Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 03:09:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781879.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_SRR1781879 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781879_1.fastq.gz SRR1781879_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 03:09:12 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781879.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	222,247,104
Mapped reads	213,630,441 / 96.12%
Unmapped reads	8,616,663 / 3.88%
Mapped paired reads	213,630,441 / 96.12%
Mapped reads, first in pair	107,530,749 / 48.38%
Mapped reads, second in pair	106,099,692 / 47.74%
Mapped reads, both in pair	210,934,626 / 94.91%
Mapped reads, singletons	2,695,815 / 1.21%
Secondary alignments	0
Supplementary alignments	1,227,661 / 0.55%
Read min/max/mean length	30 / 100 / 100.23
Duplicated reads (estimated)	25,472,570 / 11.46%
Duplication rate	11.24%
Clipped reads	14,215,457 / 6.4%

2.2. ACGT Content

Number/percentage of A's	6,179,219,969 / 29.18%
Number/percentage of C's	4,397,487,594 / 20.77%
Number/percentage of T's	6,135,905,733 / 28.98%
Number/percentage of G's	4,462,224,438 / 21.07%
Number/percentage of N's	644,510 / 0%

GC Percentage	41.84%

2.3. Coverage

Mean	6.8416
Standard Deviation	11.4301

2.4. Mapping Quality

Mean Mapping Quality	53.82

2.5. Insert size

Mean	37,478.98
Standard Deviation	1,874,821.55
P25/Median/P75	153 / 190 / 232

2.6. Mismatches and indels

General error rate	0.49%
Mismatches	99,774,805
Insertions	2,067,422
Mapped reads with at least one insertion	0.95%
Deletions	1,813,571
Mapped reads with at least one deletion	0.83%
Homopolymer indels	46.17%

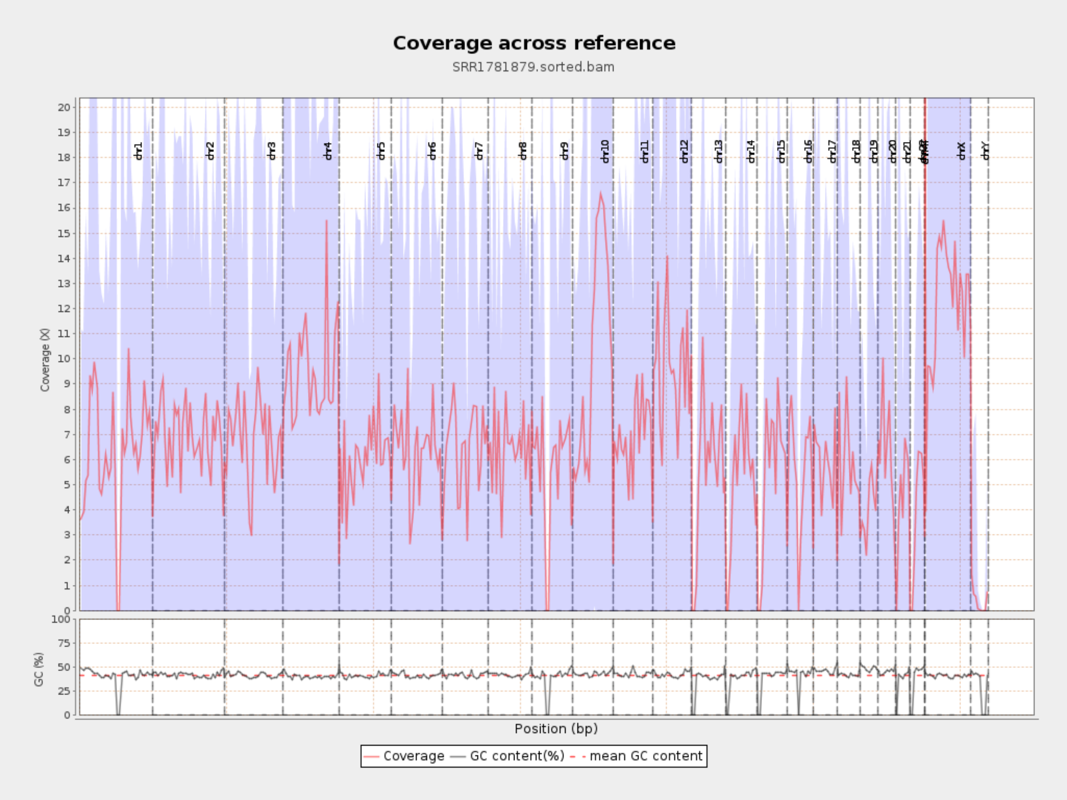
2.7. Chromosome stats

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

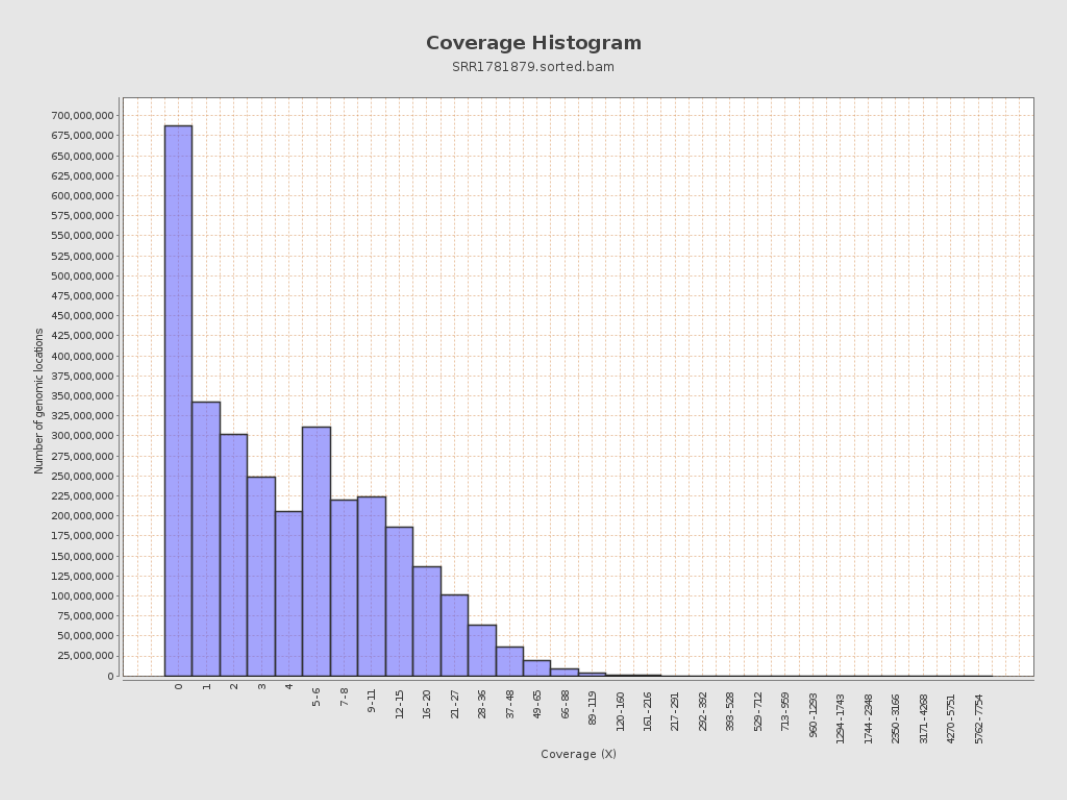
		bases	coverage	deviation
chr1	249250621	1570892112	6.3025	13.4132
chr2	243199373	1695585496	6.972	11.0409
chr3	198022430	1354415528	6.8397	9.9937
chr4	191154276	1816353566	9.502	13.0854
chr5	180915260	1099383183	6.0768	9.0157
chr6	171115067	1100205154	6.4296	9.9133
chr7	159138663	1026230892	6.4487	10.0393
chr8	146364022	933648166	6.3789	9.2747
chr9	141213431	784966232	5.5587	10.3004
chr10	135534747	1410781500	10.409	16.2818
chr11	135006516	939470580	6.9587	10.5203
chr12	133851895	1297117755	9.6907	13.2297
chr13	115169878	642060778	5.5749	8.867
chr14	107349540	554735248	5.1676	8.8662
chr15	102531392	542676462	5.2928	9.1596
chr16	90354753	486245807	5.3815	9.1234
chr17	81195210	470206217	5.7911	10.1896
chr18	78077248	472095593	6.0465	11.0362
chr19	59128983	239859297	4.0565	9.6557
chr20	63025520	395583301	6.2766	10.0422
chr21	48129895	220992798	4.5916	11.9629
chr22	51304566	196893883	3.8377	7.7977
chrMT	16571	960124	57.94	17.0603
chrX	155270560	1904644134	12.2666	15.9721

chrY	59373566	23608515	0.3976	4.0597

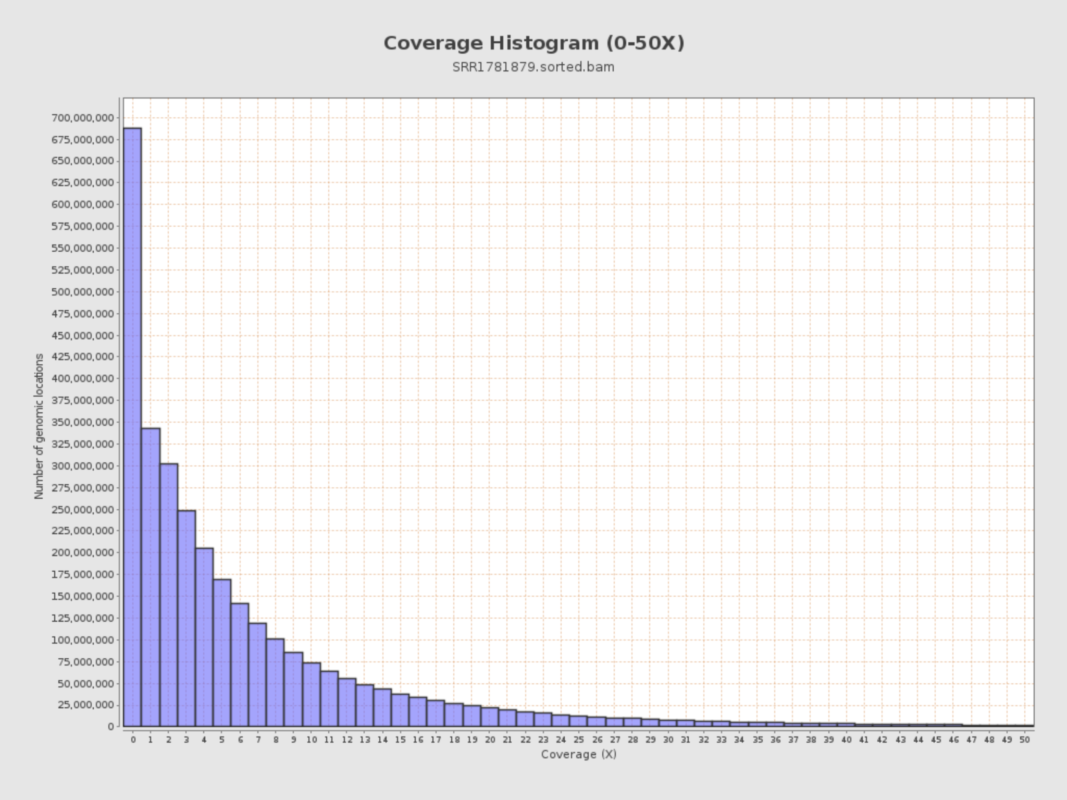
3. Results : Coverage across reference



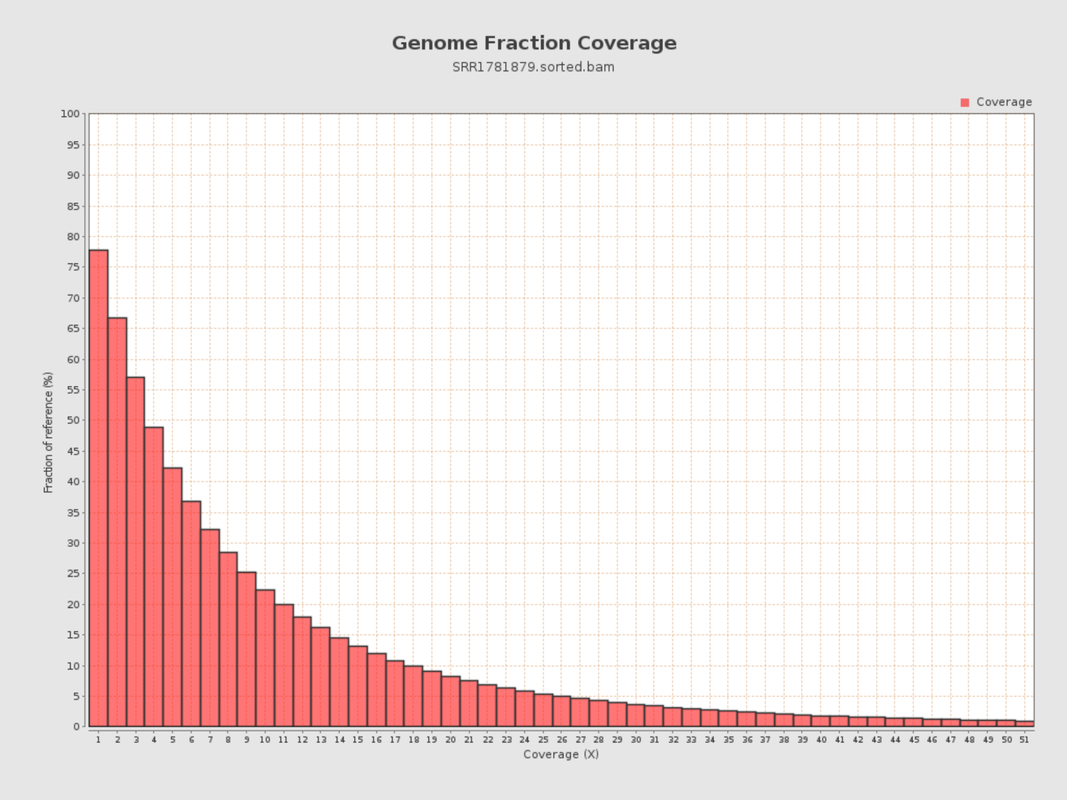
4. Results : Coverage Histogram



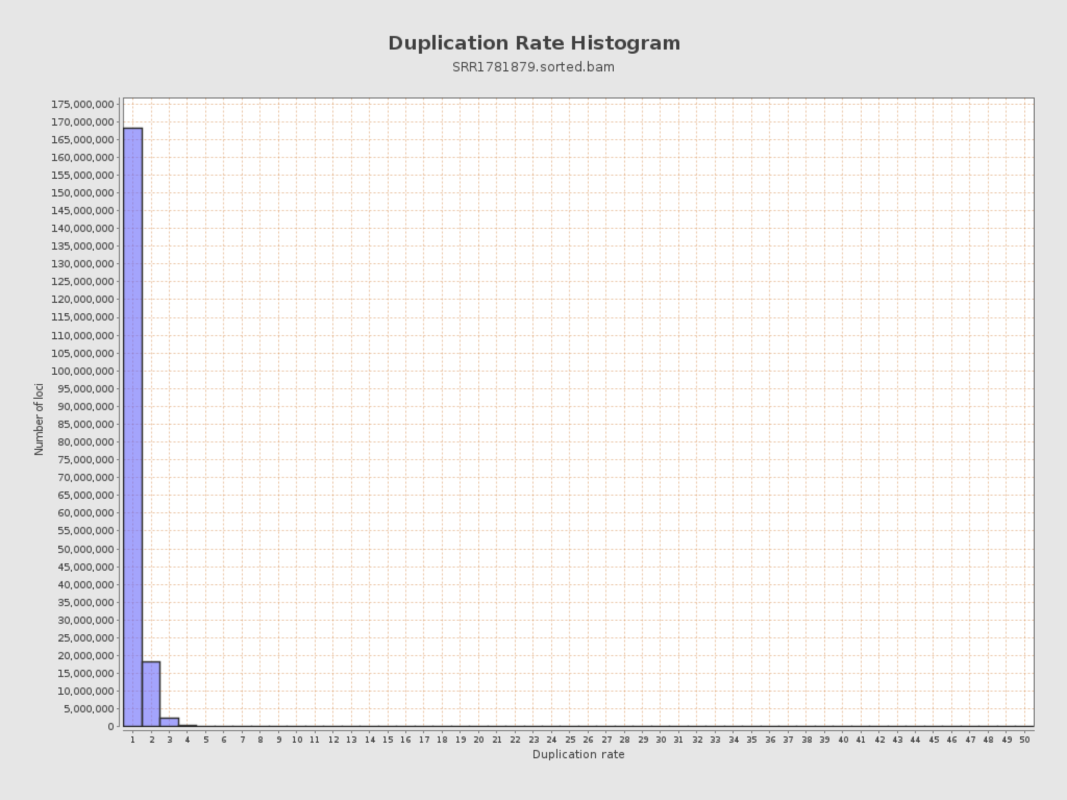
5. Results : Coverage Histogram (0-50X)



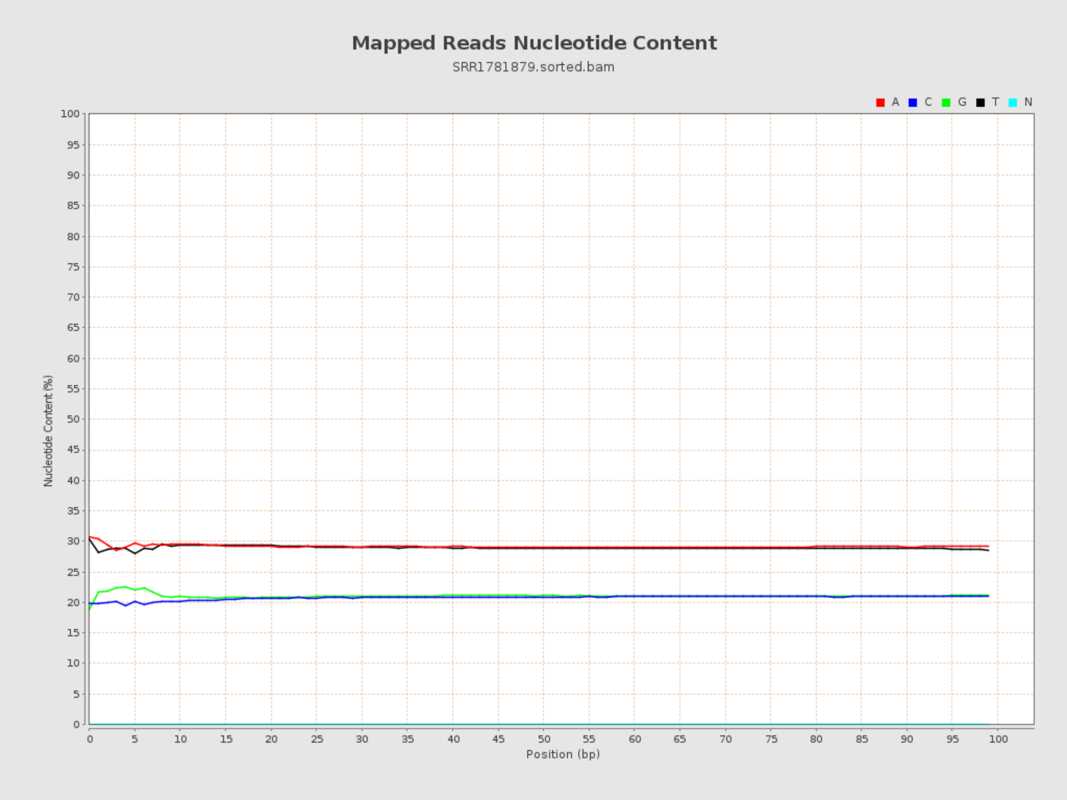
6. Results : Genome Fraction Coverage



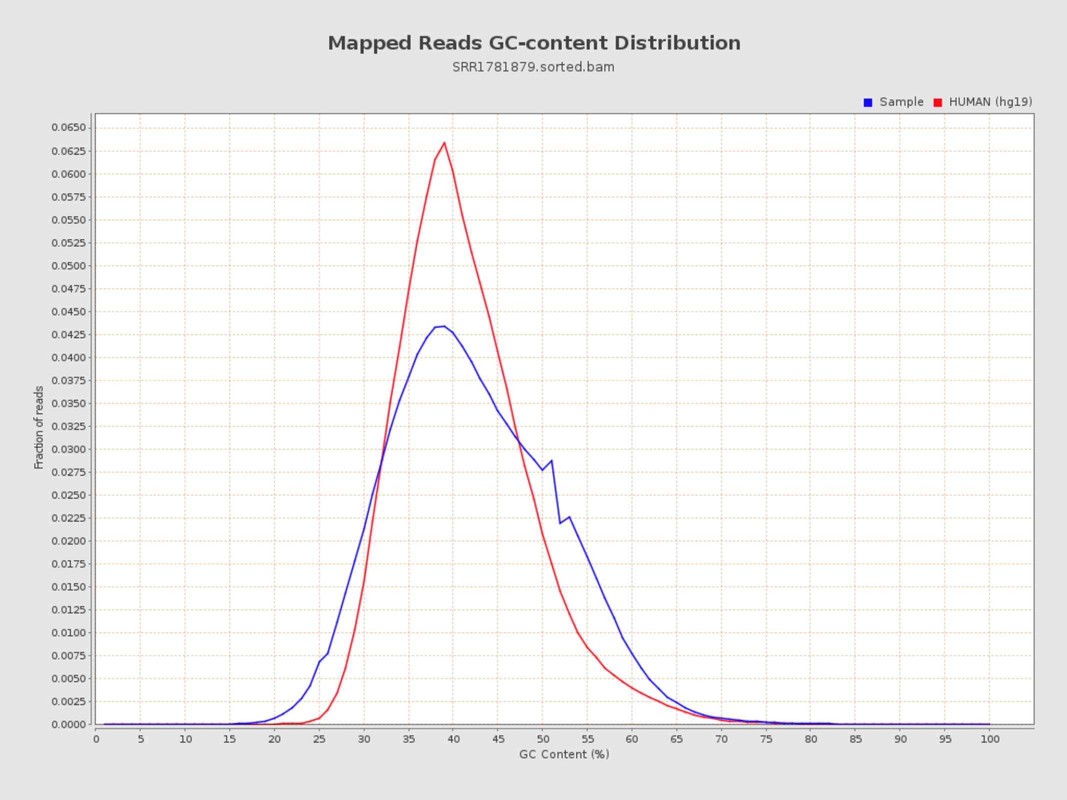
7. Results : Duplication Rate Histogram



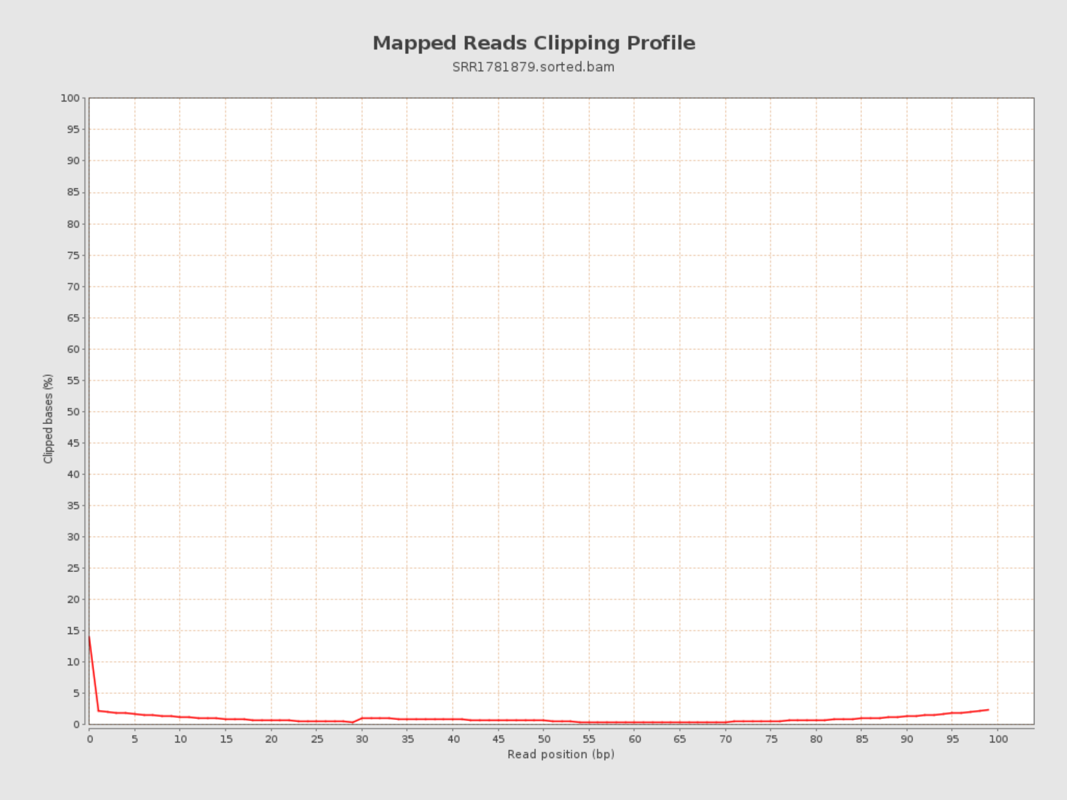
8. Results : Mapped Reads Nucleotide Content



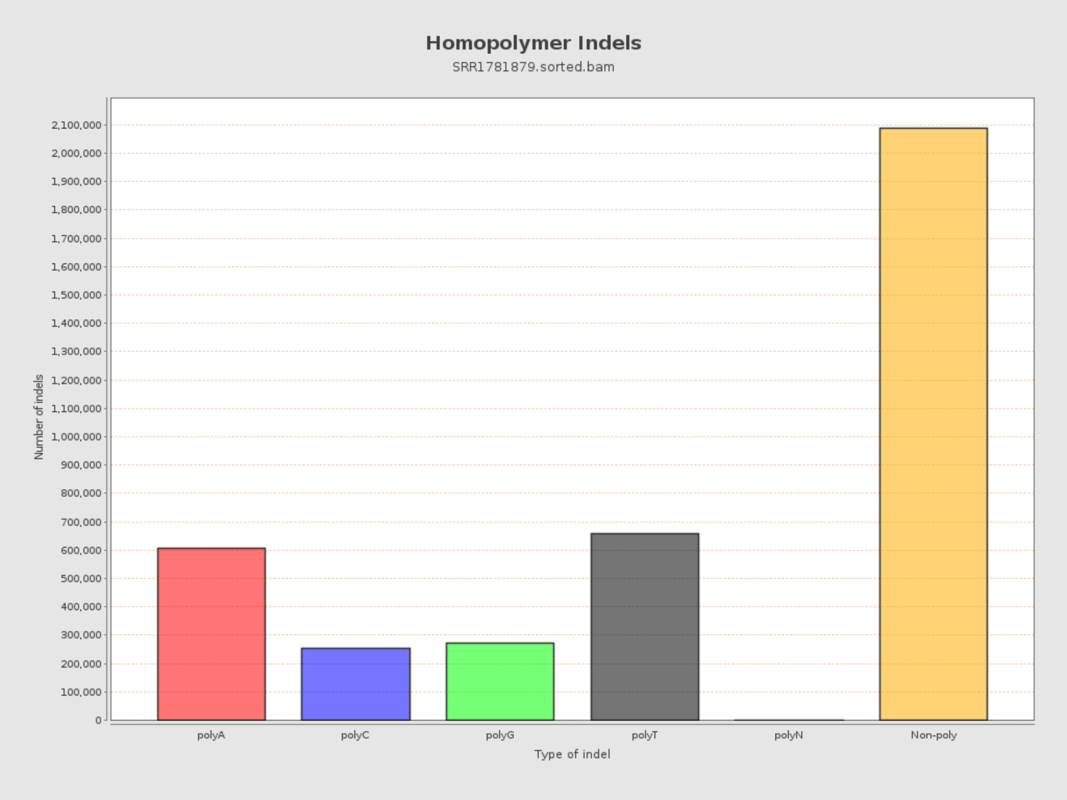
9. Results : Mapped Reads GC-content Distribution



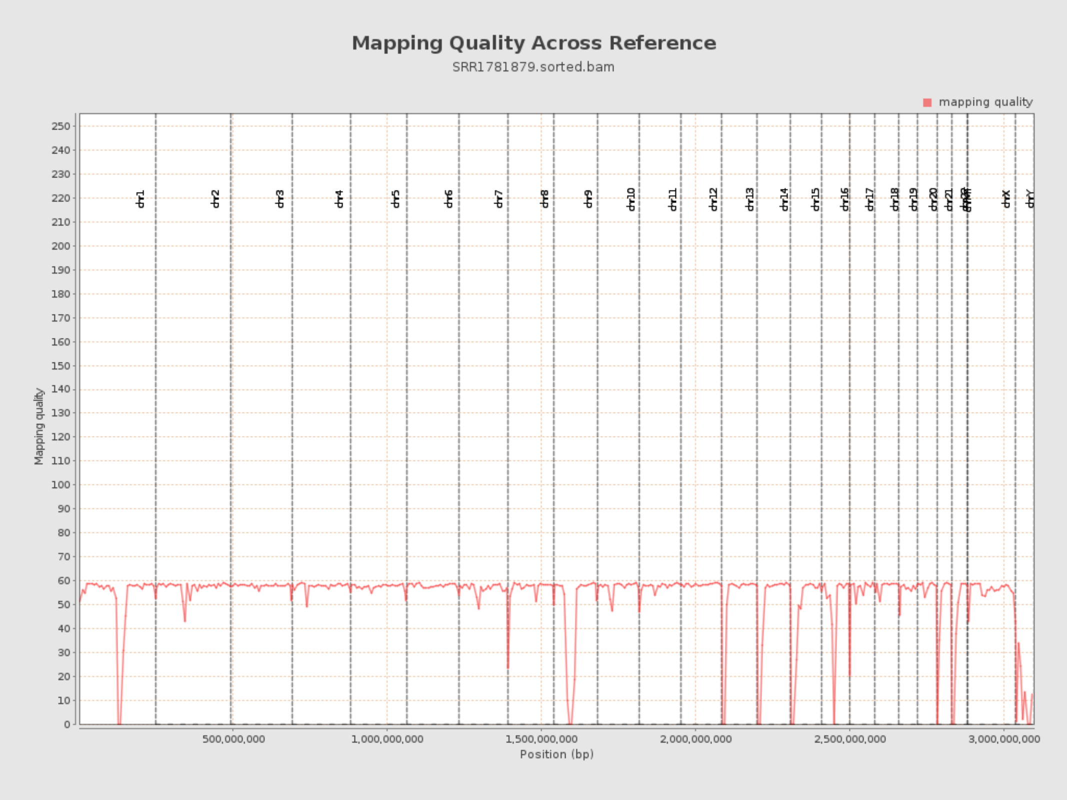
10. Results : Mapped Reads Clipping Profile



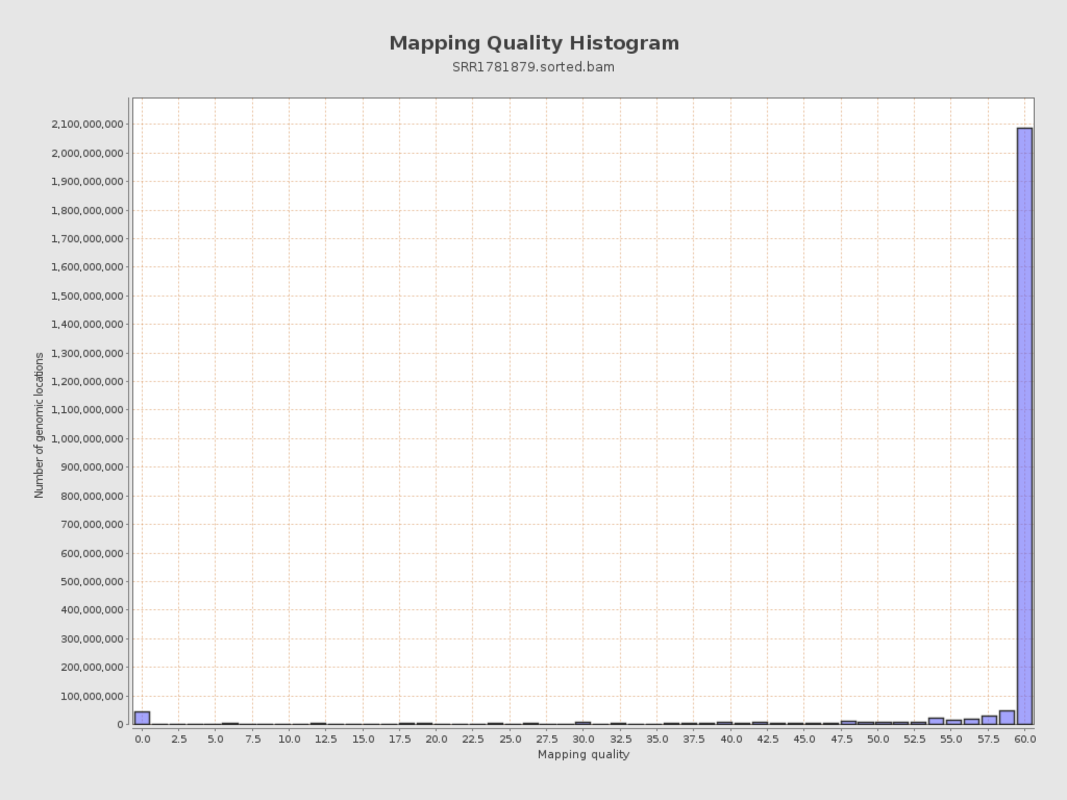
11. Results : Homopolymer Indels



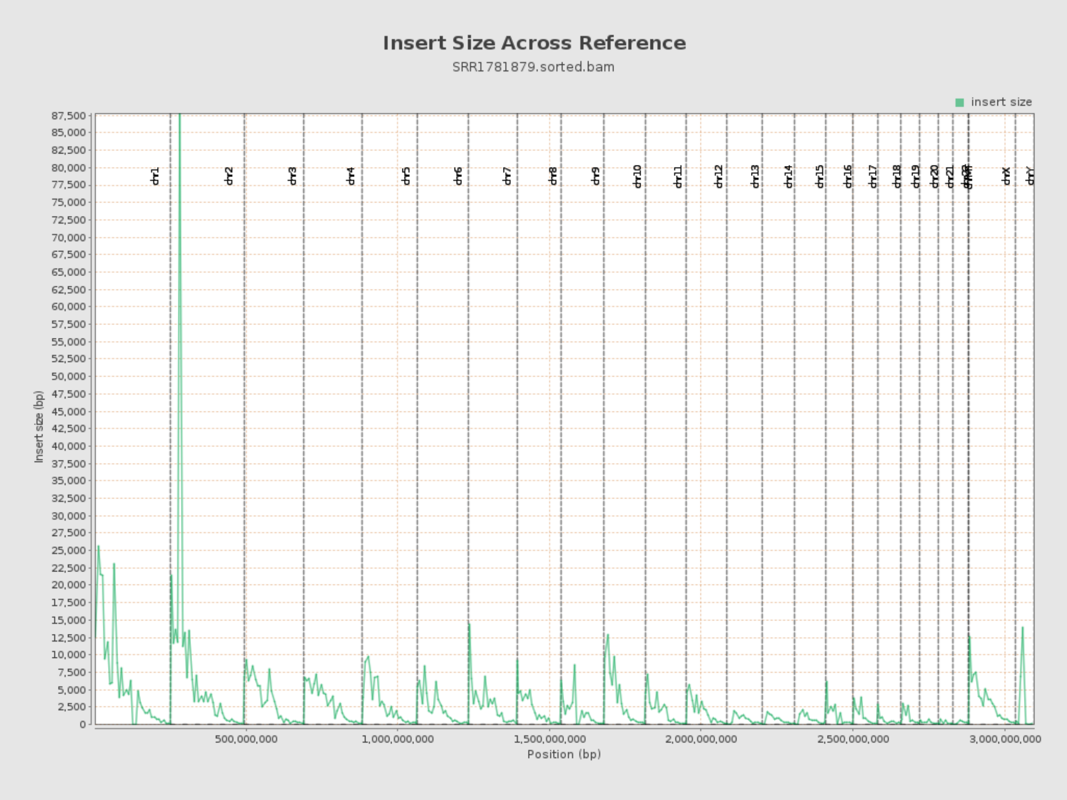
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram