

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 21:04:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779277.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_SRR1779277 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779277_1.fastq.gz SRR1779277_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 21:04:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779277.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,489,966
Mapped reads	10,773,093 / 93.76%
Unmapped reads	716,873 / 6.24%
Mapped paired reads	10,773,093 / 93.76%
Mapped reads, first in pair	5,442,939 / 47.37%
Mapped reads, second in pair	5,330,154 / 46.39%
Mapped reads, both in pair	10,638,964 / 92.59%
Mapped reads, singletons	134,129 / 1.17%
Secondary alignments	0
Supplementary alignments	25,458 / 0.22%
Read min/max/mean length	30 / 80 / 80.08
Duplicated reads (estimated)	382,545 / 3.33%
Duplication rate	3.05%
Clipped reads	367,675 / 3.2%

2.2. ACGT Content

Number/percentage of A's	263,021,703 / 30.7%
Number/percentage of C's	164,209,528 / 19.16%
Number/percentage of T's	262,400,305 / 30.62%
Number/percentage of G's	167,072,628 / 19.5%
Number/percentage of N's	161,772 / 0.02%

GC Percentage	38.66%
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2.3. Coverage

Mean	0.2768
Standard Deviation	1.4025

2.4. Mapping Quality

Mean Mapping Quality	52.56
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2.5. Insert size

Mean	37,267.43
Standard Deviation	1,825,413.9
P25/Median/P75	145 / 196 / 270

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	3,281,233
Insertions	63,643
Mapped reads with at least one insertion	0.58%
Deletions	80,203
Mapped reads with at least one deletion	0.73%
Homopolymer indels	46.59%

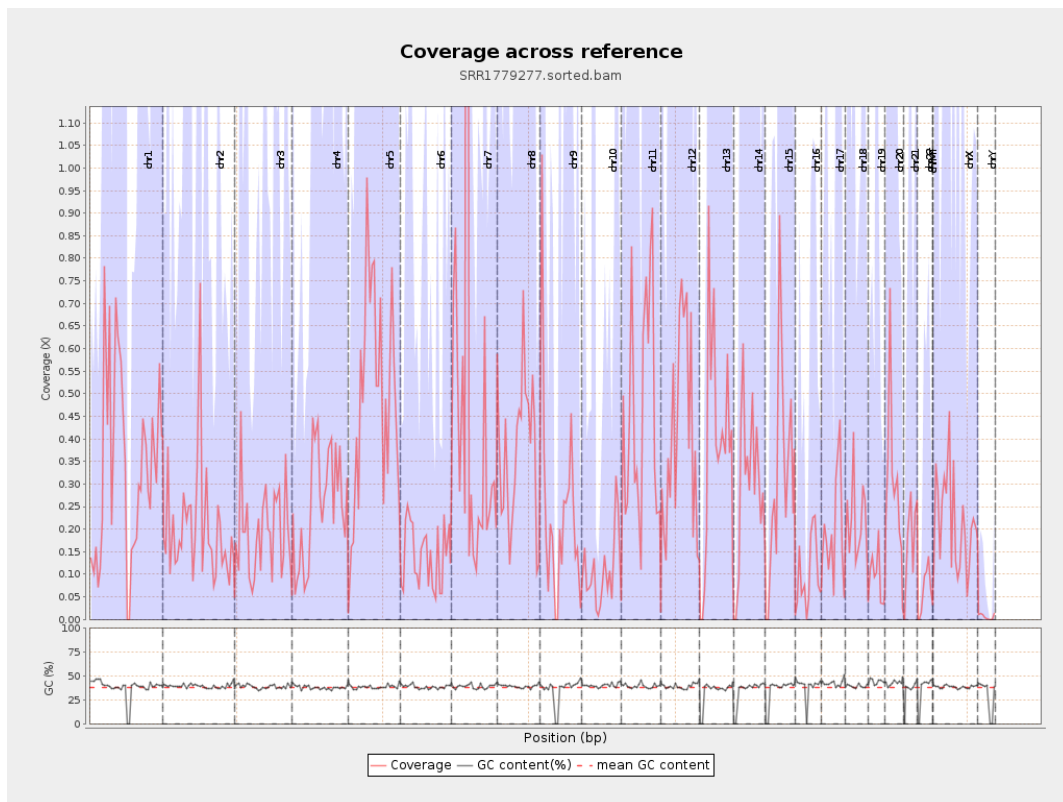
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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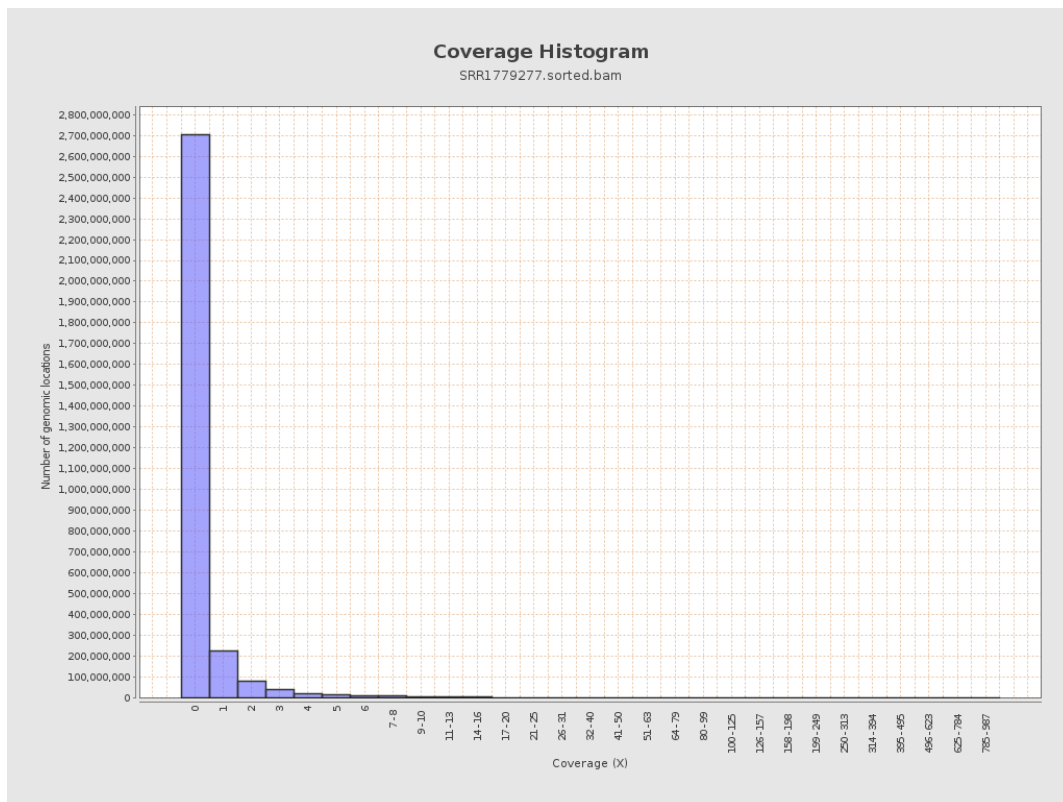
		bases	coverage	deviation
chr1	249250621	82696049	0.3318	1.5139
chr2	243199373	48593022	0.1998	0.8439
chr3	198022430	38204720	0.1929	0.8164
chr4	191154276	48266408	0.2525	0.996
chr5	180915260	88093070	0.4869	1.5082
chr6	171115067	24080415	0.1407	0.7073
chr7	159138663	88393241	0.5554	3.8958
chr8	146364022	53811068	0.3677	1.1916
chr9	141213431	32826863	0.2325	1.0392
chr10	135534747	14656109	0.1081	1.4458
chr11	135006516	60412033	0.4475	1.4568
chr12	133851895	55106738	0.4117	1.3464
chr13	115169878	44470485	0.3861	1.2591
chr14	107349540	32263156	0.3005	1.1044
chr15	102531392	31950068	0.3116	1.146
chr16	90354753	9043811	0.1001	0.5247
chr17	81195210	16812160	0.2071	0.855
chr18	78077248	17317307	0.2218	0.9096
chr19	59128983	5777647	0.0977	0.8085
chr20	63025520	19517542	0.3097	1.0334
chr21	48129895	8150776	0.1693	0.7815
chr22	51304566	3339547	0.0651	0.4148
chrMT	16571	1066	0.0643	0.2608
chrX	155270560	32865851	0.2117	0.9558

chrY	59373566	384481	0.0065	0.1324
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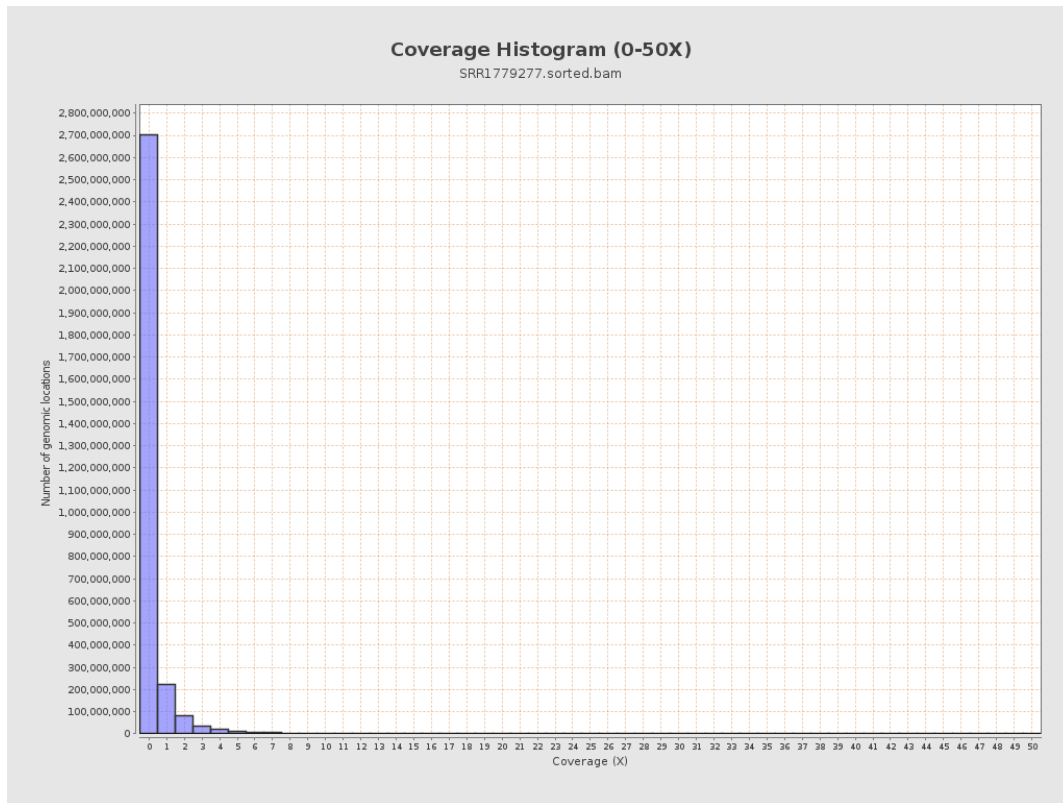
3. Results : Coverage across reference



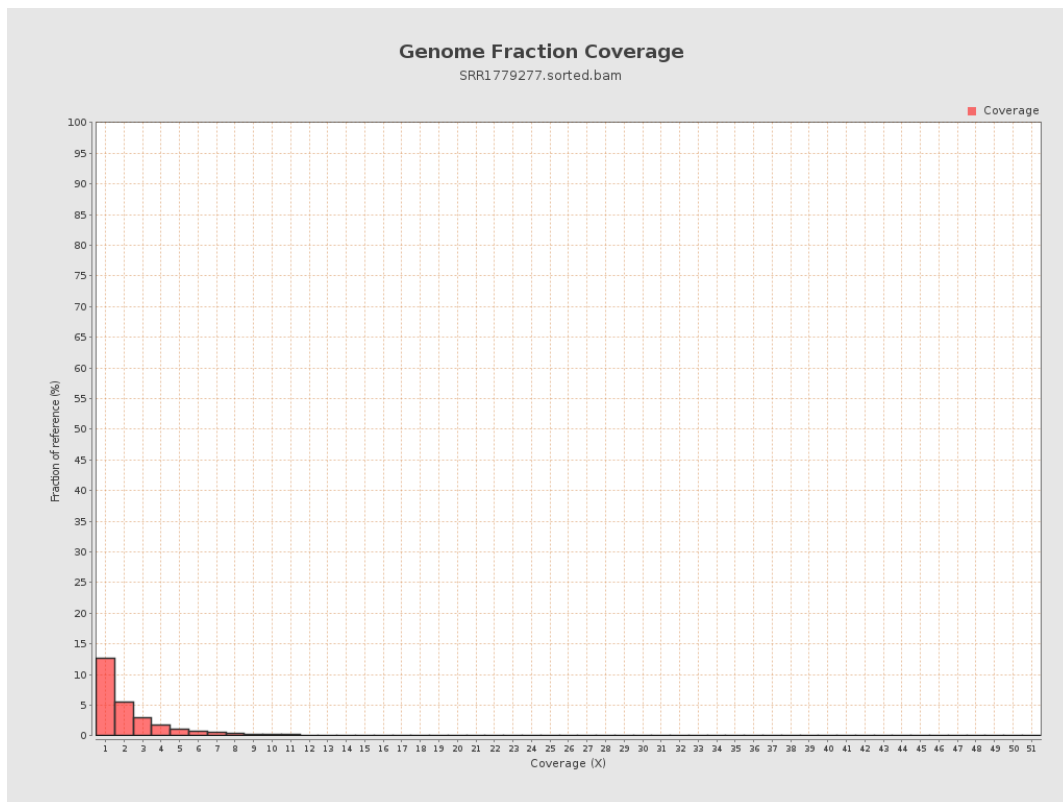
4. Results : Coverage Histogram



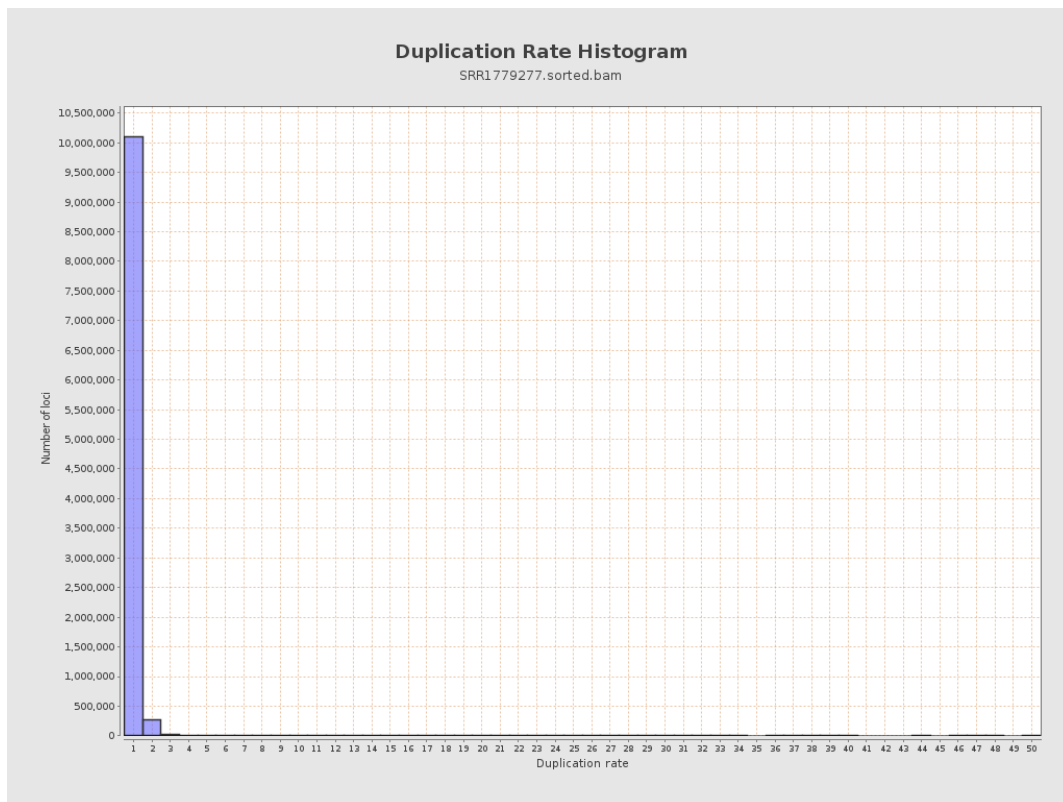
5. Results : Coverage Histogram (0-50X)



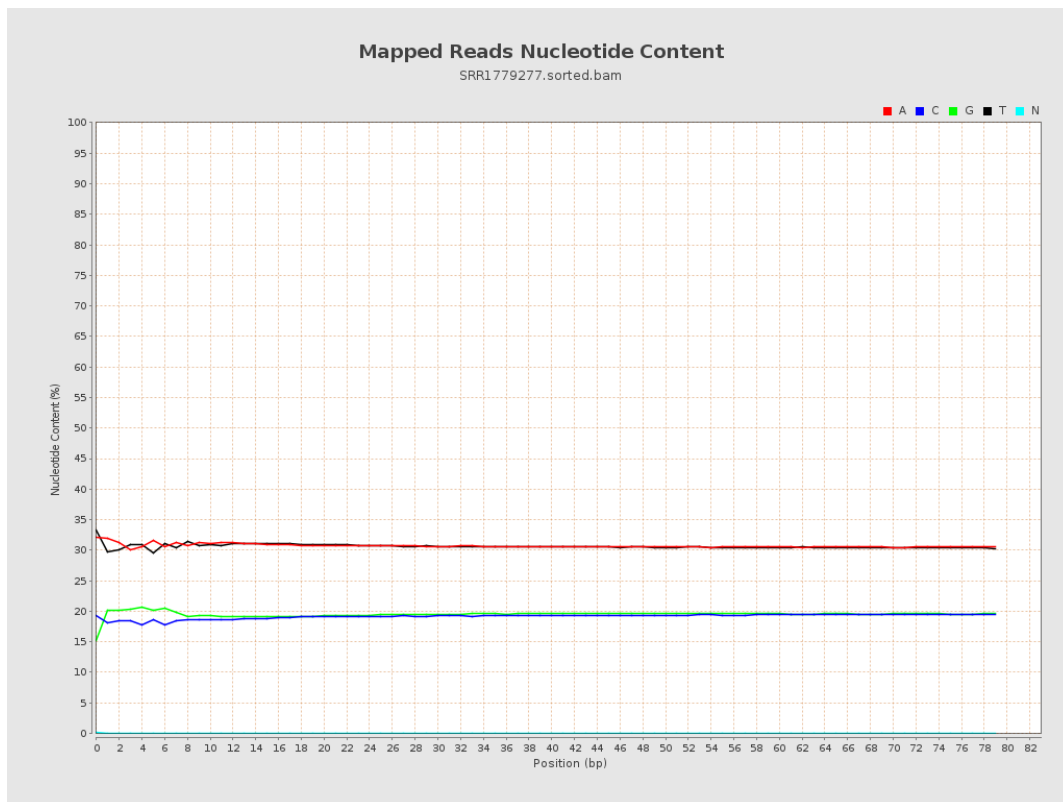
6. Results : Genome Fraction Coverage



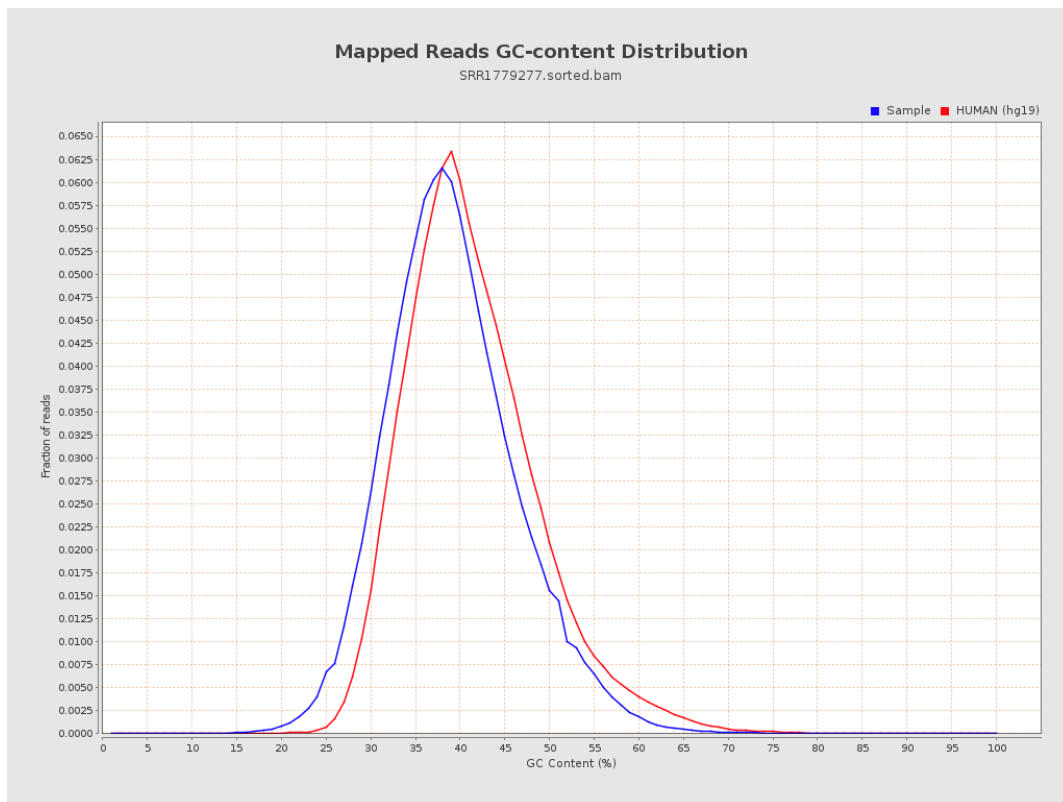
7. Results : Duplication Rate Histogram



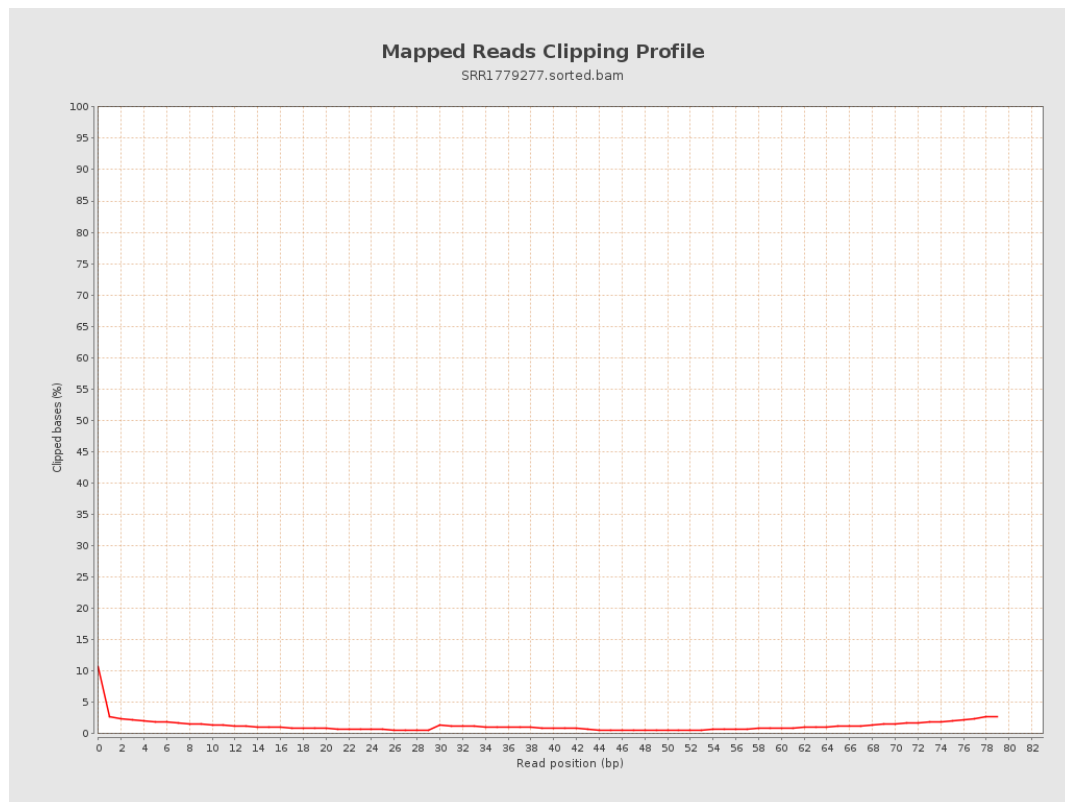
8. Results : Mapped Reads Nucleotide Content



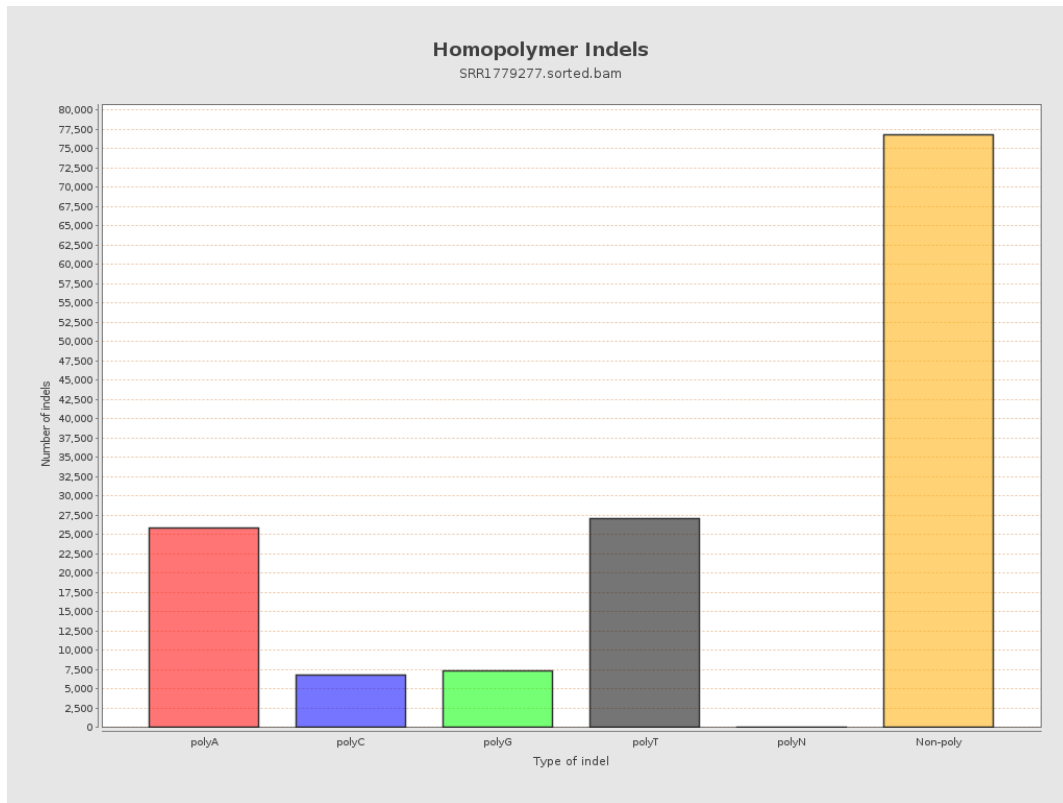
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



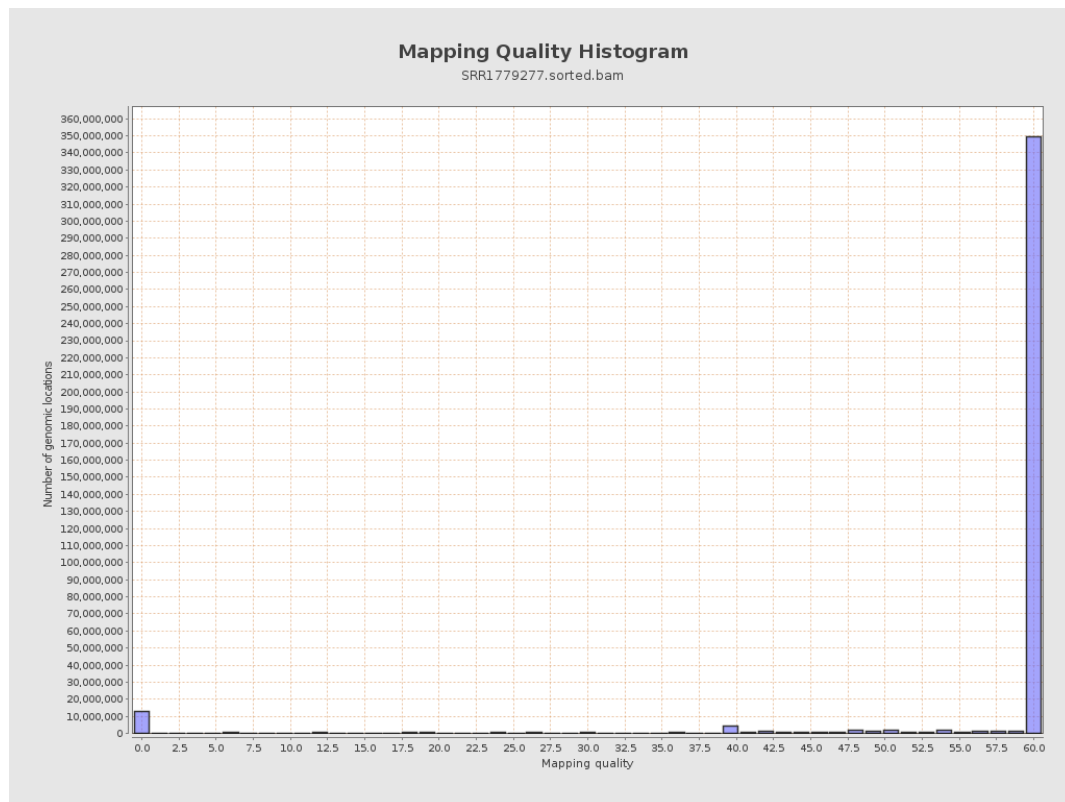
11. Results : Homopolymer Indels



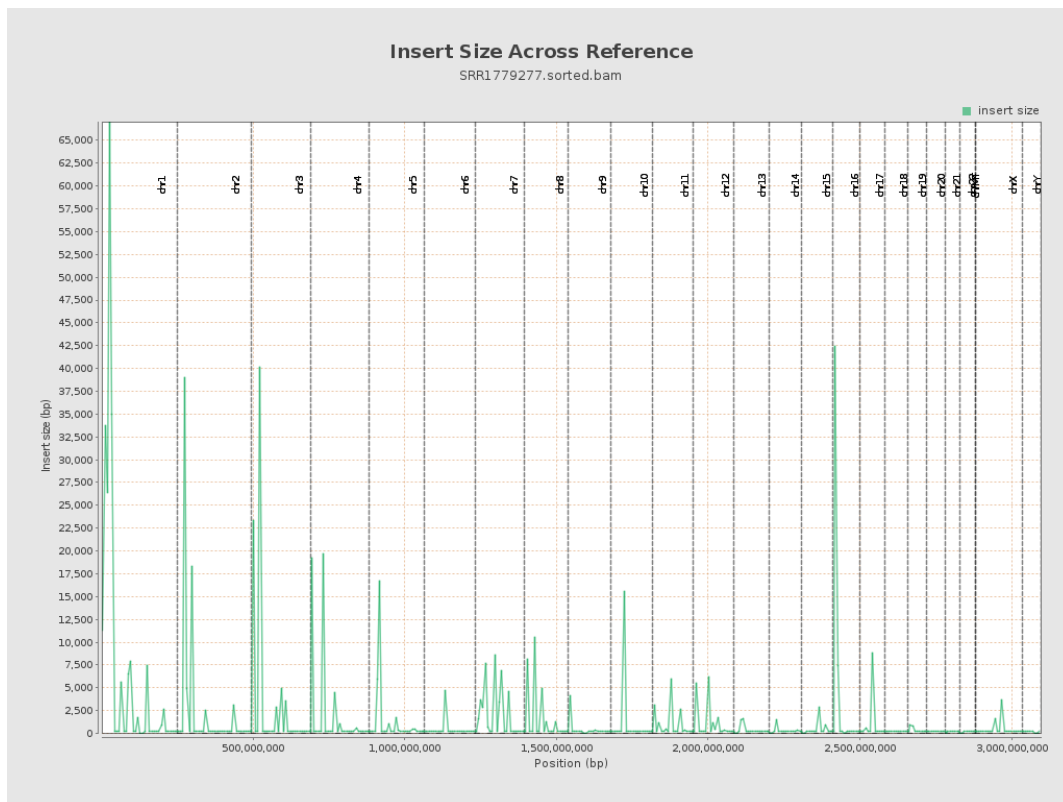
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

