Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 19:26:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084889.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_SRR3084889 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084889.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 19:26:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084889.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,566,248
Mapped reads	2,285,911 / 89.08%
Unmapped reads	280,337 / 10.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,498 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	106,244 / 4.14%
Duplication rate	3.91%
Clipped reads	785,246 / 30.6%

2.2. ACGT Content

Number/percentage of A's	46,060,277 / 29.12%
Number/percentage of C's	29,010,146 / 18.34%
Number/percentage of T's	50,684,706 / 32.04%
Number/percentage of G's	32,400,877 / 20.48%
Number/percentage of N's	24,728 / 0.02%
GC Percentage	38.82%

2.3. Coverage

Mean	0.0511

Standard Deviation	0.4171

2.4. Mapping Quality

Mean Mapping Quality	47.68

2.5. Mismatches and indels

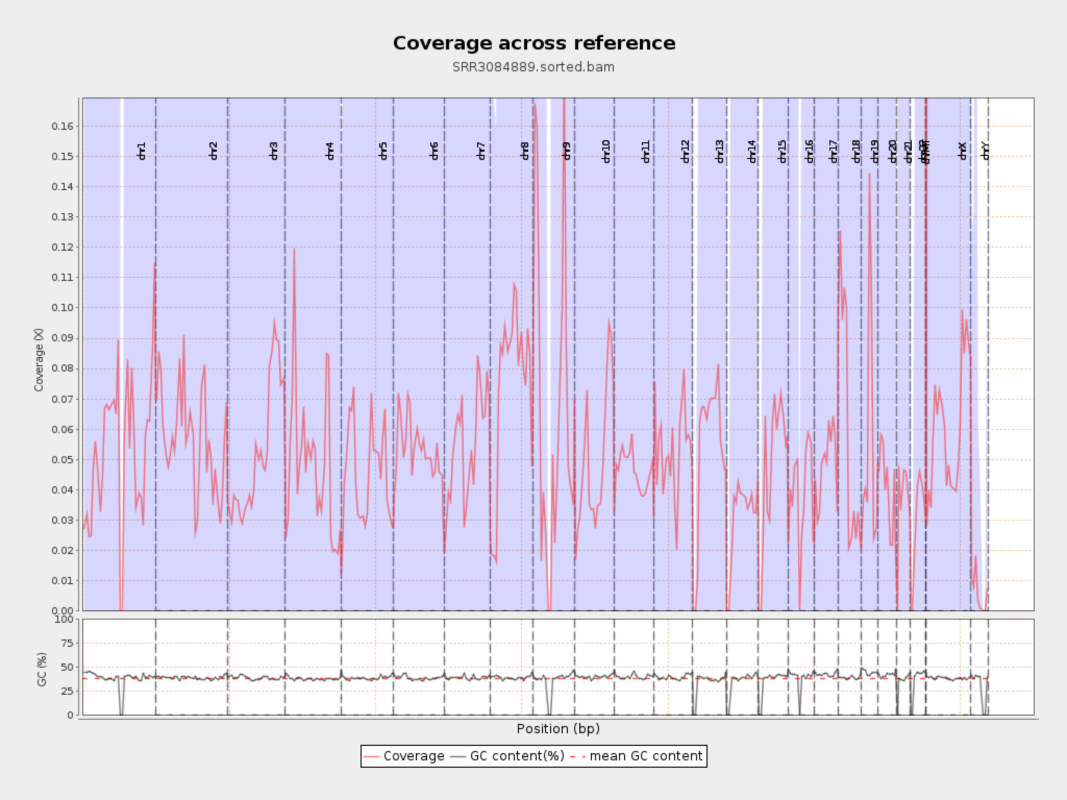
General error rate	0.84%
Mismatches	1,309,406
Insertions	12,861
Mapped reads with at least one insertion	0.56%
Deletions	34,362
Mapped reads with at least one deletion	1.49%
Homopolymer indels	48.36%

2.6. Chromosome stats

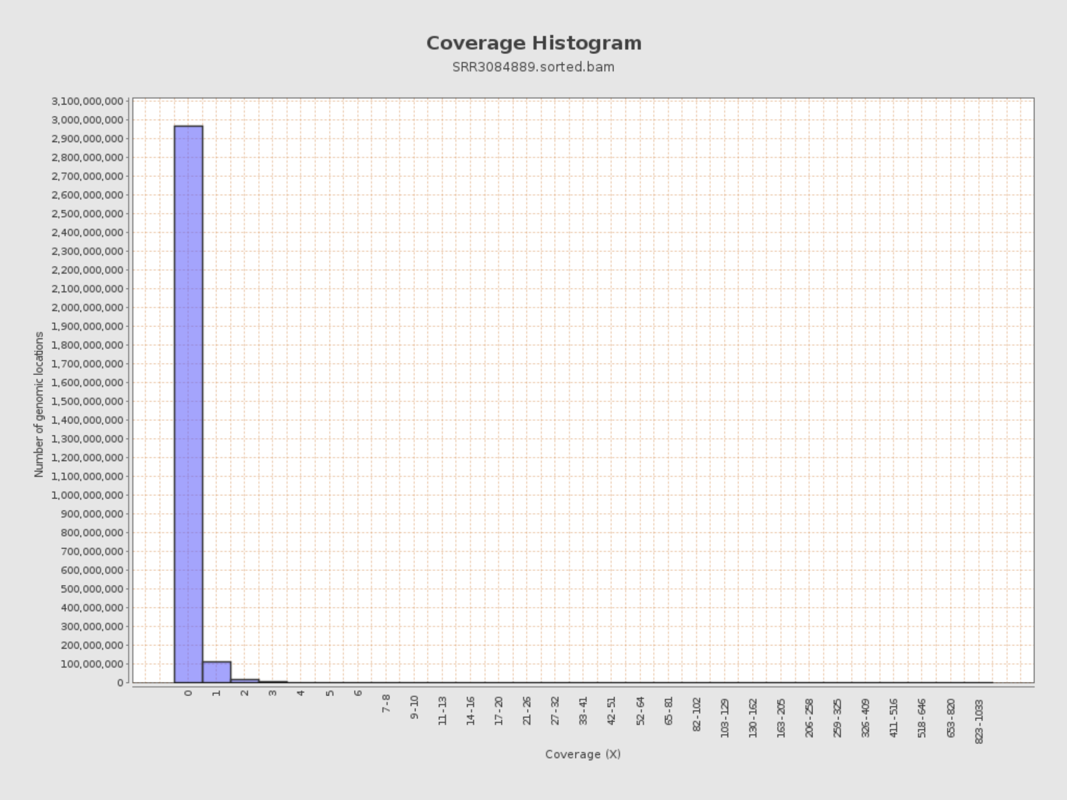
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13203481	0.053	0.858
chr2	243199373	13729471	0.0565	0.4089
chr3	198022430	10348419	0.0523	0.2631
chr4	191154276	9196261	0.0481	0.2621
chr5	180915260	8252695	0.0456	0.2594
chr6	171115067	9130406	0.0534	0.2751
chr7	159138663	8672636	0.0545	0.3768

chr8	146364022	10970610	0.075	0.7358
chr9	141213431	9250452	0.0655	0.3954
chr10	135534747	6652801	0.0491	0.3579
chr11	135006516	6262484	0.0464	0.3085
chr12	133851895	7196417	0.0538	0.2699
chr13	115169878	6167484	0.0536	0.266
chr14	107349540	3319598	0.0309	0.218
chr15	102531392	4818698	0.047	0.2494
chr16	90354753	3376990	0.0374	0.2381
chr17	81195210	3949452	0.0486	0.2632
chr18	78077248	4819660	0.0617	0.6285
chr19	59128983	3332630	0.0564	0.4778
chr20	63025520	2581480	0.041	0.2401
chr21	48129895	1788760	0.0372	0.2381
chr22	51304566	1495340	0.0291	0.1947
chrMT	16571	60473	3.6493	2.5079
chrX	155270560	9319275	0.06	0.2996
chrY	59373566	346047	0.0058	0.1203

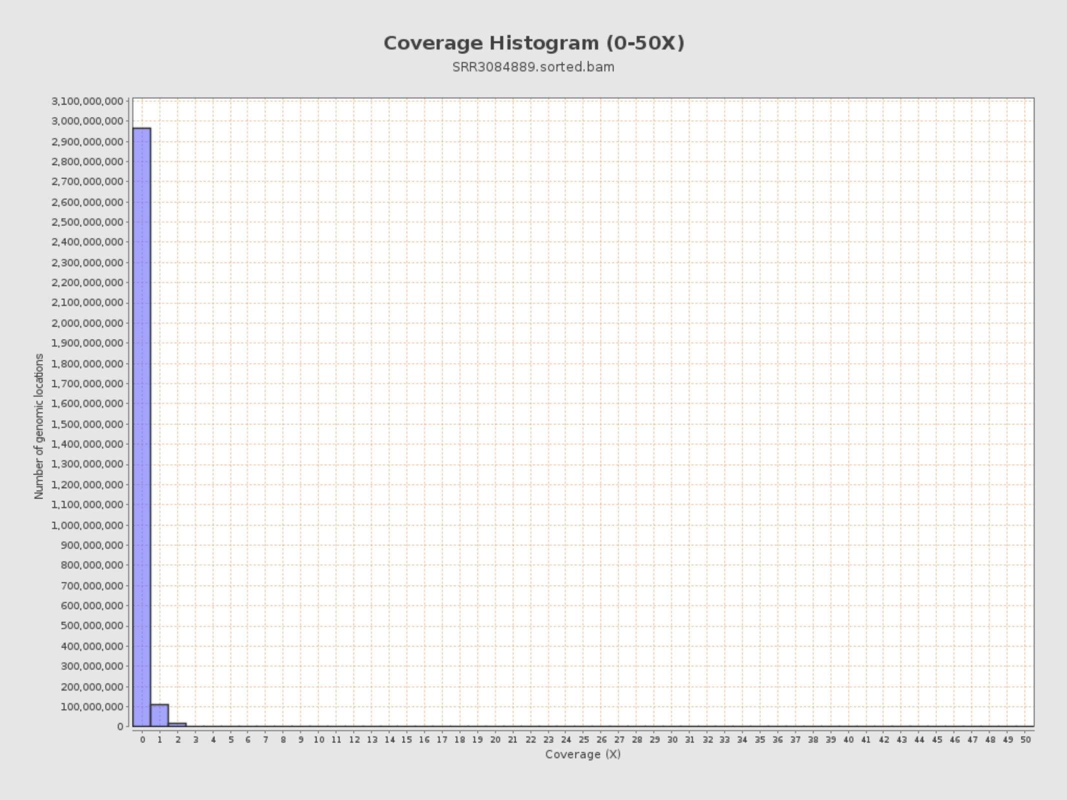
3. Results : Coverage across reference



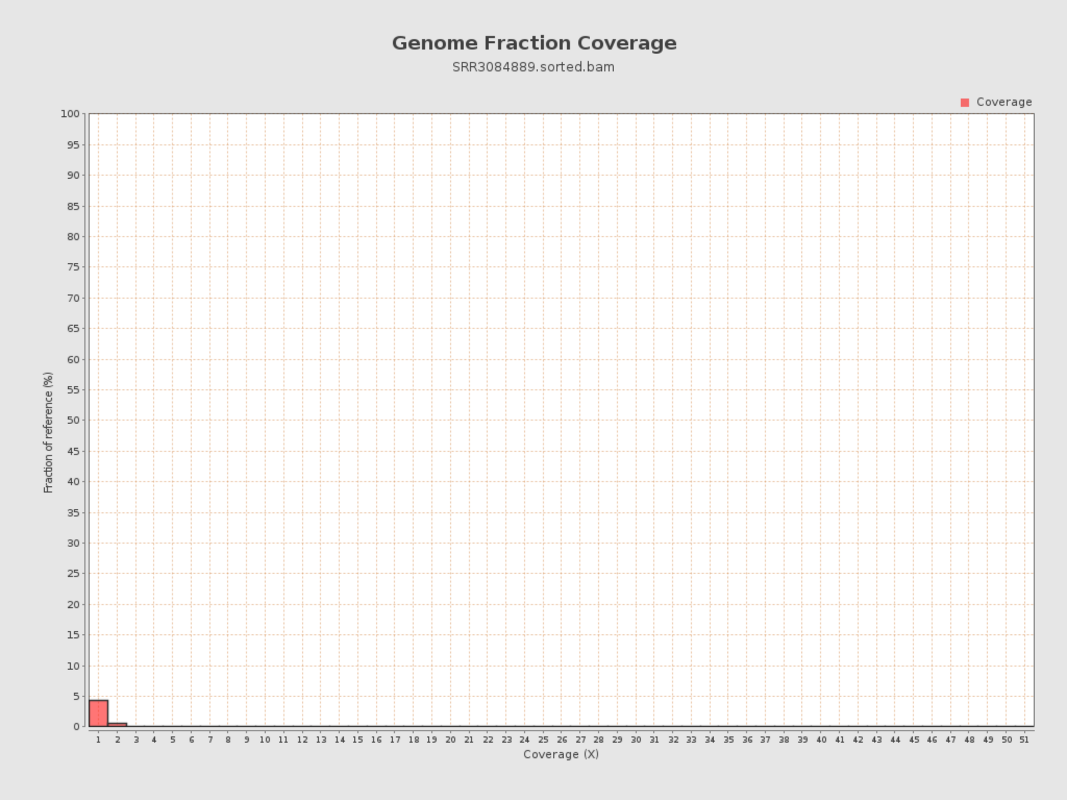
4. Results : Coverage Histogram



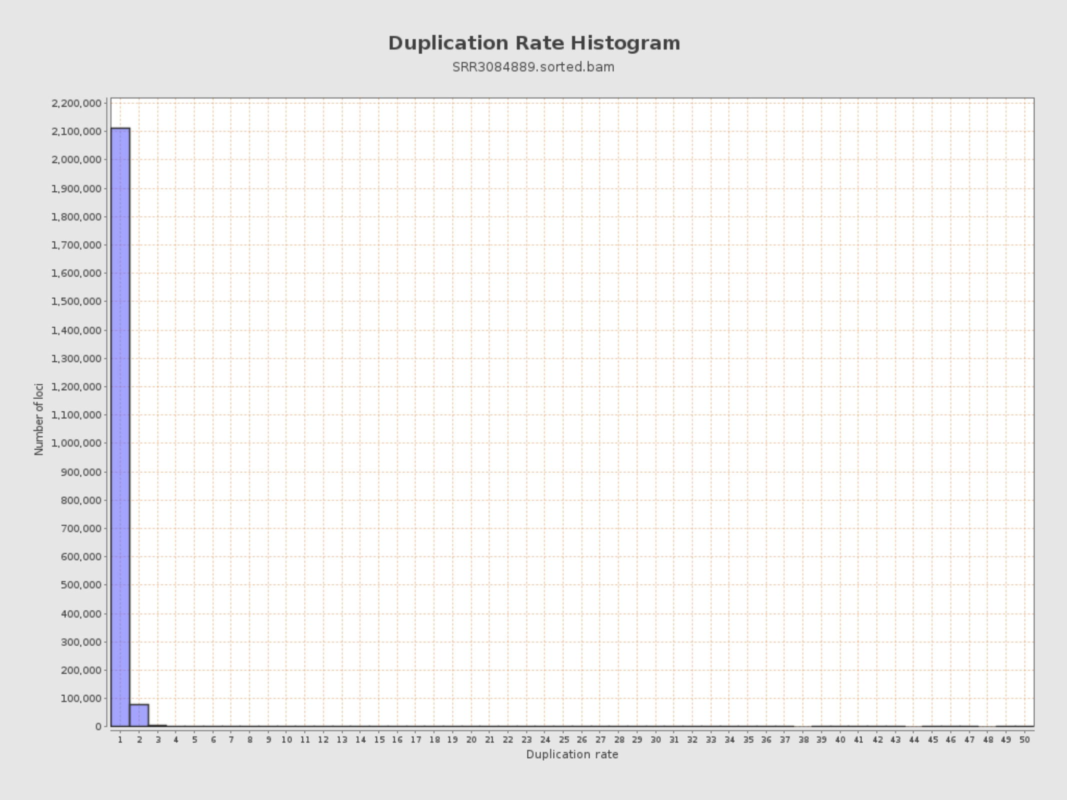
5. Results : Coverage Histogram (0-50X)



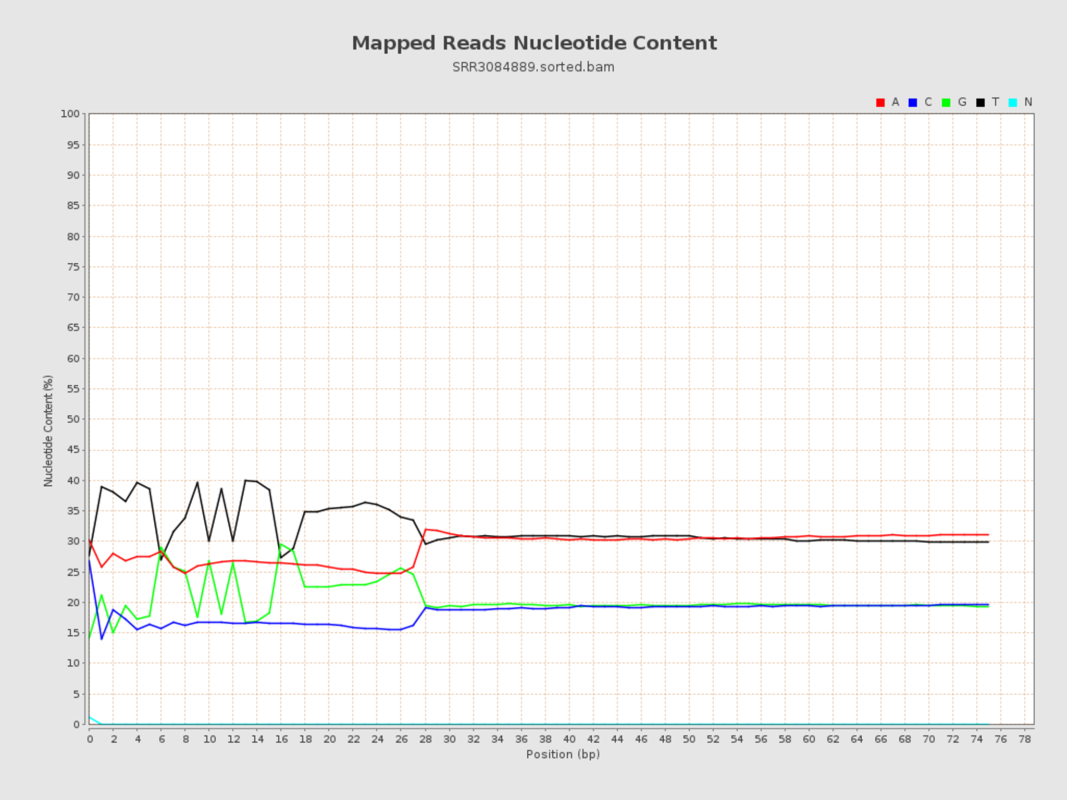
6. Results : Genome Fraction Coverage



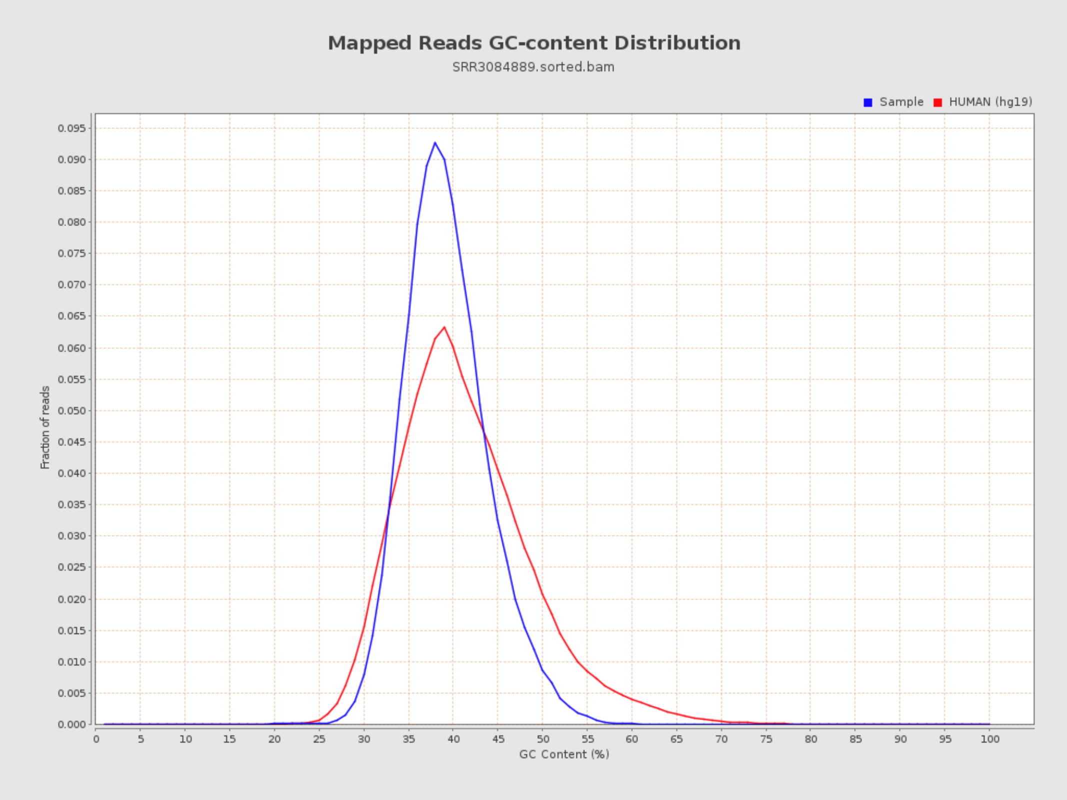
7. Results : Duplication Rate Histogram



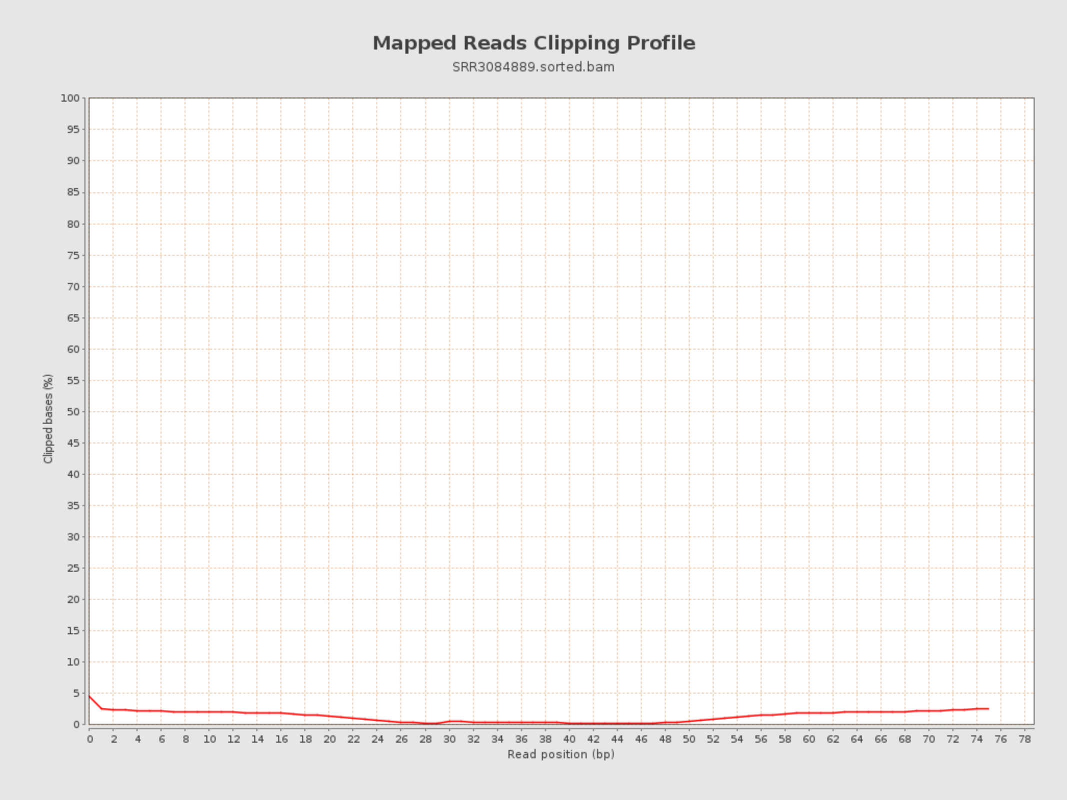
8. Results : Mapped Reads Nucleotide Content



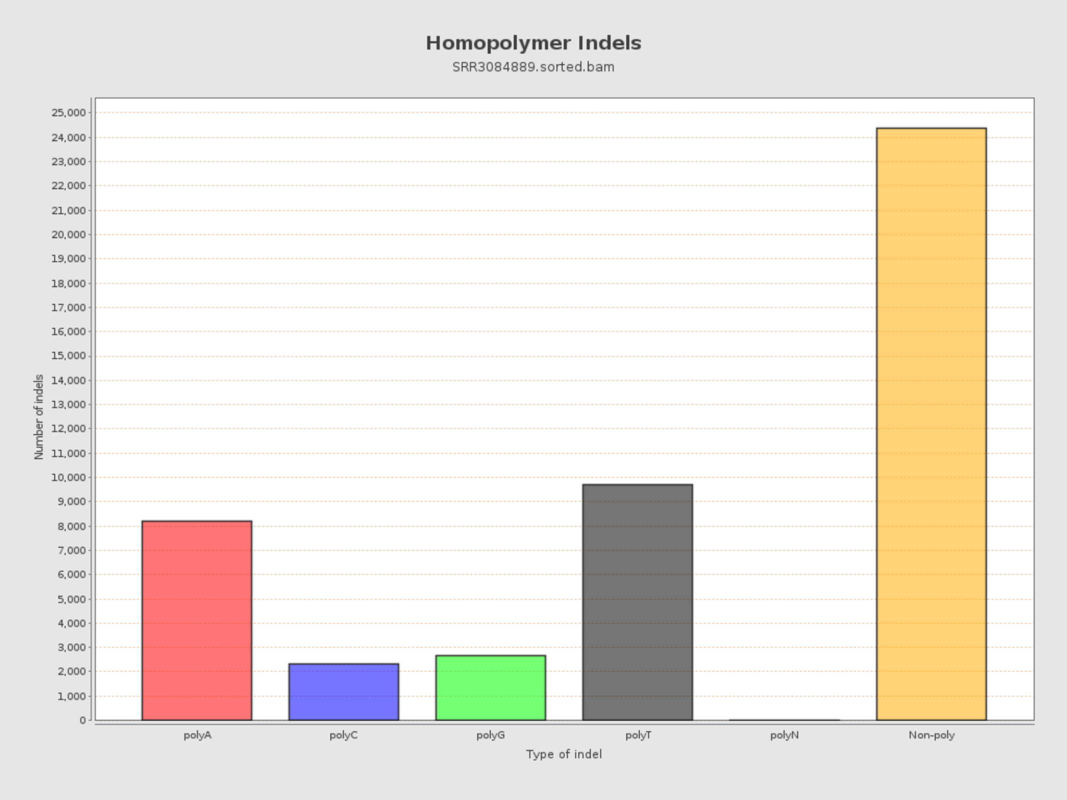
9. Results : Mapped Reads GC-content Distribution



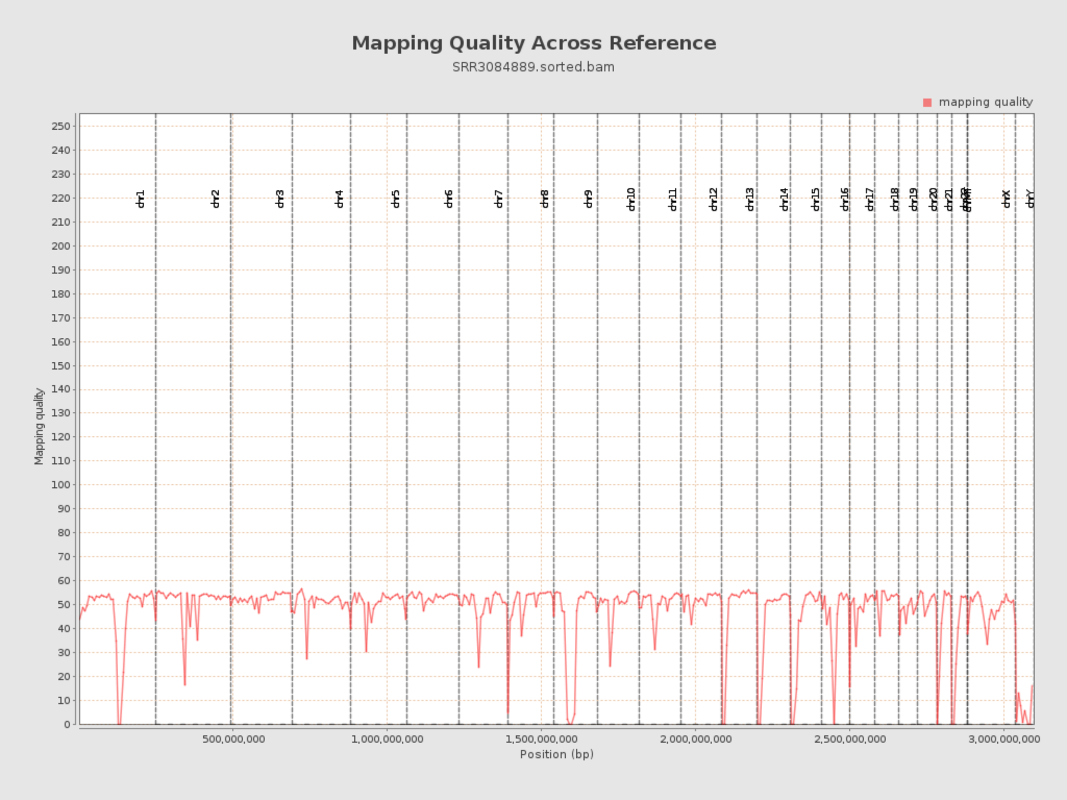
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram