Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 04:25:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777261.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_SRR1777261 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777261_1.fastq.gz SRR1777261_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 04:25:28 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777261.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	82,566,514
Mapped reads	82,373,923 / 99.77%
Unmapped reads	192,591 / 0.23%
Mapped paired reads	82,373,923 / 99.77%
Mapped reads, first in pair	41,190,527 / 49.89%
Mapped reads, second in pair	41,183,396 / 49.88%
Mapped reads, both in pair	82,315,312 / 99.7%
Mapped reads, singletons	58,611 / 0.07%
Secondary alignments	0
Supplementary alignments	2,429,965 / 2.94%
Read min/max/mean length	30 / 101 / 102.22
Duplicated reads (estimated)	44,135,968 / 53.46%
Duplication rate	43.51%
Clipped reads	8,956,753 / 10.85%

2.2. ACGT Content

Number/percentage of A's	2,274,234,720 / 27.51%
Number/percentage of C's	1,842,661,759 / 22.29%
Number/percentage of T's	2,255,666,343 / 27.28%
Number/percentage of G's	1,856,126,318 / 22.45%
Number/percentage of N's	39,092,855 / 0.47%

GC Percentage	44.74%

2.3. Coverage

Mean	2.6711
Standard Deviation	24.3865

2.4. Mapping Quality

Mean Mapping Quality	54.7

2.5. Insert size

Mean	282,107.15
Standard Deviation	5,239,592.76
P25/Median/P75	196 / 248 / 316

2.6. Mismatches and indels

General error rate	0.73%
Mismatches	58,058,127
Insertions	1,600,775
Mapped reads with at least one insertion	1.91%
Deletions	581,053
Mapped reads with at least one deletion	0.7%
Homopolymer indels	51.07%

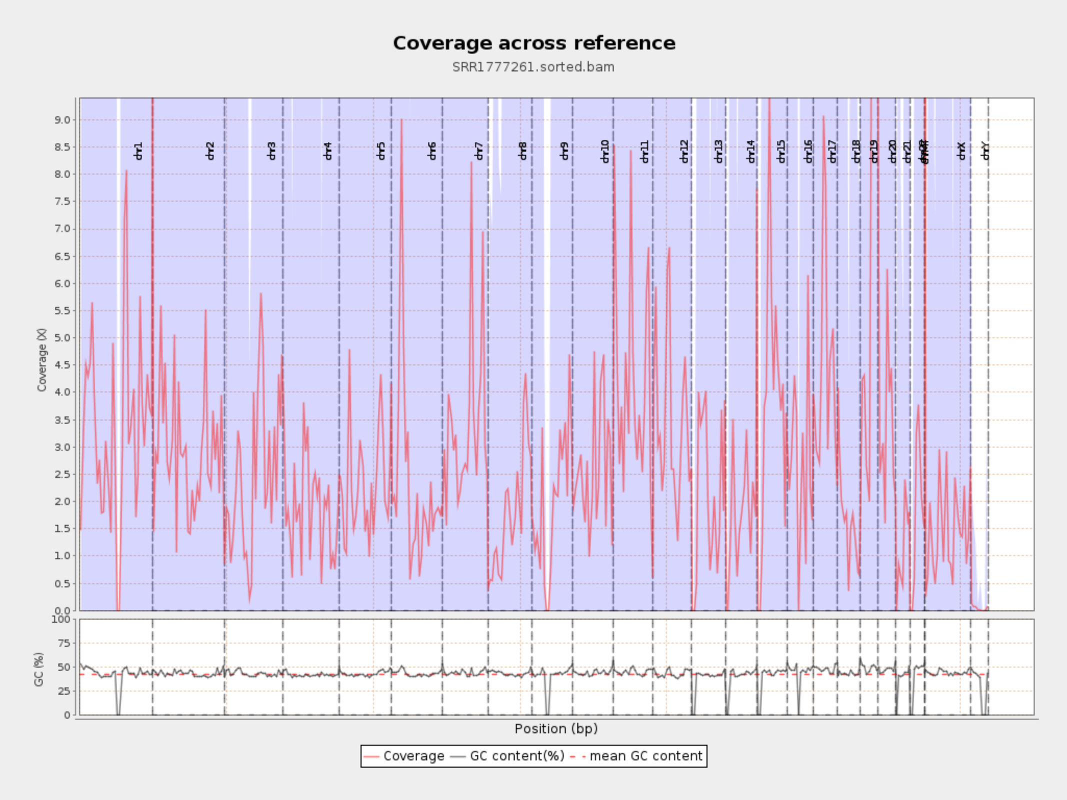
2.7. Chromosome stats

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

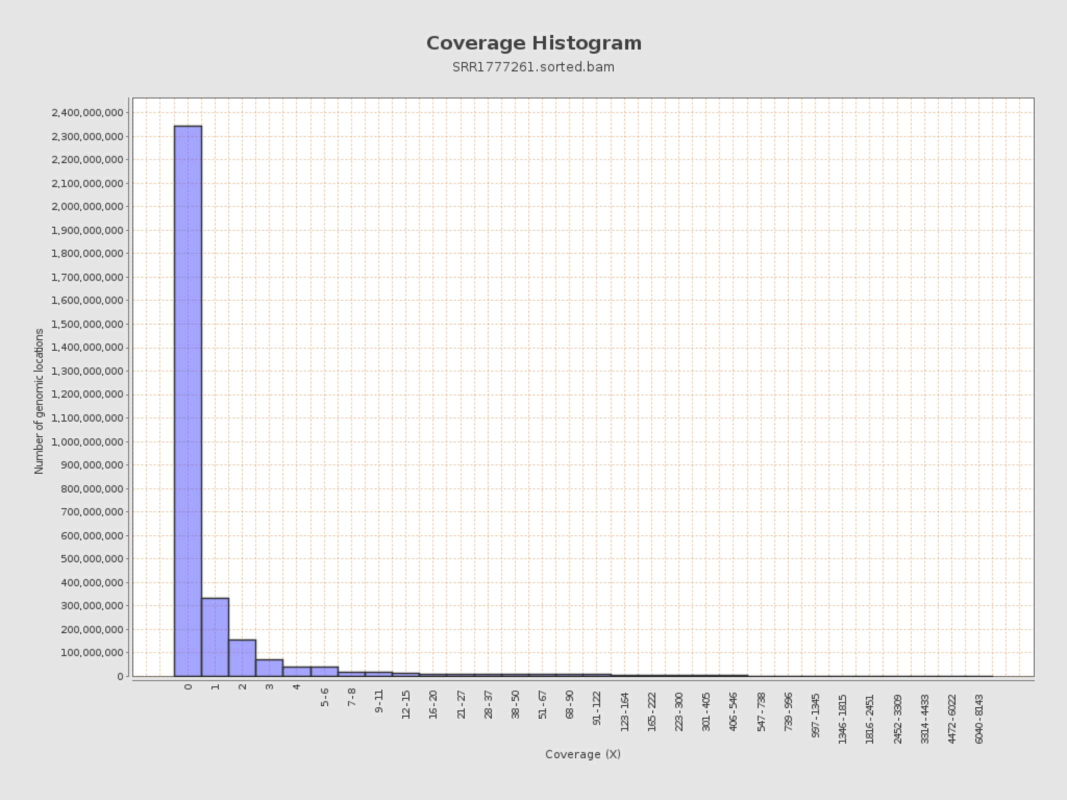
		bases	coverage	deviation
chr1	249250621	853522218	3.4244	27.7378
chr2	243199373	717485752	2.9502	25.0272
chr3	198022430	486362835	2.4561	23.1898
chr4	191154276	359947061	1.883	19.1573
chr5	180915260	421930346	2.3322	22.1005
chr6	171115067	389089568	2.2738	22.3539
chr7	159138663	539188395	3.3882	29.3585
chr8	146364022	268223091	1.8326	19.6341
chr9	141213431	279017943	1.9759	18.954
chr10	135534747	351656493	2.5946	23.4495
chr11	135006516	575379090	4.2619	34.4666
chr12	133851895	469612381	3.5084	27.7795
chr13	115169878	232966033	2.0228	21.9224
chr14	107349540	186583513	1.7381	18.6507
chr15	102531392	381244983	3.7183	30.5068
chr16	90354753	240094375	2.6572	21.0961
chr17	81195210	371279251	4.5727	32.1884
chr18	78077248	127802983	1.6369	17.3035
chr19	59128983	422500466	7.1454	42.7687
chr20	63025520	225723316	3.5815	27.9135
chr21	48129895	54689253	1.1363	14.2128
chr22	51304566	90614373	1.7662	16.065
chrMT	16571	2573029	155.273	52.3806
chrX	155270560	219155309	1.4114	16.7433

chrY	59373566	2385391	0.0402	1.6408

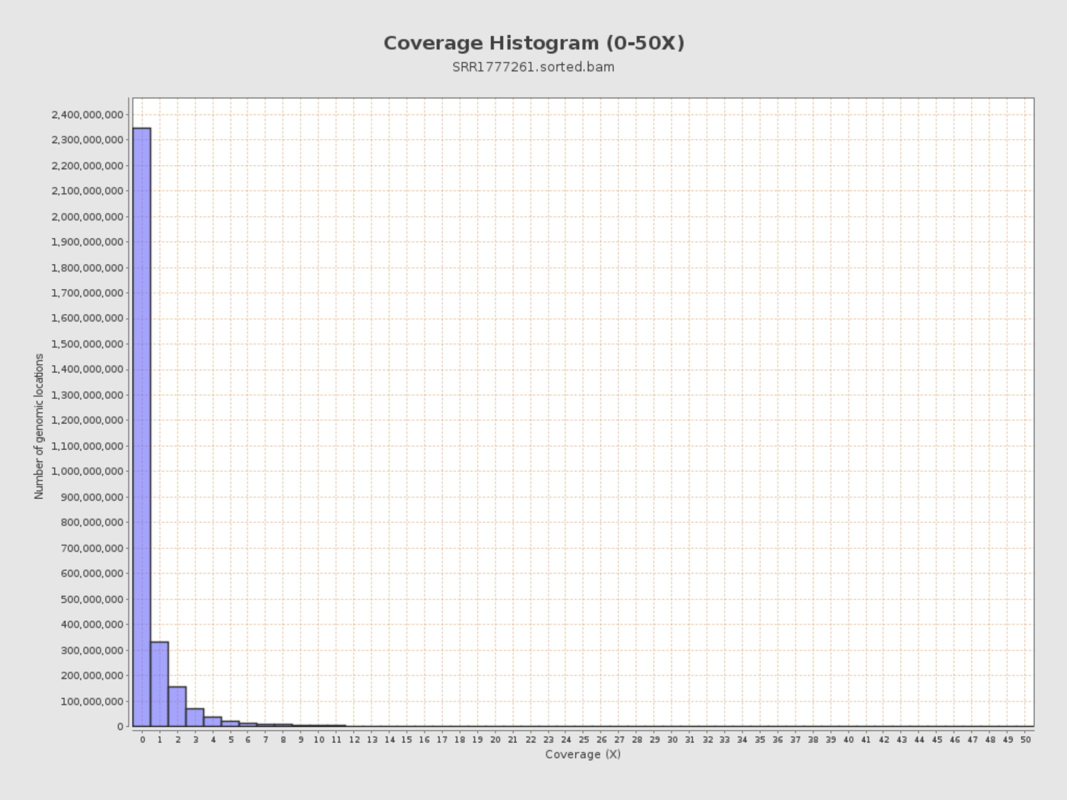
3. Results : Coverage across reference



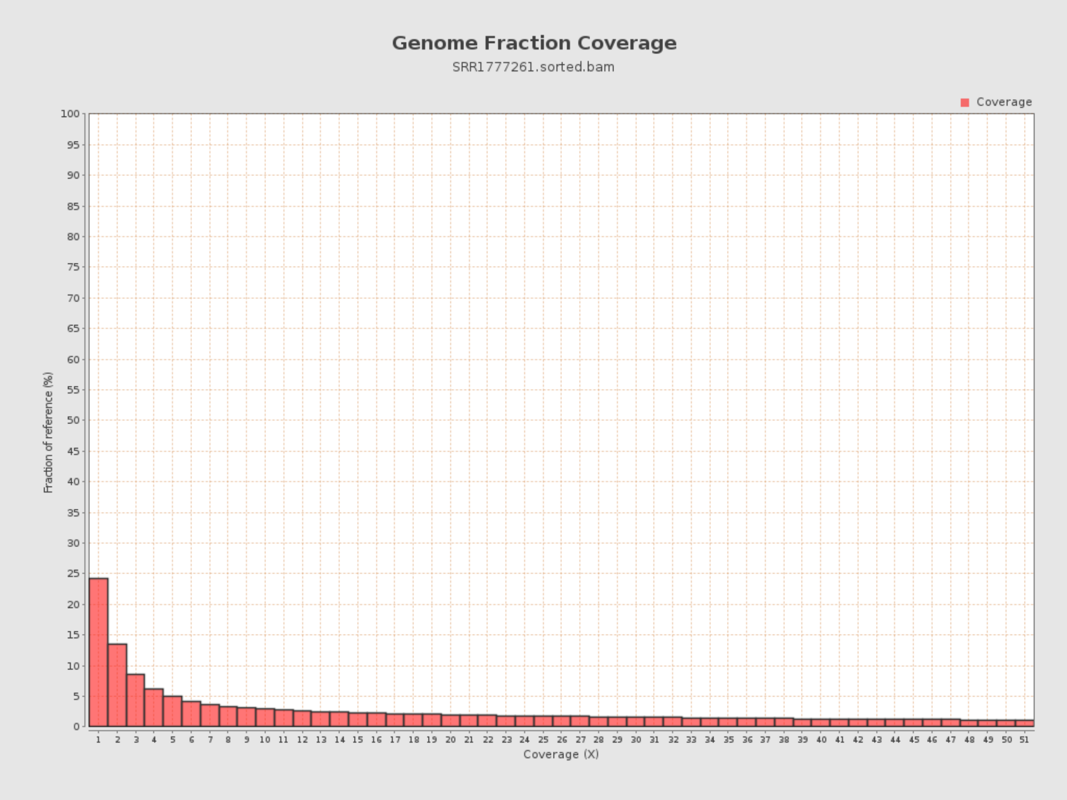
4. Results : Coverage Histogram



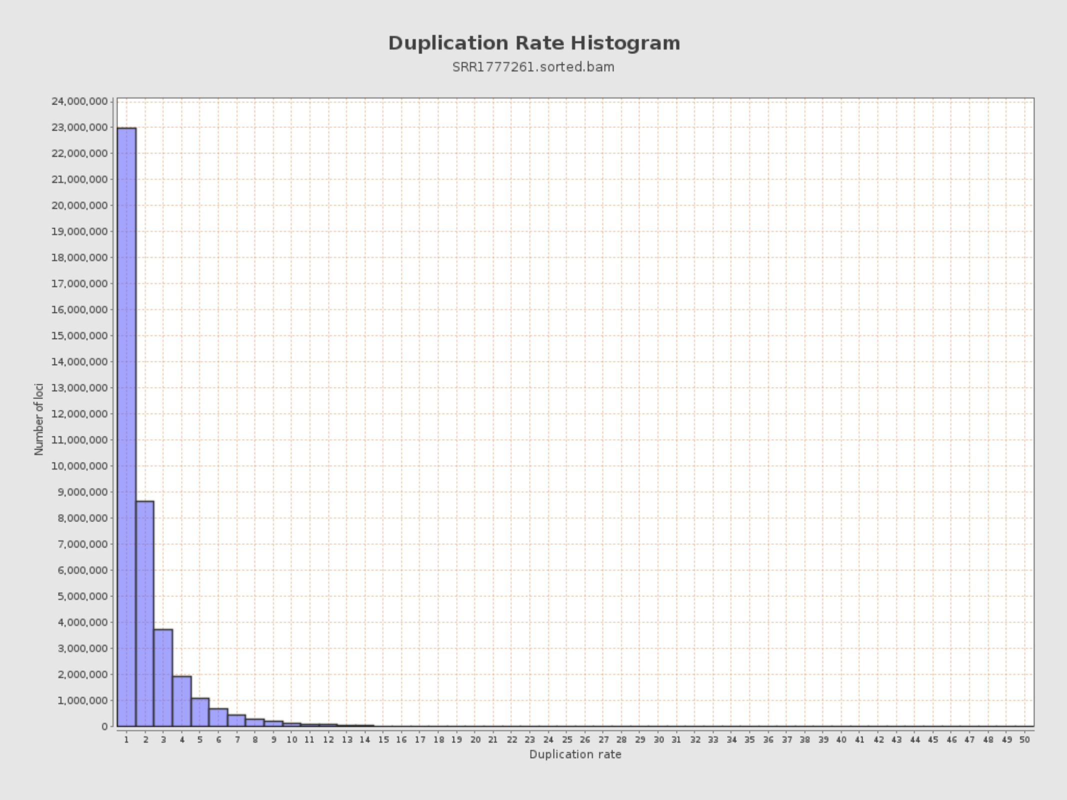
5. Results : Coverage Histogram (0-50X)



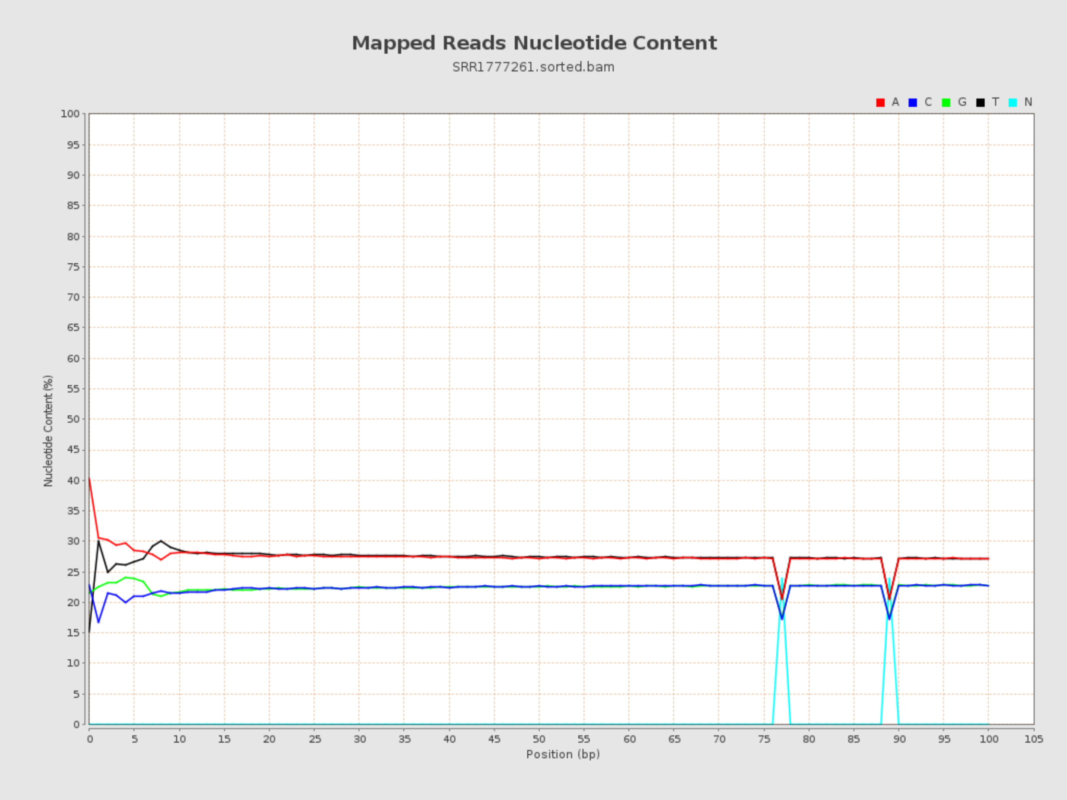
6. Results : Genome Fraction Coverage



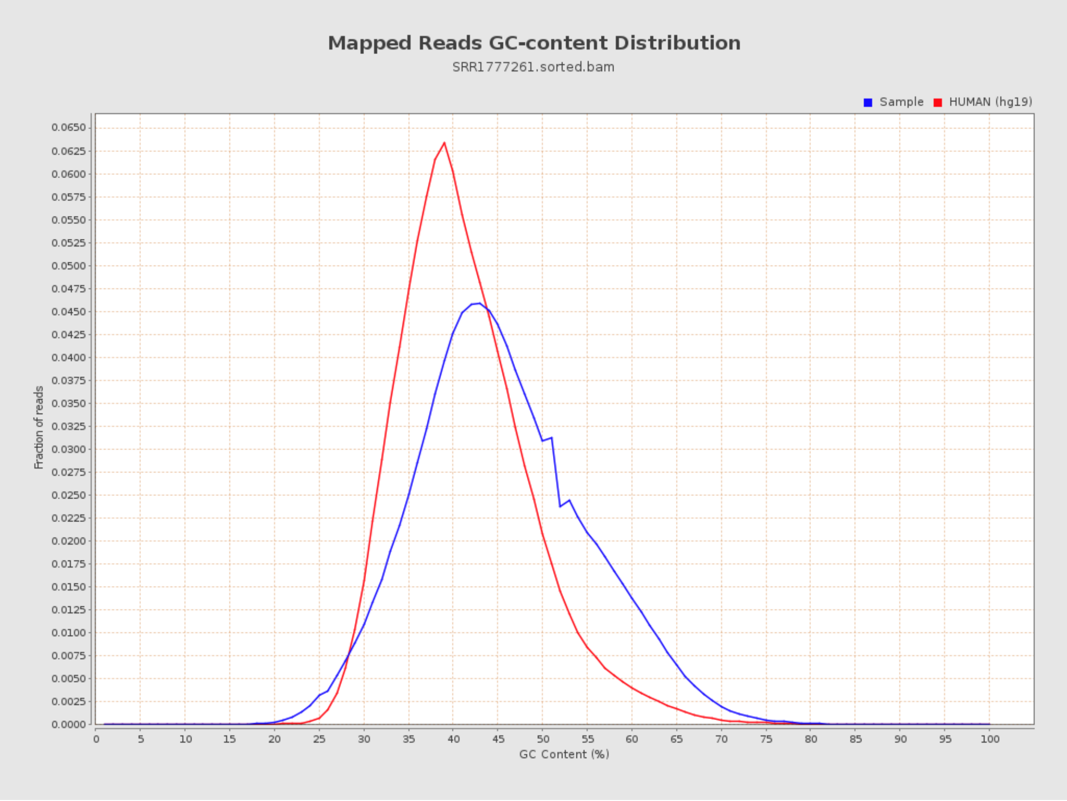
7. Results : Duplication Rate Histogram



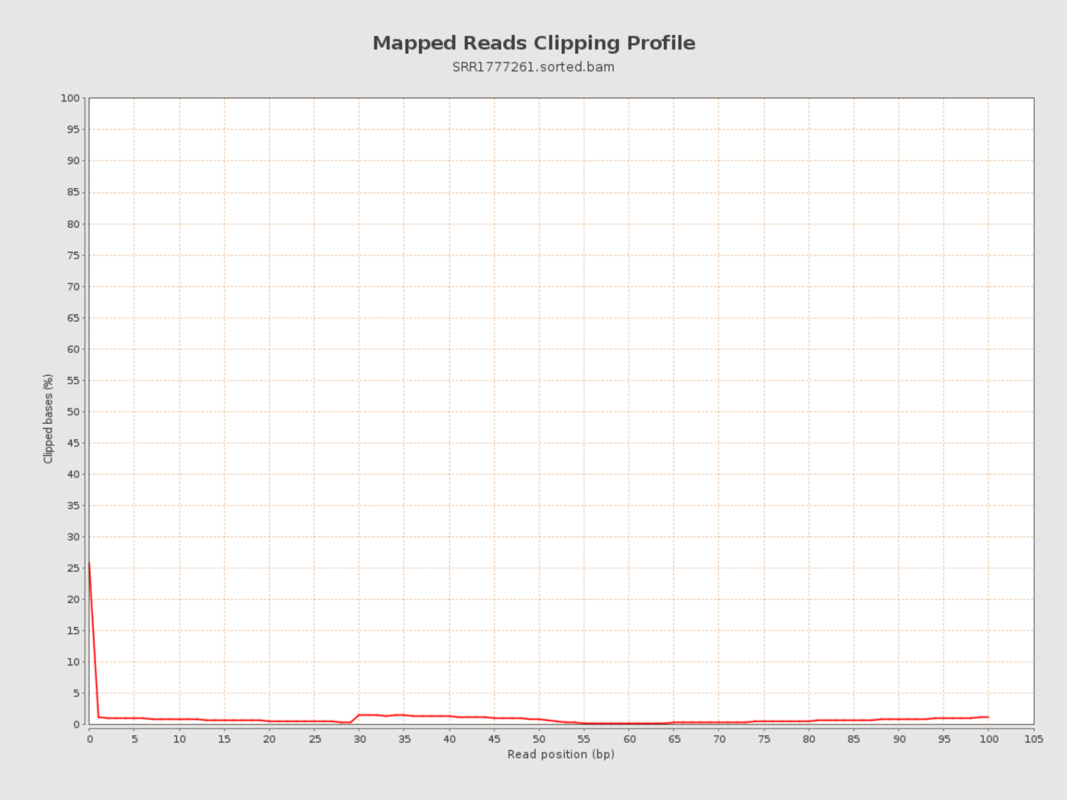
8. Results : Mapped Reads Nucleotide Content



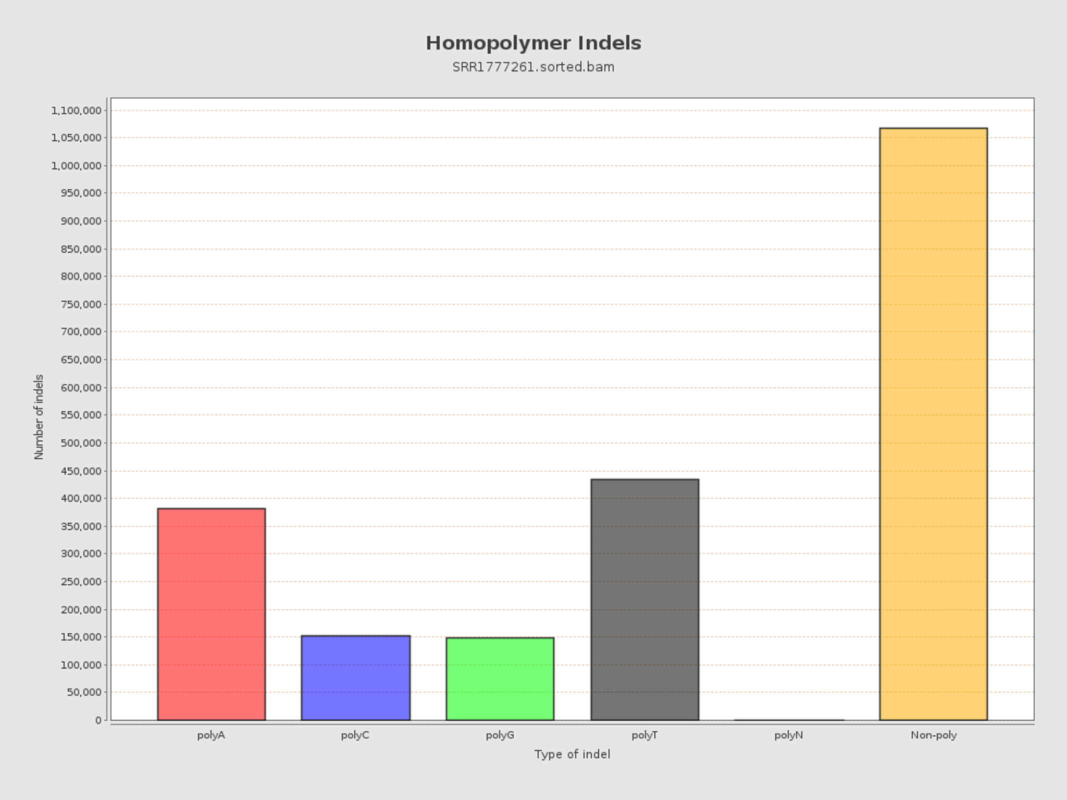
9. Results : Mapped Reads GC-content Distribution



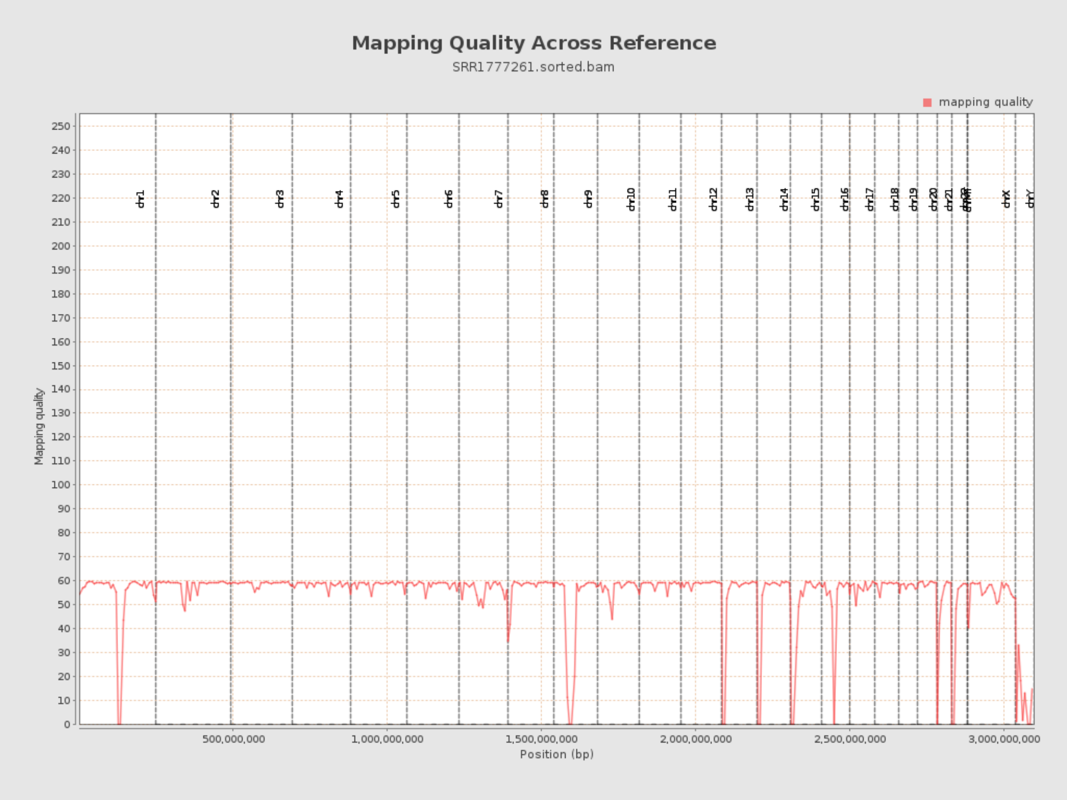
10. Results : Mapped Reads Clipping Profile



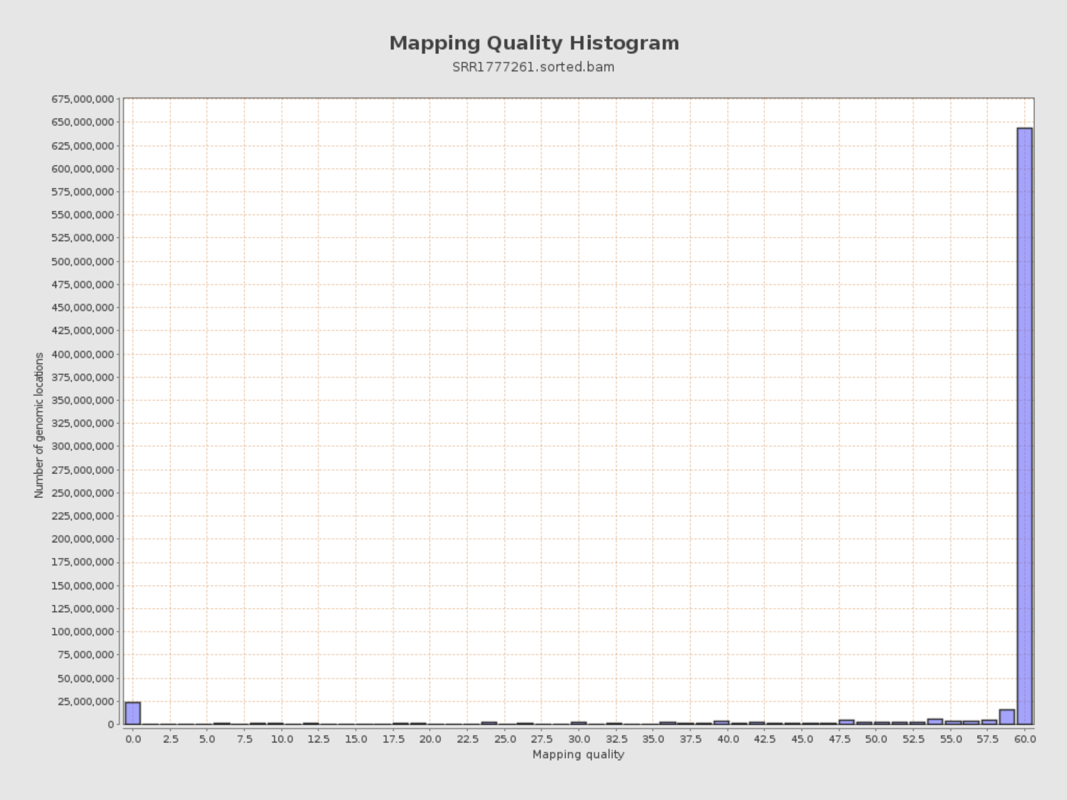
11. Results : Homopolymer Indels



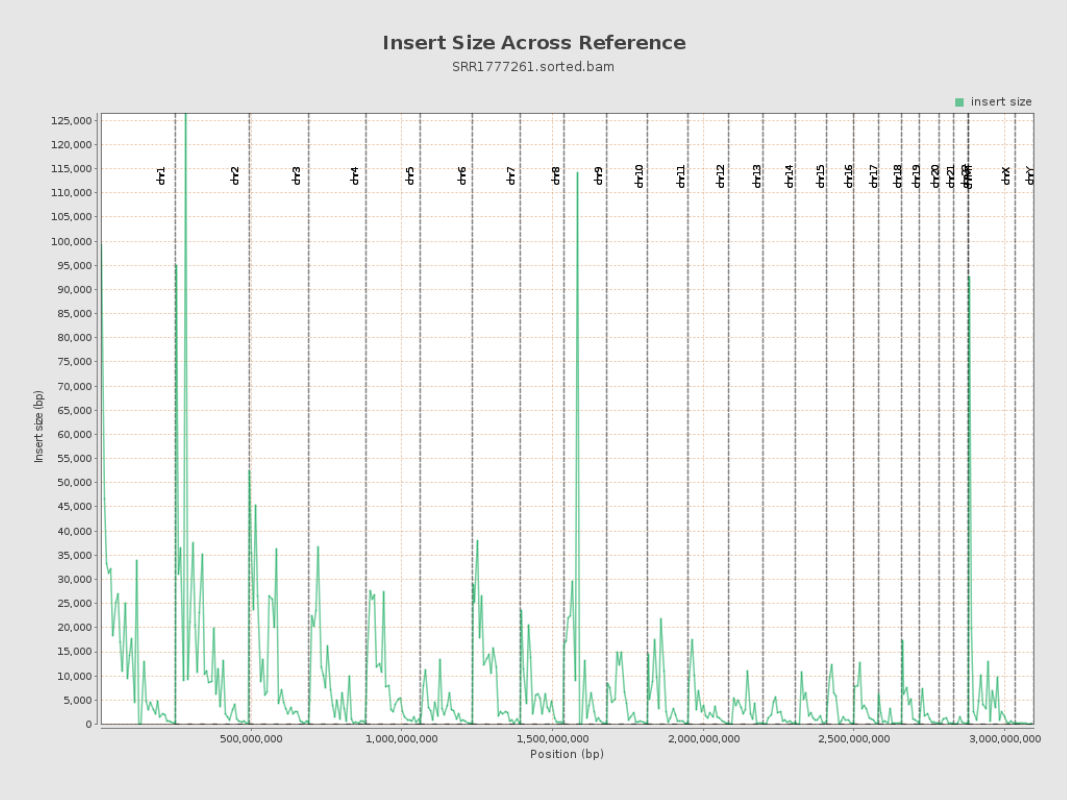
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram