Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 12:58:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089564.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_SRR089564 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089564.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 12:58:41 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089564.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,462,968
Mapped reads	9,182,408 / 80.1%
Unmapped reads	2,280,560 / 19.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	322 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,556,043 / 22.3%
Duplication rate	19.32%
Clipped reads	1,013,325 / 8.84%

2.2. ACGT Content

Number/percentage of A's	137,133,538 / 31.77%
Number/percentage of C's	82,231,399 / 19.05%
Number/percentage of T's	117,863,235 / 27.3%
Number/percentage of G's	93,956,997 / 21.77%
Number/percentage of N's	482,946 / 0.11%
GC Percentage	40.82%

2.3. Coverage

Mean	0.1395

Standard Deviation	1.1062

2.4. Mapping Quality

Mean Mapping Quality	44.86

2.5. Mismatches and indels

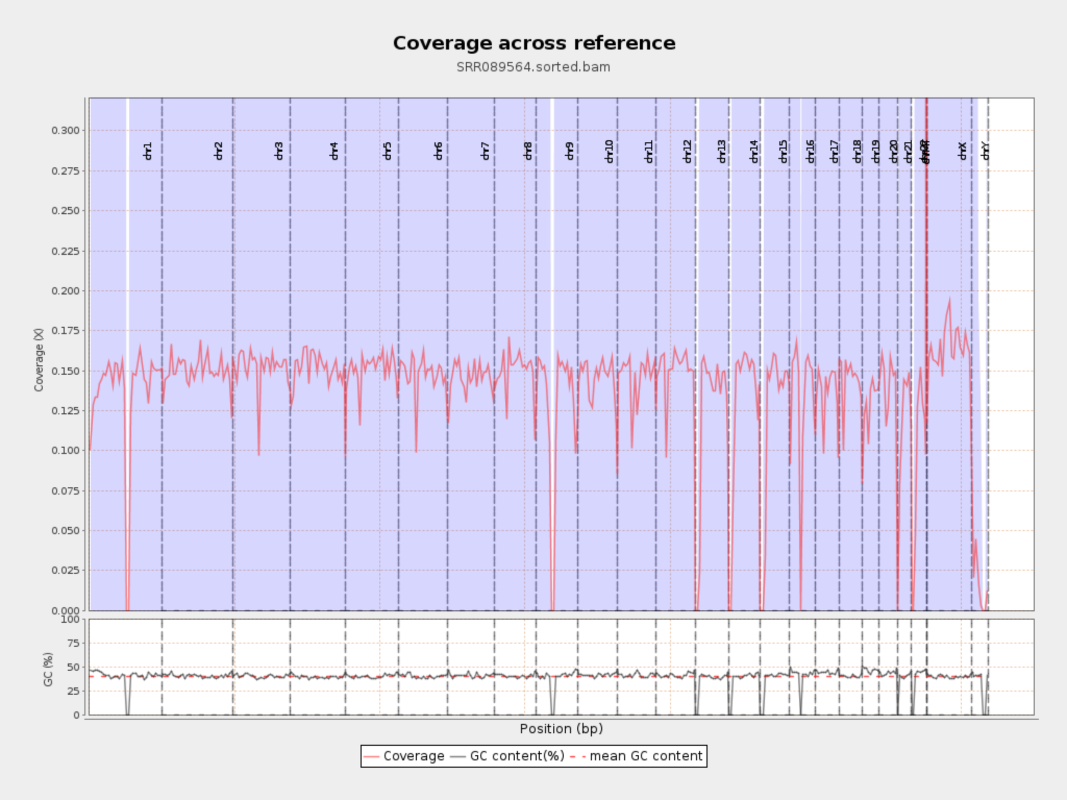
General error rate	0.76%
Mismatches	3,276,861
Insertions	17,176
Mapped reads with at least one insertion	0.19%
Deletions	53,190
Mapped reads with at least one deletion	0.58%
Homopolymer indels	44.81%

2.6. Chromosome stats

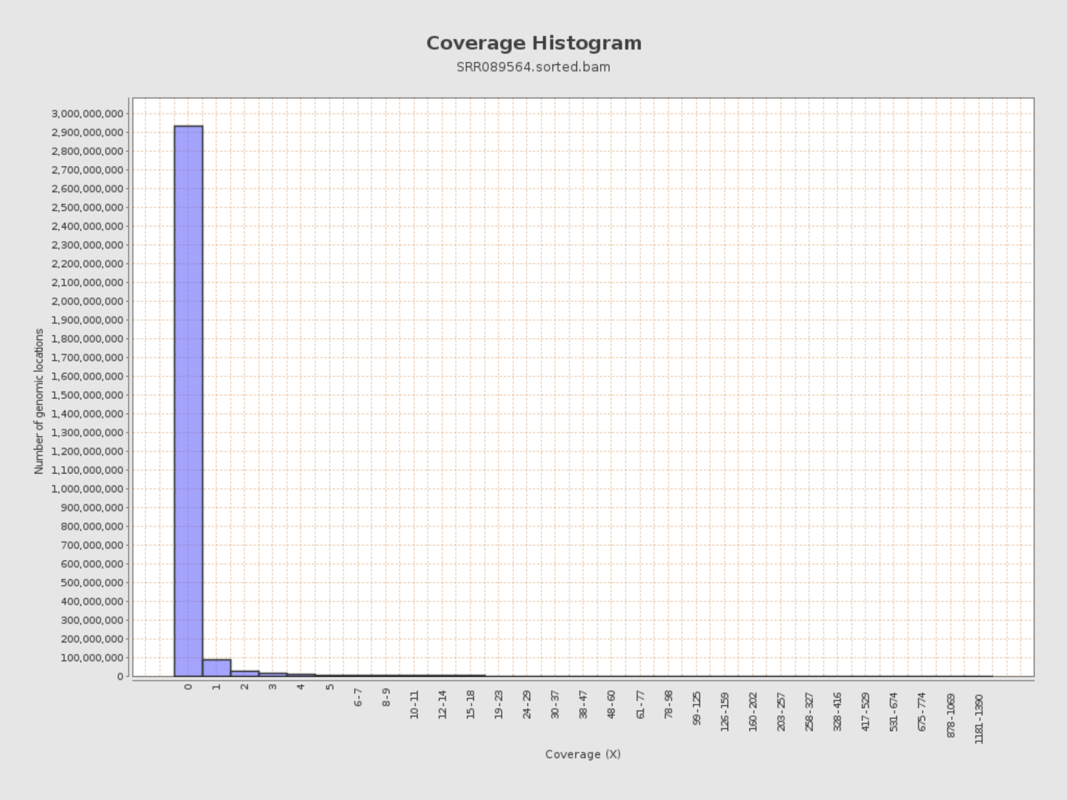
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	33837023	0.1358	1.1363
chr2	243199373	36503758	0.1501	1.2569
chr3	198022430	30179714	0.1524	1.1159
chr4	191154276	28981201	0.1516	1.1286
chr5	180915260	27372060	0.1513	1.102
chr6	171115067	25265421	0.1477	1.1285
chr7	159138663	23249090	0.1461	1.1402

chr8	146364022	21959343	0.15	1.3423
chr9	141213431	17794324	0.126	1.013
chr10	135534747	19915402	0.1469	1.1225
chr11	135006516	19667692	0.1457	1.1139
chr12	133851895	20094118	0.1501	1.0872
chr13	115169878	13945387	0.1211	0.9824
chr14	107349540	13475891	0.1255	1.0763
chr15	102531392	12193073	0.1189	0.9348
chr16	90354753	11941433	0.1322	1.0612
chr17	81195210	11020326	0.1357	0.9913
chr18	78077248	11263803	0.1443	1.1077
chr19	59128983	7613435	0.1288	1.0522
chr20	63025520	8914947	0.1414	1.0553
chr21	48129895	5423511	0.1127	0.9937
chr22	51304566	4651437	0.0907	0.8096
chrMT	16571	44037	2.6575	8.1308
chrX	155270560	25413124	0.1637	1.1737
chrY	59373566	1027922	0.0173	0.3402

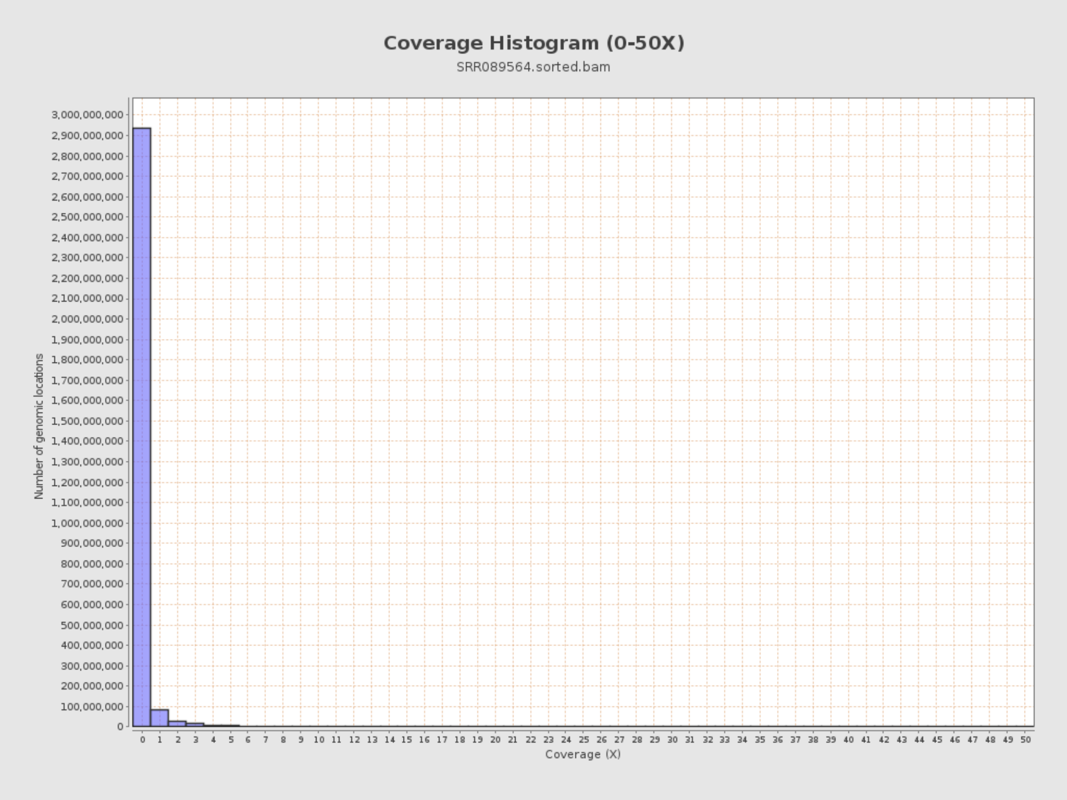
3. Results : Coverage across reference



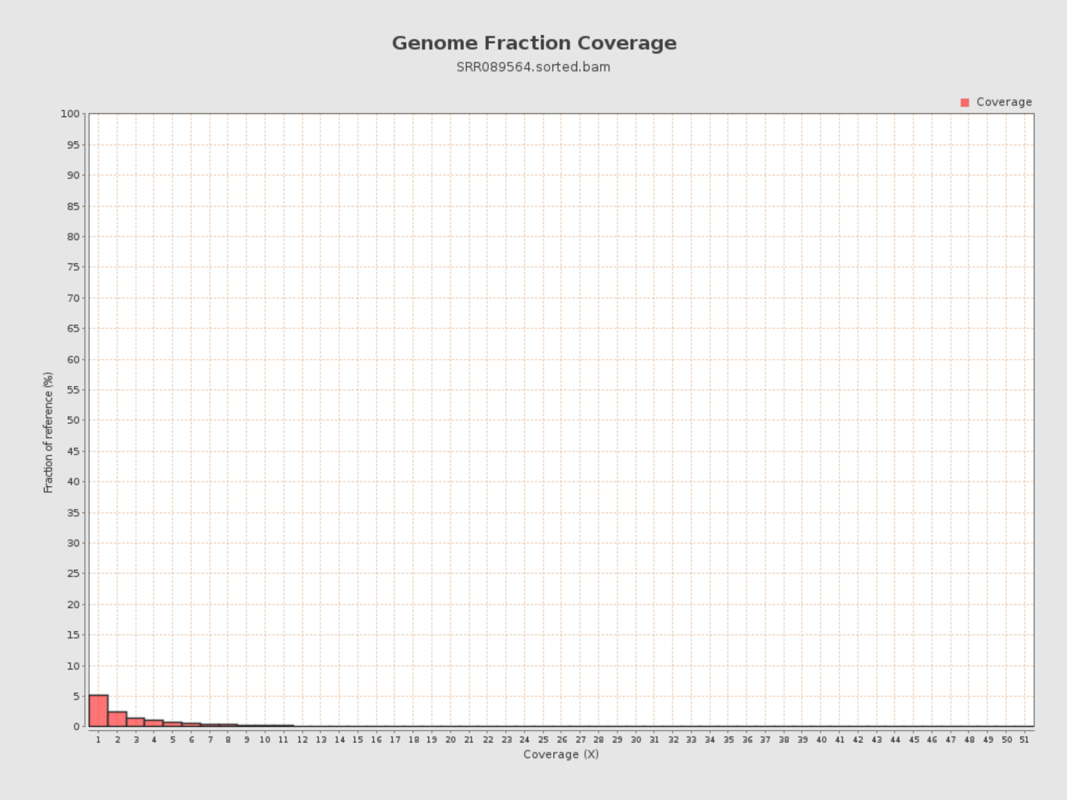
4. Results : Coverage Histogram



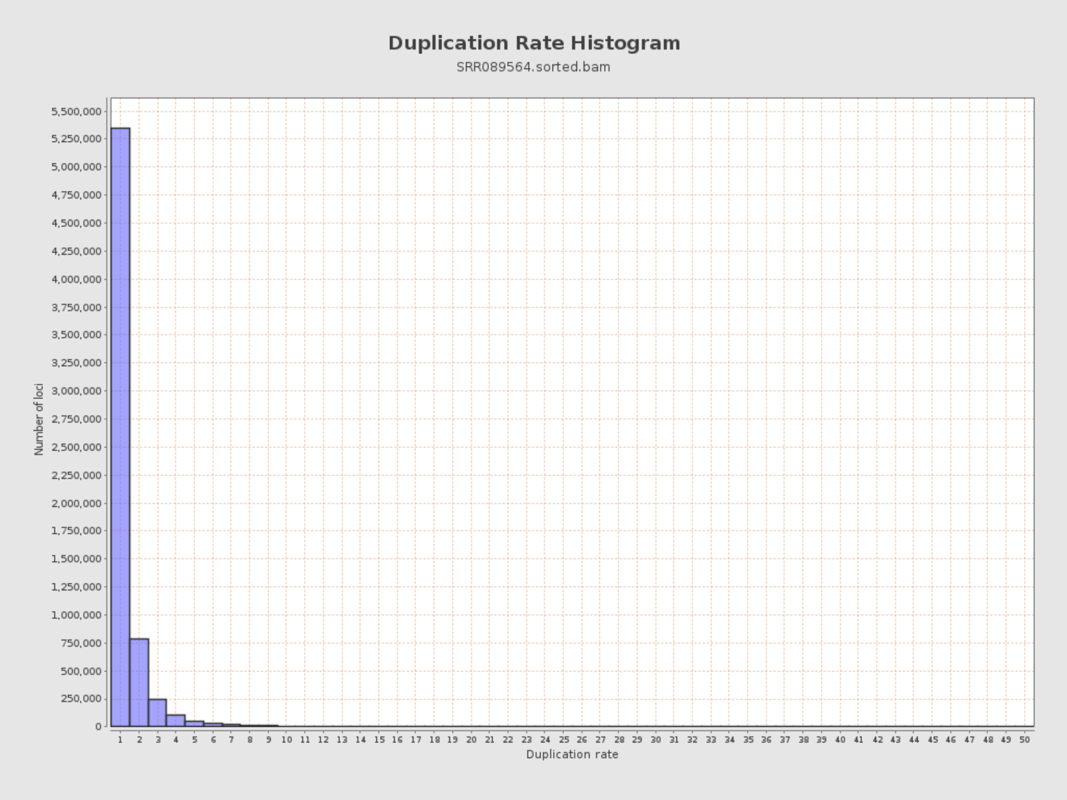
5. Results : Coverage Histogram (0-50X)



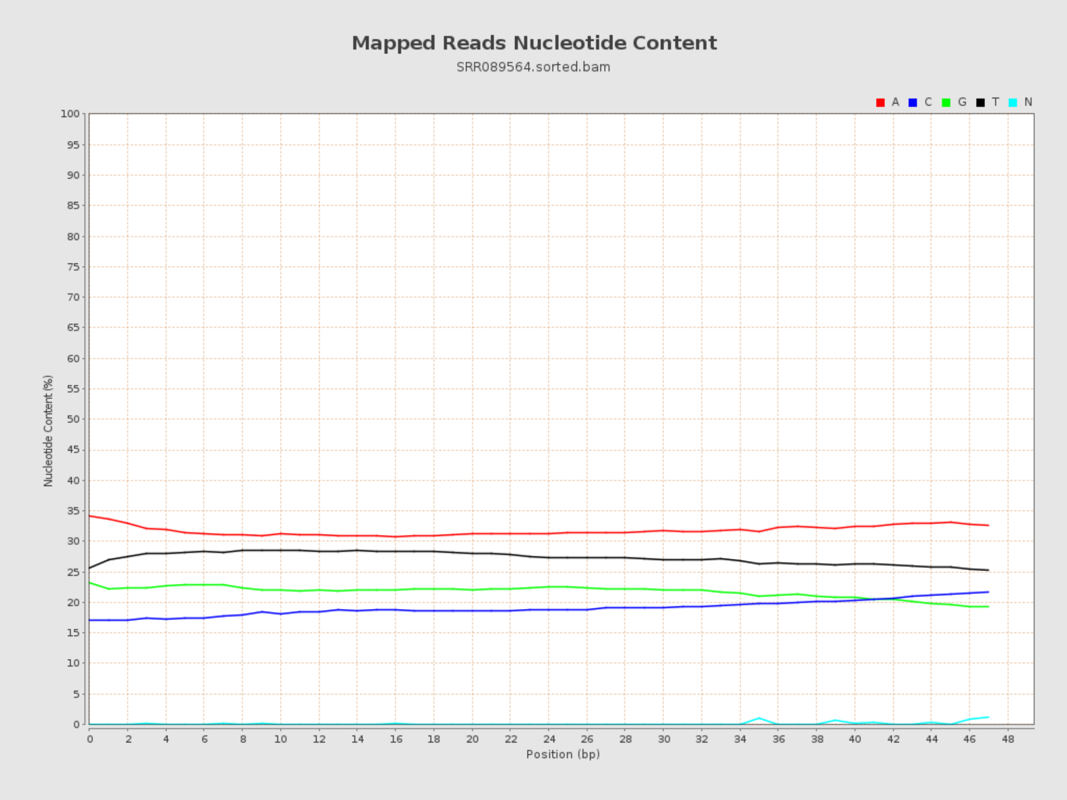
6. Results : Genome Fraction Coverage



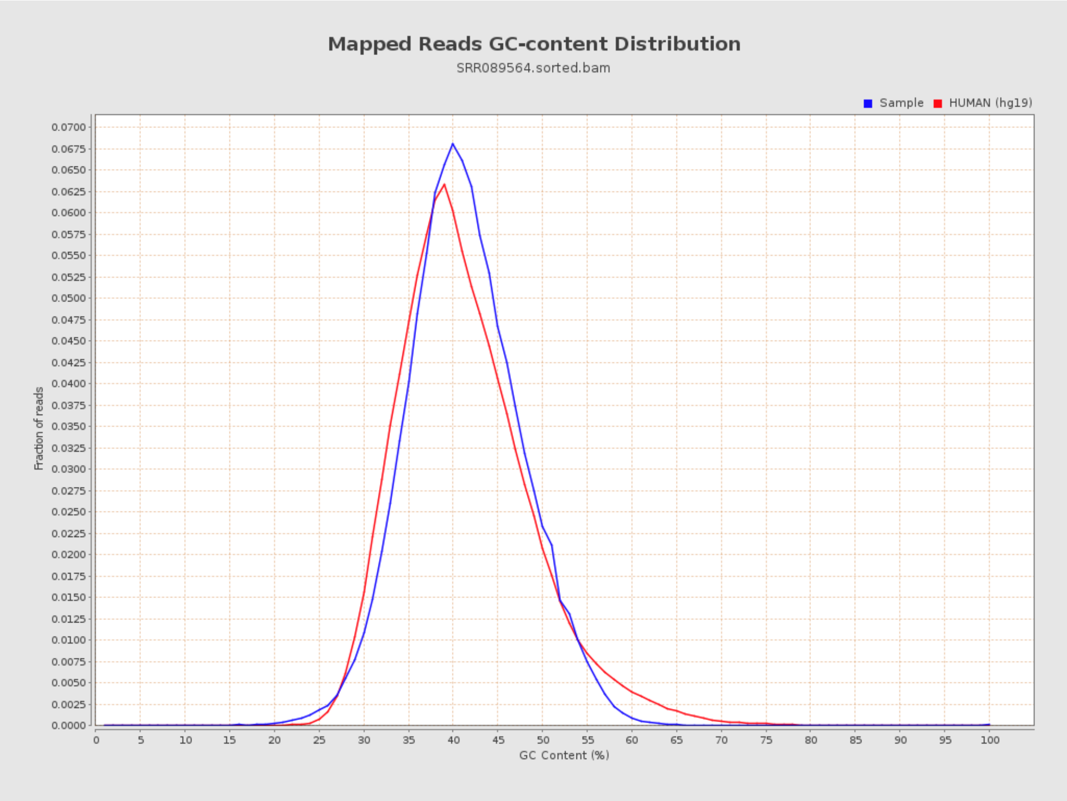
7. Results : Duplication Rate Histogram



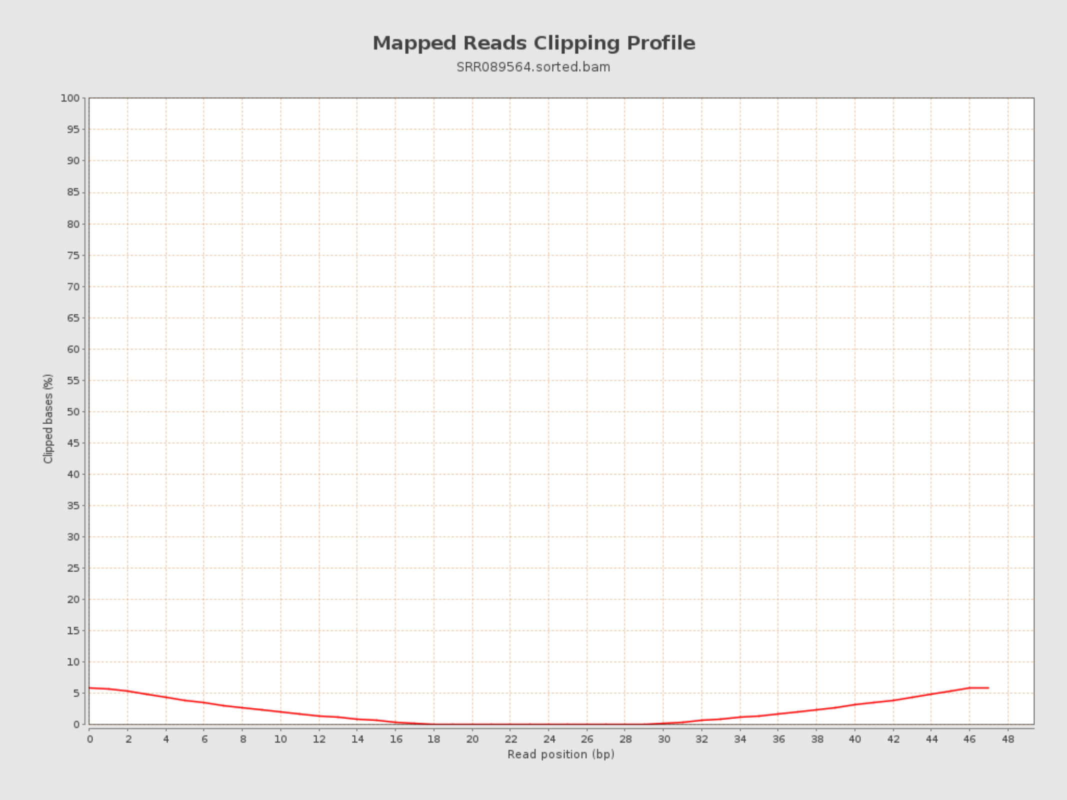
8. Results : Mapped Reads Nucleotide Content



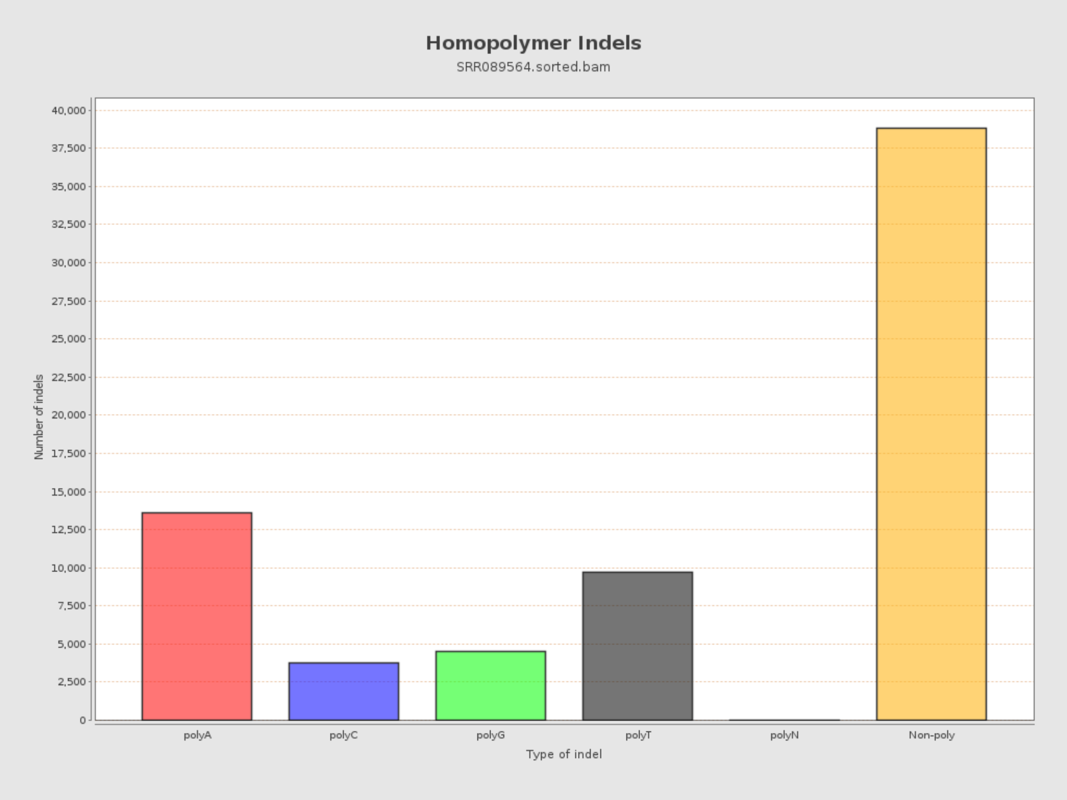
9. Results : Mapped Reads GC-content Distribution



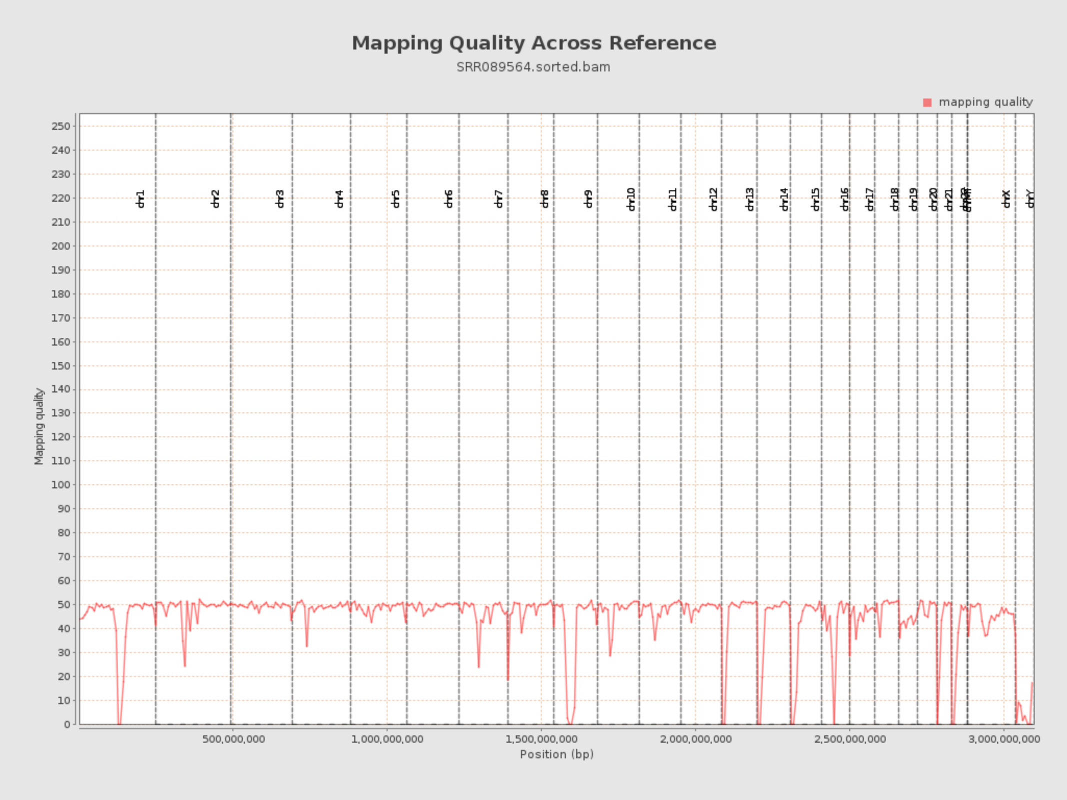
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram