Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 09:48:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089378.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_SRR089378 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089378.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 09:48:40 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089378.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	29,635,251
Mapped reads	27,990,071 / 94.45%
Unmapped reads	1,645,180 / 5.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	143,494 / 0.48%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	6,310,773 / 21.29%
Duplication rate	14.51%
Clipped reads	12,331,682 / 41.61%

2.2. ACGT Content

Number/percentage of A's	510,054,136 / 27.38%
Number/percentage of C's	335,608,778 / 18.02%
Number/percentage of T's	586,339,629 / 31.48%
Number/percentage of G's	430,569,666 / 23.11%
Number/percentage of N's	191,700 / 0.01%
GC Percentage	41.13%

2.3. Coverage

Mean	0.602

Standard Deviation	3.6954

2.4. Mapping Quality

Mean Mapping Quality	47.5

2.5. Mismatches and indels

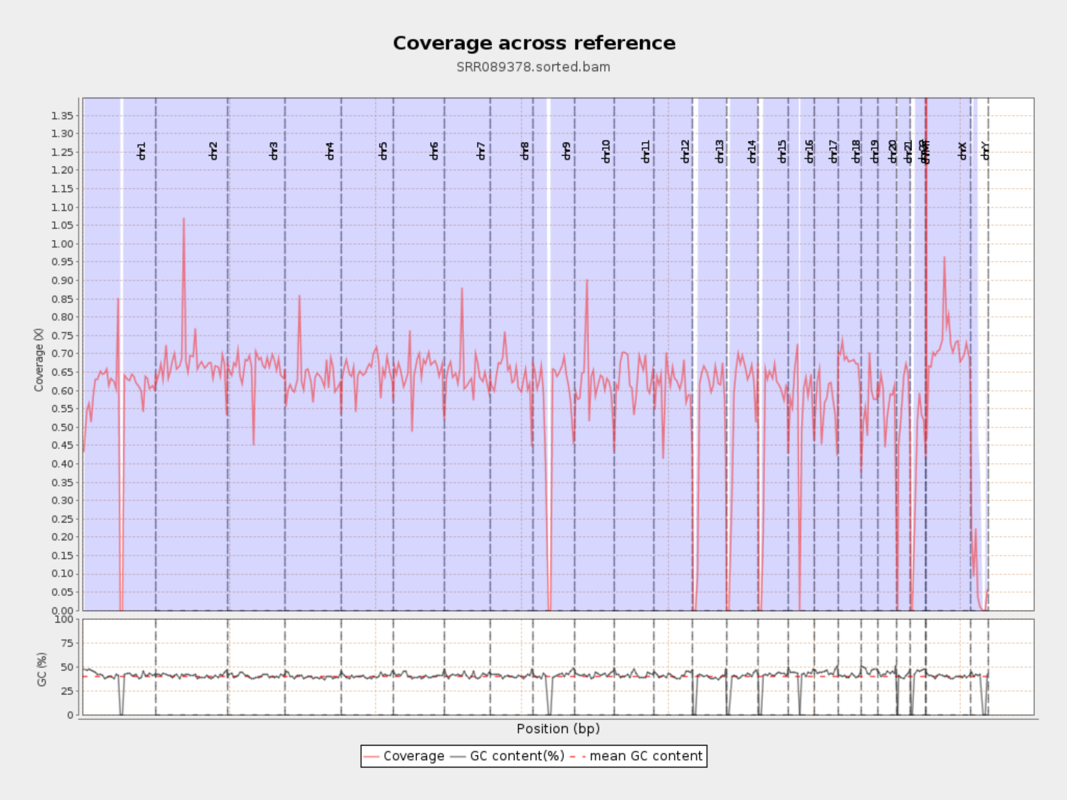
General error rate	0.58%
Mismatches	10,630,058
Insertions	133,590
Mapped reads with at least one insertion	0.47%
Deletions	427,879
Mapped reads with at least one deletion	1.51%
Homopolymer indels	49.1%

2.6. Chromosome stats

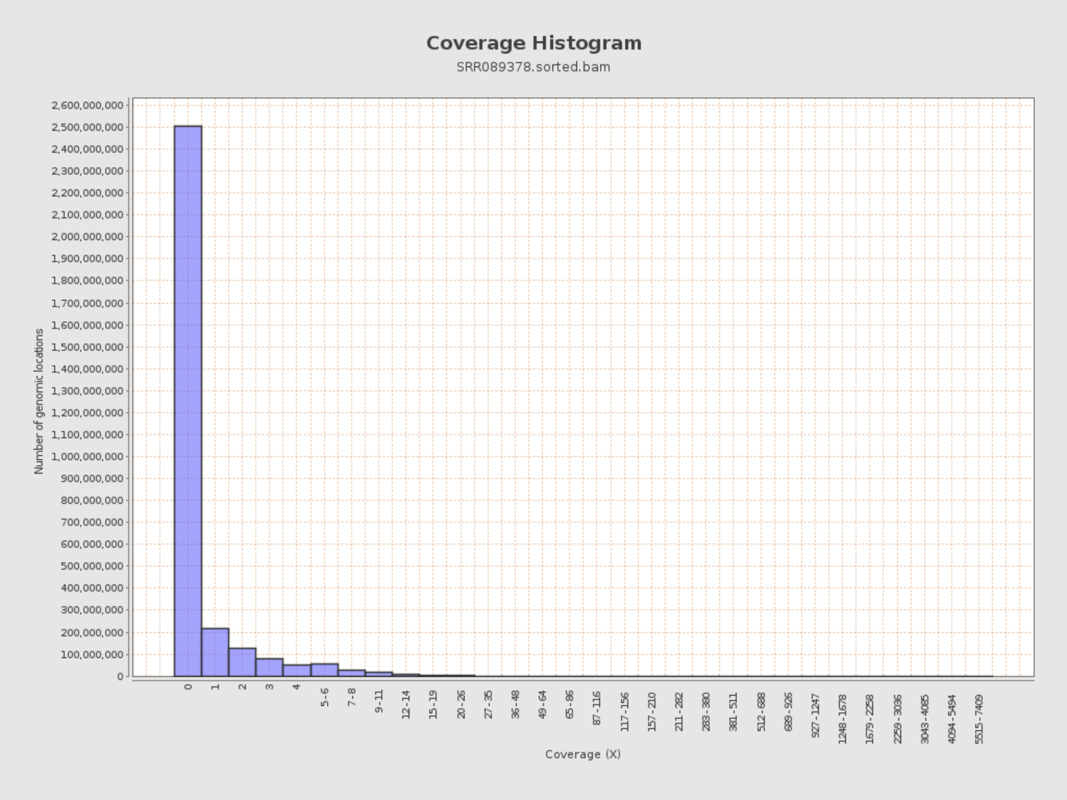
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	143972553	0.5776	6.0163
chr2	243199373	165559185	0.6808	4.3148
chr3	198022430	131032996	0.6617	1.9574
chr4	191154276	121244734	0.6343	2.3646
chr5	180915260	117715882	0.6507	1.9623
chr6	171115067	112537288	0.6577	2.7399
chr7	159138663	102516426	0.6442	4.8436

chr8	146364022	93002357	0.6354	5.1365
chr9	141213431	76991092	0.5452	4.0411
chr10	135534747	84650049	0.6246	3.9561
chr11	135006516	86078311	0.6376	4.1046
chr12	133851895	81454496	0.6085	2.0718
chr13	115169878	60099108	0.5218	1.7218
chr14	107349540	57771163	0.5382	2.0134
chr15	102531392	51950567	0.5067	1.8361
chr16	90354753	48448831	0.5362	2.3261
chr17	81195210	46250063	0.5696	2.4206
chr18	78077248	53415439	0.6841	8.0546
chr19	59128983	33316100	0.5634	3.8473
chr20	63025520	35624484	0.5652	2.0998
chr21	48129895	25060856	0.5207	2.4257
chr22	51304566	19148681	0.3732	1.4301
chrMT	16571	247182	14.9165	17.5623
chrX	155270560	111019918	0.715	2.7688
chrY	59373566	4397366	0.0741	1.4405

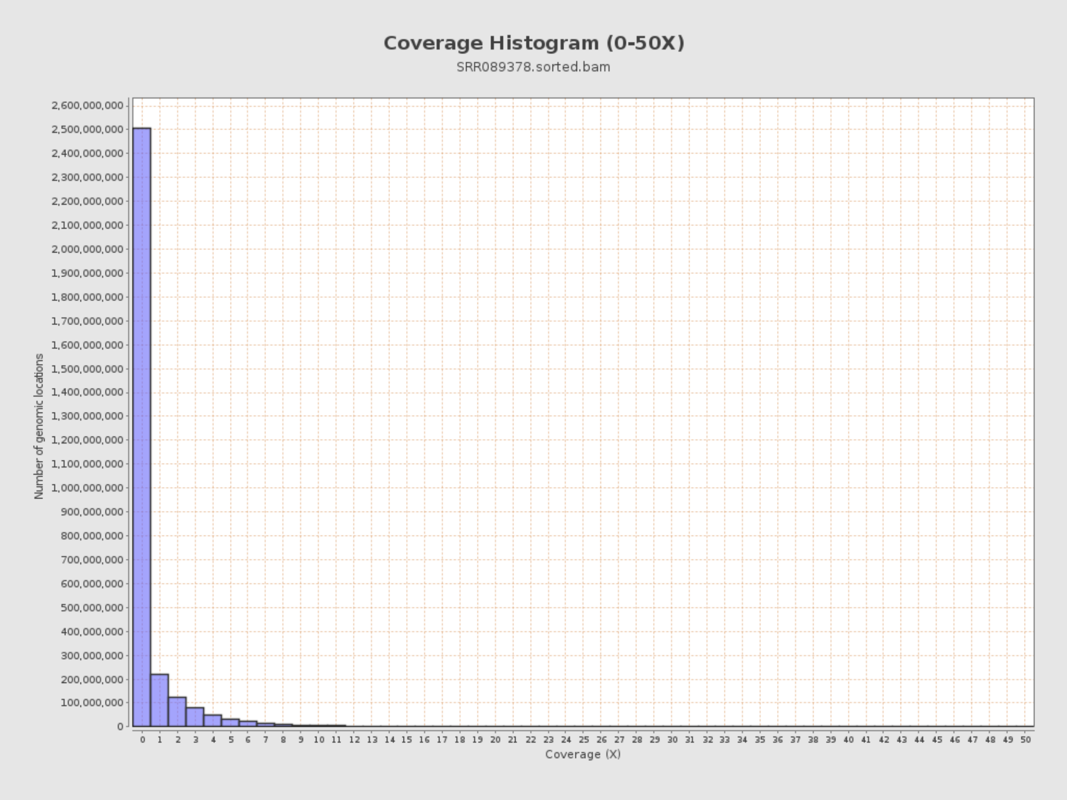
3. Results : Coverage across reference



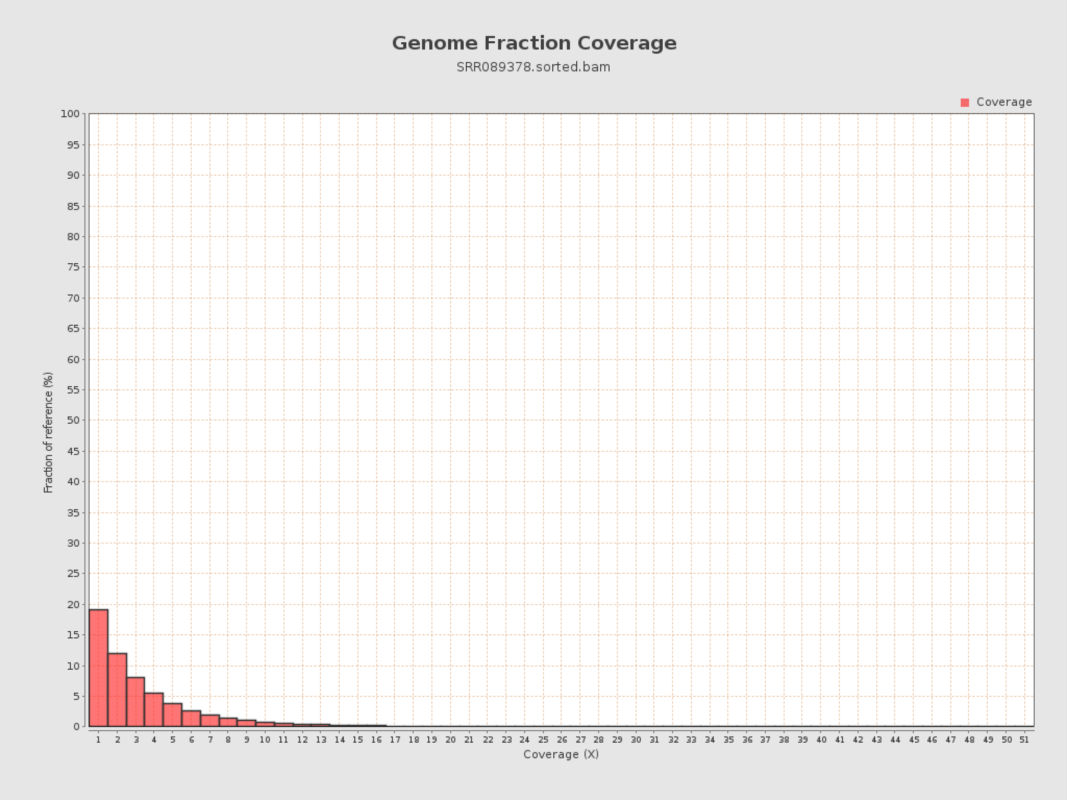
4. Results : Coverage Histogram



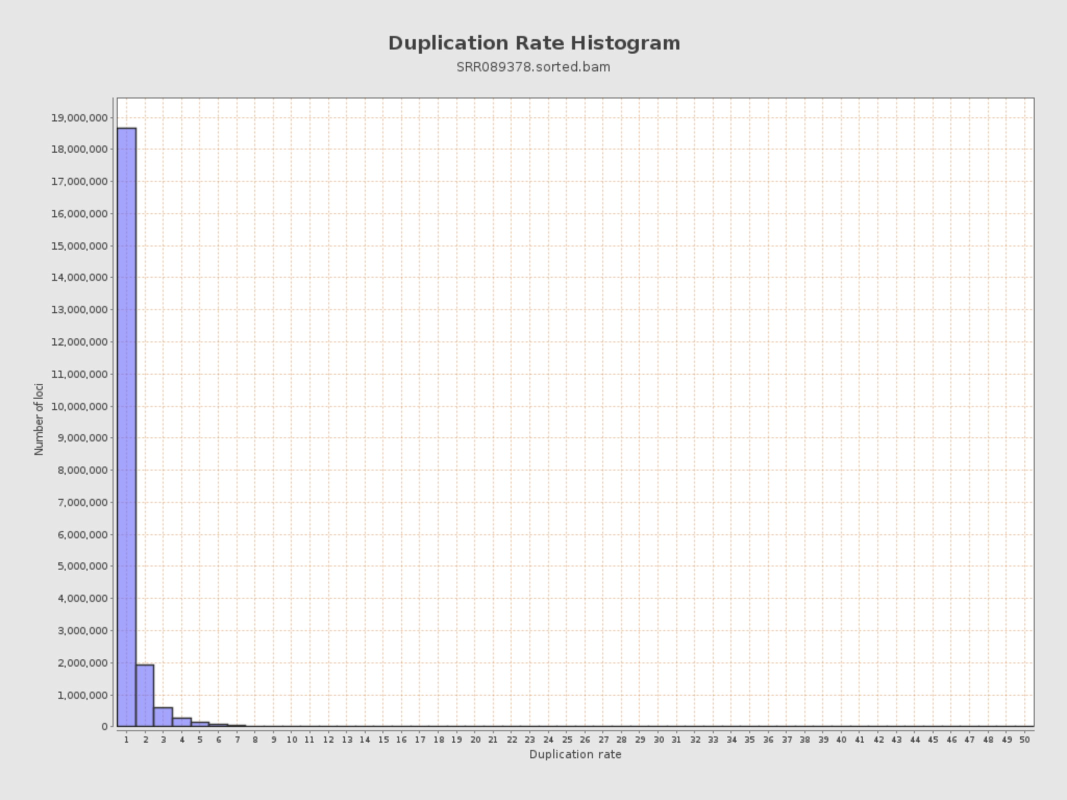
5. Results : Coverage Histogram (0-50X)



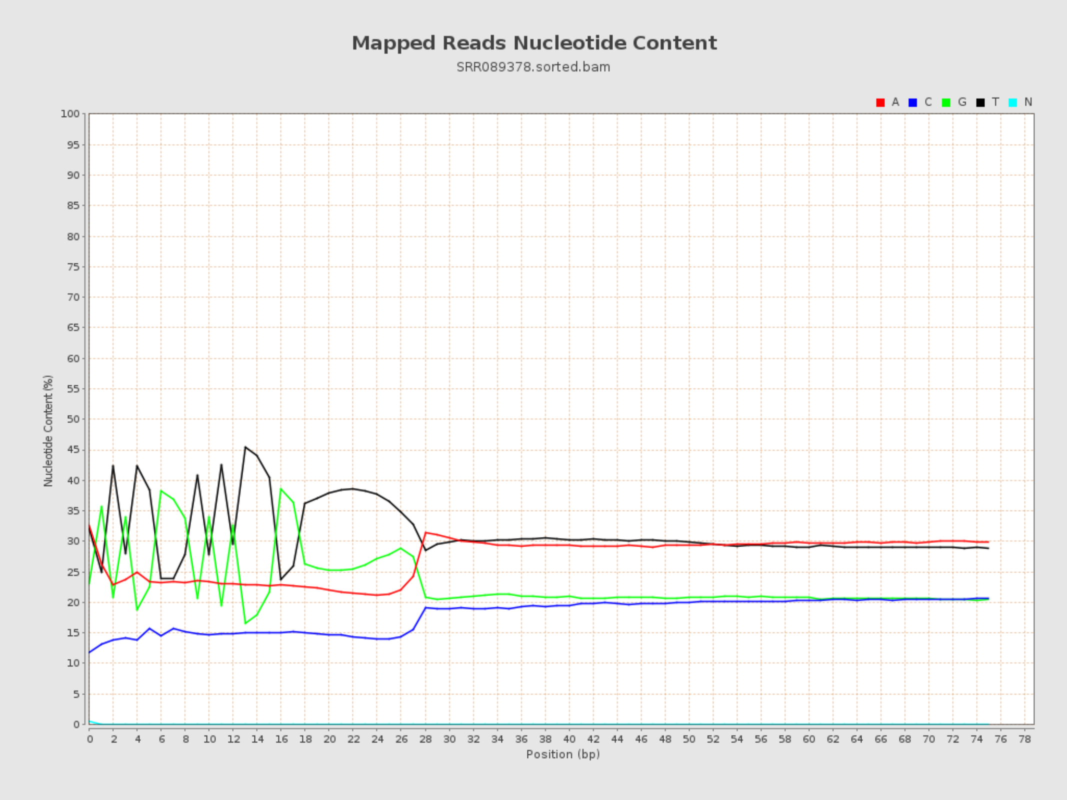
6. Results : Genome Fraction Coverage



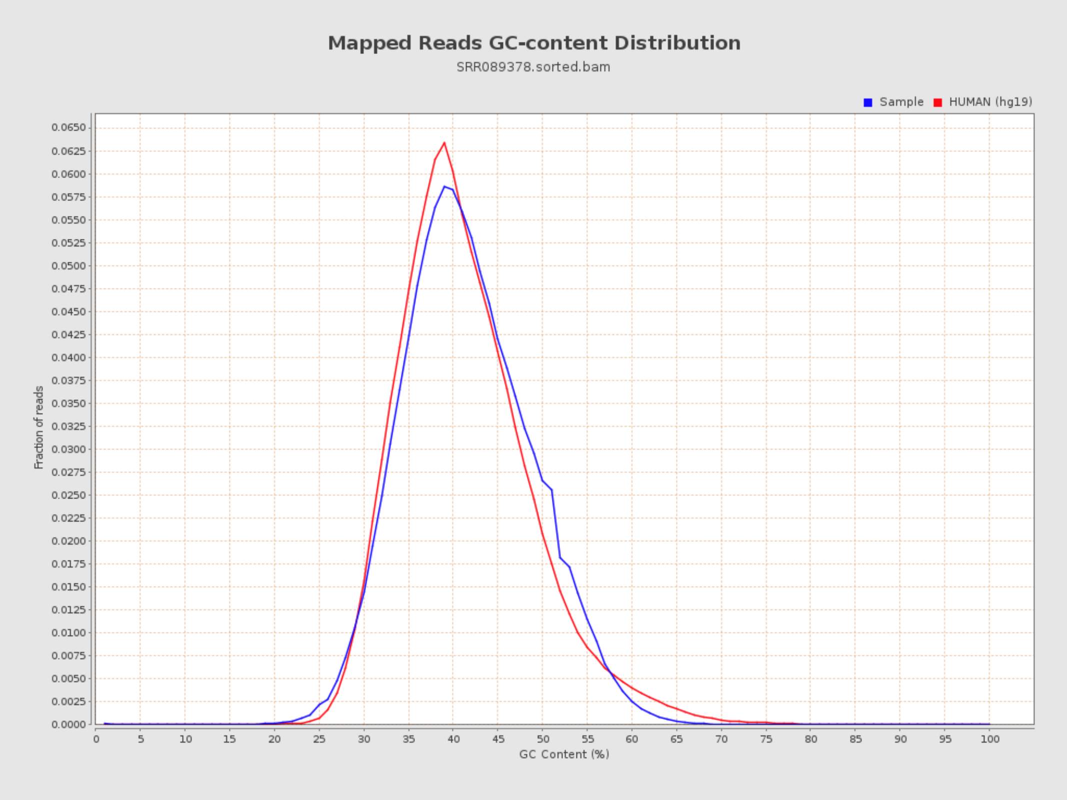
7. Results : Duplication Rate Histogram



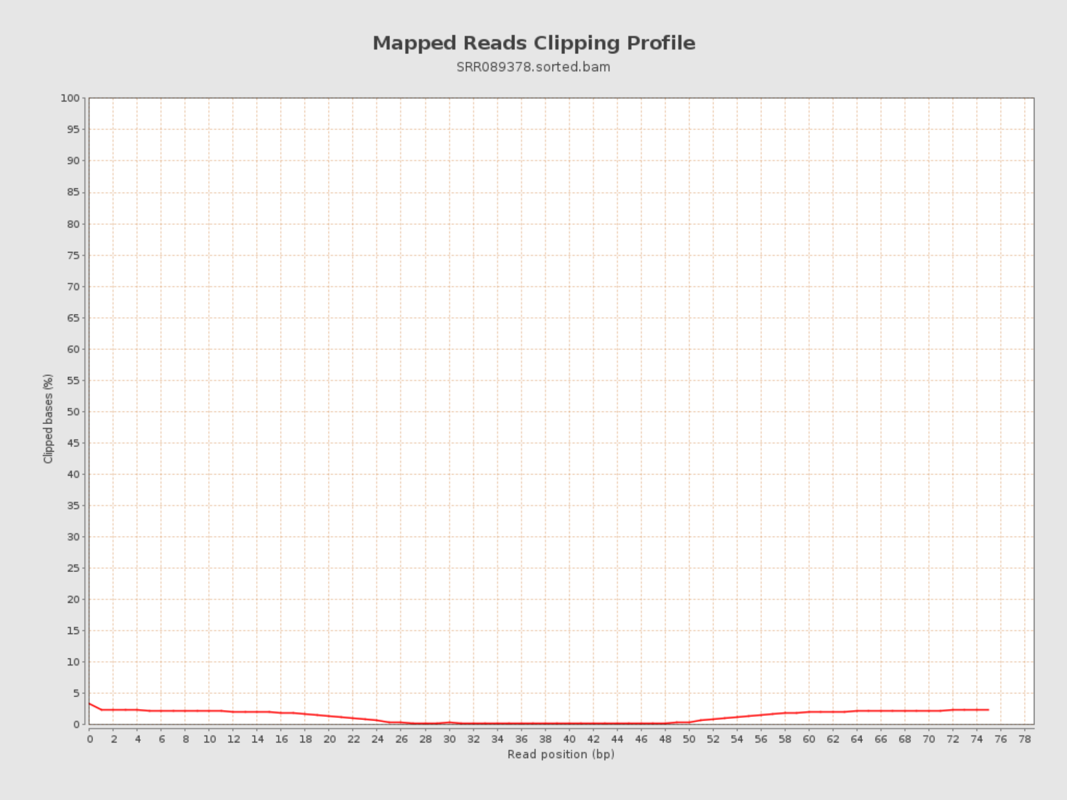
8. Results : Mapped Reads Nucleotide Content



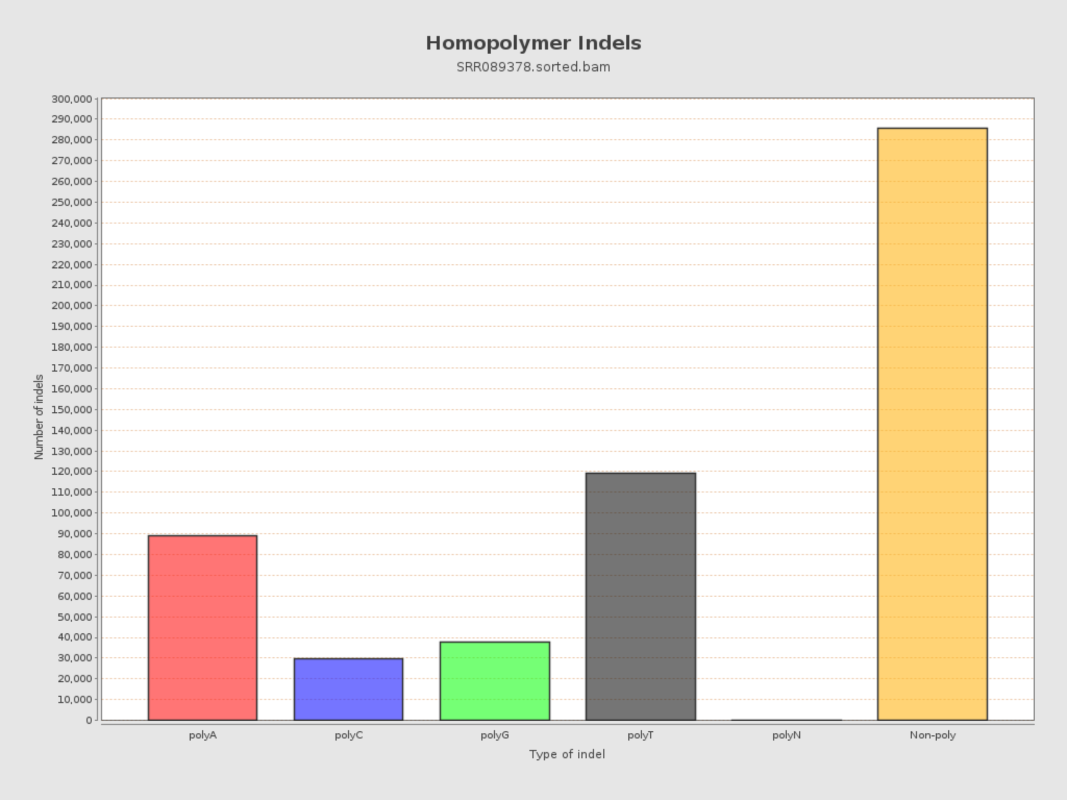
9. Results : Mapped Reads GC-content Distribution



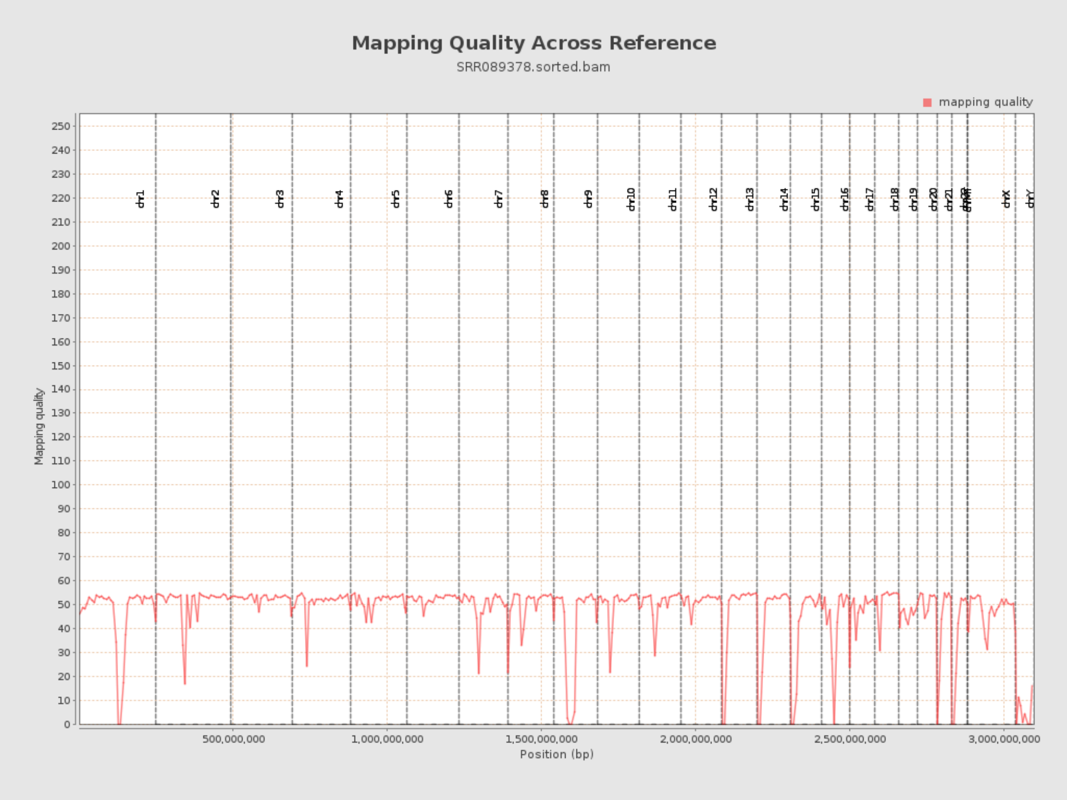
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram