

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 20:10:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046490.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_SRR2046490 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046490_1.fastq.gz SRR2046490_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 20:10:05 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046490.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,548,528
Mapped reads	9,469,759 / 99.18%
Unmapped reads	78,769 / 0.82%
Mapped paired reads	9,469,759 / 99.18%
Mapped reads, first in pair	4,761,587 / 49.87%
Mapped reads, second in pair	4,708,172 / 49.31%
Mapped reads, both in pair	9,409,210 / 98.54%
Mapped reads, singletons	60,549 / 0.63%
Secondary alignments	0
Supplementary alignments	48,818 / 0.51%
Read min/max/mean length	30 / 100 / 100.21
Duplicated reads (estimated)	7,653,535 / 80.15%
Duplication rate	26.97%
Clipped reads	1,189,694 / 12.46%

2.2. ACGT Content

Number/percentage of A's	256,655,982 / 27.69%
Number/percentage of C's	206,453,543 / 22.27%
Number/percentage of T's	257,056,018 / 27.73%
Number/percentage of G's	206,793,855 / 22.31%
Number/percentage of N's	80,030 / 0.01%

GC Percentage	44.58%
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2.3. Coverage

Mean	0.2995
Standard Deviation	60.365

2.4. Mapping Quality

Mean Mapping Quality	52.38
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2.5. Insert size

Mean	19,214.55
Standard Deviation	1,475,965.98
P25/Median/P75	124 / 156 / 193

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	3,557,311
Insertions	65,646
Mapped reads with at least one insertion	0.68%
Deletions	86,273
Mapped reads with at least one deletion	0.89%
Homopolymer indels	49.34%

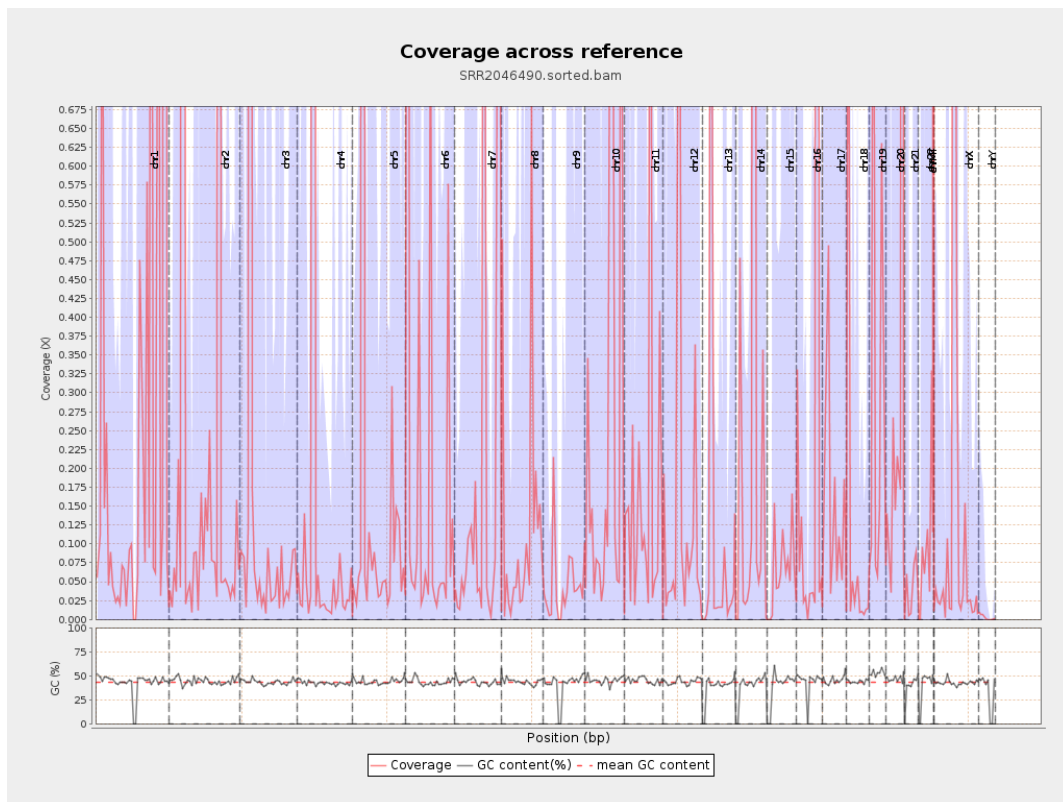
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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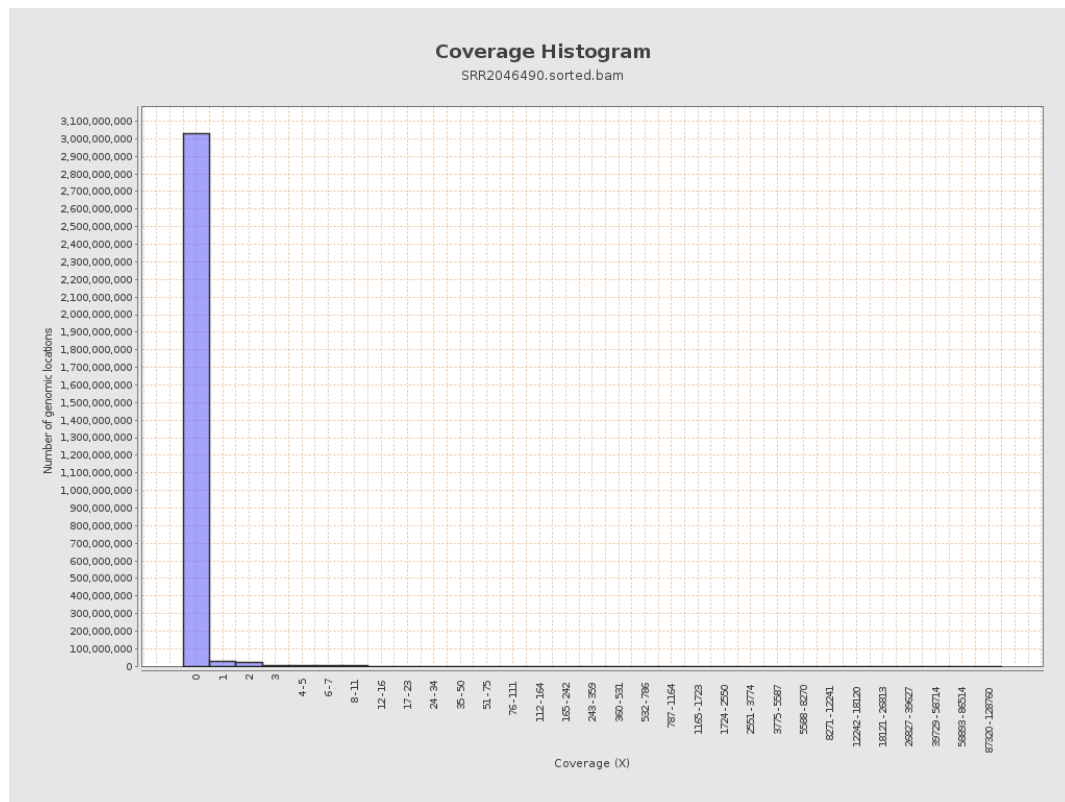
		bases	coverage	deviation
chr1	249250621	159371630	0.6394	84.5756
chr2	243199373	139690475	0.5744	83.9411
chr3	198022430	63410418	0.3202	66.6581
chr4	191154276	38013611	0.1989	43.8219
chr5	180915260	87224853	0.4821	154.6014
chr6	171115067	40831781	0.2386	42.0671
chr7	159138663	31086085	0.1953	19.5909
chr8	146364022	18206880	0.1244	15.3856
chr9	141213431	5852927	0.0414	3.3544
chr10	135534747	38301400	0.2826	25.8995
chr11	135006516	25633265	0.1899	18.0247
chr12	133851895	22570753	0.1686	17.9134
chr13	115169878	12662823	0.1099	14.0838
chr14	107349540	31812448	0.2963	20.792
chr15	102531392	6648813	0.0648	3.7501
chr16	90354753	78077372	0.8641	92.8585
chr17	81195210	12748593	0.157	16.2857
chr18	78077248	10122386	0.1296	15.9451
chr19	59128983	19114543	0.3233	20.2334
chr20	63025520	55669802	0.8833	99.3694
chr21	48129895	2007262	0.0417	2.4034
chr22	51304566	5199598	0.1013	5.5172
chrMT	16571	269103	16.2394	7.3947
chrX	155270560	22591385	0.1455	24.7733

chrY	59373566	161166	0.0027	0.123
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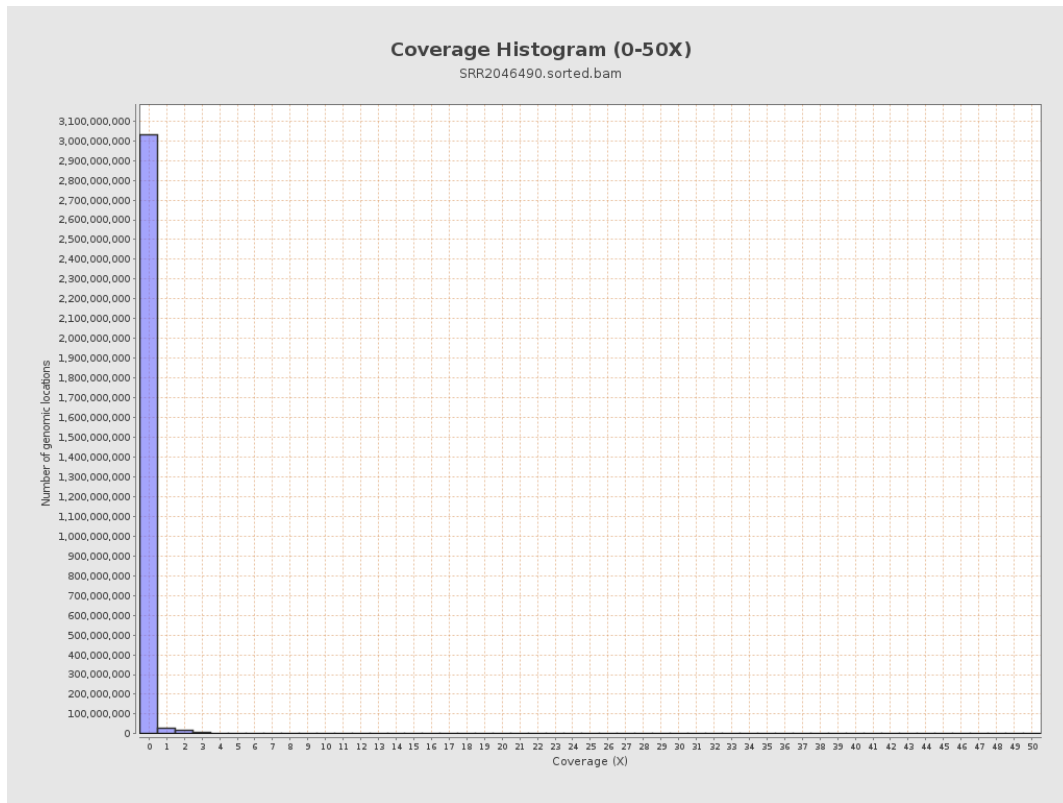
3. Results : Coverage across reference



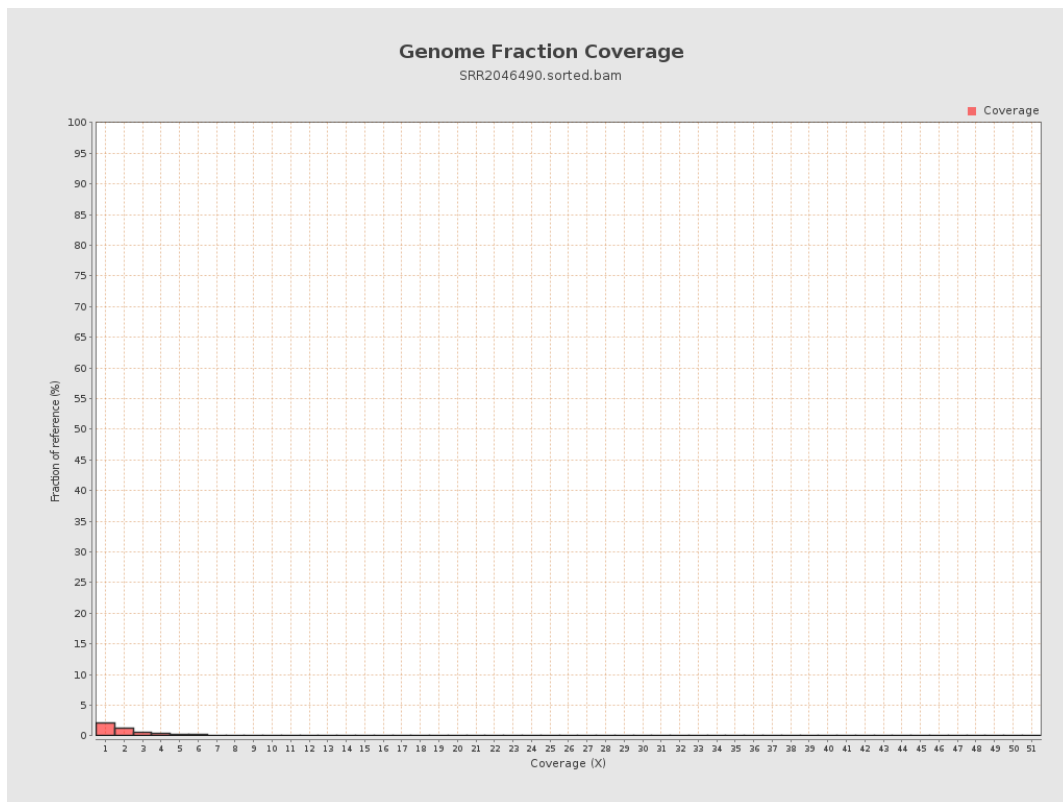
4. Results : Coverage Histogram



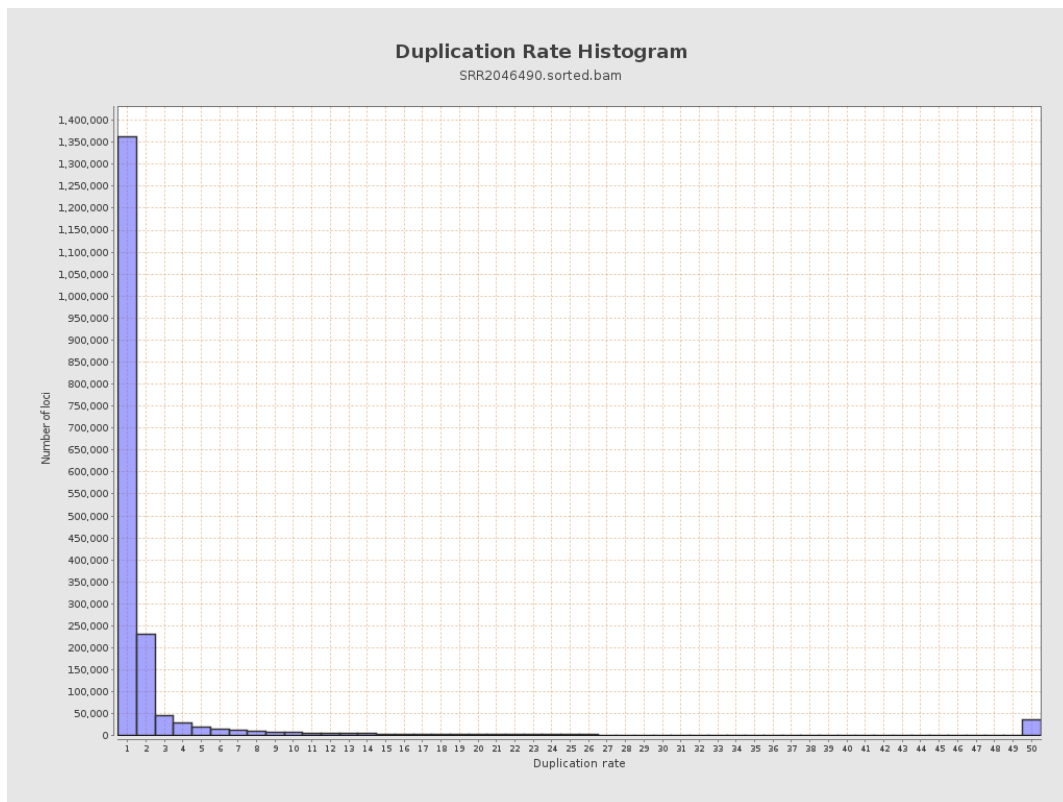
5. Results : Coverage Histogram (0-50X)



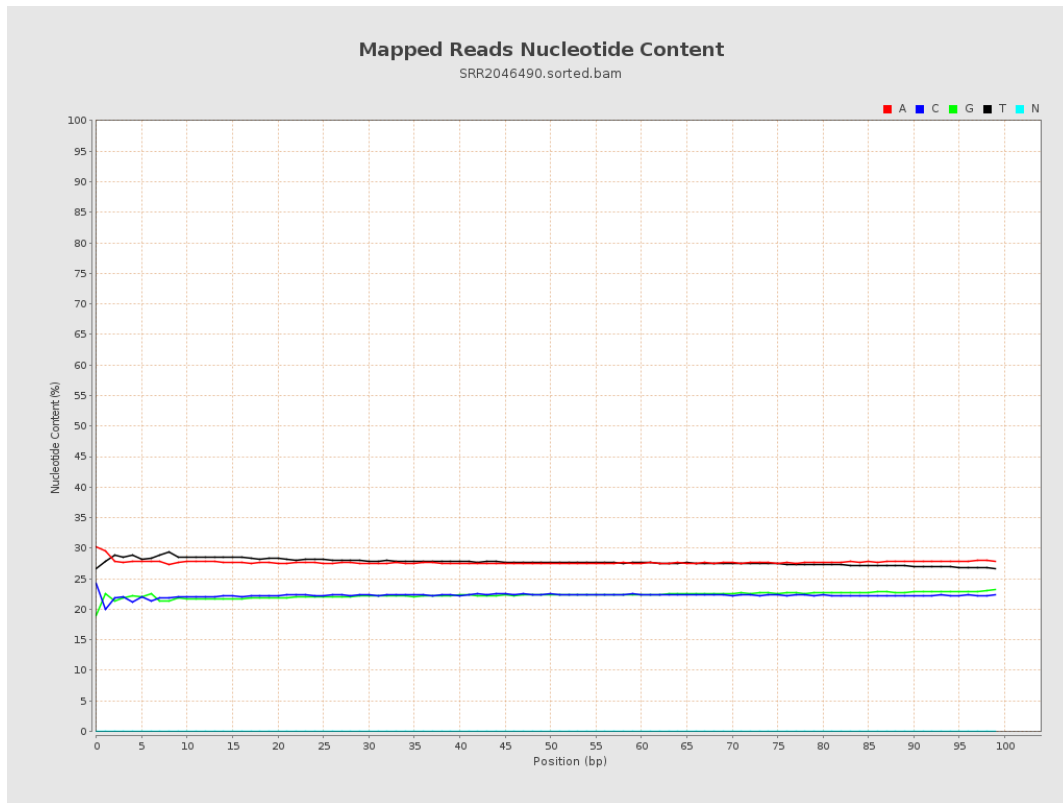
6. Results : Genome Fraction Coverage



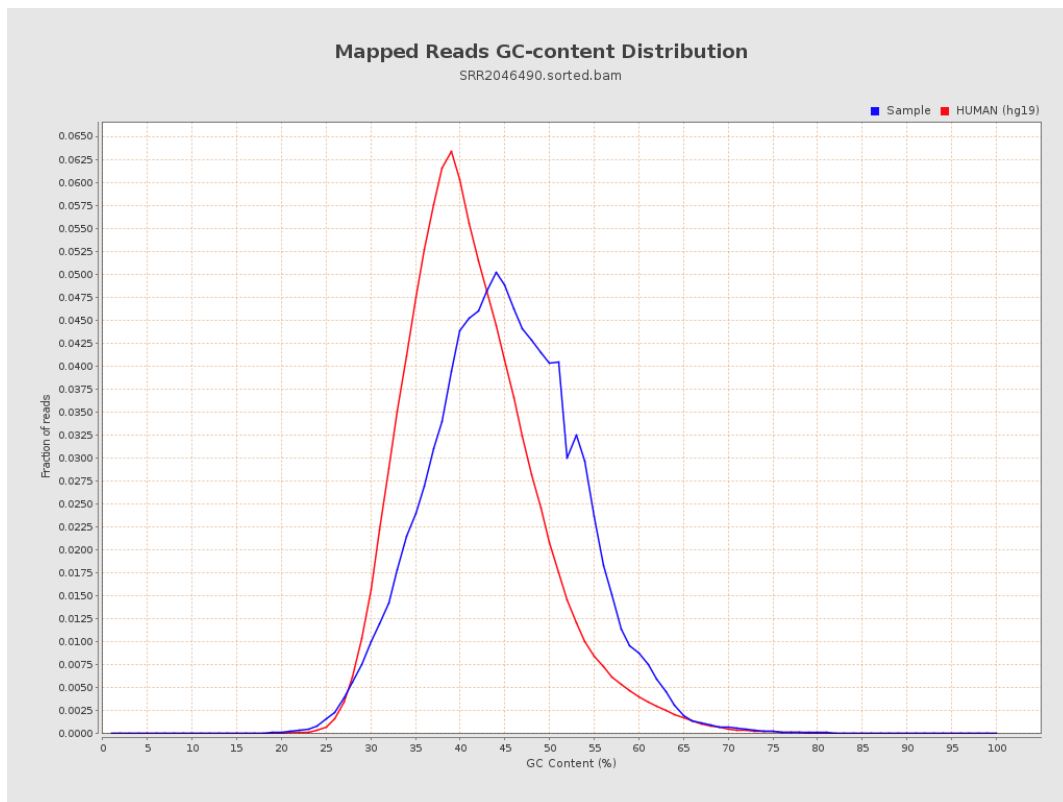
7. Results : Duplication Rate Histogram



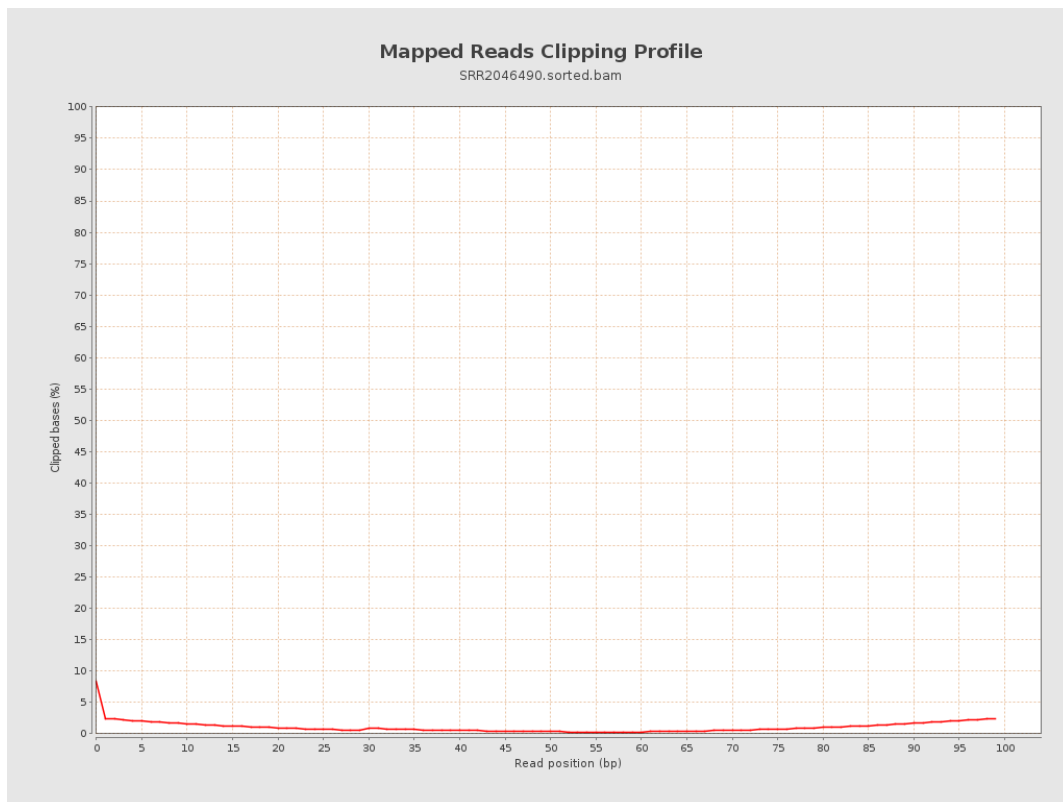
8. Results : Mapped Reads Nucleotide Content



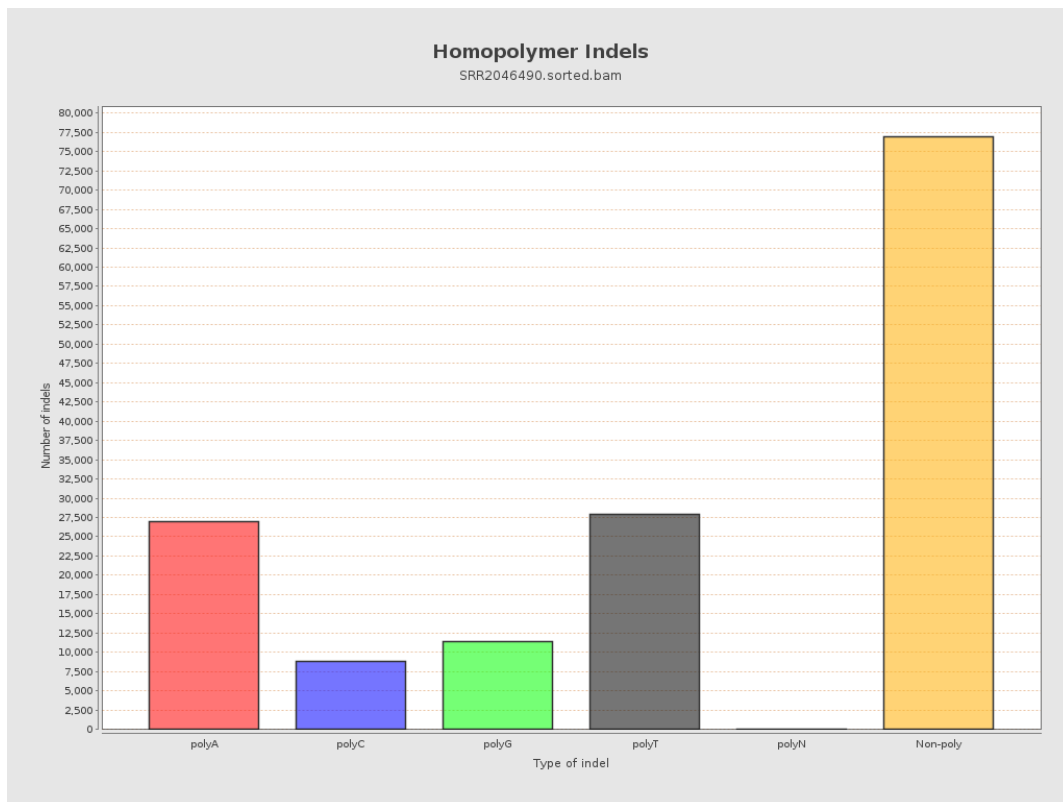
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



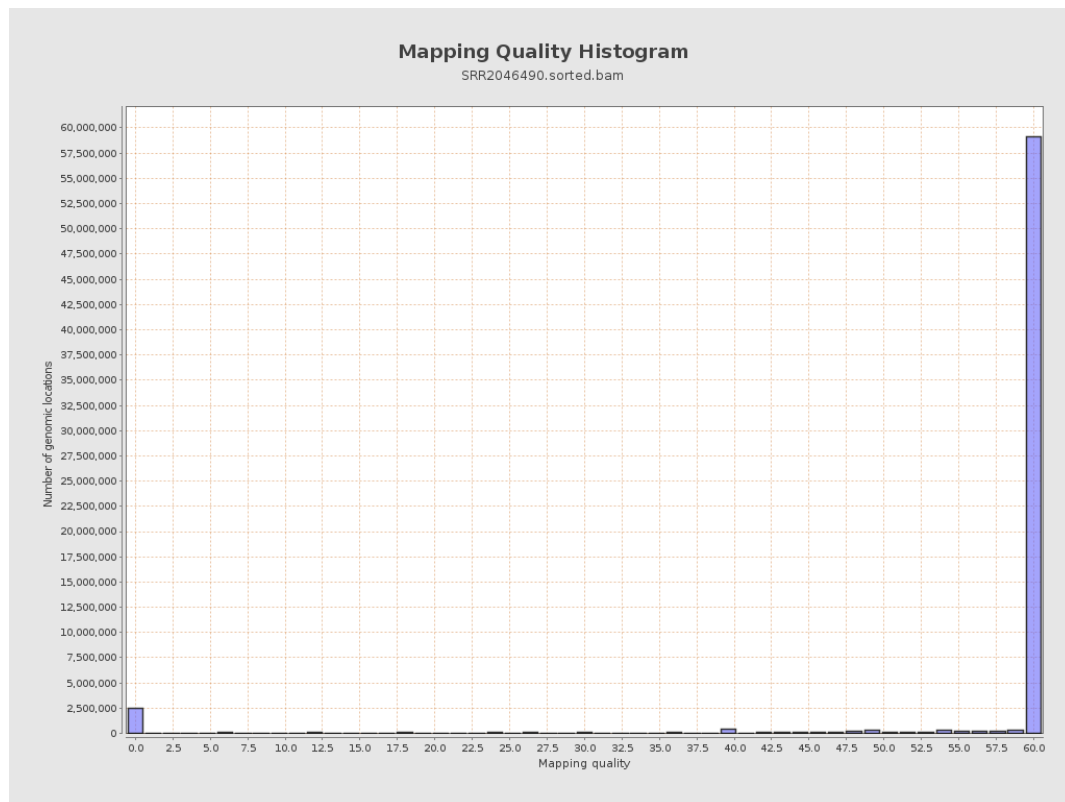
11. Results : Homopolymer Indels



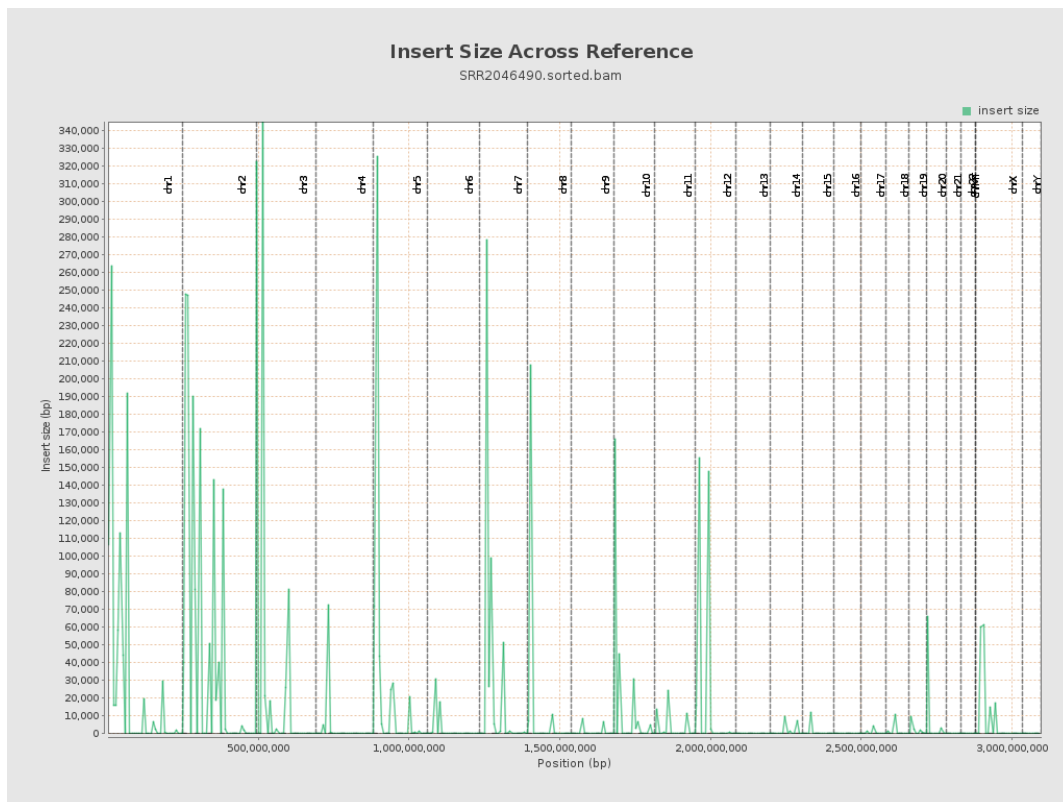
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

