

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 14:50:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046440.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_SRR2046440 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046440_1.fastq.gz SRR2046440_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 14:50:54 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046440.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,260,144
Mapped reads	9,220,107 / 99.57%
Unmapped reads	40,037 / 0.43%
Mapped paired reads	9,220,107 / 99.57%
Mapped reads, first in pair	4,617,447 / 49.86%
Mapped reads, second in pair	4,602,660 / 49.7%
Mapped reads, both in pair	9,192,642 / 99.27%
Mapped reads, singletons	27,465 / 0.3%
Secondary alignments	0
Supplementary alignments	41,557 / 0.45%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	7,376,287 / 79.66%
Duplication rate	28.15%
Clipped reads	1,496,321 / 16.16%

2.2. ACGT Content

Number/percentage of A's	246,846,678 / 27.48%
Number/percentage of C's	202,338,769 / 22.52%
Number/percentage of T's	246,961,936 / 27.49%
Number/percentage of G's	202,145,286 / 22.5%
Number/percentage of N's	77,521 / 0.01%

GC Percentage	45.02%
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2.3. Coverage

Mean	0.2903
Standard Deviation	47.7077

2.4. Mapping Quality

Mean Mapping Quality	52.43
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2.5. Insert size

Mean	14,590.6
Standard Deviation	1,138,314.87
P25/Median/P75	112 / 139 / 171

2.6. Mismatches and indels

General error rate	0.38%
Mismatches	3,234,593
Insertions	72,563
Mapped reads with at least one insertion	0.77%
Deletions	84,614
Mapped reads with at least one deletion	0.89%
Homopolymer indels	48.81%

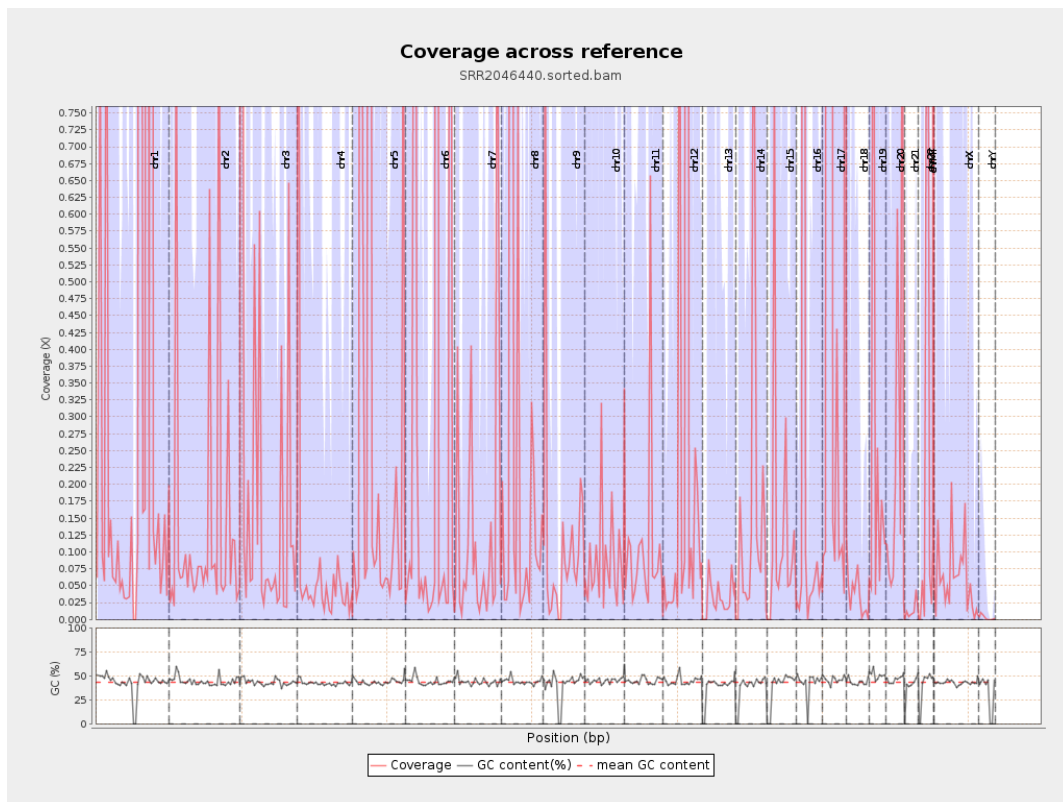
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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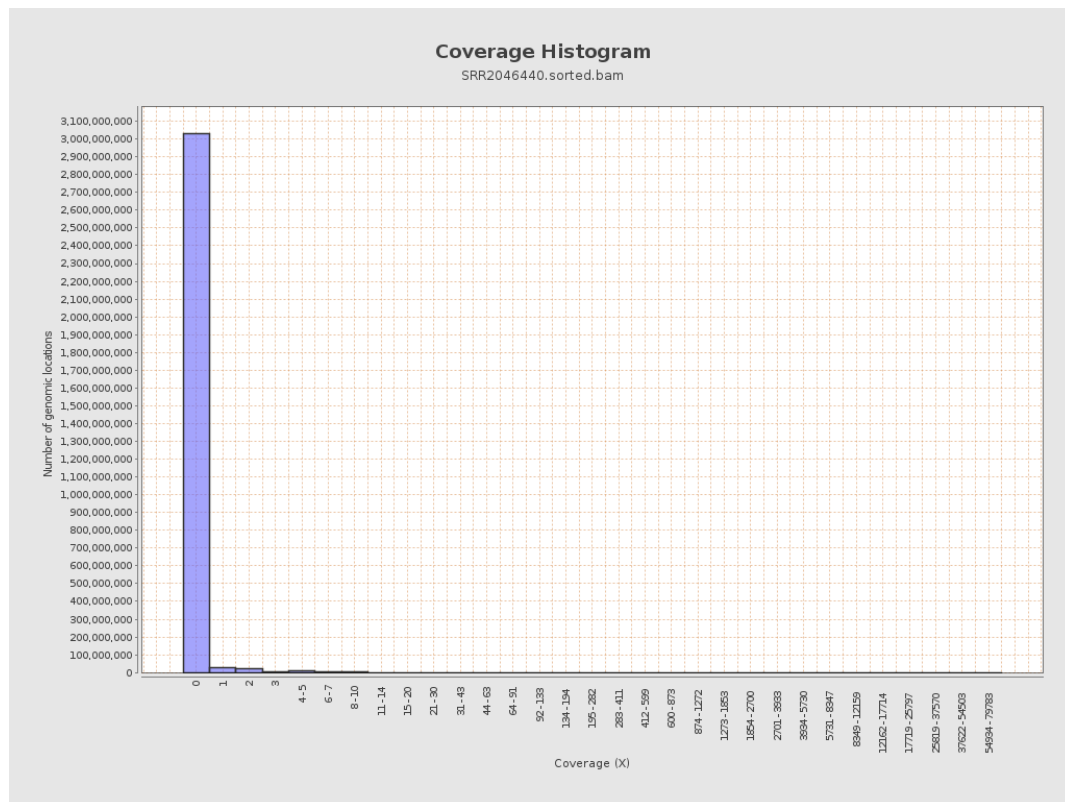
		bases	coverage	deviation
chr1	249250621	138313008	0.5549	75.778
chr2	243199373	35990447	0.148	20.8371
chr3	198022430	54476361	0.2751	73.8661
chr4	191154276	17142947	0.0897	12.3502
chr5	180915260	73646788	0.4071	45.0397
chr6	171115067	76562550	0.4474	63.7884
chr7	159138663	21642747	0.136	18.3571
chr8	146364022	45154055	0.3085	40.7035
chr9	141213431	17573814	0.1244	14.1249
chr10	135534747	11483980	0.0847	7.2788
chr11	135006516	14953120	0.1108	7.9019
chr12	133851895	87565128	0.6542	82.8975
chr13	115169878	3724367	0.0323	1.6798
chr14	107349540	16886835	0.1573	21.8371
chr15	102531392	13946271	0.136	19.6811
chr16	90354753	26389634	0.2921	32.9048
chr17	81195210	182919162	2.2528	148.2828
chr18	78077248	2784325	0.0357	1.7544
chr19	59128983	15974718	0.2702	19.6984
chr20	63025520	18685288	0.2965	26.375
chr21	48129895	660025	0.0137	0.4211
chr22	51304566	12021833	0.2343	23.6812
chrMT	16571	168369	10.1605	4.9349
chrX	155270560	9775301	0.063	6.1193

chrY	59373566	165472	0.0028	0.1204
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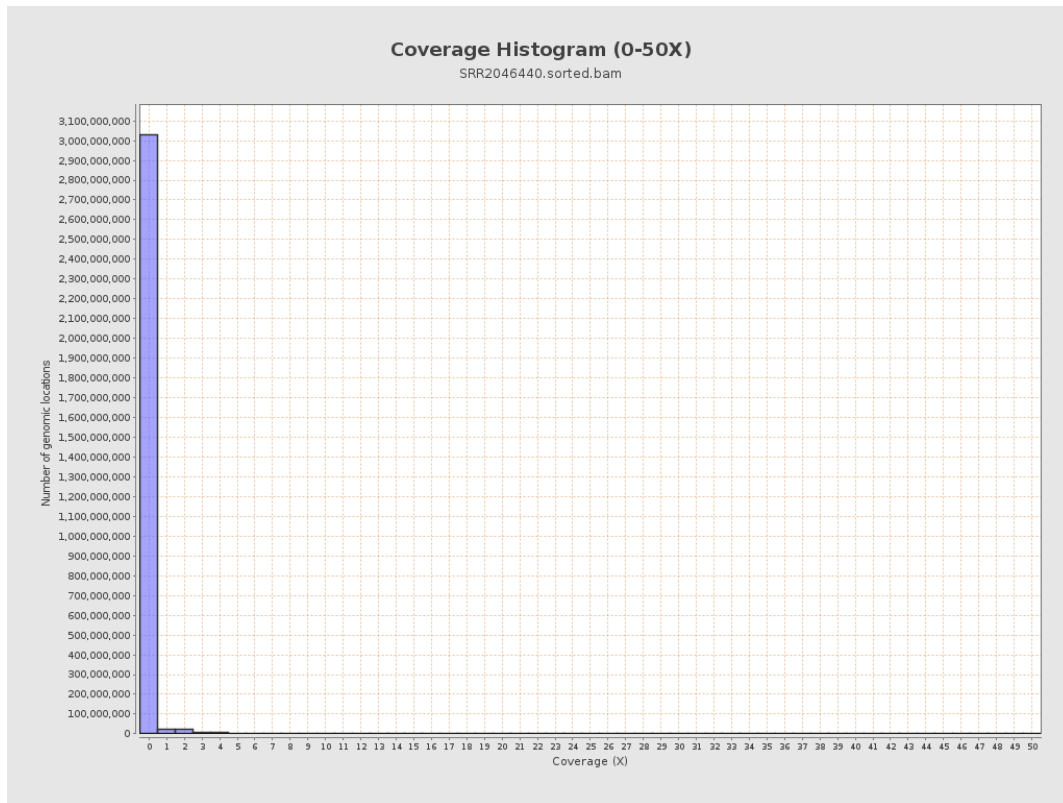
3. Results : Coverage across reference



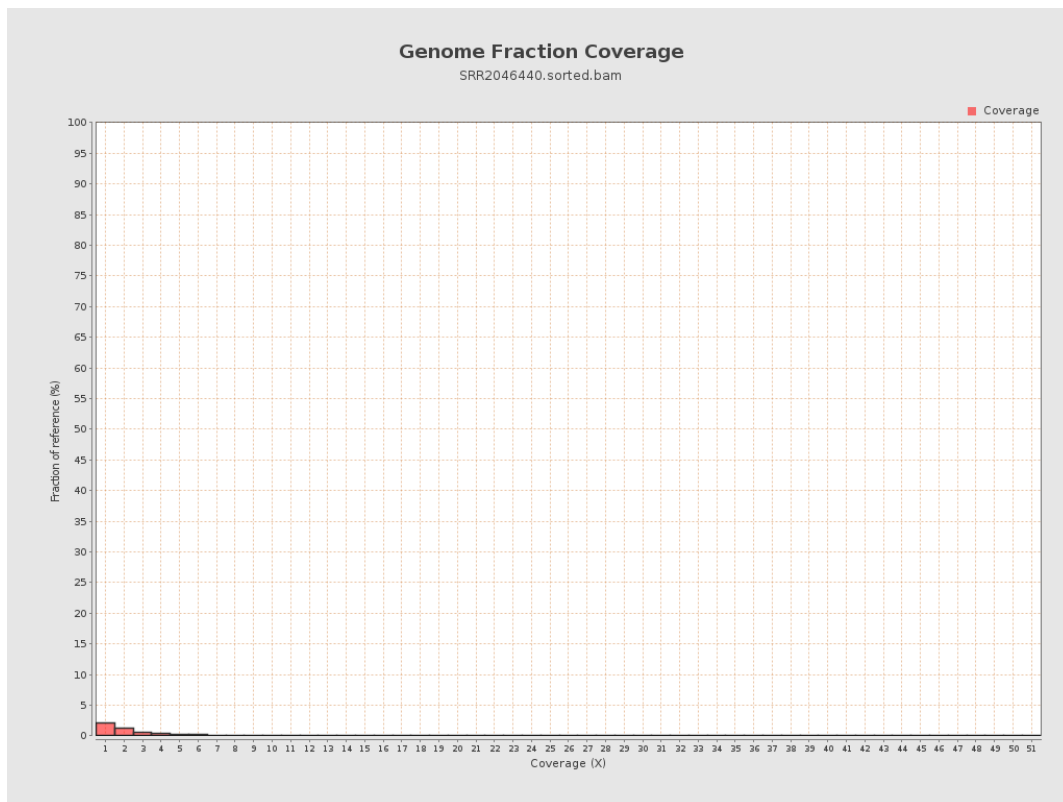
4. Results : Coverage Histogram



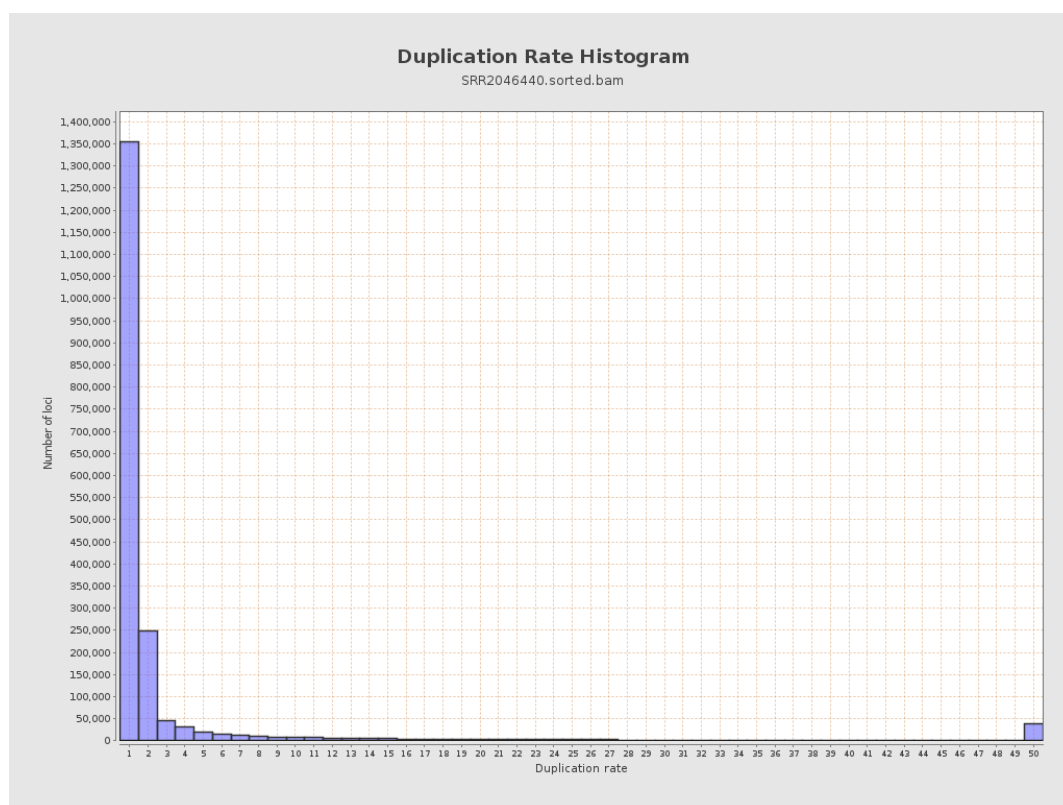
5. Results : Coverage Histogram (0-50X)



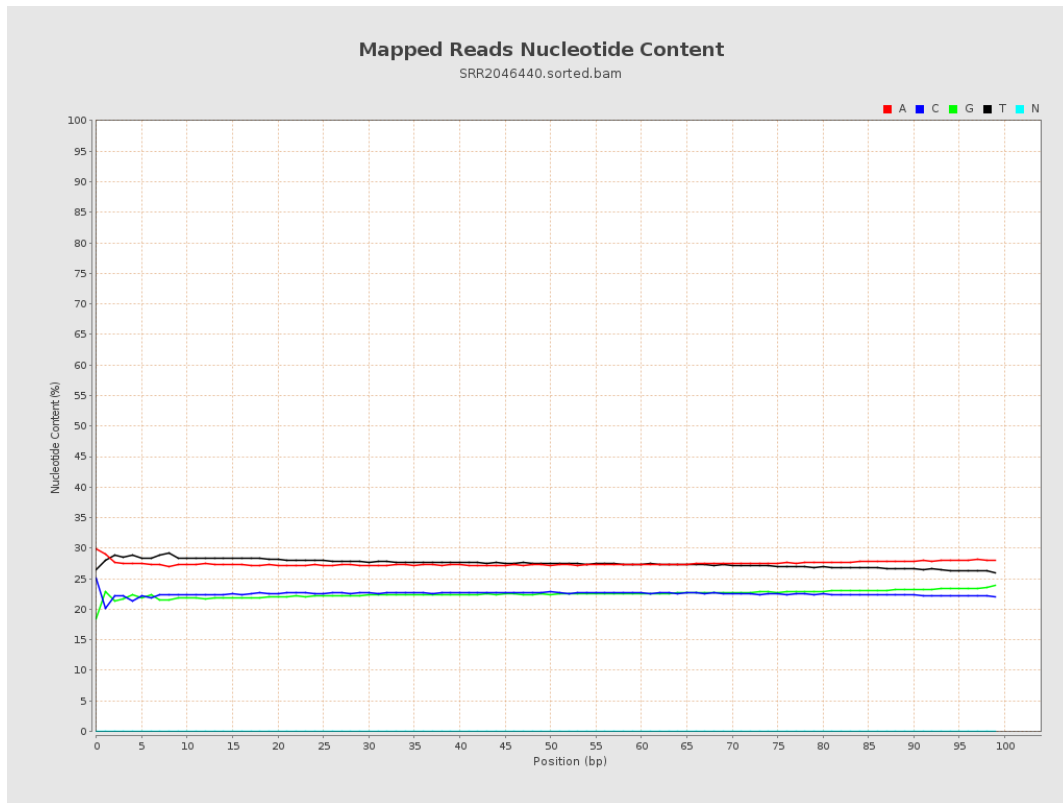
6. Results : Genome Fraction Coverage



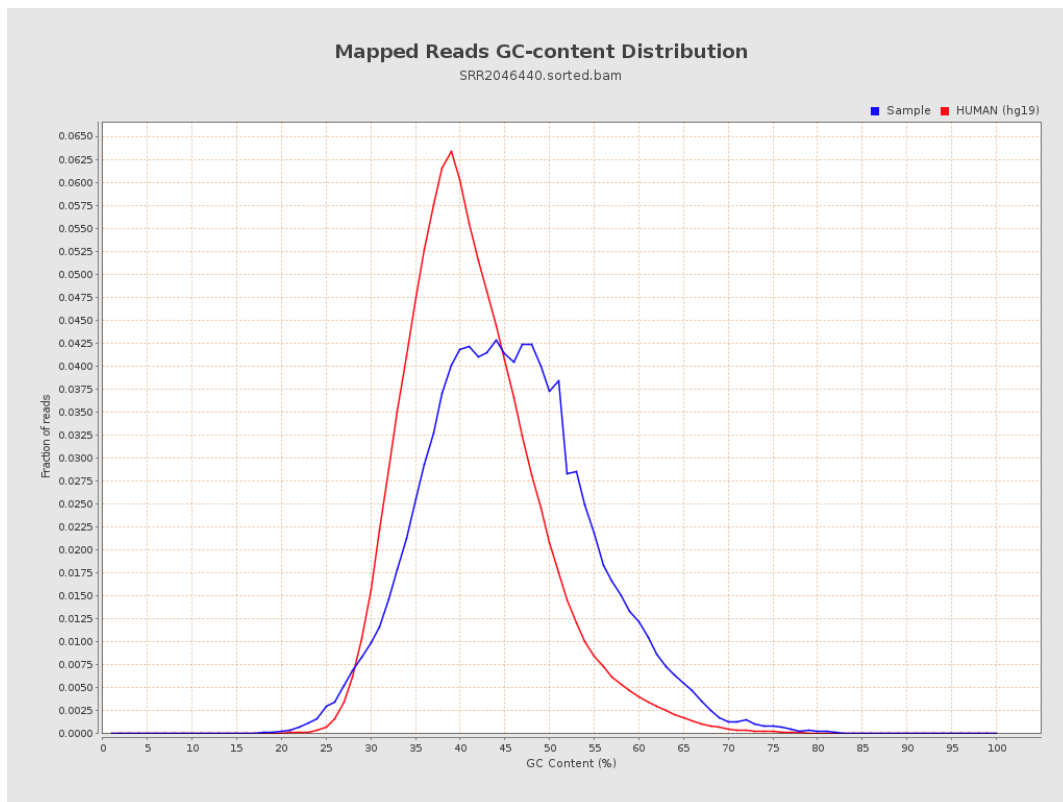
7. Results : Duplication Rate Histogram



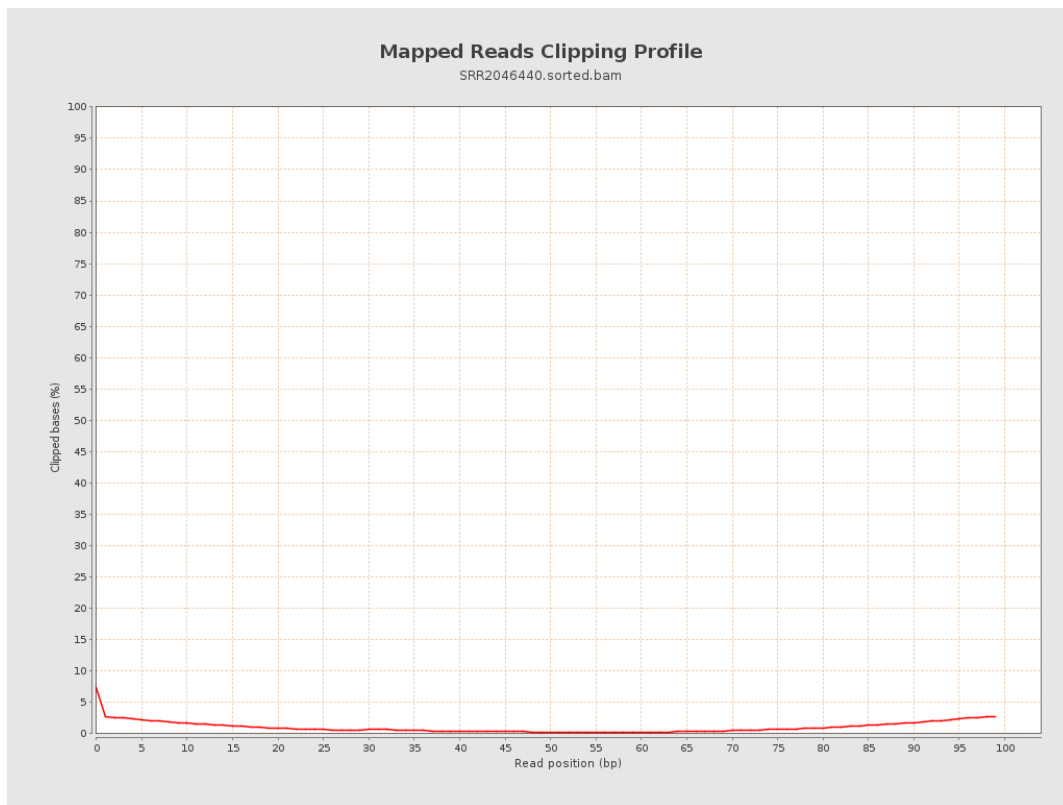
8. Results : Mapped Reads Nucleotide Content



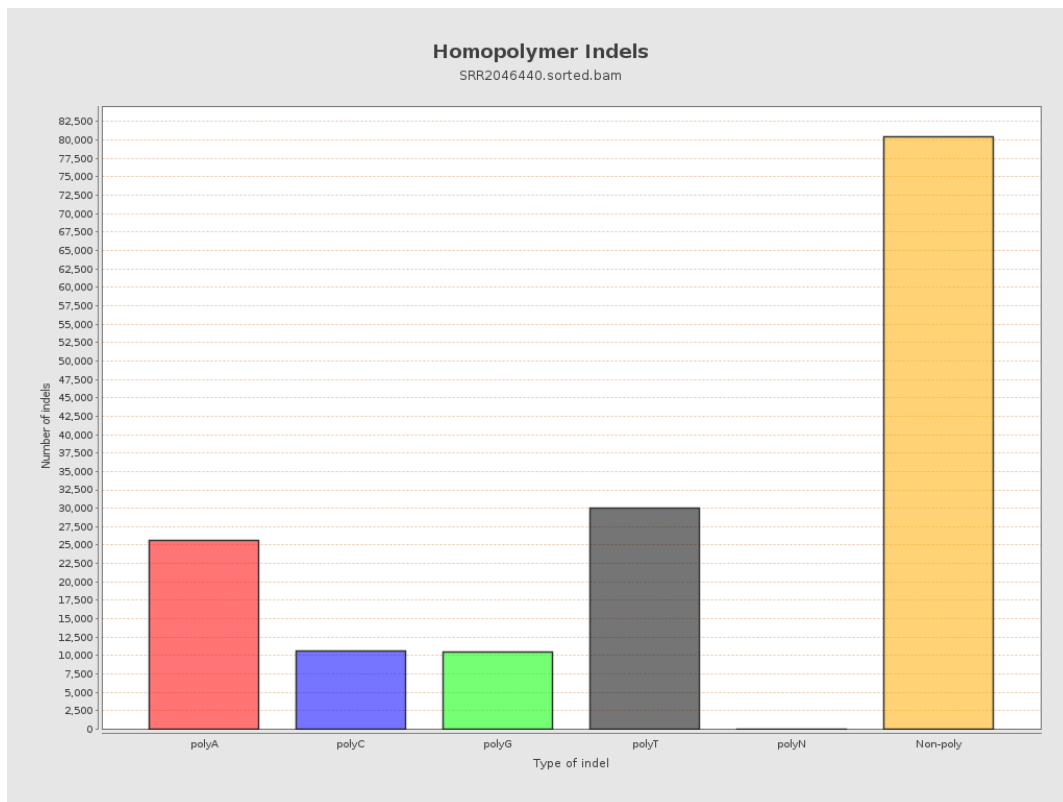
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



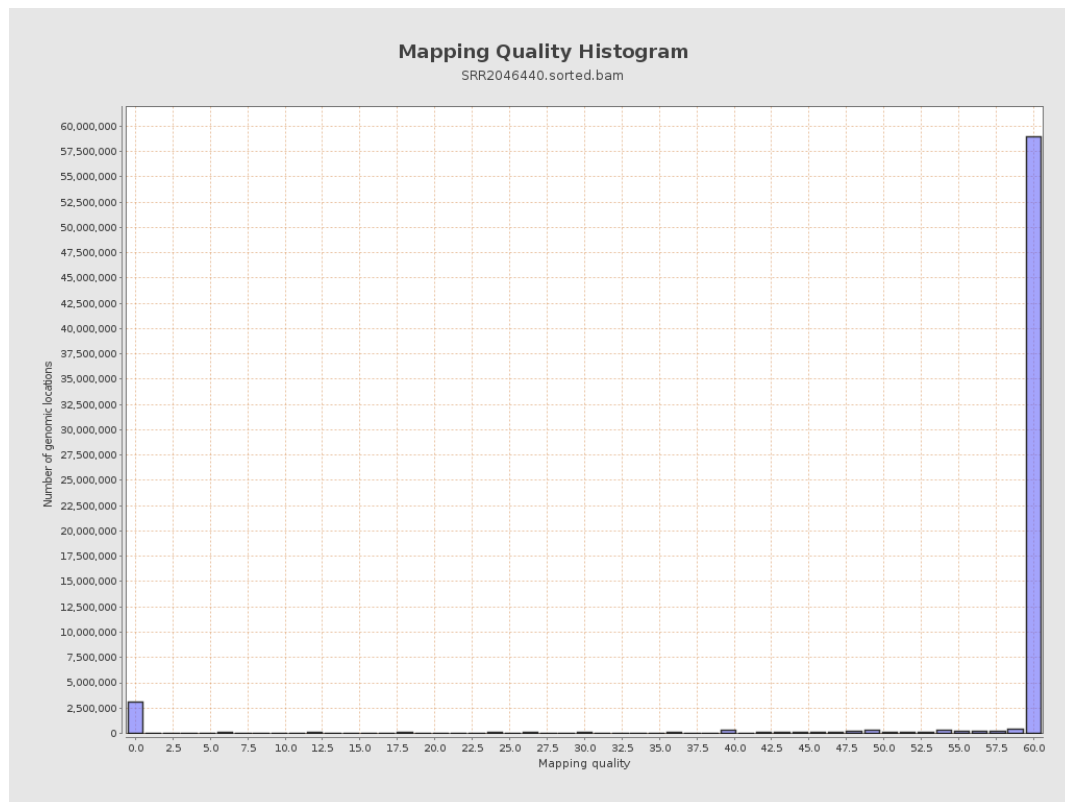
11. Results : Homopolymer Indels



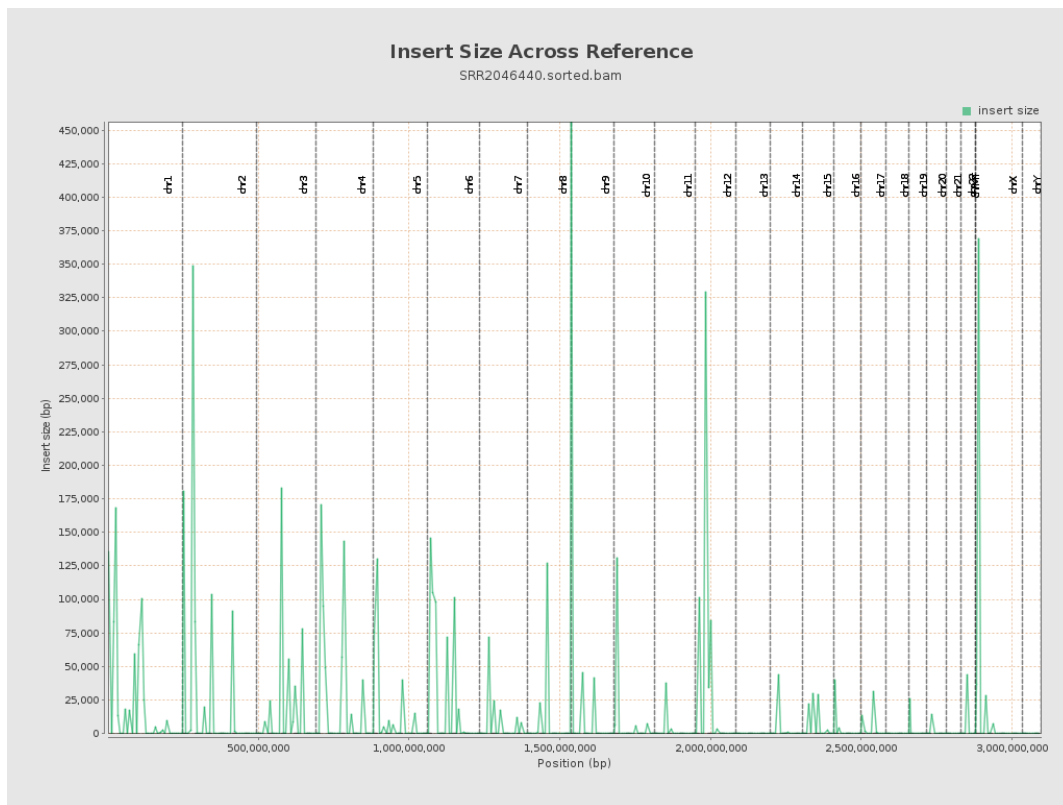
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

