Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 21:23:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006146.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_SRR1006146 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006146_1.fastq.gz SRR1006146_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 21:23:10 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006146.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	27,919,118
Mapped reads	23,233,576 / 83.22%
Unmapped reads	4,685,542 / 16.78%
Mapped paired reads	23,233,576 / 83.22%
Mapped reads, first in pair	11,840,556 / 42.41%
Mapped reads, second in pair	11,393,020 / 40.81%
Mapped reads, both in pair	20,544,472 / 73.59%
Mapped reads, singletons	2,689,104 / 9.63%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	6,879,072 / 24.64%
Duplication rate	25.71%
Clipped reads	2,618,186 / 9.38%

2.2. ACGT Content

Number/percentage of A's	237,148,542 / 26.57%
Number/percentage of C's	197,443,091 / 22.12%
Number/percentage of T's	247,250,104 / 27.7%
Number/percentage of G's	210,625,513 / 23.6%
Number/percentage of N's	33,384 / 0%
GC Percentage	45.72%

2.3. Coverage

Mean	0.2883
Standard Deviation	2.1684

2.4. Mapping Quality

Mean Mapping Quality	45.19

2.5. Insert size

Mean	87,024.44
Standard Deviation	2,935,242.06
P25/Median/P75	58 / 82 / 111

2.6. Mismatches and indels

General error rate	0.5%
Mismatches	4,419,918
Insertions	34,678
Mapped reads with at least one insertion	0.15%
Deletions	79,753
Mapped reads with at least one deletion	0.34%
Homopolymer indels	44.82%

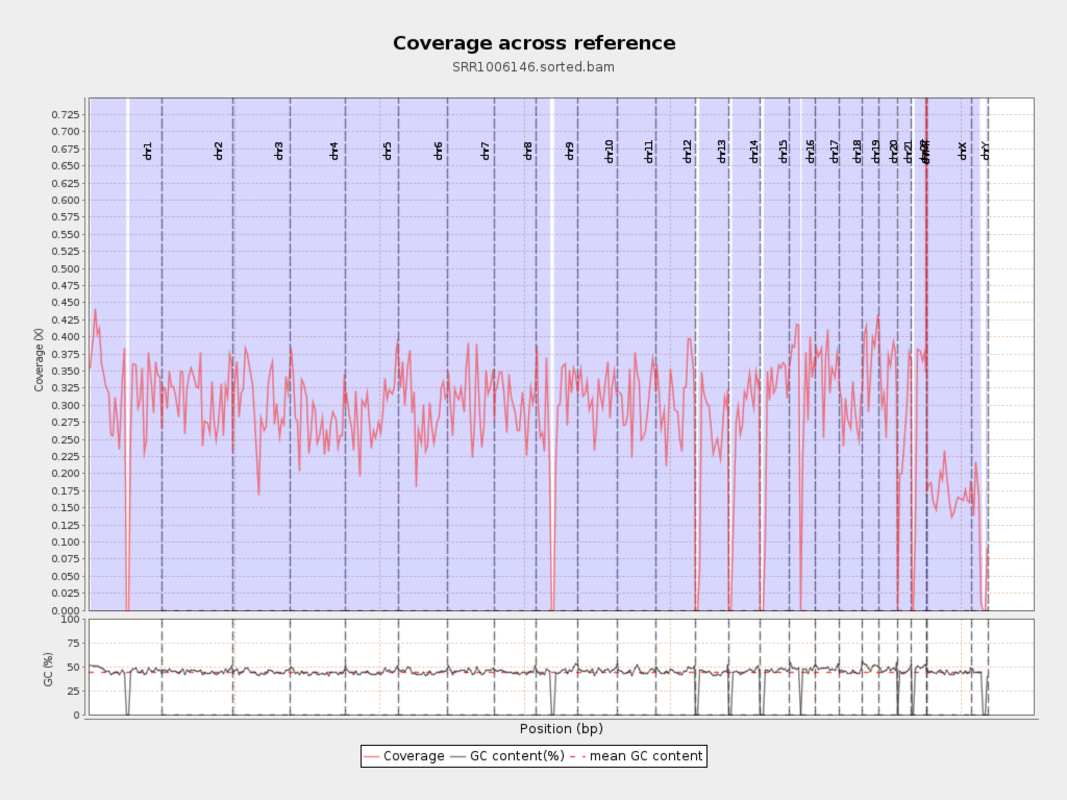
2.7. Chromosome stats

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

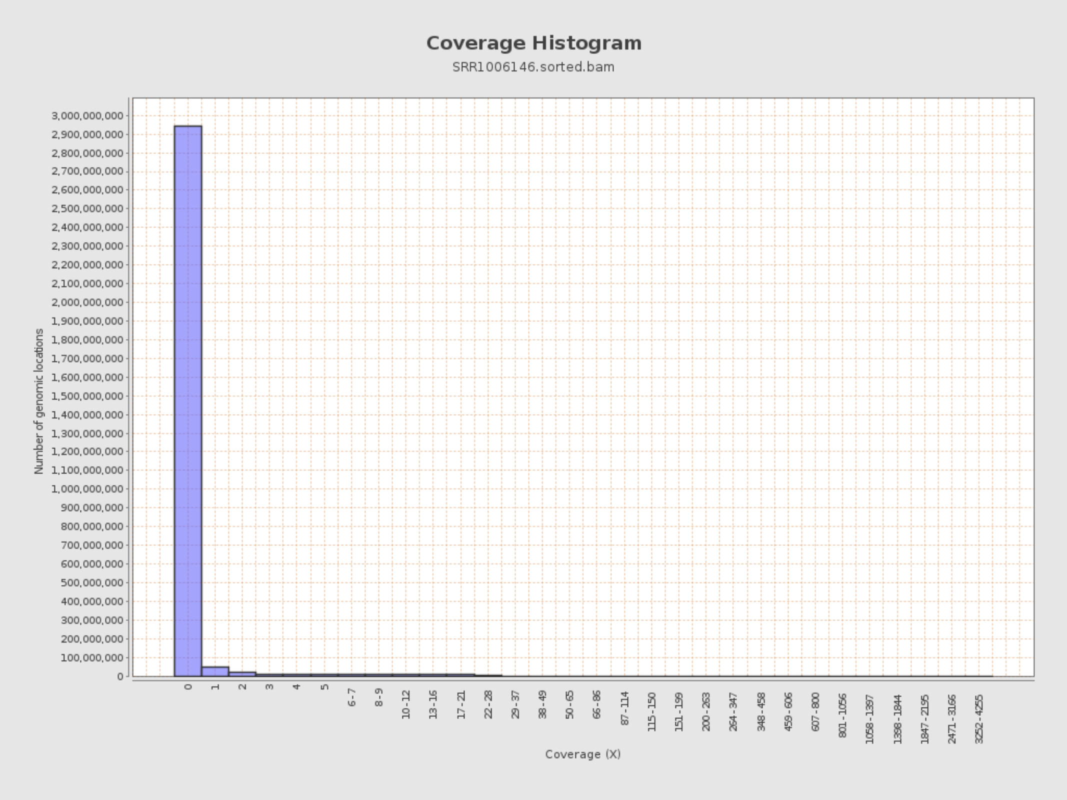
chr1	249250621	76978754	0.3088	2.7305
chr2	243199373	76182805	0.3133	2.2788
chr3	198022430	60266335	0.3043	1.9702
chr4	191154276	53324460	0.279	1.9469
chr5	180915260	52609430	0.2908	1.9146
chr6	171115067	50585861	0.2956	2.3362
chr7	159138663	49357231	0.3102	2.4757
chr8	146364022	44434281	0.3036	2.1926
chr9	141213431	37903696	0.2684	1.8965
chr10	135534747	42710221	0.3151	2.0883
chr11	135006516	41422689	0.3068	3.0071
chr12	133851895	41496444	0.31	2.0057
chr13	115169878	27043938	0.2348	1.7525
chr14	107349540	27218771	0.2536	1.8214
chr15	102531392	28162522	0.2747	1.8908
chr16	90354753	29713978	0.3289	2.0624
chr17	81195210	28977575	0.3569	2.3235
chr18	78077248	22472804	0.2878	2.2592
chr19	59128983	22457429	0.3798	2.7085
chr20	63025520	21452754	0.3404	2.1204
chr21	48129895	11990224	0.2491	1.8475
chr22	51304566	13196150	0.2572	1.8318
chrMT	16571	277446	16.7429	22.9418
chrX	155270560	26660564	0.1717	1.545

chrY	59373566	5705142	0.0961	1.0471

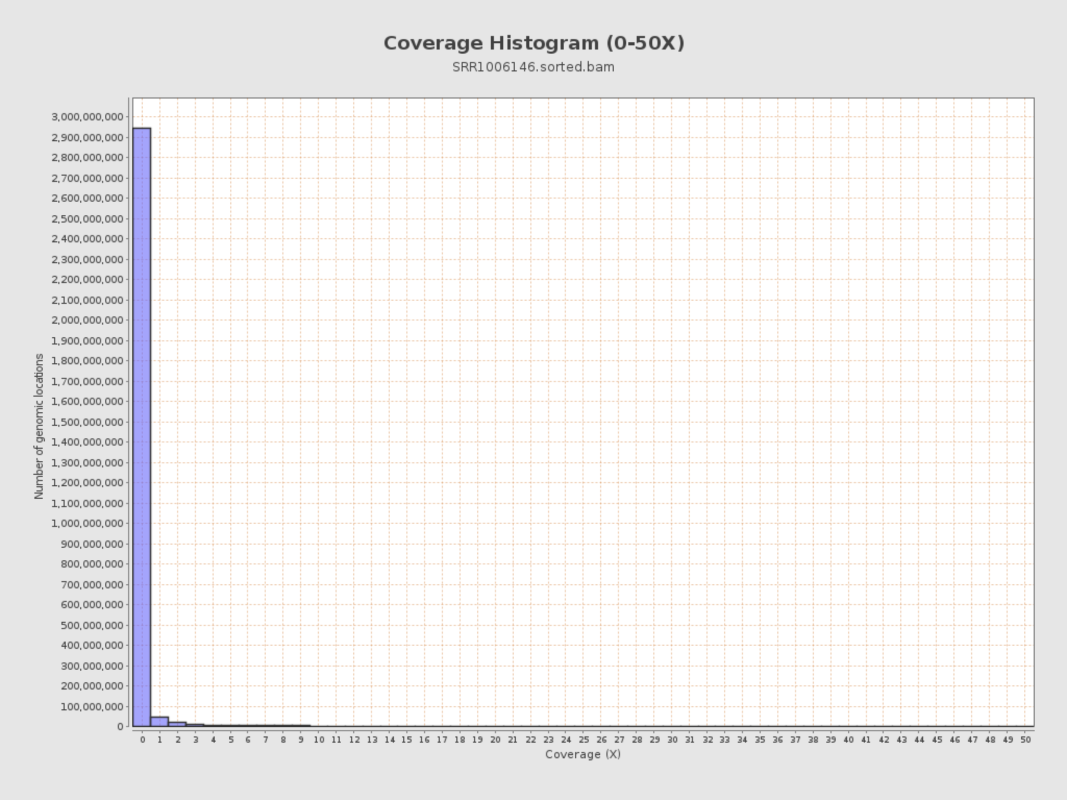
3. Results : Coverage across reference



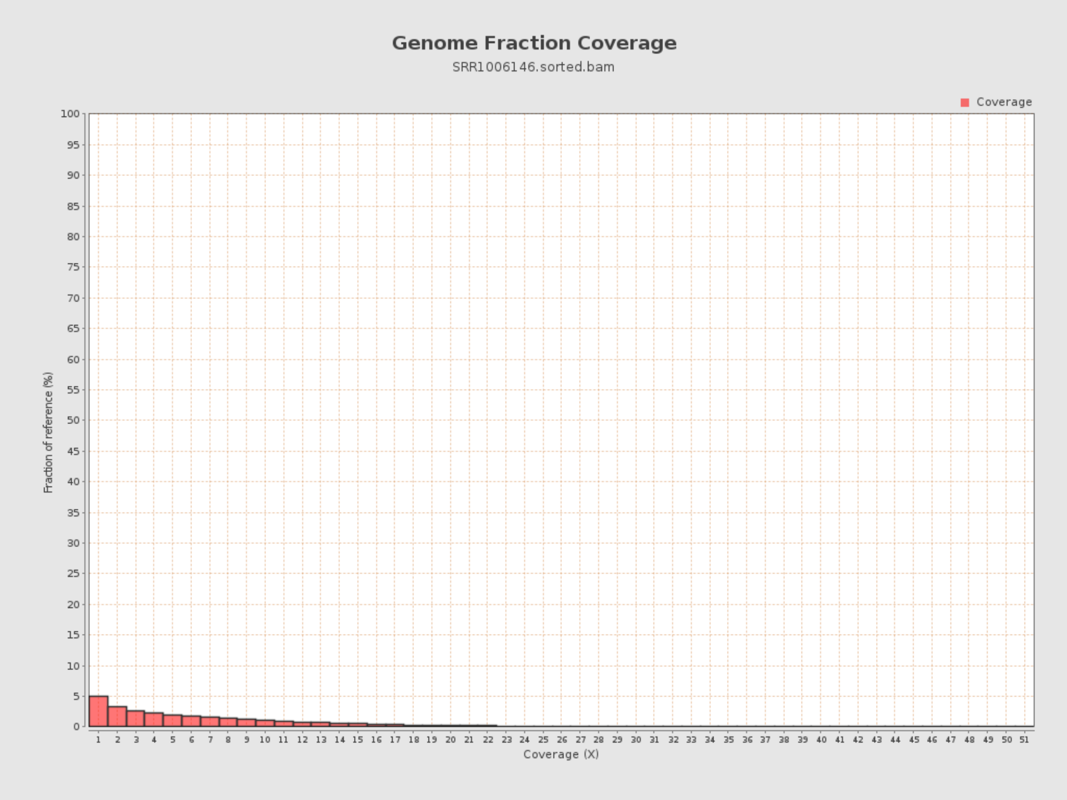
4. Results : Coverage Histogram



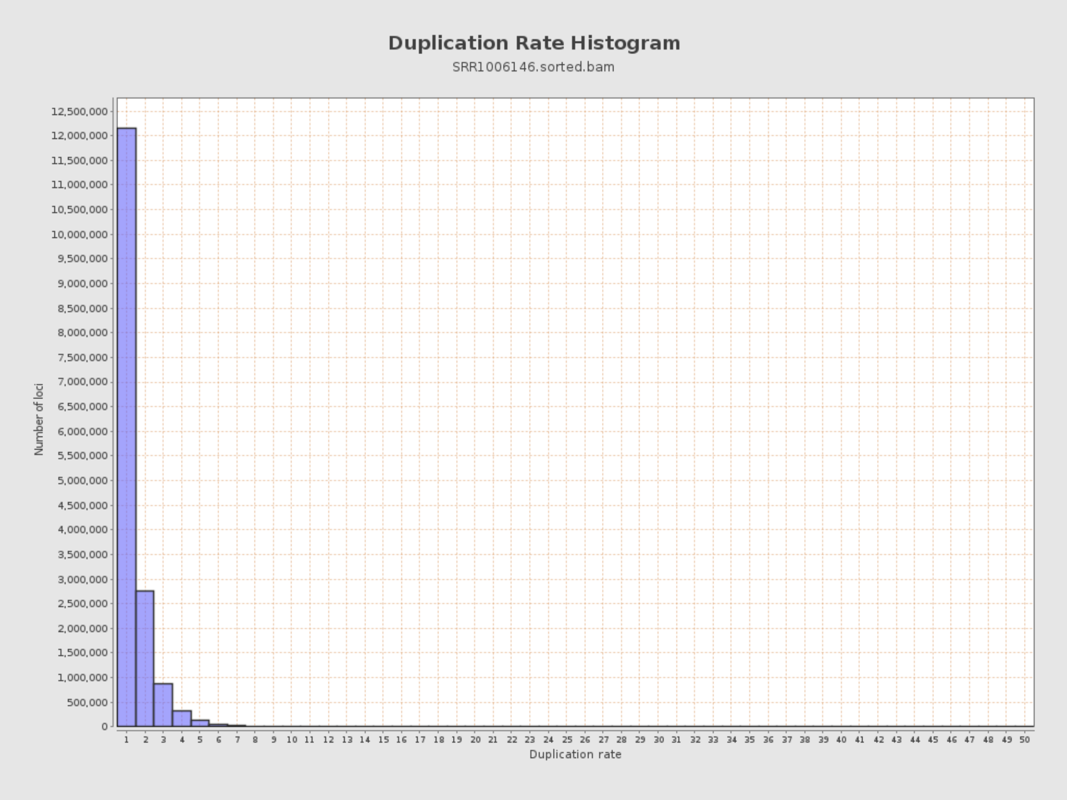
5. Results : Coverage Histogram (0-50X)



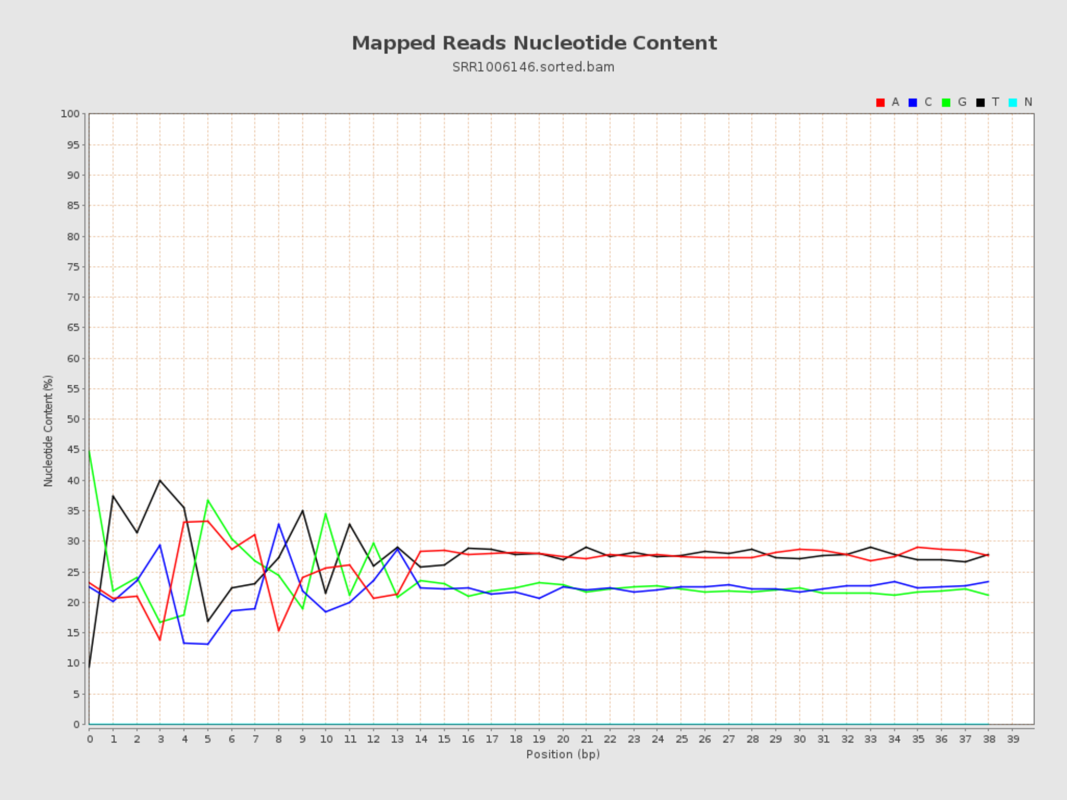
6. Results : Genome Fraction Coverage



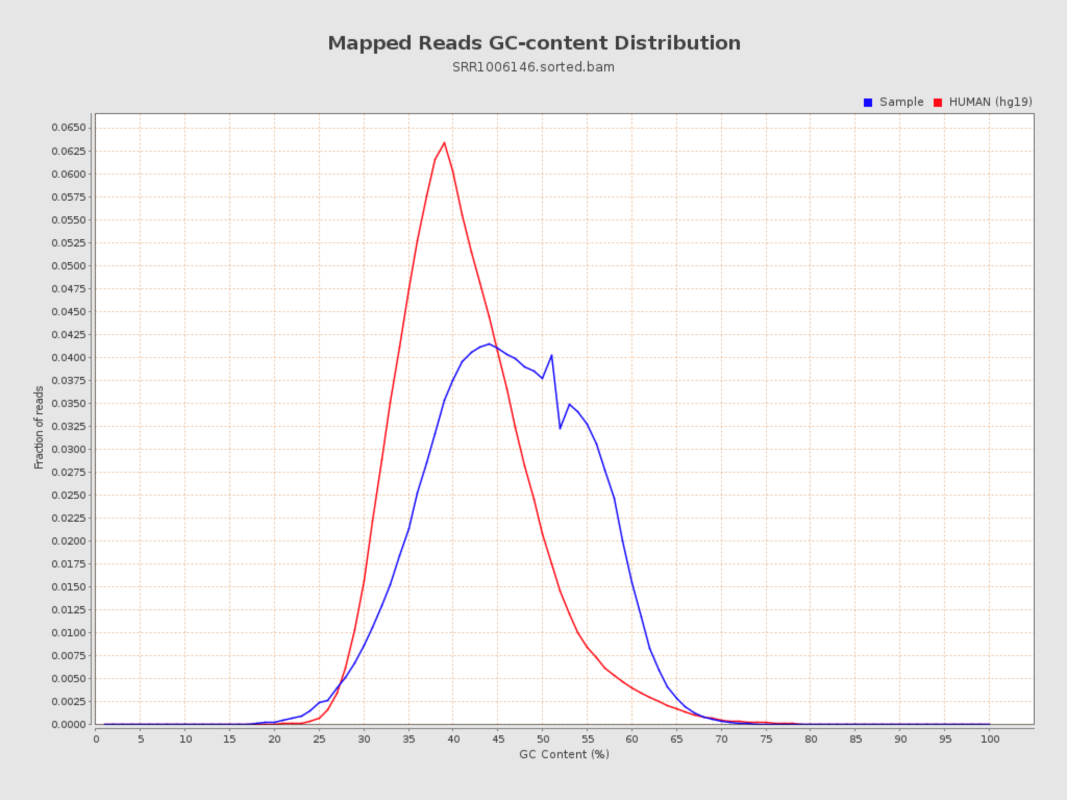
7. Results : Duplication Rate Histogram



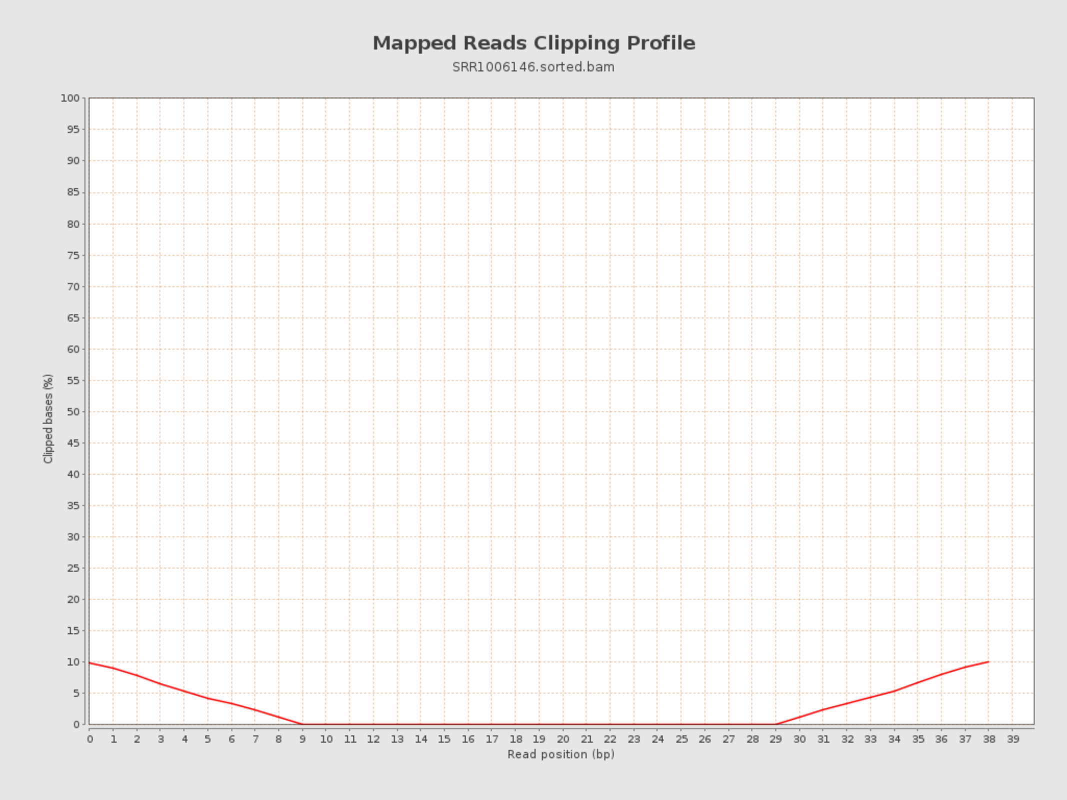
8. Results : Mapped Reads Nucleotide Content



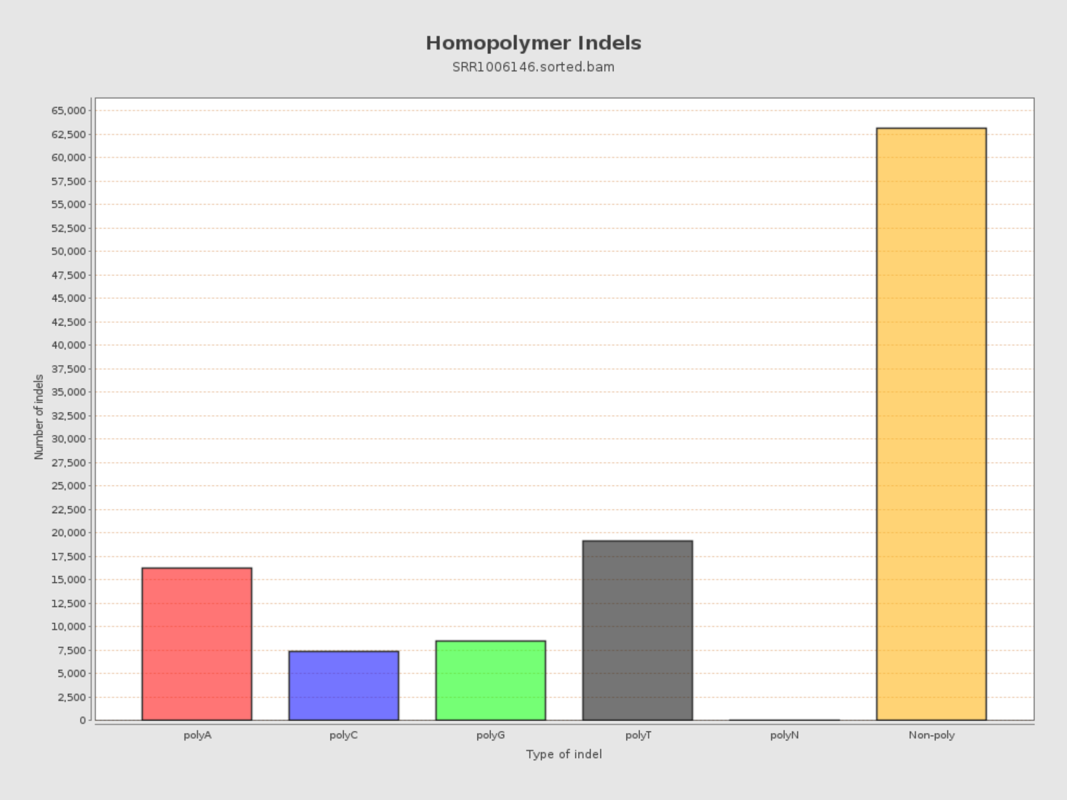
9. Results : Mapped Reads GC-content Distribution



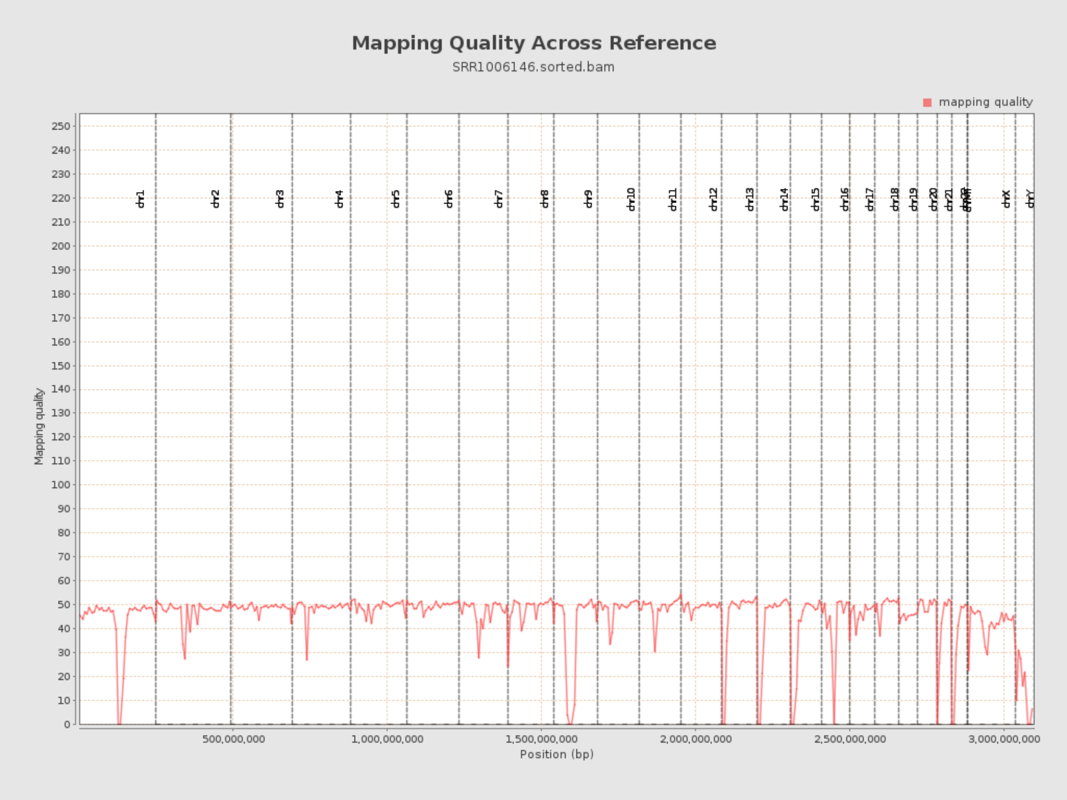
10. Results : Mapped Reads Clipping Profile



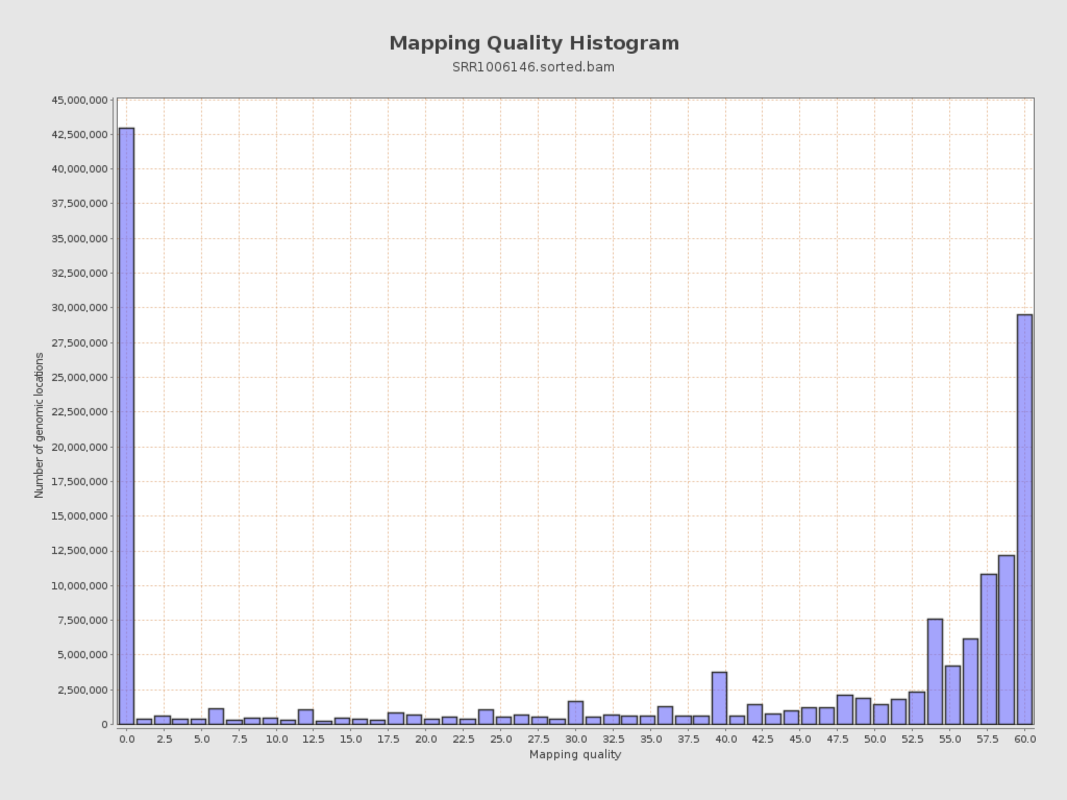
11. Results : Homopolymer Indels



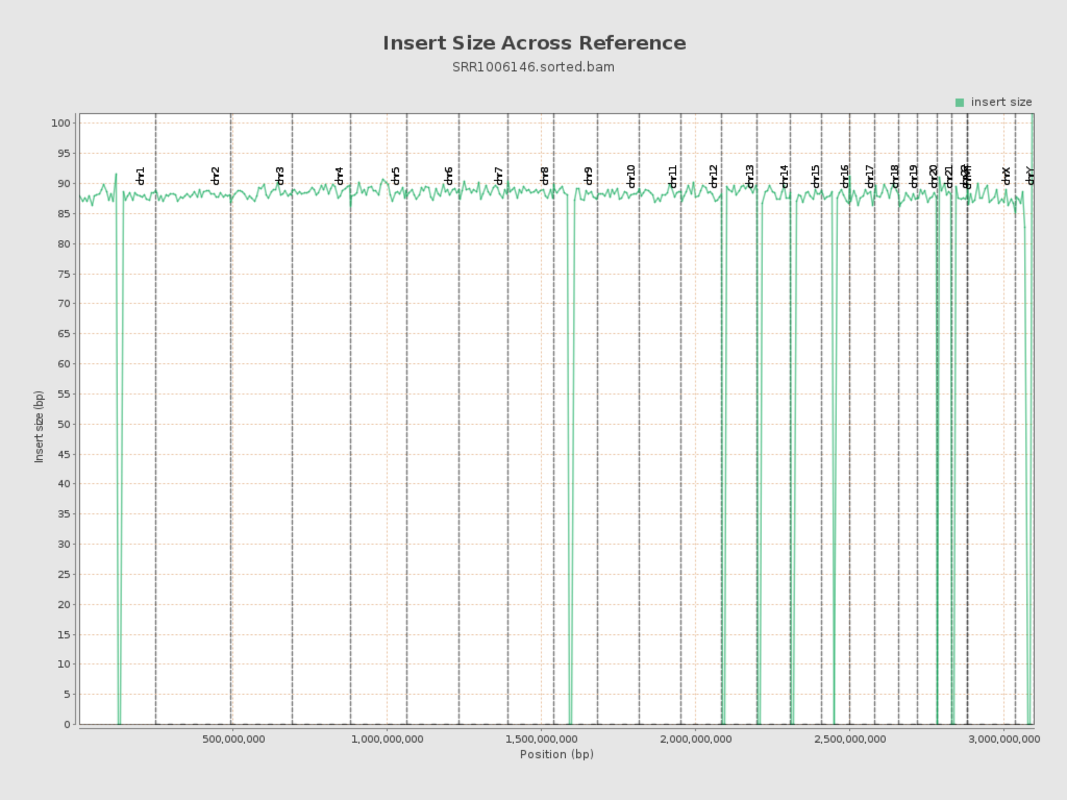
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram