

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 22:01:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779282.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_SRR1779282 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779282_1.fastq.gz SRR1779282_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 22:00:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779282.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,575,604
Mapped reads	8,367,231 / 97.57%
Unmapped reads	208,373 / 2.43%
Mapped paired reads	8,367,231 / 97.57%
Mapped reads, first in pair	4,215,710 / 49.16%
Mapped reads, second in pair	4,151,521 / 48.41%
Mapped reads, both in pair	8,292,232 / 96.7%
Mapped reads, singletons	74,999 / 0.87%
Secondary alignments	0
Supplementary alignments	18,243 / 0.21%
Read min/max/mean length	30 / 80 / 80.08
Duplicated reads (estimated)	78,376 / 0.91%
Duplication rate	0.85%
Clipped reads	272,942 / 3.18%

2.2. ACGT Content

Number/percentage of A's	203,260,124 / 30.53%
Number/percentage of C's	128,700,512 / 19.33%
Number/percentage of T's	202,926,475 / 30.48%
Number/percentage of G's	130,764,036 / 19.64%
Number/percentage of N's	124,648 / 0.02%

GC Percentage	38.97%
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2.3. Coverage

Mean	0.2151
Standard Deviation	0.6773

2.4. Mapping Quality

Mean Mapping Quality	53.14
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2.5. Insert size

Mean	43,535.17
Standard Deviation	1,968,118.77
P25/Median/P75	155 / 203 / 272

2.6. Mismatches and indels

General error rate	0.41%
Mismatches	2,622,944
Insertions	48,111
Mapped reads with at least one insertion	0.57%
Deletions	61,156
Mapped reads with at least one deletion	0.72%
Homopolymer indels	46.42%

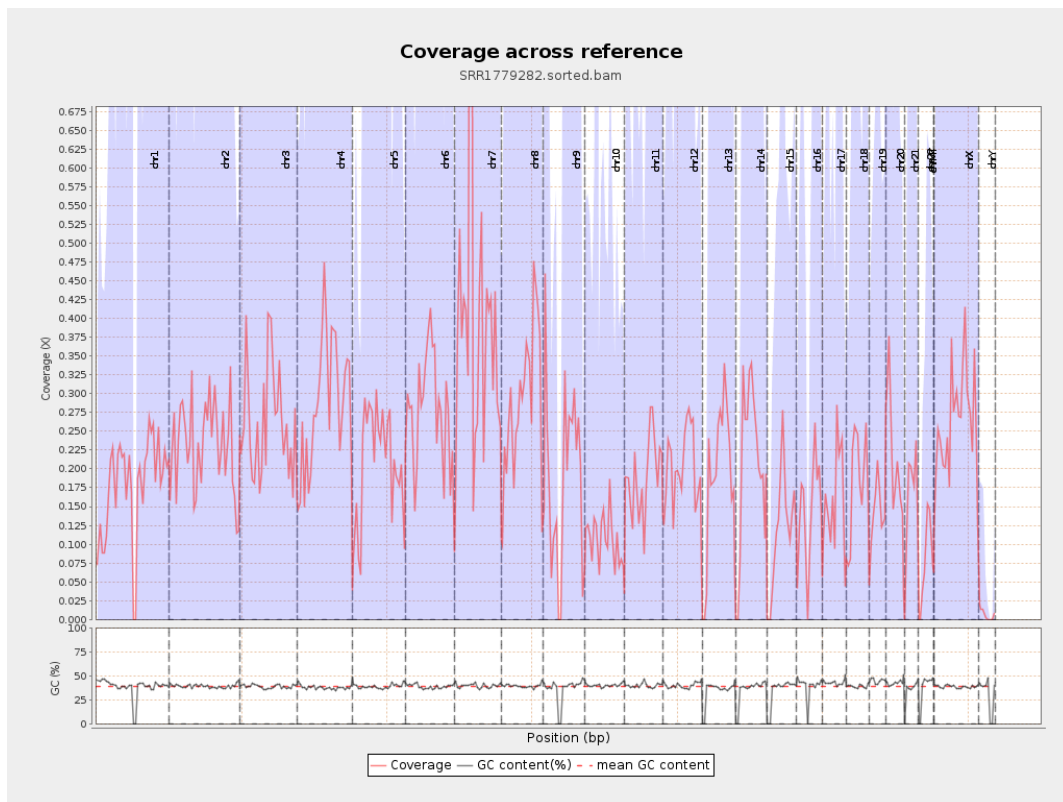
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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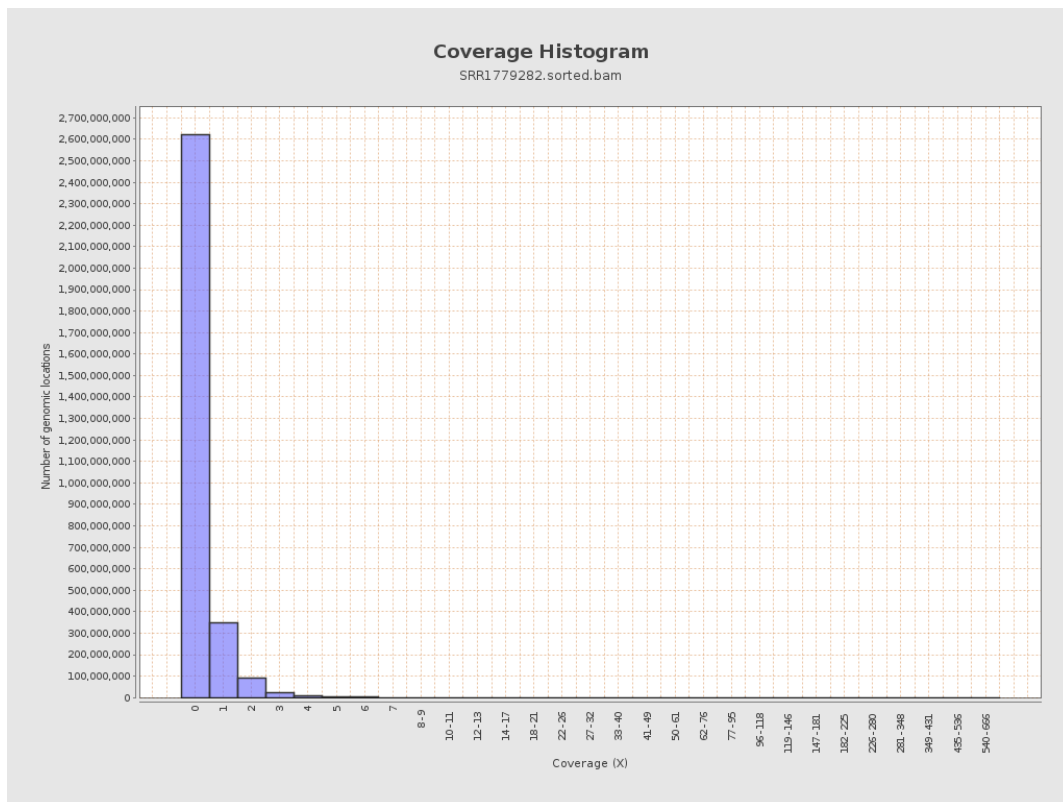
		bases	coverage	deviation
chr1	249250621	44232520	0.1775	0.8157
chr2	243199373	56382269	0.2318	0.6005
chr3	198022430	51835122	0.2618	0.6406
chr4	191154276	55362354	0.2896	0.6771
chr5	180915260	37658910	0.2082	0.5632
chr6	171115067	47629324	0.2783	0.6736
chr7	159138663	65571008	0.412	1.3284
chr8	146364022	42550183	0.2907	0.6845
chr9	141213431	26813289	0.1899	0.5676
chr10	135534747	14682503	0.1083	0.802
chr11	135006516	25438950	0.1884	0.5414
chr12	133851895	26850613	0.2006	0.5523
chr13	115169878	21794972	0.1892	0.5381
chr14	107349540	22209519	0.2069	0.5782
chr15	102531392	12249867	0.1195	0.4309
chr16	90354753	12969912	0.1435	0.4575
chr17	81195210	12613413	0.1553	0.5211
chr18	78077248	14049715	0.1799	0.534
chr19	59128983	8853666	0.1497	0.6124
chr20	63025520	13224743	0.2098	0.5789
chr21	48129895	7680044	0.1596	0.5043
chr22	51304566	4023796	0.0784	0.3426
chrMT	16571	1037	0.0626	0.2991
chrX	155270560	40828935	0.263	0.6661

chrY	59373566	396536	0.0067	0.108
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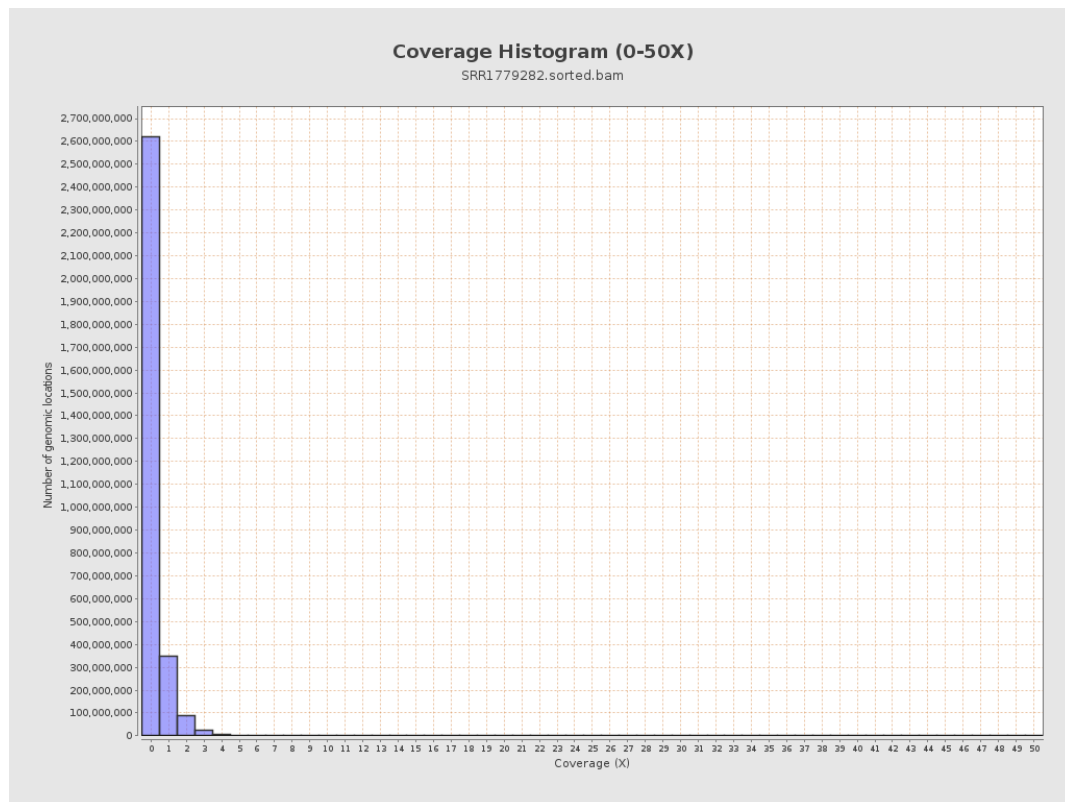
3. Results : Coverage across reference



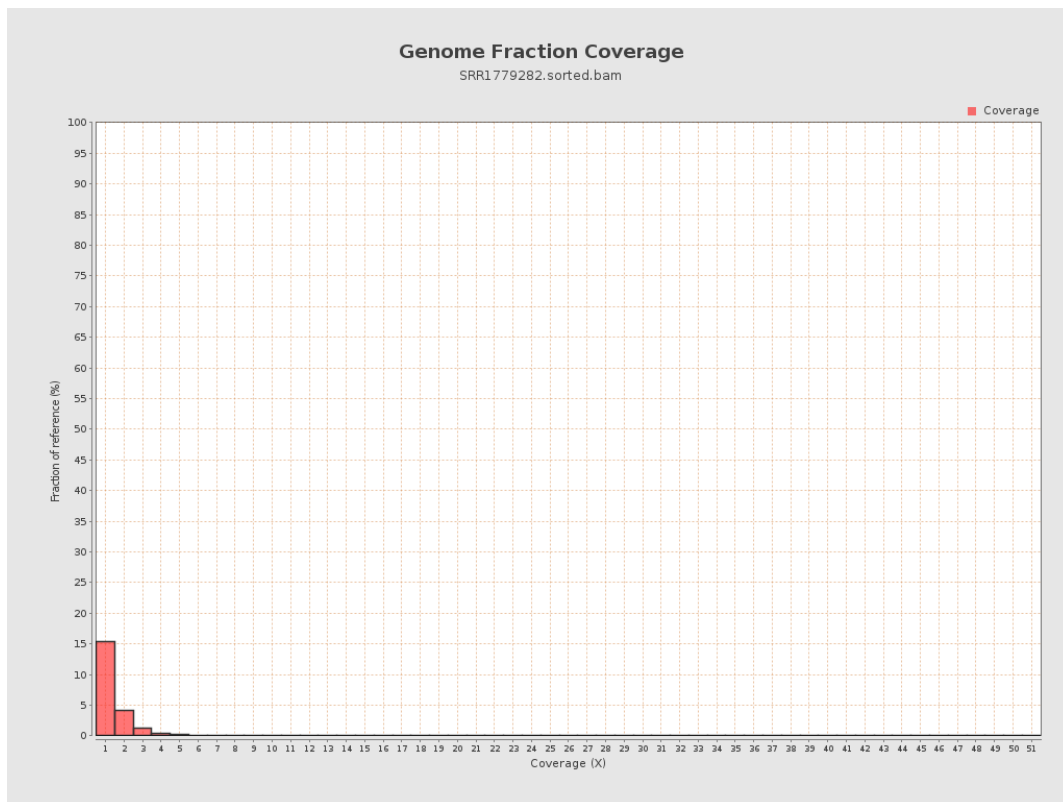
4. Results : Coverage Histogram



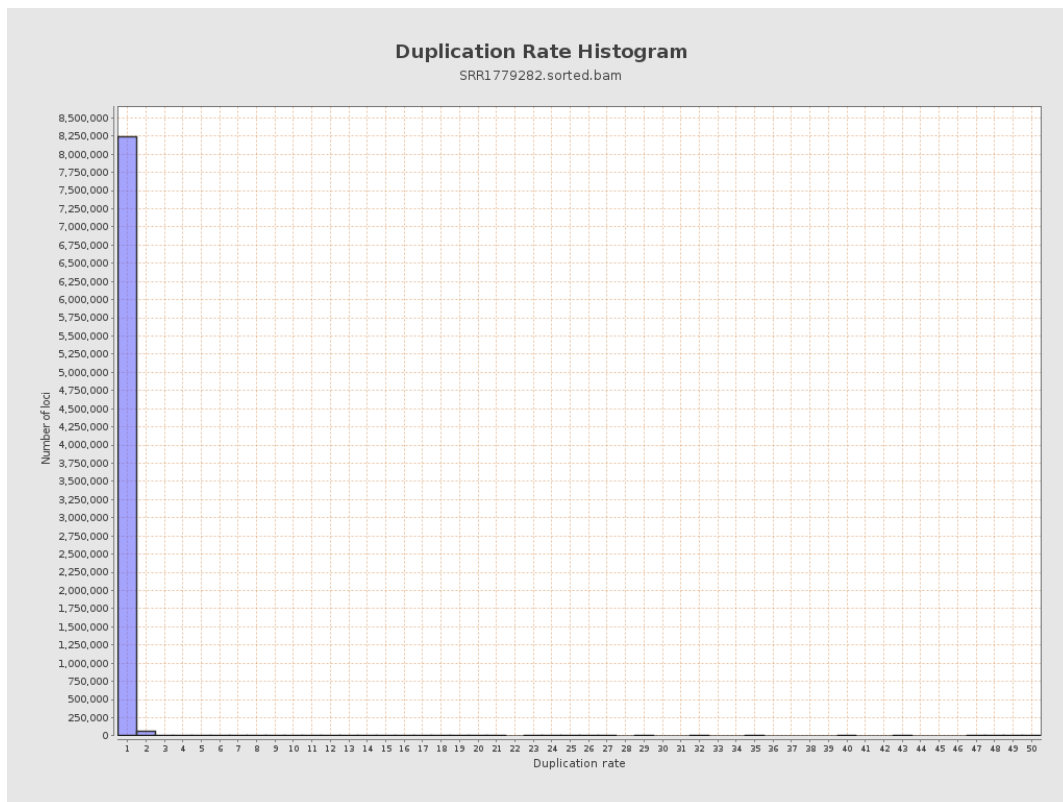
5. Results : Coverage Histogram (0-50X)



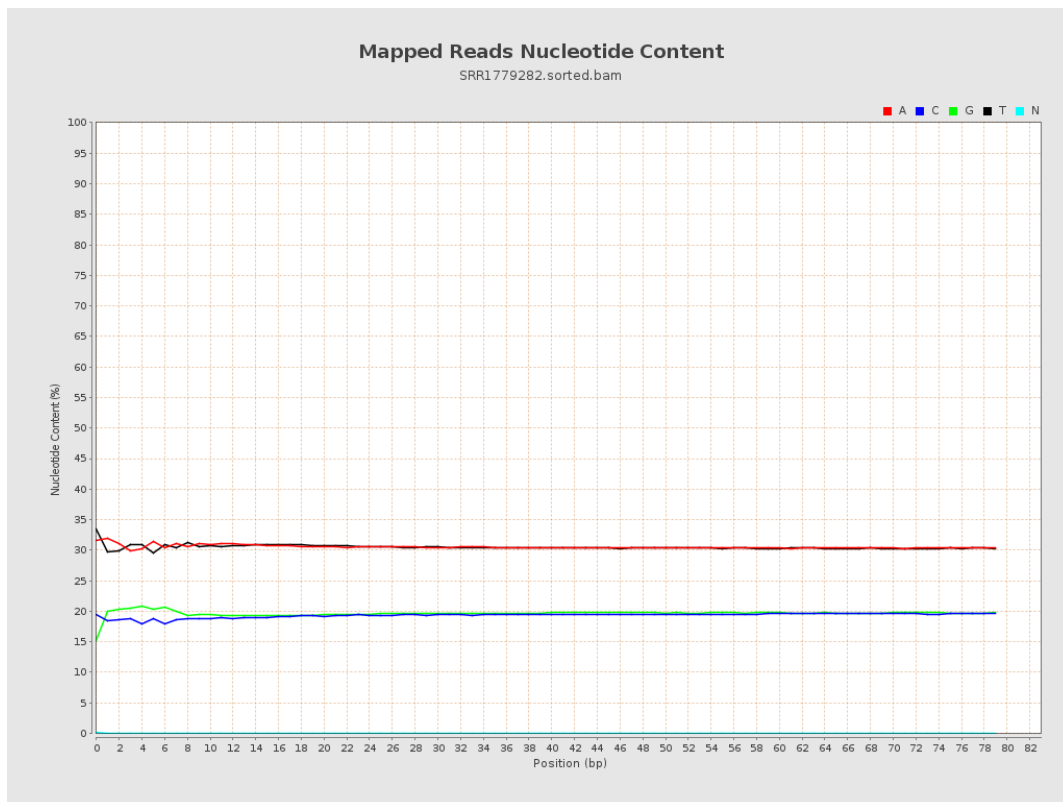
6. Results : Genome Fraction Coverage



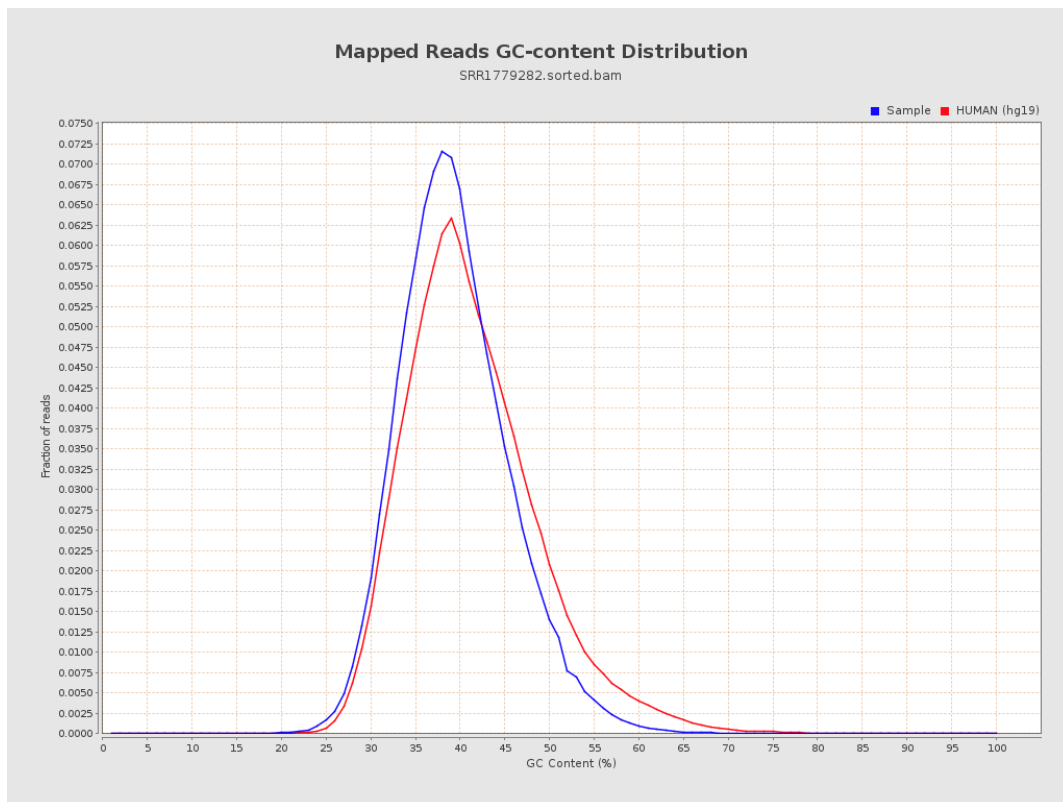
7. Results : Duplication Rate Histogram



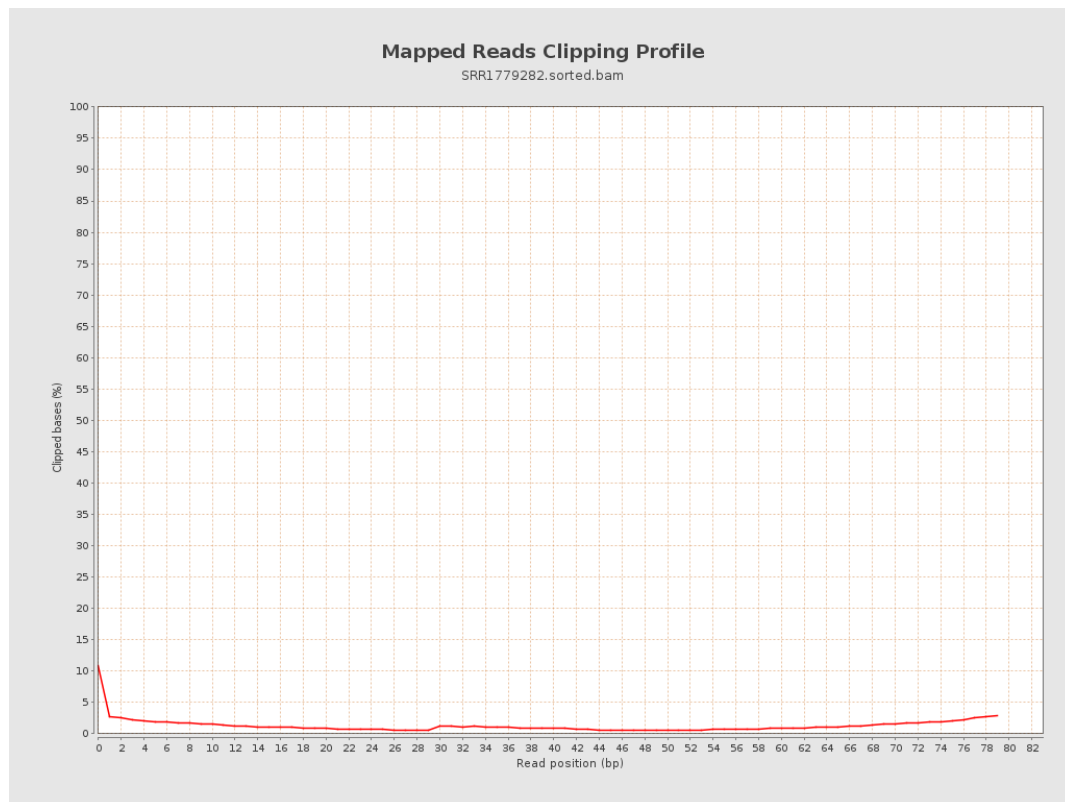
8. Results : Mapped Reads Nucleotide Content



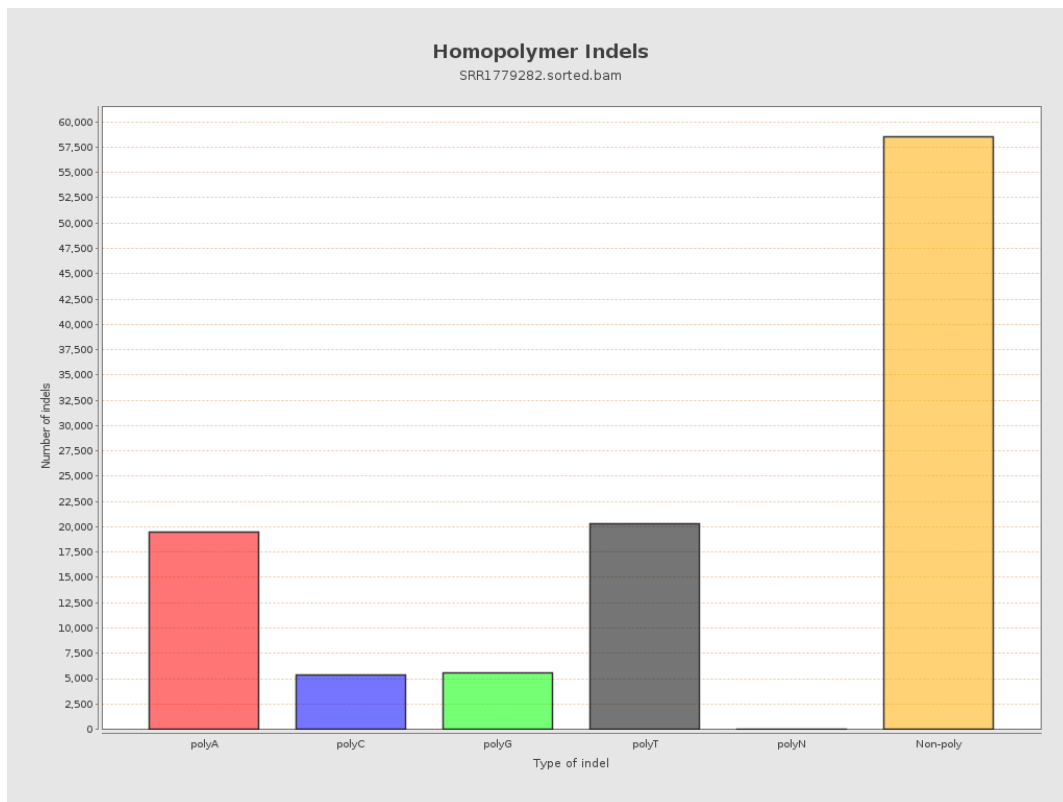
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



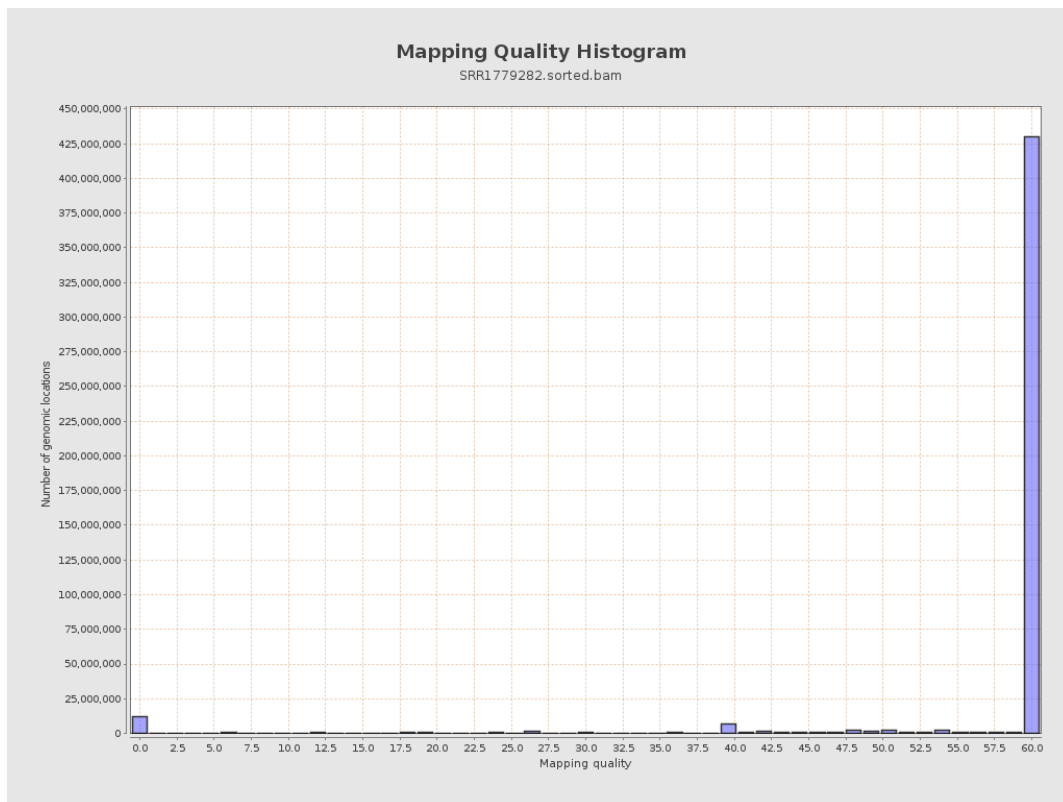
11. Results : Homopolymer Indels



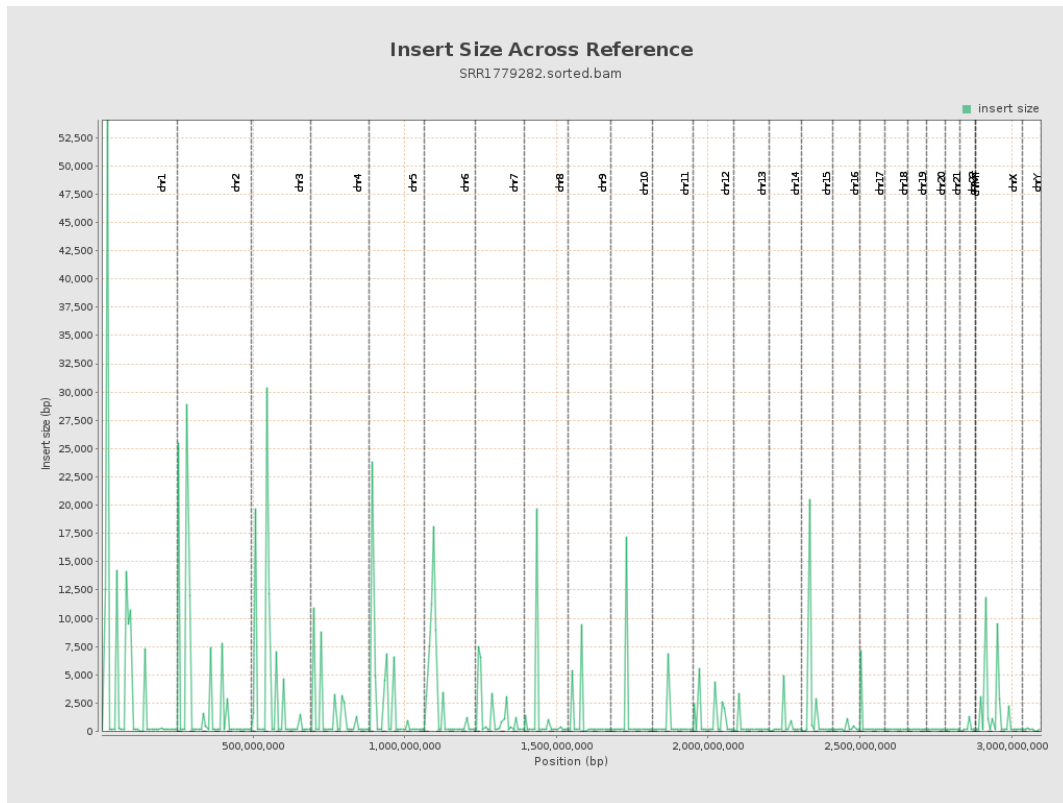
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

