Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 11:16:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089402.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_SRR089402 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089402.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 11:16:12 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089402.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,066,645
Mapped reads	20,819,912 / 90.26%
Unmapped reads	2,246,733 / 9.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	117,496 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	4,019,457 / 17.43%
Duplication rate	12.64%
Clipped reads	8,976,261 / 38.91%

2.2. ACGT Content

Number/percentage of A's	371,144,912 / 26.73%
Number/percentage of C's	265,726,515 / 19.14%
Number/percentage of T's	427,890,565 / 30.82%
Number/percentage of G's	323,588,112 / 23.3%
Number/percentage of N's	149,931 / 0.01%
GC Percentage	42.44%

2.3. Coverage

Mean	0.4487

Standard Deviation	2.9823

2.4. Mapping Quality

Mean Mapping Quality	46.48

2.5. Mismatches and indels

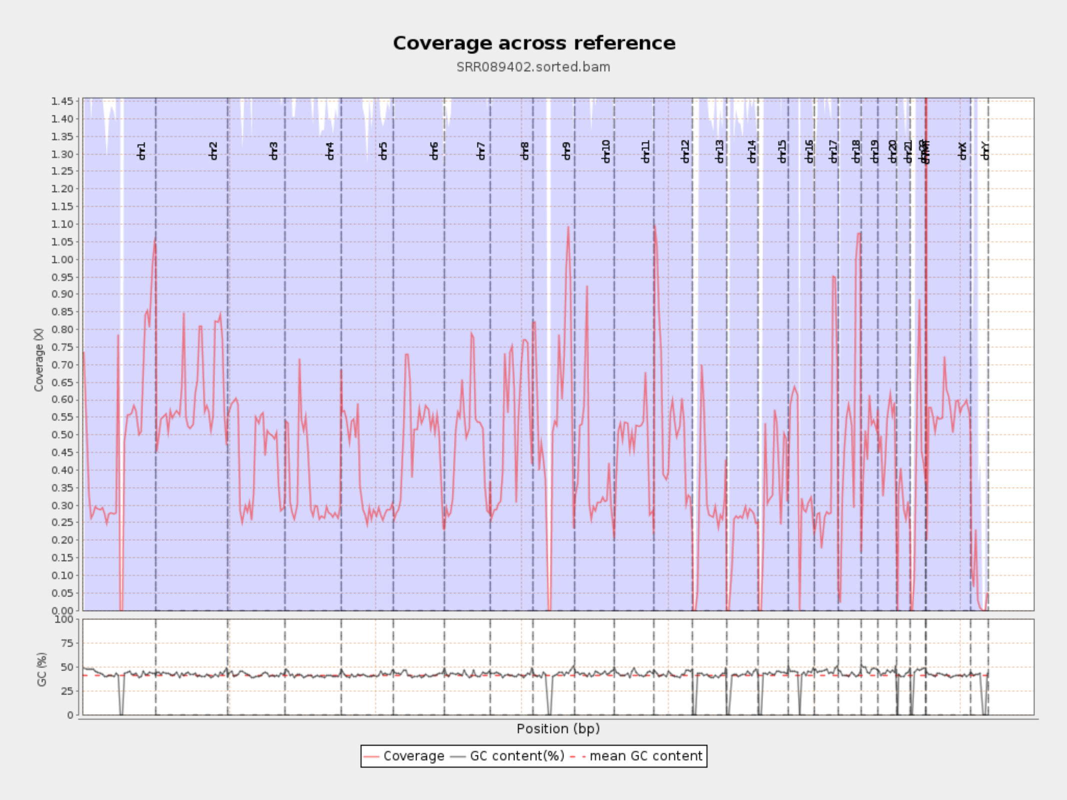
General error rate	0.66%
Mismatches	9,027,221
Insertions	91,507
Mapped reads with at least one insertion	0.44%
Deletions	276,809
Mapped reads with at least one deletion	1.31%
Homopolymer indels	45.68%

2.6. Chromosome stats

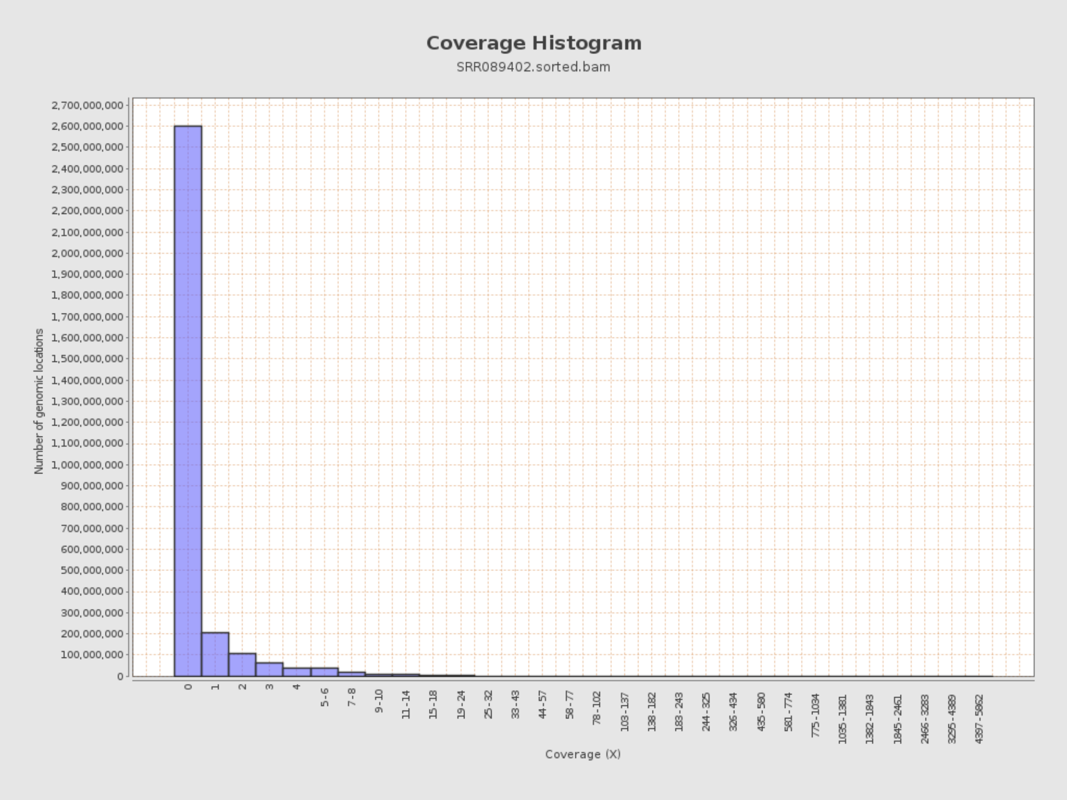
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	119460421	0.4793	5.725
chr2	243199373	148659629	0.6113	3.4986
chr3	198022430	87464501	0.4417	1.525
chr4	191154276	67808260	0.3547	2.1367
chr5	180915260	67411039	0.3726	1.3996
chr6	171115067	84685159	0.4949	2.1396
chr7	159138663	75550799	0.4747	3.5729

chr8	146364022	77905667	0.5323	2.941
chr9	141213431	78965075	0.5592	3.0316
chr10	135534747	52587071	0.388	4.2649
chr11	135006516	64869276	0.4805	3.1282
chr12	133851895	75023929	0.5605	1.7955
chr13	115169878	33508164	0.2909	1.1907
chr14	107349540	24230983	0.2257	1.3856
chr15	102531392	35058061	0.3419	1.3002
chr16	90354753	34482236	0.3816	1.8163
chr17	81195210	33546932	0.4132	1.8709
chr18	78077248	42942693	0.55	4.5039
chr19	59128983	28911814	0.489	4.0175
chr20	63025520	31252228	0.4959	1.8544
chr21	48129895	13489244	0.2803	1.9597
chr22	51304566	20029117	0.3904	1.473
chrMT	16571	187262	11.3006	8.0793
chrX	155270560	87354047	0.5626	2.1247
chrY	59373566	3606735	0.0607	1.7659

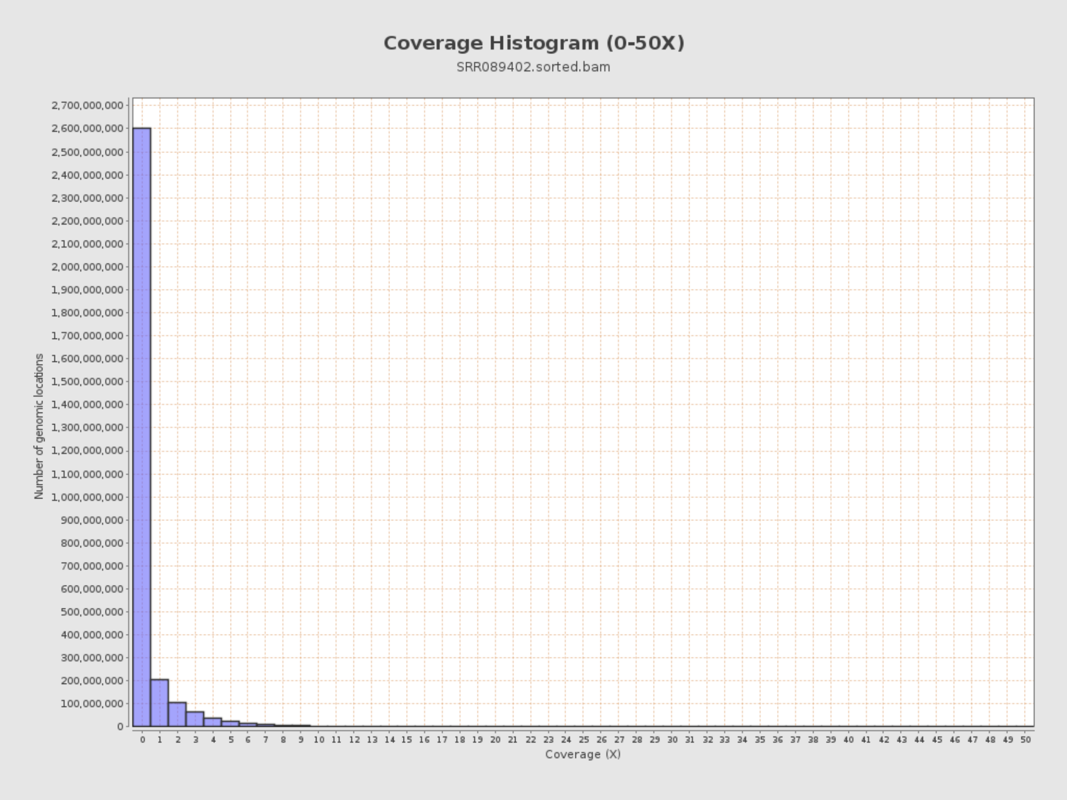
3. Results : Coverage across reference



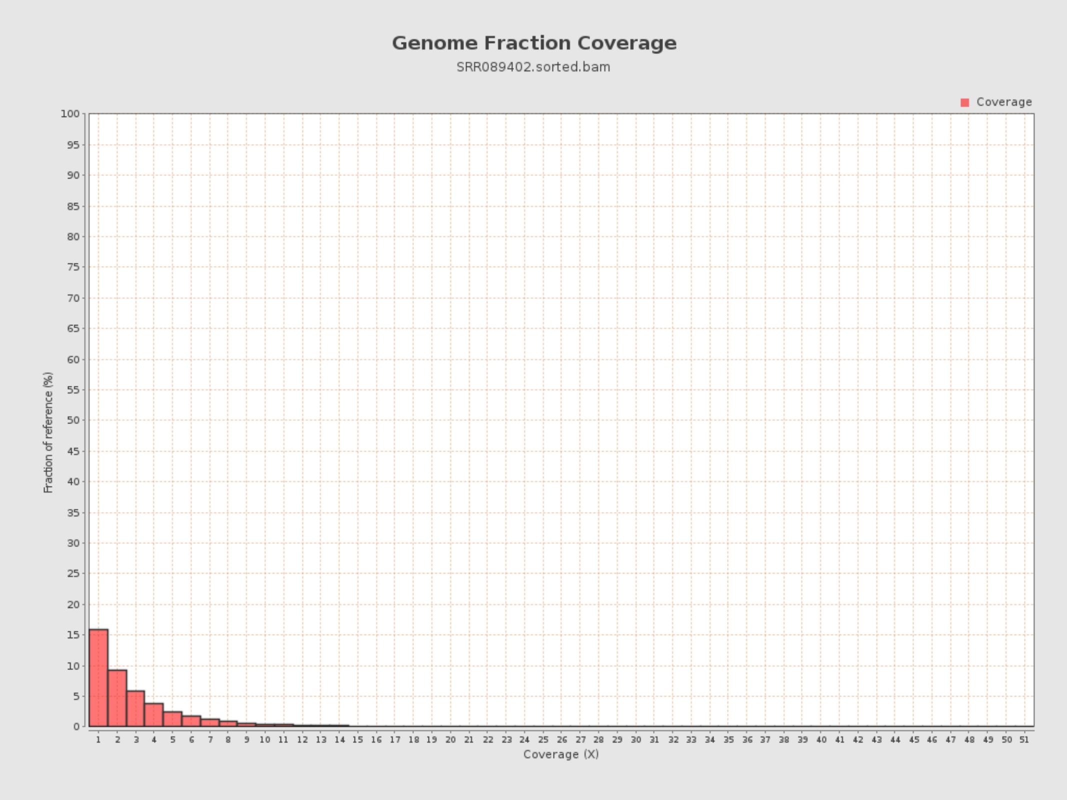
4. Results : Coverage Histogram



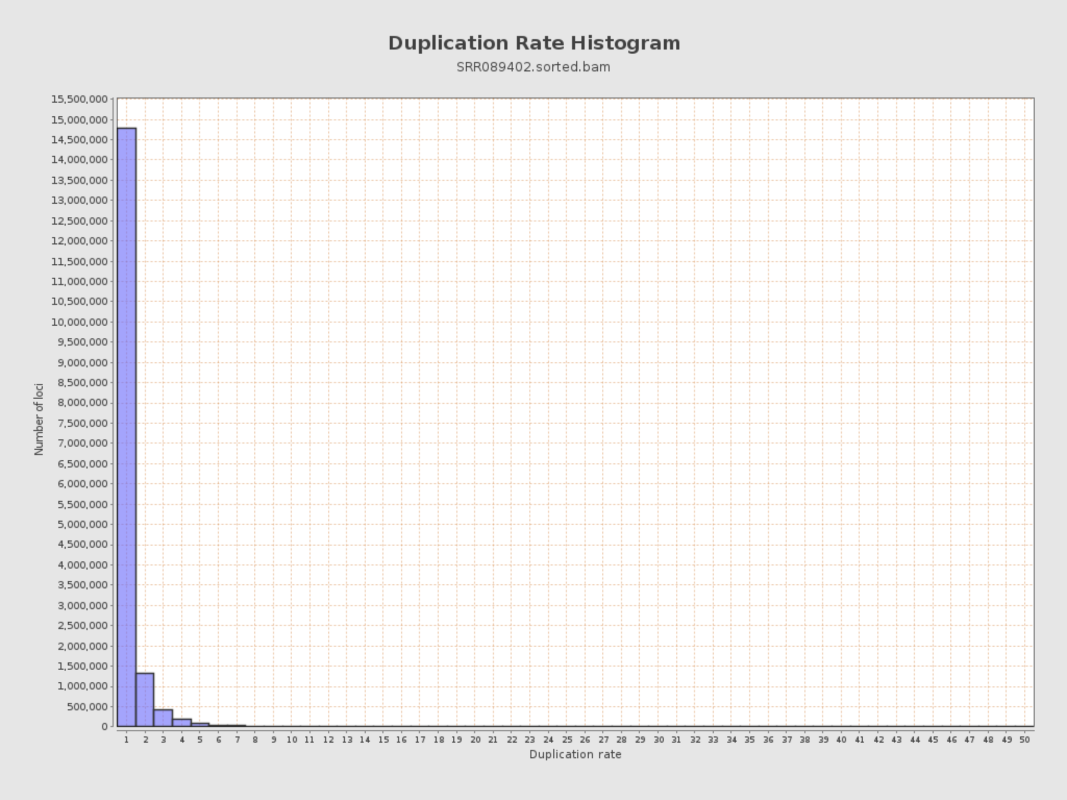
5. Results : Coverage Histogram (0-50X)



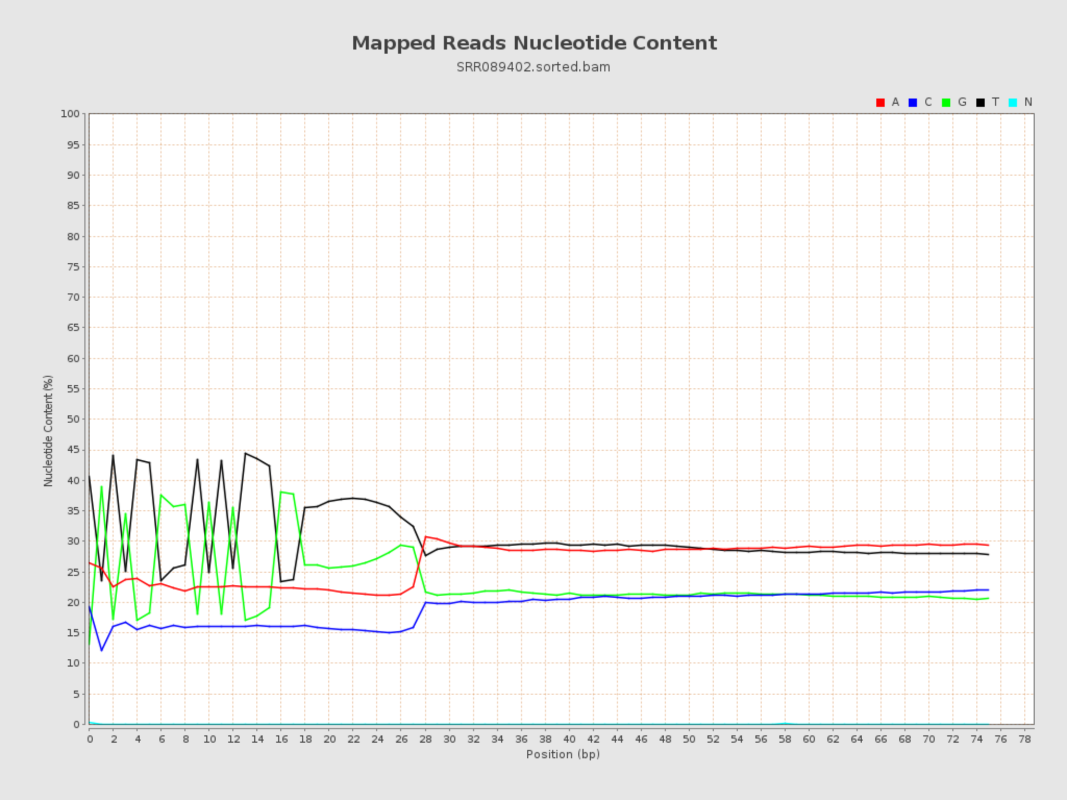
6. Results : Genome Fraction Coverage



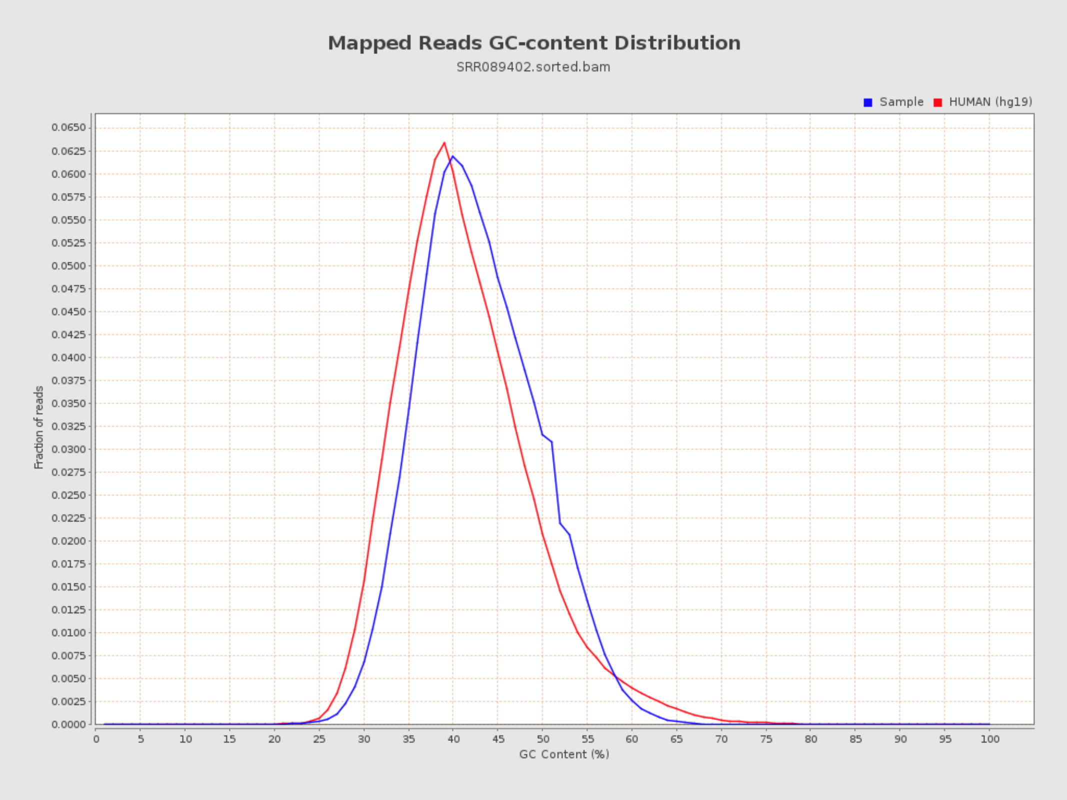
7. Results : Duplication Rate Histogram



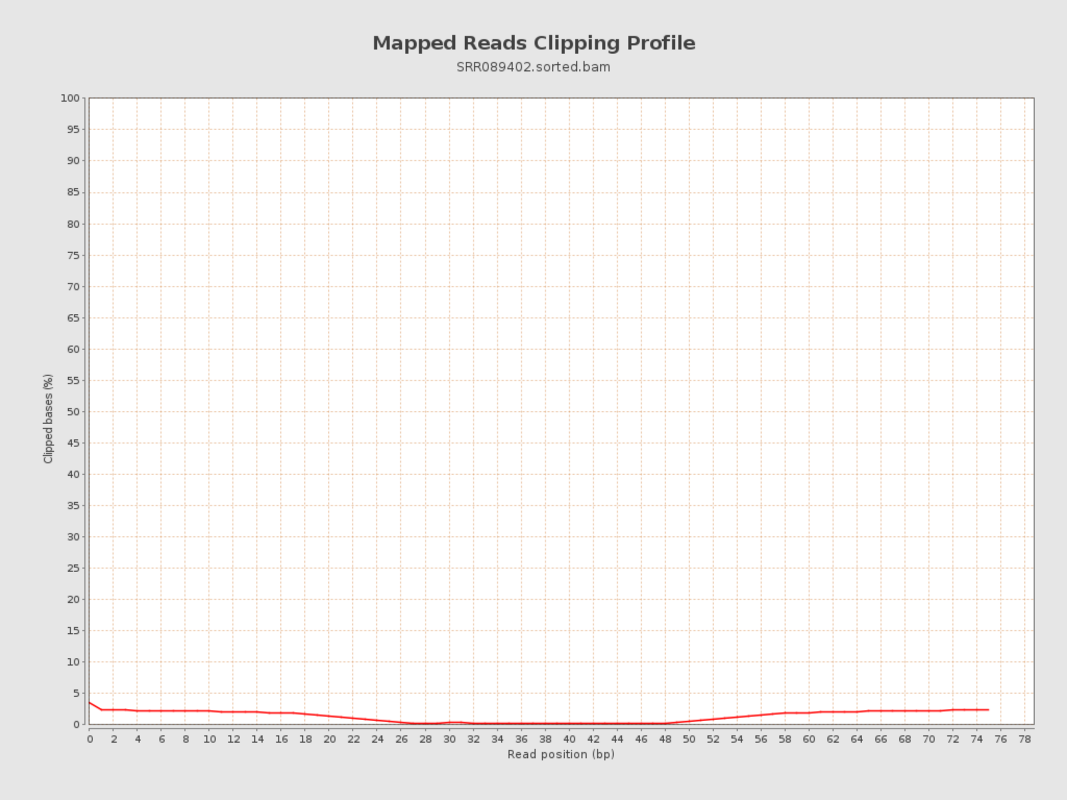
8. Results : Mapped Reads Nucleotide Content



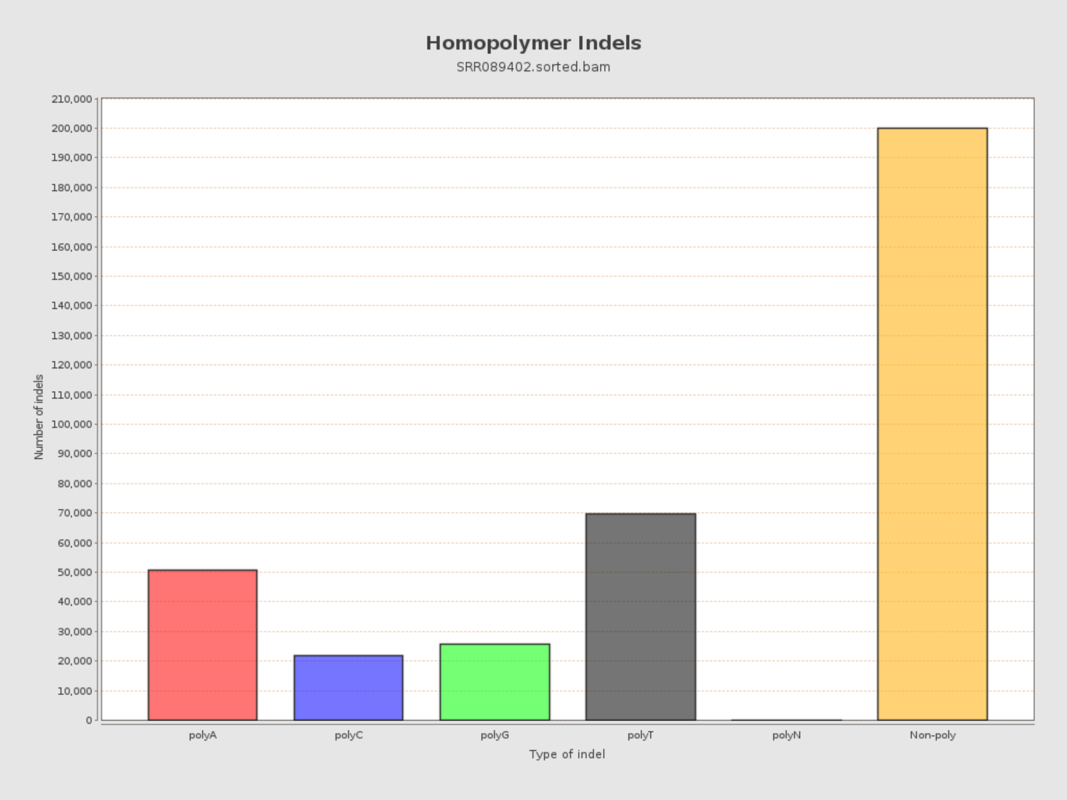
9. Results : Mapped Reads GC-content Distribution



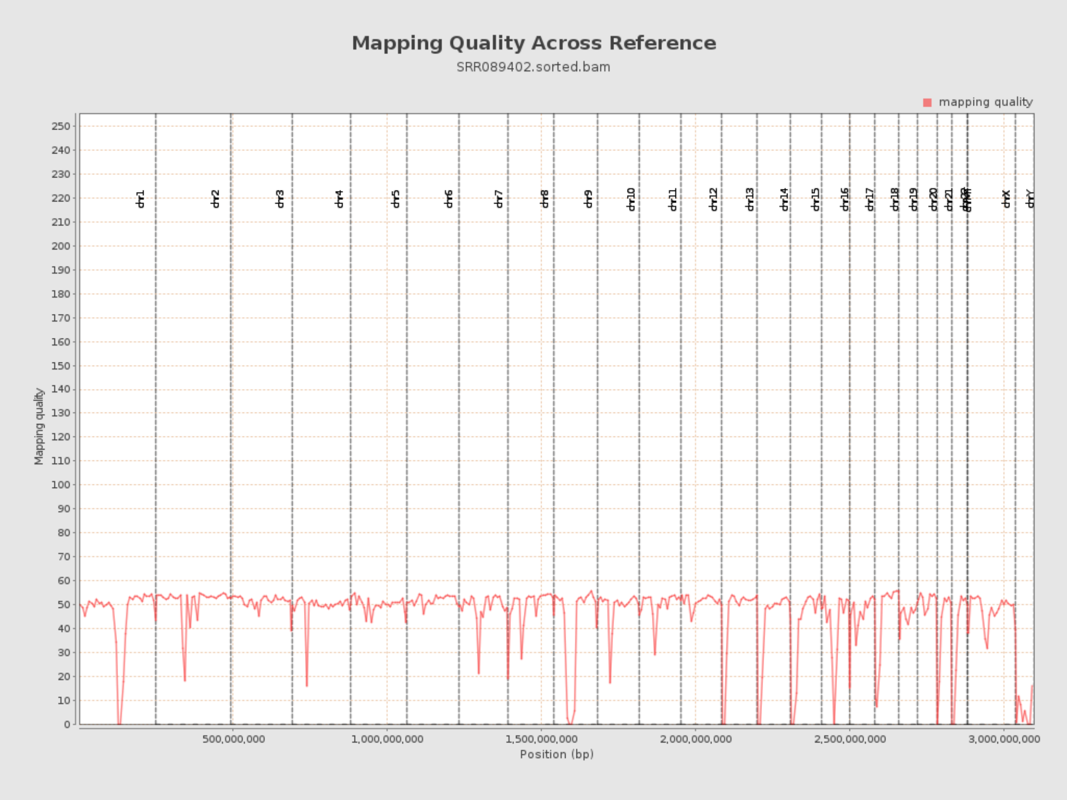
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram