Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 00:17:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089713.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_SRR089713 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089713.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 00:17:38 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089713.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,383,780
Mapped reads	15,794,878 / 85.92%
Unmapped reads	2,588,902 / 14.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	627 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	3,385,080 / 18.41%
Duplication rate	12.55%
Clipped reads	1,135,122 / 6.17%

2.2. ACGT Content

Number/percentage of A's	218,188,686 / 29.18%
Number/percentage of C's	152,809,711 / 20.44%
Number/percentage of T's	217,676,062 / 29.11%
Number/percentage of G's	159,012,865 / 21.27%
Number/percentage of N's	10,320 / 0%
GC Percentage	41.7%

2.3. Coverage

Mean	0.2416

Standard Deviation	1.5712

2.4. Mapping Quality

Mean Mapping Quality	45.15

2.5. Mismatches and indels

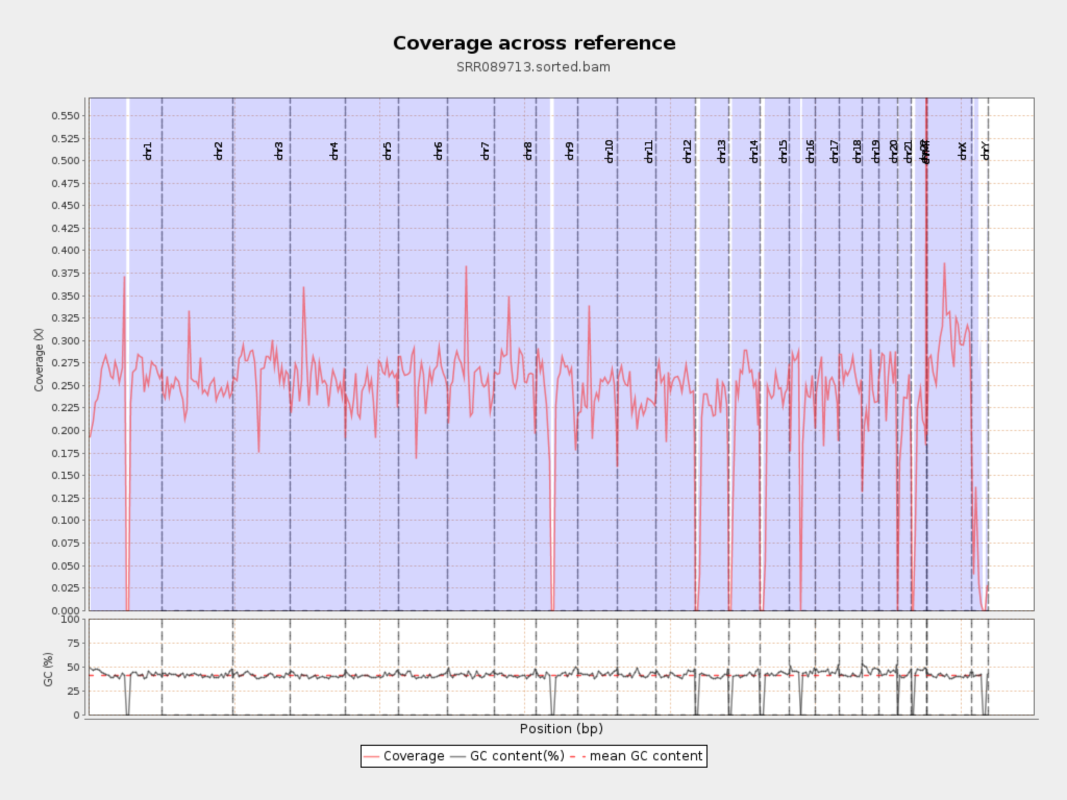
General error rate	0.55%
Mismatches	4,042,137
Insertions	29,583
Mapped reads with at least one insertion	0.19%
Deletions	86,930
Mapped reads with at least one deletion	0.55%
Homopolymer indels	47.09%

2.6. Chromosome stats

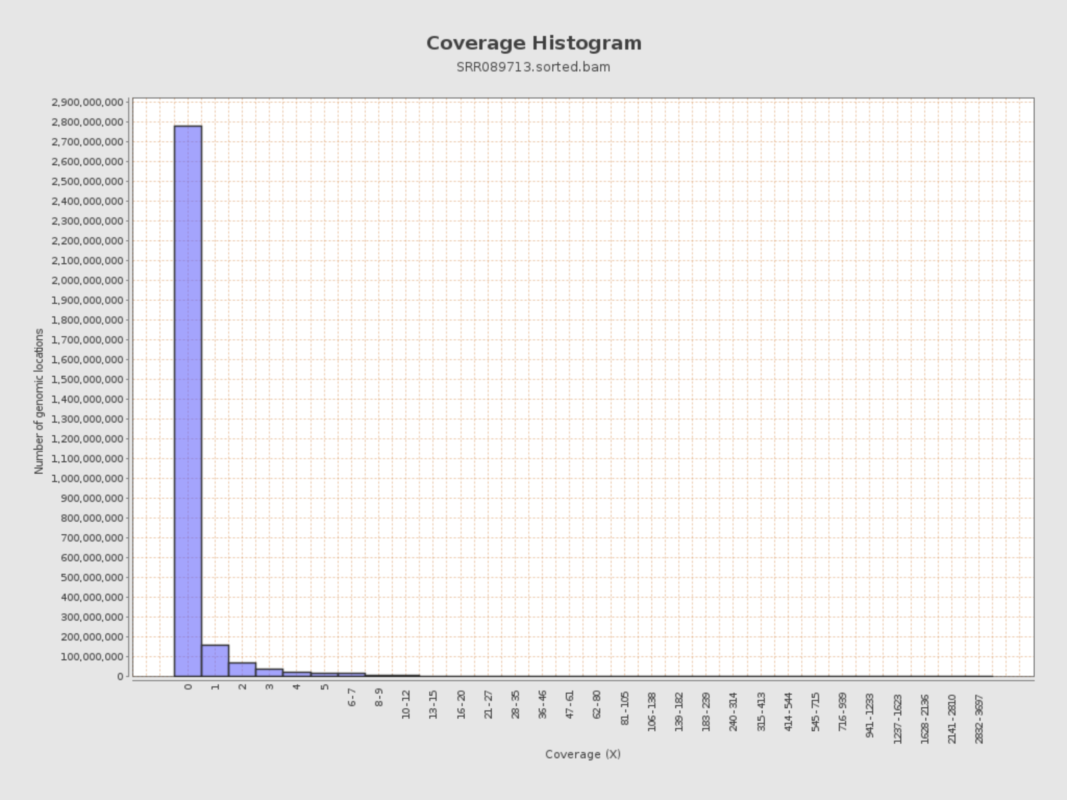
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	61411712	0.2464	2.8328
chr2	243199373	60508738	0.2488	1.472
chr3	198022430	53338621	0.2694	1.0356
chr4	191154276	49443171	0.2587	1.1318
chr5	180915260	44826172	0.2478	1.0059
chr6	171115067	44721577	0.2614	1.1334
chr7	159138663	41542341	0.261	2.1575

chr8	146364022	39356068	0.2689	2.1201
chr9	141213431	31383522	0.2222	1.3595
chr10	135534747	33186677	0.2449	1.4578
chr11	135006516	31801791	0.2356	1.4973
chr12	133851895	33631246	0.2513	1.0607
chr13	115169878	22301008	0.1936	0.875
chr14	107349540	23213139	0.2162	0.9909
chr15	102531392	20139304	0.1964	0.8913
chr16	90354753	20501190	0.2269	1.0416
chr17	81195210	19697295	0.2426	1.1801
chr18	78077248	20671622	0.2648	2.8752
chr19	59128983	13513778	0.2285	1.9746
chr20	63025520	16542606	0.2625	1.1268
chr21	48129895	9334365	0.1939	1.1102
chr22	51304566	7912443	0.1542	0.7948
chrMT	16571	27486	1.6587	2.4948
chrX	155270560	46395214	0.2988	1.2569
chrY	59373566	2430225	0.0409	1.0831

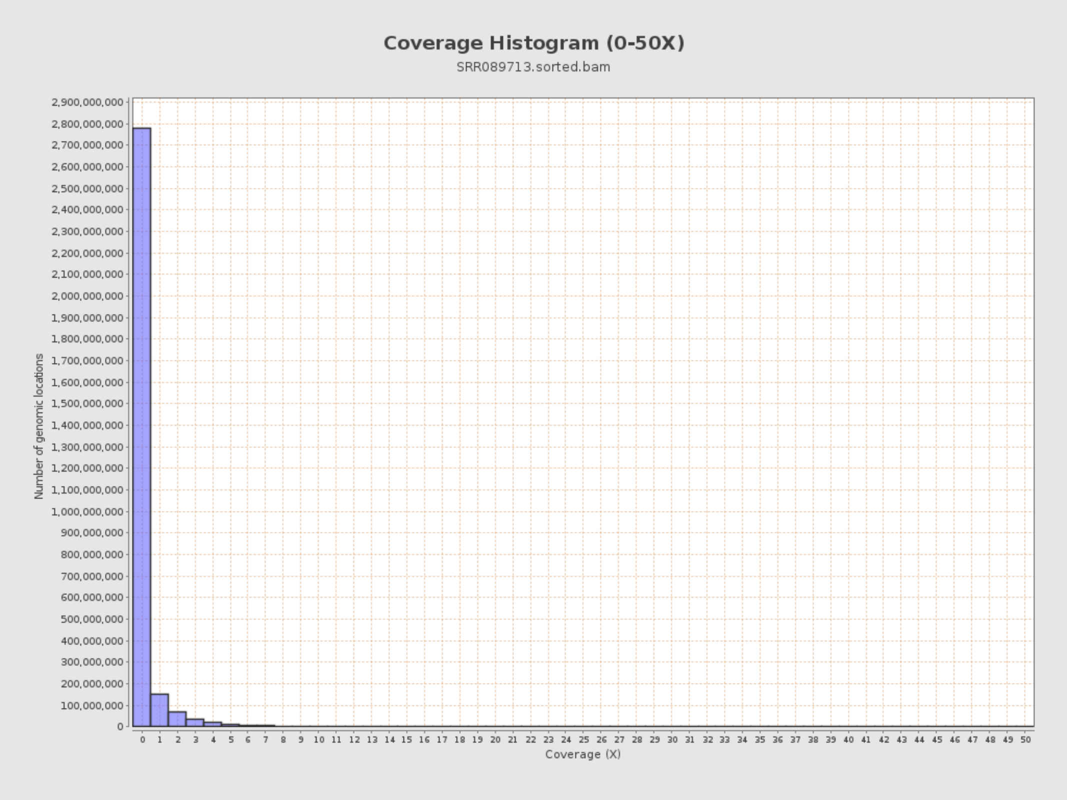
3. Results : Coverage across reference



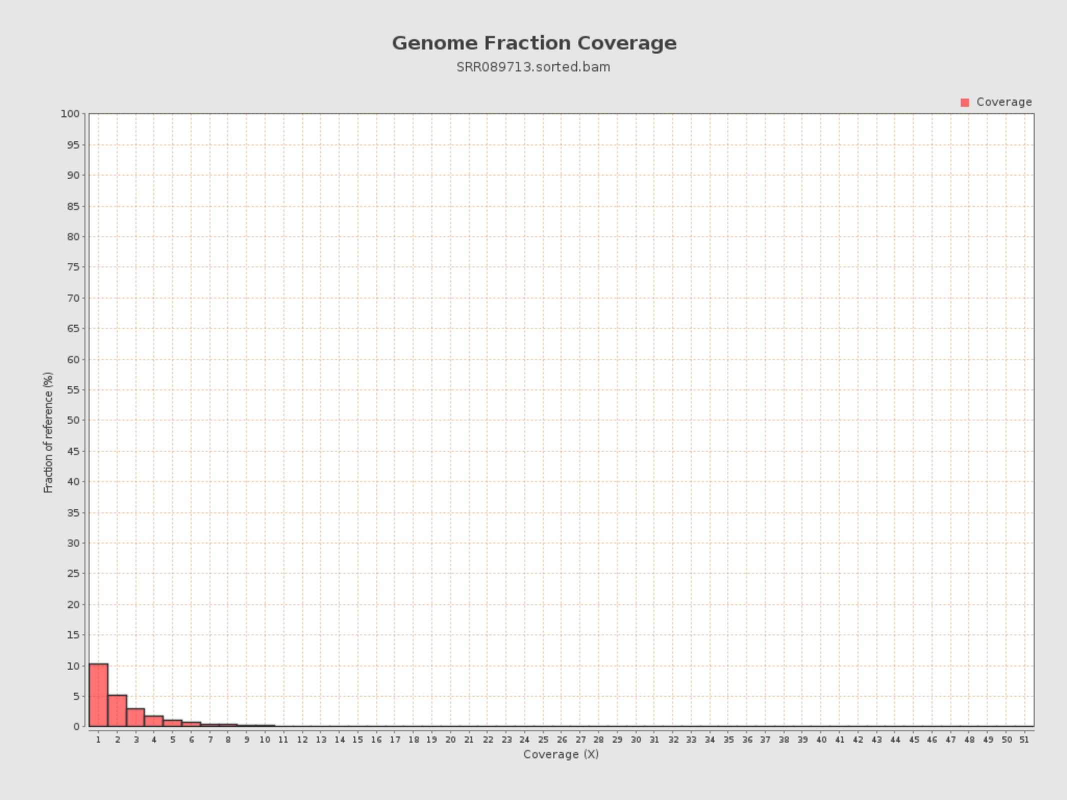
4. Results : Coverage Histogram



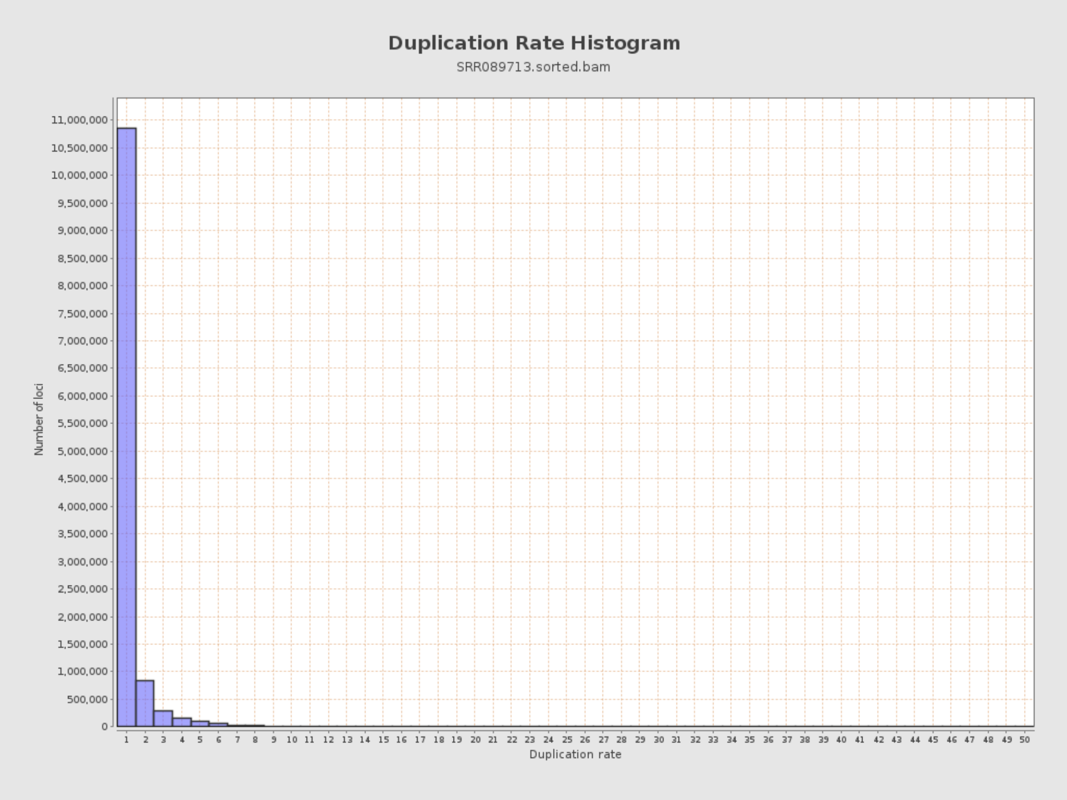
5. Results : Coverage Histogram (0-50X)



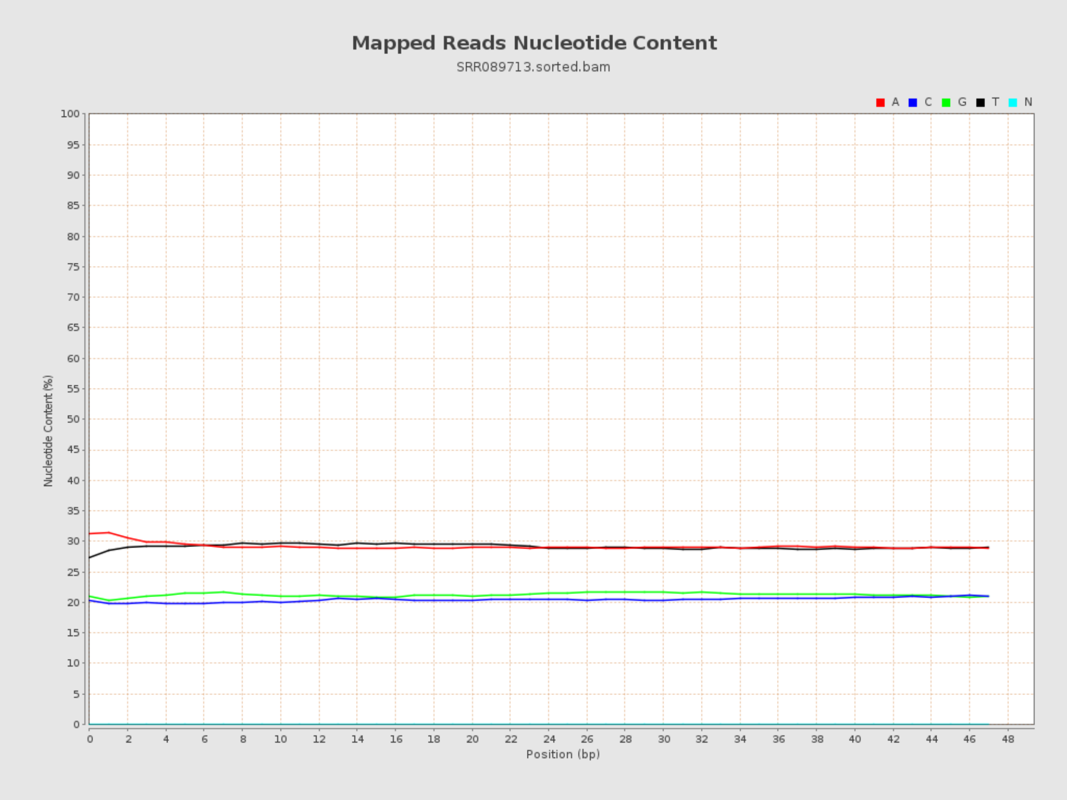
6. Results : Genome Fraction Coverage



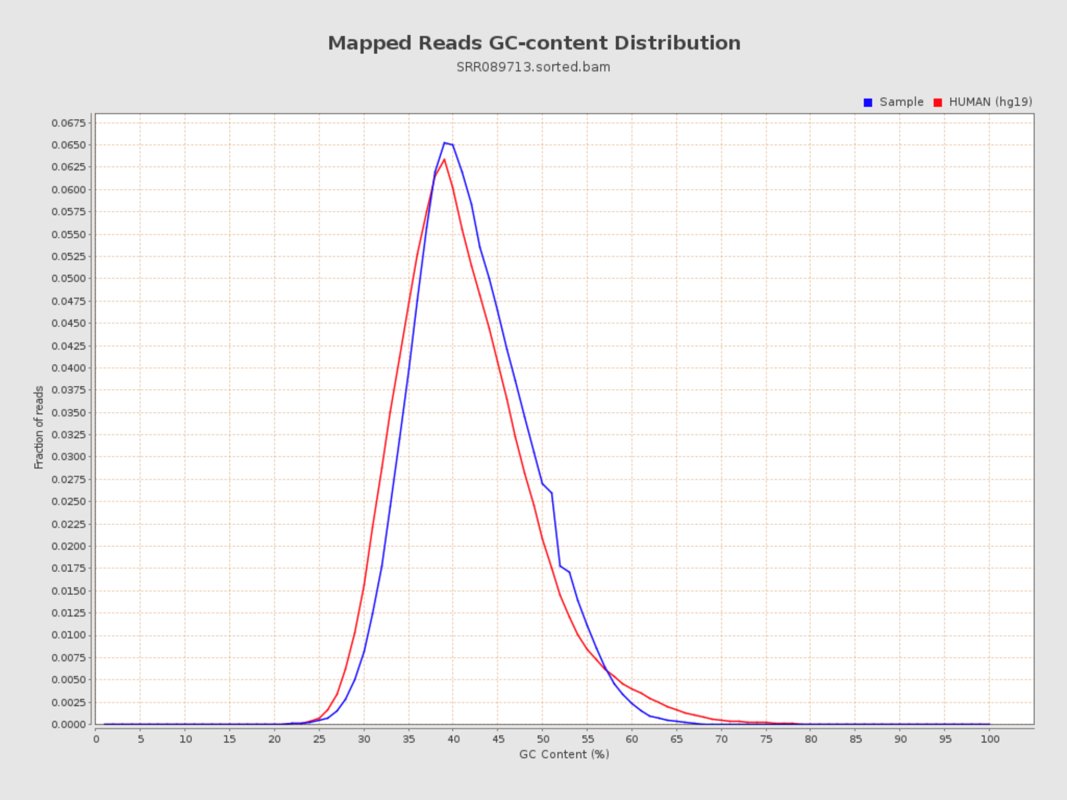
7. Results : Duplication Rate Histogram



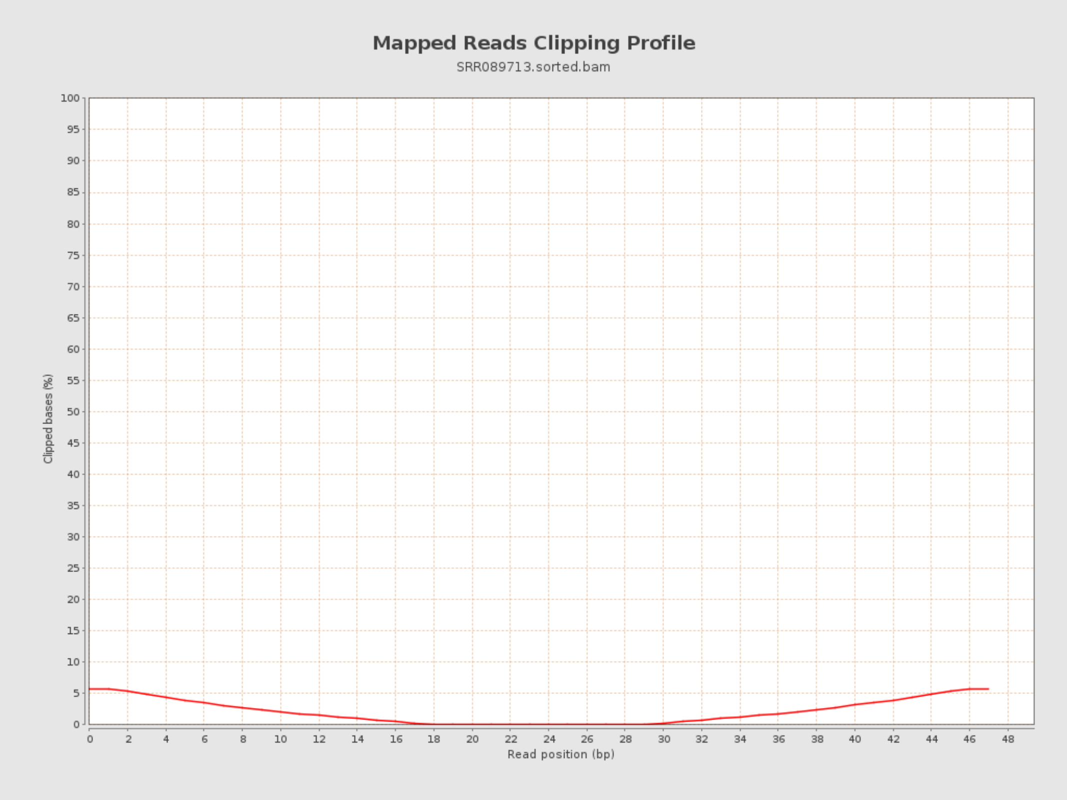
8. Results : Mapped Reads Nucleotide Content



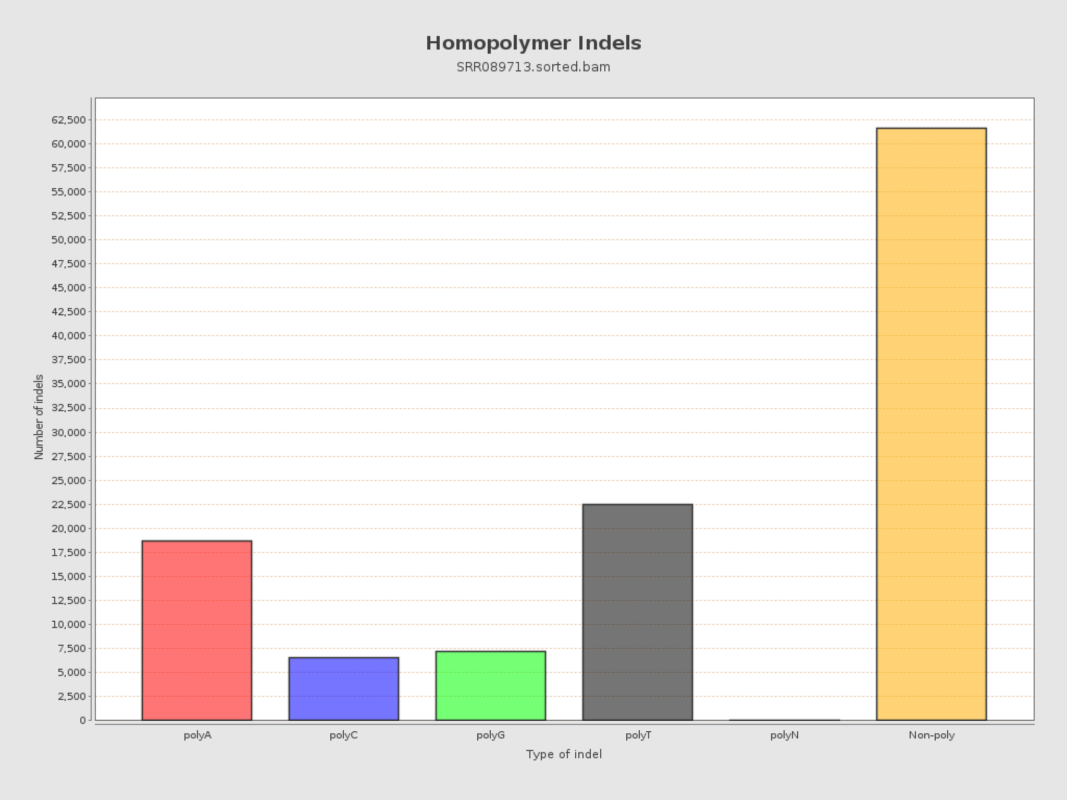
9. Results : Mapped Reads GC-content Distribution



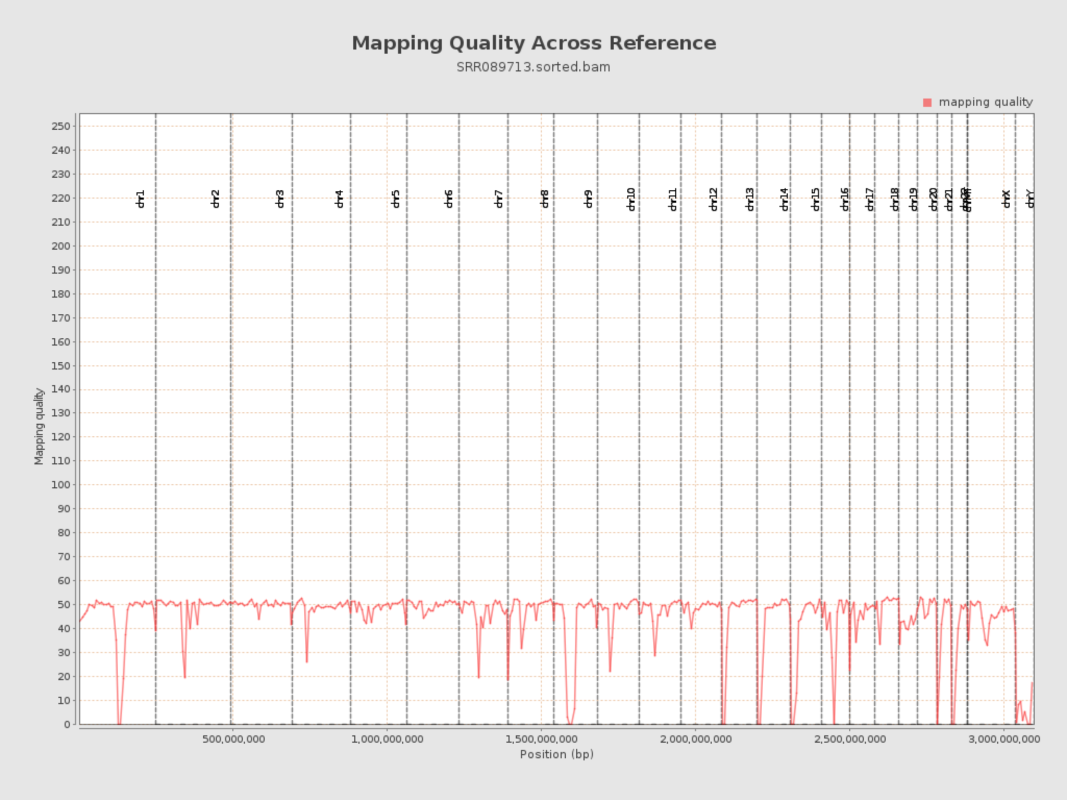
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram