Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/04 00:55:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777283.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_SRR1777283 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777283_1.fastq.gz SRR1777283_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 04 00:55:56 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777283.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	33,149,956
Mapped reads	32,785,527 / 98.9%
Unmapped reads	364,429 / 1.1%
Mapped paired reads	32,785,527 / 98.9%
Mapped reads, first in pair	16,394,309 / 49.45%
Mapped reads, second in pair	16,391,218 / 49.45%
Mapped reads, both in pair	32,626,874 / 98.42%
Mapped reads, singletons	158,653 / 0.48%
Secondary alignments	0
Supplementary alignments	1,233,876 / 3.72%
Read min/max/mean length	30 / 101 / 102.47
Duplicated reads (estimated)	15,930,096 / 48.05%
Duplication rate	36.21%
Clipped reads	5,010,036 / 15.11%

2.2. ACGT Content

Number/percentage of A's	853,339,638 / 26.36%
Number/percentage of C's	766,217,292 / 23.67%
Number/percentage of T's	851,064,366 / 26.29%
Number/percentage of G's	766,872,074 / 23.69%
Number/percentage of N's	119,427 / 0%

GC Percentage	47.35%

2.3. Coverage

Mean	1.0469
Standard Deviation	38.5688

2.4. Mapping Quality

Mean Mapping Quality	53.33

2.5. Insert size

Mean	276,712.89
Standard Deviation	5,257,267.74
P25/Median/P75	179 / 226 / 281

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	16,032,830
Insertions	1,097,550
Mapped reads with at least one insertion	3.04%
Deletions	850,141
Mapped reads with at least one deletion	2.36%
Homopolymer indels	30.45%

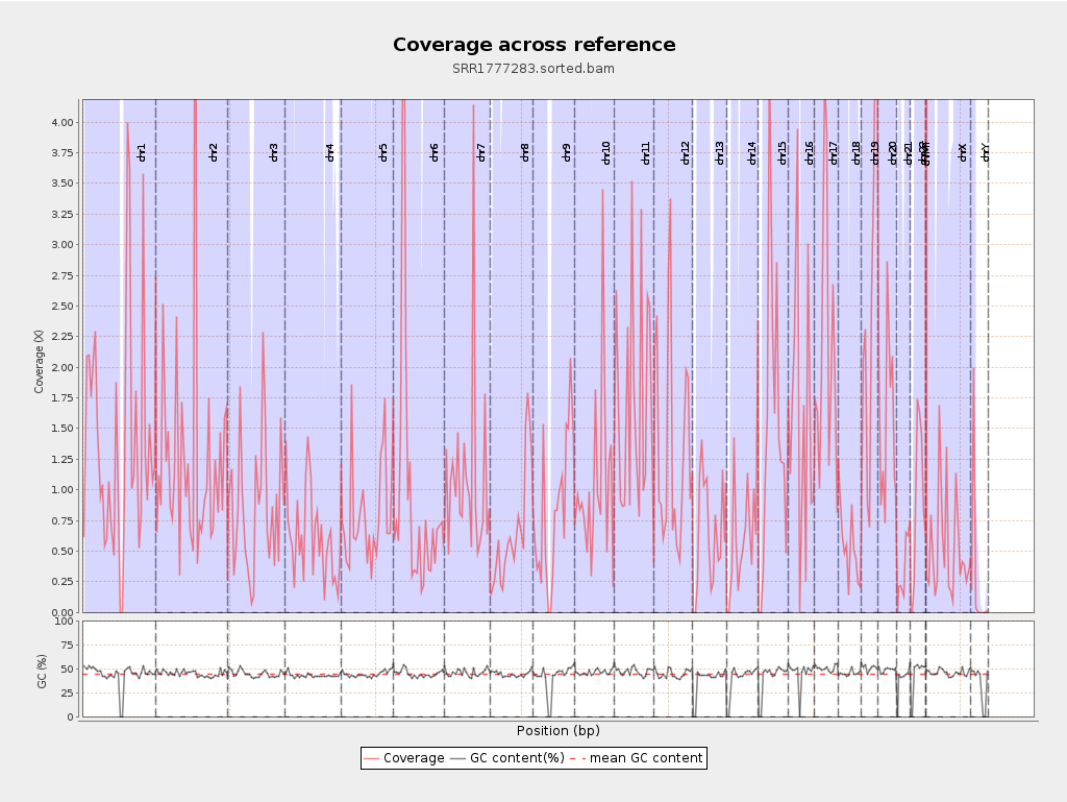
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard

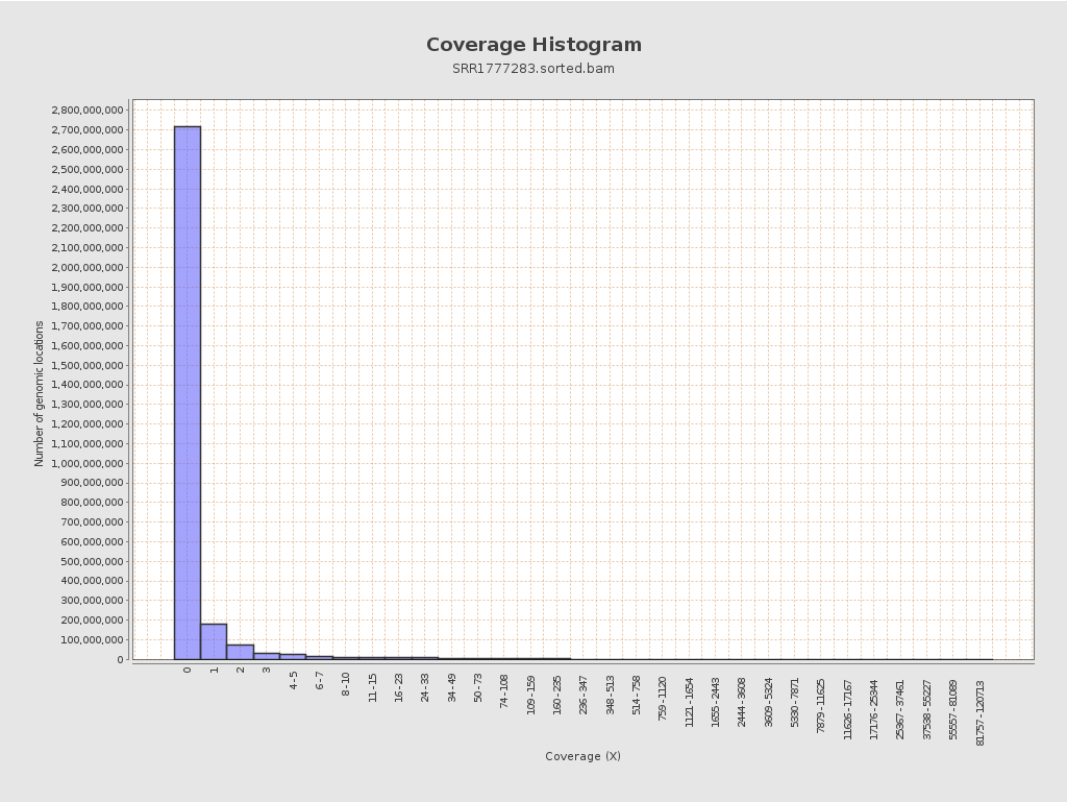
		bases	coverage	deviation
chr1	249250621	345583952	1.3865	17.7891
chr2	243199373	307612228	1.2649	88.6759
chr3	198022430	167141140	0.8441	11.5215
chr4	191154276	117025970	0.6122	22.6652
chr5	180915260	148141091	0.8188	19.6225
chr6	171115067	158968065	0.929	22.5036
chr7	159138663	173630857	1.0911	30.0285
chr8	146364022	99786161	0.6818	11.5084
chr9	141213431	115633434	0.8189	19.2304
chr10	135534747	144797419	1.0683	81.752
chr11	135006516	229848743	1.7025	33.2302
chr12	133851895	184285658	1.3768	15.688
chr13	115169878	73803173	0.6408	10.2928
chr14	107349540	63995980	0.5961	19.6684
chr15	102531392	148435653	1.4477	13.8393
chr16	90354753	138113000	1.5286	63.5994
chr17	81195210	174237734	2.1459	24.3812
chr18	78077248	42439420	0.5436	11.632
chr19	59128983	147341440	2.4919	27.1354
chr20	63025520	97106495	1.5407	17.8053
chr21	48129895	18011569	0.3742	5.7079
chr22	51304566	47153565	0.9191	15.4164
chrMT	16571	664956	40.1277	12.5316
chrX	155270560	80154626	0.5162	11.4242

chrY	59373566	16857552	0.2839	85.5088

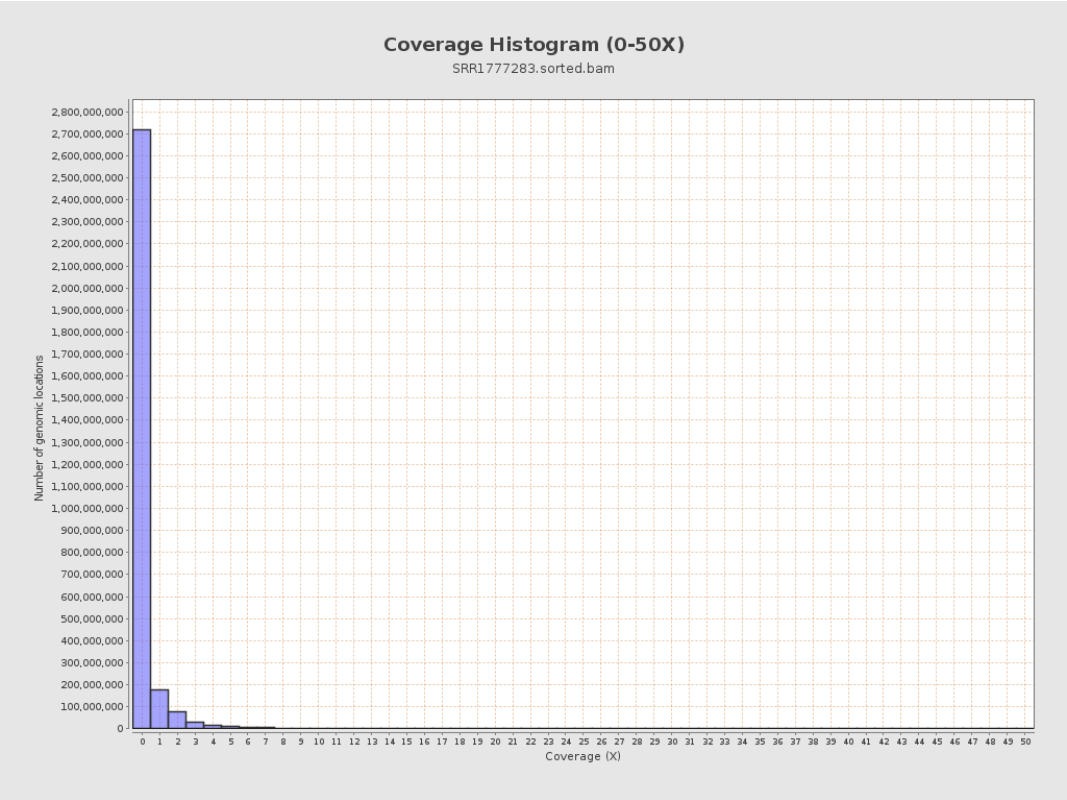
3. Results : Coverage across reference



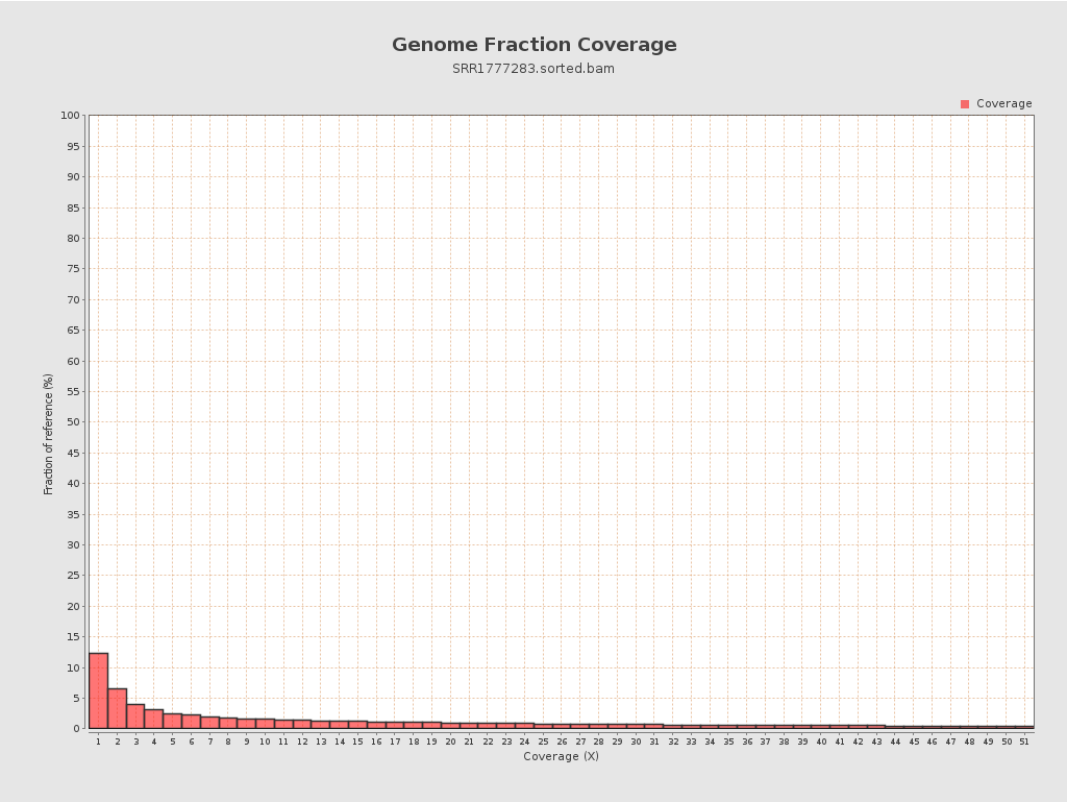
4. Results : Coverage Histogram



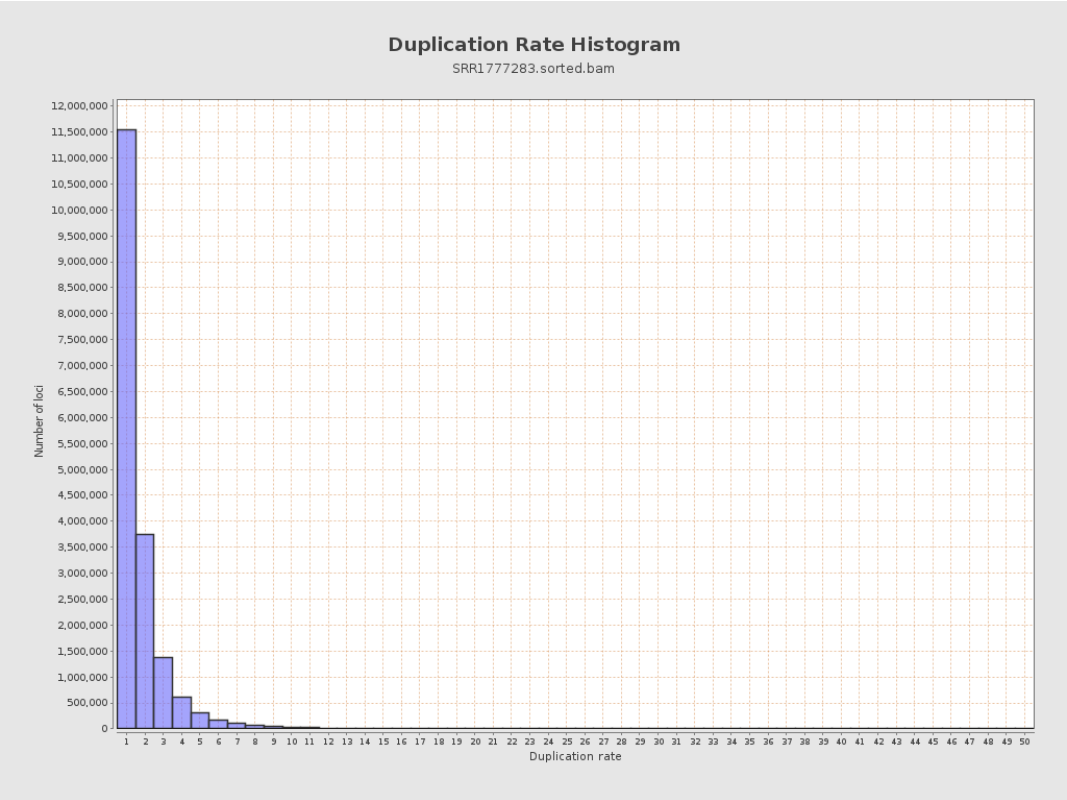
5. Results : Coverage Histogram (0-50X)



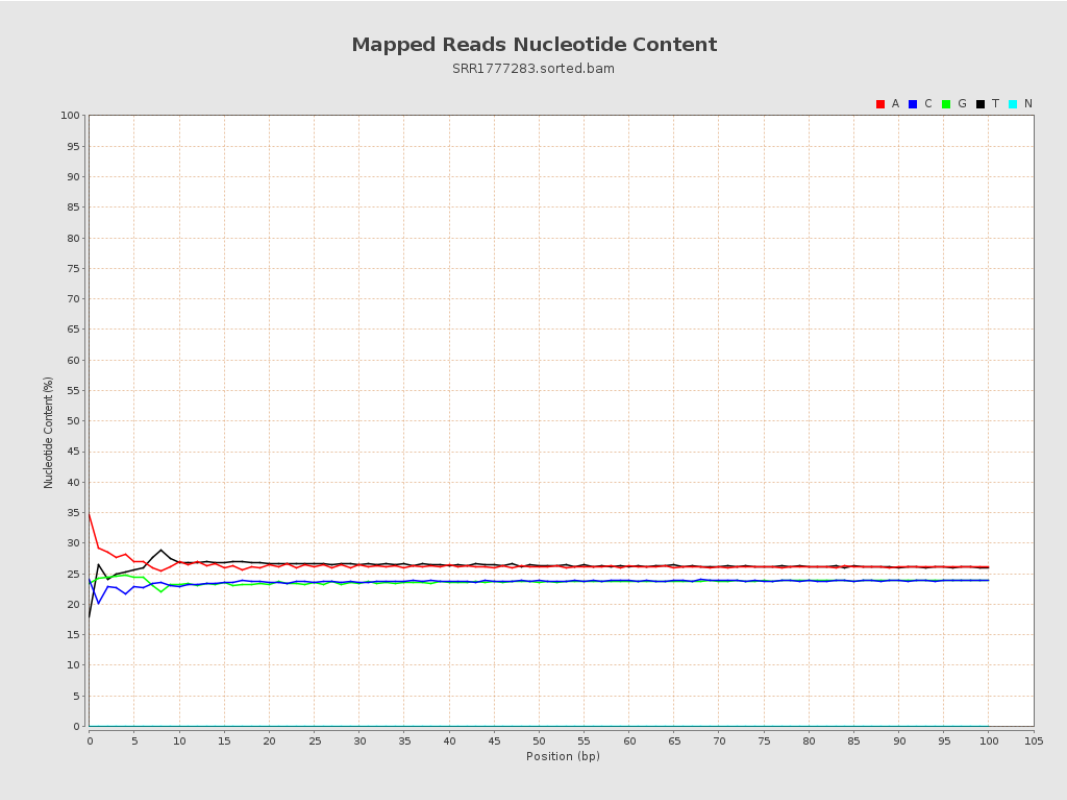
6. Results : Genome Fraction Coverage



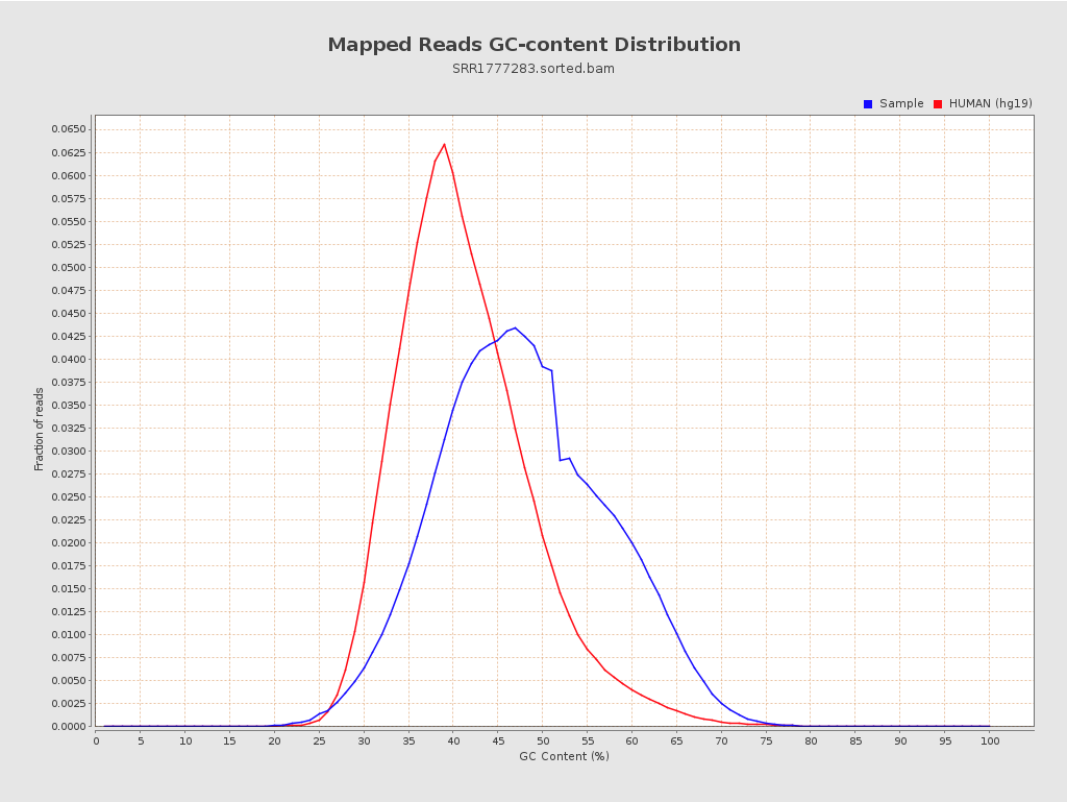
7. Results : Duplication Rate Histogram



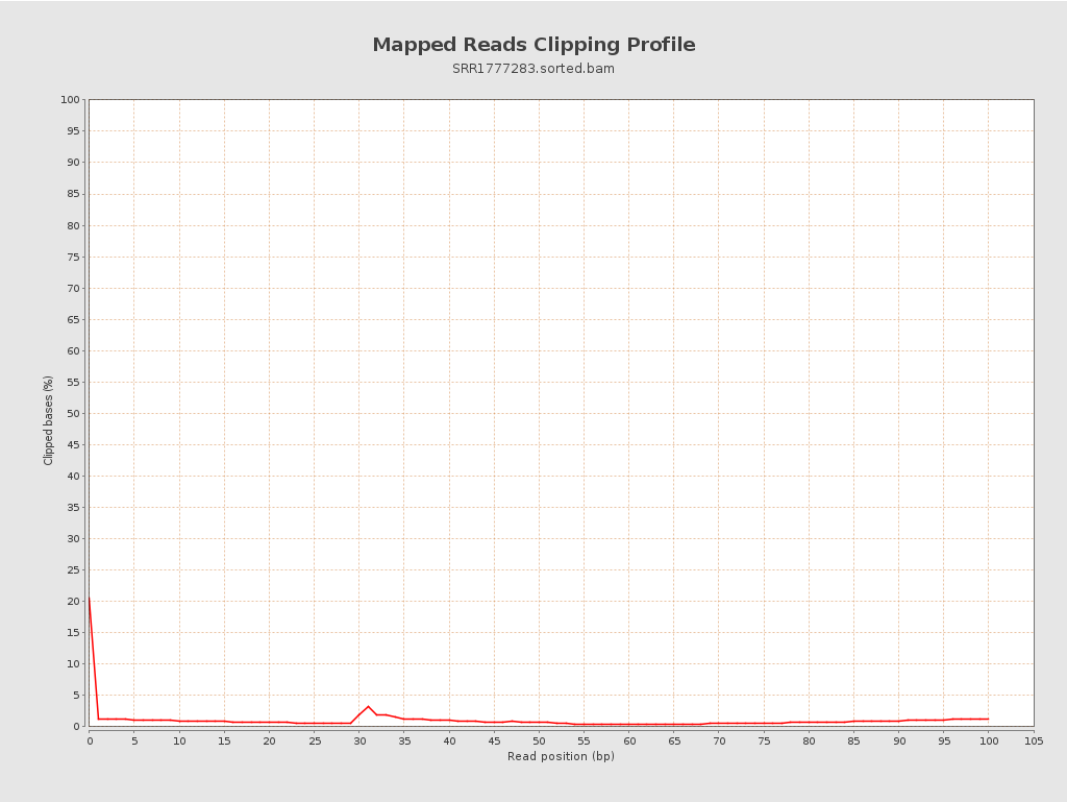
8. Results : Mapped Reads Nucleotide Content



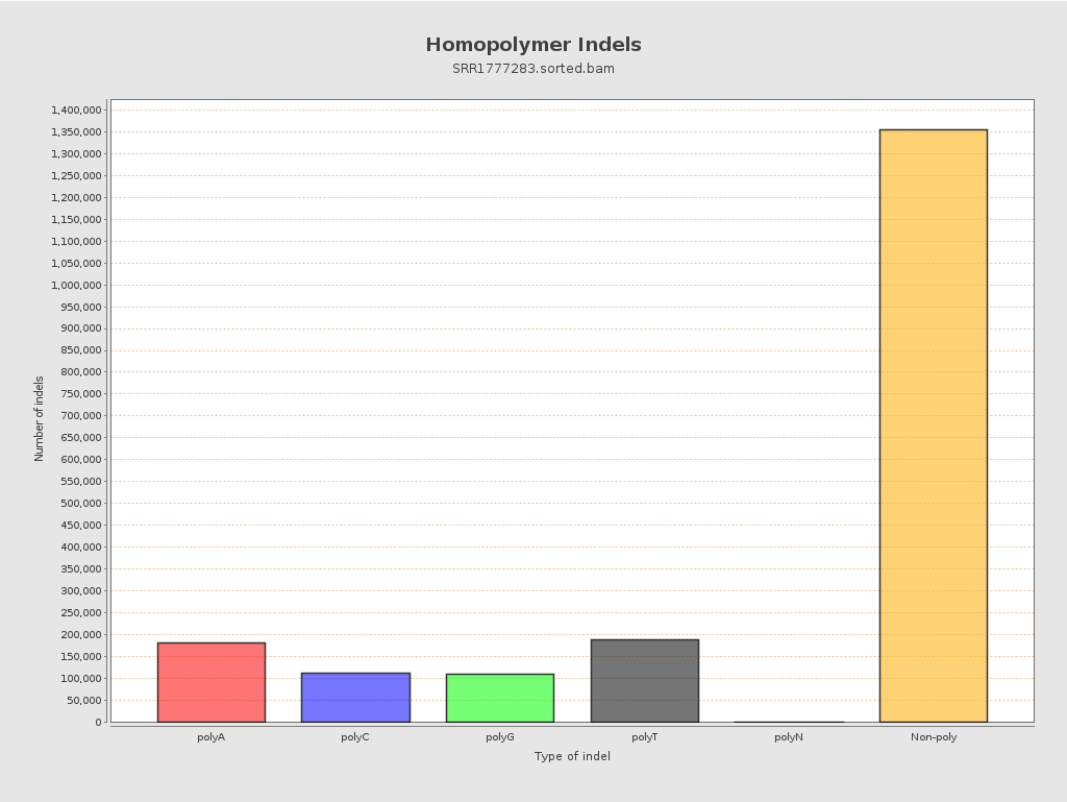
9. Results : Mapped Reads GC-content Distribution



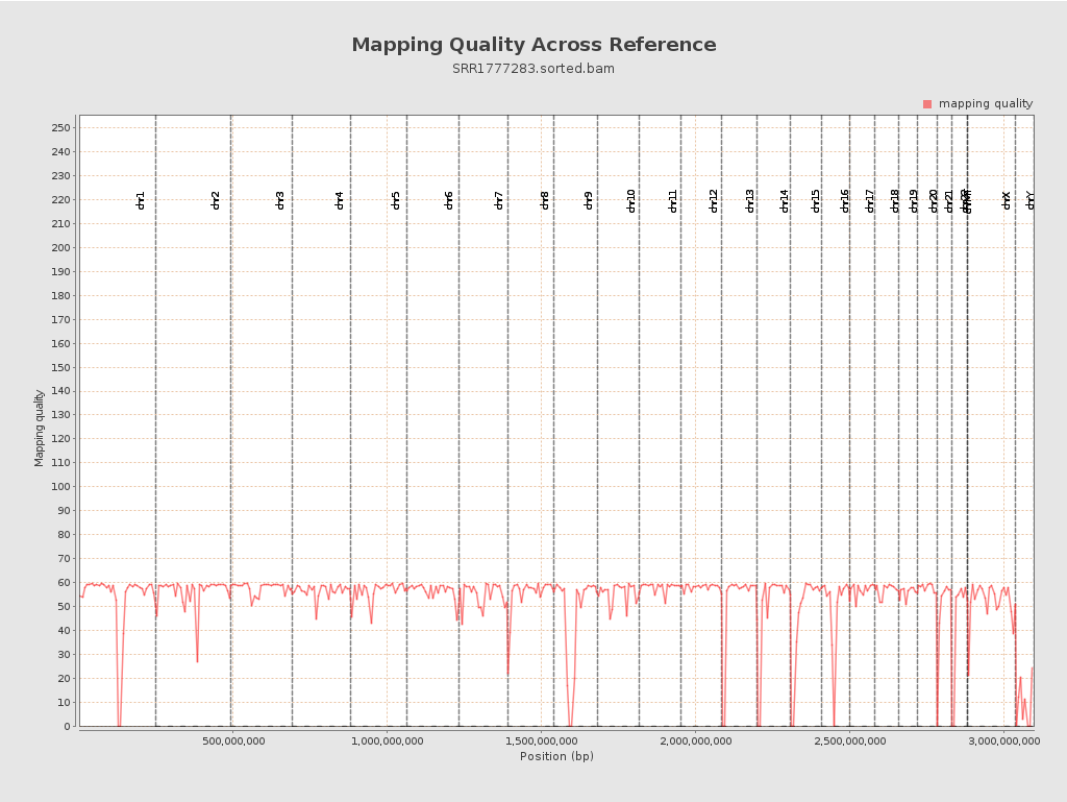
10. Results : Mapped Reads Clipping Profile



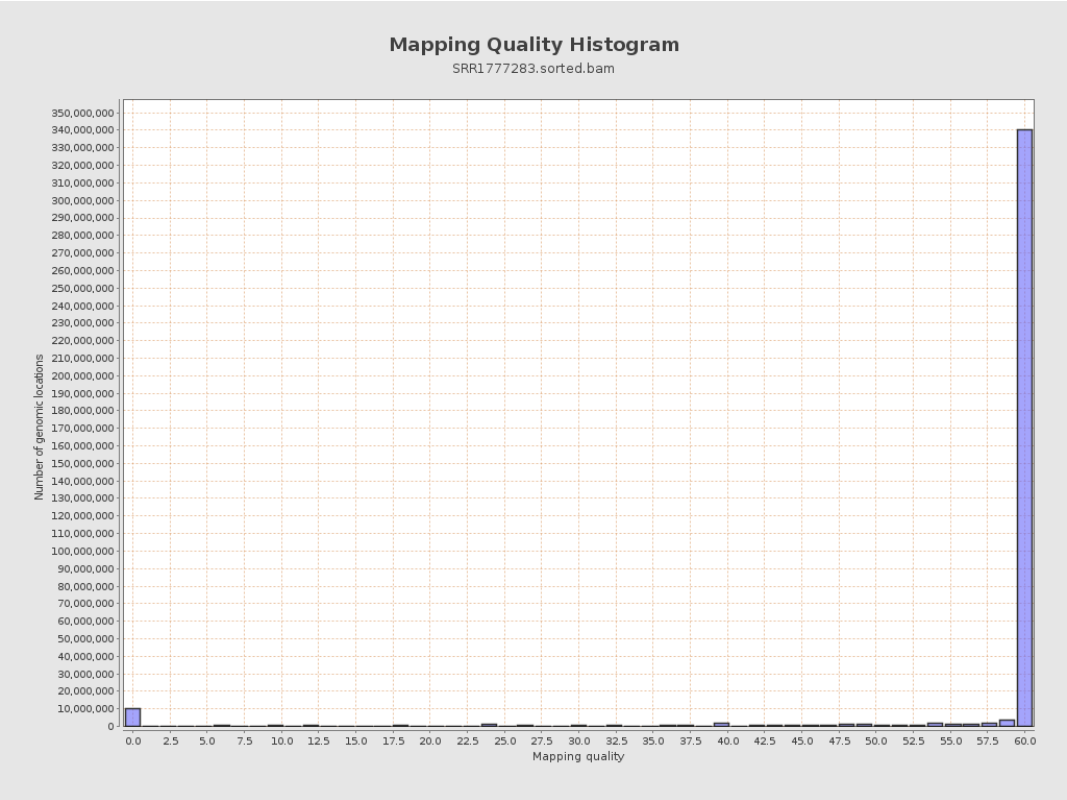
11. Results : Homopolymer Indels



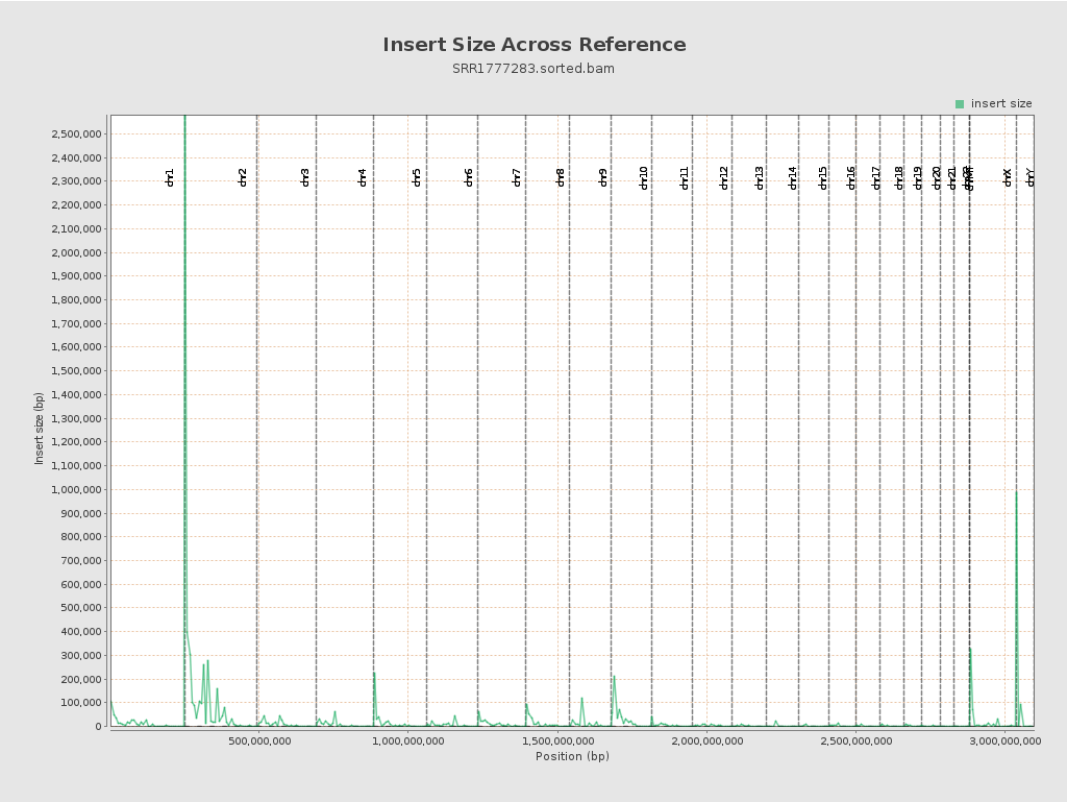
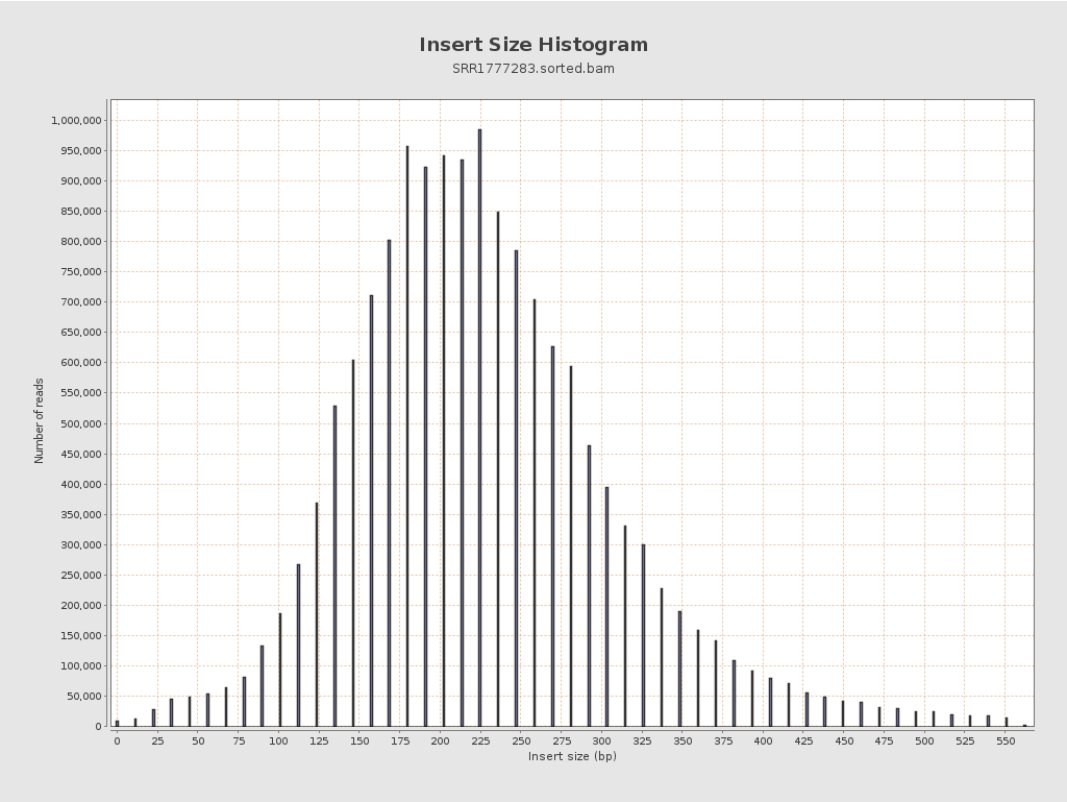
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram