Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/27 15:31:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781855.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_SRR1781855 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781855_1.fastq.gz SRR1781855_2.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Mar 27 15:31:41 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781855.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	192,274,572
Mapped reads	187,529,174 / 97.53%
Unmapped reads	4,745,398 / 2.47%
Mapped paired reads	187,529,174 / 97.53%
Mapped reads, first in pair	94,220,446 / 49%
Mapped reads, second in pair	93,308,728 / 48.53%
Mapped reads, both in pair	185,977,286 / 96.72%
Mapped reads, singletons	1,551,888 / 0.81%
Secondary alignments	0
Supplementary alignments	696,683 / 0.36%
Read min/max/mean length	30 / 100 / 99.98
Duplicated reads (estimated)	12,746,638 / 6.63%
Duplication rate	6.51%
Clipped reads	7,917,408 / 4.12%

2.2. ACGT Content

Number/percentage of A's	5,455,428,977 / 29.3%
Number/percentage of C's	3,831,888,374 / 20.58%
Number/percentage of T's	5,437,355,821 / 29.2%
Number/percentage of G's	3,868,887,927 / 20.78%
Number/percentage of N's	25,415,176 / 0.14%

GC Percentage	41.36%

2.3. Coverage

Mean	6.0157
Standard Deviation	7.4063

2.4. Mapping Quality

Mean Mapping Quality	53.97

2.5. Insert size

Mean	39,799.57
Standard Deviation	1,939,890.73
P25/Median/P75	164 / 198 / 240

2.6. Mismatches and indels

General error rate	0.56%
Mismatches	101,842,276
Insertions	1,703,666
Mapped reads with at least one insertion	0.9%
Deletions	1,696,859
Mapped reads with at least one deletion	0.89%
Homopolymer indels	45.42%

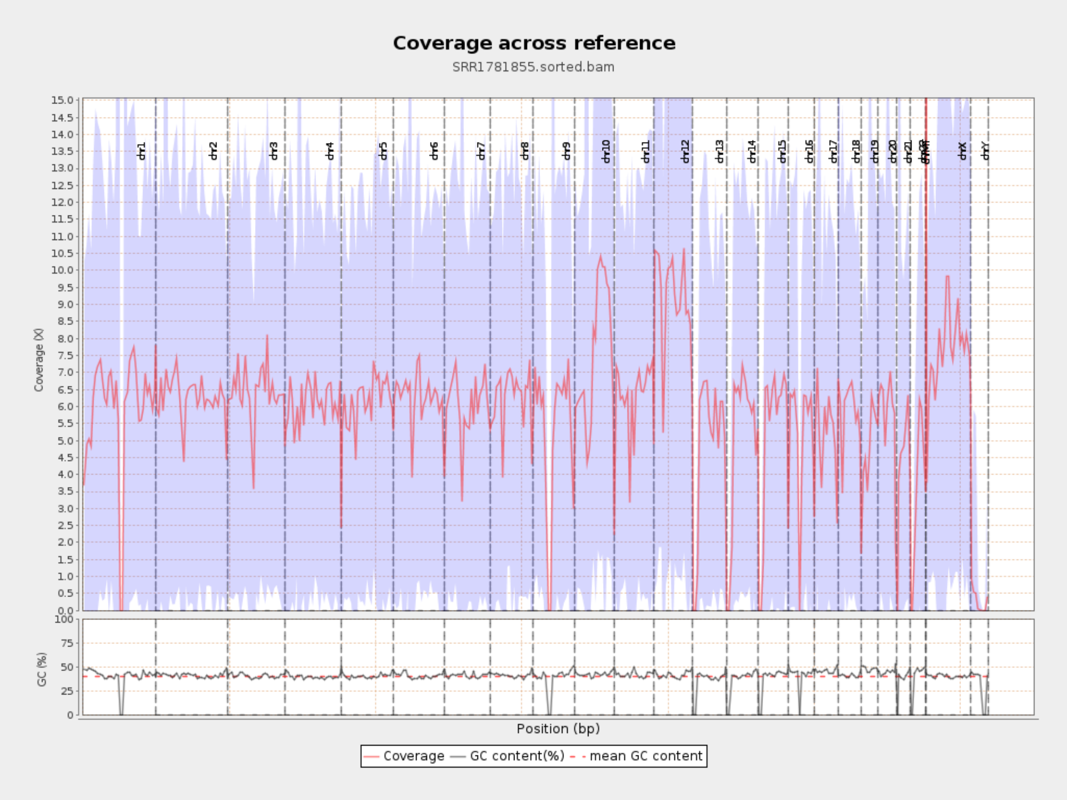
2.7. Chromosome stats

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

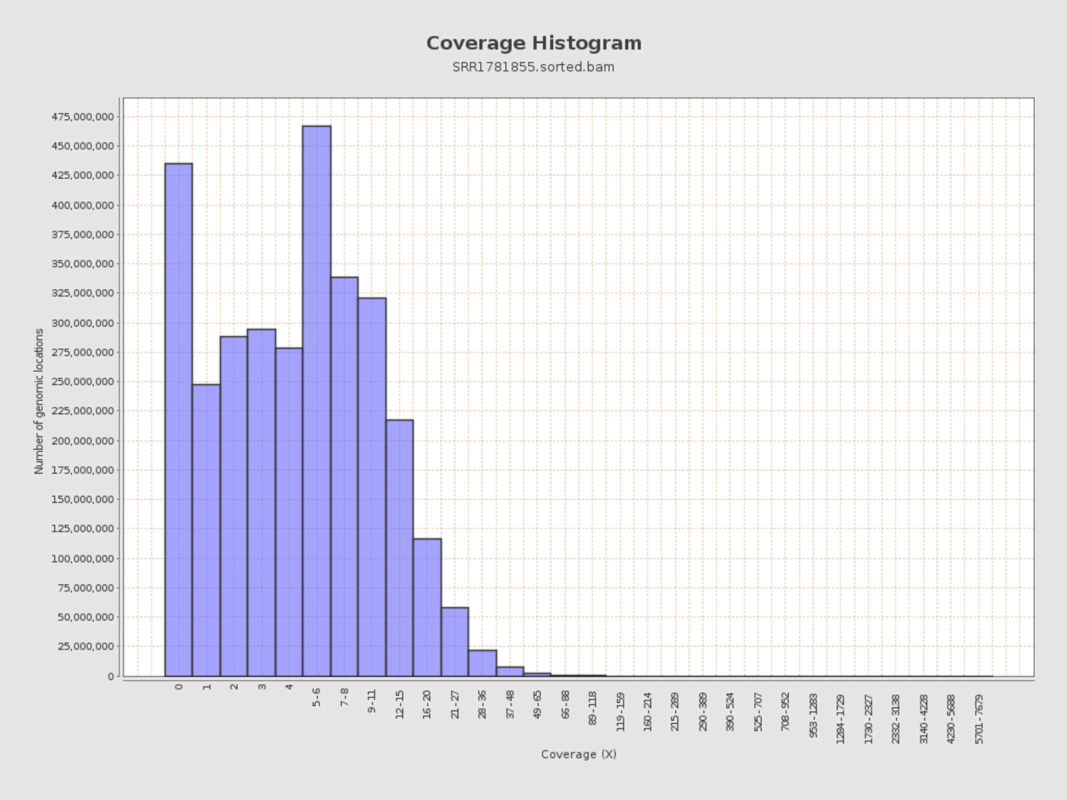
		bases	coverage	deviation
chr1	249250621	1477340881	5.9271	10.4653
chr2	243199373	1525253296	6.2716	8.085
chr3	198022430	1268150448	6.4041	5.8379
chr4	191154276	1167798253	6.1092	6.7613
chr5	180915260	1113238186	6.1534	5.5296
chr6	171115067	1074923494	6.2819	6.4043
chr7	159138663	954457730	5.9976	6.5729
chr8	146364022	917487873	6.2685	5.9044
chr9	141213431	752365173	5.3279	7.2598
chr10	135534747	1030452350	7.6029	11.7012
chr11	135006516	846267787	6.2683	6.1185
chr12	133851895	1246802727	9.3148	8.2512
chr13	115169878	563083966	4.8892	5.3025
chr14	107349540	550680341	5.1298	5.6985
chr15	102531392	523865412	5.1093	5.8078
chr16	90354753	457687577	5.0655	5.9123
chr17	81195210	431238291	5.3111	6.3351
chr18	78077248	459001787	5.8788	7.1776
chr19	59128983	283503607	4.7947	7.4607
chr20	63025520	374763183	5.9462	6.8988
chr21	48129895	214877136	4.4645	9.5823
chr22	51304566	183774479	3.582	5.259
chrMT	16571	1019153	61.5022	18.3476
chrX	155270560	1188345055	7.6534	7.0939

chrY	59373566	16417731	0.2765	3.0237

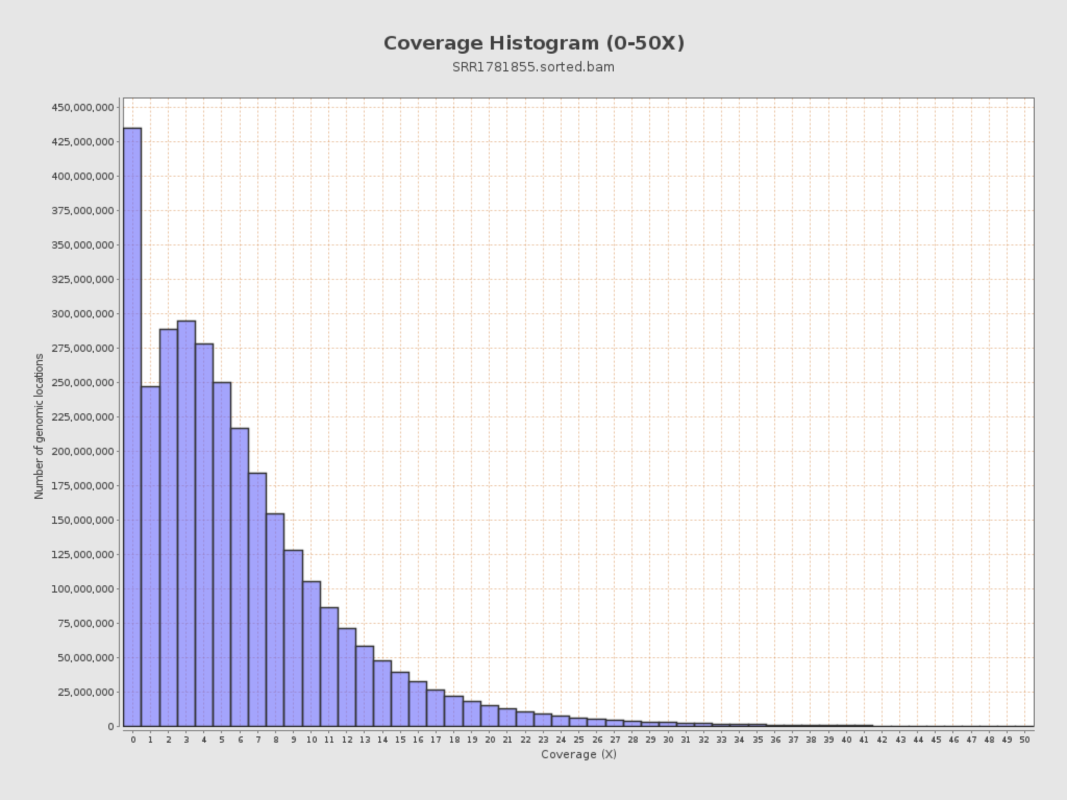
3. Results : Coverage across reference



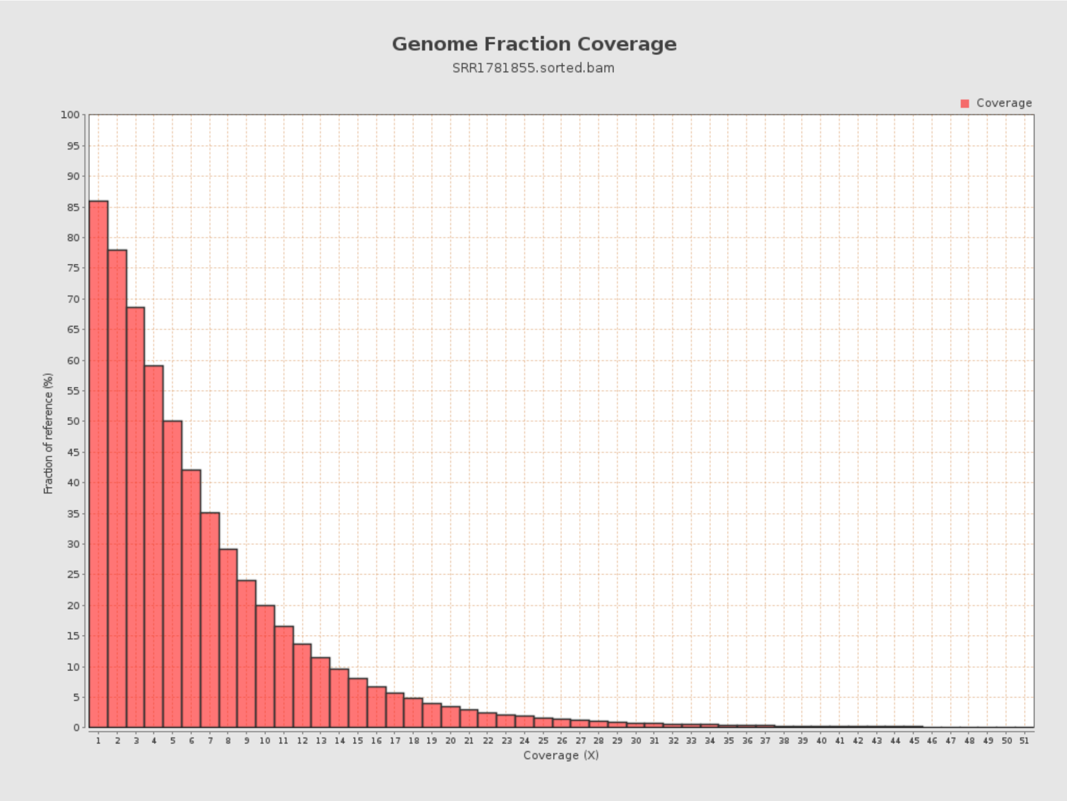
4. Results : Coverage Histogram



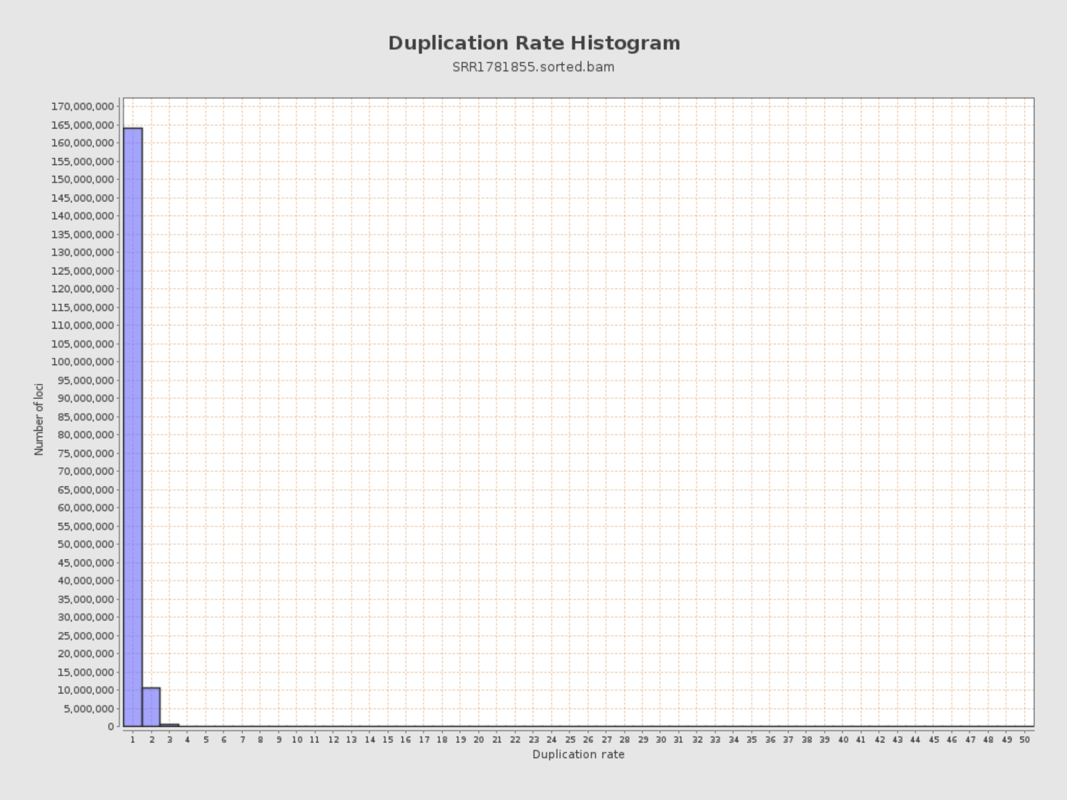
5. Results : Coverage Histogram (0-50X)



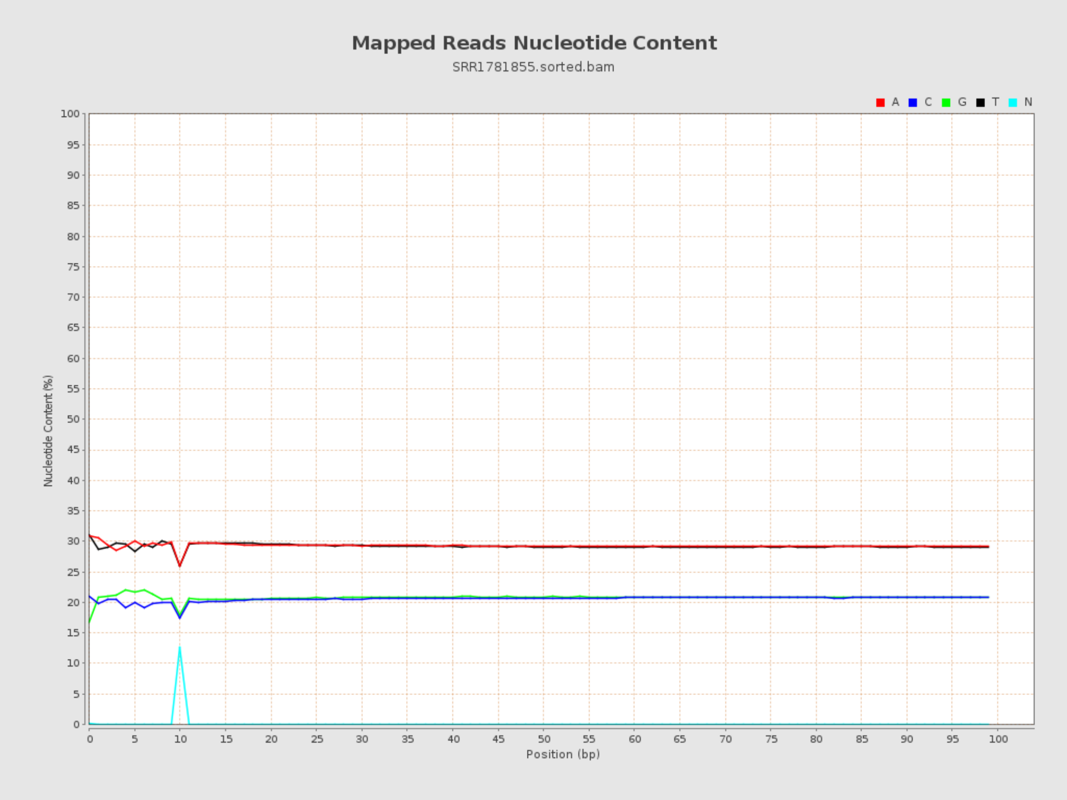
6. Results : Genome Fraction Coverage



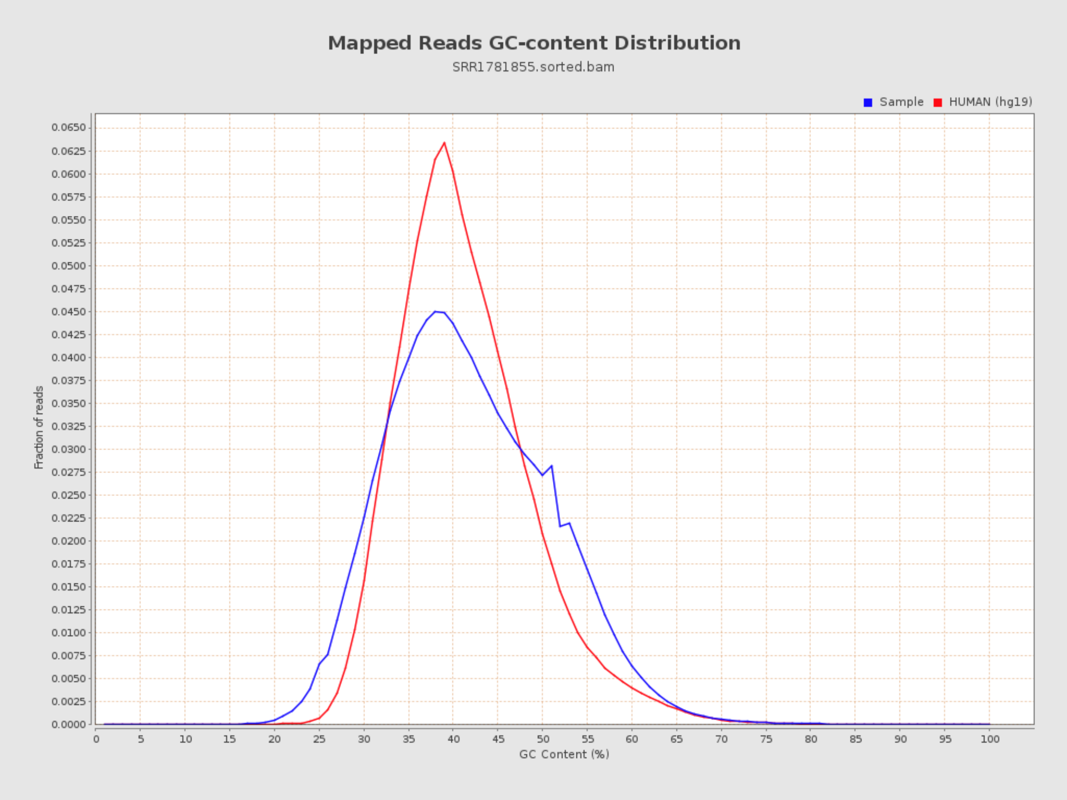
7. Results : Duplication Rate Histogram



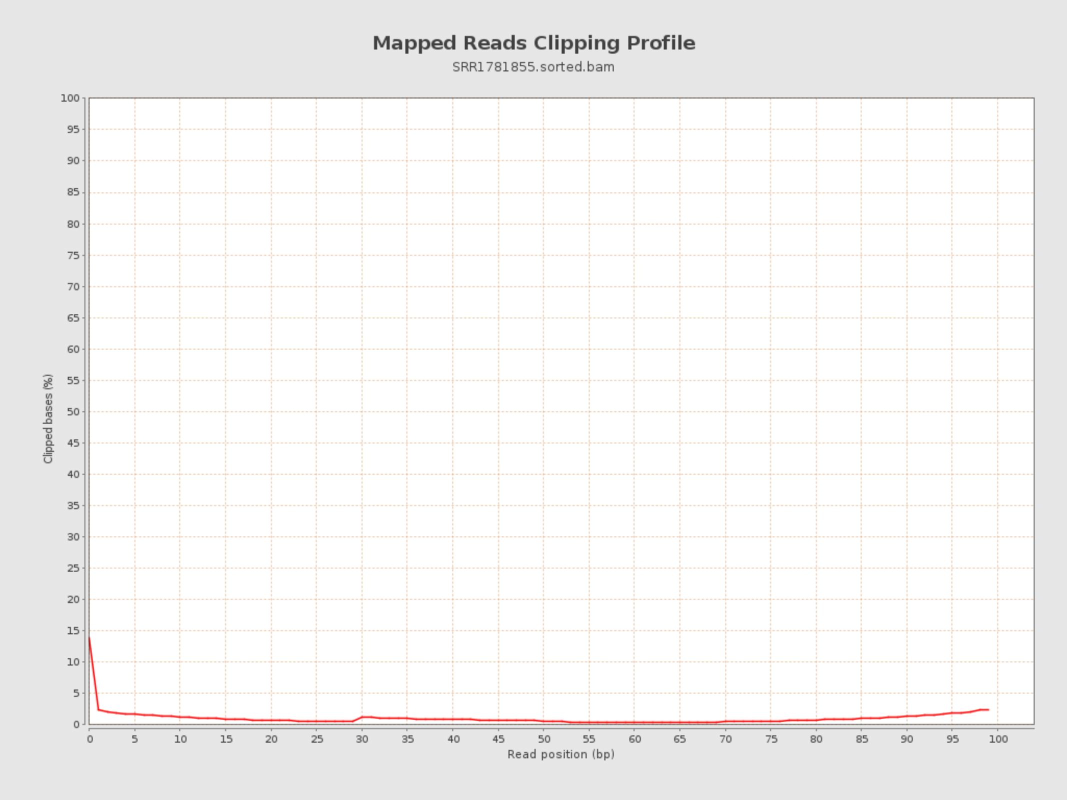
8. Results : Mapped Reads Nucleotide Content



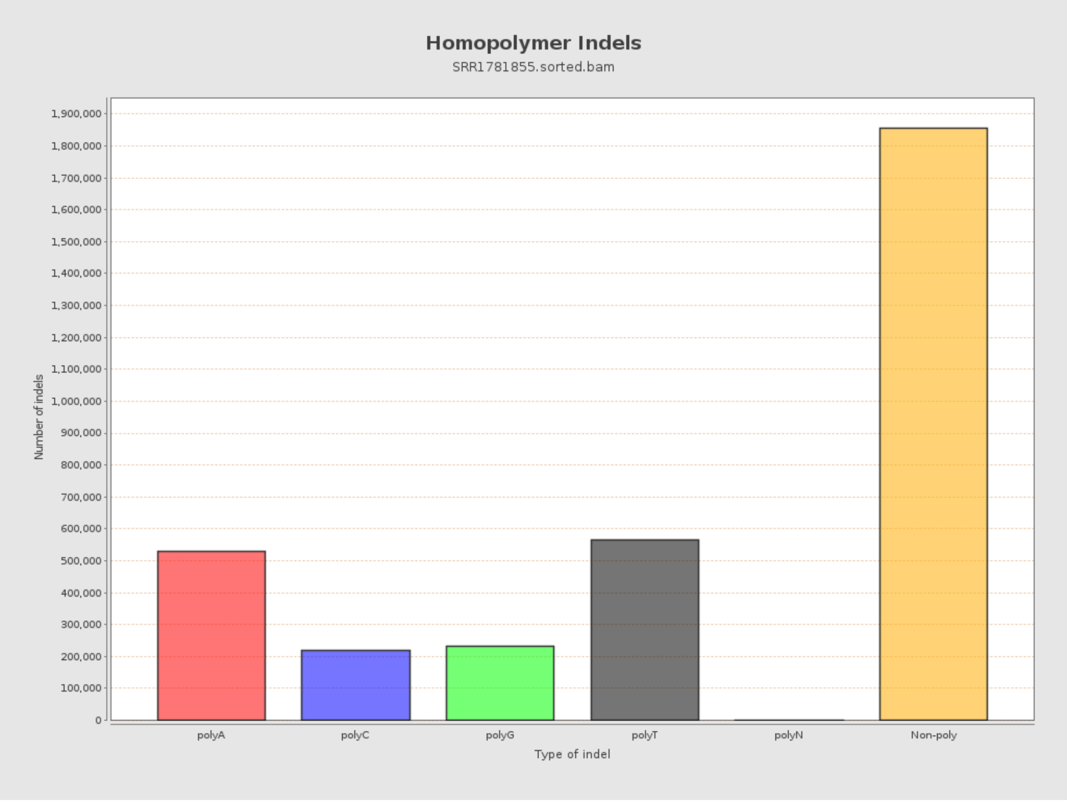
9. Results : Mapped Reads GC-content Distribution



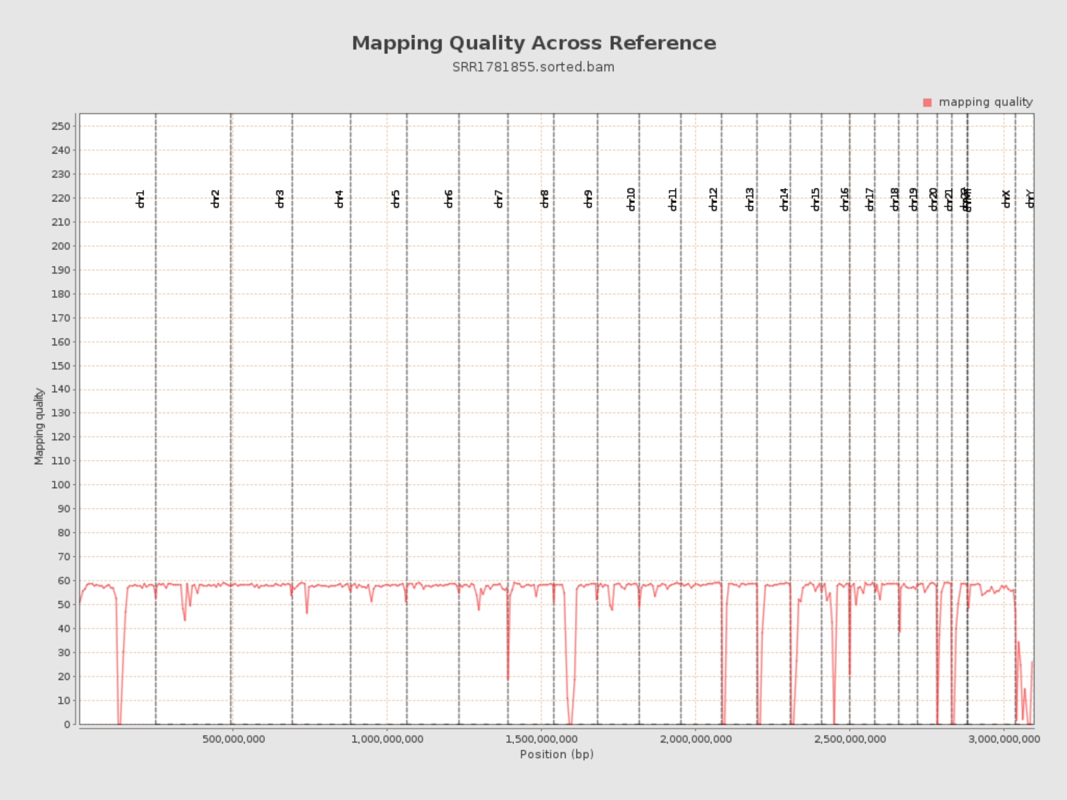
10. Results : Mapped Reads Clipping Profile



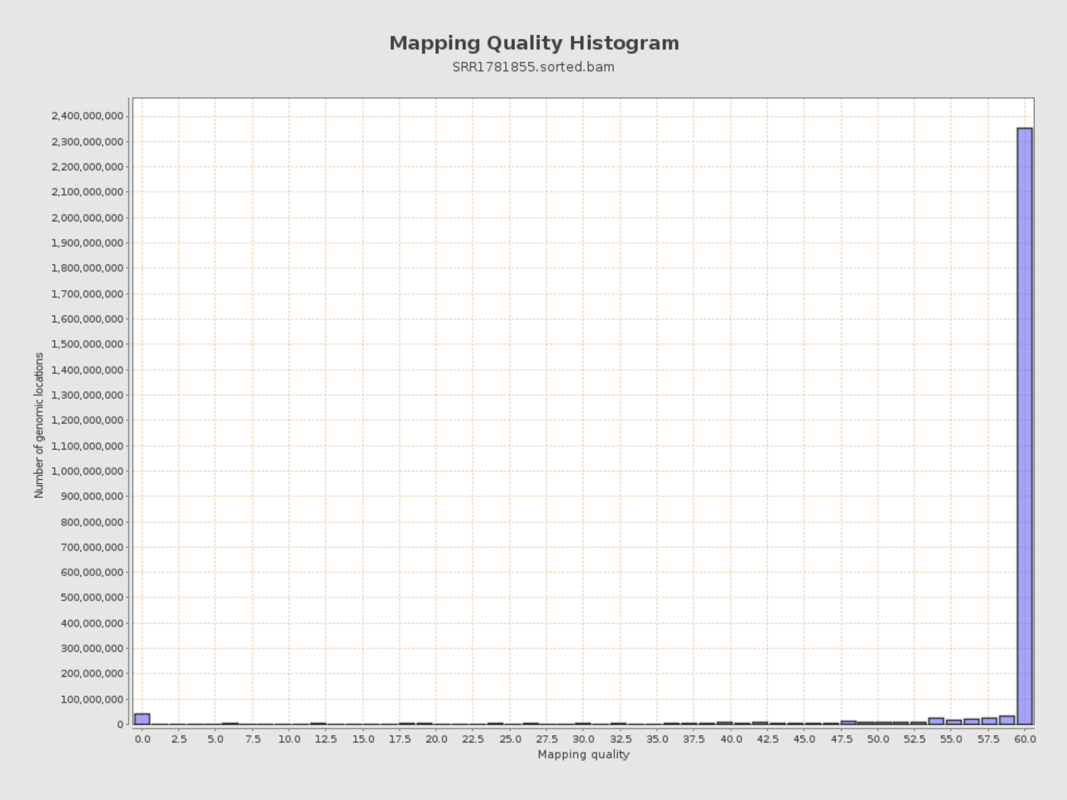
11. Results : Homopolymer Indels



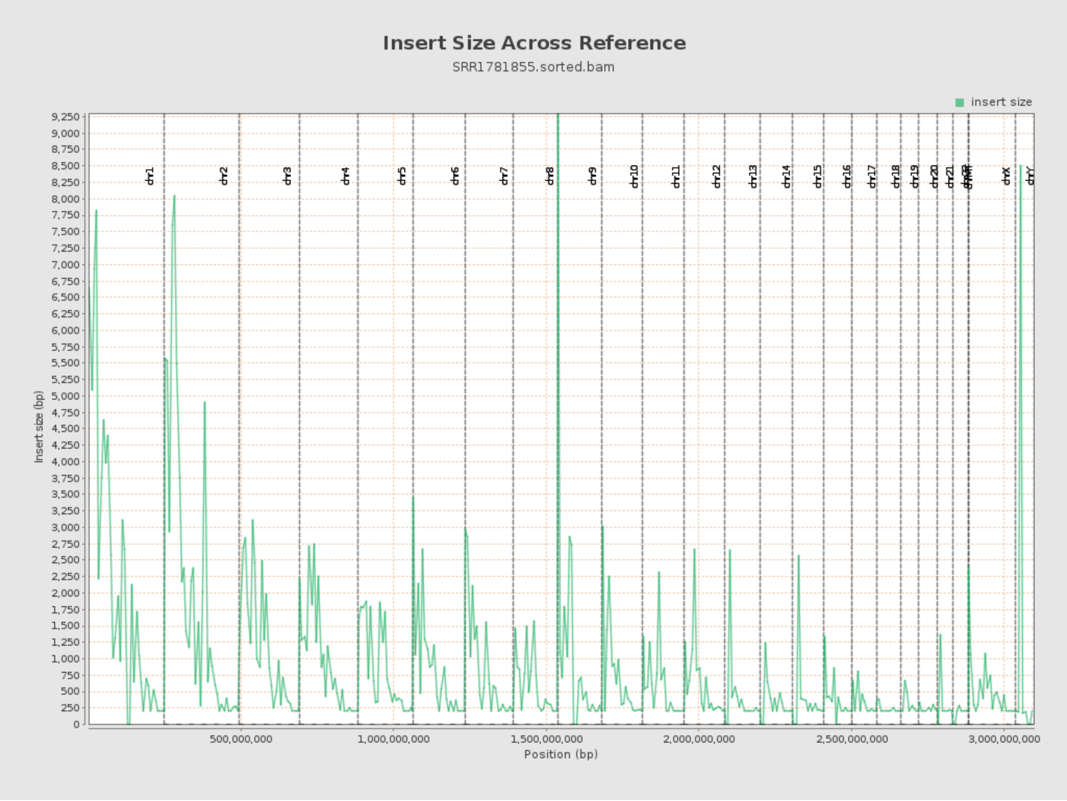
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram