Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 09:24:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089377.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_SRR089377 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089377.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 09:24:13 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089377.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	25,701,801
Mapped reads	24,049,268 / 93.57%
Unmapped reads	1,652,533 / 6.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	134,668 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	5,497,610 / 21.39%
Duplication rate	14.61%
Clipped reads	12,017,329 / 46.76%

2.2. ACGT Content

Number/percentage of A's	401,721,564 / 25.6%
Number/percentage of C's	296,593,799 / 18.9%
Number/percentage of T's	486,638,602 / 31.01%
Number/percentage of G's	384,259,888 / 24.48%
Number/percentage of N's	184,160 / 0.01%
GC Percentage	43.38%

2.3. Coverage

Mean	0.5071

Standard Deviation	3.039

2.4. Mapping Quality

Mean Mapping Quality	46.35

2.5. Mismatches and indels

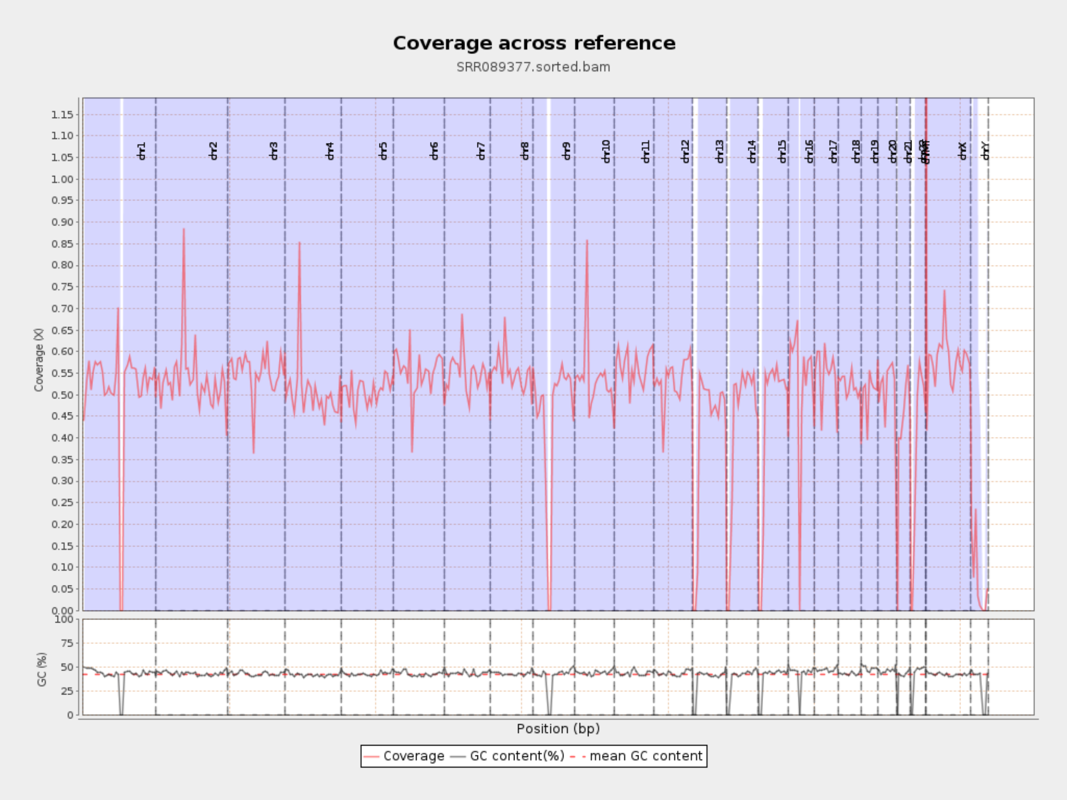
General error rate	0.62%
Mismatches	9,445,369
Insertions	105,854
Mapped reads with at least one insertion	0.44%
Deletions	315,570
Mapped reads with at least one deletion	1.3%
Homopolymer indels	46.64%

2.6. Chromosome stats

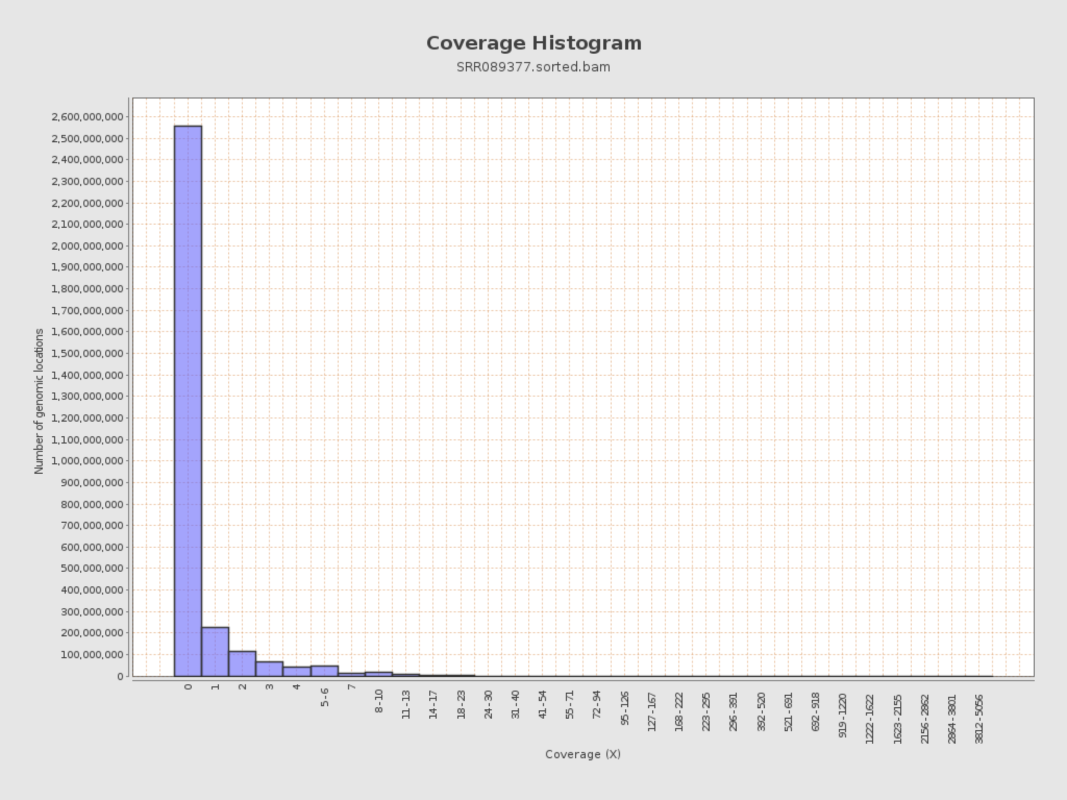
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	127054898	0.5097	4.6969
chr2	243199373	130734589	0.5376	4.0494
chr3	198022430	109061364	0.5508	1.7687
chr4	191154276	97242314	0.5087	2.3838
chr5	180915260	91996415	0.5085	1.6921
chr6	171115067	94581656	0.5527	2.459
chr7	159138663	87682265	0.551	3.7733

chr8	146364022	80733262	0.5516	2.9176
chr9	141213431	62844225	0.445	3.1991
chr10	135534747	73132317	0.5396	3.8668
chr11	135006516	75765067	0.5612	3.2203
chr12	133851895	71713095	0.5358	1.9202
chr13	115169878	47686342	0.4141	1.5111
chr14	107349540	46809822	0.4361	1.7468
chr15	102531392	44657951	0.4356	1.7585
chr16	90354753	46591882	0.5157	2.1963
chr17	81195210	44860898	0.5525	2.2957
chr18	78077248	40780238	0.5223	6.107
chr19	59128983	29788087	0.5038	3.2615
chr20	63025520	32695231	0.5188	2.0267
chr21	48129895	20423026	0.4243	2.2868
chr22	51304566	18824836	0.3669	1.4526
chrMT	16571	130012	7.8458	15.3416
chrX	155270560	90040107	0.5799	2.3215
chrY	59373566	4125009	0.0695	1.7275

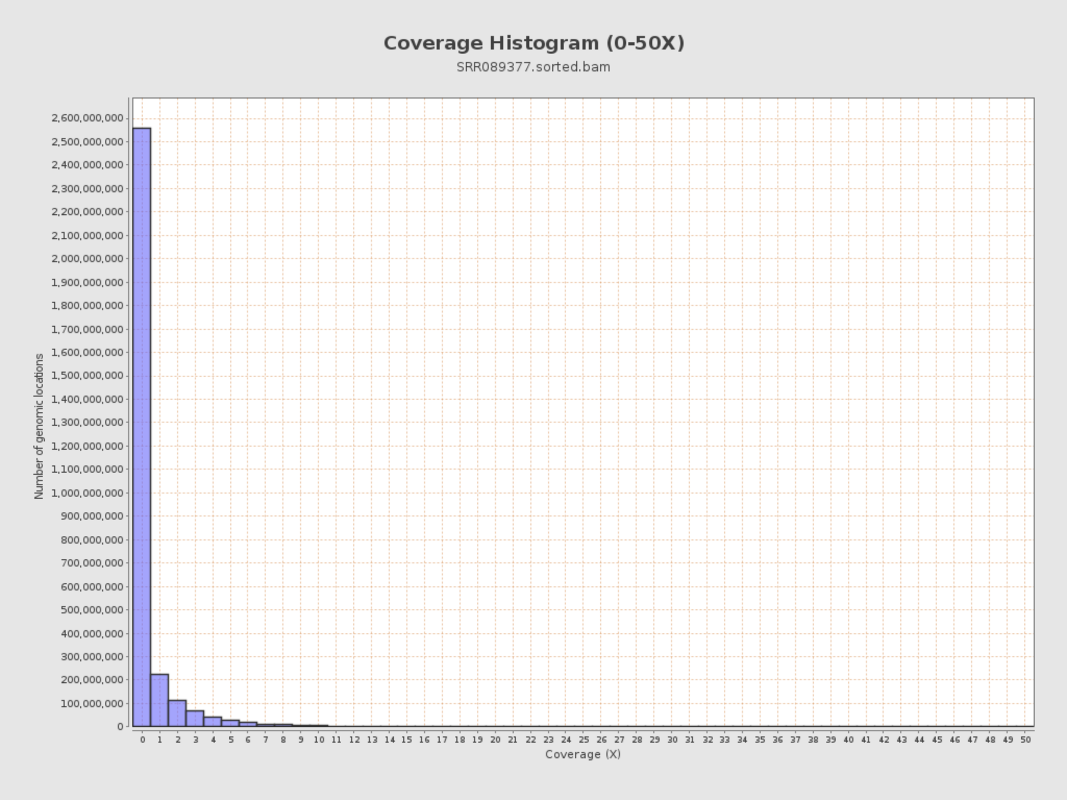
3. Results : Coverage across reference



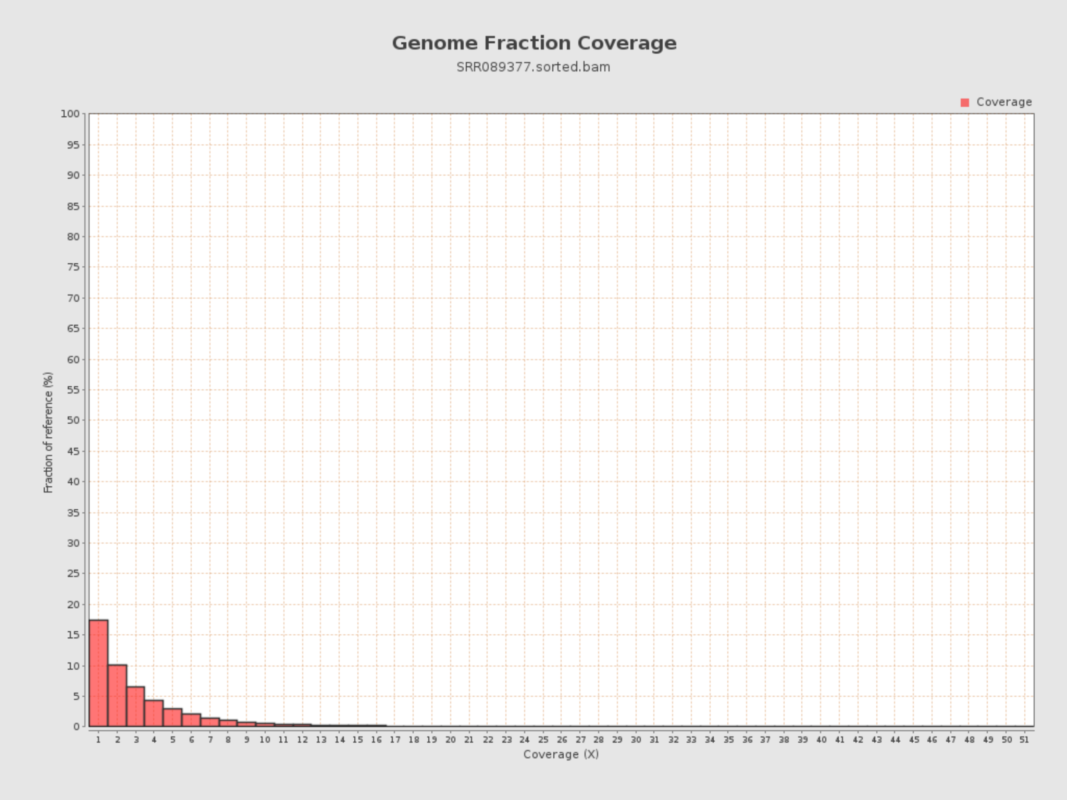
4. Results : Coverage Histogram



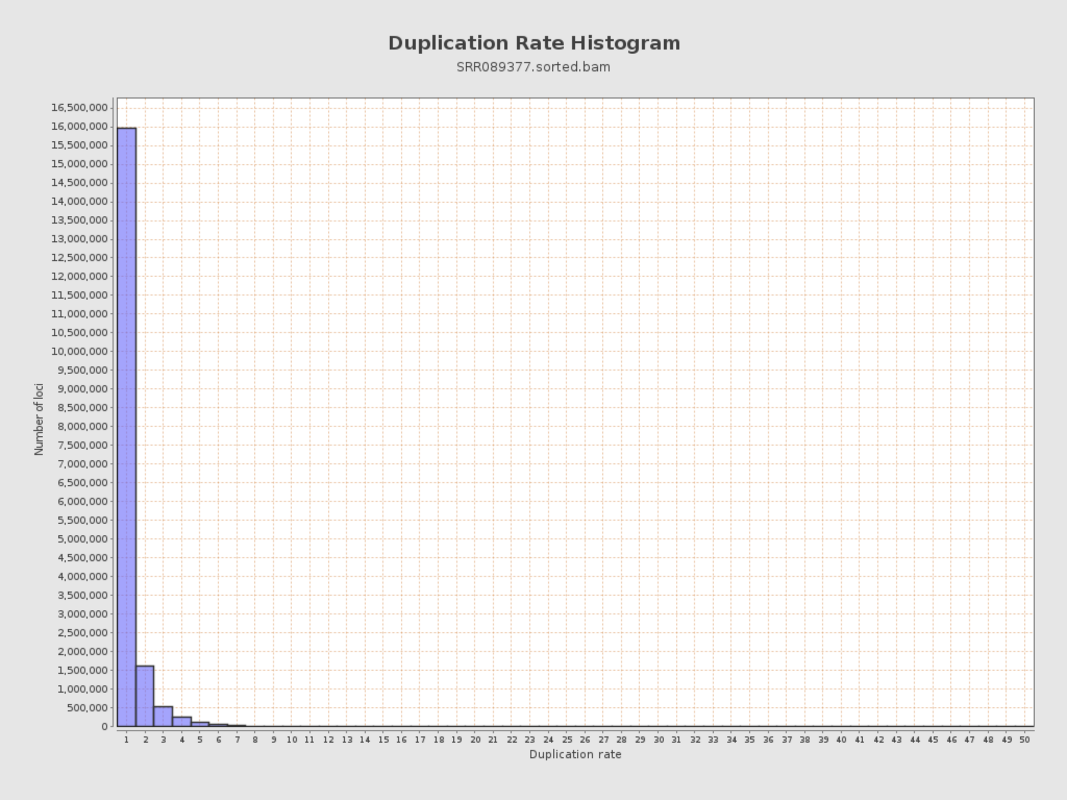
5. Results : Coverage Histogram (0-50X)



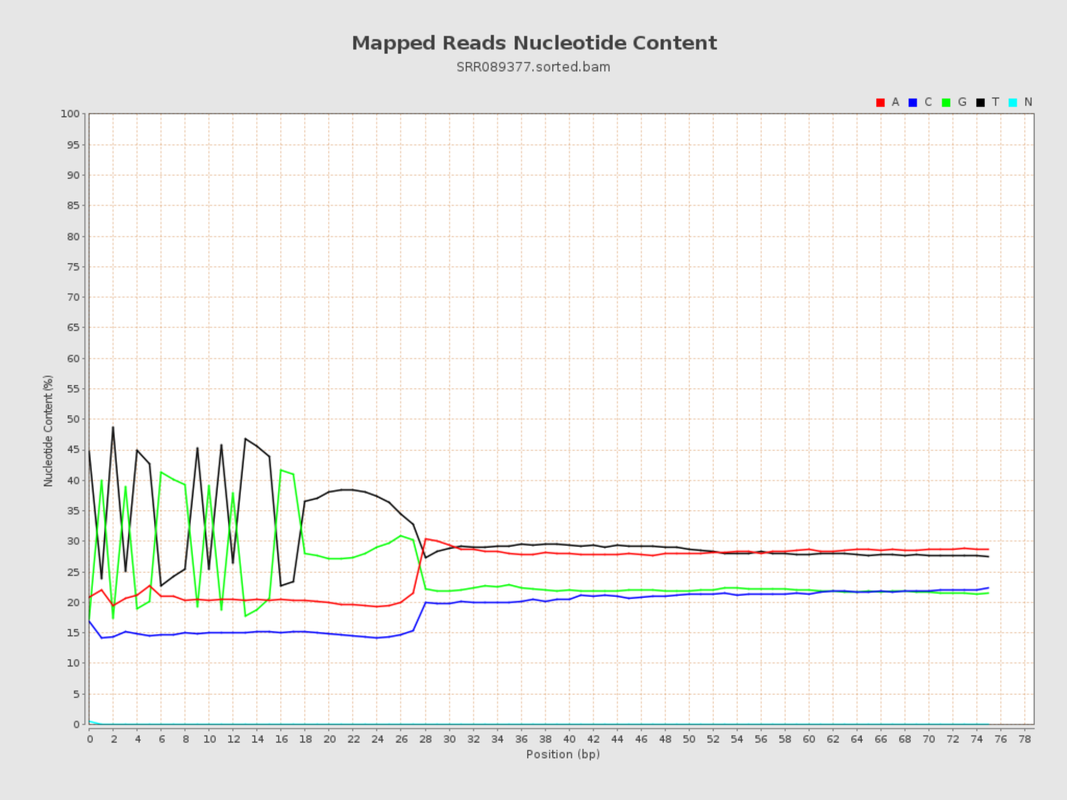
6. Results : Genome Fraction Coverage



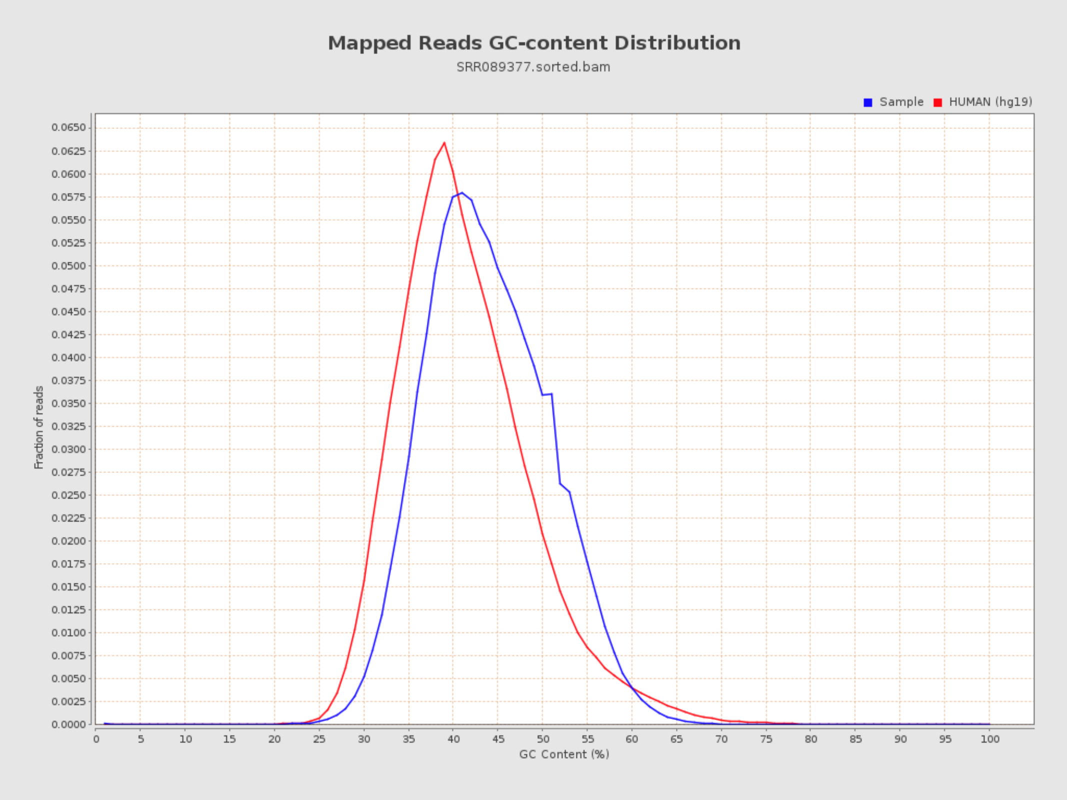
7. Results : Duplication Rate Histogram



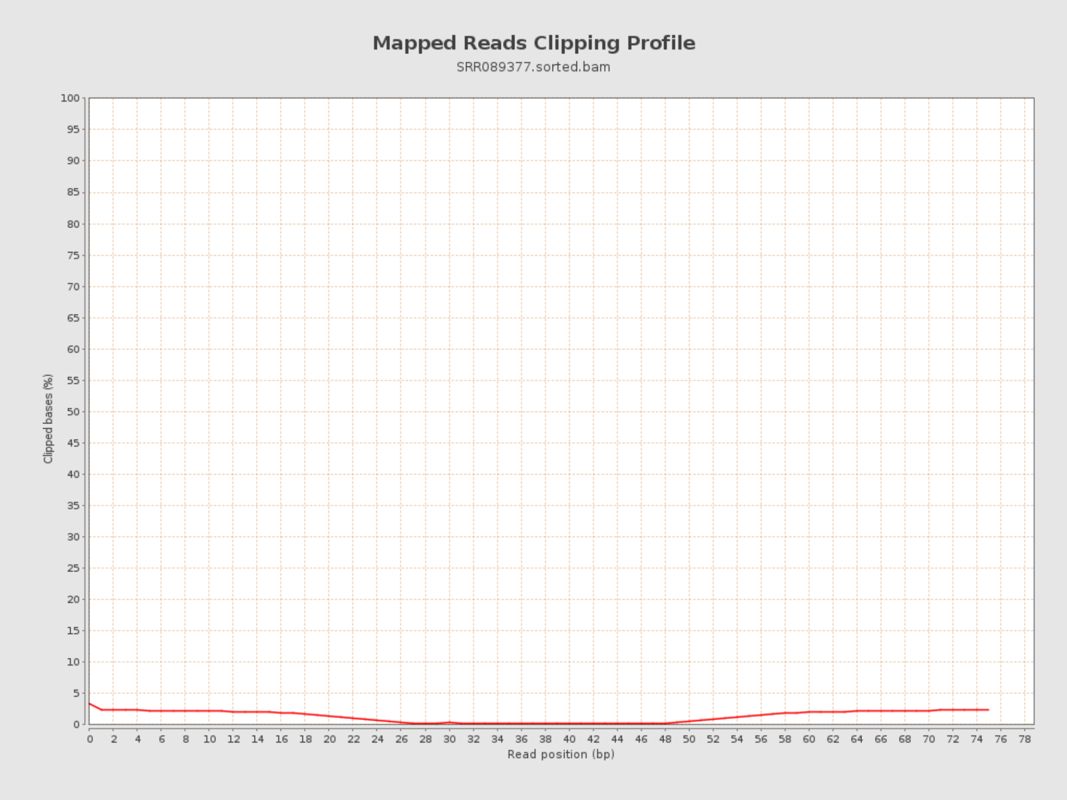
8. Results : Mapped Reads Nucleotide Content



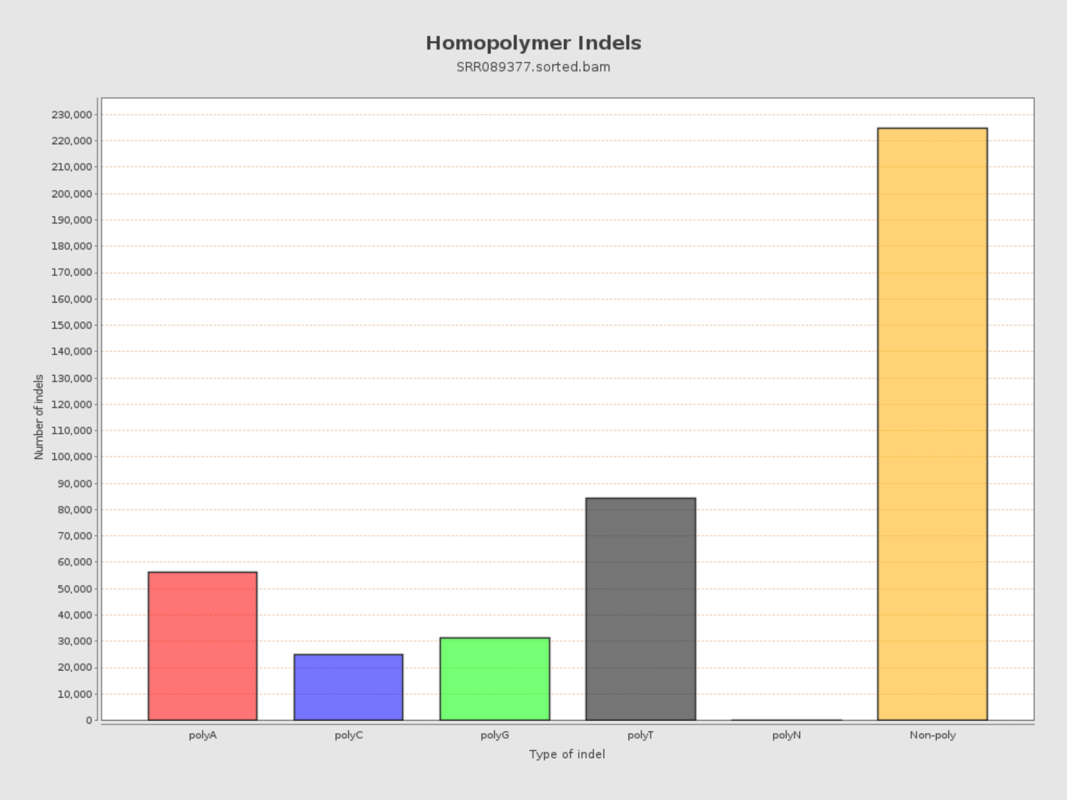
9. Results : Mapped Reads GC-content Distribution



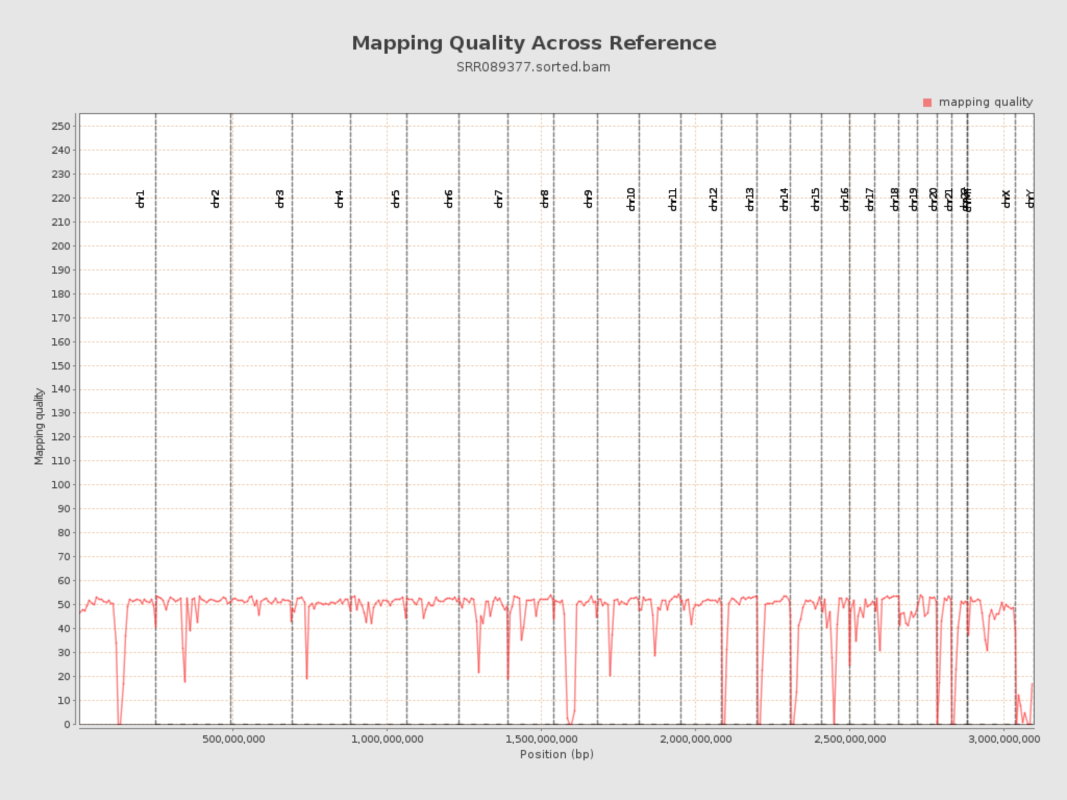
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram