

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 15:41:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779208.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_SRR1779208 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779208_1.fastq.gz SRR1779208_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 15:41:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779208.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,829,460
Mapped reads	7,503,684 / 95.84%
Unmapped reads	325,776 / 4.16%
Mapped paired reads	7,503,684 / 95.84%
Mapped reads, first in pair	3,810,447 / 48.67%
Mapped reads, second in pair	3,693,237 / 47.17%
Mapped reads, both in pair	7,376,812 / 94.22%
Mapped reads, singletons	126,872 / 1.62%
Secondary alignments	0
Supplementary alignments	17,030 / 0.22%
Read min/max/mean length	30 / 80 / 80.08
Duplicated reads (estimated)	95,054 / 1.21%
Duplication rate	1.16%
Clipped reads	267,867 / 3.42%

2.2. ACGT Content

Number/percentage of A's	182,556,903 / 30.6%
Number/percentage of C's	114,822,937 / 19.24%
Number/percentage of T's	182,081,333 / 30.52%
Number/percentage of G's	117,110,137 / 19.63%
Number/percentage of N's	106,928 / 0.02%

GC Percentage	38.87%
---------------	--------

2.3. Coverage

Mean	0.1928
Standard Deviation	0.7115

2.4. Mapping Quality

Mean Mapping Quality	52.85
----------------------	-------

2.5. Insert size

Mean	58,660.44
Standard Deviation	2,370,494.95
P25/Median/P75	198 / 268 / 342

2.6. Mismatches and indels

General error rate	0.46%
Mismatches	2,644,219
Insertions	44,643
Mapped reads with at least one insertion	0.59%
Deletions	55,954
Mapped reads with at least one deletion	0.74%
Homopolymer indels	46.95%

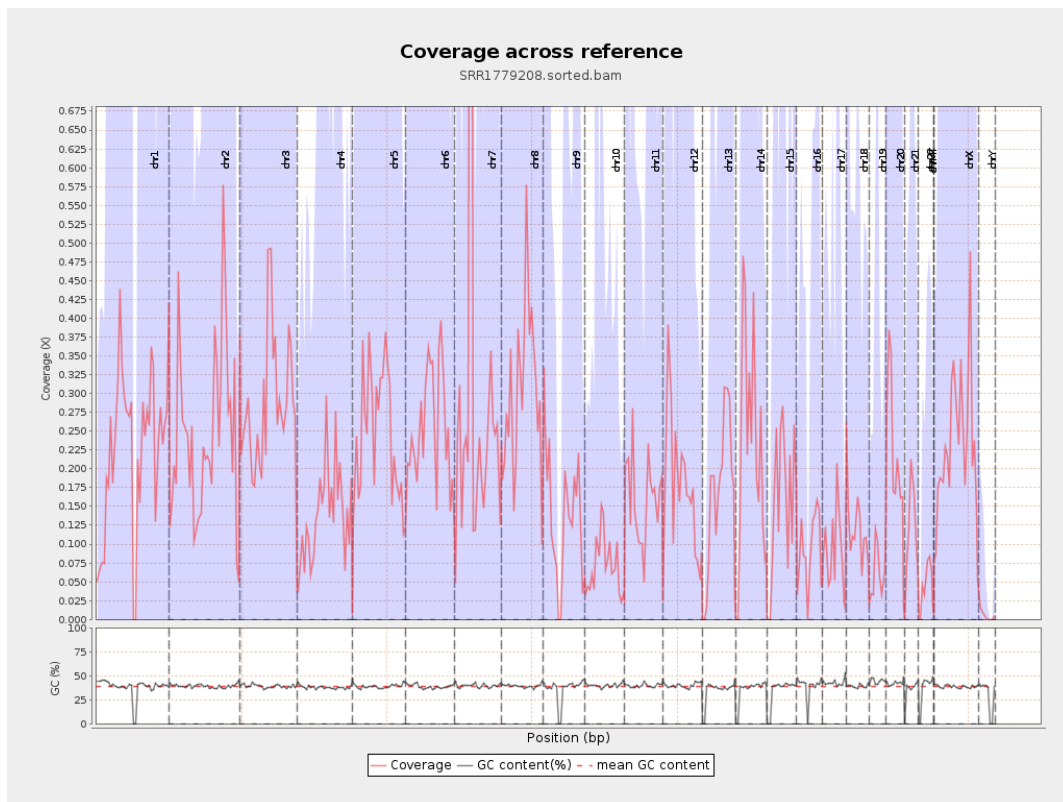
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

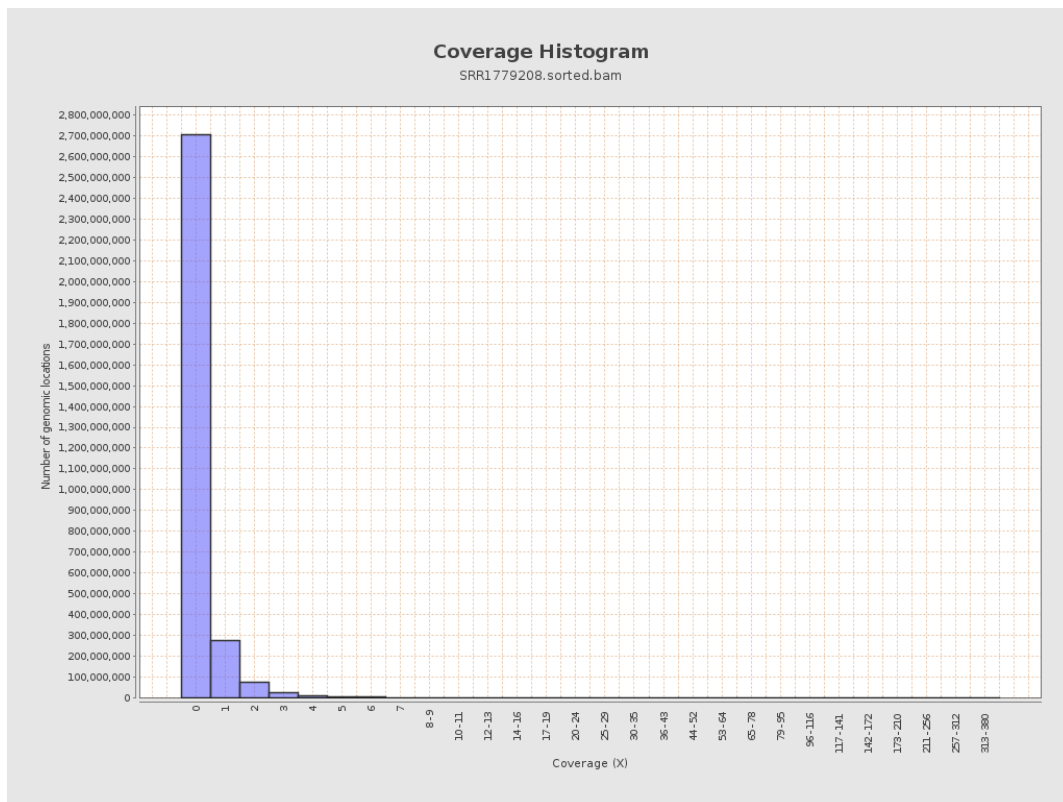
		bases	coverage	deviation
chr1	249250621	55854951	0.2241	0.7799
chr2	243199373	59832668	0.246	0.7039
chr3	198022430	56753085	0.2866	0.7586
chr4	191154276	26691091	0.1396	0.5124
chr5	180915260	44696368	0.2471	0.694
chr6	171115067	42796175	0.2501	0.7079
chr7	159138663	46500950	0.2922	1.5672
chr8	146364022	44066925	0.3011	0.7523
chr9	141213431	19021217	0.1347	0.5057
chr10	135534747	9749210	0.0719	0.6313
chr11	135006516	21278270	0.1576	0.538
chr12	133851895	23684652	0.1769	0.582
chr13	115169878	18920243	0.1643	0.5535
chr14	107349540	24048317	0.224	0.6877
chr15	102531392	15866983	0.1548	0.5611
chr16	90354753	8441064	0.0934	0.4005
chr17	81195210	7381320	0.0909	0.4241
chr18	78077248	9285116	0.1189	0.4795
chr19	59128983	3794250	0.0642	0.3935
chr20	63025520	14163810	0.2247	0.6409
chr21	48129895	5518821	0.1147	0.4597
chr22	51304566	2395042	0.0467	0.2848
chrMT	16571	80	0.0048	0.0693
chrX	155270560	35681288	0.2298	0.7042

chrY	59373566	371640	0.0063	0.1027
------	----------	--------	--------	--------

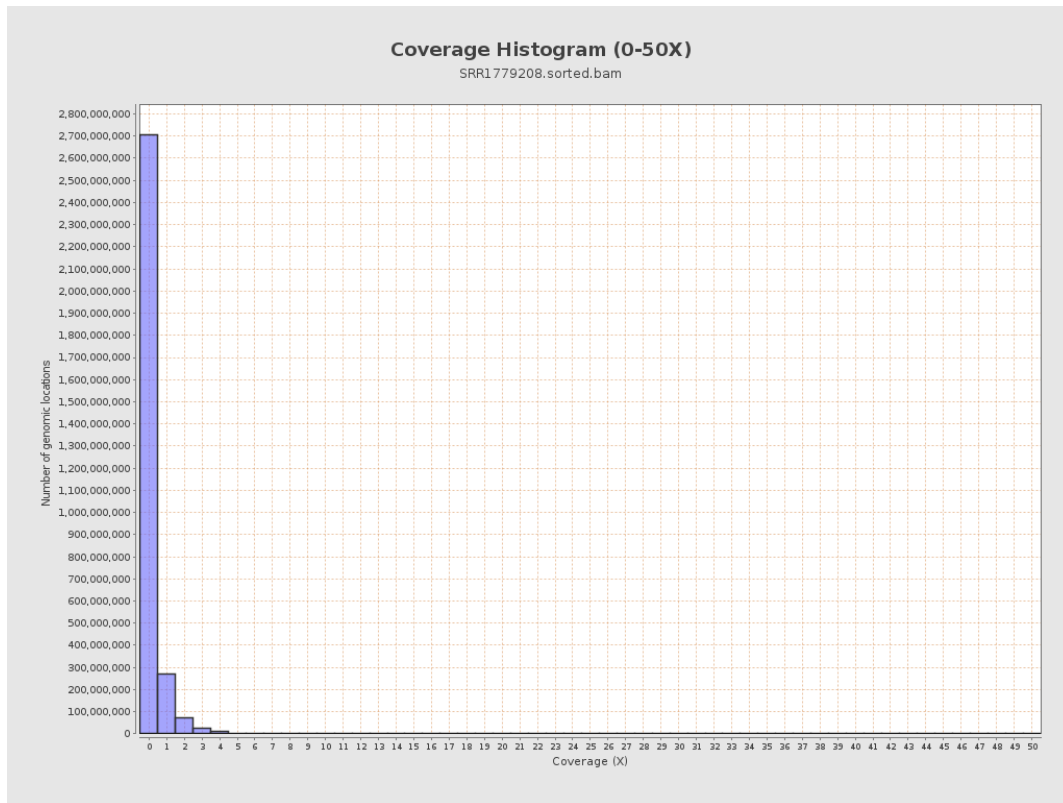
3. Results : Coverage across reference



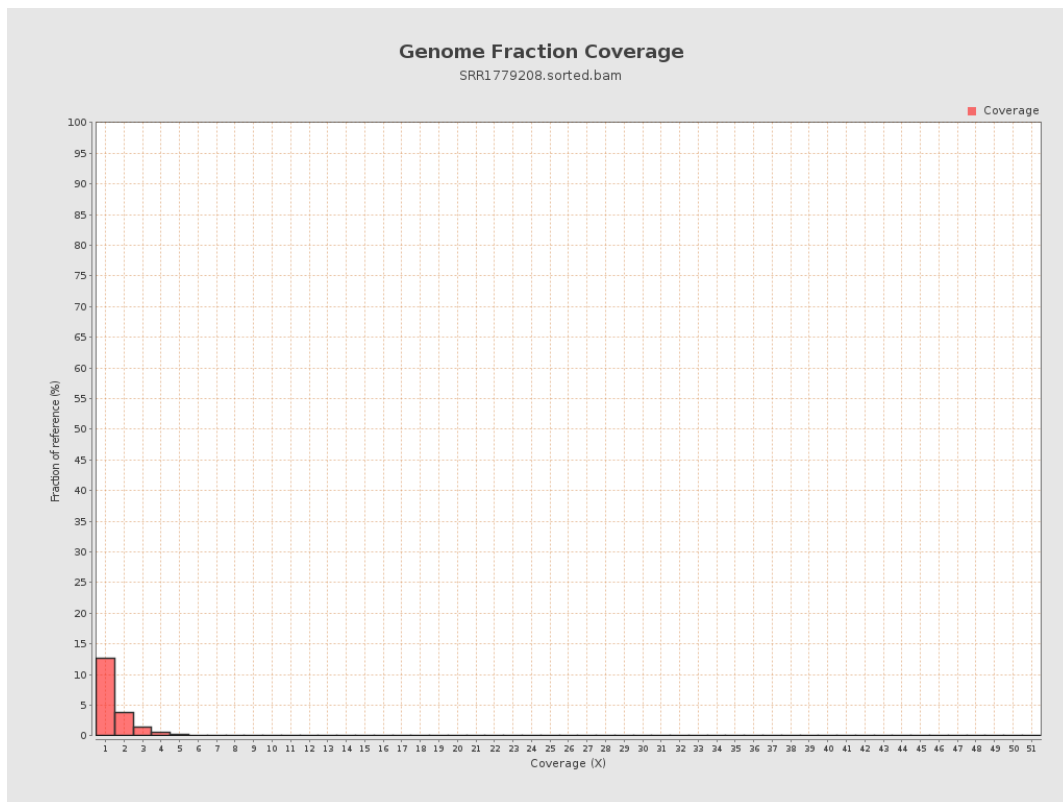
4. Results : Coverage Histogram



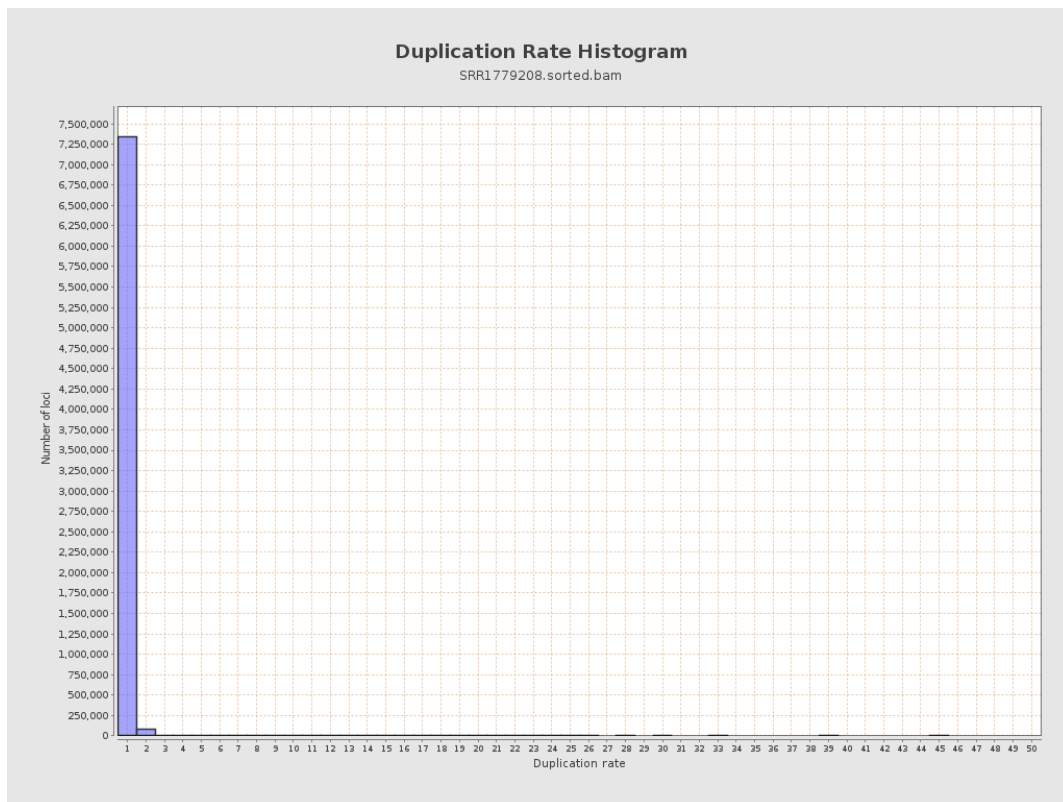
5. Results : Coverage Histogram (0-50X)



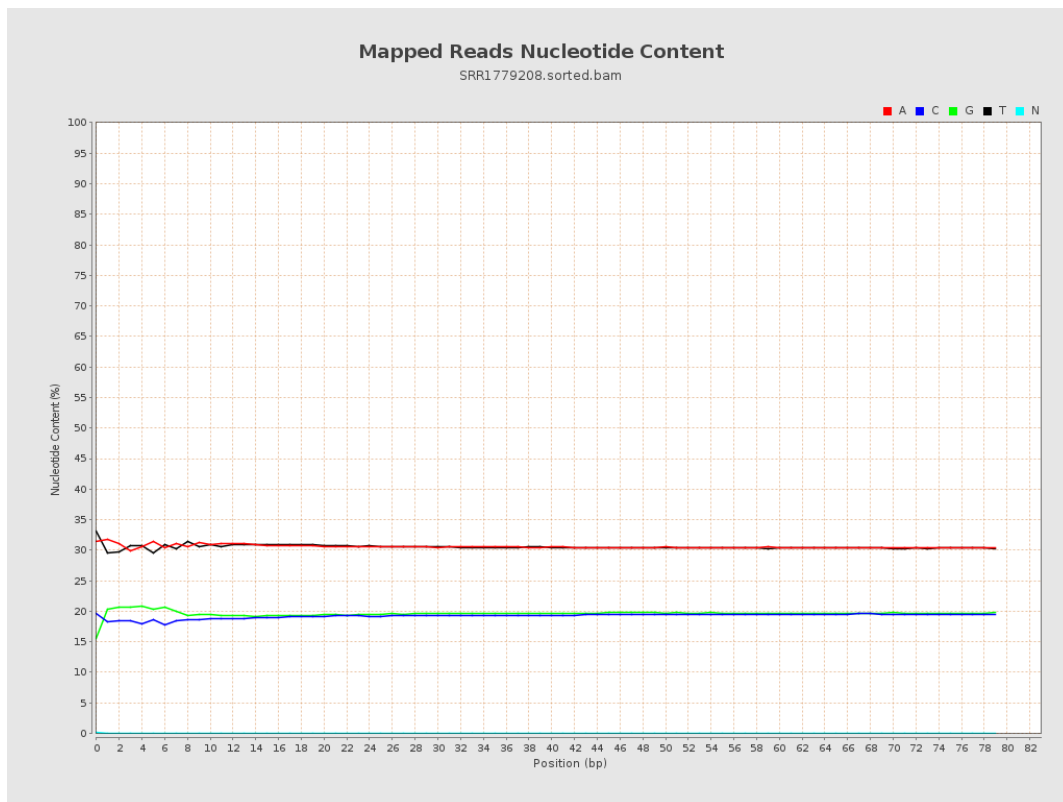
6. Results : Genome Fraction Coverage



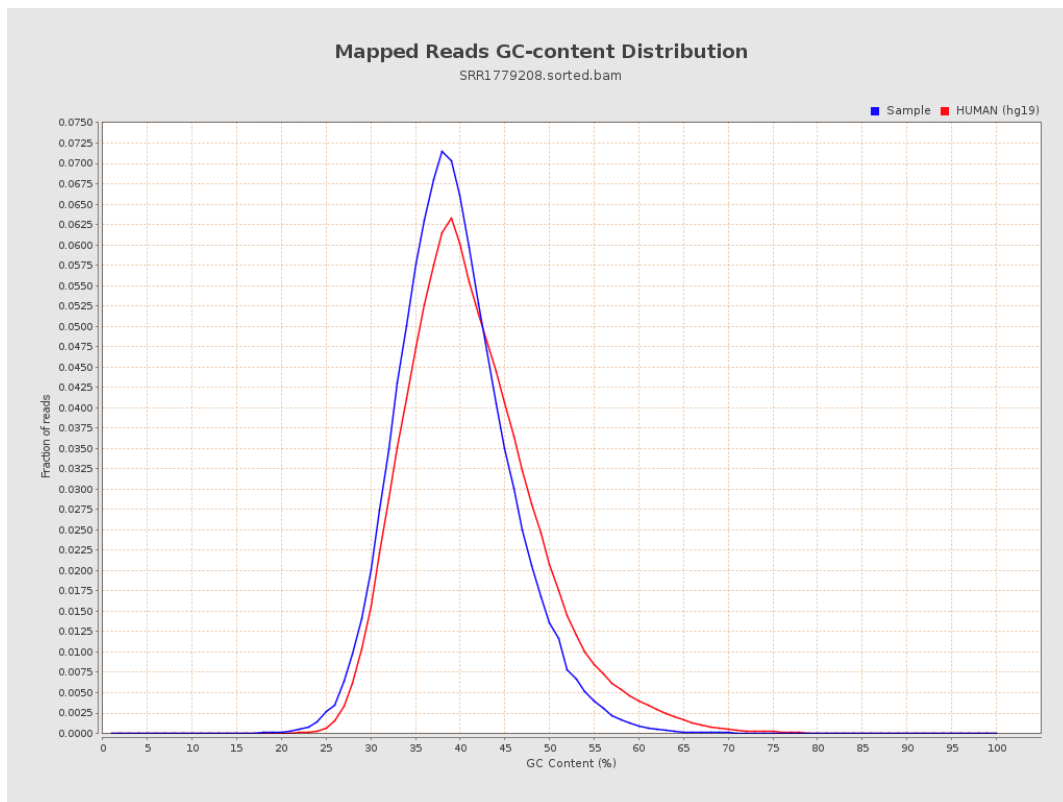
7. Results : Duplication Rate Histogram



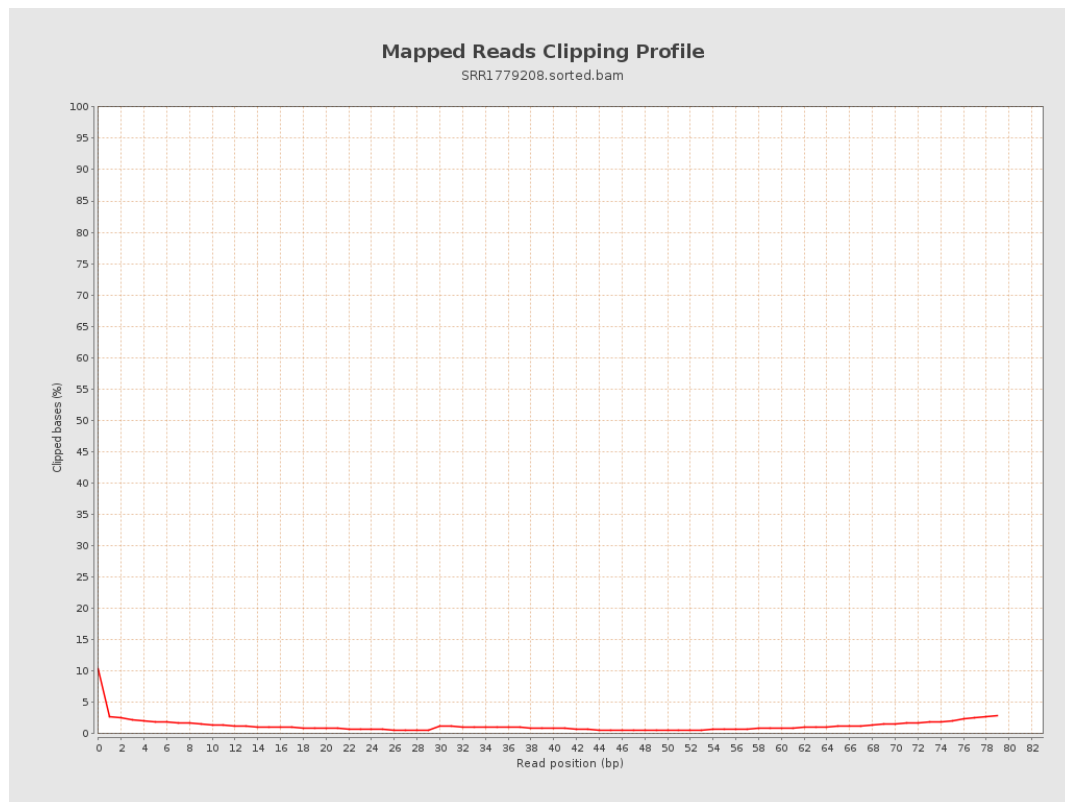
8. Results : Mapped Reads Nucleotide Content



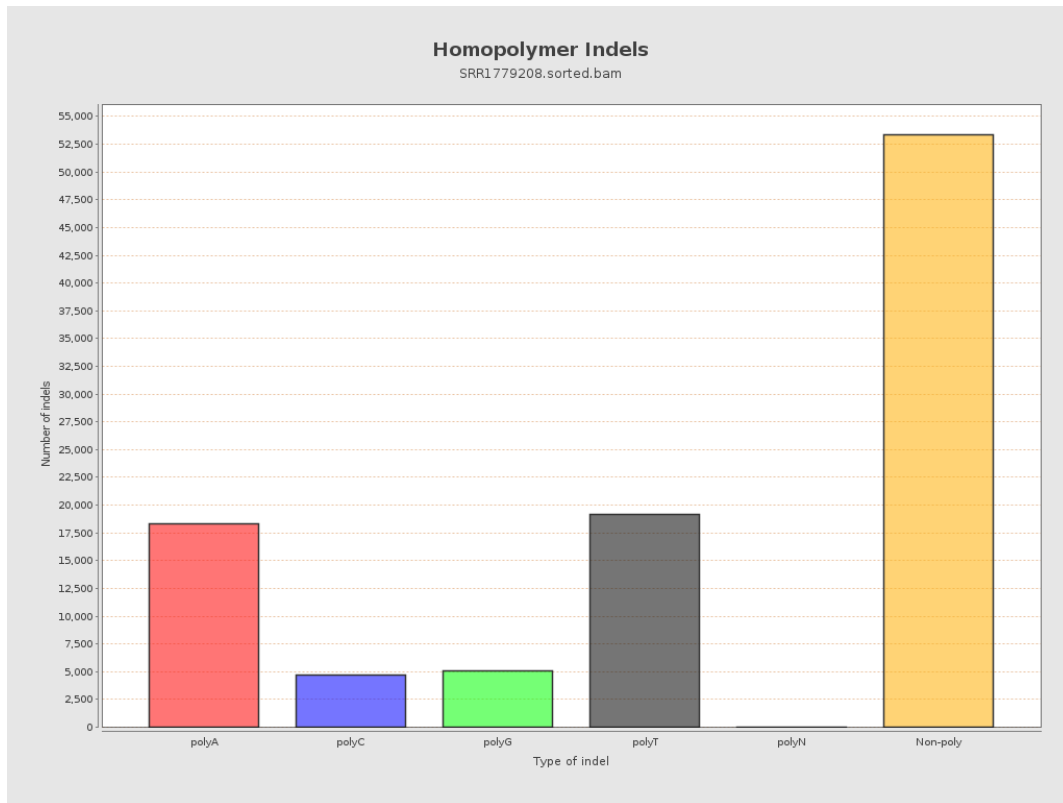
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



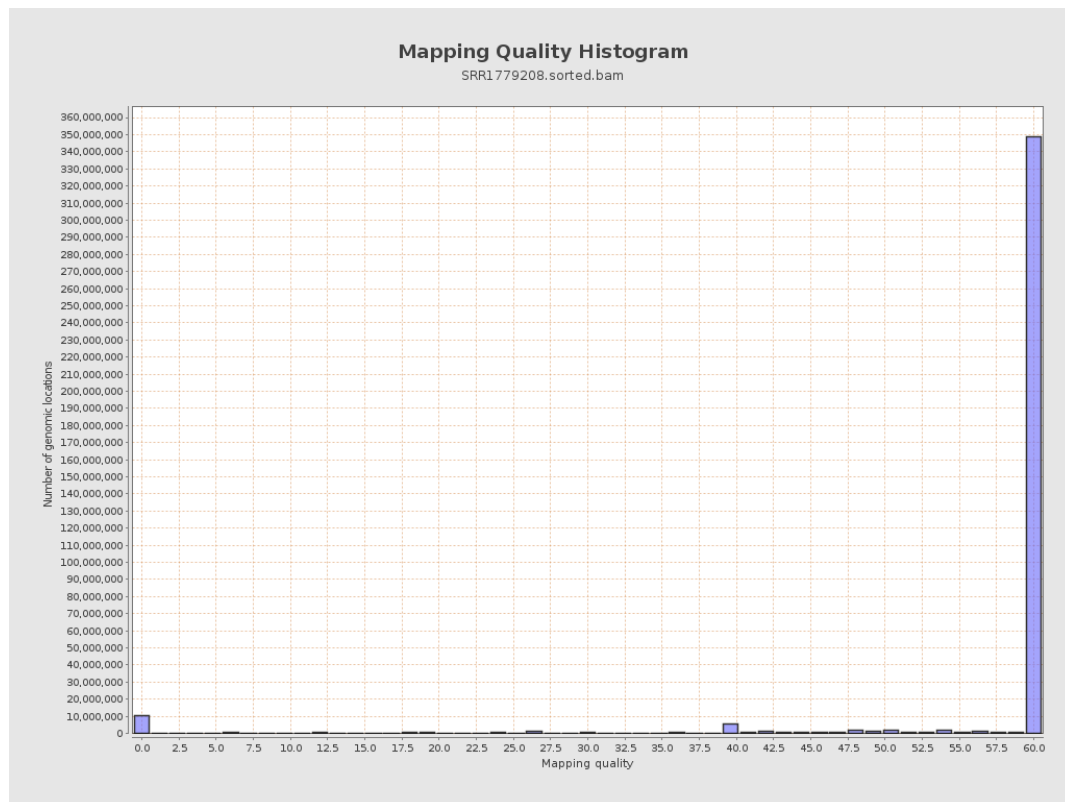
11. Results : Homopolymer Indels



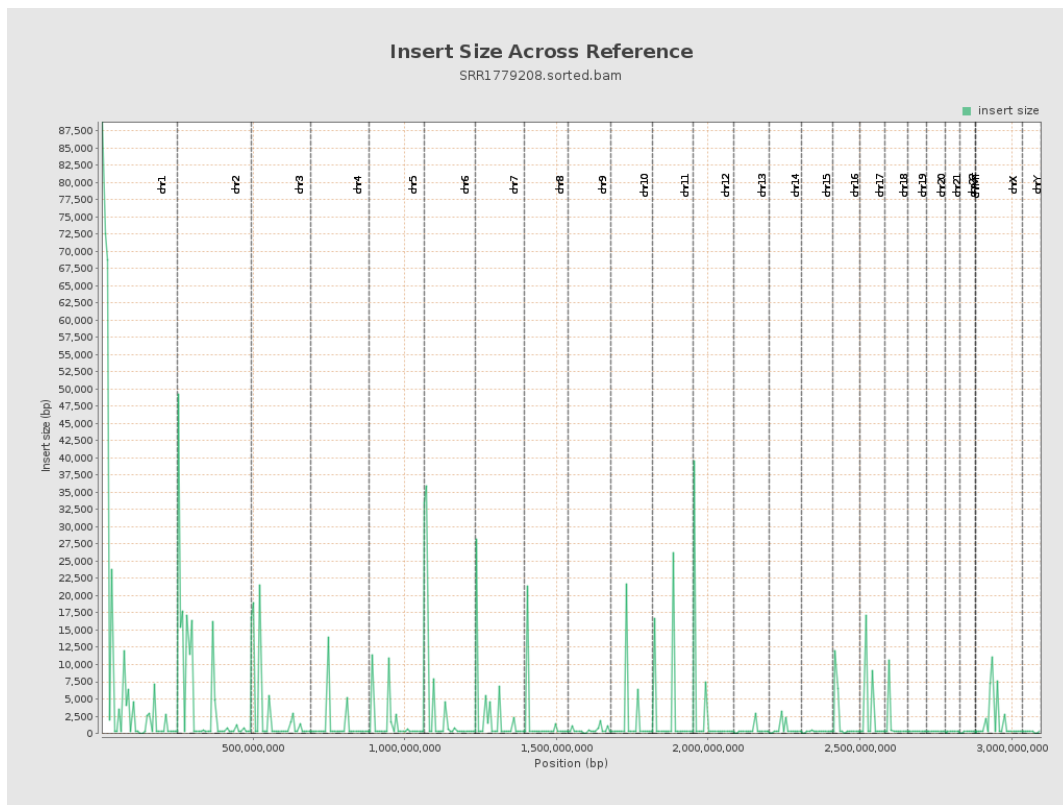
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

