Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 02:41:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777252.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_SRR1777252 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777252_1.fastq.gz SRR1777252_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 02:41:04 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777252.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	59,851,126
Mapped reads	59,652,972 / 99.67%
Unmapped reads	198,154 / 0.33%
Mapped paired reads	59,652,972 / 99.67%
Mapped reads, first in pair	29,825,624 / 49.83%
Mapped reads, second in pair	29,827,348 / 49.84%
Mapped reads, both in pair	59,613,294 / 99.6%
Mapped reads, singletons	39,678 / 0.07%
Secondary alignments	0
Supplementary alignments	1,988,421 / 3.32%
Read min/max/mean length	30 / 101 / 102.37
Duplicated reads (estimated)	32,775,407 / 54.76%
Duplication rate	47.69%
Clipped reads	7,191,141 / 12.02%

2.2. ACGT Content

Number/percentage of A's	1,681,509,828 / 28.1%
Number/percentage of C's	1,309,864,504 / 21.89%
Number/percentage of T's	1,666,867,405 / 27.85%
Number/percentage of G's	1,325,895,136 / 22.16%
Number/percentage of N's	74,063 / 0%

GC Percentage	44.05%

2.3. Coverage

Mean	1.9334
Standard Deviation	19.513

2.4. Mapping Quality

Mean Mapping Quality	54.78

2.5. Insert size

Mean	200,710.63
Standard Deviation	4,326,739.8
P25/Median/P75	183 / 233 / 297

2.6. Mismatches and indels

General error rate	0.24%
Mismatches	12,860,906
Insertions	982,521
Mapped reads with at least one insertion	1.62%
Deletions	404,178
Mapped reads with at least one deletion	0.66%
Homopolymer indels	50.66%

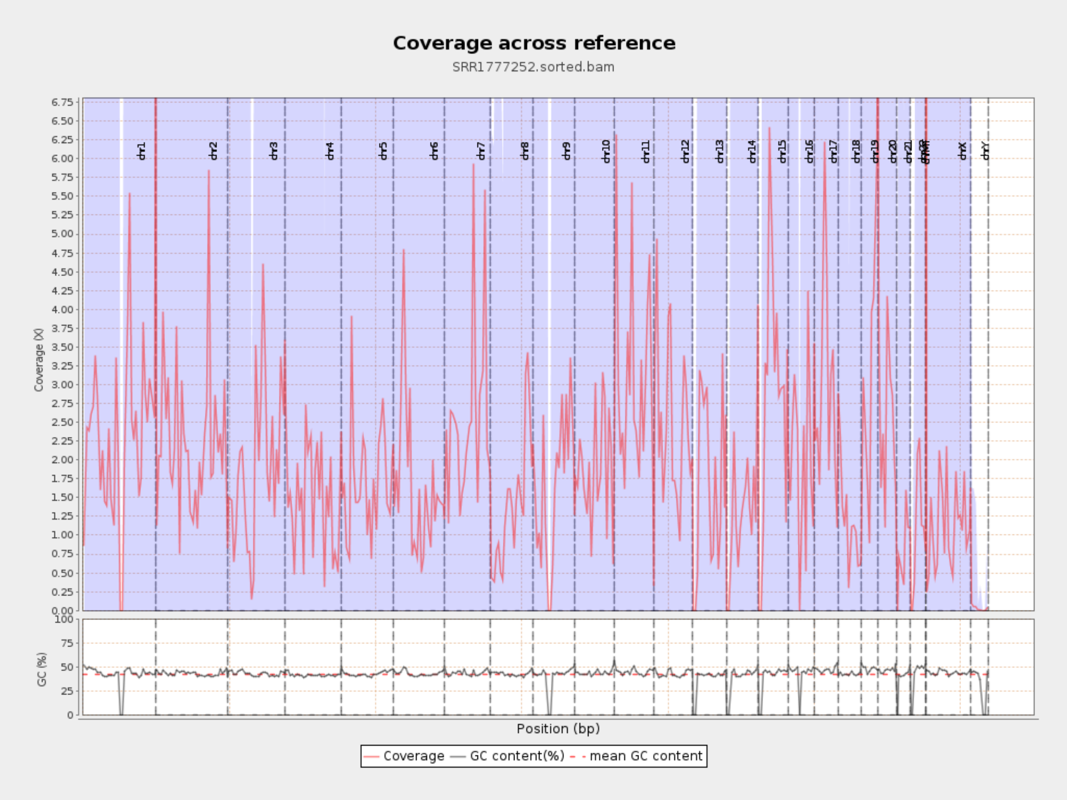
2.7. Chromosome stats

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

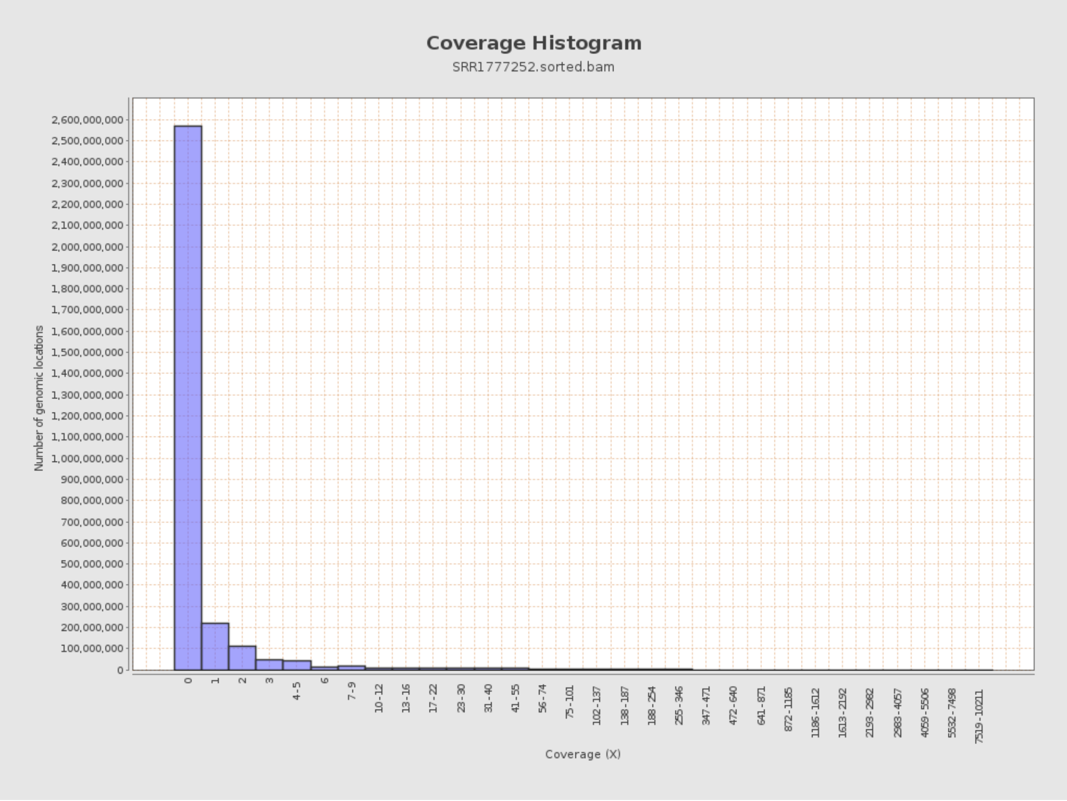
		bases	coverage	deviation
chr1	249250621	588110700	2.3595	20.7686
chr2	243199373	548065859	2.2536	20.6365
chr3	198022430	374833857	1.8929	18.4419
chr4	191154276	282934035	1.4801	16.6628
chr5	180915260	315202150	1.7423	17.6533
chr6	171115067	281325002	1.6441	16.6867
chr7	159138663	400873558	2.519	24.633
chr8	146364022	208625657	1.4254	17.1629
chr9	141213431	228410873	1.6175	22.8565
chr10	135534747	257378170	1.899	17.9502
chr11	135006516	419620166	3.1081	27.6461
chr12	133851895	340205079	2.5417	21.8072
chr13	115169878	191214594	1.6603	19.1598
chr14	107349540	133194423	1.2408	13.415
chr15	102531392	285814743	2.7876	25.3644
chr16	90354753	171904752	1.9026	17.263
chr17	81195210	241417197	2.9733	23.1509
chr18	78077248	94936549	1.2159	13.6019
chr19	59128983	191557239	3.2397	23.0748
chr20	63025520	158885339	2.521	23.0177
chr21	48129895	39235502	0.8152	12.3099
chr22	51304566	55712771	1.0859	10.8721
chrMT	16571	1322065	79.7818	42.6508
chrX	155270560	172788888	1.1128	13.2042

chrY	59373566	1548861	0.0261	0.9526

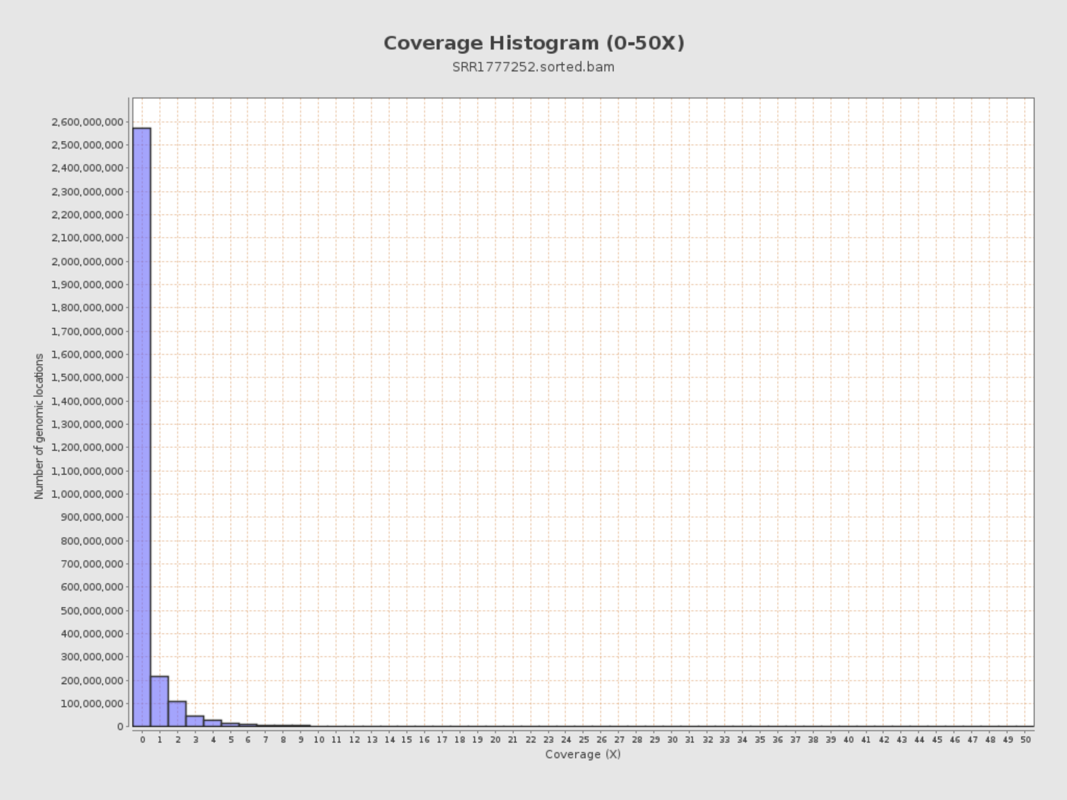
3. Results : Coverage across reference



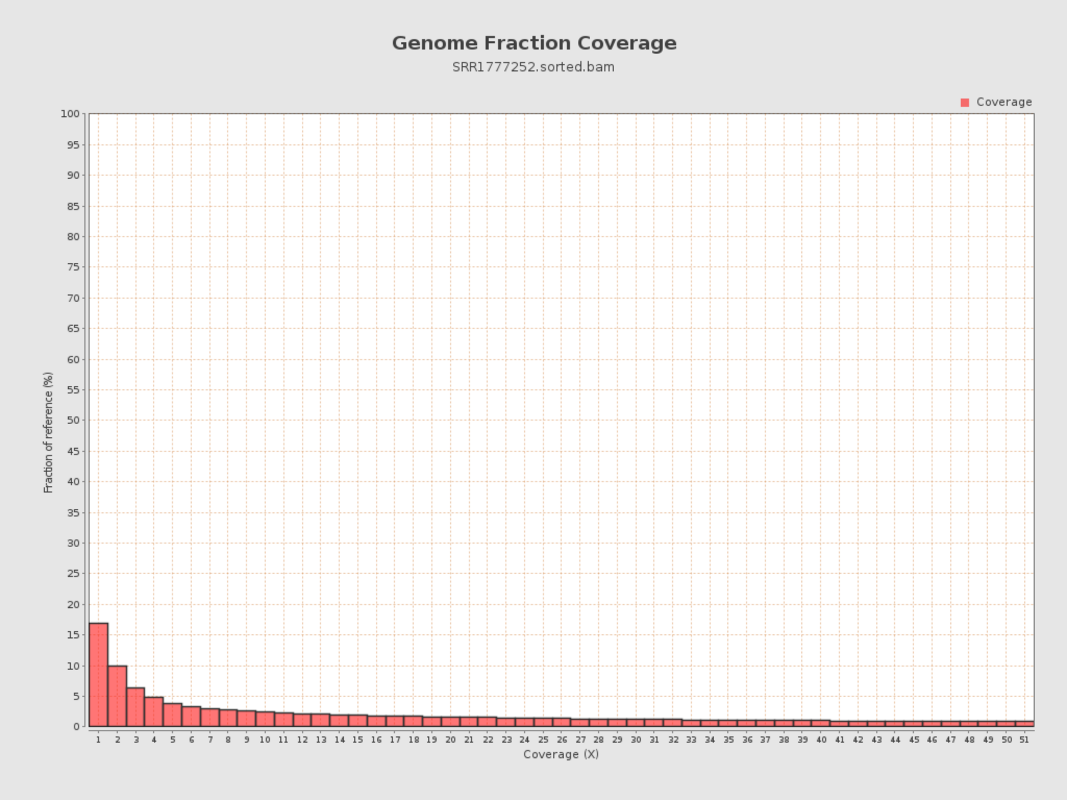
4. Results : Coverage Histogram



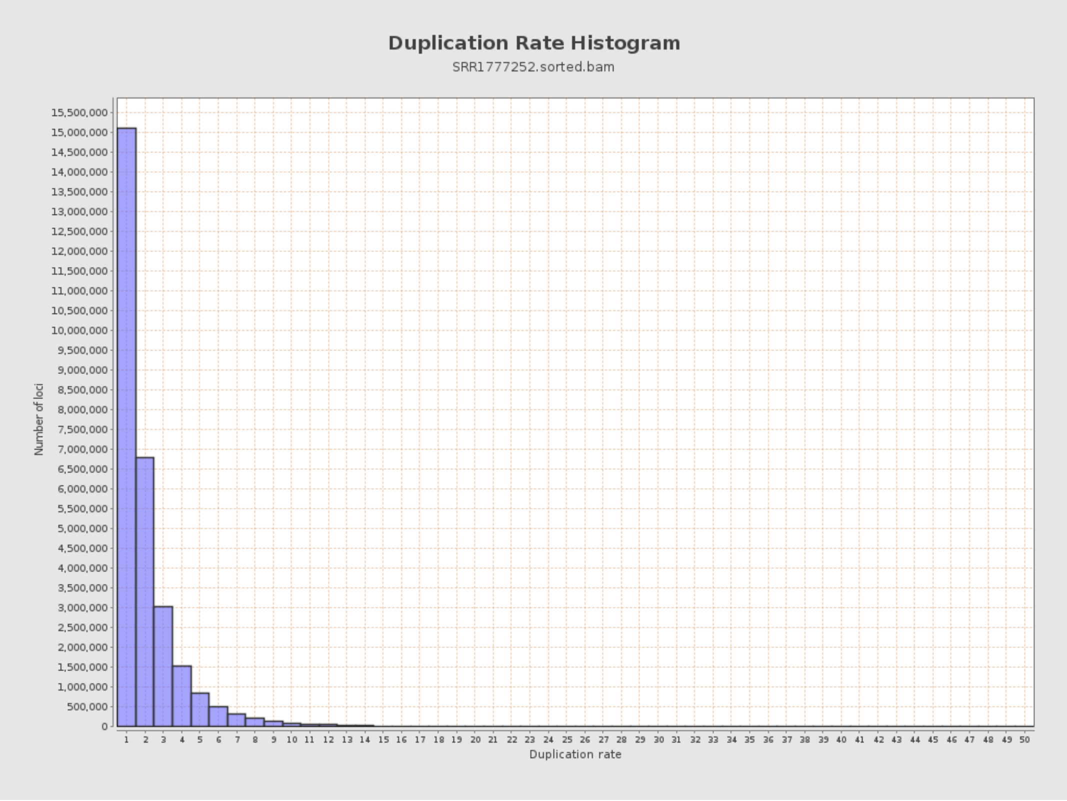
5. Results : Coverage Histogram (0-50X)



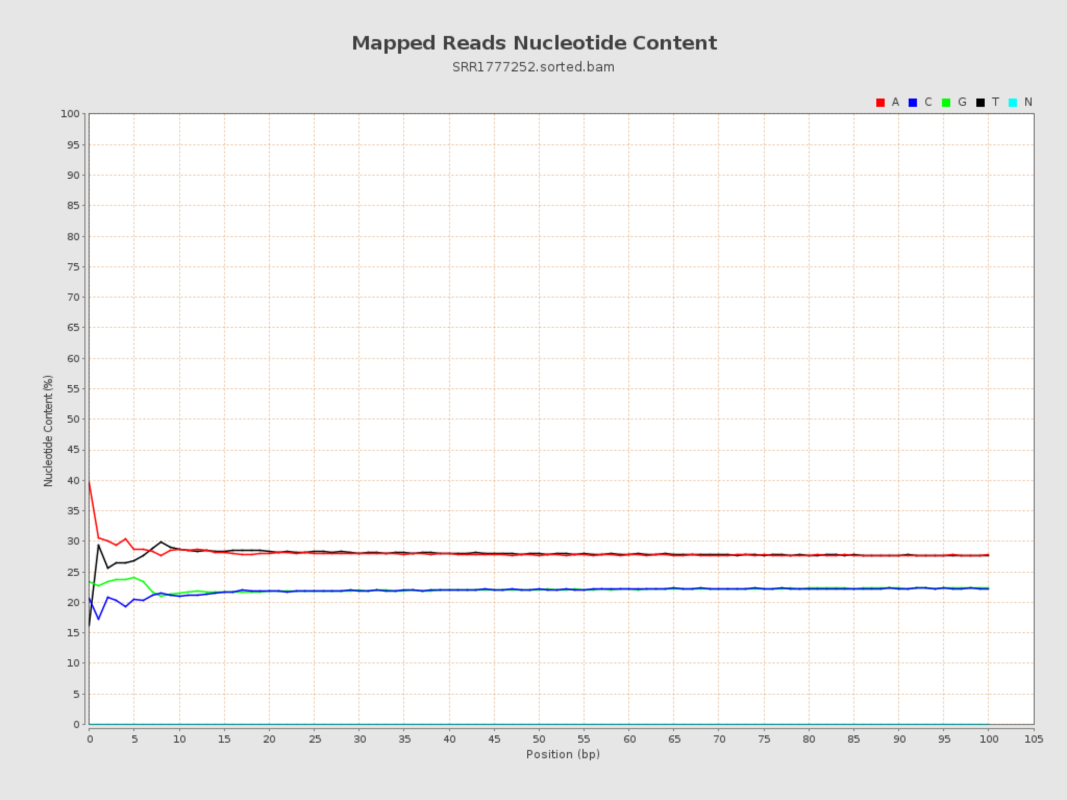
6. Results : Genome Fraction Coverage



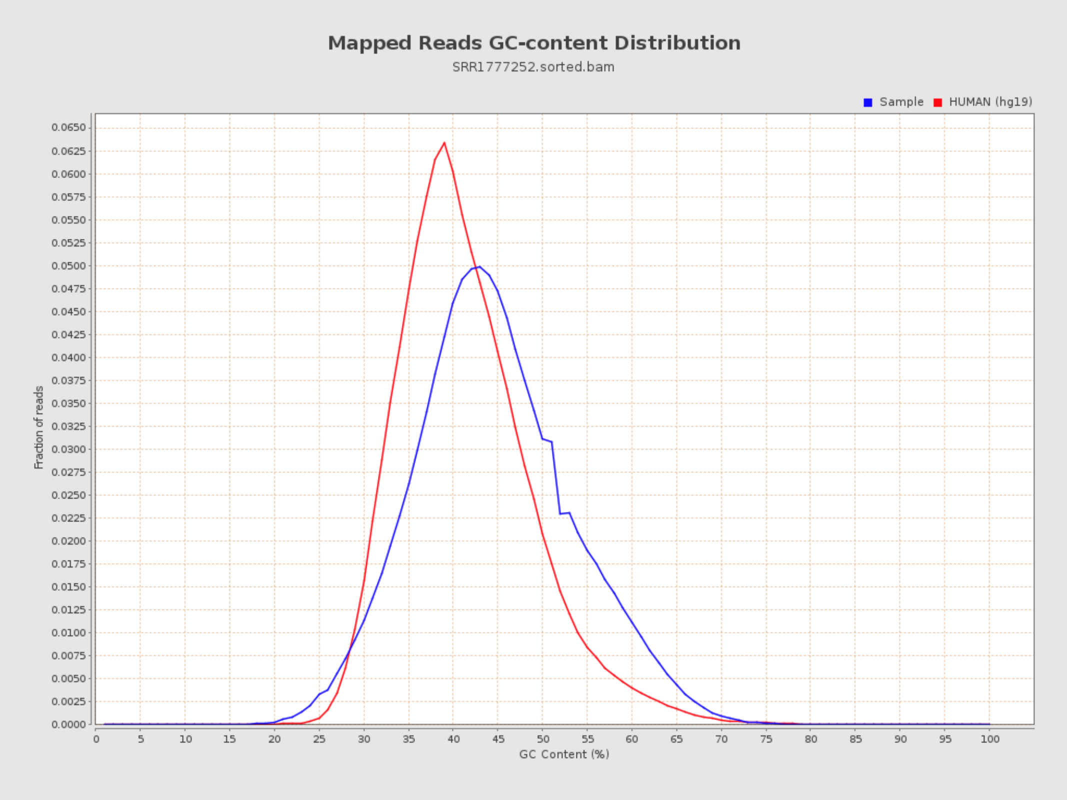
7. Results : Duplication Rate Histogram



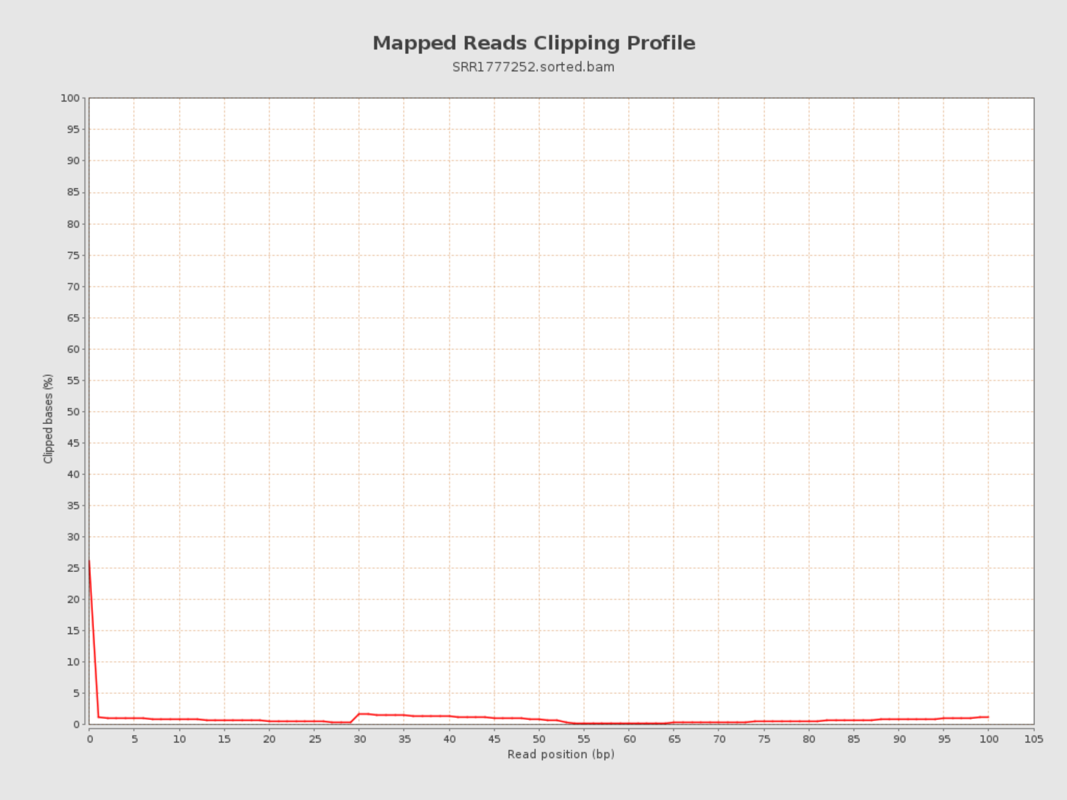
8. Results : Mapped Reads Nucleotide Content



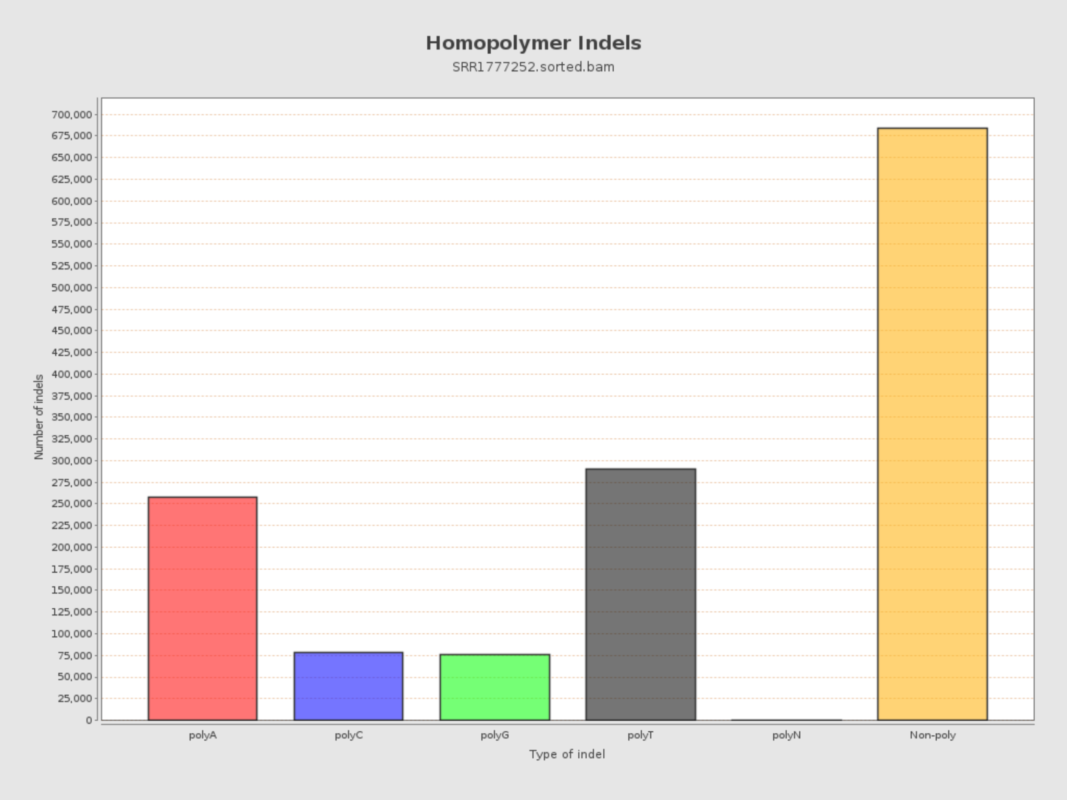
9. Results : Mapped Reads GC-content Distribution



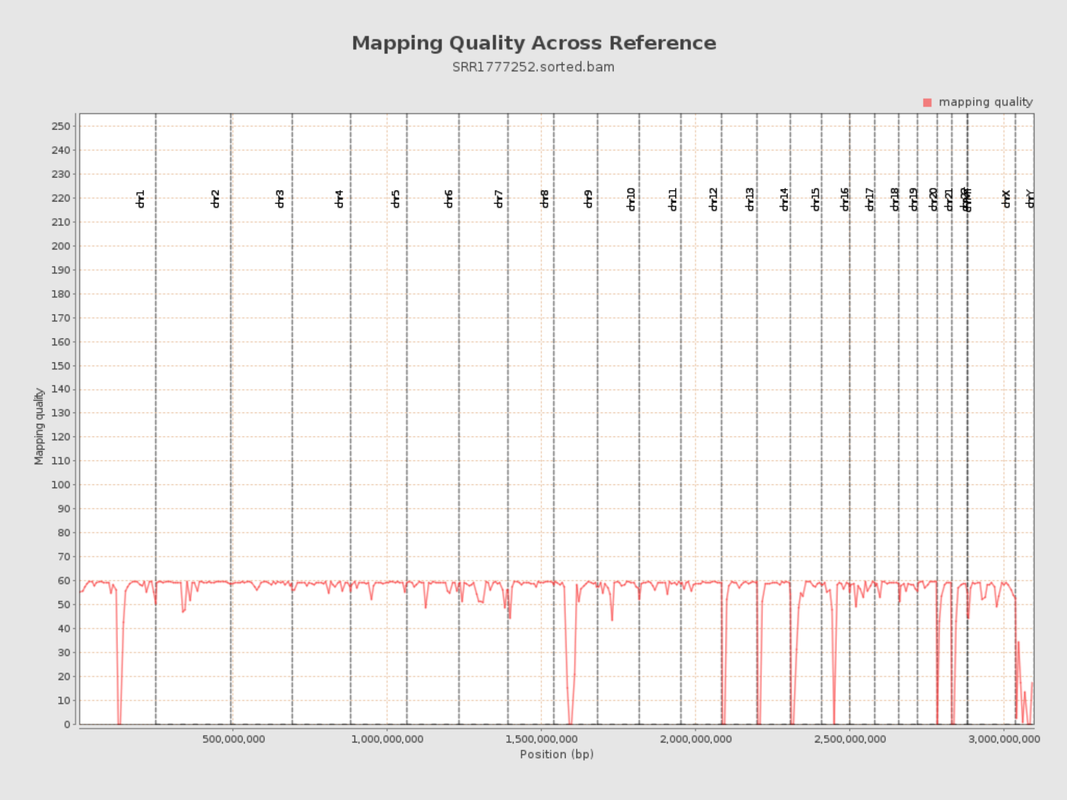
10. Results : Mapped Reads Clipping Profile



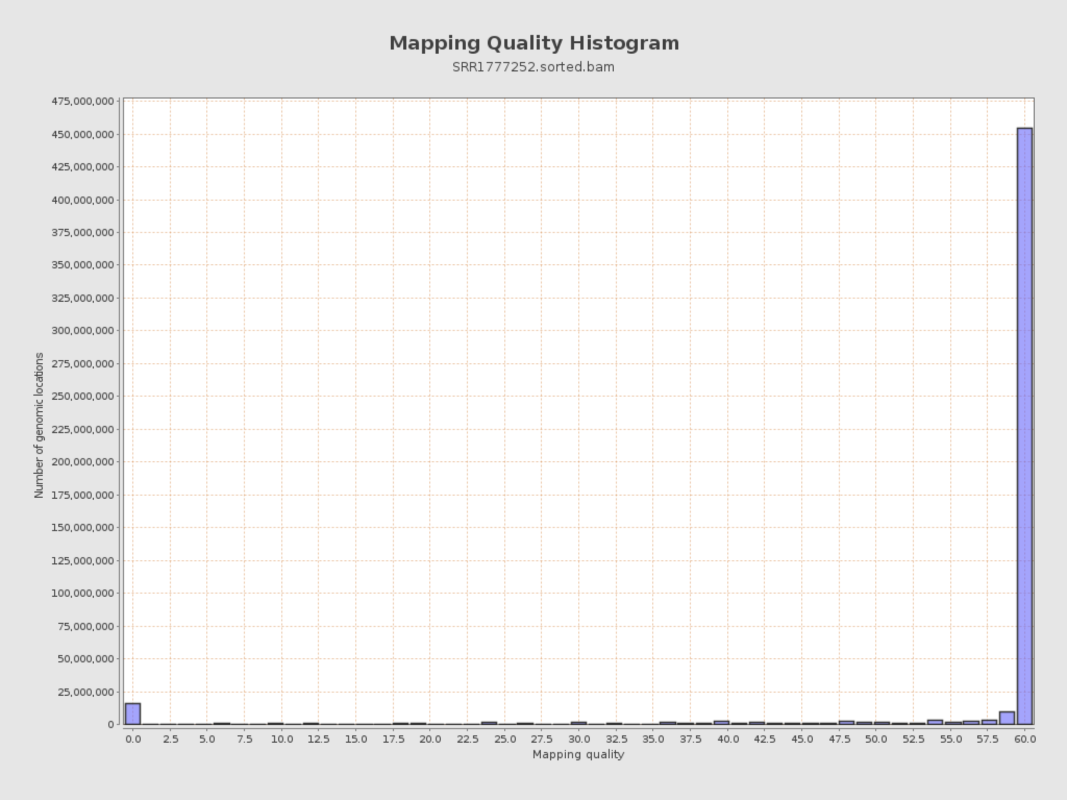
11. Results : Homopolymer Indels



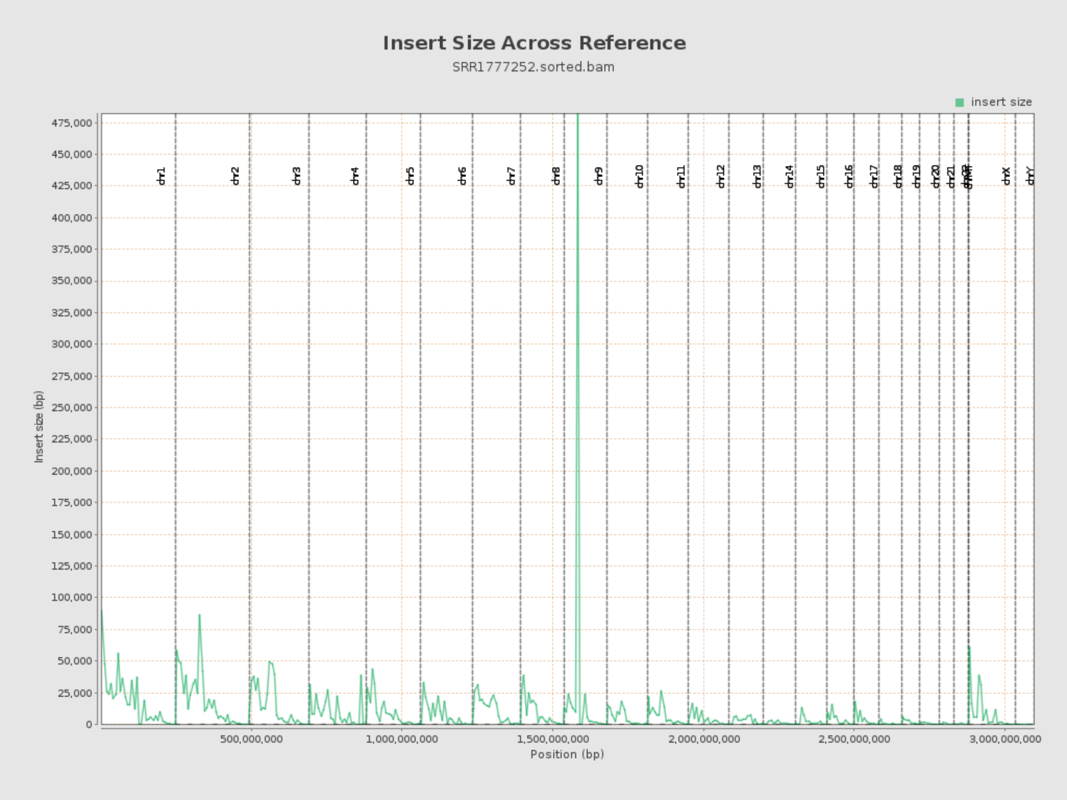
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram