Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/07 02:52:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777308.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_SRR1777308 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777308_1.fastq.gz SRR1777308_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Apr 07 02:52:12 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777308.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	364,320,754
Mapped reads	344,125,158 / 94.46%
Unmapped reads	20,195,596 / 5.54%
Mapped paired reads	344,125,158 / 94.46%
Mapped reads, first in pair	173,137,169 / 47.52%
Mapped reads, second in pair	170,987,989 / 46.93%
Mapped reads, both in pair	338,319,248 / 92.86%
Mapped reads, singletons	5,805,910 / 1.59%
Secondary alignments	0
Supplementary alignments	10,719,492 / 2.94%
Read min/max/mean length	30 / 101 / 102.22
Duplicated reads (estimated)	151,225,794 / 41.51%
Duplication rate	22.84%
Clipped reads	103,163,148 / 28.32%

2.2. ACGT Content

Number/percentage of A's	9,453,504,576 / 28.88%
Number/percentage of C's	6,954,695,447 / 21.25%
Number/percentage of T's	9,248,363,555 / 28.26%
Number/percentage of G's	7,070,982,551 / 21.6%
Number/percentage of N's	915,506 / 0%

GC Percentage	42.85%

2.3. Coverage

Mean	10.5835
Standard Deviation	386.1113

2.4. Mapping Quality

Mean Mapping Quality	52.48

2.5. Insert size

Mean	146,246.59
Standard Deviation	3,738,075.76
P25/Median/P75	114 / 164 / 239

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	302,672,865
Insertions	11,791,267
Mapped reads with at least one insertion	3.14%
Deletions	10,756,334
Mapped reads with at least one deletion	2.82%
Homopolymer indels	29.02%

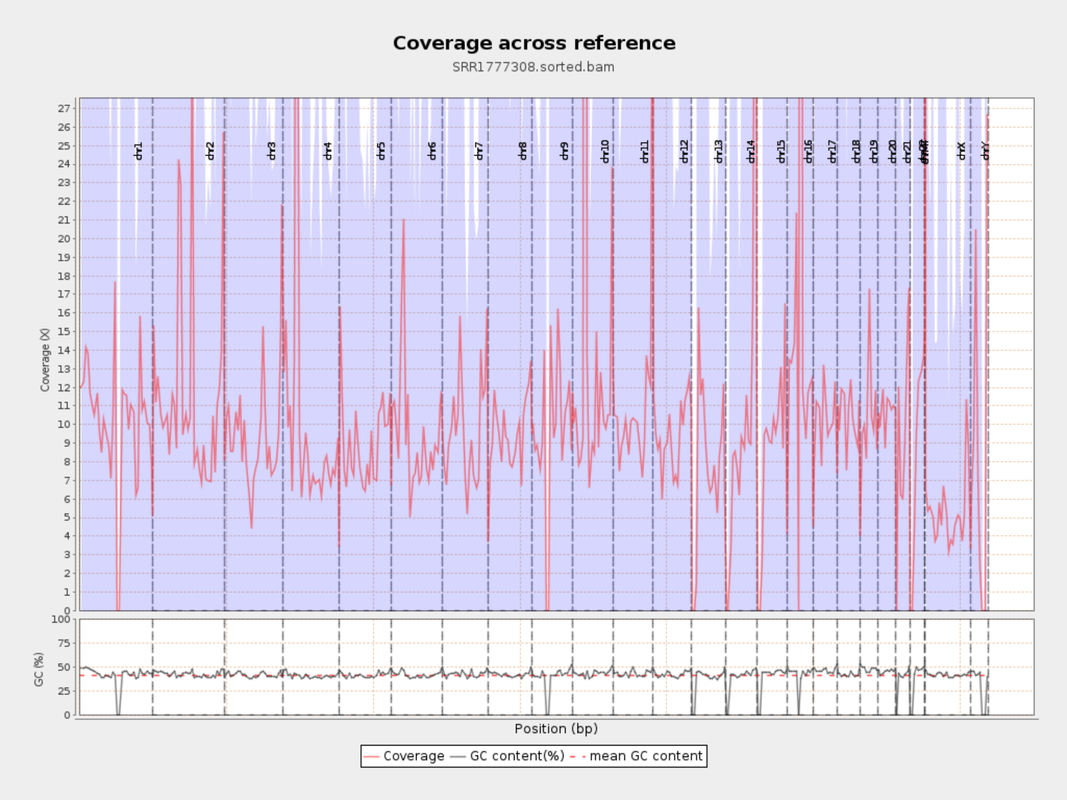
2.7. Chromosome stats

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

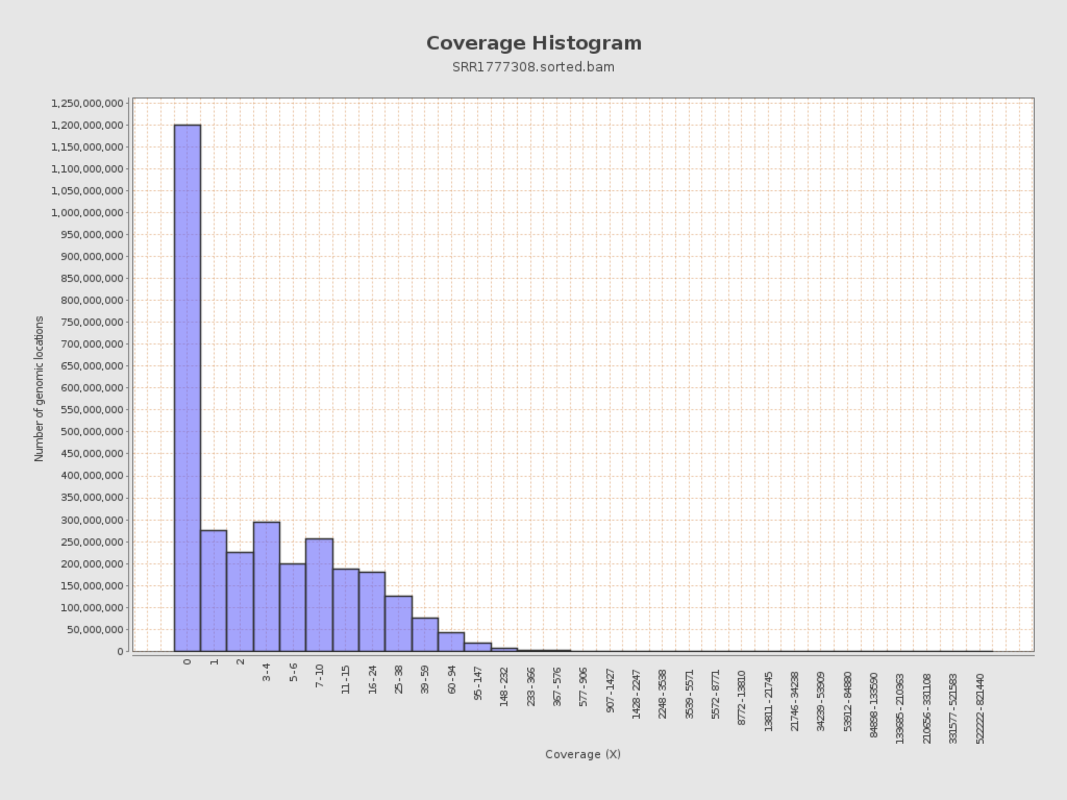
		bases	coverage	deviation
chr1	249250621	2522587245	10.1207	175.3117
chr2	243199373	2846021972	11.7024	298.9405
chr3	198022430	1844473636	9.3145	179.4116
chr4	191154276	1979310489	10.3545	285.6878
chr5	180915260	1646654251	9.1018	78.8331
chr6	171115067	1636884822	9.566	182.9405
chr7	159138663	1560880668	9.8083	95.2087
chr8	146364022	1415403550	9.6704	60.0363
chr9	141213431	1361595551	9.6421	163.1319
chr10	135534747	2688943835	19.8395	1,490.6062
chr11	135006516	1379437351	10.2176	73.1941
chr12	133851895	1258589648	9.4029	40.3595
chr13	115169878	894065054	7.763	131.8408
chr14	107349540	1197582606	11.1559	478.1095
chr15	102531392	868014045	8.4658	125.581
chr16	90354753	1797809507	19.8972	571.8297
chr17	81195210	832696288	10.2555	61.5306
chr18	78077248	812913926	10.4117	132.2033
chr19	59128983	624902685	10.5685	125.979
chr20	63025520	675689615	10.7209	86.1226
chr21	48129895	468426259	9.7325	173.1587
chr22	51304566	437826616	8.5339	78.7647
chrMT	16571	645436491	38,949.7611	6,213.6113
chrX	155270560	821211236	5.2889	111.4762

chrY	59373566	545856572	9.1936	296.5009

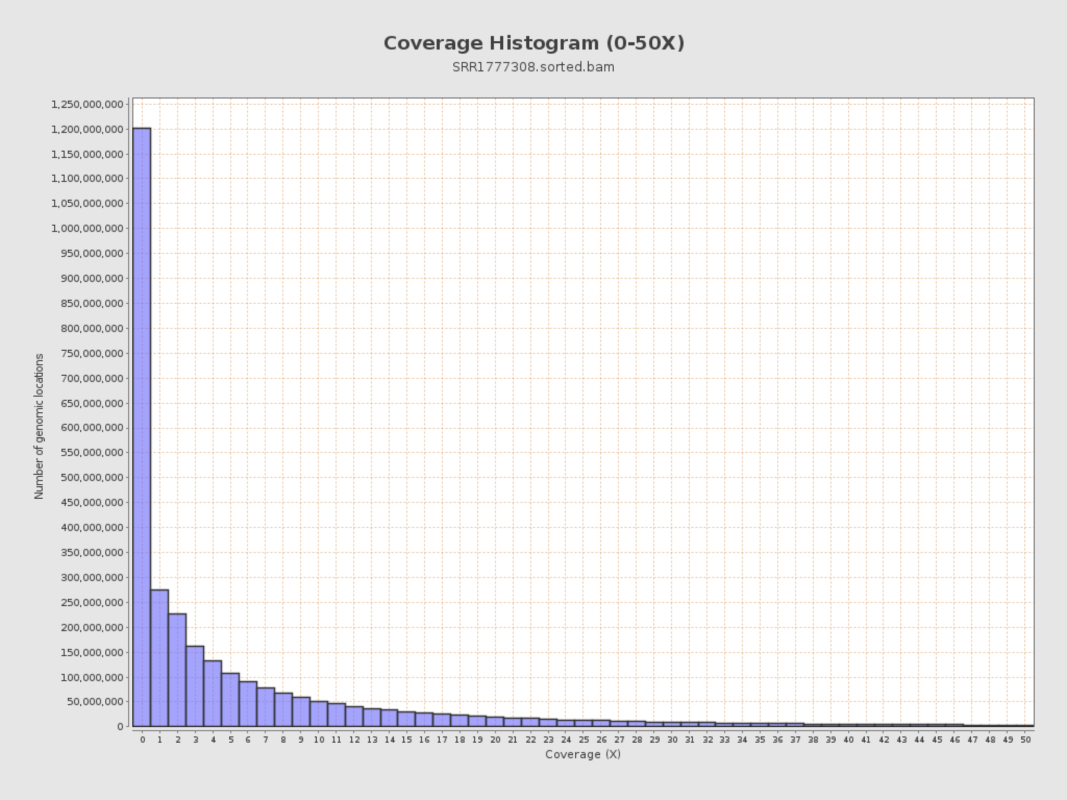
3. Results : Coverage across reference



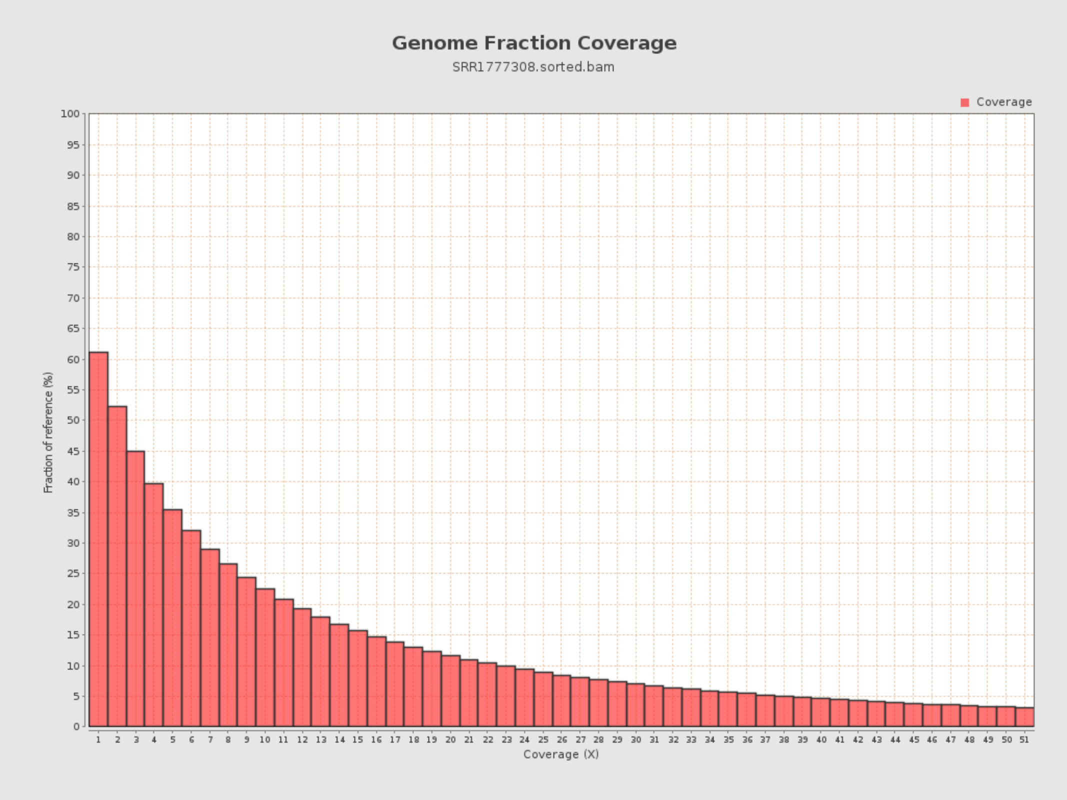
4. Results : Coverage Histogram



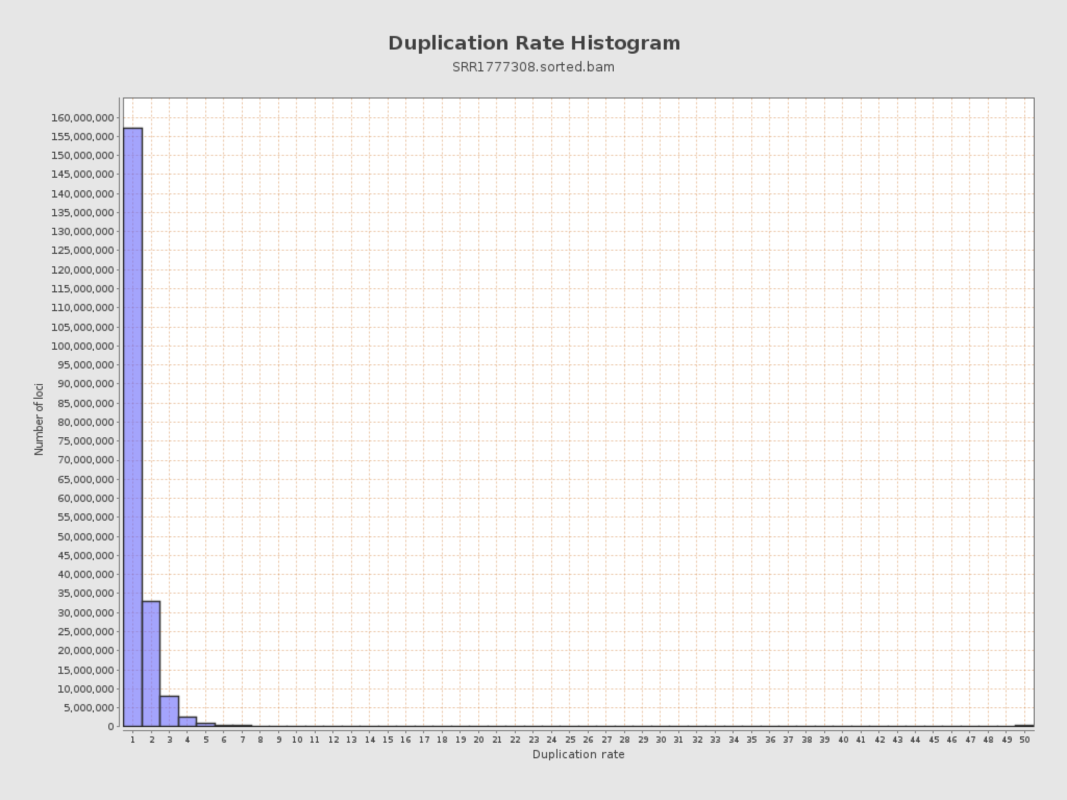
5. Results : Coverage Histogram (0-50X)



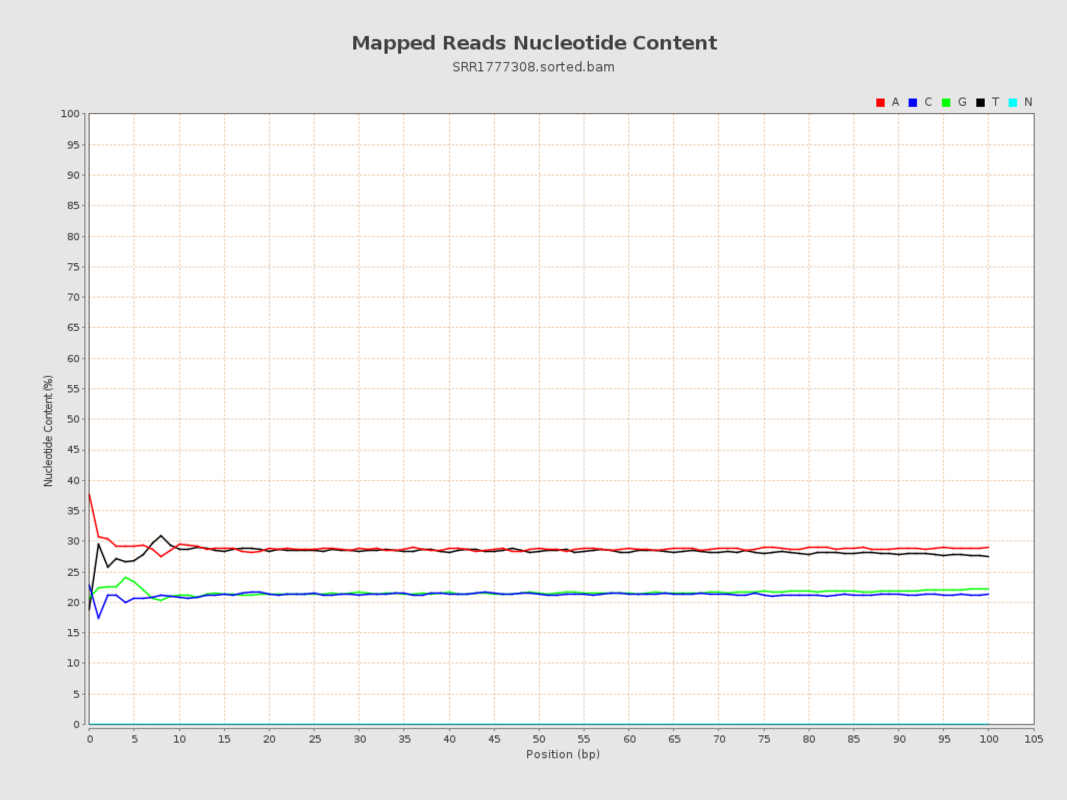
6. Results : Genome Fraction Coverage



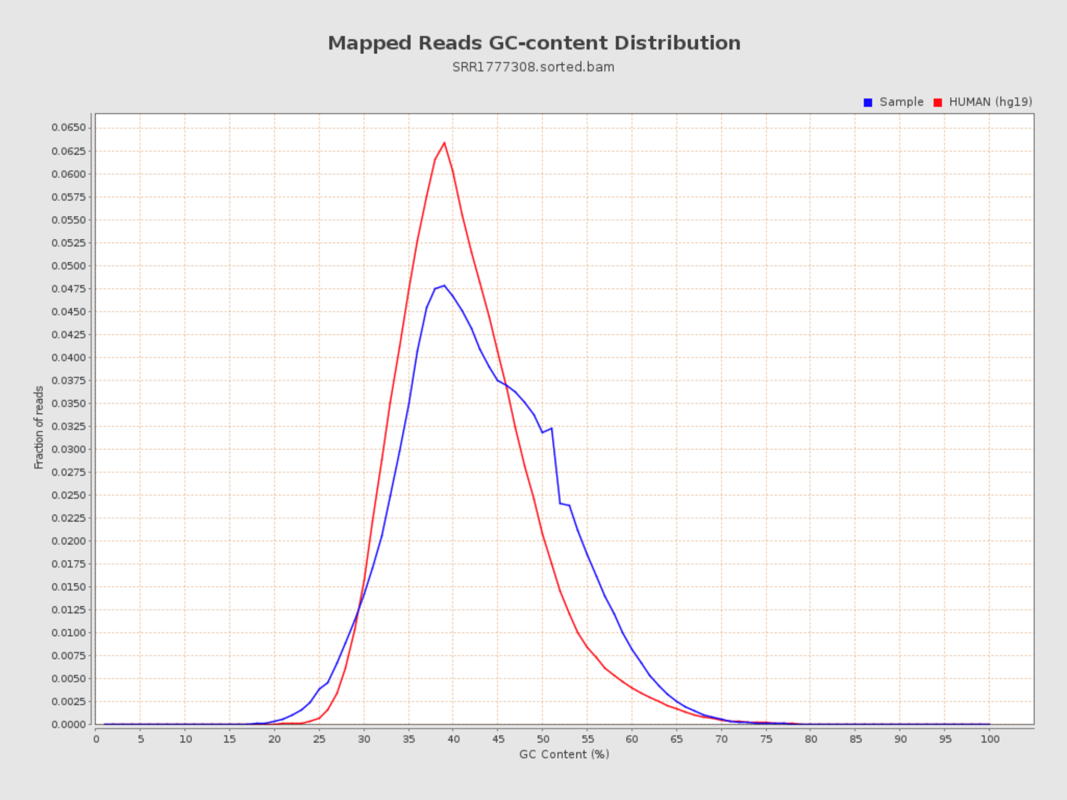
7. Results : Duplication Rate Histogram



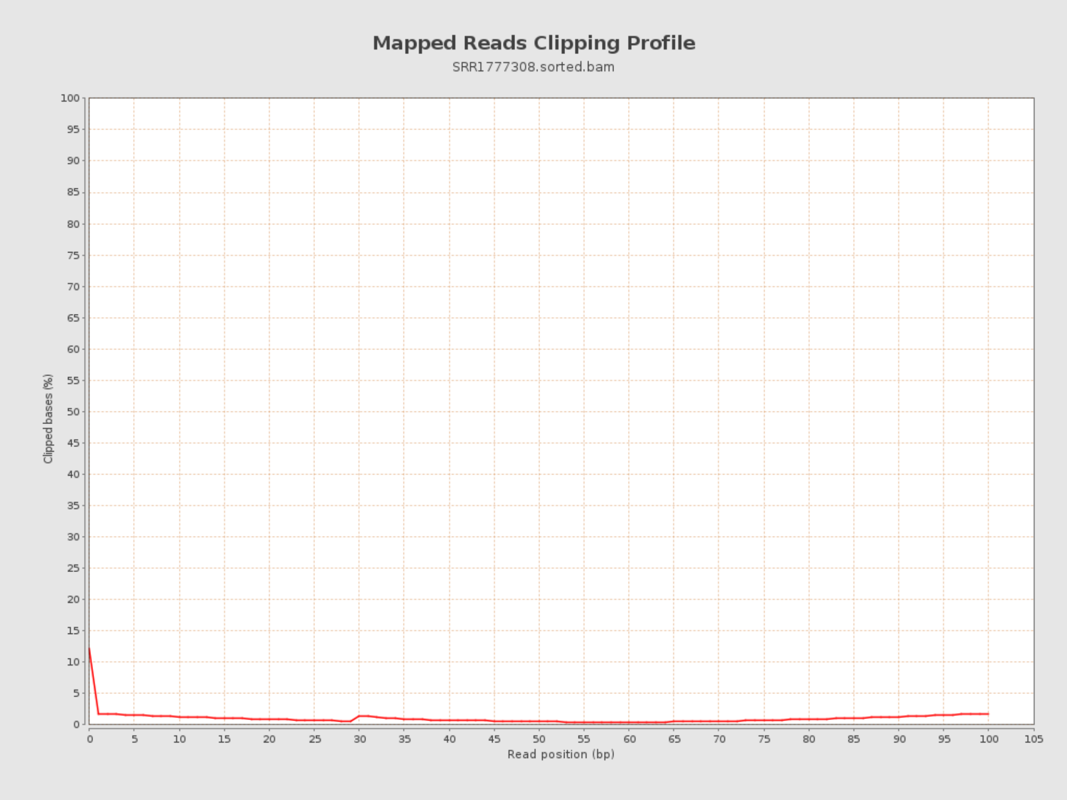
8. Results : Mapped Reads Nucleotide Content



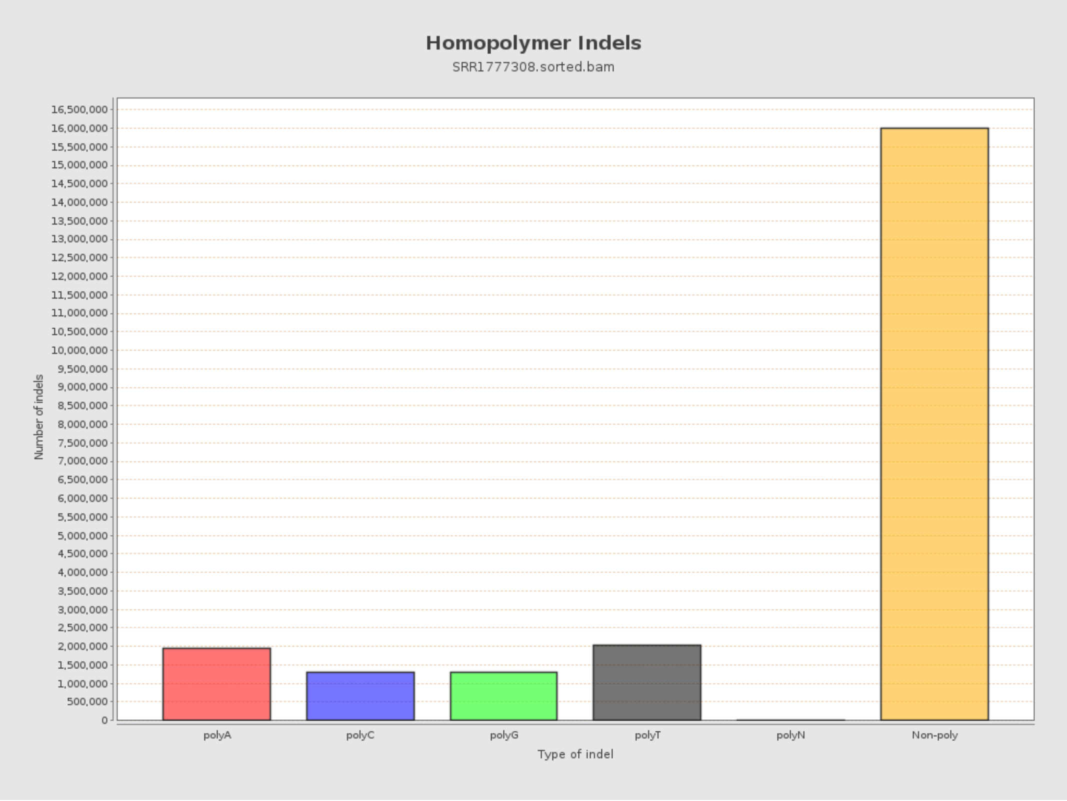
9. Results : Mapped Reads GC-content Distribution



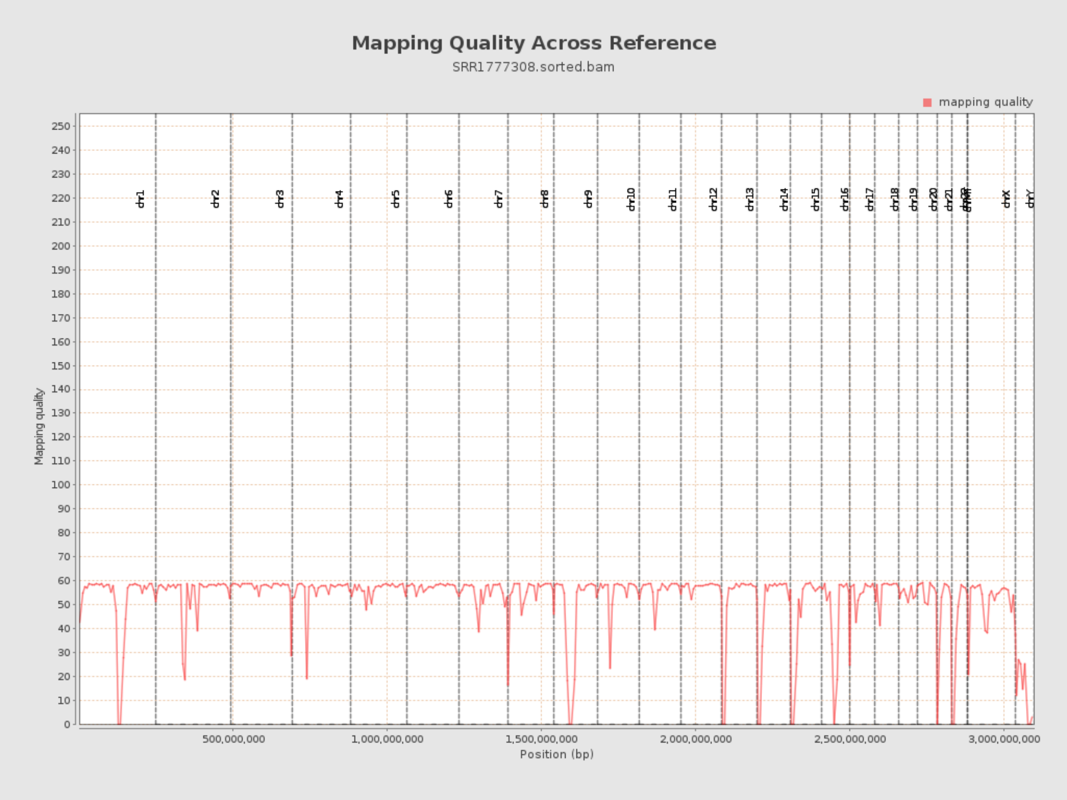
10. Results : Mapped Reads Clipping Profile



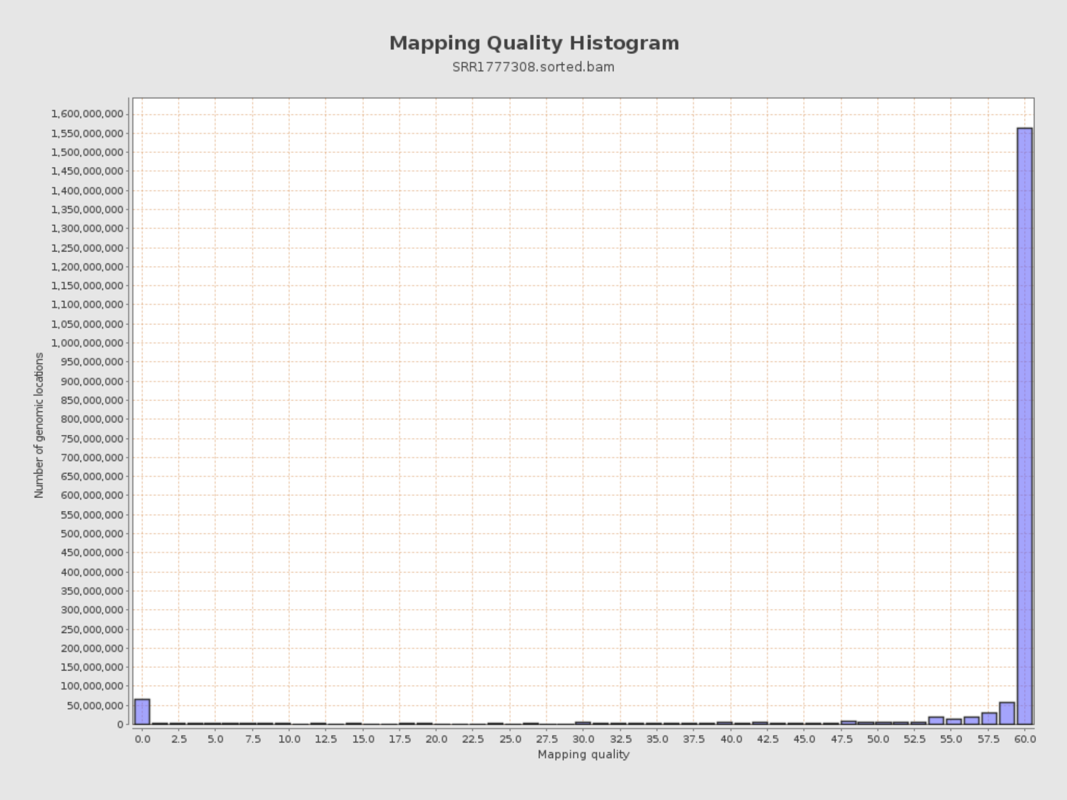
11. Results : Homopolymer Indels



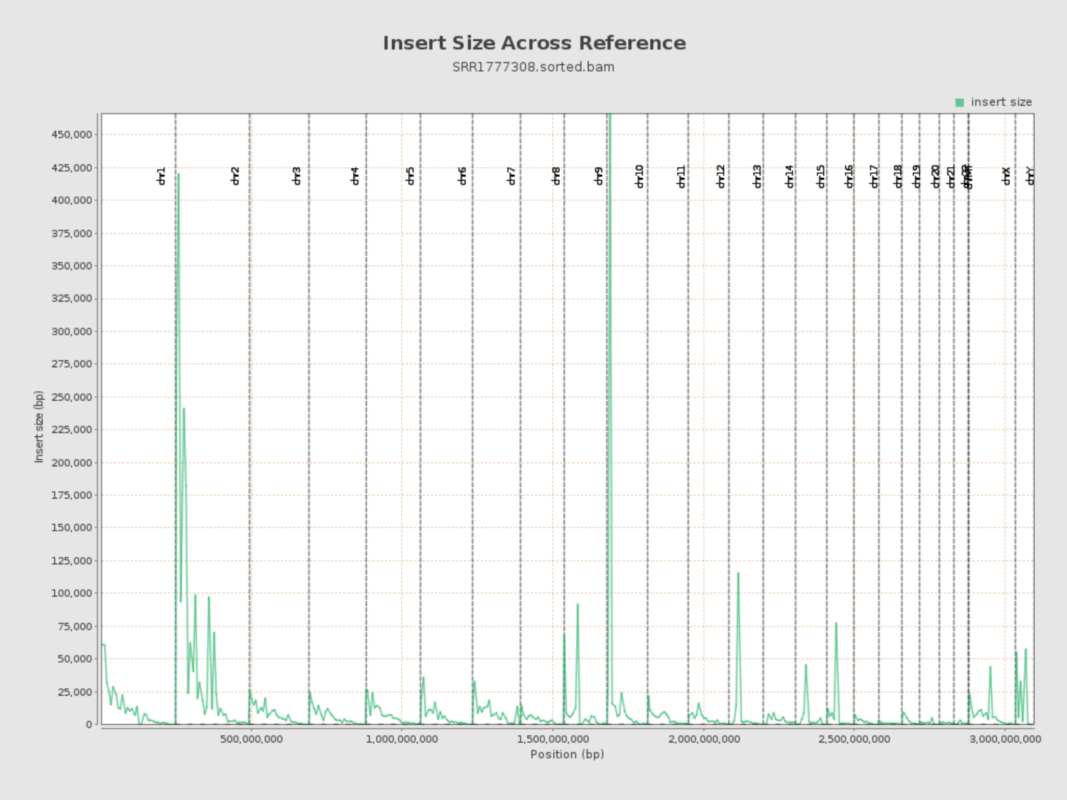
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram