Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 15:17:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089593.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_SRR089593 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089593.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 15:17:22 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089593.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	25,130,779
Mapped reads	21,642,471 / 86.12%
Unmapped reads	3,488,308 / 13.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	898 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,002,178 / 7.97%
Duplication rate	6.73%
Clipped reads	2,293,715 / 9.13%

2.2. ACGT Content

Number/percentage of A's	312,648,557 / 30.74%
Number/percentage of C's	205,564,426 / 20.21%
Number/percentage of T's	274,744,482 / 27.01%
Number/percentage of G's	223,878,564 / 22.01%
Number/percentage of N's	269,954 / 0.03%
GC Percentage	42.22%

2.3. Coverage

Mean	0.3286

Standard Deviation	1.8975

2.4. Mapping Quality

Mean Mapping Quality	42.88

2.5. Mismatches and indels

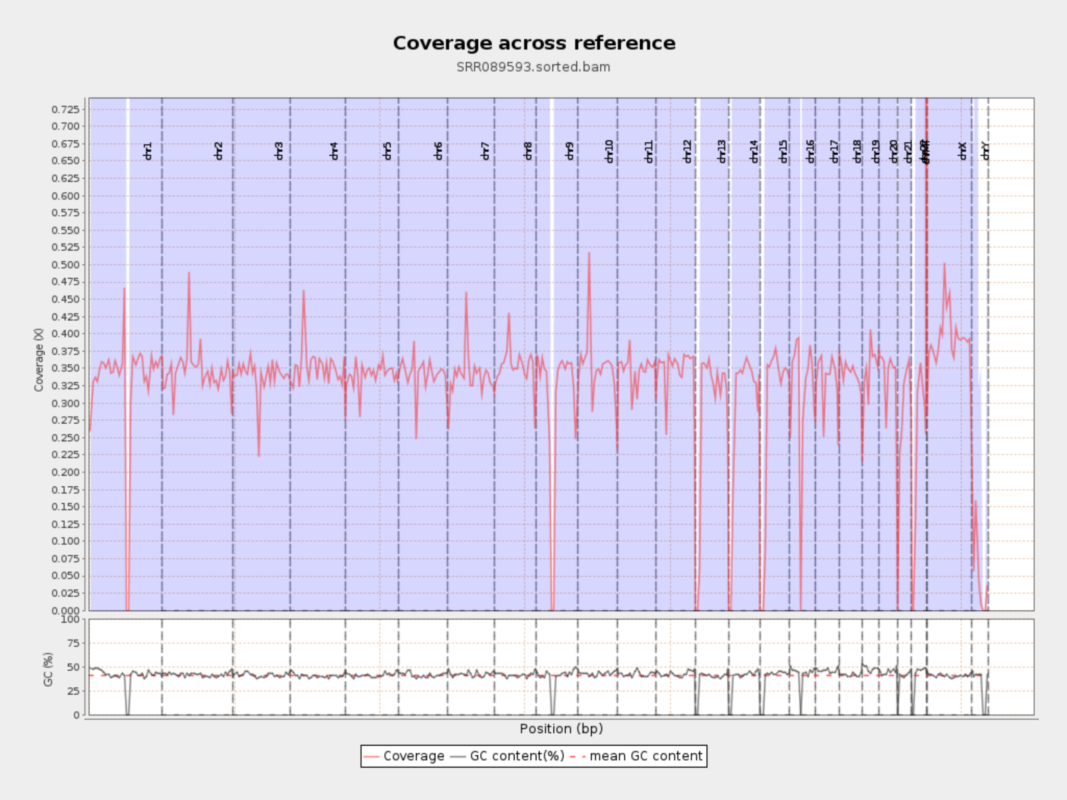
General error rate	0.45%
Mismatches	4,472,842
Insertions	42,203
Mapped reads with at least one insertion	0.19%
Deletions	134,909
Mapped reads with at least one deletion	0.62%
Homopolymer indels	44.67%

2.6. Chromosome stats

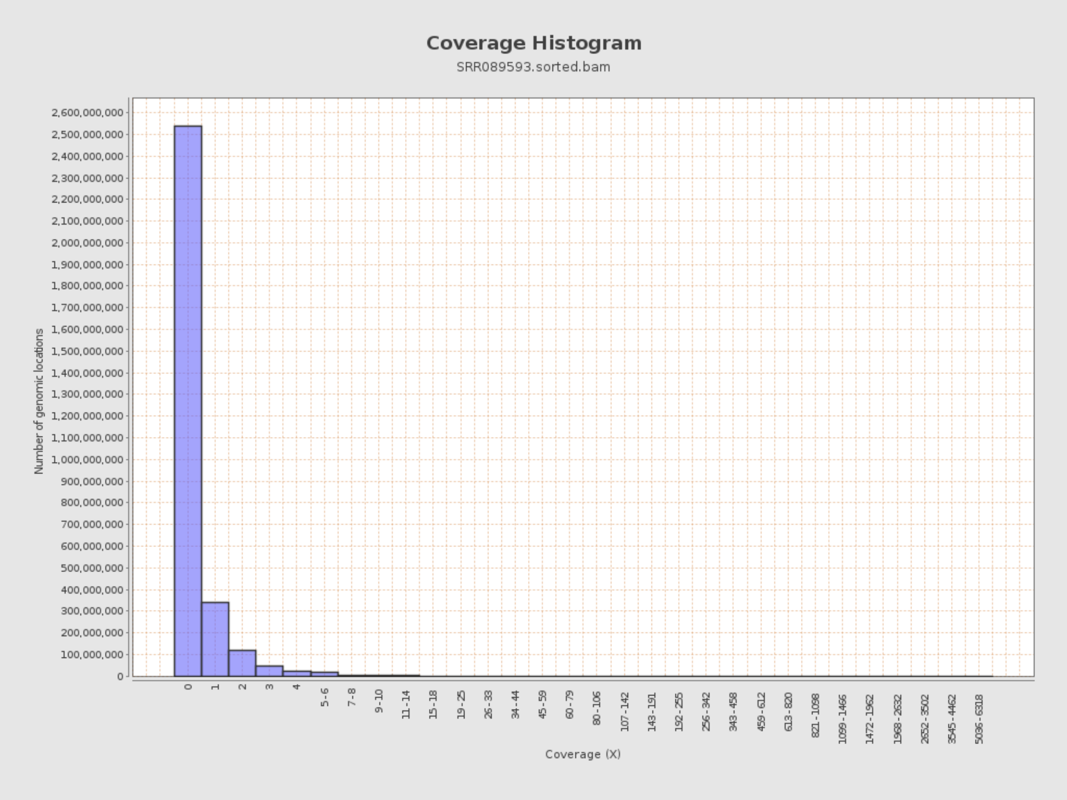
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	81959969	0.3288	3.3445
chr2	243199373	84480022	0.3474	2.0546
chr3	198022430	67147233	0.3391	0.9914
chr4	191154276	67416044	0.3527	1.1867
chr5	180915260	61800749	0.3416	1.0112
chr6	171115067	58593912	0.3424	1.2502
chr7	159138663	54431493	0.342	2.3765

chr8	146364022	51637572	0.3528	3.5732
chr9	141213431	42358940	0.3	1.6567
chr10	135534747	48243083	0.3559	2.0094
chr11	135006516	46761085	0.3464	1.6126
chr12	133851895	46925259	0.3506	1.0798
chr13	115169878	32399064	0.2813	0.895
chr14	107349540	30650647	0.2855	1.1613
chr15	102531392	28994983	0.2828	0.9029
chr16	90354753	28439405	0.3148	1.1549
chr17	81195210	26995131	0.3325	1.2351
chr18	78077248	26907932	0.3446	2.8453
chr19	59128983	20557346	0.3477	2.777
chr20	63025520	21404704	0.3396	1.1119
chr21	48129895	13235130	0.275	1.2605
chr22	51304566	11441438	0.223	0.8087
chrMT	16571	271124	16.3614	13.0112
chrX	155270560	61093655	0.3935	1.3992
chrY	59373566	3163613	0.0533	0.8849

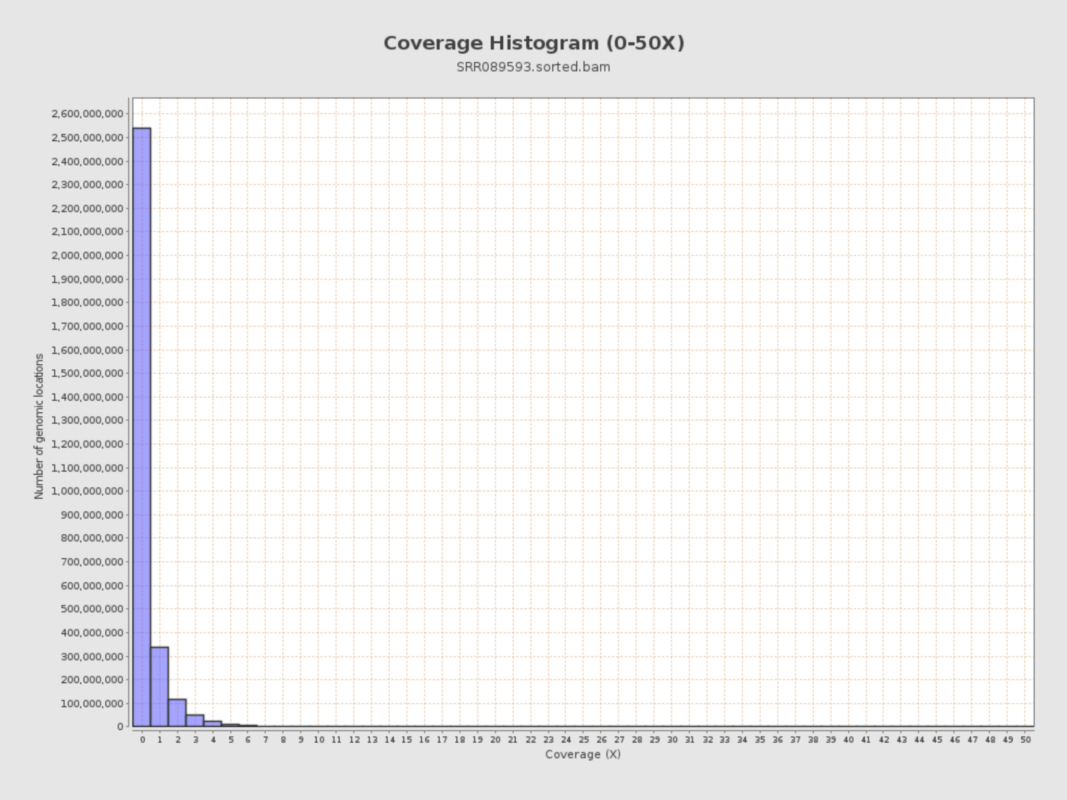
3. Results : Coverage across reference



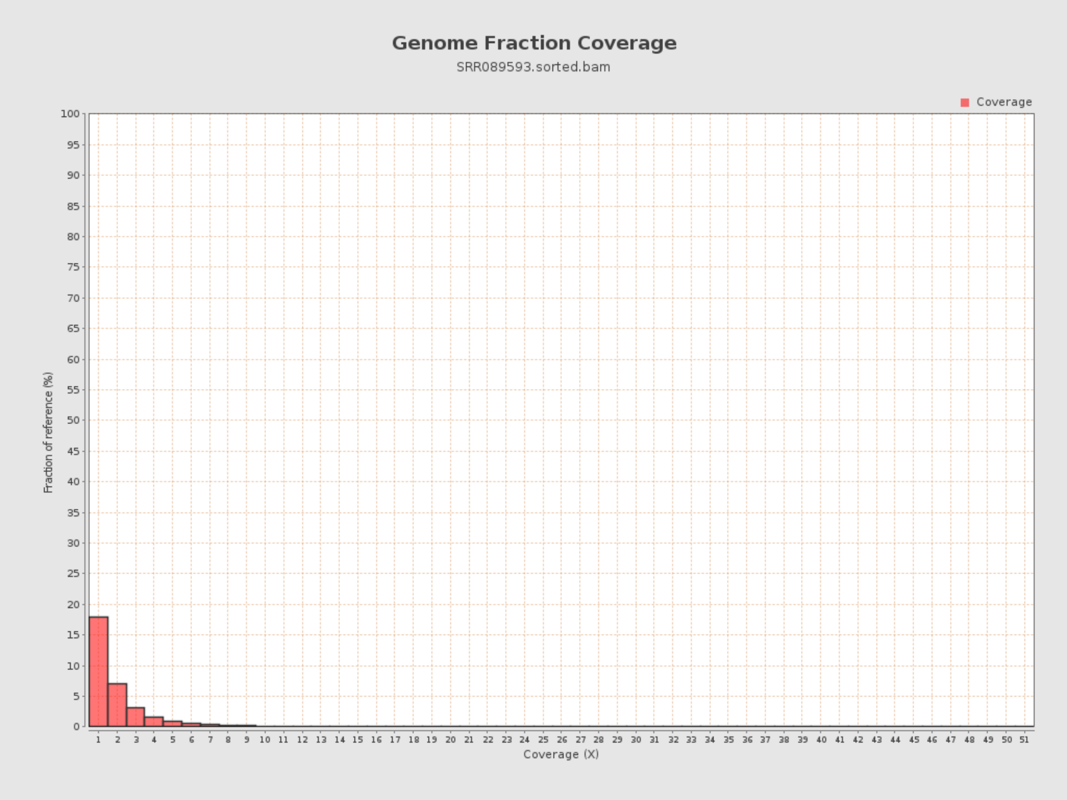
4. Results : Coverage Histogram



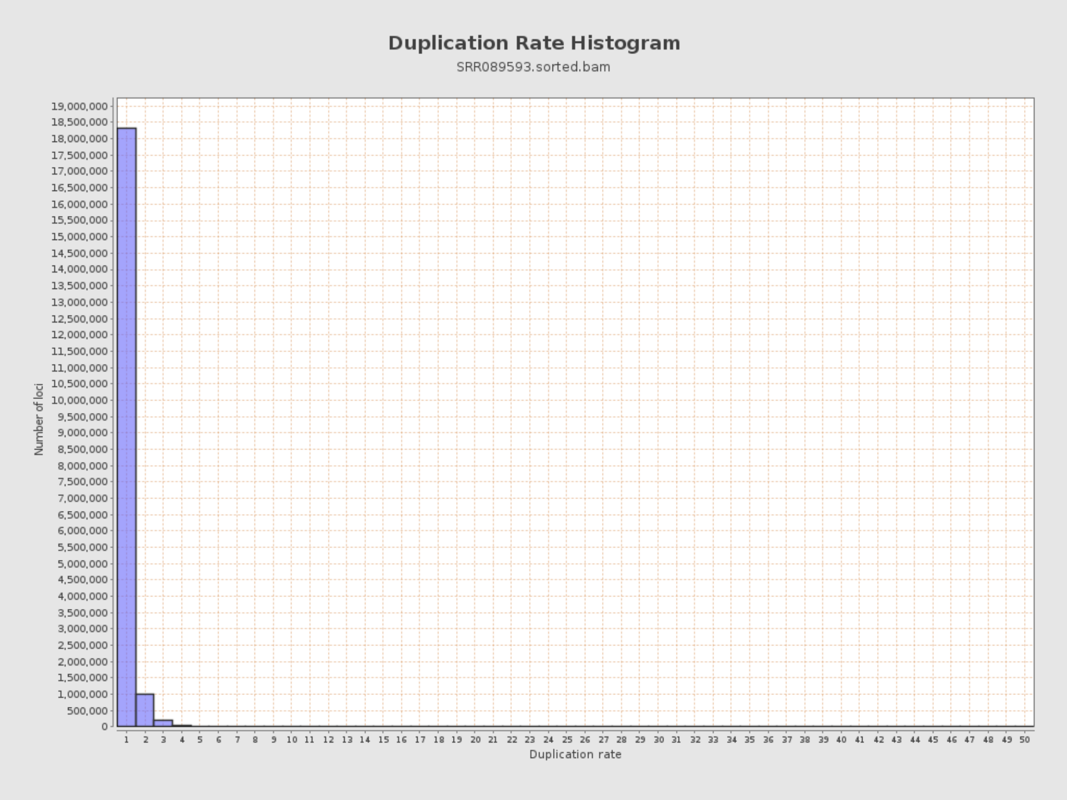
5. Results : Coverage Histogram (0-50X)



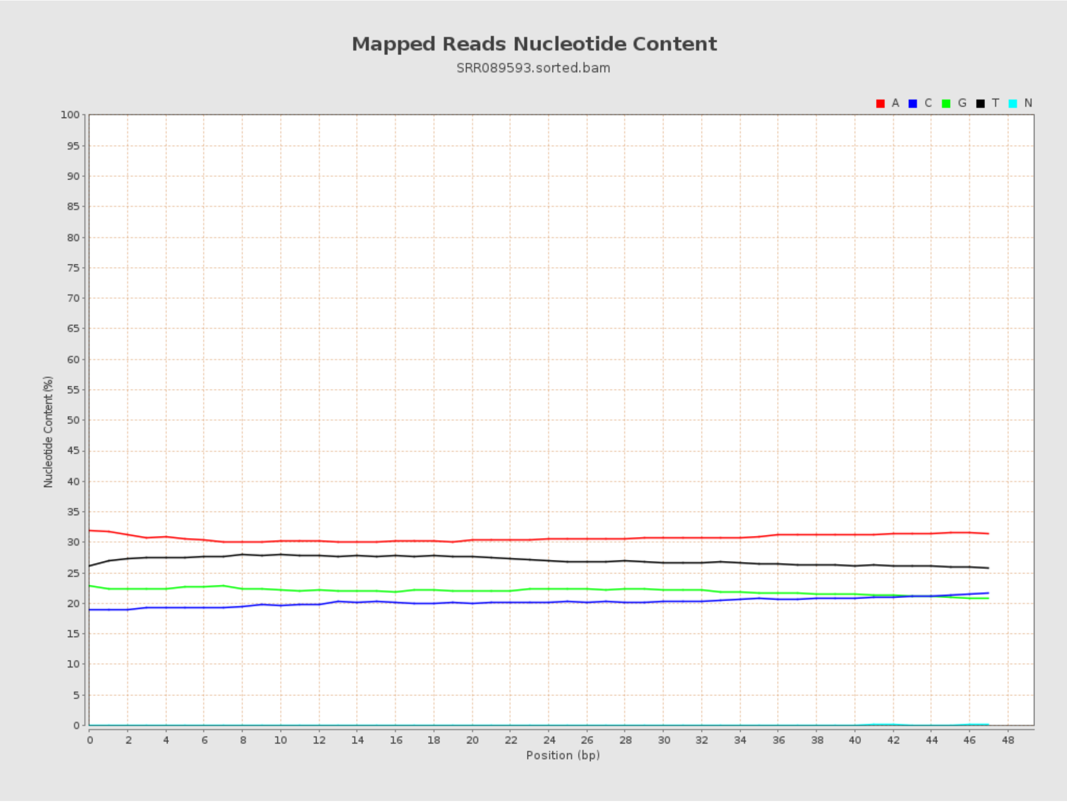
6. Results : Genome Fraction Coverage



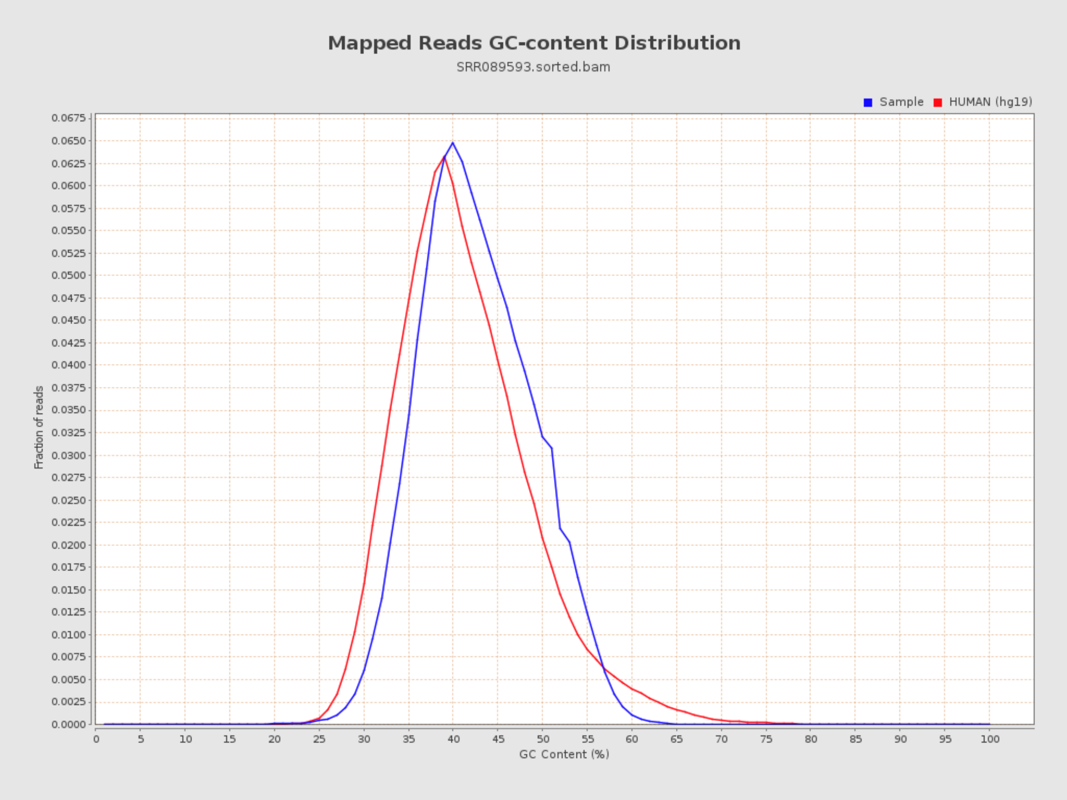
7. Results : Duplication Rate Histogram



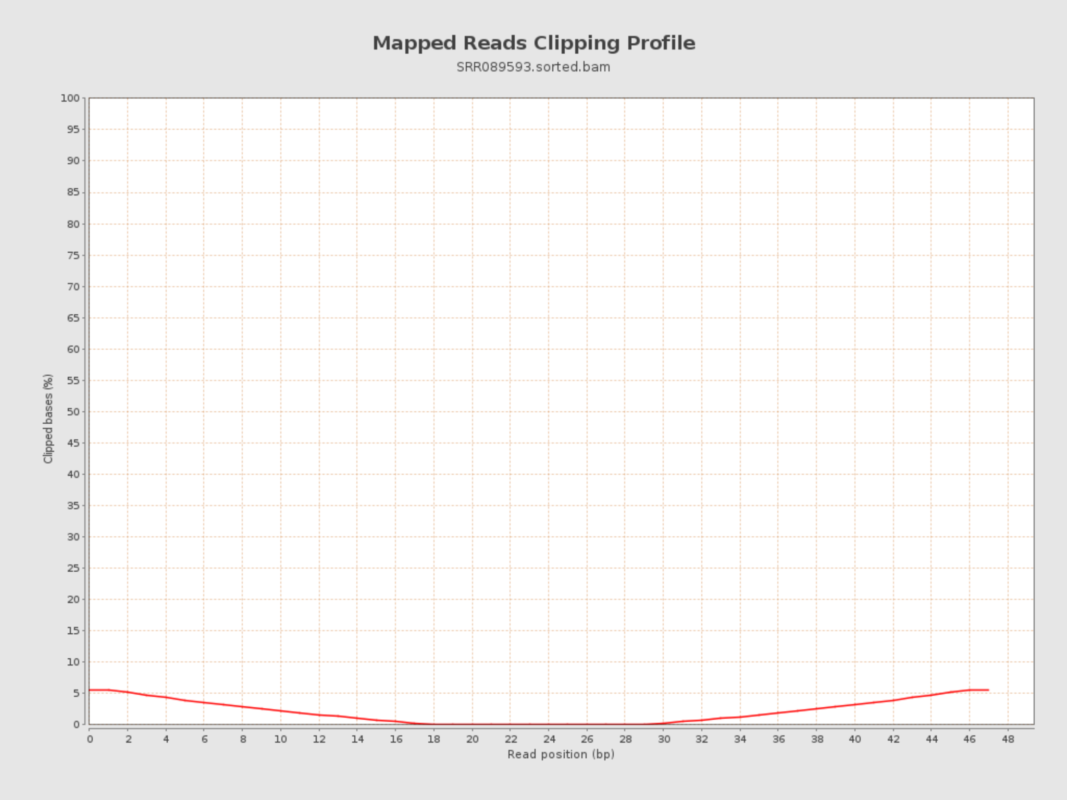
8. Results : Mapped Reads Nucleotide Content



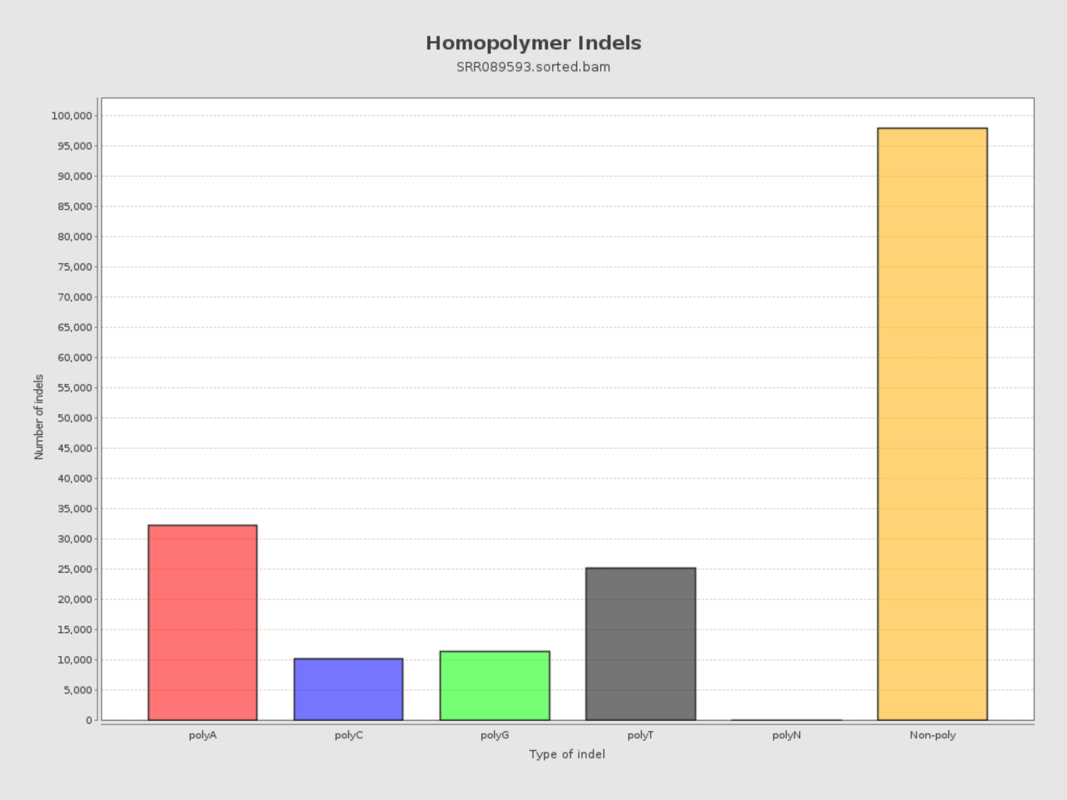
9. Results : Mapped Reads GC-content Distribution



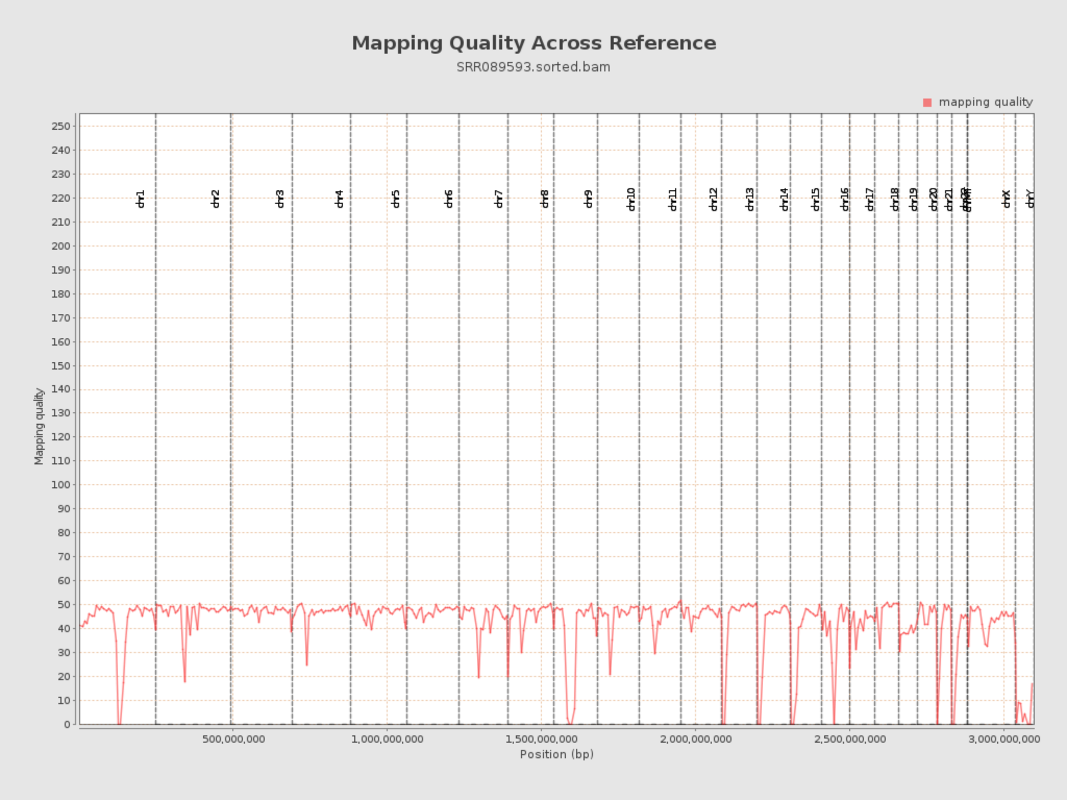
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram