Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/28 03:30:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781881.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_SRR1781881 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781881_1.fastq.gz SRR1781881_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Mar 28 03:30:34 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781881.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	207,645,696
Mapped reads	202,436,415 / 97.49%
Unmapped reads	5,209,281 / 2.51%
Mapped paired reads	202,436,415 / 97.49%
Mapped reads, first in pair	101,885,196 / 49.07%
Mapped reads, second in pair	100,551,219 / 48.42%
Mapped reads, both in pair	200,335,208 / 96.48%
Mapped reads, singletons	2,101,207 / 1.01%
Secondary alignments	0
Supplementary alignments	487,861 / 0.23%
Read min/max/mean length	30 / 100 / 99.99
Duplicated reads (estimated)	16,532,471 / 7.96%
Duplication rate	7.86%
Clipped reads	7,308,755 / 3.52%

2.2. ACGT Content

Number/percentage of A's	6,005,368,665 / 29.85%
Number/percentage of C's	4,039,535,863 / 20.08%
Number/percentage of T's	5,992,577,733 / 29.78%
Number/percentage of G's	4,081,465,327 / 20.28%
Number/percentage of N's	2,068,927 / 0.01%

GC Percentage	40.36%

2.3. Coverage

Mean	6.501
Standard Deviation	8.324

2.4. Mapping Quality

Mean Mapping Quality	54

2.5. Insert size

Mean	25,753.35
Standard Deviation	1,550,183.41
P25/Median/P75	174 / 212 / 257

2.6. Mismatches and indels

General error rate	0.45%
Mismatches	86,675,089
Insertions	2,202,047
Mapped reads with at least one insertion	1.07%
Deletions	1,855,524
Mapped reads with at least one deletion	0.9%
Homopolymer indels	47.4%

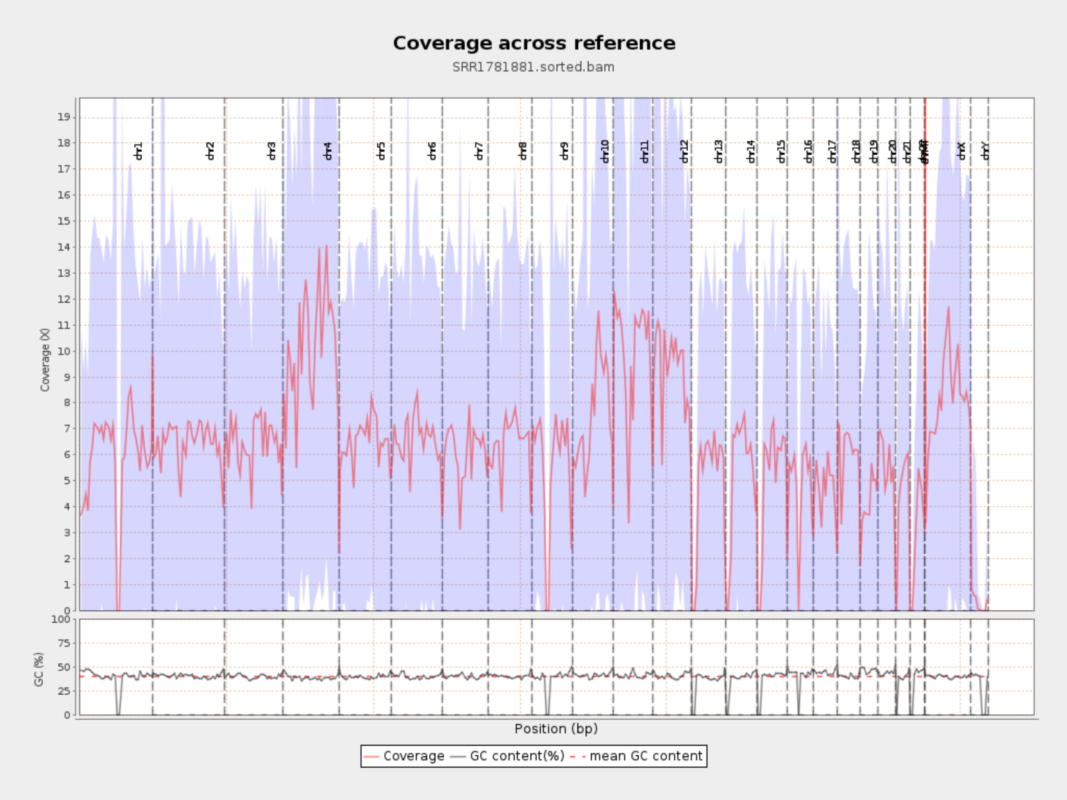
2.7. Chromosome stats

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

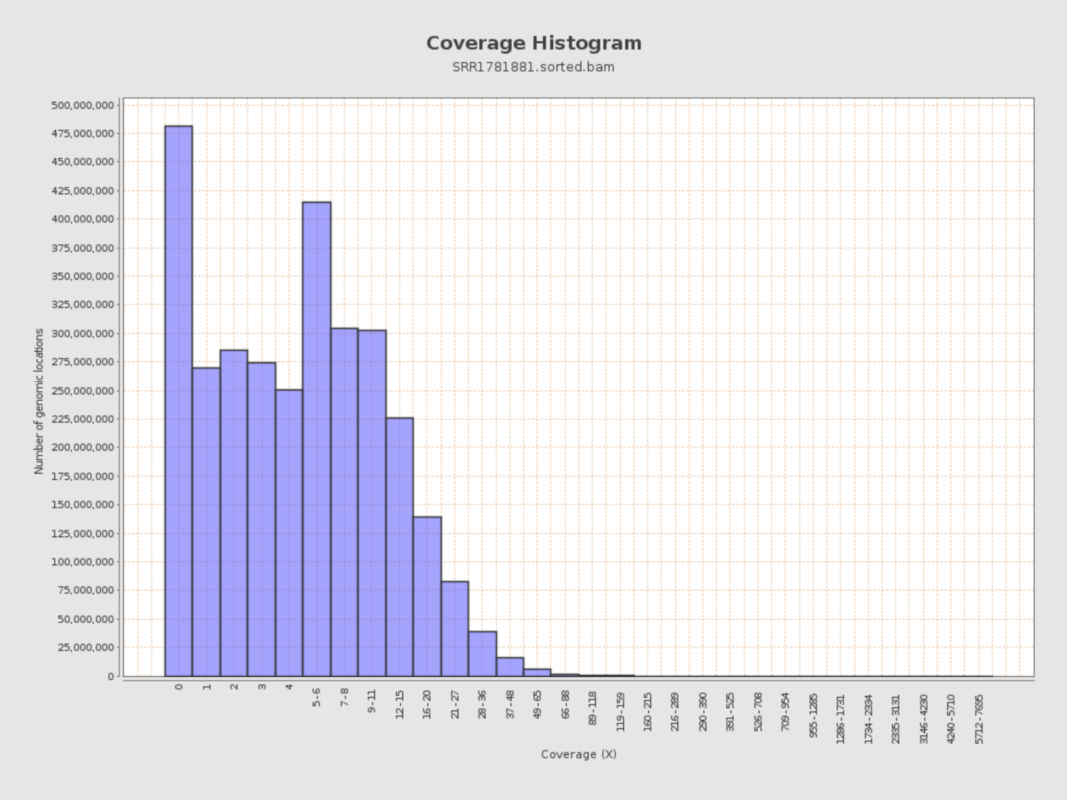
		bases	coverage	deviation
chr1	249250621	1471660165	5.9043	9.606
chr2	243199373	1569761012	6.4546	9.629
chr3	198022430	1285087834	6.4896	6.8274
chr4	191154276	1975801822	10.3362	10.0322
chr5	180915260	1172985023	6.4836	6.3854
chr6	171115067	1137279690	6.6463	7.0751
chr7	159138663	962669232	6.0492	7.2981
chr8	146364022	946247190	6.465	6.8346
chr9	141213431	775196755	5.4895	7.8097
chr10	135534747	1030399050	7.6025	10.982
chr11	135006516	1343482562	9.9512	10.4286
chr12	133851895	1248653780	9.3286	9.3221
chr13	115169878	578849357	5.026	5.9919
chr14	107349540	561853341	5.2339	6.4052
chr15	102531392	517858305	5.0507	6.3913
chr16	90354753	417085955	4.6161	6.0346
chr17	81195210	381177474	4.6946	6.1195
chr18	78077248	483738158	6.1956	7.4767
chr19	59128983	249940688	4.227	6.8454
chr20	63025520	351505677	5.5772	7.5187
chr21	48129895	221130980	4.5945	8.3842
chr22	51304566	154376018	3.009	5.1378
chrMT	16571	1082270	65.3111	21.949
chrX	155270560	1270148978	8.1802	8.7057

chrY	59373566	17181902	0.2894	3.1355

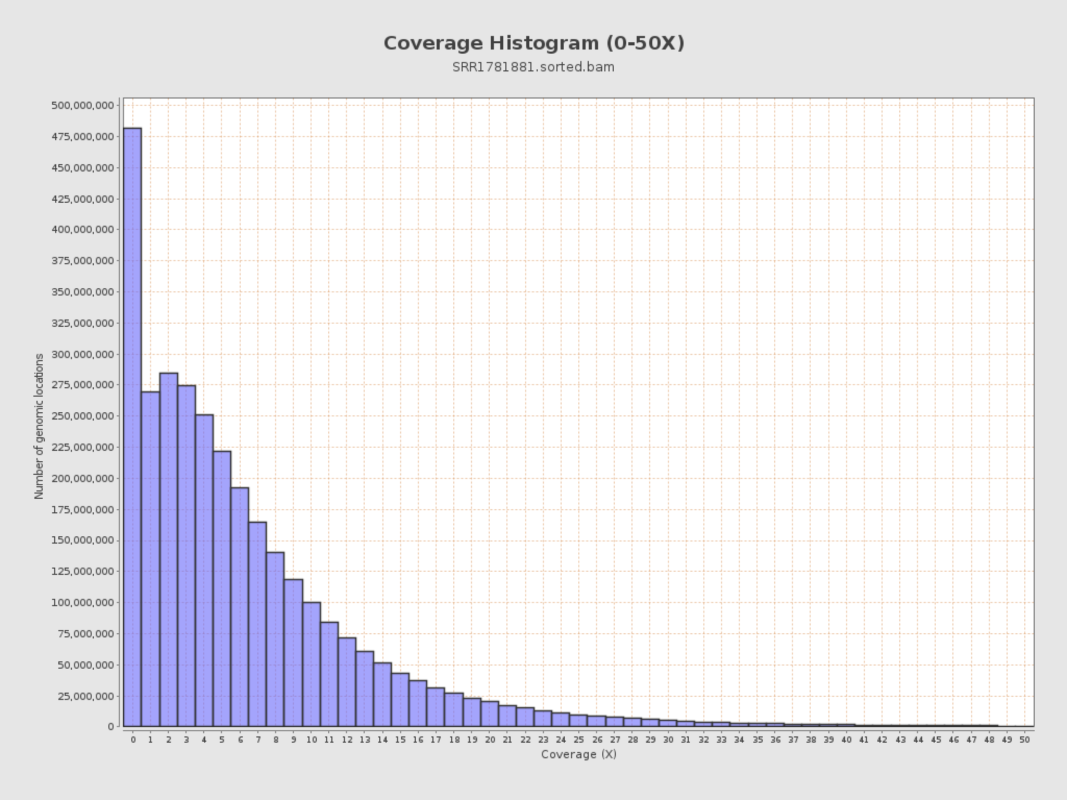
3. Results : Coverage across reference



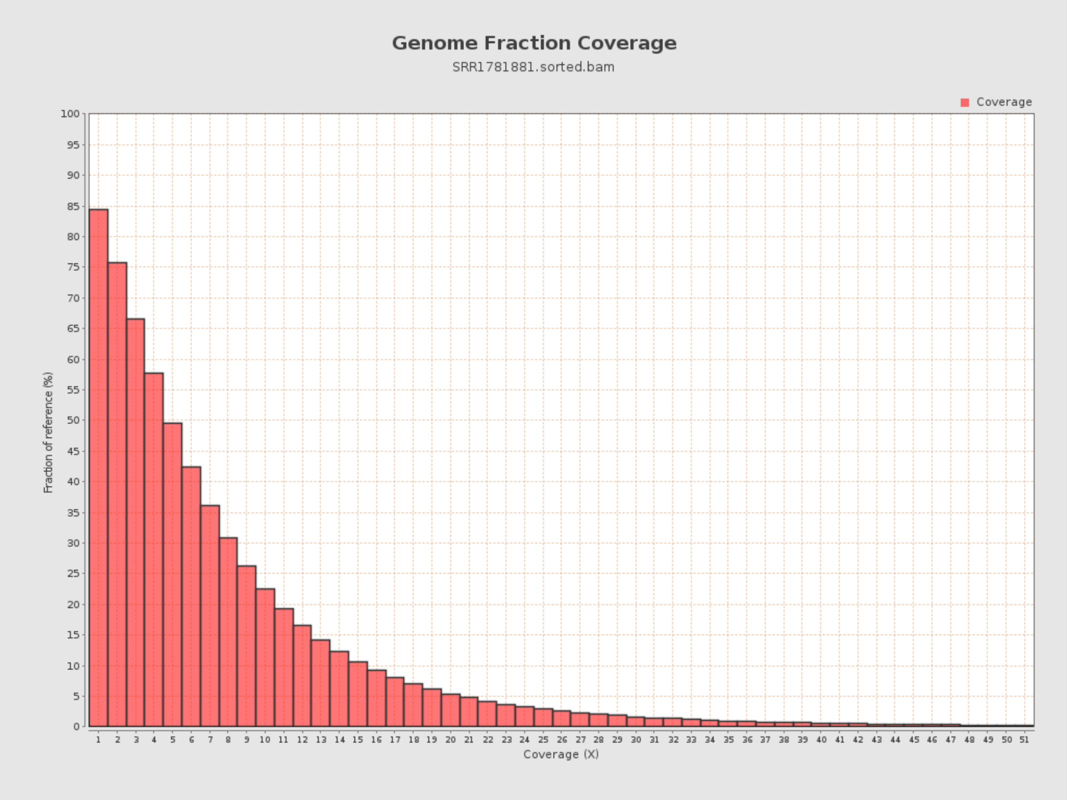
4. Results : Coverage Histogram



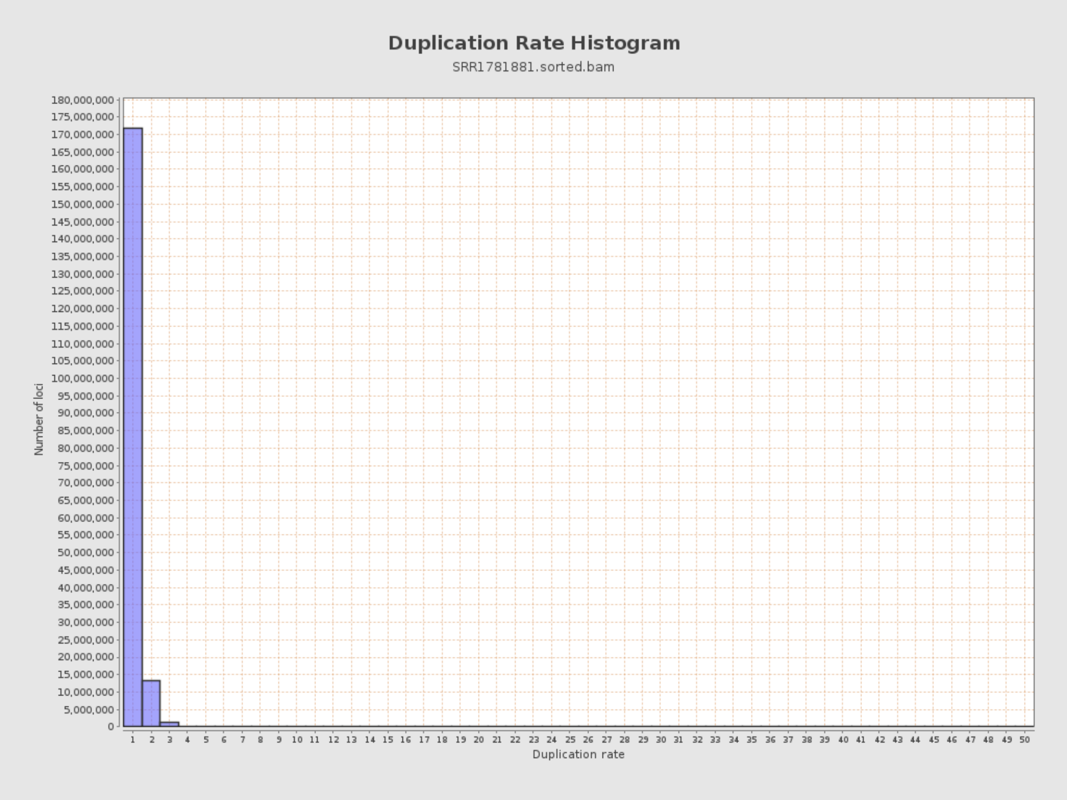
5. Results : Coverage Histogram (0-50X)



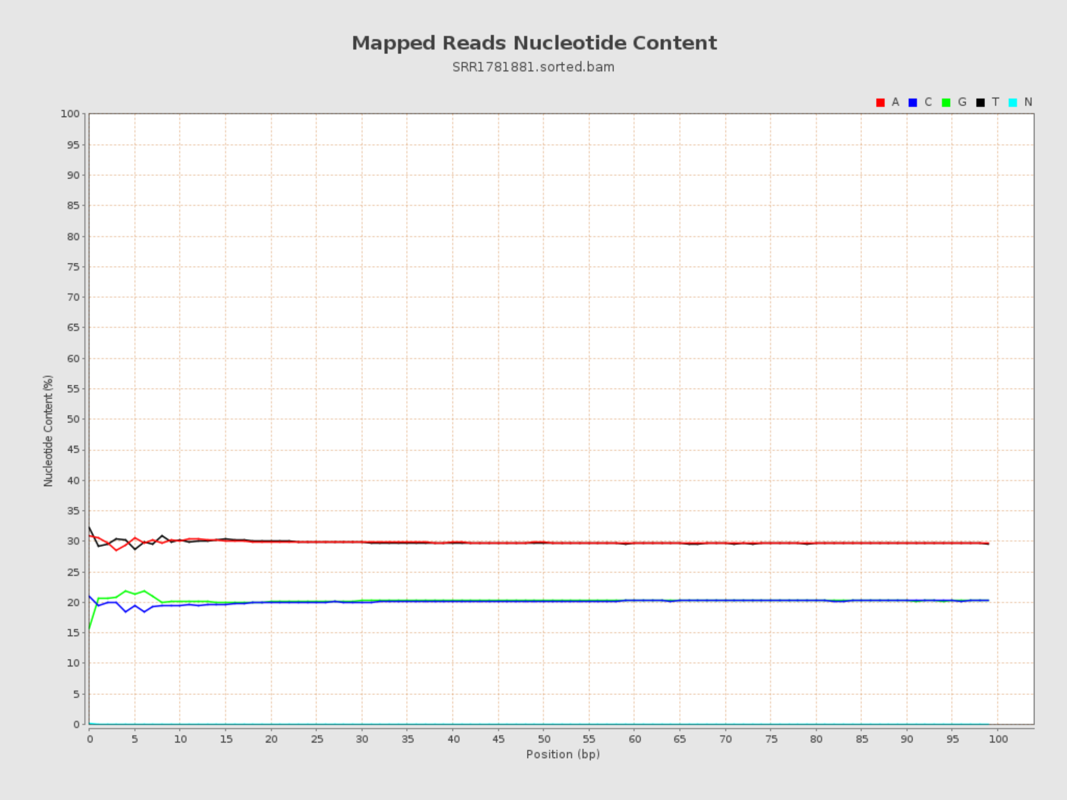
6. Results : Genome Fraction Coverage



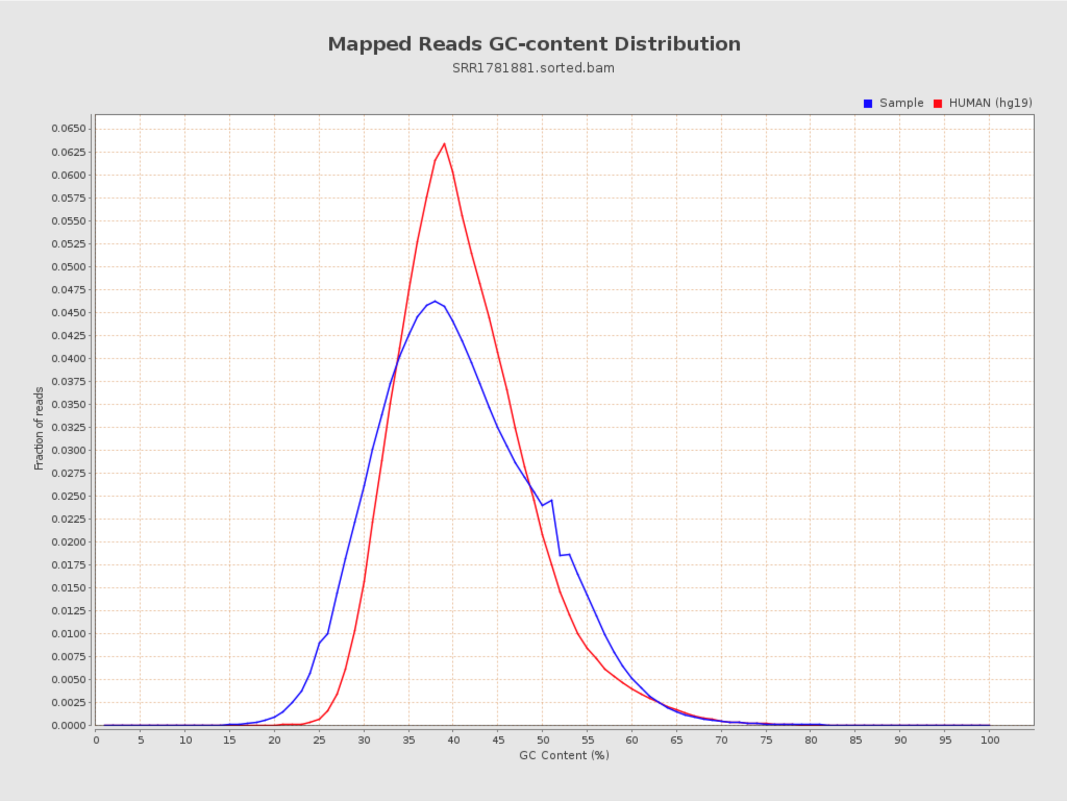
7. Results : Duplication Rate Histogram



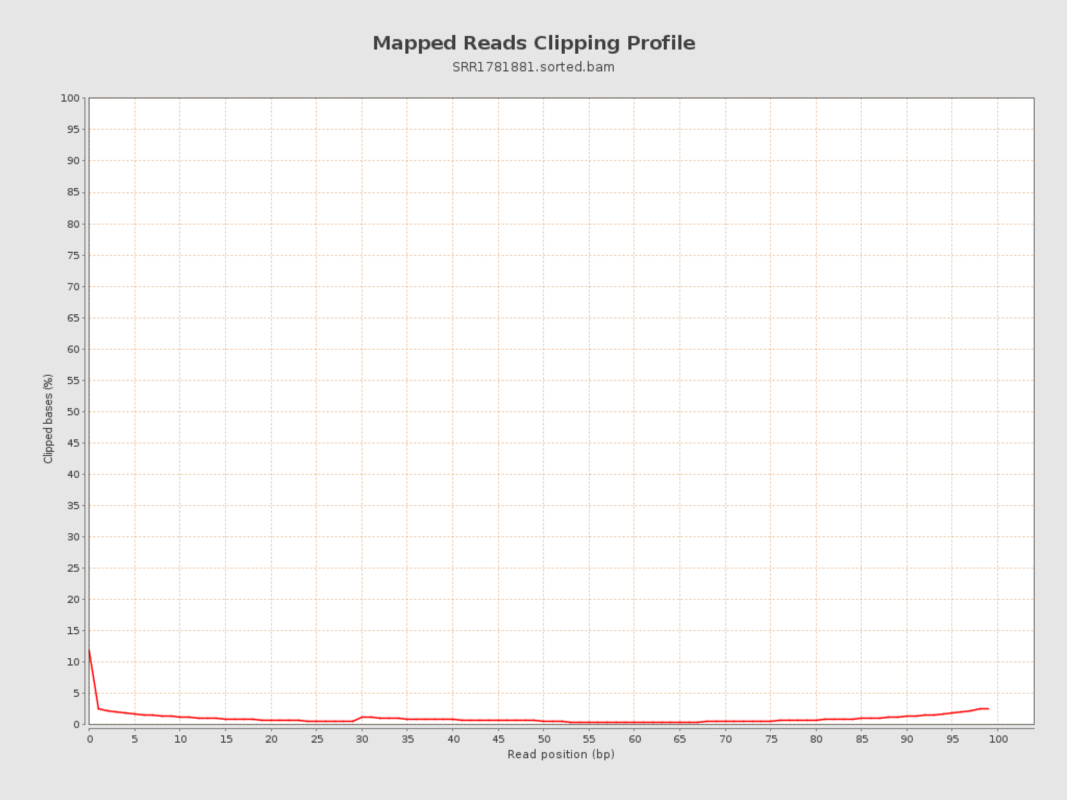
8. Results : Mapped Reads Nucleotide Content



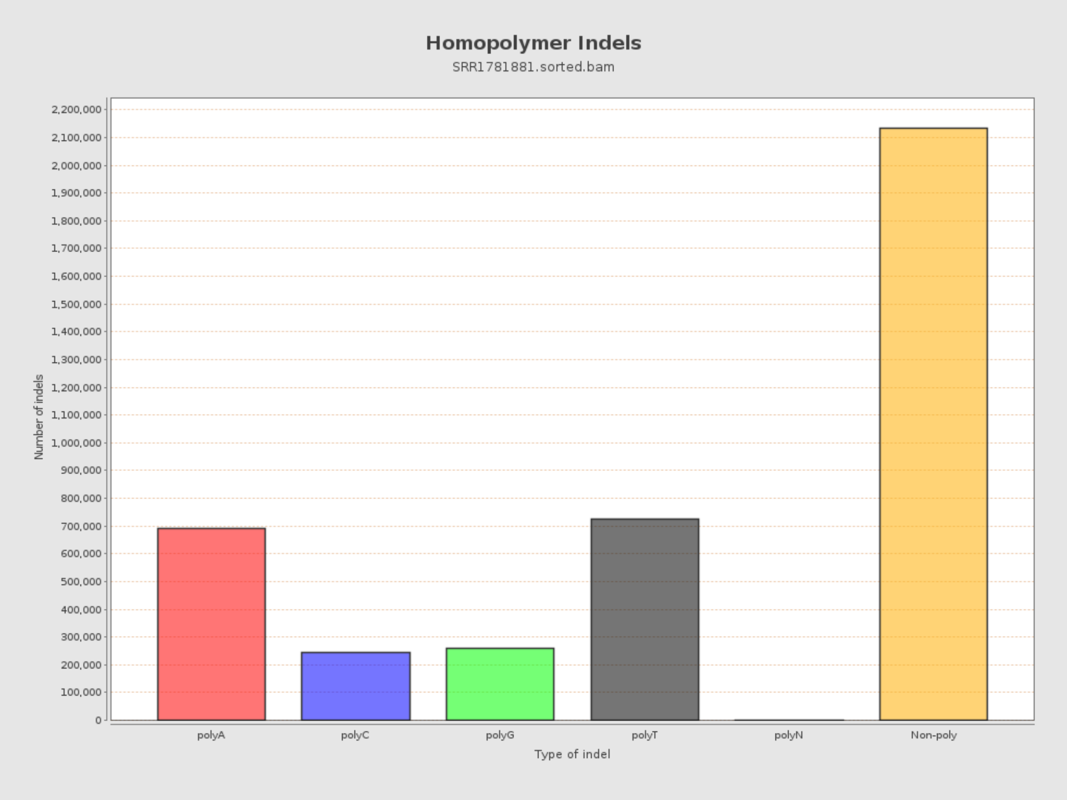
9. Results : Mapped Reads GC-content Distribution



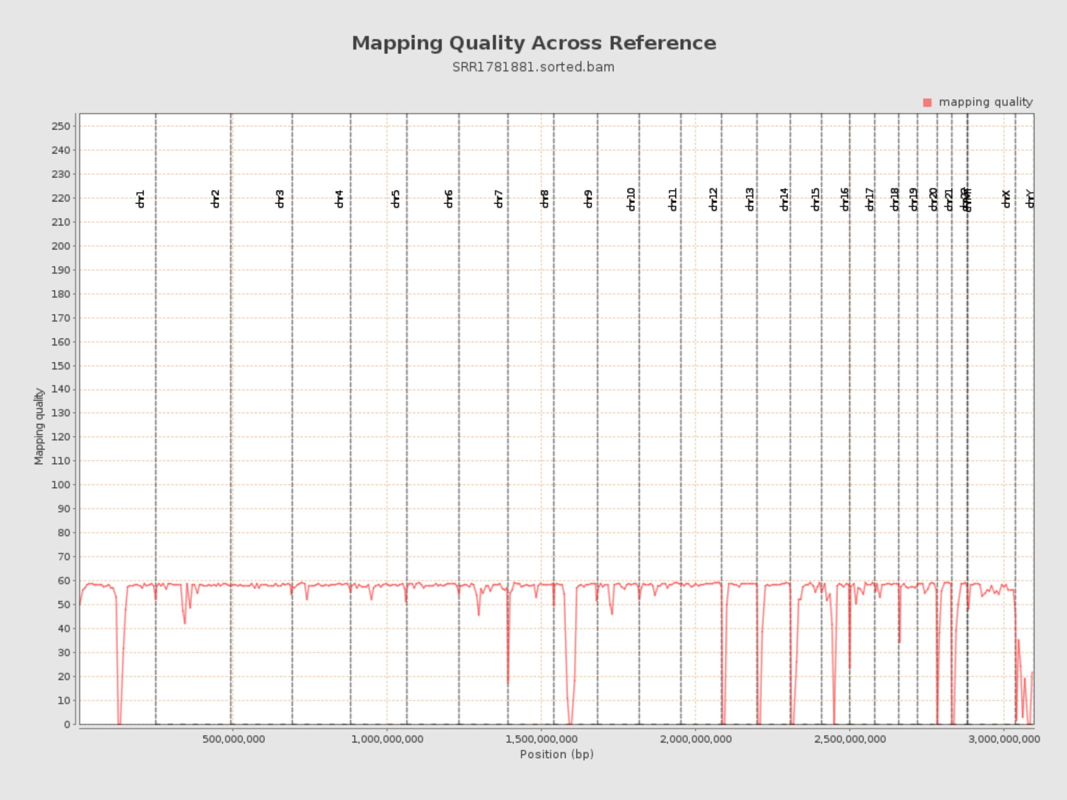
10. Results : Mapped Reads Clipping Profile



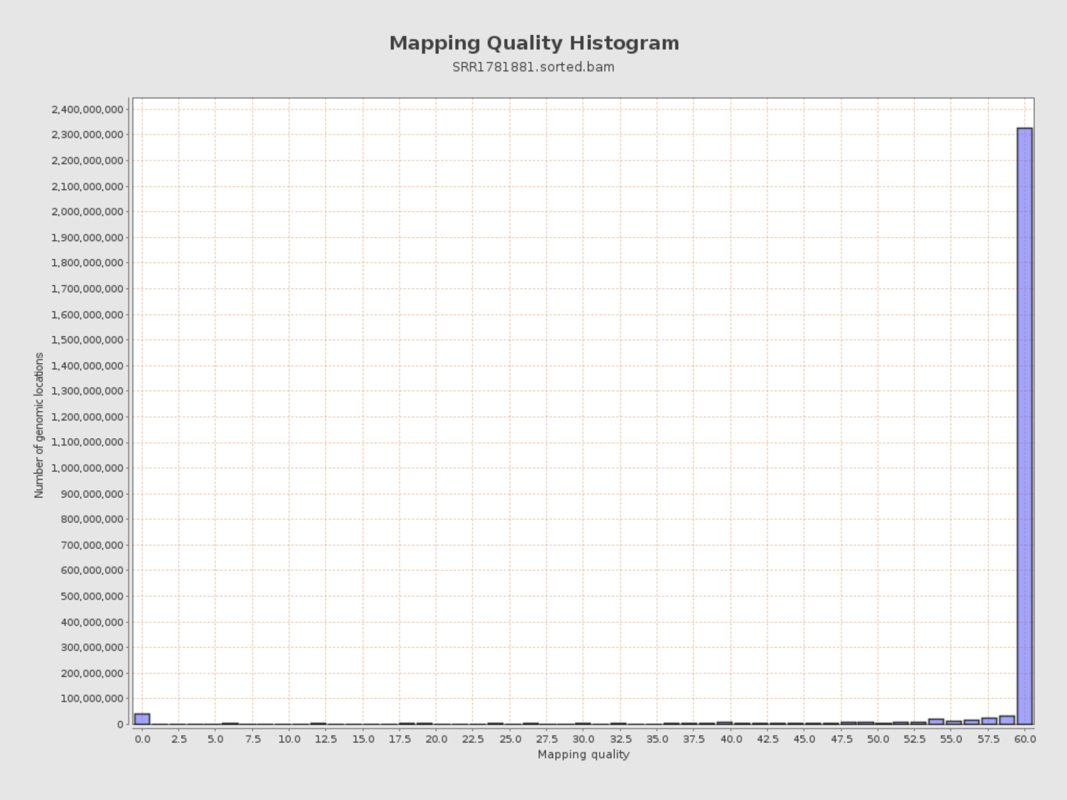
11. Results : Homopolymer Indels



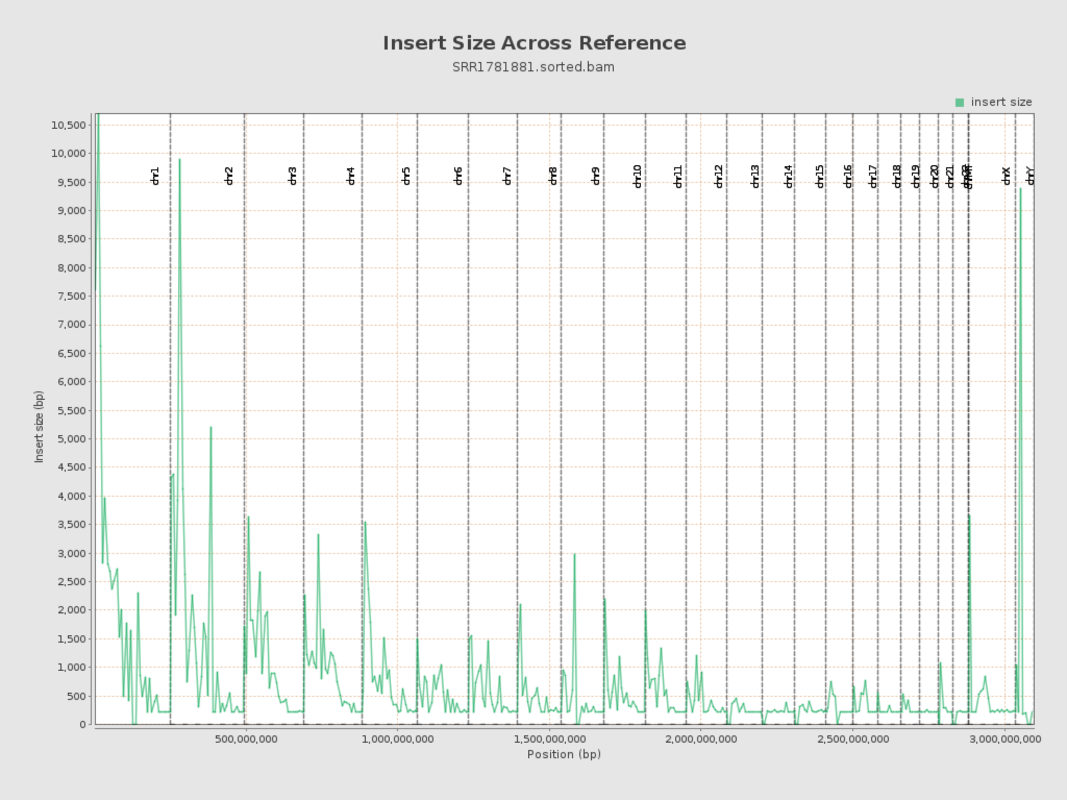
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram