Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 06:42:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777265.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_SRR1777265 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777265_1.fastq.gz SRR1777265_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 06:42:10 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777265.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	51,917,058
Mapped reads	51,639,720 / 99.47%
Unmapped reads	277,338 / 0.53%
Mapped paired reads	51,639,720 / 99.47%
Mapped reads, first in pair	25,820,651 / 49.73%
Mapped reads, second in pair	25,819,069 / 49.73%
Mapped reads, both in pair	51,543,106 / 99.28%
Mapped reads, singletons	96,614 / 0.19%
Secondary alignments	0
Supplementary alignments	1,964,095 / 3.78%
Read min/max/mean length	30 / 101 / 102.55
Duplicated reads (estimated)	26,560,164 / 51.16%
Duplication rate	46.38%
Clipped reads	6,949,770 / 13.39%

2.2. ACGT Content

Number/percentage of A's	1,431,228,259 / 27.65%
Number/percentage of C's	1,159,907,996 / 22.41%
Number/percentage of T's	1,420,949,875 / 27.45%
Number/percentage of G's	1,164,117,509 / 22.49%
Number/percentage of N's	63,157 / 0%

GC Percentage	44.9%

2.3. Coverage

Mean	1.6723
Standard Deviation	14.7407

2.4. Mapping Quality

Mean Mapping Quality	54.62

2.5. Insert size

Mean	322,681.15
Standard Deviation	5,599,118.61
P25/Median/P75	180 / 229 / 288

2.6. Mismatches and indels

General error rate	0.22%
Mismatches	10,103,784
Insertions	822,212
Mapped reads with at least one insertion	1.57%
Deletions	358,431
Mapped reads with at least one deletion	0.69%
Homopolymer indels	51.72%

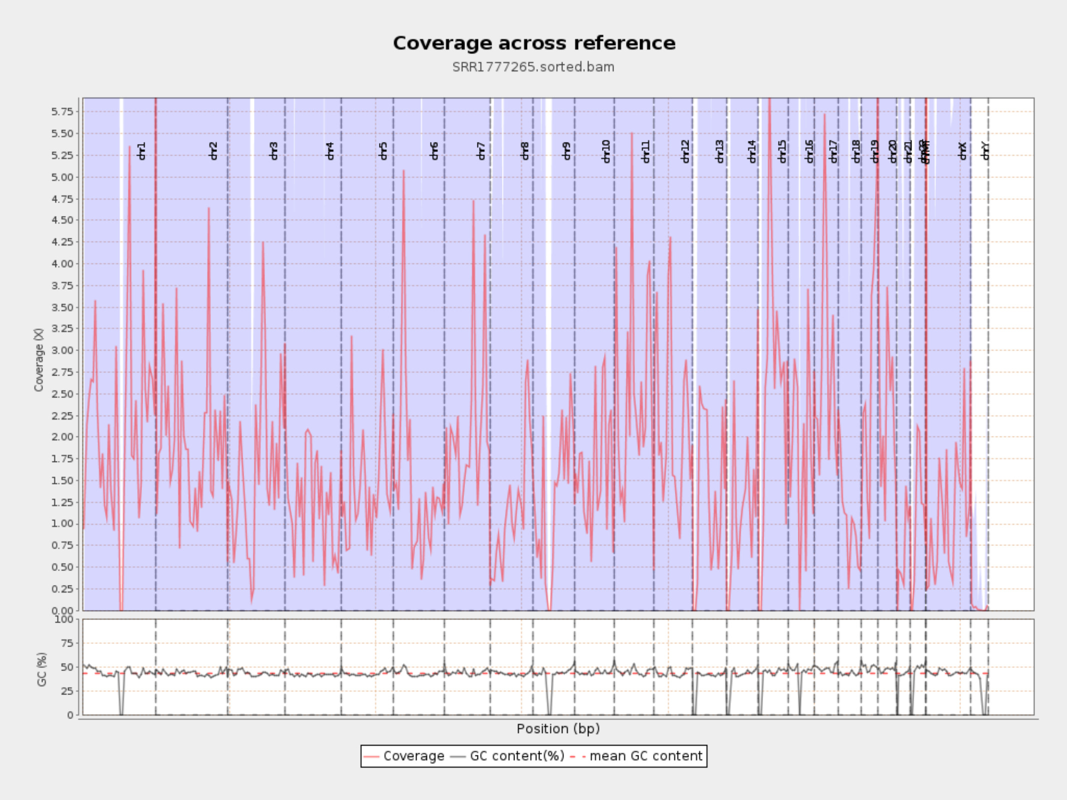
2.7. Chromosome stats

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

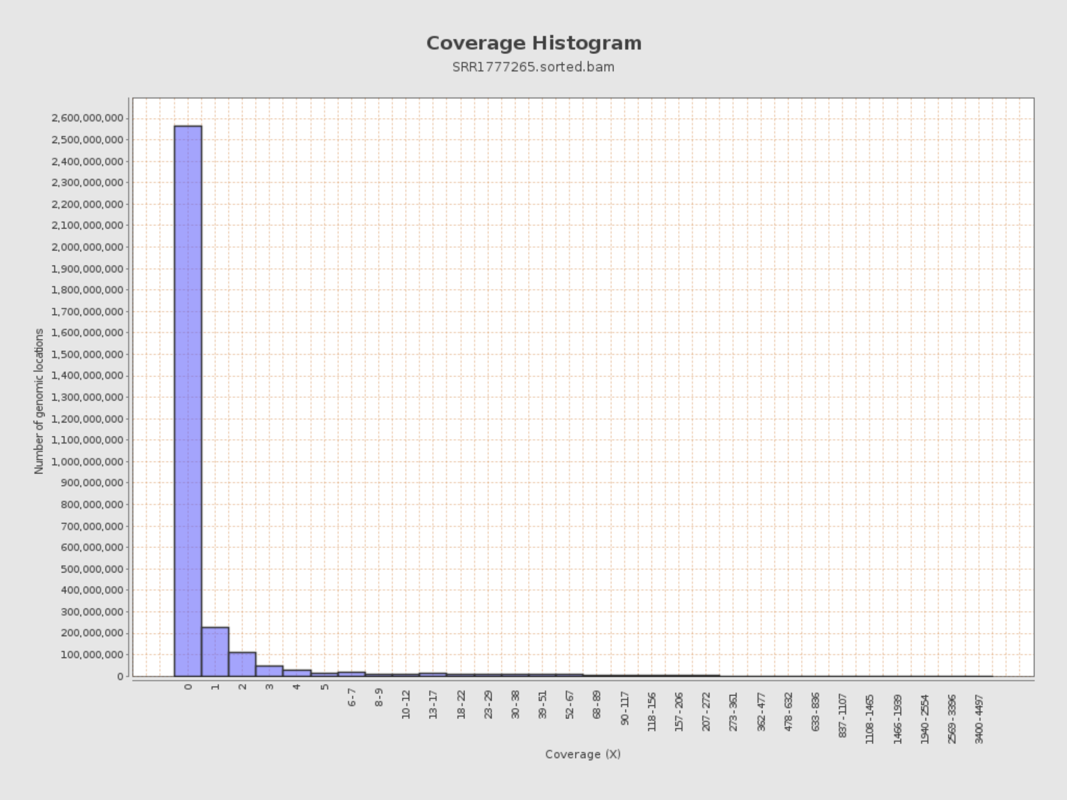
		bases	coverage	deviation
chr1	249250621	529751029	2.1254	16.6513
chr2	243199373	472822939	1.9442	16.4786
chr3	198022430	318038389	1.6061	14.3245
chr4	191154276	234382016	1.2261	12.2733
chr5	180915260	271100179	1.4985	12.9813
chr6	171115067	245377303	1.434	12.9867
chr7	159138663	326861343	2.0539	17.0243
chr8	146364022	175911989	1.2019	13.1357
chr9	141213431	178812049	1.2663	11.4994
chr10	135534747	223995306	1.6527	14.0306
chr11	135006516	338195397	2.505	19.4234
chr12	133851895	296470899	2.2149	17.1346
chr13	115169878	151223108	1.313	13.9652
chr14	107349540	118832694	1.107	11.0705
chr15	102531392	256096975	2.4977	19.9365
chr16	90354753	160175512	1.7727	13.7143
chr17	81195210	225731075	2.7801	19.1508
chr18	78077248	81144000	1.0393	10.5307
chr19	59128983	165276601	2.7952	16.9808
chr20	63025520	143334192	2.2742	17.6885
chr21	48129895	34565610	0.7182	7.9614
chr22	51304566	55621596	1.0841	9.2263
chrMT	16571	1193605	72.0298	27.9944
chrX	155270560	170519223	1.0982	12.5937

chrY	59373566	1625871	0.0274	1.334

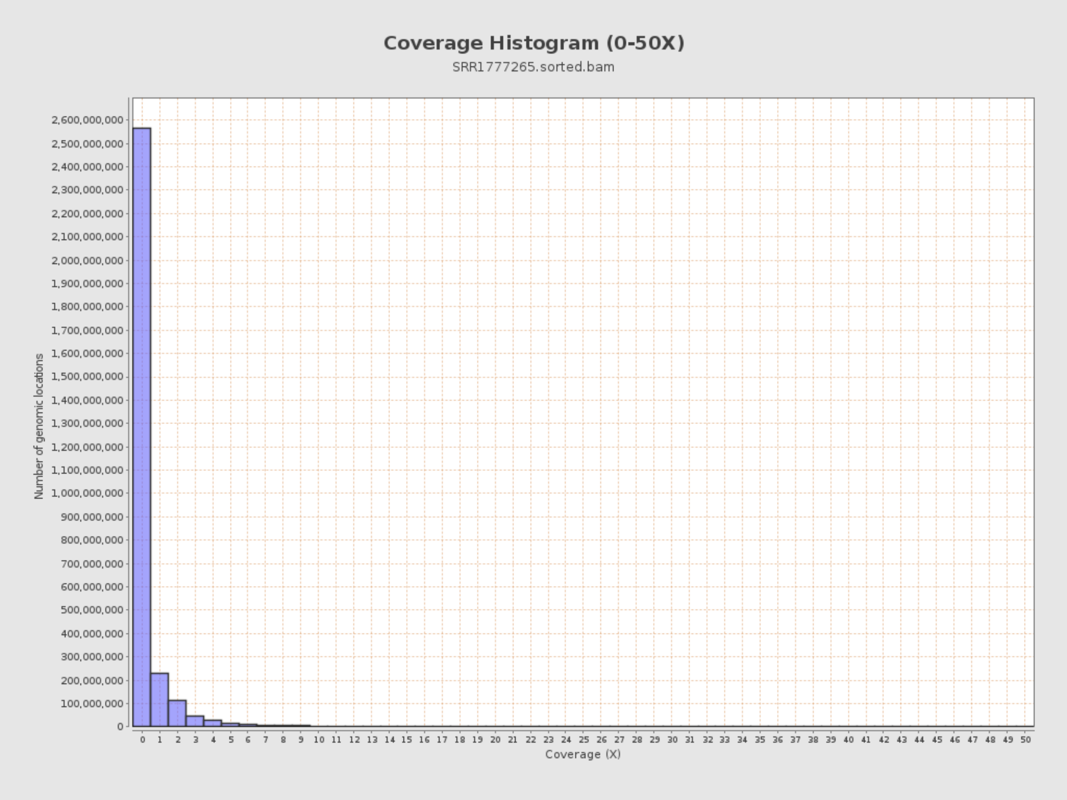
3. Results : Coverage across reference



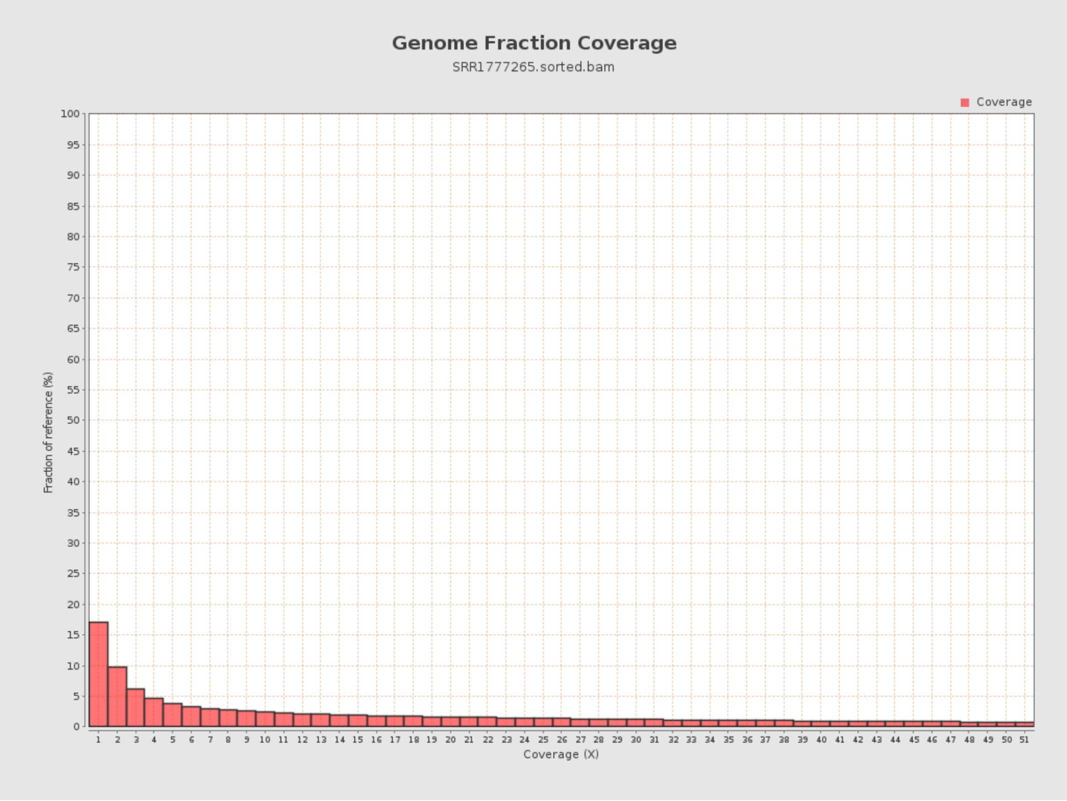
4. Results : Coverage Histogram



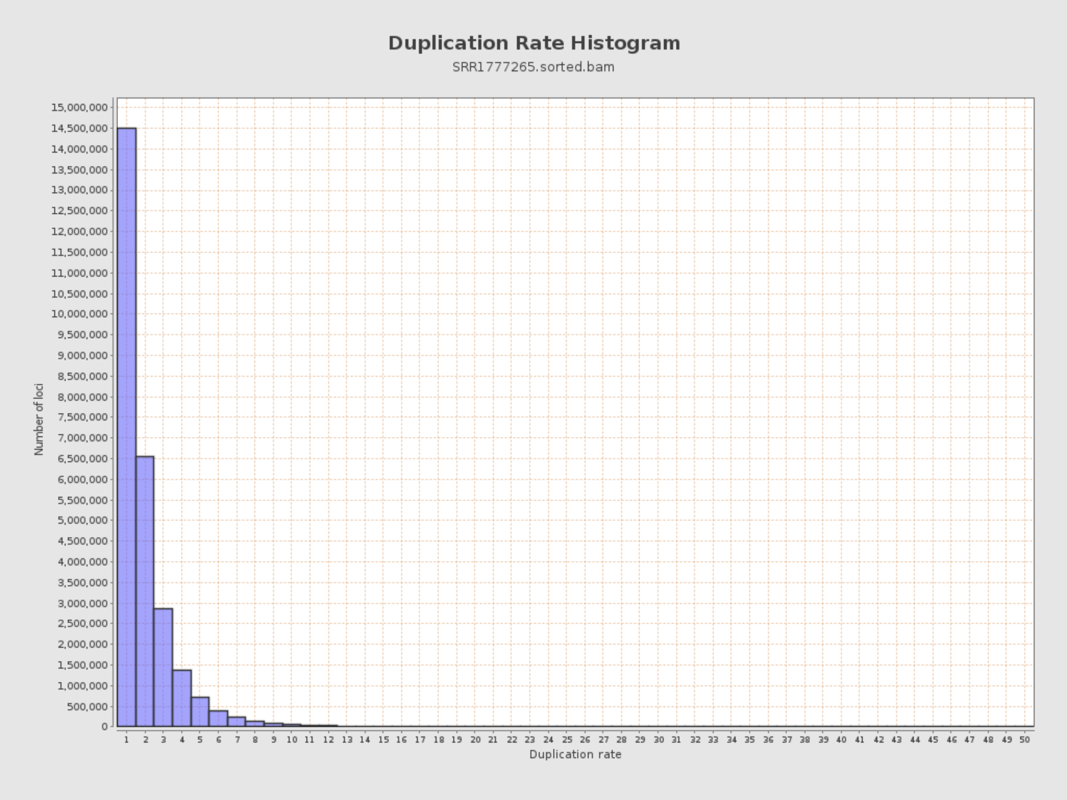
5. Results : Coverage Histogram (0-50X)



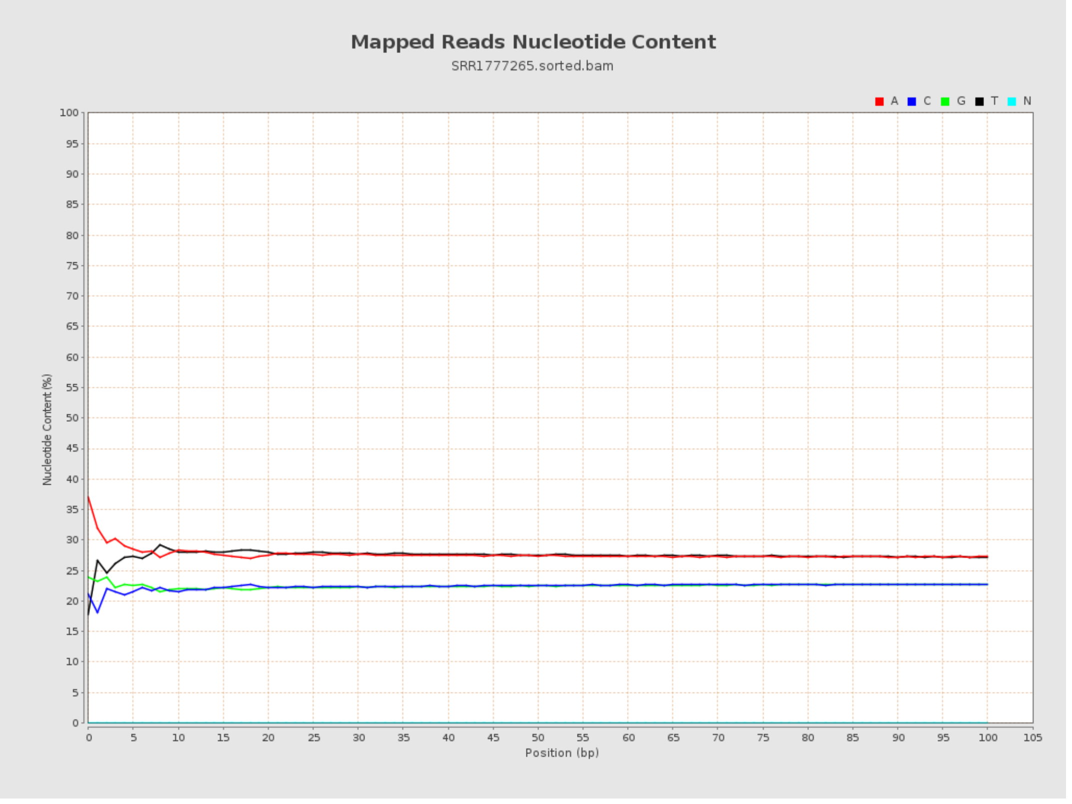
6. Results : Genome Fraction Coverage



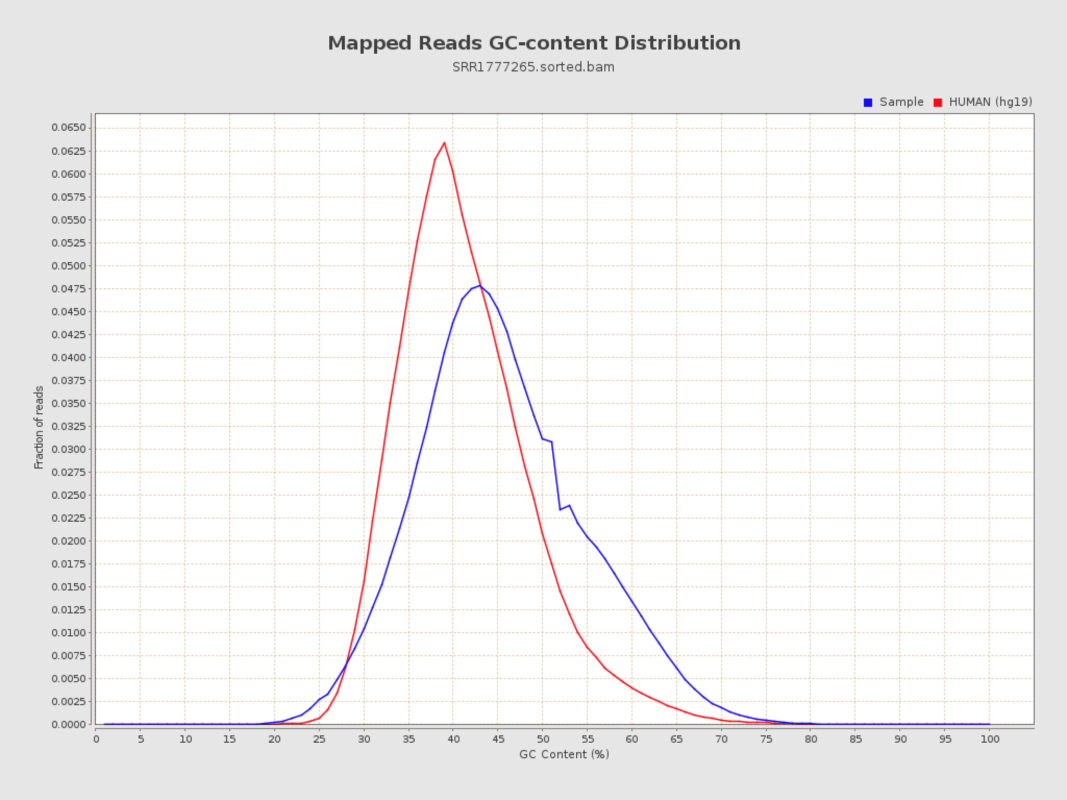
7. Results : Duplication Rate Histogram



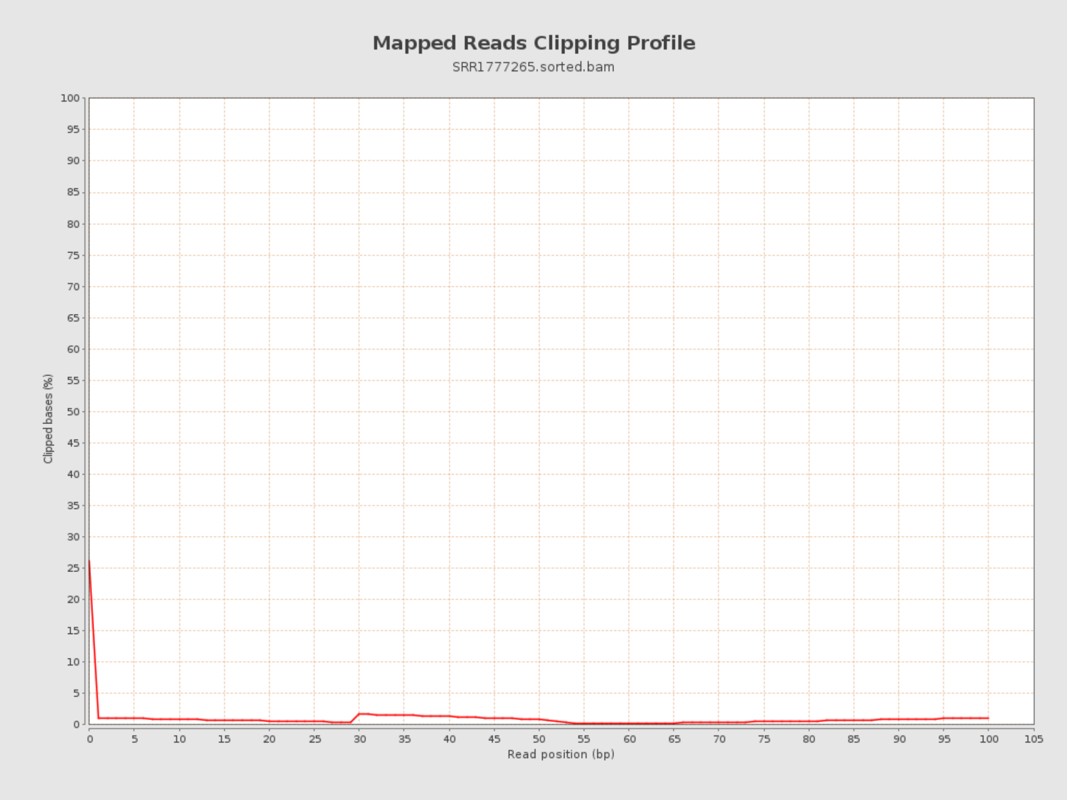
8. Results : Mapped Reads Nucleotide Content



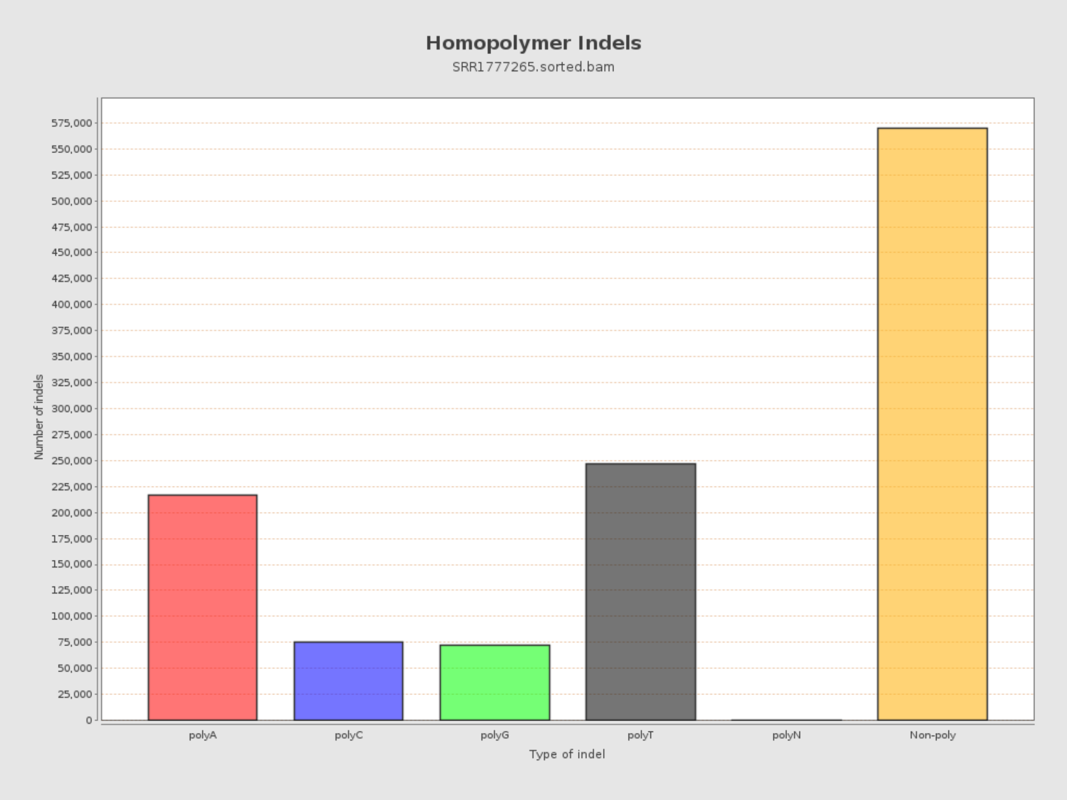
9. Results : Mapped Reads GC-content Distribution



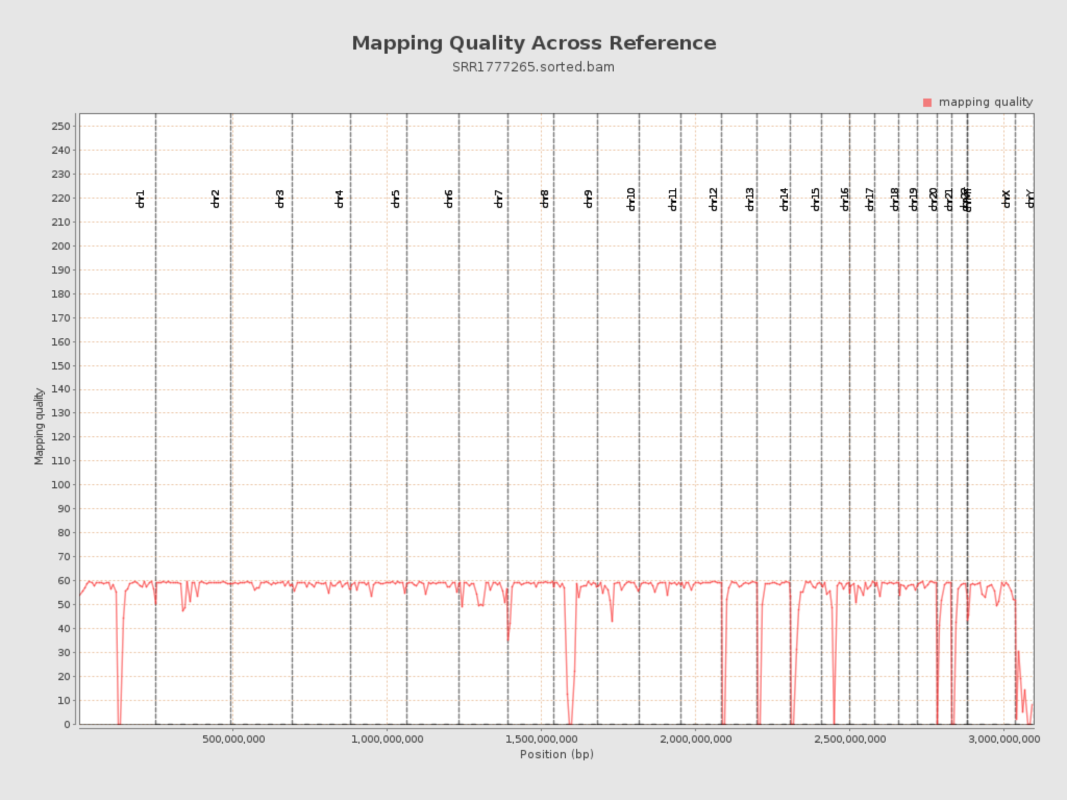
10. Results : Mapped Reads Clipping Profile



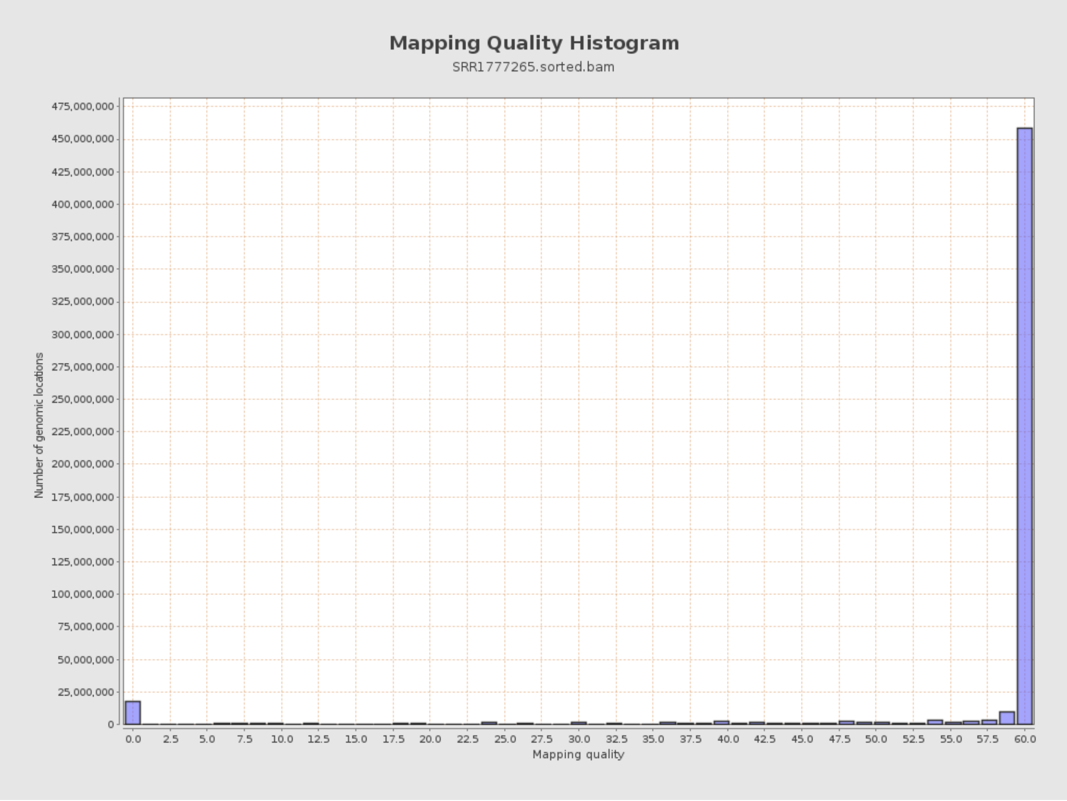
11. Results : Homopolymer Indels



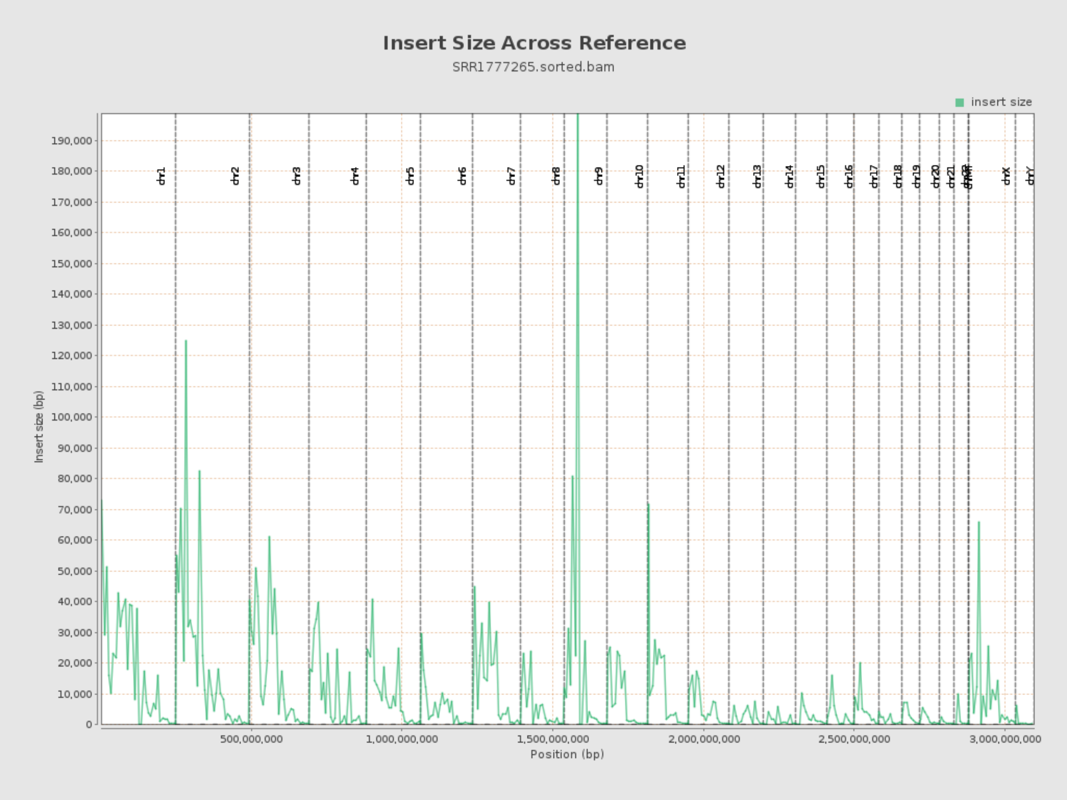
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram