Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 14:53:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777247.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_SRR1777247 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777247_1.fastq.gz SRR1777247_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 14:52:59 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777247.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,033,628
Mapped reads	17,935,216 / 99.45%
Unmapped reads	98,412 / 0.55%
Mapped paired reads	17,935,216 / 99.45%
Mapped reads, first in pair	8,968,680 / 49.73%
Mapped reads, second in pair	8,966,536 / 49.72%
Mapped reads, both in pair	17,906,556 / 99.3%
Mapped reads, singletons	28,660 / 0.16%
Secondary alignments	0
Supplementary alignments	461,367 / 2.56%
Read min/max/mean length	30 / 101 / 102
Duplicated reads (estimated)	10,062,060 / 55.8%
Duplication rate	35.76%
Clipped reads	8,746,446 / 48.5%

2.2. ACGT Content

Number/percentage of A's	416,644,695 / 25.56%
Number/percentage of C's	342,798,889 / 21.03%
Number/percentage of T's	473,658,501 / 29.06%
Number/percentage of G's	396,718,275 / 24.34%
Number/percentage of N's	57,559 / 0%

GC Percentage	45.37%

2.3. Coverage

Mean	0.5267
Standard Deviation	8.6656

2.4. Mapping Quality

Mean Mapping Quality	54.25

2.5. Insert size

Mean	295,520.57
Standard Deviation	5,386,547.01
P25/Median/P75	152 / 195 / 246

2.6. Mismatches and indels

General error rate	0.44%
Mismatches	7,039,995
Insertions	95,119
Mapped reads with at least one insertion	0.52%
Deletions	331,060
Mapped reads with at least one deletion	1.82%
Homopolymer indels	50.05%

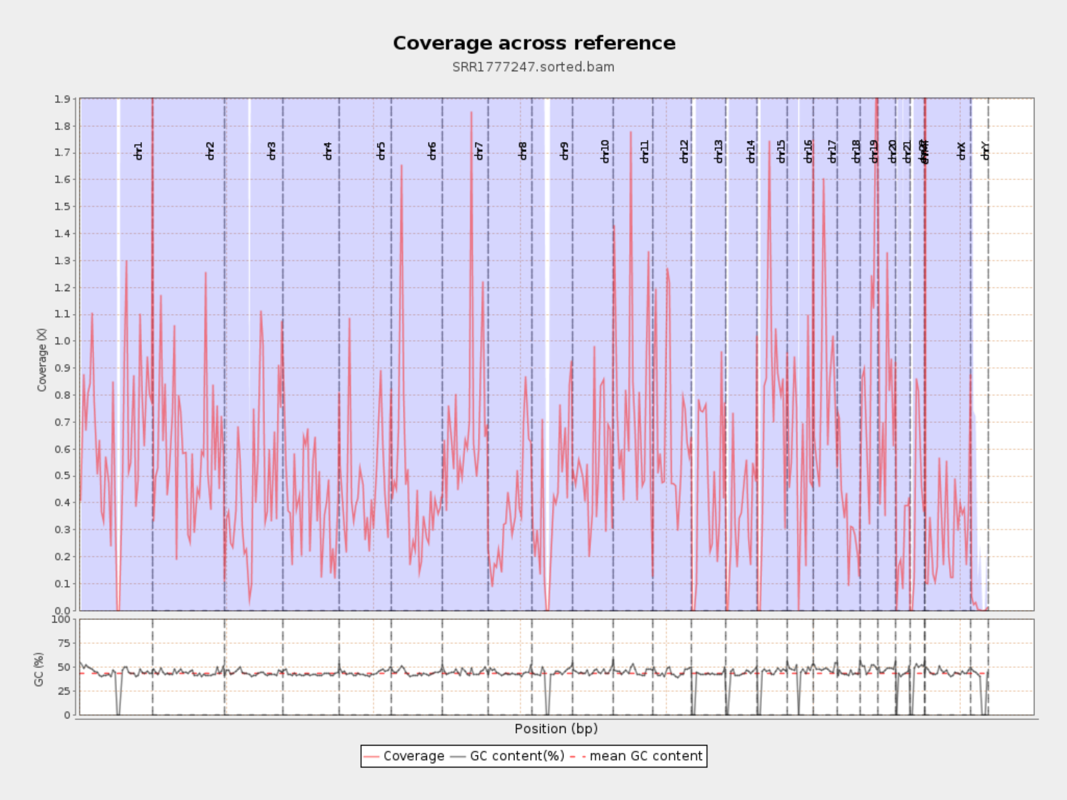
2.7. Chromosome stats

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

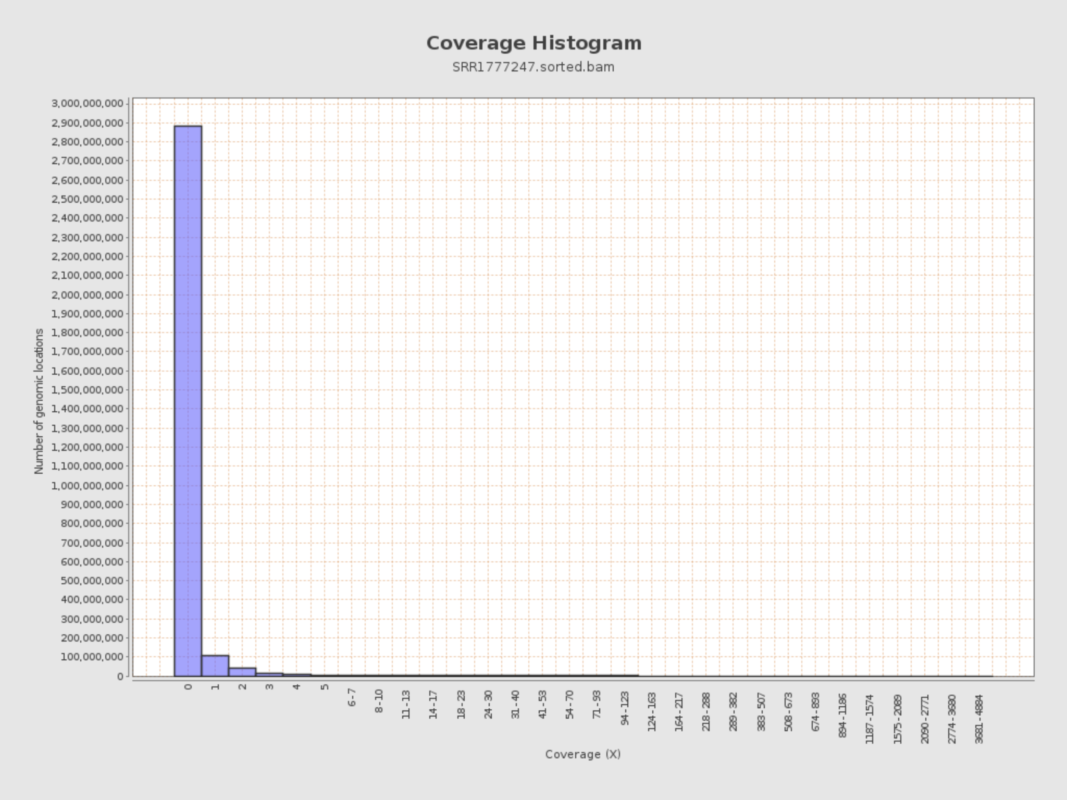
		bases	coverage	deviation
chr1	249250621	161106163	0.6464	10.161
chr2	243199373	145661070	0.5989	8.9631
chr3	198022430	93398503	0.4717	7.7674
chr4	191154276	78316695	0.4097	7.369
chr5	180915260	86091331	0.4759	7.5433
chr6	171115067	75065534	0.4387	7.7206
chr7	159138663	111704168	0.7019	11.0905
chr8	146364022	54513721	0.3725	7.2989
chr9	141213431	57759788	0.409	6.783
chr10	135534747	72701092	0.5364	8.4443
chr11	135006516	105854279	0.7841	11.2215
chr12	133851895	90512157	0.6762	9.35
chr13	115169878	51814895	0.4499	8.1675
chr14	107349540	37264128	0.3471	6.5806
chr15	102531392	74138319	0.7231	9.8694
chr16	90354753	51354769	0.5684	7.4692
chr17	81195210	68683352	0.8459	10.3958
chr18	78077248	27474208	0.3519	7.6349
chr19	59128983	59484086	1.006	13.4065
chr20	63025520	48859200	0.7752	13.5988
chr21	48129895	11448056	0.2379	5.0295
chr22	51304566	21226027	0.4137	6.5521
chrMT	16571	342737	20.6829	12.9105
chrX	155270560	44888648	0.2891	6.0038

chrY	59373566	798889	0.0135	0.8532

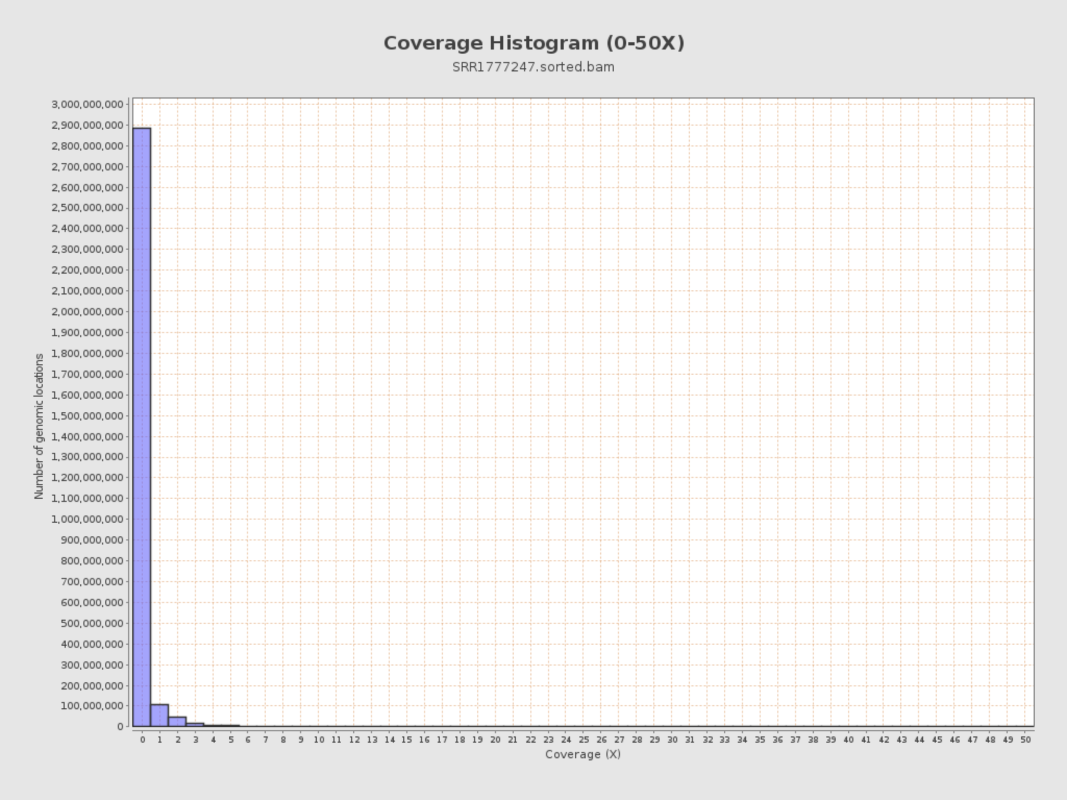
3. Results : Coverage across reference



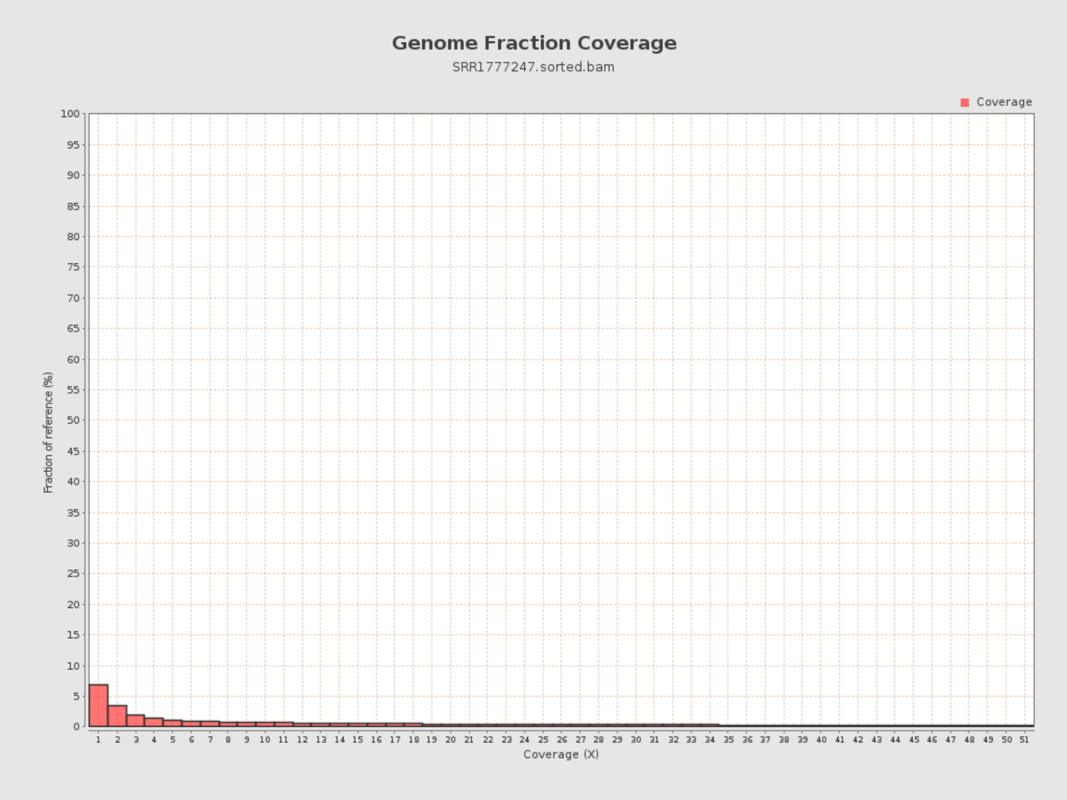
4. Results : Coverage Histogram



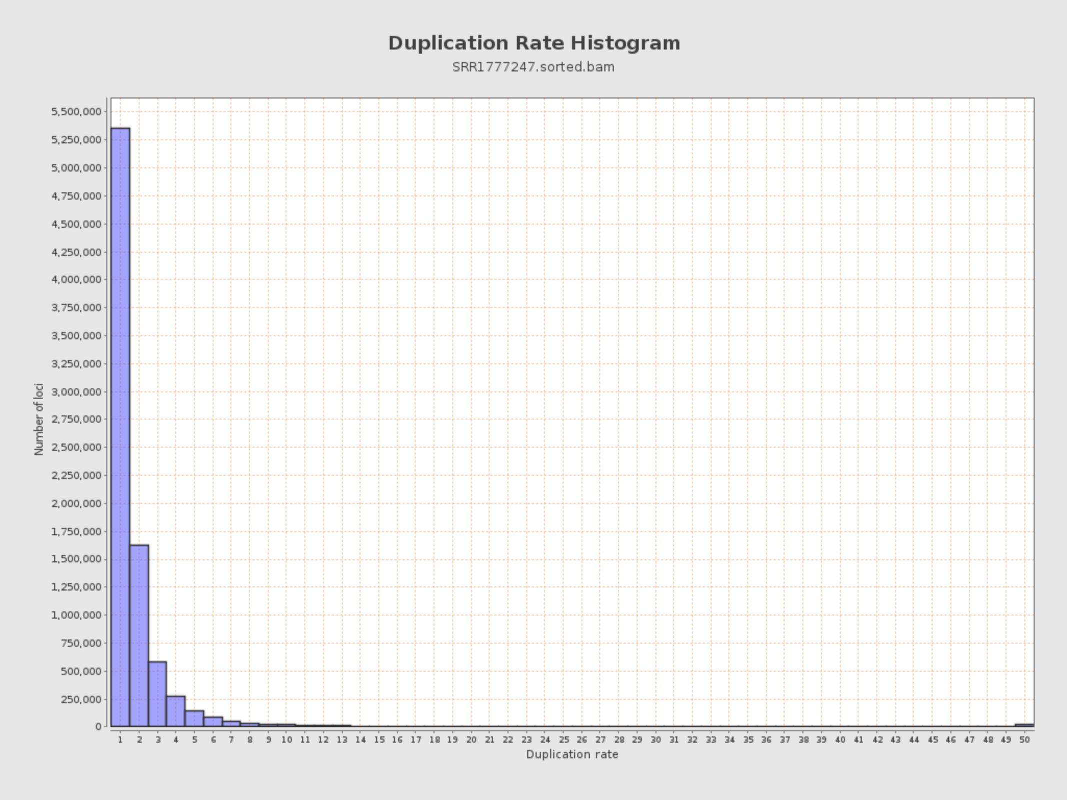
5. Results : Coverage Histogram (0-50X)



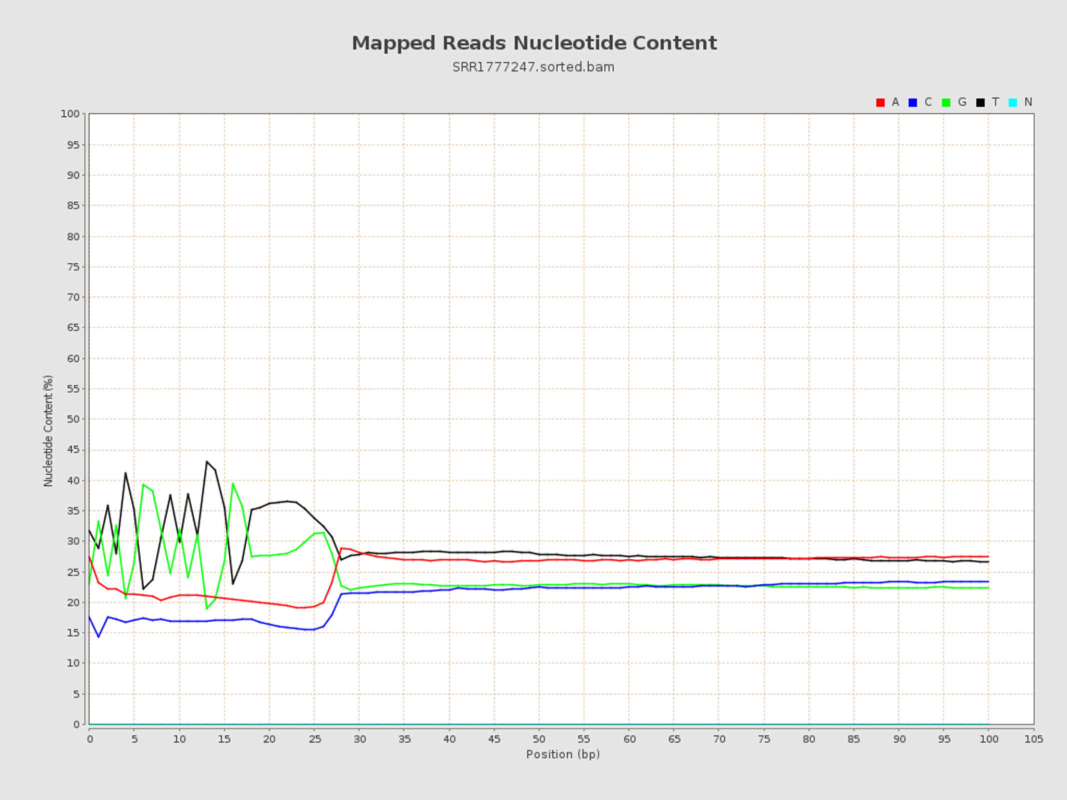
6. Results : Genome Fraction Coverage



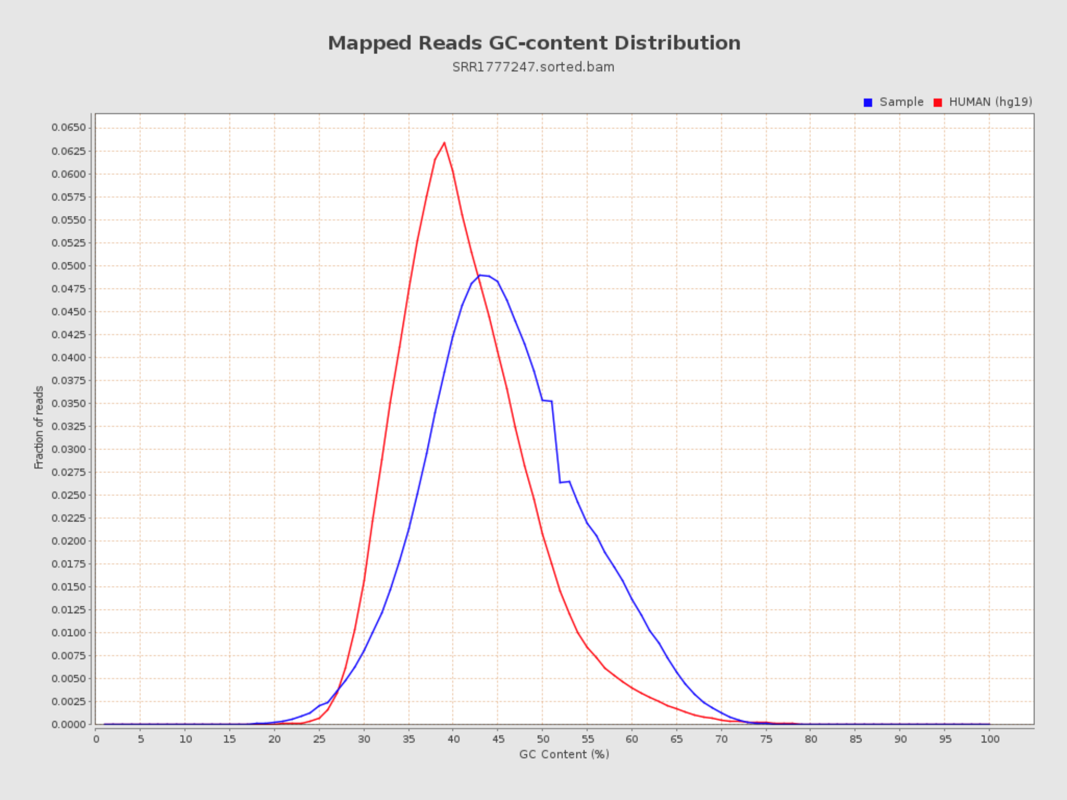
7. Results : Duplication Rate Histogram



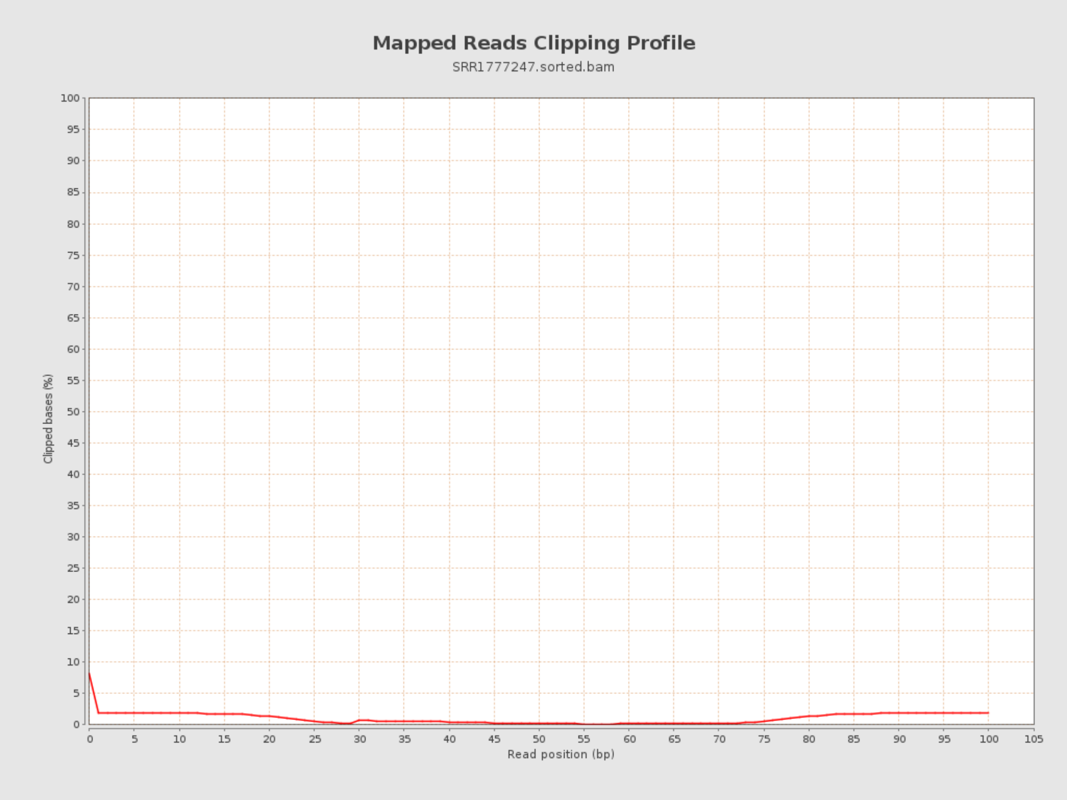
8. Results : Mapped Reads Nucleotide Content



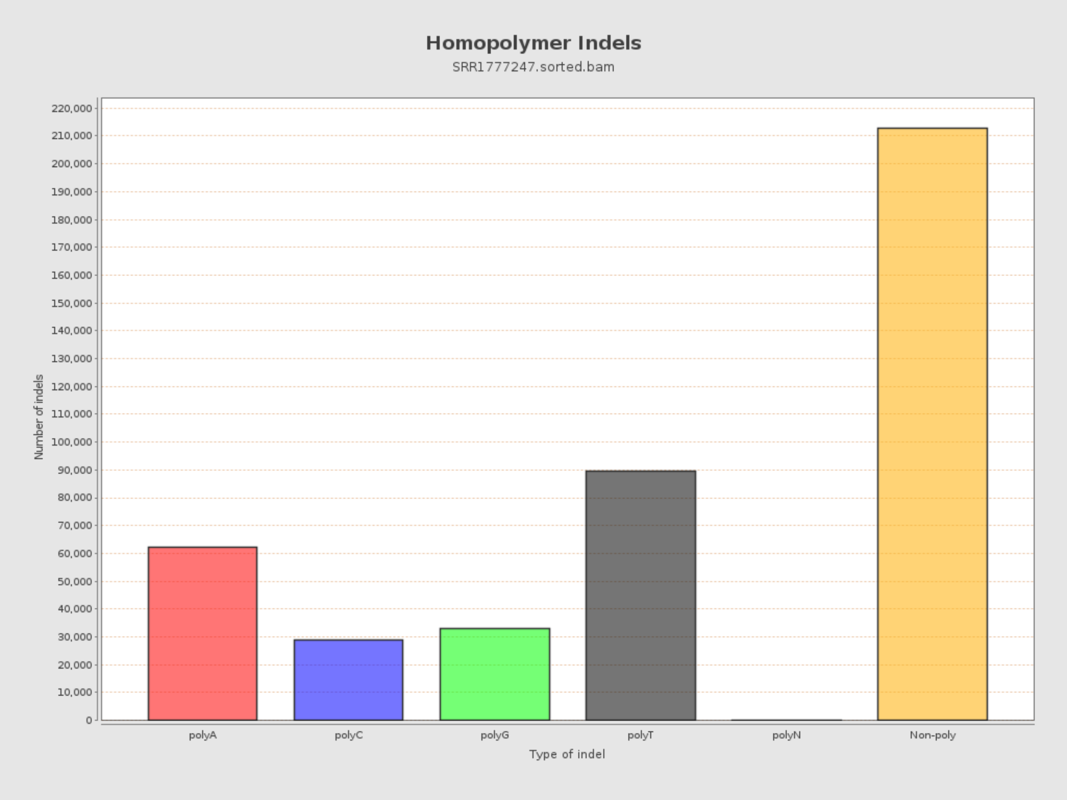
9. Results : Mapped Reads GC-content Distribution



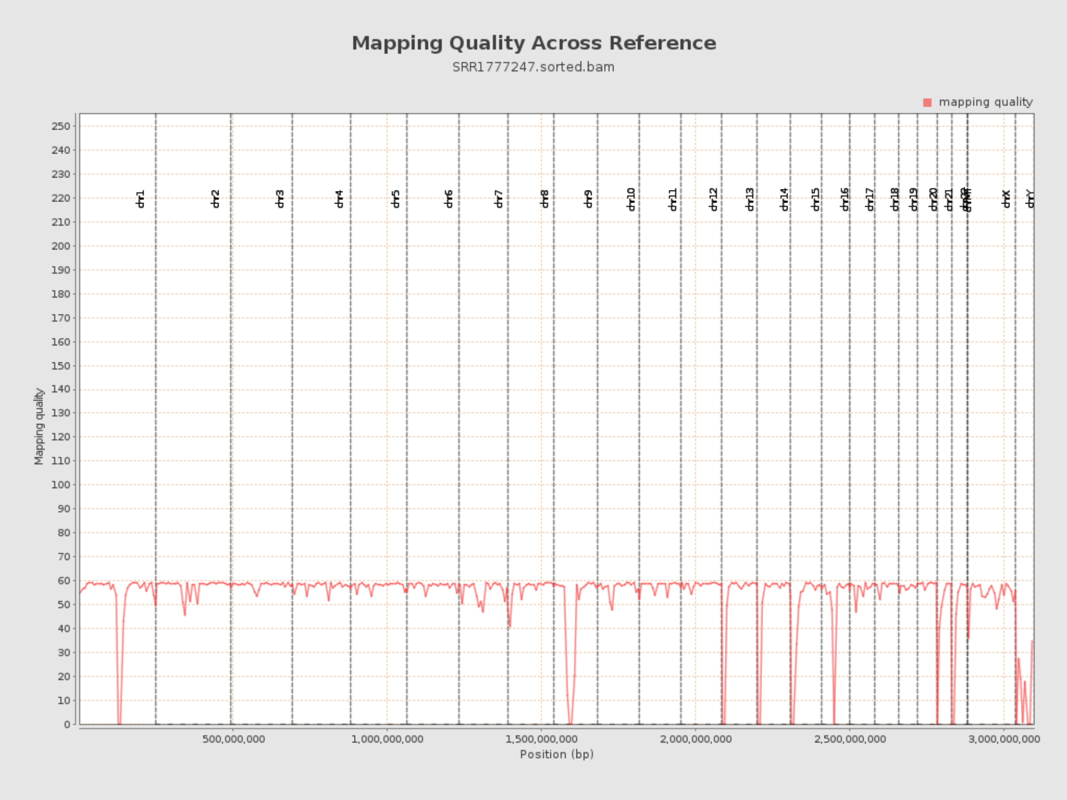
10. Results : Mapped Reads Clipping Profile



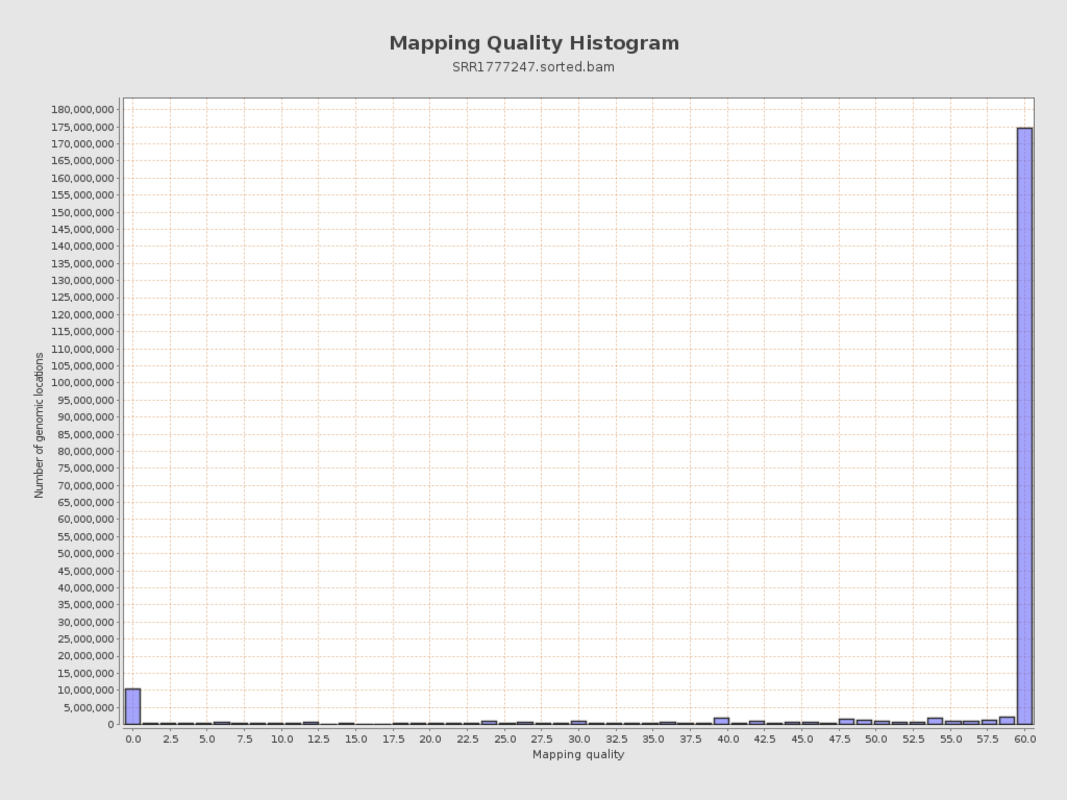
11. Results : Homopolymer Indels



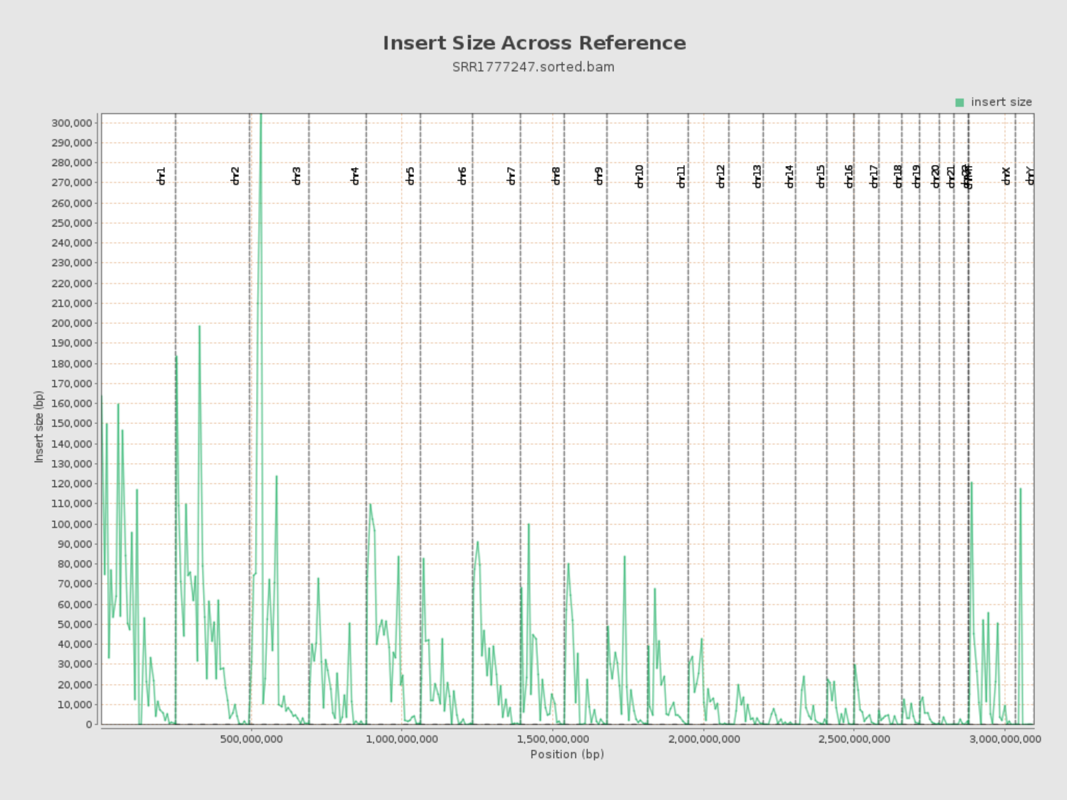
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram