

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 20:52:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046535.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_SRR2046535 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046535_1.fastq.gz SRR2046535_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 20:51:59 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046535.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,261,316
Mapped reads	11,700,259 / 95.42%
Unmapped reads	561,057 / 4.58%
Mapped paired reads	11,700,259 / 95.42%
Mapped reads, first in pair	5,878,840 / 47.95%
Mapped reads, second in pair	5,821,419 / 47.48%
Mapped reads, both in pair	11,628,118 / 94.84%
Mapped reads, singletons	72,141 / 0.59%
Secondary alignments	0
Supplementary alignments	47,917 / 0.39%
Read min/max/mean length	30 / 100 / 100.16
Duplicated reads (estimated)	7,854,847 / 64.06%
Duplication rate	32.02%
Clipped reads	1,281,078 / 10.45%

2.2. ACGT Content

Number/percentage of A's	332,549,141 / 28.93%
Number/percentage of C's	241,489,614 / 21.01%
Number/percentage of T's	333,282,108 / 29%
Number/percentage of G's	241,916,977 / 21.05%
Number/percentage of N's	113,330 / 0.01%

GC Percentage	42.06%
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2.3. Coverage

Mean	0.3714
Standard Deviation	24.2863

2.4. Mapping Quality

Mean Mapping Quality	53.79
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2.5. Insert size

Mean	18,353.68
Standard Deviation	1,335,774.36
P25/Median/P75	126 / 158 / 197

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	4,222,364
Insertions	94,279
Mapped reads with at least one insertion	0.79%
Deletions	113,390
Mapped reads with at least one deletion	0.95%
Homopolymer indels	48.89%

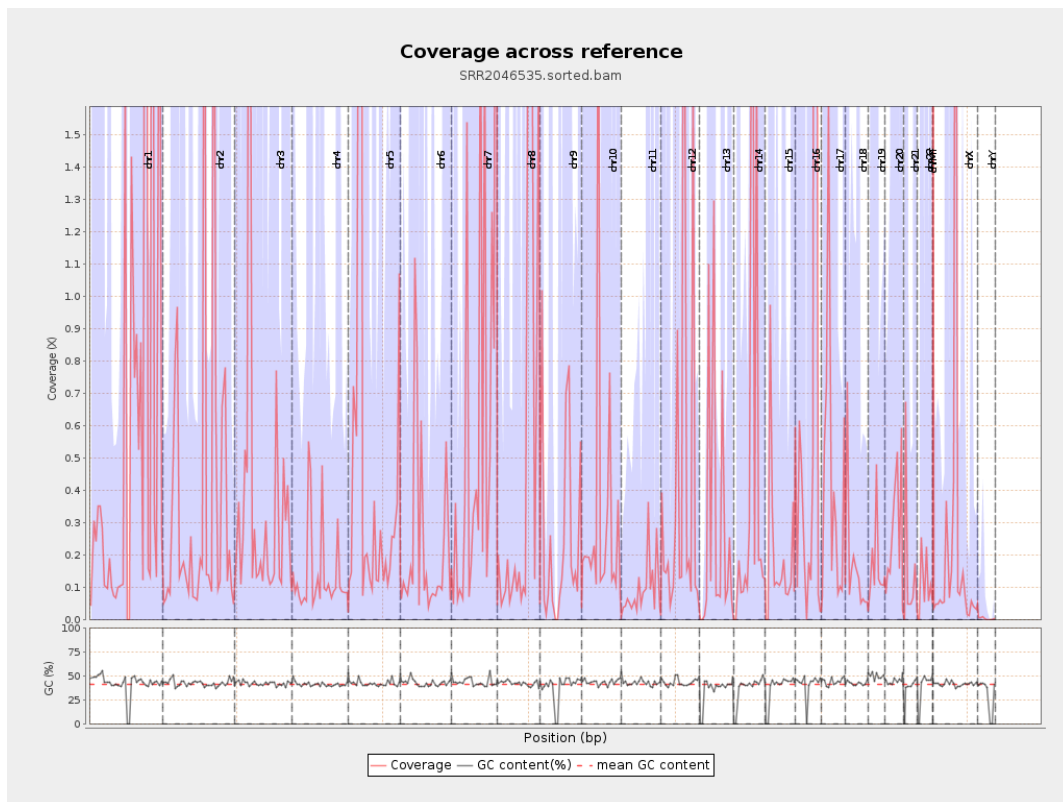
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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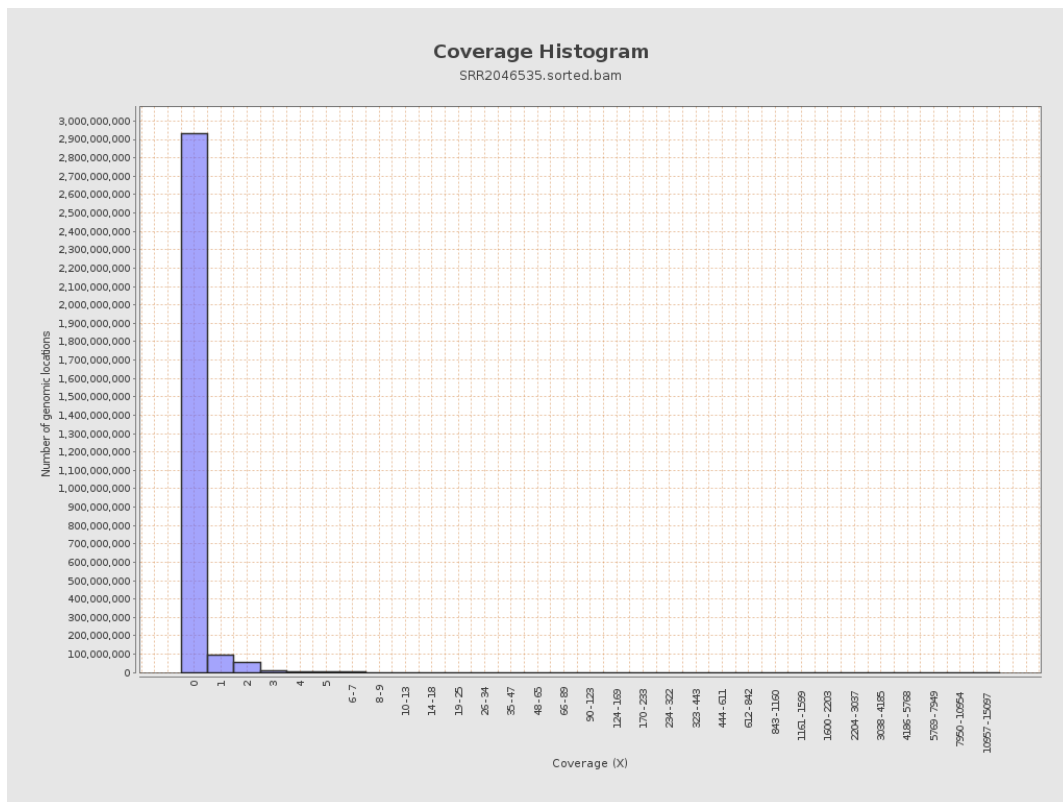
		bases	coverage	deviation
chr1	249250621	157221137	0.6308	30.7967
chr2	243199373	96946181	0.3986	22.7673
chr3	198022430	72050070	0.3638	23.9532
chr4	191154276	27410082	0.1434	7.0055
chr5	180915260	98677263	0.5454	38.0339
chr6	171115067	38678411	0.226	11.4919
chr7	159138663	118918951	0.7473	35.2234
chr8	146364022	89422290	0.611	31.7794
chr9	141213431	34549917	0.2447	14.3778
chr10	135534747	45148427	0.3331	21.9103
chr11	135006516	12621411	0.0935	5.2444
chr12	133851895	57357246	0.4285	28.9259
chr13	115169878	31383408	0.2725	19.6052
chr14	107349540	47176234	0.4395	24.0364
chr15	102531392	20274489	0.1977	9.531
chr16	90354753	76007827	0.8412	49.7078
chr17	81195210	34095527	0.4199	17.0107
chr18	78077248	13147380	0.1684	5.6083
chr19	59128983	10028133	0.1696	6.4721
chr20	63025520	17633952	0.2798	11.6215
chr21	48129895	7916368	0.1645	14.6735
chr22	51304566	5460610	0.1064	4.8586
chrMT	16571	69918	4.2193	2.8806
chrX	155270560	37300573	0.2402	27.0273

chrY	59373566	158991	0.0027	0.1702
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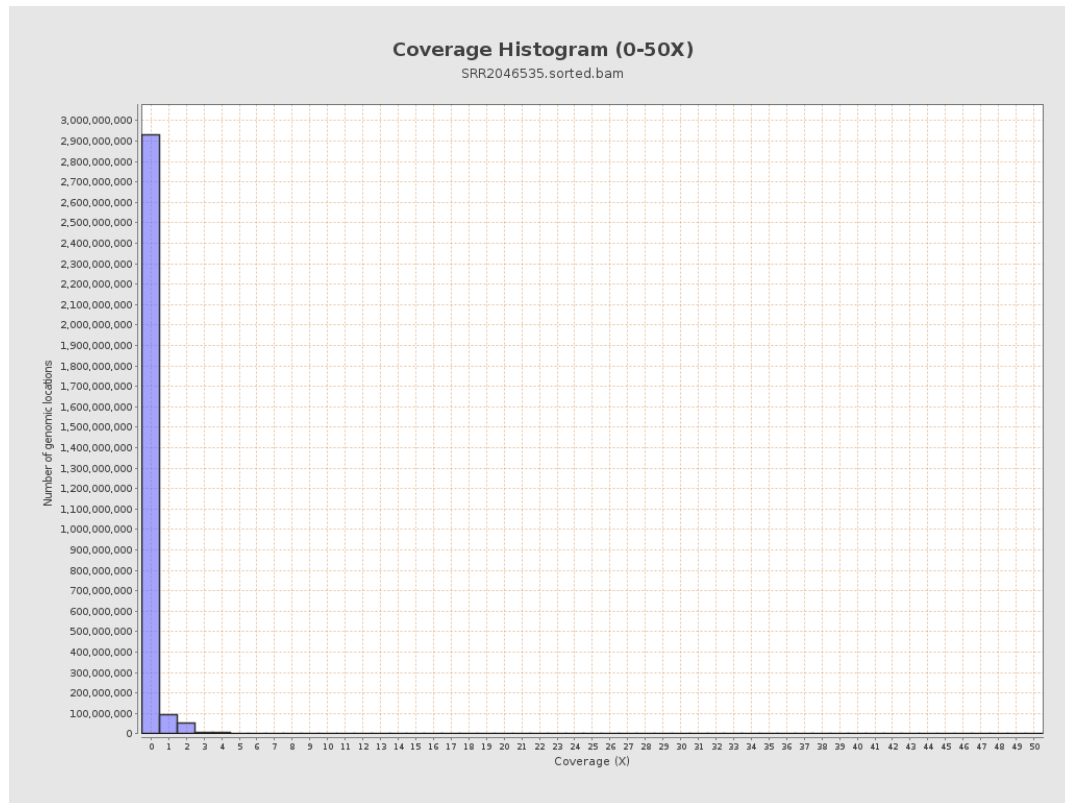
3. Results : Coverage across reference



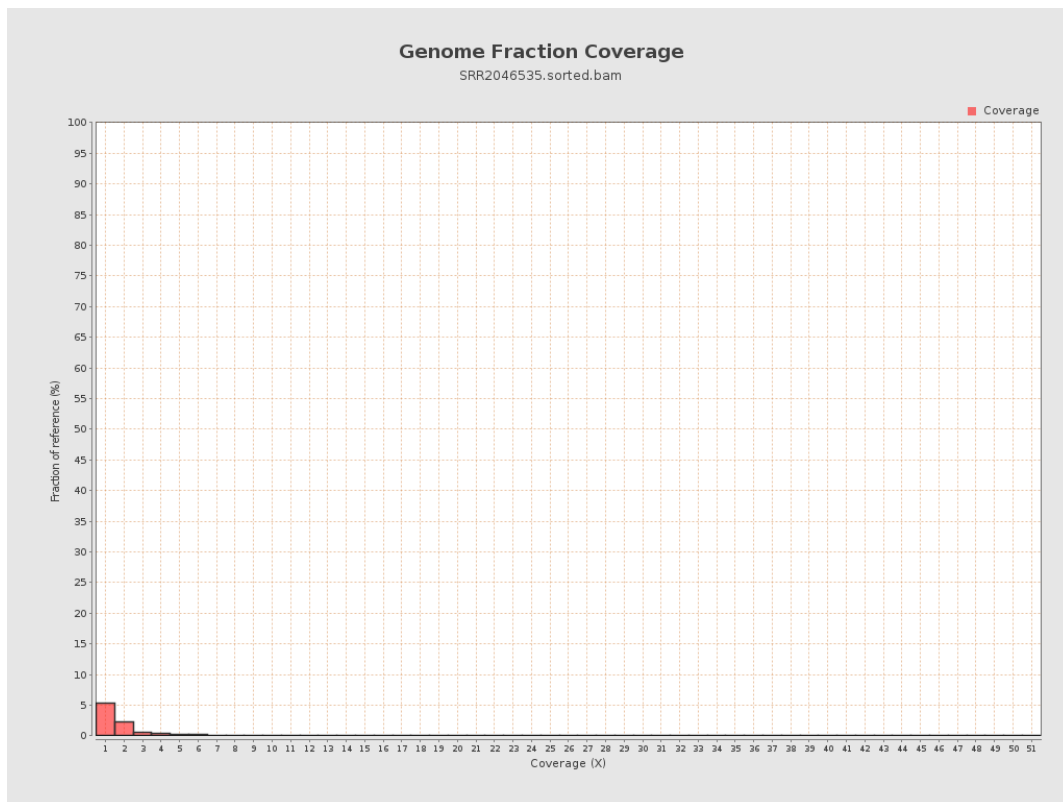
4. Results : Coverage Histogram



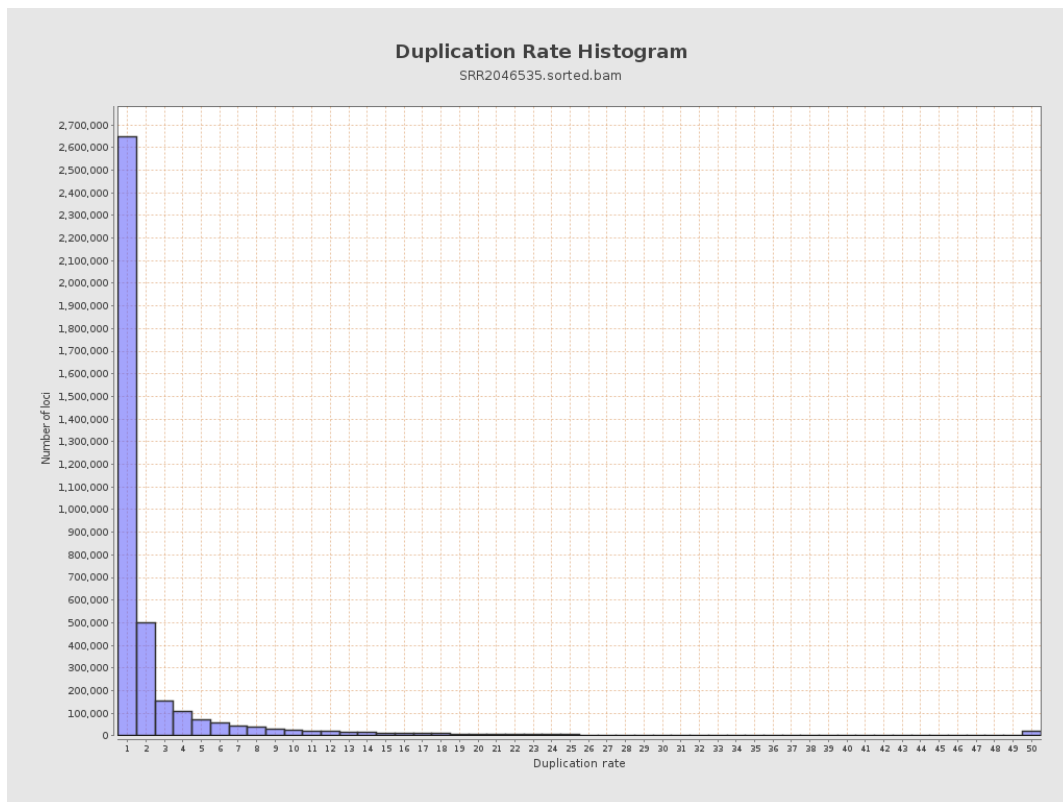
5. Results : Coverage Histogram (0-50X)



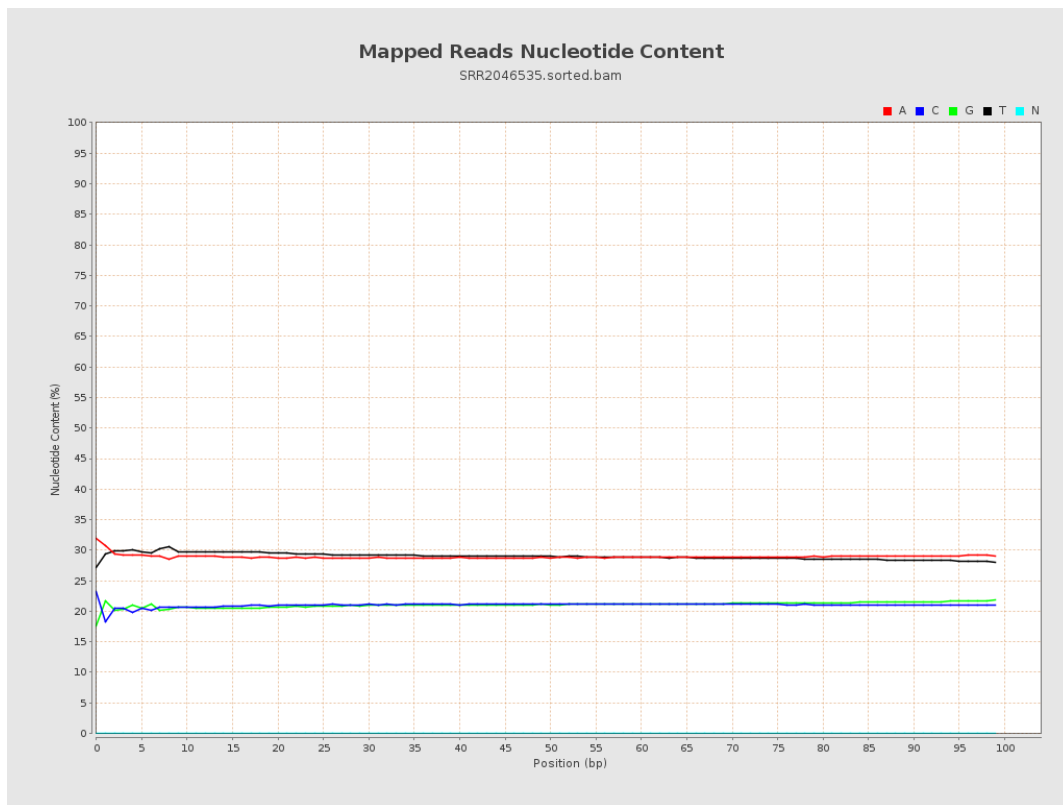
6. Results : Genome Fraction Coverage



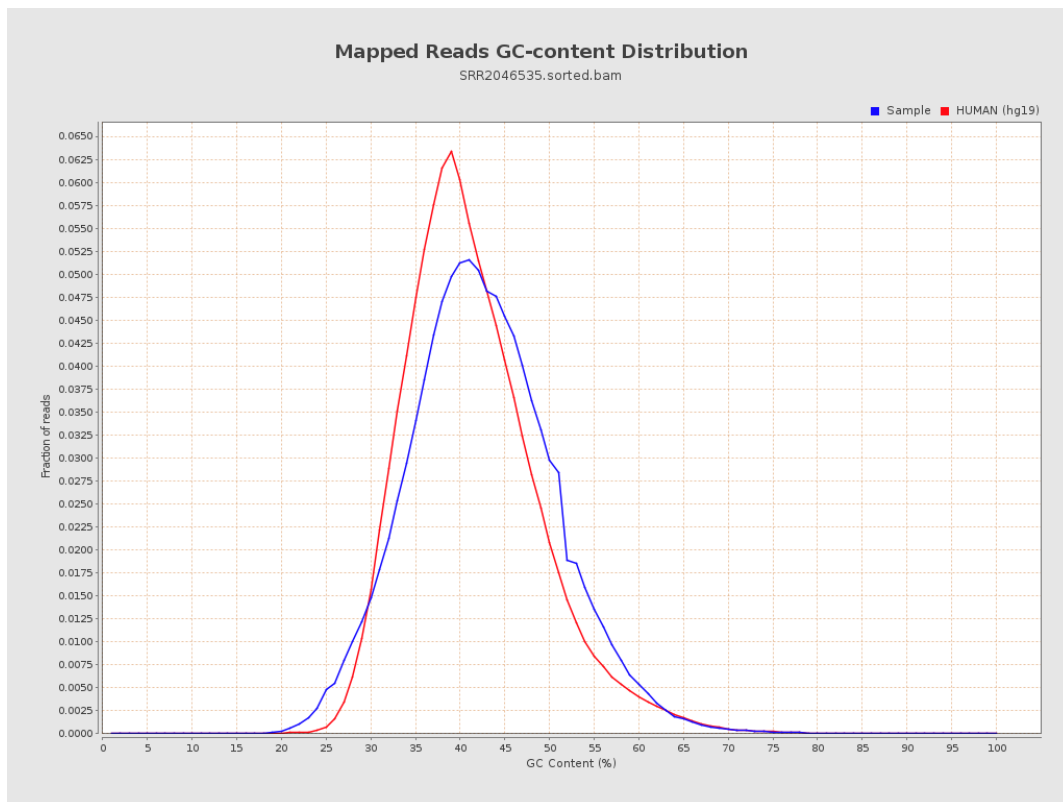
7. Results : Duplication Rate Histogram



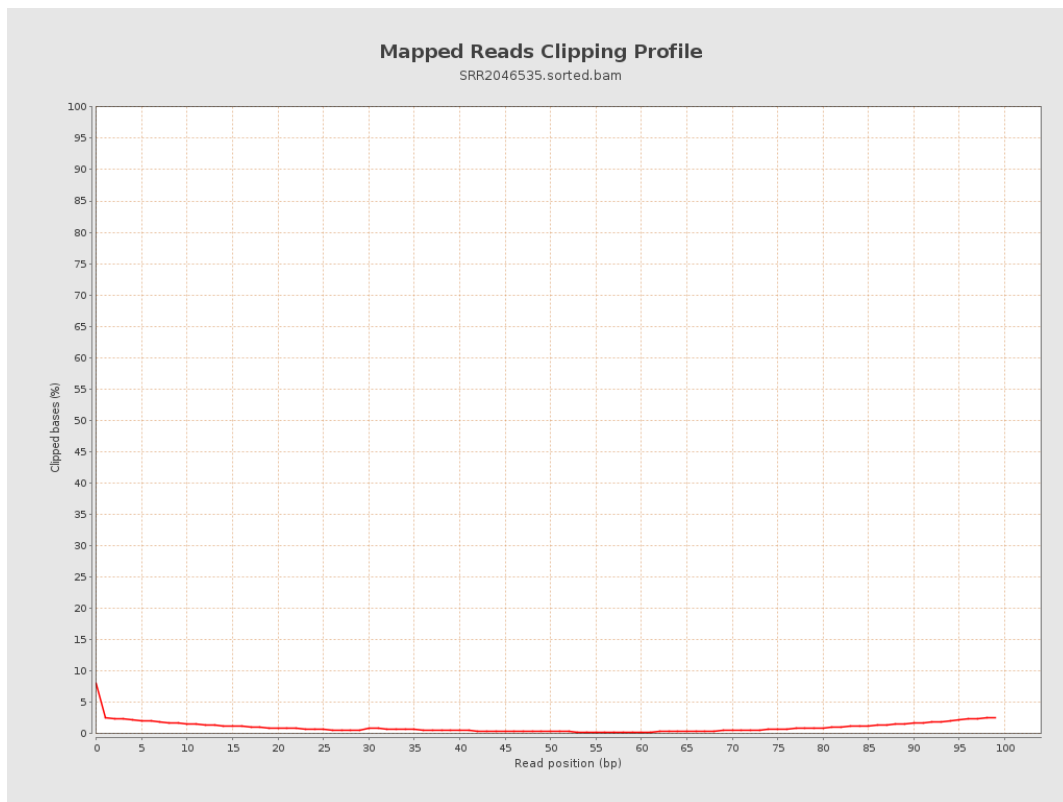
8. Results : Mapped Reads Nucleotide Content



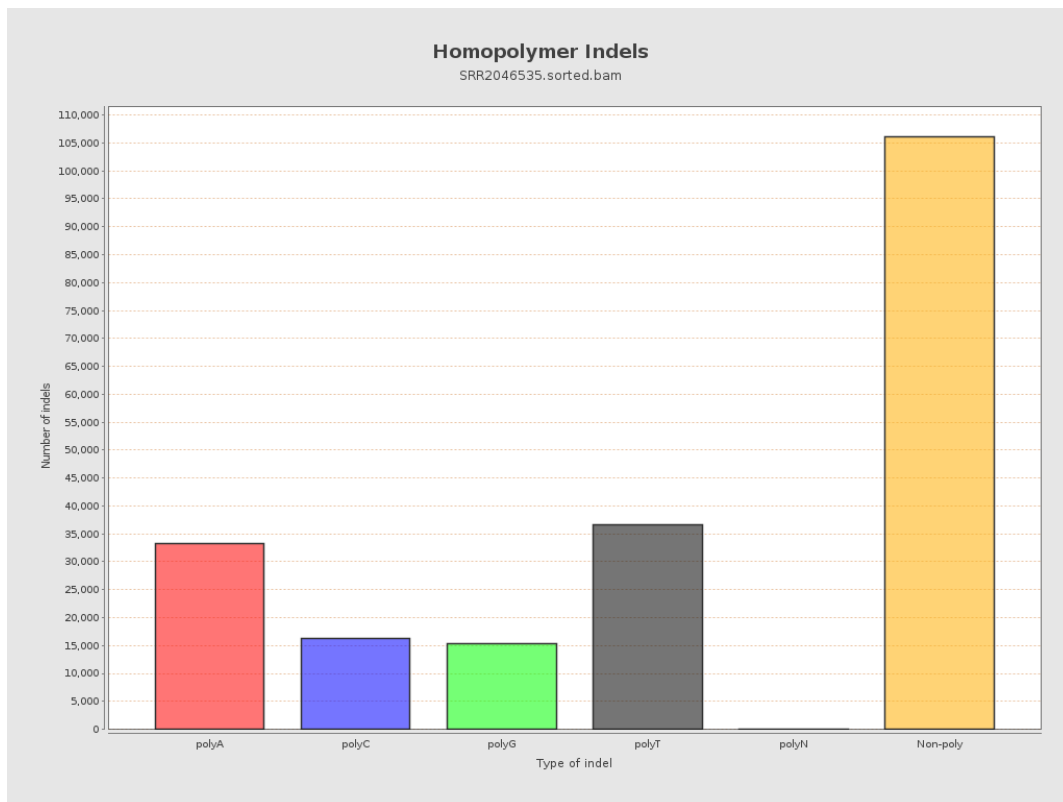
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



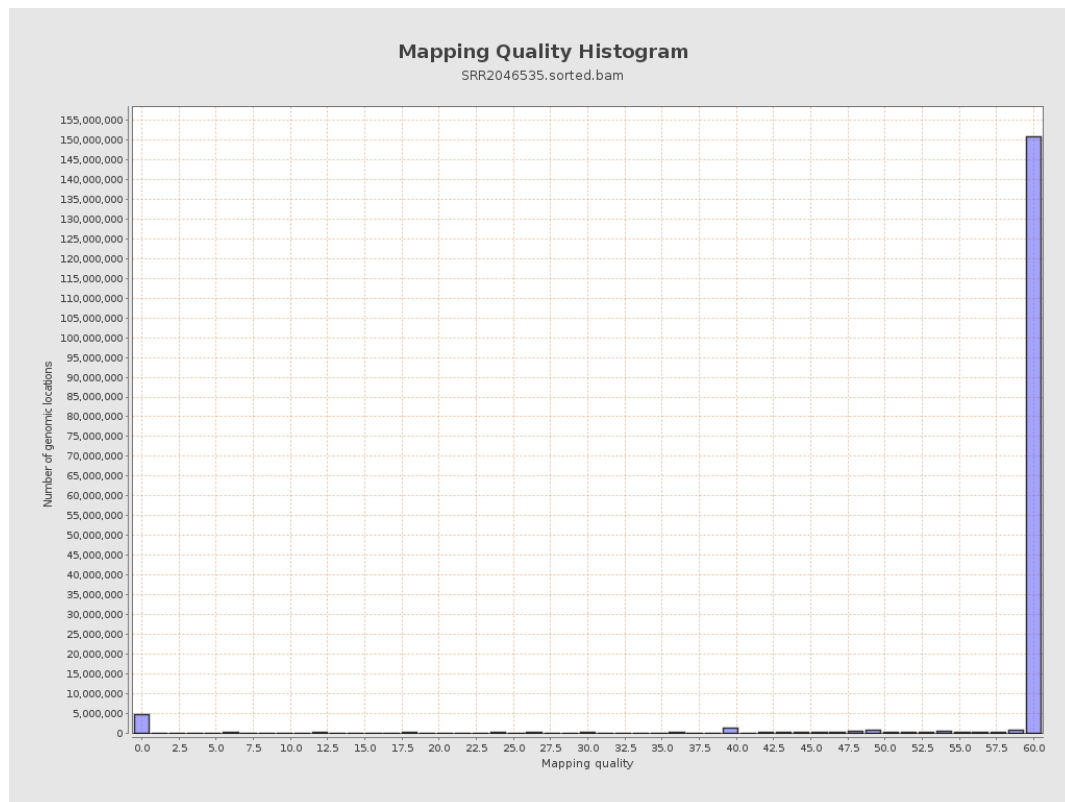
11. Results : Homopolymer Indels



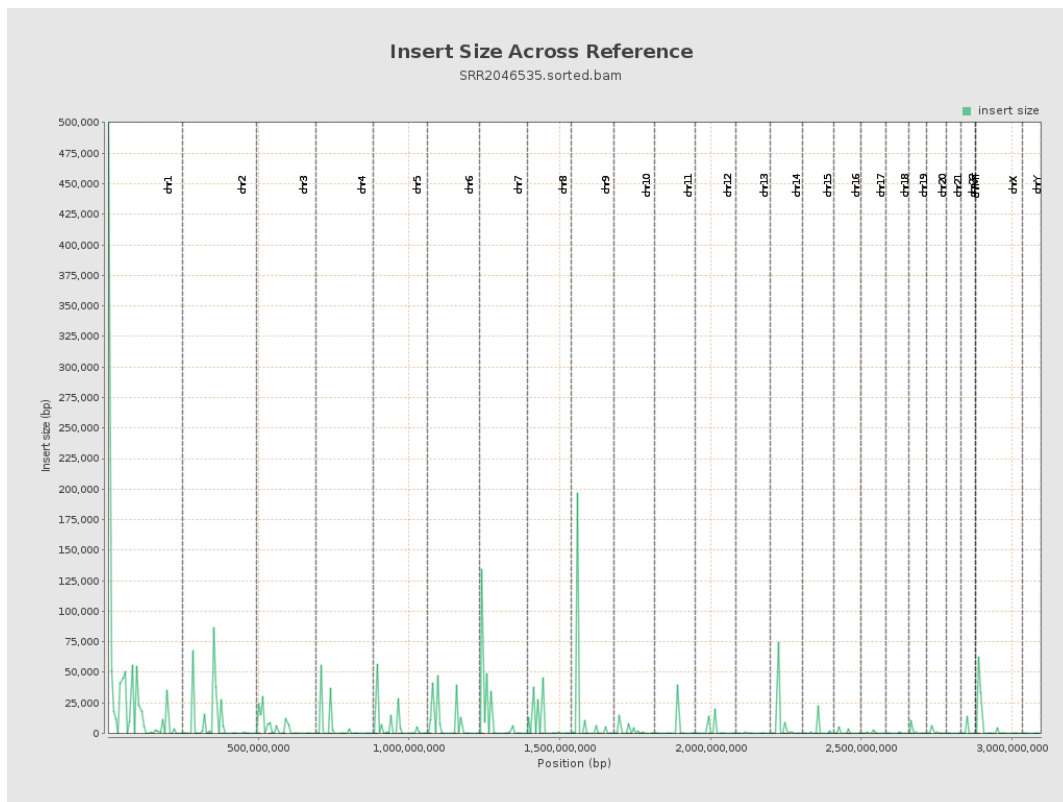
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

