

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/04 11:43:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777286.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_SRR1777286 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777286_1.fastq.gz SRR1777286_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 04 11:43:36 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777286.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	257,508,860
Mapped reads	254,295,719 / 98.75%
Unmapped reads	3,213,141 / 1.25%
Mapped paired reads	254,295,719 / 98.75%
Mapped reads, first in pair	127,413,293 / 49.48%
Mapped reads, second in pair	126,882,426 / 49.27%
Mapped reads, both in pair	253,214,136 / 98.33%
Mapped reads, singletons	1,081,583 / 0.42%
Secondary alignments	0
Supplementary alignments	938,063 / 0.36%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	33,372,451 / 12.96%
Duplication rate	8.48%
Clipped reads	41,455,876 / 16.1%

2.2. ACGT Content

Number/percentage of A's	7,132,987,598 / 29.01%
Number/percentage of C's	5,136,556,023 / 20.89%
Number/percentage of T's	7,018,516,322 / 28.54%
Number/percentage of G's	5,264,299,787 / 21.41%
Number/percentage of N's	35,268,419 / 0.14%

GC Percentage	42.3%
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2.3. Coverage

Mean	7.9448
Standard Deviation	98.0632

2.4. Mapping Quality

Mean Mapping Quality	53.57
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2.5. Insert size

Mean	108,298.22
Standard Deviation	3,225,564.09
P25/Median/P75	122 / 166 / 220

2.6. Mismatches and indels

General error rate	0.92%
Mismatches	220,655,799
Insertions	2,453,223
Mapped reads with at least one insertion	0.94%
Deletions	2,944,700
Mapped reads with at least one deletion	1.13%
Homopolymer indels	43.09%

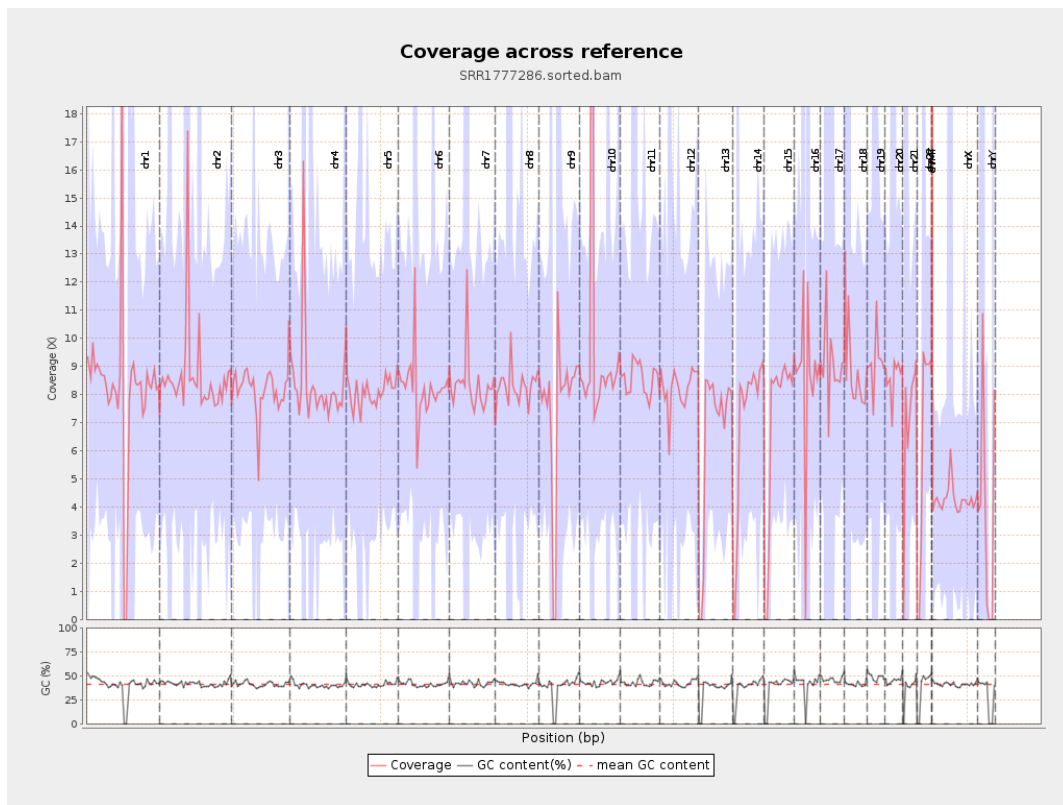
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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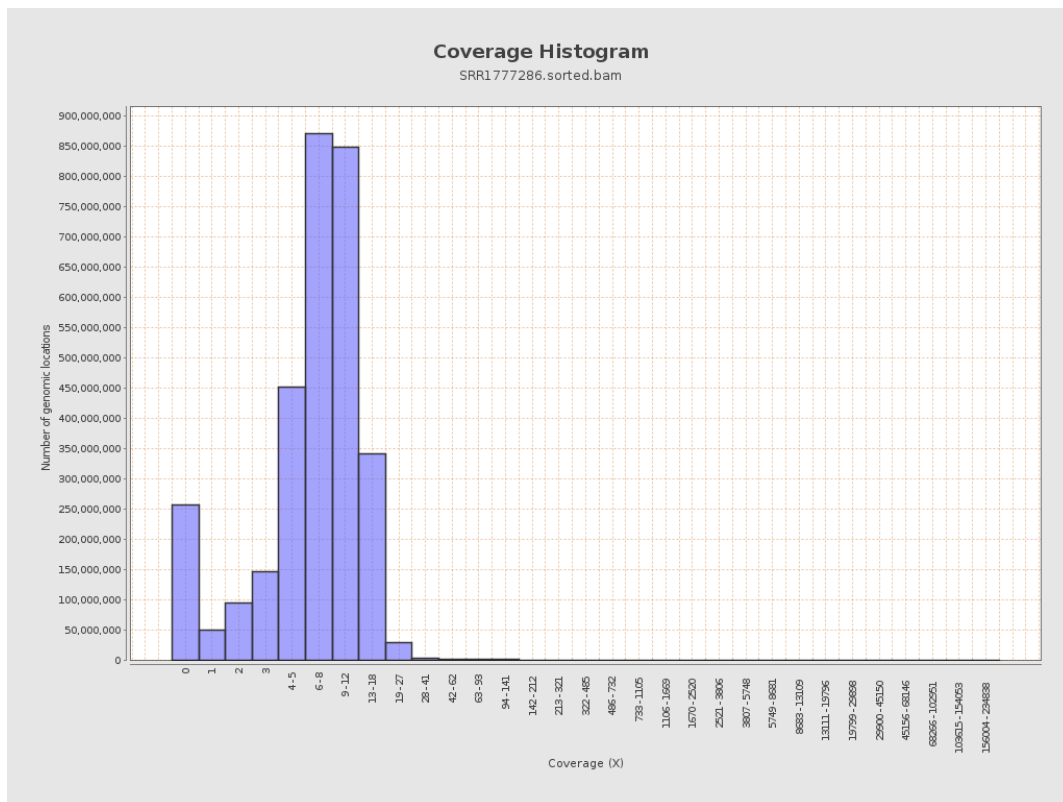
		bases	coverage	deviation
chr1	249250621	2061939216	8.2726	232.7337
chr2	243199373	2108145032	8.6684	59.0299
chr3	198022430	1612582140	8.1434	21.729
chr4	191154276	1593010453	8.3336	62.0989
chr5	180915260	1467053265	8.1091	8.6541
chr6	171115067	1413436384	8.2602	50.7962
chr7	159138663	1331472724	8.3667	80.6253
chr8	146364022	1220317103	8.3375	29.7533
chr9	141213431	1060471668	7.5097	87.3228
chr10	135534747	1364931892	10.0707	256.6786
chr11	135006516	1158172693	8.5786	52.7887
chr12	133851895	1099083119	8.2112	7.8843
chr13	115169878	759909556	6.5982	4.9164
chr14	107349540	747379793	6.9621	8.7854
chr15	102531392	712522257	6.9493	5.3391
chr16	90354753	783671250	8.6733	39.772
chr17	81195210	735449654	9.0578	52.3527
chr18	78077248	680244881	8.7125	112.2909
chr19	59128983	542618125	9.1769	109.1487
chr20	63025520	542404542	8.6061	16.8796
chr21	48129895	345218646	7.1726	29.6529
chr22	51304566	325598173	6.3464	12.4406
chrMT	16571	27275171	1,645.9581	176.7619
chrX	155270560	661092328	4.2577	23.5604

chrY	59373566	240588617	4.0521	72.0349
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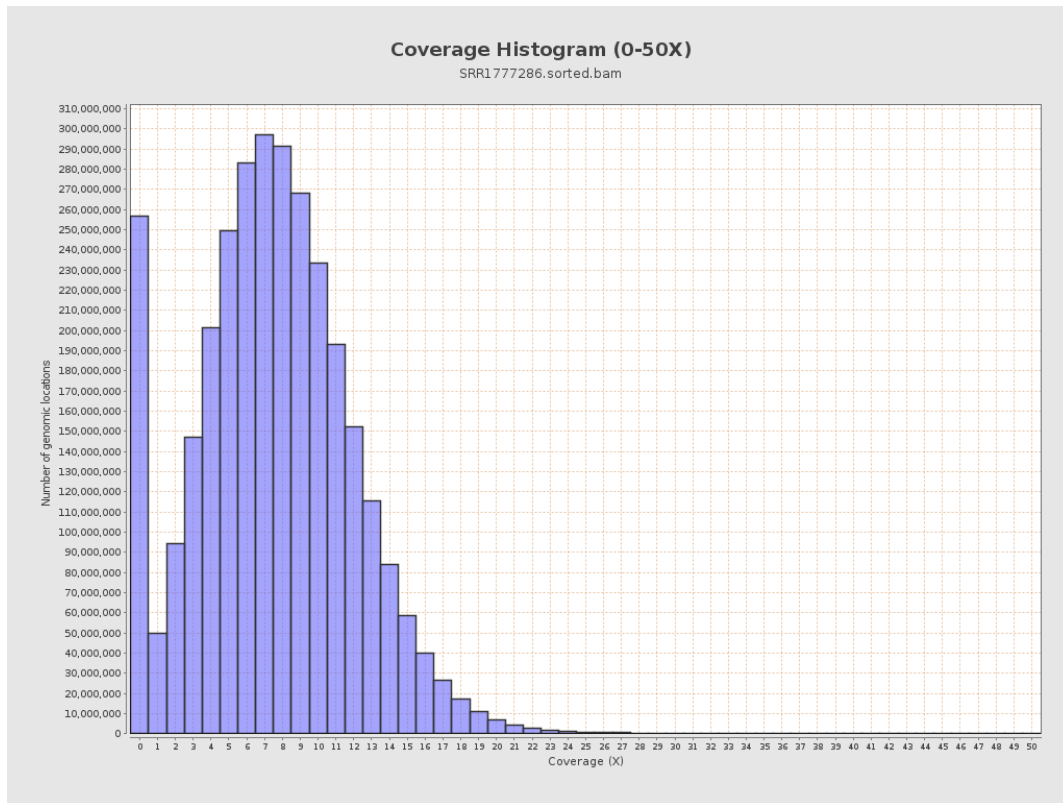
3. Results : Coverage across reference



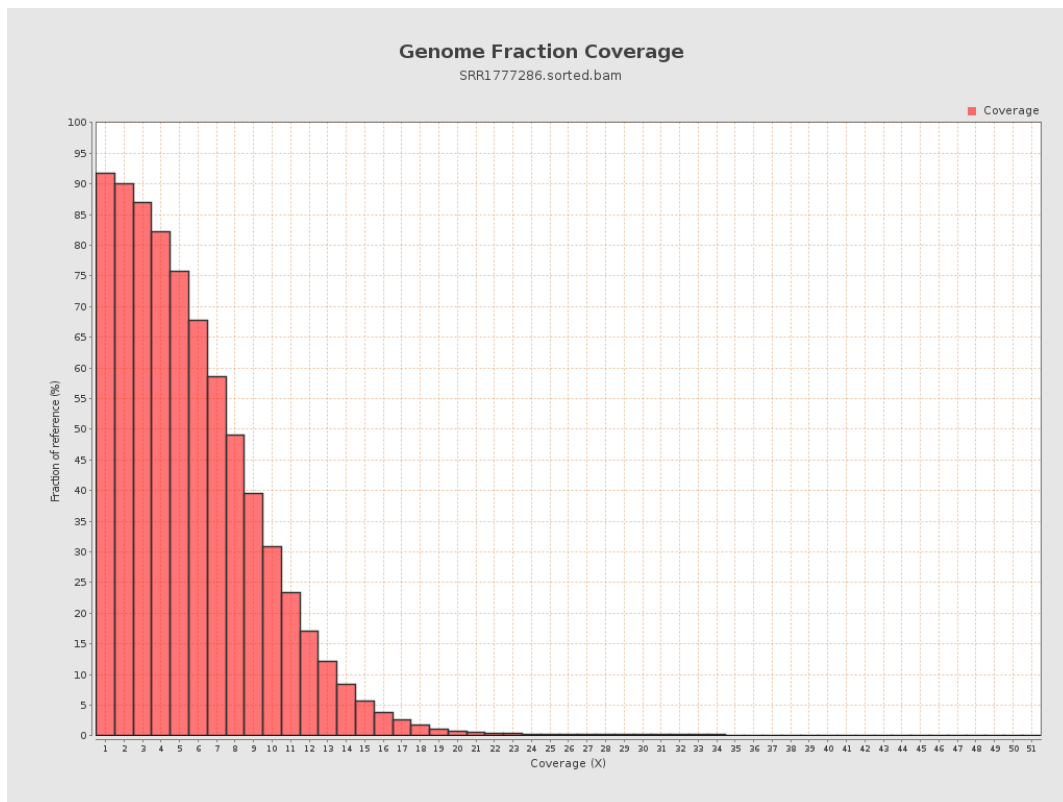
4. Results : Coverage Histogram



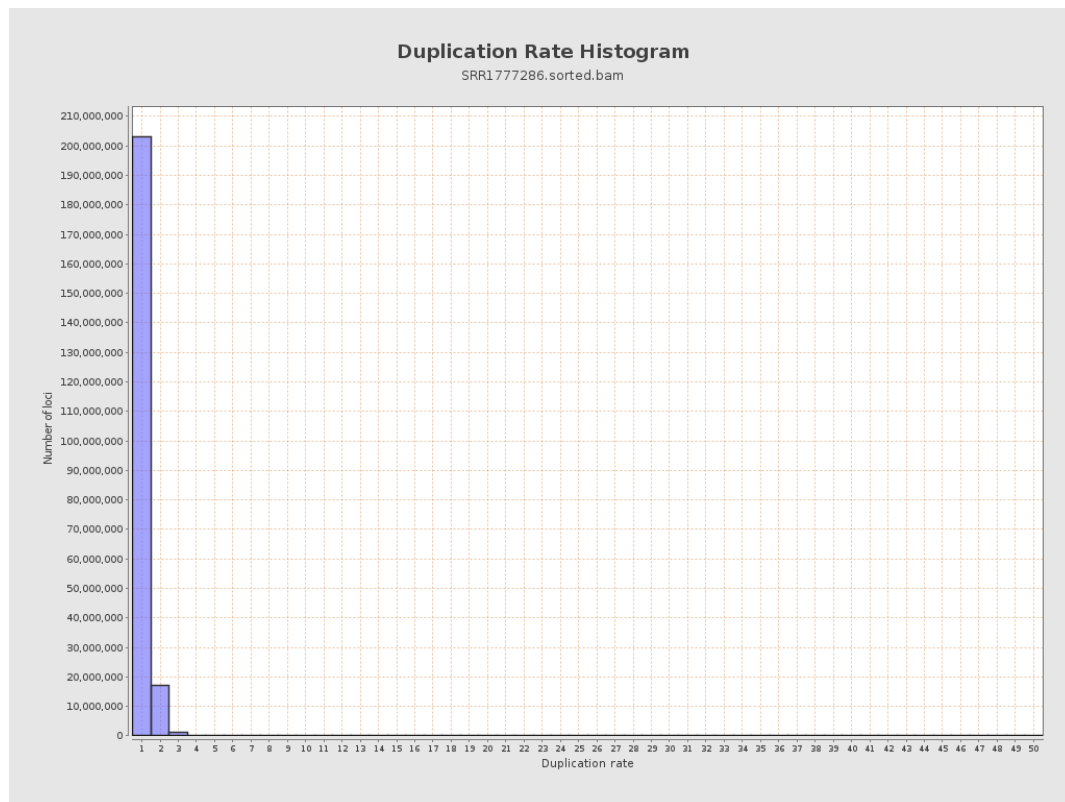
5. Results : Coverage Histogram (0-50X)



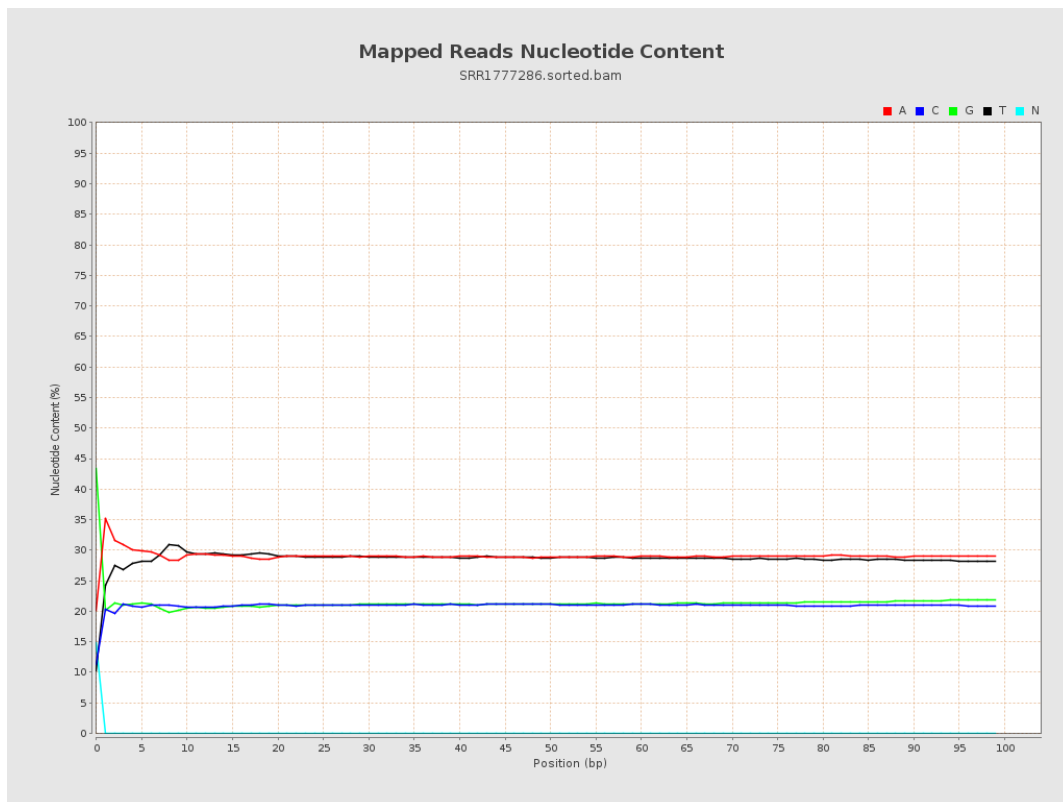
6. Results : Genome Fraction Coverage



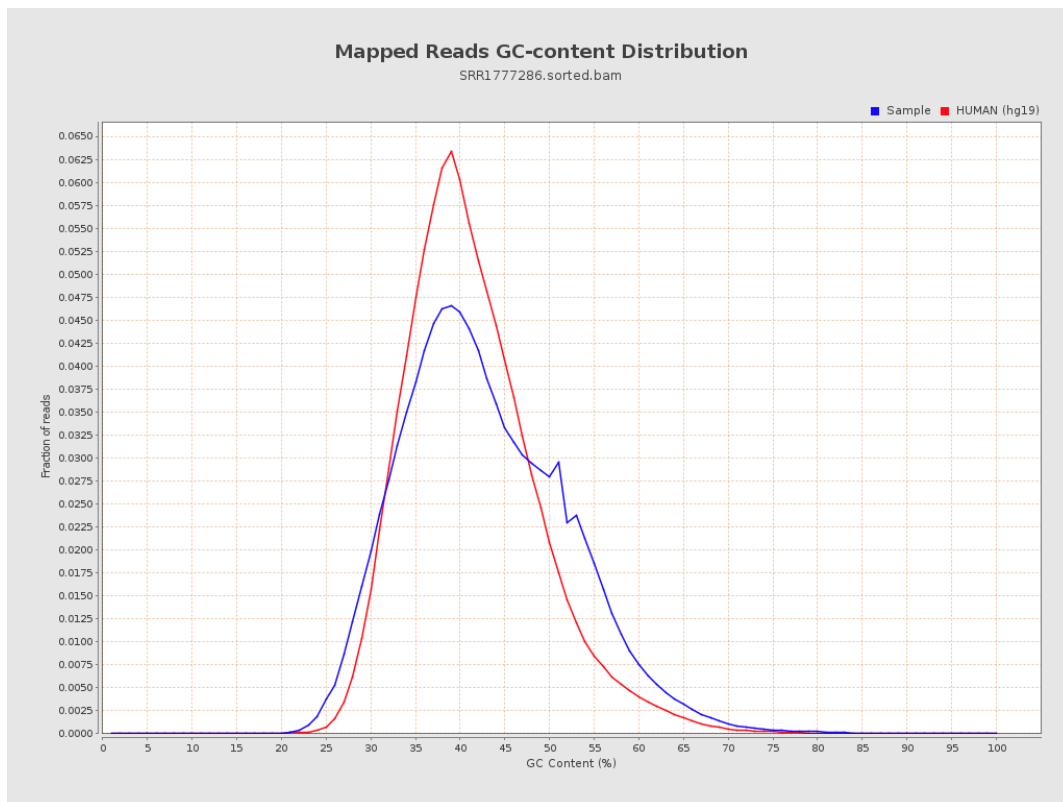
7. Results : Duplication Rate Histogram



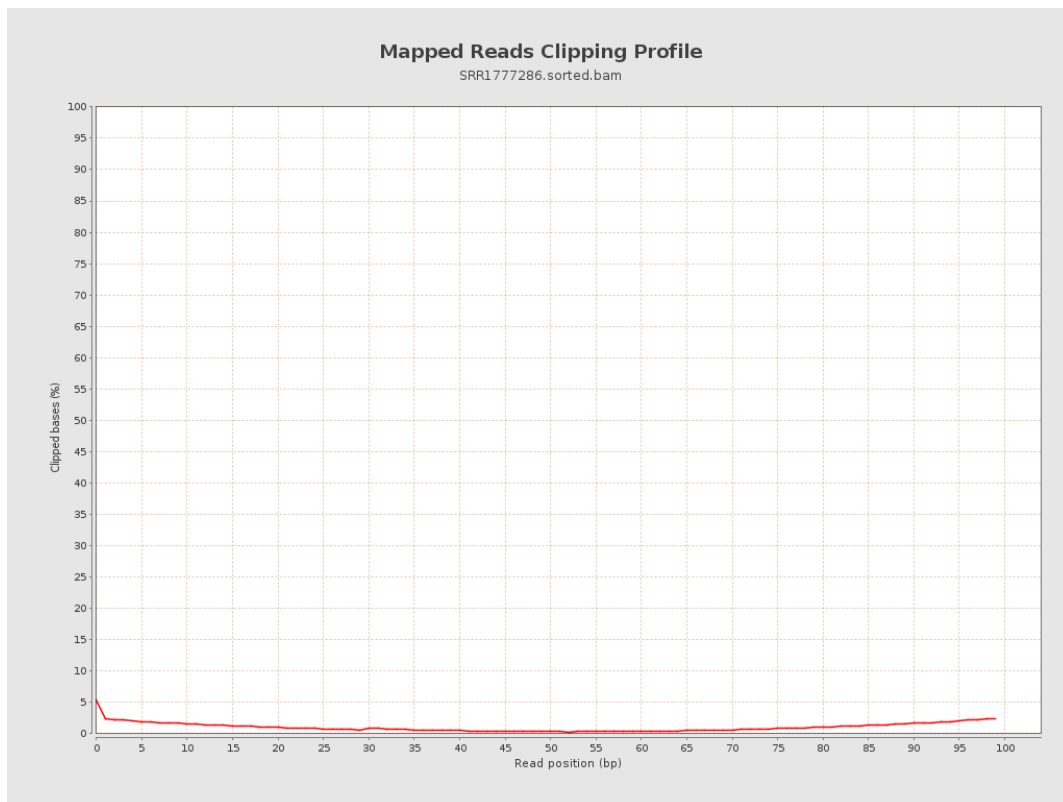
8. Results : Mapped Reads Nucleotide Content



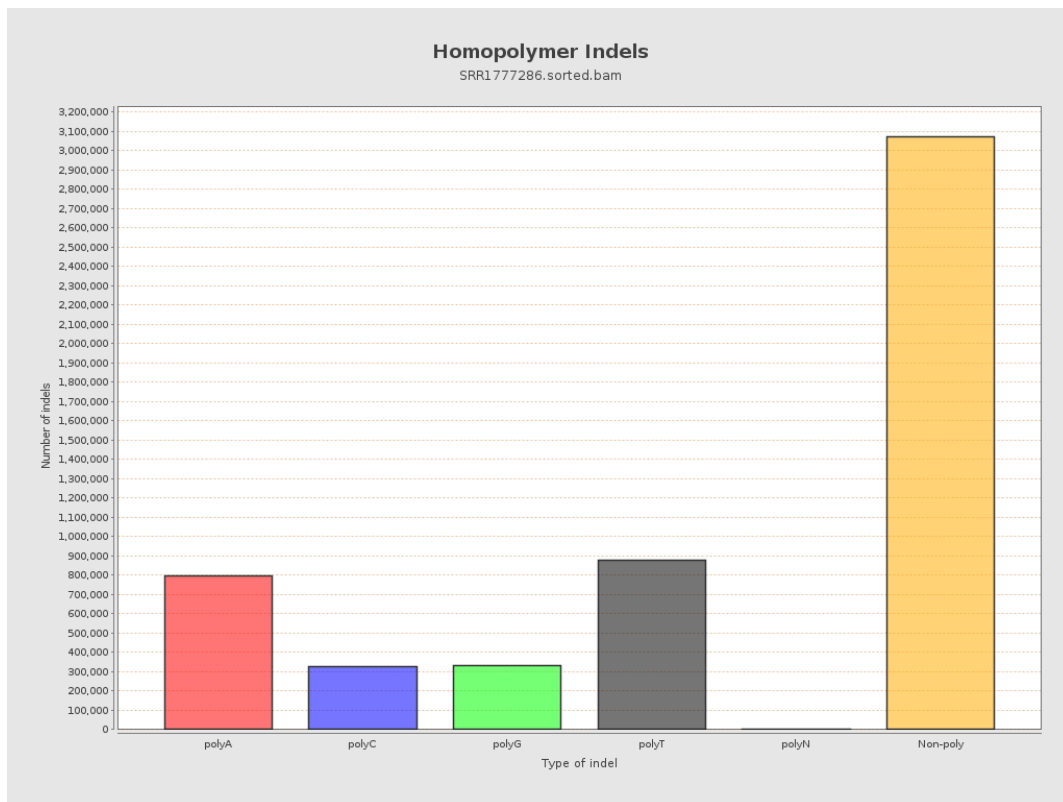
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



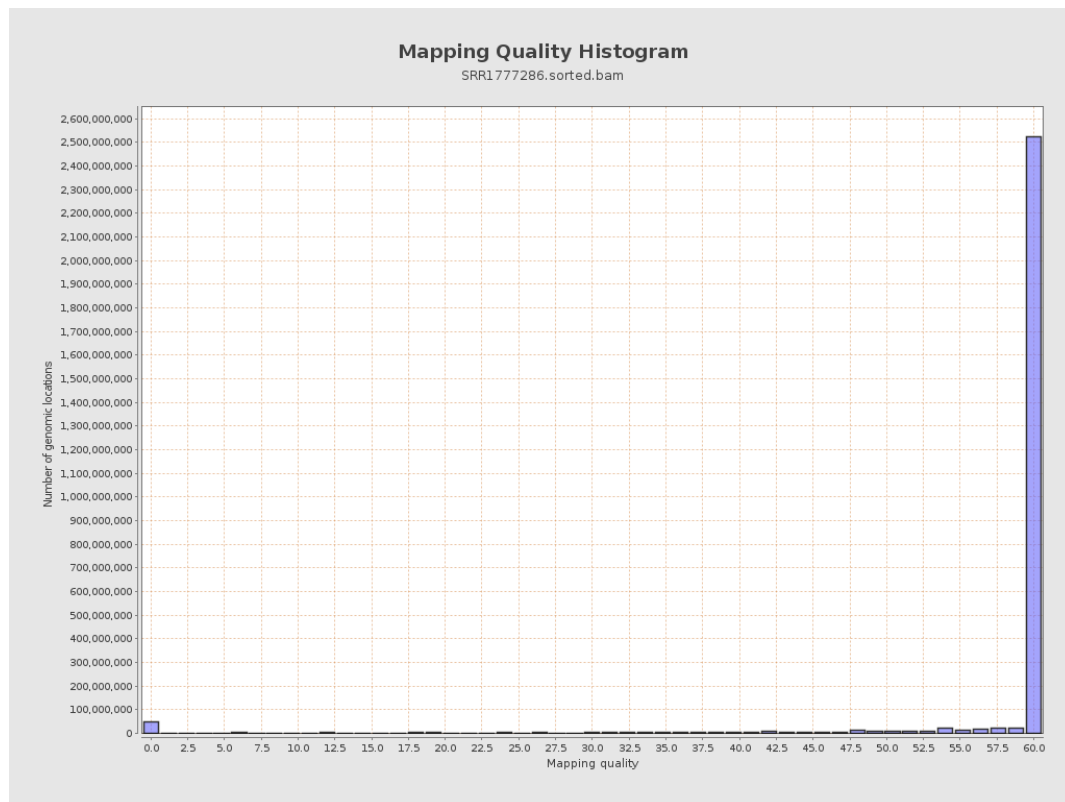
11. Results : Homopolymer Indels



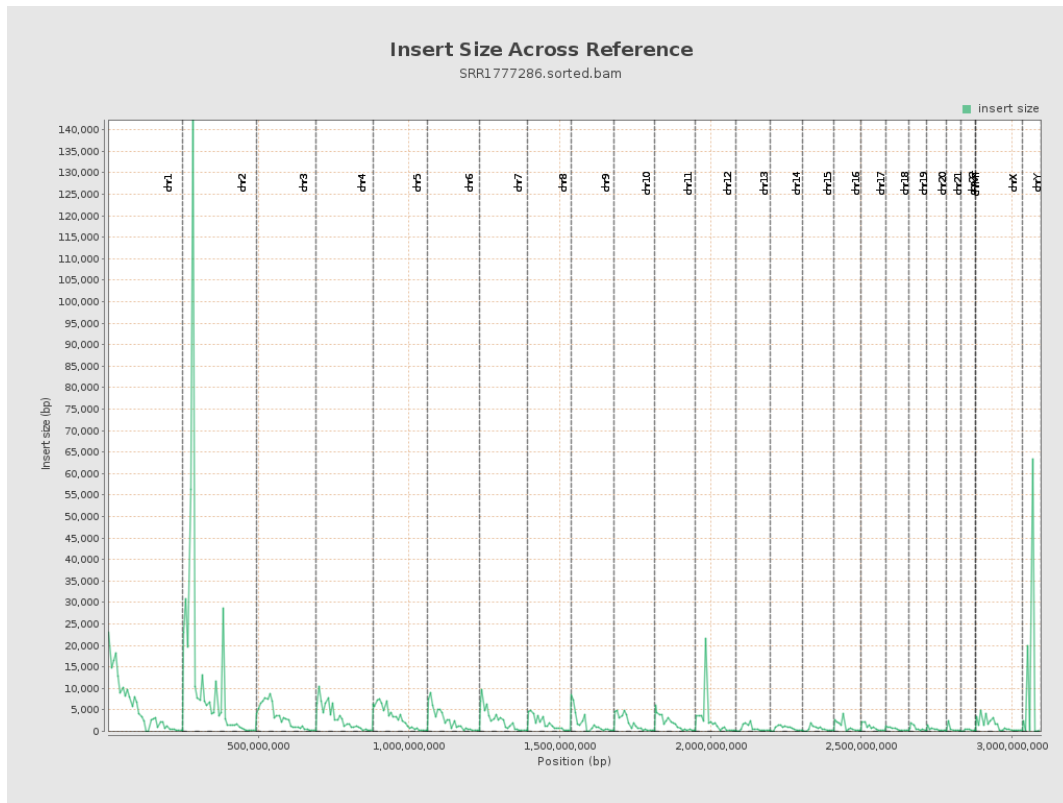
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

