

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 14:09:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779197.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_SRR1779197 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779197_1.fastq.gz SRR1779197_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 14:09:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779197.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,108,294
Mapped reads	10,805,296 / 97.27%
Unmapped reads	302,998 / 2.73%
Mapped paired reads	10,805,296 / 97.27%
Mapped reads, first in pair	5,450,518 / 49.07%
Mapped reads, second in pair	5,354,778 / 48.21%
Mapped reads, both in pair	10,694,978 / 96.28%
Mapped reads, singletons	110,318 / 0.99%
Secondary alignments	0
Supplementary alignments	27,563 / 0.25%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	149,330 / 1.34%
Duplication rate	1.29%
Clipped reads	359,153 / 3.23%

2.2. ACGT Content

Number/percentage of A's	262,542,575 / 30.54%
Number/percentage of C's	166,292,943 / 19.34%
Number/percentage of T's	261,897,412 / 30.46%
Number/percentage of G's	168,902,943 / 19.64%
Number/percentage of N's	162,014 / 0.02%

GC Percentage	38.99%
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2.3. Coverage

Mean	0.2778
Standard Deviation	0.8687

2.4. Mapping Quality

Mean Mapping Quality	52.9
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2.5. Insert size

Mean	45,110.88
Standard Deviation	1,945,830.35
P25/Median/P75	163 / 210 / 275

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	3,301,000
Insertions	62,443
Mapped reads with at least one insertion	0.57%
Deletions	77,690
Mapped reads with at least one deletion	0.71%
Homopolymer indels	46.97%

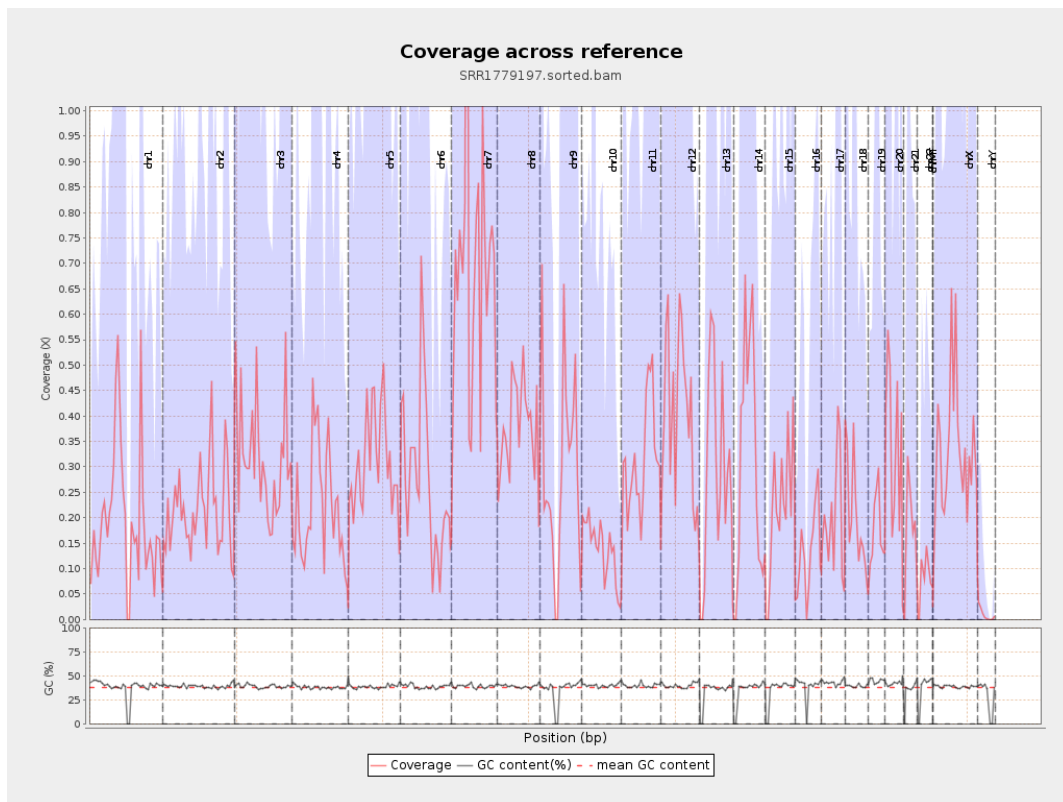
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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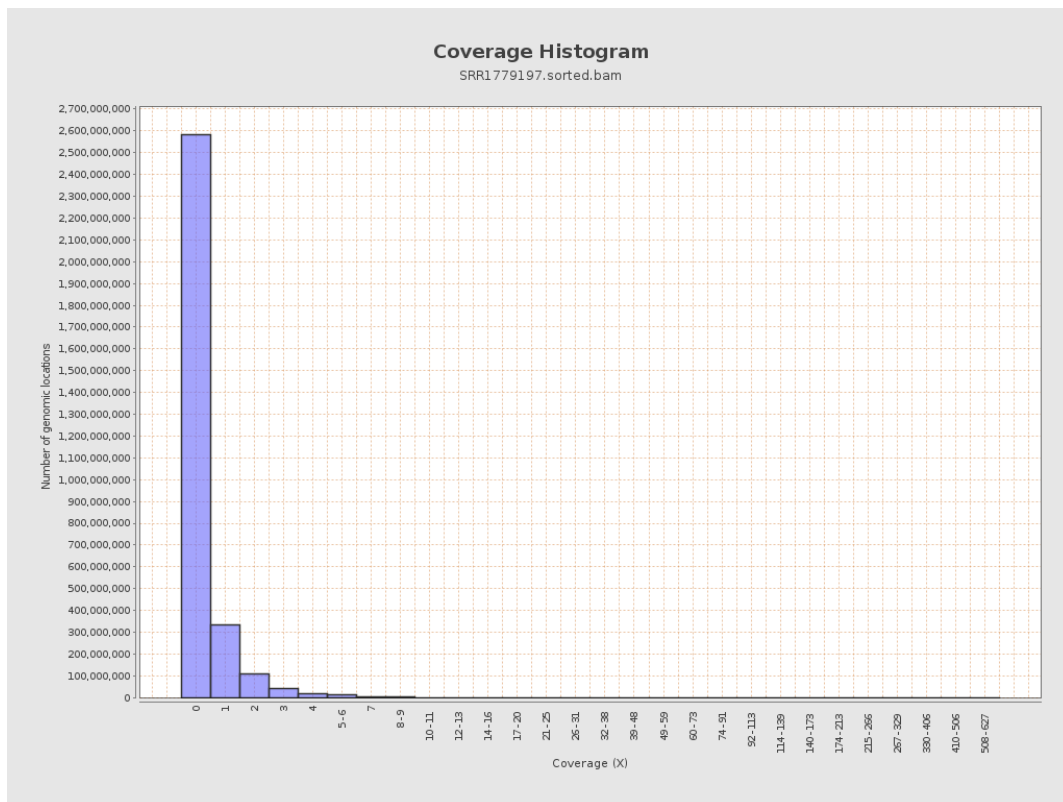
		bases	coverage	deviation
chr1	249250621	47472178	0.1905	0.6769
chr2	243199373	52078927	0.2141	0.6677
chr3	198022430	62817483	0.3172	0.8172
chr4	191154276	41917166	0.2193	0.6817
chr5	180915260	55486145	0.3067	0.8285
chr6	171115067	46852047	0.2738	0.8089
chr7	159138663	111910039	0.7032	1.7418
chr8	146364022	55029710	0.376	0.8924
chr9	141213431	41310309	0.2925	0.8393
chr10	135534747	19164330	0.1414	1.0984
chr11	135006516	42276813	0.3131	0.8335
chr12	133851895	53879729	0.4025	0.9403
chr13	115169878	32946163	0.2861	0.7937
chr14	107349540	33520476	0.3123	0.9035
chr15	102531392	22628689	0.2207	0.6968
chr16	90354753	11377334	0.1259	0.4833
chr17	81195210	16557602	0.2039	0.6305
chr18	78077248	15944426	0.2042	0.6991
chr19	59128983	10442684	0.1766	0.6168
chr20	63025520	21782060	0.3456	0.8614
chr21	48129895	8285069	0.1721	0.6304
chr22	51304566	4155573	0.081	0.3666
chrMT	16571	408	0.0246	0.2014
chrX	155270560	51602020	0.3323	0.9258

chrY	59373566	521298	0.0088	0.1456
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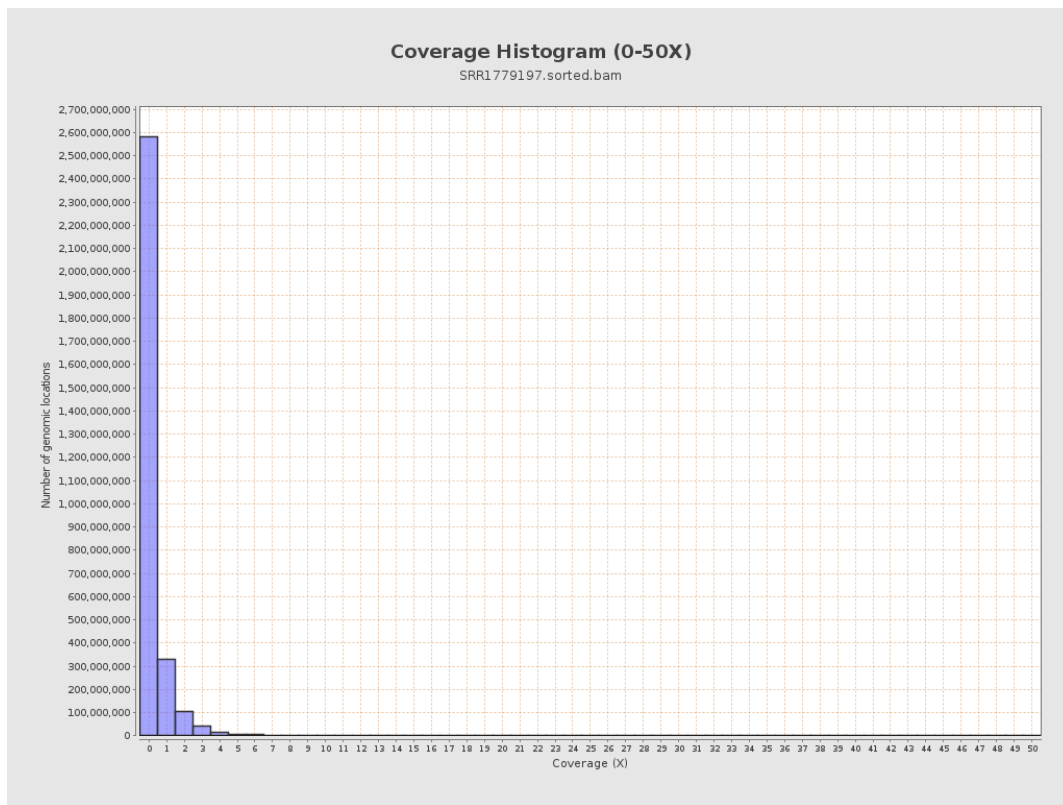
3. Results : Coverage across reference



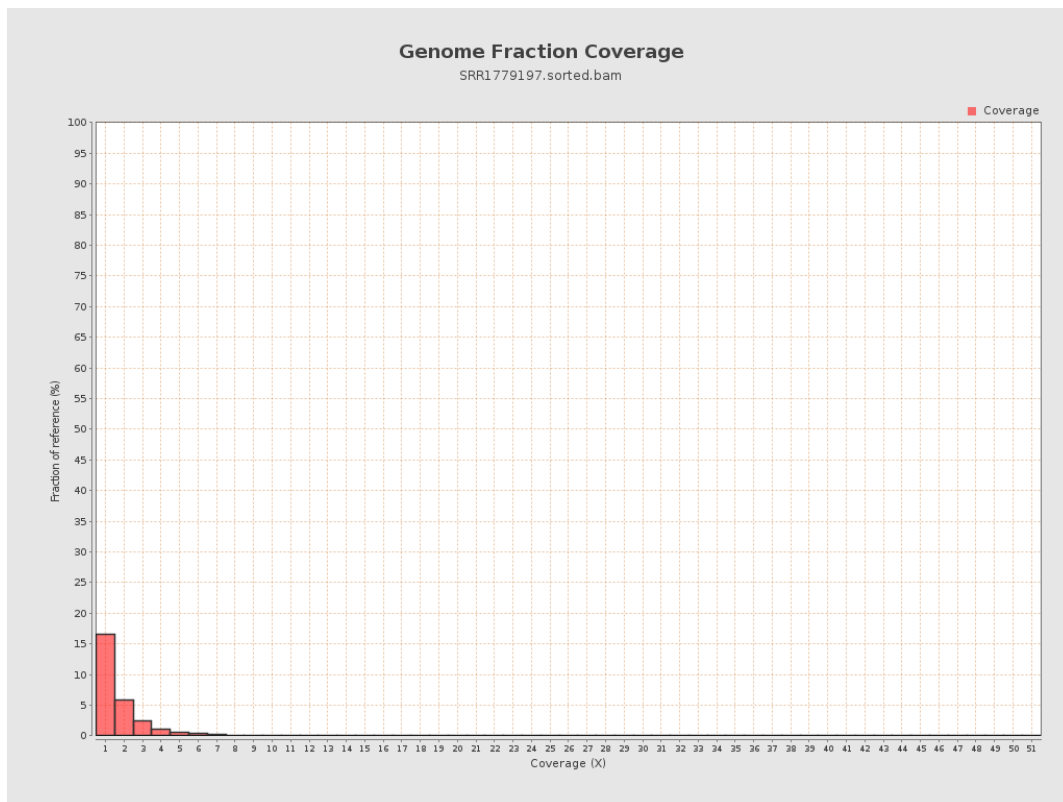
4. Results : Coverage Histogram



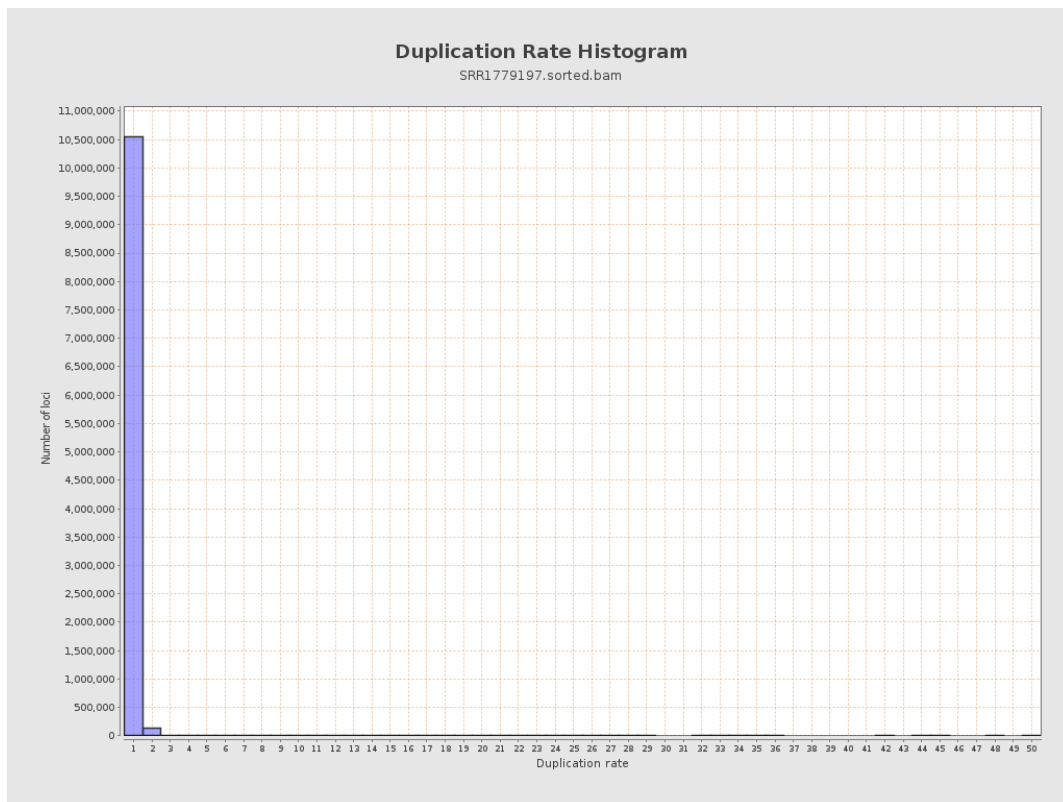
5. Results : Coverage Histogram (0-50X)



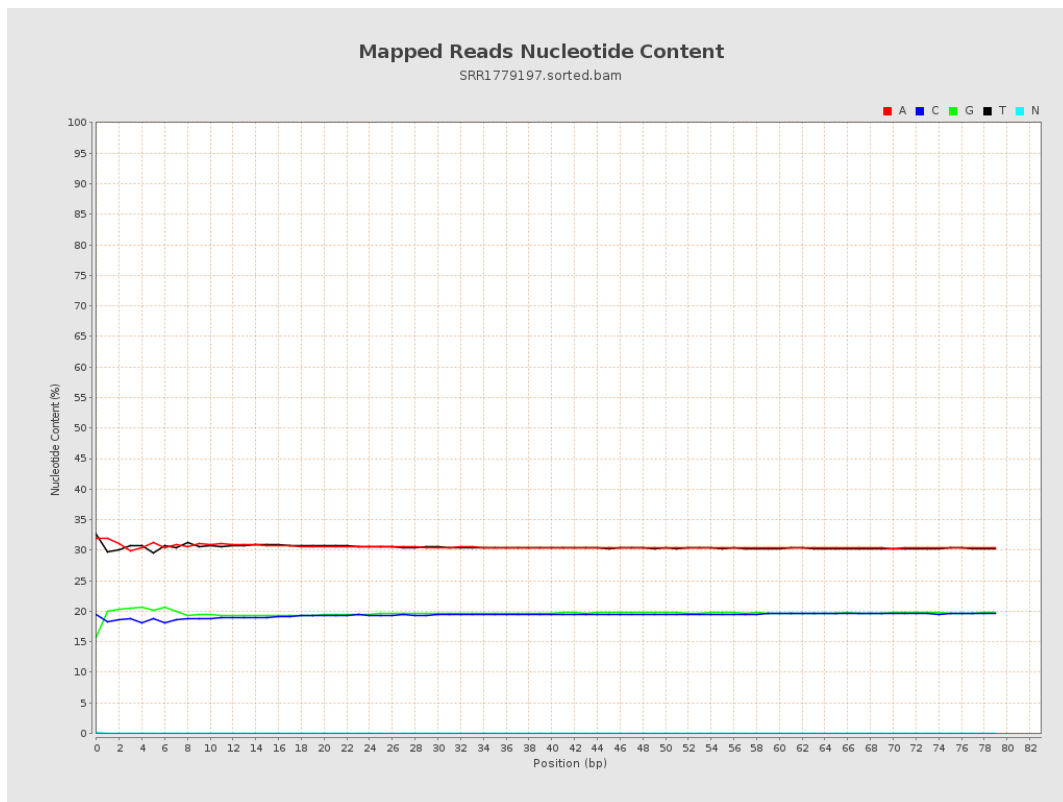
6. Results : Genome Fraction Coverage



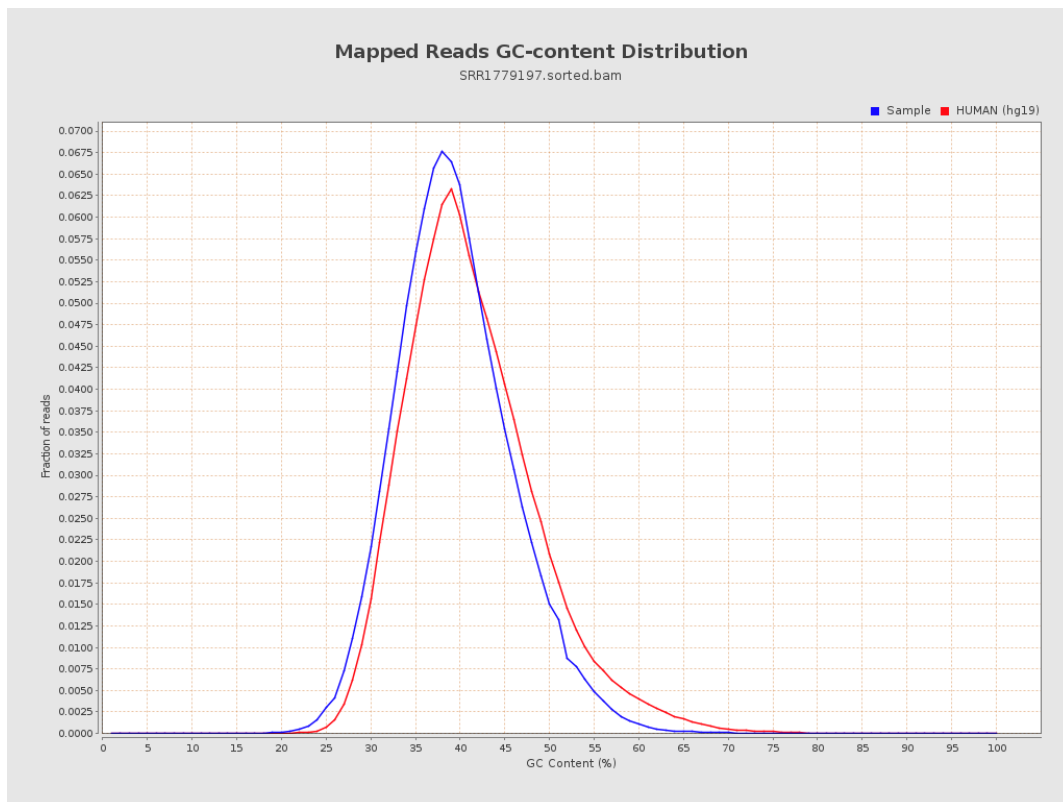
7. Results : Duplication Rate Histogram



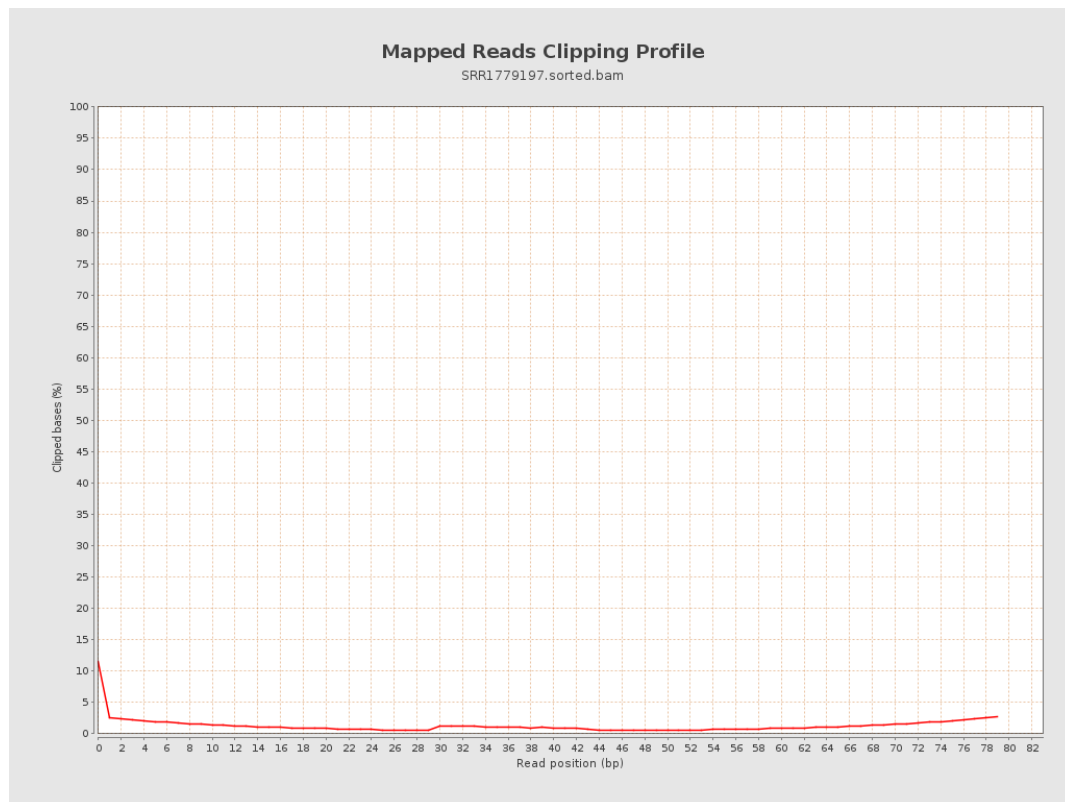
8. Results : Mapped Reads Nucleotide Content



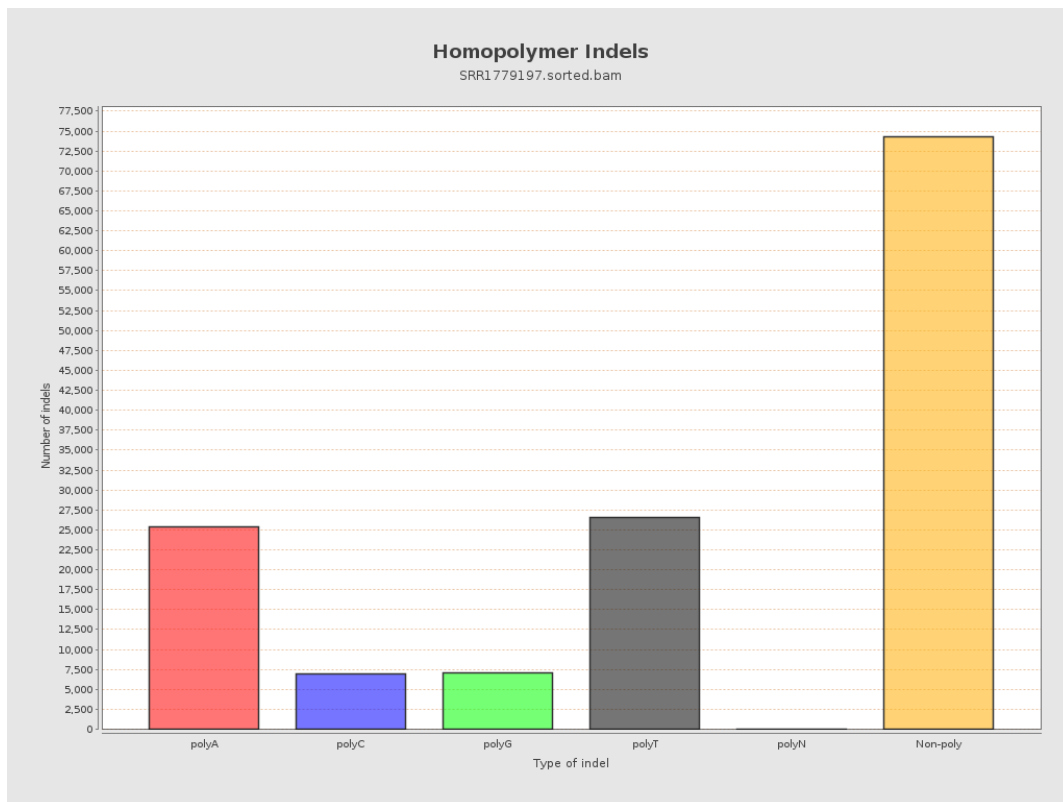
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



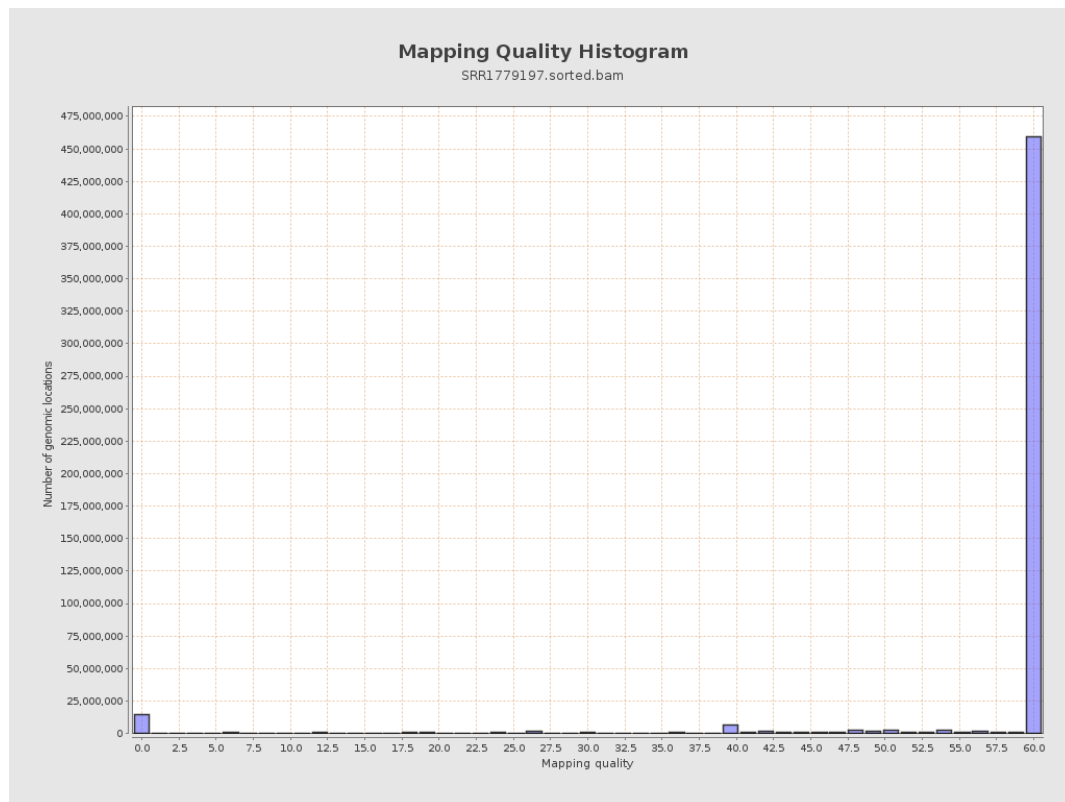
11. Results : Homopolymer Indels



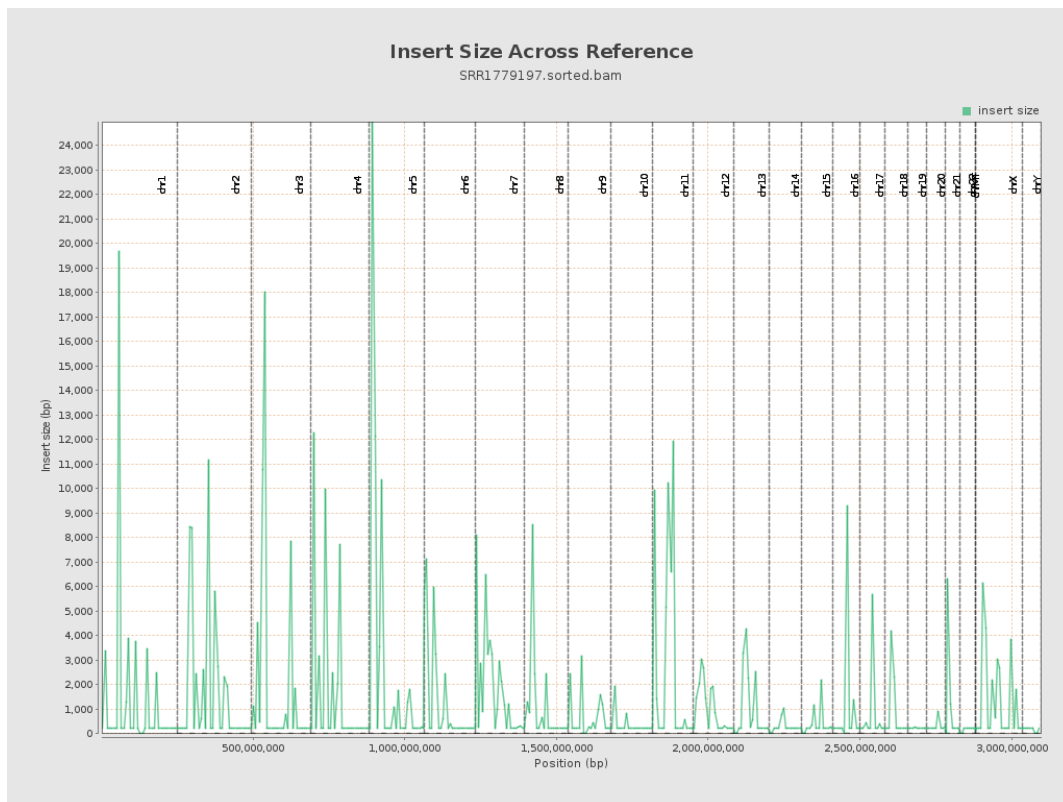
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

