Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 11:35:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089403.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_SRR089403 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089403.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 11:35:38 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089403.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,524,958
Mapped reads	21,685,914 / 92.18%
Unmapped reads	1,839,044 / 7.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	152,608 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	4,781,336 / 20.32%
Duplication rate	14.25%
Clipped reads	10,522,383 / 44.73%

2.2. ACGT Content

Number/percentage of A's	379,362,715 / 26.63%
Number/percentage of C's	271,034,791 / 19.03%
Number/percentage of T's	439,947,449 / 30.89%
Number/percentage of G's	333,963,981 / 23.45%
Number/percentage of N's	97,048 / 0.01%
GC Percentage	42.47%

2.3. Coverage

Mean	0.4603

Standard Deviation	3.0069

2.4. Mapping Quality

Mean Mapping Quality	46.25

2.5. Mismatches and indels

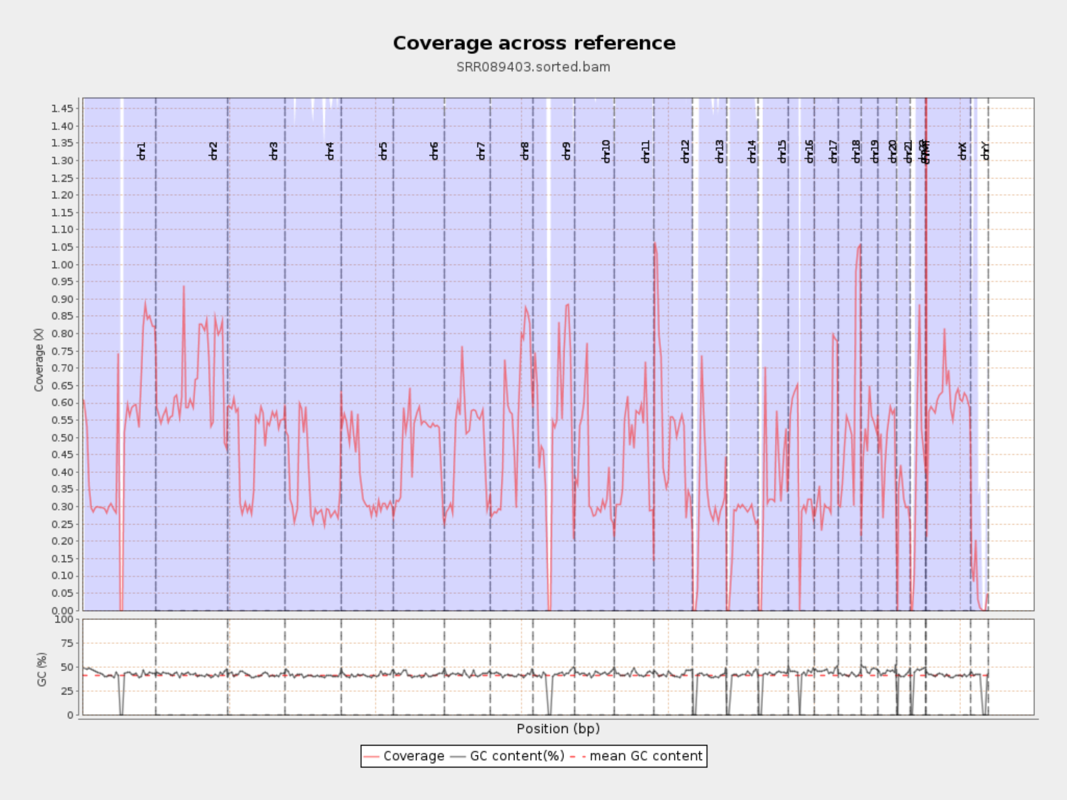
General error rate	0.65%
Mismatches	9,062,244
Insertions	89,533
Mapped reads with at least one insertion	0.41%
Deletions	275,475
Mapped reads with at least one deletion	1.26%
Homopolymer indels	46.09%

2.6. Chromosome stats

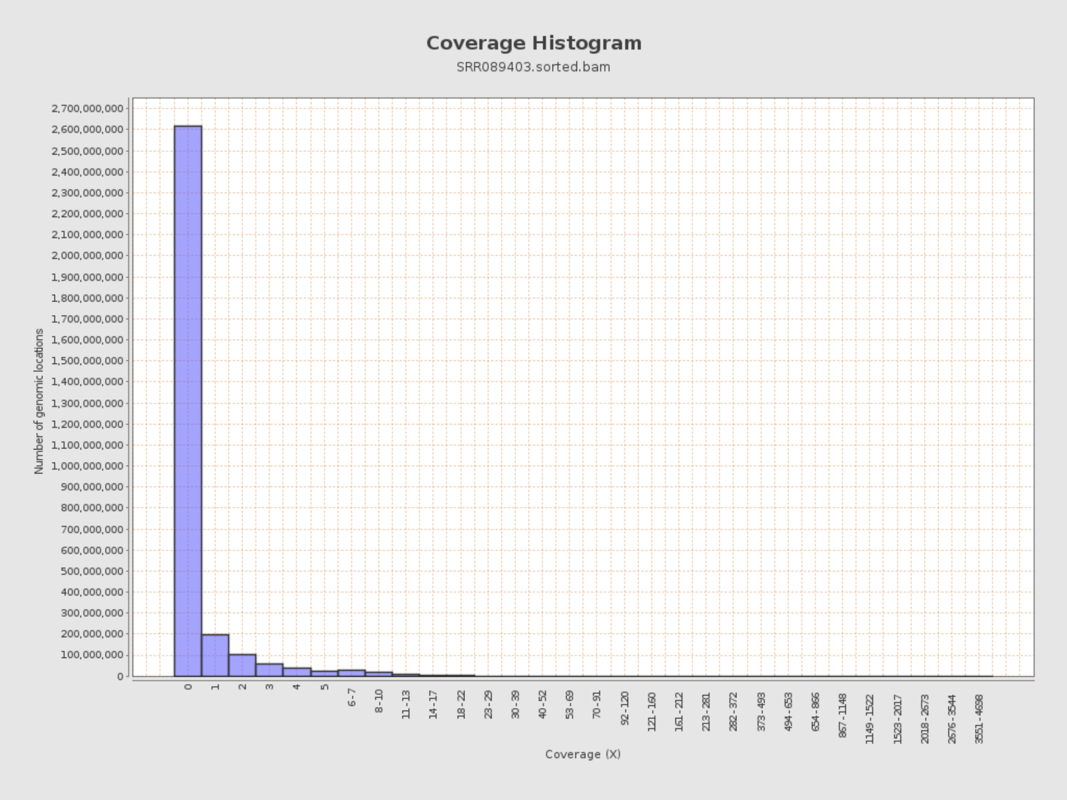
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	120925488	0.4852	4.872
chr2	243199373	159690121	0.6566	3.9451
chr3	198022430	97243223	0.4911	1.696
chr4	191154276	67811227	0.3547	1.8963
chr5	180915260	69651845	0.385	1.5427
chr6	171115067	83850892	0.49	2.3049
chr7	159138663	76875775	0.4831	4.4511

chr8	146364022	80113476	0.5474	3.2384
chr9	141213431	75292718	0.5332	3.2122
chr10	135534747	51594703	0.3807	3.4966
chr11	135006516	62924442	0.4661	3.2355
chr12	133851895	73701186	0.5506	1.9254
chr13	115169878	35082209	0.3046	1.311
chr14	107349540	26061539	0.2428	1.8487
chr15	102531392	36260354	0.3537	1.4457
chr16	90354753	34876324	0.386	1.9483
chr17	81195210	33741692	0.4156	2.0925
chr18	78077248	45618643	0.5843	4.7929
chr19	59128983	30450529	0.515	4.3813
chr20	63025520	30493314	0.4838	1.8241
chr21	48129895	14350878	0.2982	1.8683
chr22	51304566	20908801	0.4075	1.5576
chrMT	16571	110199	6.6501	6.2597
chrX	155270560	93653093	0.6032	2.4213
chrY	59373566	3599670	0.0606	1.4132

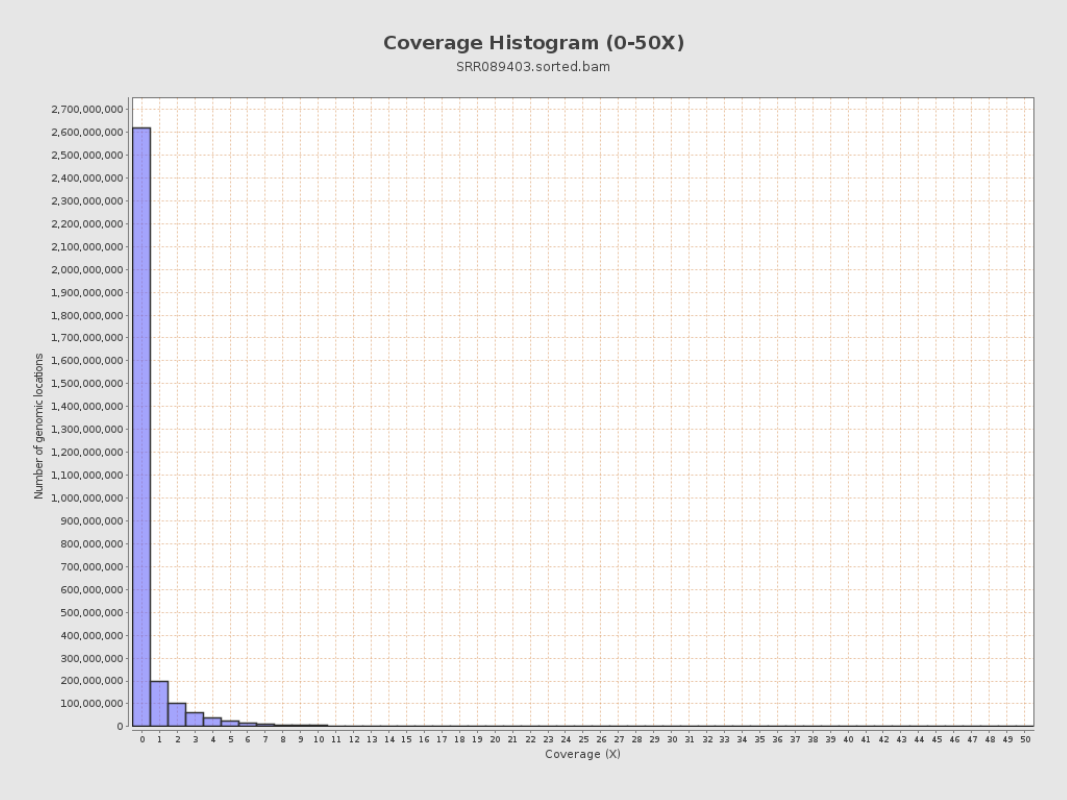
3. Results : Coverage across reference



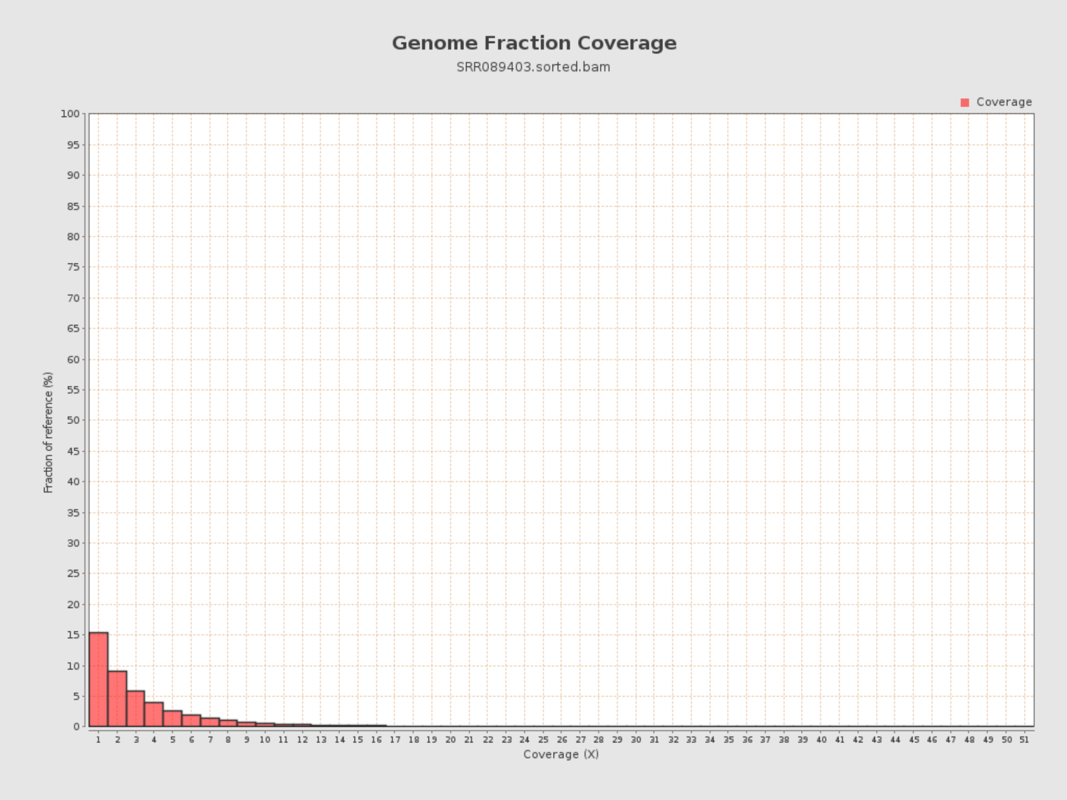
4. Results : Coverage Histogram



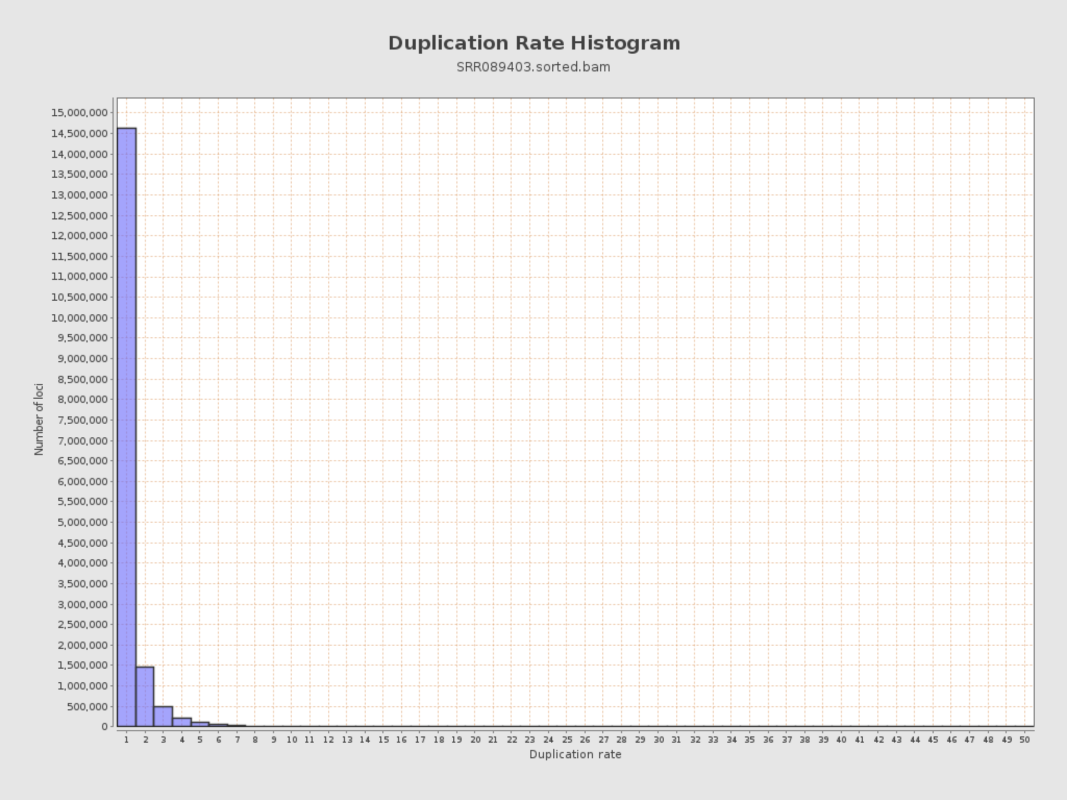
5. Results : Coverage Histogram (0-50X)



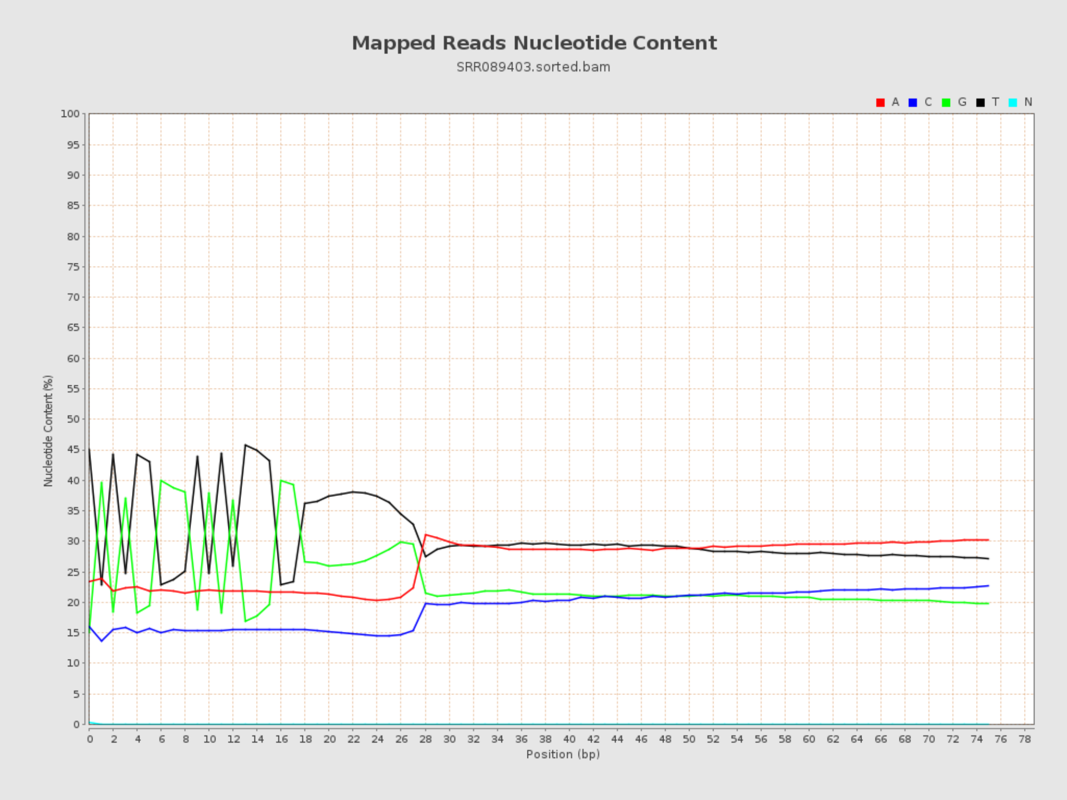
6. Results : Genome Fraction Coverage



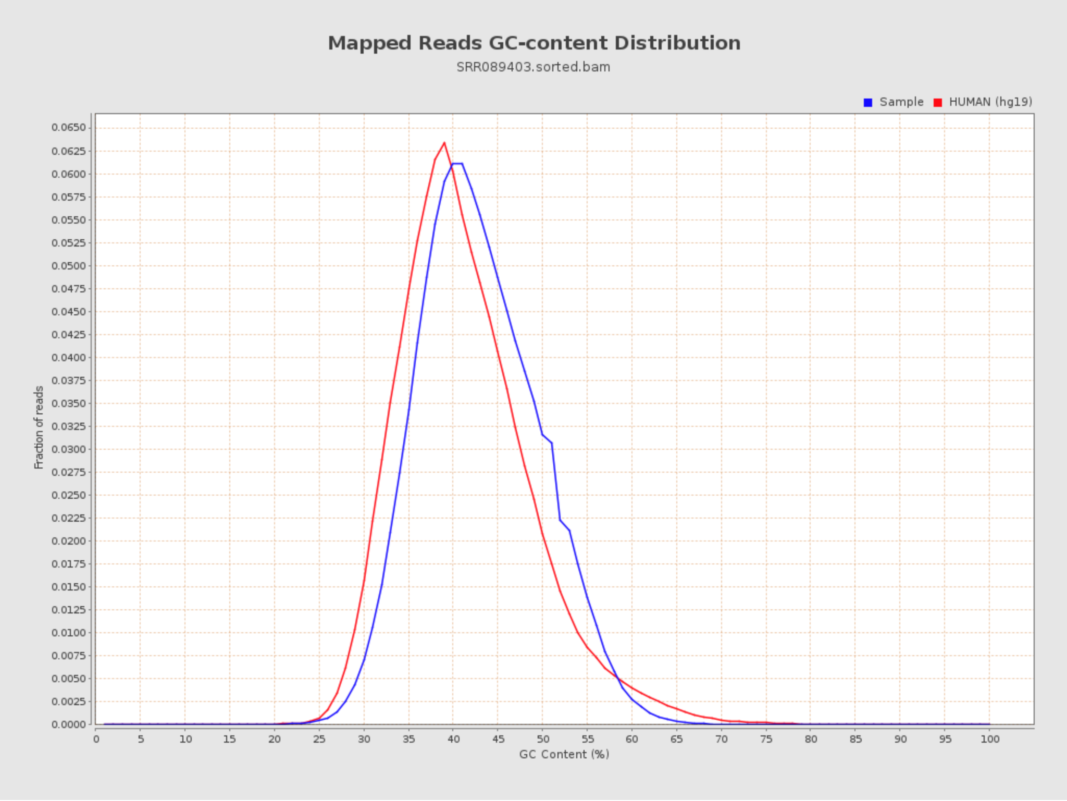
7. Results : Duplication Rate Histogram



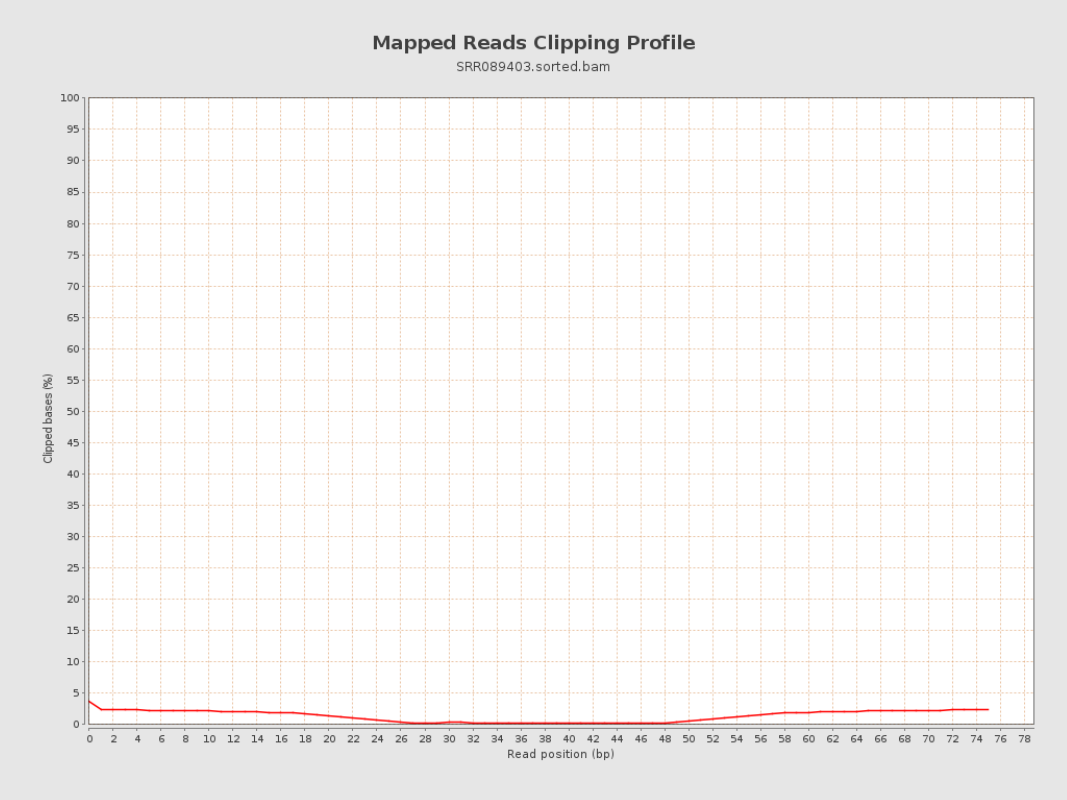
8. Results : Mapped Reads Nucleotide Content



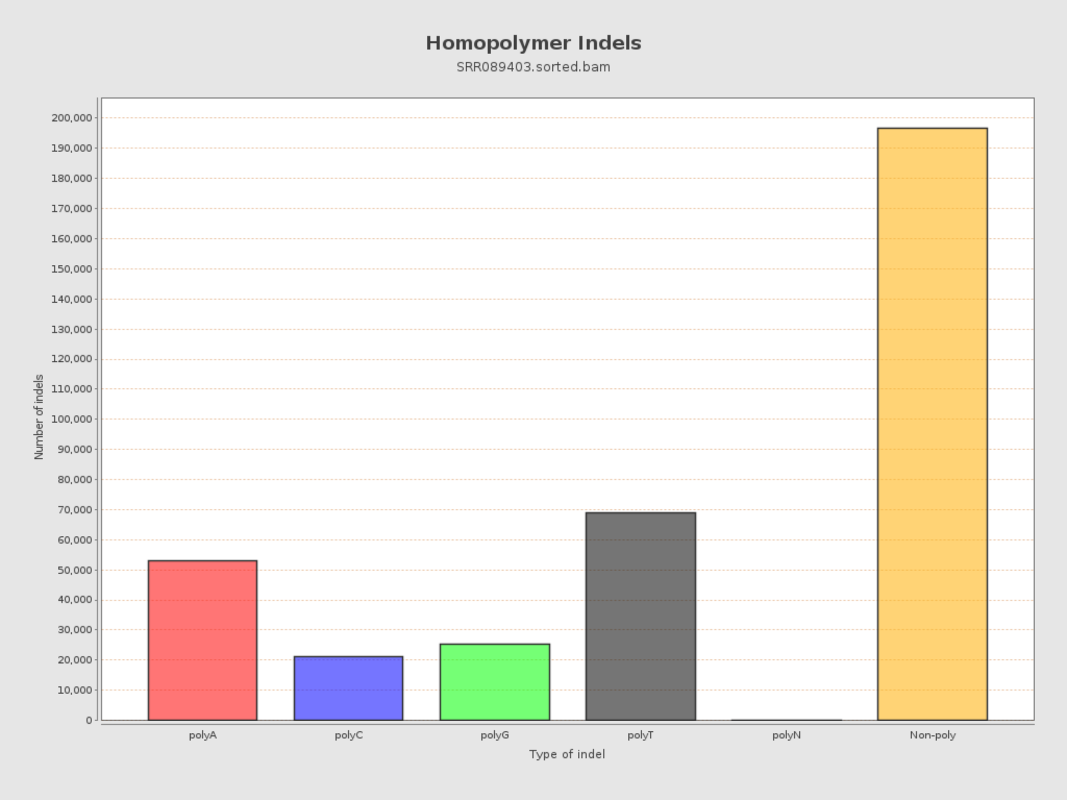
9. Results : Mapped Reads GC-content Distribution



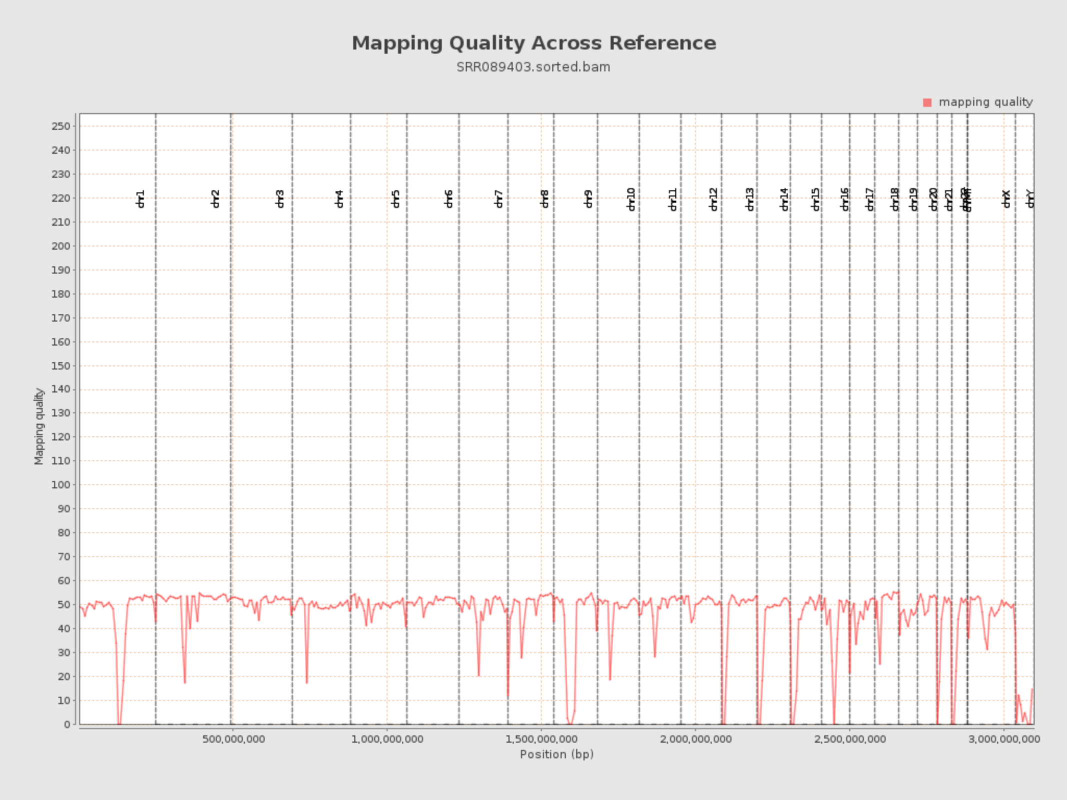
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram