

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 21:41:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046542.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_SRR2046542 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046542_1.fastq.gz SRR2046542_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 21:41:24 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046542.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,738,976
Mapped reads	7,622,439 / 98.49%
Unmapped reads	116,537 / 1.51%
Mapped paired reads	7,622,439 / 98.49%
Mapped reads, first in pair	3,857,548 / 49.85%
Mapped reads, second in pair	3,764,891 / 48.65%
Mapped reads, both in pair	7,518,894 / 97.16%
Mapped reads, singletons	103,545 / 1.34%
Secondary alignments	0
Supplementary alignments	42,890 / 0.55%
Read min/max/mean length	30 / 100 / 100.22
Duplicated reads (estimated)	5,033,493 / 65.04%
Duplication rate	36.41%
Clipped reads	1,738,211 / 22.46%

2.2. ACGT Content

Number/percentage of A's	214,827,795 / 29.46%
Number/percentage of C's	151,007,448 / 20.71%
Number/percentage of T's	213,095,969 / 29.22%
Number/percentage of G's	150,259,284 / 20.6%
Number/percentage of N's	62,563 / 0.01%

GC Percentage	41.31%
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2.3. Coverage

Mean	0.2356
Standard Deviation	16.3502

2.4. Mapping Quality

Mean Mapping Quality	53.14
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2.5. Insert size

Mean	32,911.76
Standard Deviation	1,917,240.07
P25/Median/P75	104 / 134 / 170

2.6. Mismatches and indels

General error rate	0.45%
Mismatches	3,124,187
Insertions	66,136
Mapped reads with at least one insertion	0.85%
Deletions	72,135
Mapped reads with at least one deletion	0.92%
Homopolymer indels	47.94%

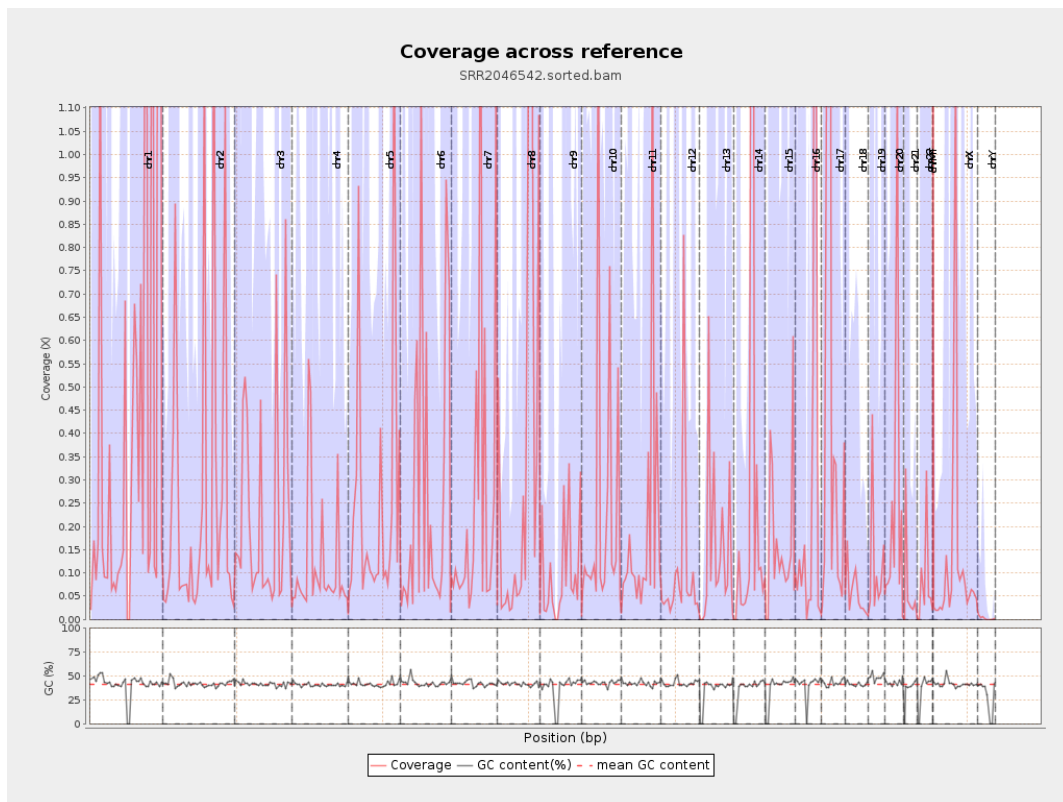
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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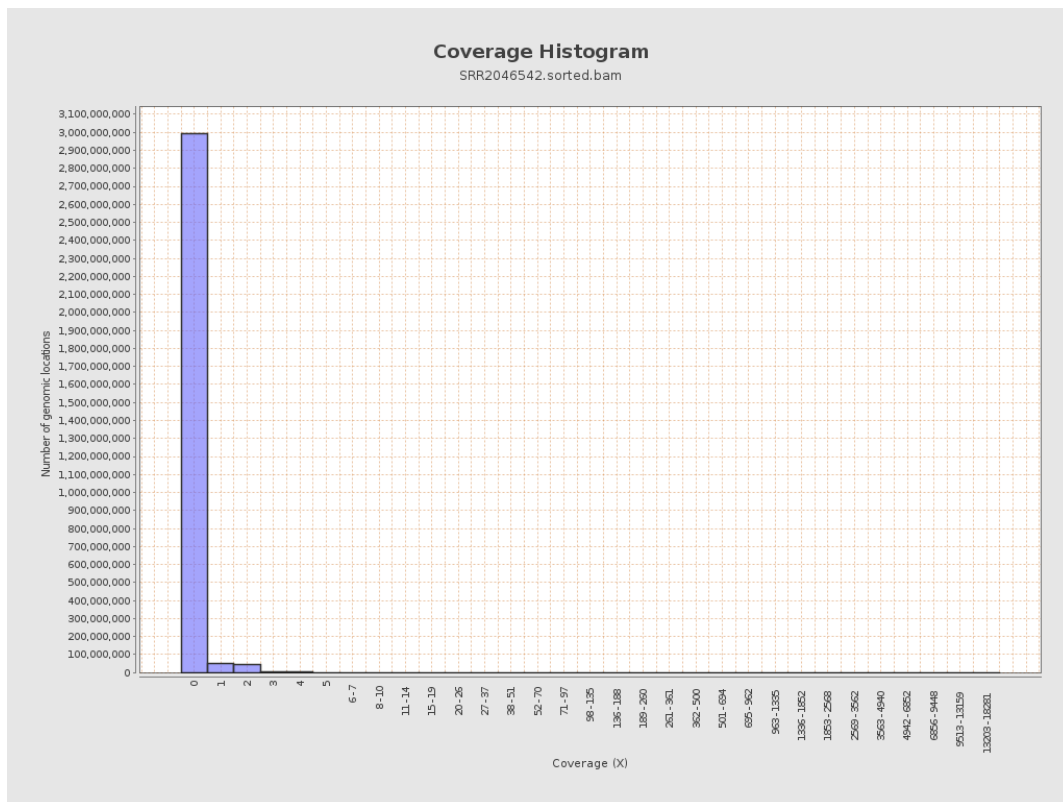
		bases	coverage	deviation
chr1	249250621	123895737	0.4971	27.4358
chr2	243199373	63895496	0.2627	14.933
chr3	198022430	43829045	0.2213	11.6789
chr4	191154276	22948274	0.1201	8.5105
chr5	180915260	43962186	0.243	17.5998
chr6	171115067	46571713	0.2722	14.7872
chr7	159138663	44913132	0.2822	22.3121
chr8	146364022	58767214	0.4015	21.4663
chr9	141213431	14267678	0.101	6.2287
chr10	135534747	32535889	0.2401	17.8101
chr11	135006516	26889511	0.1992	11.5193
chr12	133851895	13083681	0.0977	6.4197
chr13	115169878	17162272	0.149	7.0055
chr14	107349540	31070898	0.2894	17.8624
chr15	102531392	17768942	0.1733	8.9773
chr16	90354753	23912803	0.2647	15.7228
chr17	81195210	47473985	0.5847	36.5809
chr18	78077248	4463256	0.0572	1.7733
chr19	59128983	6864922	0.1161	5.6819
chr20	63025520	16102823	0.2555	18.5044
chr21	48129895	3510200	0.0729	6.3661
chr22	51304566	4354894	0.0849	5.1375
chrMT	16571	37234	2.2469	2.3093
chrX	155270560	21001878	0.1353	13.0858

chrY	59373566	165651	0.0028	0.1365
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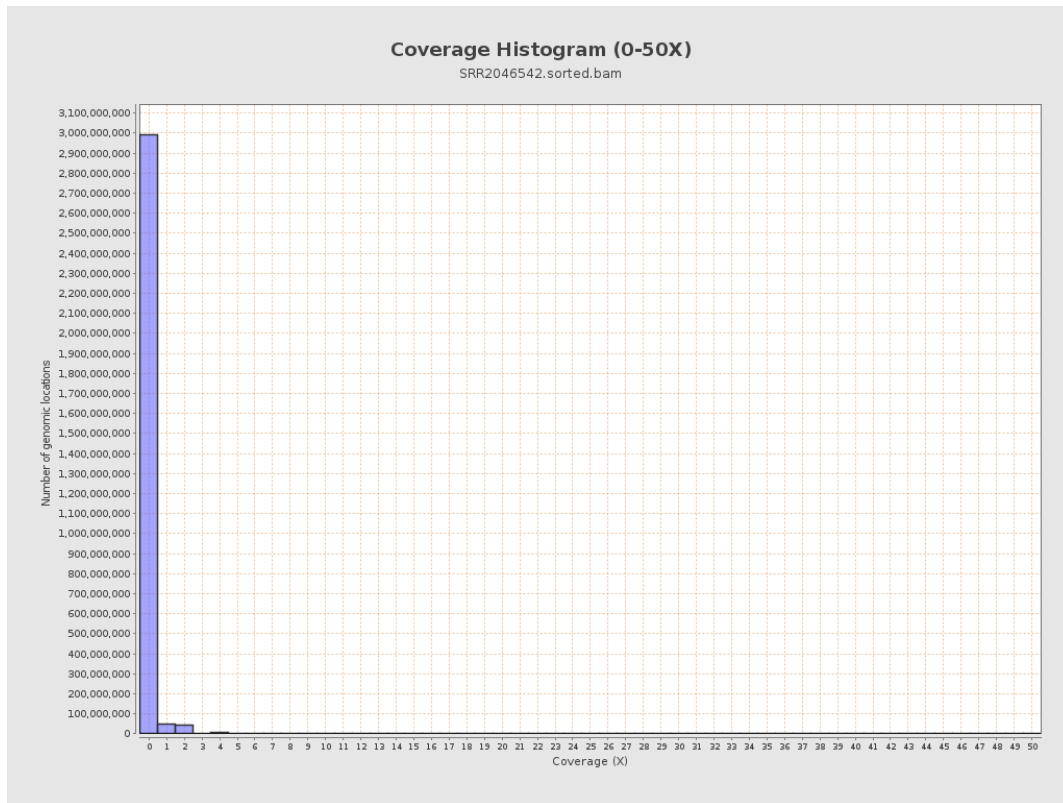
3. Results : Coverage across reference



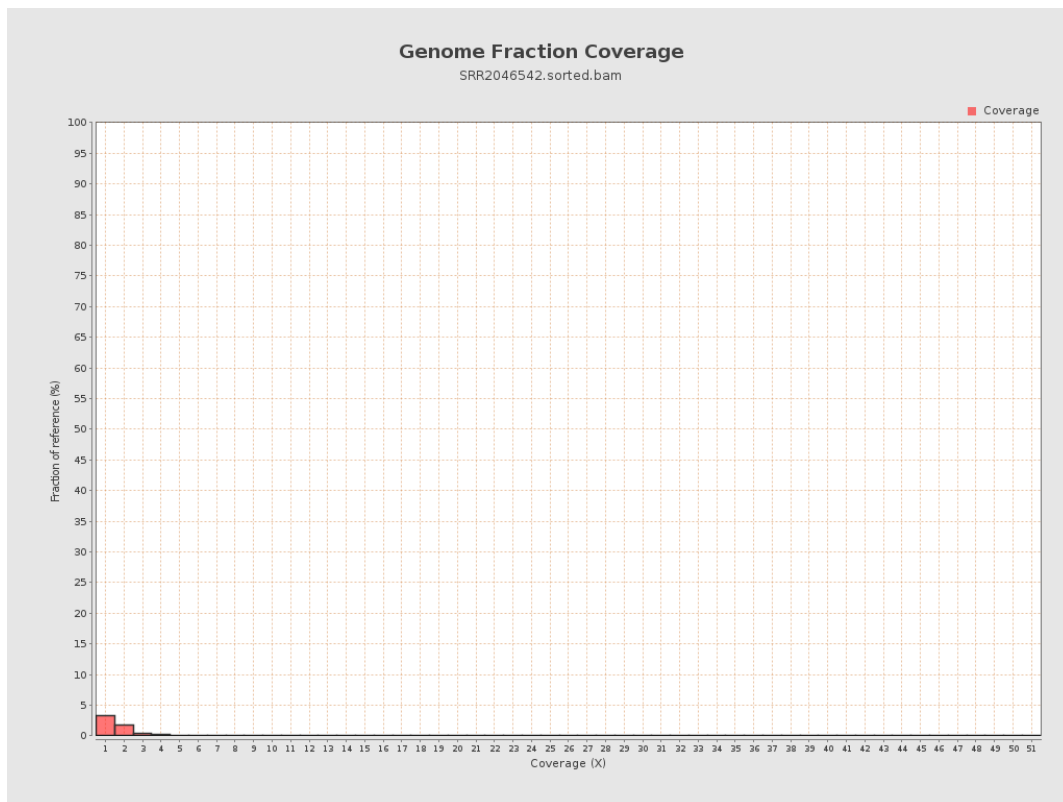
4. Results : Coverage Histogram



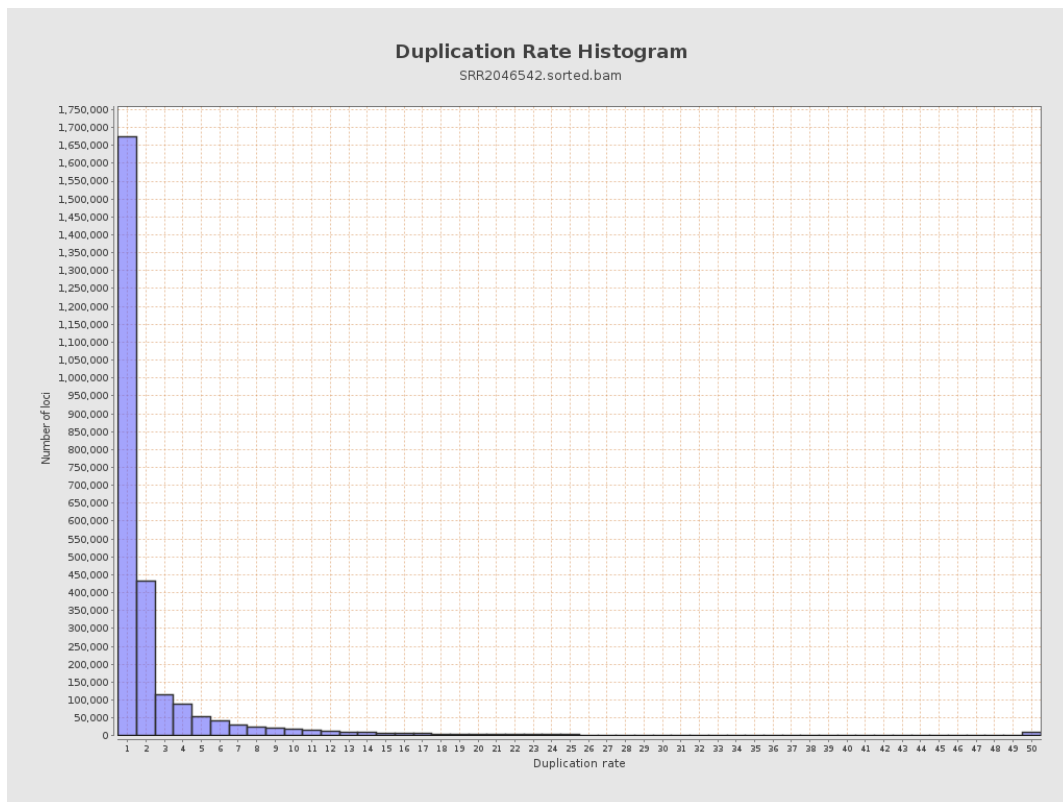
5. Results : Coverage Histogram (0-50X)



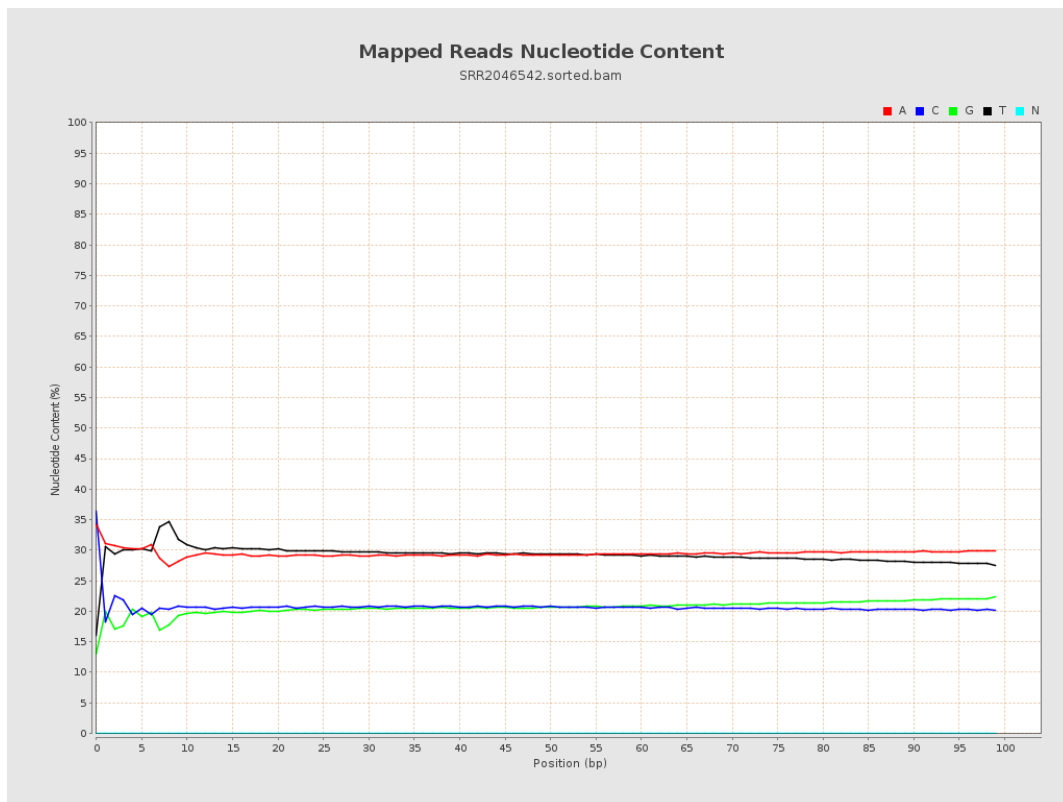
6. Results : Genome Fraction Coverage



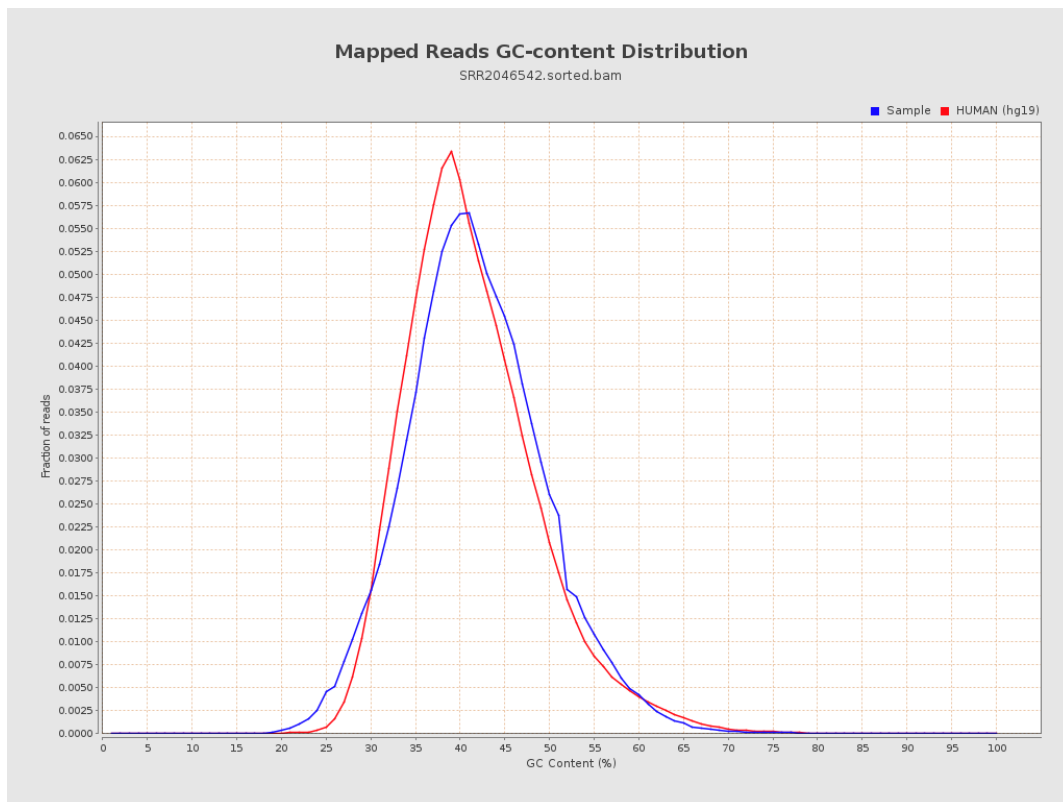
7. Results : Duplication Rate Histogram



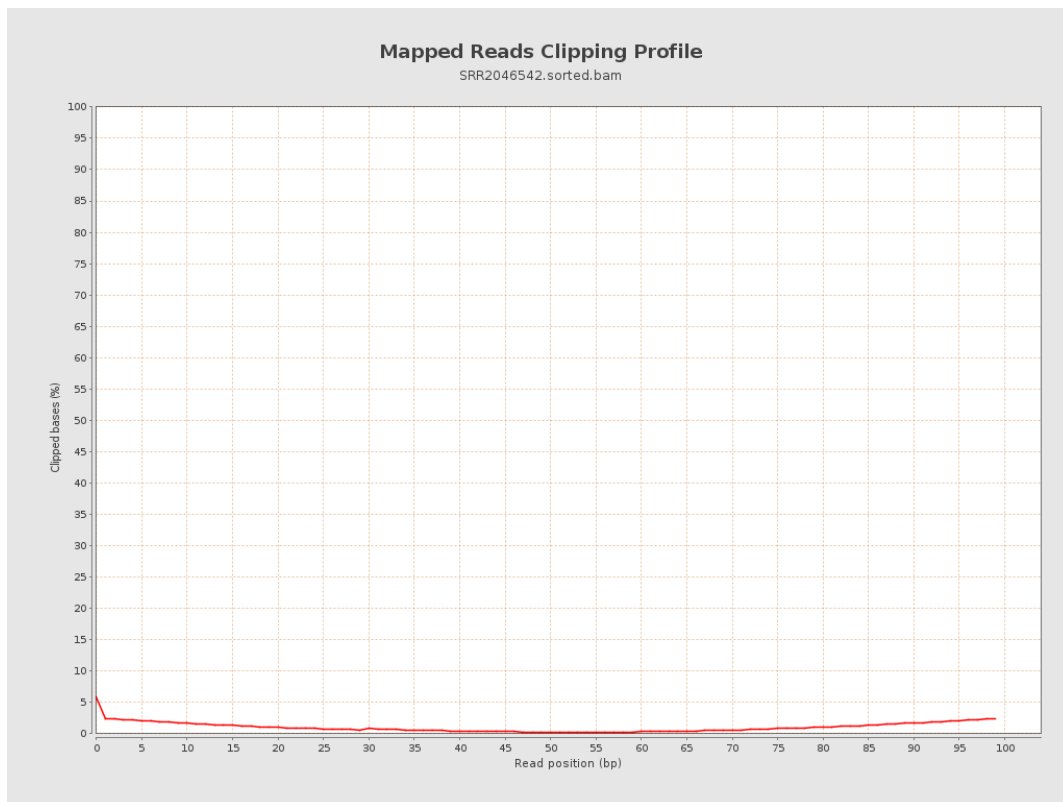
8. Results : Mapped Reads Nucleotide Content



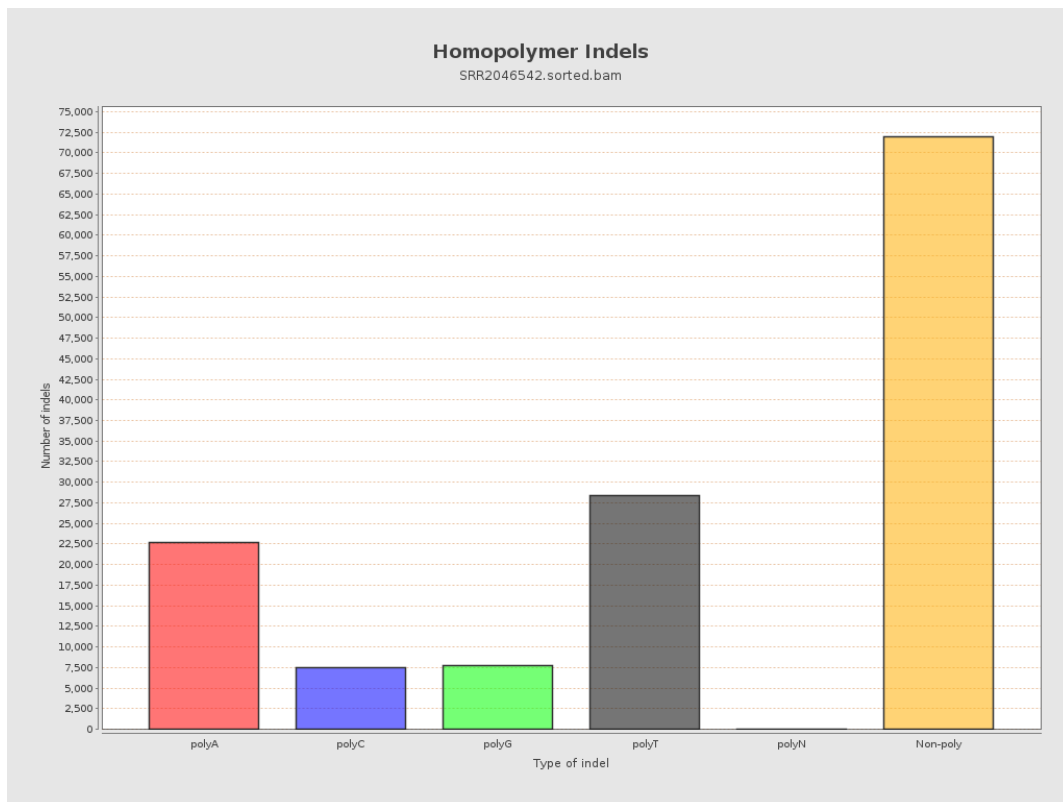
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



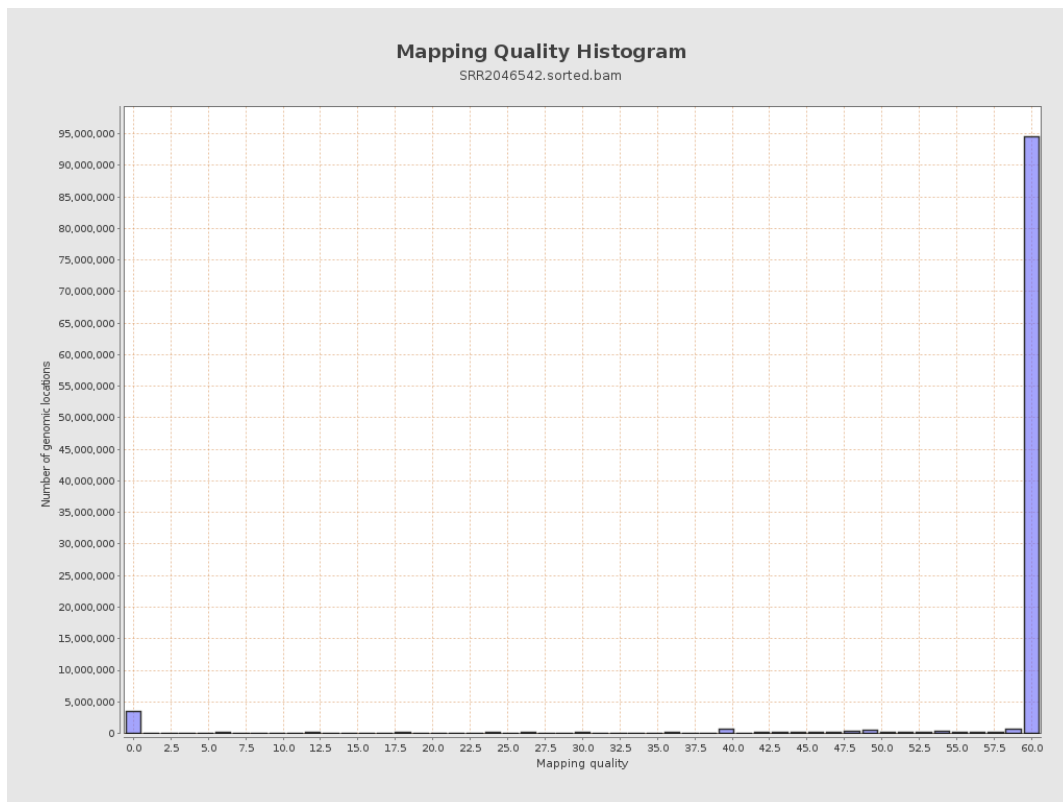
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

