

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/06 04:01:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777296.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_SRR1777296 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777296_1.fastq.gz SRR1777296_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 06 04:01:22 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777296.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,845,642
Mapped reads	1,820,540 / 98.64%
Unmapped reads	25,102 / 1.36%
Mapped paired reads	1,820,540 / 98.64%
Mapped reads, first in pair	912,424 / 49.44%
Mapped reads, second in pair	908,116 / 49.2%
Mapped reads, both in pair	1,811,722 / 98.16%
Mapped reads, singletons	8,818 / 0.48%
Secondary alignments	0
Supplementary alignments	54,331 / 2.94%
Read min/max/mean length	30 / 101 / 102.22
Duplicated reads (estimated)	119,191 / 6.46%
Duplication rate	4.94%
Clipped reads	374,815 / 20.31%

2.2. ACGT Content

Number/percentage of A's	52,125,337 / 29.17%
Number/percentage of C's	37,337,788 / 20.9%
Number/percentage of T's	51,142,879 / 28.62%
Number/percentage of G's	38,069,354 / 21.31%
Number/percentage of N's	3,076 / 0%

GC Percentage	42.2%
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2.3. Coverage

Mean	0.0577
Standard Deviation	0.7736

2.4. Mapping Quality

Mean Mapping Quality	53.31
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2.5. Insert size

Mean	166,990.87
Standard Deviation	3,931,586.96
P25/Median/P75	131 / 174 / 229

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	1,040,517
Insertions	36,155
Mapped reads with at least one insertion	1.93%
Deletions	25,018
Mapped reads with at least one deletion	1.33%
Homopolymer indels	44.16%

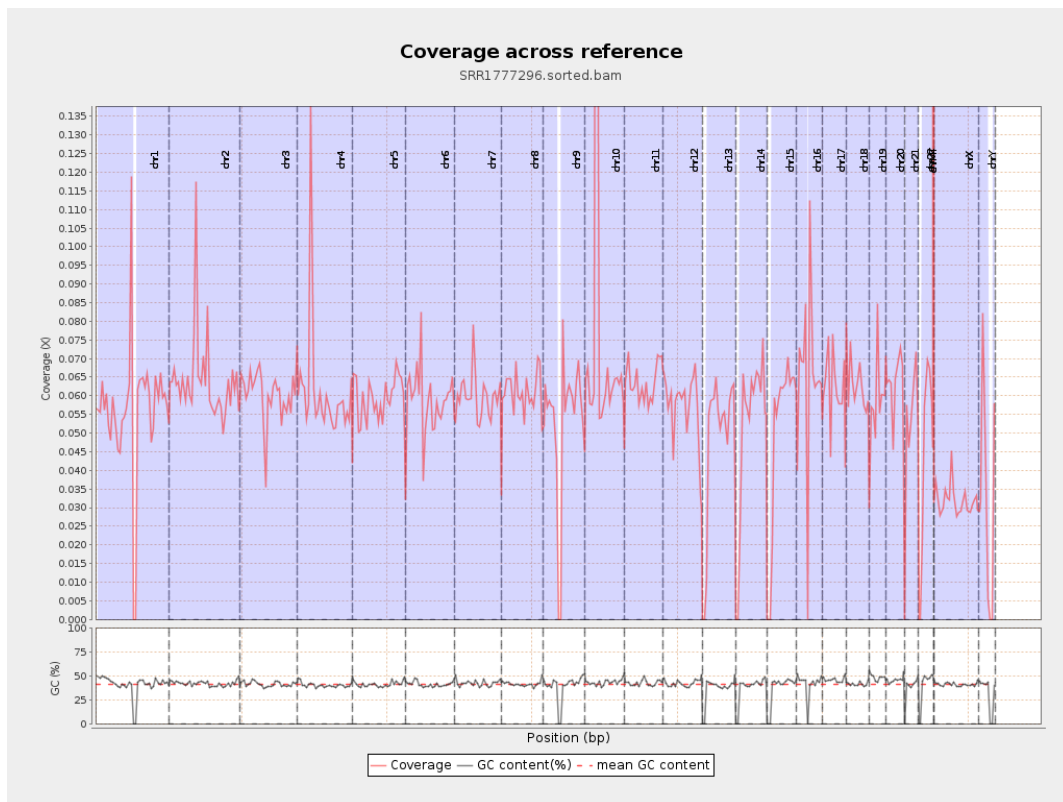
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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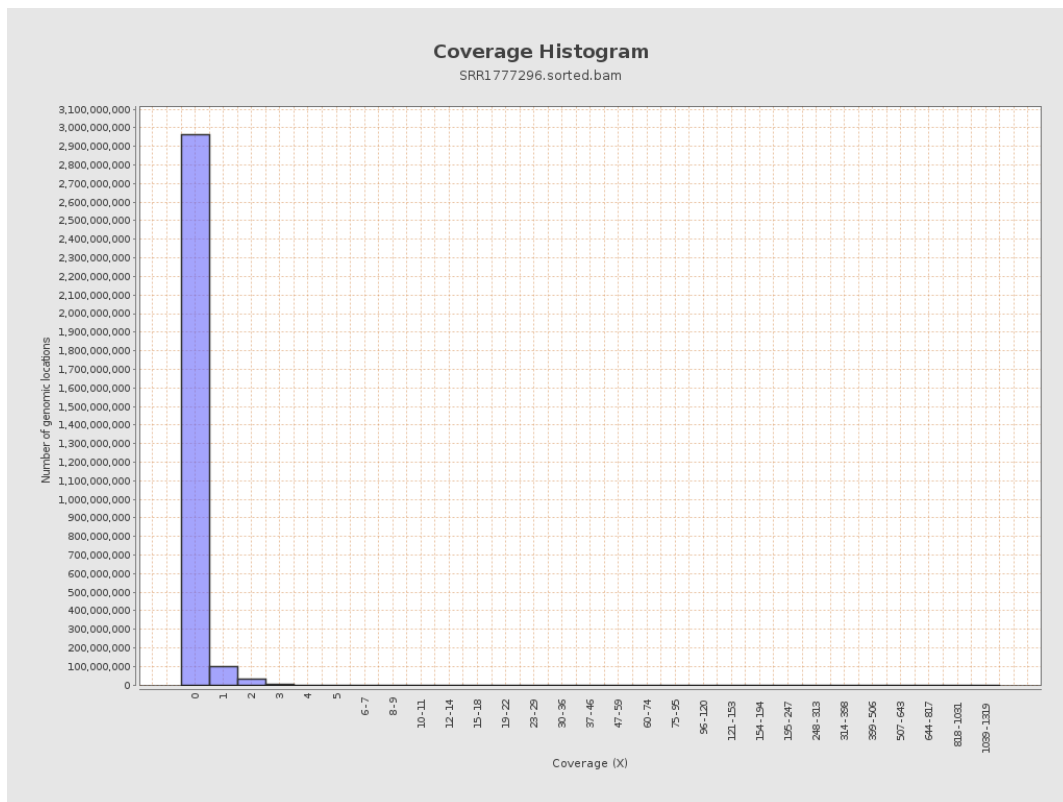
		bases	coverage	deviation
chr1	249250621	13923552	0.0559	1.2788
chr2	243199373	15598060	0.0641	0.5352
chr3	198022430	11919842	0.0602	0.3403
chr4	191154276	11600446	0.0607	0.6691
chr5	180915260	10714788	0.0592	0.3004
chr6	171115067	9989454	0.0584	0.4004
chr7	159138663	9543423	0.06	0.4819
chr8	146364022	8955930	0.0612	0.3755
chr9	141213431	7512679	0.0532	0.6539
chr10	135534747	10172452	0.0751	2.287
chr11	135006516	8530865	0.0632	0.3869
chr12	133851895	7671226	0.0573	0.2914
chr13	115169878	5474250	0.0475	0.2655
chr14	107349540	5522630	0.0514	0.2799
chr15	102531392	5162956	0.0504	0.2735
chr16	90354753	5846904	0.0647	0.5034
chr17	81195210	5036411	0.062	0.3989
chr18	78077248	4928876	0.0631	0.7946
chr19	59128983	3504166	0.0593	0.7186
chr20	63025520	3948663	0.0627	0.3393
chr21	48129895	2514654	0.0522	0.3877
chr22	51304566	2218658	0.0432	0.2547
chrMT	16571	1644750	99.2547	22.5425
chrX	155270560	4985253	0.0321	0.2453

chrY	59373566	1823576	0.0307	0.6643
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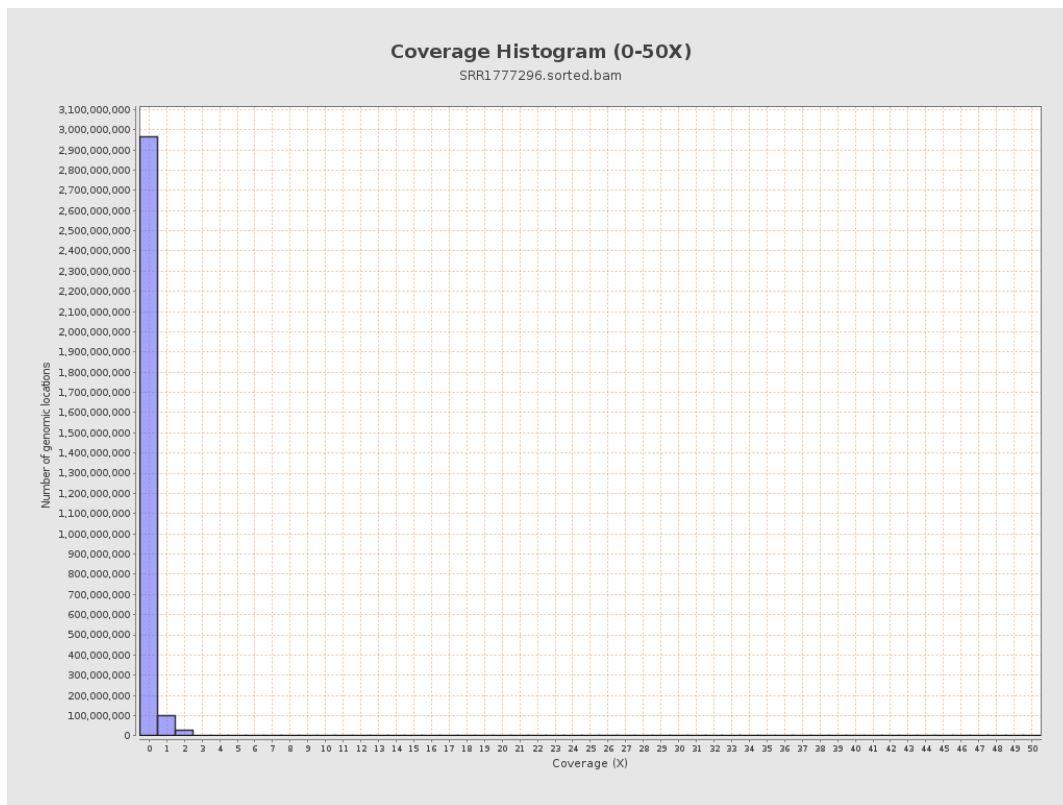
3. Results : Coverage across reference



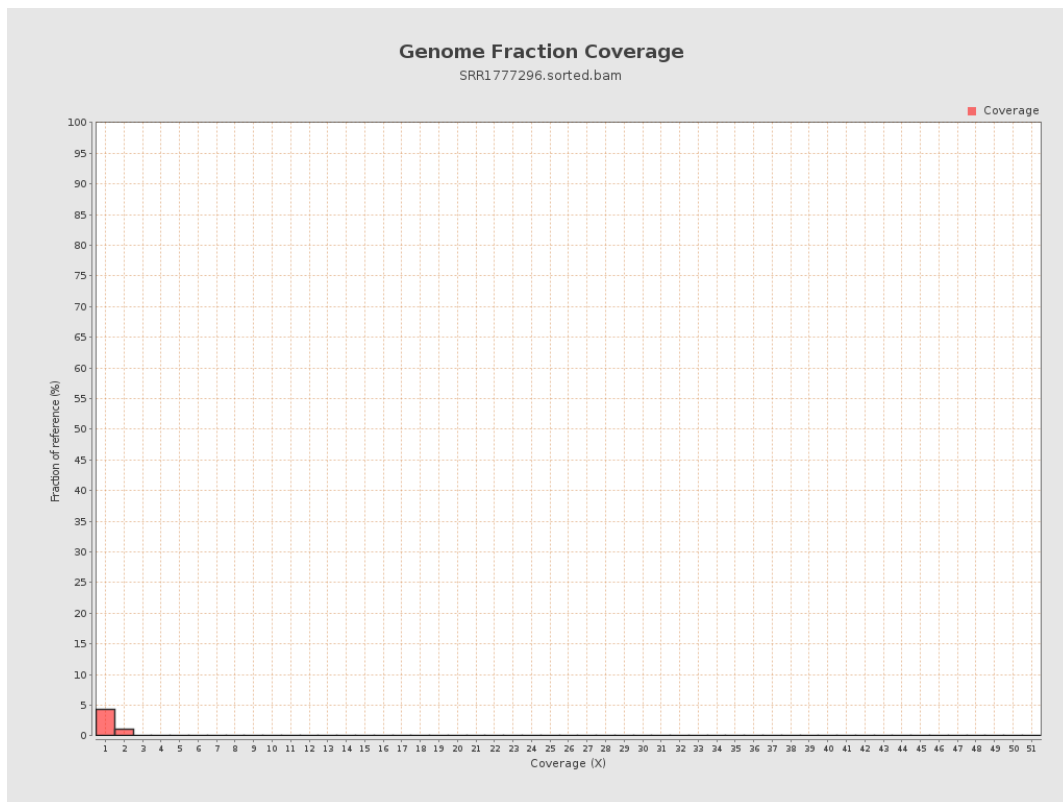
4. Results : Coverage Histogram



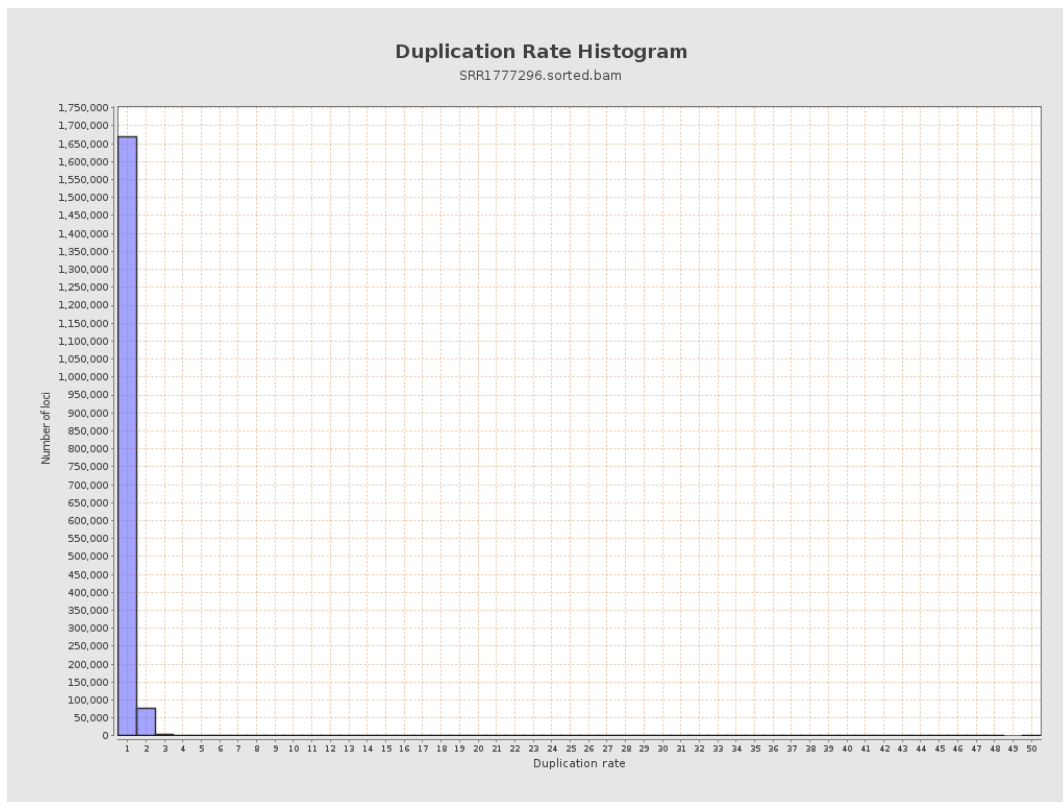
5. Results : Coverage Histogram (0-50X)



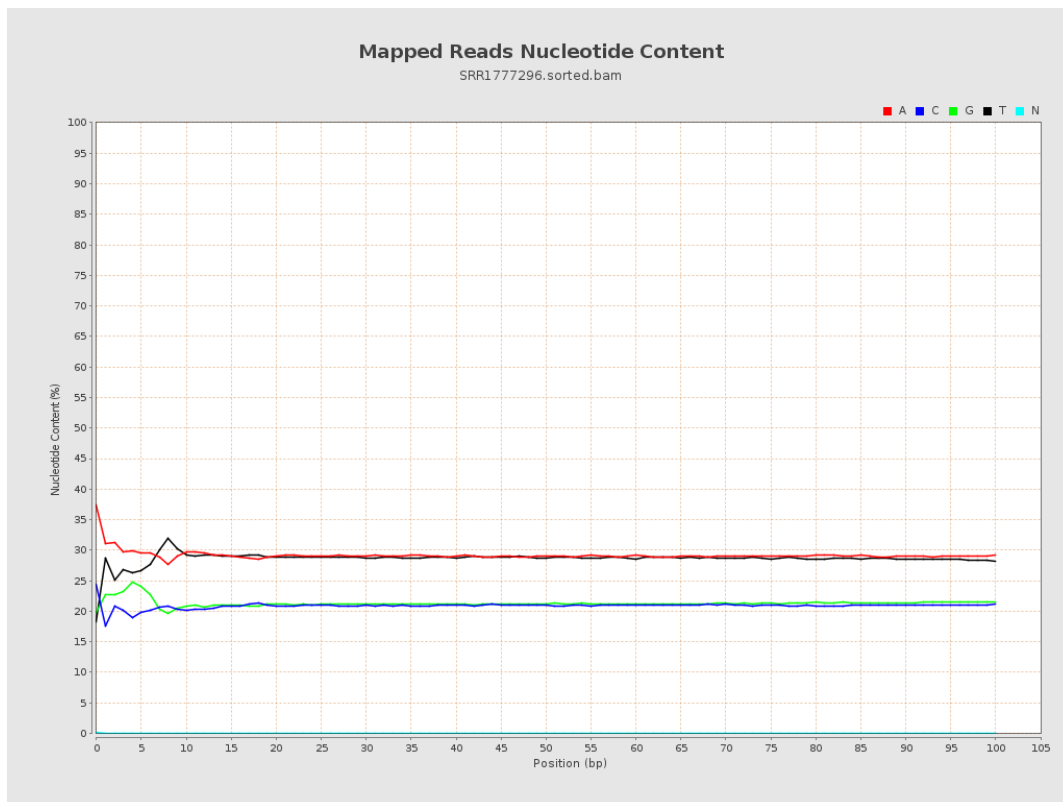
6. Results : Genome Fraction Coverage



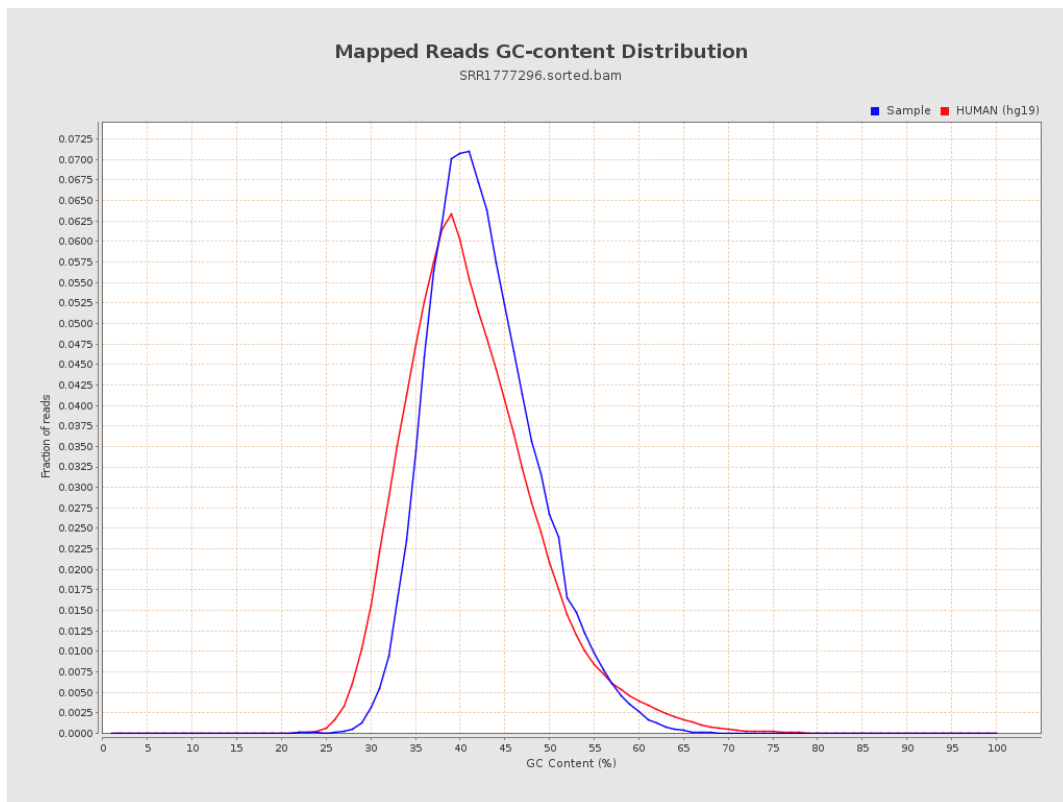
7. Results : Duplication Rate Histogram



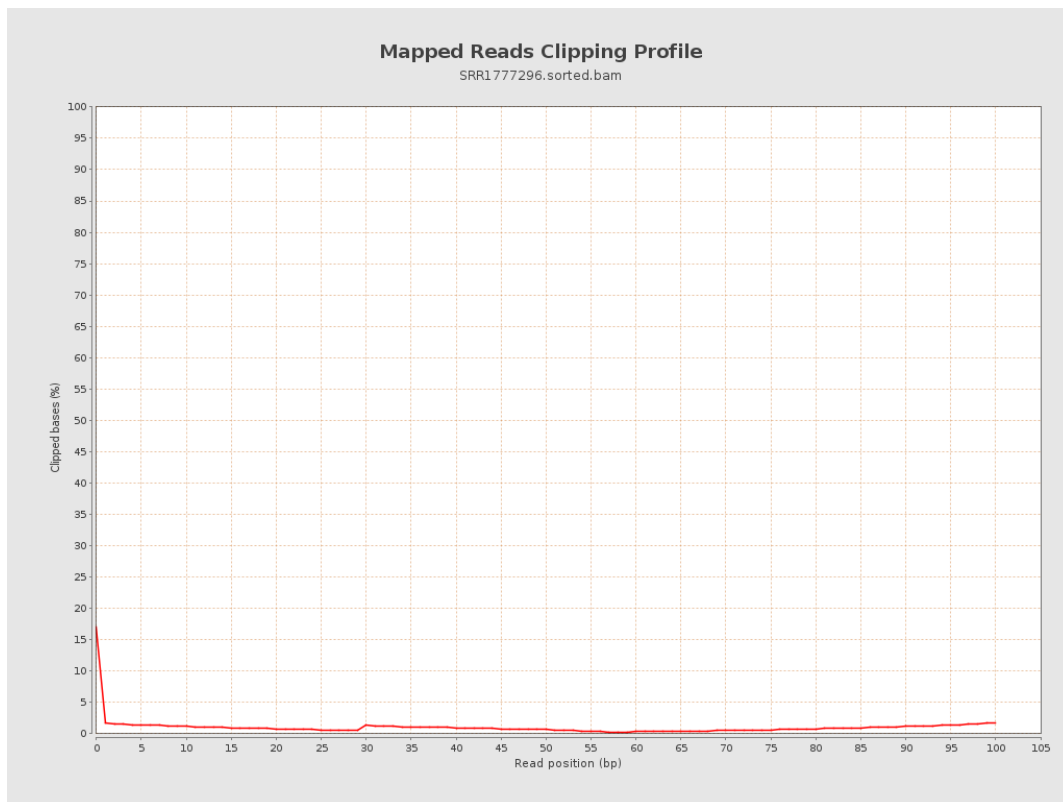
8. Results : Mapped Reads Nucleotide Content



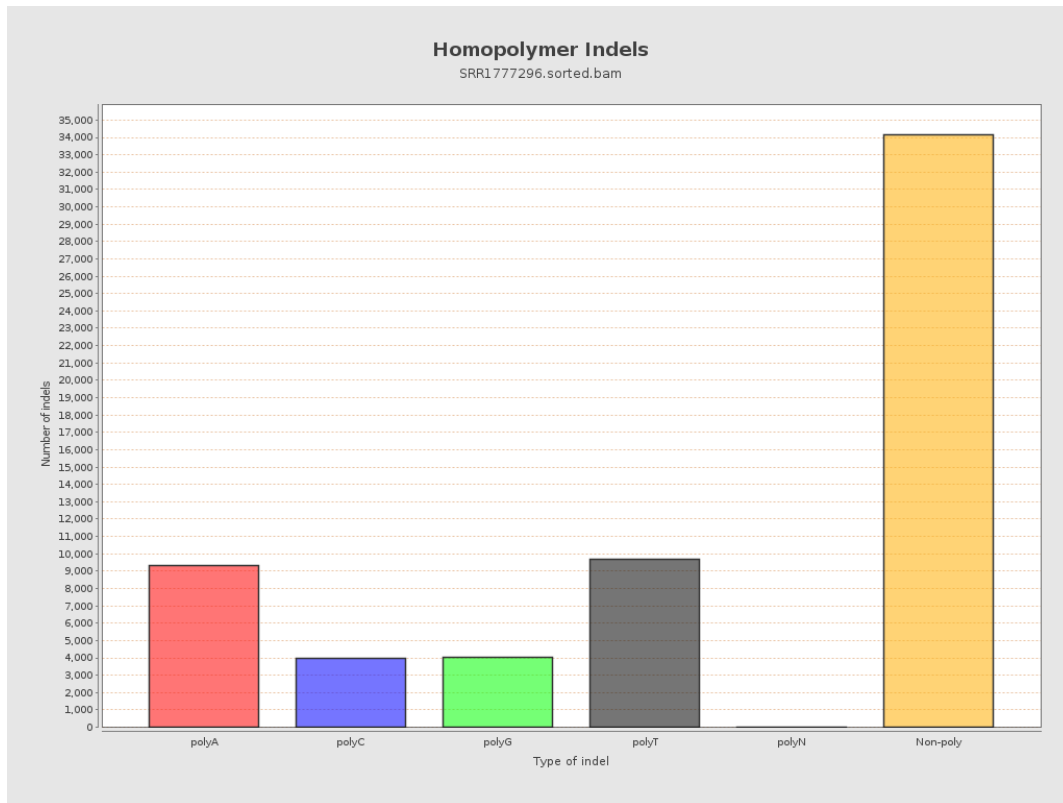
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



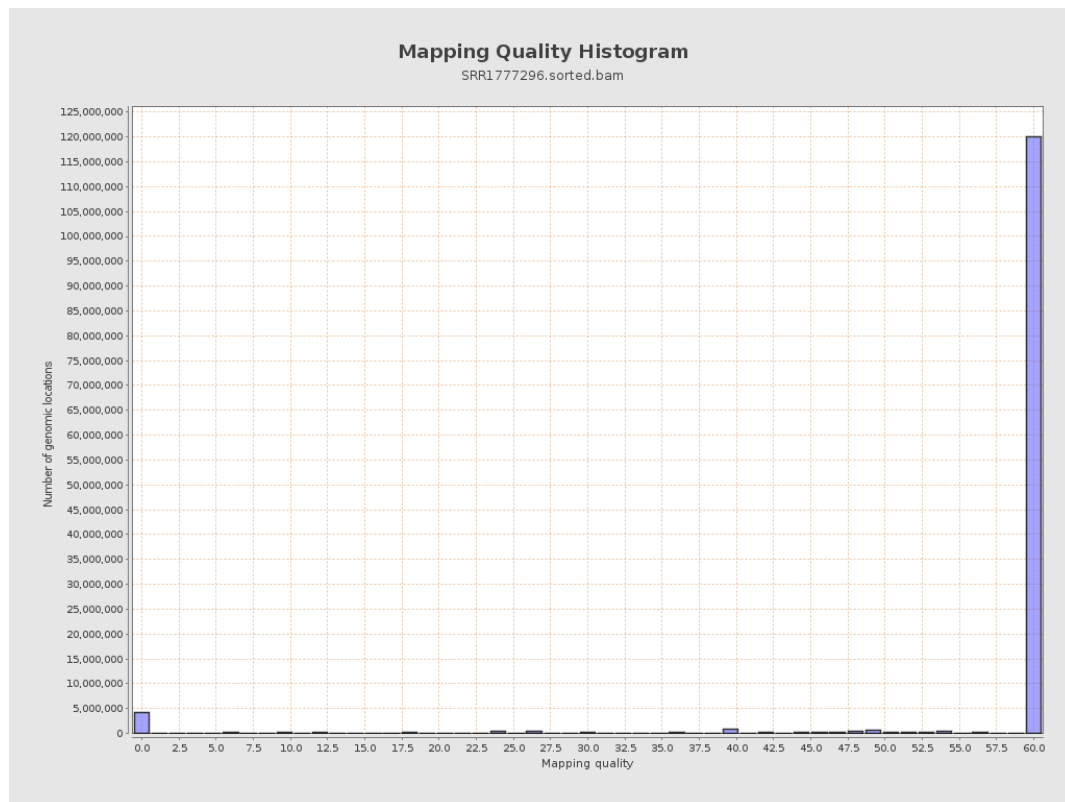
11. Results : Homopolymer Indels



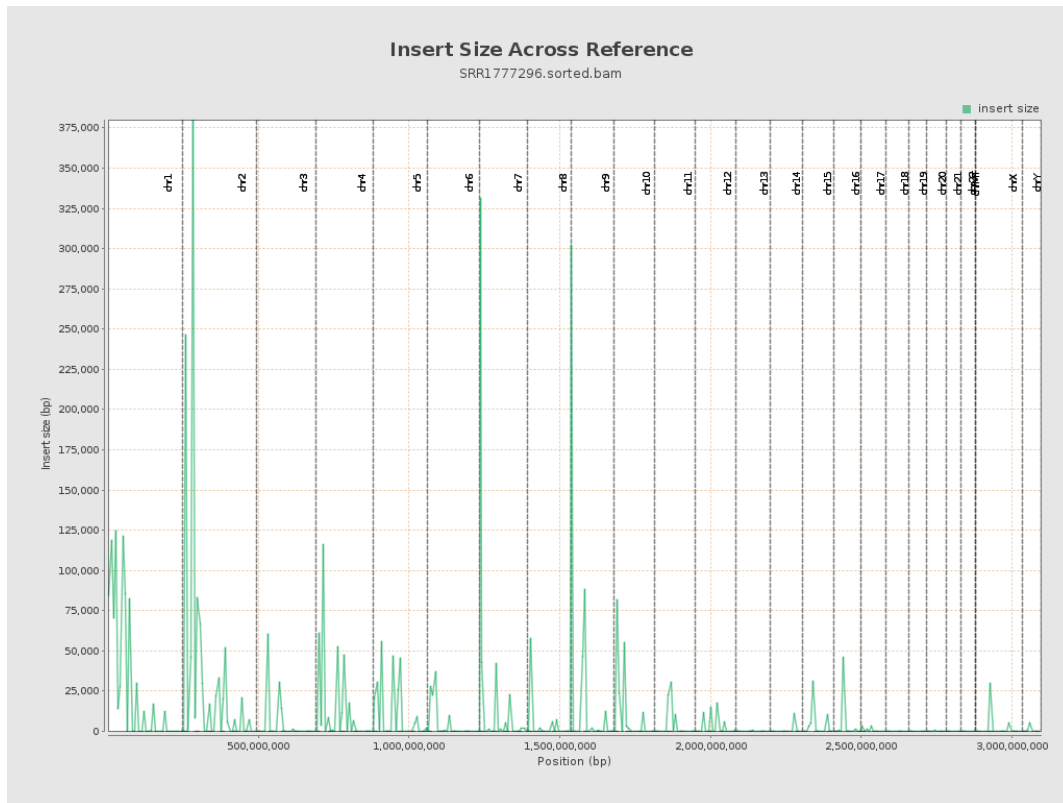
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

