Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 15:50:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779386.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_SRR1779386 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779386_1.fastq.gz SRR1779386_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 15:50:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779386.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,770,384
Mapped reads	13,178,274 / 95.7%
Unmapped reads	592,110 / 4.3%
Mapped paired reads	13,178,274 / 95.7%
Mapped reads, first in pair	6,634,595 / 48.18%
Mapped reads, second in pair	6,543,679 / 47.52%
Mapped reads, both in pair	13,061,226 / 94.85%
Mapped reads, singletons	117,048 / 0.85%
Secondary alignments	0
Supplementary alignments	51,156 / 0.37%
Read min/max/mean length	30 / 80 / 80.14
Duplicated reads (estimated)	585,478 / 4.25%
Duplication rate	4.12%
Clipped reads	581,294 / 4.22%

2.2. ACGT Content

Number/percentage of A's	313,409,218 / 29.92%
Number/percentage of C's	209,051,600 / 19.96%
Number/percentage of T's	312,371,015 / 29.82%
Number/percentage of G's	212,333,427 / 20.27%
Number/percentage of N's	237,011 / 0.02%

GC Percentage	40.23%

2.3. Coverage

Mean	0.3384
Standard Deviation	1.6148

2.4. Mapping Quality

Mean Mapping Quality	52.71

2.5. Insert size

Mean	33,417.68
Standard Deviation	1,687,635.01
P25/Median/P75	139 / 182 / 235

2.6. Mismatches and indels

General error rate	0.33%
Mismatches	3,337,555
Insertions	93,575
Mapped reads with at least one insertion	0.7%
Deletions	108,552
Mapped reads with at least one deletion	0.81%
Homopolymer indels	47.19%

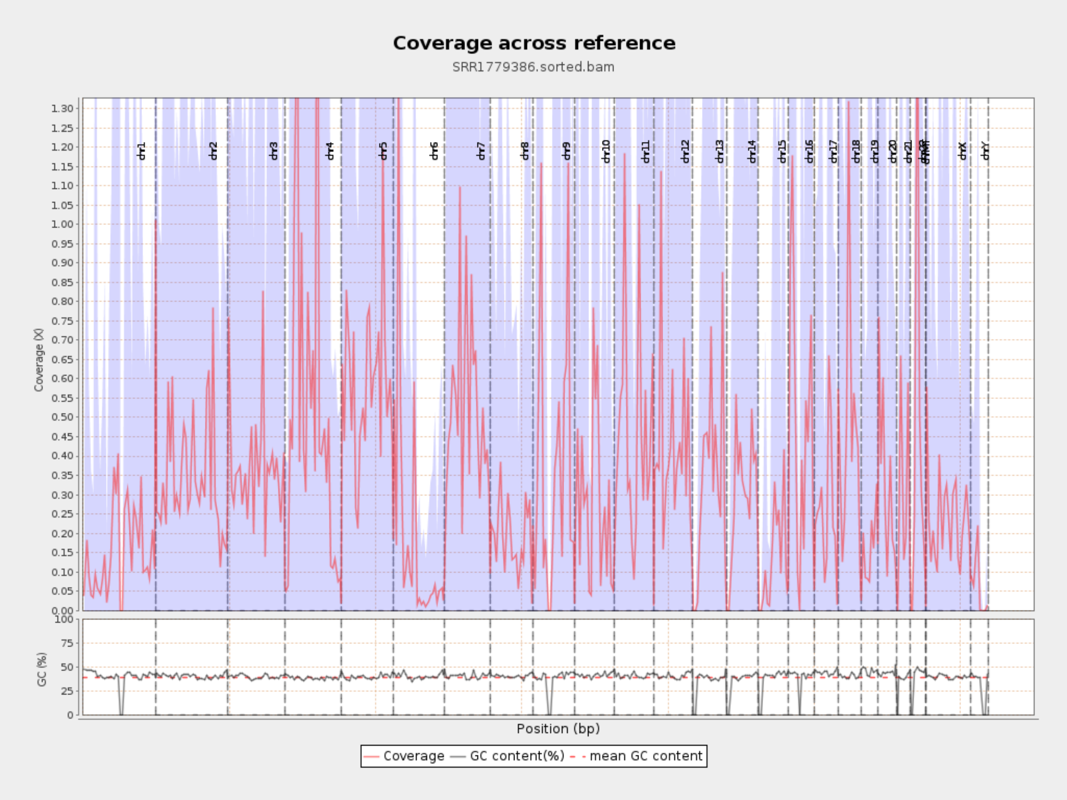
2.7. Chromosome stats

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

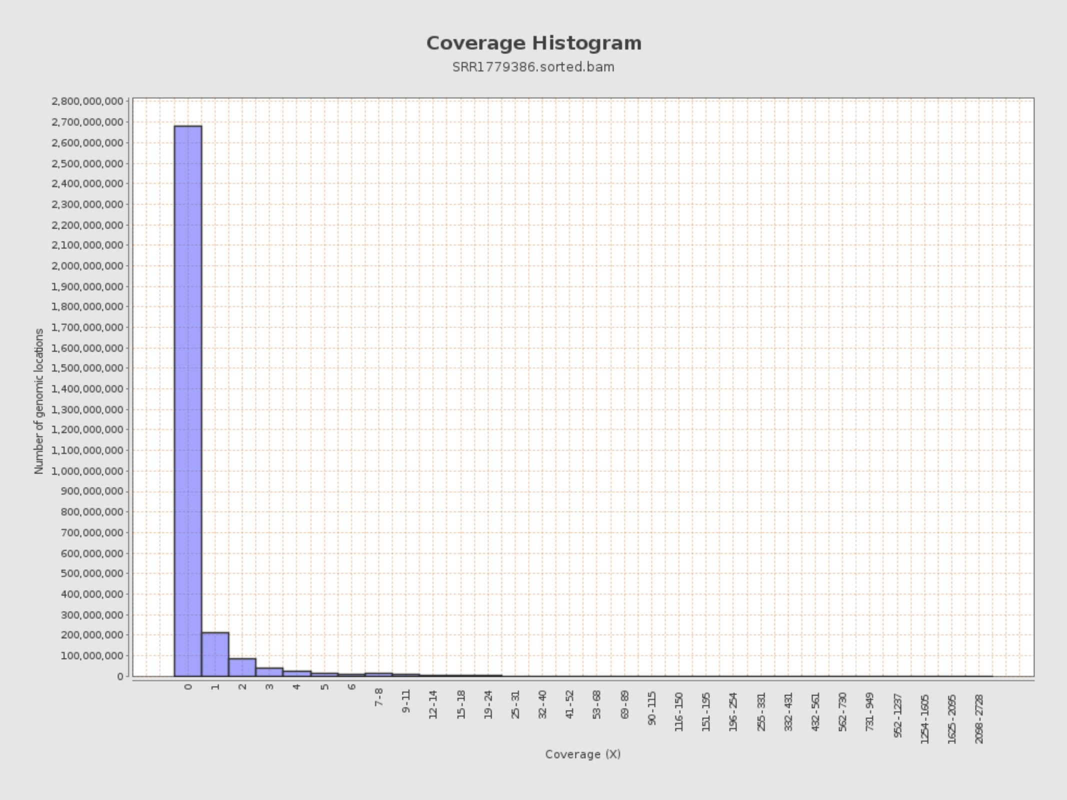
		bases	**coverage**	**deviation**
chr1	249250621	38413073	0.1541	2.821
chr2	243199373	84675744	0.3482	1.1856
chr3	198022430	73632640	0.3718	1.1675
chr4	191154276	101391158	0.5304	1.8519
chr5	180915260	105157510	0.5813	1.6687
chr6	171115067	30515518	0.1783	1.1443
chr7	159138663	82501305	0.5184	1.6185
chr8	146364022	28195658	0.1926	0.854
chr9	141213431	53572363	0.3794	1.605
chr10	135534747	38722078	0.2857	2.0523
chr11	135006516	61266660	0.4538	1.6012
chr12	133851895	57502735	0.4296	1.5699
chr13	115169878	38707731	0.3361	1.1376
chr14	107349540	32783825	0.3054	1.2917
chr15	102531392	13836656	0.135	0.8113
chr16	90354753	42123724	0.4662	2.2233
chr17	81195210	22120482	0.2724	1.089
chr18	78077248	36337715	0.4654	1.6406
chr19	59128983	9469415	0.1601	1.568
chr20	63025520	20721247	0.3288	1.5128
chr21	48129895	13663607	0.2839	1.2442
chr22	51304566	22542065	0.4394	2.0597
chrMT	16571	160	0.0097	0.0978
chrX	155270560	35879191	0.2311	0.9973

chrY	59373566	3896879	0.0656	0.5092

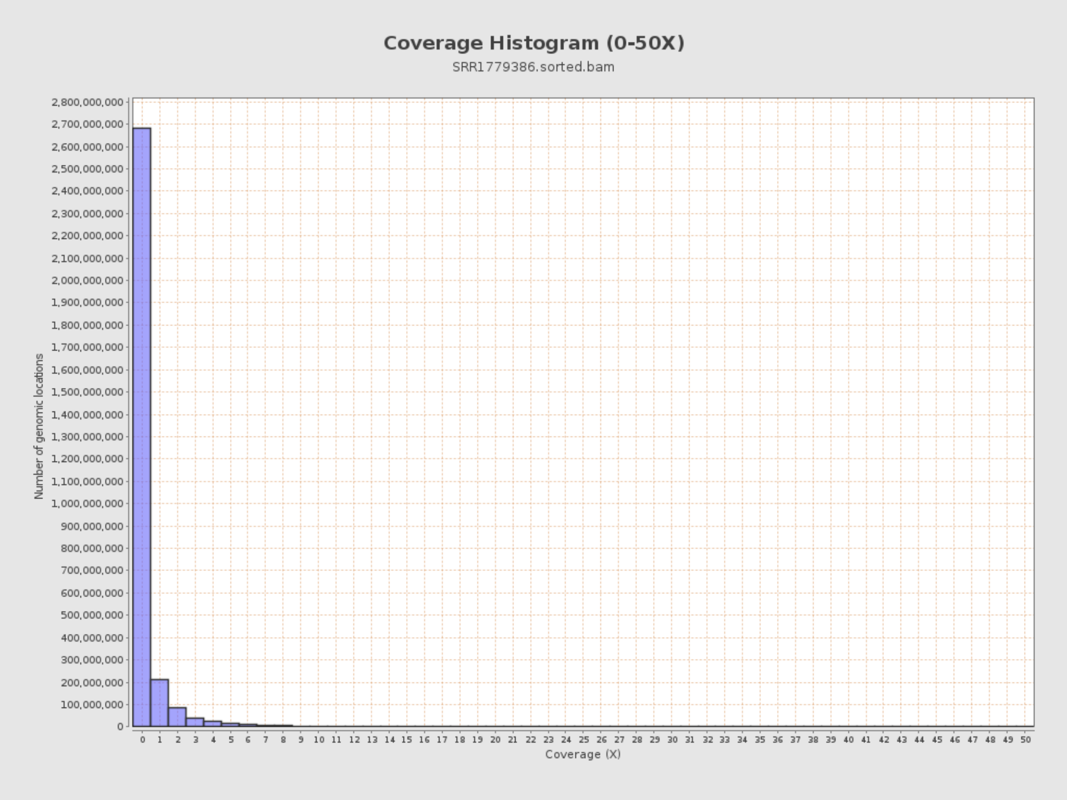
3. Results : Coverage across reference



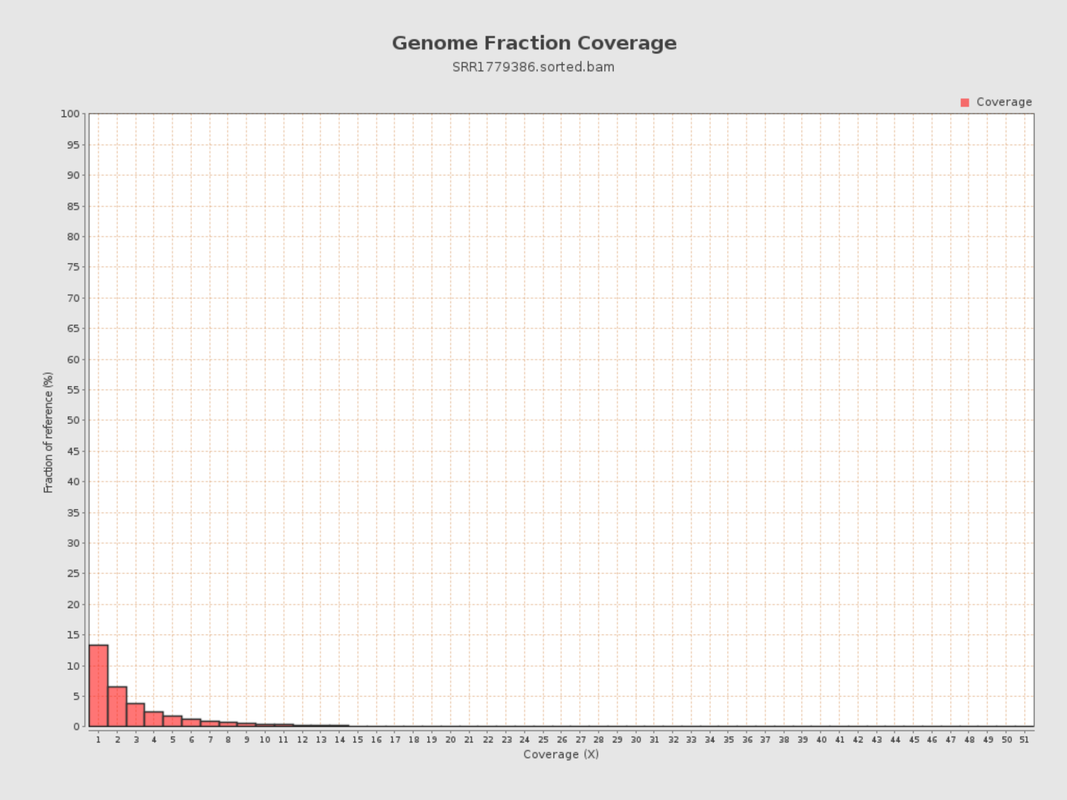
4. Results : Coverage Histogram



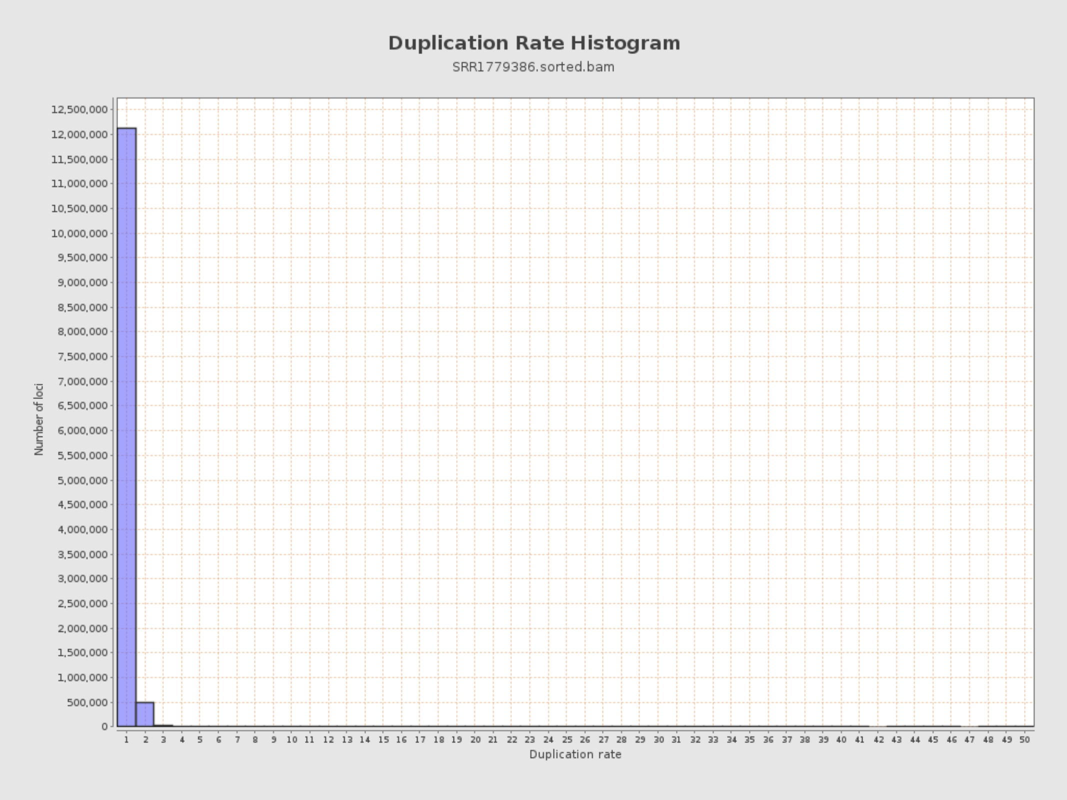
5. Results : Coverage Histogram (0-50X)



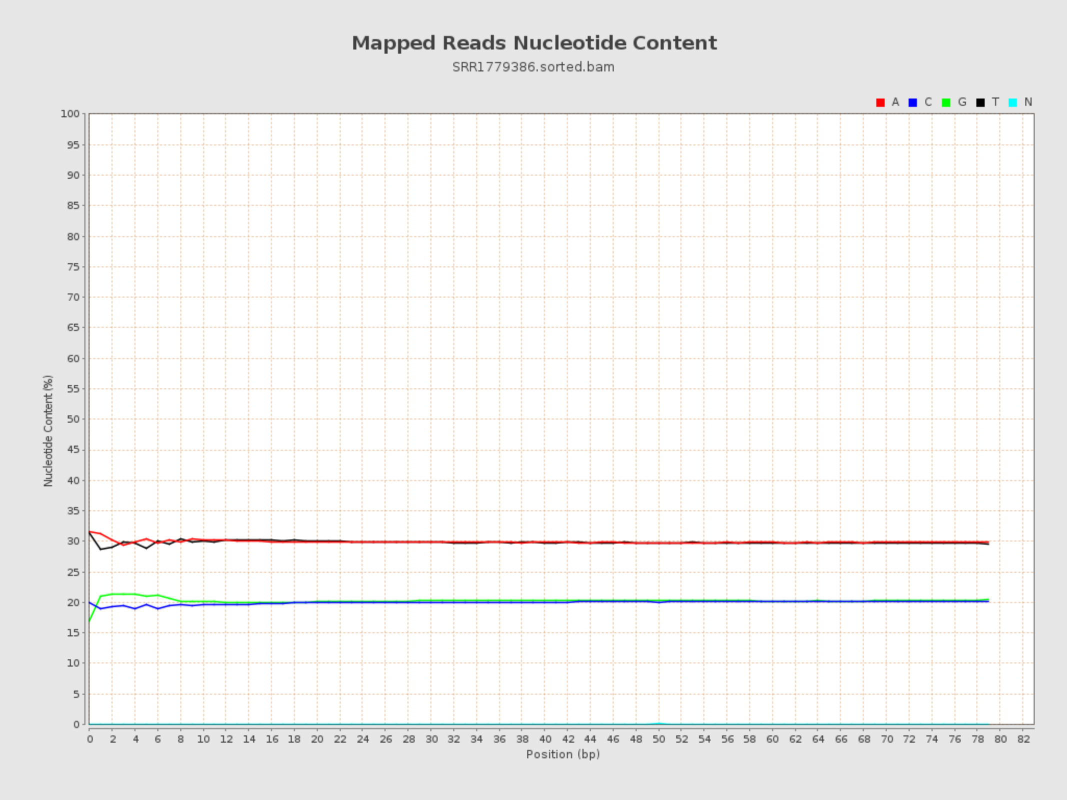
6. Results : Genome Fraction Coverage



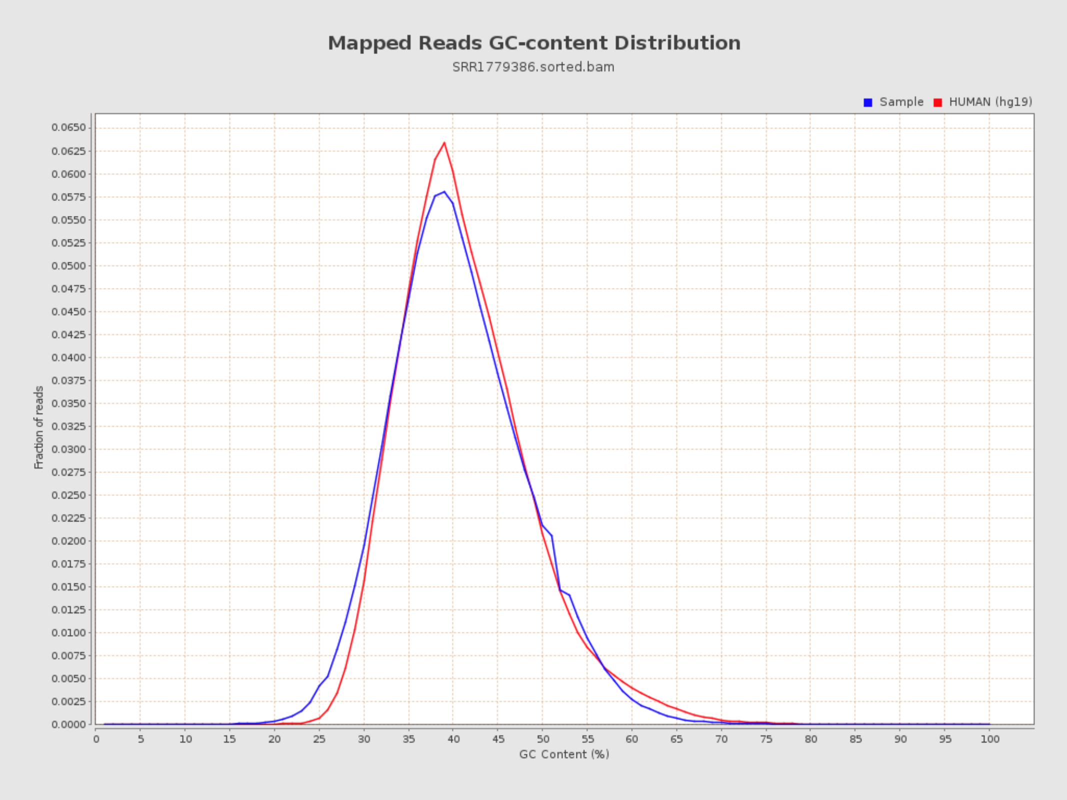
7. Results : Duplication Rate Histogram



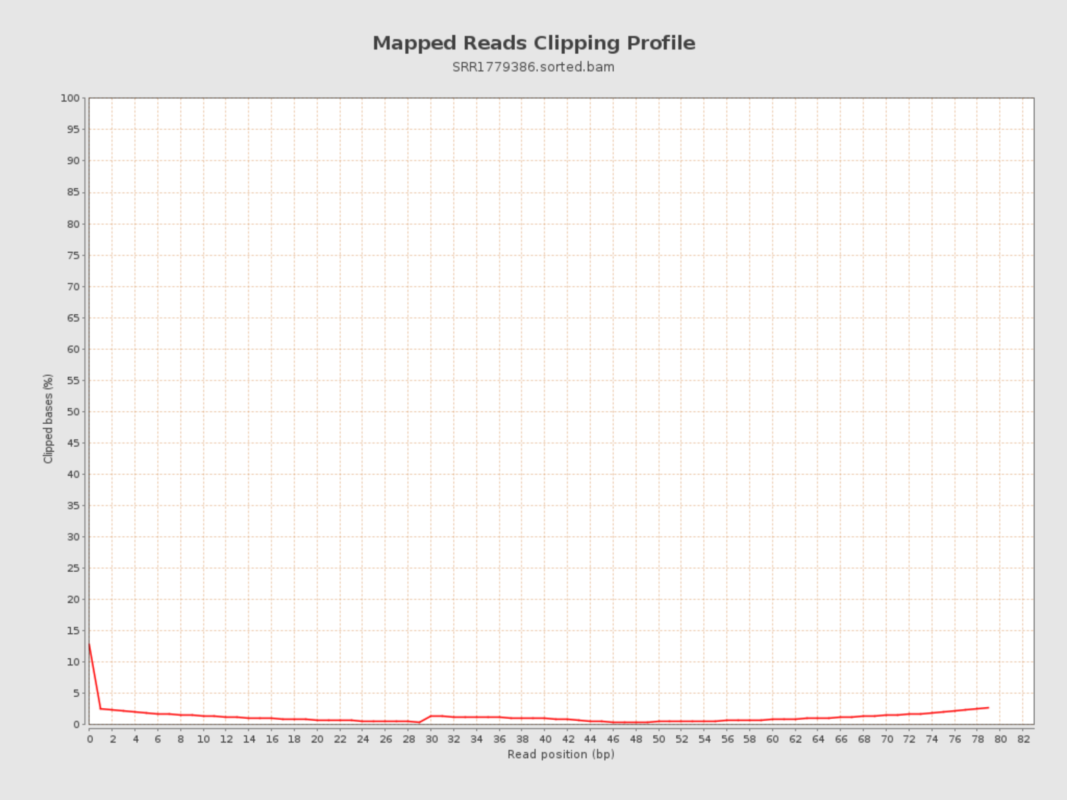
8. Results : Mapped Reads Nucleotide Content



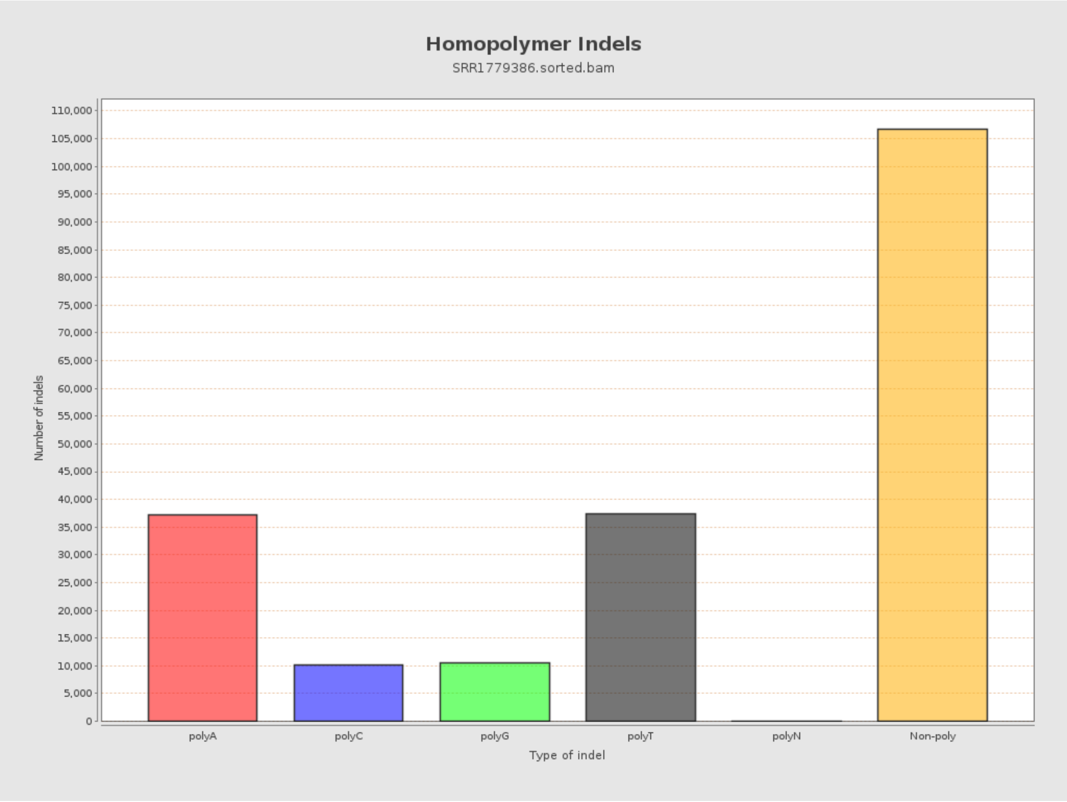
9. Results : Mapped Reads GC-content Distribution



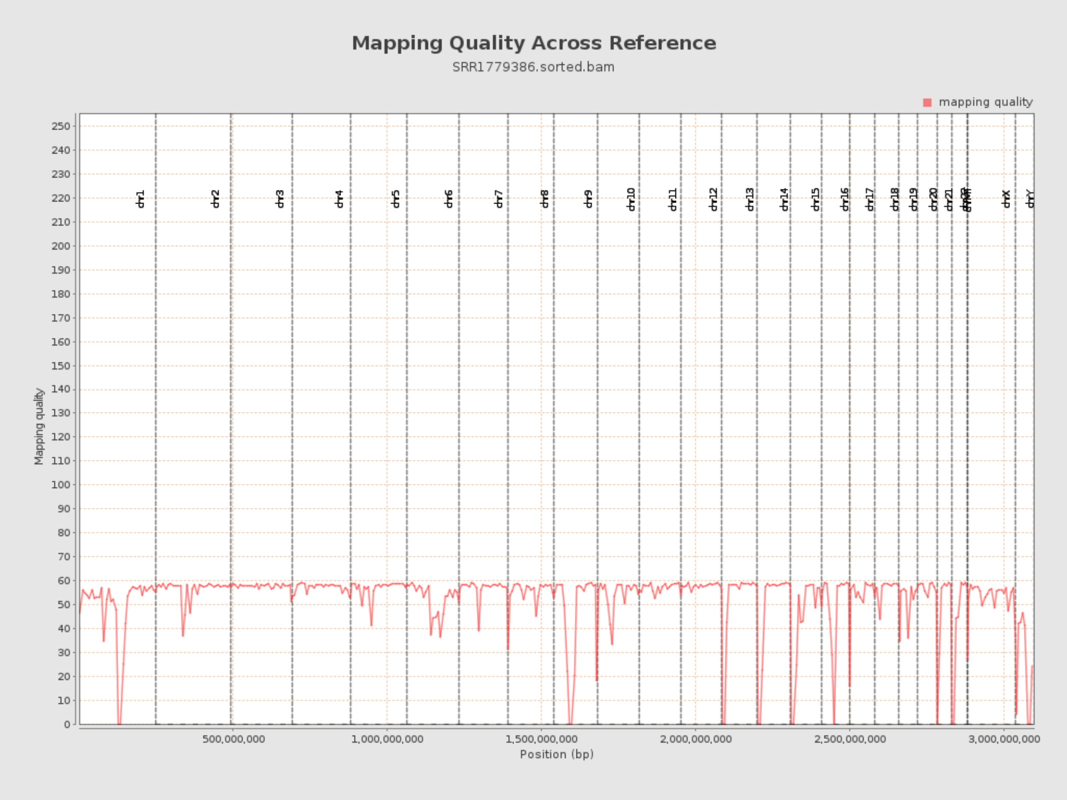
10. Results : Mapped Reads Clipping Profile



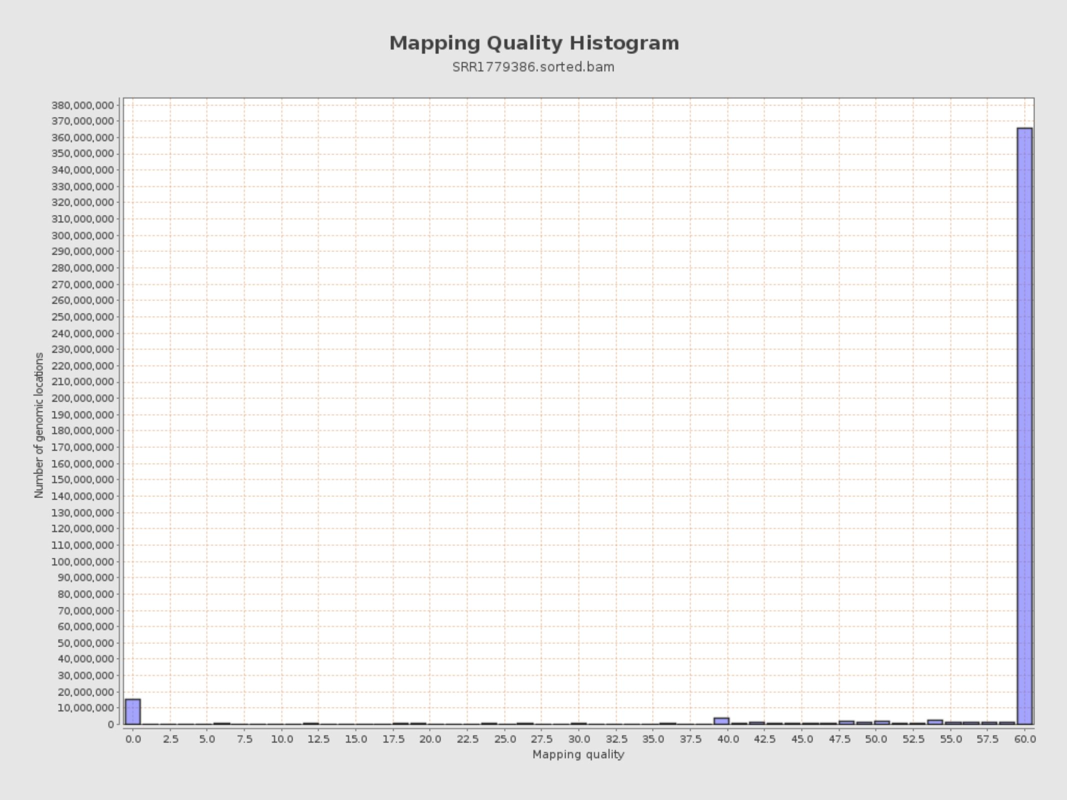
11. Results : Homopolymer Indels



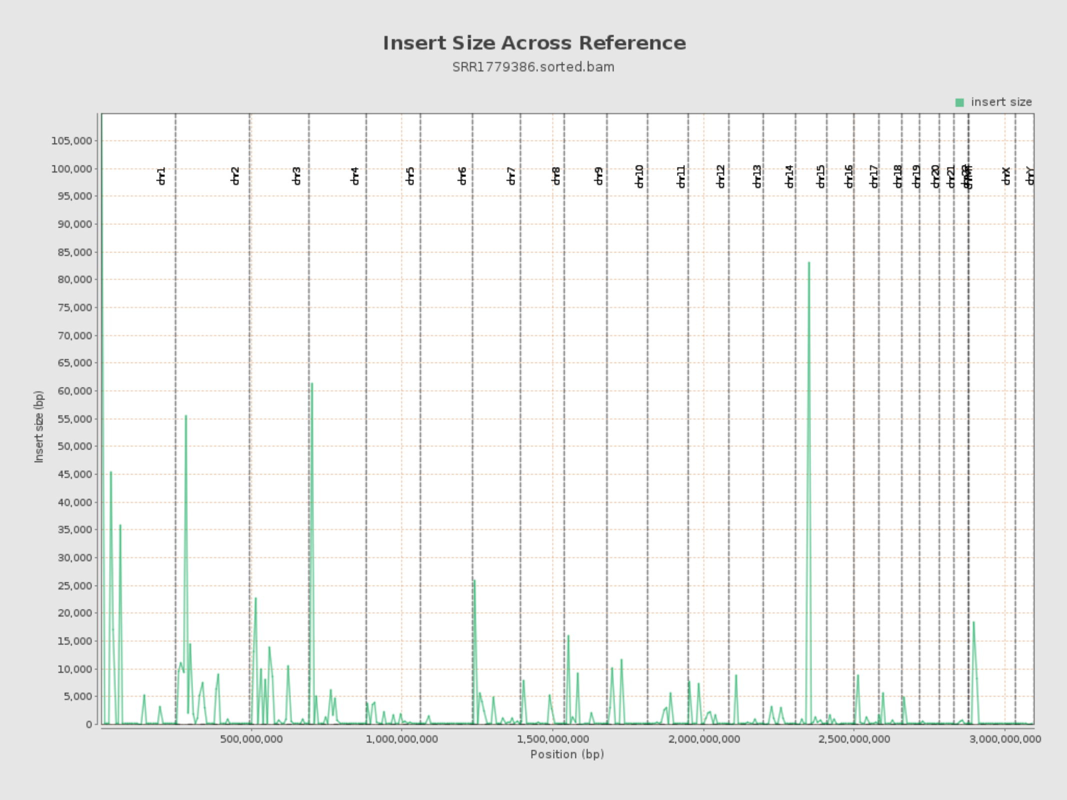
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram