Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 22:45:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006183.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_SRR1006183 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006183_1.fastq.gz SRR1006183_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 22:45:17 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006183.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,594,652
Mapped reads	4,052,686 / 88.2%
Unmapped reads	541,966 / 11.8%
Mapped paired reads	4,052,686 / 88.2%
Mapped reads, first in pair	2,032,887 / 44.24%
Mapped reads, second in pair	2,019,799 / 43.96%
Mapped reads, both in pair	3,738,038 / 81.36%
Mapped reads, singletons	314,648 / 6.85%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	135,557 / 2.95%
Duplication rate	2.76%
Clipped reads	219,386 / 4.77%

2.2. ACGT Content

Number/percentage of A's	43,847,474 / 27.95%
Number/percentage of C's	33,812,266 / 21.55%
Number/percentage of T's	44,739,765 / 28.52%
Number/percentage of G's	34,478,037 / 21.98%
Number/percentage of N's	5,940 / 0%
GC Percentage	43.53%

2.3. Coverage

Mean	0.0507
Standard Deviation	0.3515

2.4. Mapping Quality

Mean Mapping Quality	47.78

2.5. Insert size

Mean	82,665.19
Standard Deviation	2,752,719.53
P25/Median/P75	115 / 155 / 212

2.6. Mismatches and indels

General error rate	0.3%
Mismatches	462,709
Insertions	4,348
Mapped reads with at least one insertion	0.11%
Deletions	15,707
Mapped reads with at least one deletion	0.39%
Homopolymer indels	45.14%

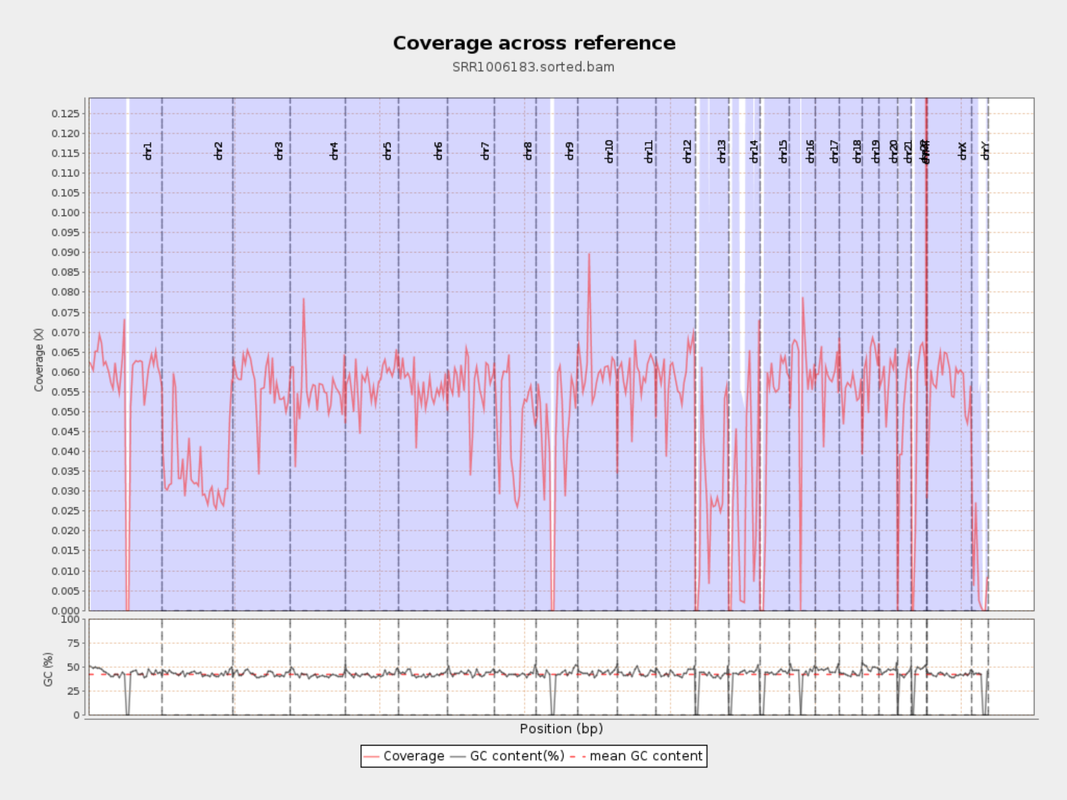
2.7. Chromosome stats

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

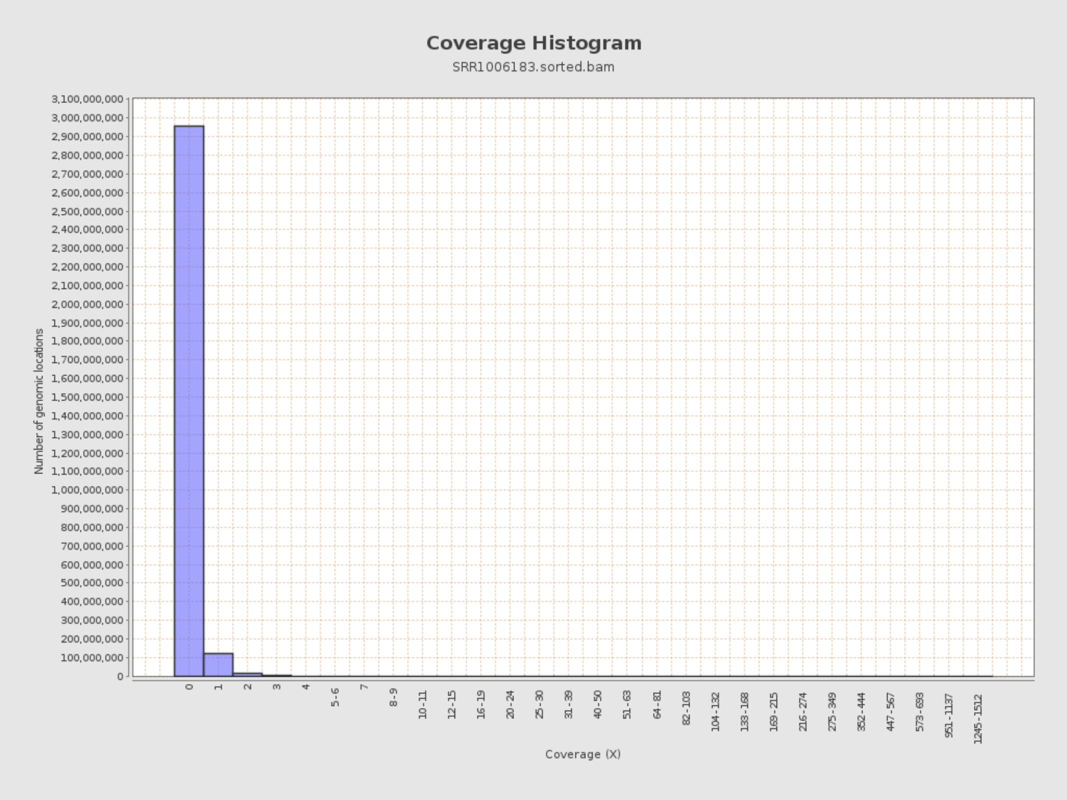
chr1	249250621	14356118	0.0576	0.5205
chr2	243199373	8374535	0.0344	0.2547
chr3	198022430	11250627	0.0568	0.2614
chr4	191154276	10559840	0.0552	0.2853
chr5	180915260	10427067	0.0576	0.2633
chr6	171115067	9574083	0.056	0.283
chr7	159138663	8997024	0.0565	0.3784
chr8	146364022	6877317	0.047	0.7726
chr9	141213431	6094063	0.0432	0.2556
chr10	135534747	8286618	0.0611	0.3943
chr11	135006516	7943487	0.0588	0.3013
chr12	133851895	7907960	0.0591	0.2675
chr13	115169878	3317659	0.0288	0.1873
chr14	107349540	2627507	0.0245	0.2399
chr15	102531392	4914197	0.0479	0.2405
chr16	90354753	5251818	0.0581	0.3395
chr17	81195210	4760060	0.0586	0.2761
chr18	78077248	4362675	0.0559	0.4162
chr19	59128983	3632932	0.0614	0.3904
chr20	63025520	3687308	0.0585	0.2744
chr21	48129895	2260812	0.047	0.2639
chr22	51304566	2257247	0.044	0.2361
chrMT	16571	20195	1.2187	1.3083
chrX	155270560	8718761	0.0562	0.2751

chrY	59373566	444814	0.0075	0.2272

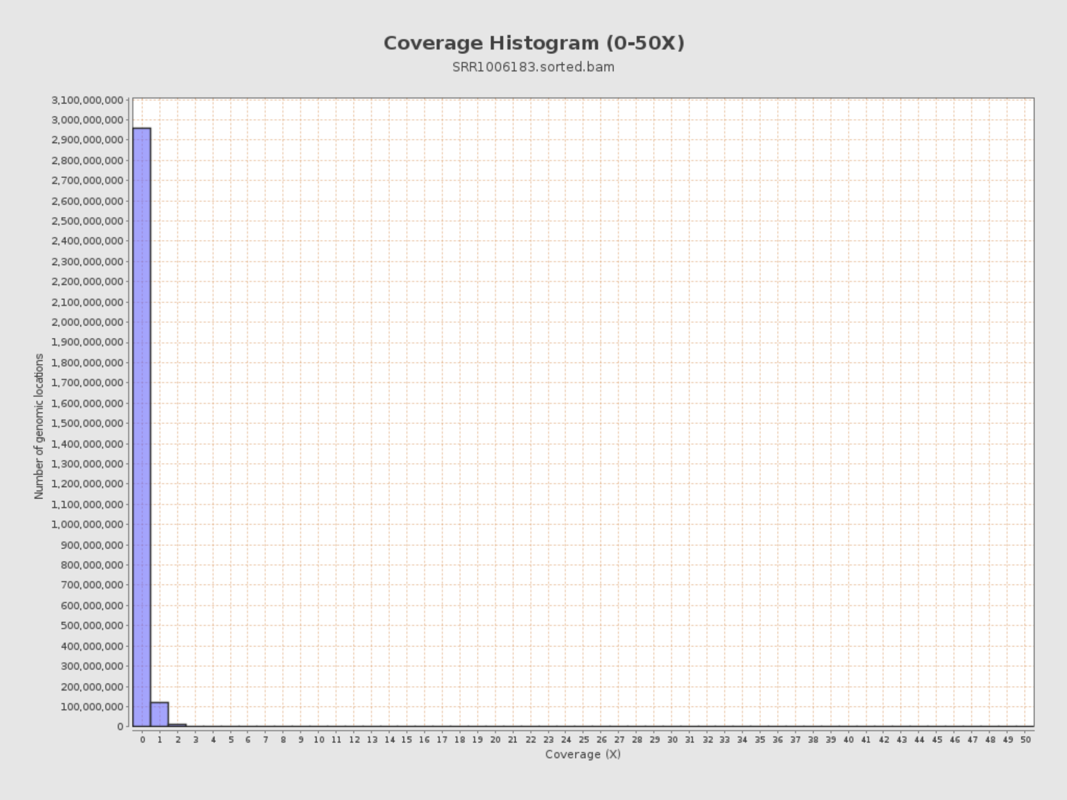
3. Results : Coverage across reference



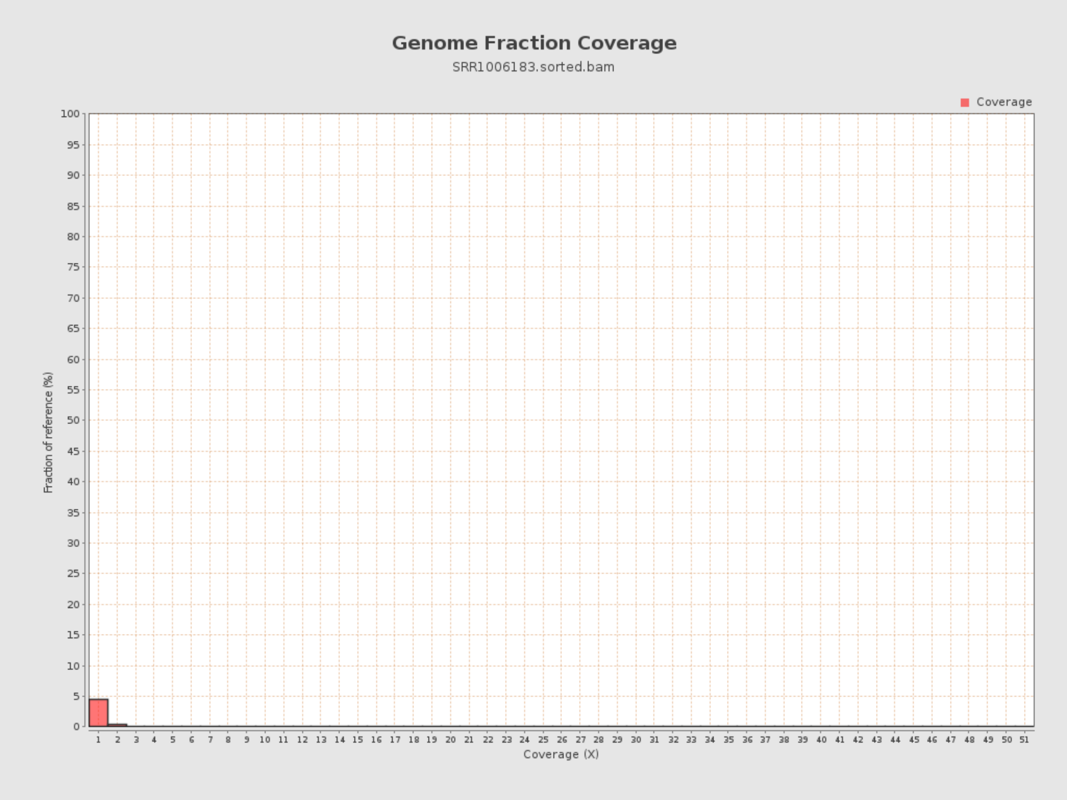
4. Results : Coverage Histogram



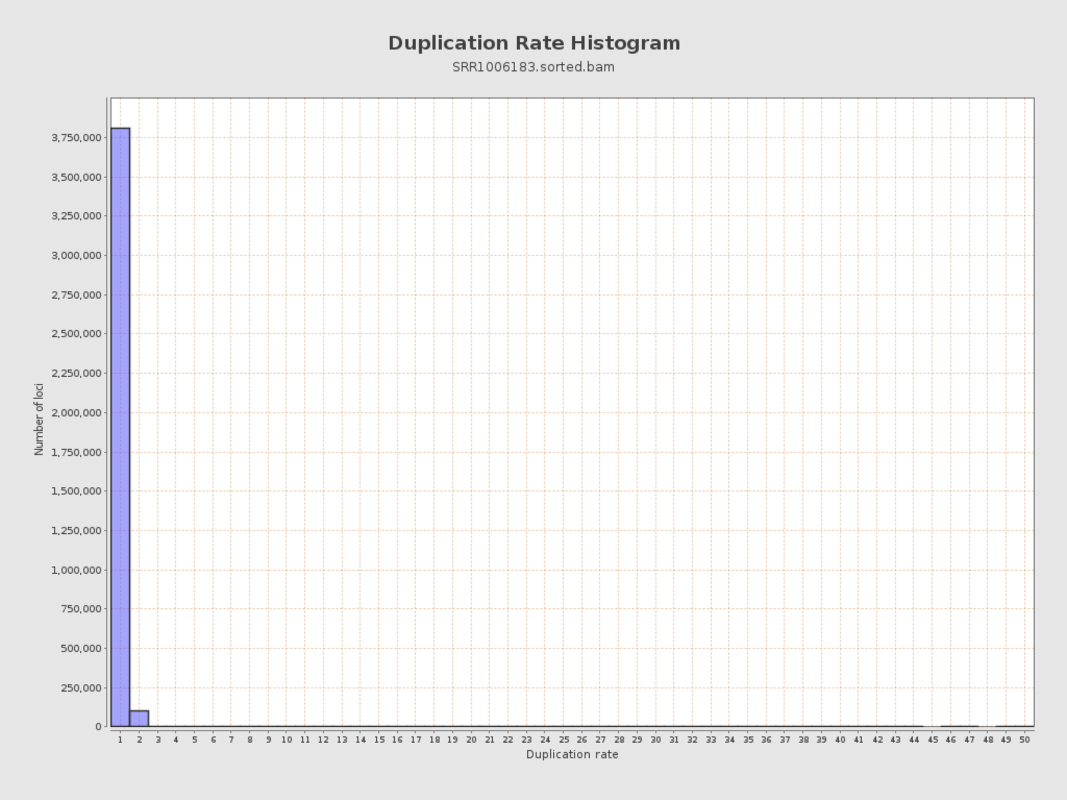
5. Results : Coverage Histogram (0-50X)



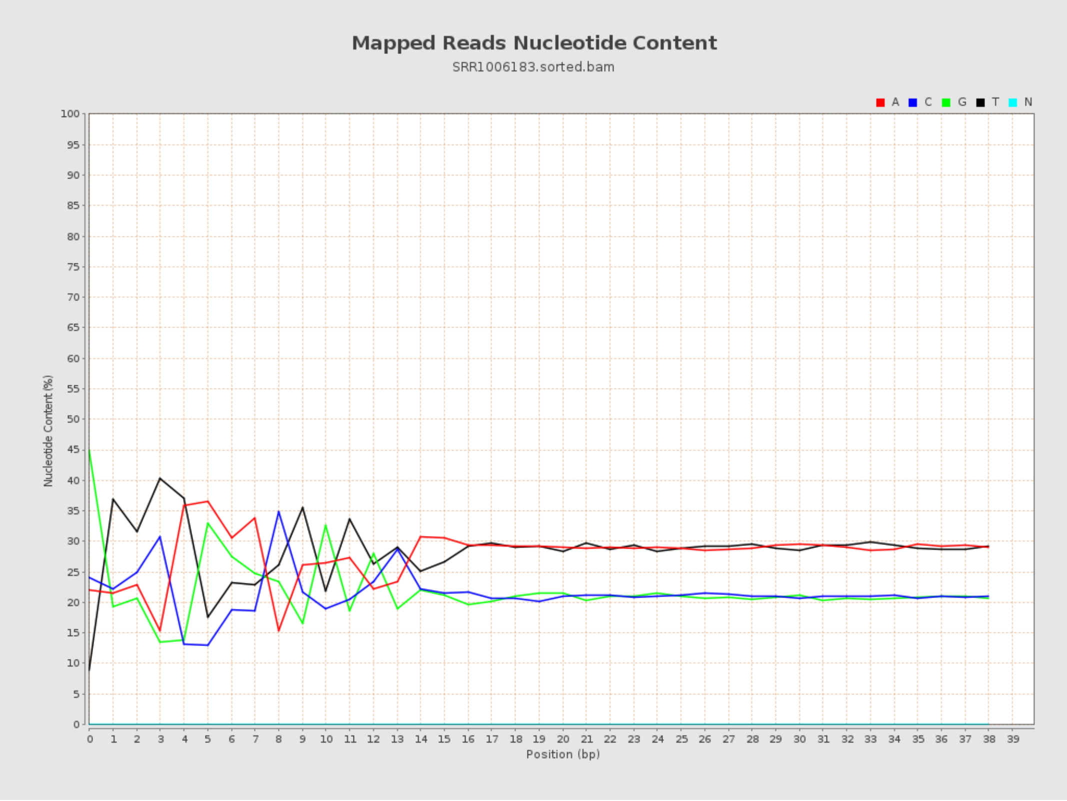
6. Results : Genome Fraction Coverage



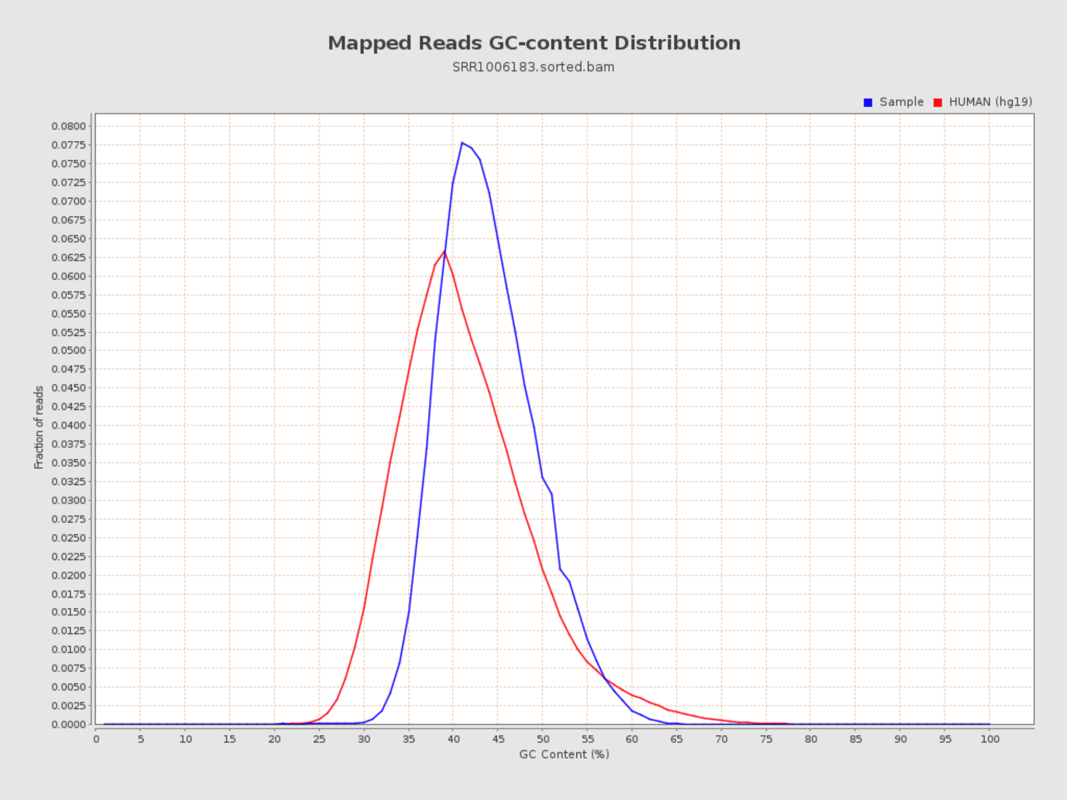
7. Results : Duplication Rate Histogram



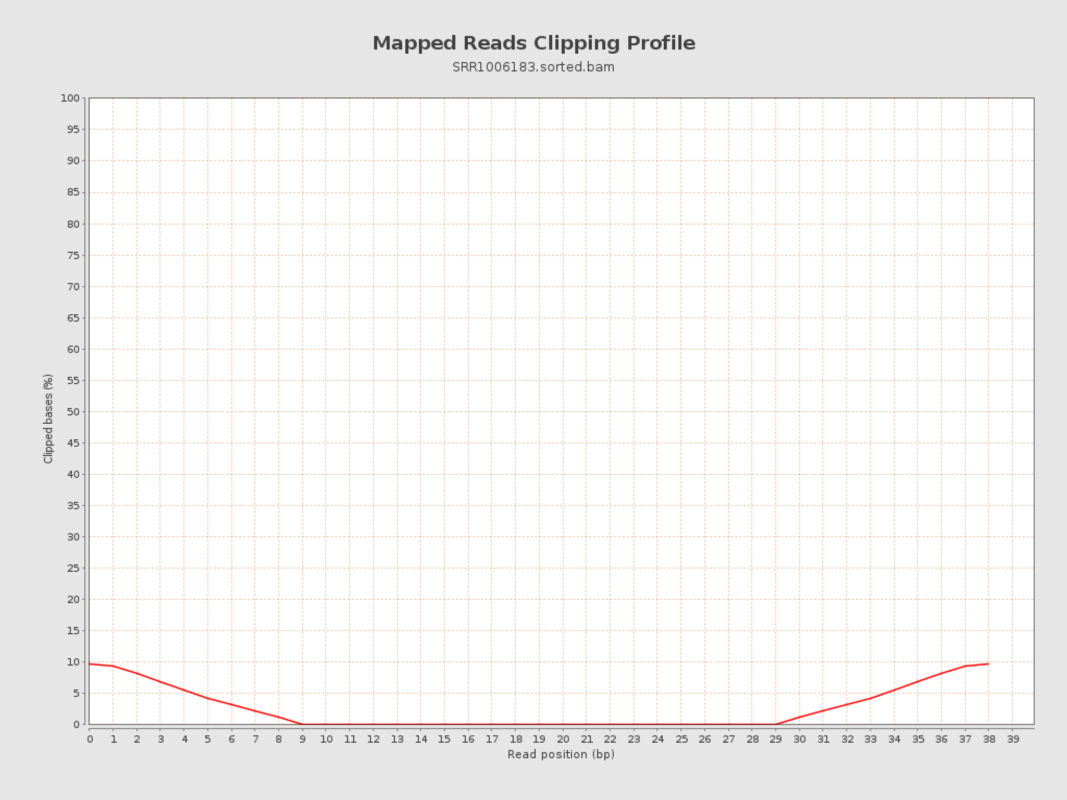
8. Results : Mapped Reads Nucleotide Content



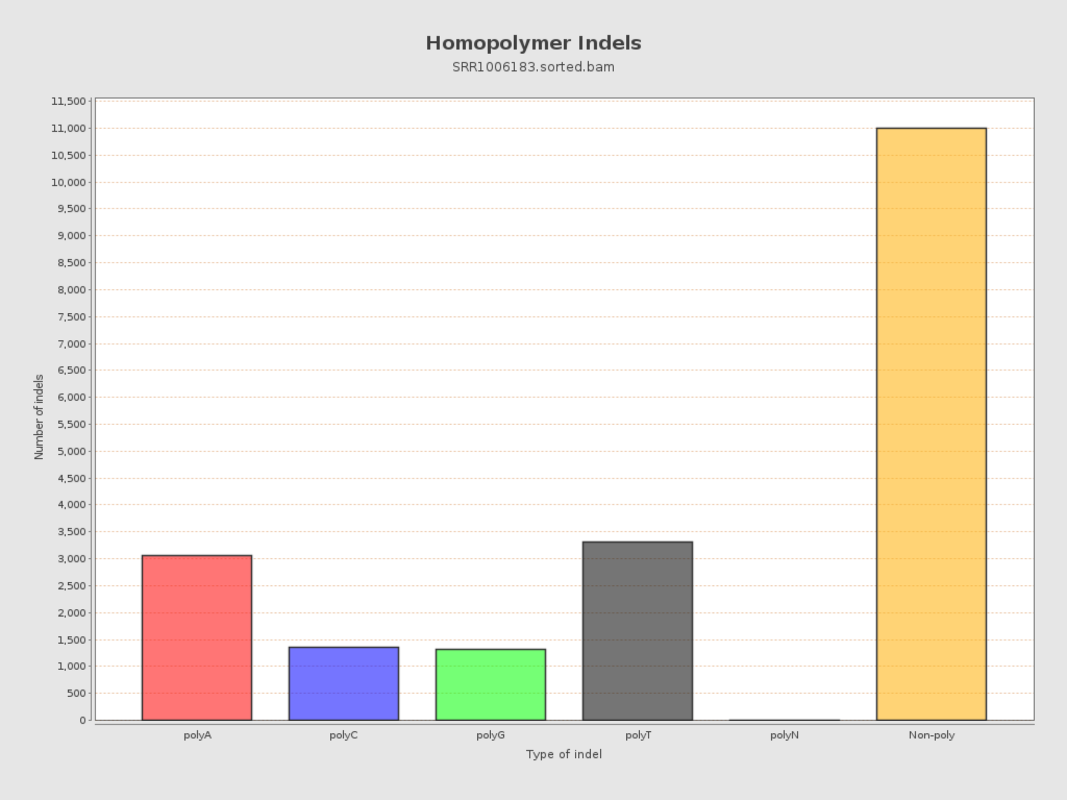
9. Results : Mapped Reads GC-content Distribution



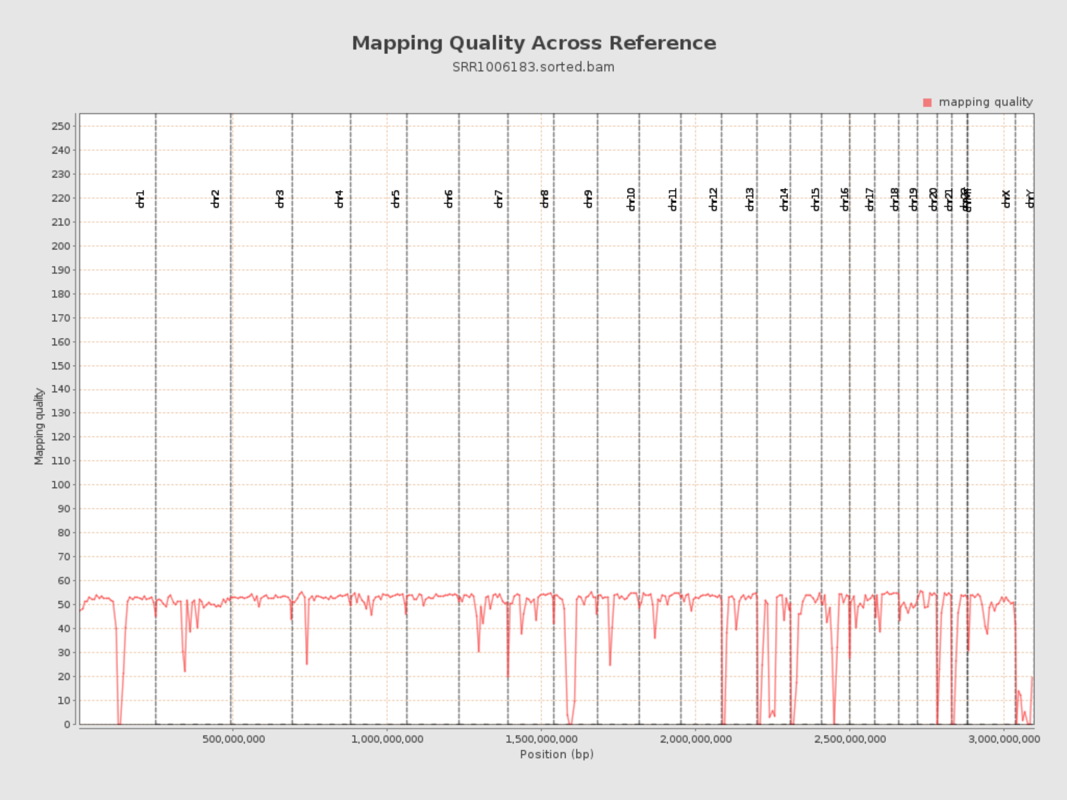
10. Results : Mapped Reads Clipping Profile



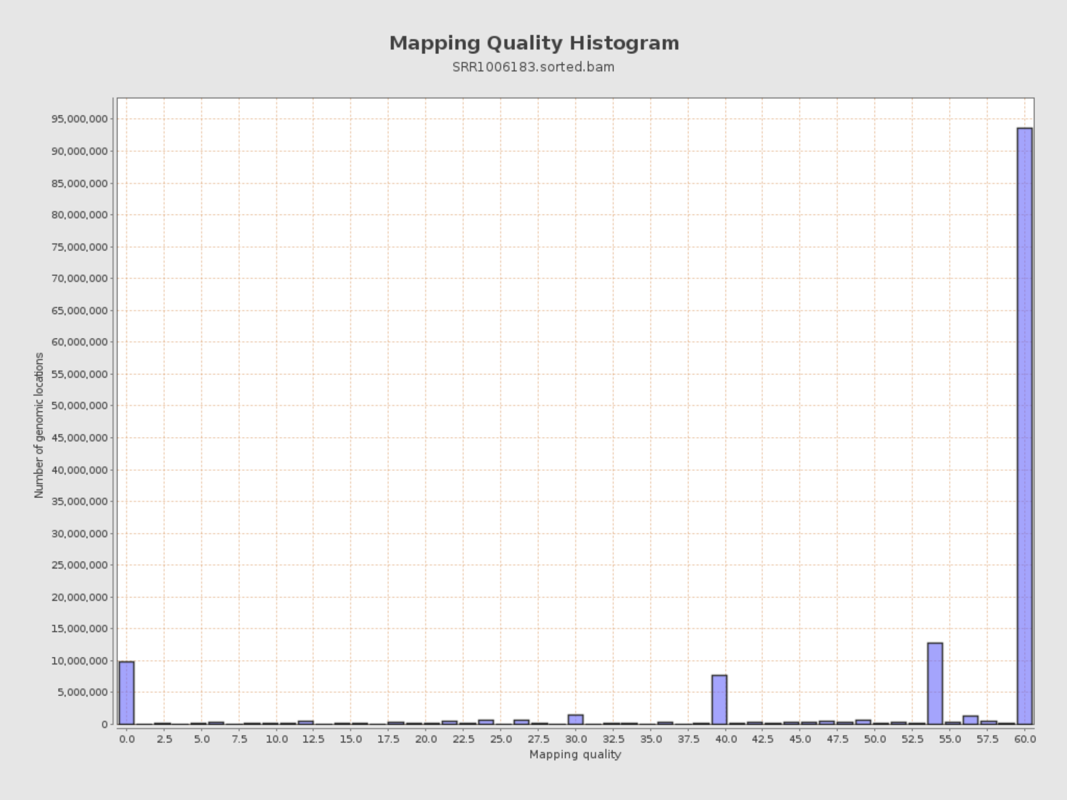
11. Results : Homopolymer Indels



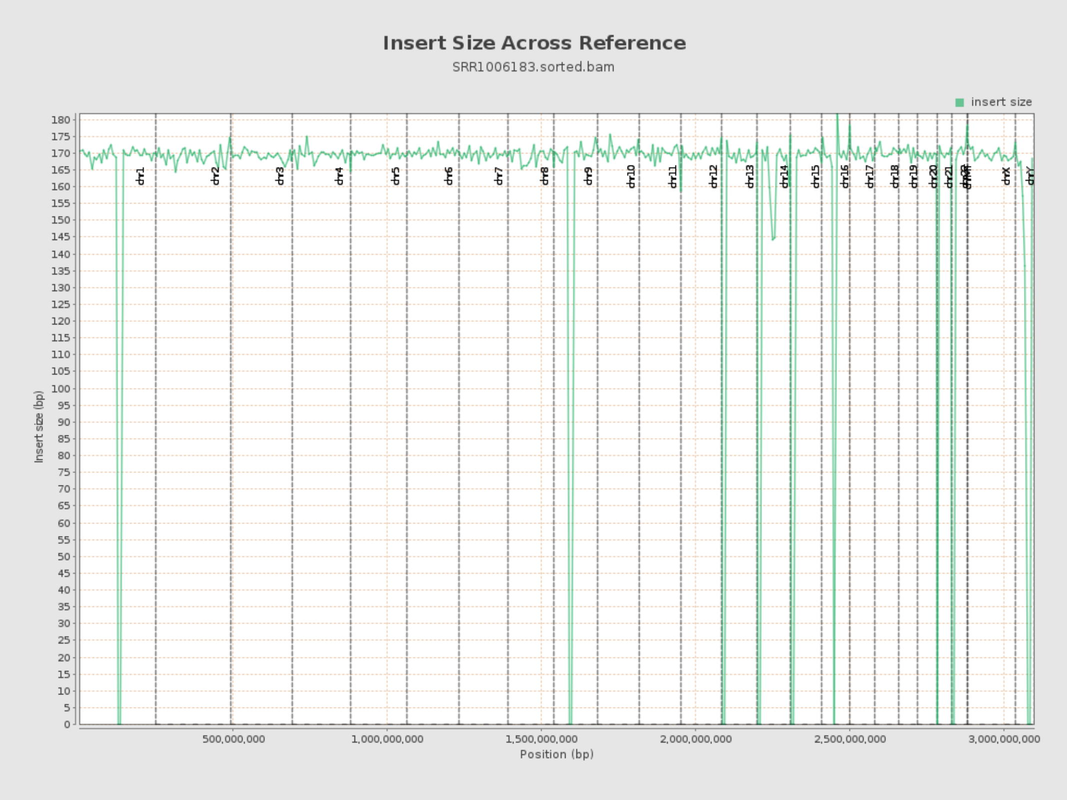
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram