Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 02:59:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053674.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_SRR053674 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053674.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 02:59:32 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053674.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,786,661
Mapped reads	6,081,609 / 69.21%
Unmapped reads	2,705,052 / 30.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	214 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,602,244 / 18.23%
Duplication rate	18.37%
Clipped reads	907,468 / 10.33%

2.2. ACGT Content

Number/percentage of A's	86,214,377 / 30.39%
Number/percentage of C's	53,979,590 / 19.03%
Number/percentage of T's	85,801,198 / 30.25%
Number/percentage of G's	57,518,799 / 20.28%
Number/percentage of N's	147,761 / 0.05%
GC Percentage	39.31%

2.3. Coverage

Mean	0.0916

Standard Deviation	1.2761

2.4. Mapping Quality

Mean Mapping Quality	43.75

2.5. Mismatches and indels

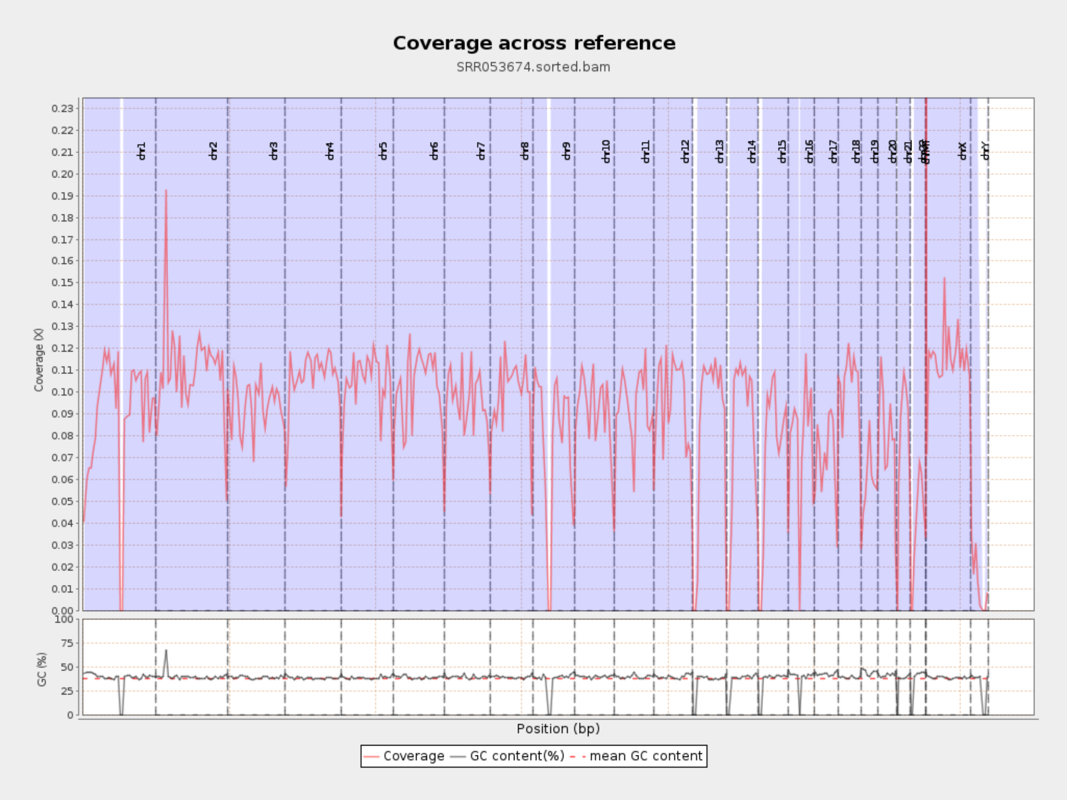
General error rate	1.07%
Mismatches	3,023,271
Insertions	17,069
Mapped reads with at least one insertion	0.28%
Deletions	40,117
Mapped reads with at least one deletion	0.66%
Homopolymer indels	44.73%

2.6. Chromosome stats

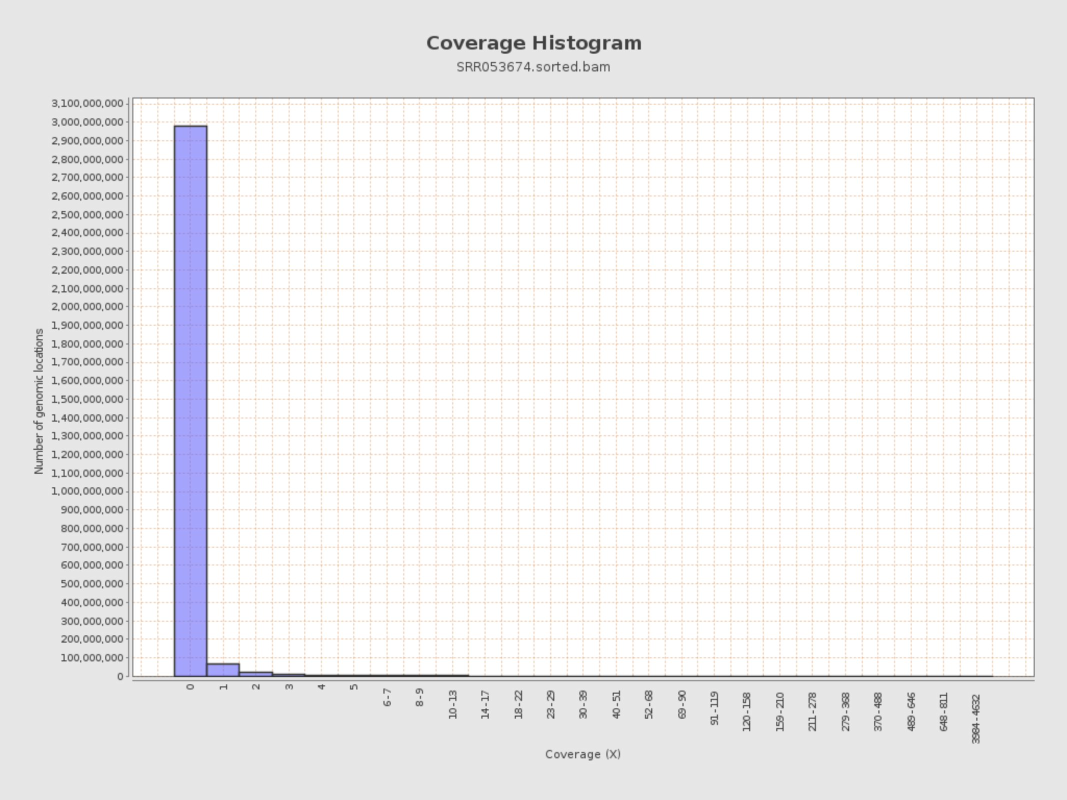
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22216893	0.0891	0.9243
chr2	243199373	26980227	0.1109	3.5479
chr3	198022430	18713062	0.0945	0.7715
chr4	191154276	20494453	0.1072	0.8461
chr5	180915260	18708440	0.1034	0.8181
chr6	171115067	17774998	0.1039	0.9466
chr7	159138663	15176956	0.0954	0.9557

chr8	146364022	14600851	0.0998	0.8878
chr9	141213431	11021395	0.078	0.7619
chr10	135534747	12512785	0.0923	0.8241
chr11	135006516	12588887	0.0932	0.9188
chr12	133851895	12864020	0.0961	0.7861
chr13	115169878	9881690	0.0858	0.7351
chr14	107349540	8869624	0.0826	0.8666
chr15	102531392	7338573	0.0716	0.6666
chr16	90354753	6824581	0.0755	0.696
chr17	81195210	5800123	0.0714	0.6701
chr18	78077248	8201251	0.105	1.0037
chr19	59128983	3513937	0.0594	0.8748
chr20	63025520	5216620	0.0828	0.7384
chr21	48129895	3750012	0.0779	0.7203
chr22	51304566	2040008	0.0398	0.4618
chrMT	16571	12301	0.7423	1.8414
chrX	155270560	17893959	0.1152	0.9468
chrY	59373566	723041	0.0122	0.2424

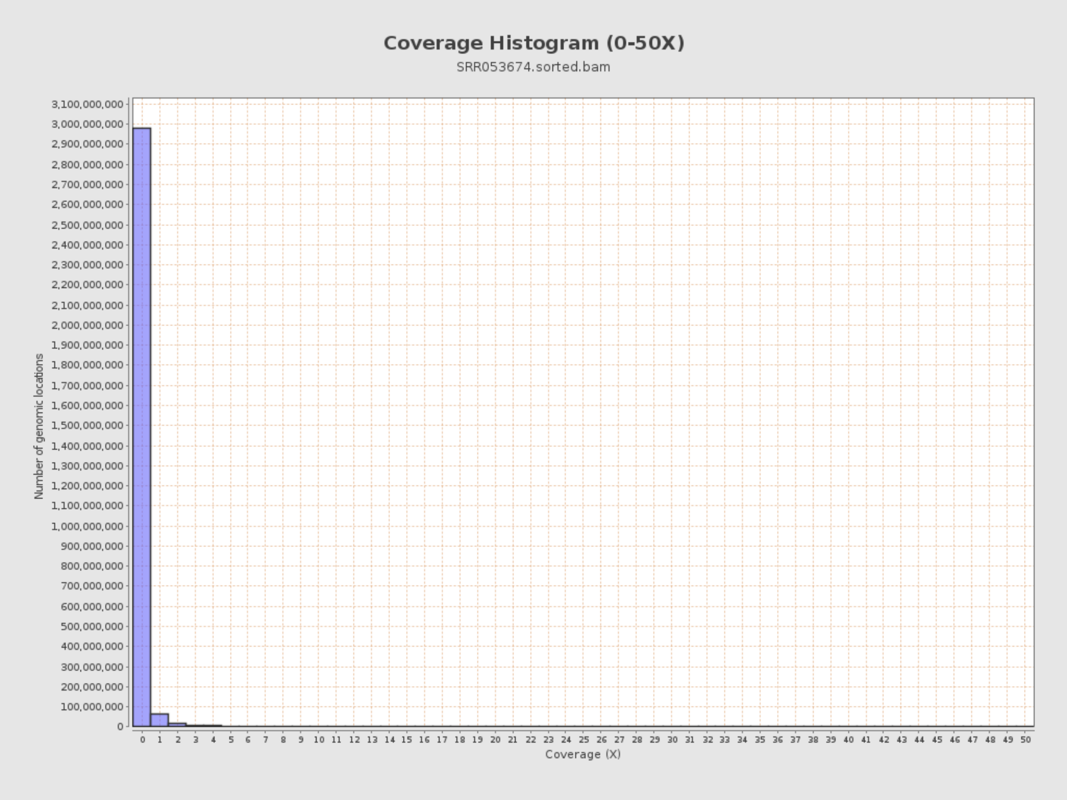
3. Results : Coverage across reference



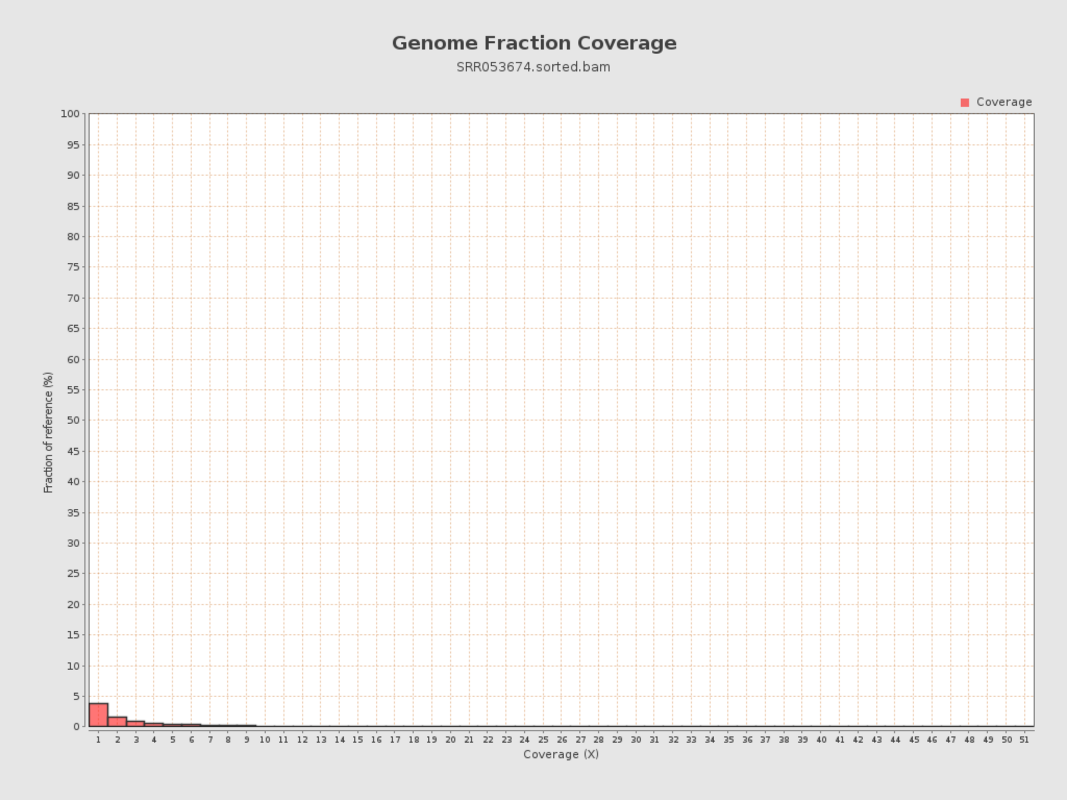
4. Results : Coverage Histogram



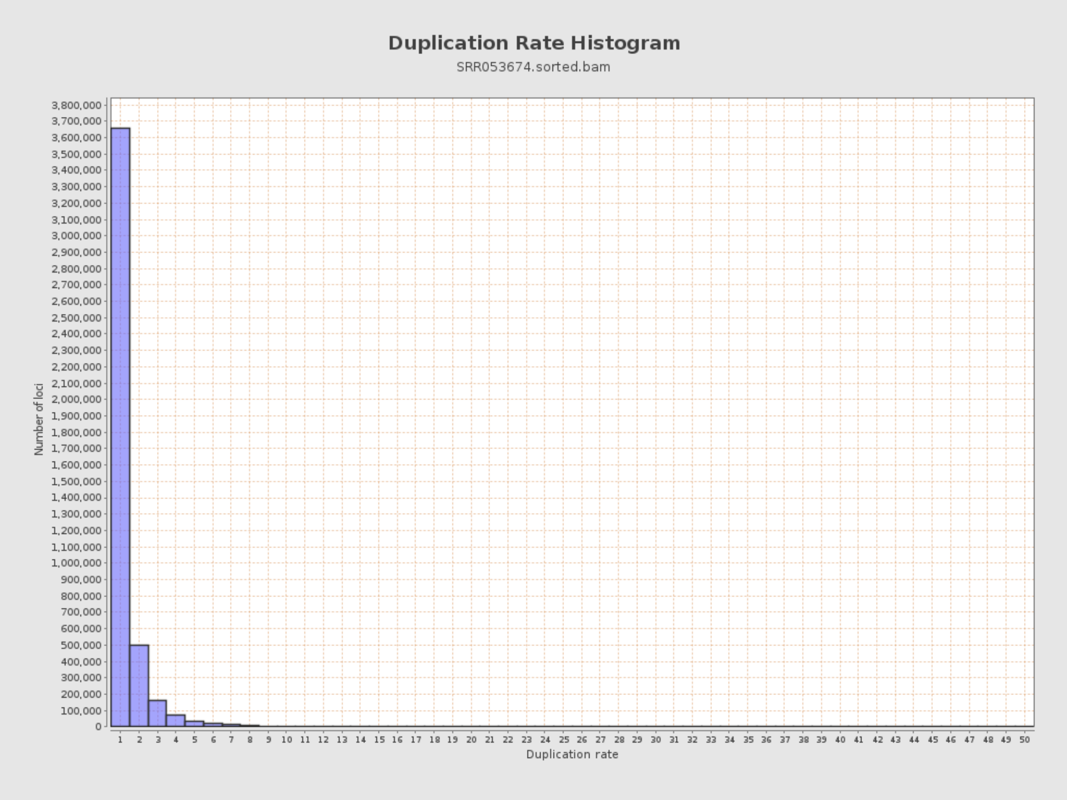
5. Results : Coverage Histogram (0-50X)



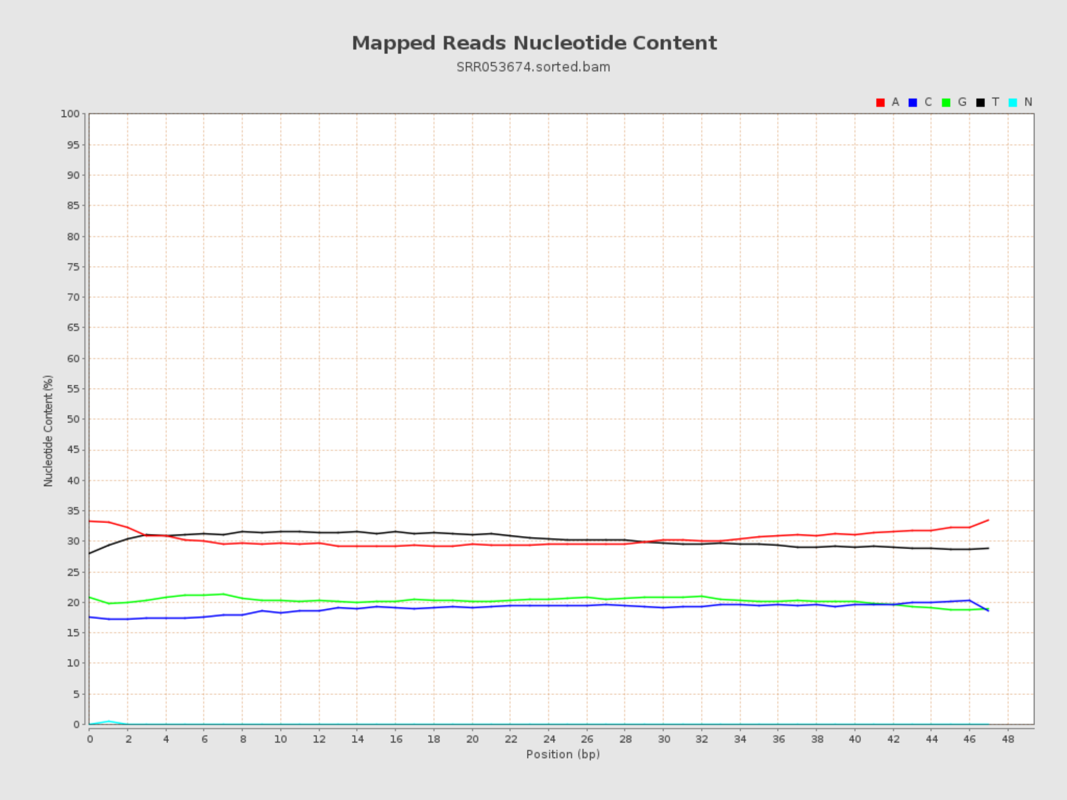
6. Results : Genome Fraction Coverage



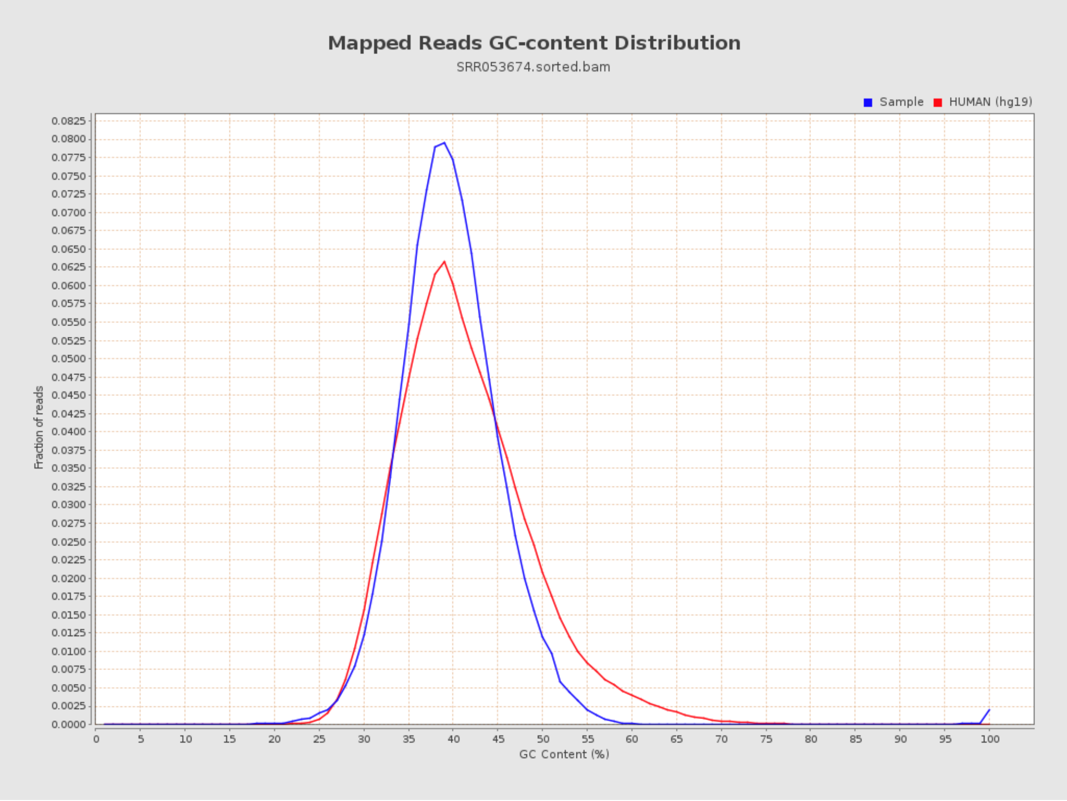
7. Results : Duplication Rate Histogram



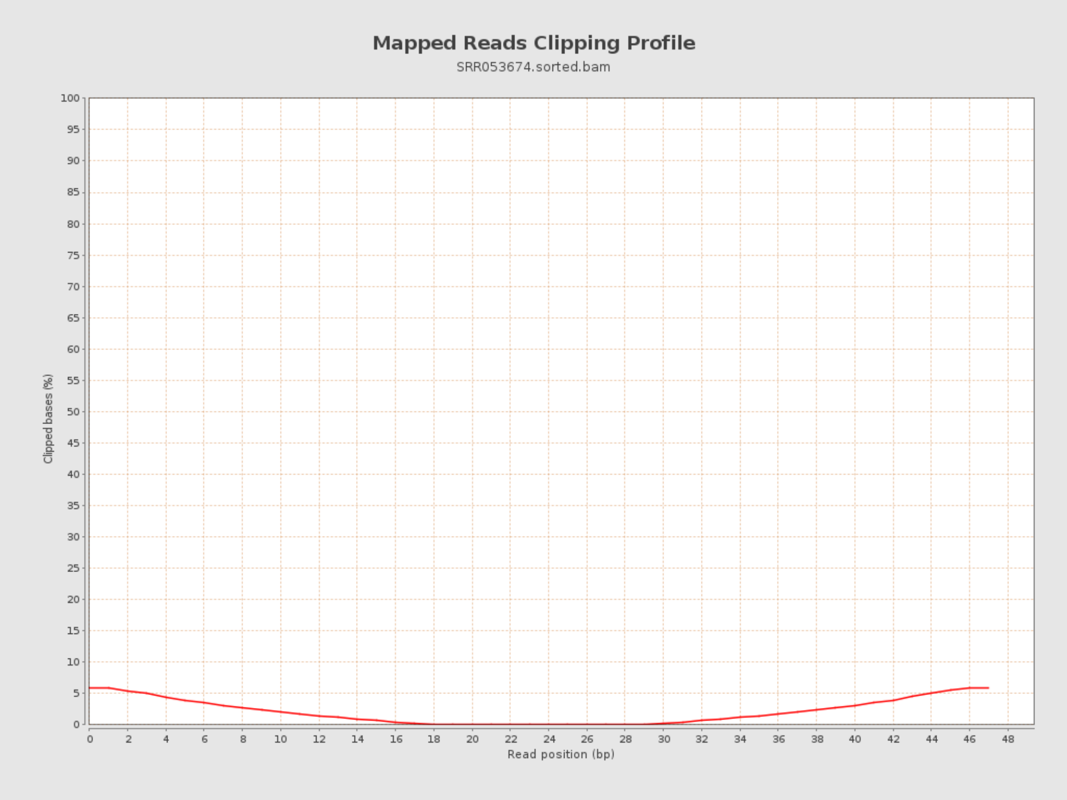
8. Results : Mapped Reads Nucleotide Content



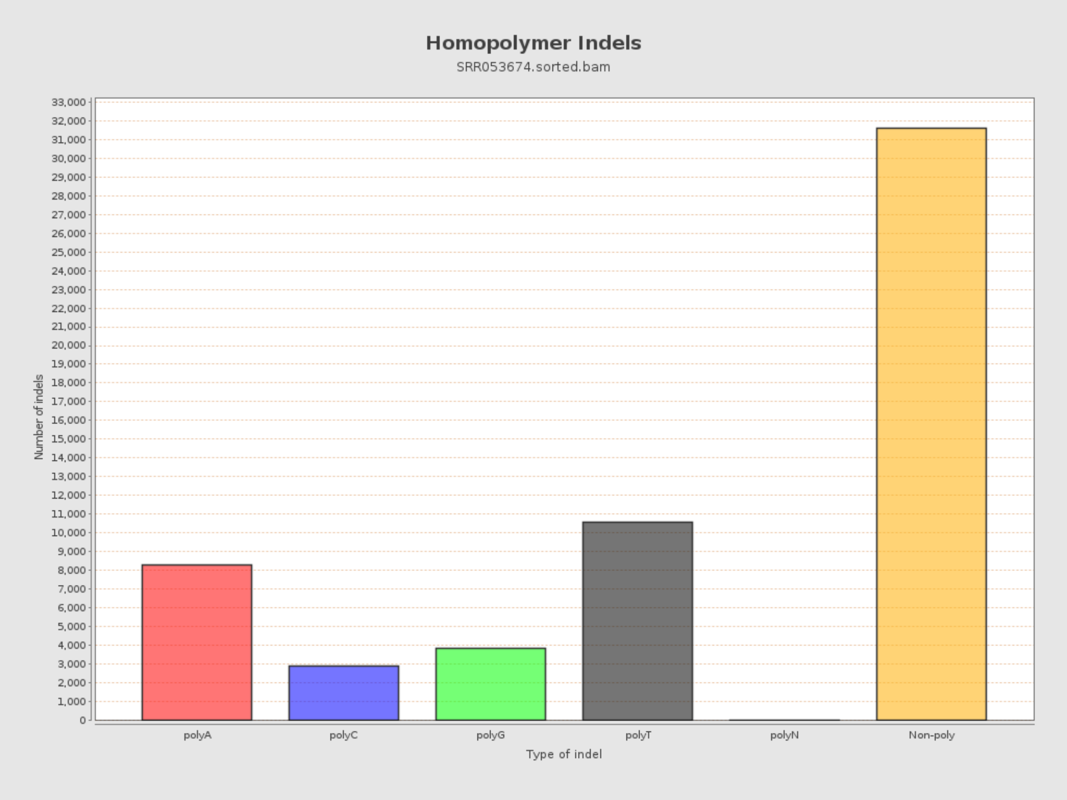
9. Results : Mapped Reads GC-content Distribution



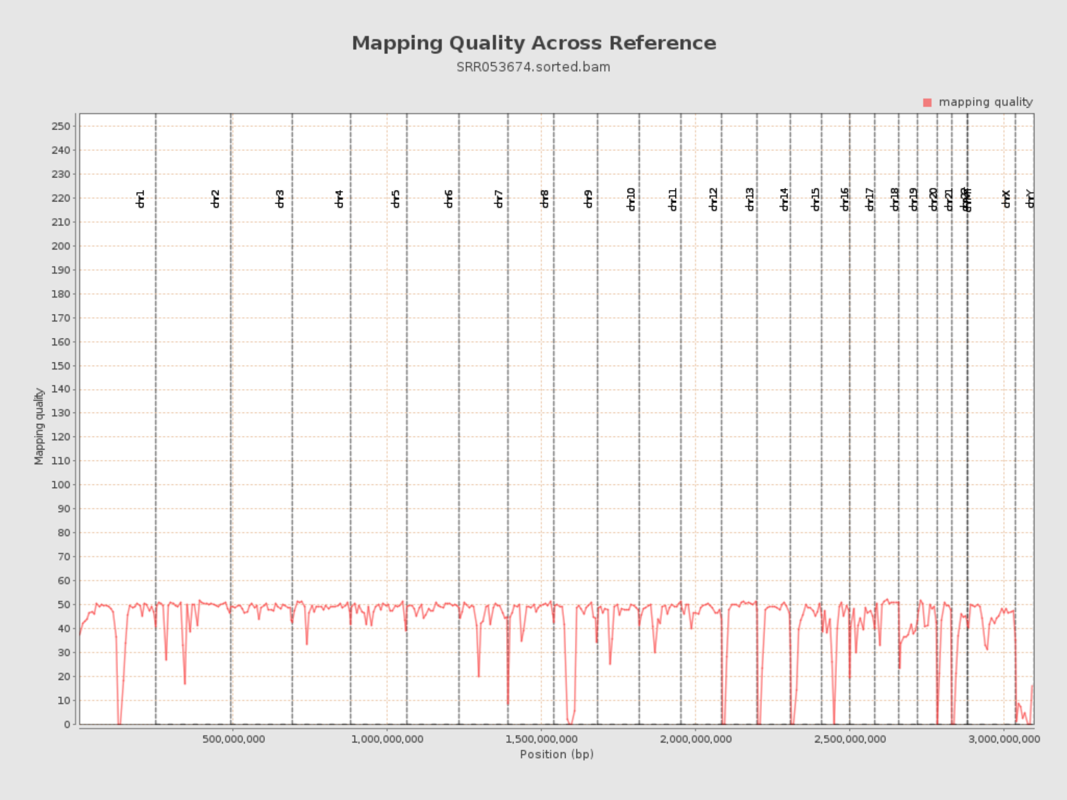
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram