Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/29 03:44:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779333.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_SRR1779333 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779333_1.fastq.gz SRR1779333_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 29 03:44:48 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779333.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	131,025,486
Mapped reads	126,308,150 / 96.4%
Unmapped reads	4,717,336 / 3.6%
Mapped paired reads	126,308,150 / 96.4%
Mapped reads, first in pair	63,856,213 / 48.74%
Mapped reads, second in pair	62,451,937 / 47.66%
Mapped reads, both in pair	124,153,596 / 94.76%
Mapped reads, singletons	2,154,554 / 1.64%
Secondary alignments	0
Supplementary alignments	525,155 / 0.4%
Read min/max/mean length	30 / 100 / 100.05
Duplicated reads (estimated)	7,679,530 / 5.86%
Duplication rate	5.79%
Clipped reads	6,140,508 / 4.69%

2.2. ACGT Content

Number/percentage of A's	3,698,479,469 / 29.53%
Number/percentage of C's	2,549,097,417 / 20.35%
Number/percentage of T's	3,680,279,584 / 29.39%
Number/percentage of G's	2,594,937,773 / 20.72%
Number/percentage of N's	798,575 / 0.01%

GC Percentage	41.07%

2.3. Coverage

Mean	4.0464
Standard Deviation	6.8896

2.4. Mapping Quality

Mean Mapping Quality	53.99

2.5. Insert size

Mean	55,015.25
Standard Deviation	2,363,281.71
P25/Median/P75	185 / 240 / 312

2.6. Mismatches and indels

General error rate	0.38%
Mismatches	45,727,110
Insertions	1,320,076
Mapped reads with at least one insertion	1.03%
Deletions	1,324,061
Mapped reads with at least one deletion	1.03%
Homopolymer indels	48.2%

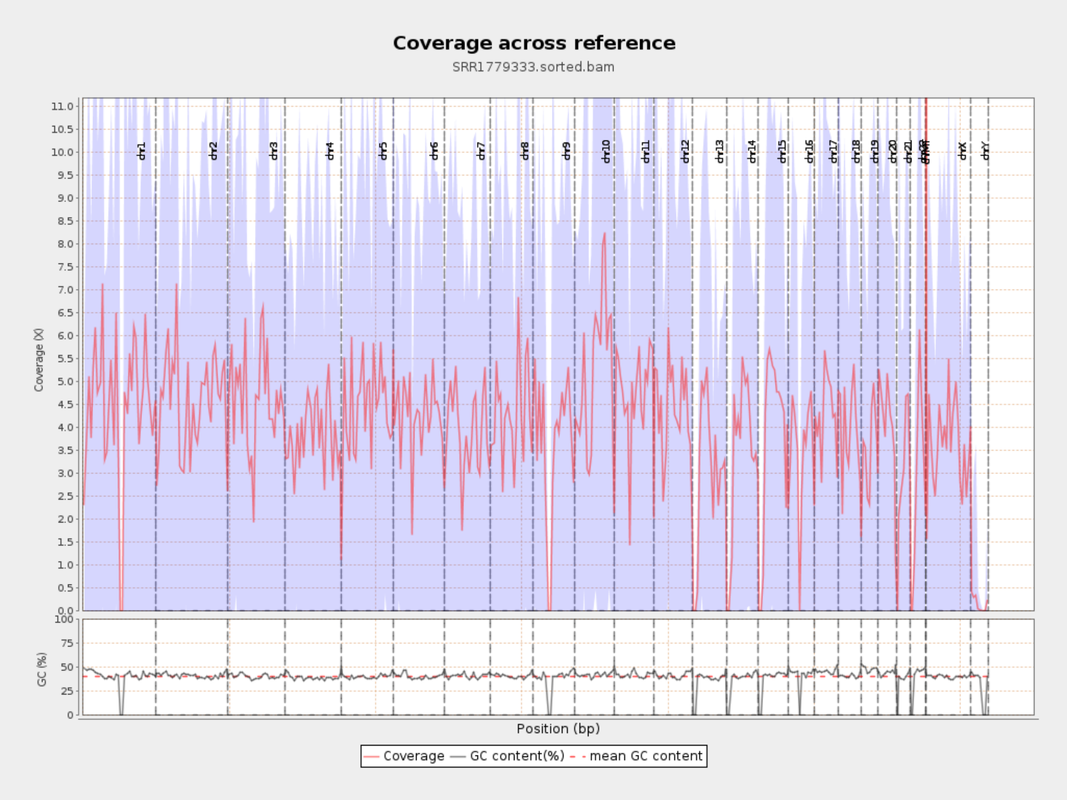
2.7. Chromosome stats

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

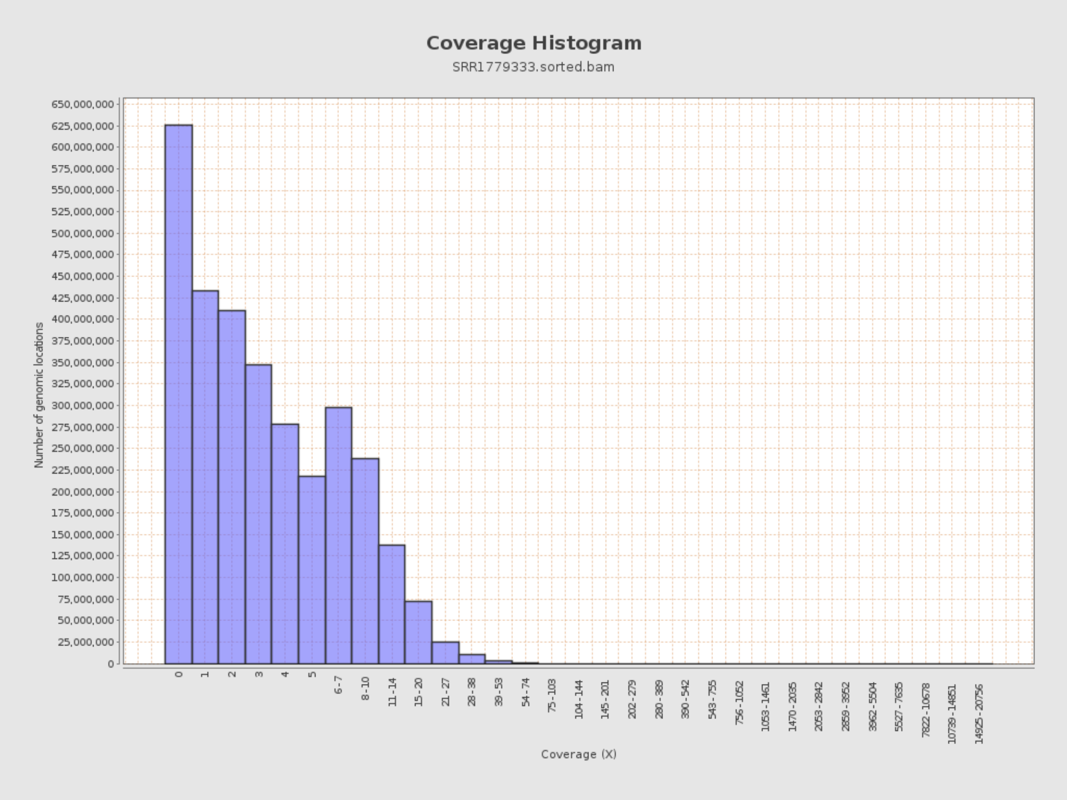
		bases	coverage	deviation
chr1	249250621	1111324973	4.4587	6.9209
chr2	243199373	1115963042	4.5887	17.0939
chr3	198022430	905370500	4.5721	5.0183
chr4	191154276	738396631	3.8628	4.4542
chr5	180915260	805534279	4.4526	4.8727
chr6	171115067	727613863	4.2522	4.6923
chr7	159138663	617681570	3.8814	4.6396
chr8	146364022	627911247	4.2901	4.8573
chr9	141213431	516078765	3.6546	4.9146
chr10	135534747	717743192	5.2956	6.549
chr11	135006516	636880332	4.7174	5.2574
chr12	133851895	596844169	4.459	5.6952
chr13	115169878	345247700	2.9977	3.9971
chr14	107349540	371565316	3.4613	4.3549
chr15	102531392	380036603	3.7065	4.7533
chr16	90354753	308036029	3.4092	4.3455
chr17	81195210	354861343	4.3705	5.3838
chr18	78077248	310789565	3.9805	4.9959
chr19	59128983	205707904	3.479	5.2214
chr20	63025520	263938904	4.1878	5.0003
chr21	48129895	145896507	3.0313	5.0762
chr22	51304566	151695312	2.9568	4.7897
chrMT	16571	1879740	113.4355	26.8618
chrX	155270560	560552375	3.6102	4.3314

chrY	59373566	8980243	0.1512	1.6983

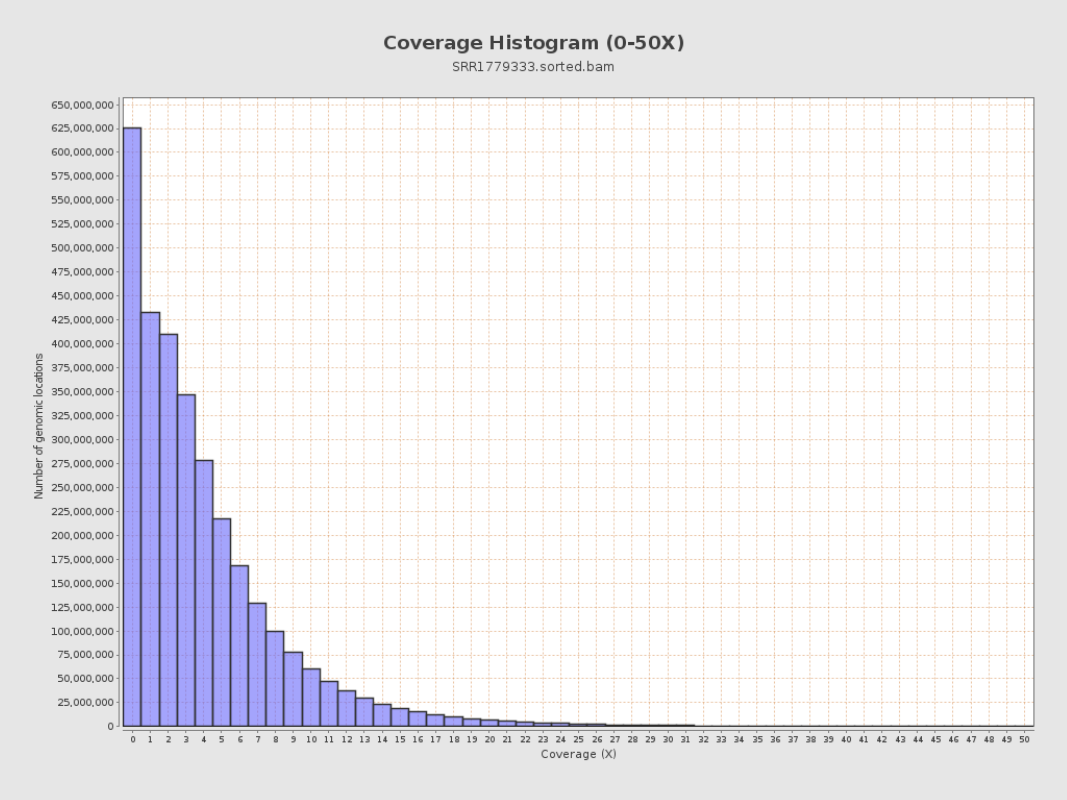
3. Results : Coverage across reference



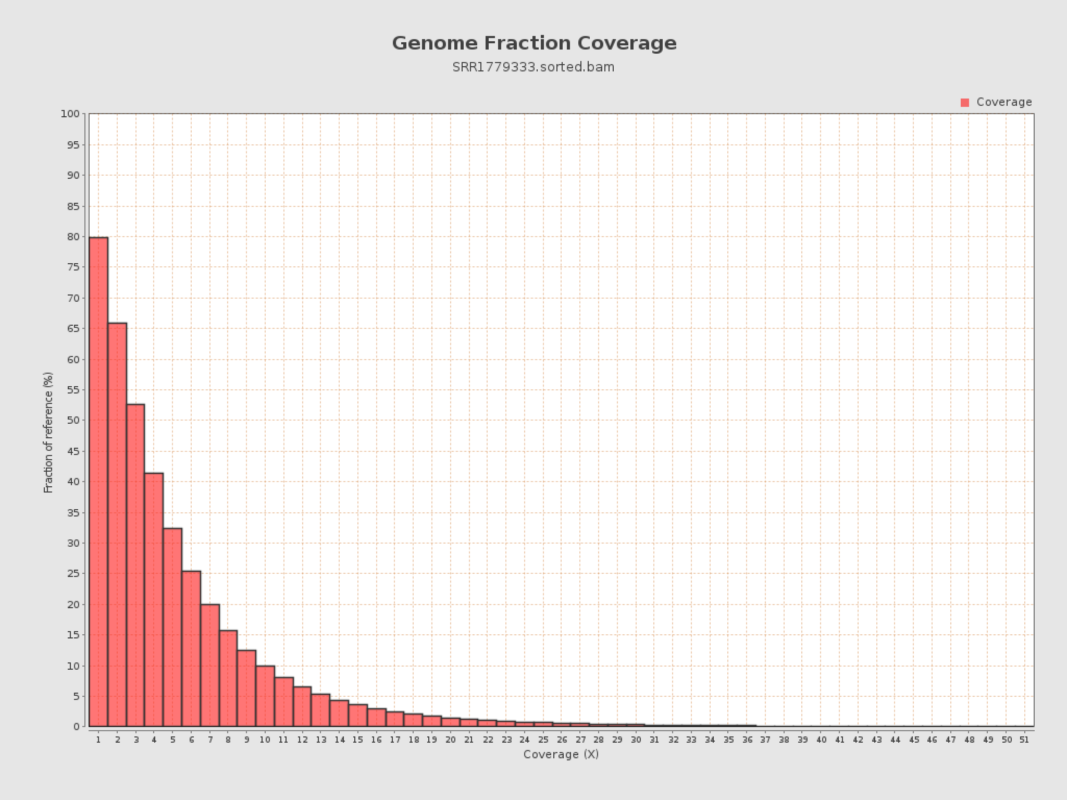
4. Results : Coverage Histogram



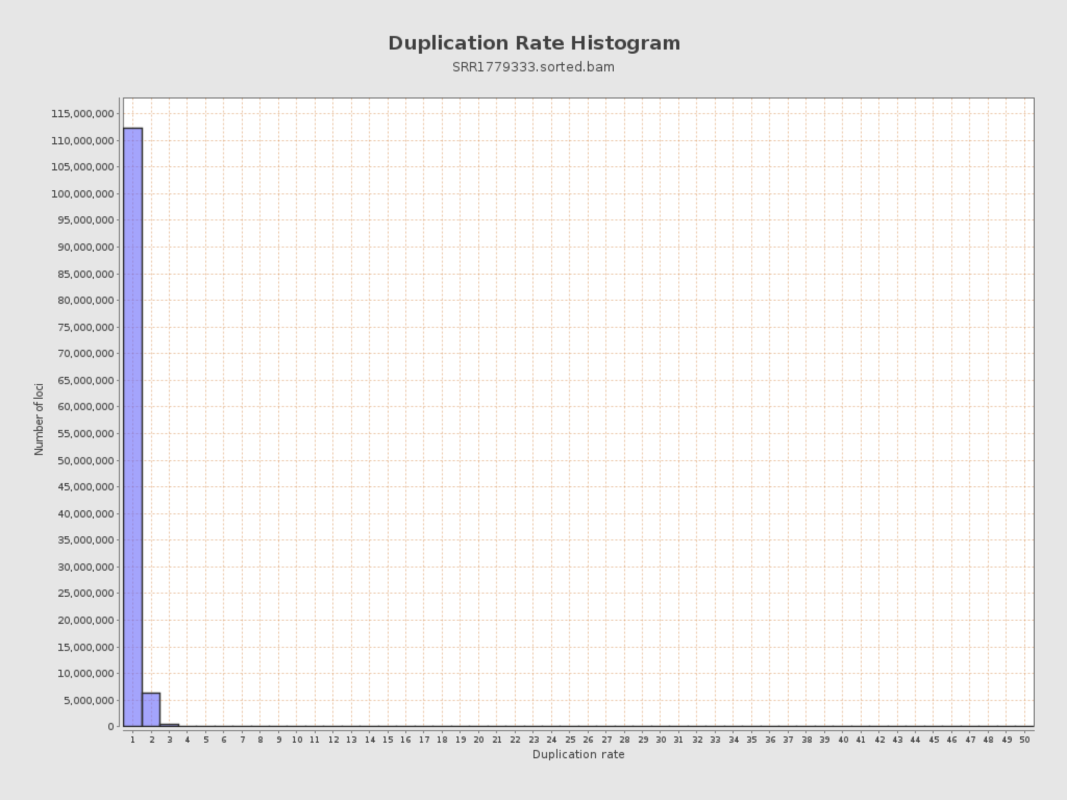
5. Results : Coverage Histogram (0-50X)



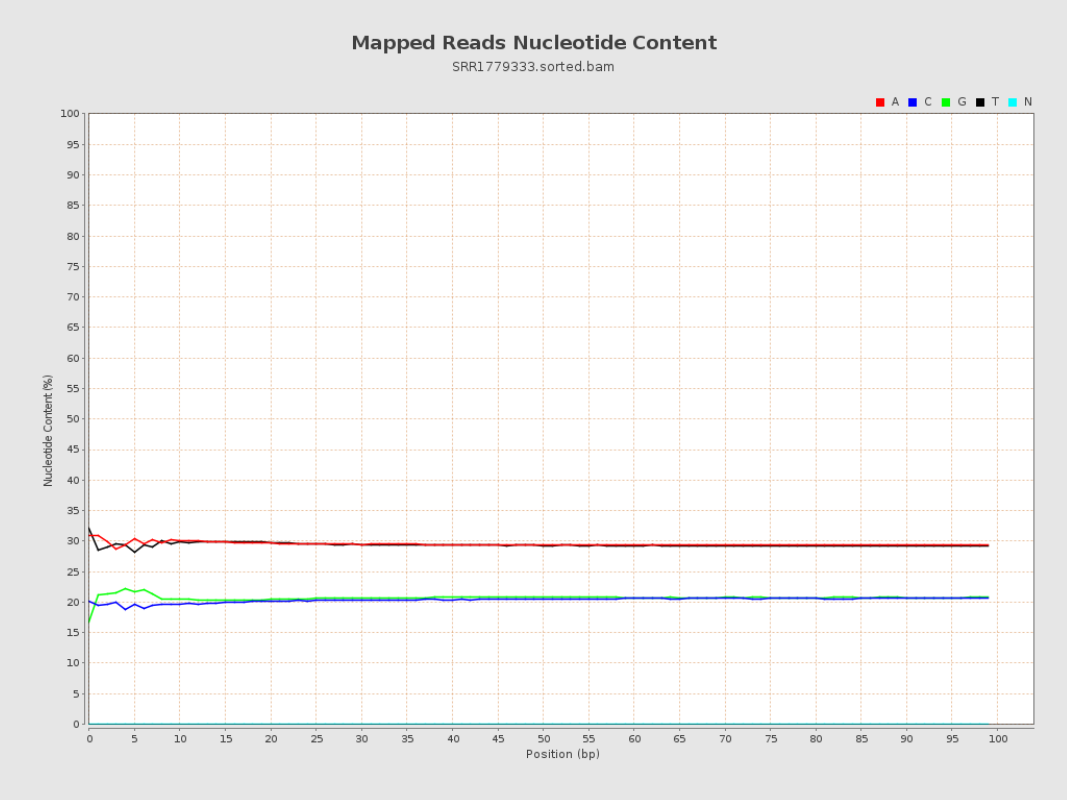
6. Results : Genome Fraction Coverage



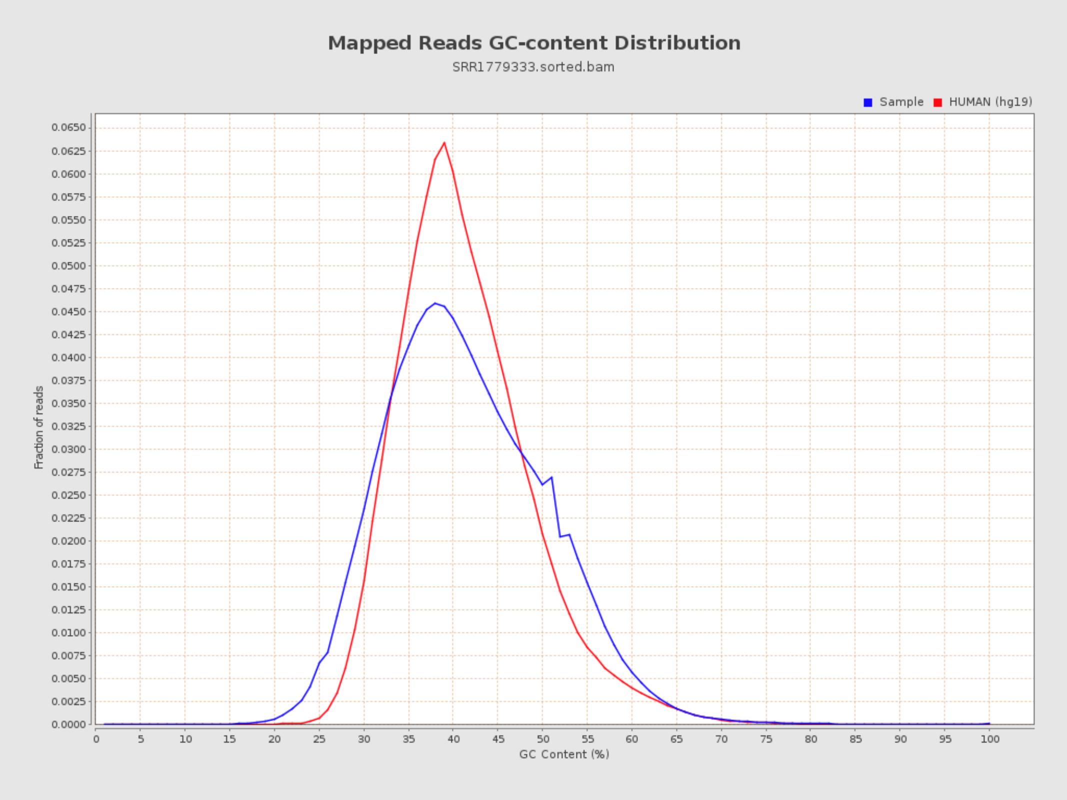
7. Results : Duplication Rate Histogram



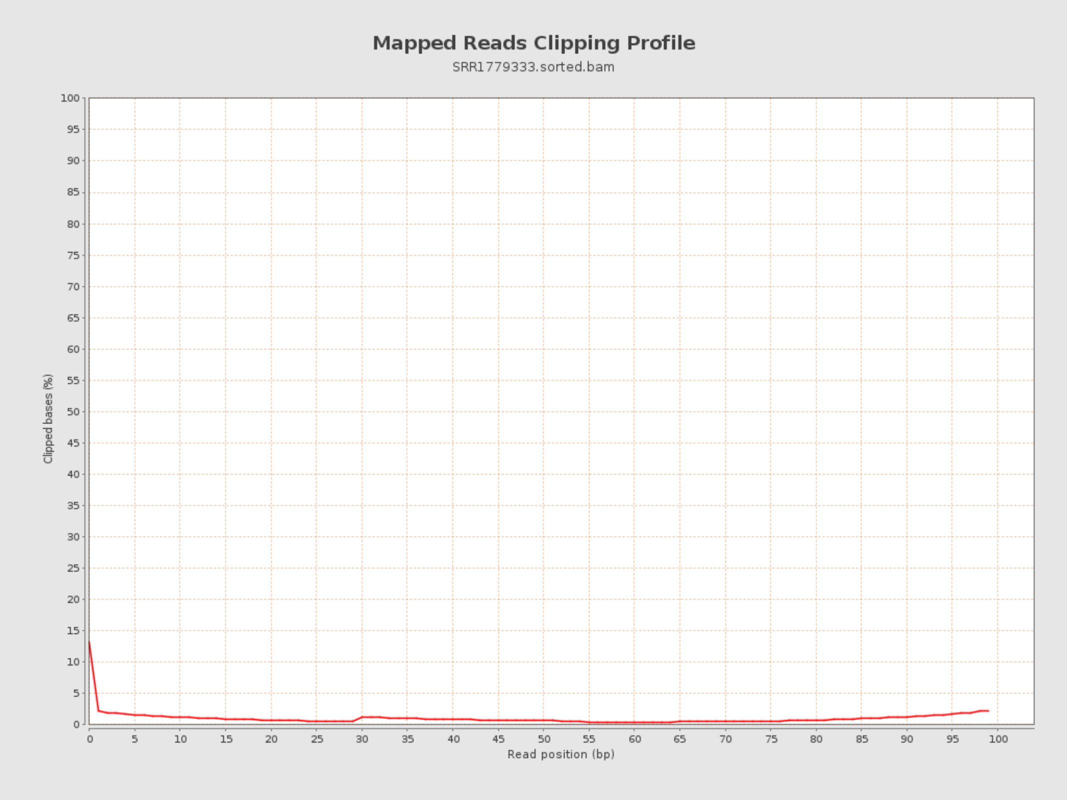
8. Results : Mapped Reads Nucleotide Content



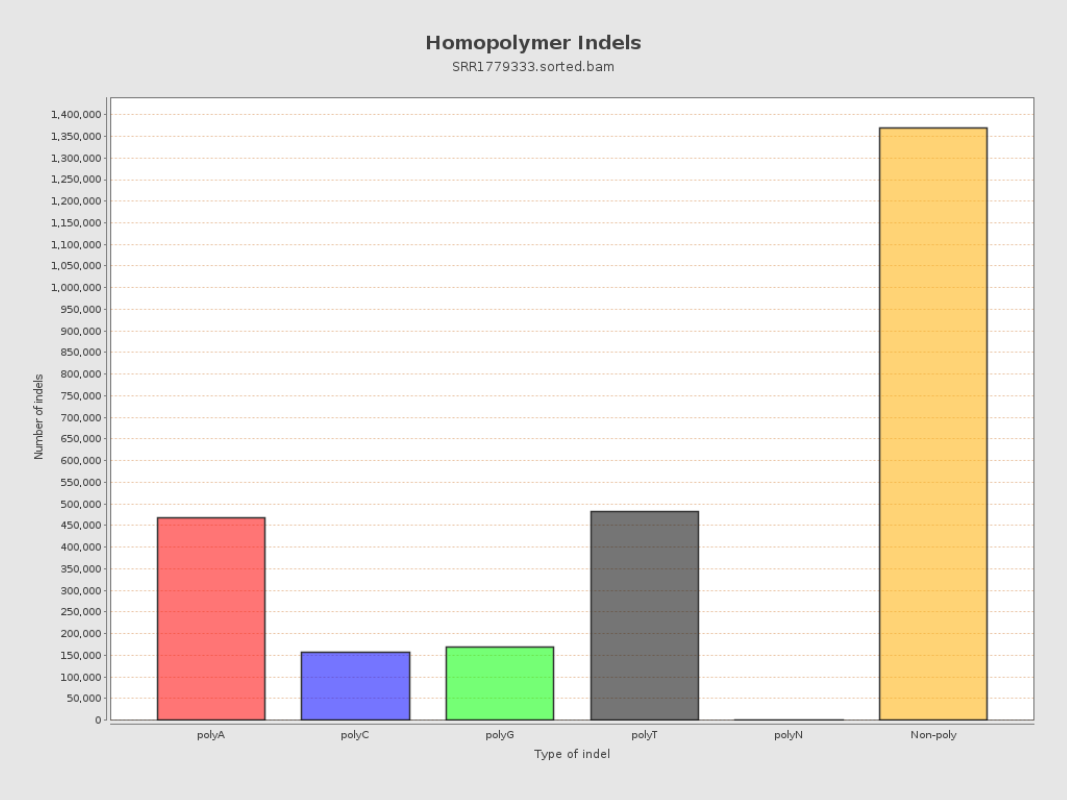
9. Results : Mapped Reads GC-content Distribution



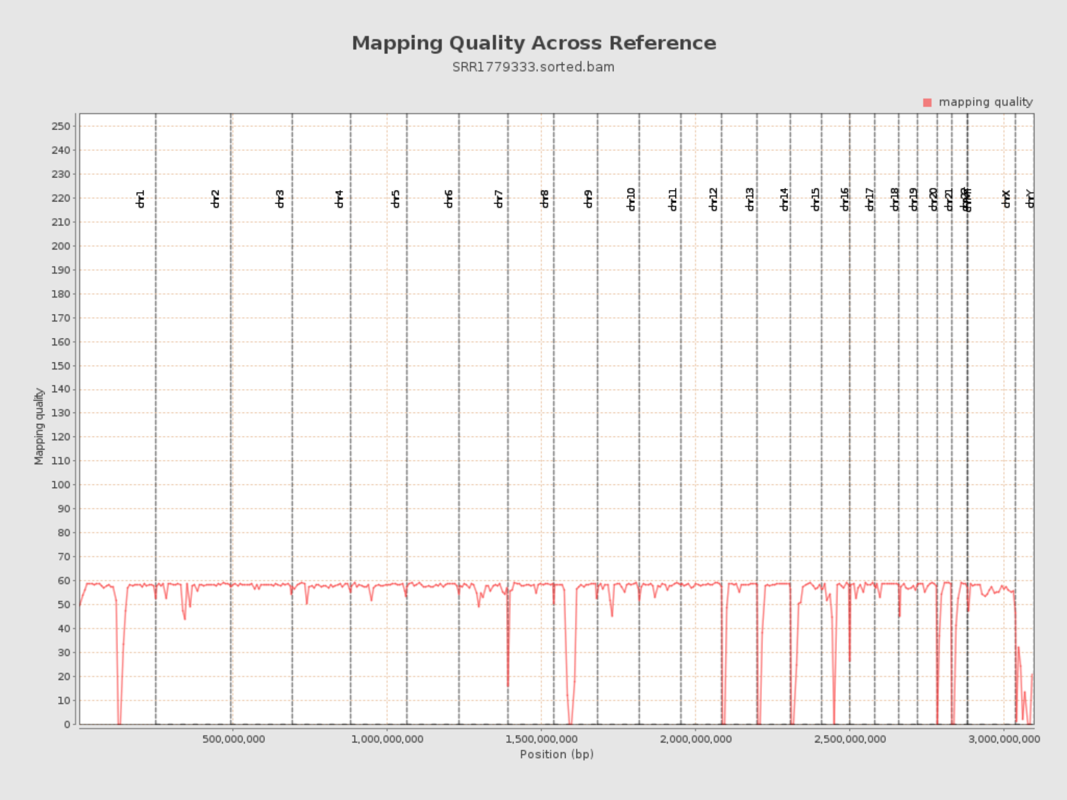
10. Results : Mapped Reads Clipping Profile



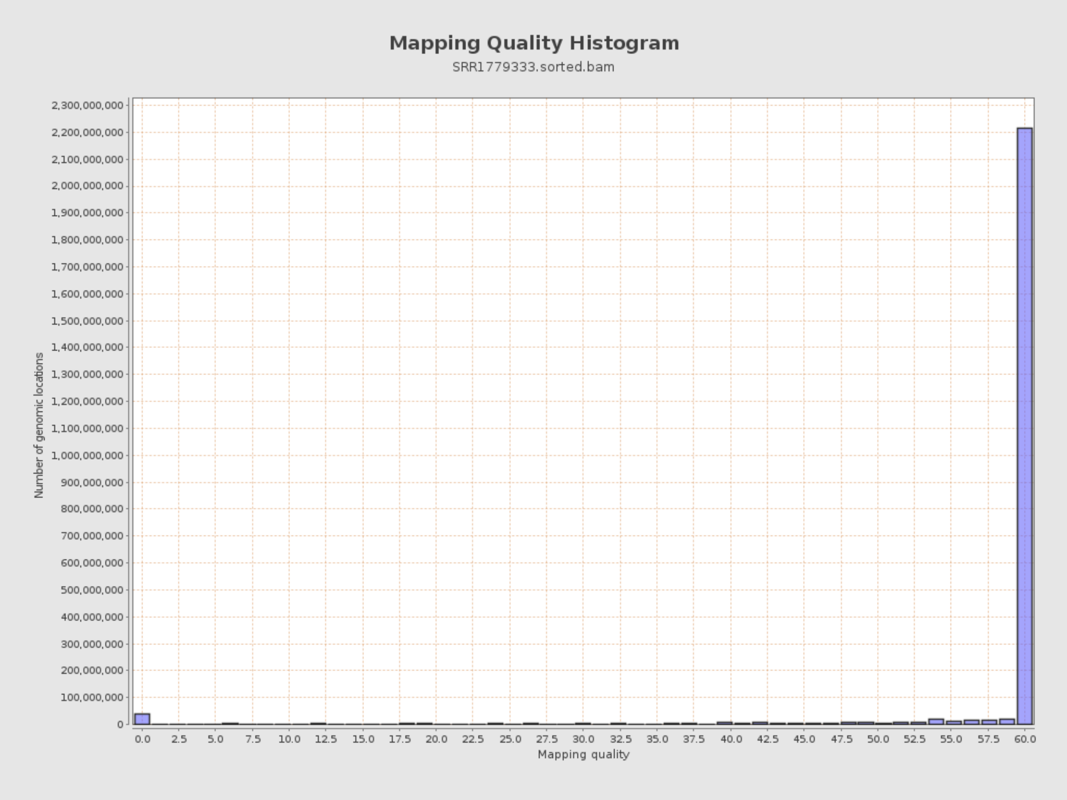
11. Results : Homopolymer Indels



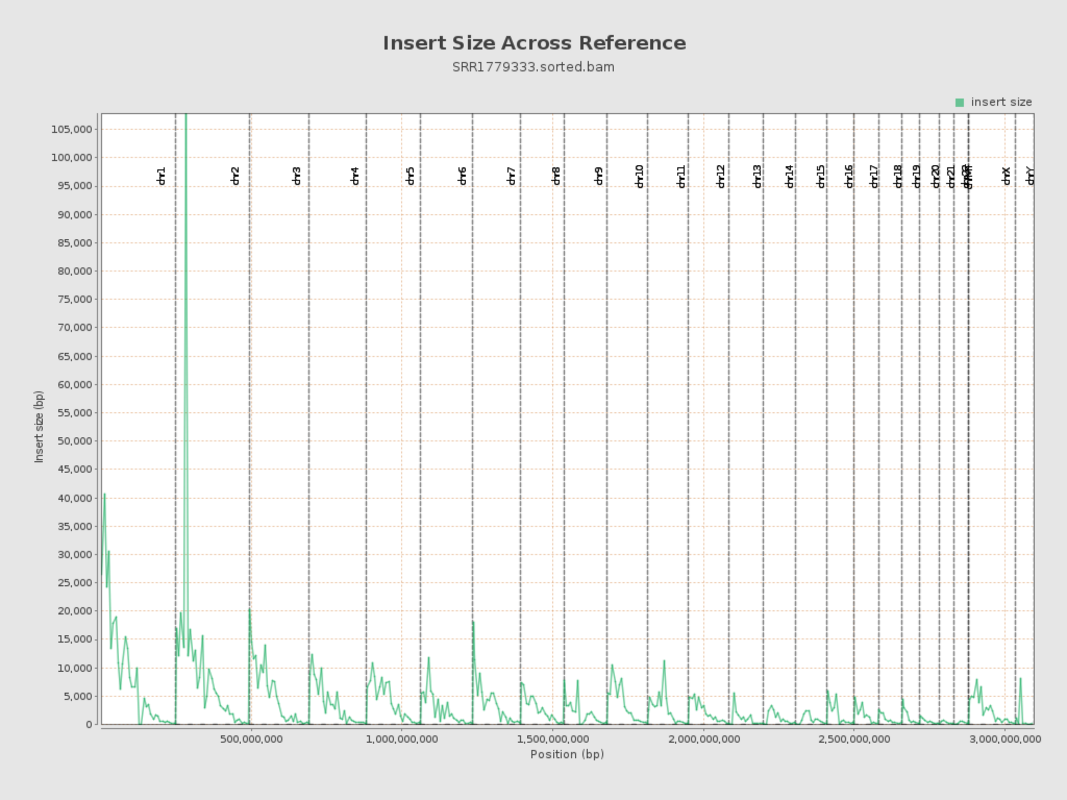
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram