Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/28 15:17:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781913.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_SRR1781913 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781913_1.fastq.gz SRR1781913_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Mar 28 15:17:36 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781913.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	44,904,082
Mapped reads	44,061,439 / 98.12%
Unmapped reads	842,643 / 1.88%
Mapped paired reads	44,061,439 / 98.12%
Mapped reads, first in pair	22,216,093 / 49.47%
Mapped reads, second in pair	21,845,346 / 48.65%
Mapped reads, both in pair	43,552,712 / 96.99%
Mapped reads, singletons	508,727 / 1.13%
Secondary alignments	0
Supplementary alignments	155,367 / 0.35%
Read min/max/mean length	30 / 100 / 99.98
Duplicated reads (estimated)	1,214,880 / 2.71%
Duplication rate	2.64%
Clipped reads	1,691,276 / 3.77%

2.2. ACGT Content

Number/percentage of A's	1,315,054,275 / 30.06%
Number/percentage of C's	866,863,369 / 19.82%
Number/percentage of T's	1,312,912,962 / 30.01%
Number/percentage of G's	879,024,337 / 20.09%
Number/percentage of N's	765,606 / 0.02%

GC Percentage	39.91%

2.3. Coverage

Mean	1.4135
Standard Deviation	2.0953

2.4. Mapping Quality

Mean Mapping Quality	53.99

2.5. Insert size

Mean	48,644.1
Standard Deviation	2,123,102.58
P25/Median/P75	218 / 277 / 358

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	16,363,545
Insertions	499,816
Mapped reads with at least one insertion	1.12%
Deletions	483,297
Mapped reads with at least one deletion	1.08%
Homopolymer indels	48.65%

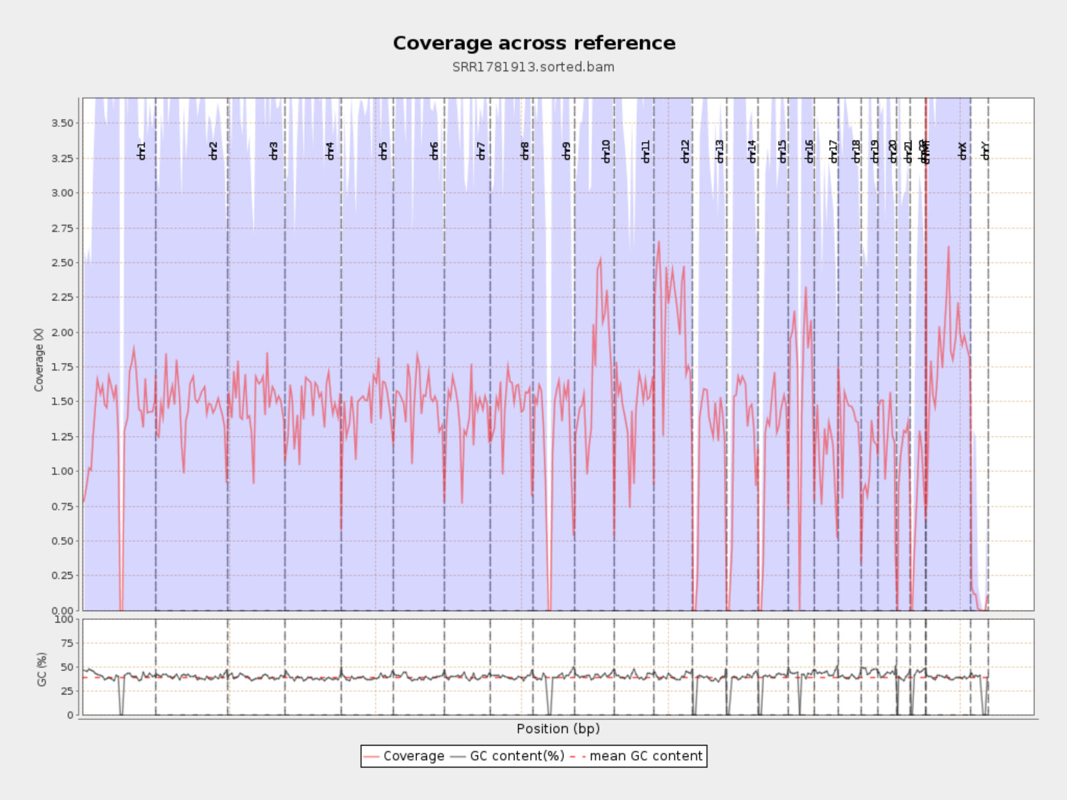
2.7. Chromosome stats

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

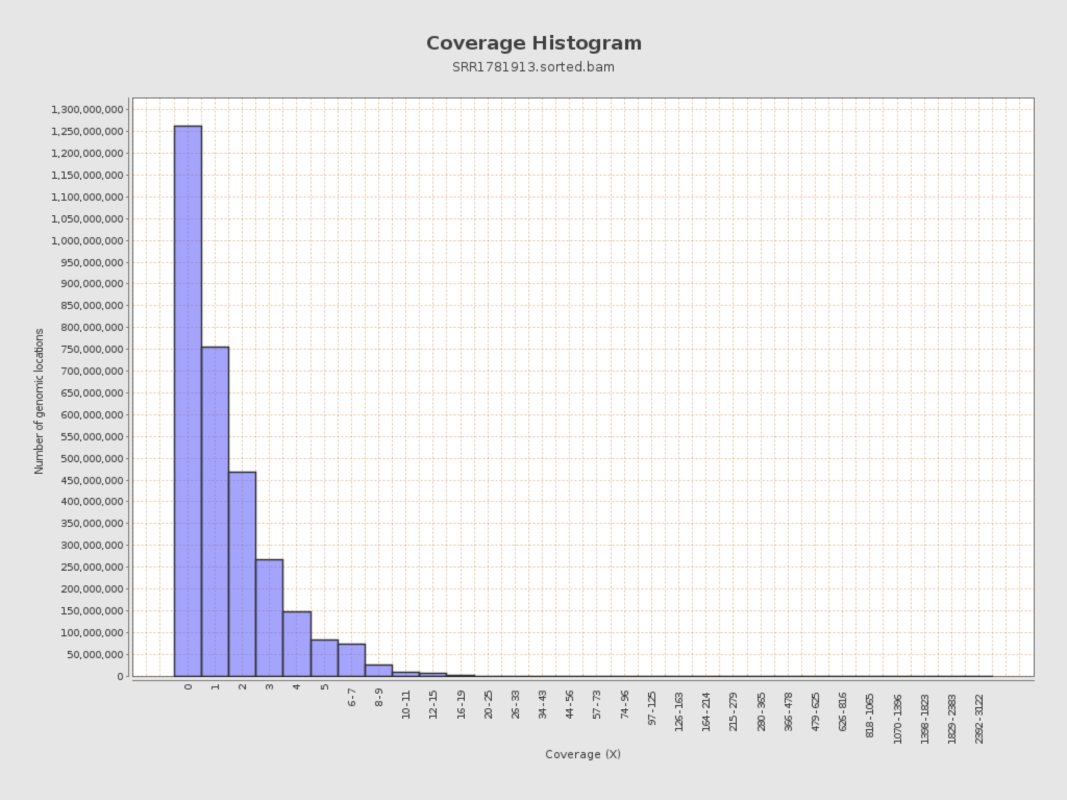
		bases	coverage	deviation
chr1	249250621	338635673	1.3586	2.3153
chr2	243199373	355806488	1.463	2.962
chr3	198022430	298570844	1.5078	1.8227
chr4	191154276	282725218	1.479	1.8529
chr5	180915260	264690831	1.4631	1.7663
chr6	171115067	258344575	1.5098	1.9199
chr7	159138663	222583335	1.3987	1.8705
chr8	146364022	214499499	1.4655	1.8236
chr9	141213431	173891698	1.2314	1.9488
chr10	135534747	234547786	1.7305	2.7346
chr11	135006516	194884481	1.4435	1.8364
chr12	133851895	287292107	2.1463	2.5943
chr13	115169878	133794413	1.1617	1.6253
chr14	107349540	129898311	1.2101	1.7246
chr15	102531392	117246259	1.1435	1.699
chr16	90354753	150238095	1.6628	2.2115
chr17	81195210	91255110	1.1239	1.6814
chr18	78077248	107981663	1.383	1.8456
chr19	59128983	60000207	1.0147	1.8673
chr20	63025520	80786988	1.2818	1.943
chr21	48129895	50020756	1.0393	2.0064
chr22	51304566	37726370	0.7353	1.3929
chrMT	16571	92070	5.5561	2.9535
chrX	155270560	286572999	1.8456	2.1749

chrY	59373566	3612827	0.0608	0.6678

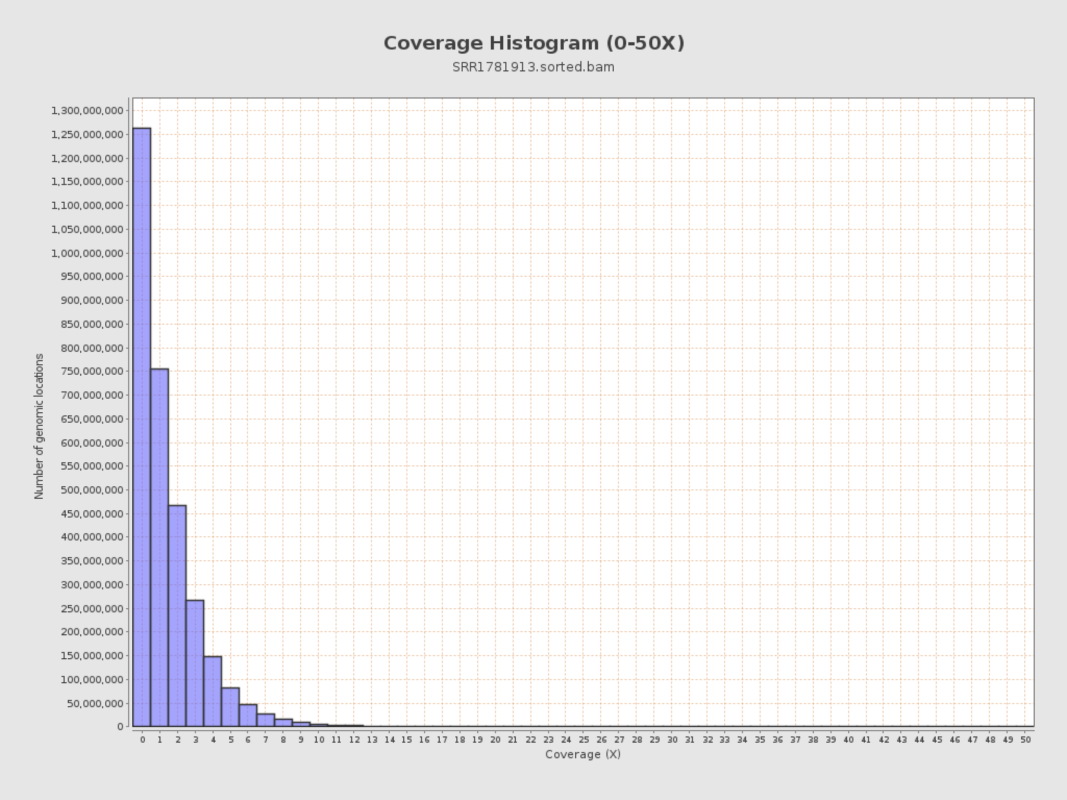
3. Results : Coverage across reference



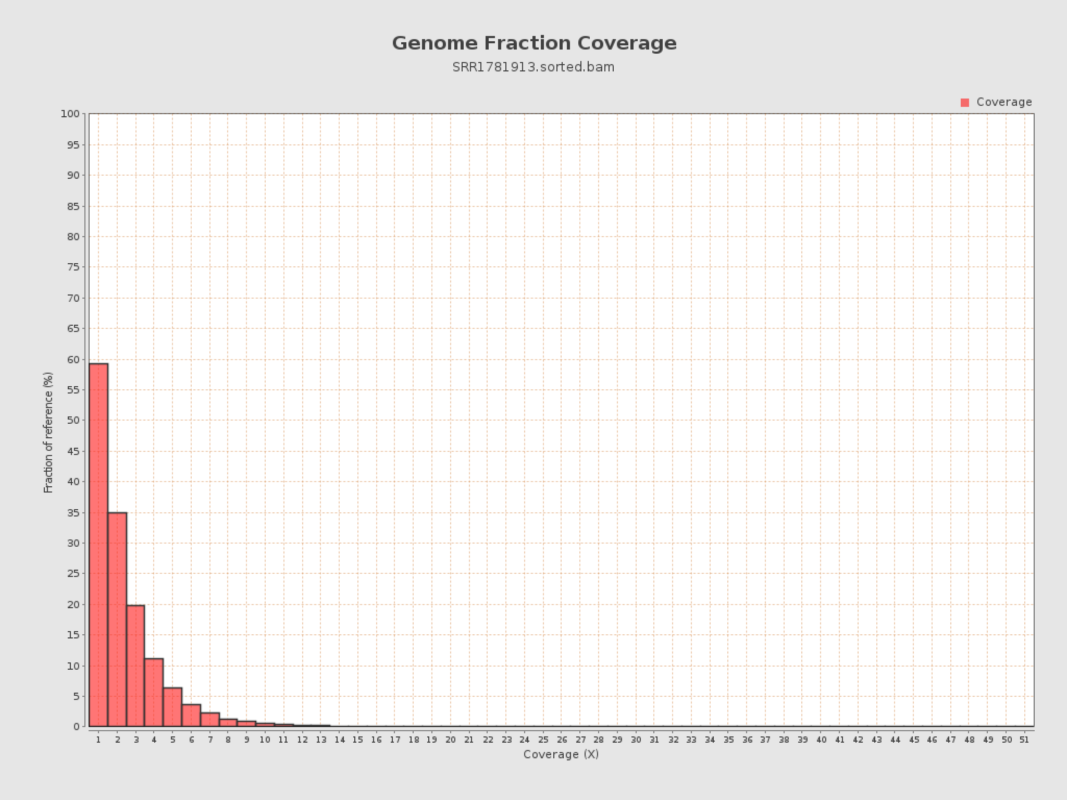
4. Results : Coverage Histogram



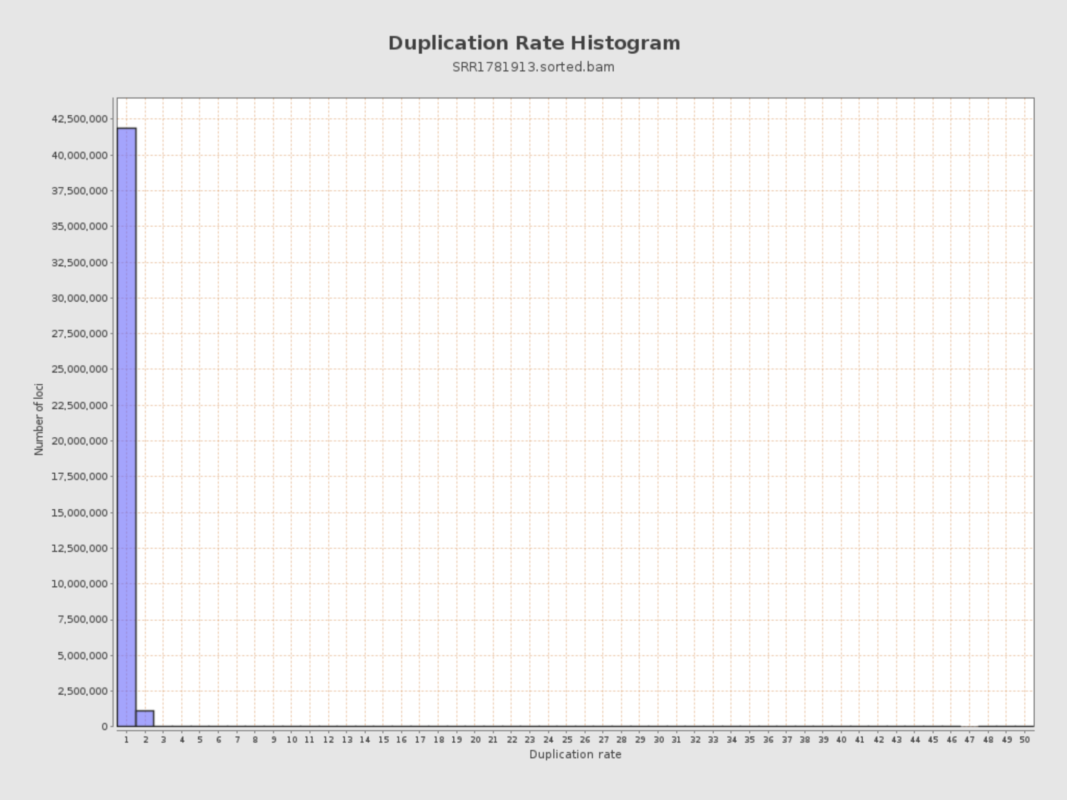
5. Results : Coverage Histogram (0-50X)



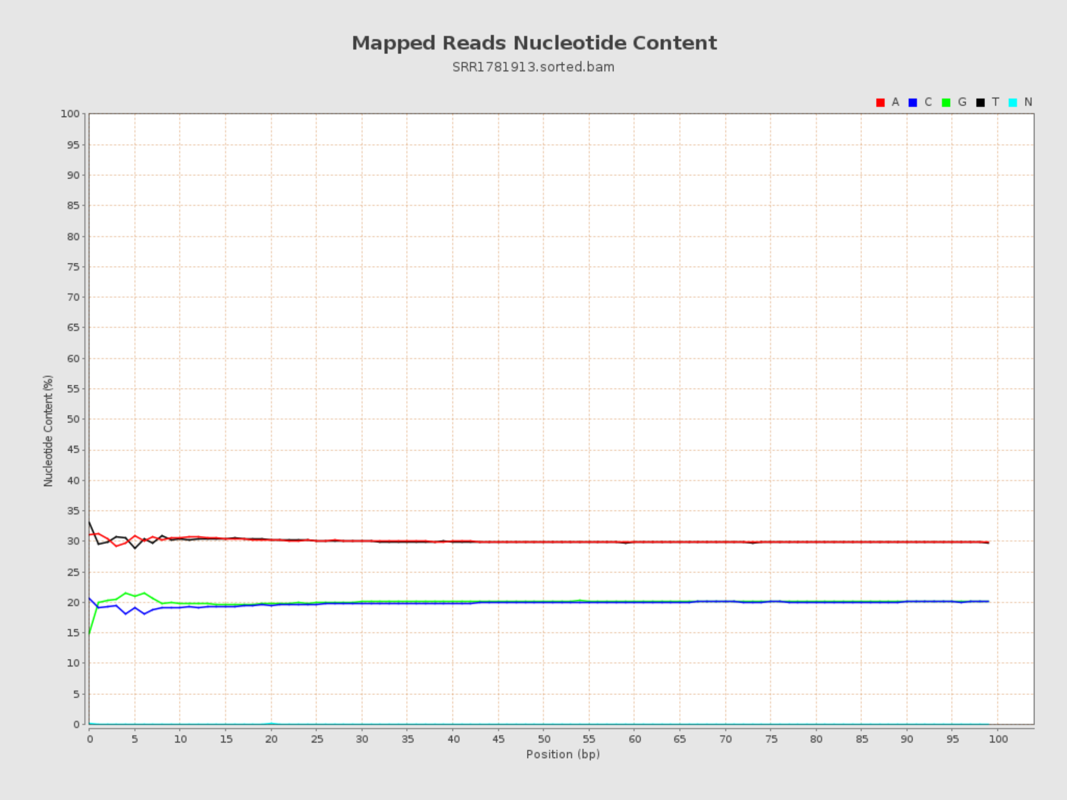
6. Results : Genome Fraction Coverage



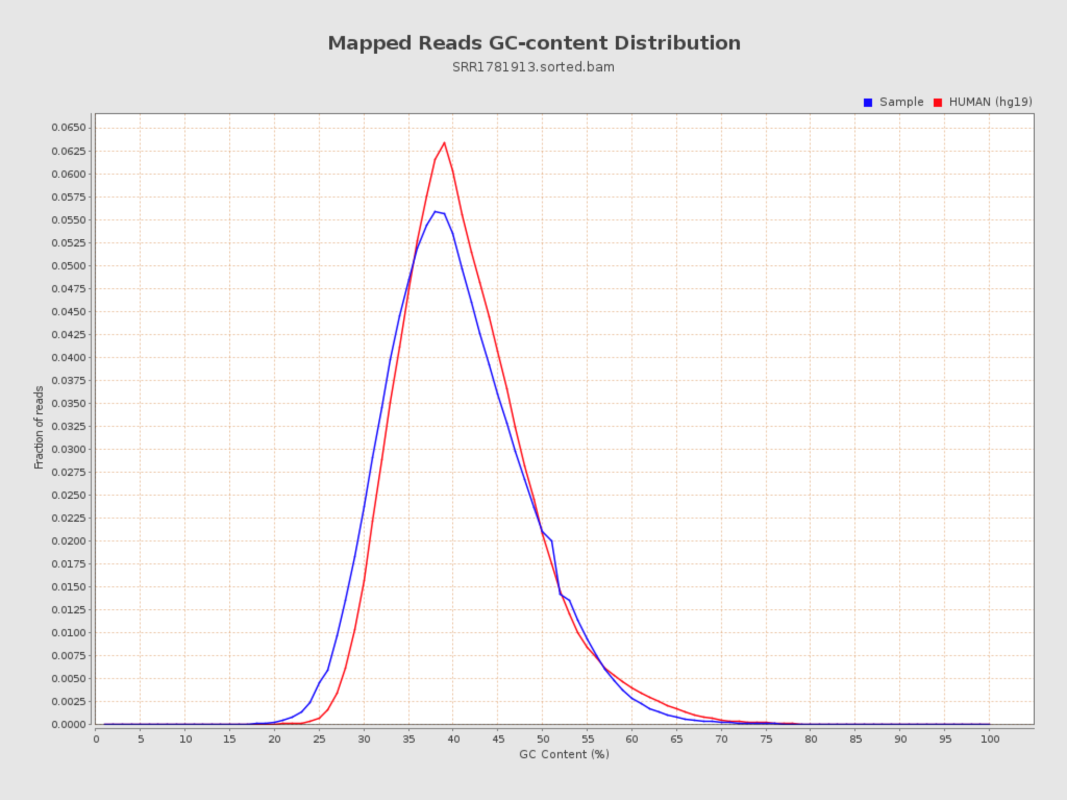
7. Results : Duplication Rate Histogram



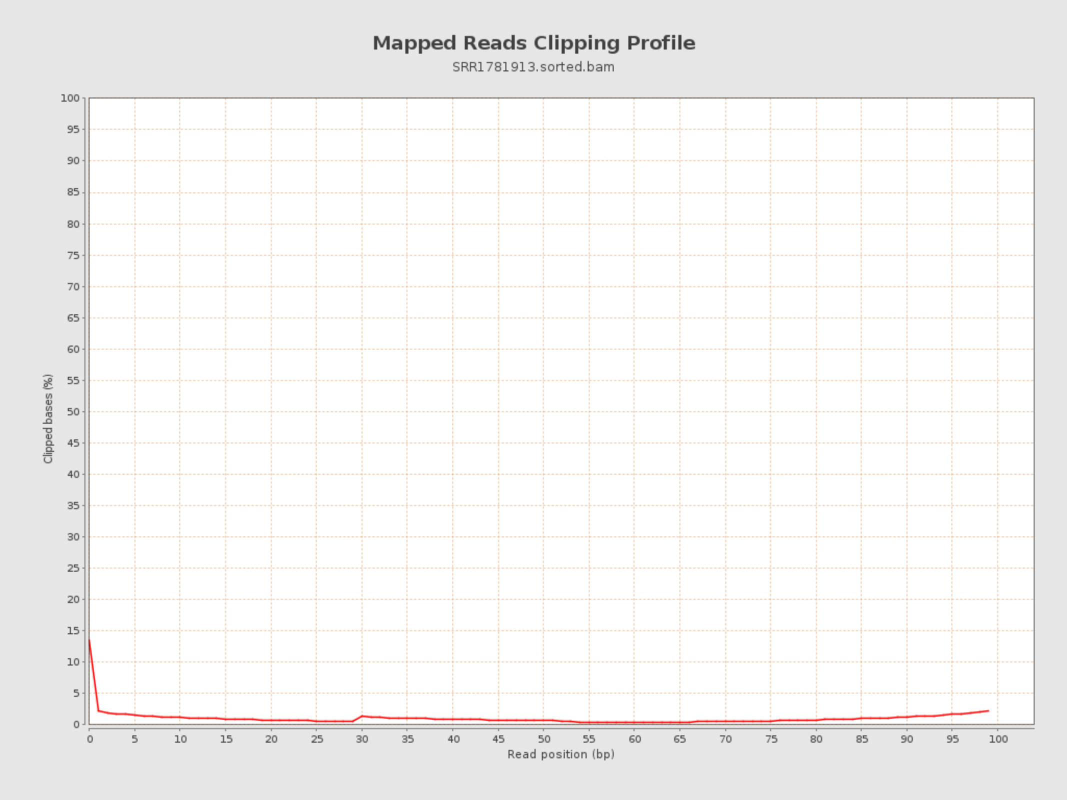
8. Results : Mapped Reads Nucleotide Content



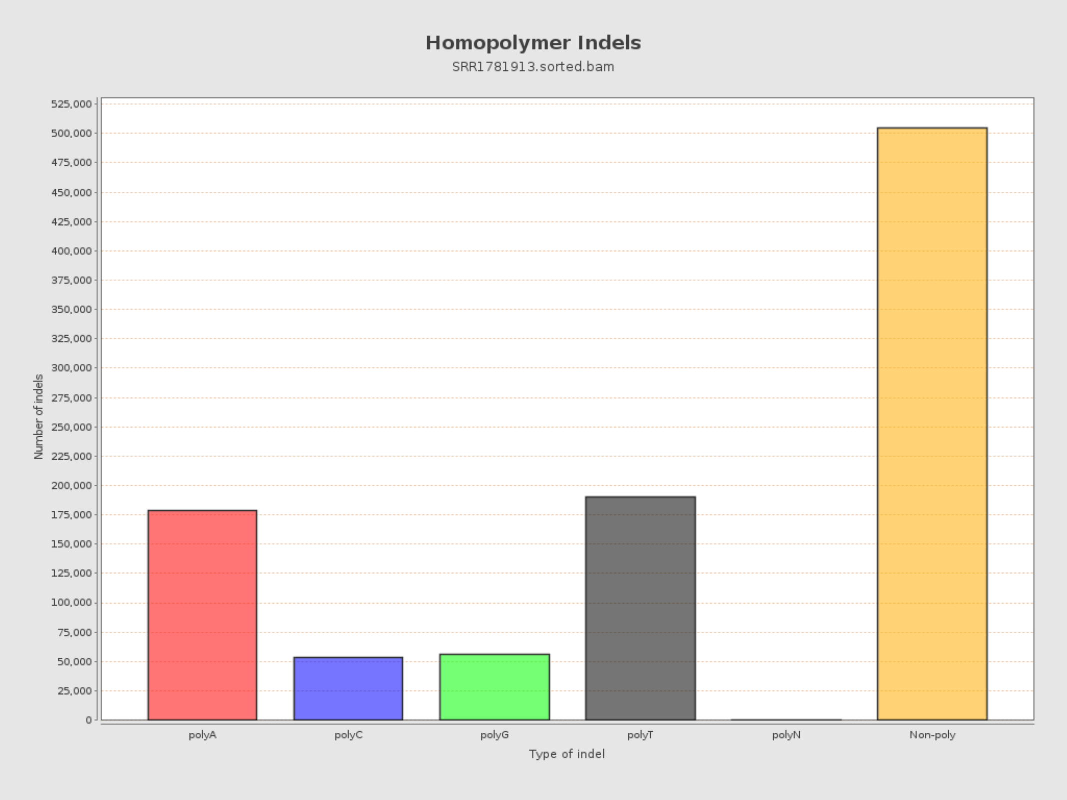
9. Results : Mapped Reads GC-content Distribution



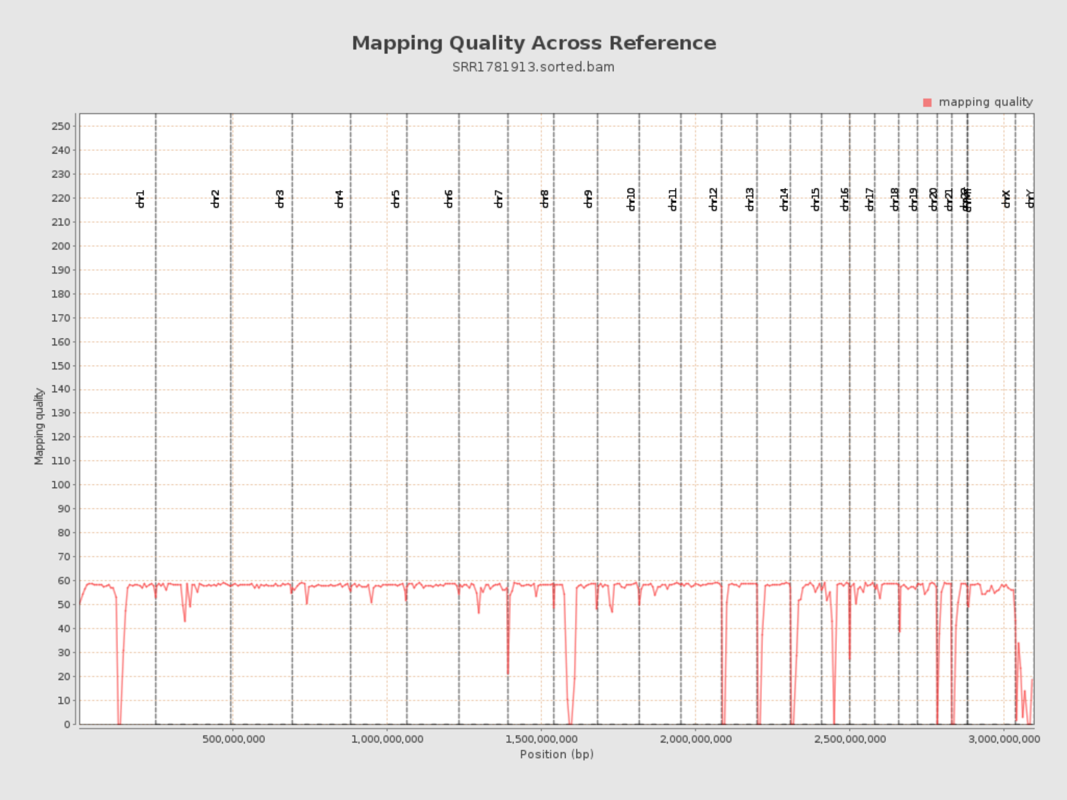
10. Results : Mapped Reads Clipping Profile



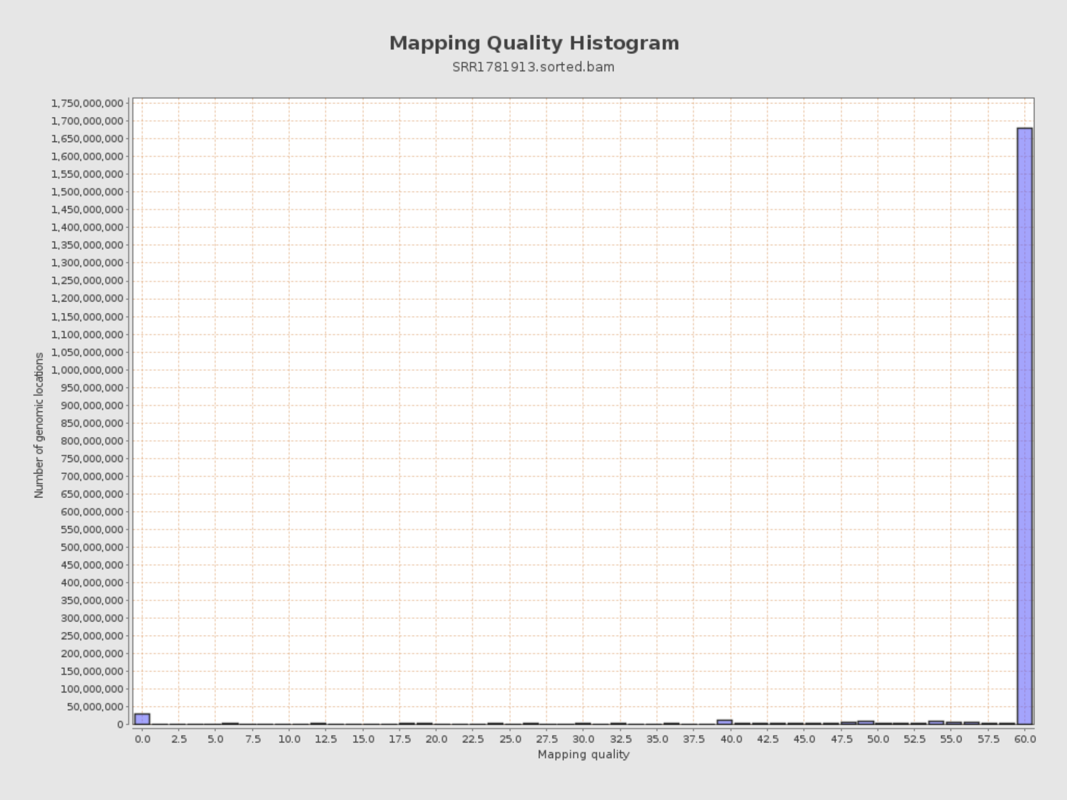
11. Results : Homopolymer Indels



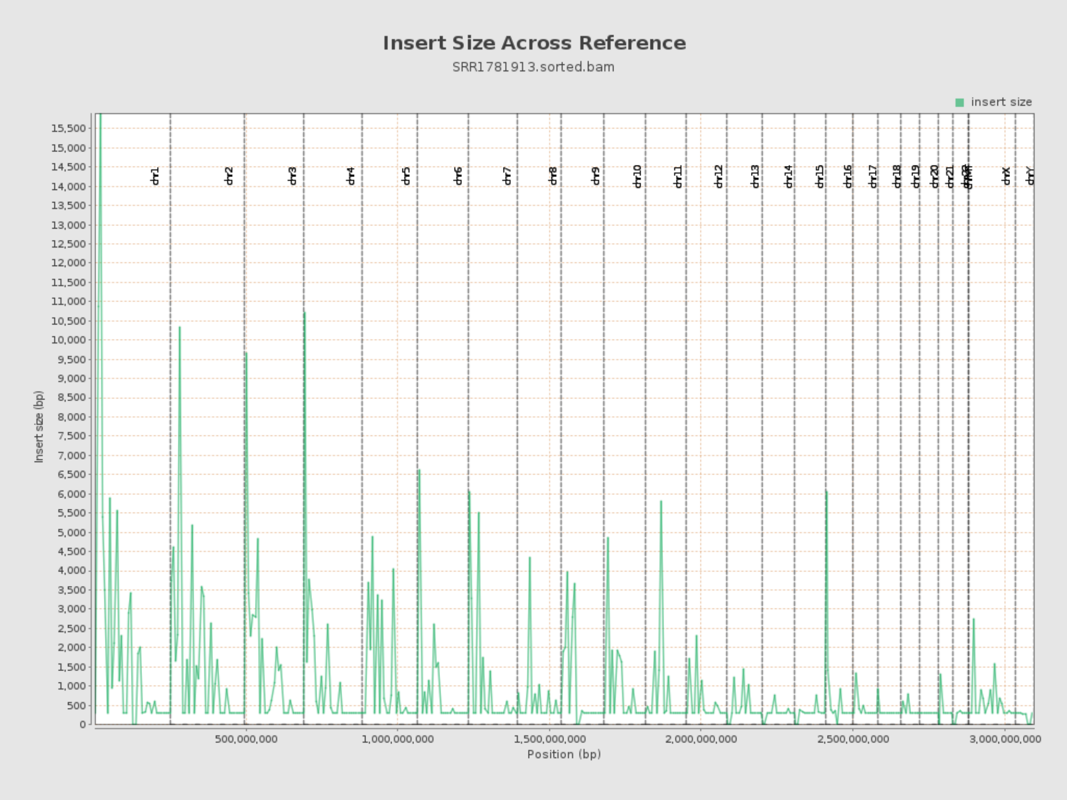
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram