Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 18:07:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089609.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_SRR089609 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089609.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 18:07:30 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089609.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,644,889
Mapped reads	15,373,763 / 87.13%
Unmapped reads	2,271,126 / 12.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	577 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	3,729,802 / 21.14%
Duplication rate	15.09%
Clipped reads	1,356,910 / 7.69%

2.2. ACGT Content

Number/percentage of A's	208,002,026 / 28.68%
Number/percentage of C's	154,329,918 / 21.28%
Number/percentage of T's	205,890,645 / 28.39%
Number/percentage of G's	156,962,700 / 21.64%
Number/percentage of N's	13,441 / 0%
GC Percentage	42.93%

2.3. Coverage

Mean	0.2343

Standard Deviation	1.559

2.4. Mapping Quality

Mean Mapping Quality	44.57

2.5. Mismatches and indels

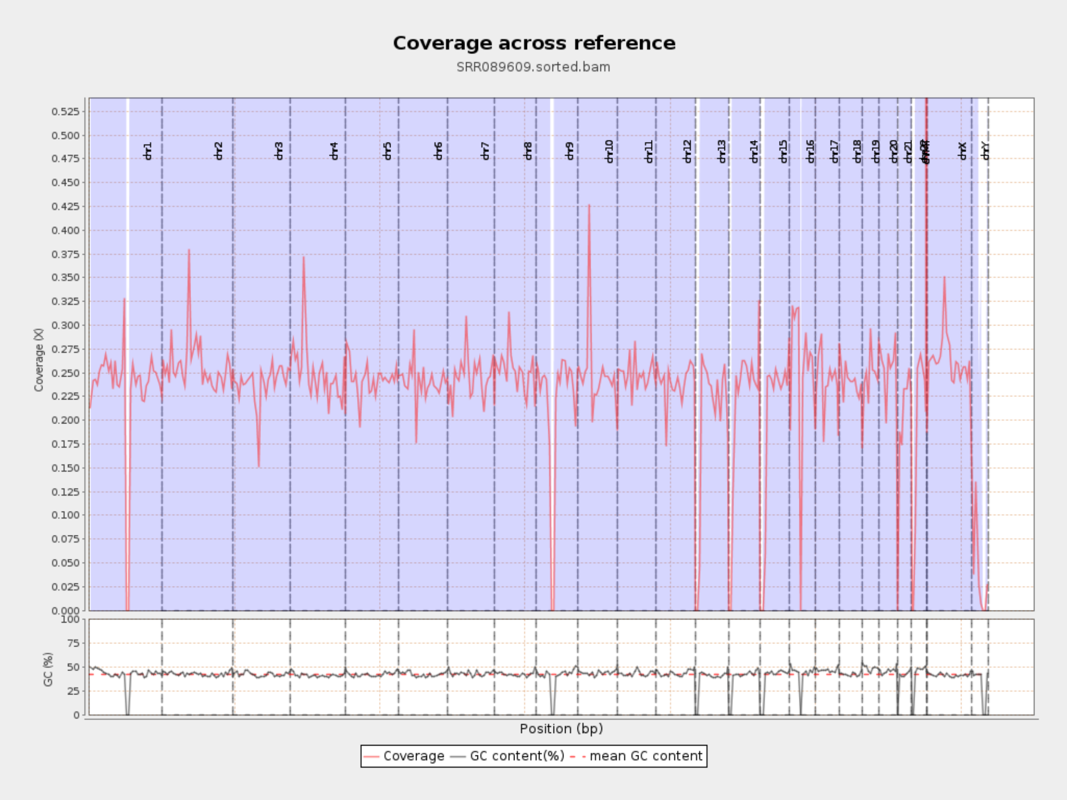
General error rate	0.44%
Mismatches	3,121,172
Insertions	27,230
Mapped reads with at least one insertion	0.18%
Deletions	89,900
Mapped reads with at least one deletion	0.58%
Homopolymer indels	44.49%

2.6. Chromosome stats

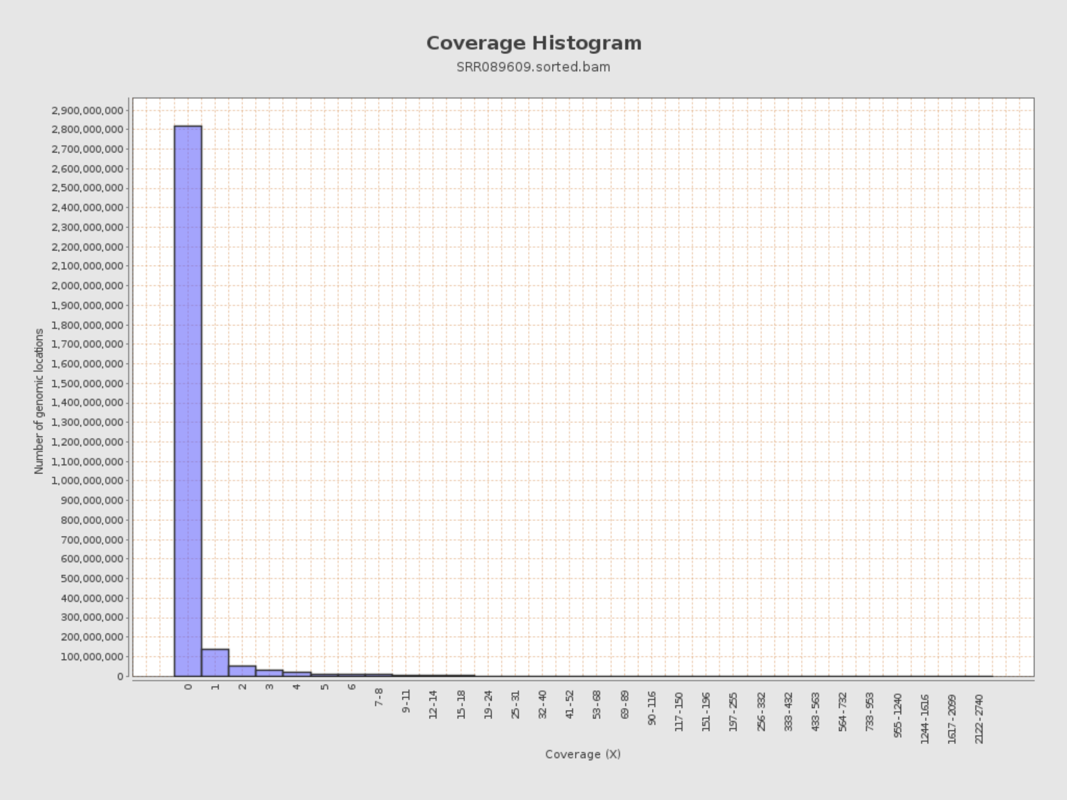
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	57865780	0.2322	2.3473
chr2	243199373	62914812	0.2587	1.9301
chr3	198022430	47193058	0.2383	1.1416
chr4	191154276	47916681	0.2507	1.3038
chr5	180915260	44035542	0.2434	1.1632
chr6	171115067	41246705	0.241	1.2952
chr7	159138663	39074908	0.2455	1.8142

chr8	146364022	36958325	0.2525	1.6316
chr9	141213431	29929417	0.2119	1.4051
chr10	135534747	33897220	0.2501	1.9636
chr11	135006516	33411071	0.2475	1.5295
chr12	133851895	32106798	0.2399	1.199
chr13	115169878	22702851	0.1971	1.0309
chr14	107349540	22289992	0.2076	1.2224
chr15	102531392	20071059	0.1958	1.0385
chr16	90354753	22757071	0.2519	1.3606
chr17	81195210	19475878	0.2399	1.2967
chr18	78077248	18897256	0.242	2.0289
chr19	59128983	14648738	0.2477	2.293
chr20	63025520	16092499	0.2553	1.3101
chr21	48129895	9494449	0.1973	1.2757
chr22	51304566	9004903	0.1755	1.0155
chrMT	16571	246695	14.8872	14.4069
chrX	155270560	40724678	0.2623	1.3385
chrY	59373566	2377774	0.04	0.9083

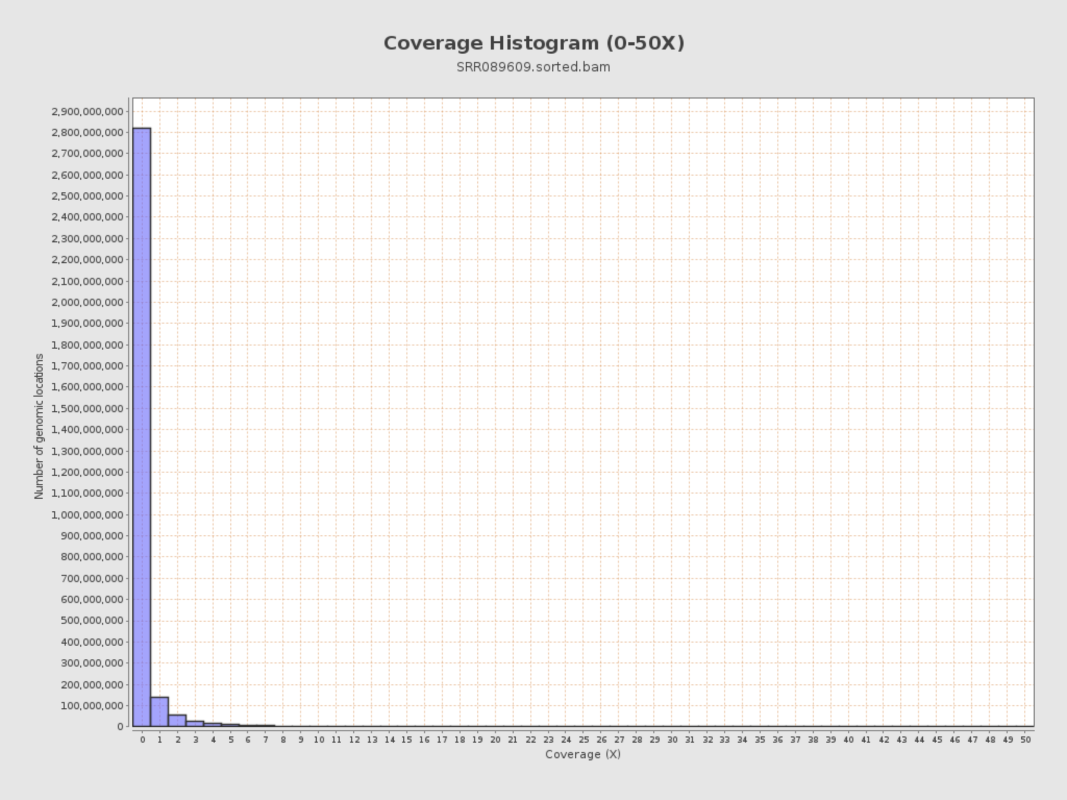
3. Results : Coverage across reference



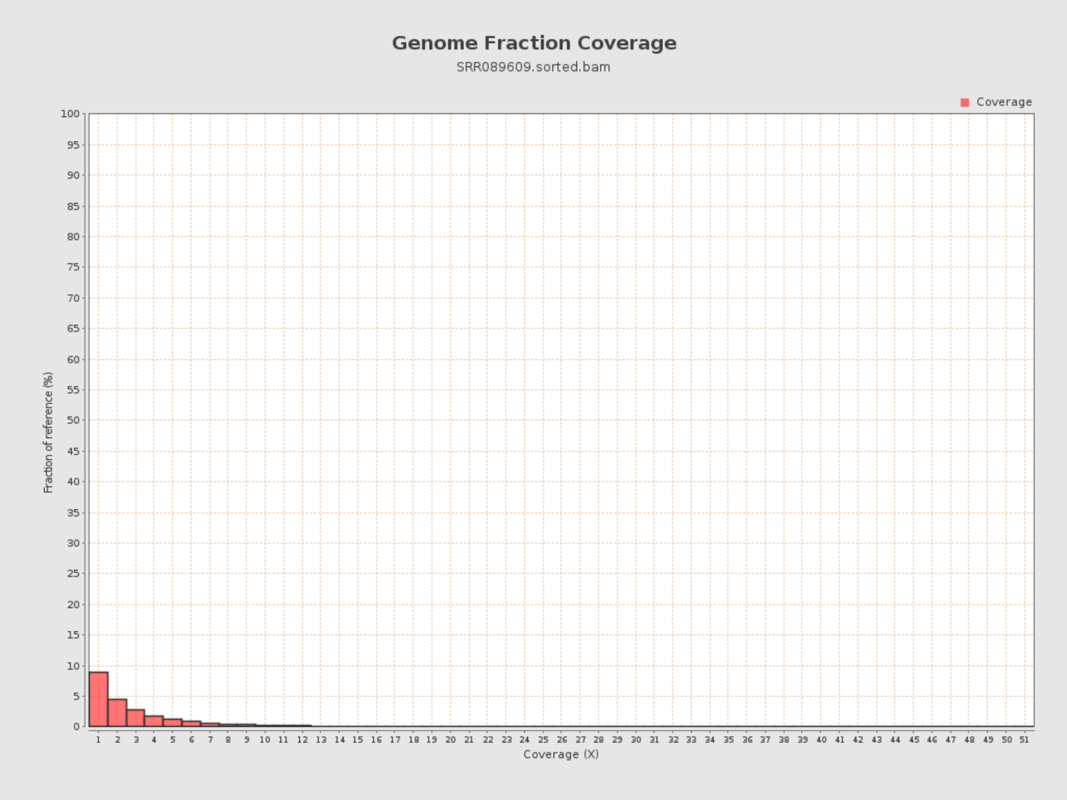
4. Results : Coverage Histogram



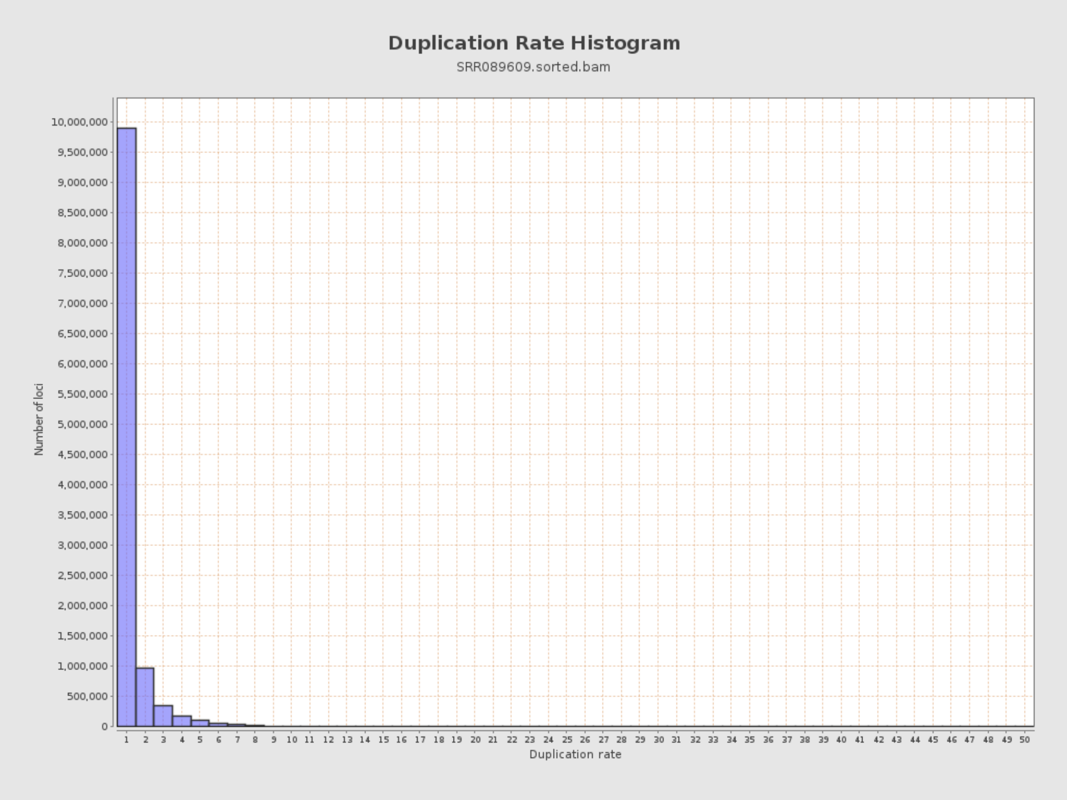
5. Results : Coverage Histogram (0-50X)



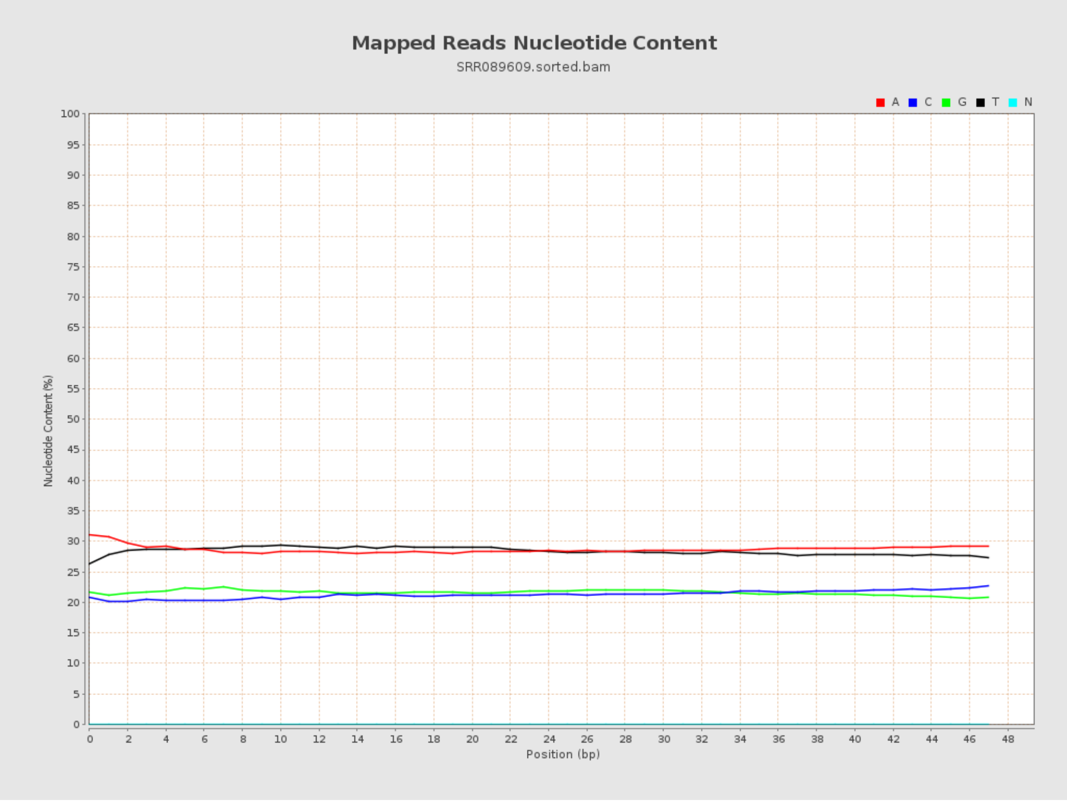
6. Results : Genome Fraction Coverage



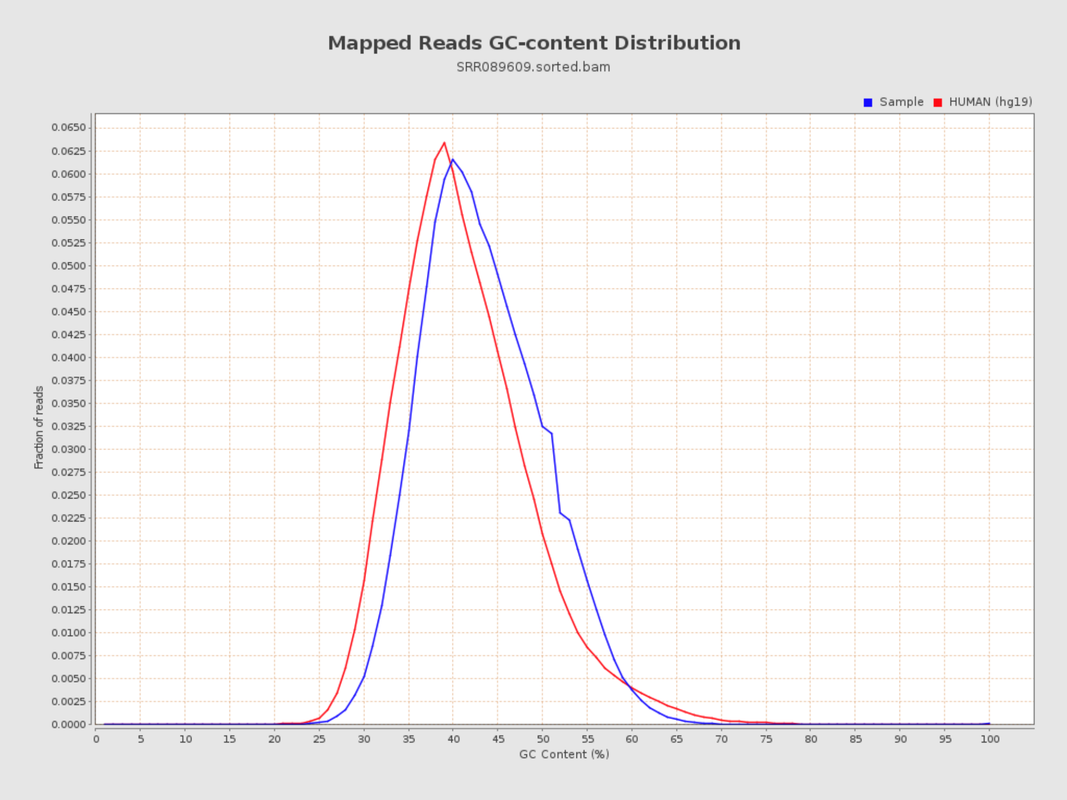
7. Results : Duplication Rate Histogram



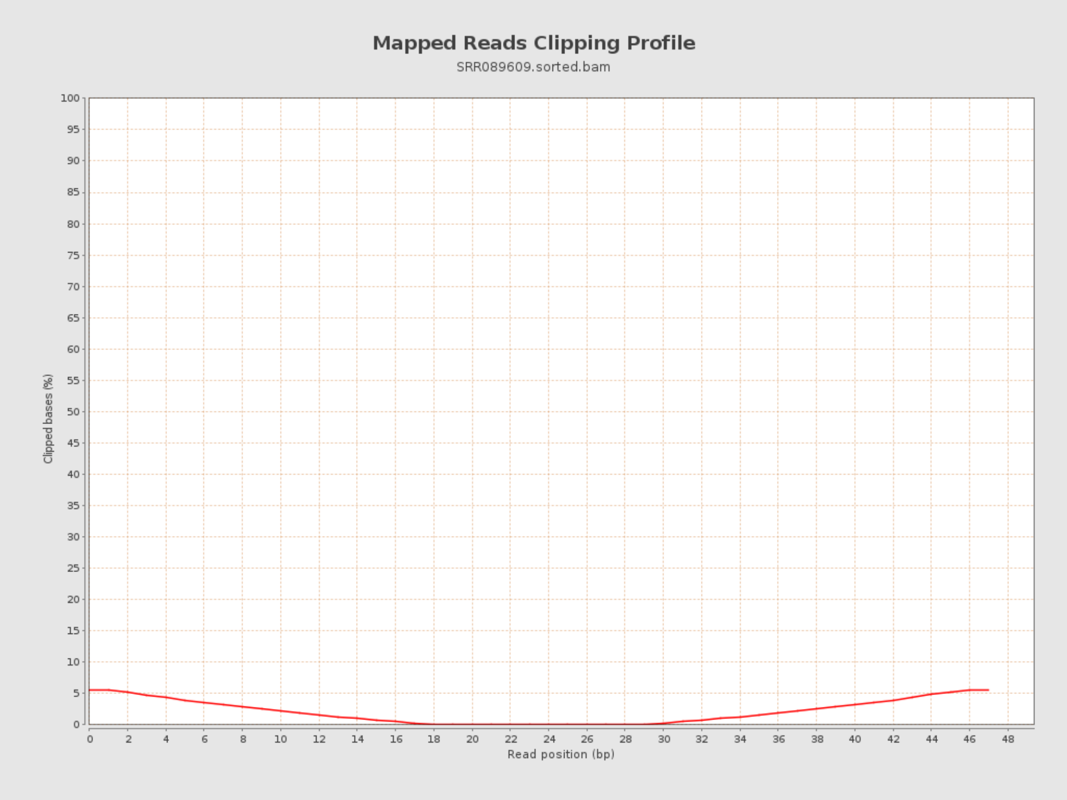
8. Results : Mapped Reads Nucleotide Content



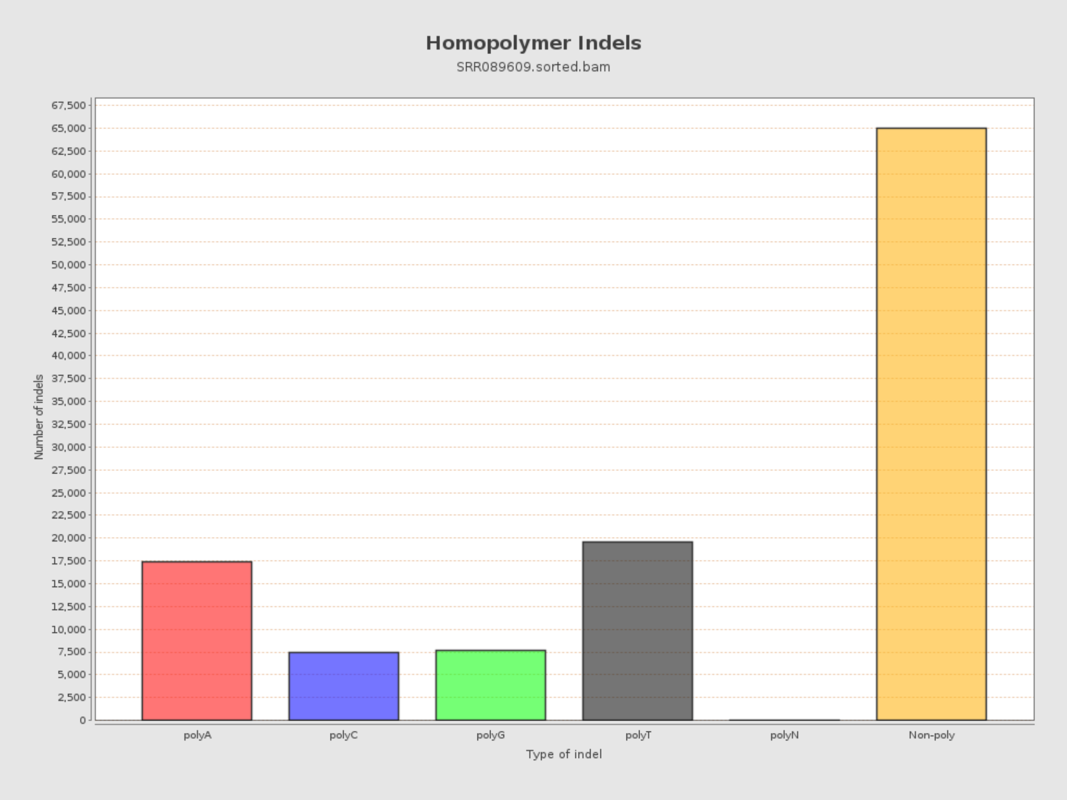
9. Results : Mapped Reads GC-content Distribution



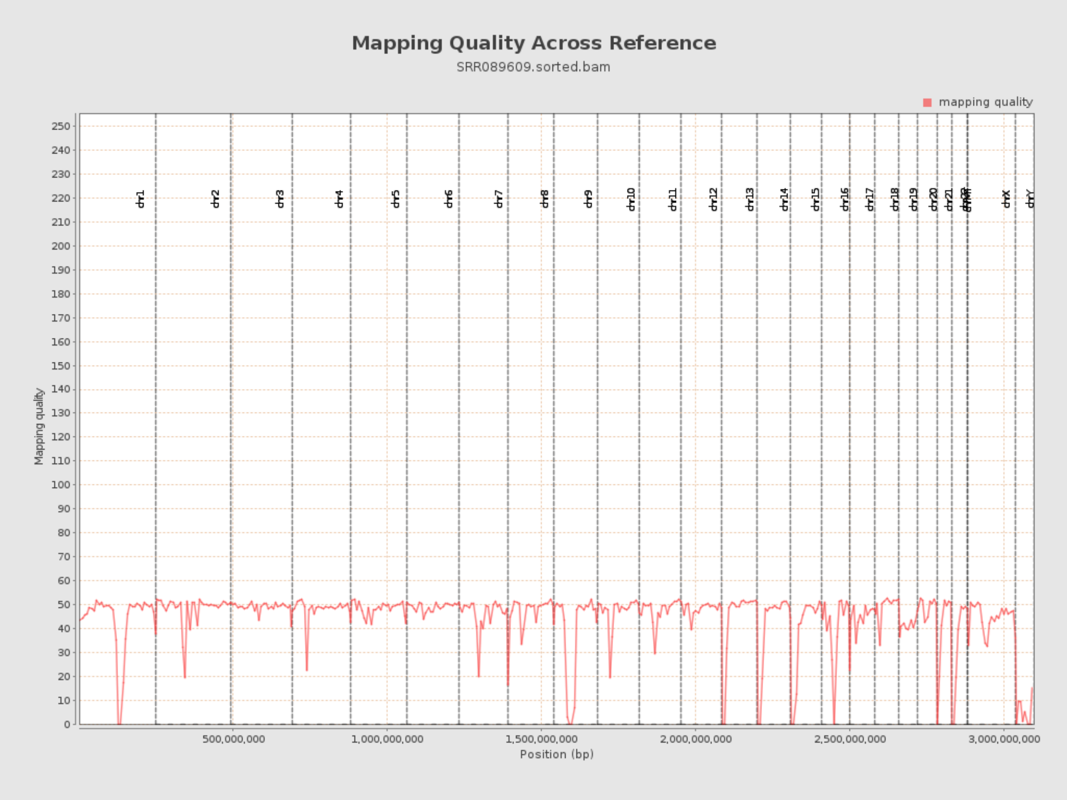
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram