Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/25 09:43:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781823.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_SRR1781823 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781823_1.fastq.gz SRR1781823_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Mar 25 09:43:35 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781823.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	168,130,146
Mapped reads	163,763,058 / 97.4%
Unmapped reads	4,367,088 / 2.6%
Mapped paired reads	163,763,058 / 97.4%
Mapped reads, first in pair	82,474,663 / 49.05%
Mapped reads, second in pair	81,288,395 / 48.35%
Mapped reads, both in pair	161,958,124 / 96.33%
Mapped reads, singletons	1,804,934 / 1.07%
Secondary alignments	0
Supplementary alignments	507,857 / 0.3%
Read min/max/mean length	30 / 100 / 99.99
Duplicated reads (estimated)	10,870,778 / 6.47%
Duplication rate	6.37%
Clipped reads	6,945,944 / 4.13%

2.2. ACGT Content

Number/percentage of A's	4,838,466,152 / 29.76%
Number/percentage of C's	3,285,387,289 / 20.2%
Number/percentage of T's	4,820,709,988 / 29.65%
Number/percentage of G's	3,314,624,521 / 20.38%
Number/percentage of N's	1,414,523 / 0.01%

GC Percentage	40.59%

2.3. Coverage

Mean	5.2537
Standard Deviation	6.8146

2.4. Mapping Quality

Mean Mapping Quality	53.91

2.5. Insert size

Mean	34,388.46
Standard Deviation	1,799,926.23
P25/Median/P75	162 / 198 / 241

2.6. Mismatches and indels

General error rate	0.46%
Mismatches	71,935,349
Insertions	1,782,419
Mapped reads with at least one insertion	1.07%
Deletions	1,509,805
Mapped reads with at least one deletion	0.91%
Homopolymer indels	46.91%

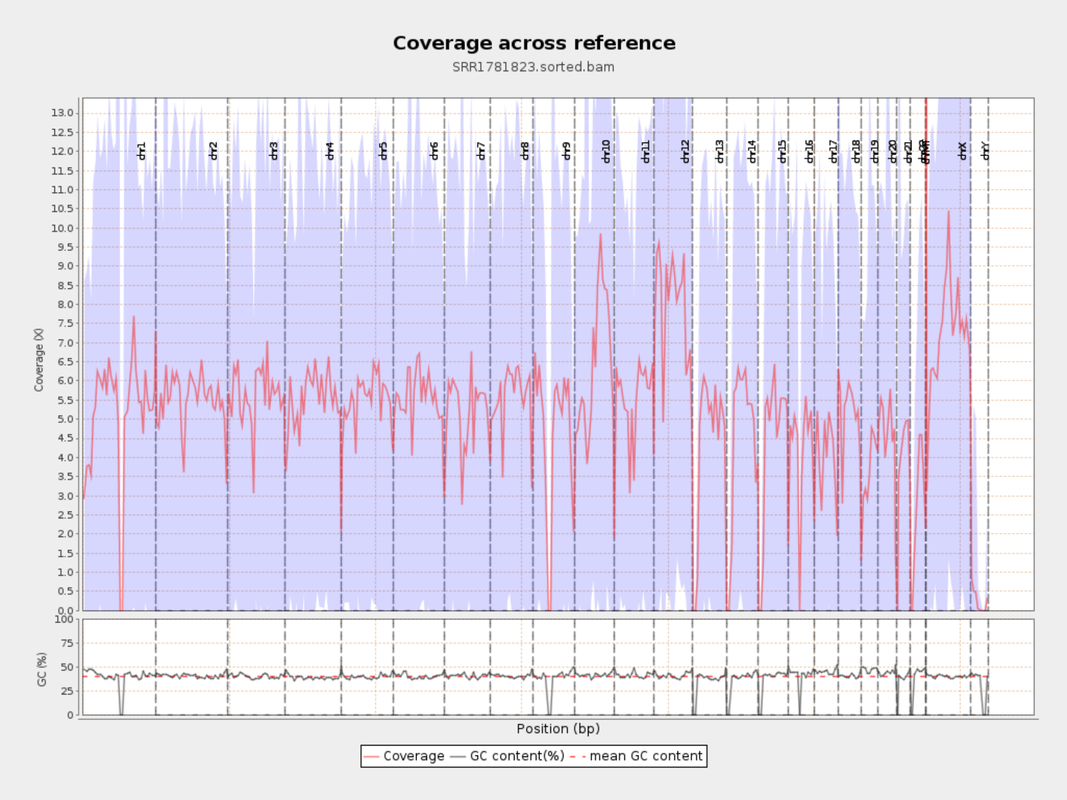
2.7. Chromosome stats

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

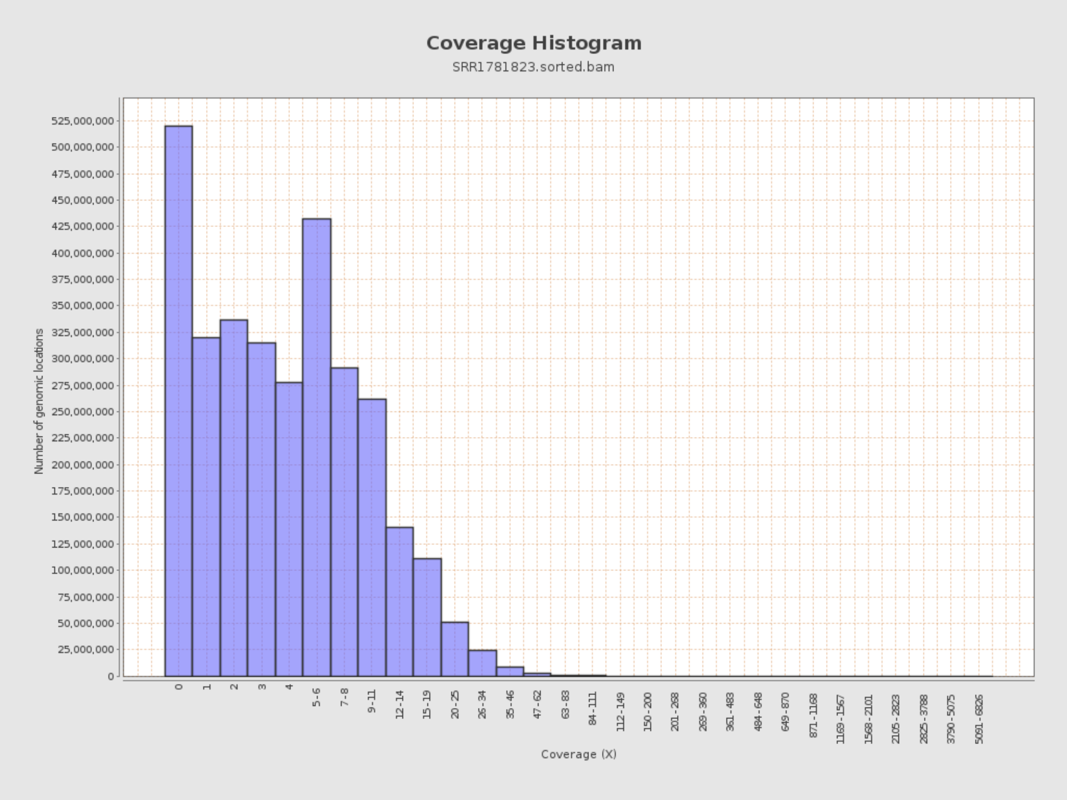
		bases	coverage	deviation
chr1	249250621	1283366842	5.1489	8.9128
chr2	243199373	1342314798	5.5194	8.2766
chr3	198022430	1116721136	5.6394	5.7332
chr4	191154276	1061997520	5.5557	5.9708
chr5	180915260	991878837	5.4826	5.3806
chr6	171115067	957665855	5.5966	5.9571
chr7	159138663	821356828	5.1613	6.2265
chr8	146364022	813919624	5.5609	5.72
chr9	141213431	658285798	4.6616	6.8682
chr10	135534747	878587605	6.4824	9.9309
chr11	135006516	742365686	5.4987	5.8473
chr12	133851895	1075231400	8.033	7.805
chr13	115169878	504165464	4.3776	4.9669
chr14	107349540	487011997	4.5367	5.4741
chr15	102531392	443743430	4.3279	5.4333
chr16	90354753	368133725	4.0743	5.1938
chr17	81195210	334454744	4.1191	5.2646
chr18	78077248	403521455	5.1682	6.2645
chr19	59128983	215304413	3.6413	6.1276
chr20	63025520	298329171	4.7335	6.418
chr21	48129895	188242178	3.9111	7.6287
chr22	51304566	138199834	2.6937	4.5249
chrMT	16571	1388092	83.7663	24.2572
chrX	155270560	1122710421	7.2307	7.3229

chrY	59373566	15051092	0.2535	2.6389

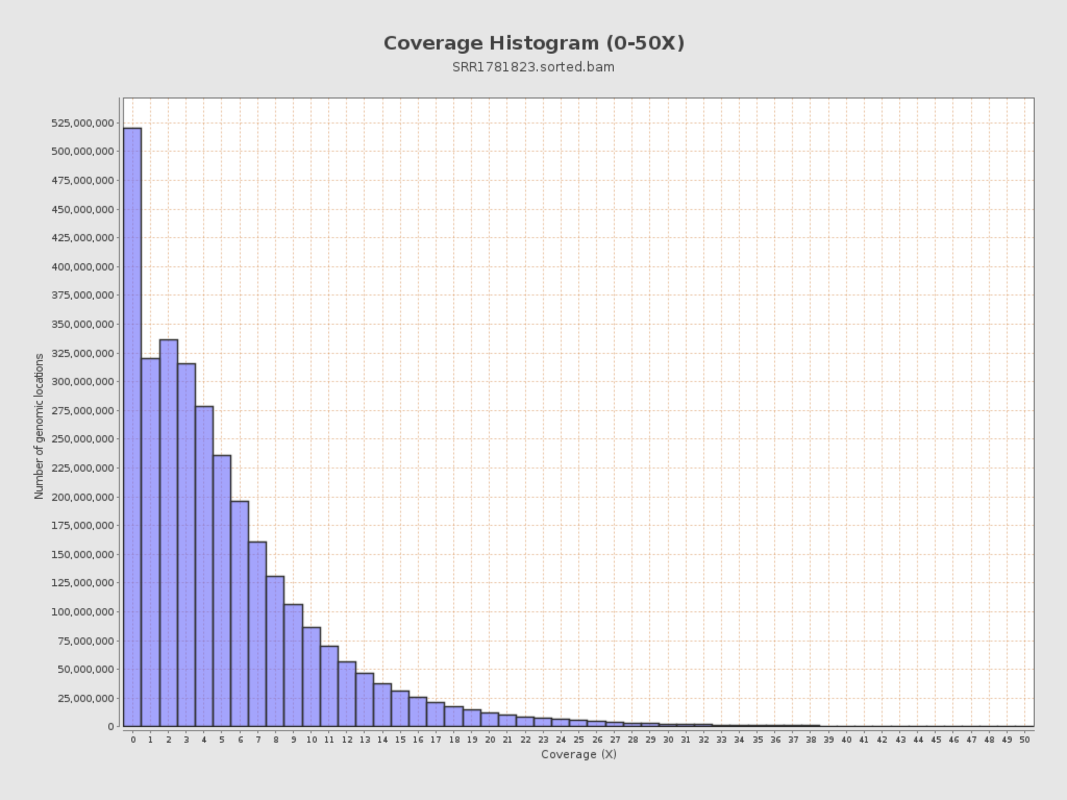
3. Results : Coverage across reference



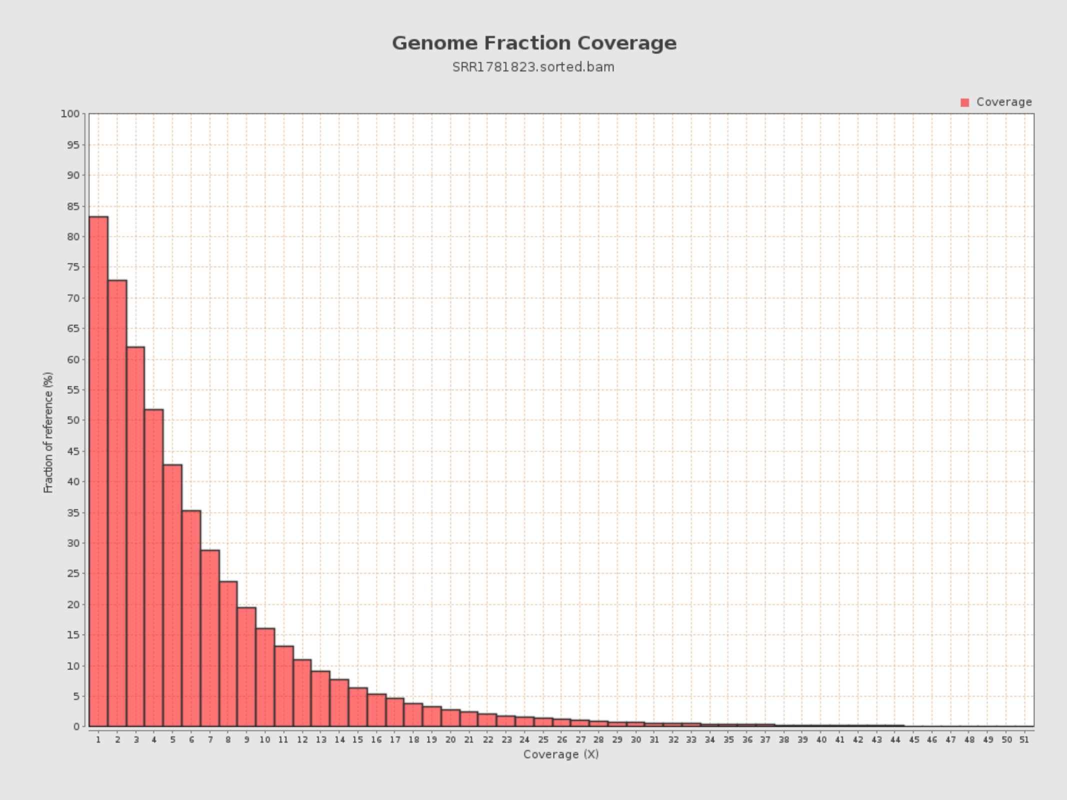
4. Results : Coverage Histogram



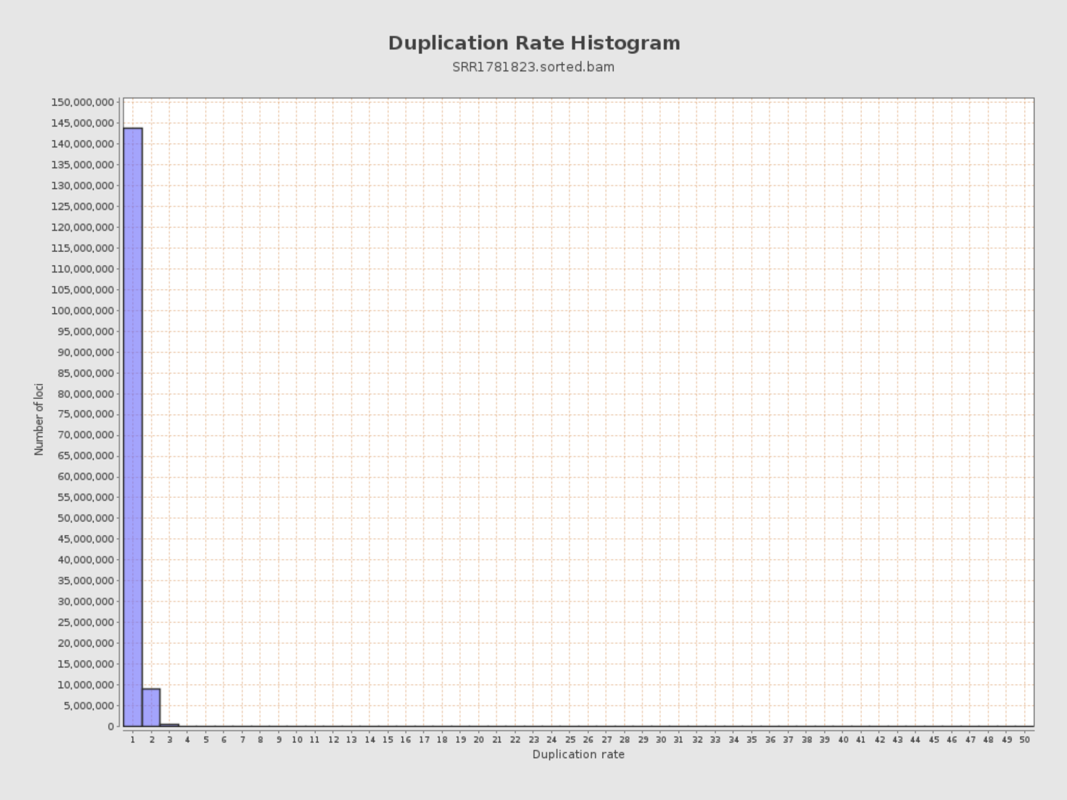
5. Results : Coverage Histogram (0-50X)



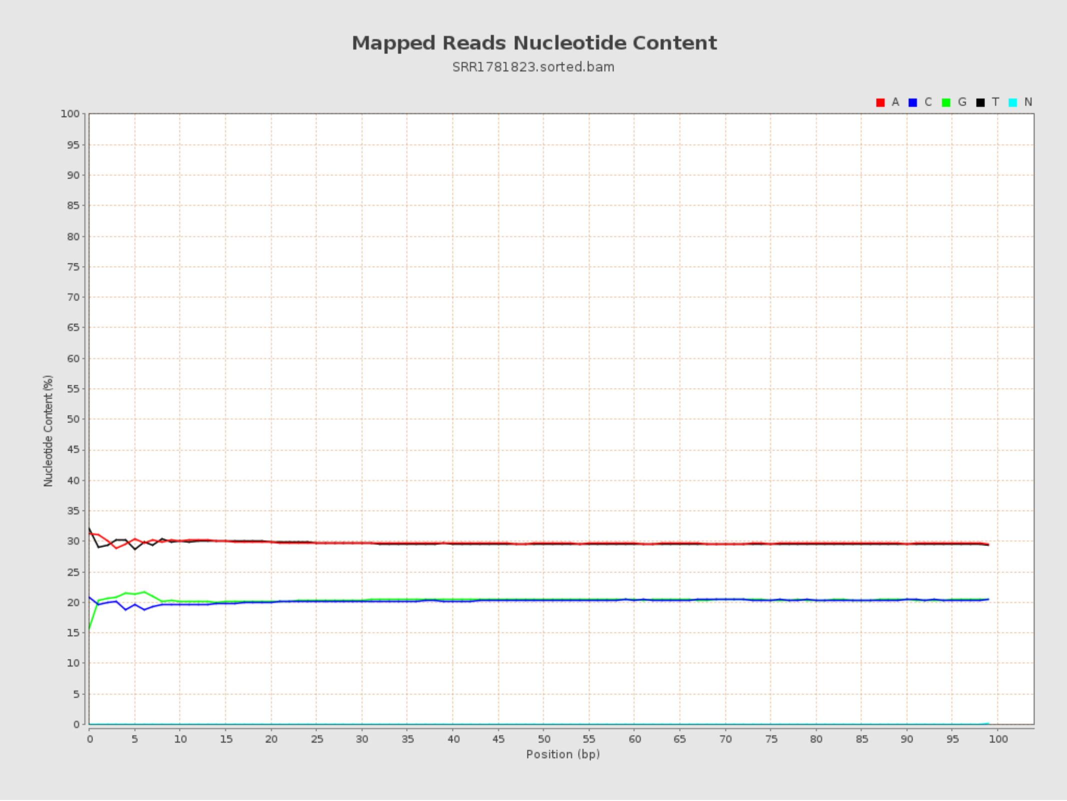
6. Results : Genome Fraction Coverage



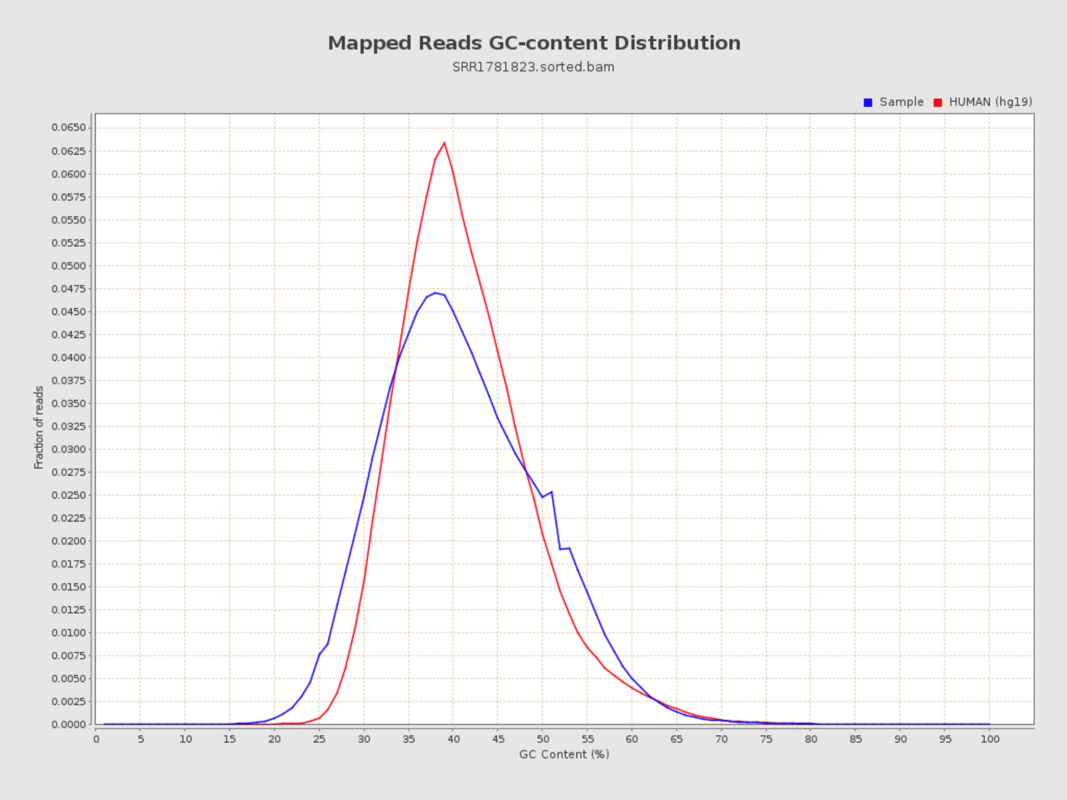
7. Results : Duplication Rate Histogram



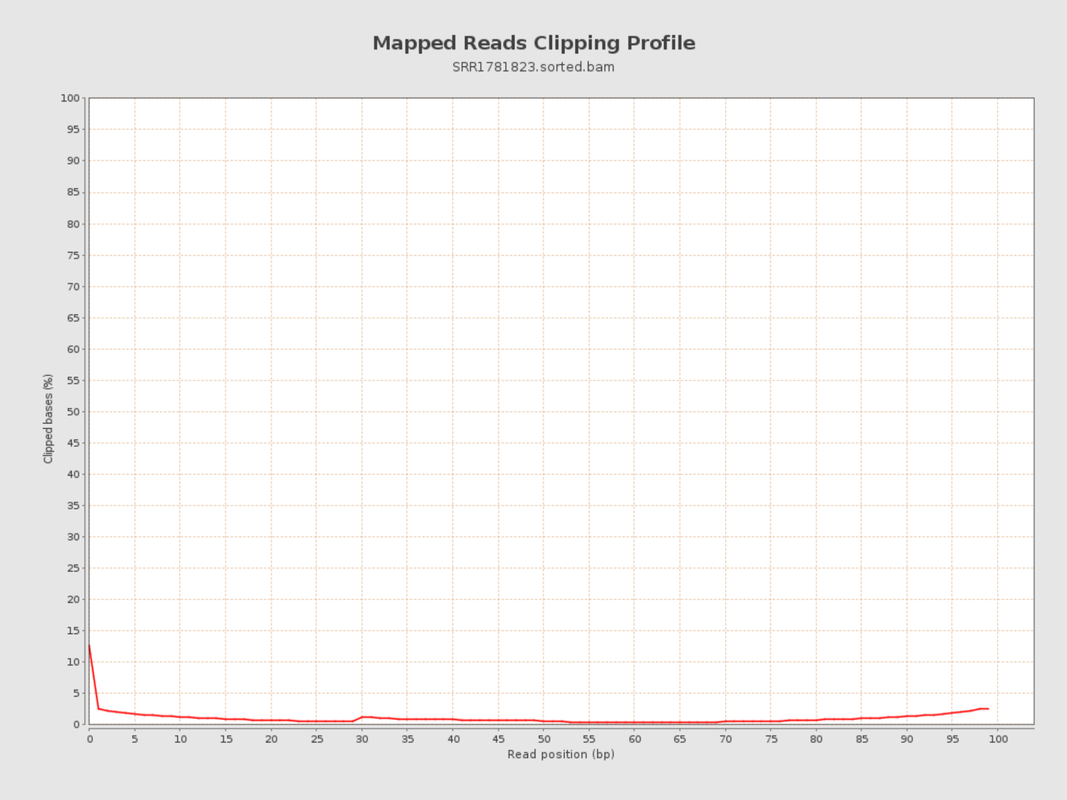
8. Results : Mapped Reads Nucleotide Content



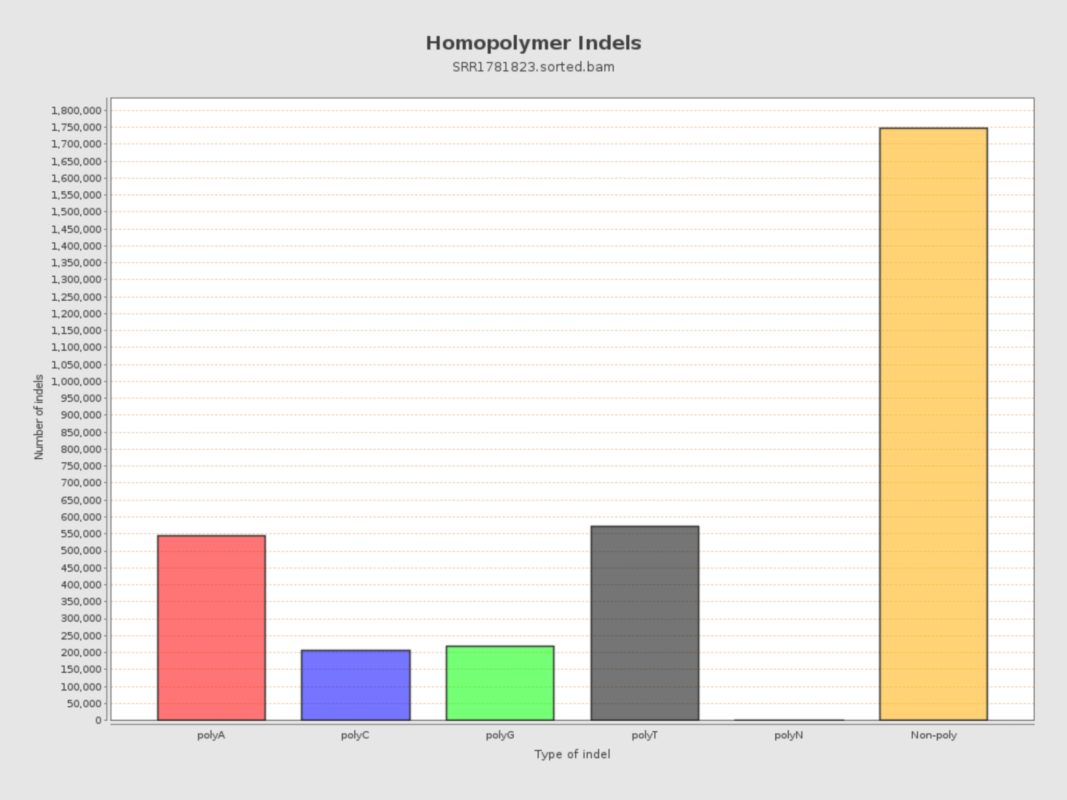
9. Results : Mapped Reads GC-content Distribution



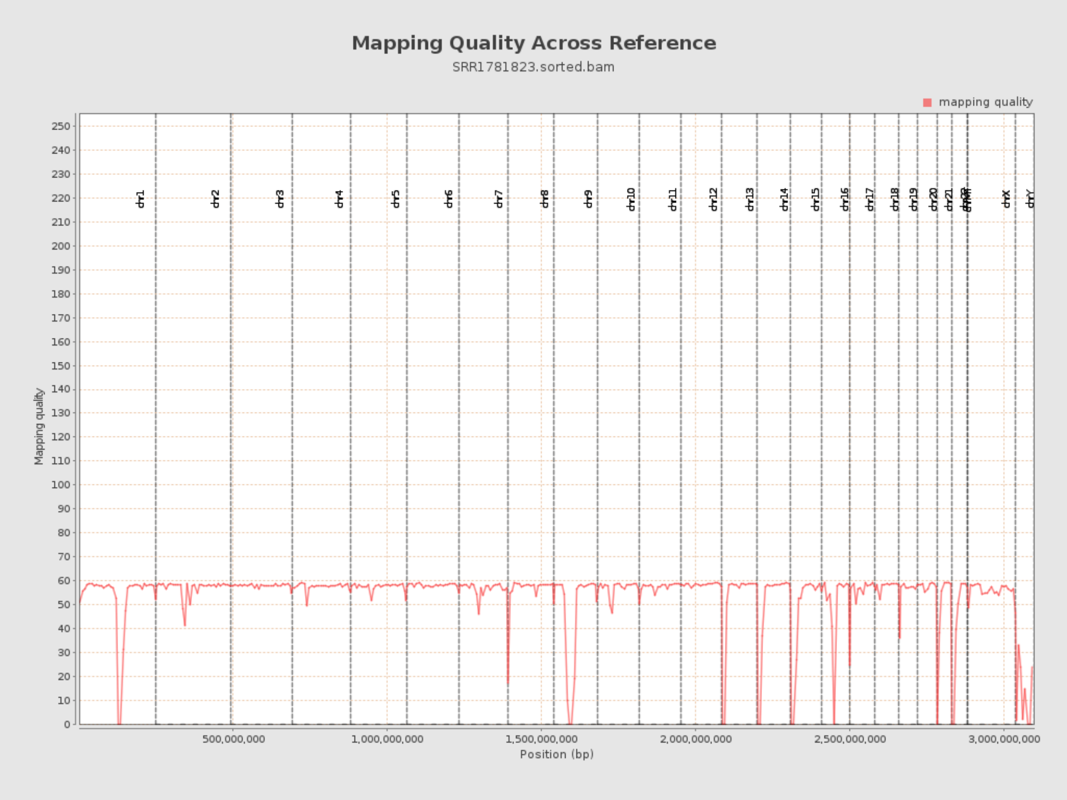
10. Results : Mapped Reads Clipping Profile



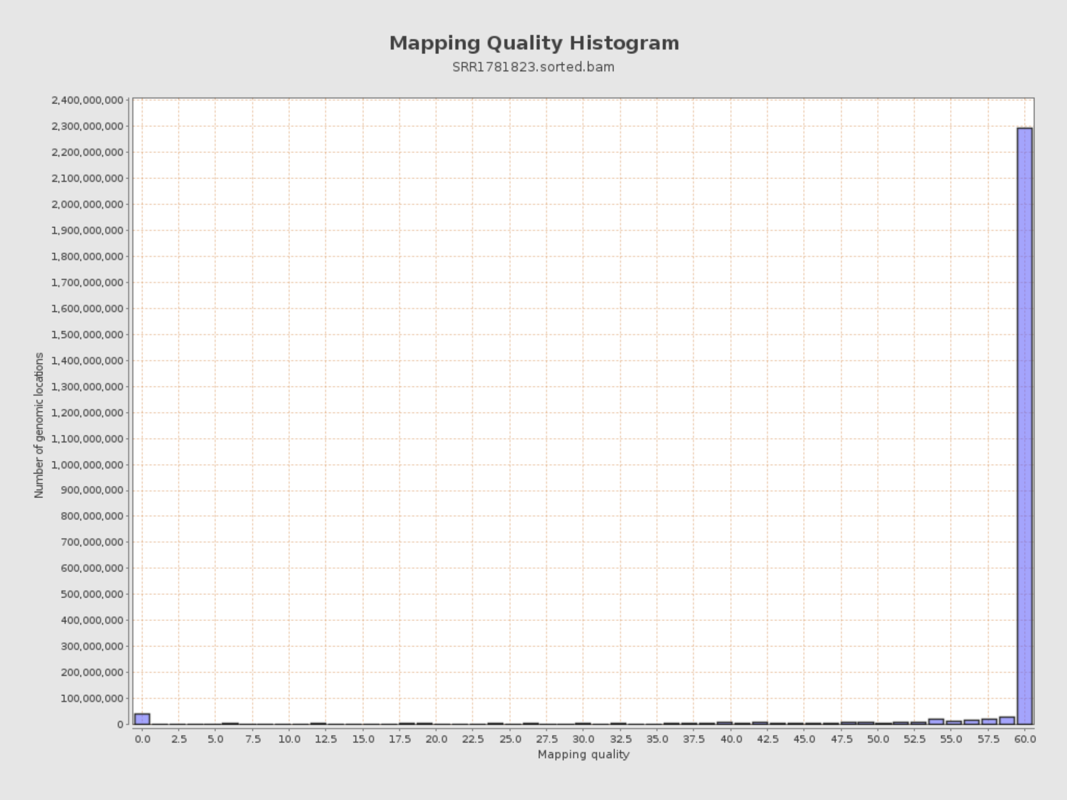
11. Results : Homopolymer Indels



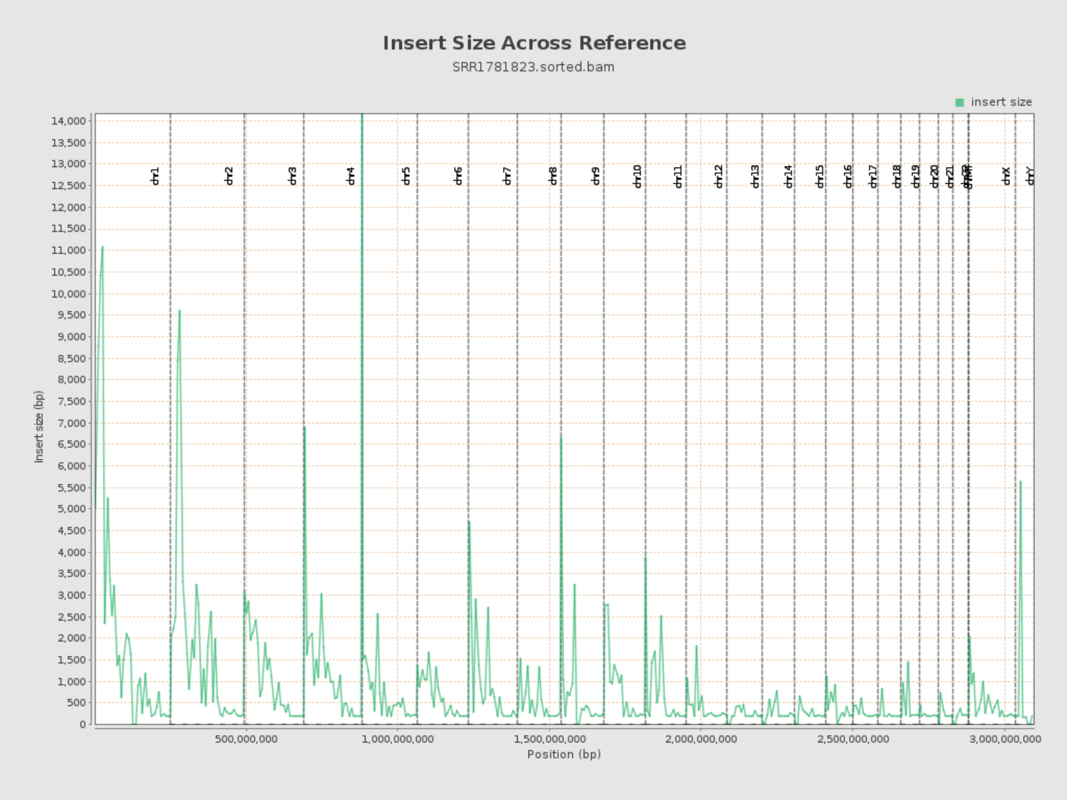
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram