Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 01:34:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053635.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_SRR053635 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053635.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 01:34:45 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053635.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,269,824
Mapped reads	9,924,272 / 74.79%
Unmapped reads	3,345,552 / 25.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	257 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	3,247,350 / 24.47%
Duplication rate	20.86%
Clipped reads	1,247,422 / 9.4%

2.2. ACGT Content

Number/percentage of A's	143,139,948 / 30.78%
Number/percentage of C's	90,485,429 / 19.46%
Number/percentage of T's	138,023,884 / 29.68%
Number/percentage of G's	93,369,253 / 20.08%
Number/percentage of N's	2,690 / 0%
GC Percentage	39.54%

2.3. Coverage

Mean	0.1502

Standard Deviation	1.3187

2.4. Mapping Quality

Mean Mapping Quality	45.1

2.5. Mismatches and indels

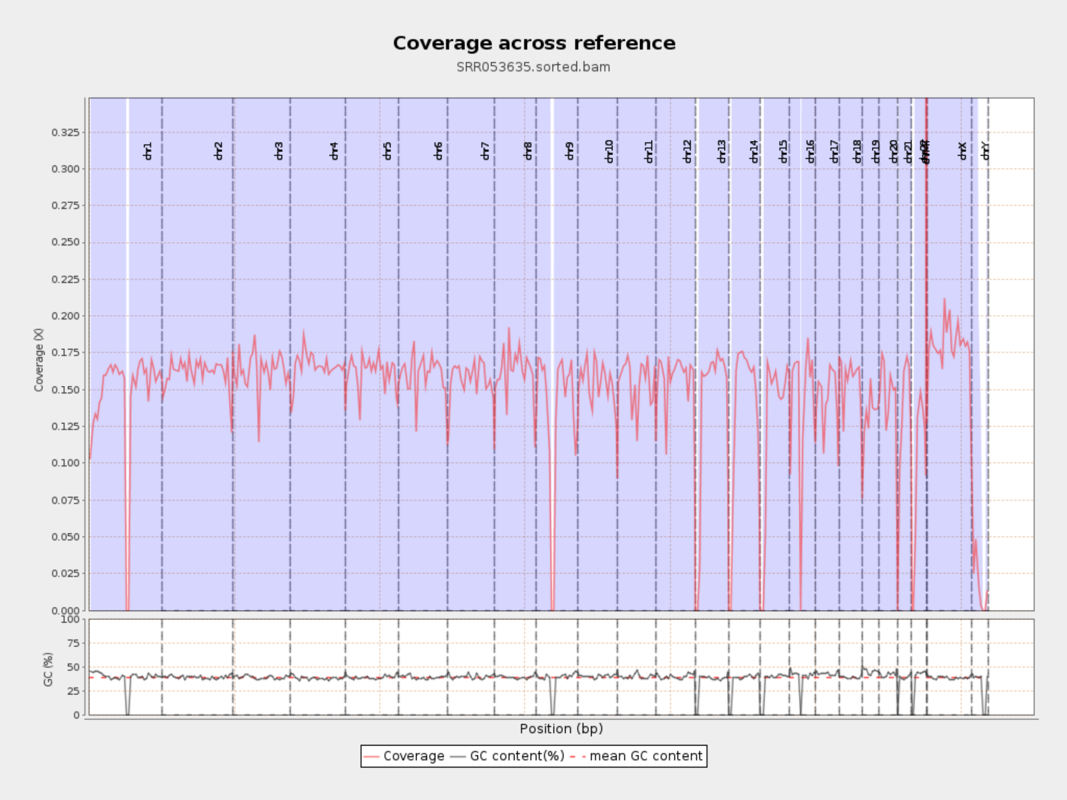
General error rate	0.56%
Mismatches	2,590,422
Insertions	20,671
Mapped reads with at least one insertion	0.21%
Deletions	64,285
Mapped reads with at least one deletion	0.65%
Homopolymer indels	46.98%

2.6. Chromosome stats

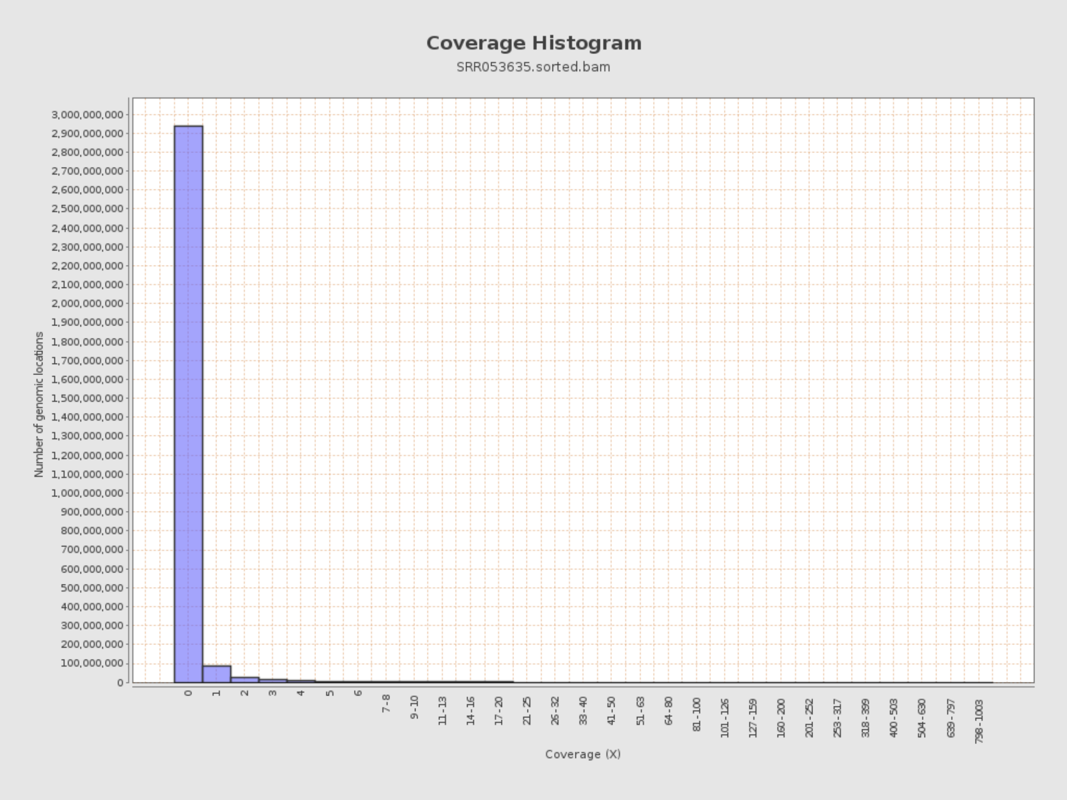
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	36205076	0.1453	1.3548
chr2	243199373	39357236	0.1618	1.4472
chr3	198022430	32351280	0.1634	1.3139
chr4	191154276	31700937	0.1658	1.3726
chr5	180915260	29313479	0.162	1.2862
chr6	171115067	27501618	0.1607	1.3671
chr7	159138663	25282202	0.1589	1.4385

chr8	146364022	23783526	0.1625	1.4359
chr9	141213431	19086956	0.1352	1.2187
chr10	135534747	21168773	0.1562	1.3352
chr11	135006516	20854514	0.1545	1.3979
chr12	133851895	21153956	0.158	1.2793
chr13	115169878	15783412	0.137	1.2043
chr14	107349540	14541459	0.1355	1.308
chr15	102531392	12920473	0.126	1.1145
chr16	90354753	12817604	0.1419	1.2218
chr17	81195210	11642711	0.1434	1.1819
chr18	78077248	12310823	0.1577	1.4263
chr19	59128983	7866584	0.133	1.259
chr20	63025520	9321298	0.1479	1.245
chr21	48129895	6140008	0.1276	1.191
chr22	51304566	4754141	0.0927	0.929
chrMT	16571	103829	6.2657	15.3755
chrX	155270560	27985319	0.1802	1.4481
chrY	59373566	1167907	0.0197	0.3872

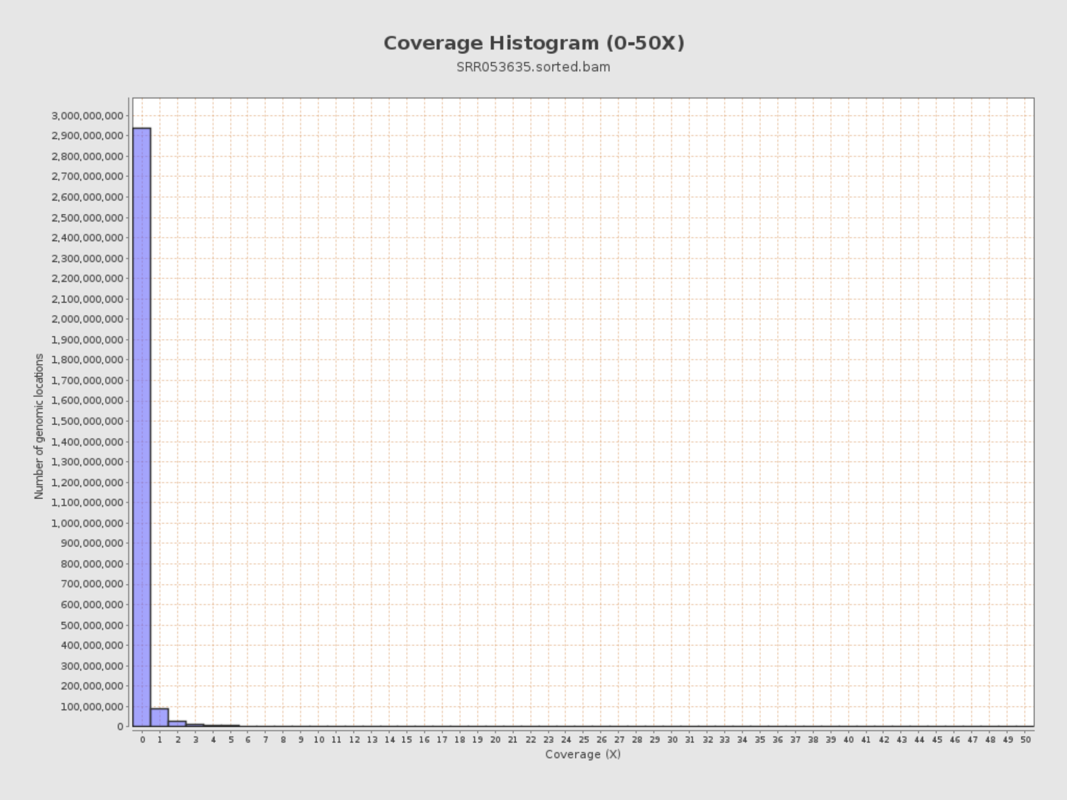
3. Results : Coverage across reference



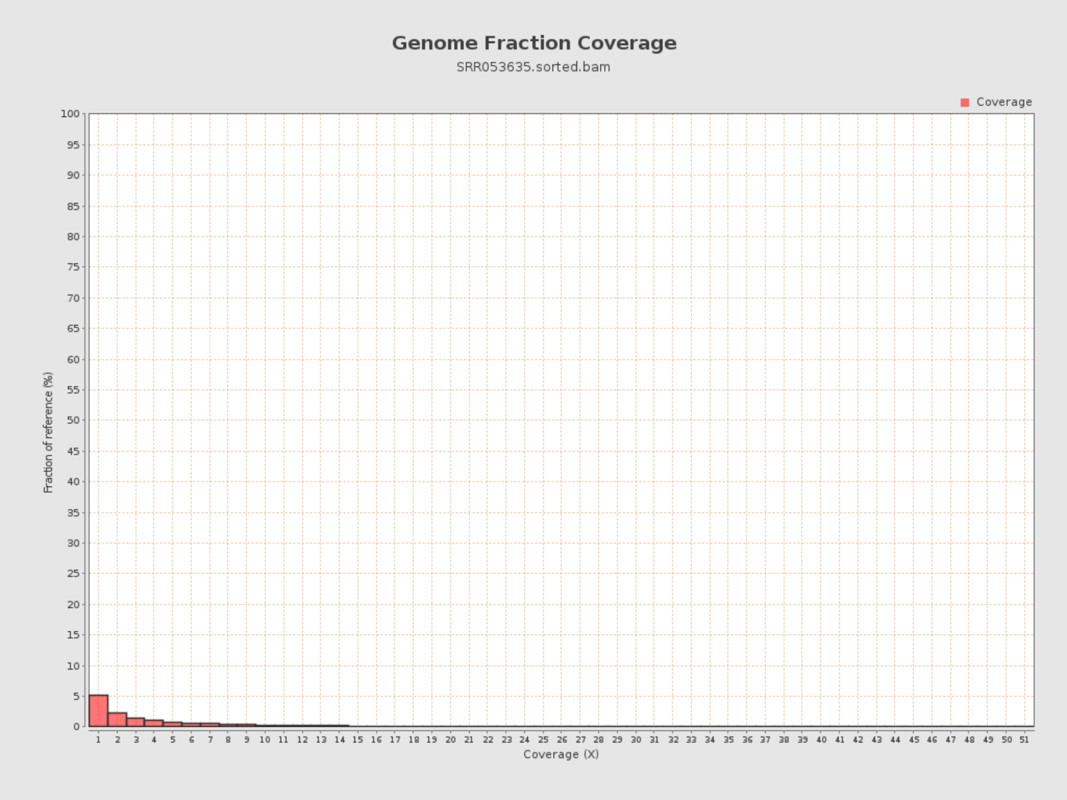
4. Results : Coverage Histogram



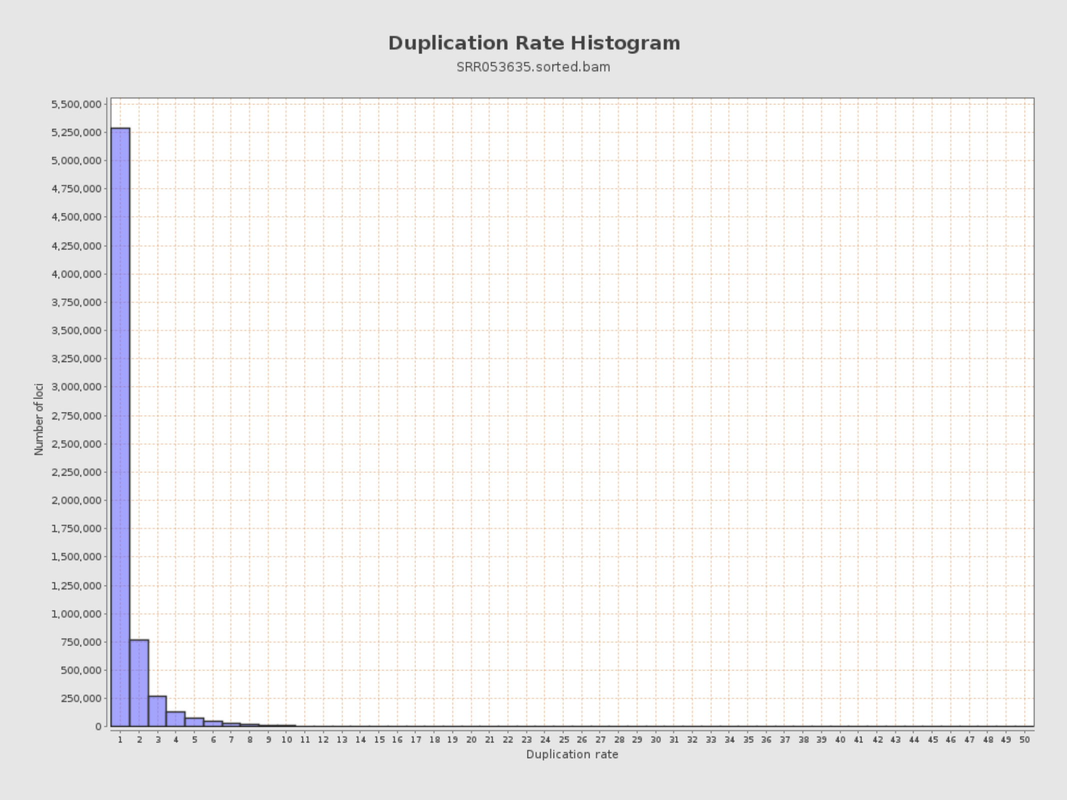
5. Results : Coverage Histogram (0-50X)



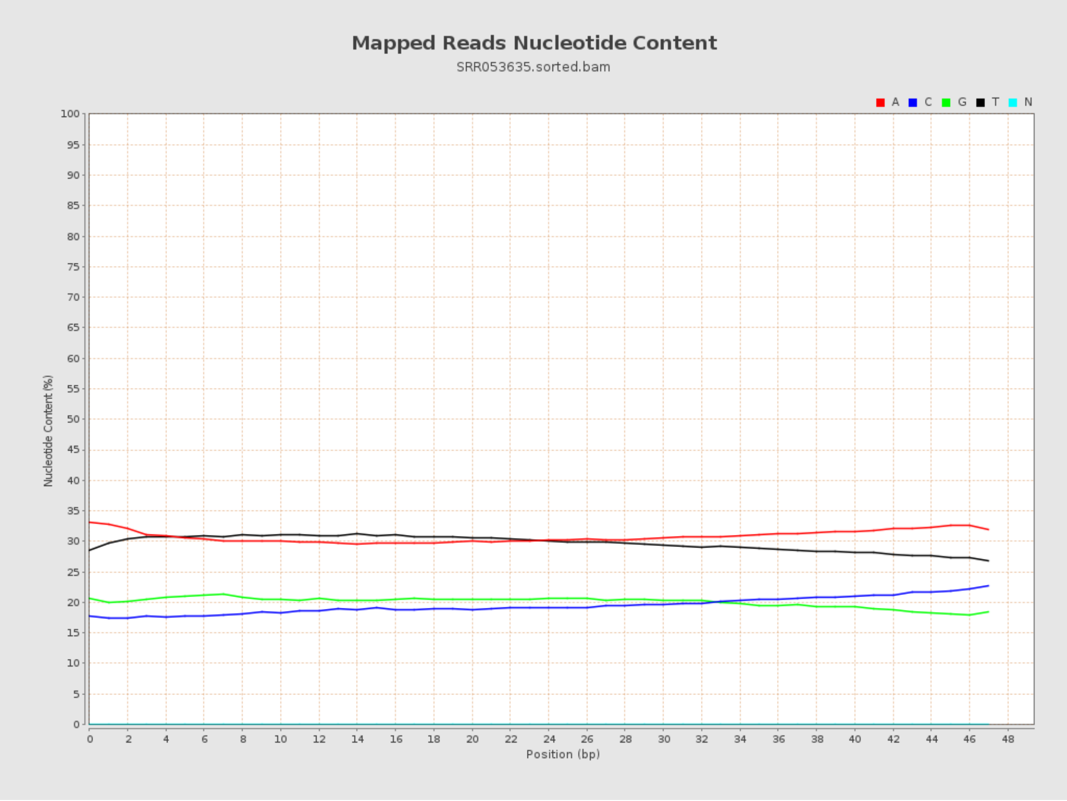
6. Results : Genome Fraction Coverage



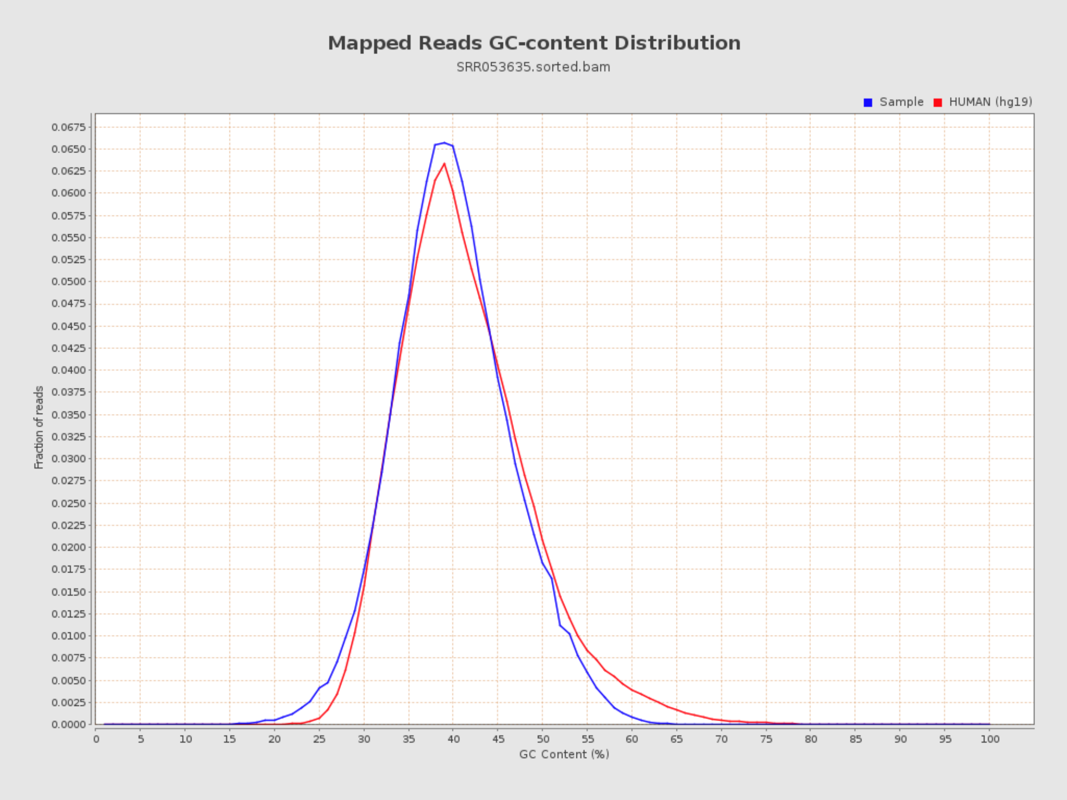
7. Results : Duplication Rate Histogram



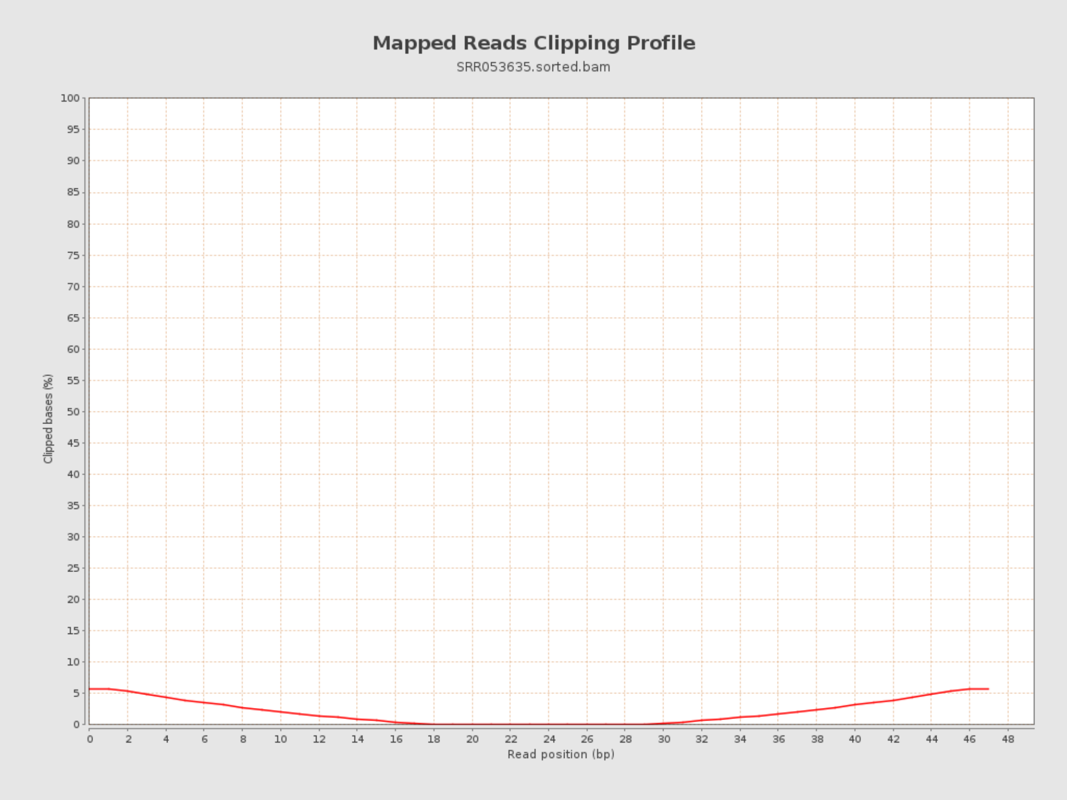
8. Results : Mapped Reads Nucleotide Content



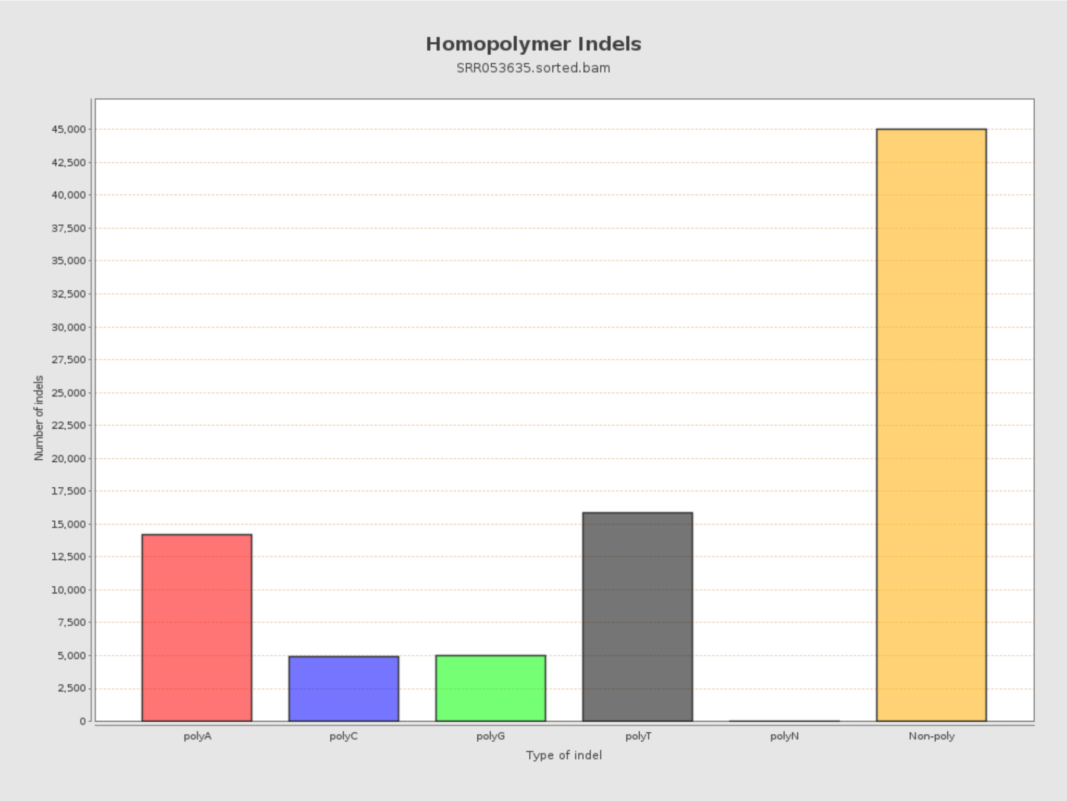
9. Results : Mapped Reads GC-content Distribution



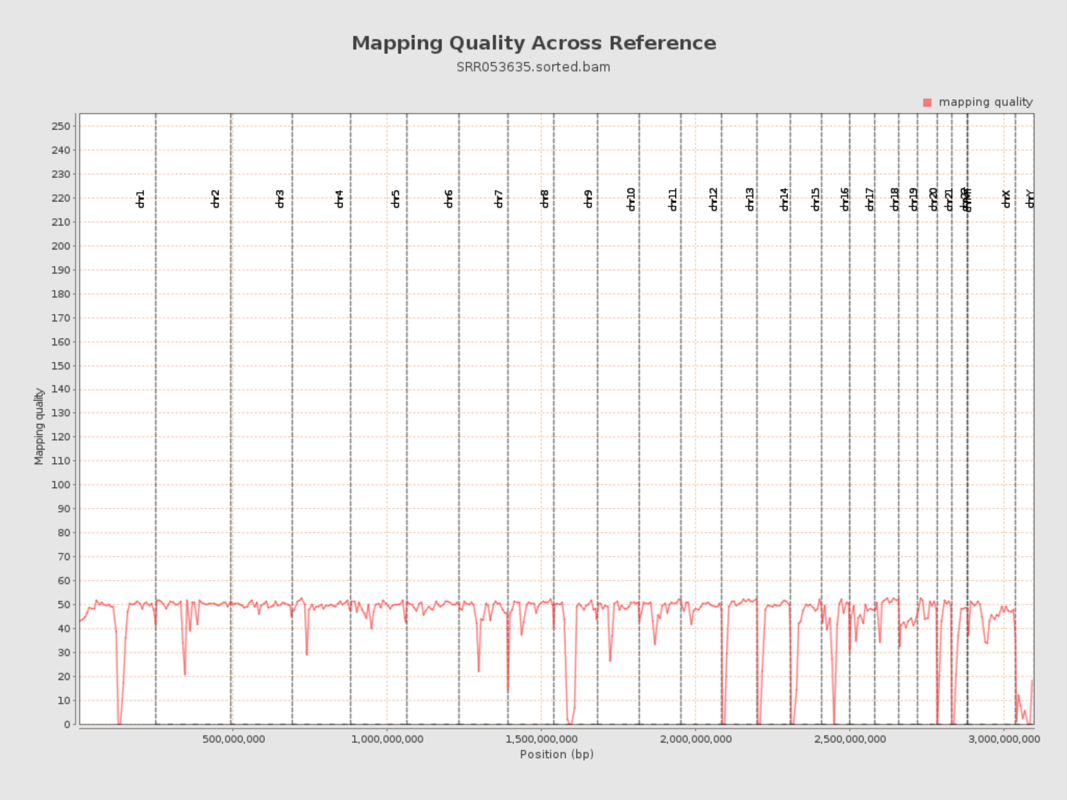
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram