Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 18:44:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006090.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_SRR1006090 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006090_1.fastq.gz SRR1006090_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 18:44:57 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006090.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,671,204
Mapped reads	9,287,839 / 87.04%
Unmapped reads	1,383,365 / 12.96%
Mapped paired reads	9,287,839 / 87.04%
Mapped reads, first in pair	4,702,040 / 44.06%
Mapped reads, second in pair	4,585,799 / 42.97%
Mapped reads, both in pair	8,481,022 / 79.48%
Mapped reads, singletons	806,817 / 7.56%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	1,157,459 / 10.85%
Duplication rate	11.26%
Clipped reads	881,022 / 8.26%

2.2. ACGT Content

Number/percentage of A's	92,900,626 / 25.96%
Number/percentage of C's	81,353,764 / 22.73%
Number/percentage of T's	96,526,795 / 26.97%
Number/percentage of G's	87,058,302 / 24.33%
Number/percentage of N's	14,427 / 0%
GC Percentage	47.06%

2.3. Coverage

Mean	0.1156
Standard Deviation	0.7547

2.4. Mapping Quality

Mean Mapping Quality	46.1

2.5. Insert size

Mean	73,748.44
Standard Deviation	2,680,864.75
P25/Median/P75	64 / 91 / 124

2.6. Mismatches and indels

General error rate	0.5%
Mismatches	1,789,582
Insertions	12,474
Mapped reads with at least one insertion	0.13%
Deletions	29,539
Mapped reads with at least one deletion	0.32%
Homopolymer indels	43.56%

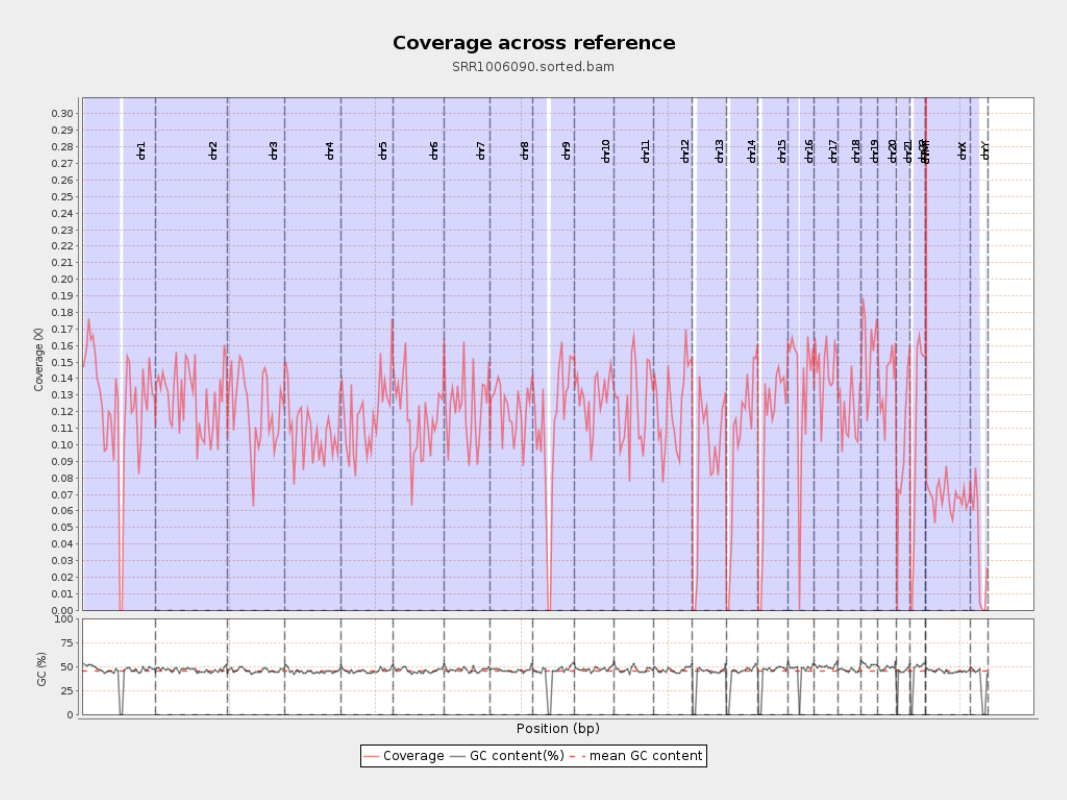
2.7. Chromosome stats

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

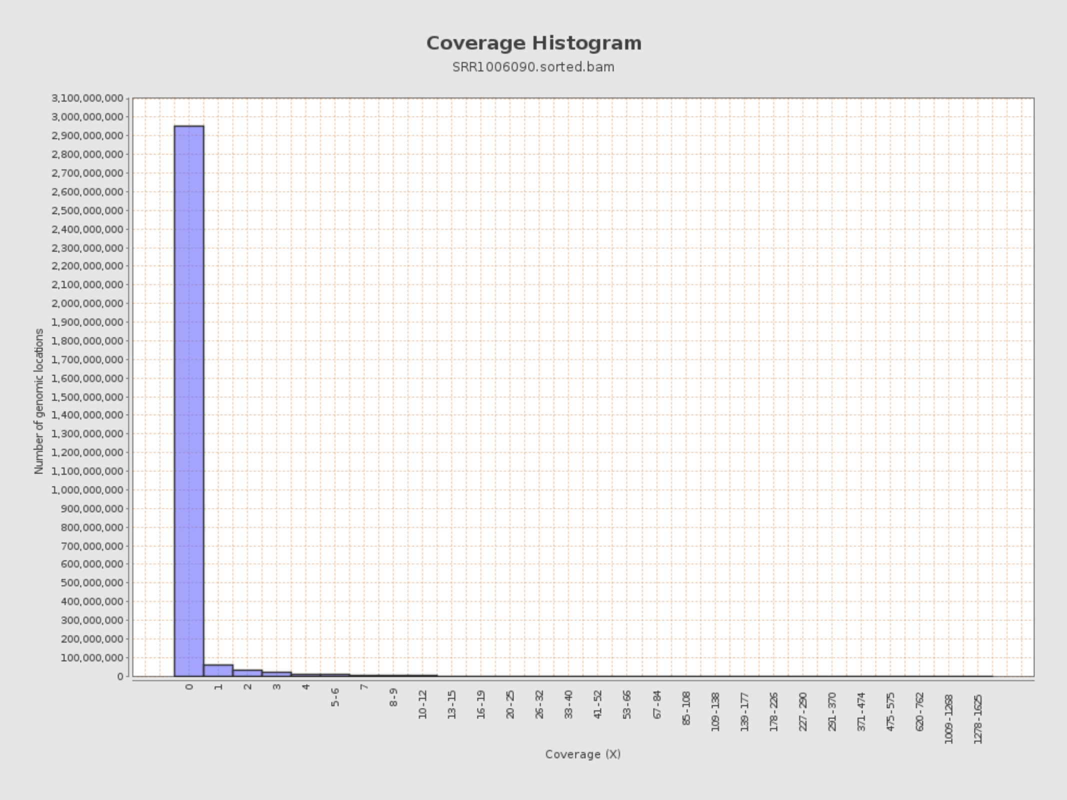
chr1	249250621	30595843	0.1228	0.8316
chr2	243199373	31143744	0.1281	0.7761
chr3	198022430	23917832	0.1208	0.7022
chr4	191154276	20623992	0.1079	0.6912
chr5	180915260	21492532	0.1188	0.6975
chr6	171115067	19858430	0.1161	0.7408
chr7	159138663	19634791	0.1234	0.8388
chr8	146364022	17760748	0.1213	0.8189
chr9	141213431	15425393	0.1092	0.6926
chr10	135534747	17423244	0.1286	0.7472
chr11	135006516	16612284	0.123	1.1013
chr12	133851895	16546517	0.1236	0.717
chr13	115169878	10529069	0.0914	0.618
chr14	107349540	11005363	0.1025	0.6624
chr15	102531392	10918491	0.1065	0.6692
chr16	90354753	12089508	0.1338	0.7785
chr17	81195210	11885246	0.1464	0.8426
chr18	78077248	9205821	0.1179	0.7612
chr19	59128983	9369779	0.1585	0.9468
chr20	63025520	8687374	0.1378	0.7755
chr21	48129895	4667967	0.097	0.681
chr22	51304566	5531547	0.1078	0.7175
chrMT	16571	24177	1.459	2.4801
chrX	155270560	10708521	0.069	0.5261

chrY	59373566	2232978	0.0376	0.3802

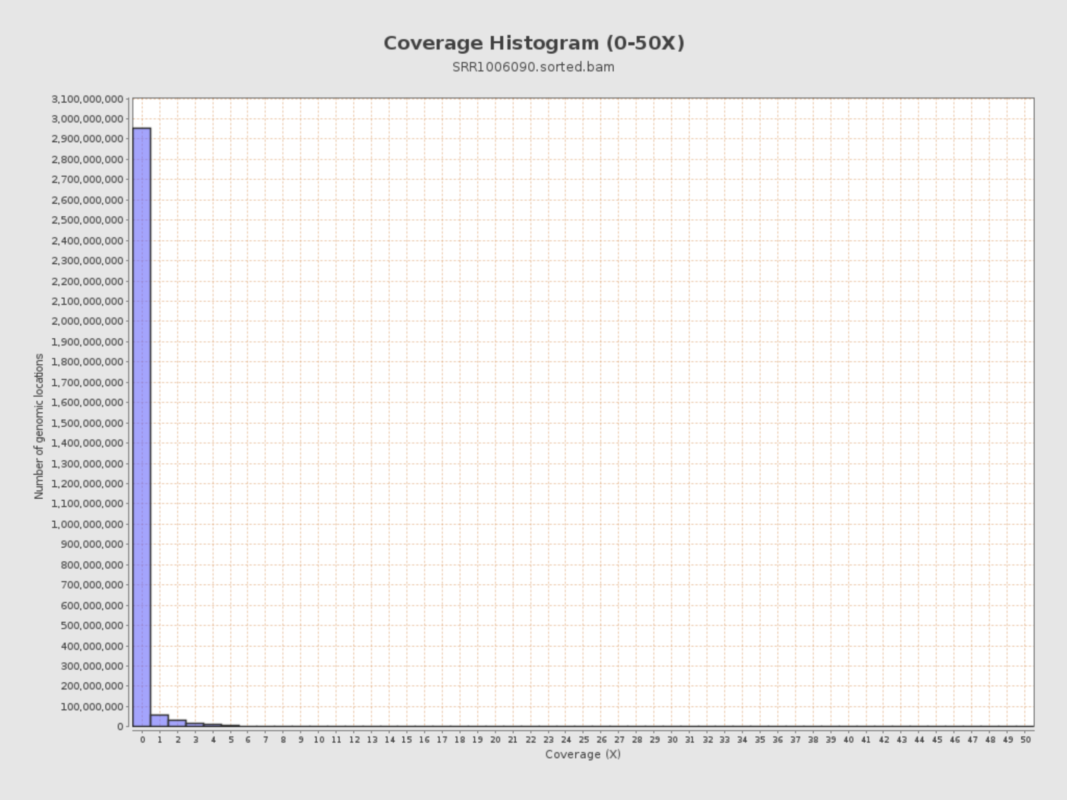
3. Results : Coverage across reference



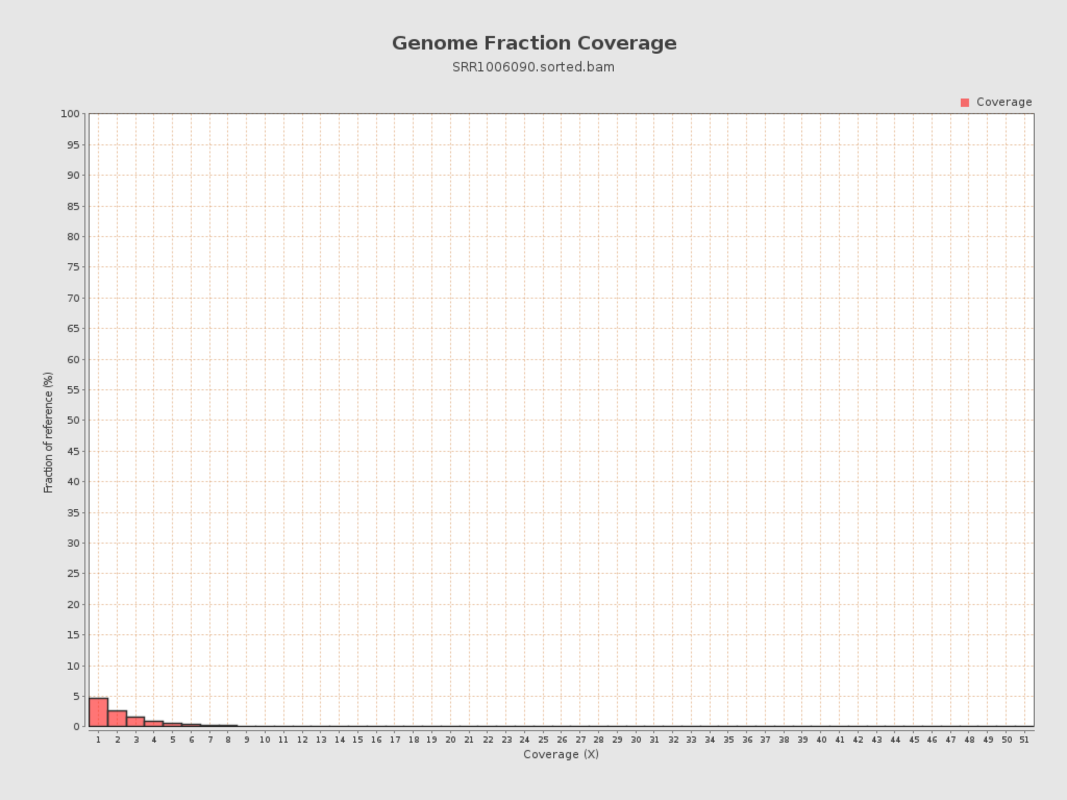
4. Results : Coverage Histogram



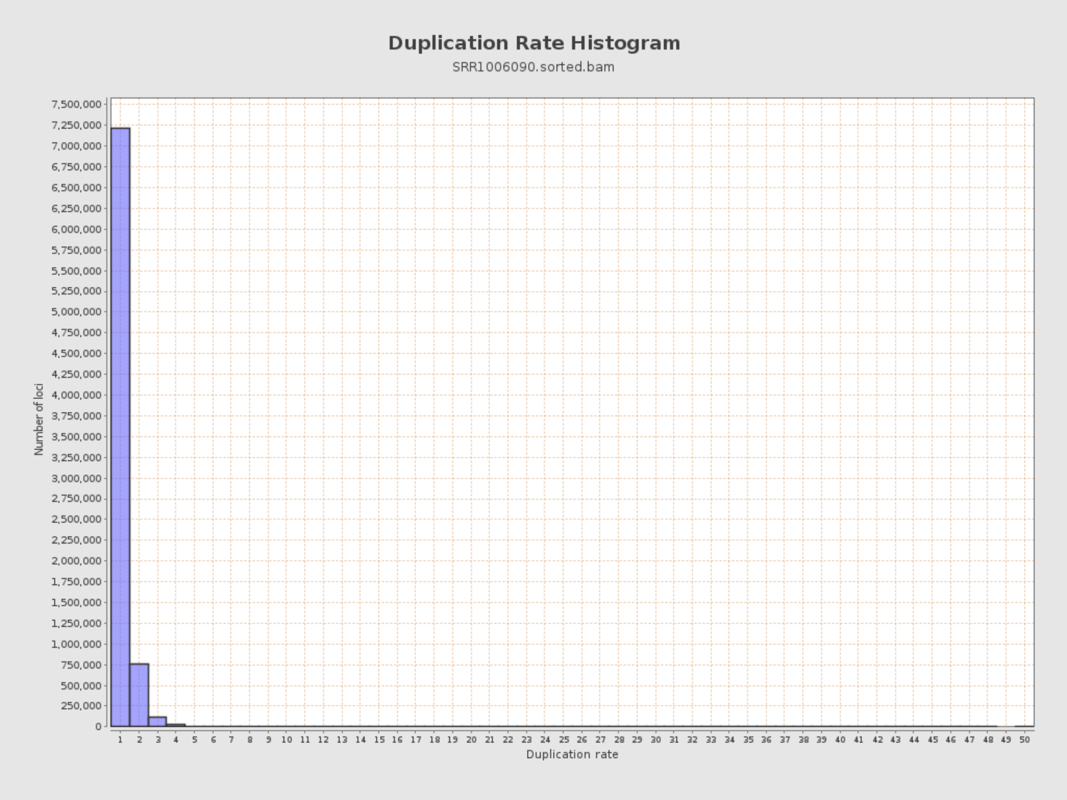
5. Results : Coverage Histogram (0-50X)



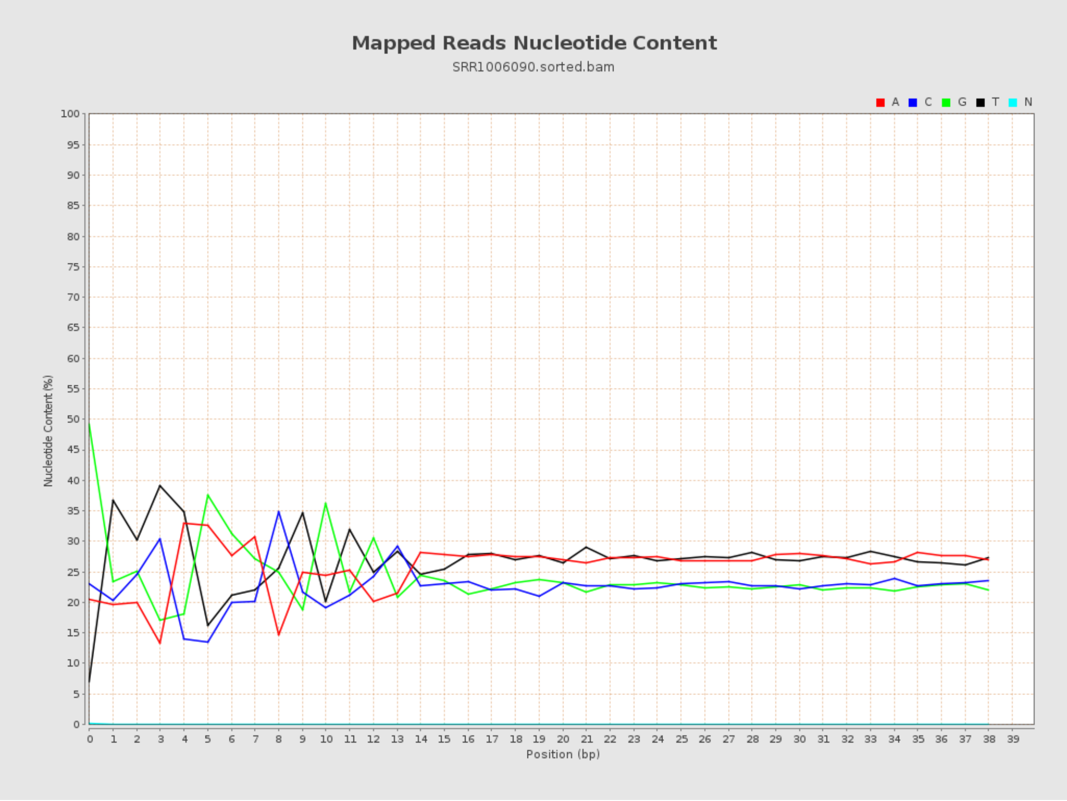
6. Results : Genome Fraction Coverage



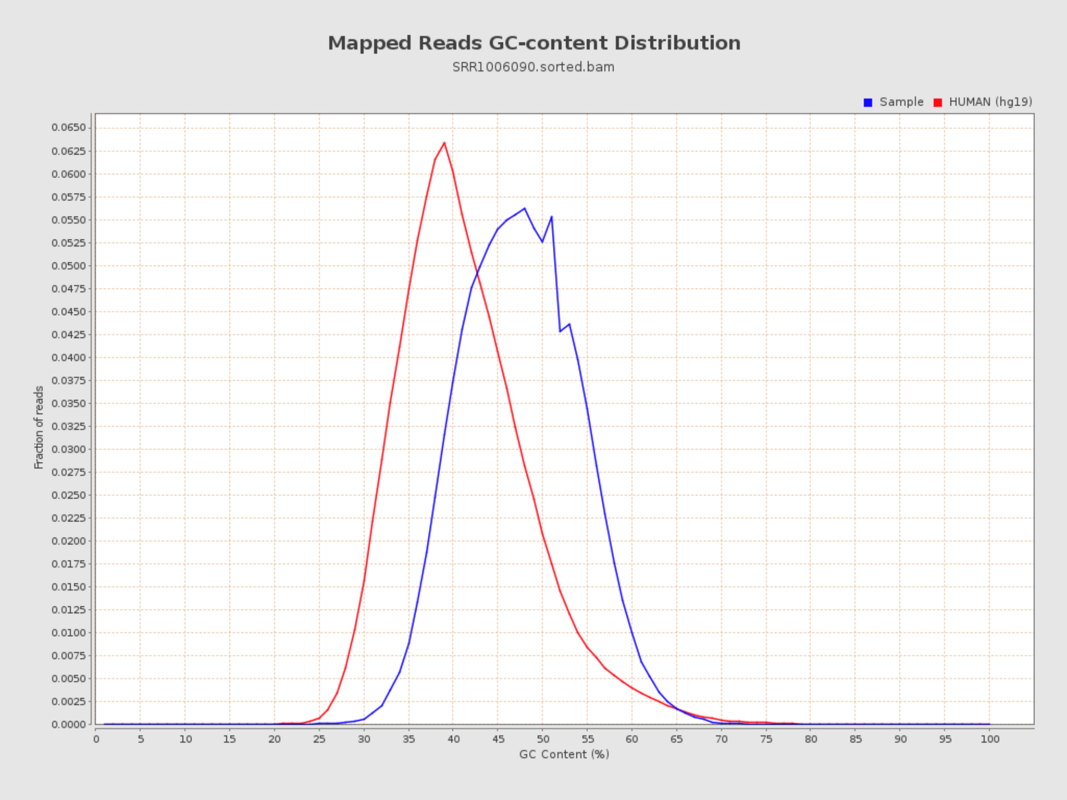
7. Results : Duplication Rate Histogram



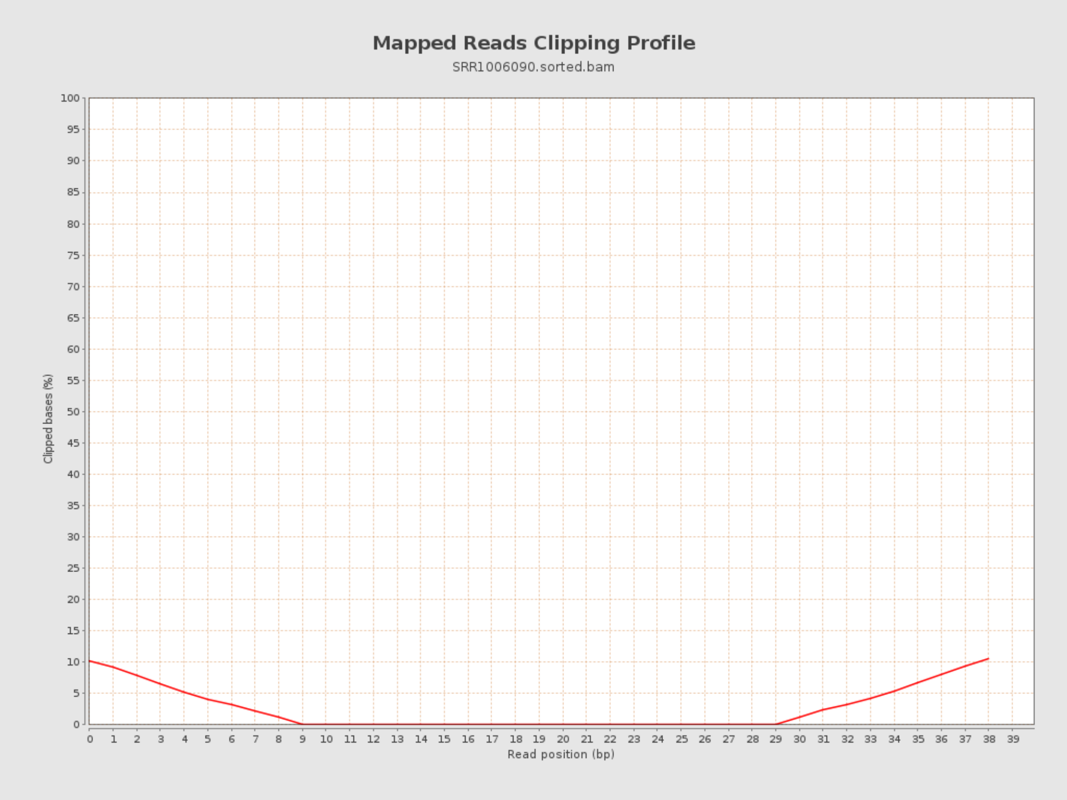
8. Results : Mapped Reads Nucleotide Content



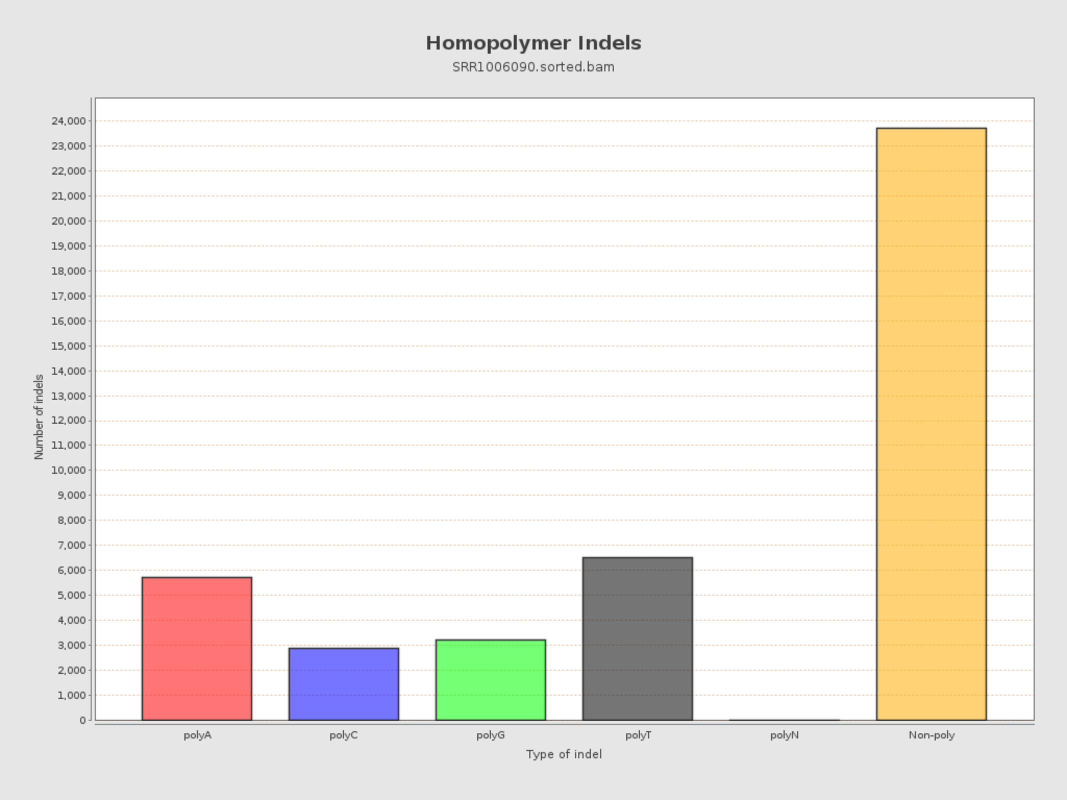
9. Results : Mapped Reads GC-content Distribution



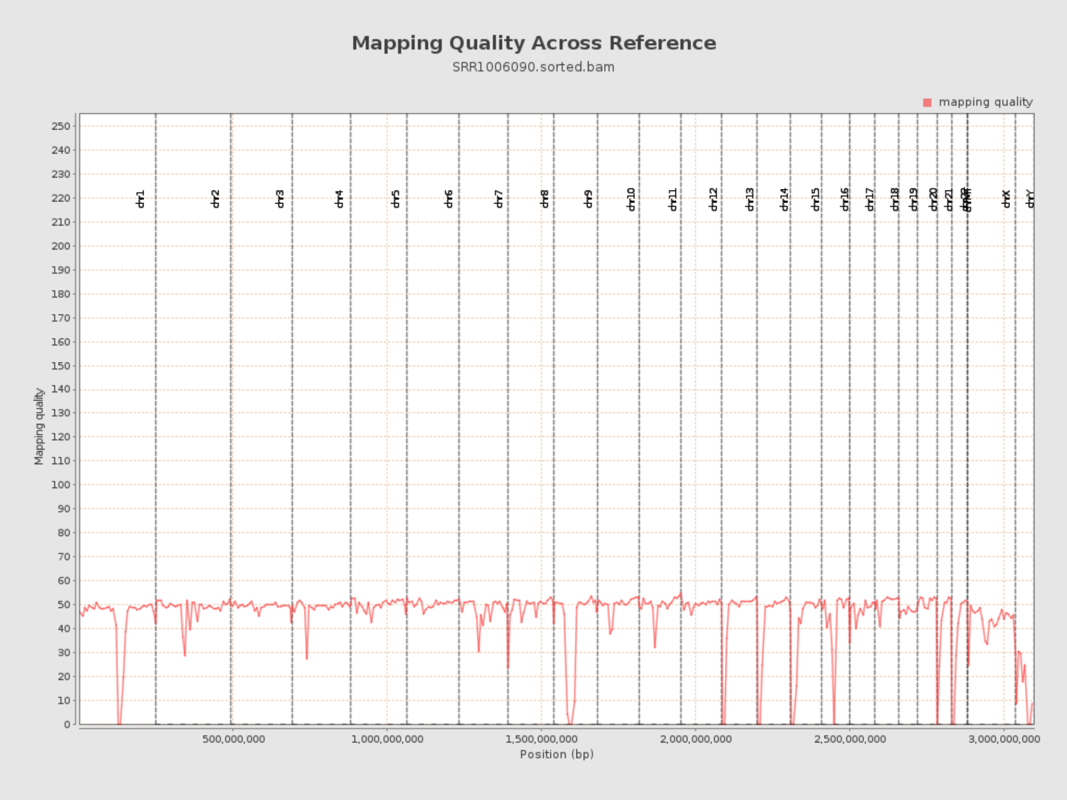
10. Results : Mapped Reads Clipping Profile



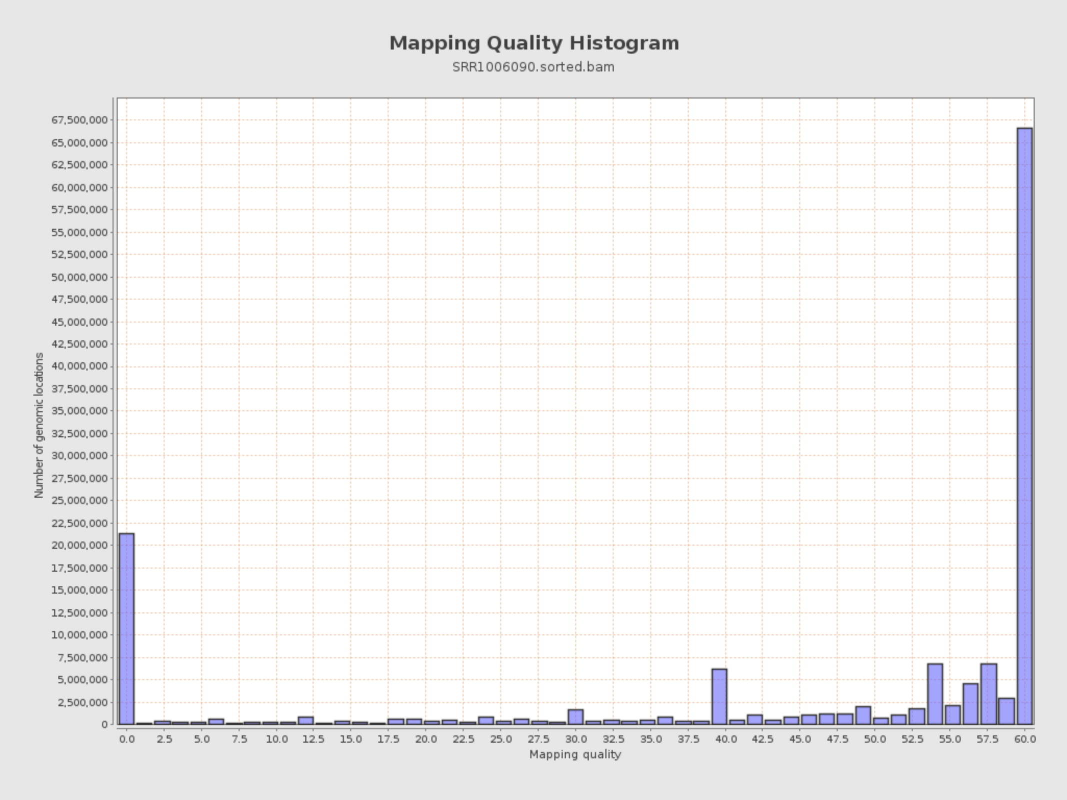
11. Results : Homopolymer Indels



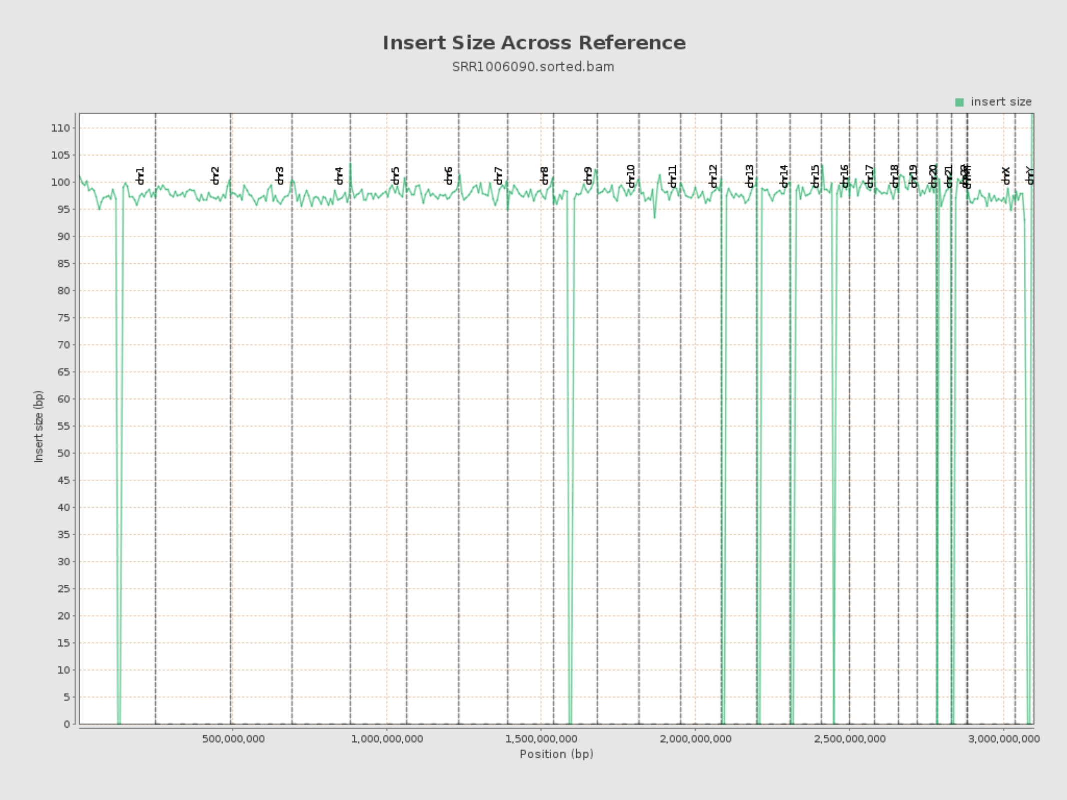
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram