Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 19:56:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089694.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_SRR089694 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089694.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 19:56:58 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089694.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,402,841
Mapped reads	15,941,072 / 82.16%
Unmapped reads	3,461,769 / 17.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	695 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,523,353 / 7.85%
Duplication rate	7.23%
Clipped reads	2,010,387 / 10.36%

2.2. ACGT Content

Number/percentage of A's	239,211,586 / 32.07%
Number/percentage of C's	147,368,828 / 19.76%
Number/percentage of T's	198,812,749 / 26.65%
Number/percentage of G's	160,501,678 / 21.52%
Number/percentage of N's	69,222 / 0.01%
GC Percentage	41.27%

2.3. Coverage

Mean	0.241

Standard Deviation	1.3181

2.4. Mapping Quality

Mean Mapping Quality	43.26

2.5. Mismatches and indels

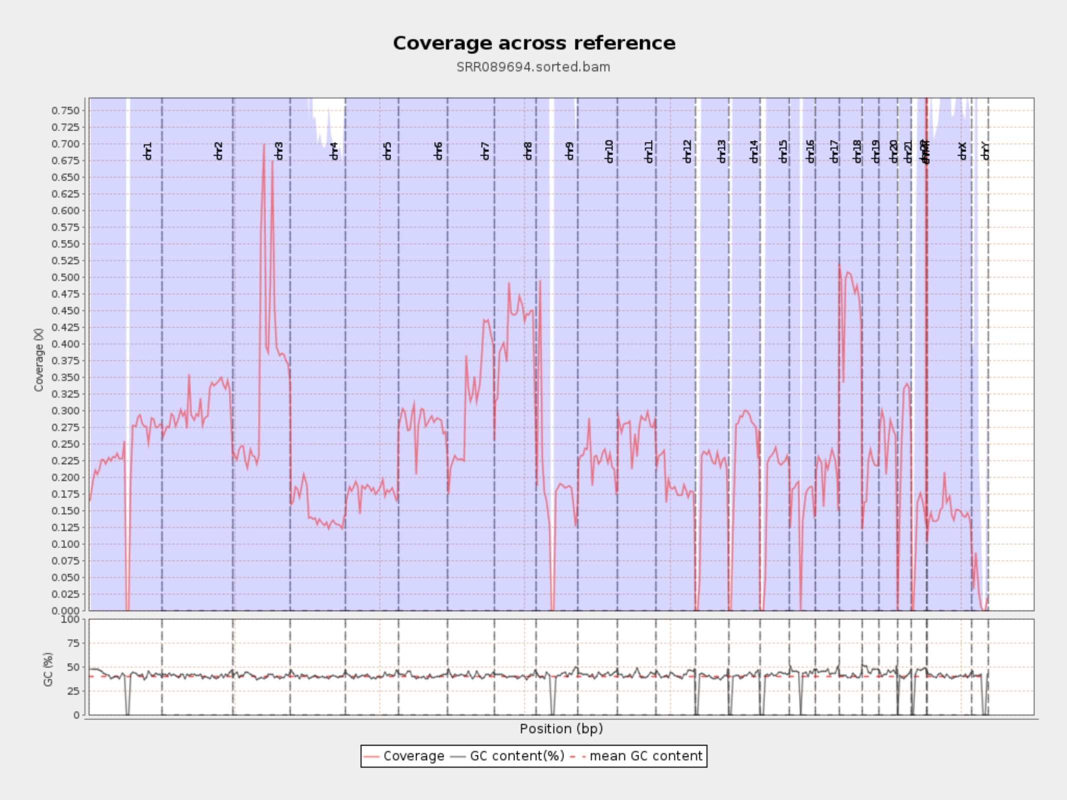
General error rate	0.48%
Mismatches	3,540,907
Insertions	32,524
Mapped reads with at least one insertion	0.2%
Deletions	102,139
Mapped reads with at least one deletion	0.64%
Homopolymer indels	44.64%

2.6. Chromosome stats

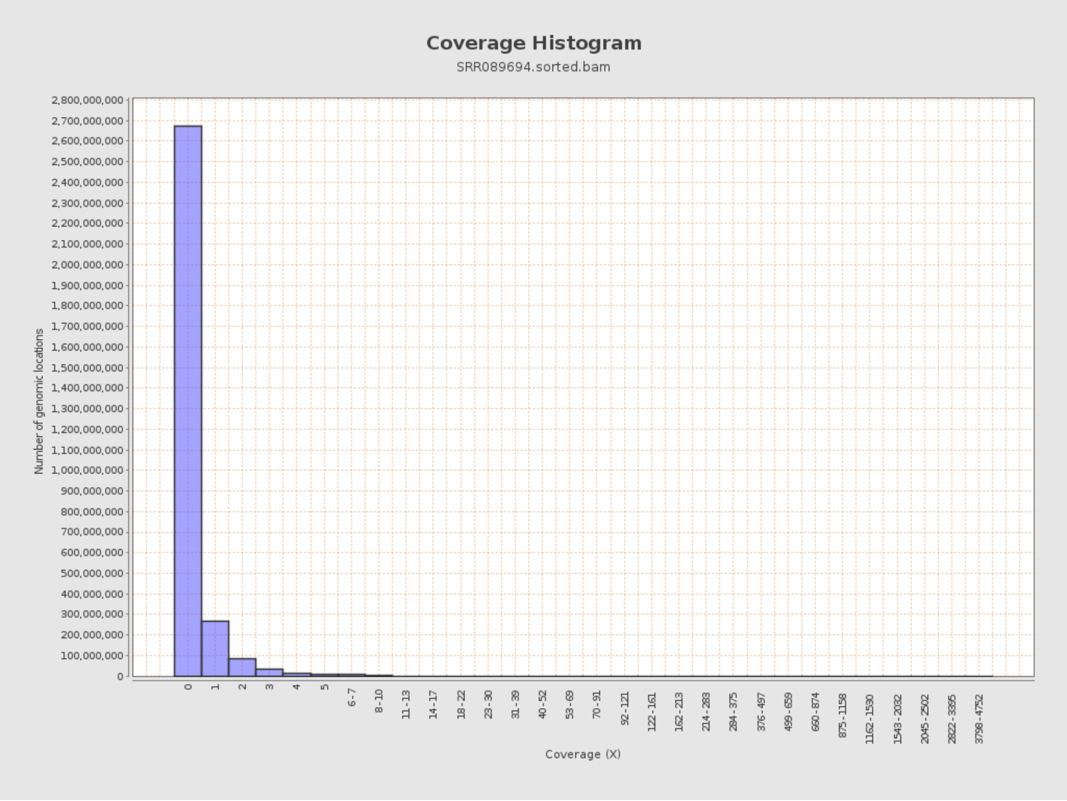
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	57315885	0.23	1.4952
chr2	243199373	74341840	0.3057	1.7638
chr3	198022430	69040505	0.3486	1.0621
chr4	191154276	28215198	0.1476	0.6522
chr5	180915260	32519206	0.1797	0.6926
chr6	171115067	48204587	0.2817	1.0778
chr7	159138663	50574469	0.3178	2.0103

chr8	146364022	61162381	0.4179	2.9473
chr9	141213431	25943714	0.1837	1.1141
chr10	135534747	31002516	0.2287	1.1816
chr11	135006516	36767720	0.2723	1.1466
chr12	133851895	25415753	0.1899	0.743
chr13	115169878	21816556	0.1894	0.7166
chr14	107349540	25243494	0.2352	0.9077
chr15	102531392	18685563	0.1822	0.7052
chr16	90354753	14260544	0.1578	0.7157
chr17	81195210	17192716	0.2117	0.8475
chr18	78077248	37027152	0.4742	1.7424
chr19	59128983	12108767	0.2048	1.4818
chr20	63025520	16466648	0.2613	0.8923
chr21	48129895	12176282	0.253	0.9572
chr22	51304566	5849282	0.114	0.5459
chrMT	16571	309032	18.649	15.3313
chrX	155270560	22825375	0.147	0.8716
chrY	59373566	1653152	0.0278	0.4884

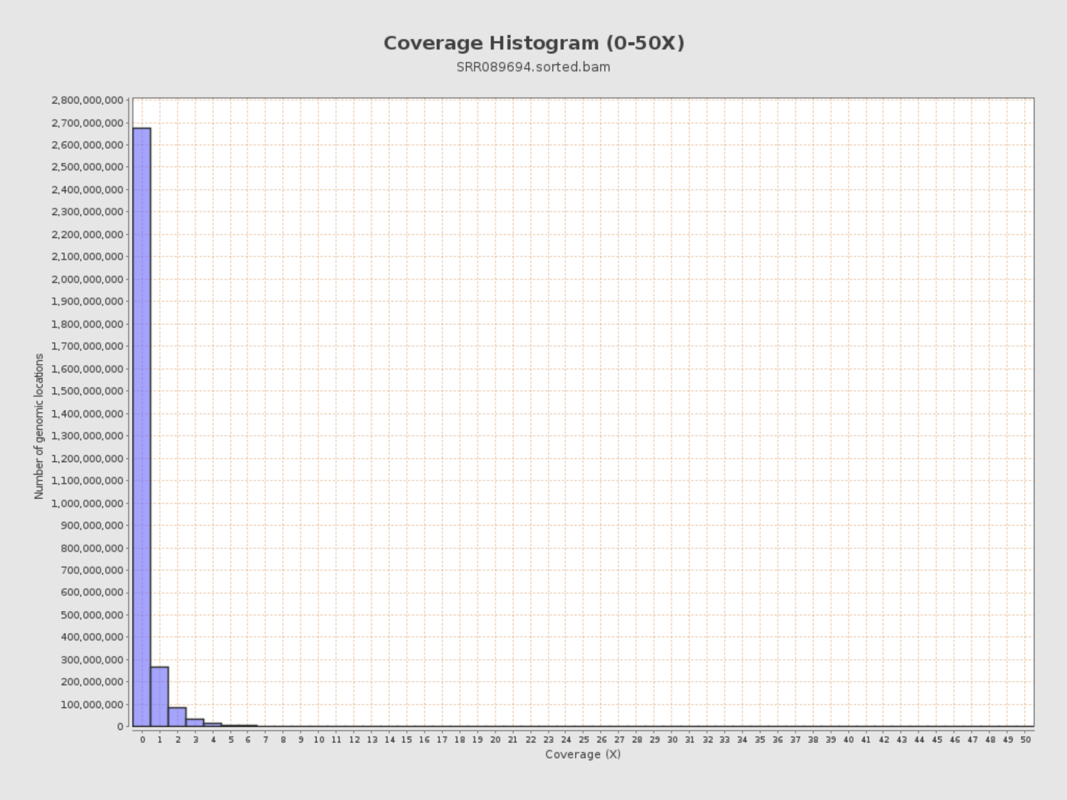
3. Results : Coverage across reference



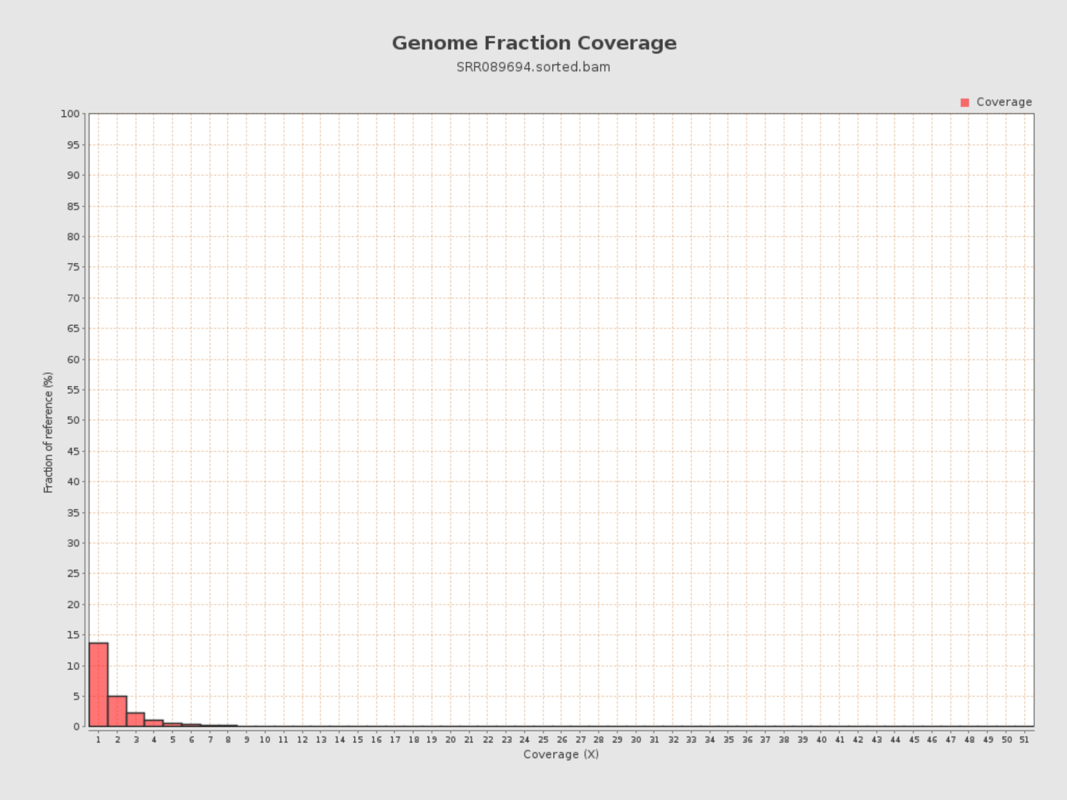
4. Results : Coverage Histogram



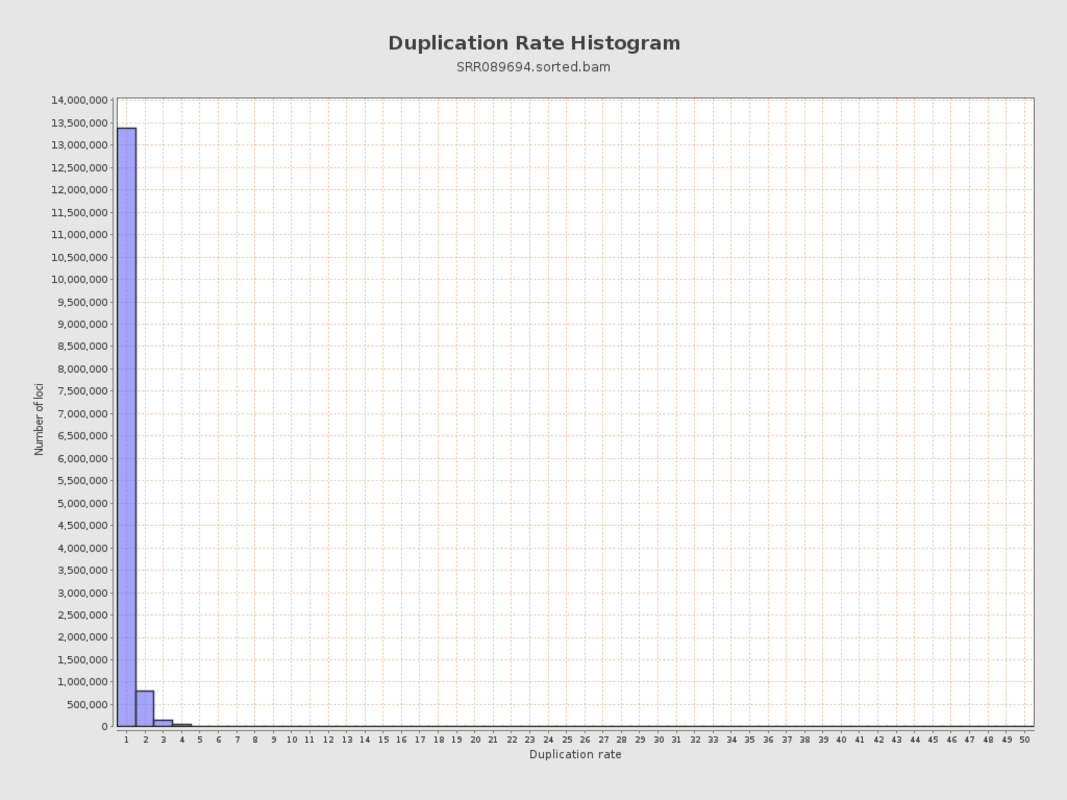
5. Results : Coverage Histogram (0-50X)



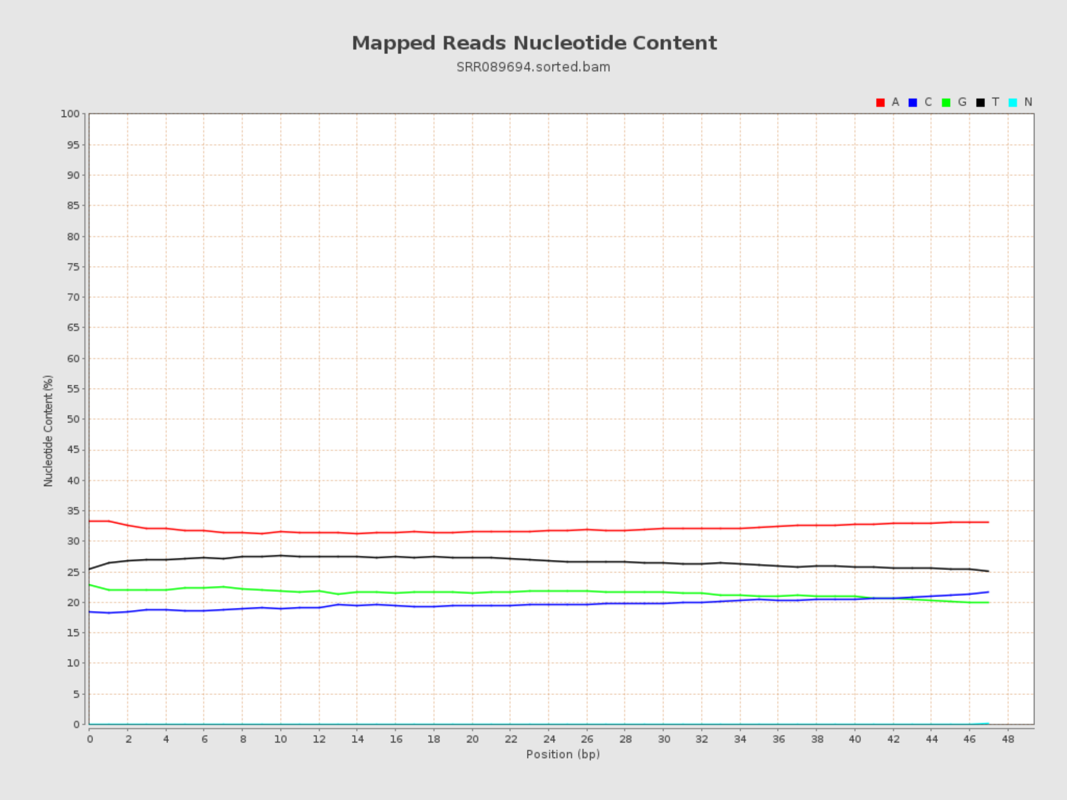
6. Results : Genome Fraction Coverage



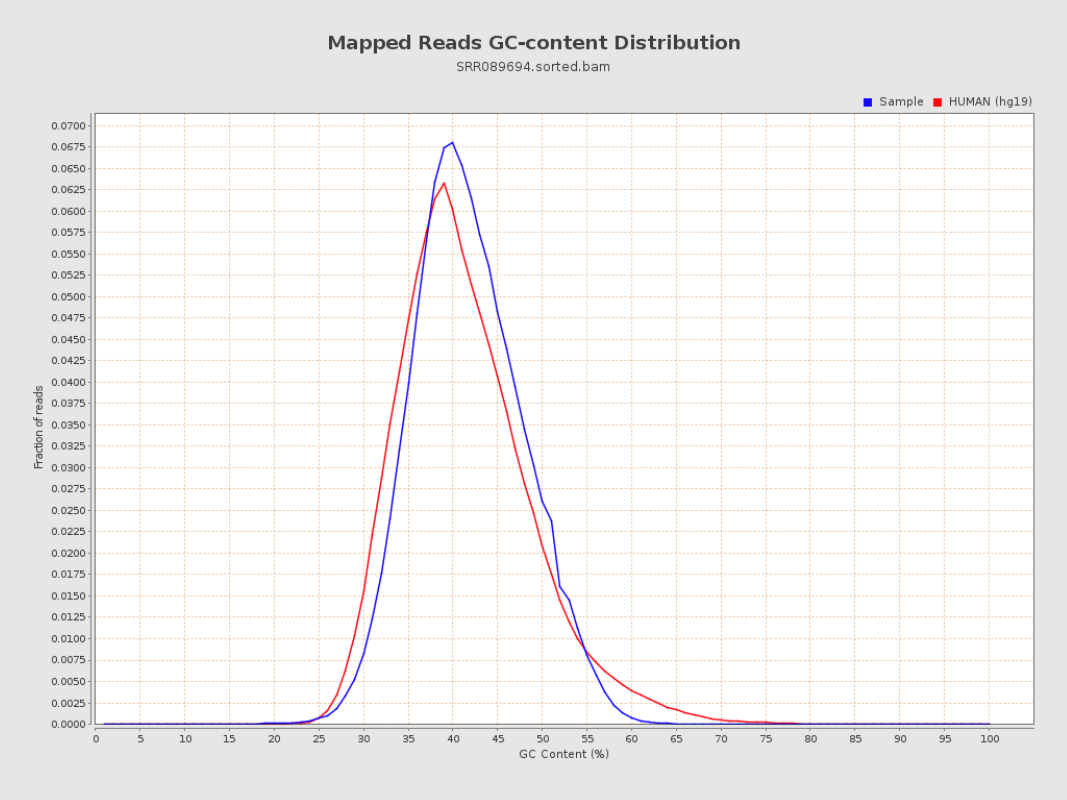
7. Results : Duplication Rate Histogram



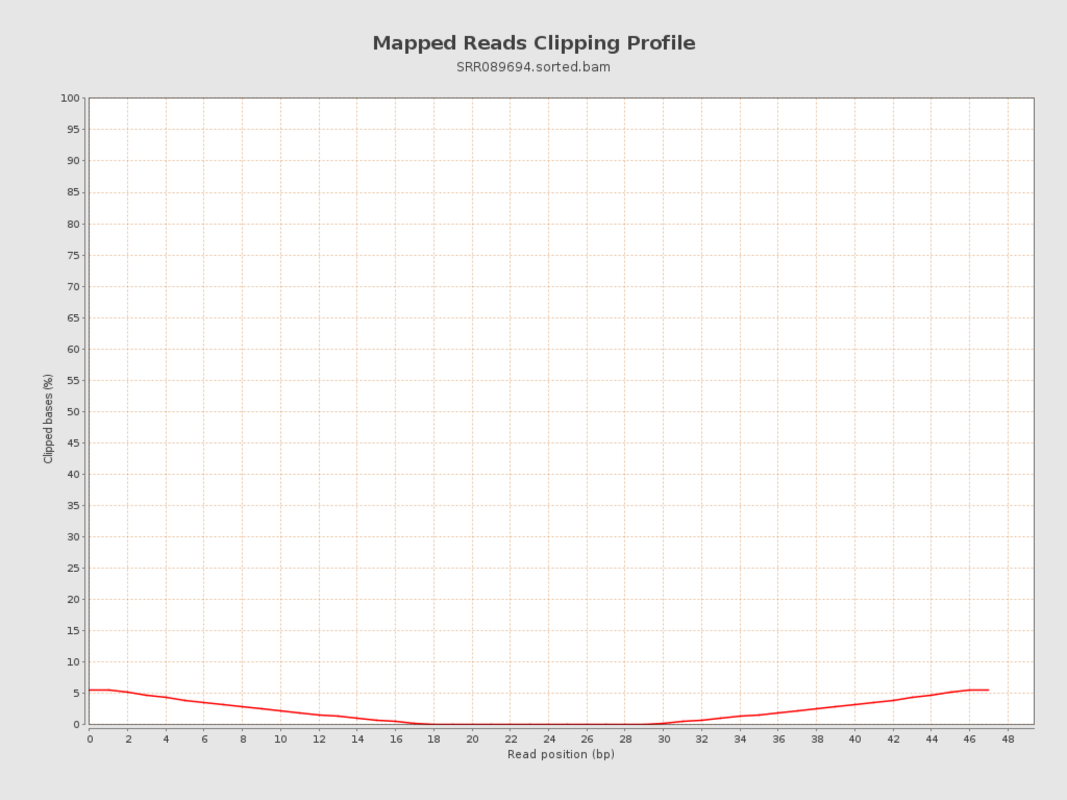
8. Results : Mapped Reads Nucleotide Content



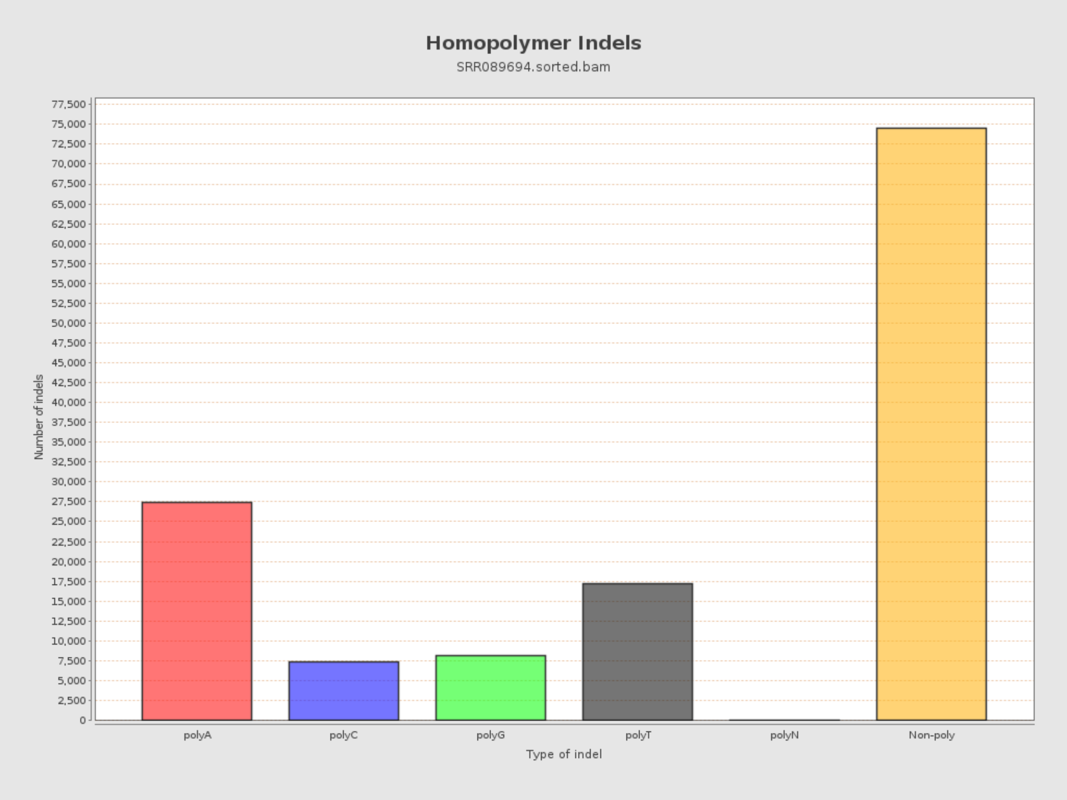
9. Results : Mapped Reads GC-content Distribution



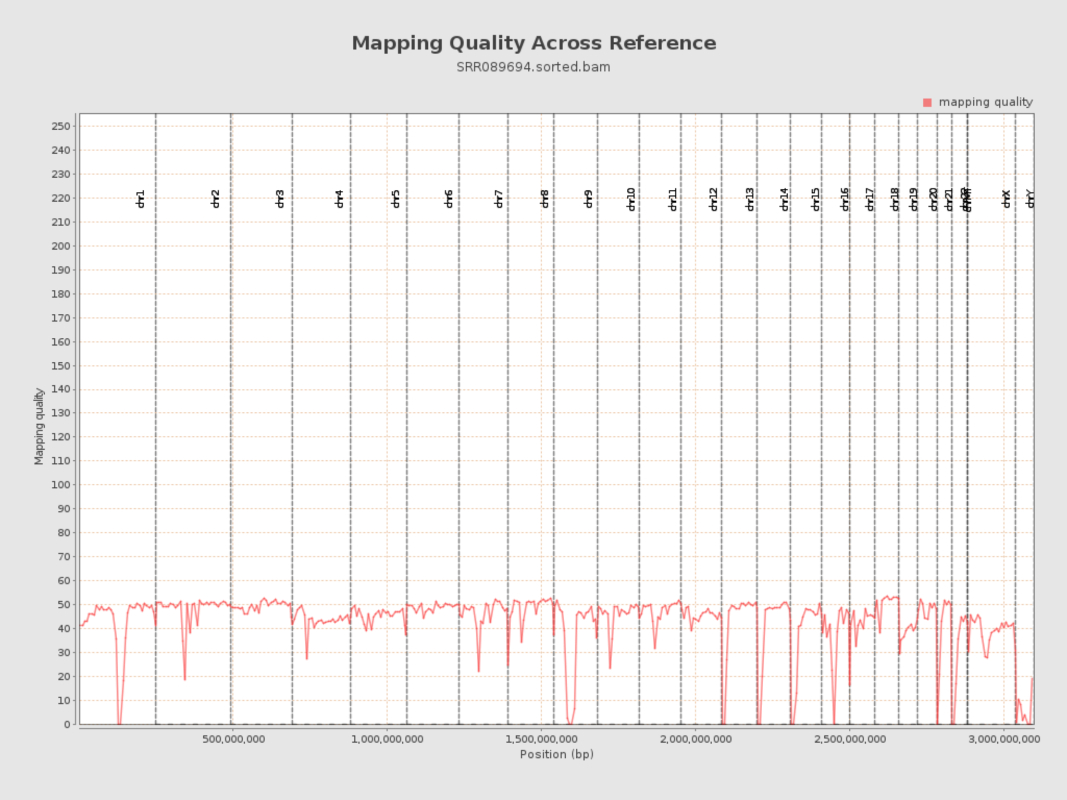
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram