Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/06 04:18:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777301.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_SRR1777301 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777301_1.fastq.gz SRR1777301_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 06 04:18:46 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777301.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,767,708
Mapped reads	1,716,191 / 97.09%
Unmapped reads	51,517 / 2.91%
Mapped paired reads	1,716,191 / 97.09%
Mapped reads, first in pair	860,510 / 48.68%
Mapped reads, second in pair	855,681 / 48.41%
Mapped reads, both in pair	1,706,432 / 96.53%
Mapped reads, singletons	9,759 / 0.55%
Secondary alignments	0
Supplementary alignments	67,542 / 3.82%
Read min/max/mean length	30 / 101 / 102.58
Duplicated reads (estimated)	190,282 / 10.76%
Duplication rate	8.96%
Clipped reads	555,964 / 31.45%

2.2. ACGT Content

Number/percentage of A's	48,398,038 / 29.51%
Number/percentage of C's	33,690,524 / 20.54%
Number/percentage of T's	47,388,599 / 28.89%
Number/percentage of G's	34,531,331 / 21.05%
Number/percentage of N's	2,698 / 0%

GC Percentage	41.6%

2.3. Coverage

Mean	0.053
Standard Deviation	0.8744

2.4. Mapping Quality

Mean Mapping Quality	52.86

2.5. Insert size

Mean	177,887.62
Standard Deviation	4,061,691.3
P25/Median/P75	107 / 154 / 218

2.6. Mismatches and indels

General error rate	0.73%
Mismatches	1,120,544
Insertions	38,178
Mapped reads with at least one insertion	2.15%
Deletions	24,513
Mapped reads with at least one deletion	1.37%
Homopolymer indels	42.18%

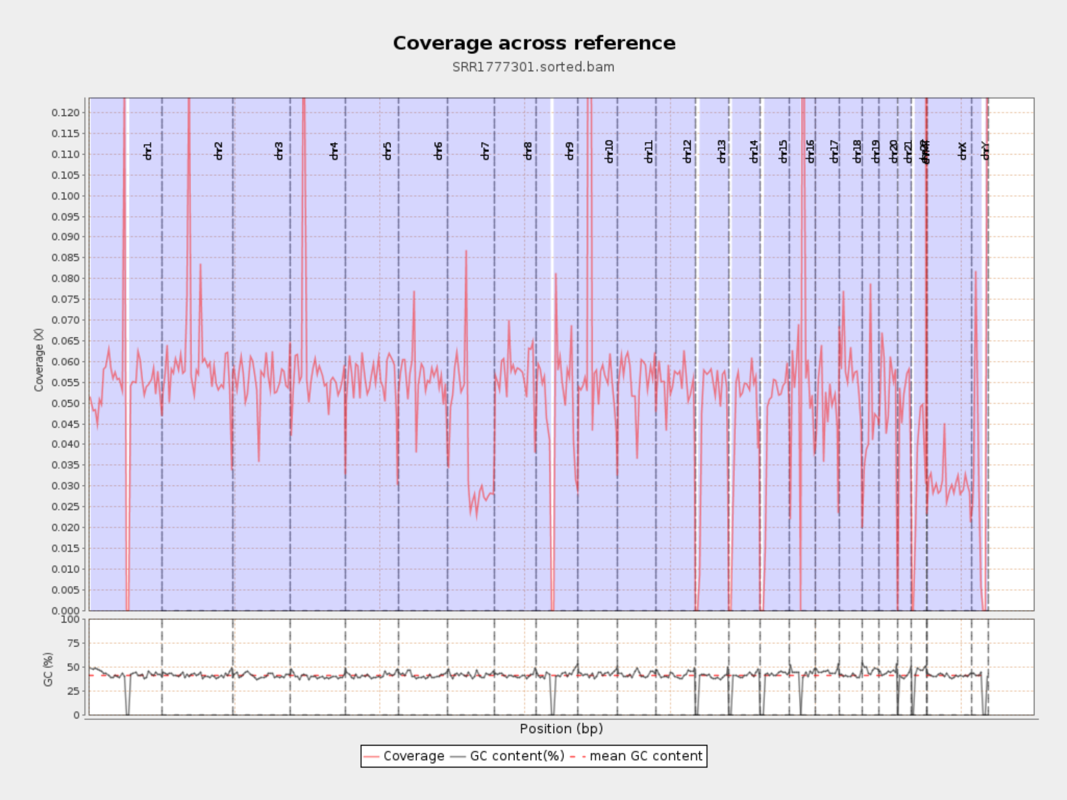
2.7. Chromosome stats

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

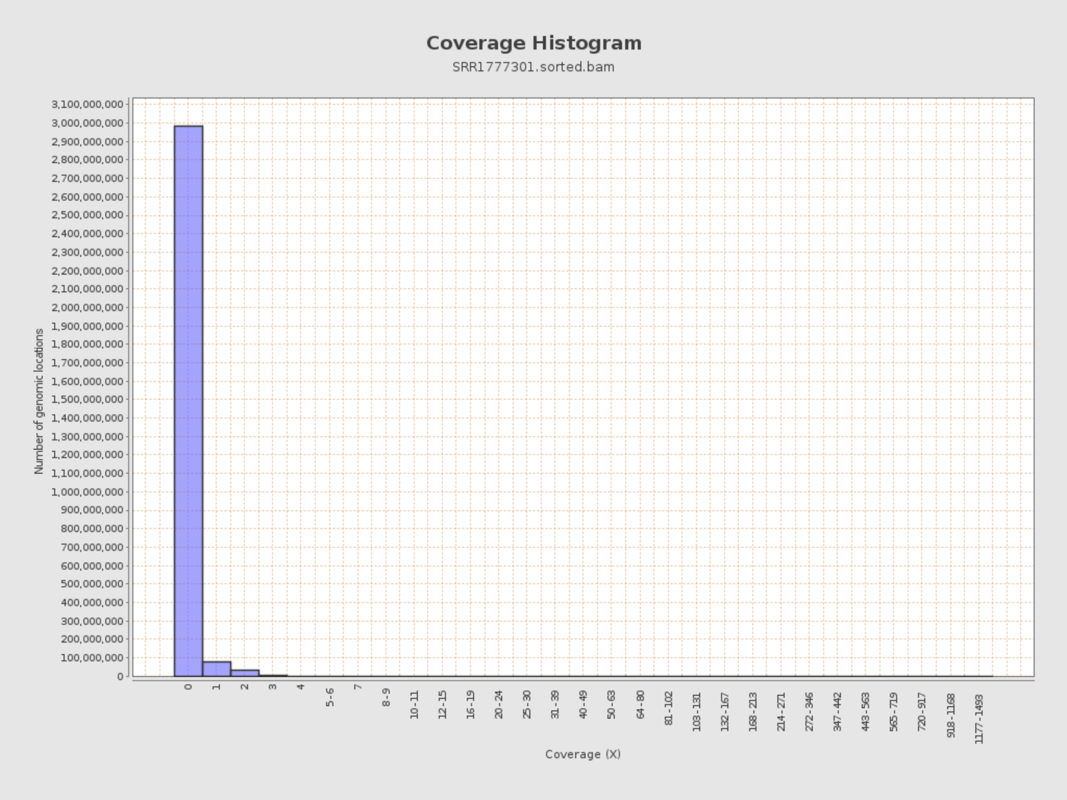
		bases	coverage	deviation
chr1	249250621	13392850	0.0537	1.5116
chr2	243199373	14770434	0.0607	0.6665
chr3	198022430	11027513	0.0557	0.3553
chr4	191154276	11352918	0.0594	0.7597
chr5	180915260	10109750	0.0559	0.3064
chr6	171115067	9584771	0.056	0.3774
chr7	159138663	6361111	0.04	0.6291
chr8	146364022	8416234	0.0575	0.4278
chr9	141213431	6866773	0.0486	0.6917
chr10	135534747	9341310	0.0689	2.072
chr11	135006516	7536475	0.0558	0.3745
chr12	133851895	7338541	0.0548	0.3011
chr13	115169878	5243924	0.0455	0.2719
chr14	107349540	4810021	0.0448	0.279
chr15	102531392	4399486	0.0429	0.2612
chr16	90354753	5392694	0.0597	0.8621
chr17	81195210	3927966	0.0484	0.4177
chr18	78077248	4591167	0.0588	0.8233
chr19	59128983	2686406	0.0454	0.8385
chr20	63025520	3403114	0.054	0.3374
chr21	48129895	2216433	0.0461	0.3854
chr22	51304566	1552145	0.0303	0.2288
chrMT	16571	2696599	162.73	40.5667
chrX	155270560	4702222	0.0303	0.2484

chrY	59373566	2359628	0.0397	0.9195

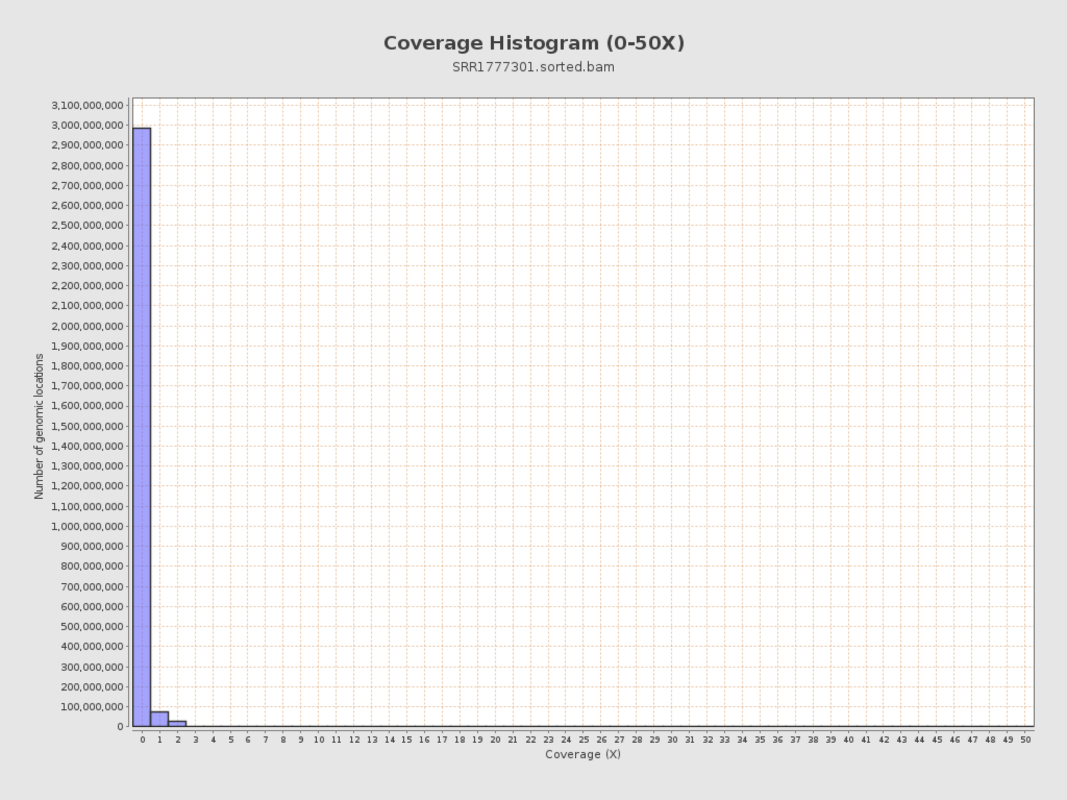
3. Results : Coverage across reference



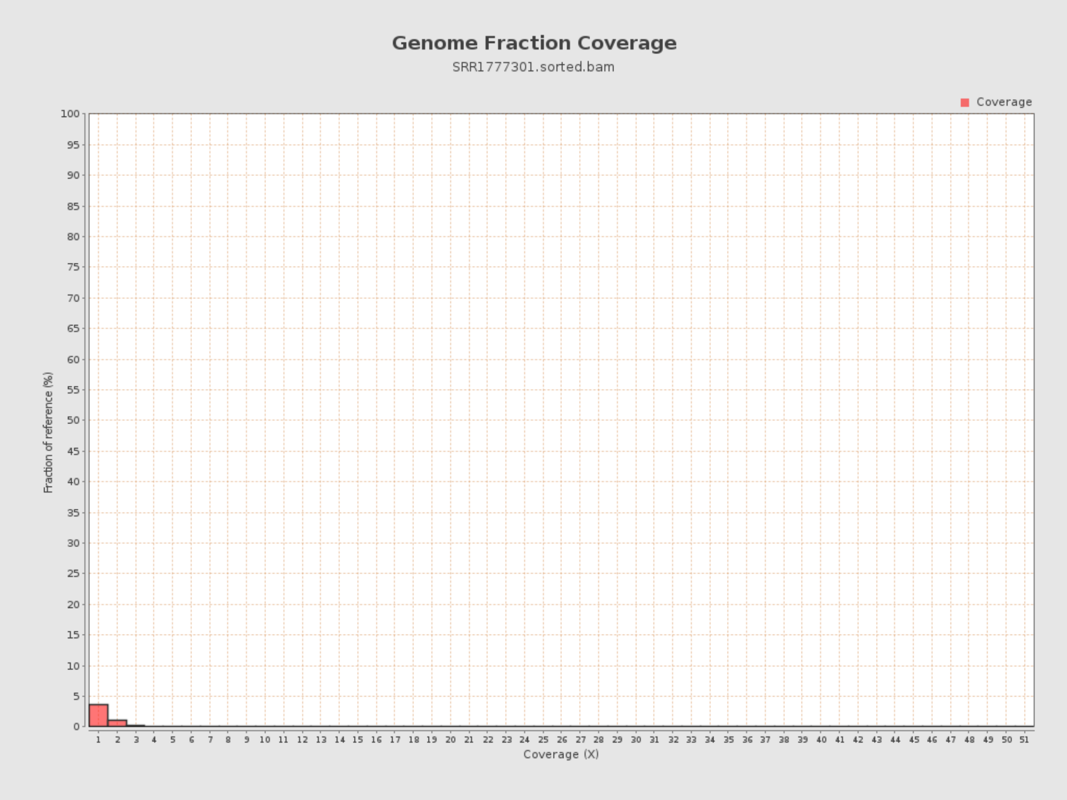
4. Results : Coverage Histogram



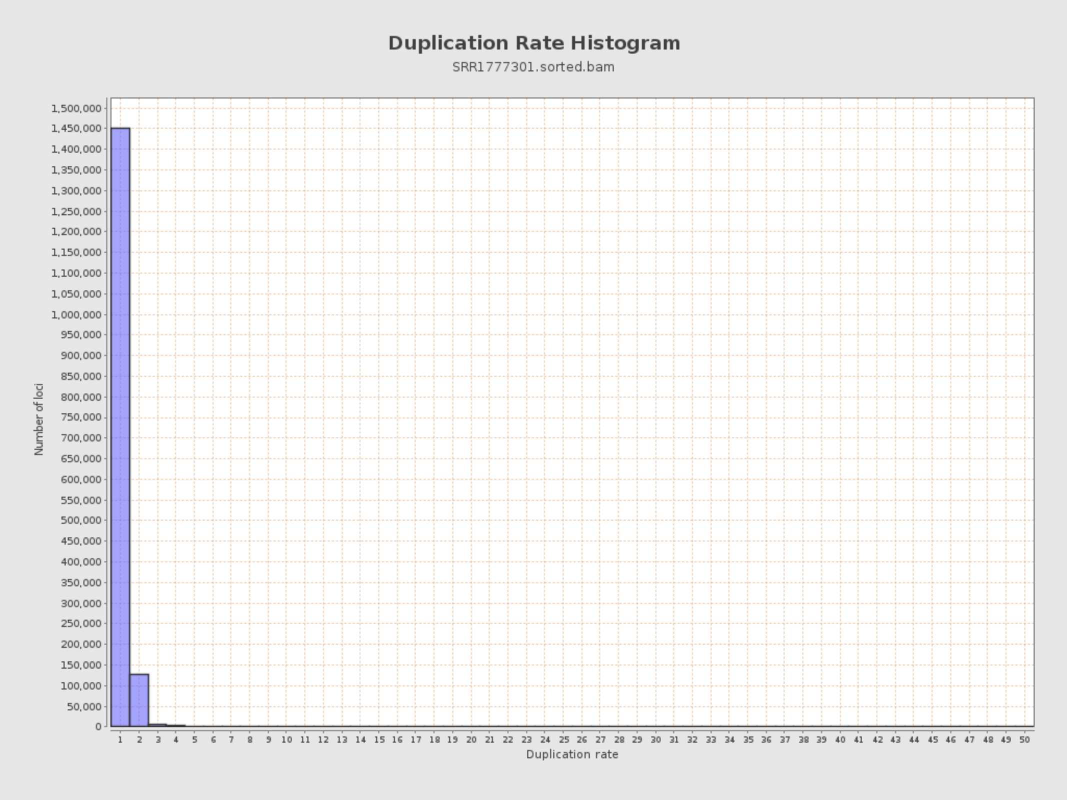
5. Results : Coverage Histogram (0-50X)



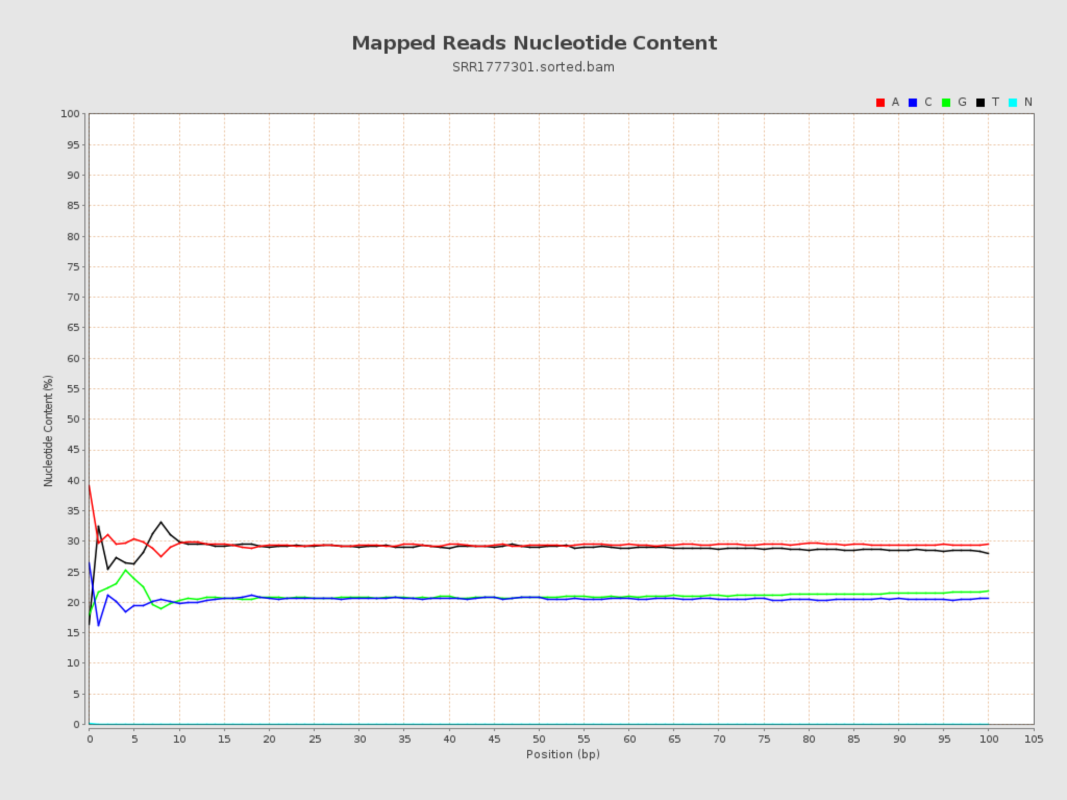
6. Results : Genome Fraction Coverage



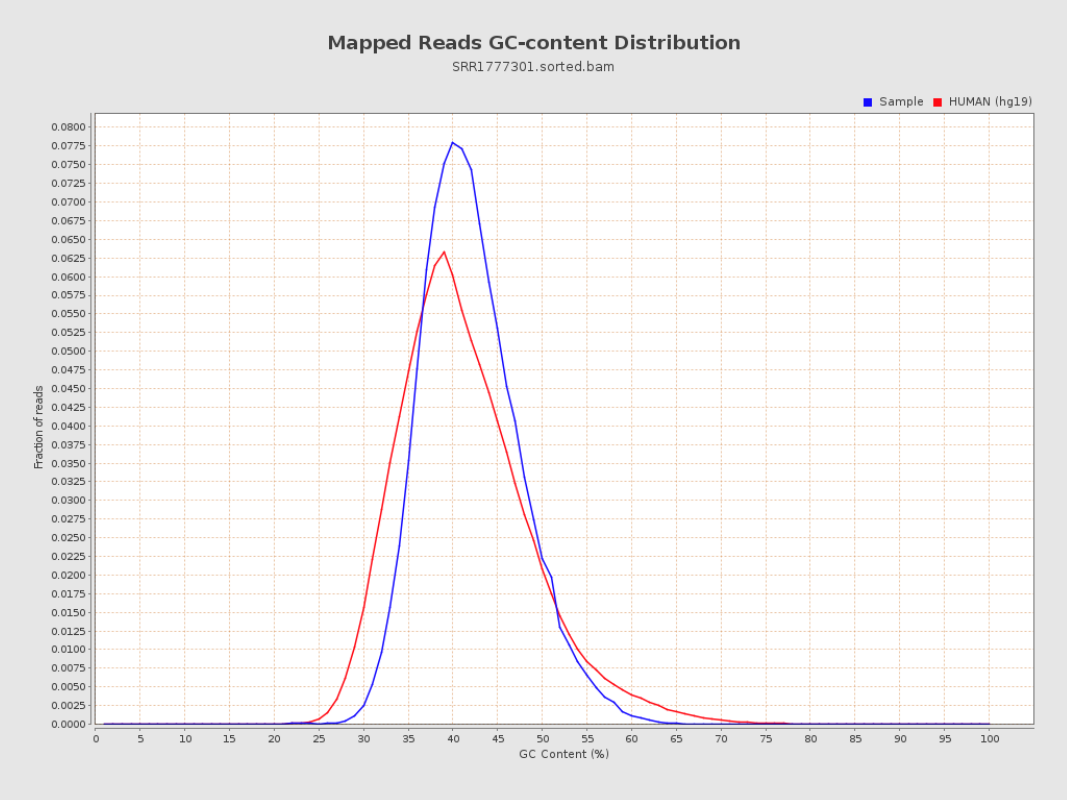
7. Results : Duplication Rate Histogram



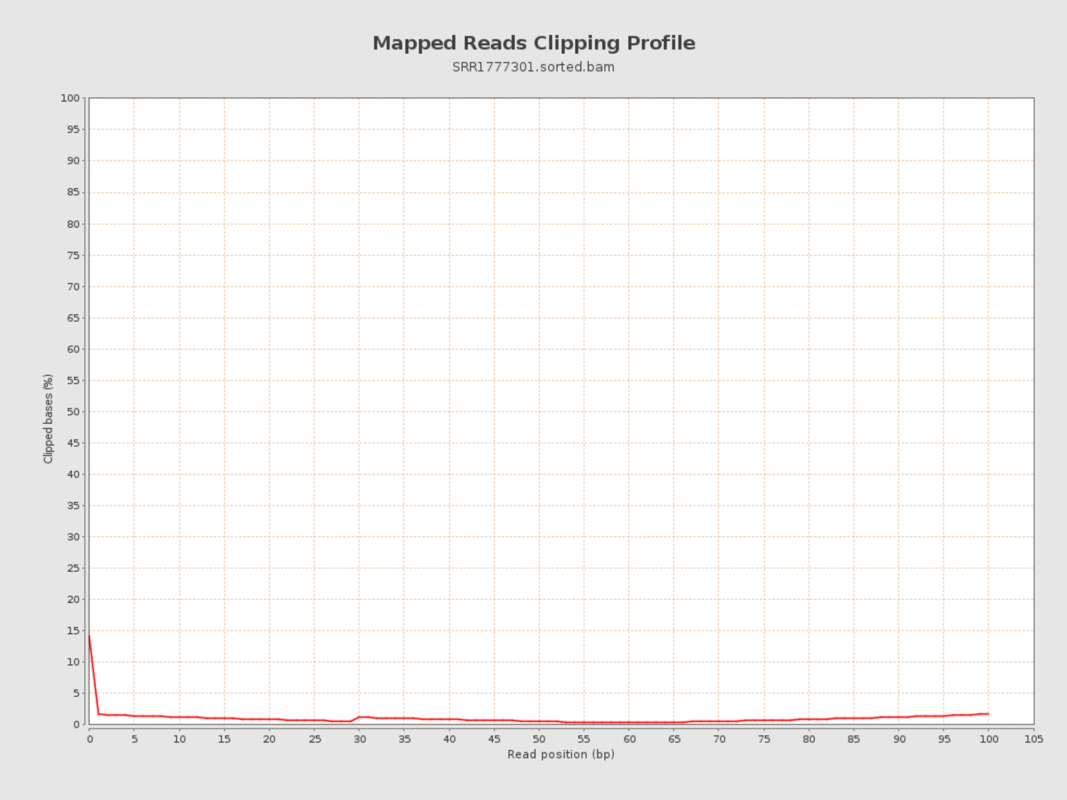
8. Results : Mapped Reads Nucleotide Content



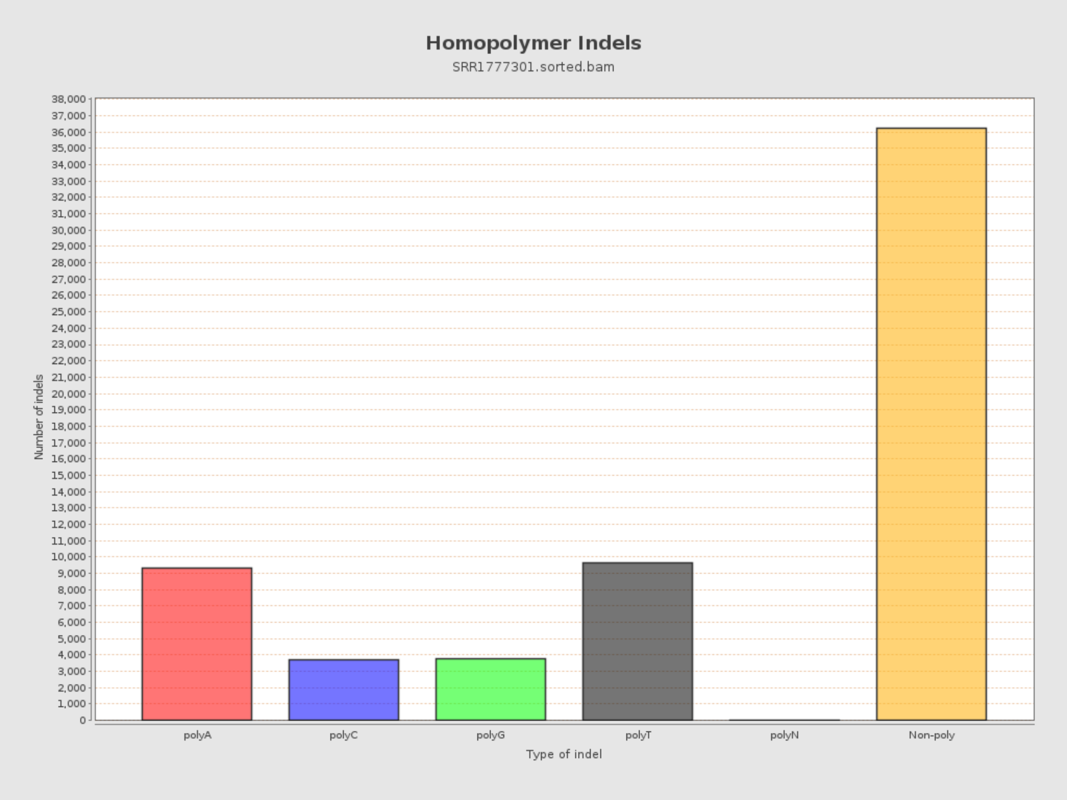
9. Results : Mapped Reads GC-content Distribution



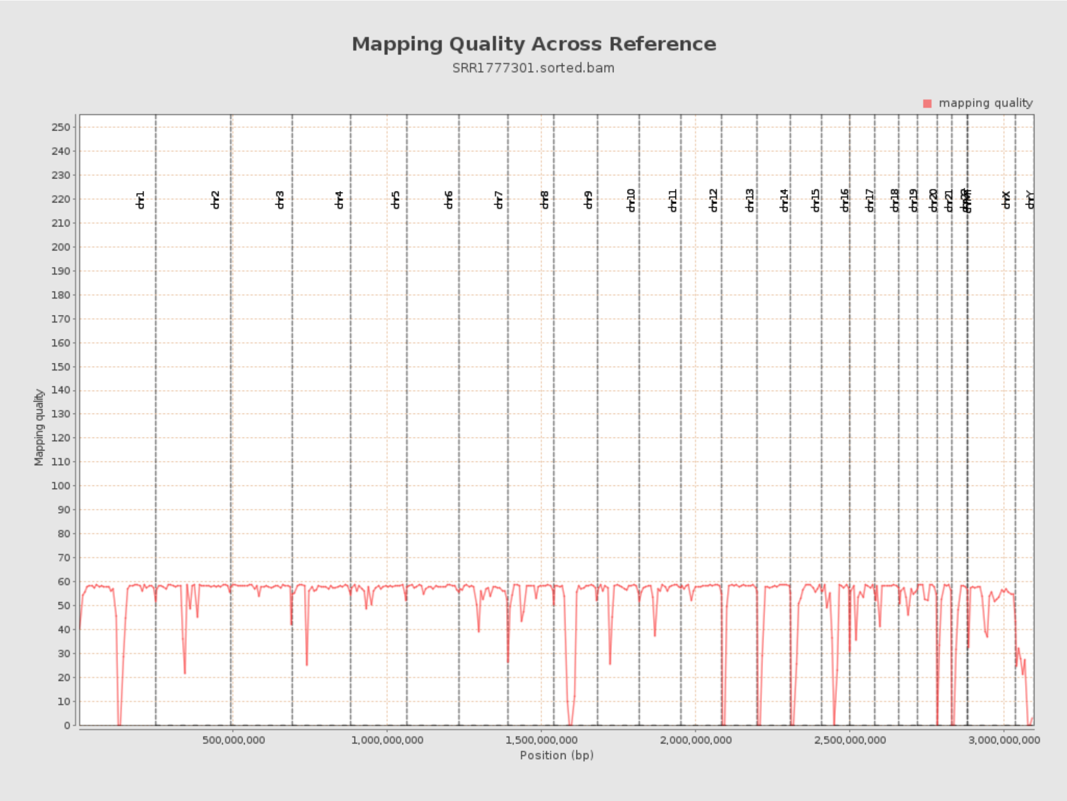
10. Results : Mapped Reads Clipping Profile



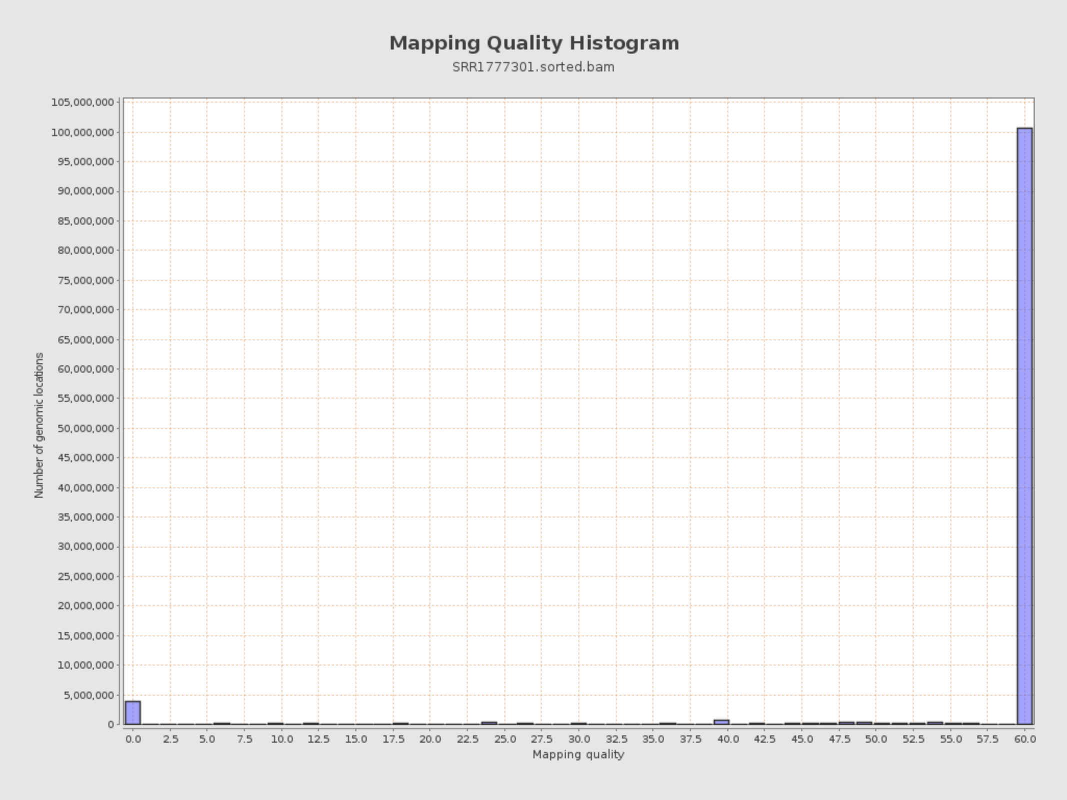
11. Results : Homopolymer Indels



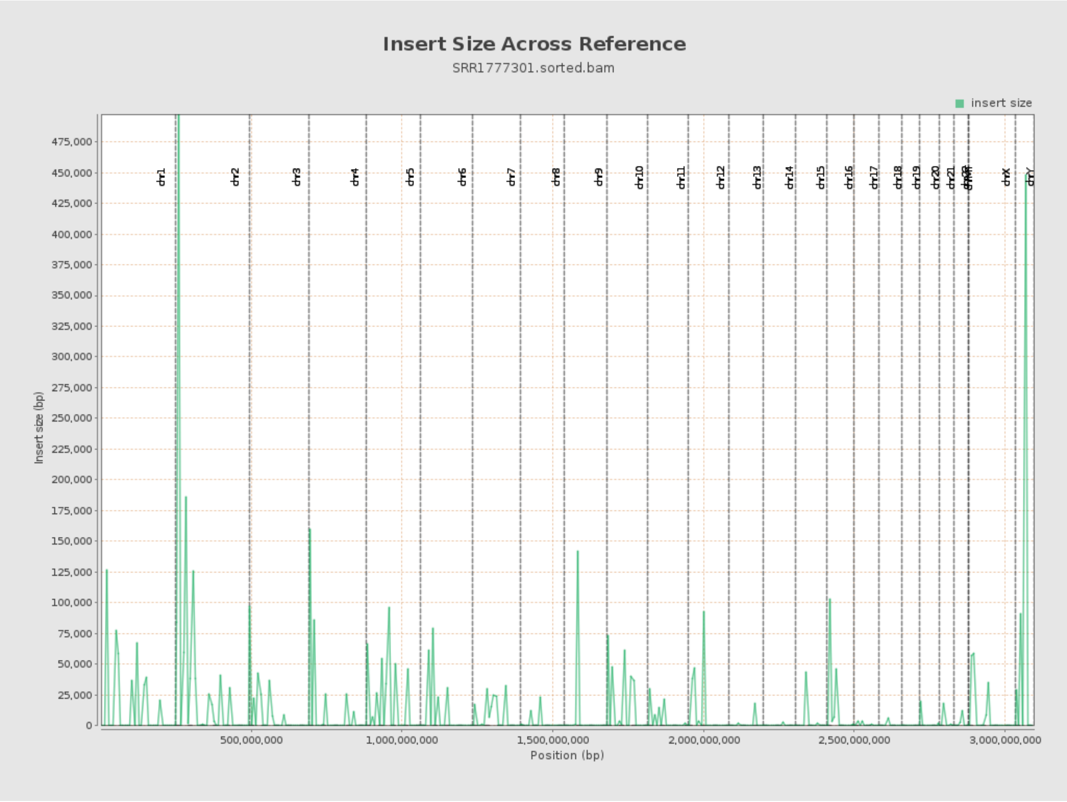
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram