Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/22 13:33:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926911.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_SRR926911 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926911_1.fastq.gz SRR926911_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 22 13:33:38 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926911.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	24,944,740
Mapped reads	23,137,674 / 92.76%
Unmapped reads	1,807,066 / 7.24%
Mapped paired reads	23,137,674 / 92.76%
Mapped reads, first in pair	11,638,272 / 46.66%
Mapped reads, second in pair	11,499,402 / 46.1%
Mapped reads, both in pair	22,862,718 / 91.65%
Mapped reads, singletons	274,956 / 1.1%
Secondary alignments	0
Supplementary alignments	182,210 / 0.73%
Read min/max/mean length	30 / 101 / 101.3
Duplicated reads (estimated)	1,306,508 / 5.24%
Duplication rate	4.68%
Clipped reads	5,186,373 / 20.79%

2.2. ACGT Content

Number/percentage of A's	629,189,571 / 28.57%
Number/percentage of C's	446,796,448 / 20.29%
Number/percentage of T's	632,985,753 / 28.74%
Number/percentage of G's	493,335,280 / 22.4%
Number/percentage of N's	218,925 / 0.01%

GC Percentage	42.68%

2.3. Coverage

Mean	0.712
Standard Deviation	2.3743

2.4. Mapping Quality

Mean Mapping Quality	53.49

2.5. Insert size

Mean	86,391.26
Standard Deviation	2,900,753.35
P25/Median/P75	153 / 194 / 258

2.6. Mismatches and indels

General error rate	1.05%
Mismatches	22,471,588
Insertions	346,271
Mapped reads with at least one insertion	1.48%
Deletions	1,215,525
Mapped reads with at least one deletion	5.11%
Homopolymer indels	53.29%

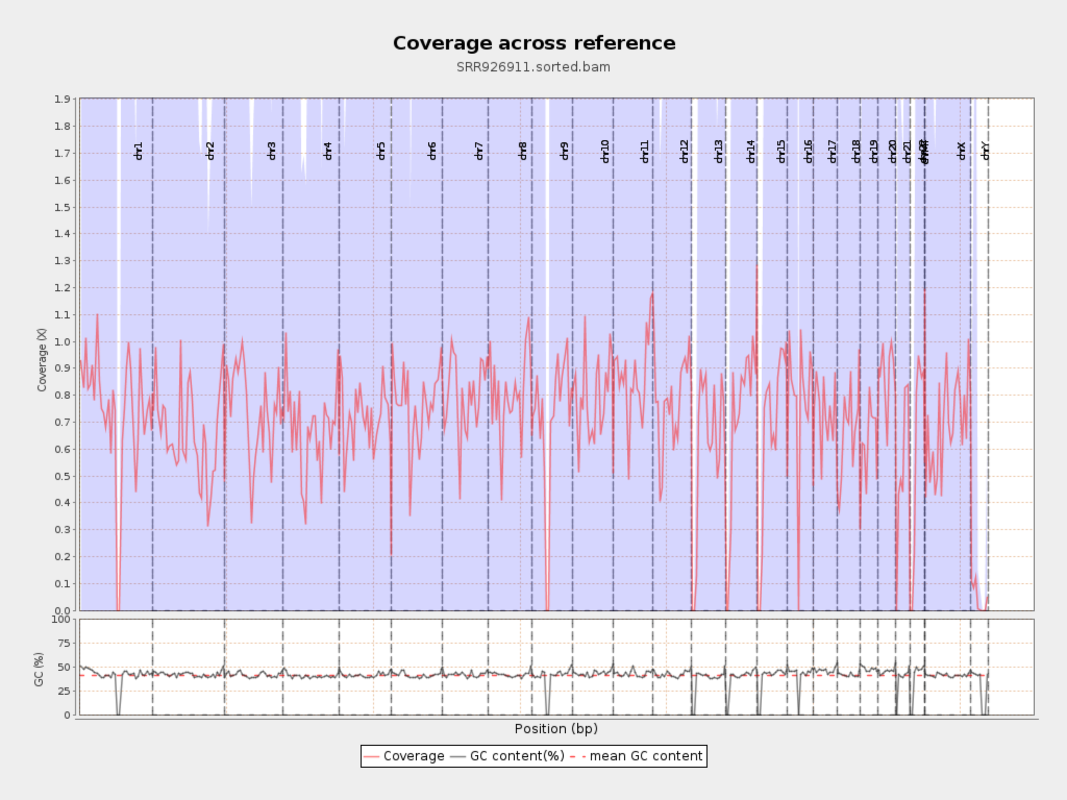
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

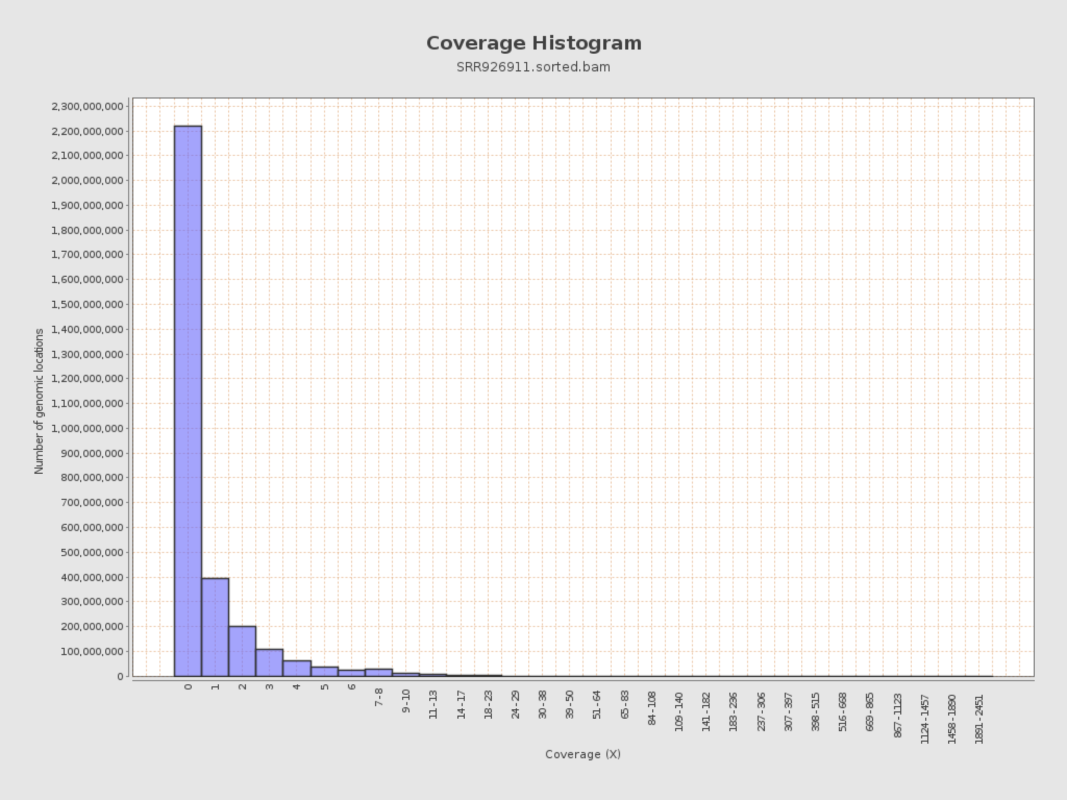
		bases	coverage	deviation
chr1	249250621	184817382	0.7415	2.5176
chr2	243199373	161369682	0.6635	3.2724
chr3	198022430	146982911	0.7423	1.6723
chr4	191154276	128020116	0.6697	1.647
chr5	180915260	128564797	0.7106	1.6139
chr6	171115067	131095215	0.7661	2.1644
chr7	159138663	127103960	0.7987	1.8606
chr8	146364022	117458625	0.8025	1.9537
chr9	141213431	99436693	0.7042	2.7798
chr10	135534747	108125709	0.7978	5.1689
chr11	135006516	116383102	0.8621	2.1873
chr12	133851895	103837514	0.7758	1.7688
chr13	115169878	69734896	0.6055	1.498
chr14	107349540	75396507	0.7023	1.6826
chr15	102531392	66516524	0.6487	1.6513
chr16	90354753	70133086	0.7762	3.4035
chr17	81195210	58872787	0.7251	1.8847
chr18	78077248	51888179	0.6646	2.5424
chr19	59128983	37920368	0.6413	1.9103
chr20	63025520	55236447	0.8764	1.9839
chr21	48129895	26017791	0.5406	1.9314
chr22	51304566	29955840	0.5839	1.6489
chrMT	16571	19842	1.1974	1.4275
chrX	155270560	106706605	0.6872	1.7075

chrY	59373566	2634646	0.0444	1.1365

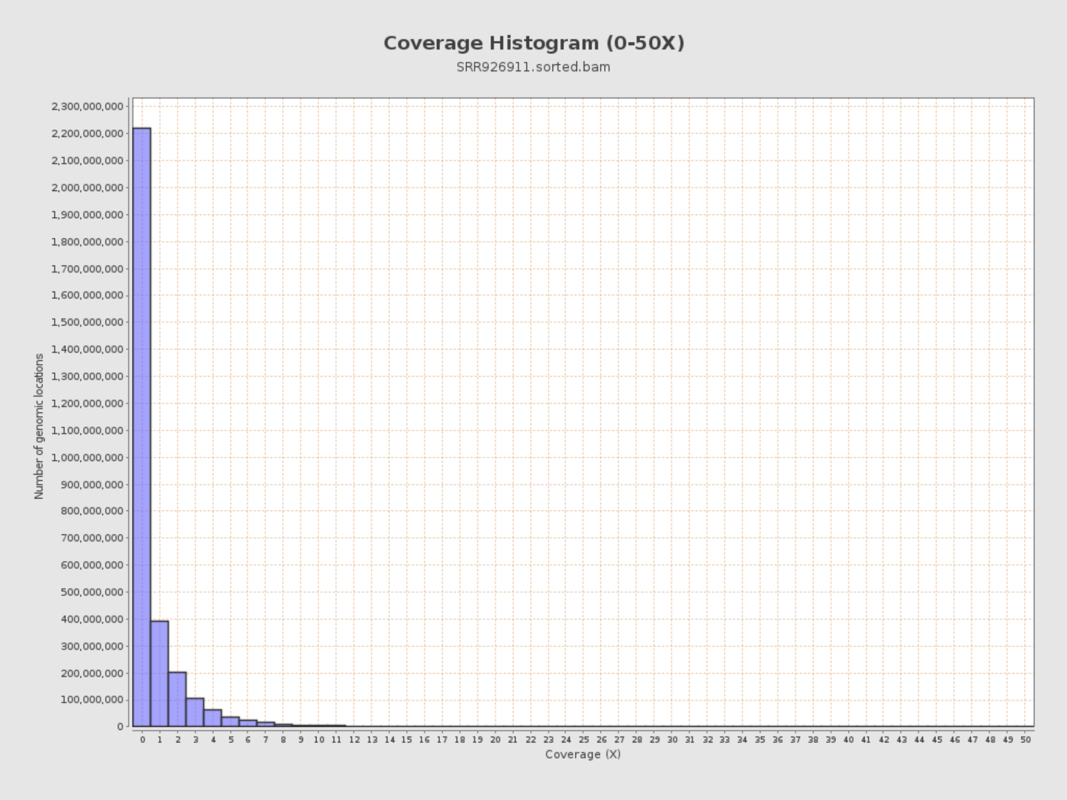
3. Results : Coverage across reference



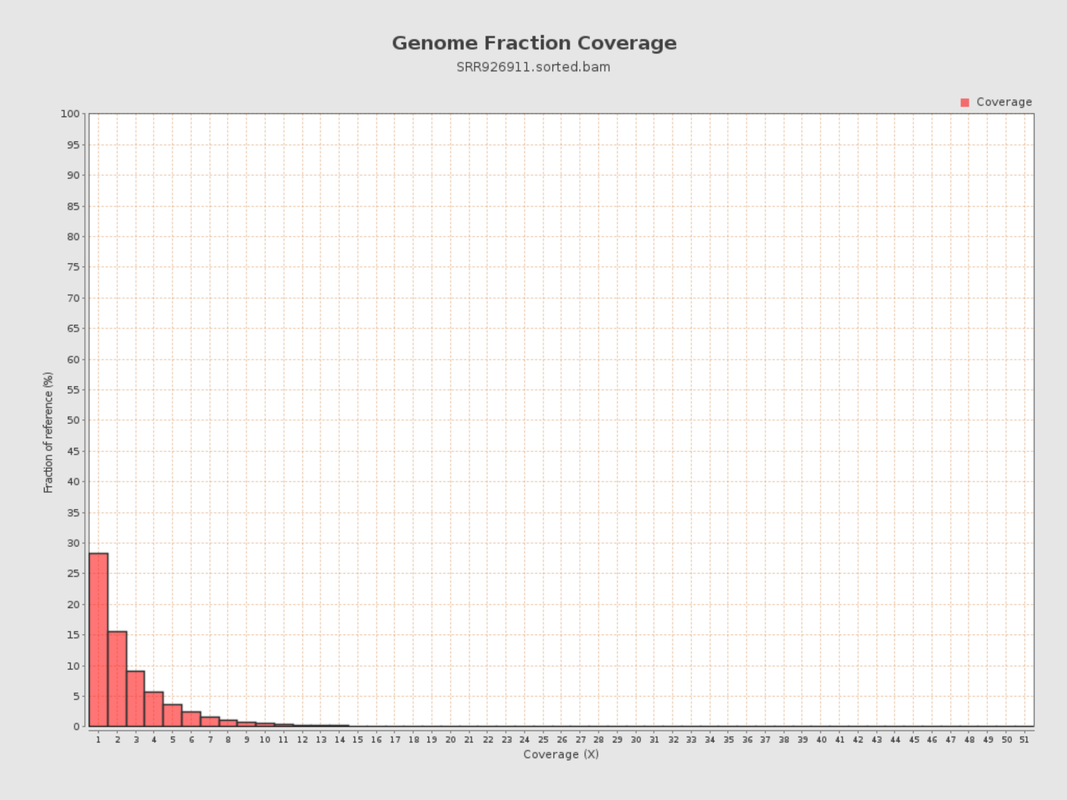
4. Results : Coverage Histogram



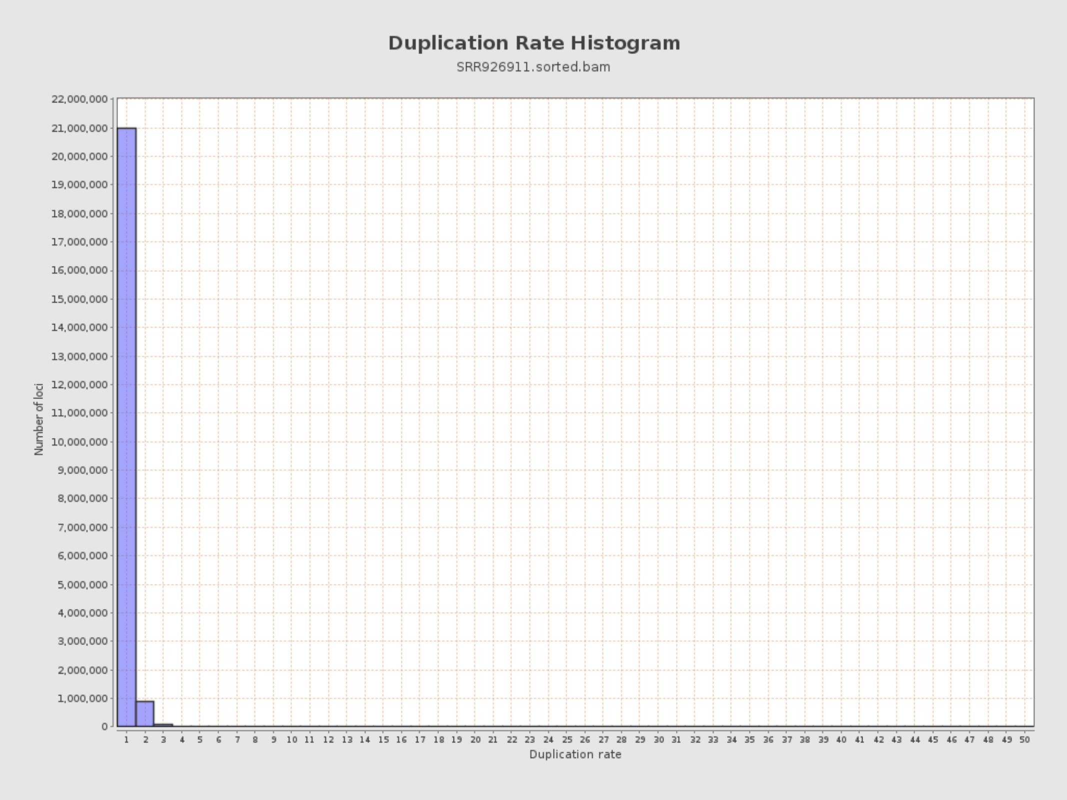
5. Results : Coverage Histogram (0-50X)



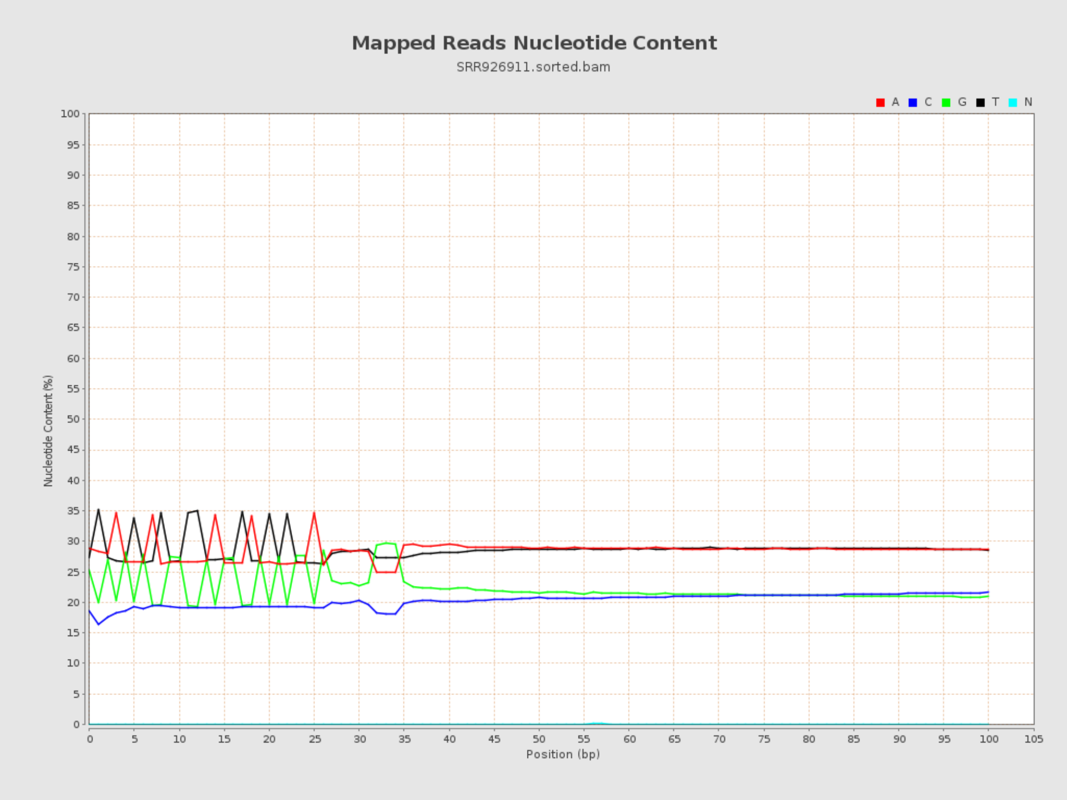
6. Results : Genome Fraction Coverage



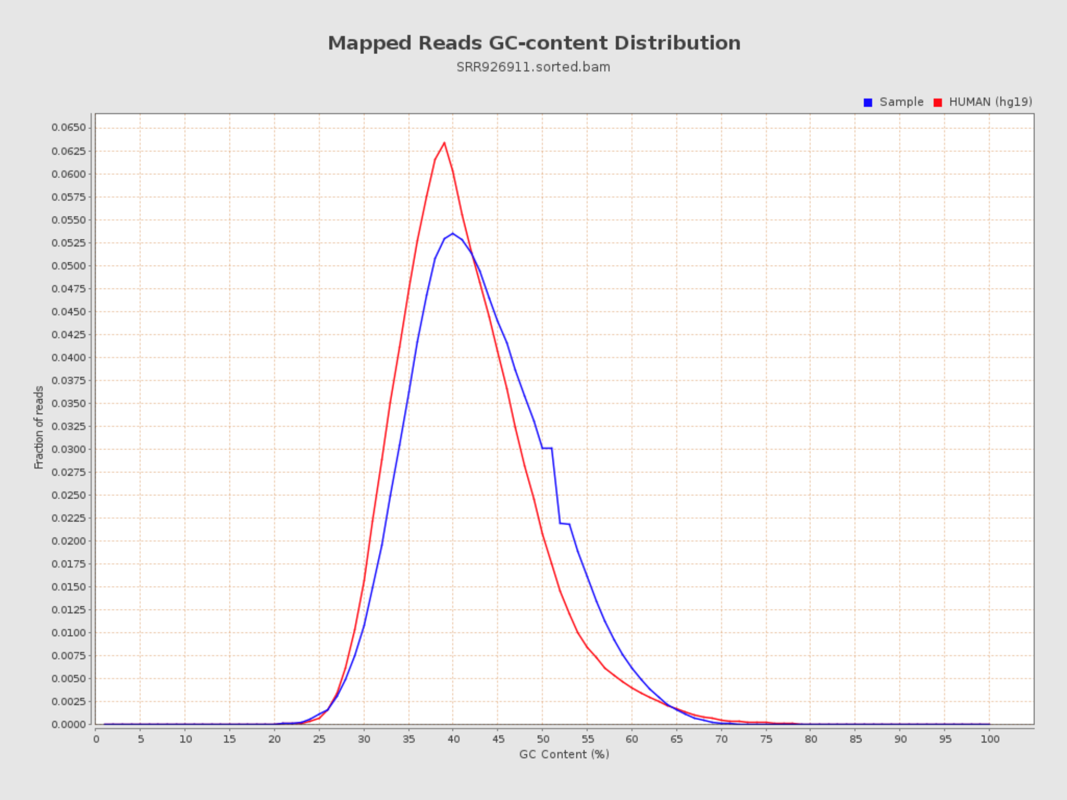
7. Results : Duplication Rate Histogram



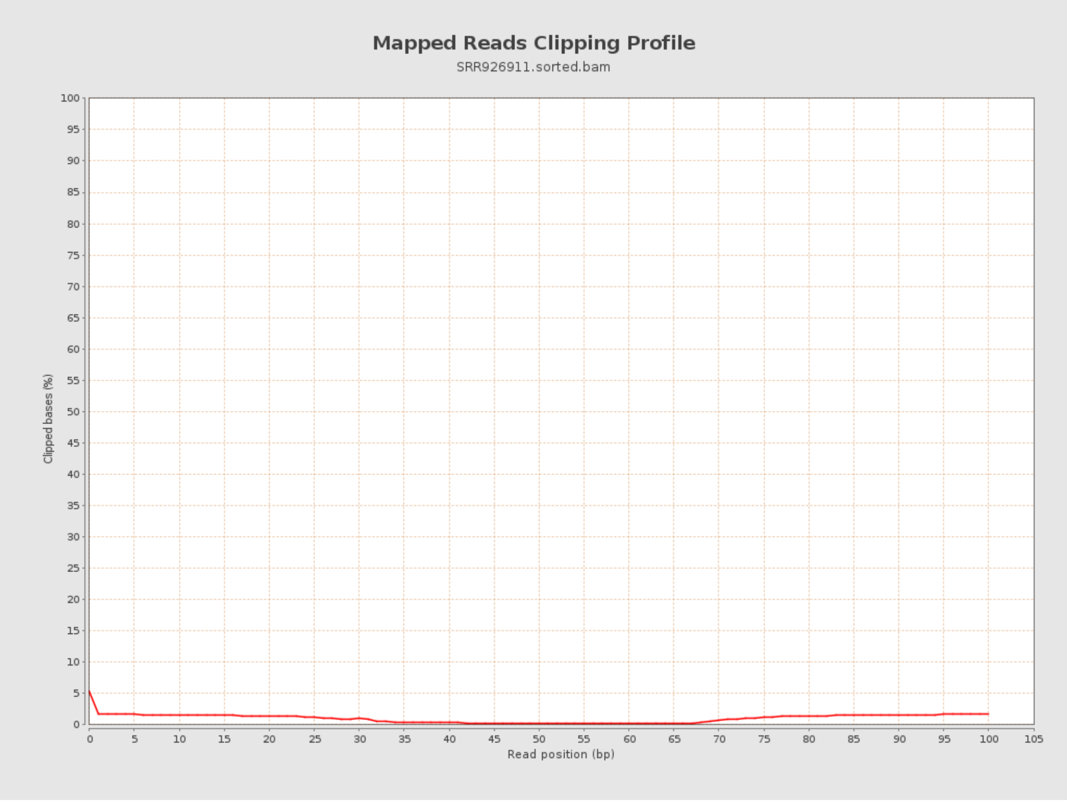
8. Results : Mapped Reads Nucleotide Content



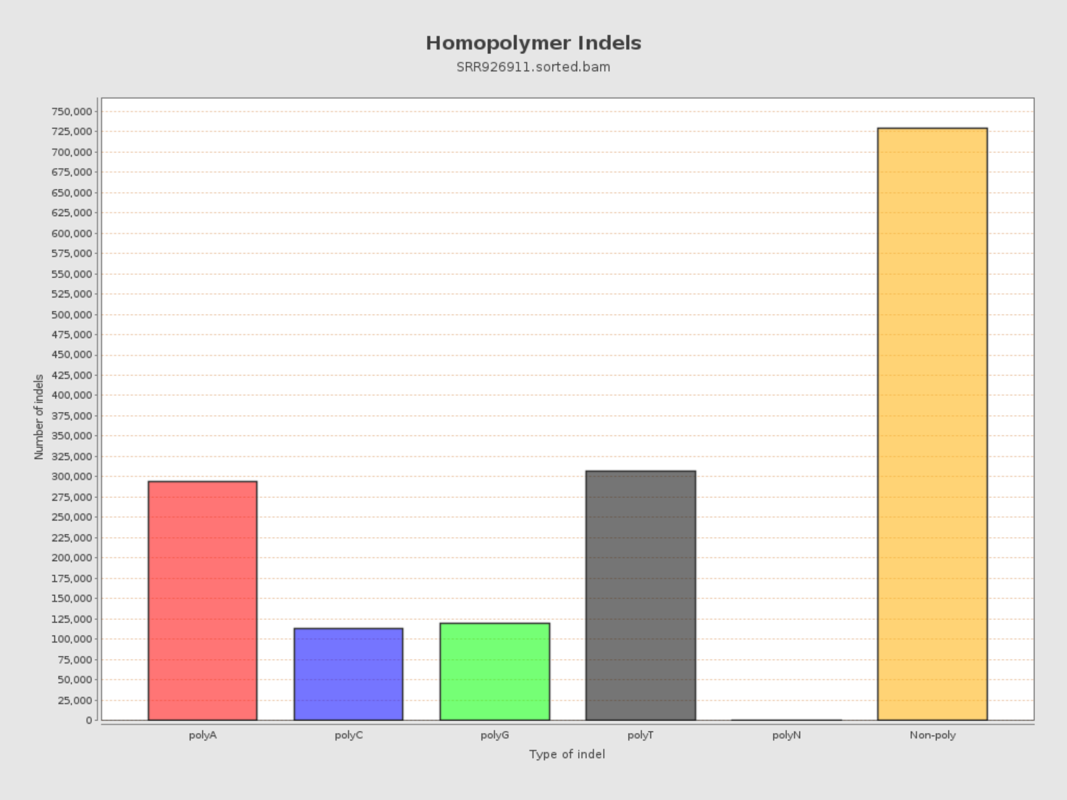
9. Results : Mapped Reads GC-content Distribution



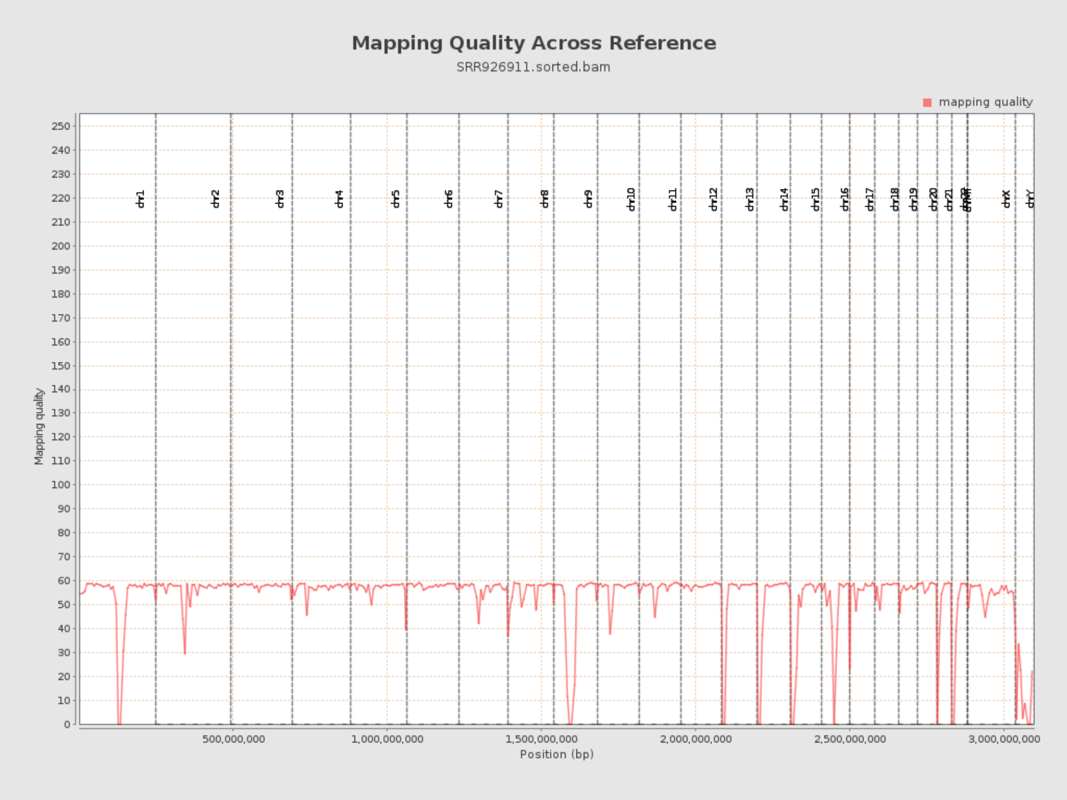
10. Results : Mapped Reads Clipping Profile



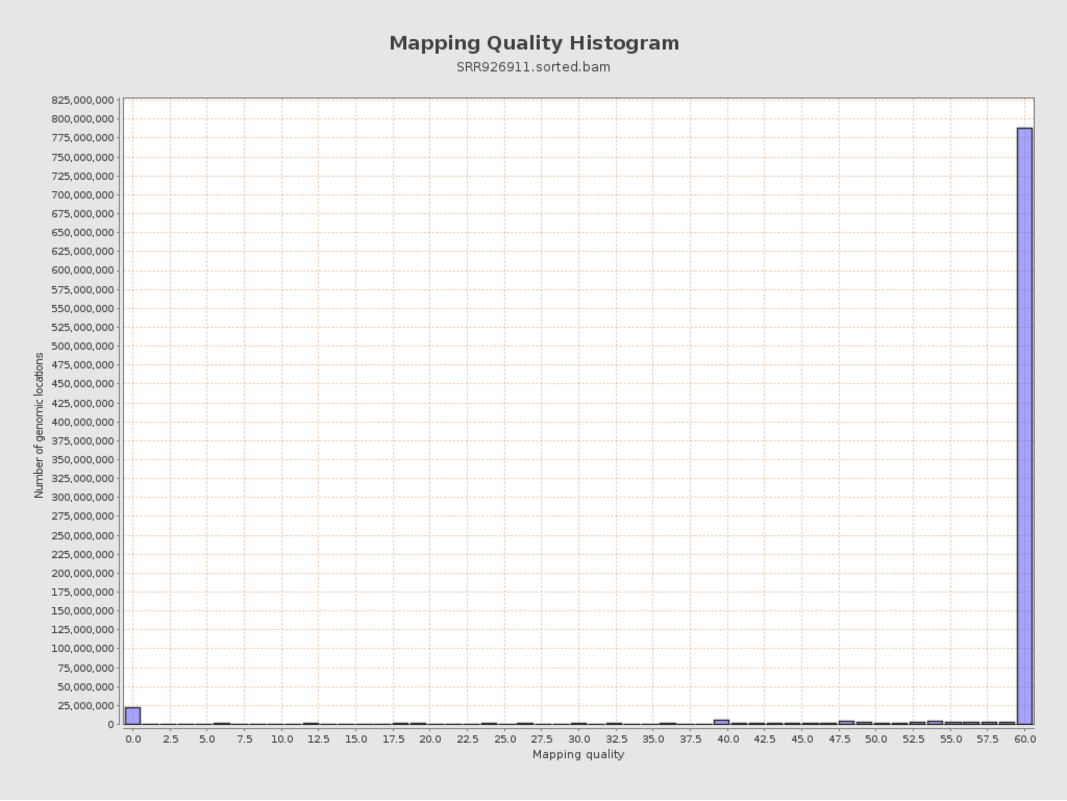
11. Results : Homopolymer Indels



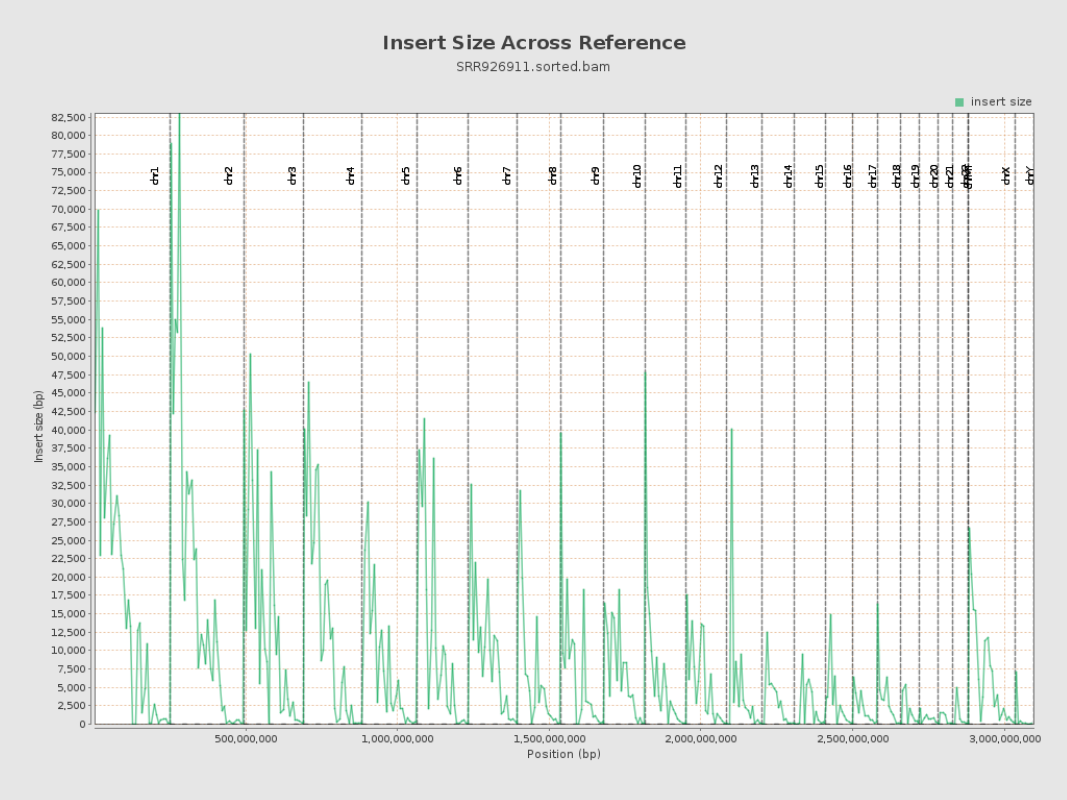
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram