Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 16:01:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779388.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_SRR1779388 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779388_1.fastq.gz SRR1779388_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 16:01:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779388.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,306,228
Mapped reads	3,369,770 / 53.44%
Unmapped reads	2,936,458 / 46.56%
Mapped paired reads	3,369,770 / 53.44%
Mapped reads, first in pair	1,709,054 / 27.1%
Mapped reads, second in pair	1,660,716 / 26.33%
Mapped reads, both in pair	3,253,728 / 51.6%
Mapped reads, singletons	116,042 / 1.84%
Secondary alignments	0
Supplementary alignments	22,495 / 0.36%
Read min/max/mean length	30 / 80 / 80.13
Duplicated reads (estimated)	204,819 / 3.25%
Duplication rate	4.28%
Clipped reads	361,269 / 5.73%

2.2. ACGT Content

Number/percentage of A's	83,713,128 / 31.51%
Number/percentage of C's	46,983,486 / 17.68%
Number/percentage of T's	80,227,638 / 30.2%
Number/percentage of G's	54,707,874 / 20.59%
Number/percentage of N's	54,851 / 0.02%

GC Percentage	38.27%

2.3. Coverage

Mean	0.0858
Standard Deviation	0.9607

2.4. Mapping Quality

Mean Mapping Quality	51.71

2.5. Insert size

Mean	54,893.27
Standard Deviation	2,126,314.37
P25/Median/P75	238 / 351 / 526

2.6. Mismatches and indels

General error rate	0.73%
Mismatches	1,904,916
Insertions	27,458
Mapped reads with at least one insertion	0.81%
Deletions	30,620
Mapped reads with at least one deletion	0.9%
Homopolymer indels	46.43%

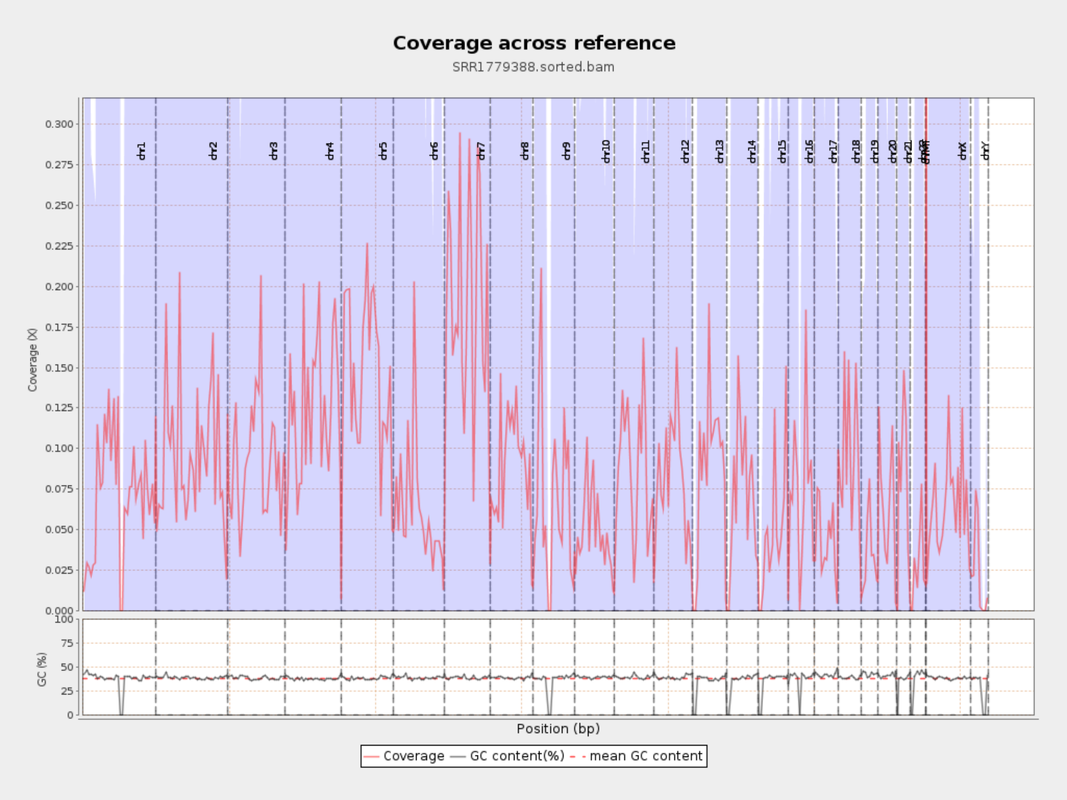
2.7. Chromosome stats

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

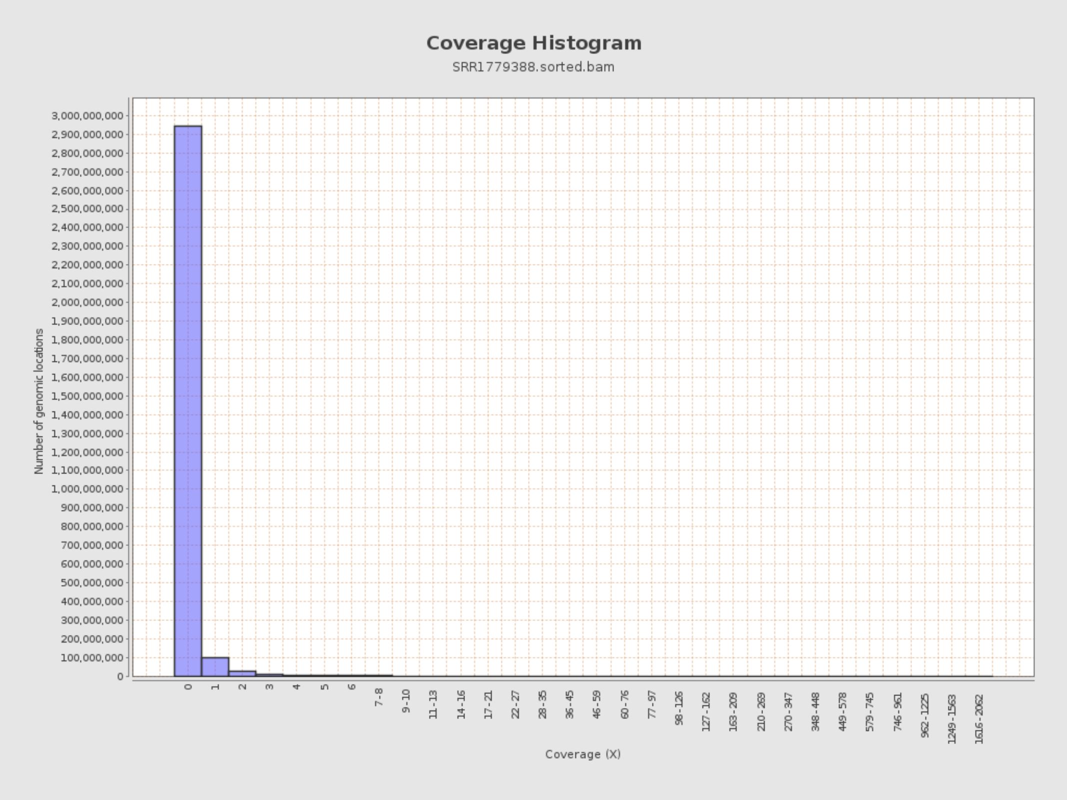
		bases	coverage	deviation
chr1	249250621	17524282	0.0703	1.4086
chr2	243199373	23101800	0.095	0.8297
chr3	198022430	18580623	0.0938	0.6935
chr4	191154276	23752375	0.1243	0.8377
chr5	180915260	26051653	0.144	0.7975
chr6	171115067	10706574	0.0626	0.4838
chr7	159138663	29553705	0.1857	0.9519
chr8	146364022	13260206	0.0906	0.63
chr9	141213431	9950514	0.0705	0.5934
chr10	135534747	6625032	0.0489	1.1914
chr11	135006516	11778388	0.0872	0.5553
chr12	133851895	10871920	0.0812	0.4975
chr13	115169878	10295108	0.0894	0.6307
chr14	107349540	7765412	0.0723	0.7223
chr15	102531392	5181380	0.0505	0.5007
chr16	90354753	6443737	0.0713	0.9775
chr17	81195210	3556292	0.0438	0.503
chr18	78077248	7716220	0.0988	0.8446
chr19	59128983	2064708	0.0349	0.9789
chr20	63025520	4244804	0.0674	3.5396
chr21	48129895	3773108	0.0784	0.5858
chr22	51304566	1489539	0.029	1.198
chrMT	16571	27491	1.659	1.6706
chrX	155270560	10009635	0.0645	0.6019

chrY	59373566	1424620	0.024	0.2869

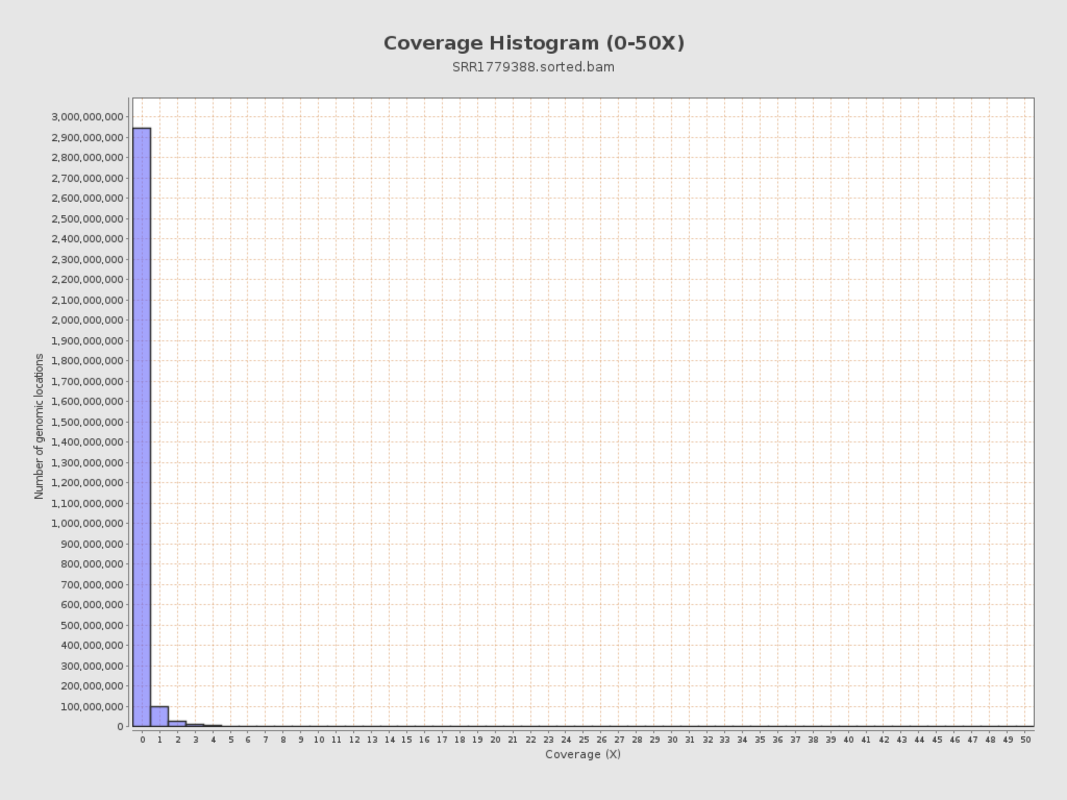
3. Results : Coverage across reference



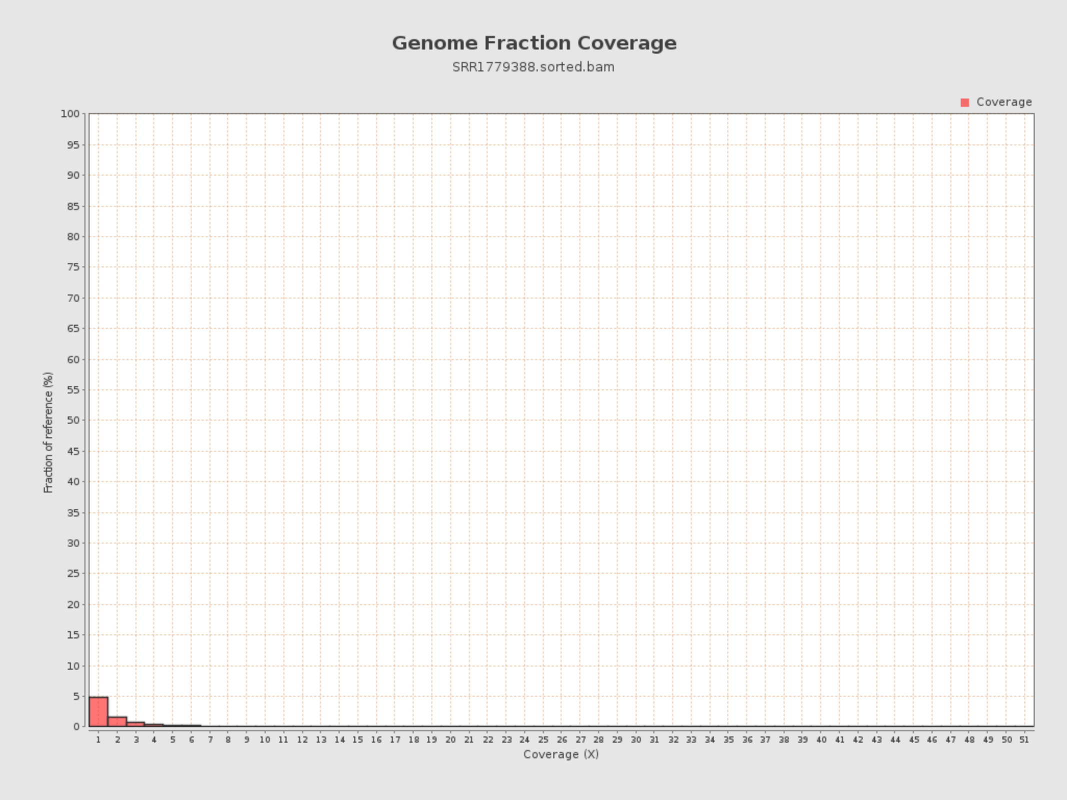
4. Results : Coverage Histogram



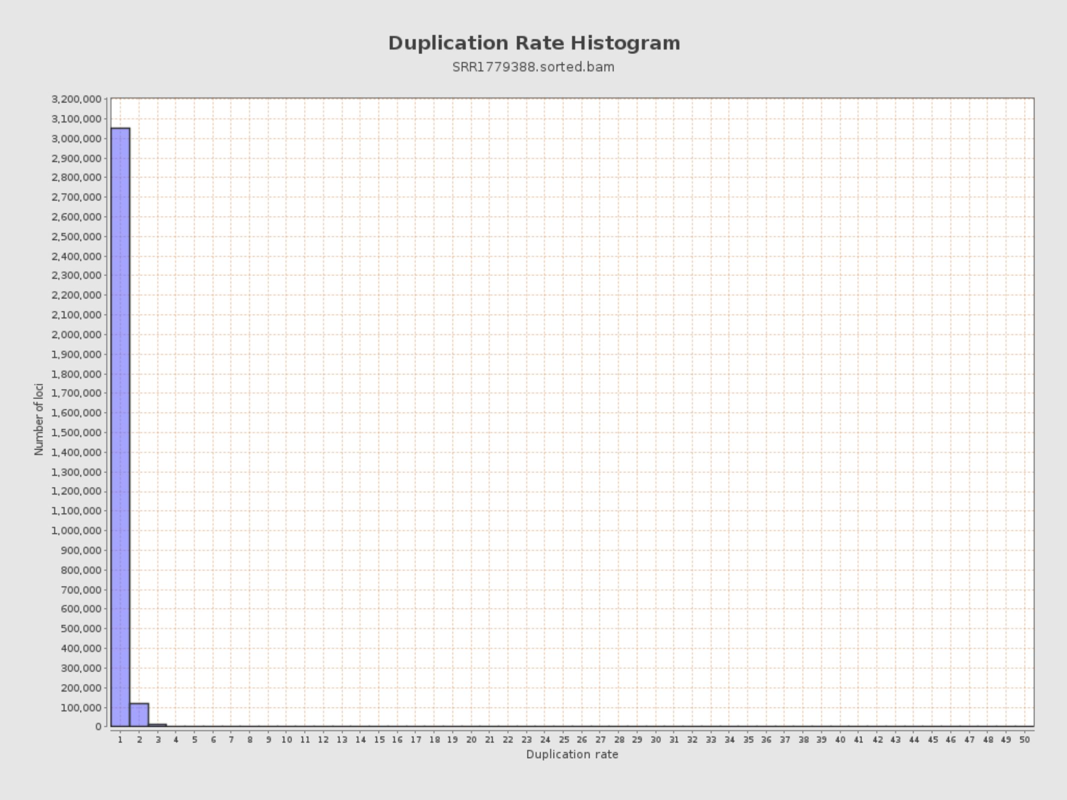
5. Results : Coverage Histogram (0-50X)



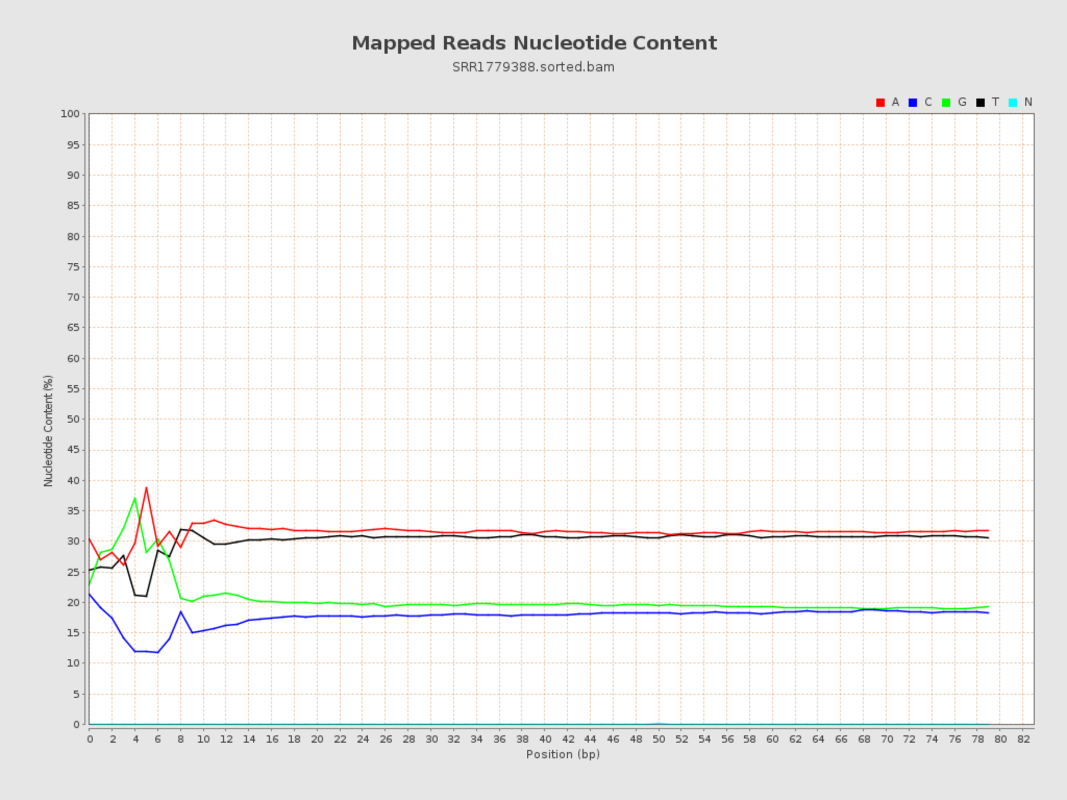
6. Results : Genome Fraction Coverage



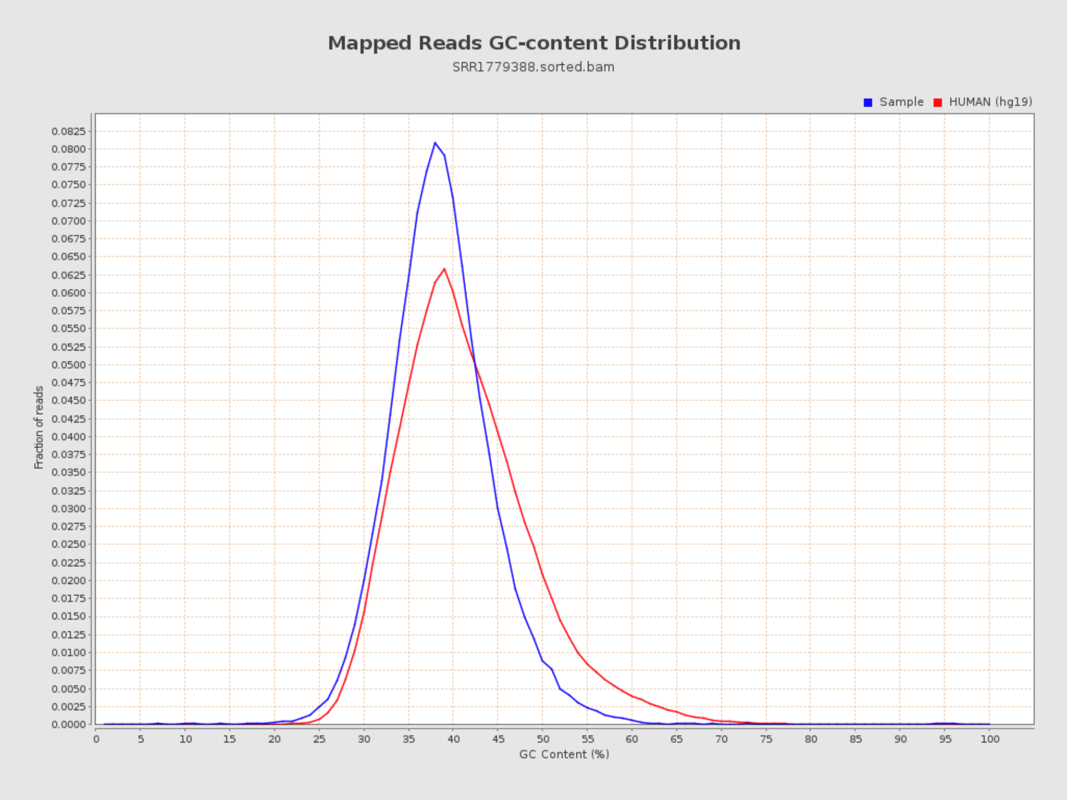
7. Results : Duplication Rate Histogram



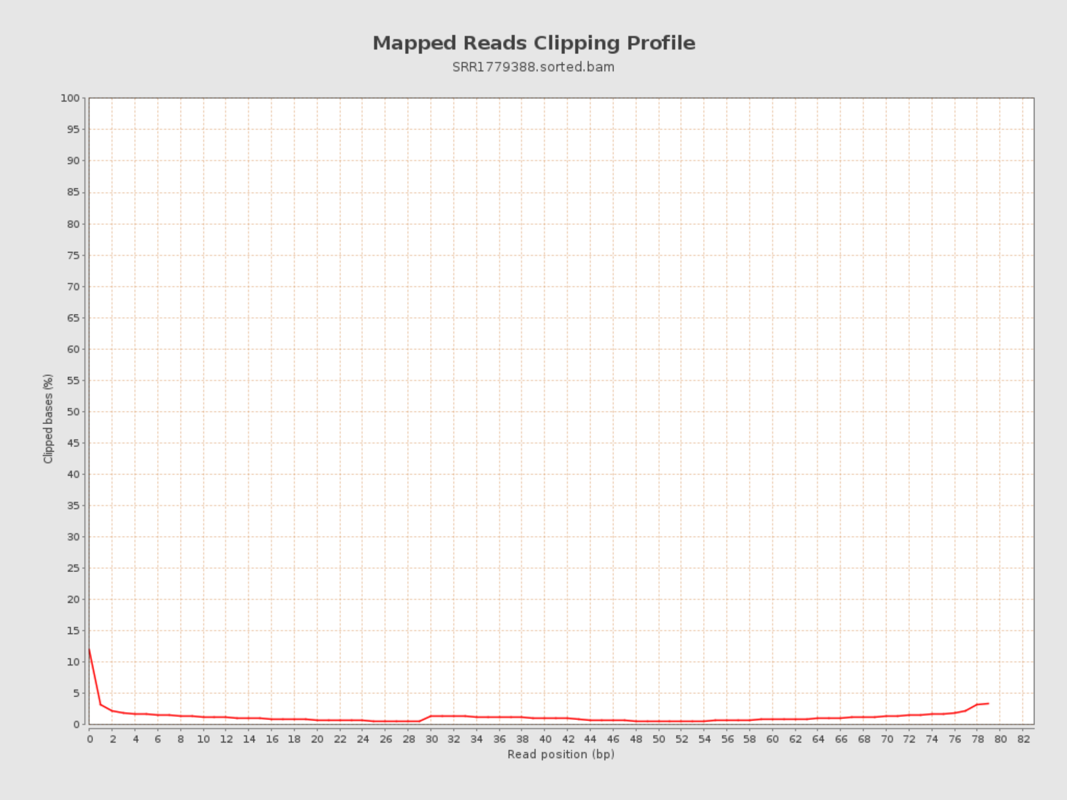
8. Results : Mapped Reads Nucleotide Content



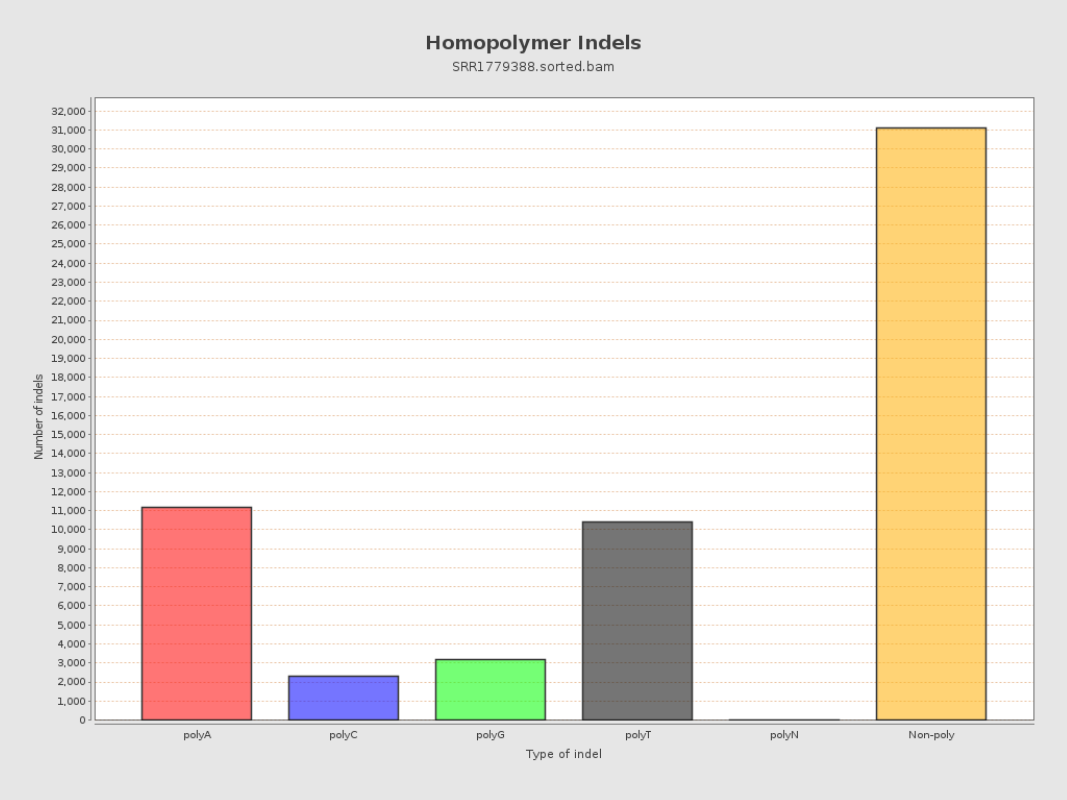
9. Results : Mapped Reads GC-content Distribution



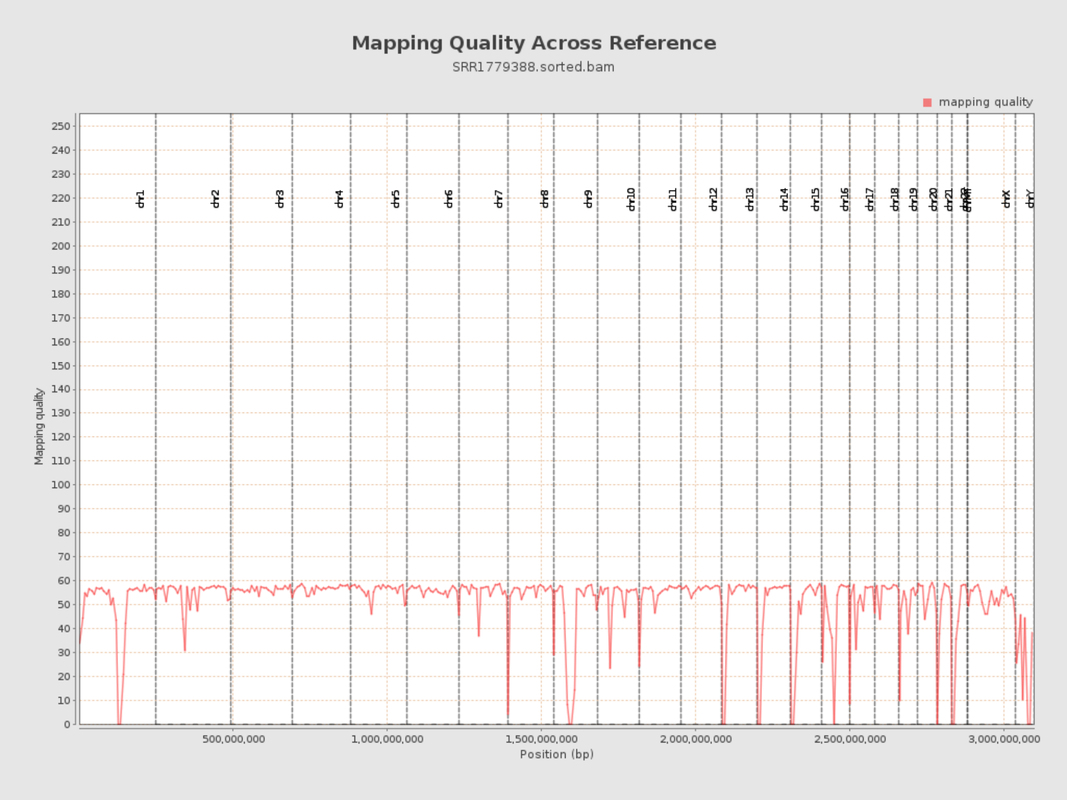
10. Results : Mapped Reads Clipping Profile



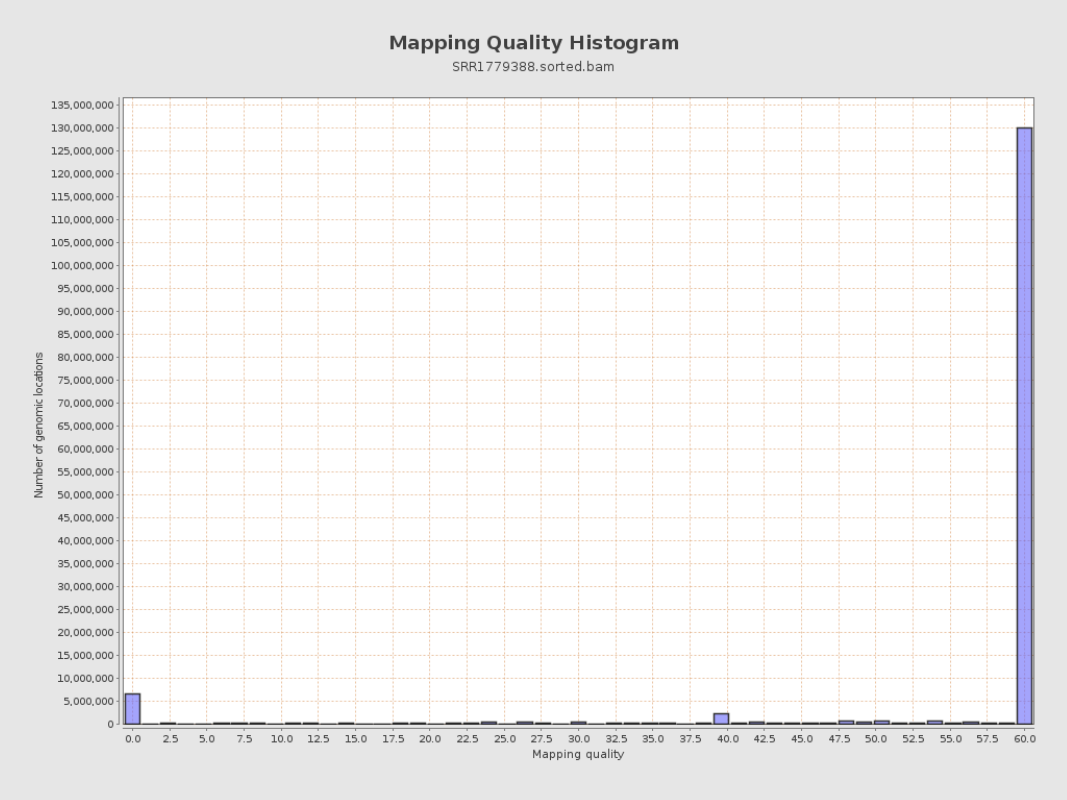
11. Results : Homopolymer Indels



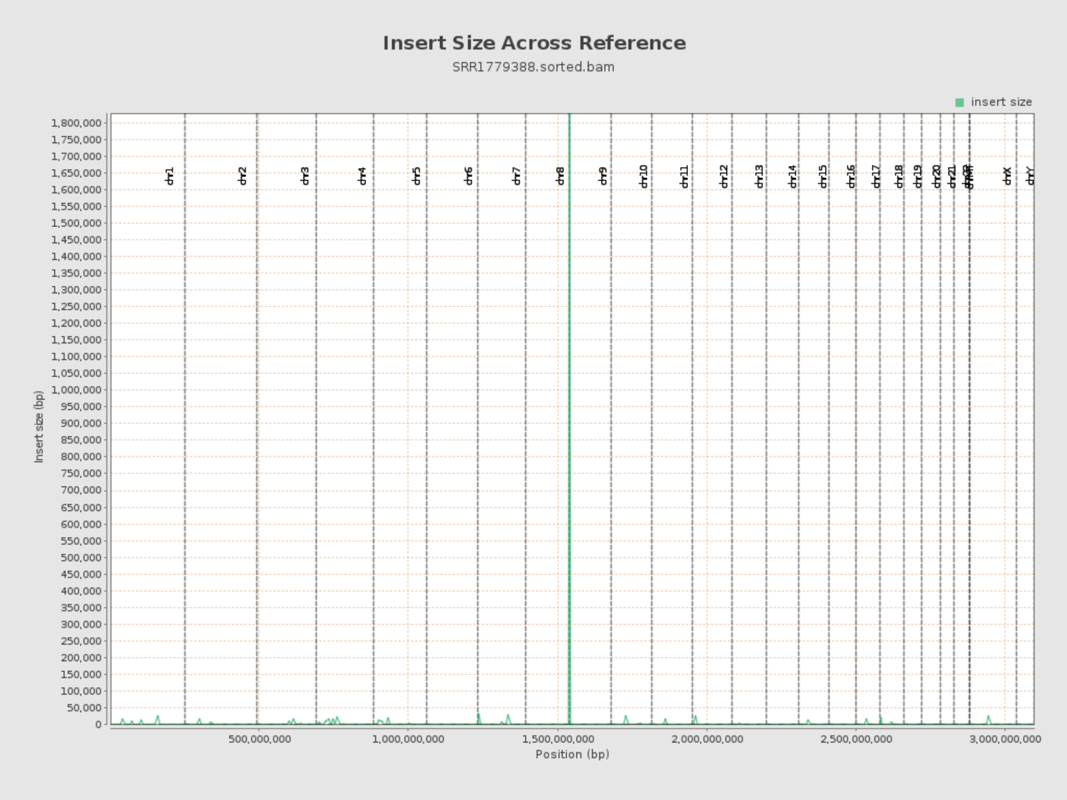
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram