Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 22:57:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006188.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_SRR1006188 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006188_1.fastq.gz SRR1006188_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 22:57:17 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006188.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,533,036
Mapped reads	8,371,928 / 87.82%
Unmapped reads	1,161,108 / 12.18%
Mapped paired reads	8,371,928 / 87.82%
Mapped reads, first in pair	4,222,188 / 44.29%
Mapped reads, second in pair	4,149,740 / 43.53%
Mapped reads, both in pair	7,743,666 / 81.23%
Mapped reads, singletons	628,262 / 6.59%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	315,869 / 3.31%
Duplication rate	3.11%
Clipped reads	492,048 / 5.16%

2.2. ACGT Content

Number/percentage of A's	88,157,070 / 27.21%
Number/percentage of C's	71,774,005 / 22.16%
Number/percentage of T's	89,957,994 / 27.77%
Number/percentage of G's	74,035,763 / 22.85%
Number/percentage of N's	38,030 / 0.01%
GC Percentage	45.01%

2.3. Coverage

Mean	0.1047
Standard Deviation	0.5622

2.4. Mapping Quality

Mean Mapping Quality	47.67

2.5. Insert size

Mean	60,056.6
Standard Deviation	2,338,215.42
P25/Median/P75	76 / 112 / 153

2.6. Mismatches and indels

General error rate	0.32%
Mismatches	1,021,835
Insertions	9,375
Mapped reads with at least one insertion	0.11%
Deletions	30,290
Mapped reads with at least one deletion	0.36%
Homopolymer indels	43.14%

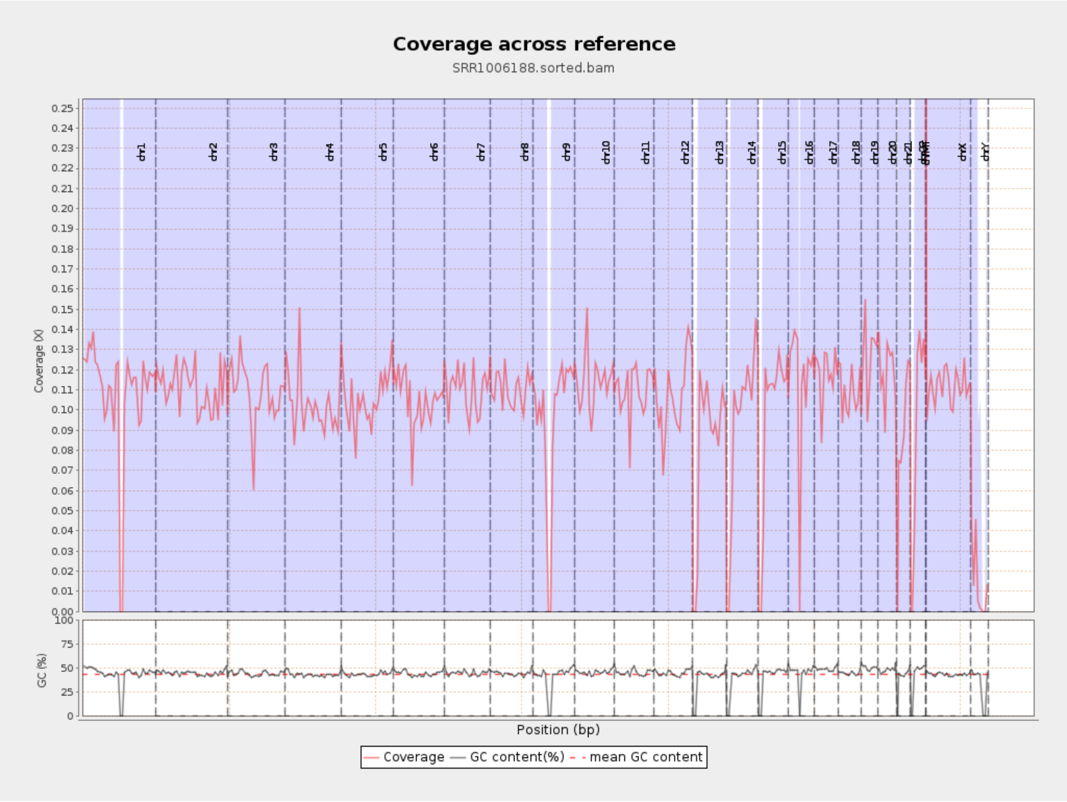
2.7. Chromosome stats

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

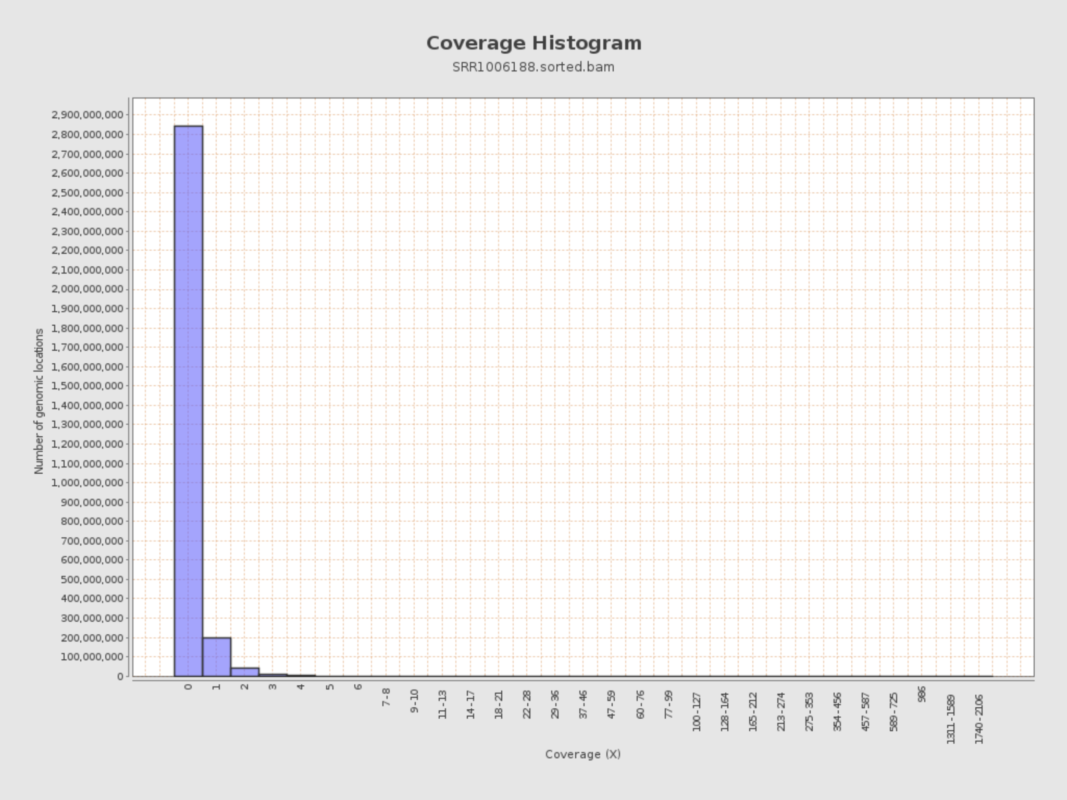
chr1	249250621	26961071	0.1082	0.7229
chr2	243199373	27075380	0.1113	0.5164
chr3	198022430	21543500	0.1088	0.3993
chr4	191154276	19687471	0.103	0.4611
chr5	180915260	19193546	0.1061	0.3982
chr6	171115067	17869849	0.1044	0.4415
chr7	159138663	17575811	0.1104	0.6067
chr8	146364022	16125839	0.1102	1.1067
chr9	141213431	13427607	0.0951	0.4495
chr10	135534747	15399973	0.1136	0.5874
chr11	135006516	14781268	0.1095	0.4847
chr12	133851895	14475378	0.1081	0.4078
chr13	115169878	9735125	0.0845	0.3525
chr14	107349540	10155248	0.0946	0.9126
chr15	102531392	9669372	0.0943	0.3783
chr16	90354753	10231120	0.1132	0.4898
chr17	81195210	9627078	0.1186	0.442
chr18	78077248	8466318	0.1084	0.68
chr19	59128983	7482120	0.1265	0.6117
chr20	63025520	7473683	0.1186	0.4439
chr21	48129895	4260569	0.0885	0.4518
chr22	51304566	4592121	0.0895	0.4091
chrMT	16571	5744	0.3466	1.0879
chrX	155270560	17349066	0.1117	0.4365

chrY	59373566	839025	0.0141	0.3309

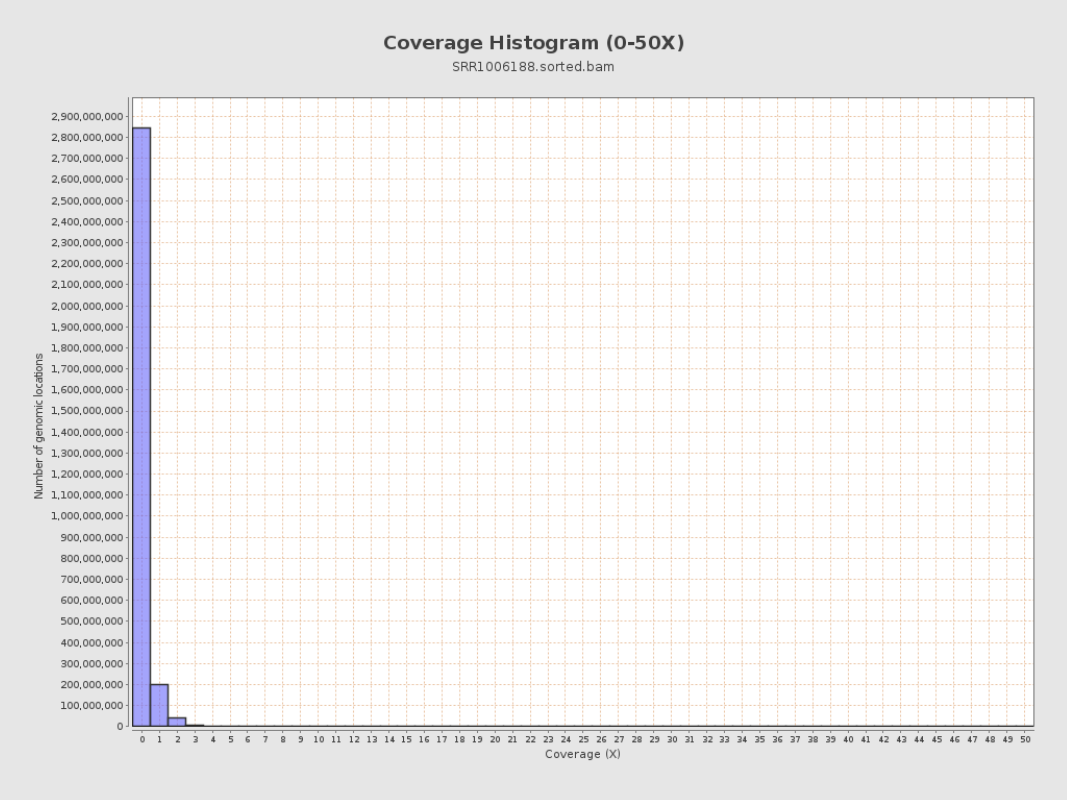
3. Results : Coverage across reference



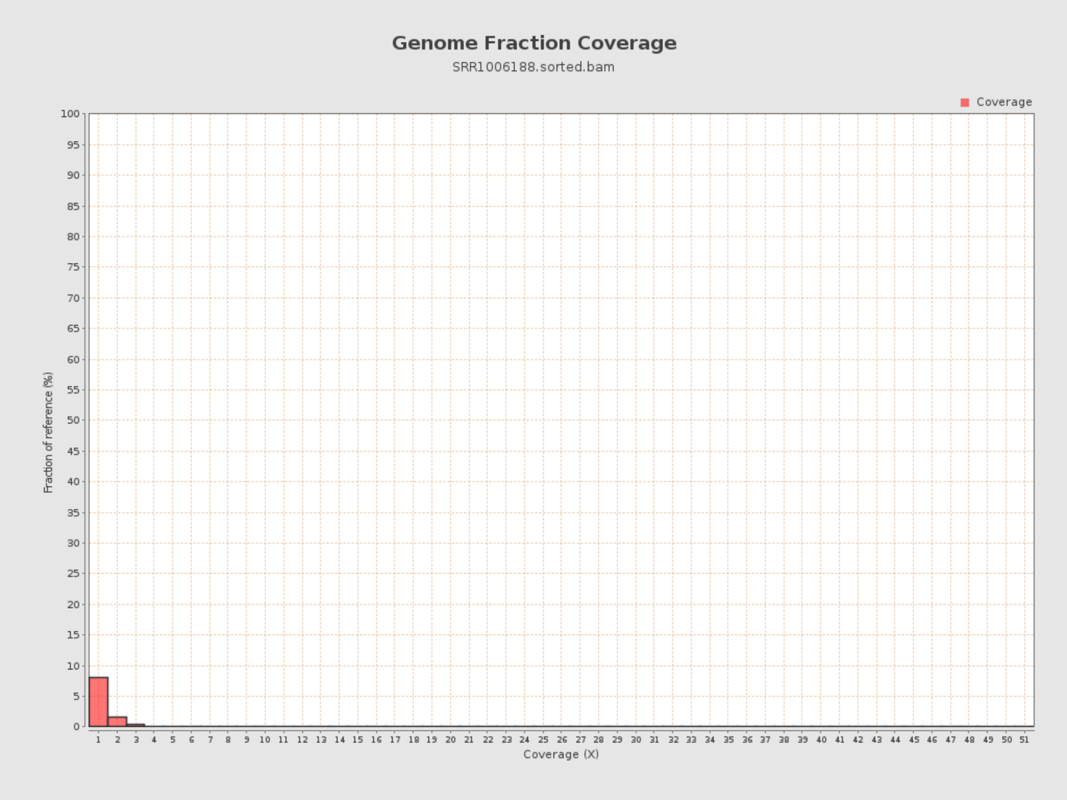
4. Results : Coverage Histogram



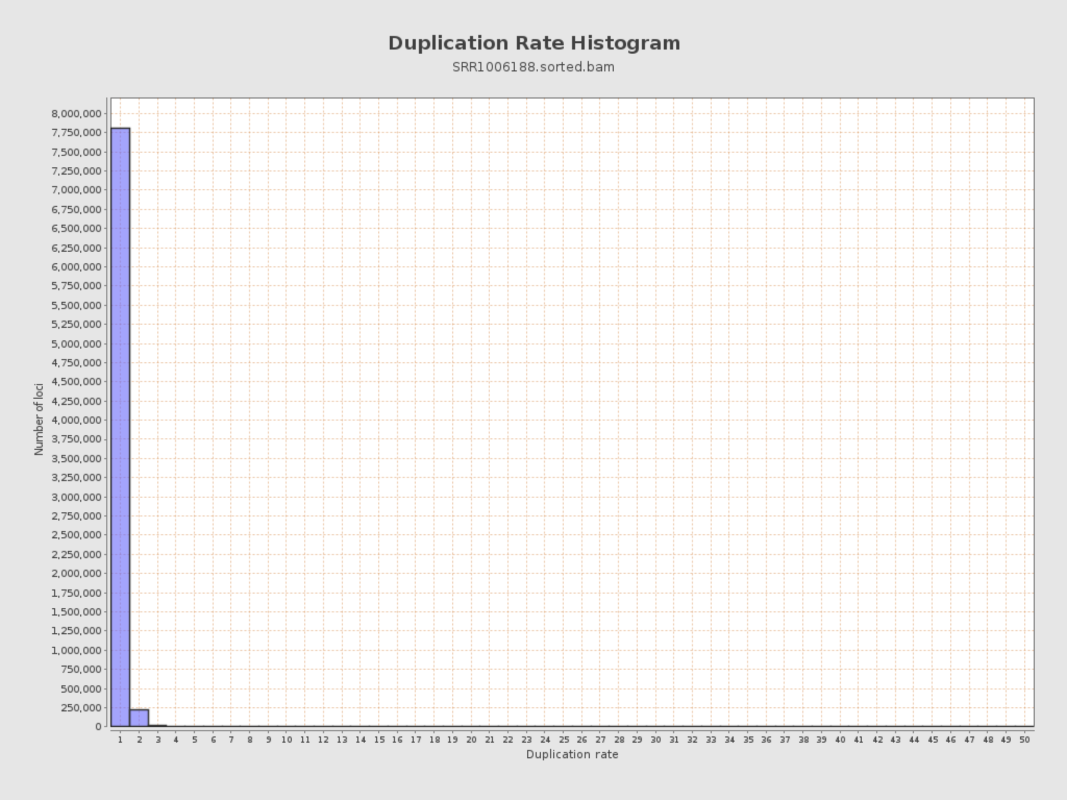
5. Results : Coverage Histogram (0-50X)



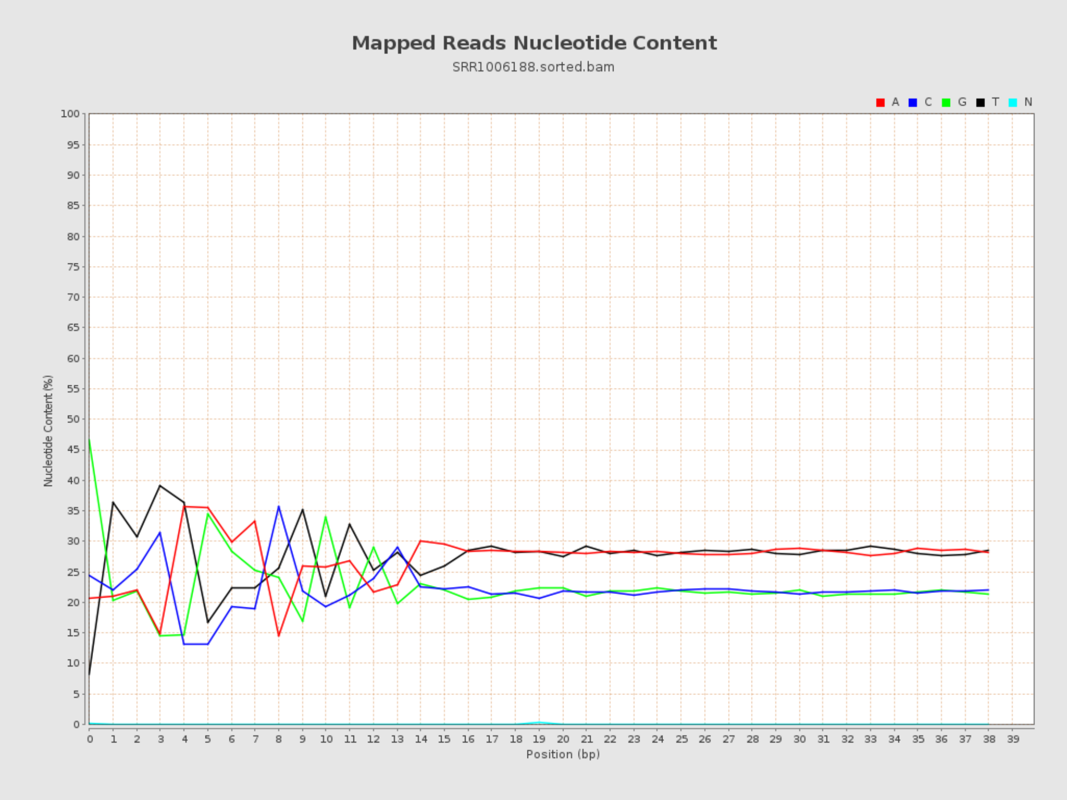
6. Results : Genome Fraction Coverage



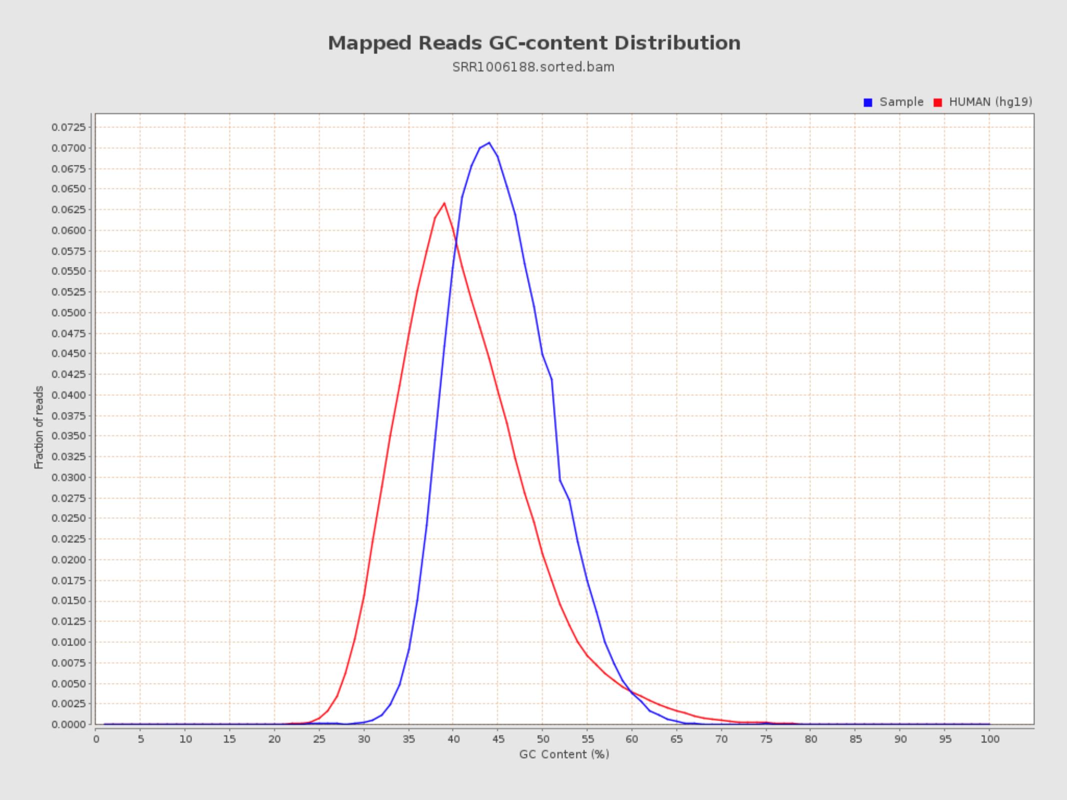
7. Results : Duplication Rate Histogram



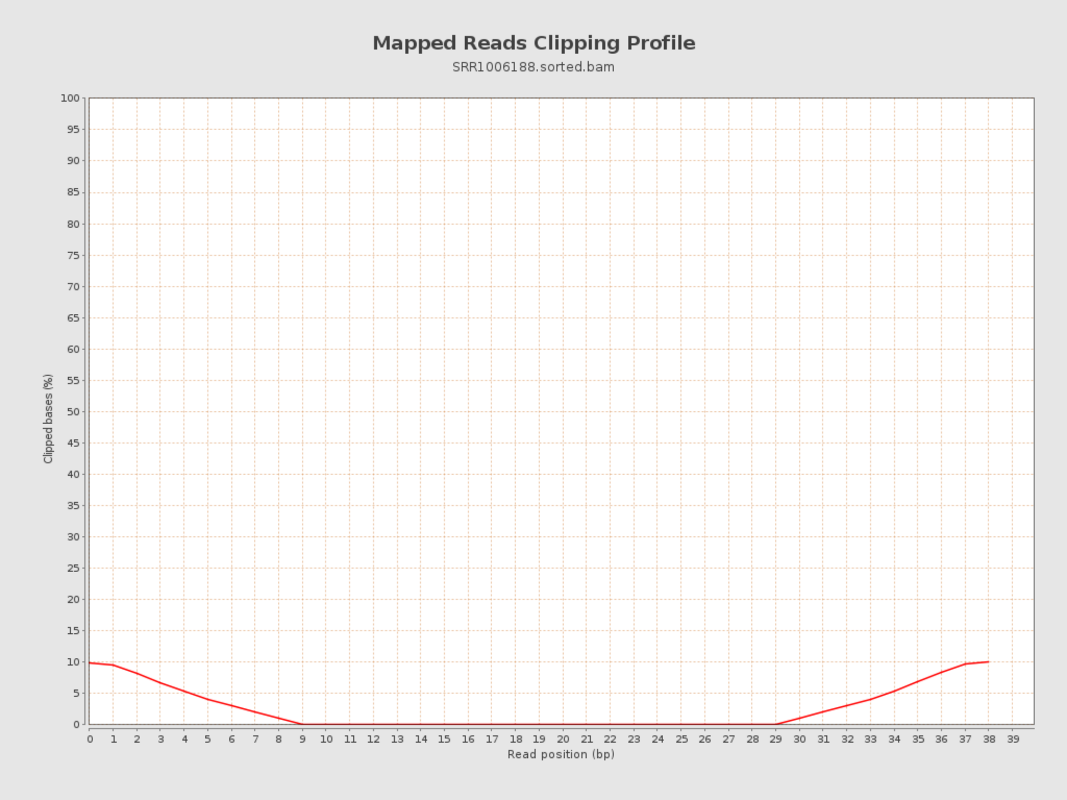
8. Results : Mapped Reads Nucleotide Content



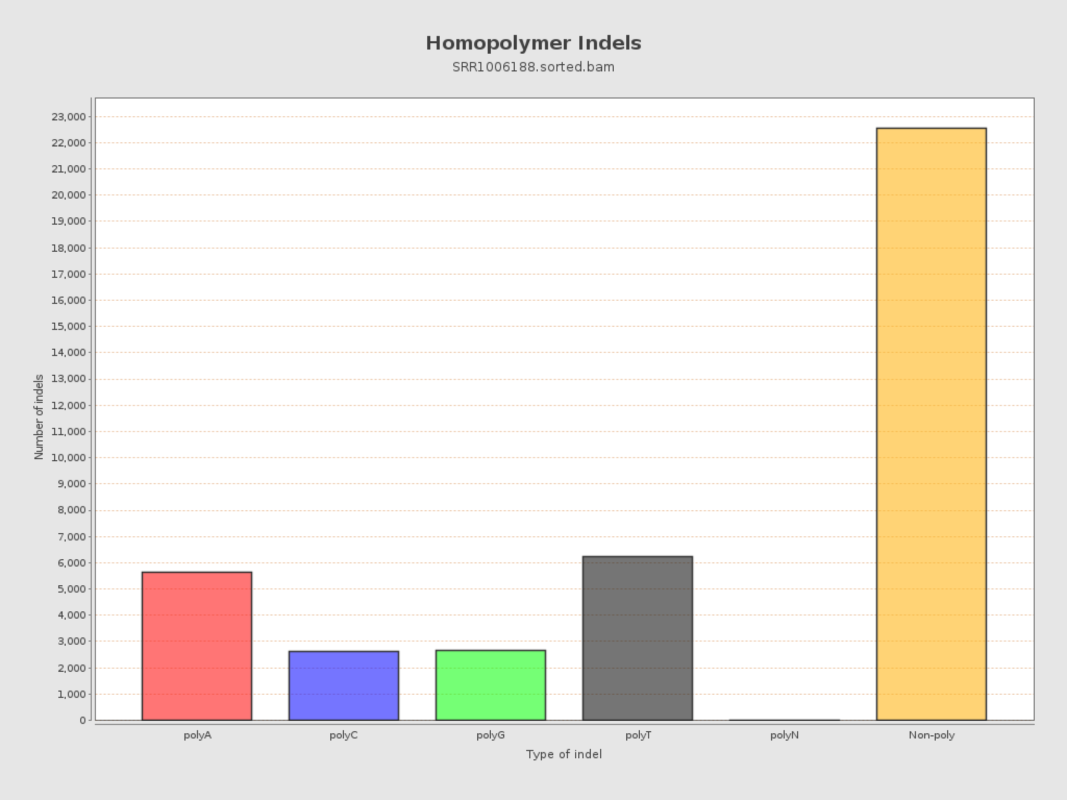
9. Results : Mapped Reads GC-content Distribution



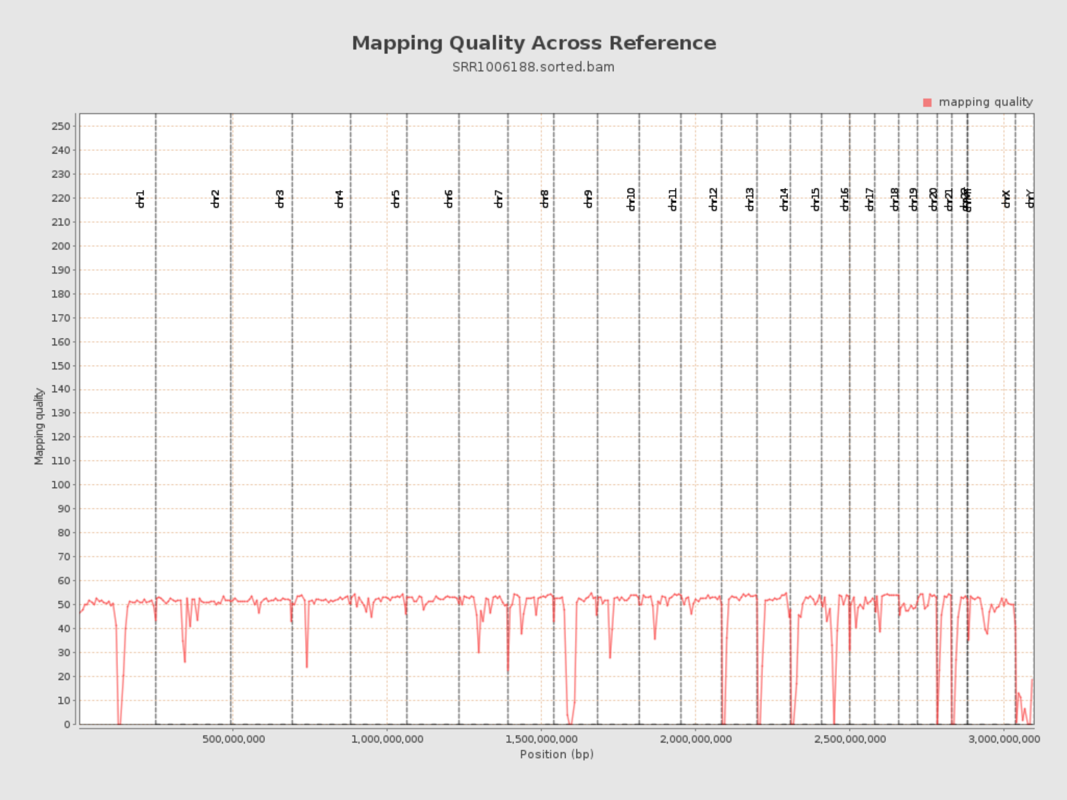
10. Results : Mapped Reads Clipping Profile



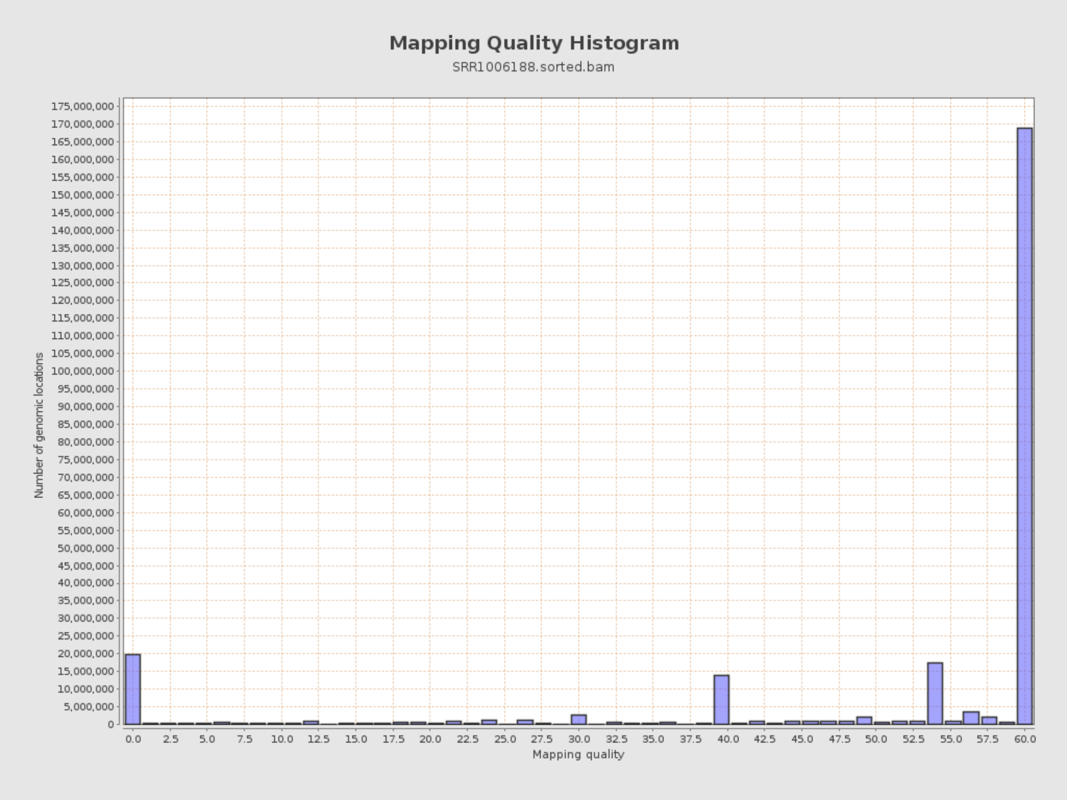
11. Results : Homopolymer Indels



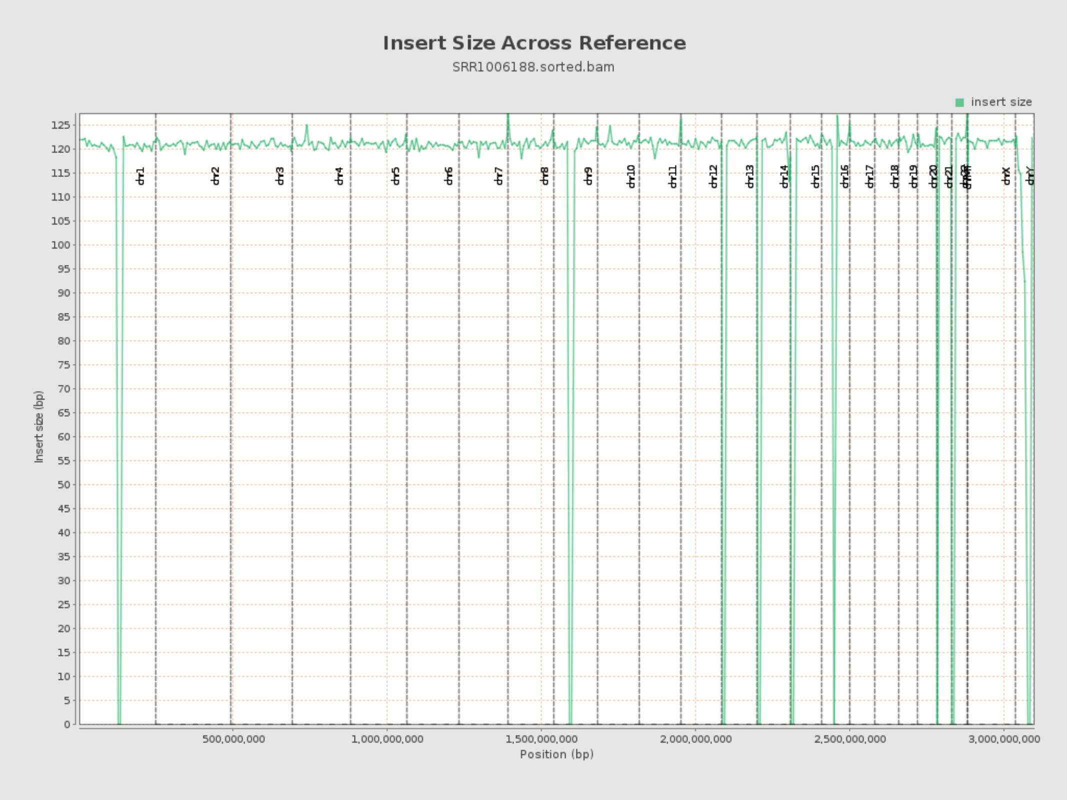
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram