Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/26 21:24:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781851.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_SRR1781851 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781851_1.fastq.gz SRR1781851_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Mar 26 21:24:01 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781851.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	162,472,042
Mapped reads	157,420,590 / 96.89%
Unmapped reads	5,051,452 / 3.11%
Mapped paired reads	157,420,590 / 96.89%
Mapped reads, first in pair	79,524,103 / 48.95%
Mapped reads, second in pair	77,896,487 / 47.94%
Mapped reads, both in pair	153,908,934 / 94.73%
Mapped reads, singletons	3,511,656 / 2.16%
Secondary alignments	0
Supplementary alignments	528,609 / 0.33%
Read min/max/mean length	30 / 100 / 99.99
Duplicated reads (estimated)	11,175,059 / 6.88%
Duplication rate	6.87%
Clipped reads	9,356,178 / 5.76%

2.2. ACGT Content

Number/percentage of A's	4,676,608,259 / 29.99%
Number/percentage of C's	3,133,169,047 / 20.09%
Number/percentage of T's	4,610,936,508 / 29.56%
Number/percentage of G's	3,170,723,426 / 20.33%
Number/percentage of N's	4,740,556 / 0.03%

GC Percentage	40.42%

2.3. Coverage

Mean	5.0391
Standard Deviation	6.2469

2.4. Mapping Quality

Mean Mapping Quality	53.82

2.5. Insert size

Mean	45,961.93
Standard Deviation	2,113,700.87
P25/Median/P75	146 / 185 / 235

2.6. Mismatches and indels

General error rate	0.47%
Mismatches	70,663,904
Insertions	1,865,472
Mapped reads with at least one insertion	1.17%
Deletions	1,405,189
Mapped reads with at least one deletion	0.88%
Homopolymer indels	47.53%

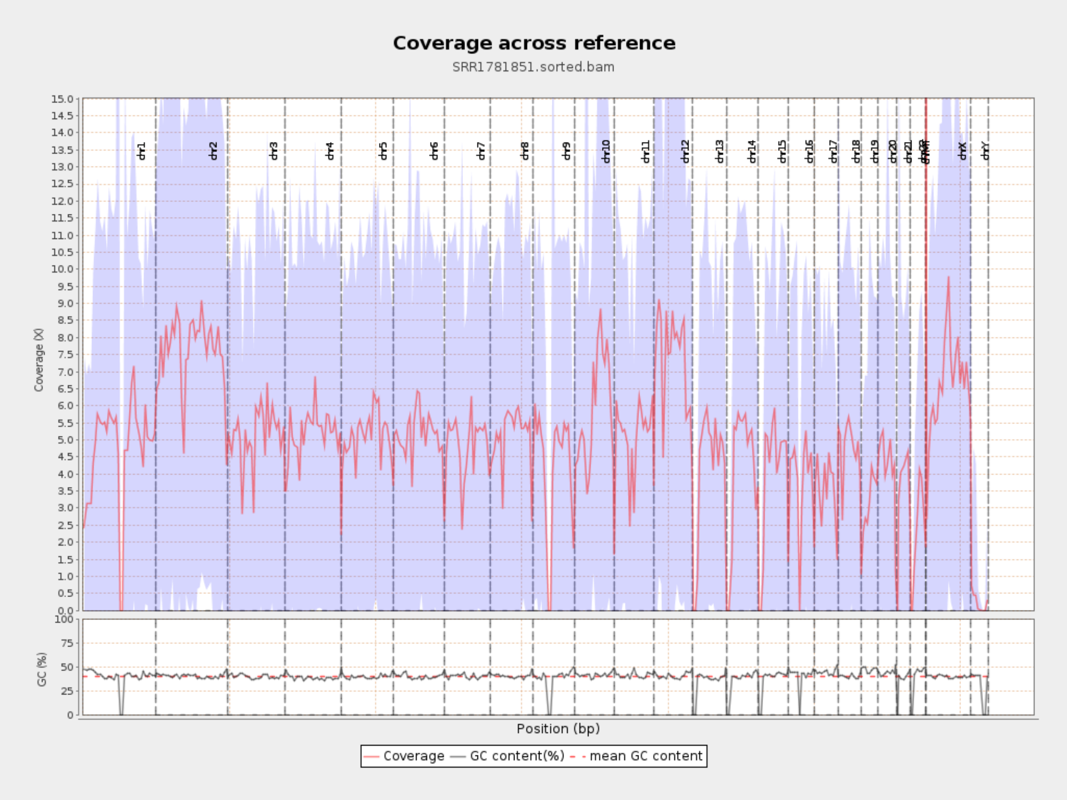
2.7. Chromosome stats

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

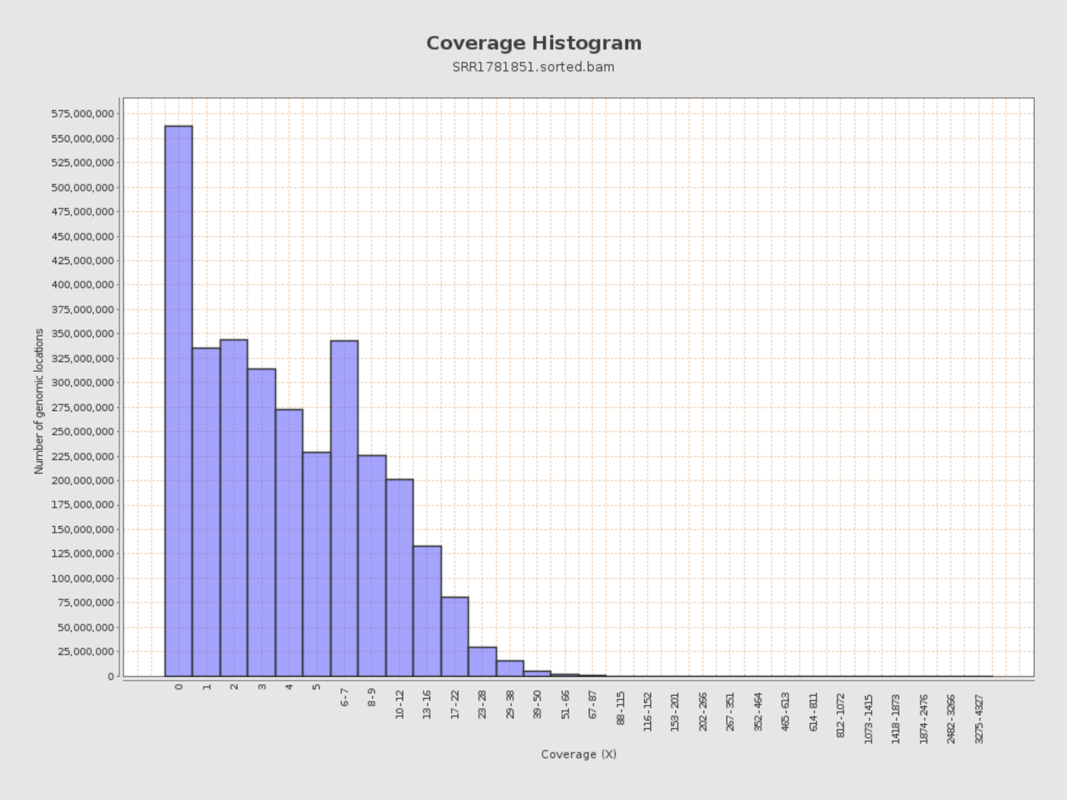
		bases	coverage	deviation
chr1	249250621	1177662326	4.7248	7.2811
chr2	243199373	1854994071	7.6275	8.1236
chr3	198022430	1016830854	5.1349	5.4451
chr4	191154276	999794314	5.2303	5.4852
chr5	180915260	922787104	5.1007	5.1221
chr6	171115067	887420849	5.1861	5.5497
chr7	159138663	765150003	4.8081	5.7139
chr8	146364022	750436017	5.1272	5.3456
chr9	141213431	598396838	4.2375	5.9935
chr10	135534747	805705346	5.9446	7.9532
chr11	135006516	685611362	5.0784	5.5021
chr12	133851895	999372546	7.4663	7.5369
chr13	115169878	476091261	4.1338	4.9268
chr14	107349540	448005641	4.1733	5.1627
chr15	102531392	403514840	3.9355	5.0379
chr16	90354753	332737926	3.6826	4.8039
chr17	81195210	294773039	3.6304	4.8328
chr18	78077248	372061633	4.7653	5.5172
chr19	59128983	186881581	3.1606	5.1288
chr20	63025520	275694589	4.3743	6.1479
chr21	48129895	173087878	3.5963	6.5395
chr22	51304566	120341808	2.3456	3.9505
chrMT	16571	582547	35.1546	10.2293
chrX	155270560	1037734106	6.6834	7.0129

chrY	59373566	13688994	0.2306	2.3345

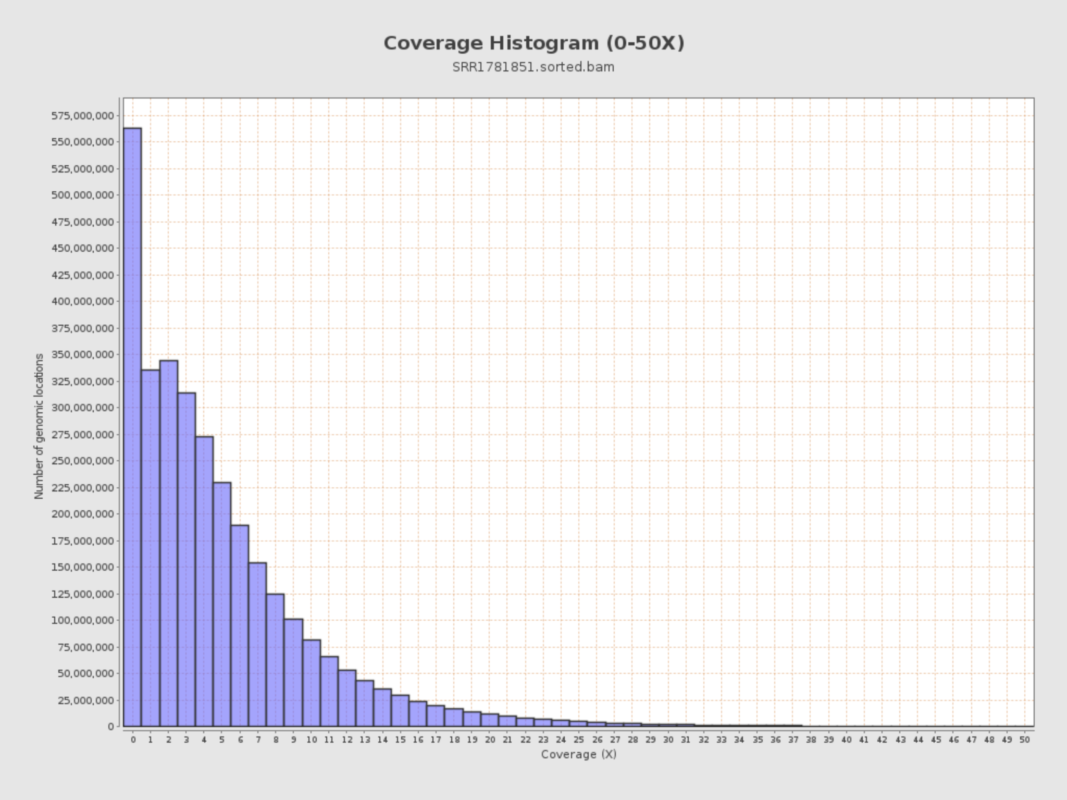
3. Results : Coverage across reference



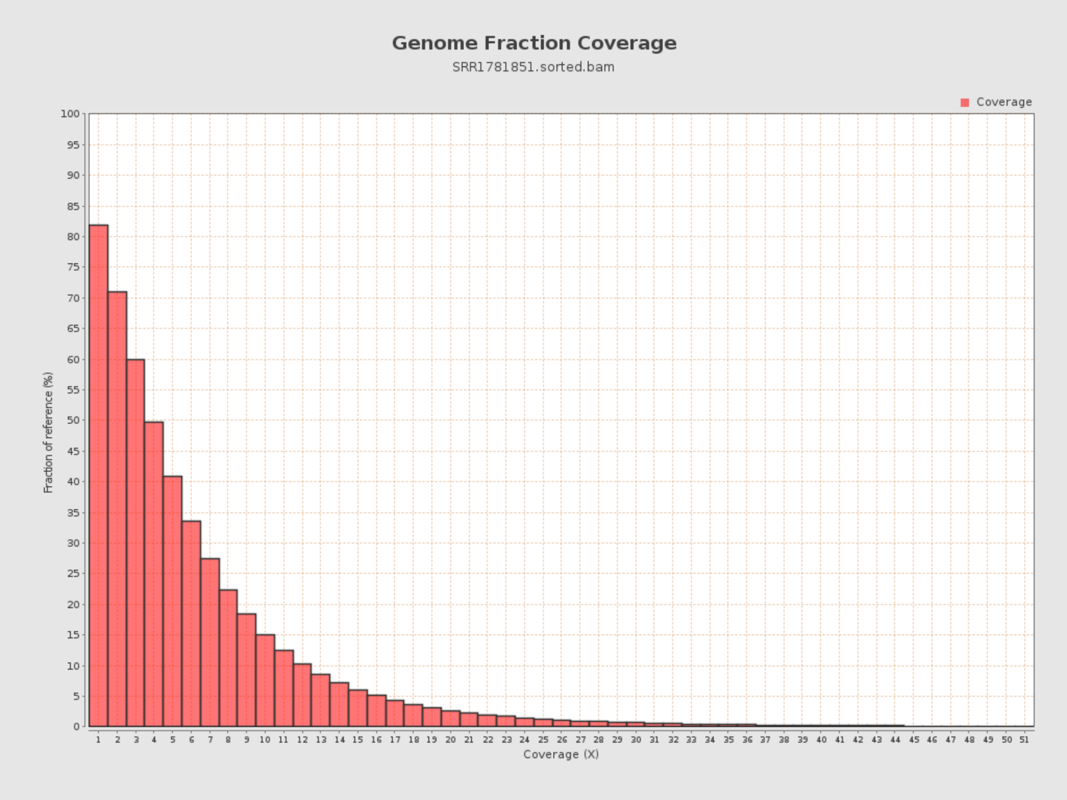
4. Results : Coverage Histogram



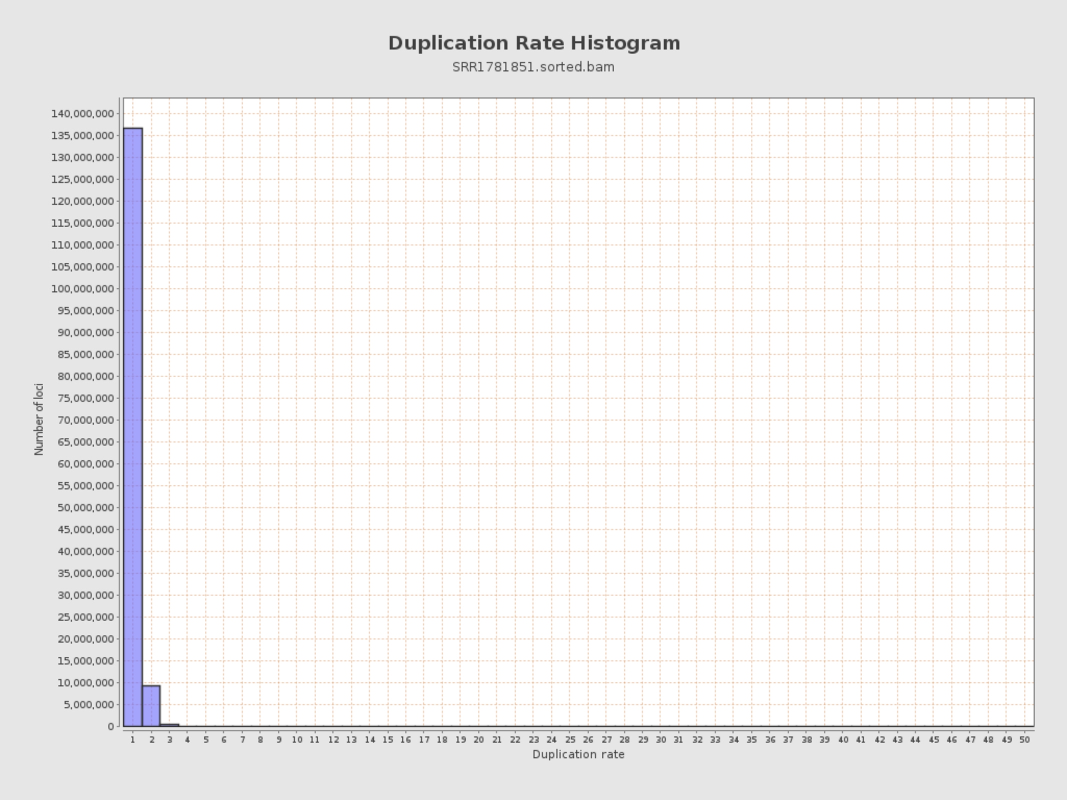
5. Results : Coverage Histogram (0-50X)



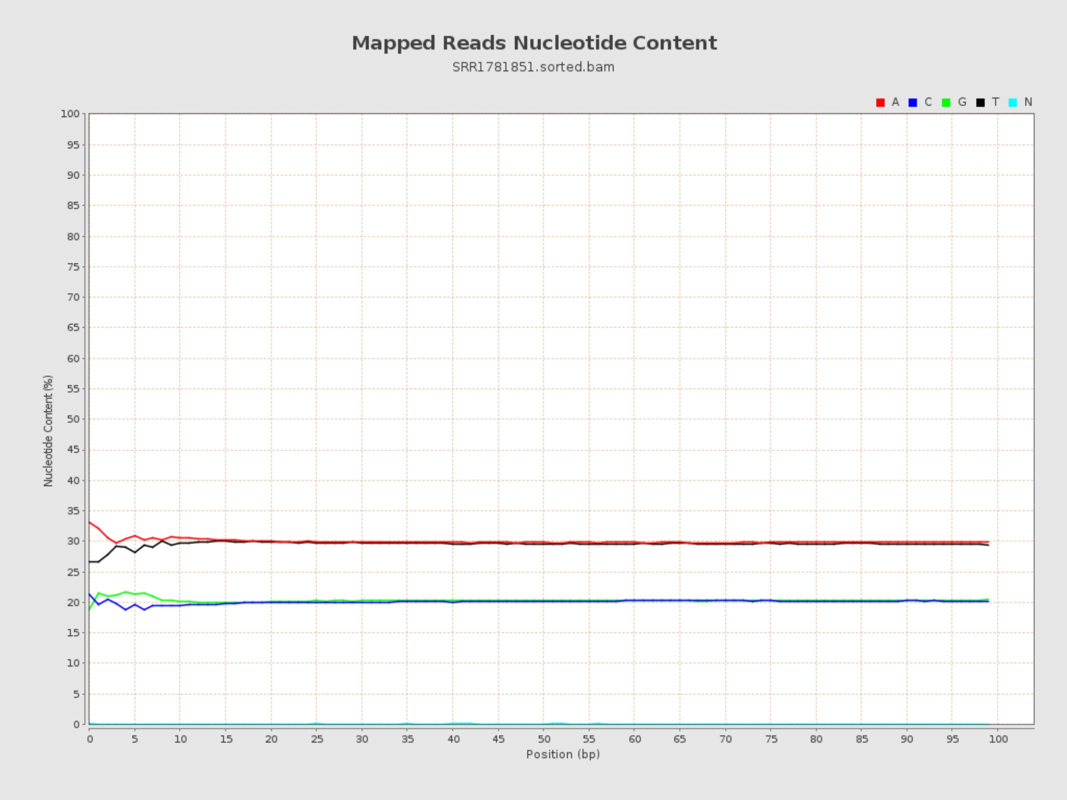
6. Results : Genome Fraction Coverage



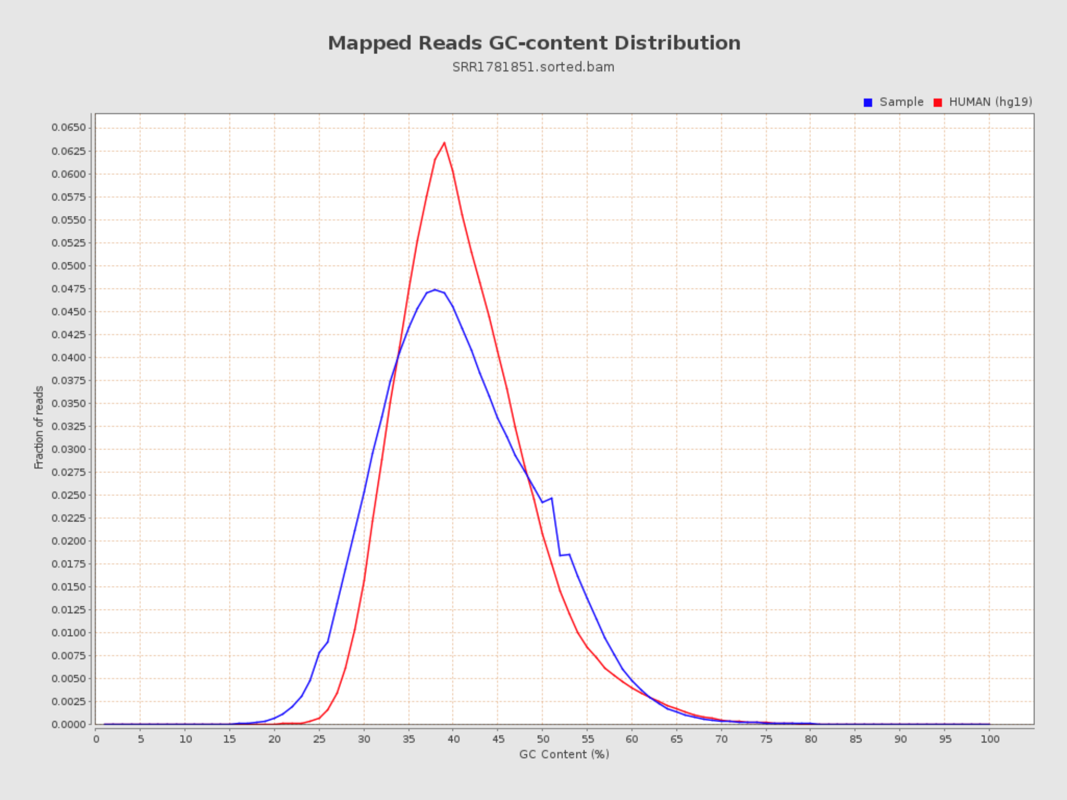
7. Results : Duplication Rate Histogram



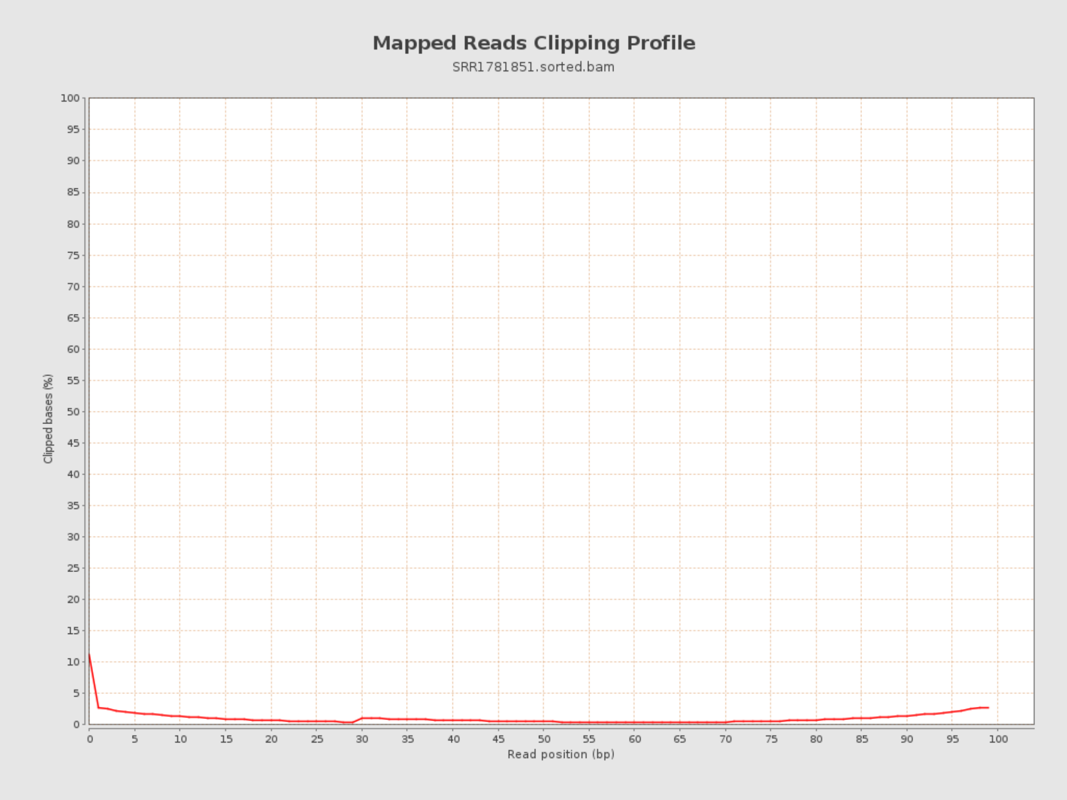
8. Results : Mapped Reads Nucleotide Content



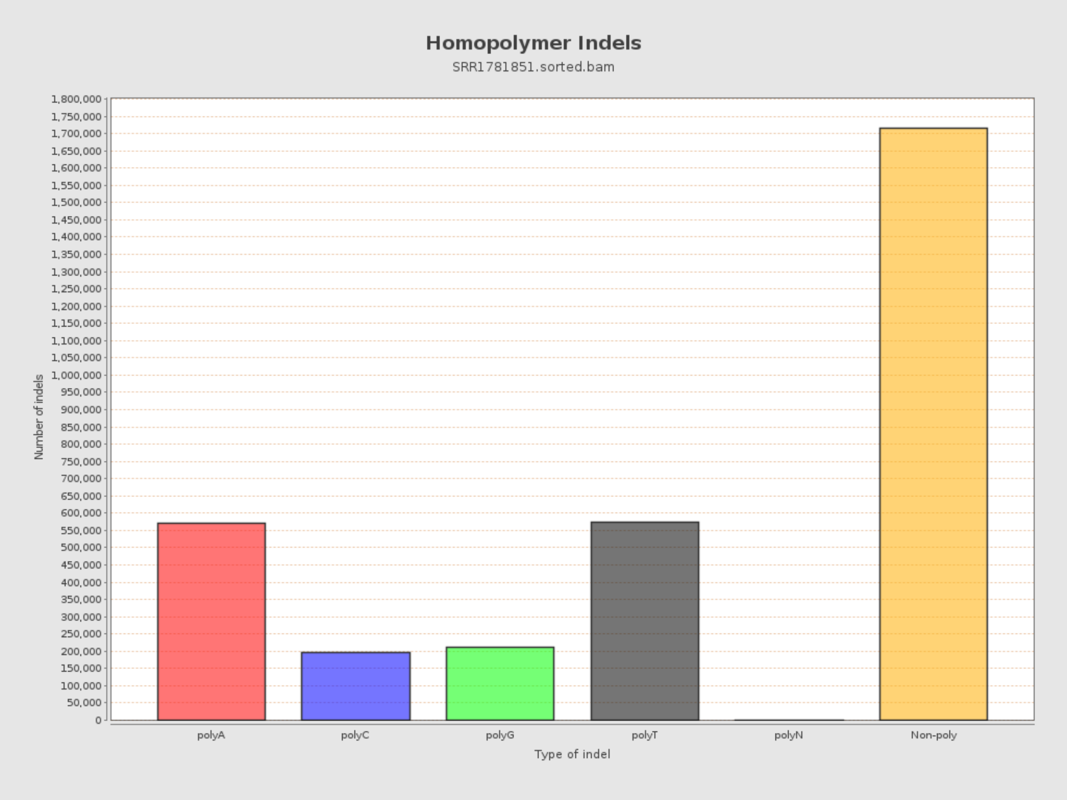
9. Results : Mapped Reads GC-content Distribution



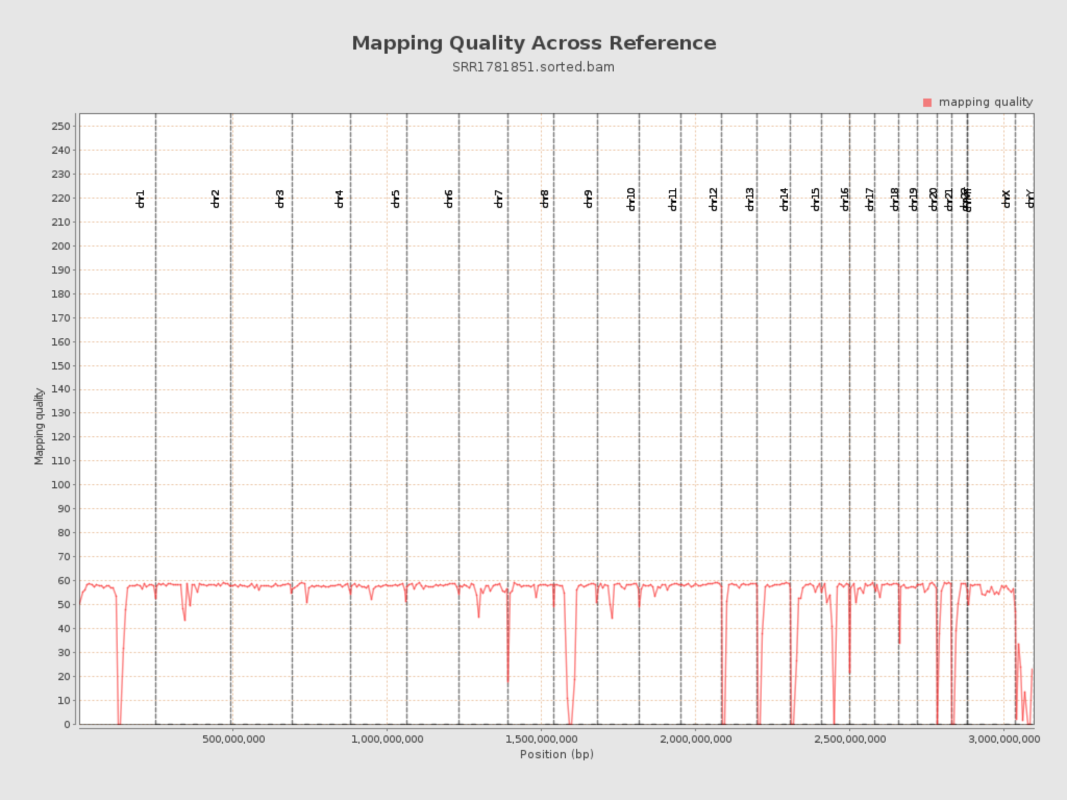
10. Results : Mapped Reads Clipping Profile



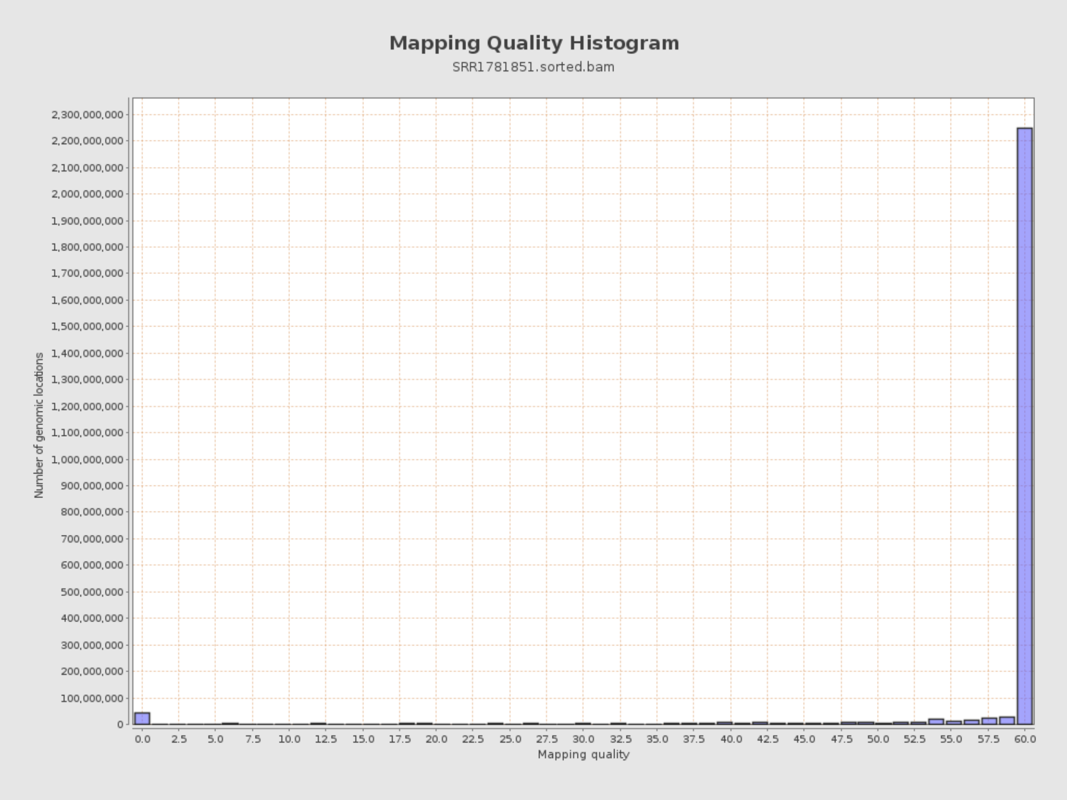
11. Results : Homopolymer Indels



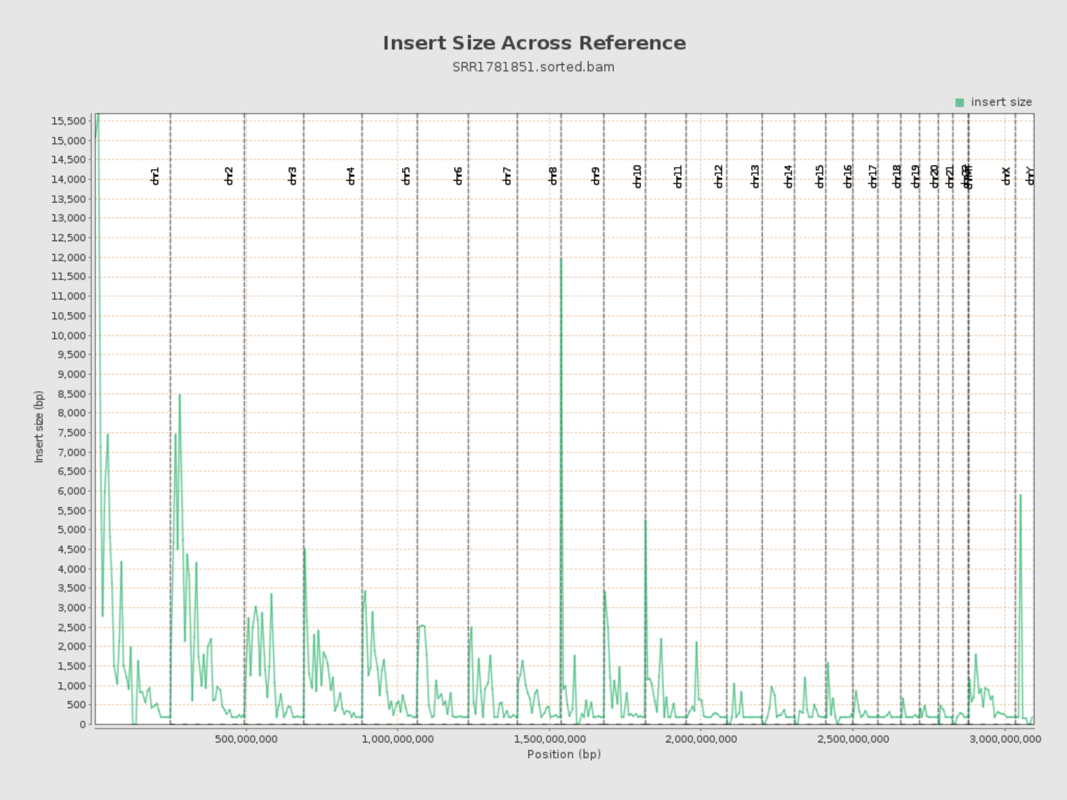
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram