Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 04:57:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089754.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_SRR089754 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089754.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 04:57:03 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089754.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,322,982
Mapped reads	26,990,777 / 83.5%
Unmapped reads	5,332,205 / 16.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,264 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	5,003,563 / 15.48%
Duplication rate	12.01%
Clipped reads	2,076,425 / 6.42%

2.2. ACGT Content

Number/percentage of A's	392,542,506 / 30.77%
Number/percentage of C's	253,753,784 / 19.89%
Number/percentage of T's	366,235,353 / 28.71%
Number/percentage of G's	262,899,538 / 20.61%
Number/percentage of N's	137,859 / 0.01%
GC Percentage	40.5%

2.3. Coverage

Mean	0.4121

Standard Deviation	2.929

2.4. Mapping Quality

Mean Mapping Quality	45.52

2.5. Mismatches and indels

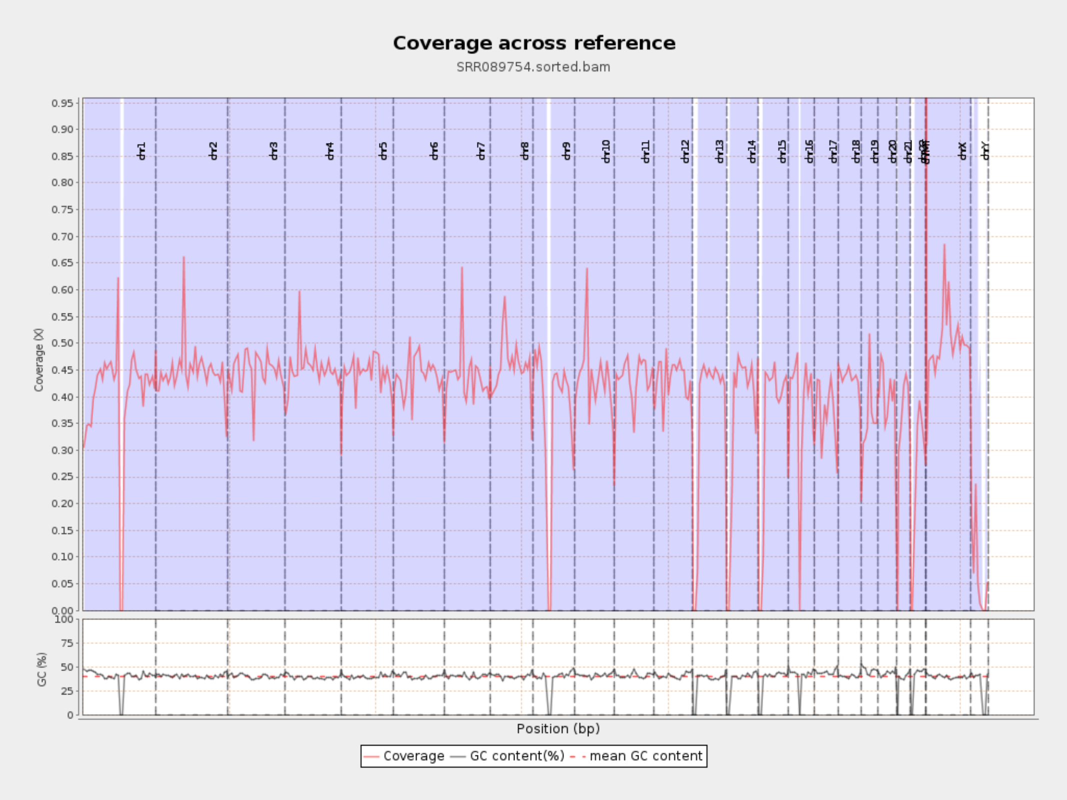
General error rate	0.43%
Mismatches	5,426,229
Insertions	48,652
Mapped reads with at least one insertion	0.18%
Deletions	155,426
Mapped reads with at least one deletion	0.57%
Homopolymer indels	47.7%

2.6. Chromosome stats

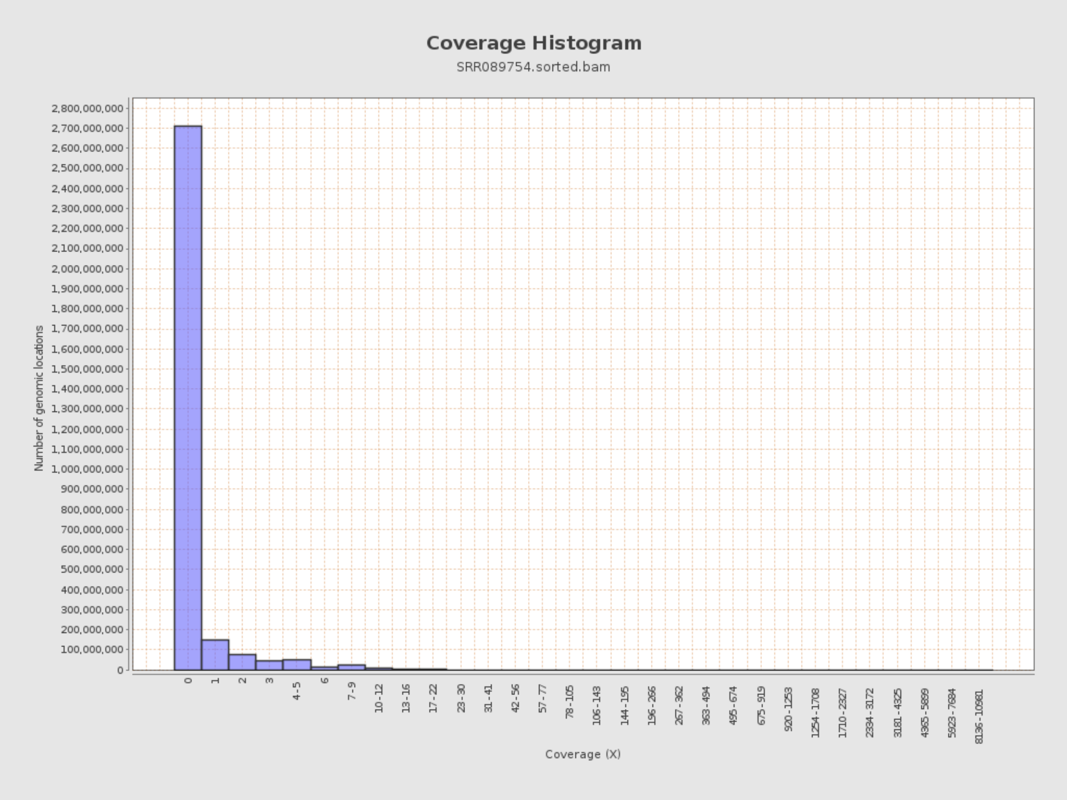
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	100149410	0.4018	5.0367
chr2	243199373	108875023	0.4477	2.7679
chr3	198022430	88597381	0.4474	1.7208
chr4	191154276	86761563	0.4539	1.9441
chr5	180915260	79889749	0.4416	1.735
chr6	171115067	75437227	0.4409	1.9596
chr7	159138663	69617102	0.4375	3.4978

chr8	146364022	66897473	0.4571	6.1978
chr9	141213431	52434667	0.3713	2.4884
chr10	135534747	59100504	0.4361	2.5487
chr11	135006516	58337068	0.4321	2.6533
chr12	133851895	57789286	0.4317	1.8053
chr13	115169878	41951669	0.3643	1.5565
chr14	107349540	39039442	0.3637	1.7916
chr15	102531392	35037271	0.3417	1.515
chr16	90354753	33477417	0.3705	1.717
chr17	81195210	30306037	0.3732	1.9785
chr18	78077248	34018343	0.4357	4.3688
chr19	59128983	21294816	0.3601	3.8153
chr20	63025520	25535064	0.4052	1.7325
chr21	48129895	16427975	0.3413	1.8616
chr22	51304566	12639565	0.2464	1.2494
chrMT	16571	174691	10.542	10.2949
chrX	155270560	77842424	0.5013	2.1811
chrY	59373566	4170628	0.0702	1.6705

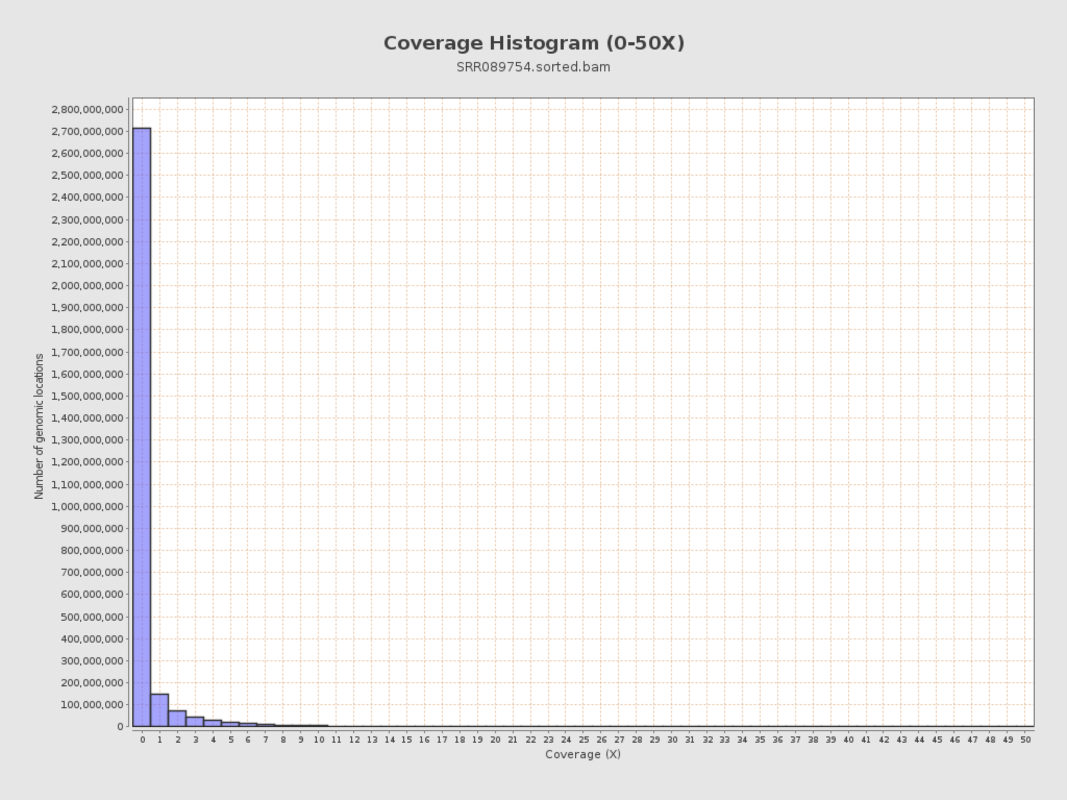
3. Results : Coverage across reference



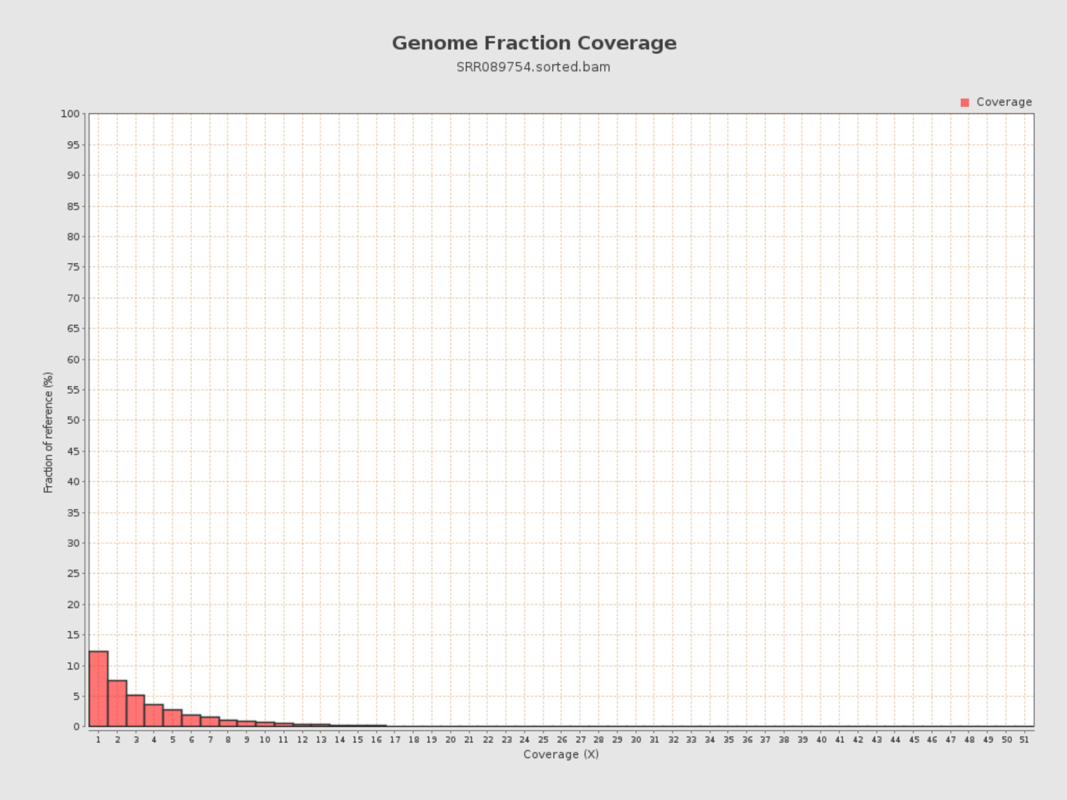
4. Results : Coverage Histogram



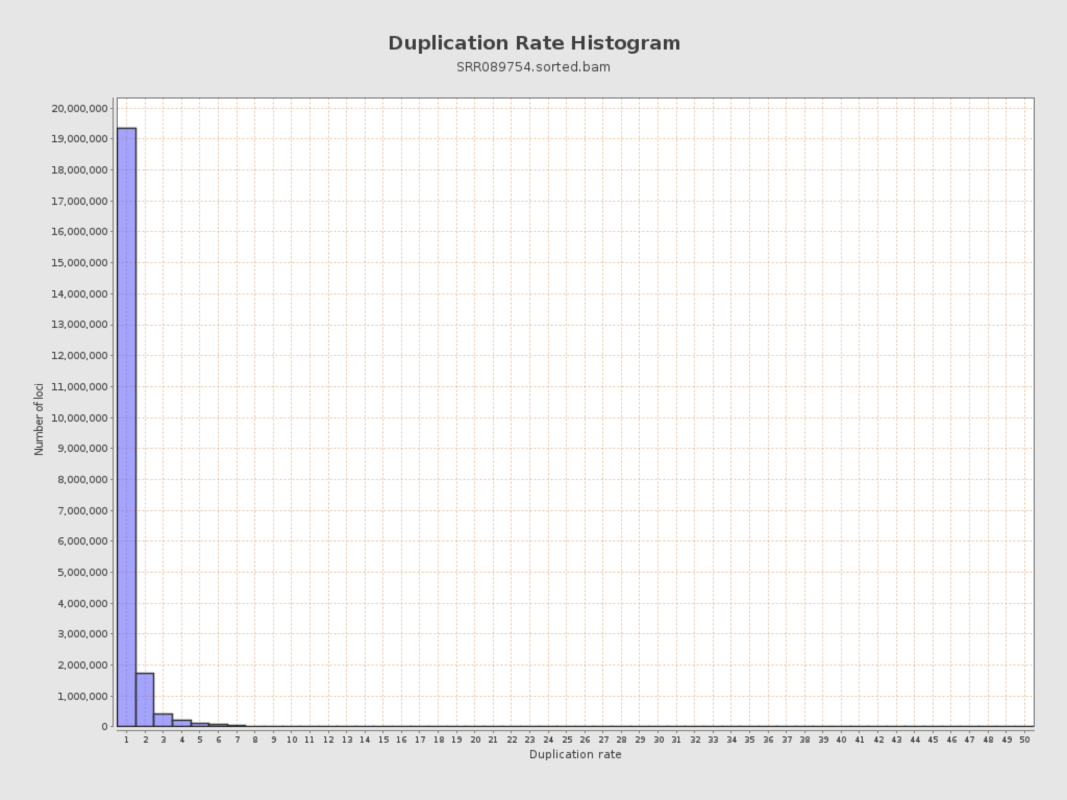
5. Results : Coverage Histogram (0-50X)



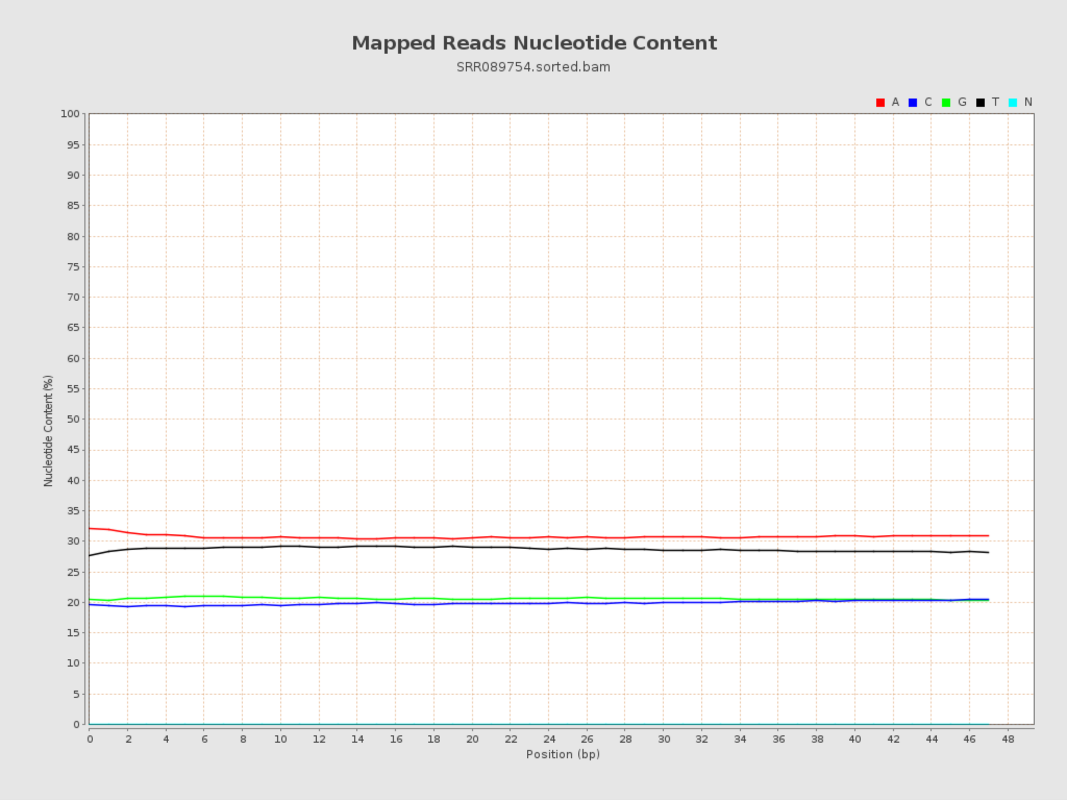
6. Results : Genome Fraction Coverage



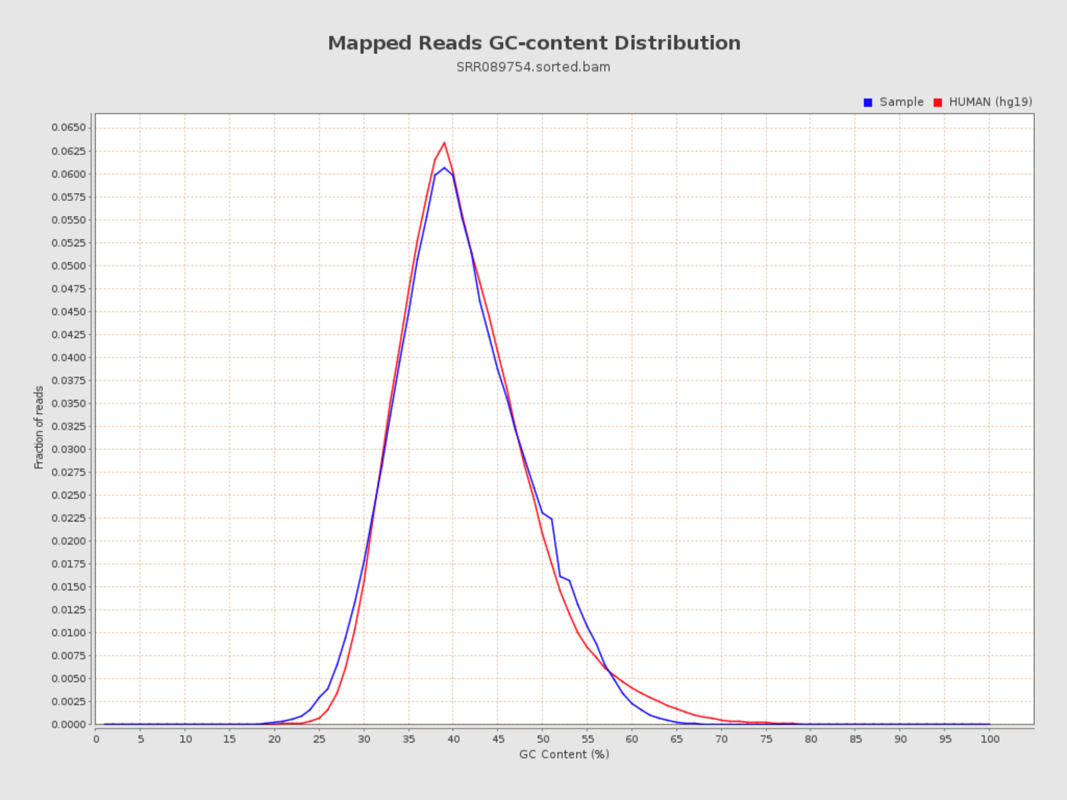
7. Results : Duplication Rate Histogram



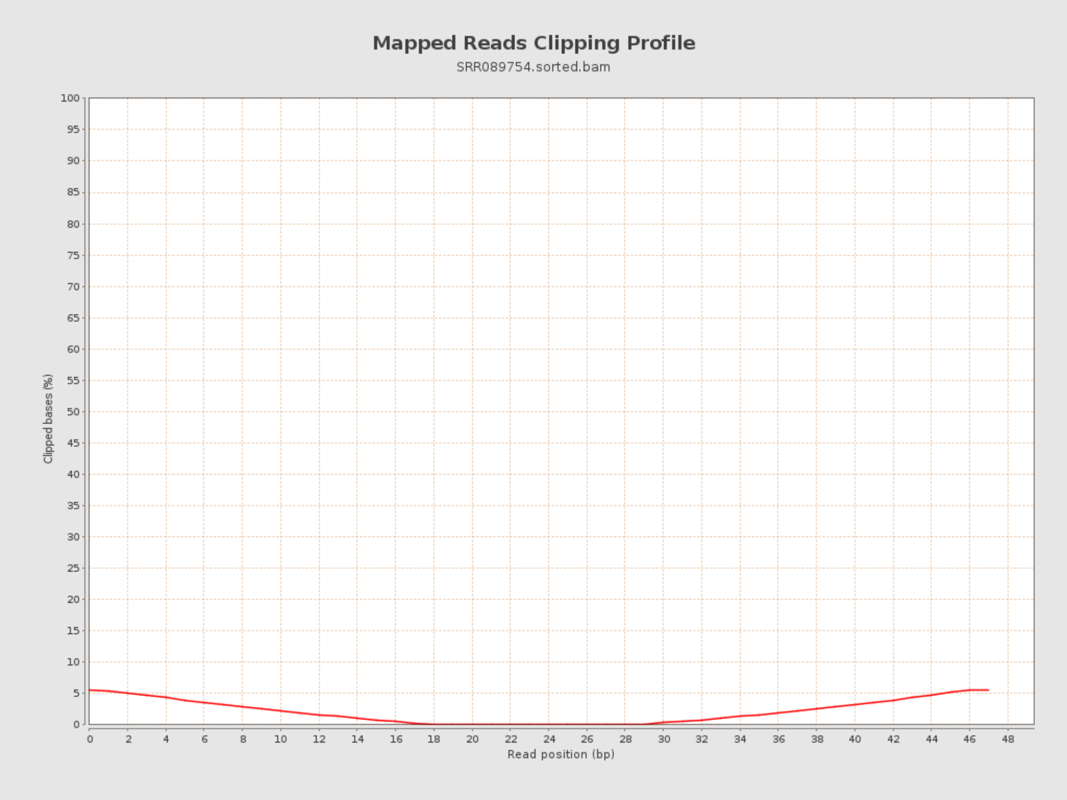
8. Results : Mapped Reads Nucleotide Content



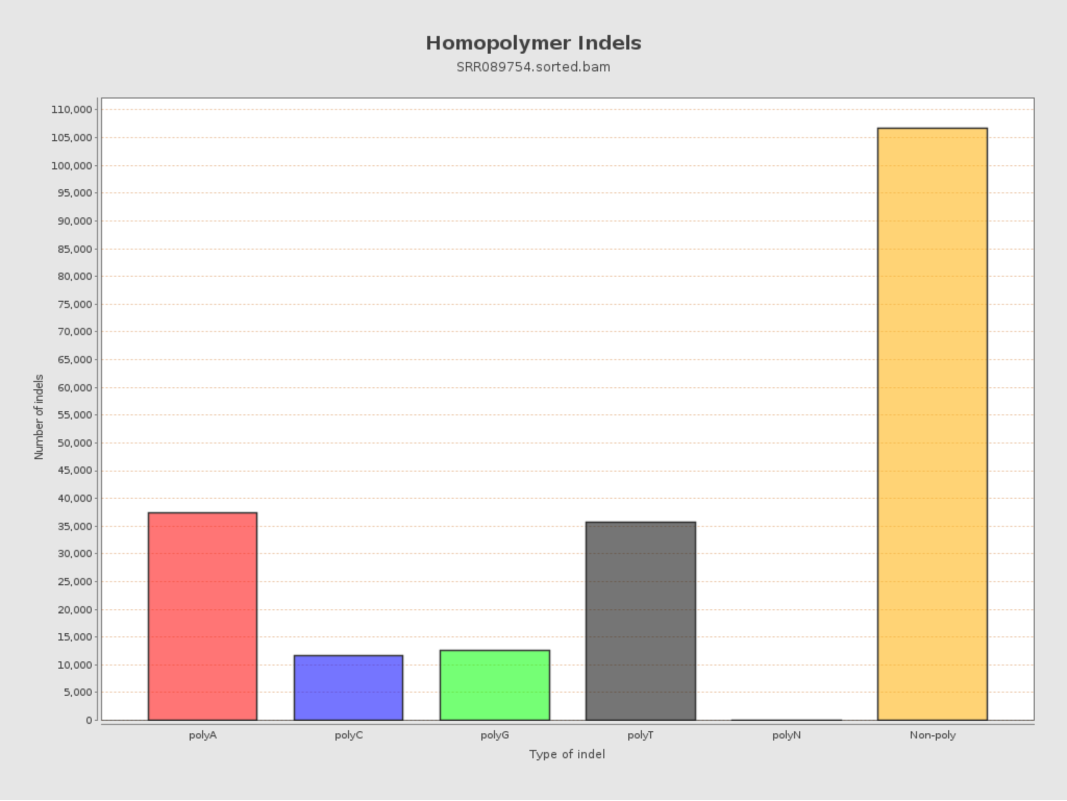
9. Results : Mapped Reads GC-content Distribution



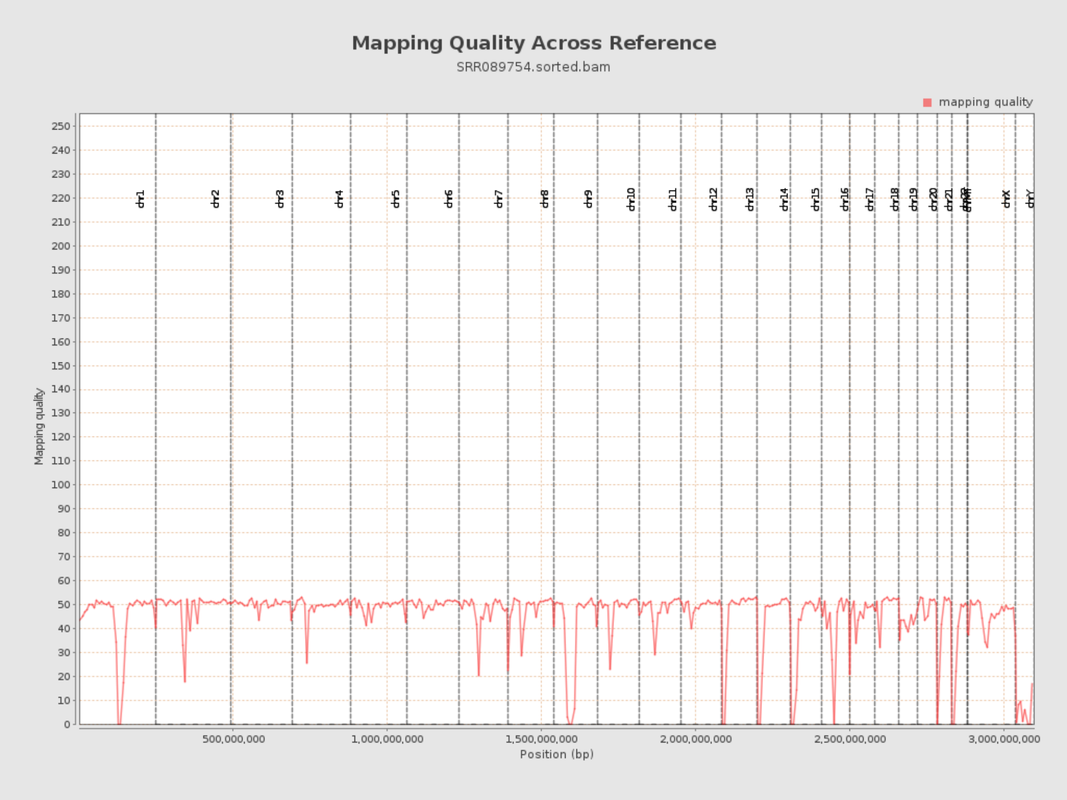
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram