Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 22:58:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089708.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_SRR089708 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089708.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 22:58:04 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089708.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,895,852
Mapped reads	19,439,099 / 93.03%
Unmapped reads	1,456,753 / 6.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	99,632 / 0.48%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	5,451,870 / 26.09%
Duplication rate	17.61%
Clipped reads	10,090,840 / 48.29%

2.2. ACGT Content

Number/percentage of A's	319,975,271 / 25.53%
Number/percentage of C's	228,665,750 / 18.24%
Number/percentage of T's	397,389,640 / 31.7%
Number/percentage of G's	307,443,210 / 24.53%
Number/percentage of N's	54,925 / 0%
GC Percentage	42.77%

2.3. Coverage

Mean	0.4051

Standard Deviation	2.4965

2.4. Mapping Quality

Mean Mapping Quality	46.68

2.5. Mismatches and indels

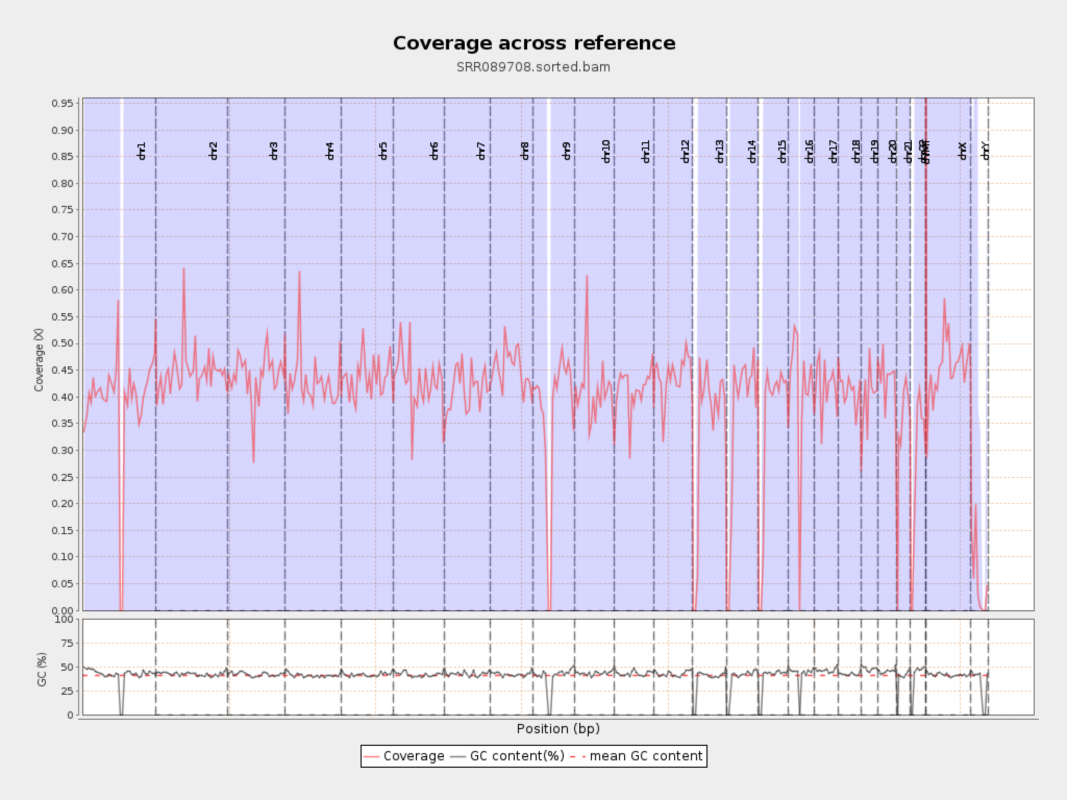
General error rate	0.63%
Mismatches	7,777,172
Insertions	84,765
Mapped reads with at least one insertion	0.43%
Deletions	265,211
Mapped reads with at least one deletion	1.35%
Homopolymer indels	47.88%

2.6. Chromosome stats

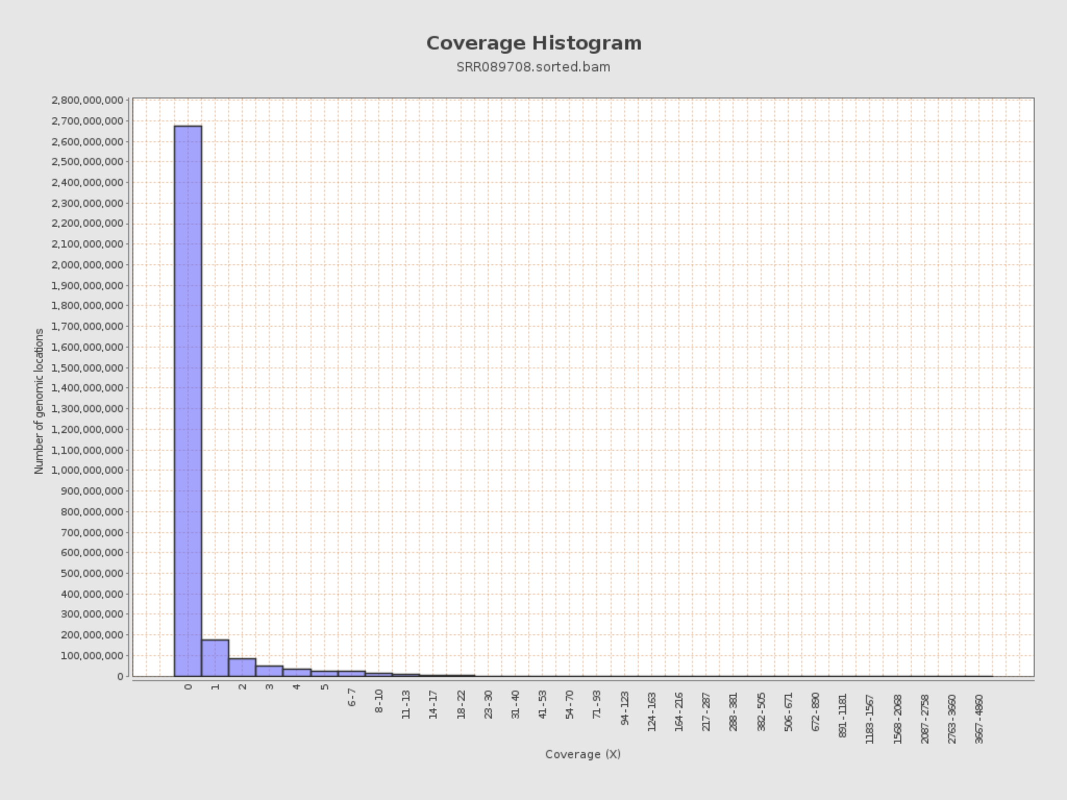
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	97501226	0.3912	4.2138
chr2	243199373	108934723	0.4479	3.0198
chr3	198022430	86866096	0.4387	1.6251
chr4	191154276	82141408	0.4297	1.8938
chr5	180915260	78854574	0.4359	1.596
chr6	171115067	73577920	0.43	2.2898
chr7	159138663	66103231	0.4154	2.7682

chr8	146364022	66148296	0.4519	3.0683
chr9	141213431	52123832	0.3691	2.1989
chr10	135534747	55782299	0.4116	2.7861
chr11	135006516	55841639	0.4136	2.0474
chr12	133851895	59107792	0.4416	1.9461
chr13	115169878	39133210	0.3398	1.3856
chr14	107349540	39003677	0.3633	1.6166
chr15	102531392	34804063	0.3394	1.8724
chr16	90354753	36405041	0.4029	1.8318
chr17	81195210	34276493	0.4221	1.9552
chr18	78077248	32103239	0.4112	4.6077
chr19	59128983	23734126	0.4014	2.6794
chr20	63025520	27522286	0.4367	1.7702
chr21	48129895	16382582	0.3404	1.9176
chr22	51304566	13577596	0.2646	1.2649
chrMT	16571	24763	1.4944	2.261
chrX	155270560	70628334	0.4549	1.865
chrY	59373566	3414673	0.0575	1.3812

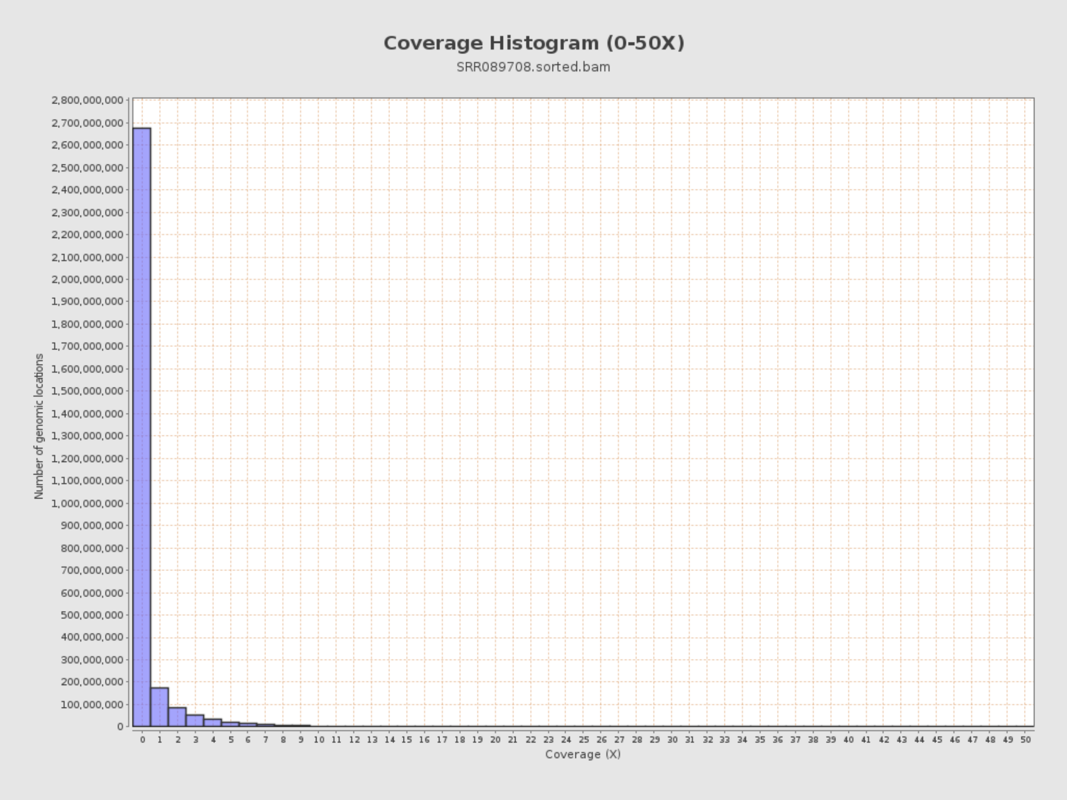
3. Results : Coverage across reference



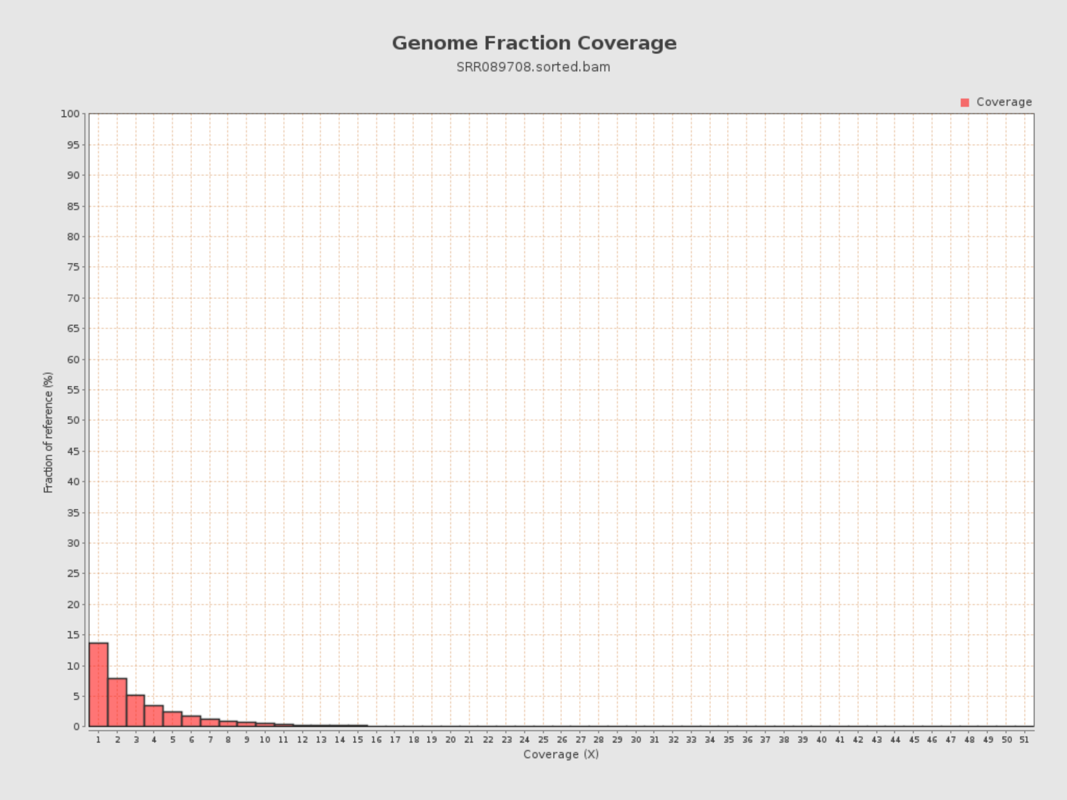
4. Results : Coverage Histogram



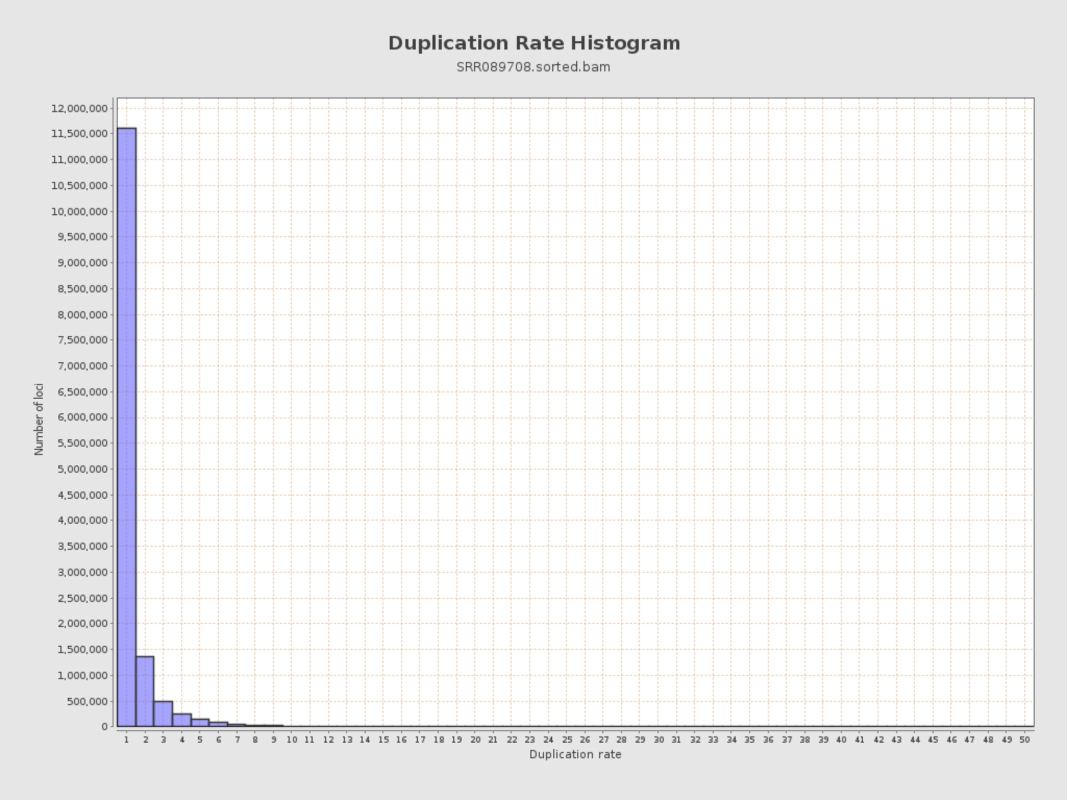
5. Results : Coverage Histogram (0-50X)



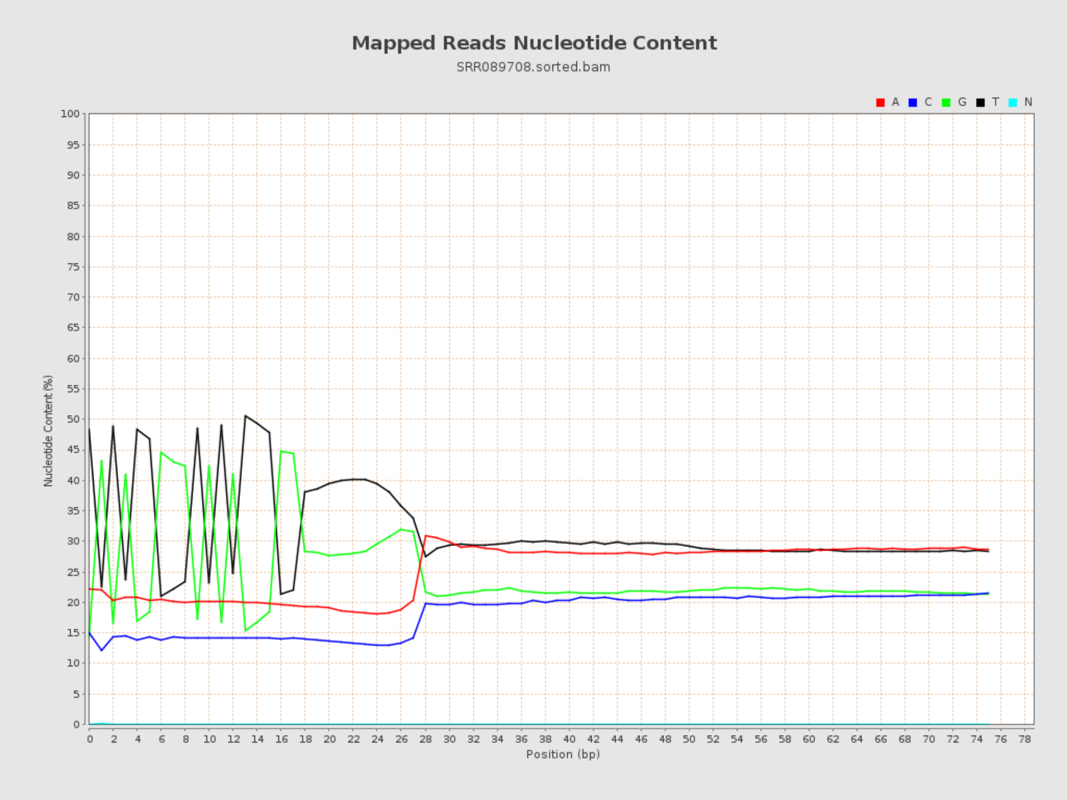
6. Results : Genome Fraction Coverage



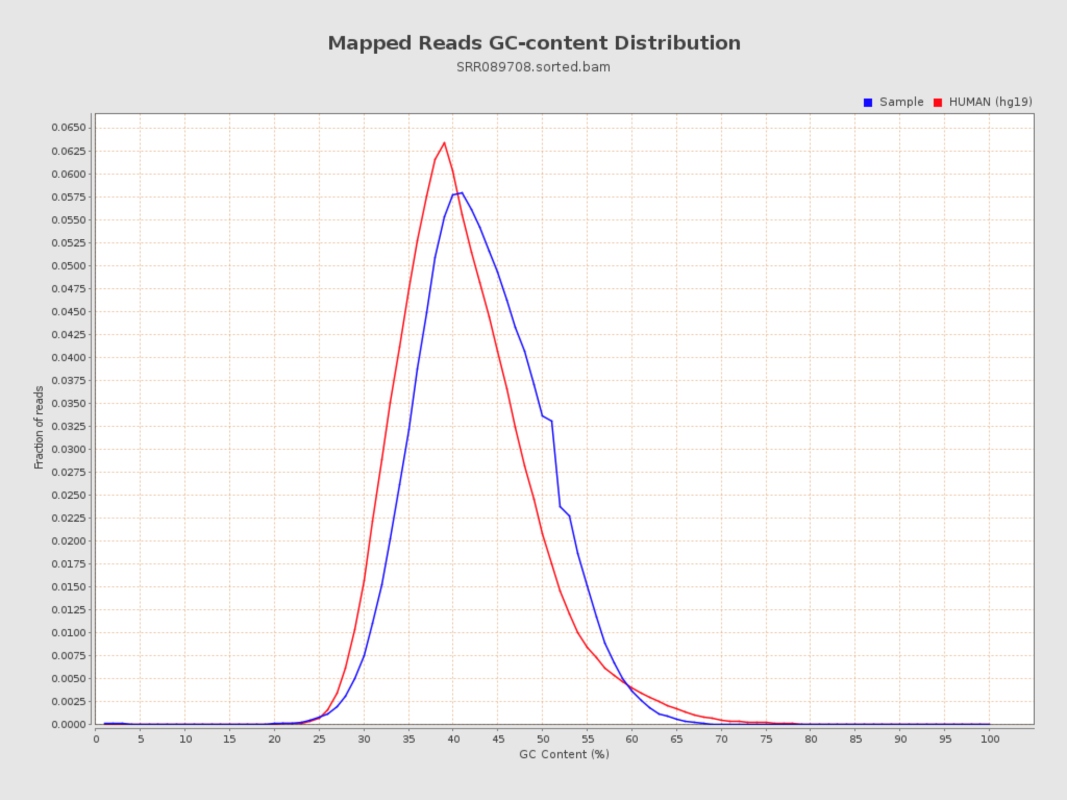
7. Results : Duplication Rate Histogram



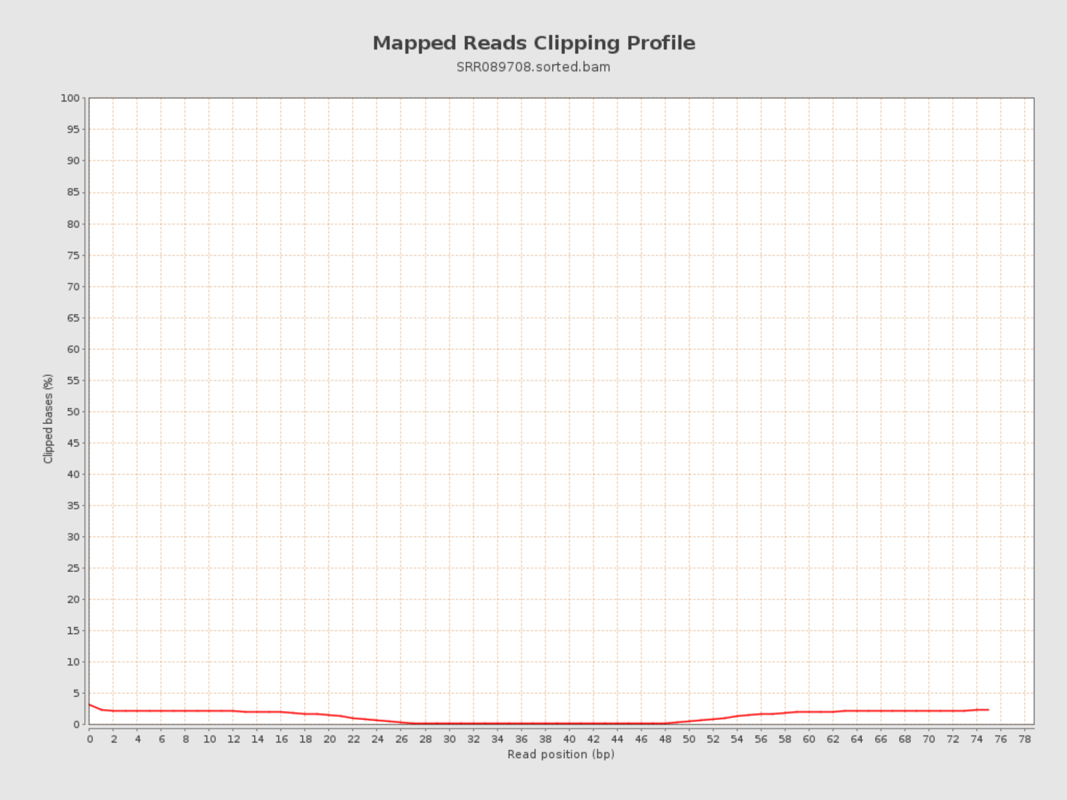
8. Results : Mapped Reads Nucleotide Content



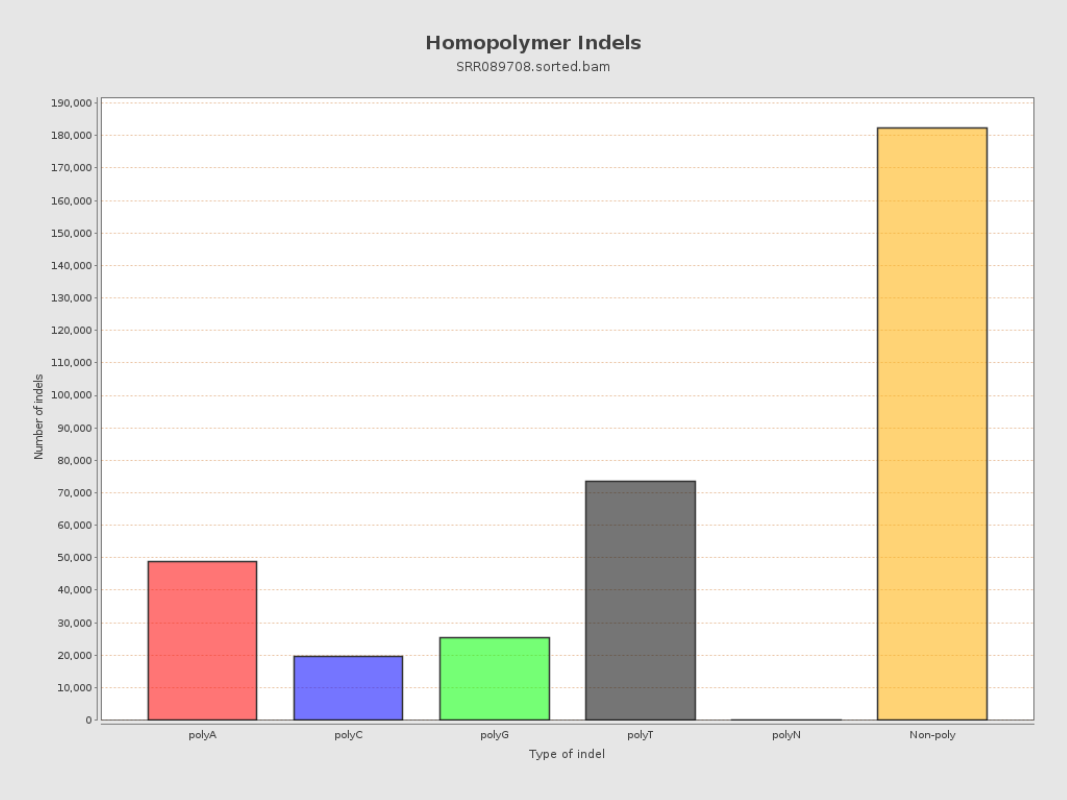
9. Results : Mapped Reads GC-content Distribution



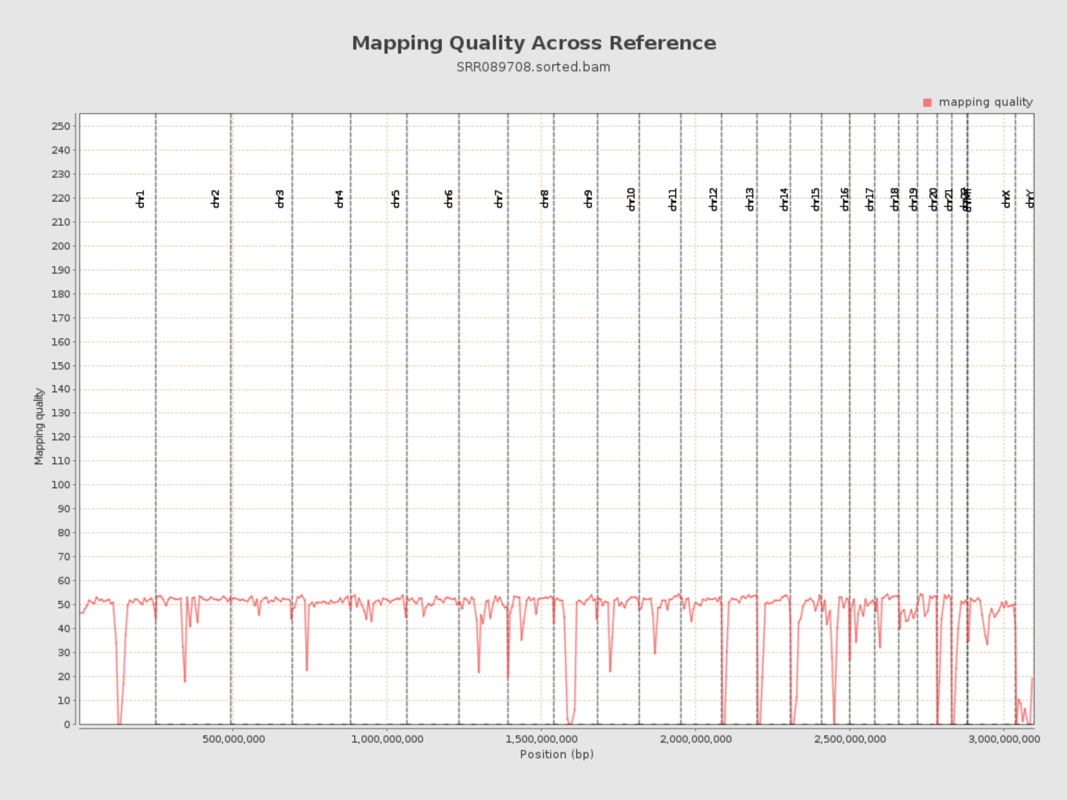
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram