Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 23:25:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006192.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_SRR1006192 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006192_1.fastq.gz SRR1006192_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 23:25:46 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006192.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,033,628
Mapped reads	6,054,922 / 86.09%
Unmapped reads	978,706 / 13.91%
Mapped paired reads	6,054,922 / 86.09%
Mapped reads, first in pair	3,053,468 / 43.41%
Mapped reads, second in pair	3,001,454 / 42.67%
Mapped reads, both in pair	5,566,460 / 79.14%
Mapped reads, singletons	488,462 / 6.94%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	278,927 / 3.97%
Duplication rate	3.98%
Clipped reads	358,990 / 5.1%

2.2. ACGT Content

Number/percentage of A's	65,321,295 / 27.88%
Number/percentage of C's	50,216,635 / 21.43%
Number/percentage of T's	66,546,101 / 28.4%
Number/percentage of G's	52,170,296 / 22.27%
Number/percentage of N's	27,630 / 0.01%
GC Percentage	43.7%

2.3. Coverage

Mean	0.0757
Standard Deviation	0.5279

2.4. Mapping Quality

Mean Mapping Quality	47.86

2.5. Insert size

Mean	53,099.31
Standard Deviation	2,184,281.5
P25/Median/P75	74 / 101 / 136

2.6. Mismatches and indels

General error rate	0.32%
Mismatches	749,325
Insertions	6,788
Mapped reads with at least one insertion	0.11%
Deletions	25,961
Mapped reads with at least one deletion	0.43%
Homopolymer indels	41.75%

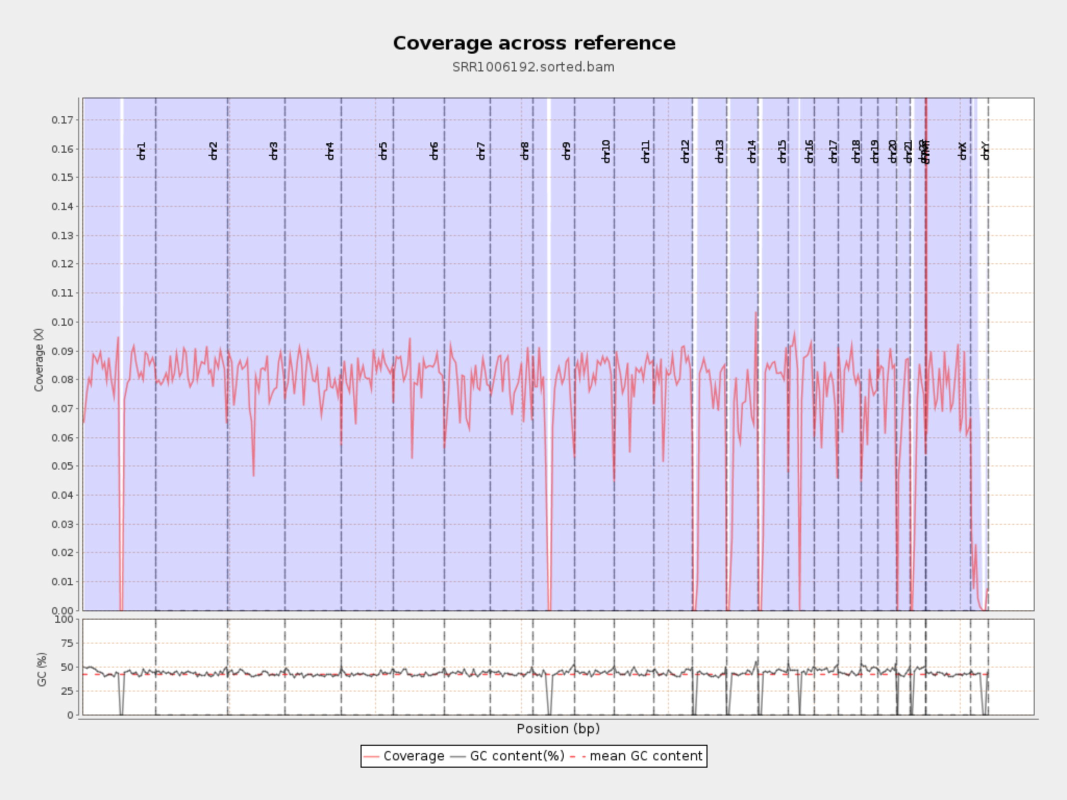
2.7. Chromosome stats

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

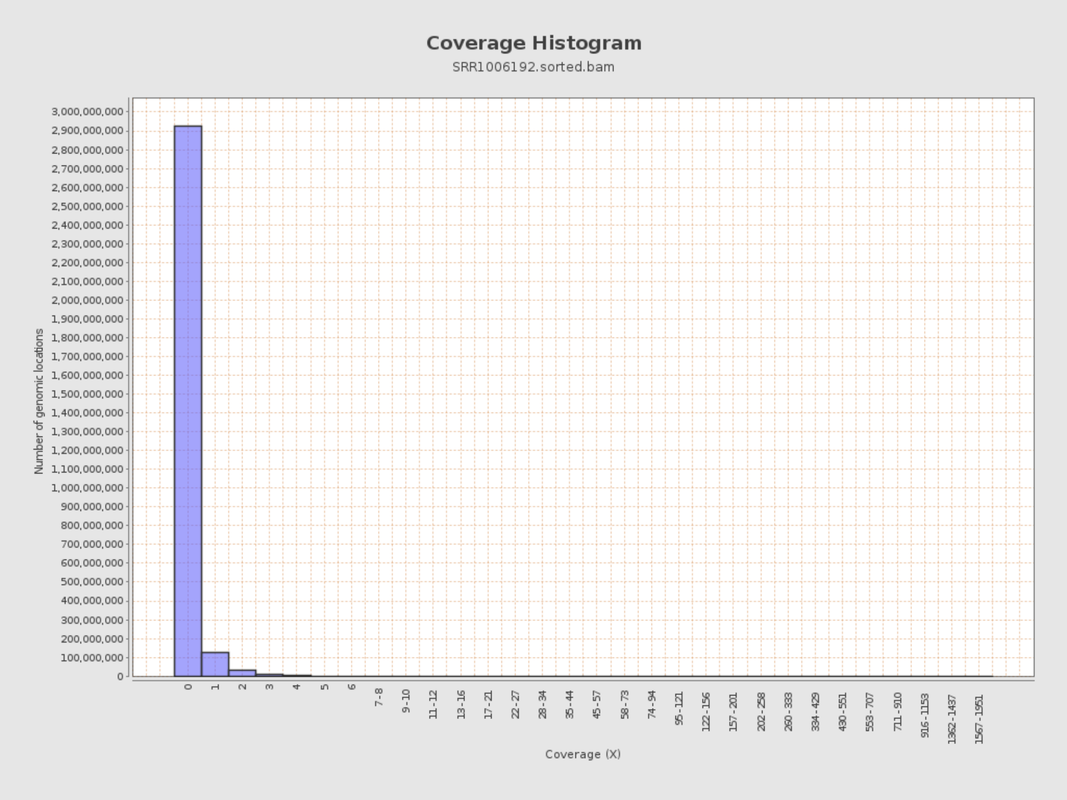
chr1	249250621	19512804	0.0783	0.6133
chr2	243199373	20247908	0.0833	0.4344
chr3	198022430	15716621	0.0794	0.3688
chr4	191154276	15353313	0.0803	0.386
chr5	180915260	14806860	0.0818	0.3751
chr6	171115067	14147192	0.0827	0.4155
chr7	159138663	12365667	0.0777	0.5216
chr8	146364022	11620971	0.0794	1.0177
chr9	141213431	9659402	0.0684	0.3846
chr10	135534747	11225975	0.0828	0.4375
chr11	135006516	10879591	0.0806	0.4659
chr12	133851895	10932824	0.0817	0.3798
chr13	115169878	7675125	0.0666	0.3381
chr14	107349540	6524788	0.0608	1.3112
chr15	102531392	6964092	0.0679	0.3443
chr16	90354753	6952599	0.0769	0.3886
chr17	81195210	6005707	0.074	0.3803
chr18	78077248	6363799	0.0815	0.5743
chr19	59128983	4232784	0.0716	0.4861
chr20	63025520	5035116	0.0799	0.3992
chr21	48129895	3058085	0.0635	0.358
chr22	51304566	2701557	0.0527	0.3275
chrMT	16571	15962	0.9632	1.7354
chrX	155270560	11844937	0.0763	0.3884

chrY	59373566	473924	0.008	0.1636

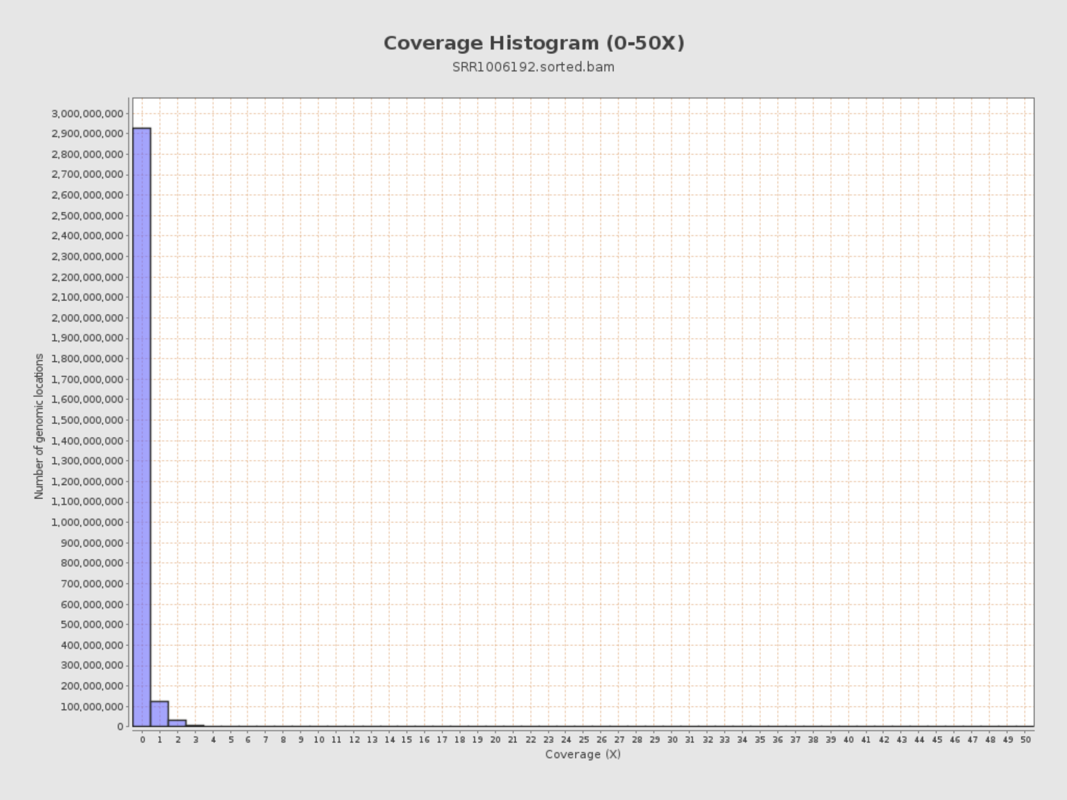
3. Results : Coverage across reference



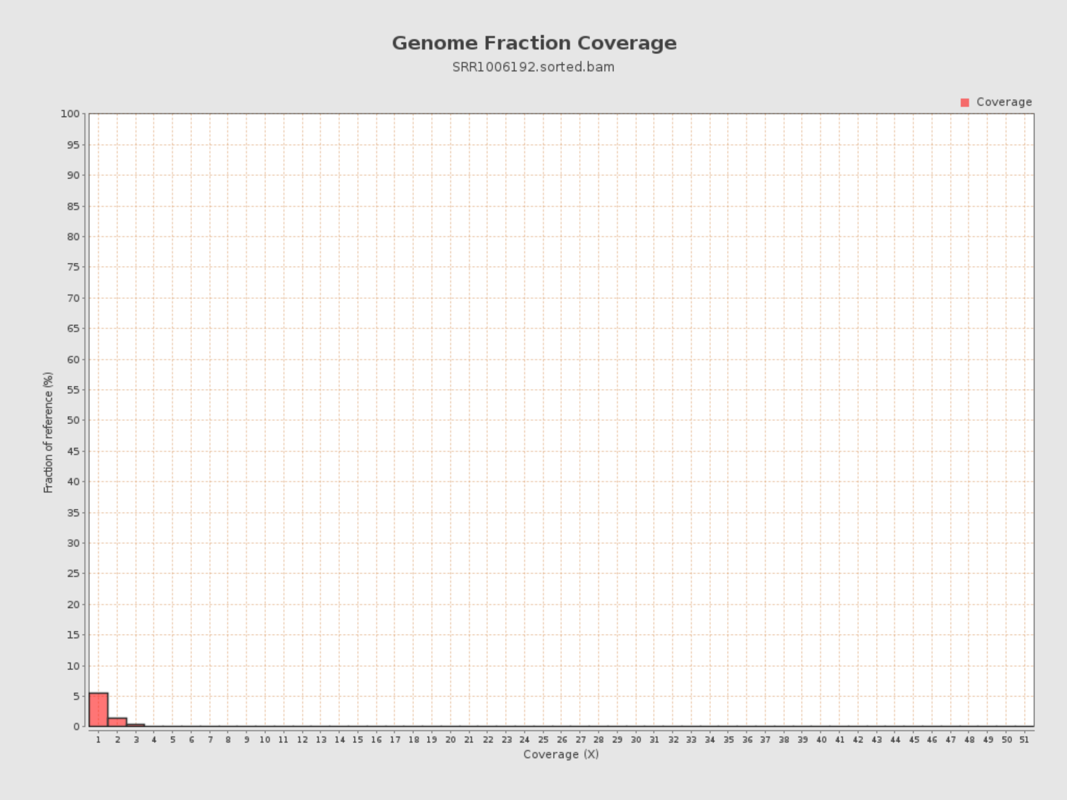
4. Results : Coverage Histogram



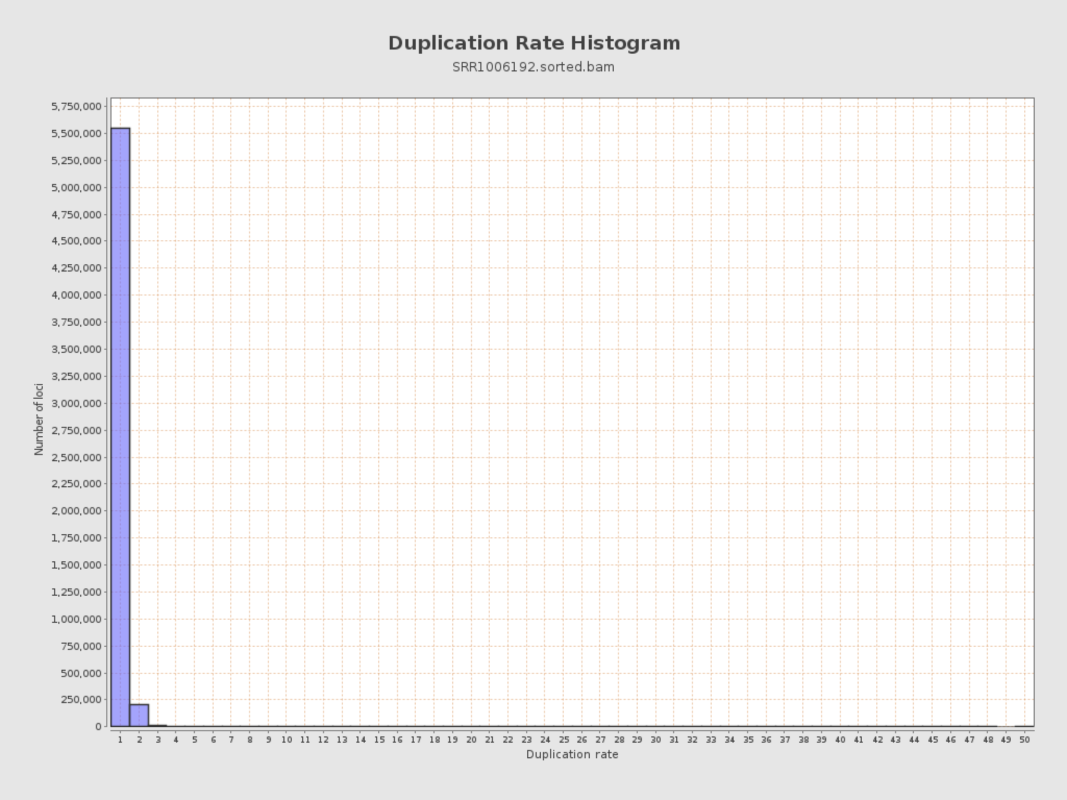
5. Results : Coverage Histogram (0-50X)



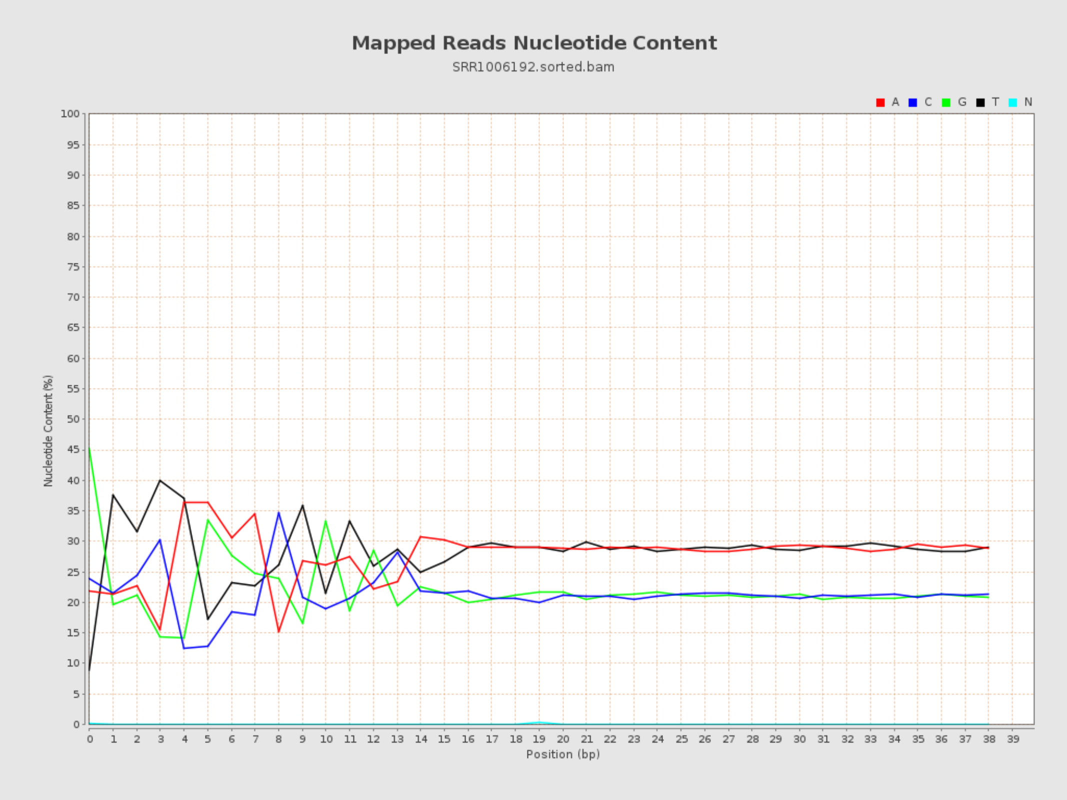
6. Results : Genome Fraction Coverage



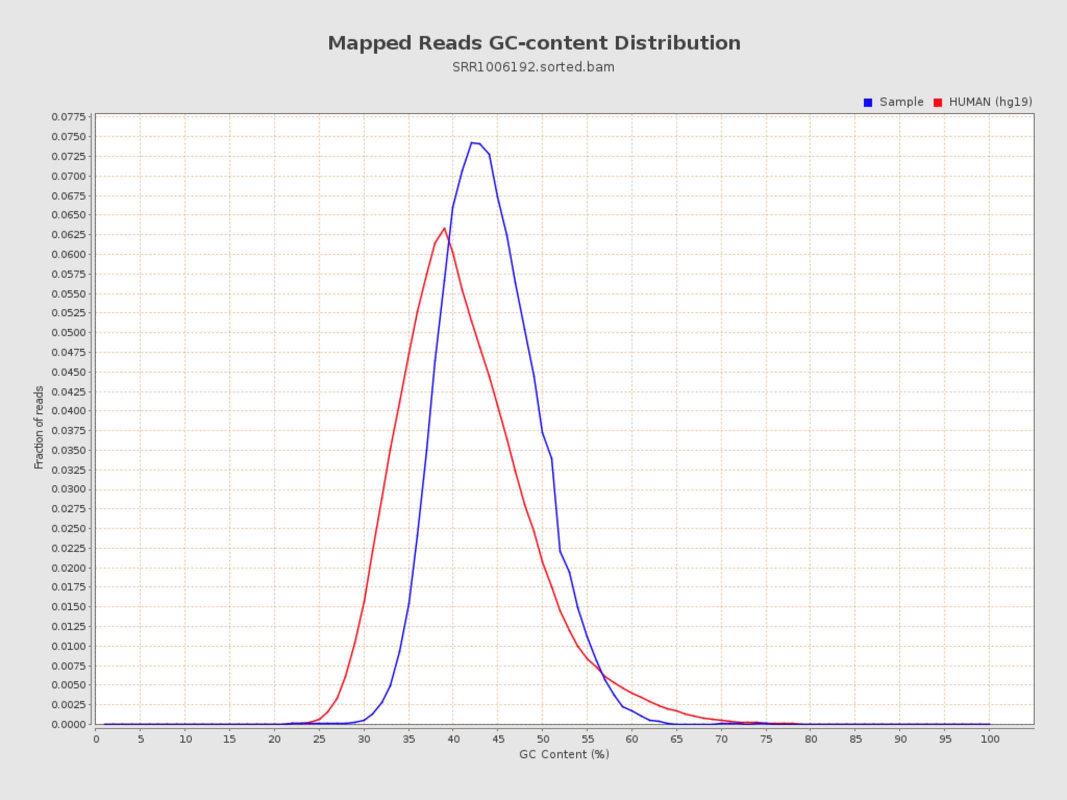
7. Results : Duplication Rate Histogram



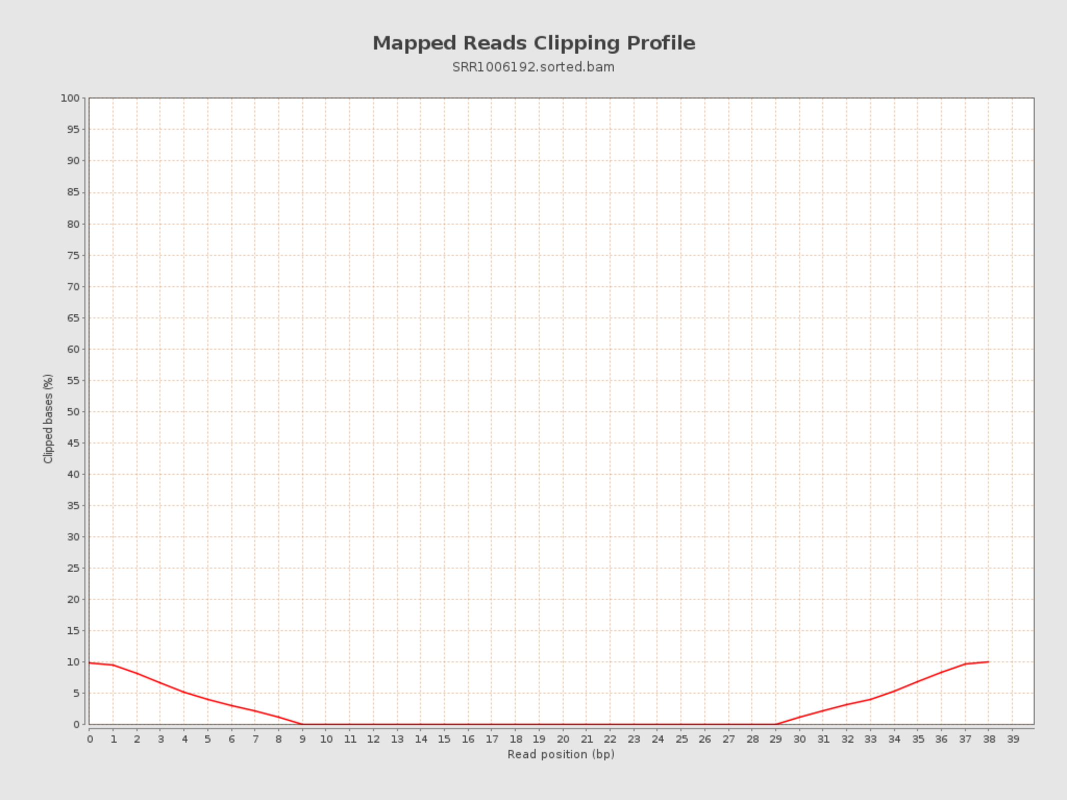
8. Results : Mapped Reads Nucleotide Content



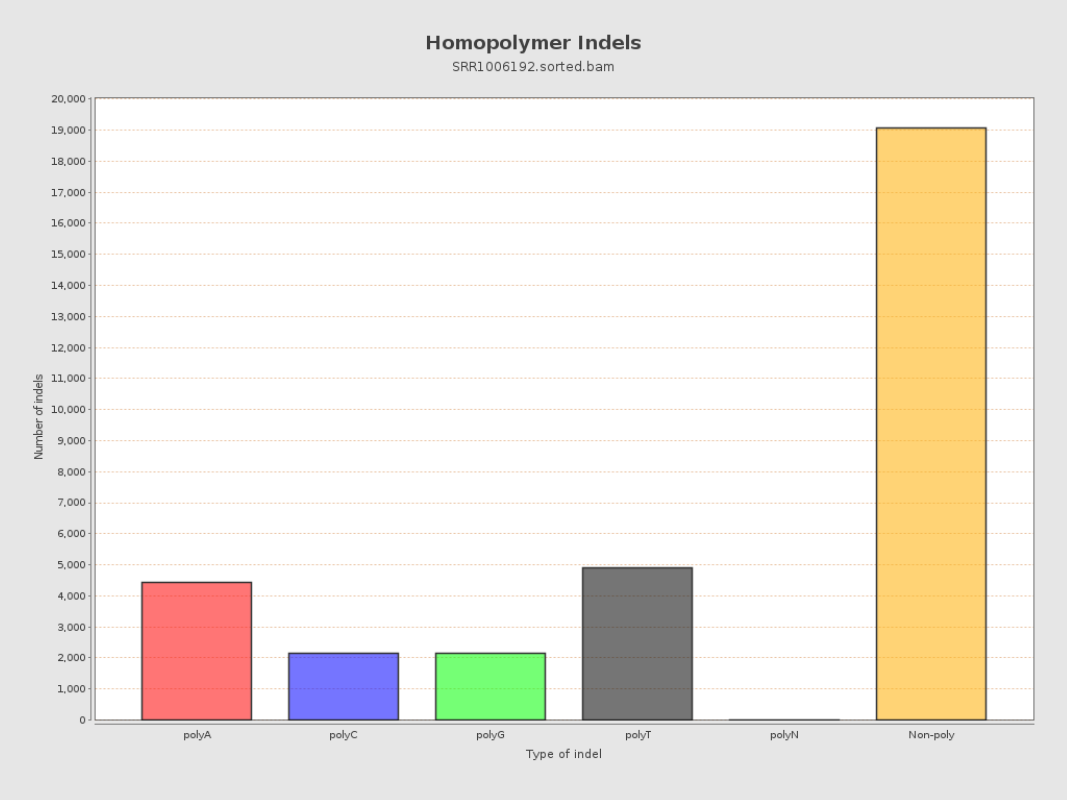
9. Results : Mapped Reads GC-content Distribution



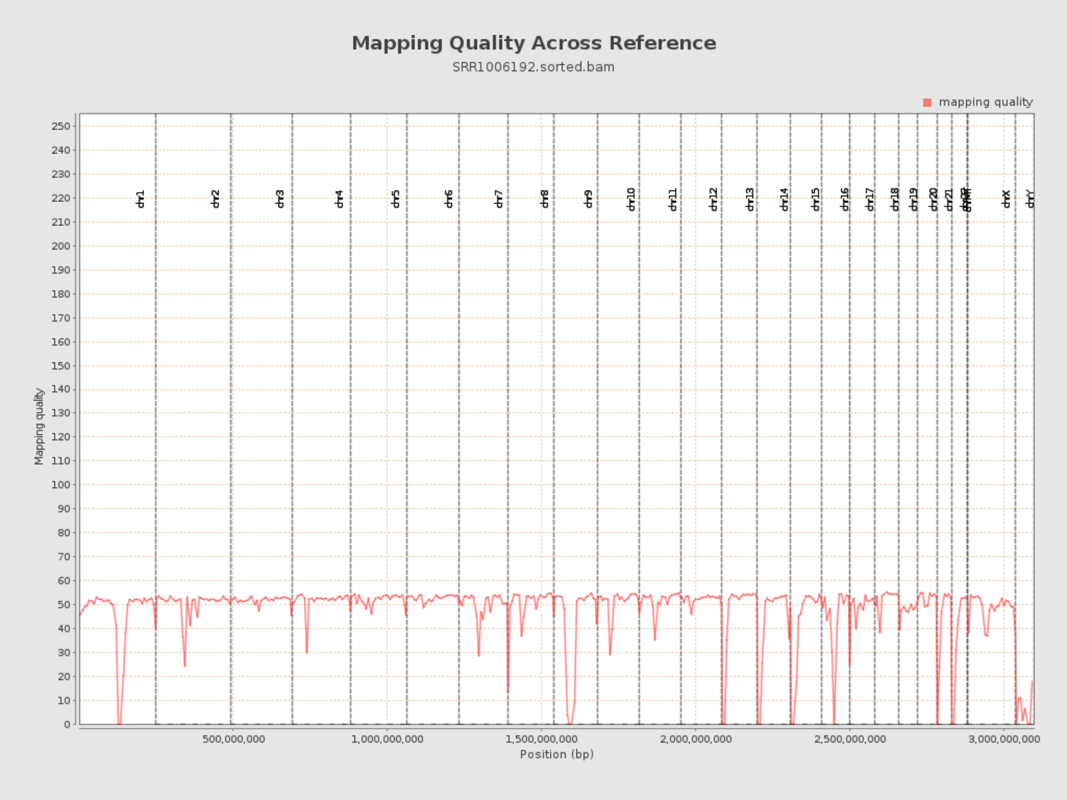
10. Results : Mapped Reads Clipping Profile



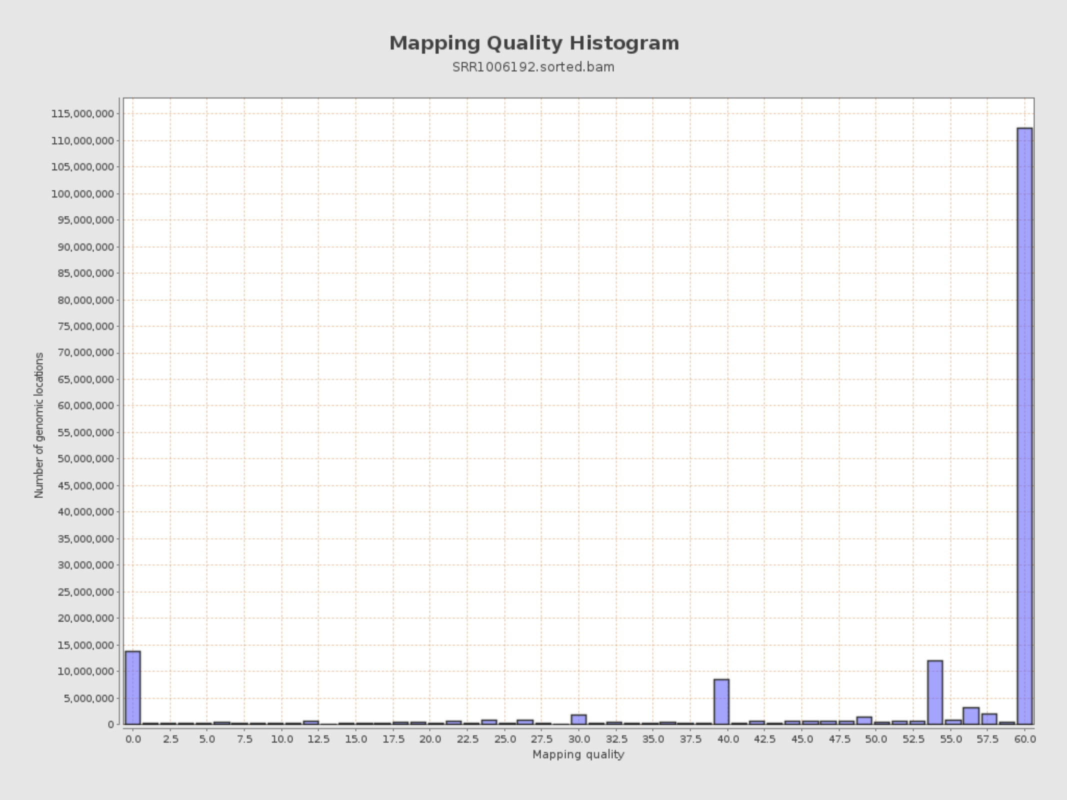
11. Results : Homopolymer Indels



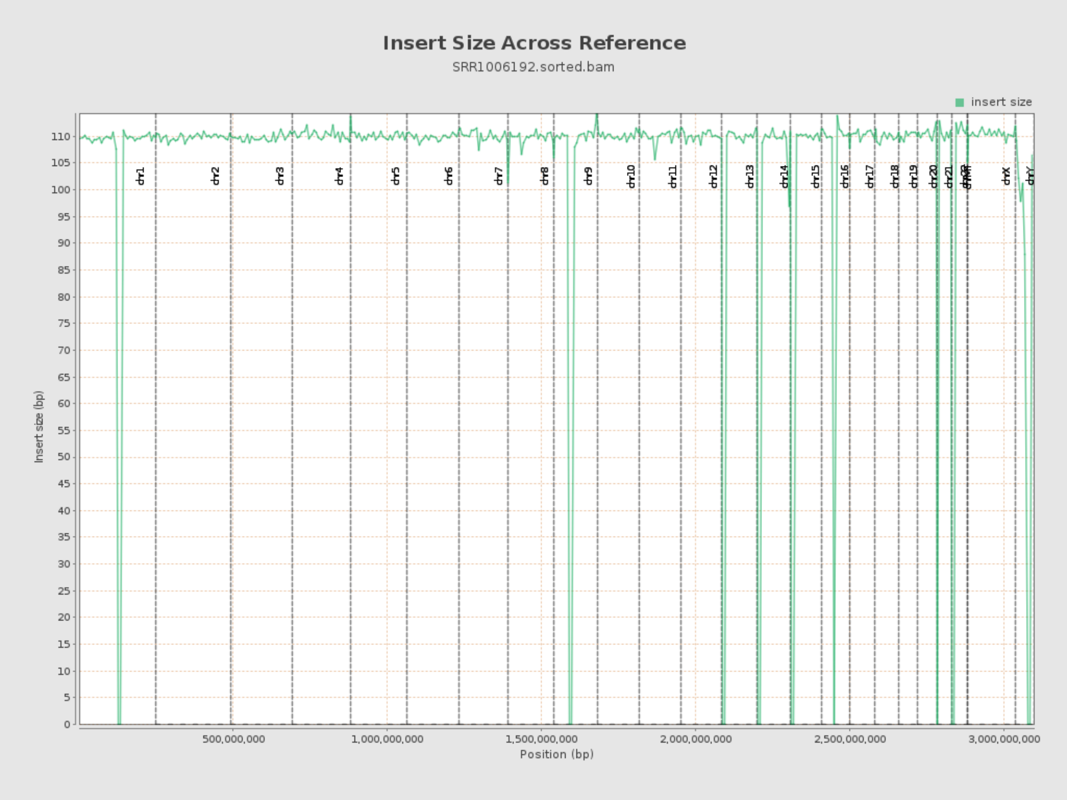
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram