

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 17:34:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238489.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_SRR6238489 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238489.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 17:34:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238489.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,484,539
Mapped reads	1,170,448 / 78.84%
Unmapped reads	314,091 / 21.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,605 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	307,945 / 20.74%
Duplication rate	17.25%
Clipped reads	820,123 / 55.24%

2.2. ACGT Content

Number/percentage of A's	16,760,492 / 24.04%
Number/percentage of C's	11,861,264 / 17.01%
Number/percentage of T's	24,144,905 / 34.62%
Number/percentage of G's	16,962,539 / 24.32%
Number/percentage of N's	3,863 / 0.01%
GC Percentage	41.33%

2.3. Coverage

Mean	0.0225

Standard Deviation	0.502
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2.4. Mapping Quality

Mean Mapping Quality	43.43
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2.5. Mismatches and indels

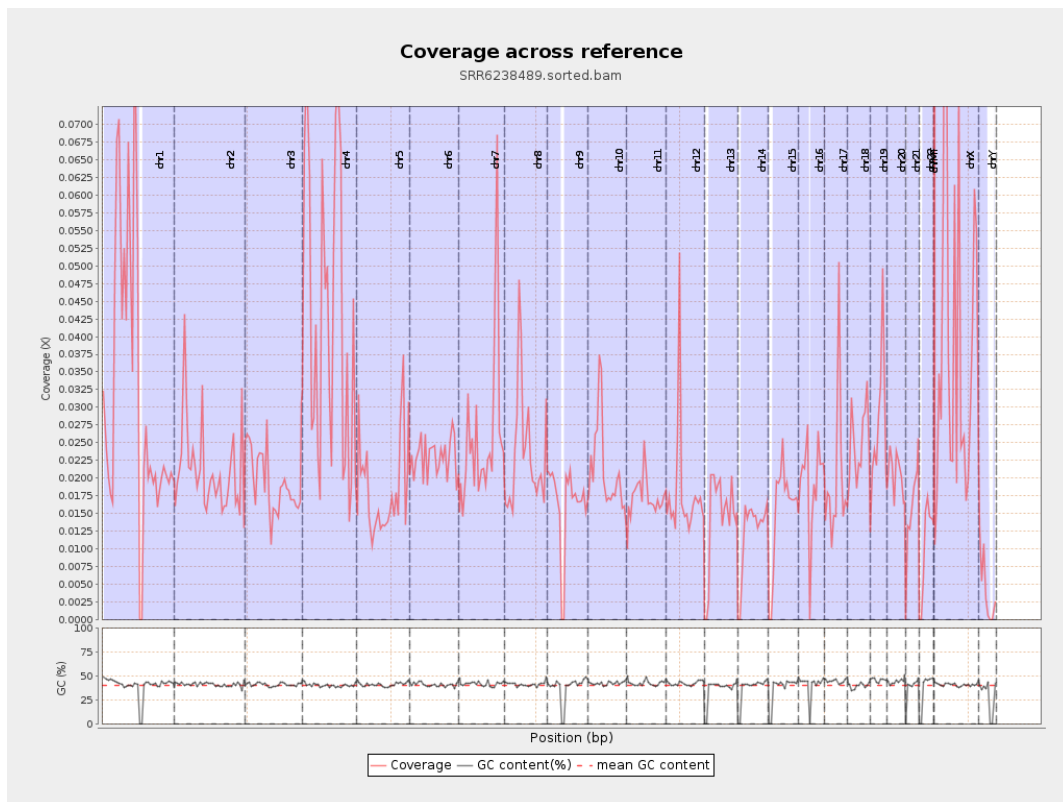
General error rate	0.71%
Mismatches	485,954
Insertions	4,501
Mapped reads with at least one insertion	0.38%
Deletions	22,528
Mapped reads with at least one deletion	1.9%
Homopolymer indels	40.28%

2.6. Chromosome stats

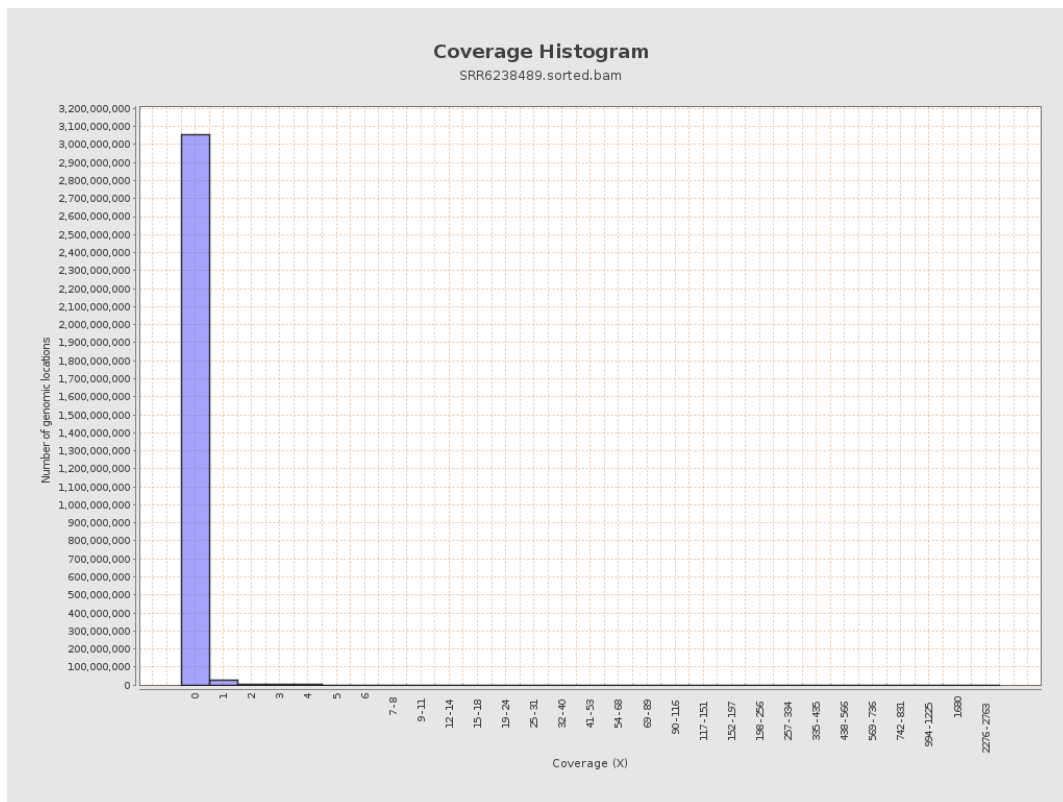
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7873434	0.0316	0.6306
chr2	243199373	5133417	0.0211	1.2319
chr3	198022430	3827090	0.0193	0.2555
chr4	191154276	7953347	0.0416	0.3753
chr5	180915260	3316430	0.0183	0.2389
chr6	171115067	3925951	0.0229	0.4607
chr7	159138663	4030771	0.0253	0.3621

chr8	146364022	3456475	0.0236	0.4303
chr9	141213431	2306801	0.0163	0.2429
chr10	135534747	2872685	0.0212	0.2788
chr11	135006516	2350762	0.0174	0.2427
chr12	133851895	2412493	0.018	0.2416
chr13	115169878	1649246	0.0143	0.332
chr14	107349540	1322092	0.0123	0.1926
chr15	102531392	1572019	0.0153	0.3047
chr16	90354753	1712377	0.019	0.2487
chr17	81195210	1564032	0.0193	0.2468
chr18	78077248	1944400	0.0249	0.9164
chr19	59128983	1617409	0.0274	0.3965
chr20	63025520	1293920	0.0205	0.2476
chr21	48129895	758234	0.0158	0.2176
chr22	51304566	547049	0.0107	0.181
chrMT	16571	43941	2.6517	2.968
chrX	155270560	6048643	0.039	0.3647
chrY	59373566	237565	0.004	0.2011

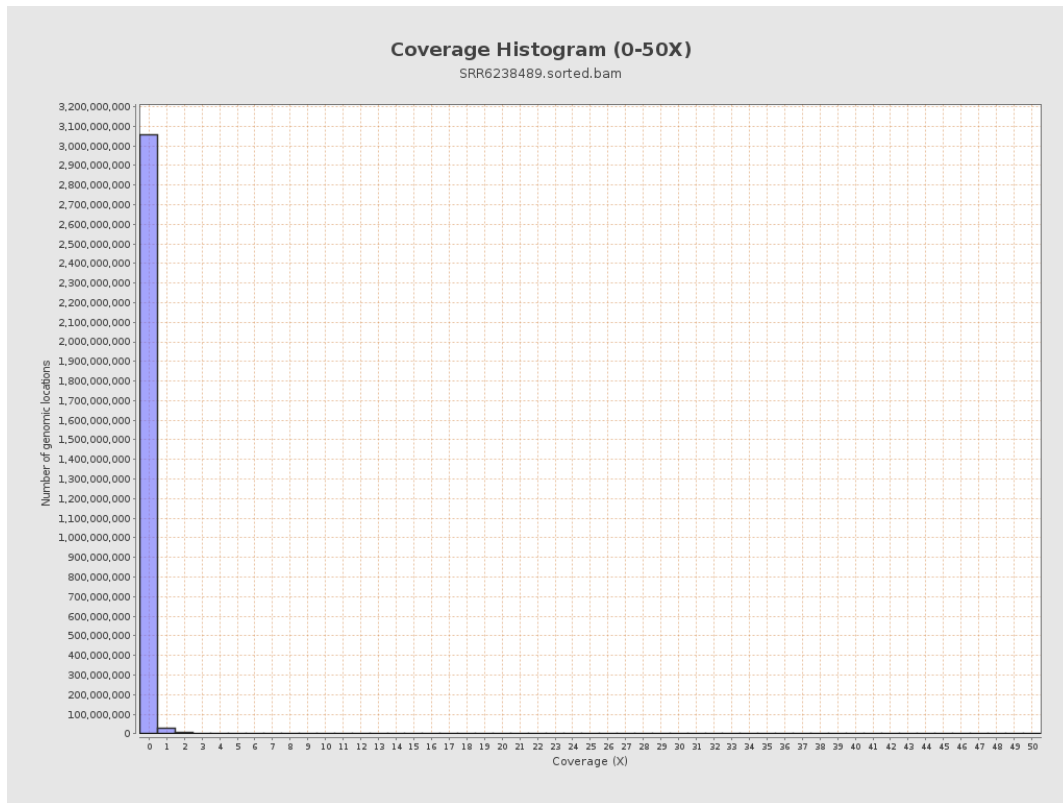
3. Results : Coverage across reference



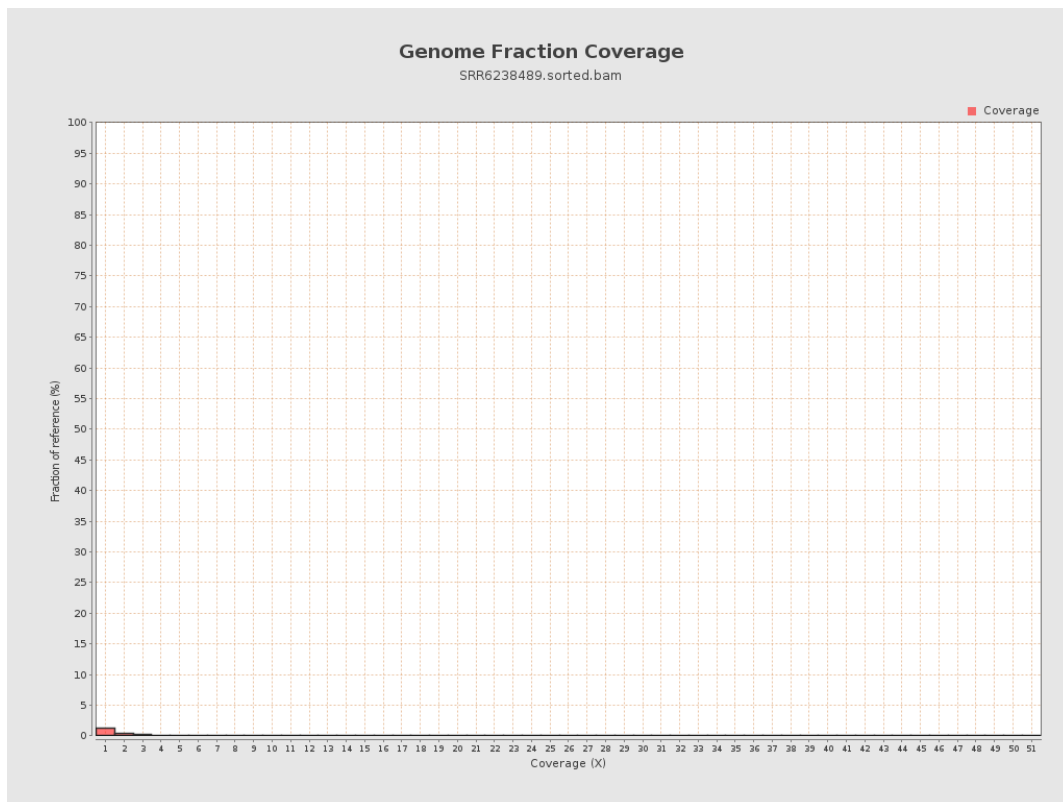
4. Results : Coverage Histogram



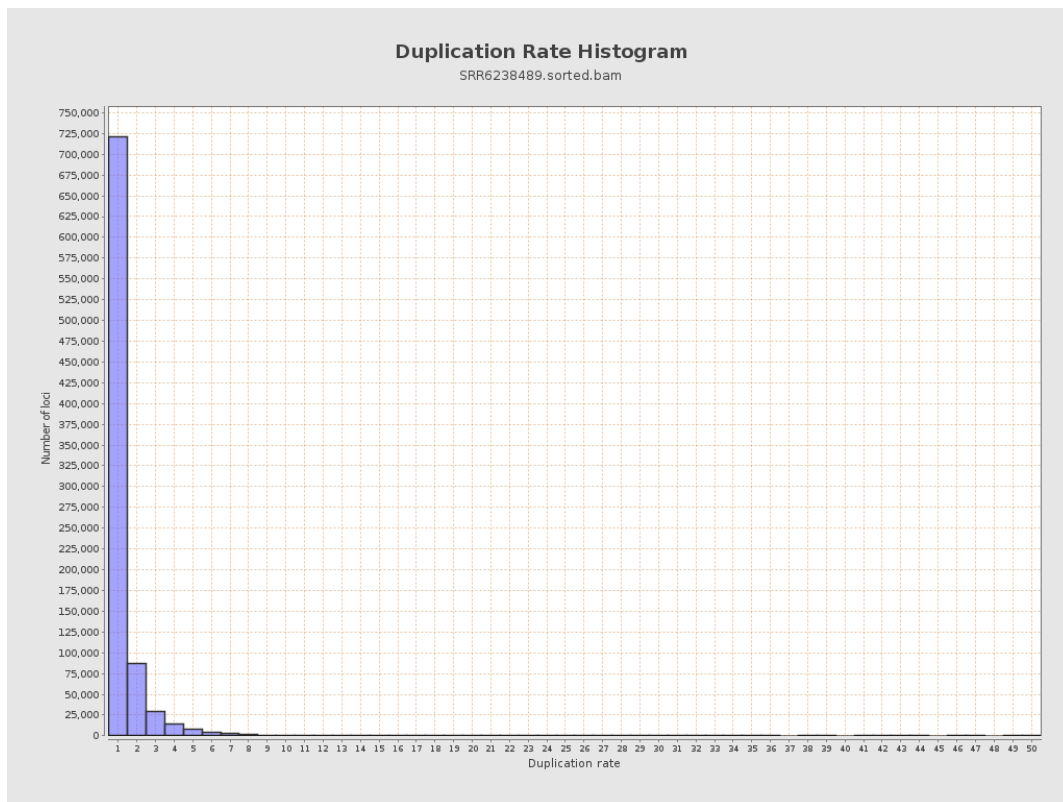
5. Results : Coverage Histogram (0-50X)



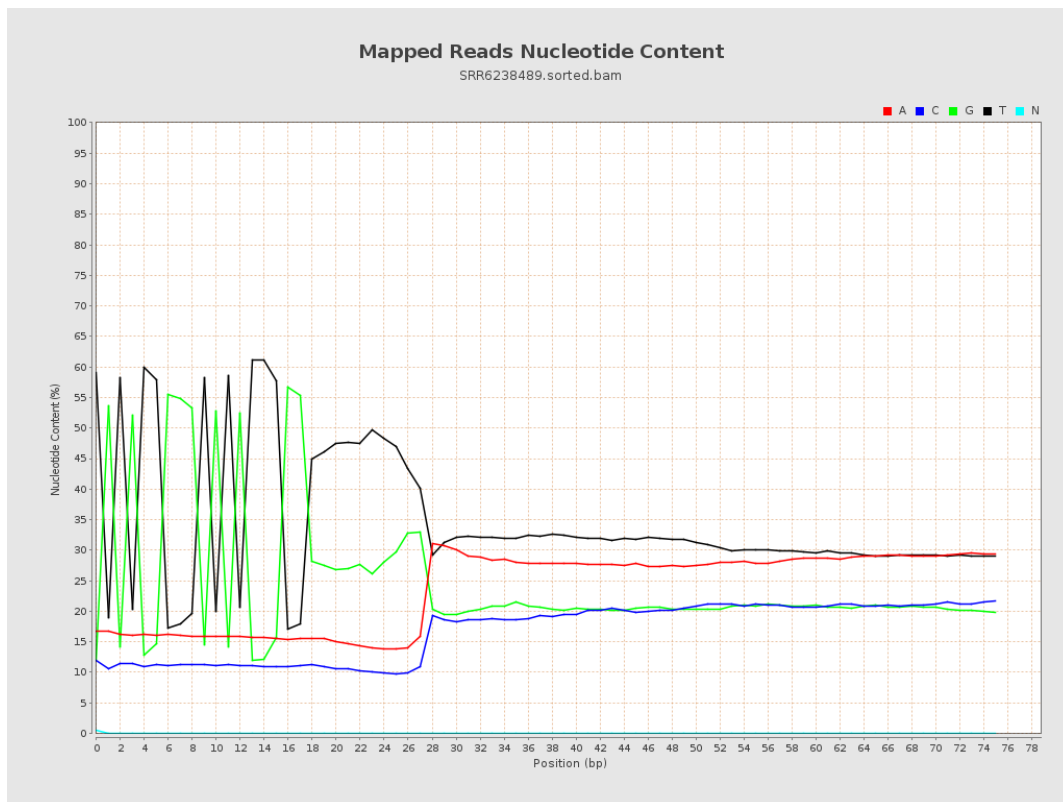
6. Results : Genome Fraction Coverage



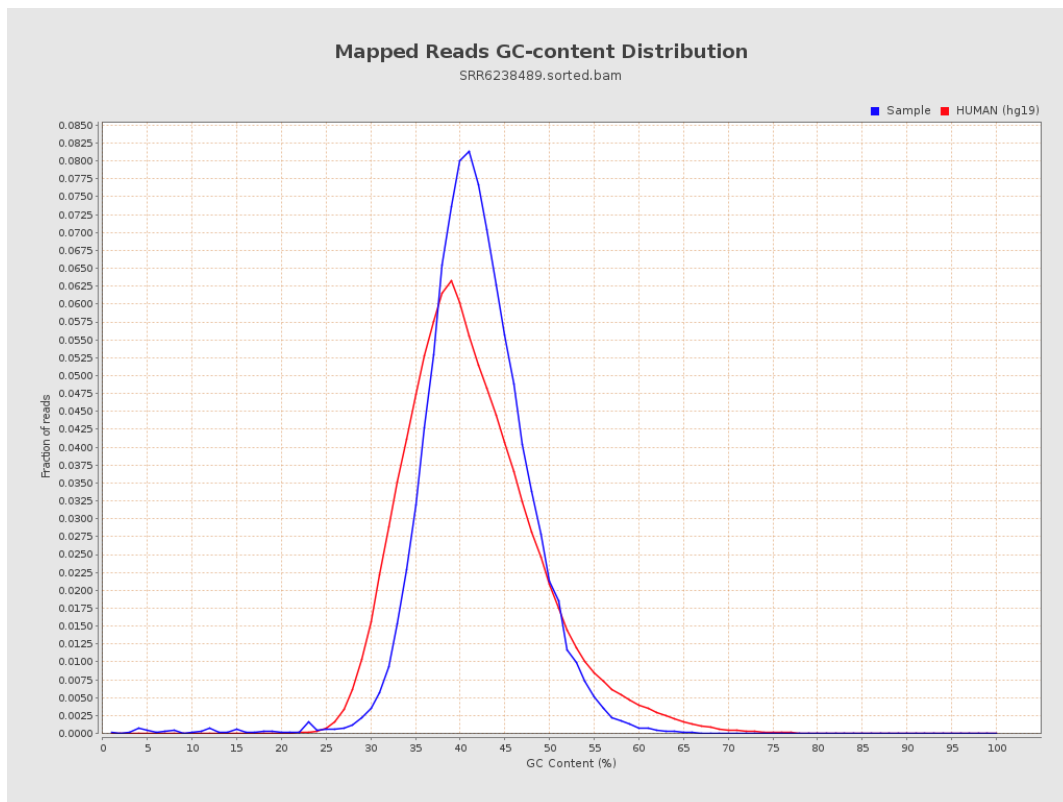
7. Results : Duplication Rate Histogram



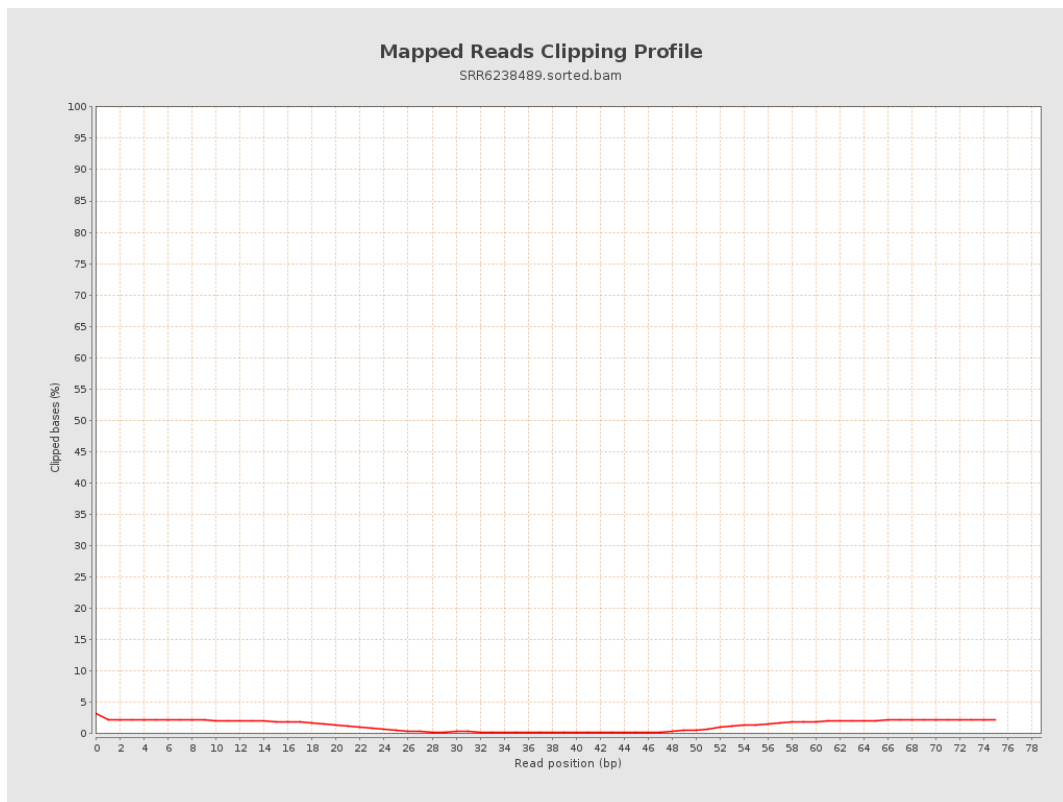
8. Results : Mapped Reads Nucleotide Content



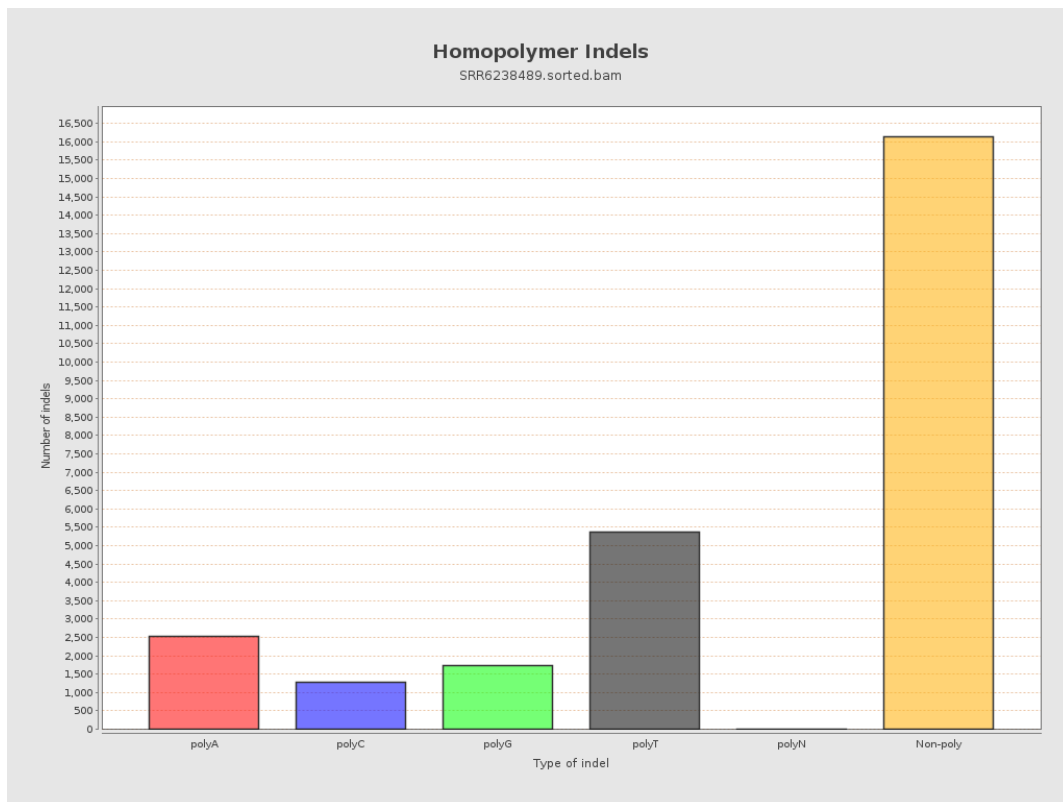
9. Results : Mapped Reads GC-content Distribution



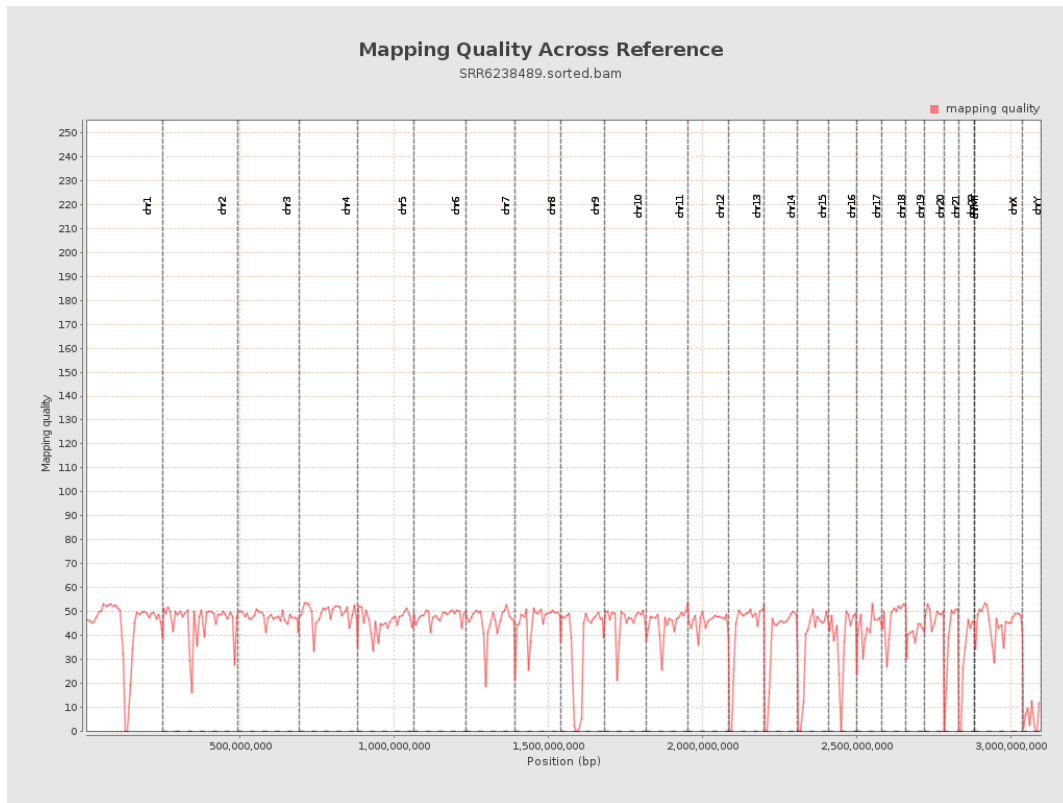
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

