

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 12:06:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524989.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_SRR10524989 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524989.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 12:06:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524989.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,297,844
Mapped reads	1,144,529 / 88.19%
Unmapped reads	153,315 / 11.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,368 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	26,361 / 2.03%
Duplication rate	1.59%
Clipped reads	1,145,854 / 88.29%

2.2. ACGT Content

Number/percentage of A's	16,956,518 / 25.96%
Number/percentage of C's	12,115,555 / 18.55%
Number/percentage of T's	21,008,986 / 32.16%
Number/percentage of G's	15,246,908 / 23.34%
Number/percentage of N's	1,990 / 0%
GC Percentage	41.88%

2.3. Coverage

Mean	0.0211

Standard Deviation	0.2061
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2.4. Mapping Quality

Mean Mapping Quality	44.58
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2.5. Mismatches and indels

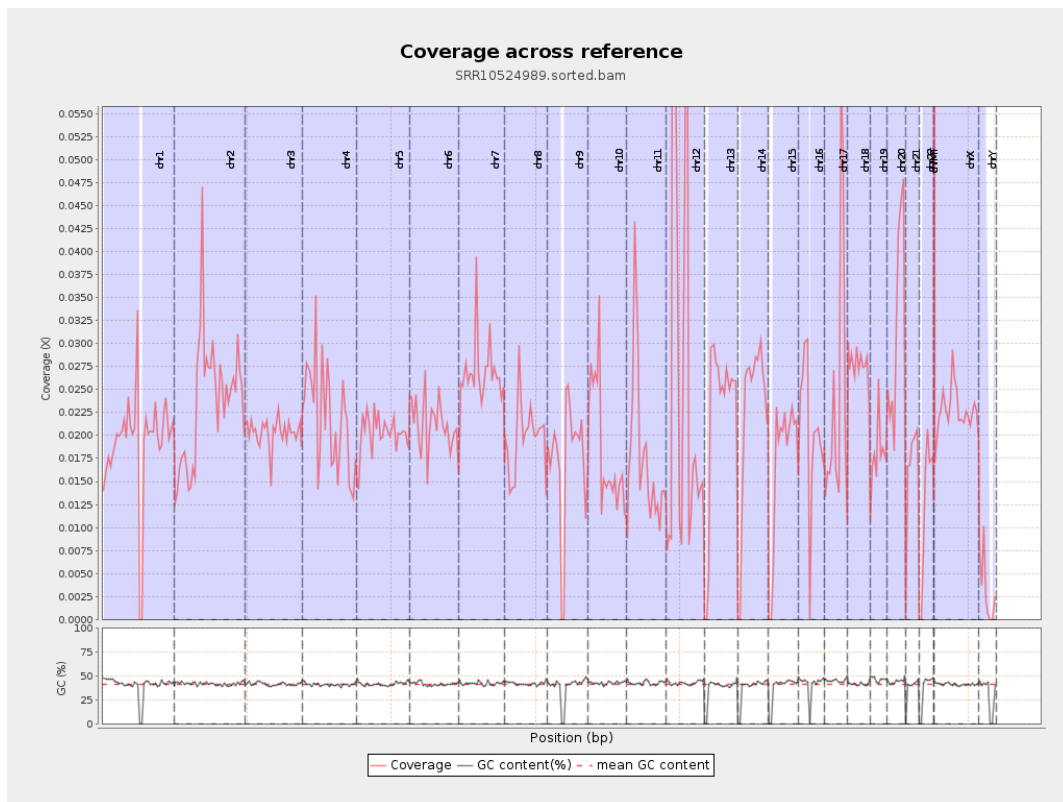
General error rate	0.49%
Mismatches	311,447
Insertions	4,831
Mapped reads with at least one insertion	0.42%
Deletions	9,791
Mapped reads with at least one deletion	0.85%
Homopolymer indels	41.98%

2.6. Chromosome stats

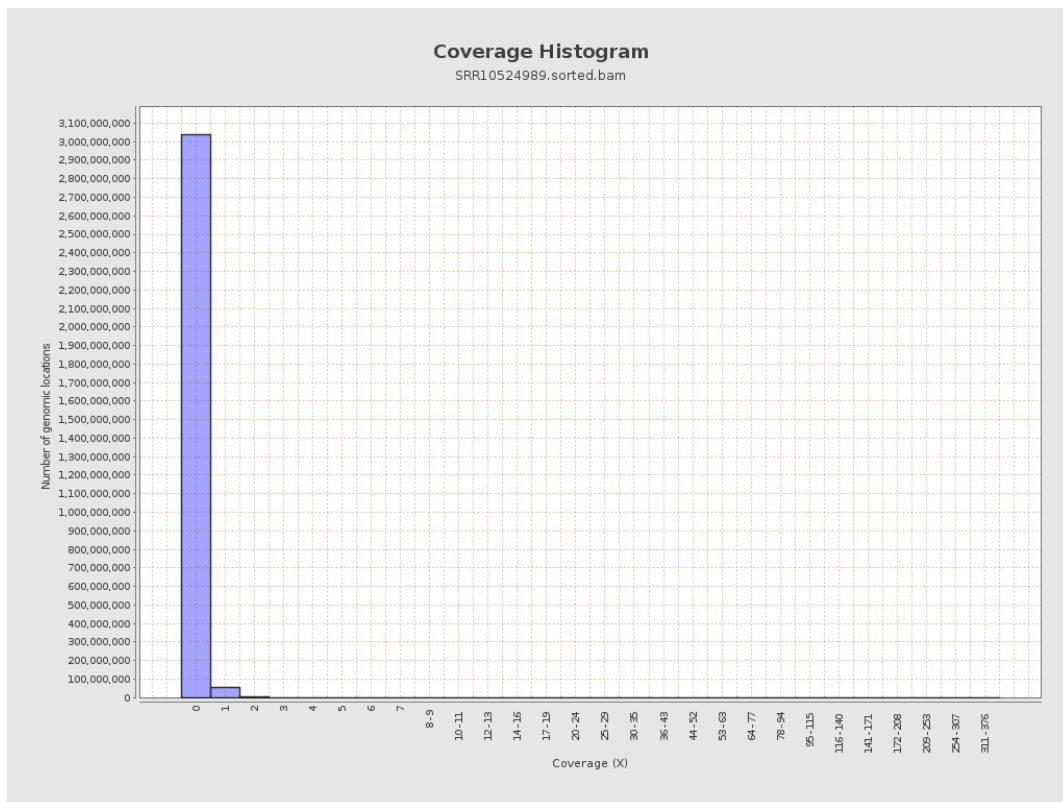
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4795749	0.0192	0.3229
chr2	243199373	5749628	0.0236	0.2308
chr3	198022430	4028802	0.0203	0.1499
chr4	191154276	4144068	0.0217	0.1668
chr5	180915260	3676003	0.0203	0.1517
chr6	171115067	3636453	0.0213	0.1663
chr7	159138663	4271206	0.0268	0.2777

chr8	146364022	2906007	0.0199	0.1949
chr9	141213431	2444724	0.0173	0.2046
chr10	135534747	2499158	0.0184	0.1993
chr11	135006516	2373366	0.0176	0.1767
chr12	133851895	3901389	0.0291	0.1999
chr13	115169878	2548210	0.0221	0.1566
chr14	107349540	2395159	0.0223	0.1675
chr15	102531392	1739634	0.017	0.1383
chr16	90354753	1829208	0.0202	0.1586
chr17	81195210	1970311	0.0243	0.1688
chr18	78077248	2164976	0.0277	0.3464
chr19	59128983	1085118	0.0184	0.2542
chr20	63025520	2026392	0.0322	0.1947
chr21	48129895	798906	0.0166	0.149
chr22	51304566	638519	0.0124	0.1175
chrMT	16571	2386	0.144	0.4272
chrX	155270560	3536928	0.0228	0.1782
chrY	59373566	184120	0.0031	0.082

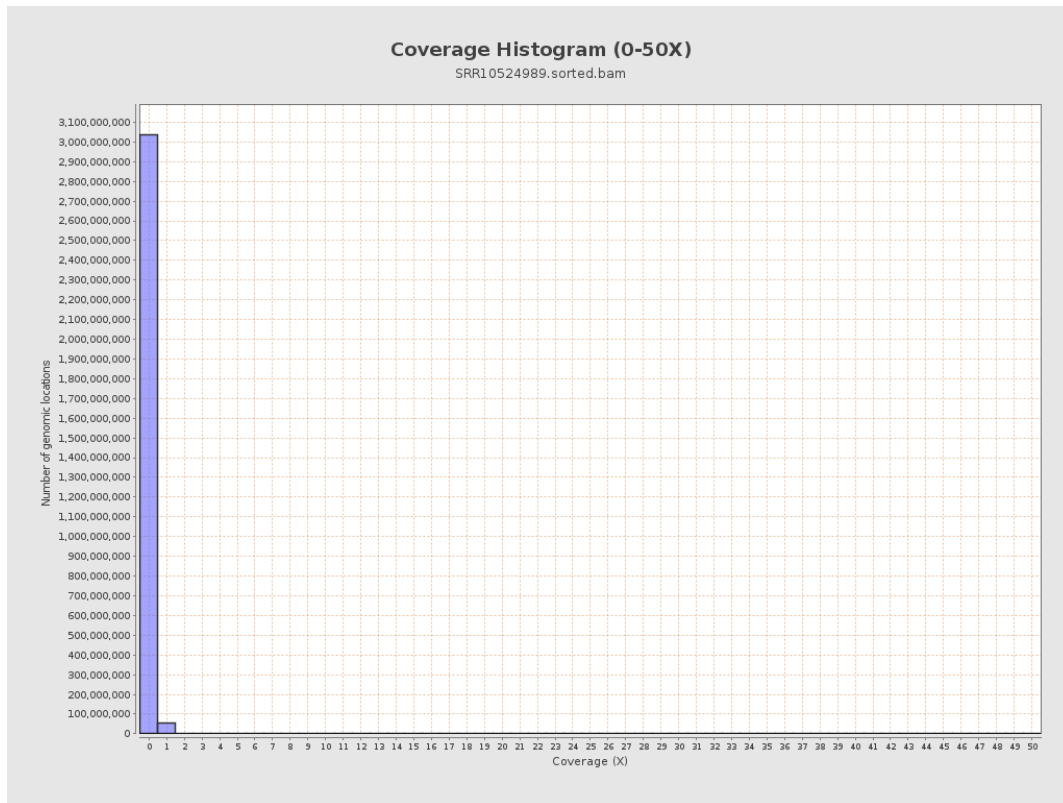
3. Results : Coverage across reference



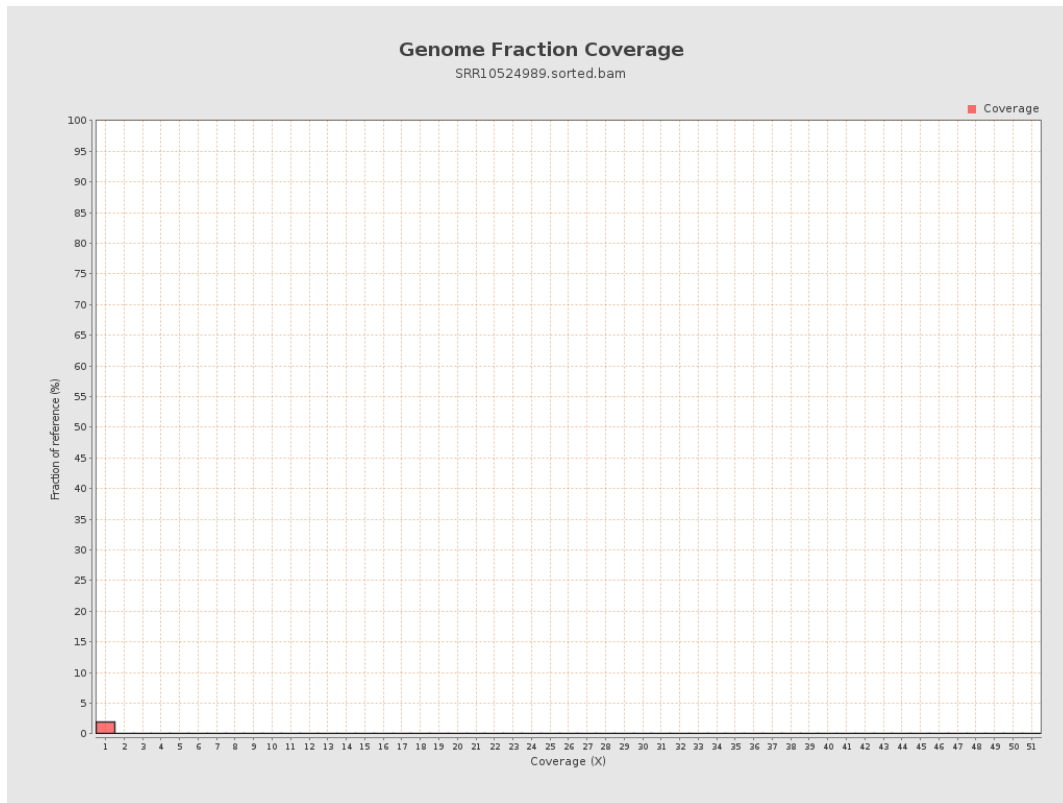
4. Results : Coverage Histogram



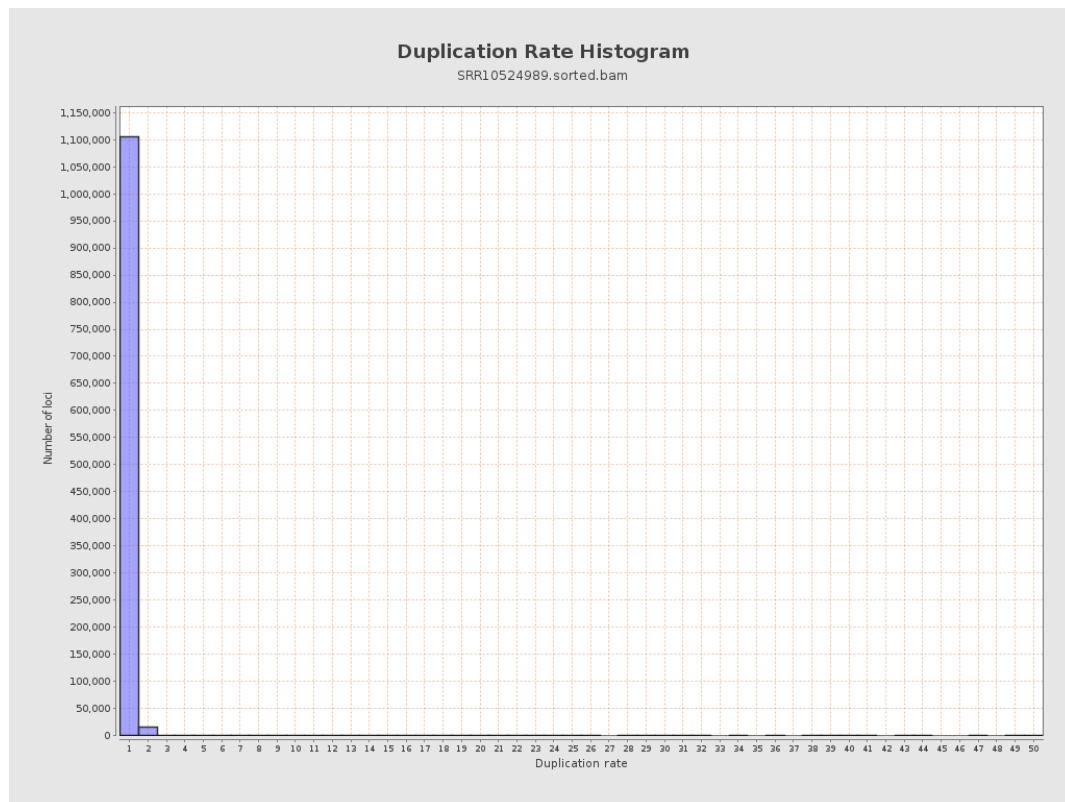
5. Results : Coverage Histogram (0-50X)



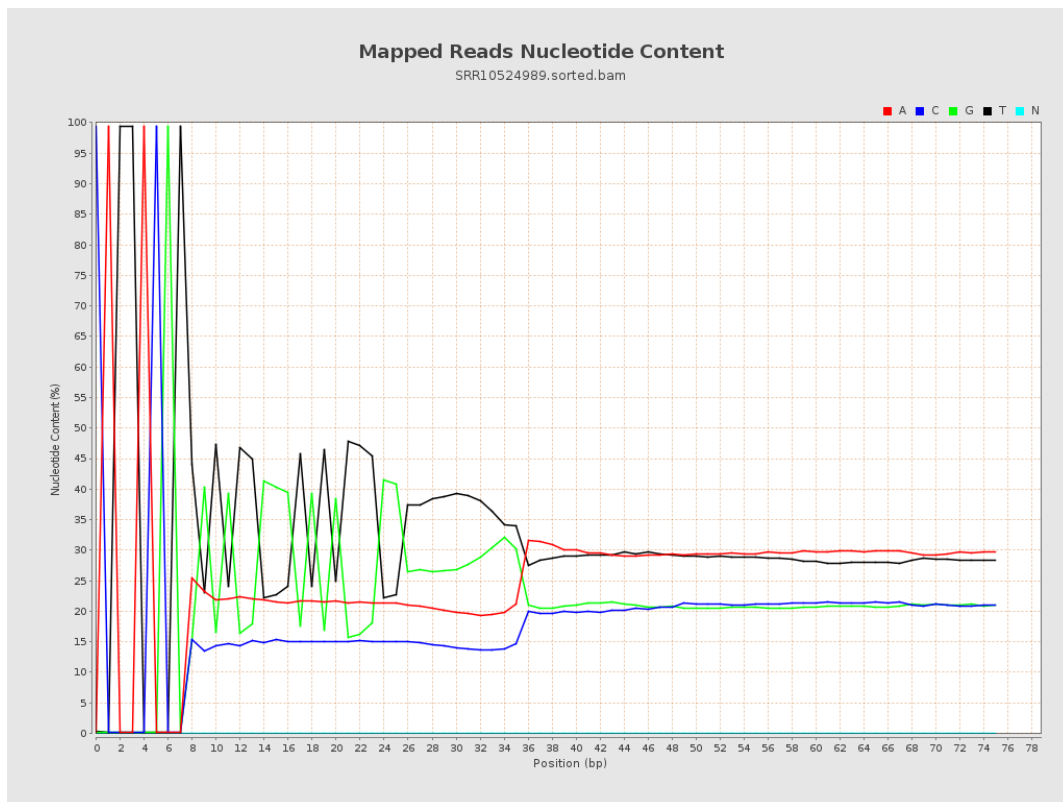
6. Results : Genome Fraction Coverage



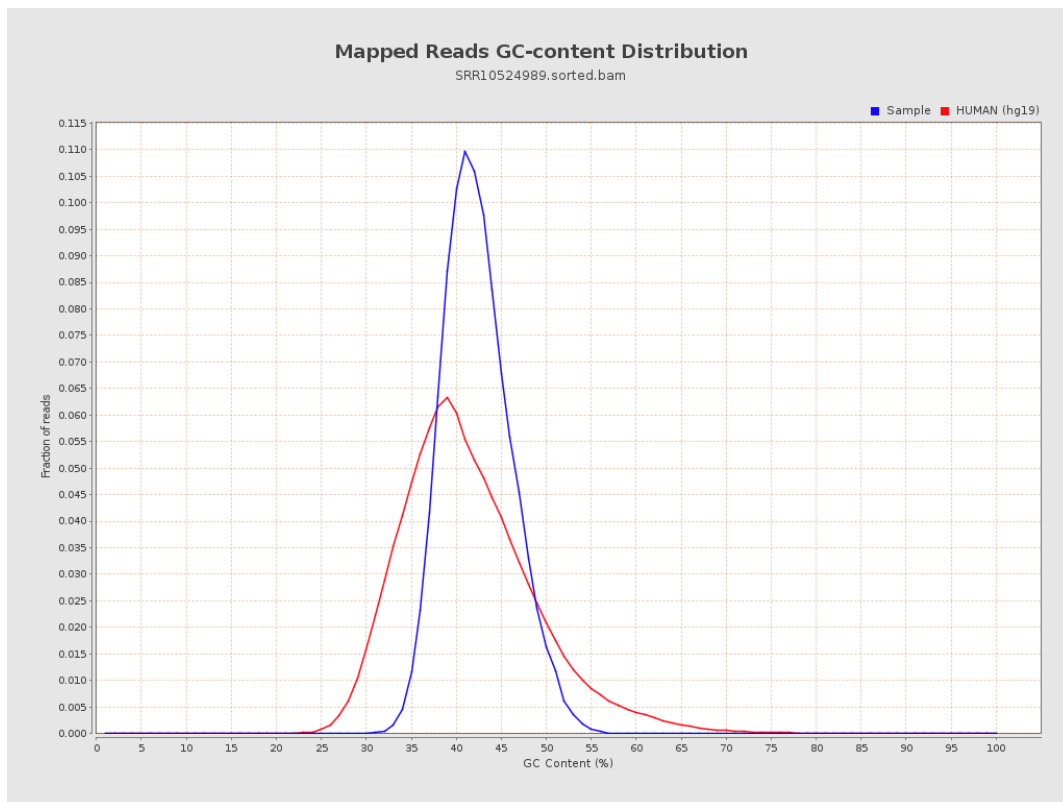
7. Results : Duplication Rate Histogram



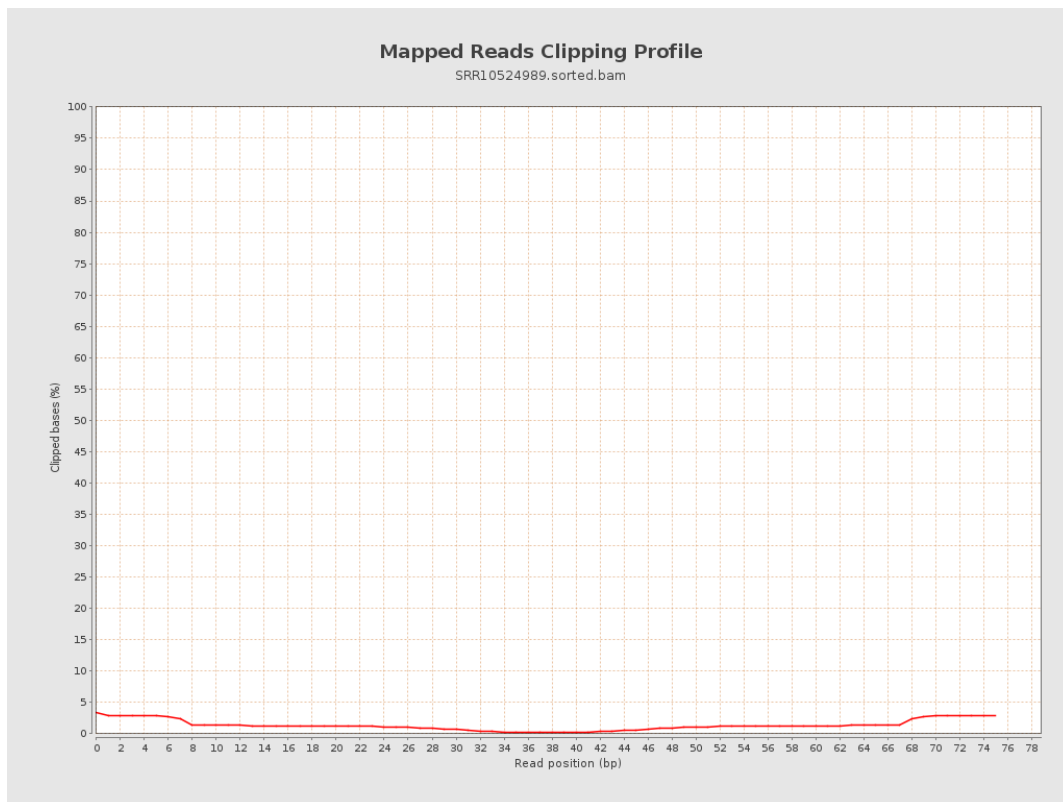
8. Results : Mapped Reads Nucleotide Content



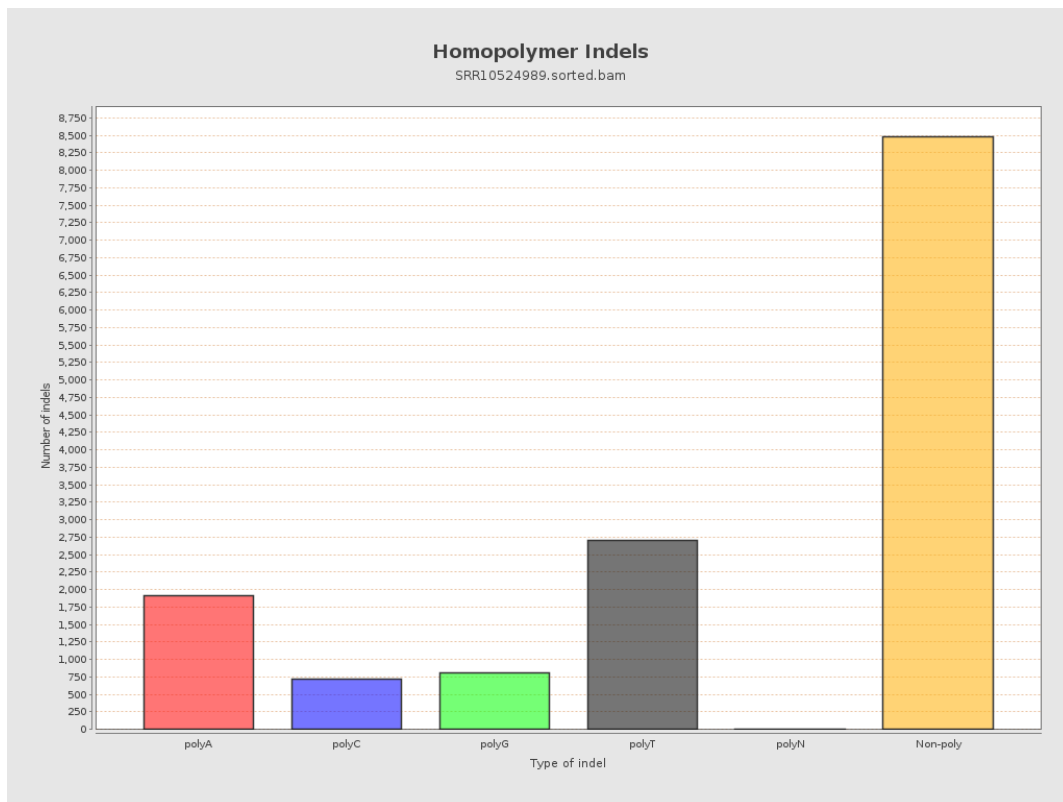
9. Results : Mapped Reads GC-content Distribution



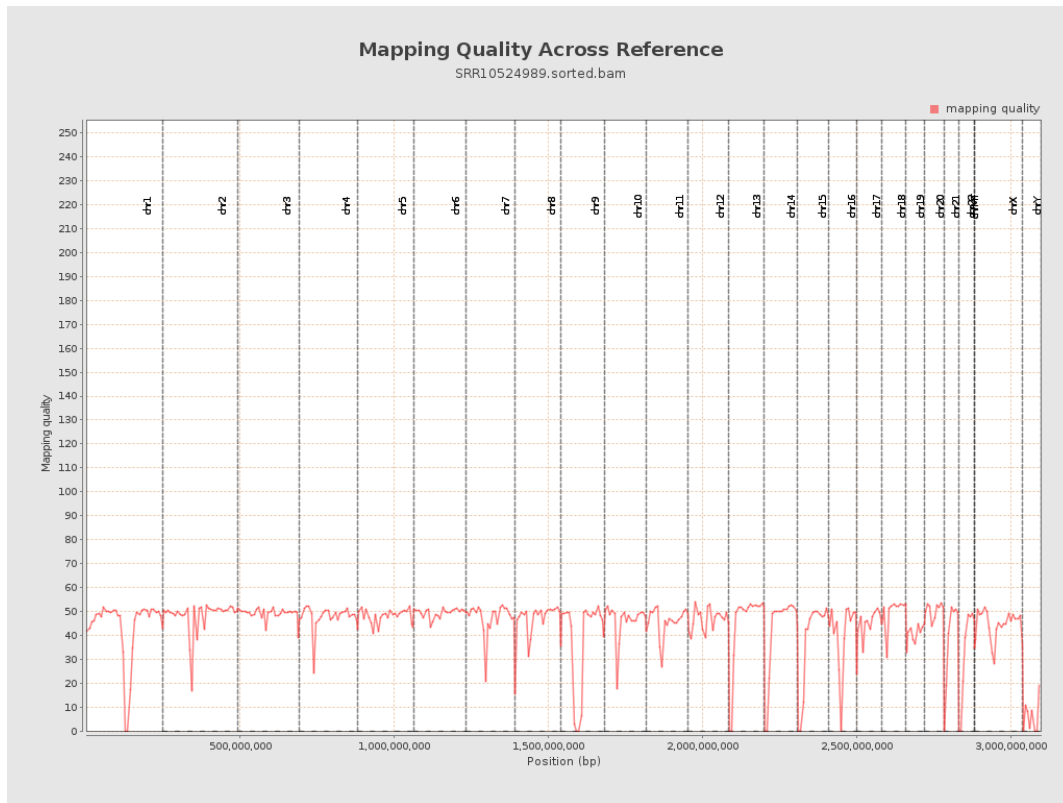
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

