Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 23:01:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549088.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_SRR1549088 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549088.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 23:01:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549088.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,863,682
Mapped reads	6,923,007 / 88.04%
Unmapped reads	940,675 / 11.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	229,228 / 2.92%
Duplication rate	2.08%
Clipped reads	319,201 / 4.06%

2.2. ACGT Content

Number/percentage of A's	82,593,229 / 30.03%
Number/percentage of C's	55,043,291 / 20.01%
Number/percentage of T's	83,608,138 / 30.4%
Number/percentage of G's	53,715,000 / 19.53%
Number/percentage of N's	67,448 / 0.02%
GC Percentage	39.54%

2.3. Coverage

Mean	0.0888
Standard Deviation	0.7442

2.4. Mapping Quality

Mean Mapping Quality	44.29

2.5. Mismatches and indels

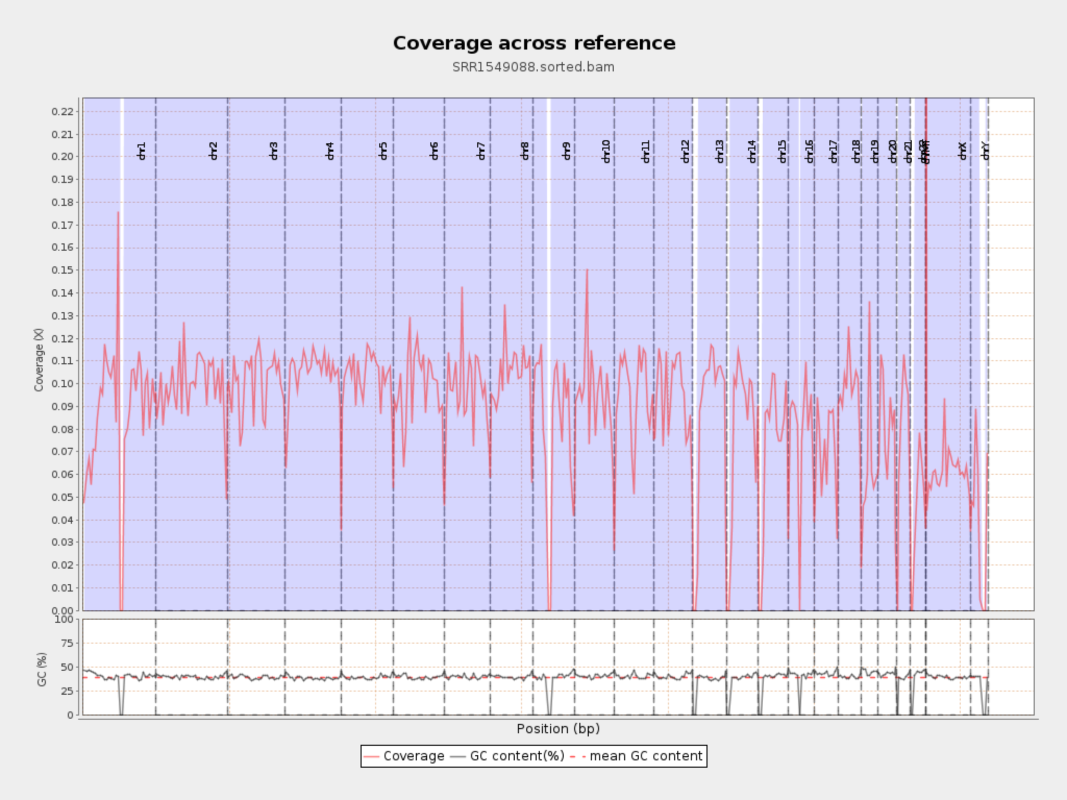
General error rate	0.4%
Mismatches	1,088,643
Insertions	6,303
Mapped reads with at least one insertion	0.09%
Deletions	19,859
Mapped reads with at least one deletion	0.29%
Homopolymer indels	46.12%

2.6. Chromosome stats

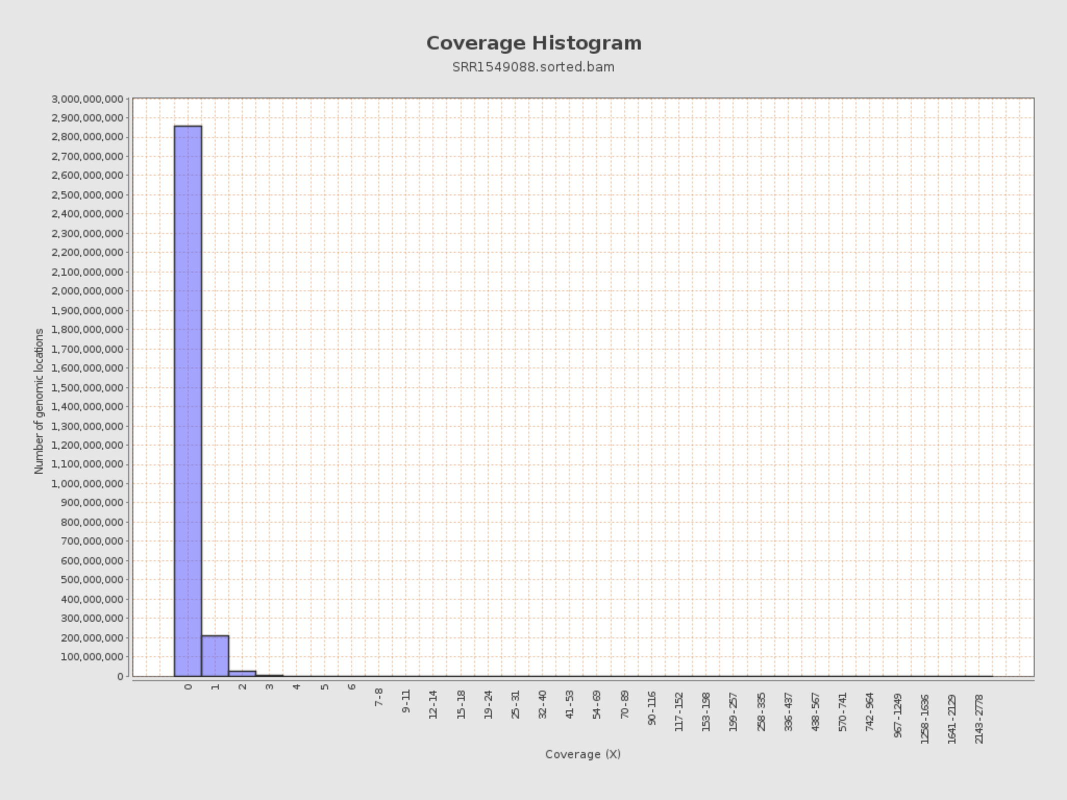
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21733464	0.0872	1.8769
chr2	243199373	24183598	0.0994	0.5539
chr3	198022430	19956001	0.1008	0.3627
chr4	191154276	20075094	0.105	0.3697
chr5	180915260	18609752	0.1029	0.3698
chr6	171115067	16987474	0.0993	0.4818
chr7	159138663	15460845	0.0972	0.7739
chr8	146364022	15142841	0.1035	0.6213

chr9	141213431	11538233	0.0817	0.5224
chr10	135534747	13000474	0.0959	0.6515
chr11	135006516	12813299	0.0949	0.5744
chr12	133851895	12703000	0.0949	0.3709
chr13	115169878	9872533	0.0857	0.3185
chr14	107349540	8485979	0.079	0.3958
chr15	102531392	7271629	0.0709	0.2938
chr16	90354753	6861642	0.0759	0.4029
chr17	81195210	5818157	0.0717	0.3616
chr18	78077248	7741808	0.0992	1.1555
chr19	59128983	3786118	0.064	1.4199
chr20	63025520	5183718	0.0822	0.3394
chr21	48129895	3715693	0.0772	0.3694
chr22	51304566	2257524	0.044	0.279
chrMT	16571	16533	0.9977	1.5214
chrX	155270560	9480170	0.0611	0.374
chrY	59373566	2356104	0.0397	0.365

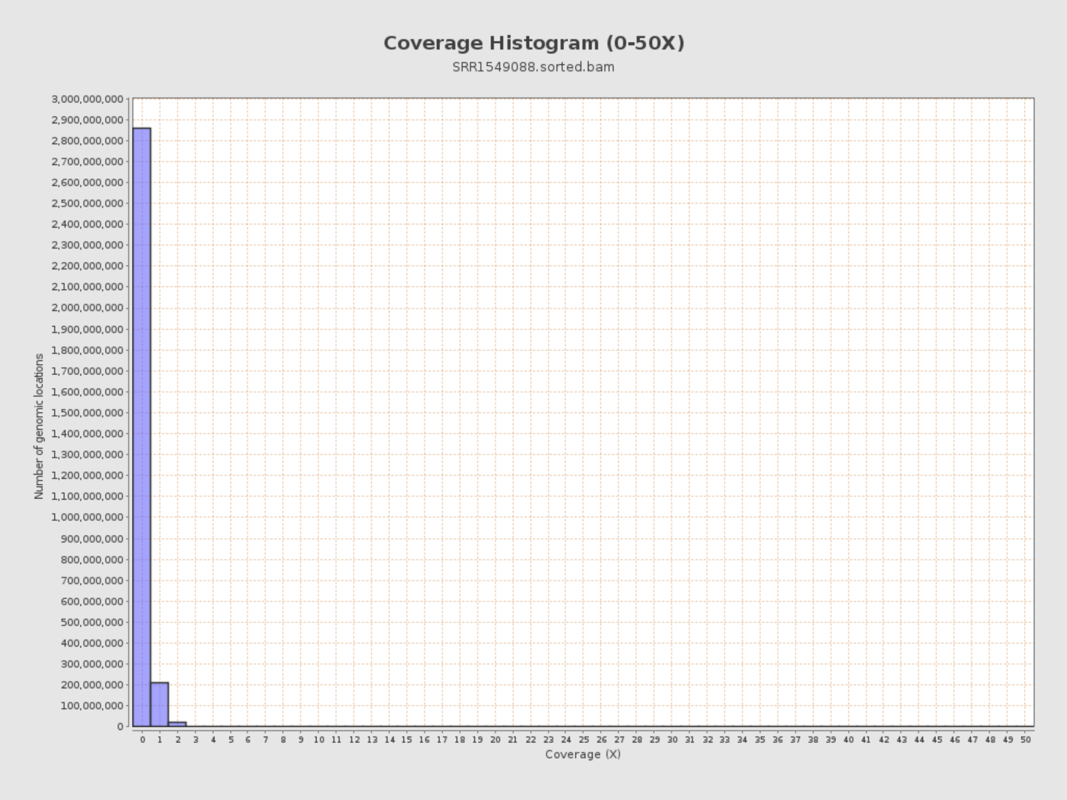
3. Results : Coverage across reference



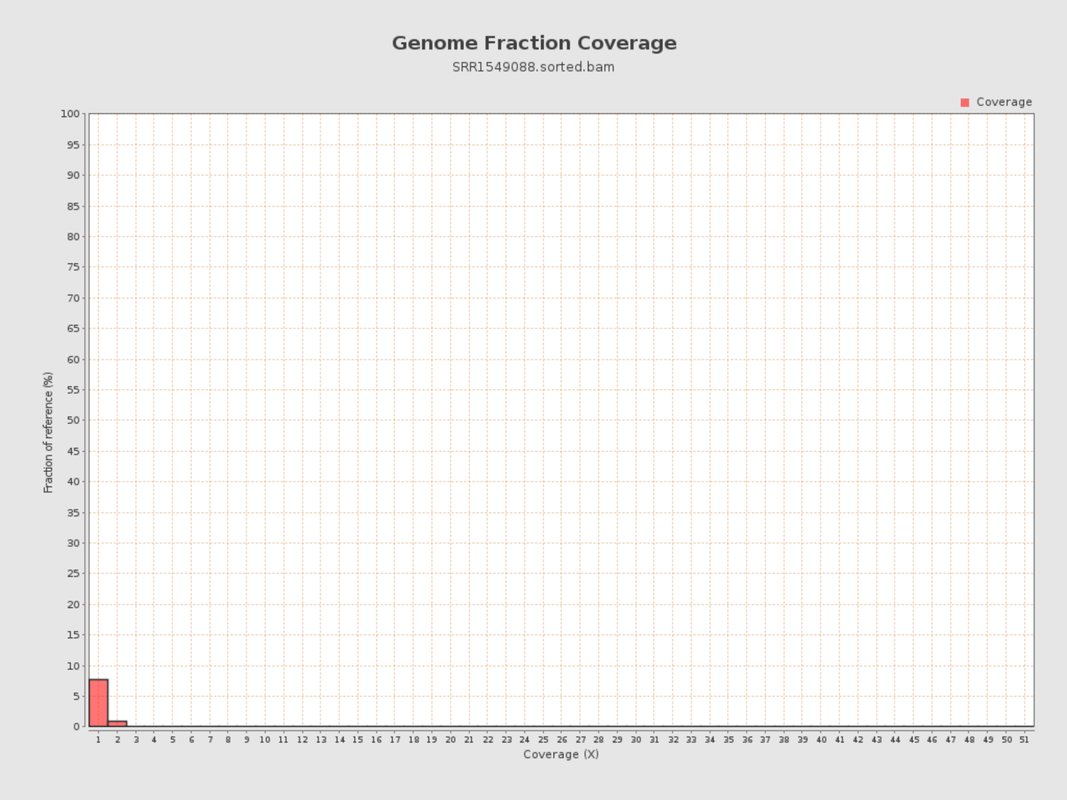
4. Results : Coverage Histogram



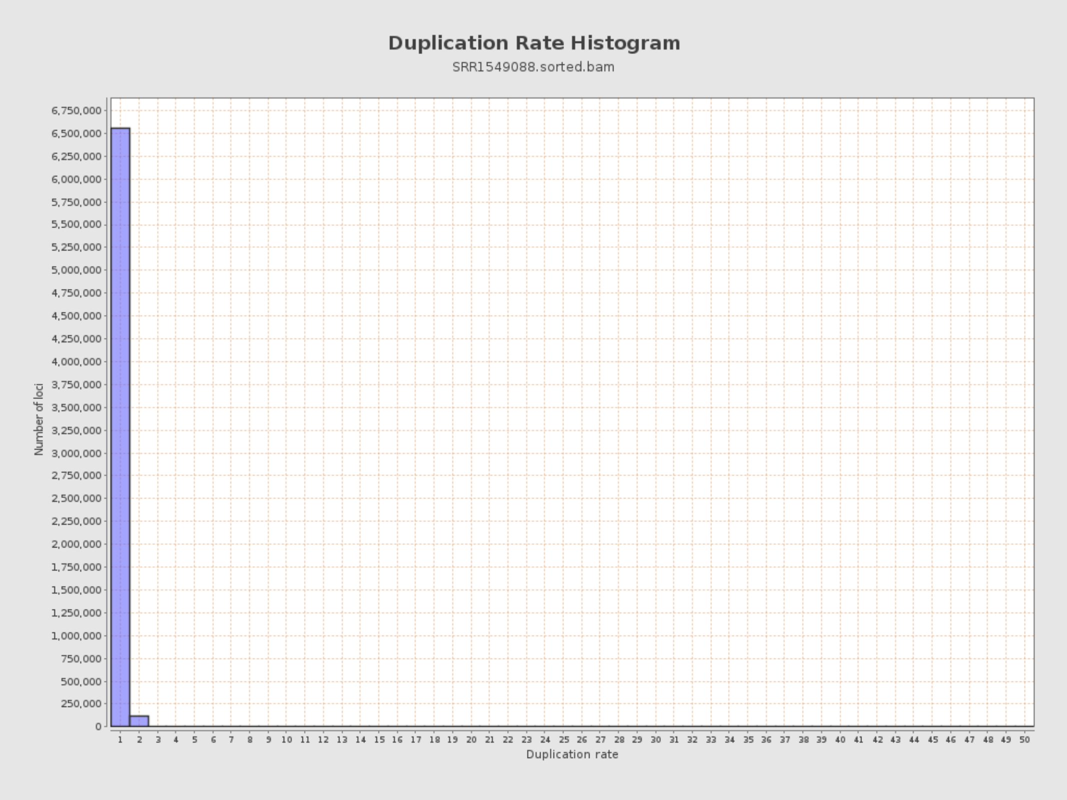
5. Results : Coverage Histogram (0-50X)



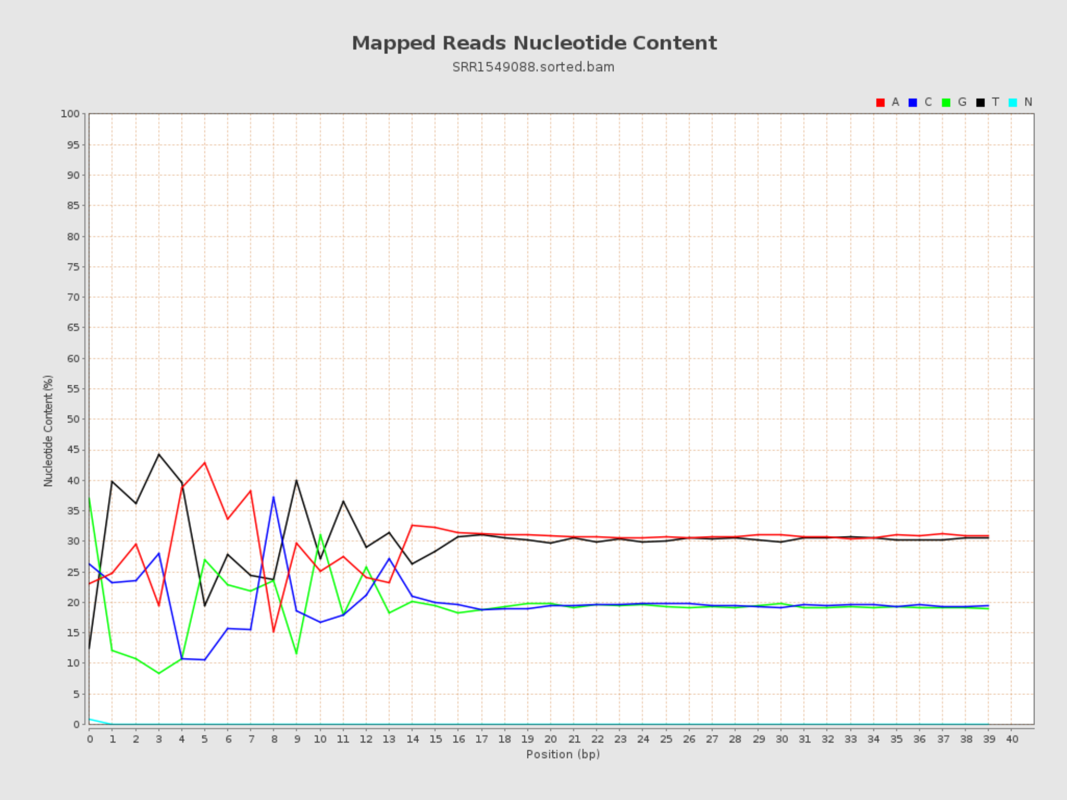
6. Results : Genome Fraction Coverage



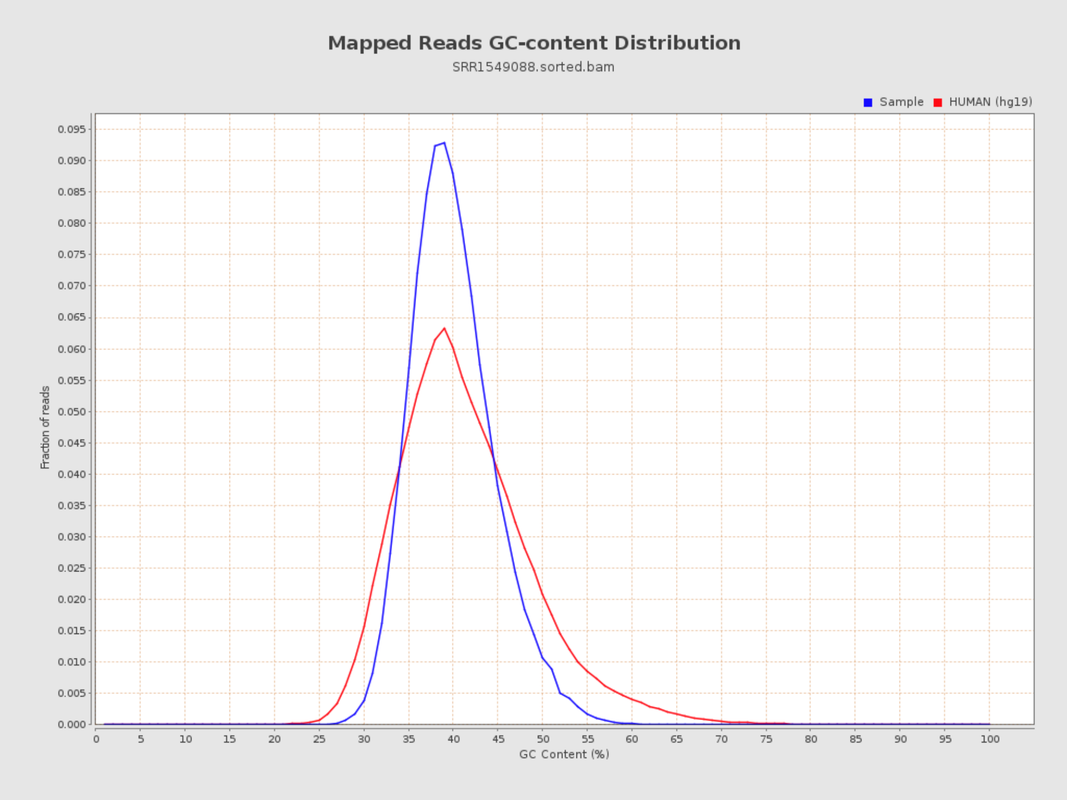
7. Results : Duplication Rate Histogram



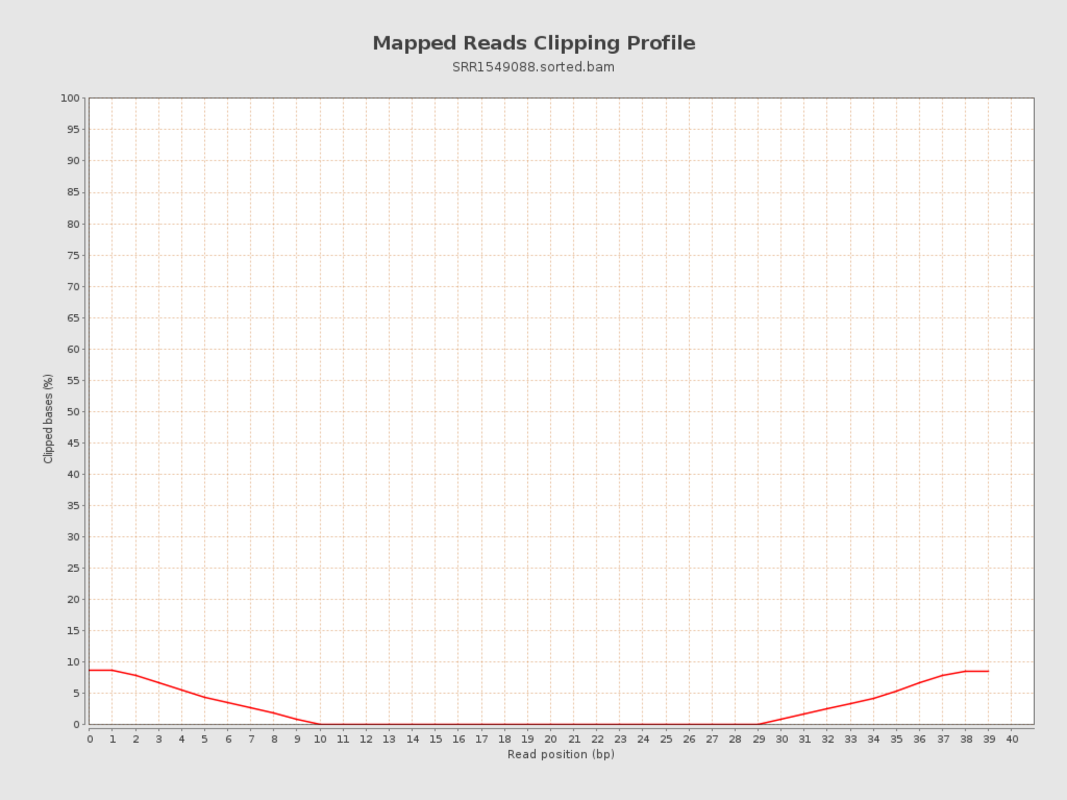
8. Results : Mapped Reads Nucleotide Content



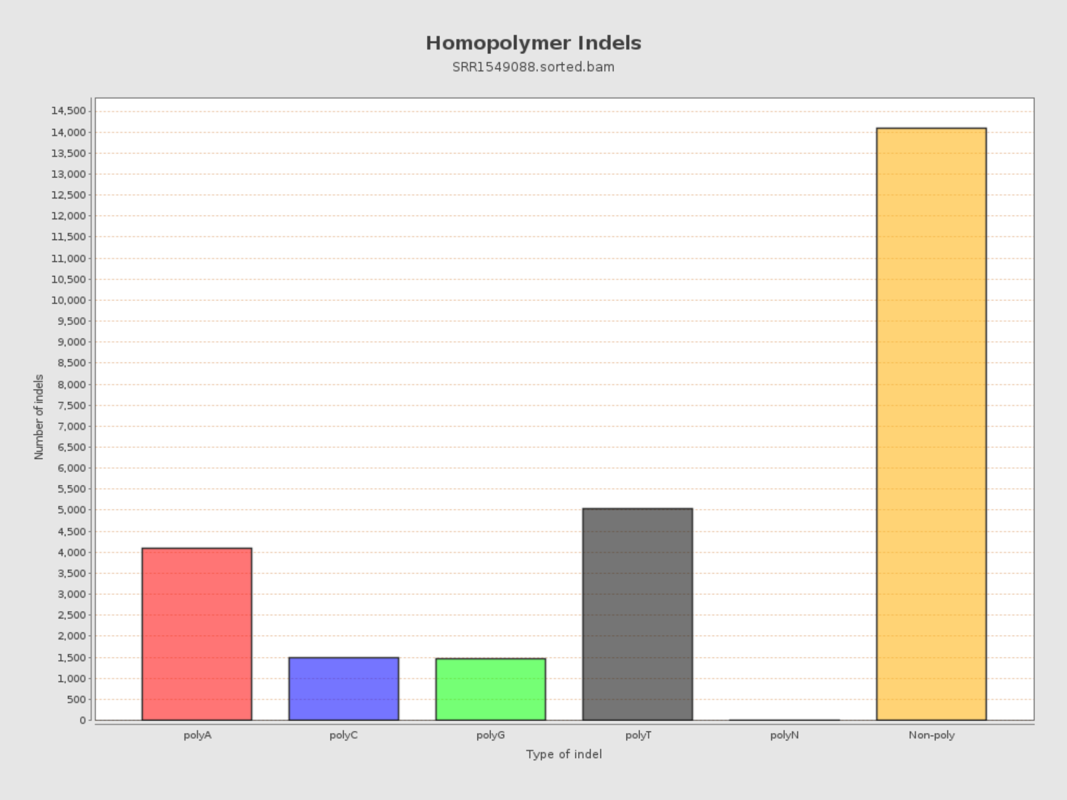
9. Results : Mapped Reads GC-content Distribution



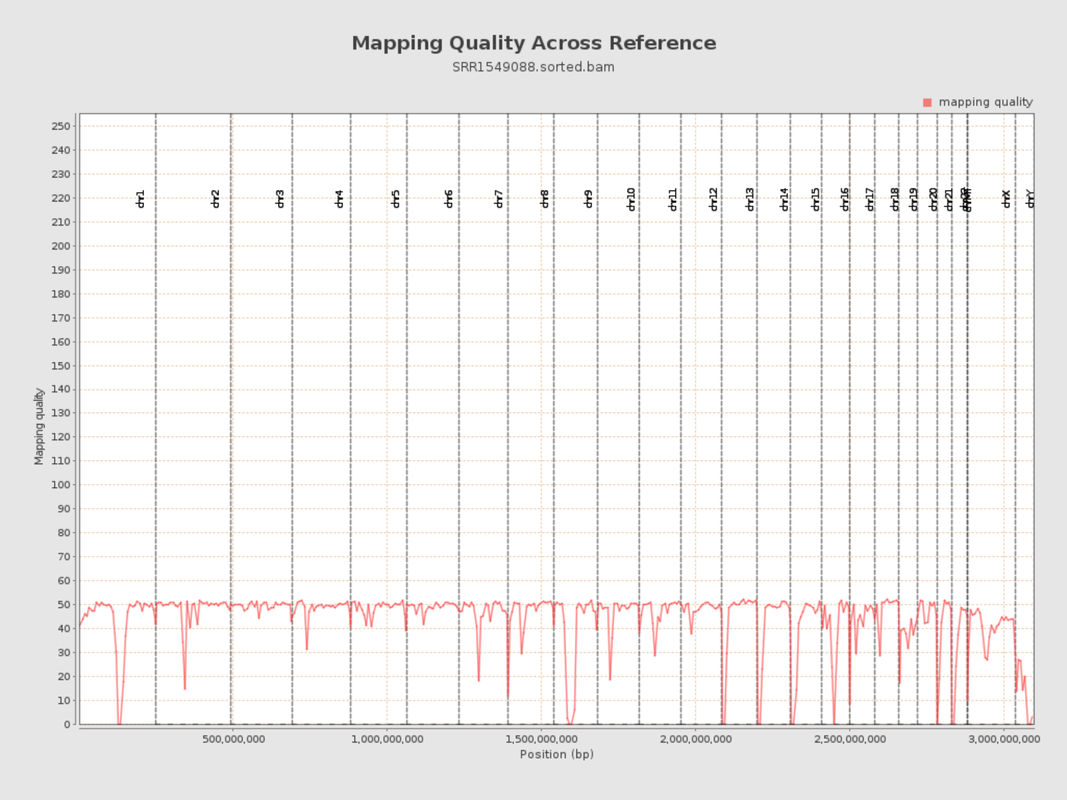
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram