

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/06 04:11:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777299.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_SRR1777299 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777299_1.fastq.gz SRR1777299_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 06 04:11:36 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777299.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,481,956
Mapped reads	1,452,322 / 98%
Unmapped reads	29,634 / 2%
Mapped paired reads	1,452,322 / 98%
Mapped reads, first in pair	727,693 / 49.1%
Mapped reads, second in pair	724,629 / 48.9%
Mapped reads, both in pair	1,444,494 / 97.47%
Mapped reads, singletons	7,828 / 0.53%
Secondary alignments	0
Supplementary alignments	57,615 / 3.89%
Read min/max/mean length	30 / 101 / 102.61
Duplicated reads (estimated)	137,835 / 9.3%
Duplication rate	7.72%
Clipped reads	435,909 / 29.41%

2.2. ACGT Content

Number/percentage of A's	41,661,017 / 29.77%
Number/percentage of C's	28,454,199 / 20.33%
Number/percentage of T's	40,867,121 / 29.2%
Number/percentage of G's	28,956,908 / 20.69%
Number/percentage of N's	2,259 / 0%

GC Percentage	41.03%
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2.3. Coverage

Mean	0.0452
Standard Deviation	0.6721

2.4. Mapping Quality

Mean Mapping Quality	52.79
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2.5. Insert size

Mean	165,660.97
Standard Deviation	3,872,185.06
P25/Median/P75	112 / 157 / 219

2.6. Mismatches and indels

General error rate	0.72%
Mismatches	938,521
Insertions	35,184
Mapped reads with at least one insertion	2.34%
Deletions	22,004
Mapped reads with at least one deletion	1.45%
Homopolymer indels	41.99%

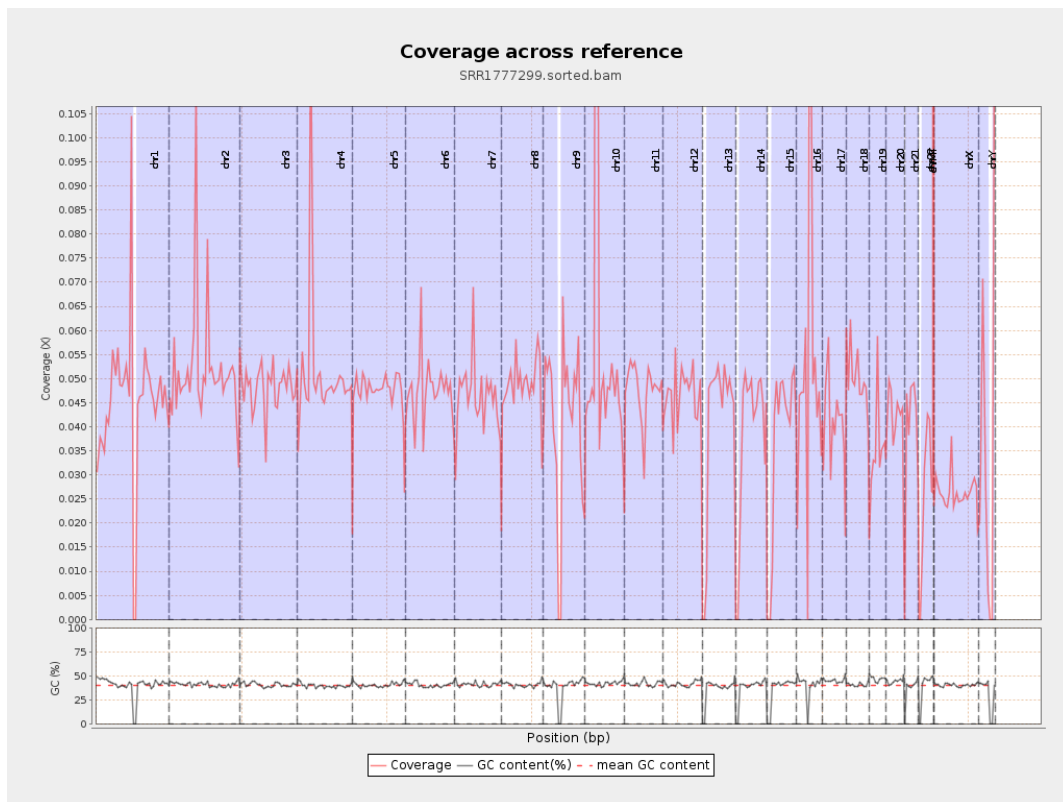
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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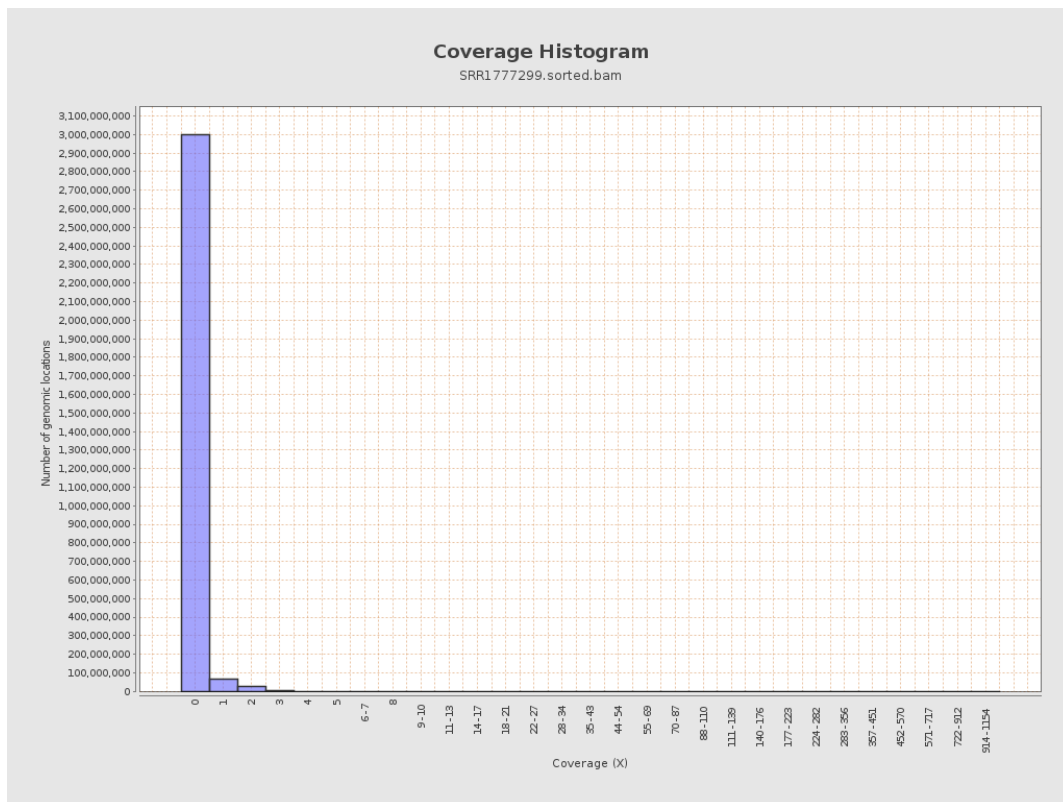
		bases	coverage	deviation
chr1	249250621	11267960	0.0452	1.1515
chr2	243199373	12659460	0.0521	0.6306
chr3	198022430	9559990	0.0483	0.3409
chr4	191154276	9734137	0.0509	0.6095
chr5	180915260	8605515	0.0476	0.2807
chr6	171115067	8118276	0.0474	0.3349
chr7	159138663	7424847	0.0467	0.4711
chr8	146364022	7168123	0.049	0.4242
chr9	141213431	5880843	0.0416	0.577
chr10	135534747	7882092	0.0582	1.8497
chr11	135006516	6388449	0.0473	0.3271
chr12	133851895	6213524	0.0464	0.2823
chr13	115169878	4637479	0.0403	0.2594
chr14	107349540	4109088	0.0383	0.2603
chr15	102531392	3778910	0.0369	0.2416
chr16	90354753	4825792	0.0534	0.9082
chr17	81195210	3244945	0.04	0.3621
chr18	78077248	3923433	0.0503	0.6808
chr19	59128983	2106416	0.0356	0.6695
chr20	63025520	2642646	0.0419	0.2931
chr21	48129895	1891629	0.0393	0.3243
chr22	51304566	1260255	0.0246	0.2141
chrMT	16571	559379	33.7565	10.8444
chrX	155270560	4103145	0.0264	0.2303

chrY	59373566	2017170	0.034	0.7691
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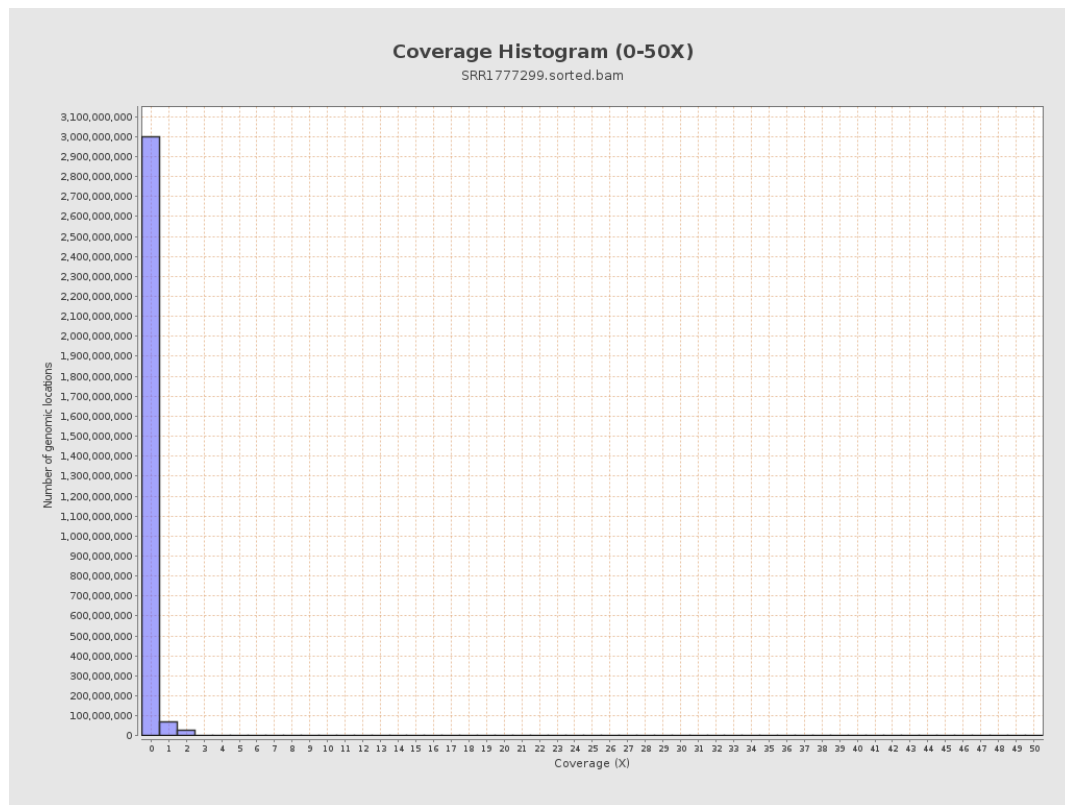
3. Results : Coverage across reference



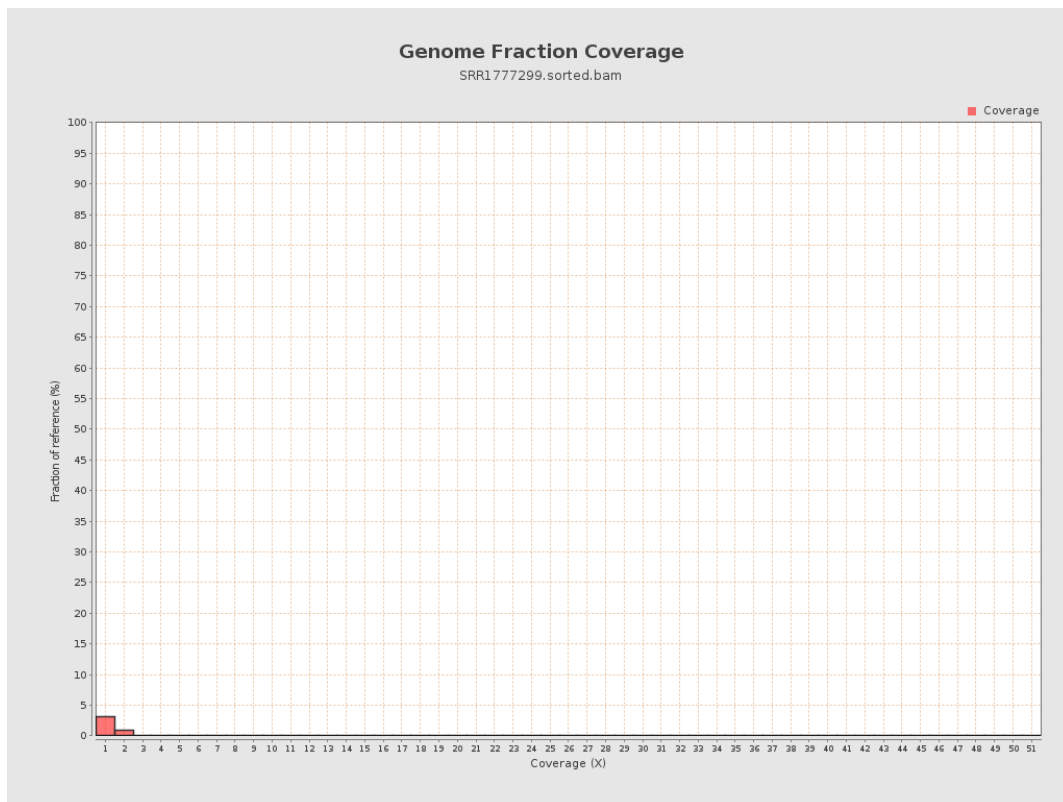
4. Results : Coverage Histogram



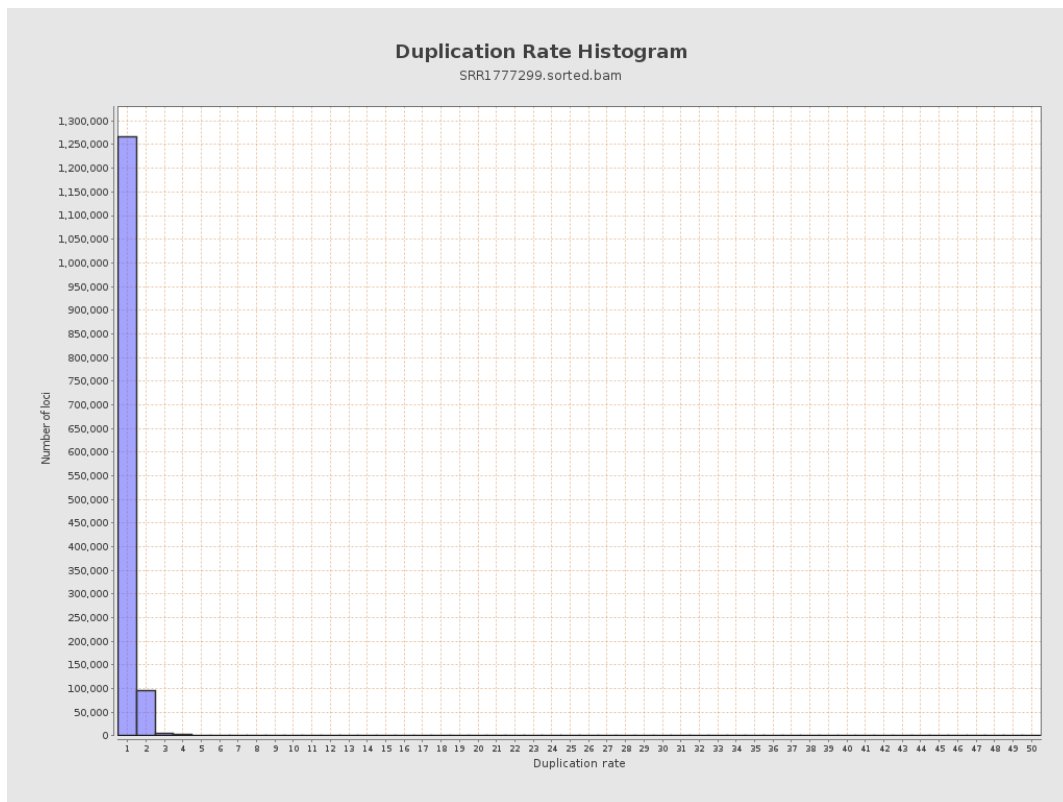
5. Results : Coverage Histogram (0-50X)



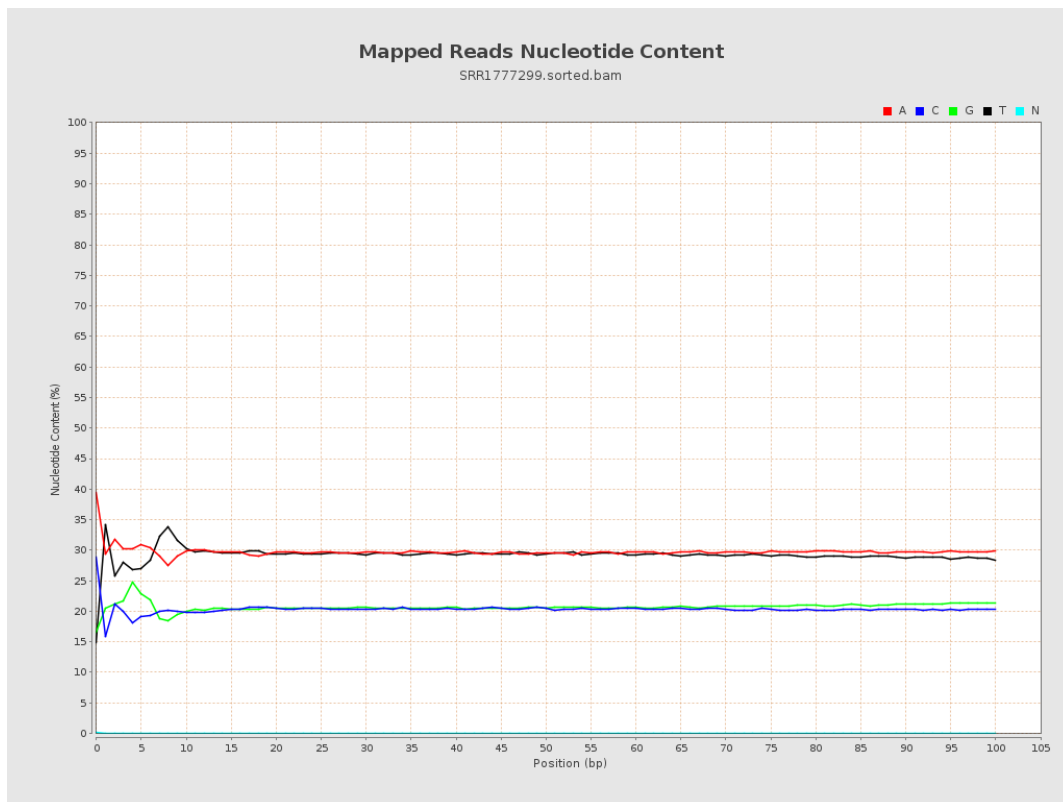
6. Results : Genome Fraction Coverage



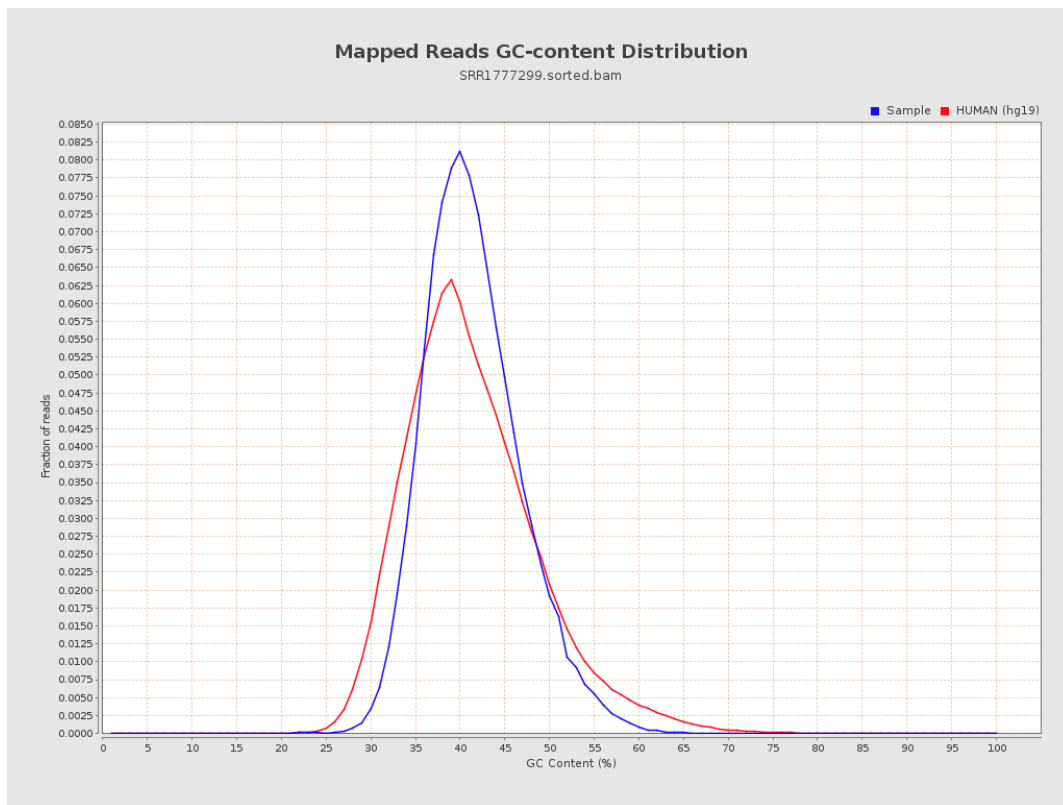
7. Results : Duplication Rate Histogram



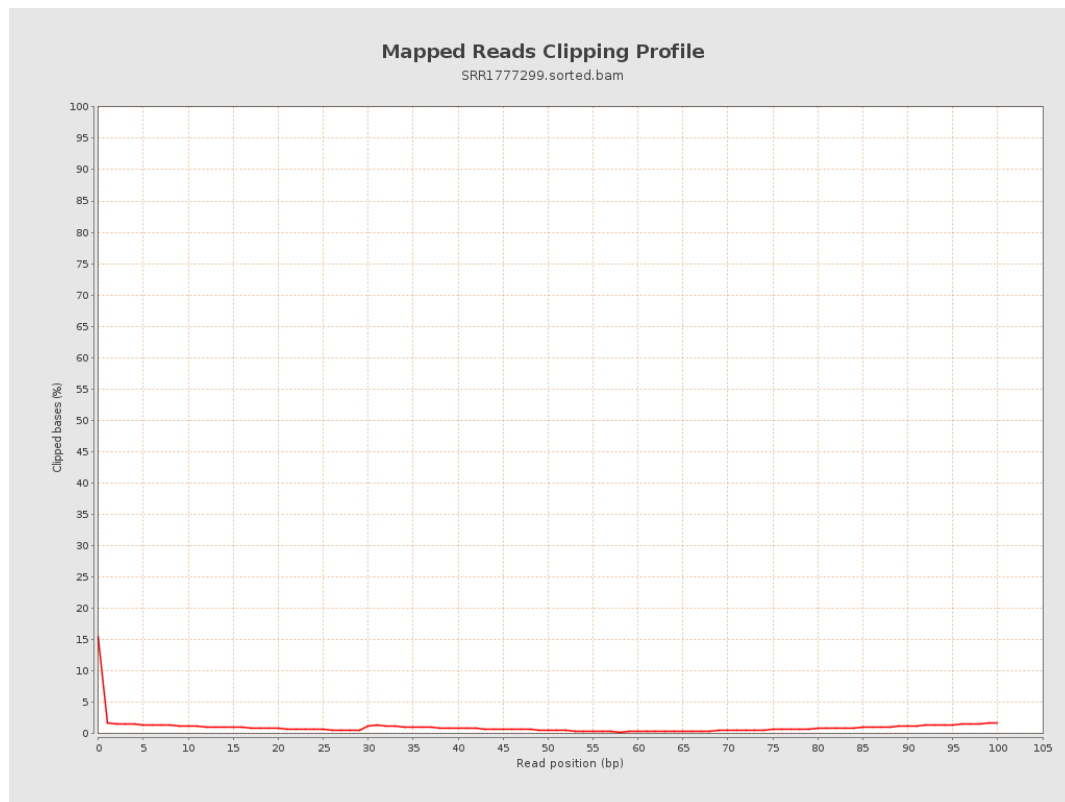
8. Results : Mapped Reads Nucleotide Content



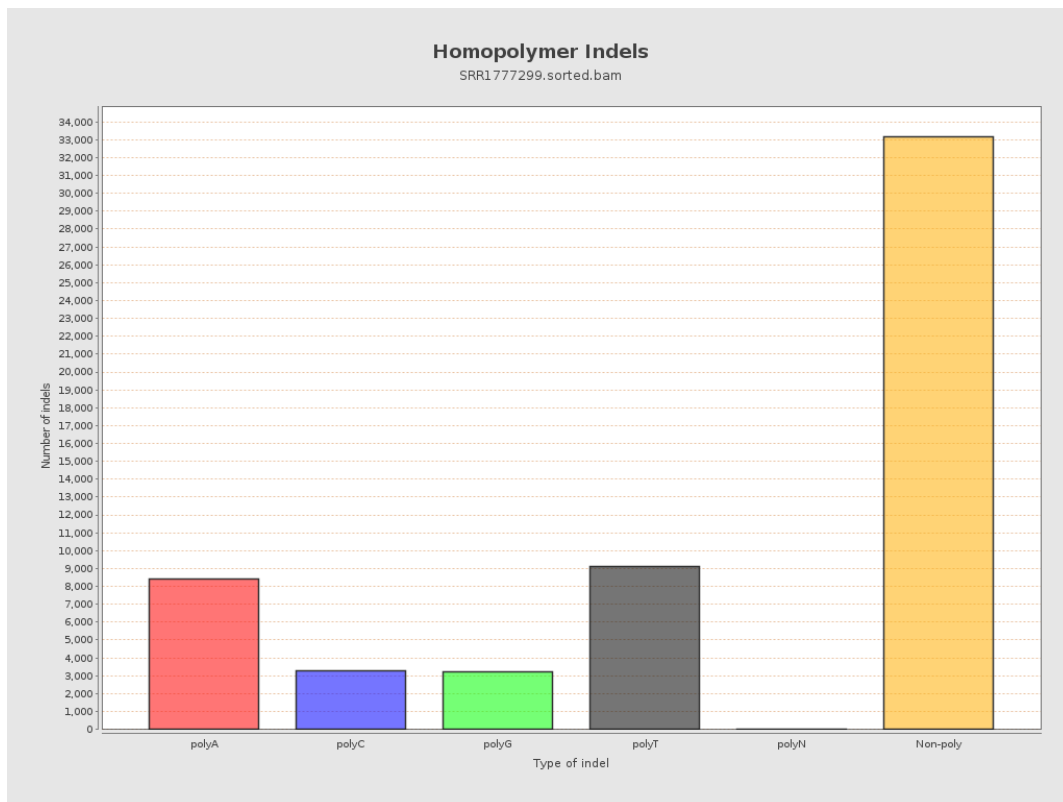
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



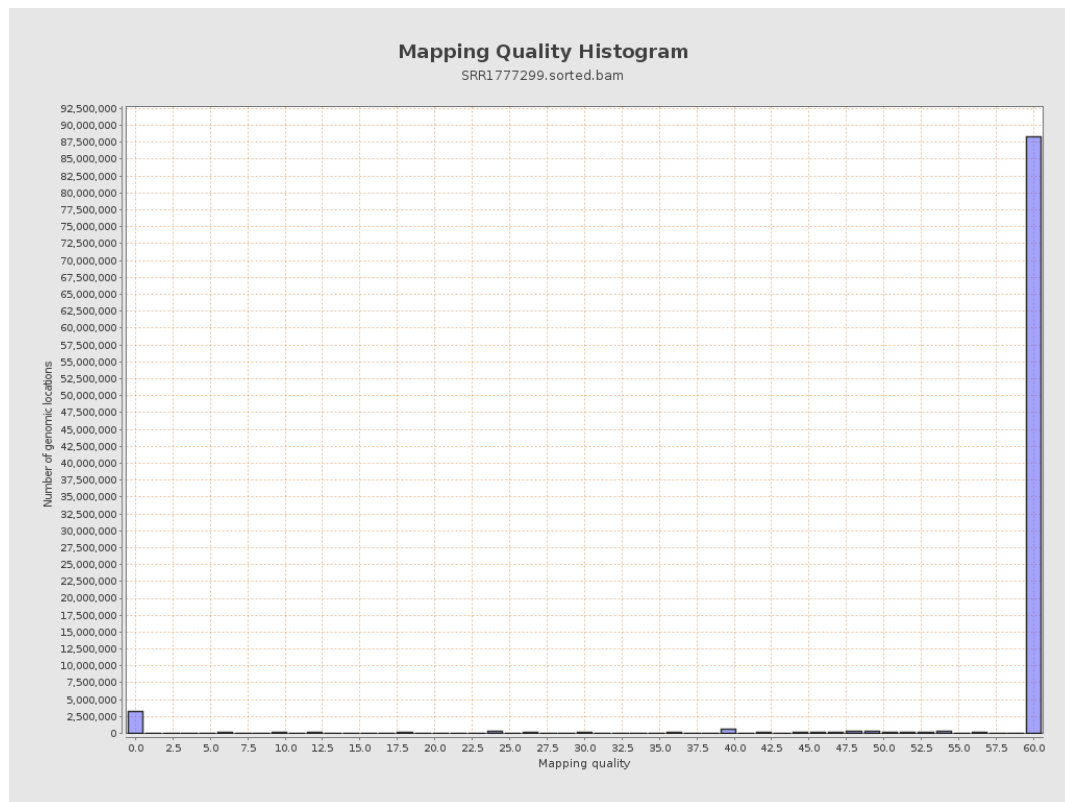
11. Results : Homopolymer Indels



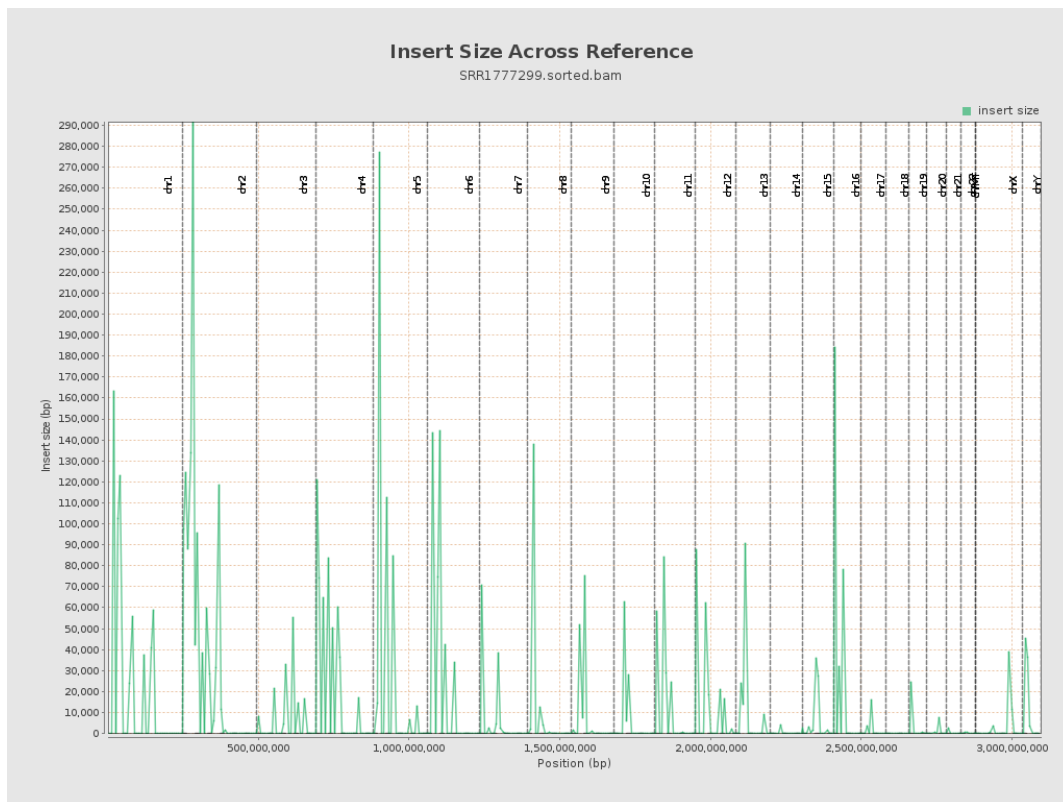
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

