

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/03 09:02:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777279.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_SRR1777279 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777279_1.fastq.gz SRR1777279_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 03 09:02:55 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777279.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,196,784
Mapped reads	11,398,263 / 93.45%
Unmapped reads	798,521 / 6.55%
Mapped paired reads	11,398,263 / 93.45%
Mapped reads, first in pair	5,718,269 / 46.88%
Mapped reads, second in pair	5,679,994 / 46.57%
Mapped reads, both in pair	11,151,474 / 91.43%
Mapped reads, singletons	246,789 / 2.02%
Secondary alignments	0
Supplementary alignments	1,131,204 / 9.27%
Read min/max/mean length	30 / 101 / 104.62
Duplicated reads (estimated)	5,366,697 / 44%
Duplication rate	8.34%
Clipped reads	5,819,254 / 47.71%

2.2. ACGT Content

Number/percentage of A's	295,894,516 / 28.79%
Number/percentage of C's	219,473,658 / 21.35%
Number/percentage of T's	289,759,734 / 28.19%
Number/percentage of G's	222,660,215 / 21.66%
Number/percentage of N's	18,225 / 0%

GC Percentage	43.02%
---------------	--------

2.3. Coverage

Mean	0.3334
Standard Deviation	49.9174

2.4. Mapping Quality

Mean Mapping Quality	49.01
----------------------	-------

2.5. Insert size

Mean	621,278.64
Standard Deviation	7,522,458.17
P25/Median/P75	104 / 156 / 226

2.6. Mismatches and indels

General error rate	1.88%
Mismatches	15,547,444
Insertions	1,121,128
Mapped reads with at least one insertion	8.58%
Deletions	1,118,654
Mapped reads with at least one deletion	8.62%
Homopolymer indels	21.53%

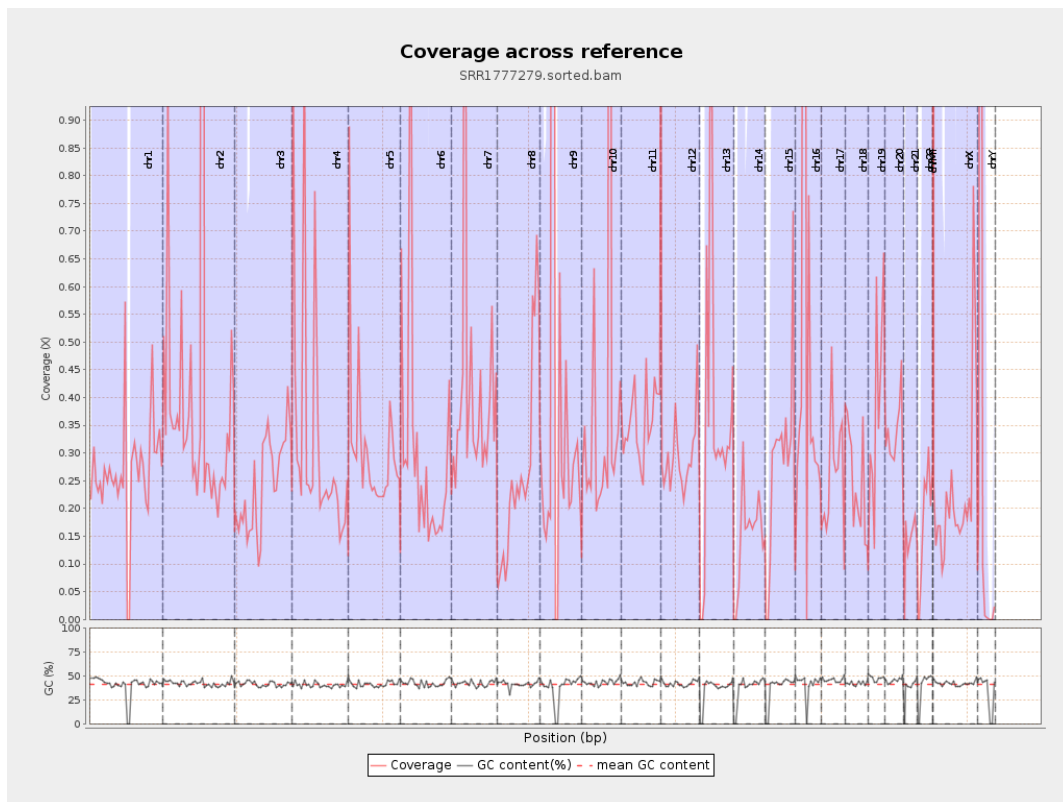
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

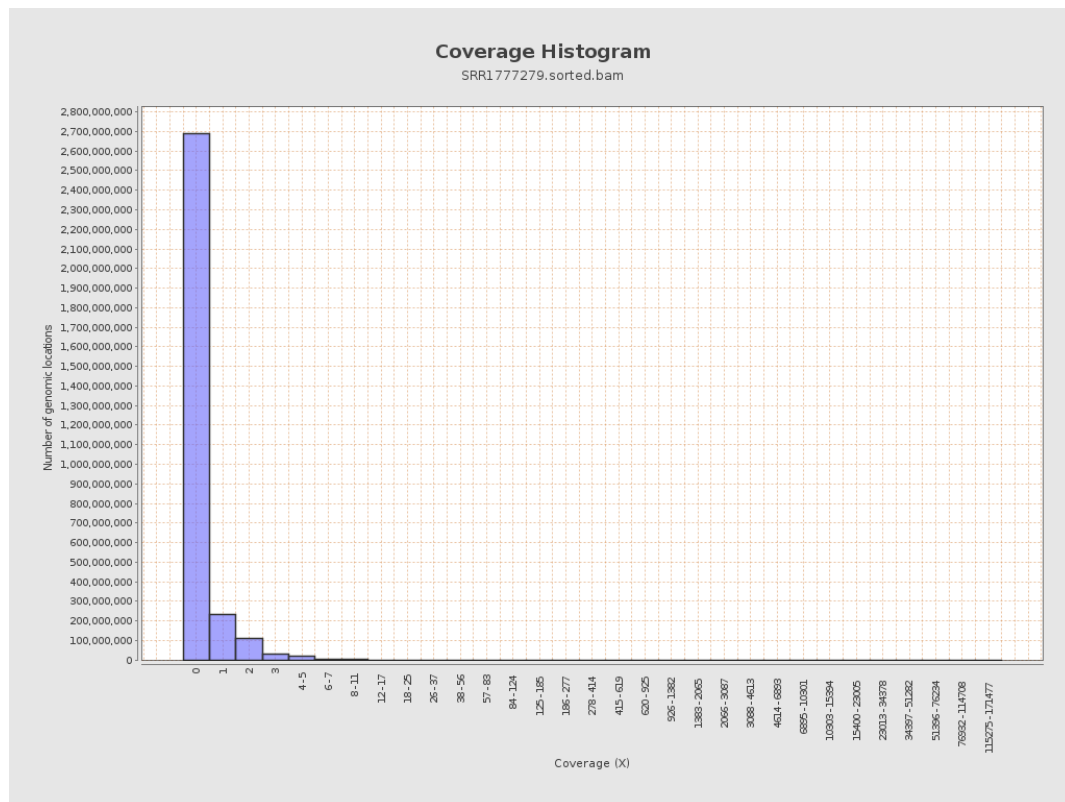
		bases	coverage	deviation
chr1	249250621	66386767	0.2663	14.3093
chr2	243199373	142349423	0.5853	122.054
chr3	198022430	48360943	0.2442	5.9323
chr4	191154276	61747503	0.323	29.7857
chr5	180915260	55822279	0.3086	19.8573
chr6	171115067	50335175	0.2942	26.8632
chr7	159138663	67277336	0.4228	34.3895
chr8	146364022	39884351	0.2725	9.3011
chr9	141213431	60283119	0.4269	41.3381
chr10	135534747	56745081	0.4187	110.038
chr11	135006516	48217896	0.3572	14.8805
chr12	133851895	39397120	0.2943	7.2362
chr13	115169878	41105534	0.3569	19.7799
chr14	107349540	16639041	0.155	21.0652
chr15	102531392	29231526	0.2851	7.7145
chr16	90354753	47199199	0.5224	77.5526
chr17	81195210	21401738	0.2636	7.6125
chr18	78077248	19636275	0.2515	18.1888
chr19	59128983	22473008	0.3801	24.0138
chr20	63025520	21418012	0.3398	13.7514
chr21	48129895	6845504	0.1422	3.8235
chr22	51304566	8967049	0.1748	13.6641
chrMT	16571	4714304	284.4912	49.6867
chrX	155270560	33951739	0.2187	15.7607

chrY	59373566	21766539	0.3666	114.5491
------	----------	----------	--------	----------

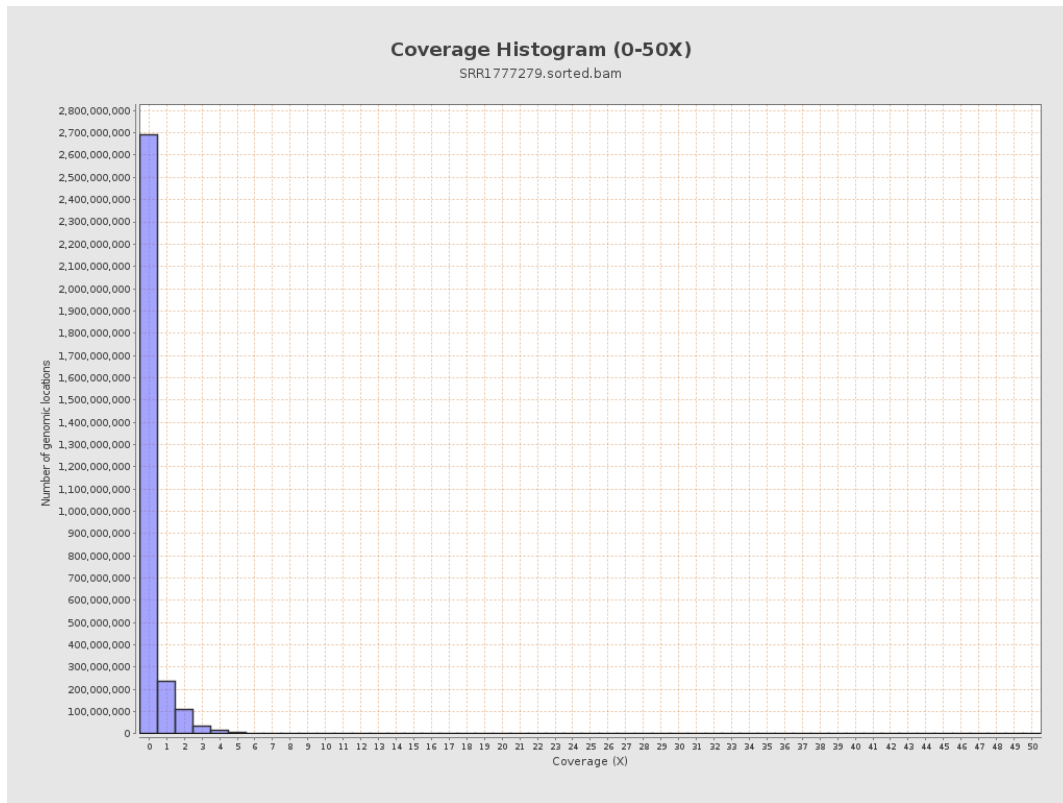
3. Results : Coverage across reference



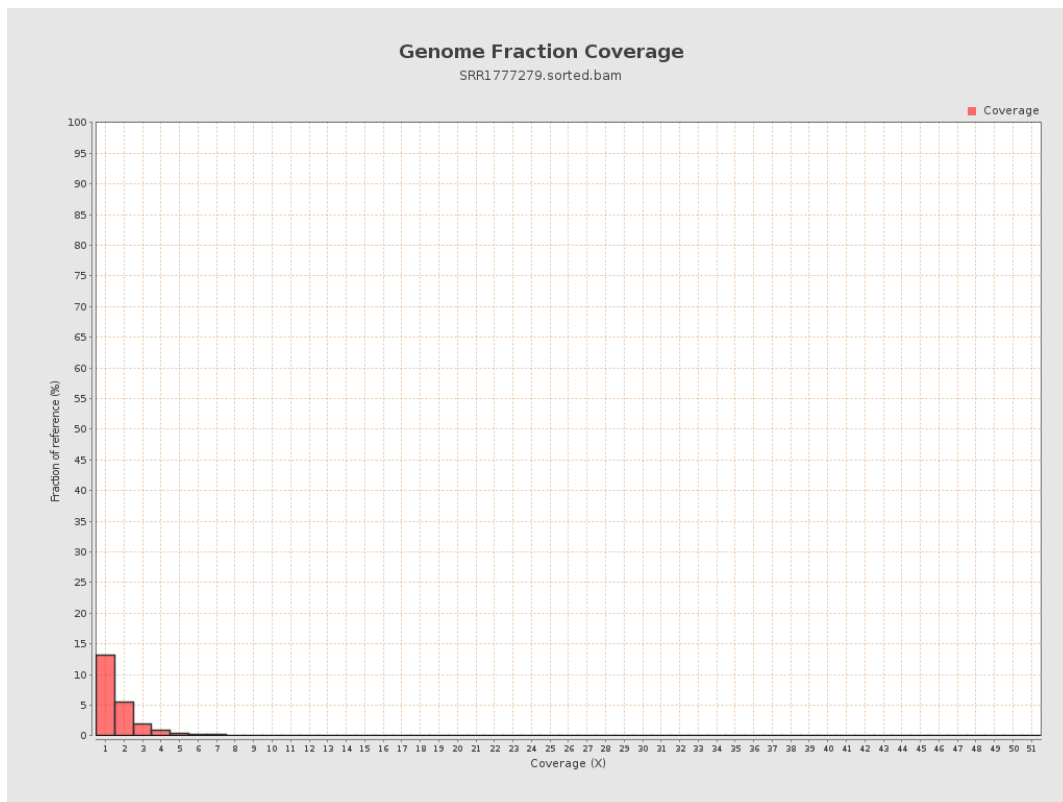
4. Results : Coverage Histogram



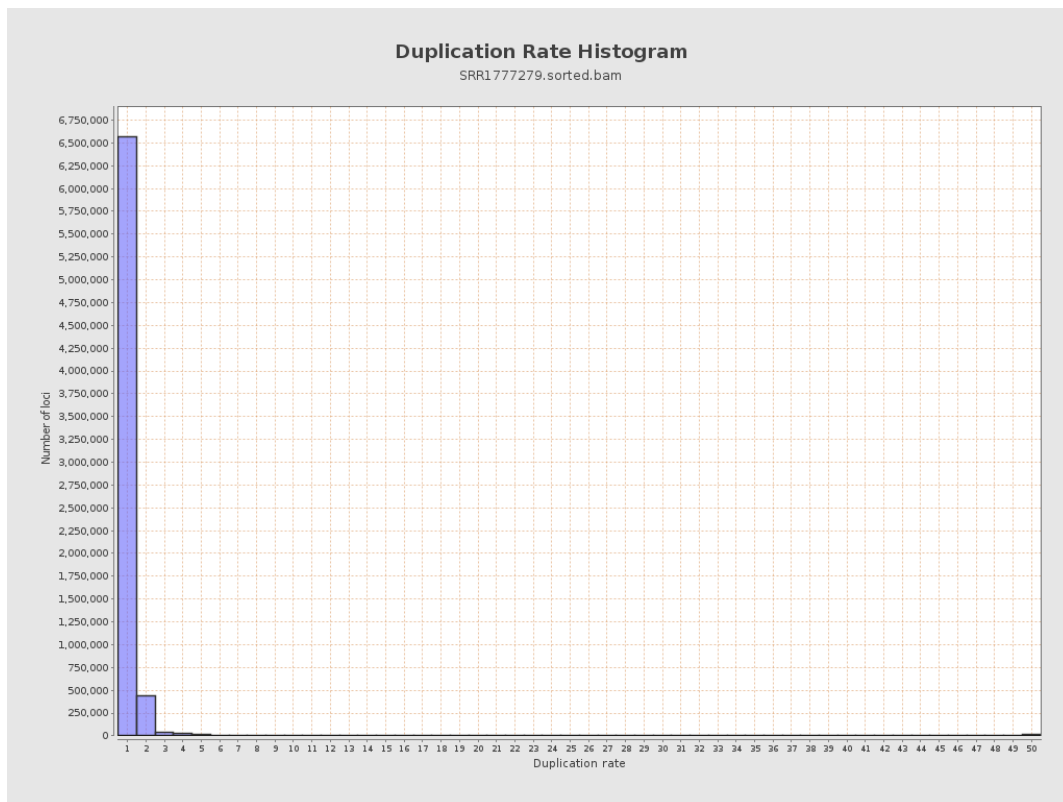
5. Results : Coverage Histogram (0-50X)



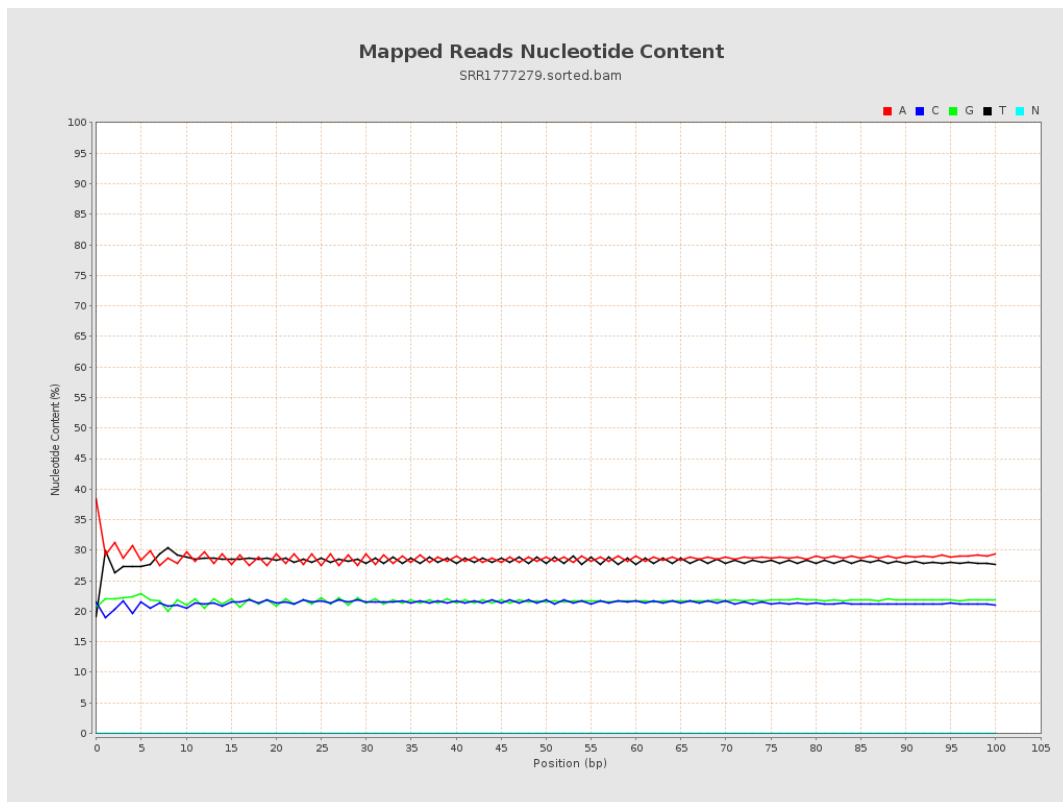
6. Results : Genome Fraction Coverage



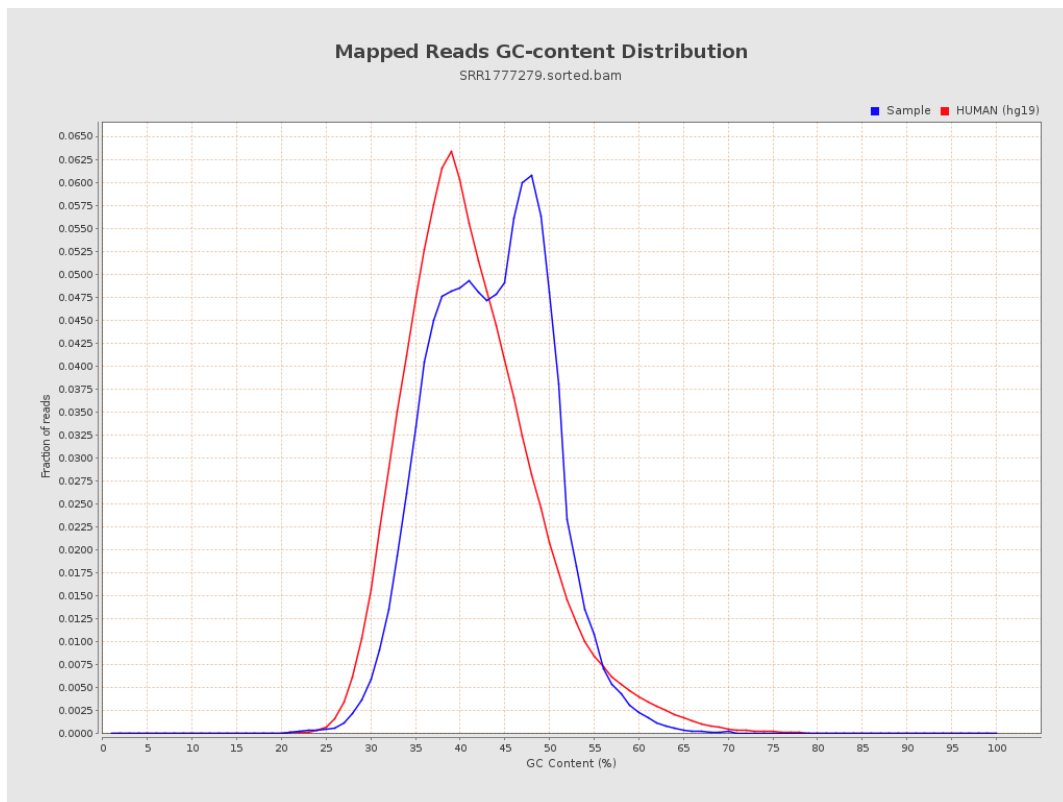
7. Results : Duplication Rate Histogram



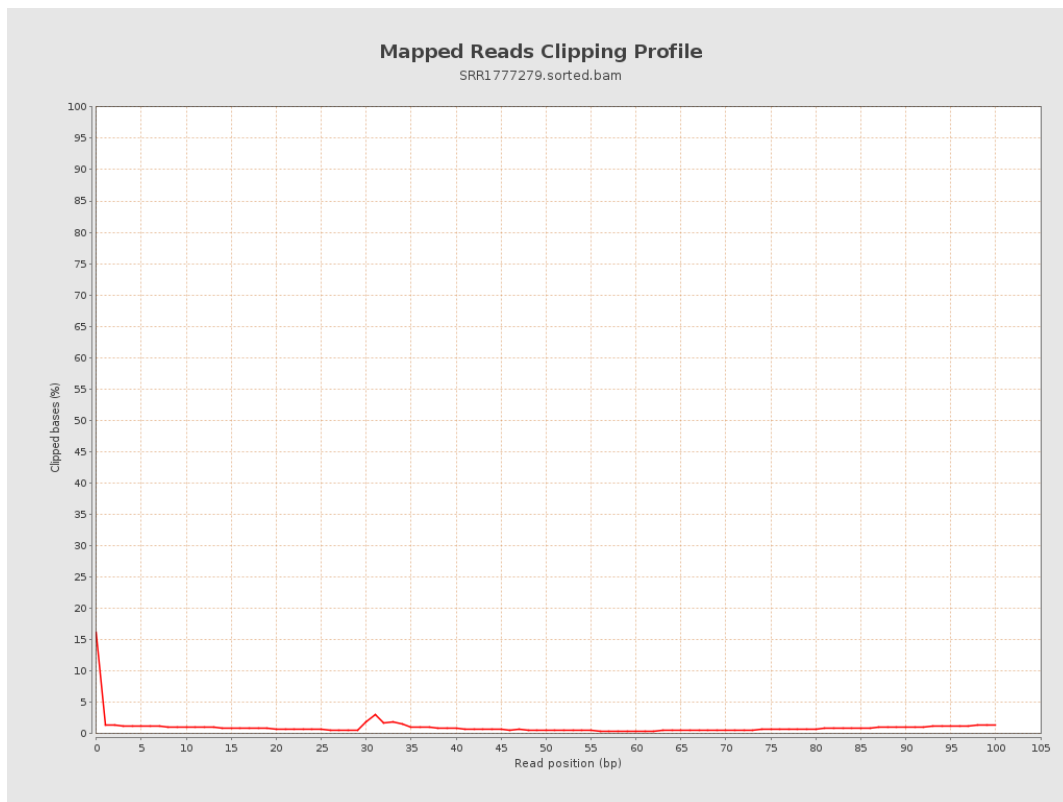
8. Results : Mapped Reads Nucleotide Content



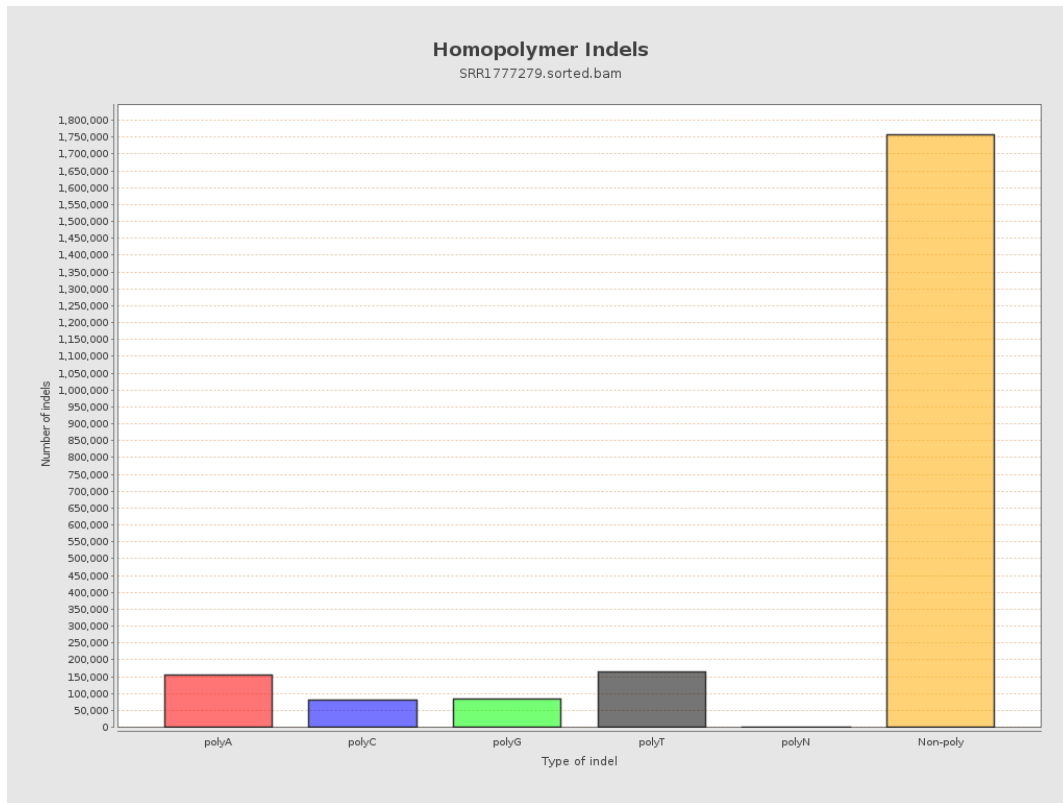
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



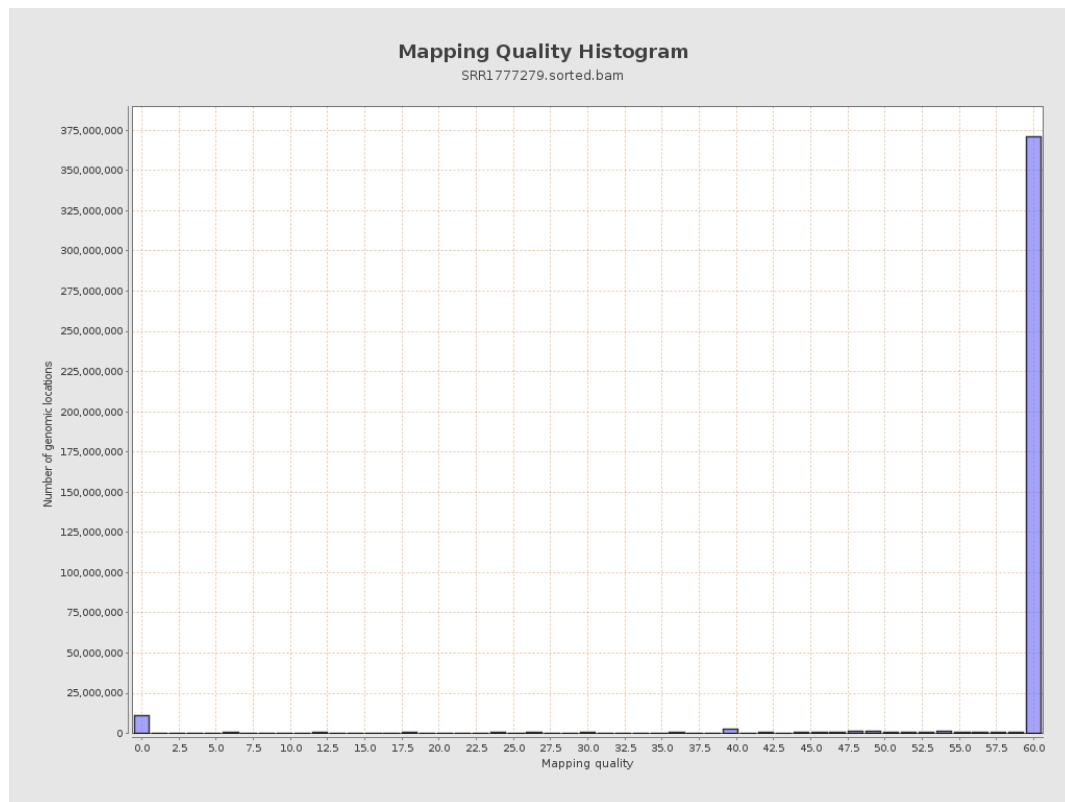
11. Results : Homopolymer Indels



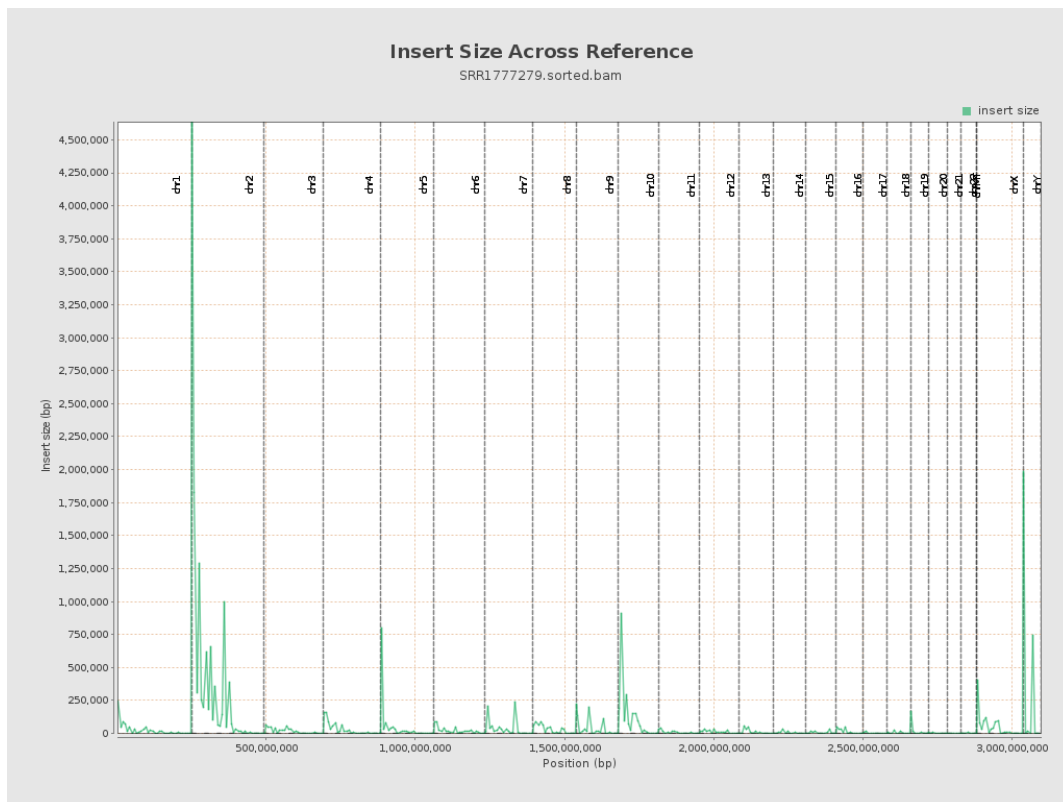
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

