Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/28 06:22:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781882.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_SRR1781882 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781882_1.fastq.gz SRR1781882_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Mar 28 06:22:31 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781882.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	143,224,038
Mapped reads	140,017,925 / 97.76%
Unmapped reads	3,206,113 / 2.24%
Mapped paired reads	140,017,925 / 97.76%
Mapped reads, first in pair	70,521,993 / 49.24%
Mapped reads, second in pair	69,495,932 / 48.52%
Mapped reads, both in pair	138,579,452 / 96.76%
Mapped reads, singletons	1,438,473 / 1%
Secondary alignments	0
Supplementary alignments	369,845 / 0.26%
Read min/max/mean length	30 / 100 / 99.99
Duplicated reads (estimated)	7,997,941 / 5.58%
Duplication rate	5.51%
Clipped reads	5,095,865 / 3.56%

2.2. ACGT Content

Number/percentage of A's	4,150,432,588 / 29.82%
Number/percentage of C's	2,798,080,860 / 20.1%
Number/percentage of T's	4,139,711,435 / 29.74%
Number/percentage of G's	2,827,842,272 / 20.32%
Number/percentage of N's	1,425,702 / 0.01%

GC Percentage	40.42%

2.3. Coverage

Mean	4.4967
Standard Deviation	5.5515

2.4. Mapping Quality

Mean Mapping Quality	54.05

2.5. Insert size

Mean	31,845.4
Standard Deviation	1,738,359.67
P25/Median/P75	182 / 221 / 266

2.6. Mismatches and indels

General error rate	0.44%
Mismatches	58,401,308
Insertions	1,482,527
Mapped reads with at least one insertion	1.04%
Deletions	1,253,950
Mapped reads with at least one deletion	0.88%
Homopolymer indels	46.98%

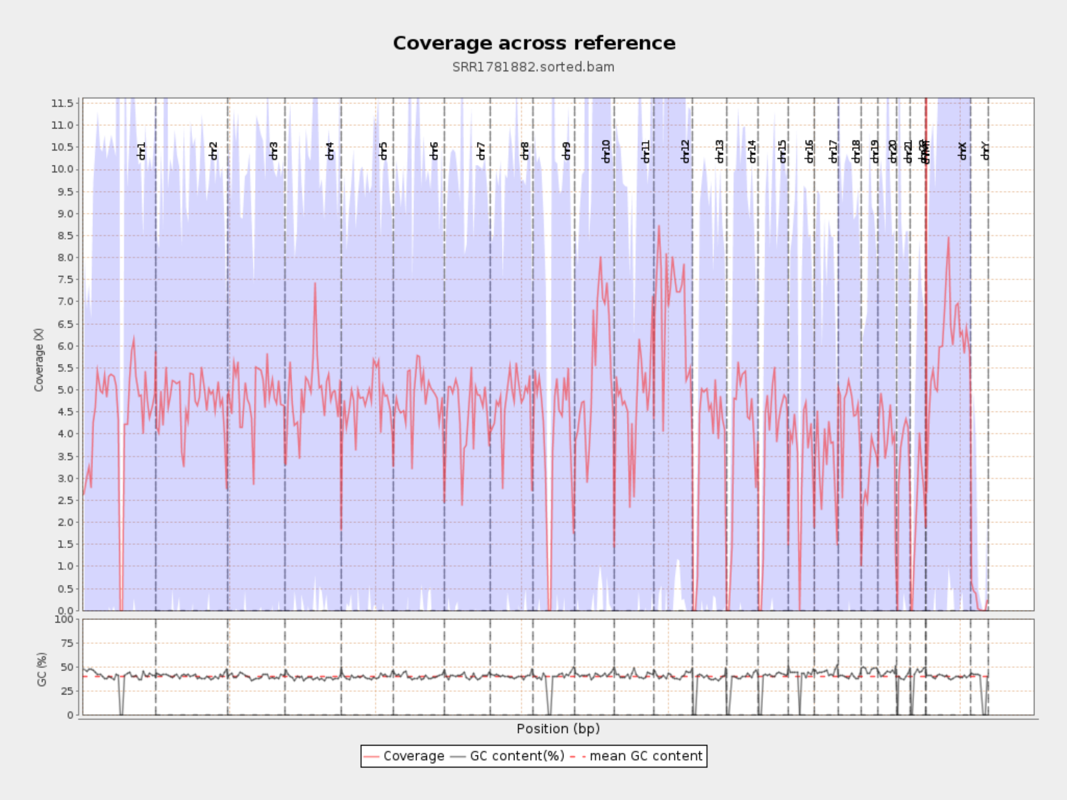
2.7. Chromosome stats

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

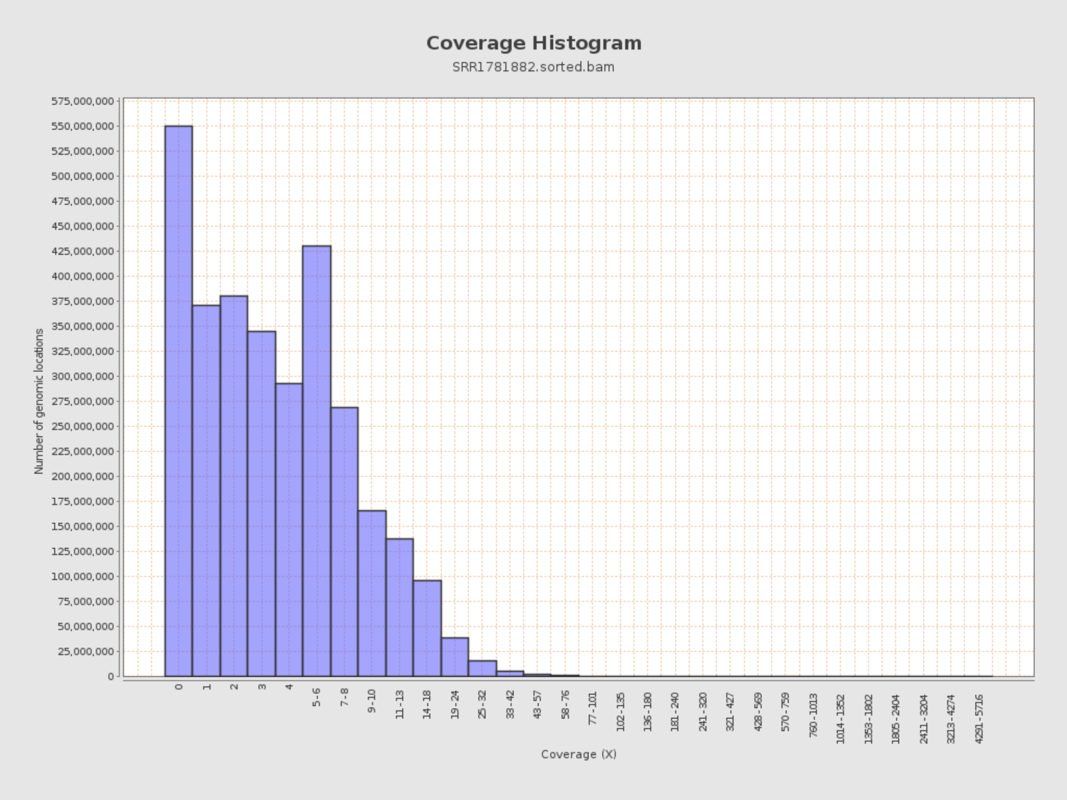
		bases	coverage	deviation
chr1	249250621	1095784379	4.3963	6.6348
chr2	243199373	1143218562	4.7007	6.881
chr3	198022430	966616592	4.8813	4.8081
chr4	191154276	948198777	4.9604	5.0087
chr5	180915260	851617755	4.7073	4.5118
chr6	171115067	828244261	4.8403	4.9602
chr7	159138663	709838112	4.4605	5.2108
chr8	146364022	684619584	4.6775	4.6475
chr9	141213431	561640049	3.9772	5.5581
chr10	135534747	745455965	5.5001	7.6095
chr11	135006516	637800478	4.7242	5.0355
chr12	133851895	925117604	6.9115	6.6536
chr13	115169878	436299778	3.7883	4.271
chr14	107349540	412925110	3.8465	4.5878
chr15	102531392	382172617	3.7274	4.5797
chr16	90354753	307723742	3.4057	4.4296
chr17	81195210	278710836	3.4326	4.3452
chr18	78077248	350733825	4.4921	5.0275
chr19	59128983	179620097	3.0378	4.6952
chr20	63025520	253812436	4.0271	5.3803
chr21	48129895	161591662	3.3574	5.8033
chr22	51304566	112857124	2.1997	3.5539
chrMT	16571	742843	44.8279	14.6478
chrX	155270560	933034156	6.0091	6.0761

chrY	59373566	11925197	0.2009	2.2398

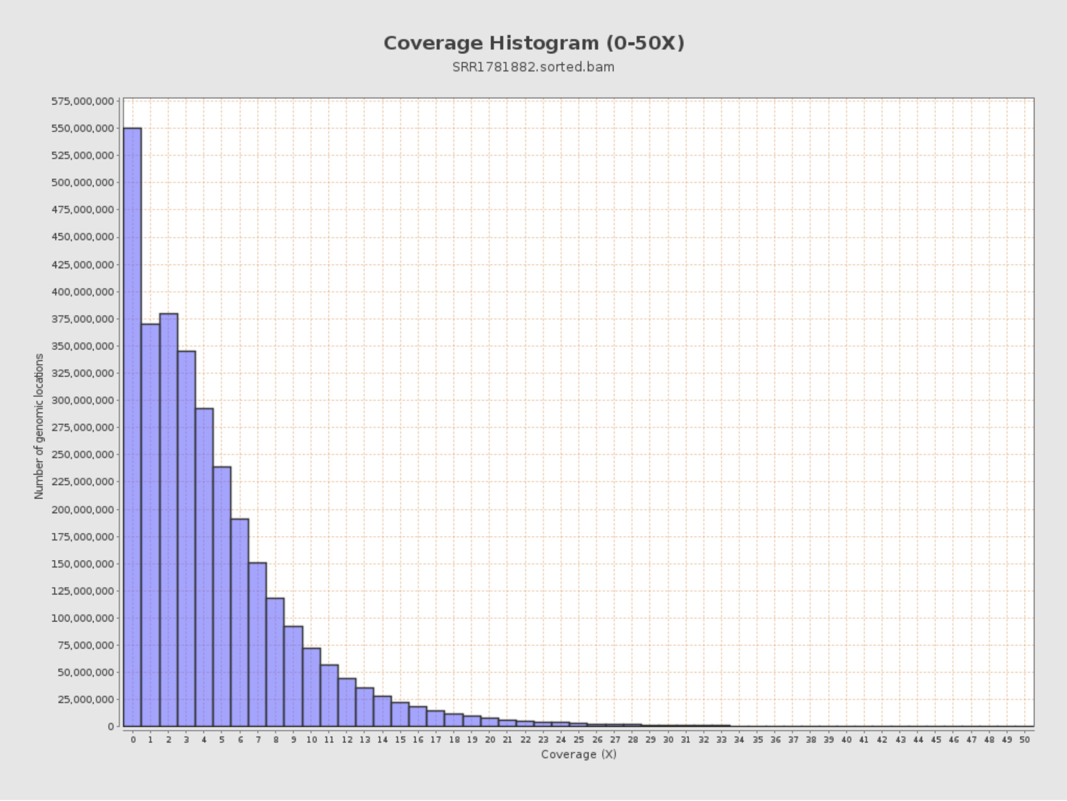
3. Results : Coverage across reference



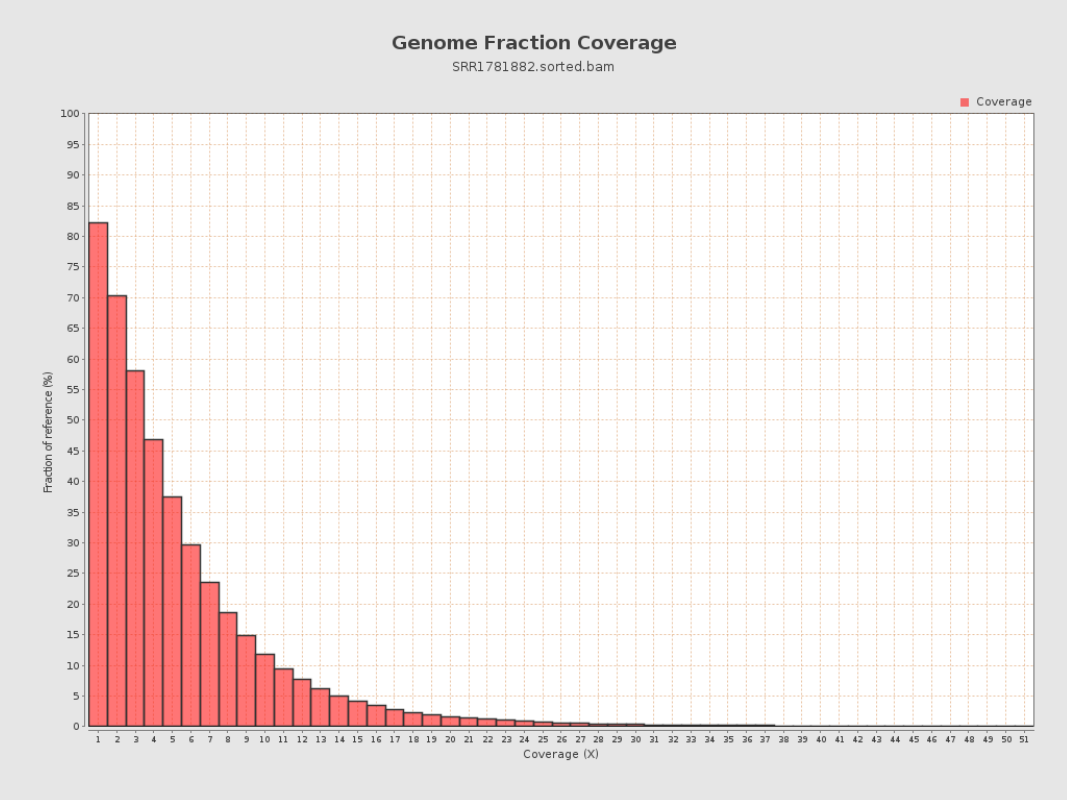
4. Results : Coverage Histogram



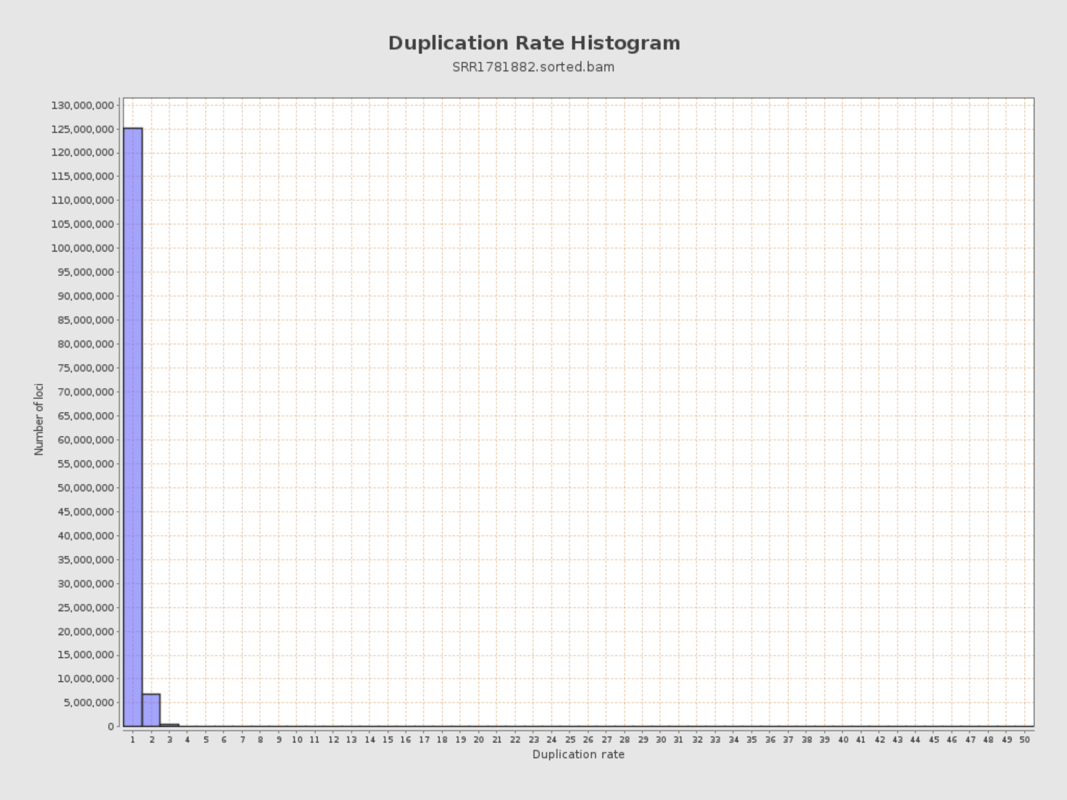
5. Results : Coverage Histogram (0-50X)



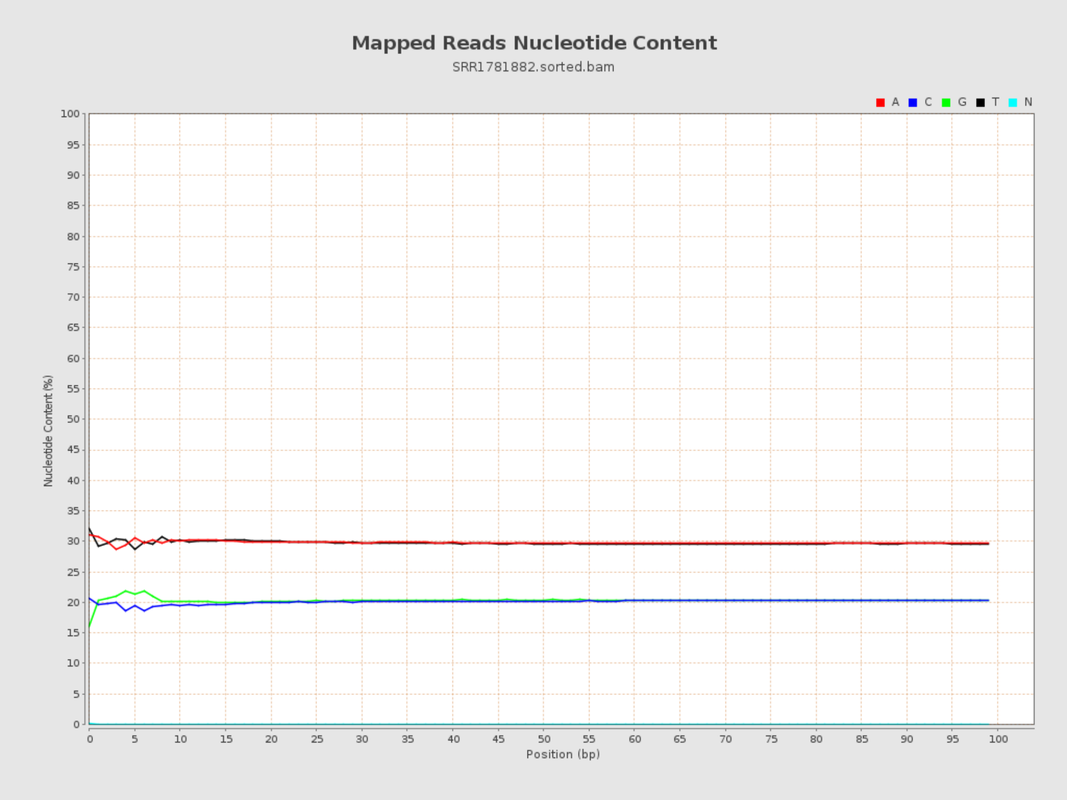
6. Results : Genome Fraction Coverage



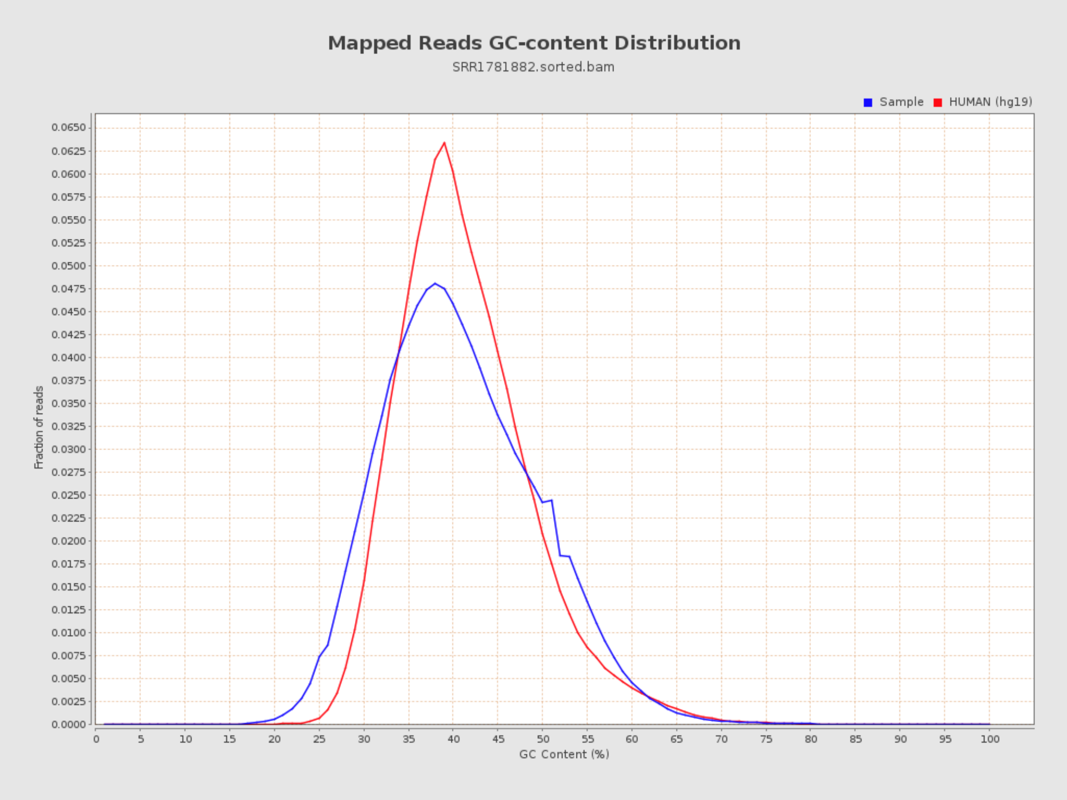
7. Results : Duplication Rate Histogram



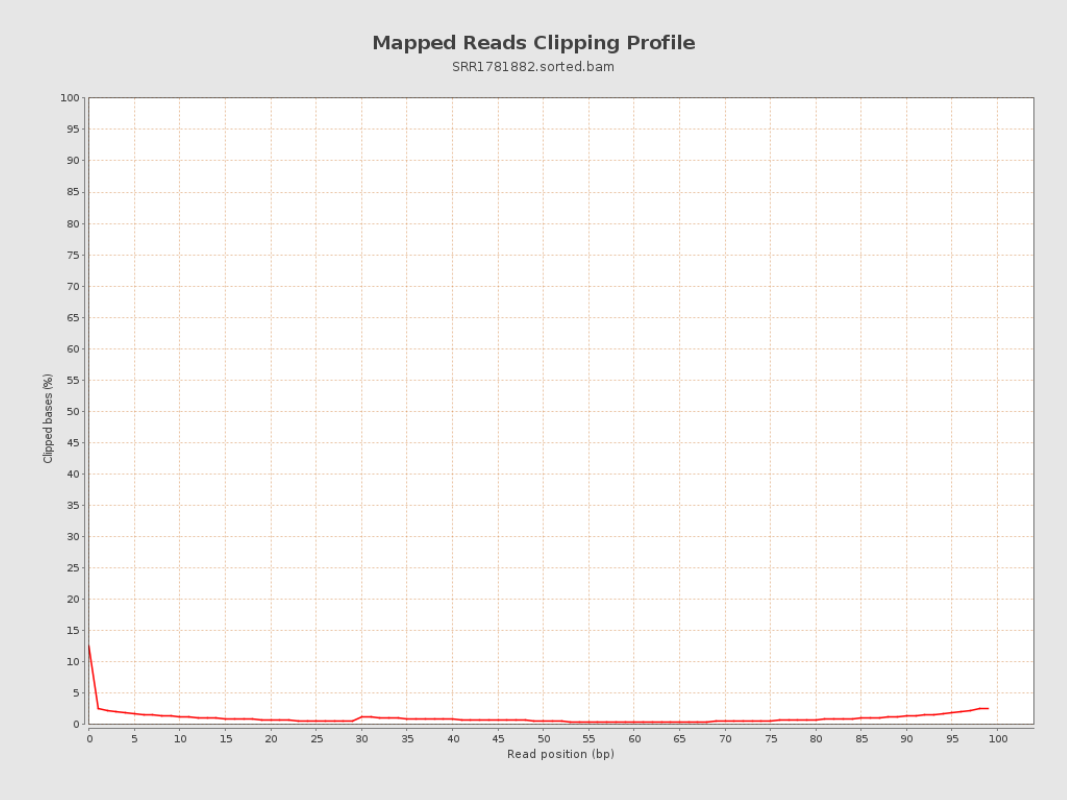
8. Results : Mapped Reads Nucleotide Content



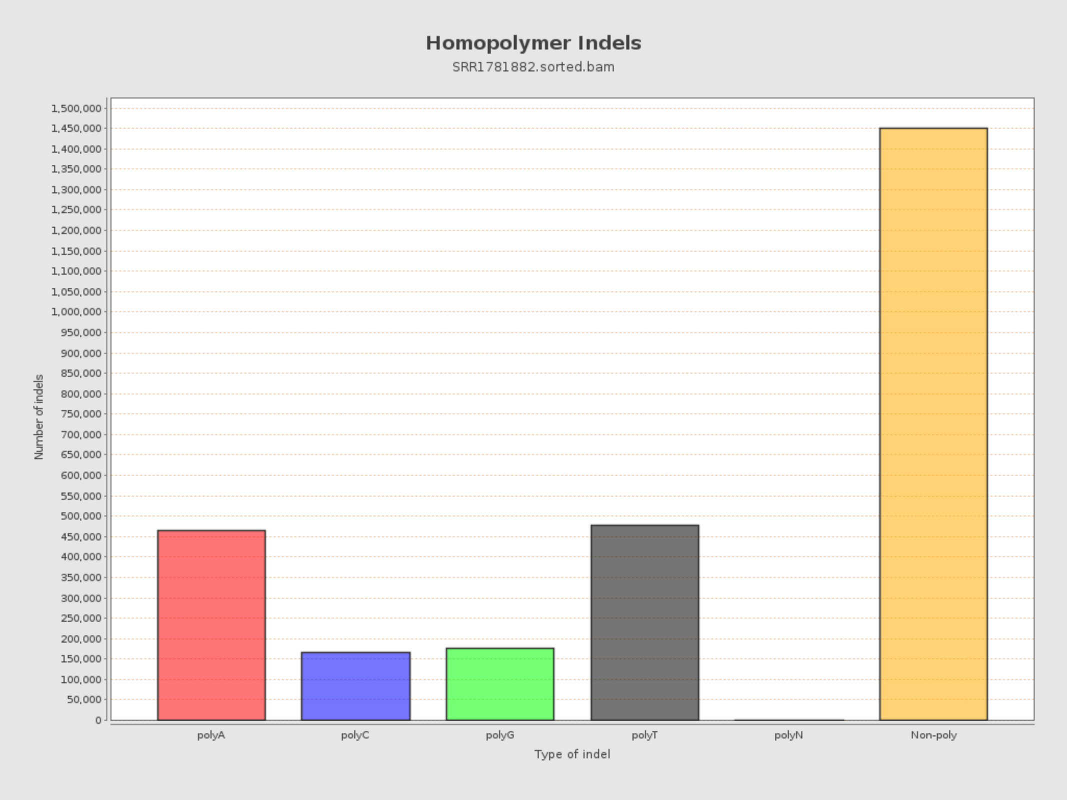
9. Results : Mapped Reads GC-content Distribution



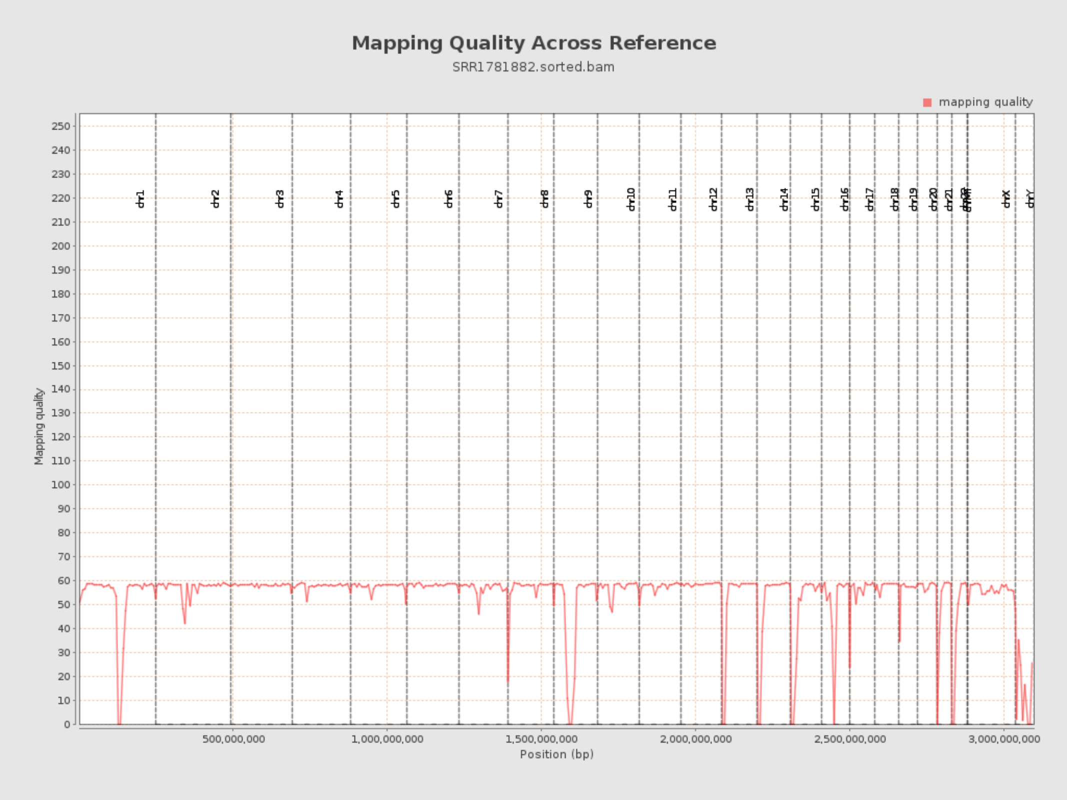
10. Results : Mapped Reads Clipping Profile



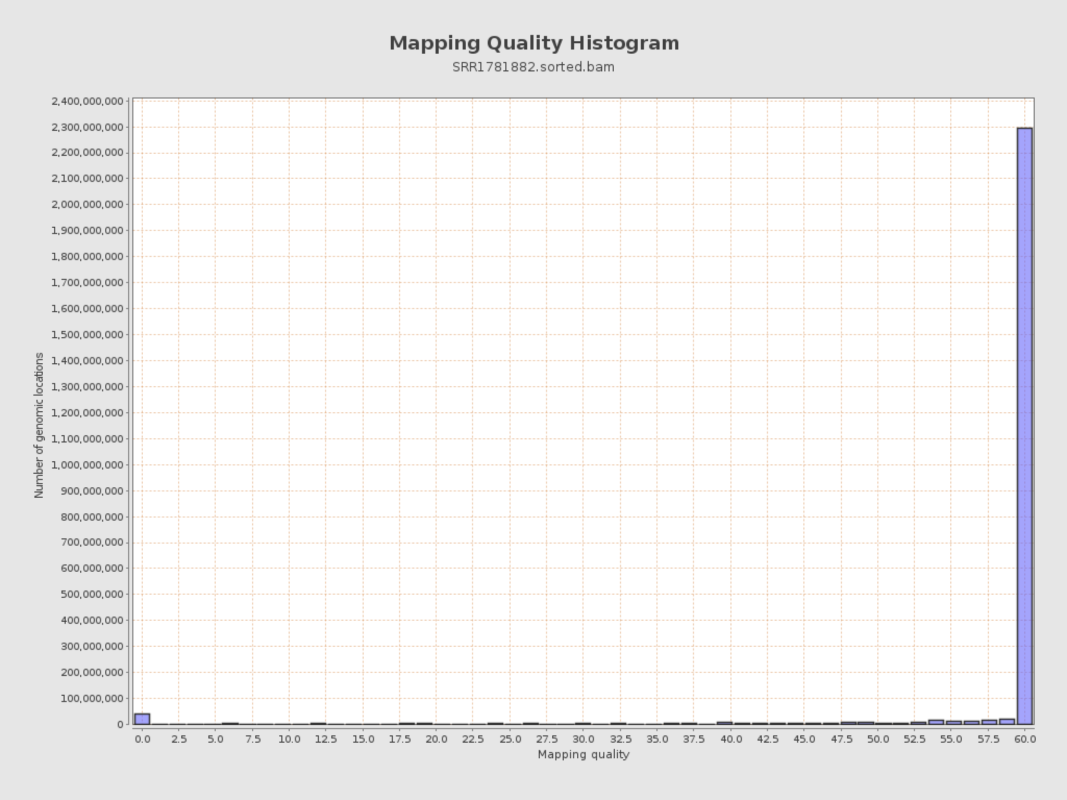
11. Results : Homopolymer Indels



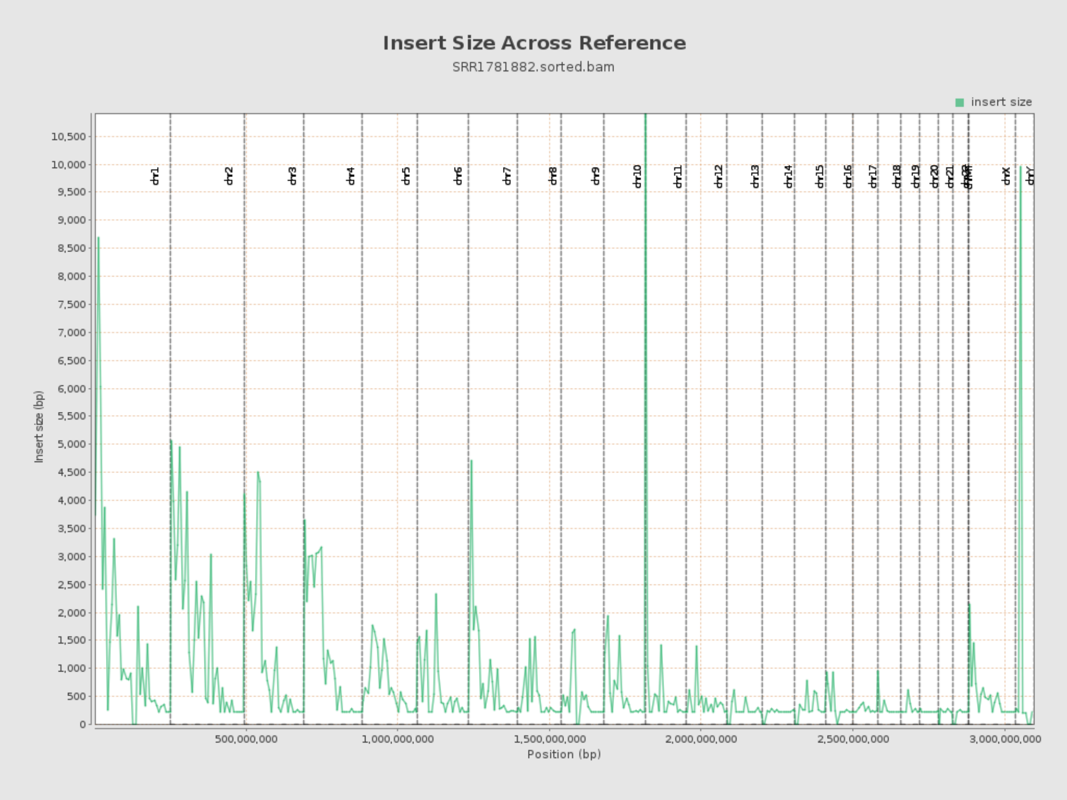
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram