Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 08:04:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926968.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_SRR926968 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926968_1.fastq.gz SRR926968_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 08:04:00 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926968.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	24,095,590
Mapped reads	23,711,901 / 98.41%
Unmapped reads	383,689 / 1.59%
Mapped paired reads	23,711,901 / 98.41%
Mapped reads, first in pair	11,914,035 / 49.44%
Mapped reads, second in pair	11,797,866 / 48.96%
Mapped reads, both in pair	23,508,316 / 97.56%
Mapped reads, singletons	203,585 / 0.84%
Secondary alignments	0
Supplementary alignments	174,137 / 0.72%
Read min/max/mean length	30 / 101 / 101.29
Duplicated reads (estimated)	1,357,031 / 5.63%
Duplication rate	4.36%
Clipped reads	4,779,331 / 19.83%

2.2. ACGT Content

Number/percentage of A's	645,455,666 / 28.41%
Number/percentage of C's	466,326,245 / 20.53%
Number/percentage of T's	651,895,161 / 28.7%
Number/percentage of G's	507,746,829 / 22.35%
Number/percentage of N's	165,559 / 0.01%

GC Percentage	42.88%

2.3. Coverage

Mean	0.7343
Standard Deviation	3.0324

2.4. Mapping Quality

Mean Mapping Quality	53.65

2.5. Insert size

Mean	75,627.11
Standard Deviation	2,709,171.91
P25/Median/P75	147 / 183 / 236

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	21,764,012
Insertions	362,643
Mapped reads with at least one insertion	1.5%
Deletions	1,187,345
Mapped reads with at least one deletion	4.88%
Homopolymer indels	52.82%

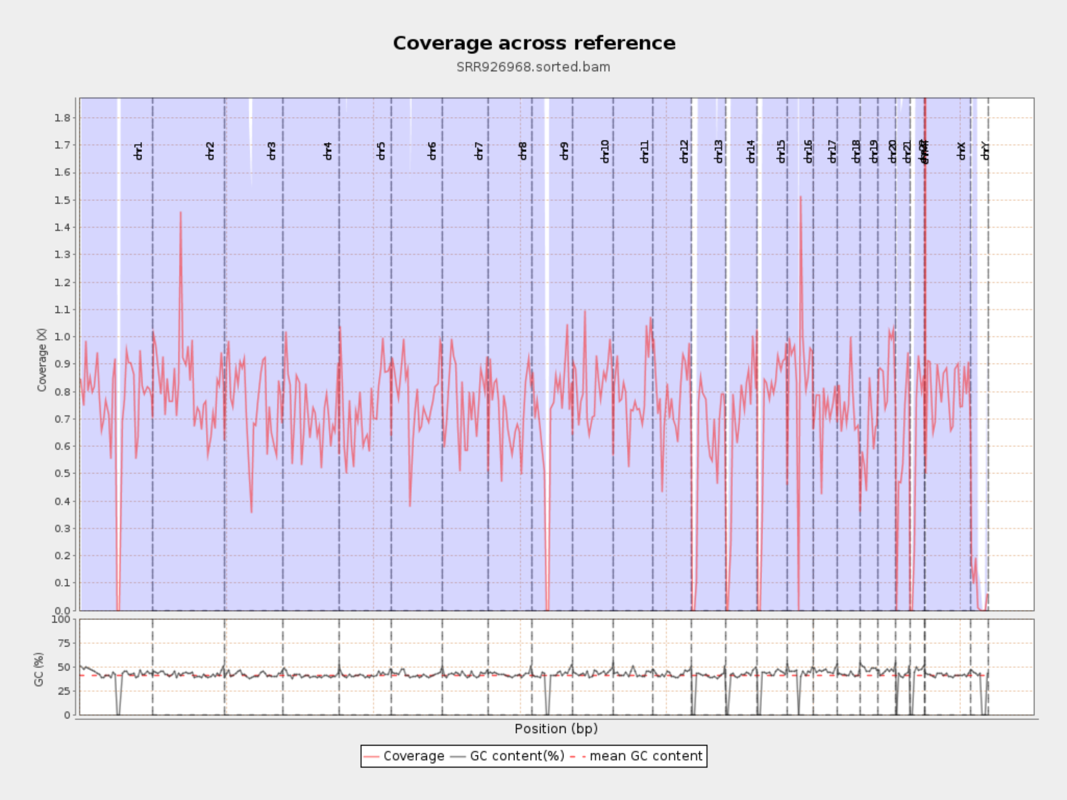
2.7. Chromosome stats

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

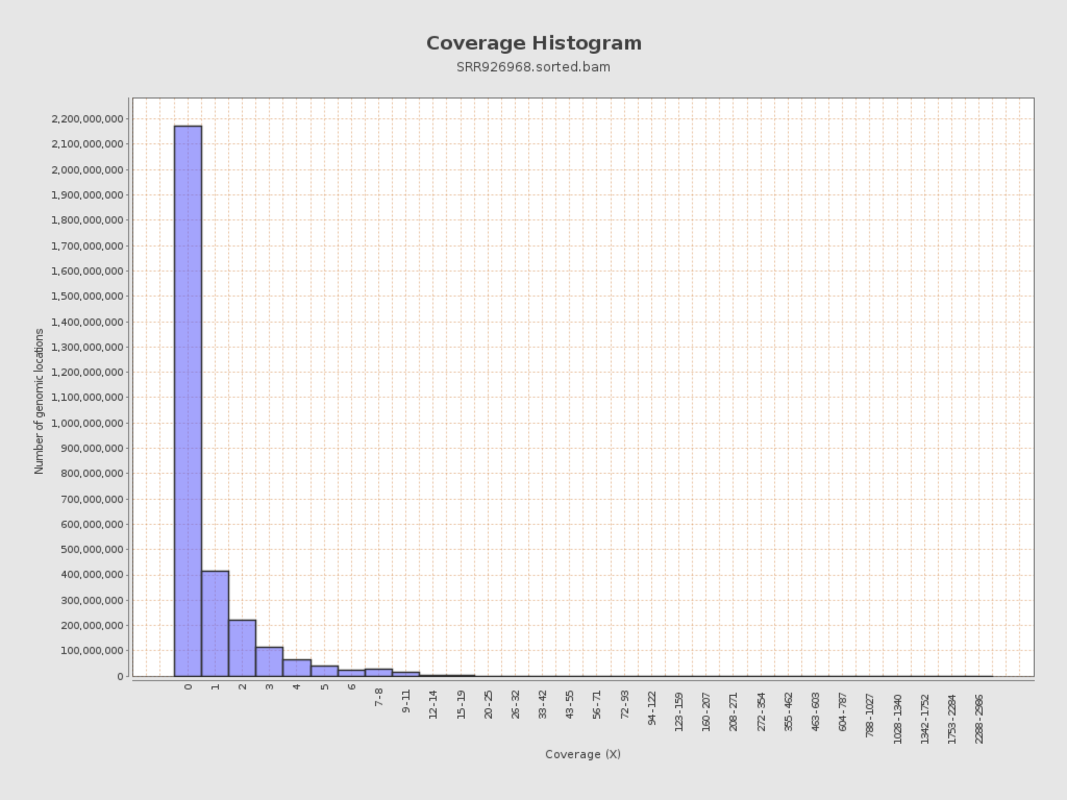
		bases	coverage	deviation
chr1	249250621	186570601	0.7485	3.6534
chr2	243199373	201341125	0.8279	5.0513
chr3	198022430	149834582	0.7567	1.6248
chr4	191154276	138728816	0.7257	2.3377
chr5	180915260	134163313	0.7416	1.6033
chr6	171115067	133743712	0.7816	2.0957
chr7	159138663	121125187	0.7611	2.4691
chr8	146364022	105709388	0.7222	1.8644
chr9	141213431	97221081	0.6885	4.2704
chr10	135534747	112023880	0.8265	4.3336
chr11	135006516	107599995	0.797	2.8551
chr12	133851895	103565955	0.7737	1.7628
chr13	115169878	67012906	0.5819	1.441
chr14	107349540	69668496	0.649	1.5743
chr15	102531392	71587559	0.6982	1.6542
chr16	90354753	78462729	0.8684	6.0671
chr17	81195210	58962256	0.7262	2.9961
chr18	78077248	58597626	0.7505	4.1673
chr19	59128983	36492541	0.6172	2.3317
chr20	63025520	56100509	0.8901	1.933
chr21	48129895	28238894	0.5867	2.6081
chr22	51304566	28905666	0.5634	1.5682
chrMT	16571	387229	23.3679	16.4936
chrX	155270560	123517327	0.7955	1.9374

chrY	59373566	3713672	0.0625	1.7818

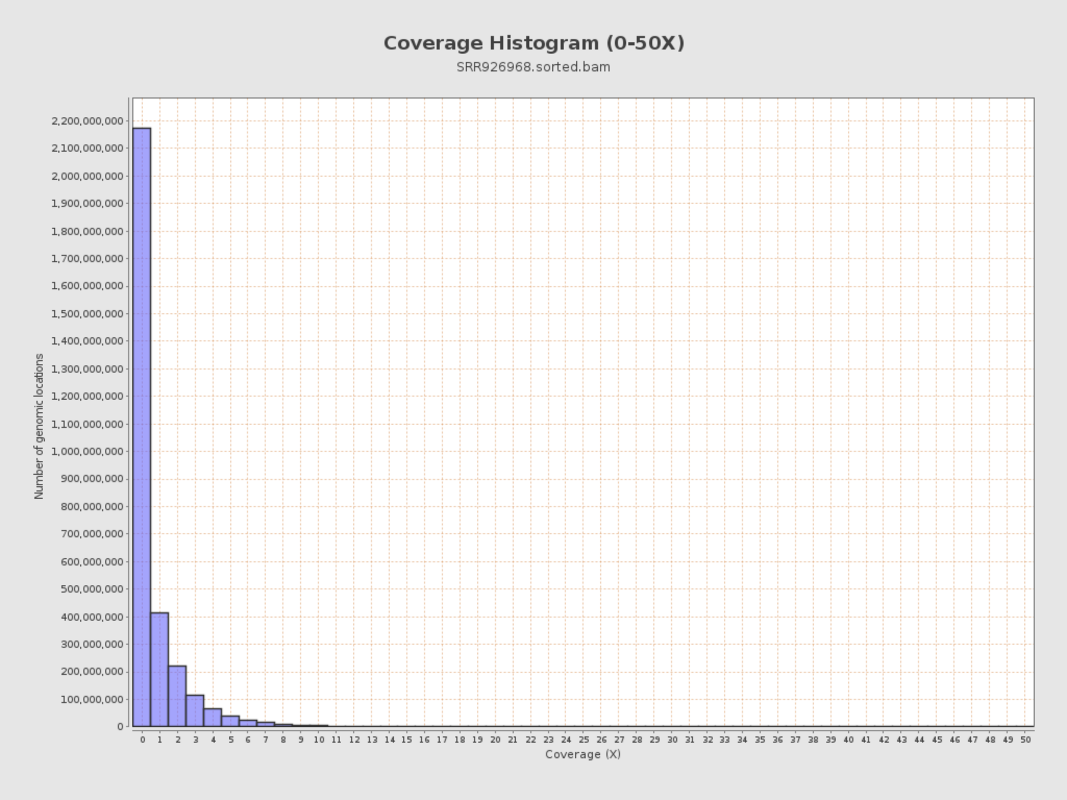
3. Results : Coverage across reference



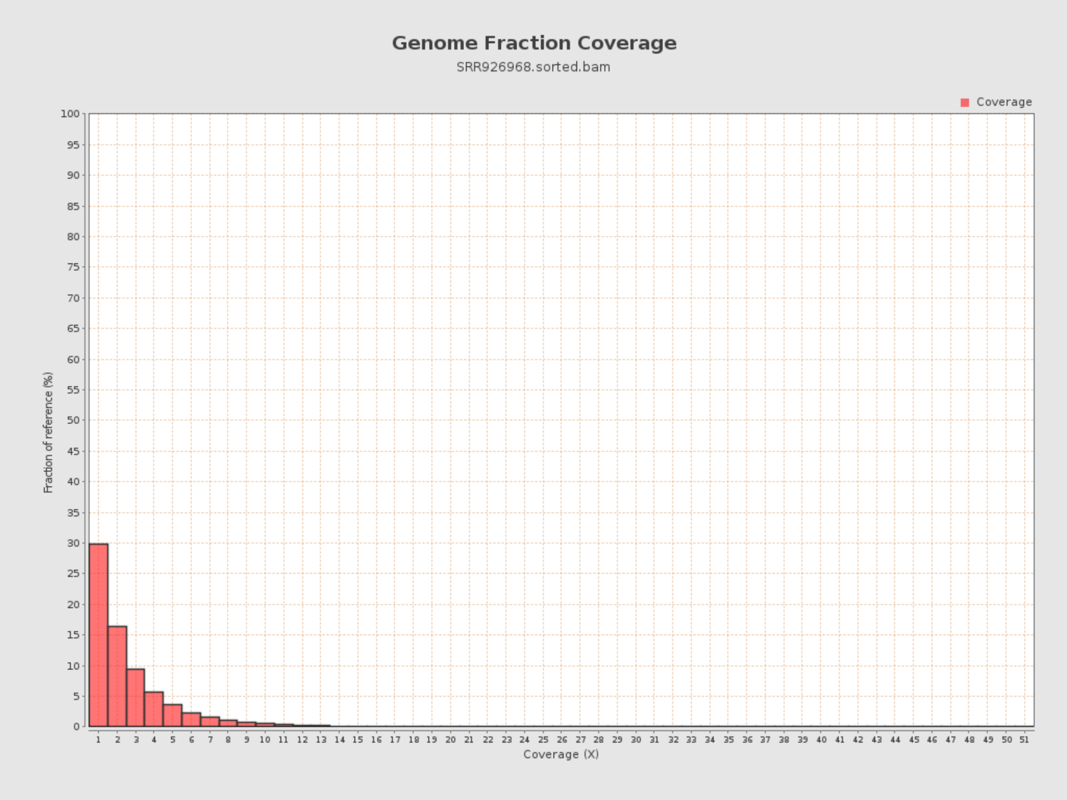
4. Results : Coverage Histogram



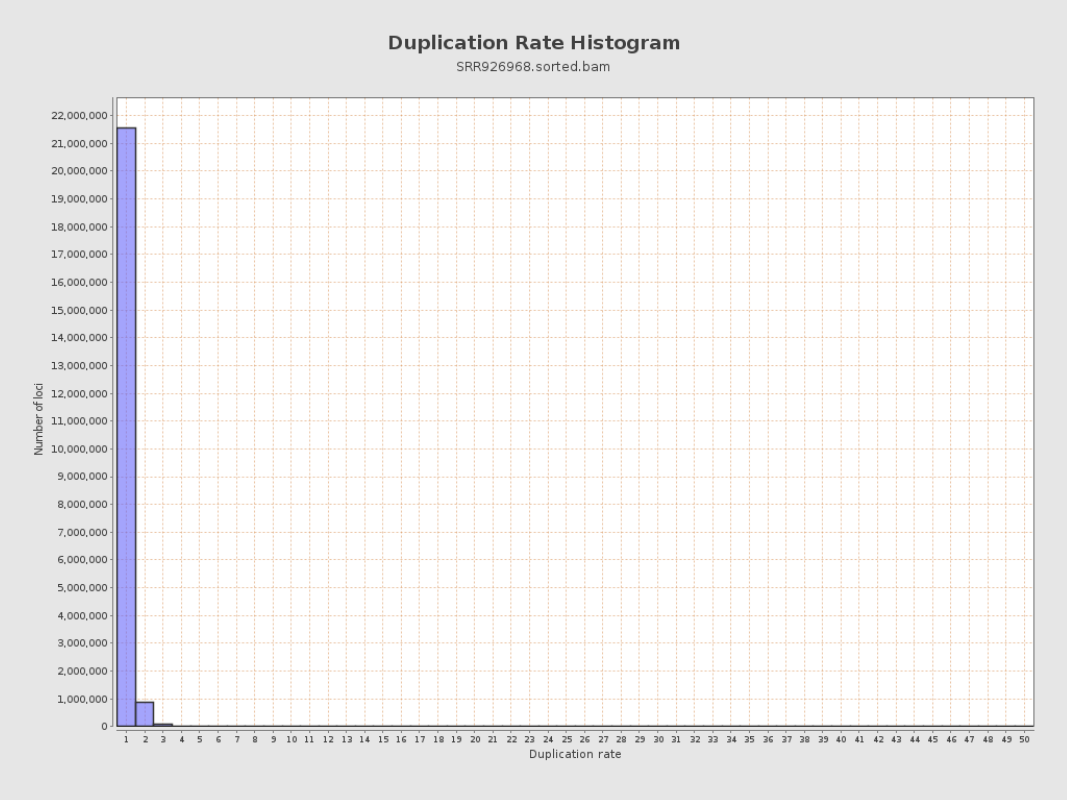
5. Results : Coverage Histogram (0-50X)



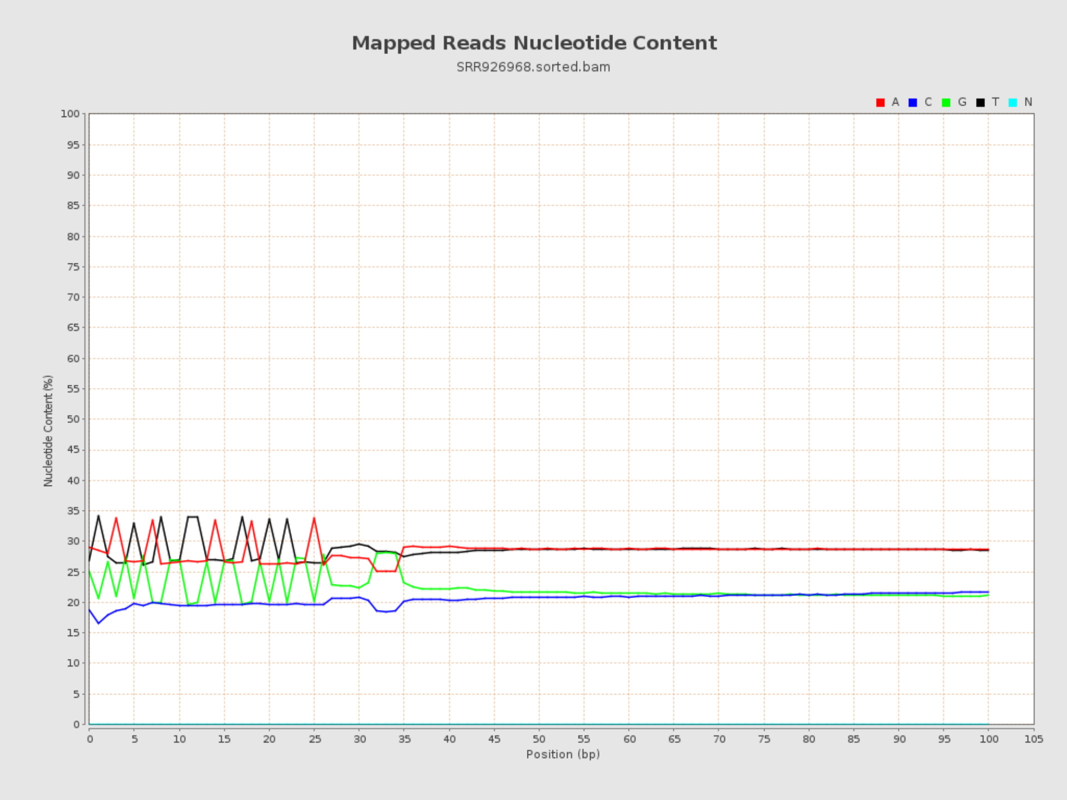
6. Results : Genome Fraction Coverage



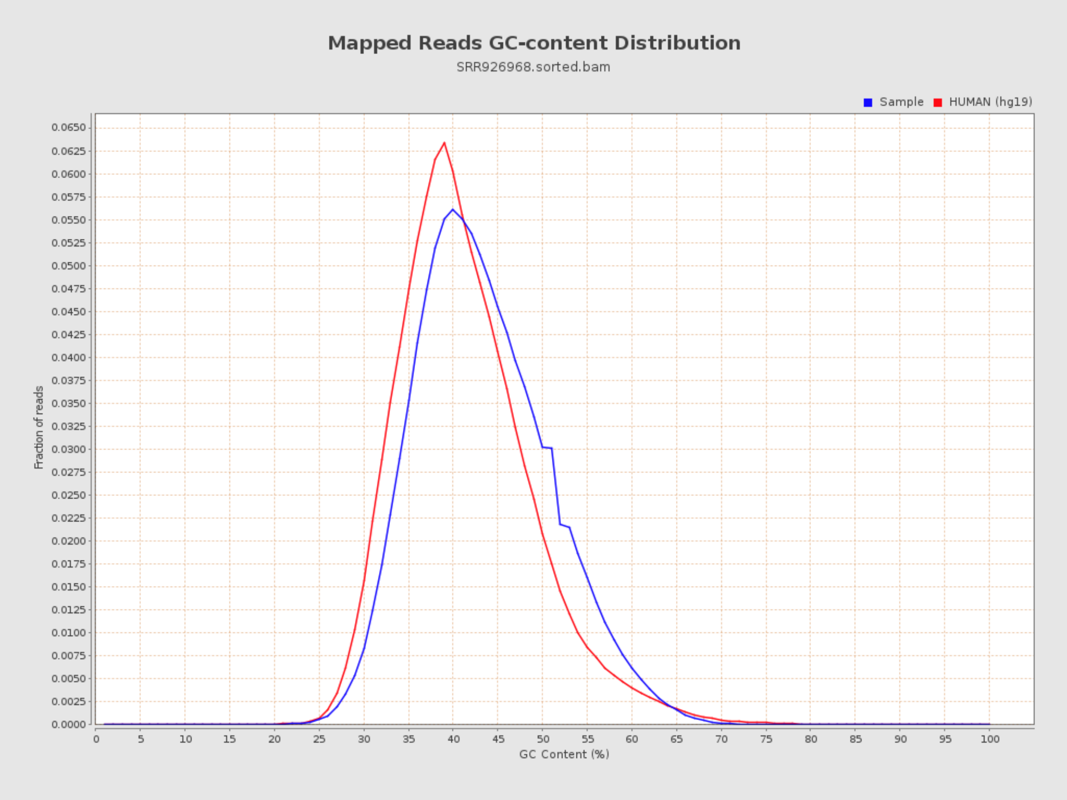
7. Results : Duplication Rate Histogram



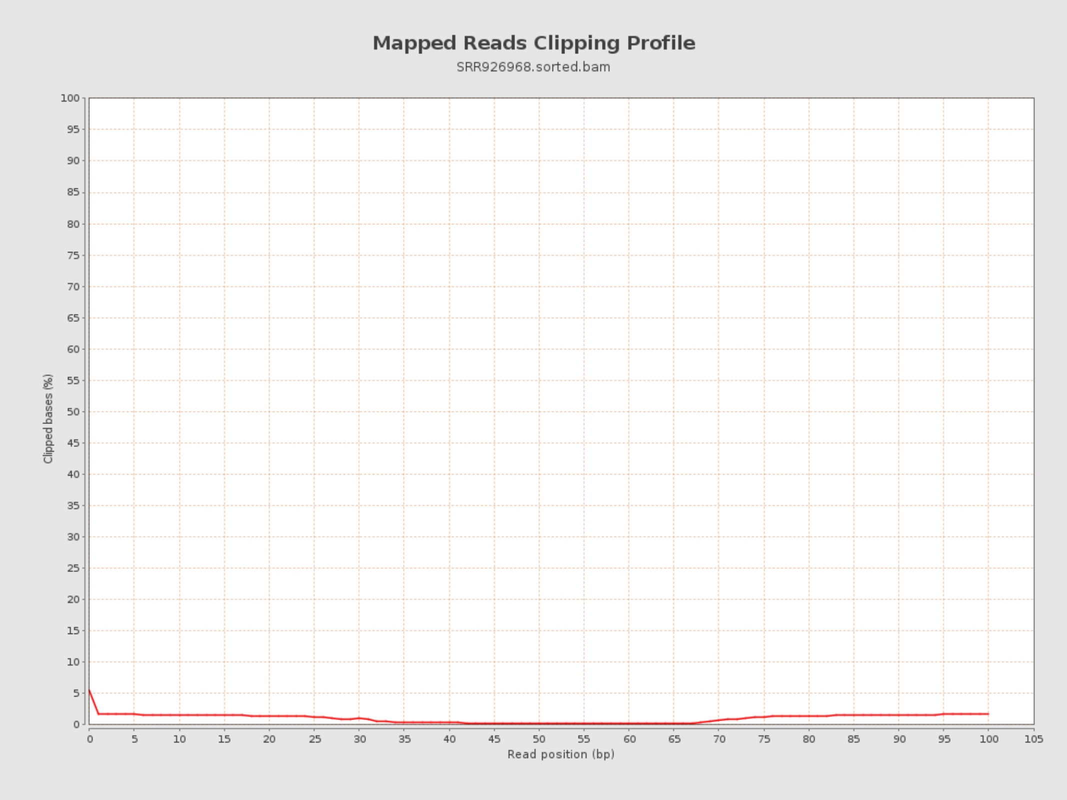
8. Results : Mapped Reads Nucleotide Content



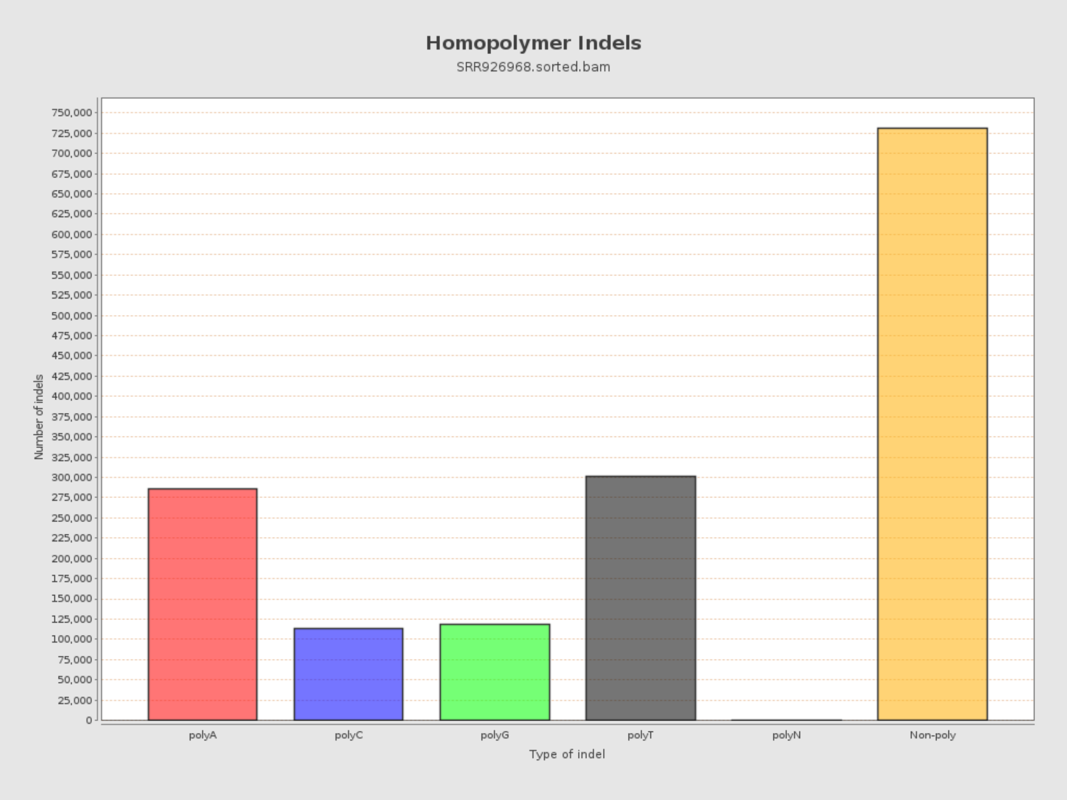
9. Results : Mapped Reads GC-content Distribution



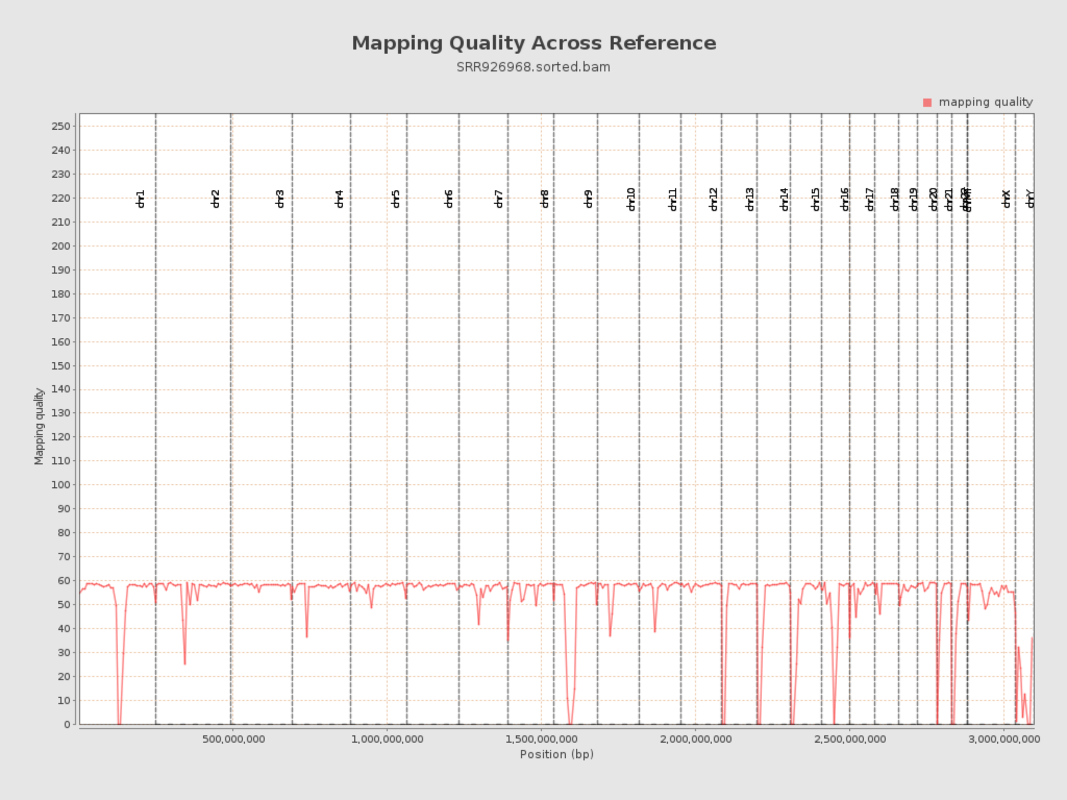
10. Results : Mapped Reads Clipping Profile



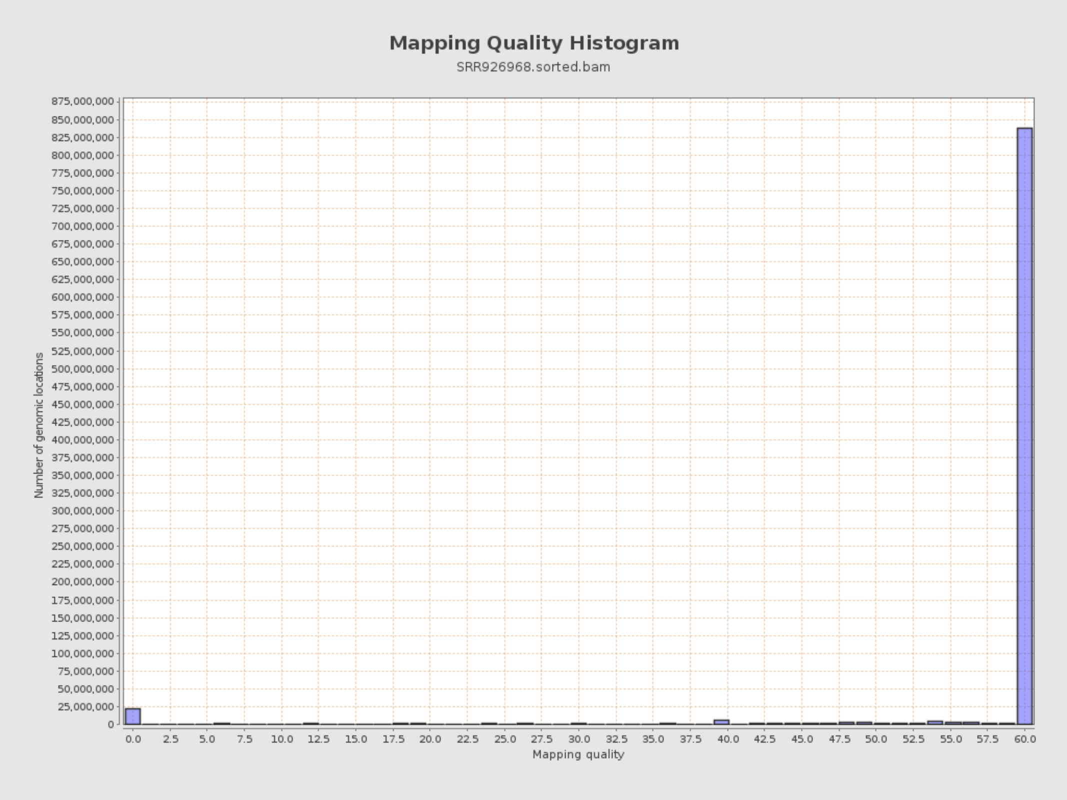
11. Results : Homopolymer Indels



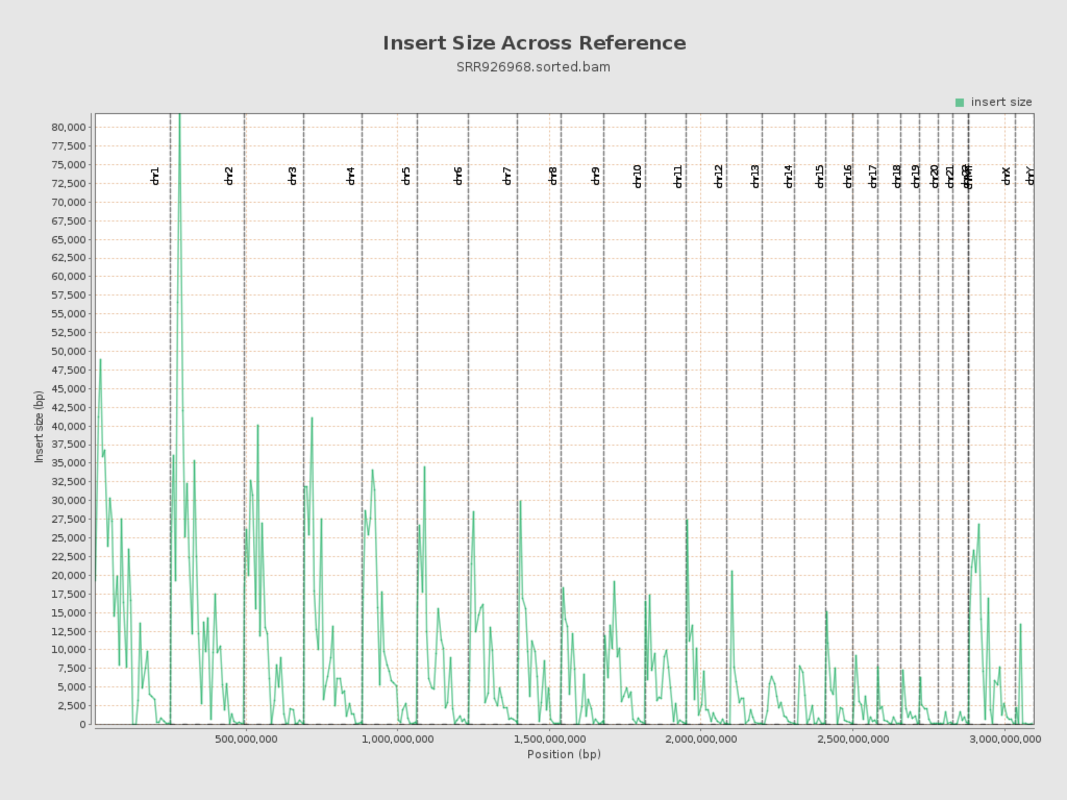
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram