Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/24 02:39:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1778442.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_SRR1778442 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1778442_1.fastq.gz SRR1778442_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Mar 24 02:39:54 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1778442.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	457,417,538
Mapped reads	413,507,277 / 90.4%
Unmapped reads	43,910,261 / 9.6%
Mapped paired reads	413,507,277 / 90.4%
Mapped reads, first in pair	207,618,664 / 45.39%
Mapped reads, second in pair	205,888,613 / 45.01%
Mapped reads, both in pair	402,976,804 / 88.1%
Mapped reads, singletons	10,530,473 / 2.3%
Secondary alignments	0
Supplementary alignments	947,544 / 0.21%
Read min/max/mean length	30 / 101 / 101.08
Duplicated reads (estimated)	56,252,485 / 12.3%
Duplication rate	8.71%
Clipped reads	26,922,153 / 5.89%

2.2. ACGT Content

Number/percentage of A's	12,064,340,724 / 29.47%
Number/percentage of C's	8,424,981,566 / 20.58%
Number/percentage of T's	11,993,775,648 / 29.3%
Number/percentage of G's	8,453,059,626 / 20.65%
Number/percentage of N's	4,777,654 / 0.01%

GC Percentage	41.23%

2.3. Coverage

Mean	13.2294
Standard Deviation	128.9662

2.4. Mapping Quality

Mean Mapping Quality	53.57

2.5. Insert size

Mean	49,750.94
Standard Deviation	2,176,576.45
P25/Median/P75	178 / 242 / 329

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	221,581,702
Insertions	4,439,404
Mapped reads with at least one insertion	1.04%
Deletions	5,658,573
Mapped reads with at least one deletion	1.33%
Homopolymer indels	44.36%

2.7. Chromosome stats

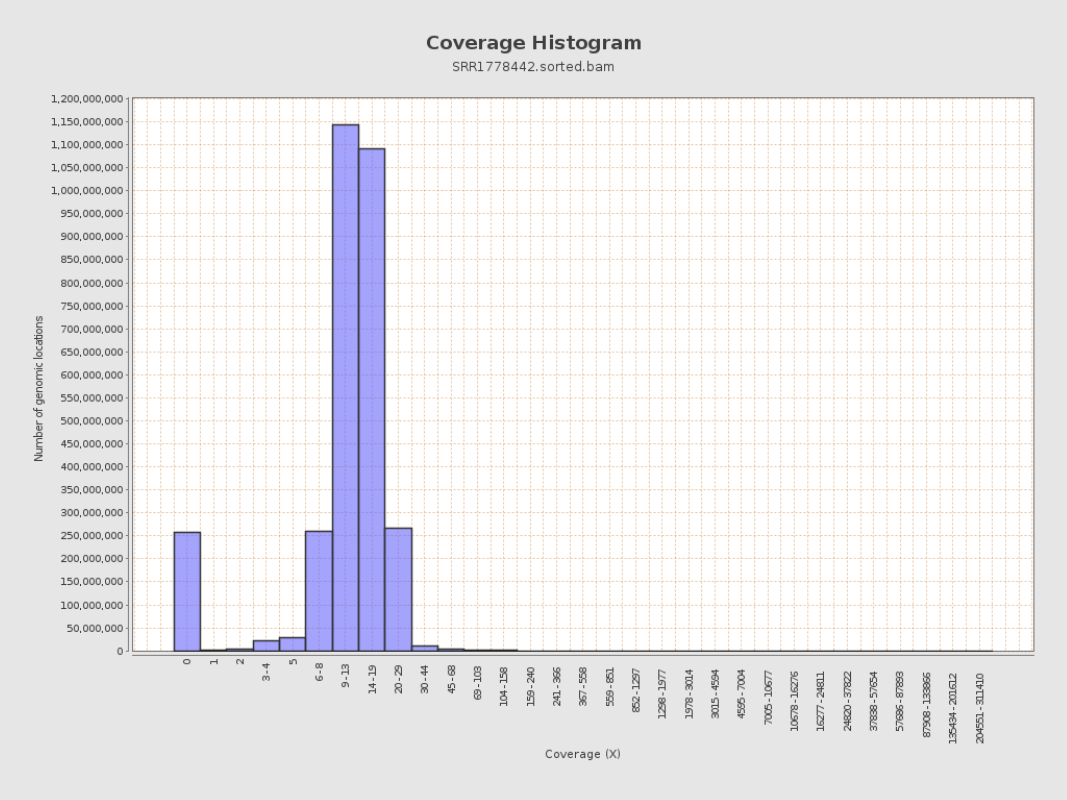
Name	**Length**	**Mapped**	**Mean**	**Standard**

		bases	coverage	deviation
chr1	249250621	3270242916	13.1203	321.5349
chr2	243199373	3391926582	13.9471	85.0674
chr3	198022430	2625728149	13.2598	11.5595
chr4	191154276	2639215308	13.8067	111.9737
chr5	180915260	2380363452	13.1573	12.8509
chr6	171115067	2275665002	13.299	52.5456
chr7	159138663	2169457125	13.6325	138.6987
chr8	146364022	1976815815	13.5062	134.7747
chr9	141213431	1707960549	12.0949	147.9528
chr10	135534747	2490184386	18.373	200.0083
chr11	135006516	1822149029	13.4967	49.9803
chr12	133851895	2198655756	16.426	17.5343
chr13	115169878	1256454489	10.9096	8.1837
chr14	107349540	1191841543	11.1024	11.7718
chr15	102531392	1119326685	10.9169	9.7764
chr16	90354753	1224624689	13.5535	64.8259
chr17	81195210	1119837529	13.7919	51.2826
chr18	78077248	1082451003	13.8638	149.2498
chr19	59128983	825325119	13.958	150.5848
chr20	63025520	832890897	13.2151	27.5769
chr21	48129895	551905575	11.467	41.6852
chr22	51304566	493570358	9.6204	11.7229
chrMT	16571	168050444	10,141.2373	916.7209
chrX	155270560	2009858683	12.9442	31.768

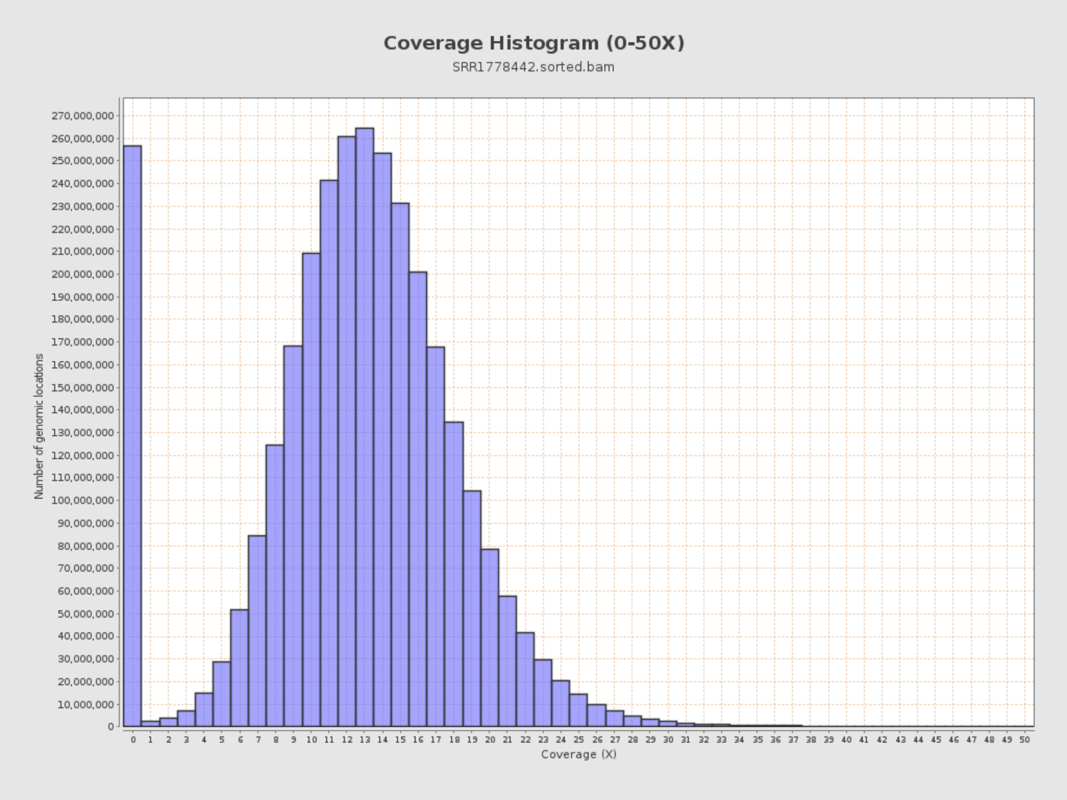
chrY	59373566	129751366	2.1853	108.0582

3. Results : Coverage across reference

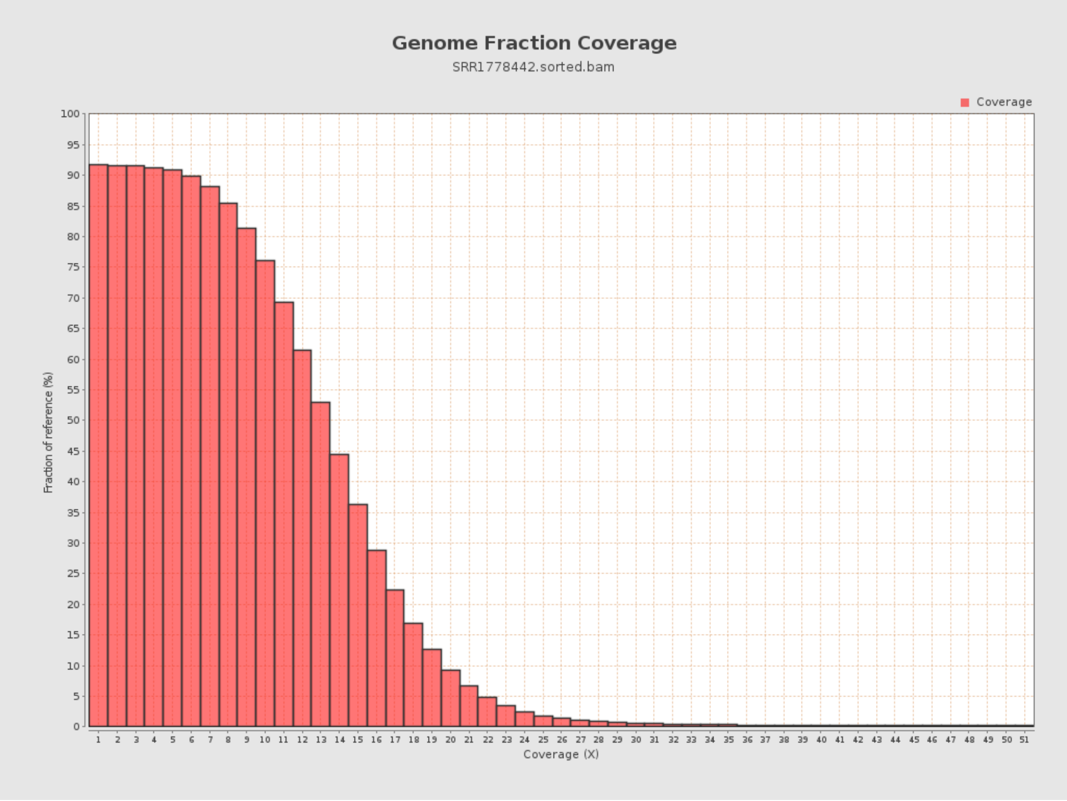
4. Results : Coverage Histogram



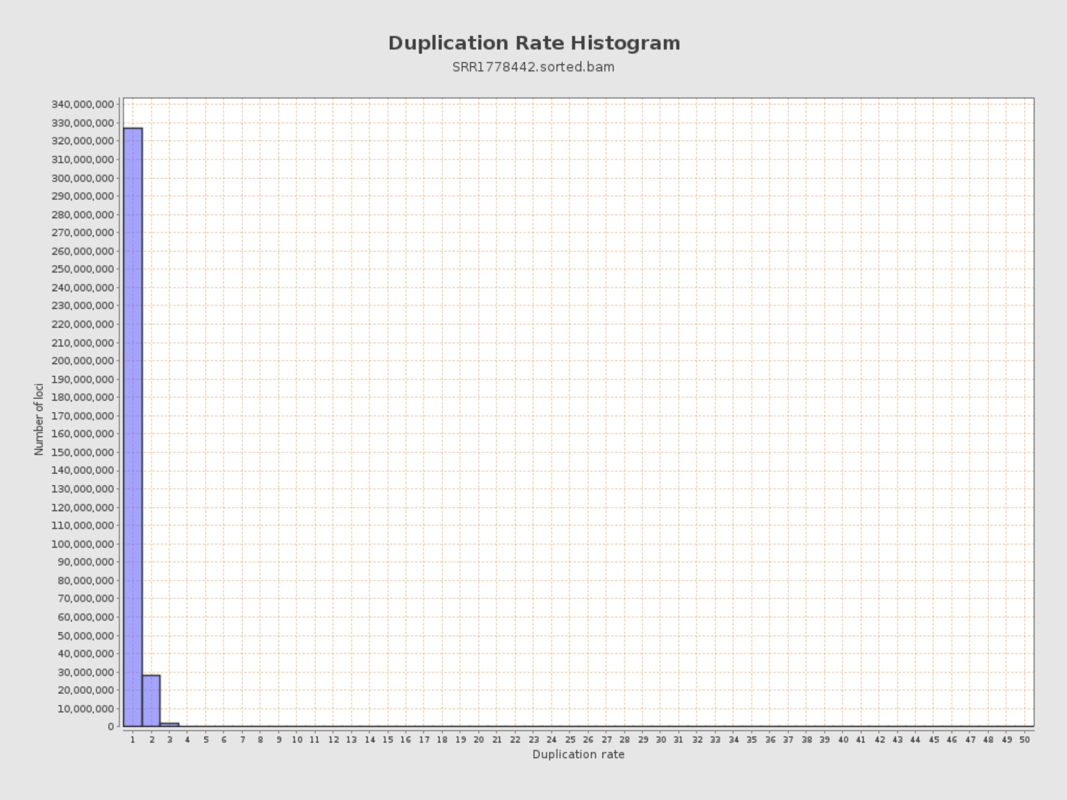
5. Results : Coverage Histogram (0-50X)



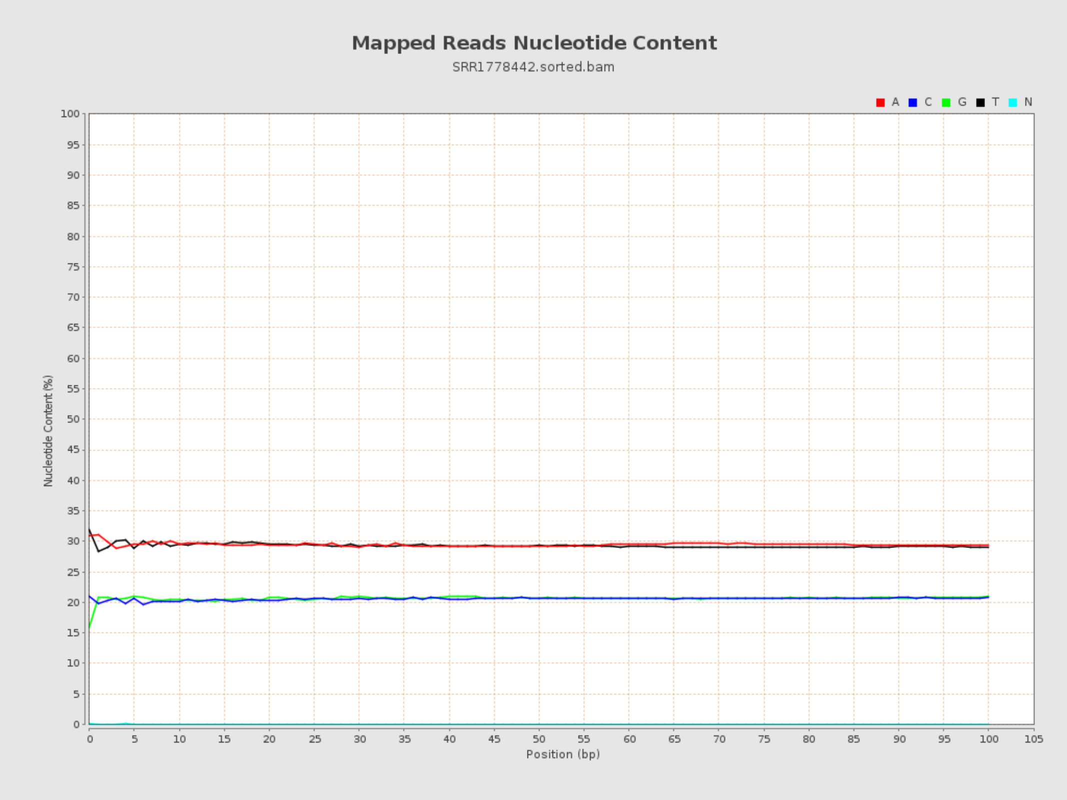
6. Results : Genome Fraction Coverage



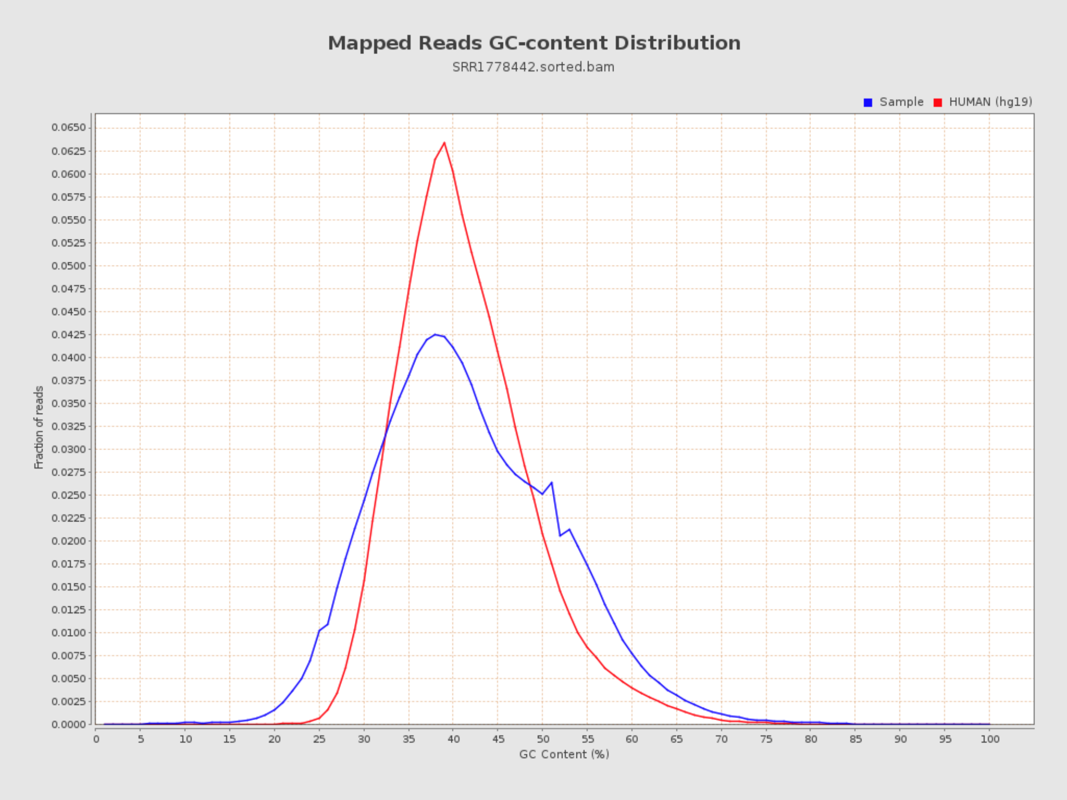
7. Results : Duplication Rate Histogram



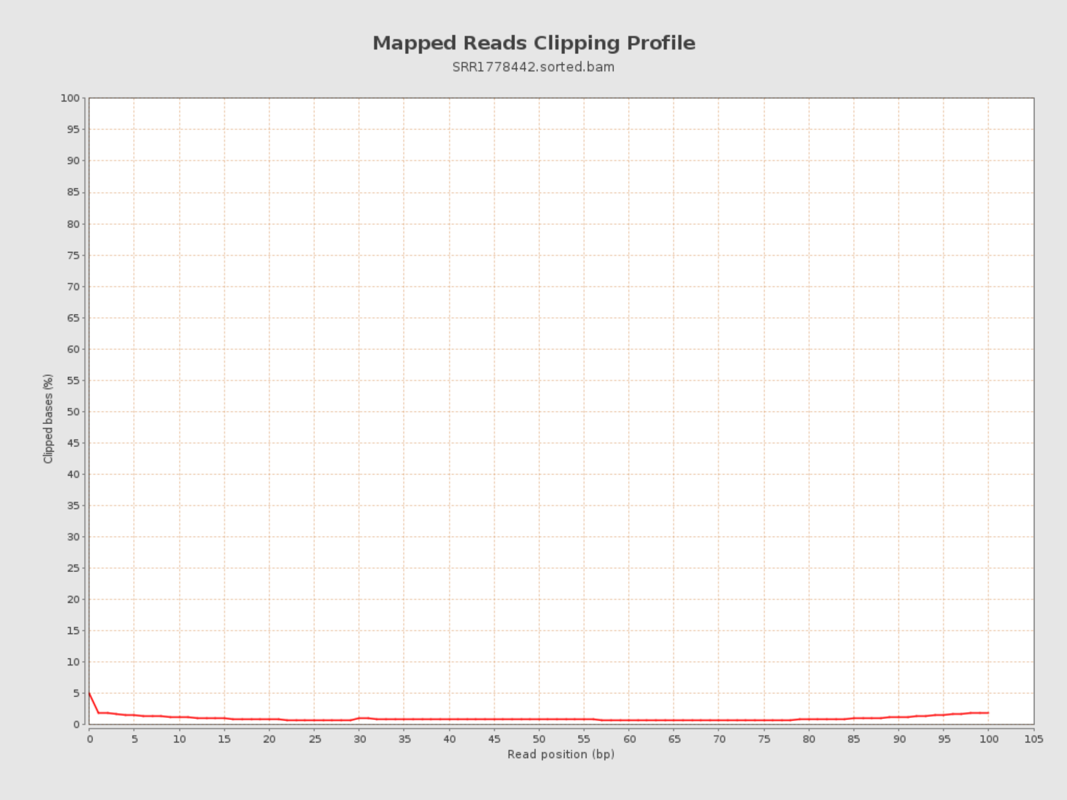
8. Results : Mapped Reads Nucleotide Content



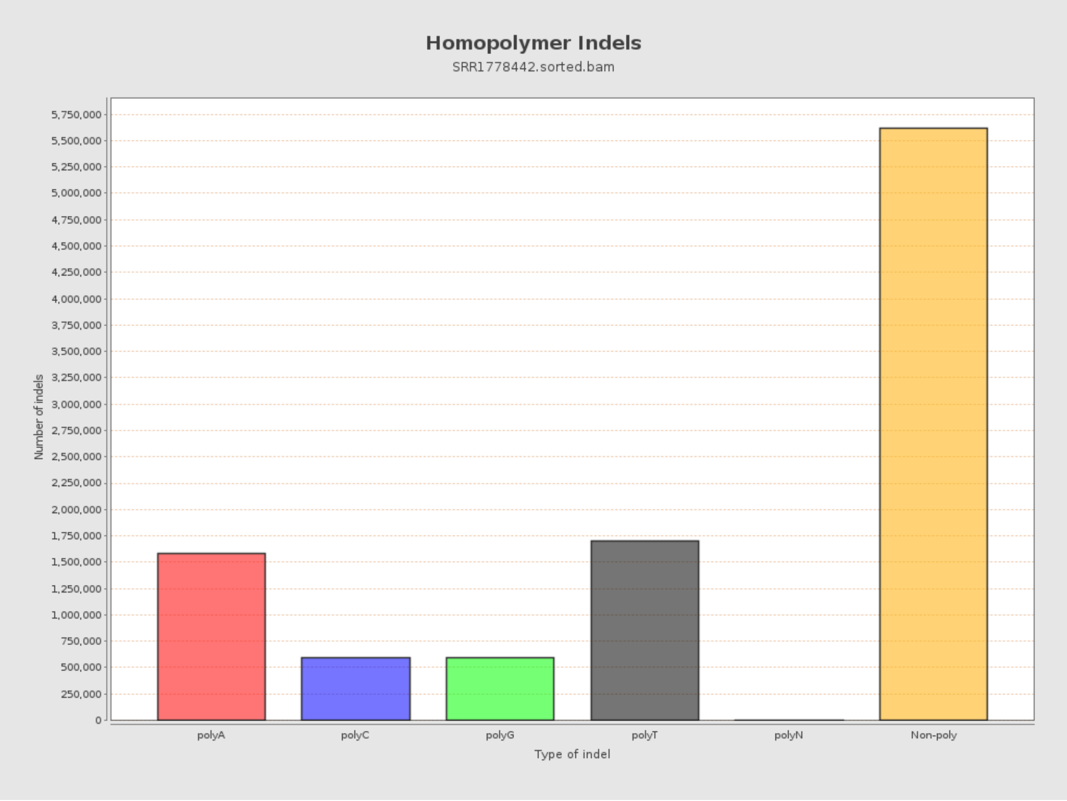
9. Results : Mapped Reads GC-content Distribution



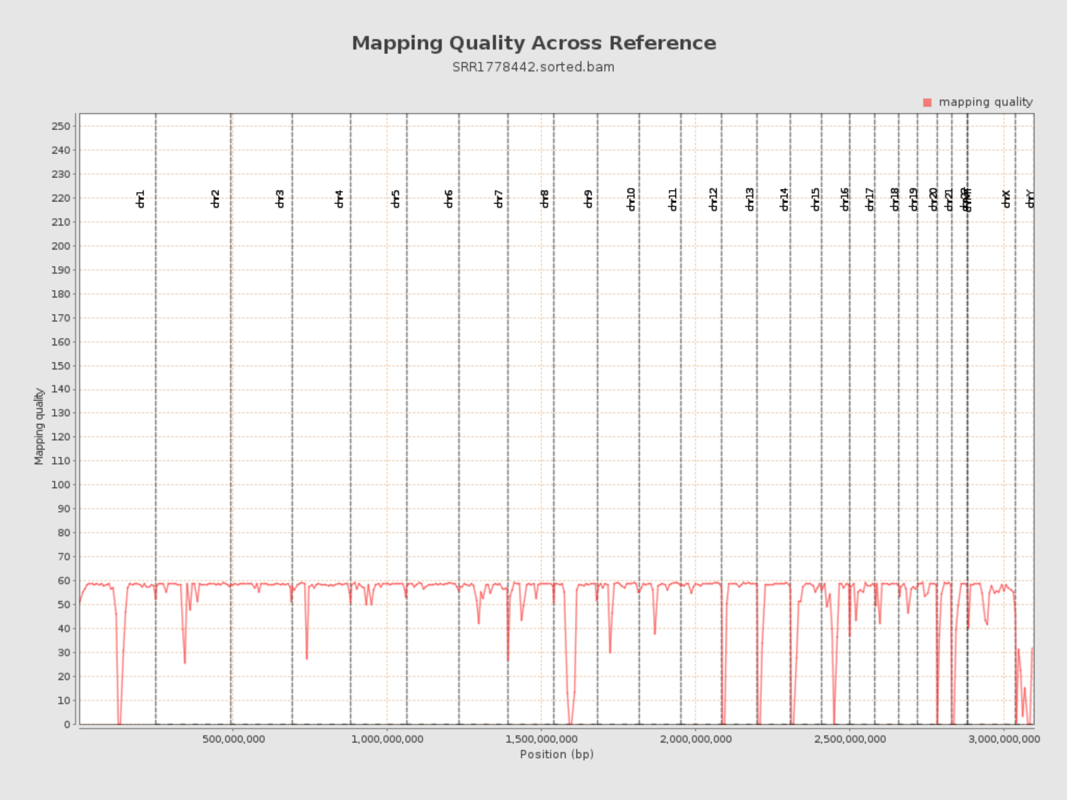
10. Results : Mapped Reads Clipping Profile



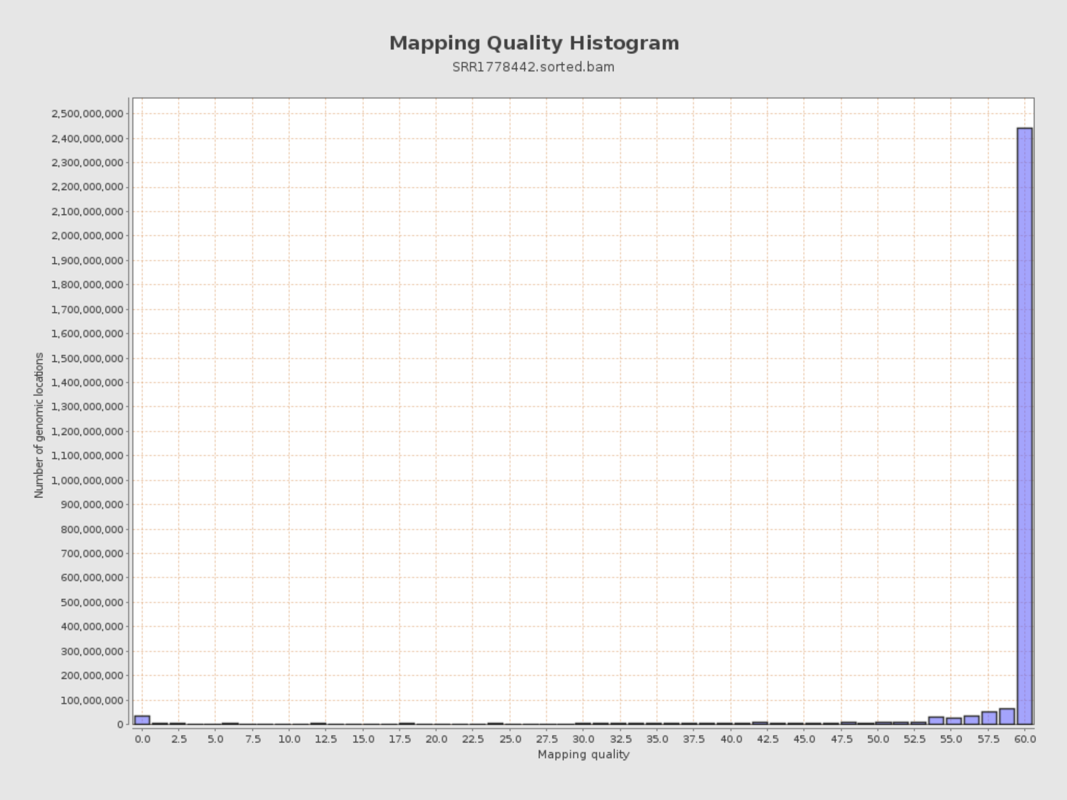
11. Results : Homopolymer Indels



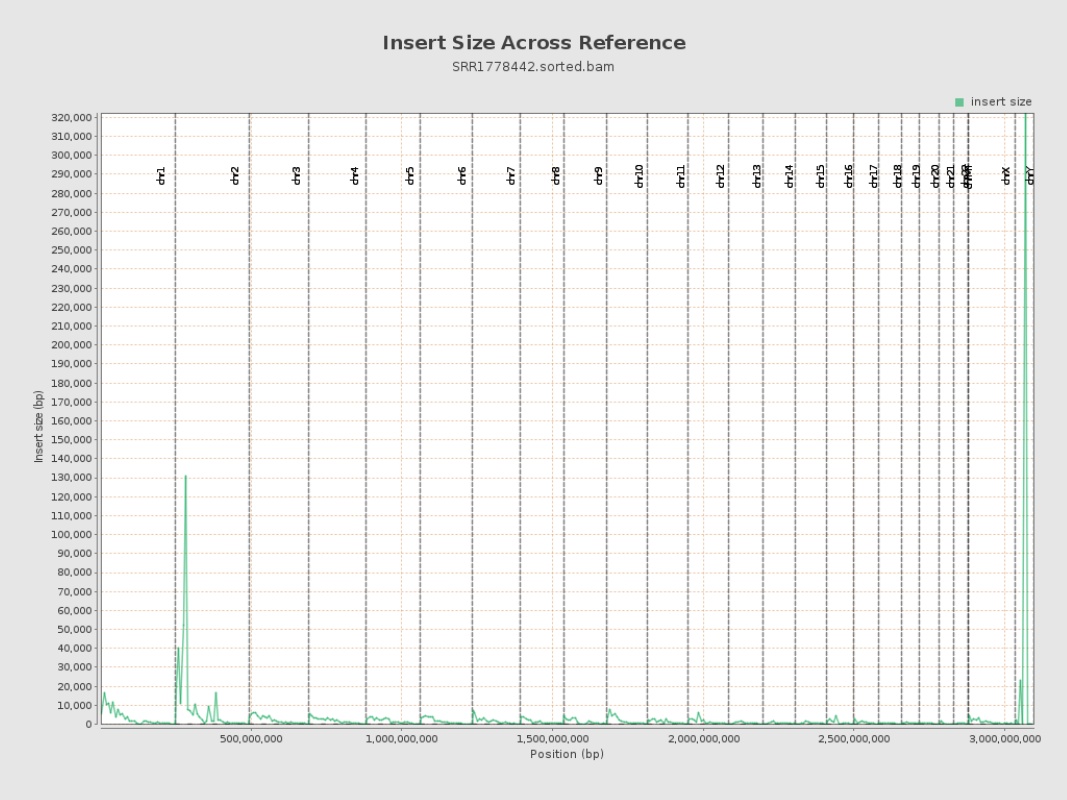
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram