Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 15:41:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926984.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_SRR926984 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926984_1.fastq.gz SRR926984_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 15:41:03 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926984.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	34,190,246
Mapped reads	33,677,771 / 98.5%
Unmapped reads	512,475 / 1.5%
Mapped paired reads	33,677,771 / 98.5%
Mapped reads, first in pair	16,907,655 / 49.45%
Mapped reads, second in pair	16,770,116 / 49.05%
Mapped reads, both in pair	33,368,732 / 97.6%
Mapped reads, singletons	309,039 / 0.9%
Secondary alignments	0
Supplementary alignments	633,024 / 1.85%
Read min/max/mean length	30 / 101 / 101.76
Duplicated reads (estimated)	2,608,739 / 7.63%
Duplication rate	5.96%
Clipped reads	8,753,935 / 25.6%

2.2. ACGT Content

Number/percentage of A's	904,739,869 / 28.29%
Number/percentage of C's	657,418,215 / 20.56%
Number/percentage of T's	915,953,845 / 28.64%
Number/percentage of G's	719,719,691 / 22.5%
Number/percentage of N's	254,042 / 0.01%

GC Percentage	43.06%

2.3. Coverage

Mean	1.0339
Standard Deviation	4.2258

2.4. Mapping Quality

Mean Mapping Quality	53.29

2.5. Insert size

Mean	175,242.98
Standard Deviation	4,090,135.26
P25/Median/P75	138 / 174 / 228

2.6. Mismatches and indels

General error rate	0.96%
Mismatches	29,765,018
Insertions	514,262
Mapped reads with at least one insertion	1.5%
Deletions	1,688,598
Mapped reads with at least one deletion	4.88%
Homopolymer indels	52.55%

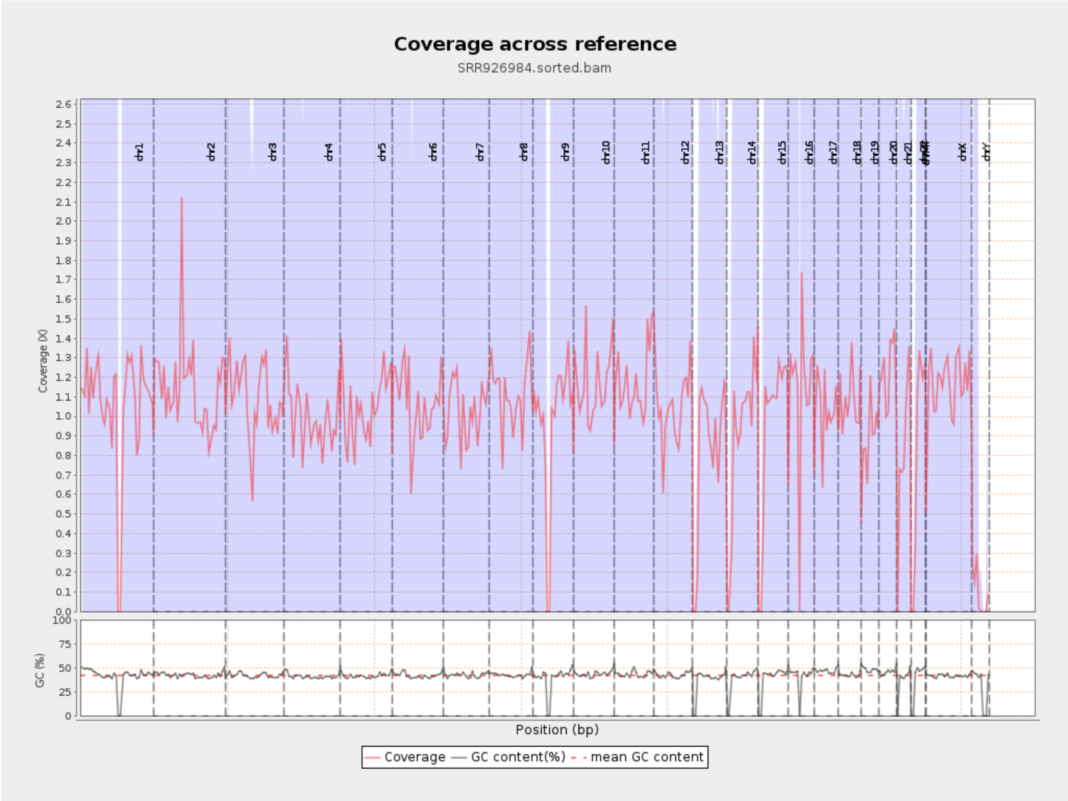
2.7. Chromosome stats

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

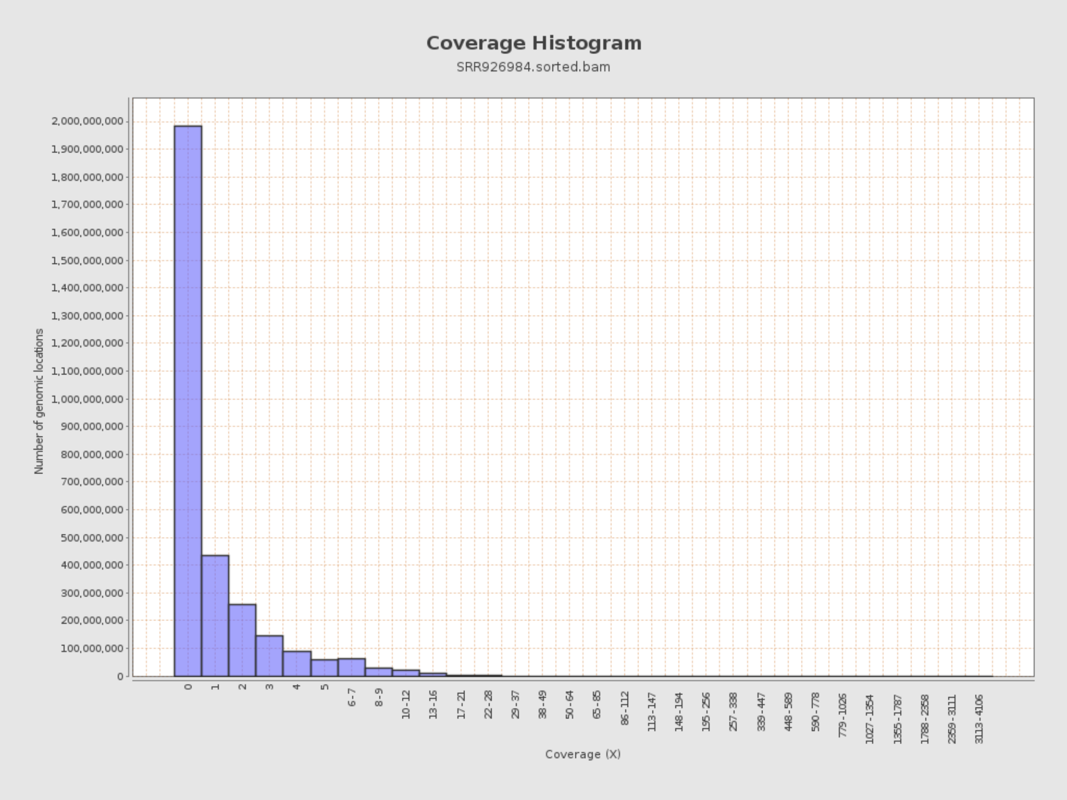
		bases	coverage	deviation
chr1	249250621	262956004	1.055	4.8968
chr2	243199373	278659543	1.1458	7.3891
chr3	198022430	216539268	1.0935	2.1733
chr4	191154276	190639469	0.9973	3.2189
chr5	180915260	190584831	1.0534	2.0993
chr6	171115067	184178826	1.0763	3.8
chr7	159138663	163409847	1.0268	3.2331
chr8	146364022	163057962	1.1141	2.703
chr9	141213431	136989392	0.9701	5.1605
chr10	135534747	159168576	1.1744	6.3629
chr11	135006516	157339655	1.1654	6.1937
chr12	133851895	140398312	1.0489	2.5941
chr13	115169878	94164131	0.8176	1.9411
chr14	107349540	95193686	0.8868	2.041
chr15	102531392	96538643	0.9416	2.1768
chr16	90354753	101927597	1.1281	6.0338
chr17	81195210	83720147	1.0311	3.0547
chr18	78077248	85280880	1.0923	5.763
chr19	59128983	52579164	0.8892	3.0388
chr20	63025520	77441118	1.2287	2.5555
chr21	48129895	41195380	0.8559	3.4375
chr22	51304566	42763117	0.8335	2.1216
chrMT	16571	8412	0.5076	1.8138
chrX	155270560	180208011	1.1606	3.0474

chrY	59373566	5550380	0.0935	2.8806

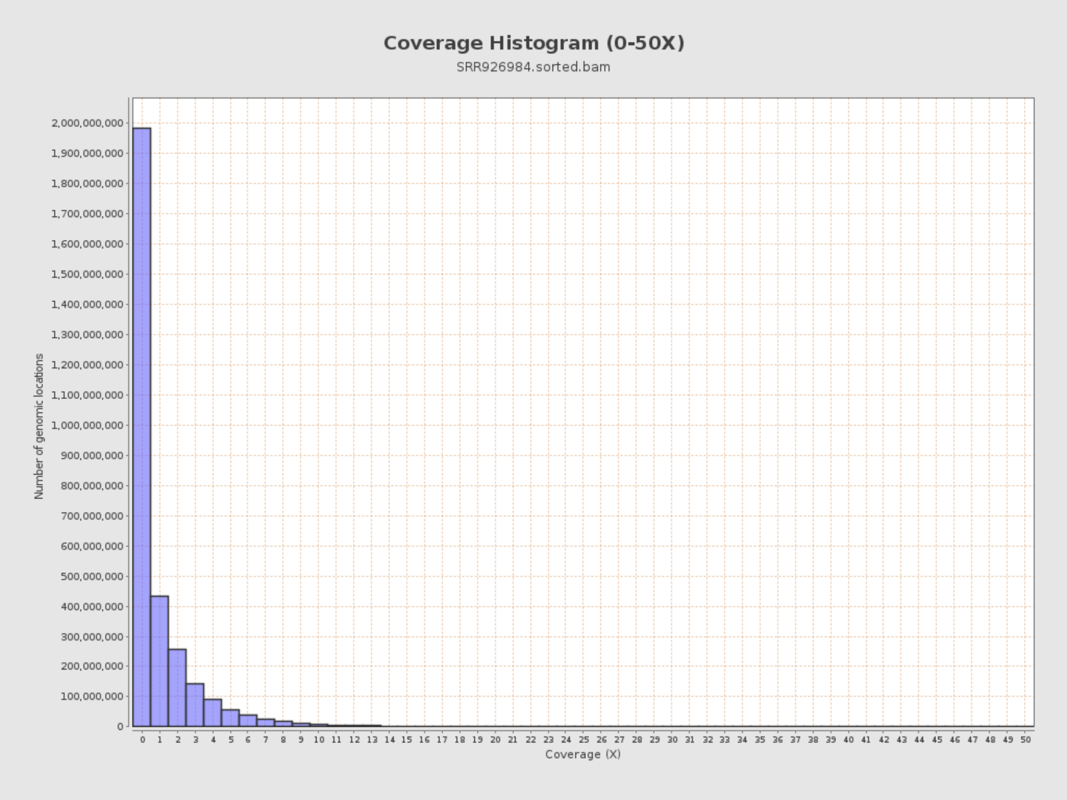
3. Results : Coverage across reference



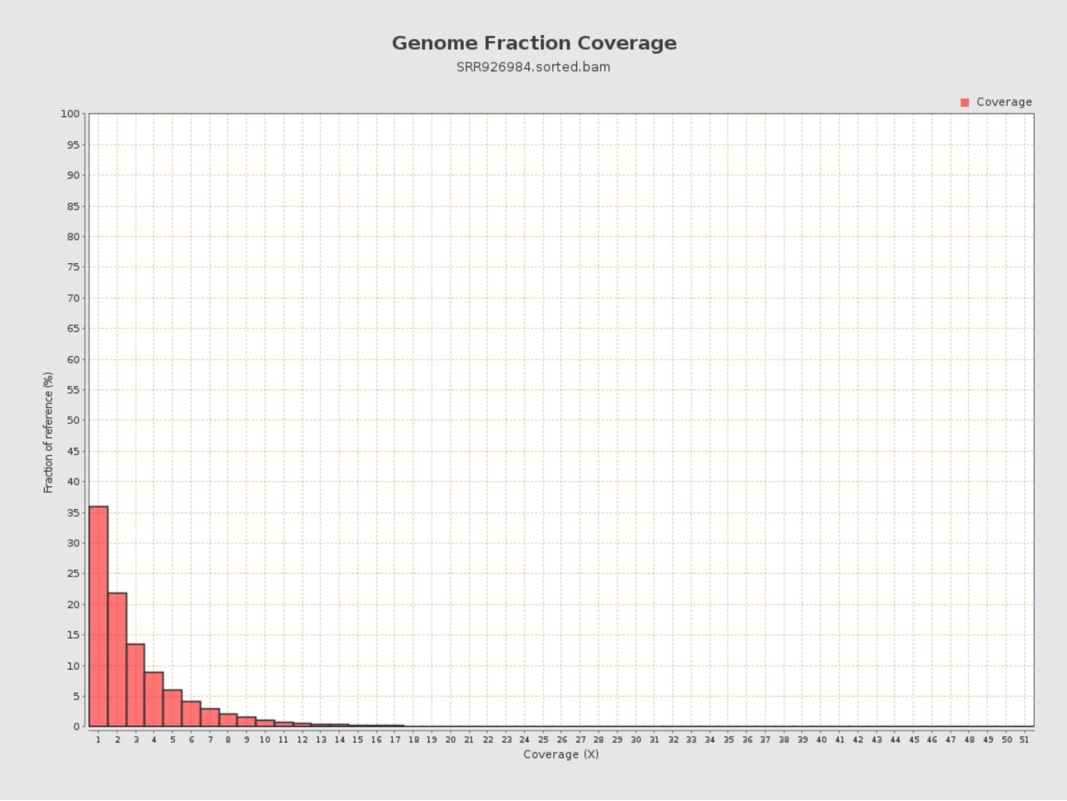
4. Results : Coverage Histogram



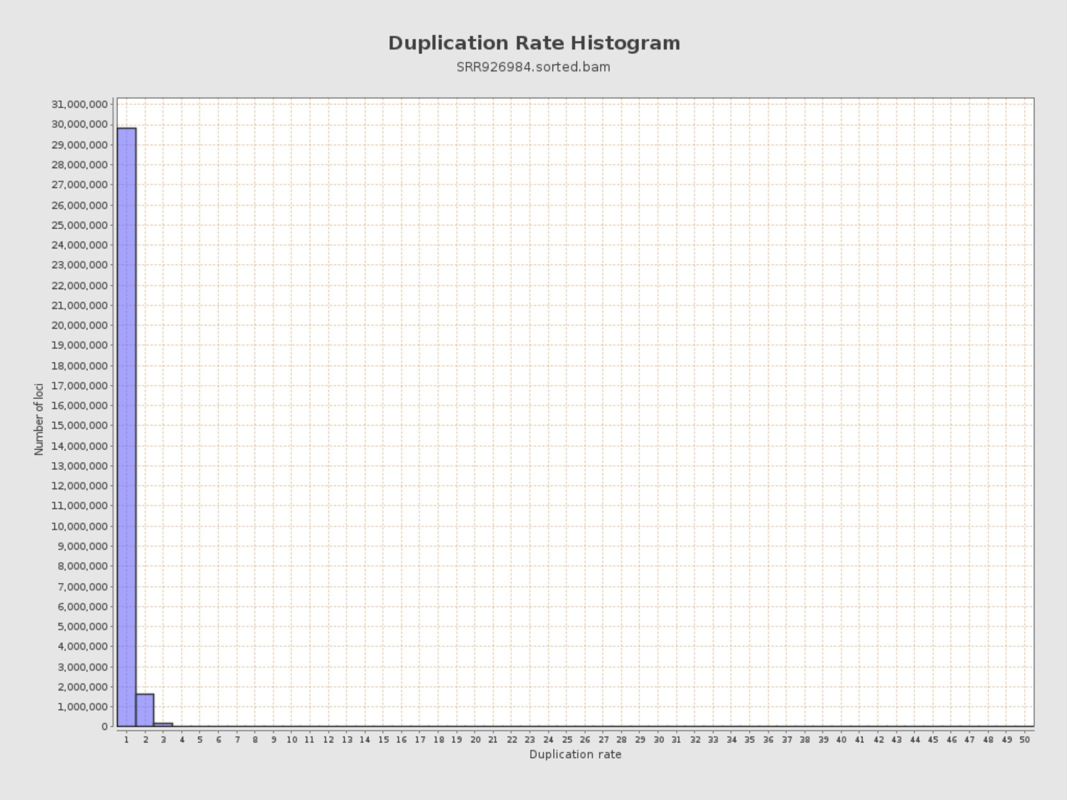
5. Results : Coverage Histogram (0-50X)



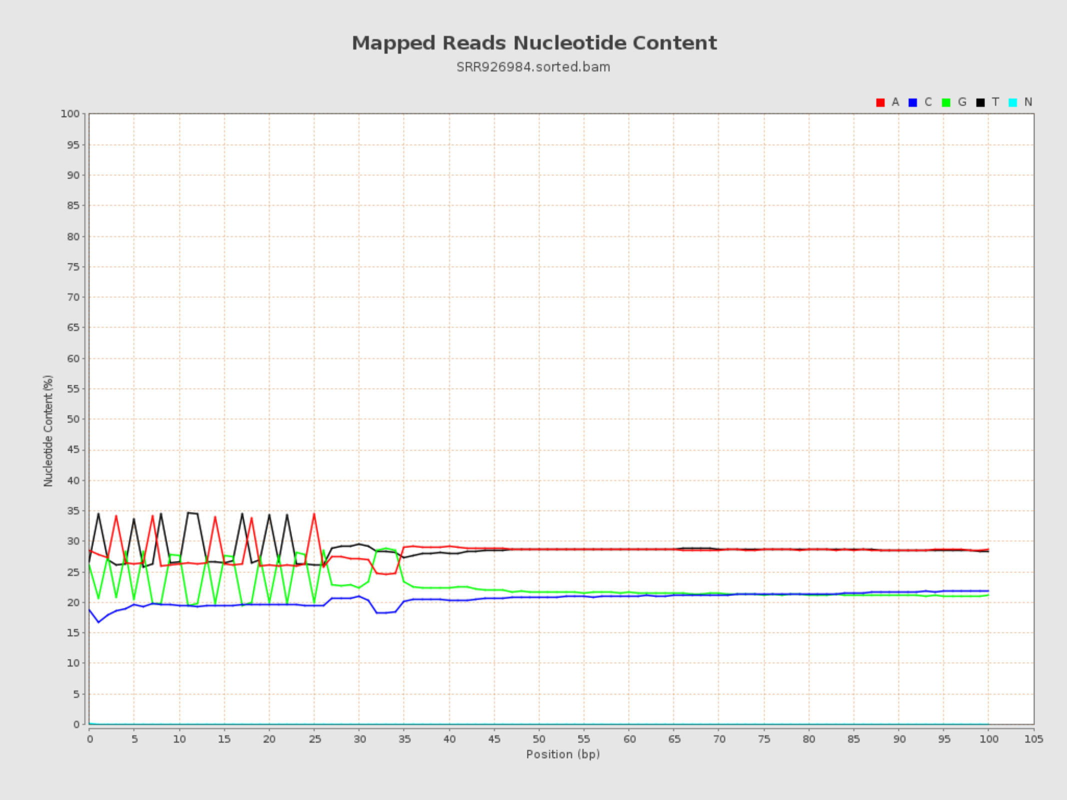
6. Results : Genome Fraction Coverage



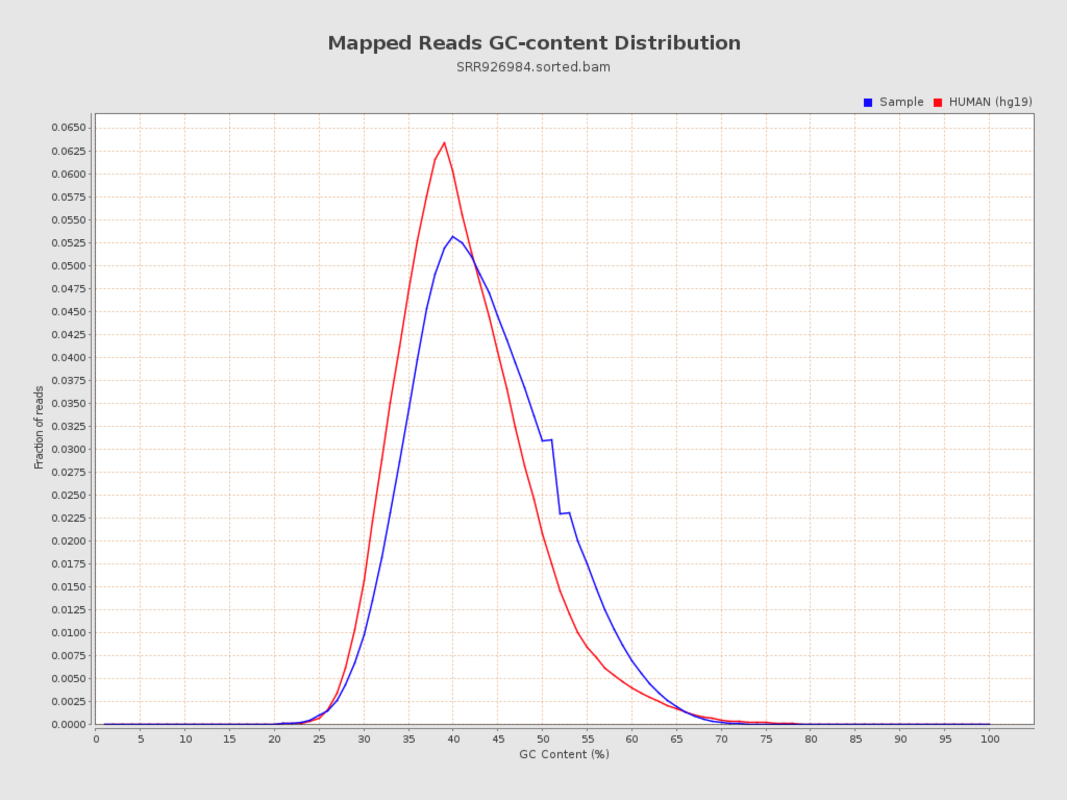
7. Results : Duplication Rate Histogram



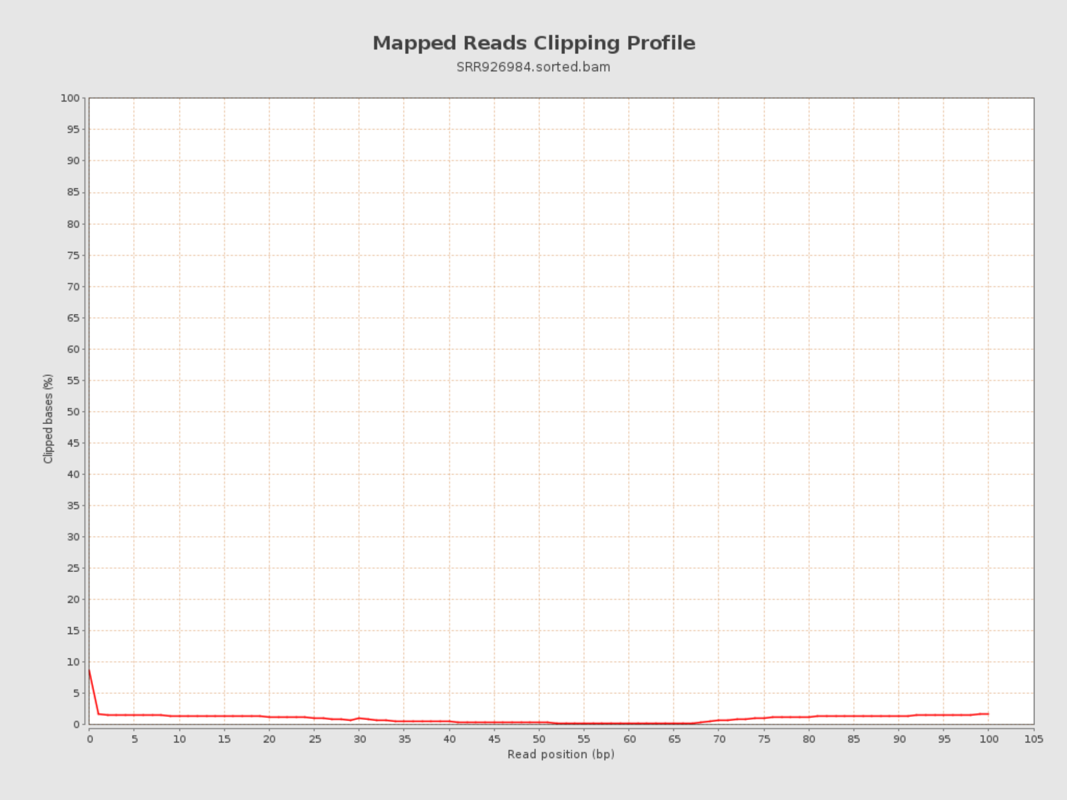
8. Results : Mapped Reads Nucleotide Content



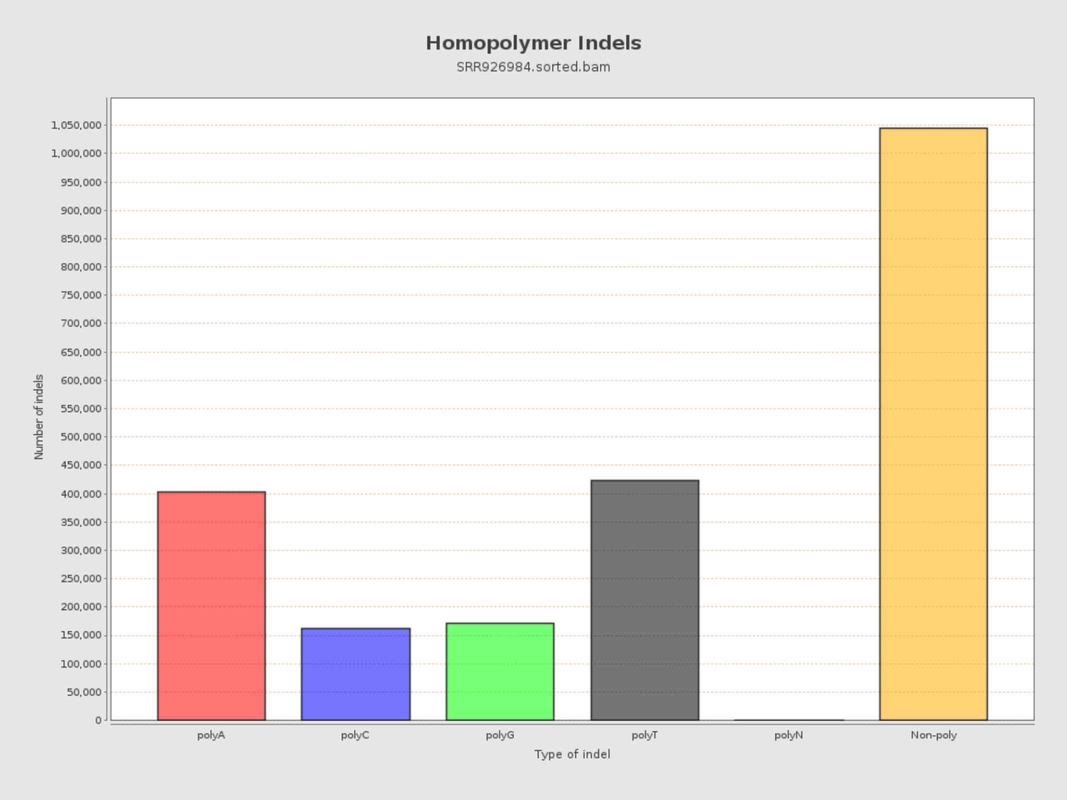
9. Results : Mapped Reads GC-content Distribution



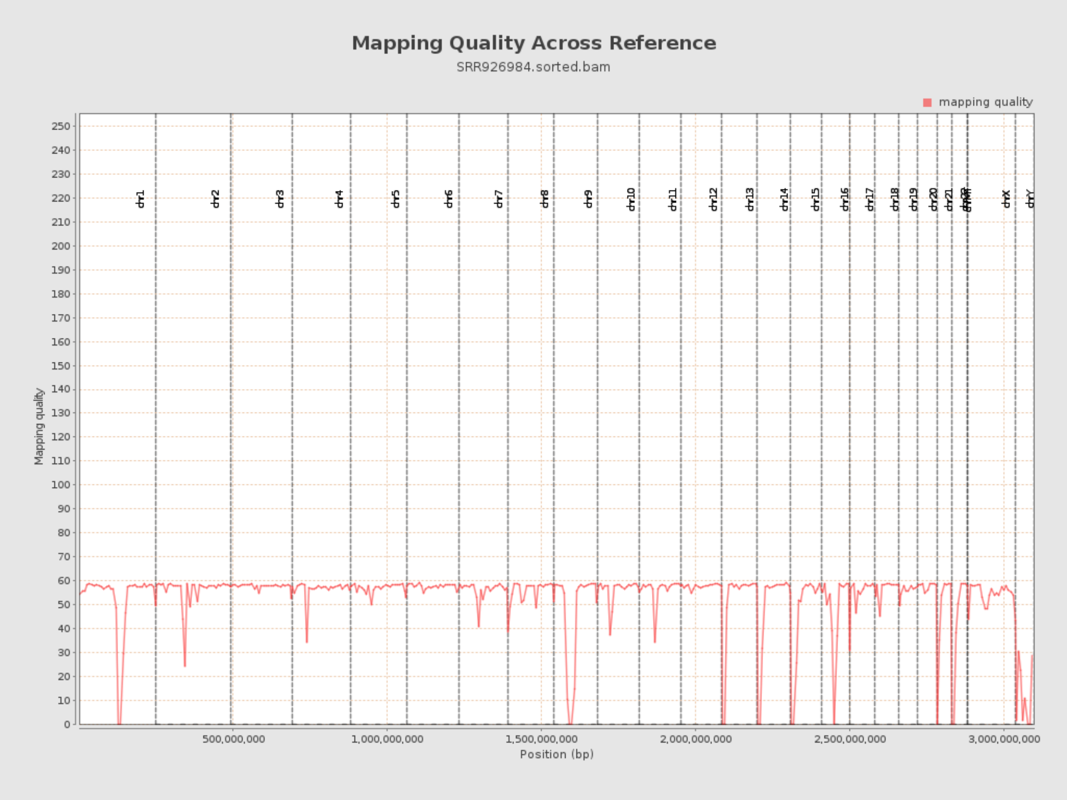
10. Results : Mapped Reads Clipping Profile



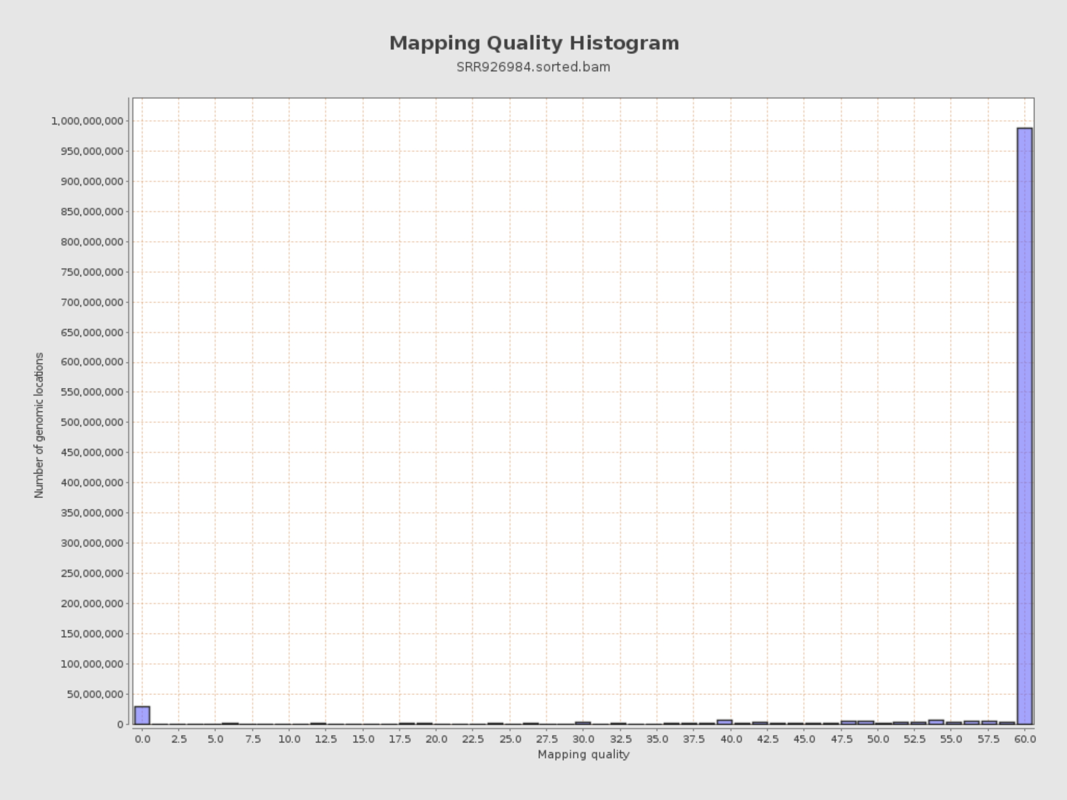
11. Results : Homopolymer Indels



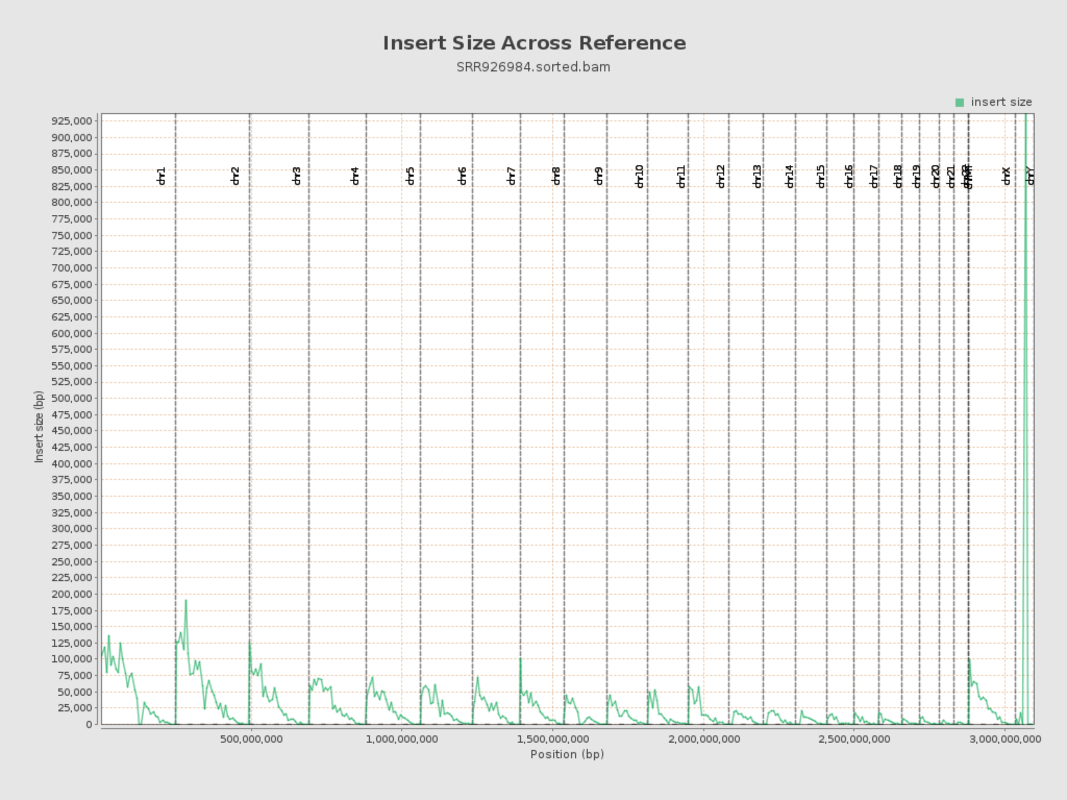
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram