Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/25 18:15:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781825.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_SRR1781825 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781825_1.fastq.gz SRR1781825_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Mar 25 18:15:33 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781825.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	146,096,708
Mapped reads	142,646,447 / 97.64%
Unmapped reads	3,450,261 / 2.36%
Mapped paired reads	142,646,447 / 97.64%
Mapped reads, first in pair	71,935,496 / 49.24%
Mapped reads, second in pair	70,710,951 / 48.4%
Mapped reads, both in pair	140,321,610 / 96.05%
Mapped reads, singletons	2,324,837 / 1.59%
Secondary alignments	0
Supplementary alignments	485,832 / 0.33%
Read min/max/mean length	30 / 100 / 99.99
Duplicated reads (estimated)	8,208,280 / 5.62%
Duplication rate	5.53%
Clipped reads	6,018,661 / 4.12%

2.2. ACGT Content

Number/percentage of A's	4,176,865,488 / 29.5%
Number/percentage of C's	2,888,234,093 / 20.4%
Number/percentage of T's	4,159,569,590 / 29.38%
Number/percentage of G's	2,932,097,048 / 20.71%
Number/percentage of N's	2,009,701 / 0.01%

GC Percentage	41.11%

2.3. Coverage

Mean	4.5746
Standard Deviation	5.5839

2.4. Mapping Quality

Mean Mapping Quality	53.96

2.5. Insert size

Mean	41,832.29
Standard Deviation	2,029,126.63
P25/Median/P75	167 / 204 / 250

2.6. Mismatches and indels

General error rate	0.46%
Mismatches	62,637,212
Insertions	1,286,115
Mapped reads with at least one insertion	0.89%
Deletions	1,276,757
Mapped reads with at least one deletion	0.88%
Homopolymer indels	46.14%

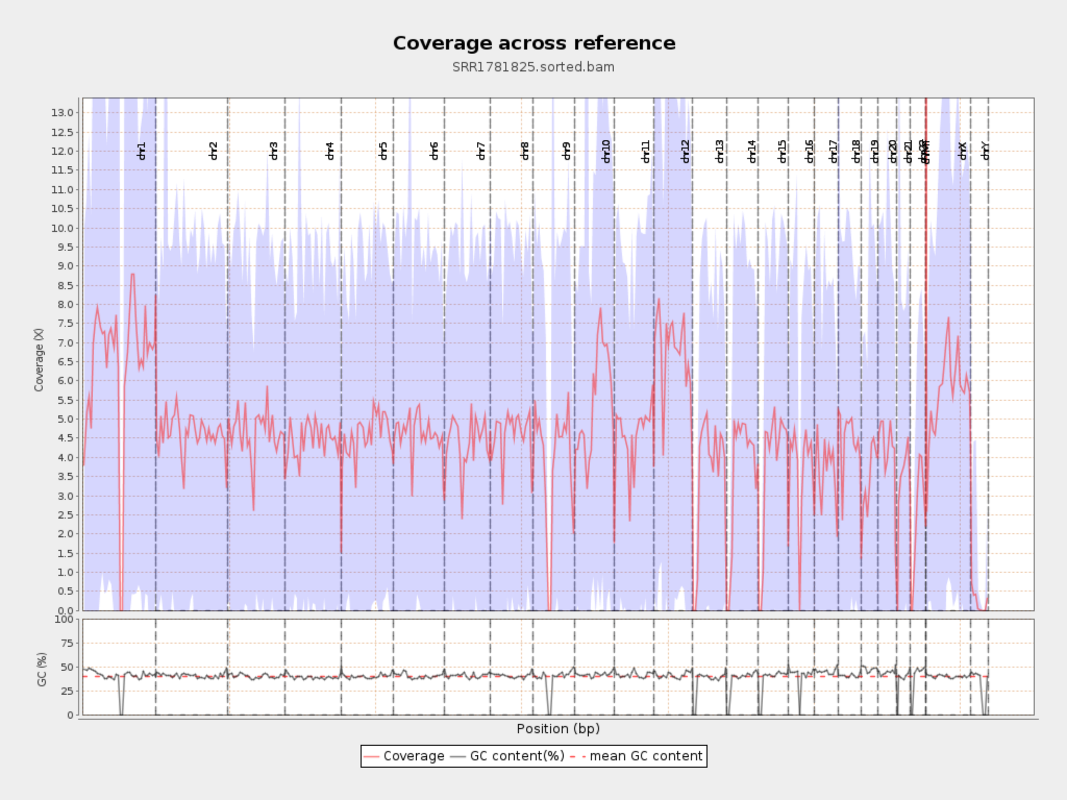
2.7. Chromosome stats

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

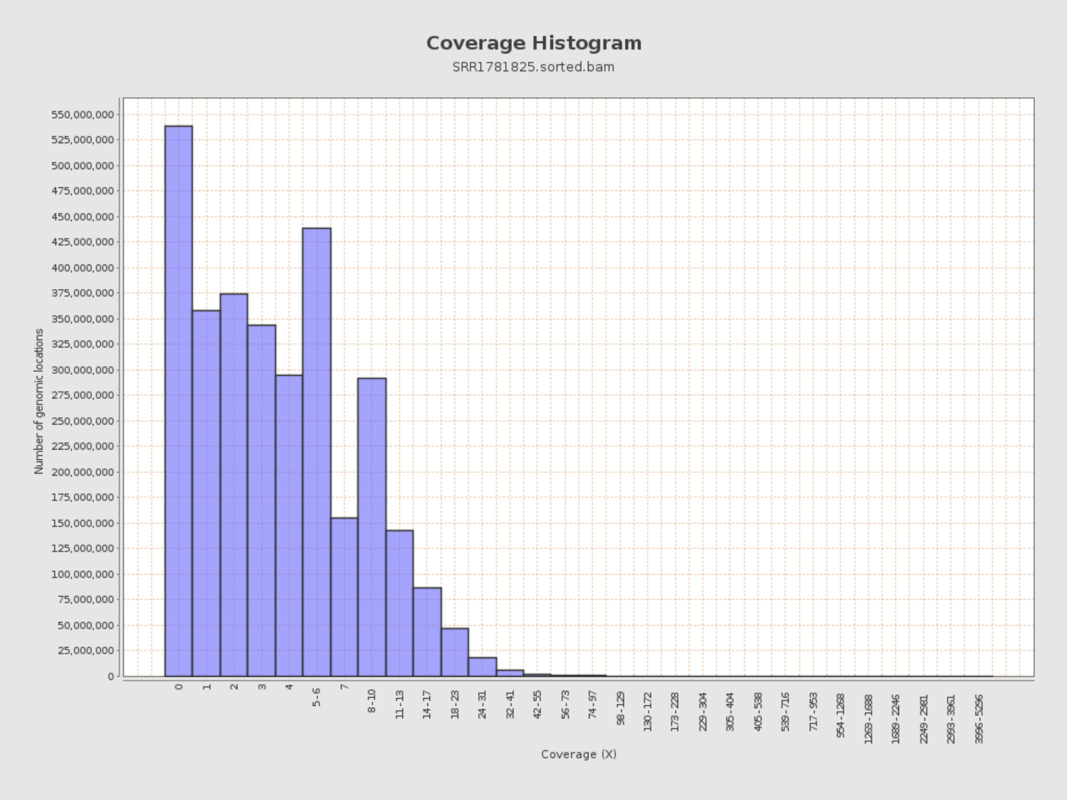
		bases	coverage	deviation
chr1	249250621	1608036555	6.4515	8.789
chr2	243199373	1125395539	4.6275	5.4845
chr3	198022430	918816406	4.64	4.5018
chr4	191154276	858390725	4.4906	4.7946
chr5	180915260	827555705	4.5743	4.3651
chr6	171115067	792680031	4.6324	4.8462
chr7	159138663	697850196	4.3852	4.8207
chr8	146364022	675328398	4.614	4.564
chr9	141213431	549881150	3.894	5.3976
chr10	135534747	746518461	5.5079	7.5984
chr11	135006516	618429790	4.5807	4.698
chr12	133851895	914186711	6.8298	6.3947
chr13	115169878	413549976	3.5908	4.084
chr14	107349540	397309021	3.7011	4.3713
chr15	102531392	382034993	3.726	4.502
chr16	90354753	325785592	3.6056	4.5807
chr17	81195210	301281087	3.7106	4.6484
chr18	78077248	347893738	4.4558	5.3505
chr19	59128983	201942335	3.4153	5.3227
chr20	63025520	270074342	4.2852	5.1752
chr21	48129895	160260019	3.3297	6.2451
chr22	51304566	124290701	2.4226	3.6673
chrMT	16571	731498	44.1433	13.1237
chrX	155270560	890487458	5.7351	5.5838

chrY	59373566	12954941	0.2182	2.2838

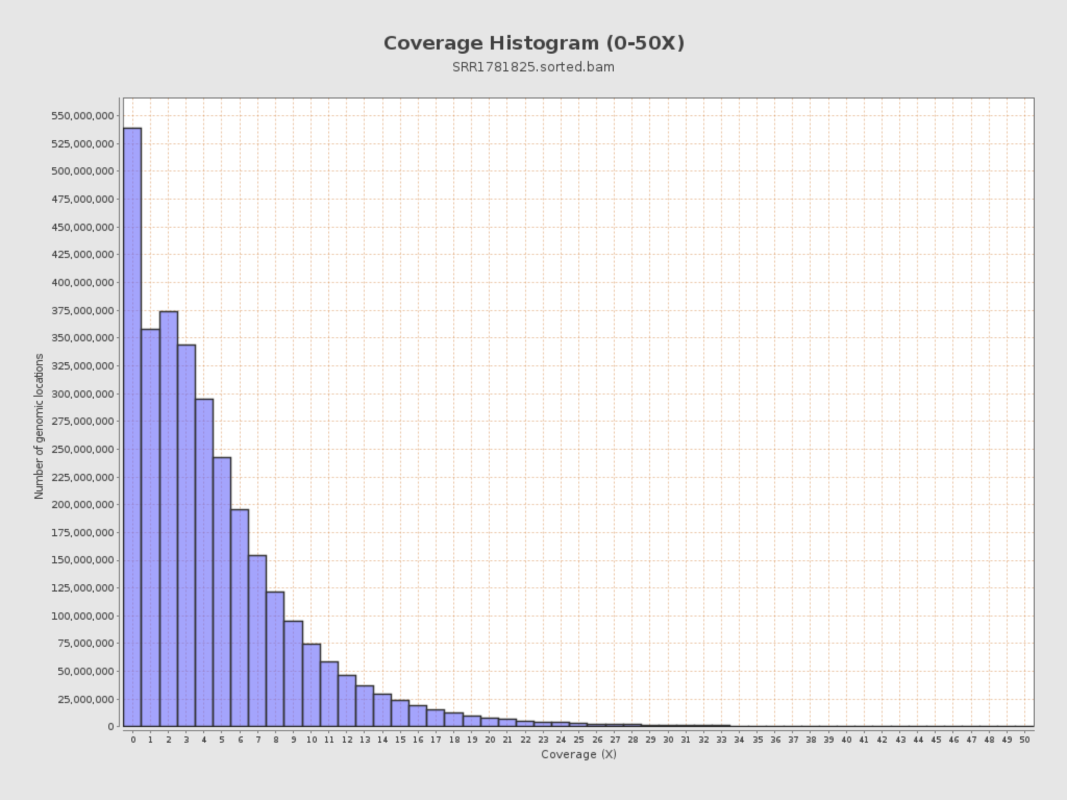
3. Results : Coverage across reference



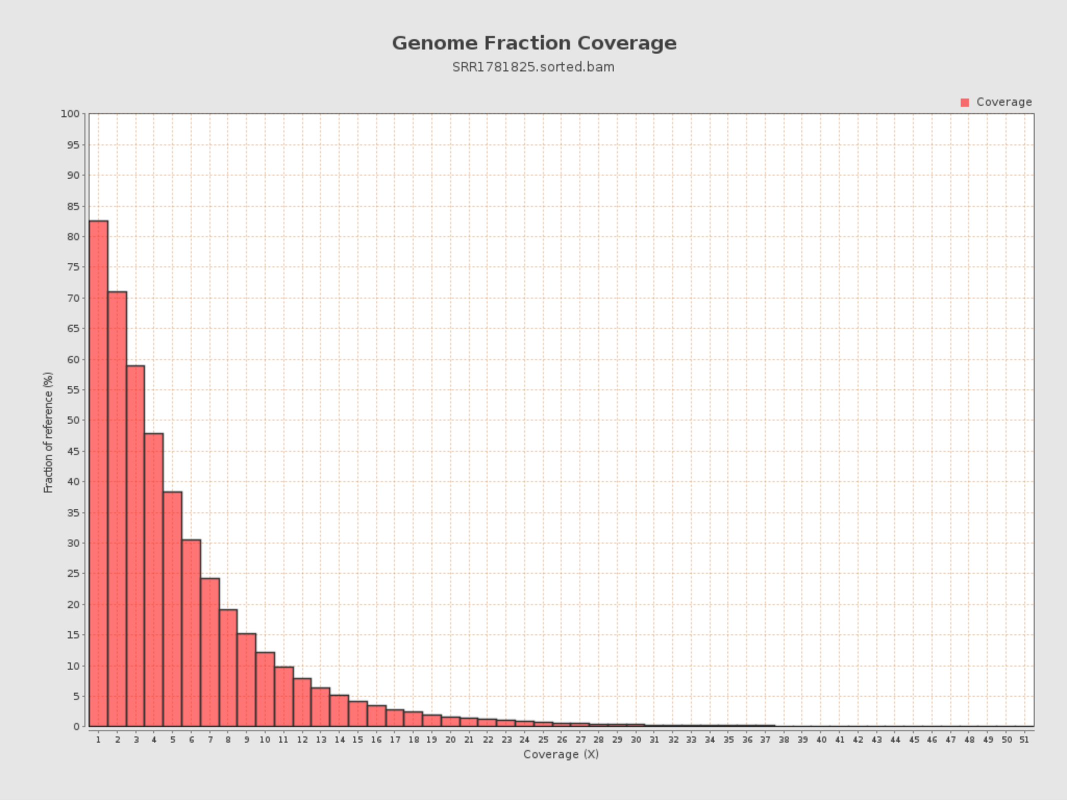
4. Results : Coverage Histogram



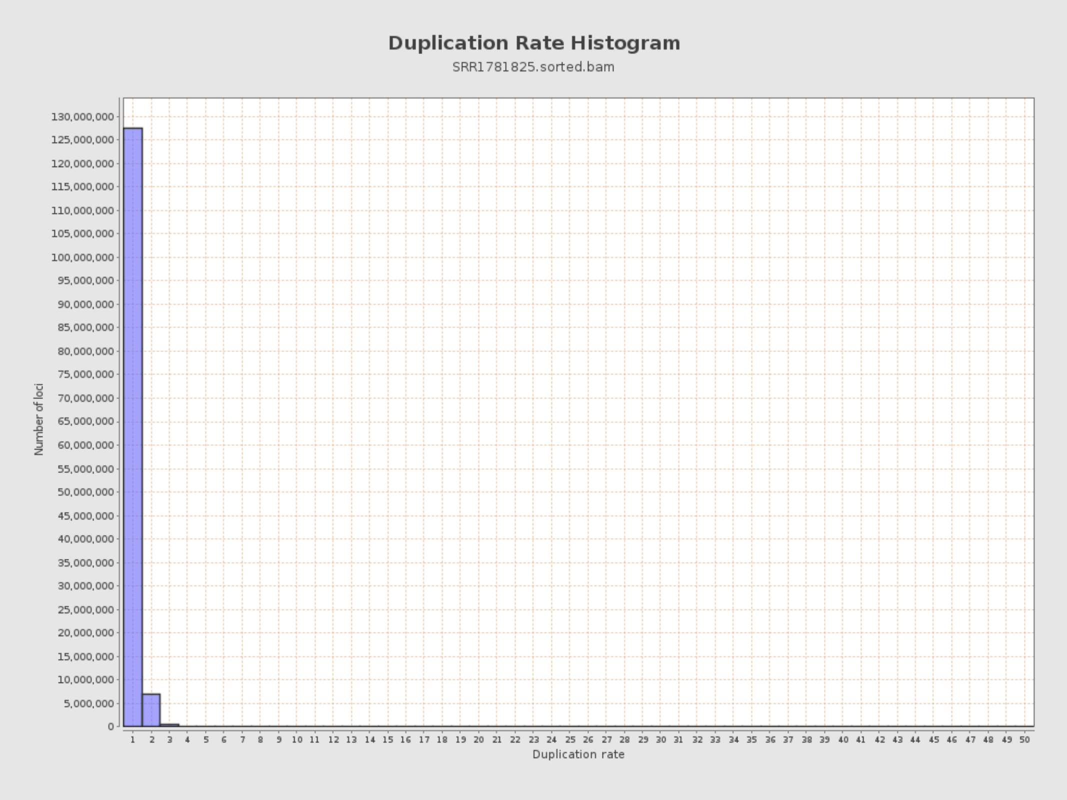
5. Results : Coverage Histogram (0-50X)



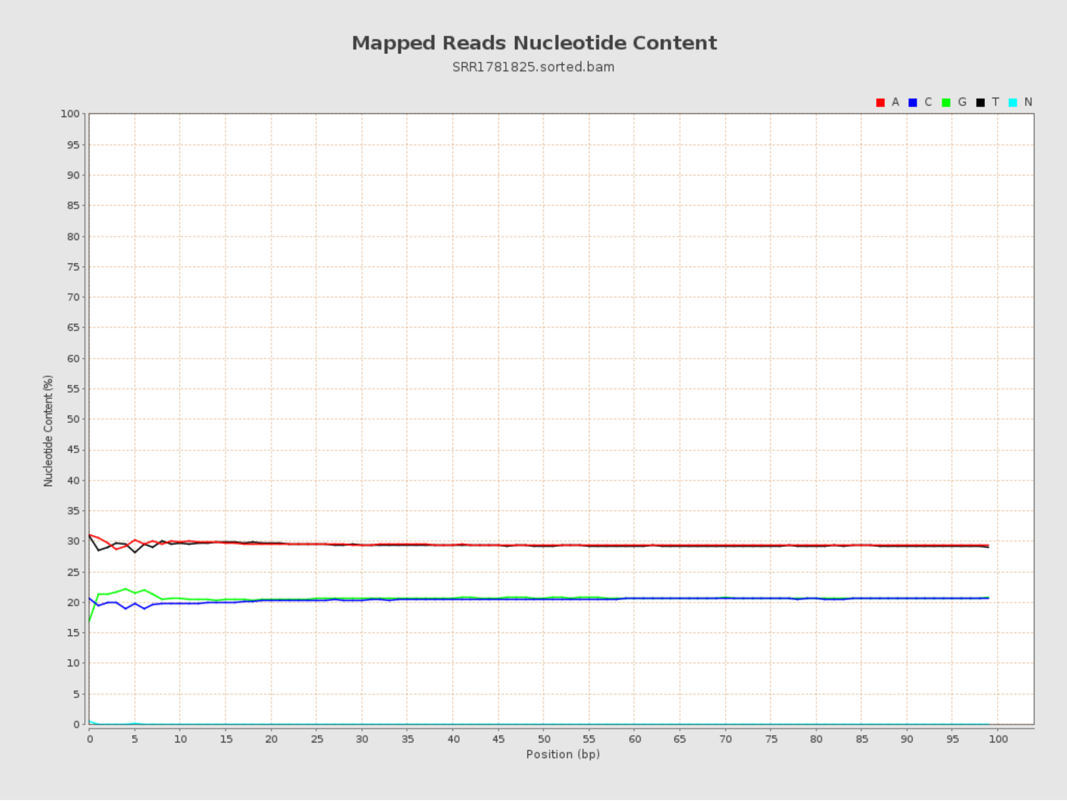
6. Results : Genome Fraction Coverage



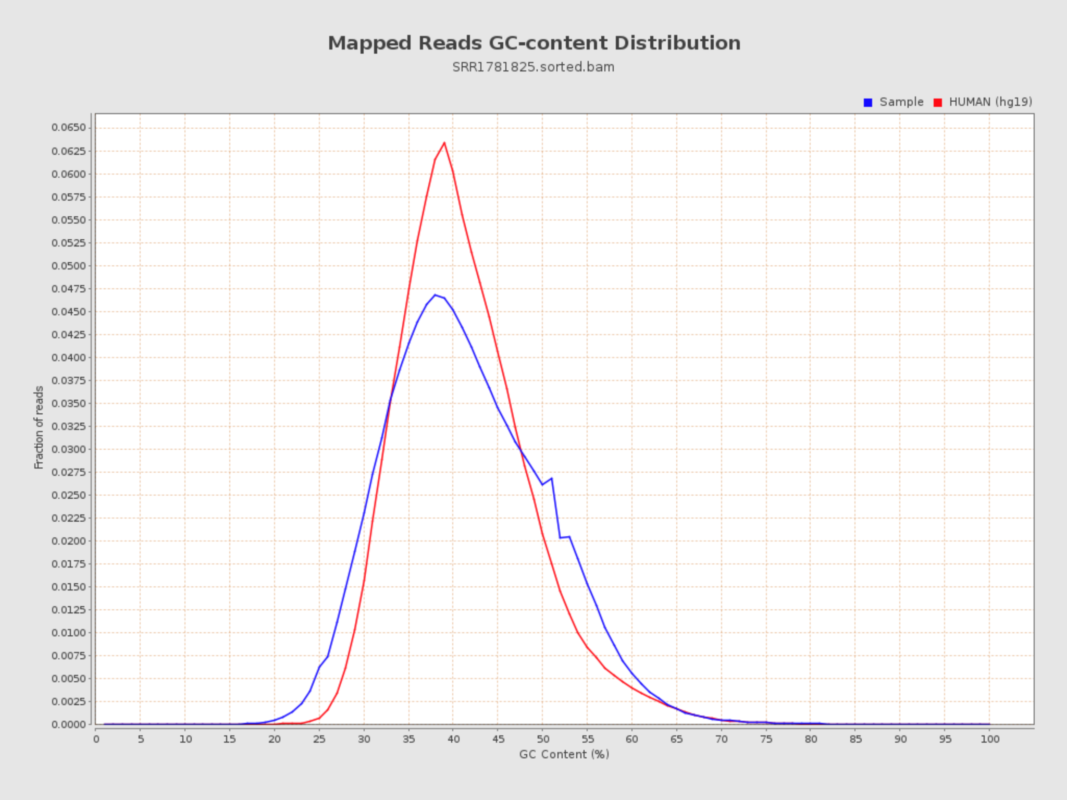
7. Results : Duplication Rate Histogram



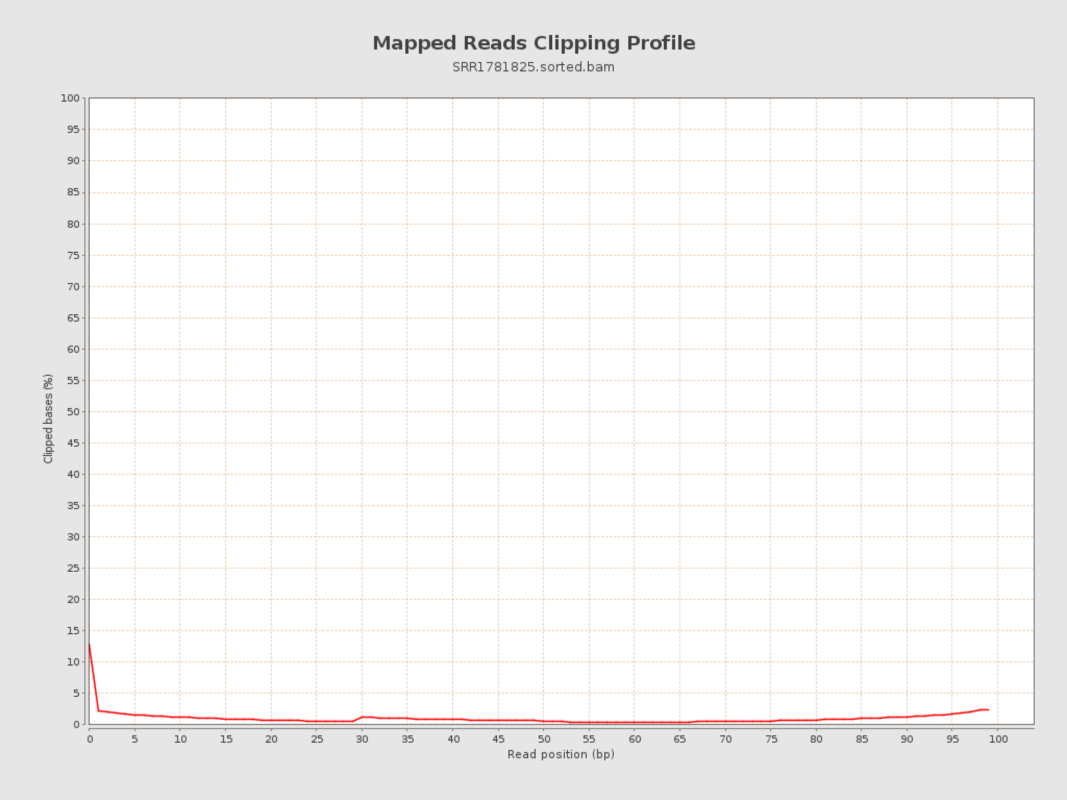
8. Results : Mapped Reads Nucleotide Content



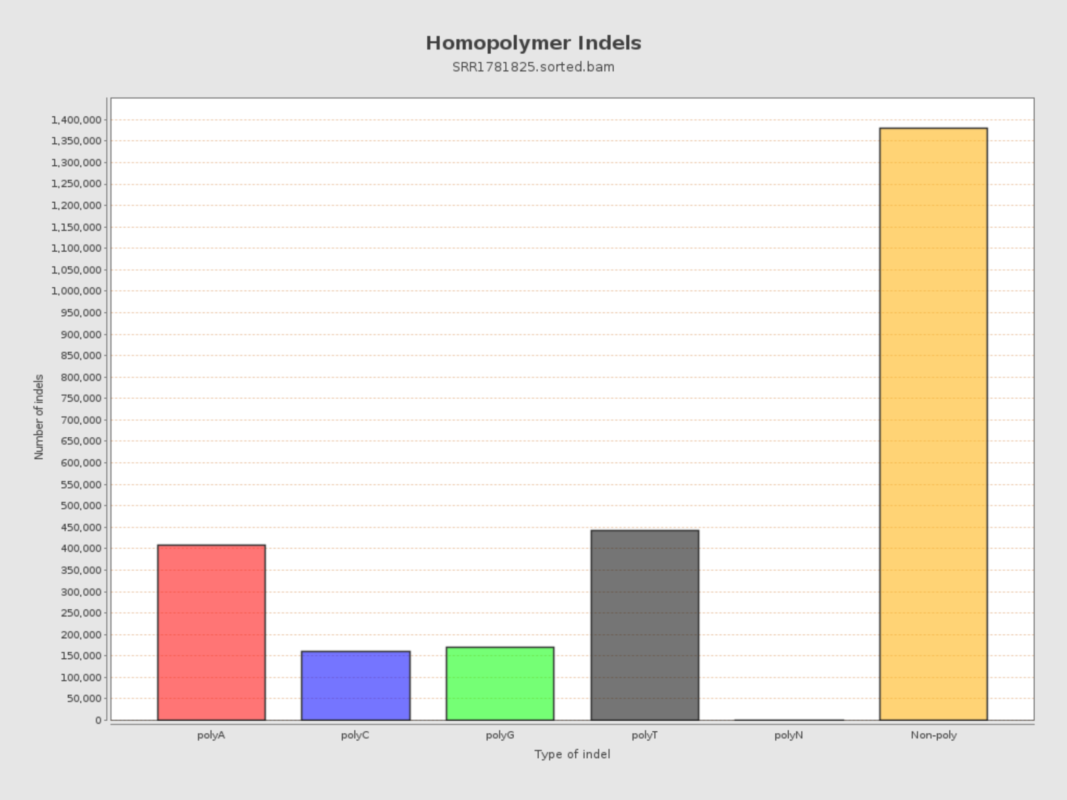
9. Results : Mapped Reads GC-content Distribution



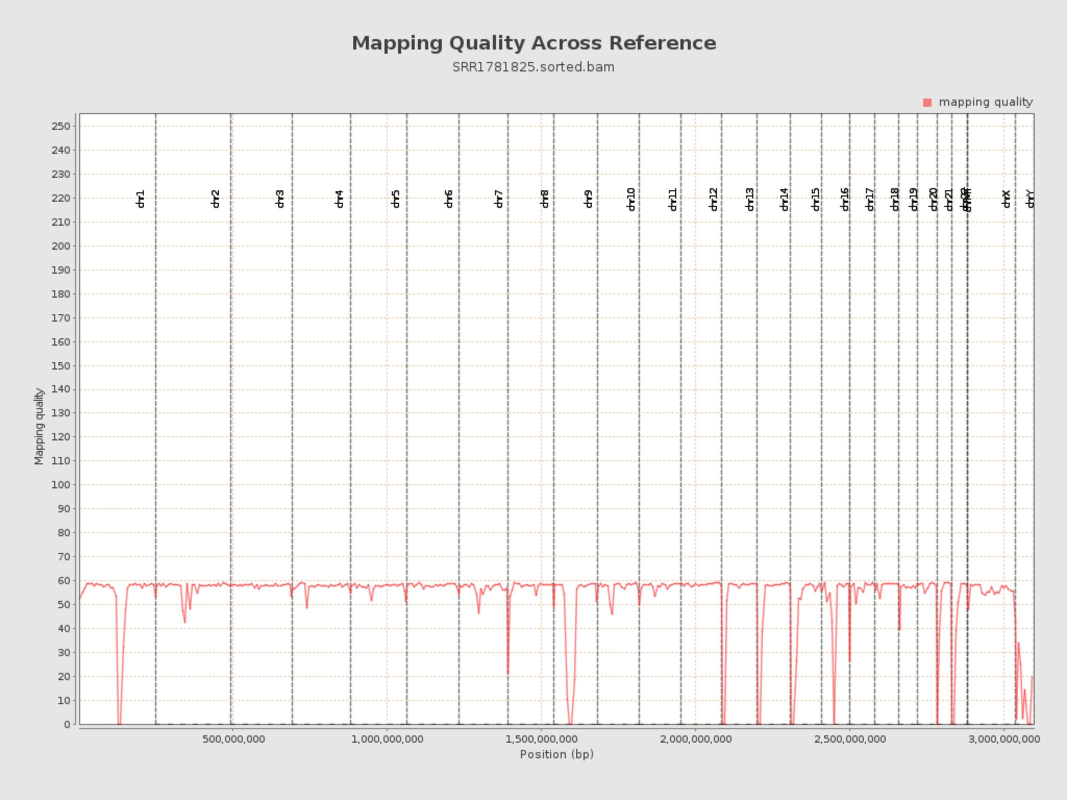
10. Results : Mapped Reads Clipping Profile



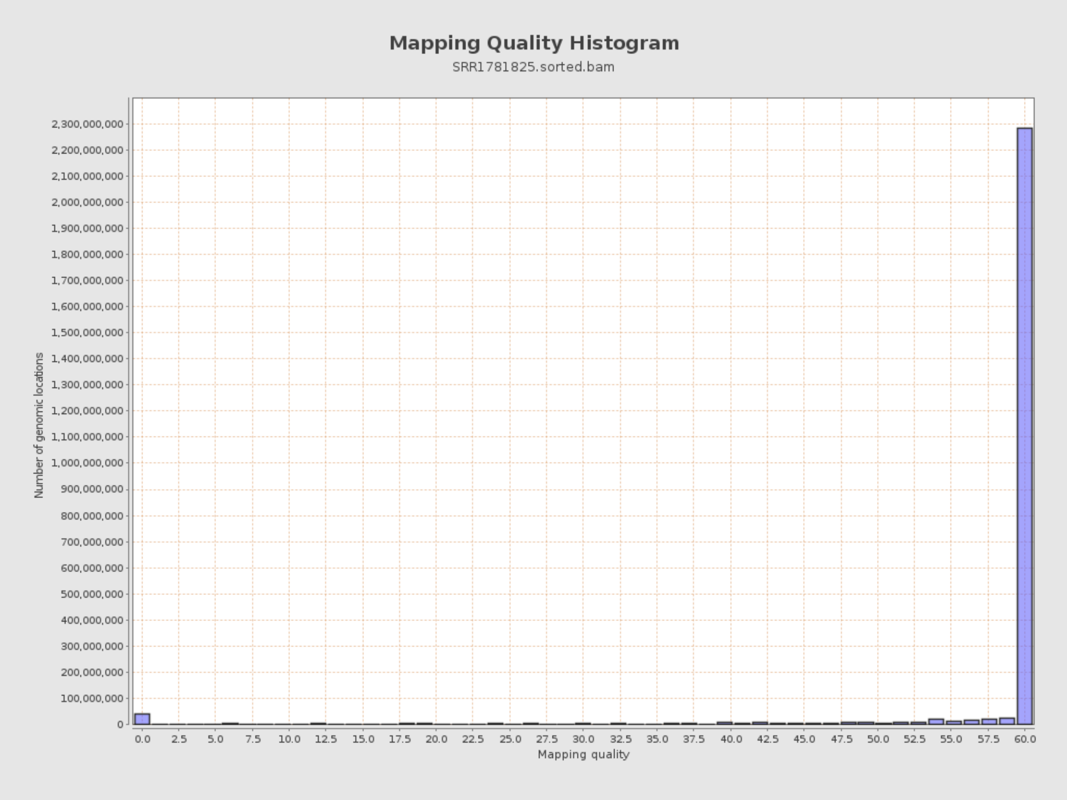
11. Results : Homopolymer Indels



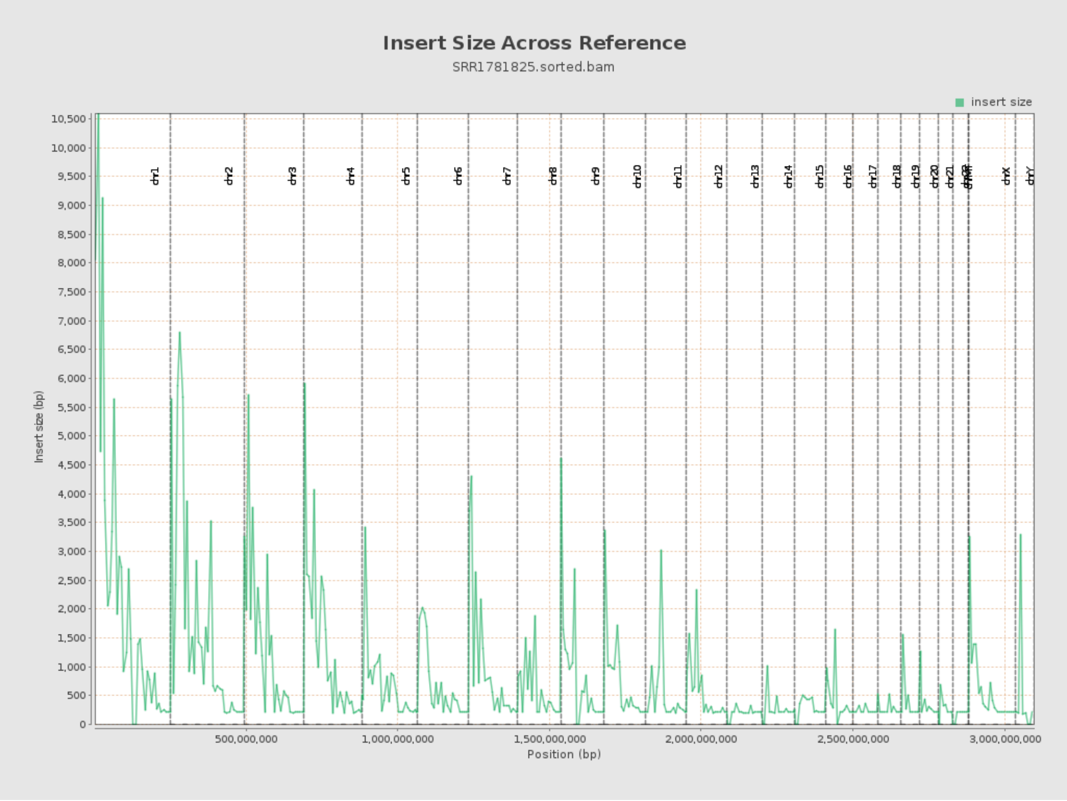
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram