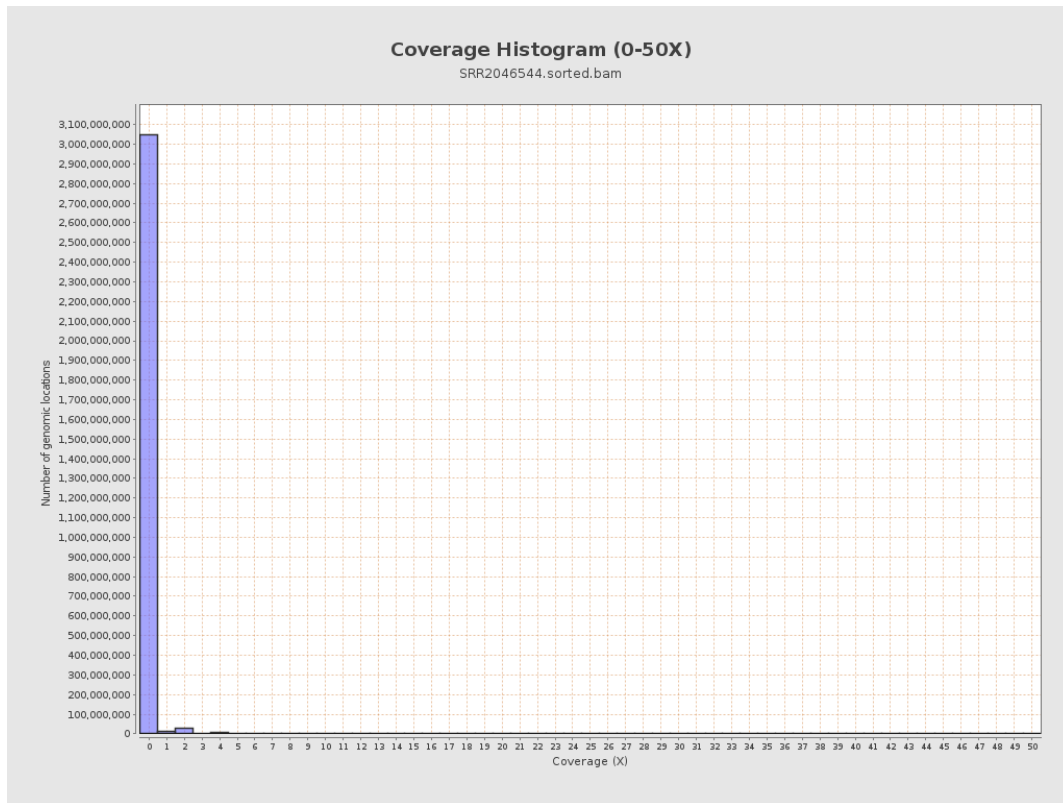
3. Results : Coverage across reference



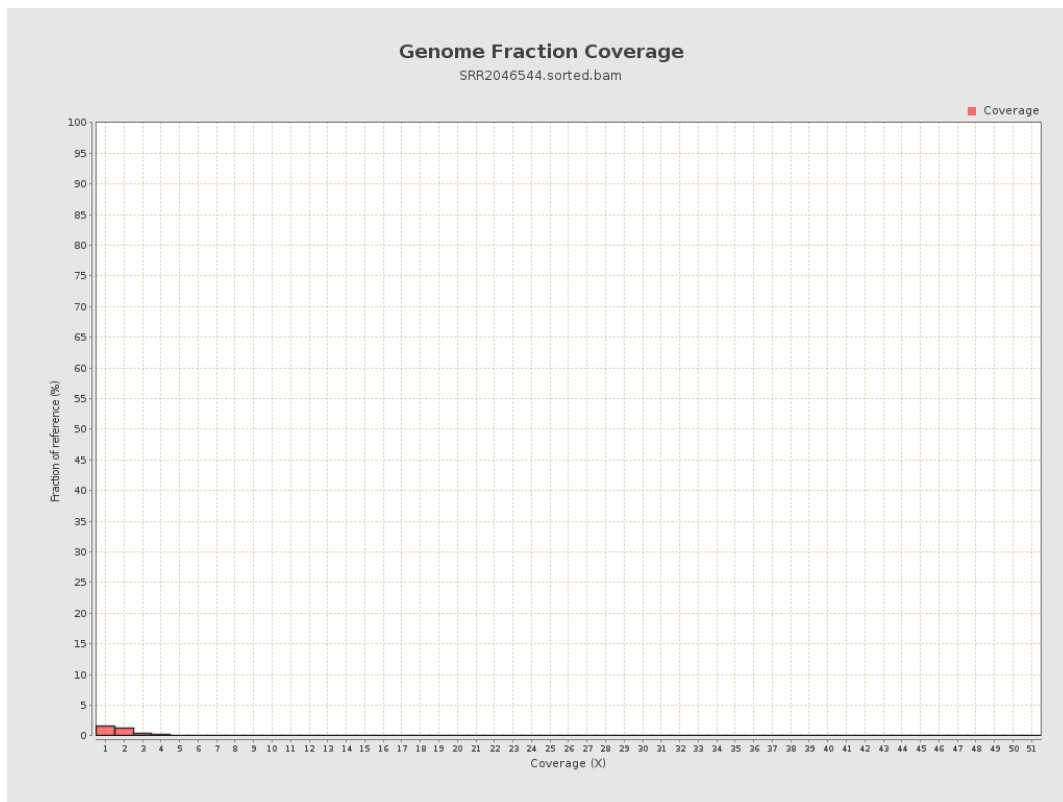
4. Results : Coverage Histogram



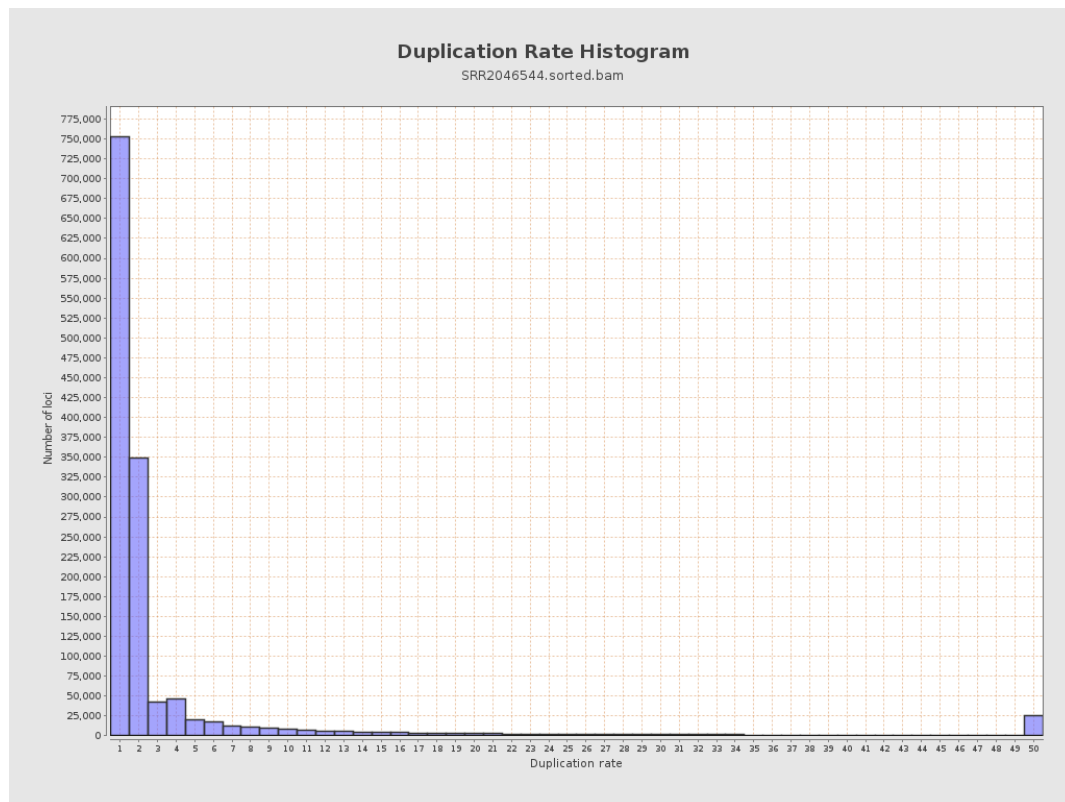
5. Results : Coverage Histogram (0-50X)



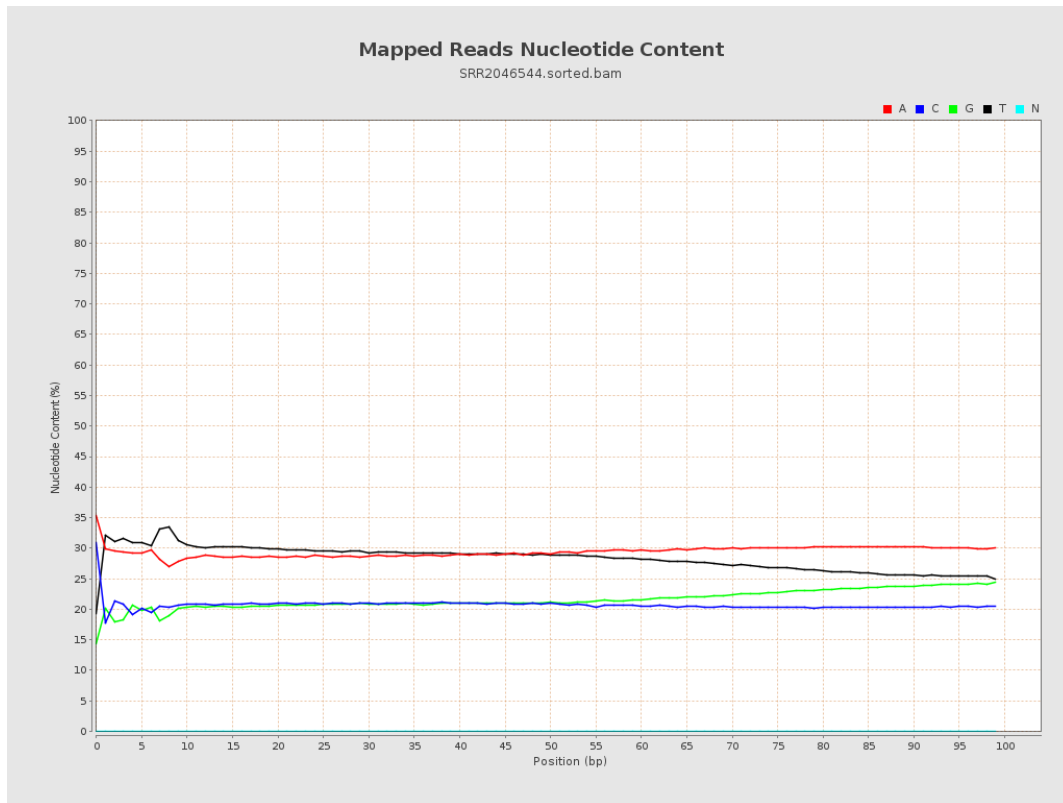
6. Results : Genome Fraction Coverage



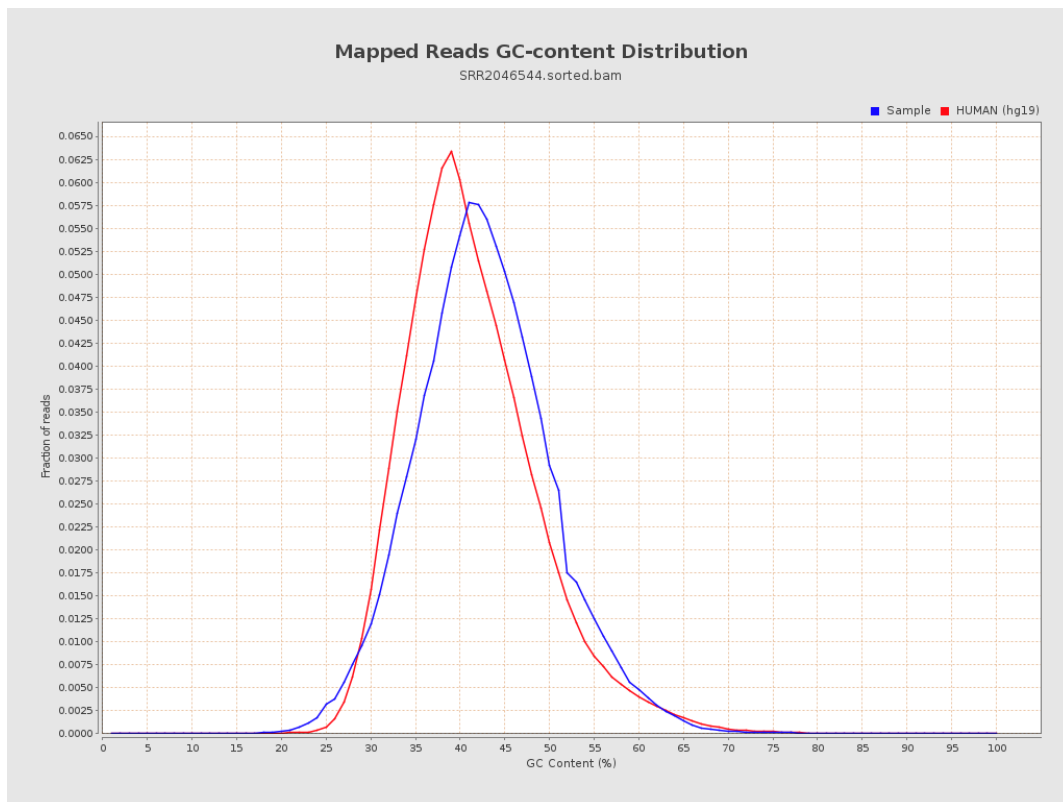
7. Results : Duplication Rate Histogram



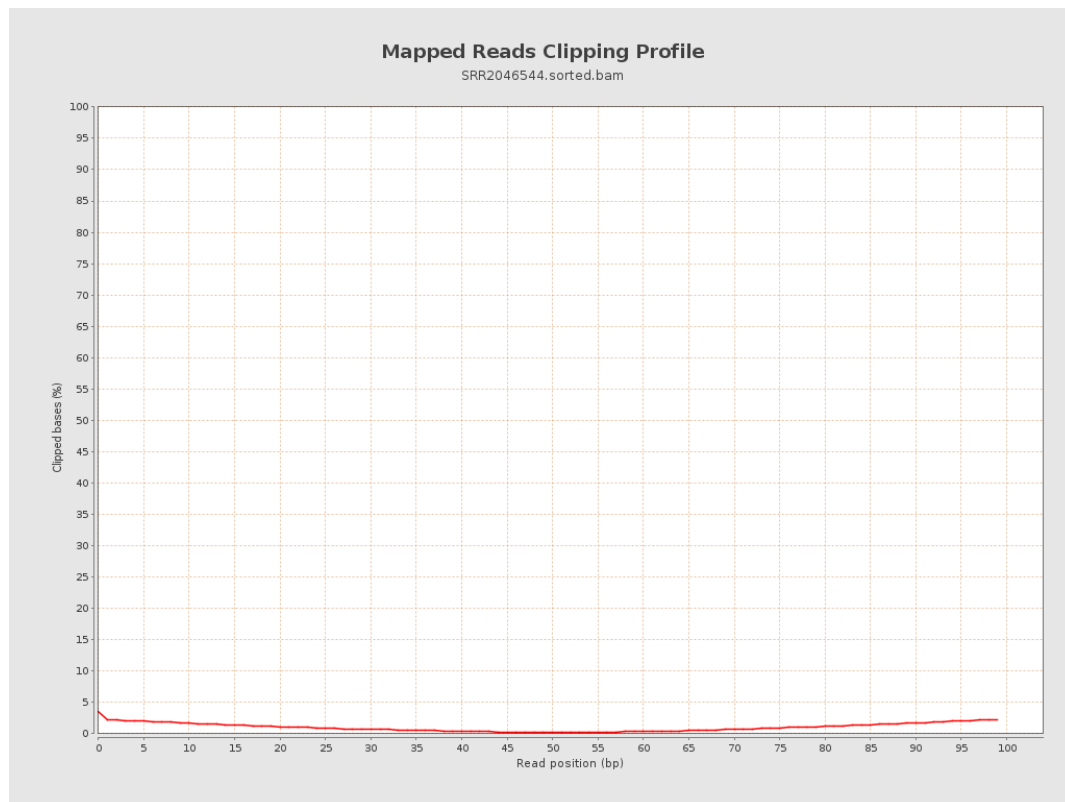
8. Results : Mapped Reads Nucleotide Content



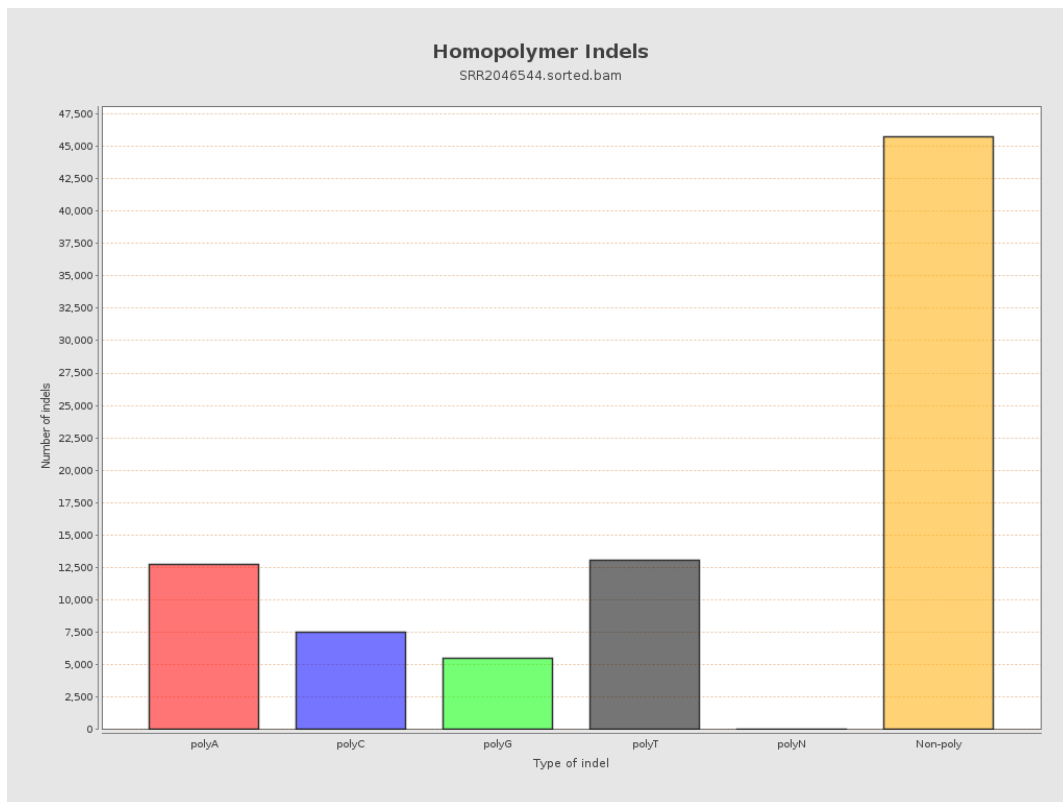
9. Results : Mapped Reads GC-content Distribution



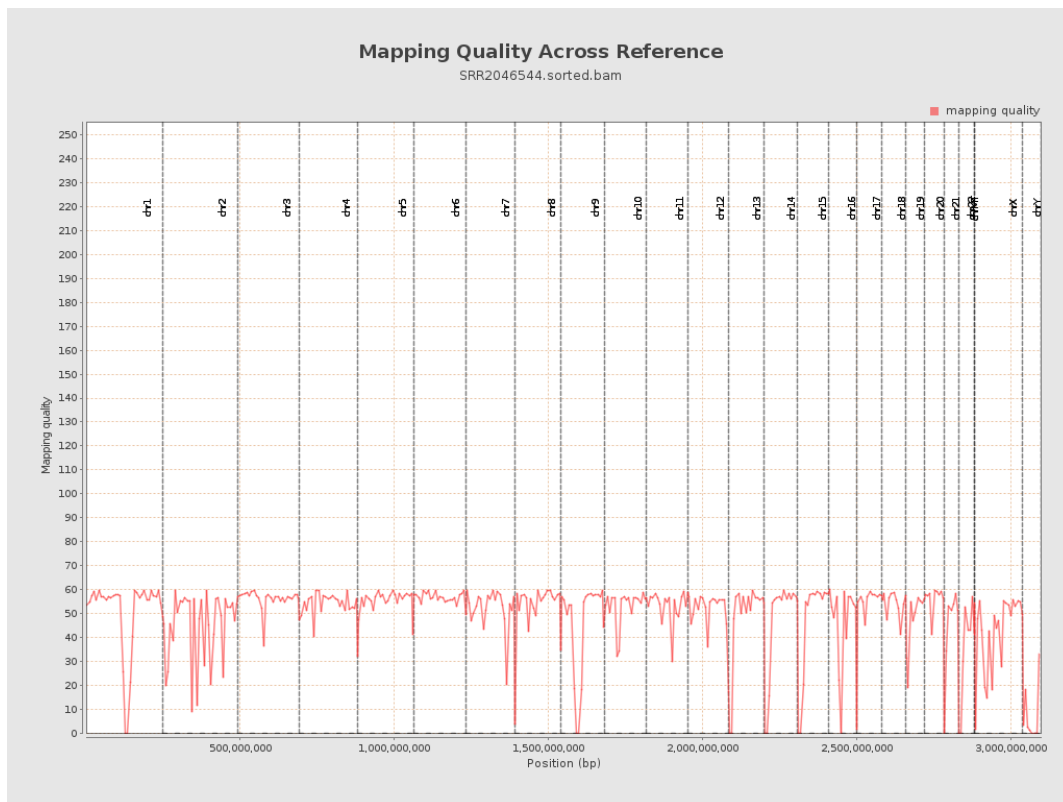
10. Results : Mapped Reads Clipping Profile



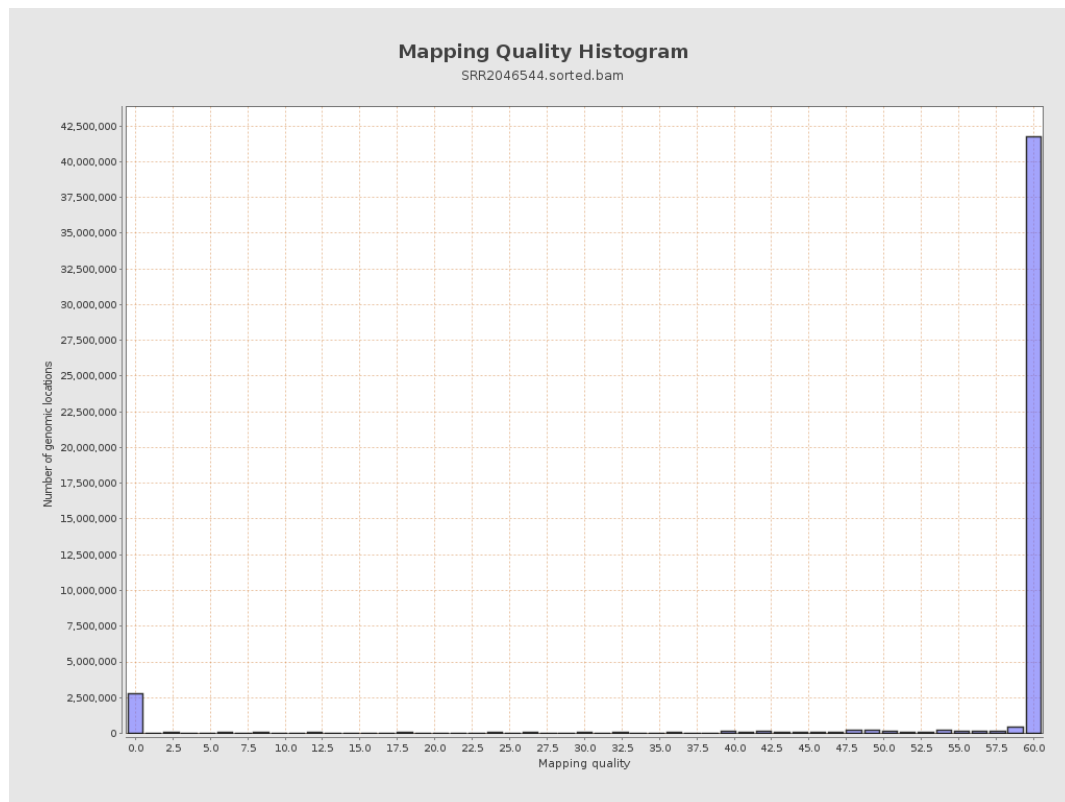
11. Results : Homopolymer Indels



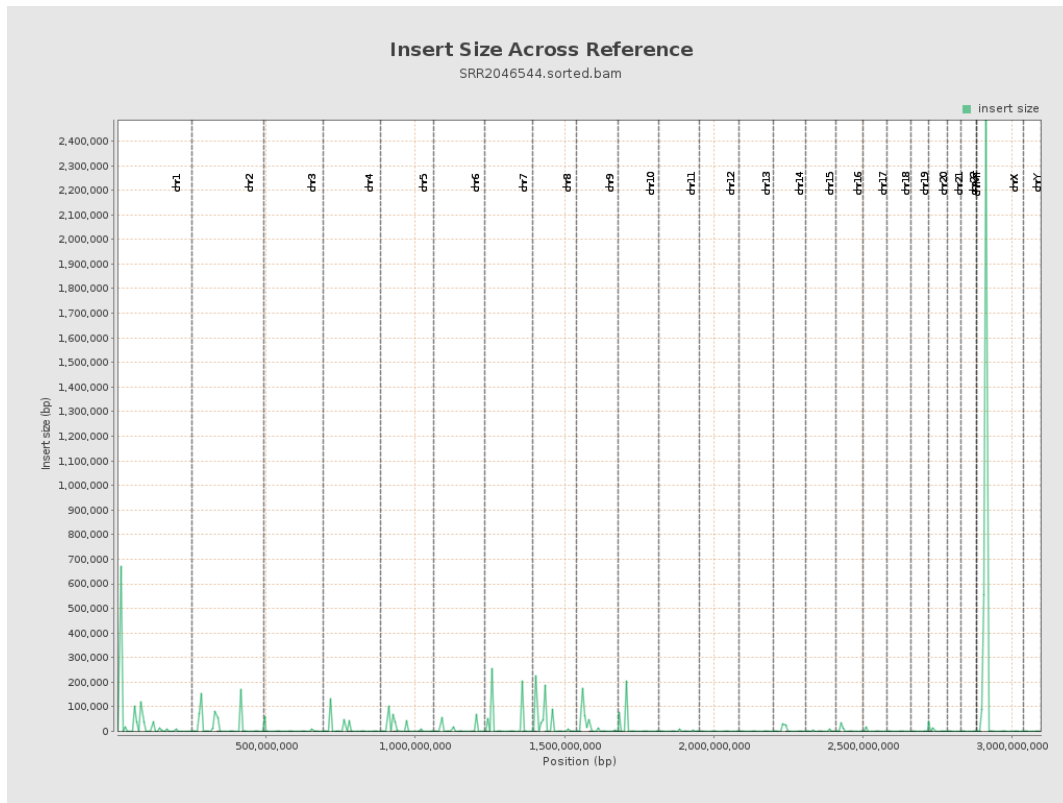
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

