Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 19:00:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082899.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_SRR3082899 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082899.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 19:00:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082899.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,118,636
Mapped reads	2,673,880 / 85.74%
Unmapped reads	444,756 / 14.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,133 / 0.65%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	155,185 / 4.98%
Duplication rate	4.66%
Clipped reads	1,106,343 / 35.48%

2.2. ACGT Content

Number/percentage of A's	51,137,236 / 28.31%
Number/percentage of C's	32,578,905 / 18.03%
Number/percentage of T's	59,136,954 / 32.74%
Number/percentage of G's	37,787,004 / 20.92%
Number/percentage of N's	10,068 / 0.01%
GC Percentage	38.95%

2.3. Coverage

Mean	0.0584

Standard Deviation	0.505

2.4. Mapping Quality

Mean Mapping Quality	47.26

2.5. Mismatches and indels

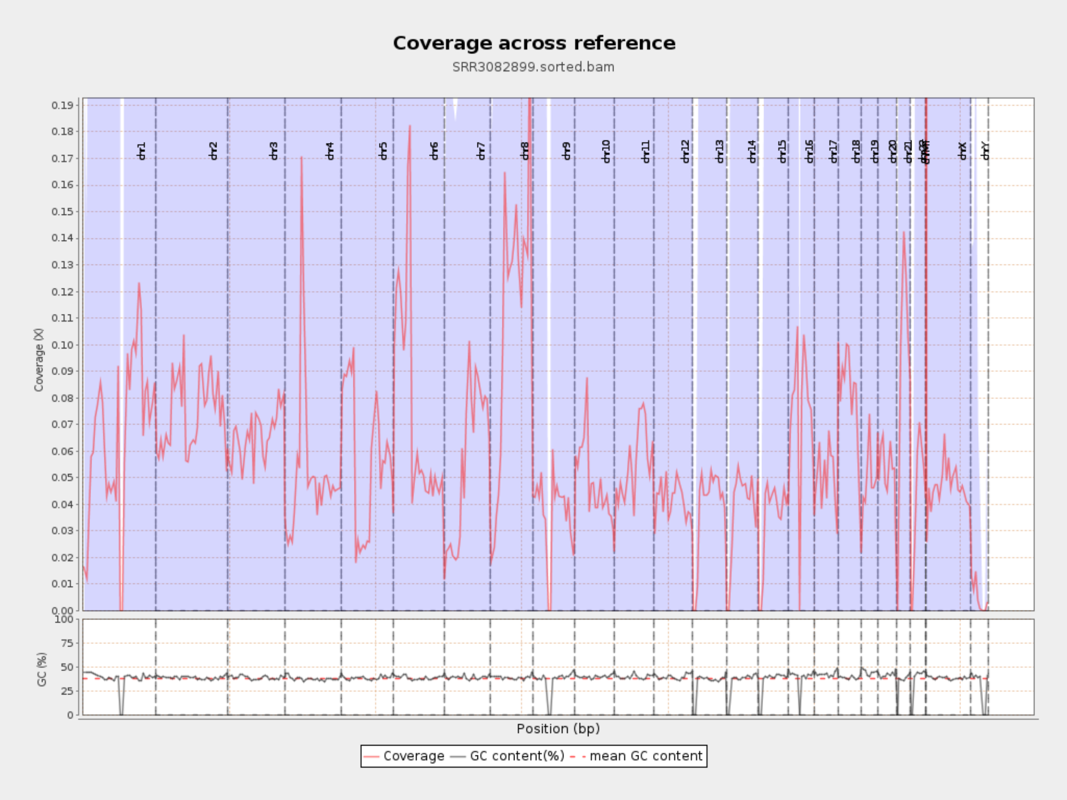
General error rate	0.89%
Mismatches	1,583,215
Insertions	14,420
Mapped reads with at least one insertion	0.54%
Deletions	39,641
Mapped reads with at least one deletion	1.47%
Homopolymer indels	47.83%

2.6. Chromosome stats

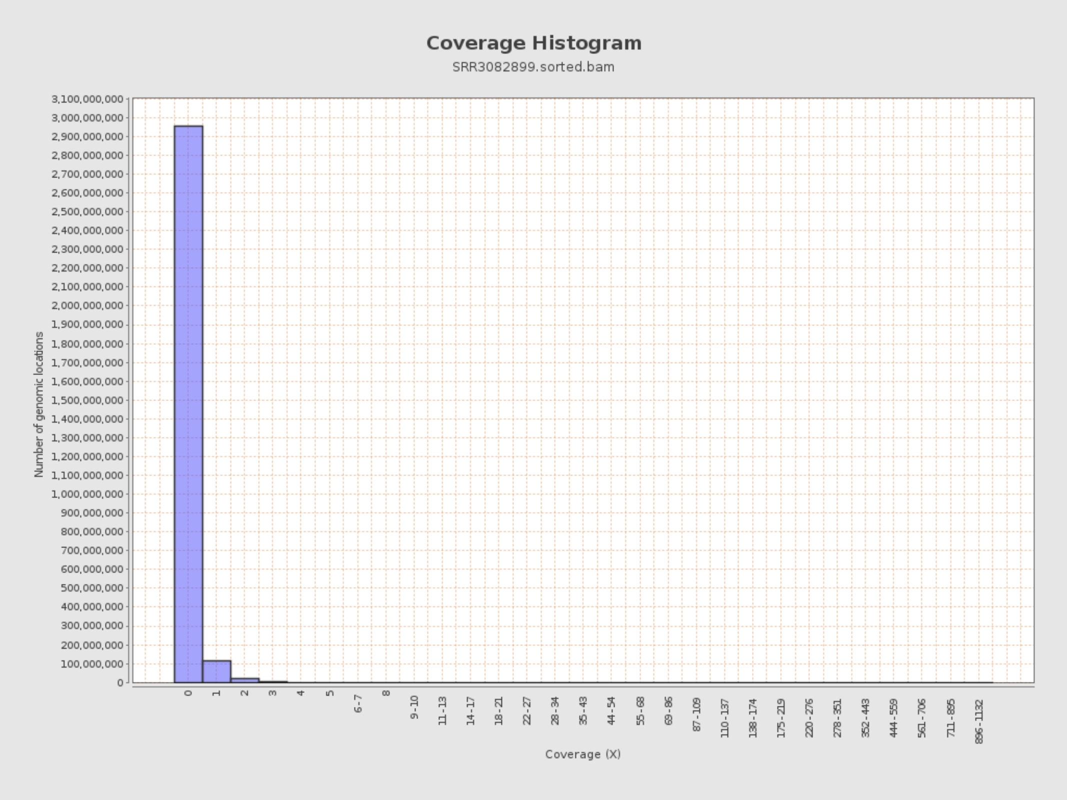
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16459138	0.066	1.0169
chr2	243199373	18185167	0.0748	0.5524
chr3	198022430	12971468	0.0655	0.3153
chr4	191154276	10213770	0.0534	0.2881
chr5	180915260	10353476	0.0572	0.2924
chr6	171115067	13054164	0.0763	0.5315
chr7	159138663	8925942	0.0561	0.3885

chr8	146364022	16131133	0.1102	0.7322
chr9	141213431	5178426	0.0367	0.3968
chr10	135534747	6618631	0.0488	0.4564
chr11	135006516	7450073	0.0552	0.3578
chr12	133851895	5537415	0.0414	0.2579
chr13	115169878	4424345	0.0384	0.2376
chr14	107349540	4083579	0.038	0.2837
chr15	102531392	3463586	0.0338	0.2211
chr16	90354753	6618862	0.0733	0.3738
chr17	81195210	4142548	0.051	0.3289
chr18	78077248	6411790	0.0821	1.0053
chr19	59128983	2943971	0.0498	0.6481
chr20	63025520	3403449	0.054	0.3041
chr21	48129895	4355159	0.0905	0.374
chr22	51304566	2154334	0.042	0.2446
chrMT	16571	151266	9.1284	5.7402
chrX	155270560	7188981	0.0463	0.3047
chrY	59373566	296575	0.005	0.1035

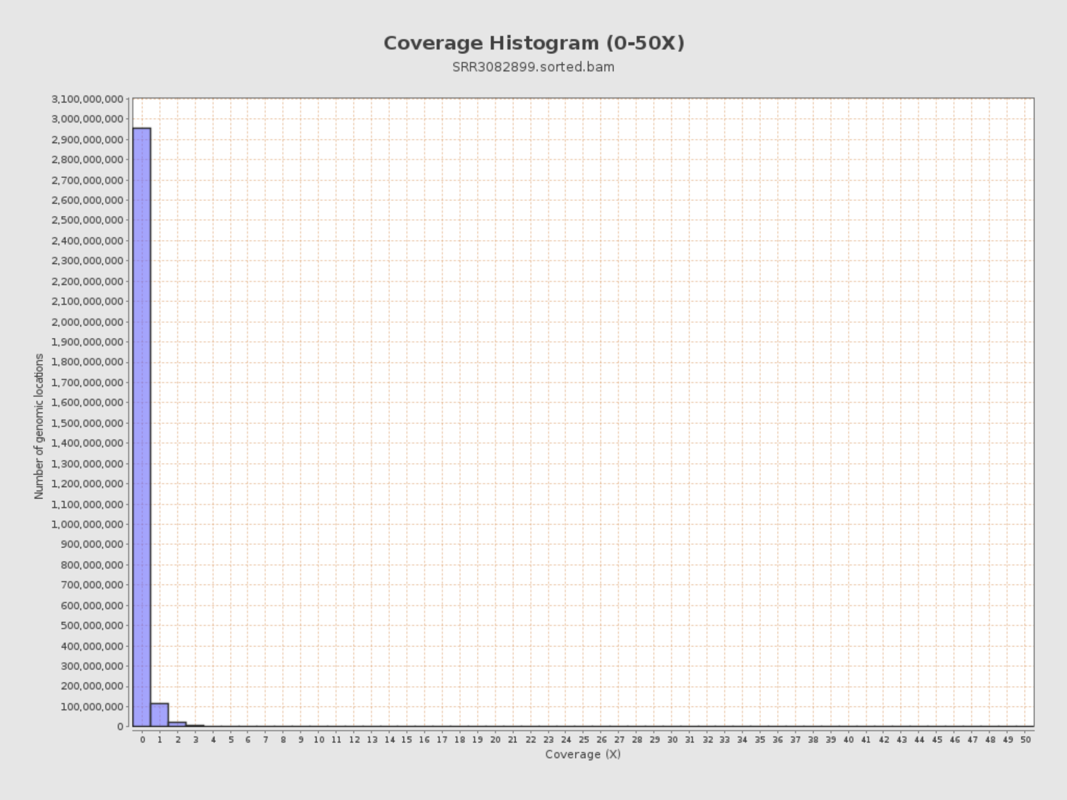
3. Results : Coverage across reference



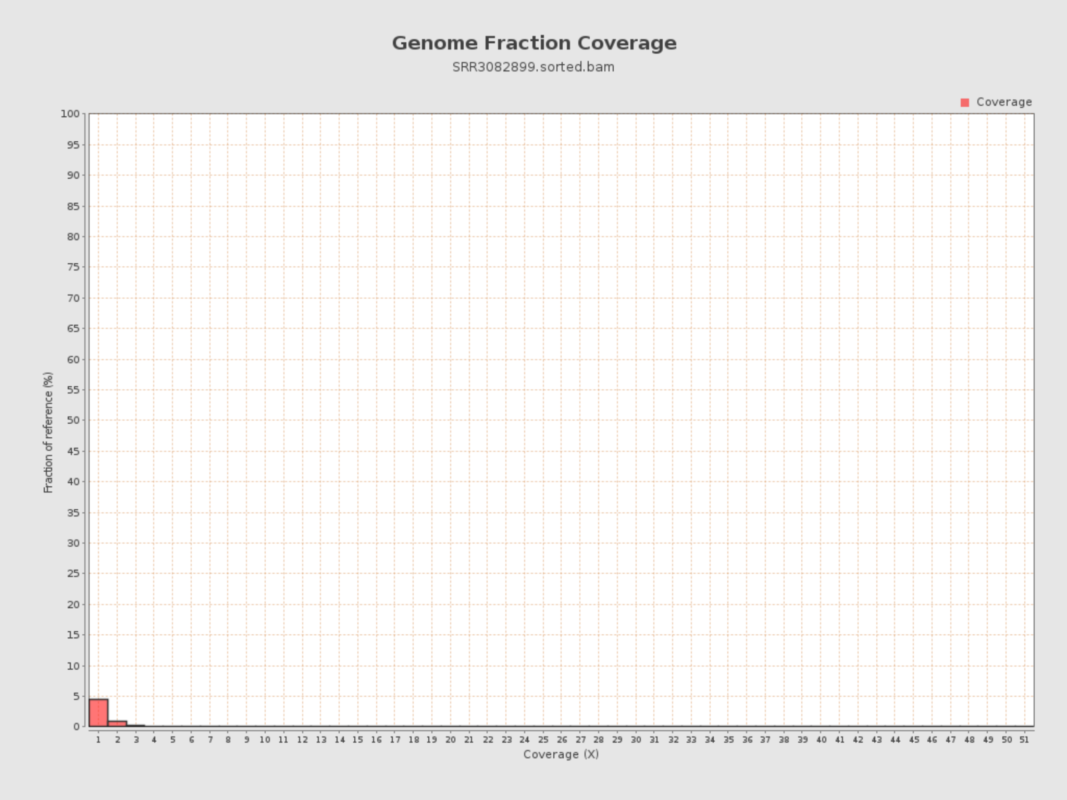
4. Results : Coverage Histogram



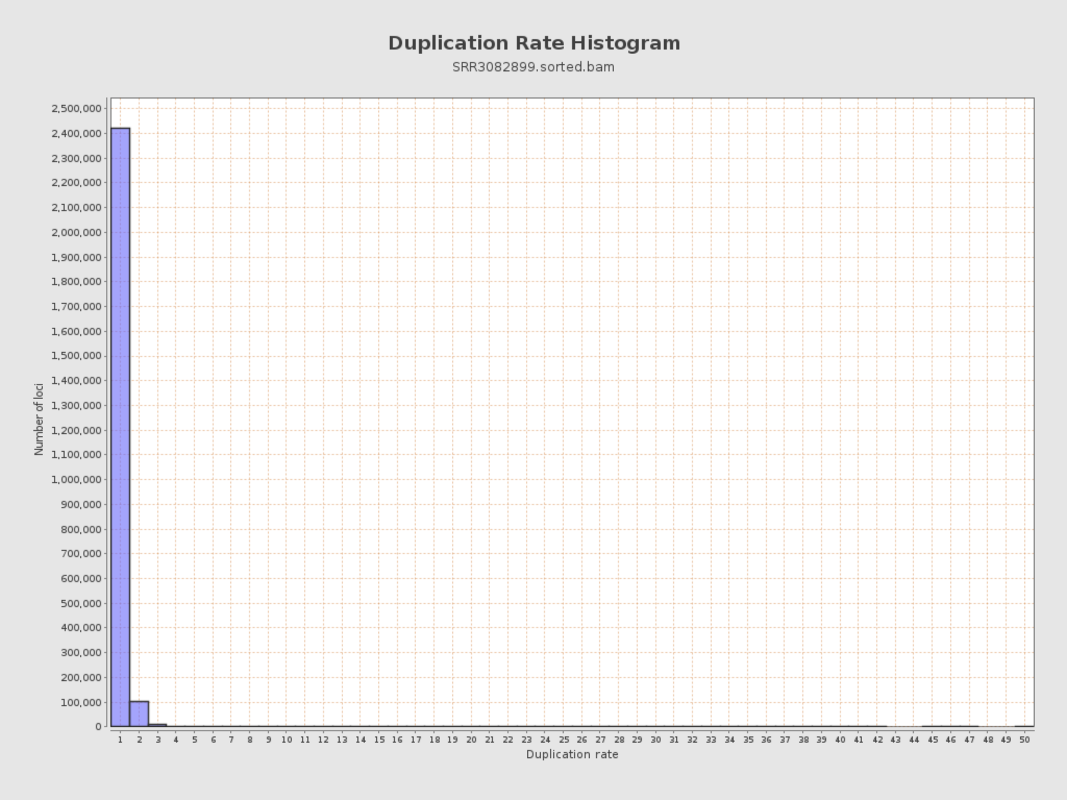
5. Results : Coverage Histogram (0-50X)



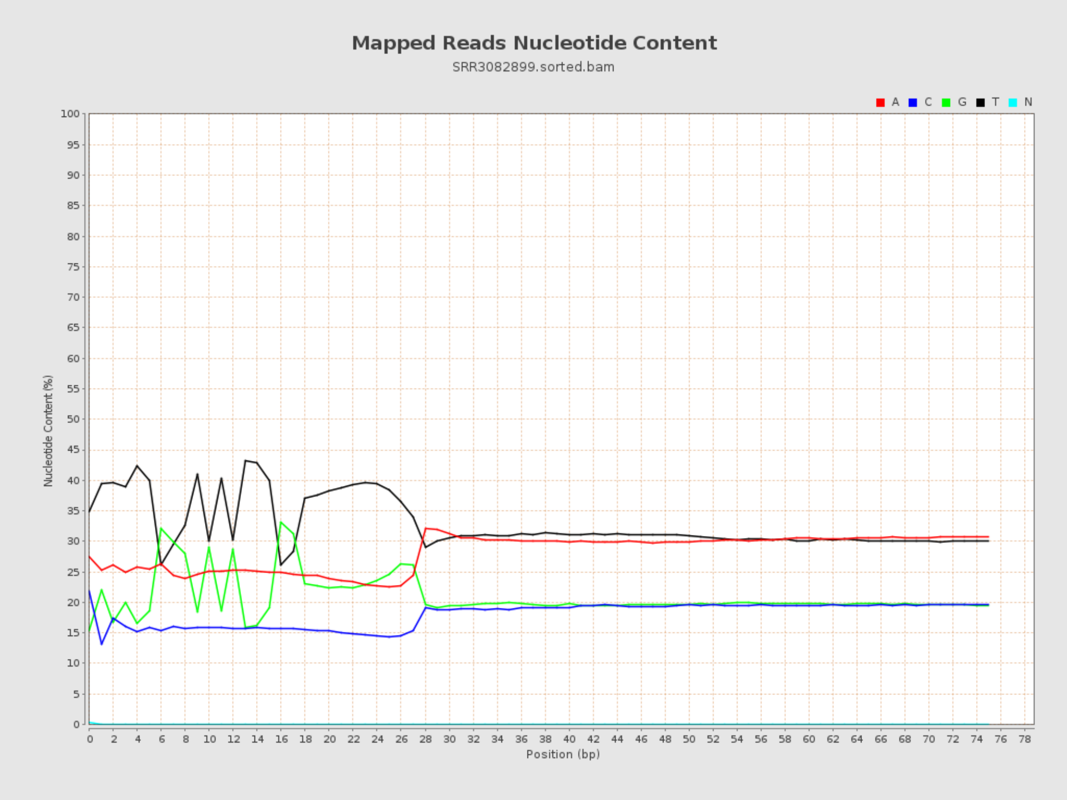
6. Results : Genome Fraction Coverage



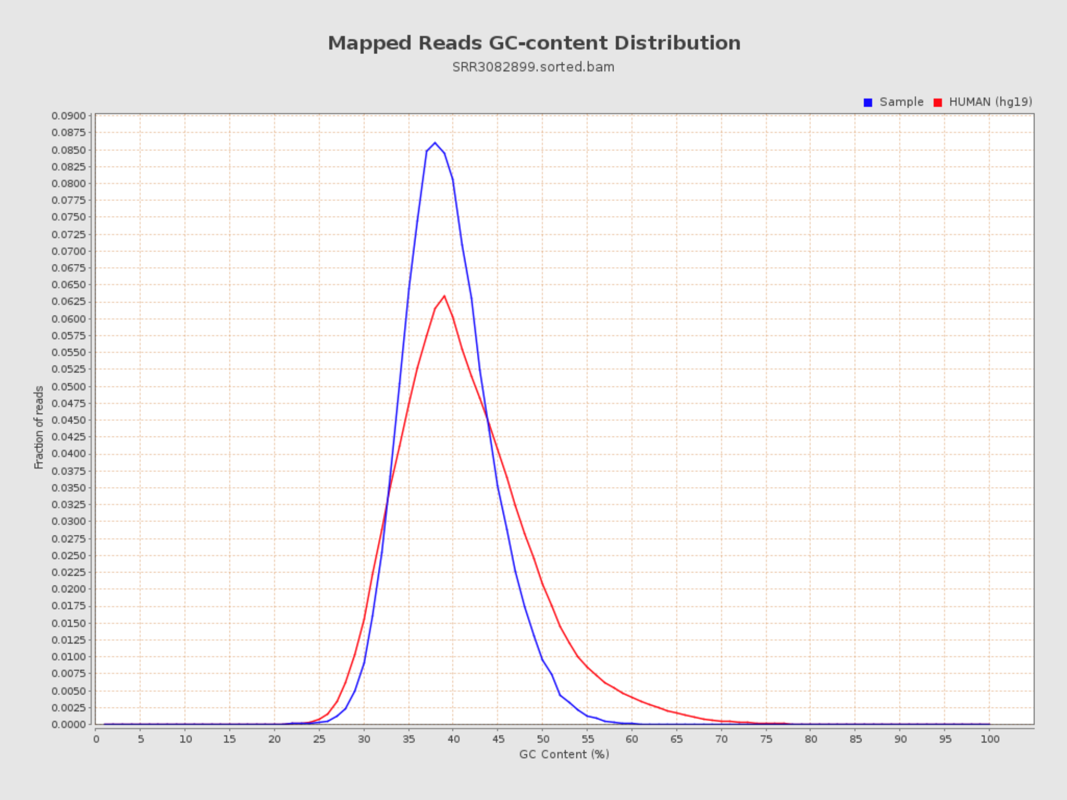
7. Results : Duplication Rate Histogram



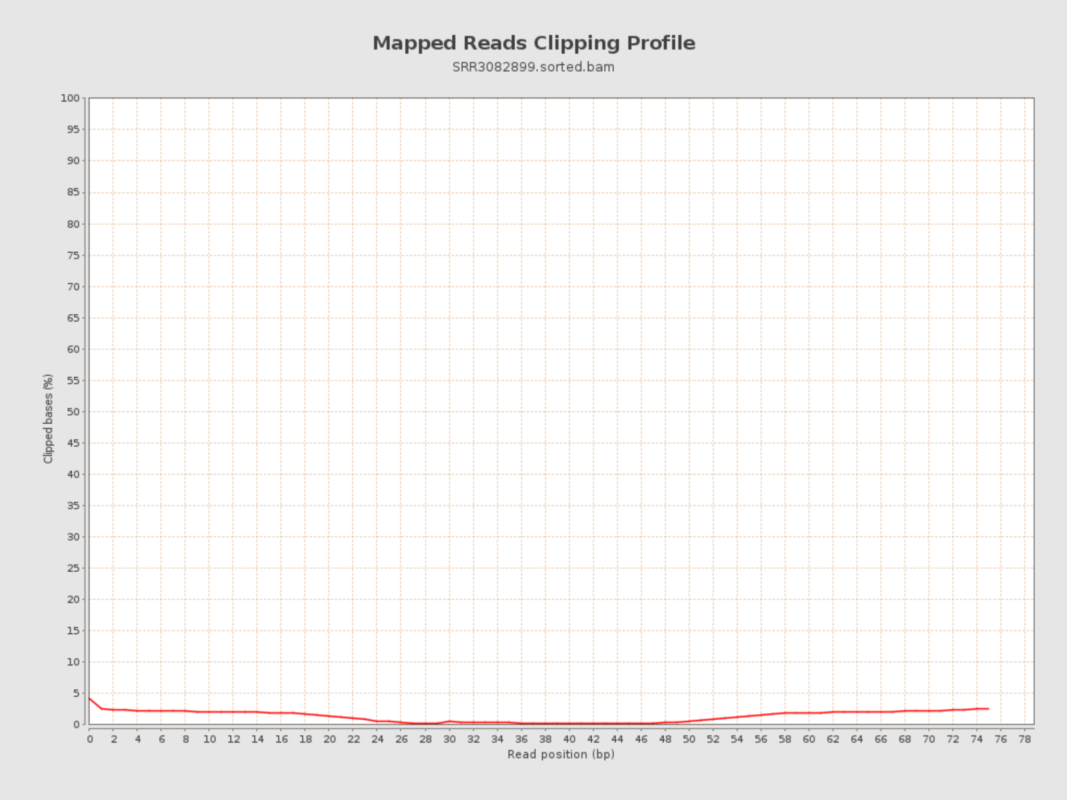
8. Results : Mapped Reads Nucleotide Content



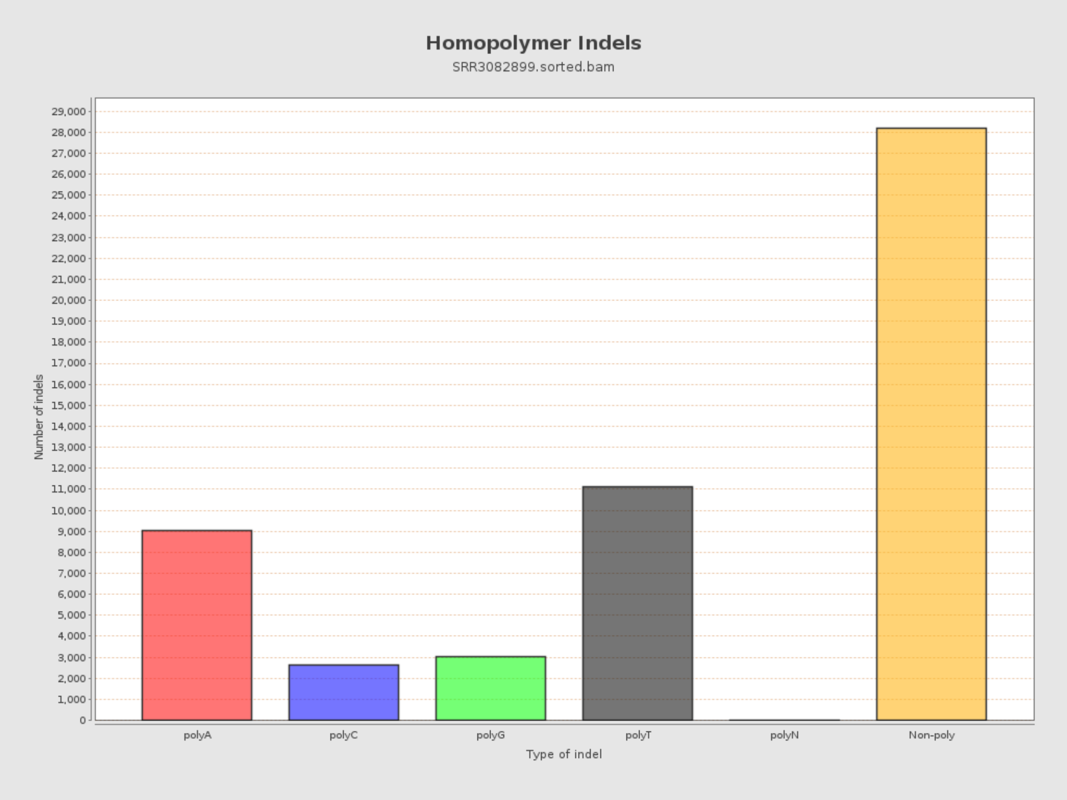
9. Results : Mapped Reads GC-content Distribution



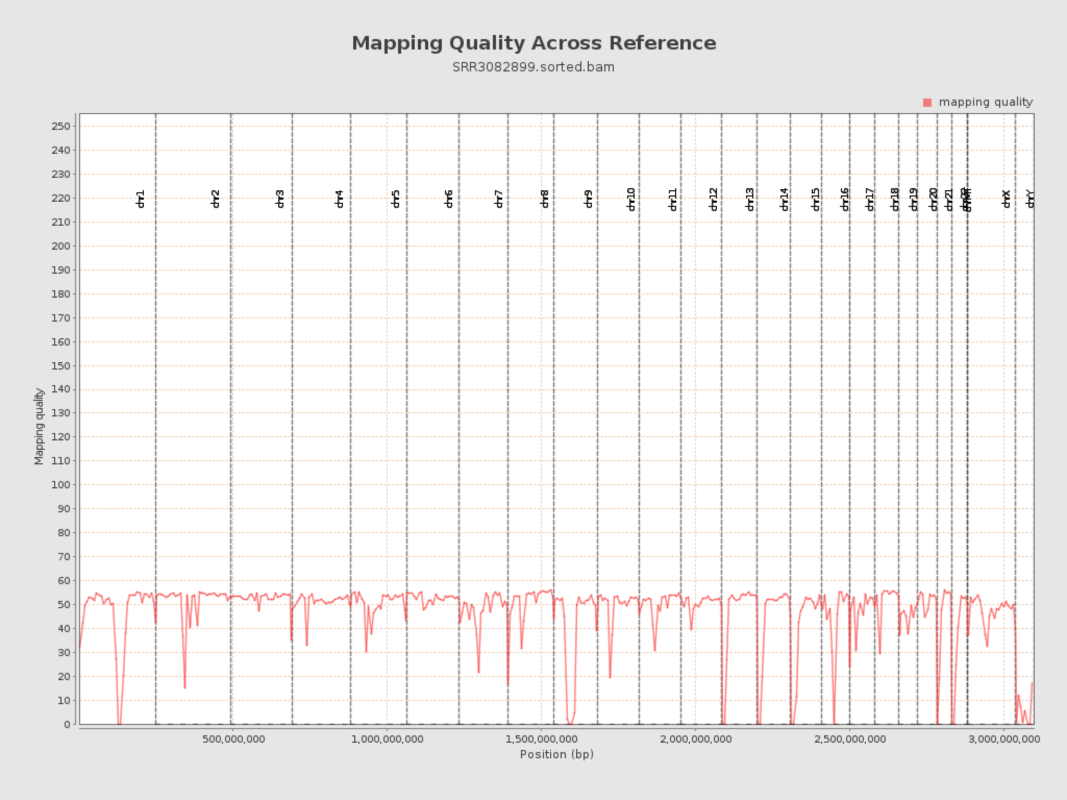
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram