

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/27 05:22:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781853.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_SRR1781853 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781853_1.fastq.gz SRR1781853_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Mar 27 05:22:43 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1781853.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	368,621,820
Mapped reads	354,135,047 / 96.07%
Unmapped reads	14,486,773 / 3.93%
Mapped paired reads	354,135,047 / 96.07%
Mapped reads, first in pair	178,498,201 / 48.42%
Mapped reads, second in pair	175,636,846 / 47.65%
Mapped reads, both in pair	348,471,806 / 94.53%
Mapped reads, singletons	5,663,241 / 1.54%
Secondary alignments	0
Supplementary alignments	920,077 / 0.25%
Read min/max/mean length	30 / 100 / 99.99
Duplicated reads (estimated)	42,766,198 / 11.6%
Duplication rate	11.61%
Clipped reads	16,457,353 / 4.46%

2.2. ACGT Content

Number/percentage of A's	10,392,736,643 / 29.57%
Number/percentage of C's	7,179,400,924 / 20.43%
Number/percentage of T's	10,310,688,581 / 29.34%
Number/percentage of G's	7,249,948,795 / 20.63%
Number/percentage of N's	9,063,921 / 0.03%

GC Percentage	41.06%
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2.3. Coverage

Mean	11.3541
Standard Deviation	13.4652

2.4. Mapping Quality

Mean Mapping Quality	53.94
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2.5. Insert size

Mean	28,630.55
Standard Deviation	1,636,375.35
P25/Median/P75	153 / 185 / 224

2.6. Mismatches and indels

General error rate	0.5%
Mismatches	169,885,856
Insertions	3,546,541
Mapped reads with at least one insertion	0.99%
Deletions	3,010,382
Mapped reads with at least one deletion	0.83%
Homopolymer indels	46.28%

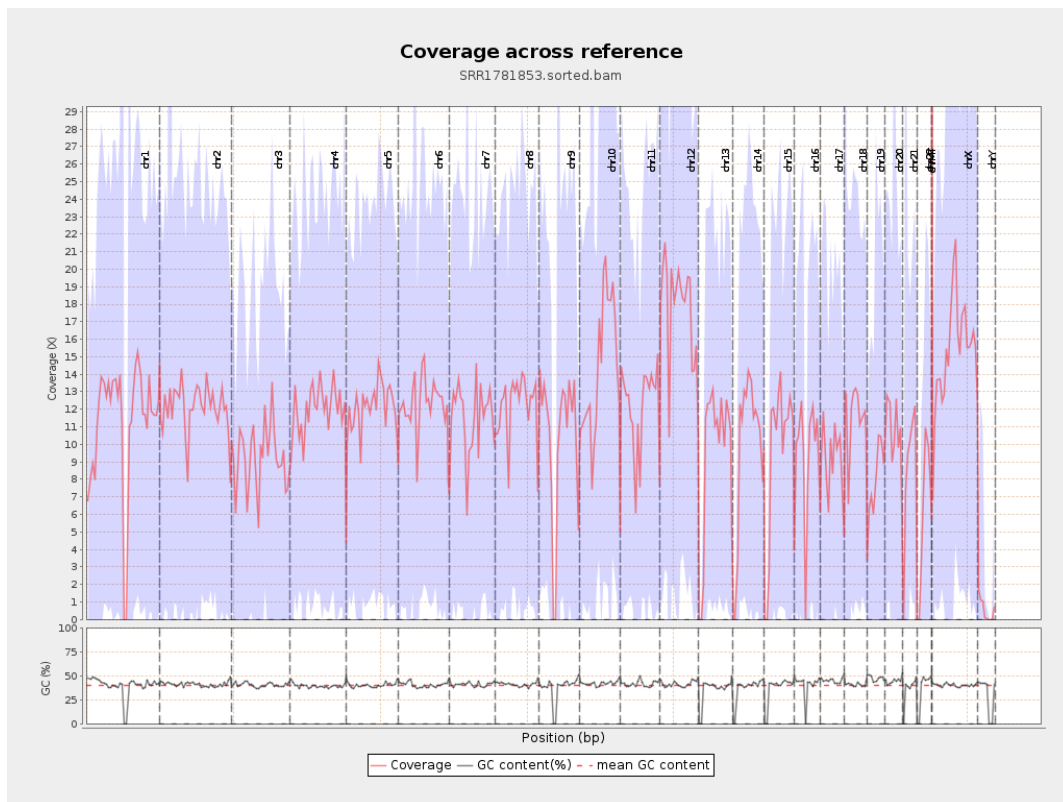
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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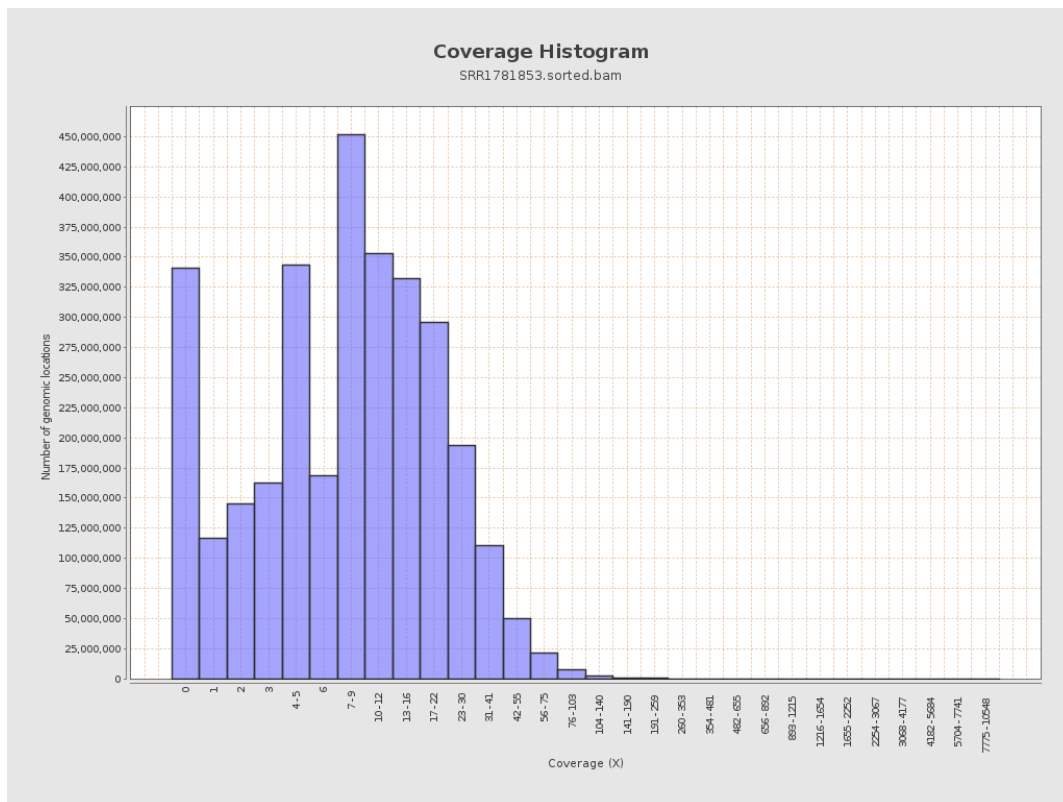
		bases	coverage	deviation
chr1	249250621	2826138800	11.3385	16.8635
chr2	243199373	2947187601	12.1184	14.9582
chr3	198022430	1818590379	9.1838	9.6726
chr4	191154276	2308946169	12.079	11.9183
chr5	180915260	2184725723	12.076	11.0973
chr6	171115067	2117799011	12.3765	12.3673
chr7	159138663	1824732779	11.4663	12.6859
chr8	146364022	1786375196	12.205	11.7425
chr9	141213431	1434105551	10.1556	13.9067
chr10	135534747	1960423105	14.4644	17.9102
chr11	135006516	1641668097	12.1599	12.1926
chr12	133851895	2384286881	17.8129	16.5817
chr13	115169878	1106000505	9.6032	10.5344
chr14	107349540	1052103315	9.8007	11.2888
chr15	102531392	973759802	9.4972	11.3208
chr16	90354753	821619525	9.0933	11.1061
chr17	81195210	735981570	9.0643	10.7522
chr18	78077248	911789505	11.678	13.1943
chr19	59128983	481285031	8.1396	12.082
chr20	63025520	674932290	10.7089	13.4111
chr21	48129895	428518282	8.9034	15.5779
chr22	51304566	308592112	6.0149	9.2416
chrMT	16571	699978	42.2411	13.0977
chrX	155270560	2385905552	15.3661	14.8244

chrY	59373566	32526534	0.5478	5.9322
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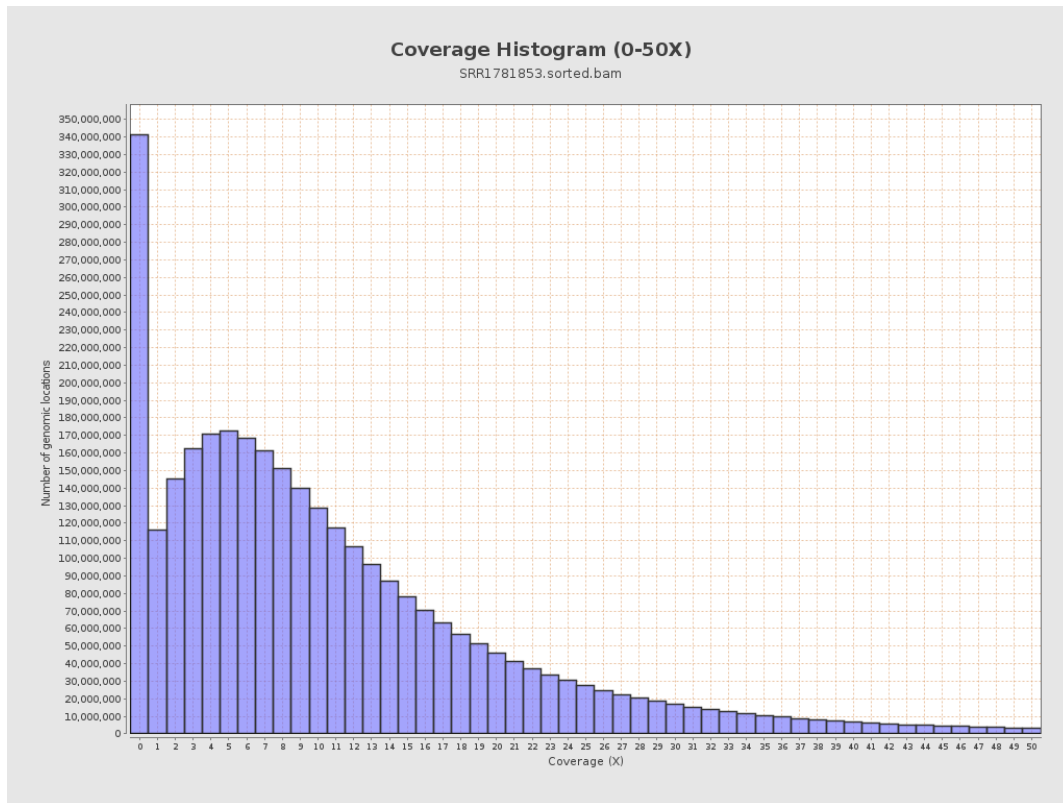
3. Results : Coverage across reference



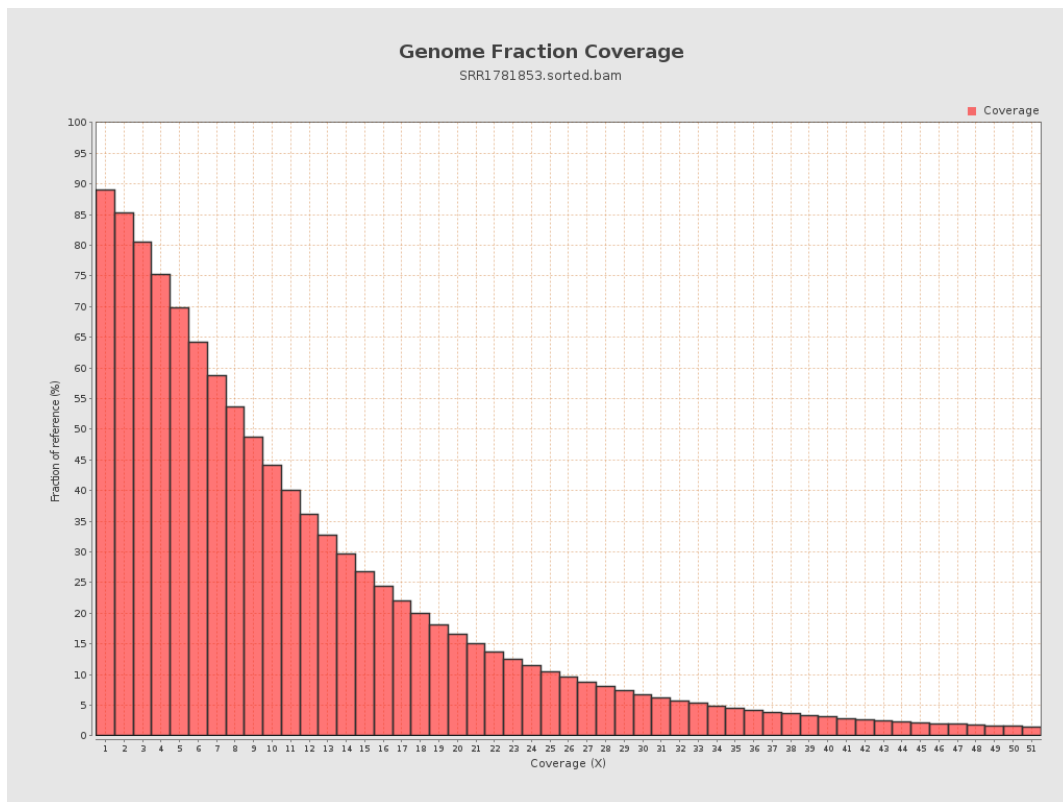
4. Results : Coverage Histogram



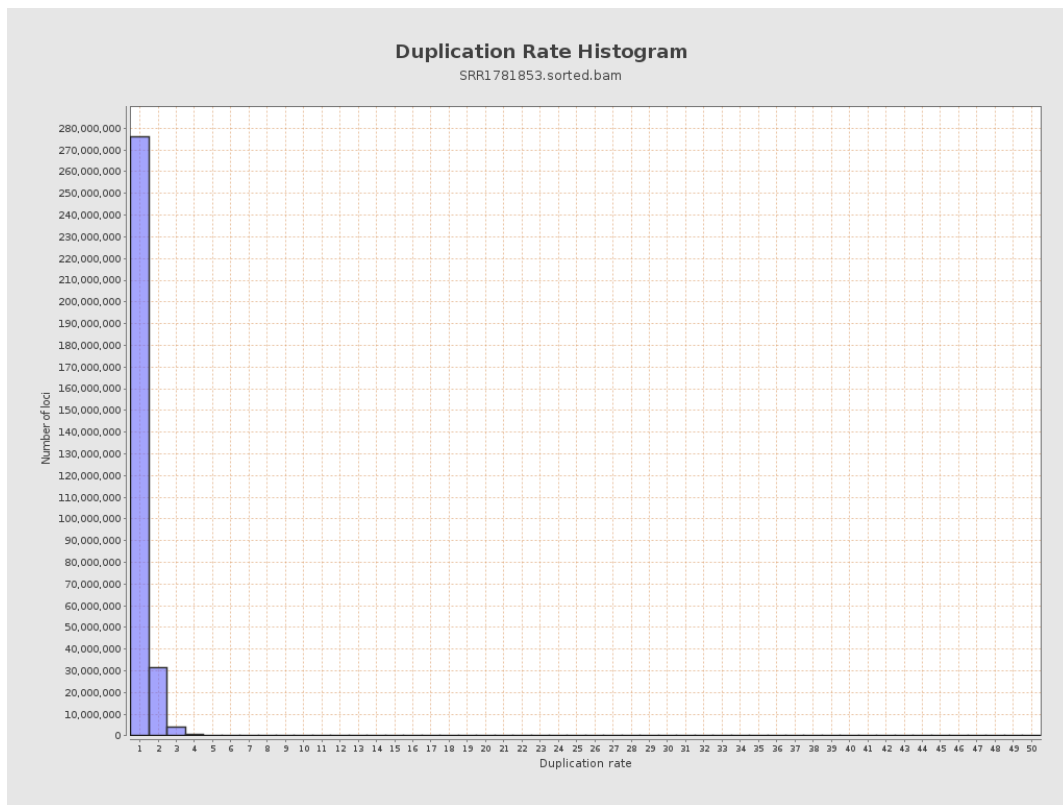
5. Results : Coverage Histogram (0-50X)



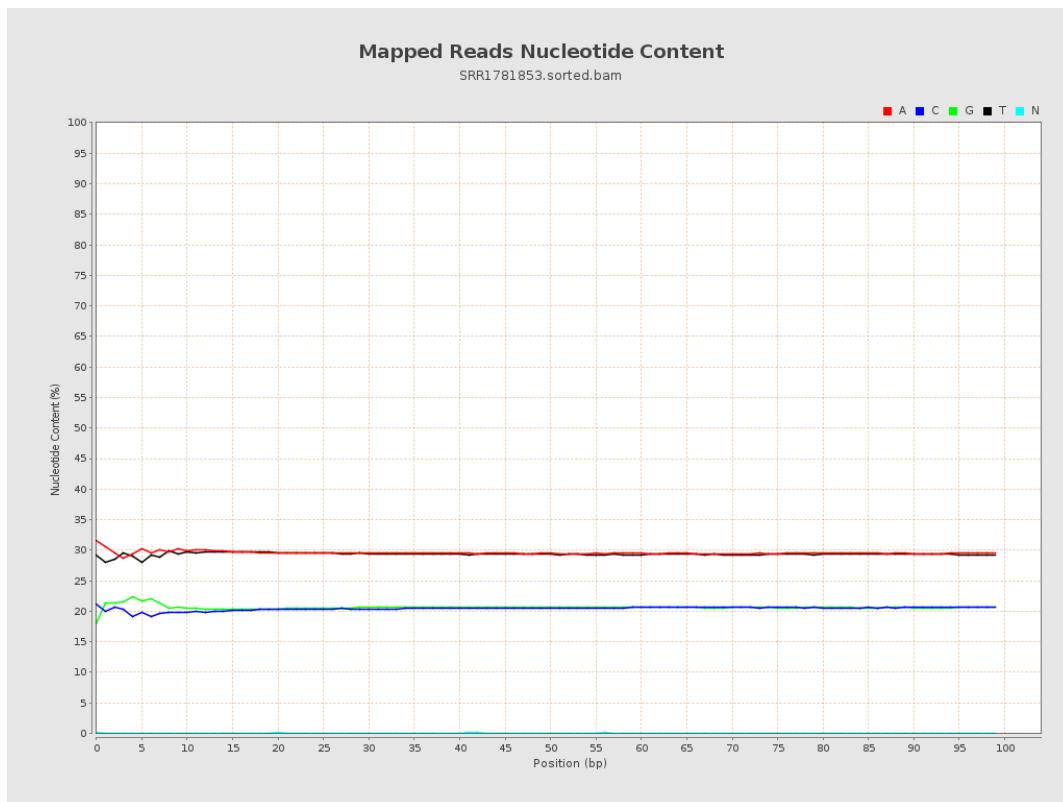
6. Results : Genome Fraction Coverage



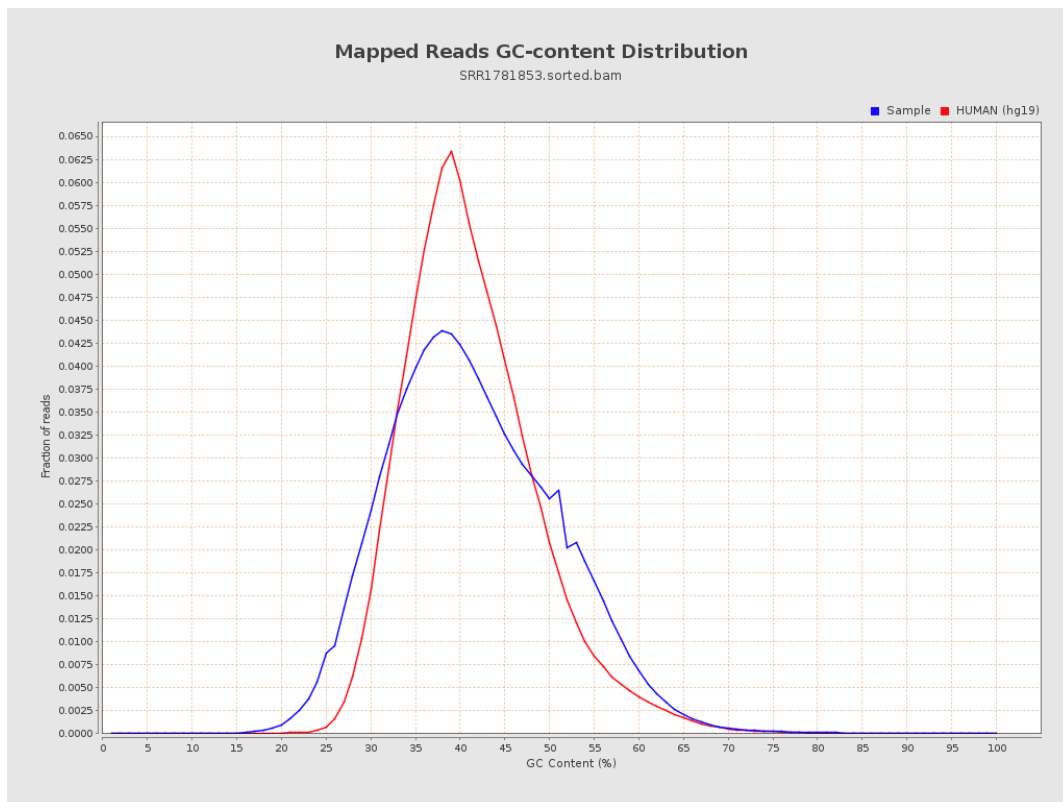
7. Results : Duplication Rate Histogram



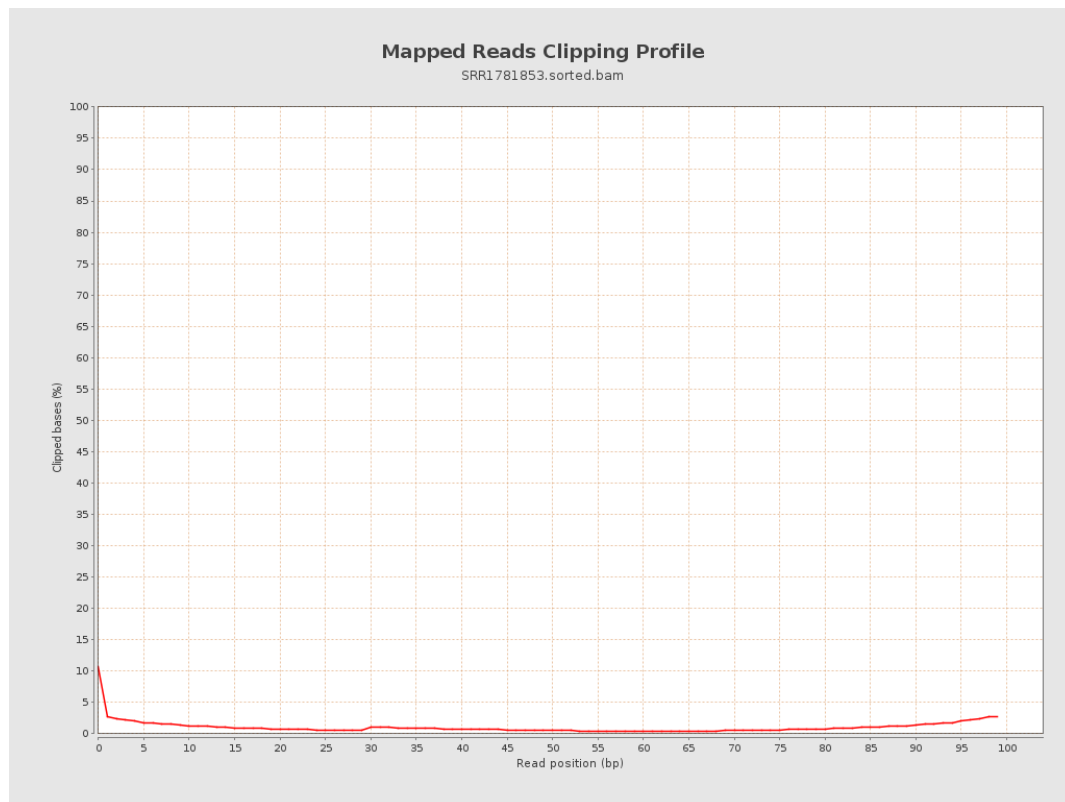
8. Results : Mapped Reads Nucleotide Content



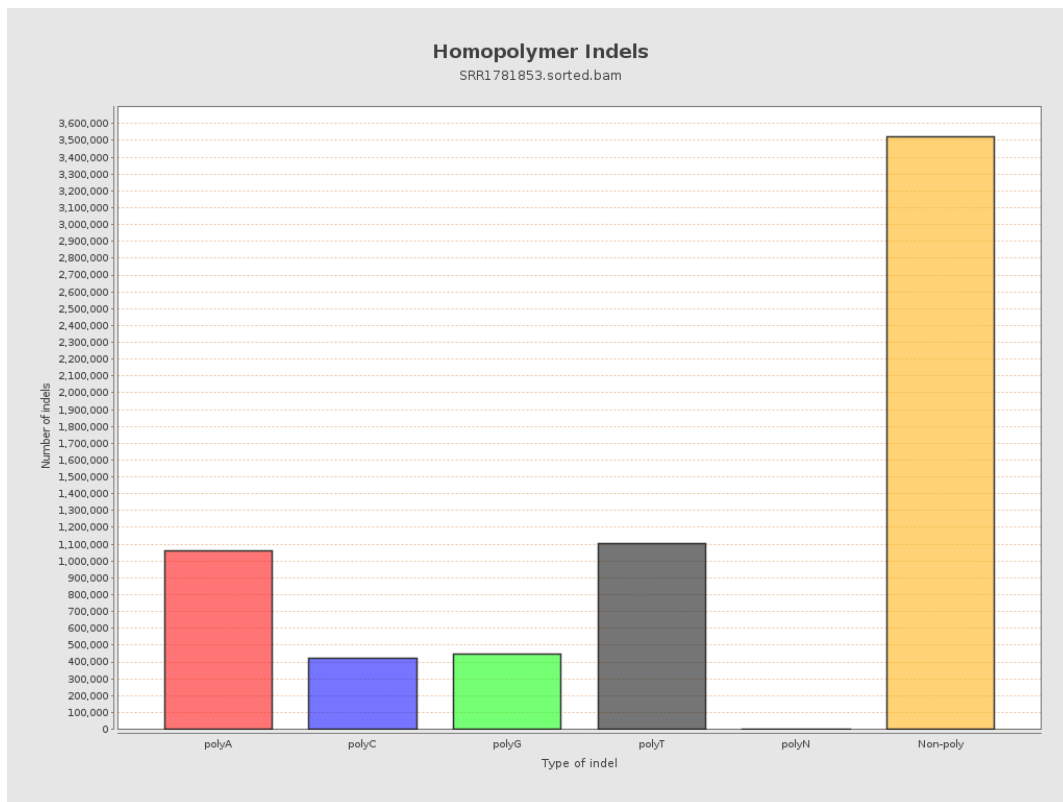
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



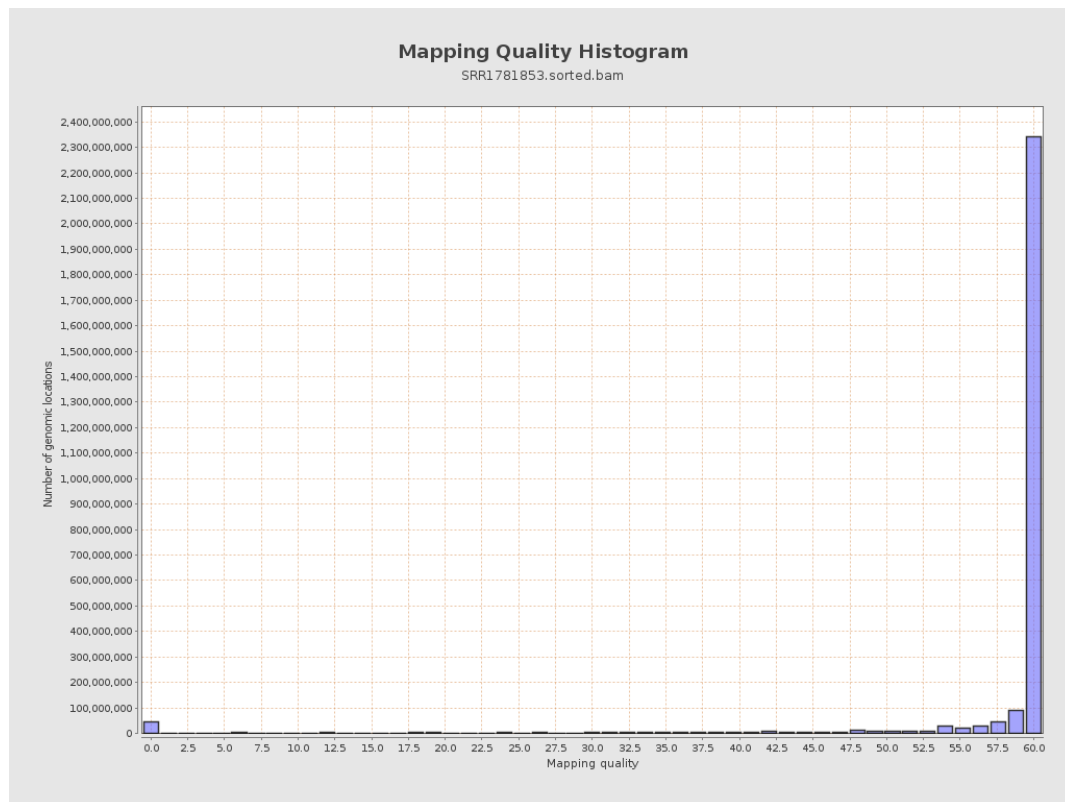
11. Results : Homopolymer Indels



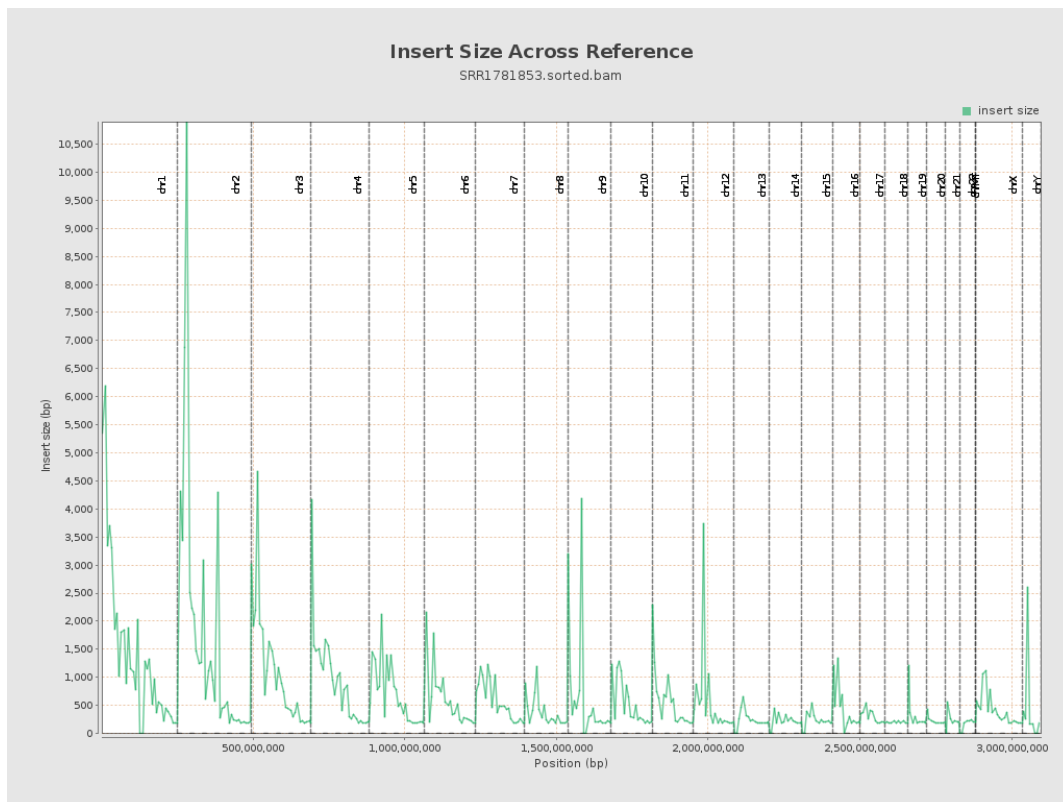
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

