Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 00:11:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006228.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_SRR1006228 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006228_1.fastq.gz SRR1006228_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 00:11:05 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006228.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,224,110
Mapped reads	10,817,744 / 88.5%
Unmapped reads	1,406,366 / 11.5%
Mapped paired reads	10,817,744 / 88.5%
Mapped reads, first in pair	5,470,901 / 44.76%
Mapped reads, second in pair	5,346,843 / 43.74%
Mapped reads, both in pair	9,917,324 / 81.13%
Mapped reads, singletons	900,420 / 7.37%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	664,187 / 5.43%
Duplication rate	5.38%
Clipped reads	681,339 / 5.57%

2.2. ACGT Content

Number/percentage of A's	117,546,270 / 28.1%
Number/percentage of C's	89,281,988 / 21.34%
Number/percentage of T's	120,018,970 / 28.69%
Number/percentage of G's	91,520,289 / 21.87%
Number/percentage of N's	17,598 / 0%
GC Percentage	43.21%

2.3. Coverage

Mean	0.1352
Standard Deviation	0.7162

2.4. Mapping Quality

Mean Mapping Quality	48.18

2.5. Insert size

Mean	81,889.78
Standard Deviation	2,730,294.06
P25/Median/P75	124 / 162 / 219

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	1,661,572
Insertions	12,075
Mapped reads with at least one insertion	0.11%
Deletions	38,963
Mapped reads with at least one deletion	0.36%
Homopolymer indels	44.67%

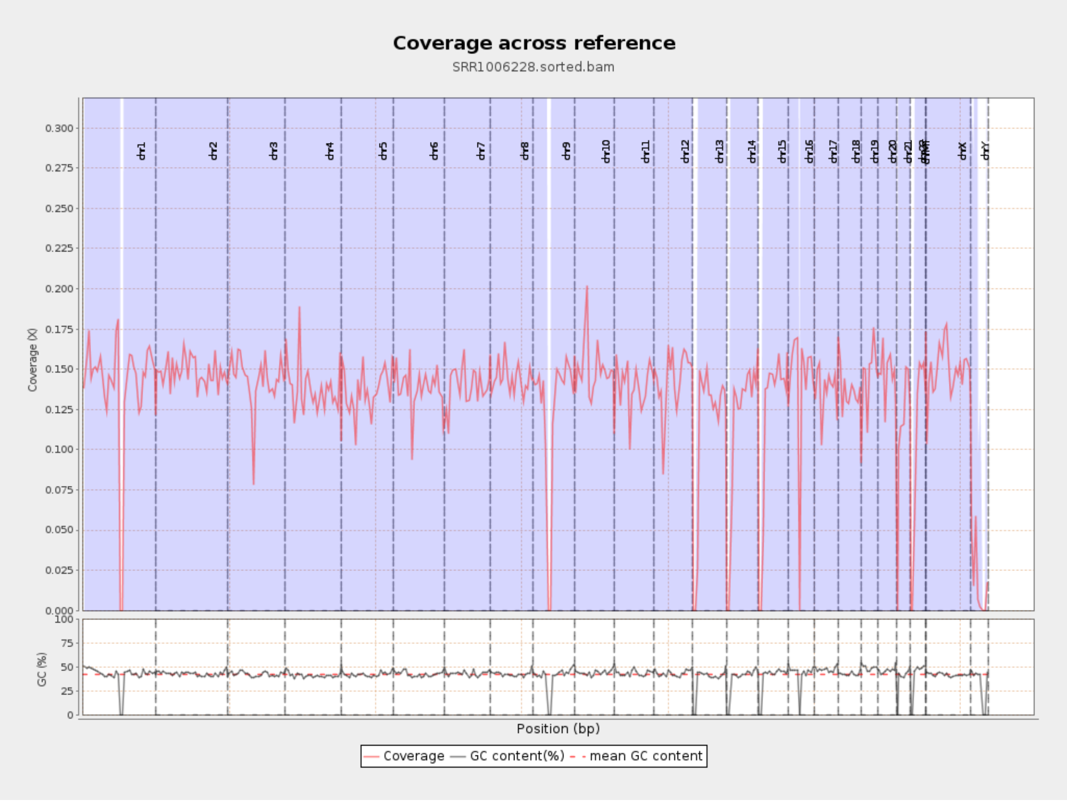
2.7. Chromosome stats

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

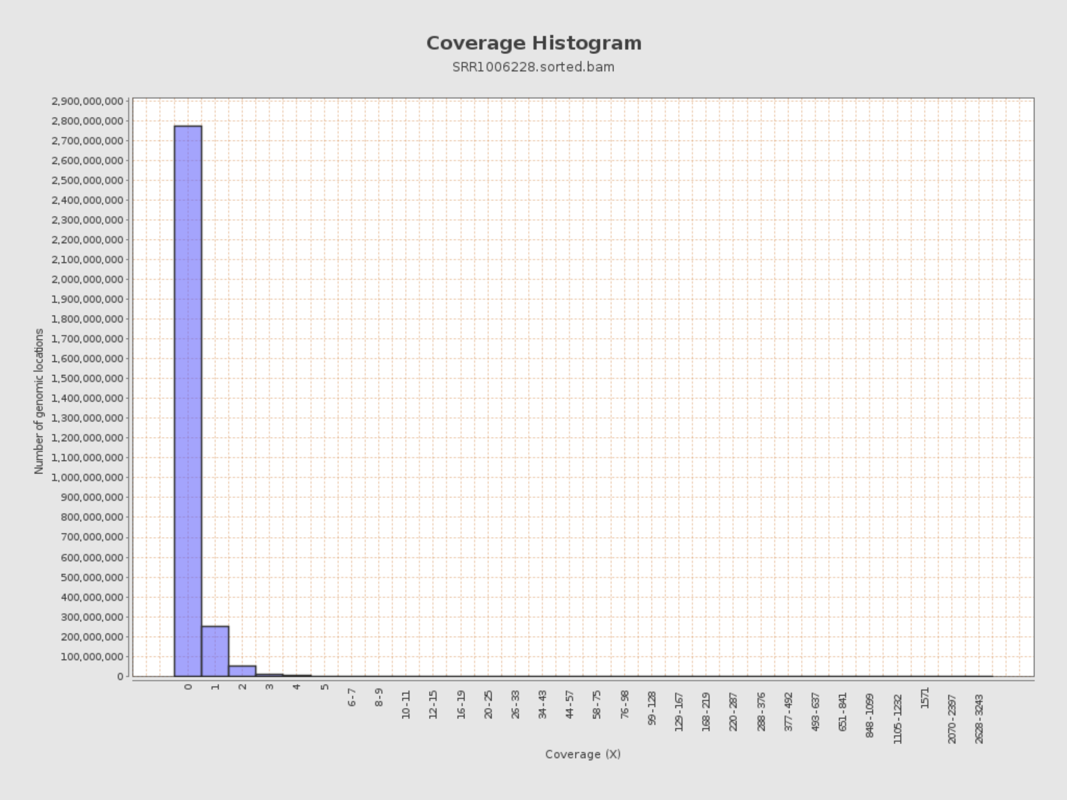
chr1	249250621	34855721	0.1398	1.0837
chr2	243199373	36063635	0.1483	0.6337
chr3	198022430	28360505	0.1432	0.4634
chr4	191154276	26495599	0.1386	0.5241
chr5	180915260	24808728	0.1371	0.4552
chr6	171115067	23719186	0.1386	0.5366
chr7	159138663	22120014	0.139	0.8055
chr8	146364022	21072751	0.144	1.6485
chr9	141213431	17536338	0.1242	0.5368
chr10	135534747	20312725	0.1499	0.7561
chr11	135006516	18770195	0.139	0.6003
chr12	133851895	19319293	0.1443	0.4709
chr13	115169878	13061231	0.1134	0.4136
chr14	107349540	12422899	0.1157	0.4806
chr15	102531392	11979004	0.1168	0.418
chr16	90354753	12699076	0.1405	0.6042
chr17	81195210	11206108	0.138	0.4872
chr18	78077248	10701673	0.1371	0.9738
chr19	59128983	8644943	0.1462	0.7848
chr20	63025520	9297023	0.1475	0.5001
chr21	48129895	5517226	0.1146	0.4965
chr22	51304566	5249770	0.1023	0.407
chrMT	16571	2878	0.1737	0.5355
chrX	155270560	23192402	0.1494	0.5415

chrY	59373566	1027581	0.0173	0.413

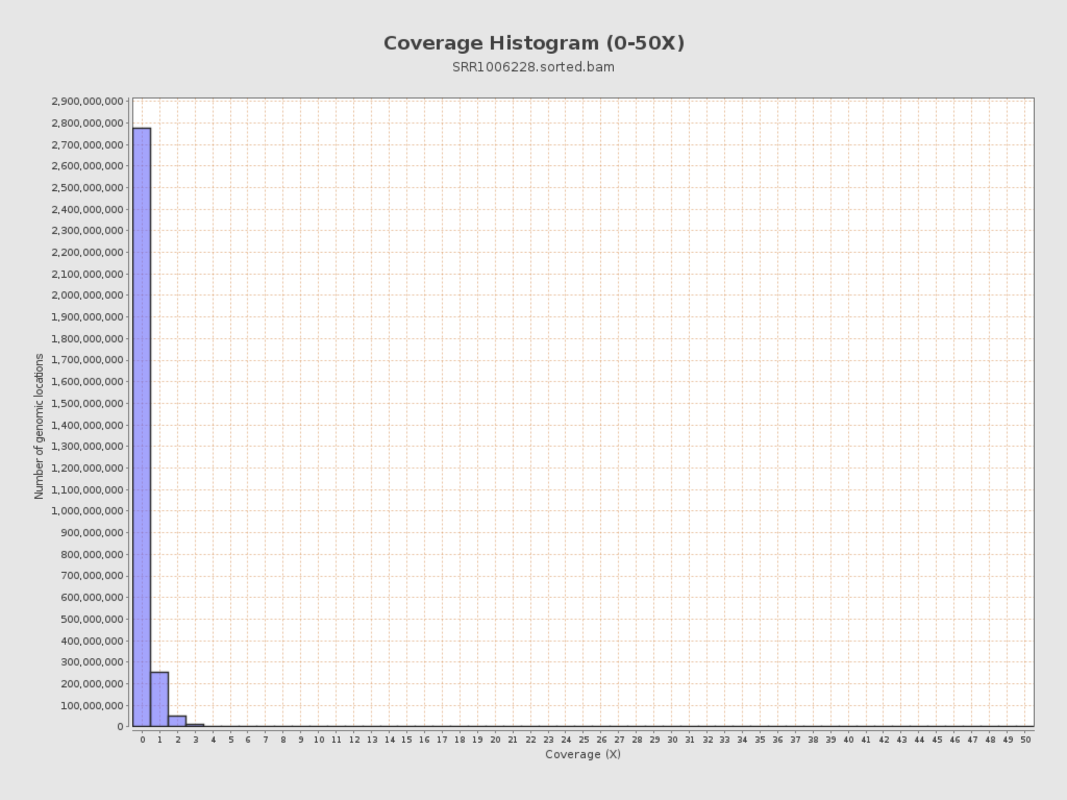
3. Results : Coverage across reference



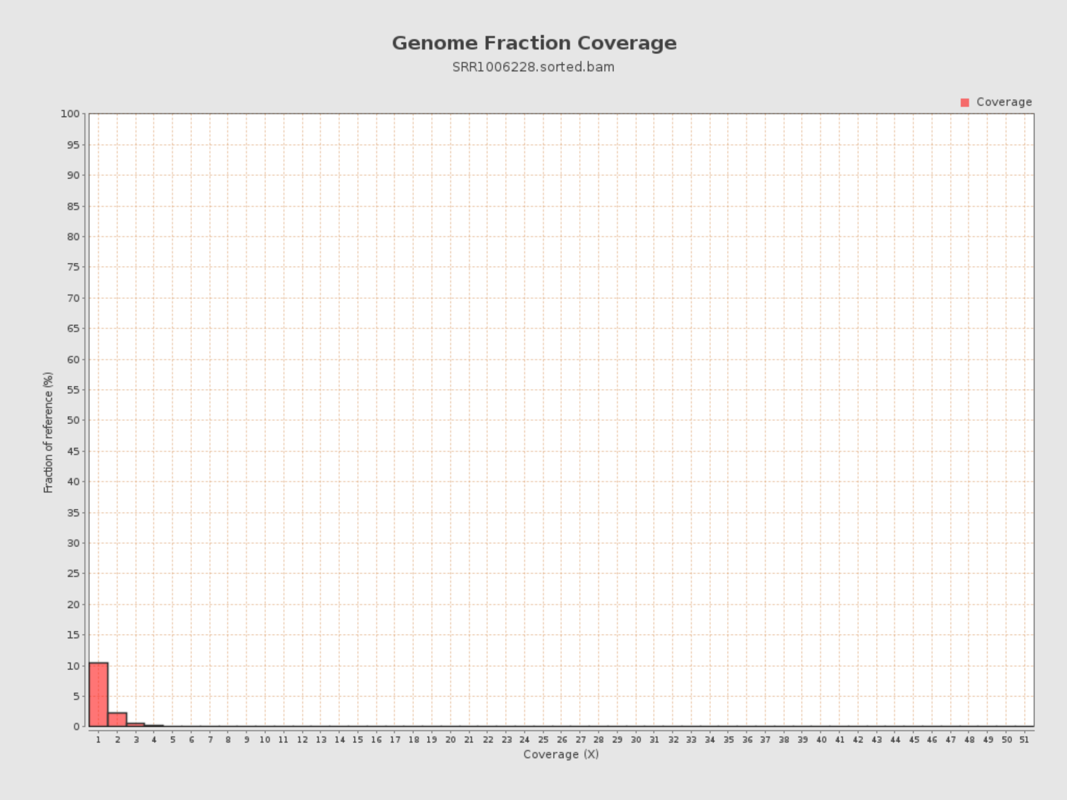
4. Results : Coverage Histogram



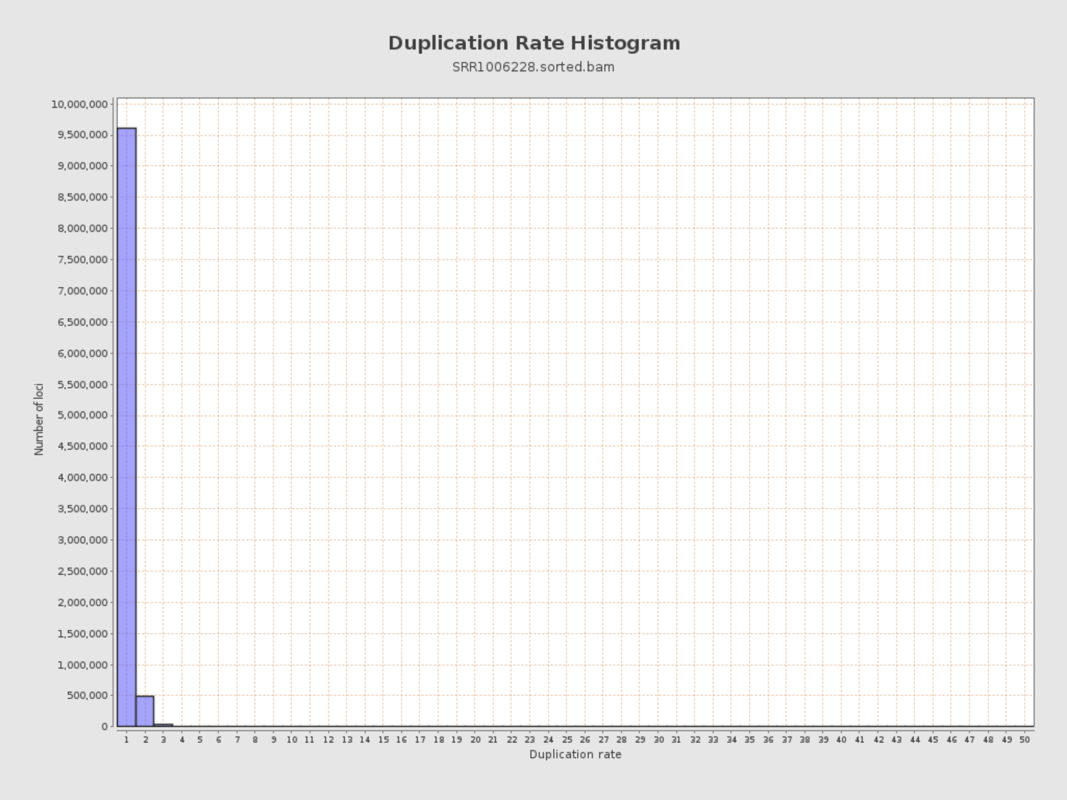
5. Results : Coverage Histogram (0-50X)



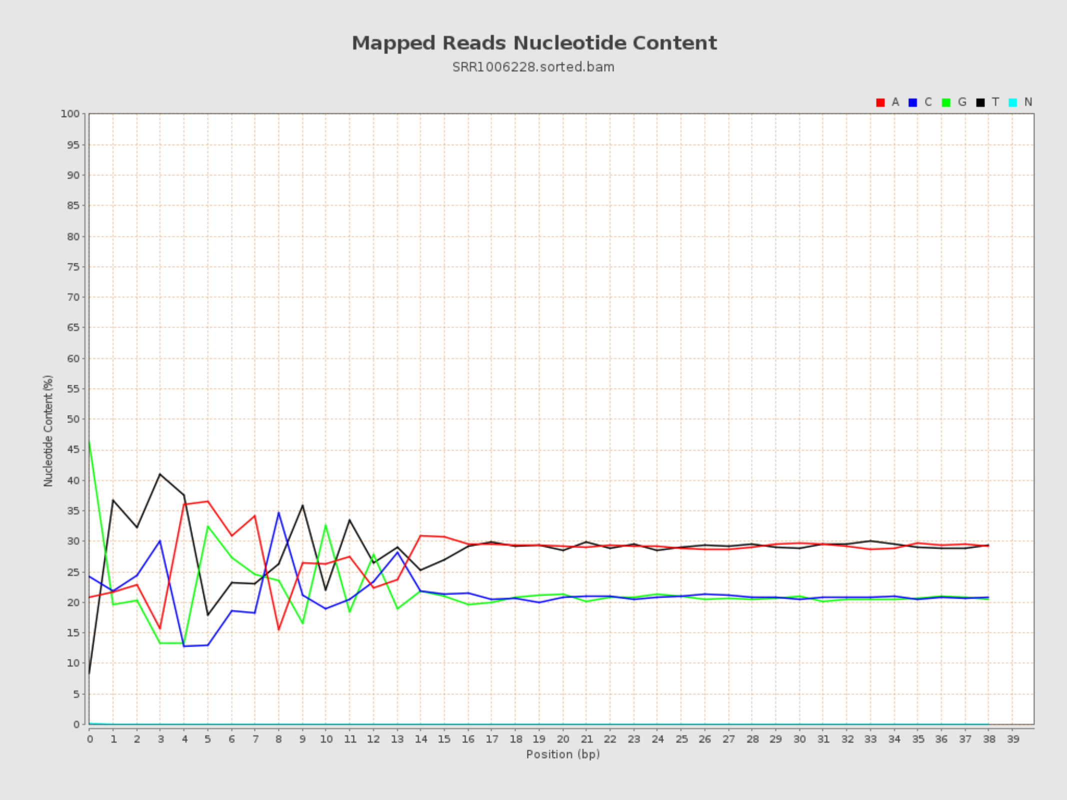
6. Results : Genome Fraction Coverage



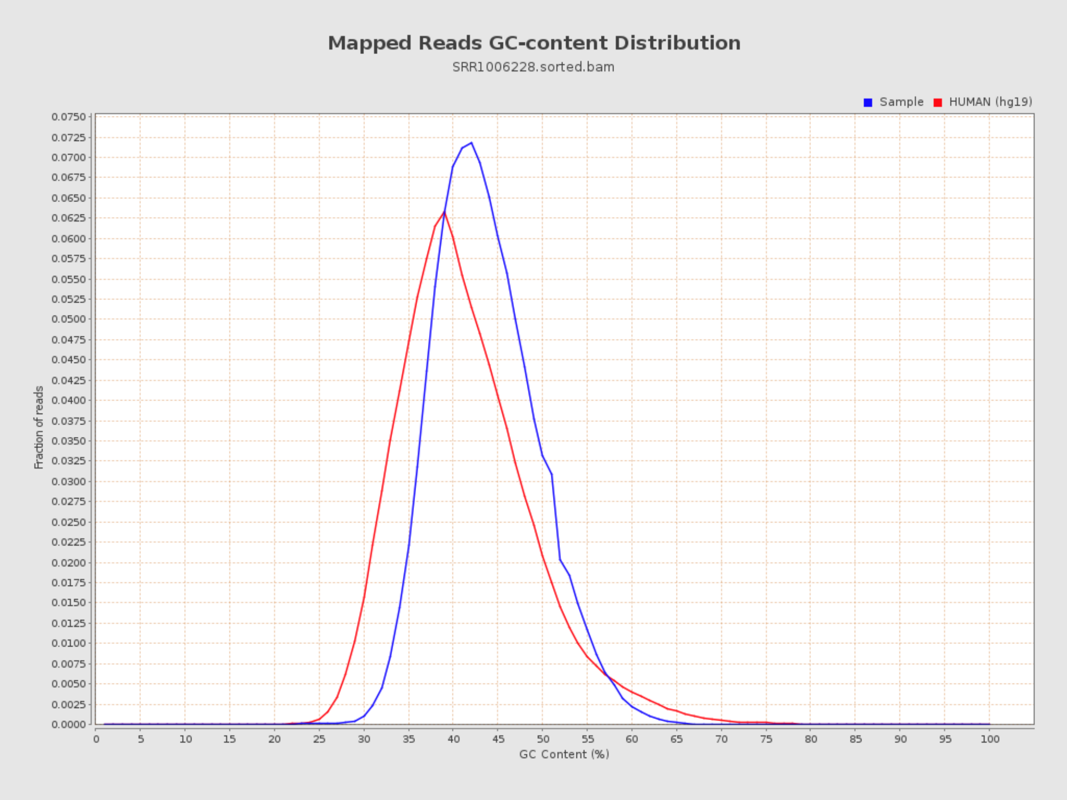
7. Results : Duplication Rate Histogram



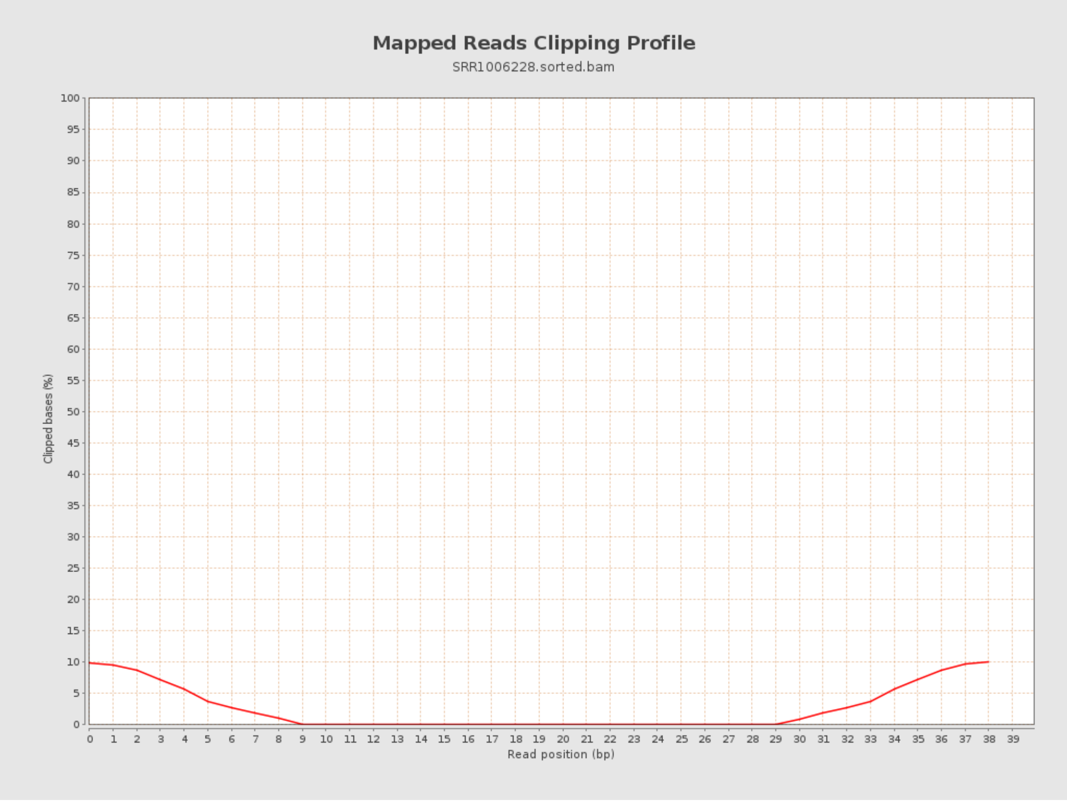
8. Results : Mapped Reads Nucleotide Content



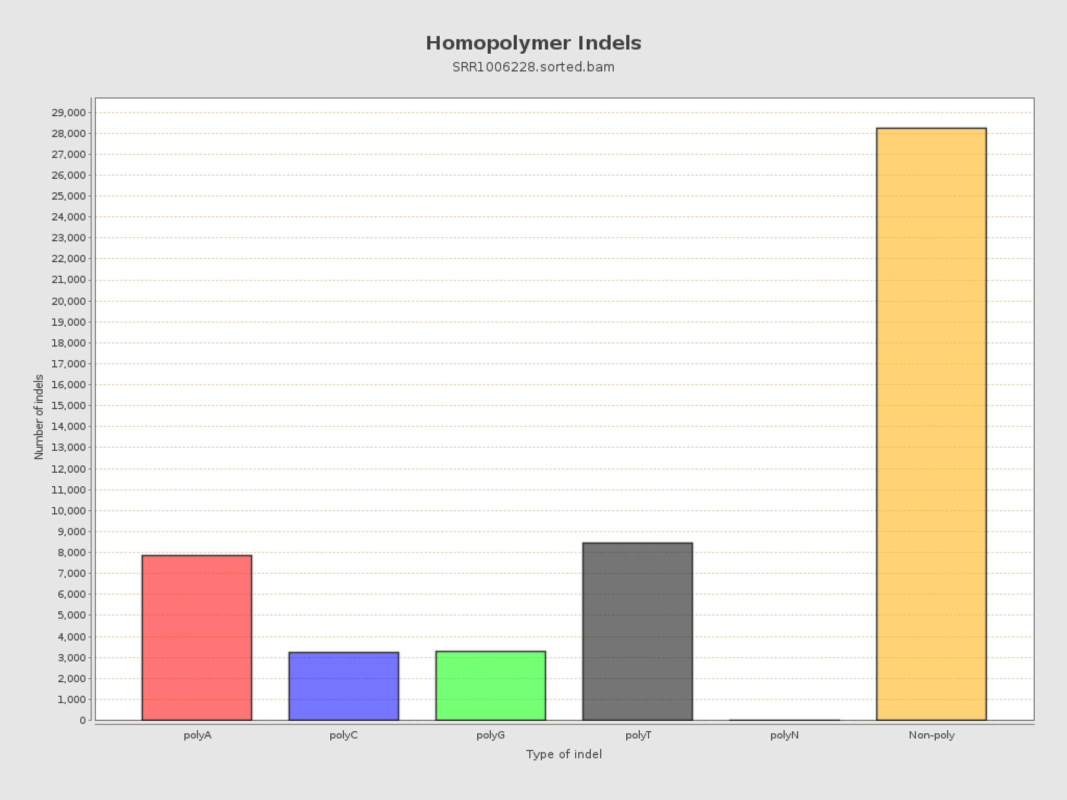
9. Results : Mapped Reads GC-content Distribution



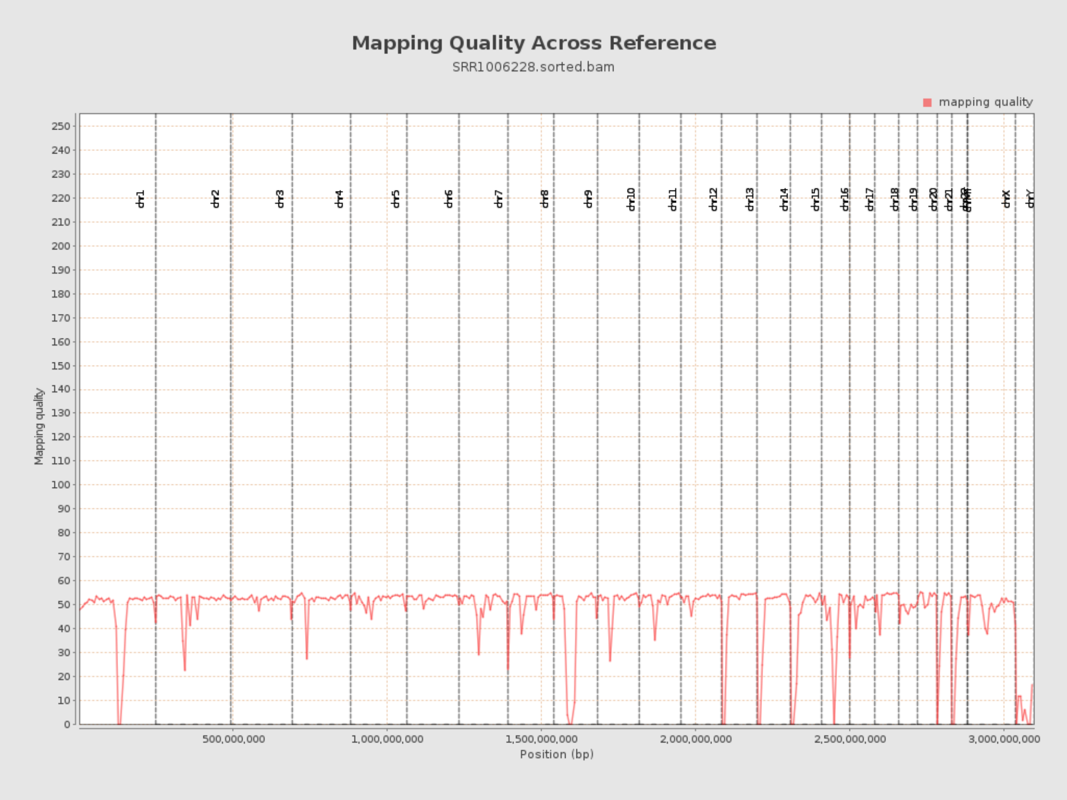
10. Results : Mapped Reads Clipping Profile



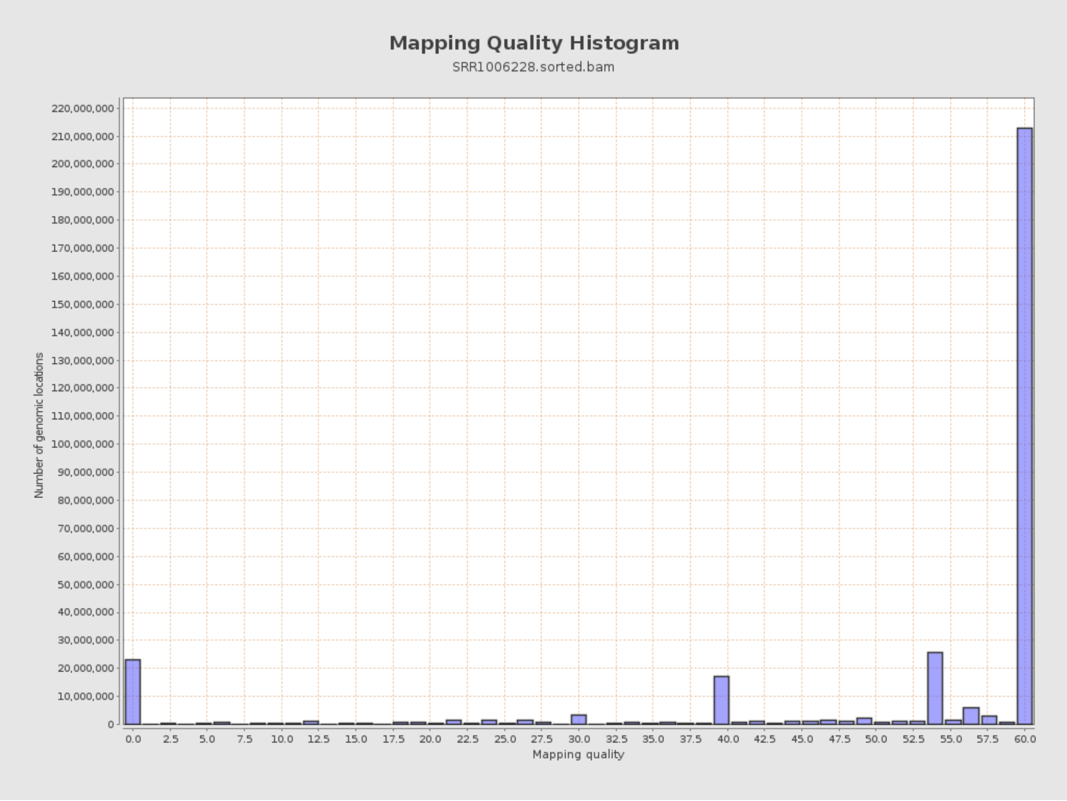
11. Results : Homopolymer Indels



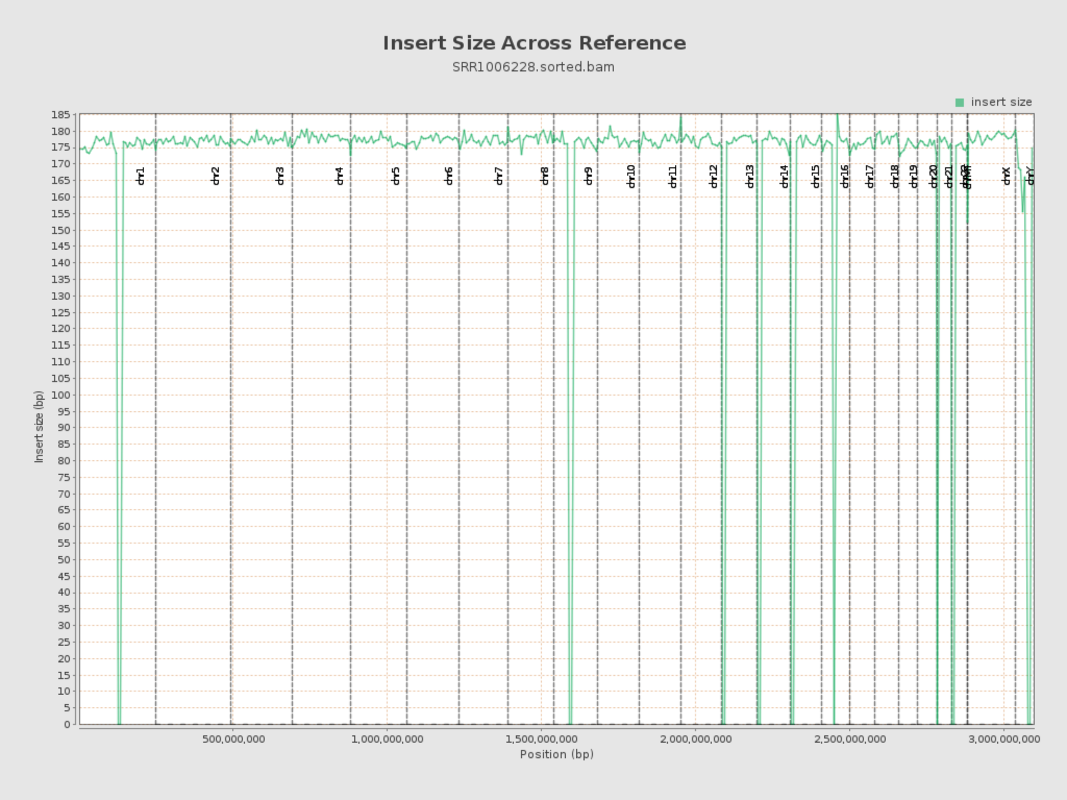
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram