

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 22:43:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779412.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_SRR1779412 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779412_1.fastq.gz SRR1779412_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 22:43:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779412.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,292,530
Mapped reads	15,751,235 / 96.68%
Unmapped reads	541,295 / 3.32%
Mapped paired reads	15,751,235 / 96.68%
Mapped reads, first in pair	7,972,632 / 48.93%
Mapped reads, second in pair	7,778,603 / 47.74%
Mapped reads, both in pair	15,527,512 / 95.3%
Mapped reads, singletons	223,723 / 1.37%
Secondary alignments	0
Supplementary alignments	61,000 / 0.37%
Read min/max/mean length	30 / 80 / 80.14
Duplicated reads (estimated)	546,606 / 3.35%
Duplication rate	3.13%
Clipped reads	653,421 / 4.01%

2.2. ACGT Content

Number/percentage of A's	381,803,187 / 30.5%
Number/percentage of C's	244,683,796 / 19.55%
Number/percentage of T's	372,615,184 / 29.77%
Number/percentage of G's	252,318,509 / 20.16%
Number/percentage of N's	274,488 / 0.02%

GC Percentage	39.71%
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2.3. Coverage

Mean	0.4044
Standard Deviation	1.4993

2.4. Mapping Quality

Mean Mapping Quality	53.23
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2.5. Insert size

Mean	229,795.23
Standard Deviation	4,653,181.64
P25/Median/P75	156 / 199 / 253

2.6. Mismatches and indels

General error rate	0.35%
Mismatches	4,209,619
Insertions	112,555
Mapped reads with at least one insertion	0.71%
Deletions	127,096
Mapped reads with at least one deletion	0.8%
Homopolymer indels	47.49%

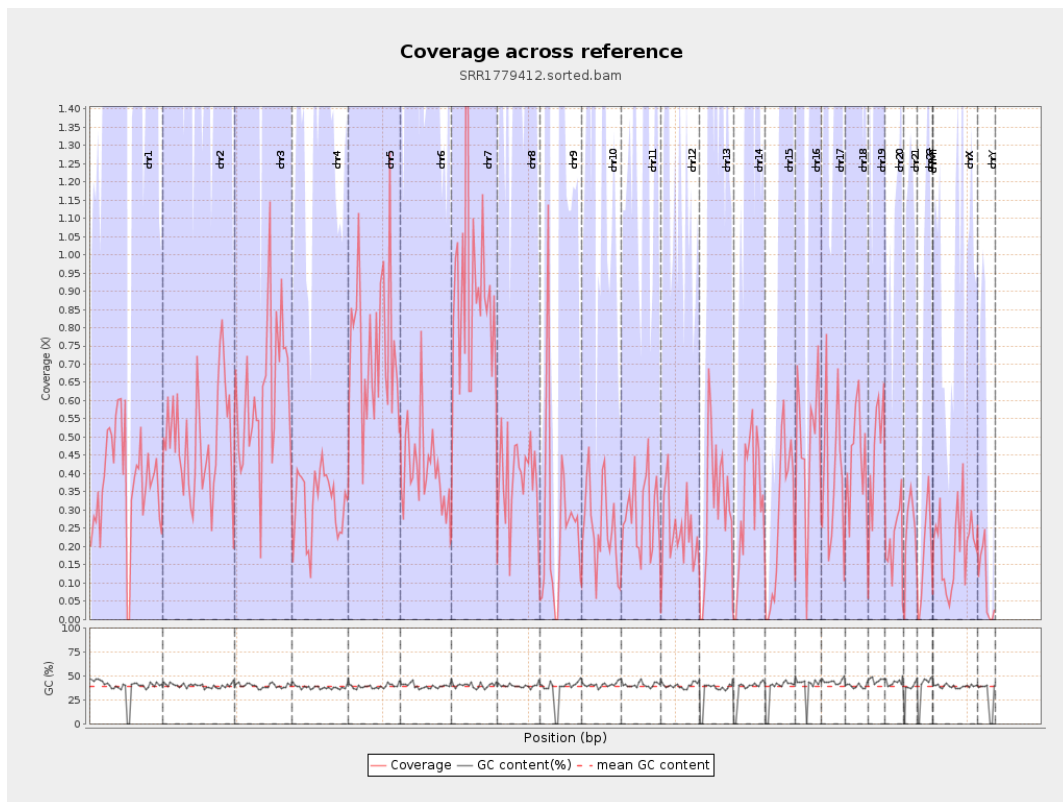
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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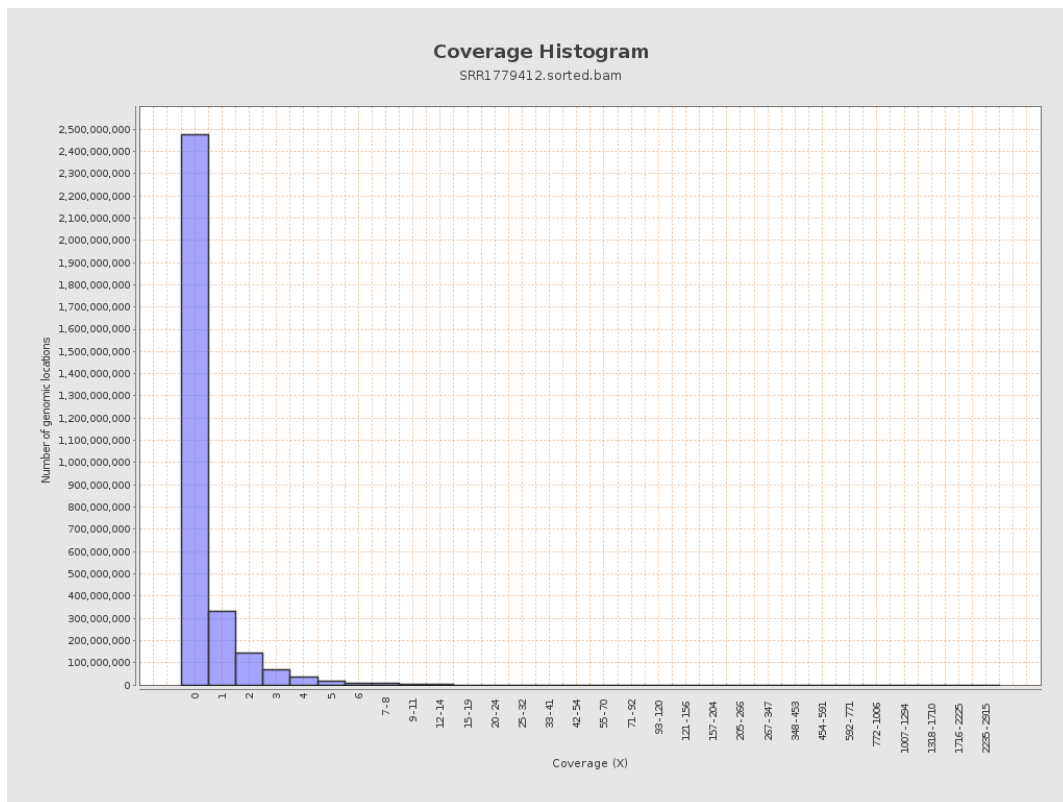
		bases	coverage	deviation
chr1	249250621	94171719	0.3778	3.099
chr2	243199373	117807343	0.4844	1.1912
chr3	198022430	122828074	0.6203	1.3206
chr4	191154276	60942001	0.3188	0.9108
chr5	180915260	133454212	0.7377	1.4662
chr6	171115067	70004267	0.4091	1.1202
chr7	159138663	144323644	0.9069	2.533
chr8	146364022	56419245	0.3855	1.0223
chr9	141213431	38393051	0.2719	1.0345
chr10	135534747	34642015	0.2556	1.5057
chr11	135006516	38704219	0.2867	0.9332
chr12	133851895	32764050	0.2448	0.8547
chr13	115169878	36272779	0.315	0.968
chr14	107349540	34714362	0.3234	0.9523
chr15	102531392	27447792	0.2677	0.9106
chr16	90354753	41628685	0.4607	1.1723
chr17	81195210	33241102	0.4094	1.2243
chr18	78077248	34227062	0.4384	1.2339
chr19	59128983	27523273	0.4655	2.2562
chr20	63025520	14104763	0.2238	0.8136
chr21	48129895	11564262	0.2403	0.7933
chr22	51304566	9510435	0.1854	0.7279
chrMT	16571	2195	0.1325	0.4115
chrX	155270560	31462003	0.2026	0.7617

chrY	59373566	5807042	0.0978	0.4905
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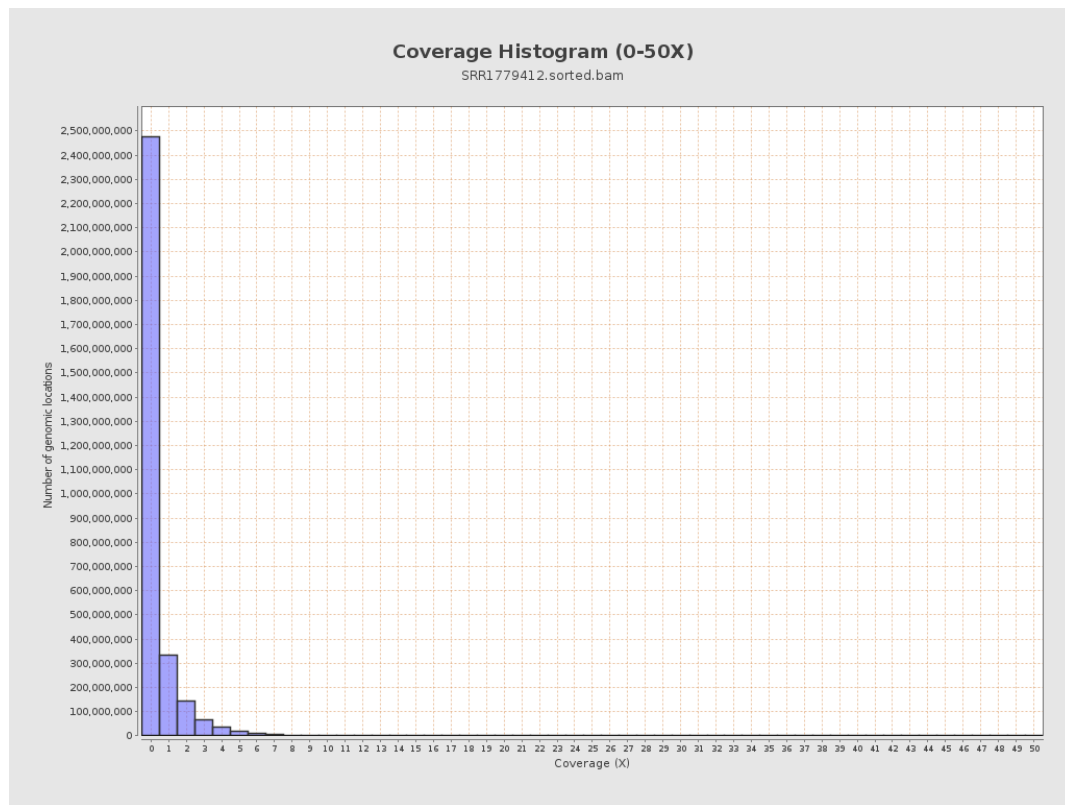
3. Results : Coverage across reference



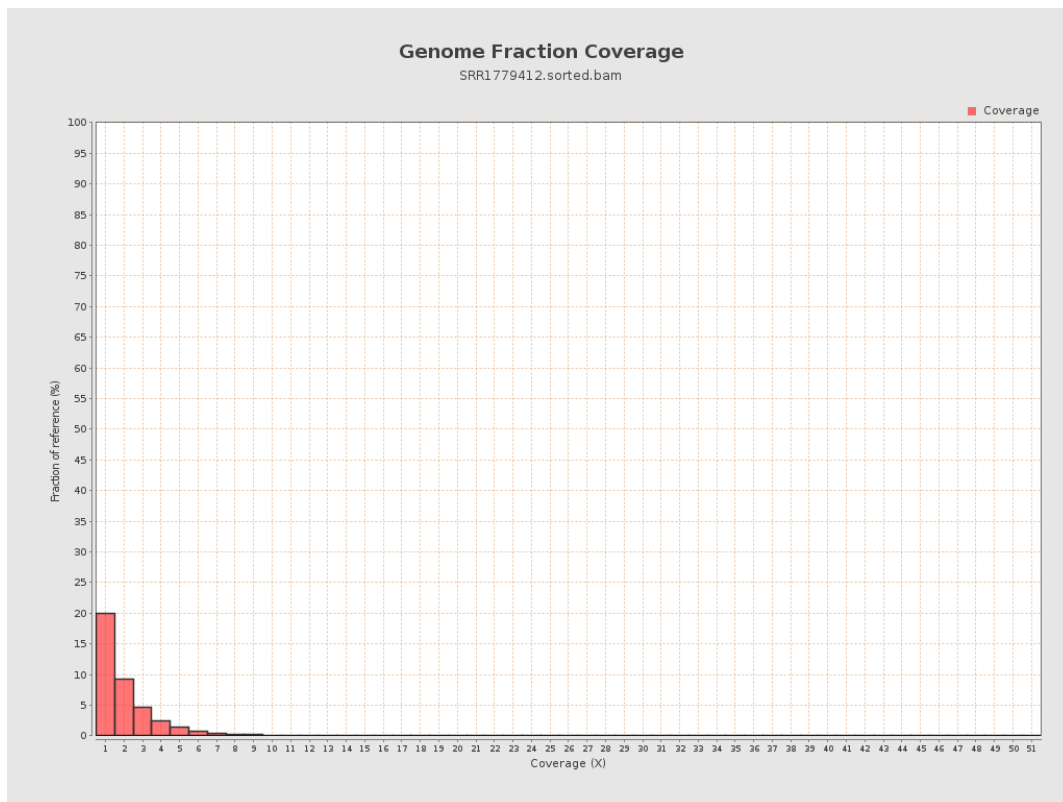
4. Results : Coverage Histogram



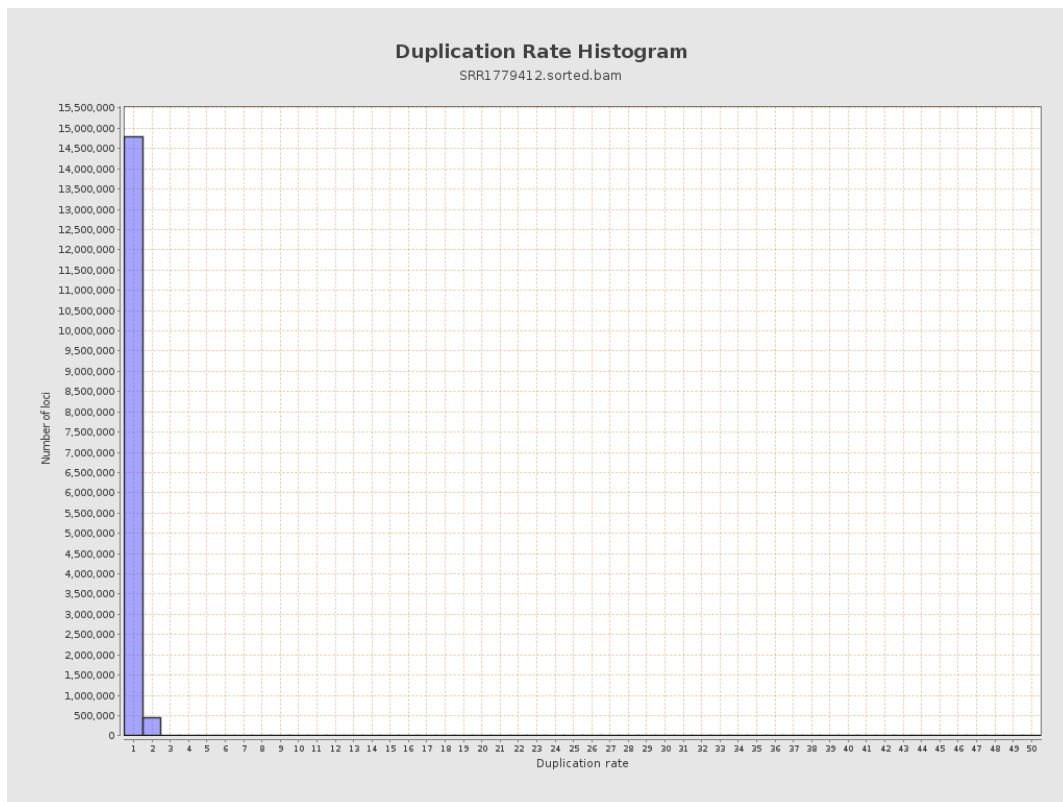
5. Results : Coverage Histogram (0-50X)



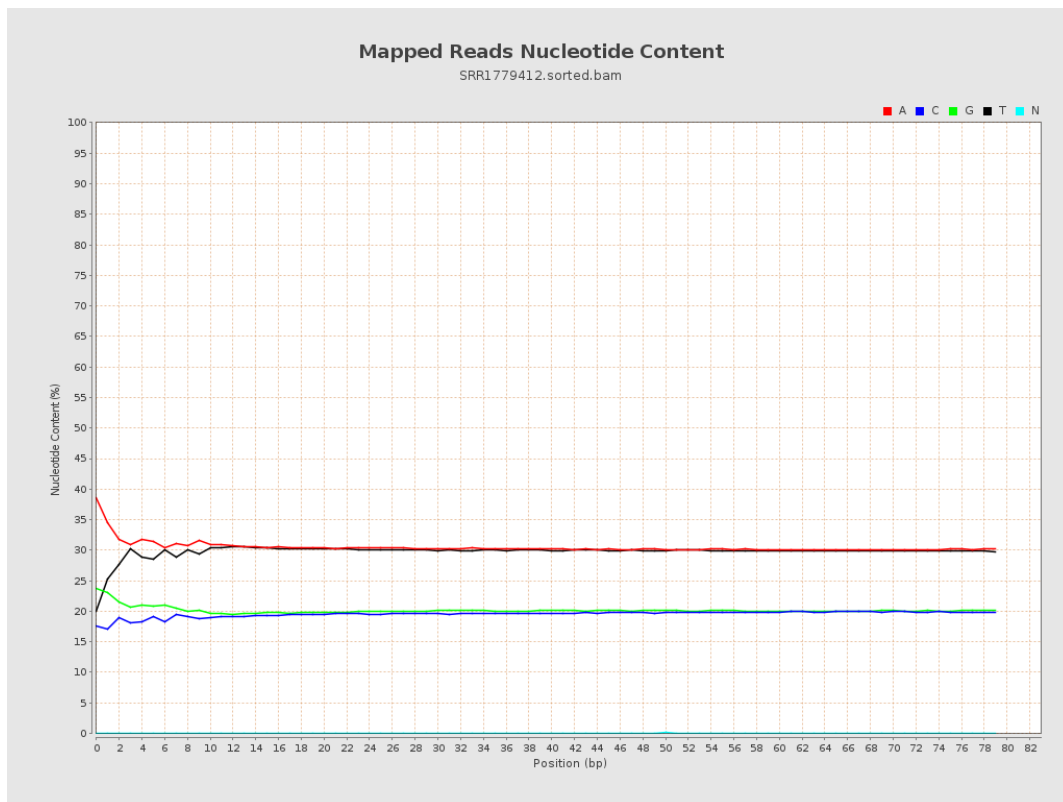
6. Results : Genome Fraction Coverage



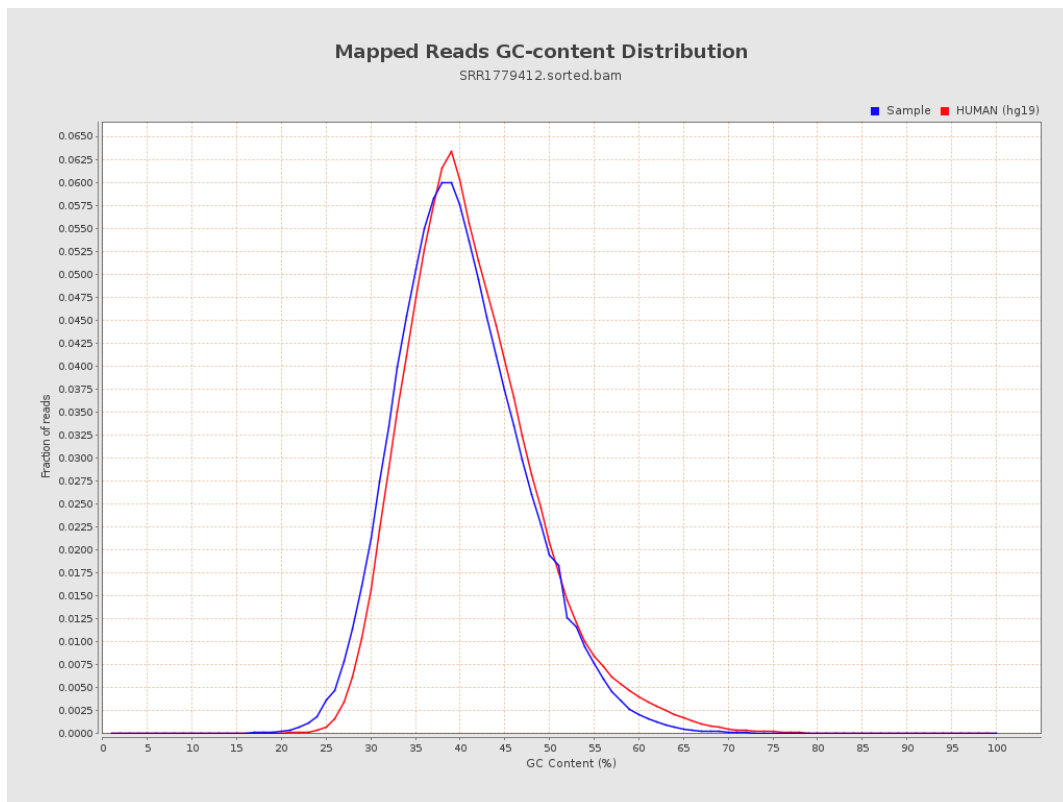
7. Results : Duplication Rate Histogram



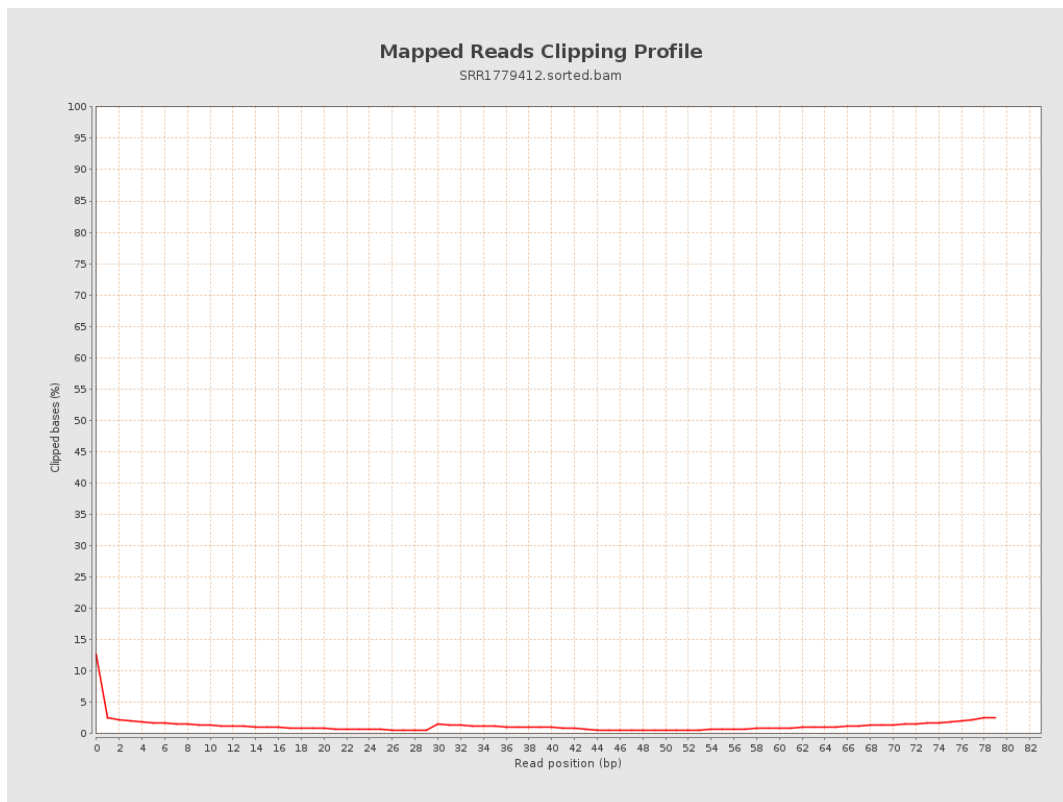
8. Results : Mapped Reads Nucleotide Content



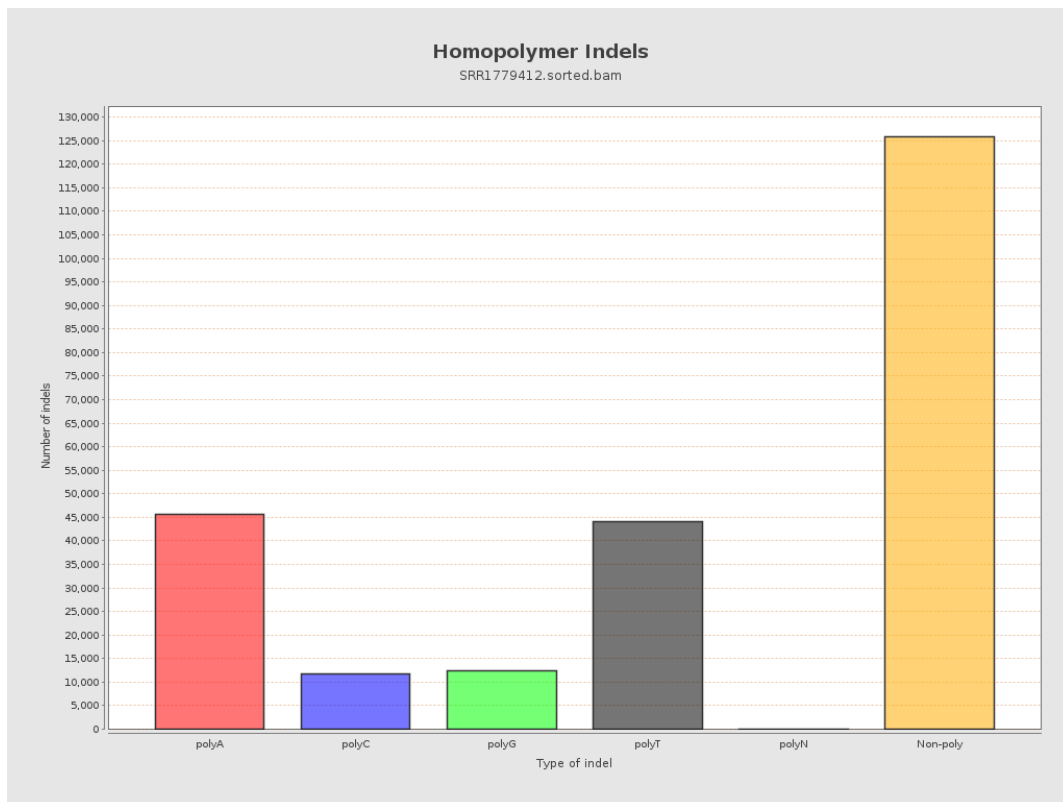
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



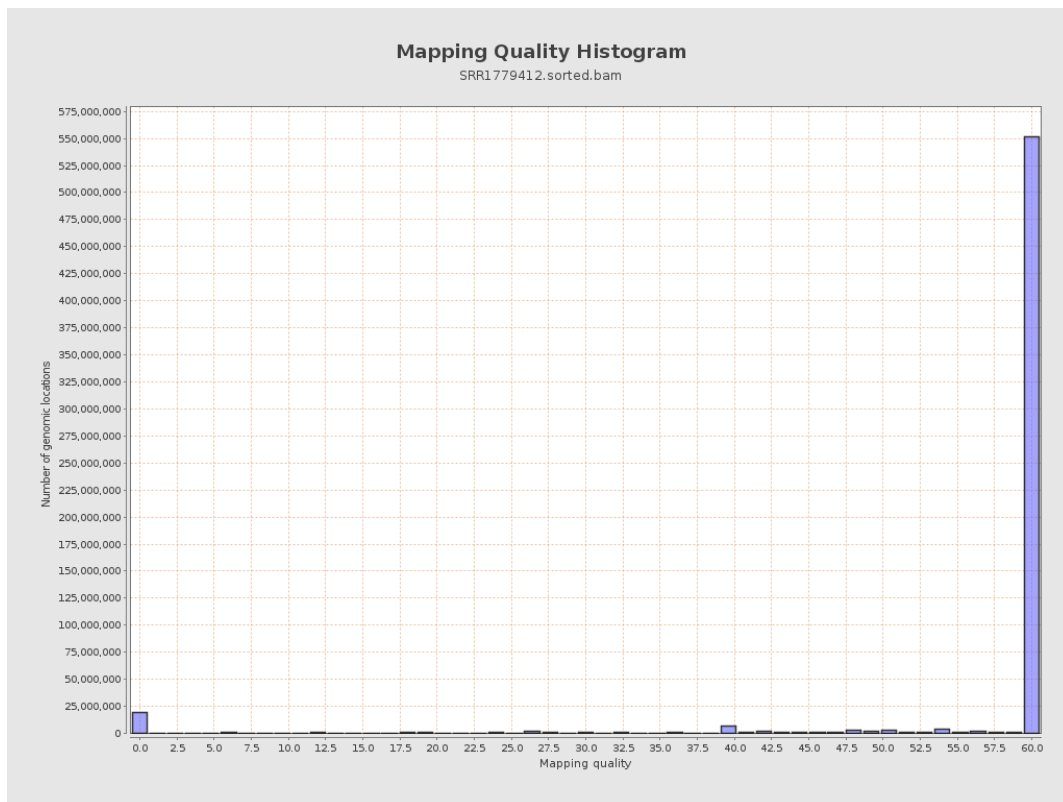
11. Results : Homopolymer Indels



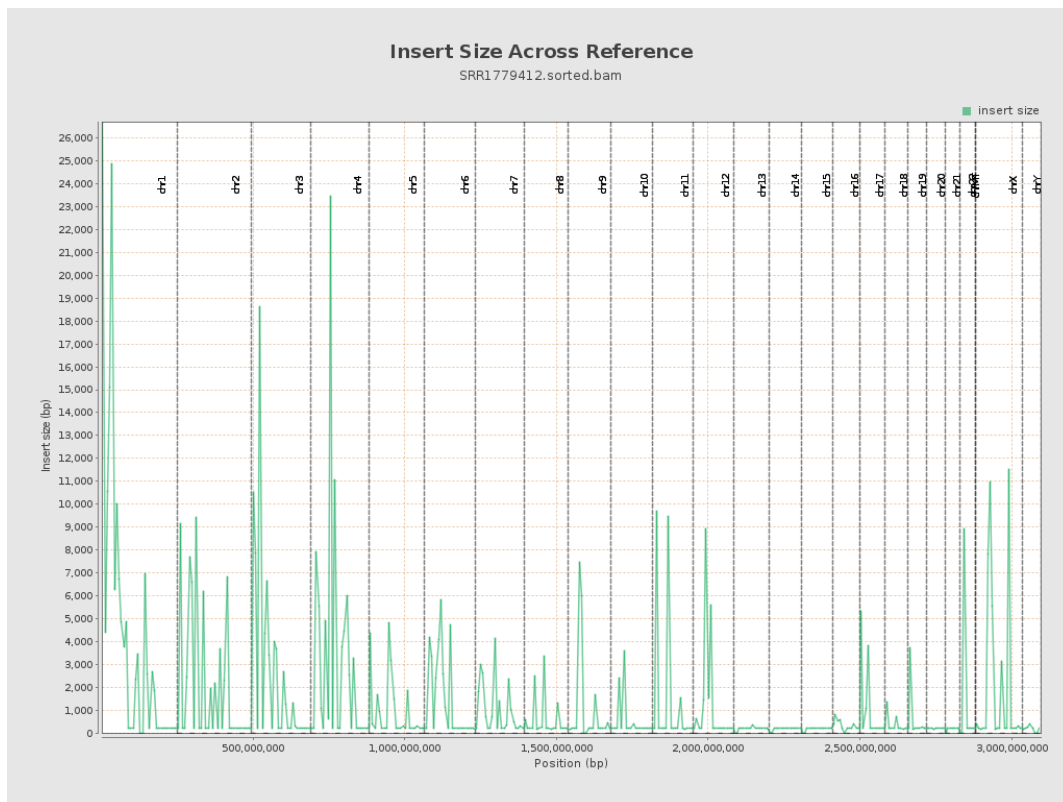
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

