Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 15:48:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777254.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_SRR1777254 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777254_1.fastq.gz SRR1777254_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 15:48:56 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777254.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,849,002
Mapped reads	20,684,202 / 99.21%
Unmapped reads	164,800 / 0.79%
Mapped paired reads	20,684,202 / 99.21%
Mapped reads, first in pair	10,344,057 / 49.61%
Mapped reads, second in pair	10,340,145 / 49.6%
Mapped reads, both in pair	20,612,336 / 98.86%
Mapped reads, singletons	71,866 / 0.34%
Secondary alignments	0
Supplementary alignments	836,243 / 4.01%
Read min/max/mean length	30 / 101 / 102.62
Duplicated reads (estimated)	8,202,335 / 39.34%
Duplication rate	31.51%
Clipped reads	3,272,352 / 15.7%

2.2. ACGT Content

Number/percentage of A's	560,052,178 / 27.37%
Number/percentage of C's	461,957,329 / 22.57%
Number/percentage of T's	558,469,102 / 27.29%
Number/percentage of G's	465,784,499 / 22.76%
Number/percentage of N's	85,713 / 0%

GC Percentage	45.34%

2.3. Coverage

Mean	0.6614
Standard Deviation	33.3236

2.4. Mapping Quality

Mean Mapping Quality	54.54

2.5. Insert size

Mean	245,421.75
Standard Deviation	3,576,507.96
P25/Median/P75	179 / 226 / 283

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	7,200,395
Insertions	482,812
Mapped reads with at least one insertion	2.23%
Deletions	340,435
Mapped reads with at least one deletion	1.48%
Homopolymer indels	36.45%

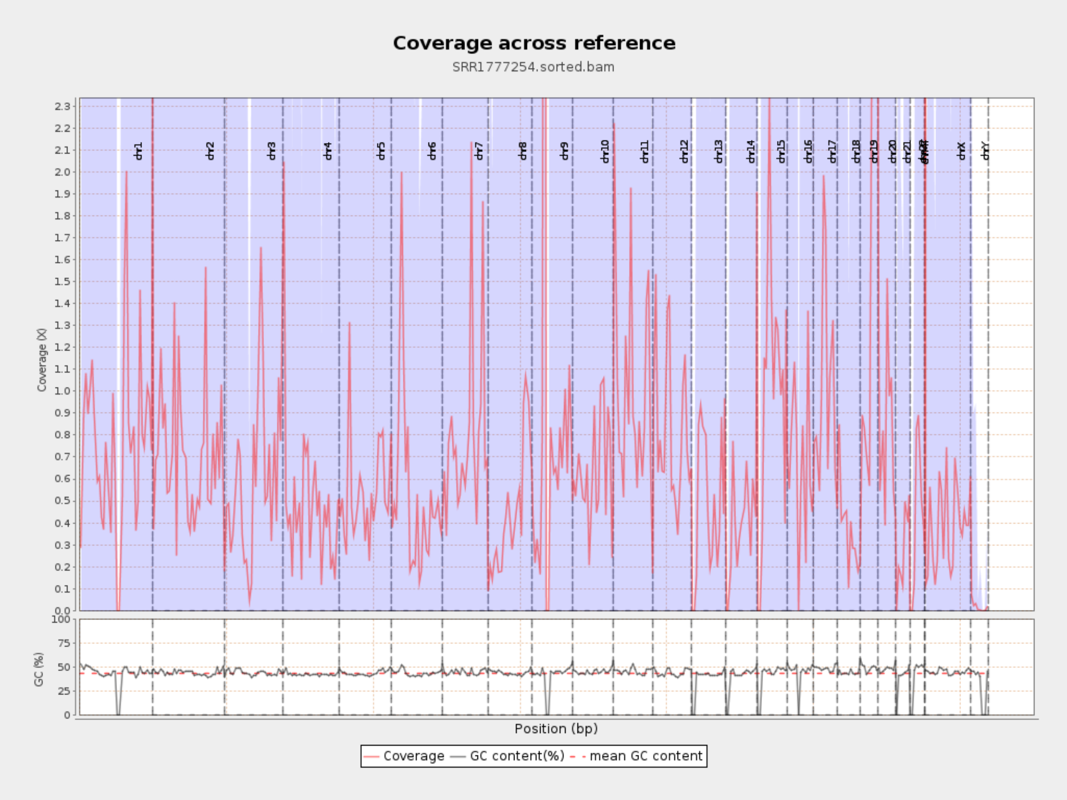
2.7. Chromosome stats

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

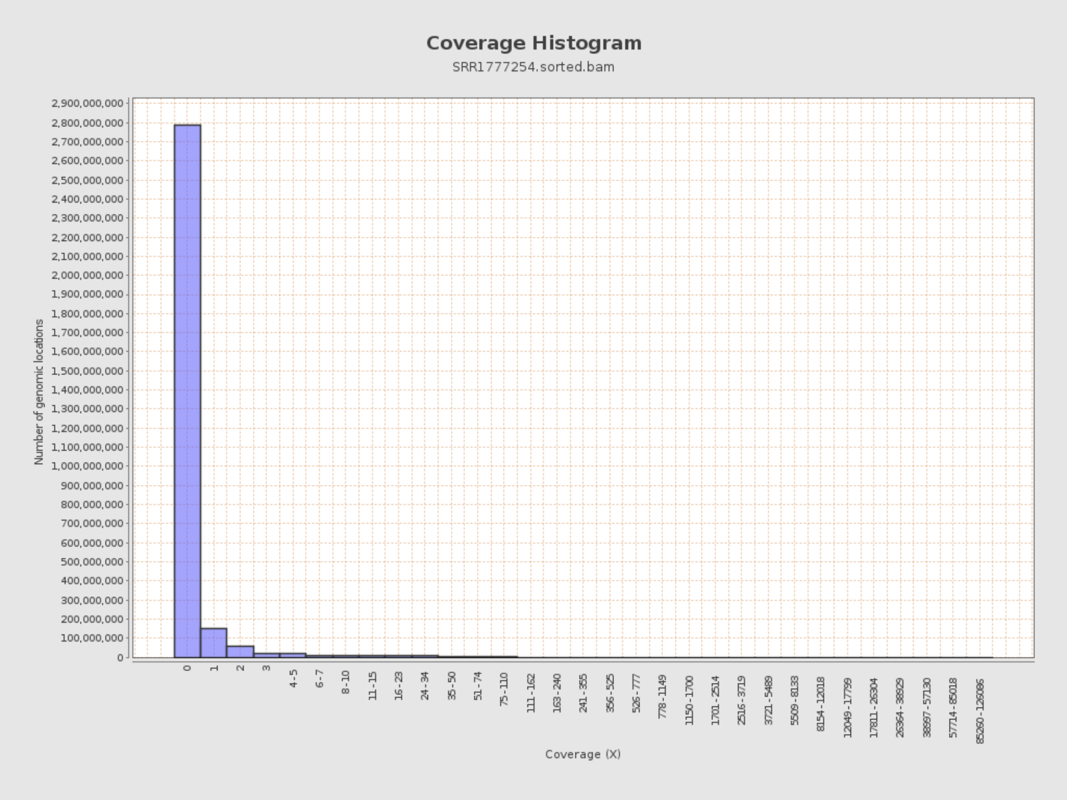
		bases	**coverage**	**deviation**
chr1	249250621	193848538	0.7777	6.4844
chr2	243199373	174773161	0.7186	6.3481
chr3	198022430	118424178	0.598	5.6755
chr4	191154276	92607114	0.4845	22.4638
chr5	180915260	97112269	0.5368	5.074
chr6	171115067	89018693	0.5202	5.0838
chr7	159138663	126853212	0.7971	9.6337
chr8	146364022	66860768	0.4568	5.2084
chr9	141213431	136641187	0.9676	151.1861
chr10	135534747	86632025	0.6392	5.8786
chr11	135006516	136470178	1.0108	8.3639
chr12	133851895	110898967	0.8285	6.7709
chr13	115169878	55002229	0.4776	5.1977
chr14	107349540	42209846	0.3932	4.0383
chr15	102531392	99964699	0.975	8.5139
chr16	90354753	60256725	0.6669	5.49
chr17	81195210	82909823	1.0211	7.9363
chr18	78077248	30209967	0.3869	5.5049
chr19	59128983	98751412	1.6701	11.8699
chr20	63025520	53265273	0.8451	6.9055
chr21	48129895	13236801	0.275	3.4751
chr22	51304566	21621460	0.4214	4.0277
chrMT	16571	768289	46.3635	20.9667
chrX	155270560	58096972	0.3742	4.5085

chrY	59373566	971008	0.0164	0.8206

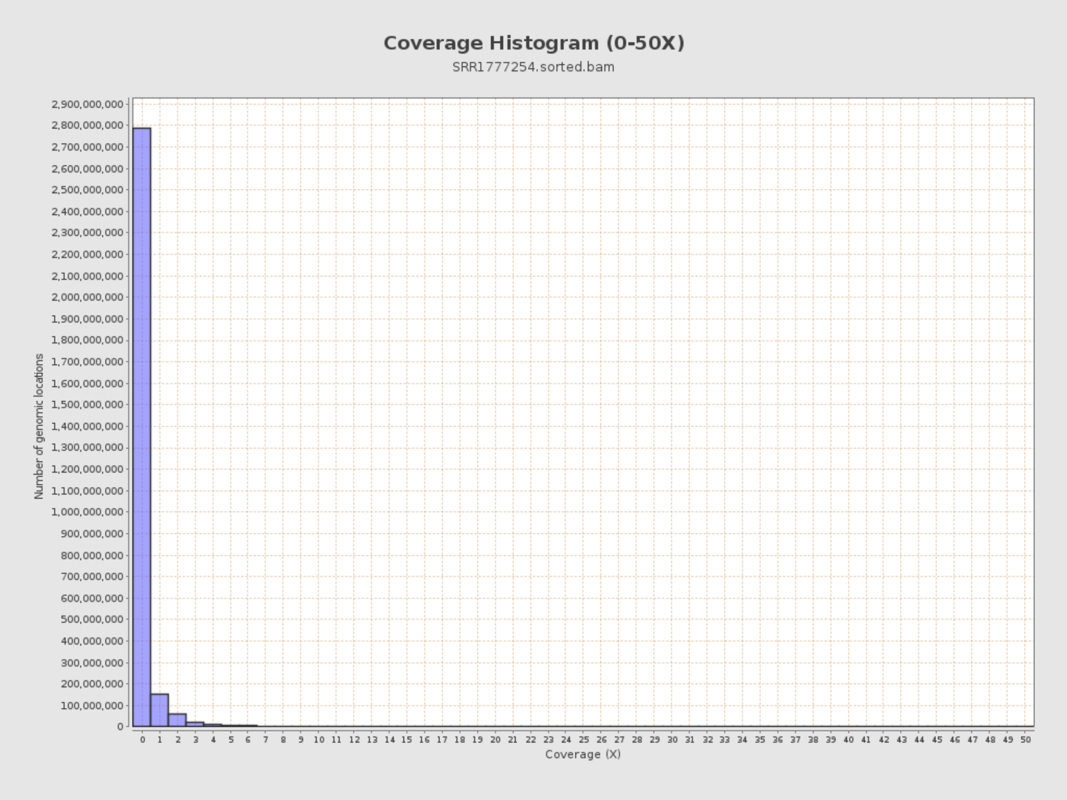
3. Results : Coverage across reference



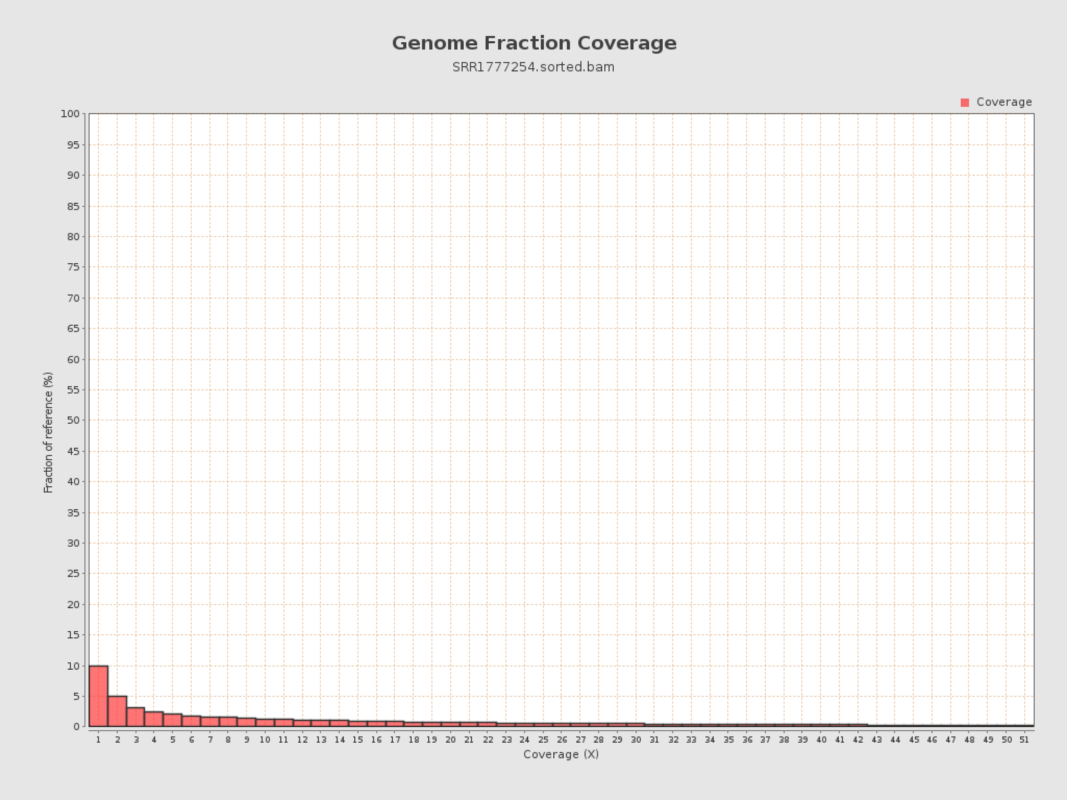
4. Results : Coverage Histogram



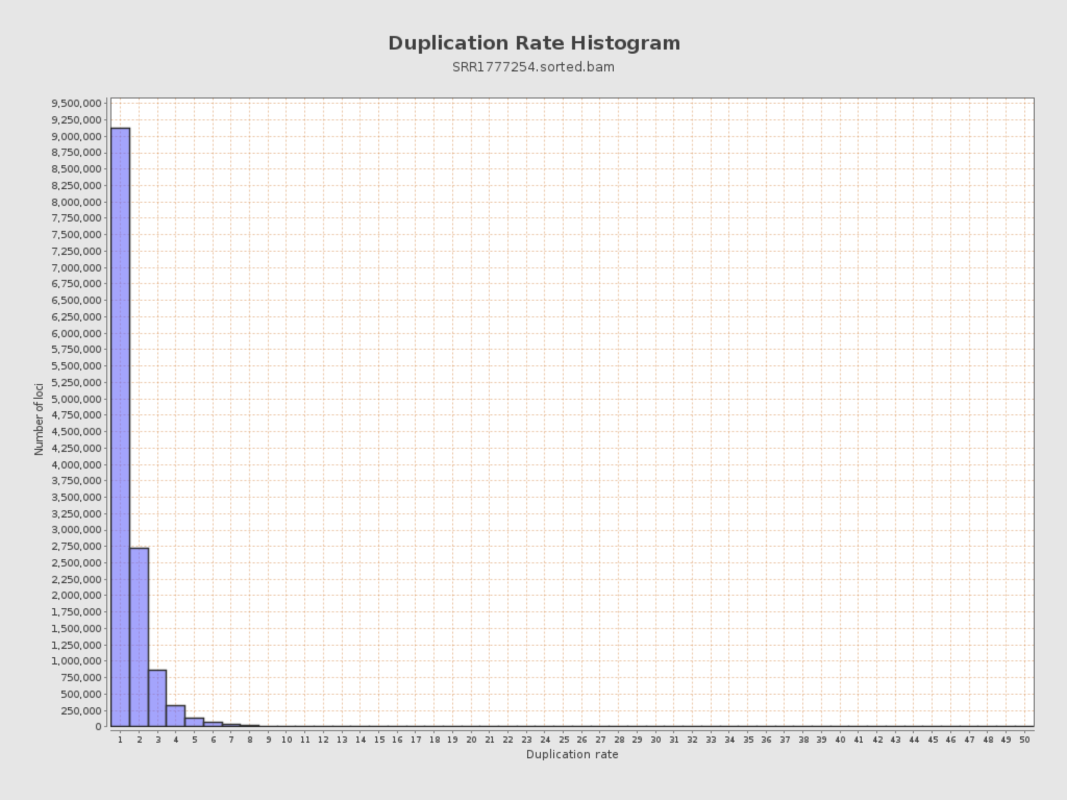
5. Results : Coverage Histogram (0-50X)



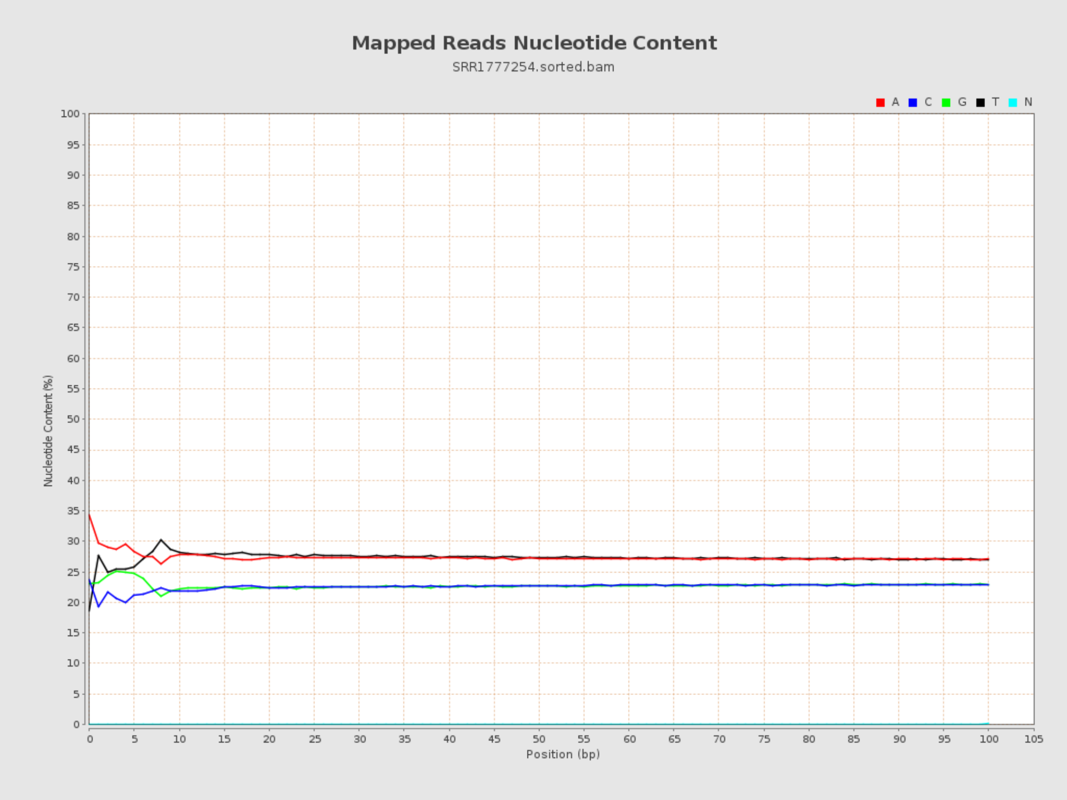
6. Results : Genome Fraction Coverage



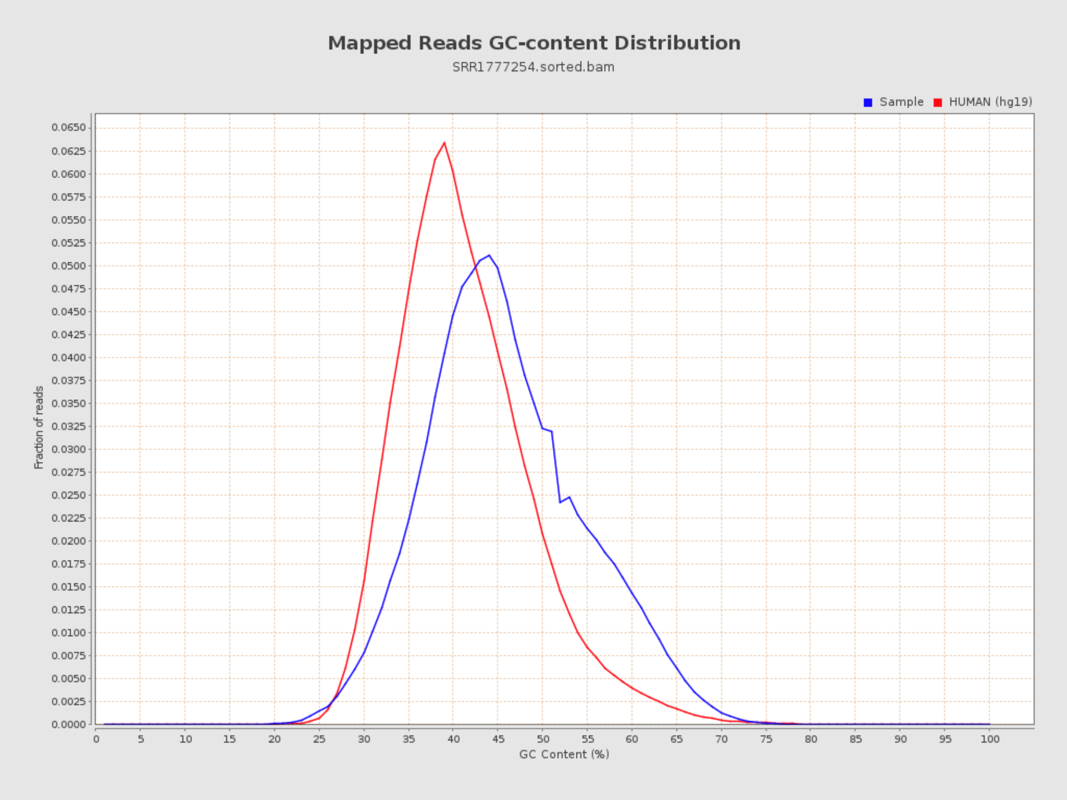
7. Results : Duplication Rate Histogram



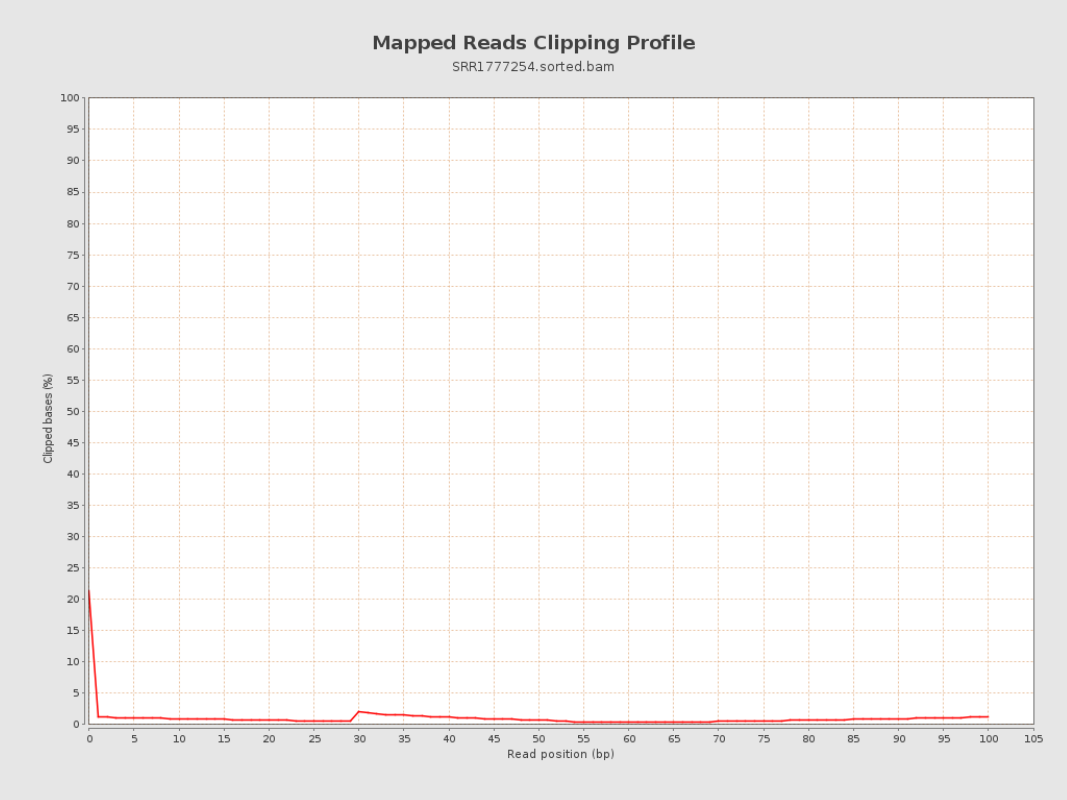
8. Results : Mapped Reads Nucleotide Content



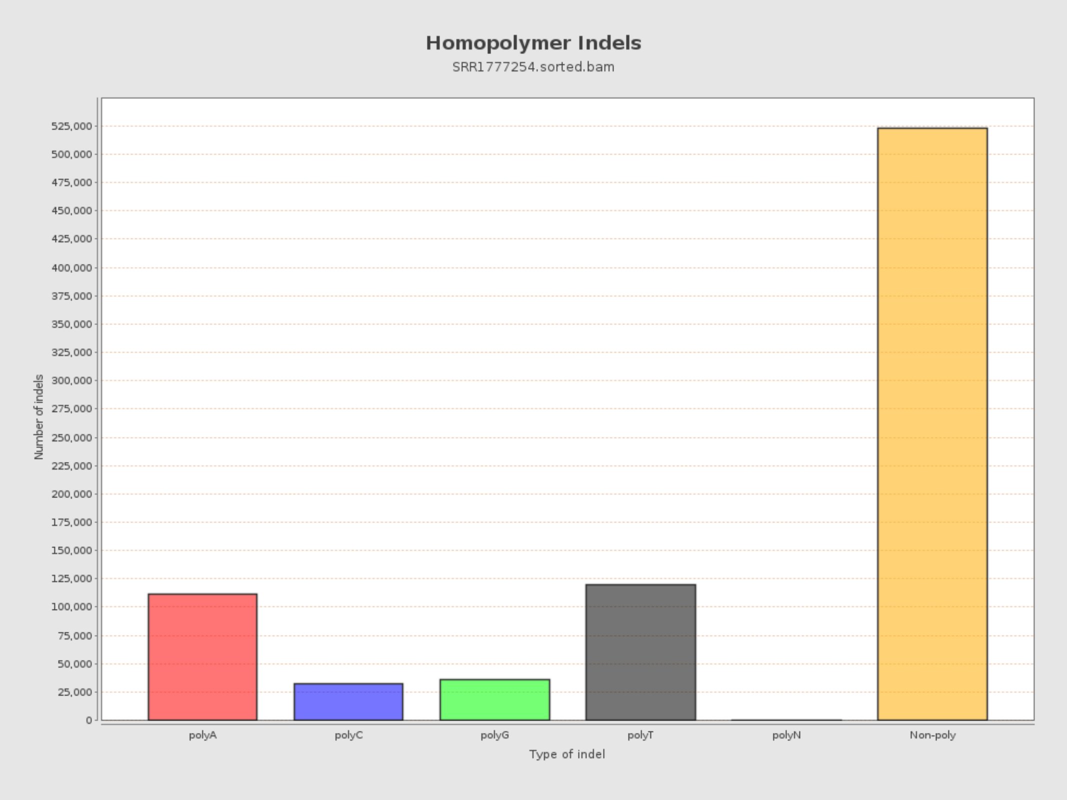
9. Results : Mapped Reads GC-content Distribution



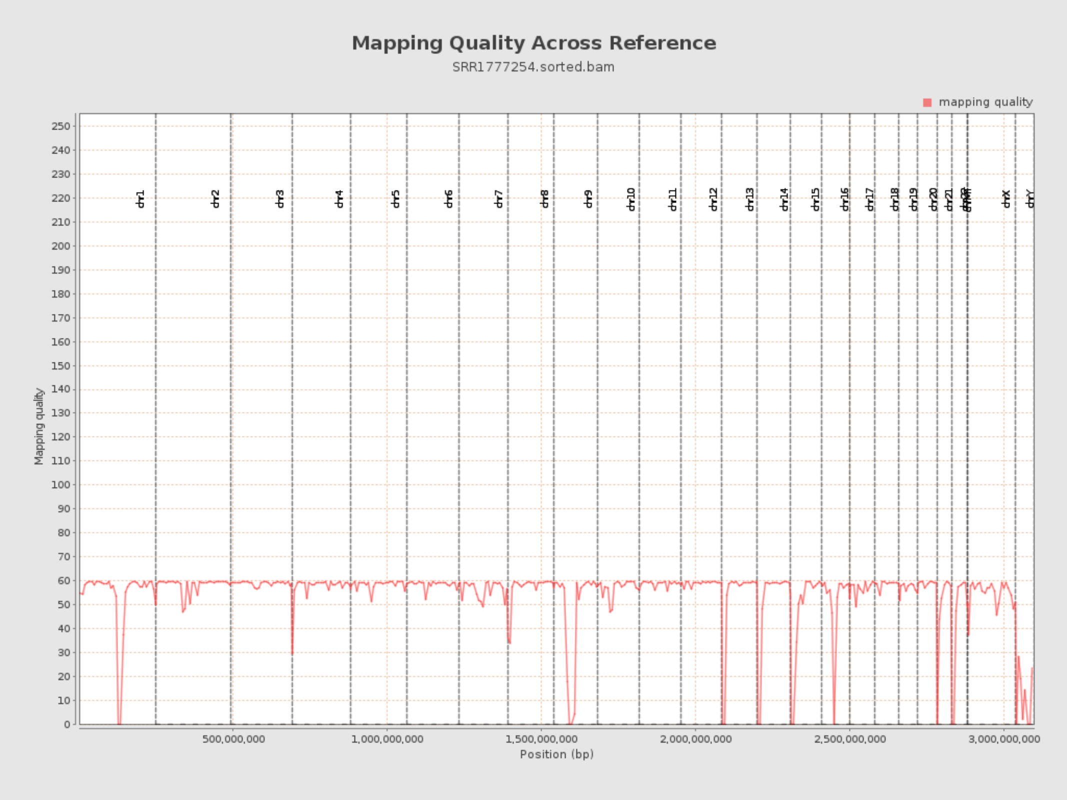
10. Results : Mapped Reads Clipping Profile



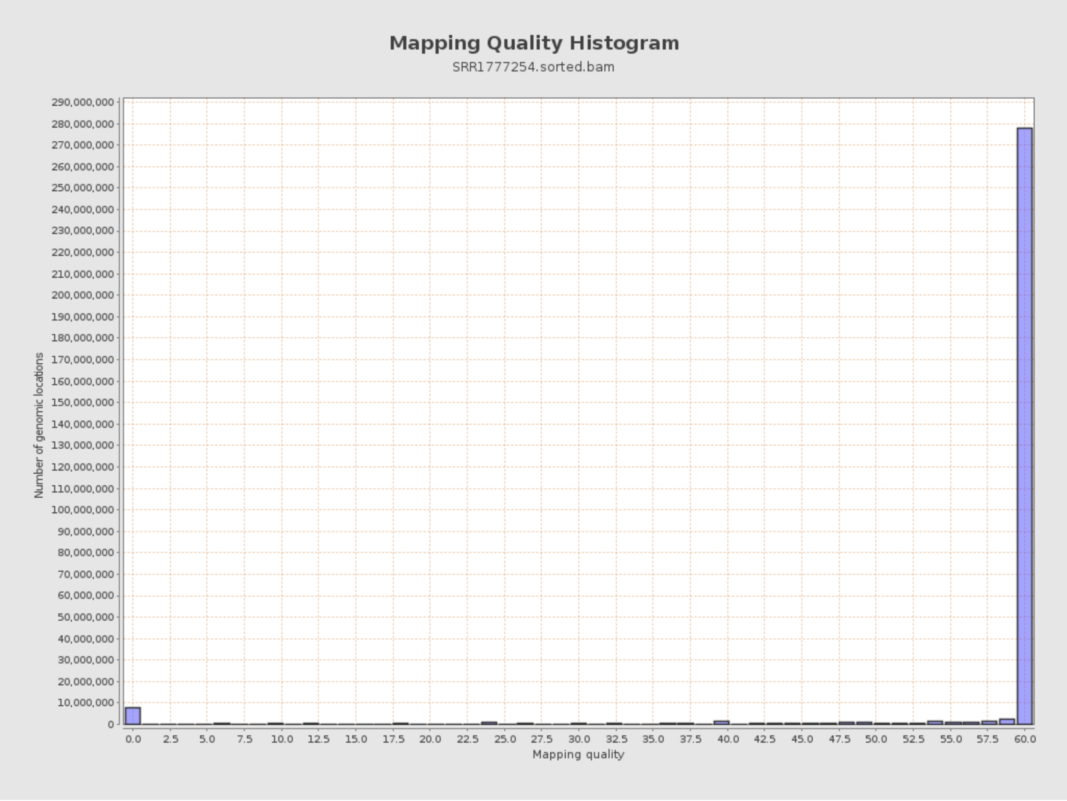
11. Results : Homopolymer Indels



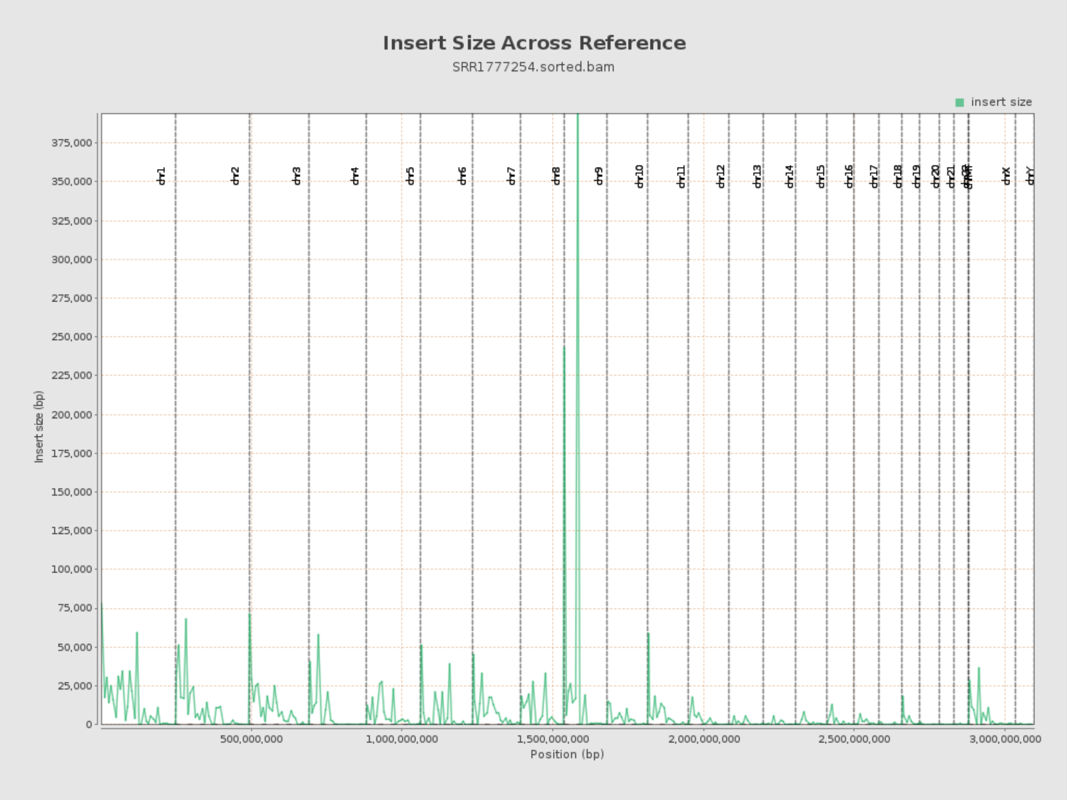
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram