Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 17:56:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089608.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_SRR089608 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089608.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 17:56:35 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089608.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,247,529
Mapped reads	9,363,468 / 83.25%
Unmapped reads	1,884,061 / 16.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	359 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	3,523,427 / 31.33%
Duplication rate	29.38%
Clipped reads	1,020,053 / 9.07%

2.2. ACGT Content

Number/percentage of A's	140,574,030 / 31.93%
Number/percentage of C's	86,559,139 / 19.66%
Number/percentage of T's	111,227,123 / 25.26%
Number/percentage of G's	101,889,148 / 23.14%
Number/percentage of N's	8,653 / 0%
GC Percentage	42.8%

2.3. Coverage

Mean	0.1422

Standard Deviation	1.2476

2.4. Mapping Quality

Mean Mapping Quality	43.07

2.5. Mismatches and indels

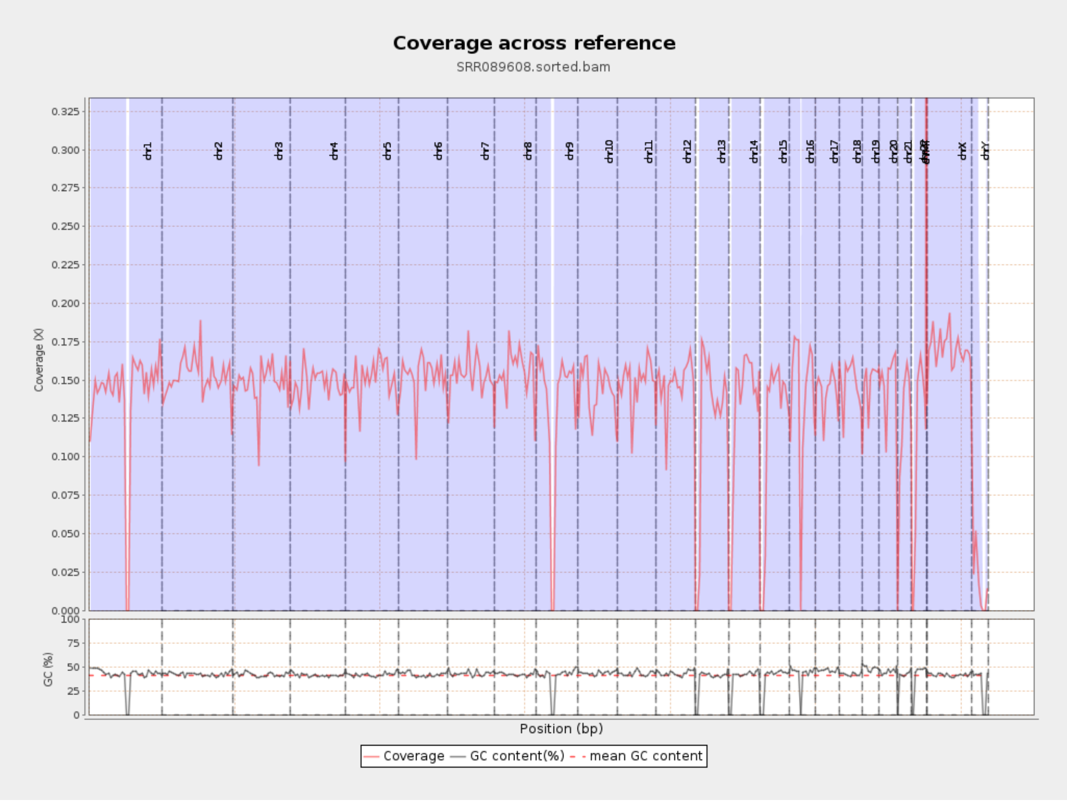
General error rate	0.48%
Mismatches	2,099,543
Insertions	17,753
Mapped reads with at least one insertion	0.19%
Deletions	54,868
Mapped reads with at least one deletion	0.58%
Homopolymer indels	44.22%

2.6. Chromosome stats

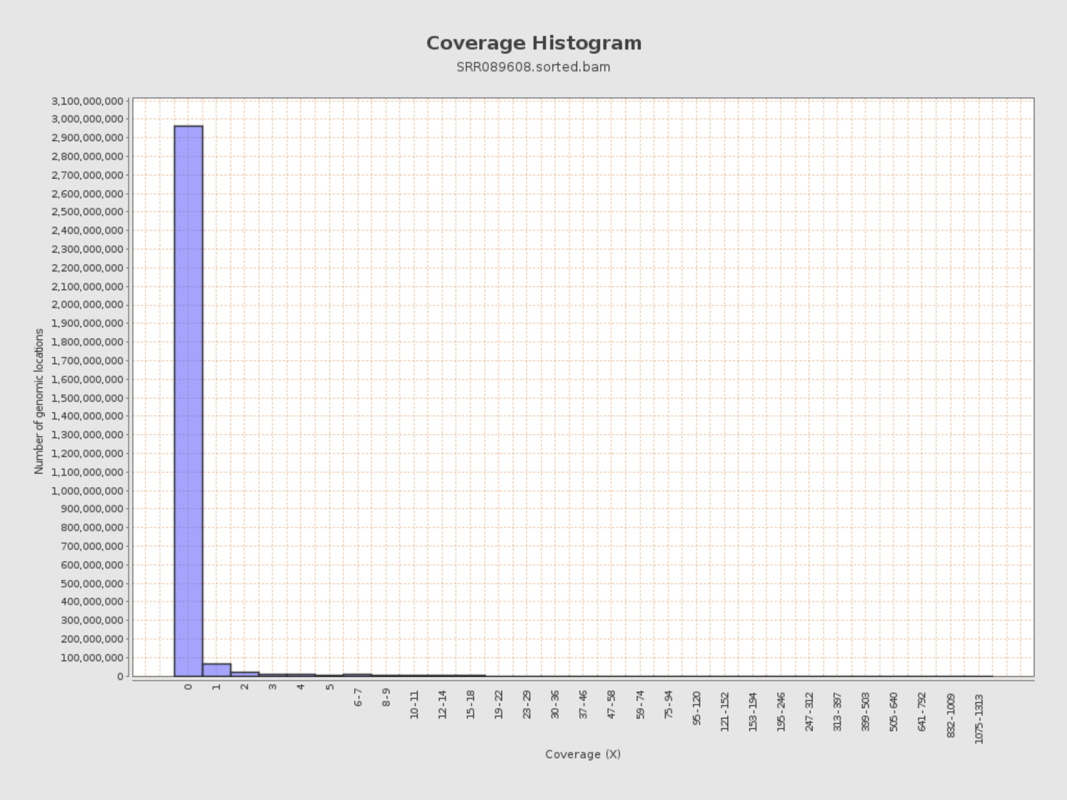
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	34754506	0.1394	1.3052
chr2	243199373	37281271	0.1533	1.3281
chr3	198022430	29369977	0.1483	1.2138
chr4	191154276	28260230	0.1478	1.2688
chr5	180915260	27329092	0.1511	1.2172
chr6	171115067	26015536	0.152	1.2862
chr7	159138663	24535234	0.1542	1.3562

chr8	146364022	22779153	0.1556	1.4784
chr9	141213431	18540799	0.1313	1.196
chr10	135534747	19602964	0.1446	1.2669
chr11	135006516	20086248	0.1488	1.3088
chr12	133851895	19762501	0.1476	1.2083
chr13	115169878	14054628	0.122	1.0996
chr14	107349540	13572328	0.1264	1.1836
chr15	102531392	12029900	0.1173	1.0636
chr16	90354753	12674949	0.1403	1.1725
chr17	81195210	11532713	0.142	1.1374
chr18	78077248	11552715	0.148	1.2762
chr19	59128983	8728711	0.1476	1.2496
chr20	63025520	9295520	0.1475	1.2109
chr21	48129895	5629336	0.117	1.1395
chr22	51304566	5307032	0.1034	0.9647
chrMT	16571	47034	2.8383	8.1894
chrX	155270560	26369395	0.1698	1.3522
chrY	59373566	1230648	0.0207	0.4446

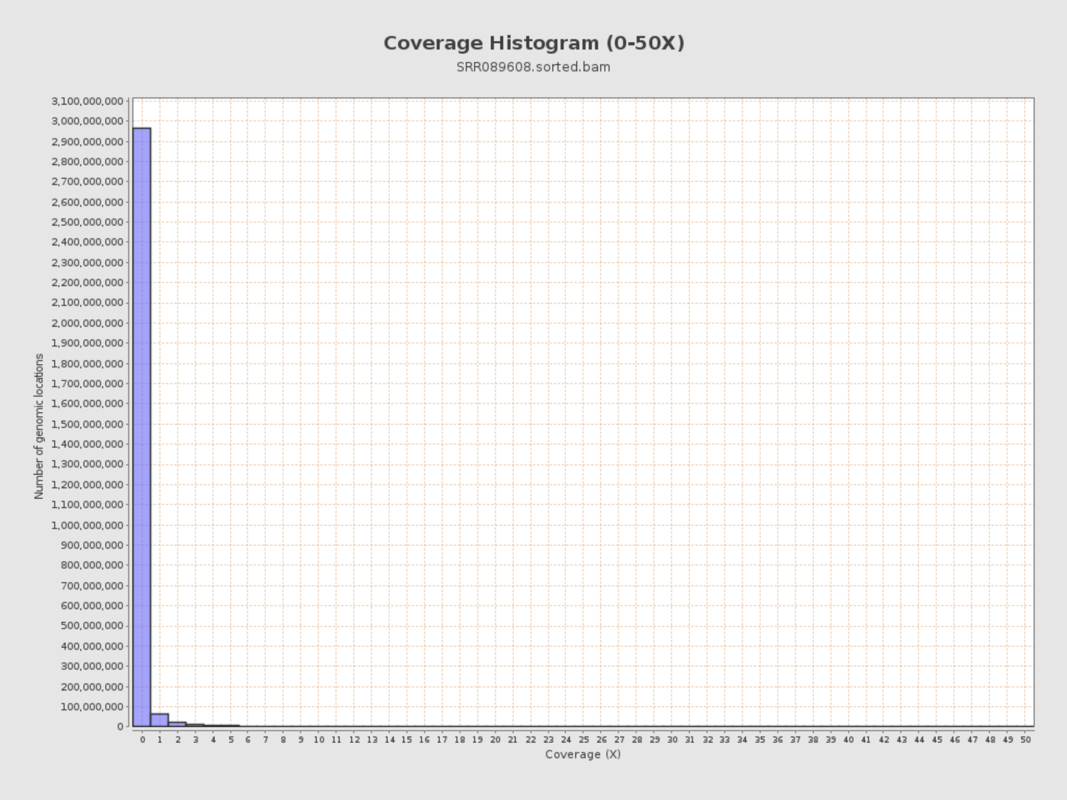
3. Results : Coverage across reference



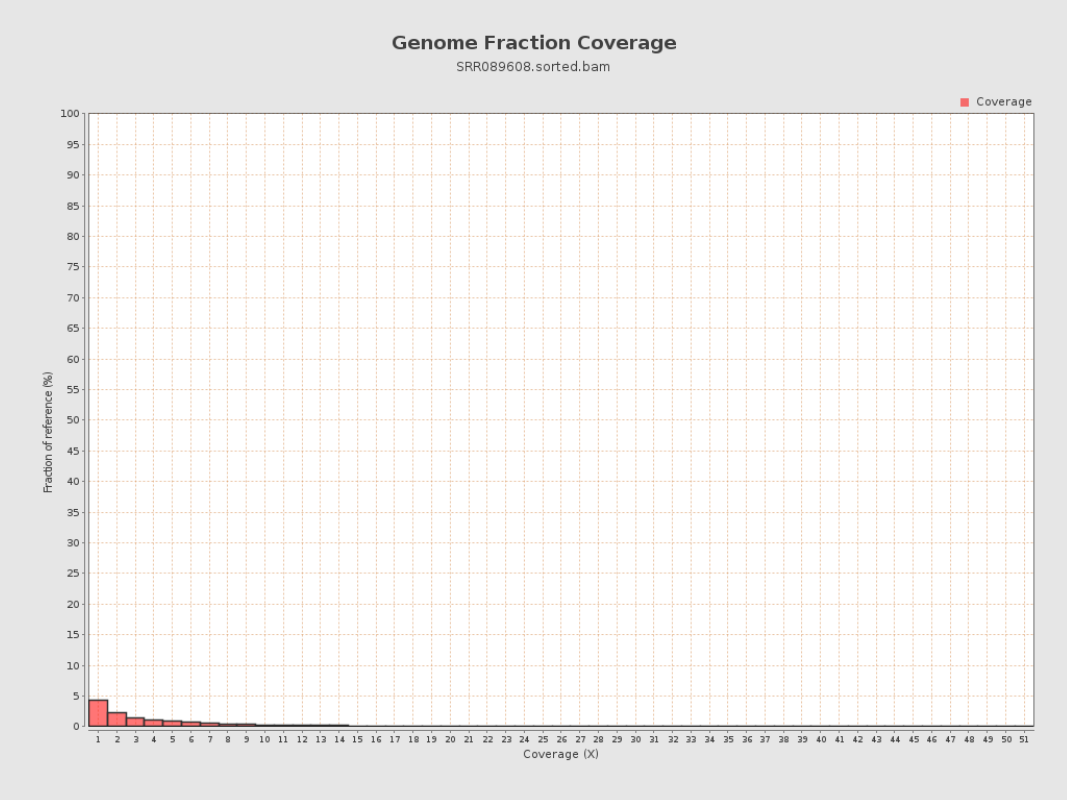
4. Results : Coverage Histogram



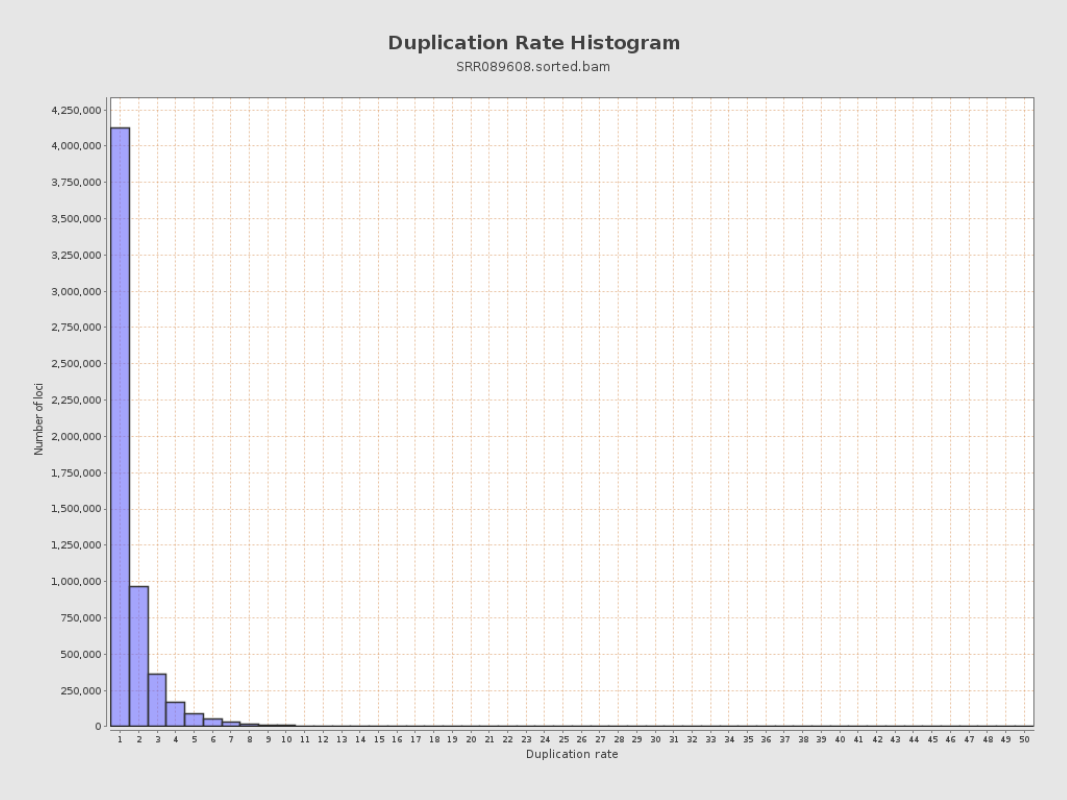
5. Results : Coverage Histogram (0-50X)



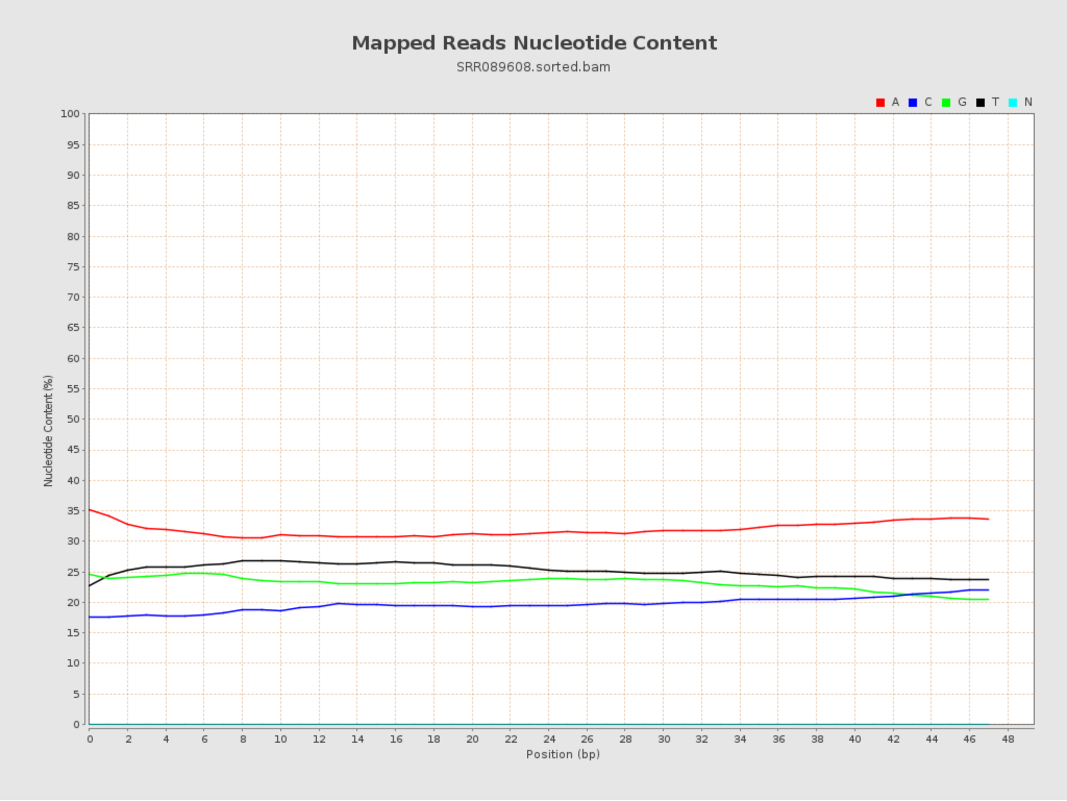
6. Results : Genome Fraction Coverage



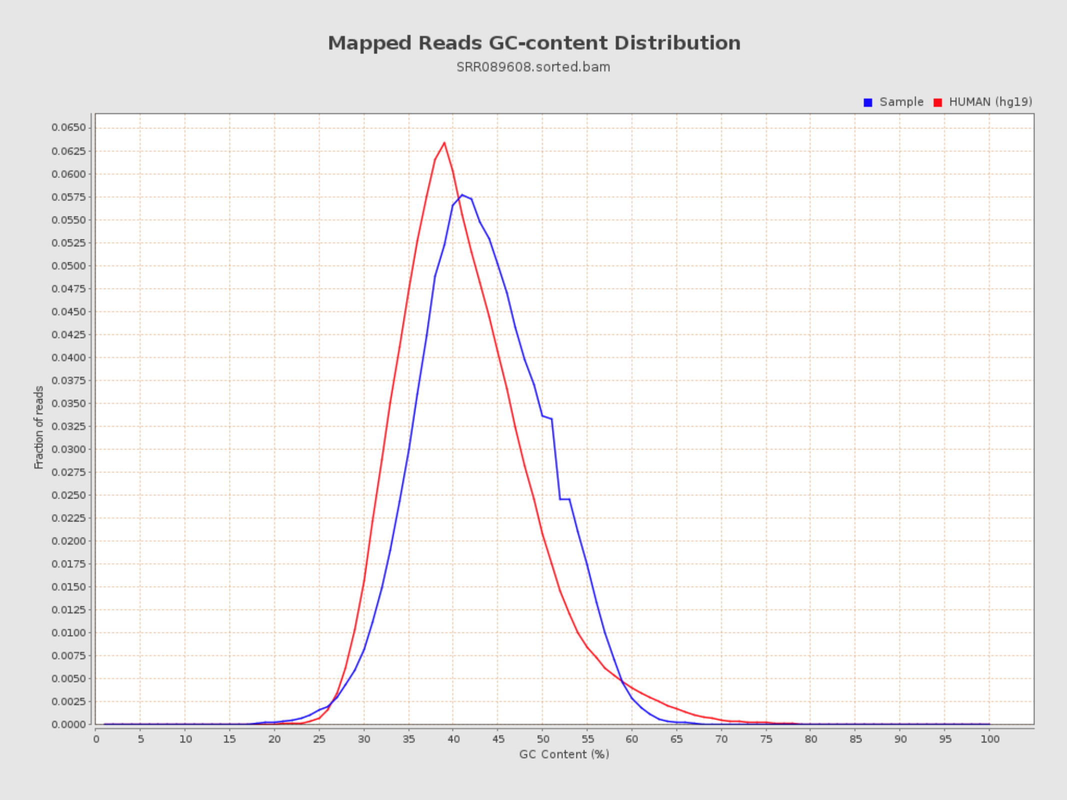
7. Results : Duplication Rate Histogram



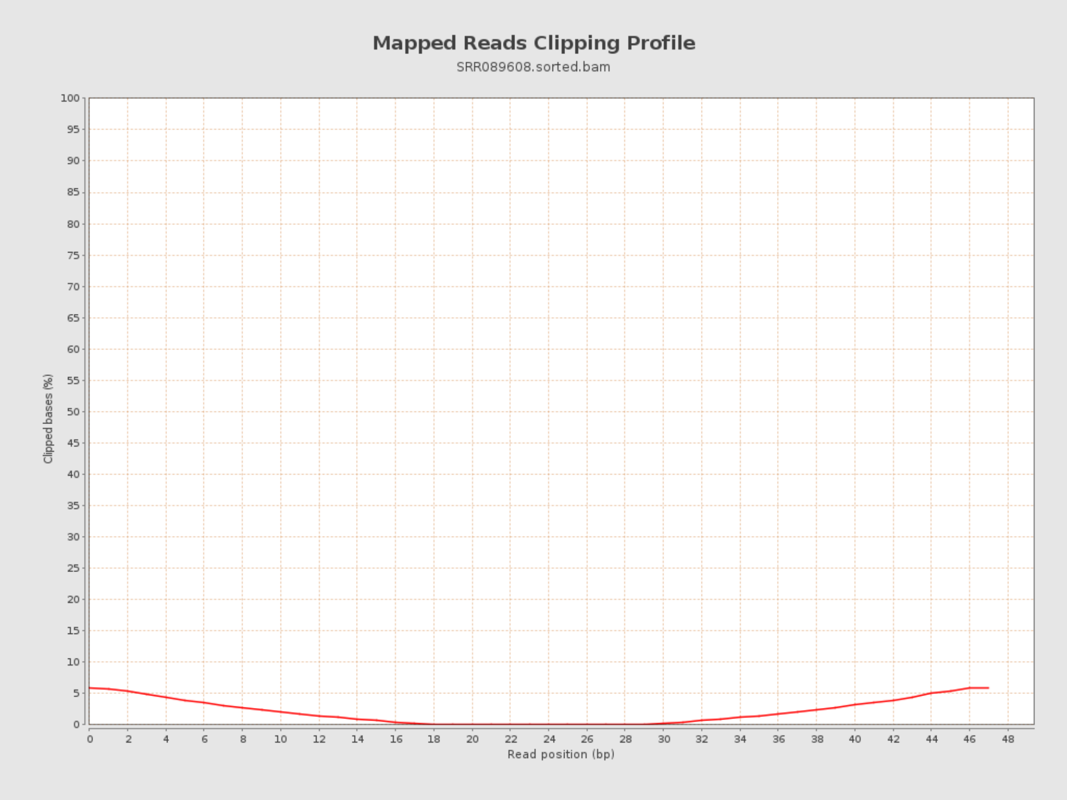
8. Results : Mapped Reads Nucleotide Content



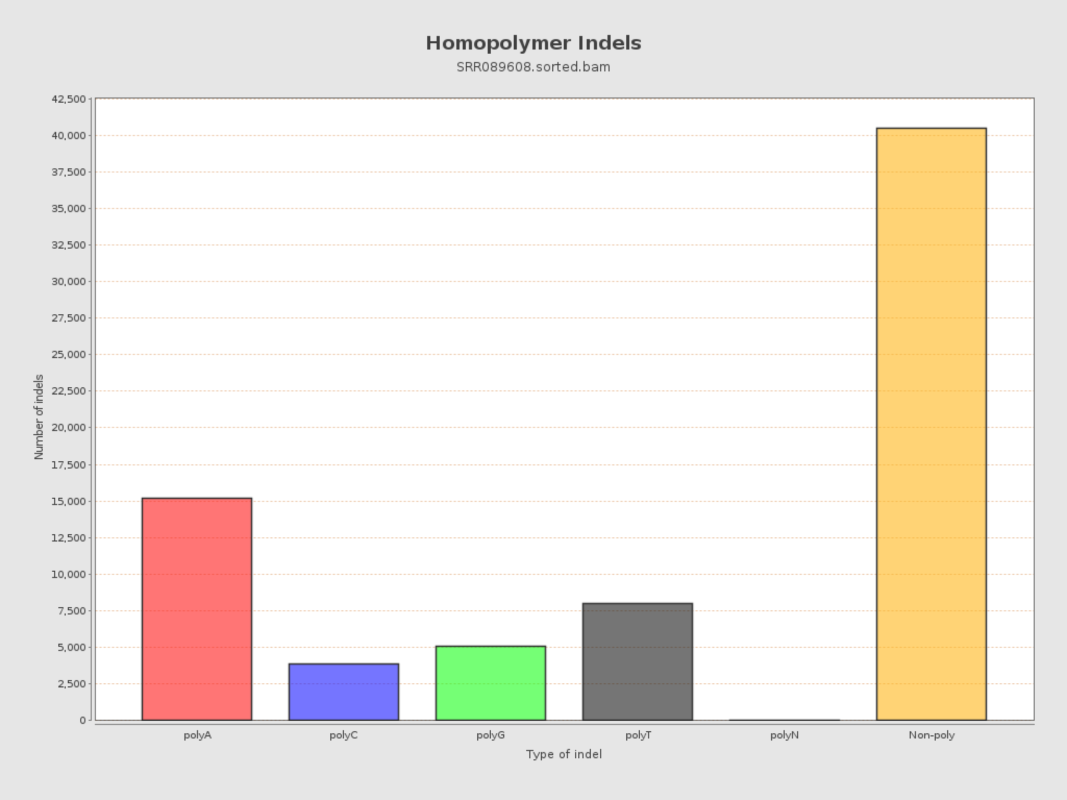
9. Results : Mapped Reads GC-content Distribution



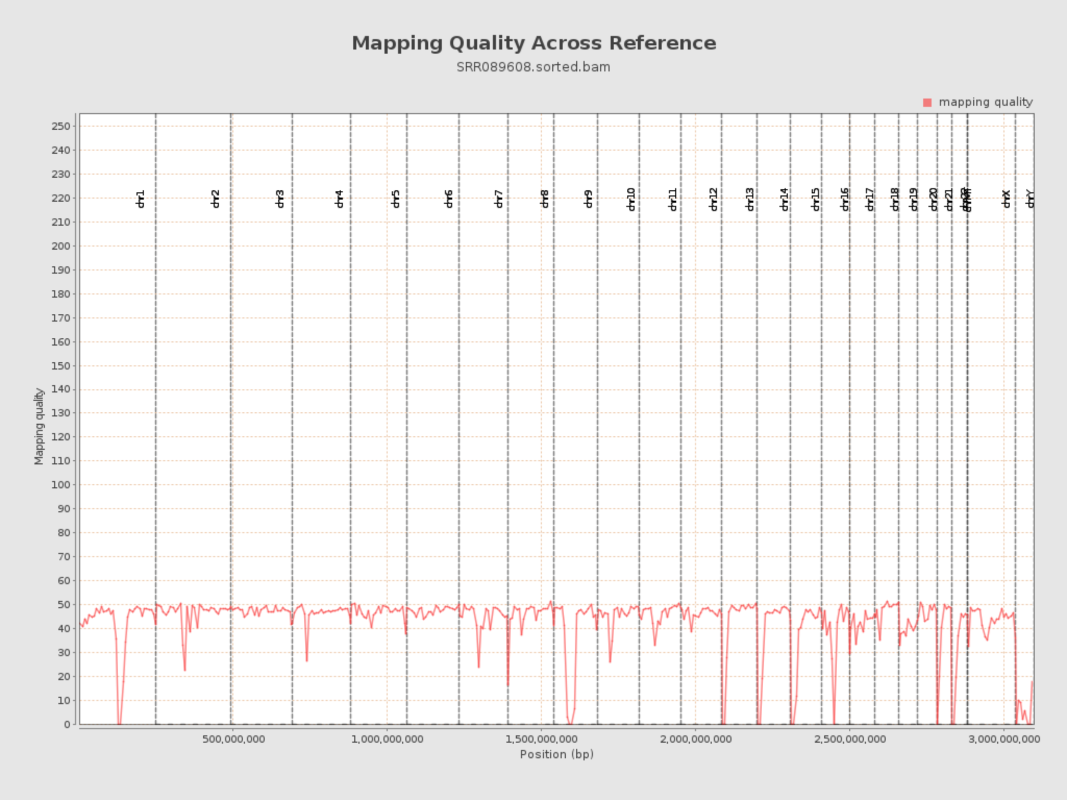
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram