Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/23 19:33:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR926992.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_SRR926992 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926992_1.fastq.gz SRR926992_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 23 19:33:44 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR926992.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	37,371,514
Mapped reads	36,804,429 / 98.48%
Unmapped reads	567,085 / 1.52%
Mapped paired reads	36,804,429 / 98.48%
Mapped reads, first in pair	18,469,460 / 49.42%
Mapped reads, second in pair	18,334,969 / 49.06%
Mapped reads, both in pair	36,509,690 / 97.69%
Mapped reads, singletons	294,739 / 0.79%
Secondary alignments	0
Supplementary alignments	529,883 / 1.42%
Read min/max/mean length	30 / 101 / 101.58
Duplicated reads (estimated)	2,877,088 / 7.7%
Duplication rate	6.03%
Clipped reads	8,589,230 / 22.98%

2.2. ACGT Content

Number/percentage of A's	996,862,924 / 28.39%
Number/percentage of C's	720,898,242 / 20.53%
Number/percentage of T's	1,008,429,091 / 28.72%
Number/percentage of G's	784,944,749 / 22.35%
Number/percentage of N's	316,755 / 0.01%

GC Percentage	42.88%

2.3. Coverage

Mean	1.1352
Standard Deviation	4.5052

2.4. Mapping Quality

Mean Mapping Quality	53.45

2.5. Insert size

Mean	134,260.06
Standard Deviation	3,560,595.11
P25/Median/P75	140 / 176 / 231

2.6. Mismatches and indels

General error rate	0.95%
Mismatches	32,476,770
Insertions	562,832
Mapped reads with at least one insertion	1.5%
Deletions	1,838,883
Mapped reads with at least one deletion	4.87%
Homopolymer indels	52.68%

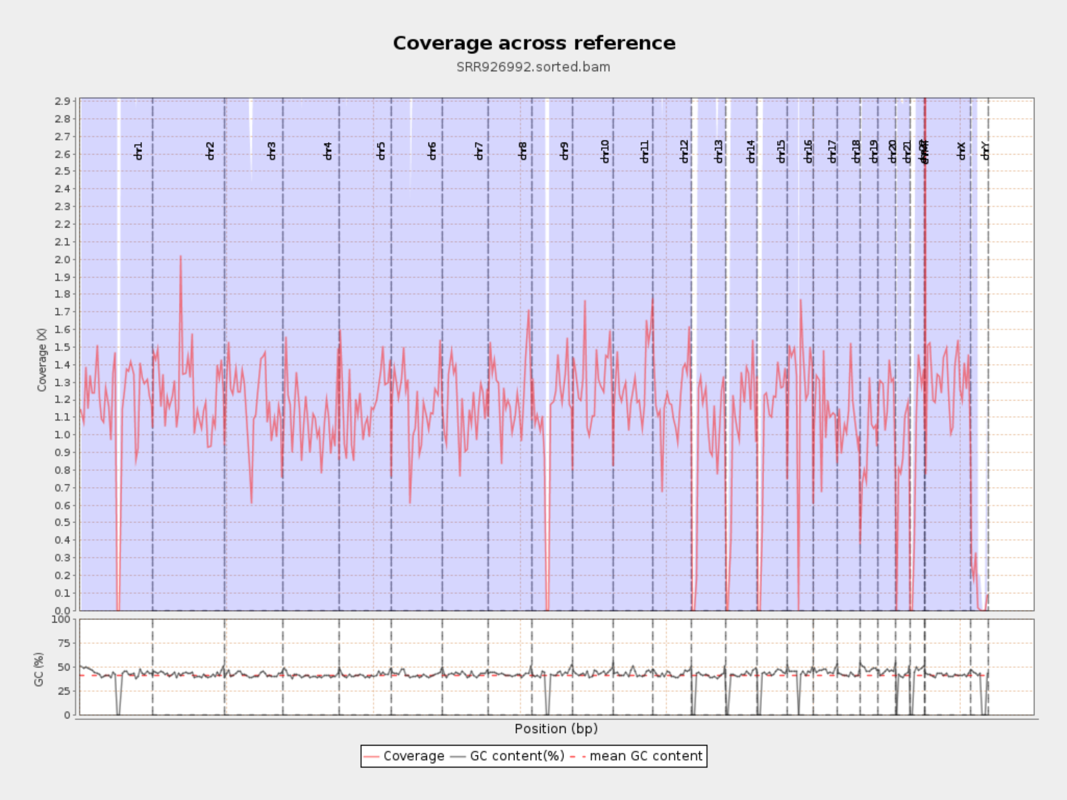
2.7. Chromosome stats

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

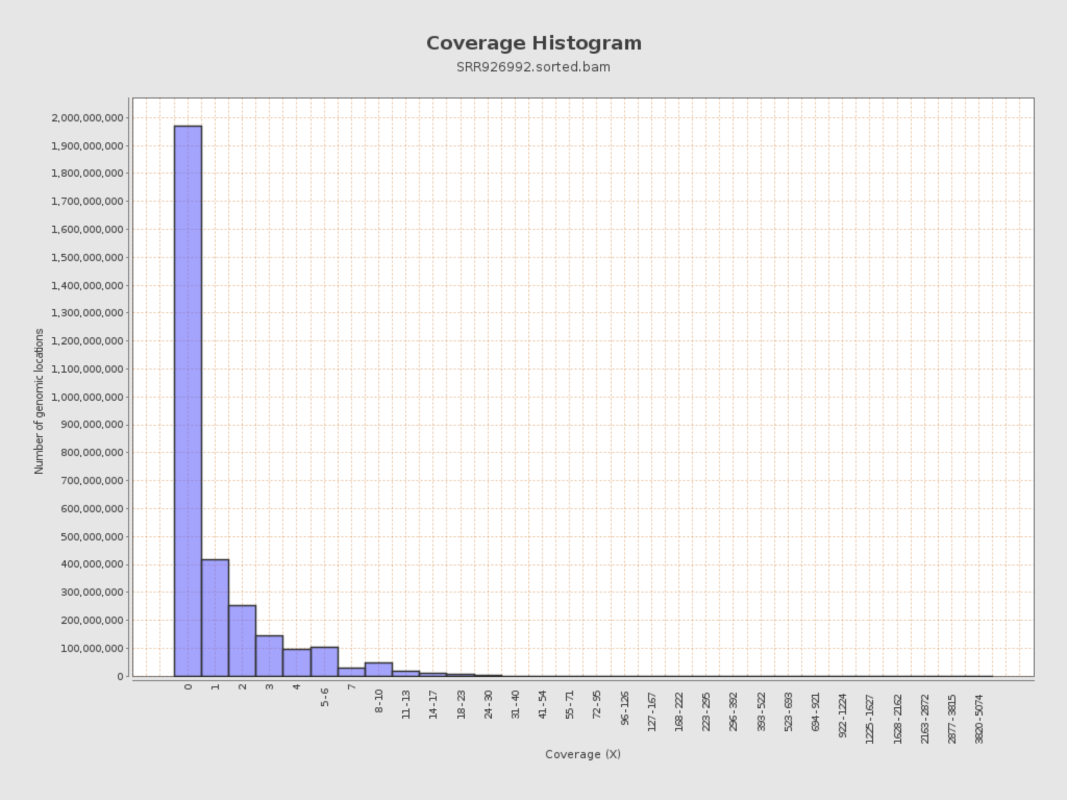
		bases	coverage	deviation
chr1	249250621	288924319	1.1592	6.1668
chr2	243199373	304449925	1.2519	6.8981
chr3	198022430	234641154	1.1849	2.3905
chr4	191154276	209350984	1.0952	3.6233
chr5	180915260	212988460	1.1773	2.3713
chr6	171115067	201189385	1.1758	3.2928
chr7	159138663	182211467	1.145	3.1657
chr8	146364022	182196266	1.2448	2.9784
chr9	141213431	150945409	1.0689	5.8721
chr10	135534747	177691902	1.311	6.8745
chr11	135006516	171972776	1.2738	6.3606
chr12	133851895	159869076	1.1944	2.7801
chr13	115169878	107348254	0.9321	2.1715
chr14	107349540	107074576	0.9974	2.299
chr15	102531392	103724133	1.0116	2.3652
chr16	90354753	115188290	1.2748	6.3447
chr17	81195210	91213282	1.1234	4.6583
chr18	78077248	86044968	1.102	5.8924
chr19	59128983	55258386	0.9345	3.7998
chr20	63025520	77655974	1.2321	2.7636
chr21	48129895	41441150	0.861	3.7783
chr22	51304566	45493859	0.8867	2.3733
chrMT	16571	205729	12.415	11.1508
chrX	155270560	200892979	1.2938	3.3212

chrY	59373566	6106070	0.1028	3.3831

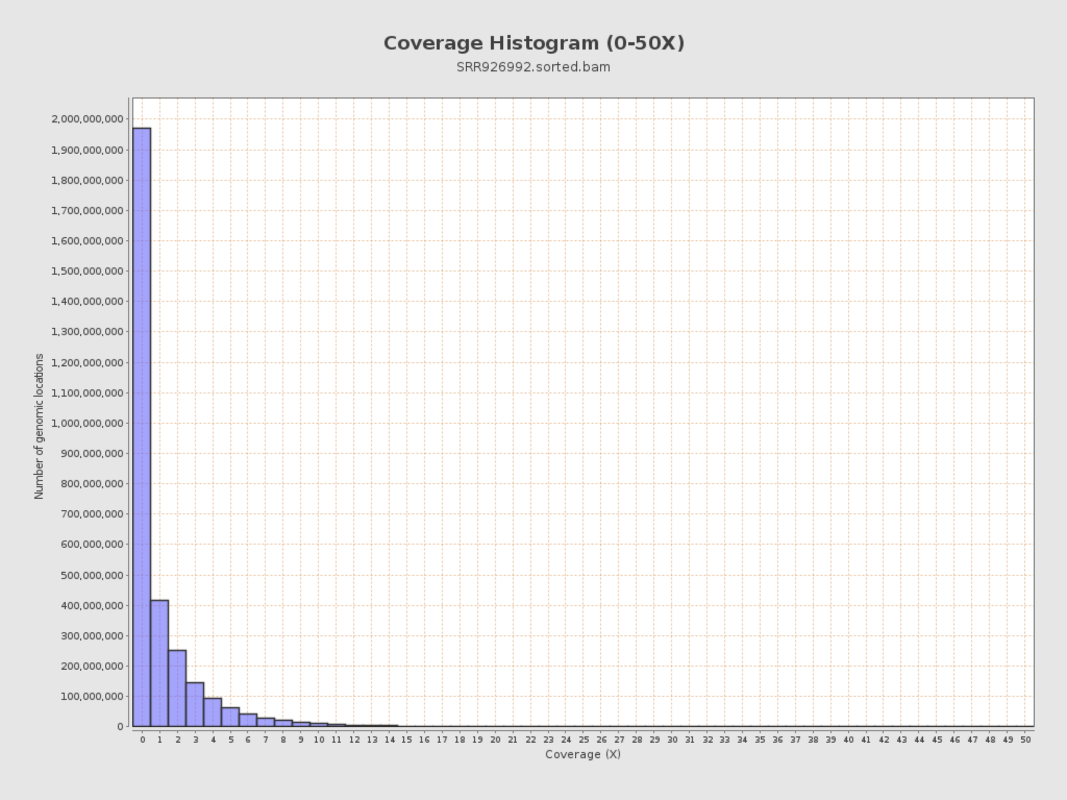
3. Results : Coverage across reference



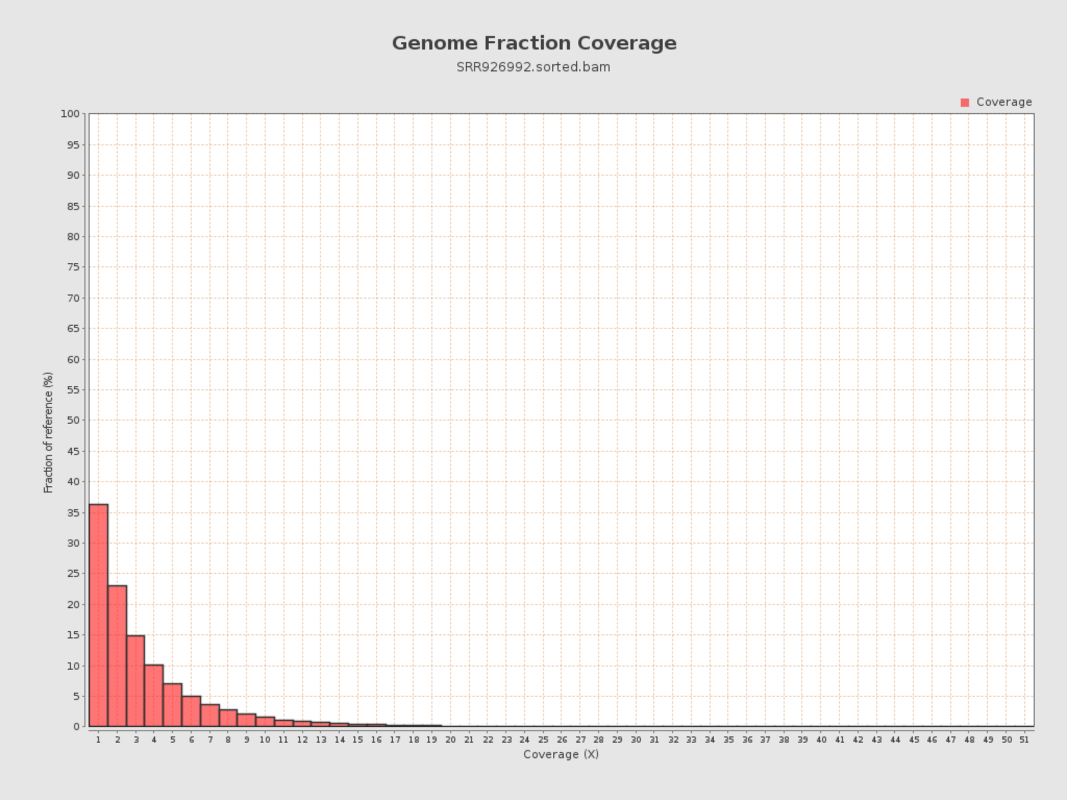
4. Results : Coverage Histogram



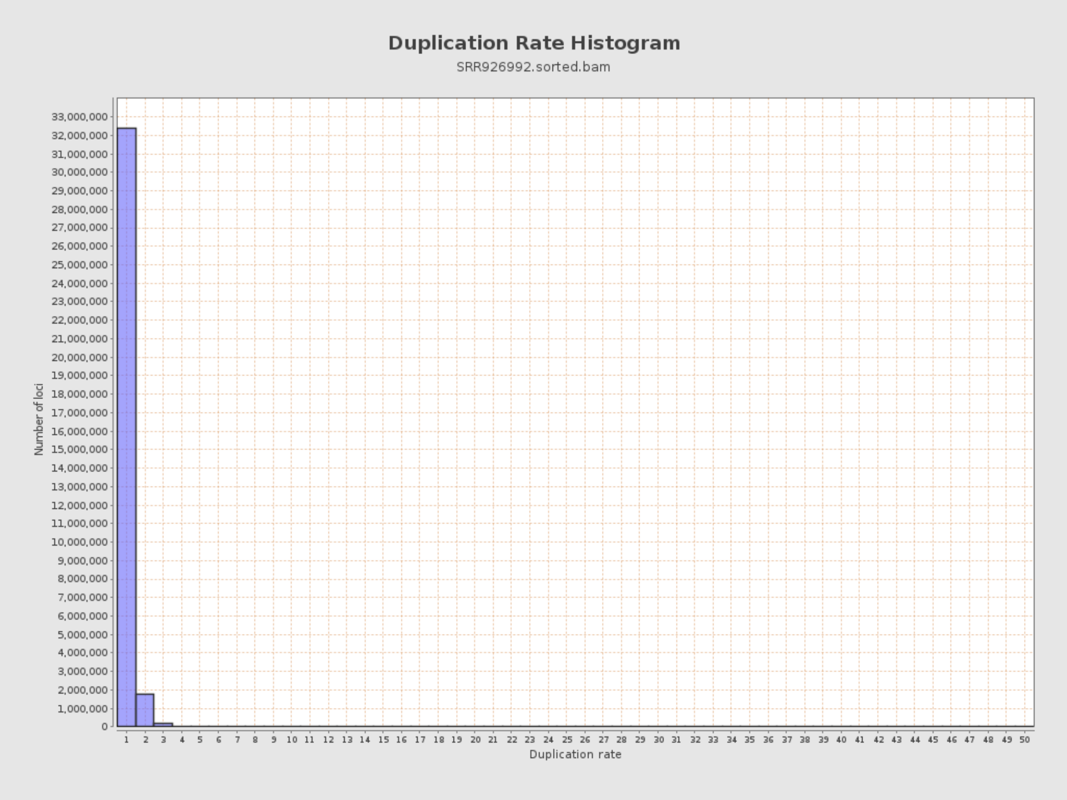
5. Results : Coverage Histogram (0-50X)



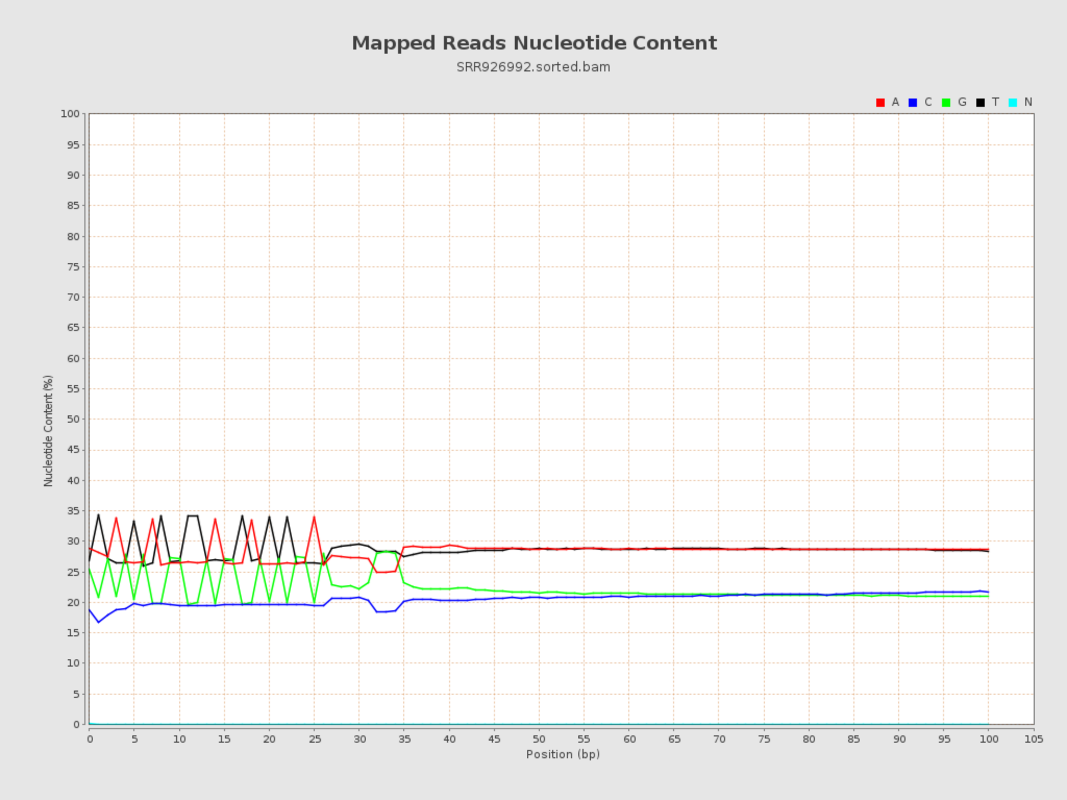
6. Results : Genome Fraction Coverage



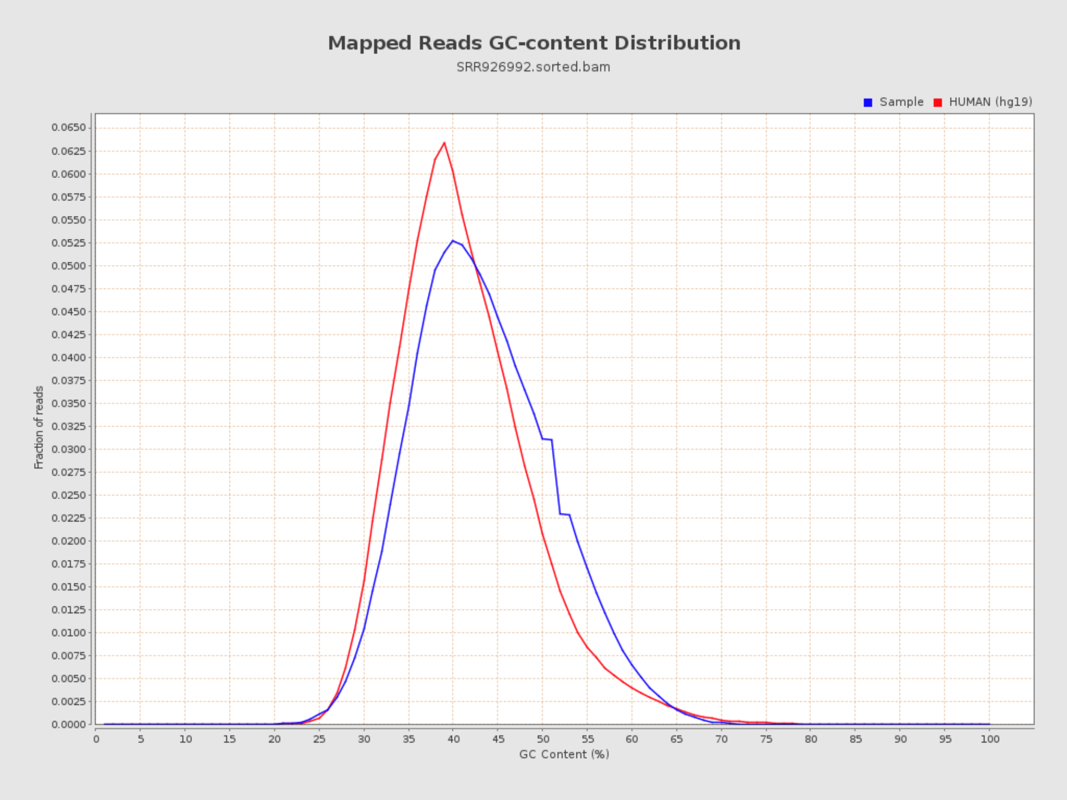
7. Results : Duplication Rate Histogram



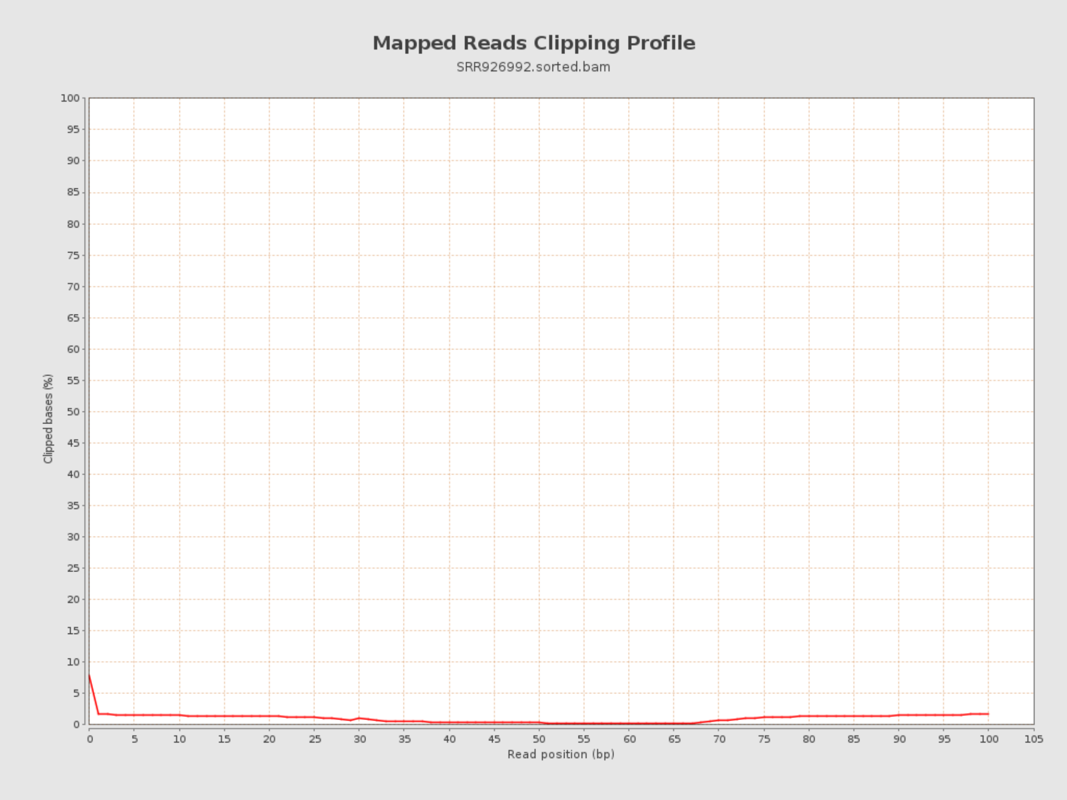
8. Results : Mapped Reads Nucleotide Content



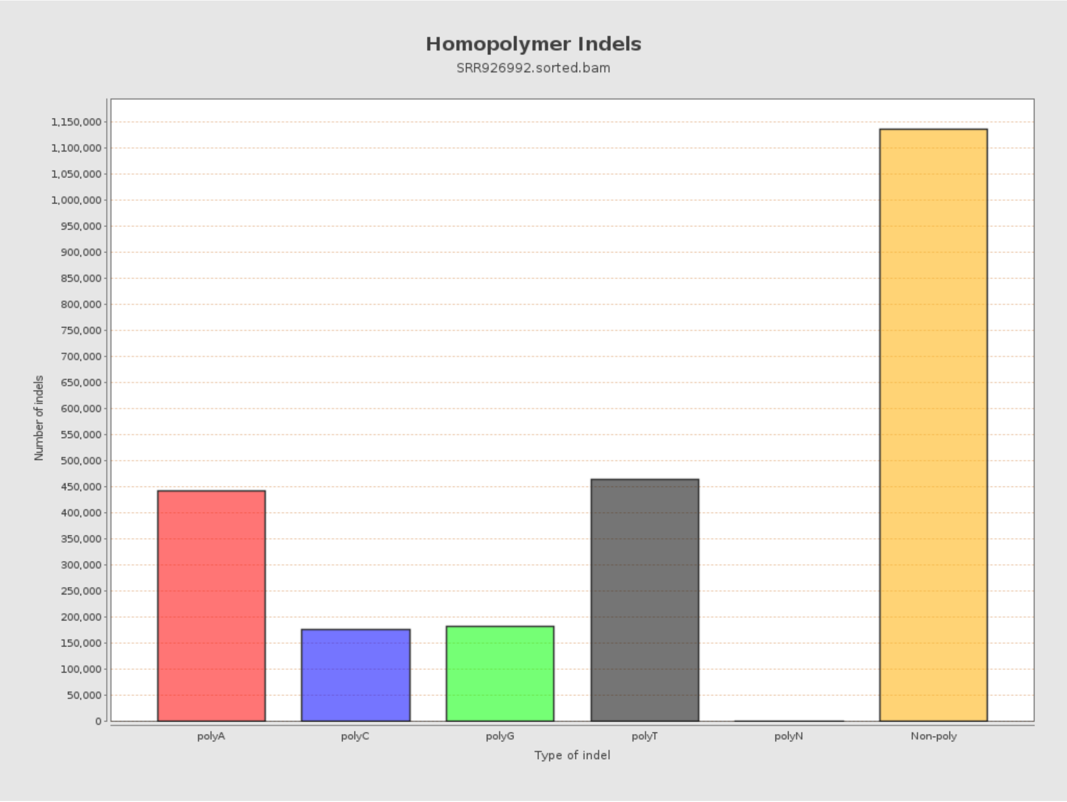
9. Results : Mapped Reads GC-content Distribution



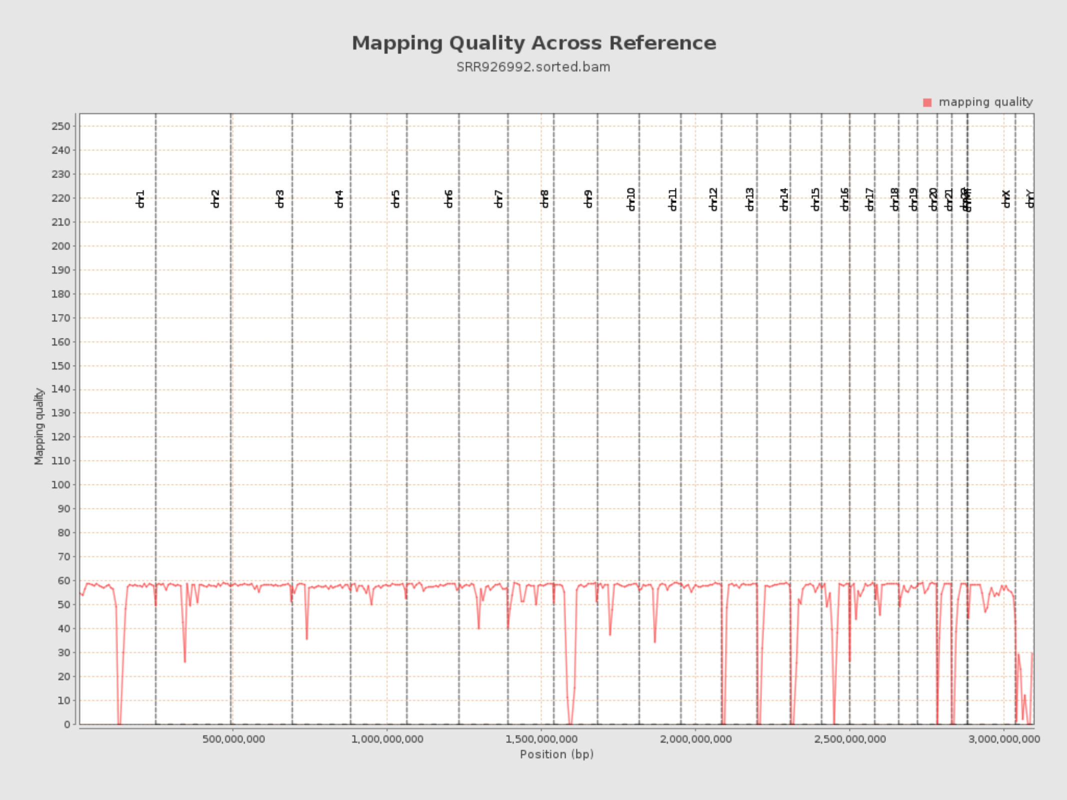
10. Results : Mapped Reads Clipping Profile



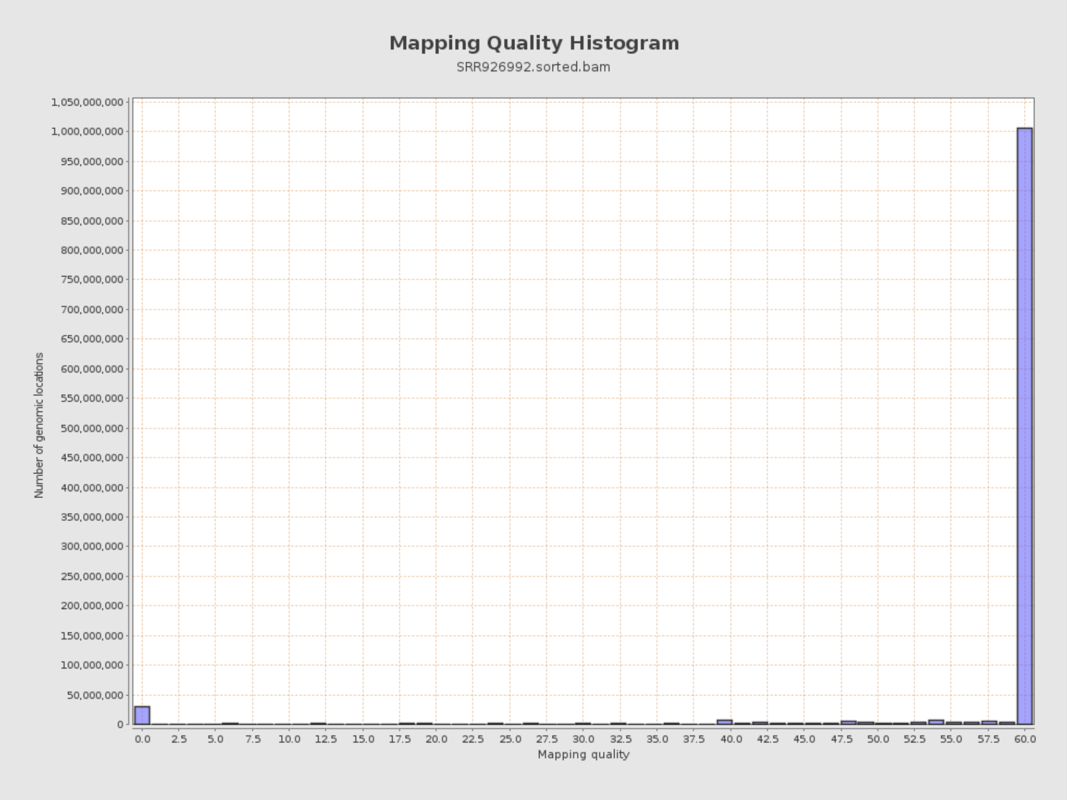
11. Results : Homopolymer Indels



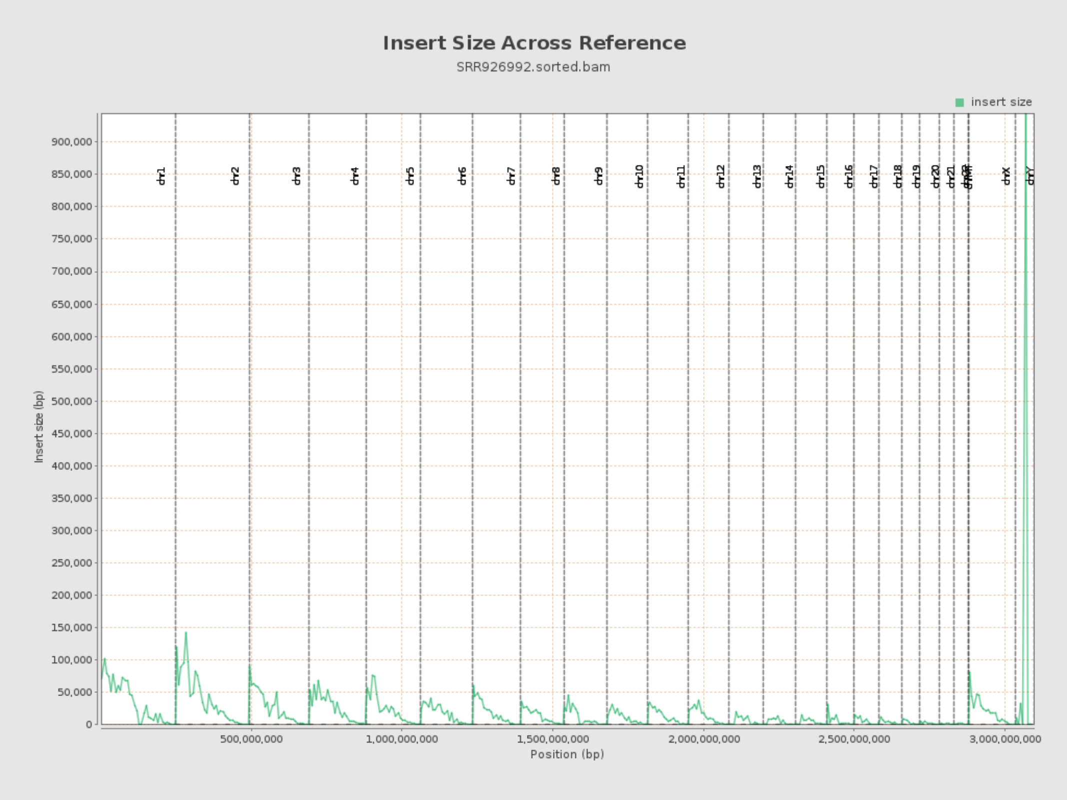
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram