Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 02:54:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053673.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_SRR053673 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053673.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 02:54:07 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053673.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,768,677
Mapped reads	4,570,163 / 79.22%
Unmapped reads	1,198,514 / 20.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	120 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	864,699 / 14.99%
Duplication rate	13.76%
Clipped reads	483,591 / 8.38%

2.2. ACGT Content

Number/percentage of A's	62,312,762 / 28.98%
Number/percentage of C's	43,414,474 / 20.19%
Number/percentage of T's	62,211,450 / 28.93%
Number/percentage of G's	46,979,361 / 21.85%
Number/percentage of N's	96,318 / 0.04%
GC Percentage	42.04%

2.3. Coverage

Mean	0.0695

Standard Deviation	0.5939

2.4. Mapping Quality

Mean Mapping Quality	44.4

2.5. Mismatches and indels

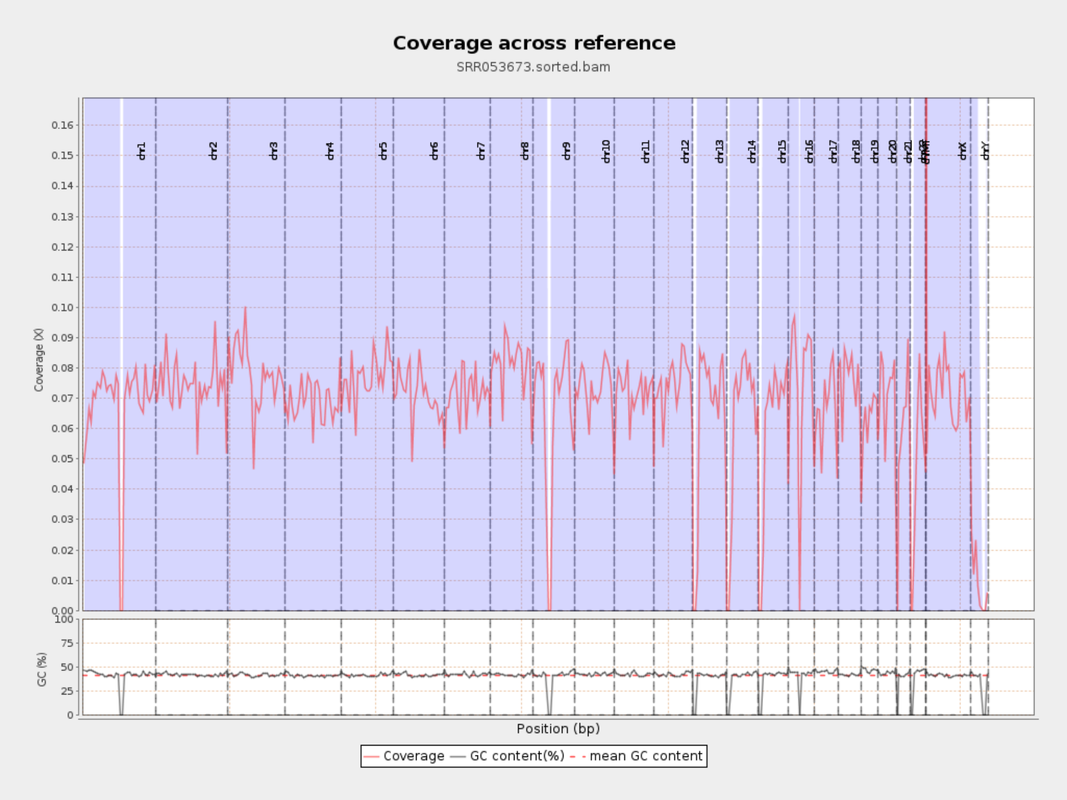
General error rate	0.71%
Mismatches	1,511,424
Insertions	9,778
Mapped reads with at least one insertion	0.21%
Deletions	28,848
Mapped reads with at least one deletion	0.63%
Homopolymer indels	45.2%

2.6. Chromosome stats

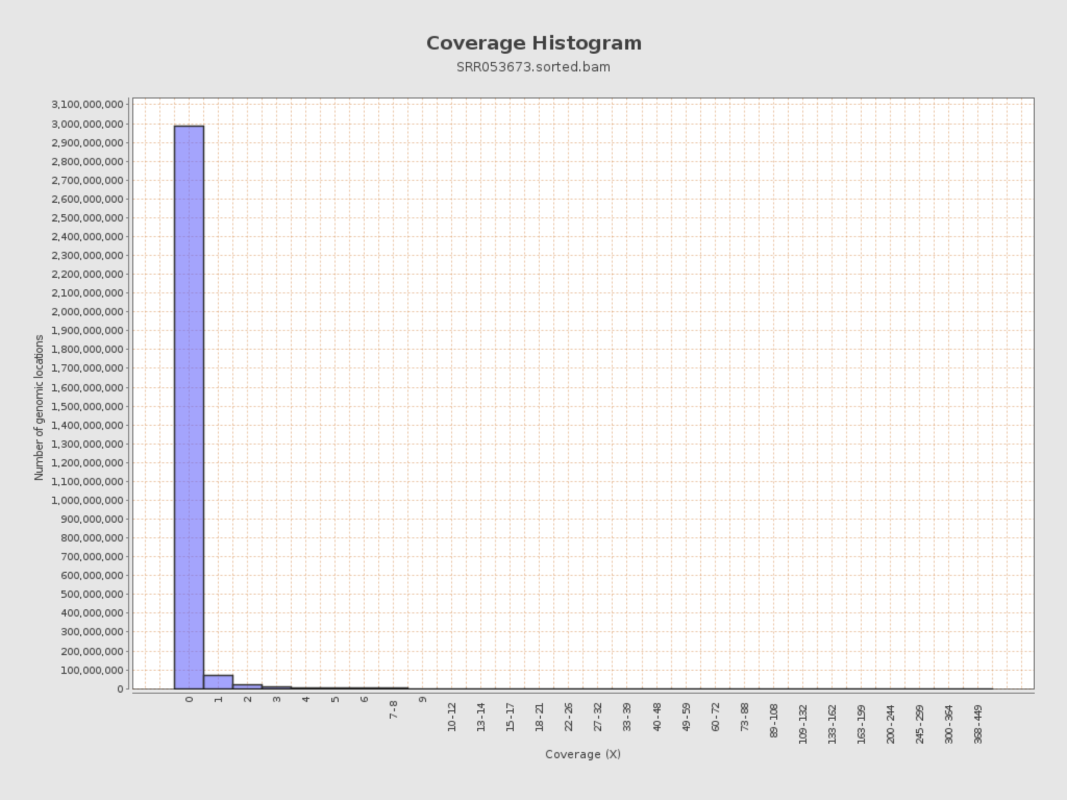
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16779310	0.0673	0.6128
chr2	243199373	18129266	0.0745	0.6633
chr3	198022430	15462463	0.0781	0.5949
chr4	191154276	13234467	0.0692	0.5706
chr5	180915260	13924162	0.077	0.592
chr6	171115067	12238164	0.0715	0.6226
chr7	159138663	11367212	0.0714	0.6398

chr8	146364022	11831706	0.0808	0.6669
chr9	141213431	9282132	0.0657	0.5555
chr10	135534747	10008470	0.0738	0.61
chr11	135006516	9705156	0.0719	0.6108
chr12	133851895	10107081	0.0755	0.5888
chr13	115169878	7267299	0.0631	0.5316
chr14	107349540	6694182	0.0624	0.5683
chr15	102531392	5984898	0.0584	0.5104
chr16	90354753	6526850	0.0722	0.5824
chr17	81195210	5456343	0.0672	0.5308
chr18	78077248	5969157	0.0765	0.634
chr19	59128983	3751625	0.0634	0.6155
chr20	63025520	4517161	0.0717	0.5996
chr21	48129895	2779602	0.0578	0.5639
chr22	51304566	2352125	0.0458	0.4267
chrMT	16571	20237	1.2212	2.1805
chrX	155270560	11143524	0.0718	0.605
chrY	59373566	522704	0.0088	0.2096

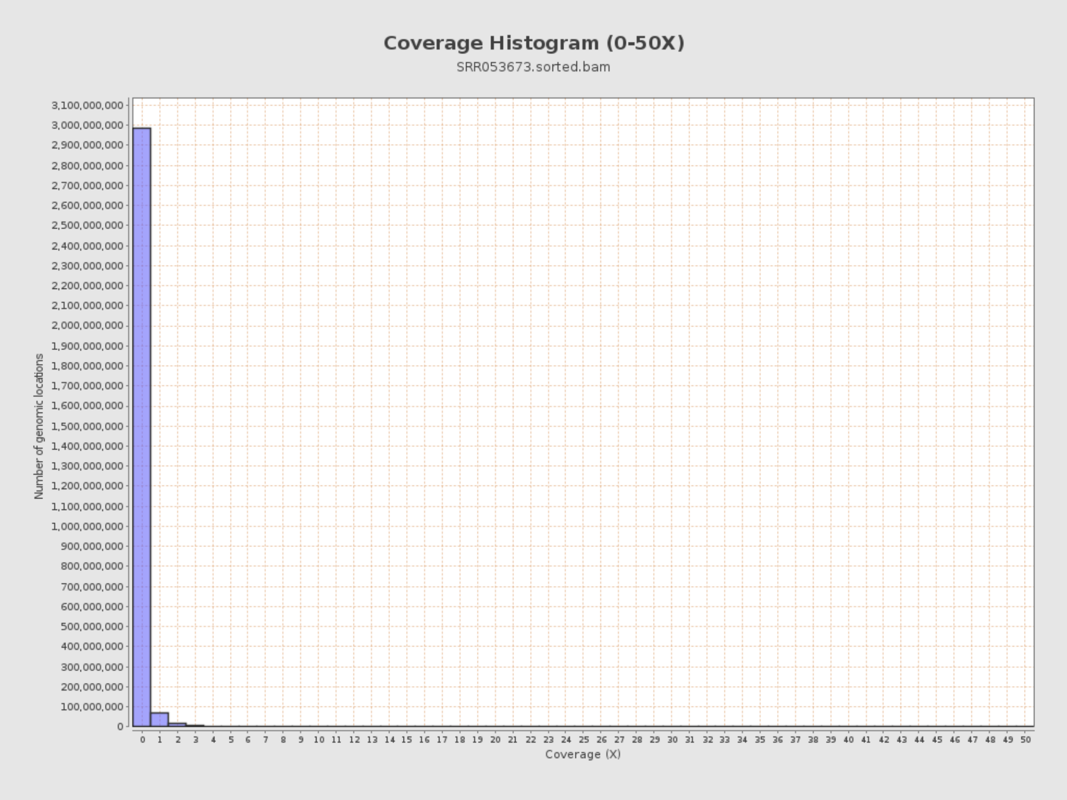
3. Results : Coverage across reference



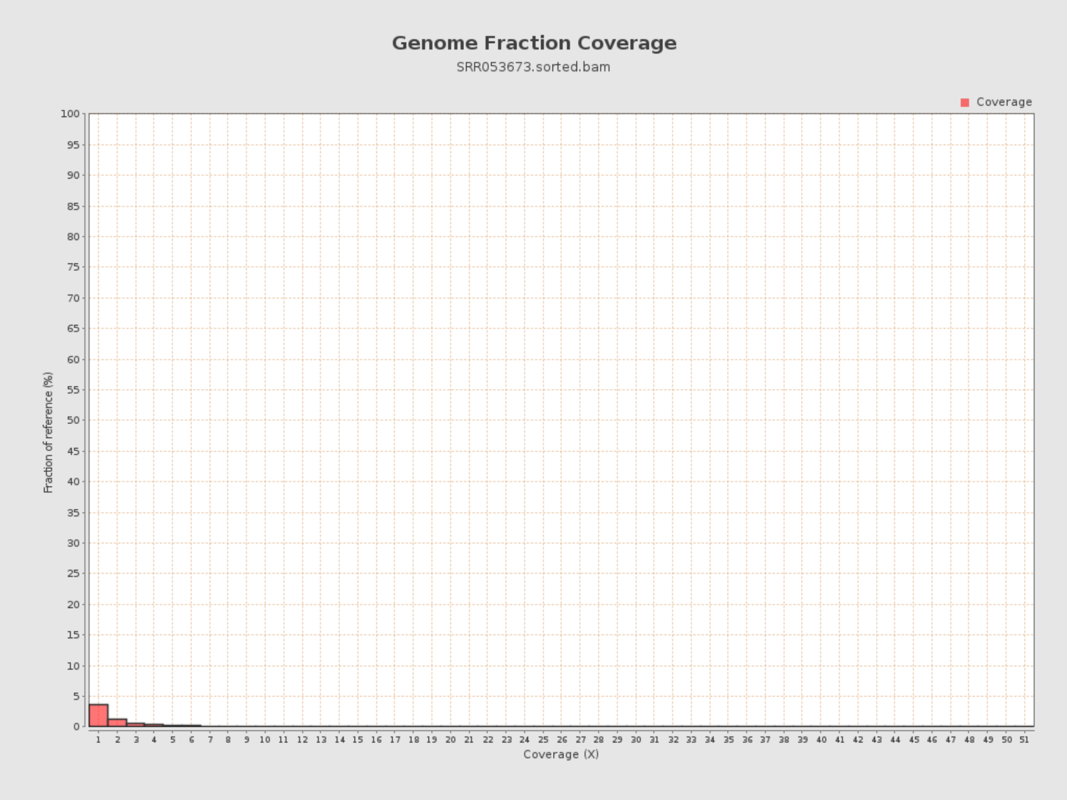
4. Results : Coverage Histogram



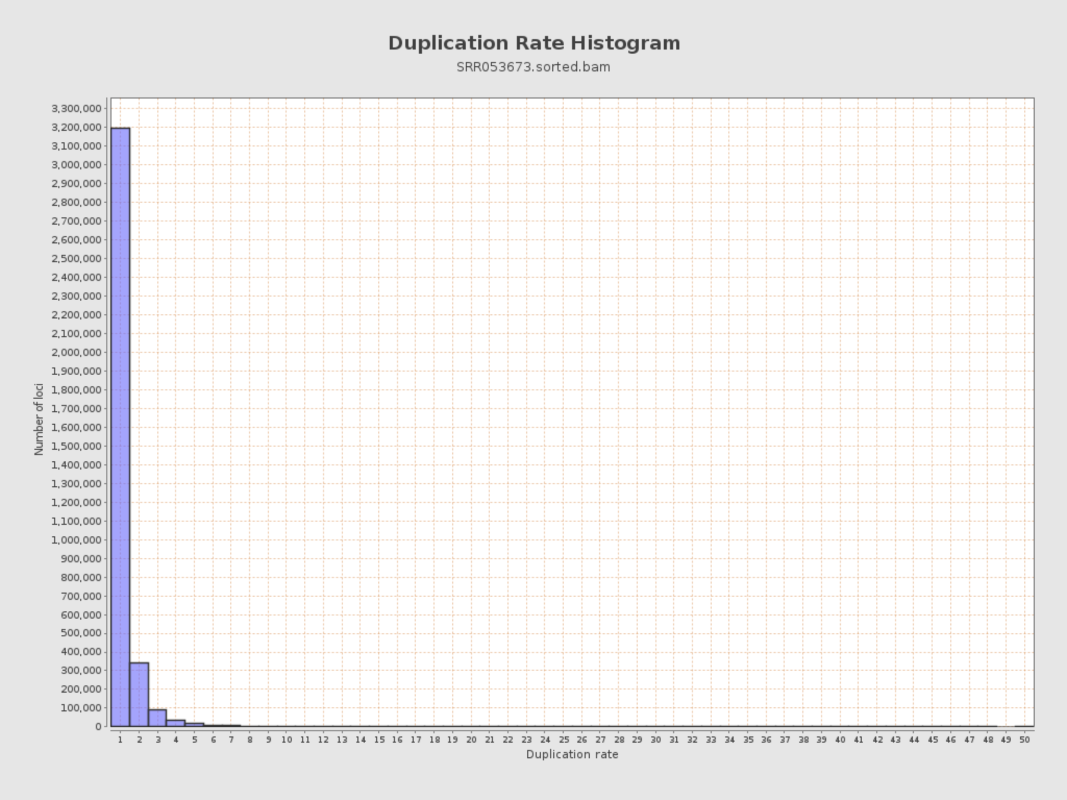
5. Results : Coverage Histogram (0-50X)



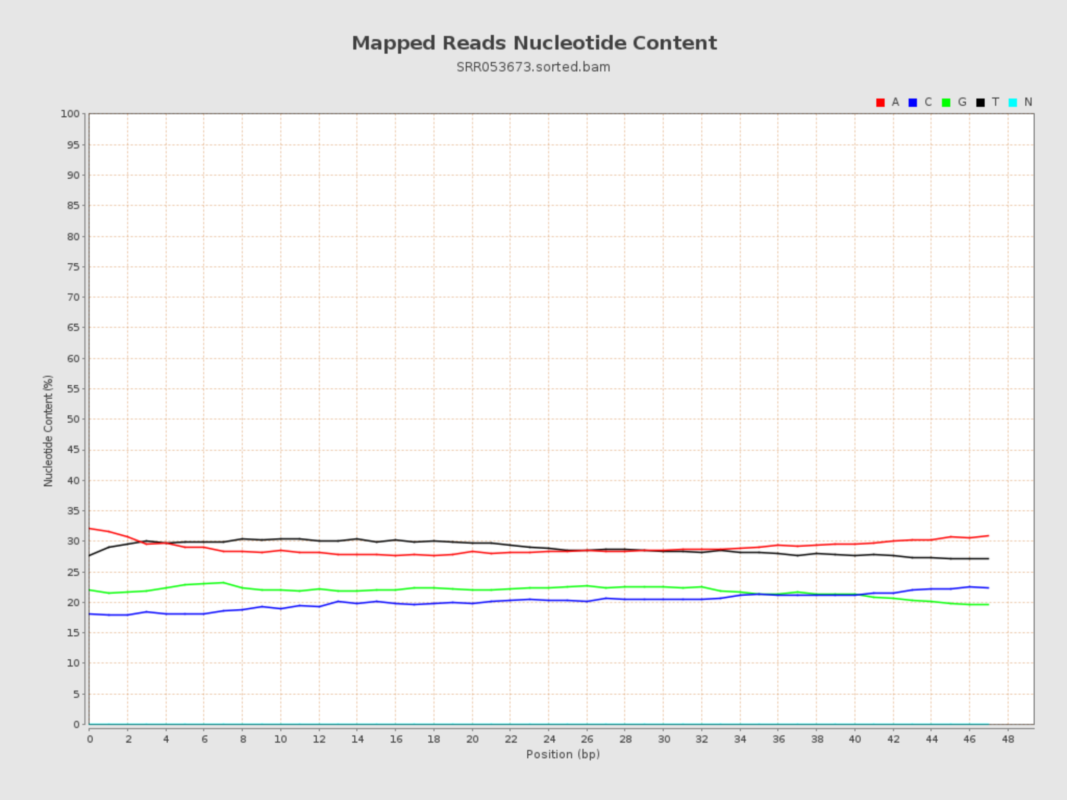
6. Results : Genome Fraction Coverage



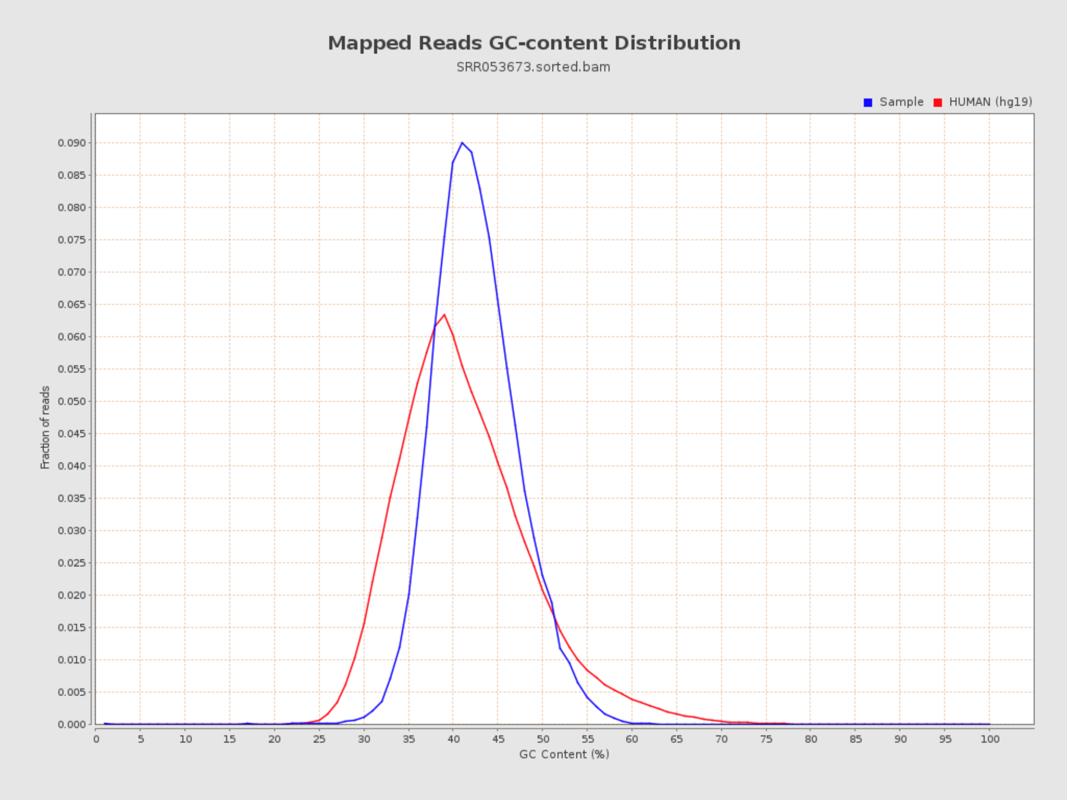
7. Results : Duplication Rate Histogram



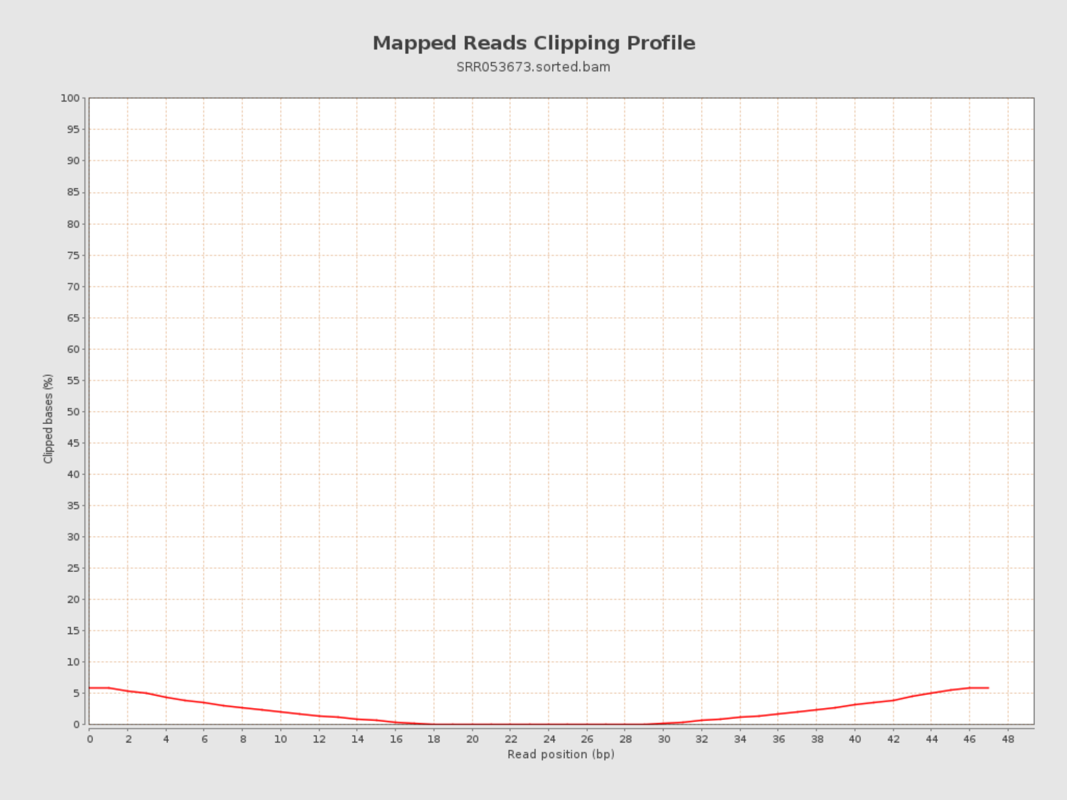
8. Results : Mapped Reads Nucleotide Content



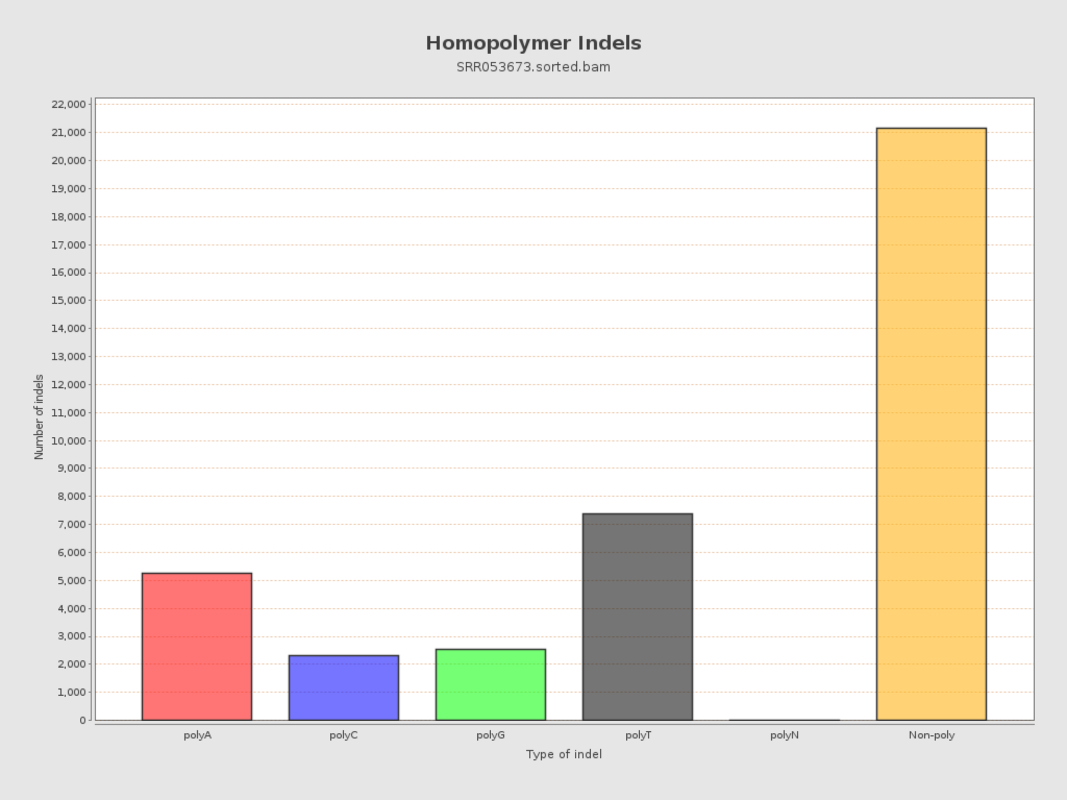
9. Results : Mapped Reads GC-content Distribution



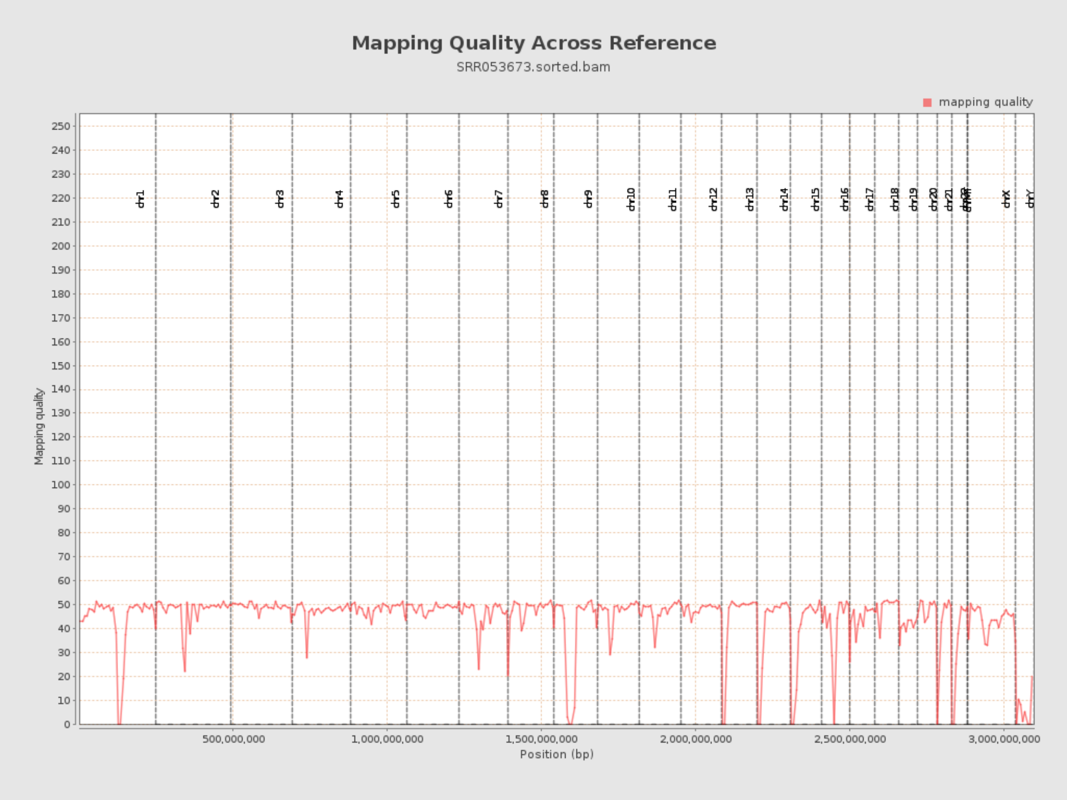
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram