Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 08:26:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777271.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_SRR1777271 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777271_1.fastq.gz SRR1777271_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 08:26:04 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777271.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,658,004
Mapped reads	3,572,603 / 97.67%
Unmapped reads	85,401 / 2.33%
Mapped paired reads	3,572,603 / 97.67%
Mapped reads, first in pair	1,795,676 / 49.09%
Mapped reads, second in pair	1,776,927 / 48.58%
Mapped reads, both in pair	3,546,182 / 96.94%
Mapped reads, singletons	26,421 / 0.72%
Secondary alignments	0
Supplementary alignments	52,463 / 1.43%
Read min/max/mean length	30 / 76 / 76.51
Duplicated reads (estimated)	62,894 / 1.72%
Duplication rate	1.68%
Clipped reads	428,505 / 11.71%

2.2. ACGT Content

Number/percentage of A's	80,328,707 / 30.08%
Number/percentage of C's	53,550,782 / 20.05%
Number/percentage of T's	78,724,162 / 29.48%
Number/percentage of G's	54,407,896 / 20.38%
Number/percentage of N's	14,749 / 0.01%

GC Percentage	40.43%

2.3. Coverage

Mean	0.0863
Standard Deviation	0.3694

2.4. Mapping Quality

Mean Mapping Quality	52.74

2.5. Insert size

Mean	226,906.09
Standard Deviation	4,606,525.07
P25/Median/P75	122 / 166 / 224

2.6. Mismatches and indels

General error rate	0.57%
Mismatches	1,447,774
Insertions	55,519
Mapped reads with at least one insertion	1.54%
Deletions	24,165
Mapped reads with at least one deletion	0.67%
Homopolymer indels	50.09%

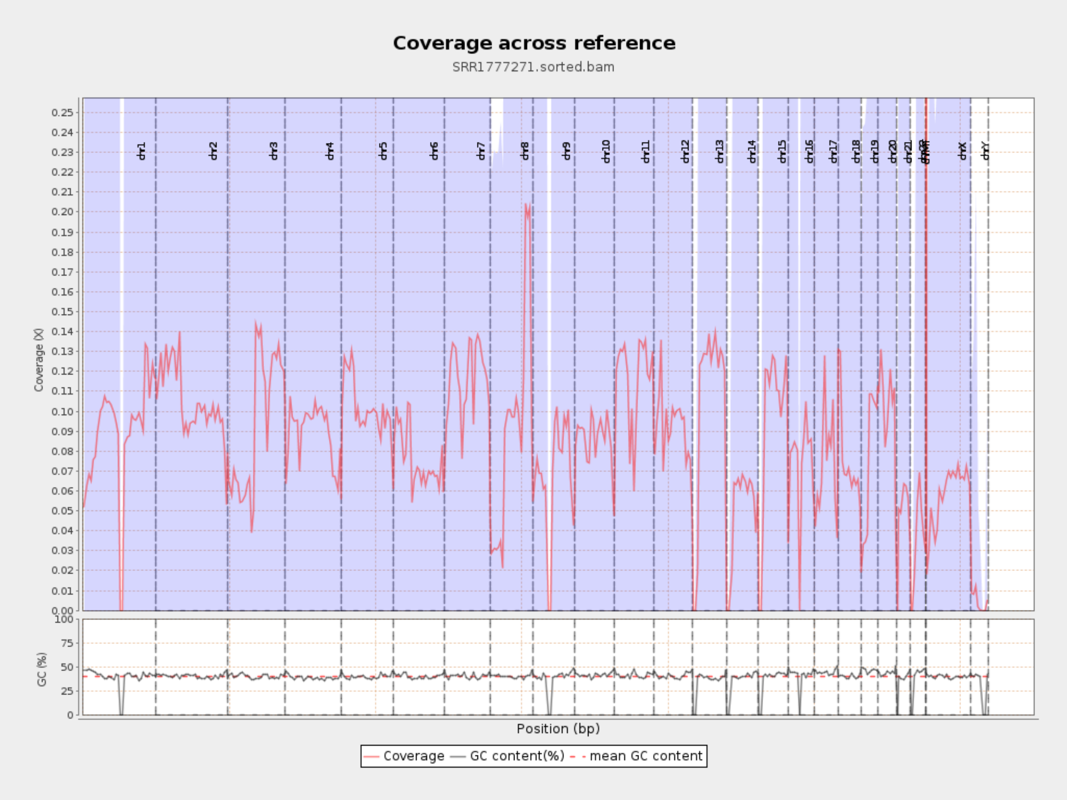
2.7. Chromosome stats

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

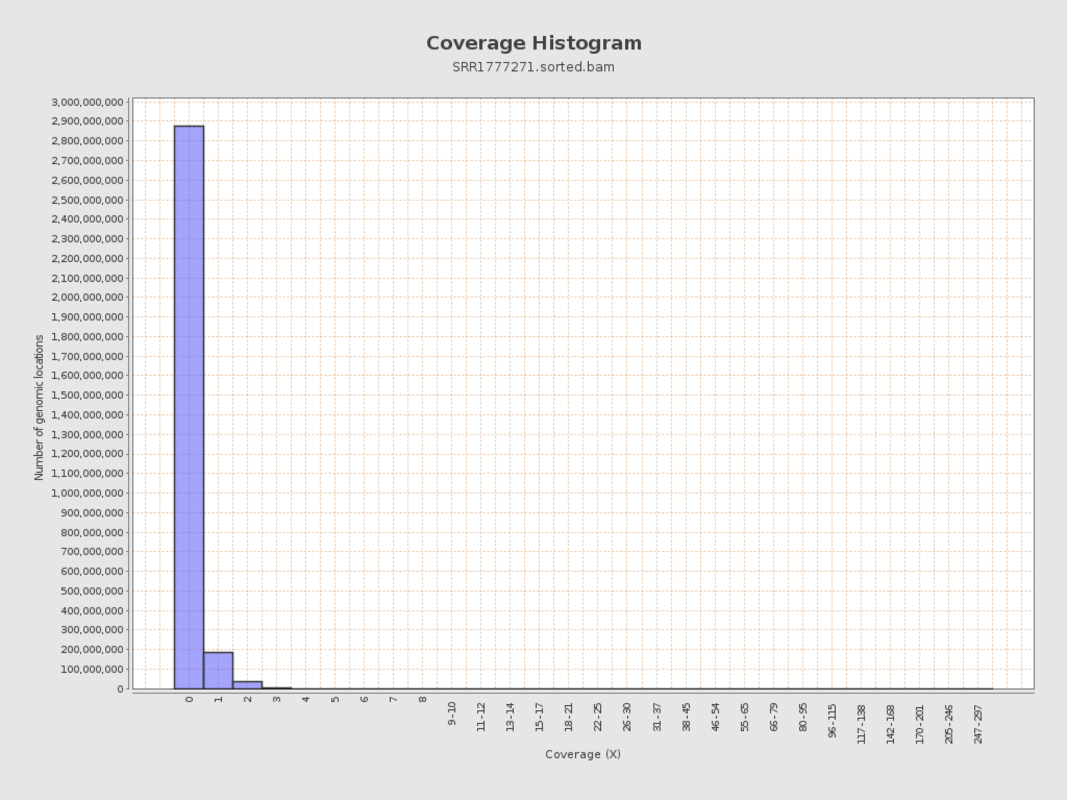
		bases	coverage	deviation
chr1	249250621	22198397	0.0891	0.4389
chr2	243199373	25586942	0.1052	0.3765
chr3	198022430	18392245	0.0929	0.3459
chr4	191154276	17169912	0.0898	0.339
chr5	180915260	18361246	0.1015	0.3598
chr6	171115067	13036273	0.0762	0.3252
chr7	159138663	18395257	0.1156	0.4014
chr8	146364022	13548744	0.0926	0.3504
chr9	141213431	9657786	0.0684	0.3344
chr10	135534747	11854316	0.0875	0.3794
chr11	135006516	15611209	0.1156	0.3905
chr12	133851895	12337980	0.0922	0.3426
chr13	115169878	12198575	0.1059	0.3703
chr14	107349540	5426373	0.0505	0.2538
chr15	102531392	9753338	0.0951	0.3519
chr16	90354753	6541891	0.0724	0.3175
chr17	81195210	5949413	0.0733	0.318
chr18	78077248	5907146	0.0757	0.3551
chr19	59128983	4399831	0.0744	0.3536
chr20	63025520	6601336	0.1047	0.3674
chr21	48129895	2358447	0.049	0.259
chr22	51304566	1825399	0.0356	0.2137
chrMT	16571	784337	47.3319	13.6516
chrX	155270560	8909903	0.0574	0.2715

chrY	59373566	266308	0.0045	0.1003

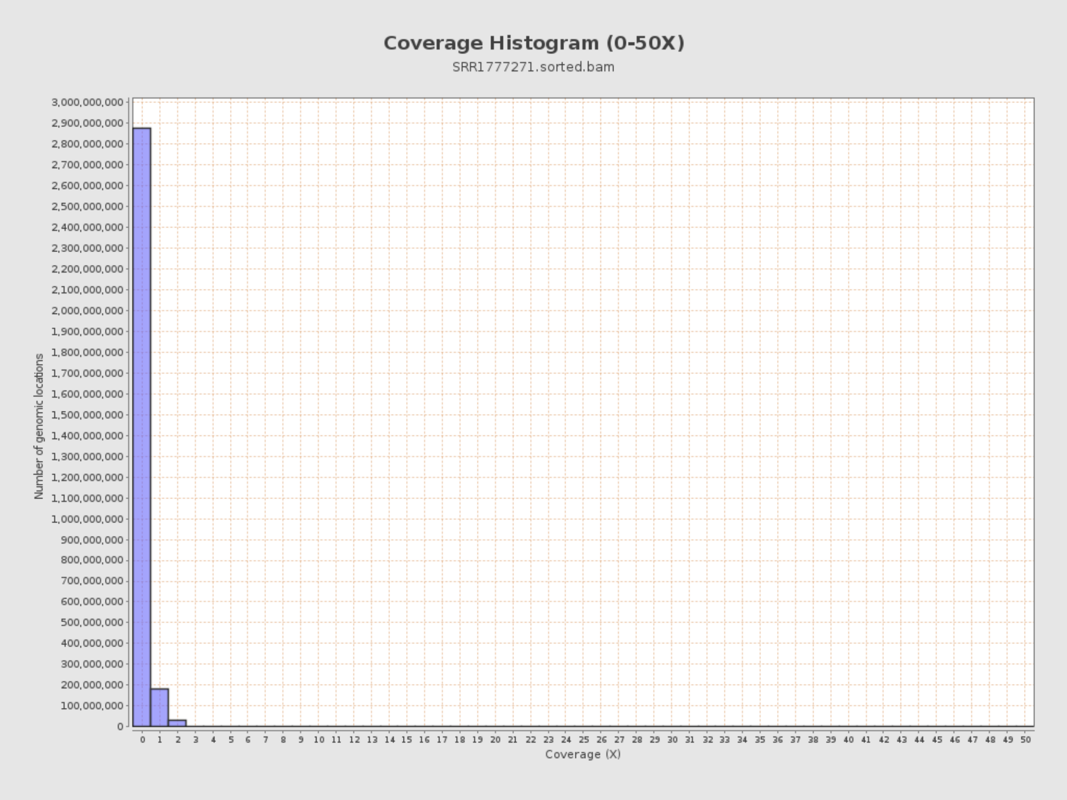
3. Results : Coverage across reference



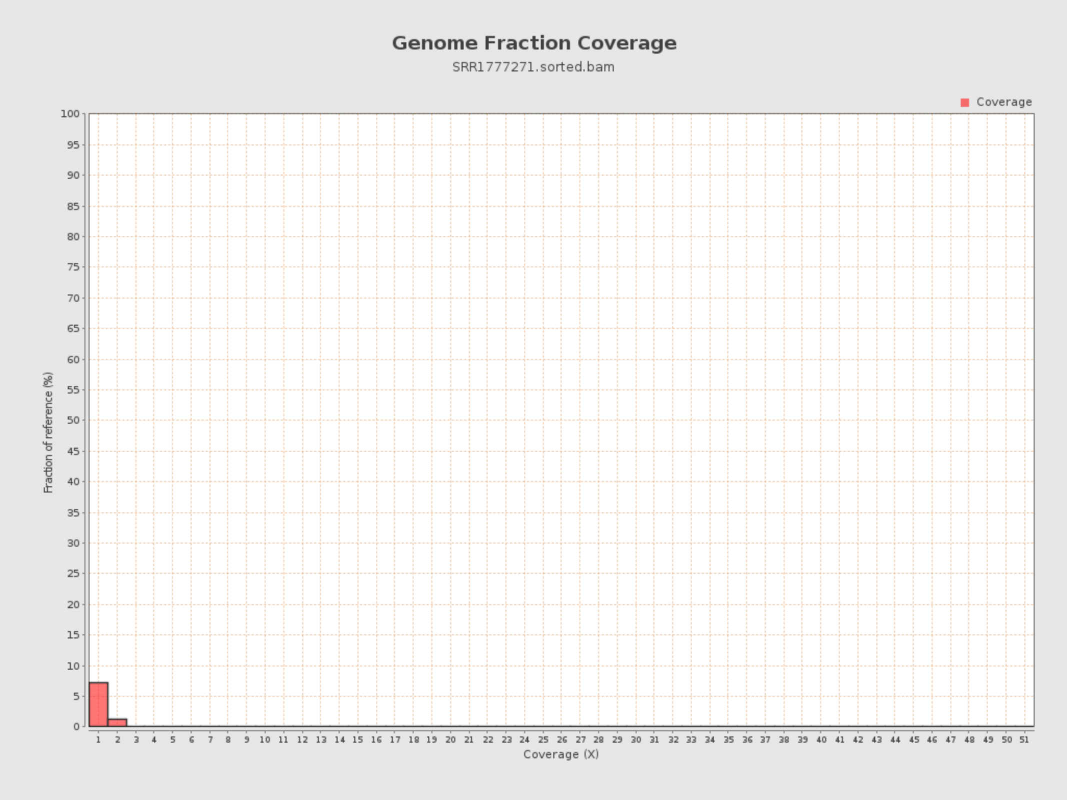
4. Results : Coverage Histogram



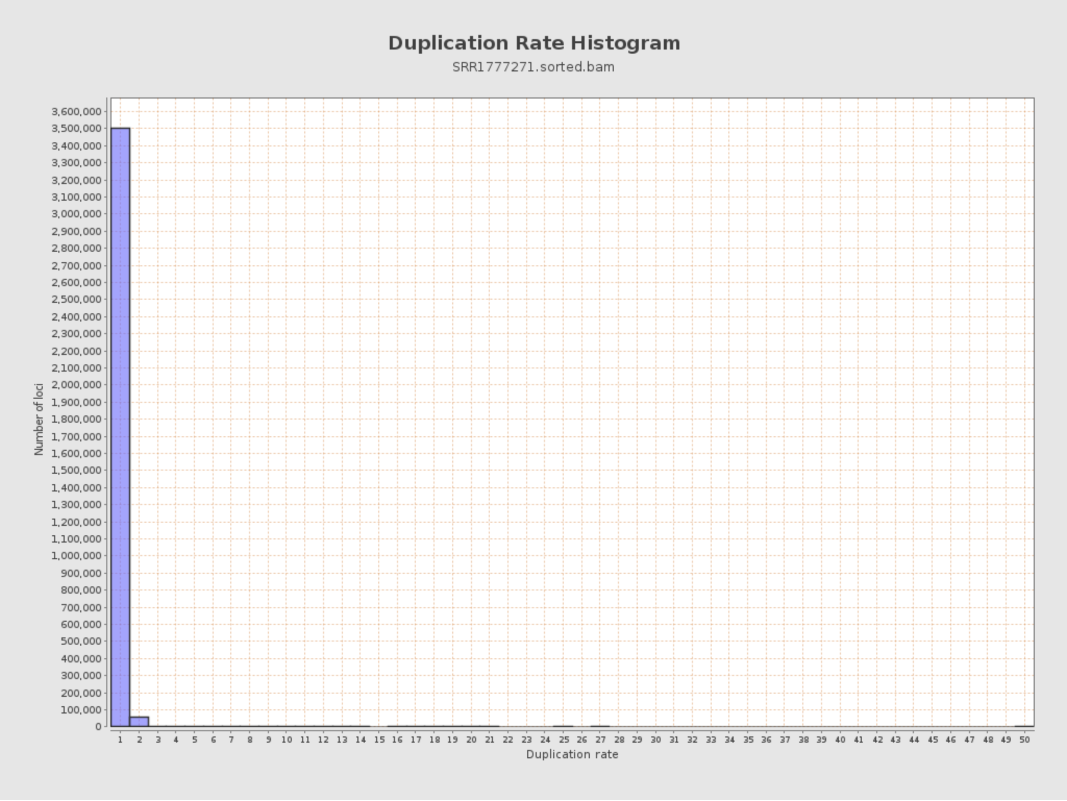
5. Results : Coverage Histogram (0-50X)



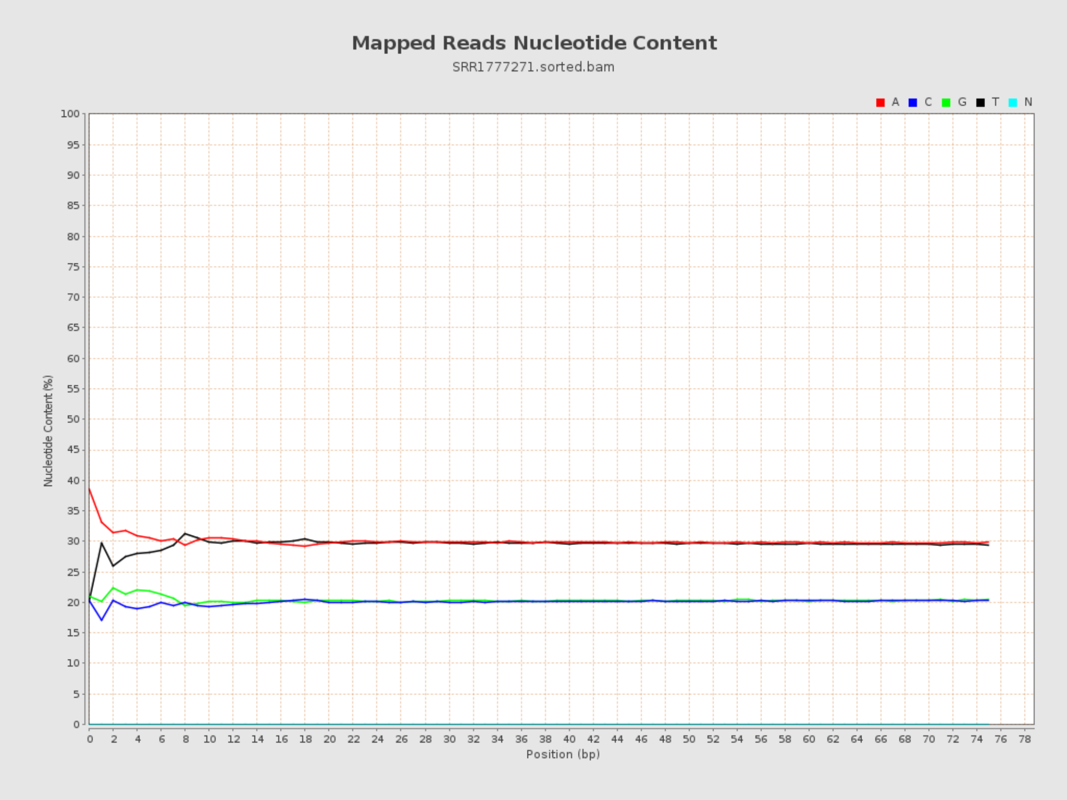
6. Results : Genome Fraction Coverage



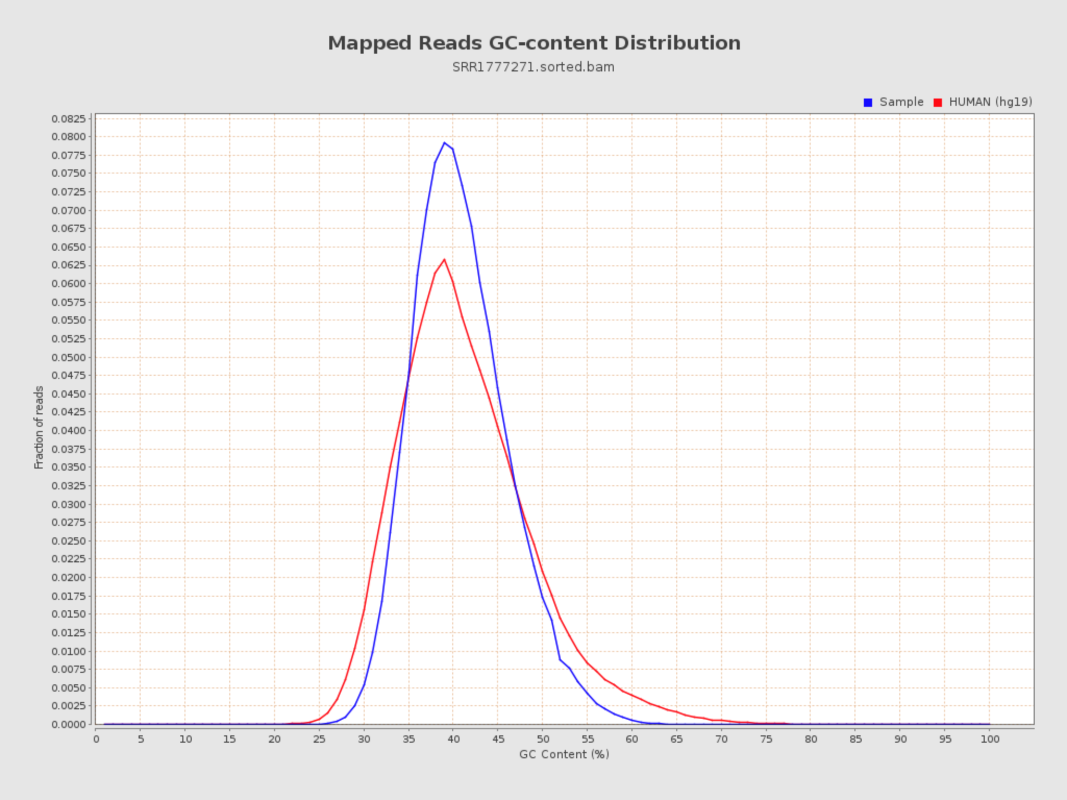
7. Results : Duplication Rate Histogram



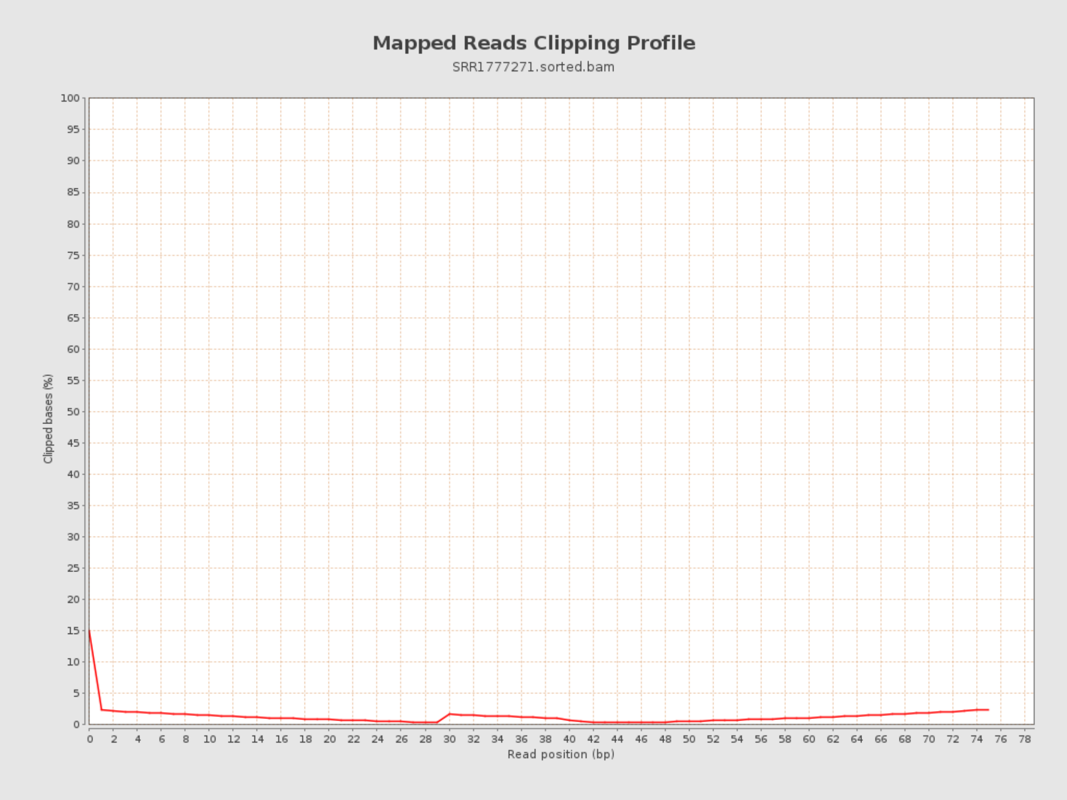
8. Results : Mapped Reads Nucleotide Content



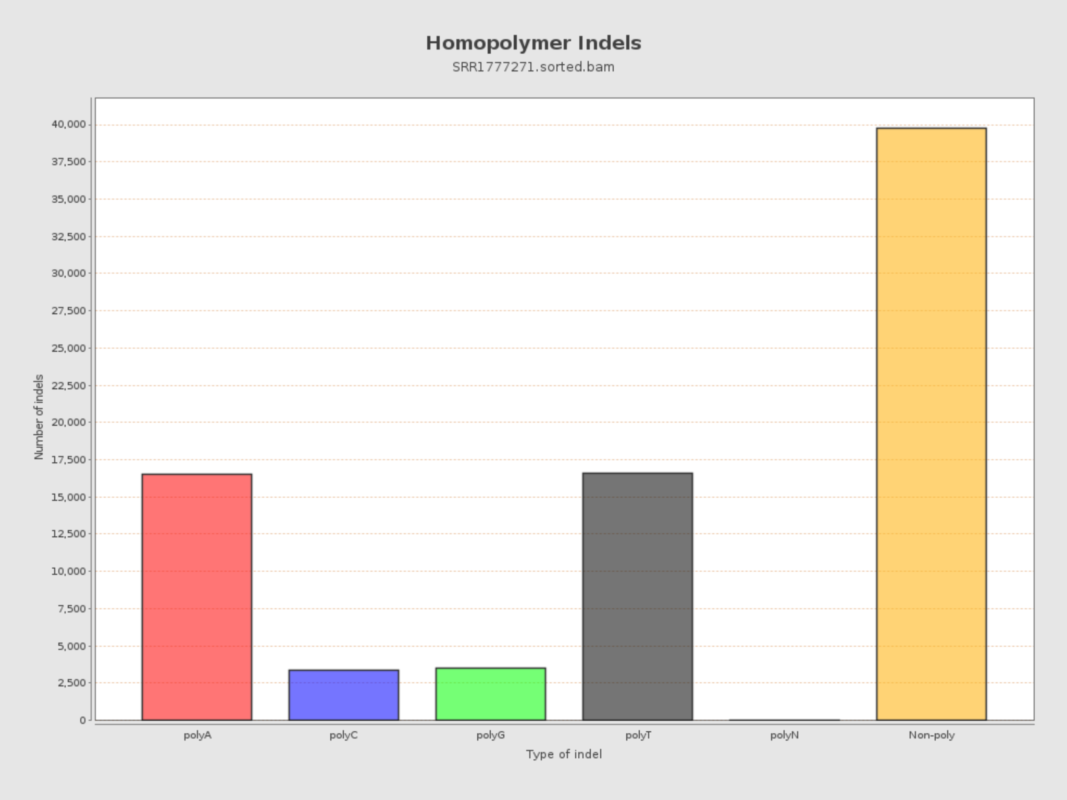
9. Results : Mapped Reads GC-content Distribution



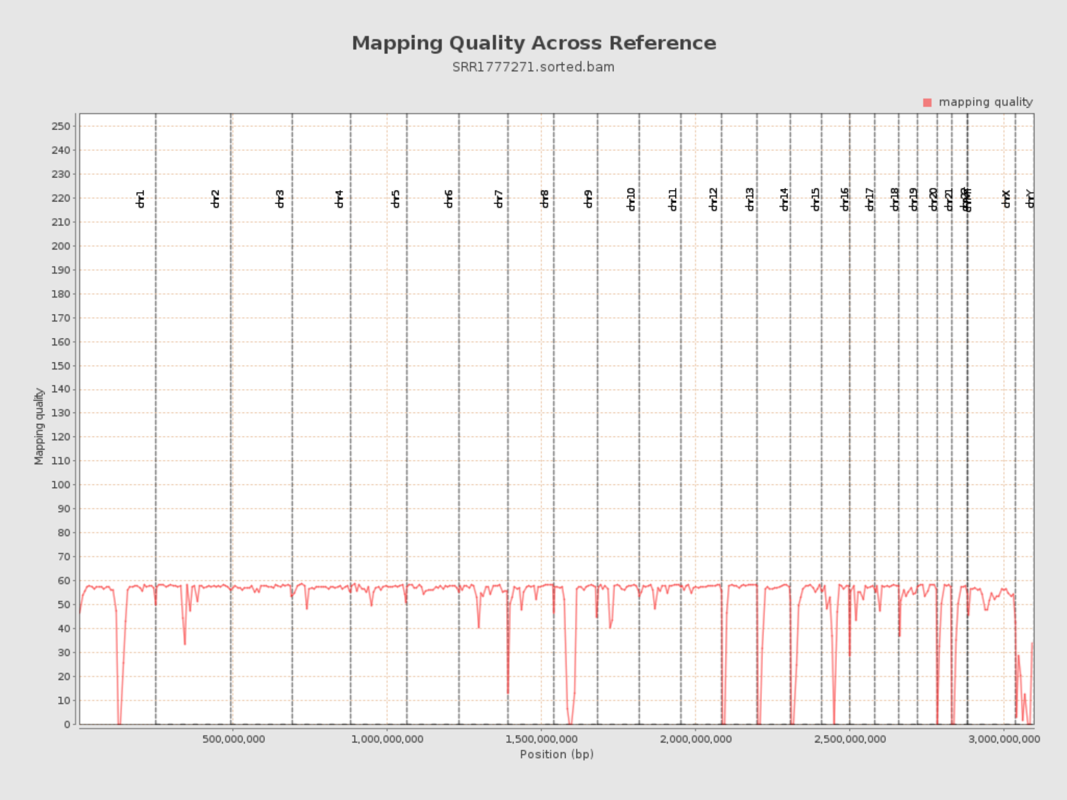
10. Results : Mapped Reads Clipping Profile



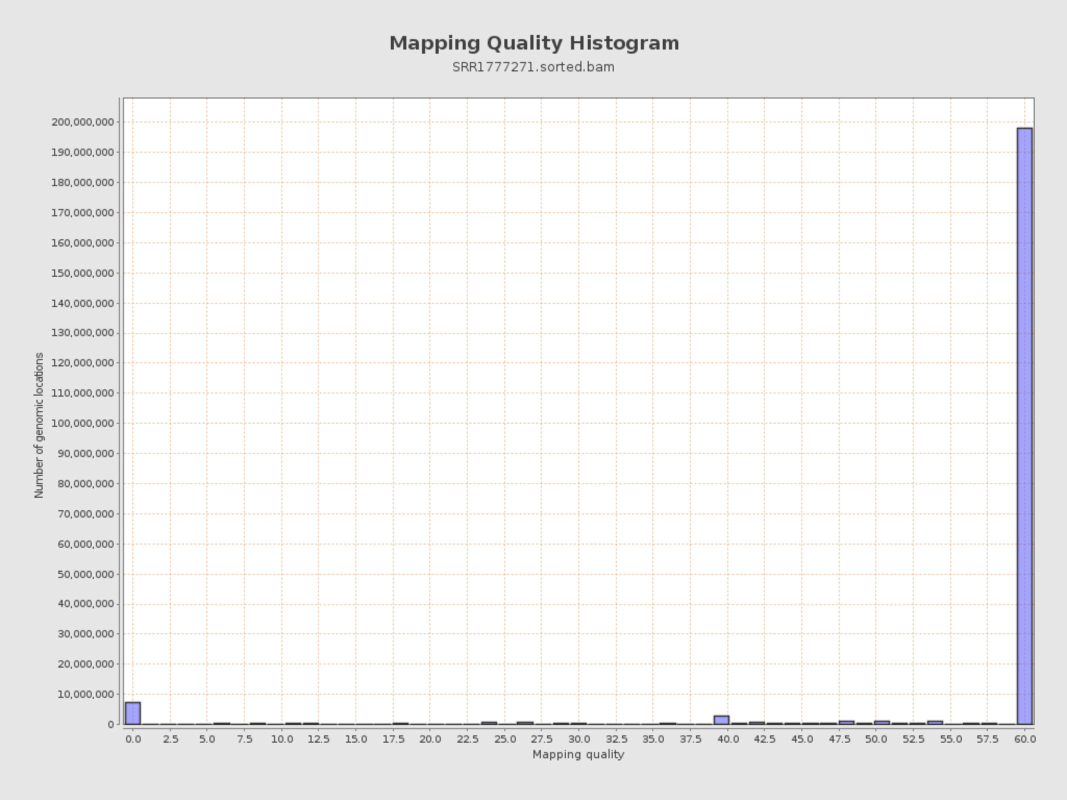
11. Results : Homopolymer Indels



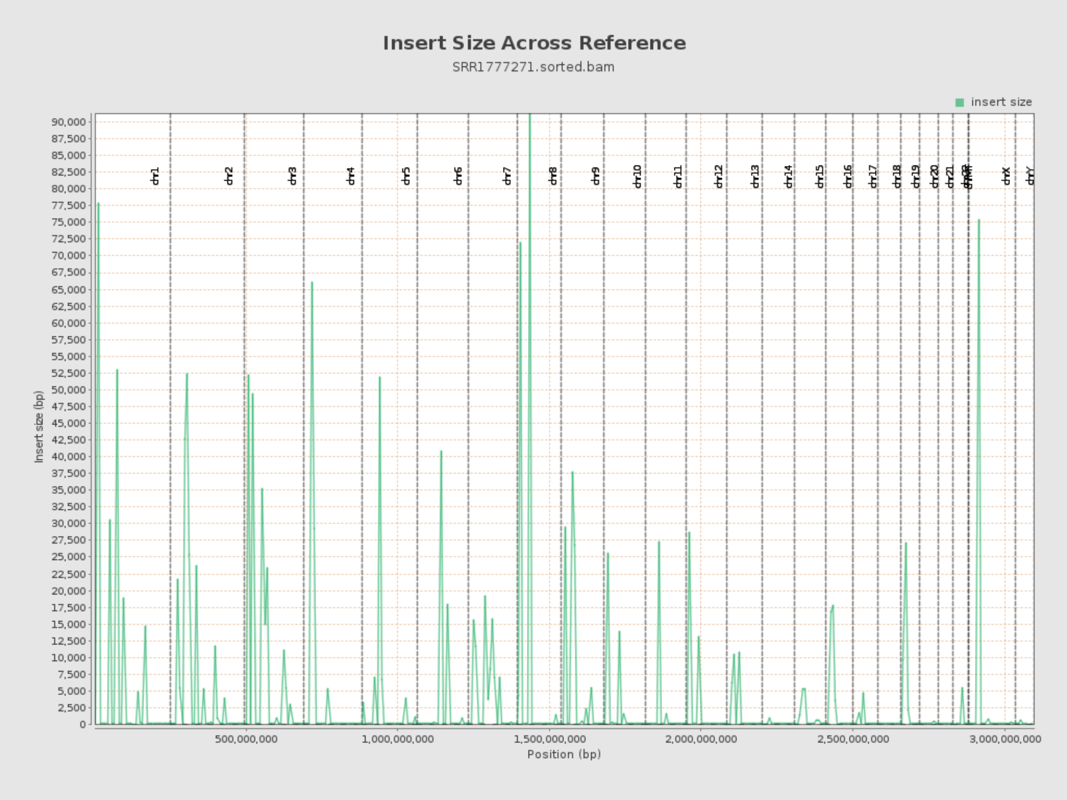
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram