

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 02:47:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231789.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_SRR6231789 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231789.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 02:47:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231789.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,790,807
Mapped reads	1,223,329 / 43.83%
Unmapped reads	1,567,478 / 56.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,219 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	60,715 / 2.18%
Duplication rate	1.95%
Clipped reads	714,637 / 25.61%

2.2. ACGT Content

Number/percentage of A's	21,778,096 / 28.15%
Number/percentage of C's	15,570,568 / 20.13%
Number/percentage of T's	21,194,767 / 27.4%
Number/percentage of G's	18,809,080 / 24.31%
Number/percentage of N's	5,340 / 0.01%
GC Percentage	44.44%

2.3. Coverage

Mean	0.025

Standard Deviation	3.7895
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2.4. Mapping Quality

Mean Mapping Quality	41.71
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2.5. Mismatches and indels

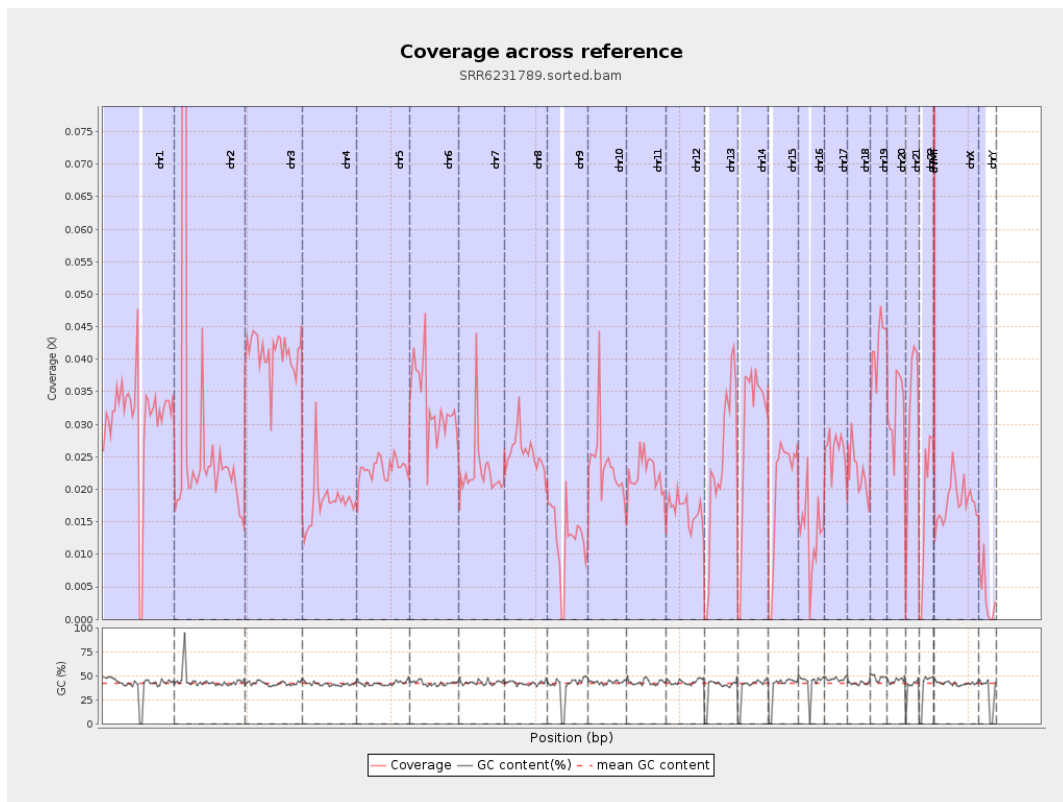
General error rate	0.75%
Mismatches	570,550
Insertions	7,105
Mapped reads with at least one insertion	0.57%
Deletions	20,199
Mapped reads with at least one deletion	1.63%
Homopolymer indels	42.96%

2.6. Chromosome stats

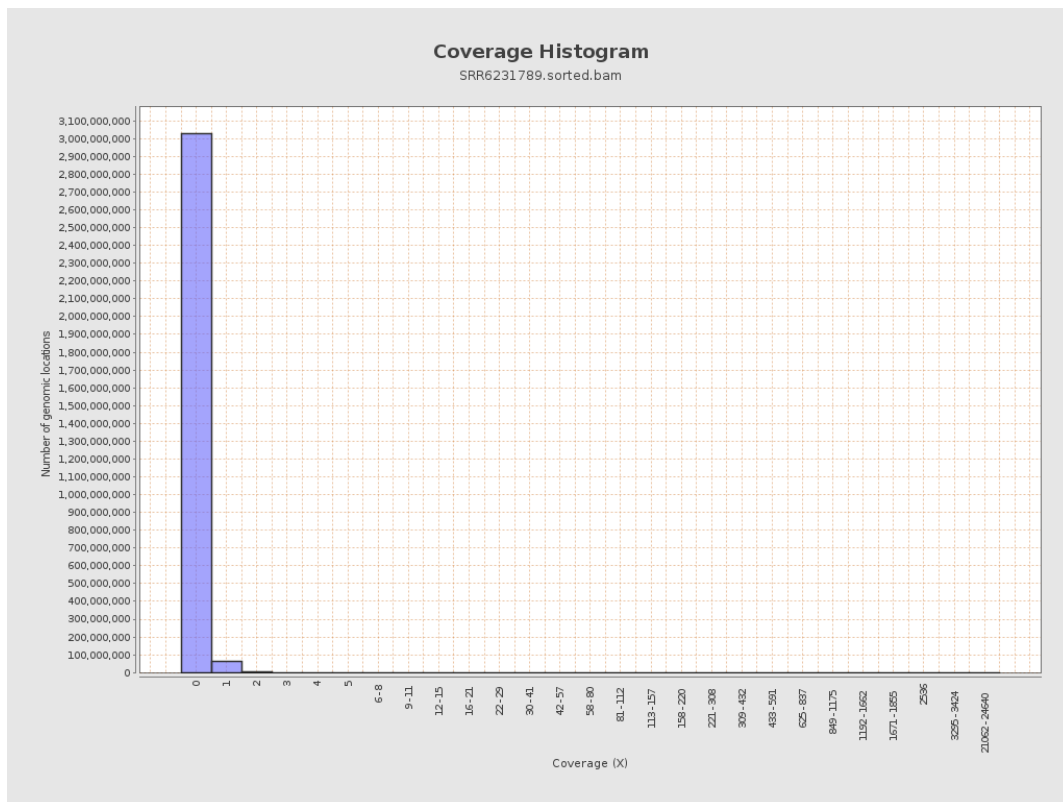
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7663870	0.0307	0.4641
chr2	243199373	7496293	0.0308	13.4935
chr3	198022430	8117805	0.041	0.2164
chr4	191154276	3468174	0.0181	0.1527
chr5	180915260	4227166	0.0234	0.1627
chr6	171115067	5644012	0.033	0.2343
chr7	159138663	3623352	0.0228	0.3289

chr8	146364022	3753348	0.0256	0.2835
chr9	141213431	1774703	0.0126	0.1839
chr10	135534747	3221201	0.0238	0.241
chr11	135006516	3041727	0.0225	0.2603
chr12	133851895	2247477	0.0168	0.1392
chr13	115169878	2750982	0.0239	0.1639
chr14	107349540	3179922	0.0296	0.2048
chr15	102531392	2093474	0.0204	0.1537
chr16	90354753	1185415	0.0131	0.1379
chr17	81195210	2107648	0.026	0.1854
chr18	78077248	1757584	0.0225	0.3556
chr19	59128983	2480567	0.042	0.3158
chr20	63025520	2003147	0.0318	0.192
chr21	48129895	1532520	0.0318	0.1945
chr22	51304566	922573	0.018	0.1419
chrMT	16571	65633	3.9607	2.9961
chrX	155270560	2818846	0.0182	0.159
chrY	59373566	212556	0.0036	0.0875

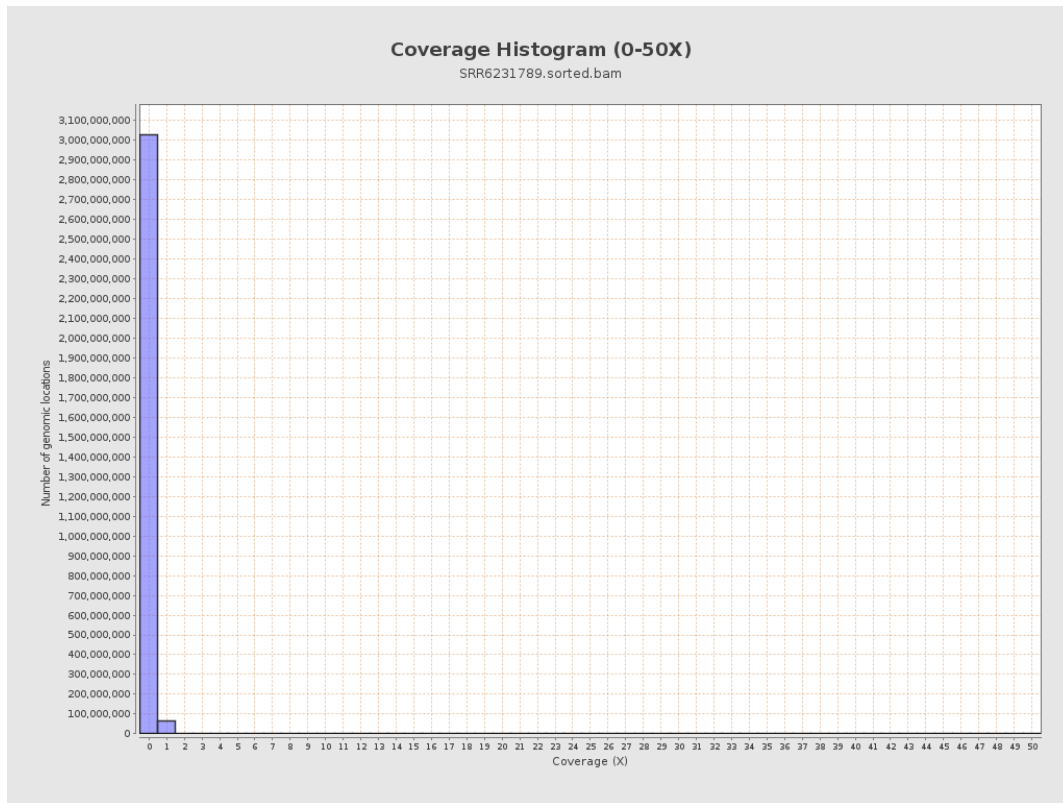
3. Results : Coverage across reference



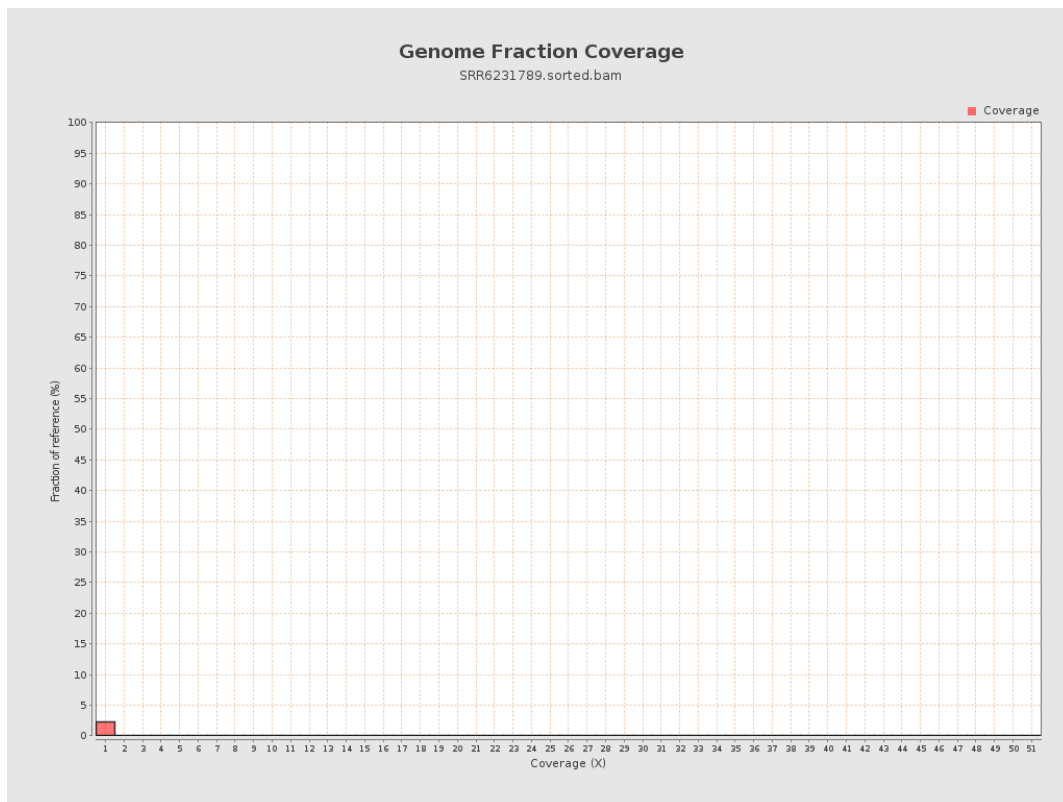
4. Results : Coverage Histogram



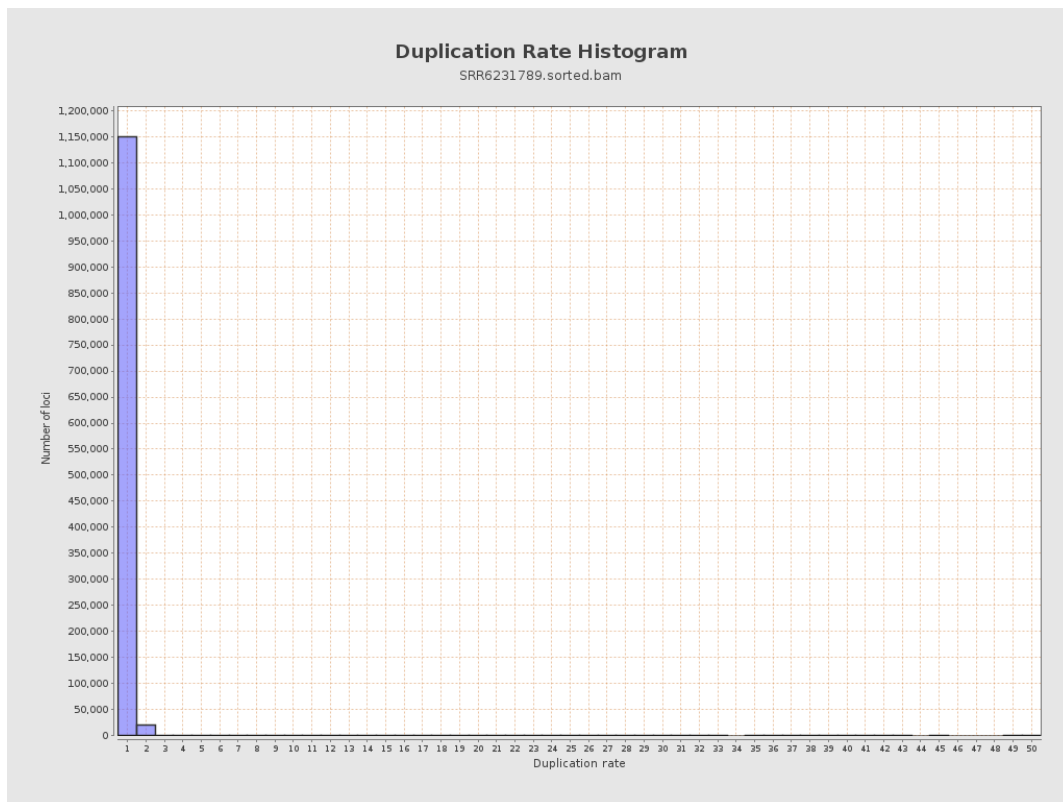
5. Results : Coverage Histogram (0-50X)



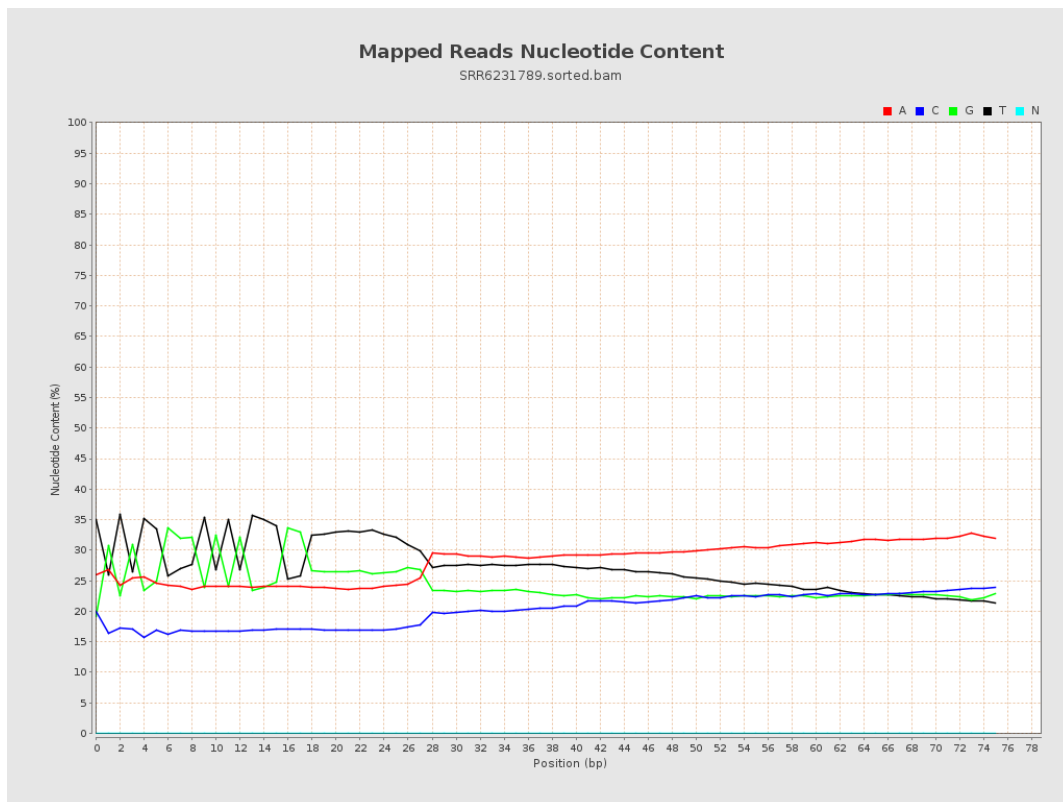
6. Results : Genome Fraction Coverage



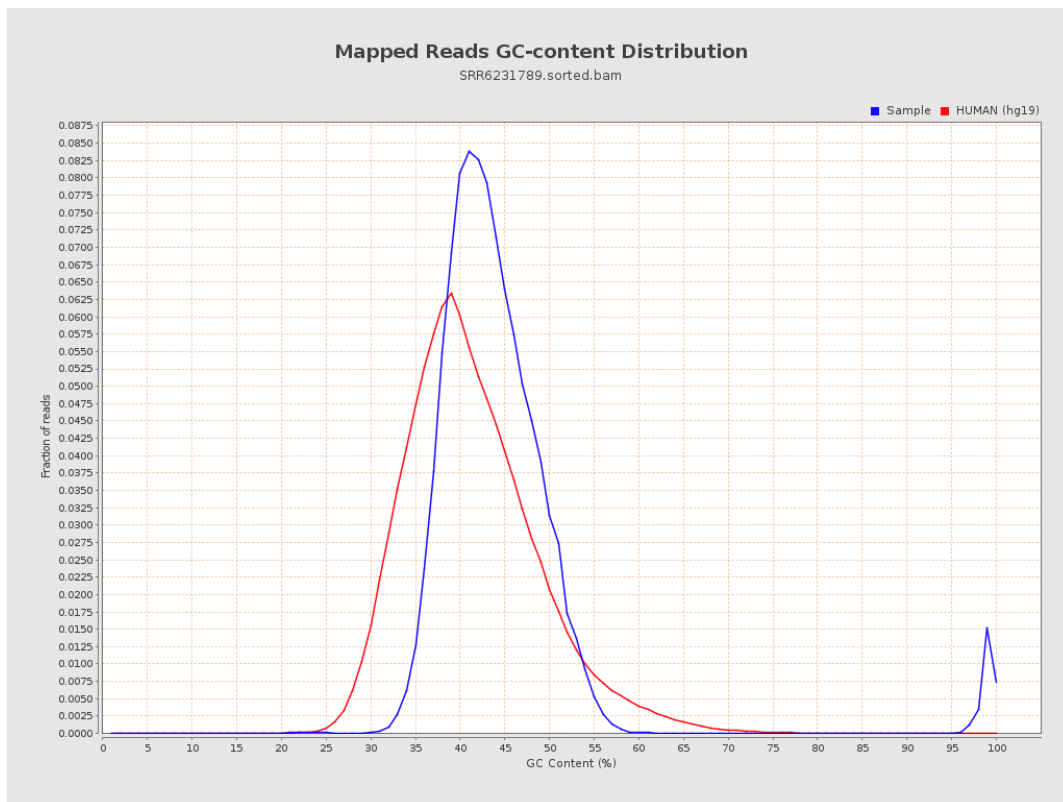
7. Results : Duplication Rate Histogram



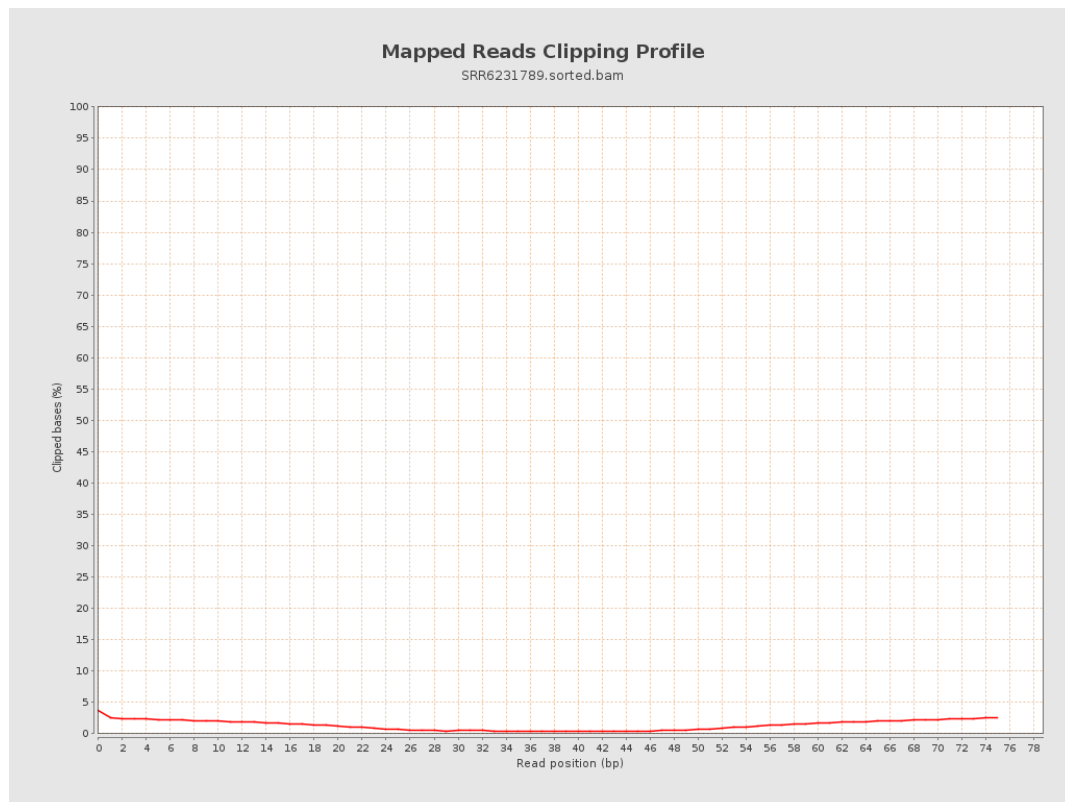
8. Results : Mapped Reads Nucleotide Content



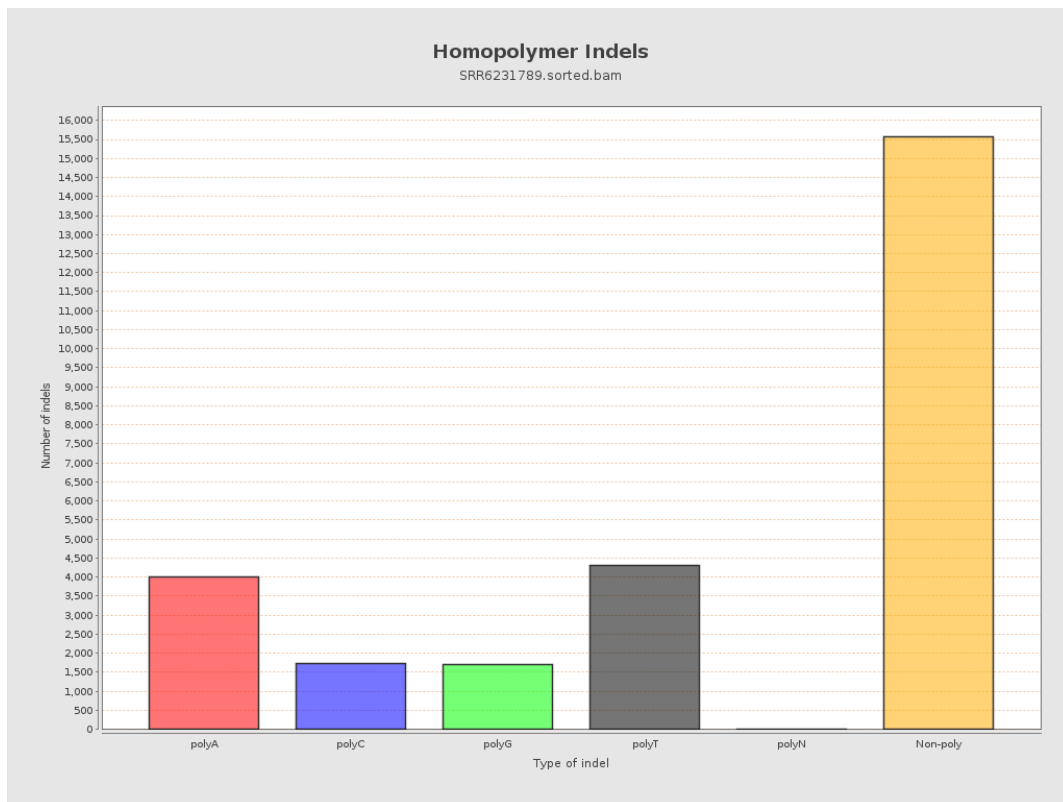
9. Results : Mapped Reads GC-content Distribution



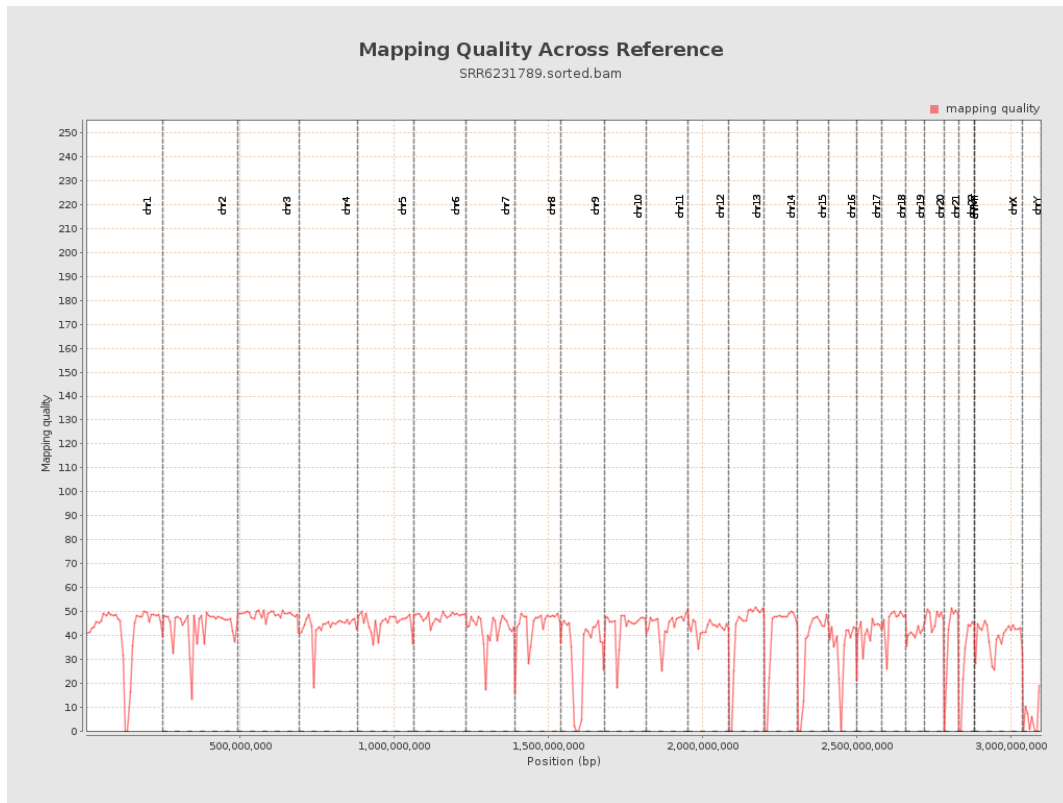
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

