Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 23:26:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927051.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_SRR927051 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927051_1.fastq.gz SRR927051_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 23:26:38 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927051.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,551,060
Mapped reads	20,809,721 / 96.56%
Unmapped reads	741,339 / 3.44%
Mapped paired reads	20,809,721 / 96.56%
Mapped reads, first in pair	10,445,925 / 48.47%
Mapped reads, second in pair	10,363,796 / 48.09%
Mapped reads, both in pair	20,368,656 / 94.51%
Mapped reads, singletons	441,065 / 2.05%
Secondary alignments	0
Supplementary alignments	461,932 / 2.14%
Read min/max/mean length	30 / 101 / 101.88
Duplicated reads (estimated)	1,887,675 / 8.76%
Duplication rate	7.19%
Clipped reads	10,853,198 / 50.36%

2.2. ACGT Content

Number/percentage of A's	520,770,635 / 28.35%
Number/percentage of C's	350,024,954 / 19.05%
Number/percentage of T's	541,861,327 / 29.5%
Number/percentage of G's	424,279,834 / 23.09%
Number/percentage of N's	188,617 / 0.01%

GC Percentage	42.15%

2.3. Coverage

Mean	0.5939
Standard Deviation	2.3314

2.4. Mapping Quality

Mean Mapping Quality	52.85

2.5. Insert size

Mean	211,074.38
Standard Deviation	4,500,263.36
P25/Median/P75	138 / 182 / 244

2.6. Mismatches and indels

General error rate	1.1%
Mismatches	19,673,883
Insertions	299,561
Mapped reads with at least one insertion	1.42%
Deletions	903,716
Mapped reads with at least one deletion	4.24%
Homopolymer indels	51.44%

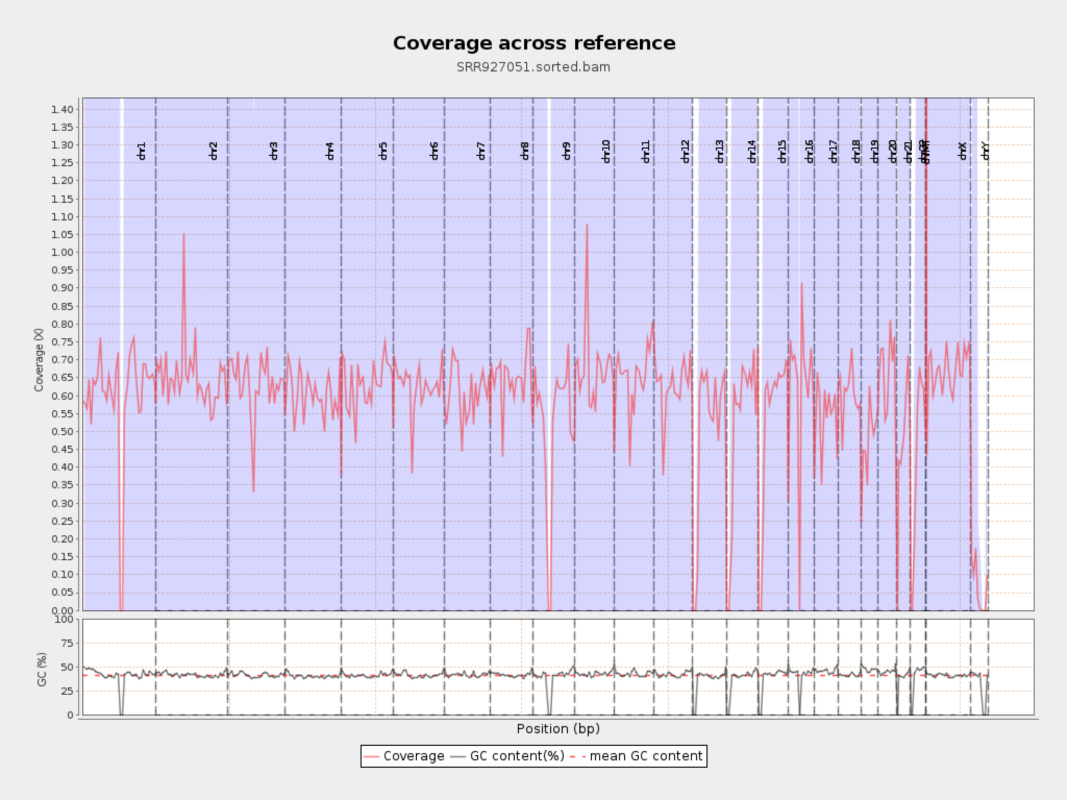
2.7. Chromosome stats

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

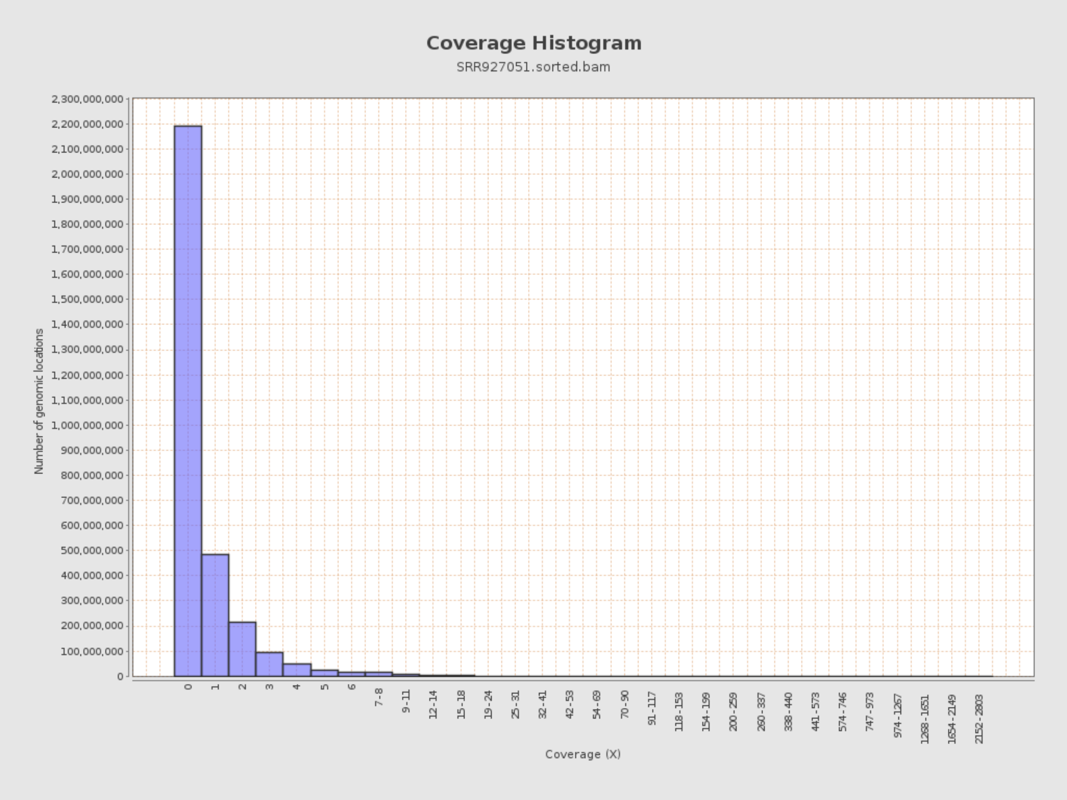
		bases	coverage	deviation
chr1	249250621	149488576	0.5998	3.0019
chr2	243199373	158806174	0.653	3.8077
chr3	198022430	125072691	0.6316	1.3485
chr4	191154276	116259792	0.6082	1.8961
chr5	180915260	114727592	0.6342	1.3277
chr6	171115067	107273622	0.6269	1.3949
chr7	159138663	96398768	0.6058	1.8364
chr8	146364022	95329816	0.6513	1.5489
chr9	141213431	73595028	0.5212	2.586
chr10	135534747	91375468	0.6742	5.0508
chr11	135006516	88156725	0.653	1.8566
chr12	133851895	84404789	0.6306	1.3402
chr13	115169878	57760366	0.5015	1.1782
chr14	107349540	55543229	0.5174	1.2733
chr15	102531392	53394782	0.5208	1.253
chr16	90354753	55963890	0.6194	3.3006
chr17	81195210	44812503	0.5519	1.8133
chr18	78077248	47174780	0.6042	2.5811
chr19	59128983	28466500	0.4814	1.8463
chr20	63025520	42480688	0.674	1.484
chr21	48129895	22804975	0.4738	1.6491
chr22	51304566	21712888	0.4232	1.1671
chrMT	16571	214630	12.9521	8.913
chrX	155270560	103325587	0.6655	1.5422

chrY	59373566	3908859	0.0658	1.5994

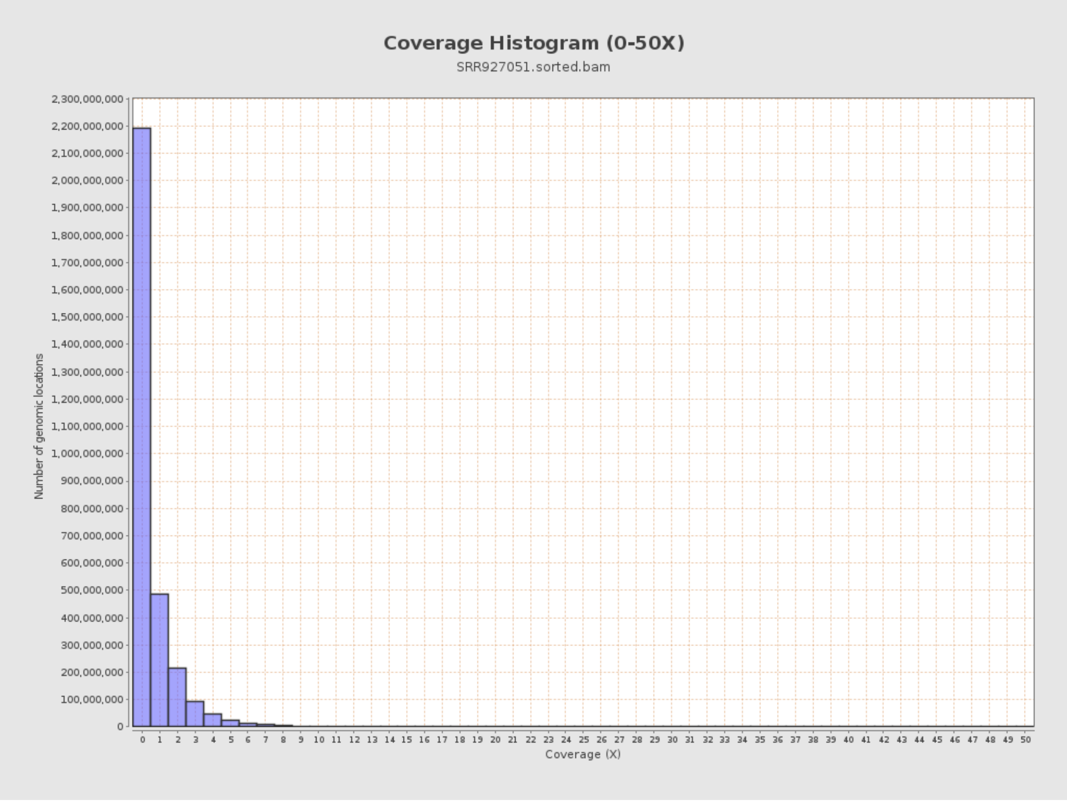
3. Results : Coverage across reference



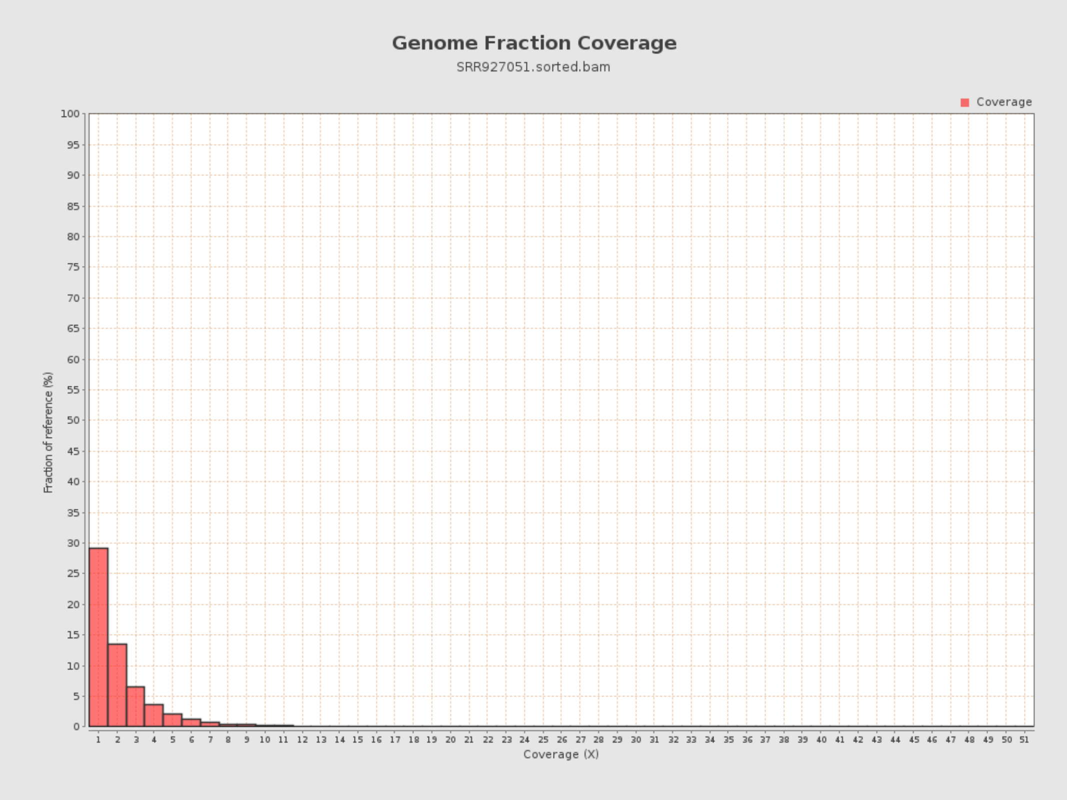
4. Results : Coverage Histogram



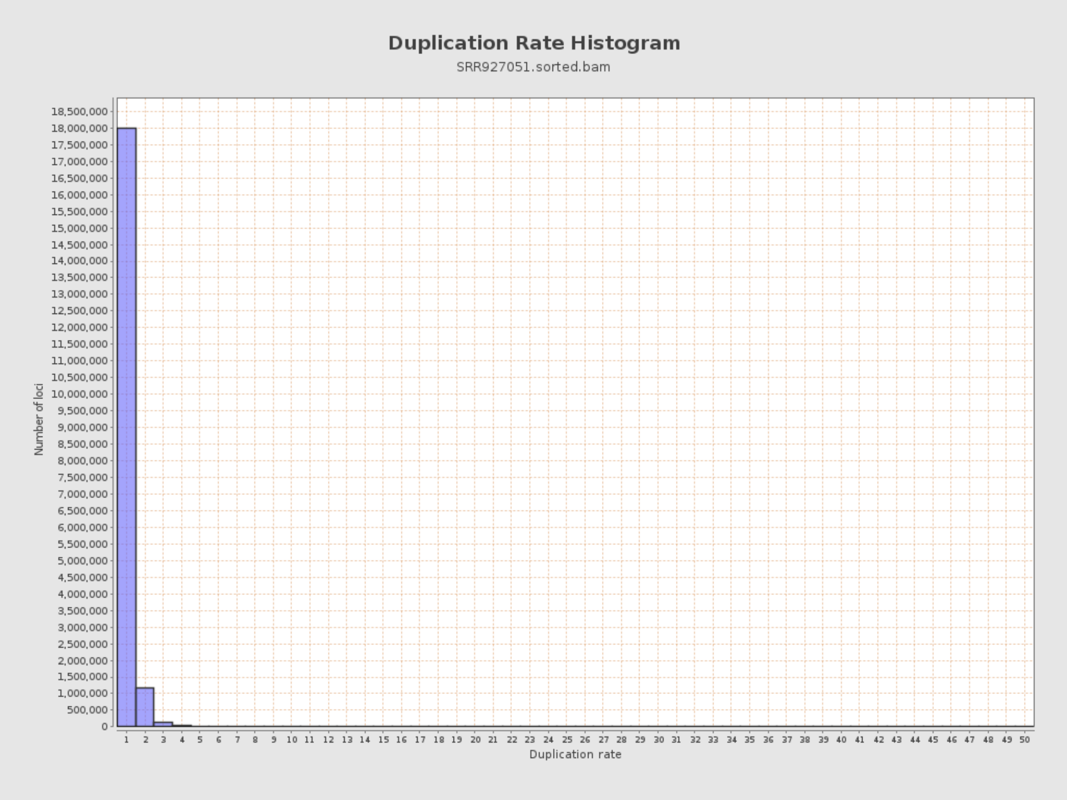
5. Results : Coverage Histogram (0-50X)



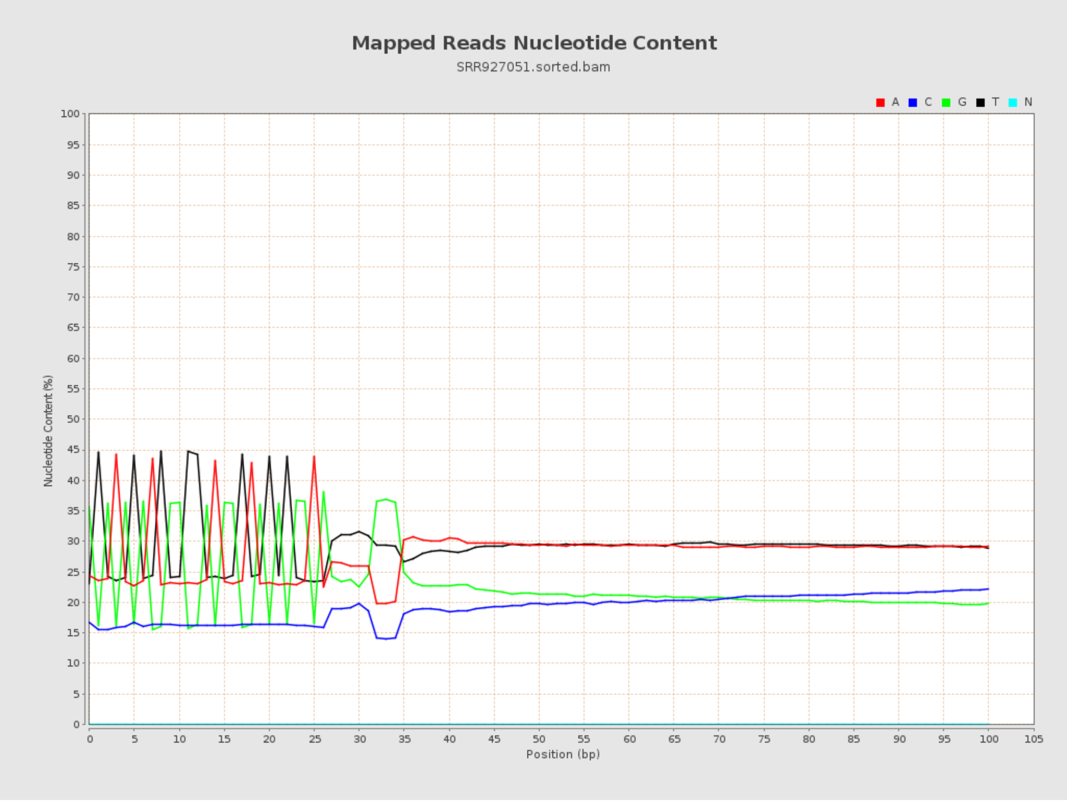
6. Results : Genome Fraction Coverage



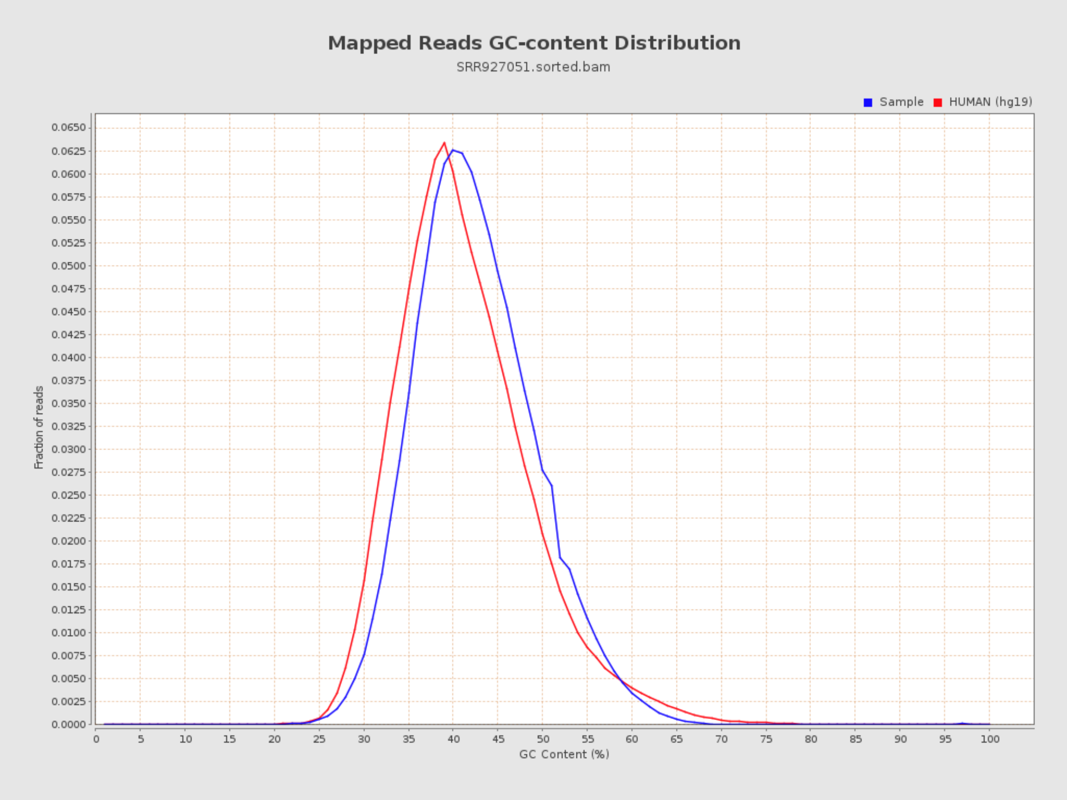
7. Results : Duplication Rate Histogram



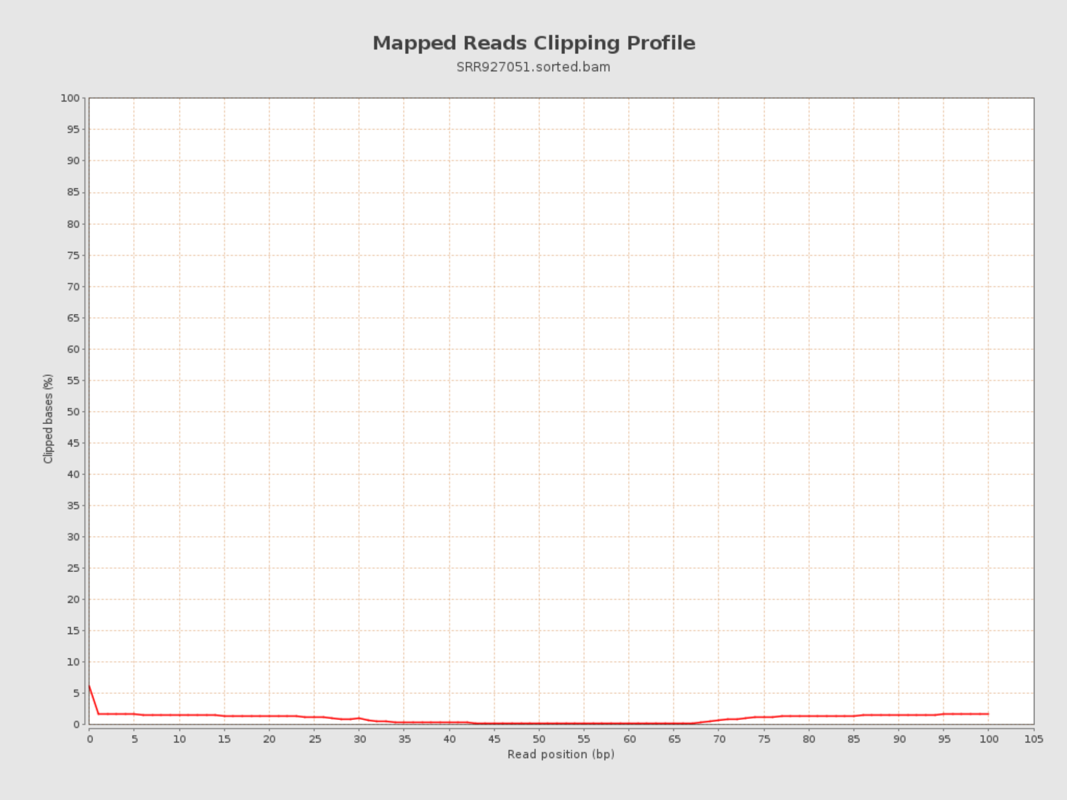
8. Results : Mapped Reads Nucleotide Content



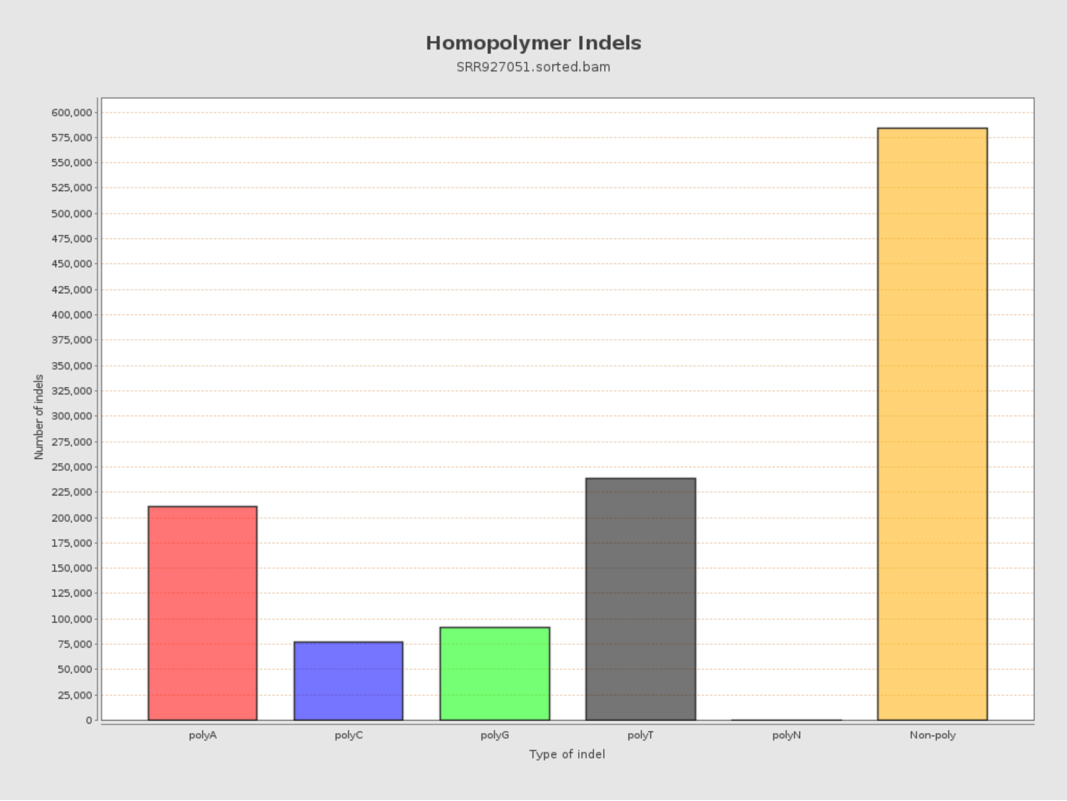
9. Results : Mapped Reads GC-content Distribution



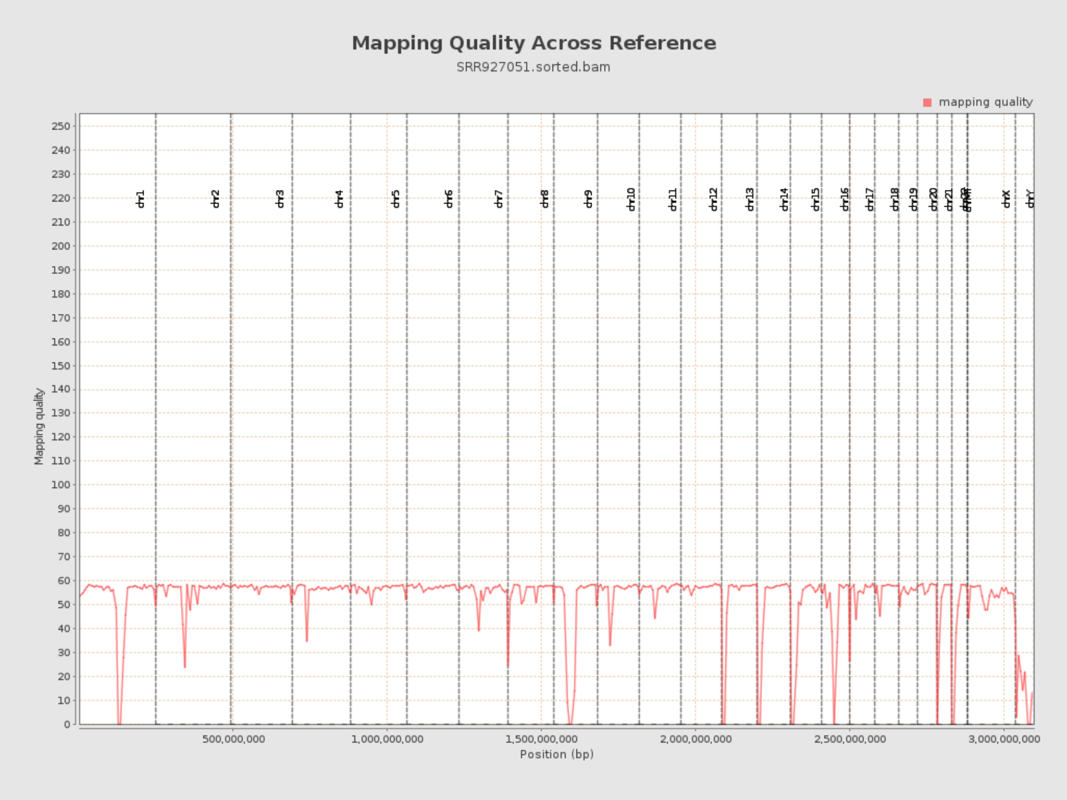
10. Results : Mapped Reads Clipping Profile



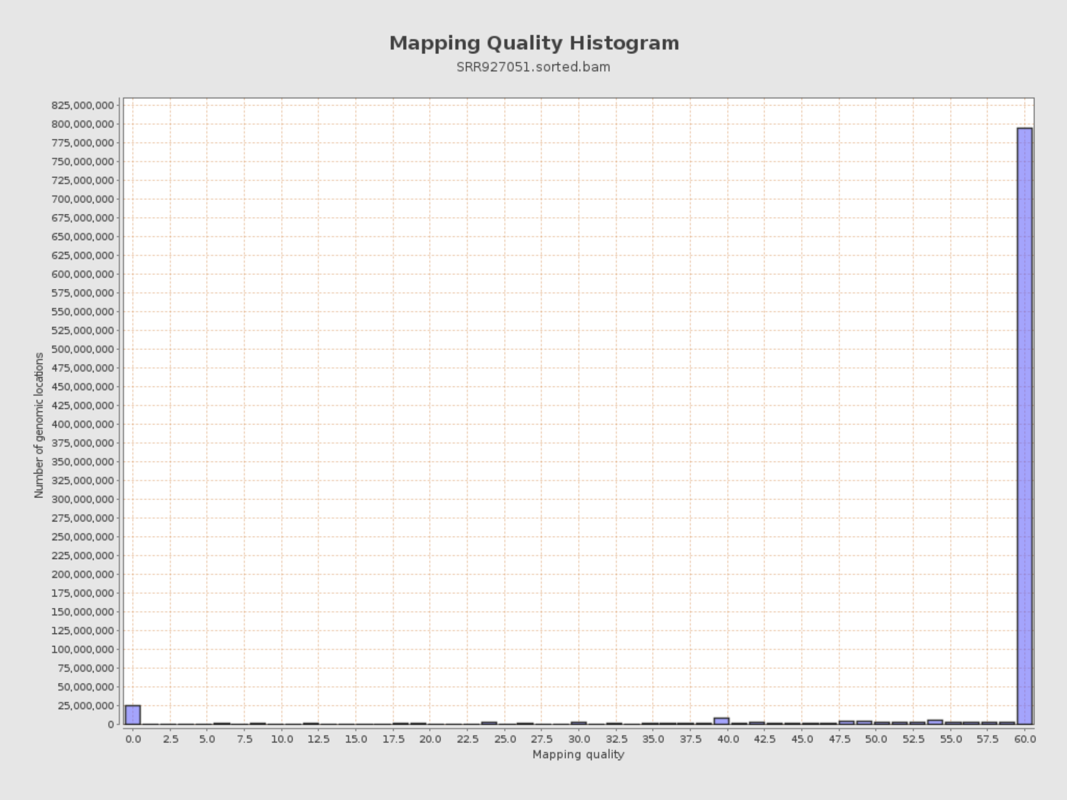
11. Results : Homopolymer Indels



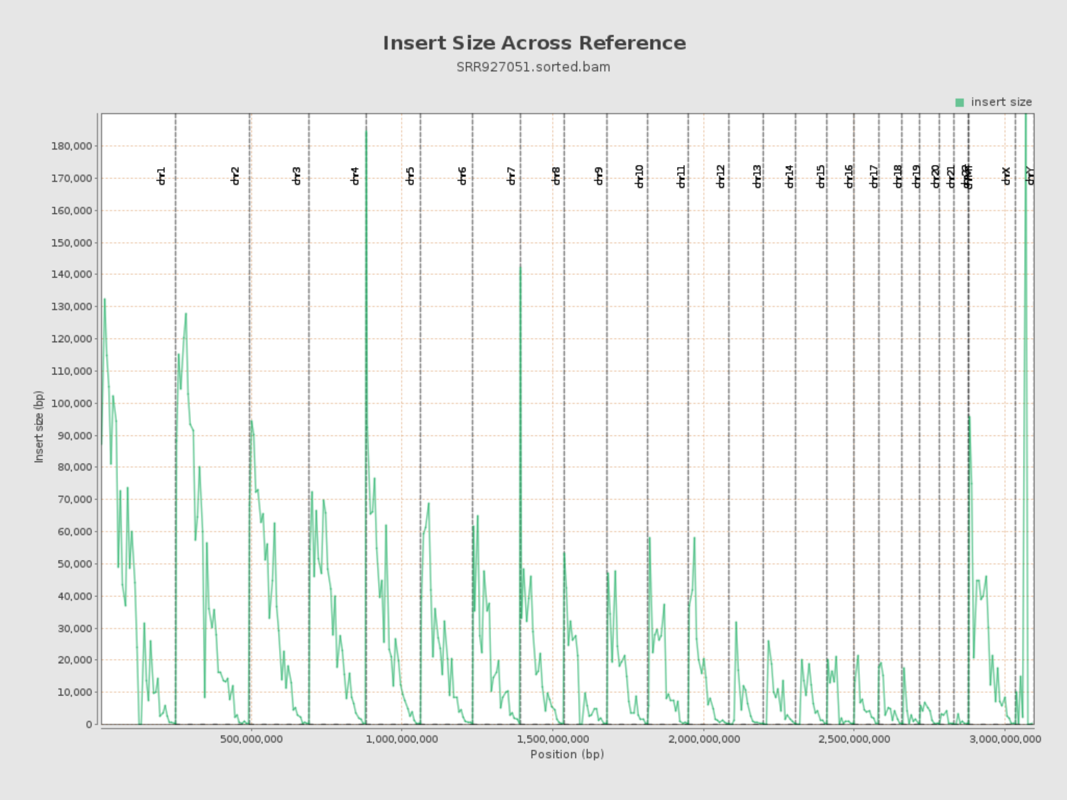
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram