Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 08:27:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779316.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_SRR1779316 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779316_1.fastq.gz SRR1779316_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 08:27:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779316.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,282,076
Mapped reads	14,120,986 / 92.4%
Unmapped reads	1,161,090 / 7.6%
Mapped paired reads	14,120,986 / 92.4%
Mapped reads, first in pair	7,150,322 / 46.79%
Mapped reads, second in pair	6,970,664 / 45.61%
Mapped reads, both in pair	13,906,500 / 91%
Mapped reads, singletons	214,486 / 1.4%
Secondary alignments	0
Supplementary alignments	38,798 / 0.25%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	561,030 / 3.67%
Duplication rate	3.67%
Clipped reads	480,574 / 3.14%

2.2. ACGT Content

Number/percentage of A's	347,945,838 / 30.97%
Number/percentage of C's	211,725,751 / 18.85%
Number/percentage of T's	347,682,841 / 30.95%
Number/percentage of G's	215,678,455 / 19.2%
Number/percentage of N's	294,926 / 0.03%

GC Percentage	38.05%

2.3. Coverage

Mean	0.3629
Standard Deviation	1.5993

2.4. Mapping Quality

Mean Mapping Quality	52.93

2.5. Insert size

Mean	37,418.89
Standard Deviation	1,822,244.4
P25/Median/P75	183 / 241 / 322

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	4,314,741
Insertions	83,010
Mapped reads with at least one insertion	0.58%
Deletions	106,539
Mapped reads with at least one deletion	0.74%
Homopolymer indels	47.34%

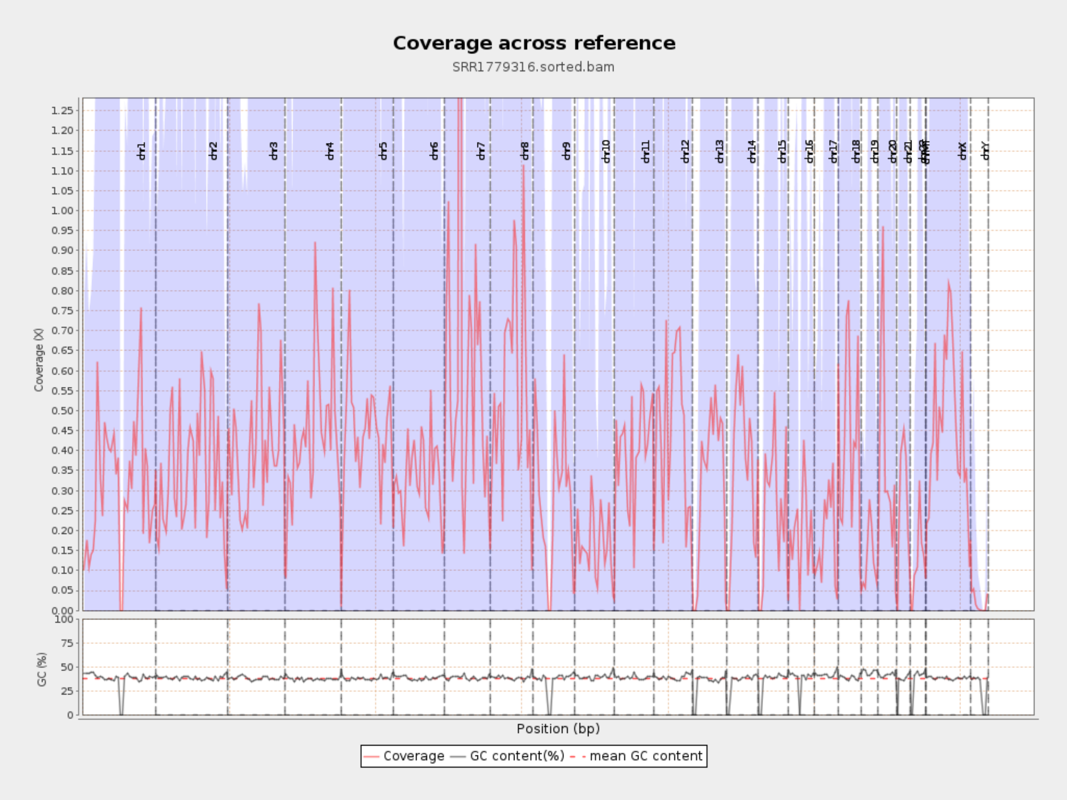
2.7. Chromosome stats

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

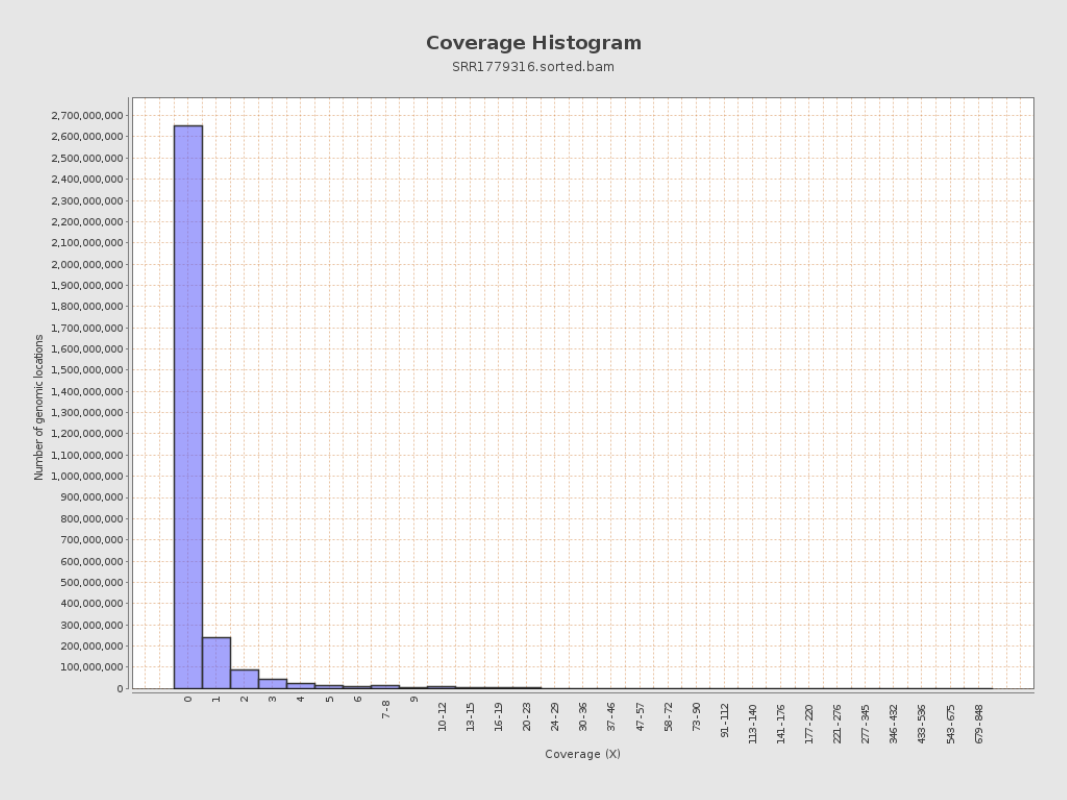
		bases	coverage	deviation
chr1	249250621	78331293	0.3143	1.5253
chr2	243199373	84571560	0.3477	1.3872
chr3	198022430	80596401	0.407	1.54
chr4	191154276	85421180	0.4469	1.8731
chr5	180915260	79248436	0.438	1.5426
chr6	171115067	57466304	0.3358	1.3937
chr7	159138663	103481245	0.6503	3.0097
chr8	146364022	82009898	0.5603	1.7422
chr9	141213431	41086873	0.291	1.2726
chr10	135534747	22792231	0.1682	1.2431
chr11	135006516	53904927	0.3993	1.6734
chr12	133851895	59582965	0.4451	1.8494
chr13	115169878	38706989	0.3361	1.3355
chr14	107349540	38206723	0.3559	1.3274
chr15	102531392	25877778	0.2524	1.1553
chr16	90354753	16992805	0.1881	0.9127
chr17	81195210	15131826	0.1864	1.0142
chr18	78077248	34378805	0.4403	1.8859
chr19	59128983	7930935	0.1341	0.9626
chr20	63025520	24669432	0.3914	1.6861
chr21	48129895	12775224	0.2654	1.0643
chr22	51304566	6580153	0.1283	1.0983
chrMT	16571	1677	0.1012	0.3447
chrX	155270560	72673398	0.468	1.6709

chrY	59373566	1130011	0.019	0.2659

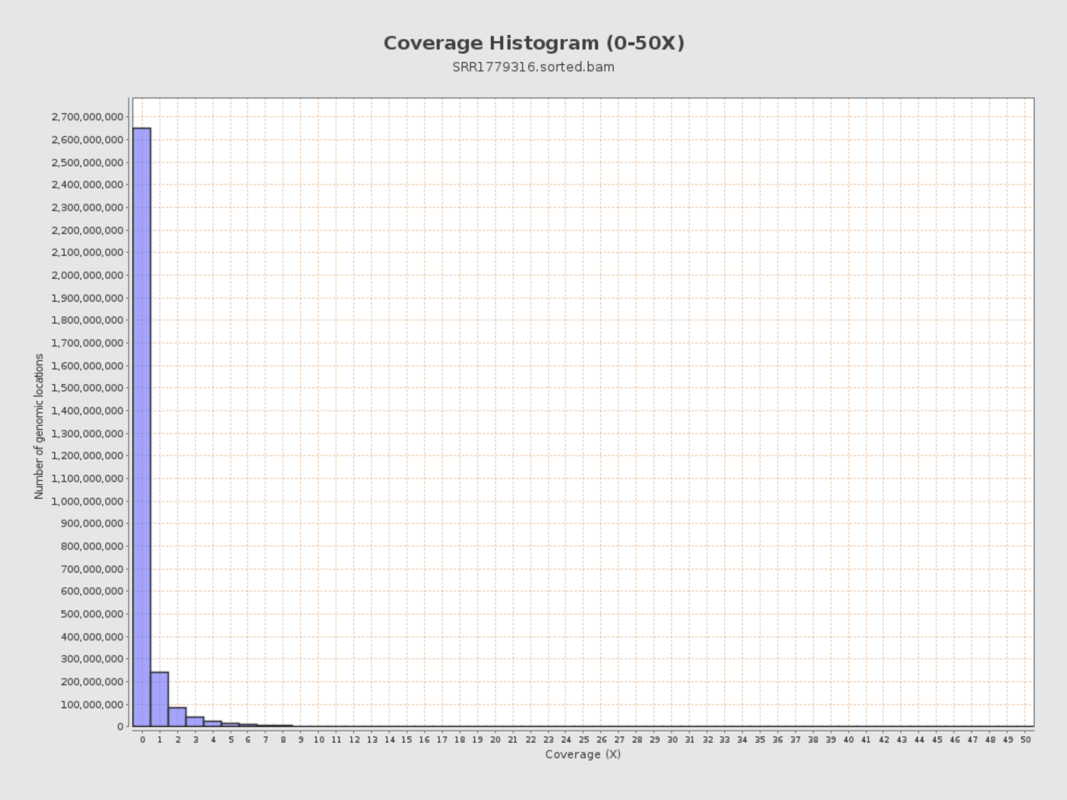
3. Results : Coverage across reference



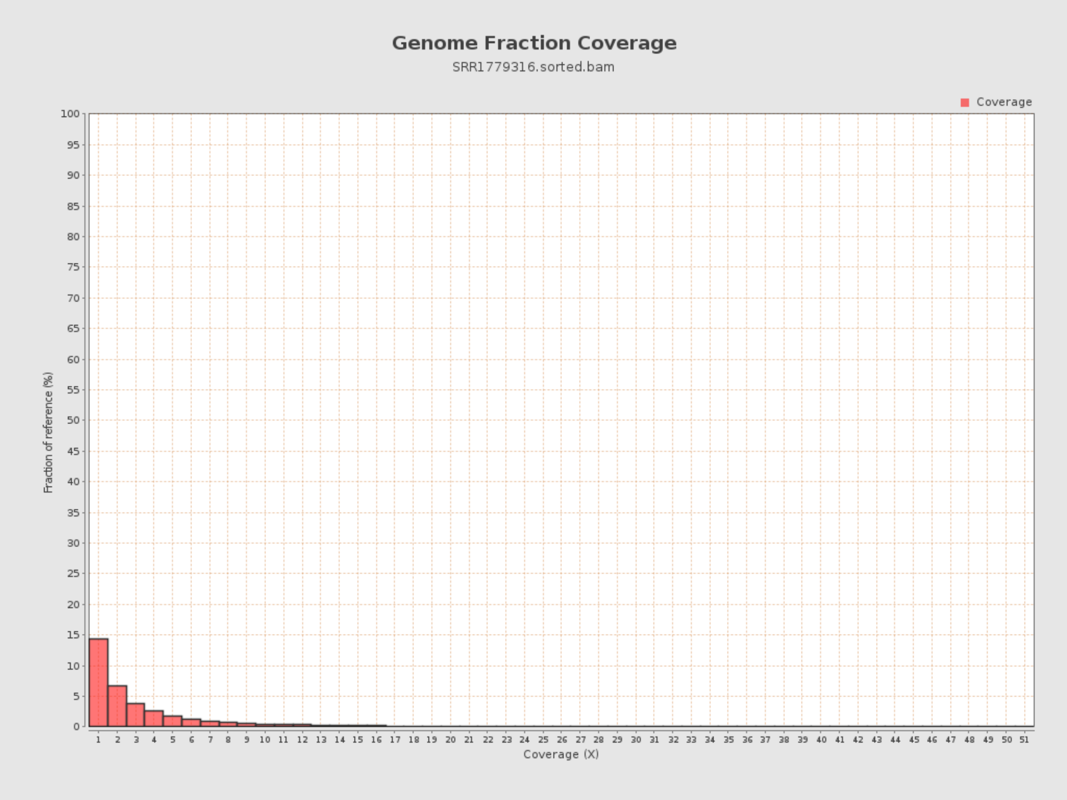
4. Results : Coverage Histogram



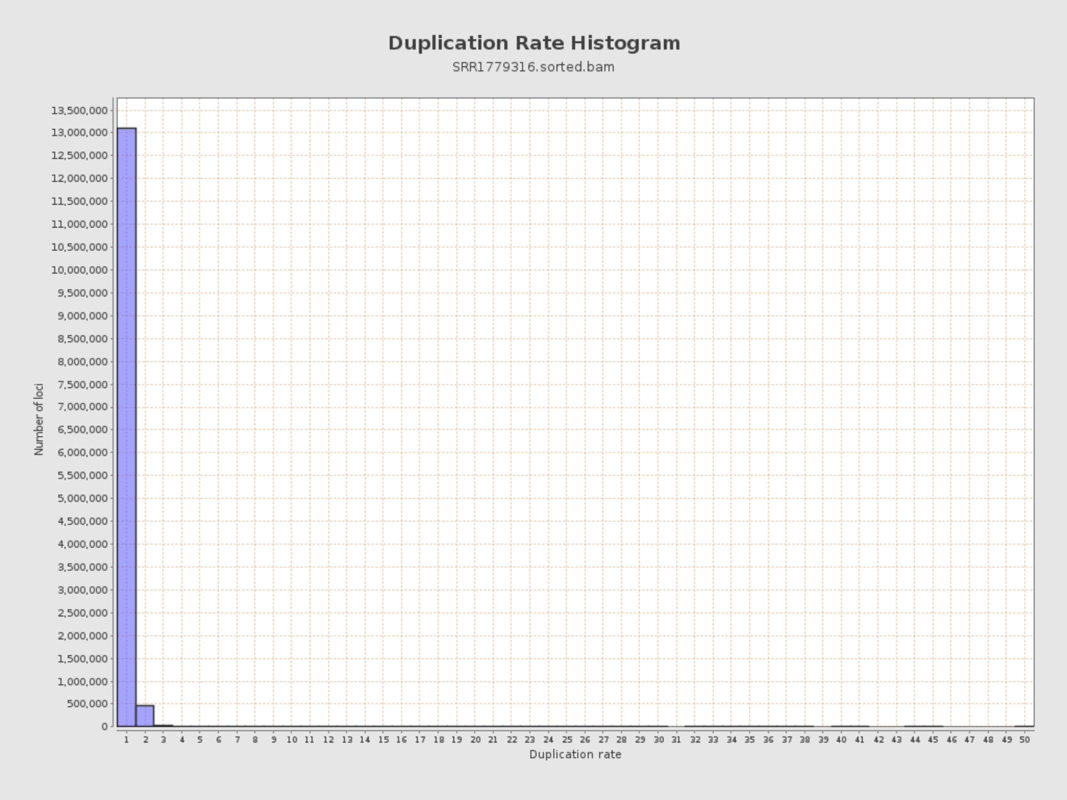
5. Results : Coverage Histogram (0-50X)



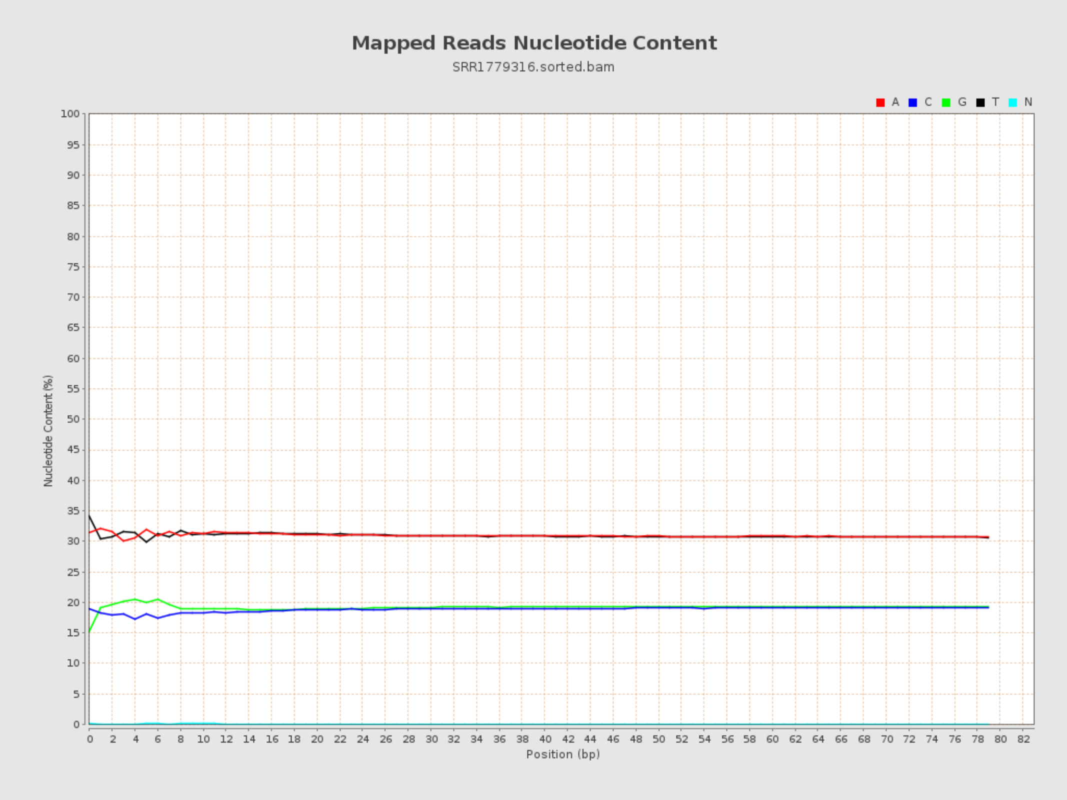
6. Results : Genome Fraction Coverage



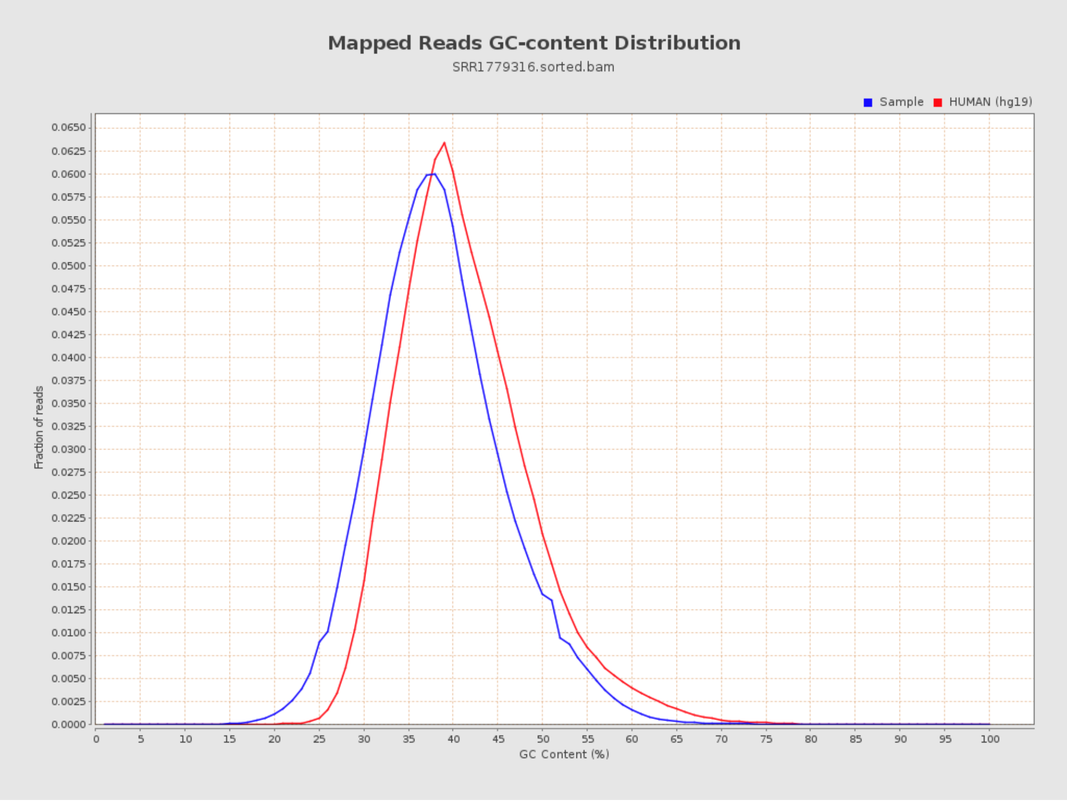
7. Results : Duplication Rate Histogram



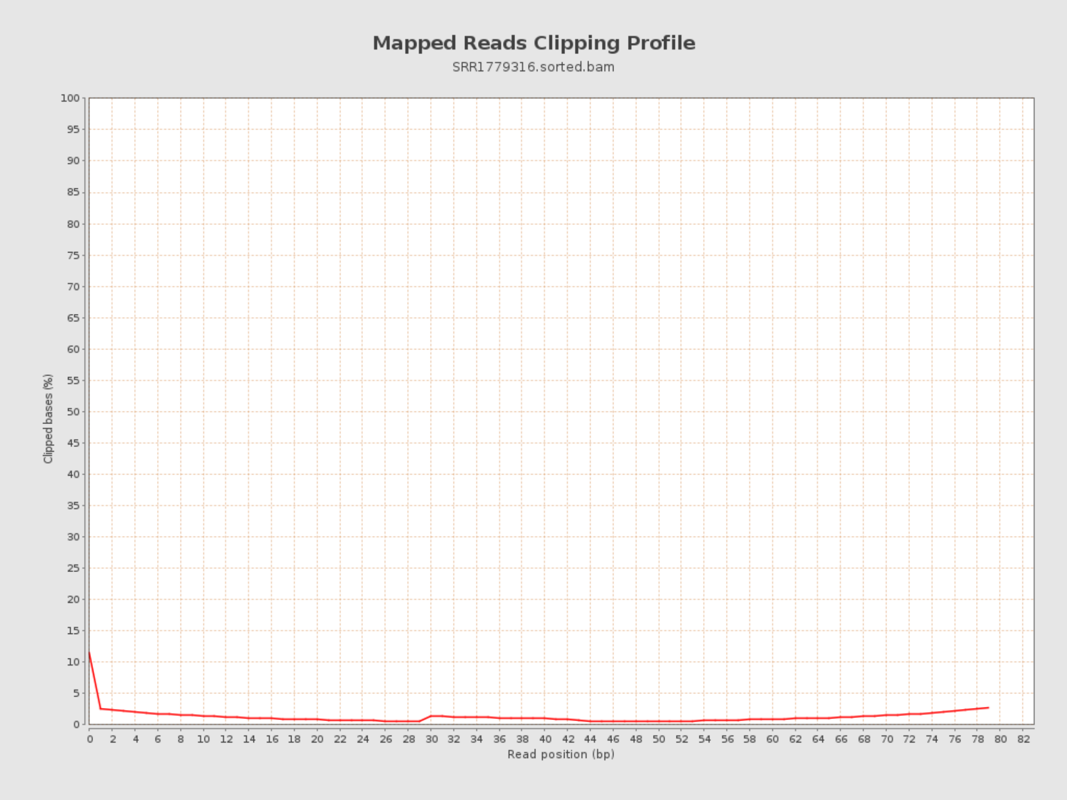
8. Results : Mapped Reads Nucleotide Content



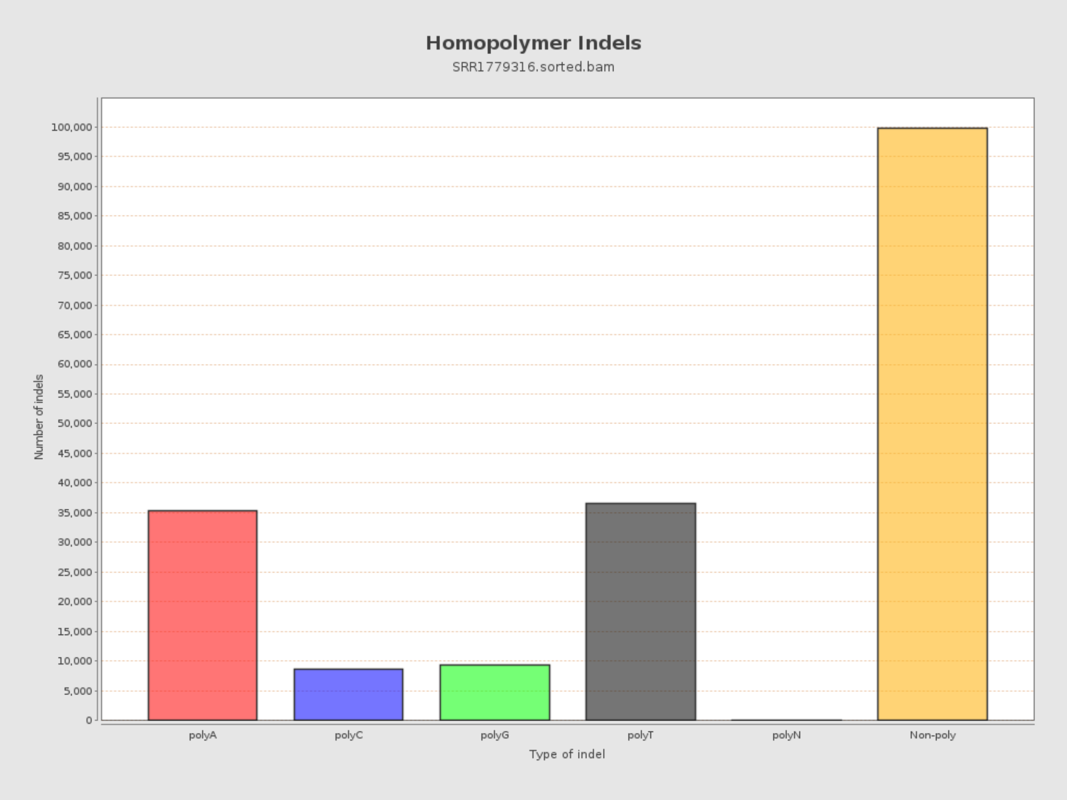
9. Results : Mapped Reads GC-content Distribution



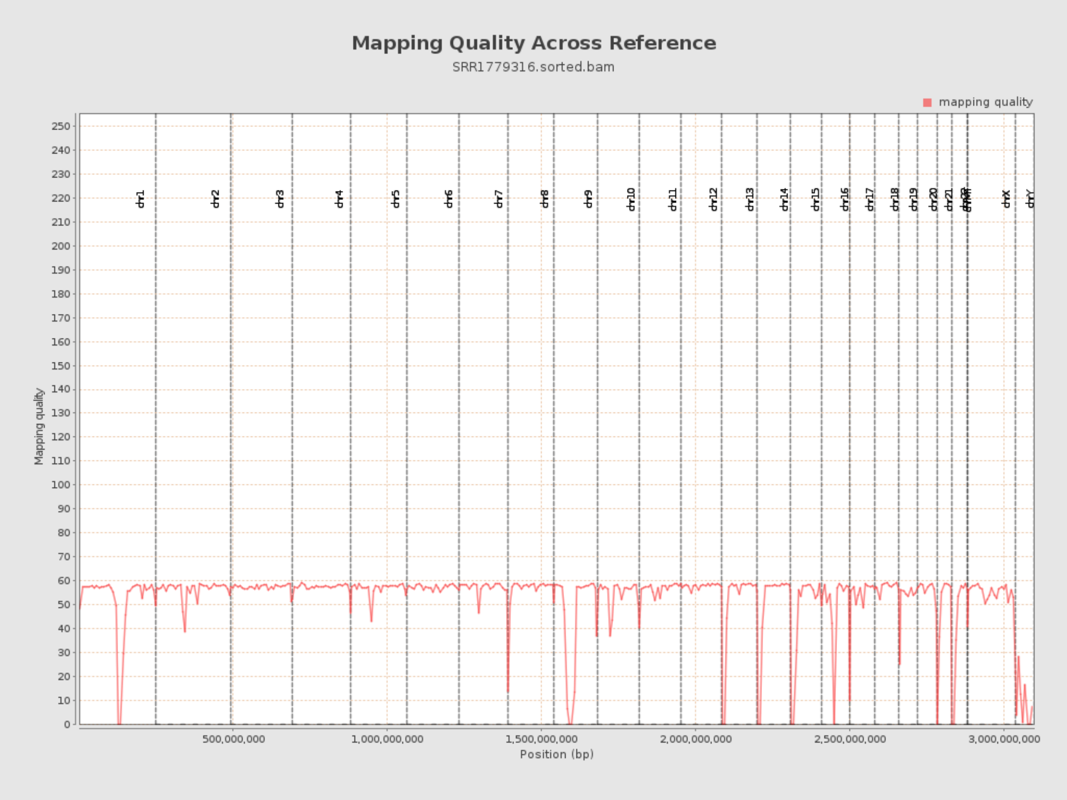
10. Results : Mapped Reads Clipping Profile



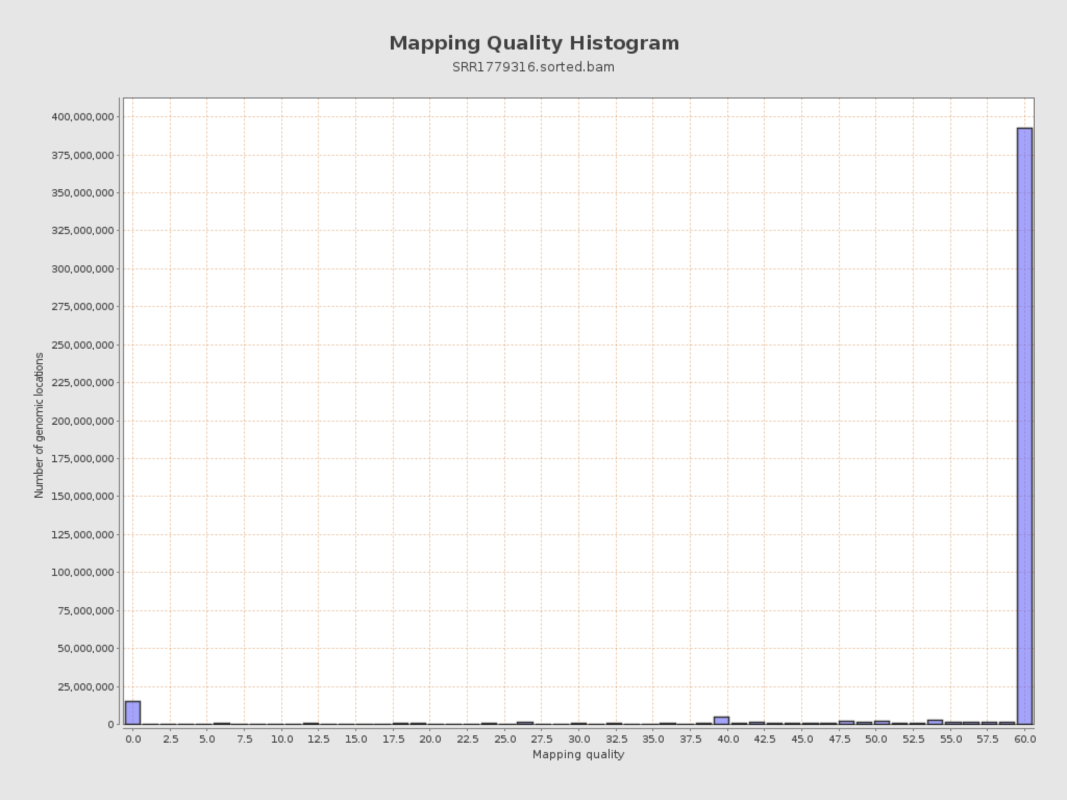
11. Results : Homopolymer Indels



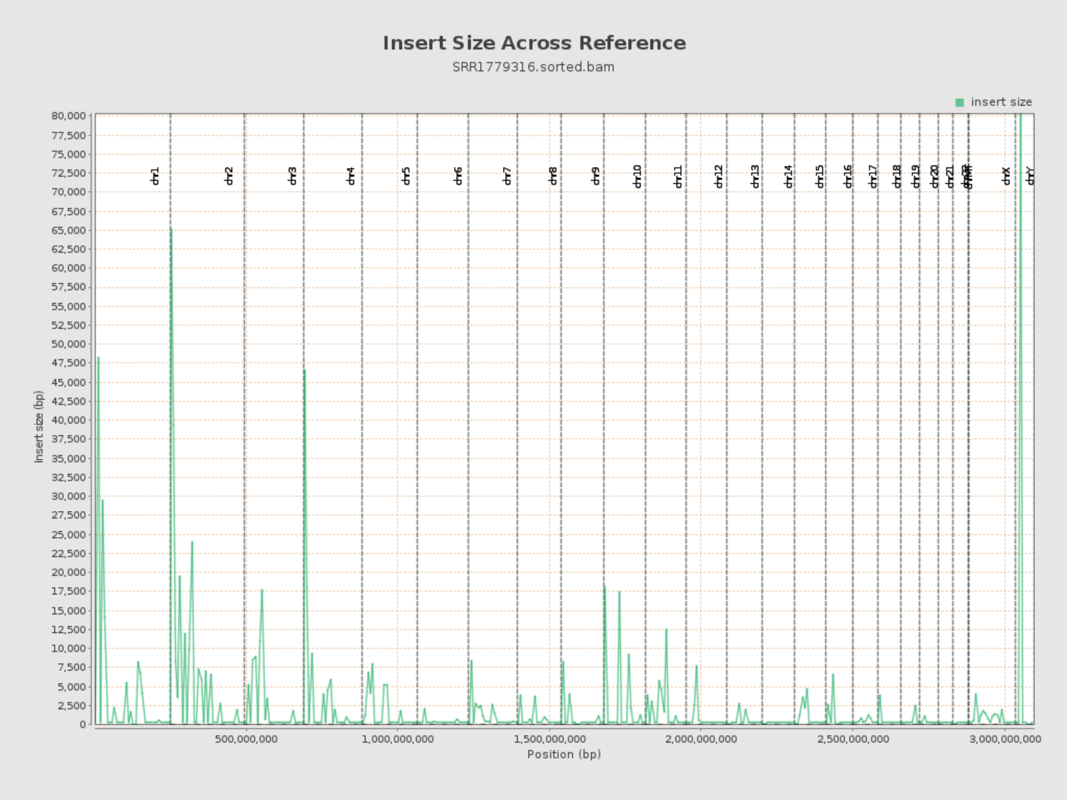
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram