Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 01:52:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089722.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_SRR089722 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089722.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 01:52:59 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089722.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,935,979
Mapped reads	20,085,038 / 87.57%
Unmapped reads	2,850,941 / 12.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,056 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	4,928,887 / 21.49%
Duplication rate	14.51%
Clipped reads	1,454,689 / 6.34%

2.2. ACGT Content

Number/percentage of A's	286,913,723 / 30.19%
Number/percentage of C's	187,445,886 / 19.72%
Number/percentage of T's	278,794,281 / 29.34%
Number/percentage of G's	197,162,480 / 20.75%
Number/percentage of N's	4,664 / 0%
GC Percentage	40.47%

2.3. Coverage

Mean	0.307

Standard Deviation	2.1237

2.4. Mapping Quality

Mean Mapping Quality	45.56

2.5. Mismatches and indels

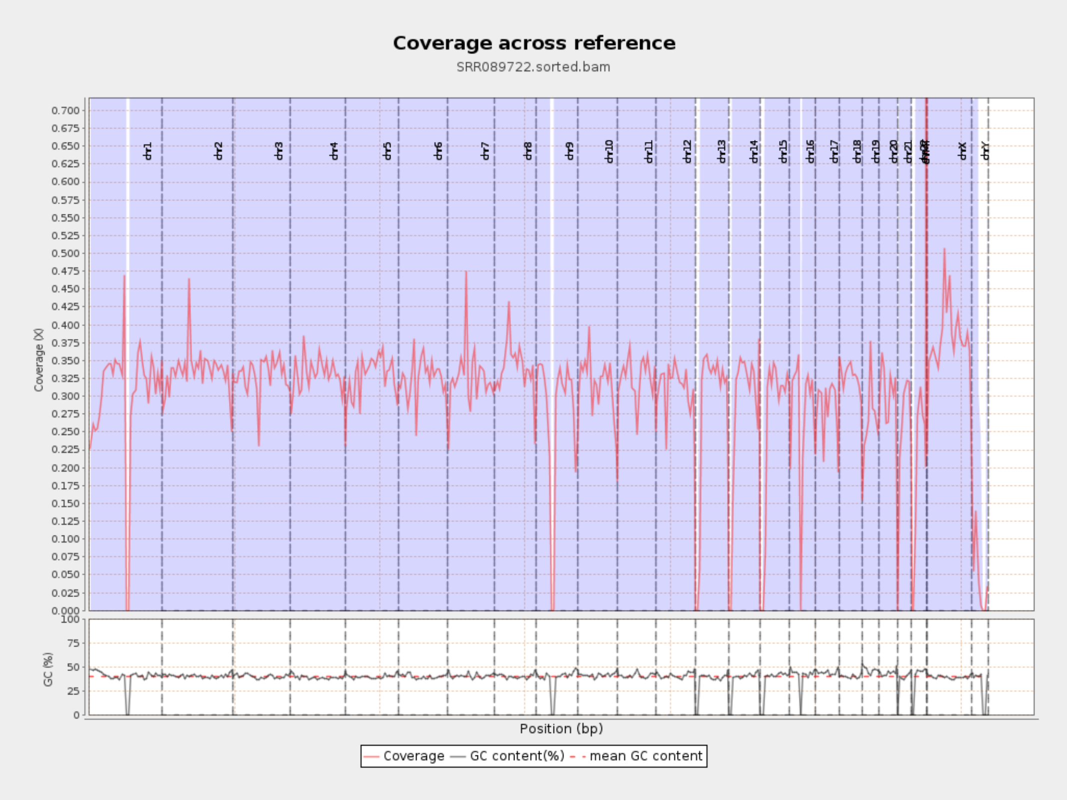
General error rate	0.39%
Mismatches	3,622,966
Insertions	37,542
Mapped reads with at least one insertion	0.19%
Deletions	127,209
Mapped reads with at least one deletion	0.63%
Homopolymer indels	48.67%

2.6. Chromosome stats

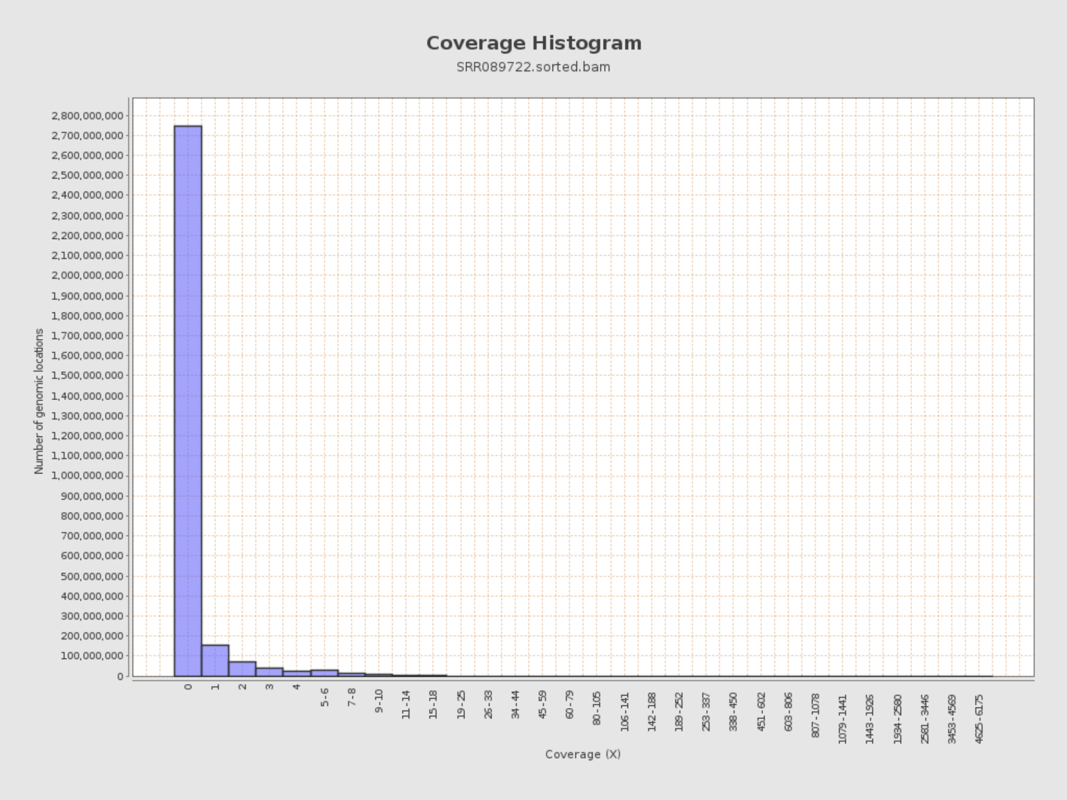
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	75327205	0.3022	3.8799
chr2	243199373	81632939	0.3357	2.0143
chr3	198022430	65383964	0.3302	1.2827
chr4	191154276	63187117	0.3306	1.3532
chr5	180915260	59507904	0.3289	1.2985
chr6	171115067	55655784	0.3253	1.4826
chr7	159138663	52214049	0.3281	2.8073

chr8	146364022	49738321	0.3398	3.5983
chr9	141213431	38679929	0.2739	1.8256
chr10	135534747	43399793	0.3202	1.7107
chr11	135006516	43691543	0.3236	2.0894
chr12	133851895	41812769	0.3124	1.3551
chr13	115169878	32065546	0.2784	1.1947
chr14	107349540	29333182	0.2732	1.2865
chr15	102531392	26403546	0.2575	1.1289
chr16	90354753	24956759	0.2762	1.2495
chr17	81195210	22836053	0.2812	1.4415
chr18	78077248	25662614	0.3287	3.5848
chr19	59128983	15949683	0.2697	2.9262
chr20	63025520	19271040	0.3058	1.3262
chr21	48129895	12086890	0.2511	1.2844
chr22	51304566	9898697	0.1929	0.9679
chrMT	16571	80308	4.8463	5.384
chrX	155270560	58982160	0.3799	1.6535
chrY	59373566	2751948	0.0463	0.9227

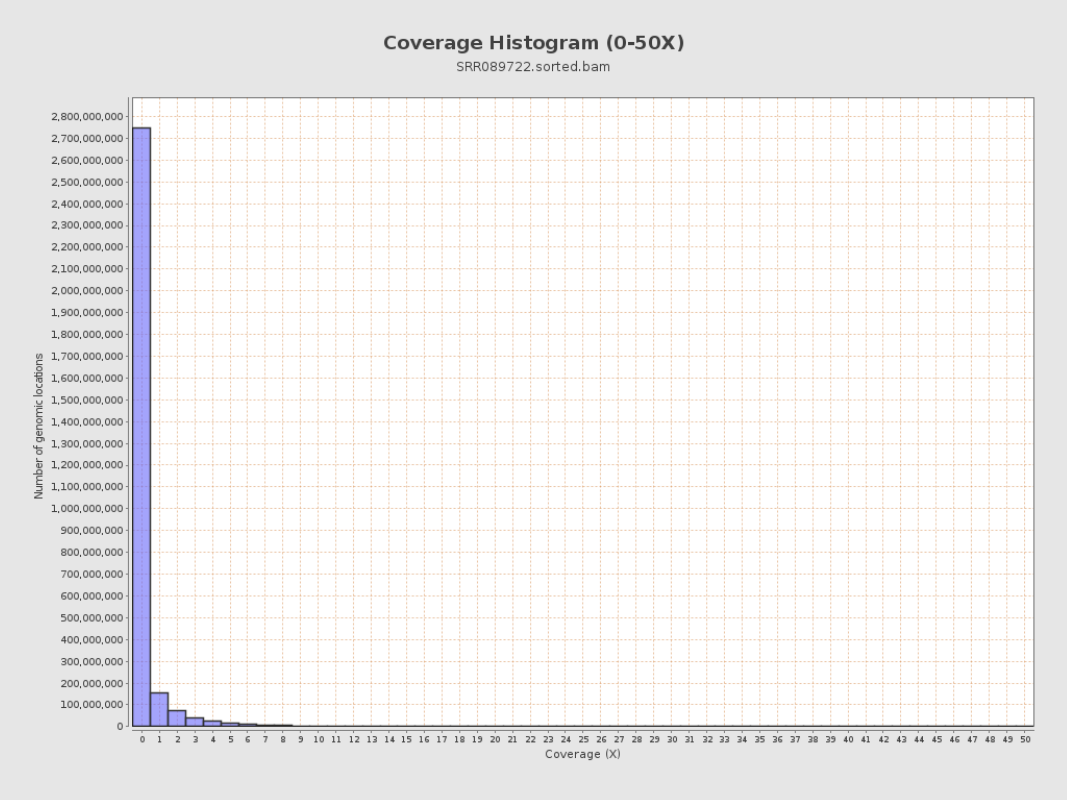
3. Results : Coverage across reference



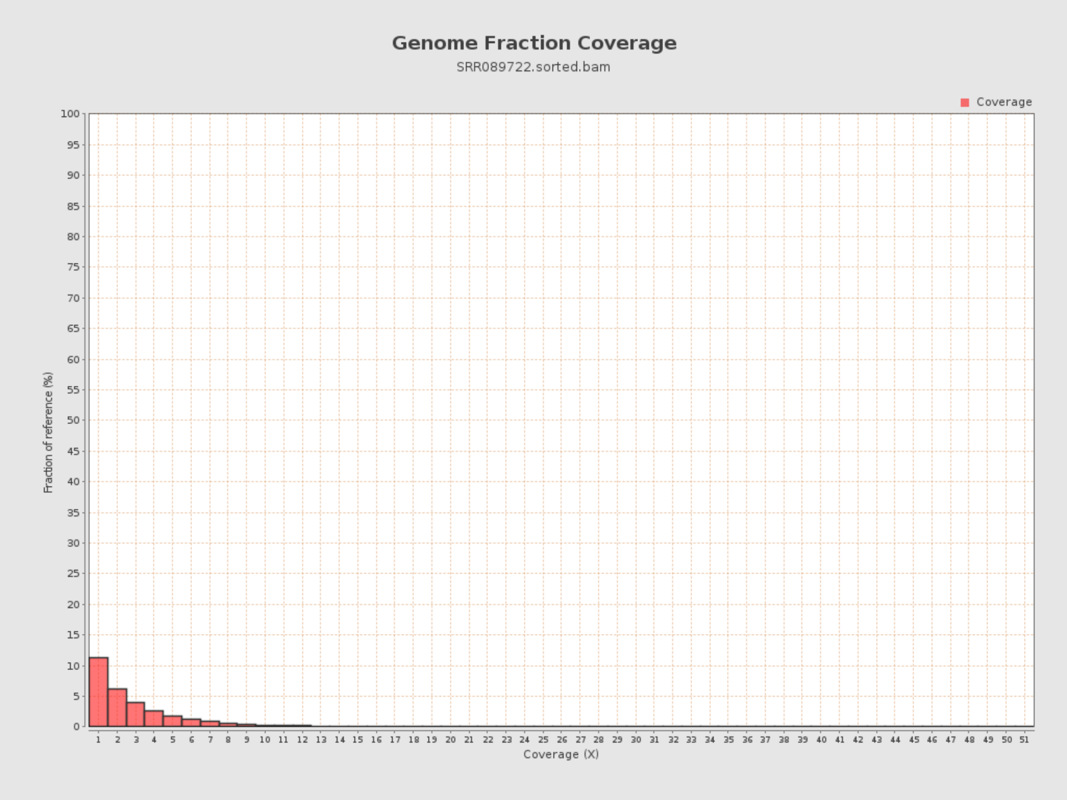
4. Results : Coverage Histogram



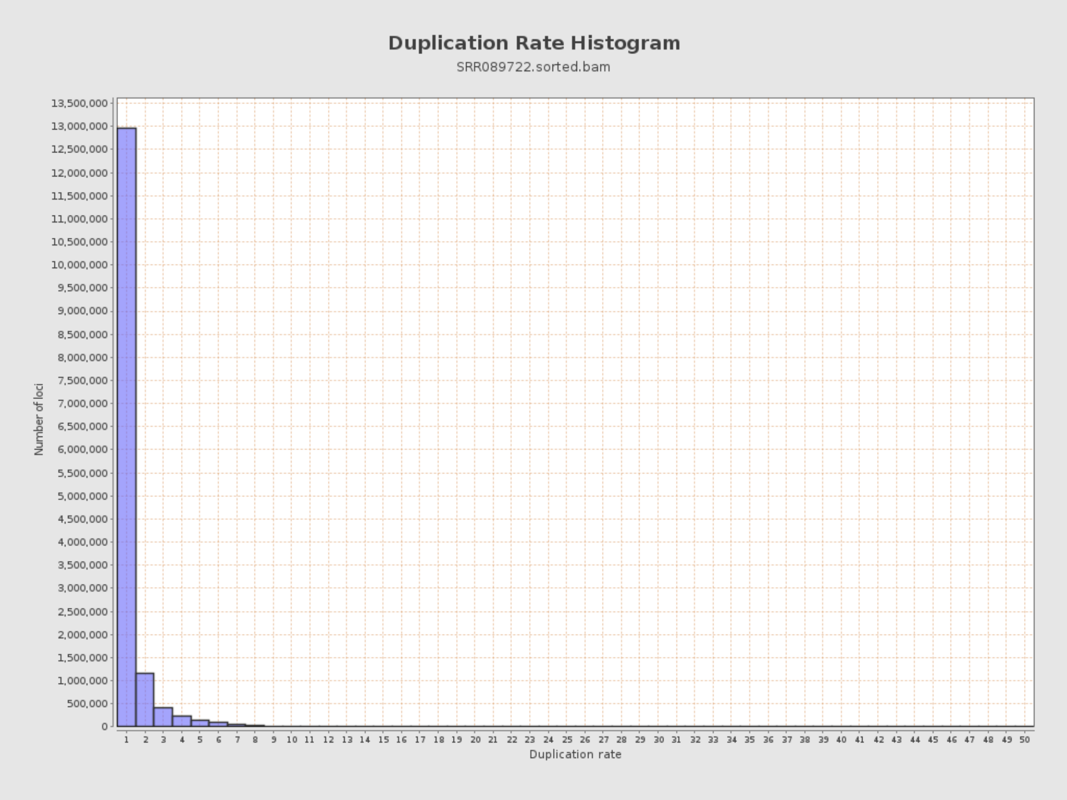
5. Results : Coverage Histogram (0-50X)



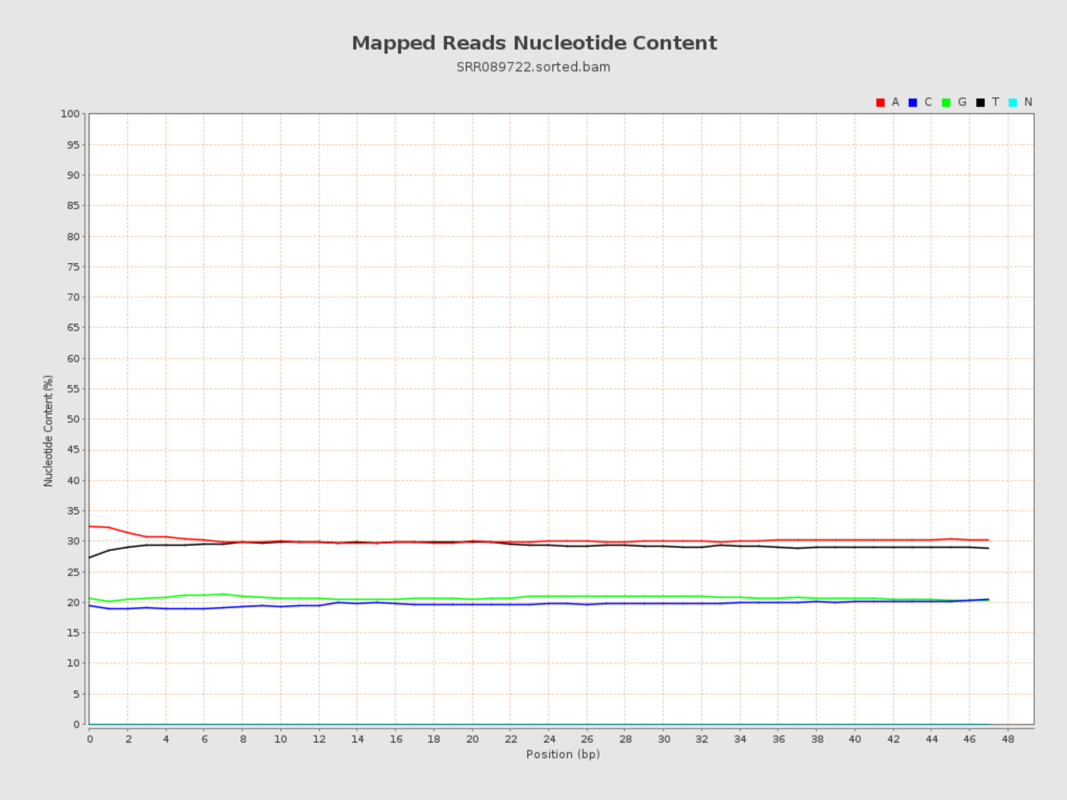
6. Results : Genome Fraction Coverage



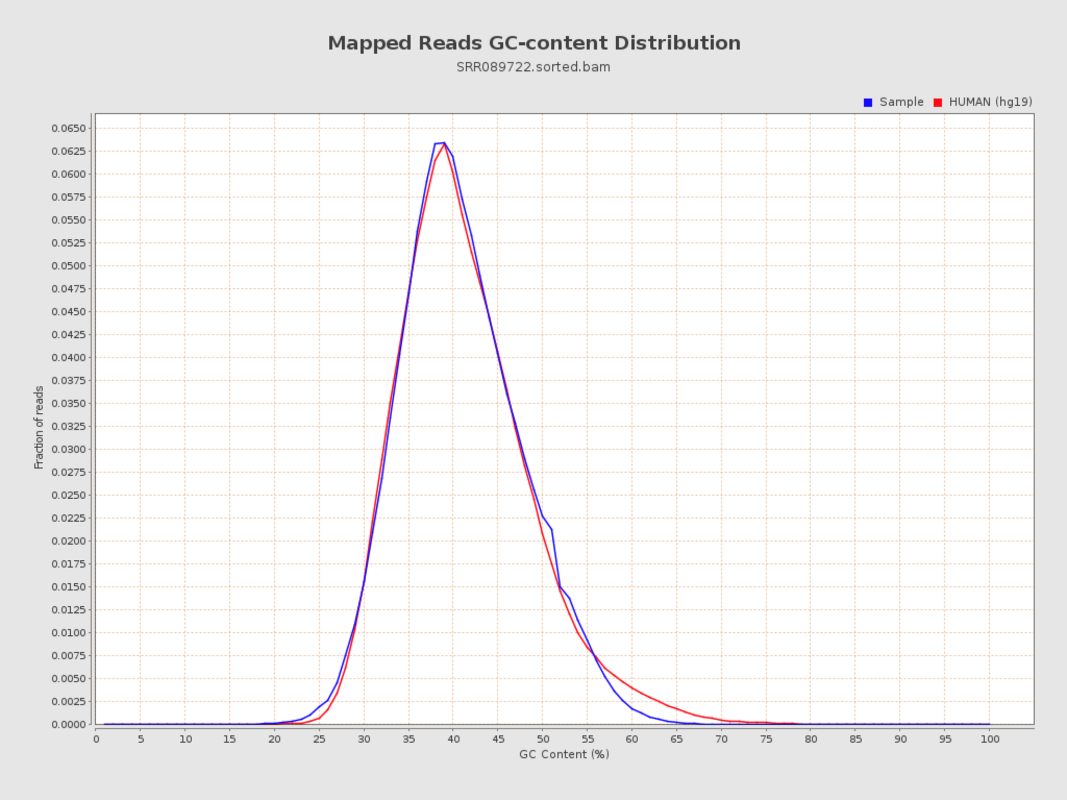
7. Results : Duplication Rate Histogram



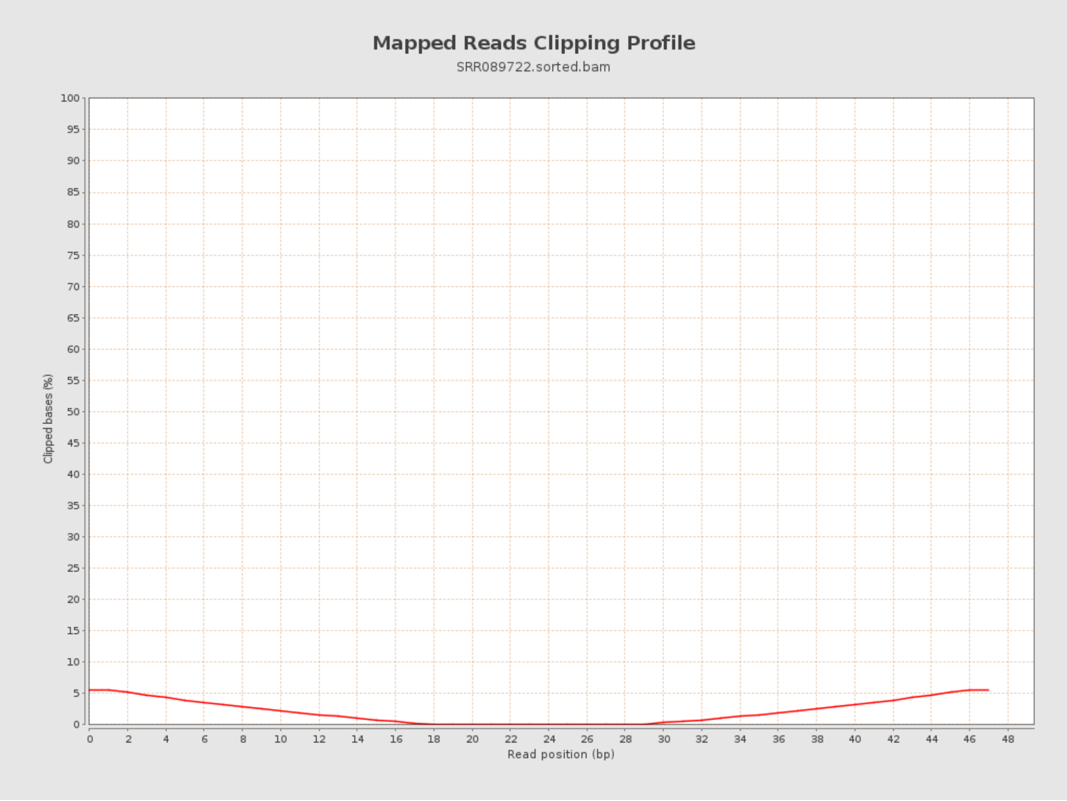
8. Results : Mapped Reads Nucleotide Content



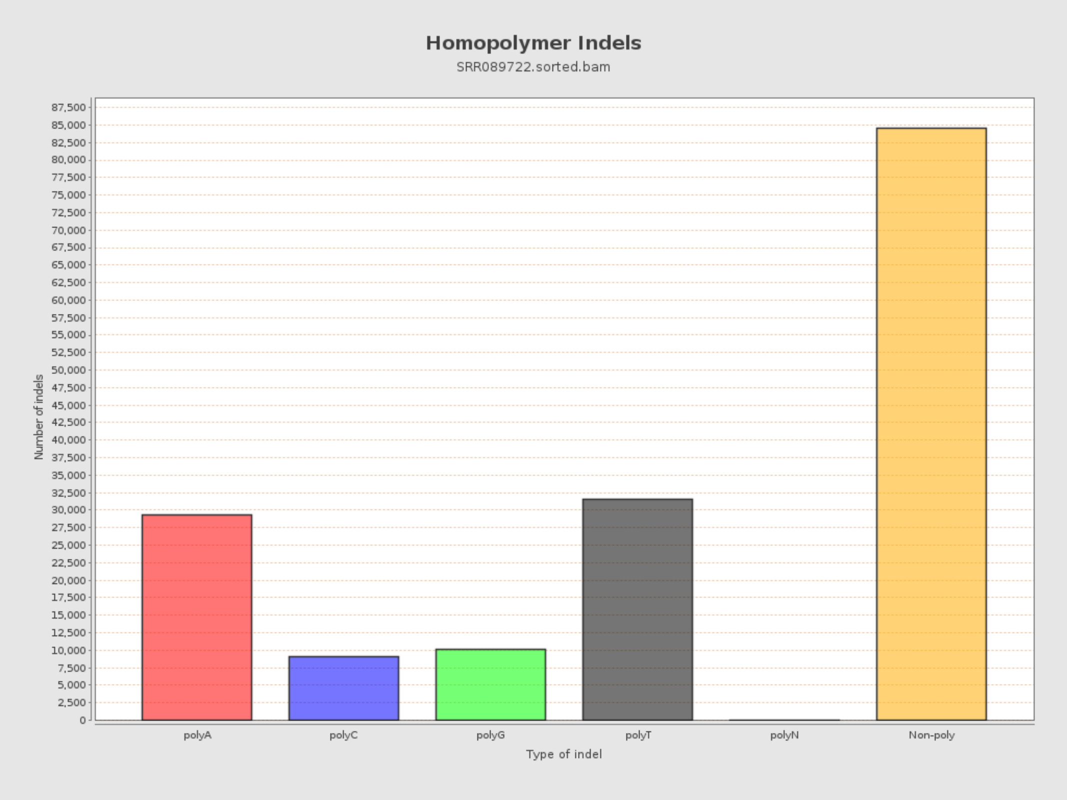
9. Results : Mapped Reads GC-content Distribution



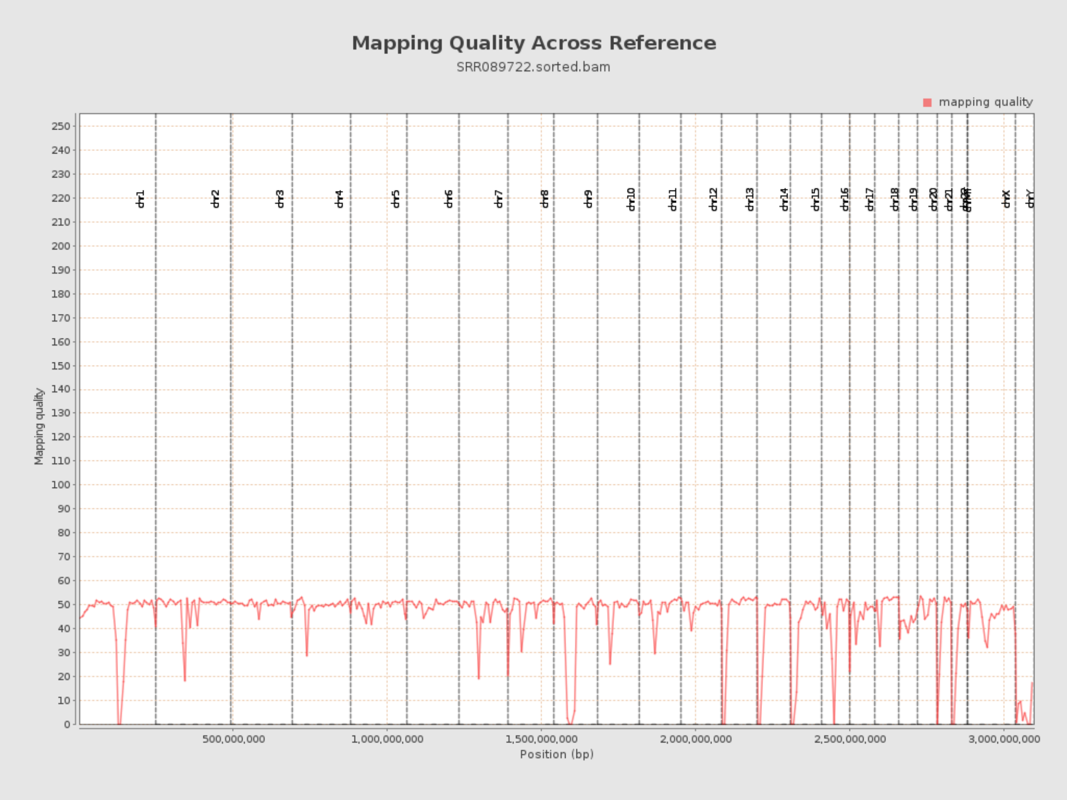
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram