Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/06 00:40:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777290.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_SRR1777290 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777290_1.fastq.gz SRR1777290_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 06 00:40:18 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777290.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	102,540,314
Mapped reads	100,841,214 / 98.34%
Unmapped reads	1,699,100 / 1.66%
Mapped paired reads	100,841,214 / 98.34%
Mapped reads, first in pair	50,565,502 / 49.31%
Mapped reads, second in pair	50,275,712 / 49.03%
Mapped reads, both in pair	100,323,292 / 97.84%
Mapped reads, singletons	517,922 / 0.51%
Secondary alignments	0
Supplementary alignments	4,863,257 / 4.74%
Read min/max/mean length	30 / 101 / 102.96
Duplicated reads (estimated)	18,635,175 / 18.17%
Duplication rate	12.72%
Clipped reads	31,674,592 / 30.89%

2.2. ACGT Content

Number/percentage of A's	2,847,201,520 / 29.22%
Number/percentage of C's	2,027,997,375 / 20.81%
Number/percentage of T's	2,780,554,577 / 28.53%
Number/percentage of G's	2,088,897,120 / 21.44%
Number/percentage of N's	161,728 / 0%

GC Percentage	42.25%

2.3. Coverage

Mean	3.1488
Standard Deviation	28.4806

2.4. Mapping Quality

Mean Mapping Quality	53

2.5. Insert size

Mean	145,482.68
Standard Deviation	3,659,520.78
P25/Median/P75	111 / 155 / 214

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	59,643,598
Insertions	2,224,755
Mapped reads with at least one insertion	2.16%
Deletions	1,222,445
Mapped reads with at least one deletion	1.18%
Homopolymer indels	46.38%

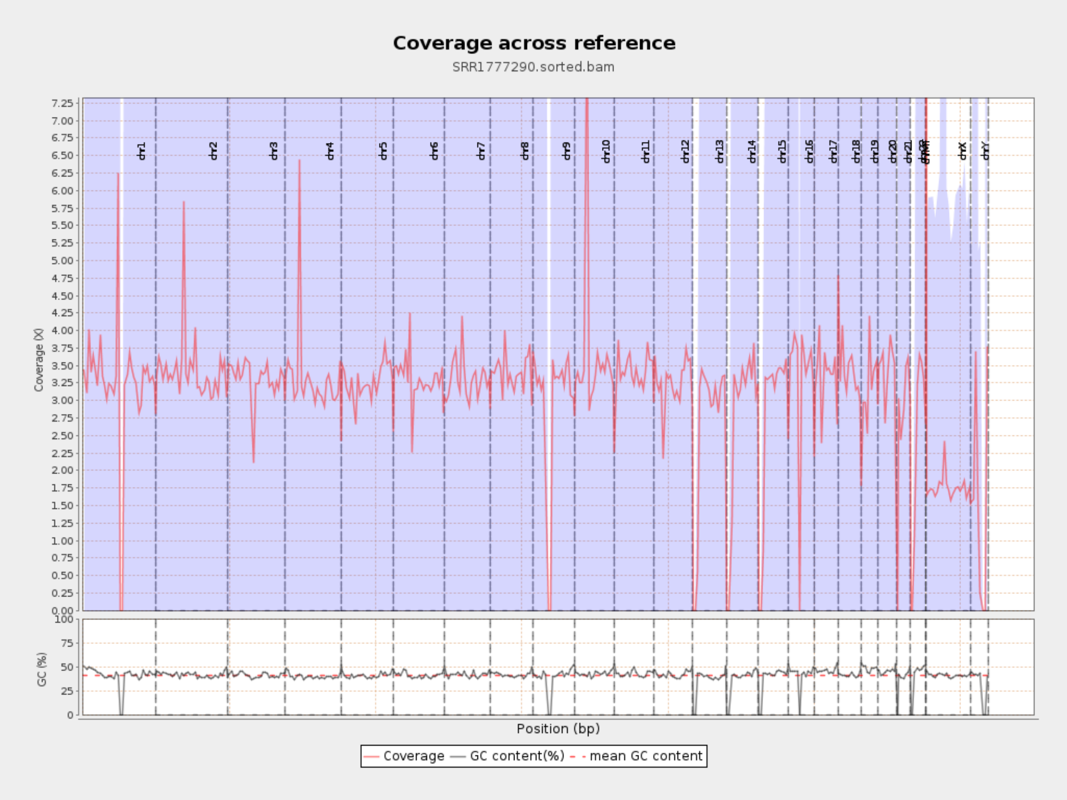
2.7. Chromosome stats

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

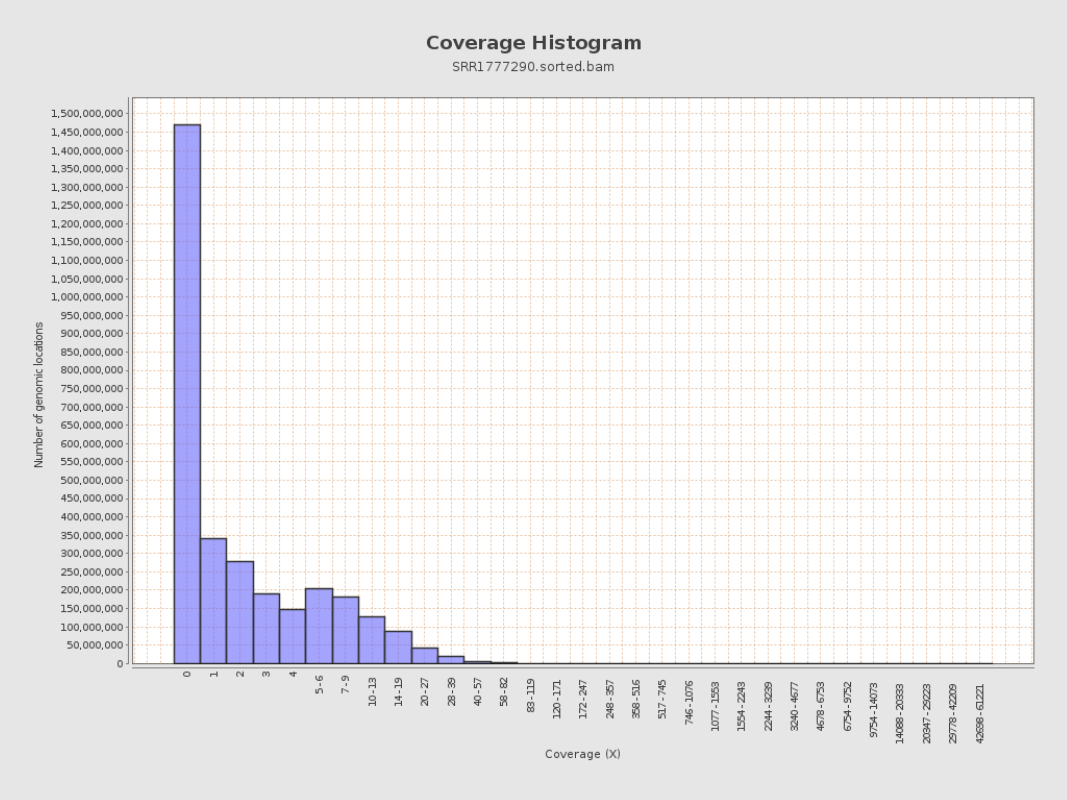
		bases	coverage	deviation
chr1	249250621	803895200	3.2252	61.2552
chr2	243199373	836145934	3.4381	19.4794
chr3	198022430	653359761	3.2994	6.8072
chr4	191154276	639109622	3.3434	22.8355
chr5	180915260	590925896	3.2663	5.9473
chr6	171115067	566400390	3.3101	13.2716
chr7	159138663	526735472	3.3099	26.1108
chr8	146364022	497314341	3.3978	14.2556
chr9	141213431	409004041	2.8964	24.8261
chr10	135534747	496241139	3.6614	44.9417
chr11	135006516	461503223	3.4184	22.0773
chr12	133851895	437182452	3.2662	5.8486
chr13	115169878	304362950	2.6427	5.2662
chr14	107349540	297333656	2.7698	5.805
chr15	102531392	277778126	2.7092	5.2487
chr16	90354753	295629796	3.2719	12.3095
chr17	81195210	274412378	3.3797	14.3751
chr18	78077248	269362032	3.4499	38.1947
chr19	59128983	187922814	3.1782	32.7896
chr20	63025520	215533241	3.4198	8.4963
chr21	48129895	134491353	2.7943	12.9099
chr22	51304566	119613759	2.3314	6.6041
chrMT	16571	87503731	5,280.5341	1,174.4679
chrX	155270560	273085376	1.7588	9.4613

chrY	59373566	93016182	1.5666	25.1435

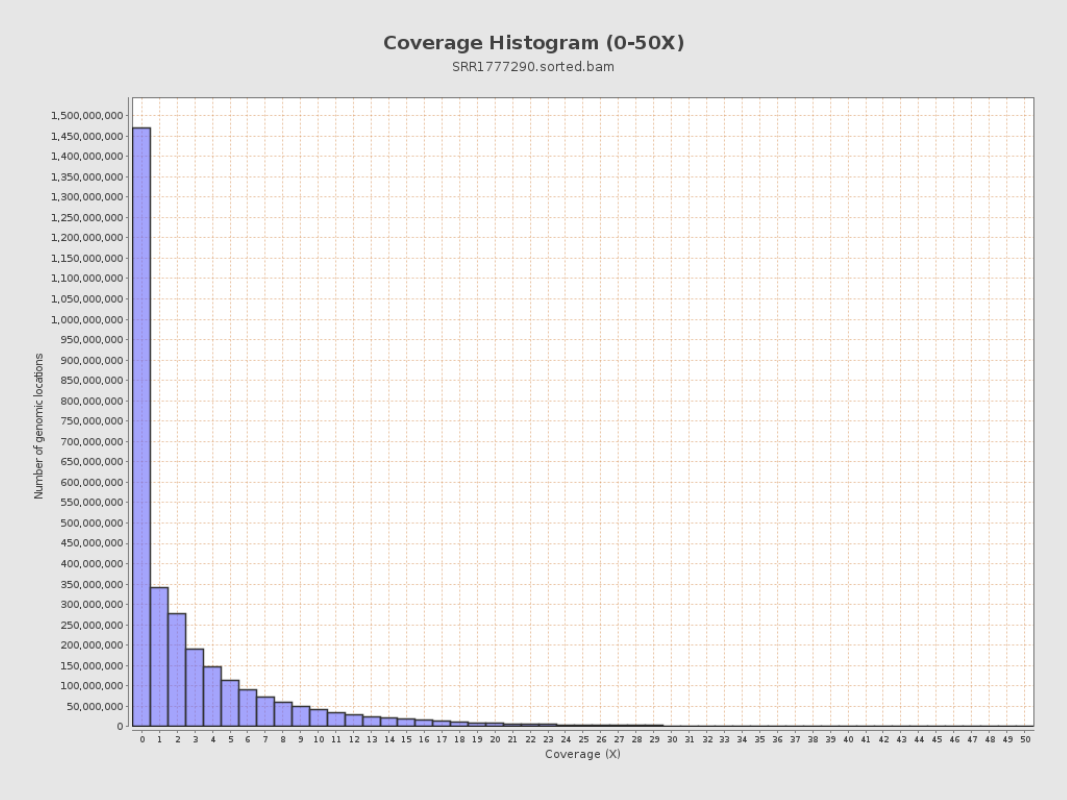
3. Results : Coverage across reference



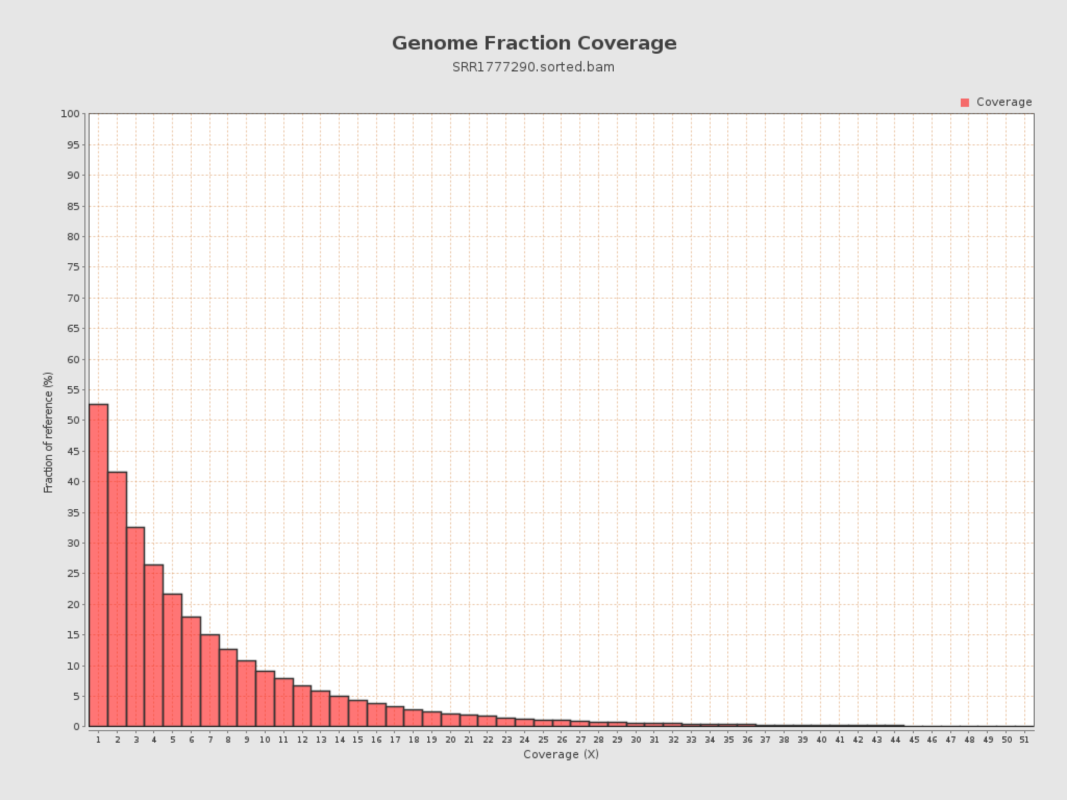
4. Results : Coverage Histogram



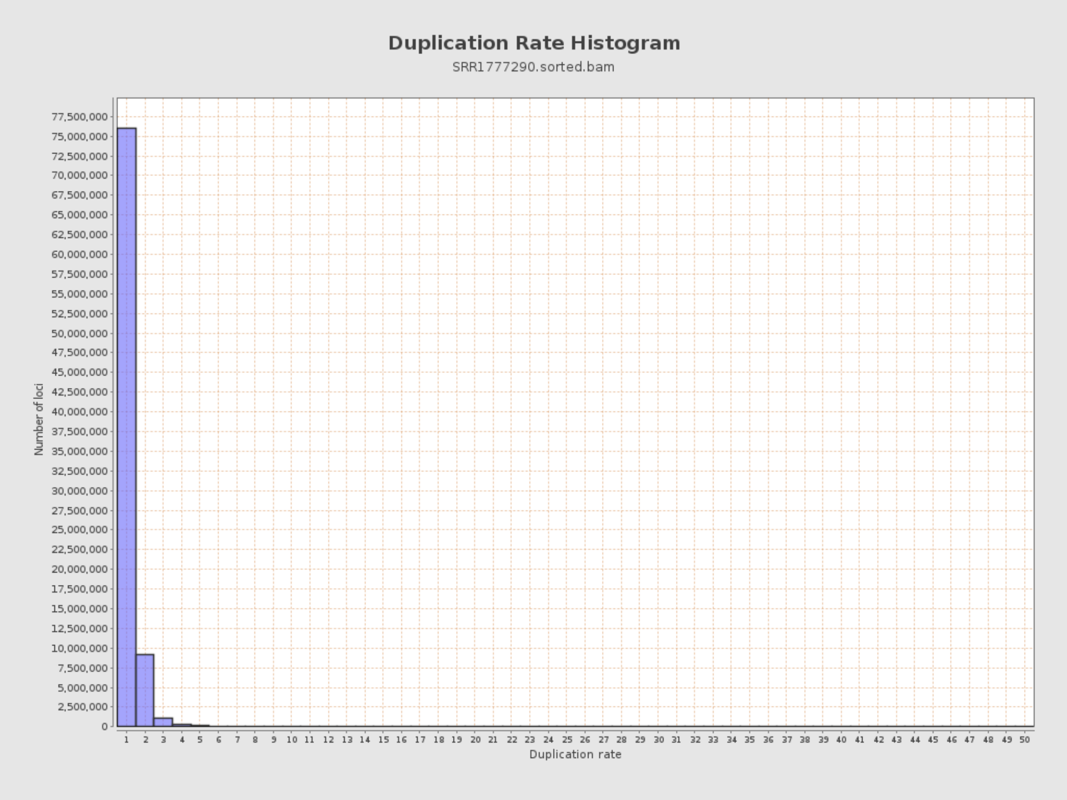
5. Results : Coverage Histogram (0-50X)



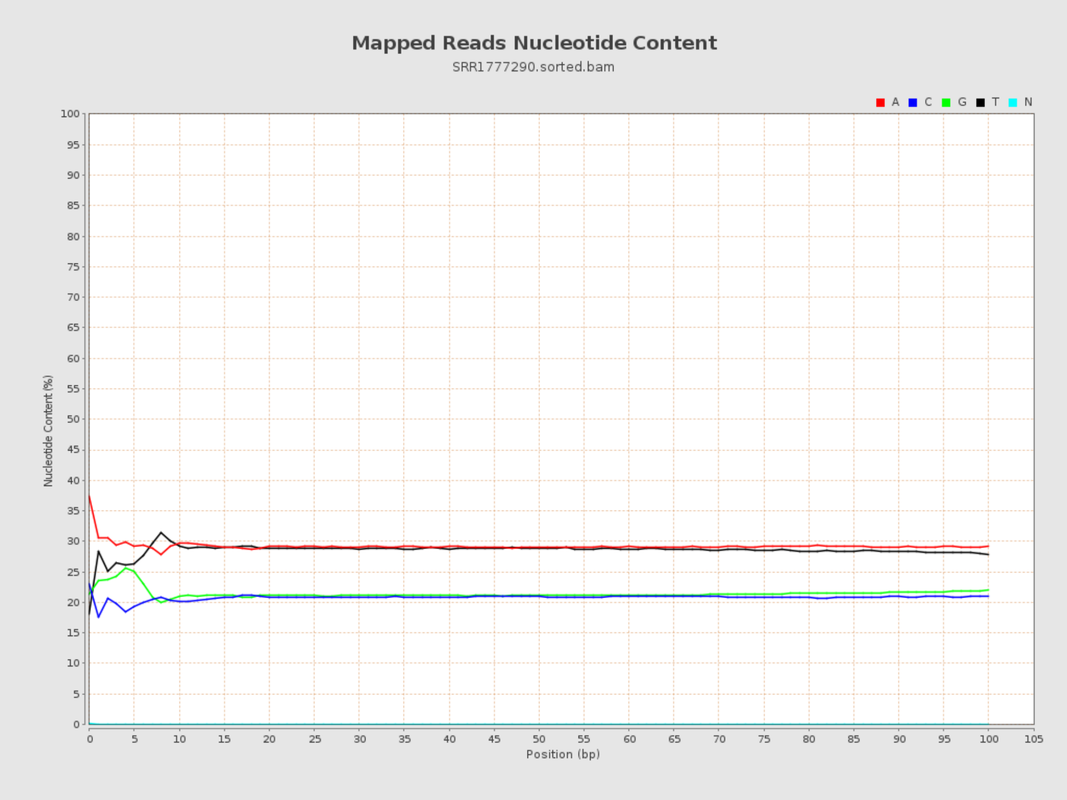
6. Results : Genome Fraction Coverage



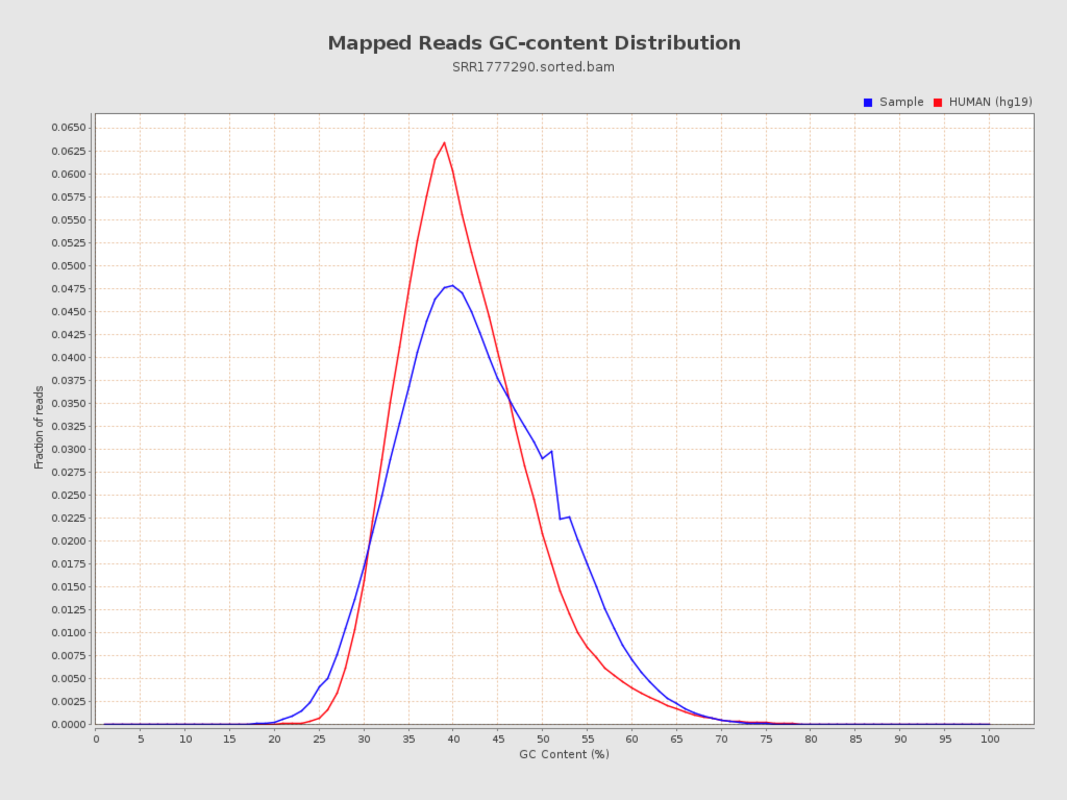
7. Results : Duplication Rate Histogram



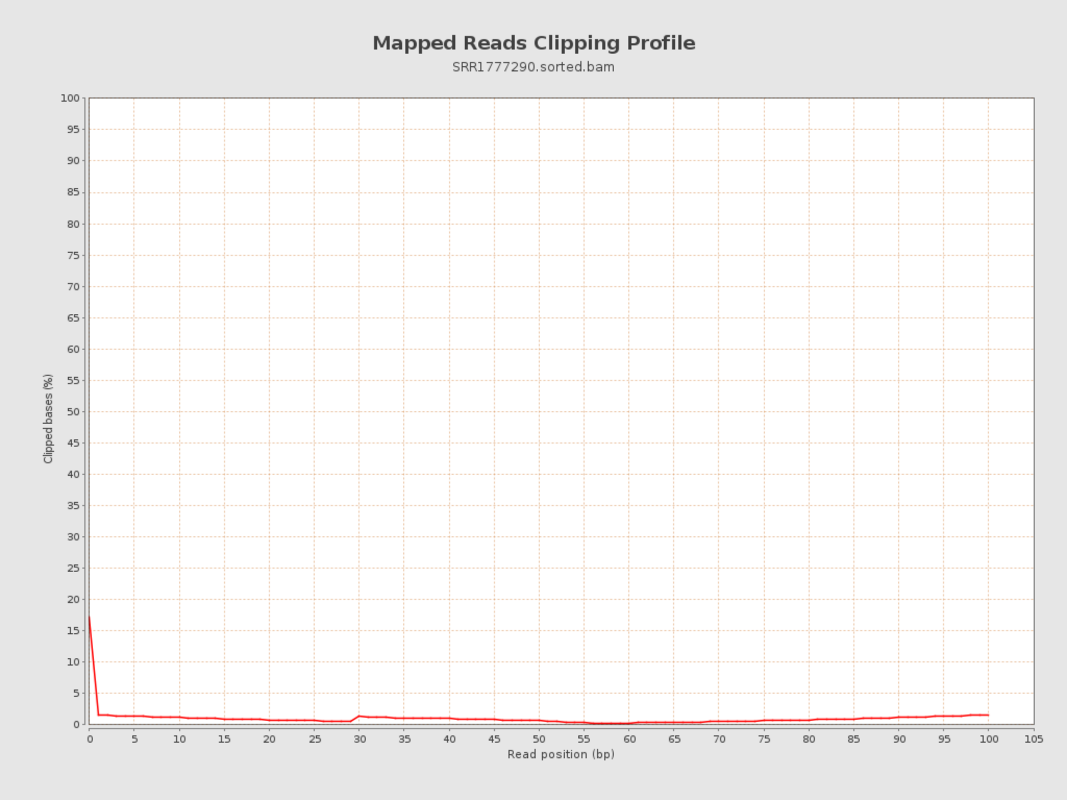
8. Results : Mapped Reads Nucleotide Content



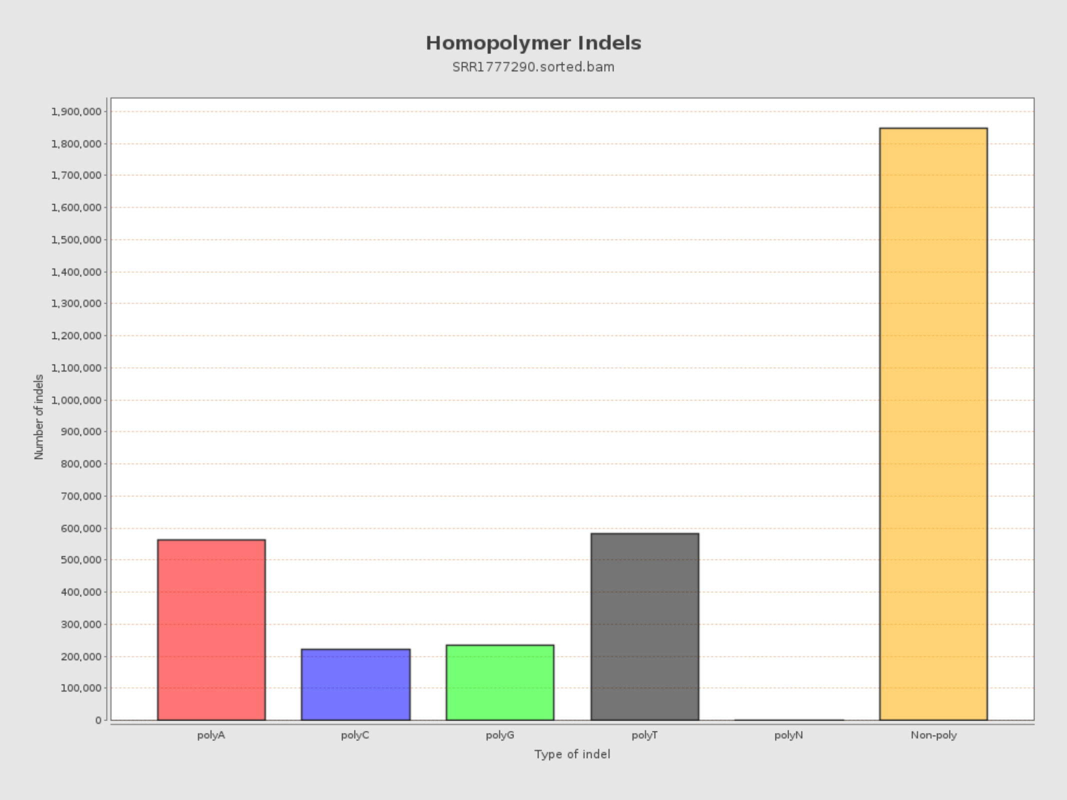
9. Results : Mapped Reads GC-content Distribution



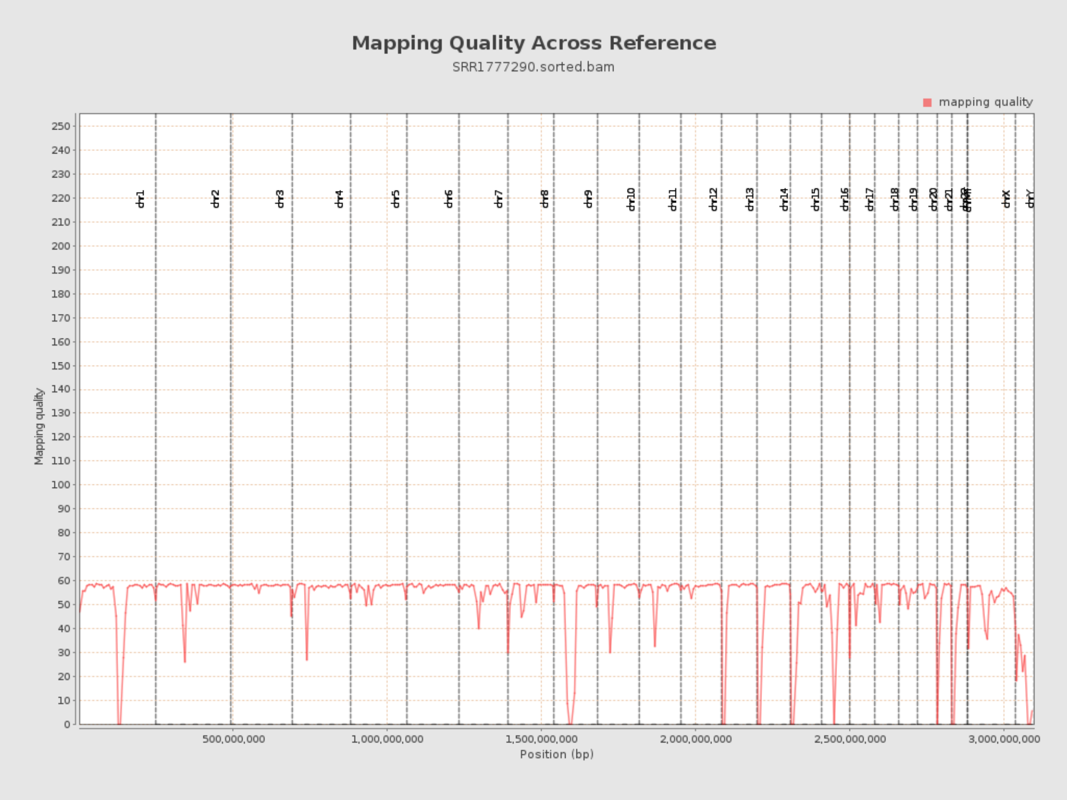
10. Results : Mapped Reads Clipping Profile



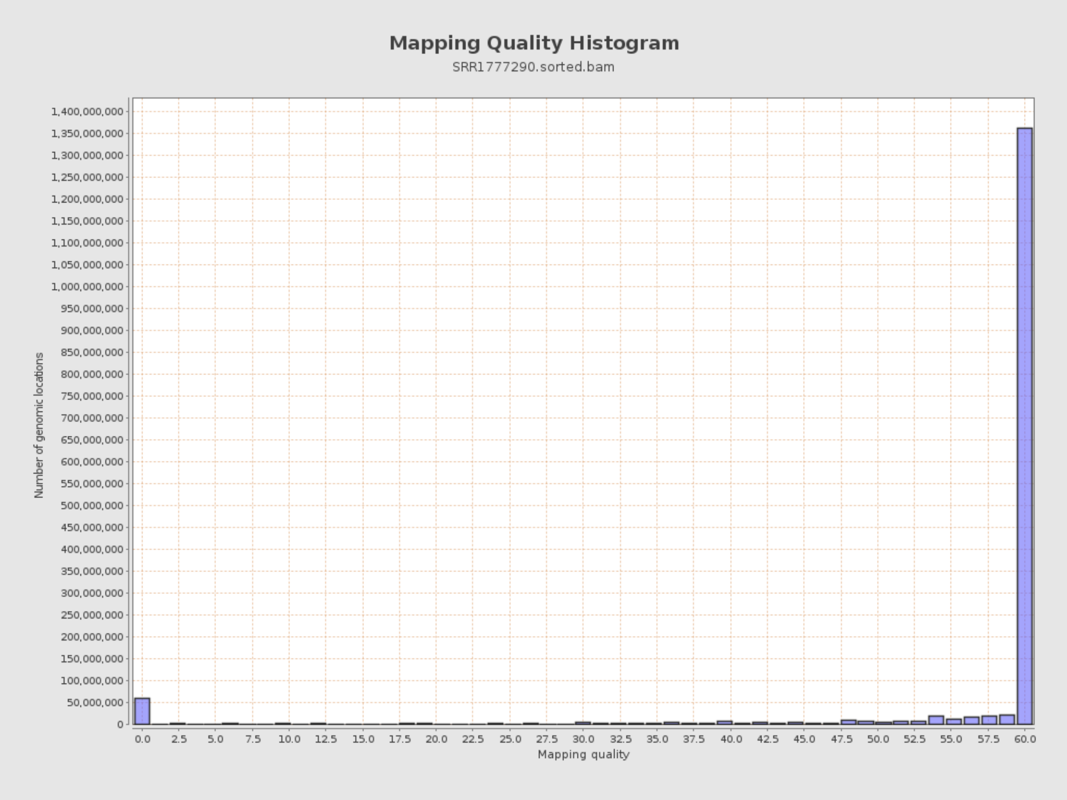
11. Results : Homopolymer Indels



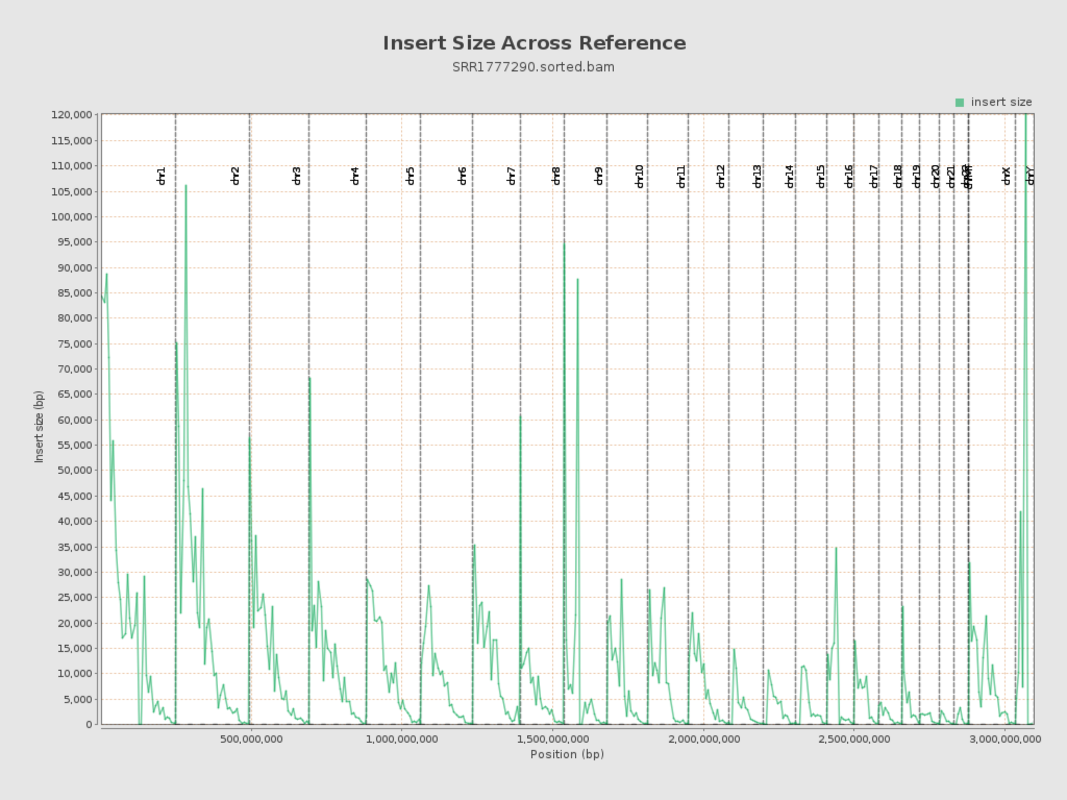
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram