Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/29 05:57:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779334.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_SRR1779334 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779334_1.fastq.gz SRR1779334_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 29 05:57:46 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779334.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	141,092,640
Mapped reads	134,642,568 / 95.43%
Unmapped reads	6,450,072 / 4.57%
Mapped paired reads	134,642,568 / 95.43%
Mapped reads, first in pair	68,183,792 / 48.33%
Mapped reads, second in pair	66,458,776 / 47.1%
Mapped reads, both in pair	131,960,934 / 93.53%
Mapped reads, singletons	2,681,634 / 1.9%
Secondary alignments	0
Supplementary alignments	578,084 / 0.41%
Read min/max/mean length	30 / 100 / 100.05
Duplicated reads (estimated)	8,218,868 / 5.83%
Duplication rate	5.78%
Clipped reads	6,623,284 / 4.69%

2.2. ACGT Content

Number/percentage of A's	3,960,773,452 / 29.69%
Number/percentage of C's	2,693,186,237 / 20.19%
Number/percentage of T's	3,942,140,613 / 29.55%
Number/percentage of G's	2,744,851,779 / 20.57%
Number/percentage of N's	859,019 / 0.01%

GC Percentage	40.76%

2.3. Coverage

Mean	4.3108
Standard Deviation	7.4256

2.4. Mapping Quality

Mean Mapping Quality	54.07

2.5. Insert size

Mean	58,948.84
Standard Deviation	2,411,896.55
P25/Median/P75	187 / 242 / 311

2.6. Mismatches and indels

General error rate	0.37%
Mismatches	46,994,697
Insertions	1,421,779
Mapped reads with at least one insertion	1.04%
Deletions	1,432,634
Mapped reads with at least one deletion	1.05%
Homopolymer indels	48.35%

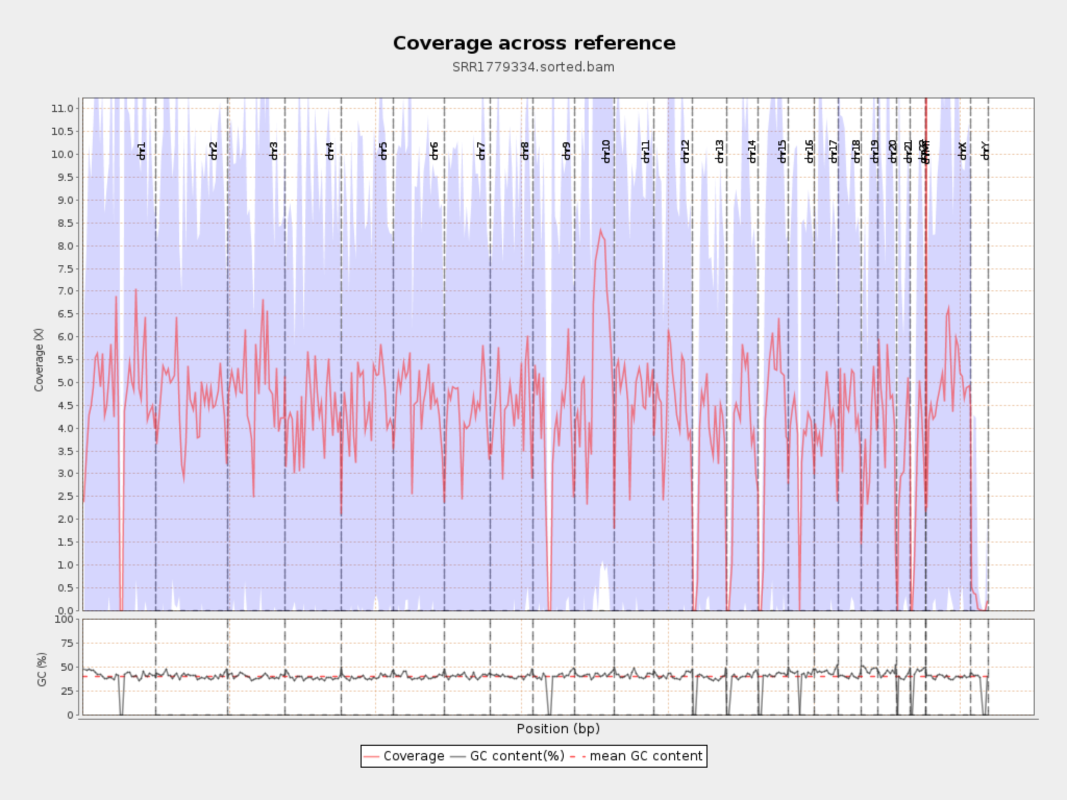
2.7. Chromosome stats

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

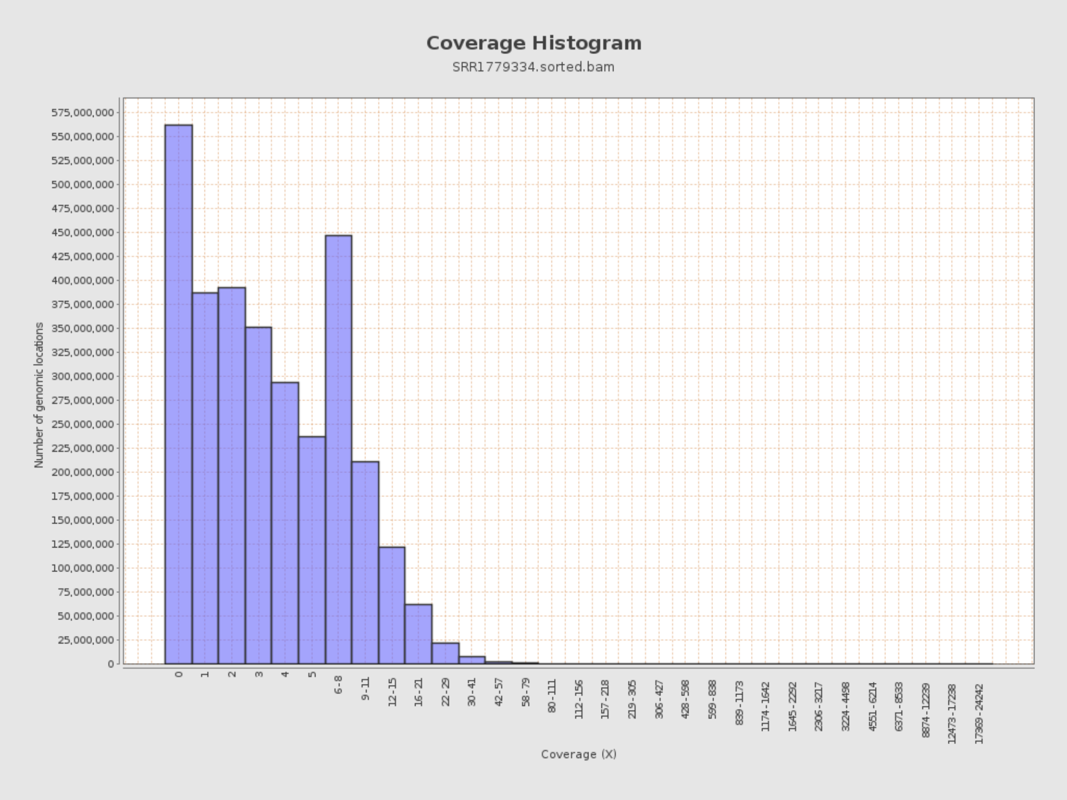
		bases	coverage	deviation
chr1	249250621	1145359212	4.5952	6.6462
chr2	243199373	1115903223	4.5884	19.3982
chr3	198022430	961431402	4.8552	4.8517
chr4	191154276	823288686	4.3069	4.68
chr5	180915260	819753235	4.5311	4.4634
chr6	171115067	790034551	4.617	4.9657
chr7	159138663	685752765	4.3092	4.7481
chr8	146364022	656566605	4.4858	4.5904
chr9	141213431	544110892	3.8531	5.3153
chr10	135534747	779588828	5.7519	7.3283
chr11	135006516	639140069	4.7341	5.0042
chr12	133851895	608073911	4.5429	6.2339
chr13	115169878	394270364	3.4234	4.0195
chr14	107349540	392594897	3.6572	4.3239
chr15	102531392	418875860	4.0853	5.0684
chr16	90354753	324511178	3.5915	4.5086
chr17	81195210	333946009	4.1129	5.5012
chr18	78077248	349046029	4.4705	5.3637
chr19	59128983	210249082	3.5558	5.083
chr20	63025520	282601738	4.4839	5.4476
chr21	48129895	153593485	3.1912	5.6025
chr22	51304566	138757633	2.7046	4.1559
chrMT	16571	819051	49.4268	13.9526
chrX	155270560	766309647	4.9353	4.9901

chrY	59373566	10403731	0.1752	2.143

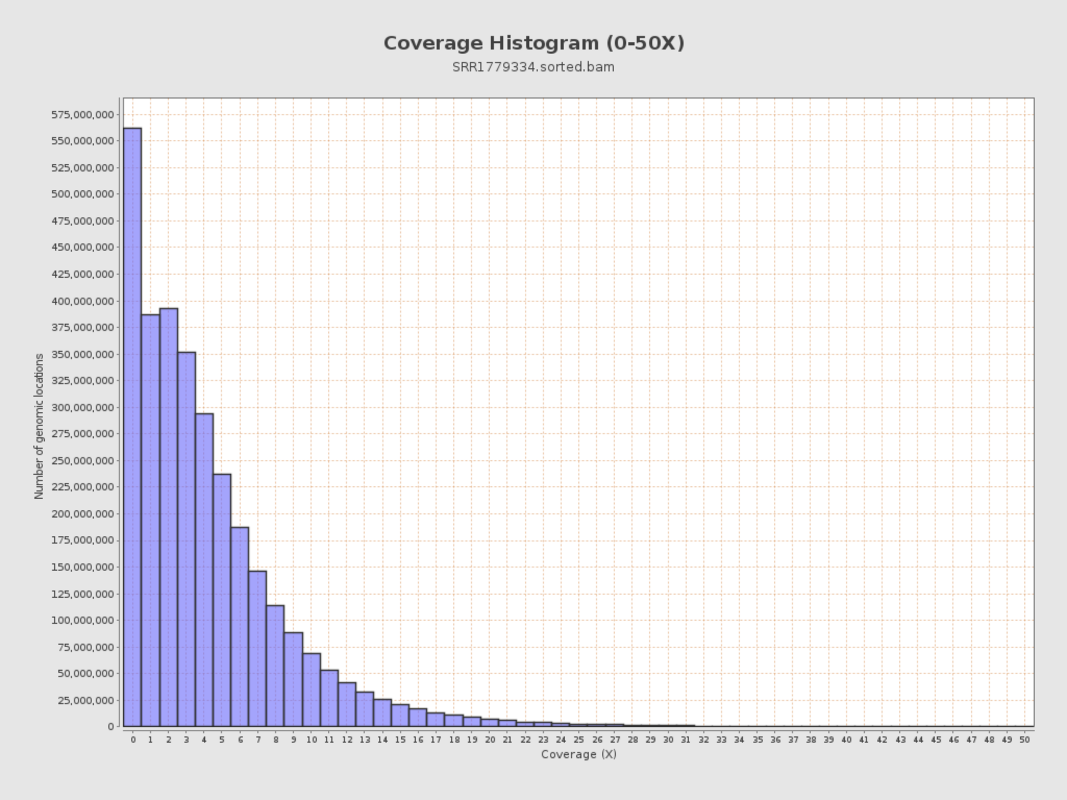
3. Results : Coverage across reference



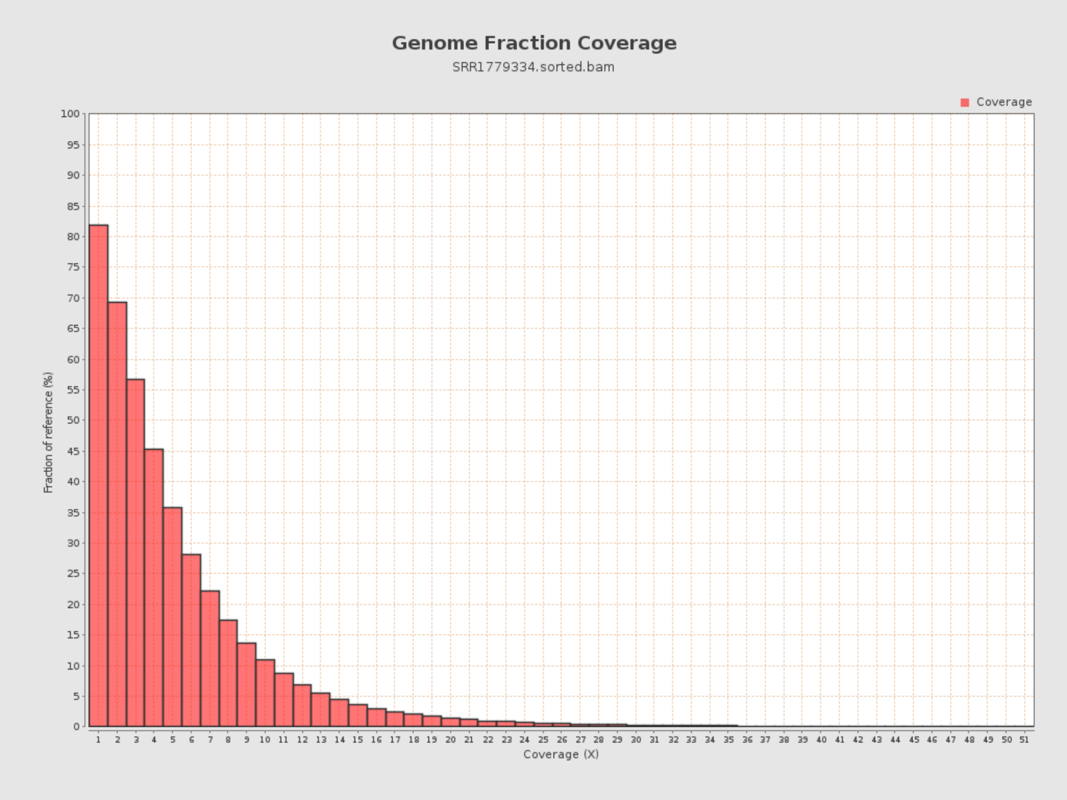
4. Results : Coverage Histogram



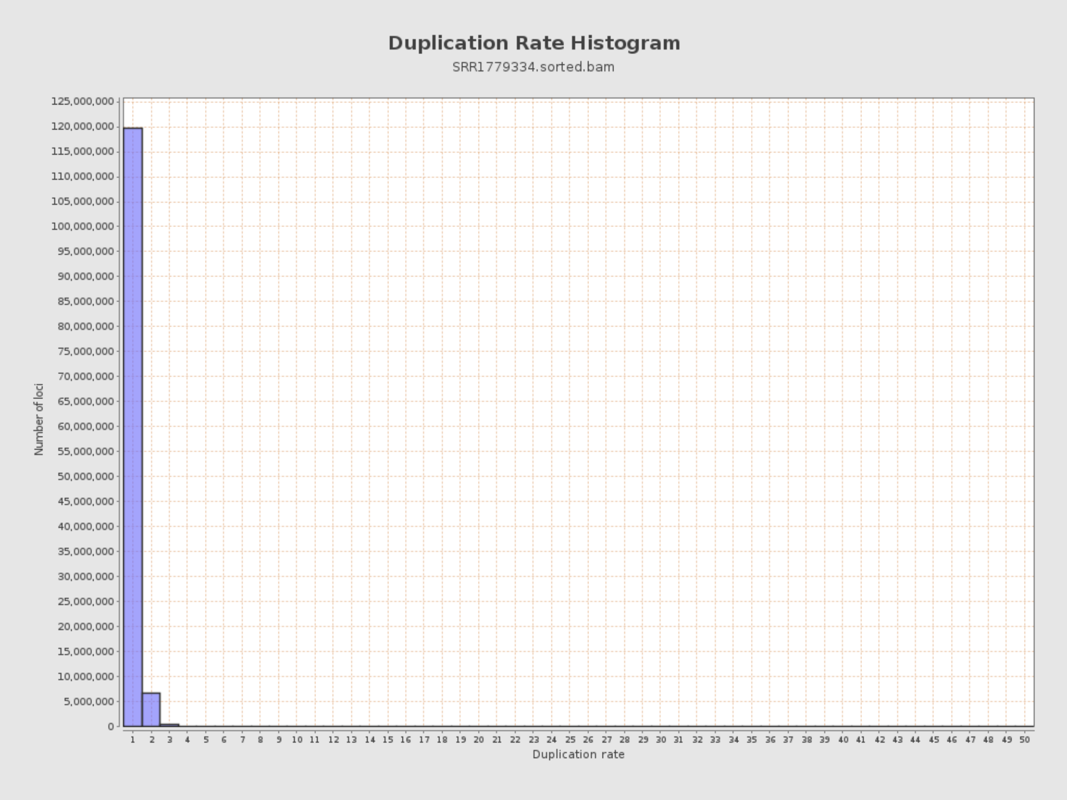
5. Results : Coverage Histogram (0-50X)



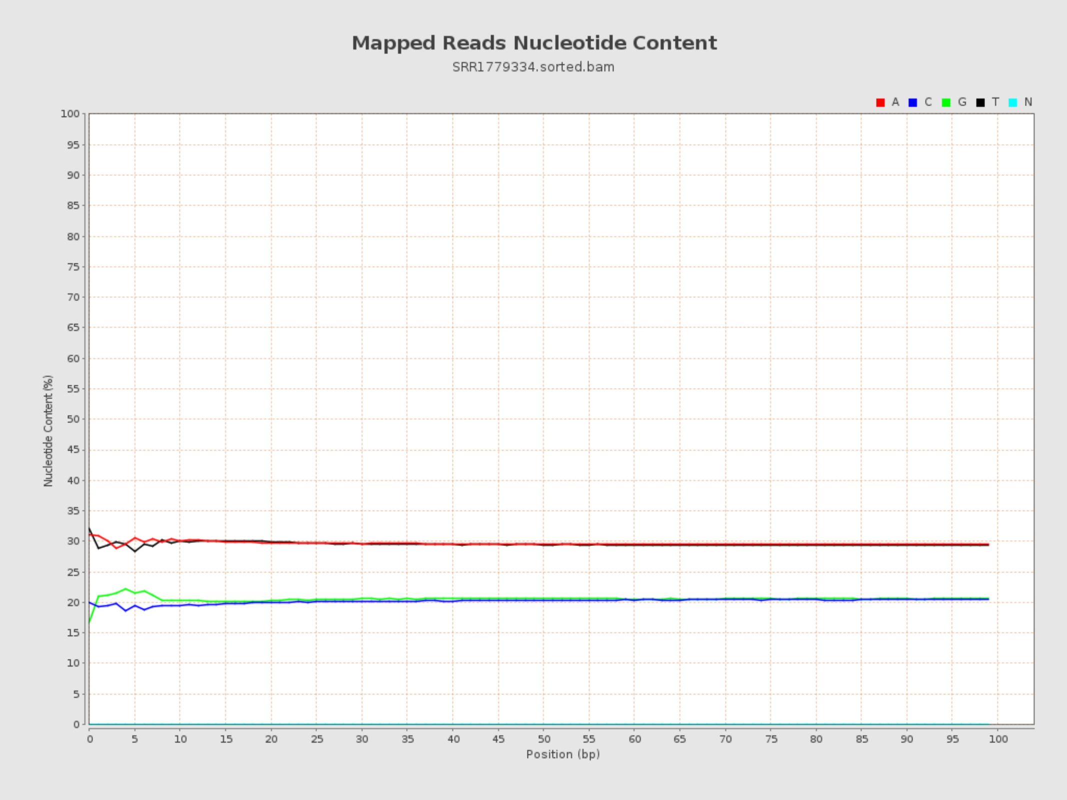
6. Results : Genome Fraction Coverage



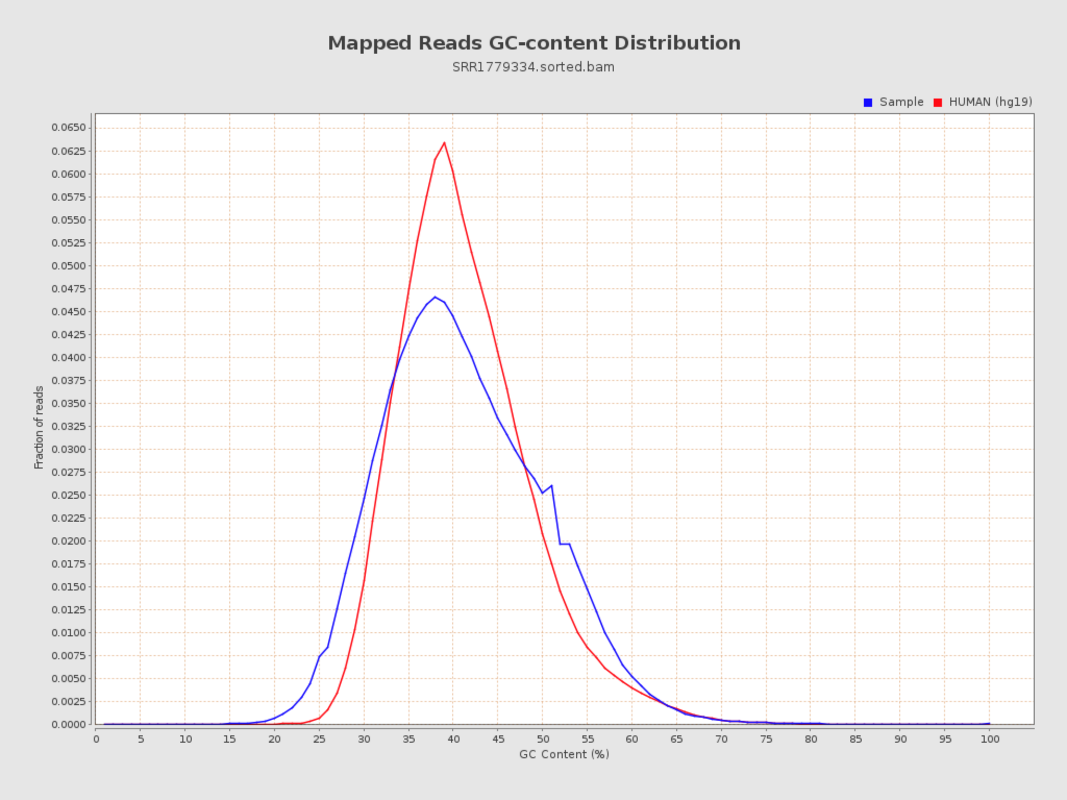
7. Results : Duplication Rate Histogram



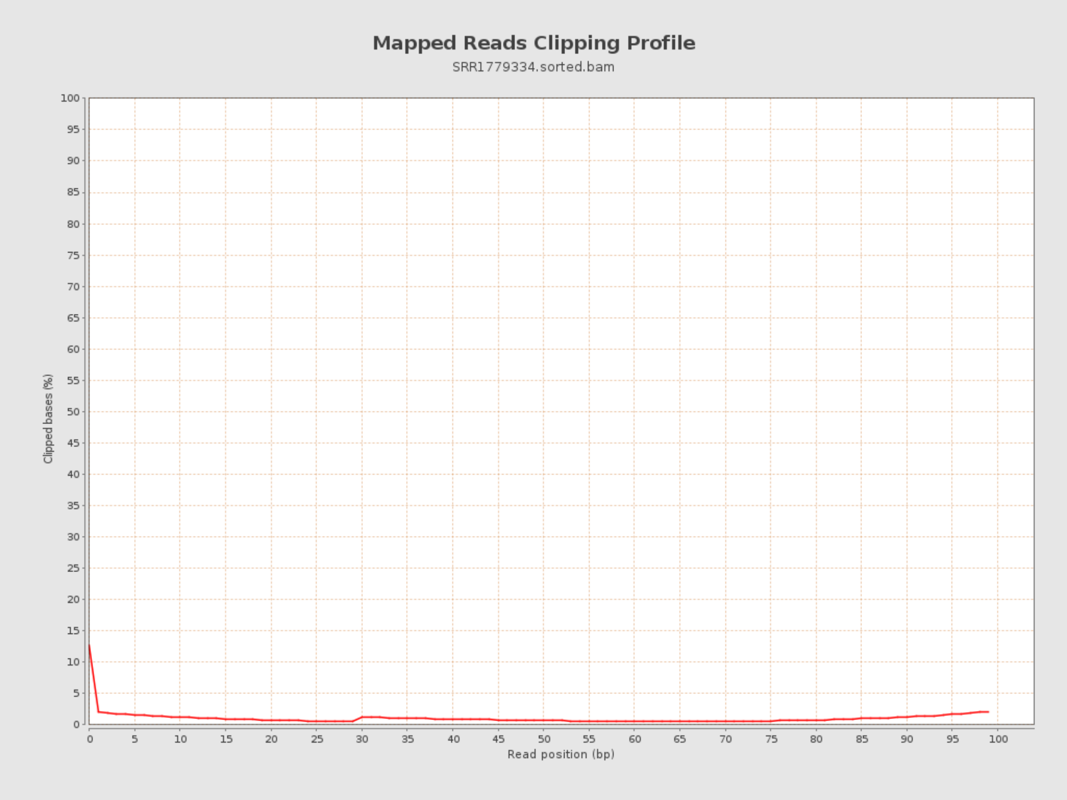
8. Results : Mapped Reads Nucleotide Content



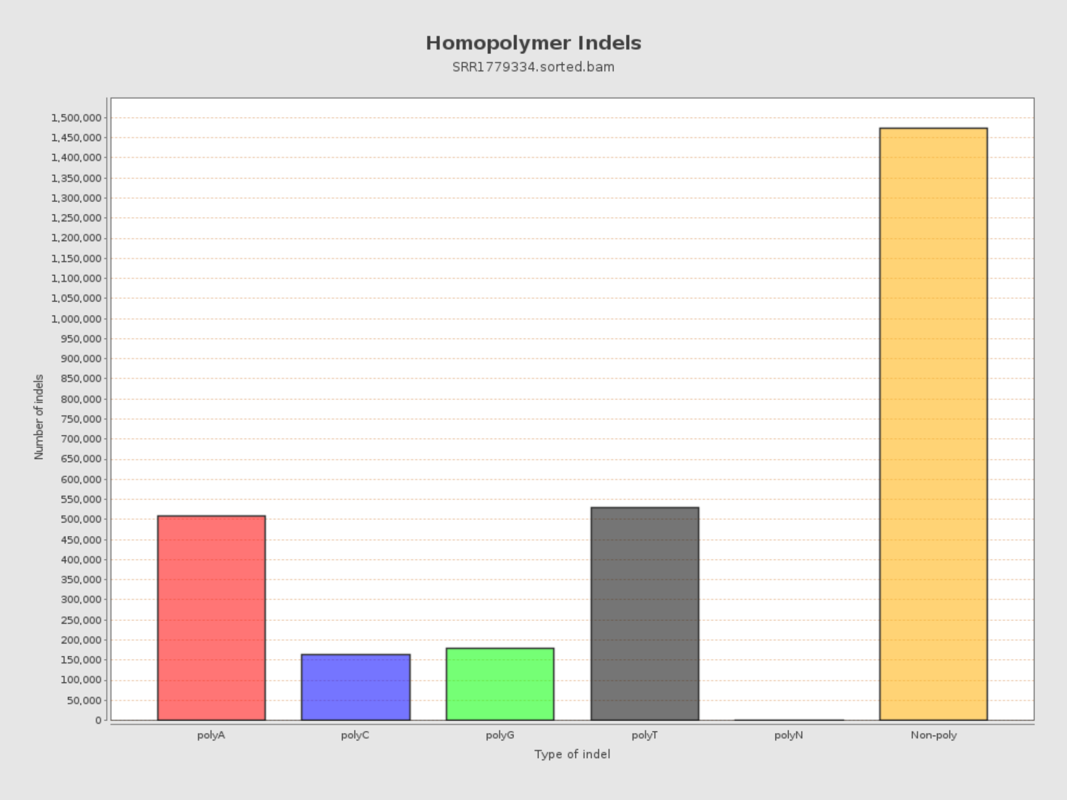
9. Results : Mapped Reads GC-content Distribution



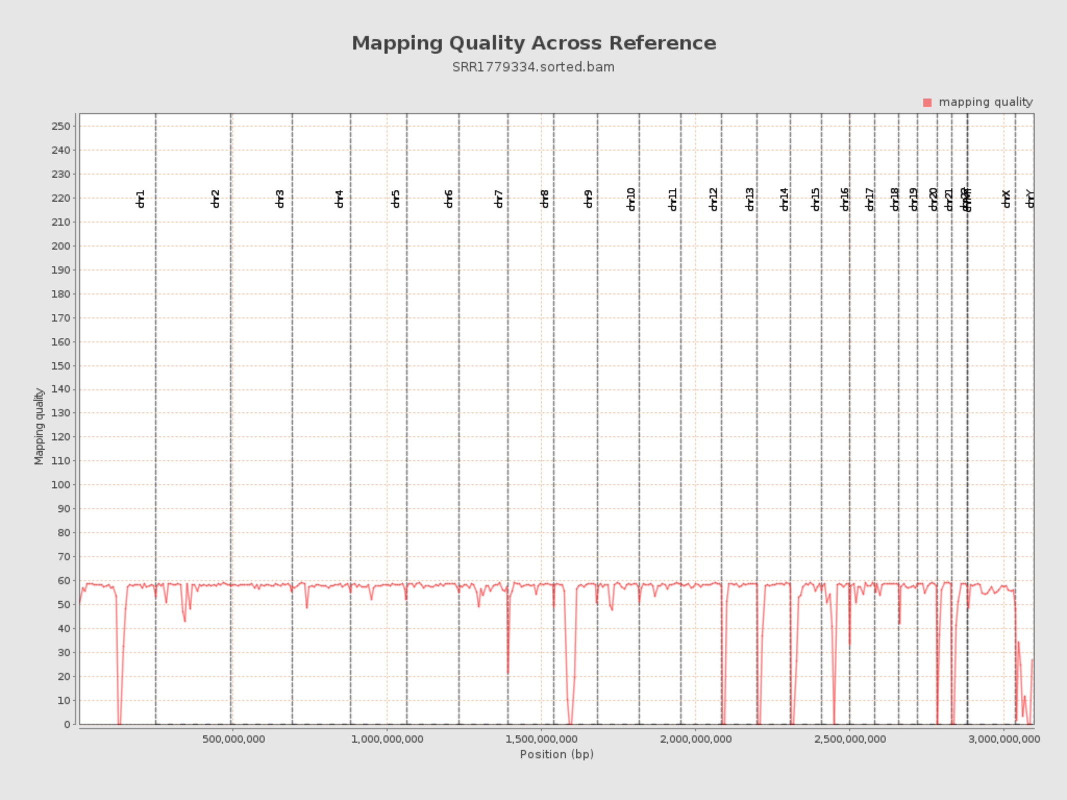
10. Results : Mapped Reads Clipping Profile



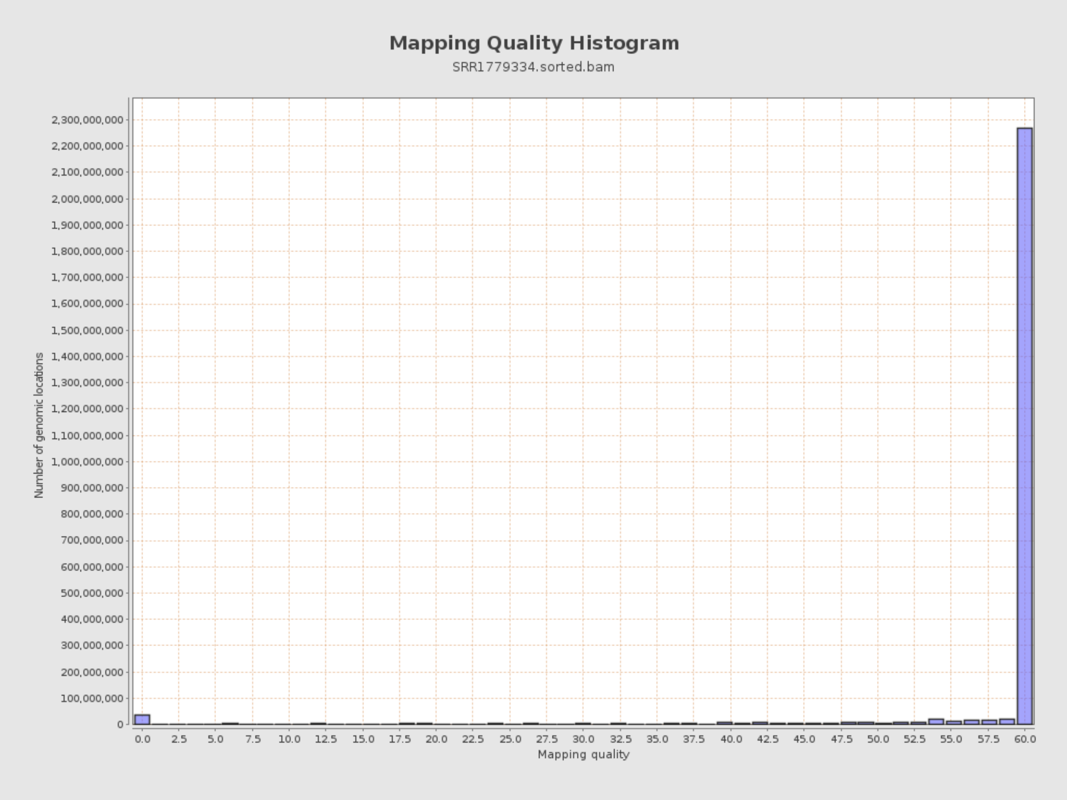
11. Results : Homopolymer Indels



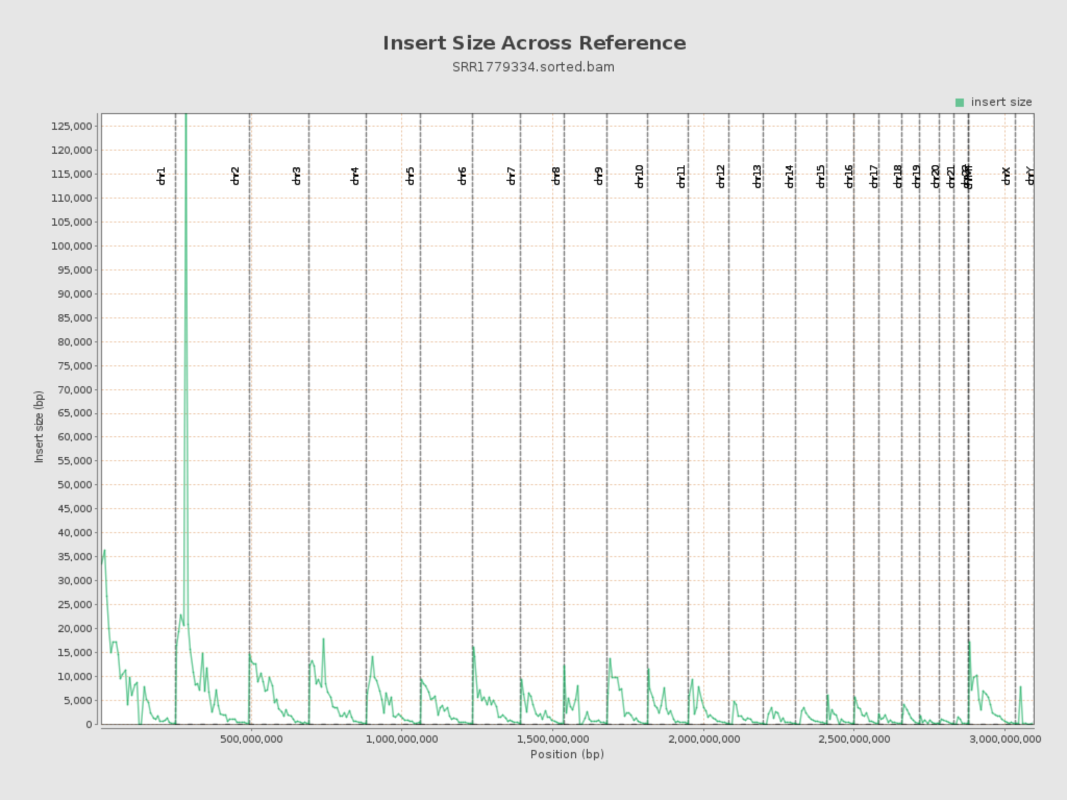
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram