Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/24 08:50:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR927023.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_SRR927023 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927023_1.fastq.gz SRR927023_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 24 08:50:20 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR927023.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	35,718,702
Mapped reads	35,194,038 / 98.53%
Unmapped reads	524,664 / 1.47%
Mapped paired reads	35,194,038 / 98.53%
Mapped reads, first in pair	17,645,740 / 49.4%
Mapped reads, second in pair	17,548,298 / 49.13%
Mapped reads, both in pair	34,885,034 / 97.67%
Mapped reads, singletons	309,004 / 0.87%
Secondary alignments	0
Supplementary alignments	321,701 / 0.9%
Read min/max/mean length	30 / 101 / 101.37
Duplicated reads (estimated)	2,738,394 / 7.67%
Duplication rate	5.75%
Clipped reads	8,960,203 / 25.09%

2.2. ACGT Content

Number/percentage of A's	955,057,290 / 28.76%
Number/percentage of C's	659,728,577 / 19.86%
Number/percentage of T's	966,444,833 / 29.1%
Number/percentage of G's	739,404,470 / 22.26%
Number/percentage of N's	717,539 / 0.02%

GC Percentage	42.13%

2.3. Coverage

Mean	1.0737
Standard Deviation	5.157

2.4. Mapping Quality

Mean Mapping Quality	53.51

2.5. Insert size

Mean	96,245.84
Standard Deviation	3,039,352.47
P25/Median/P75	155 / 198 / 264

2.6. Mismatches and indels

General error rate	0.95%
Mismatches	30,506,027
Insertions	535,732
Mapped reads with at least one insertion	1.5%
Deletions	1,755,164
Mapped reads with at least one deletion	4.86%
Homopolymer indels	52.99%

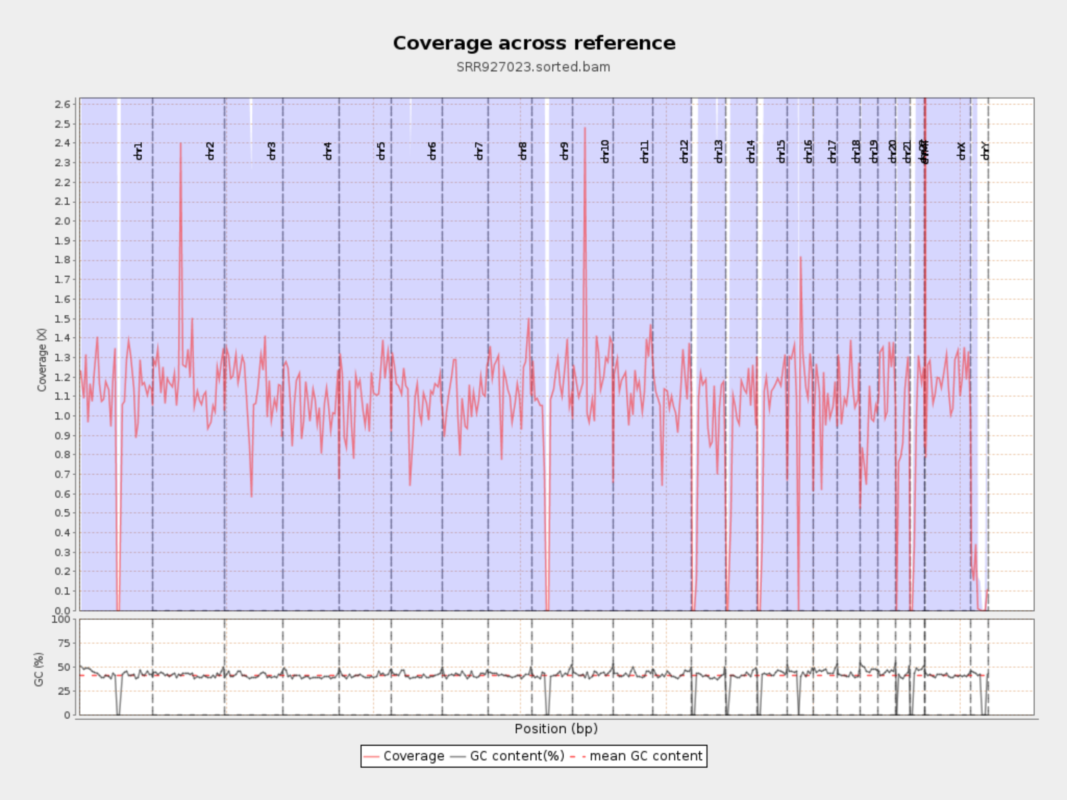
2.7. Chromosome stats

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

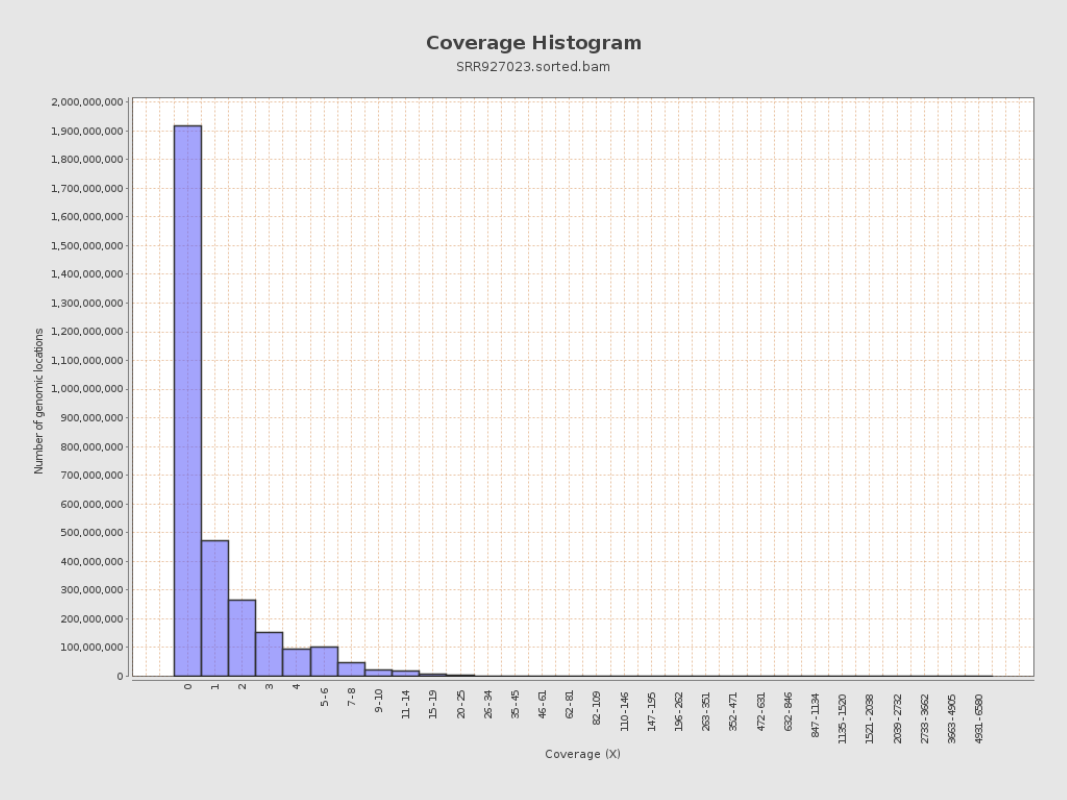
		bases	coverage	deviation
chr1	249250621	270556519	1.0855	6.6071
chr2	243199373	294708043	1.2118	8.1814
chr3	198022430	226650364	1.1446	2.2075
chr4	191154276	203960856	1.067	3.3331
chr5	180915260	200619895	1.1089	2.1015
chr6	171115067	188294804	1.1004	2.1641
chr7	159138663	171711296	1.079	3.26
chr8	146364022	171218530	1.1698	2.5992
chr9	141213431	142159295	1.0067	5.952
chr10	135534747	171469323	1.2651	13.7761
chr11	135006516	158923472	1.1772	5.356
chr12	133851895	146885843	1.0974	2.1182
chr13	115169878	100116266	0.8693	1.8512
chr14	107349540	98145366	0.9143	1.9945
chr15	102531392	96469460	0.9409	1.9985
chr16	90354753	103837417	1.1492	6.7038
chr17	81195210	84901391	1.0456	2.7212
chr18	78077248	89847273	1.1507	5.9705
chr19	59128983	53157055	0.899	3.9433
chr20	63025520	76918509	1.2204	2.4936
chr21	48129895	42971931	0.8928	2.9465
chr22	51304566	40814199	0.7955	1.9547
chrMT	16571	551938	33.3075	26.7877
chrX	155270560	182981143	1.1785	2.8297

chrY	59373566	5982855	0.1008	3.2802

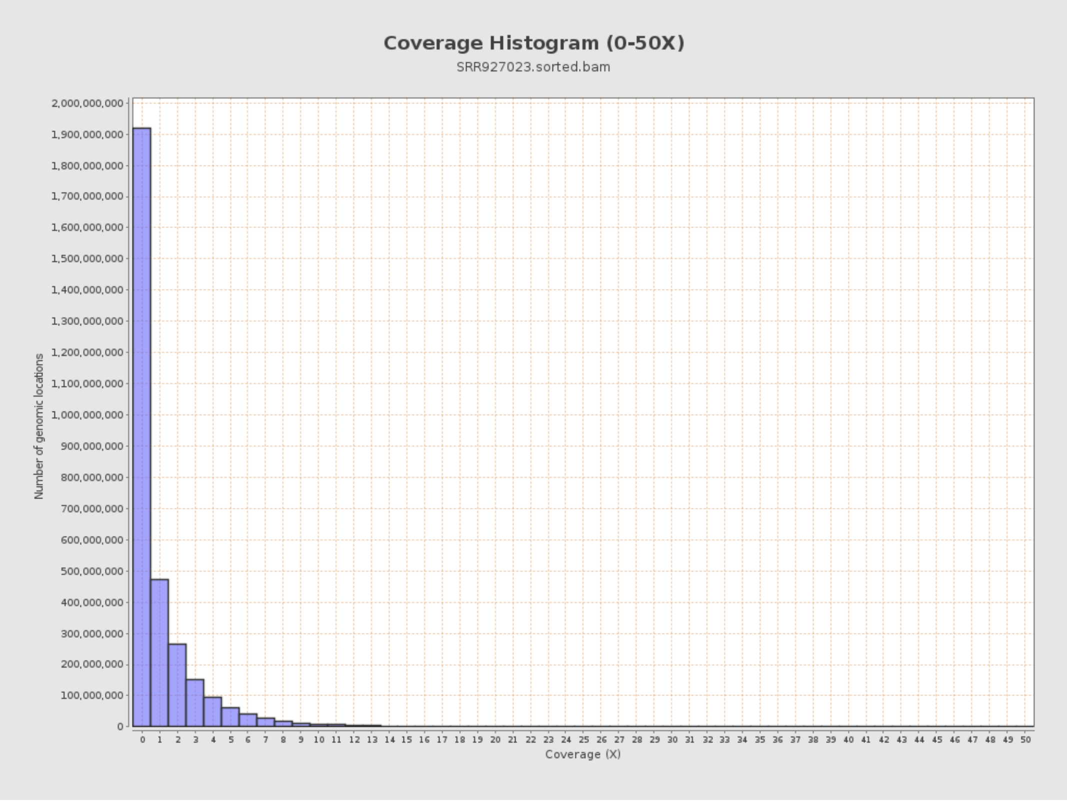
3. Results : Coverage across reference



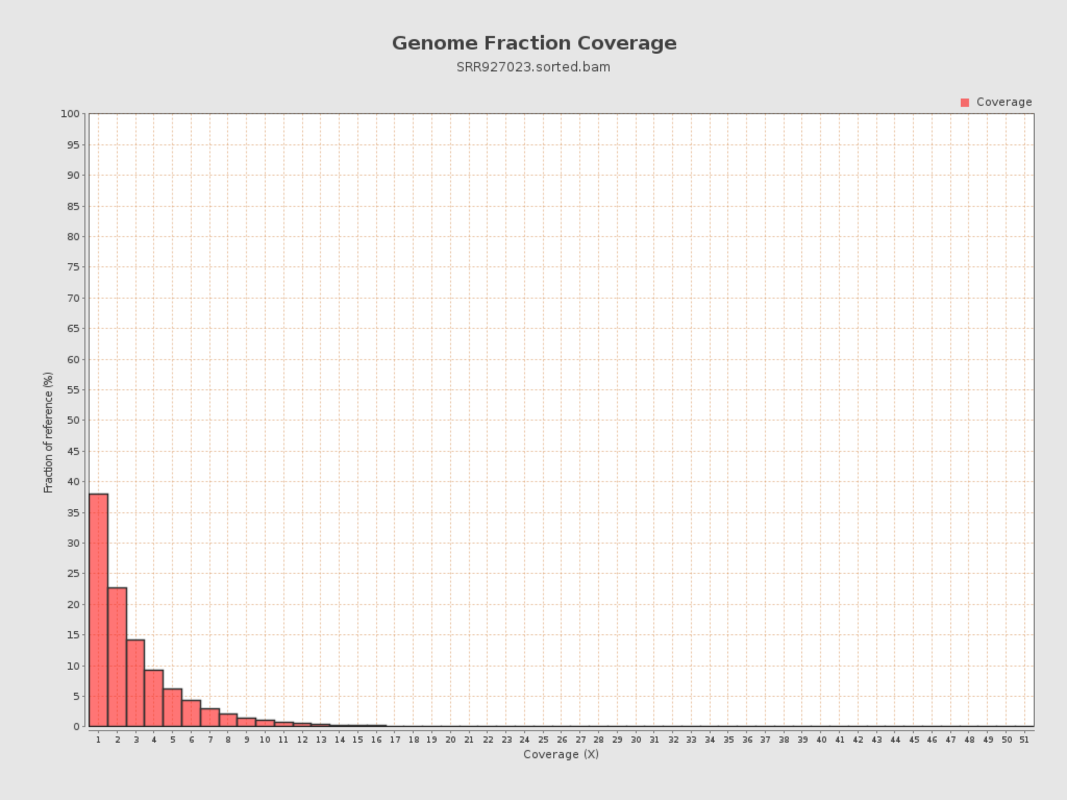
4. Results : Coverage Histogram



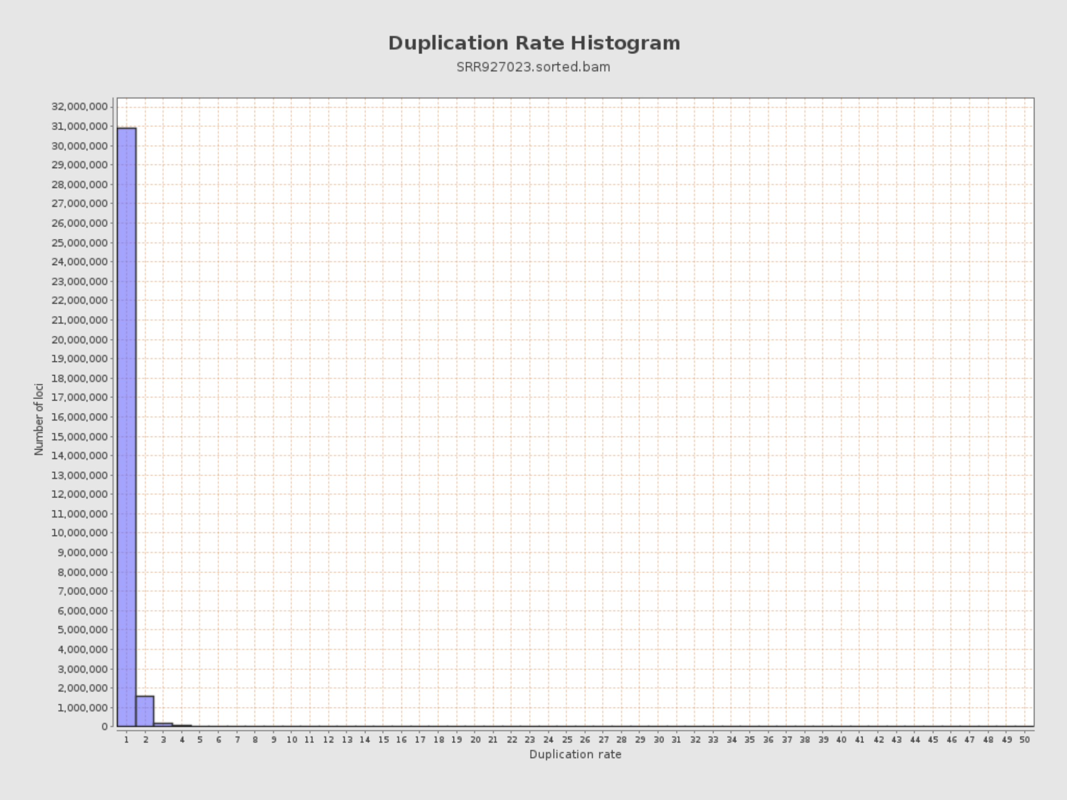
5. Results : Coverage Histogram (0-50X)



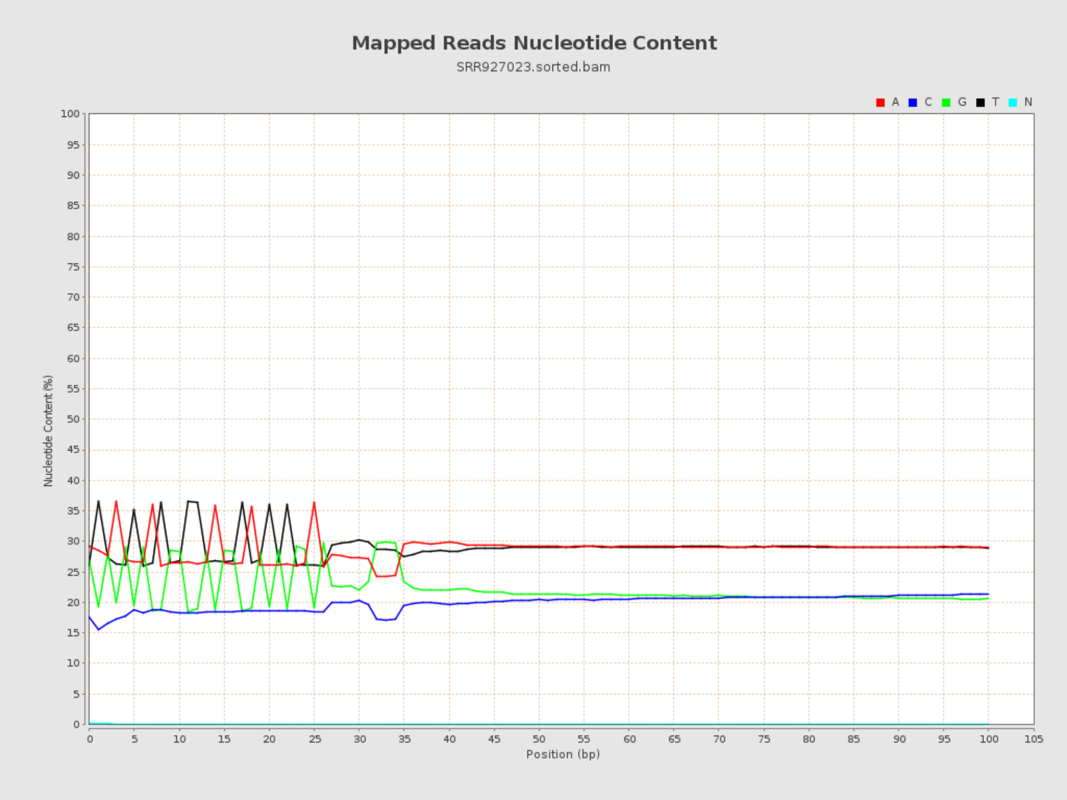
6. Results : Genome Fraction Coverage



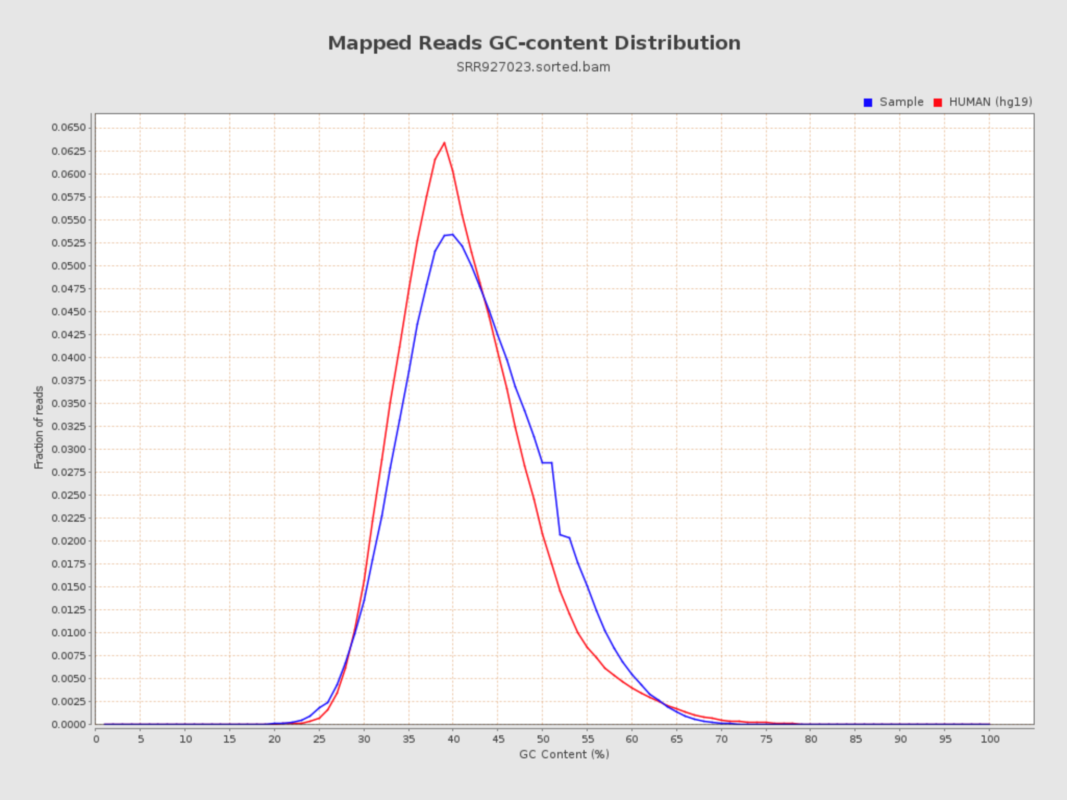
7. Results : Duplication Rate Histogram



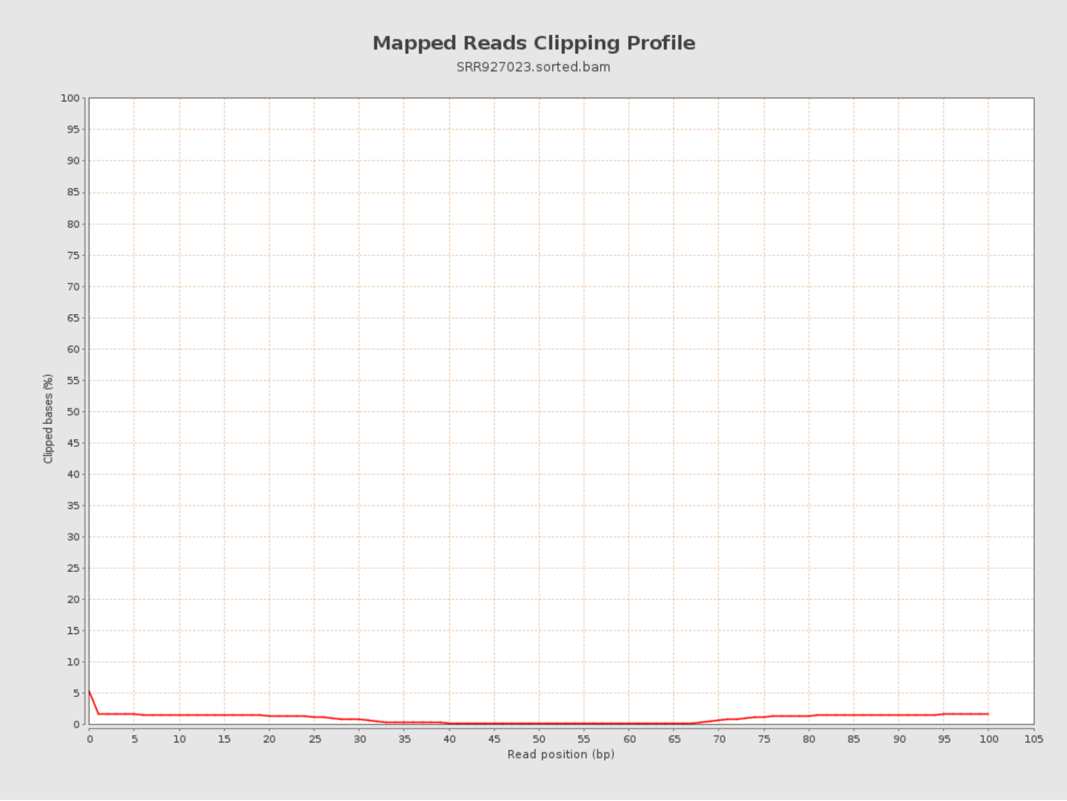
8. Results : Mapped Reads Nucleotide Content



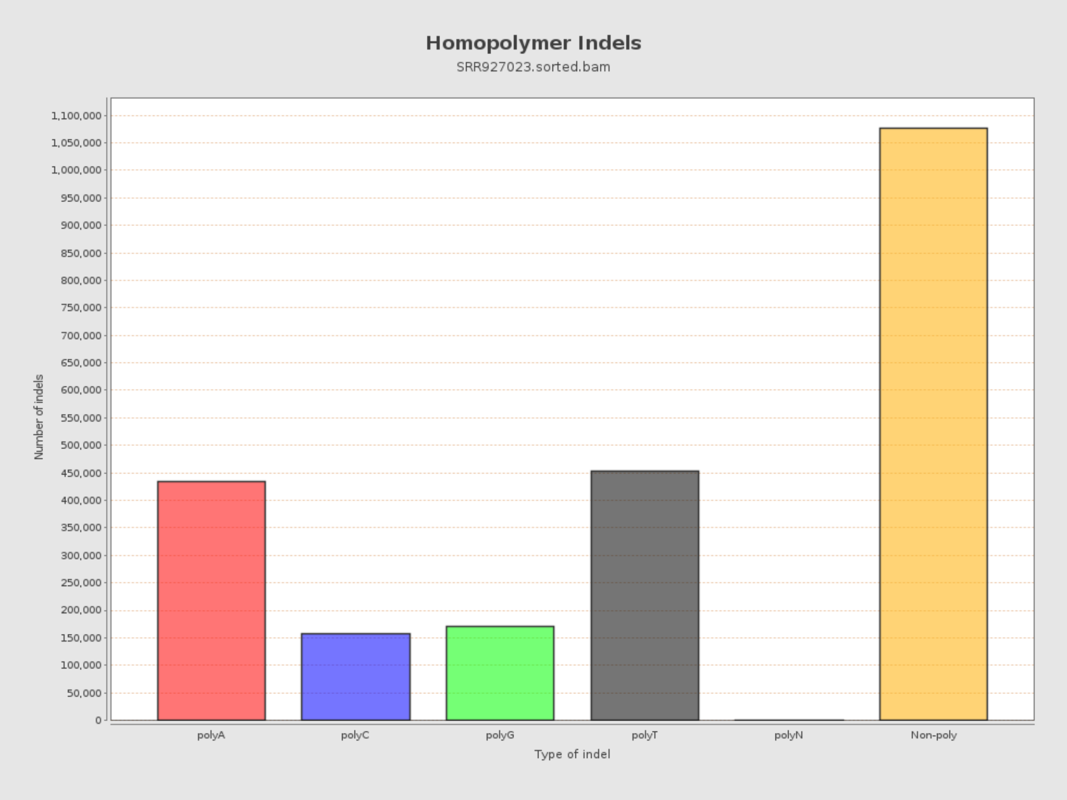
9. Results : Mapped Reads GC-content Distribution



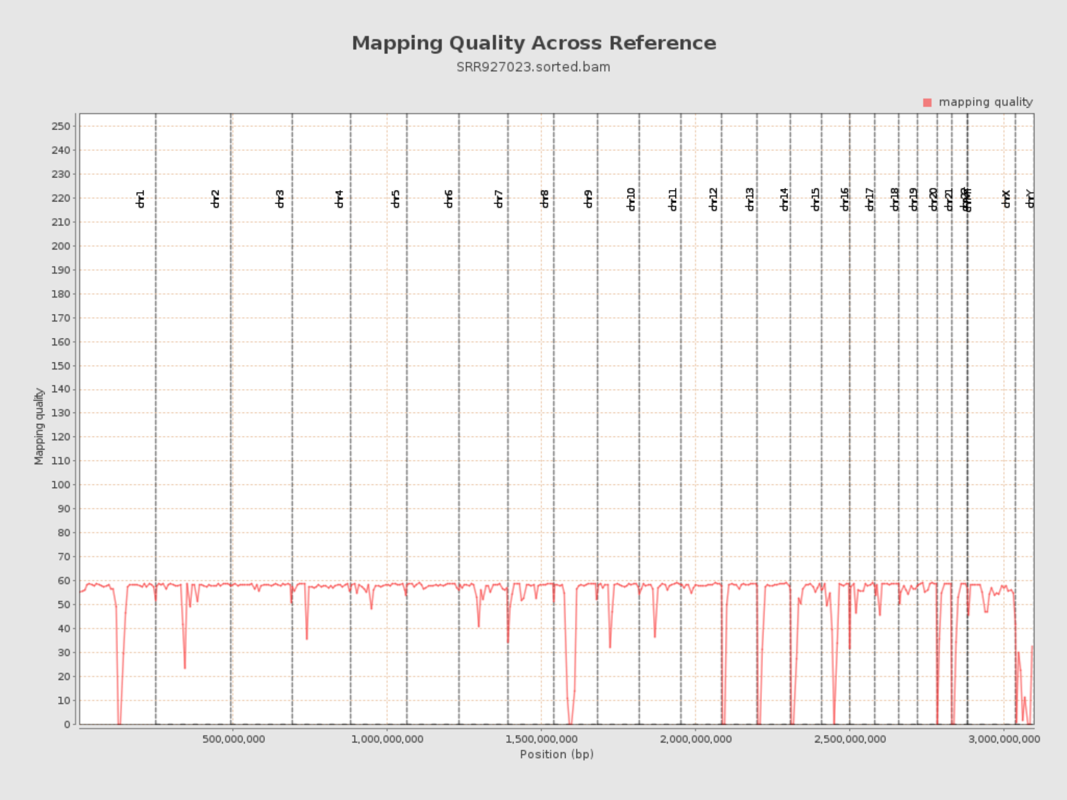
10. Results : Mapped Reads Clipping Profile



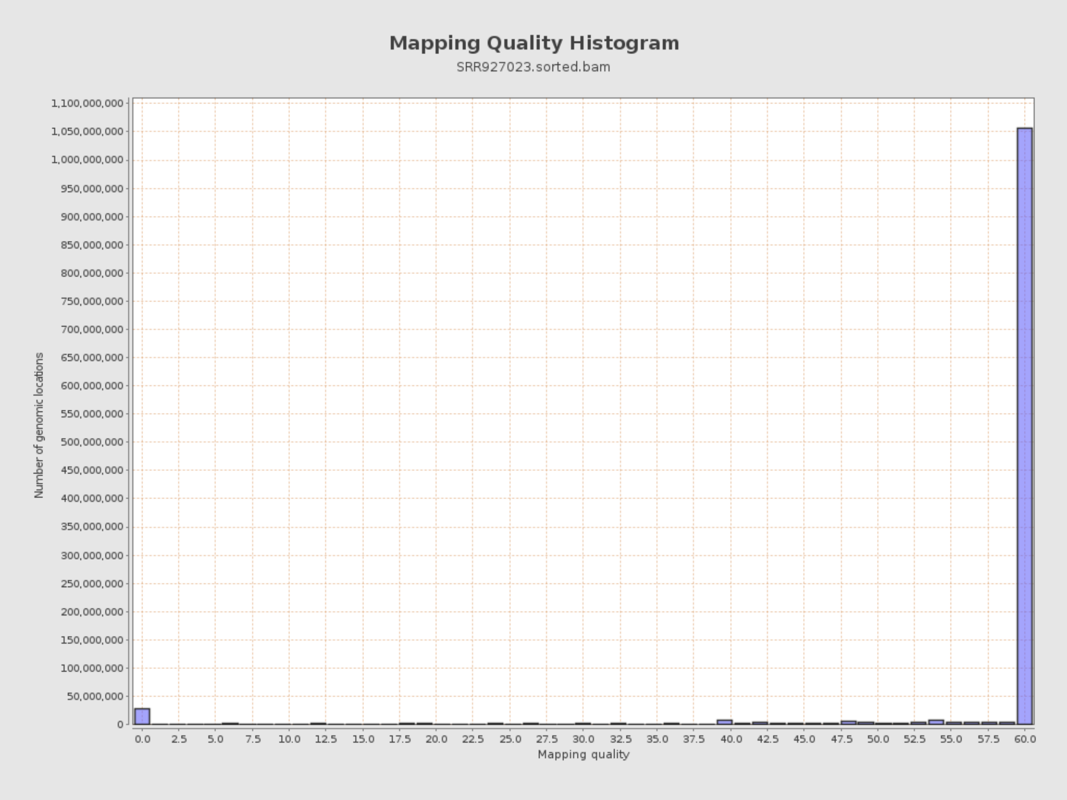
11. Results : Homopolymer Indels



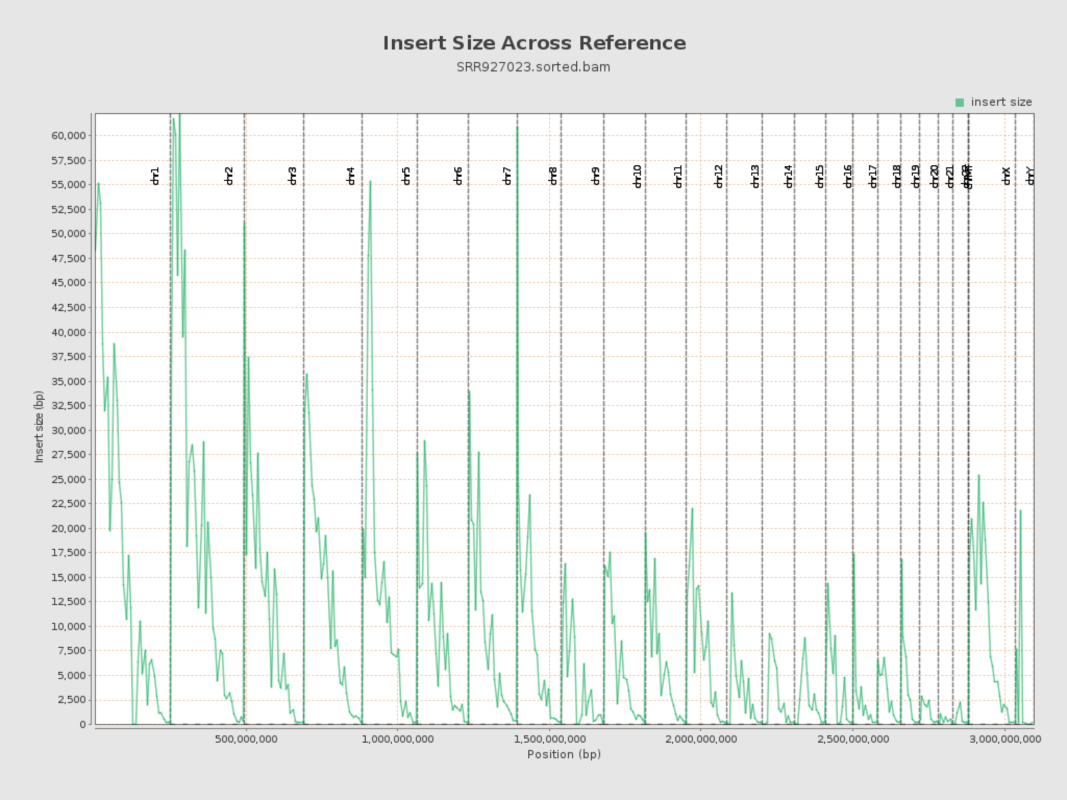
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram