

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/06 04:08:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777298.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_SRR1777298 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777298_1.fastq.gz SRR1777298_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 06 04:08:11 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777298.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,395,970
Mapped reads	1,322,508 / 94.74%
Unmapped reads	73,462 / 5.26%
Mapped paired reads	1,322,508 / 94.74%
Mapped reads, first in pair	662,651 / 47.47%
Mapped reads, second in pair	659,857 / 47.27%
Mapped reads, both in pair	1,316,498 / 94.31%
Mapped reads, singletons	6,010 / 0.43%
Secondary alignments	0
Supplementary alignments	44,010 / 3.15%
Read min/max/mean length	30 / 101 / 102.31
Duplicated reads (estimated)	109,062 / 7.81%
Duplication rate	7.16%
Clipped reads	355,948 / 25.5%

2.2. ACGT Content

Number/percentage of A's	37,924,048 / 29.64%
Number/percentage of C's	26,116,422 / 20.41%
Number/percentage of T's	37,120,522 / 29.02%
Number/percentage of G's	26,769,222 / 20.92%
Number/percentage of N's	2,084 / 0%

GC Percentage	41.34%
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2.3. Coverage

Mean	0.0413
Standard Deviation	0.5241

2.4. Mapping Quality

Mean Mapping Quality	53.25
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2.5. Insert size

Mean	133,575.19
Standard Deviation	3,490,384.29
P25/Median/P75	114 / 159 / 217

2.6. Mismatches and indels

General error rate	0.61%
Mismatches	719,235
Insertions	31,957
Mapped reads with at least one insertion	2.35%
Deletions	18,356
Mapped reads with at least one deletion	1.34%
Homopolymer indels	45.08%

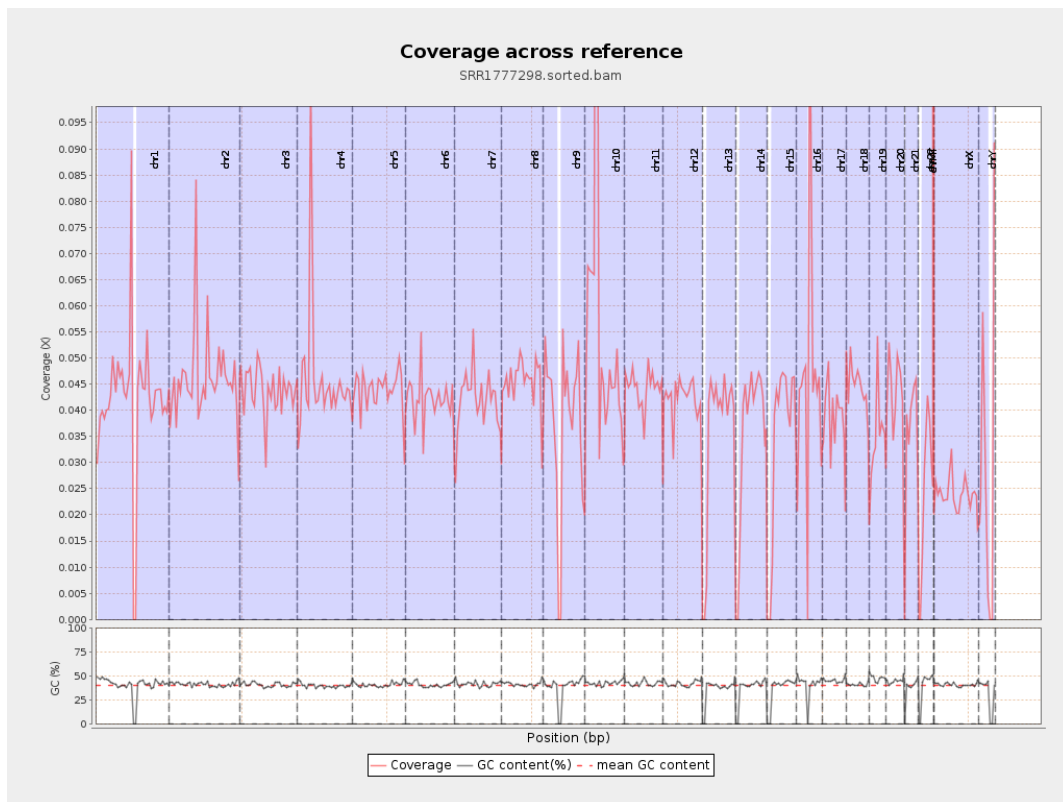
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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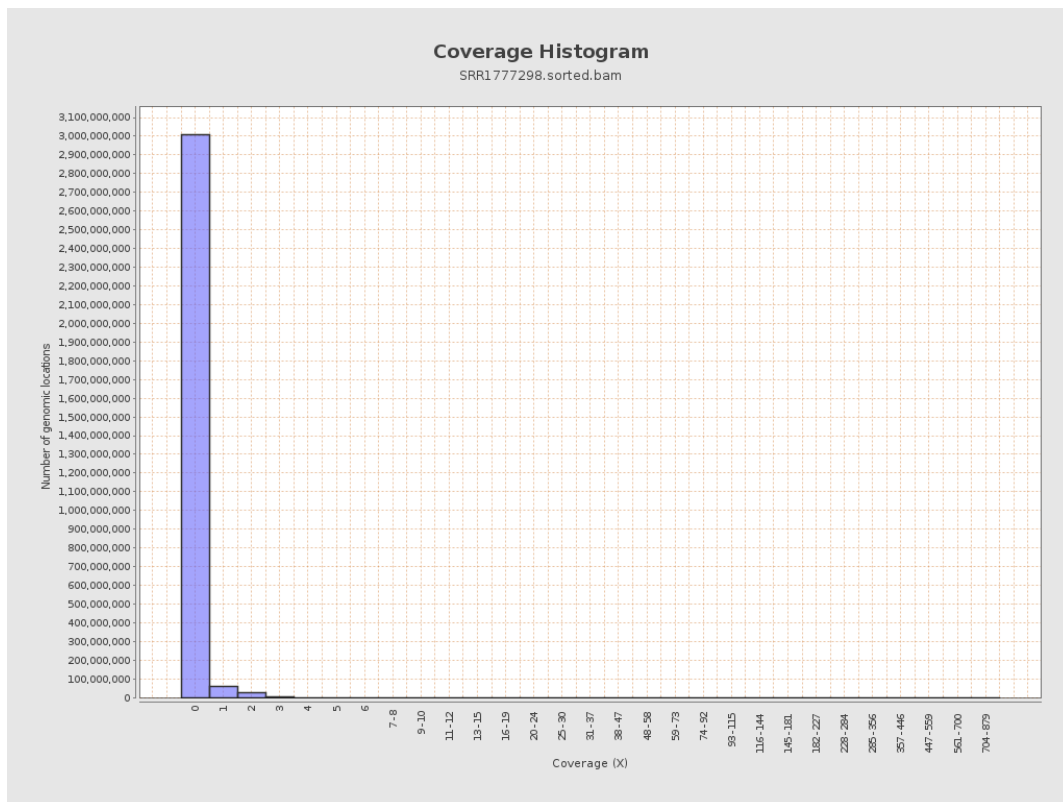
		bases	coverage	deviation
chr1	249250621	10443562	0.0419	0.9369
chr2	243199373	11262041	0.0463	0.4504
chr3	198022430	8688843	0.0439	0.2891
chr4	191154276	8683196	0.0454	0.5134
chr5	180915260	7919366	0.0438	0.2657
chr6	171115067	7194286	0.042	0.2931
chr7	159138663	6741730	0.0424	0.3643
chr8	146364022	6678940	0.0456	0.3668
chr9	141213431	5355338	0.0379	0.4666
chr10	135534747	7683024	0.0567	1.3288
chr11	135006516	5961515	0.0442	0.2959
chr12	133851895	5644634	0.0422	0.2601
chr13	115169878	4041724	0.0351	0.2348
chr14	107349540	3812207	0.0355	0.2411
chr15	102531392	3528013	0.0344	0.2327
chr16	90354753	4122481	0.0456	0.5847
chr17	81195210	3089515	0.0381	0.3082
chr18	78077248	3501735	0.0448	0.5493
chr19	59128983	2081606	0.0352	0.5421
chr20	63025520	2710595	0.043	0.285
chr21	48129895	1684804	0.035	0.2841
chr22	51304566	1227789	0.0239	0.1991
chrMT	16571	533974	32.2234	9.3283
chrX	155270560	3736875	0.0241	0.2112

chrY	59373566	1654274	0.0279	0.6055
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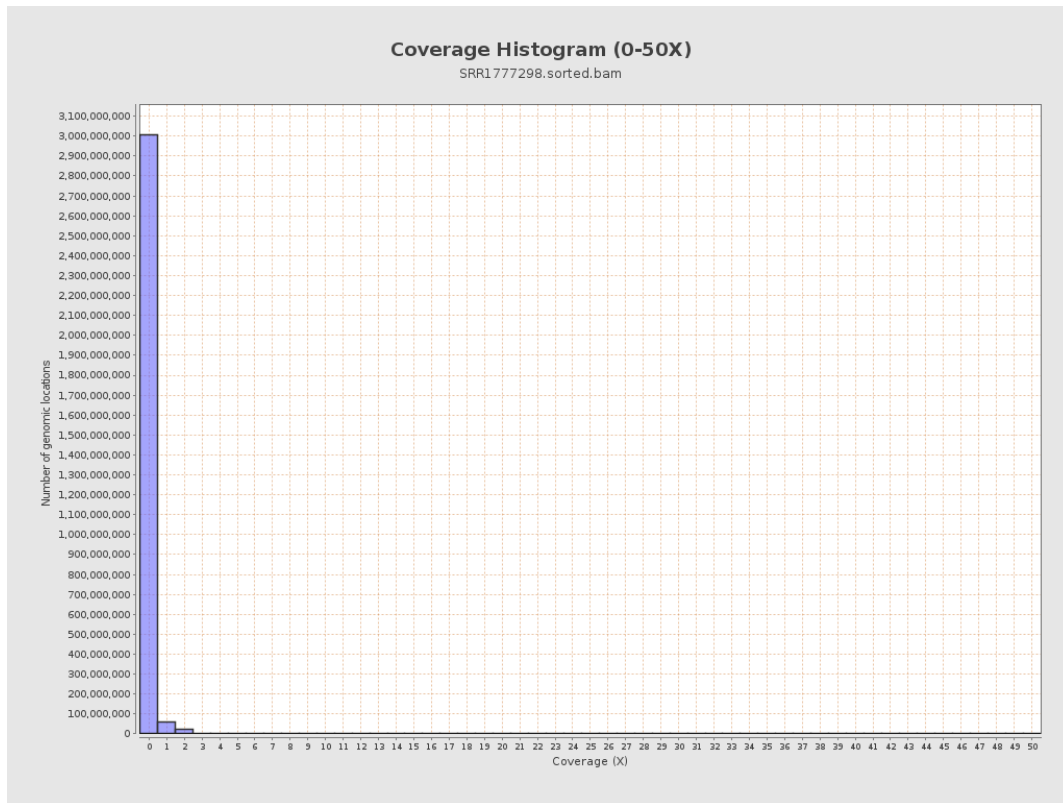
3. Results : Coverage across reference



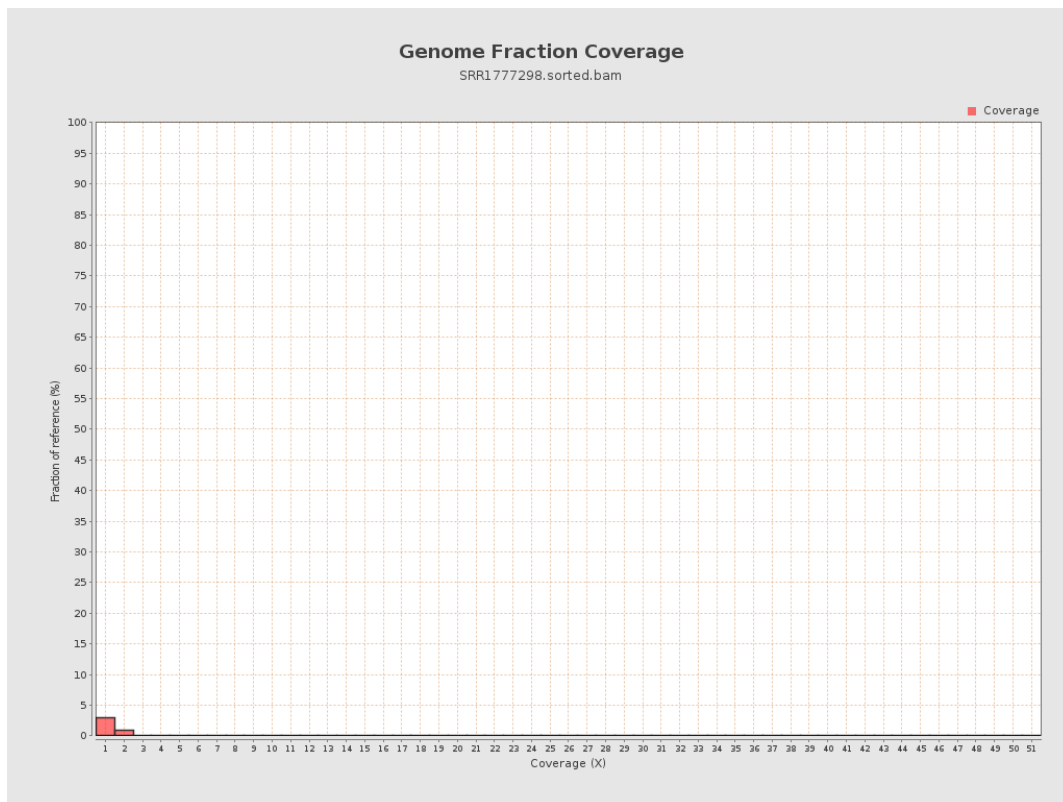
4. Results : Coverage Histogram



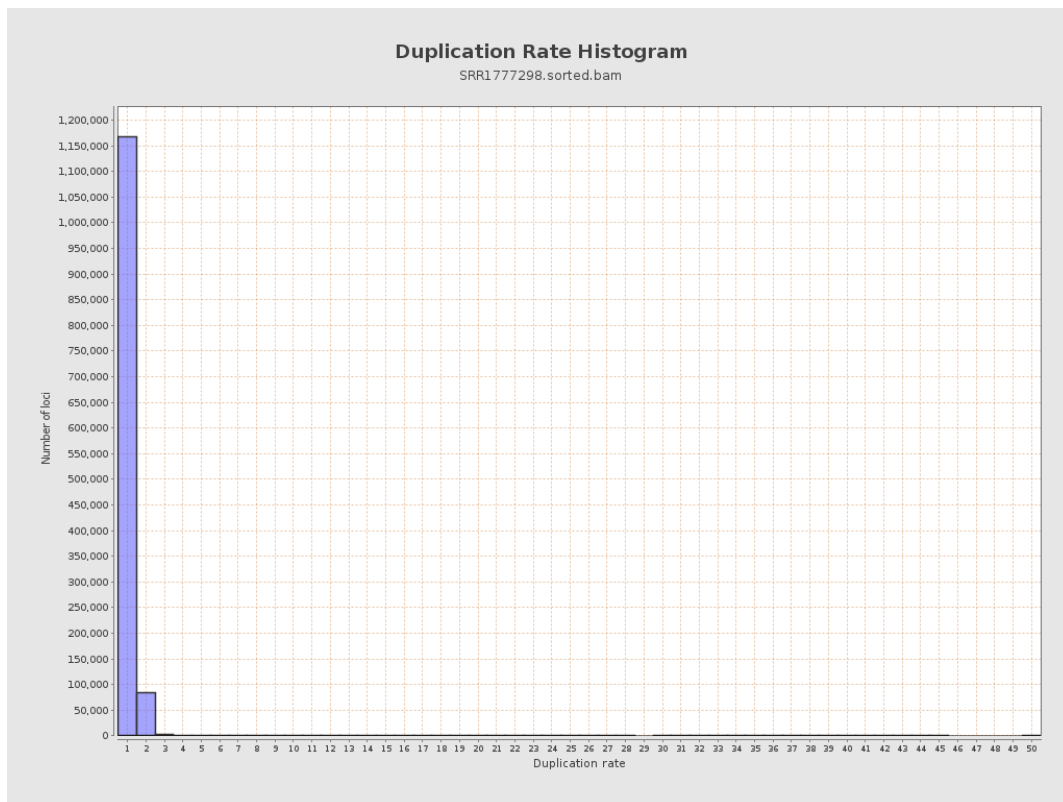
5. Results : Coverage Histogram (0-50X)



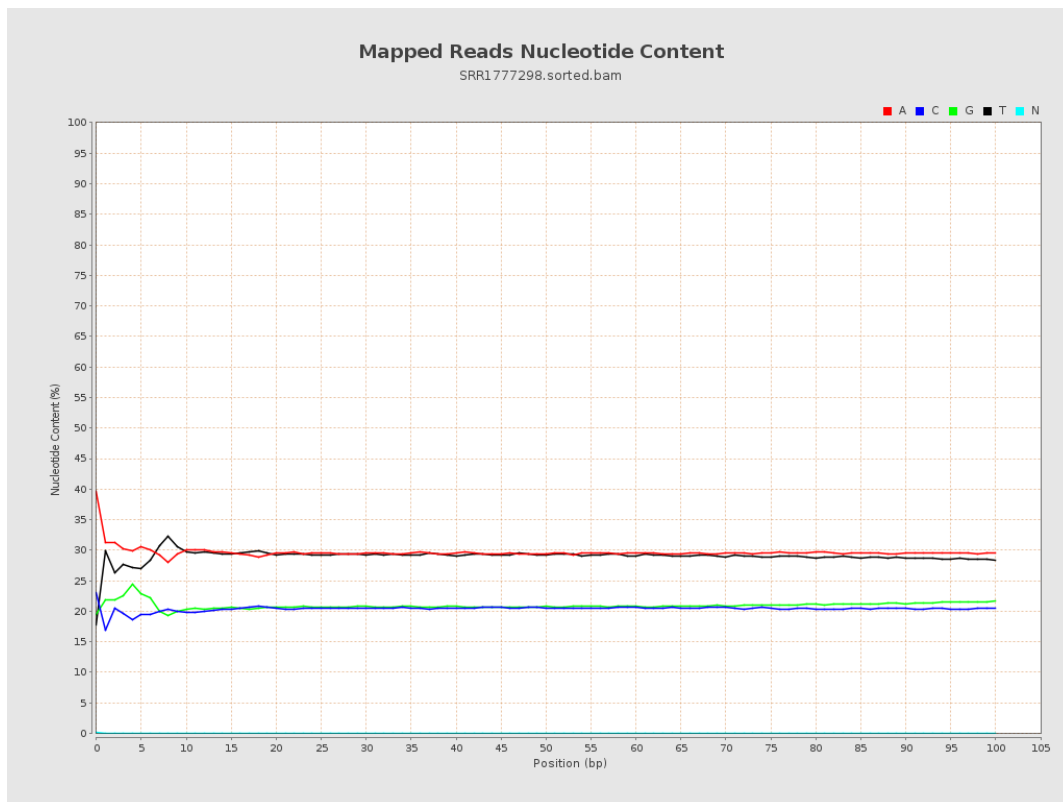
6. Results : Genome Fraction Coverage



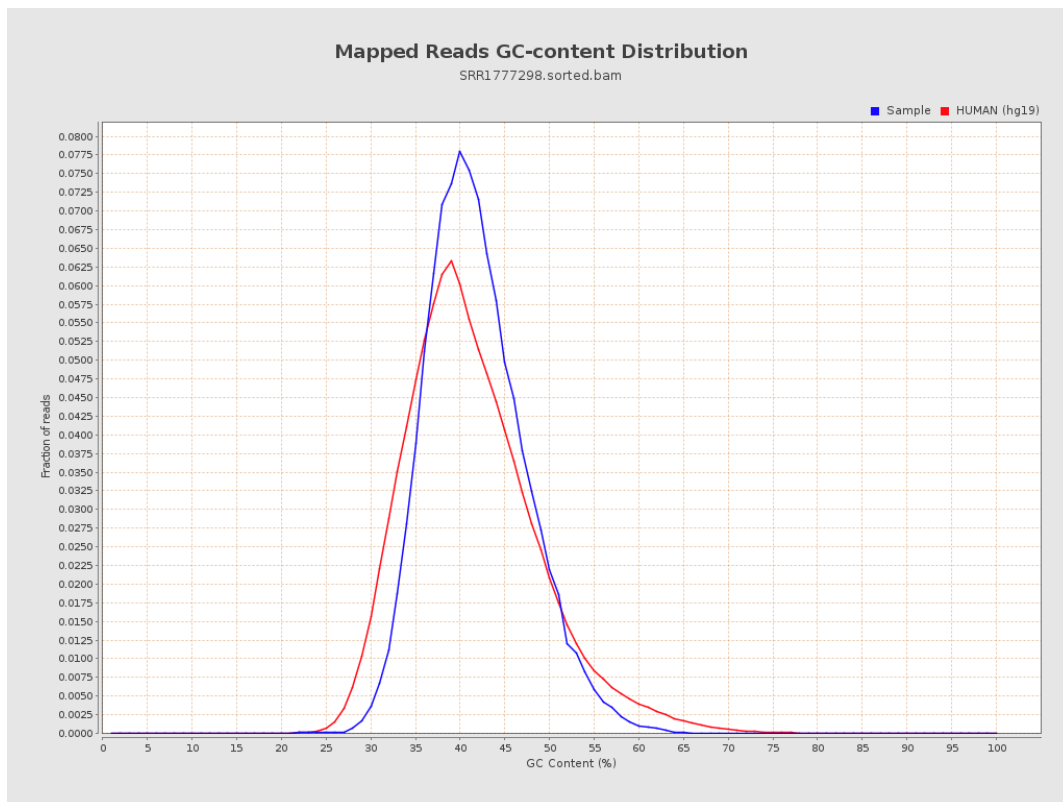
7. Results : Duplication Rate Histogram



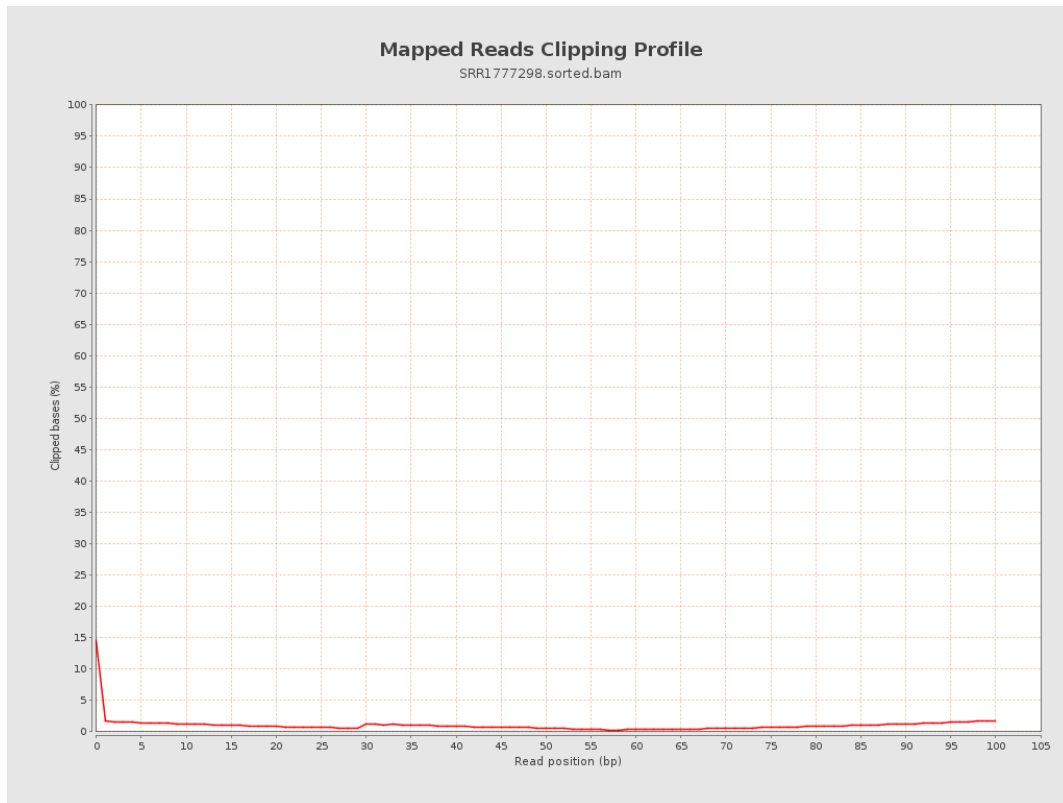
8. Results : Mapped Reads Nucleotide Content



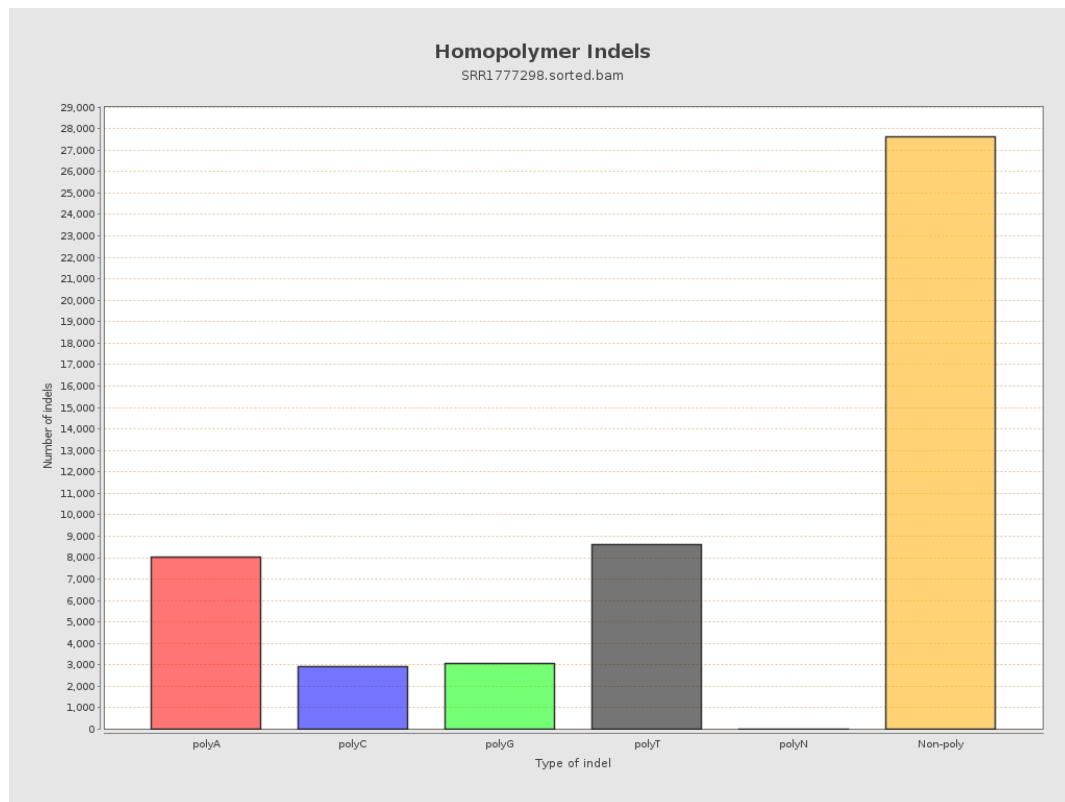
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



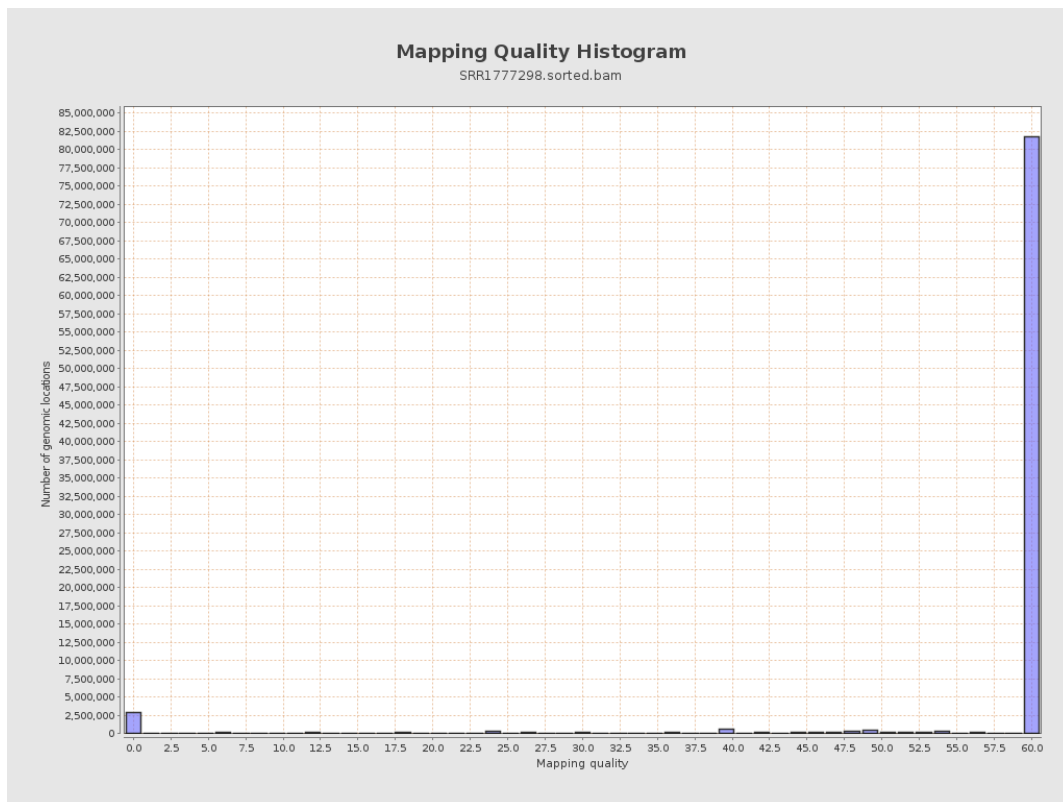
11. Results : Homopolymer Indels



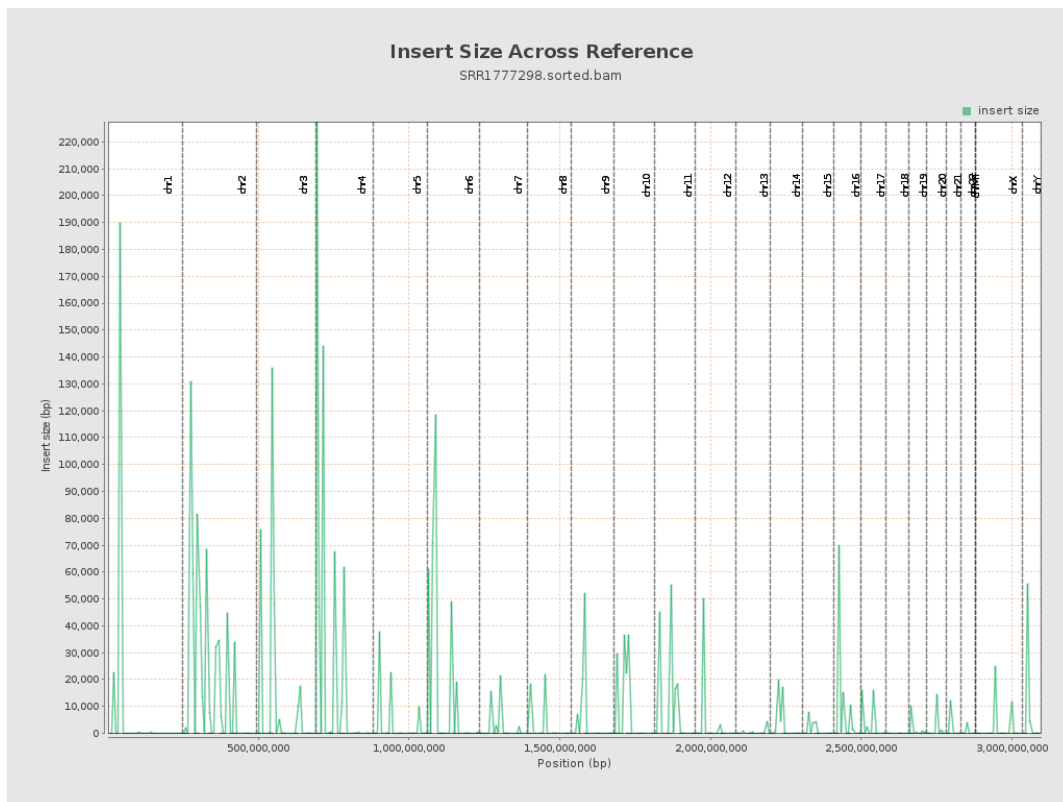
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

