

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 21:46:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777275.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_SRR1777275 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777275_1.fastq.gz SRR1777275_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 21:45:58 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777275.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	64,891,842
Mapped reads	64,764,106 / 99.8%
Unmapped reads	127,736 / 0.2%
Mapped paired reads	64,764,106 / 99.8%
Mapped reads, first in pair	32,386,622 / 49.91%
Mapped reads, second in pair	32,377,484 / 49.89%
Mapped reads, both in pair	64,734,908 / 99.76%
Mapped reads, singletons	29,198 / 0.04%
Secondary alignments	0
Supplementary alignments	227,006 / 0.35%
Read min/max/mean length	30 / 101 / 101.14
Duplicated reads (estimated)	38,880,050 / 59.92%
Duplication rate	48.25%
Clipped reads	4,342,628 / 6.69%

2.2. ACGT Content

Number/percentage of A's	1,563,215,540 / 24.25%
Number/percentage of C's	1,632,357,537 / 25.32%
Number/percentage of T's	1,567,230,507 / 24.31%
Number/percentage of G's	1,653,959,525 / 25.66%
Number/percentage of N's	30,086,738 / 0.47%

GC Percentage	50.98%
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2.3. Coverage

Mean	2.0836
Standard Deviation	28.8881

2.4. Mapping Quality

Mean Mapping Quality	55.02
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2.5. Insert size

Mean	131,839.67
Standard Deviation	3,710,285.99
P25/Median/P75	181 / 226 / 277

2.6. Mismatches and indels

General error rate	1.11%
Mismatches	70,780,817
Insertions	705,828
Mapped reads with at least one insertion	1.08%
Deletions	2,673,484
Mapped reads with at least one deletion	4.04%
Homopolymer indels	54.64%

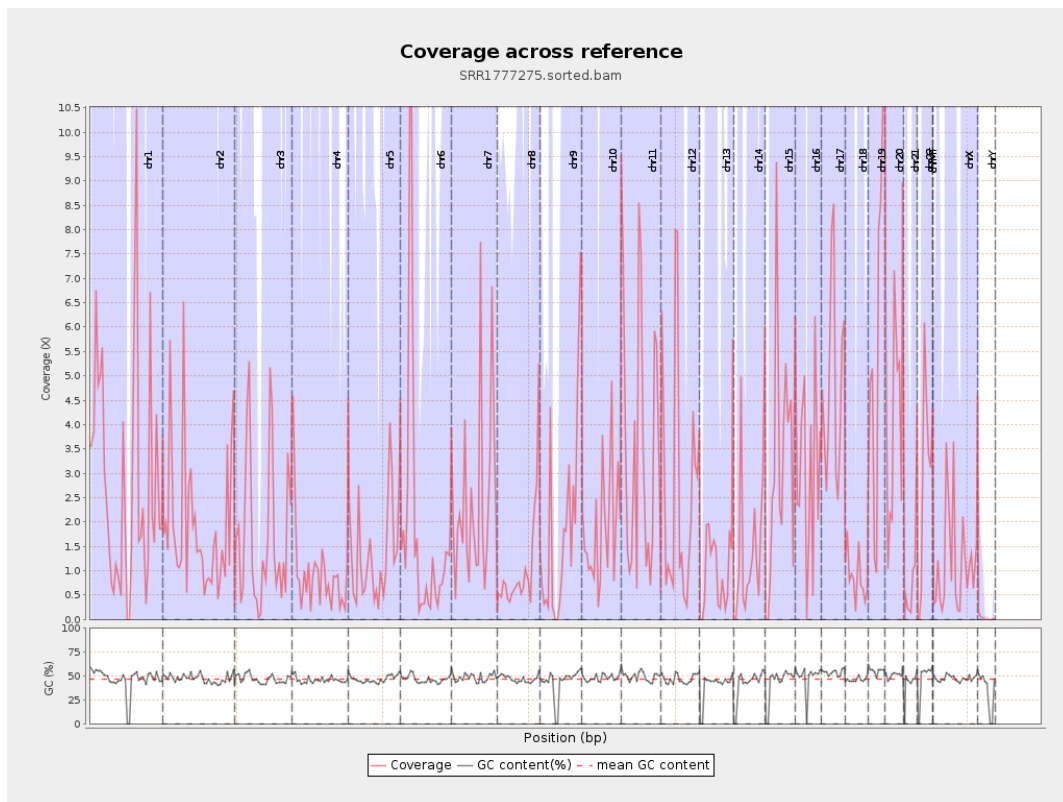
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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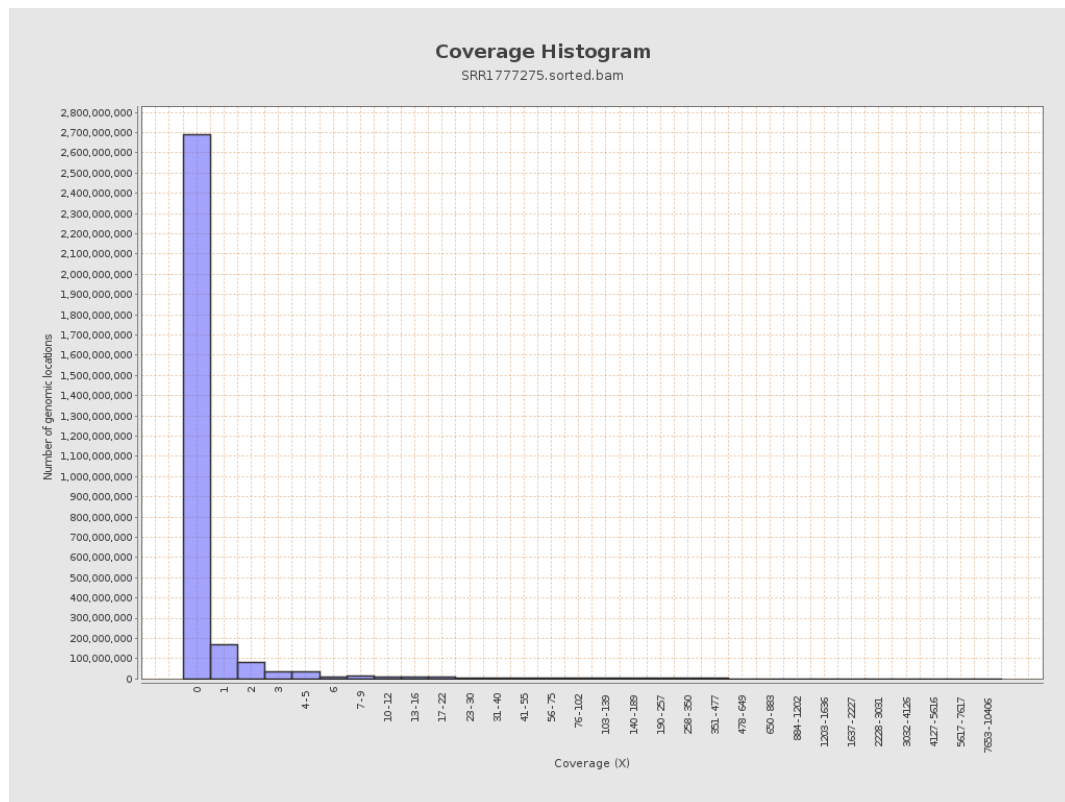
		bases	coverage	deviation
chr1	249250621	703138991	2.821	33.1917
chr2	243199373	461781247	1.8988	26.2067
chr3	198022430	342192976	1.7281	25.5742
chr4	191154276	177468317	0.9284	19.0332
chr5	180915260	261475910	1.4453	20.5153
chr6	171115067	303262460	1.7723	26.608
chr7	159138663	391845465	2.4623	33.6429
chr8	146364022	160943759	1.0996	18.8244
chr9	141213431	259698754	1.8391	26.021
chr10	135534747	258715123	1.9088	27.0657
chr11	135006516	476713600	3.531	39.5641
chr12	133851895	365863253	2.7333	36.2946
chr13	115169878	120260018	1.0442	20.1258
chr14	107349540	146188298	1.3618	20.424
chr15	102531392	312082865	3.0438	37.2026
chr16	90354753	278587445	3.0833	34.9881
chr17	81195210	385161929	4.7437	44.8853
chr18	78077248	67607828	0.8659	13.8212
chr19	59128983	341738710	5.7795	48.1735
chr20	63025520	257531564	4.0861	47.132
chr21	48129895	44808776	0.931	15.1126
chr22	51304566	145537828	2.8367	32.1809
chrMT	16571	50404	3.0417	3.7406
chrX	155270560	185923816	1.1974	20.2582

chrY	59373566	1671835	0.0282	1.1479
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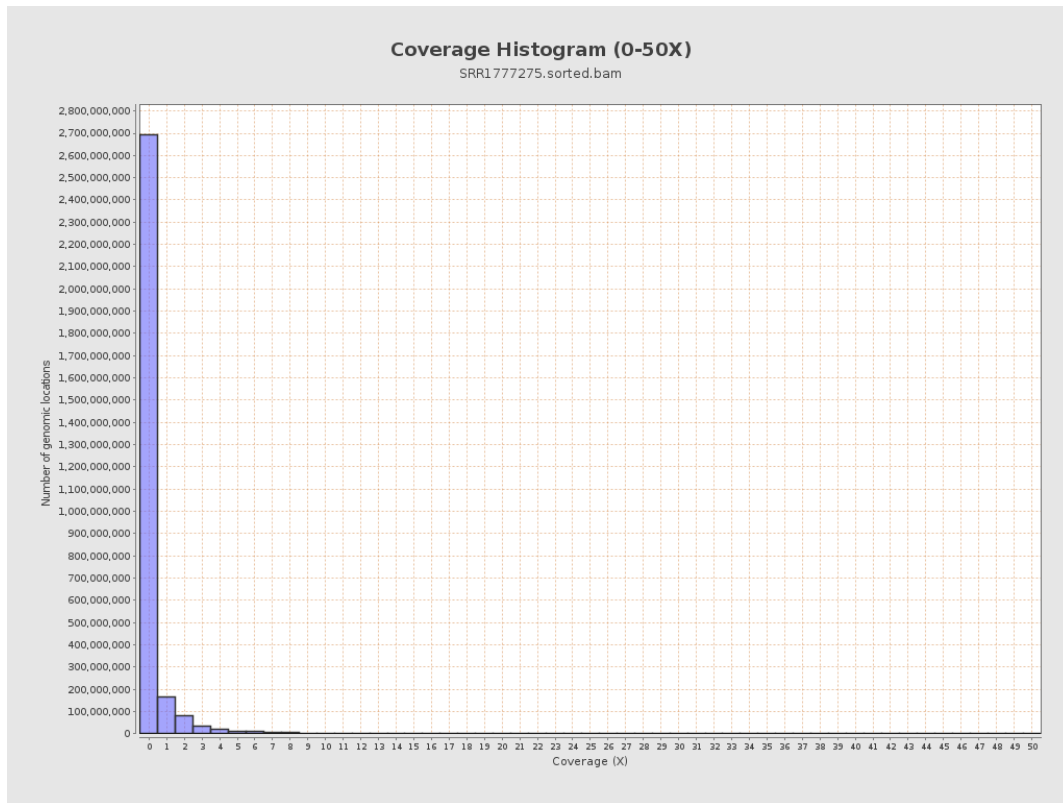
3. Results : Coverage across reference



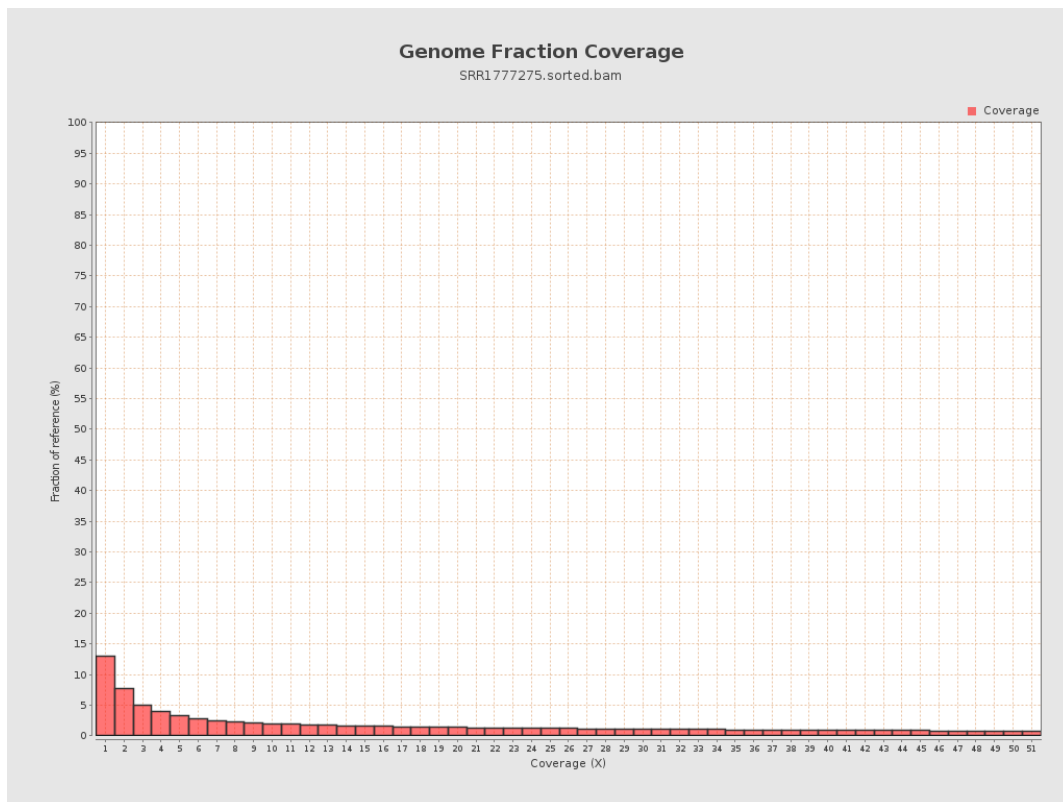
4. Results : Coverage Histogram



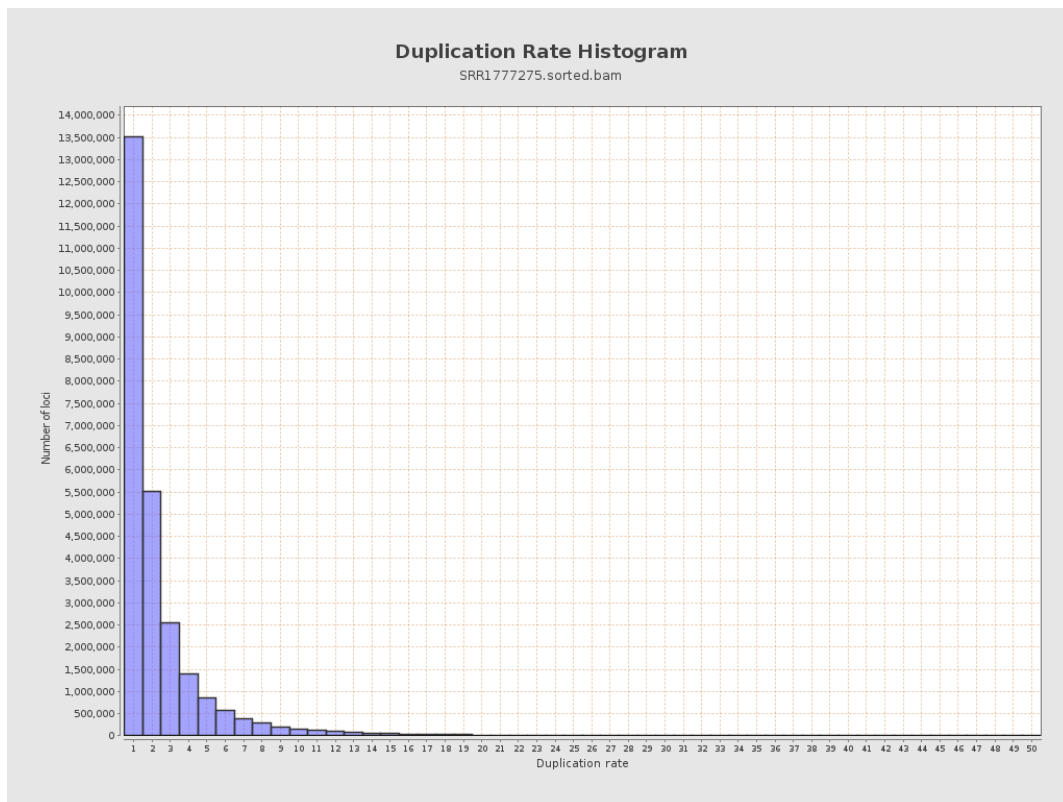
5. Results : Coverage Histogram (0-50X)



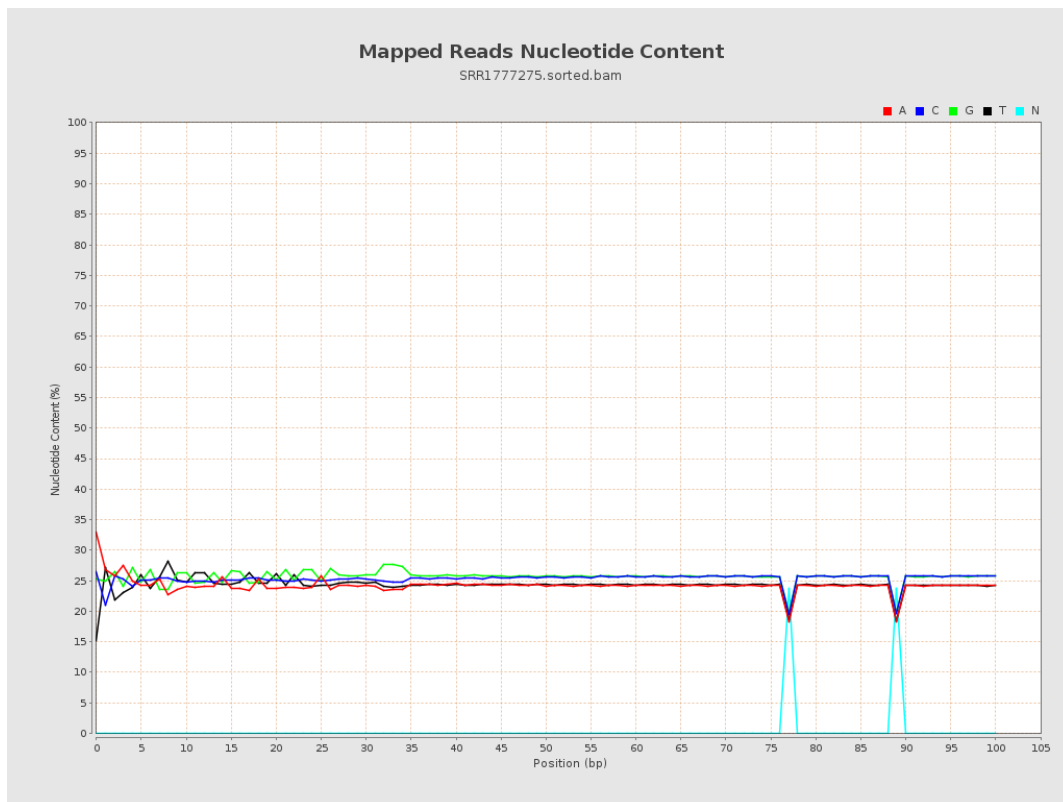
6. Results : Genome Fraction Coverage



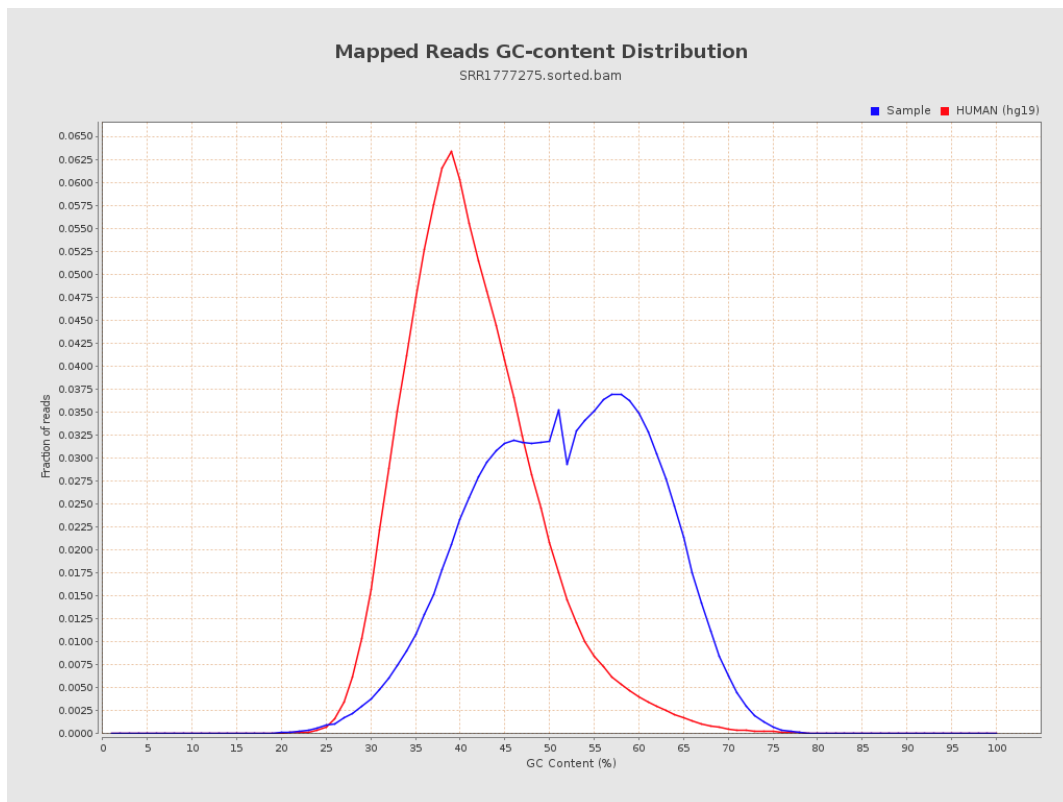
7. Results : Duplication Rate Histogram



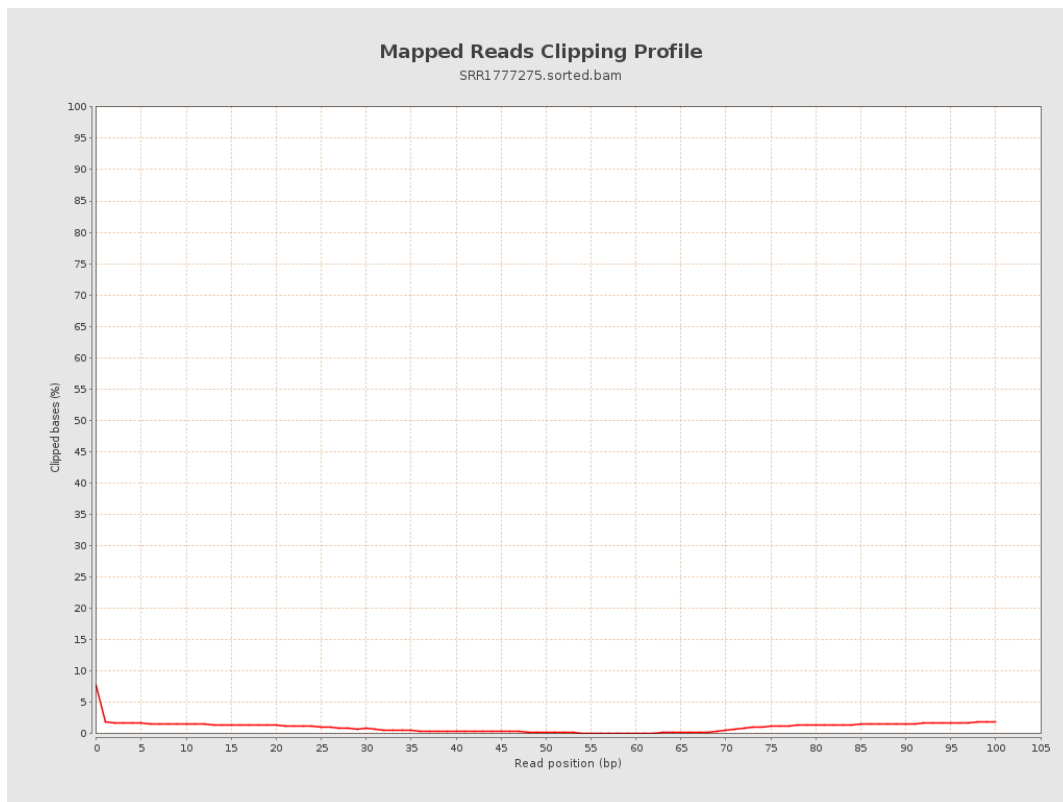
8. Results : Mapped Reads Nucleotide Content



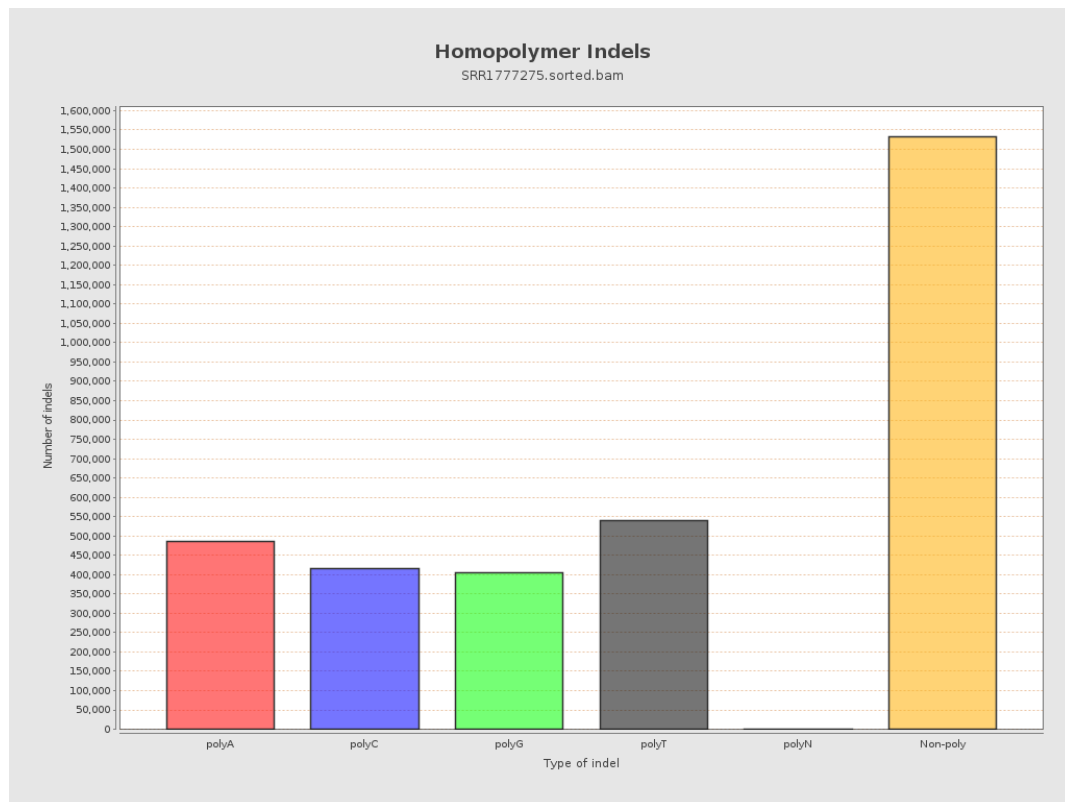
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



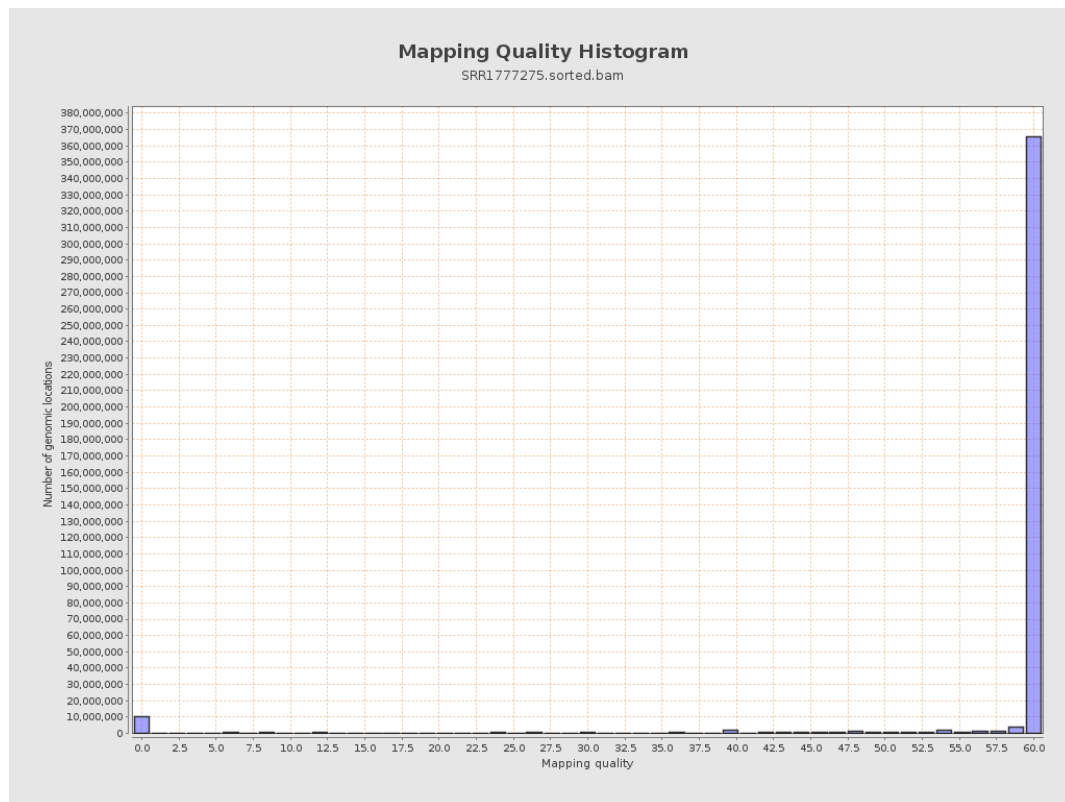
11. Results : Homopolymer Indels



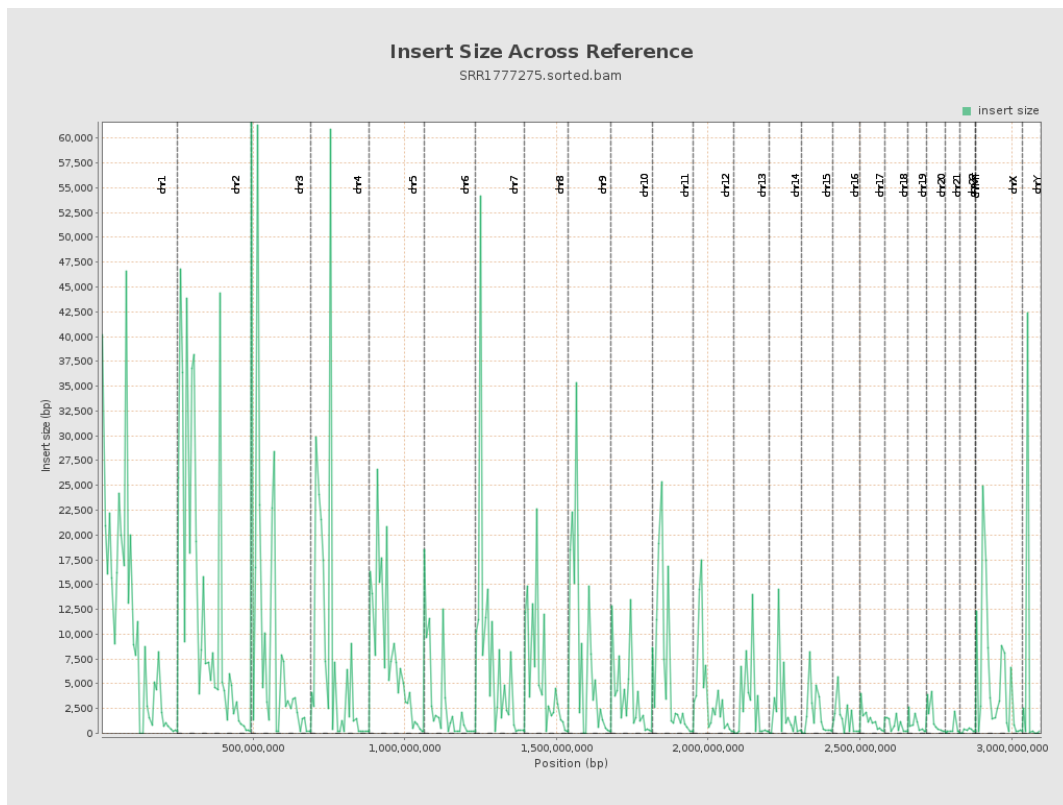
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

