Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 13:21:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006016.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_SRR1006016 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006016_1.fastq.gz SRR1006016_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 13:21:32 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006016.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,674,582
Mapped reads	11,365,167 / 72.51%
Unmapped reads	4,309,415 / 27.49%
Mapped paired reads	11,365,167 / 72.51%
Mapped reads, first in pair	5,720,644 / 36.5%
Mapped reads, second in pair	5,644,523 / 36.01%
Mapped reads, both in pair	10,072,904 / 64.26%
Mapped reads, singletons	1,292,263 / 8.24%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	498,573 / 3.18%
Duplication rate	3.66%
Clipped reads	917,002 / 5.85%

2.2. ACGT Content

Number/percentage of A's	128,233,862 / 29.2%
Number/percentage of C's	90,955,296 / 20.71%
Number/percentage of T's	127,331,603 / 29%
Number/percentage of G's	92,229,409 / 21%
Number/percentage of N's	338,729 / 0.08%
GC Percentage	41.72%

2.3. Coverage

Mean	0.1419
Standard Deviation	0.8213

2.4. Mapping Quality

Mean Mapping Quality	47.56

2.5. Insert size

Mean	68,223.94
Standard Deviation	2,484,469.57
P25/Median/P75	73 / 108 / 159

2.6. Mismatches and indels

General error rate	0.67%
Mismatches	2,927,881
Insertions	12,399
Mapped reads with at least one insertion	0.11%
Deletions	42,720
Mapped reads with at least one deletion	0.38%
Homopolymer indels	44.34%

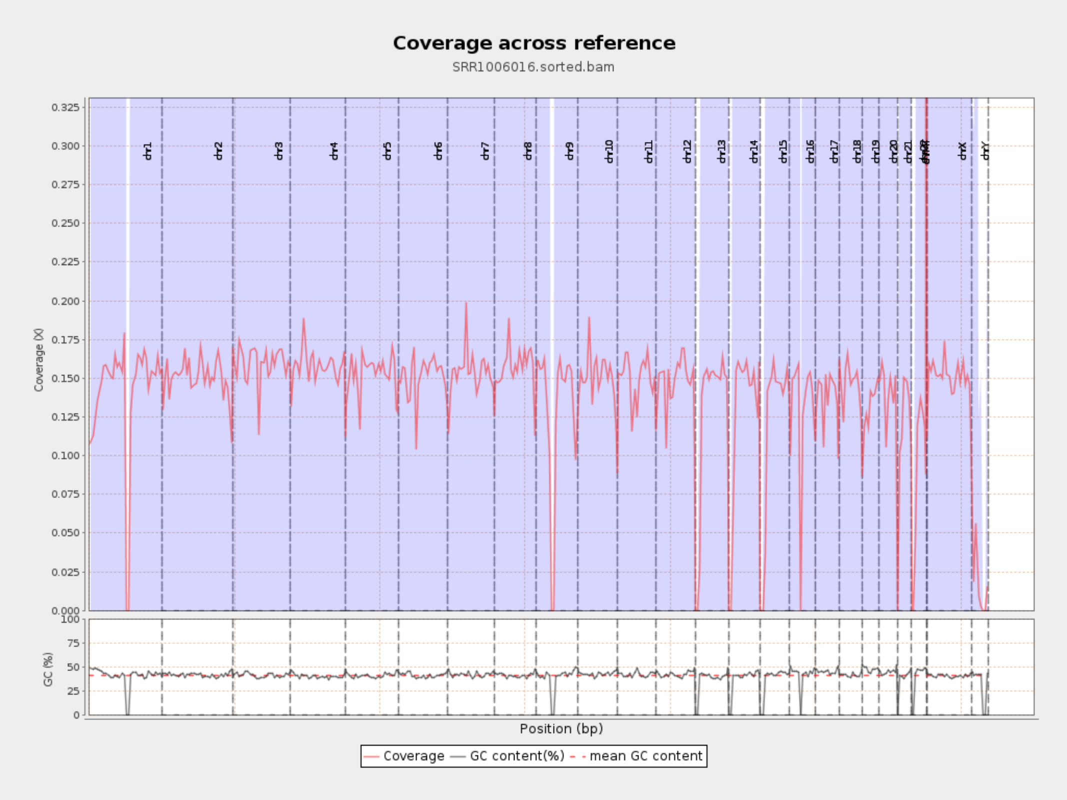
2.7. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**

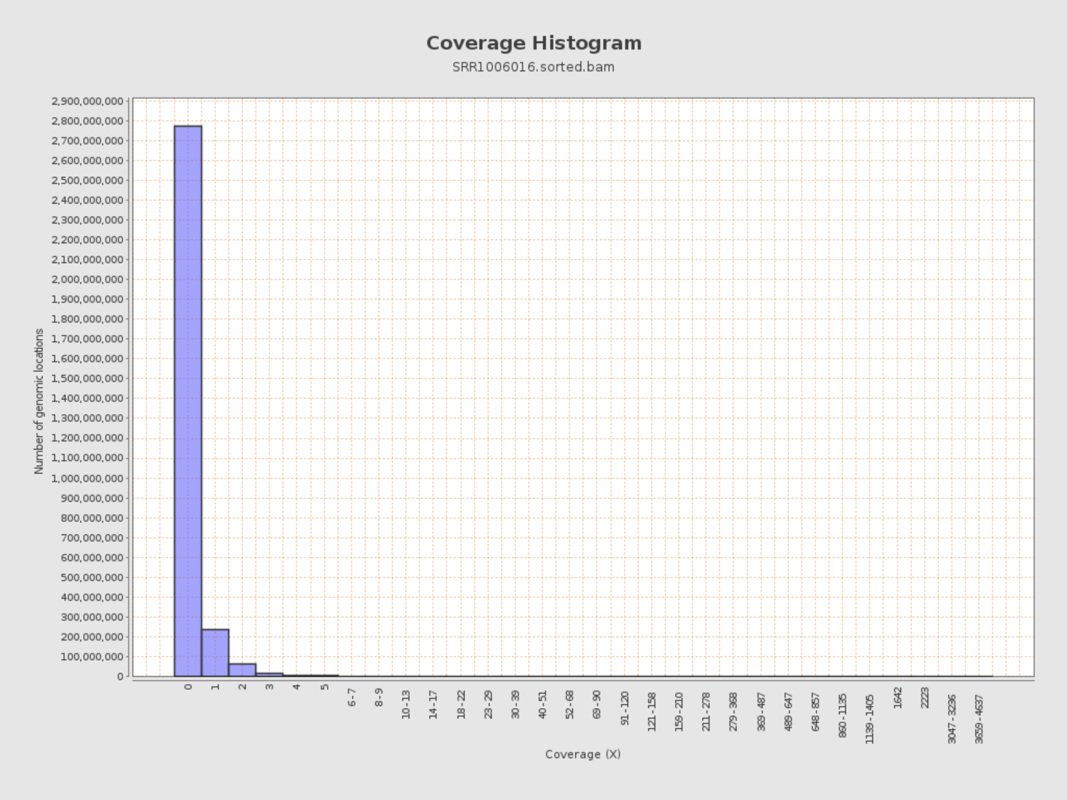
chr1	249250621	35244370	0.1414	1.1429
chr2	243199373	36644799	0.1507	0.6483
chr3	198022430	31698504	0.1601	0.5077
chr4	191154276	30226601	0.1581	0.5623
chr5	180915260	27628951	0.1527	0.496
chr6	171115067	25916492	0.1515	0.6047
chr7	159138663	24606109	0.1546	0.9951
chr8	146364022	23010519	0.1572	2.3081
chr9	141213431	18126007	0.1284	0.554
chr10	135534747	20527231	0.1515	0.7038
chr11	135006516	20171239	0.1494	0.5934
chr12	133851895	19852584	0.1483	0.4963
chr13	115169878	14531346	0.1262	0.4498
chr14	107349540	13384852	0.1247	0.4824
chr15	102531392	12188814	0.1189	0.4374
chr16	90354753	11757680	0.1301	0.5299
chr17	81195210	11156787	0.1374	0.5125
chr18	78077248	11457534	0.1467	0.8969
chr19	59128983	7773680	0.1315	0.8582
chr20	63025520	8773793	0.1392	0.4925
chr21	48129895	5541520	0.1151	0.487
chr22	51304566	4424128	0.0862	0.3852
chrMT	16571	44092	2.6608	2.3091
chrX	155270560	23408073	0.1508	0.5609

chrY	59373566	1049539	0.0177	0.3554

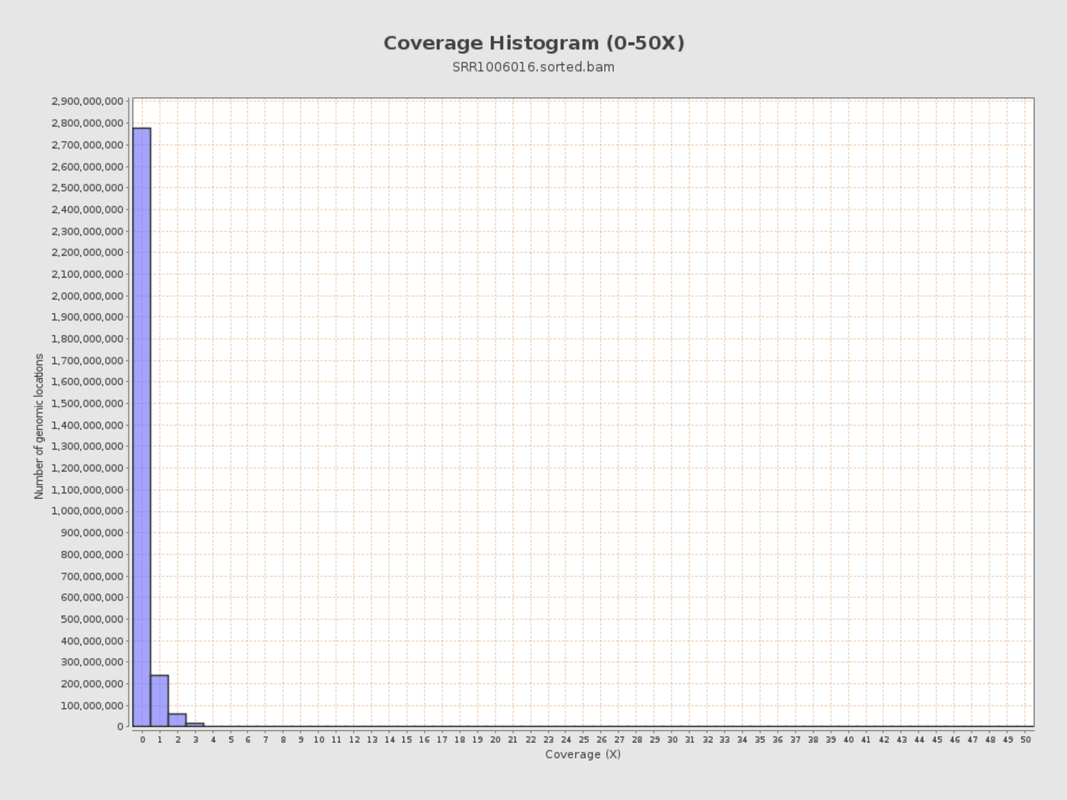
3. Results : Coverage across reference



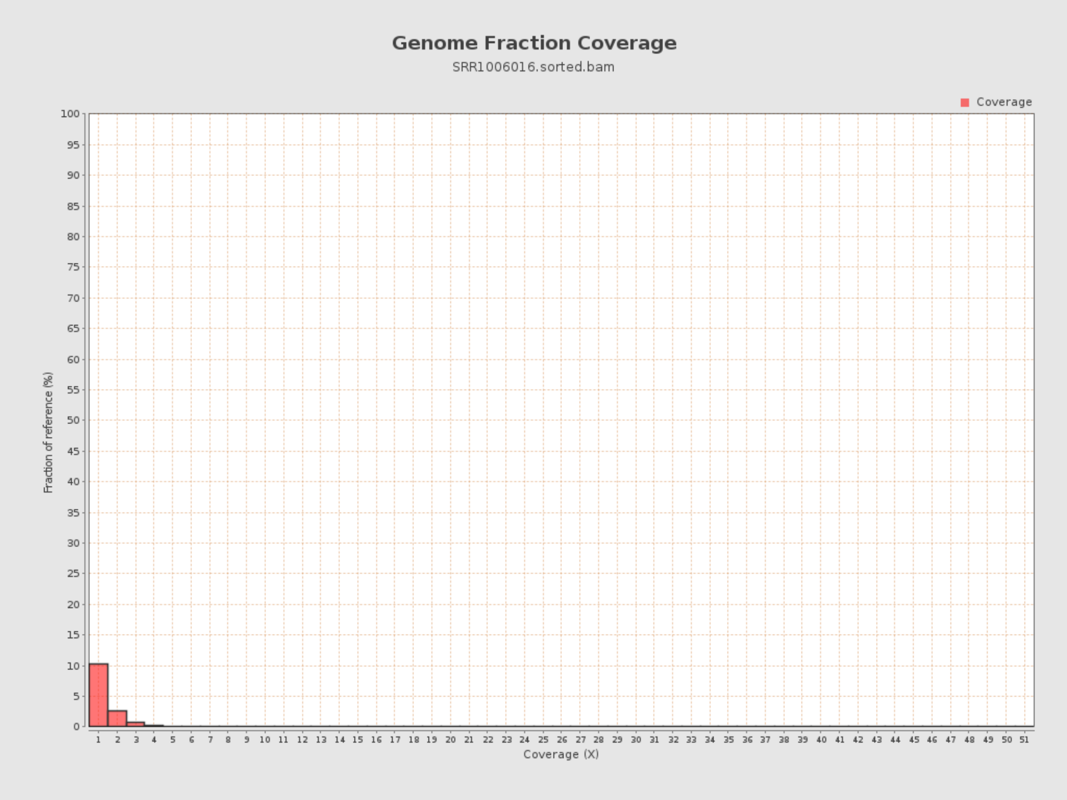
4. Results : Coverage Histogram



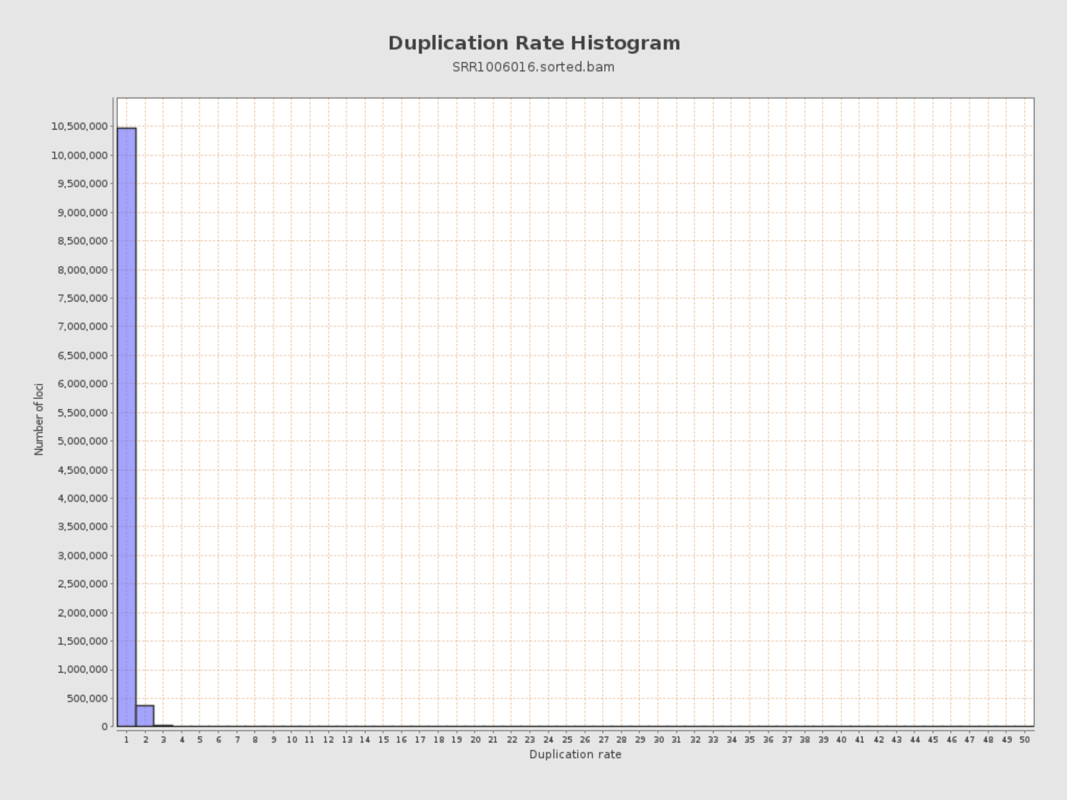
5. Results : Coverage Histogram (0-50X)



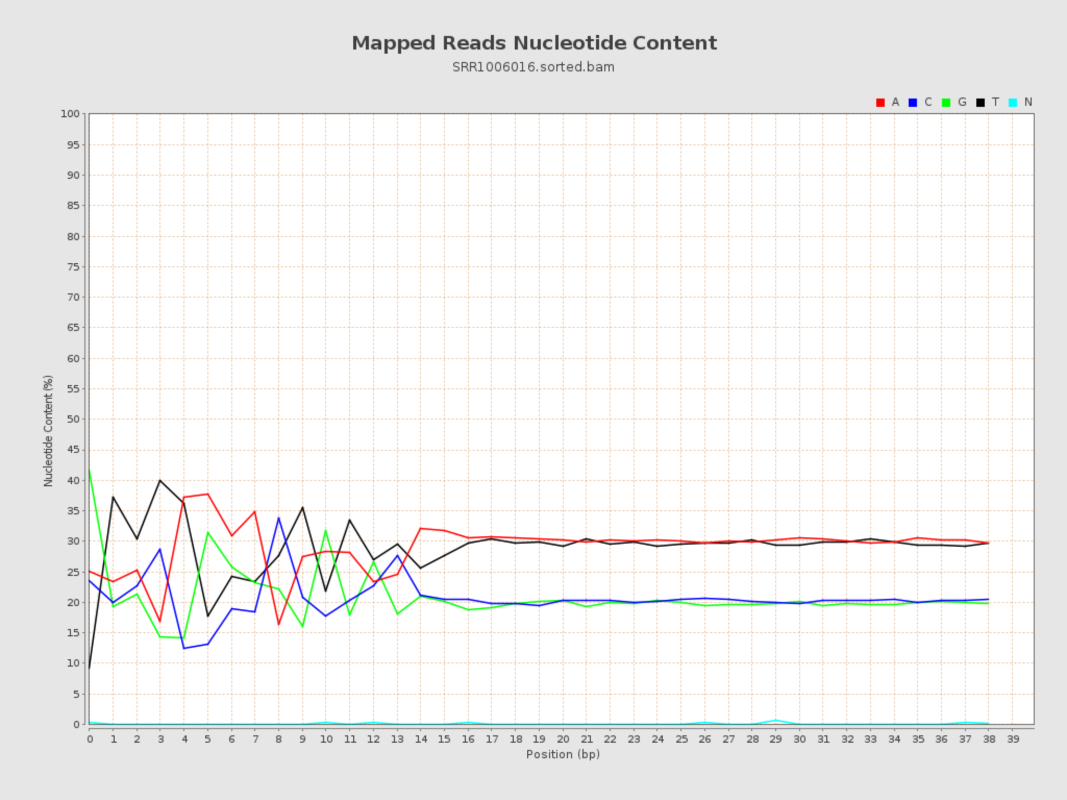
6. Results : Genome Fraction Coverage



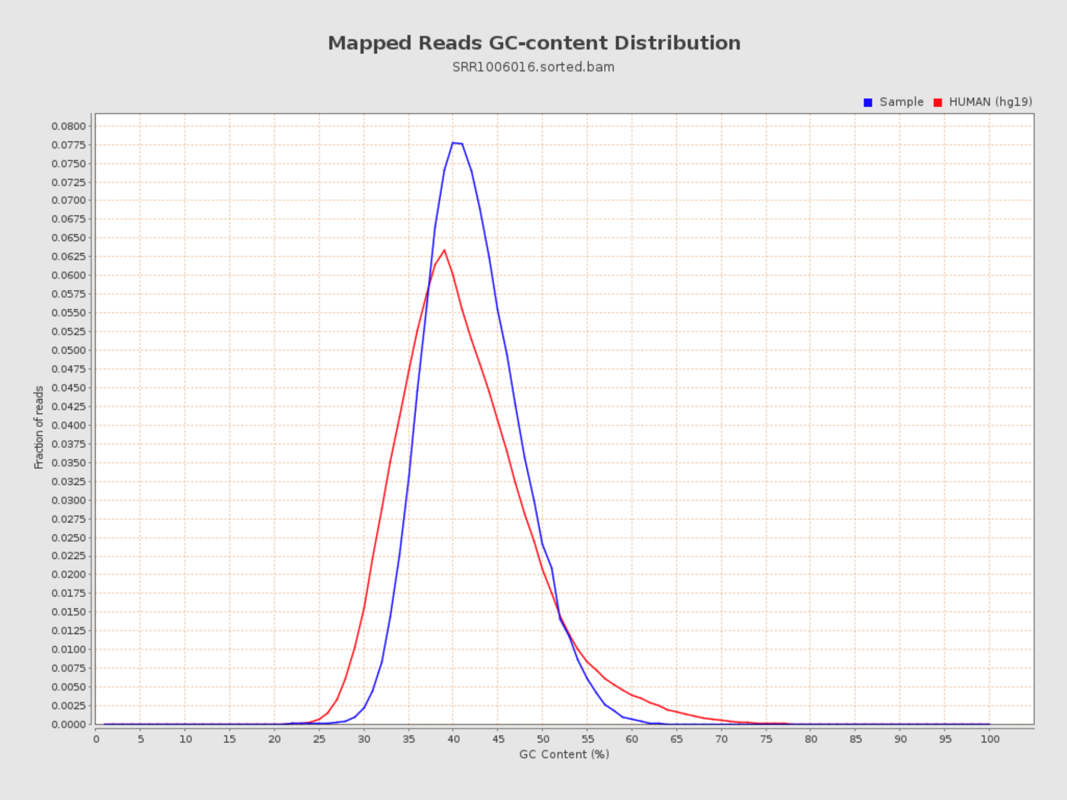
7. Results : Duplication Rate Histogram



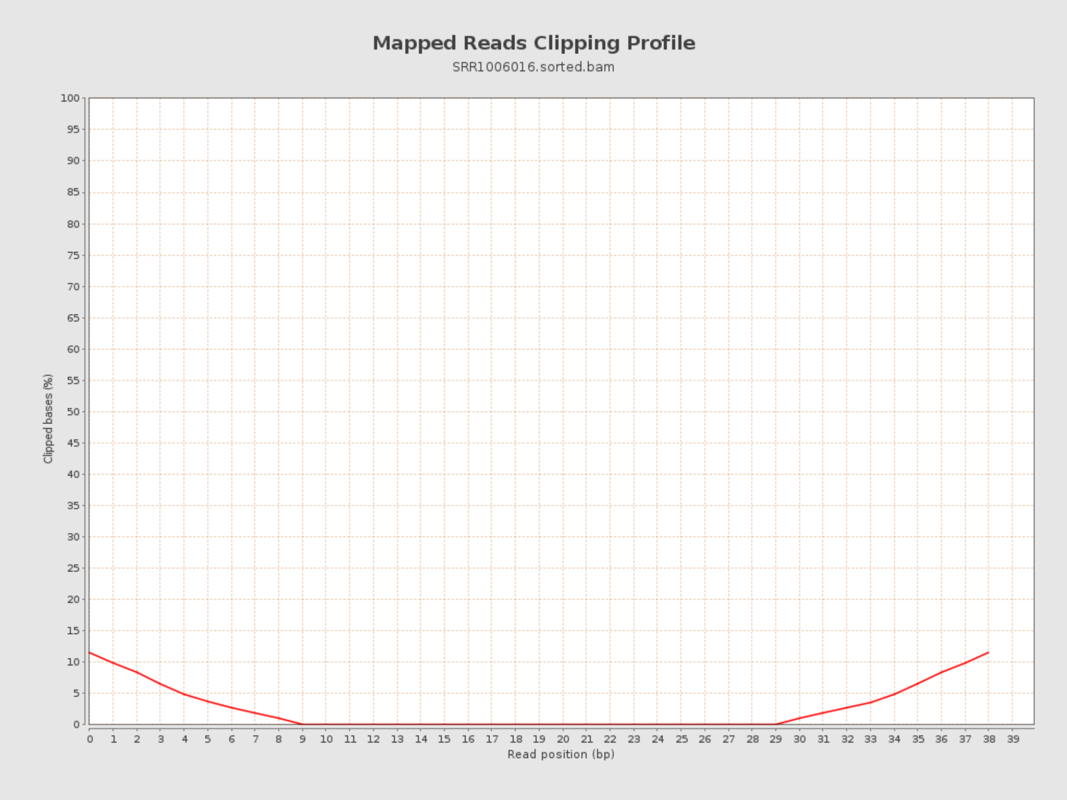
8. Results : Mapped Reads Nucleotide Content



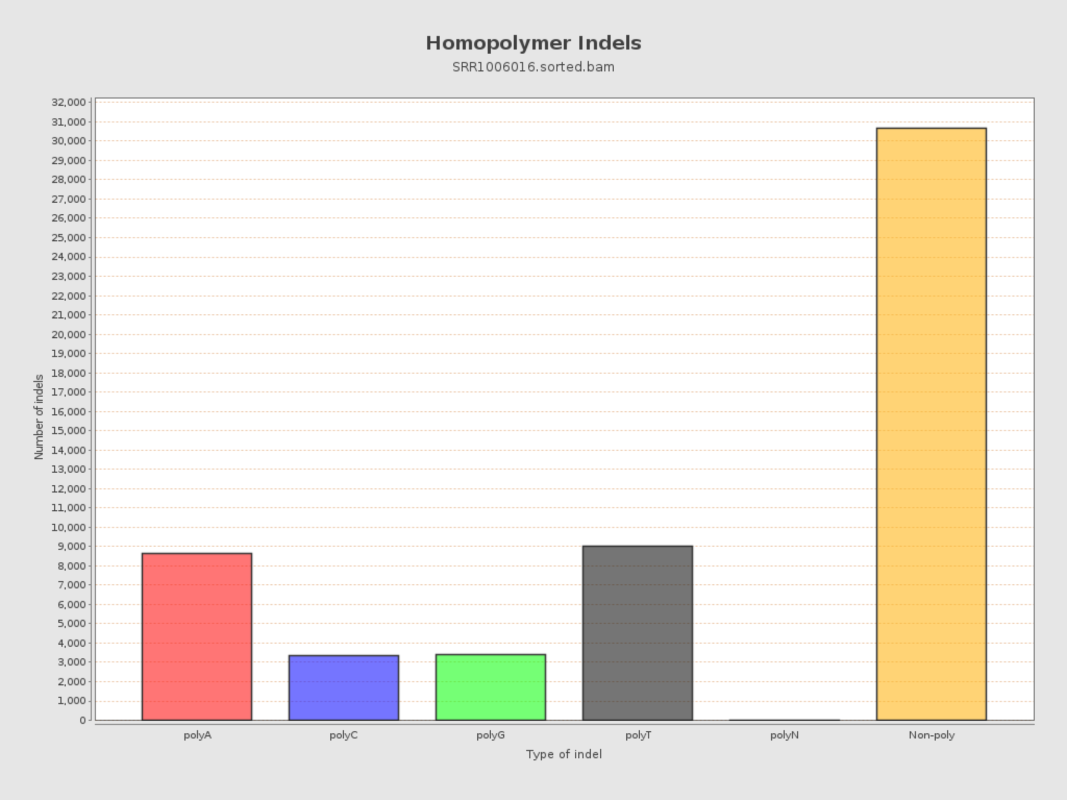
9. Results : Mapped Reads GC-content Distribution



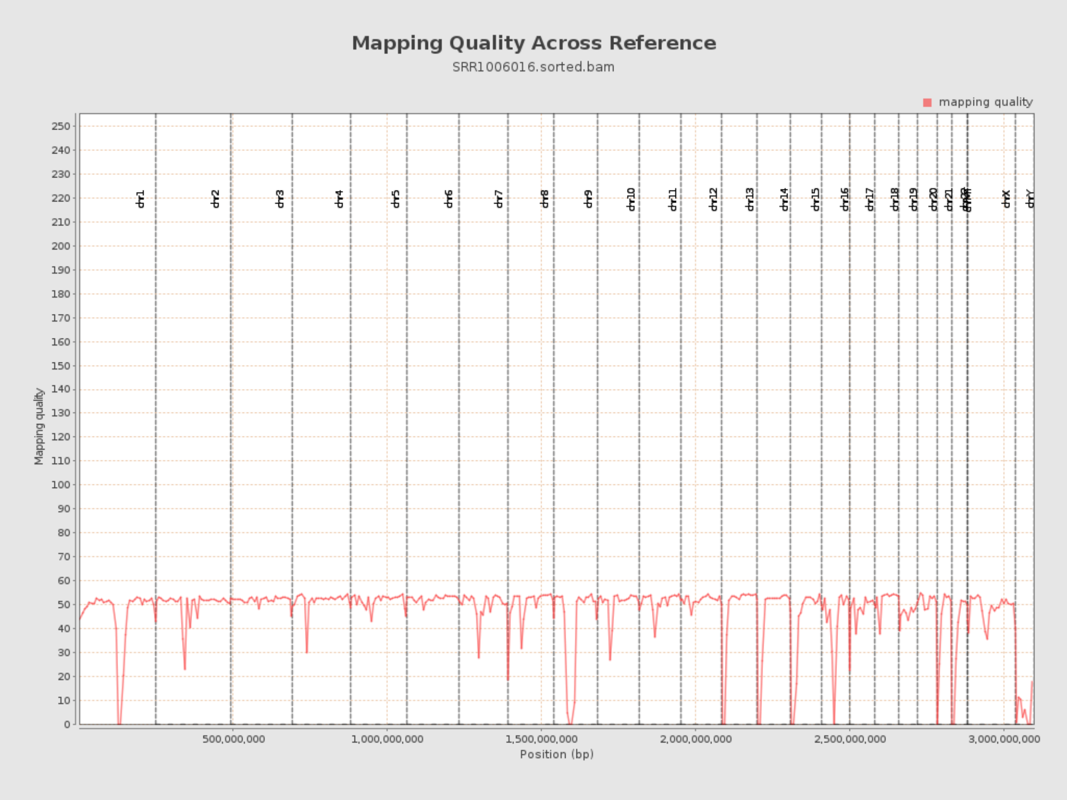
10. Results : Mapped Reads Clipping Profile



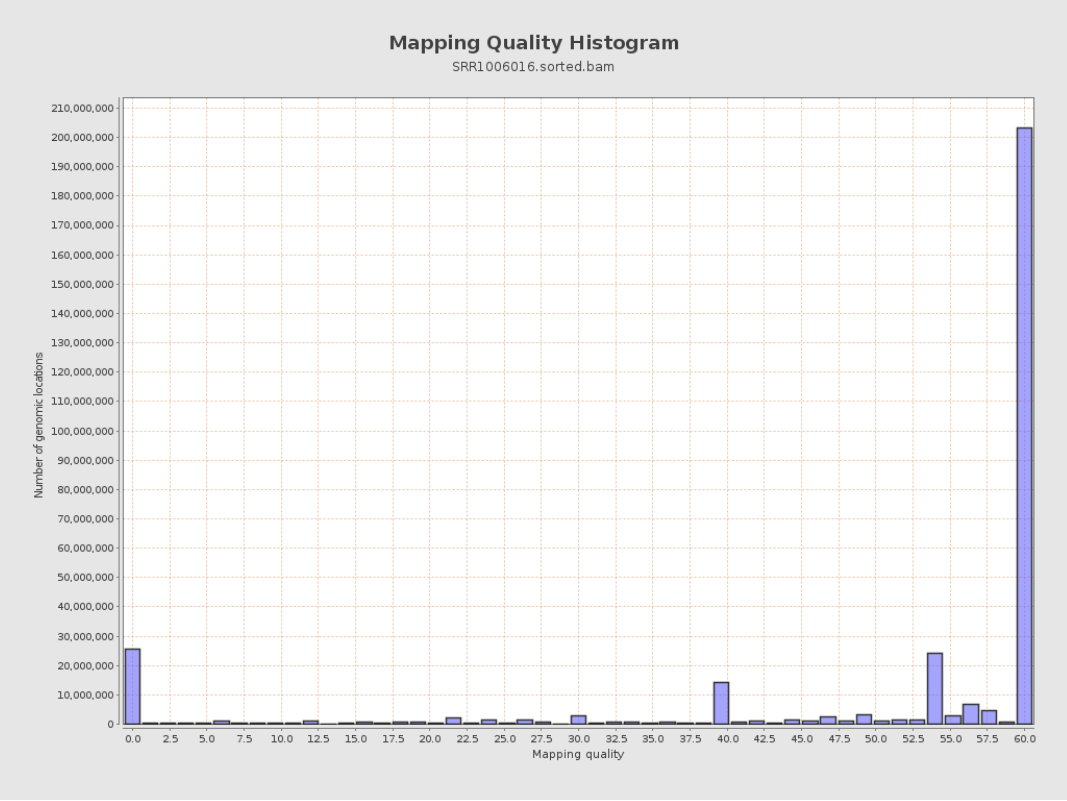
11. Results : Homopolymer Indels



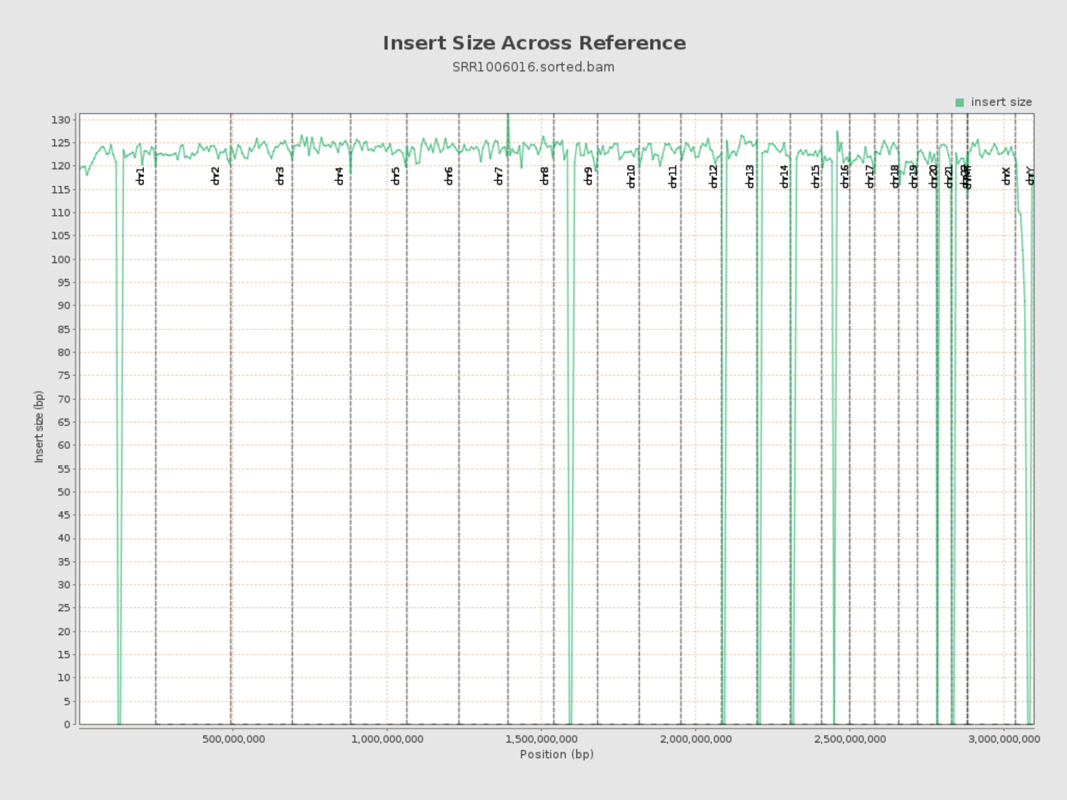
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram