Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 02:10:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089730.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_SRR089730 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089730.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 02:10:07 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089730.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,127,005
Mapped reads	18,430,507 / 87.24%
Unmapped reads	2,696,498 / 12.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	98,283 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	4,787,873 / 22.66%
Duplication rate	13.22%
Clipped reads	7,433,416 / 35.18%

2.2. ACGT Content

Number/percentage of A's	333,961,582 / 26.99%
Number/percentage of C's	236,644,116 / 19.12%
Number/percentage of T's	381,465,099 / 30.83%
Number/percentage of G's	283,652,280 / 22.92%
Number/percentage of N's	1,730,919 / 0.14%
GC Percentage	42.05%

2.3. Coverage

Mean	0.3999

Standard Deviation	3.1402

2.4. Mapping Quality

Mean Mapping Quality	47.32

2.5. Mismatches and indels

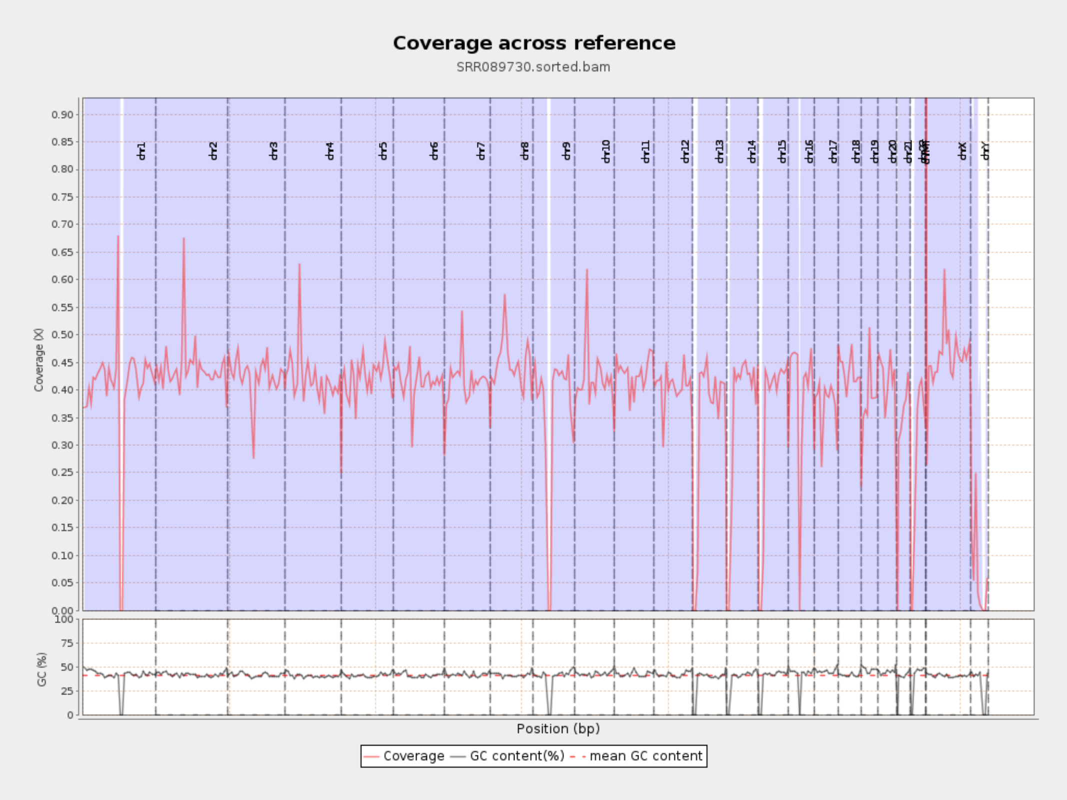
General error rate	0.87%
Mismatches	10,626,245
Insertions	84,549
Mapped reads with at least one insertion	0.45%
Deletions	237,289
Mapped reads with at least one deletion	1.27%
Homopolymer indels	46.43%

2.6. Chromosome stats

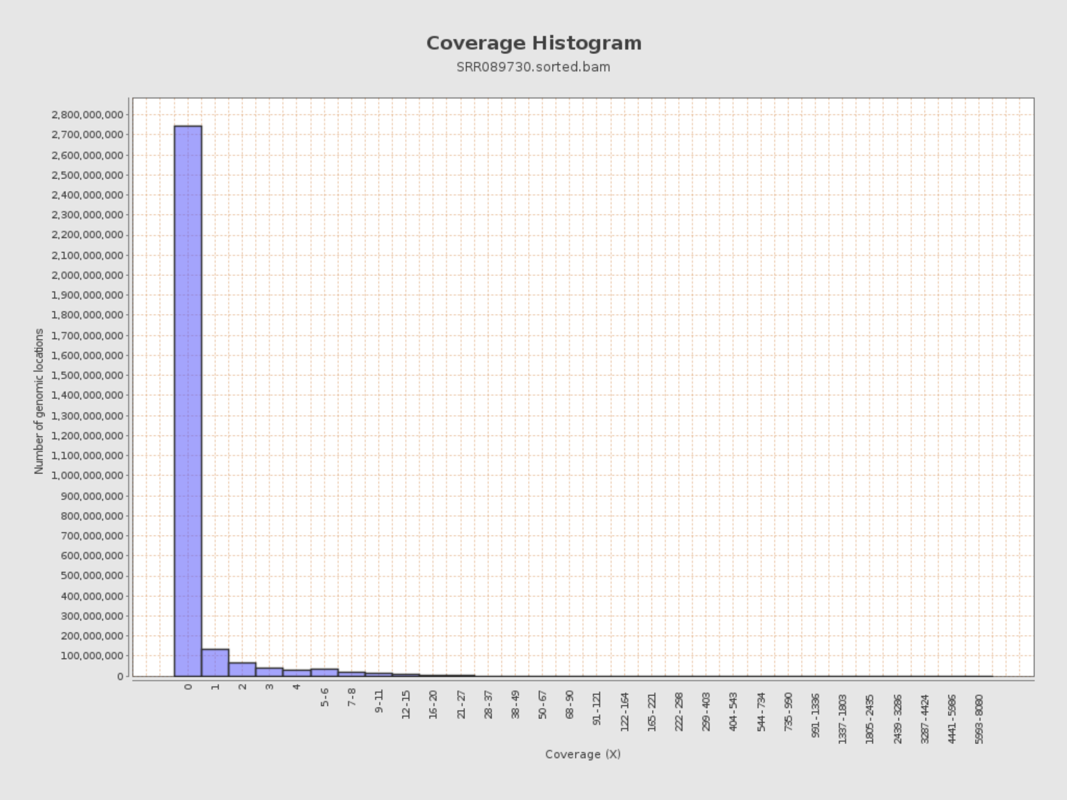
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	100309472	0.4024	6.85
chr2	243199373	107204233	0.4408	3.4476
chr3	198022430	83958179	0.424	1.7253
chr4	191154276	81198109	0.4248	2.0297
chr5	180915260	76775871	0.4244	1.7393
chr6	171115067	71338338	0.4169	1.9963
chr7	159138663	66029028	0.4149	3.0962

chr8	146364022	65618538	0.4483	4.5089
chr9	141213431	50933294	0.3607	2.8256
chr10	135534747	57117638	0.4214	2.7624
chr11	135006516	57802759	0.4281	2.3658
chr12	133851895	54414611	0.4065	1.8083
chr13	115169878	39117971	0.3397	1.5483
chr14	107349540	38319365	0.357	1.7279
chr15	102531392	34829548	0.3397	1.6465
chr16	90354753	34649426	0.3835	1.8142
chr17	81195210	30565488	0.3764	2.0034
chr18	78077248	33801055	0.4329	4.5631
chr19	59128983	22804653	0.3857	4.0075
chr20	63025520	26427311	0.4193	1.8545
chr21	48129895	15919287	0.3308	1.8496
chr22	51304566	13821889	0.2694	1.44
chrMT	16571	54042	3.2612	4.7338
chrX	155270560	71034675	0.4575	2.0424
chrY	59373566	3829367	0.0645	2.0845

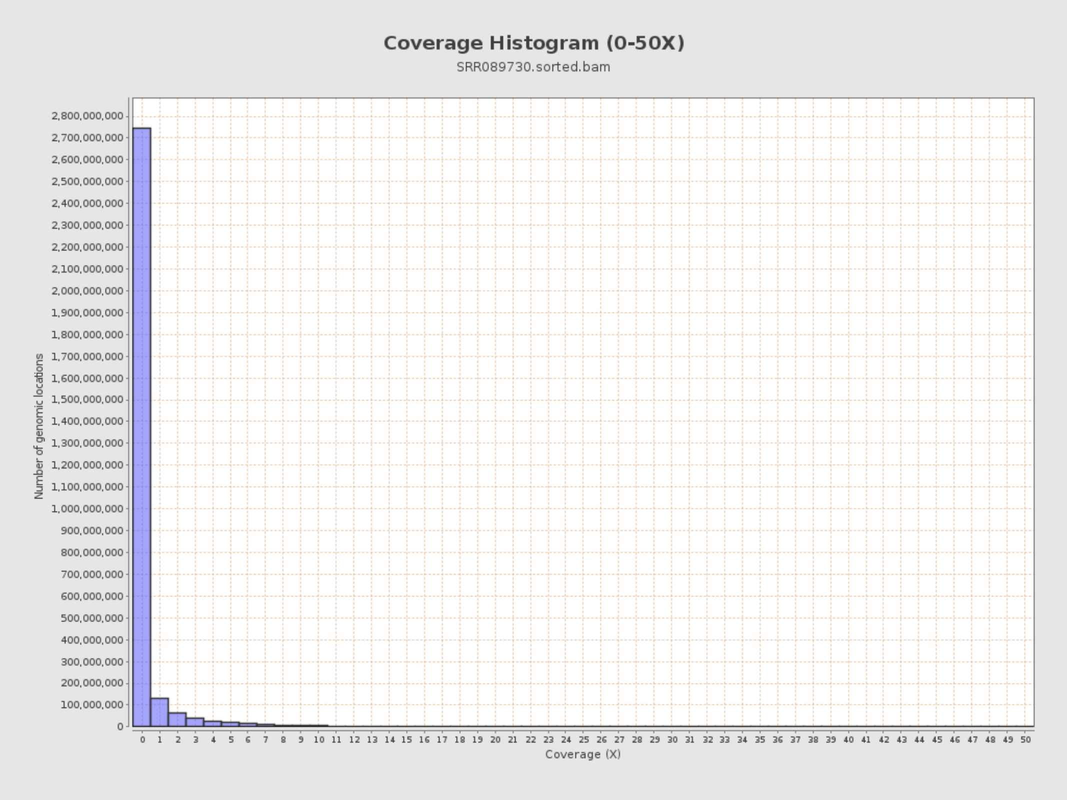
3. Results : Coverage across reference



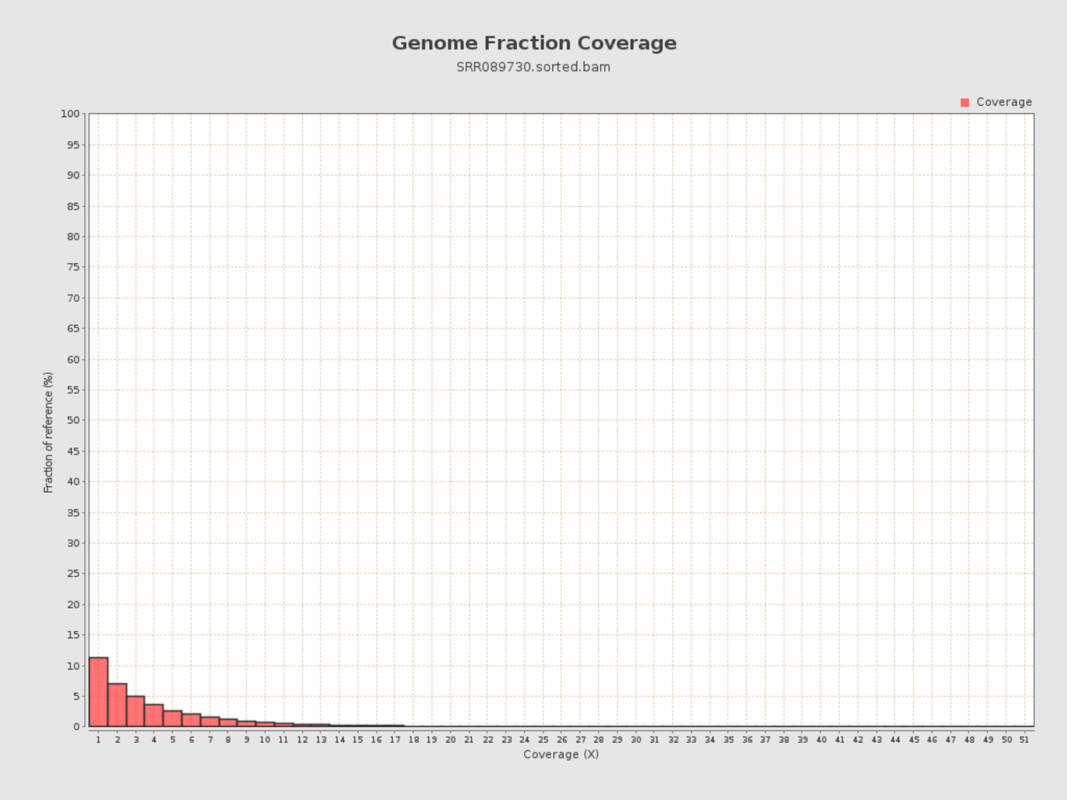
4. Results : Coverage Histogram



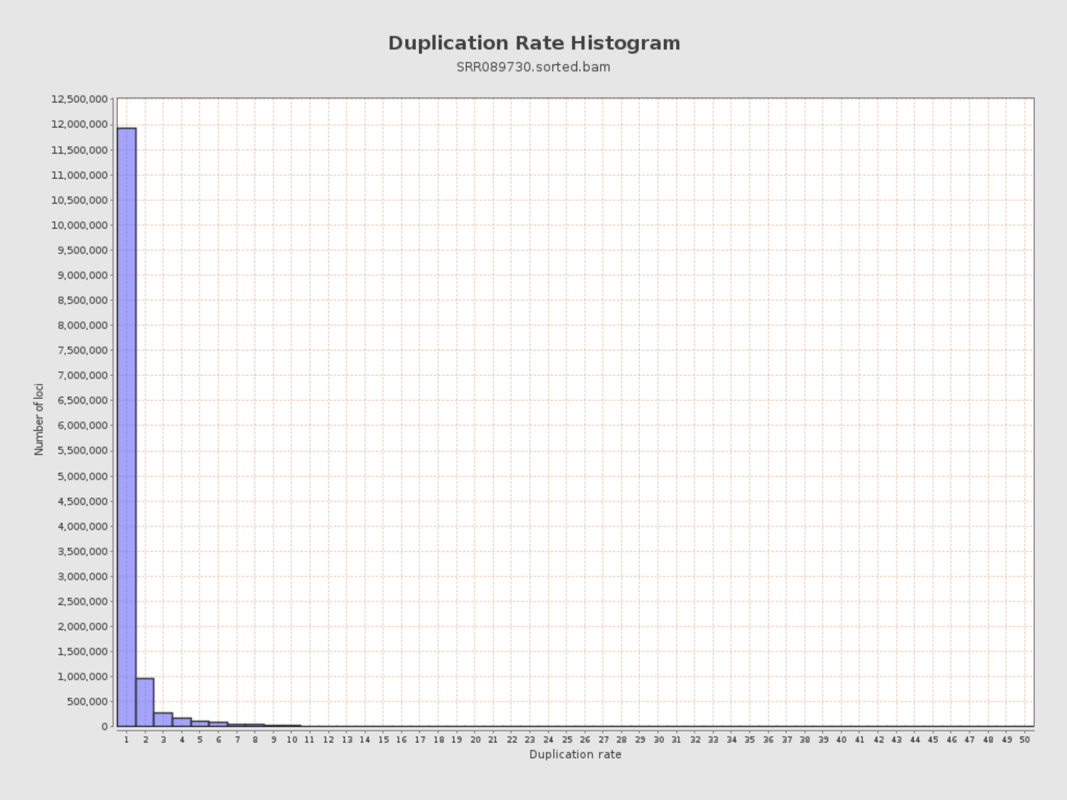
5. Results : Coverage Histogram (0-50X)



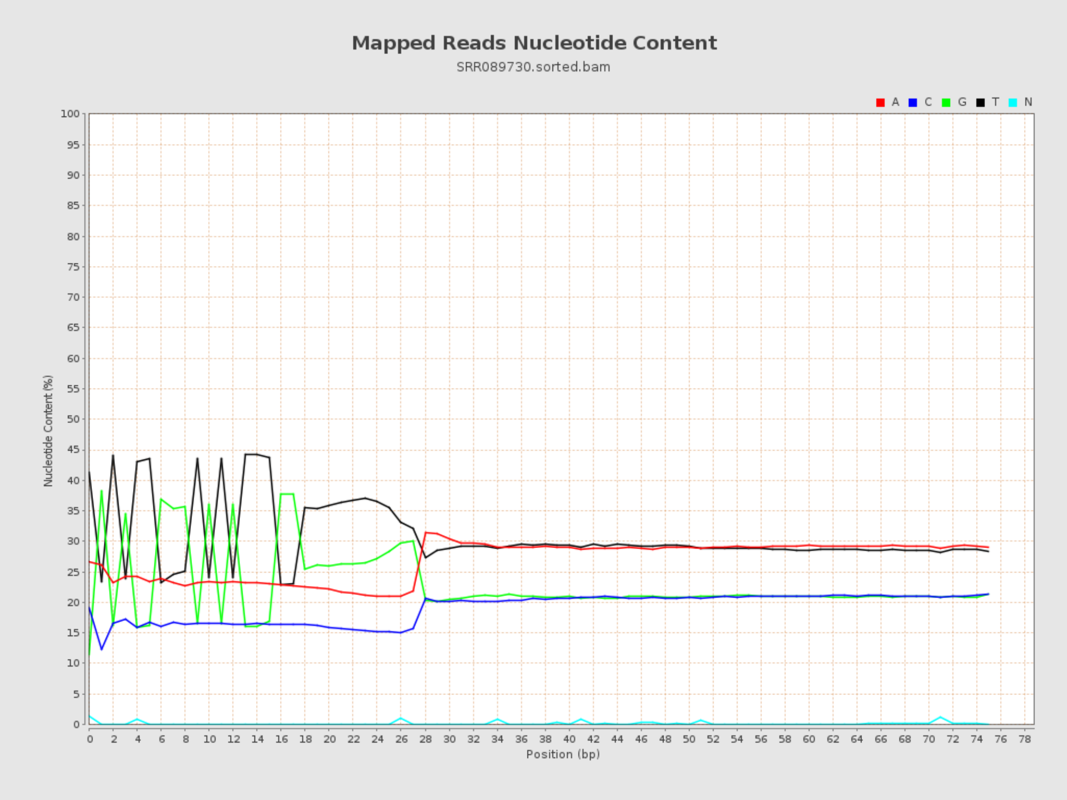
6. Results : Genome Fraction Coverage



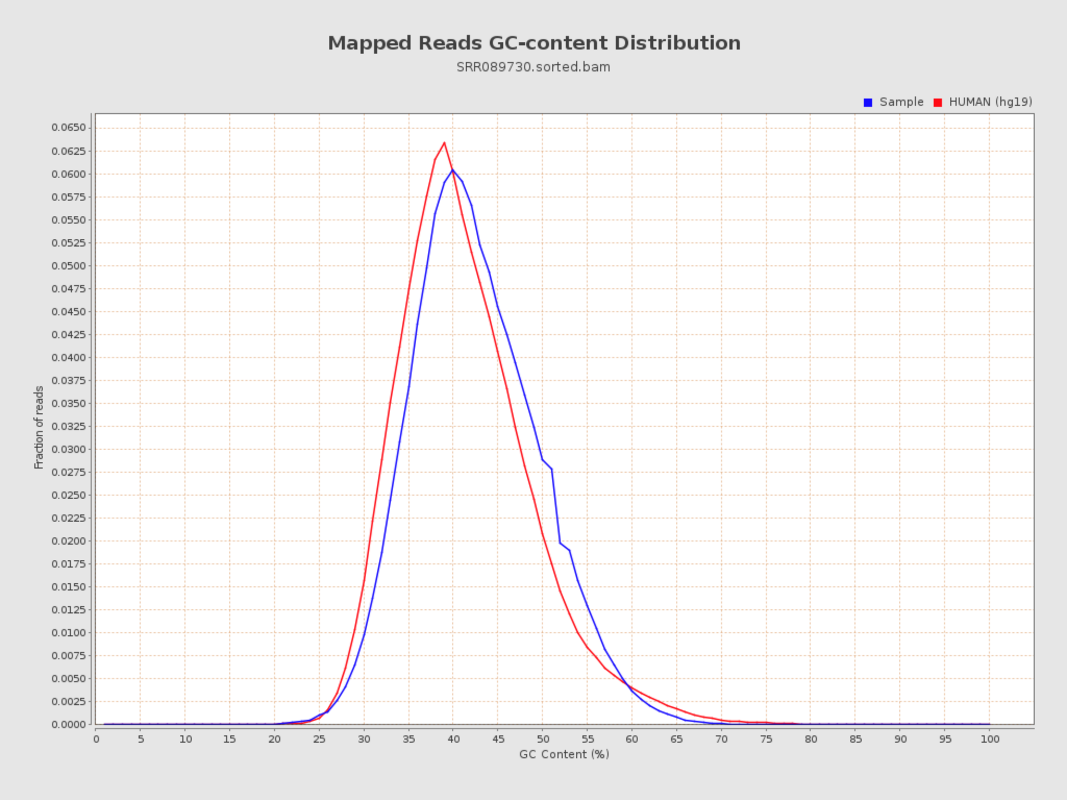
7. Results : Duplication Rate Histogram



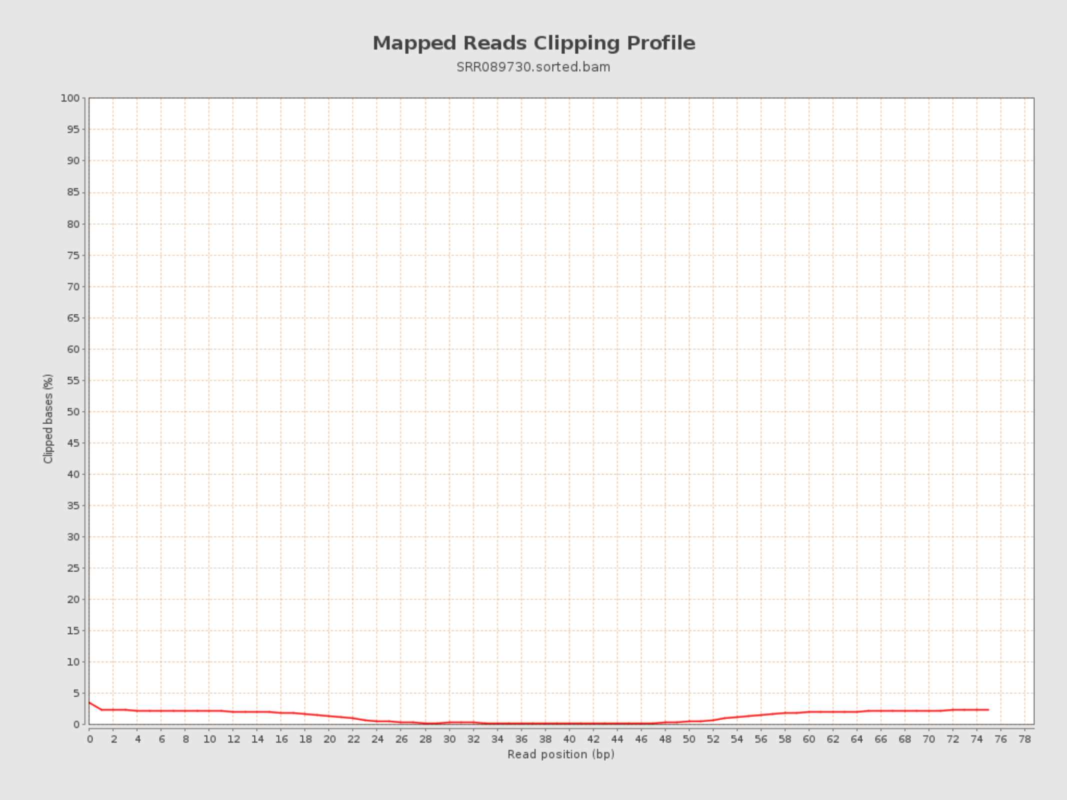
8. Results : Mapped Reads Nucleotide Content



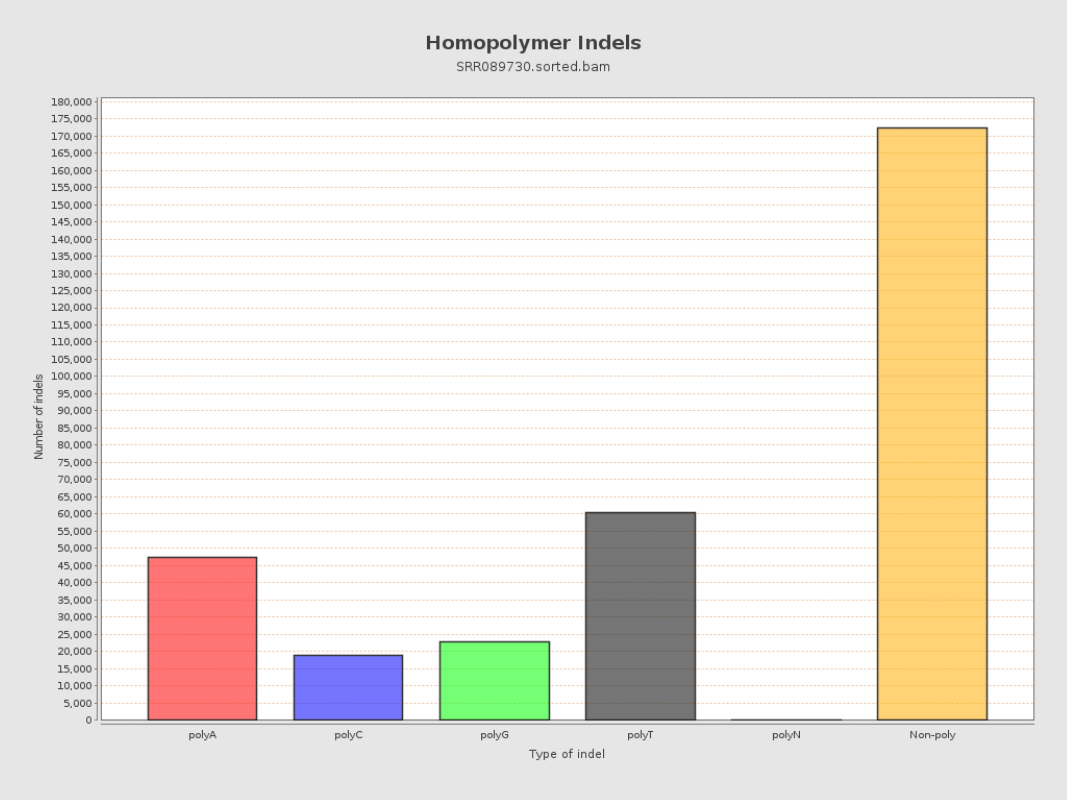
9. Results : Mapped Reads GC-content Distribution



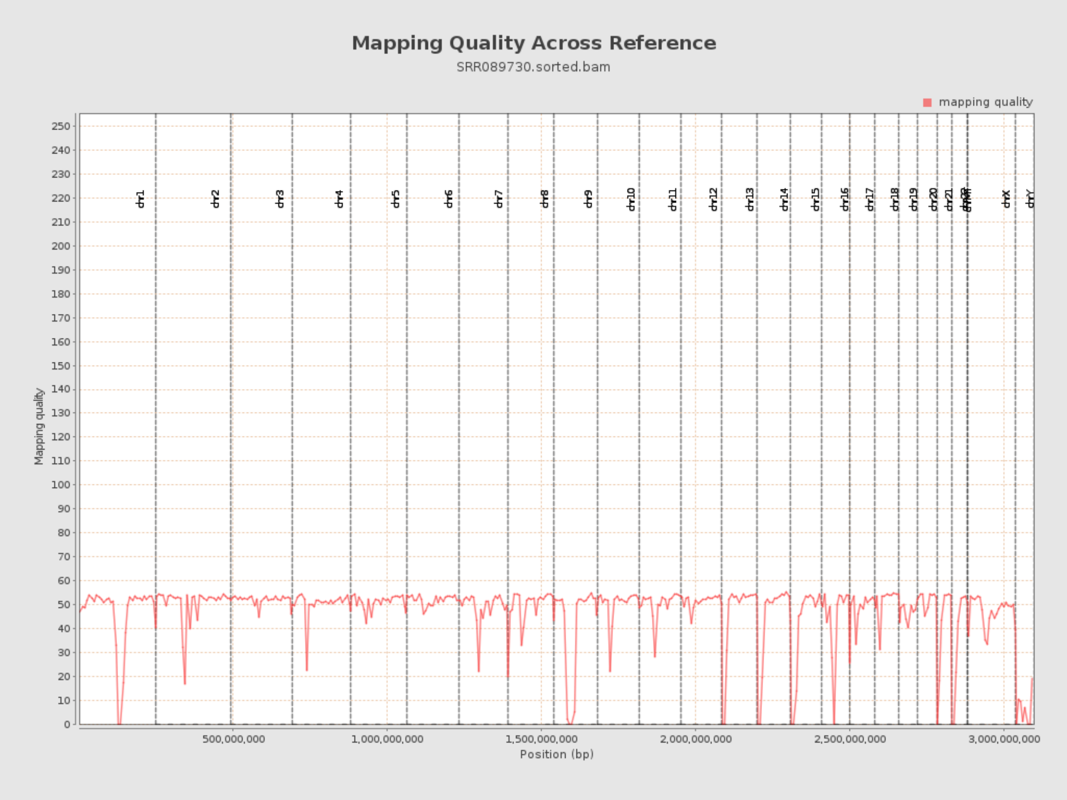
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram