Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 07:36:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1778915.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_SRR1778915 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1778915_1.fastq.gz SRR1778915_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 07:36:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1778915.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	36,584,512
Mapped reads	35,370,280 / 96.68%
Unmapped reads	1,214,232 / 3.32%
Mapped paired reads	35,370,280 / 96.68%
Mapped reads, first in pair	17,901,566 / 48.93%
Mapped reads, second in pair	17,468,714 / 47.75%
Mapped reads, both in pair	34,804,738 / 95.14%
Mapped reads, singletons	565,542 / 1.55%
Secondary alignments	0
Supplementary alignments	245,973 / 0.67%
Read min/max/mean length	30 / 101 / 101.27
Duplicated reads (estimated)	1,030,691 / 2.82%
Duplication rate	2.13%
Clipped reads	2,344,539 / 6.41%

2.2. ACGT Content

Number/percentage of A's	1,059,019,740 / 30%
Number/percentage of C's	700,463,933 / 19.84%
Number/percentage of T's	1,054,977,065 / 29.89%
Number/percentage of G's	714,282,969 / 20.24%
Number/percentage of N's	1,164,925 / 0.03%

GC Percentage	40.08%

2.3. Coverage

Mean	1.1406
Standard Deviation	4.6659

2.4. Mapping Quality

Mean Mapping Quality	53.72

2.5. Insert size

Mean	64,886.14
Standard Deviation	2,445,639.65
P25/Median/P75	212 / 278 / 353

2.6. Mismatches and indels

General error rate	0.58%
Mismatches	19,836,325
Insertions	350,000
Mapped reads with at least one insertion	0.98%
Deletions	406,715
Mapped reads with at least one deletion	1.13%
Homopolymer indels	46.91%

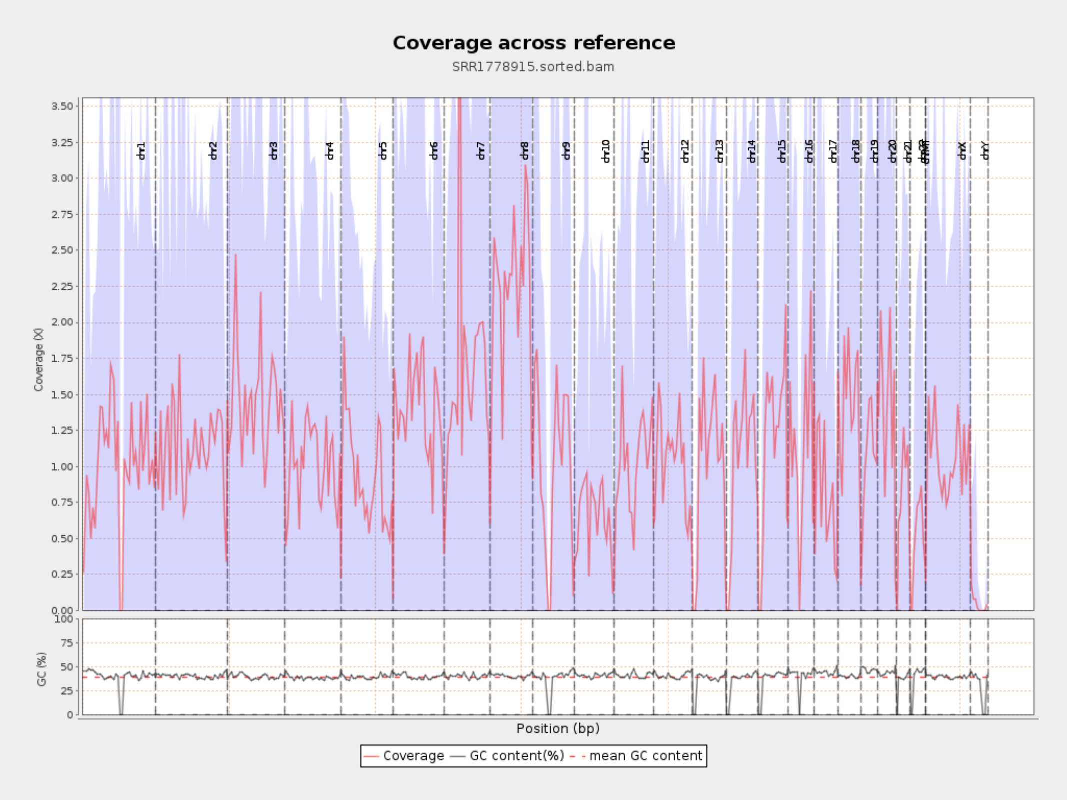
2.7. Chromosome stats

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

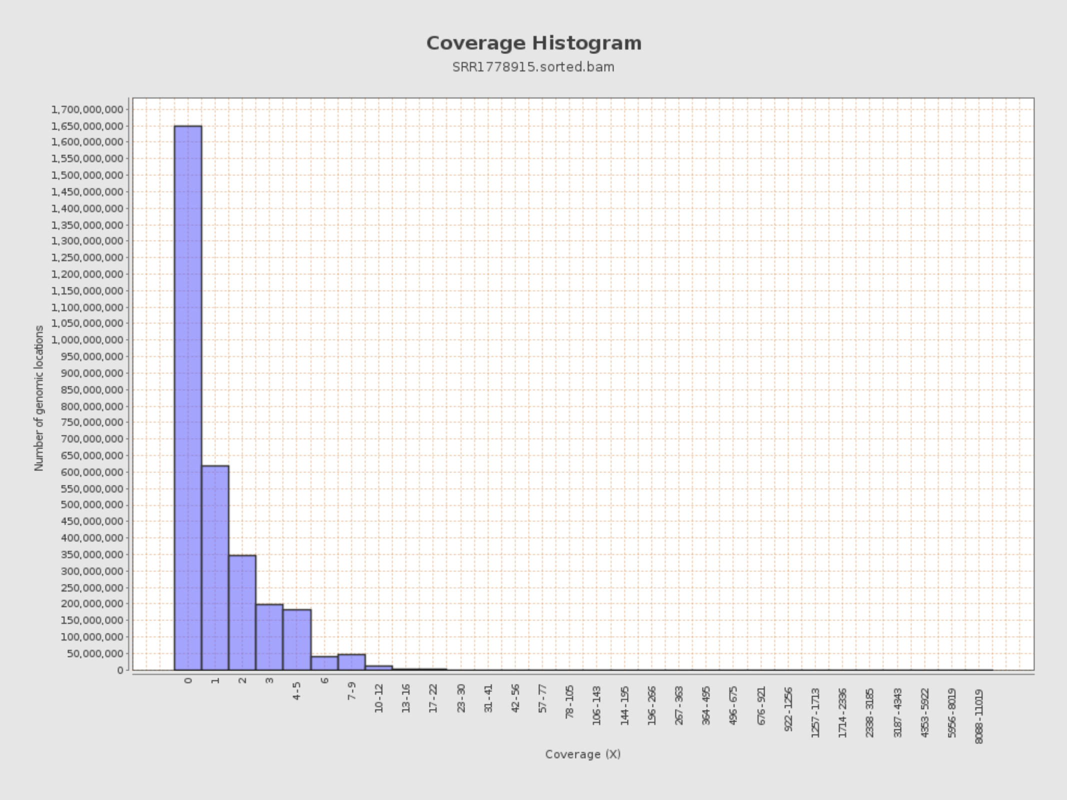
		bases	coverage	deviation
chr1	249250621	248321951	0.9963	11.7116
chr2	243199373	271648037	1.117	2.6124
chr3	198022430	289349023	1.4612	1.9721
chr4	191154276	195367386	1.022	1.8854
chr5	180915260	165735425	0.9161	1.5248
chr6	171115067	241555969	1.4117	2.6527
chr7	159138663	267222624	1.6792	4.7499
chr8	146364022	328722445	2.2459	2.6814
chr9	141213431	145103886	1.0276	3.5529
chr10	135534747	88646971	0.6541	9.9482
chr11	135006516	139315440	1.0319	1.8288
chr12	133851895	138384874	1.0339	1.801
chr13	115169878	118542506	1.0293	1.7314
chr14	107349540	114234617	1.0641	1.7806
chr15	102531392	120487663	1.1751	1.9751
chr16	90354753	96394723	1.0668	1.8984
chr17	81195210	62071953	0.7645	4.039
chr18	78077248	113042648	1.4478	3.7353
chr19	59128983	64835370	1.0965	6.4682
chr20	63025520	90293923	1.4327	2.2034
chr21	48129895	38219319	0.7941	1.6034
chr22	51304566	25479023	0.4966	1.2388
chrMT	16571	3149	0.19	0.6193
chrX	155270560	165283209	1.0645	1.7644

chrY	59373566	2546388	0.0429	0.5671

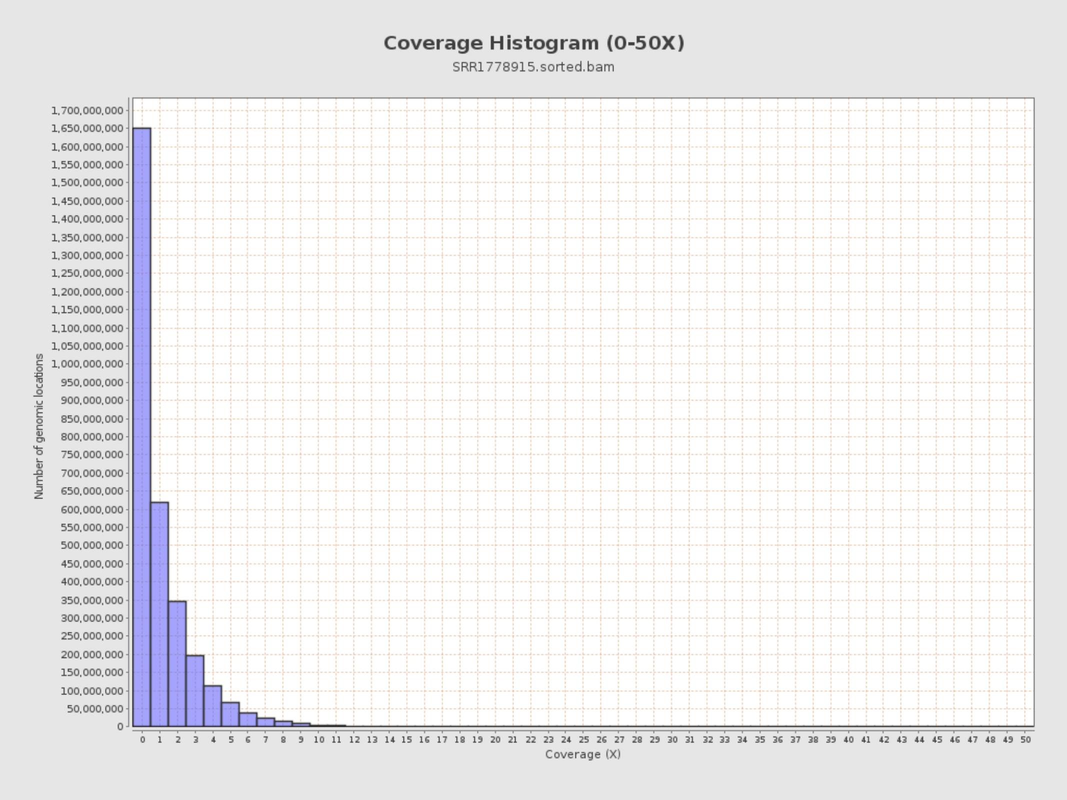
3. Results : Coverage across reference



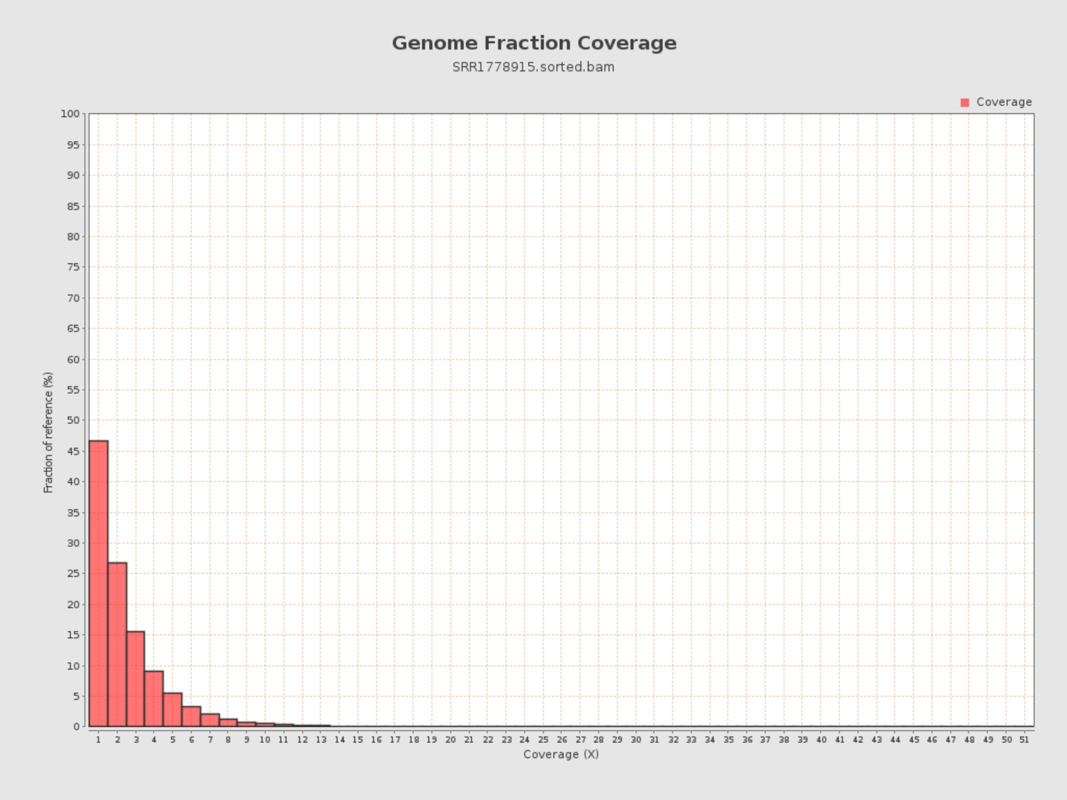
4. Results : Coverage Histogram



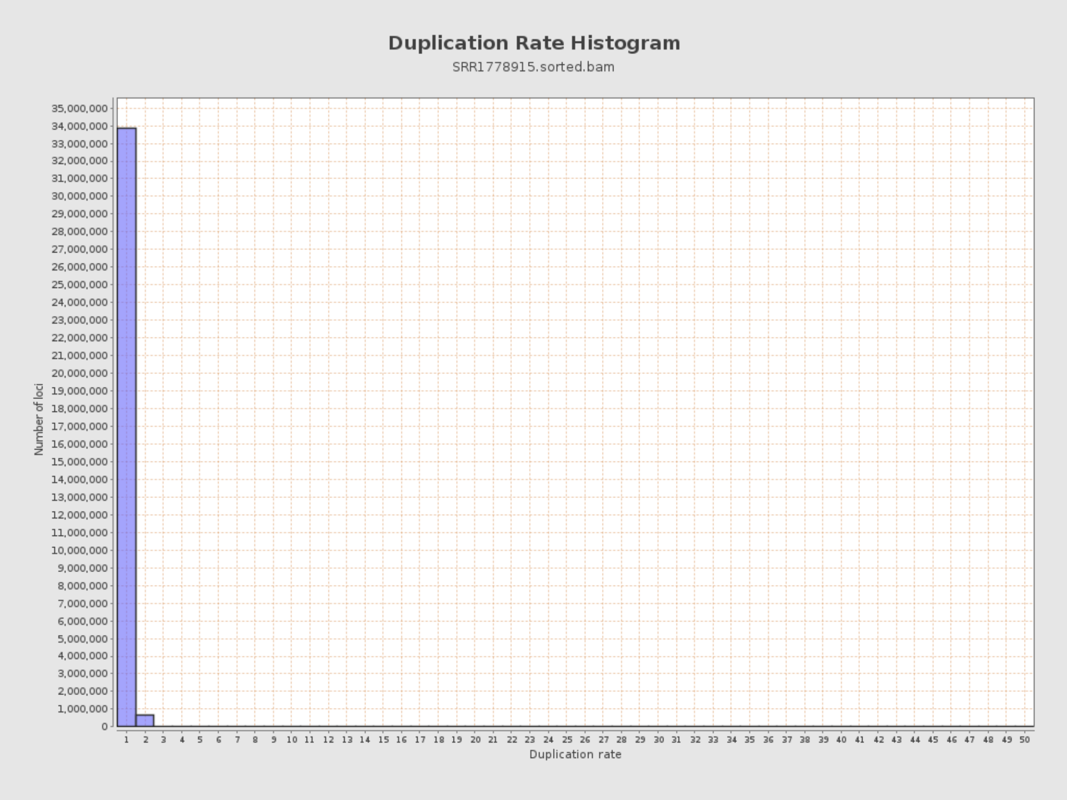
5. Results : Coverage Histogram (0-50X)



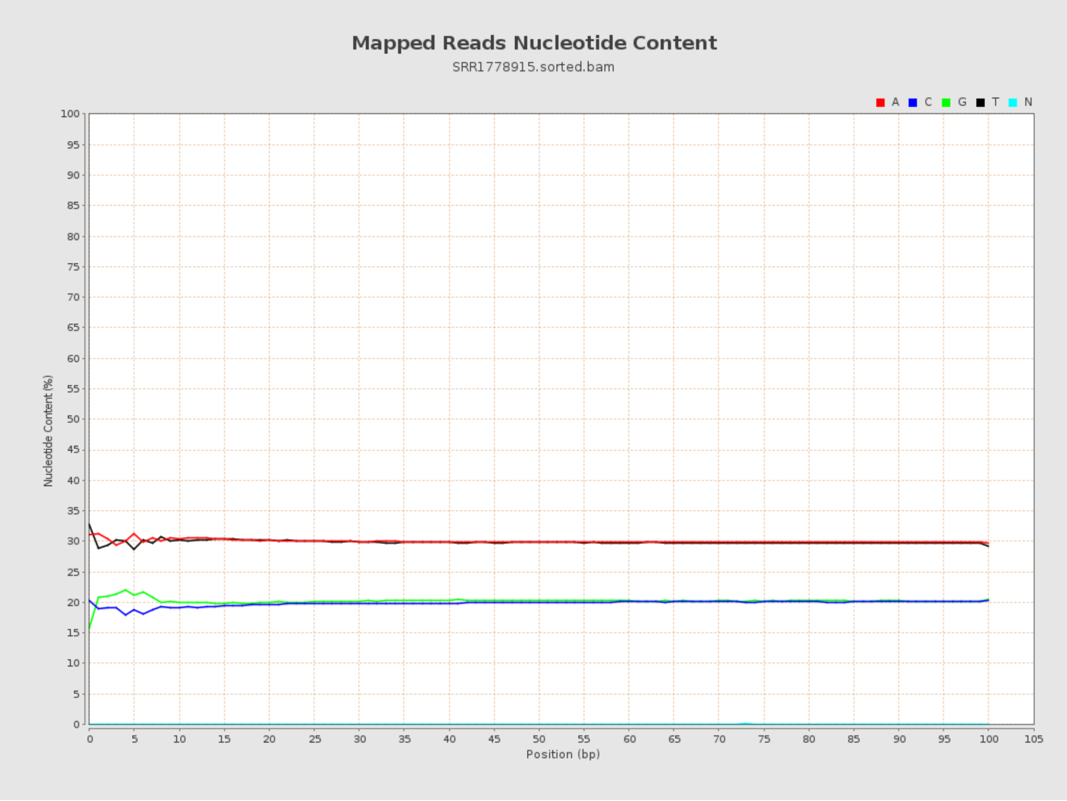
6. Results : Genome Fraction Coverage



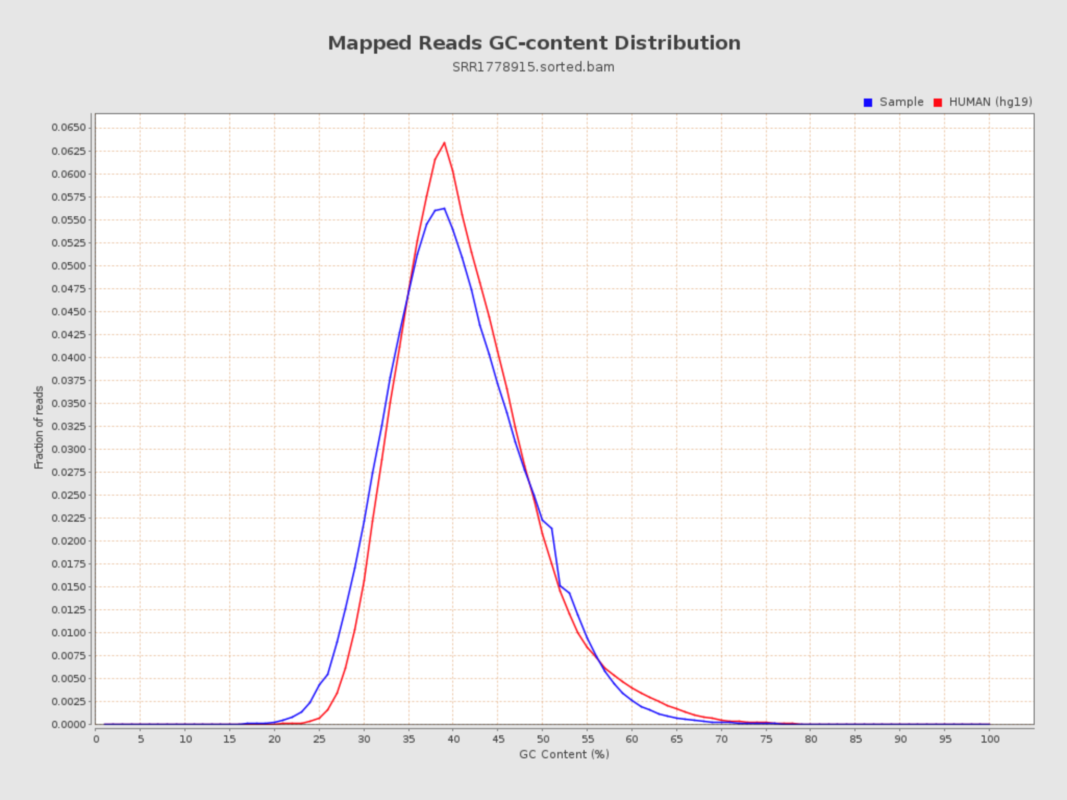
7. Results : Duplication Rate Histogram



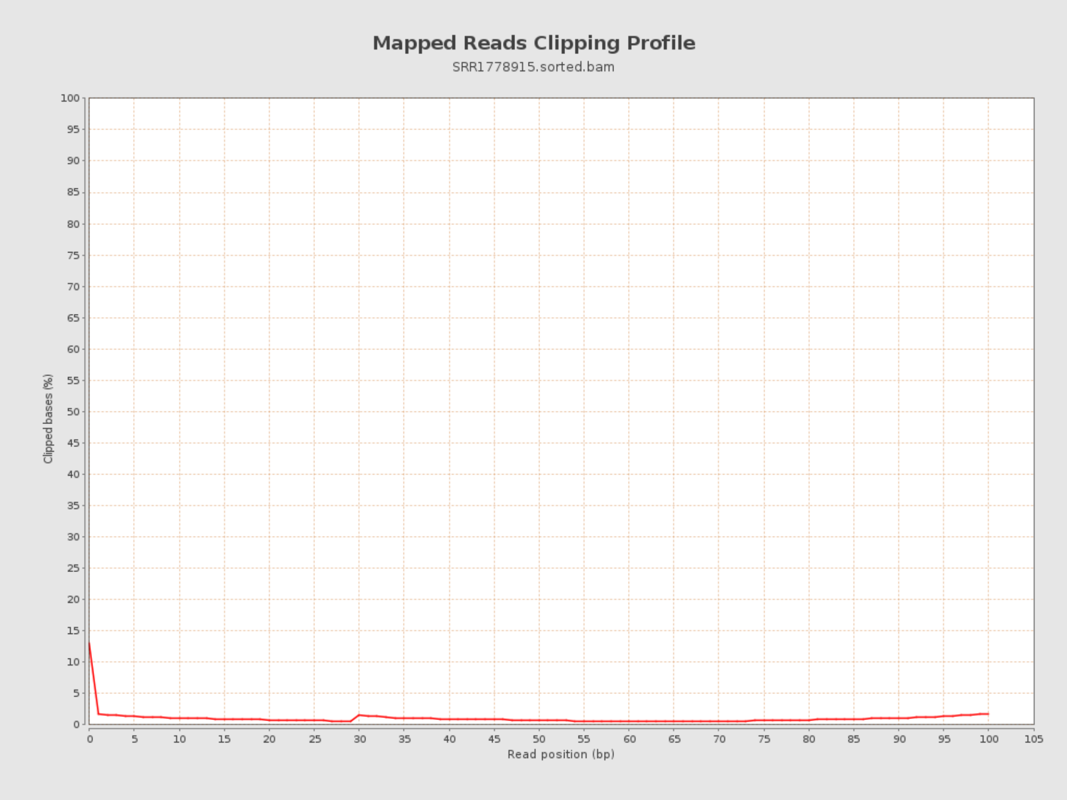
8. Results : Mapped Reads Nucleotide Content



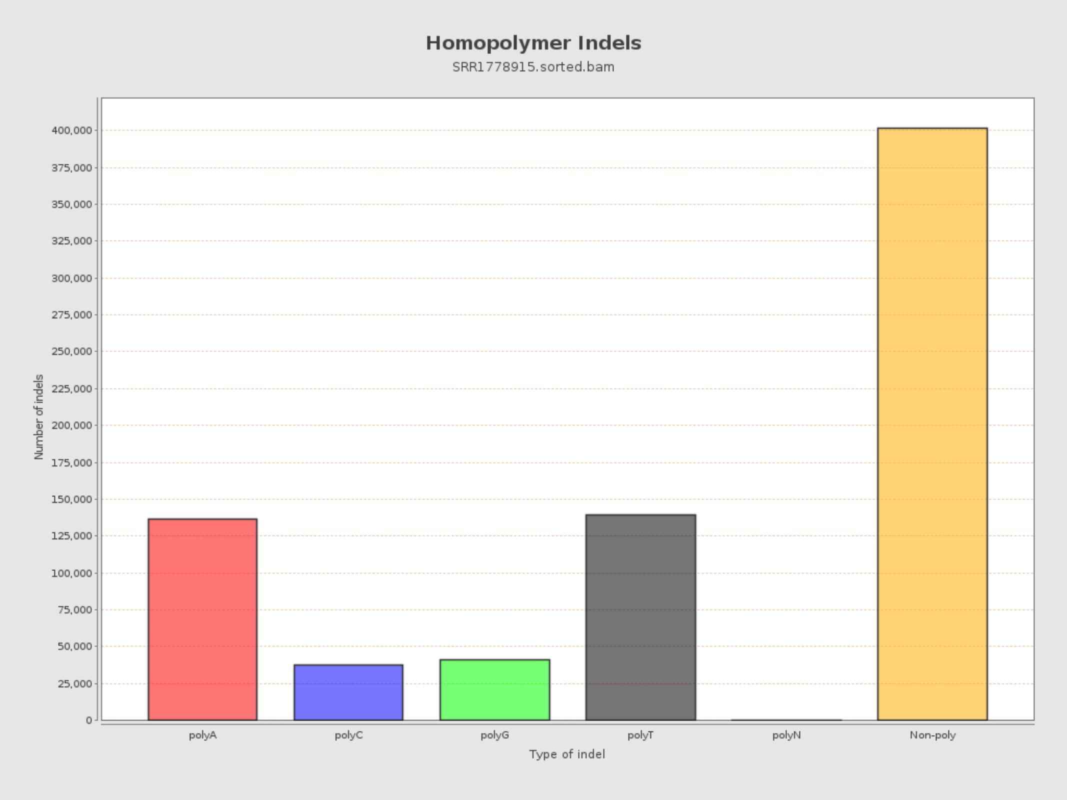
9. Results : Mapped Reads GC-content Distribution



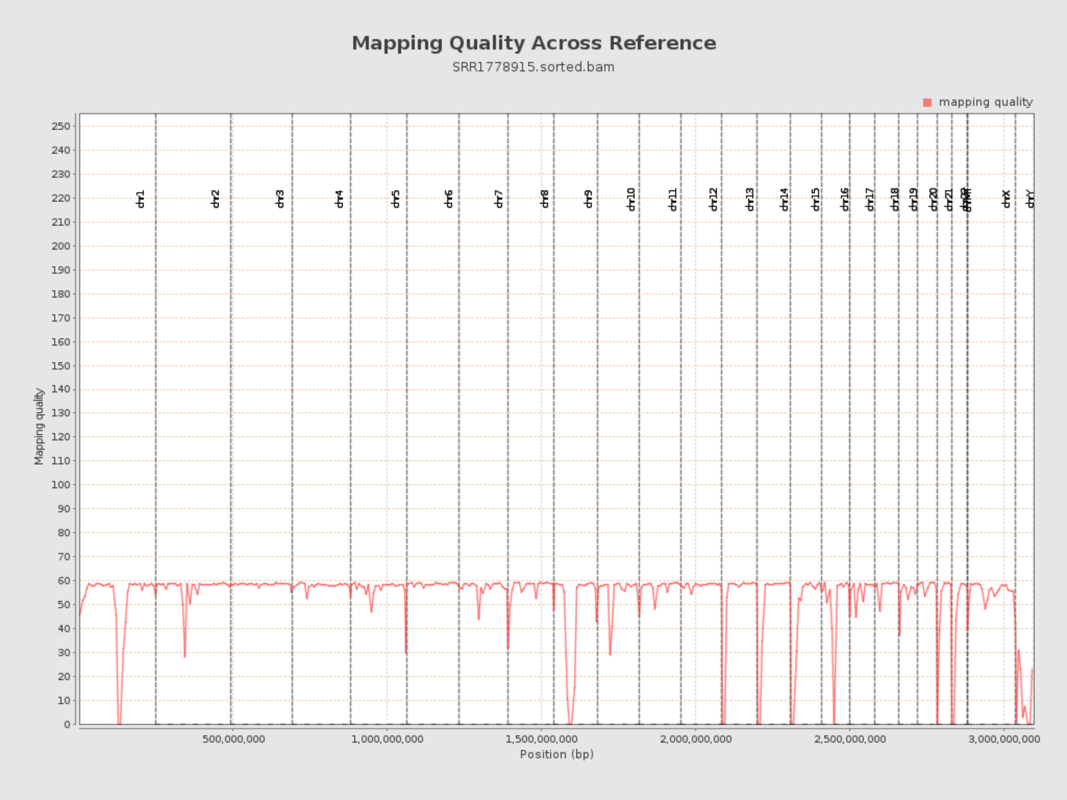
10. Results : Mapped Reads Clipping Profile



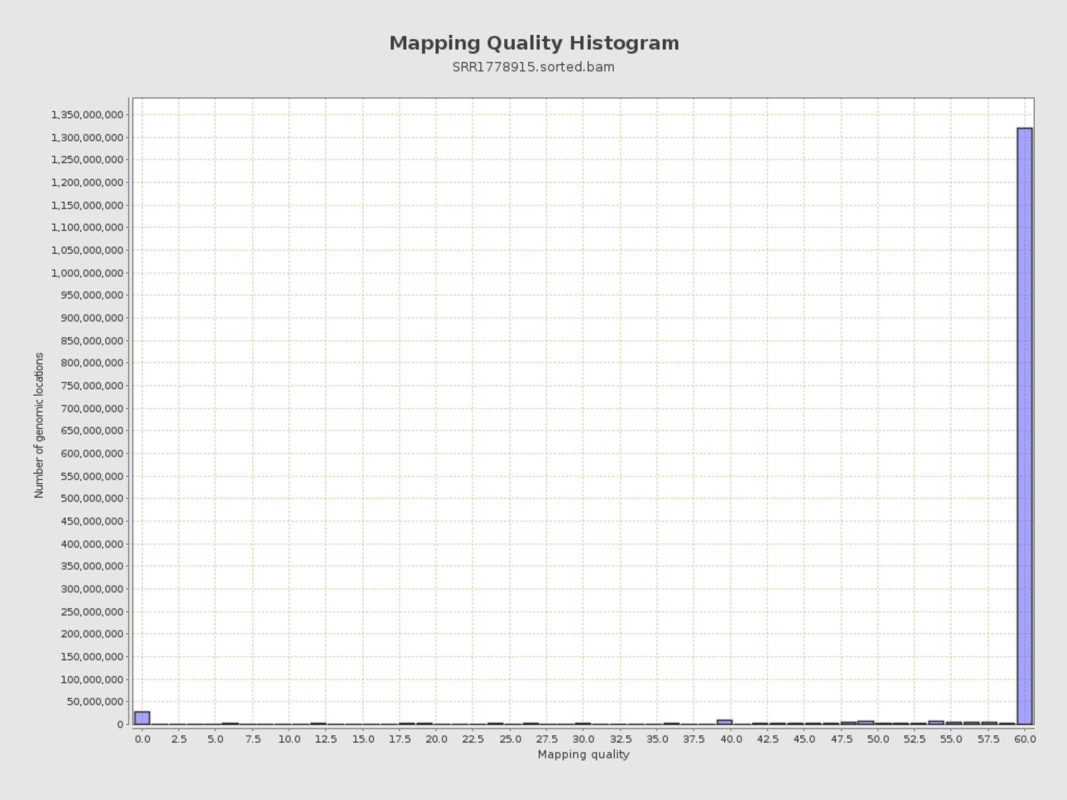
11. Results : Homopolymer Indels



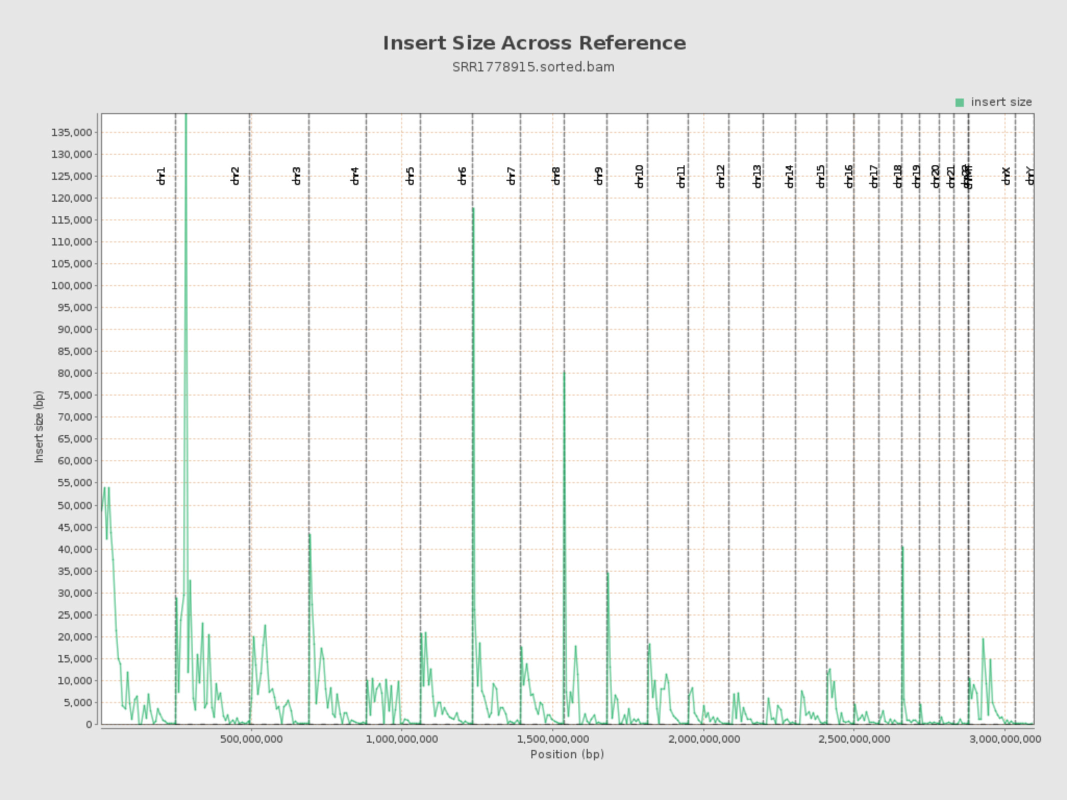
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram