Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 16:41:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926986.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_SRR926986 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926986_1.fastq.gz SRR926986_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 16:41:16 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926986.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,739,428
Mapped reads	17,407,500 / 98.13%
Unmapped reads	331,928 / 1.87%
Mapped paired reads	17,407,500 / 98.13%
Mapped reads, first in pair	8,751,613 / 49.33%
Mapped reads, second in pair	8,655,887 / 48.79%
Mapped reads, both in pair	17,210,056 / 97.02%
Mapped reads, singletons	197,444 / 1.11%
Secondary alignments	0
Supplementary alignments	307,013 / 1.73%
Read min/max/mean length	30 / 101 / 101.71
Duplicated reads (estimated)	1,037,394 / 5.85%
Duplication rate	4.69%
Clipped reads	5,419,975 / 30.55%

2.2. ACGT Content

Number/percentage of A's	462,830,705 / 28.47%
Number/percentage of C's	325,038,280 / 20%
Number/percentage of T's	470,035,560 / 28.92%
Number/percentage of G's	367,370,702 / 22.6%
Number/percentage of N's	126,776 / 0.01%

GC Percentage	42.6%

2.3. Coverage

Mean	0.5254
Standard Deviation	2.0513

2.4. Mapping Quality

Mean Mapping Quality	53

2.5. Insert size

Mean	197,789.44
Standard Deviation	4,417,942.17
P25/Median/P75	140 / 177 / 232

2.6. Mismatches and indels

General error rate	0.96%
Mismatches	15,050,916
Insertions	271,546
Mapped reads with at least one insertion	1.53%
Deletions	833,841
Mapped reads with at least one deletion	4.67%
Homopolymer indels	52.16%

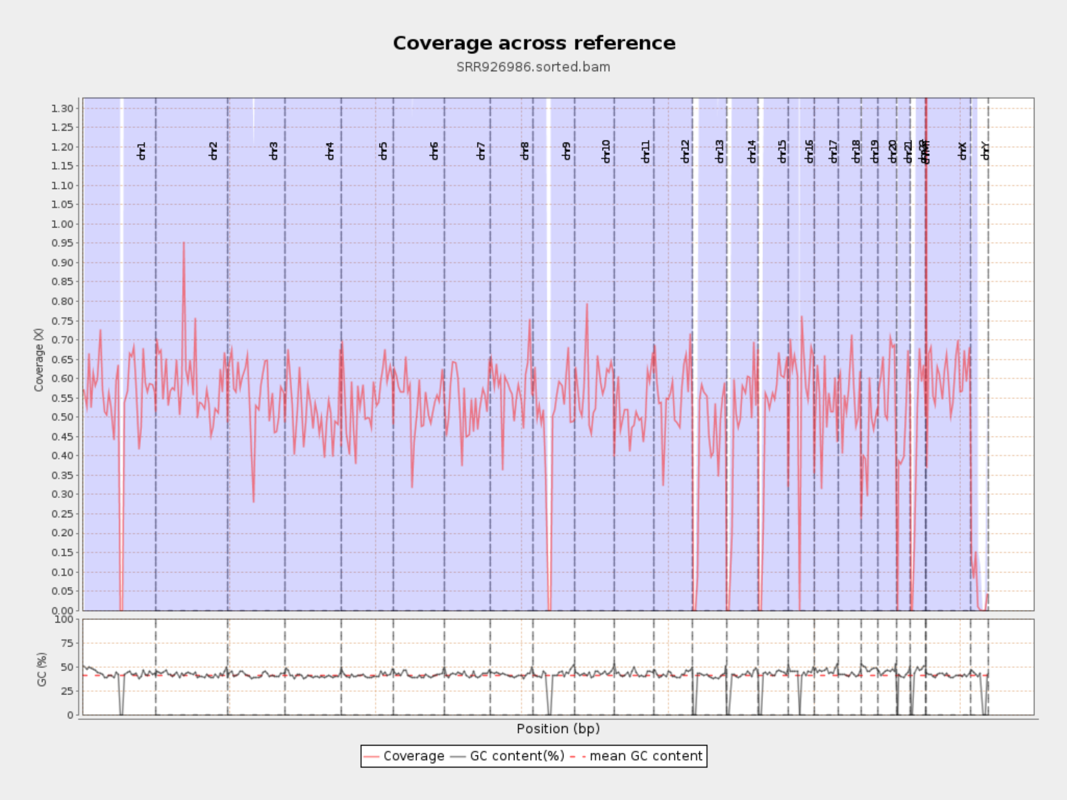
2.7. Chromosome stats

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

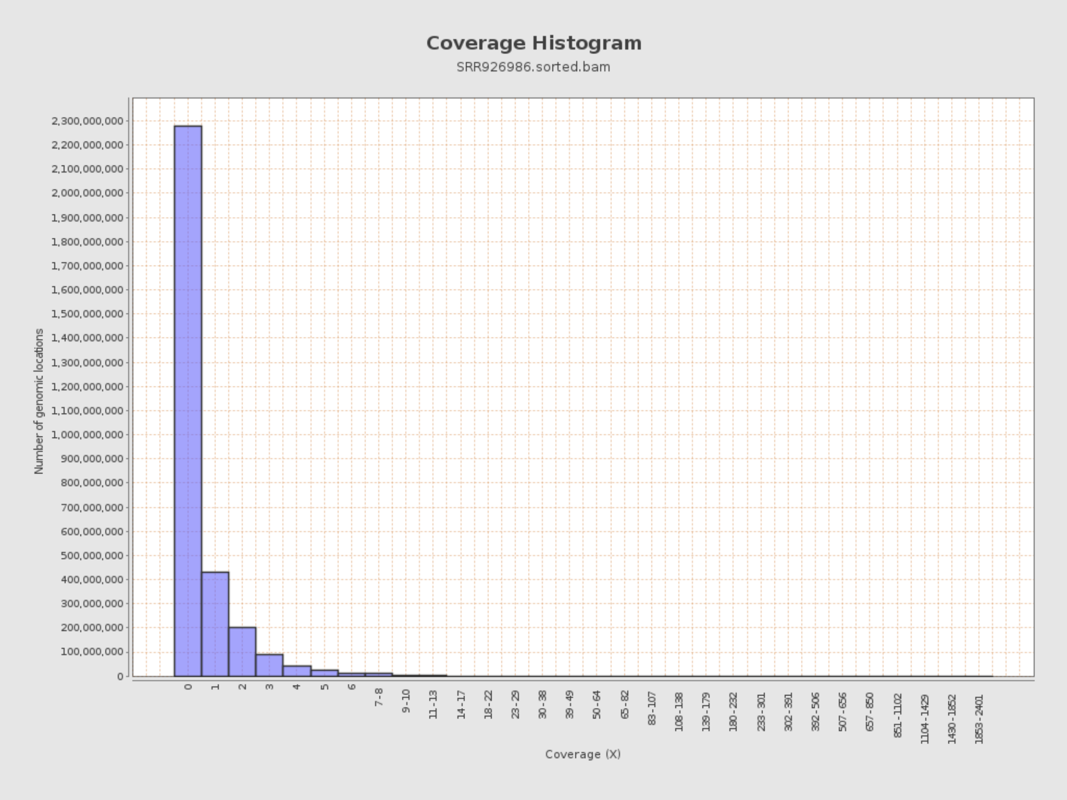
		bases	coverage	deviation
chr1	249250621	134957534	0.5415	2.5005
chr2	243199373	144115171	0.5926	3.6754
chr3	198022430	110050285	0.5557	1.2066
chr4	191154276	98687049	0.5163	1.8164
chr5	180915260	99057514	0.5475	1.1836
chr6	171115067	92584525	0.5411	1.4109
chr7	159138663	84558349	0.5314	1.6778
chr8	146364022	84278122	0.5758	1.4253
chr9	141213431	67518393	0.4781	2.4093
chr10	135534747	78612586	0.58	3.0262
chr11	135006516	69823960	0.5172	2.5172
chr12	133851895	74896238	0.5595	1.4436
chr13	115169878	48197551	0.4185	1.1002
chr14	107349540	49742241	0.4634	1.1508
chr15	102531392	48796773	0.4759	1.1918
chr16	90354753	51858661	0.5739	2.7704
chr17	81195210	42903806	0.5284	1.5103
chr18	78077248	43261278	0.5541	2.3493
chr19	59128983	26327926	0.4453	1.6318
chr20	63025520	38392193	0.6092	1.3677
chr21	48129895	20969237	0.4357	1.7132
chr22	51304566	21073344	0.4107	1.1189
chrMT	16571	145125	8.7578	7.8232
chrX	155270560	92866201	0.5981	1.4894

chrY	59373566	2937382	0.0495	1.555

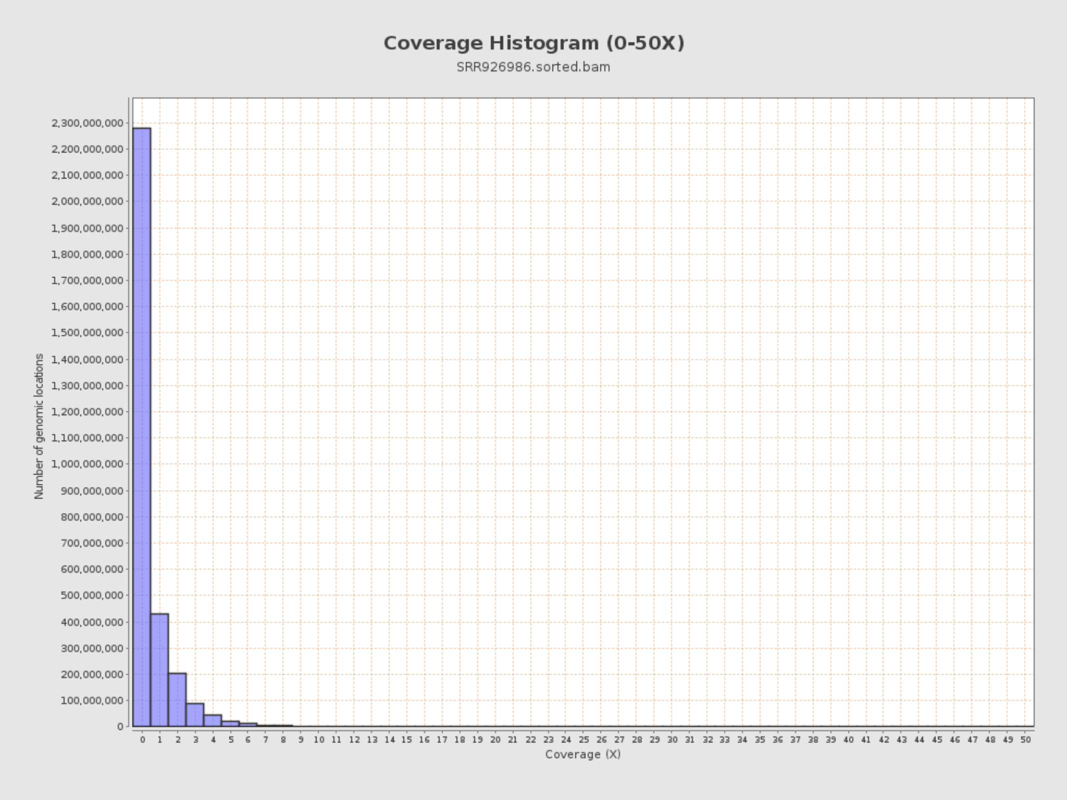
3. Results : Coverage across reference



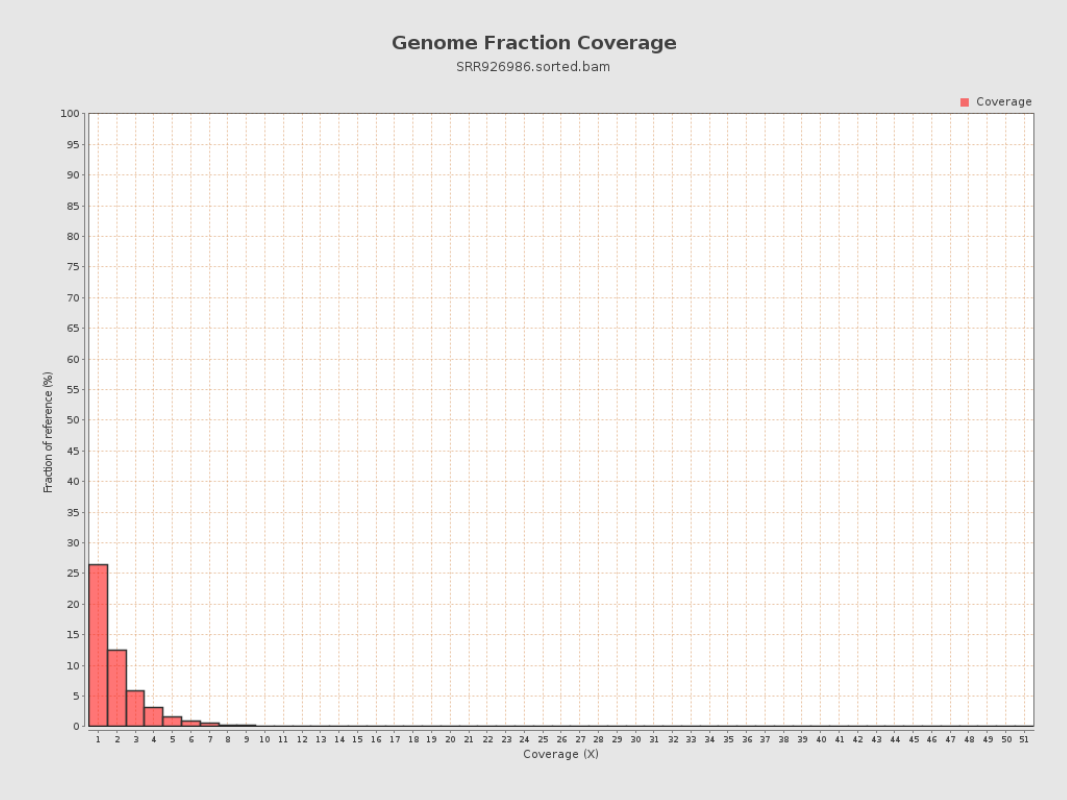
4. Results : Coverage Histogram



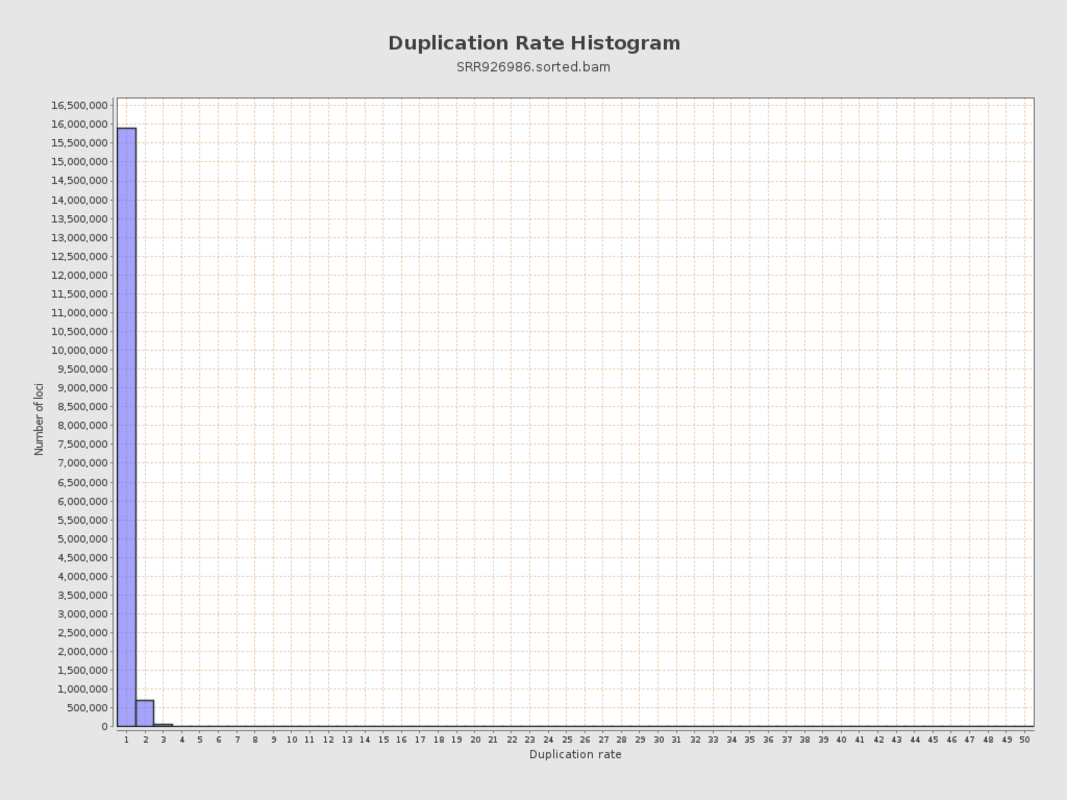
5. Results : Coverage Histogram (0-50X)



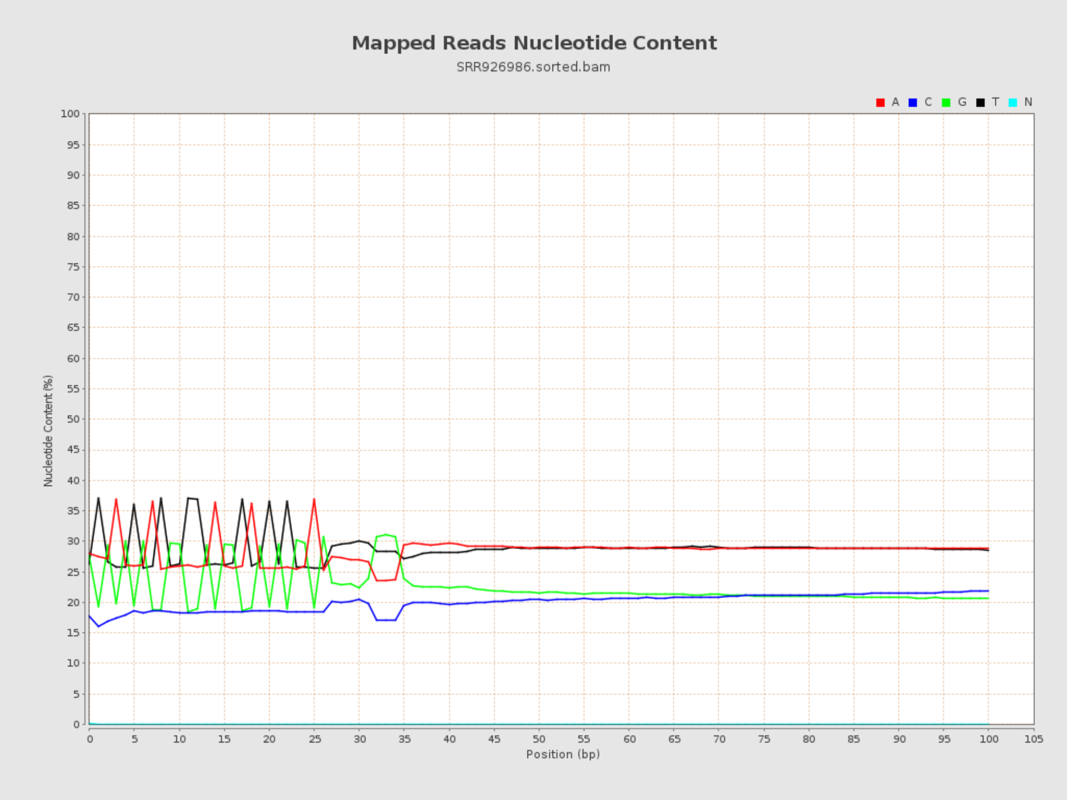
6. Results : Genome Fraction Coverage



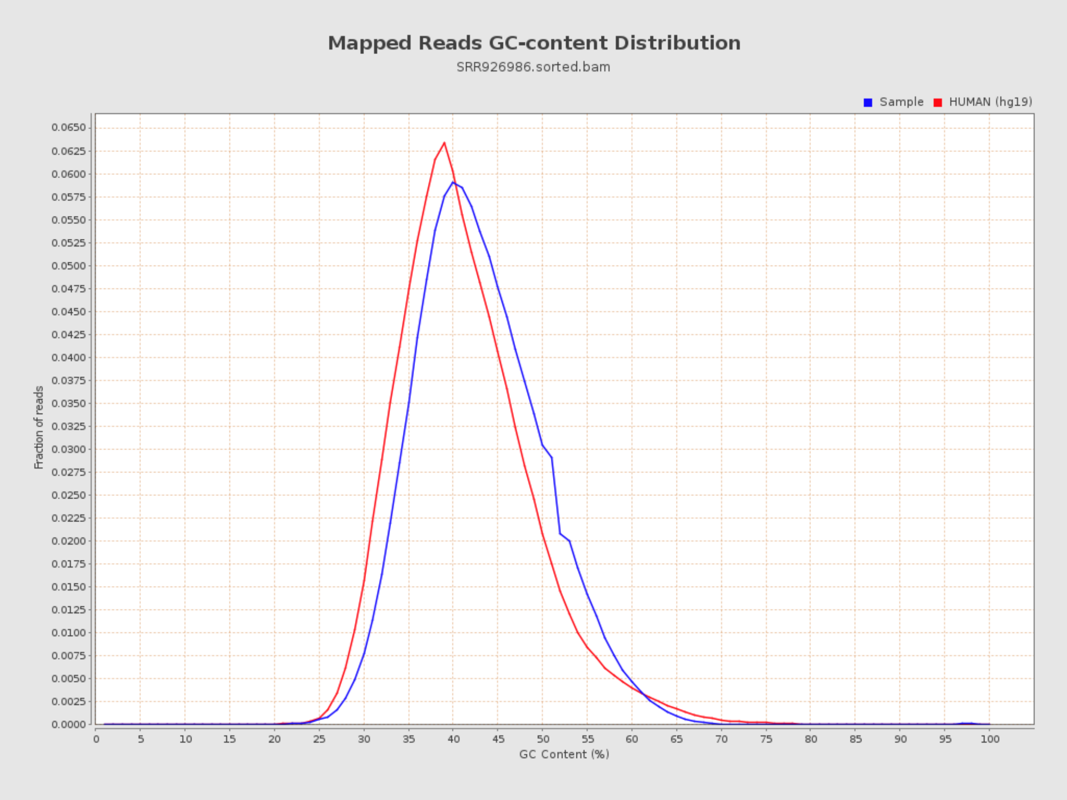
7. Results : Duplication Rate Histogram



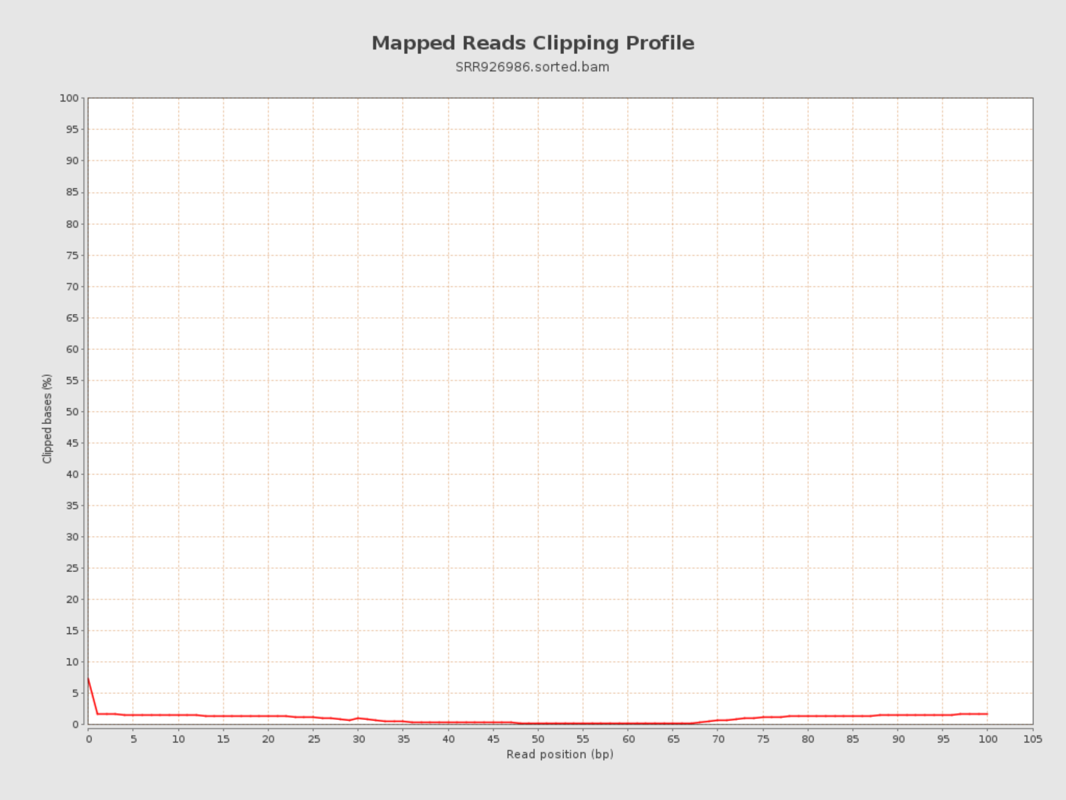
8. Results : Mapped Reads Nucleotide Content



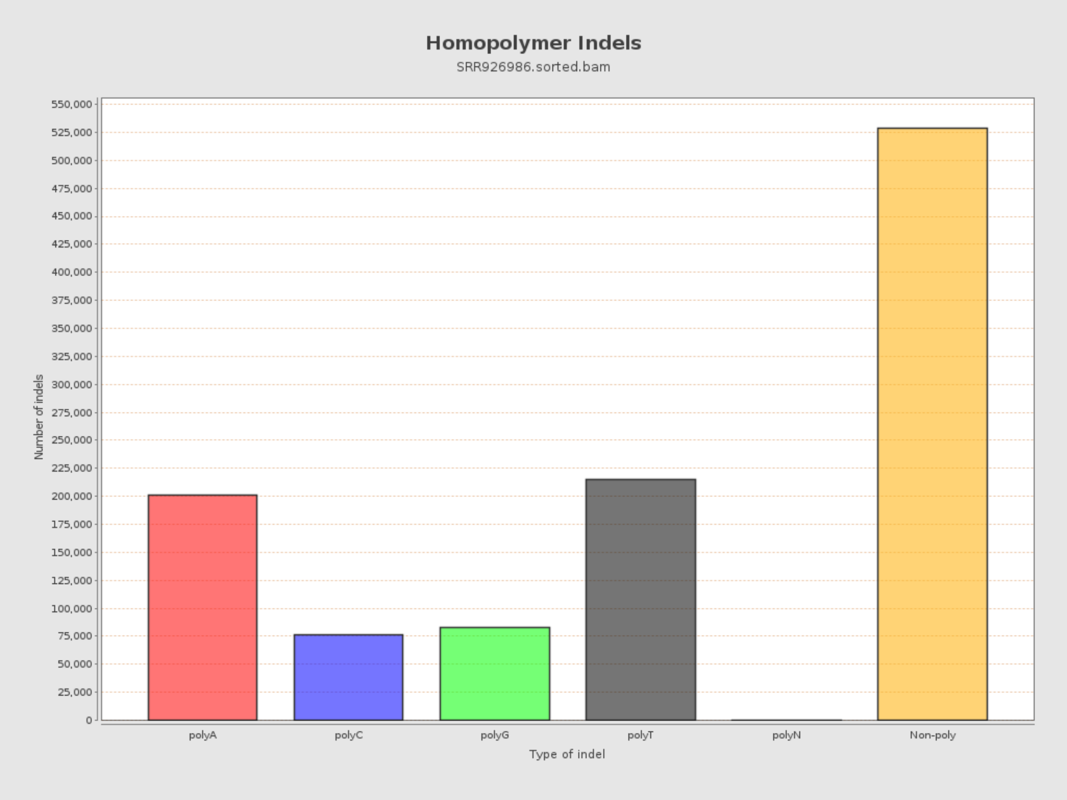
9. Results : Mapped Reads GC-content Distribution



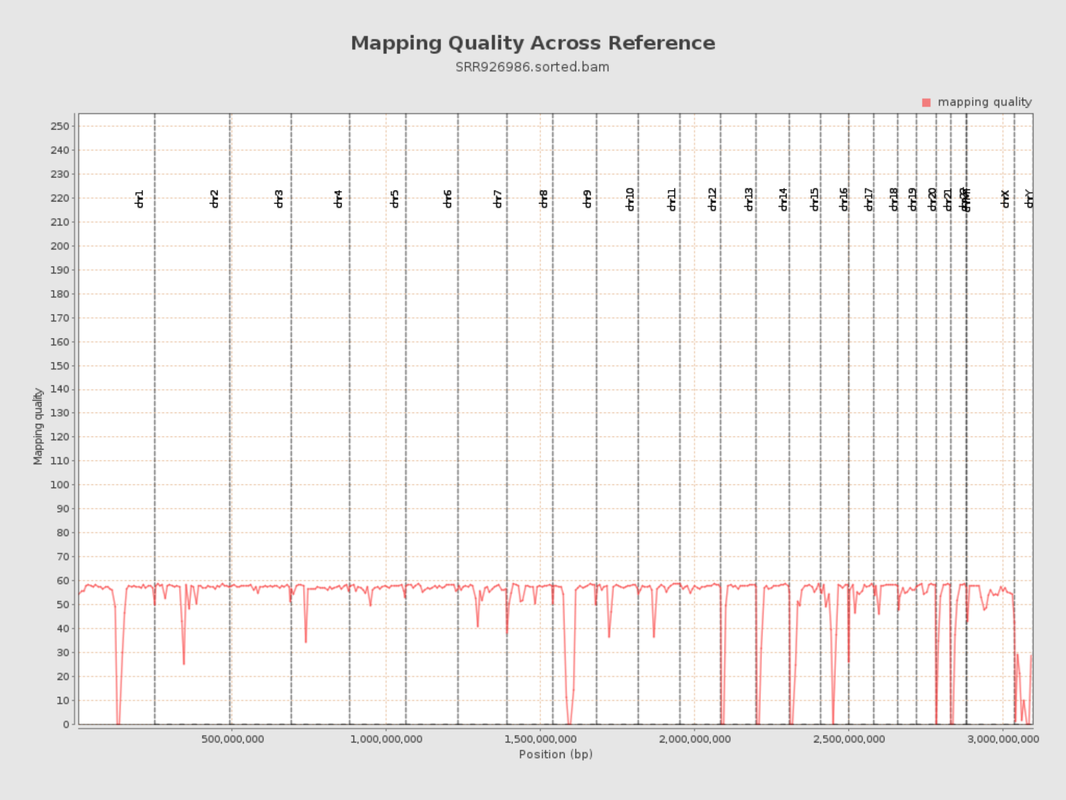
10. Results : Mapped Reads Clipping Profile



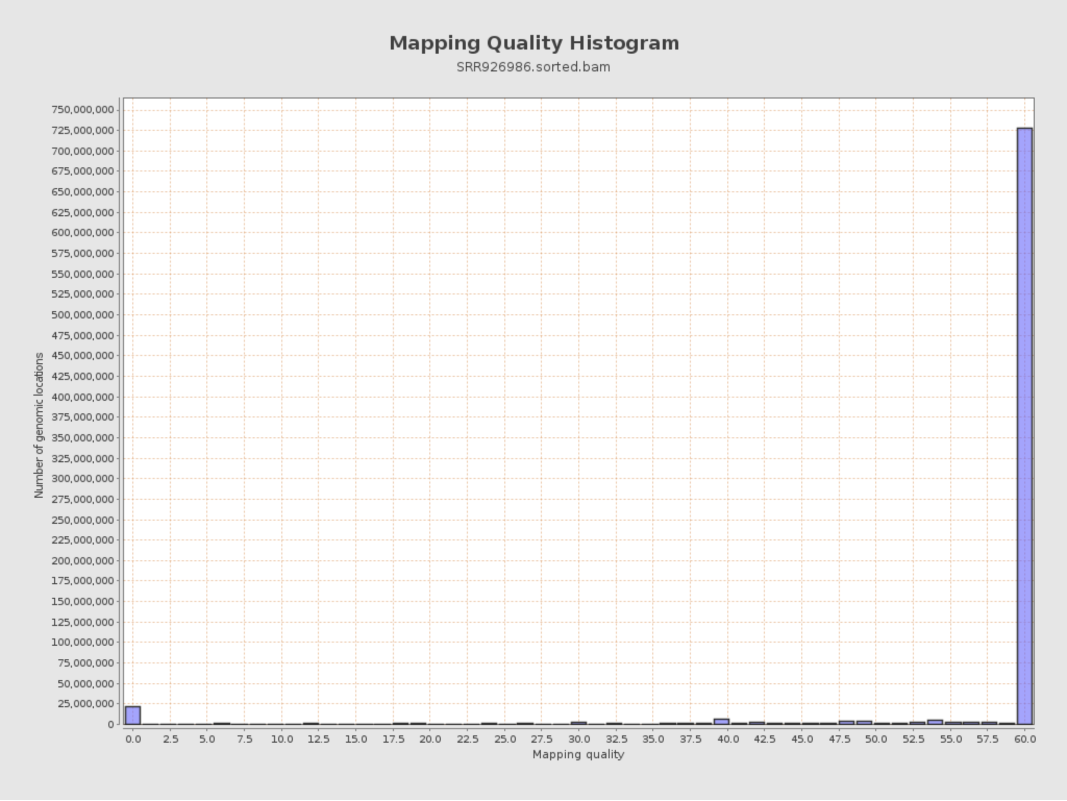
11. Results : Homopolymer Indels



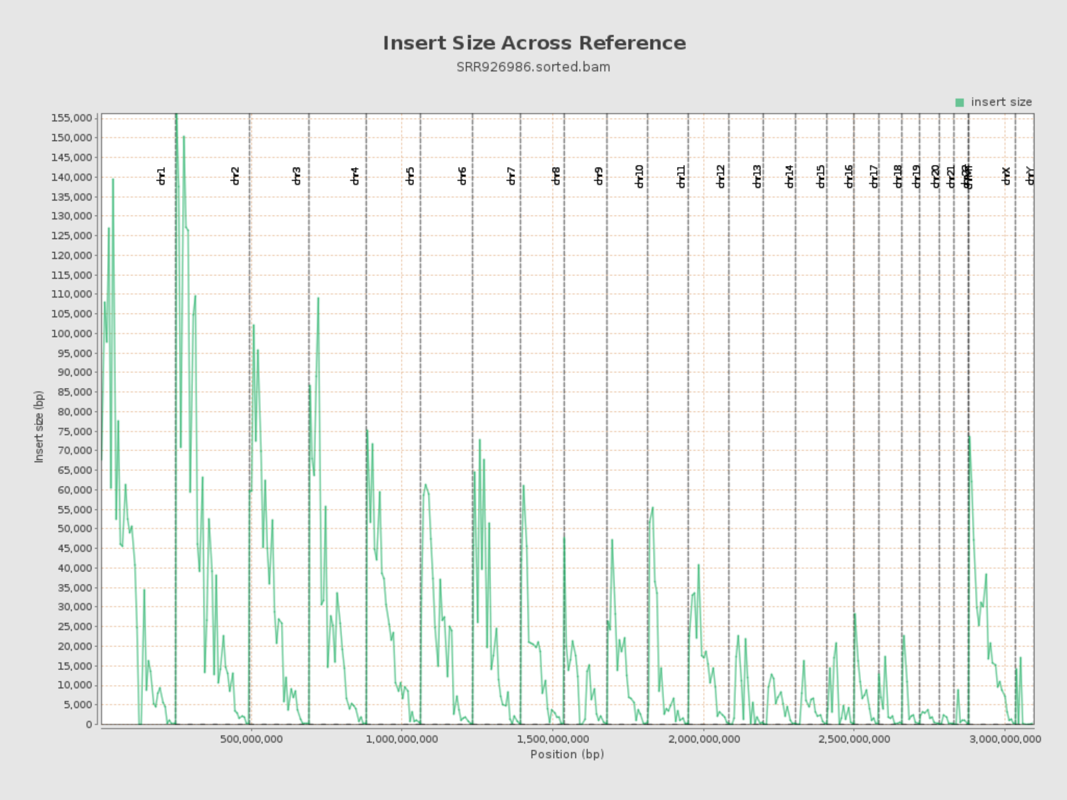
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram