

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 20:30:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046492.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_SRR2046492 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046492_1.fastq.gz SRR2046492_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 20:30:27 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046492.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,903,854
Mapped reads	7,725,388 / 97.74%
Unmapped reads	178,466 / 2.26%
Mapped paired reads	7,725,388 / 97.74%
Mapped reads, first in pair	3,940,322 / 49.85%
Mapped reads, second in pair	3,785,066 / 47.89%
Mapped reads, both in pair	7,560,758 / 95.66%
Mapped reads, singletons	164,630 / 2.08%
Secondary alignments	0
Supplementary alignments	50,702 / 0.64%
Read min/max/mean length	30 / 100 / 100.26
Duplicated reads (estimated)	5,375,593 / 68.01%
Duplication rate	35.76%
Clipped reads	1,345,253 / 17.02%

2.2. ACGT Content

Number/percentage of A's	223,047,793 / 29.79%
Number/percentage of C's	151,688,567 / 20.26%
Number/percentage of T's	223,323,616 / 29.83%
Number/percentage of G's	150,539,047 / 20.11%
Number/percentage of N's	58,842 / 0.01%

GC Percentage	40.37%
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2.3. Coverage

Mean	0.2419
Standard Deviation	18.918

2.4. Mapping Quality

Mean Mapping Quality	52.98
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2.5. Insert size

Mean	37,193.3
Standard Deviation	1,862,617.89
P25/Median/P75	113 / 143 / 178

2.6. Mismatches and indels

General error rate	0.47%
Mismatches	3,382,399
Insertions	61,683
Mapped reads with at least one insertion	0.78%
Deletions	70,471
Mapped reads with at least one deletion	0.88%
Homopolymer indels	49.07%

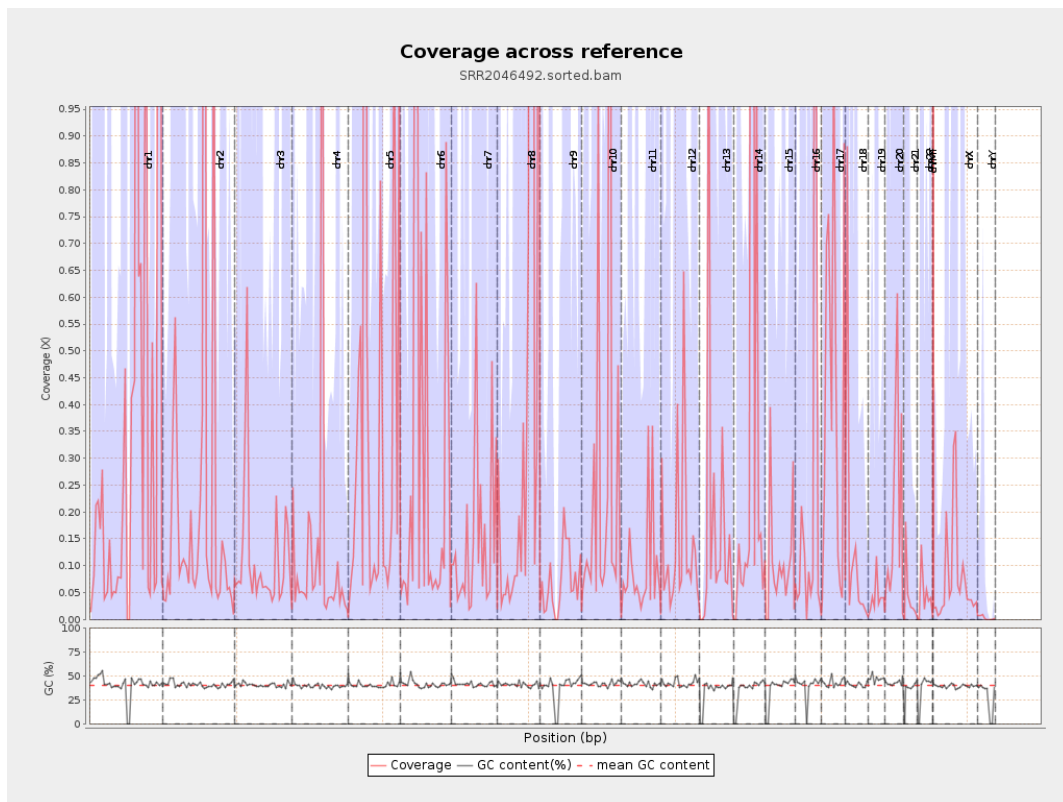
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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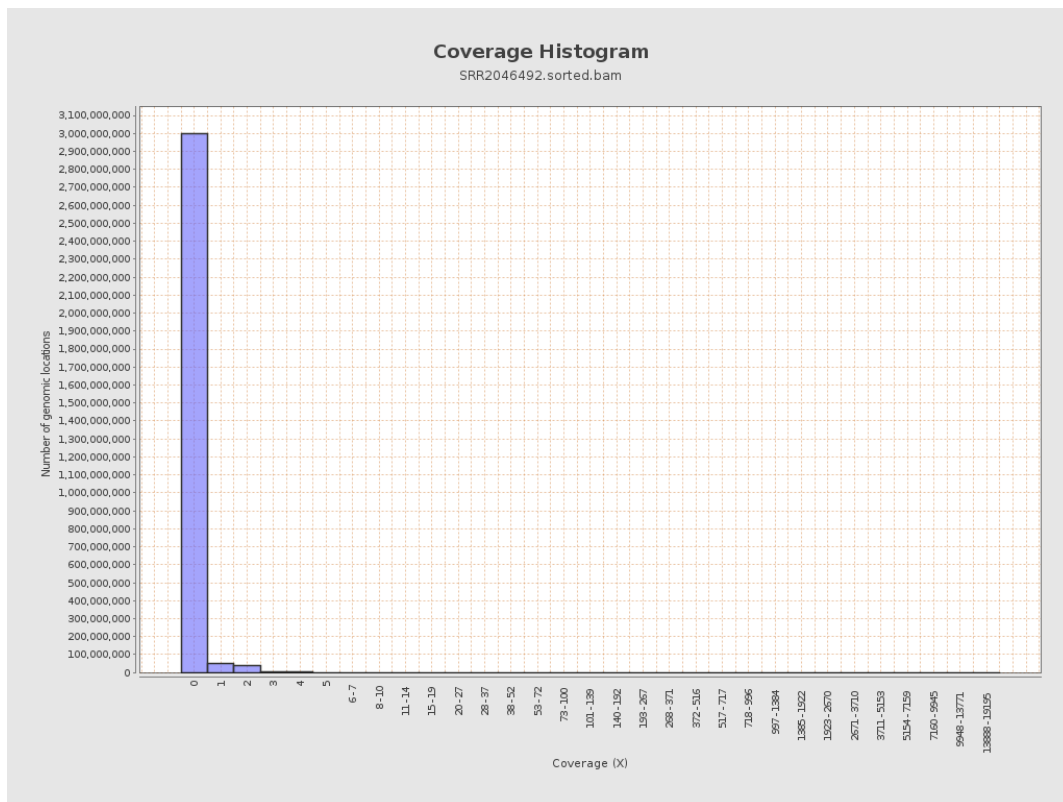
		bases	coverage	deviation
chr1	249250621	102068742	0.4095	22.0652
chr2	243199373	61711232	0.2537	17.2105
chr3	198022430	22912564	0.1157	5.5027
chr4	191154276	26001165	0.136	13.0641
chr5	180915260	83714472	0.4627	38.5088
chr6	171115067	54359530	0.3177	17.6566
chr7	159138663	24066417	0.1512	7.4208
chr8	146364022	113445395	0.7751	40.3196
chr9	141213431	10032637	0.071	2.9725
chr10	135534747	39196733	0.2892	27.4125
chr11	135006516	13156225	0.0974	4.433
chr12	133851895	19116384	0.1428	7.3141
chr13	115169878	20775148	0.1804	12.2517
chr14	107349540	51821861	0.4827	33.4481
chr15	102531392	11229730	0.1095	4.1715
chr16	90354753	18990850	0.2102	10.5655
chr17	81195210	33616637	0.414	17.0977
chr18	78077248	10768380	0.1379	8.4802
chr19	59128983	2421536	0.041	2.356
chr20	63025520	12826337	0.2035	12.5714
chr21	48129895	2234753	0.0464	3.5147
chr22	51304566	2237805	0.0436	2.7124
chrMT	16571	61805	3.7297	2.5575
chrX	155270560	11911814	0.0767	5.4977

chrY	59373566	174143	0.0029	0.2797
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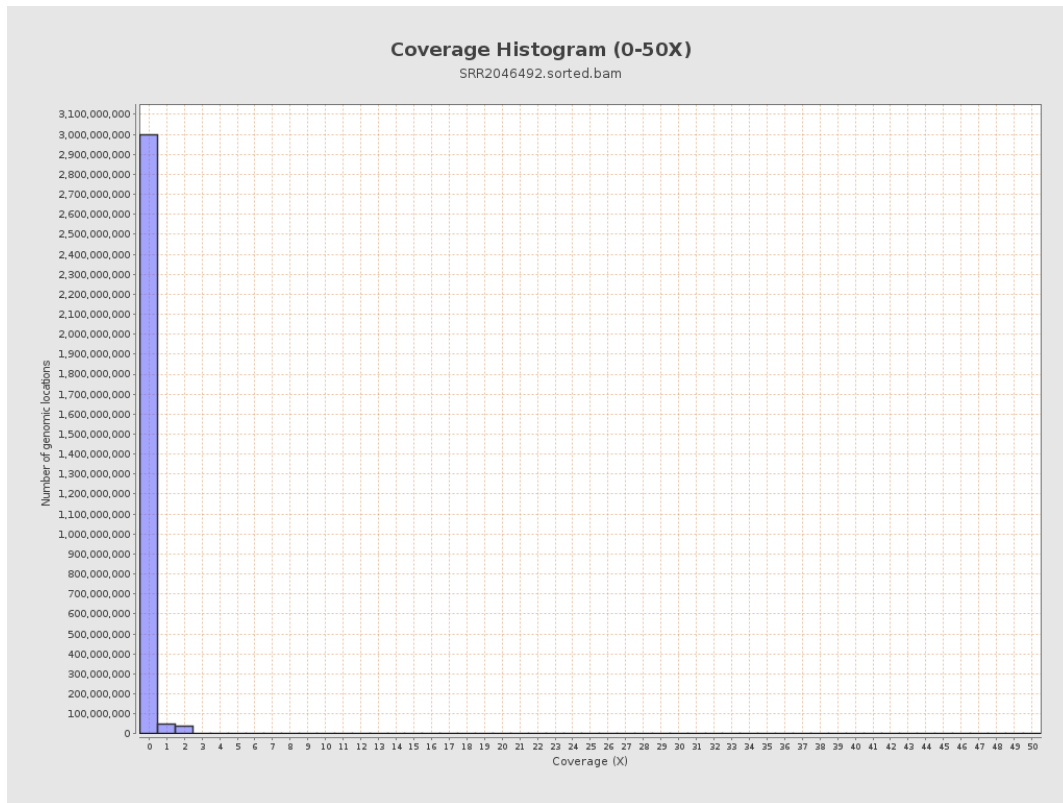
3. Results : Coverage across reference



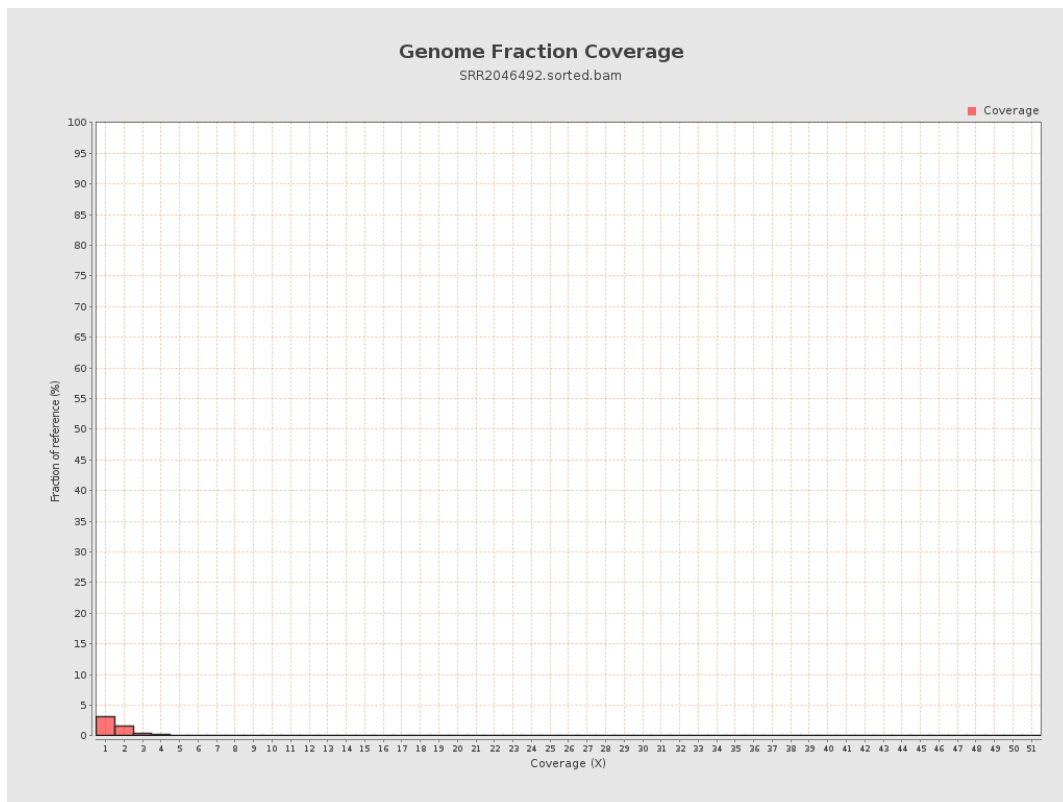
4. Results : Coverage Histogram



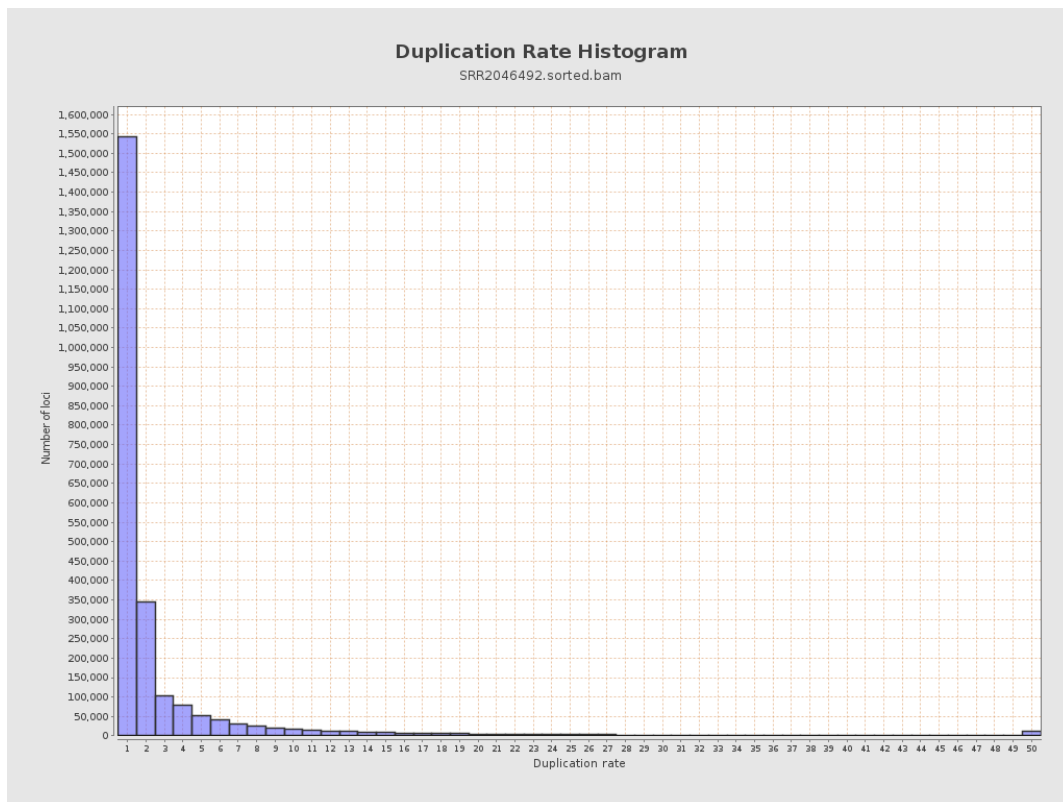
5. Results : Coverage Histogram (0-50X)



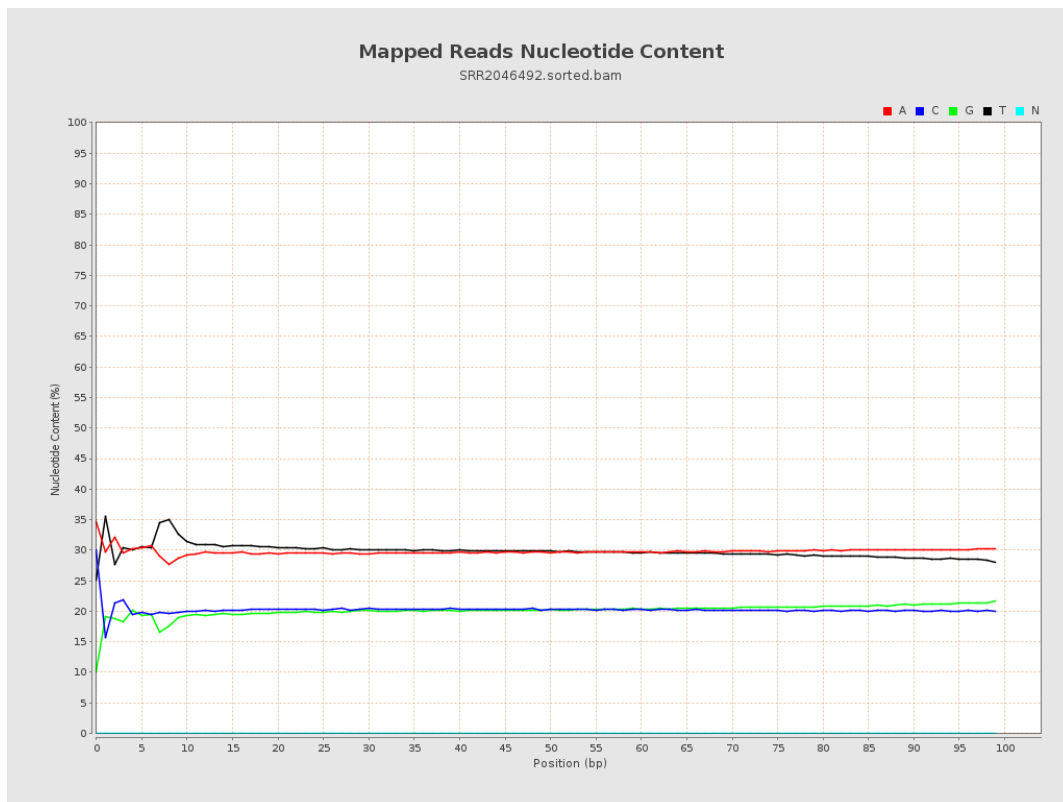
6. Results : Genome Fraction Coverage



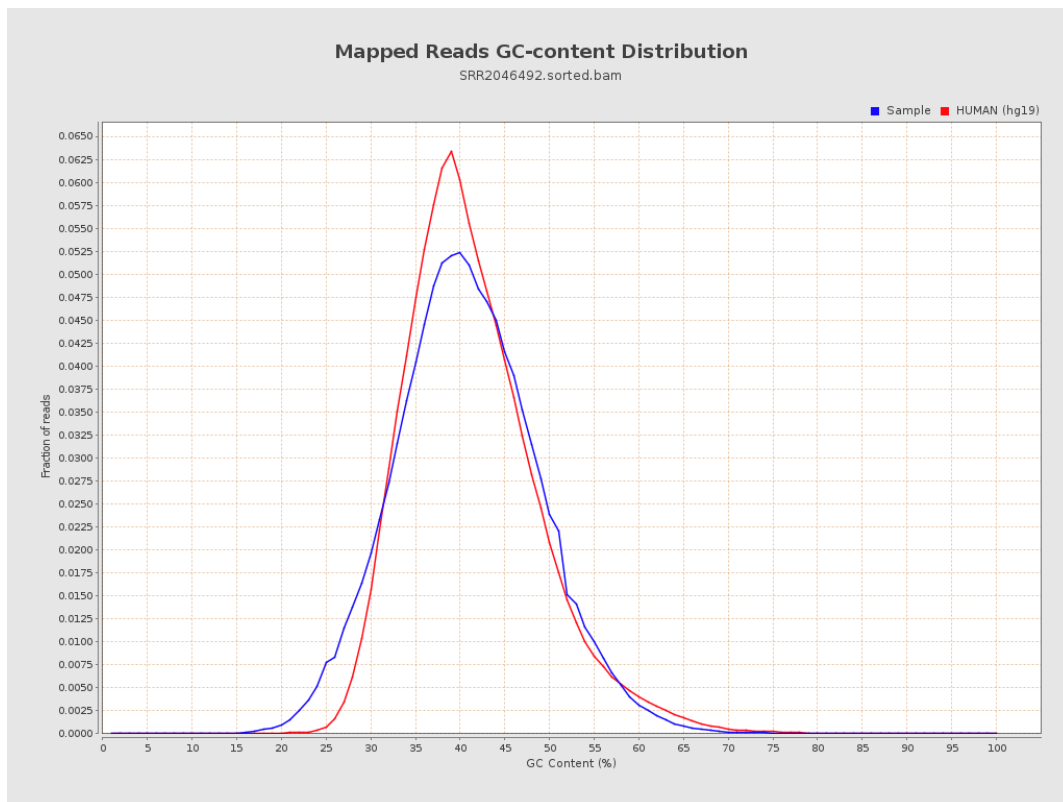
7. Results : Duplication Rate Histogram



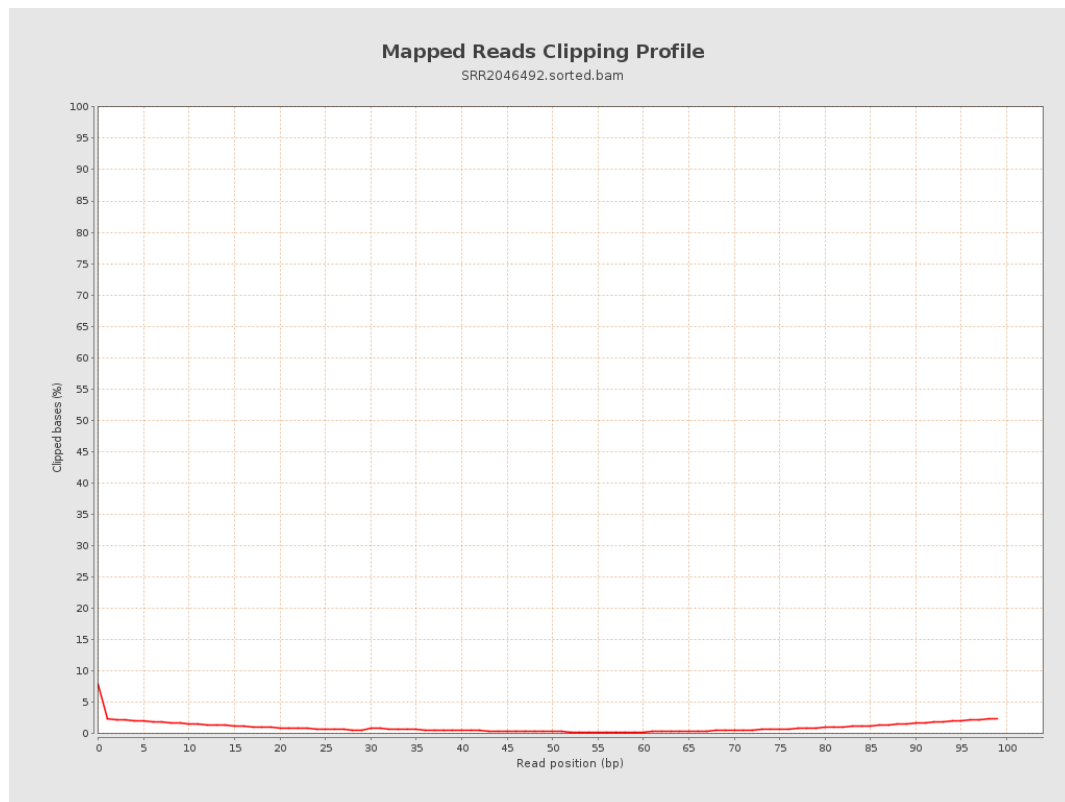
8. Results : Mapped Reads Nucleotide Content



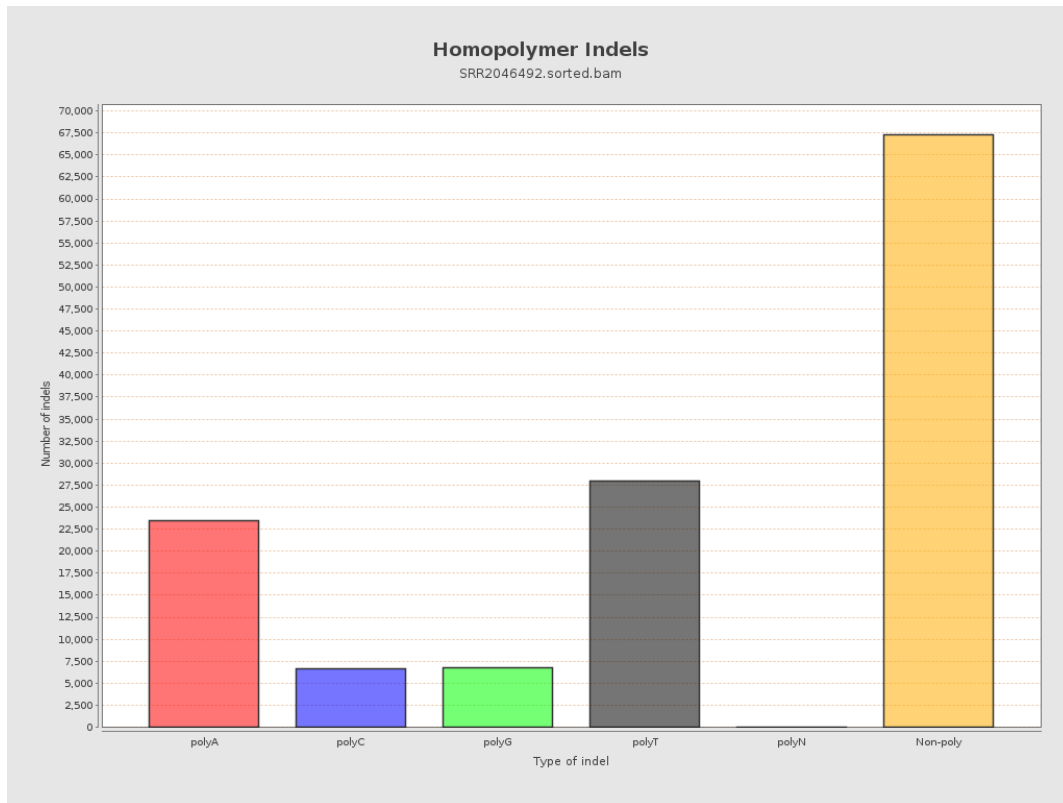
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



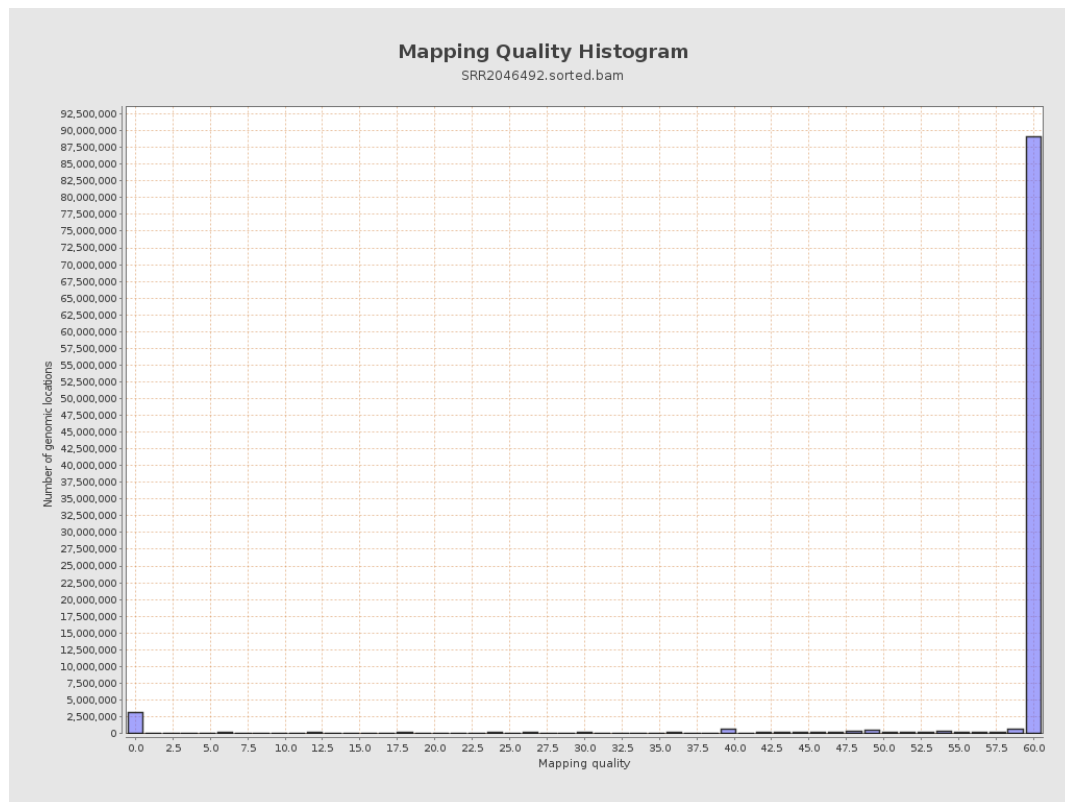
11. Results : Homopolymer Indels



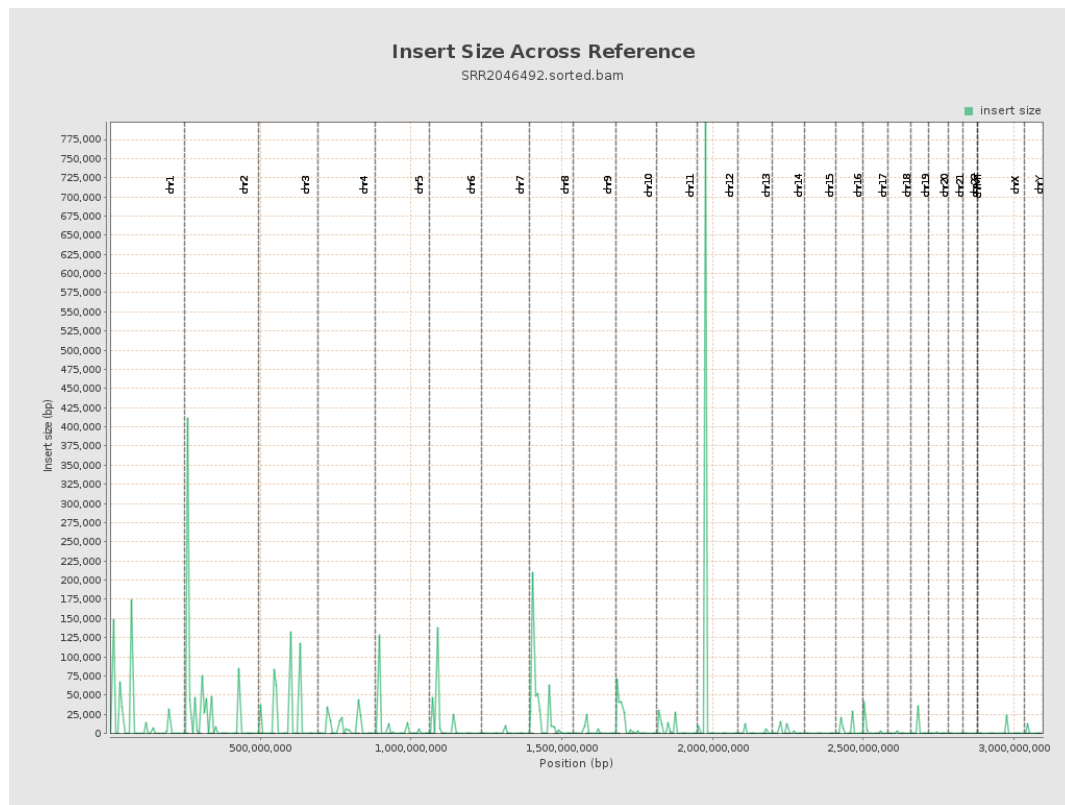
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

