Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 08:35:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777274.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_SRR1777274 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777274_1.fastq.gz SRR1777274_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 08:35:31 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777274.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,625,652
Mapped reads	12,330,507 / 97.66%
Unmapped reads	295,145 / 2.34%
Mapped paired reads	12,330,507 / 97.66%
Mapped reads, first in pair	6,183,997 / 48.98%
Mapped reads, second in pair	6,146,510 / 48.68%
Mapped reads, both in pair	12,276,932 / 97.24%
Mapped reads, singletons	53,575 / 0.42%
Secondary alignments	0
Supplementary alignments	84,320 / 0.67%
Read min/max/mean length	30 / 101 / 101.27
Duplicated reads (estimated)	893,678 / 7.08%
Duplication rate	7.05%
Clipped reads	2,592,026 / 20.53%

2.2. ACGT Content

Number/percentage of A's	323,774,502 / 27.32%
Number/percentage of C's	266,739,219 / 22.51%
Number/percentage of T's	318,244,135 / 26.85%
Number/percentage of G's	276,380,593 / 23.32%
Number/percentage of N's	22,155 / 0%

GC Percentage	45.83%

2.3. Coverage

Mean	0.3831
Standard Deviation	2.9519

2.4. Mapping Quality

Mean Mapping Quality	54.06

2.5. Insert size

Mean	84,570.82
Standard Deviation	3,003,143.1
P25/Median/P75	120 / 164 / 220

2.6. Mismatches and indels

General error rate	0.76%
Mismatches	8,646,183
Insertions	194,132
Mapped reads with at least one insertion	1.55%
Deletions	584,724
Mapped reads with at least one deletion	4.63%
Homopolymer indels	54.17%

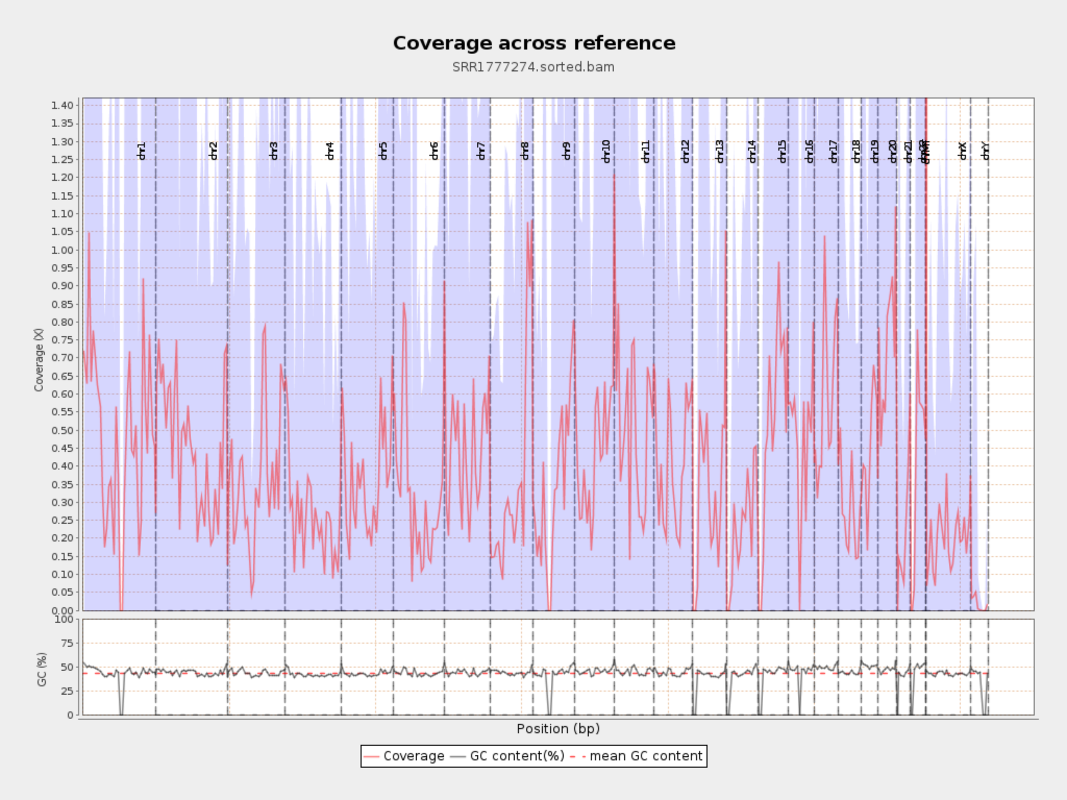
2.7. Chromosome stats

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

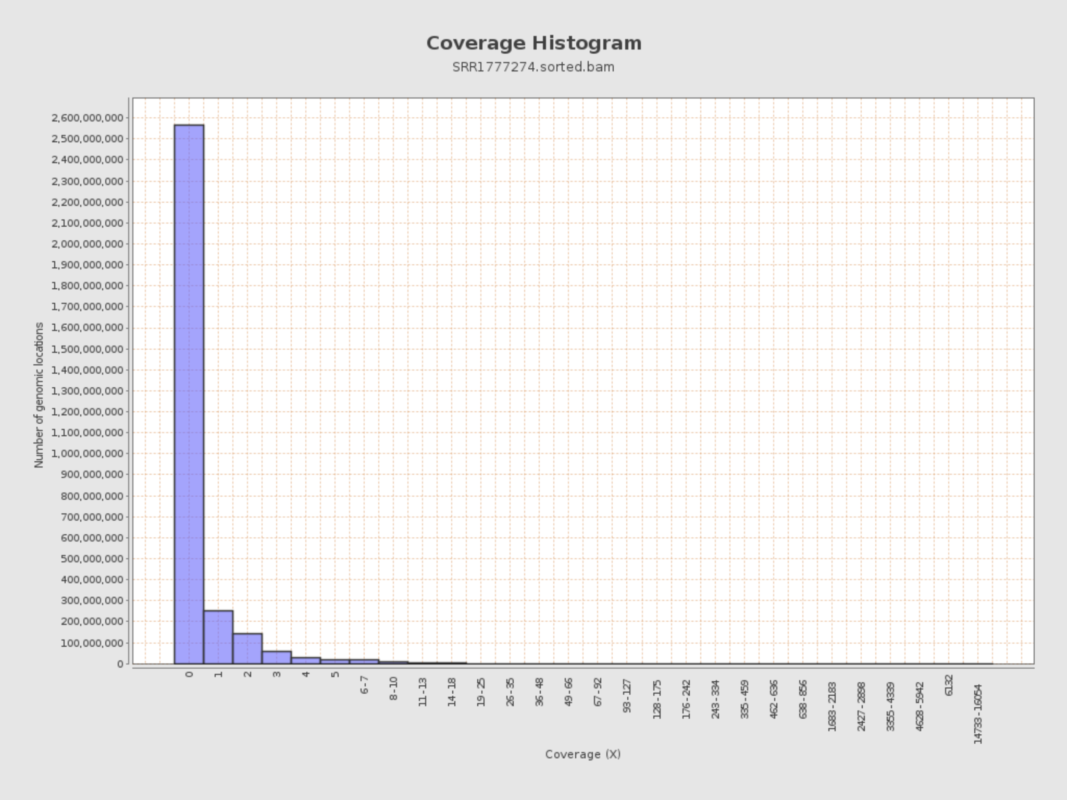
		bases	coverage	deviation
chr1	249250621	118901714	0.477	1.4319
chr2	243199373	110218293	0.4532	1.5415
chr3	198022430	71804976	0.3626	1.1396
chr4	191154276	49587804	0.2594	0.9059
chr5	180915260	67103946	0.3709	1.1117
chr6	171115067	53840011	0.3146	11.4087
chr7	159138663	71319351	0.4482	1.2891
chr8	146364022	53181752	0.3634	1.2289
chr9	141213431	47630365	0.3373	1.2337
chr10	135534747	57799457	0.4265	1.2555
chr11	135006516	68228670	0.5054	1.4378
chr12	133851895	55066962	0.4114	1.198
chr13	115169878	37097493	0.3221	1.0881
chr14	107349540	24694401	0.23	0.8261
chr15	102531392	52155395	0.5087	1.474
chr16	90354753	42778587	0.4735	1.6718
chr17	81195210	47705843	0.5875	1.645
chr18	78077248	21190759	0.2714	1.0598
chr19	59128983	26261356	0.4441	1.3591
chr20	63025520	46026860	0.7303	1.7919
chr21	48129895	10556339	0.2193	1.0292
chr22	51304566	20642055	0.4023	1.3341
chrMT	16571	225547	13.6109	12.8051
chrX	155270560	30887227	0.1989	0.7228

chrY	59373566	1063075	0.0179	0.5008

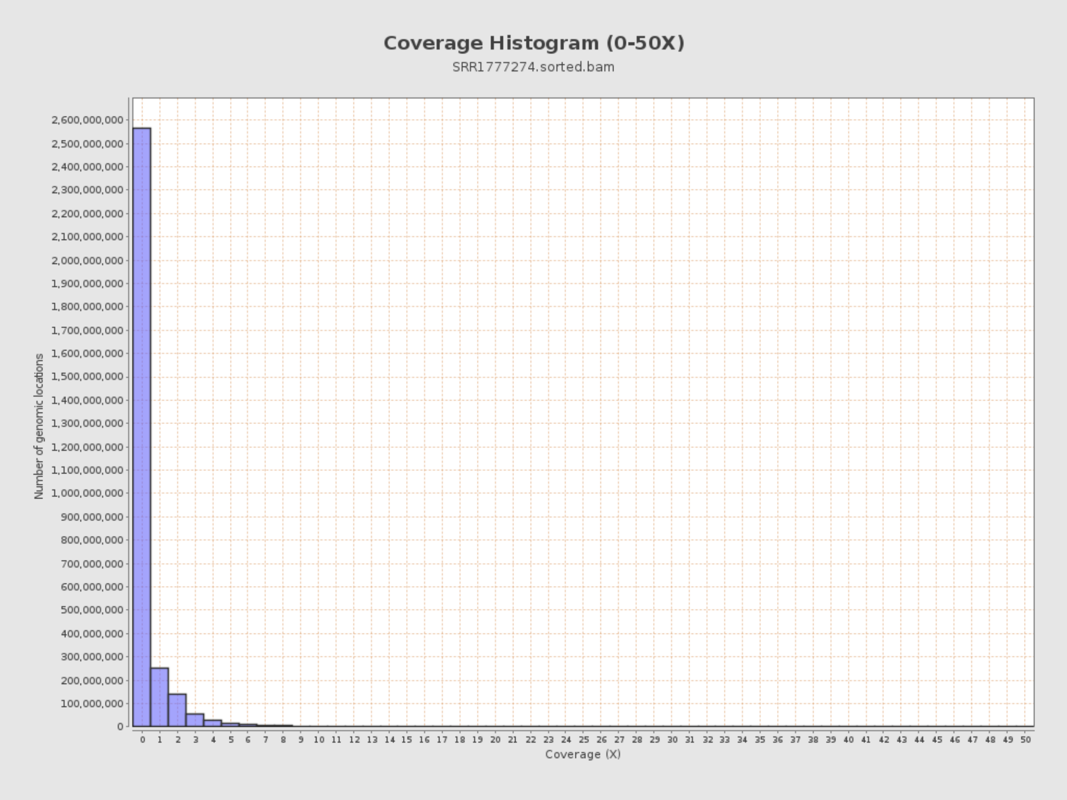
3. Results : Coverage across reference



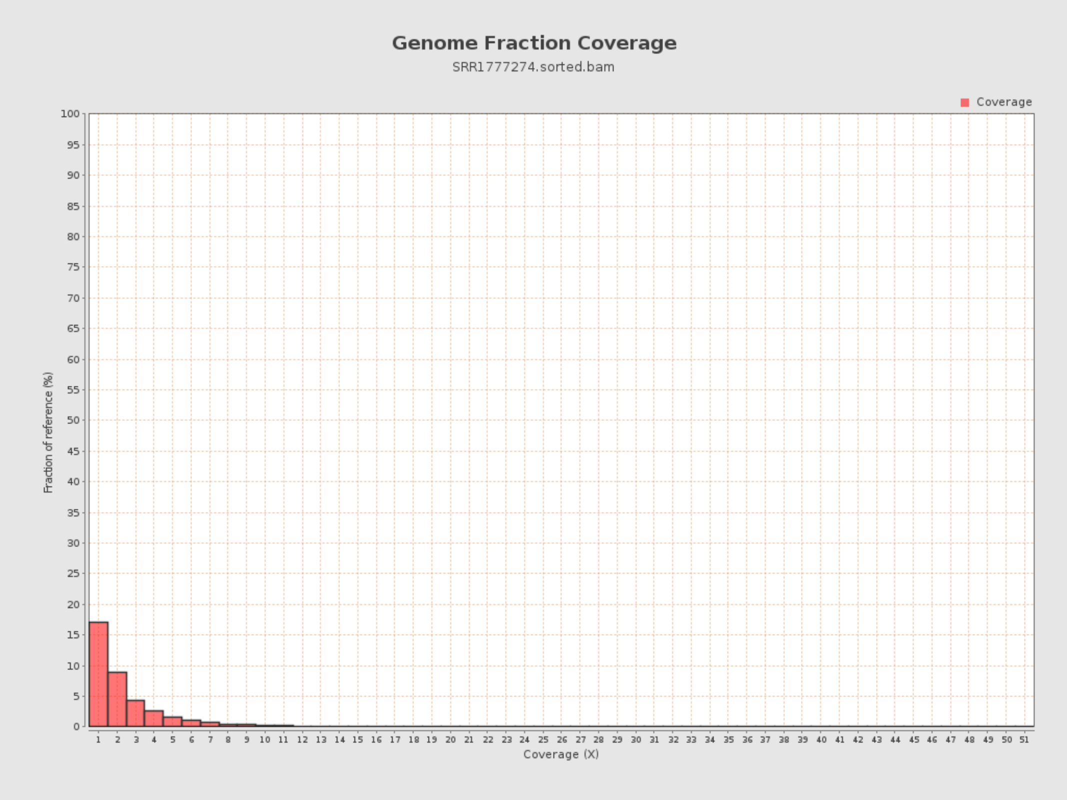
4. Results : Coverage Histogram



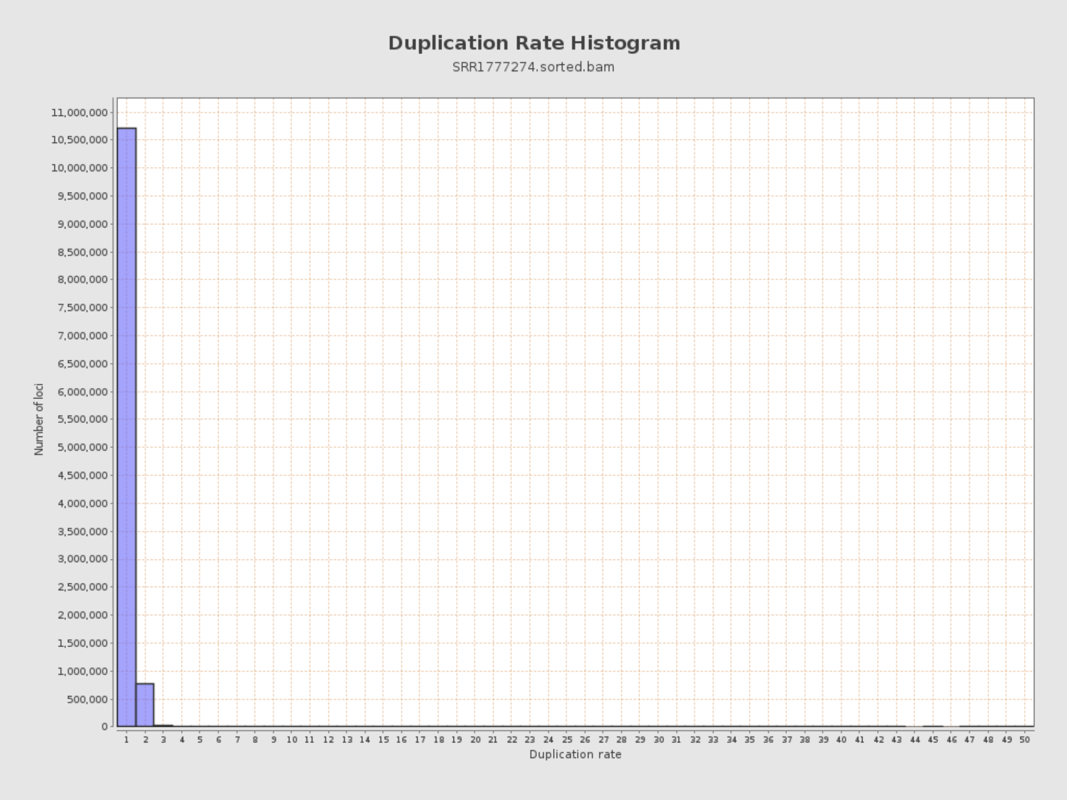
5. Results : Coverage Histogram (0-50X)



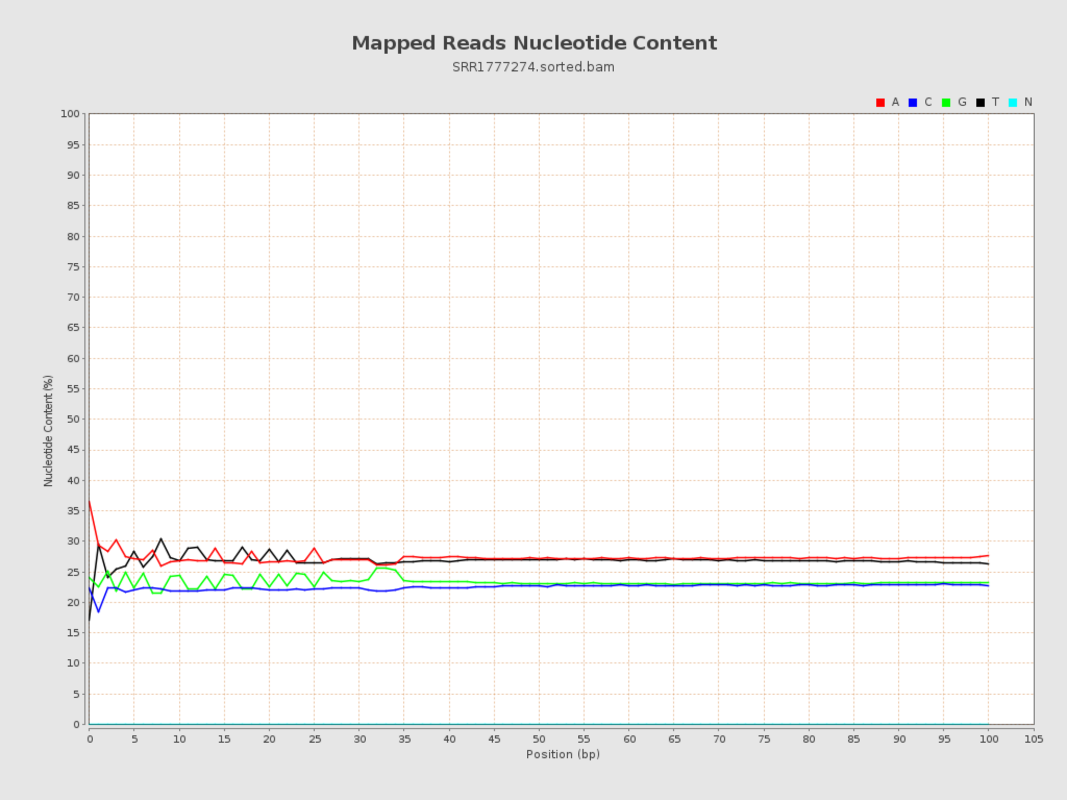
6. Results : Genome Fraction Coverage



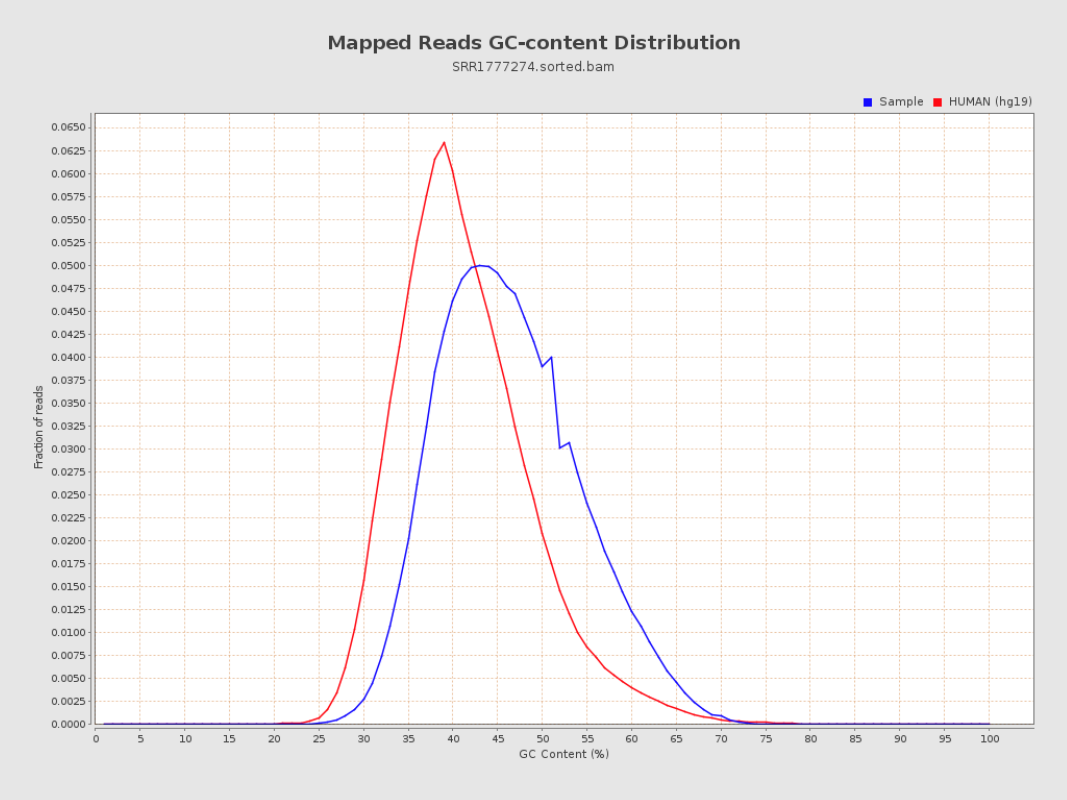
7. Results : Duplication Rate Histogram



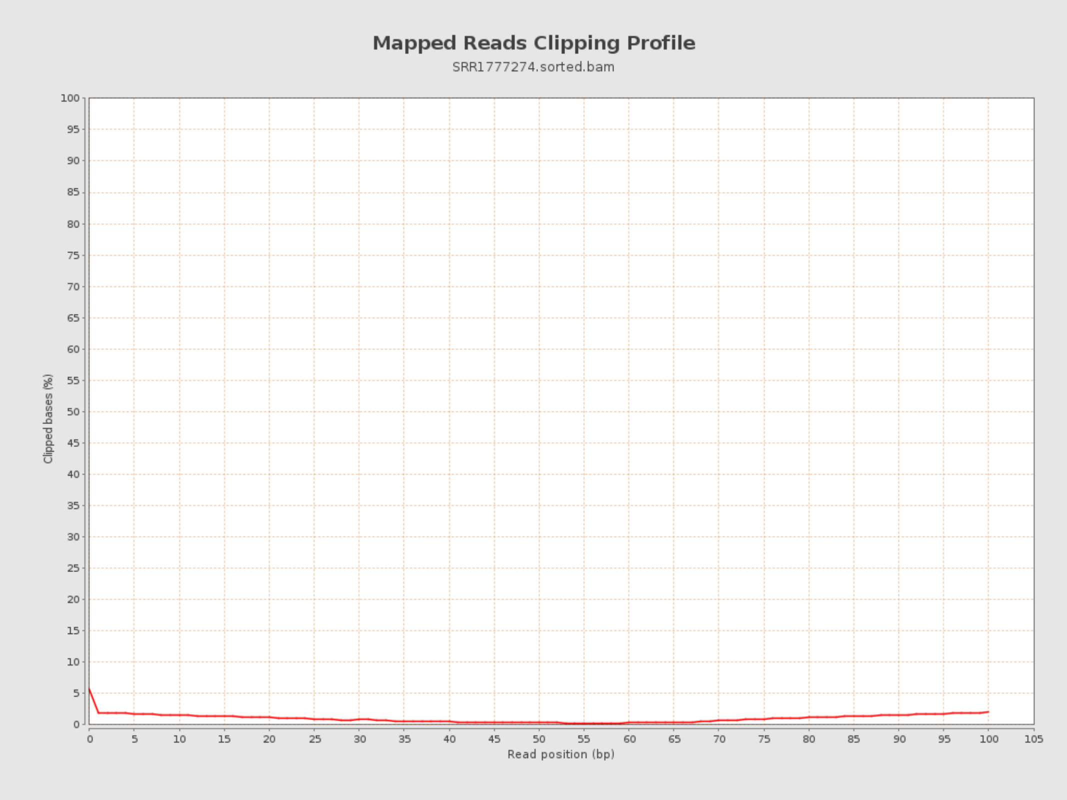
8. Results : Mapped Reads Nucleotide Content



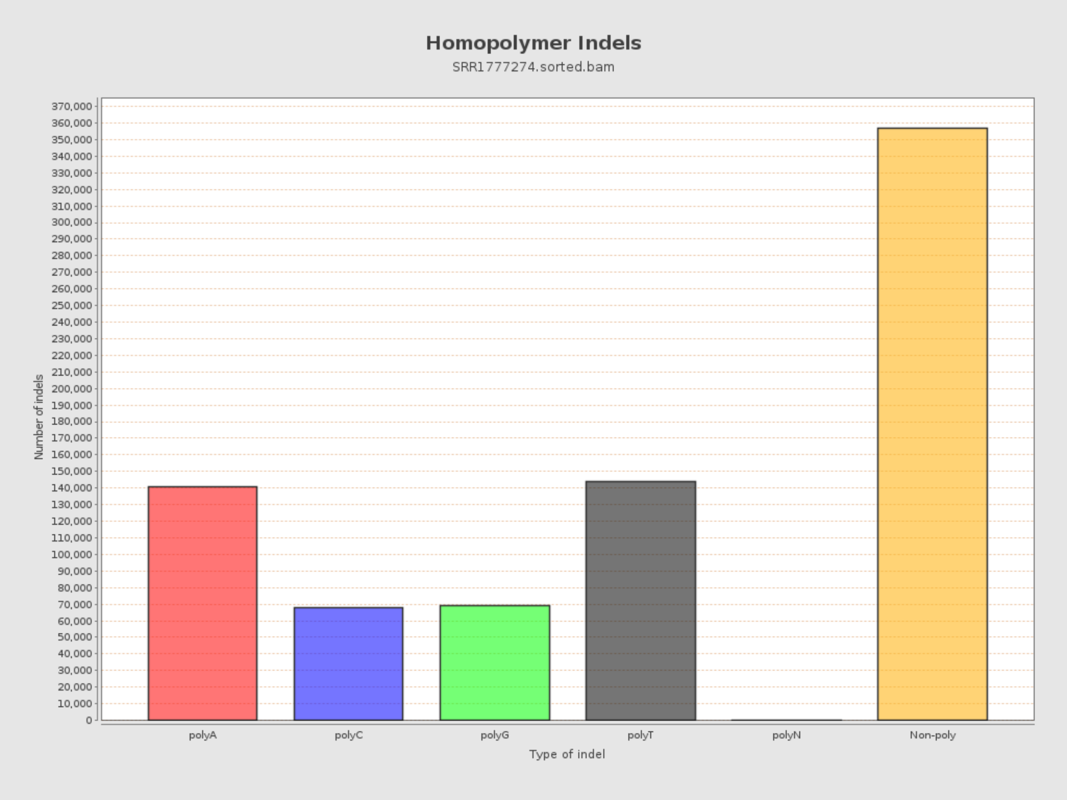
9. Results : Mapped Reads GC-content Distribution



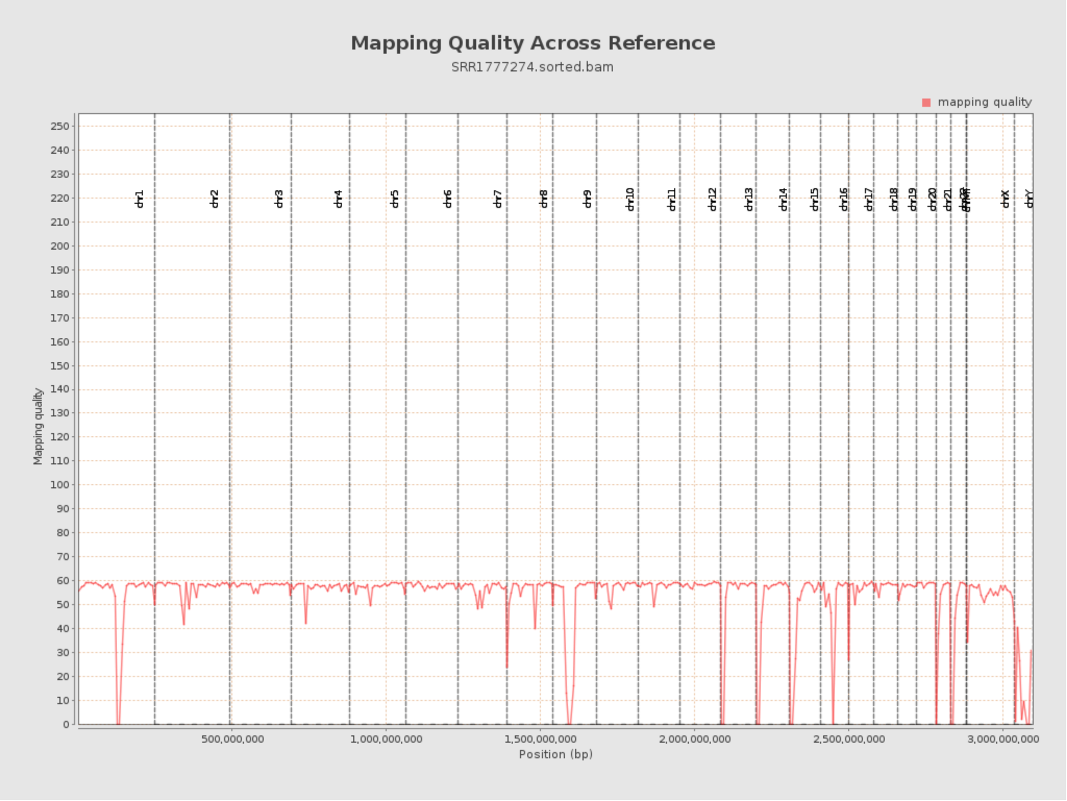
10. Results : Mapped Reads Clipping Profile



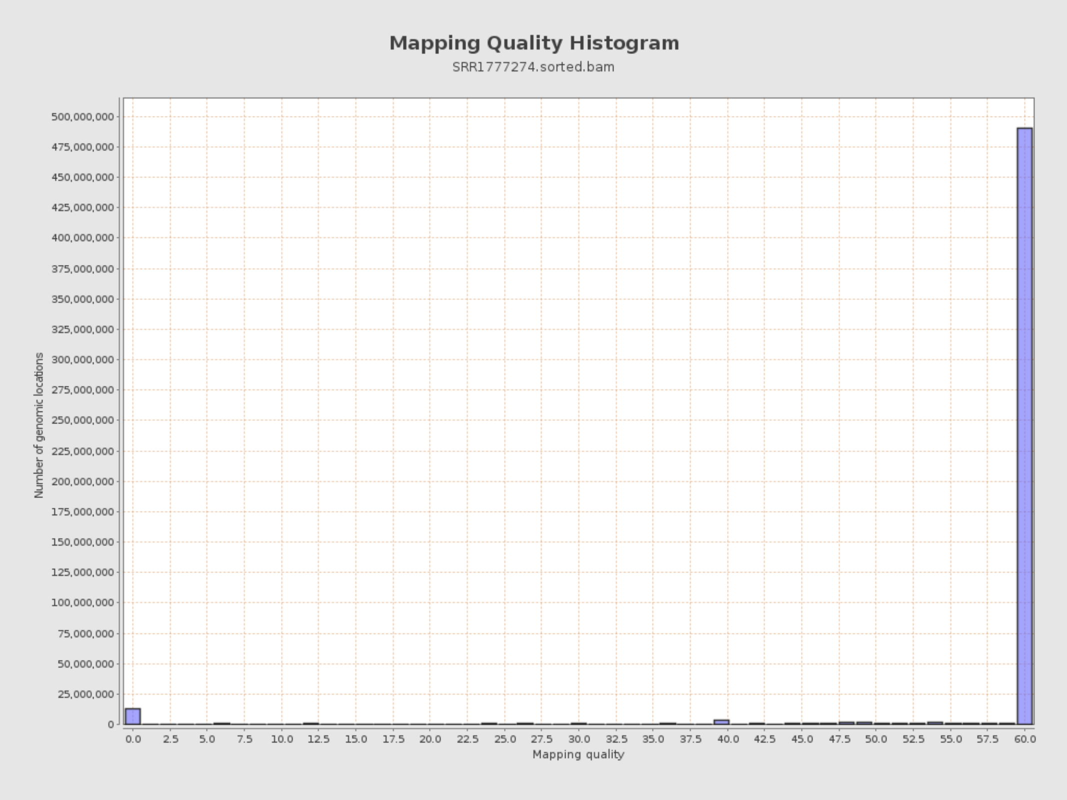
11. Results : Homopolymer Indels



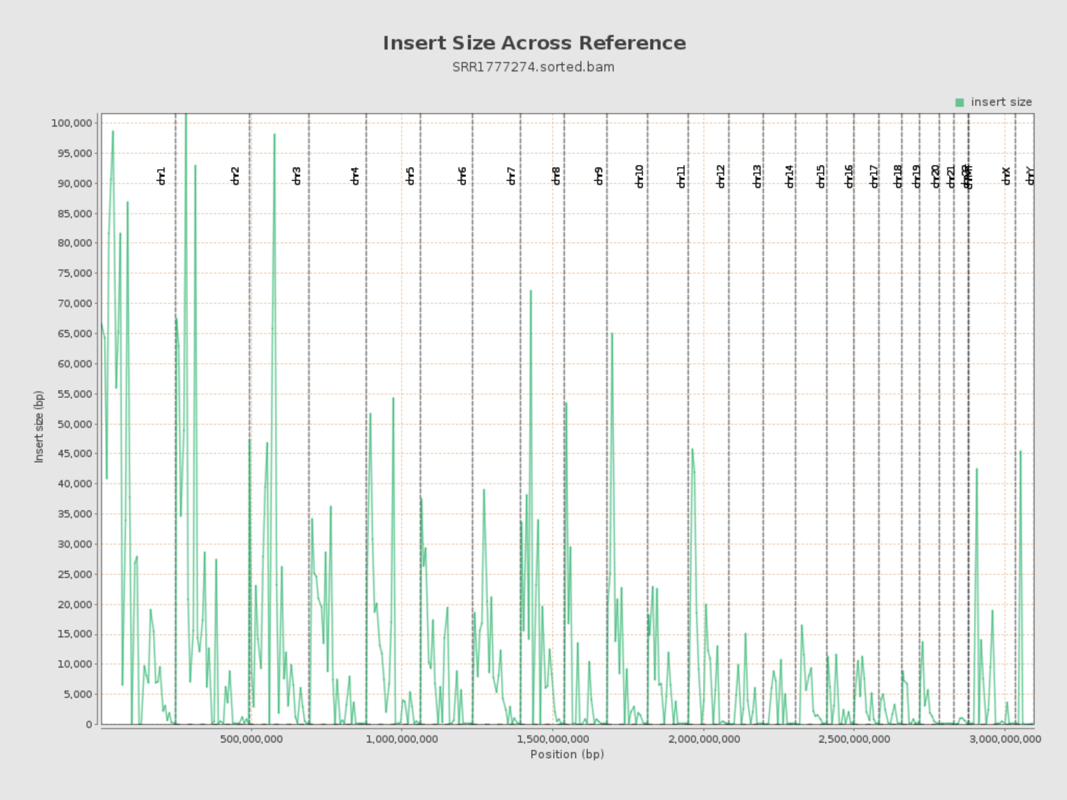
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram