Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/27 00:18:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781852.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_SRR1781852 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781852_1.fastq.gz SRR1781852_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Mar 27 00:18:49 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781852.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	140,060,140
Mapped reads	136,046,123 / 97.13%
Unmapped reads	4,014,017 / 2.87%
Mapped paired reads	136,046,123 / 97.13%
Mapped reads, first in pair	68,550,913 / 48.94%
Mapped reads, second in pair	67,495,210 / 48.19%
Mapped reads, both in pair	133,341,040 / 95.2%
Mapped reads, singletons	2,705,083 / 1.93%
Secondary alignments	0
Supplementary alignments	394,386 / 0.28%
Read min/max/mean length	30 / 100 / 99.99
Duplicated reads (estimated)	8,027,980 / 5.73%
Duplication rate	5.67%
Clipped reads	6,108,627 / 4.36%

2.2. ACGT Content

Number/percentage of A's	4,029,478,038 / 29.84%
Number/percentage of C's	2,727,839,863 / 20.2%
Number/percentage of T's	3,991,193,621 / 29.56%
Number/percentage of G's	2,749,446,553 / 20.36%
Number/percentage of N's	4,084,461 / 0.03%

GC Percentage	40.57%

2.3. Coverage

Mean	4.3624
Standard Deviation	5.6483

2.4. Mapping Quality

Mean Mapping Quality	53.88

2.5. Insert size

Mean	43,687.75
Standard Deviation	2,063,375.76
P25/Median/P75	163 / 203 / 252

2.6. Mismatches and indels

General error rate	0.48%
Mismatches	61,545,581
Insertions	1,601,807
Mapped reads with at least one insertion	1.16%
Deletions	1,191,830
Mapped reads with at least one deletion	0.86%
Homopolymer indels	47.41%

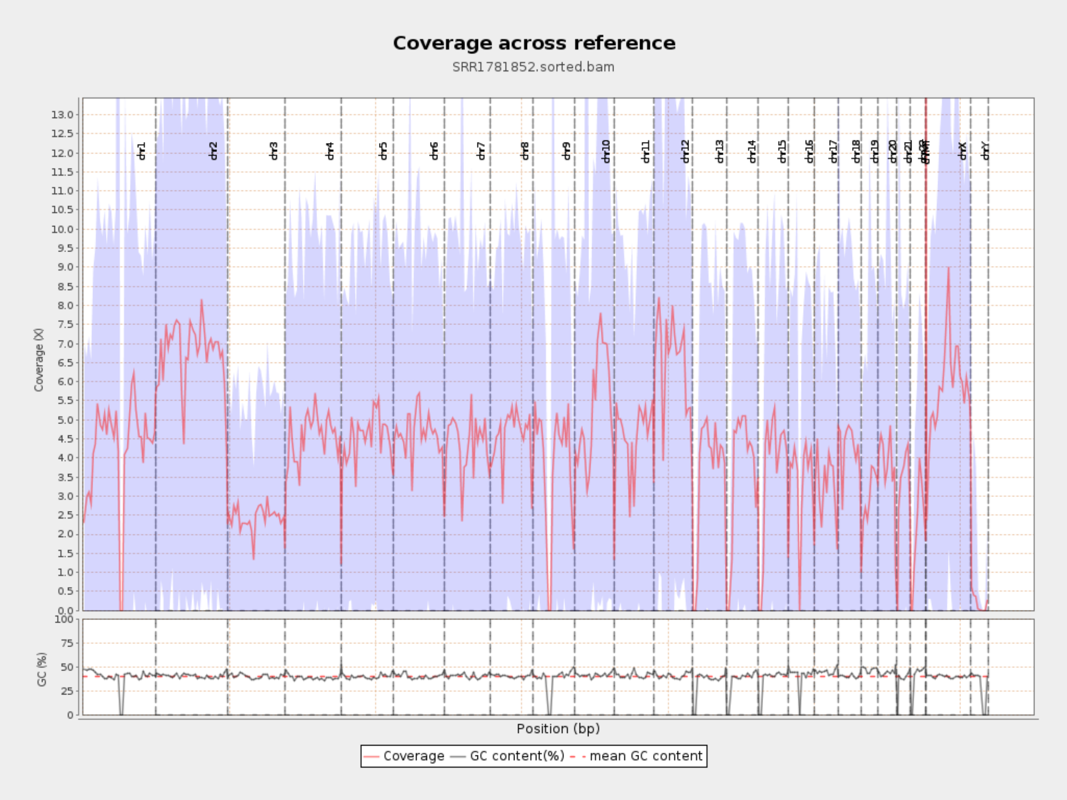
2.7. Chromosome stats

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

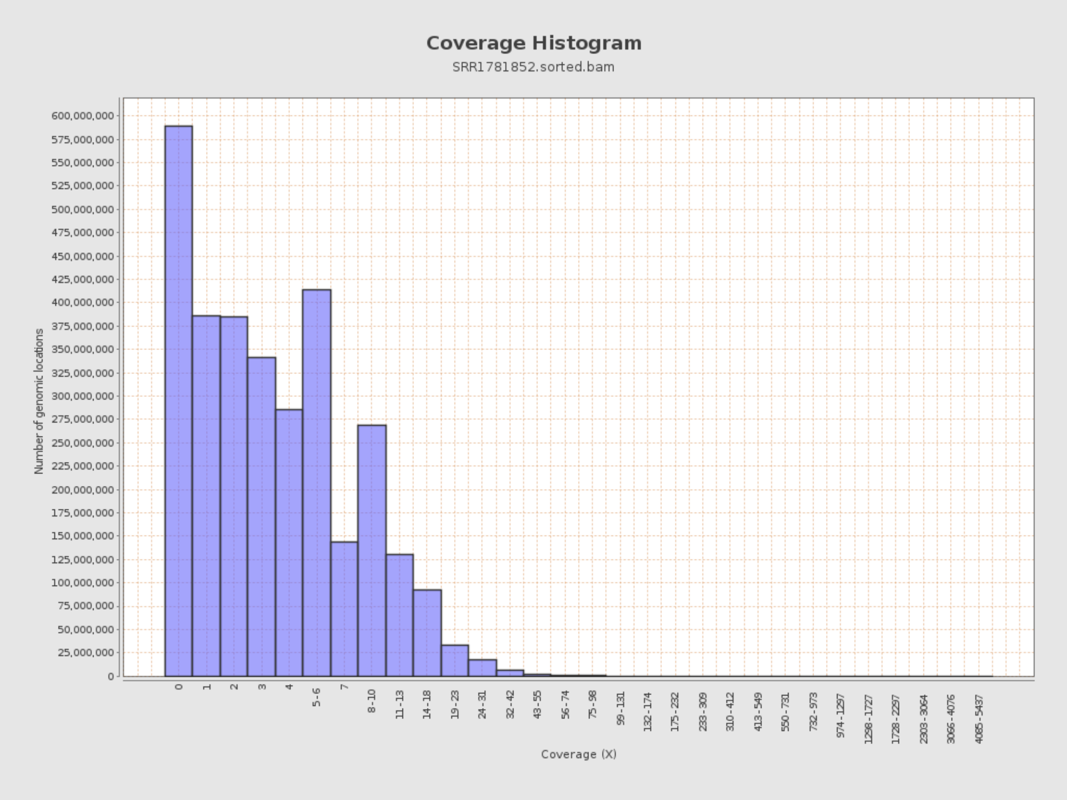
		bases	coverage	deviation
chr1	249250621	1060354855	4.2542	7.5775
chr2	243199373	1648699614	6.7792	7.117
chr3	198022430	480930387	2.4287	2.8686
chr4	191154276	878905160	4.5979	4.807
chr5	180915260	819343400	4.5289	4.4367
chr6	171115067	794004914	4.6402	4.8598
chr7	159138663	690830299	4.3411	5.479
chr8	146364022	672481005	4.5946	4.6116
chr9	141213431	542110281	3.8389	5.6165
chr10	135534747	726535028	5.3605	8.2887
chr11	135006516	617086105	4.5708	4.8129
chr12	133851895	885555867	6.6159	6.4999
chr13	115169878	413657630	3.5917	4.158
chr14	107349540	393545825	3.666	4.4222
chr15	102531392	369065204	3.5995	4.4971
chr16	90354753	297083182	3.288	4.2739
chr17	81195210	271848692	3.3481	4.3262
chr18	78077248	333772538	4.2749	5.0042
chr19	59128983	175076628	2.9609	5.1013
chr20	63025520	243982751	3.8712	5.3198
chr21	48129895	155365109	3.228	5.7974
chr22	51304566	110639557	2.1565	3.4843
chrMT	16571	315097	19.015	6.8913
chrX	155270560	911716386	5.8718	6.04

chrY	59373566	11837960	0.1994	2.1399

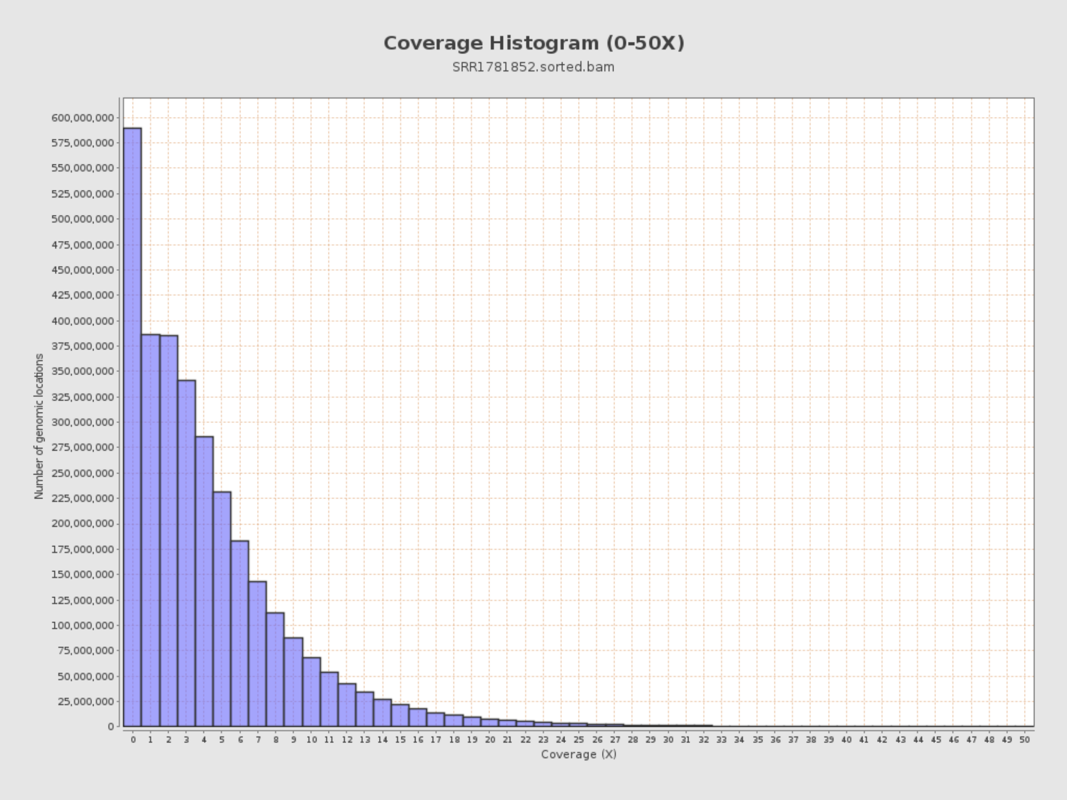
3. Results : Coverage across reference



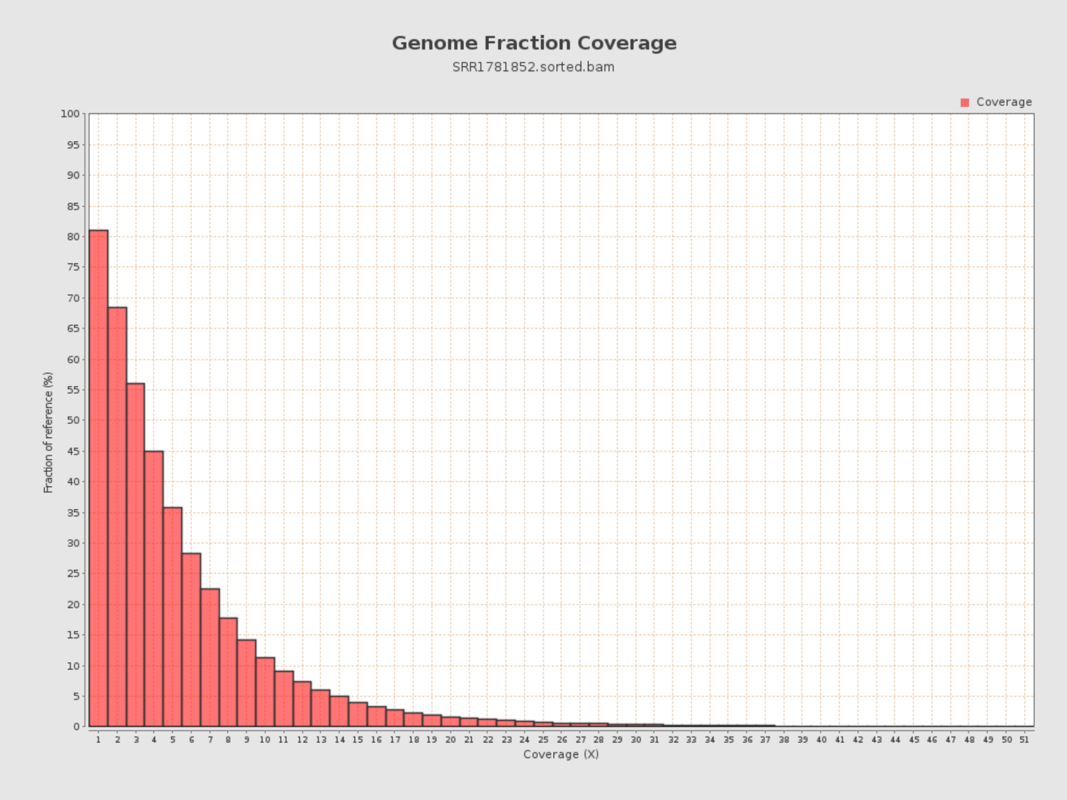
4. Results : Coverage Histogram



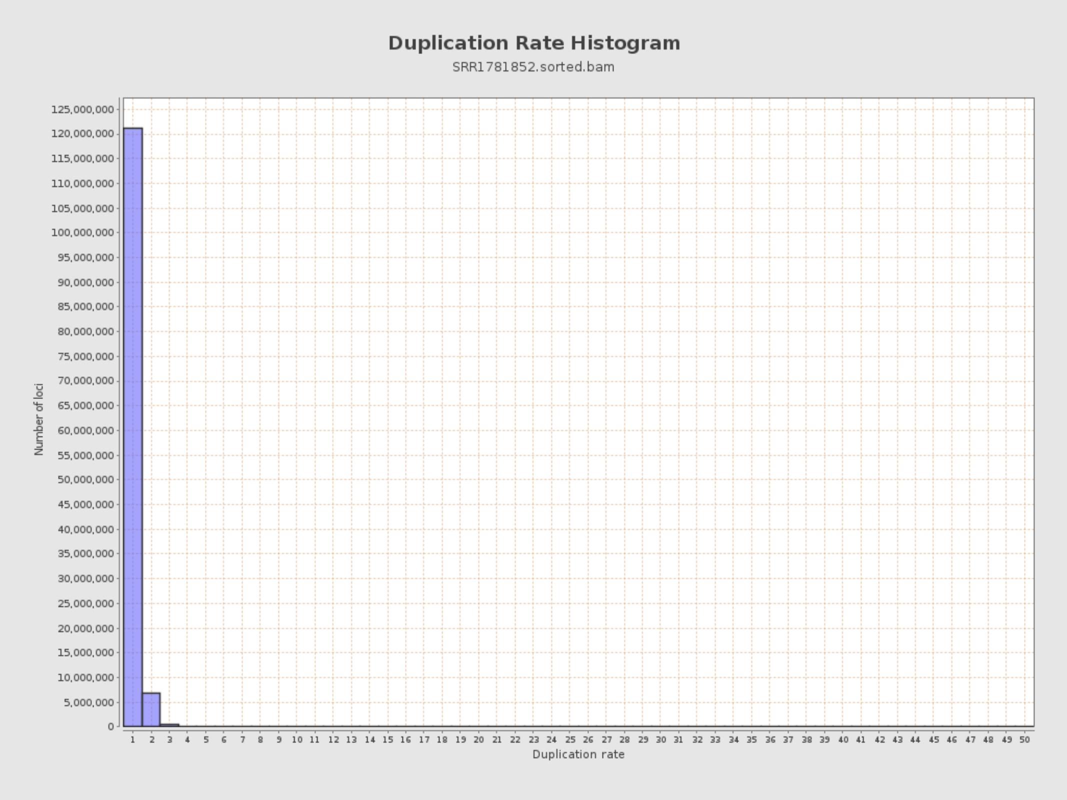
5. Results : Coverage Histogram (0-50X)



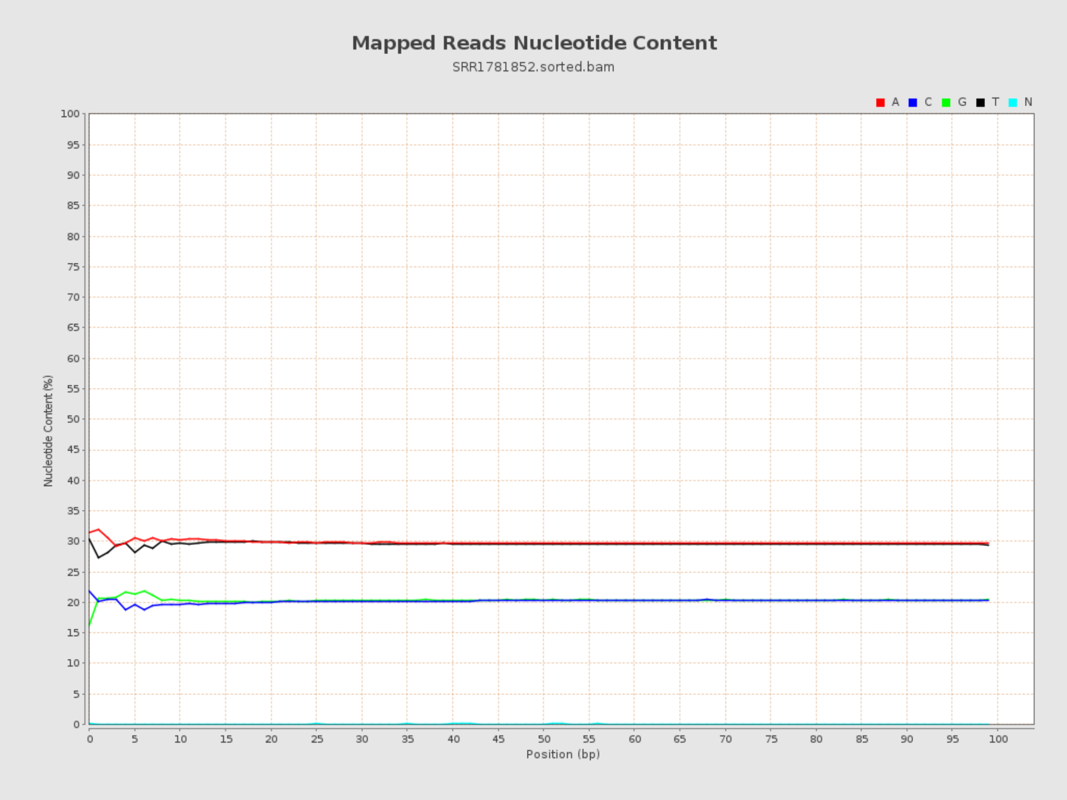
6. Results : Genome Fraction Coverage



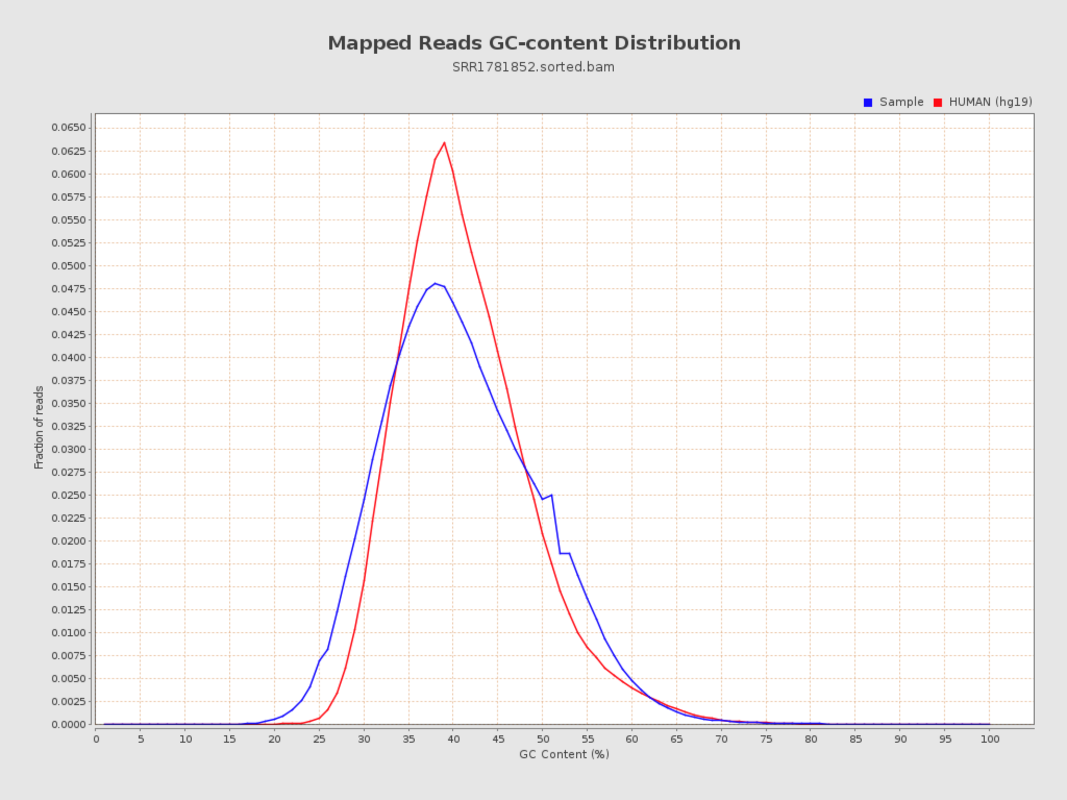
7. Results : Duplication Rate Histogram



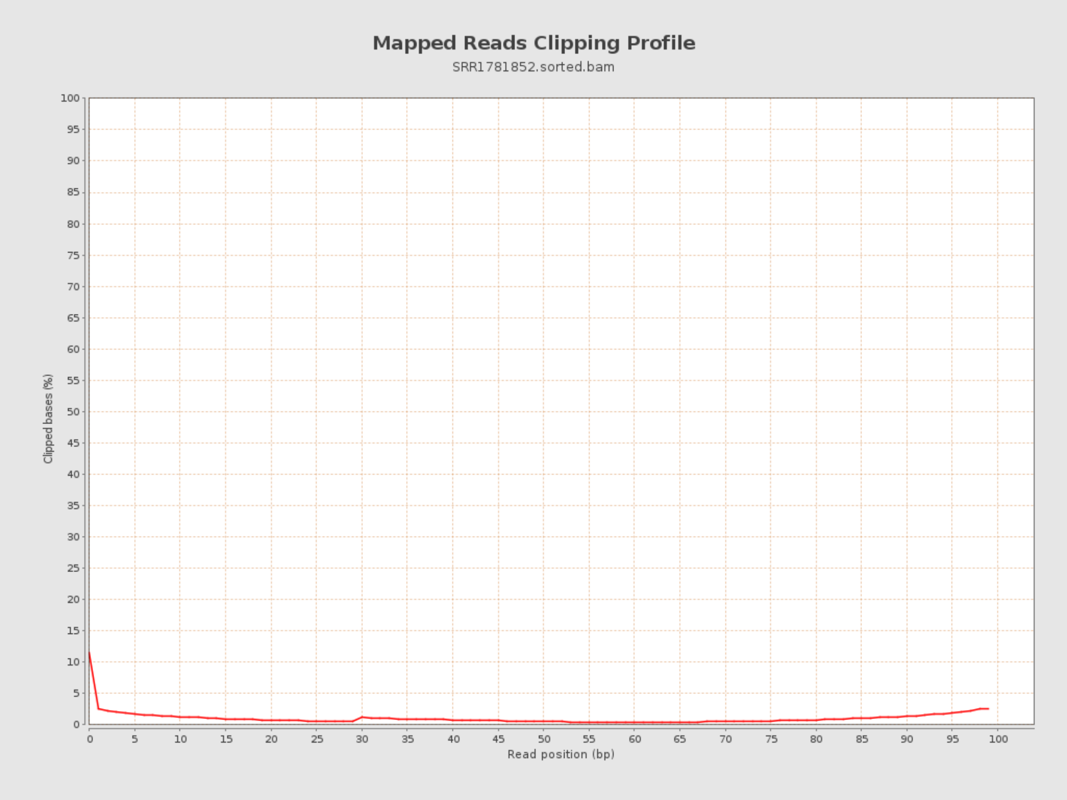
8. Results : Mapped Reads Nucleotide Content



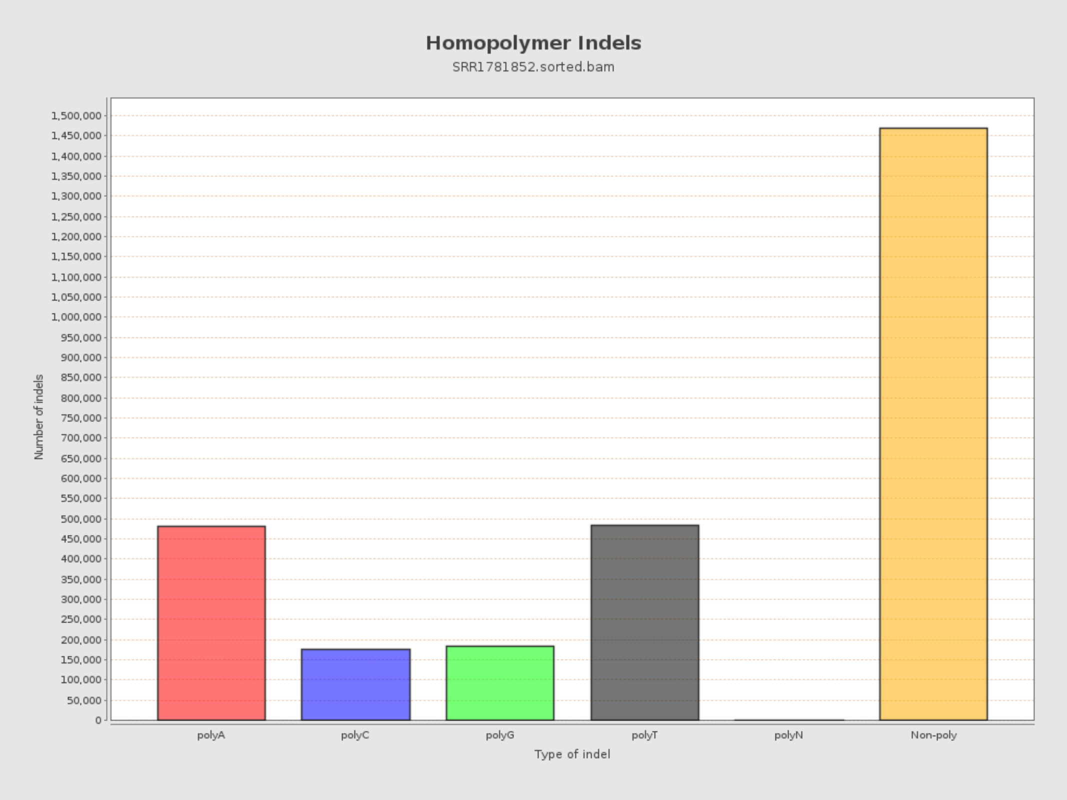
9. Results : Mapped Reads GC-content Distribution



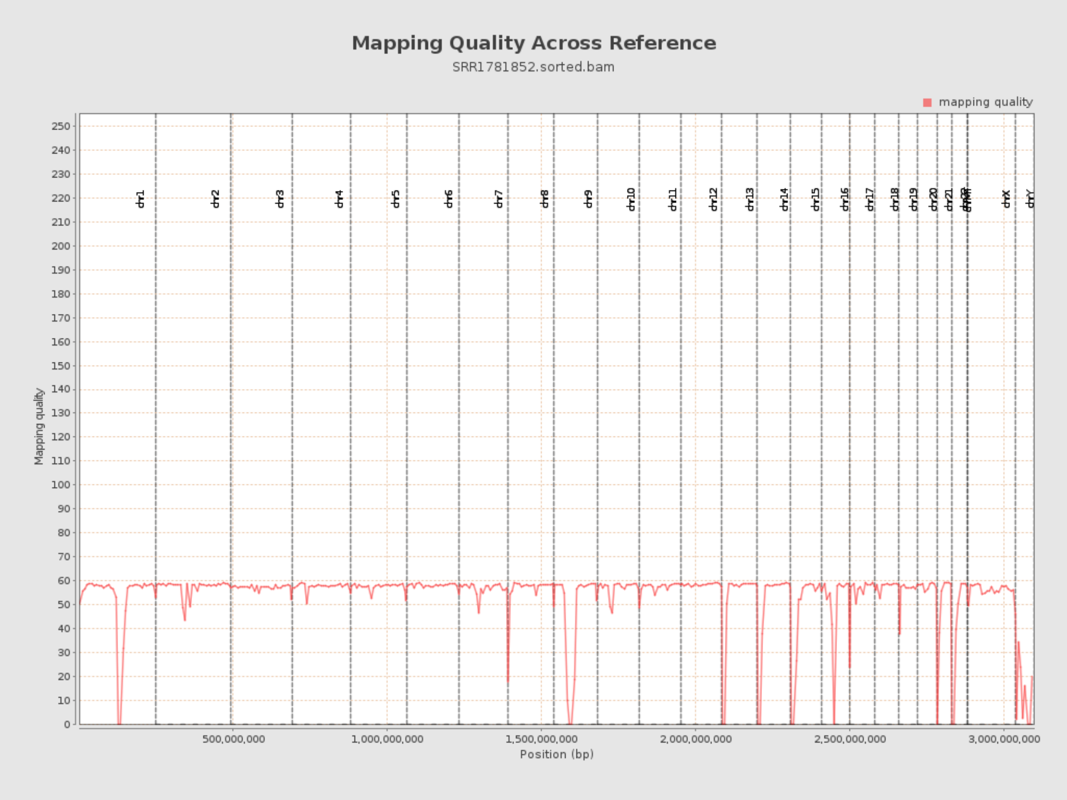
10. Results : Mapped Reads Clipping Profile



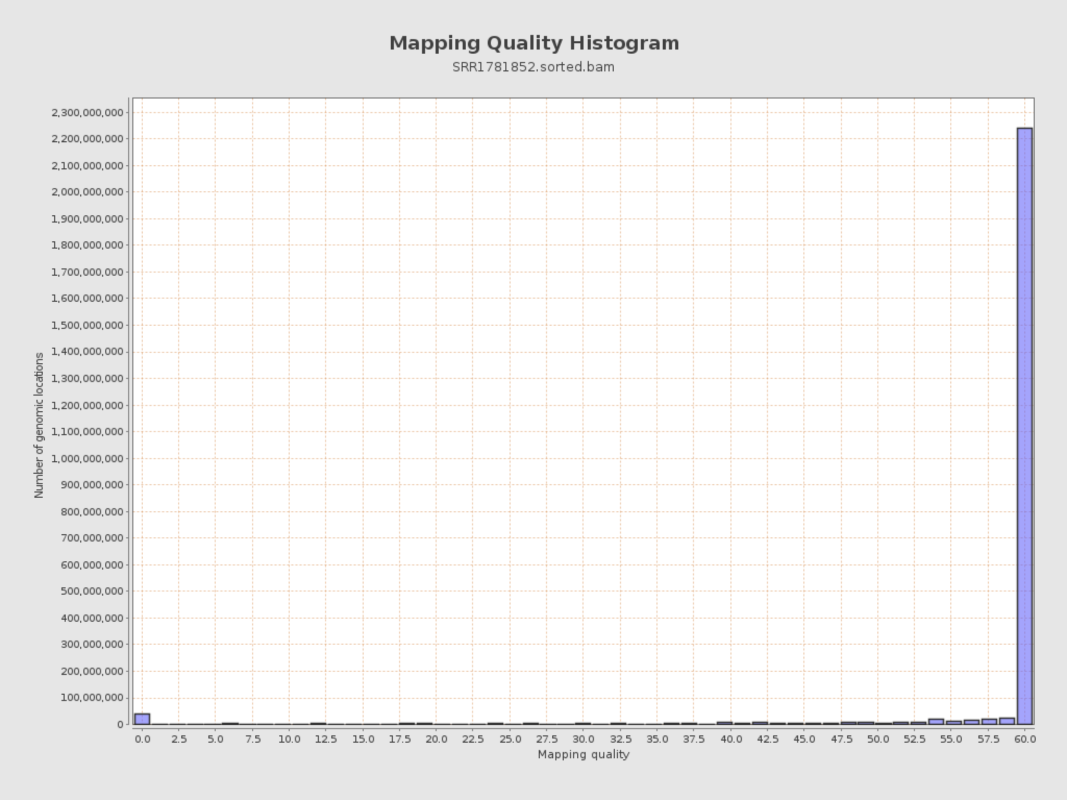
11. Results : Homopolymer Indels



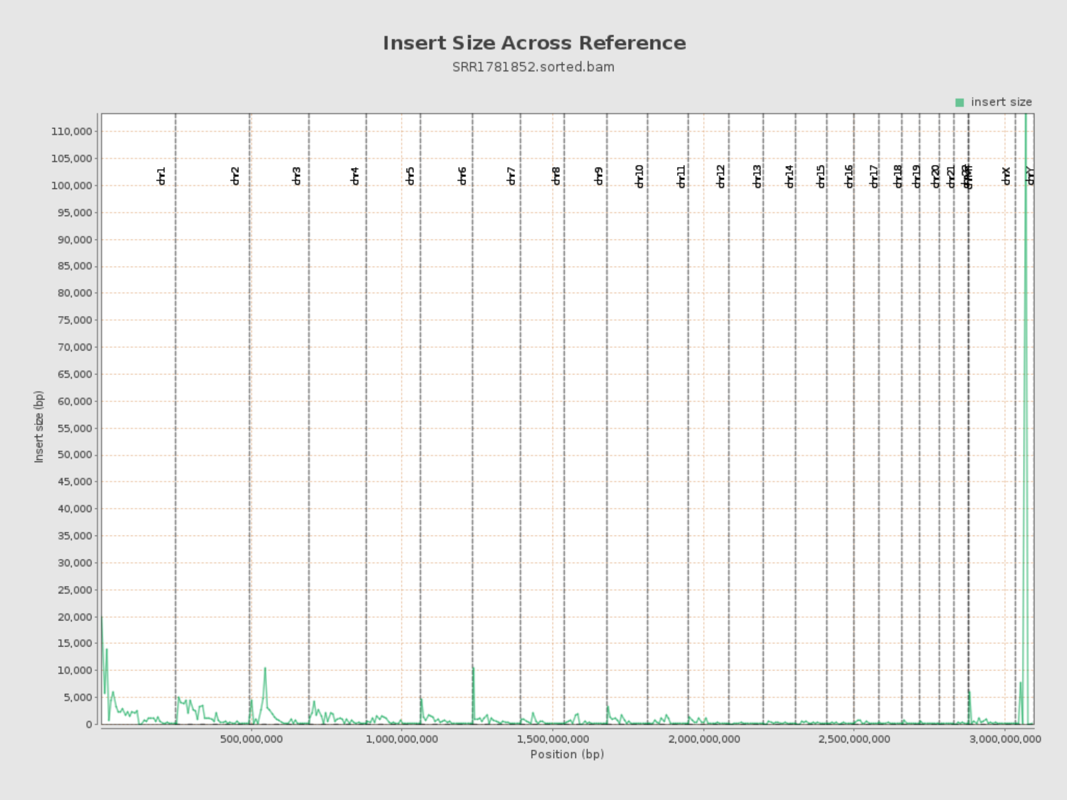
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram