Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/06 02:51:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777291.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_SRR1777291 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777291_1.fastq.gz SRR1777291_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 06 02:51:53 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777291.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	105,013,456
Mapped reads	103,303,951 / 98.37%
Unmapped reads	1,709,505 / 1.63%
Mapped paired reads	103,303,951 / 98.37%
Mapped reads, first in pair	51,798,689 / 49.33%
Mapped reads, second in pair	51,505,262 / 49.05%
Mapped reads, both in pair	102,787,226 / 97.88%
Mapped reads, singletons	516,725 / 0.49%
Secondary alignments	0
Supplementary alignments	5,018,236 / 4.78%
Read min/max/mean length	30 / 101 / 102.98
Duplicated reads (estimated)	19,244,745 / 18.33%
Duplication rate	12.8%
Clipped reads	32,278,751 / 30.74%

2.2. ACGT Content

Number/percentage of A's	2,920,633,365 / 29.24%
Number/percentage of C's	2,078,355,465 / 20.81%
Number/percentage of T's	2,853,386,397 / 28.56%
Number/percentage of G's	2,137,141,067 / 21.39%
Number/percentage of N's	158,774 / 0%

GC Percentage	42.2%

2.3. Coverage

Mean	3.228
Standard Deviation	29.2806

2.4. Mapping Quality

Mean Mapping Quality	53.01

2.5. Insert size

Mean	147,566.57
Standard Deviation	3,690,342.58
P25/Median/P75	112 / 156 / 214

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	56,170,751
Insertions	2,268,718
Mapped reads with at least one insertion	2.15%
Deletions	1,255,464
Mapped reads with at least one deletion	1.18%
Homopolymer indels	46.57%

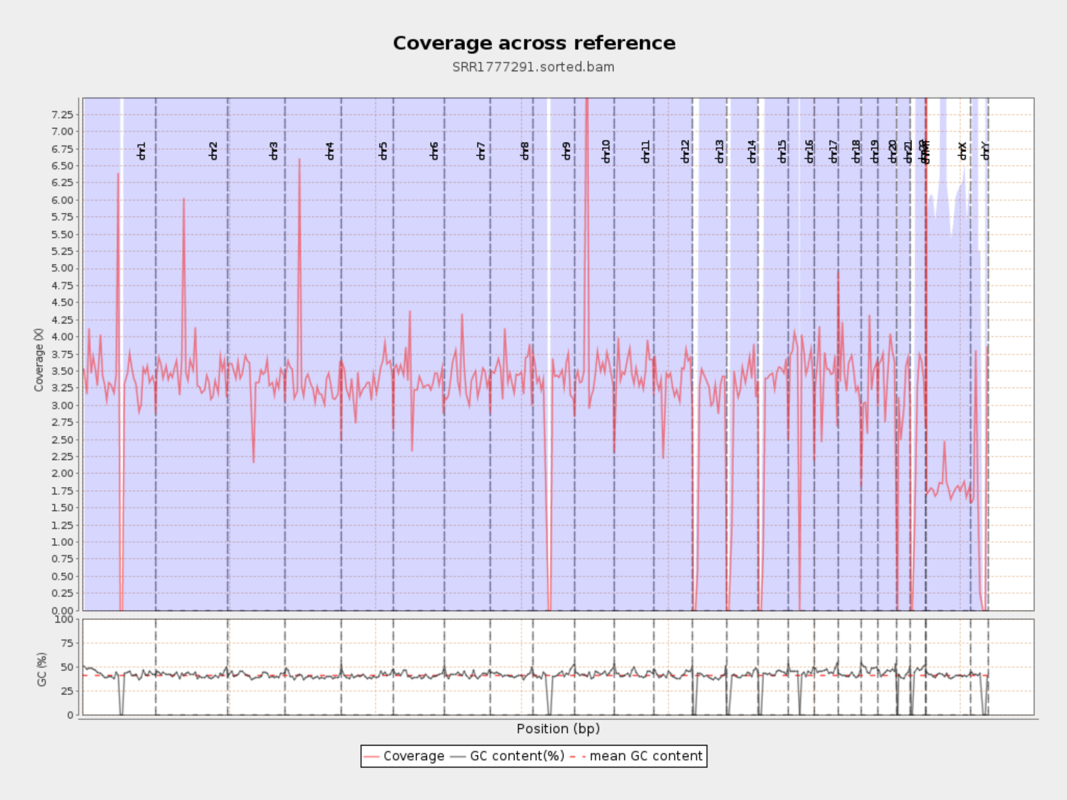
2.7. Chromosome stats

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

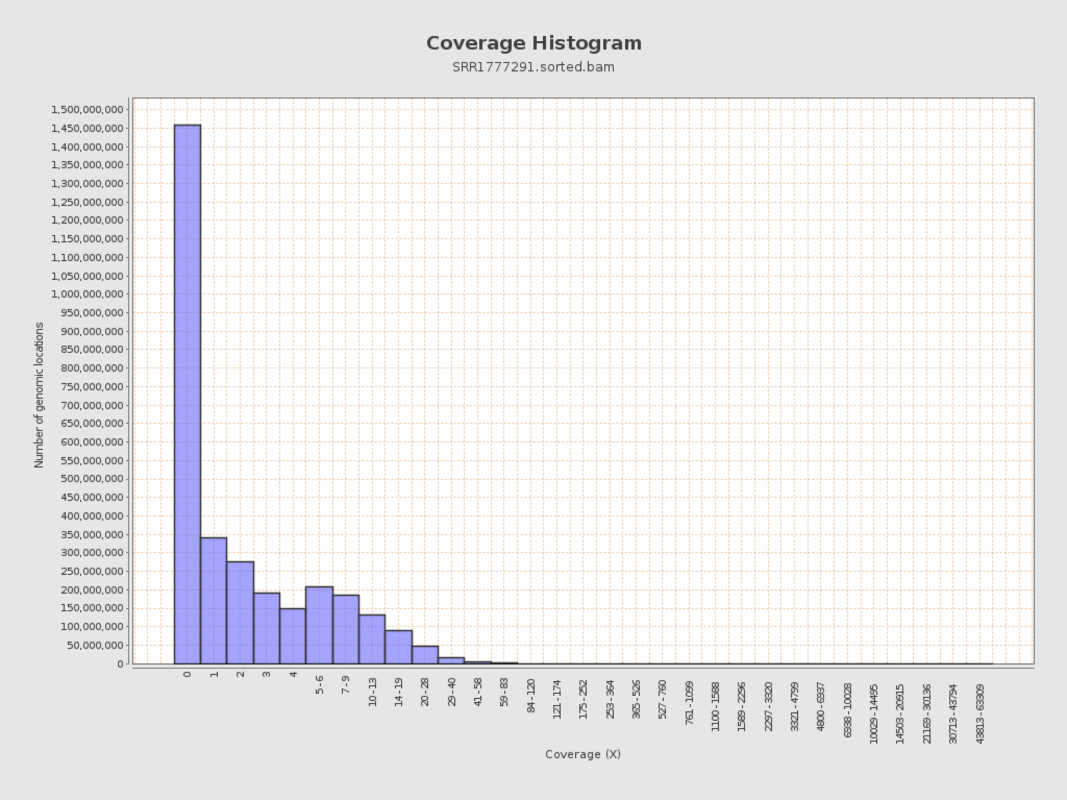
		bases	coverage	deviation
chr1	249250621	822677585	3.3006	63.1124
chr2	243199373	857230954	3.5248	20.0123
chr3	198022430	670651008	3.3867	6.9916
chr4	191154276	655635705	3.4299	23.3121
chr5	180915260	606293157	3.3513	6.0974
chr6	171115067	580788197	3.3941	13.5757
chr7	159138663	540169700	3.3943	26.7012
chr8	146364022	509896120	3.4838	14.975
chr9	141213431	419290167	2.9692	25.6467
chr10	135534747	509260840	3.7574	46.279
chr11	135006516	473507040	3.5073	23.1317
chr12	133851895	448791170	3.3529	5.998
chr13	115169878	312609654	2.7143	5.3805
chr14	107349540	304453661	2.8361	5.9342
chr15	102531392	284396636	2.7738	5.3612
chr16	90354753	302477834	3.3477	12.5533
chr17	81195210	280901247	3.4596	14.6791
chr18	78077248	276623447	3.5429	39.3171
chr19	59128983	192021731	3.2475	33.7818
chr20	63025520	220777131	3.503	8.6991
chr21	48129895	137629903	2.8596	13.3867
chr22	51304566	122206541	2.382	6.8247
chrMT	16571	89329160	5,390.6922	1,191.1562
chrX	155270560	279933135	1.8029	9.8443

chrY	59373566	95247862	1.6042	25.8646

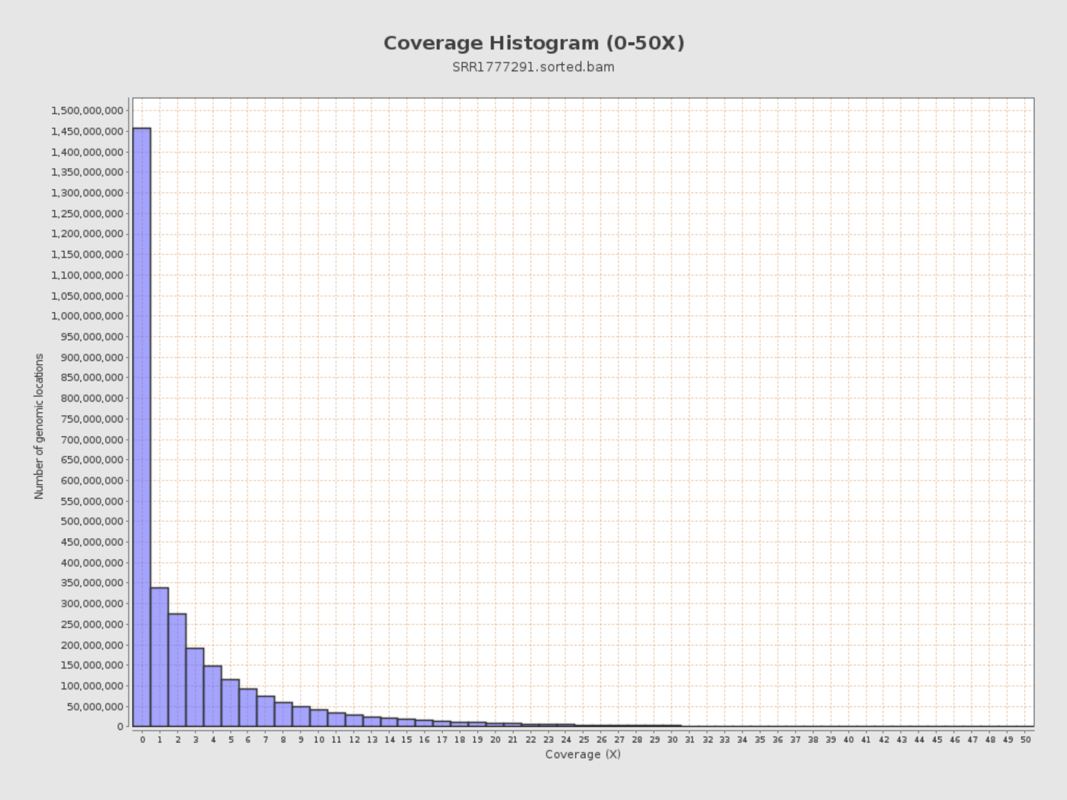
3. Results : Coverage across reference



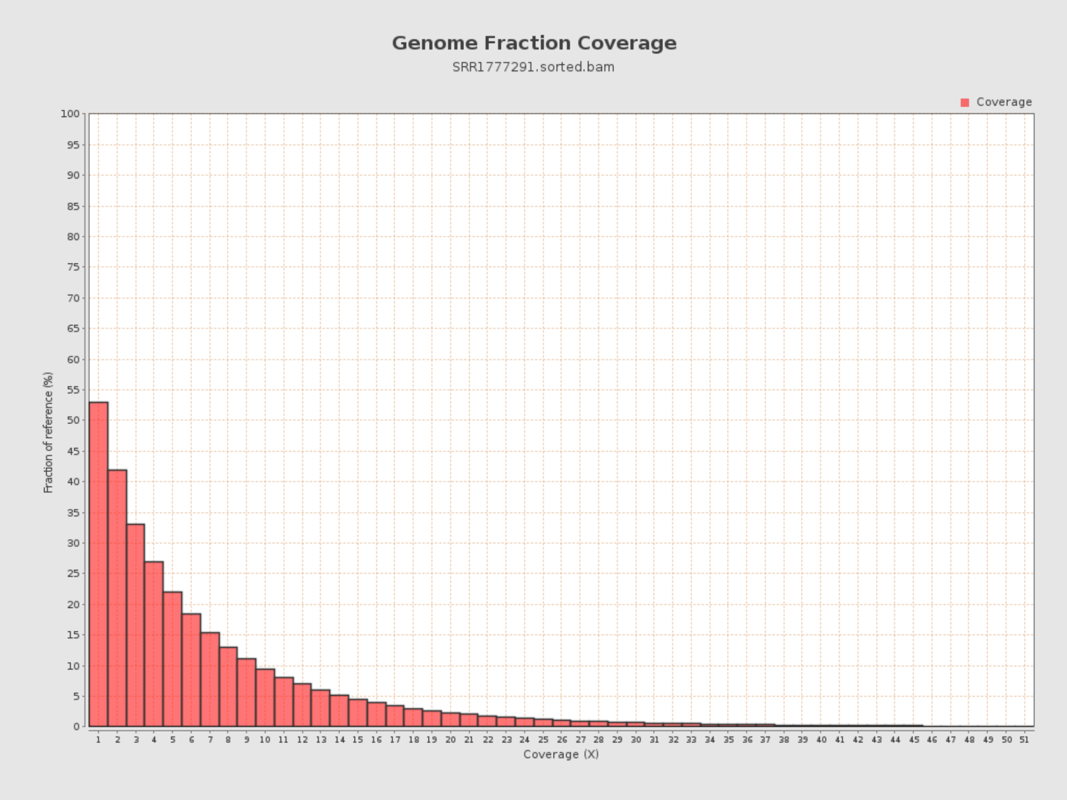
4. Results : Coverage Histogram



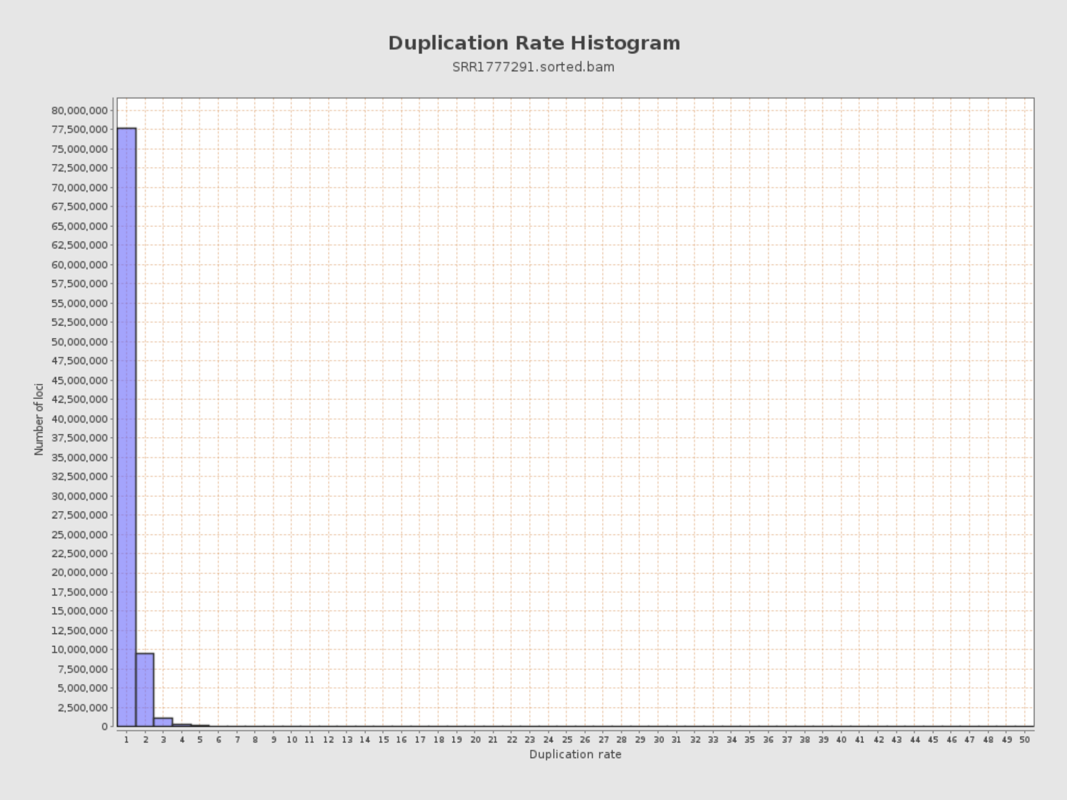
5. Results : Coverage Histogram (0-50X)



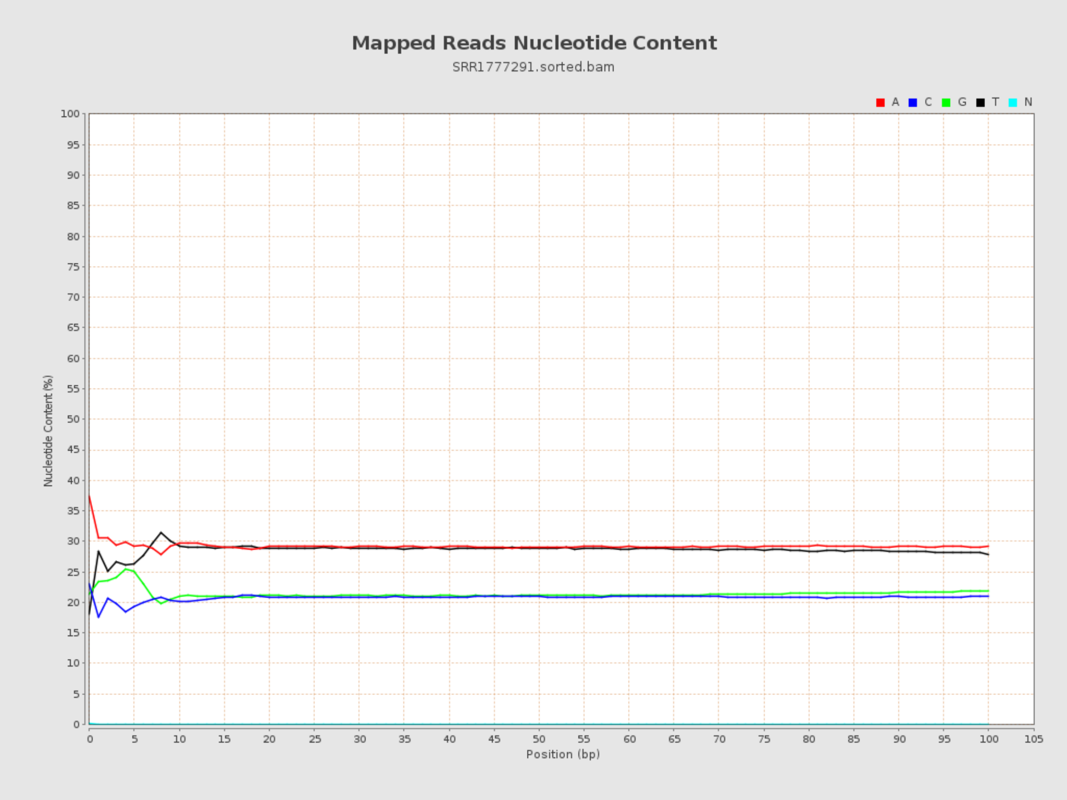
6. Results : Genome Fraction Coverage



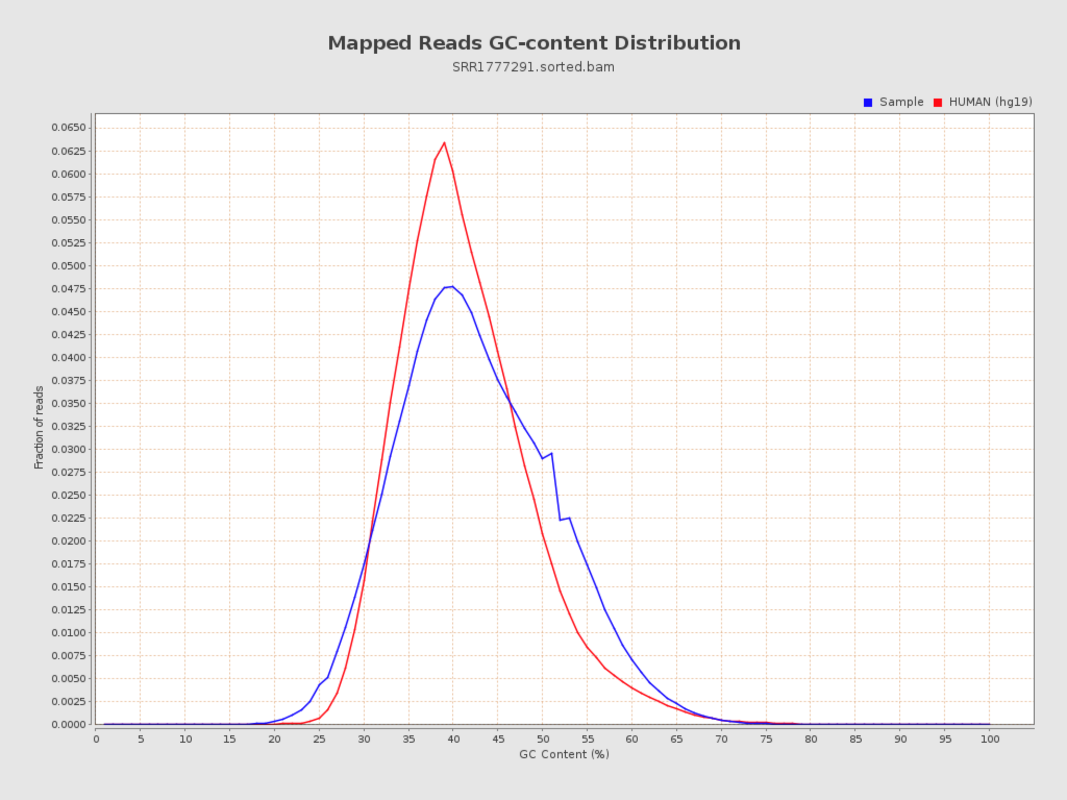
7. Results : Duplication Rate Histogram



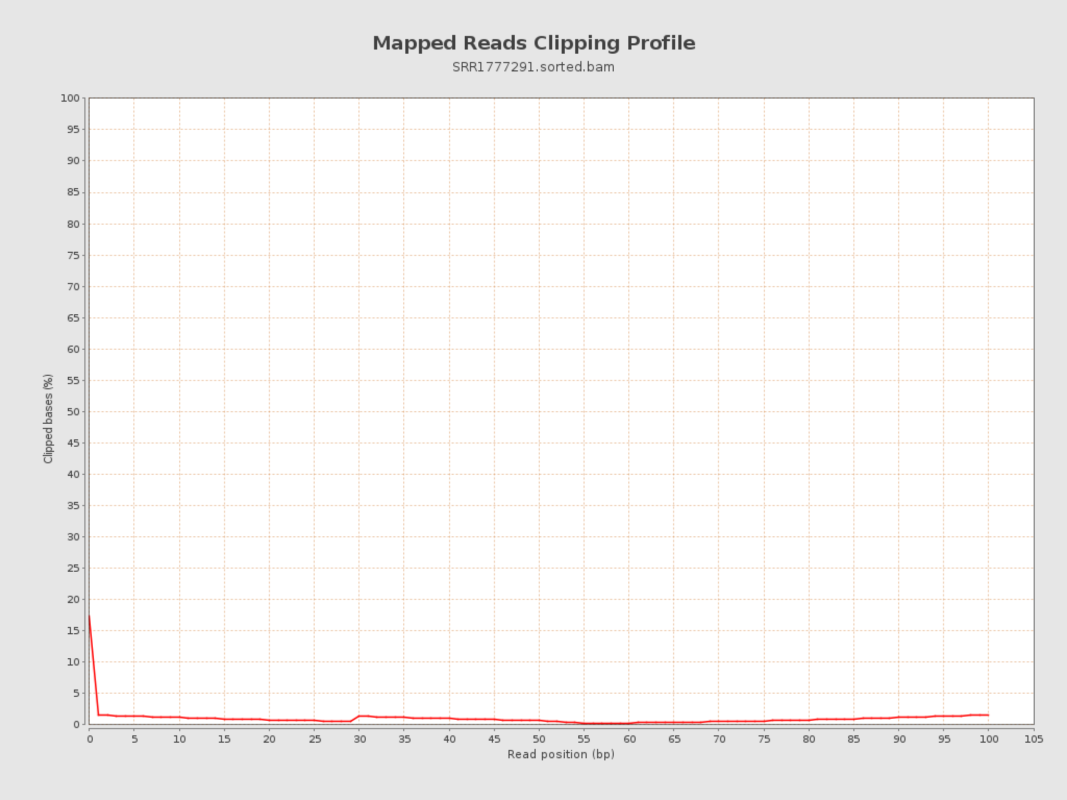
8. Results : Mapped Reads Nucleotide Content



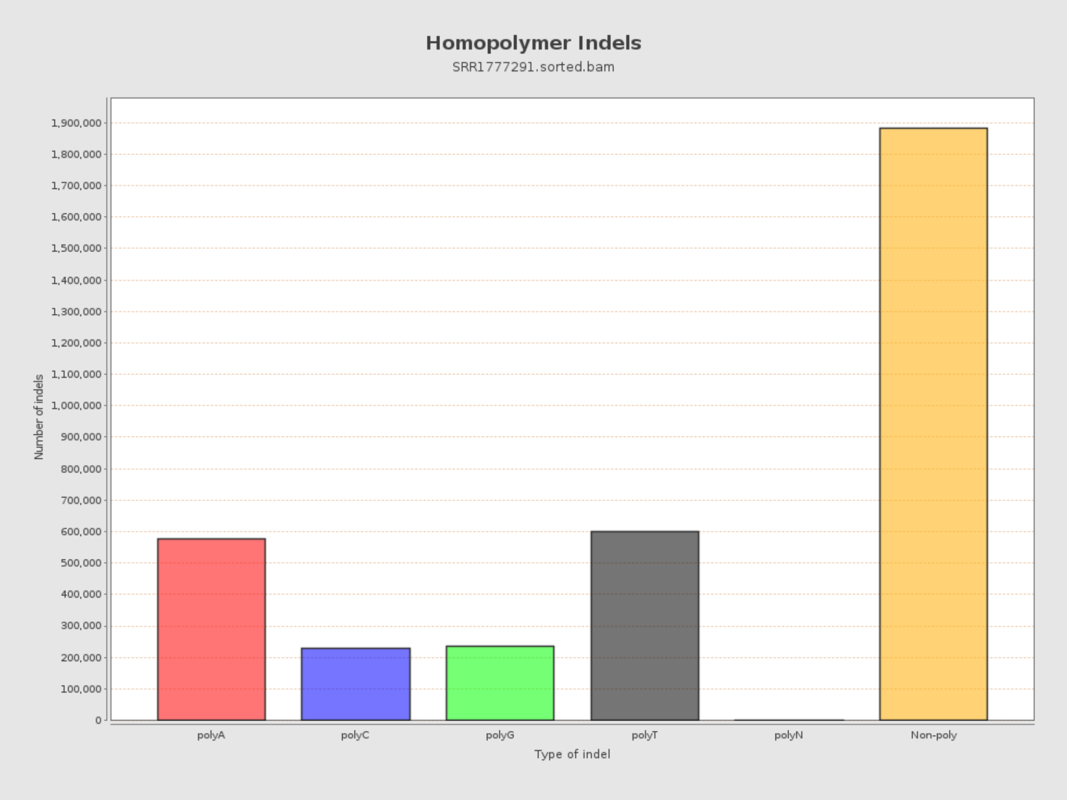
9. Results : Mapped Reads GC-content Distribution



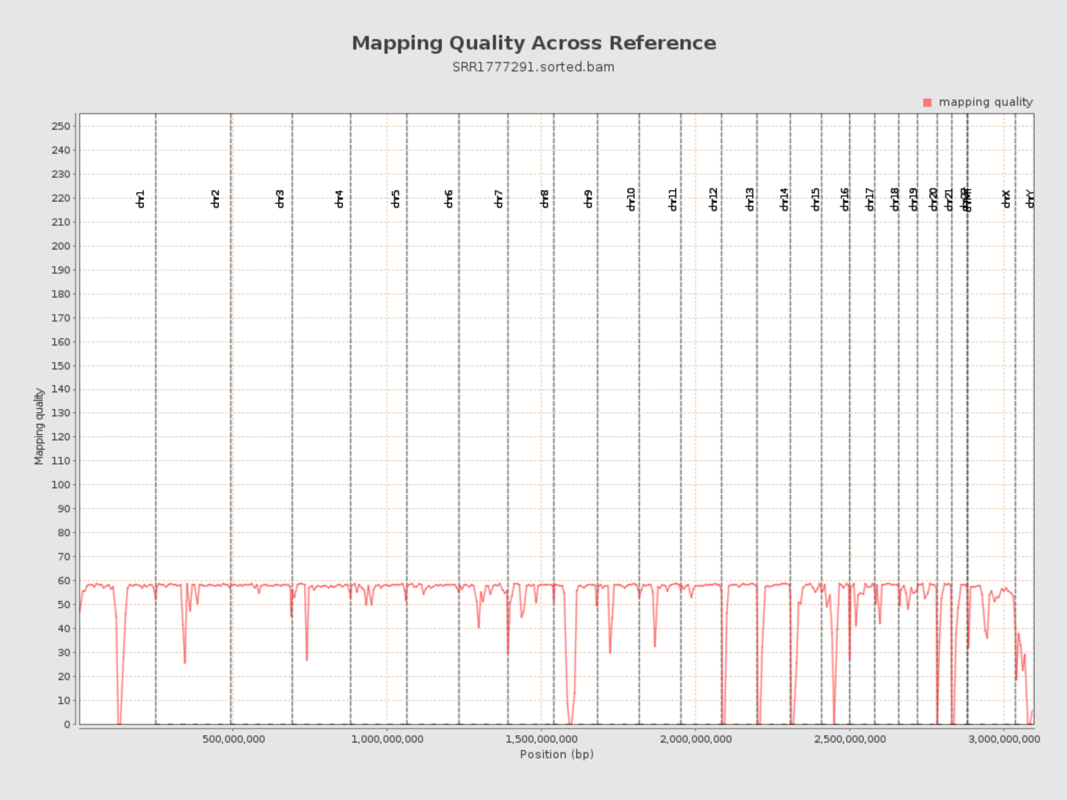
10. Results : Mapped Reads Clipping Profile



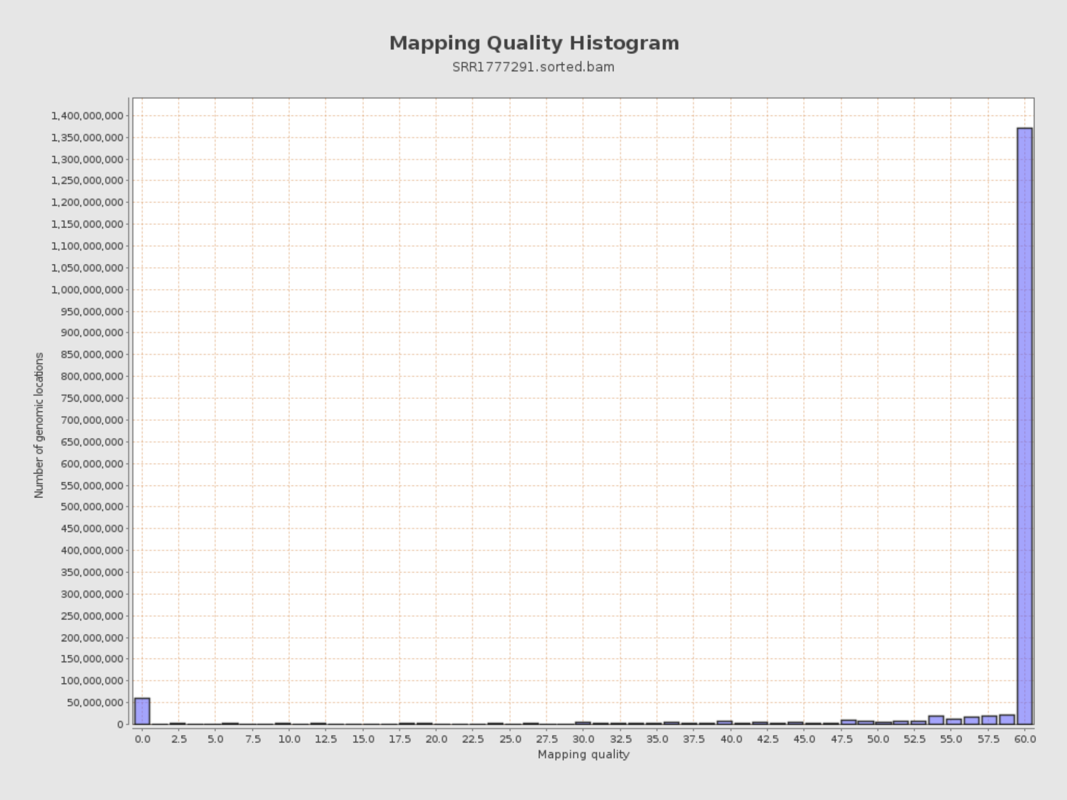
11. Results : Homopolymer Indels



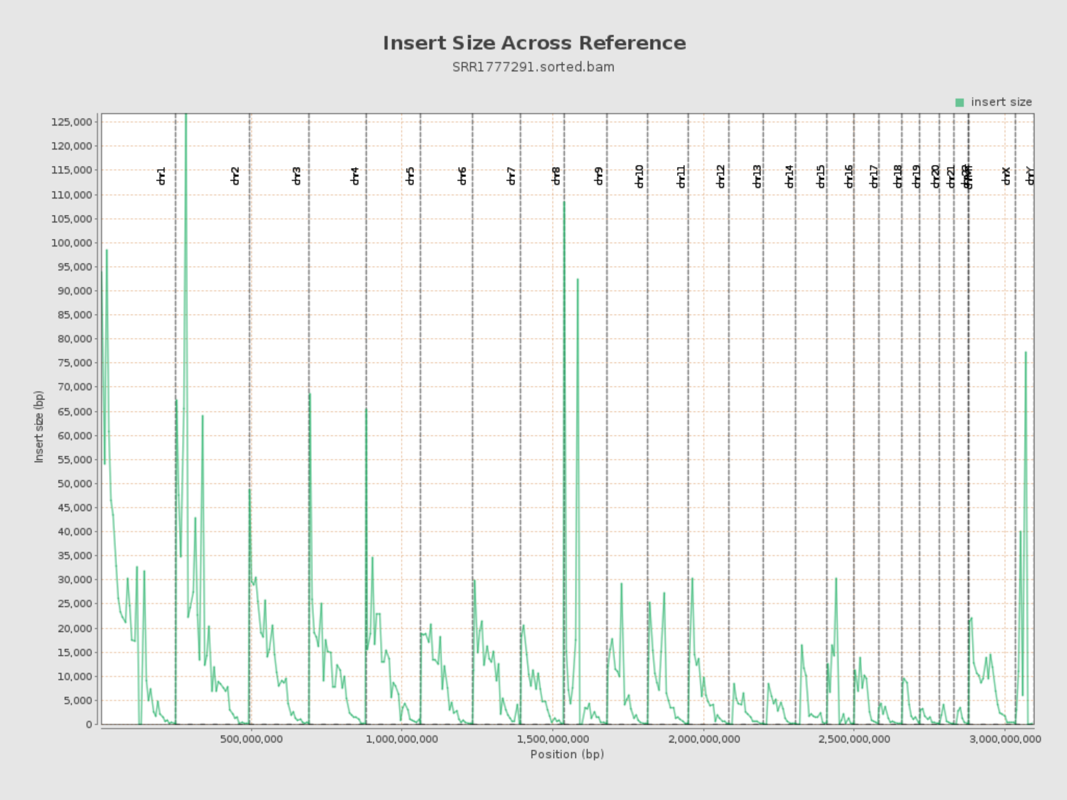
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram