

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 21:50:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046543.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_SRR2046543 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046543_1.fastq.gz SRR2046543_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 21:50:49 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046543.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,134,932
Mapped reads	9,984,225 / 98.51%
Unmapped reads	150,707 / 1.49%
Mapped paired reads	9,984,225 / 98.51%
Mapped reads, first in pair	5,051,050 / 49.84%
Mapped reads, second in pair	4,933,175 / 48.67%
Mapped reads, both in pair	9,851,126 / 97.2%
Mapped reads, singletons	133,099 / 1.31%
Secondary alignments	0
Supplementary alignments	53,882 / 0.53%
Read min/max/mean length	30 / 100 / 100.21
Duplicated reads (estimated)	7,411,870 / 73.13%
Duplication rate	34.43%
Clipped reads	2,584,038 / 25.5%

2.2. ACGT Content

Number/percentage of A's	283,976,653 / 29.78%
Number/percentage of C's	193,588,819 / 20.3%
Number/percentage of T's	281,873,256 / 29.56%
Number/percentage of G's	193,979,972 / 20.34%
Number/percentage of N's	81,906 / 0.01%

GC Percentage	40.65%
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2.3. Coverage

Mean	0.3081
Standard Deviation	35.5863

2.4. Mapping Quality

Mean Mapping Quality	52.48
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2.5. Insert size

Mean	31,857.34
Standard Deviation	1,874,211.47
P25/Median/P75	100 / 122 / 149

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	3,686,063
Insertions	81,735
Mapped reads with at least one insertion	0.81%
Deletions	90,133
Mapped reads with at least one deletion	0.88%
Homopolymer indels	48.67%

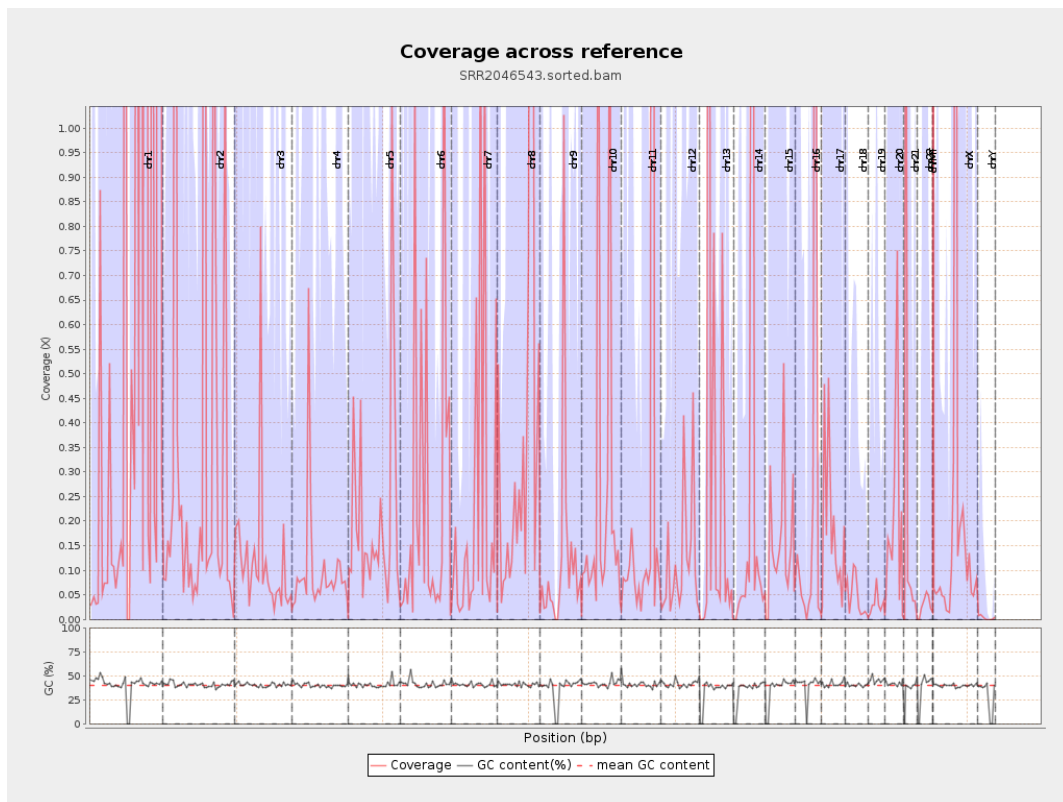
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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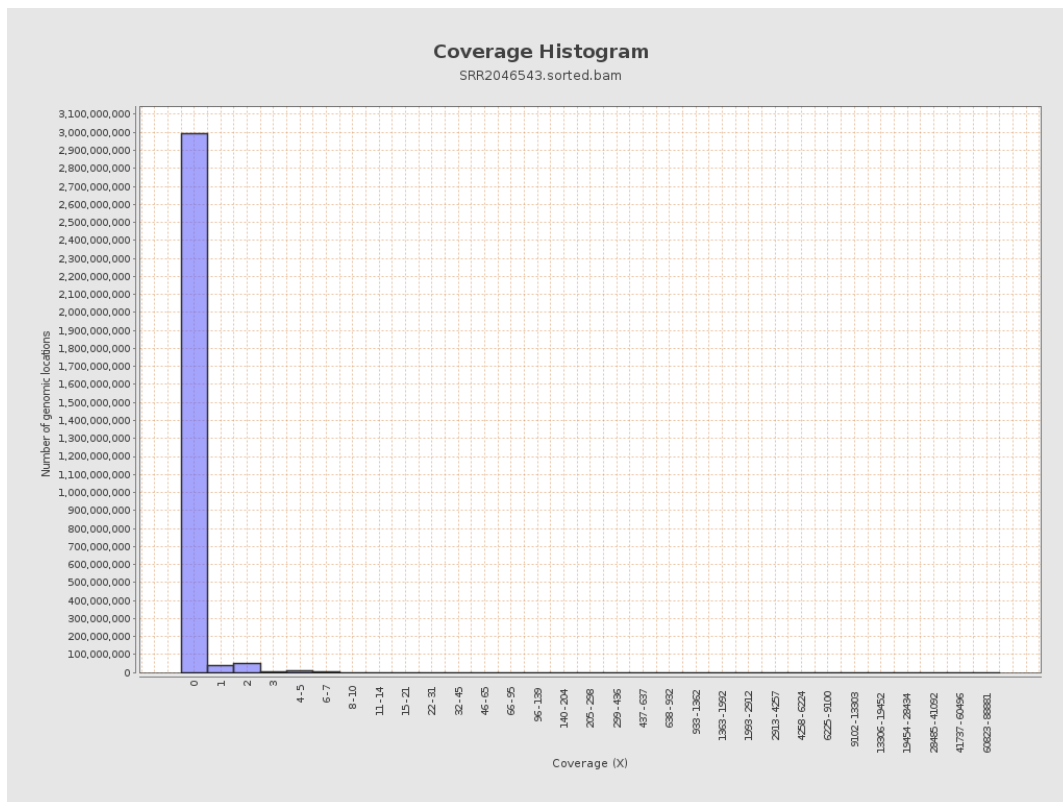
		bases	coverage	deviation
chr1	249250621	294070693	1.1798	100.0085
chr2	243199373	103029946	0.4236	31.613
chr3	198022430	23550228	0.1189	9.6586
chr4	191154276	19763539	0.1034	6.4544
chr5	180915260	37123837	0.2052	13.5428
chr6	171115067	45423539	0.2655	18.8053
chr7	159138663	39819455	0.2502	19.5638
chr8	146364022	65933380	0.4505	24.3127
chr9	141213431	17769018	0.1258	18.858
chr10	135534747	38877477	0.2868	30.506
chr11	135006516	68834286	0.5099	56.9589
chr12	133851895	15736070	0.1176	8.0039
chr13	115169878	36065009	0.3131	22.9396
chr14	107349540	27807547	0.259	20.772
chr15	102531392	16571409	0.1616	11.1329
chr16	90354753	20193759	0.2235	17.7853
chr17	81195210	14921177	0.1838	10.2082
chr18	78077248	3544237	0.0454	0.5471
chr19	59128983	1885945	0.0319	0.5925
chr20	63025520	13514012	0.2144	17.2431
chr21	48129895	15564782	0.3234	37.3671
chr22	51304566	1516630	0.0296	1.5843
chrMT	16571	99078	5.979	3.6221
chrX	155270560	31917277	0.2056	18.093

chrY	59373566	217178	0.0037	0.1887
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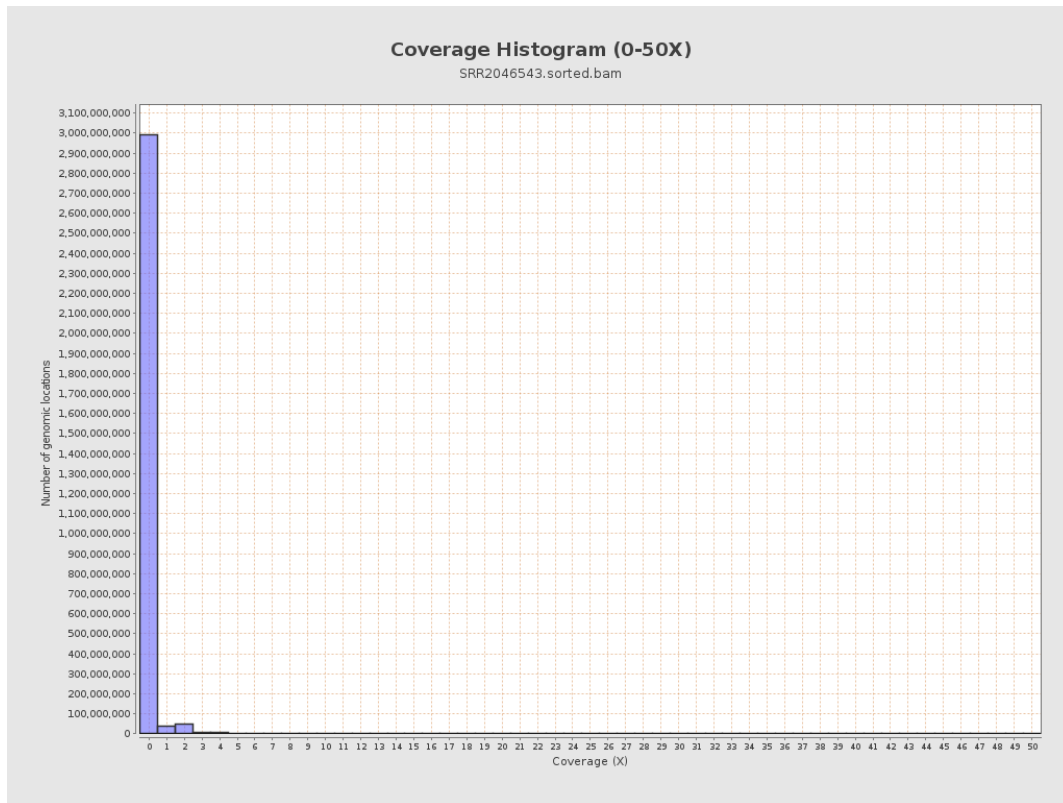
3. Results : Coverage across reference



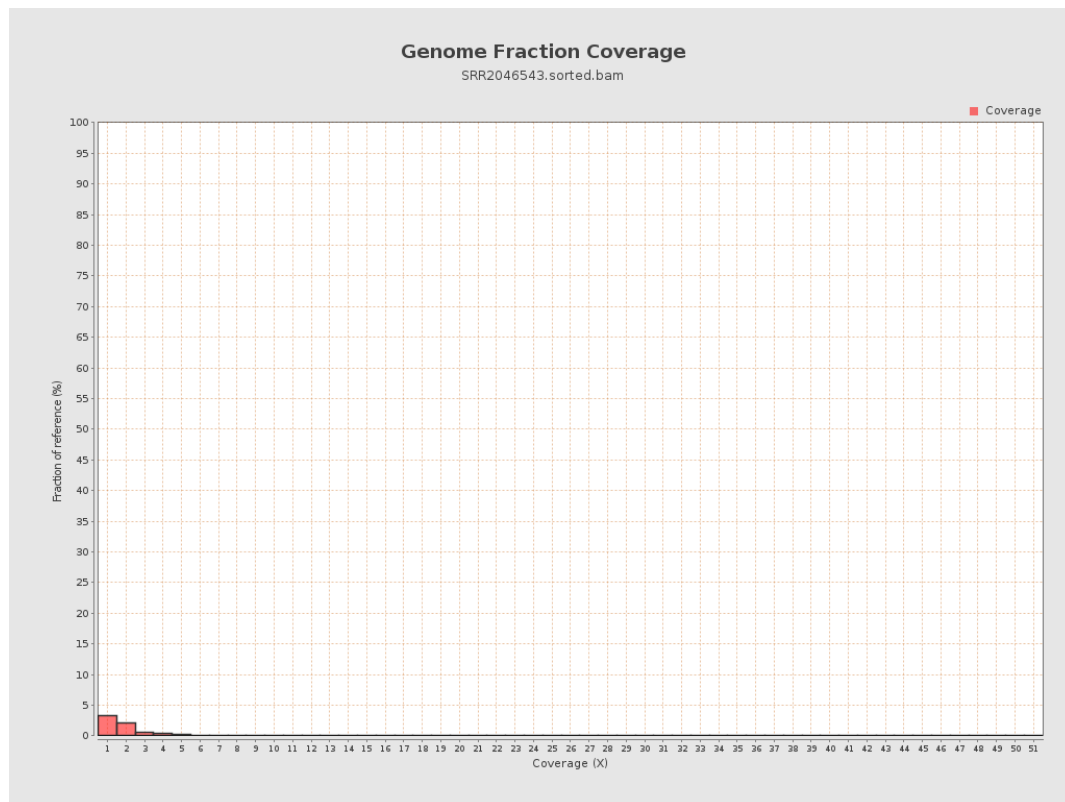
4. Results : Coverage Histogram



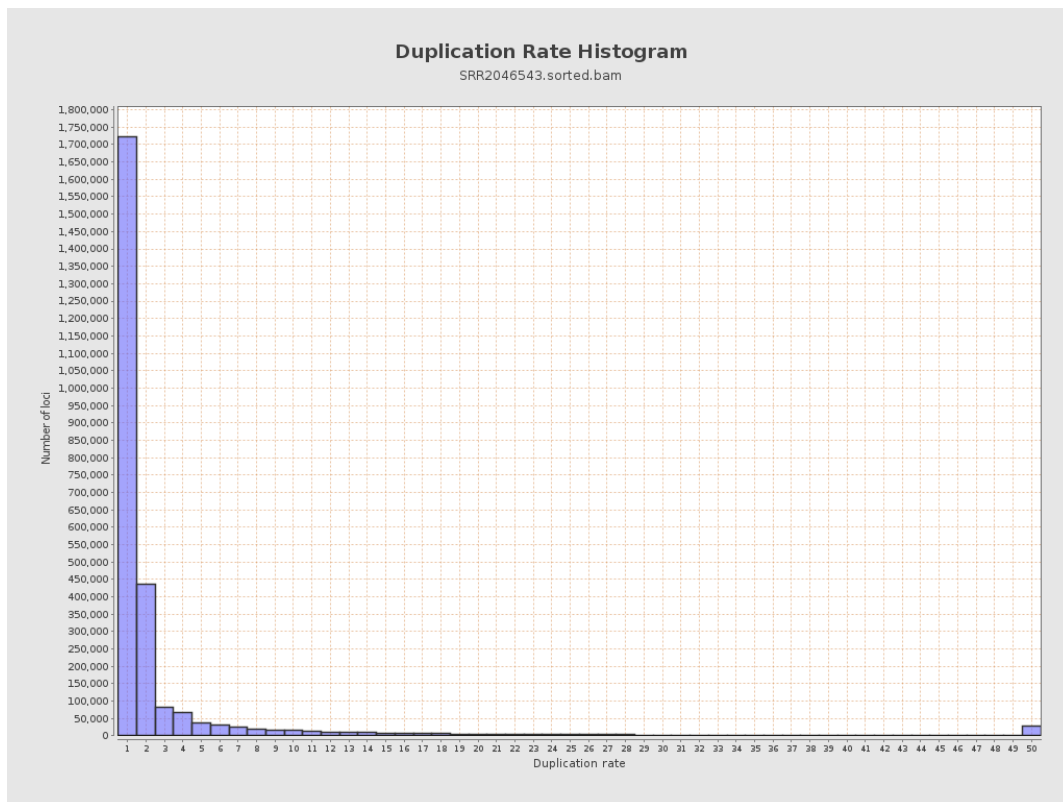
5. Results : Coverage Histogram (0-50X)



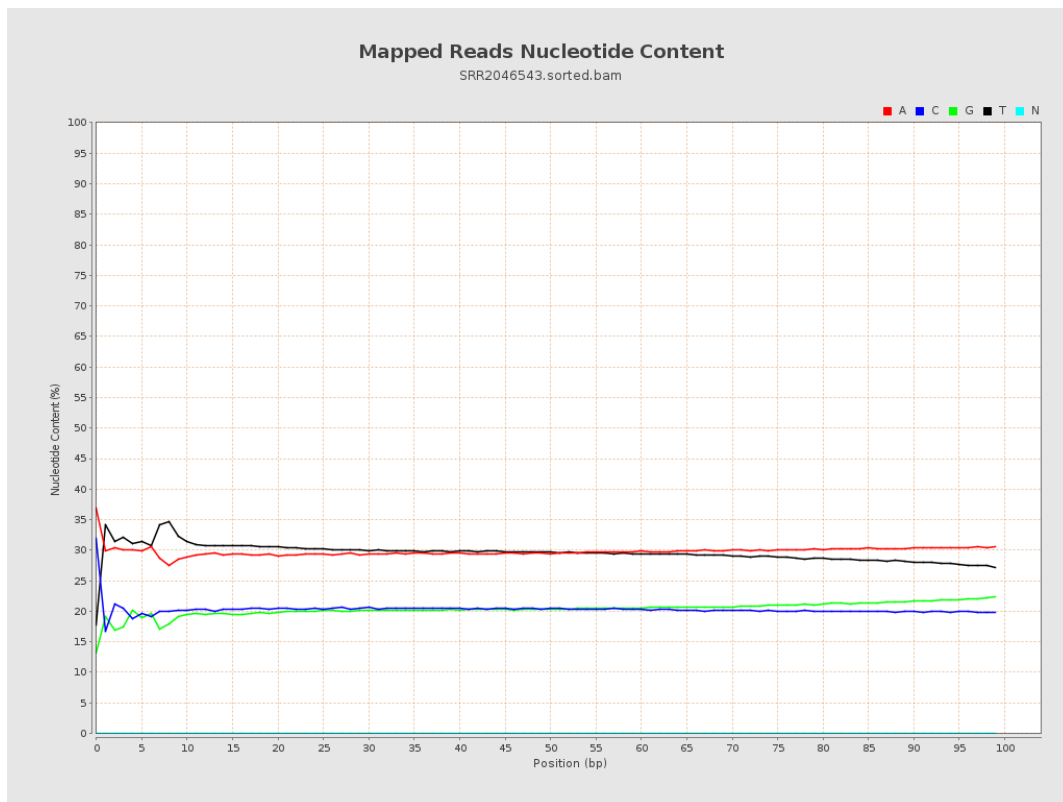
6. Results : Genome Fraction Coverage



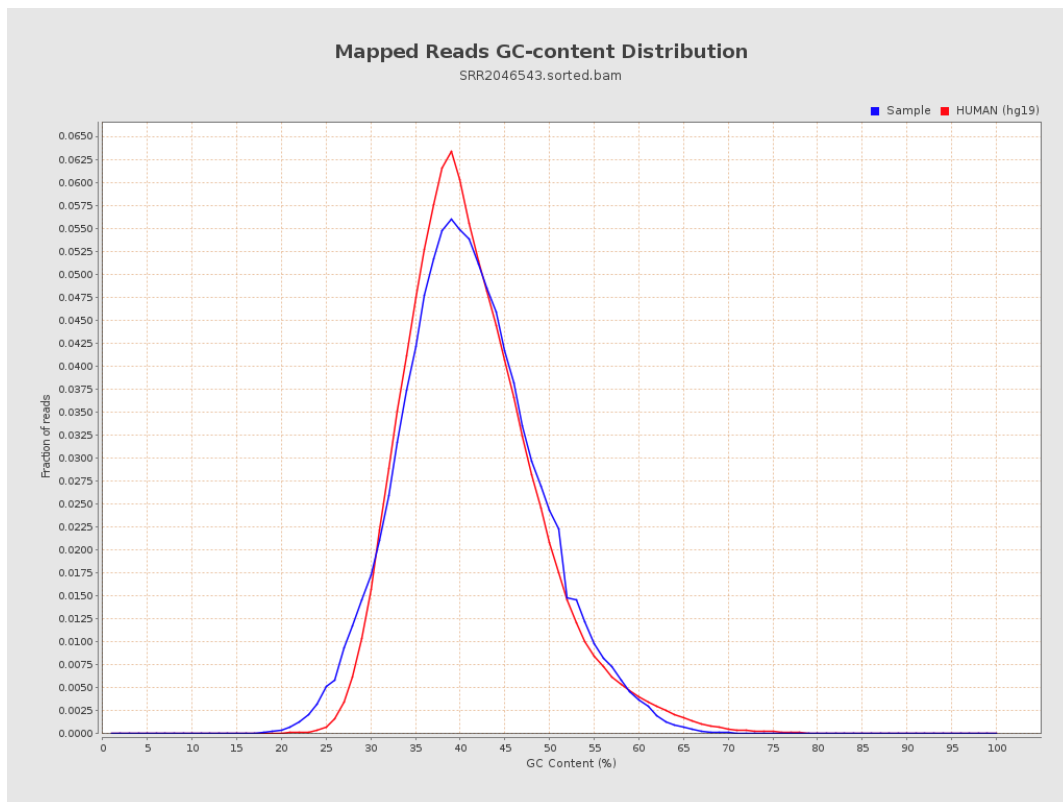
7. Results : Duplication Rate Histogram



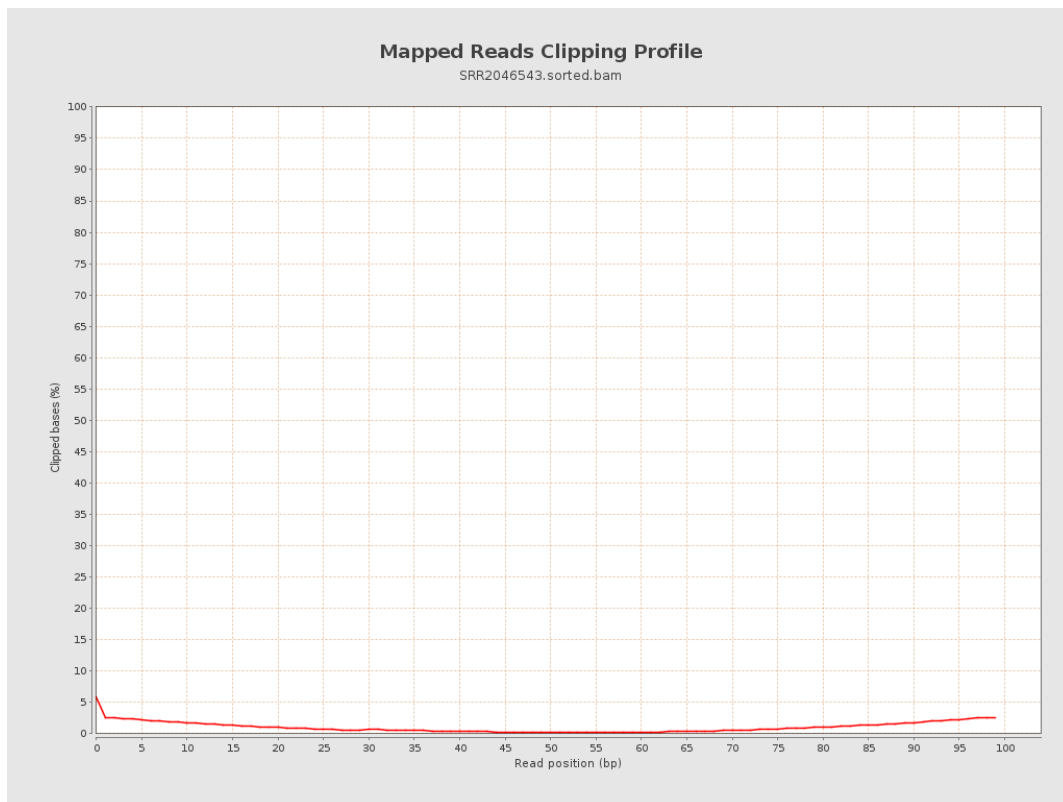
8. Results : Mapped Reads Nucleotide Content



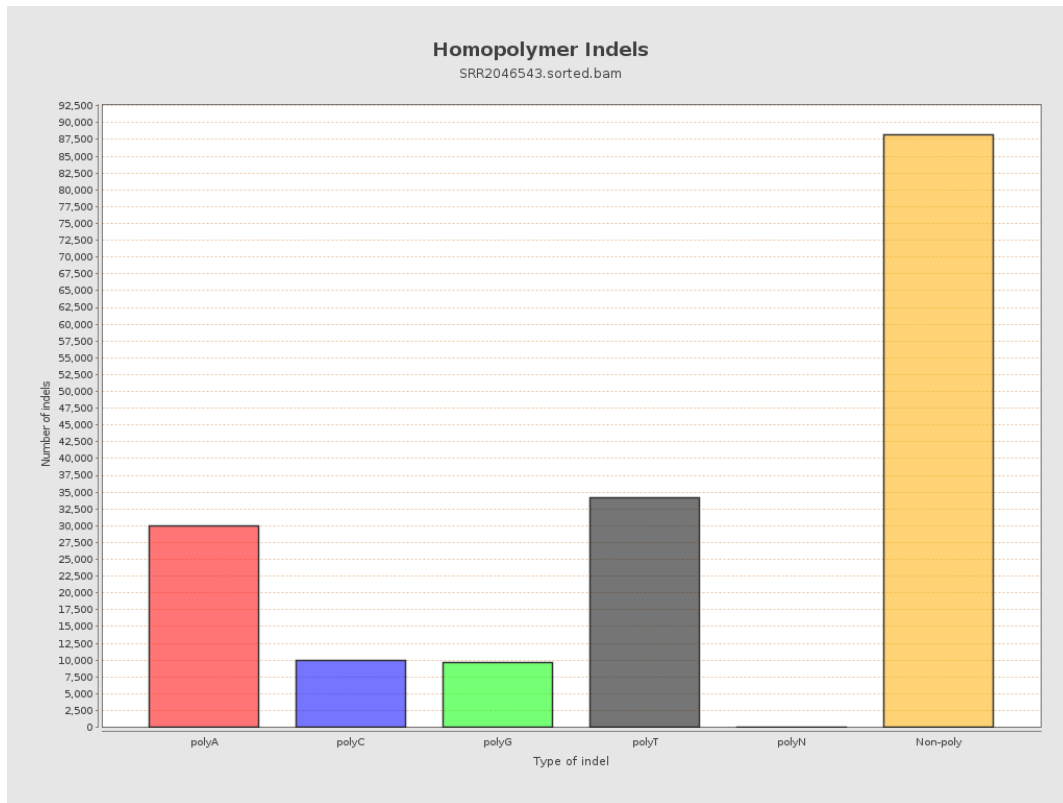
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



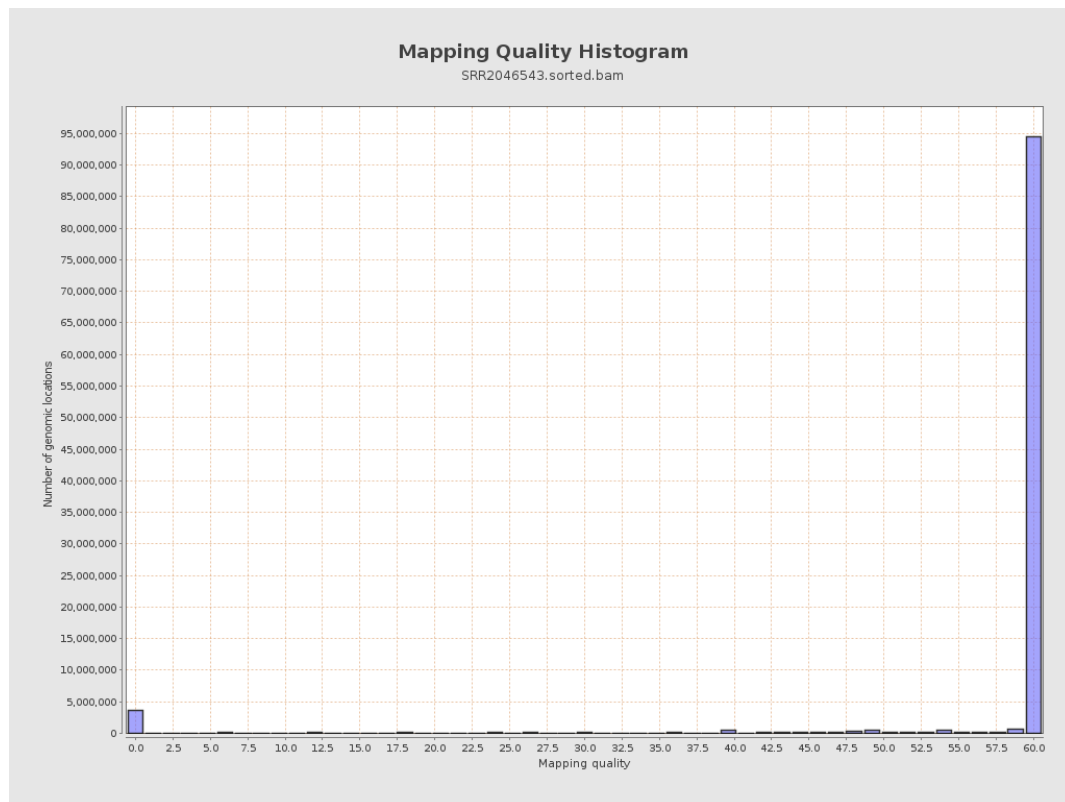
11. Results : Homopolymer Indels



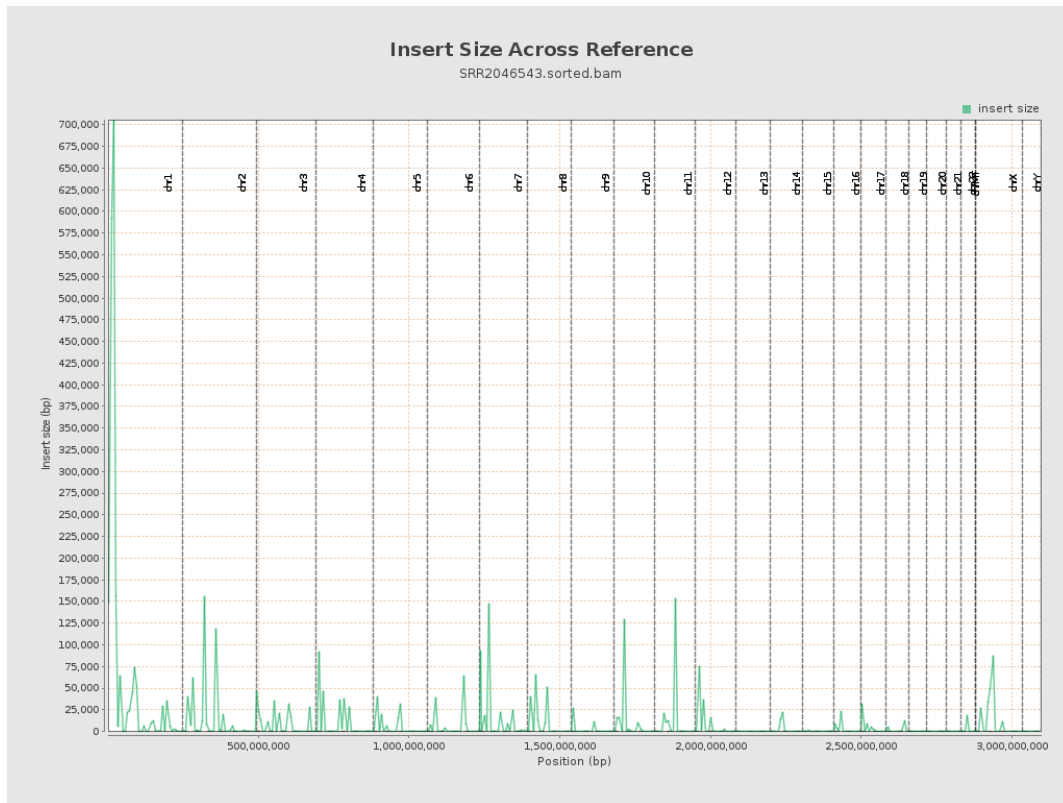
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

