Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 07:46:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779314.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_SRR1779314 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779314_1.fastq.gz SRR1779314_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 07:46:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779314.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,763,222
Mapped reads	17,126,618 / 96.42%
Unmapped reads	636,604 / 3.58%
Mapped paired reads	17,126,618 / 96.42%
Mapped reads, first in pair	8,624,953 / 48.56%
Mapped reads, second in pair	8,501,665 / 47.86%
Mapped reads, both in pair	16,976,558 / 95.57%
Mapped reads, singletons	150,060 / 0.84%
Secondary alignments	0
Supplementary alignments	42,397 / 0.24%
Read min/max/mean length	30 / 80 / 80.09
Duplicated reads (estimated)	604,838 / 3.41%
Duplication rate	3.32%
Clipped reads	526,924 / 2.97%

2.2. ACGT Content

Number/percentage of A's	421,011,571 / 30.88%
Number/percentage of C's	258,798,457 / 18.98%
Number/percentage of T's	420,421,136 / 30.84%
Number/percentage of G's	262,782,161 / 19.27%
Number/percentage of N's	361,586 / 0.03%

GC Percentage	38.26%

2.3. Coverage

Mean	0.4405
Standard Deviation	1.6698

2.4. Mapping Quality

Mean Mapping Quality	52.87

2.5. Insert size

Mean	41,922.29
Standard Deviation	1,929,795.44
P25/Median/P75	163 / 220 / 297

2.6. Mismatches and indels

General error rate	0.36%
Mismatches	4,787,920
Insertions	98,043
Mapped reads with at least one insertion	0.57%
Deletions	125,544
Mapped reads with at least one deletion	0.72%
Homopolymer indels	46.99%

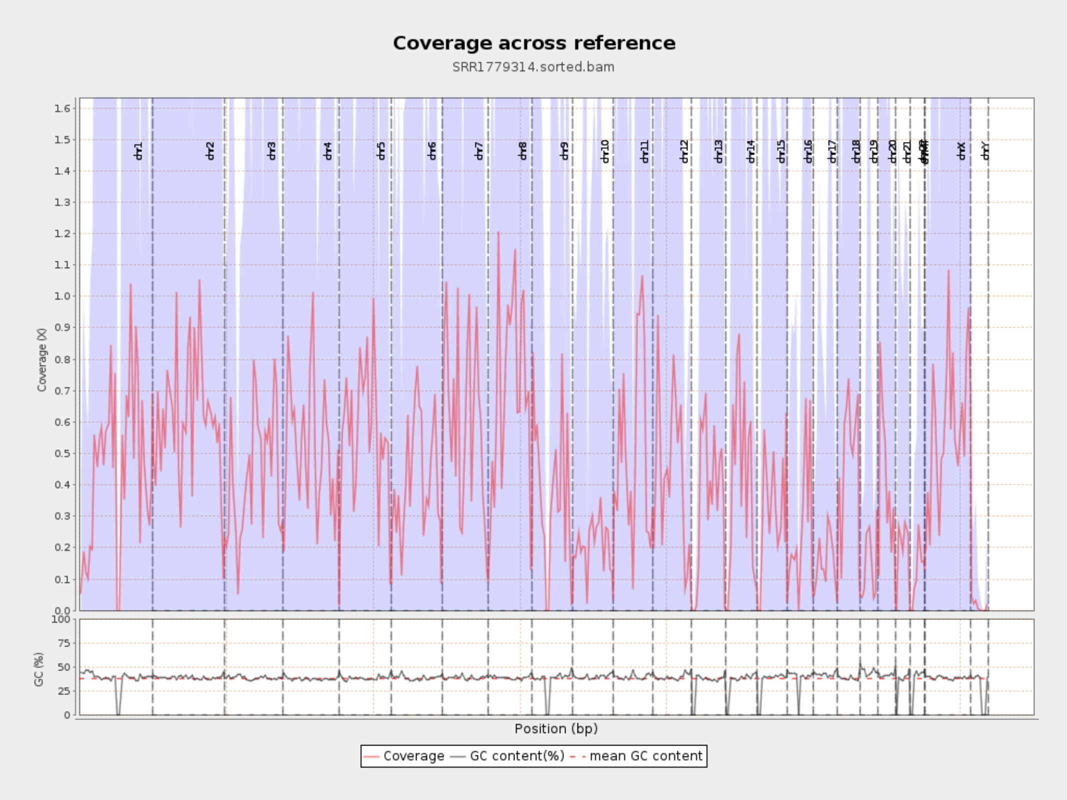
2.7. Chromosome stats

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

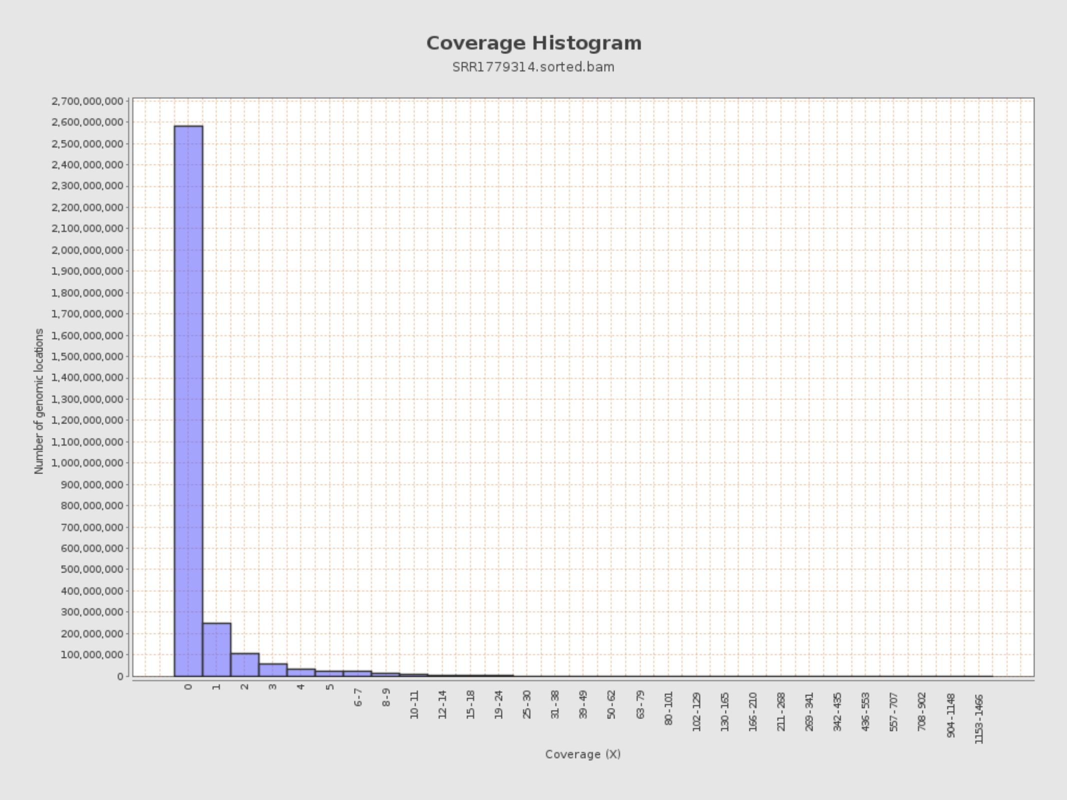
		bases	coverage	deviation
chr1	249250621	113100320	0.4538	2.1425
chr2	243199373	150290658	0.618	1.8453
chr3	198022430	85882909	0.4337	1.4606
chr4	191154276	99766517	0.5219	1.675
chr5	180915260	100944283	0.558	1.7544
chr6	171115067	74074248	0.4329	1.4695
chr7	159138663	96517406	0.6065	2.1341
chr8	146364022	103602387	0.7078	1.9777
chr9	141213431	51498262	0.3647	1.4099
chr10	135534747	28787969	0.2124	1.6427
chr11	135006516	68388618	0.5066	1.8385
chr12	133851895	58995943	0.4408	1.6302
chr13	115169878	41176875	0.3575	1.3336
chr14	107349540	44050649	0.4103	1.5219
chr15	102531392	31848900	0.3106	1.4255
chr16	90354753	22288725	0.2467	1.1315
chr17	81195210	12494970	0.1539	0.8363
chr18	78077248	38906232	0.4983	1.66
chr19	59128983	7623465	0.1289	0.9639
chr20	63025520	25375441	0.4026	1.2878
chr21	48129895	9850429	0.2047	0.895
chr22	51304566	6109769	0.1191	0.645
chrMT	16571	3259	0.1967	0.4607
chrX	155270560	91203881	0.5874	2.0794

chrY	59373566	849307	0.0143	0.1917

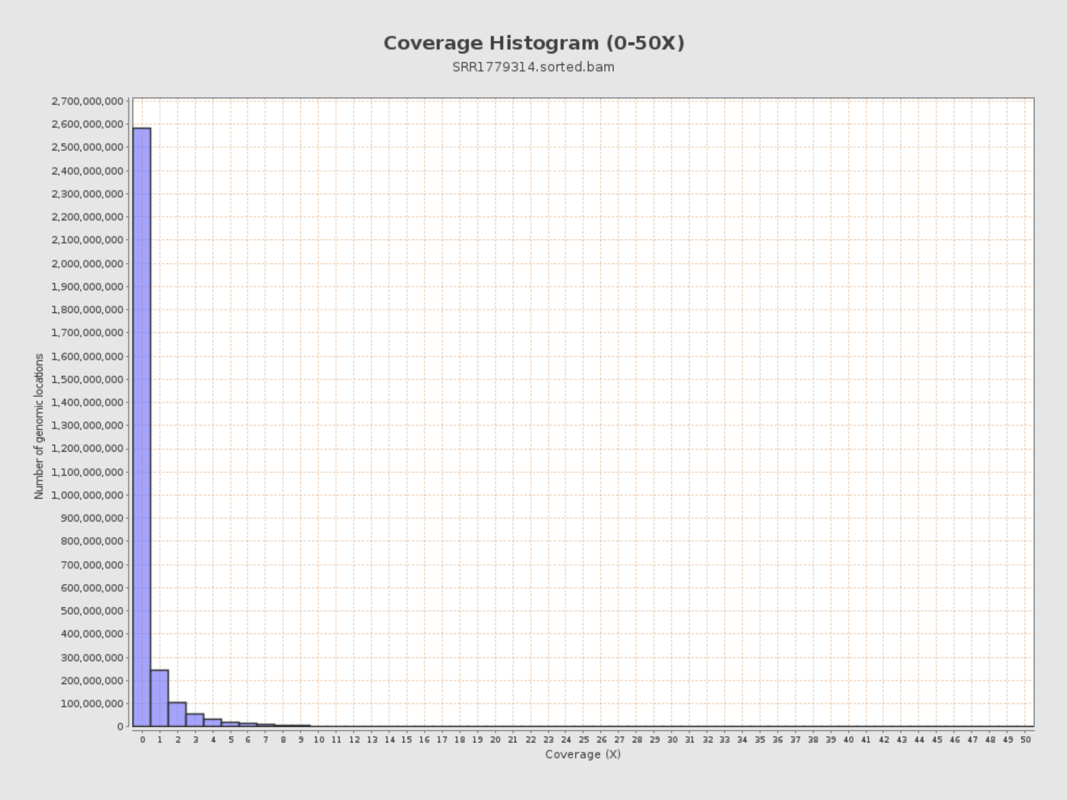
3. Results : Coverage across reference



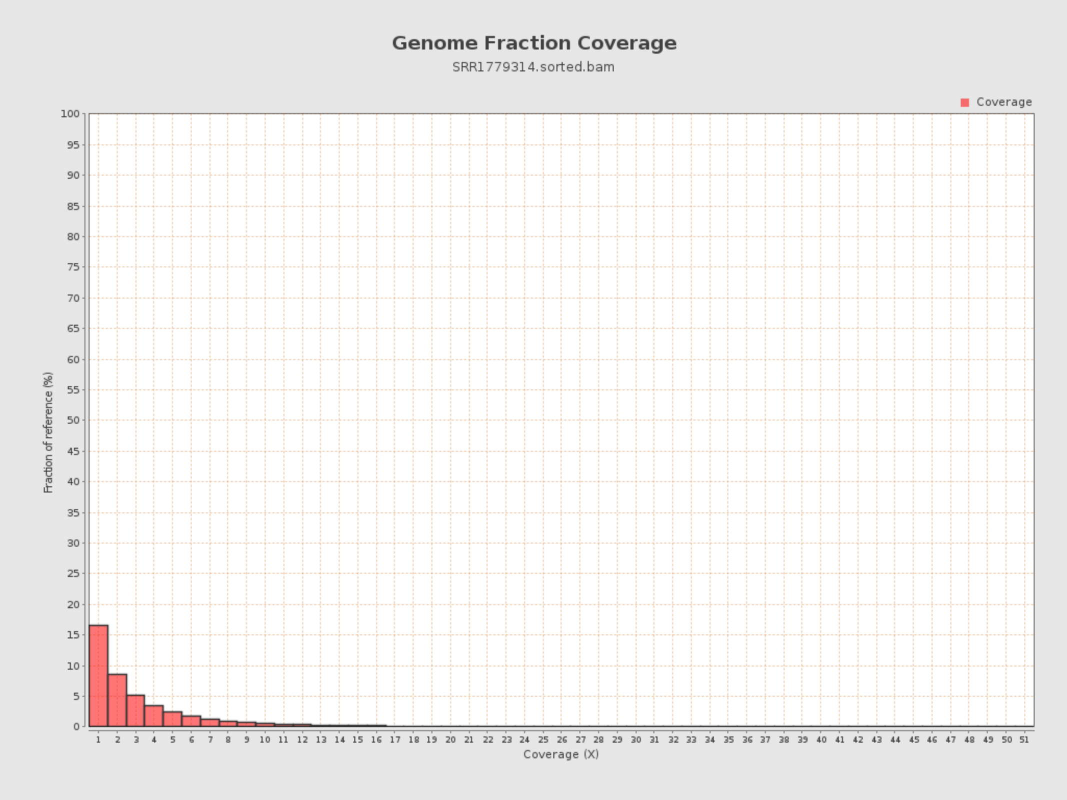
4. Results : Coverage Histogram



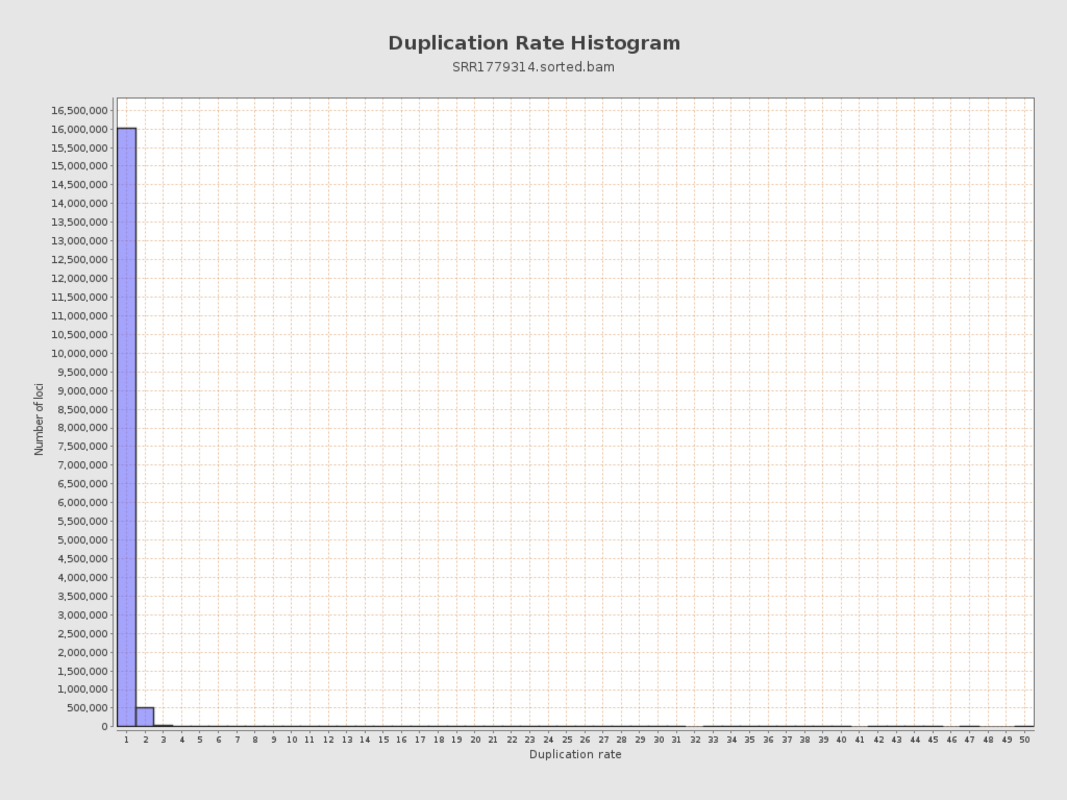
5. Results : Coverage Histogram (0-50X)



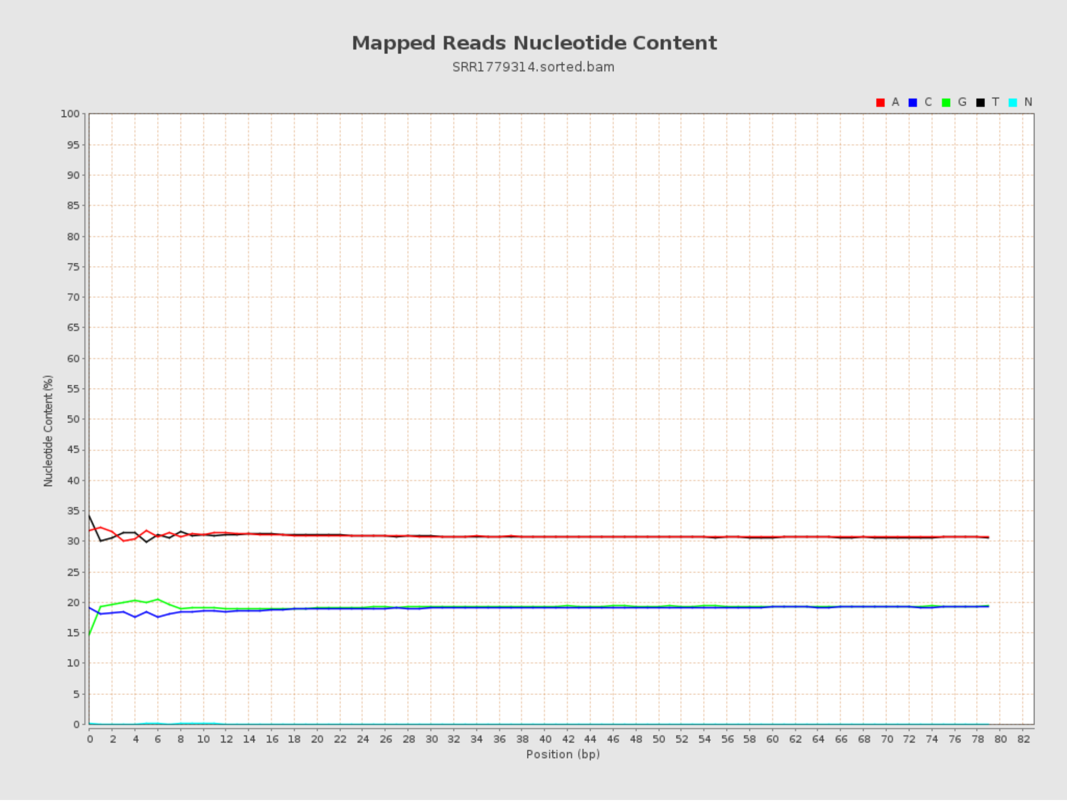
6. Results : Genome Fraction Coverage



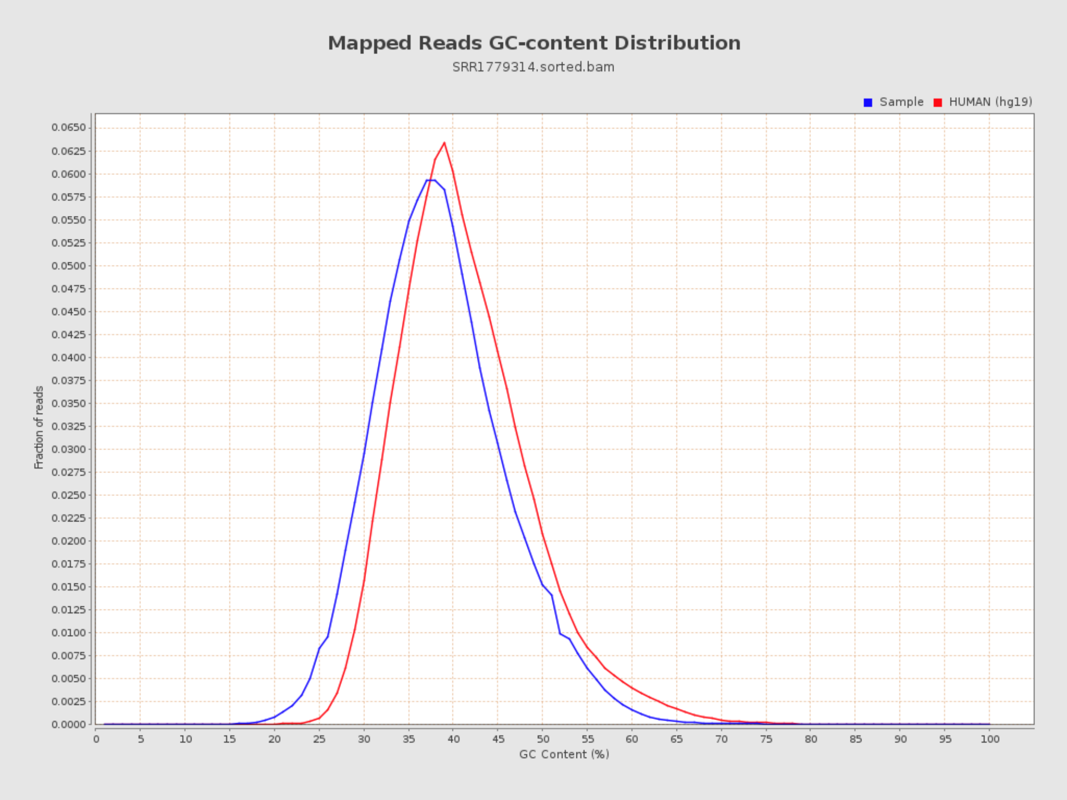
7. Results : Duplication Rate Histogram



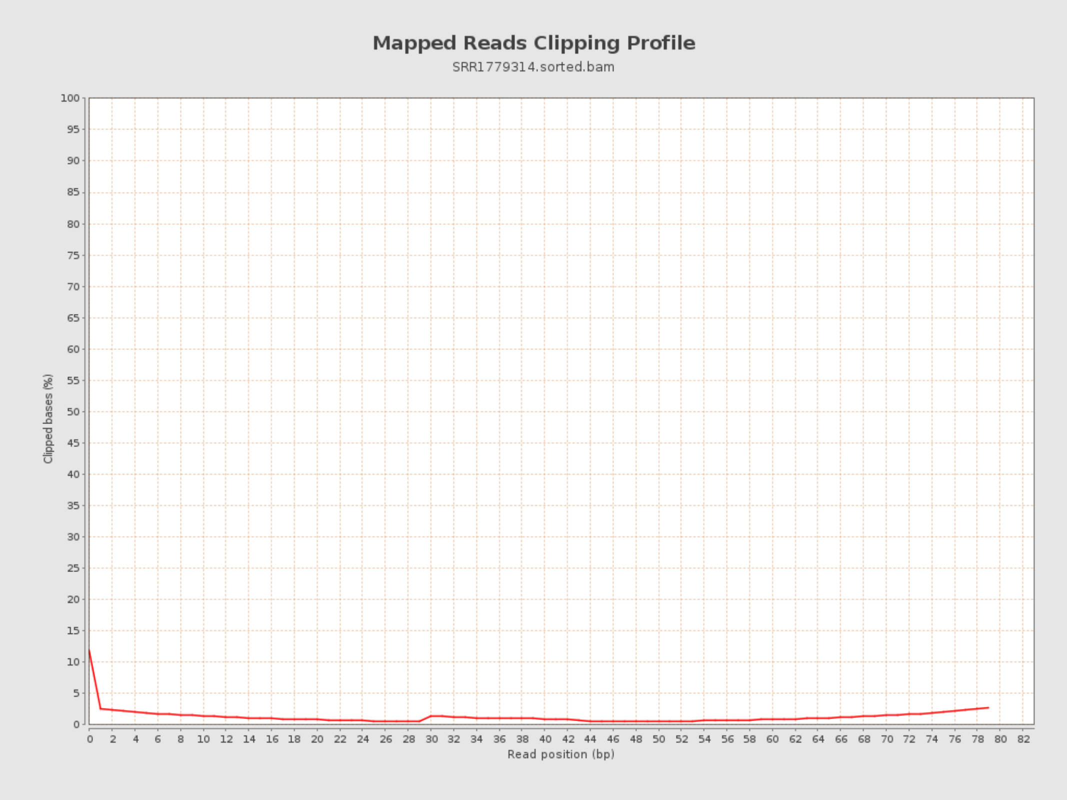
8. Results : Mapped Reads Nucleotide Content



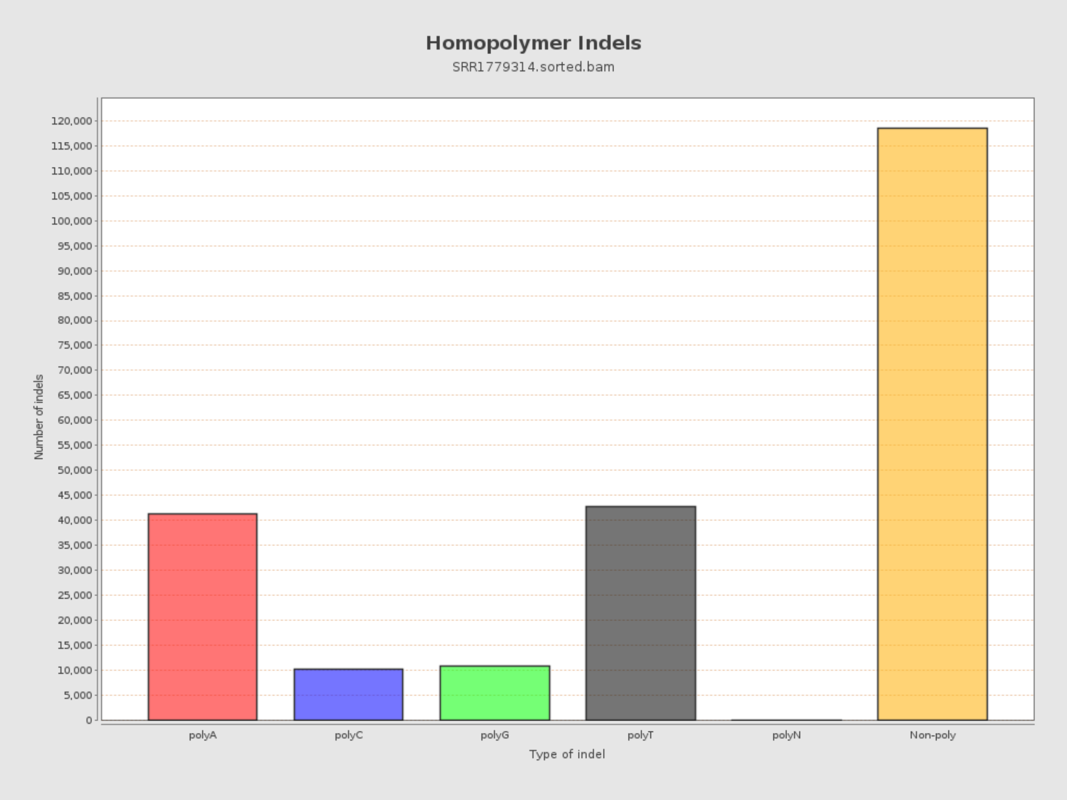
9. Results : Mapped Reads GC-content Distribution



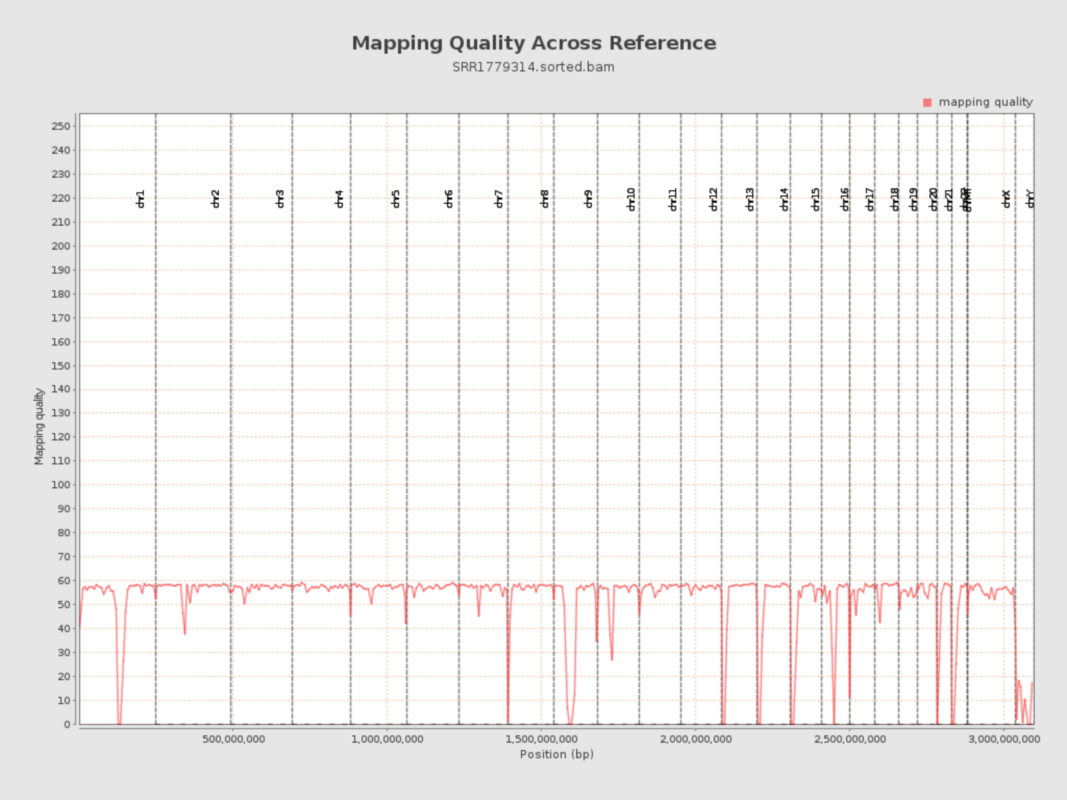
10. Results : Mapped Reads Clipping Profile



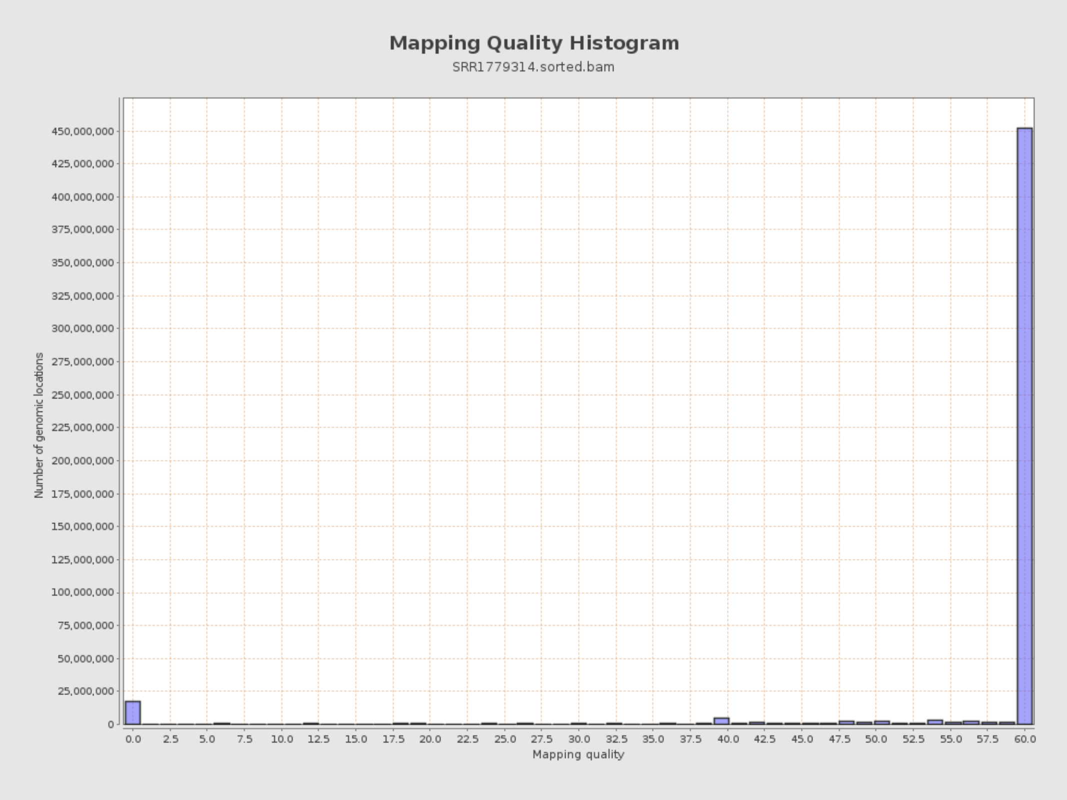
11. Results : Homopolymer Indels



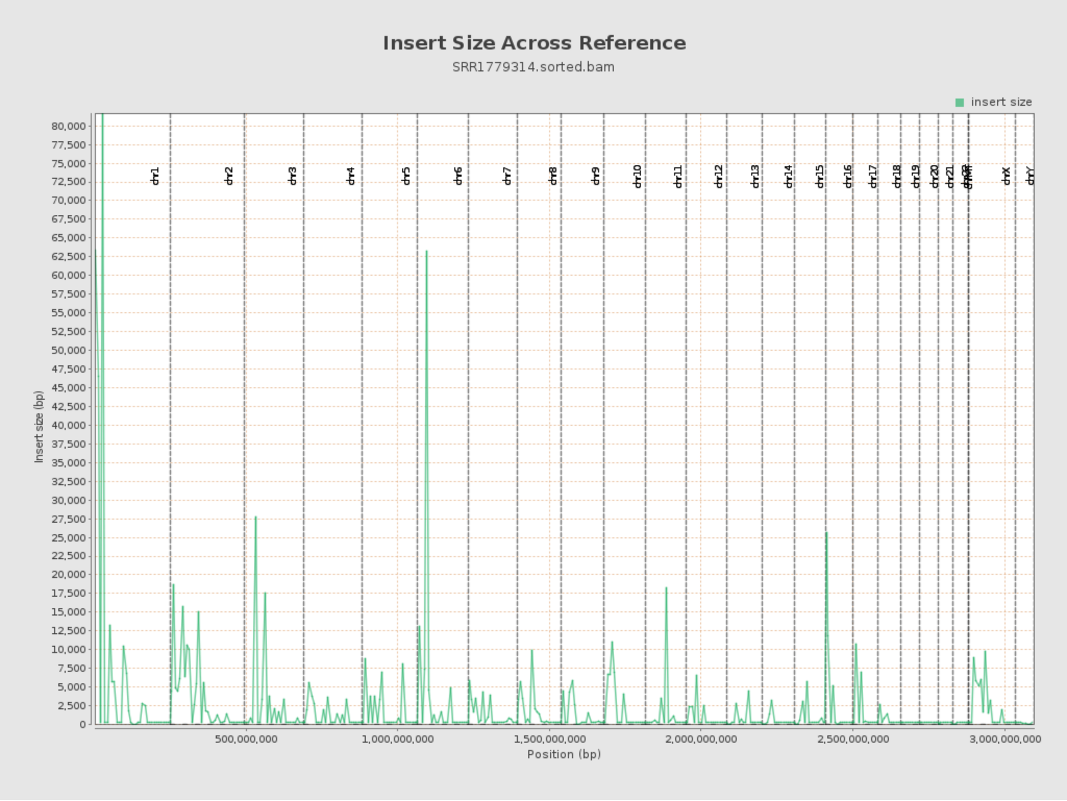
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram