

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 13:46:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046415.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_SRR2046415 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046415_1.fastq.gz SRR2046415_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 13:46:04 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046415.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,898,138
Mapped reads	7,868,811 / 99.63%
Unmapped reads	29,327 / 0.37%
Mapped paired reads	7,868,811 / 99.63%
Mapped reads, first in pair	3,940,441 / 49.89%
Mapped reads, second in pair	3,928,370 / 49.74%
Mapped reads, both in pair	7,848,426 / 99.37%
Mapped reads, singletons	20,385 / 0.26%
Secondary alignments	0
Supplementary alignments	35,359 / 0.45%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	5,447,052 / 68.97%
Duplication rate	39.9%
Clipped reads	1,299,261 / 16.45%

2.2. ACGT Content

Number/percentage of A's	217,139,028 / 28.4%
Number/percentage of C's	164,568,115 / 21.52%
Number/percentage of T's	217,457,601 / 28.44%
Number/percentage of G's	165,393,530 / 21.63%
Number/percentage of N's	72,351 / 0.01%

GC Percentage	43.15%
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2.3. Coverage

Mean	0.2471
Standard Deviation	19.2151

2.4. Mapping Quality

Mean Mapping Quality	53.48
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2.5. Insert size

Mean	15,615.41
Standard Deviation	1,241,673.75
P25/Median/P75	113 / 142 / 176

2.6. Mismatches and indels

General error rate	0.42%
Mismatches	3,057,472
Insertions	55,975
Mapped reads with at least one insertion	0.7%
Deletions	71,884
Mapped reads with at least one deletion	0.89%
Homopolymer indels	47.33%

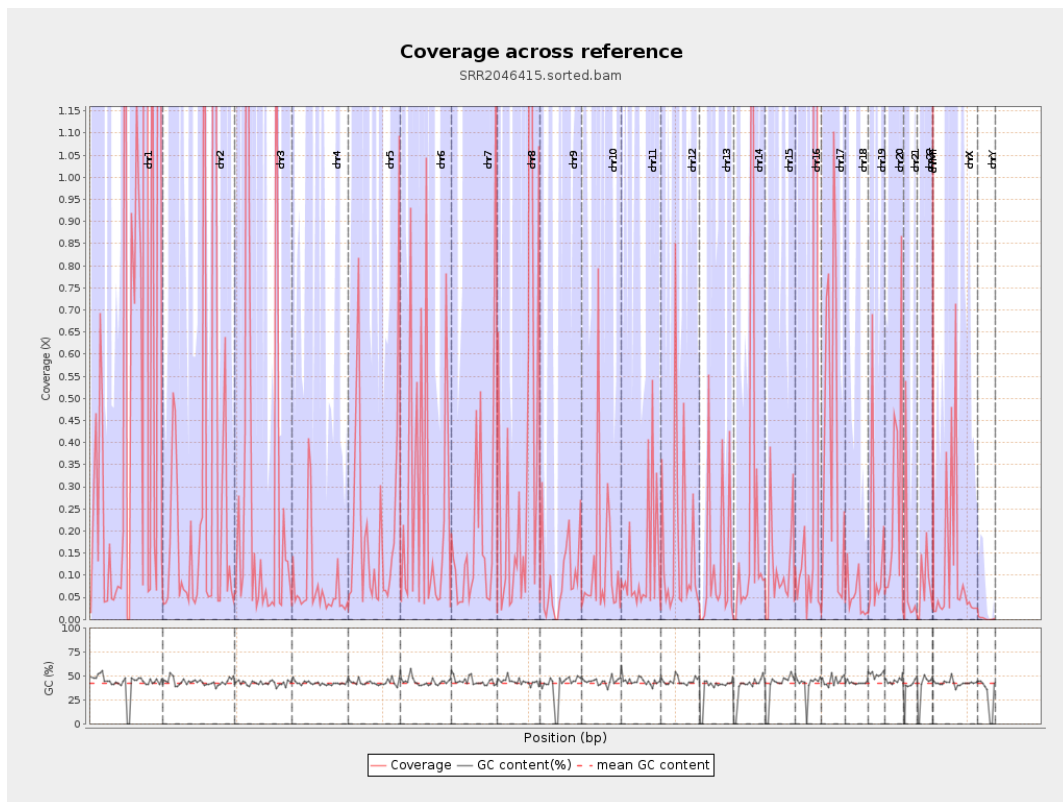
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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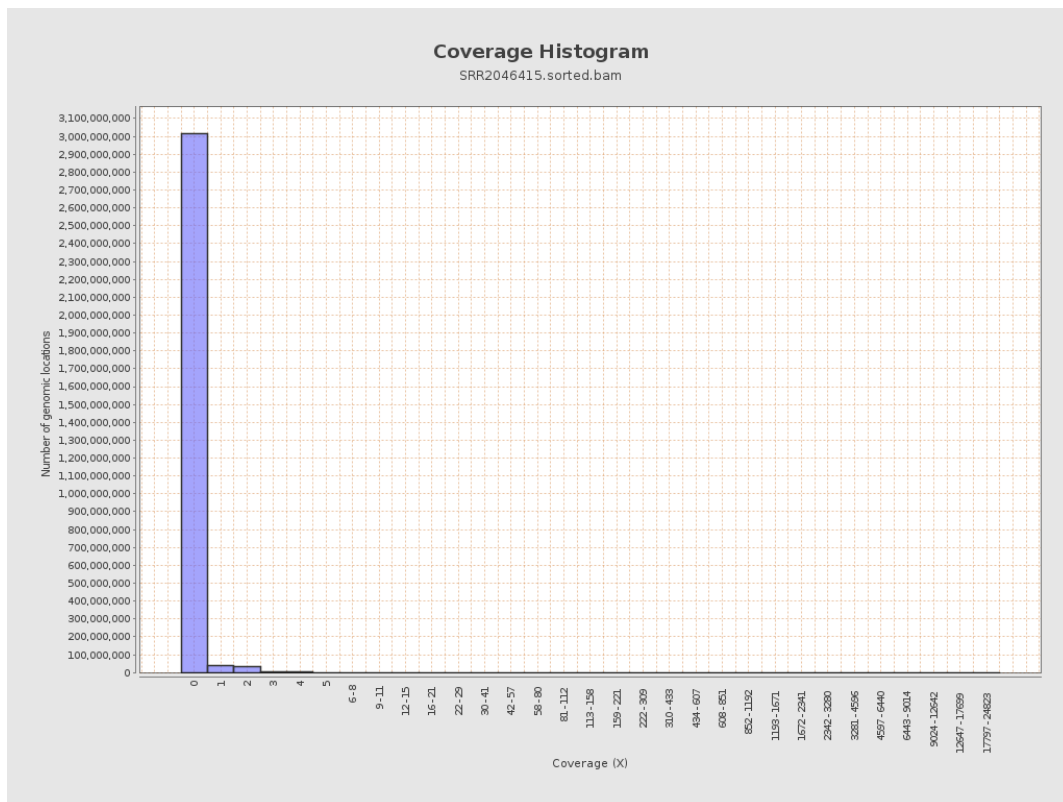
		bases	coverage	deviation
chr1	249250621	181166859	0.7268	48.7842
chr2	243199373	77699668	0.3195	18.8948
chr3	198022430	54517975	0.2753	18.8749
chr4	191154276	14584776	0.0763	4.2012
chr5	180915260	39741073	0.2197	12.8014
chr6	171115067	44722169	0.2614	11.7766
chr7	159138663	35495582	0.223	11.2375
chr8	146364022	63738245	0.4355	21.1908
chr9	141213431	13490371	0.0955	5.2868
chr10	135534747	16932567	0.1249	9.4283
chr11	135006516	17512928	0.1297	7.4198
chr12	133851895	22924935	0.1713	8.2503
chr13	115169878	14558970	0.1264	7.4541
chr14	107349540	25464988	0.2372	16.0451
chr15	102531392	12444817	0.1214	6.4226
chr16	90354753	38414266	0.4251	26.5913
chr17	81195210	33691205	0.4149	30.4061
chr18	78077248	4066926	0.0521	2.2247
chr19	59128983	9309431	0.1574	9.5218
chr20	63025520	17415754	0.2763	17.1491
chr21	48129895	5005970	0.104	11.814
chr22	51304566	4268100	0.0832	4.1866
chrMT	16571	23437	1.4143	1.5272
chrX	155270560	17510576	0.1128	7.2188

chrY	59373566	133861	0.0023	0.1073
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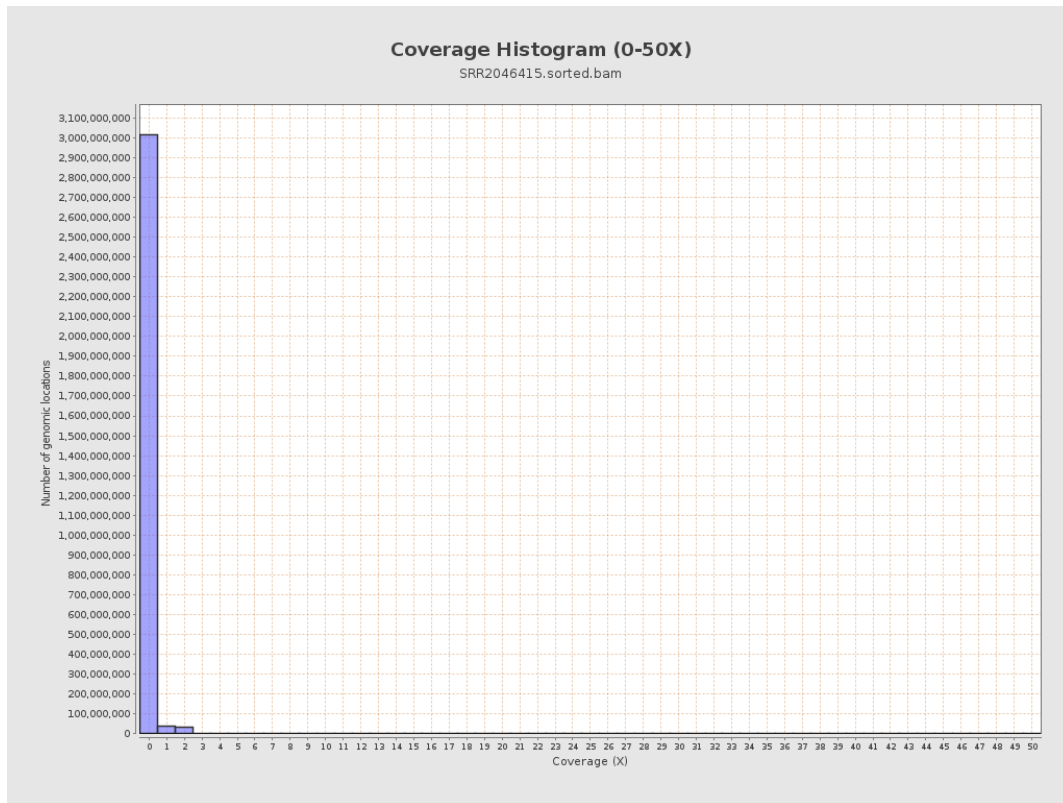
3. Results : Coverage across reference



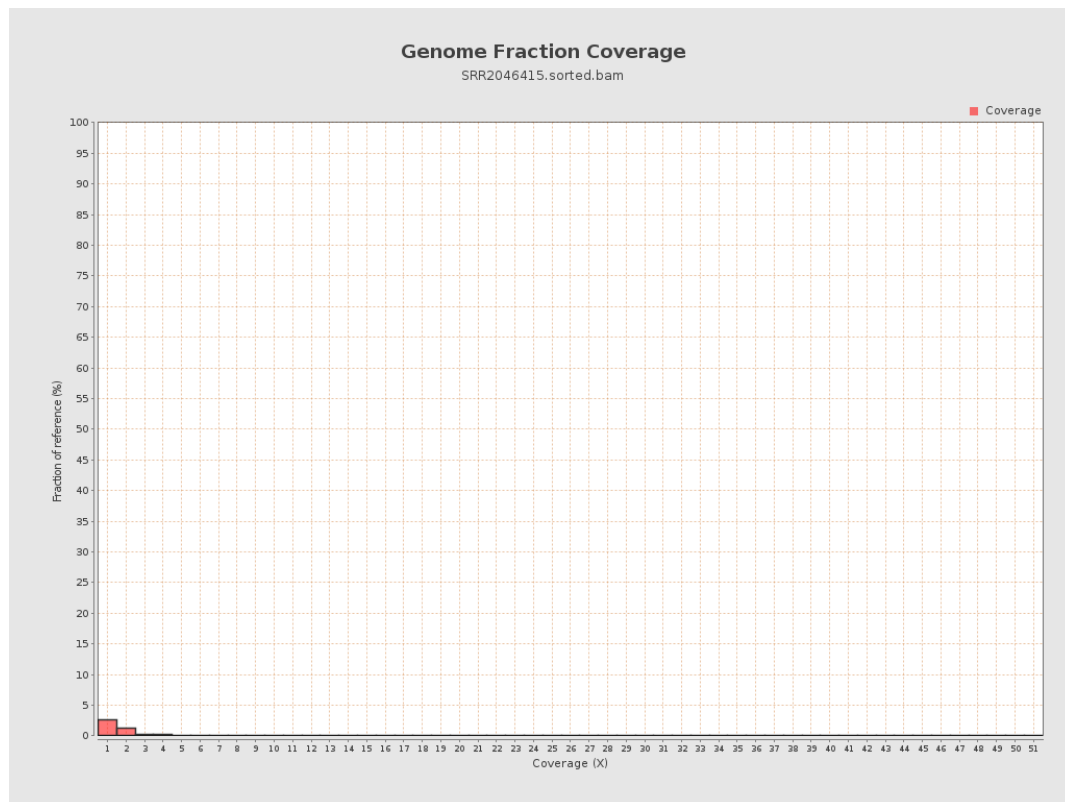
4. Results : Coverage Histogram



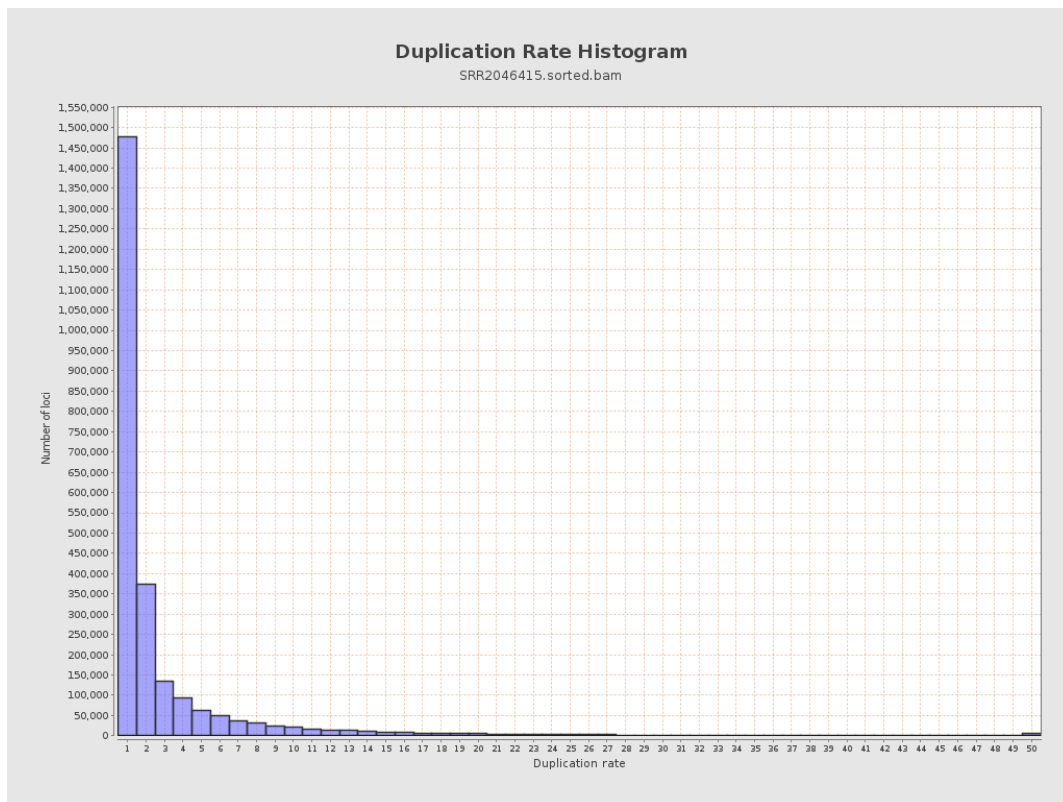
5. Results : Coverage Histogram (0-50X)



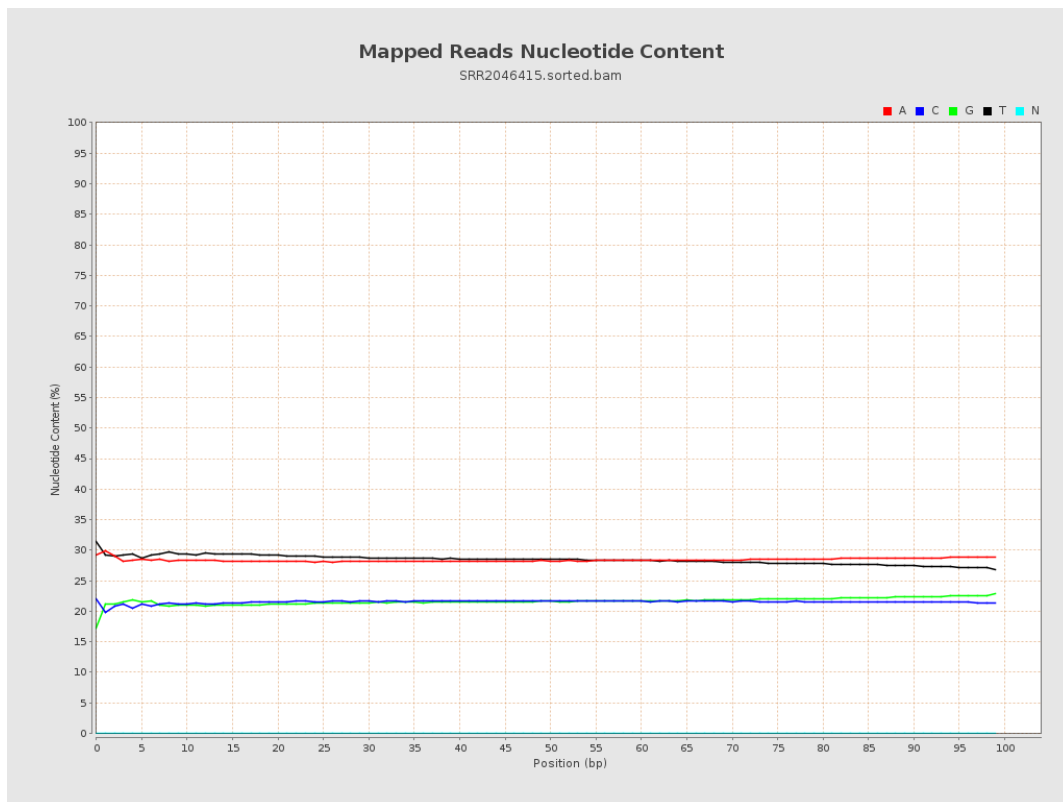
6. Results : Genome Fraction Coverage



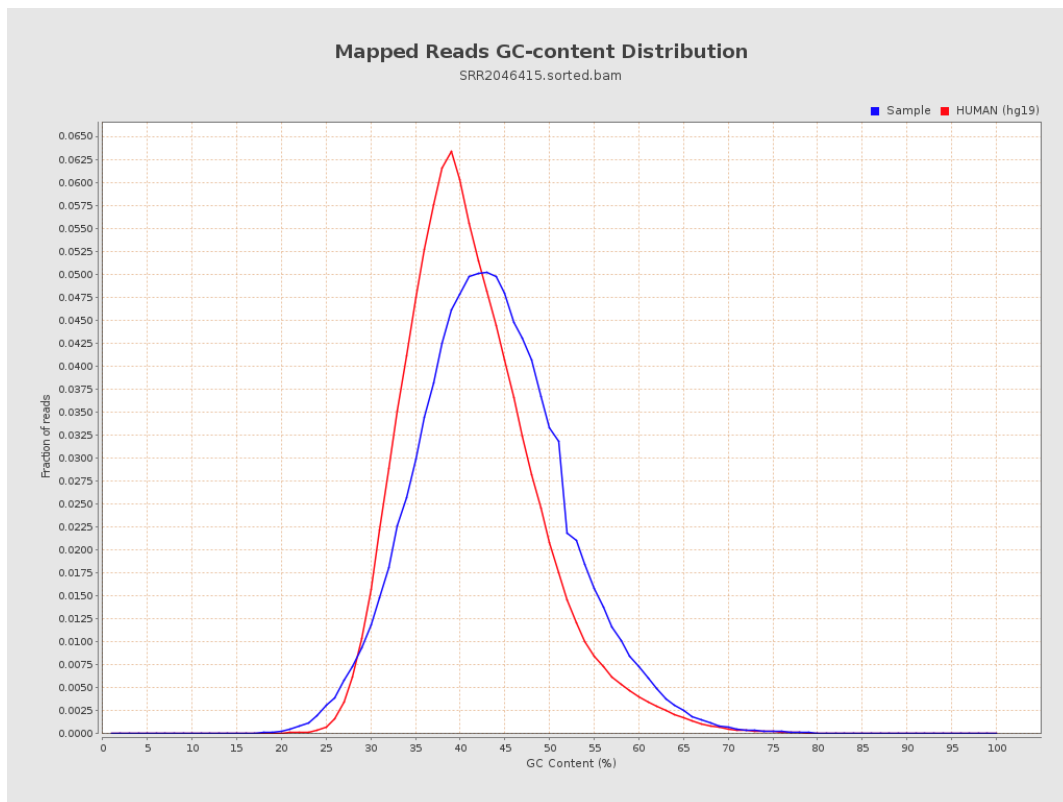
7. Results : Duplication Rate Histogram



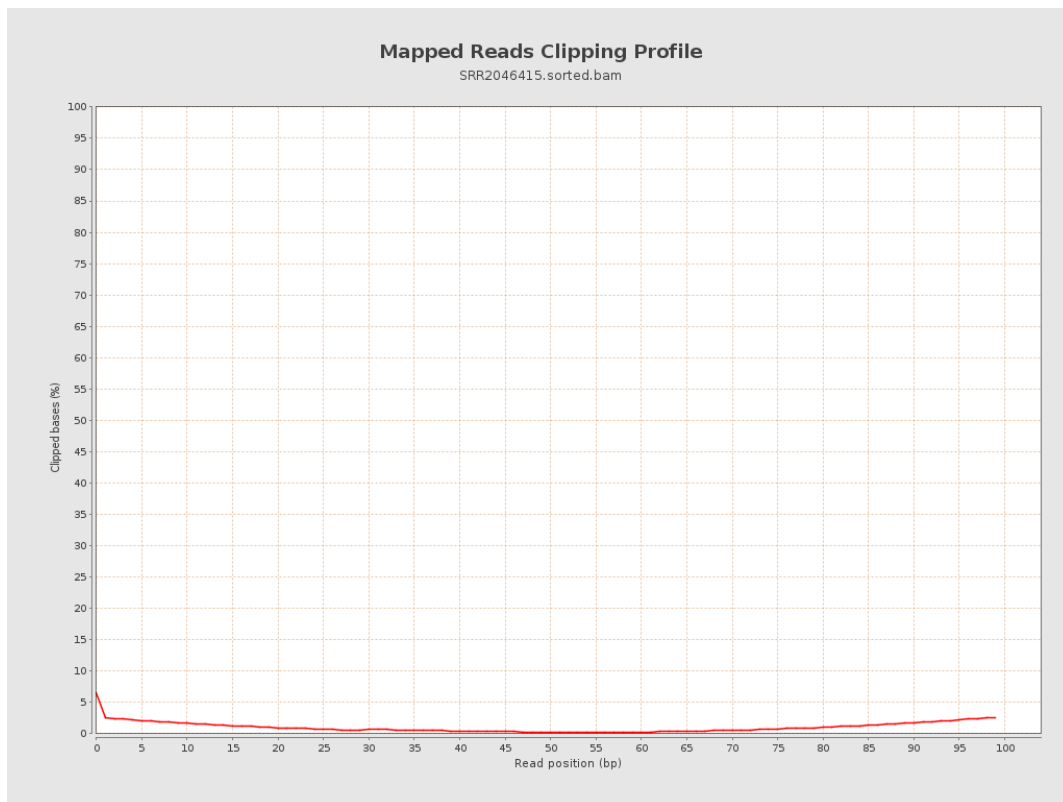
8. Results : Mapped Reads Nucleotide Content



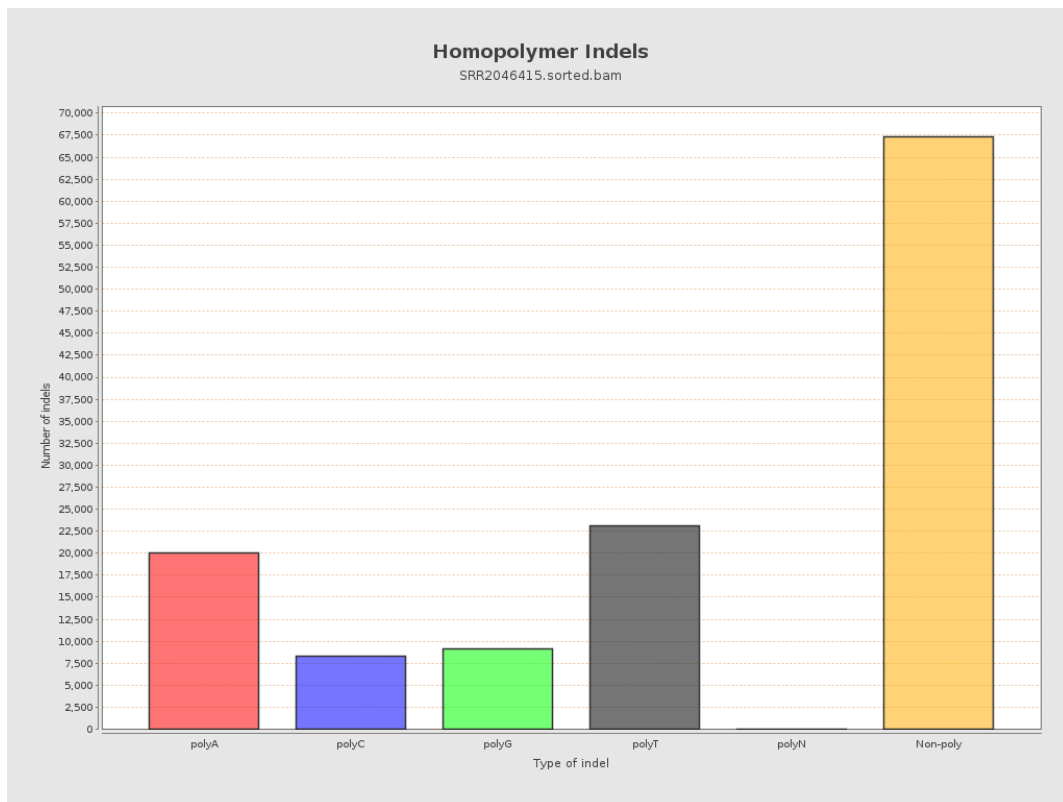
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



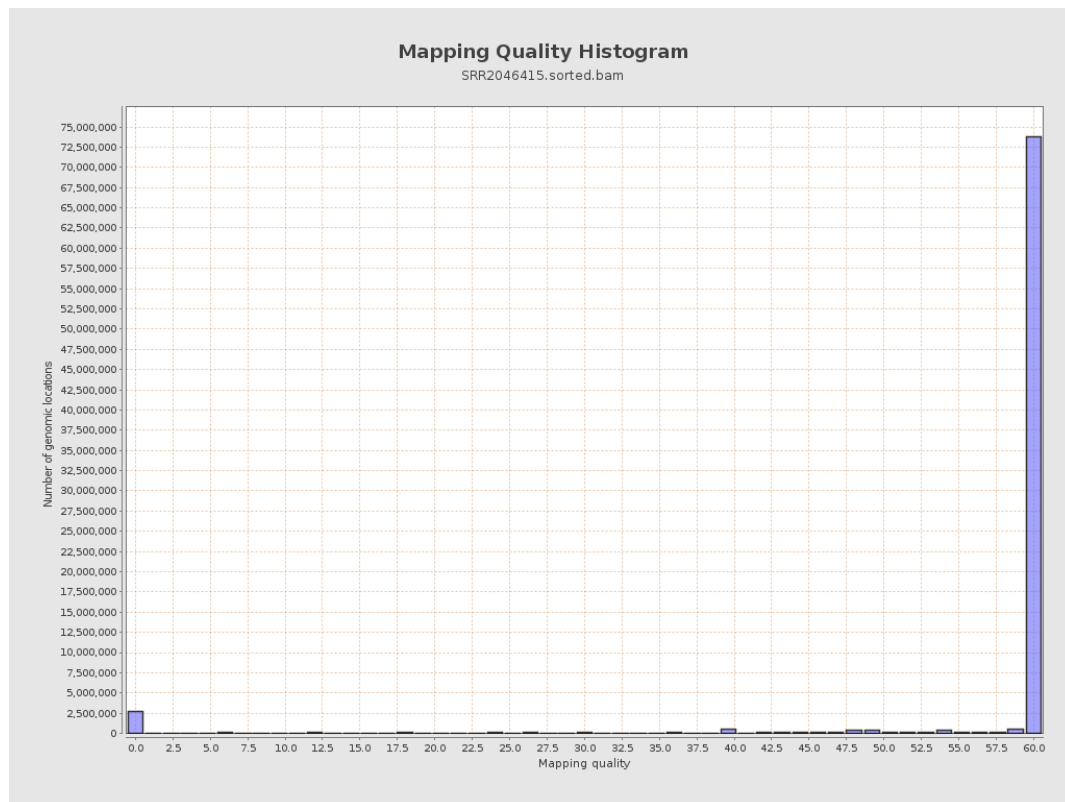
11. Results : Homopolymer Indels



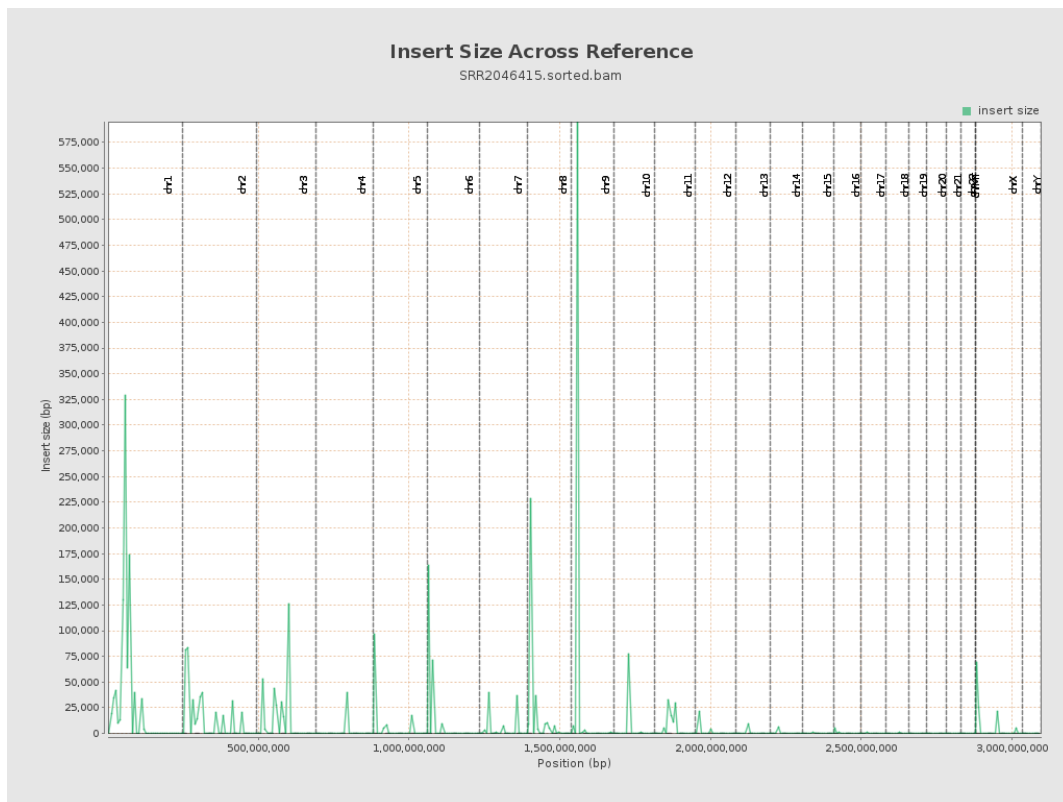
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

