Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 03:27:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089750.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_SRR089750 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089750.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 03:27:55 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089750.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	26,210,053
Mapped reads	22,697,810 / 86.6%
Unmapped reads	3,512,243 / 13.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,091 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	4,477,443 / 17.08%
Duplication rate	11.46%
Clipped reads	1,298,109 / 4.95%

2.2. ACGT Content

Number/percentage of A's	326,539,447 / 30.32%
Number/percentage of C's	213,313,998 / 19.8%
Number/percentage of T's	312,665,638 / 29.03%
Number/percentage of G's	224,591,495 / 20.85%
Number/percentage of N's	21,739 / 0%
GC Percentage	40.65%

2.3. Coverage

Mean	0.348

Standard Deviation	2.5905

2.4. Mapping Quality

Mean Mapping Quality	46.16

2.5. Mismatches and indels

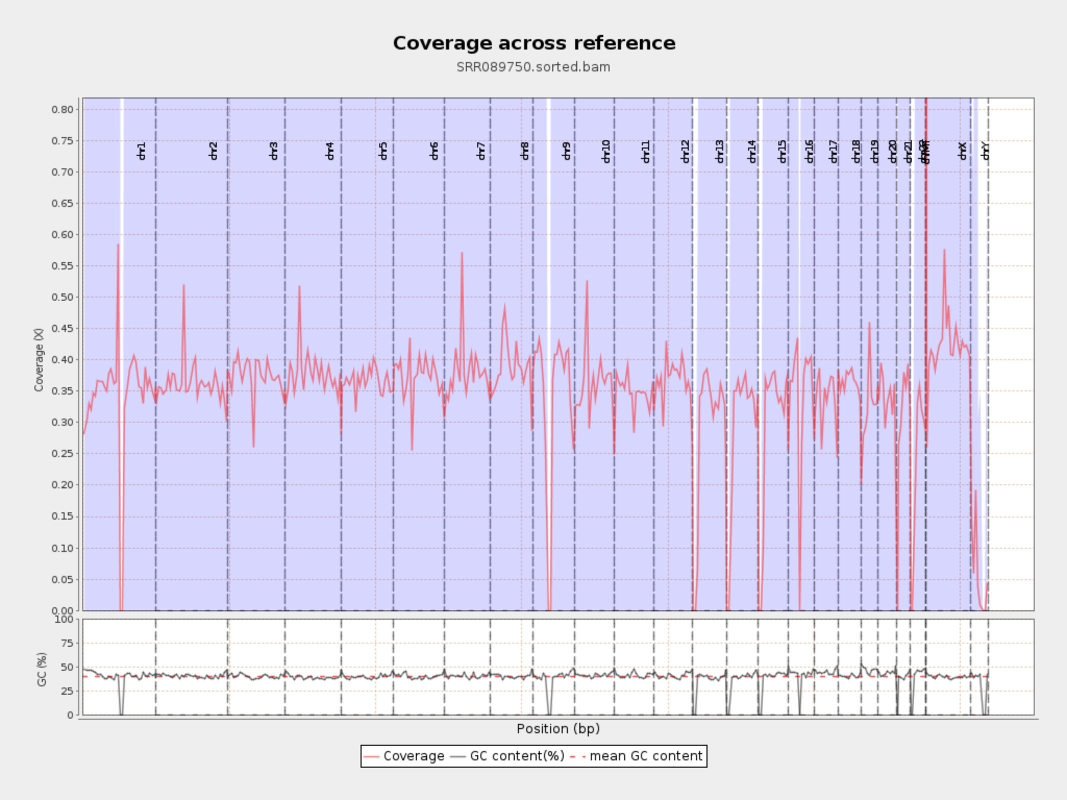
General error rate	0.36%
Mismatches	3,847,355
Insertions	41,727
Mapped reads with at least one insertion	0.18%
Deletions	142,194
Mapped reads with at least one deletion	0.63%
Homopolymer indels	48.99%

2.6. Chromosome stats

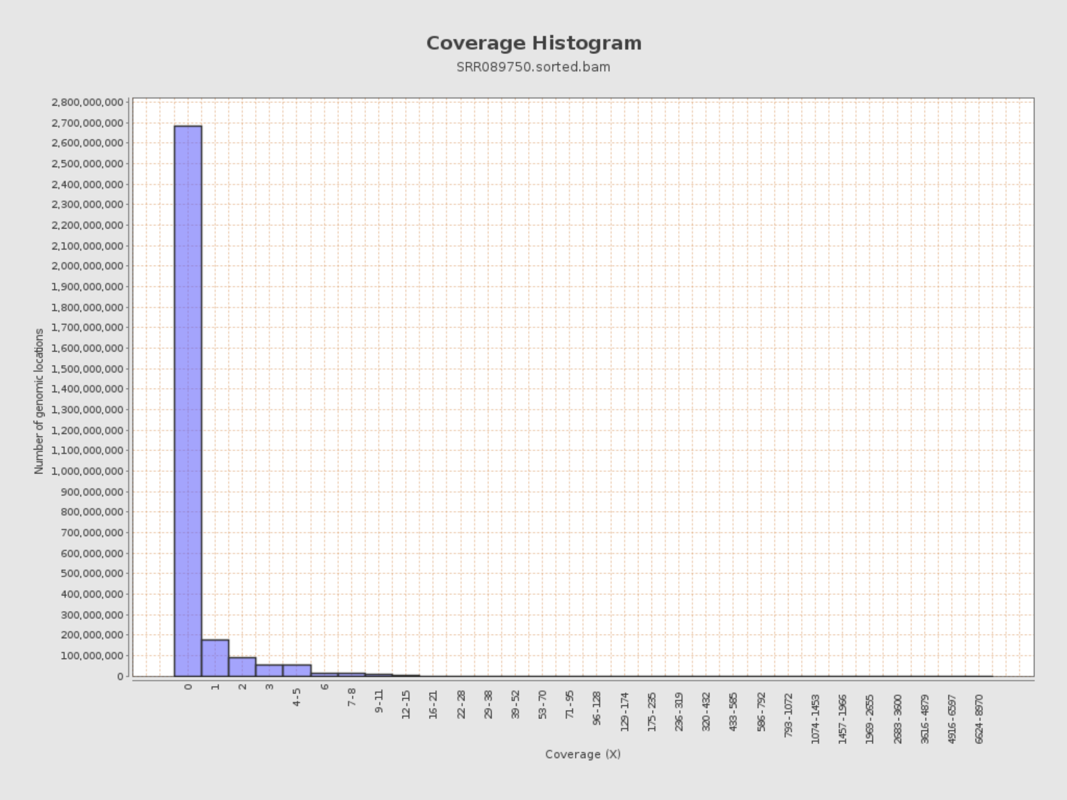
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	85064040	0.3413	5.2971
chr2	243199373	88251446	0.3629	2.133
chr3	198022430	74233272	0.3749	1.2764
chr4	191154276	72565979	0.3796	1.4636
chr5	180915260	66148687	0.3656	1.289
chr6	171115067	64006993	0.3741	1.5446
chr7	159138663	60765149	0.3818	3.0642

chr8	146364022	56566711	0.3865	4.9135
chr9	141213431	47948465	0.3395	2.0543
chr10	135534747	49216570	0.3631	2.1372
chr11	135006516	46925527	0.3476	2.0443
chr12	133851895	49376336	0.3689	1.416
chr13	115169878	33123249	0.2876	1.107
chr14	107349540	31323428	0.2918	1.2541
chr15	102531392	29264360	0.2854	1.1048
chr16	90354753	30188504	0.3341	1.3454
chr17	81195210	27557637	0.3394	1.5486
chr18	78077248	28559415	0.3658	4.7369
chr19	59128983	19447824	0.3289	3.4426
chr20	63025520	21339280	0.3386	1.3562
chr21	48129895	14622451	0.3038	1.5079
chr22	51304566	11743195	0.2289	0.965
chrMT	16571	350436	21.1475	15.0533
chrX	155270560	65366998	0.421	1.7622
chrY	59373566	3394059	0.0572	1.5176

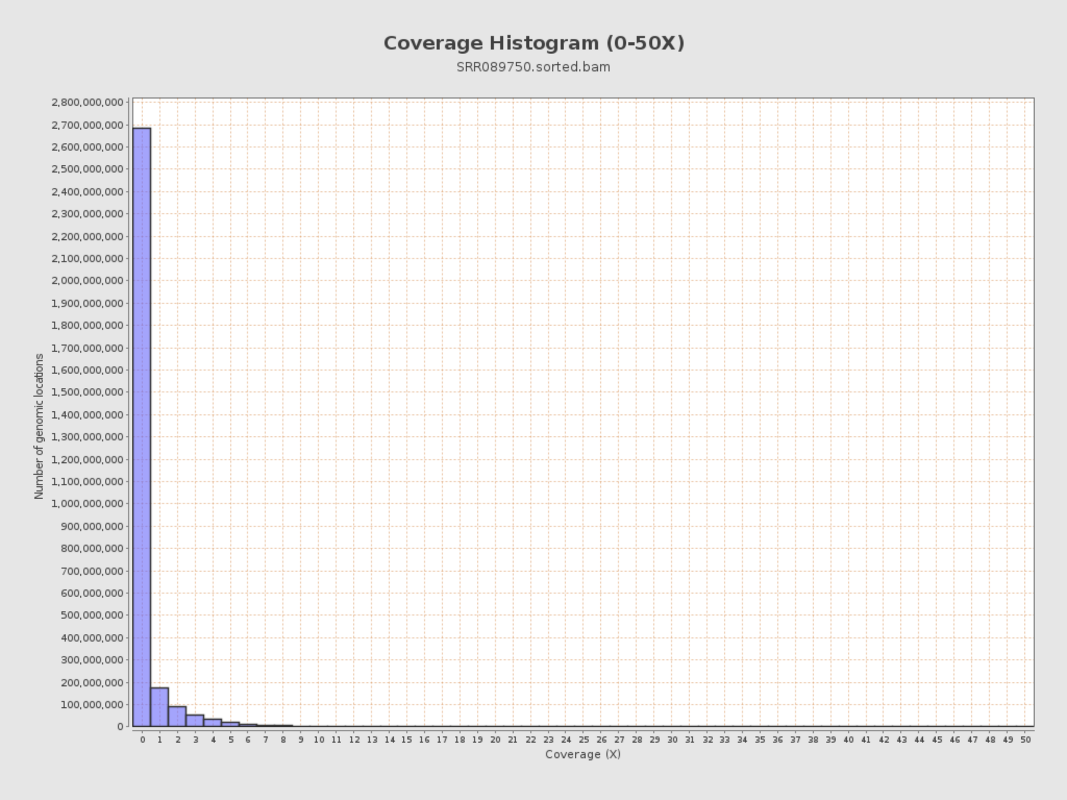
3. Results : Coverage across reference



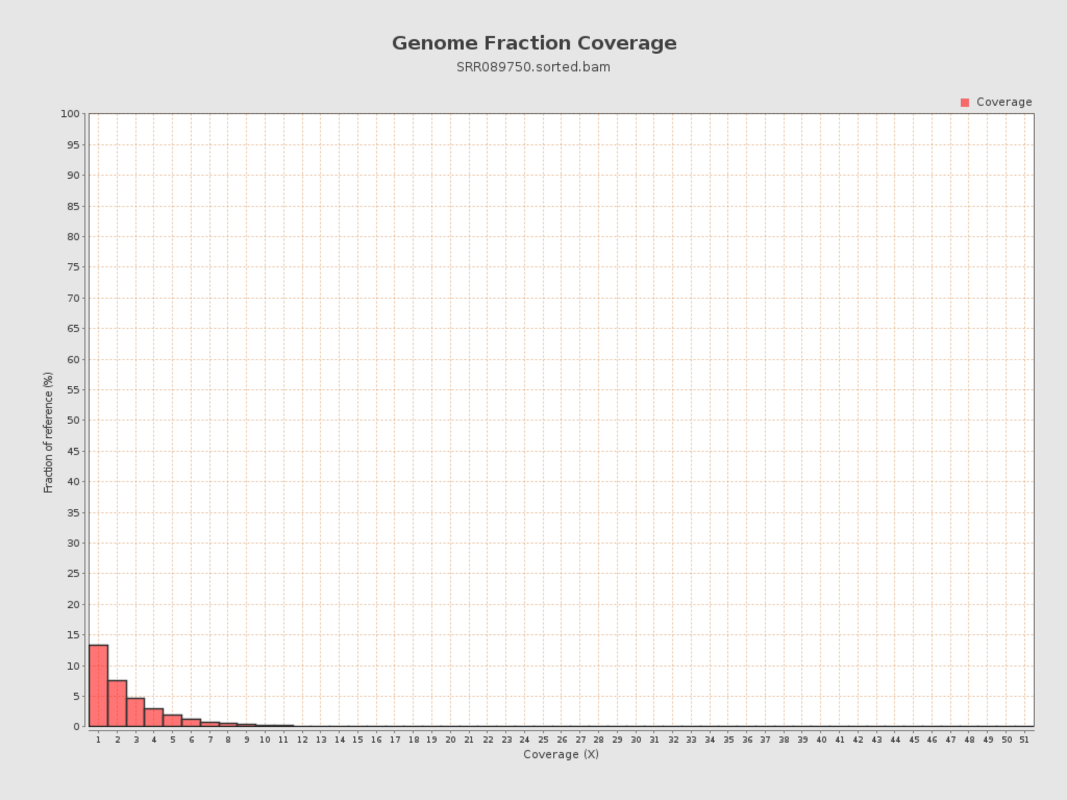
4. Results : Coverage Histogram



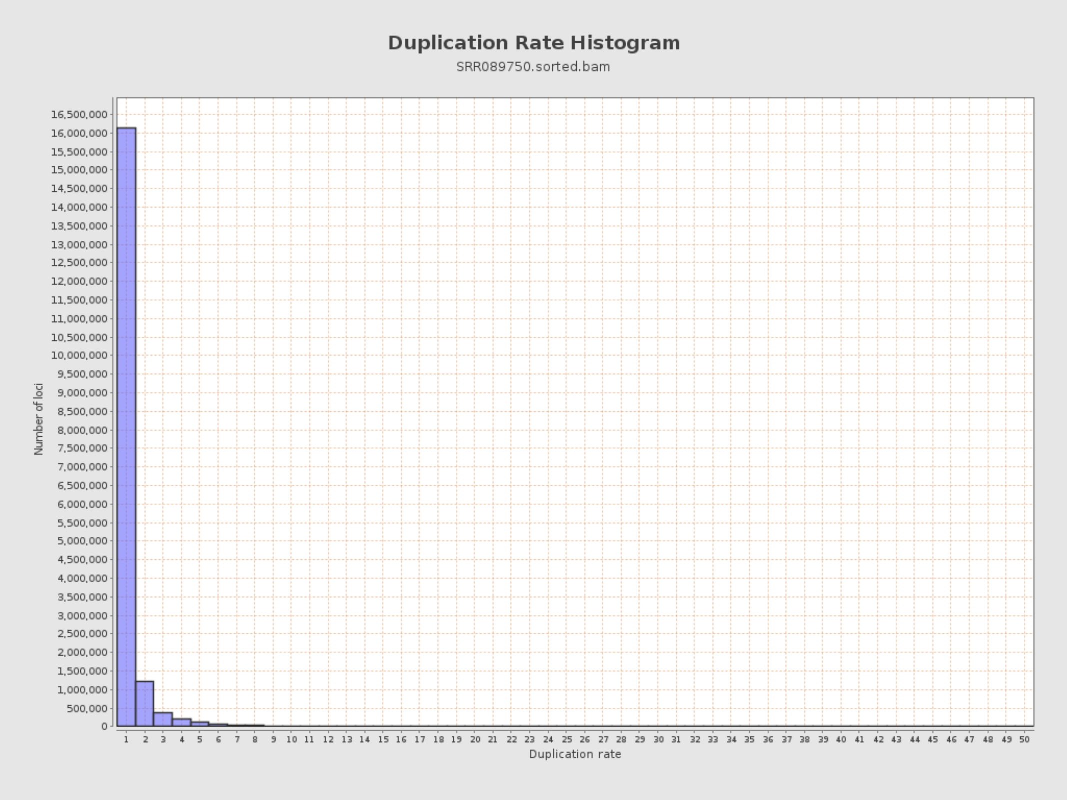
5. Results : Coverage Histogram (0-50X)



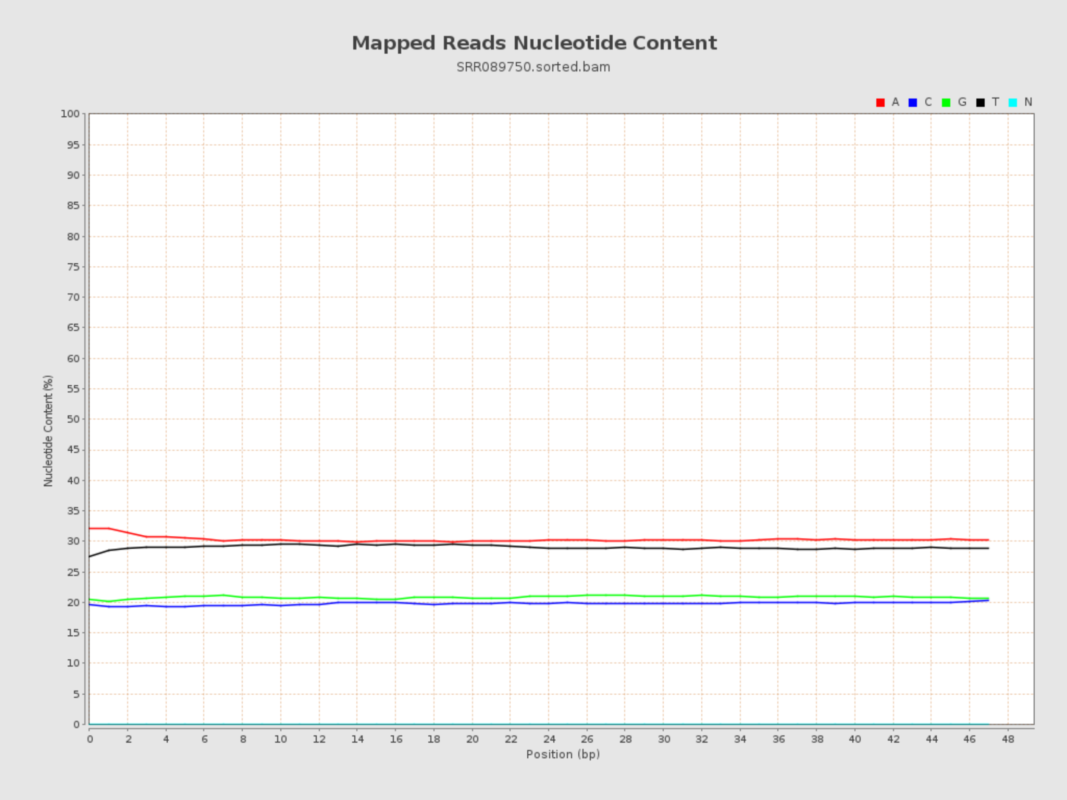
6. Results : Genome Fraction Coverage



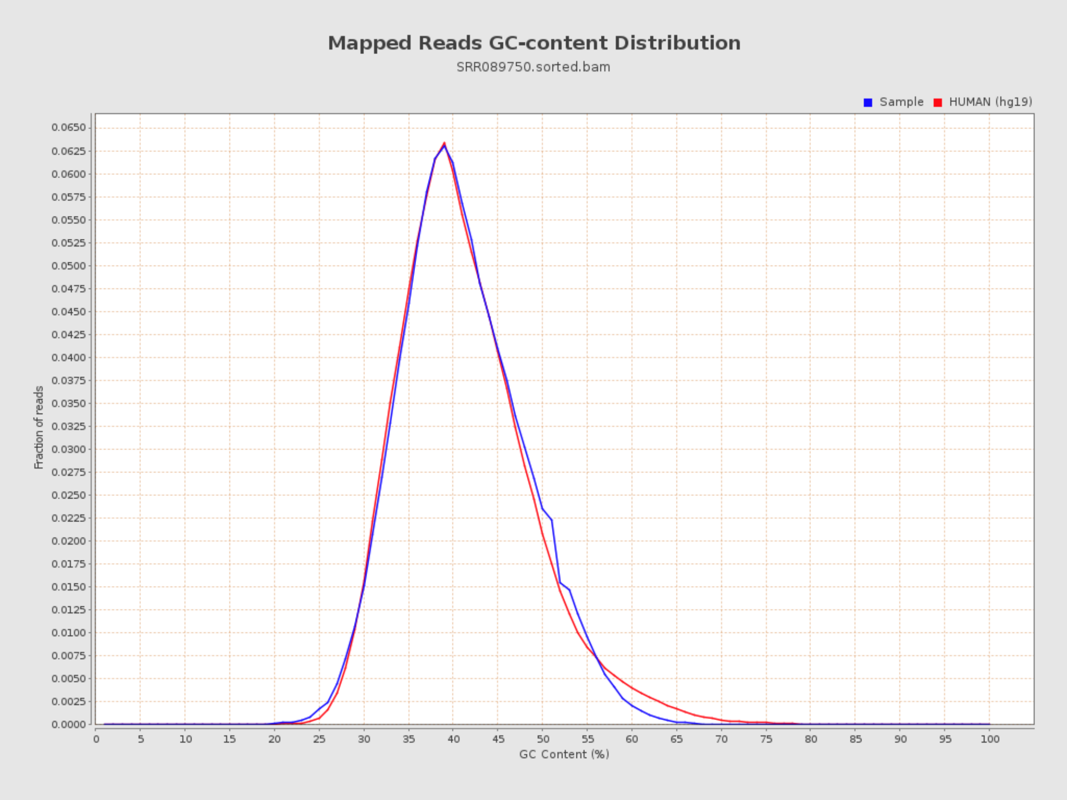
7. Results : Duplication Rate Histogram



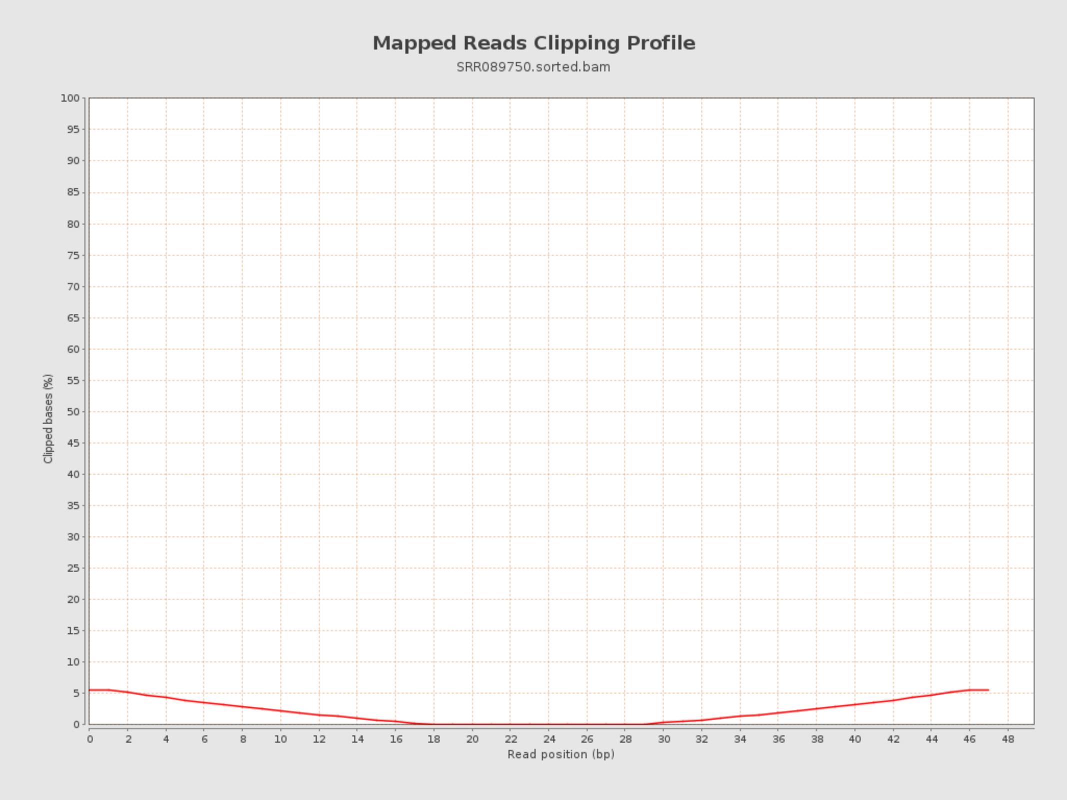
8. Results : Mapped Reads Nucleotide Content



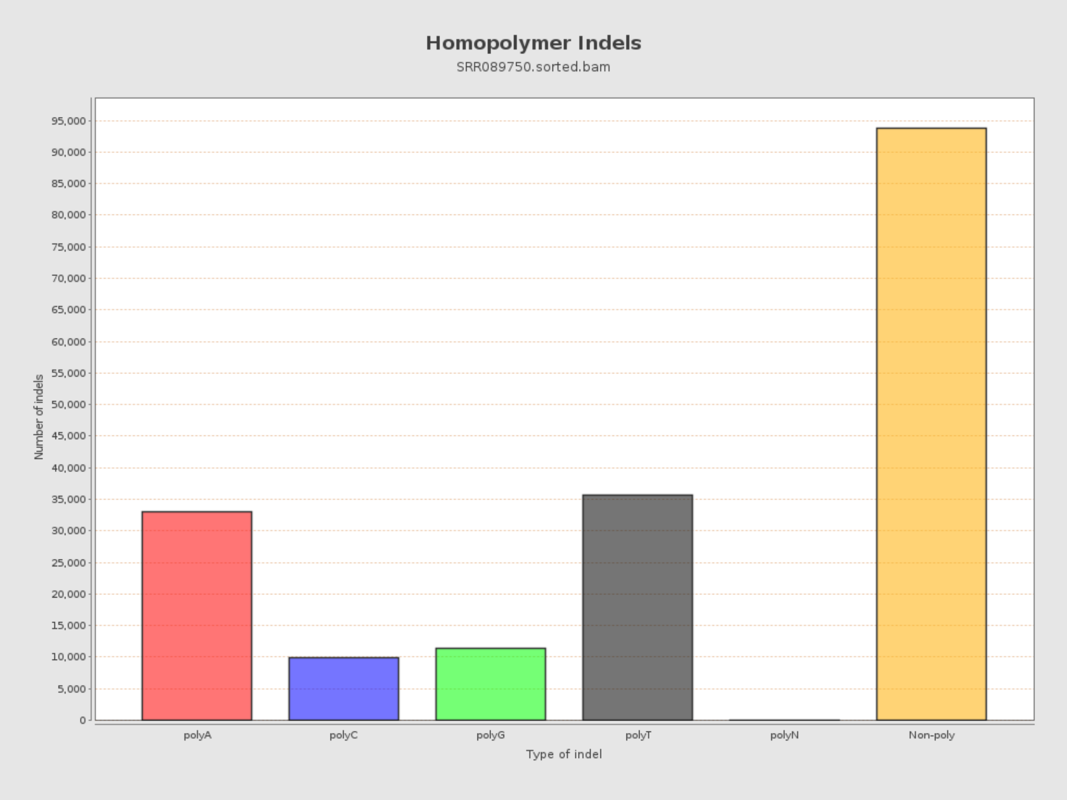
9. Results : Mapped Reads GC-content Distribution



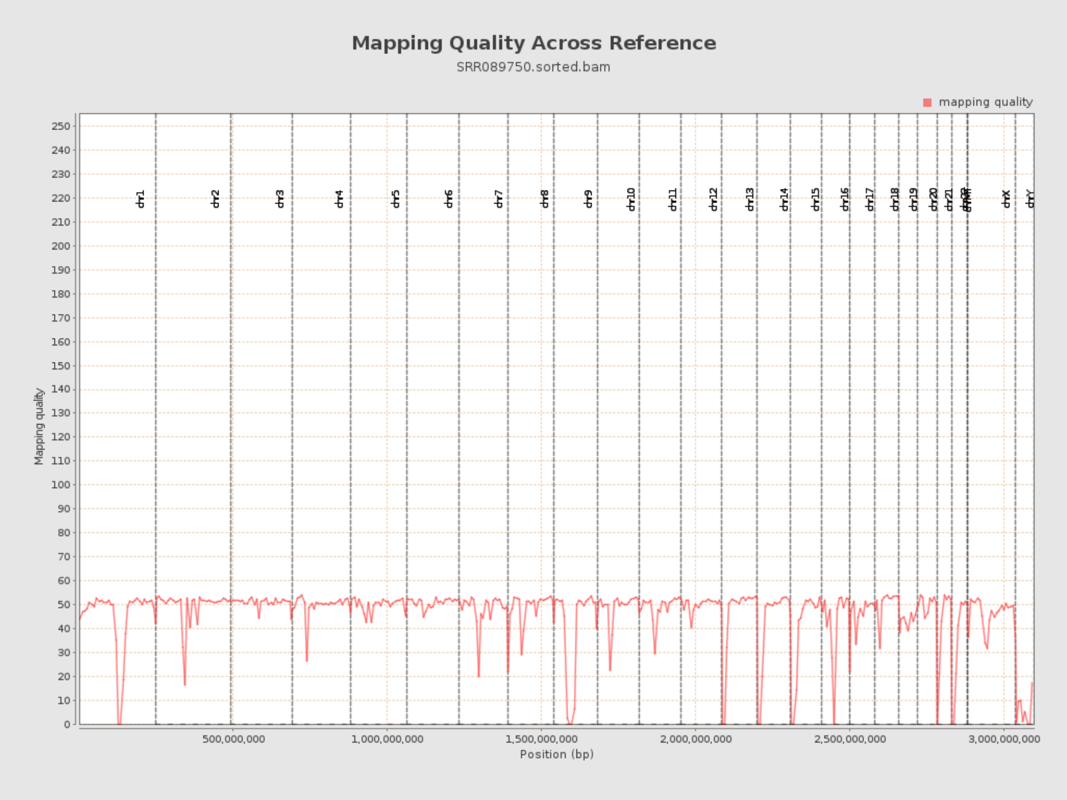
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram