Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 22:43:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777276.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_SRR1777276 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777276_1.fastq.gz SRR1777276_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 22:43:04 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777276.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	60,091,208
Mapped reads	58,405,595 / 97.19%
Unmapped reads	1,685,613 / 2.81%
Mapped paired reads	58,405,595 / 97.19%
Mapped reads, first in pair	29,204,052 / 48.6%
Mapped reads, second in pair	29,201,543 / 48.6%
Mapped reads, both in pair	58,365,622 / 97.13%
Mapped reads, singletons	39,973 / 0.07%
Secondary alignments	0
Supplementary alignments	199,590 / 0.33%
Read min/max/mean length	30 / 101 / 101.14
Duplicated reads (estimated)	33,979,460 / 56.55%
Duplication rate	45.06%
Clipped reads	4,154,143 / 6.91%

2.2. ACGT Content

Number/percentage of A's	1,389,850,463 / 23.95%
Number/percentage of C's	1,496,537,805 / 25.79%
Number/percentage of T's	1,393,158,432 / 24.01%
Number/percentage of G's	1,523,431,645 / 26.25%
Number/percentage of N's	237,128 / 0%

GC Percentage	52.04%

2.3. Coverage

Mean	1.8756
Standard Deviation	27.6997

2.4. Mapping Quality

Mean Mapping Quality	55.12

2.5. Insert size

Mean	96,283.11
Standard Deviation	3,202,604.79
P25/Median/P75	185 / 231 / 284

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	36,131,278
Insertions	601,198
Mapped reads with at least one insertion	1.02%
Deletions	2,329,987
Mapped reads with at least one deletion	3.91%
Homopolymer indels	55.39%

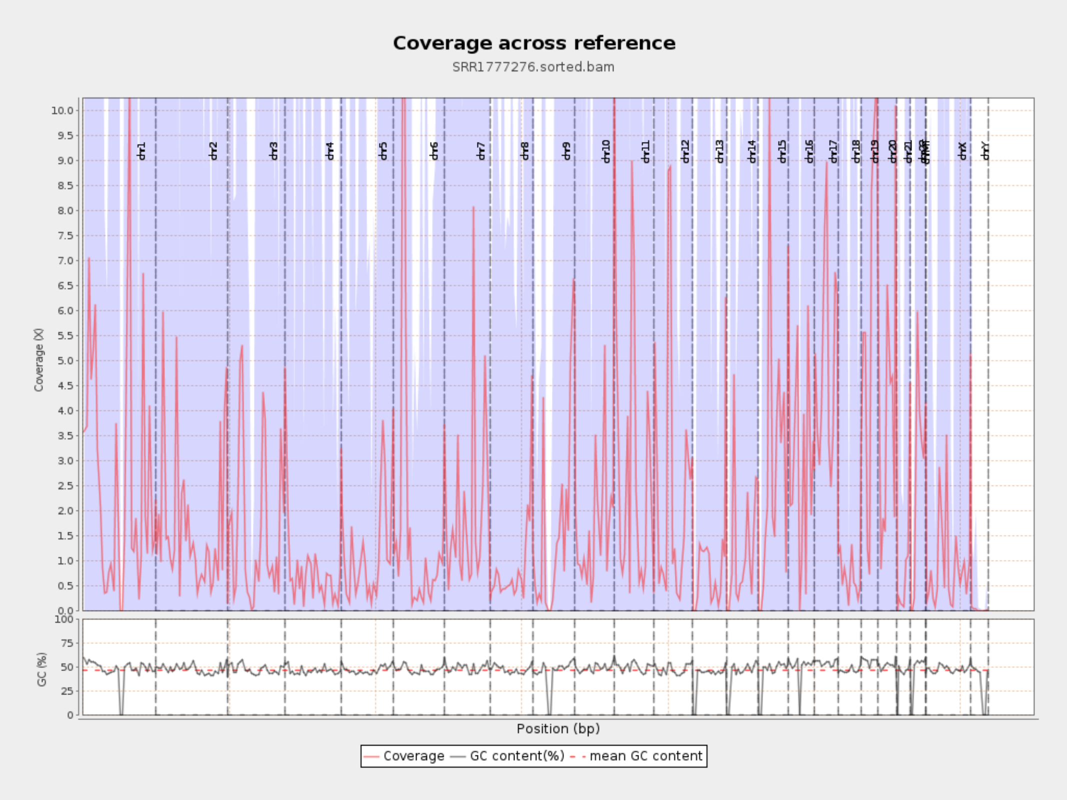
2.7. Chromosome stats

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

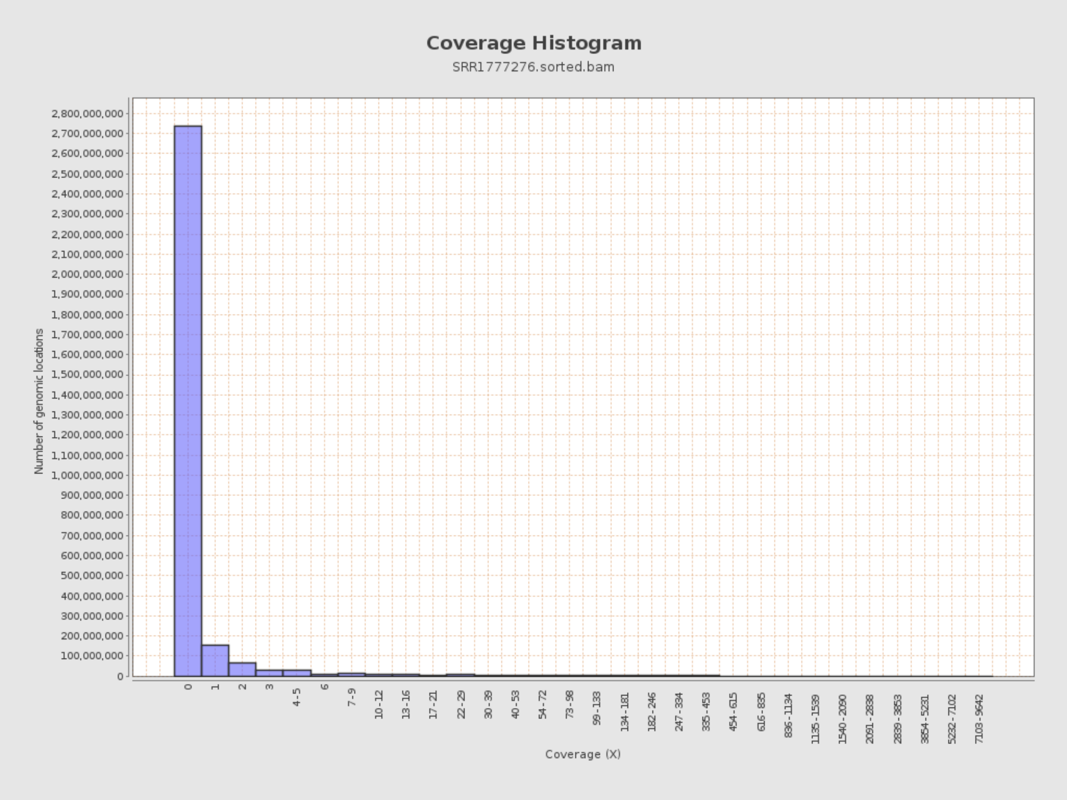
		bases	coverage	deviation
chr1	249250621	669809034	2.6873	32.9371
chr2	243199373	407884983	1.6772	25.0159
chr3	198022430	317165433	1.6017	25.2579
chr4	191154276	140639964	0.7357	15.5463
chr5	180915260	221460006	1.2241	18.8094
chr6	171115067	281243648	1.6436	27.155
chr7	159138663	325859092	2.0476	32.2174
chr8	146364022	132105207	0.9026	17.2454
chr9	141213431	227659079	1.6122	23.4824
chr10	135534747	224118692	1.6536	23.9756
chr11	135006516	393511654	2.9148	34.6625
chr12	133851895	339181586	2.534	34.6296
chr13	115169878	92131507	0.8	14.8993
chr14	107349540	128060039	1.1929	18.1924
chr15	102531392	280228619	2.7331	34.8829
chr16	90354753	270270721	2.9912	34.6983
chr17	81195210	399686513	4.9225	50.5578
chr18	78077248	52220670	0.6688	12.1969
chr19	59128983	348046672	5.8862	51.51
chr20	63025520	229413753	3.64	43.6203
chr21	48129895	42375551	0.8804	15.319
chr22	51304566	137237804	2.675	31.1311
chrMT	16571	59095	3.5662	4.3768
chrX	155270560	144793460	0.9325	17.4637

chrY	59373566	997114	0.0168	0.9023

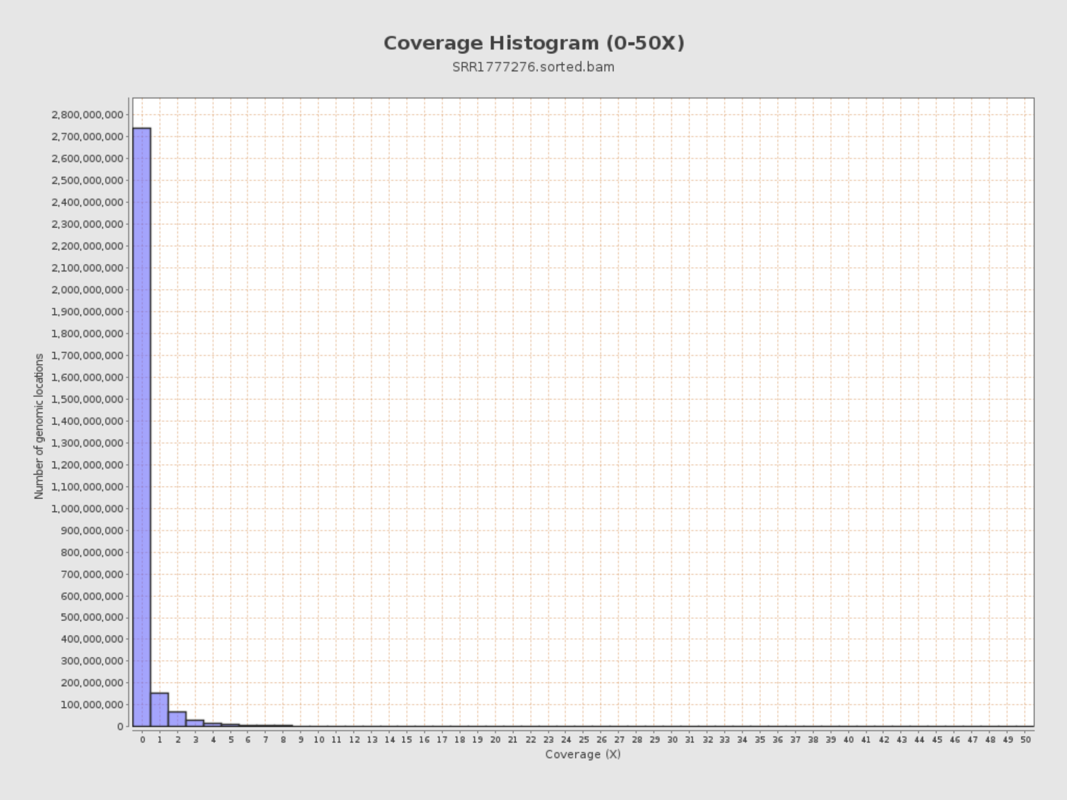
3. Results : Coverage across reference



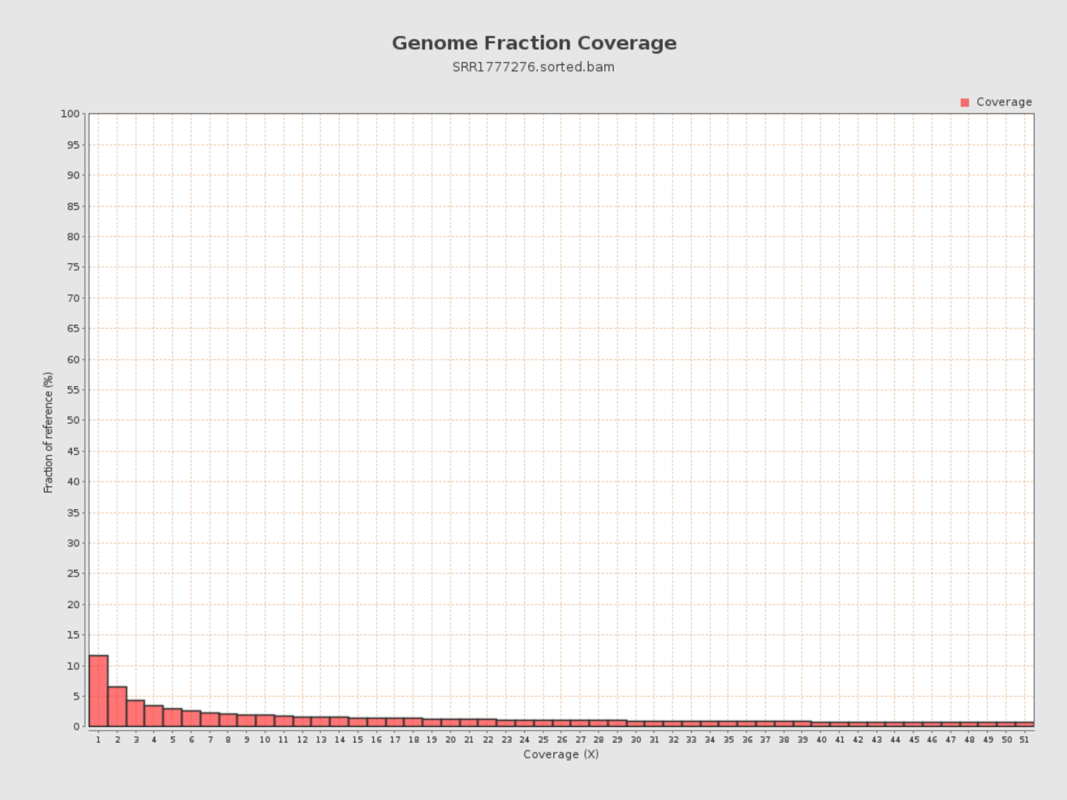
4. Results : Coverage Histogram



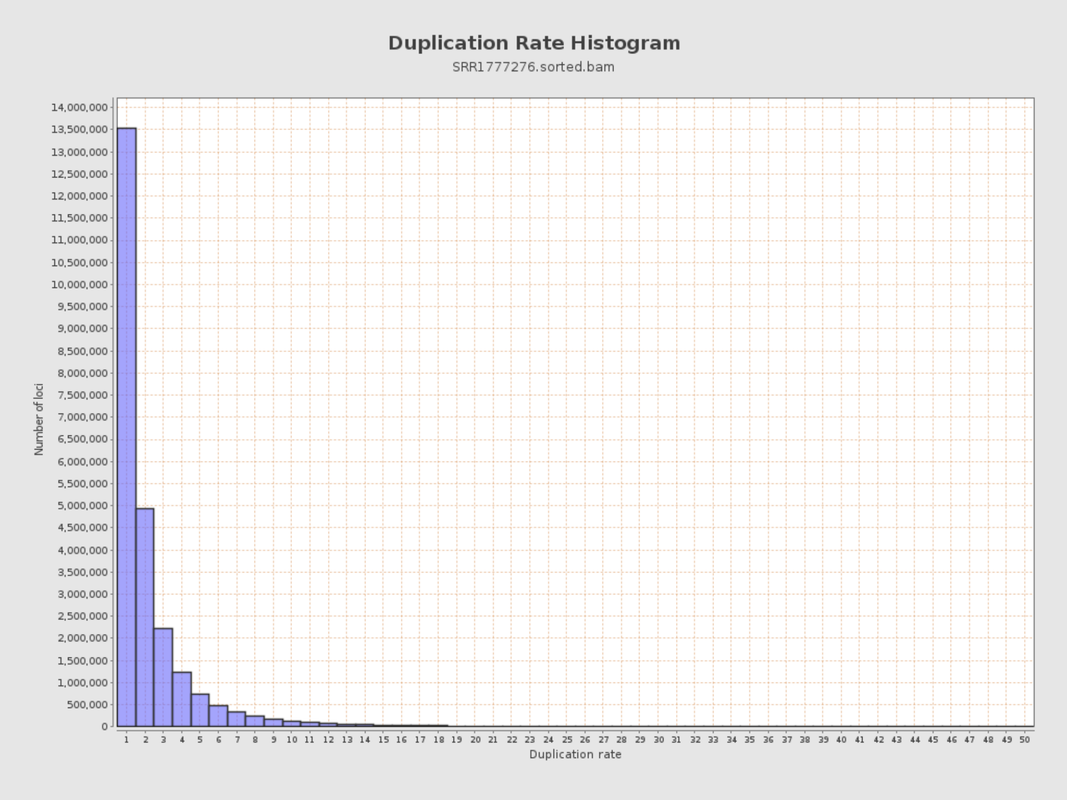
5. Results : Coverage Histogram (0-50X)



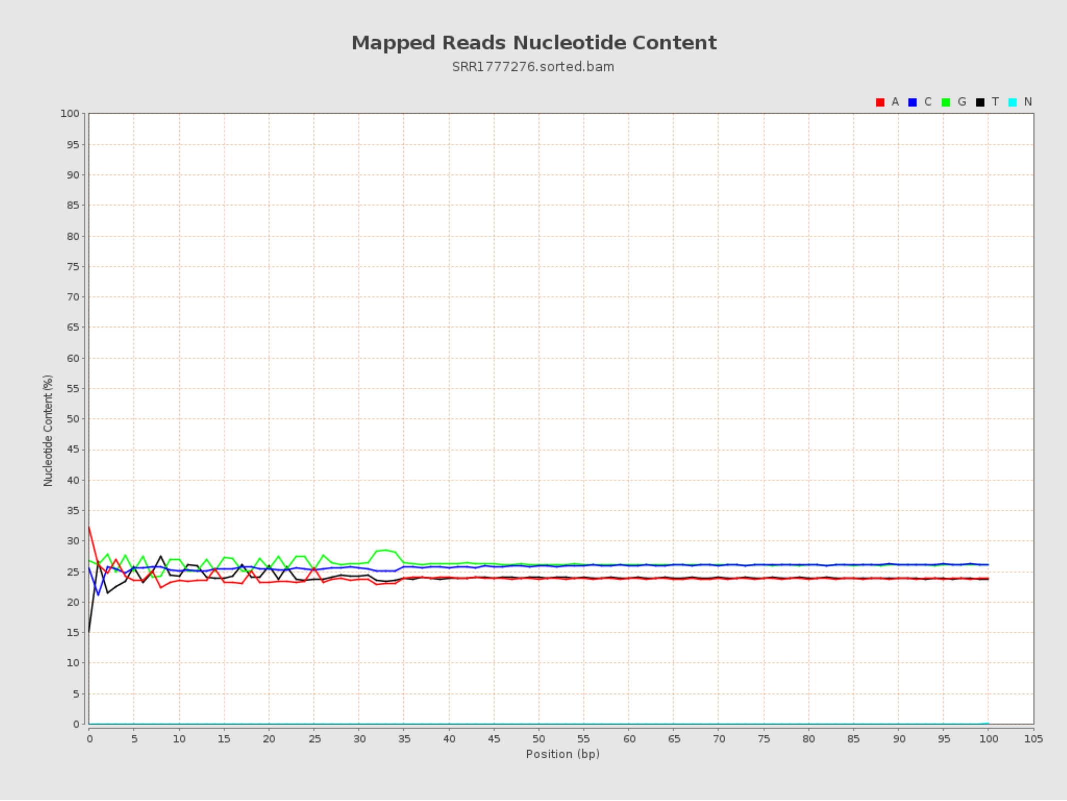
6. Results : Genome Fraction Coverage



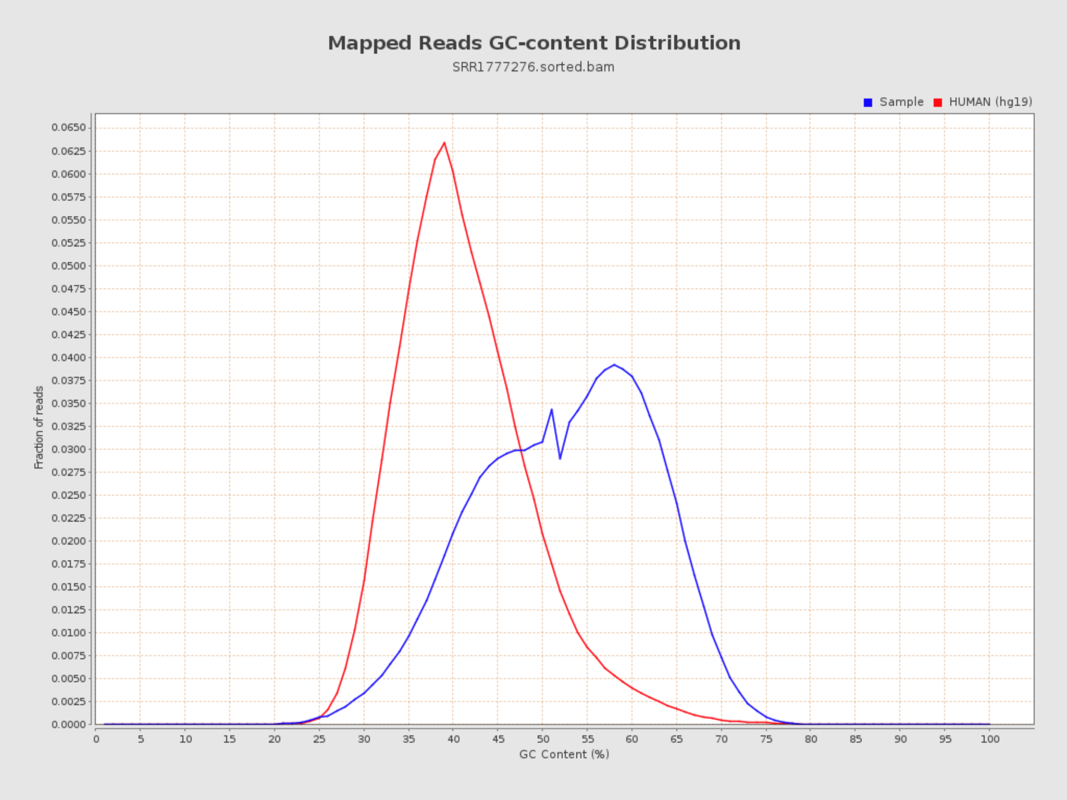
7. Results : Duplication Rate Histogram



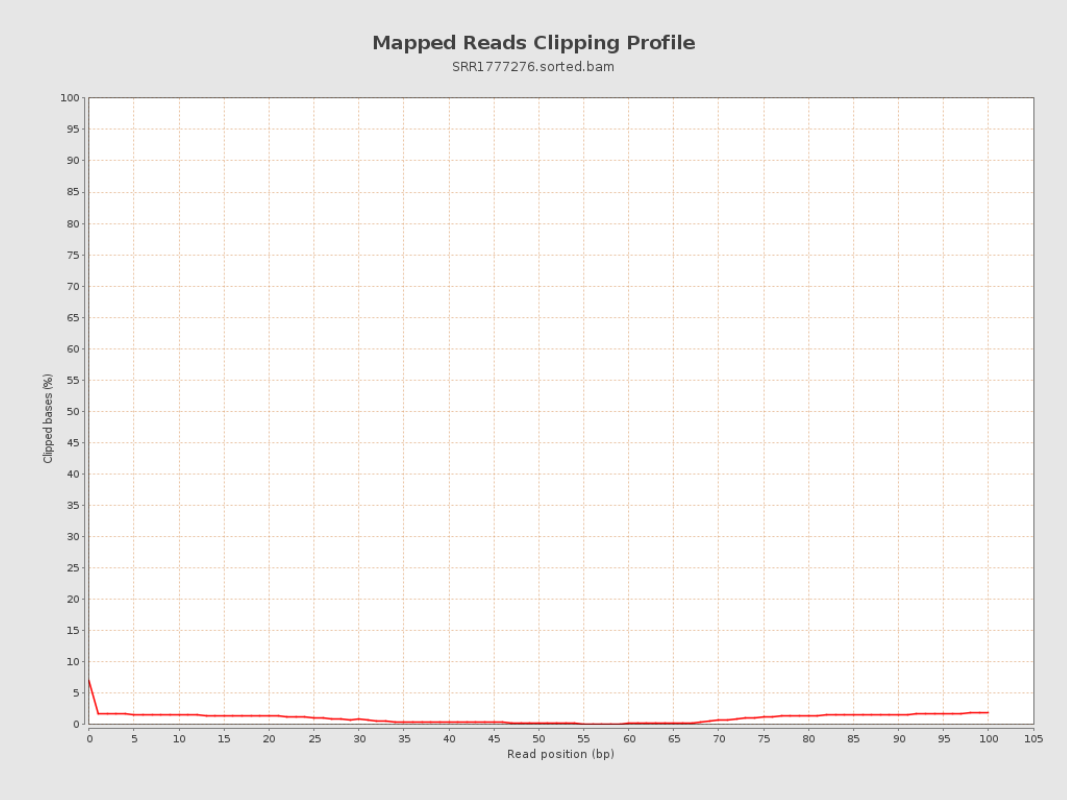
8. Results : Mapped Reads Nucleotide Content



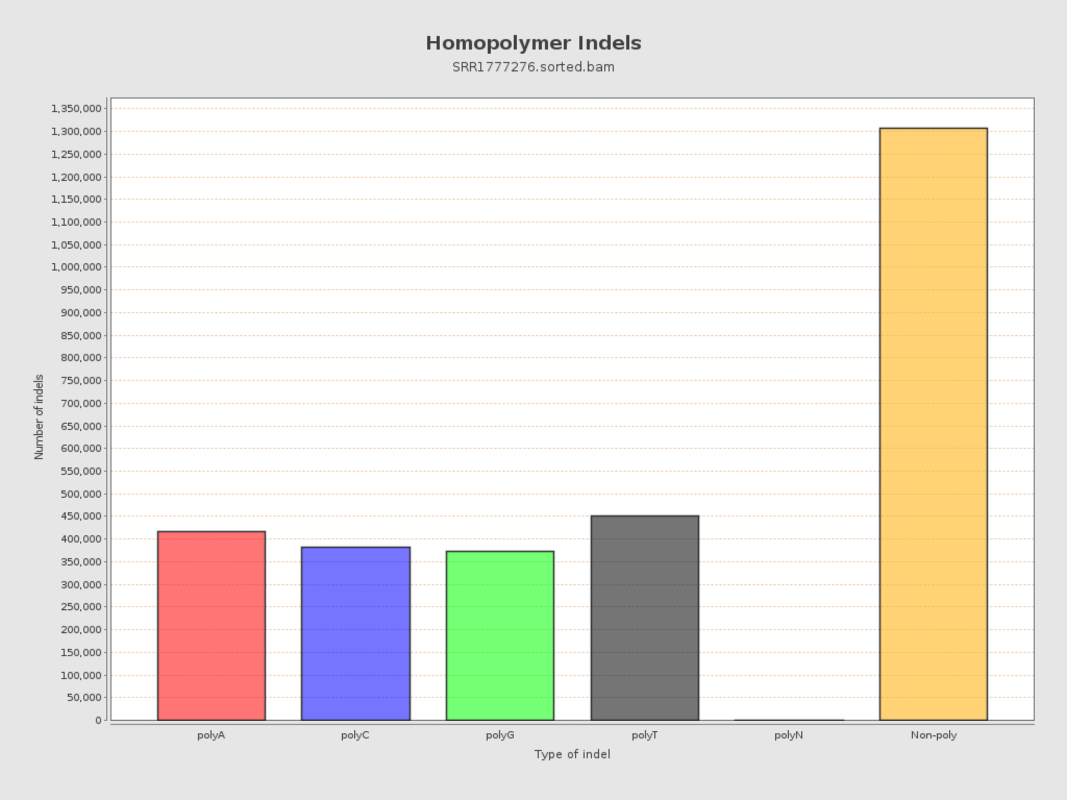
9. Results : Mapped Reads GC-content Distribution



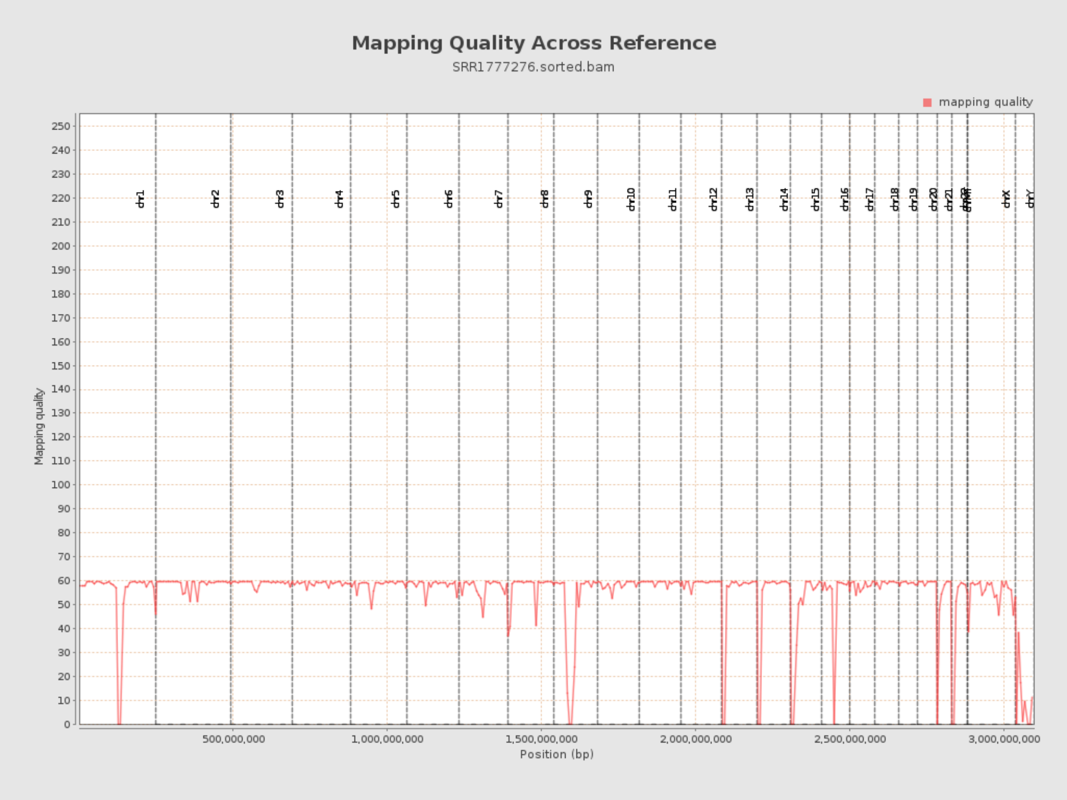
10. Results : Mapped Reads Clipping Profile



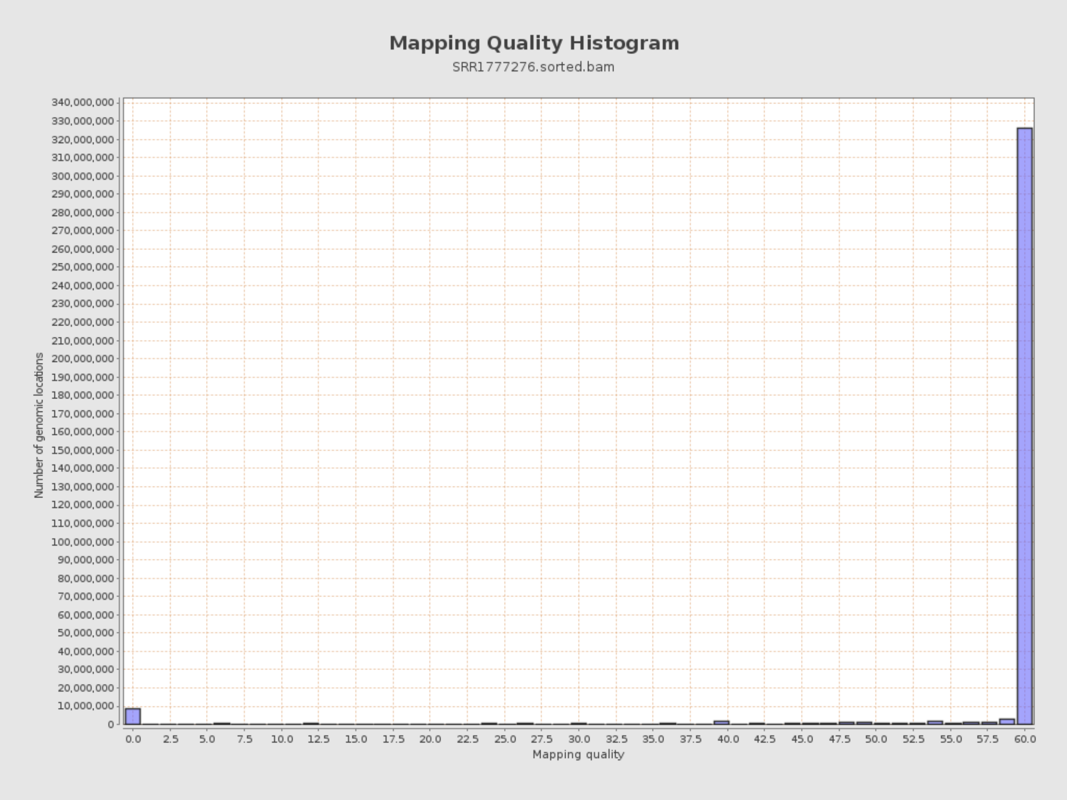
11. Results : Homopolymer Indels



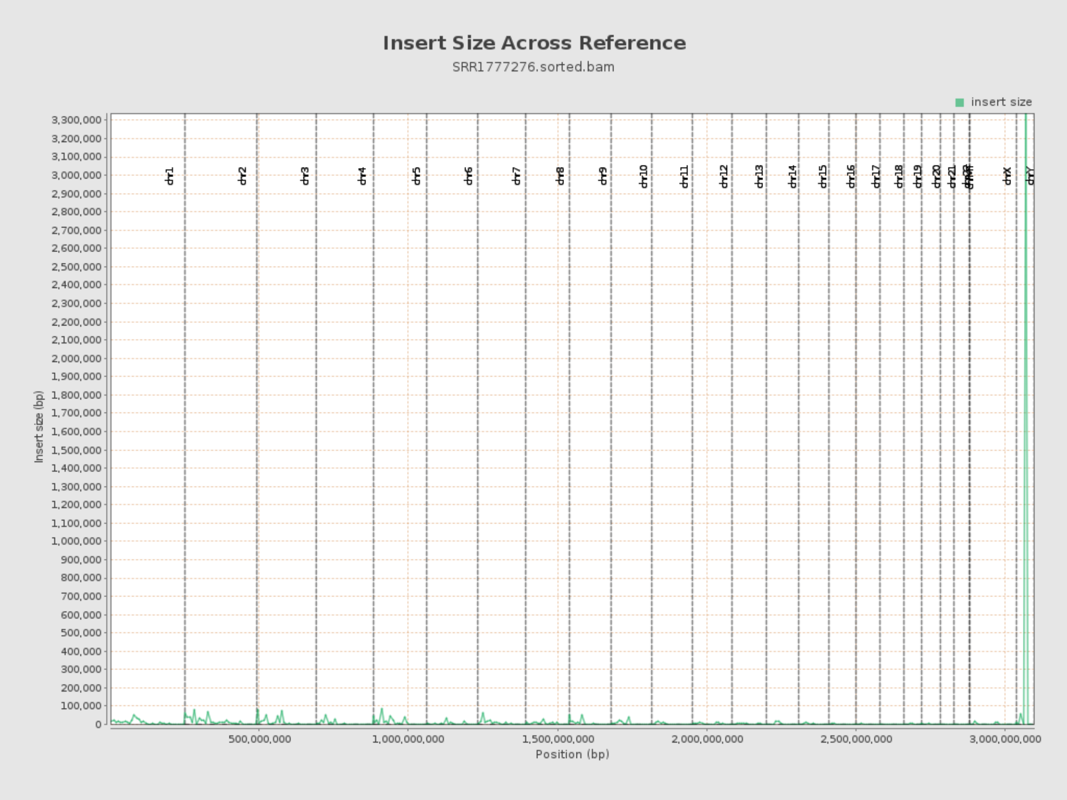
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram