Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/27 21:08:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781857.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_SRR1781857 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781857_1.fastq.gz SRR1781857_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Mar 27 21:08:18 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781857.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	147,673,722
Mapped reads	144,839,944 / 98.08%
Unmapped reads	2,833,778 / 1.92%
Mapped paired reads	144,839,944 / 98.08%
Mapped reads, first in pair	72,798,555 / 49.3%
Mapped reads, second in pair	72,041,389 / 48.78%
Mapped reads, both in pair	143,608,712 / 97.25%
Mapped reads, singletons	1,231,232 / 0.83%
Secondary alignments	0
Supplementary alignments	452,134 / 0.31%
Read min/max/mean length	30 / 100 / 99.98
Duplicated reads (estimated)	8,836,715 / 5.98%
Duplication rate	5.88%
Clipped reads	5,979,705 / 4.05%

2.2. ACGT Content

Number/percentage of A's	4,287,562,664 / 29.79%
Number/percentage of C's	2,896,423,927 / 20.13%
Number/percentage of T's	4,272,695,712 / 29.69%
Number/percentage of G's	2,932,124,542 / 20.38%
Number/percentage of N's	1,479,749 / 0.01%

GC Percentage	40.5%

2.3. Coverage

Mean	4.6495
Standard Deviation	5.8613

2.4. Mapping Quality

Mean Mapping Quality	53.93

2.5. Insert size

Mean	33,606.42
Standard Deviation	1,783,281.08
P25/Median/P75	168 / 205 / 249

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	53,416,170
Insertions	1,628,865
Mapped reads with at least one insertion	1.11%
Deletions	1,335,770
Mapped reads with at least one deletion	0.91%
Homopolymer indels	47.2%

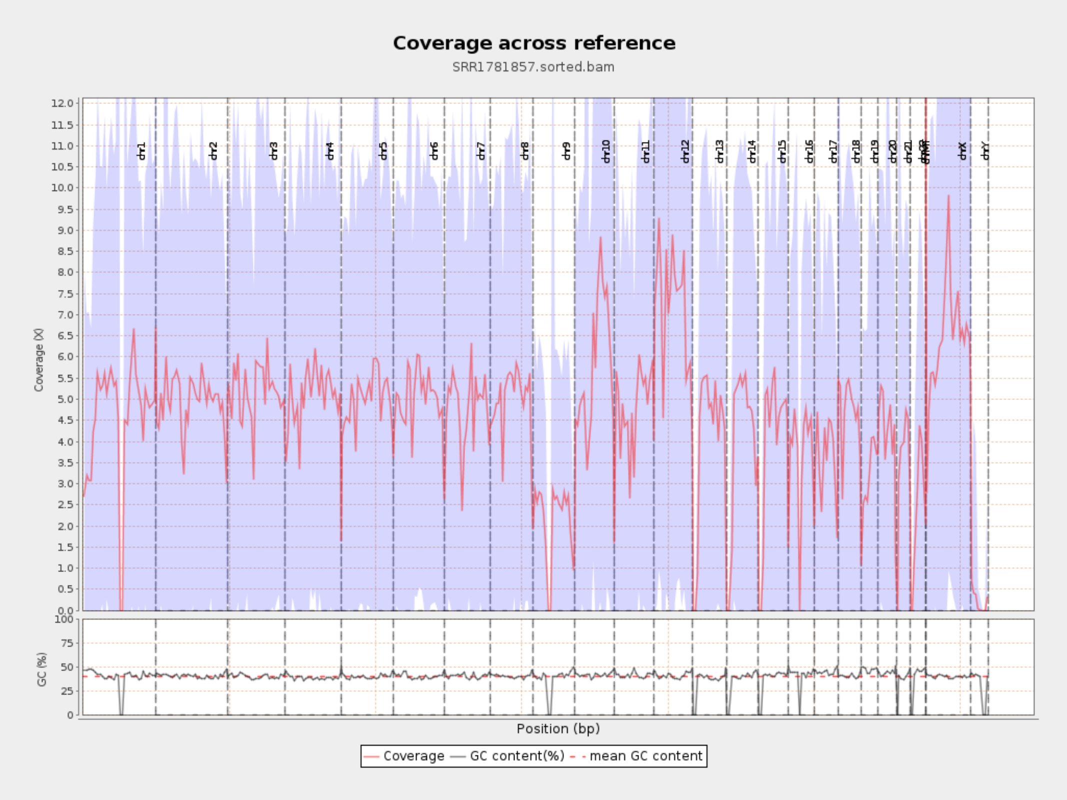
2.7. Chromosome stats

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

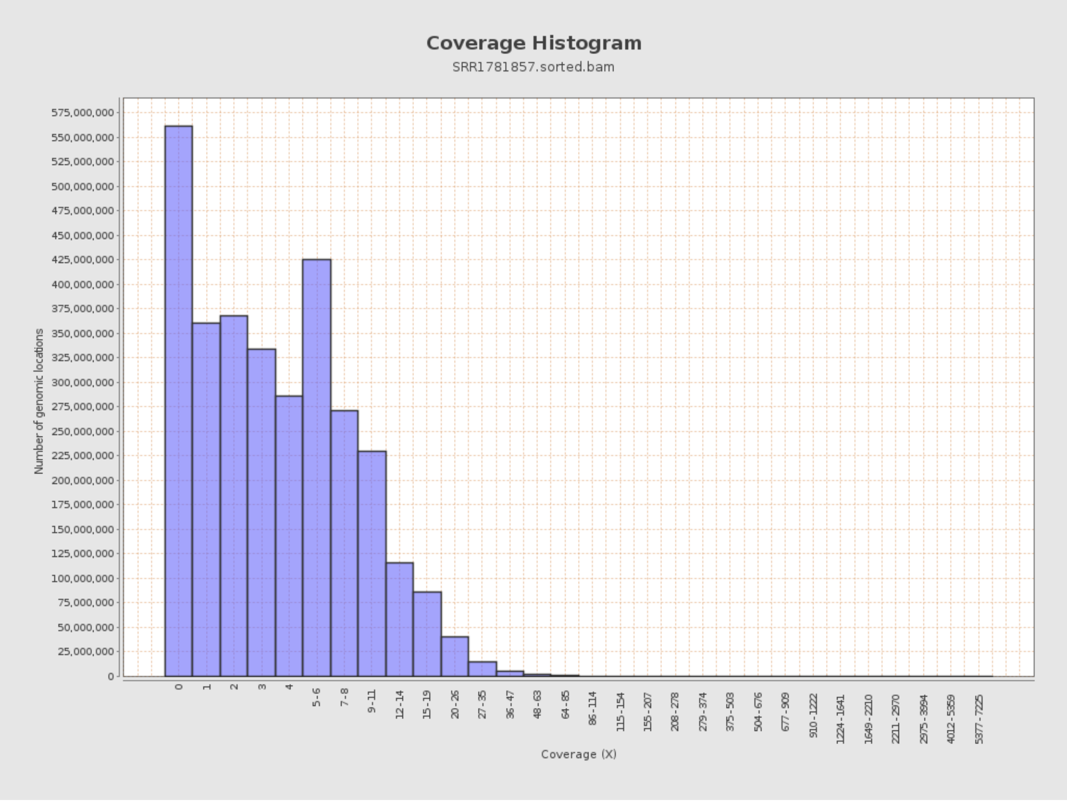
		bases	coverage	deviation
chr1	249250621	1138917157	4.5694	6.7221
chr2	243199373	1200172564	4.9349	7.9584
chr3	198022430	1026389755	5.1832	5.1193
chr4	191154276	978327930	5.118	5.2174
chr5	180915260	903560880	4.9944	4.8744
chr6	171115067	866802811	5.0656	5.2568
chr7	159138663	756389812	4.753	5.414
chr8	146364022	732472937	5.0045	4.9683
chr9	141213431	305791234	2.1655	4.1395
chr10	135534747	795002550	5.8657	7.7121
chr11	135006516	644524982	4.774	5.113
chr12	133851895	977946523	7.3062	7.2
chr13	115169878	465732838	4.0439	4.6311
chr14	107349540	431116398	4.016	4.7751
chr15	102531392	402162737	3.9223	4.8853
chr16	90354753	322865572	3.5733	4.6347
chr17	81195210	298586608	3.6774	4.5882
chr18	78077248	367356297	4.705	5.3145
chr19	59128983	188581309	3.1893	4.8124
chr20	63025520	272601422	4.3253	5.8239
chr21	48129895	169942901	3.5309	6.1249
chr22	51304566	124858725	2.4337	3.994
chrMT	16571	223508	13.4879	5.5362
chrX	155270560	1010173847	6.5059	6.5766

chrY	59373566	12773743	0.2151	2.2181

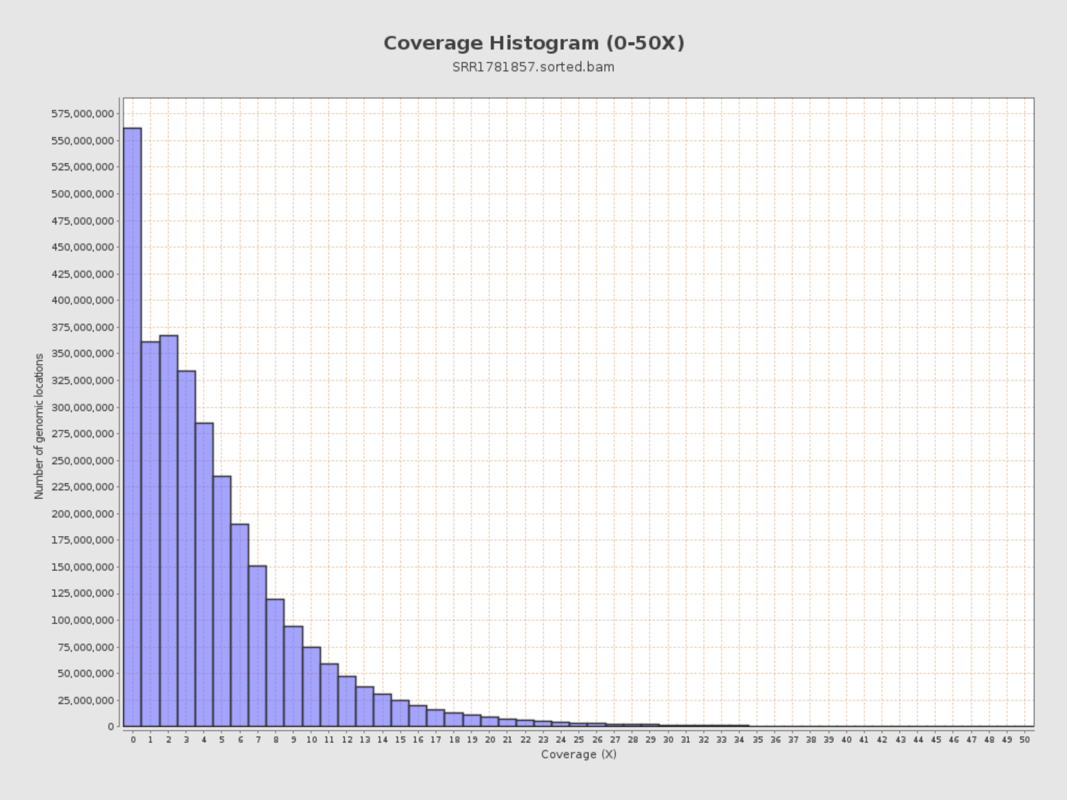
3. Results : Coverage across reference



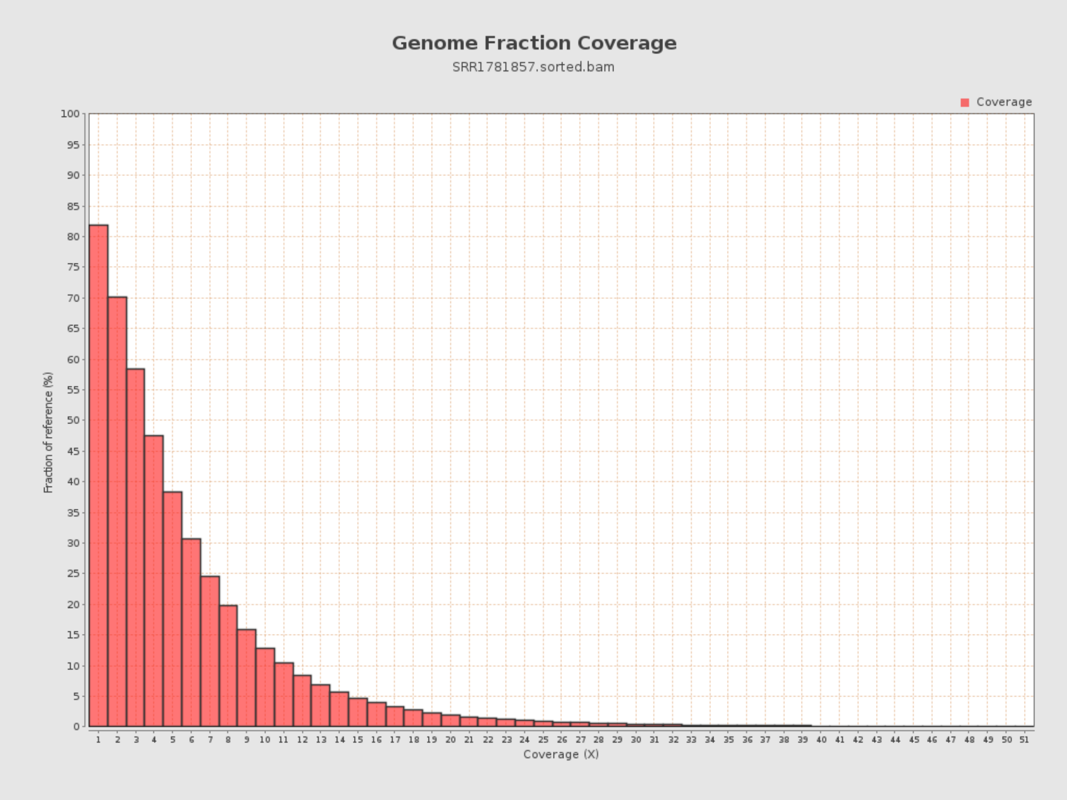
4. Results : Coverage Histogram



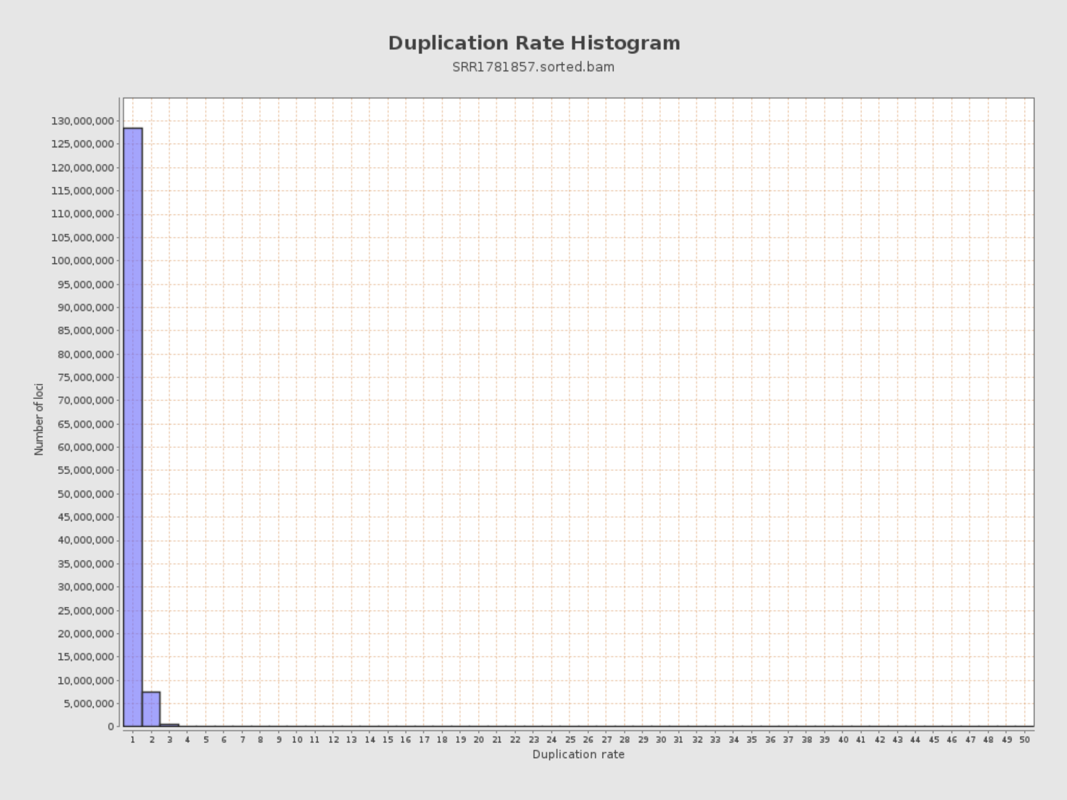
5. Results : Coverage Histogram (0-50X)



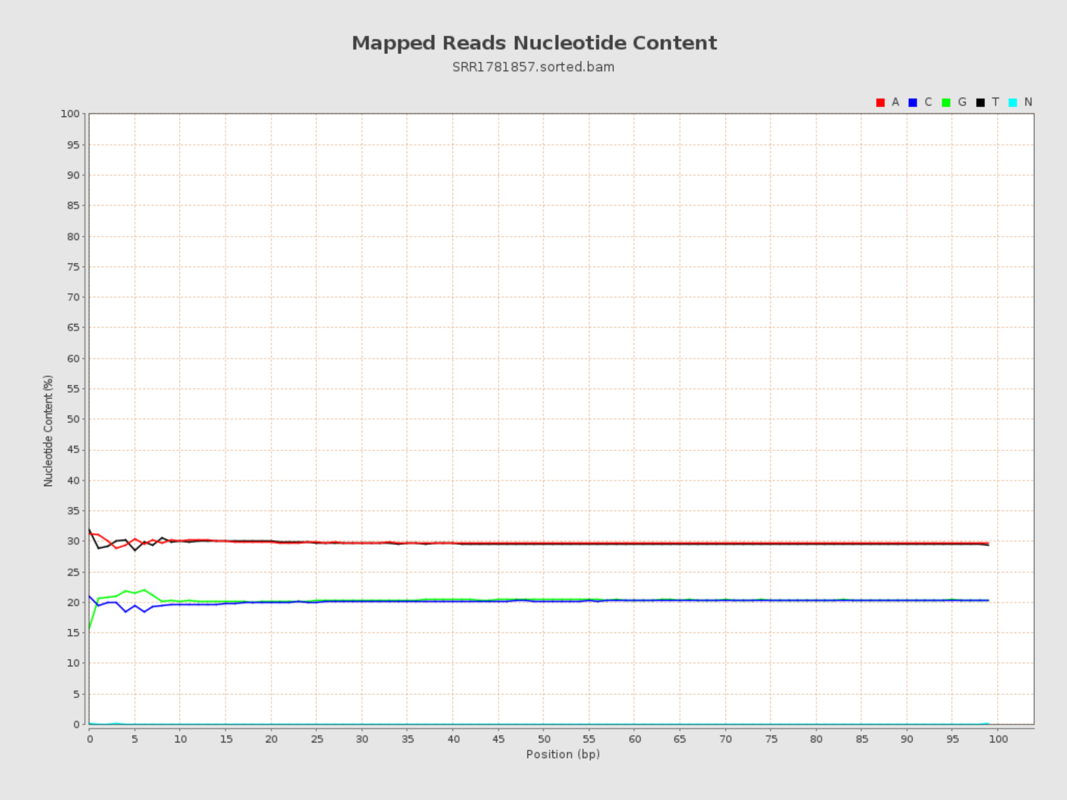
6. Results : Genome Fraction Coverage



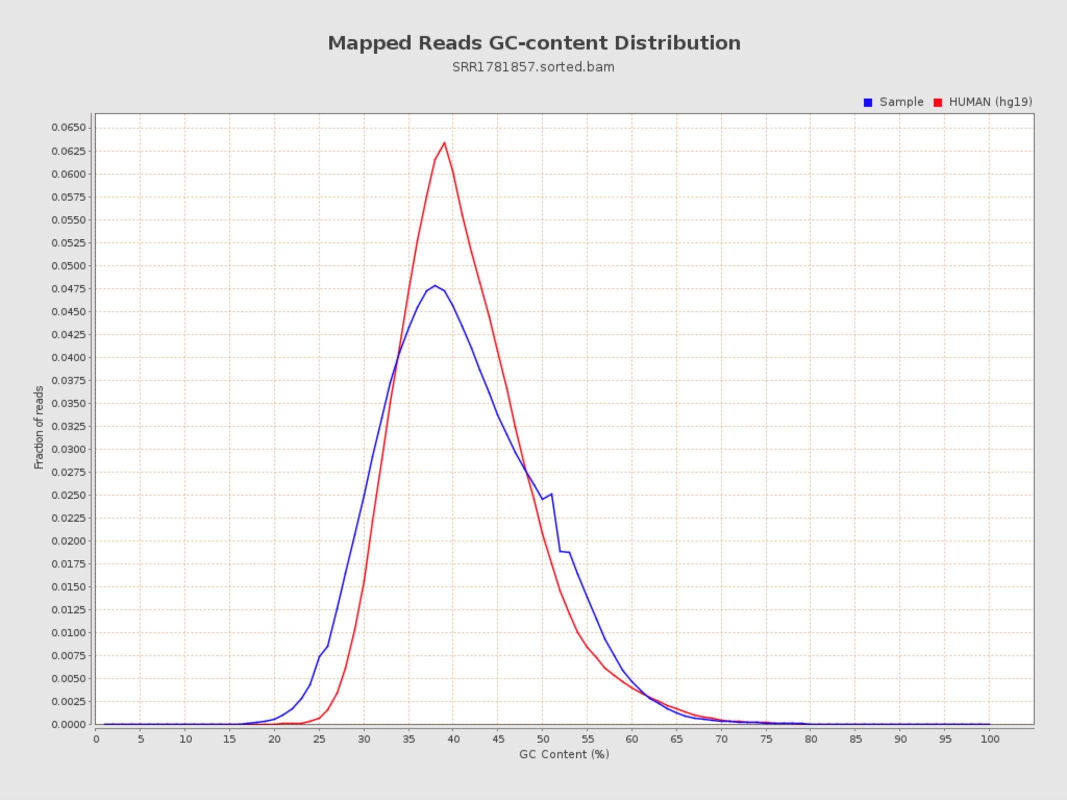
7. Results : Duplication Rate Histogram



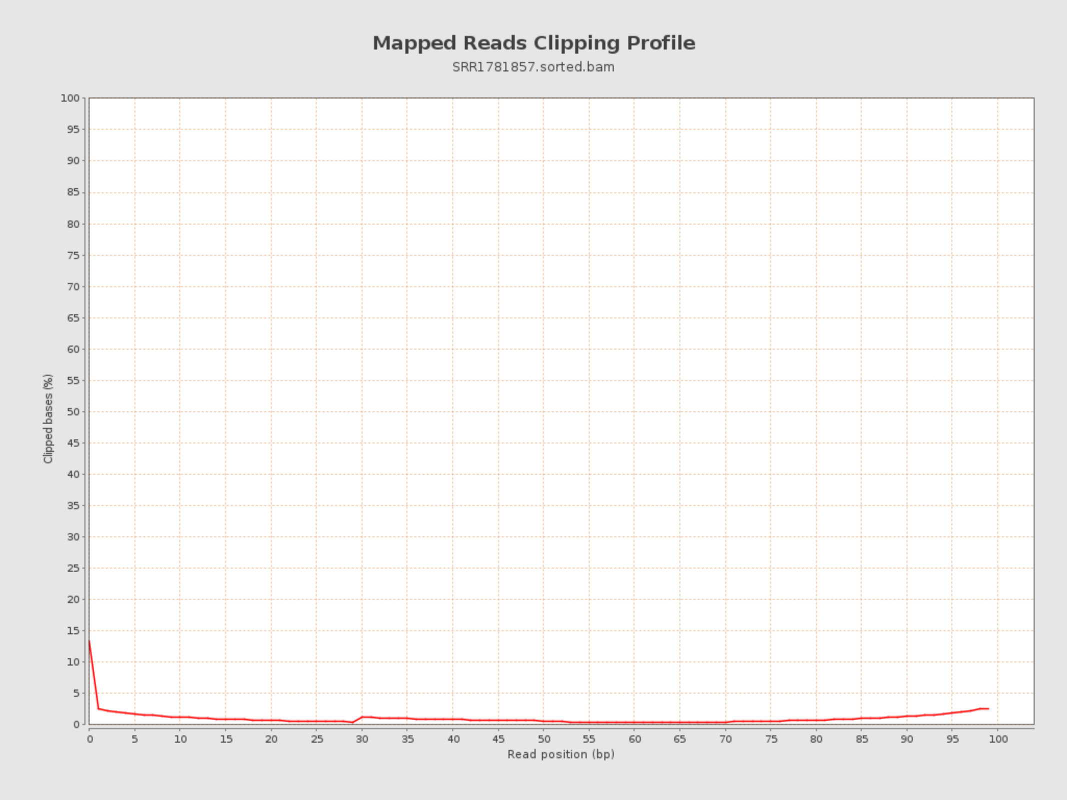
8. Results : Mapped Reads Nucleotide Content



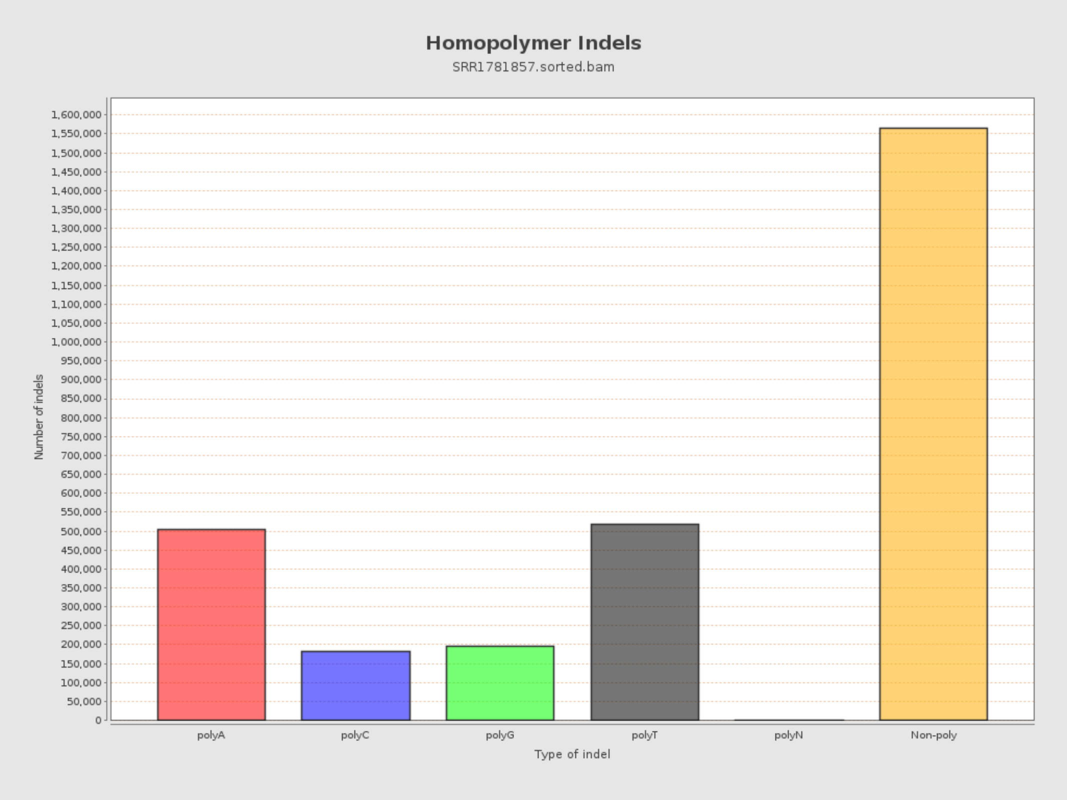
9. Results : Mapped Reads GC-content Distribution



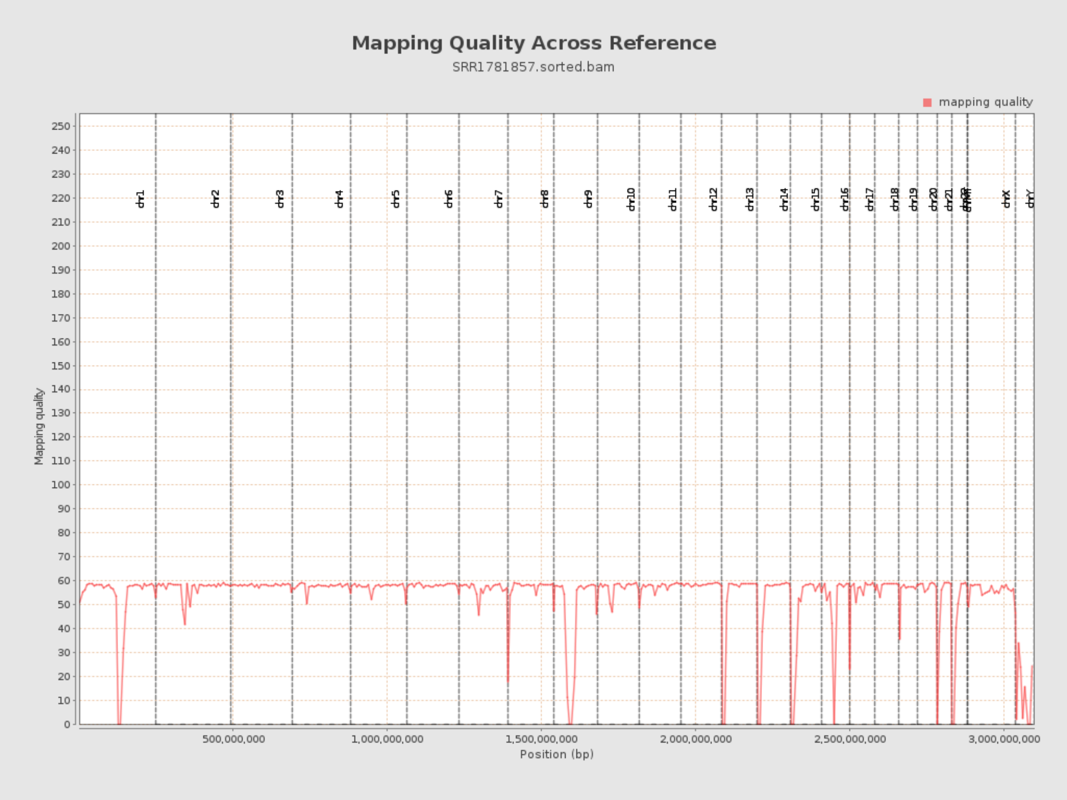
10. Results : Mapped Reads Clipping Profile



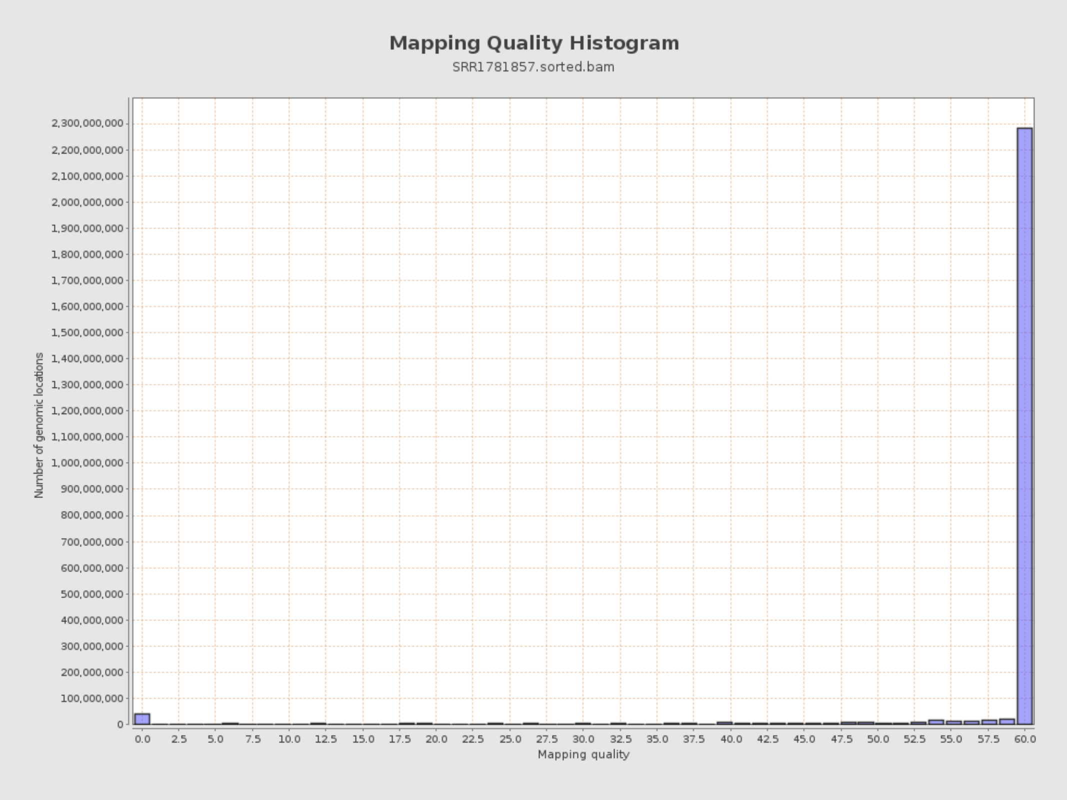
11. Results : Homopolymer Indels



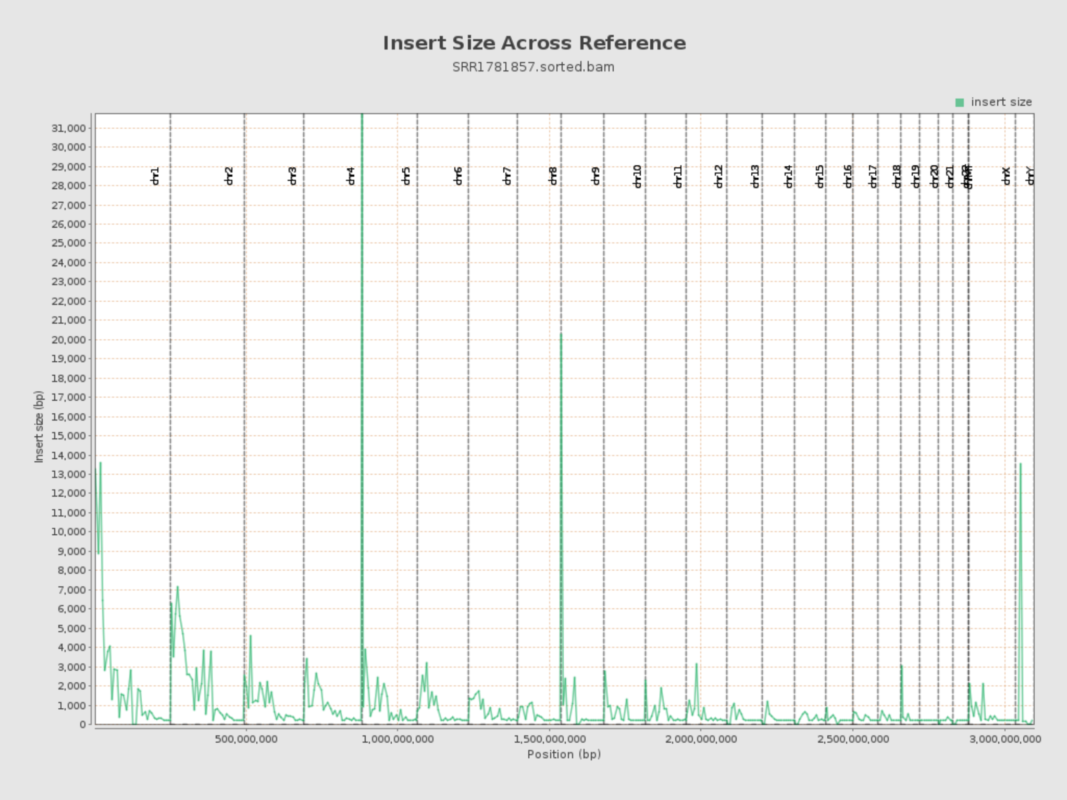
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram