Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/29 10:59:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779336.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_SRR1779336 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779336_1.fastq.gz SRR1779336_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Mar 29 10:59:48 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1779336.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	154,379,068
Mapped reads	148,805,103 / 96.39%
Unmapped reads	5,573,965 / 3.61%
Mapped paired reads	148,805,103 / 96.39%
Mapped reads, first in pair	75,312,227 / 48.78%
Mapped reads, second in pair	73,492,876 / 47.61%
Mapped reads, both in pair	146,134,818 / 94.66%
Mapped reads, singletons	2,670,285 / 1.73%
Secondary alignments	0
Supplementary alignments	669,092 / 0.43%
Read min/max/mean length	30 / 100 / 100.06
Duplicated reads (estimated)	9,565,484 / 6.2%
Duplication rate	6.13%
Clipped reads	7,797,960 / 5.05%

2.2. ACGT Content

Number/percentage of A's	4,371,936,456 / 29.64%
Number/percentage of C's	2,991,747,760 / 20.28%
Number/percentage of T's	4,349,266,487 / 29.48%
Number/percentage of G's	3,037,467,954 / 20.59%
Number/percentage of N's	693,829 / 0%

GC Percentage	40.87%

2.3. Coverage

Mean	4.7661
Standard Deviation	8.2891

2.4. Mapping Quality

Mean Mapping Quality	53.92

2.5. Insert size

Mean	61,375.53
Standard Deviation	2,465,407.16
P25/Median/P75	171 / 222 / 289

2.6. Mismatches and indels

General error rate	0.42%
Mismatches	58,989,486
Insertions	1,520,891
Mapped reads with at least one insertion	1%
Deletions	1,541,172
Mapped reads with at least one deletion	1.02%
Homopolymer indels	47.71%

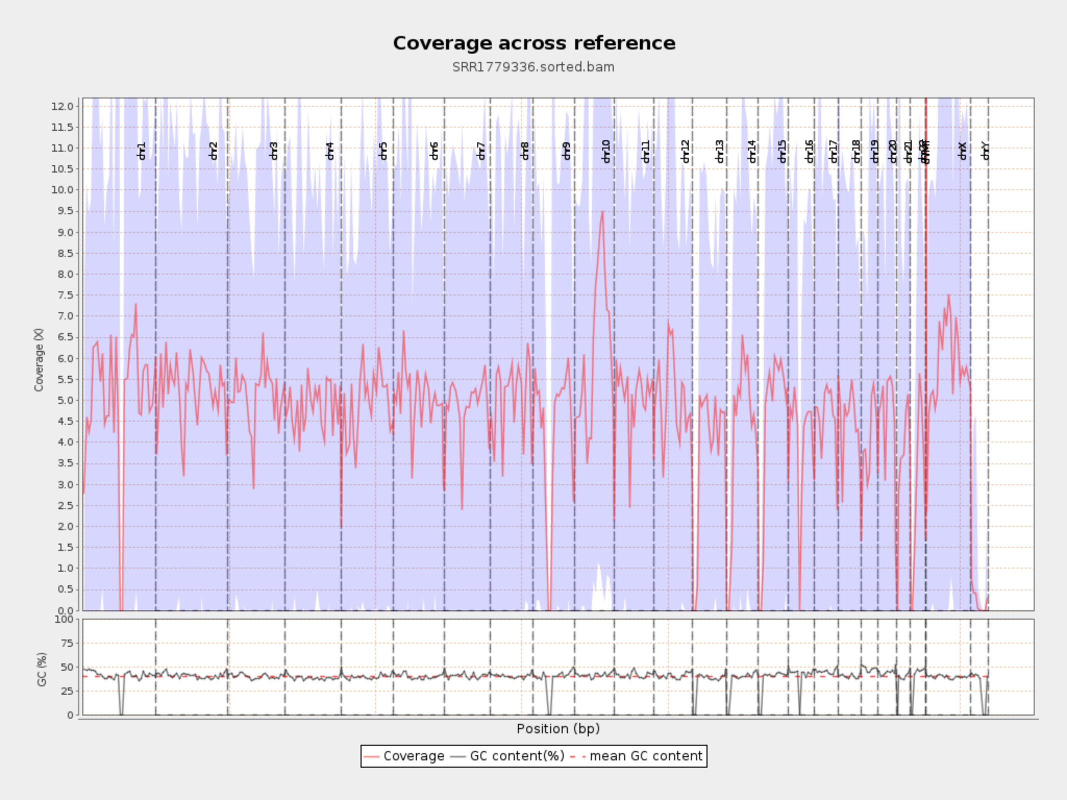
2.7. Chromosome stats

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

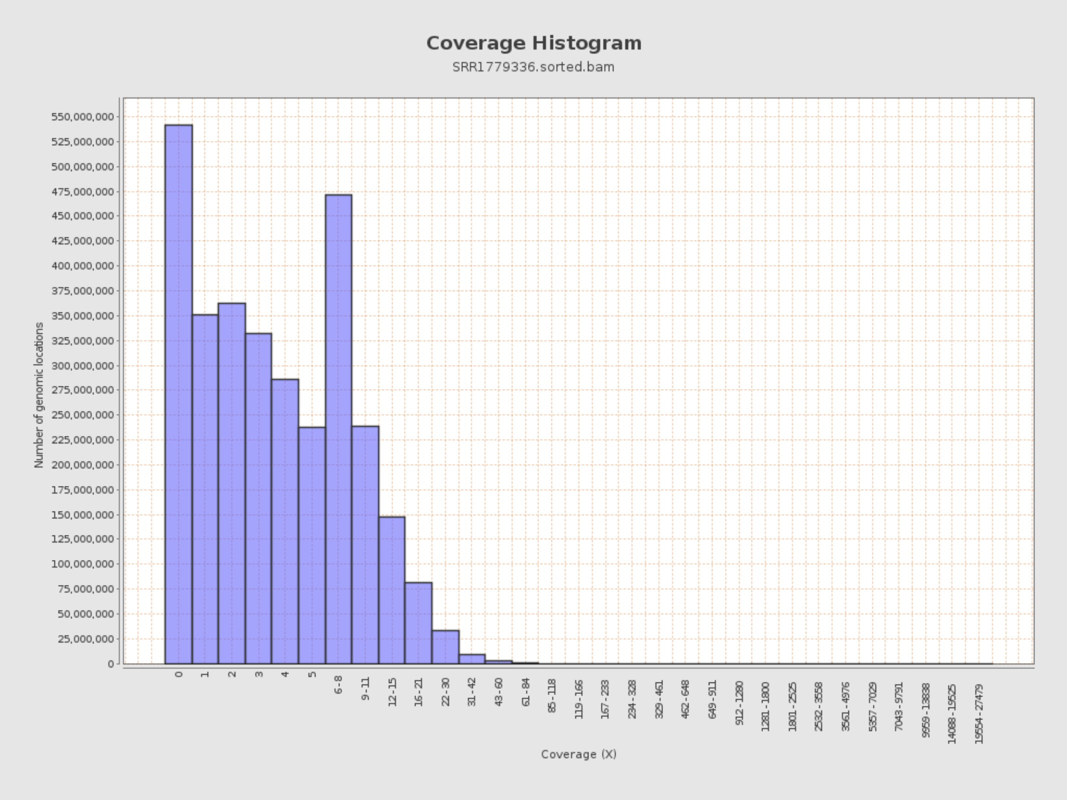
		bases	coverage	deviation
chr1	249250621	1262268028	5.0643	7.8338
chr2	243199373	1273589370	5.2368	21.8461
chr3	198022430	1013738799	5.1193	5.0752
chr4	191154276	931137481	4.8711	5.2482
chr5	180915260	888478920	4.911	4.9033
chr6	171115067	865282215	5.0567	5.6883
chr7	159138663	767840777	4.825	5.3317
chr8	146364022	741904350	5.0689	5.2195
chr9	141213431	597793464	4.2333	5.8287
chr10	135534747	842190016	6.2138	7.8826
chr11	135006516	683137842	5.06	5.3613
chr12	133851895	681573549	5.092	5.9622
chr13	115169878	438630616	3.8086	4.4995
chr14	107349540	455589009	4.244	5.0603
chr15	102531392	449358236	4.3826	5.386
chr16	90354753	355560164	3.9352	4.7118
chr17	81195210	379222373	4.6705	5.7906
chr18	78077248	351758265	4.5053	5.7264
chr19	59128983	235962614	3.9906	5.9155
chr20	63025520	296030357	4.697	5.5838
chr21	48129895	173623473	3.6074	6.5845
chr22	51304566	153801621	2.9978	4.4742
chrMT	16571	653071	39.4105	10.4821
chrX	155270560	902402802	5.8118	5.9636

chrY	59373566	12991988	0.2188	2.323

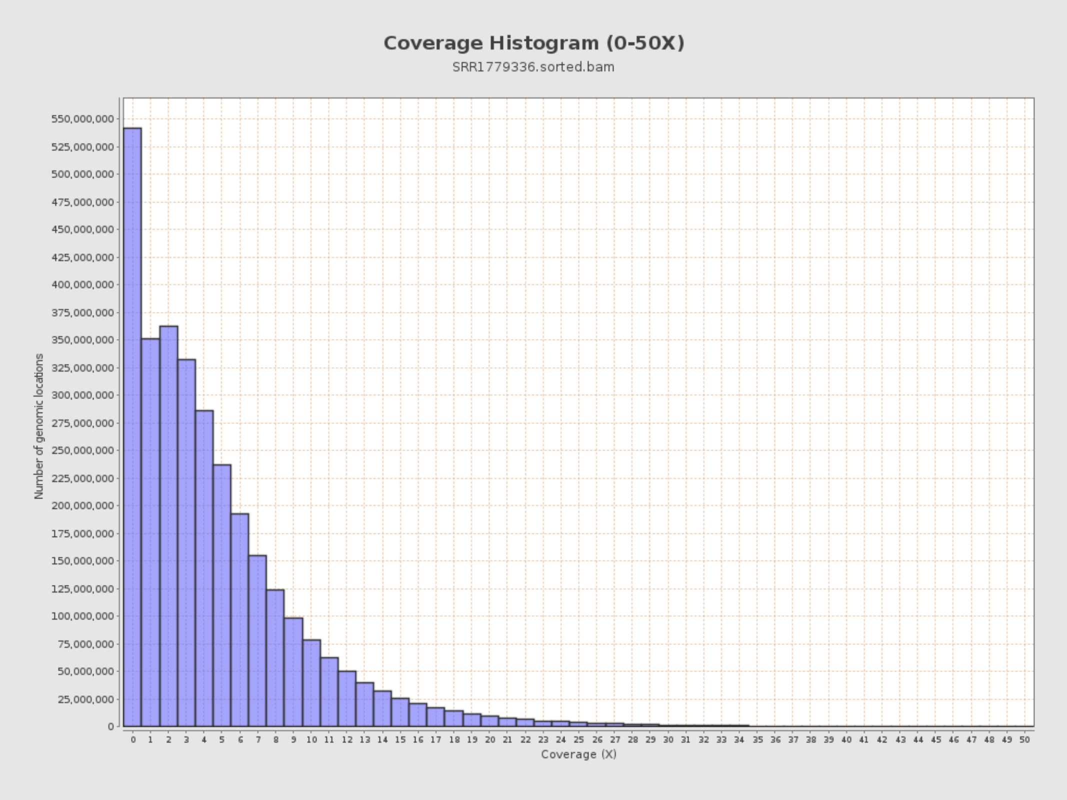
3. Results : Coverage across reference



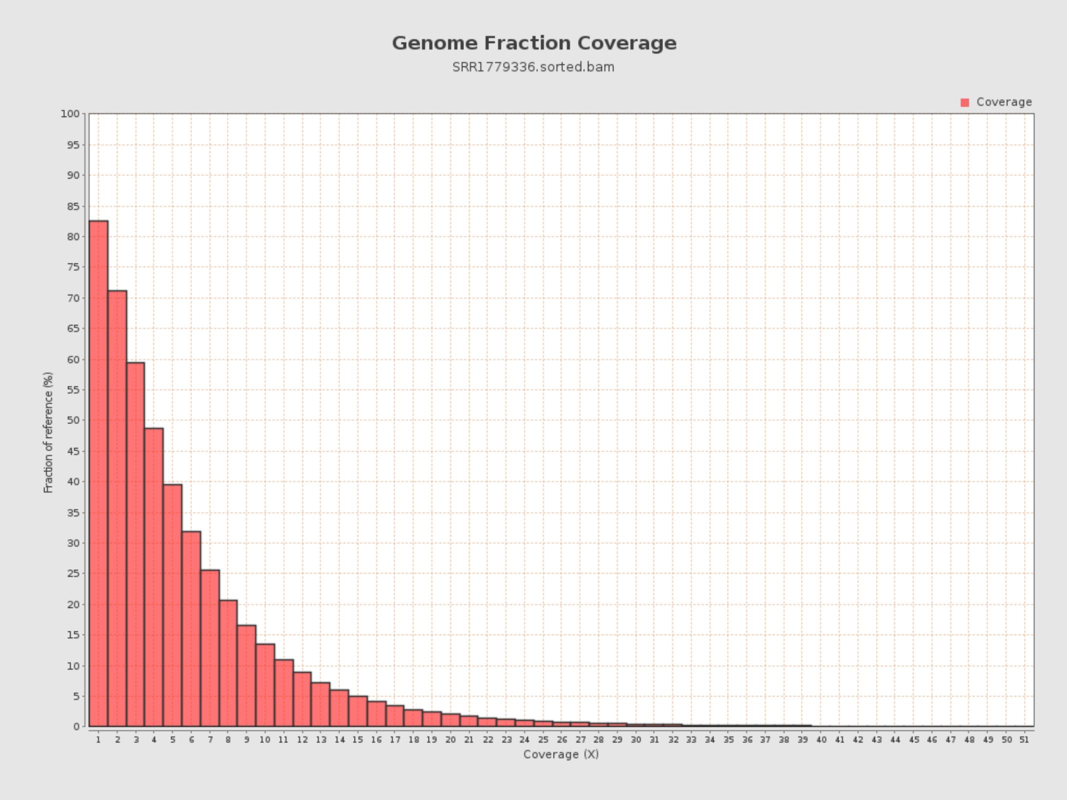
4. Results : Coverage Histogram



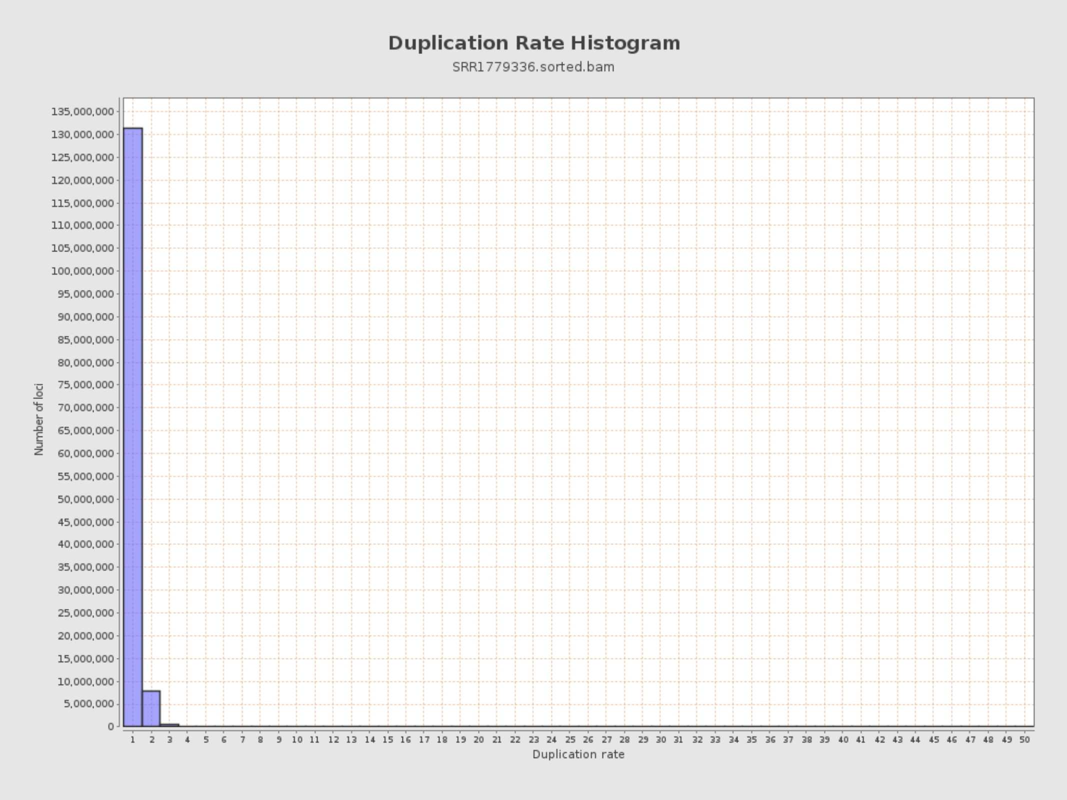
5. Results : Coverage Histogram (0-50X)



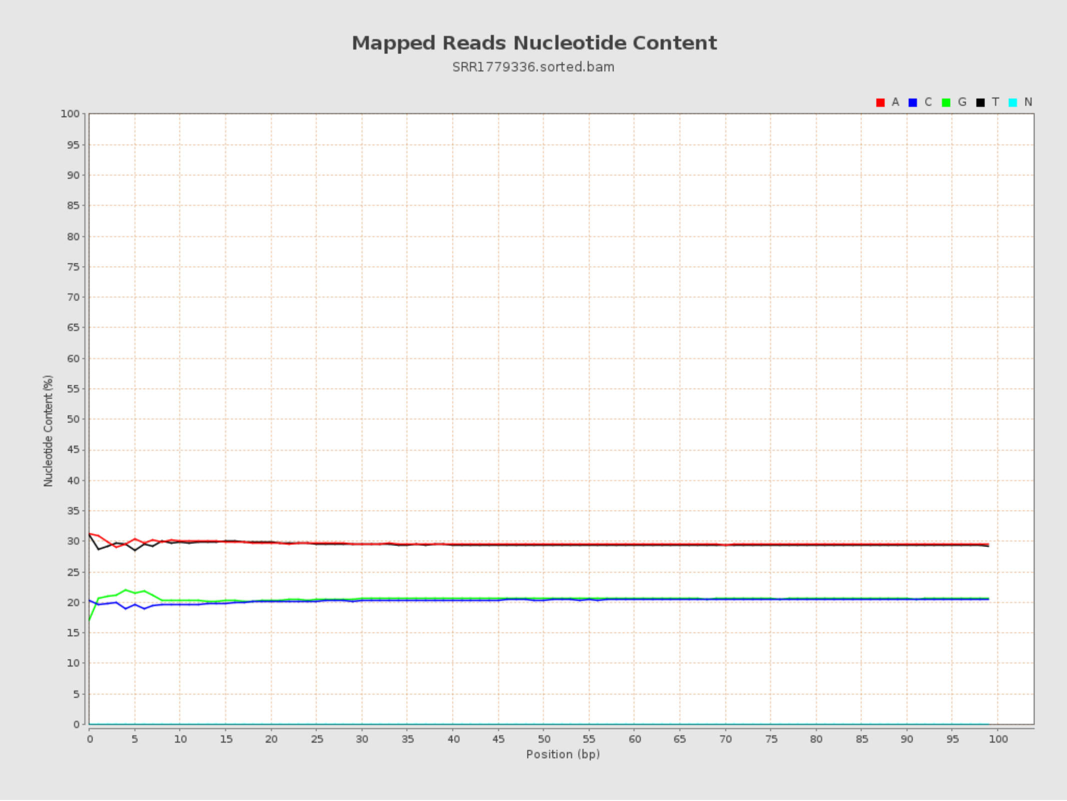
6. Results : Genome Fraction Coverage



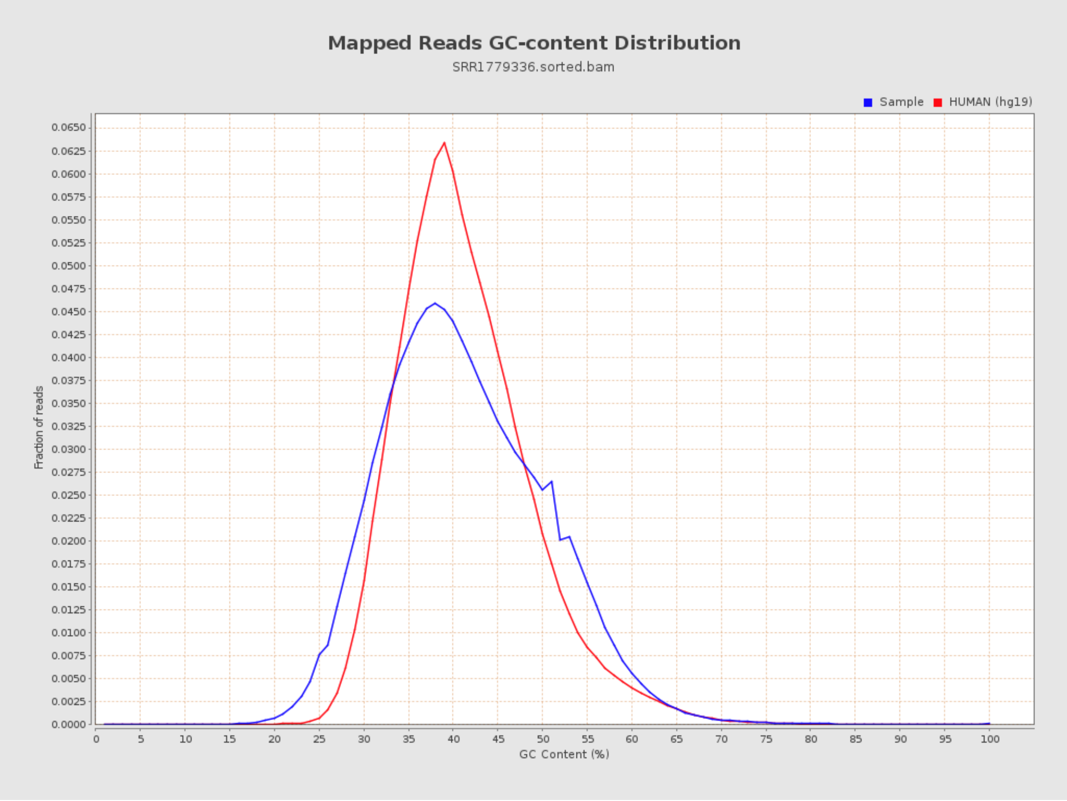
7. Results : Duplication Rate Histogram



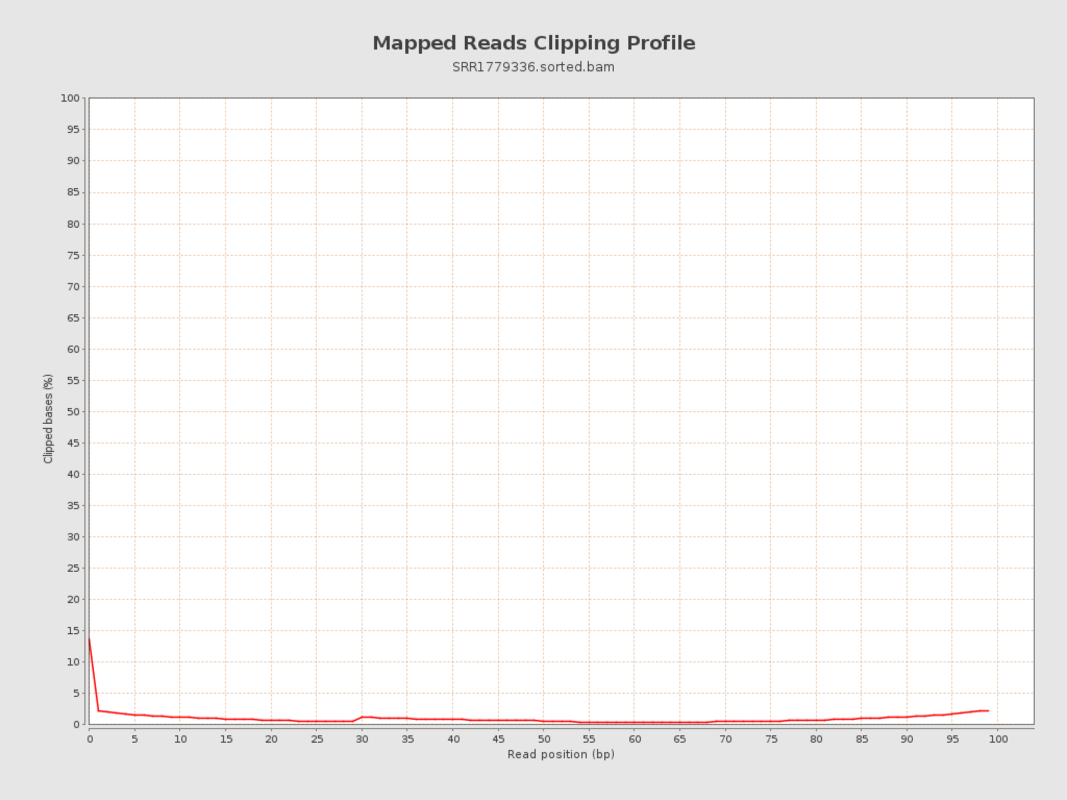
8. Results : Mapped Reads Nucleotide Content



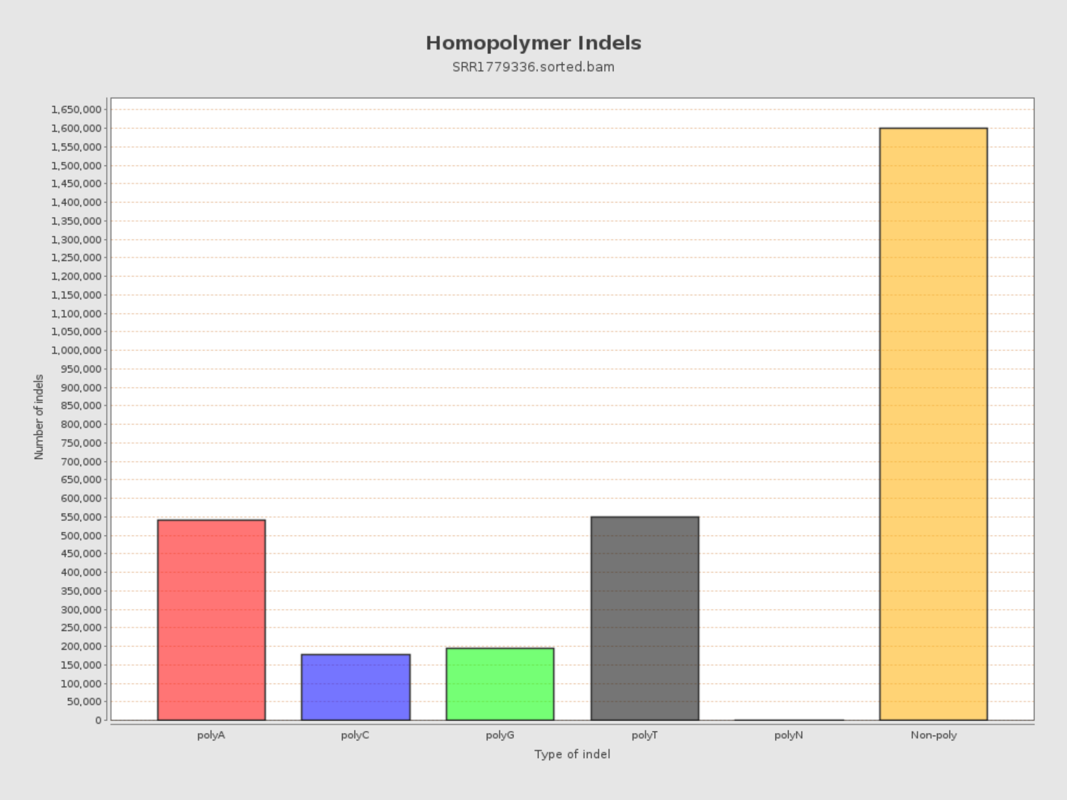
9. Results : Mapped Reads GC-content Distribution



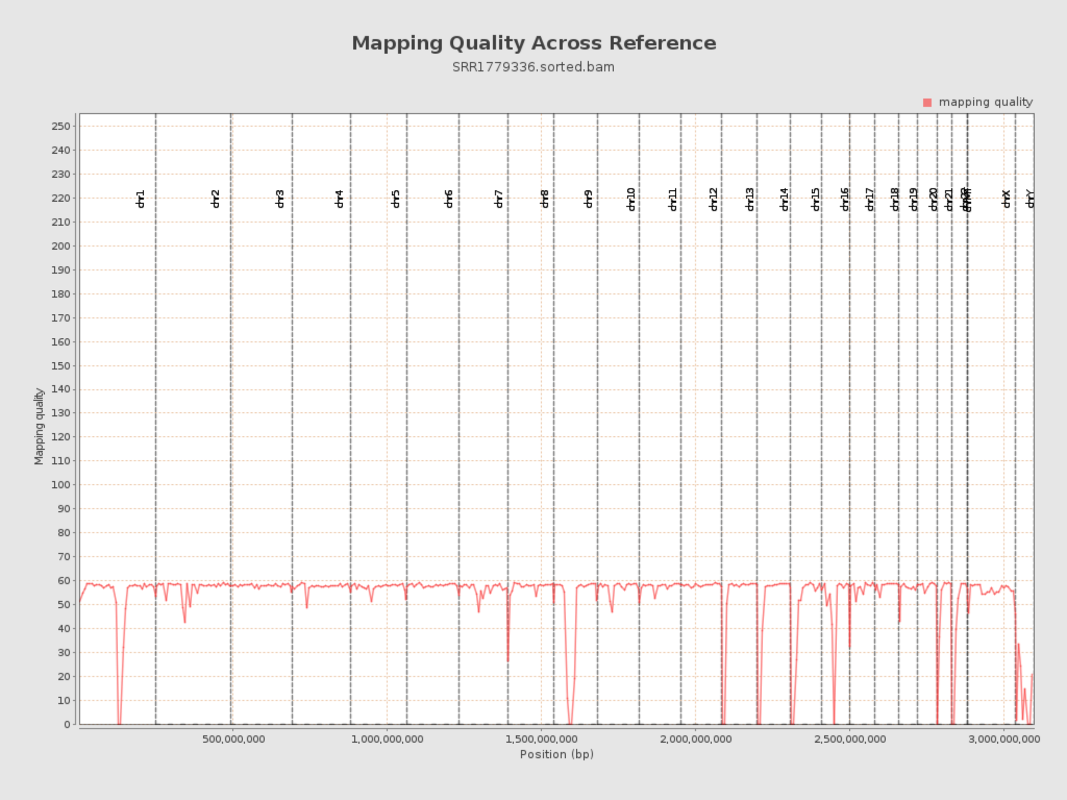
10. Results : Mapped Reads Clipping Profile



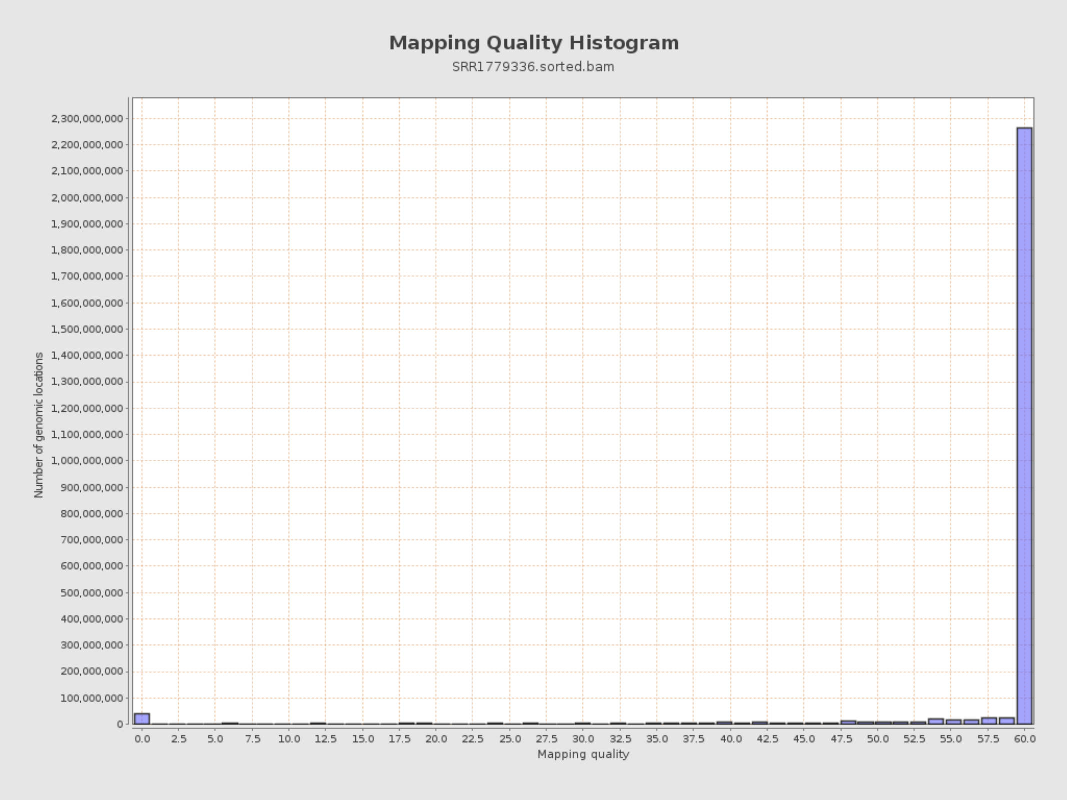
11. Results : Homopolymer Indels



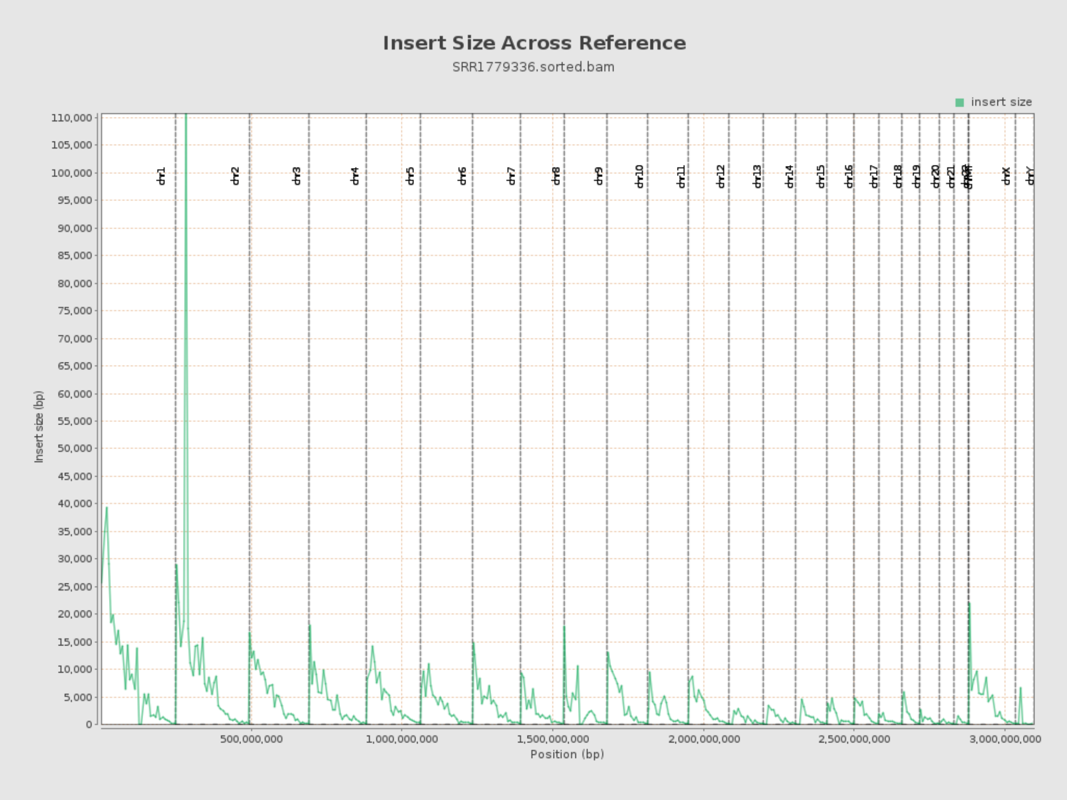
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram