Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/06 15:51:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR960913.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_SRR960913 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR960913_1.fastq.gz SRR960913_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Jan 06 15:51:02 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR960913.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	198,413,316
Mapped reads	188,621,312 / 95.06%
Unmapped reads	9,792,004 / 4.94%
Mapped paired reads	188,621,312 / 95.06%
Mapped reads, first in pair	94,980,140 / 47.87%
Mapped reads, second in pair	93,641,172 / 47.2%
Mapped reads, both in pair	183,319,382 / 92.39%
Mapped reads, singletons	5,301,930 / 2.67%
Secondary alignments	0
Supplementary alignments	2,973,626 / 1.5%
Read min/max/mean length	30 / 101 / 101.58
Duplicated reads (estimated)	24,634,726 / 12.42%
Duplication rate	7.32%
Clipped reads	107,777,122 / 54.32%

2.2. ACGT Content

Number/percentage of A's	4,678,289,681 / 29.21%
Number/percentage of C's	3,269,974,082 / 20.42%
Number/percentage of T's	4,805,444,380 / 30%
Number/percentage of G's	3,261,240,708 / 20.36%
Number/percentage of N's	1,167,907 / 0.01%

GC Percentage	40.78%

2.3. Coverage

Mean	5.175
Standard Deviation	68.8936

2.4. Mapping Quality

Mean Mapping Quality	52.21

2.5. Insert size

Mean	159,624.27
Standard Deviation	4,092,123.08
P25/Median/P75	136 / 149 / 161

2.6. Mismatches and indels

General error rate	1.72%
Mismatches	271,508,254
Insertions	2,339,909
Mapped reads with at least one insertion	1.22%
Deletions	2,009,390
Mapped reads with at least one deletion	1.04%
Homopolymer indels	36.78%

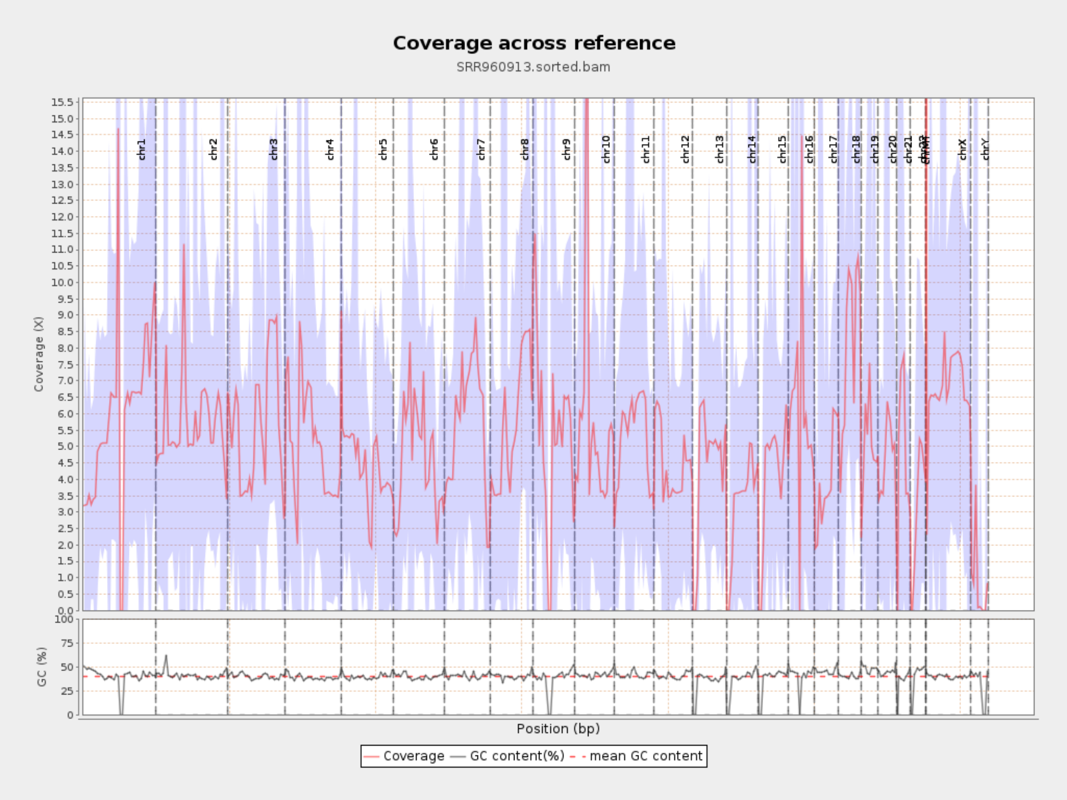
2.7. Chromosome stats

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

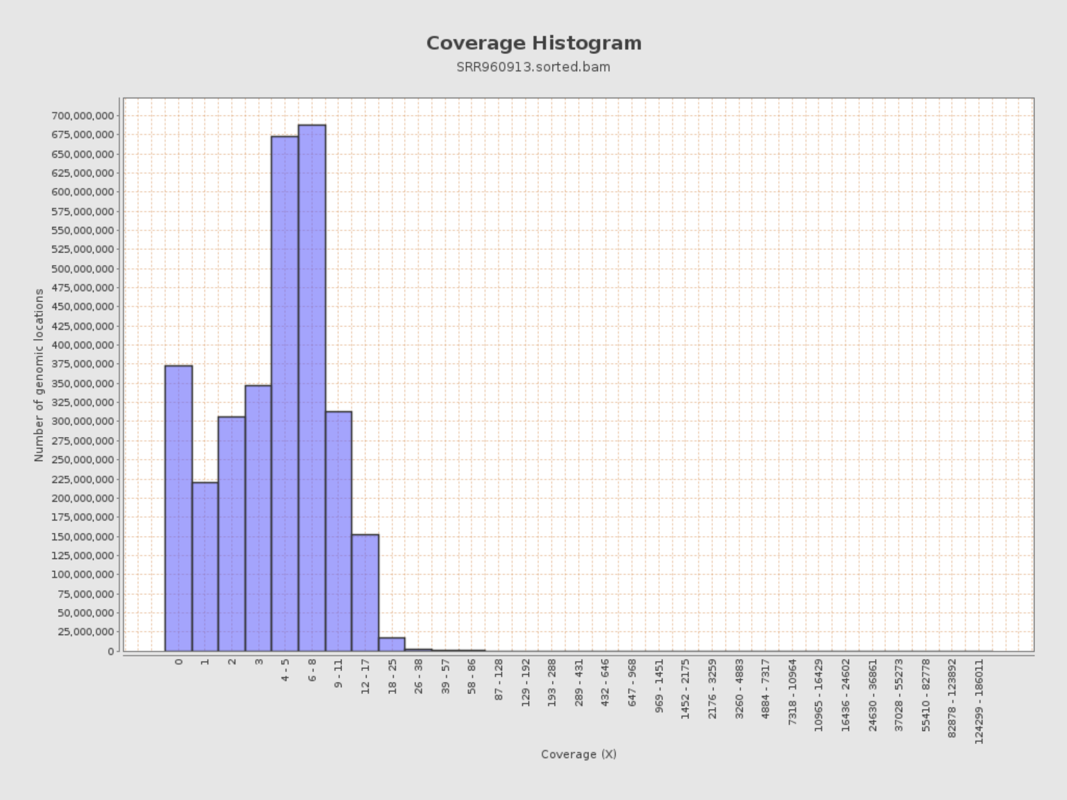
		bases	coverage	deviation
chr1	249250621	1475643366	5.9203	177.8196
chr2	243199373	1391203286	5.7204	93.2107
chr3	198022430	1118251674	5.6471	11.1057
chr4	191154276	980278961	5.1282	29.0126
chr5	180915260	787939954	4.3553	6.7516
chr6	171115067	807342481	4.7181	22.1563
chr7	159138663	910819037	5.7234	46.4355
chr8	146364022	838744696	5.7305	60.5284
chr9	141213431	764758608	5.4156	52.5018
chr10	135534747	769379311	5.6766	112.0736
chr11	135006516	724019862	5.3629	32.4376
chr12	133851895	598989899	4.475	6.1869
chr13	115169878	506754068	4.4001	4.1054
chr14	107349540	353096734	3.2892	27.1254
chr15	102531392	414133292	4.0391	5.0096
chr16	90354753	551094512	6.0992	58.8718
chr17	81195210	308441701	3.7988	16.9585
chr18	78077248	623175245	7.9815	64.6977
chr19	59128983	305479000	5.1663	78.4041
chr20	63025520	293863849	4.6626	13.878
chr21	48129895	228006226	4.7373	20.8425
chr22	51304566	160805258	3.1343	4.7637
chrMT	16571	3215927	194.0696	40.4009
chrX	155270560	1055512447	6.7979	22.6289

chrY	59373566	49409249	0.8322	35.4733

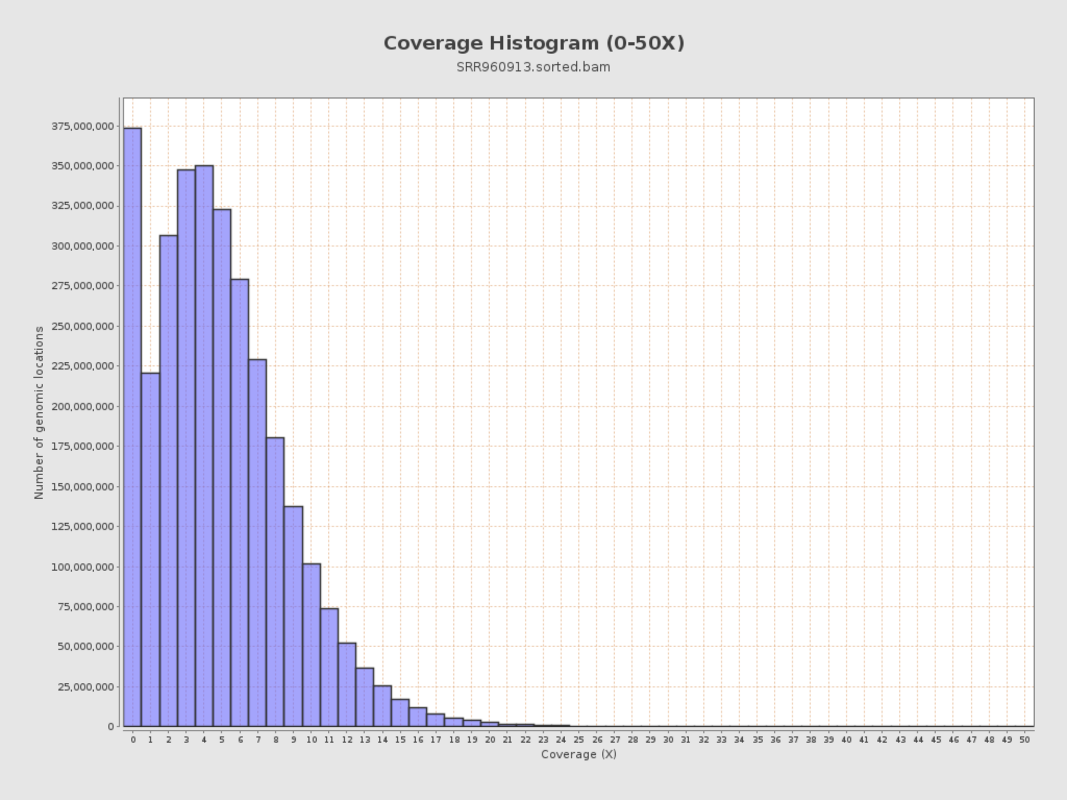
3. Results : Coverage across reference



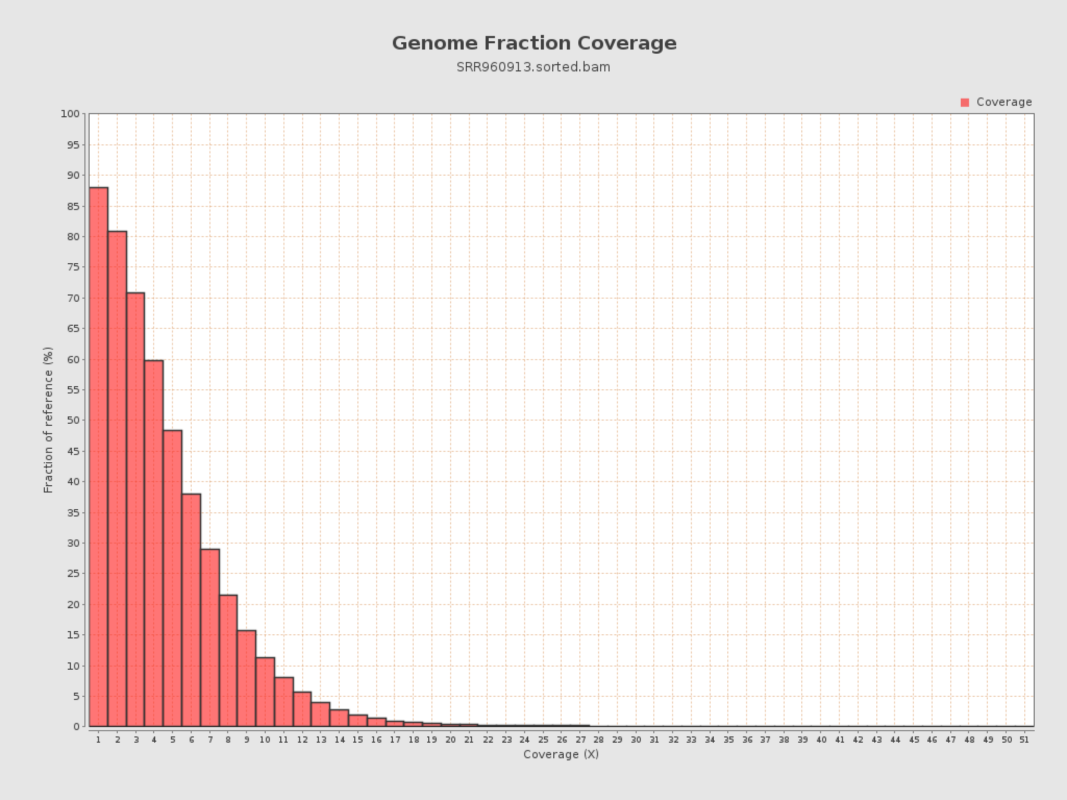
4. Results : Coverage Histogram



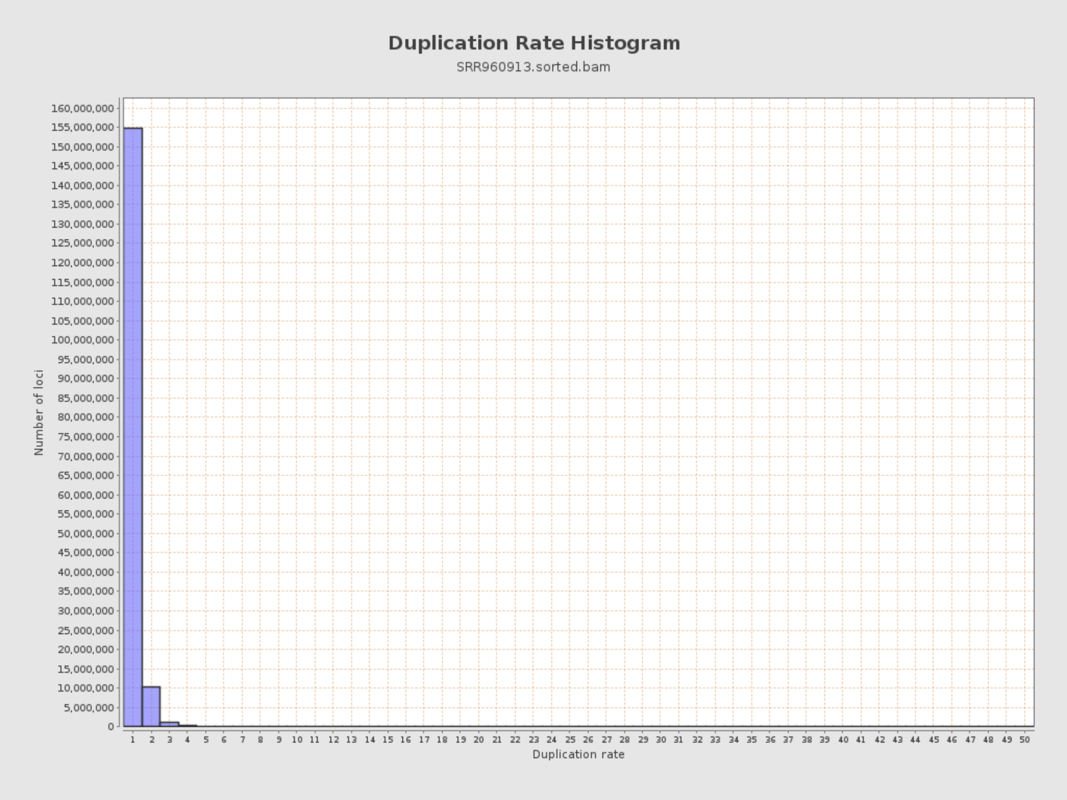
5. Results : Coverage Histogram (0-50X)



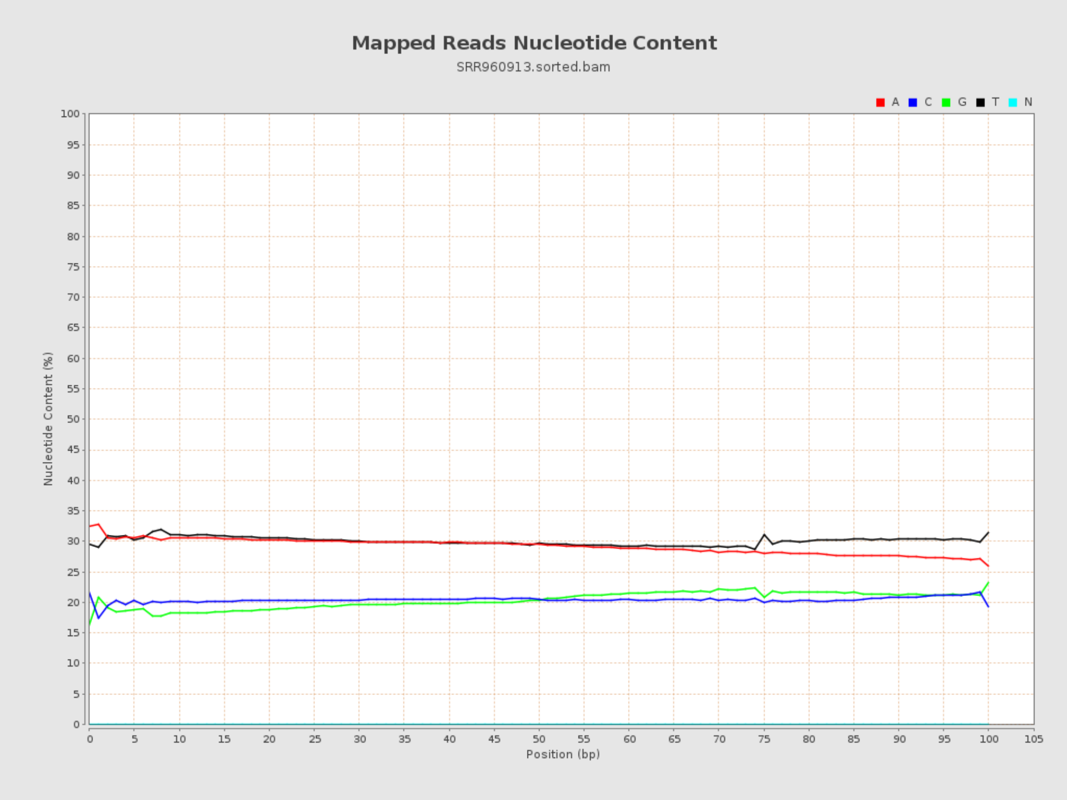
6. Results : Genome Fraction Coverage



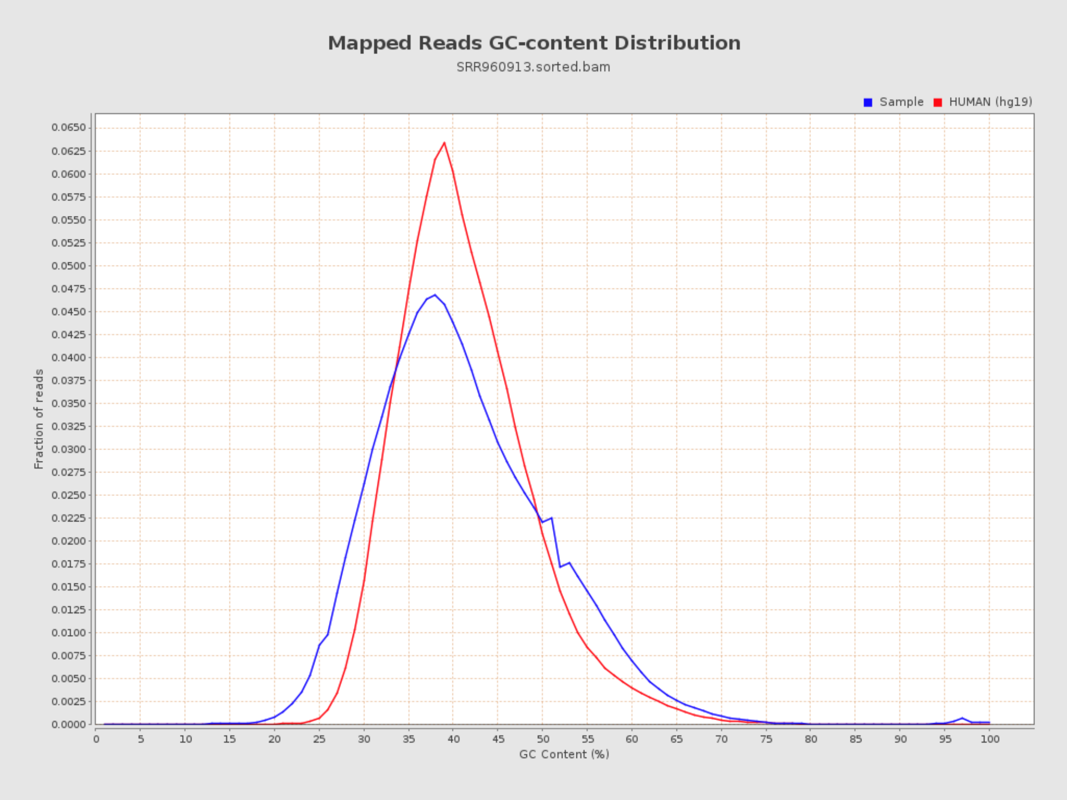
7. Results : Duplication Rate Histogram



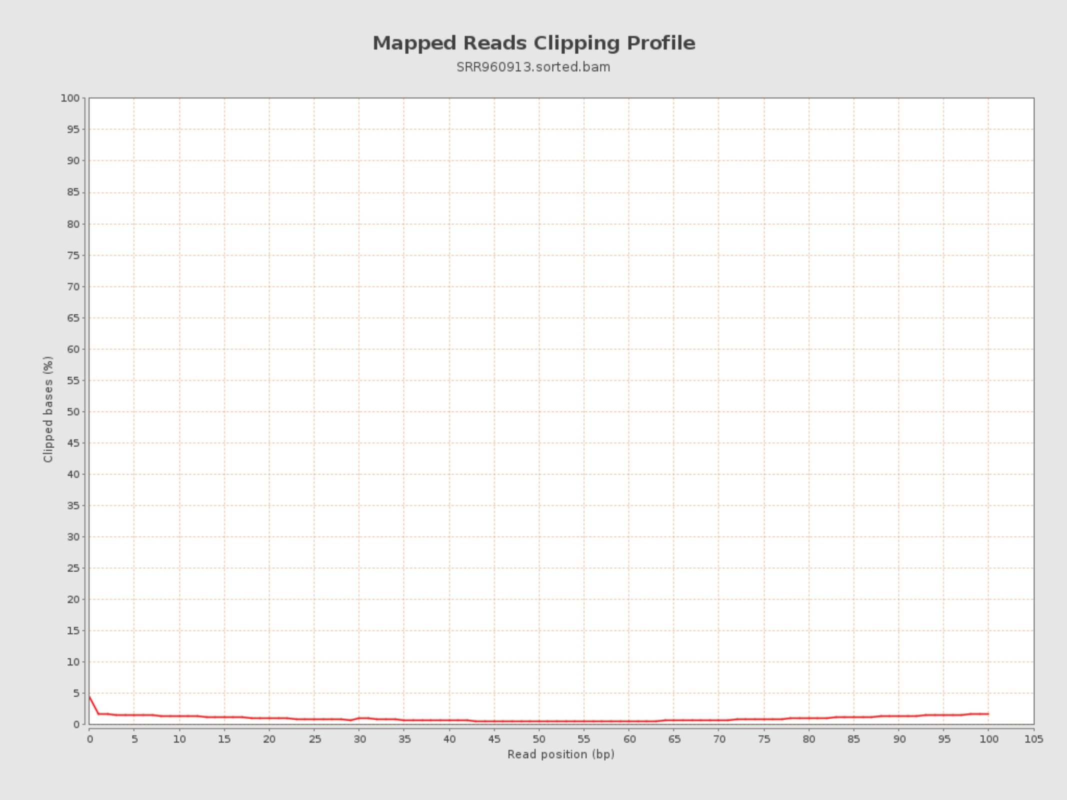
8. Results : Mapped Reads Nucleotide Content



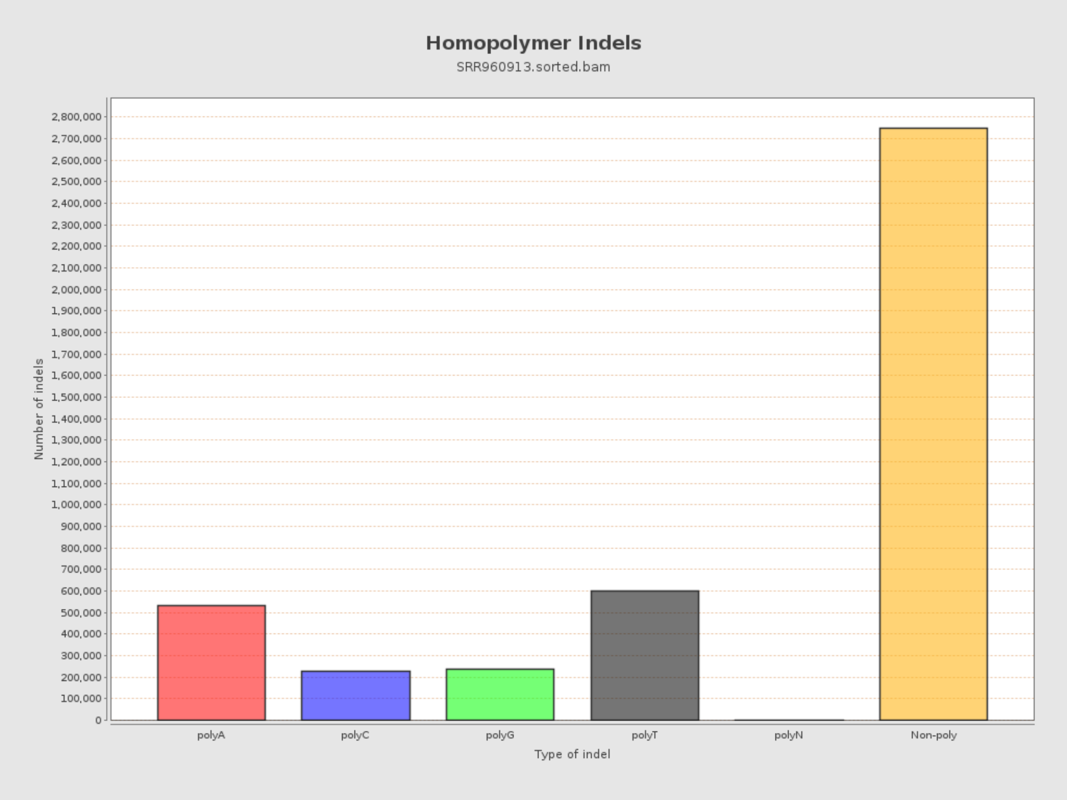
9. Results : Mapped Reads GC-content Distribution



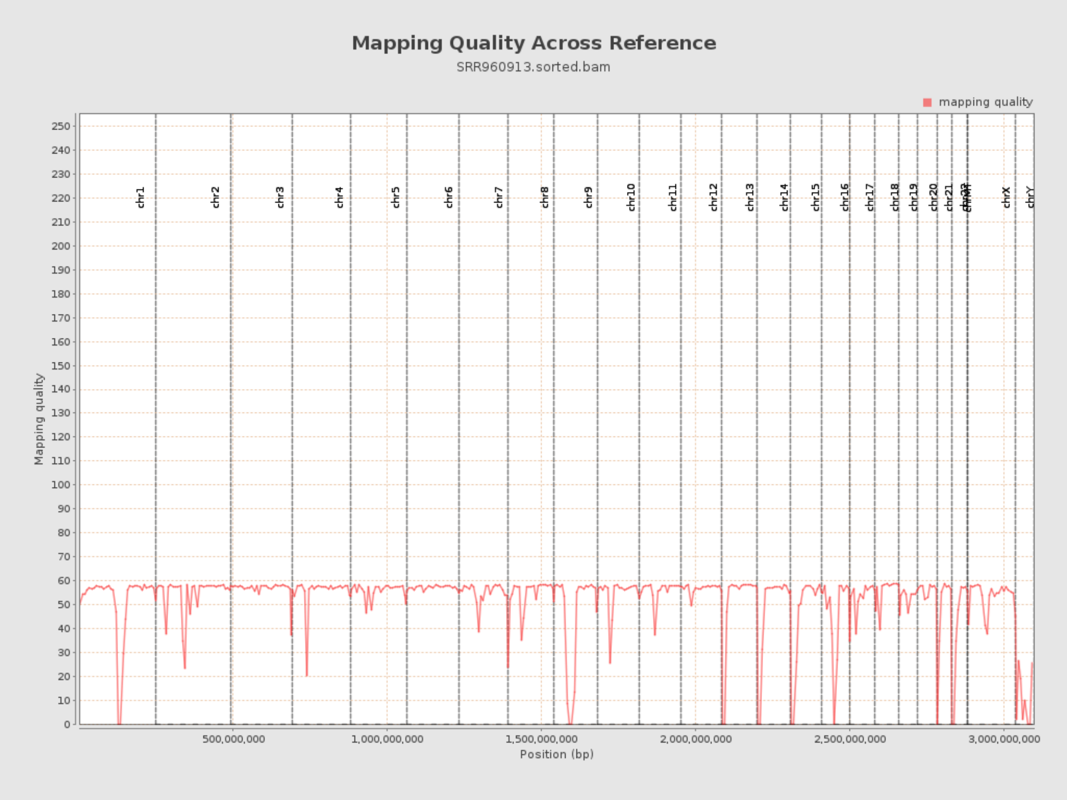
10. Results : Mapped Reads Clipping Profile



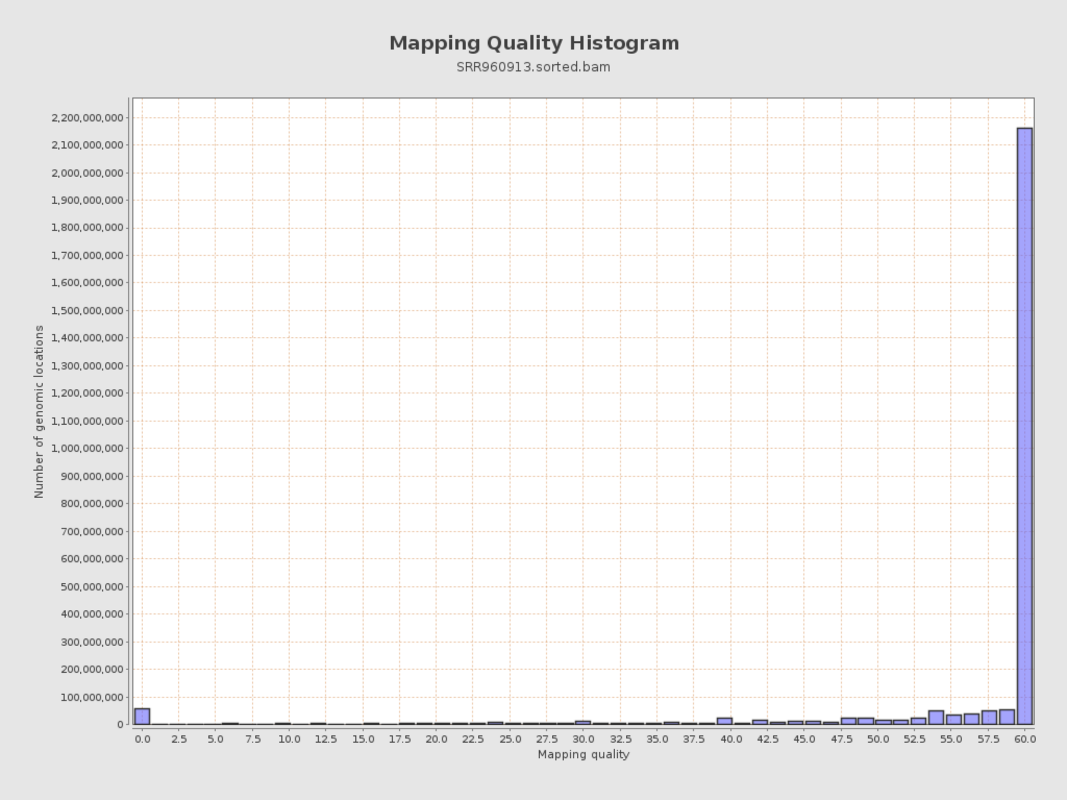
11. Results : Homopolymer Indels



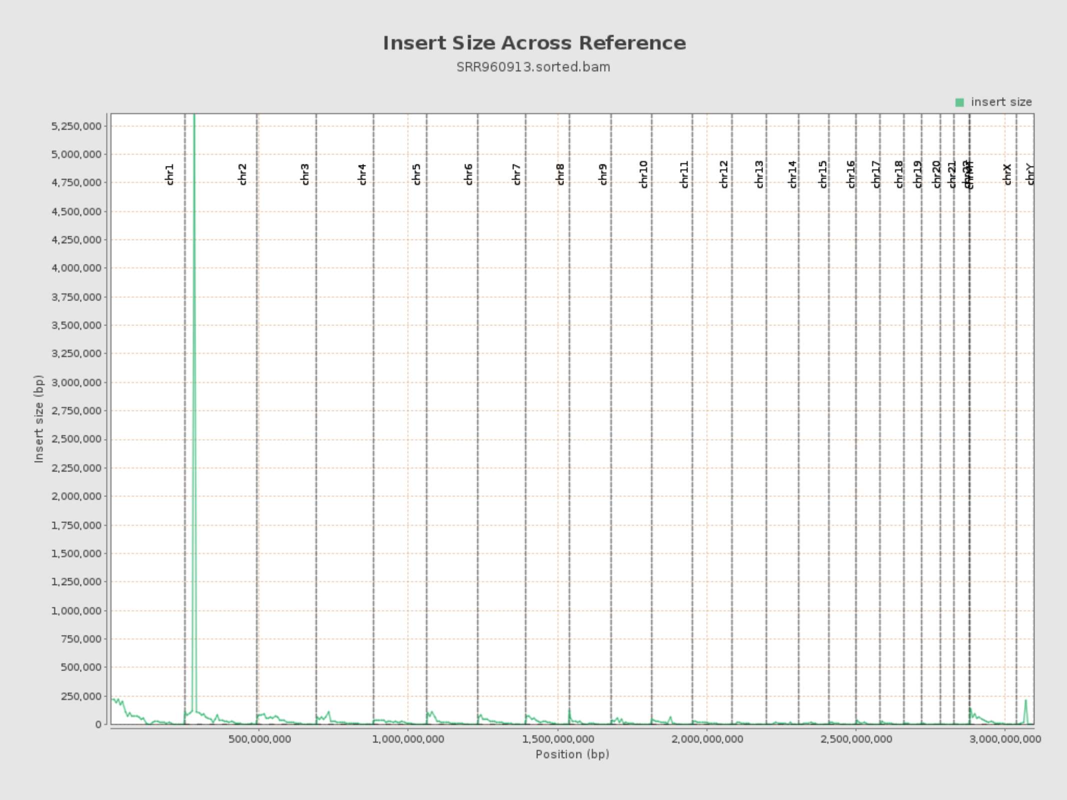
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram