Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 21:52:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089702.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_SRR089702 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089702.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 21:52:32 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089702.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	26,790,716
Mapped reads	22,155,787 / 82.7%
Unmapped reads	4,634,929 / 17.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	873 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,486,859 / 9.28%
Duplication rate	8.16%
Clipped reads	3,330,177 / 12.43%

2.2. ACGT Content

Number/percentage of A's	328,418,524 / 31.81%
Number/percentage of C's	209,400,557 / 20.28%
Number/percentage of T's	268,964,987 / 26.05%
Number/percentage of G's	225,629,724 / 21.85%
Number/percentage of N's	33,364 / 0%
GC Percentage	42.14%

2.3. Coverage

Mean	0.3336

Standard Deviation	1.7449

2.4. Mapping Quality

Mean Mapping Quality	42.57

2.5. Mismatches and indels

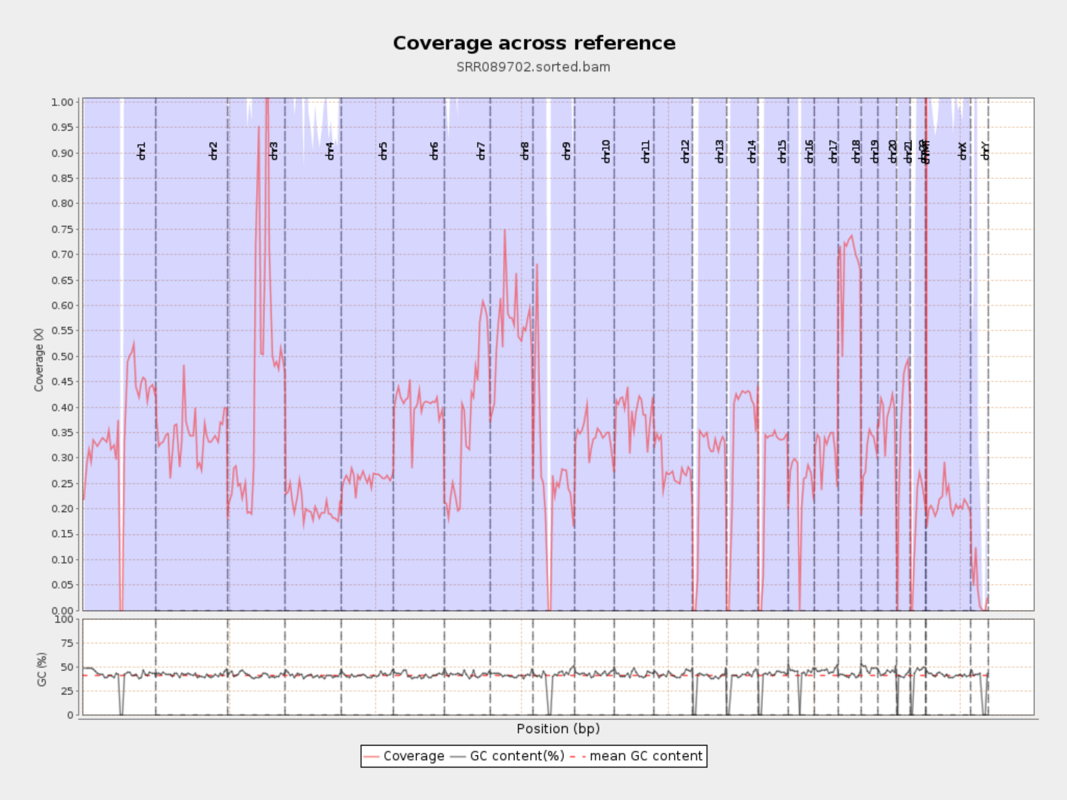
General error rate	0.54%
Mismatches	5,536,703
Insertions	47,865
Mapped reads with at least one insertion	0.22%
Deletions	143,562
Mapped reads with at least one deletion	0.65%
Homopolymer indels	43.34%

2.6. Chromosome stats

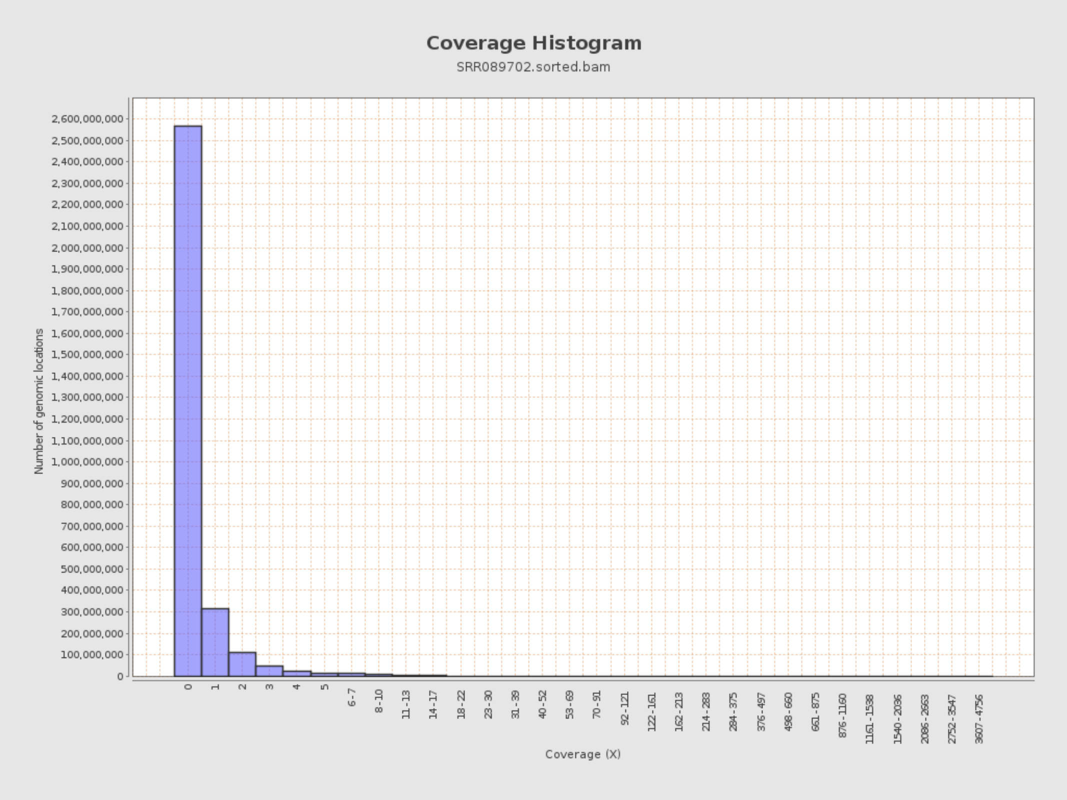
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	88990080	0.357	2.0624
chr2	243199373	83656795	0.344	2.7194
chr3	198022430	87298389	0.4409	1.3687
chr4	191154276	38897292	0.2035	0.8655
chr5	180915260	46984827	0.2597	0.9276
chr6	171115067	69345525	0.4053	1.5194
chr7	159138663	59298798	0.3726	2.2772

chr8	146364022	81360104	0.5559	3.2988
chr9	141213431	37313889	0.2642	1.6418
chr10	135534747	46481970	0.343	1.5941
chr11	135006516	52377518	0.388	1.6709
chr12	133851895	37607980	0.281	1.0135
chr13	115169878	31880407	0.2768	0.9616
chr14	107349540	37209049	0.3466	1.2363
chr15	102531392	28014513	0.2732	0.9502
chr16	90354753	21668054	0.2398	1.0028
chr17	81195210	26174475	0.3224	1.1904
chr18	78077248	53903324	0.6904	2.5109
chr19	59128983	18464021	0.3123	2.0467
chr20	63025520	24035626	0.3814	1.2302
chr21	48129895	17530289	0.3642	1.3295
chr22	51304566	8929357	0.174	0.7399
chrMT	16571	195124	11.775	11.0502
chrX	155270560	32631704	0.2102	1.2923
chrY	59373566	2411214	0.0406	0.66

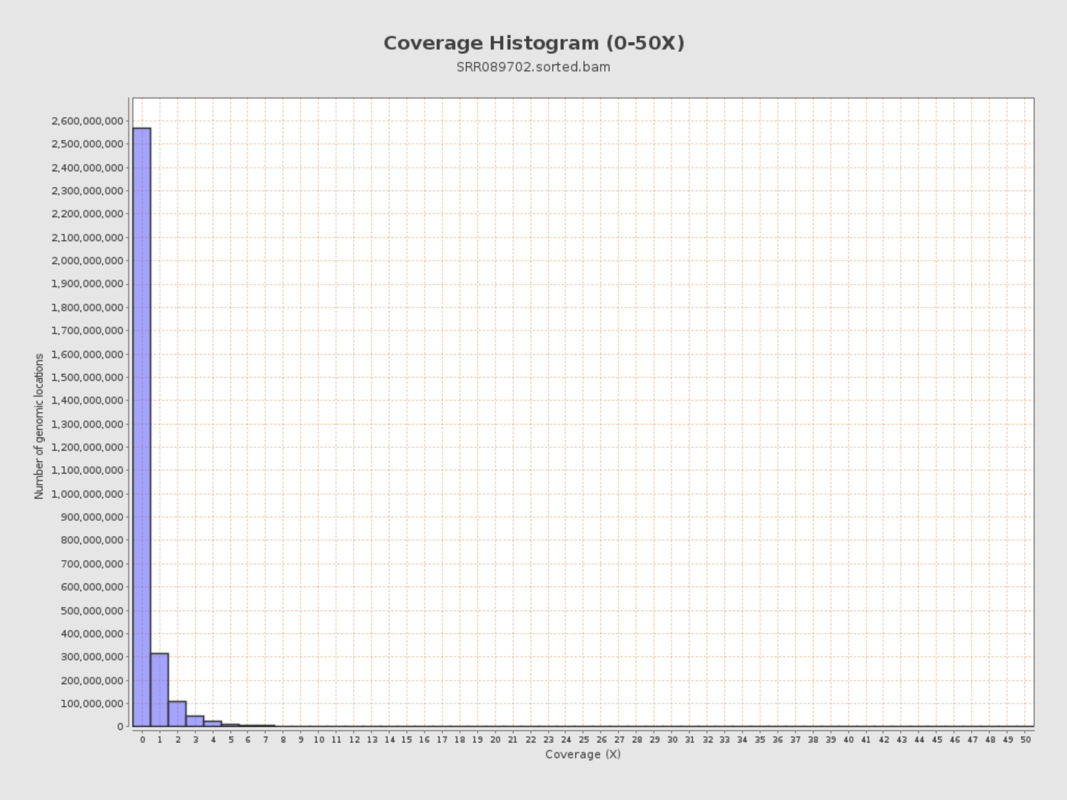
3. Results : Coverage across reference



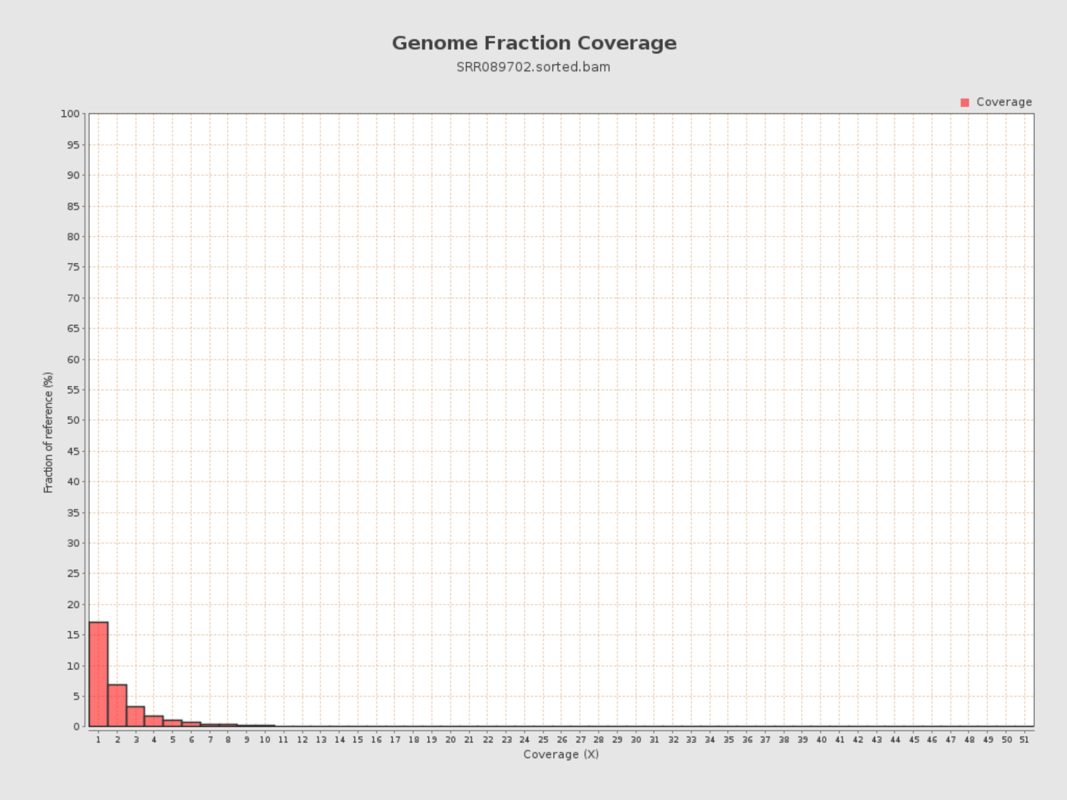
4. Results : Coverage Histogram



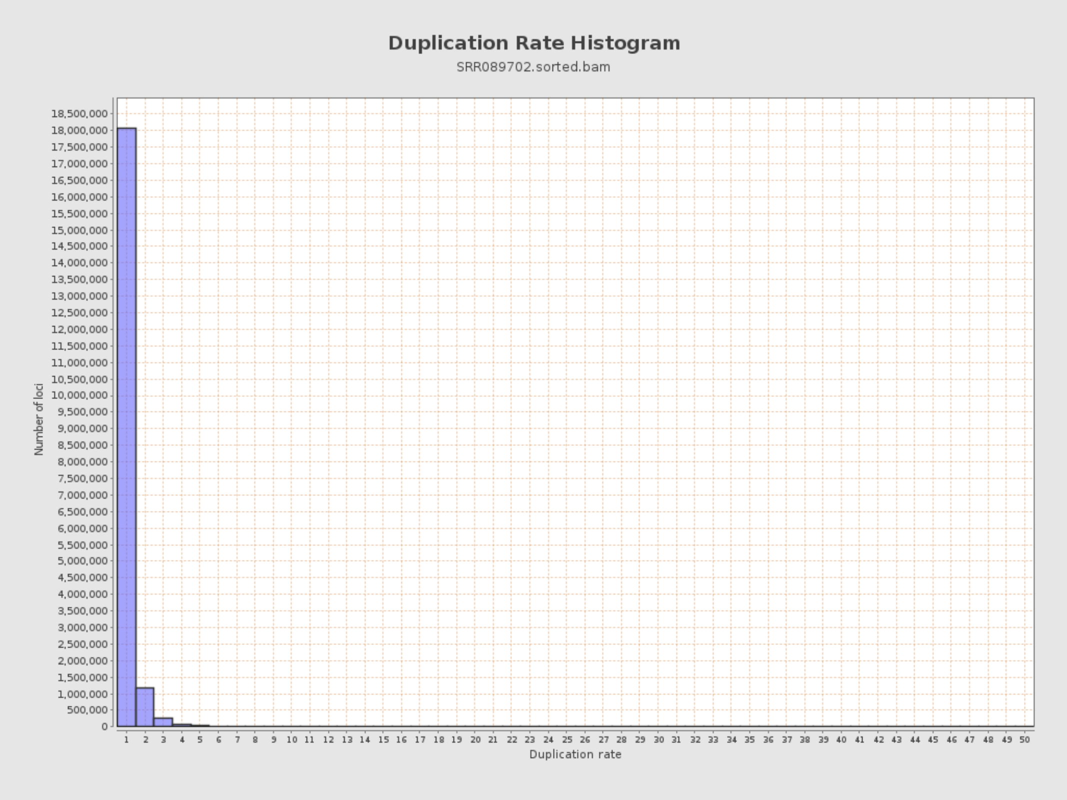
5. Results : Coverage Histogram (0-50X)



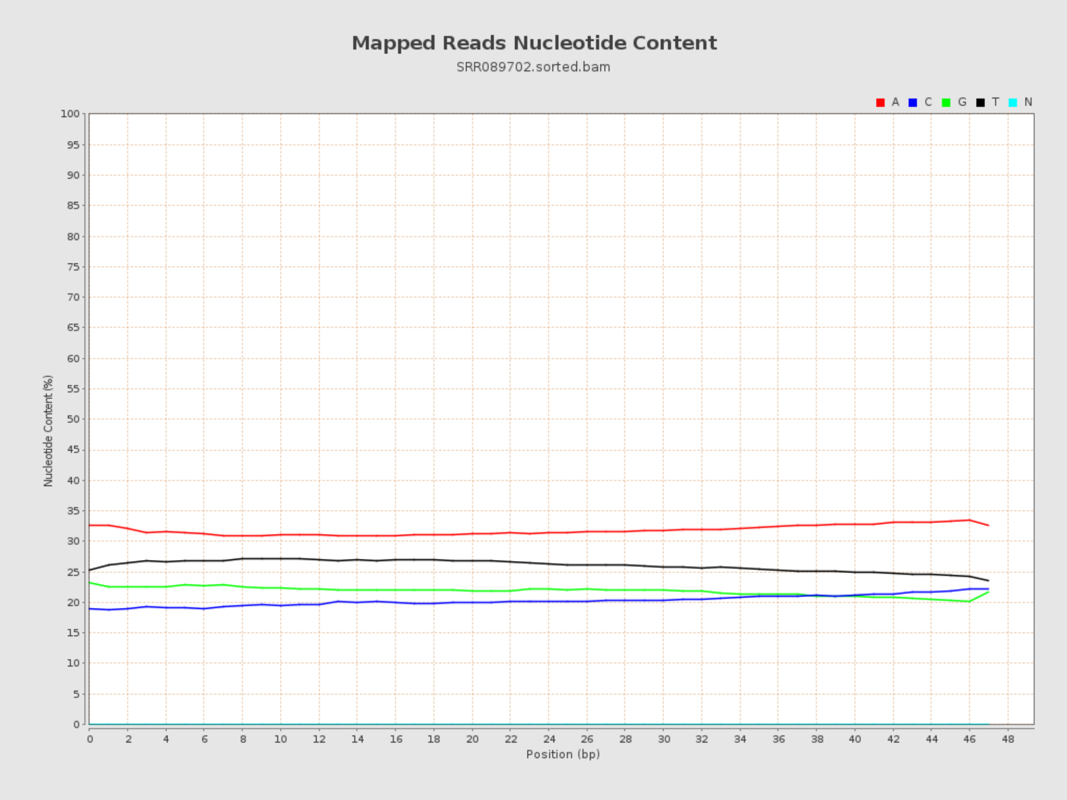
6. Results : Genome Fraction Coverage



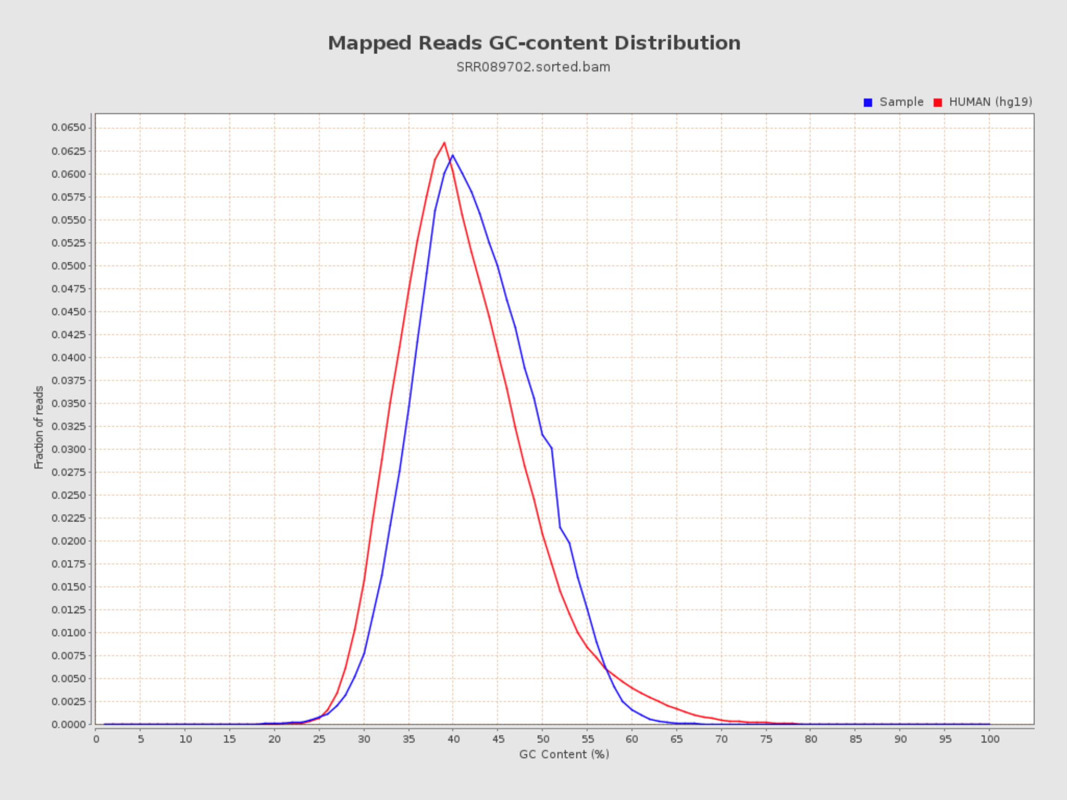
7. Results : Duplication Rate Histogram



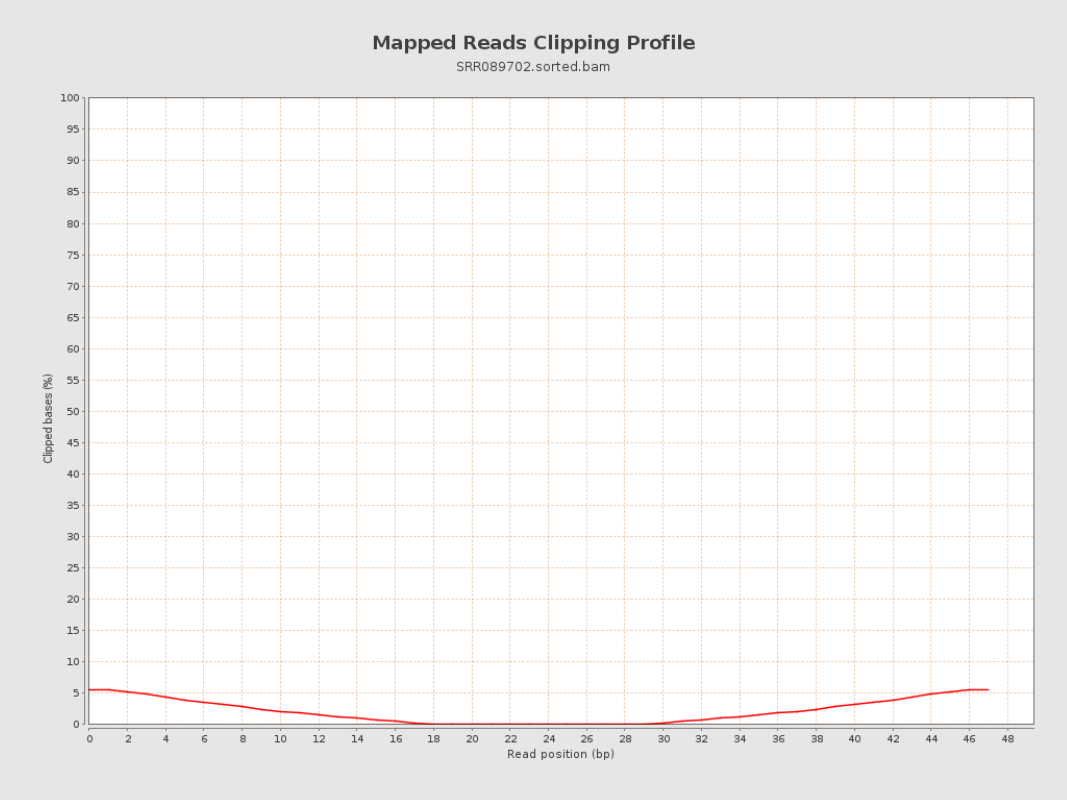
8. Results : Mapped Reads Nucleotide Content



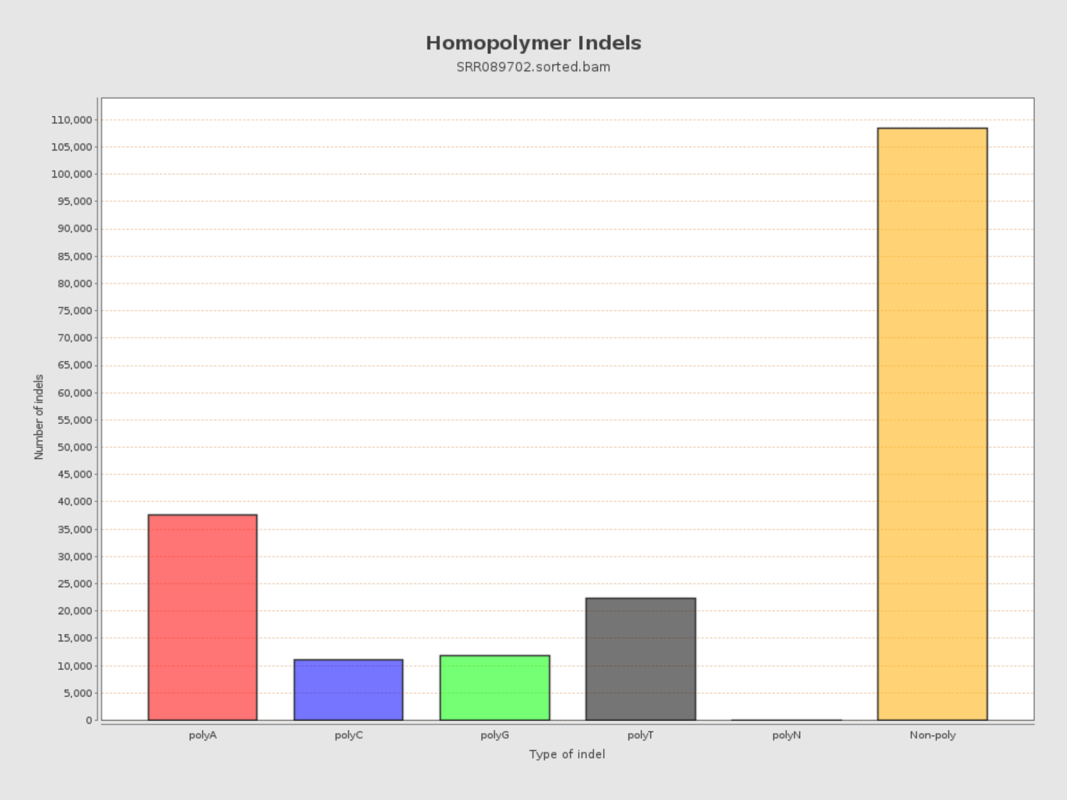
9. Results : Mapped Reads GC-content Distribution



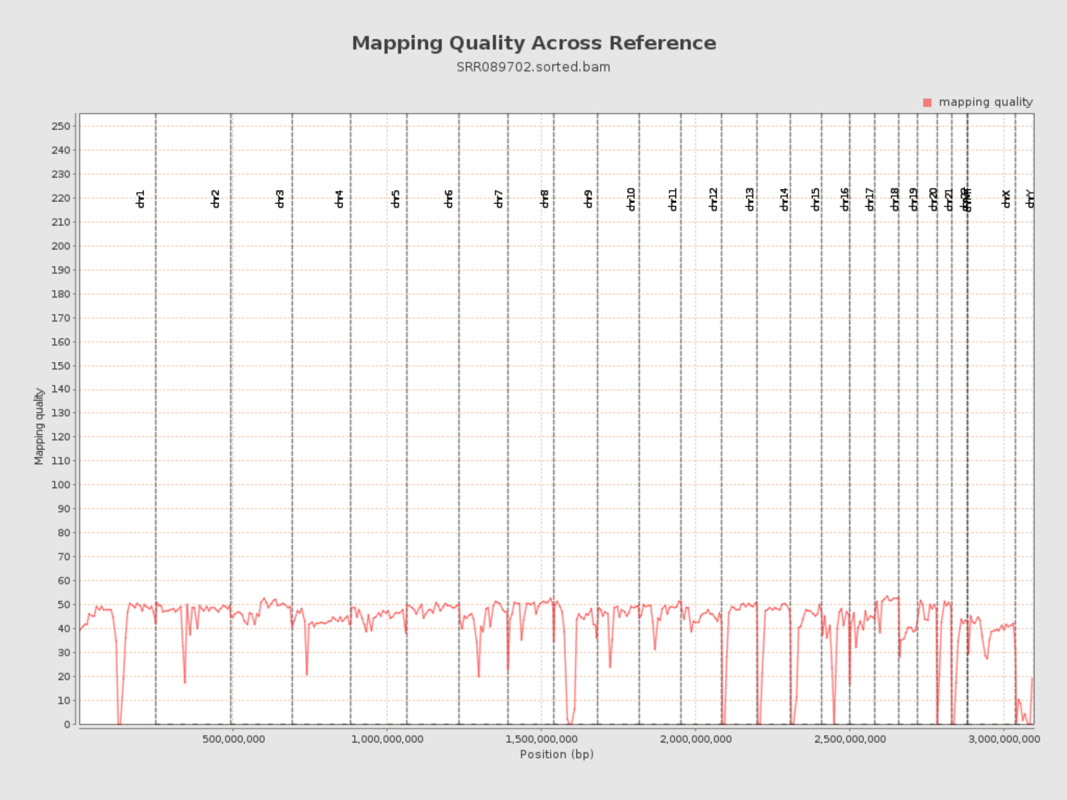
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram