

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/04 00:20:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777282.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_SRR1777282 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777282_1.fastq.gz SRR1777282_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 04 00:20:53 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1777282.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	33,661,894
Mapped reads	33,291,489 / 98.9%
Unmapped reads	370,405 / 1.1%
Mapped paired reads	33,291,489 / 98.9%
Mapped reads, first in pair	16,647,214 / 49.45%
Mapped reads, second in pair	16,644,275 / 49.45%
Mapped reads, both in pair	33,131,928 / 98.43%
Mapped reads, singletons	159,561 / 0.47%
Secondary alignments	0
Supplementary alignments	1,247,035 / 3.7%
Read min/max/mean length	30 / 101 / 102.47
Duplicated reads (estimated)	16,267,186 / 48.33%
Duplication rate	36.49%
Clipped reads	5,062,618 / 15.04%

2.2. ACGT Content

Number/percentage of A's	867,580,665 / 26.39%
Number/percentage of C's	777,333,674 / 23.64%
Number/percentage of T's	865,221,003 / 26.31%
Number/percentage of G's	777,826,799 / 23.66%
Number/percentage of N's	135,423 / 0%

GC Percentage	47.3%
---------------	-------

2.3. Coverage

Mean	1.0632
Standard Deviation	38.882

2.4. Mapping Quality

Mean Mapping Quality	53.35
----------------------	-------

2.5. Insert size

Mean	274,137.3
Standard Deviation	5,236,916.5
P25/Median/P75	179 / 225 / 281

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	16,182,613
Insertions	1,105,654
Mapped reads with at least one insertion	3.02%
Deletions	860,593
Mapped reads with at least one deletion	2.35%
Homopolymer indels	30.5%

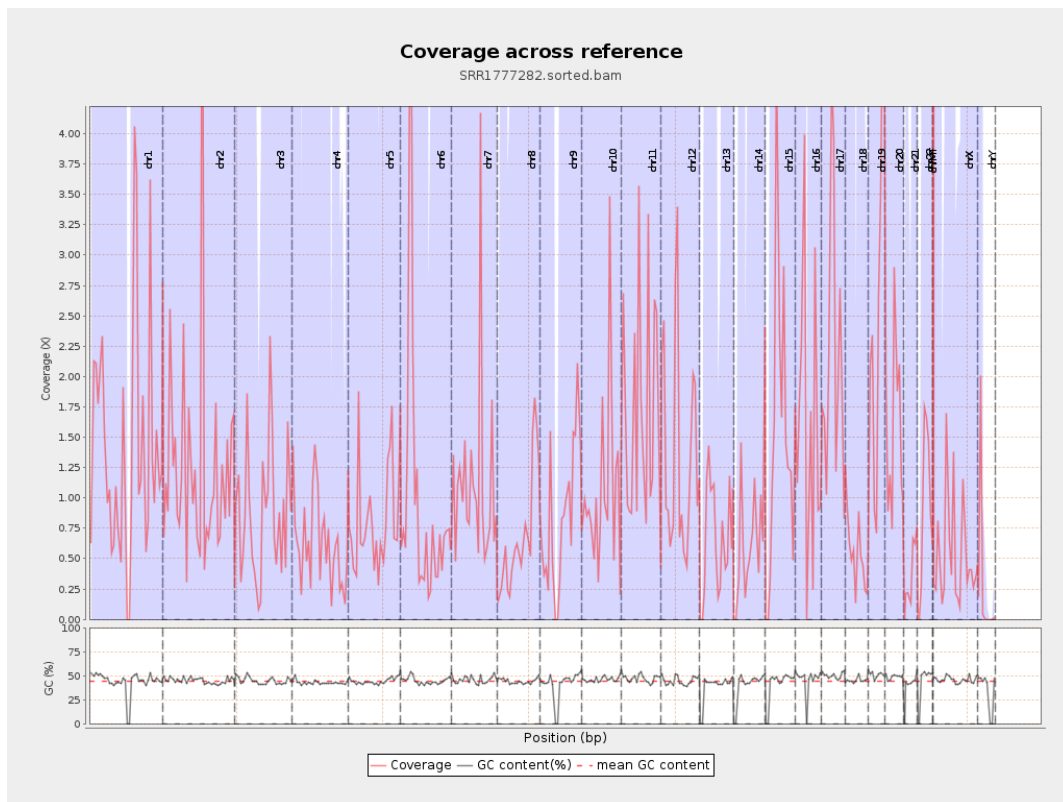
2.7. Chromosome stats

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

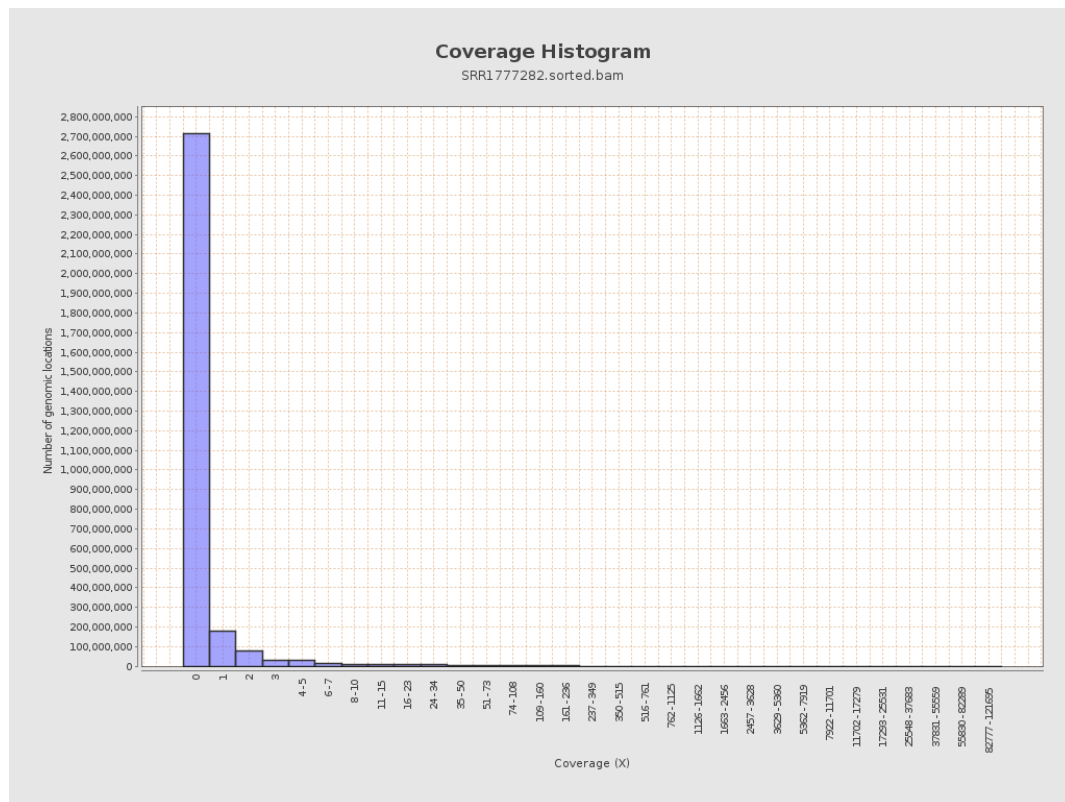
		bases	coverage	deviation
chr1	249250621	351518544	1.4103	18.095
chr2	243199373	312035460	1.283	89.428
chr3	198022430	170094566	0.859	11.6888
chr4	191154276	119187095	0.6235	22.7864
chr5	180915260	150619196	0.8325	19.7438
chr6	171115067	161330278	0.9428	22.6335
chr7	159138663	176335390	1.1081	30.2703
chr8	146364022	101612069	0.6942	11.7658
chr9	141213431	117186721	0.8299	19.3668
chr10	135534747	146968086	1.0844	82.3332
chr11	135006516	233403018	1.7288	33.749
chr12	133851895	186963000	1.3968	15.795
chr13	115169878	75202439	0.653	10.4429
chr14	107349540	65092963	0.6064	19.9571
chr15	102531392	151054239	1.4732	14.0969
chr16	90354753	139713437	1.5463	63.8126
chr17	81195210	176860221	2.1782	24.7718
chr18	78077248	42944035	0.55	11.7813
chr19	59128983	149738260	2.5324	27.4494
chr20	63025520	98515585	1.5631	18.0199
chr21	48129895	18294404	0.3801	5.7671
chr22	51304566	47683966	0.9294	15.6028
chrMT	16571	670837	40.4826	11.7296
chrX	155270560	81259845	0.5233	11.5162

chrY	59373566	17010207	0.2865	86.0279
------	----------	----------	--------	---------

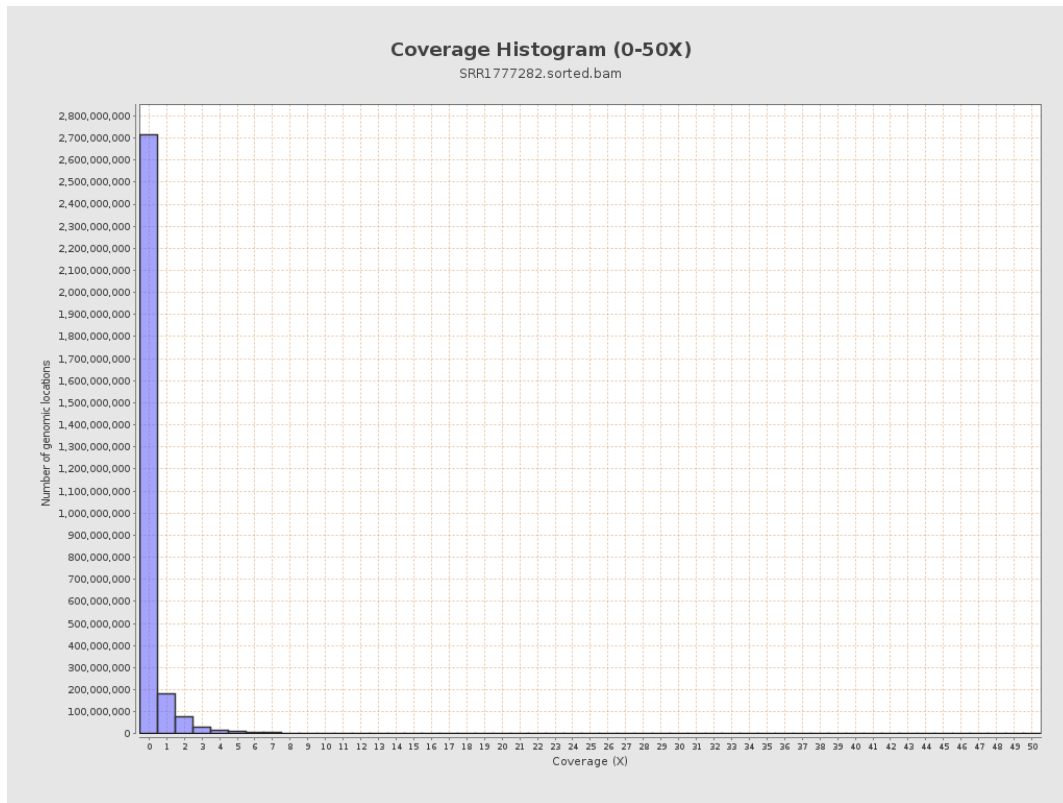
3. Results : Coverage across reference



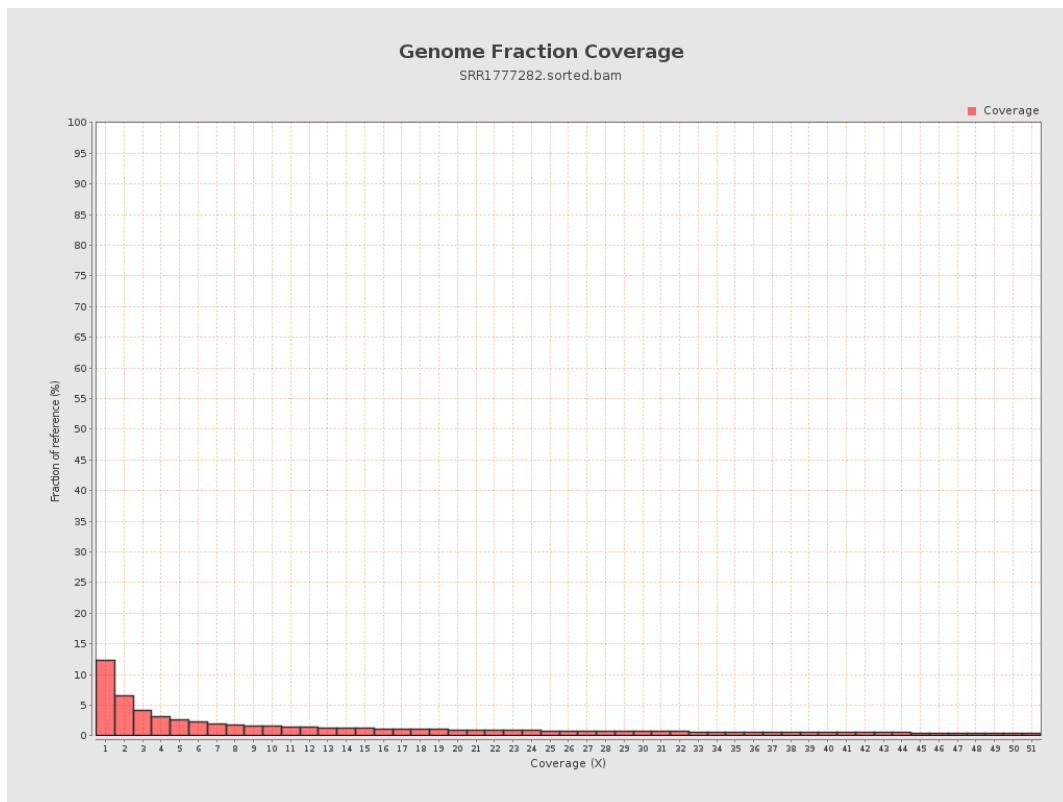
4. Results : Coverage Histogram



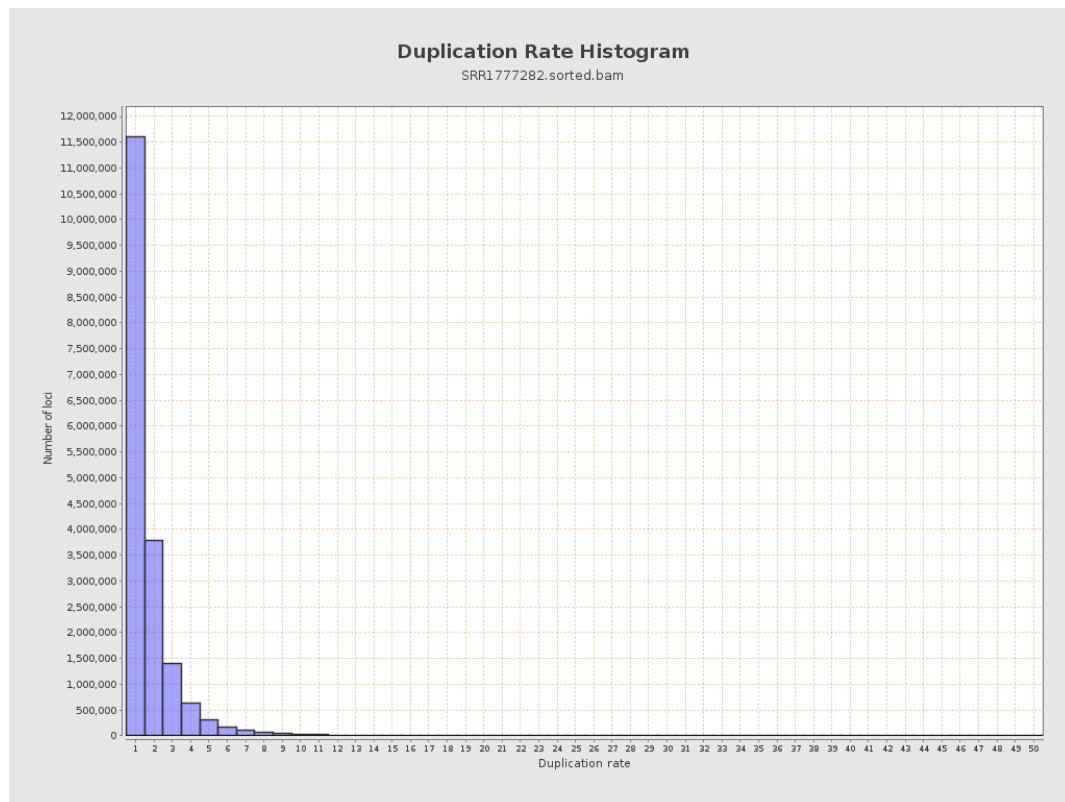
5. Results : Coverage Histogram (0-50X)



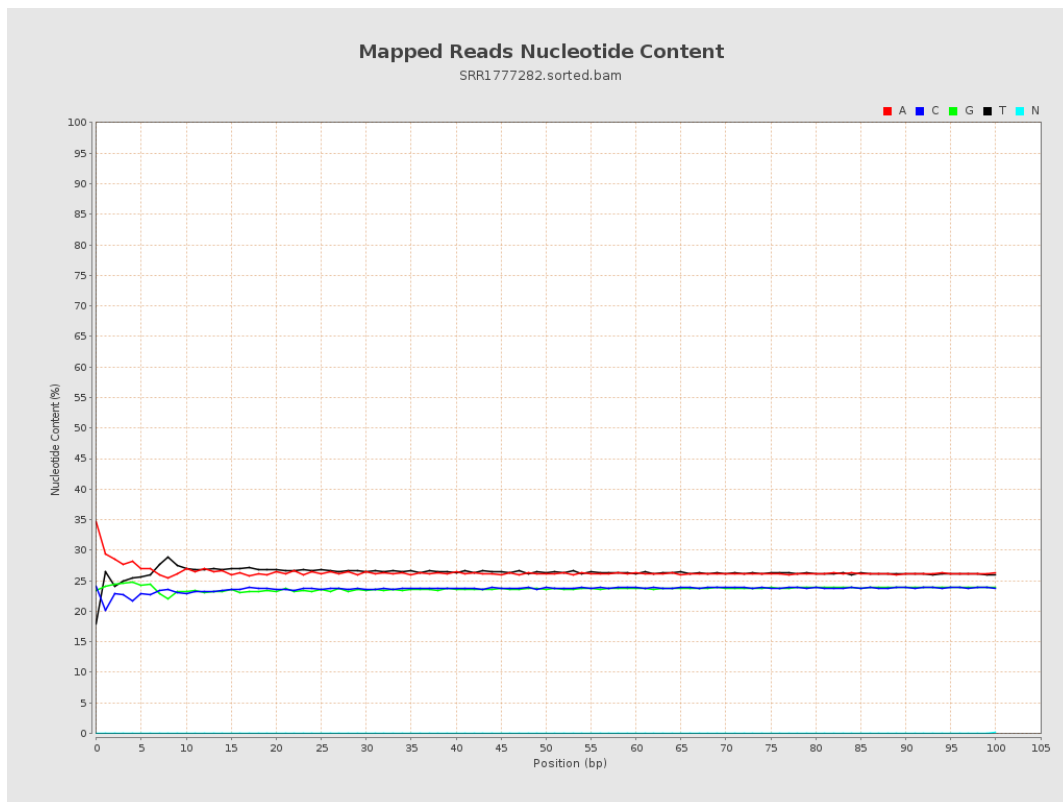
6. Results : Genome Fraction Coverage



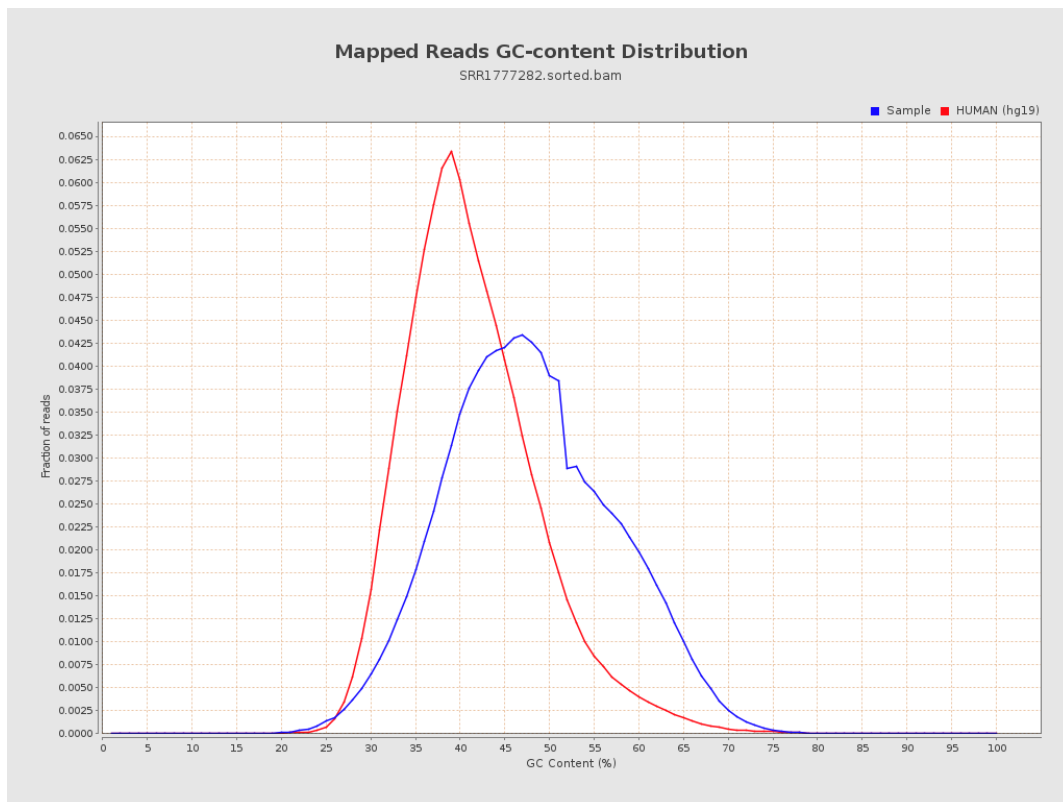
7. Results : Duplication Rate Histogram



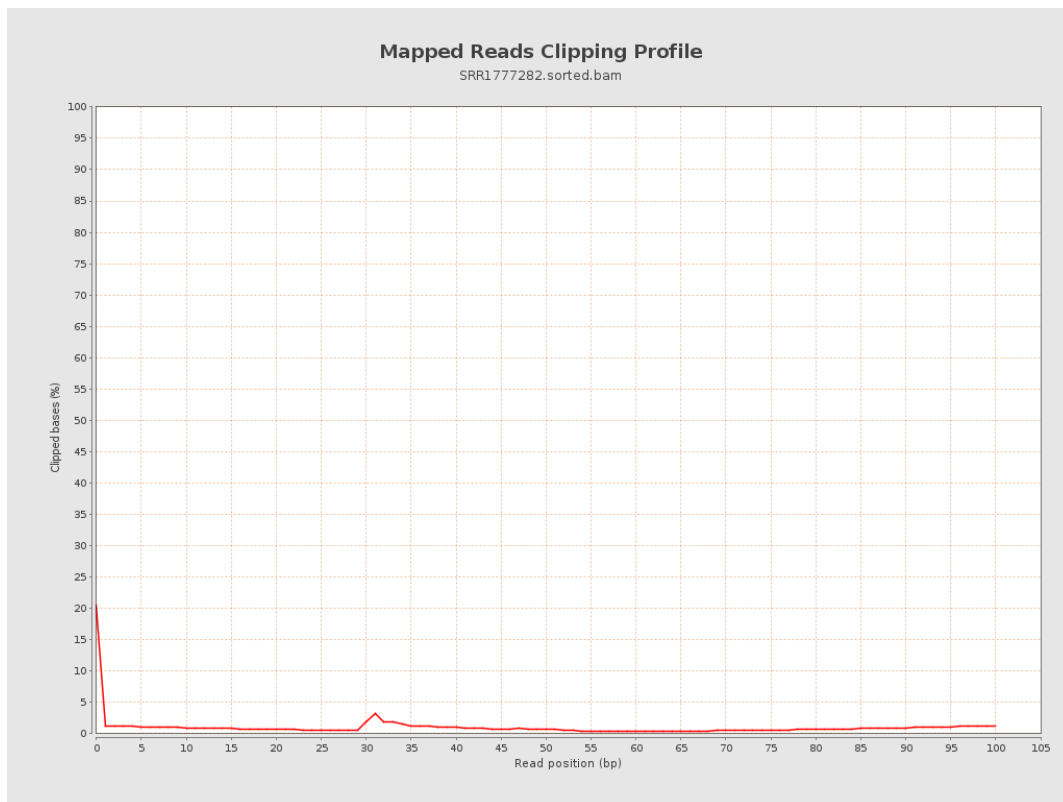
8. Results : Mapped Reads Nucleotide Content



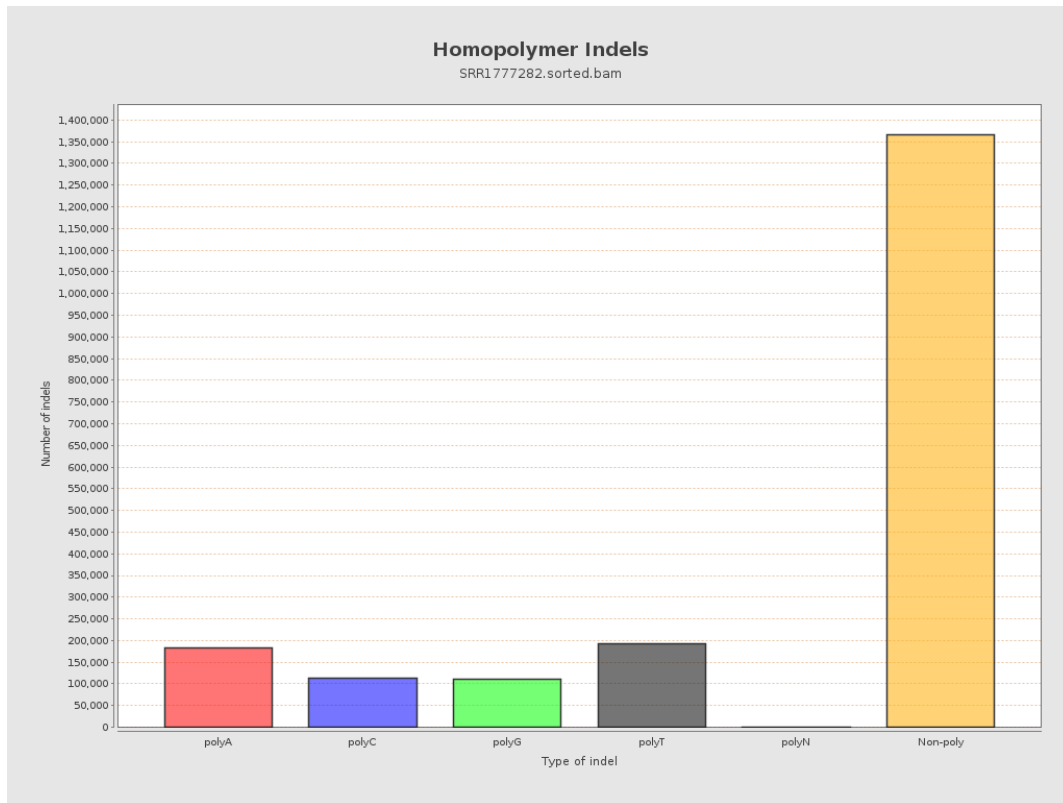
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



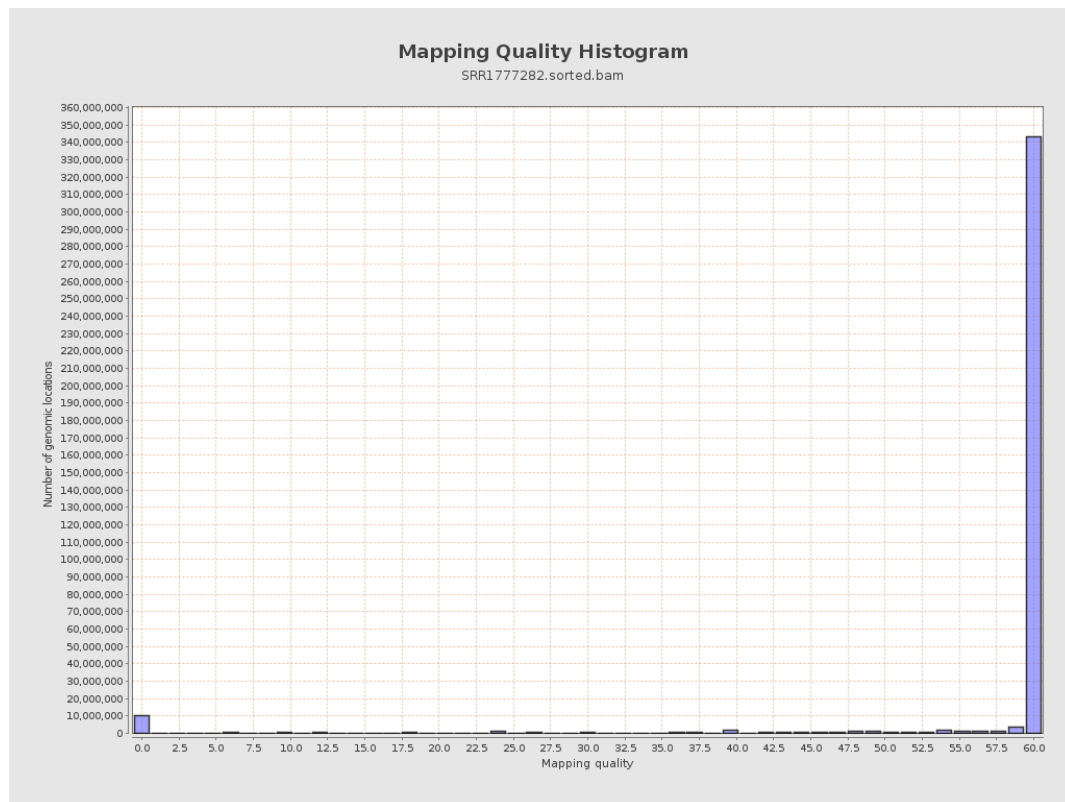
11. Results : Homopolymer Indels



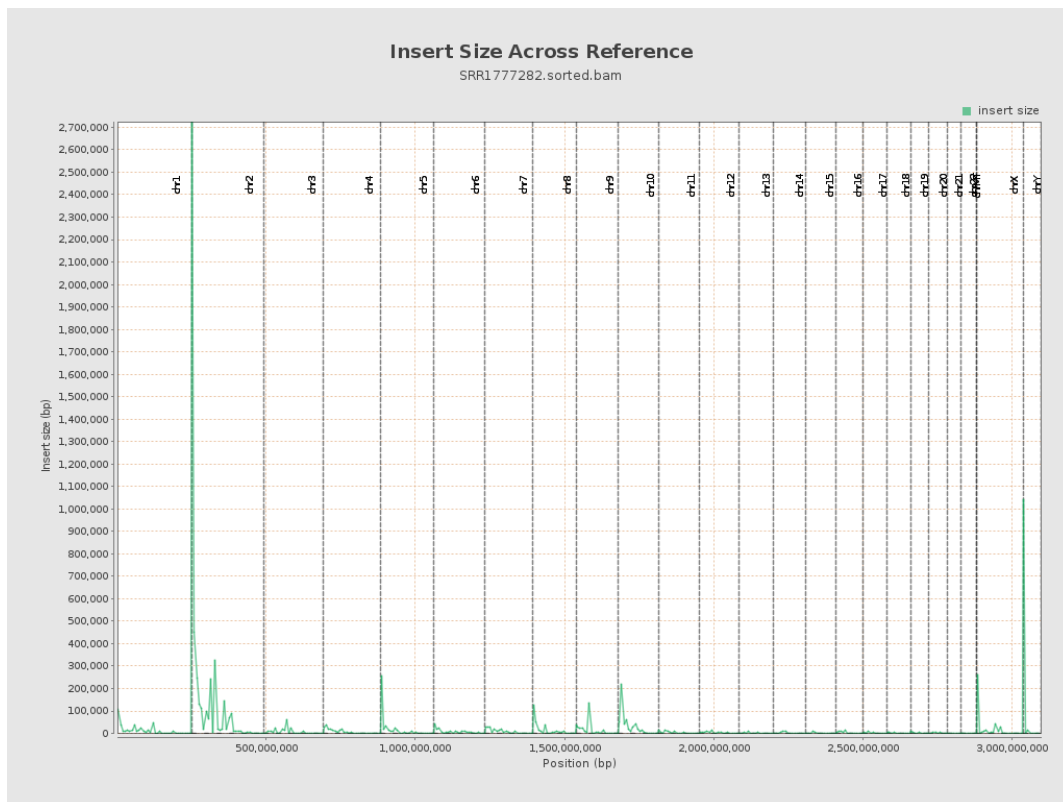
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

