Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 22:27:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089706.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_SRR089706 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089706.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 22:27:34 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089706.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,149,283
Mapped reads	6,073,263 / 74.53%
Unmapped reads	2,076,020 / 25.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	438 / 0.01%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,615,316 / 19.82%
Duplication rate	15.33%
Clipped reads	515,817 / 6.33%

2.2. ACGT Content

Number/percentage of A's	78,397,022 / 27.35%
Number/percentage of C's	61,988,746 / 21.62%
Number/percentage of T's	79,685,724 / 27.8%
Number/percentage of G's	66,596,382 / 23.23%
Number/percentage of N's	7,786 / 0%
GC Percentage	44.85%

2.3. Coverage

Mean	0.0926

Standard Deviation	0.685

2.4. Mapping Quality

Mean Mapping Quality	43.16

2.5. Mismatches and indels

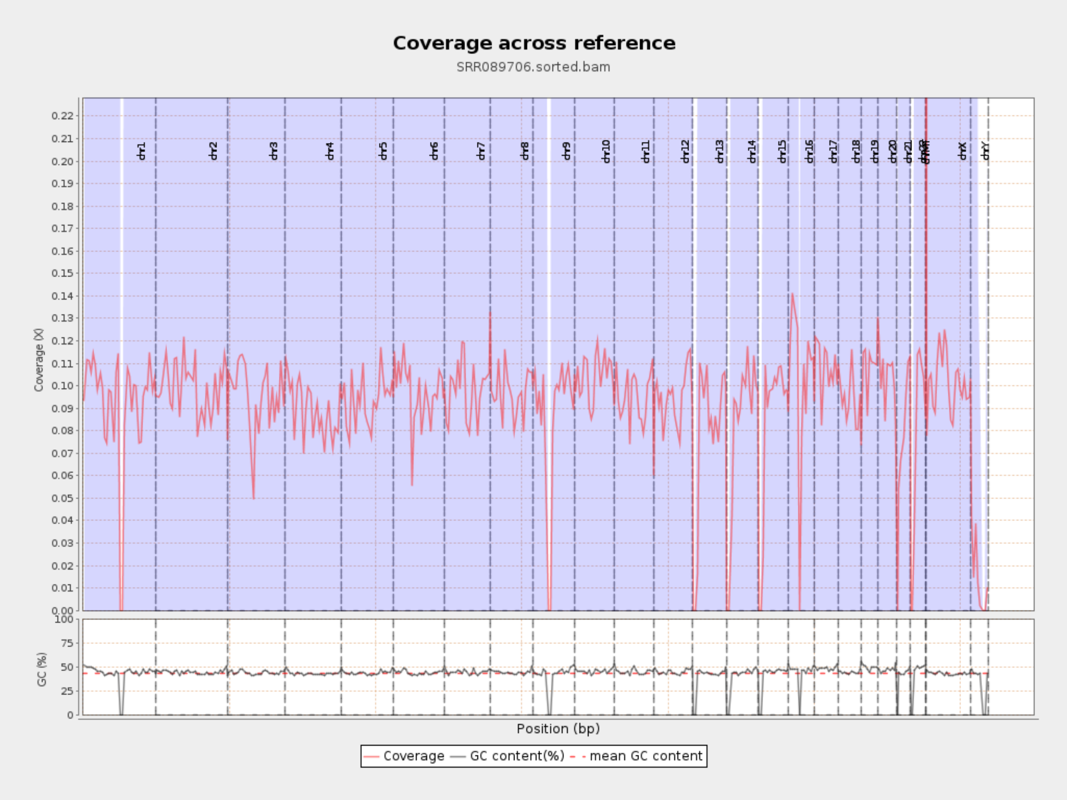
General error rate	0.52%
Mismatches	1,476,005
Insertions	11,278
Mapped reads with at least one insertion	0.19%
Deletions	36,184
Mapped reads with at least one deletion	0.59%
Homopolymer indels	46.19%

2.6. Chromosome stats

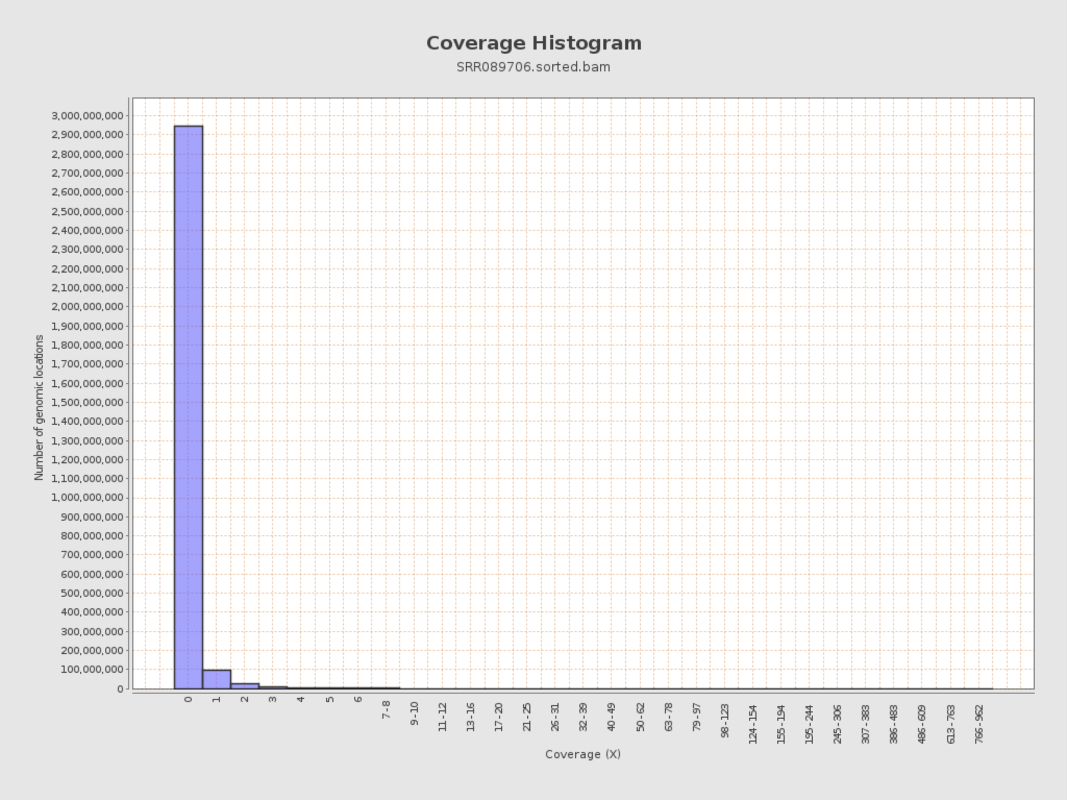
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22863074	0.0917	0.9187
chr2	243199373	24165148	0.0994	0.7089
chr3	198022430	18798728	0.0949	0.6052
chr4	191154276	17063858	0.0893	0.5955
chr5	180915260	16959100	0.0937	0.6043
chr6	171115067	16545428	0.0967	0.6794
chr7	159138663	15621942	0.0982	0.7695

chr8	146364022	14159470	0.0967	0.648
chr9	141213431	12060598	0.0854	0.641
chr10	135534747	14113758	0.1041	0.7201
chr11	135006516	12801122	0.0948	0.6687
chr12	133851895	12820965	0.0958	0.6246
chr13	115169878	9021227	0.0783	0.5576
chr14	107349540	8799366	0.082	0.5658
chr15	102531392	8313443	0.0811	0.5584
chr16	90354753	9297233	0.1029	0.6596
chr17	81195210	8863209	0.1092	0.6732
chr18	78077248	7339259	0.094	1.0457
chr19	59128983	6384337	0.108	0.7937
chr20	63025520	6546631	0.1039	0.6976
chr21	48129895	3698655	0.0768	0.578
chr22	51304566	3883845	0.0757	0.561
chrMT	16571	86969	5.2483	5.325
chrX	155270560	15705403	0.1011	0.6658
chrY	59373566	817224	0.0138	0.2617

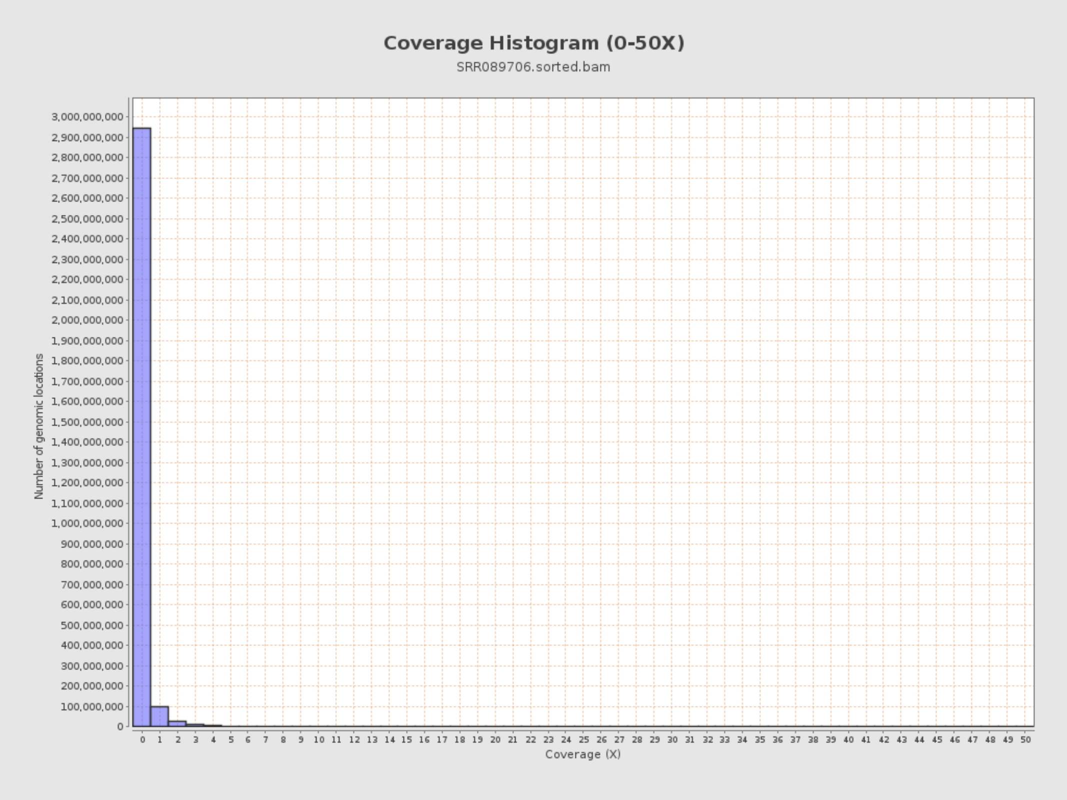
3. Results : Coverage across reference



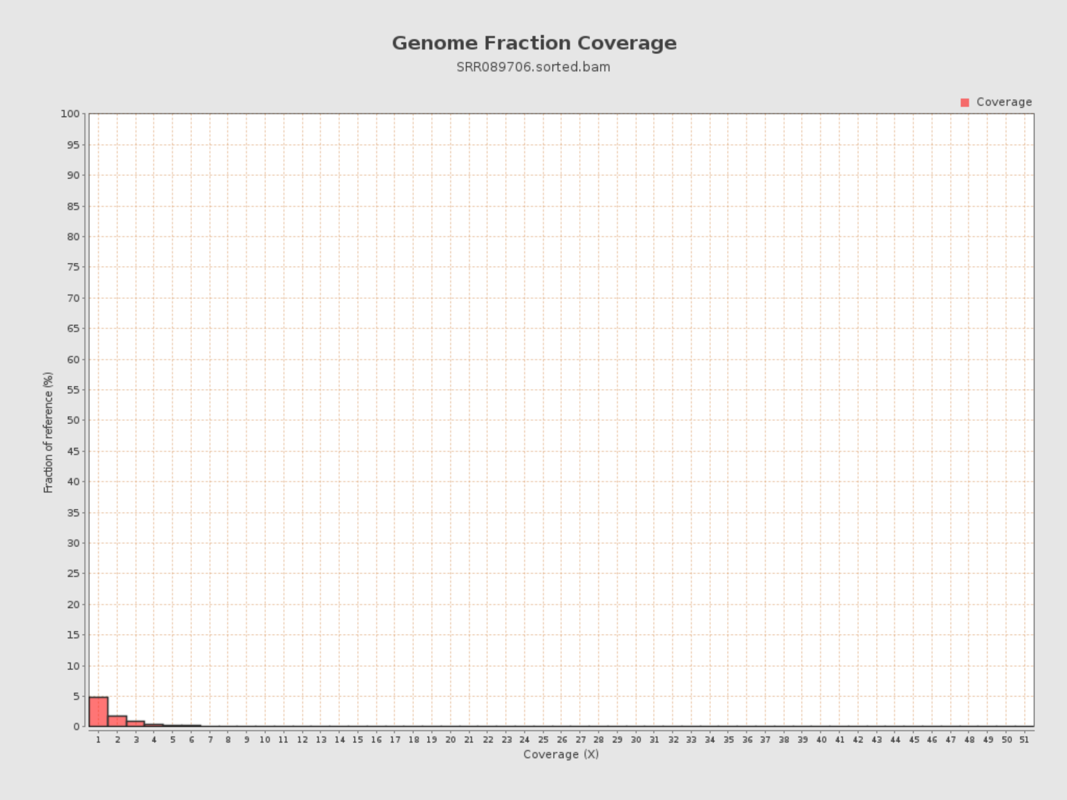
4. Results : Coverage Histogram



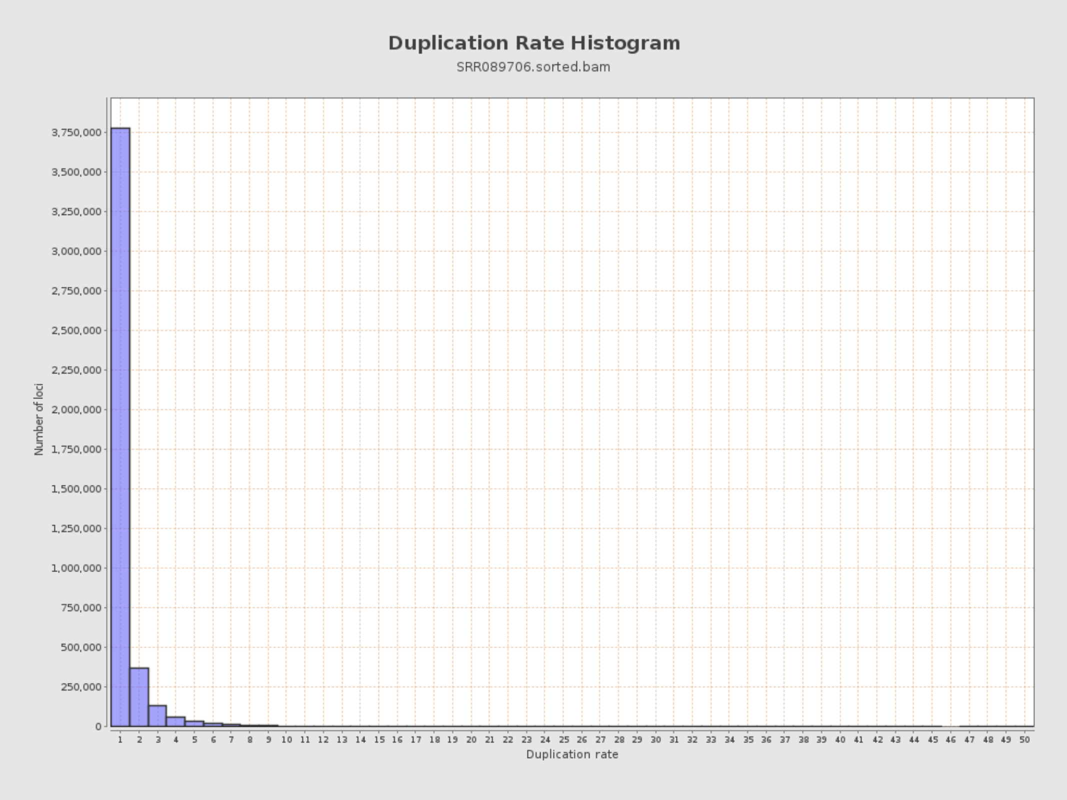
5. Results : Coverage Histogram (0-50X)



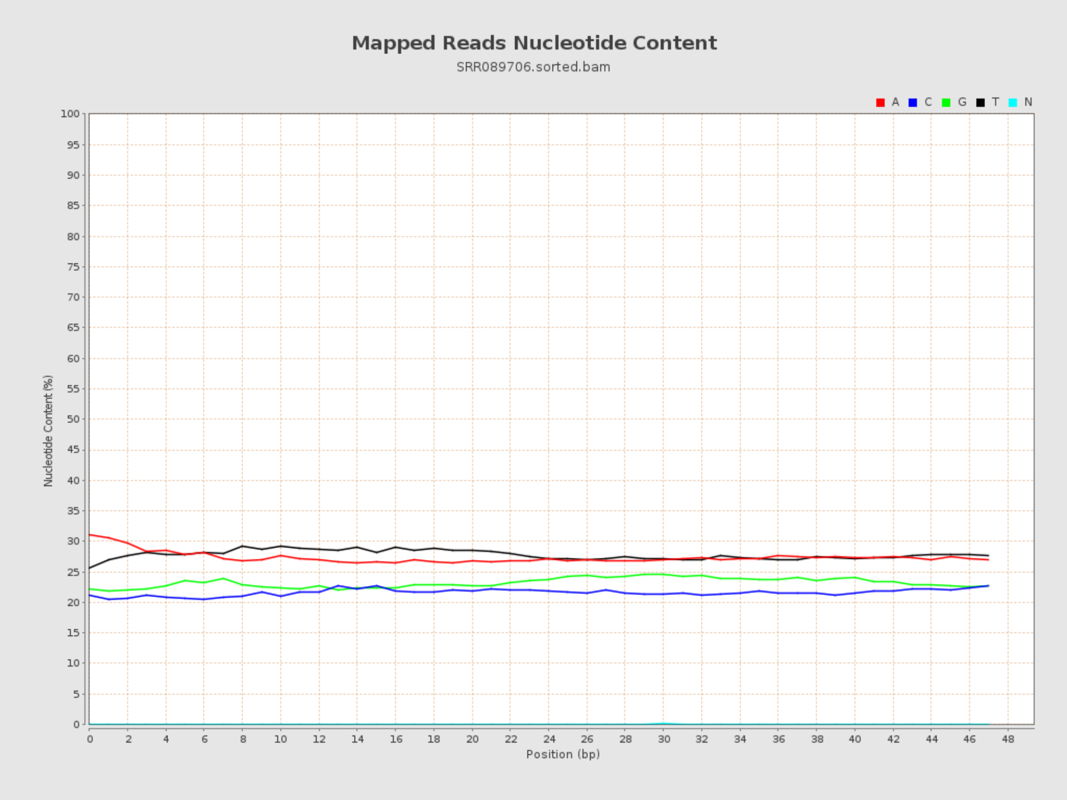
6. Results : Genome Fraction Coverage



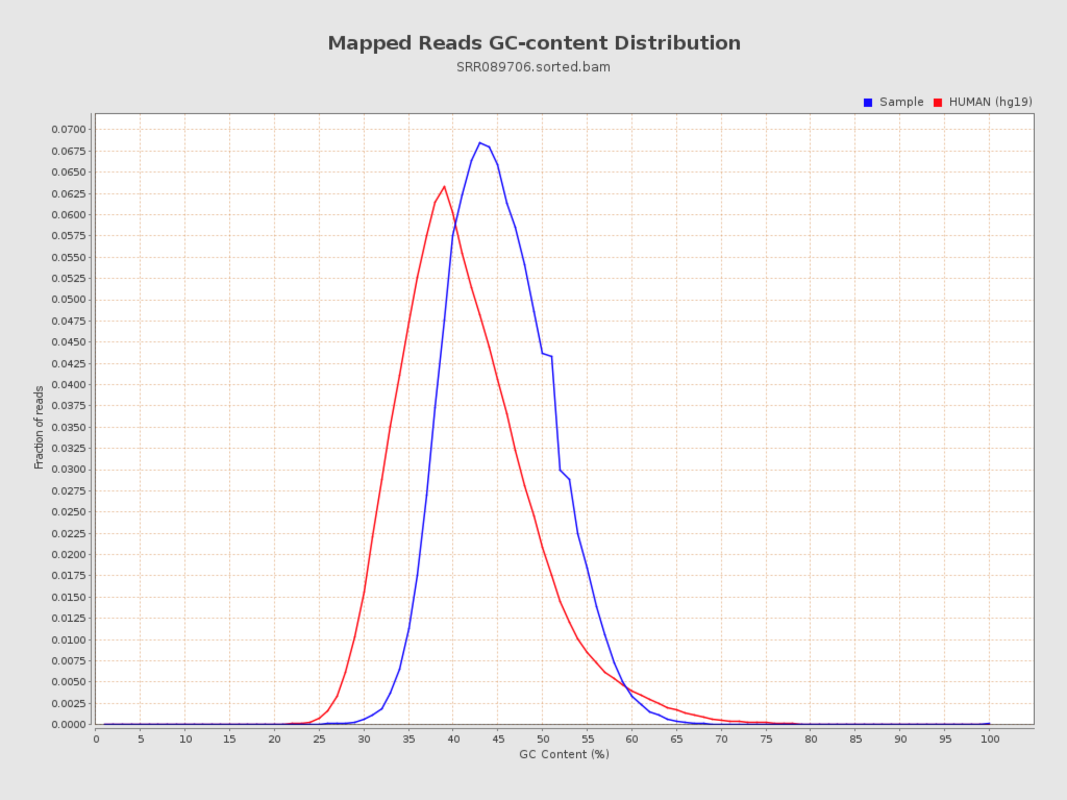
7. Results : Duplication Rate Histogram



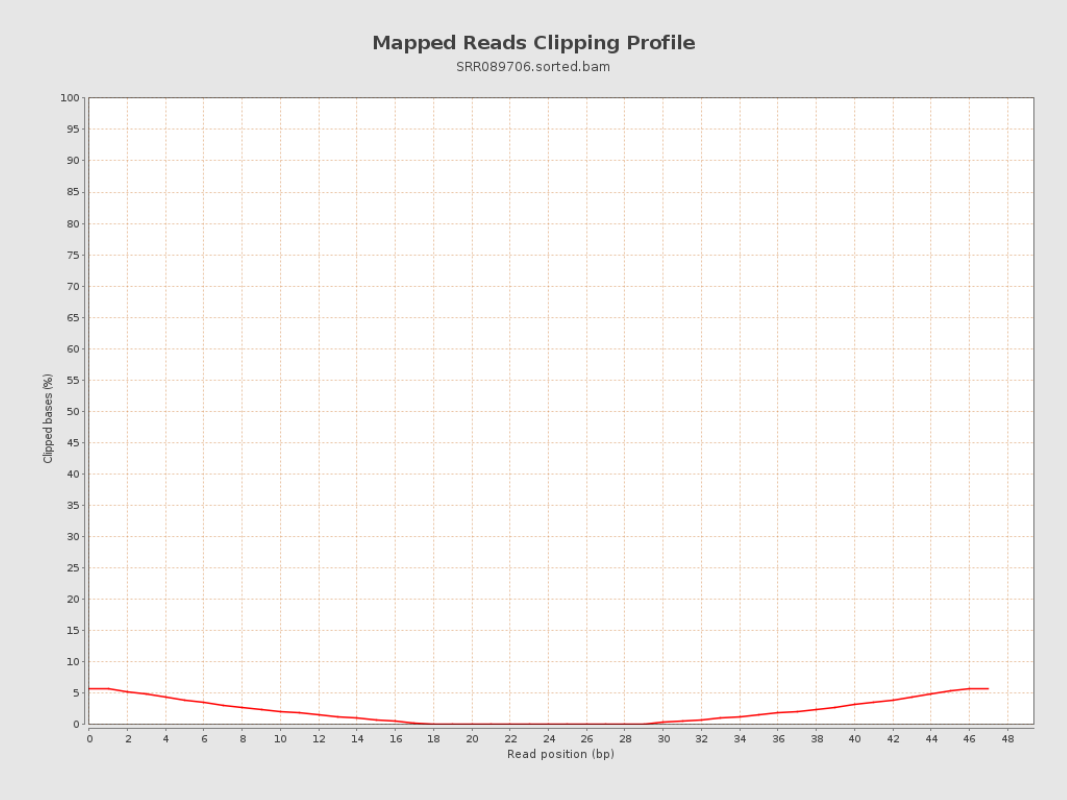
8. Results : Mapped Reads Nucleotide Content



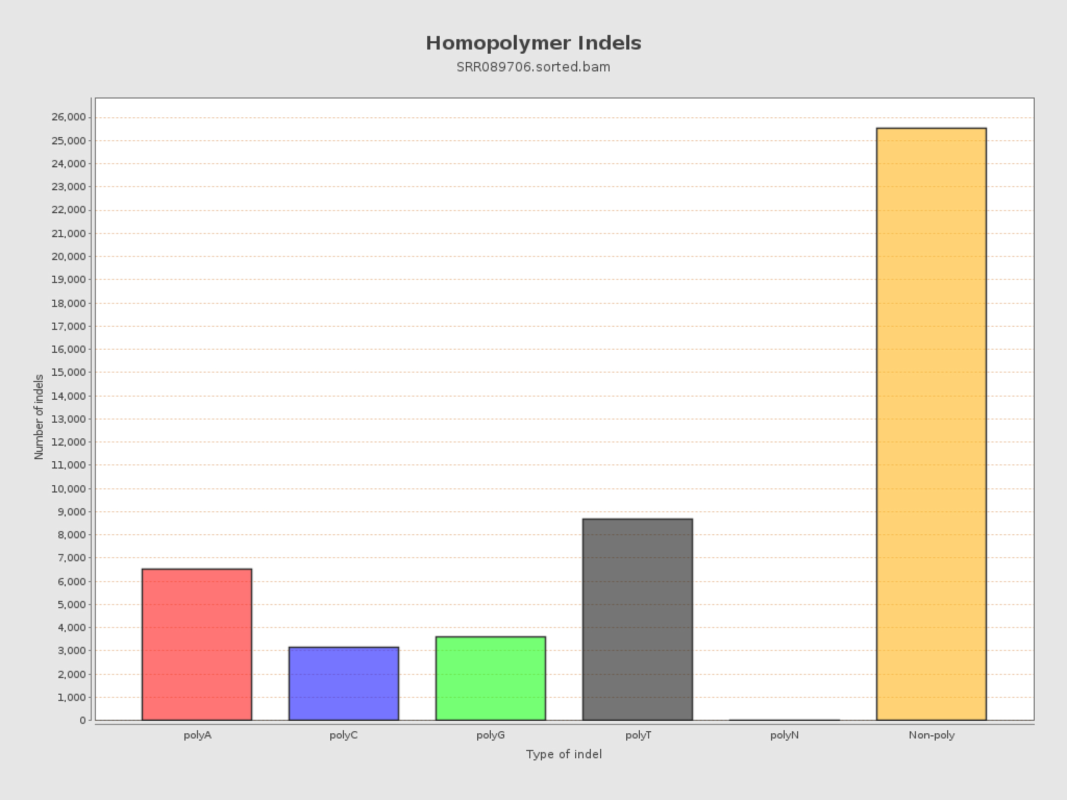
9. Results : Mapped Reads GC-content Distribution



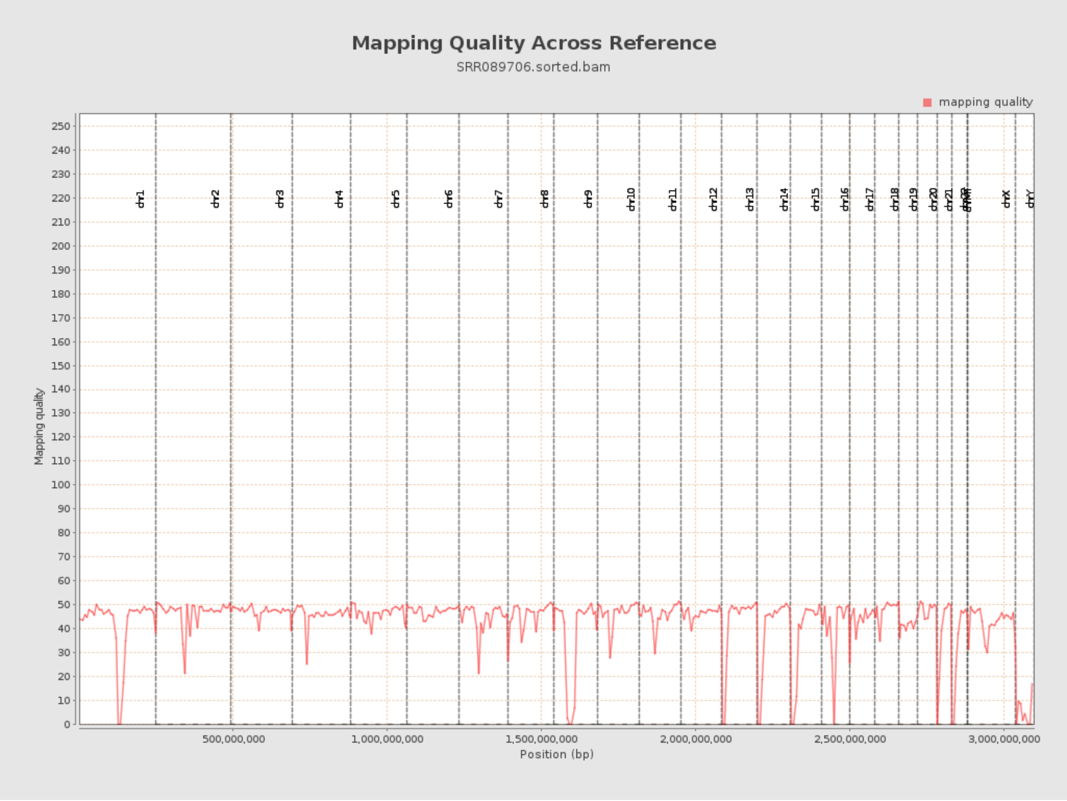
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram