Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 18:36:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006088.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_SRR1006088 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006088_1.fastq.gz SRR1006088_2.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 18:36:08 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006088.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,989,502
Mapped reads	6,150,889 / 88%
Unmapped reads	838,613 / 12%
Mapped paired reads	6,150,889 / 88%
Mapped reads, first in pair	3,111,134 / 44.51%
Mapped reads, second in pair	3,039,755 / 43.49%
Mapped reads, both in pair	5,633,848 / 80.6%
Mapped reads, singletons	517,041 / 7.4%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	315,737 / 4.52%
Duplication rate	4.66%
Clipped reads	502,080 / 7.18%

2.2. ACGT Content

Number/percentage of A's	62,739,292 / 26.42%
Number/percentage of C's	53,126,808 / 22.37%
Number/percentage of T's	65,001,391 / 27.37%
Number/percentage of G's	56,584,574 / 23.83%
Number/percentage of N's	9,960 / 0%
GC Percentage	46.2%

2.3. Coverage

Mean	0.0767
Standard Deviation	0.4273

2.4. Mapping Quality

Mean Mapping Quality	47.04

2.5. Insert size

Mean	63,552.56
Standard Deviation	2,462,895.94
P25/Median/P75	73 / 103 / 136

2.6. Mismatches and indels

General error rate	0.49%
Mismatches	1,161,196
Insertions	7,460
Mapped reads with at least one insertion	0.12%
Deletions	19,899
Mapped reads with at least one deletion	0.32%
Homopolymer indels	43.81%

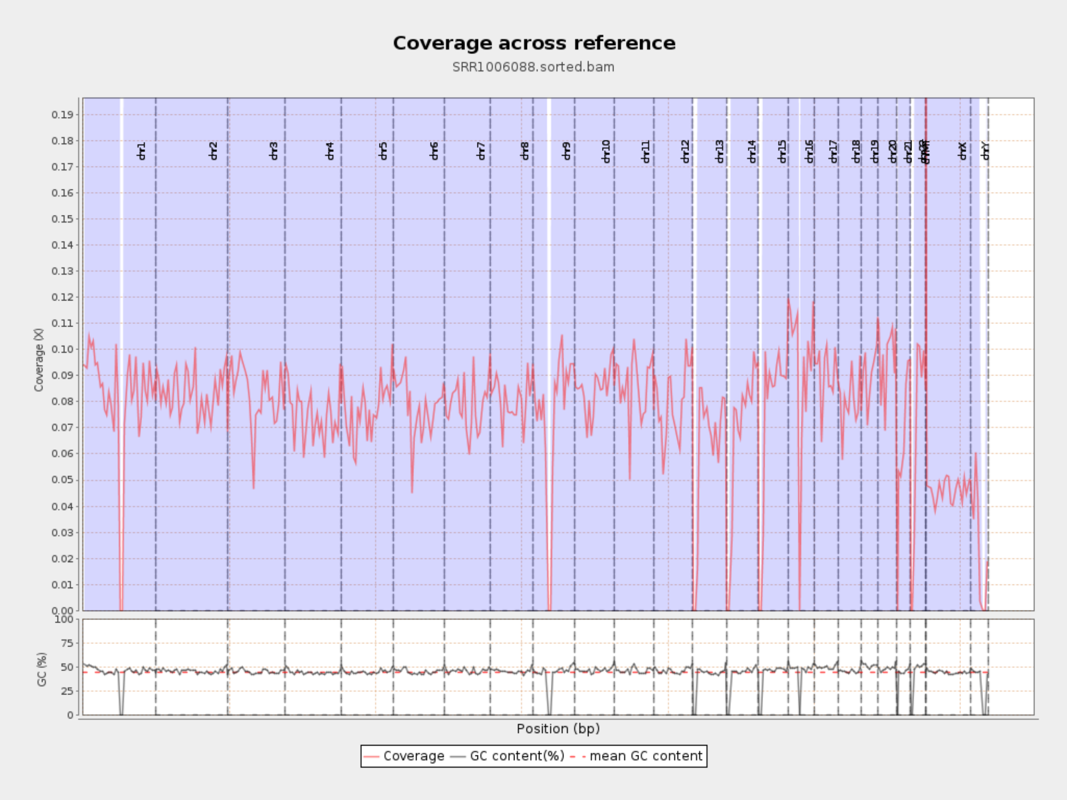
2.7. Chromosome stats

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

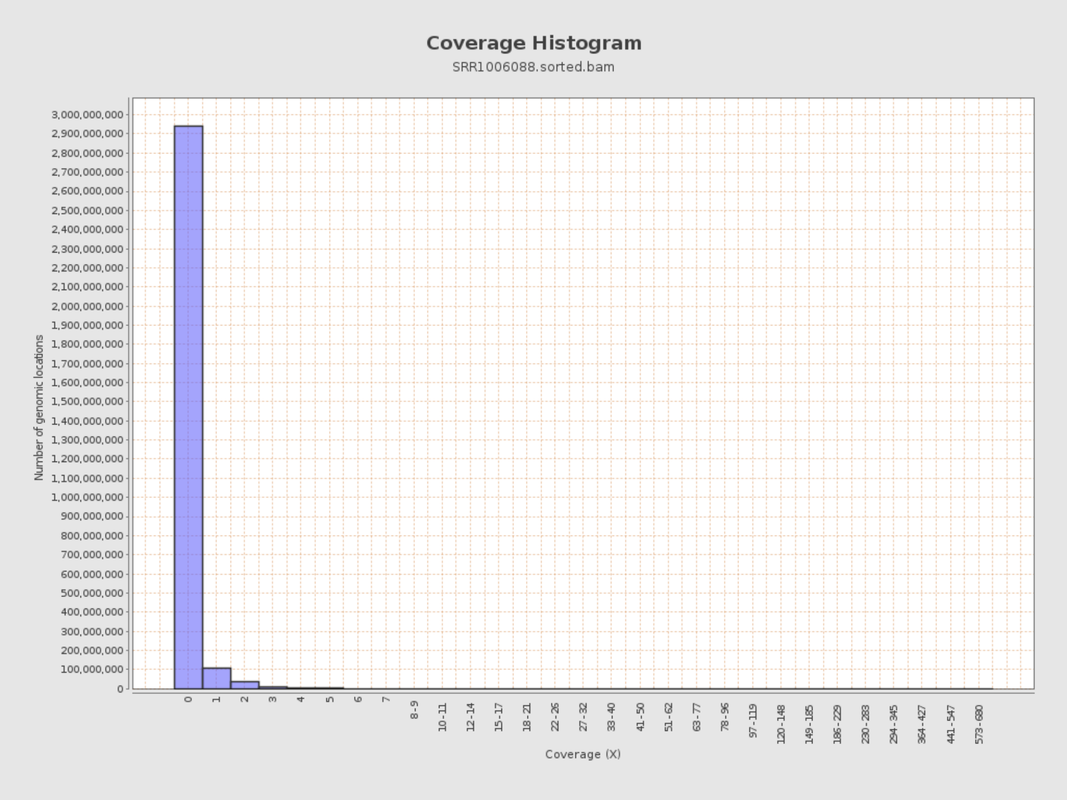
chr1	249250621	20337027	0.0816	0.4571
chr2	243199373	20269467	0.0833	0.4635
chr3	198022430	16388616	0.0828	0.4052
chr4	191154276	14325336	0.0749	0.3984
chr5	180915260	14047138	0.0776	0.3915
chr6	171115067	13313772	0.0778	0.4278
chr7	159138663	12534614	0.0788	0.4811
chr8	146364022	11758981	0.0803	0.4544
chr9	141213431	10444641	0.074	0.4065
chr10	135534747	11430354	0.0843	0.4235
chr11	135006516	11597359	0.0859	0.5541
chr12	133851895	10690296	0.0799	0.4004
chr13	115169878	7111001	0.0617	0.3533
chr14	107349540	7224140	0.0673	0.3752
chr15	102531392	7512867	0.0733	0.3892
chr16	90354753	8327360	0.0922	0.4806
chr17	81195210	7371843	0.0908	0.458
chr18	78077248	6221047	0.0797	0.4585
chr19	59128983	5348817	0.0905	0.4887
chr20	63025520	6006494	0.0953	0.4494
chr21	48129895	3167988	0.0658	0.4069
chr22	51304566	3417720	0.0666	0.4044
chrMT	16571	4658	0.2811	0.7783
chrX	155270560	7172429	0.0462	0.3058

chrY	59373566	1463512	0.0246	0.2519

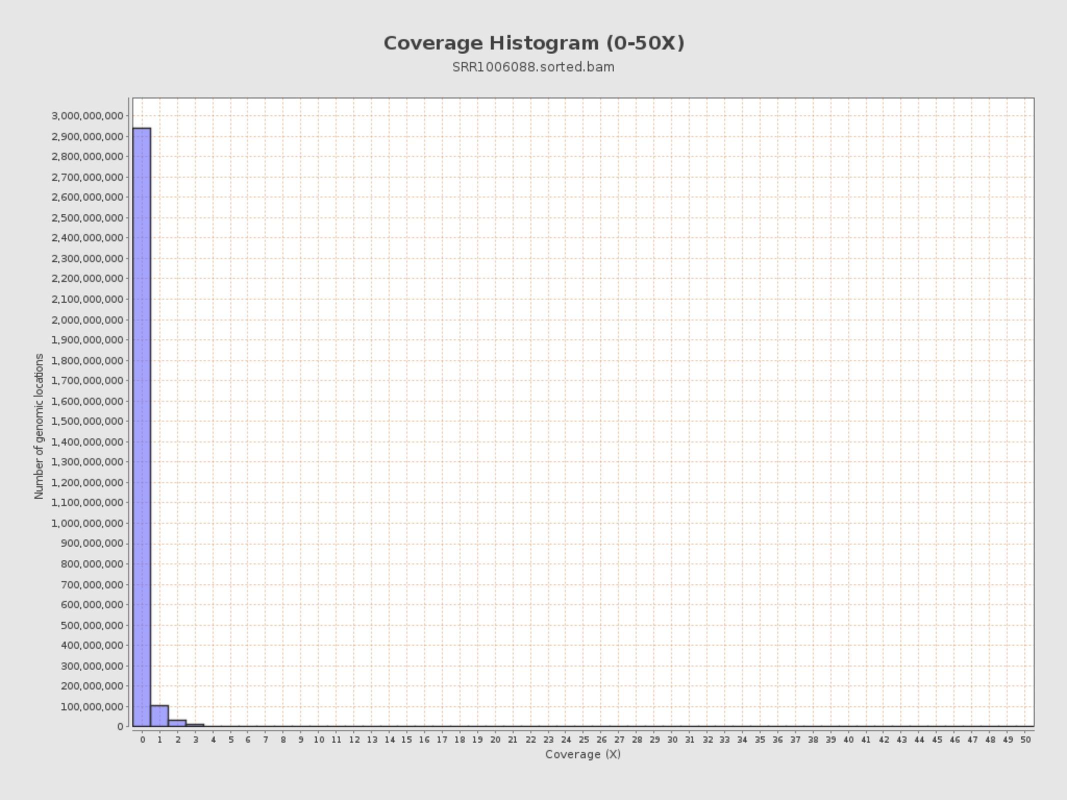
3. Results : Coverage across reference



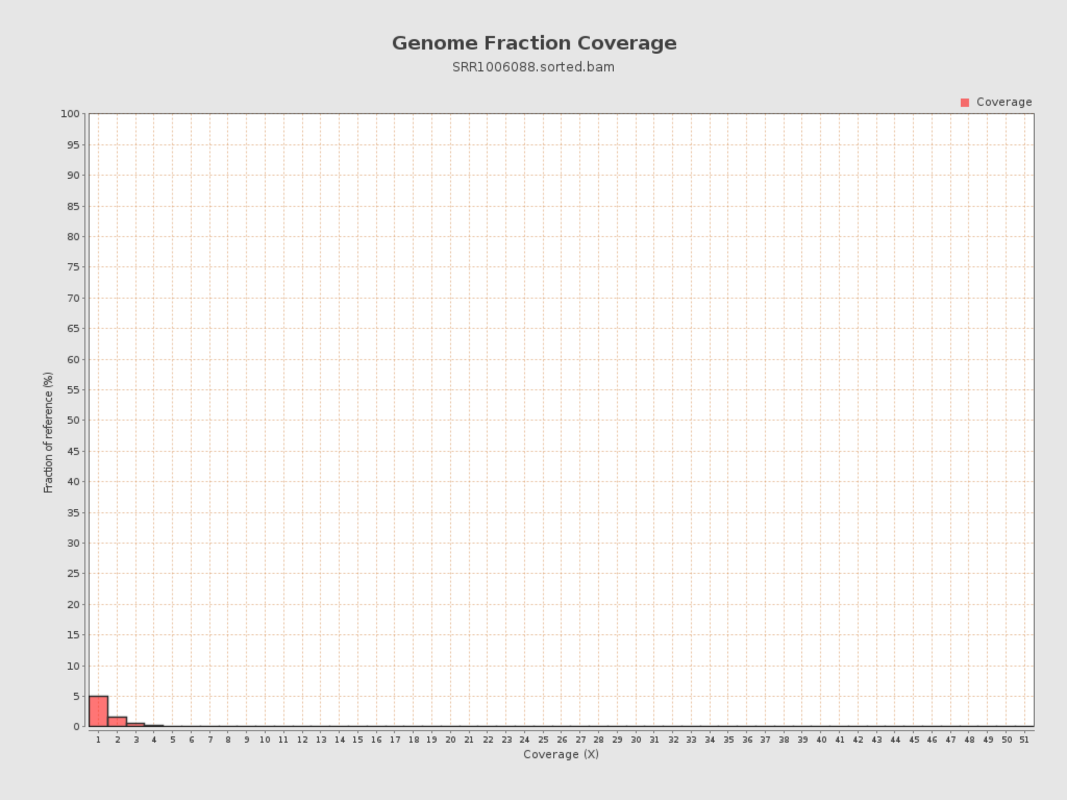
4. Results : Coverage Histogram



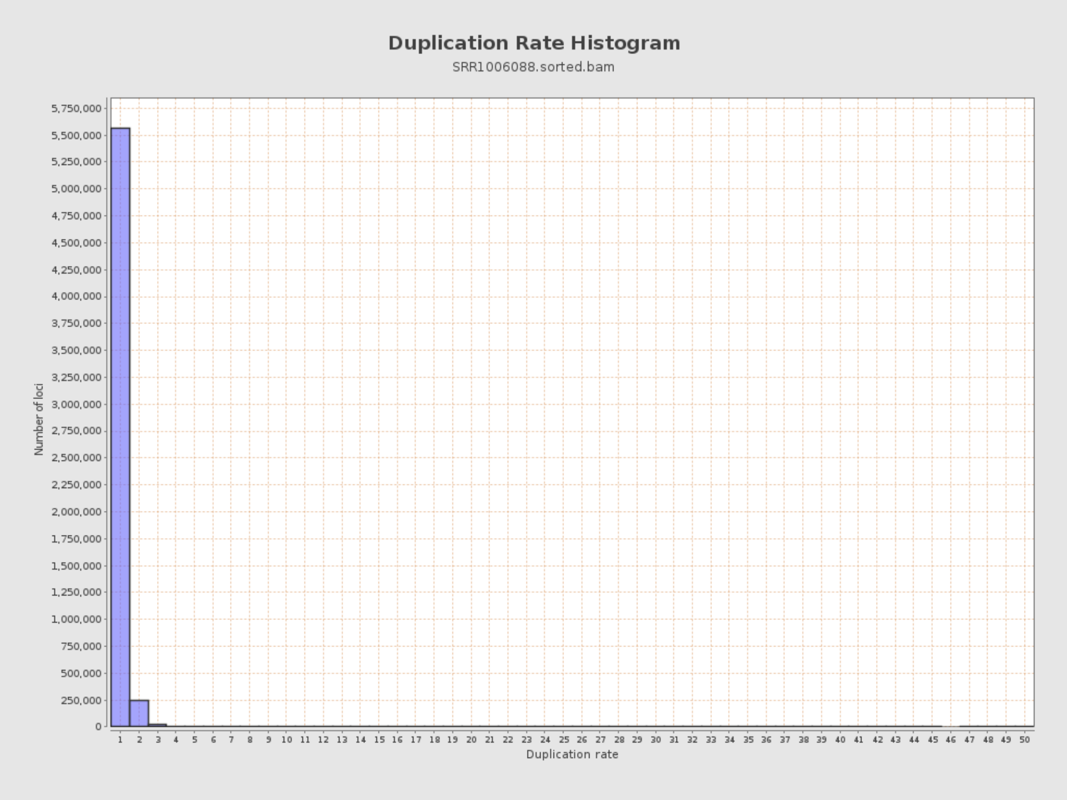
5. Results : Coverage Histogram (0-50X)



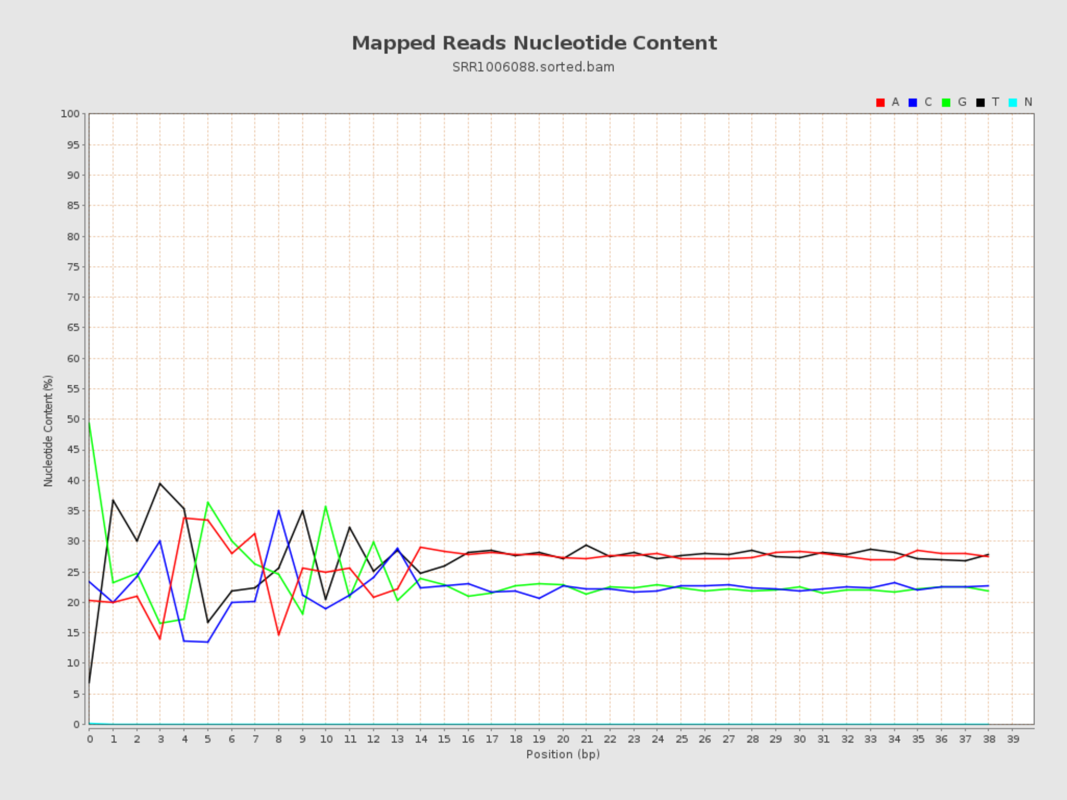
6. Results : Genome Fraction Coverage



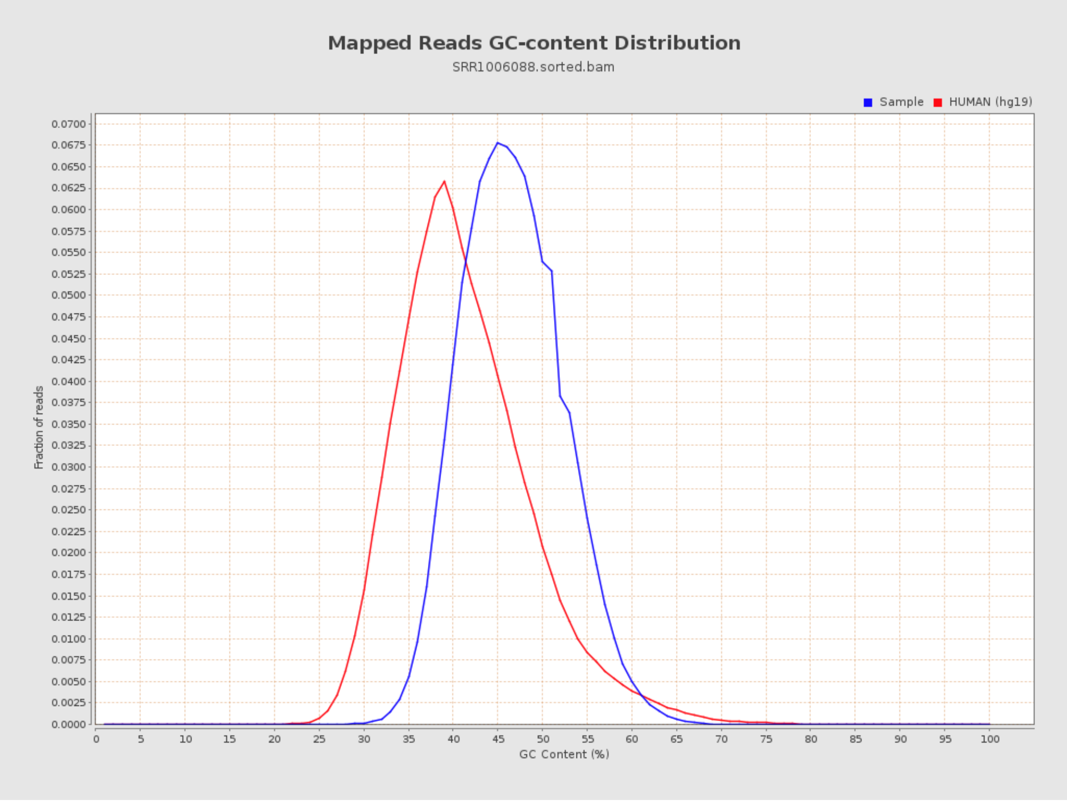
7. Results : Duplication Rate Histogram



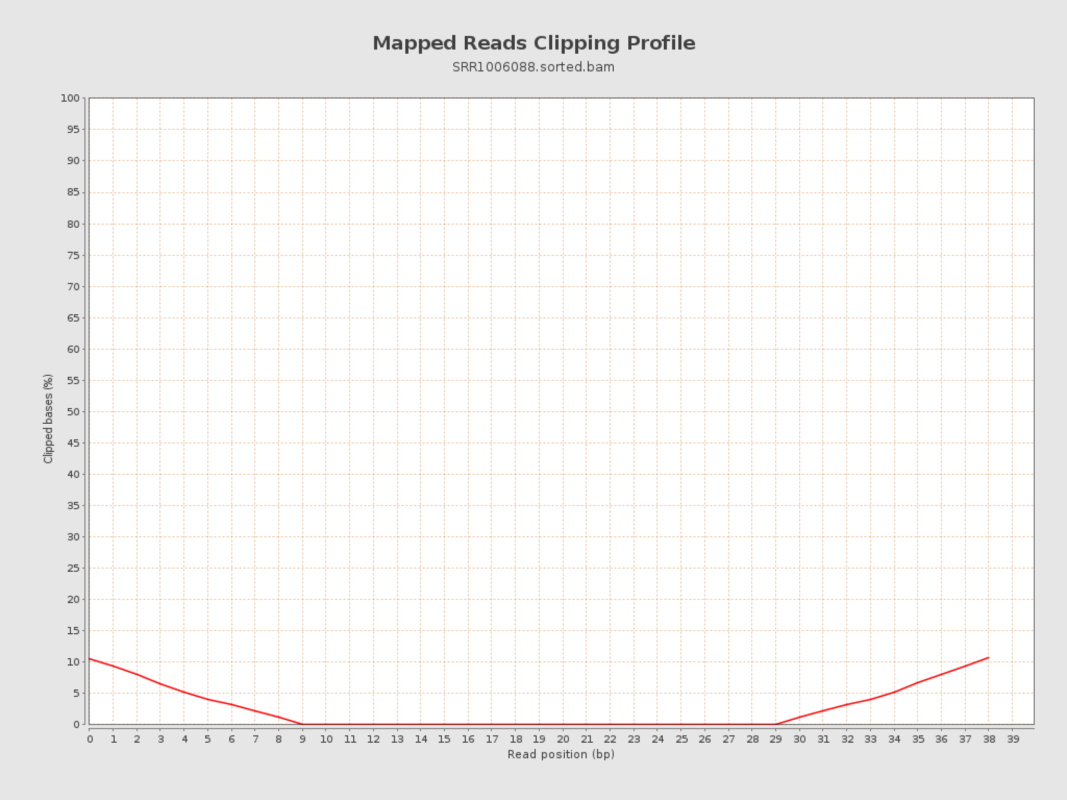
8. Results : Mapped Reads Nucleotide Content



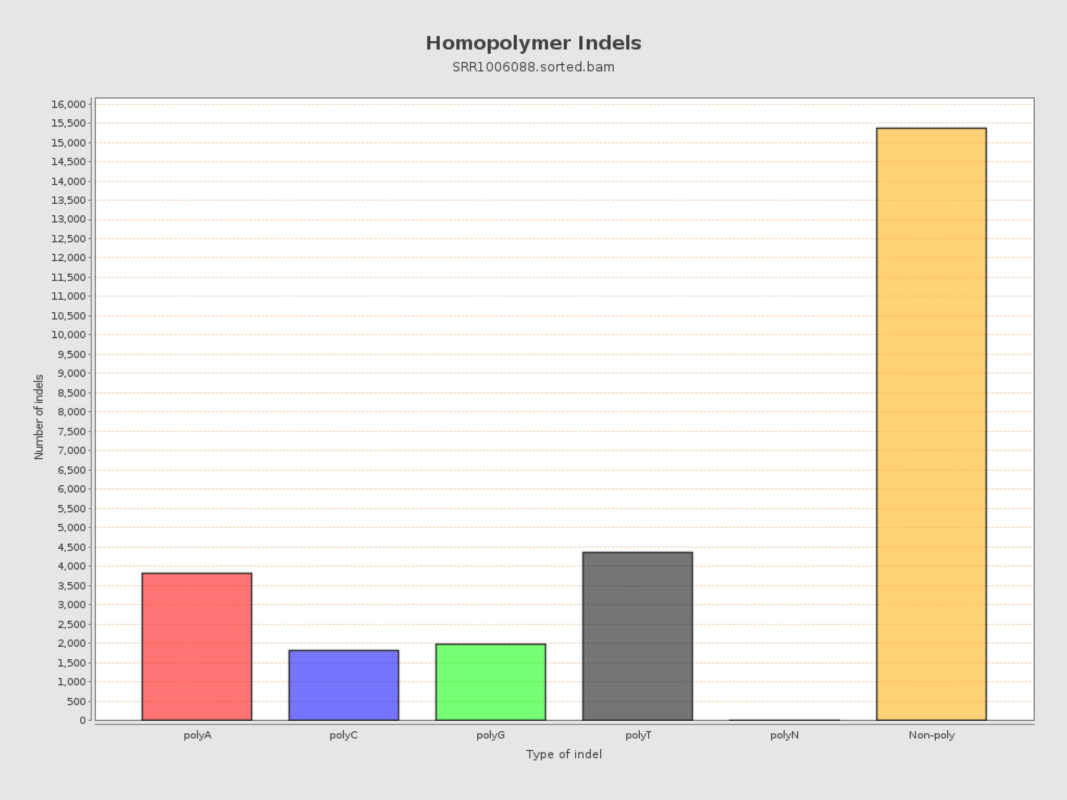
9. Results : Mapped Reads GC-content Distribution



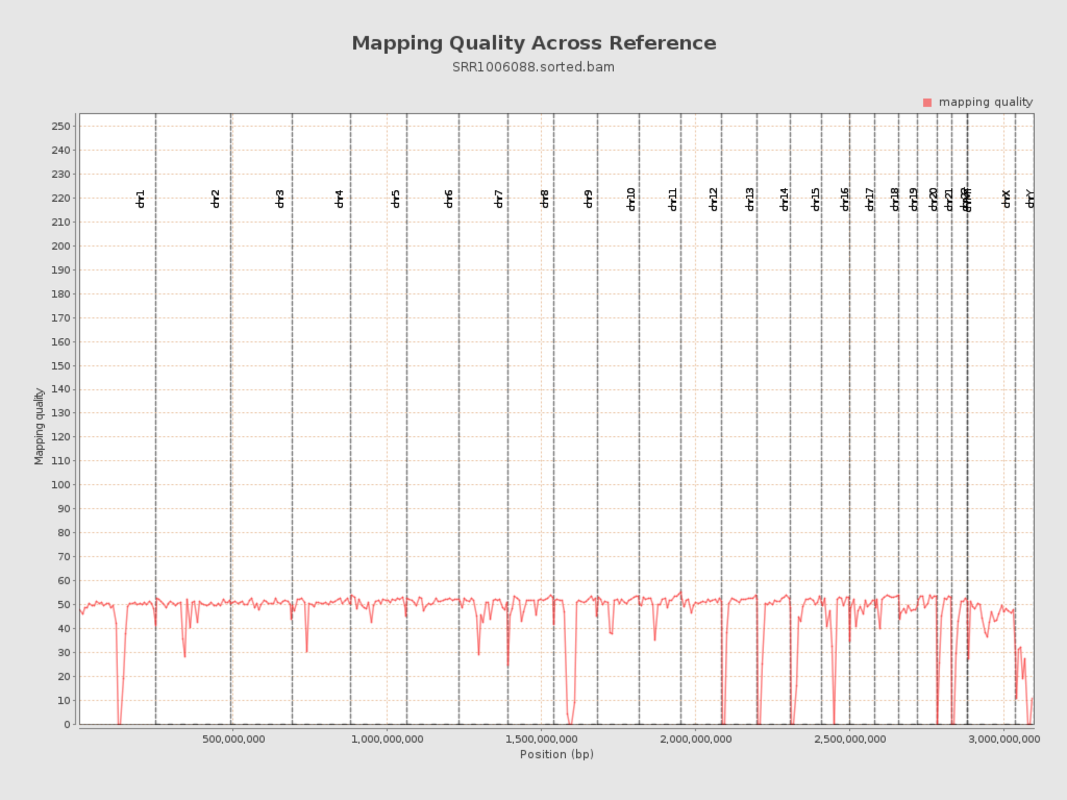
10. Results : Mapped Reads Clipping Profile



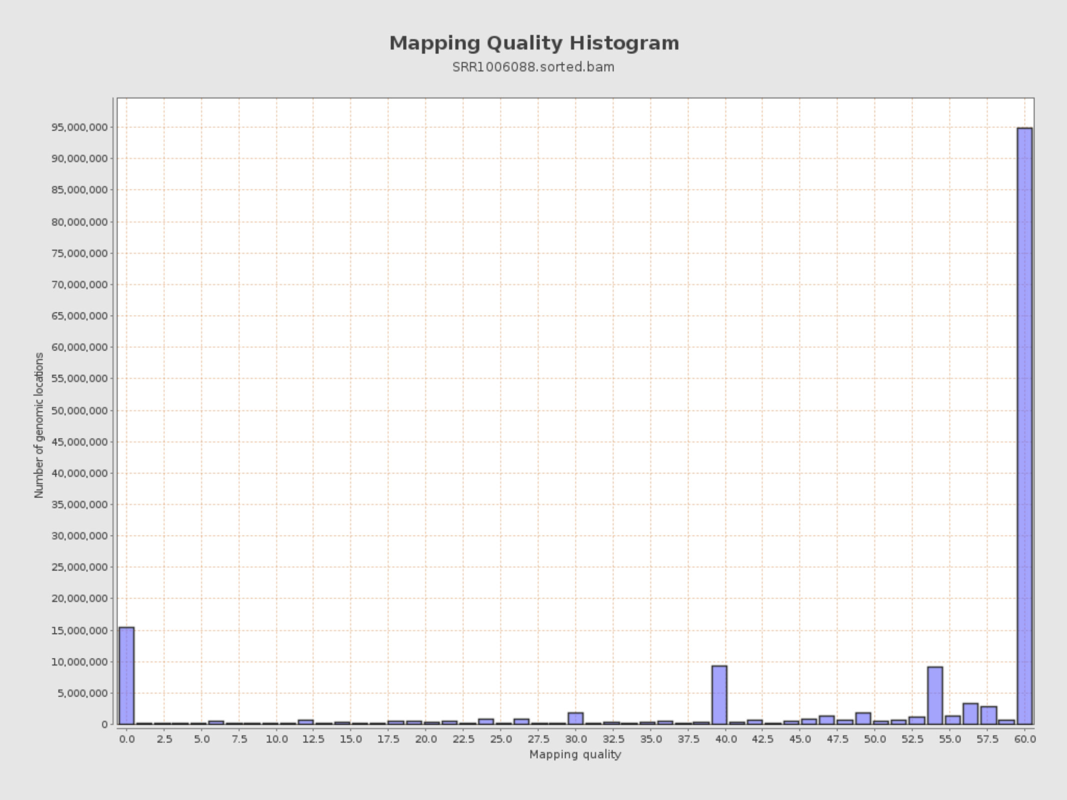
11. Results : Homopolymer Indels



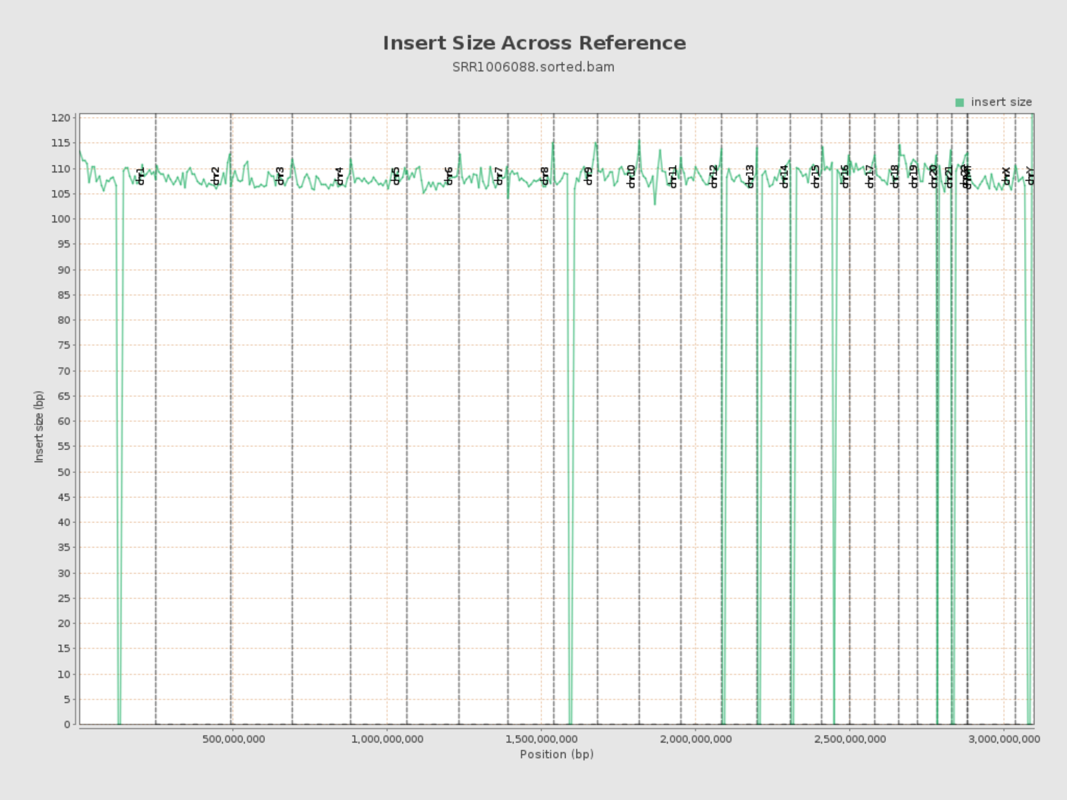
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram