Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 14:28:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777246.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_SRR1777246 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777246_1.fastq.gz SRR1777246_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 14:28:00 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777246.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,250,648
Mapped reads	18,148,240 / 99.44%
Unmapped reads	102,408 / 0.56%
Mapped paired reads	18,148,240 / 99.44%
Mapped reads, first in pair	9,075,352 / 49.73%
Mapped reads, second in pair	9,072,888 / 49.71%
Mapped reads, both in pair	18,119,292 / 99.28%
Mapped reads, singletons	28,948 / 0.16%
Secondary alignments	0
Supplementary alignments	466,704 / 2.56%
Read min/max/mean length	30 / 101 / 102
Duplicated reads (estimated)	10,217,947 / 55.99%
Duplication rate	35.98%
Clipped reads	8,832,091 / 48.39%

2.2. ACGT Content

Number/percentage of A's	422,184,340 / 25.59%
Number/percentage of C's	346,651,584 / 21.01%
Number/percentage of T's	479,774,264 / 29.08%
Number/percentage of G's	400,974,758 / 24.31%
Number/percentage of N's	62,439 / 0%

GC Percentage	45.32%

2.3. Coverage

Mean	0.5331
Standard Deviation	8.7739

2.4. Mapping Quality

Mean Mapping Quality	54.25

2.5. Insert size

Mean	292,981.08
Standard Deviation	5,368,566.92
P25/Median/P75	152 / 195 / 246

2.6. Mismatches and indels

General error rate	0.44%
Mismatches	7,085,625
Insertions	95,503
Mapped reads with at least one insertion	0.52%
Deletions	333,585
Mapped reads with at least one deletion	1.81%
Homopolymer indels	49.91%

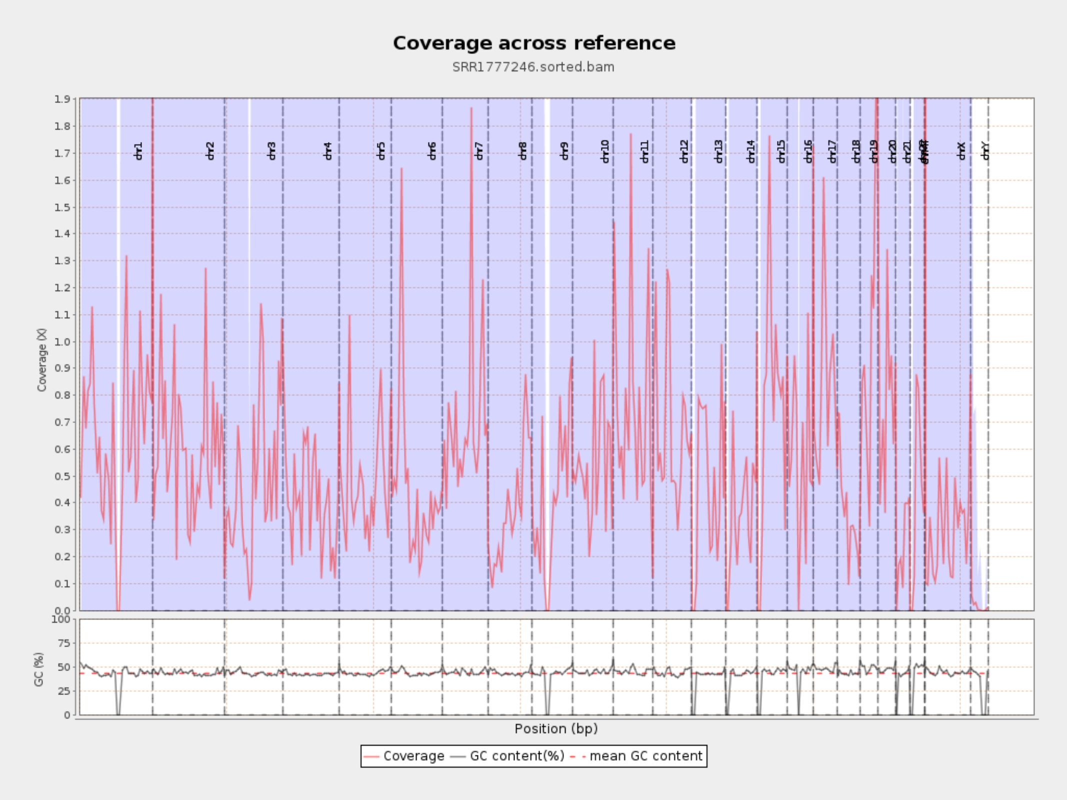
2.7. Chromosome stats

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

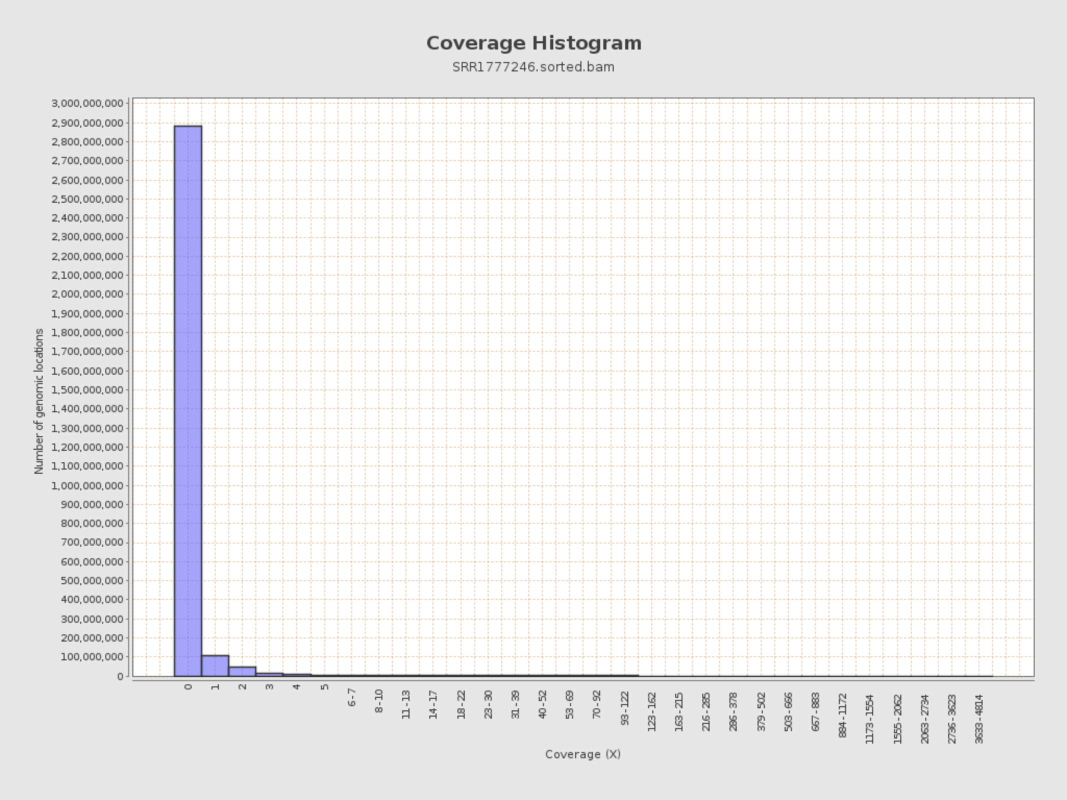
		bases	coverage	deviation
chr1	249250621	163123479	0.6545	10.2975
chr2	243199373	147730711	0.6074	9.0837
chr3	198022430	94640070	0.4779	7.8884
chr4	191154276	79442885	0.4156	7.497
chr5	180915260	87190760	0.4819	7.6385
chr6	171115067	75639680	0.442	7.7528
chr7	159138663	113277001	0.7118	11.2966
chr8	146364022	55304480	0.3779	7.372
chr9	141213431	58603995	0.415	6.9063
chr10	135534747	73760131	0.5442	8.5674
chr11	135006516	106710989	0.7904	11.369
chr12	133851895	91603888	0.6844	9.4646
chr13	115169878	52536825	0.4562	8.2837
chr14	107349540	37747642	0.3516	6.6724
chr15	102531392	74975335	0.7312	9.9803
chr16	90354753	51968224	0.5752	7.5554
chr17	81195210	69161801	0.8518	10.4351
chr18	78077248	27962912	0.3581	7.7274
chr19	59128983	59778059	1.011	13.4664
chr20	63025520	49499273	0.7854	13.7229
chr21	48129895	11674747	0.2426	5.1174
chr22	51304566	21473762	0.4186	6.6363
chrMT	16571	348879	21.0536	12.595
chrX	155270560	45262673	0.2915	6.0622

chrY	59373566	814921	0.0137	0.8065

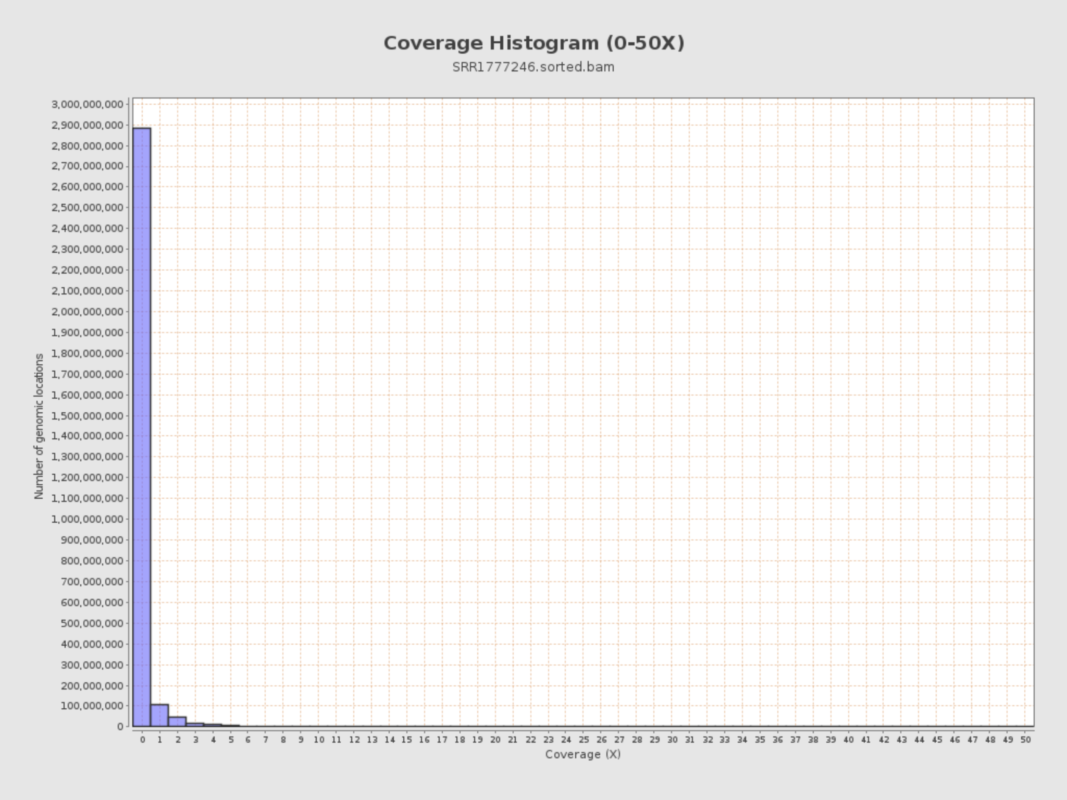
3. Results : Coverage across reference



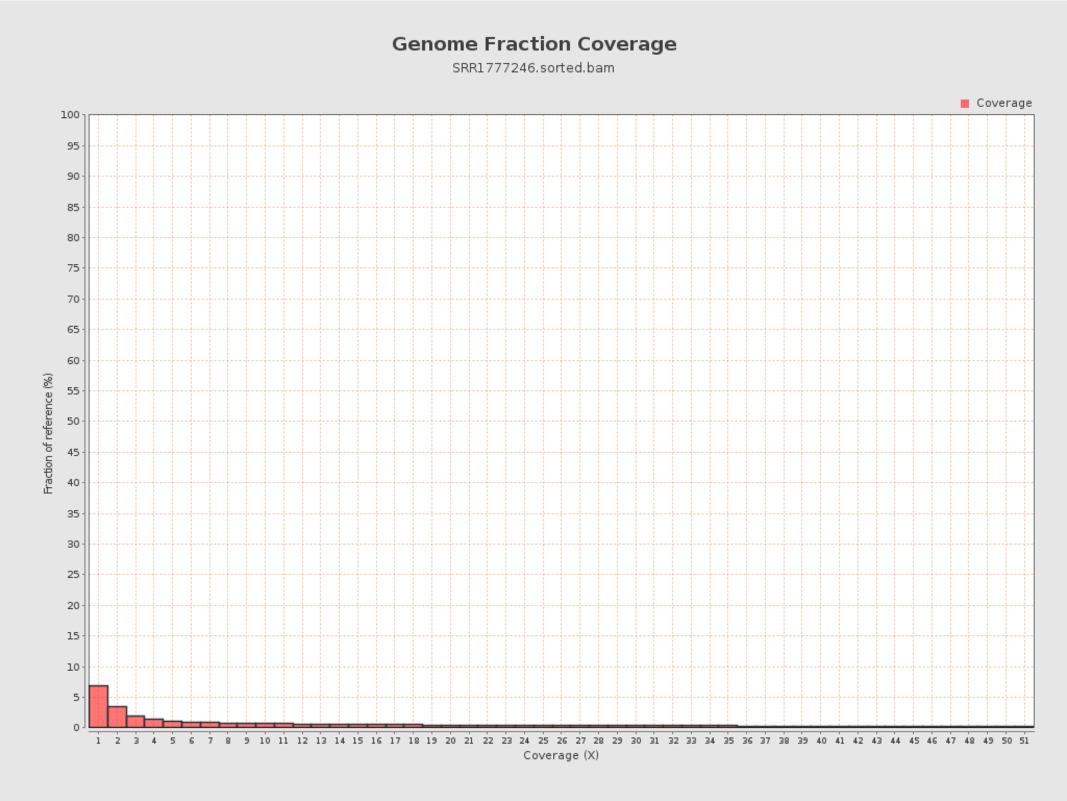
4. Results : Coverage Histogram



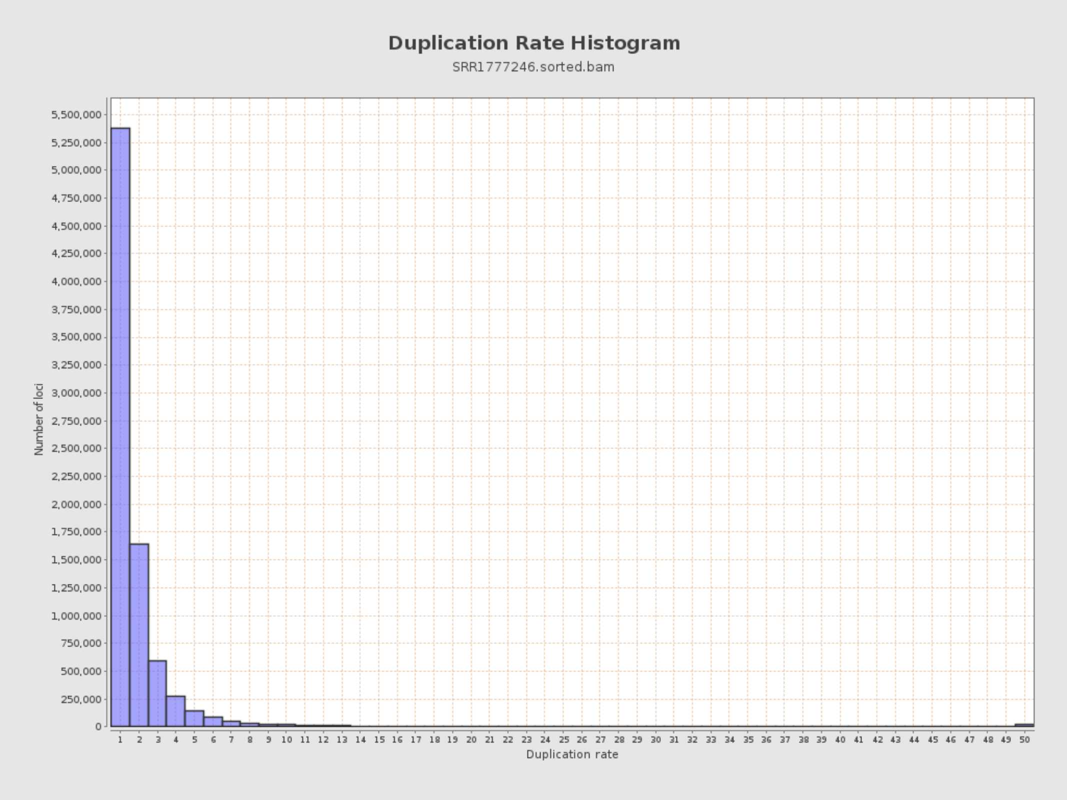
5. Results : Coverage Histogram (0-50X)



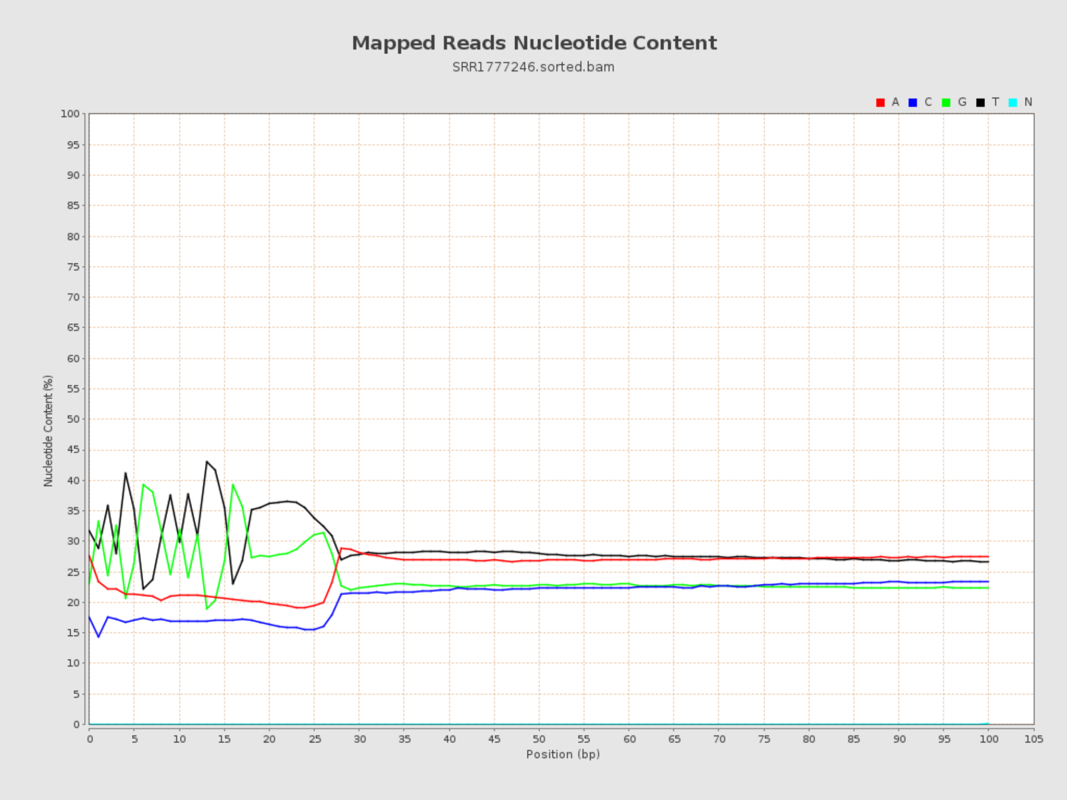
6. Results : Genome Fraction Coverage



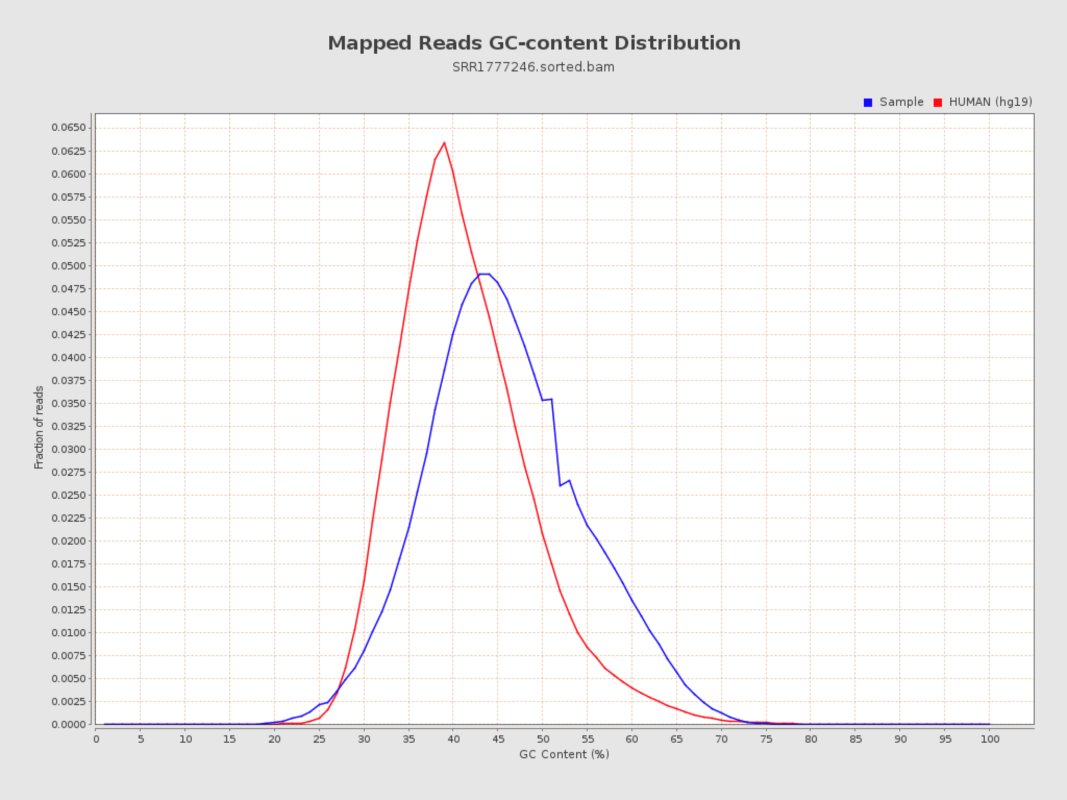
7. Results : Duplication Rate Histogram



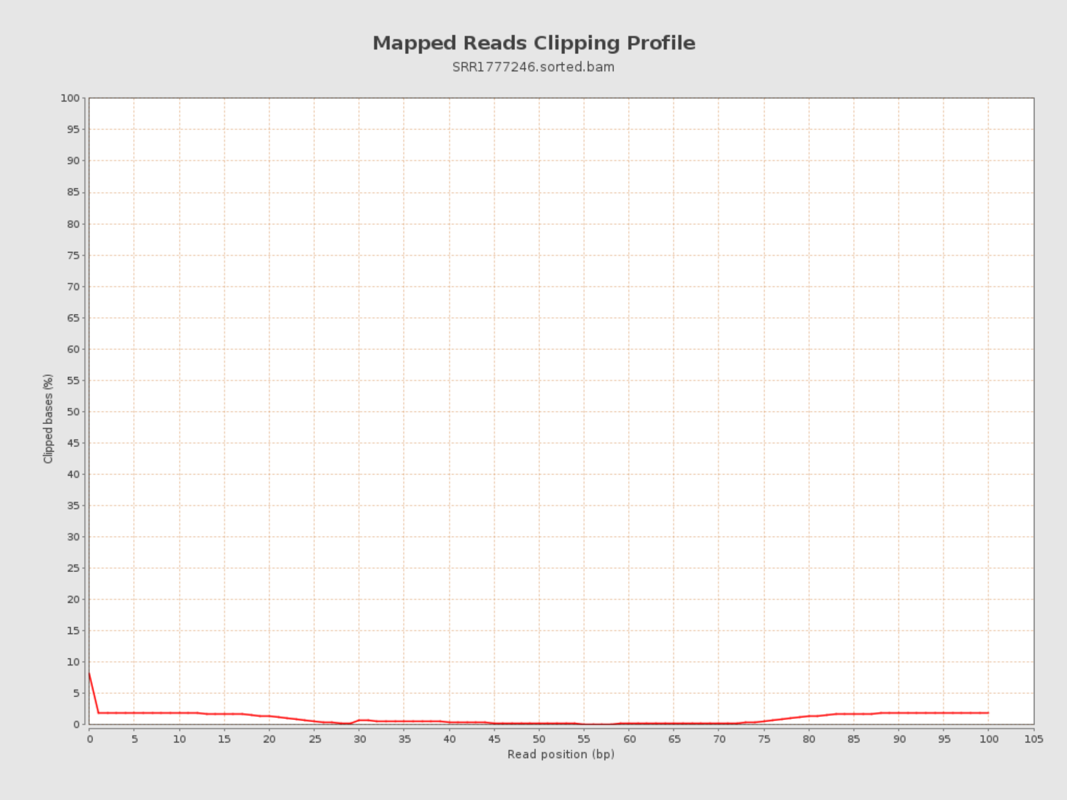
8. Results : Mapped Reads Nucleotide Content



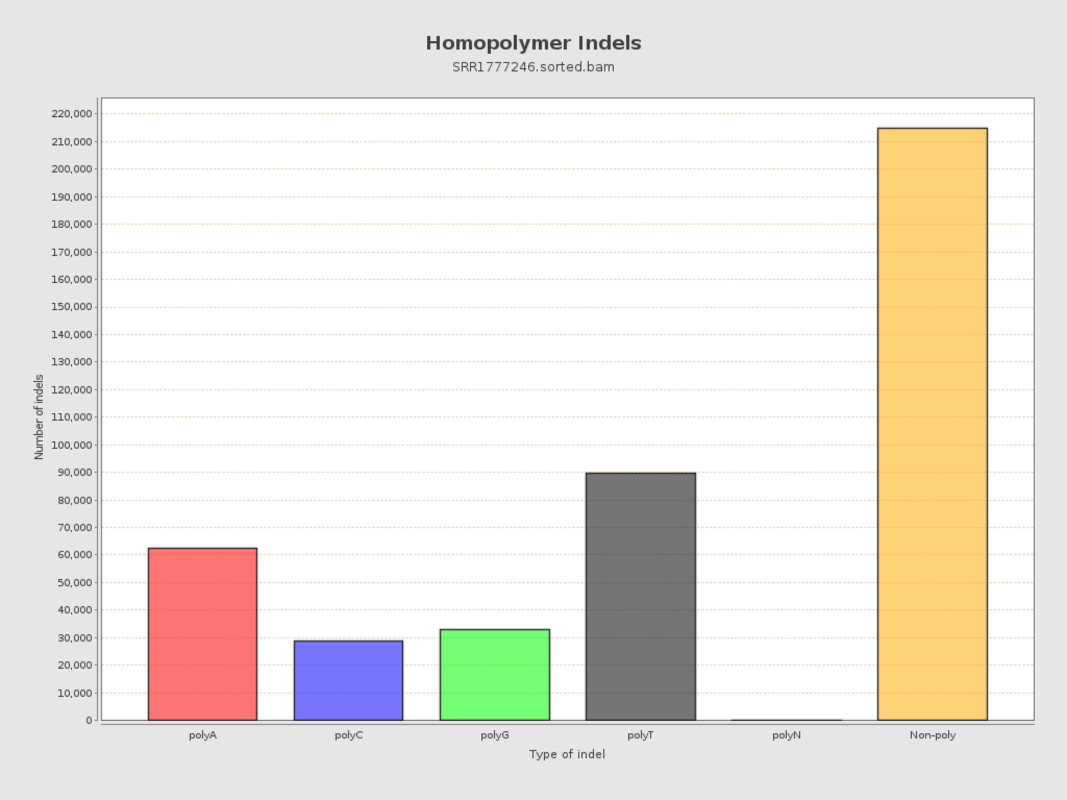
9. Results : Mapped Reads GC-content Distribution



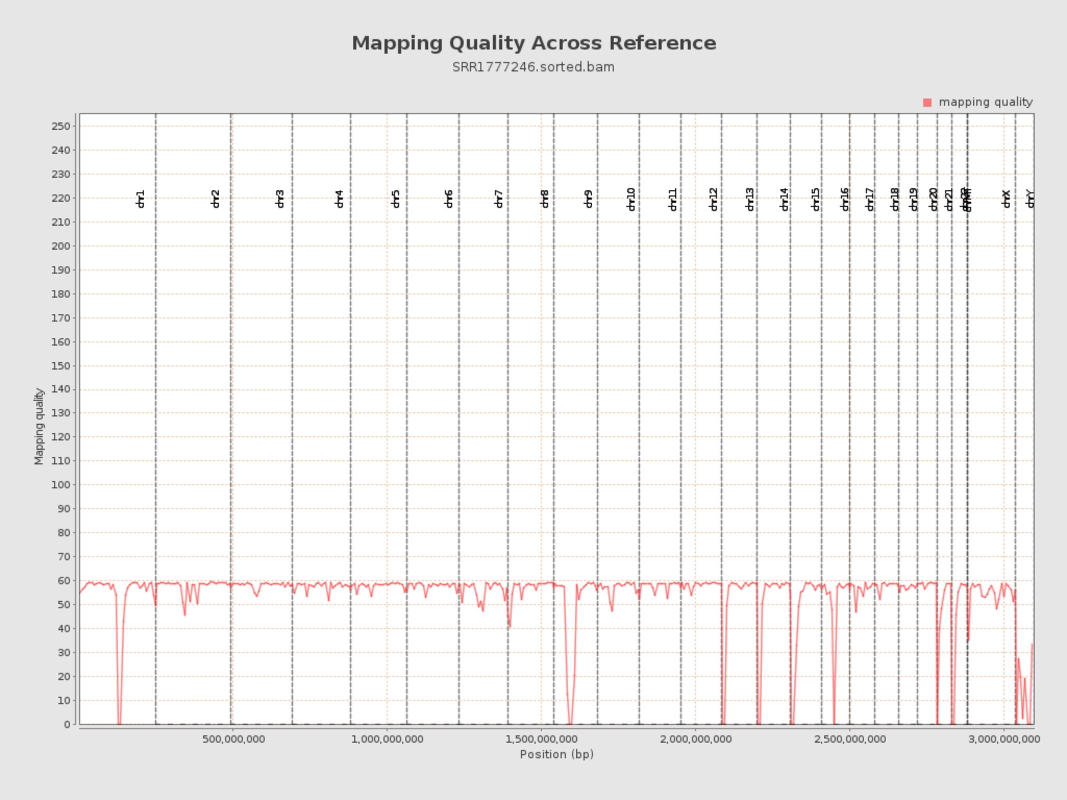
10. Results : Mapped Reads Clipping Profile



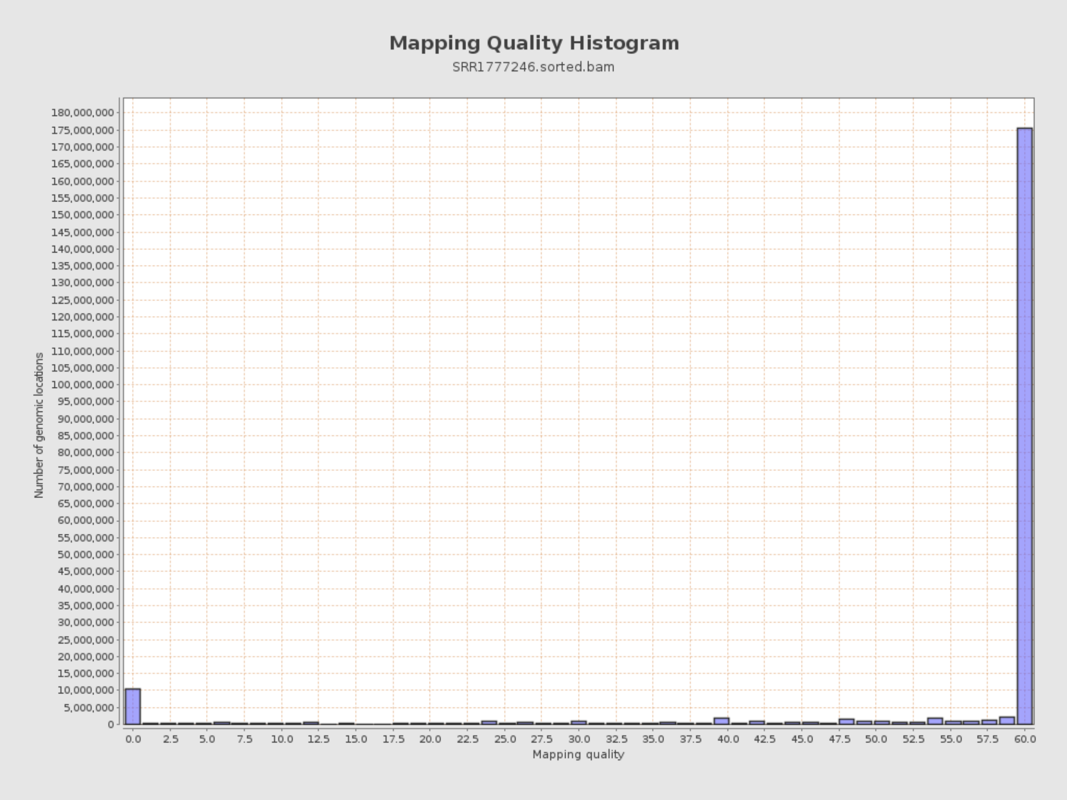
11. Results : Homopolymer Indels



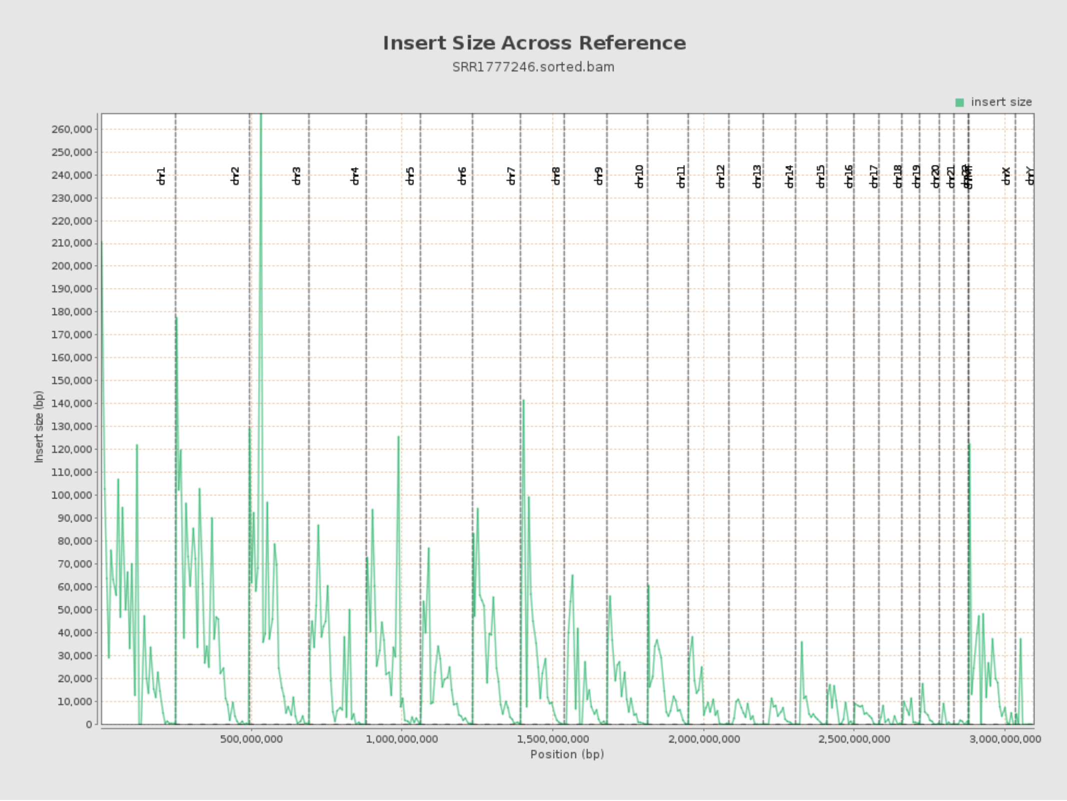
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram