Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 14:43:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006026.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_SRR1006026 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006026_1.fastq.gz SRR1006026_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 14:43:03 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006026.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,354,842
Mapped reads	8,263,403 / 66.88%
Unmapped reads	4,091,439 / 33.12%
Mapped paired reads	8,263,403 / 66.88%
Mapped reads, first in pair	4,186,436 / 33.88%
Mapped reads, second in pair	4,076,967 / 33%
Mapped reads, both in pair	7,189,276 / 58.19%
Mapped reads, singletons	1,074,127 / 8.69%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	262,142 / 2.12%
Duplication rate	2.49%
Clipped reads	691,944 / 5.6%

2.2. ACGT Content

Number/percentage of A's	95,025,112 / 29.78%
Number/percentage of C's	64,821,336 / 20.32%
Number/percentage of T's	93,466,051 / 29.29%
Number/percentage of G's	65,619,156 / 20.57%
Number/percentage of N's	121,047 / 0.04%
GC Percentage	40.88%

2.3. Coverage

Mean	0.1031
Standard Deviation	0.5917

2.4. Mapping Quality

Mean Mapping Quality	47.08

2.5. Insert size

Mean	69,878.68
Standard Deviation	2,563,100.99
P25/Median/P75	69 / 97 / 139

2.6. Mismatches and indels

General error rate	0.71%
Mismatches	2,267,097
Insertions	8,978
Mapped reads with at least one insertion	0.11%
Deletions	27,435
Mapped reads with at least one deletion	0.33%
Homopolymer indels	45.48%

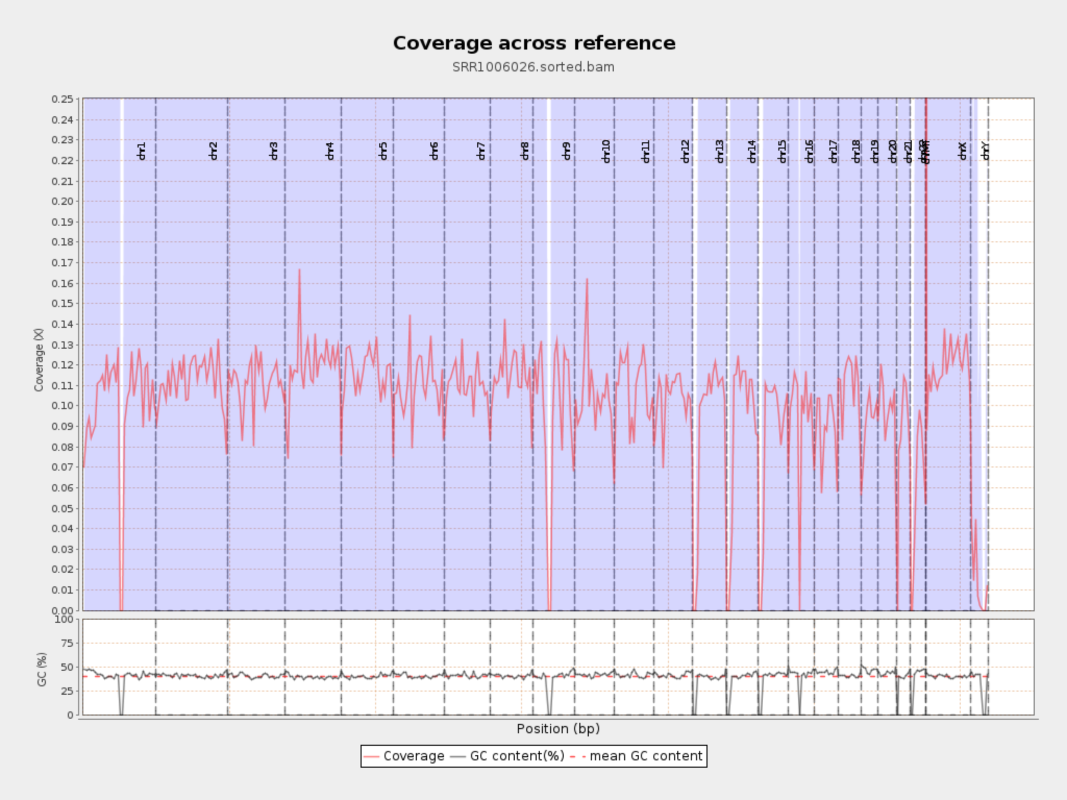
2.7. Chromosome stats

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

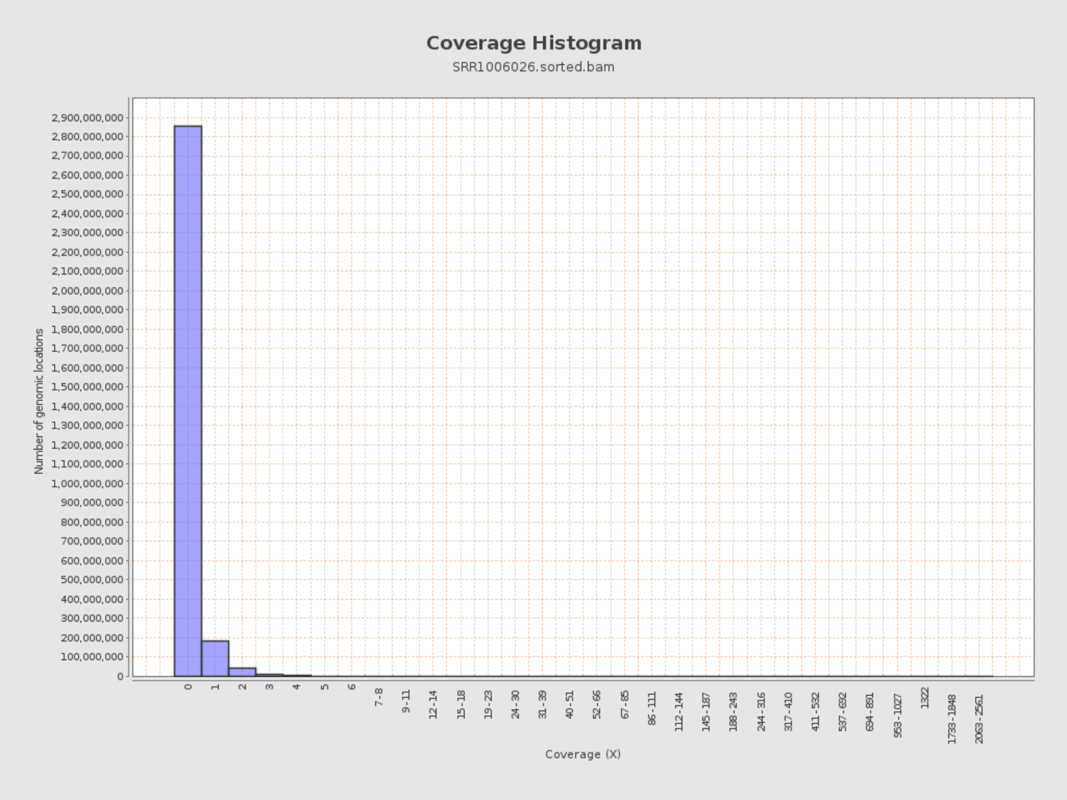
chr1	249250621	24935993	0.1	0.8407
chr2	243199373	27361493	0.1125	0.541
chr3	198022430	22024603	0.1112	0.4153
chr4	191154276	22896519	0.1198	0.4914
chr5	180915260	20932029	0.1157	0.4256
chr6	171115067	18996748	0.111	0.5477
chr7	159138663	17530750	0.1102	0.687
chr8	146364022	16771466	0.1146	1.3199
chr9	141213431	13692925	0.097	0.4619
chr10	135534747	14270400	0.1053	0.629
chr11	135006516	14694298	0.1088	0.4771
chr12	133851895	13879949	0.1037	0.4028
chr13	115169878	10417106	0.0904	0.3732
chr14	107349540	9725915	0.0906	0.4107
chr15	102531392	8435043	0.0823	0.3567
chr16	90354753	8291355	0.0918	0.4456
chr17	81195210	7317853	0.0901	0.3946
chr18	78077248	8667663	0.111	0.6917
chr19	59128983	5455431	0.0923	0.6577
chr20	63025520	6281569	0.0997	0.4144
chr21	48129895	4095157	0.0851	0.419
chr22	51304566	3002523	0.0585	0.3016
chrMT	16571	45712	2.7586	2.7304
chrX	155270560	18528842	0.1193	0.4737

chrY	59373566	836058	0.0141	0.2949

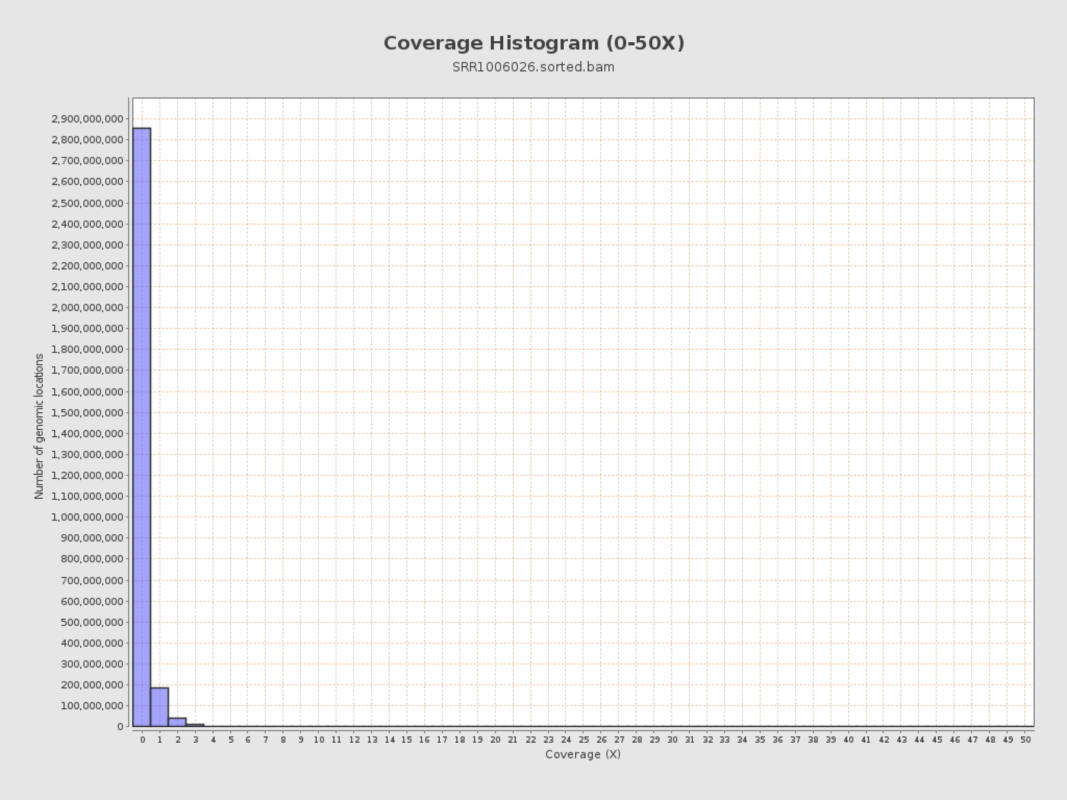
3. Results : Coverage across reference



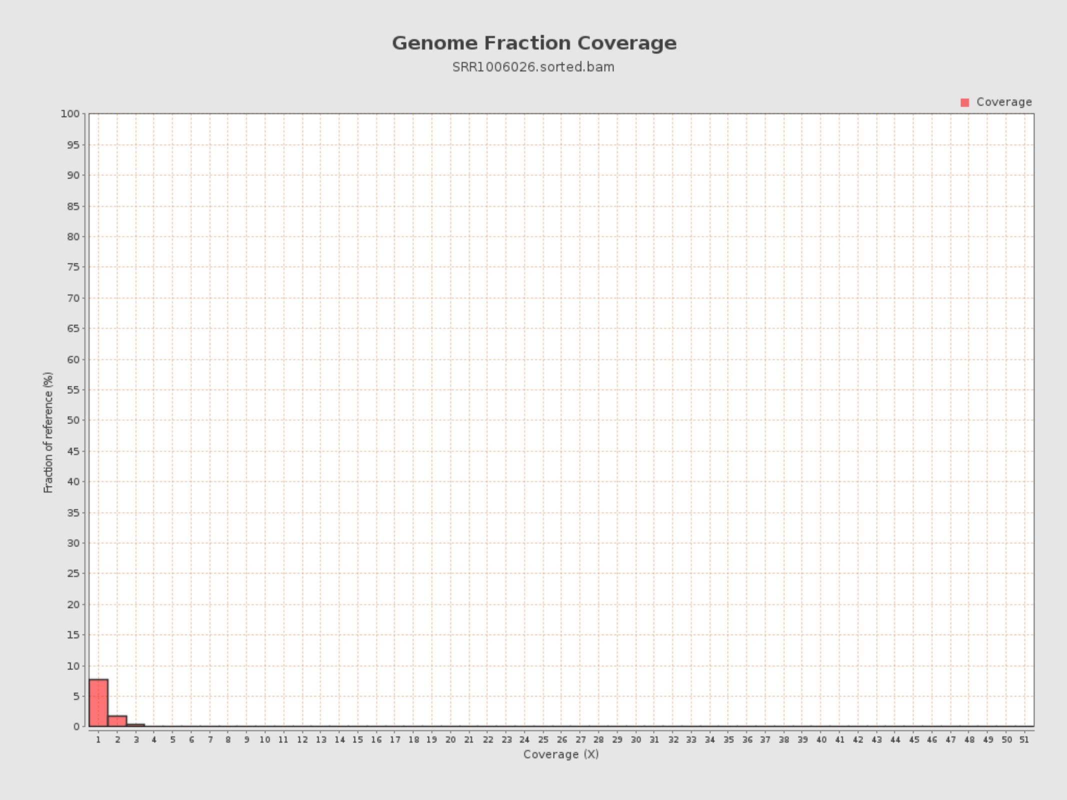
4. Results : Coverage Histogram



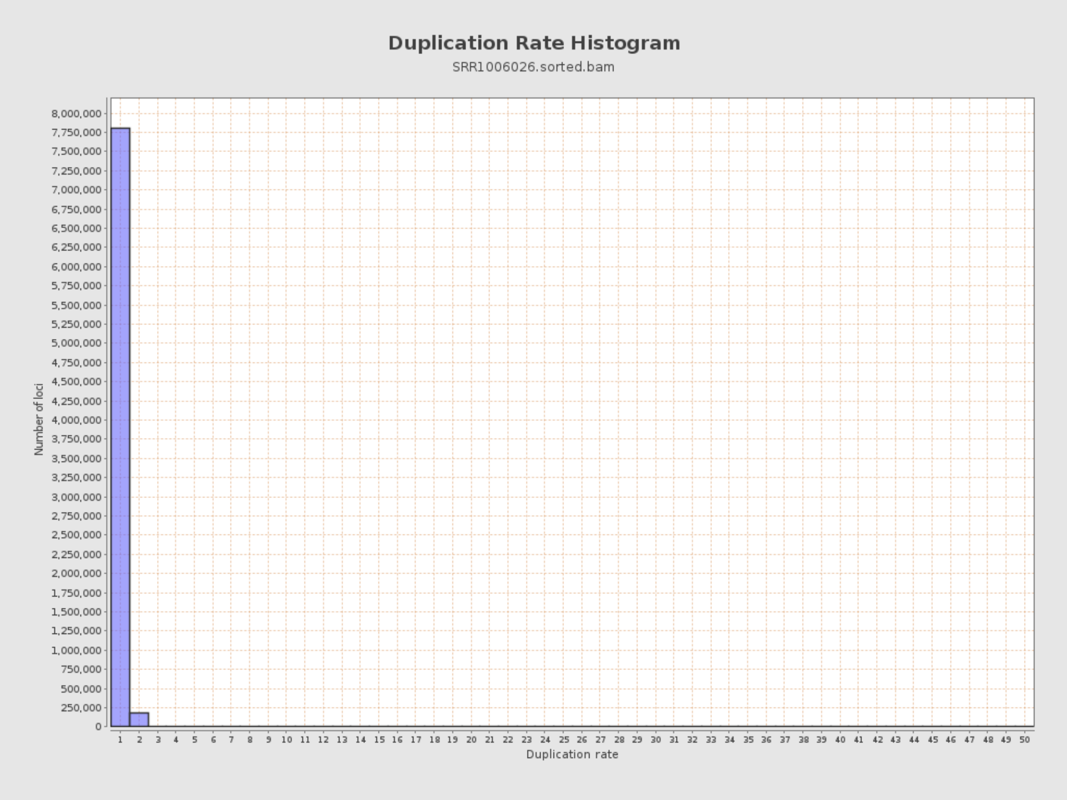
5. Results : Coverage Histogram (0-50X)



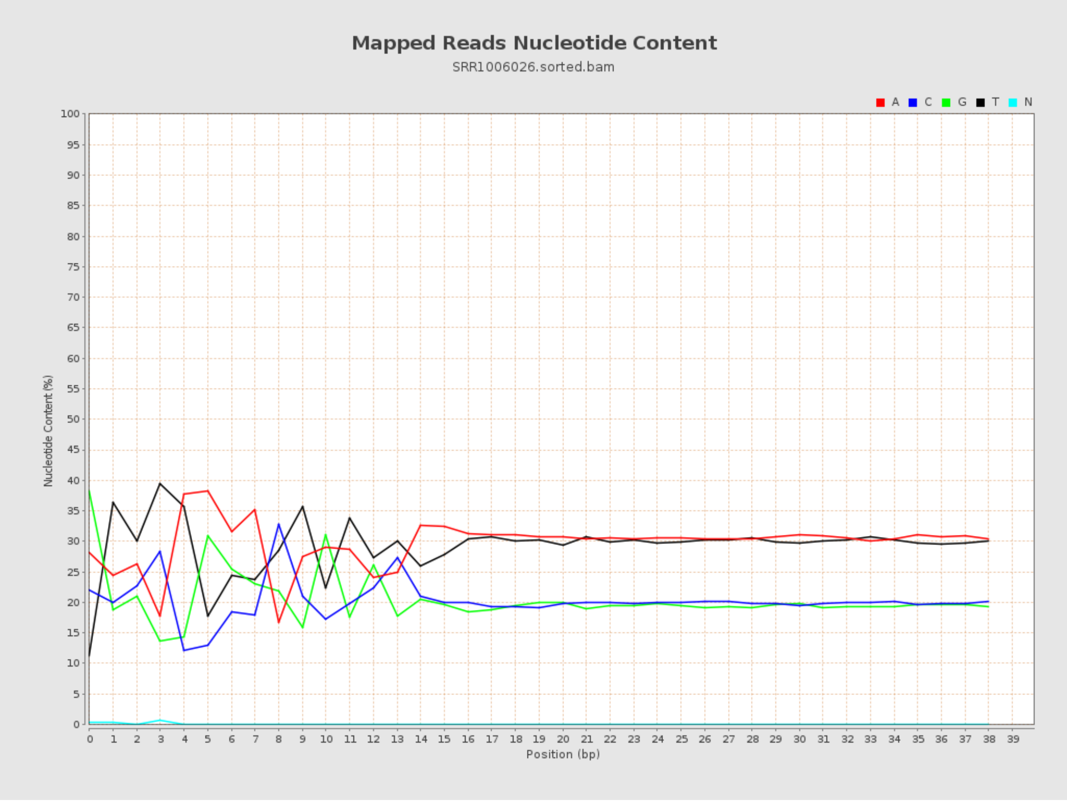
6. Results : Genome Fraction Coverage



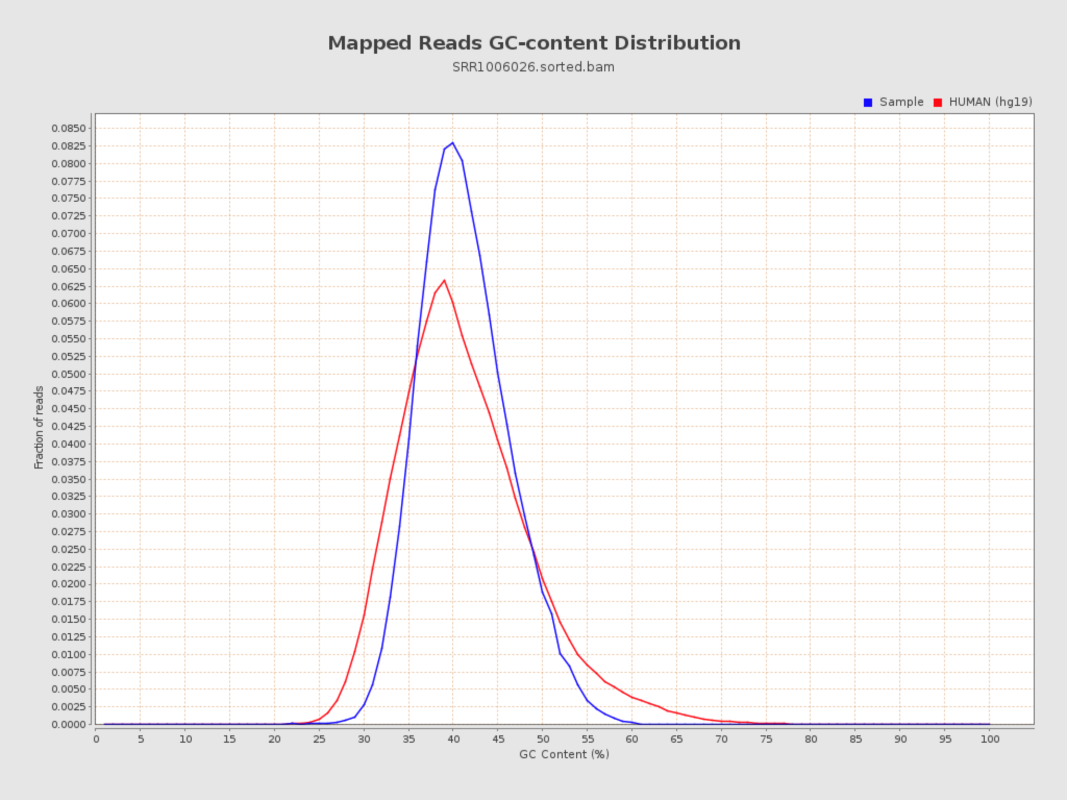
7. Results : Duplication Rate Histogram



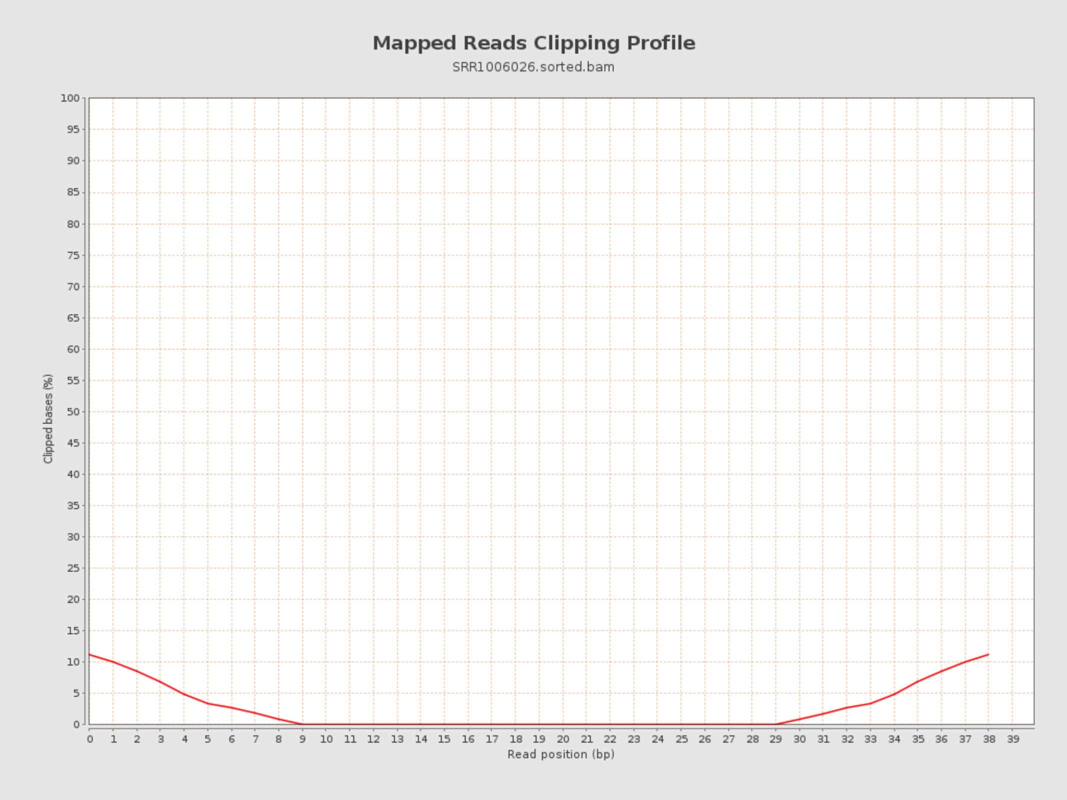
8. Results : Mapped Reads Nucleotide Content



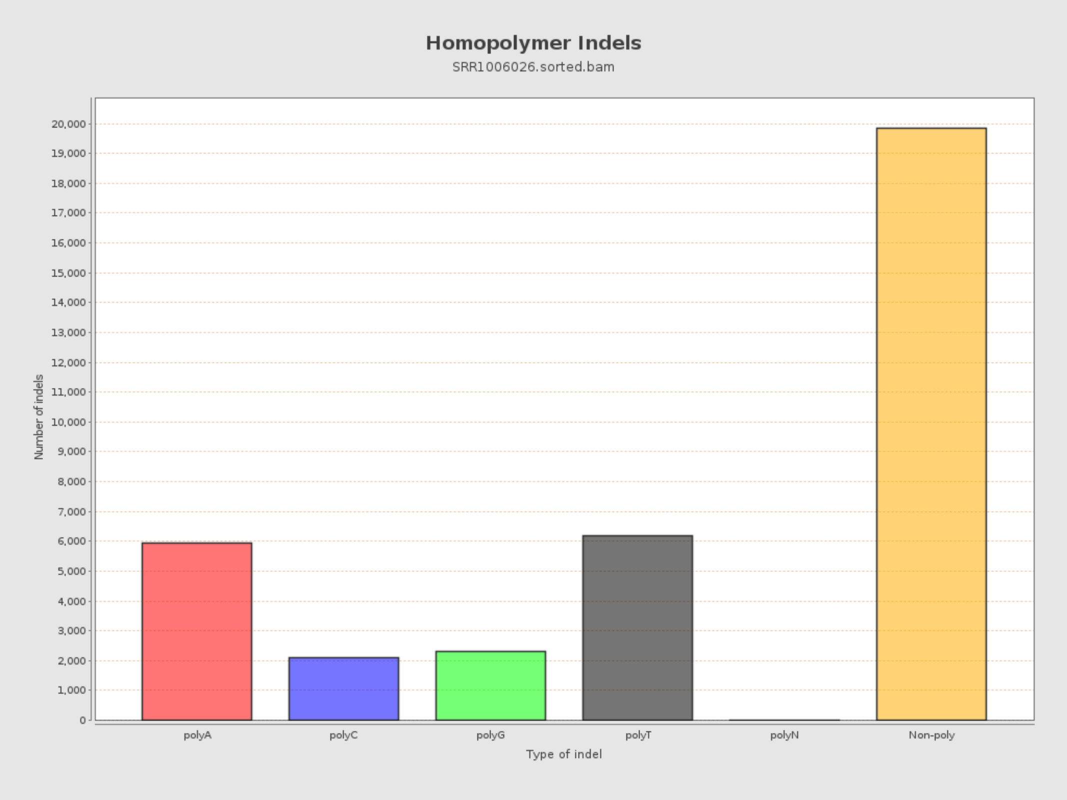
9. Results : Mapped Reads GC-content Distribution



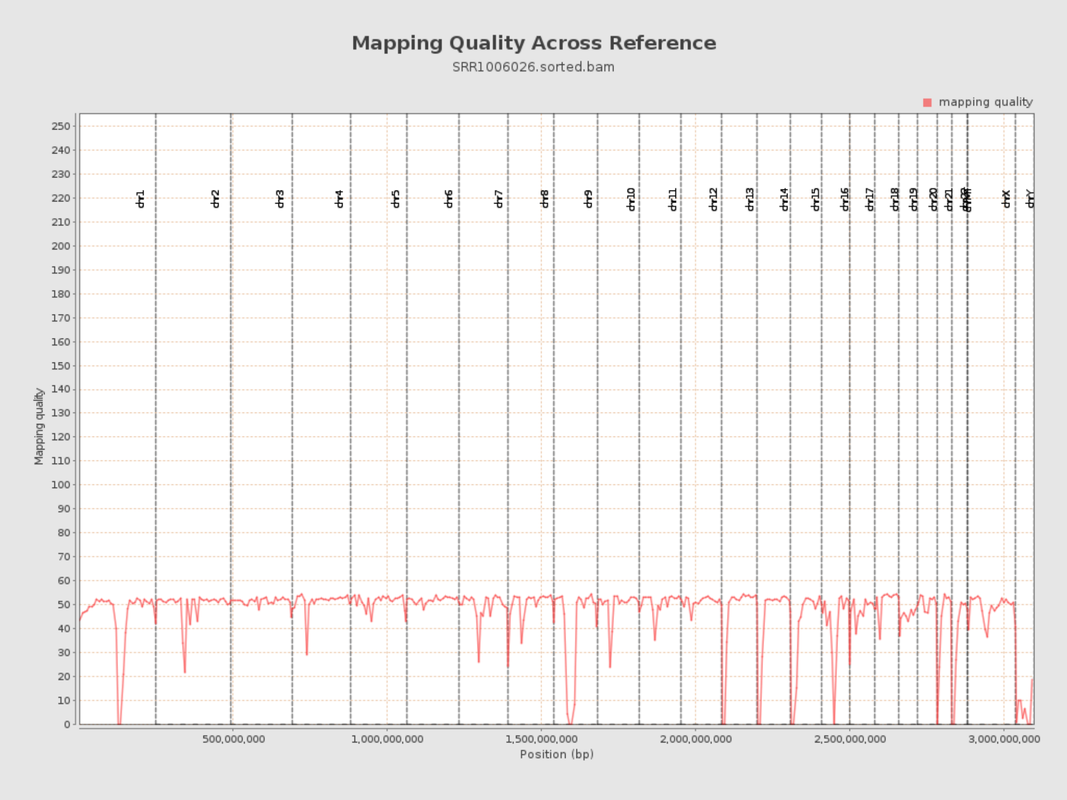
10. Results : Mapped Reads Clipping Profile



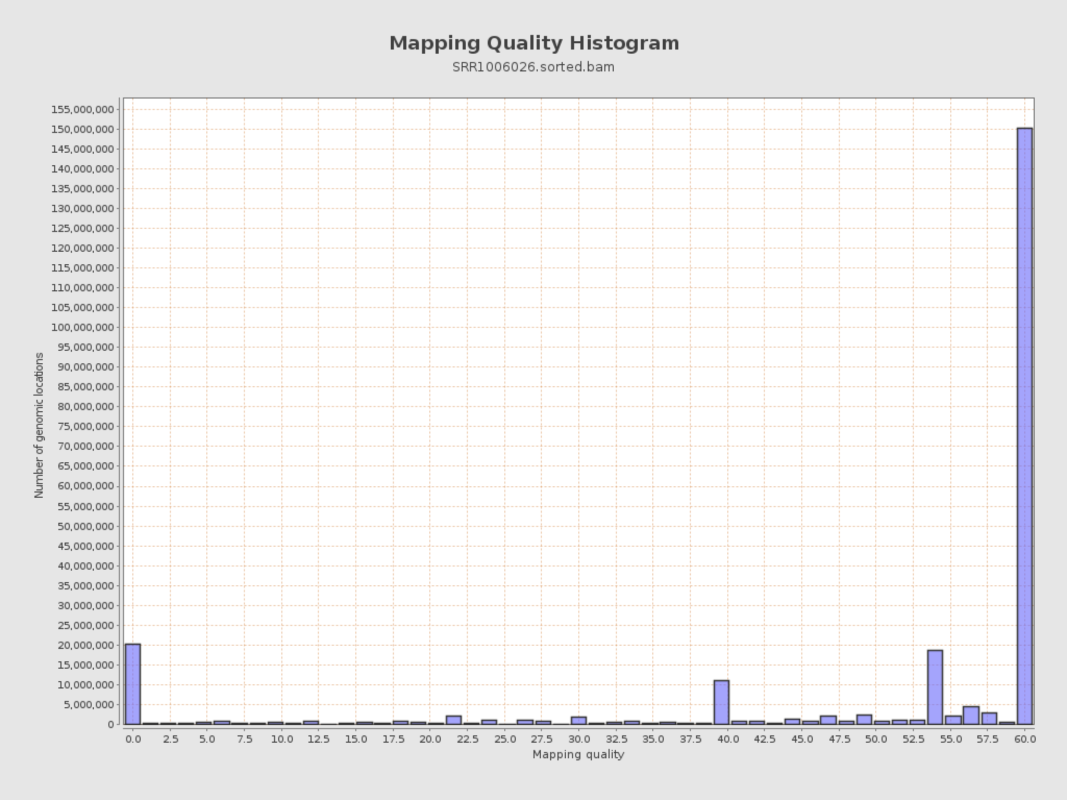
11. Results : Homopolymer Indels



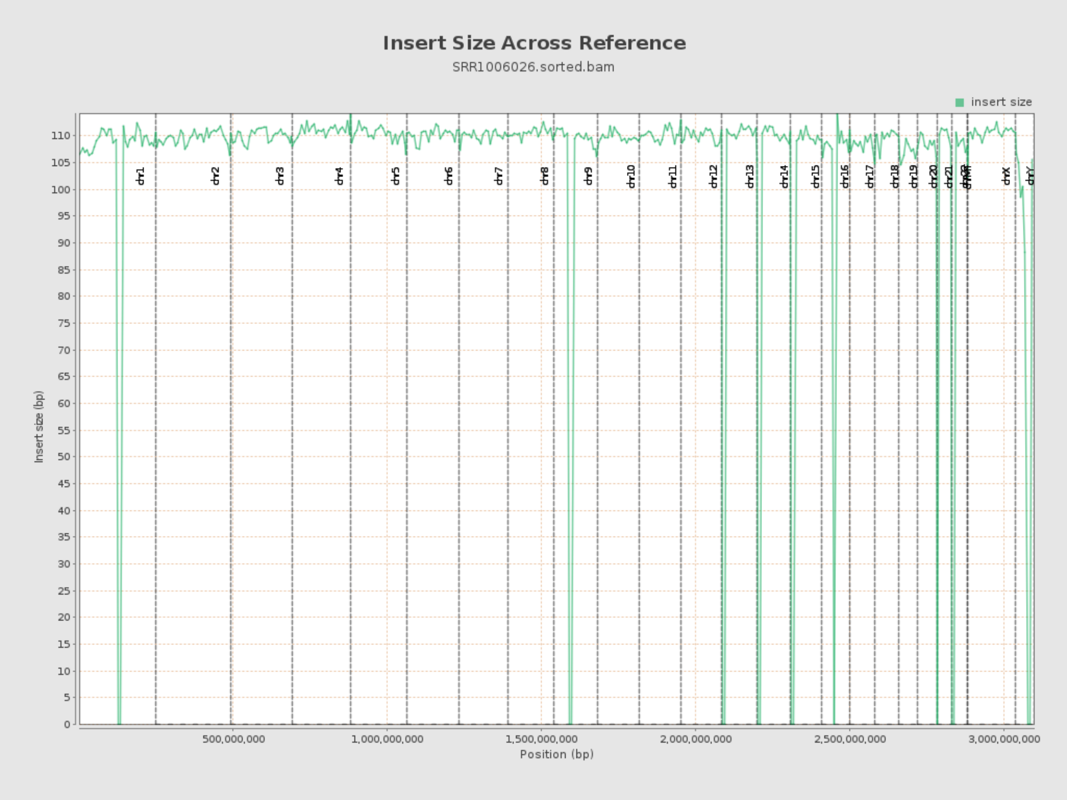
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram