Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/11 03:23:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779427.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_SRR1779427 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779427_1.fastq.gz SRR1779427_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Oct 11 03:23:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779427.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,770,268
Mapped reads	15,308,778 / 97.07%
Unmapped reads	461,490 / 2.93%
Mapped paired reads	15,308,778 / 97.07%
Mapped reads, first in pair	7,688,066 / 48.75%
Mapped reads, second in pair	7,620,712 / 48.32%
Mapped reads, both in pair	15,215,270 / 96.48%
Mapped reads, singletons	93,508 / 0.59%
Secondary alignments	0
Supplementary alignments	73,372 / 0.47%
Read min/max/mean length	30 / 80 / 80.17
Duplicated reads (estimated)	590,587 / 3.74%
Duplication rate	3.68%
Clipped reads	1,156,714 / 7.33%

2.2. ACGT Content

Number/percentage of A's	360,510,954 / 29.75%
Number/percentage of C's	244,556,197 / 20.18%
Number/percentage of T's	358,115,851 / 29.55%
Number/percentage of G's	248,386,907 / 20.5%
Number/percentage of N's	262,808 / 0.02%

GC Percentage	40.68%

2.3. Coverage

Mean	0.3916
Standard Deviation	1.3223

2.4. Mapping Quality

Mean Mapping Quality	52.52

2.5. Insert size

Mean	70,196.45
Standard Deviation	2,549,735.94
P25/Median/P75	112 / 151 / 200

2.6. Mismatches and indels

General error rate	0.32%
Mismatches	3,659,929
Insertions	132,426
Mapped reads with at least one insertion	0.86%
Deletions	135,808
Mapped reads with at least one deletion	0.88%
Homopolymer indels	47.35%

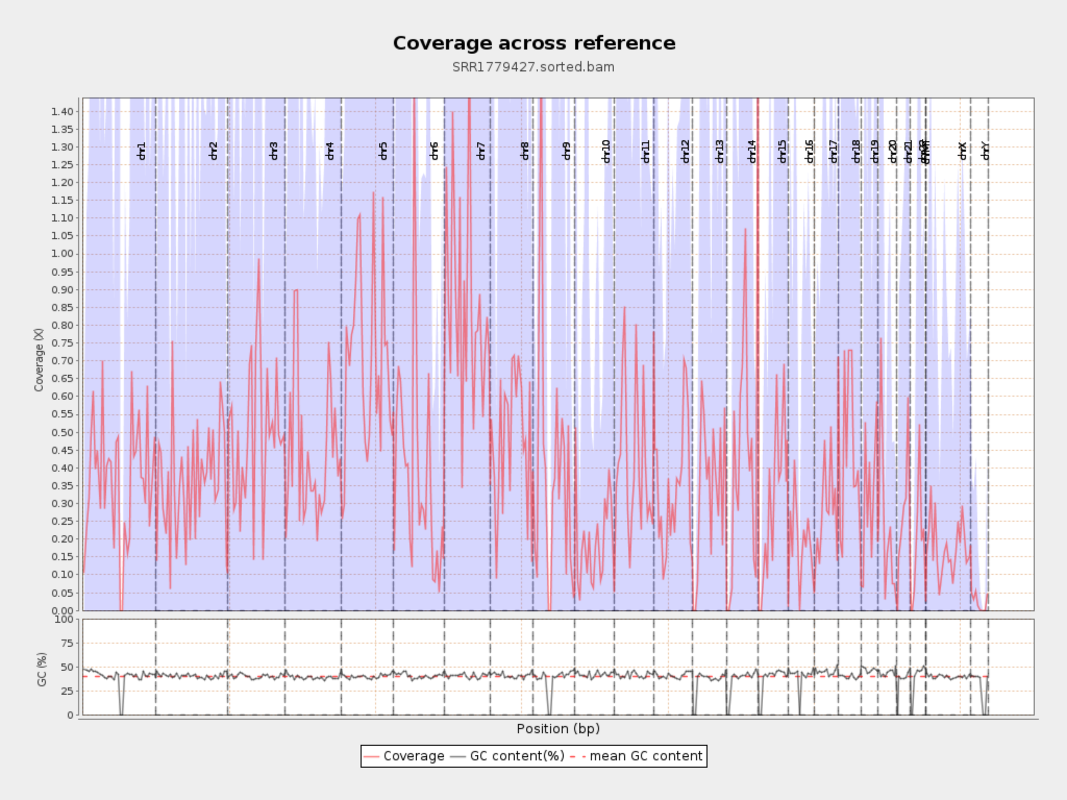
2.7. Chromosome stats

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

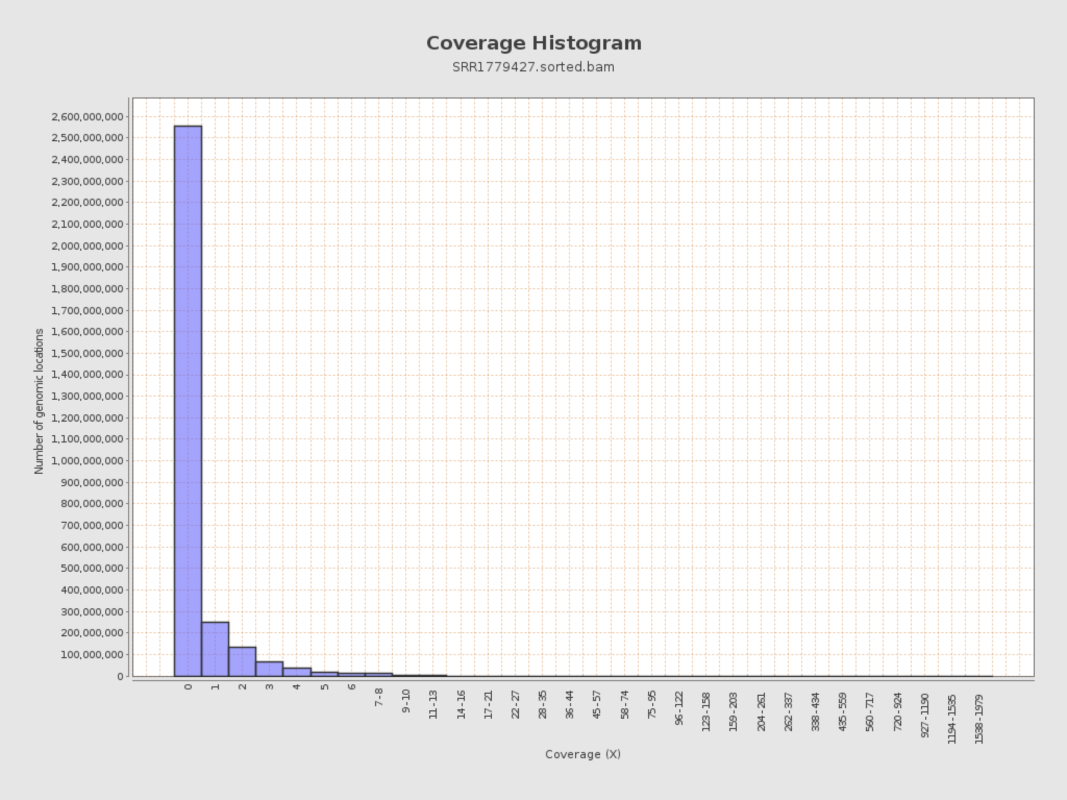
		bases	coverage	deviation
chr1	249250621	91714645	0.368	2.2544
chr2	243199373	89881685	0.3696	1.092
chr3	198022430	97126114	0.4905	1.2538
chr4	191154276	83828350	0.4385	1.1703
chr5	180915260	124916857	0.6905	1.5004
chr6	171115067	64387058	0.3763	1.3183
chr7	159138663	134223659	0.8434	1.7269
chr8	146364022	69899429	0.4776	1.2696
chr9	141213431	55610757	0.3938	1.378
chr10	135534747	26557318	0.1959	1.111
chr11	135006516	55506160	0.4111	1.1991
chr12	133851895	46326550	0.3461	1.0294
chr13	115169878	39666750	0.3444	1.0045
chr14	107349540	42106425	0.3922	1.1504
chr15	102531392	30800339	0.3004	1.0258
chr16	90354753	16541420	0.1831	0.7923
chr17	81195210	22564085	0.2779	0.9493
chr18	78077248	34703578	0.4445	1.3509
chr19	59128983	18638741	0.3152	1.5876
chr20	63025520	15129030	0.24	0.9034
chr21	48129895	12794672	0.2658	0.9519
chr22	51304566	9922397	0.1934	0.8512
chrMT	16571	625	0.0377	0.2792
chrX	155270560	27863793	0.1795	0.7586

chrY	59373566	1410649	0.0238	0.251

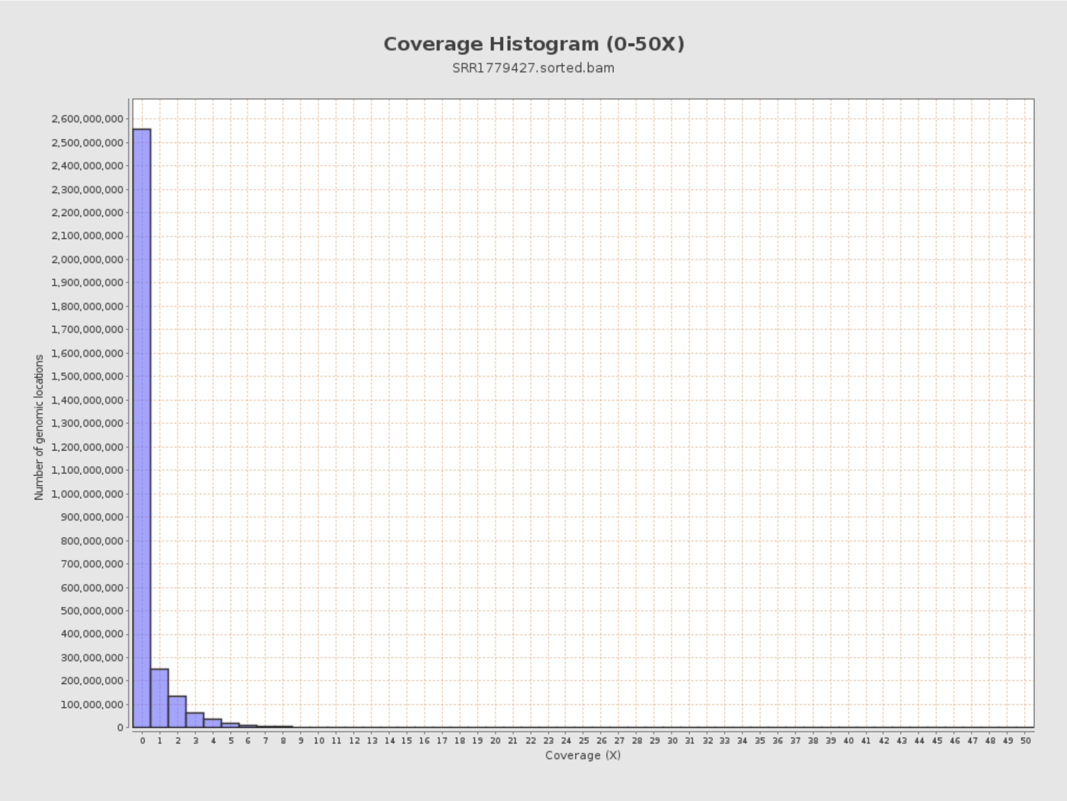
3. Results : Coverage across reference



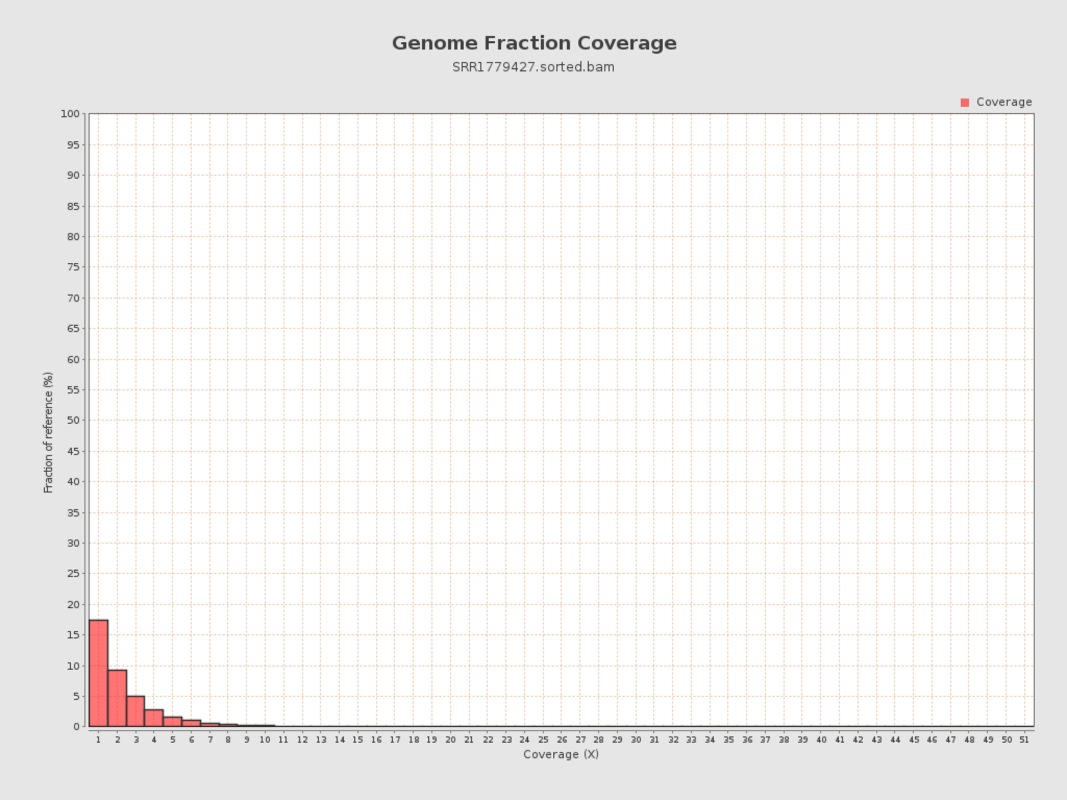
4. Results : Coverage Histogram



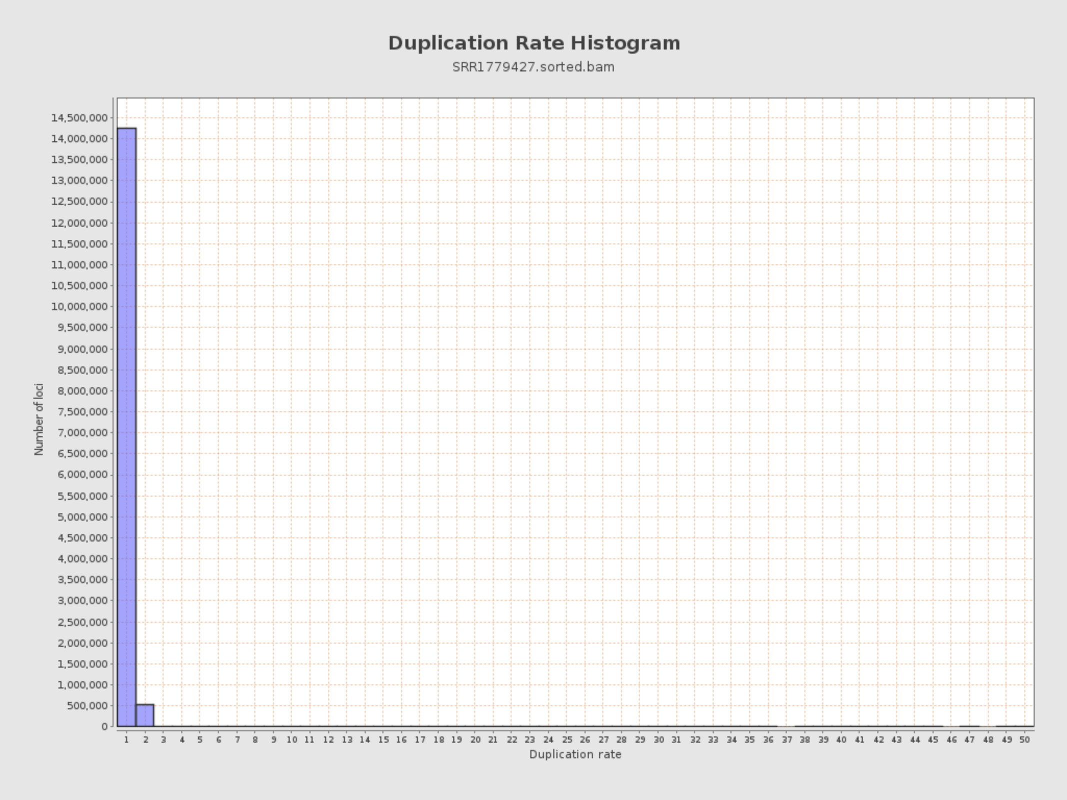
5. Results : Coverage Histogram (0-50X)



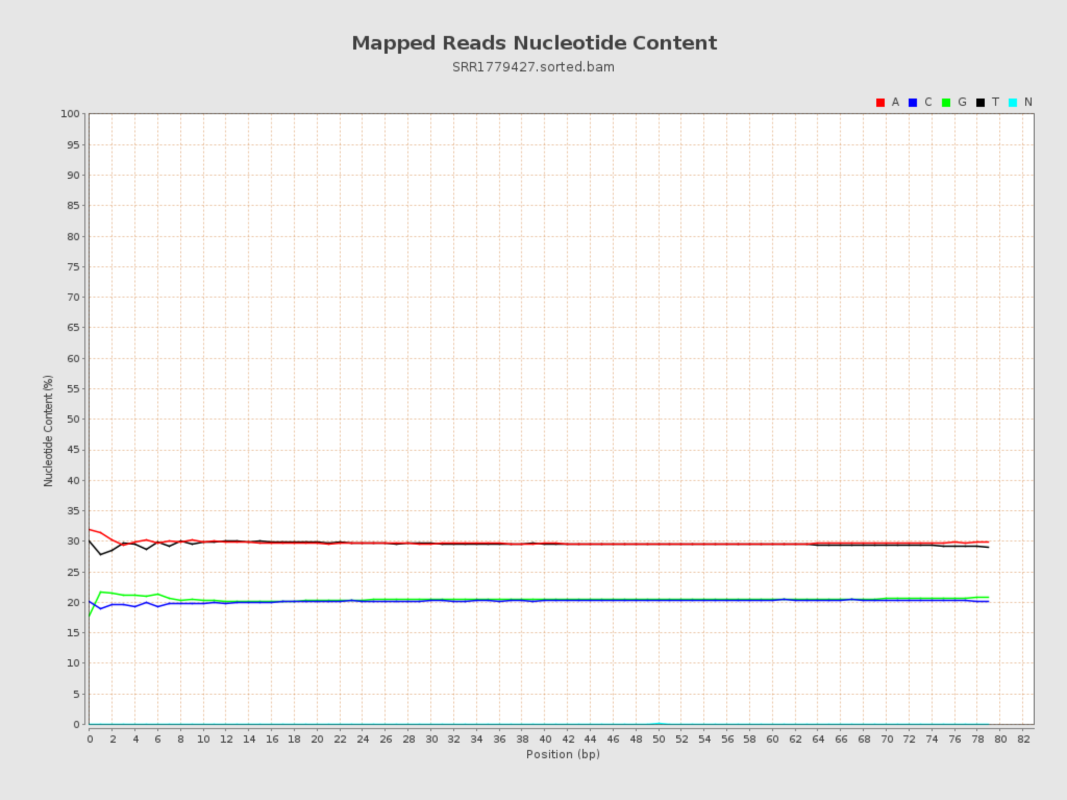
6. Results : Genome Fraction Coverage



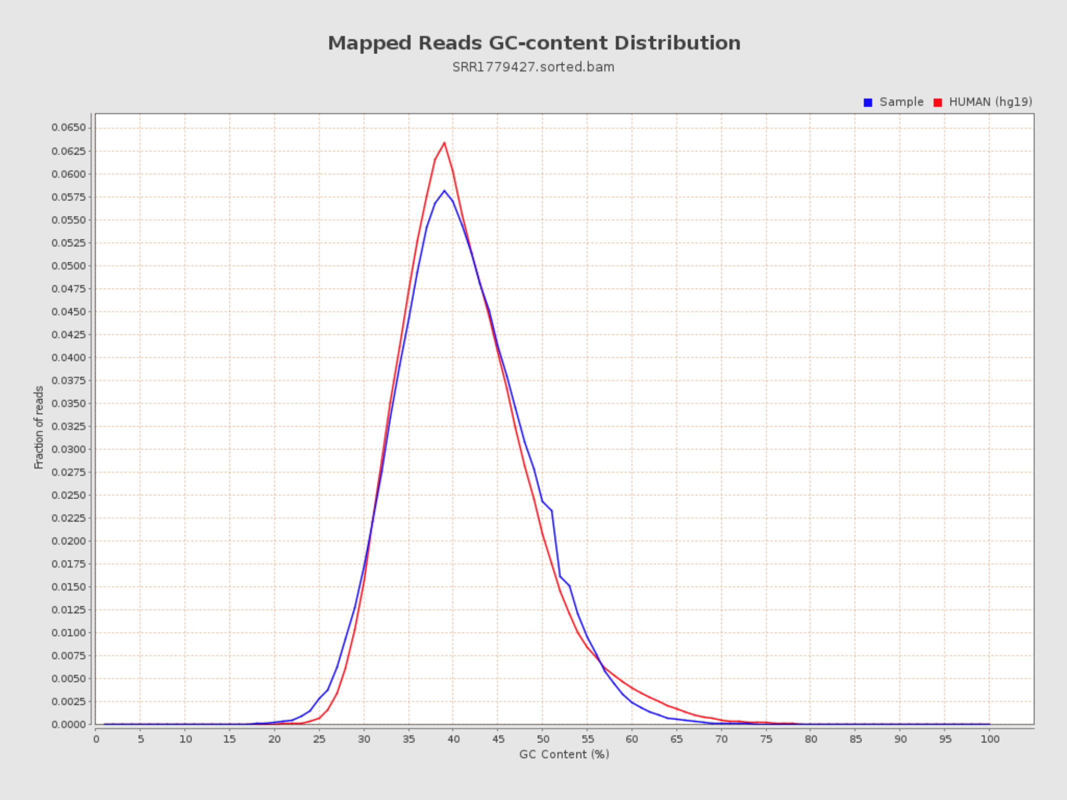
7. Results : Duplication Rate Histogram



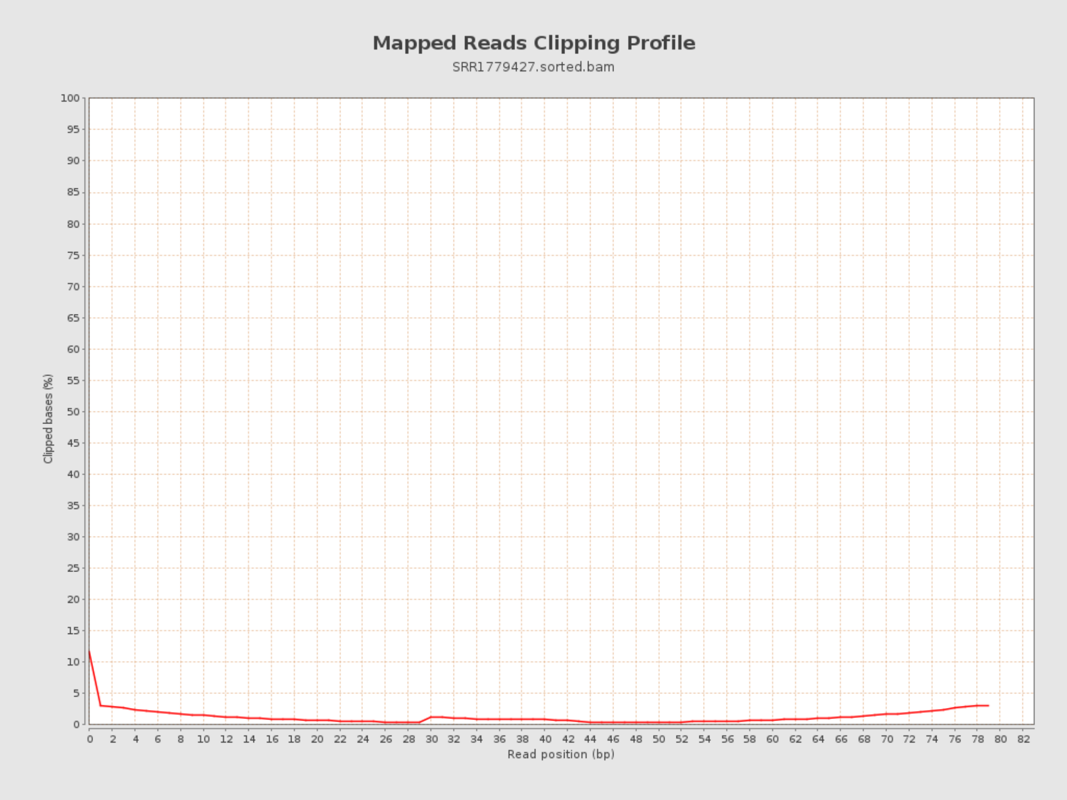
8. Results : Mapped Reads Nucleotide Content



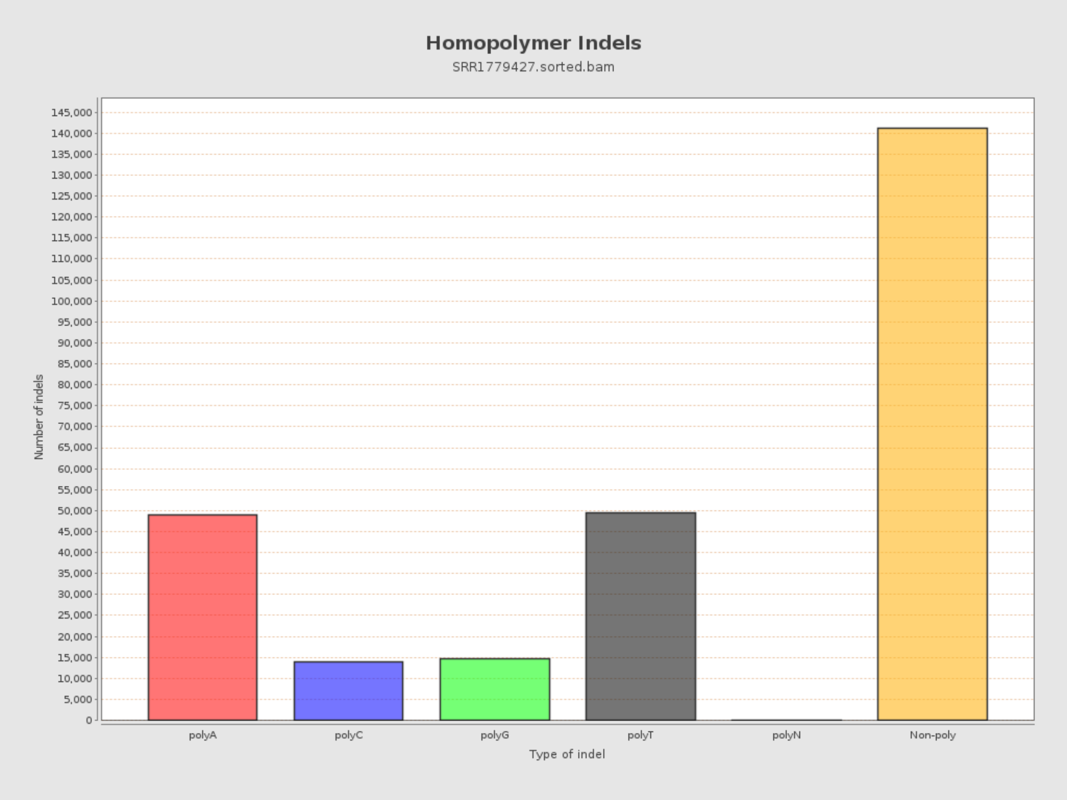
9. Results : Mapped Reads GC-content Distribution



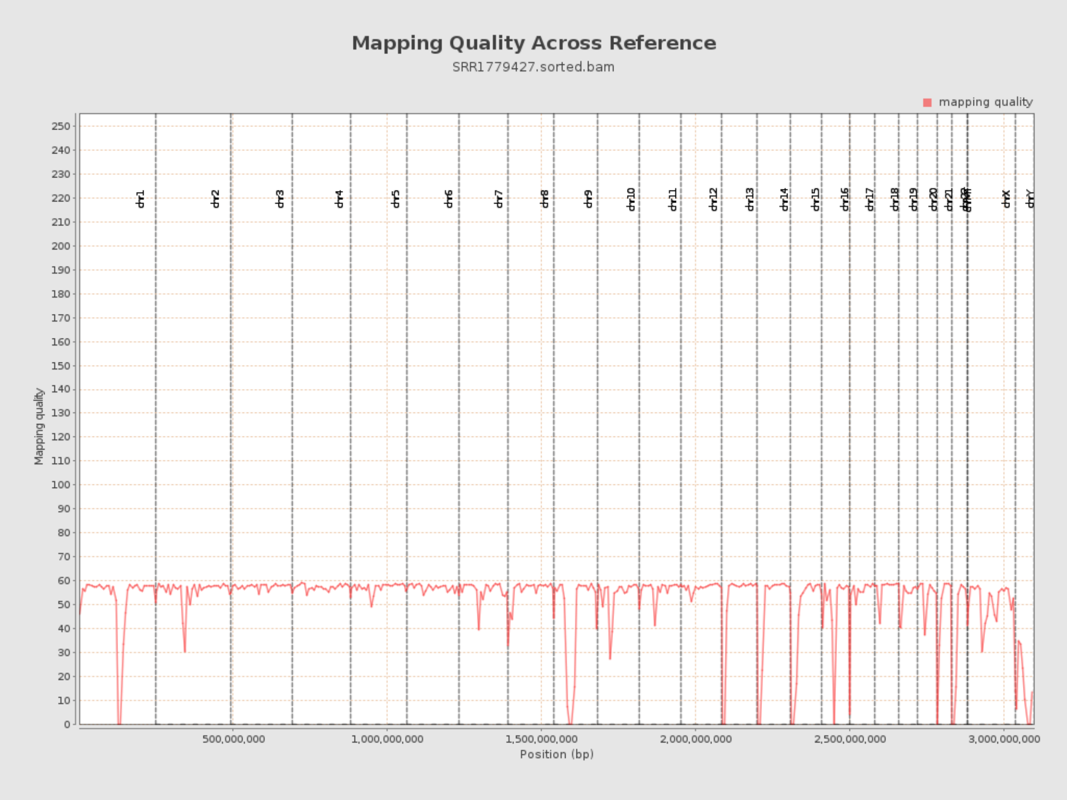
10. Results : Mapped Reads Clipping Profile



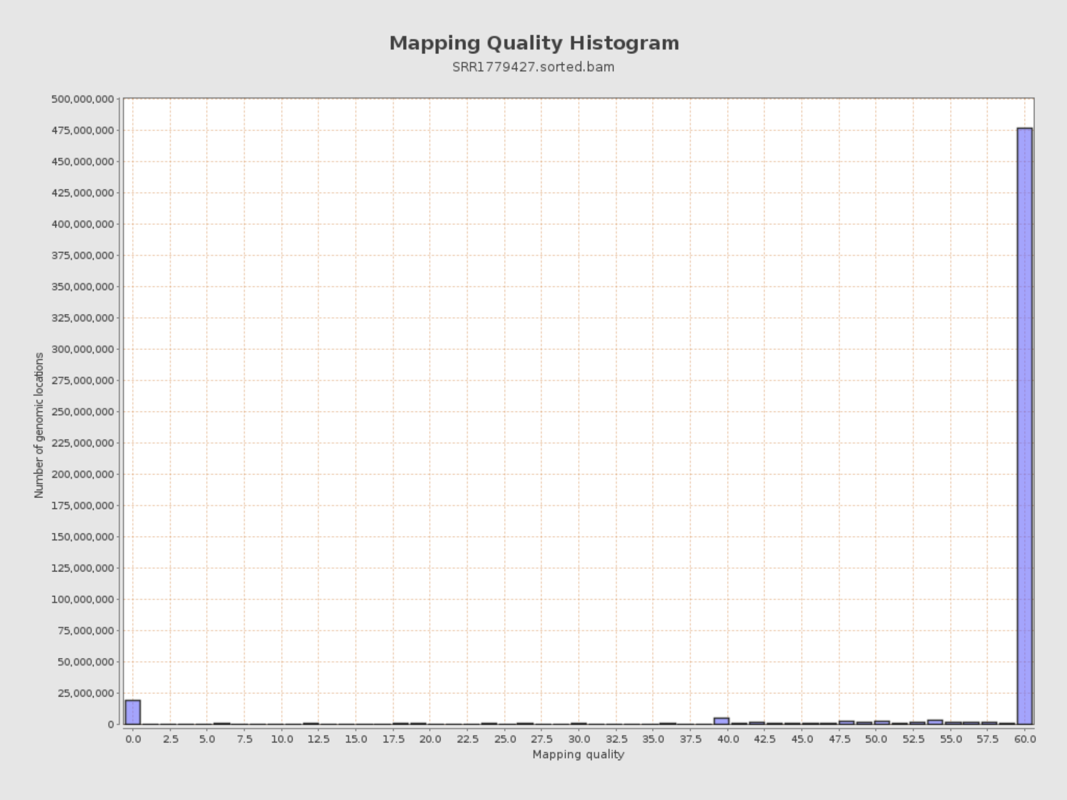
11. Results : Homopolymer Indels



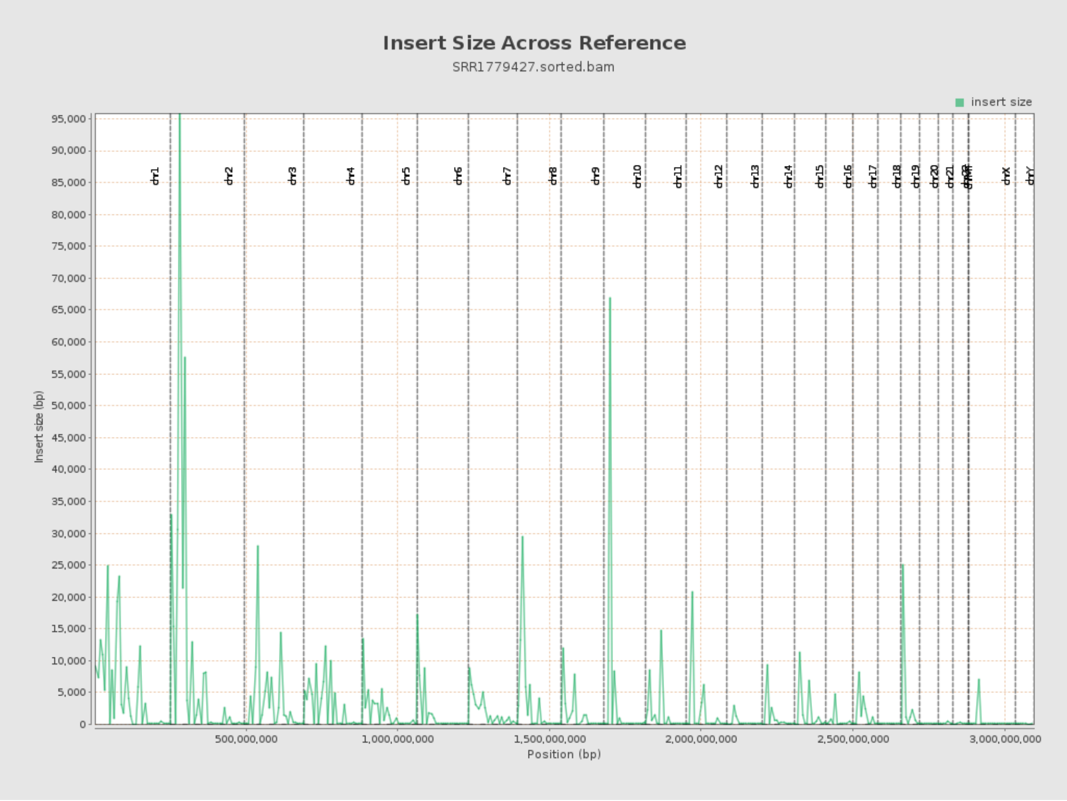
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram