Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 14:09:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089580.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_SRR089580 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089580.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 14:09:05 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089580.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	24,458,524
Mapped reads	21,230,032 / 86.8%
Unmapped reads	3,228,492 / 13.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	771 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,343,603 / 9.58%
Duplication rate	8.15%
Clipped reads	2,179,451 / 8.91%

2.2. ACGT Content

Number/percentage of A's	309,181,179 / 30.96%
Number/percentage of C's	202,238,330 / 20.25%
Number/percentage of T's	269,197,634 / 26.96%
Number/percentage of G's	217,644,728 / 21.8%
Number/percentage of N's	256,439 / 0.03%
GC Percentage	42.05%

2.3. Coverage

Mean	0.3226

Standard Deviation	1.6866

2.4. Mapping Quality

Mean Mapping Quality	44.26

2.5. Mismatches and indels

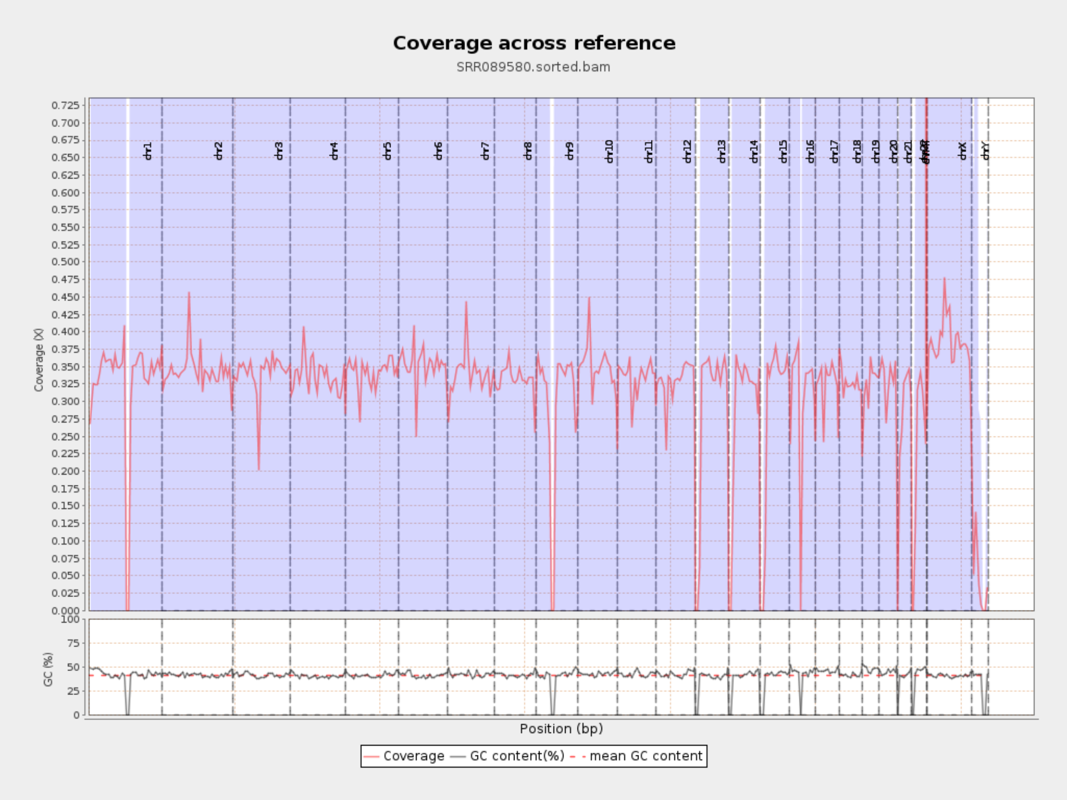
General error rate	0.43%
Mismatches	4,259,744
Insertions	39,598
Mapped reads with at least one insertion	0.19%
Deletions	132,120
Mapped reads with at least one deletion	0.62%
Homopolymer indels	45.22%

2.6. Chromosome stats

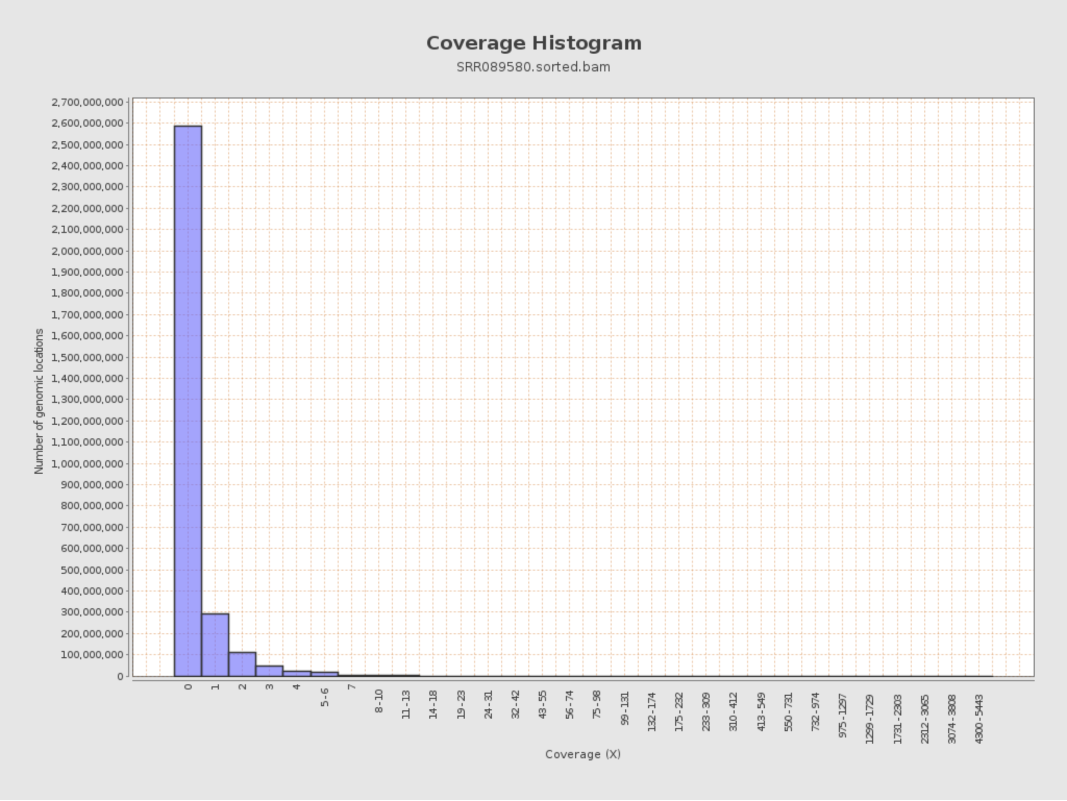
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	81172547	0.3257	2.544
chr2	243199373	83917160	0.3451	1.8346
chr3	198022430	67441556	0.3406	1.0328
chr4	191154276	64239705	0.3361	1.1474
chr5	180915260	61733824	0.3412	1.051
chr6	171115067	60259248	0.3522	1.3359
chr7	159138663	54325249	0.3414	2.3645

chr8	146364022	48488120	0.3313	3.1574
chr9	141213431	41537414	0.2941	1.4795
chr10	135534747	47740465	0.3522	1.7035
chr11	135006516	45070898	0.3338	1.4798
chr12	133851895	44063864	0.3292	1.0796
chr13	115169878	33221786	0.2885	0.9535
chr14	107349540	30051307	0.2799	1.1862
chr15	102531392	28871566	0.2816	0.9439
chr16	90354753	27797917	0.3077	1.1288
chr17	81195210	26357336	0.3246	1.2274
chr18	78077248	25601578	0.3279	2.4704
chr19	59128983	19211671	0.3249	2.2683
chr20	63025520	20721982	0.3288	1.1101
chr21	48129895	13025019	0.2706	1.1559
chr22	51304566	11020747	0.2148	0.8204
chrMT	16571	449297	27.1135	20.5814
chrX	155270560	59571070	0.3837	1.3946
chrY	59373566	2826048	0.0476	0.7509

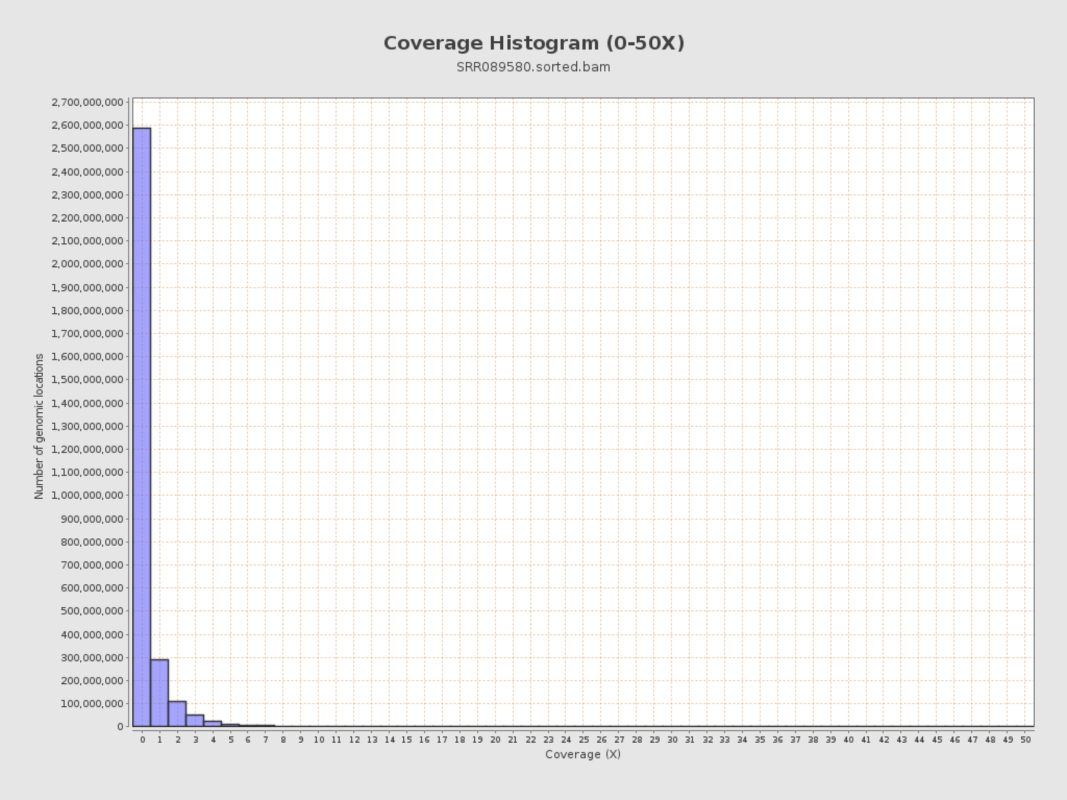
3. Results : Coverage across reference



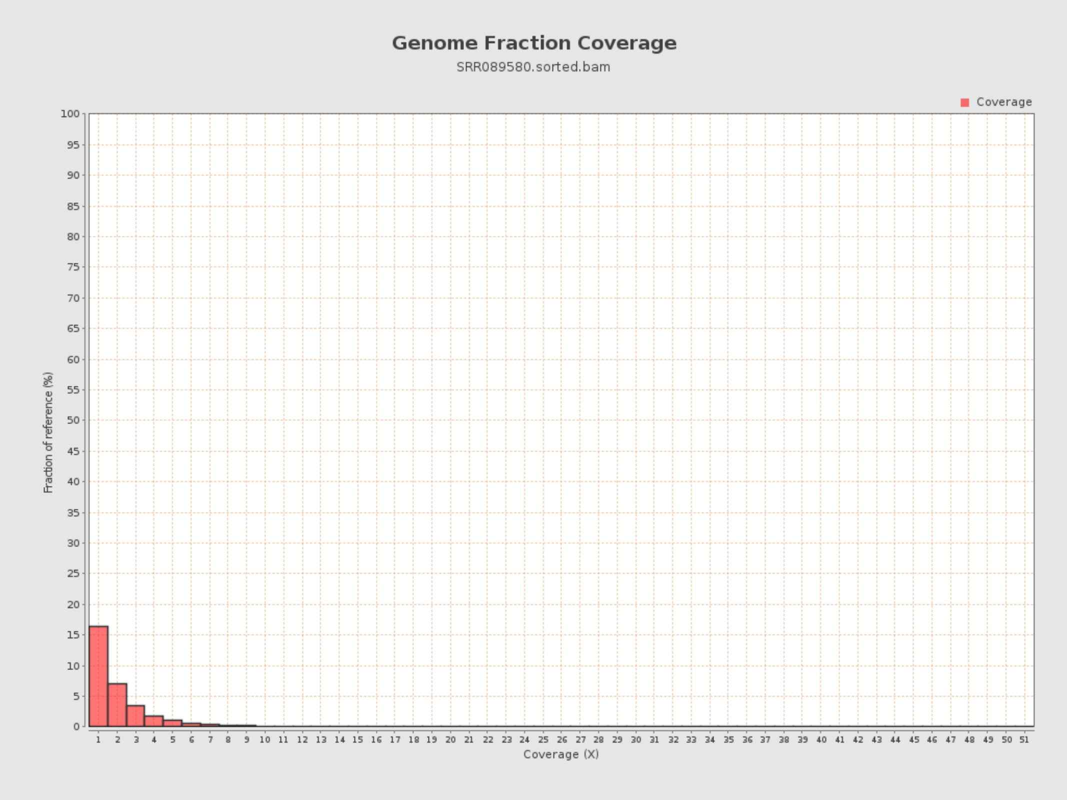
4. Results : Coverage Histogram



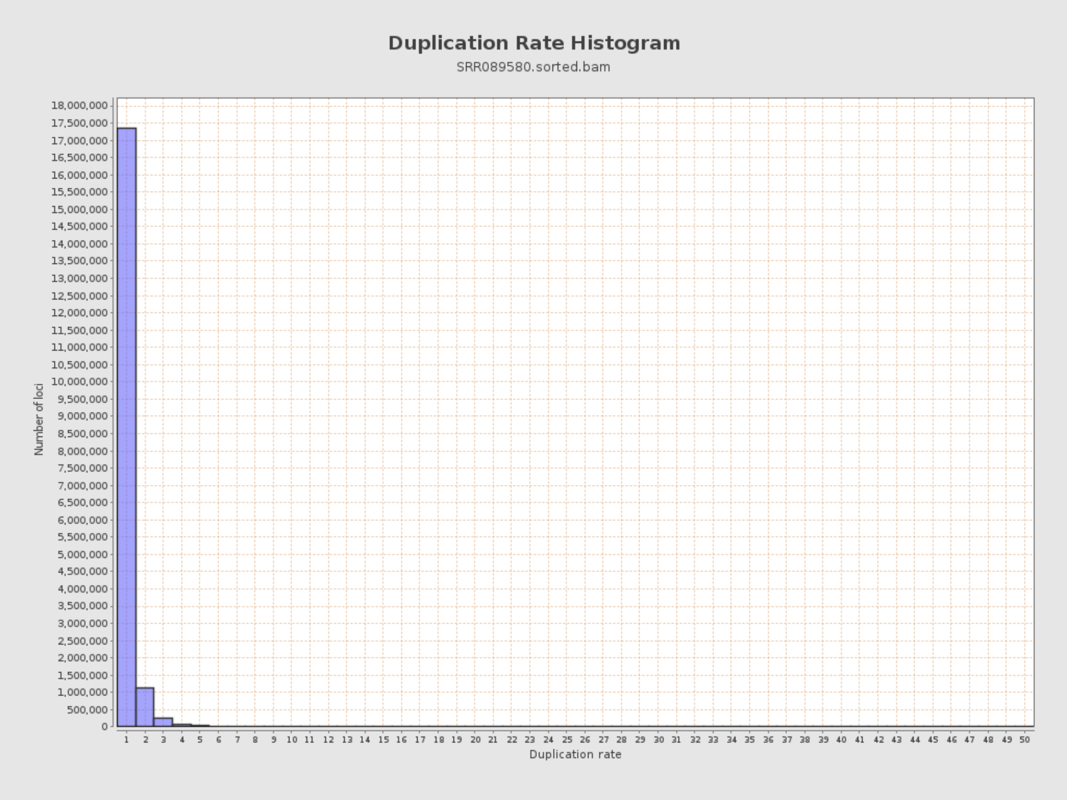
5. Results : Coverage Histogram (0-50X)



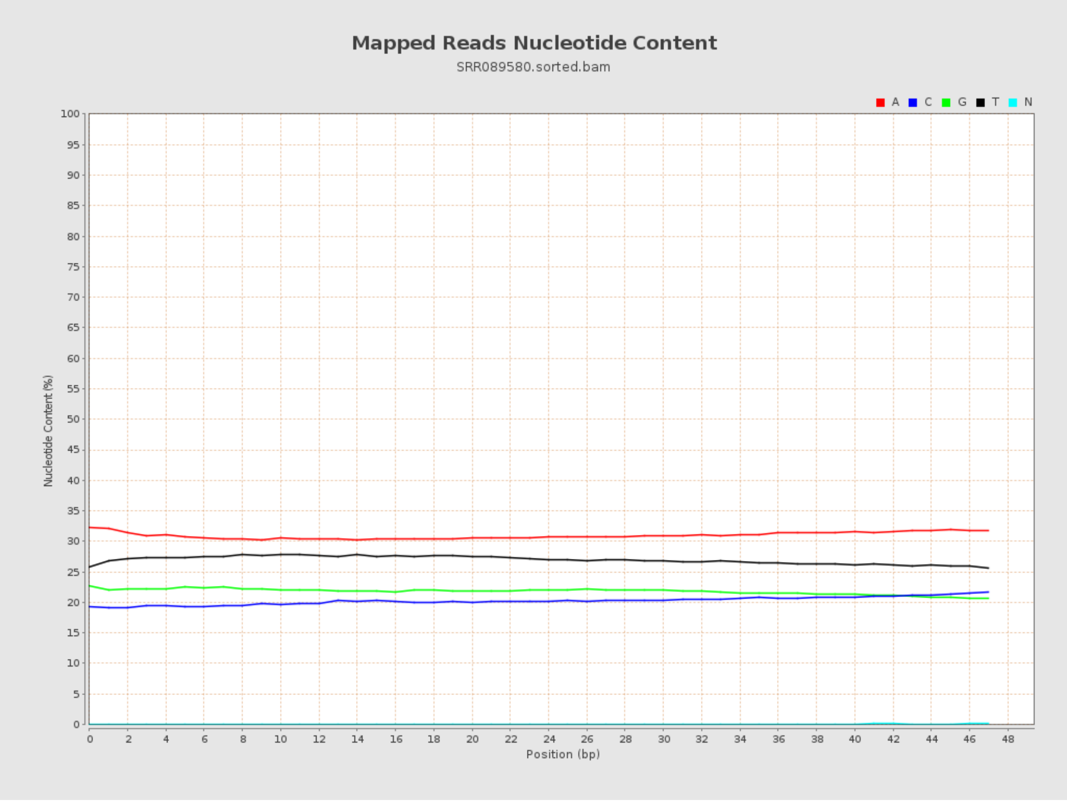
6. Results : Genome Fraction Coverage



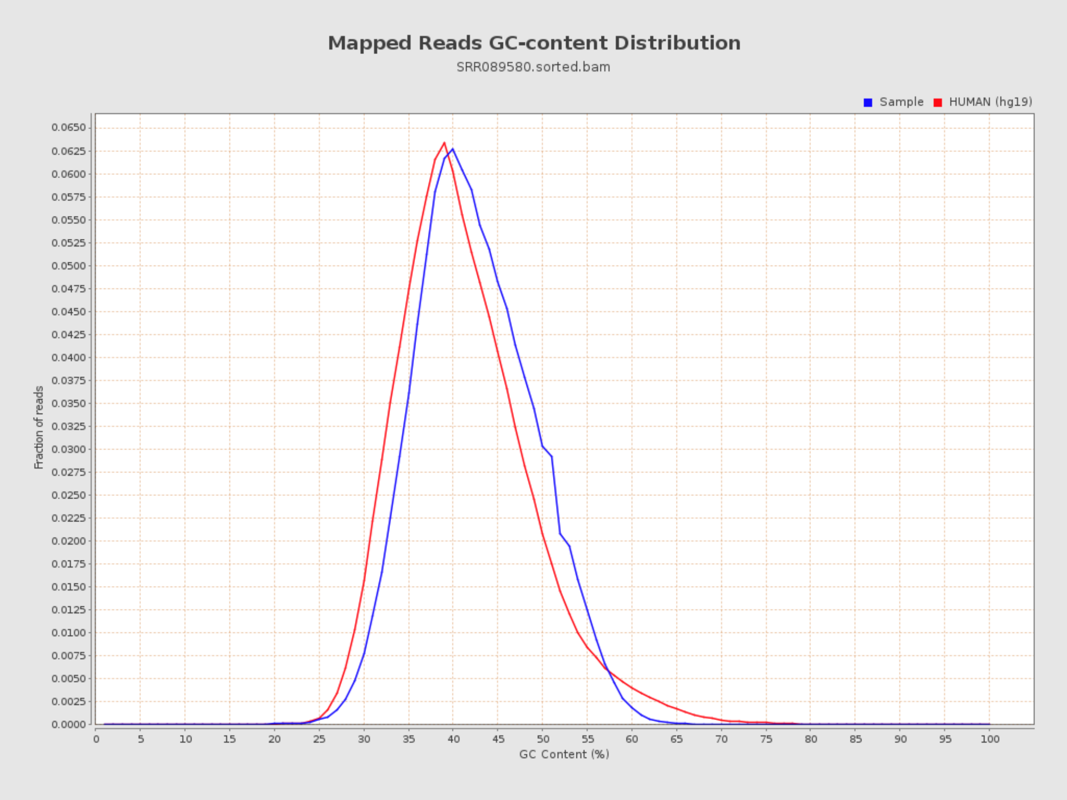
7. Results : Duplication Rate Histogram



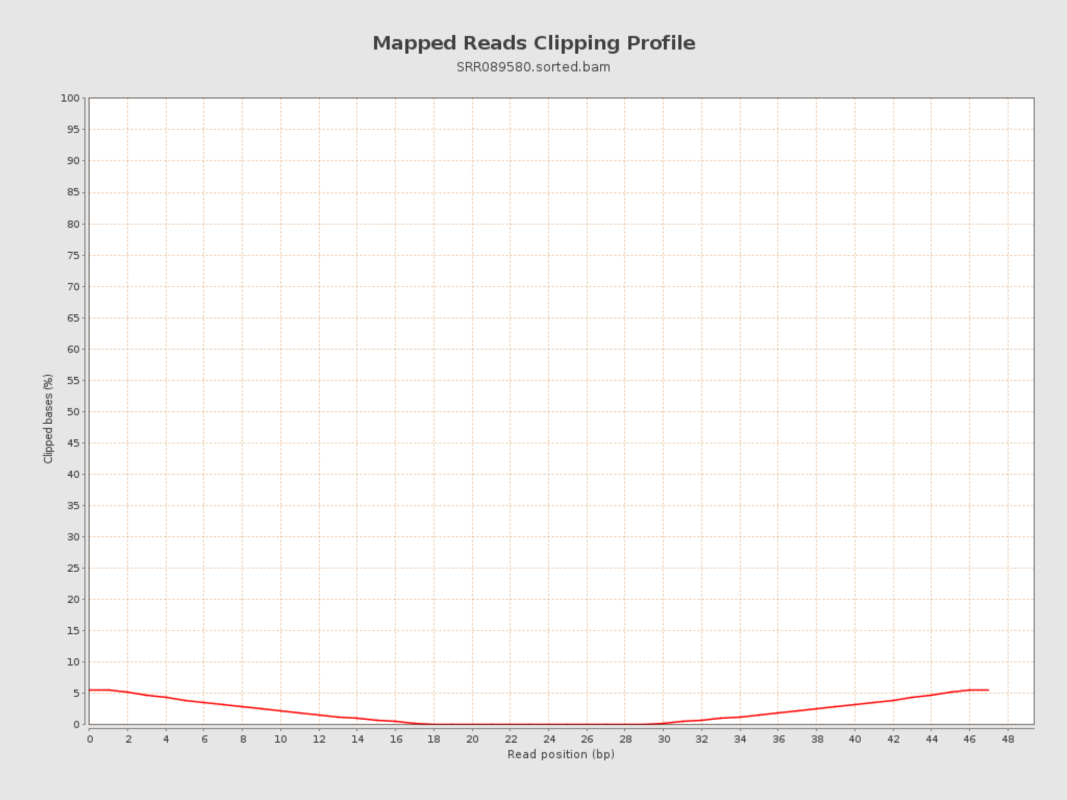
8. Results : Mapped Reads Nucleotide Content



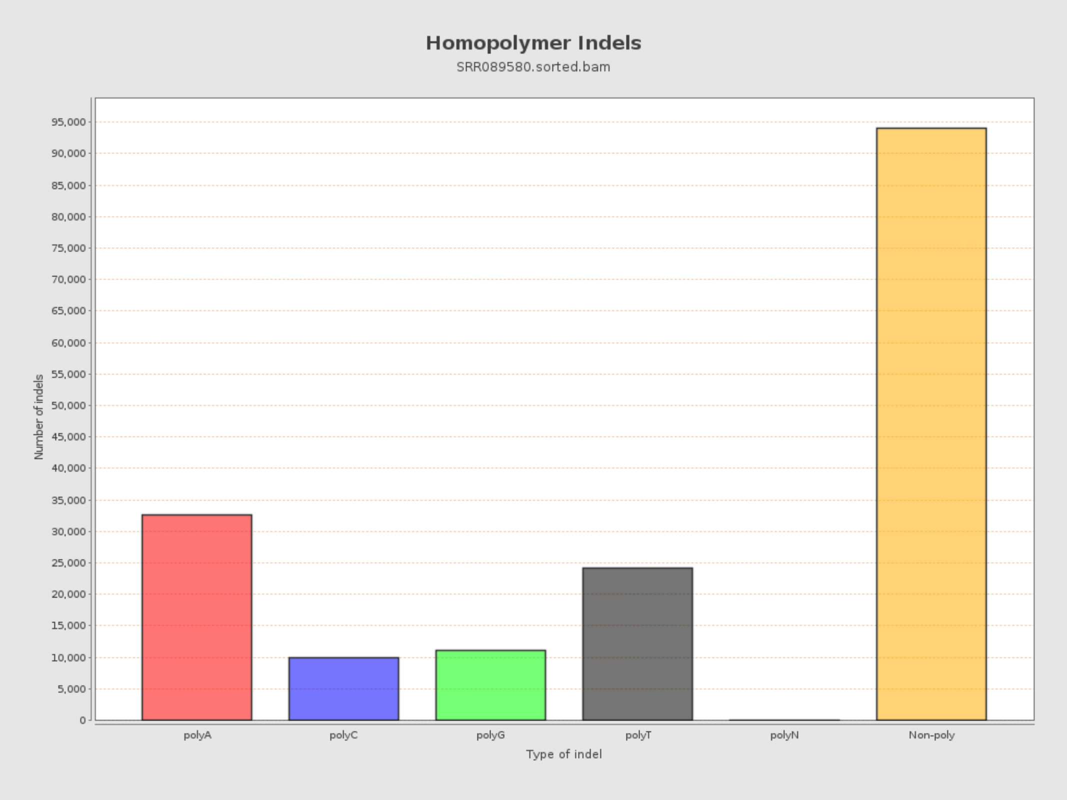
9. Results : Mapped Reads GC-content Distribution



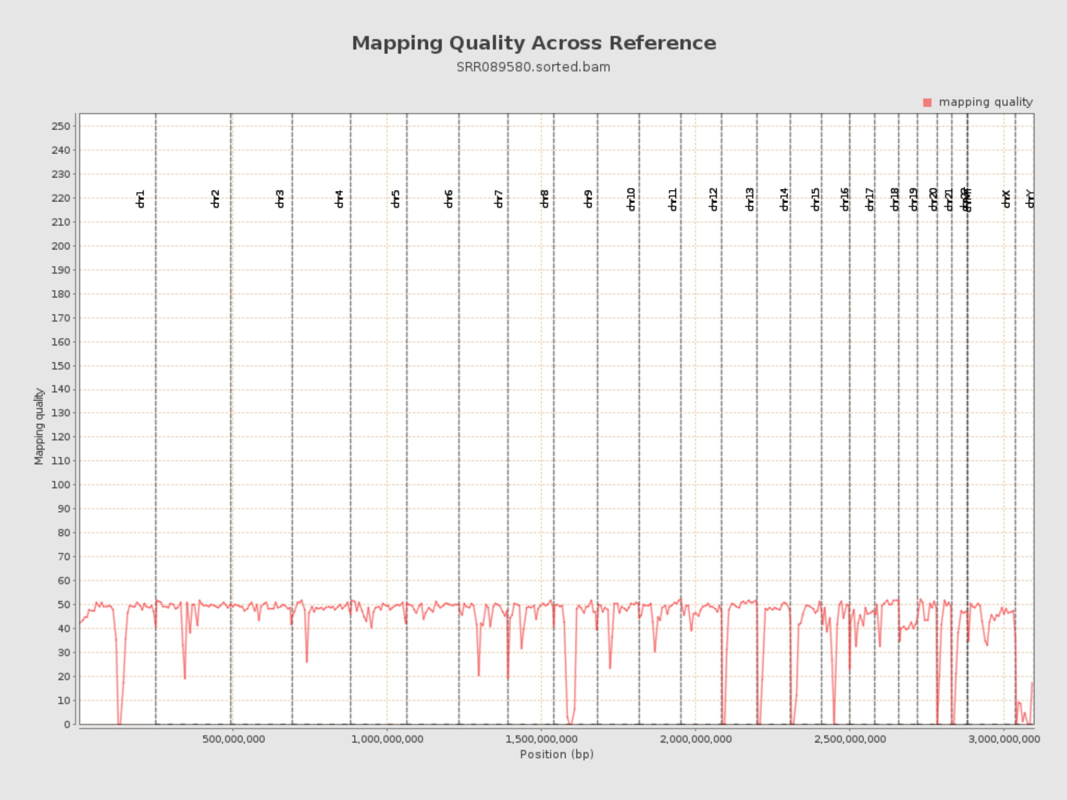
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram