

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 01:58:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472579.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_SRR3472579 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472579_1.fastq.gz SRR3472579_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 01:58:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472579.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,404,600
Mapped reads	7,707,250 / 91.7%
Unmapped reads	697,350 / 8.3%
Mapped paired reads	7,707,250 / 91.7%
Mapped reads, first in pair	3,887,004 / 46.25%
Mapped reads, second in pair	3,820,246 / 45.45%
Mapped reads, both in pair	7,523,198 / 89.51%
Mapped reads, singletons	184,052 / 2.19%
Secondary alignments	0
Supplementary alignments	252,278 / 3%
Read min/max/mean length	30 / 100 / 101.17
Duplicated reads (estimated)	1,162,109 / 13.83%
Duplication rate	12.77%
Clipped reads	5,890,768 / 70.09%

2.2. ACGT Content

Number/percentage of A's	161,700,981 / 25.75%
Number/percentage of C's	125,666,671 / 20.01%
Number/percentage of T's	186,867,638 / 29.75%
Number/percentage of G's	153,410,658 / 24.43%
Number/percentage of N's	423,449 / 0.07%

GC Percentage	44.43%
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2.3. Coverage

Mean	0.203
Standard Deviation	2.1389

2.4. Mapping Quality

Mean Mapping Quality	50.34
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2.5. Insert size

Mean	255,247.47
Standard Deviation	4,892,314.17
P25/Median/P75	92 / 129 / 176

2.6. Mismatches and indels

General error rate	1.22%
Mismatches	7,557,427
Insertions	61,481
Mapped reads with at least one insertion	0.78%
Deletions	142,098
Mapped reads with at least one deletion	1.81%
Homopolymer indels	42.45%

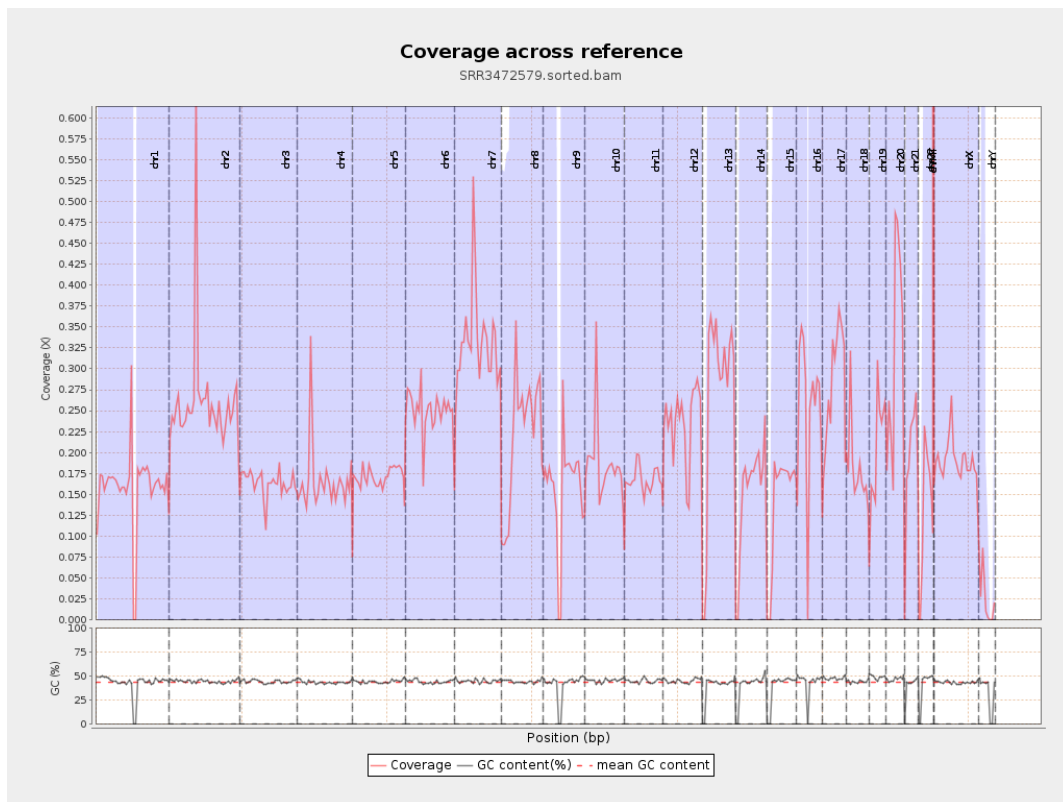
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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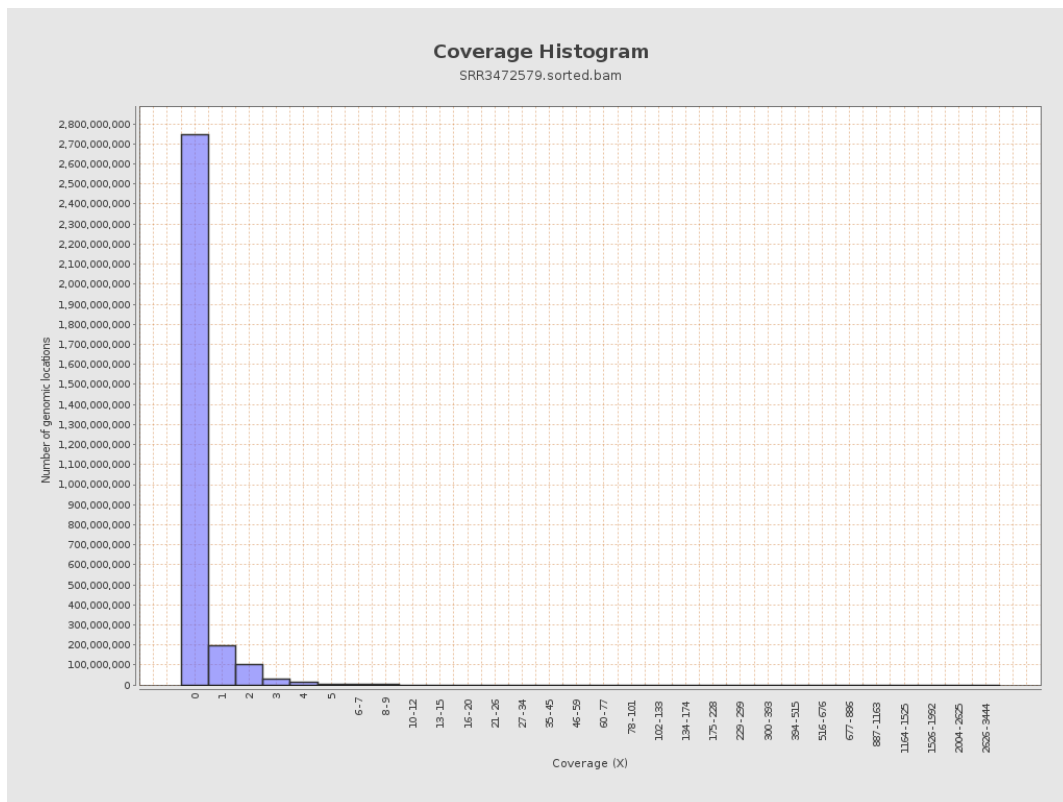
		bases	coverage	deviation
chr1	249250621	39260276	0.1575	2.5457
chr2	243199373	63284967	0.2602	3.1398
chr3	198022430	32306232	0.1631	0.6036
chr4	191154276	31444324	0.1645	1.1727
chr5	180915260	30941844	0.171	0.6785
chr6	171115067	42550092	0.2487	1.1756
chr7	159138663	53425986	0.3357	3.9536
chr8	146364022	32204534	0.22	1.8226
chr9	141213431	22228694	0.1574	2.4202
chr10	135534747	25138800	0.1855	1.8576
chr11	135006516	22333491	0.1654	1.6229
chr12	133851895	31493889	0.2353	0.801
chr13	115169878	30800746	0.2674	0.8247
chr14	107349540	16384834	0.1526	4.587
chr15	102531392	14629420	0.1427	0.5737
chr16	90354753	23011911	0.2547	1.1557
chr17	81195210	23159365	0.2852	1.9006
chr18	78077248	14256824	0.1826	4.2988
chr19	59128983	12365242	0.2091	1.7946
chr20	63025520	20136155	0.3195	1.1998
chr21	48129895	9209479	0.1913	0.8609
chr22	51304566	6532314	0.1273	0.5474
chrMT	16571	174671	10.5408	7.941
chrX	155270560	29614826	0.1907	1.0203

chrY	59373566	1448136	0.0244	0.9198
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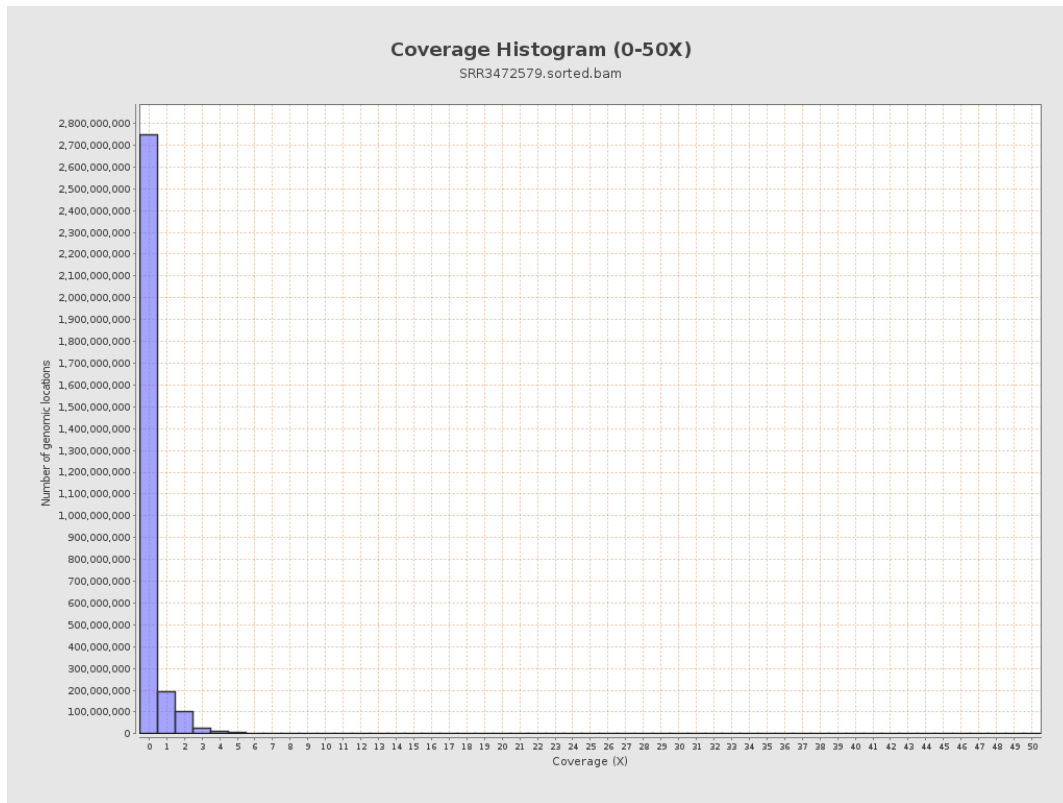
3. Results : Coverage across reference



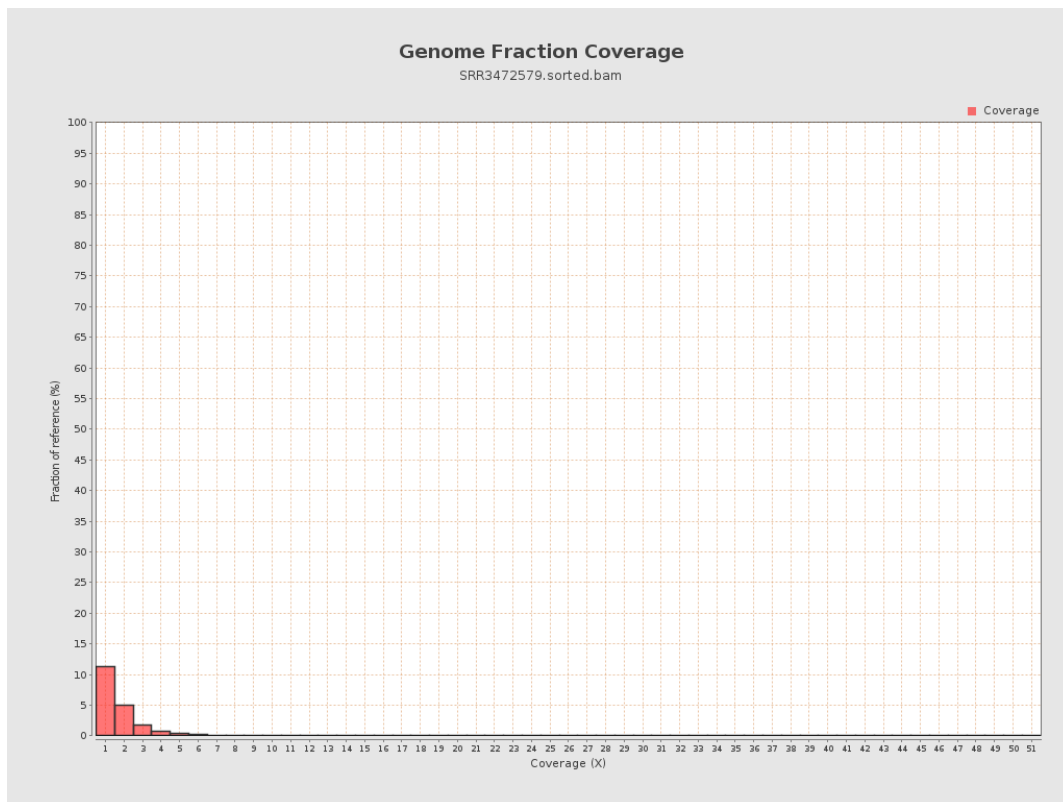
4. Results : Coverage Histogram



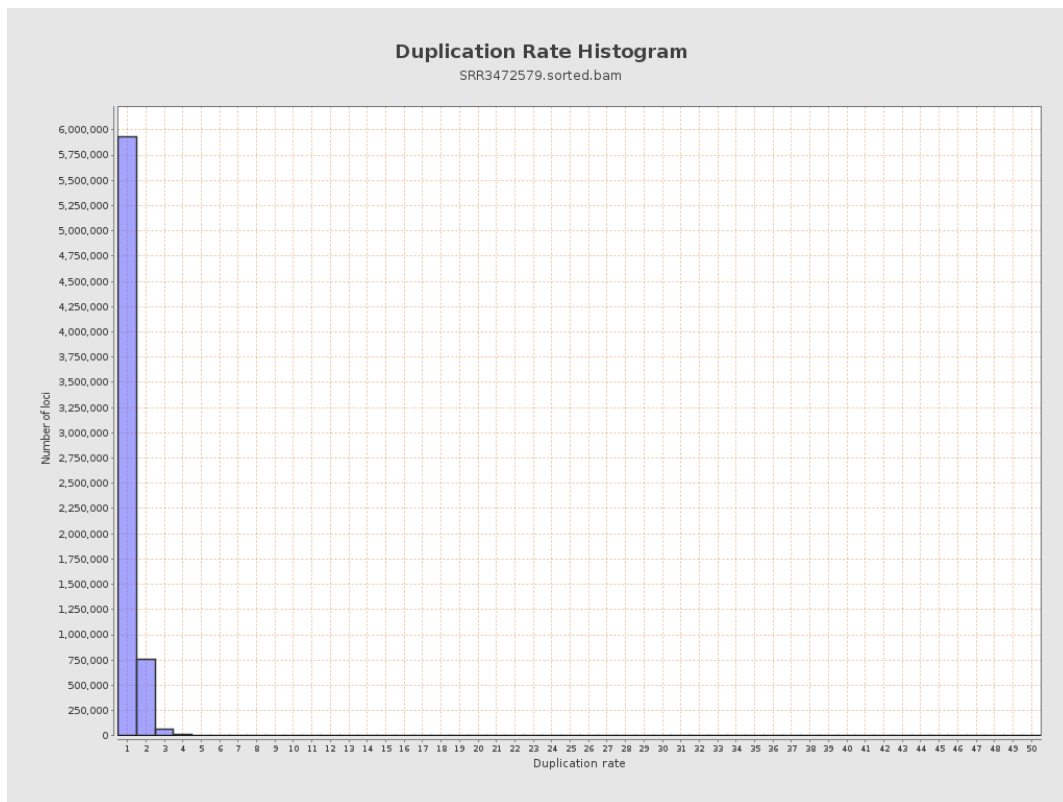
5. Results : Coverage Histogram (0-50X)



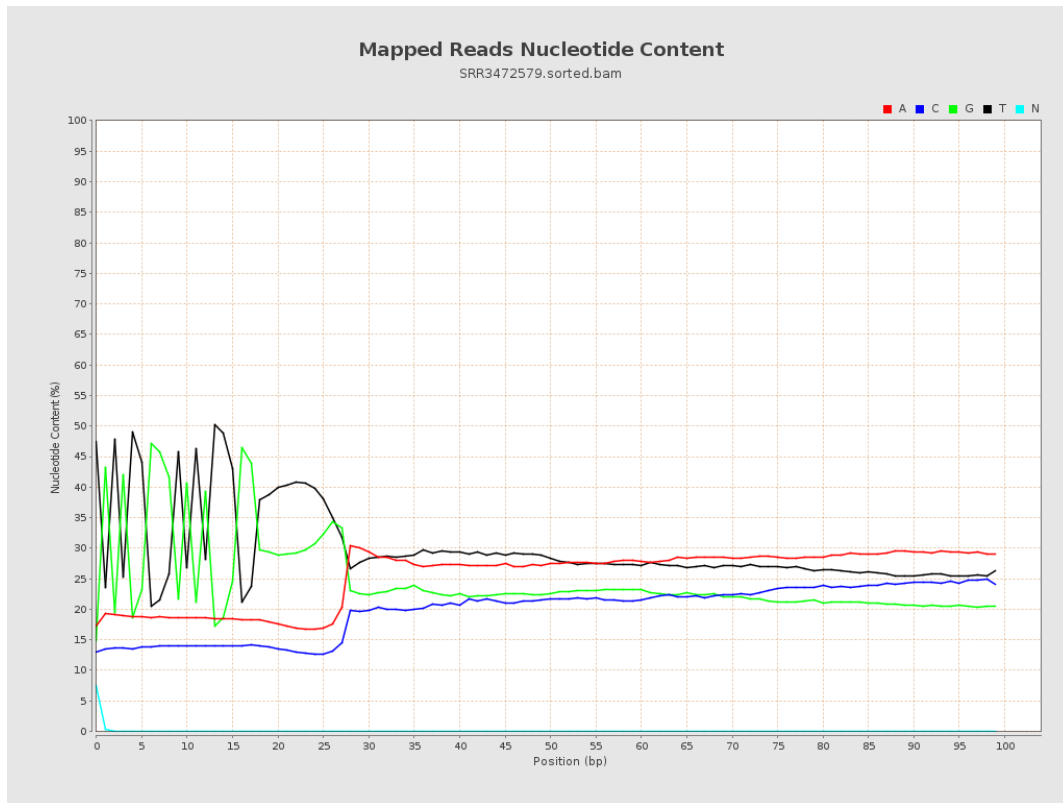
6. Results : Genome Fraction Coverage



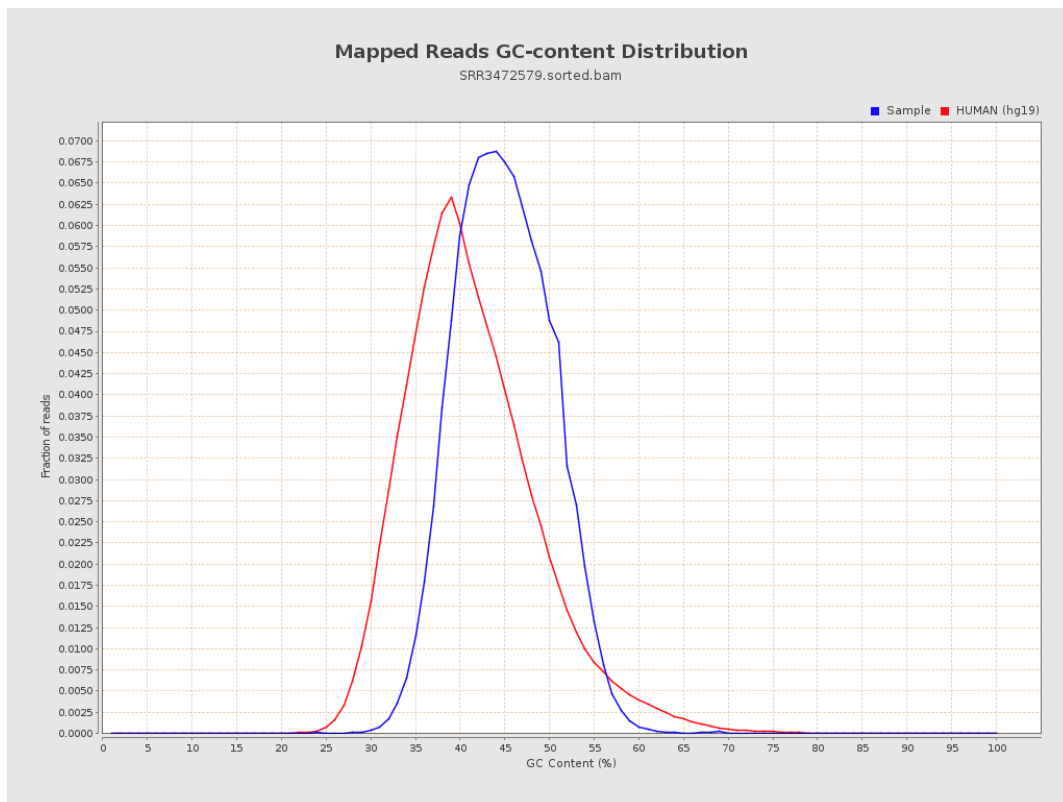
7. Results : Duplication Rate Histogram



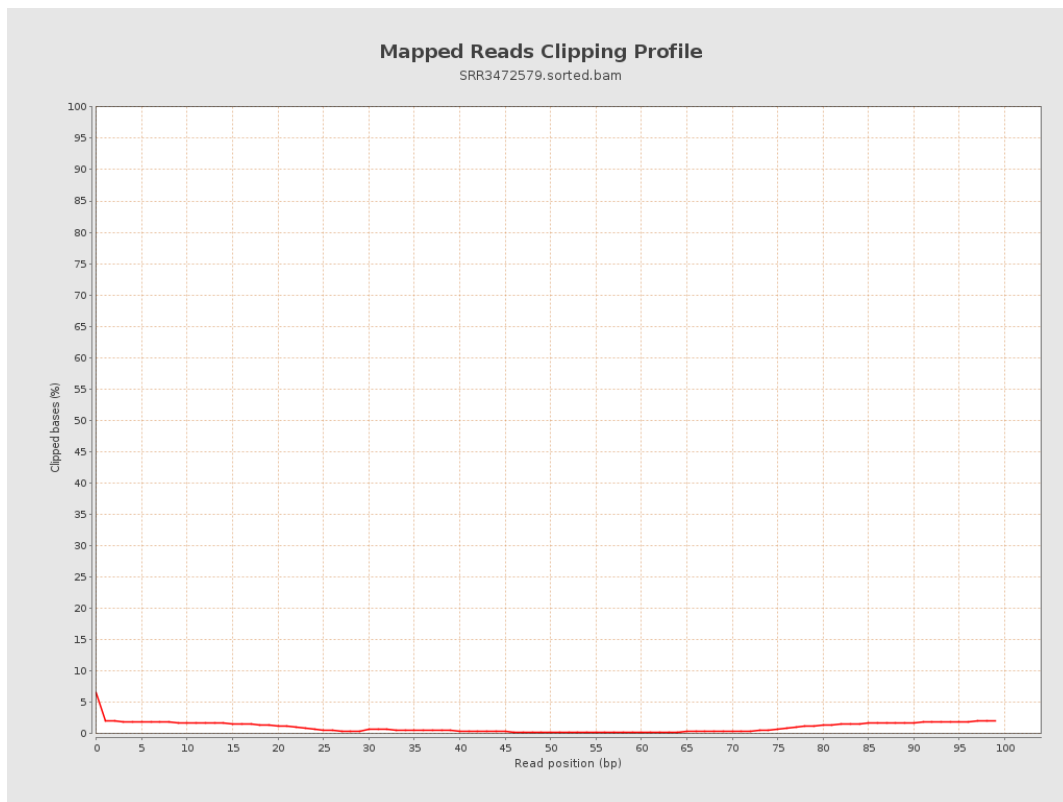
8. Results : Mapped Reads Nucleotide Content



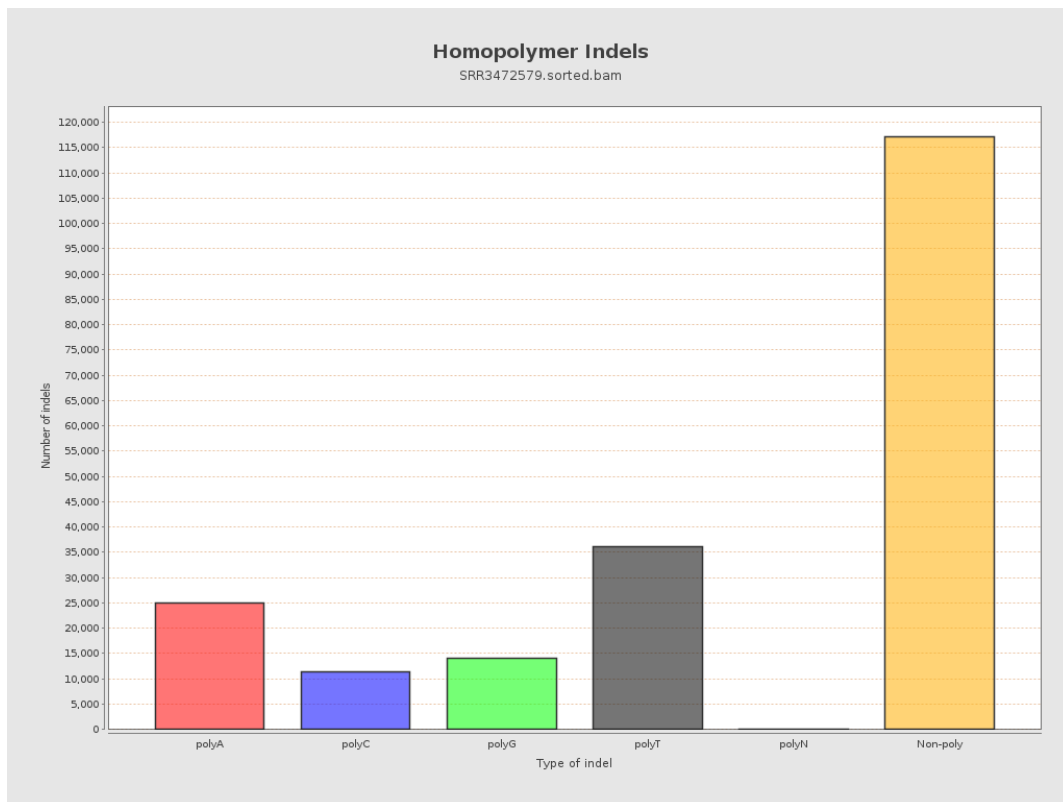
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



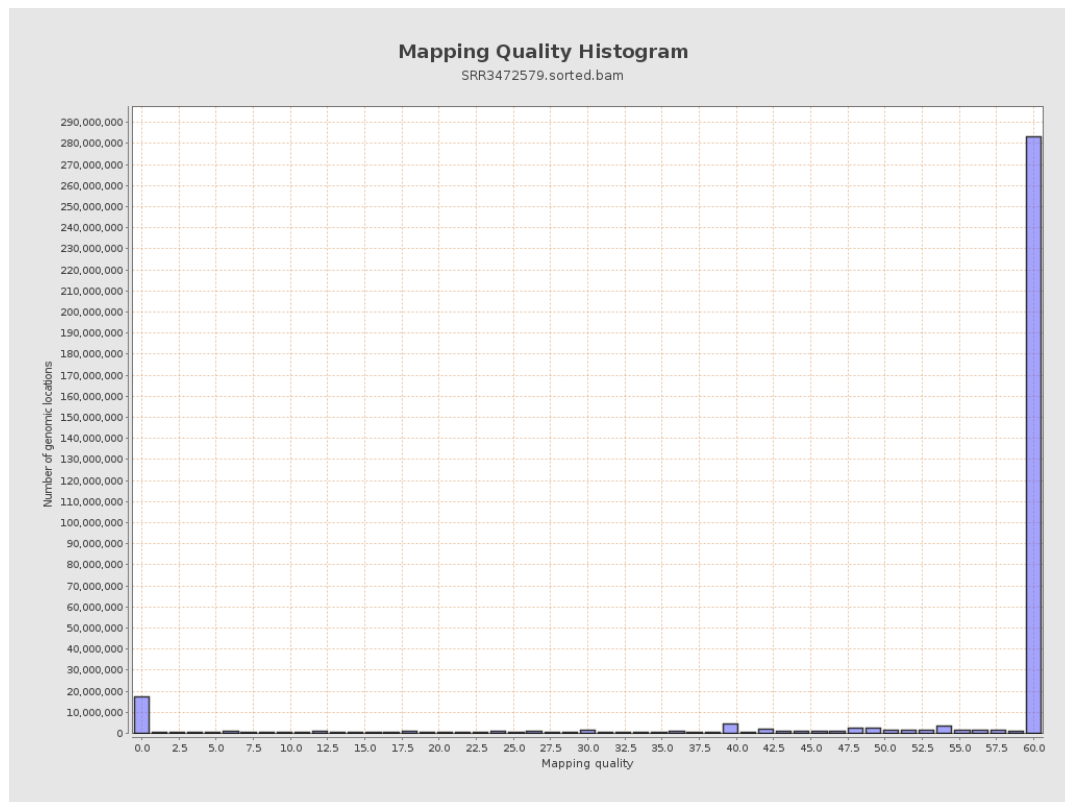
11. Results : Homopolymer Indels



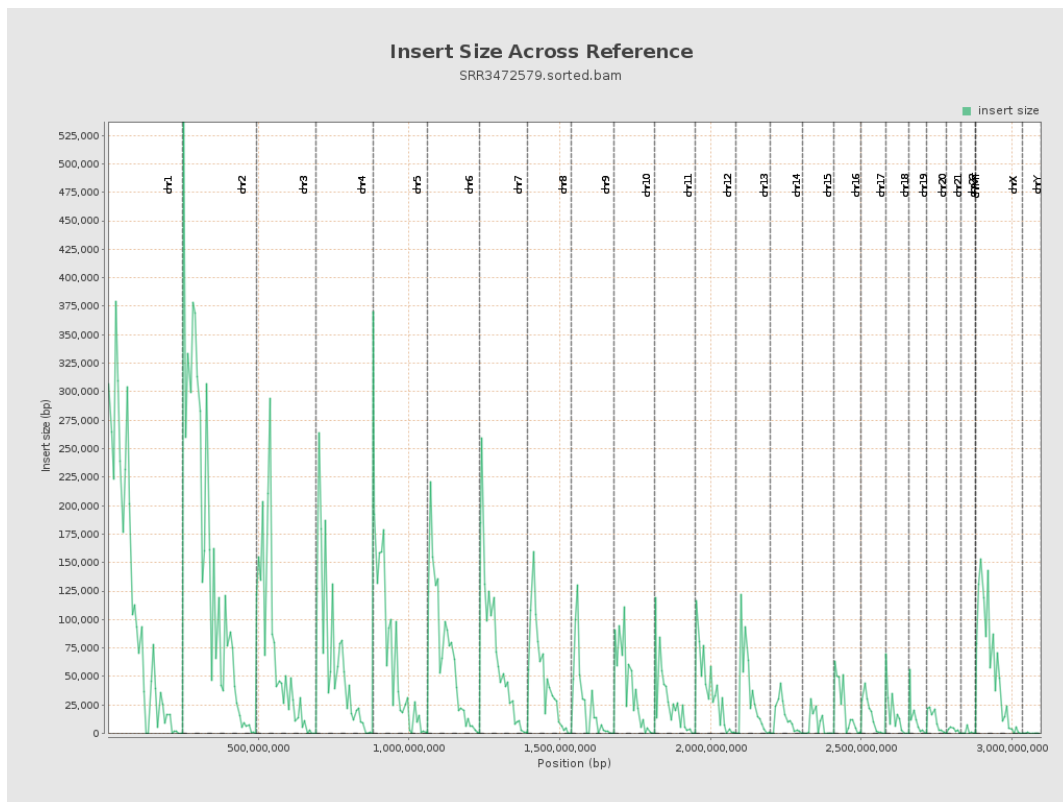
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

