

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 16:27:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046483.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_SRR2046483 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046483_1.fastq.gz SRR2046483_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 16:27:01 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046483.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,330,850
Mapped reads	7,295,937 / 99.52%
Unmapped reads	34,913 / 0.48%
Mapped paired reads	7,295,937 / 99.52%
Mapped reads, first in pair	3,653,161 / 49.83%
Mapped reads, second in pair	3,642,776 / 49.69%
Mapped reads, both in pair	7,275,952 / 99.25%
Mapped reads, singletons	19,985 / 0.27%
Secondary alignments	0
Supplementary alignments	31,330 / 0.43%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	5,020,291 / 68.48%
Duplication rate	47.29%
Clipped reads	3,308,318 / 45.13%

2.2. ACGT Content

Number/percentage of A's	192,211,969 / 29.1%
Number/percentage of C's	138,809,313 / 21.02%
Number/percentage of T's	186,205,304 / 28.19%
Number/percentage of G's	143,216,647 / 21.68%
Number/percentage of N's	49,677 / 0.01%

GC Percentage	42.7%
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2.3. Coverage

Mean	0.2134
Standard Deviation	13.4001

2.4. Mapping Quality

Mean Mapping Quality	52.8
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2.5. Insert size

Mean	19,265.09
Standard Deviation	1,286,987.97
P25/Median/P75	83 / 103 / 134

2.6. Mismatches and indels

General error rate	0.47%
Mismatches	2,996,611
Insertions	52,320
Mapped reads with at least one insertion	0.71%
Deletions	64,771
Mapped reads with at least one deletion	0.86%
Homopolymer indels	46.24%

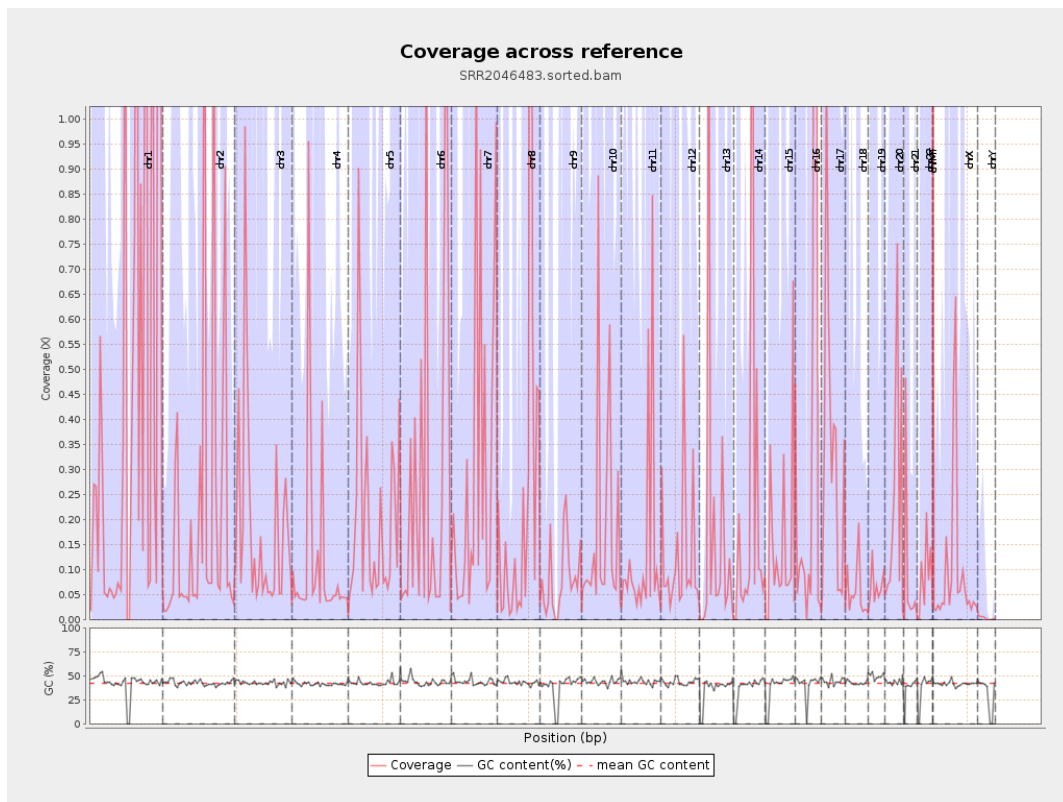
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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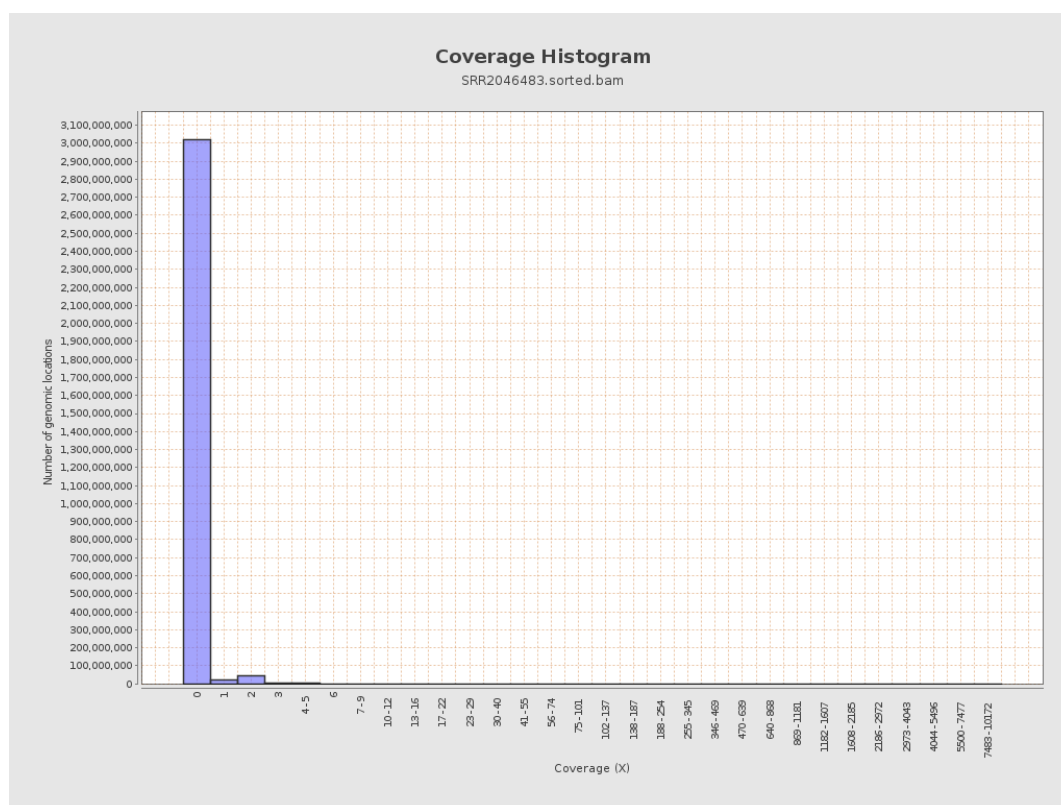
		bases	coverage	deviation
chr1	249250621	129209687	0.5184	26.9663
chr2	243199373	53831232	0.2213	14.7971
chr3	198022430	36538491	0.1845	9.6639
chr4	191154276	22793070	0.1192	7.696
chr5	180915260	37205696	0.2057	11.5302
chr6	171115067	48091703	0.281	12.3232
chr7	159138663	49425156	0.3106	14.9621
chr8	146364022	43300867	0.2958	15.0064
chr9	141213431	11546701	0.0818	4.2627
chr10	135534747	24560785	0.1812	11.5563
chr11	135006516	18559642	0.1375	6.8462
chr12	133851895	17039037	0.1273	6.2788
chr13	115169878	19434500	0.1687	10.3622
chr14	107349540	22890455	0.2132	11.2847
chr15	102531392	16123520	0.1573	9.111
chr16	90354753	35079418	0.3882	24.4801
chr17	81195210	27326816	0.3366	15.5321
chr18	78077248	4277792	0.0548	3.0037
chr19	59128983	3881351	0.0656	1.7309
chr20	63025520	14992340	0.2379	15.5318
chr21	48129895	4647336	0.0966	10.0781
chr22	51304566	4547606	0.0886	4.3714
chrMT	16571	45533	2.7478	2.5673
chrX	155270560	15144044	0.0975	8.1729

chrY	59373566	179564	0.003	0.1495
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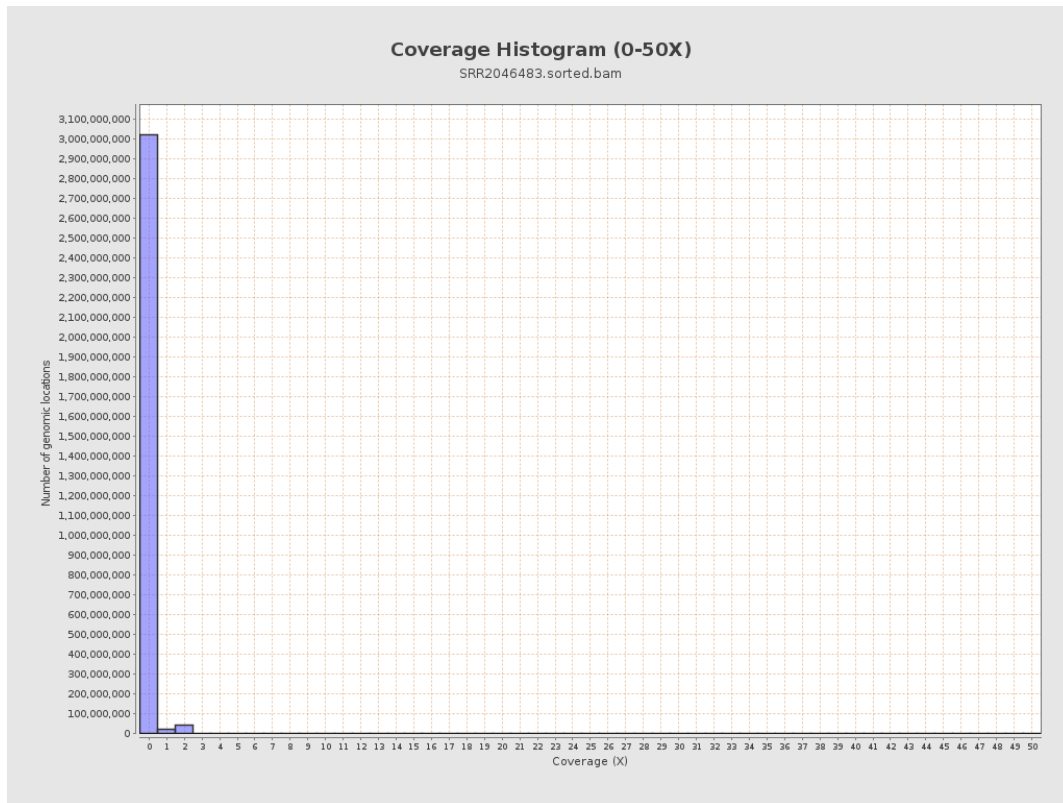
3. Results : Coverage across reference



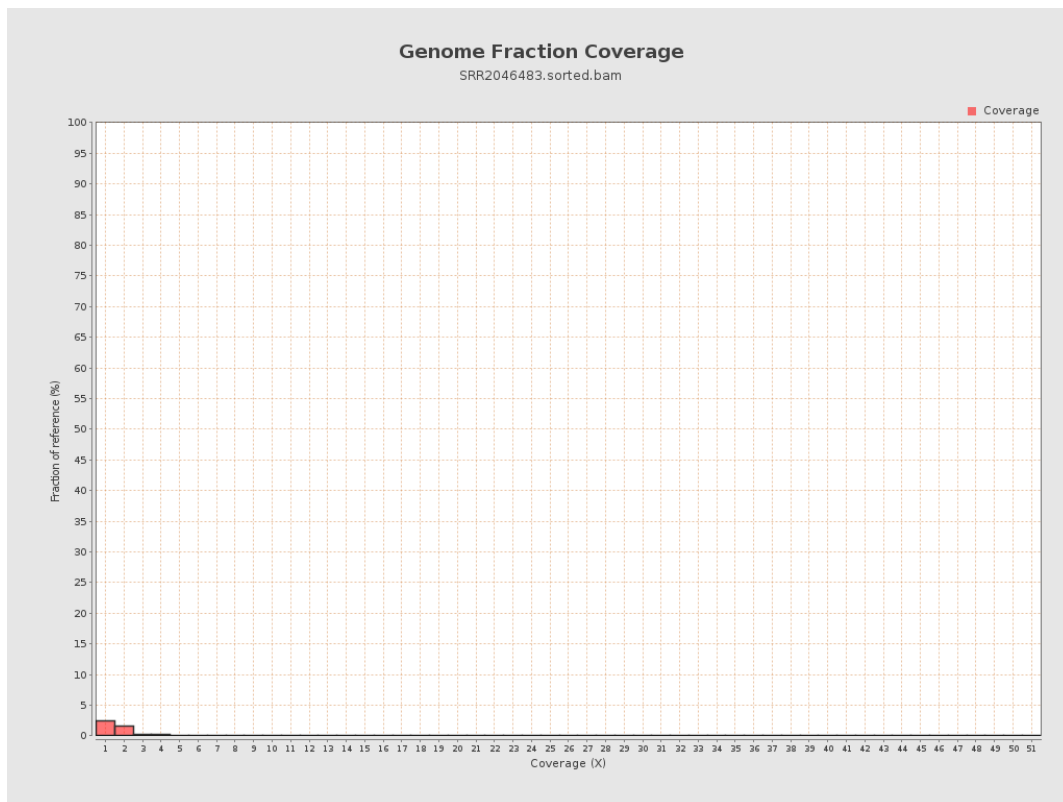
4. Results : Coverage Histogram



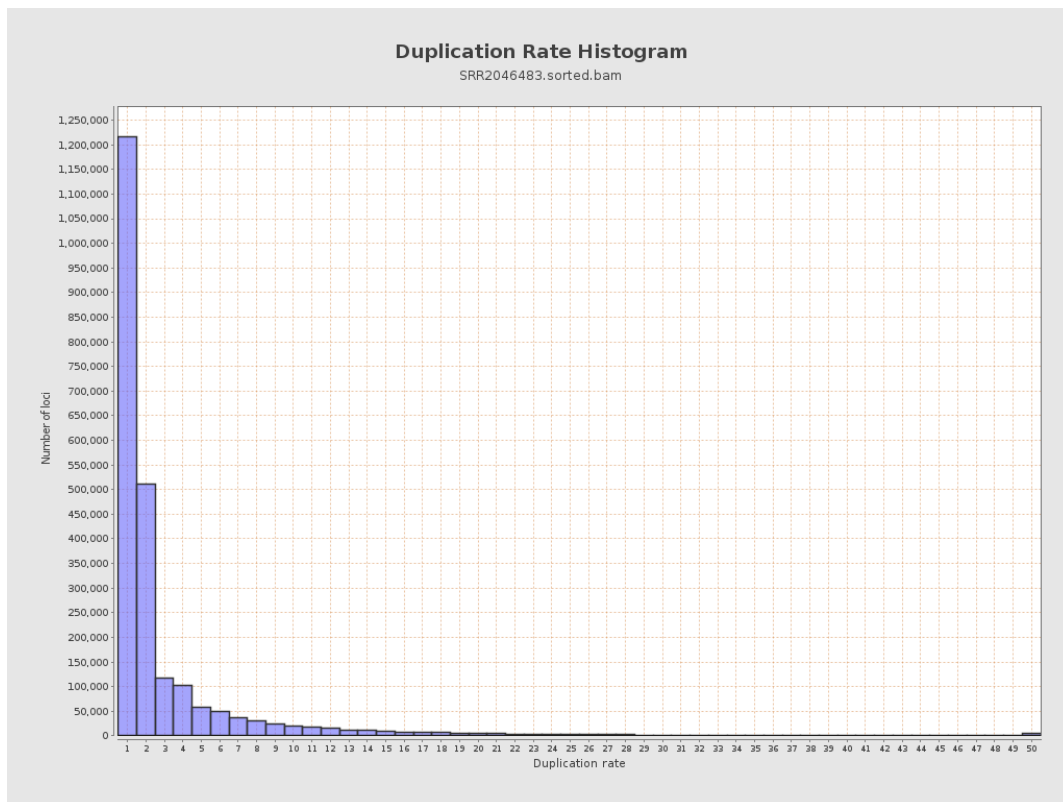
5. Results : Coverage Histogram (0-50X)



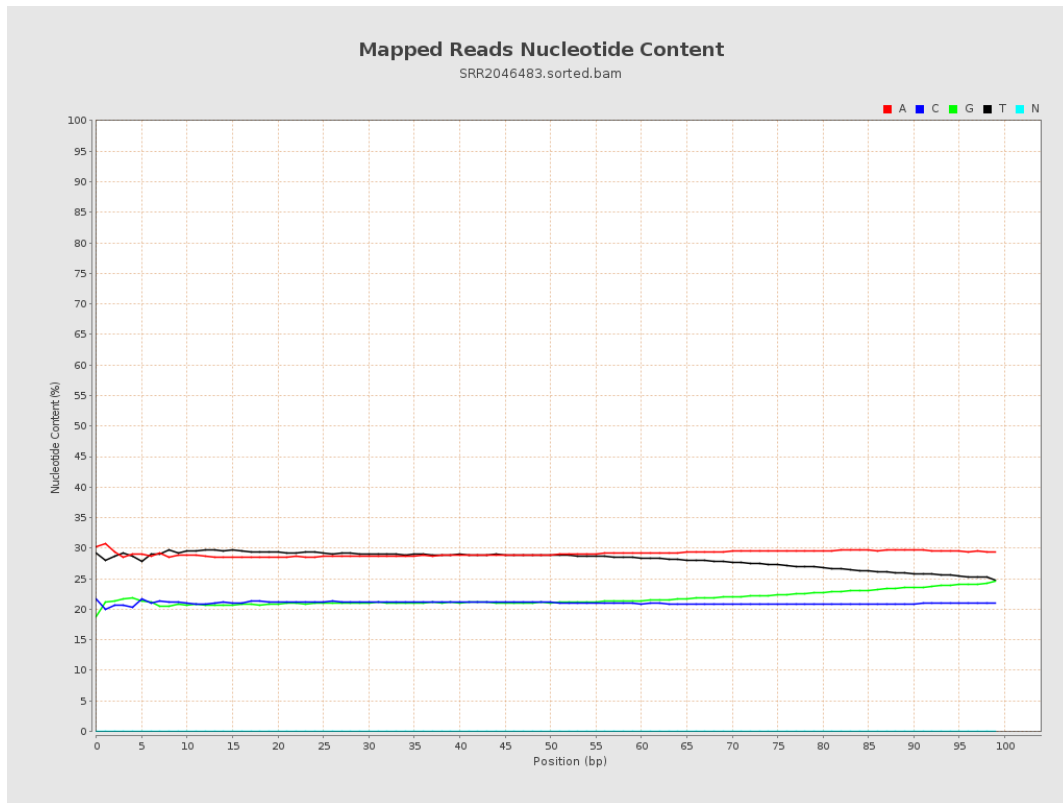
6. Results : Genome Fraction Coverage



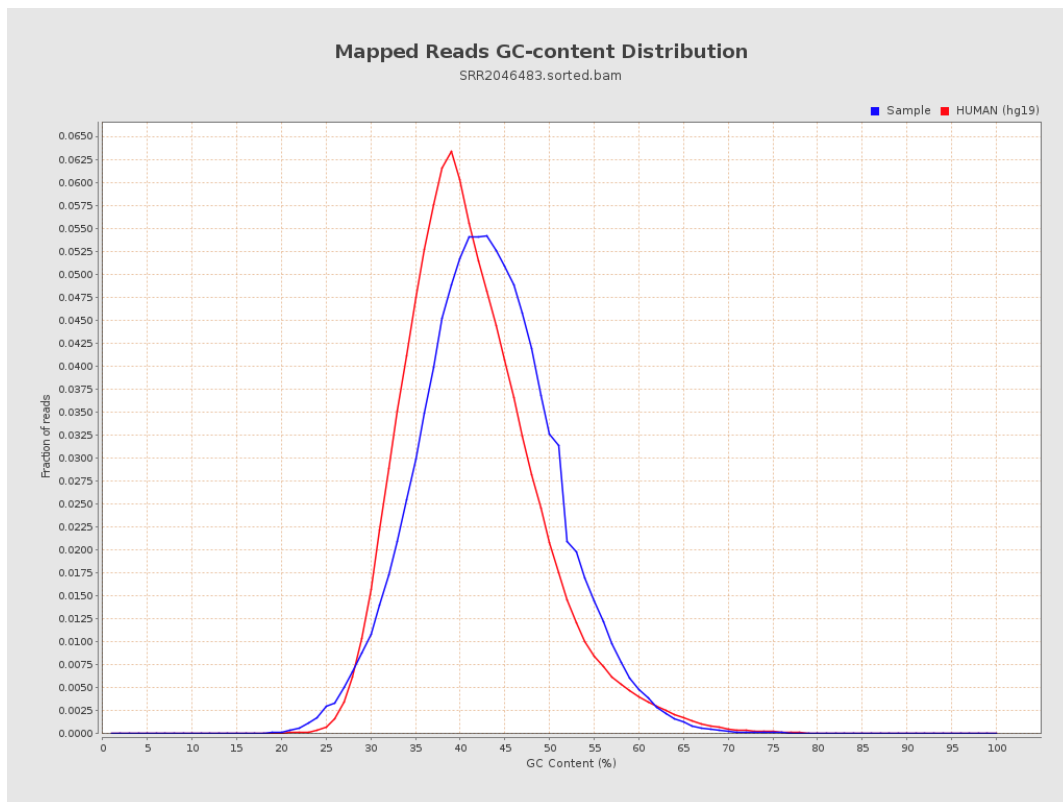
7. Results : Duplication Rate Histogram



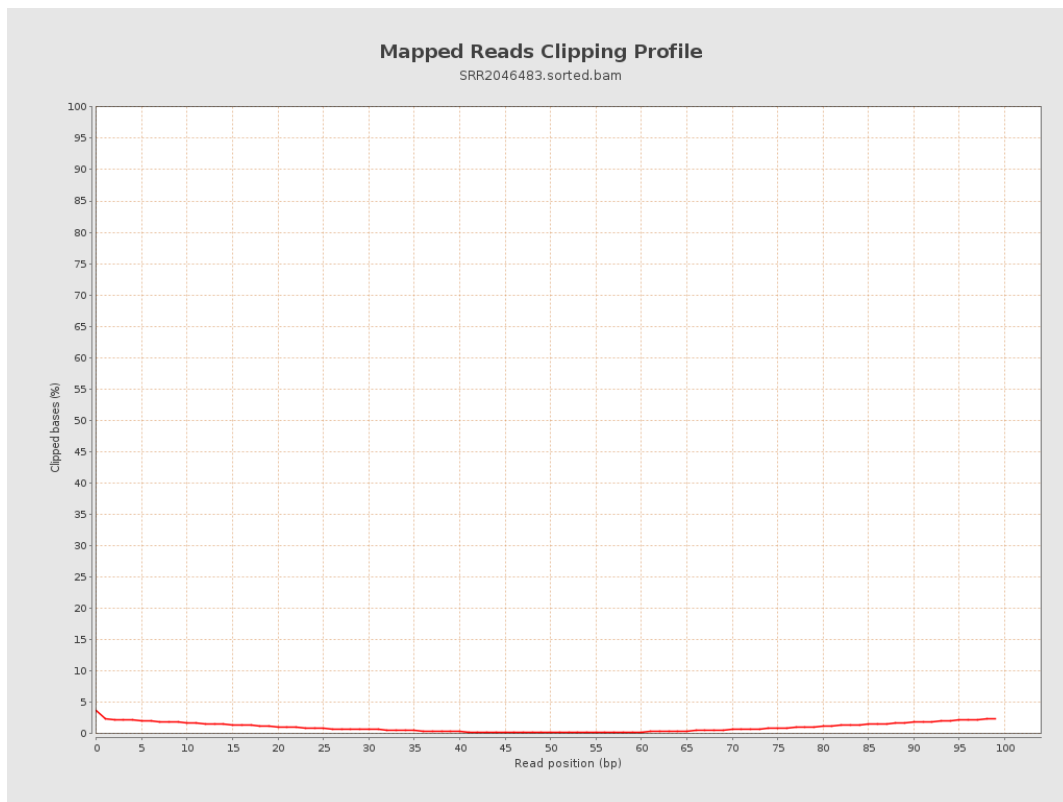
8. Results : Mapped Reads Nucleotide Content



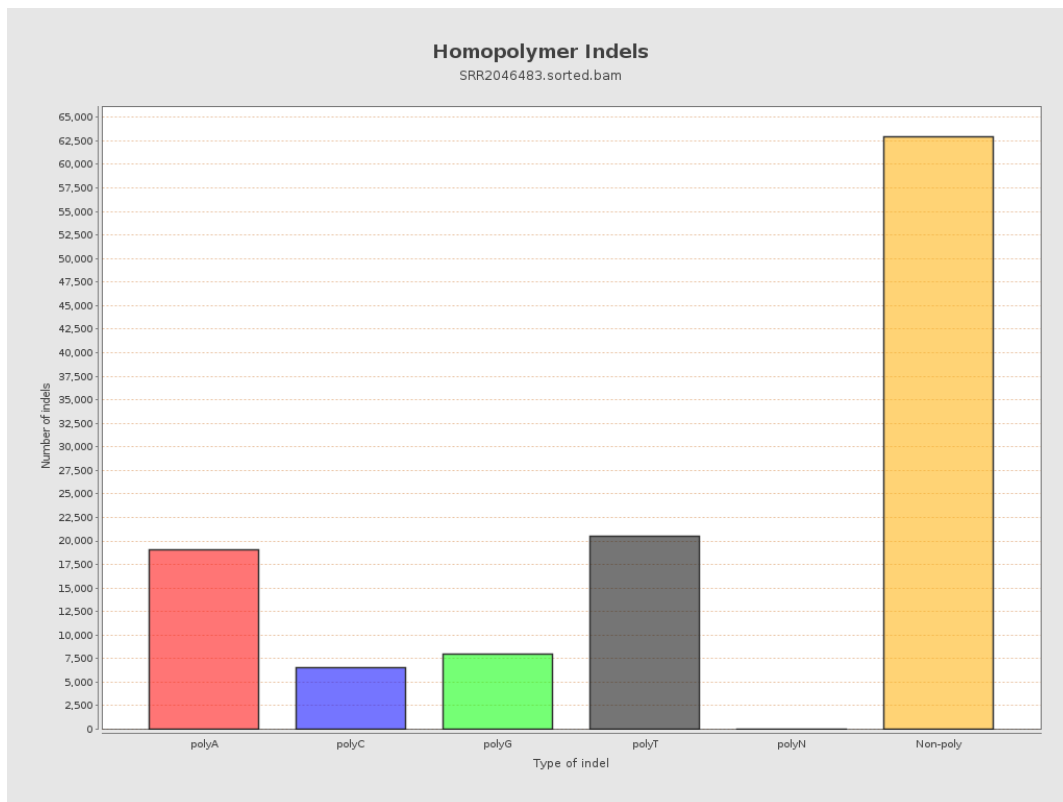
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



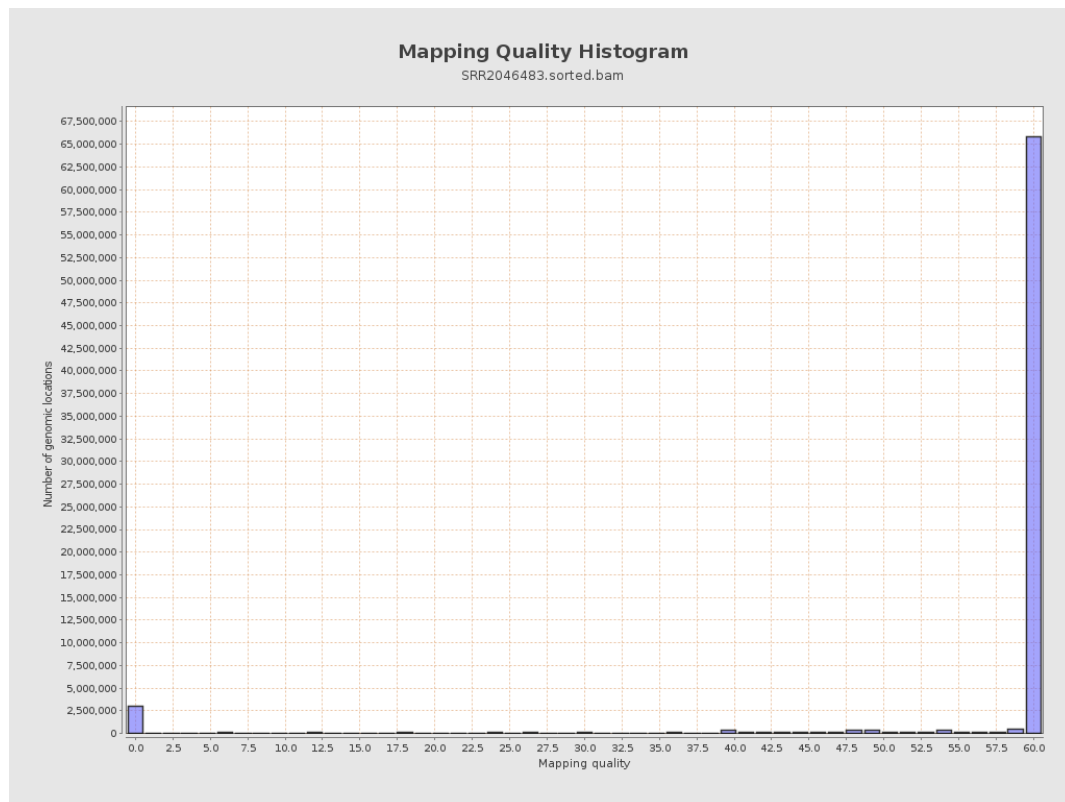
11. Results : Homopolymer Indels



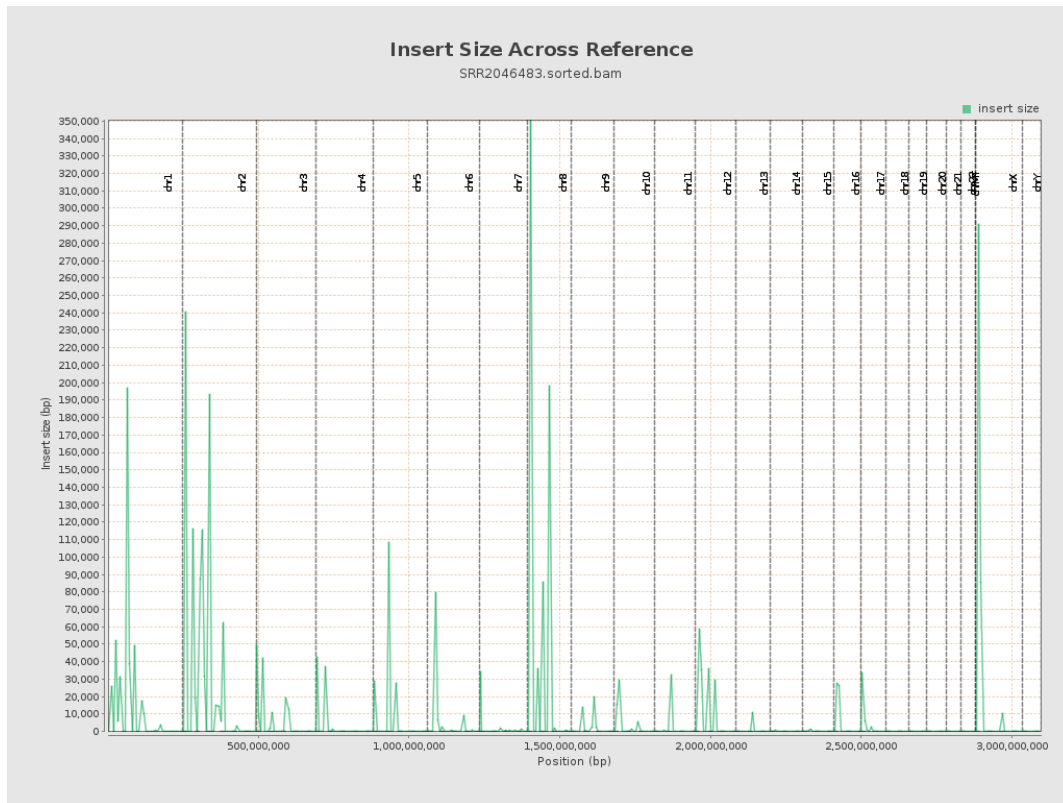
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

