Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 23:45:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089711.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_SRR089711 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089711.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 23:45:08 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089711.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,638,886
Mapped reads	18,300,096 / 84.57%
Unmapped reads	3,338,790 / 15.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	927 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	4,057,363 / 18.75%
Duplication rate	13%
Clipped reads	1,241,419 / 5.74%

2.2. ACGT Content

Number/percentage of A's	253,124,640 / 29.2%
Number/percentage of C's	177,260,834 / 20.45%
Number/percentage of T's	251,813,083 / 29.05%
Number/percentage of G's	184,582,692 / 21.29%
Number/percentage of N's	65,181 / 0.01%
GC Percentage	41.74%

2.3. Coverage

Mean	0.2801

Standard Deviation	1.9877

2.4. Mapping Quality

Mean Mapping Quality	45.14

2.5. Mismatches and indels

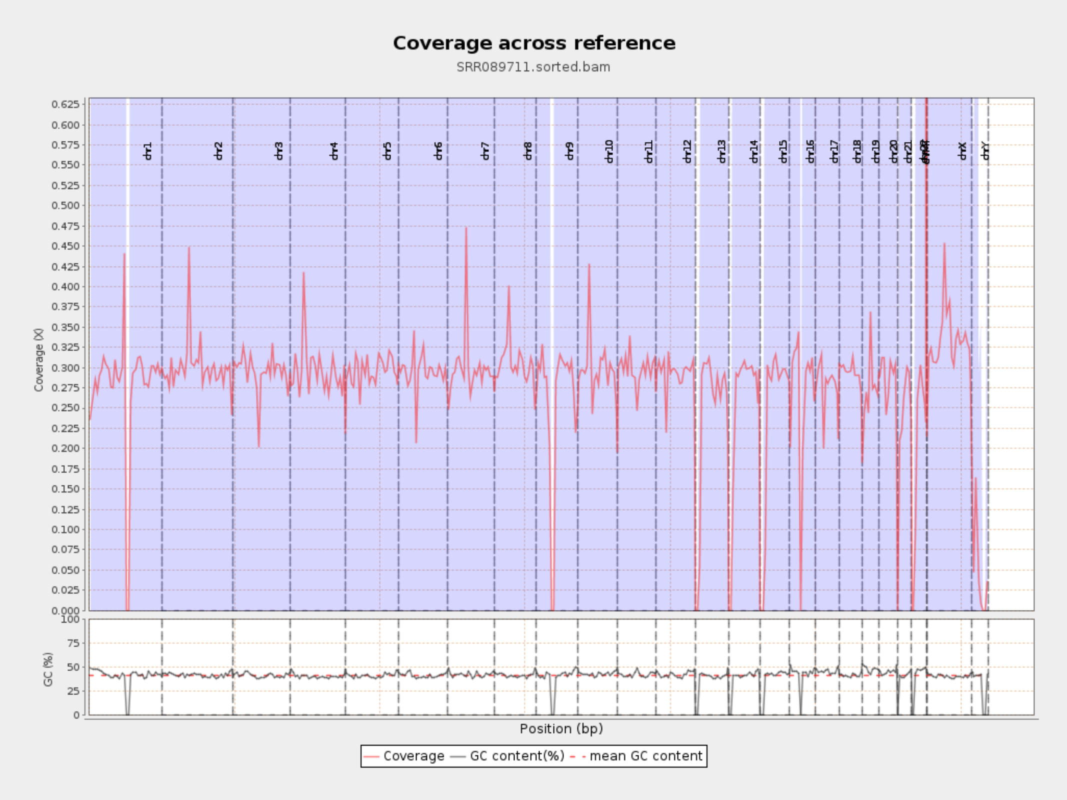
General error rate	0.46%
Mismatches	3,955,446
Insertions	34,347
Mapped reads with at least one insertion	0.19%
Deletions	109,019
Mapped reads with at least one deletion	0.59%
Homopolymer indels	47.06%

2.6. Chromosome stats

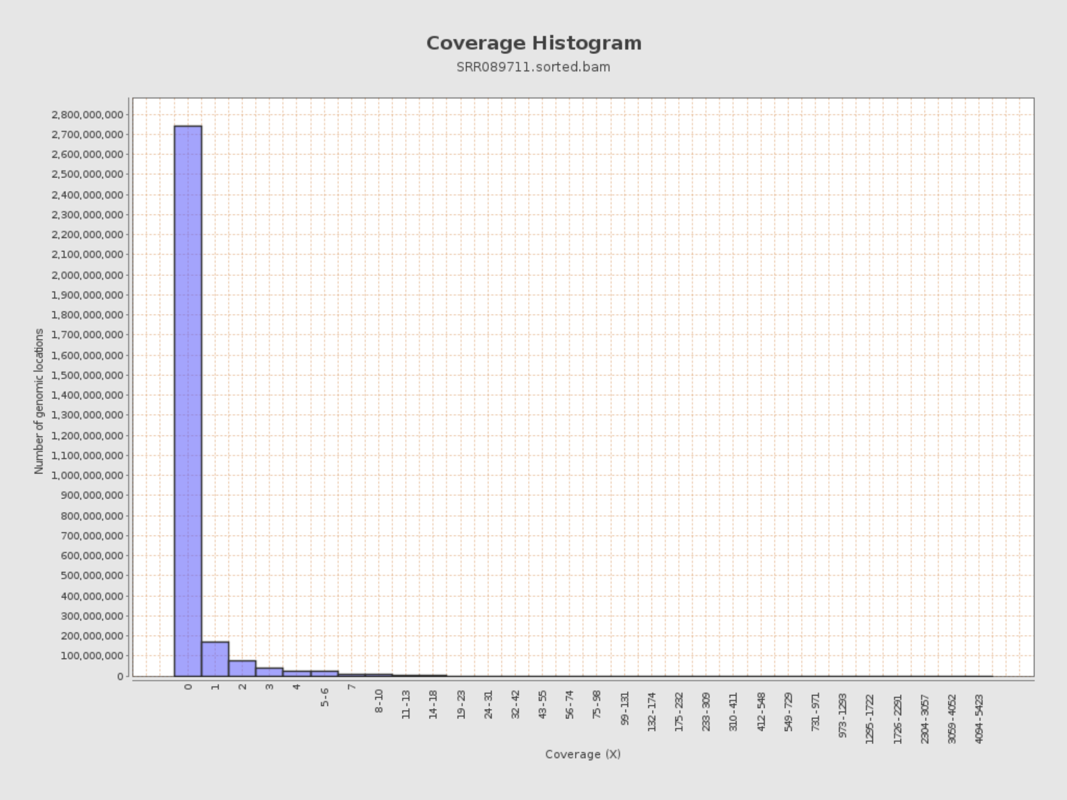
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	68950330	0.2766	3.8669
chr2	243199373	73229798	0.3011	1.8699
chr3	198022430	58388821	0.2949	1.1012
chr4	191154276	56569341	0.2959	1.27
chr5	180915260	53582135	0.2962	1.1338
chr6	171115067	50429240	0.2947	1.2821
chr7	159138663	47886132	0.3009	2.724

chr8	146364022	44609124	0.3048	2.6589
chr9	141213431	36334891	0.2573	1.7179
chr10	135534747	40624833	0.2997	1.7798
chr11	135006516	39980617	0.2961	1.9076
chr12	133851895	39147107	0.2925	1.2261
chr13	115169878	27348450	0.2375	0.9908
chr14	107349540	26420843	0.2461	1.096
chr15	102531392	24347587	0.2375	1.0022
chr16	90354753	24005407	0.2657	1.1732
chr17	81195210	22369969	0.2755	1.3522
chr18	78077248	23085748	0.2957	3.9134
chr19	59128983	16199242	0.274	2.5971
chr20	63025520	18051735	0.2864	1.2445
chr21	48129895	11164980	0.232	1.288
chr22	51304566	9692662	0.1889	0.8916
chrMT	16571	215453	13.0018	9.9214
chrX	155270560	51539979	0.3319	1.4086
chrY	59373566	2835360	0.0478	1.2261

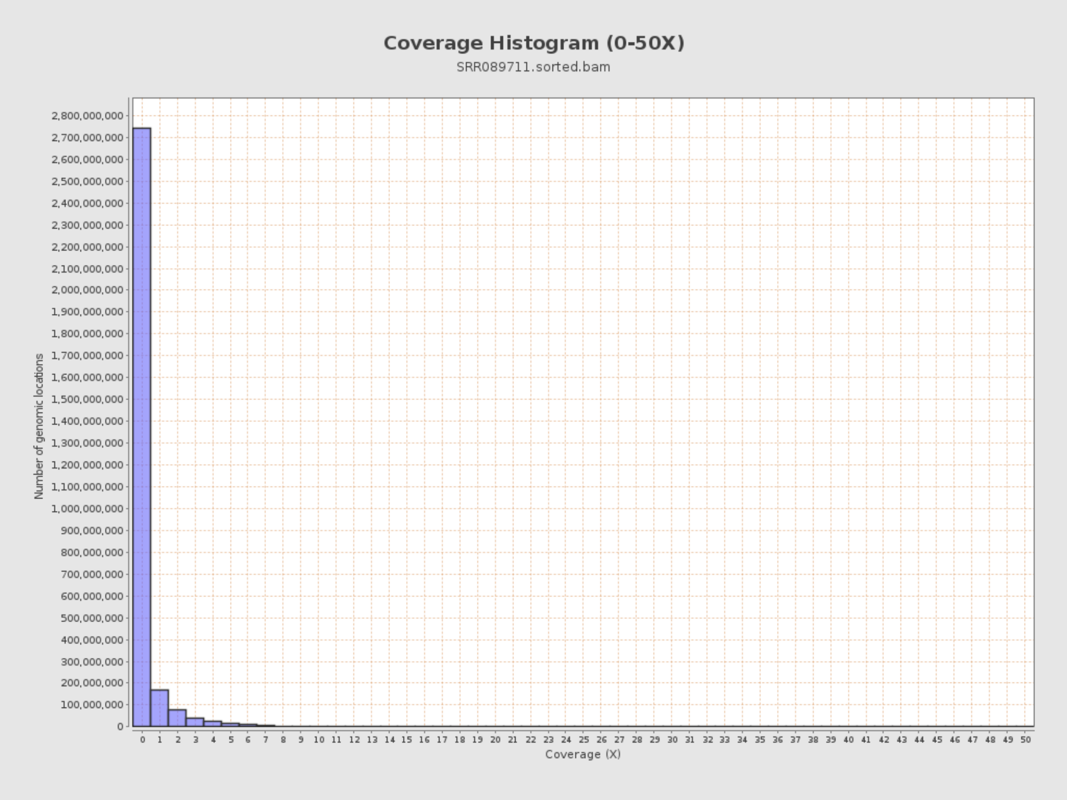
3. Results : Coverage across reference



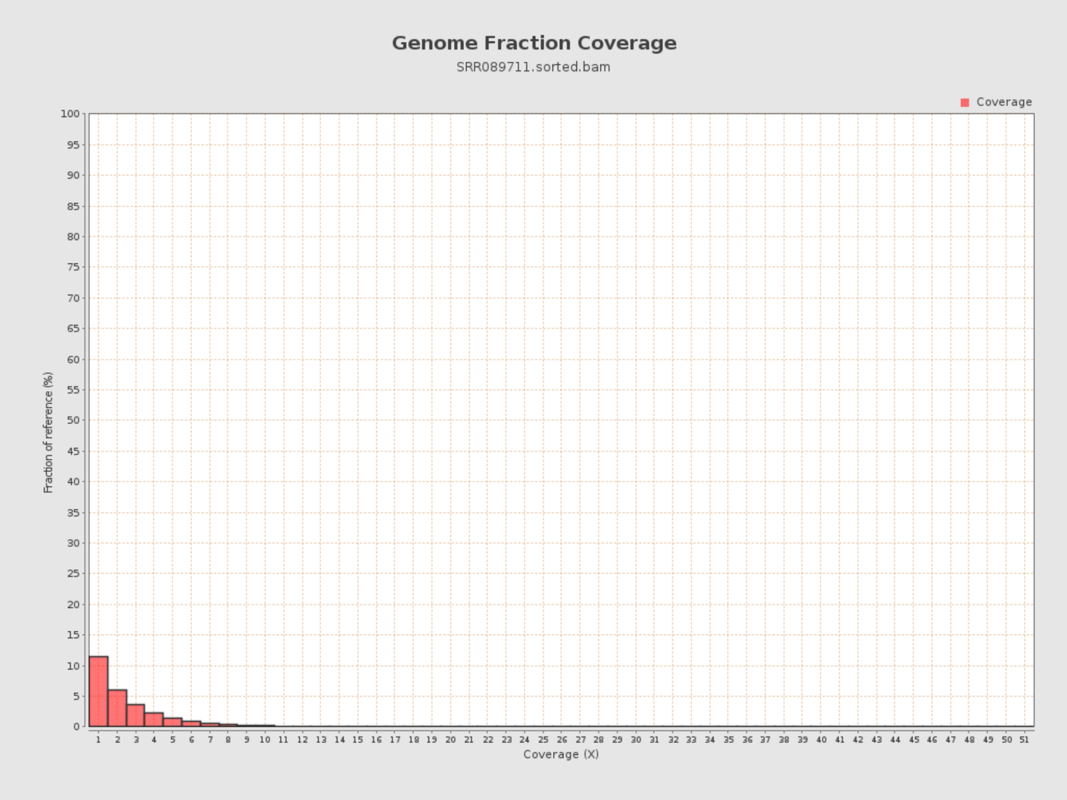
4. Results : Coverage Histogram



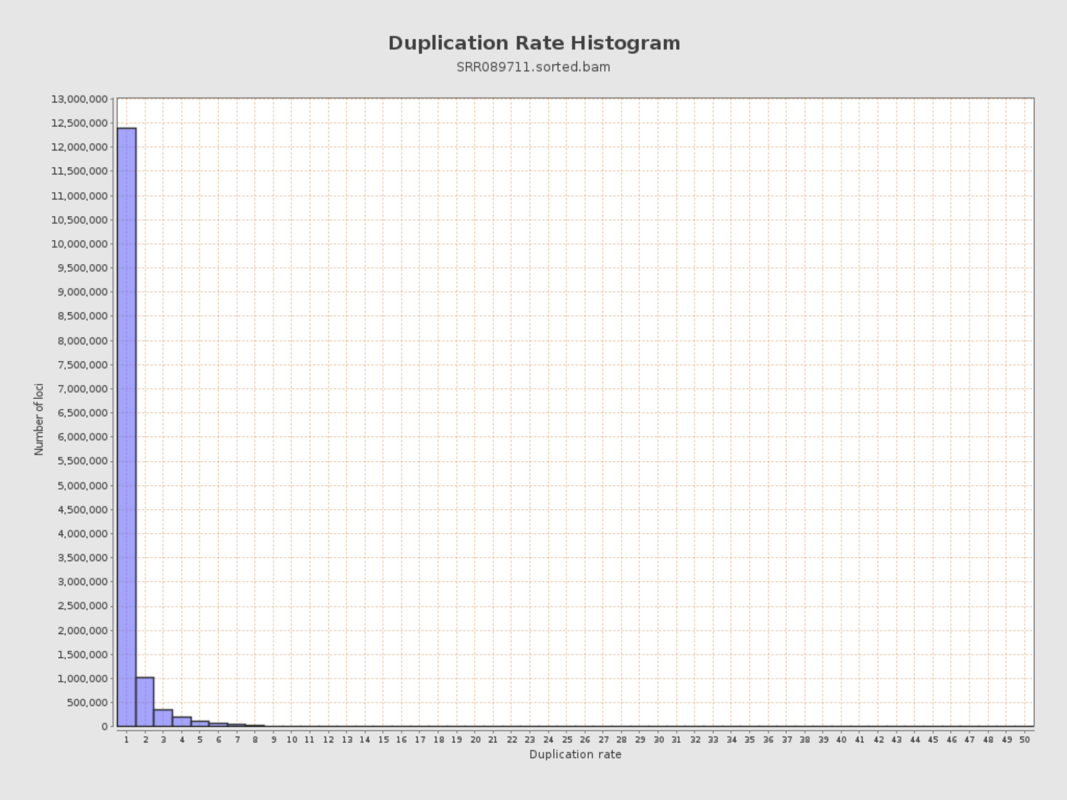
5. Results : Coverage Histogram (0-50X)



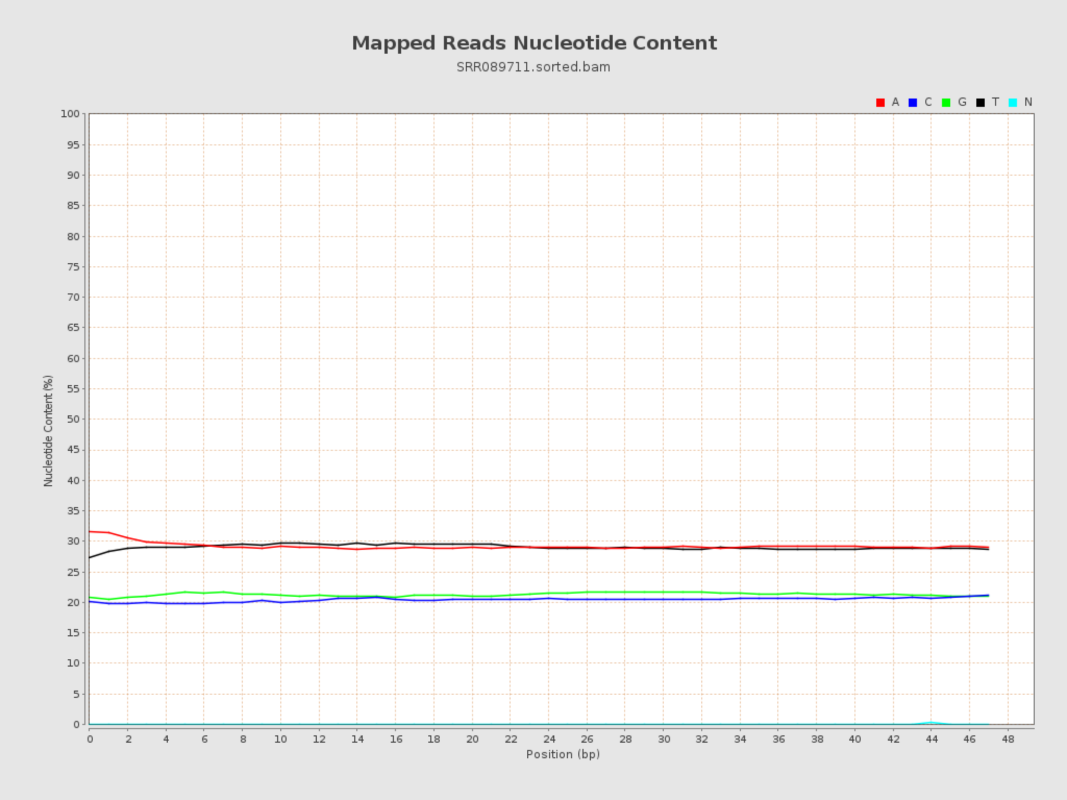
6. Results : Genome Fraction Coverage



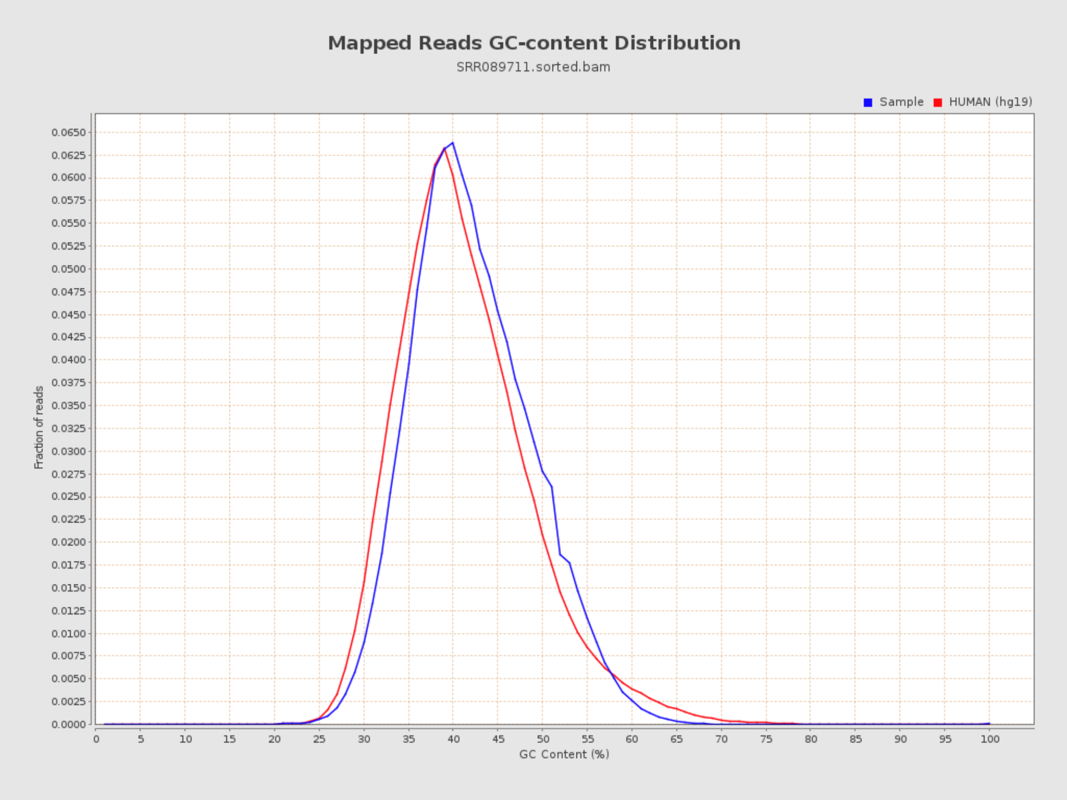
7. Results : Duplication Rate Histogram



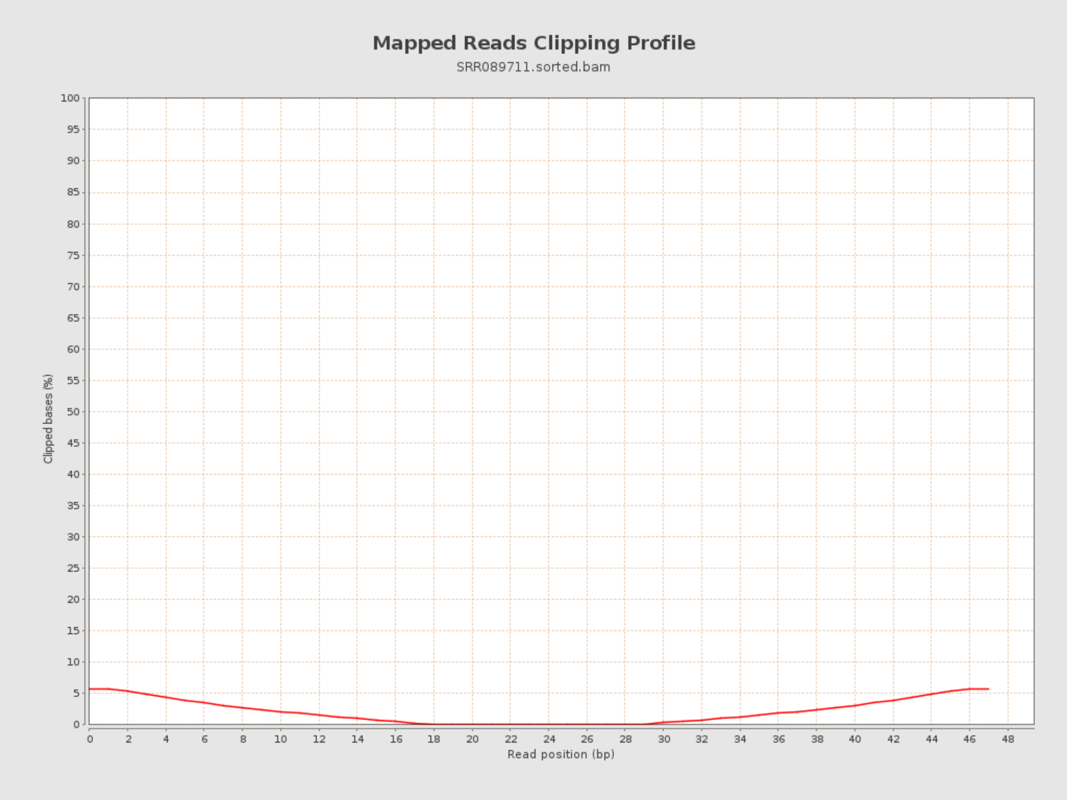
8. Results : Mapped Reads Nucleotide Content



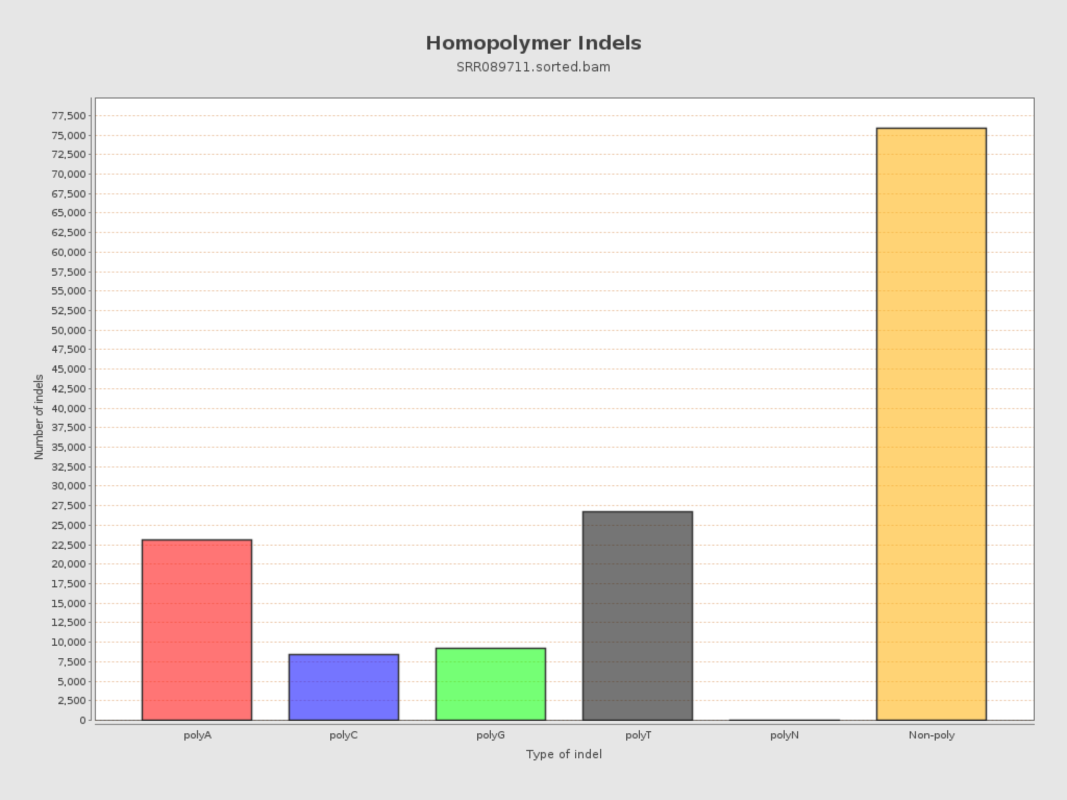
9. Results : Mapped Reads GC-content Distribution



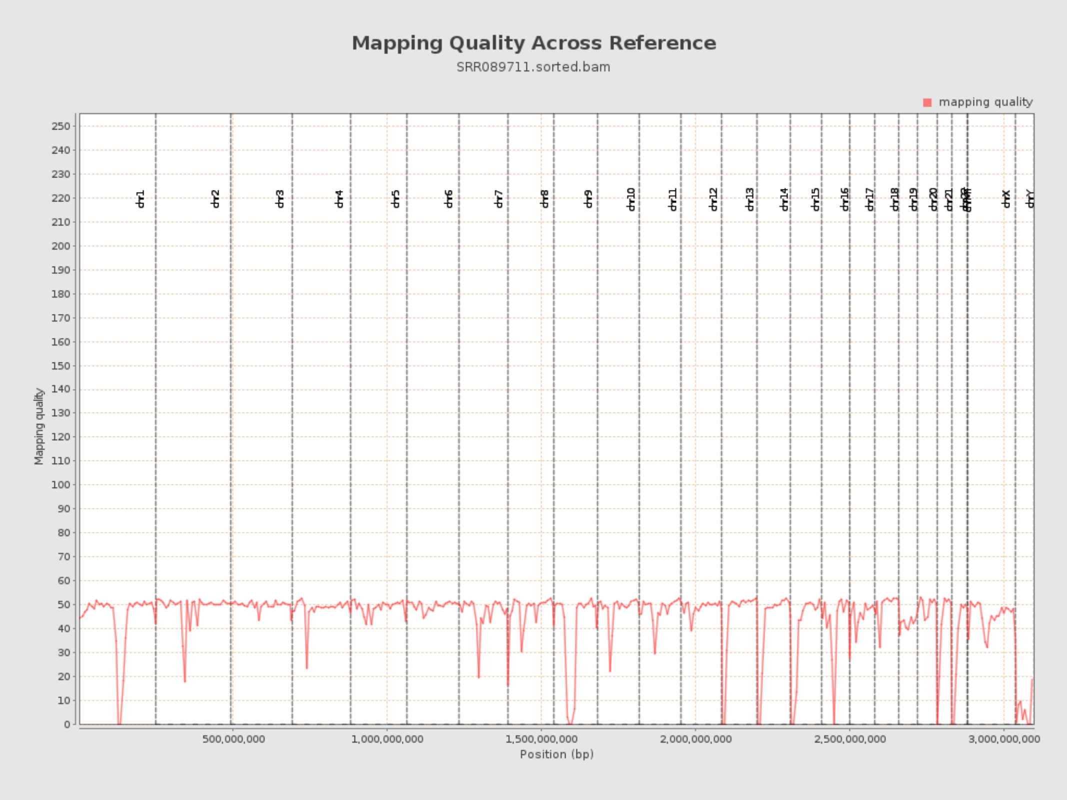
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram