Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:56:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080823.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_SRR3080823 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080823.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:56:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080823.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,555,251
Mapped reads	1,291,730 / 83.06%
Unmapped reads	263,521 / 16.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,427 / 1.18%
Read min/max/mean length	30 / 76 / 76.41
Duplicated reads (estimated)	53,431 / 3.44%
Duplication rate	2.44%
Clipped reads	476,787 / 30.66%

2.2. ACGT Content

Number/percentage of A's	27,441,225 / 30.6%
Number/percentage of C's	16,759,018 / 18.69%
Number/percentage of T's	26,082,779 / 29.08%
Number/percentage of G's	19,396,489 / 21.63%
Number/percentage of N's	11,736 / 0.01%
GC Percentage	40.31%

2.3. Coverage

Mean	0.029

Standard Deviation	0.5404

2.4. Mapping Quality

Mean Mapping Quality	44.54

2.5. Mismatches and indels

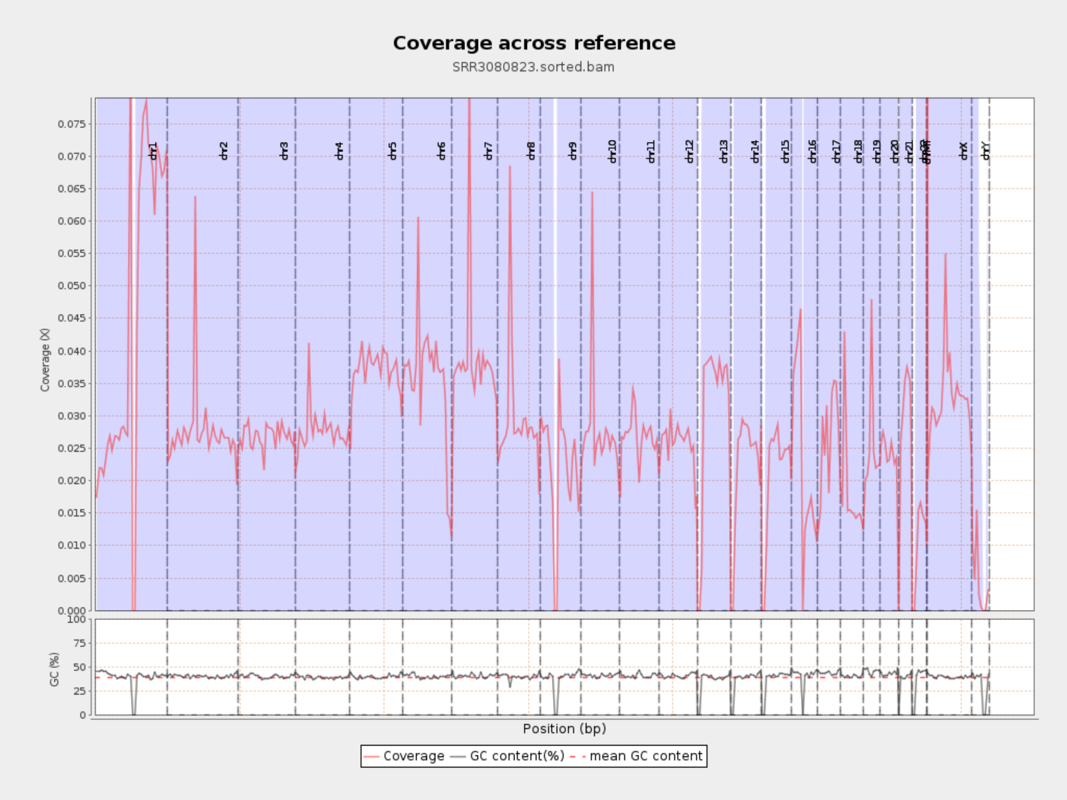
General error rate	0.99%
Mismatches	876,635
Insertions	8,112
Mapped reads with at least one insertion	0.62%
Deletions	17,437
Mapped reads with at least one deletion	1.33%
Homopolymer indels	43.83%

2.6. Chromosome stats

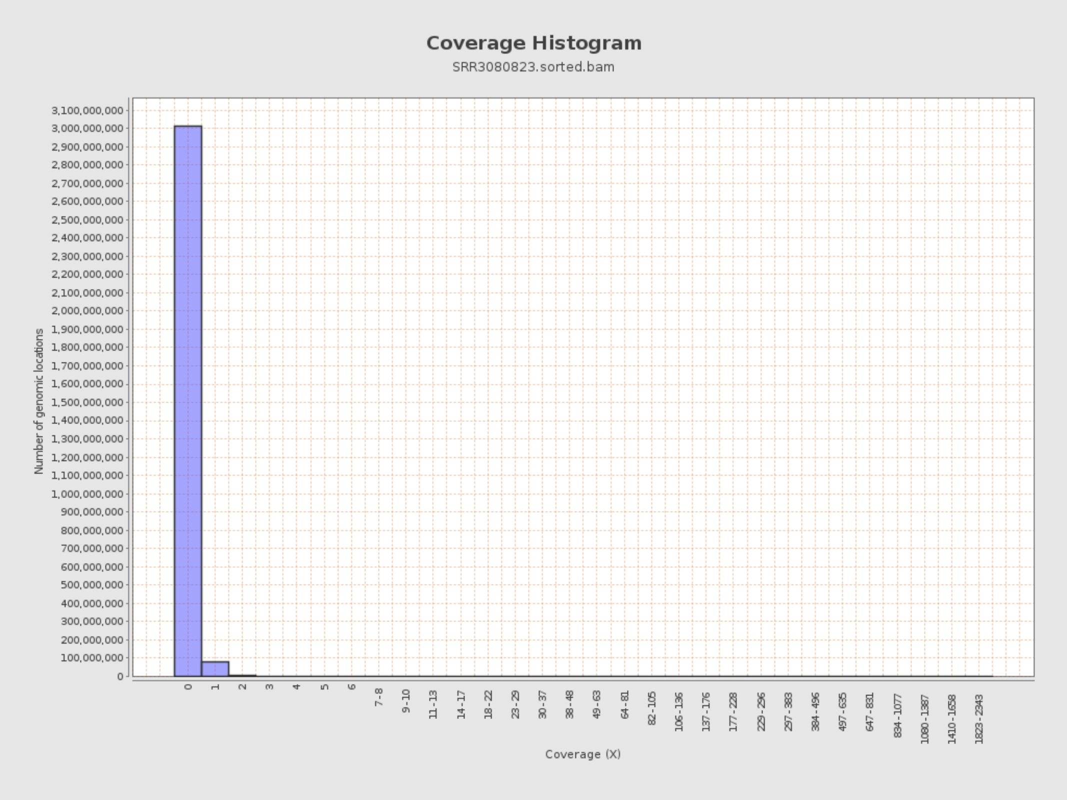
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11052332	0.0443	1.1151
chr2	243199373	6724989	0.0277	0.3179
chr3	198022430	5313662	0.0268	0.1741
chr4	191154276	5279896	0.0276	0.19
chr5	180915260	6756249	0.0373	0.208
chr6	171115067	6116959	0.0357	0.305
chr7	159138663	6191173	0.0389	0.6614

chr8	146364022	4346921	0.0297	1.4776
chr9	141213431	3132439	0.0222	0.3154
chr10	135534747	3774052	0.0278	0.3488
chr11	135006516	3634420	0.0269	0.2884
chr12	133851895	3444914	0.0257	0.1752
chr13	115169878	3541277	0.0307	0.1842
chr14	107349540	2359629	0.022	0.1987
chr15	102531392	2117936	0.0207	0.1523
chr16	90354753	2029447	0.0225	0.2157
chr17	81195210	2130752	0.0262	0.2067
chr18	78077248	1396984	0.0179	0.6889
chr19	59128983	1490831	0.0252	0.6956
chr20	63025520	1513829	0.024	0.1889
chr21	48129895	1406817	0.0292	0.2011
chr22	51304566	543073	0.0106	0.1067
chrMT	16571	35074	2.1166	1.9905
chrX	155270560	5129280	0.033	0.2205
chrY	59373566	259067	0.0044	0.1447

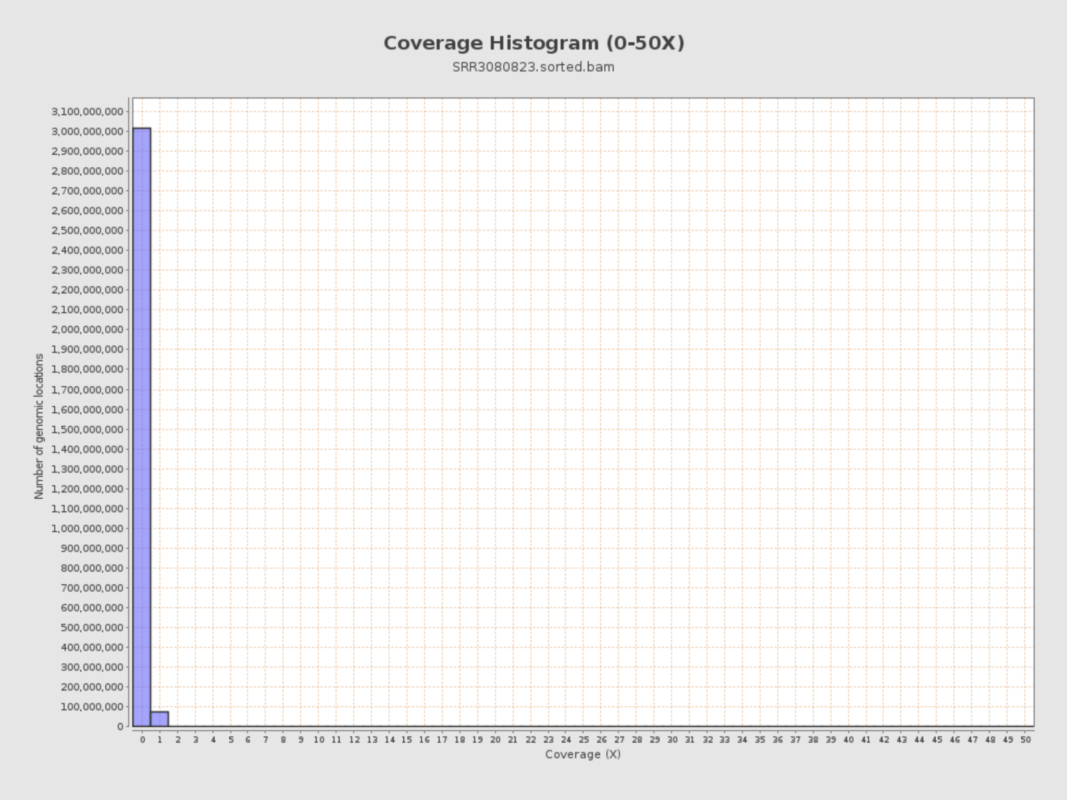
3. Results : Coverage across reference



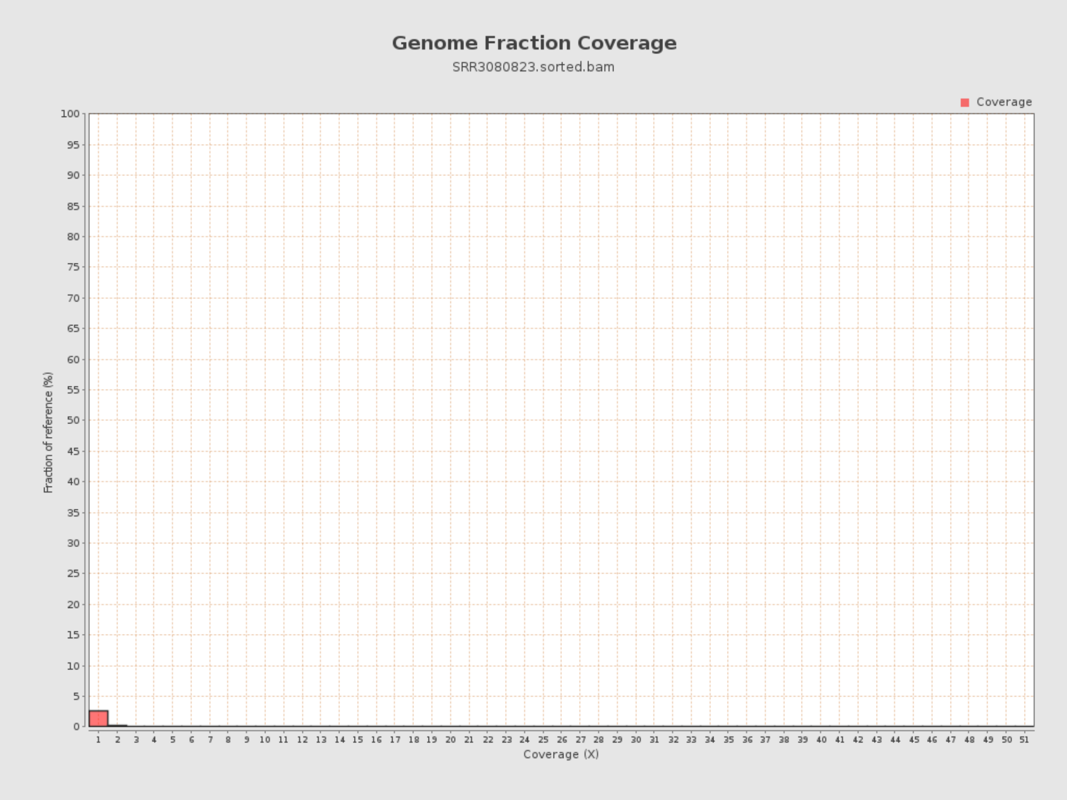
4. Results : Coverage Histogram



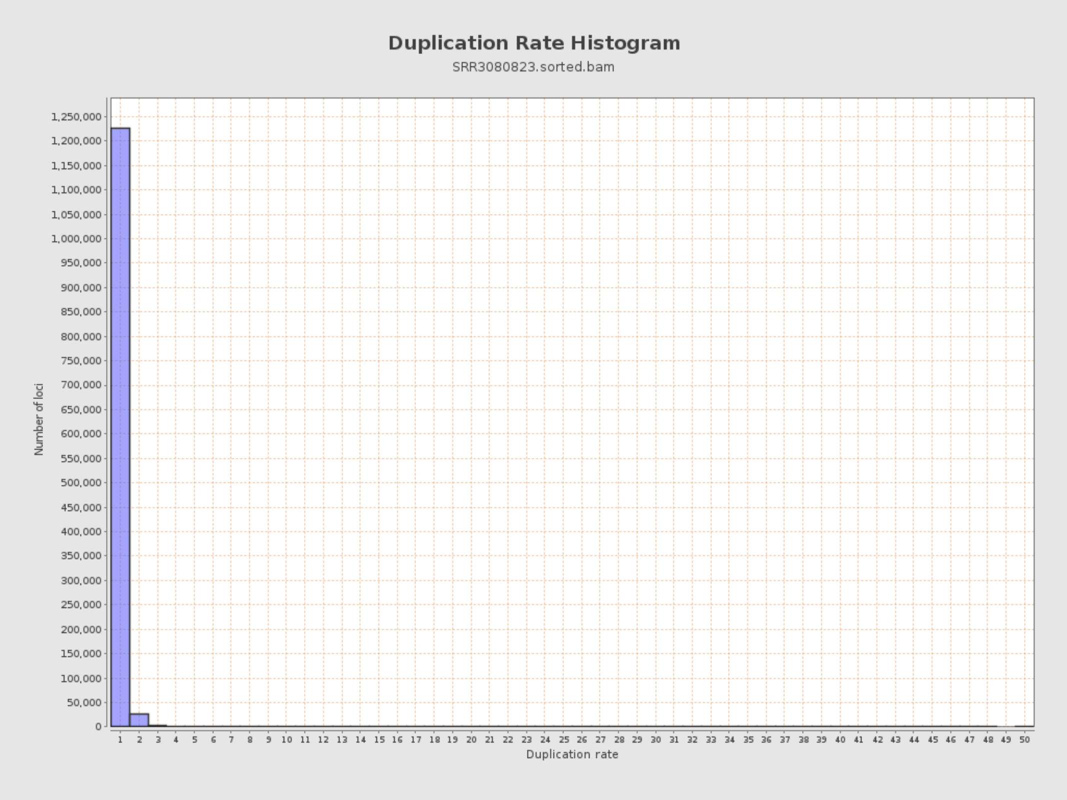
5. Results : Coverage Histogram (0-50X)



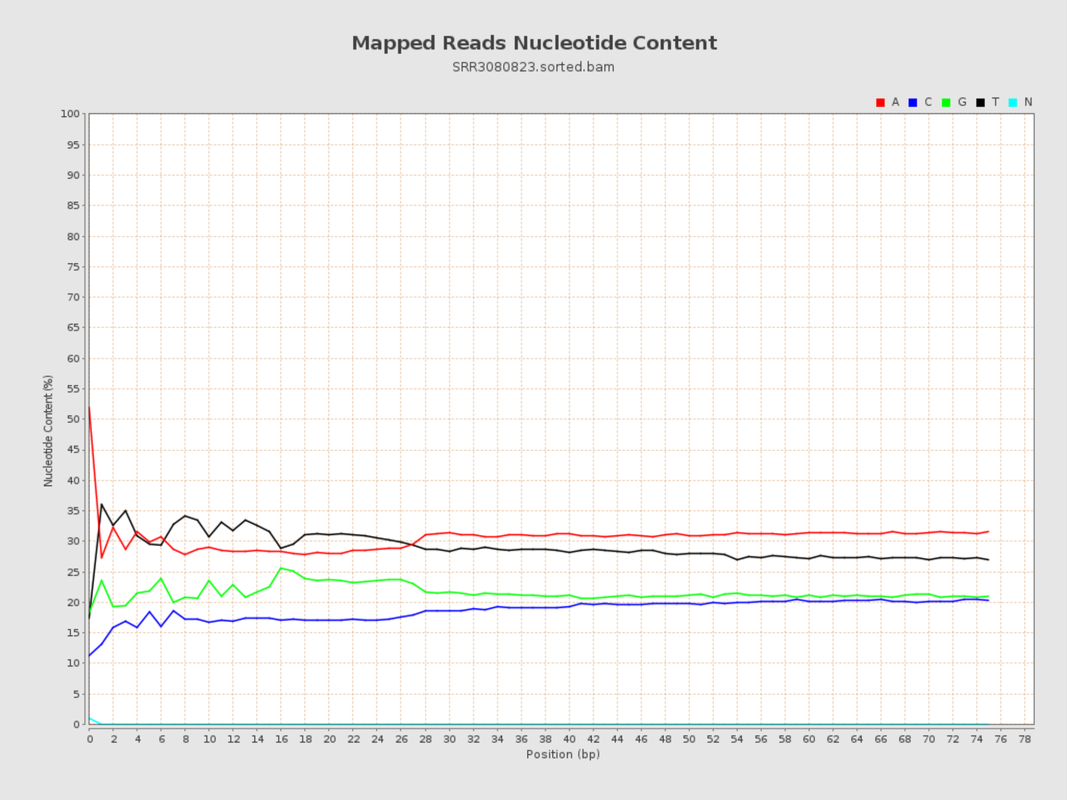
6. Results : Genome Fraction Coverage



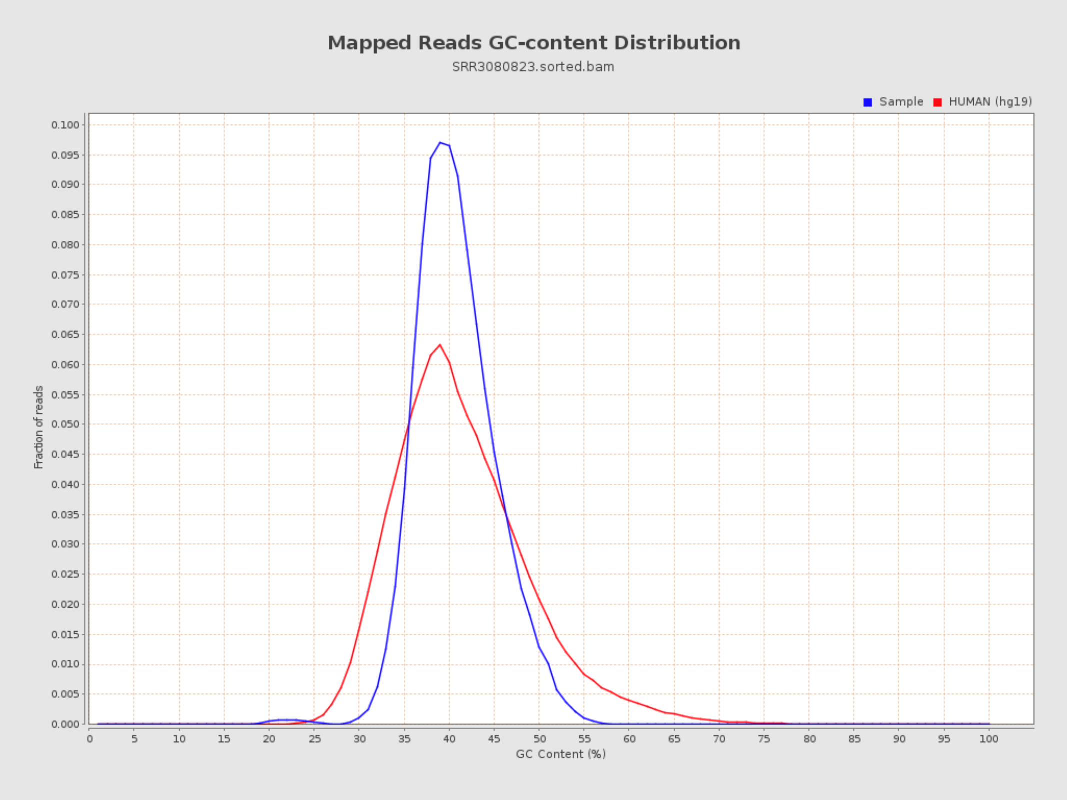
7. Results : Duplication Rate Histogram



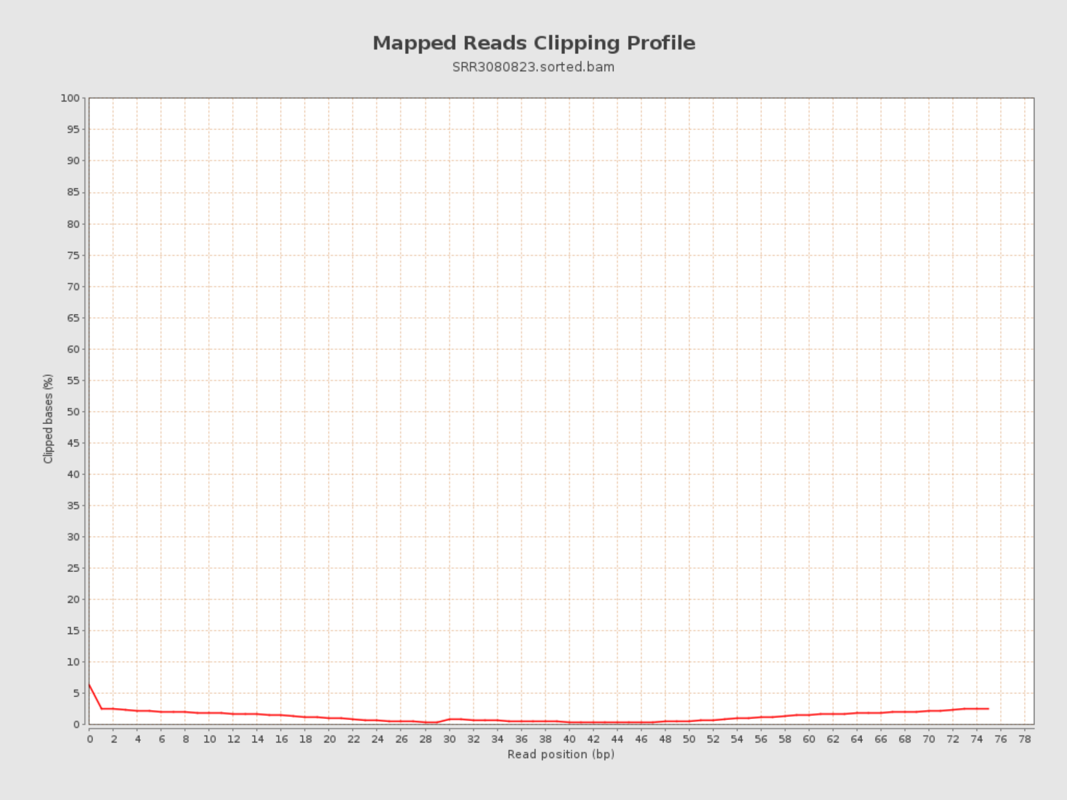
8. Results : Mapped Reads Nucleotide Content



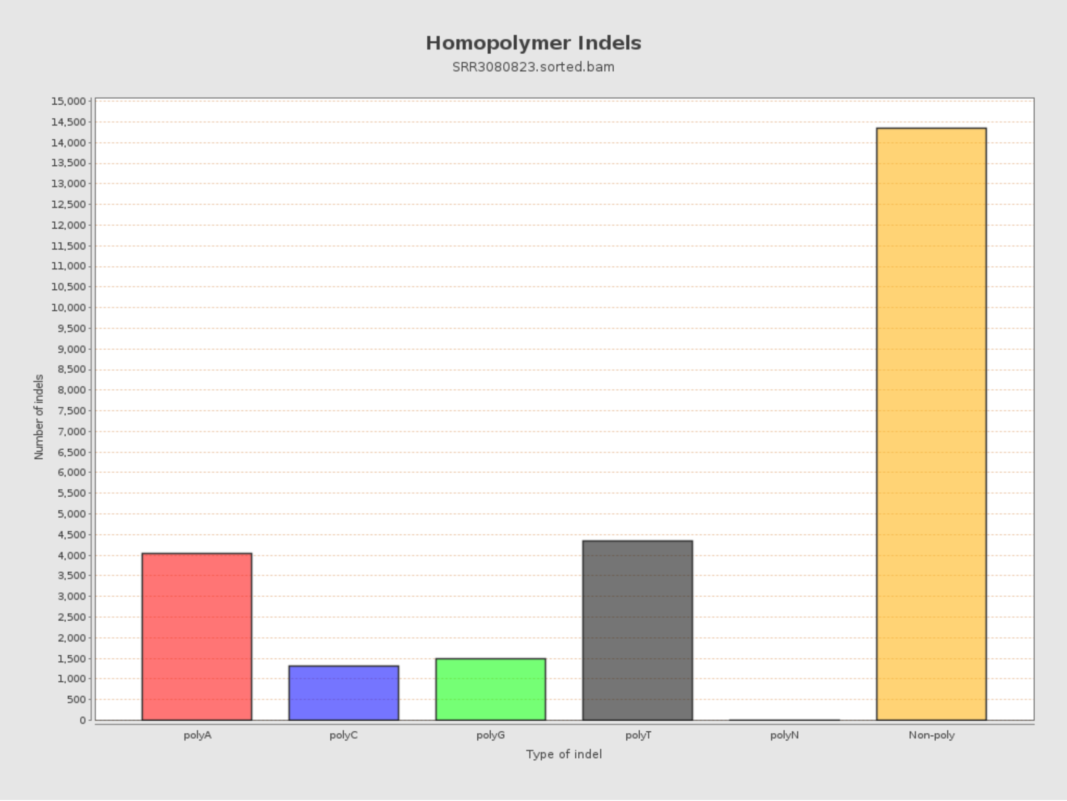
9. Results : Mapped Reads GC-content Distribution



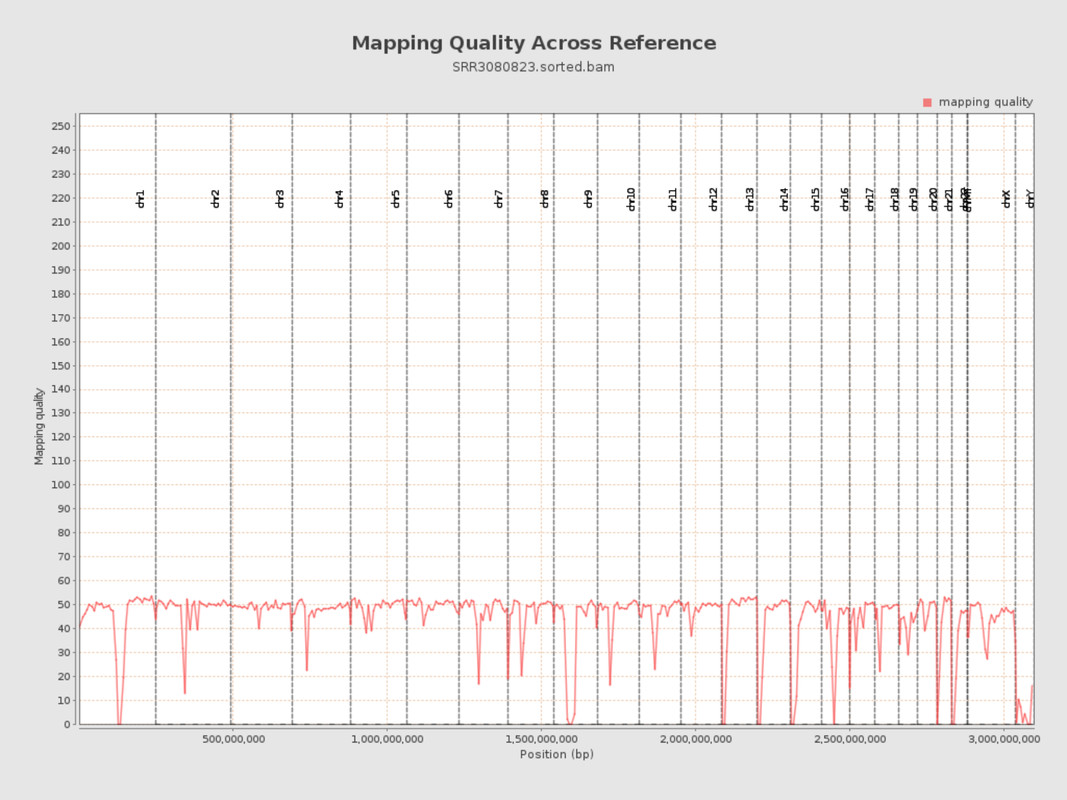
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram