Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/24 19:34:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781810.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_SRR1781810 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781810_1.fastq.gz SRR1781810_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Mar 24 19:34:52 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781810.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	160,906,540
Mapped reads	157,650,362 / 97.98%
Unmapped reads	3,256,178 / 2.02%
Mapped paired reads	157,650,362 / 97.98%
Mapped reads, first in pair	79,475,430 / 49.39%
Mapped reads, second in pair	78,174,932 / 48.58%
Mapped reads, both in pair	155,825,320 / 96.84%
Mapped reads, singletons	1,825,042 / 1.13%
Secondary alignments	0
Supplementary alignments	562,027 / 0.35%
Read min/max/mean length	30 / 100 / 99.98
Duplicated reads (estimated)	9,471,599 / 5.89%
Duplication rate	5.77%
Clipped reads	6,557,927 / 4.08%

2.2. ACGT Content

Number/percentage of A's	4,605,306,847 / 29.42%
Number/percentage of C's	3,204,492,468 / 20.47%
Number/percentage of T's	4,590,629,303 / 29.33%
Number/percentage of G's	3,251,477,460 / 20.77%
Number/percentage of N's	1,285,934 / 0.01%

GC Percentage	41.24%

2.3. Coverage

Mean	5.0575
Standard Deviation	6.0253

2.4. Mapping Quality

Mean Mapping Quality	54.03

2.5. Insert size

Mean	40,524.71
Standard Deviation	1,970,576.43
P25/Median/P75	166 / 203 / 249

2.6. Mismatches and indels

General error rate	0.45%
Mismatches	67,673,597
Insertions	1,454,354
Mapped reads with at least one insertion	0.91%
Deletions	1,444,969
Mapped reads with at least one deletion	0.9%
Homopolymer indels	46.25%

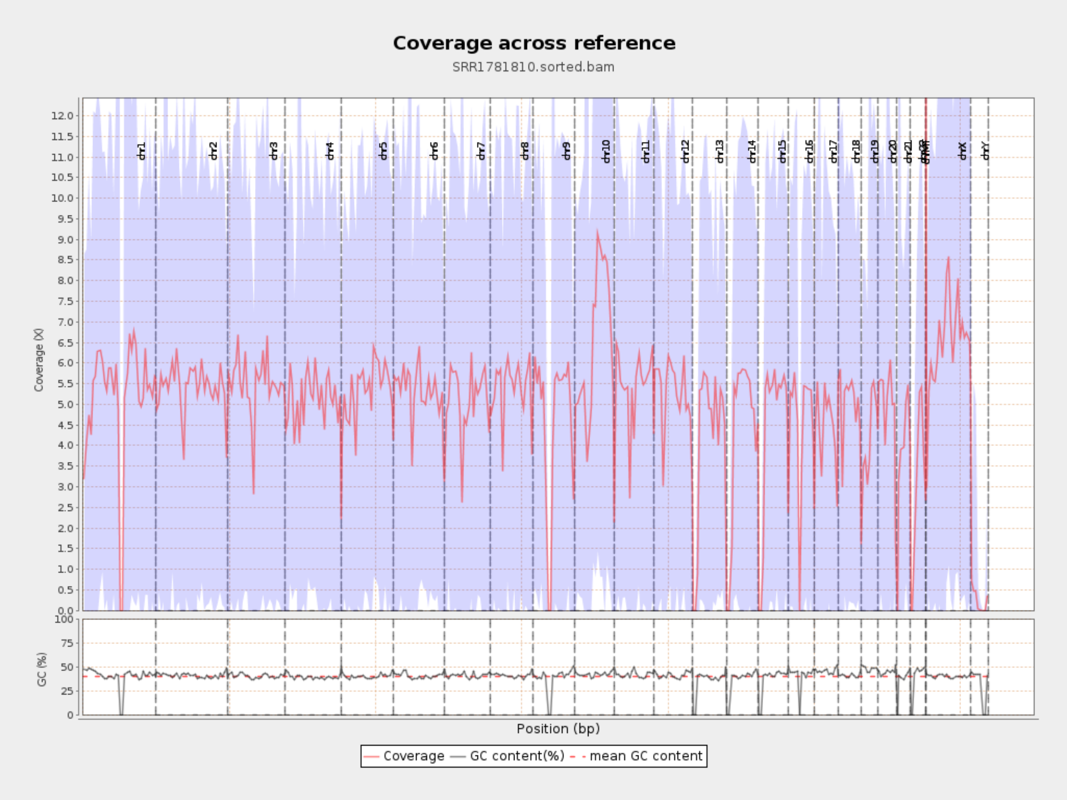
2.7. Chromosome stats

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

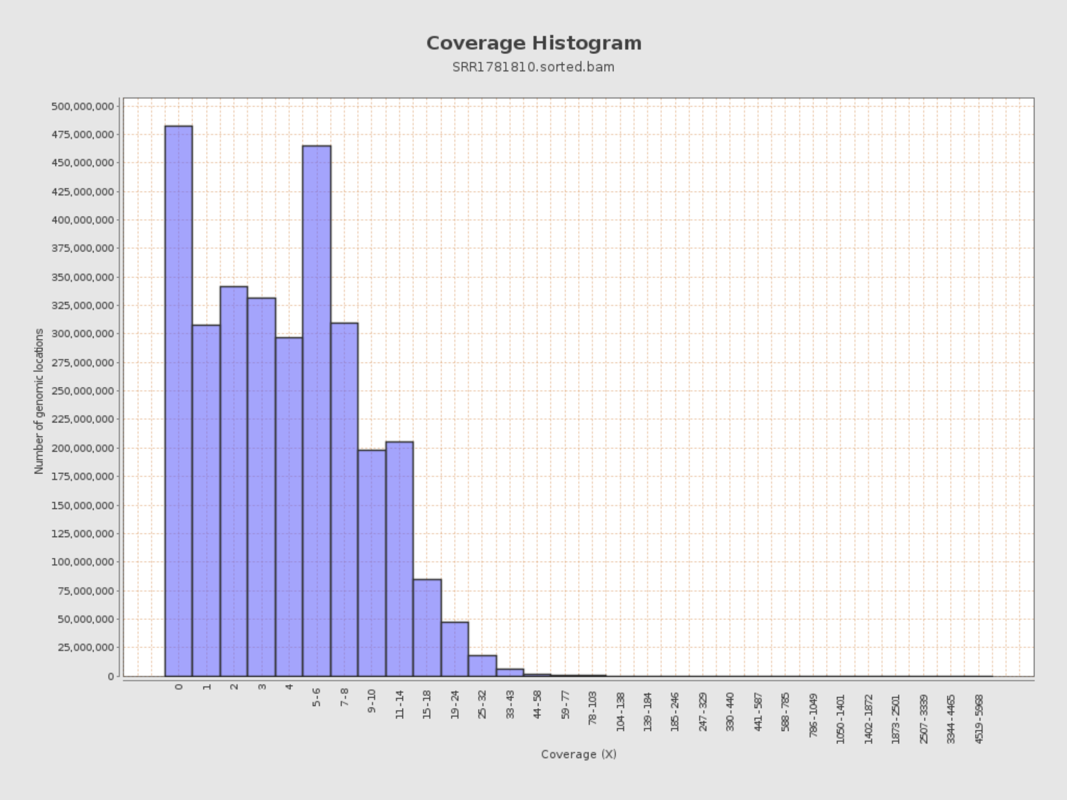
		bases	**coverage**	**deviation**
chr1	249250621	1289979498	5.1754	8.591
chr2	243199373	1318703694	5.4223	6.1195
chr3	198022430	1086493094	5.4867	5.0916
chr4	191154276	989217113	5.175	5.5315
chr5	180915260	965865928	5.3388	4.8913
chr6	171115067	913812162	5.3403	5.4588
chr7	159138663	808129032	5.0781	5.5119
chr8	146364022	790581105	5.4015	5.187
chr9	141213431	653345789	4.6267	6.1229
chr10	135534747	886943577	6.544	8.7111
chr11	135006516	732105548	5.4227	5.3311
chr12	133851895	714687211	5.3394	5.1933
chr13	115169878	482950404	4.1934	4.5666
chr14	107349540	471826545	4.3952	4.9063
chr15	102531392	448325720	4.3726	5.0157
chr16	90354753	400996425	4.438	5.1843
chr17	81195210	369105052	4.5459	5.4819
chr18	78077248	394144995	5.0481	6.0071
chr19	59128983	244413702	4.1336	6.2836
chr20	63025520	319139919	5.0637	5.8588
chr21	48129895	186740355	3.8799	7.6461
chr22	51304566	159061216	3.1003	4.5924
chrMT	16571	274947	16.5921	5.9684
chrX	155270560	1015359374	6.5393	6.1409

chrY	59373566	14242141	0.2399	2.6868

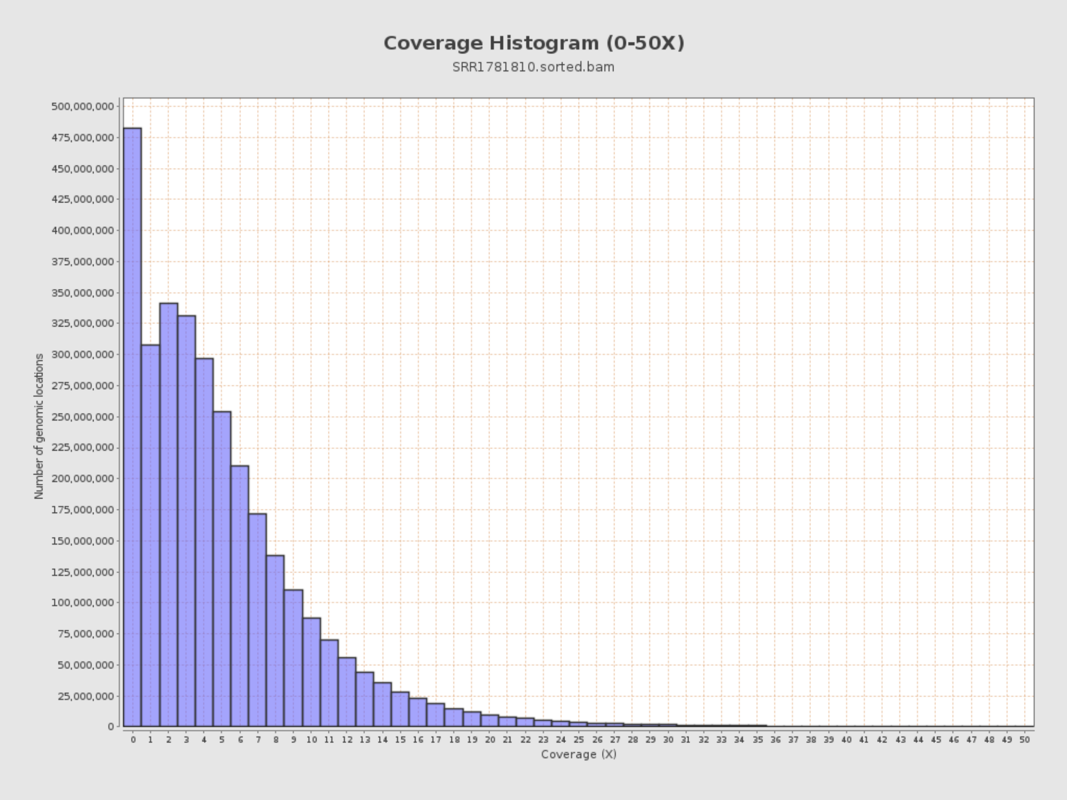
3. Results : Coverage across reference



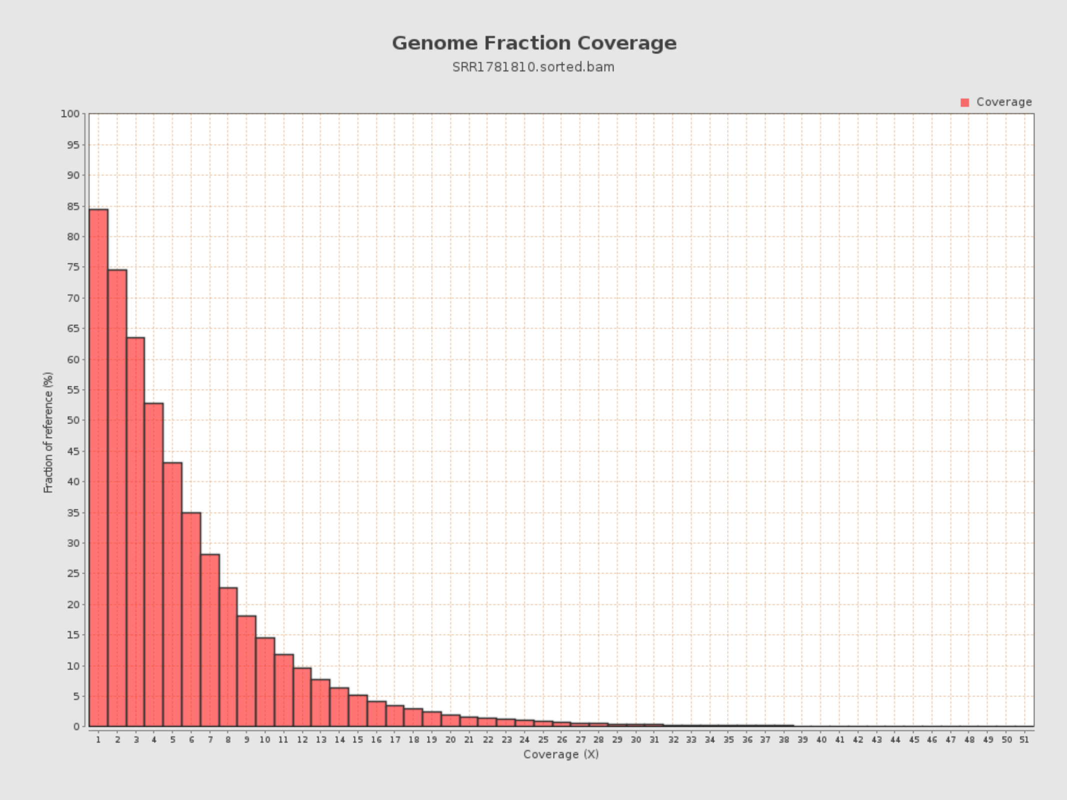
4. Results : Coverage Histogram



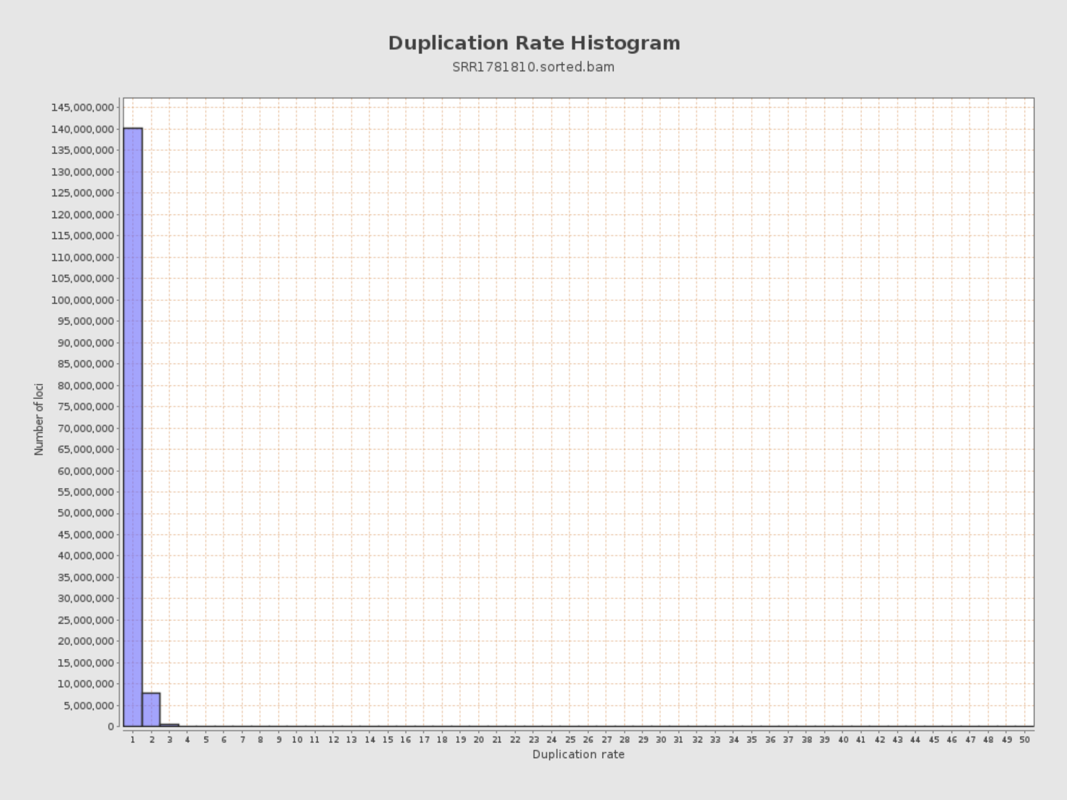
5. Results : Coverage Histogram (0-50X)



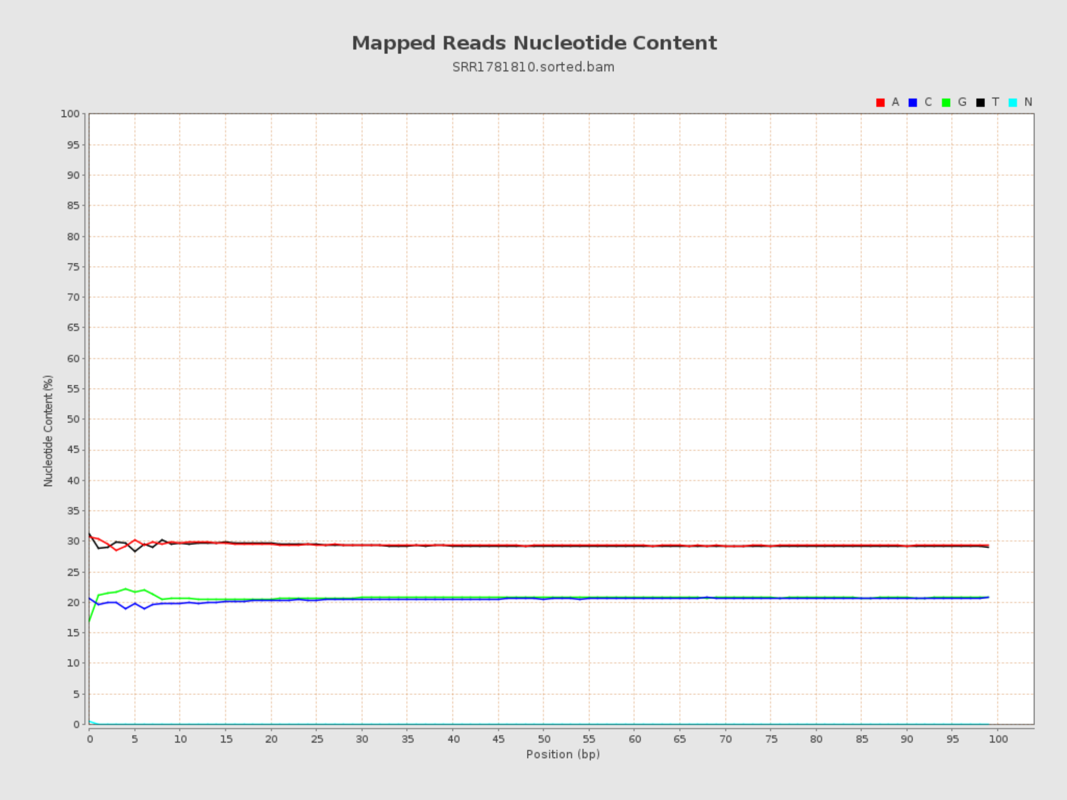
6. Results : Genome Fraction Coverage



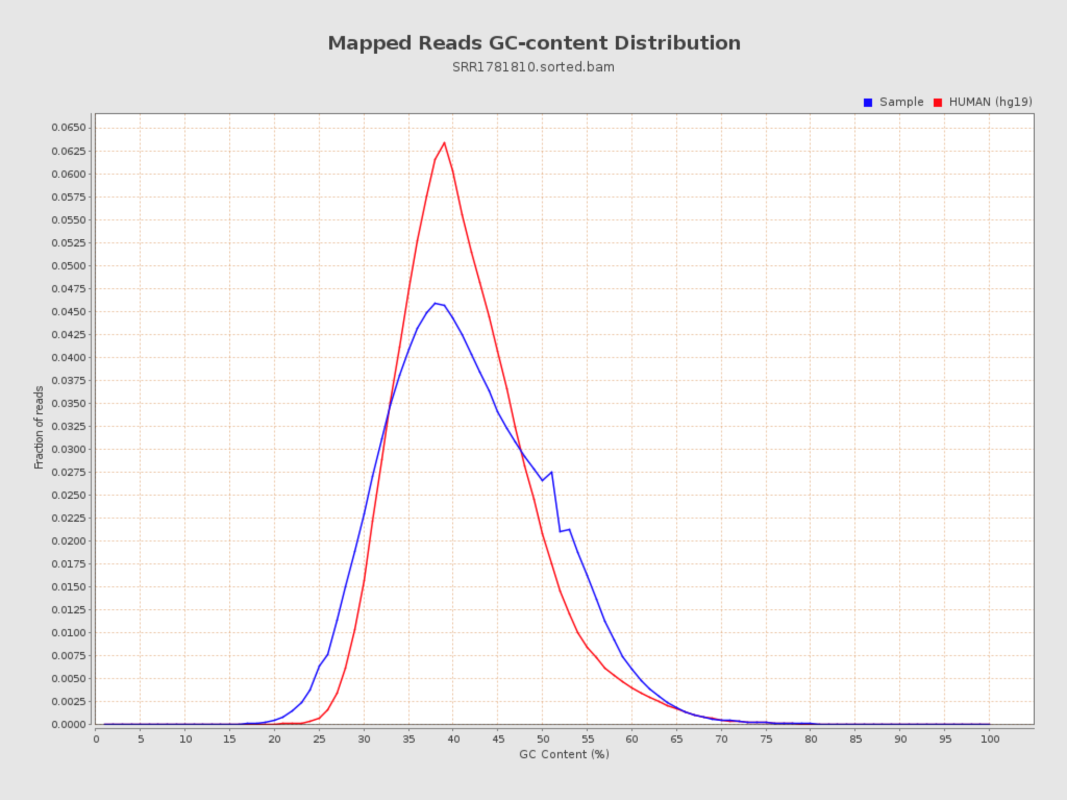
7. Results : Duplication Rate Histogram



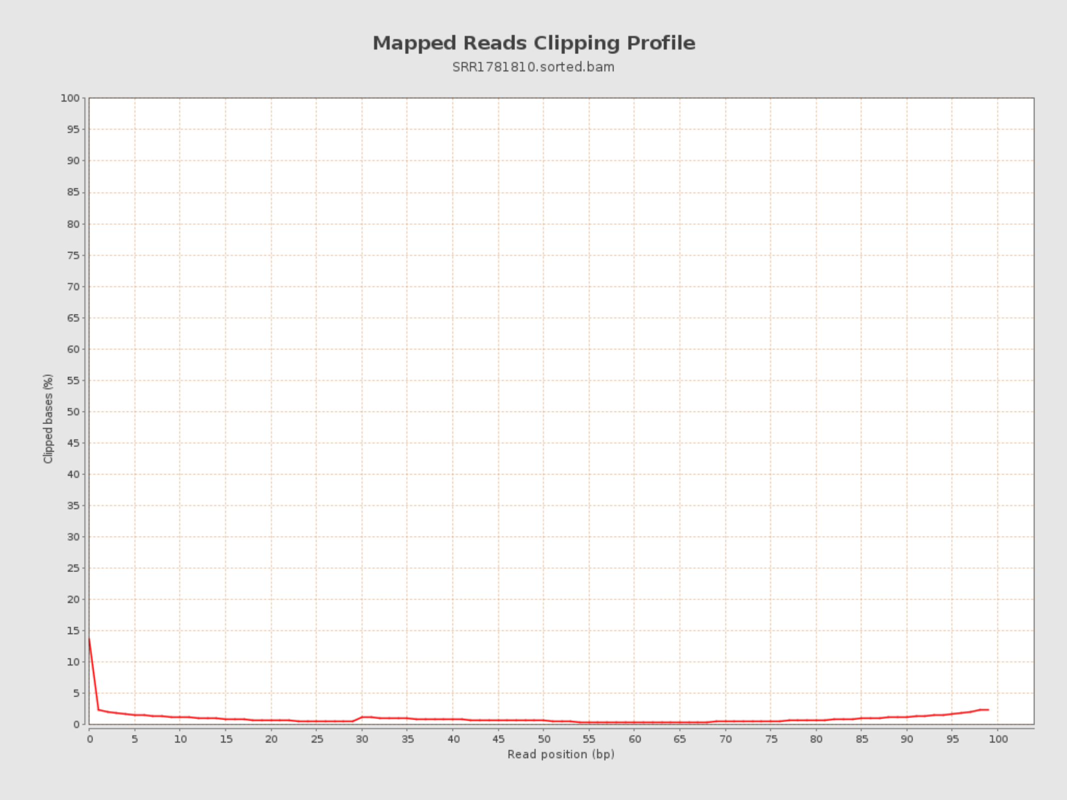
8. Results : Mapped Reads Nucleotide Content



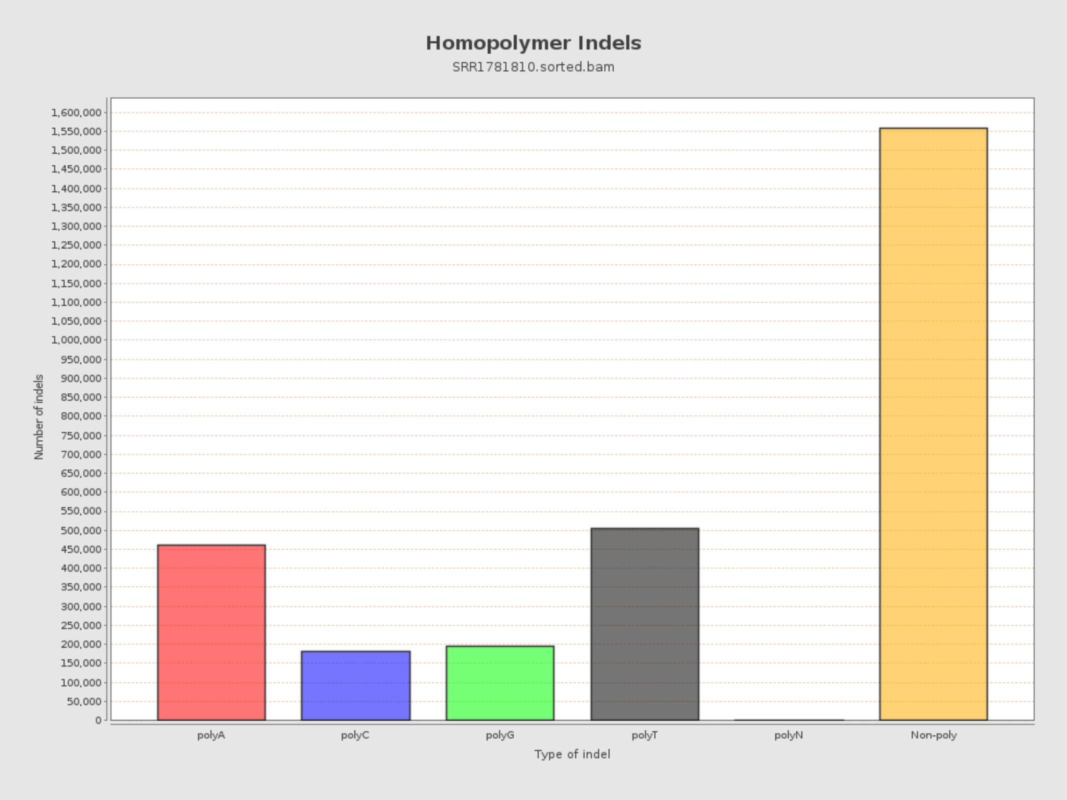
9. Results : Mapped Reads GC-content Distribution



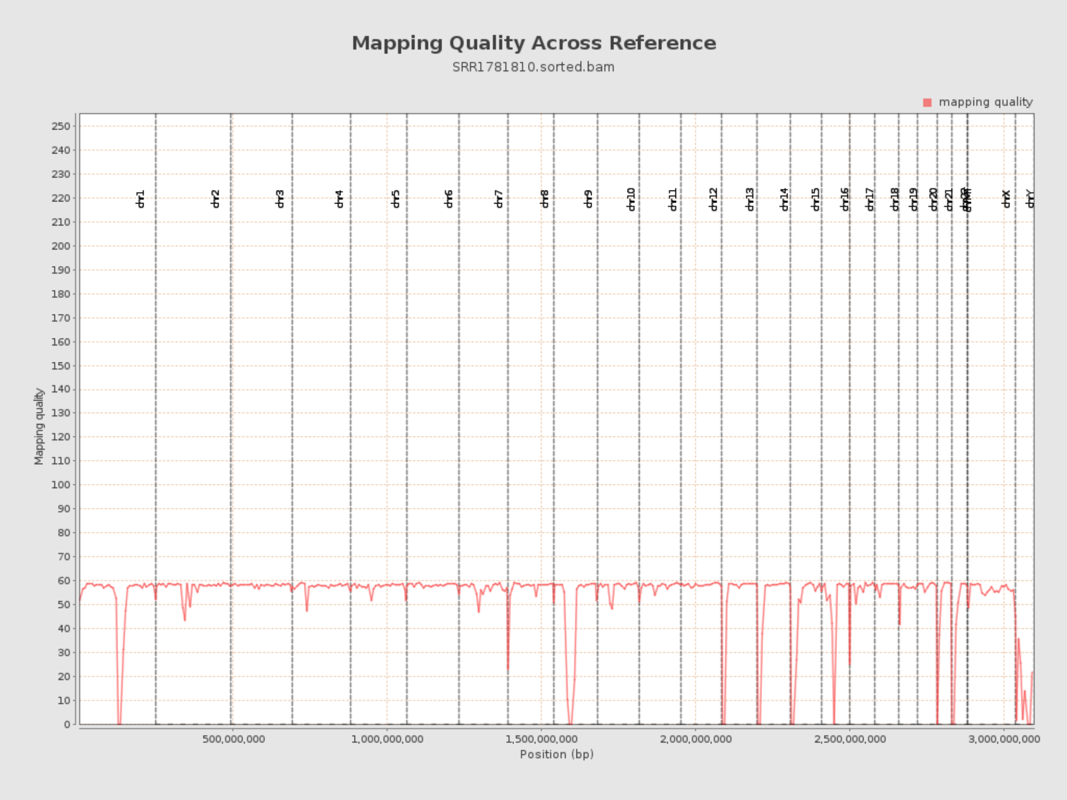
10. Results : Mapped Reads Clipping Profile



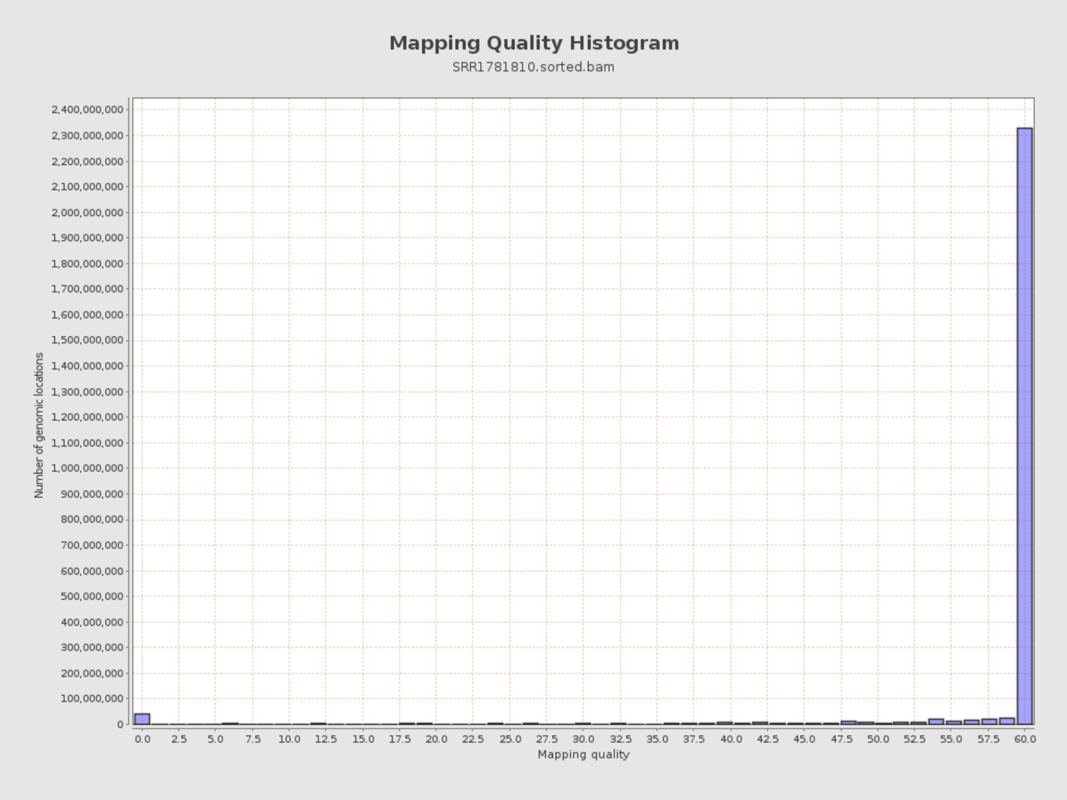
11. Results : Homopolymer Indels



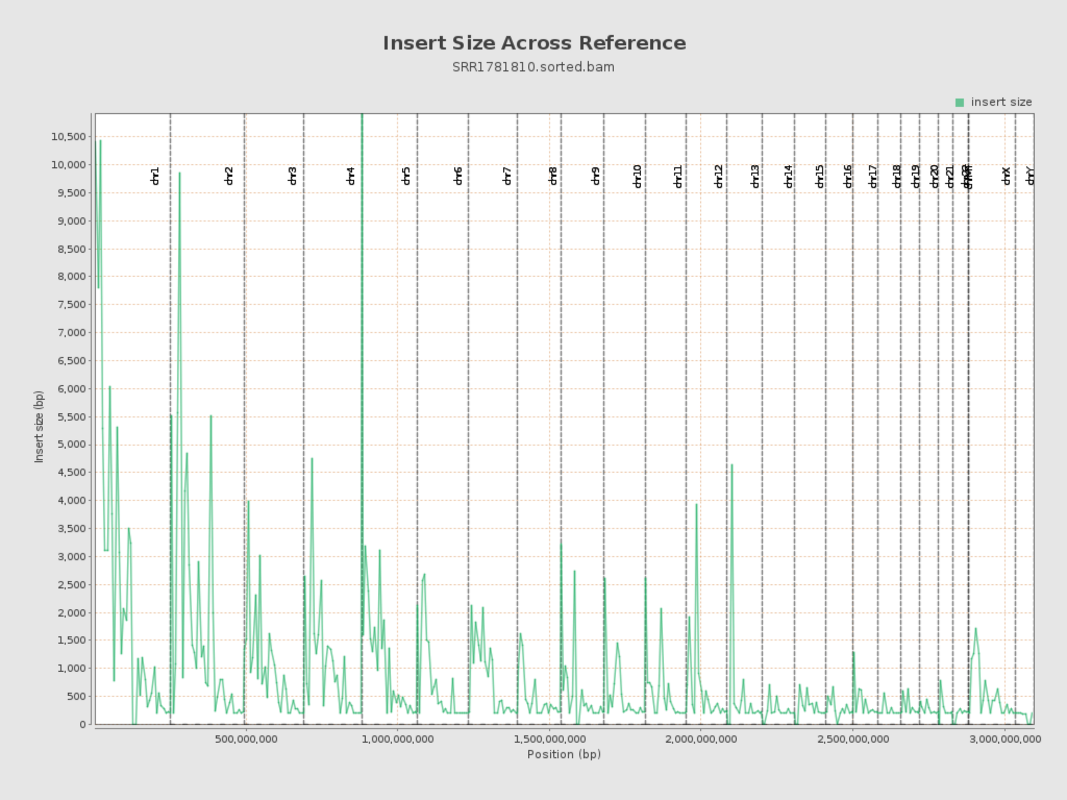
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram