Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 19:53:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777272.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_SRR1777272 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777272_1.fastq.gz SRR1777272_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 19:53:03 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777272.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	50,384,732
Mapped reads	50,210,168 / 99.65%
Unmapped reads	174,564 / 0.35%
Mapped paired reads	50,210,168 / 99.65%
Mapped reads, first in pair	25,106,223 / 49.83%
Mapped reads, second in pair	25,103,945 / 49.82%
Mapped reads, both in pair	50,150,964 / 99.54%
Mapped reads, singletons	59,204 / 0.12%
Secondary alignments	0
Supplementary alignments	1,605,032 / 3.19%
Read min/max/mean length	30 / 101 / 102.31
Duplicated reads (estimated)	21,411,989 / 42.5%
Duplication rate	35.75%
Clipped reads	5,838,833 / 11.59%

2.2. ACGT Content

Number/percentage of A's	1,408,654,630 / 27.97%
Number/percentage of C's	1,111,256,969 / 22.06%
Number/percentage of T's	1,399,852,938 / 27.79%
Number/percentage of G's	1,117,201,366 / 22.18%
Number/percentage of N's	210,363 / 0%

GC Percentage	44.24%

2.3. Coverage

Mean	1.6274
Standard Deviation	13.9563

2.4. Mapping Quality

Mean Mapping Quality	54.69

2.5. Insert size

Mean	436,677.88
Standard Deviation	6,499,023.96
P25/Median/P75	184 / 232 / 291

2.6. Mismatches and indels

General error rate	0.25%
Mismatches	11,515,790
Insertions	856,881
Mapped reads with at least one insertion	1.68%
Deletions	338,484
Mapped reads with at least one deletion	0.67%
Homopolymer indels	52.25%

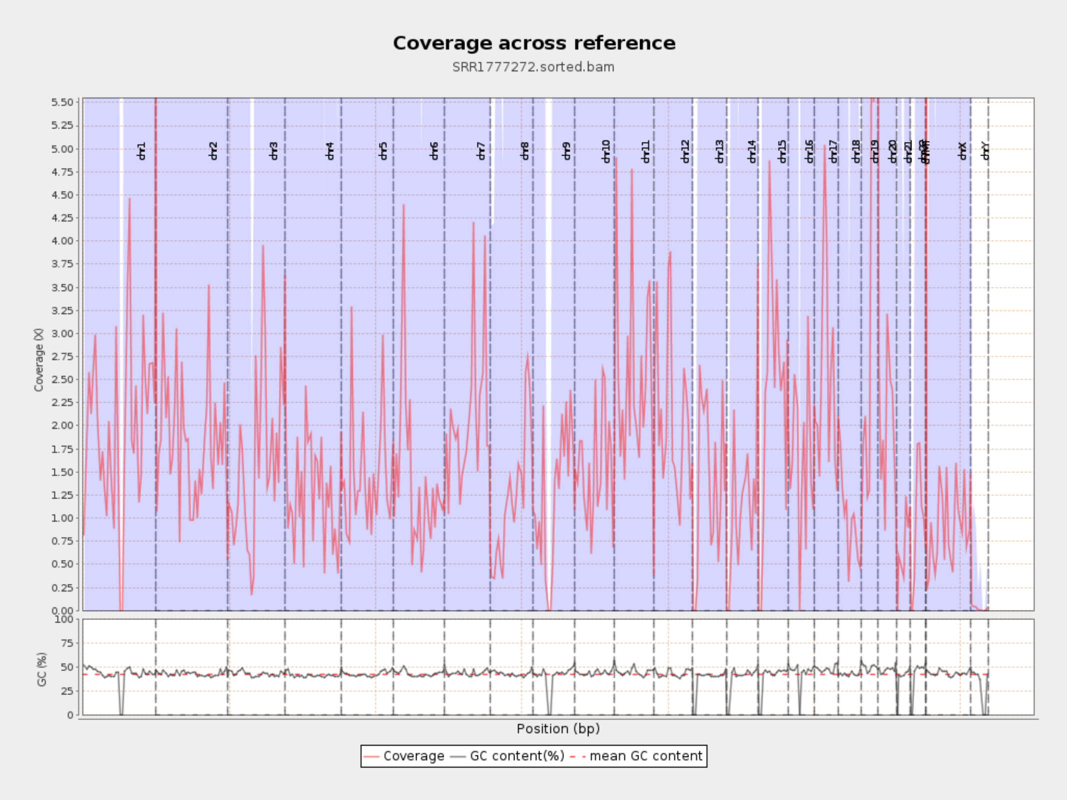
2.7. Chromosome stats

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

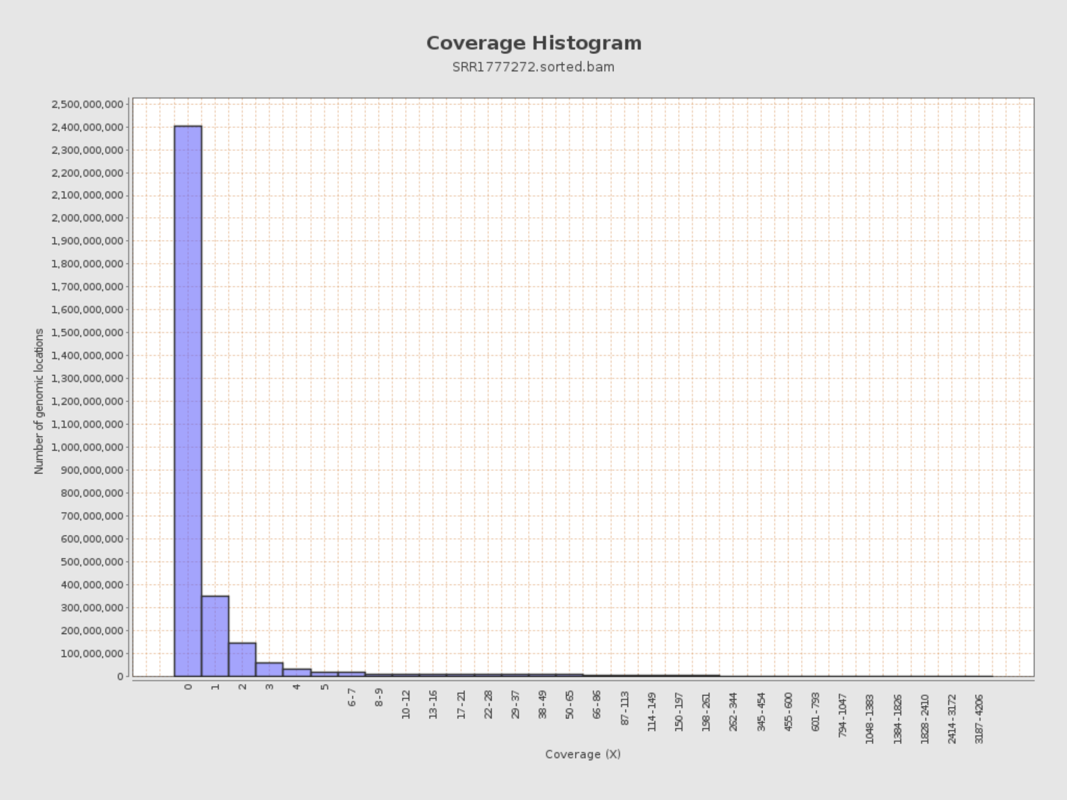
		bases	coverage	deviation
chr1	249250621	500849737	2.0094	16.1394
chr2	243199373	450534103	1.8525	14.6278
chr3	198022430	314029352	1.5858	13.7643
chr4	191154276	238451474	1.2474	11.5452
chr5	180915260	268746283	1.4855	12.4517
chr6	171115067	236977191	1.3849	12.1554
chr7	159138663	328883456	2.0666	16.9559
chr8	146364022	182291708	1.2455	12.3314
chr9	141213431	173722041	1.2302	11.4326
chr10	135534747	211311251	1.5591	12.7349
chr11	135006516	343824433	2.5467	19.3722
chr12	133851895	284679783	2.1268	16.1695
chr13	115169878	160184376	1.3909	13.988
chr14	107349540	112967563	1.0523	9.6323
chr15	102531392	233451042	2.2769	17.8764
chr16	90354753	144346269	1.5976	12.6389
chr17	81195210	206814018	2.5471	17.123
chr18	78077248	80090892	1.0258	9.5079
chr19	59128983	217272151	3.6745	22.3838
chr20	63025520	126270593	2.0035	14.852
chr21	48129895	33379991	0.6935	8.3752
chr22	51304566	48519771	0.9457	8.9288
chrMT	16571	1661979	100.2944	28.9718
chrX	155270560	137283323	0.8842	9.0682

chrY	59373566	1372620	0.0231	0.6395

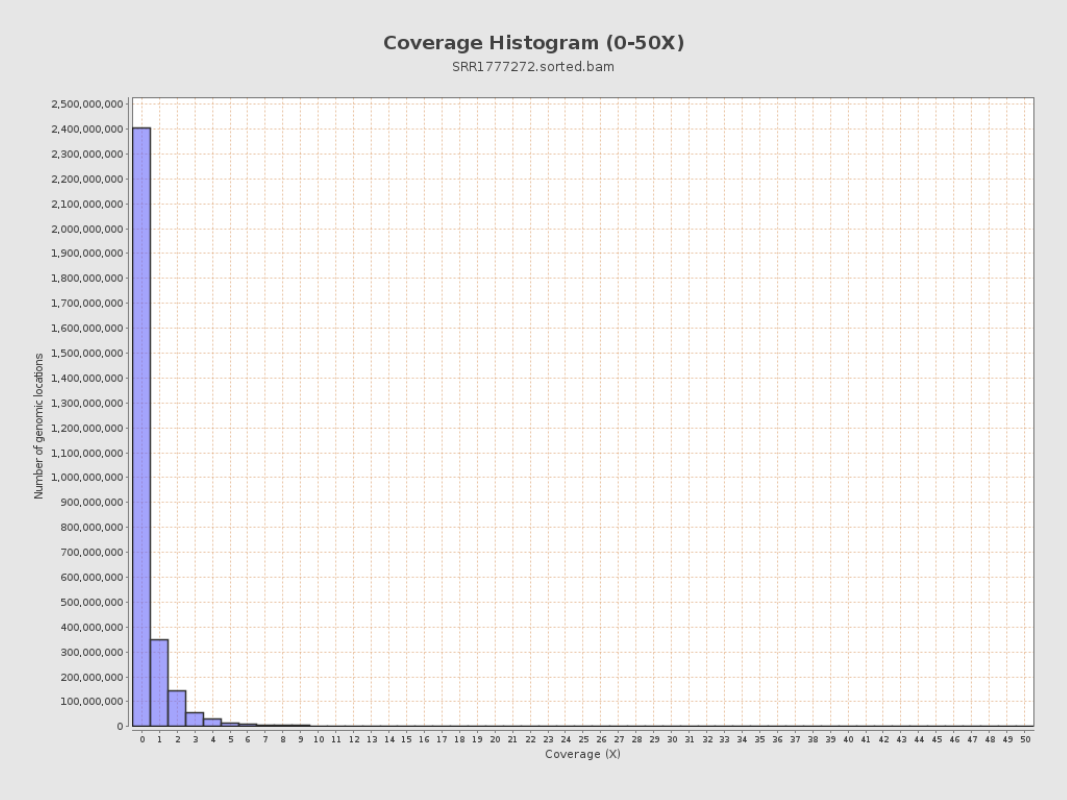
3. Results : Coverage across reference



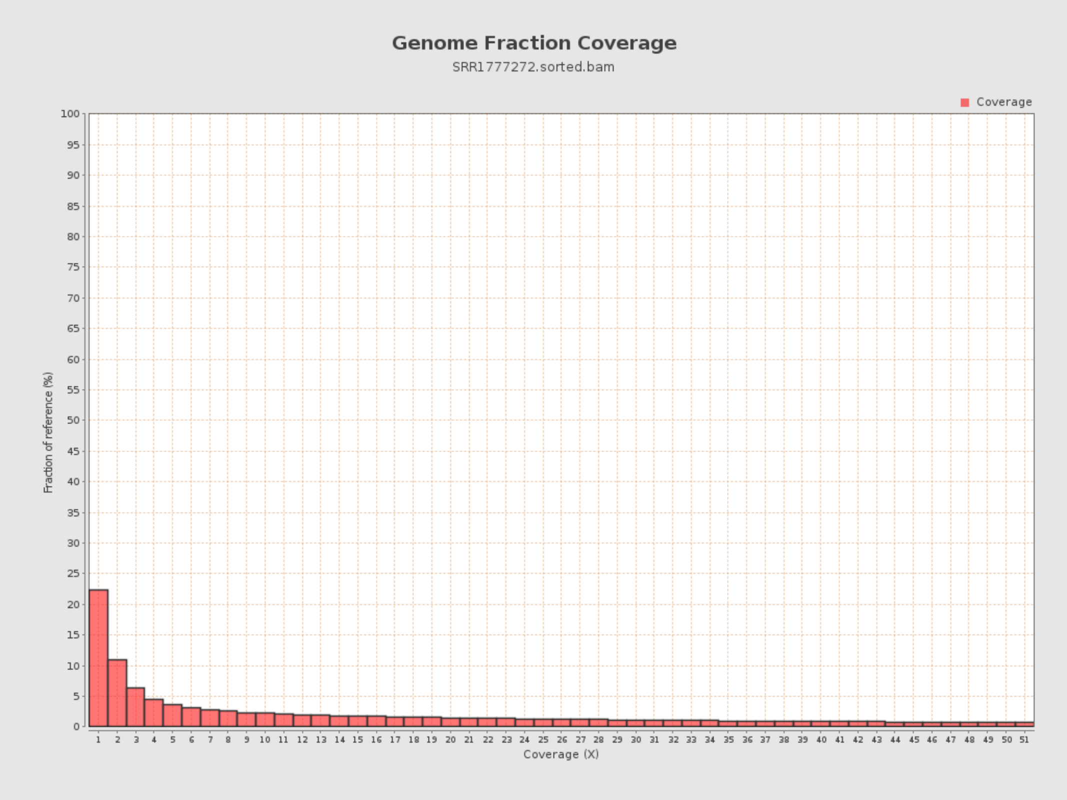
4. Results : Coverage Histogram



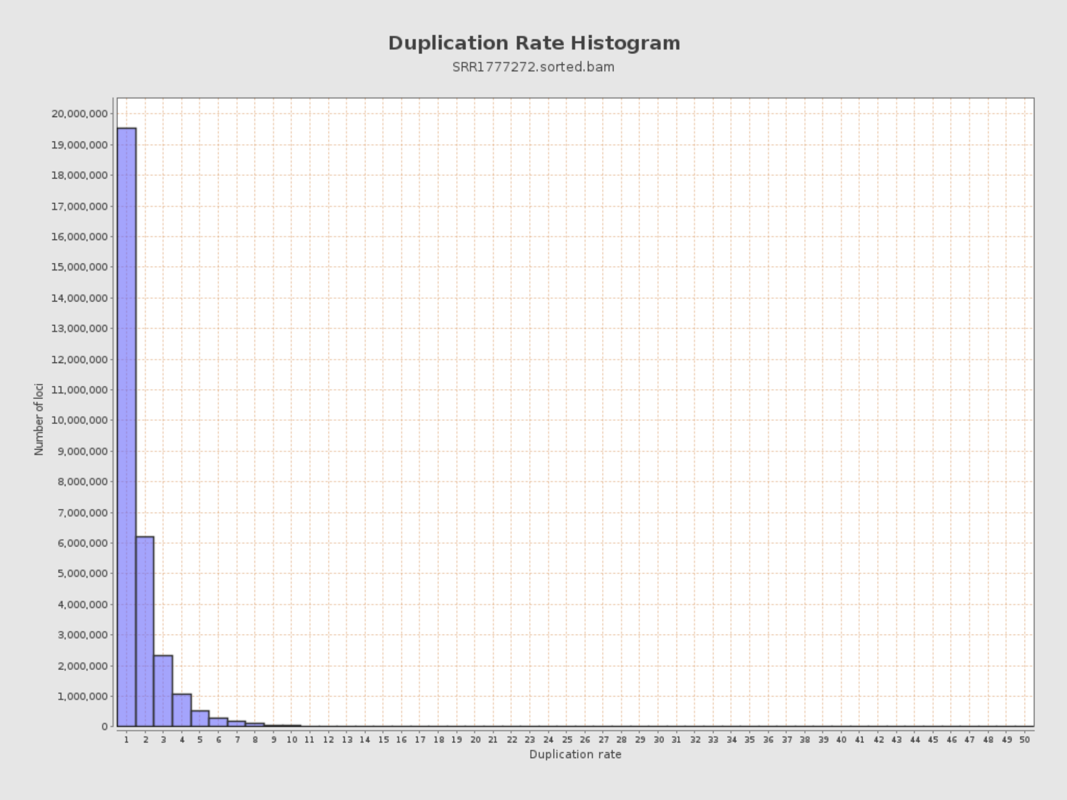
5. Results : Coverage Histogram (0-50X)



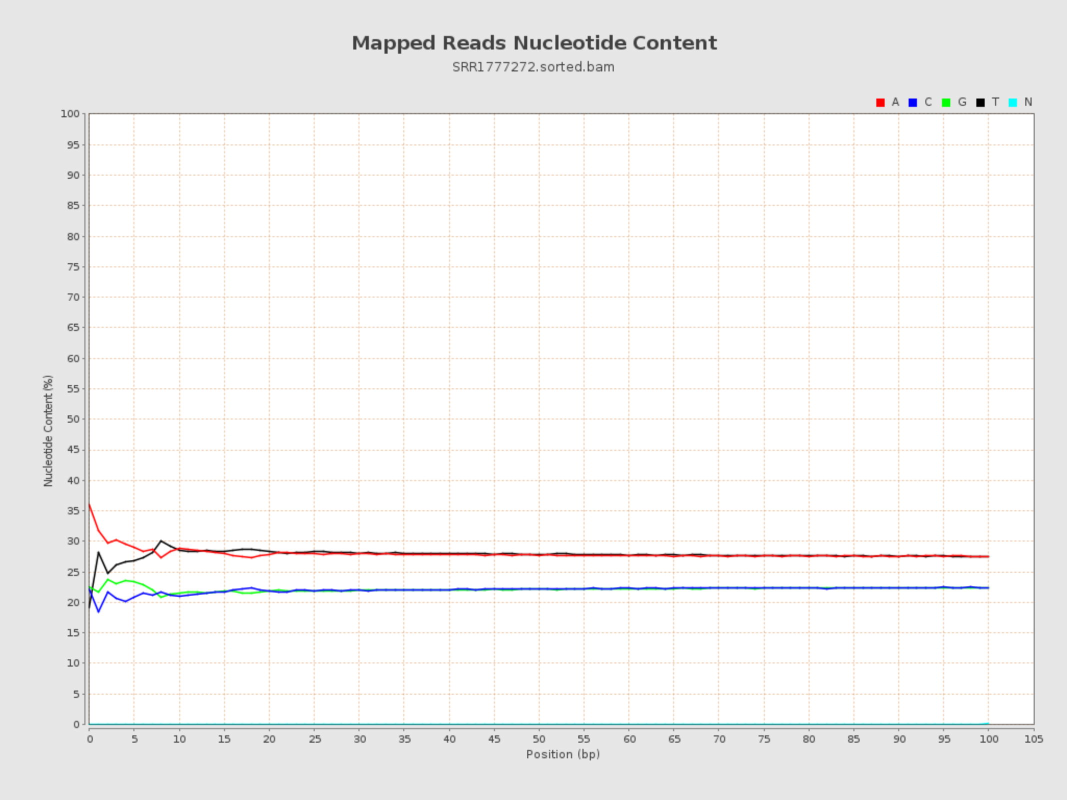
6. Results : Genome Fraction Coverage



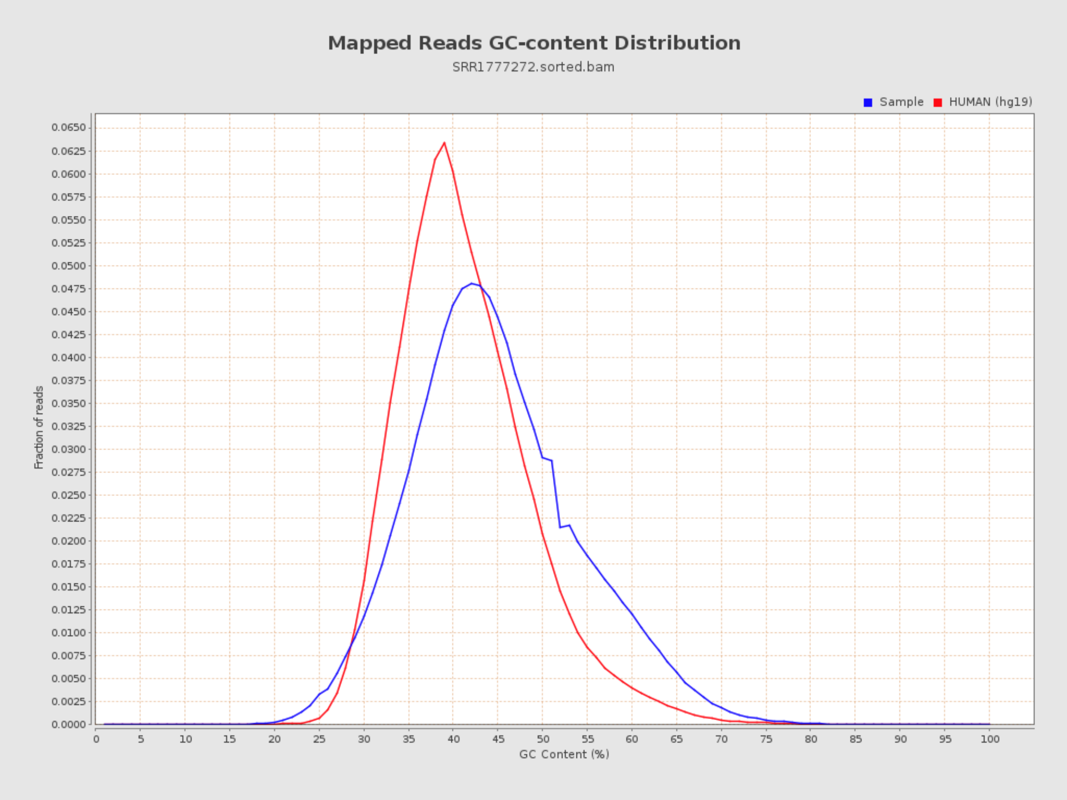
7. Results : Duplication Rate Histogram



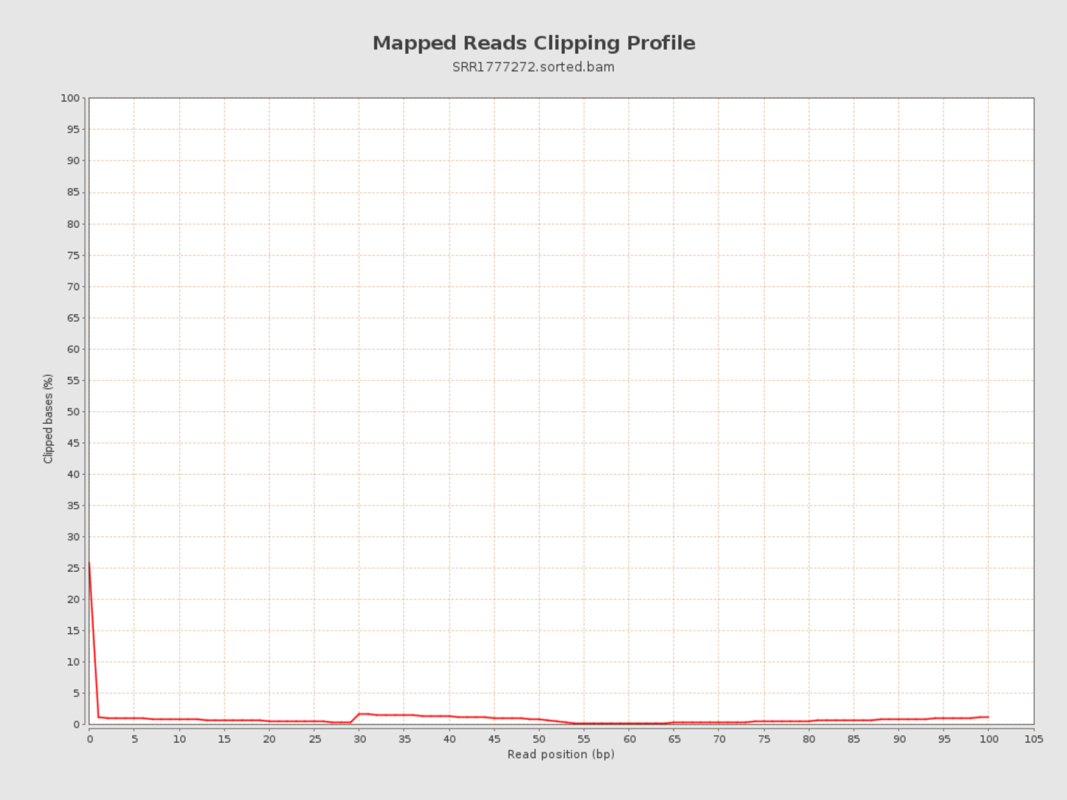
8. Results : Mapped Reads Nucleotide Content



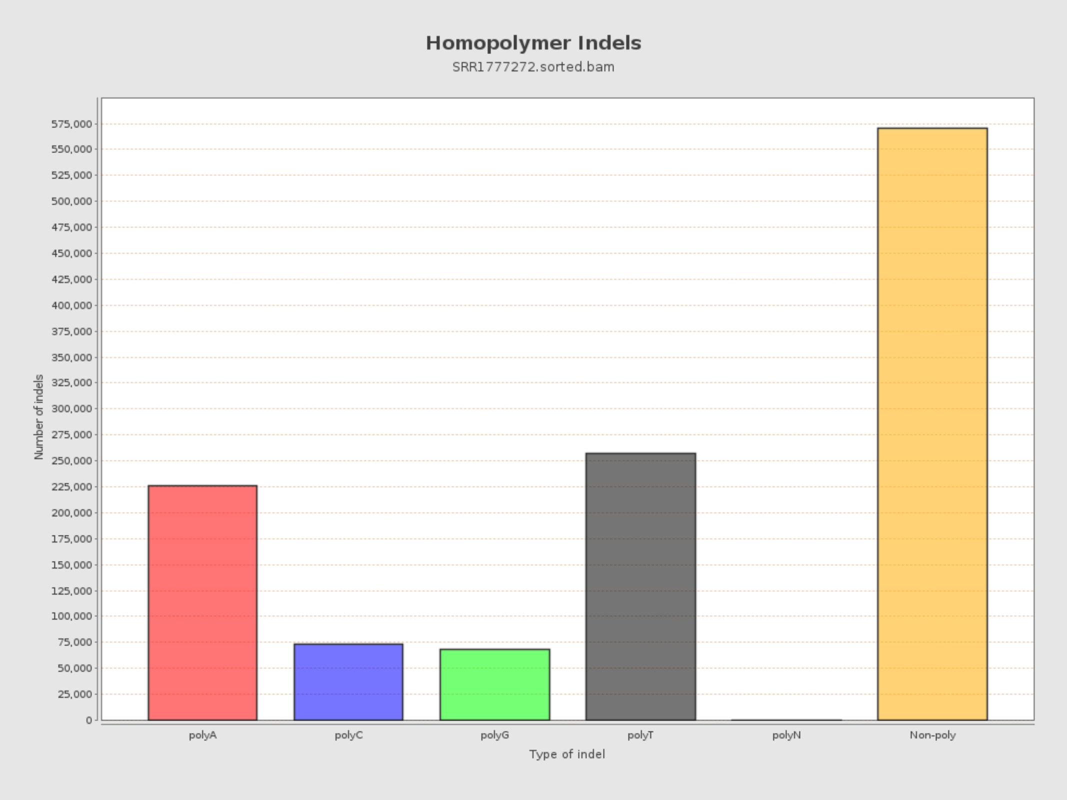
9. Results : Mapped Reads GC-content Distribution



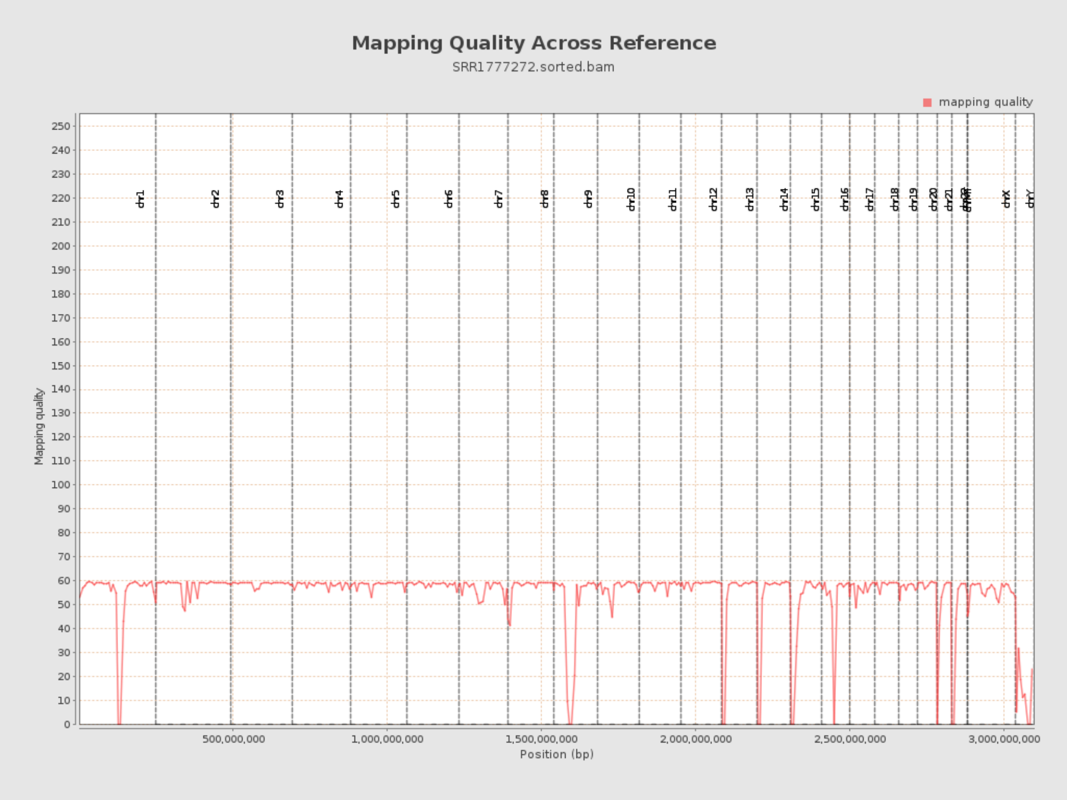
10. Results : Mapped Reads Clipping Profile



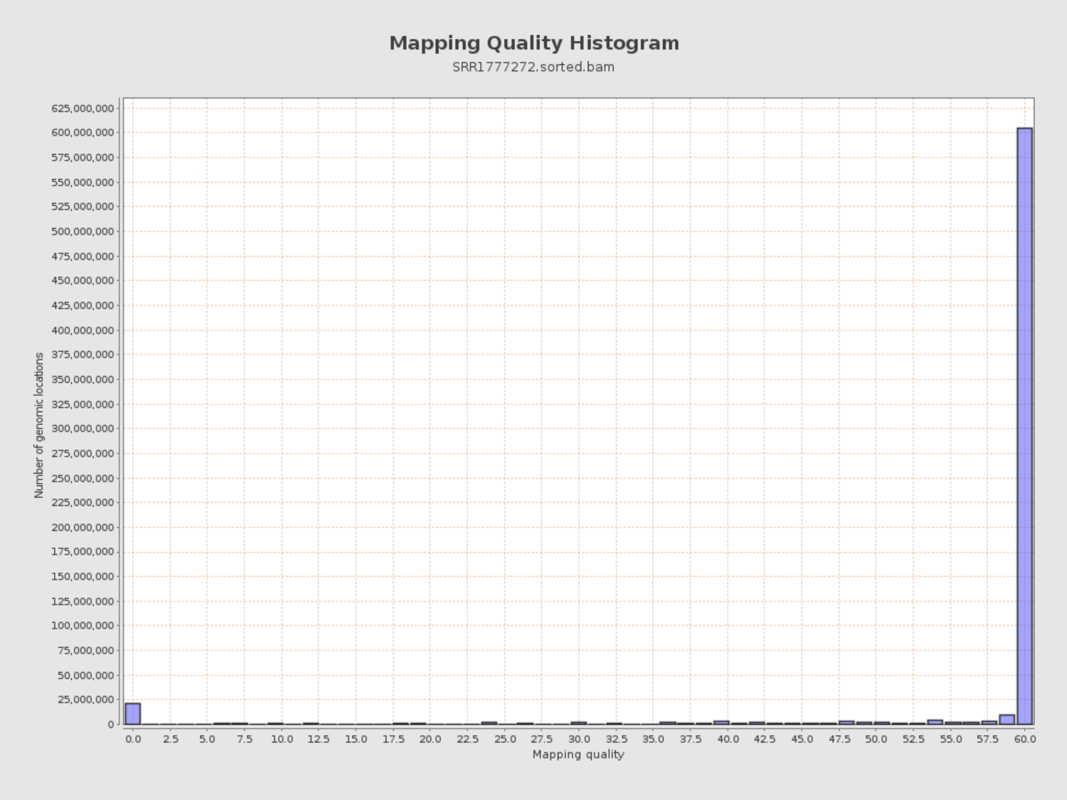
11. Results : Homopolymer Indels



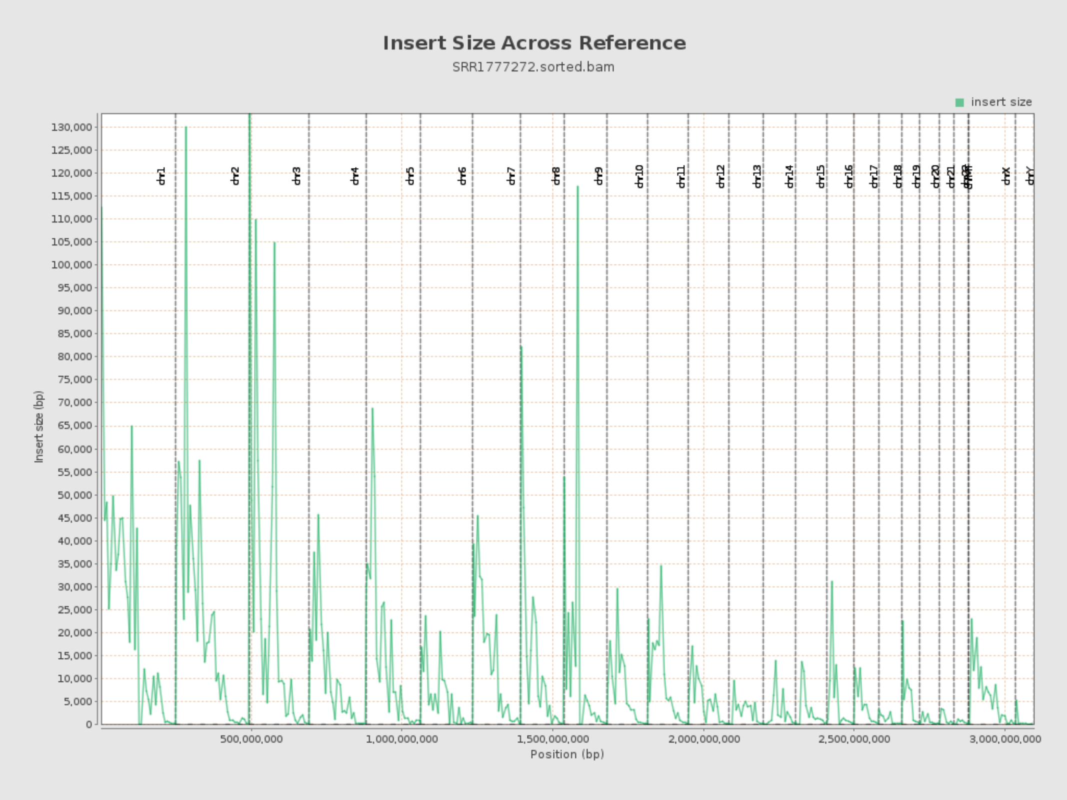
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram