Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 01:26:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089717.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_SRR089717 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089717.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 01:26:18 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089717.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	25,035,994
Mapped reads	21,548,477 / 86.07%
Unmapped reads	3,487,517 / 13.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	947 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	4,977,479 / 19.88%
Duplication rate	12.65%
Clipped reads	1,455,250 / 5.81%

2.2. ACGT Content

Number/percentage of A's	303,449,020 / 29.73%
Number/percentage of C's	207,059,299 / 20.29%
Number/percentage of T's	292,994,245 / 28.71%
Number/percentage of G's	217,126,563 / 21.27%
Number/percentage of N's	8,252 / 0%
GC Percentage	41.56%

2.3. Coverage

Mean	0.3298

Standard Deviation	2.211

2.4. Mapping Quality

Mean Mapping Quality	42.05

2.5. Mismatches and indels

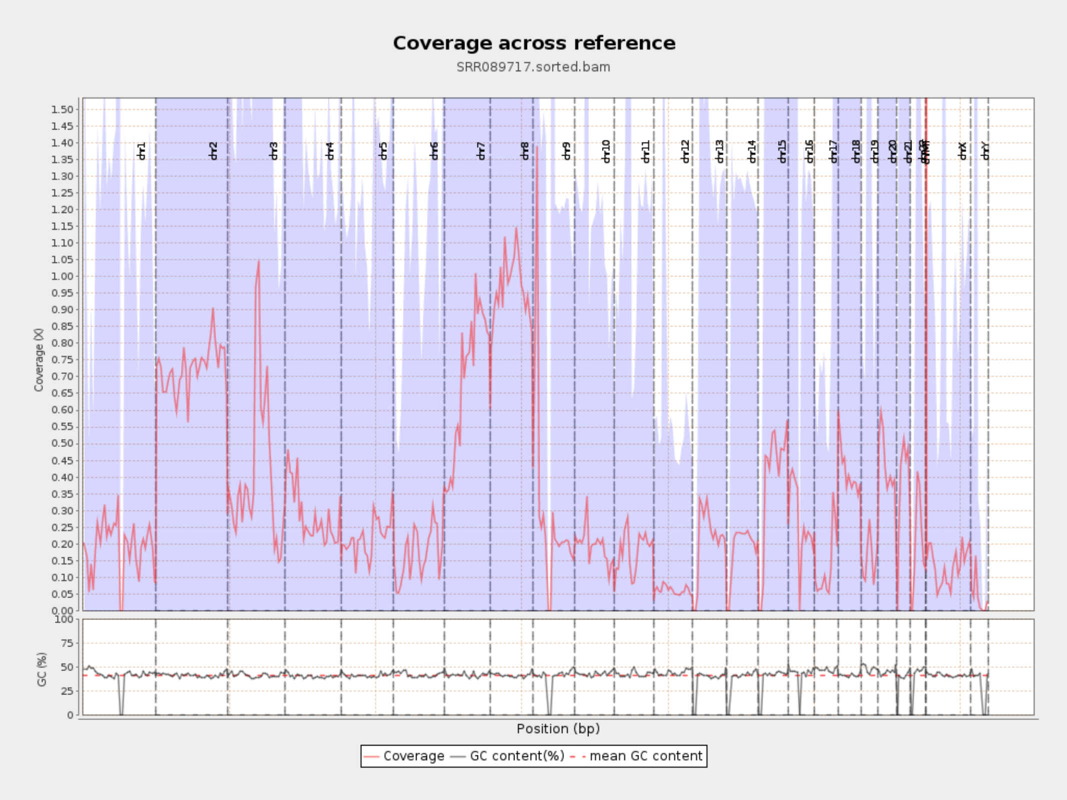
General error rate	0.37%
Mismatches	3,688,723
Insertions	36,443
Mapped reads with at least one insertion	0.17%
Deletions	125,346
Mapped reads with at least one deletion	0.58%
Homopolymer indels	47.63%

2.6. Chromosome stats

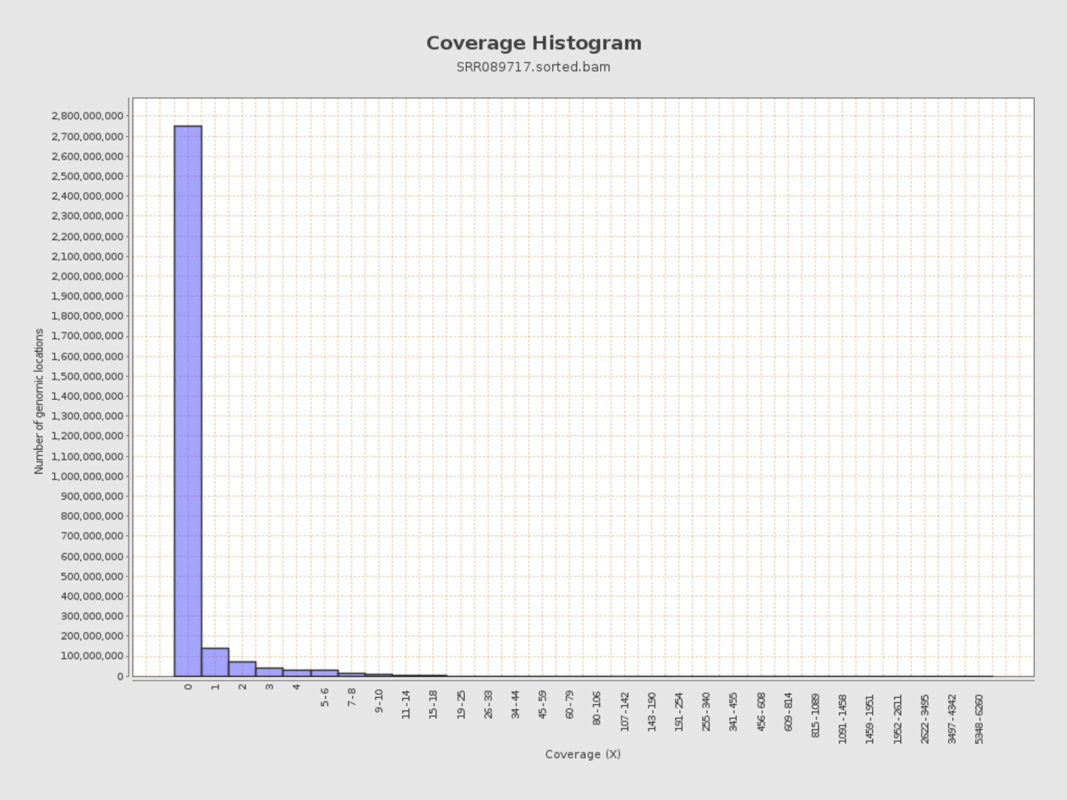
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	46983617	0.1885	2.5501
chr2	243199373	177515071	0.7299	2.8337
chr3	198022430	80406927	0.406	1.4857
chr4	191154276	54936544	0.2874	1.2556
chr5	180915260	39424416	0.2179	1.0609
chr6	171115067	29459622	0.1722	0.9257
chr7	159138663	109639514	0.689	4.9068

chr8	146364022	141744972	0.9684	4.4767
chr9	141213431	41592106	0.2945	1.964
chr10	135534747	26141338	0.1929	1.4935
chr11	135006516	23943108	0.1773	1.2074
chr12	133851895	8178300	0.0611	0.6758
chr13	115169878	24679091	0.2143	1.0314
chr14	107349540	19996079	0.1863	0.9793
chr15	102531392	39294930	0.3832	1.4456
chr16	90354753	23622889	0.2614	1.1996
chr17	81195210	10523969	0.1296	0.8429
chr18	78077248	32458173	0.4157	2.9513
chr19	59128983	9396530	0.1589	1.9223
chr20	63025520	27808078	0.4412	1.6277
chr21	48129895	17770074	0.3692	1.5313
chr22	51304566	10250757	0.1998	1.0164
chrMT	16571	1809567	109.2008	58.7569
chrX	155270560	20765901	0.1337	0.9974
chrY	59373566	2484739	0.0418	1.66

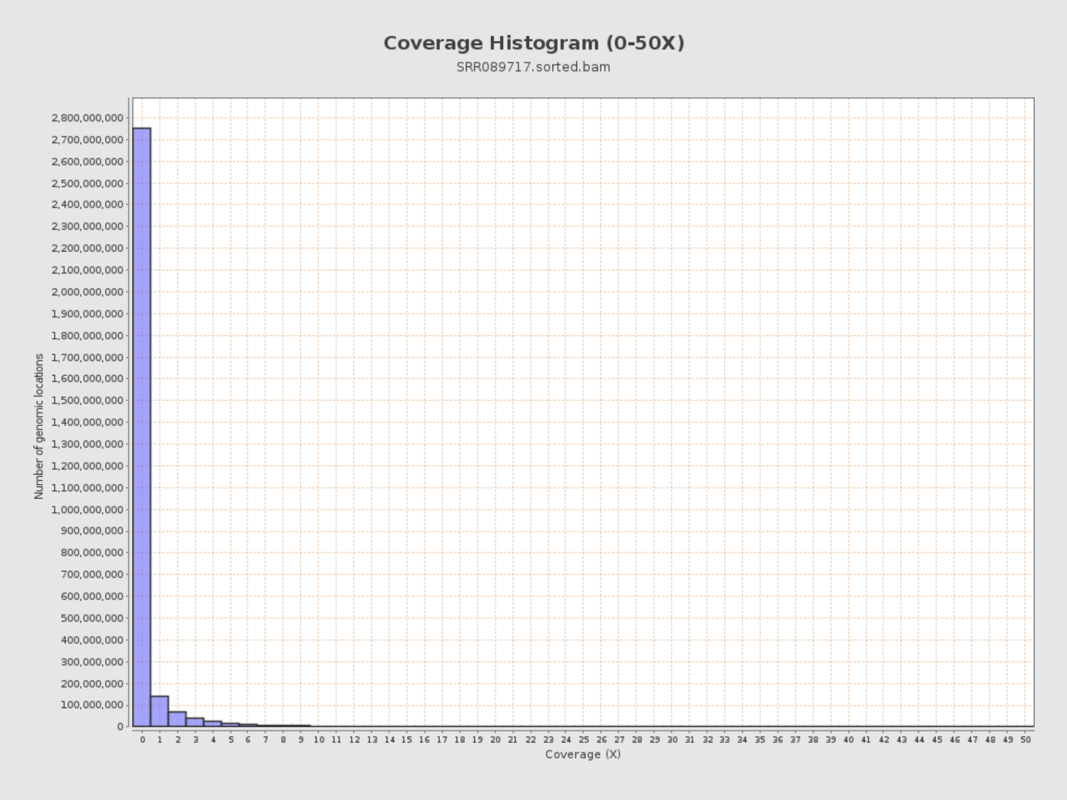
3. Results : Coverage across reference



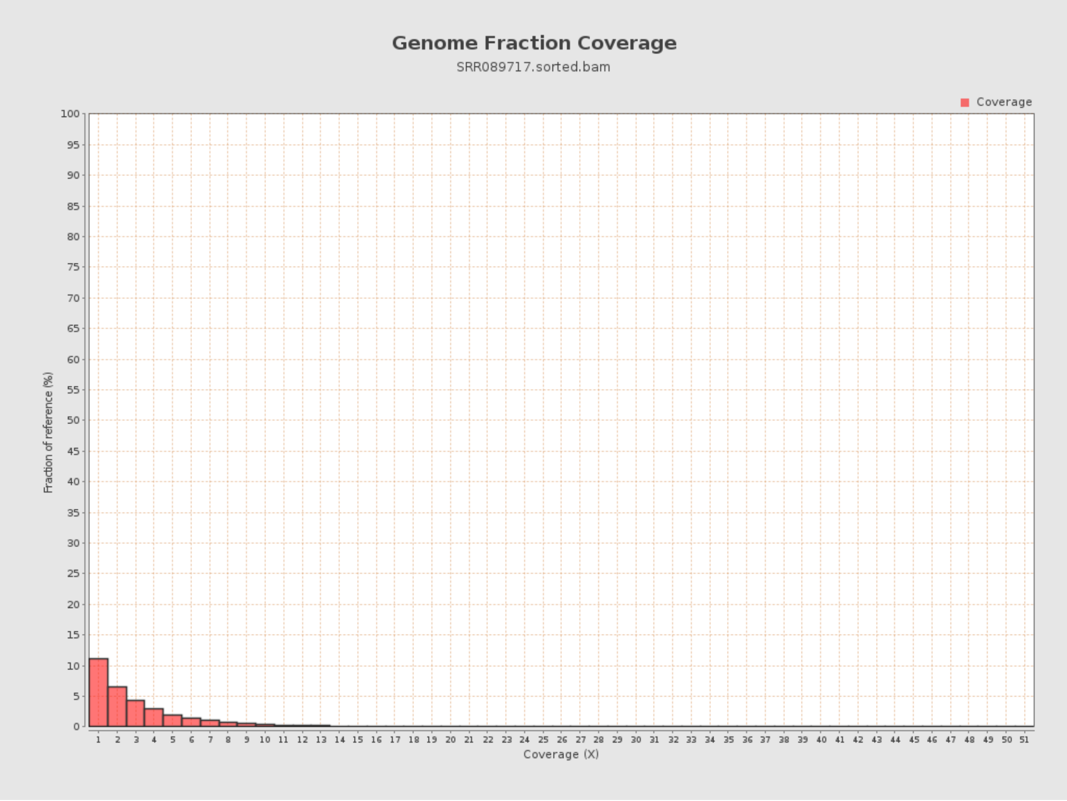
4. Results : Coverage Histogram



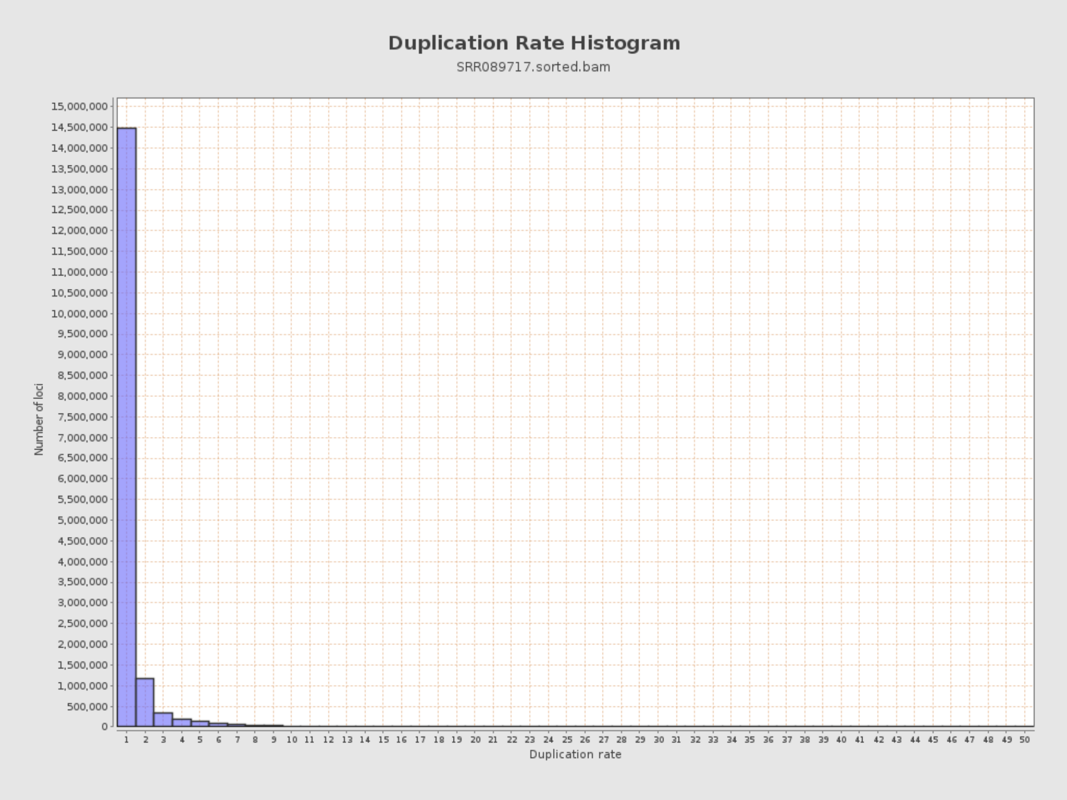
5. Results : Coverage Histogram (0-50X)



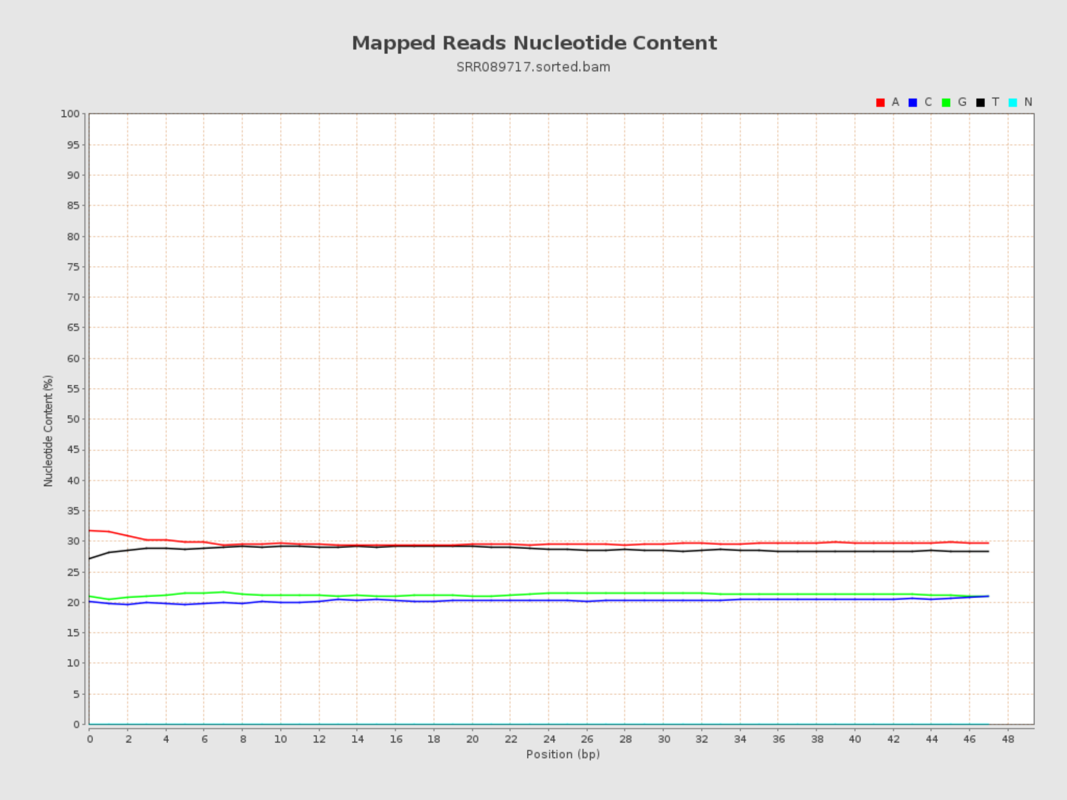
6. Results : Genome Fraction Coverage



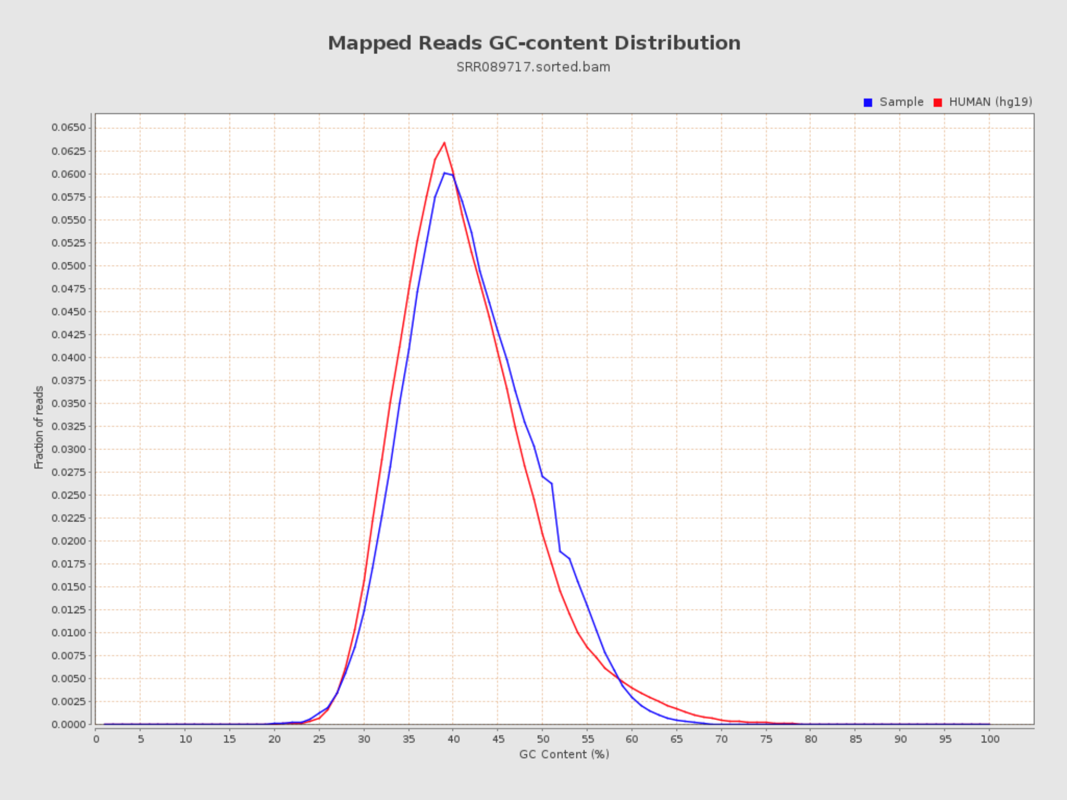
7. Results : Duplication Rate Histogram



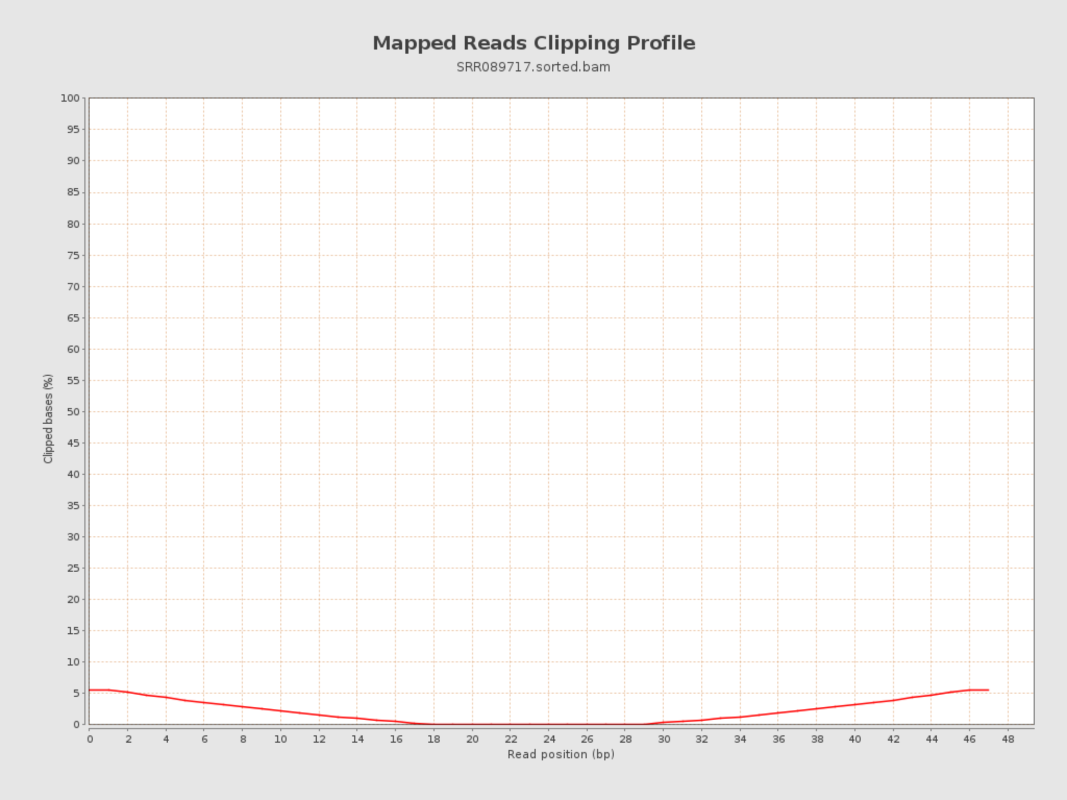
8. Results : Mapped Reads Nucleotide Content



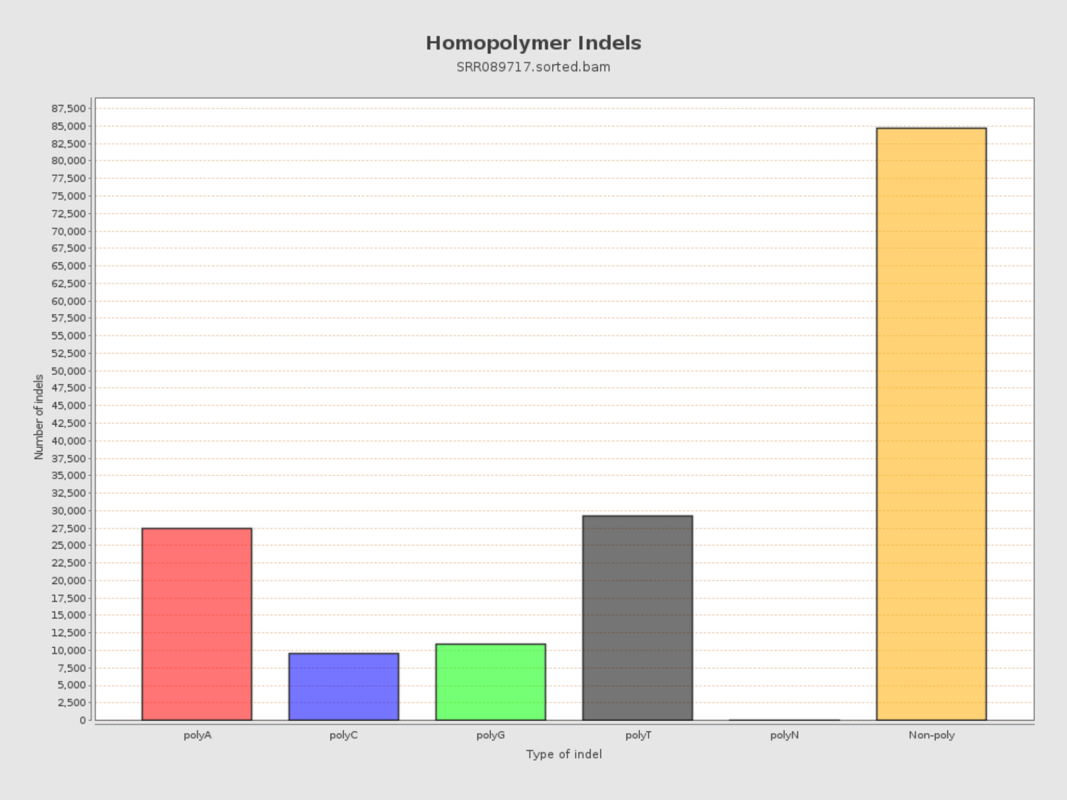
9. Results : Mapped Reads GC-content Distribution



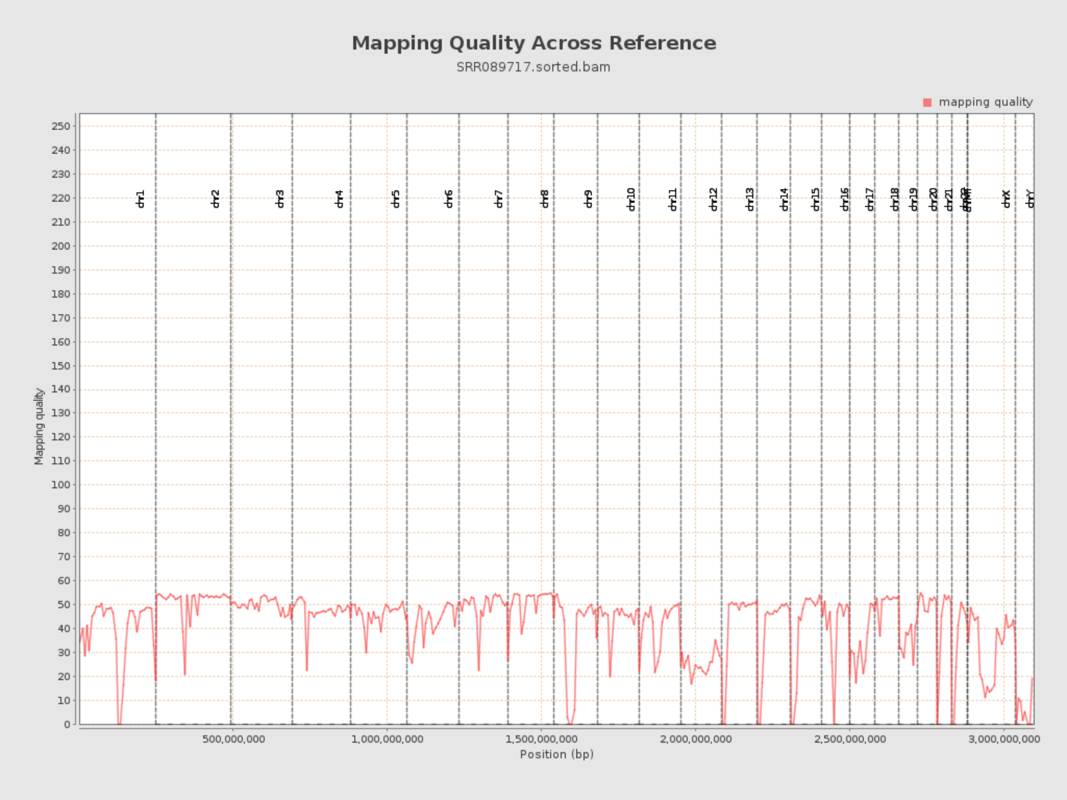
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram