Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 02:01:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053639.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_SRR053639 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053639.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 02:01:25 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053639.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,548,560
Mapped reads	10,036,248 / 68.98%
Unmapped reads	4,512,312 / 31.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	230 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	3,167,718 / 21.77%
Duplication rate	20.11%
Clipped reads	1,073,817 / 7.38%

2.2. ACGT Content

Number/percentage of A's	140,864,153 / 29.83%
Number/percentage of C's	94,495,816 / 20.01%
Number/percentage of T's	137,854,442 / 29.19%
Number/percentage of G's	99,014,416 / 20.97%
Number/percentage of N's	997 / 0%
GC Percentage	40.98%

2.3. Coverage

Mean	0.1526

Standard Deviation	1.3731

2.4. Mapping Quality

Mean Mapping Quality	44.89

2.5. Mismatches and indels

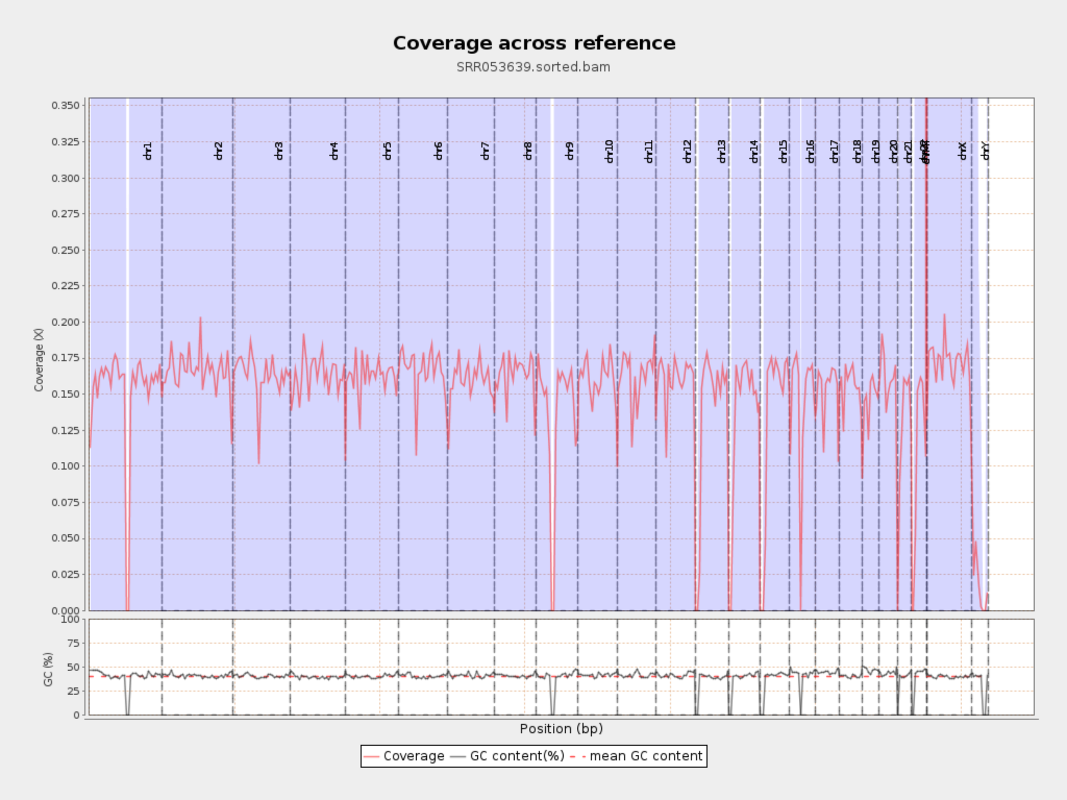
General error rate	0.57%
Mismatches	2,661,031
Insertions	19,617
Mapped reads with at least one insertion	0.2%
Deletions	63,693
Mapped reads with at least one deletion	0.63%
Homopolymer indels	46.84%

2.6. Chromosome stats

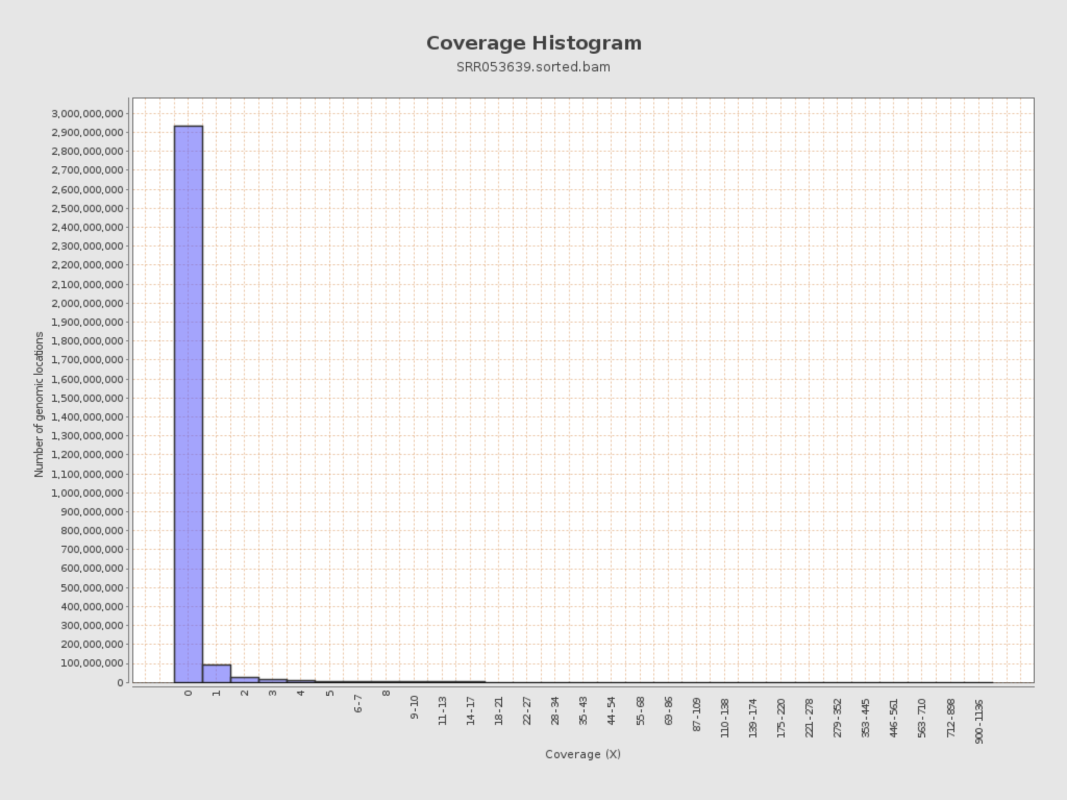
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	37625191	0.151	1.4157
chr2	243199373	40565237	0.1668	1.6019
chr3	198022430	32355791	0.1634	1.3346
chr4	191154276	31156549	0.163	1.3888
chr5	180915260	29379056	0.1624	1.3221
chr6	171115067	28509259	0.1666	1.4697
chr7	159138663	25536185	0.1605	1.4937

chr8	146364022	24015456	0.1641	1.4625
chr9	141213431	19040311	0.1348	1.2456
chr10	135534747	21973095	0.1621	1.4157
chr11	135006516	21863250	0.1619	1.4843
chr12	133851895	21406569	0.1599	1.3145
chr13	115169878	15421751	0.1339	1.1948
chr14	107349540	14308801	0.1333	1.3399
chr15	102531392	13708355	0.1337	1.1991
chr16	90354753	13069878	0.1447	1.3162
chr17	81195210	12328887	0.1518	1.2367
chr18	78077248	12188479	0.1561	1.4461
chr19	59128983	8615619	0.1457	1.3744
chr20	63025520	10106671	0.1604	1.3299
chr21	48129895	5953792	0.1237	1.2029
chr22	51304566	5232928	0.102	0.9637
chrMT	16571	80382	4.8508	9.618
chrX	155270560	26726444	0.1721	1.4251
chrY	59373566	1155917	0.0195	0.4118

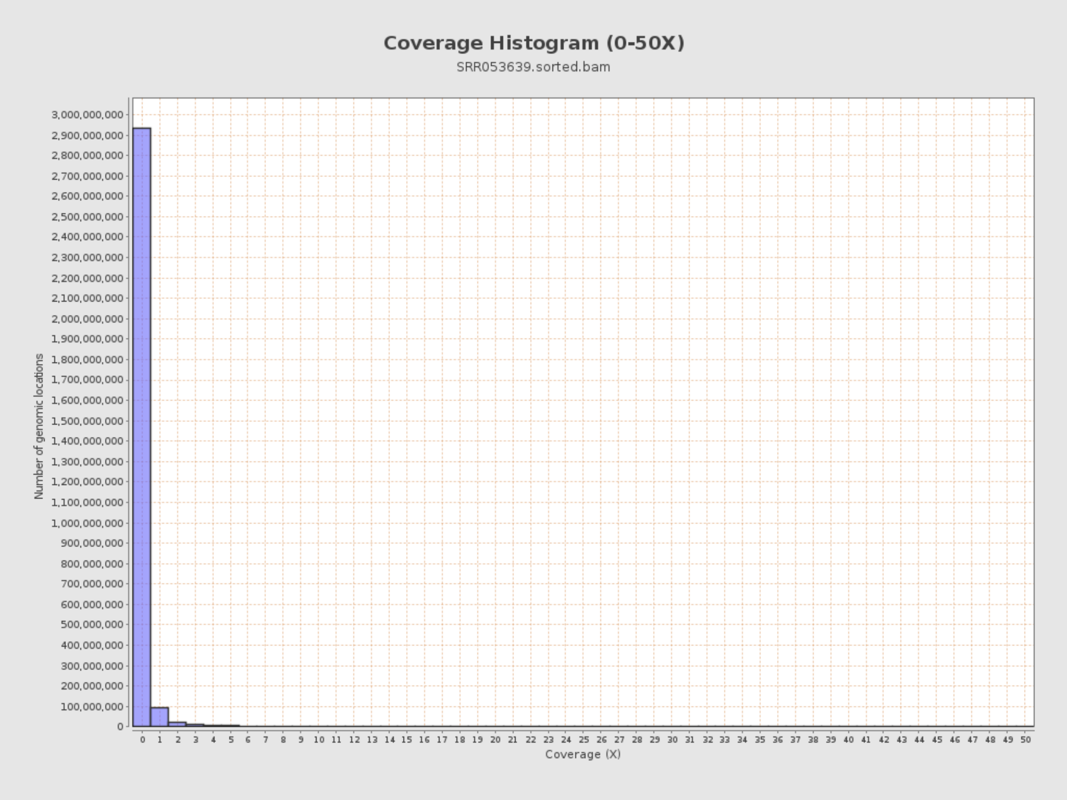
3. Results : Coverage across reference



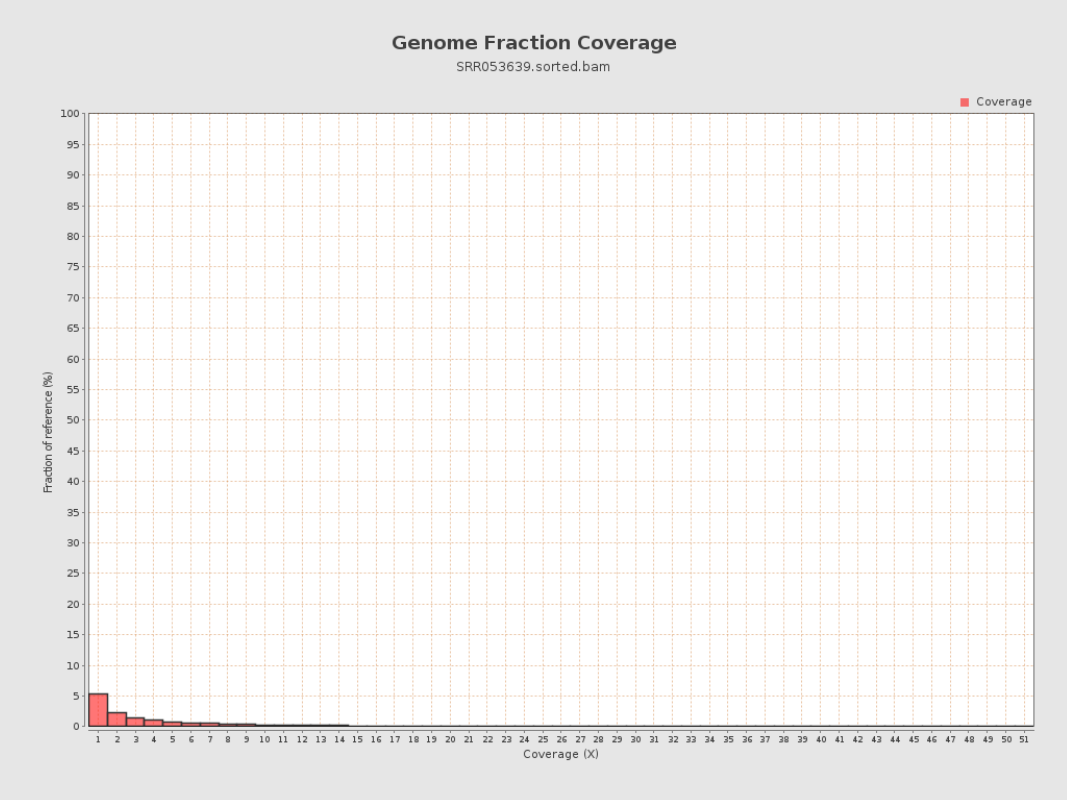
4. Results : Coverage Histogram



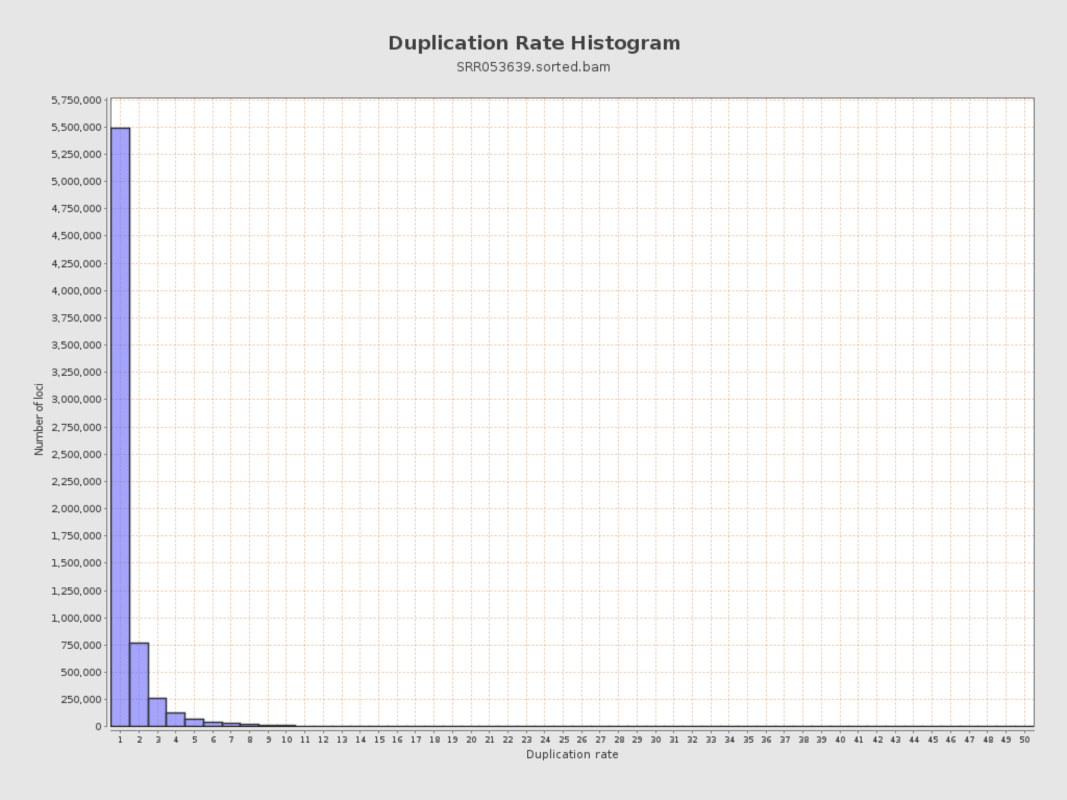
5. Results : Coverage Histogram (0-50X)



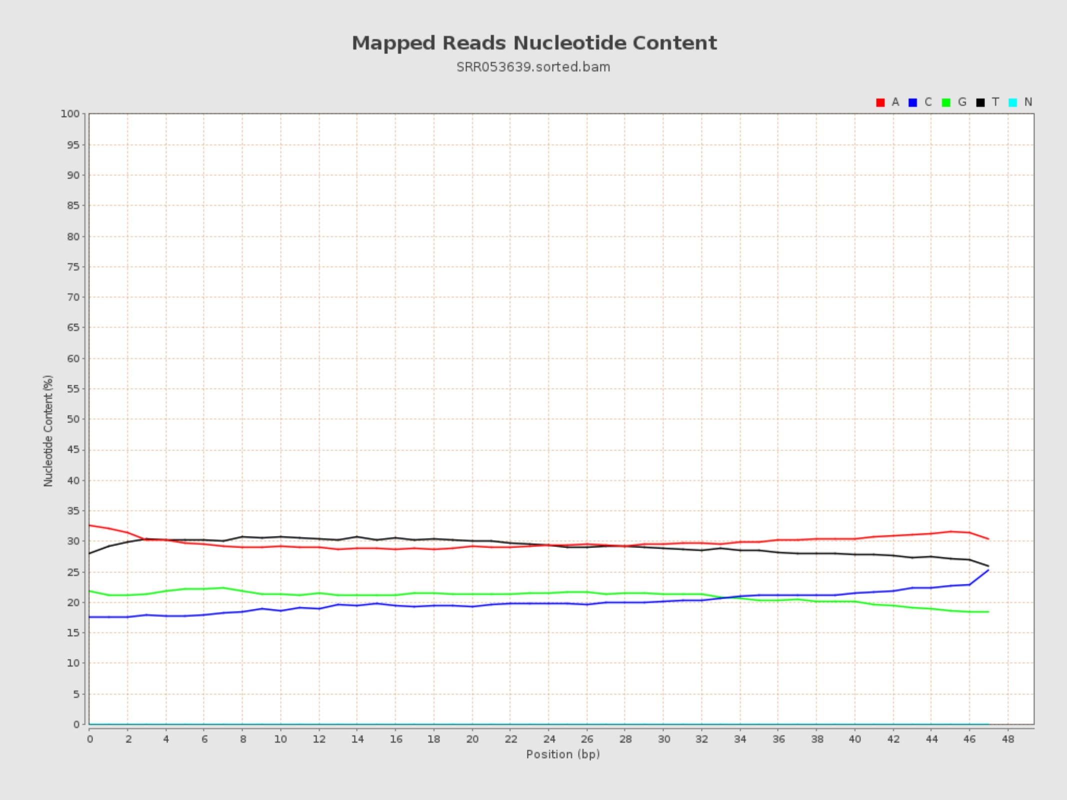
6. Results : Genome Fraction Coverage



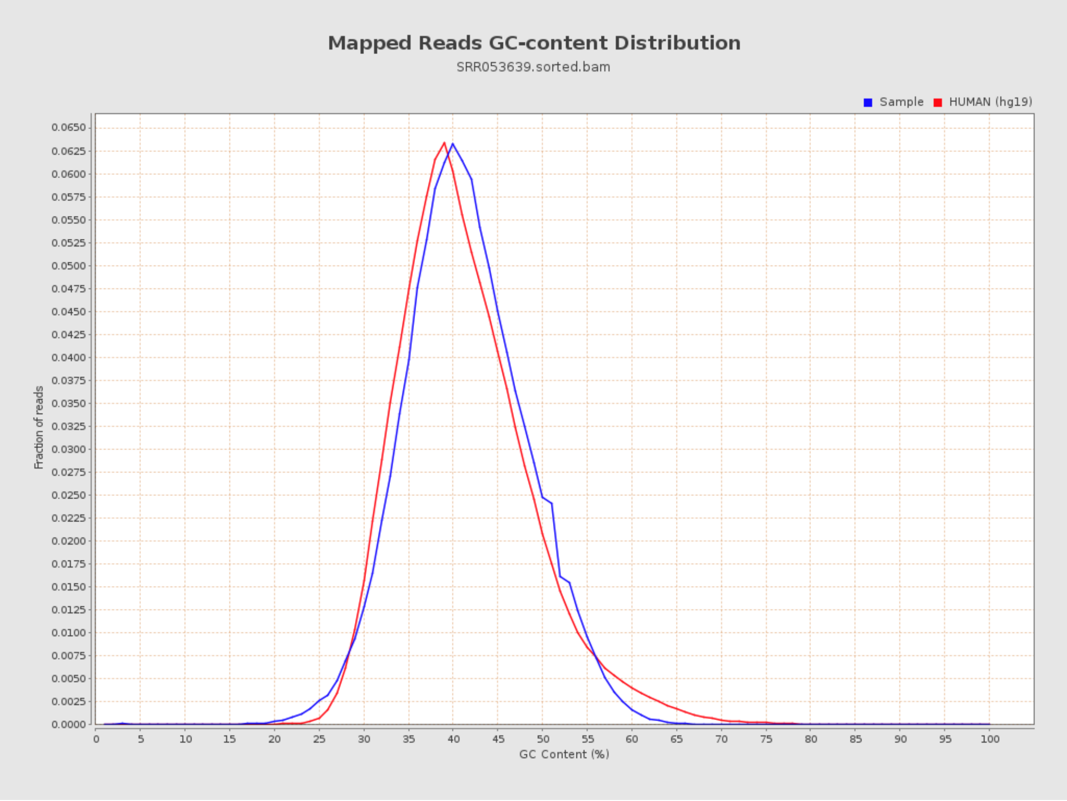
7. Results : Duplication Rate Histogram



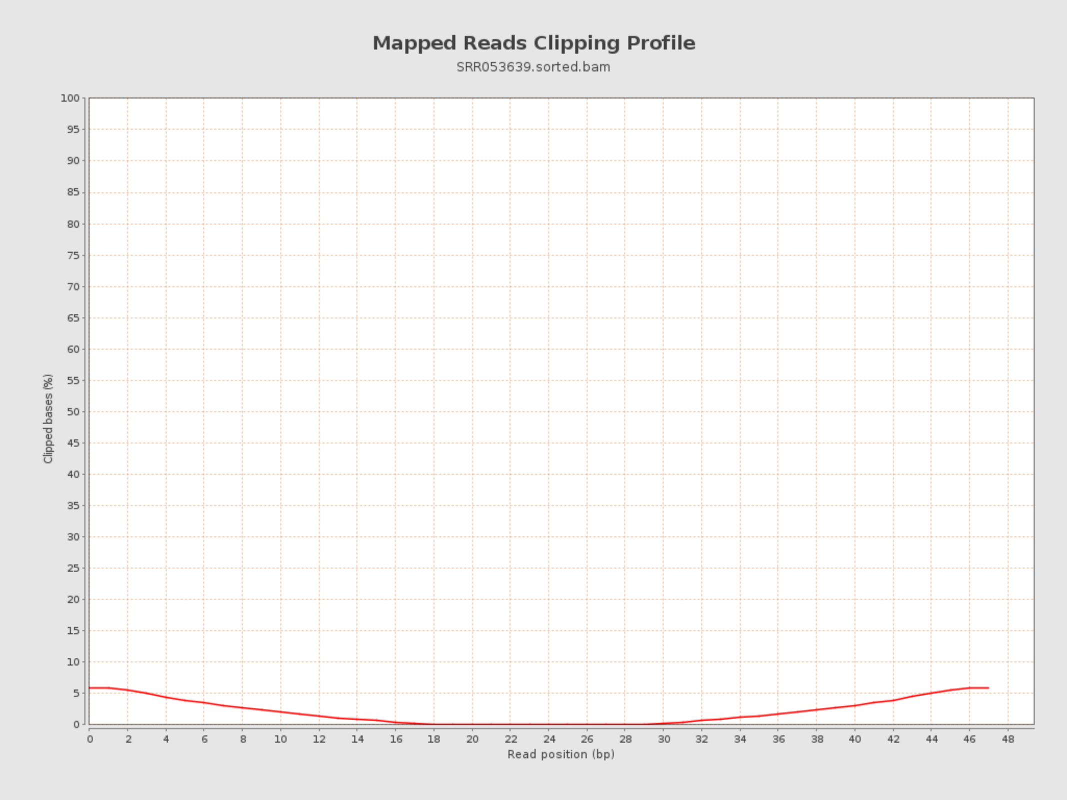
8. Results : Mapped Reads Nucleotide Content



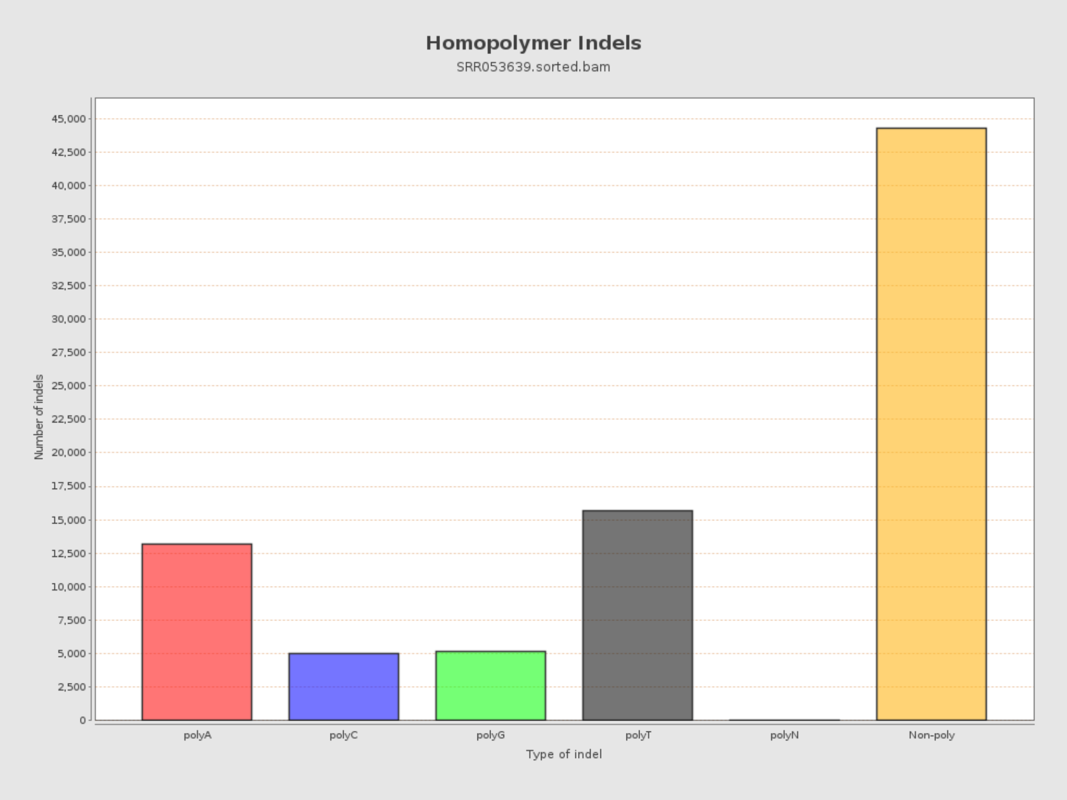
9. Results : Mapped Reads GC-content Distribution



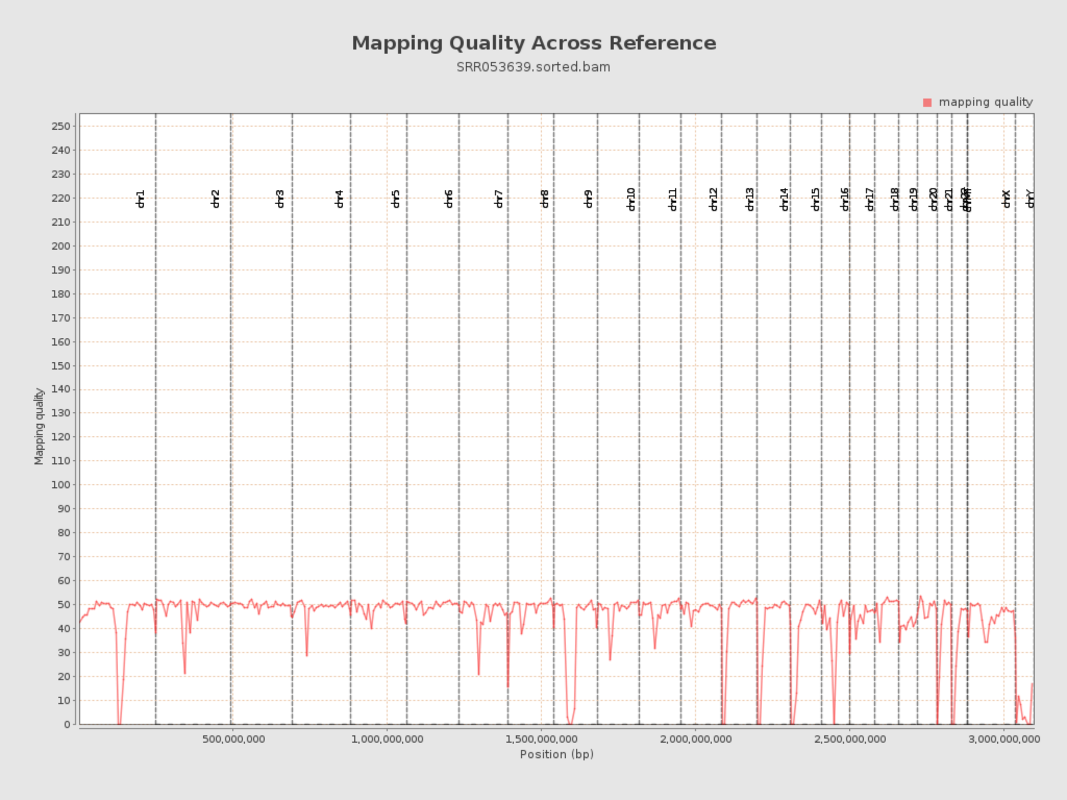
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram