Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 03:05:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053675.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_SRR053675 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053675.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 03:05:38 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053675.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,320,293
Mapped reads	6,074,957 / 73.01%
Unmapped reads	2,245,336 / 26.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	211 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,531,627 / 18.41%
Duplication rate	18.19%
Clipped reads	691,593 / 8.31%

2.2. ACGT Content

Number/percentage of A's	87,258,277 / 30.58%
Number/percentage of C's	54,606,034 / 19.14%
Number/percentage of T's	86,110,141 / 30.18%
Number/percentage of G's	57,285,605 / 20.08%
Number/percentage of N's	80,928 / 0.03%
GC Percentage	39.21%

2.3. Coverage

Mean	0.0922

Standard Deviation	0.7753

2.4. Mapping Quality

Mean Mapping Quality	45.81

2.5. Mismatches and indels

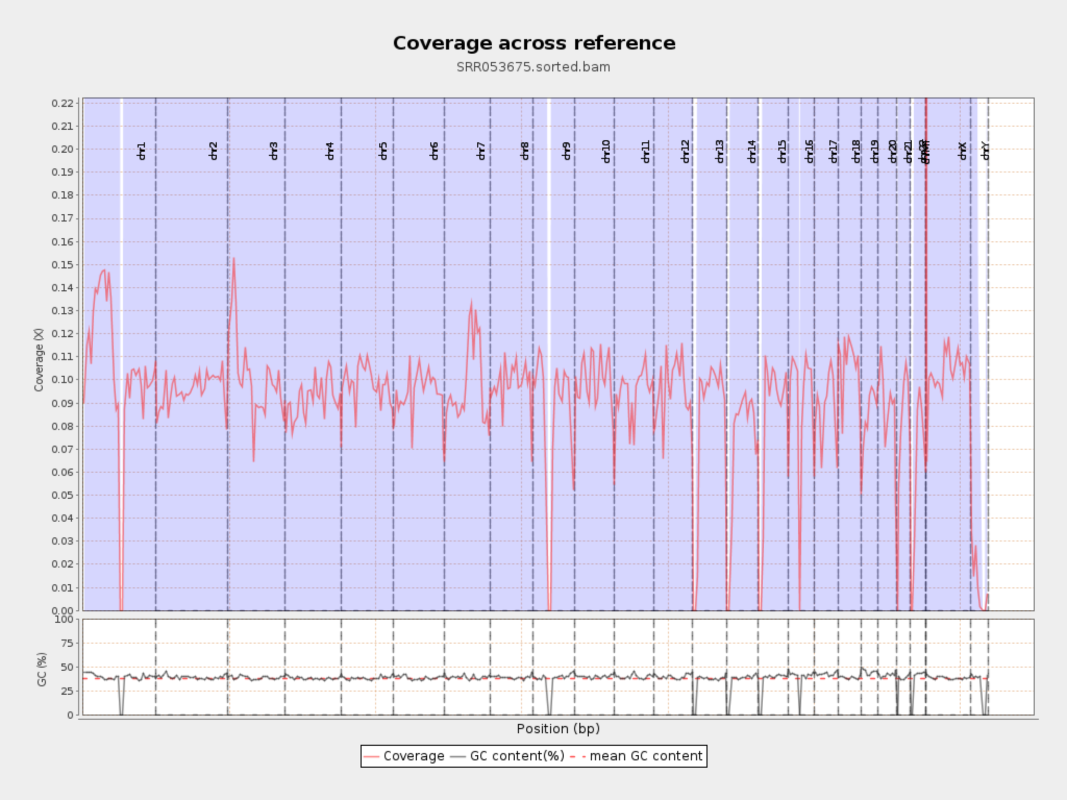
General error rate	0.63%
Mismatches	1,783,304
Insertions	13,298
Mapped reads with at least one insertion	0.22%
Deletions	42,020
Mapped reads with at least one deletion	0.69%
Homopolymer indels	47.34%

2.6. Chromosome stats

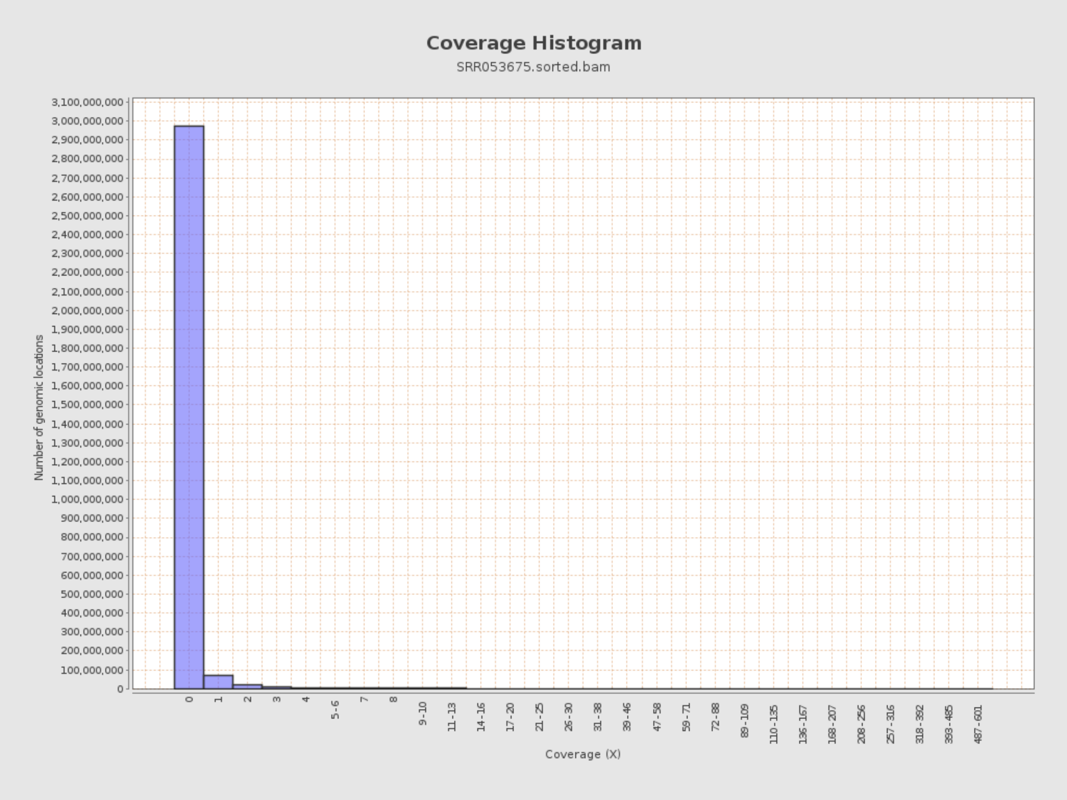
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26146477	0.1049	0.8551
chr2	243199373	23289278	0.0958	0.8877
chr3	198022430	20110937	0.1016	0.764
chr4	191154276	17580340	0.092	0.7478
chr5	180915260	17840832	0.0986	0.7542
chr6	171115067	16310884	0.0953	0.7744
chr7	159138663	15468055	0.0972	0.8311

chr8	146364022	14391499	0.0983	0.8377
chr9	141213431	11685304	0.0827	0.6999
chr10	135534747	13652897	0.1007	0.7921
chr11	135006516	12742980	0.0944	0.7886
chr12	133851895	12854445	0.096	0.7501
chr13	115169878	9479999	0.0823	0.6799
chr14	107349540	7669103	0.0714	0.6697
chr15	102531392	8169675	0.0797	0.6569
chr16	90354753	8025086	0.0888	0.7689
chr17	81195210	7213777	0.0888	0.6985
chr18	78077248	8337550	0.1068	0.8382
chr19	59128983	5038685	0.0852	0.7751
chr20	63025520	5675179	0.09	0.724
chr21	48129895	3722984	0.0774	0.6986
chr22	51304566	3017652	0.0588	0.557
chrMT	16571	314586	18.9841	34.2234
chrX	155270560	16016190	0.1032	0.8104
chrY	59373566	648921	0.0109	0.2371

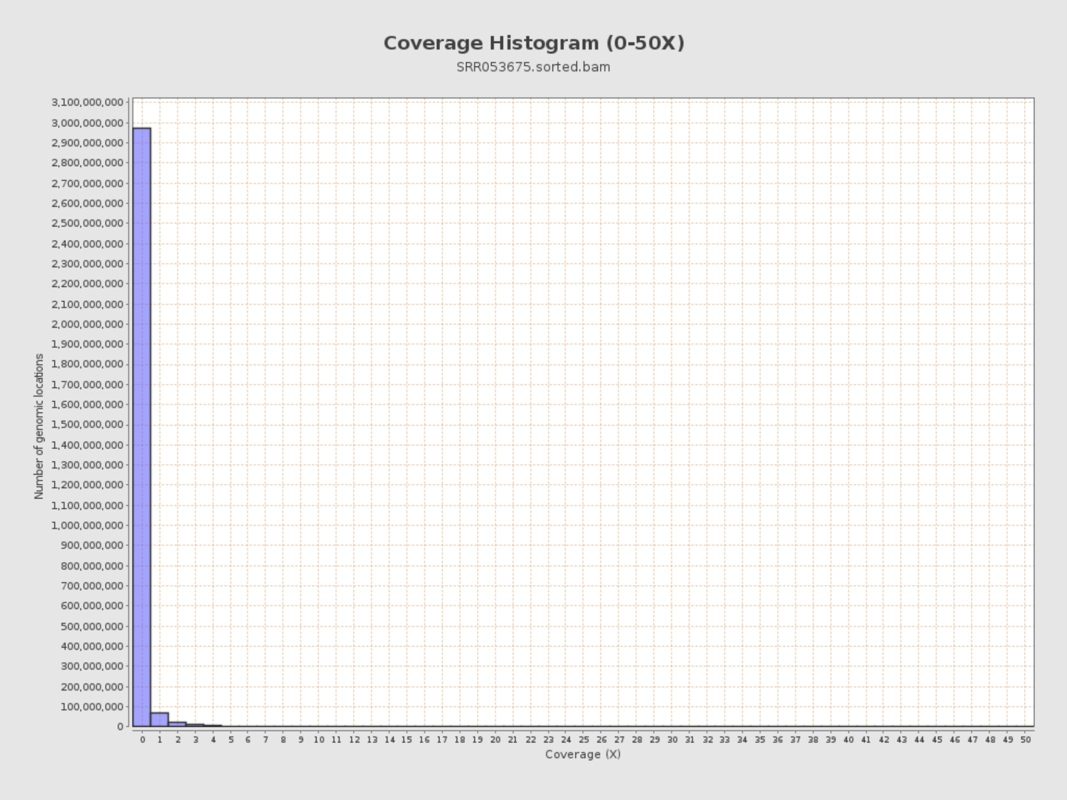
3. Results : Coverage across reference



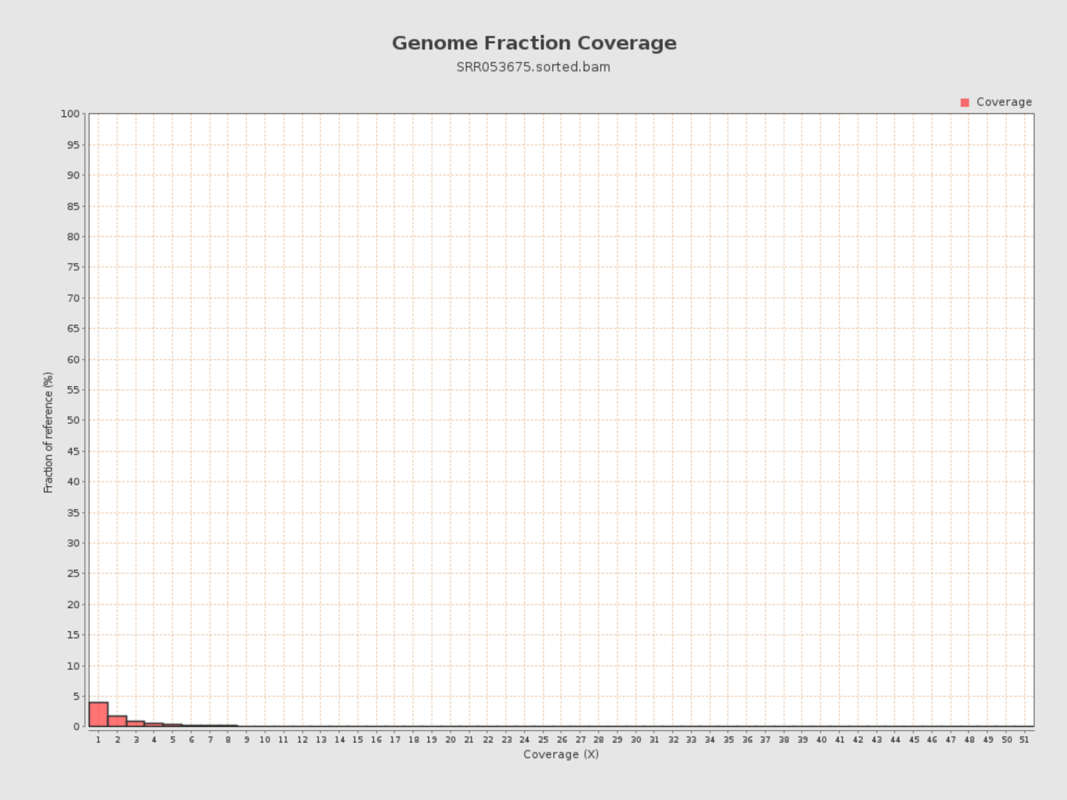
4. Results : Coverage Histogram



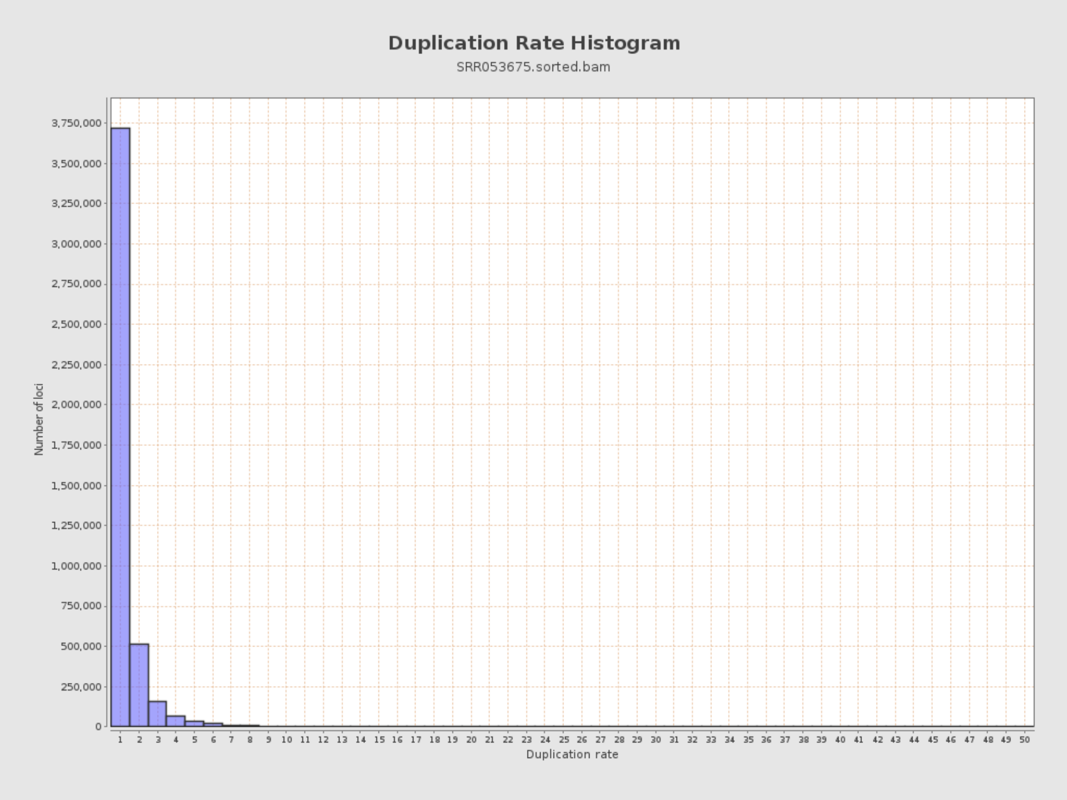
5. Results : Coverage Histogram (0-50X)



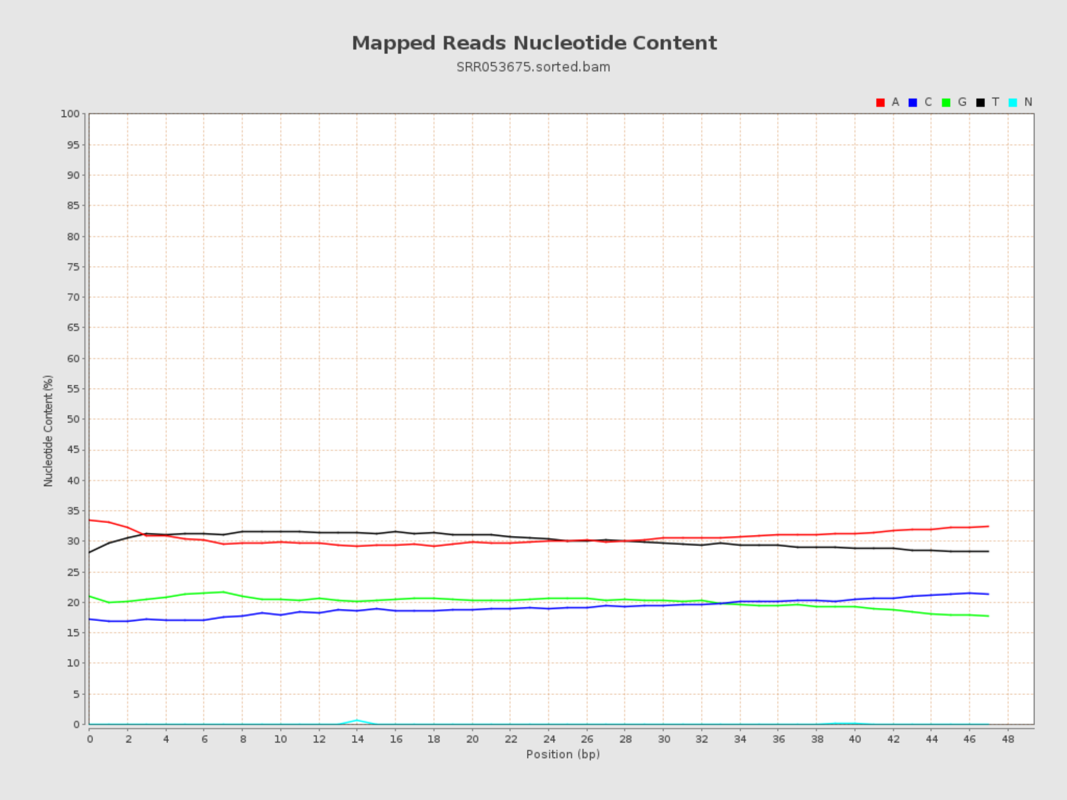
6. Results : Genome Fraction Coverage



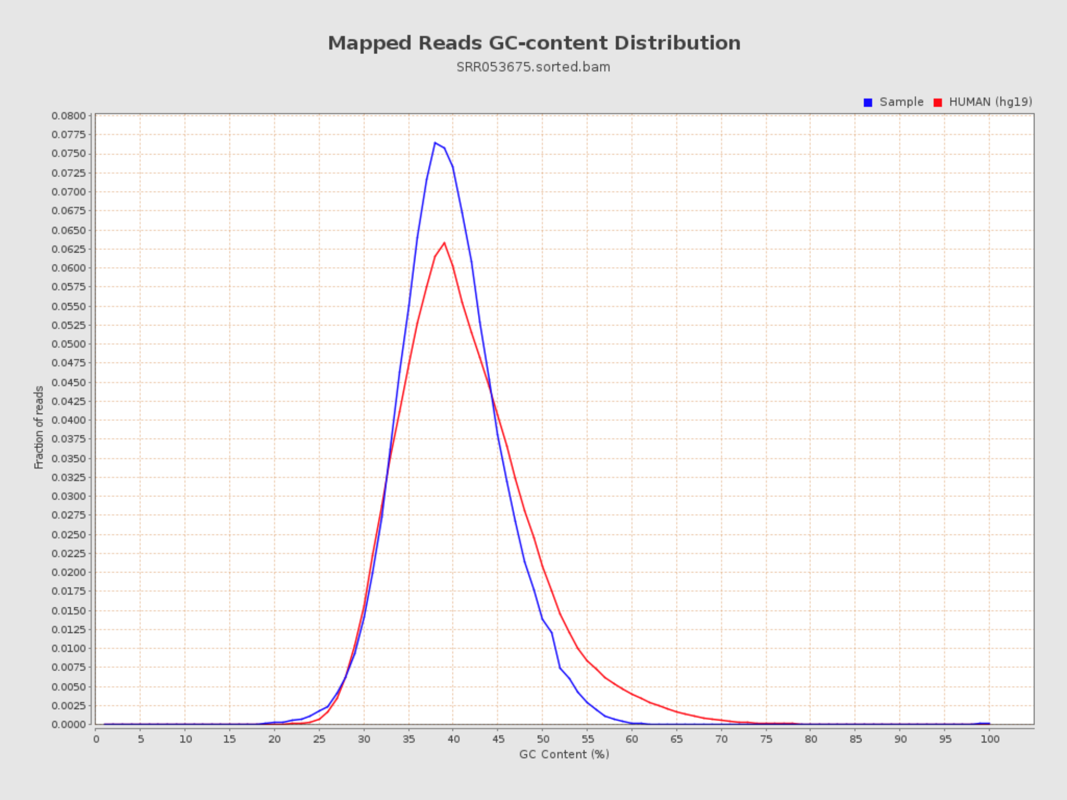
7. Results : Duplication Rate Histogram



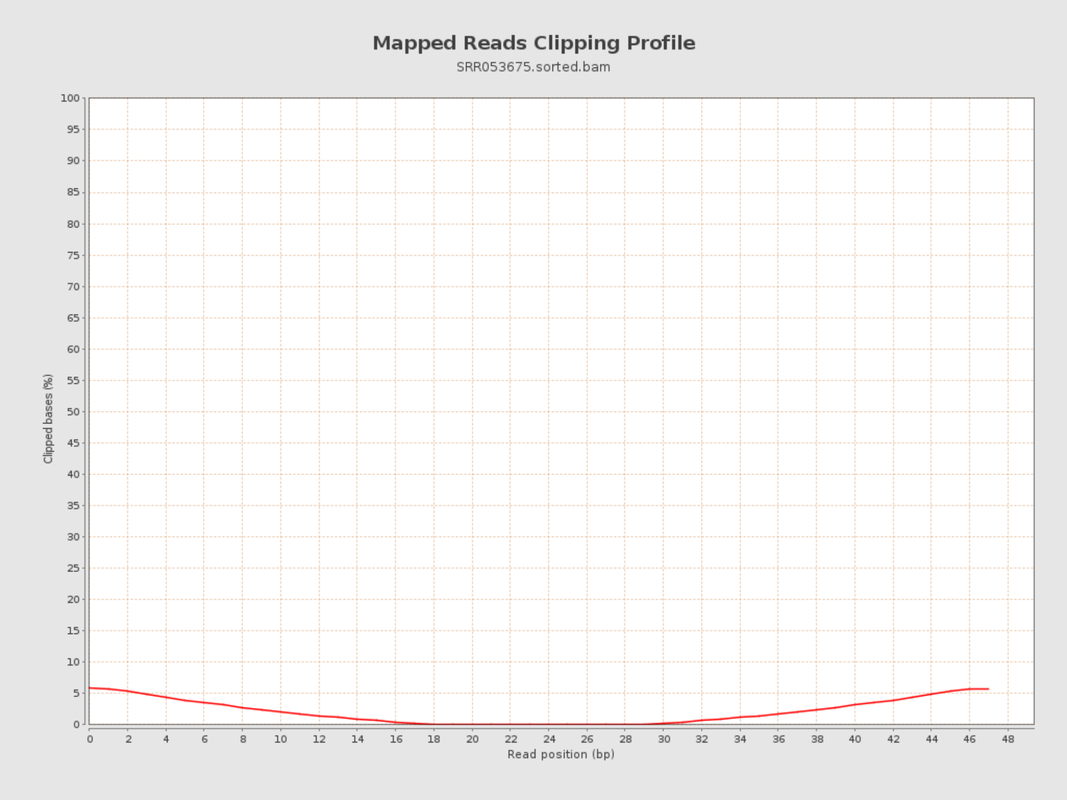
8. Results : Mapped Reads Nucleotide Content



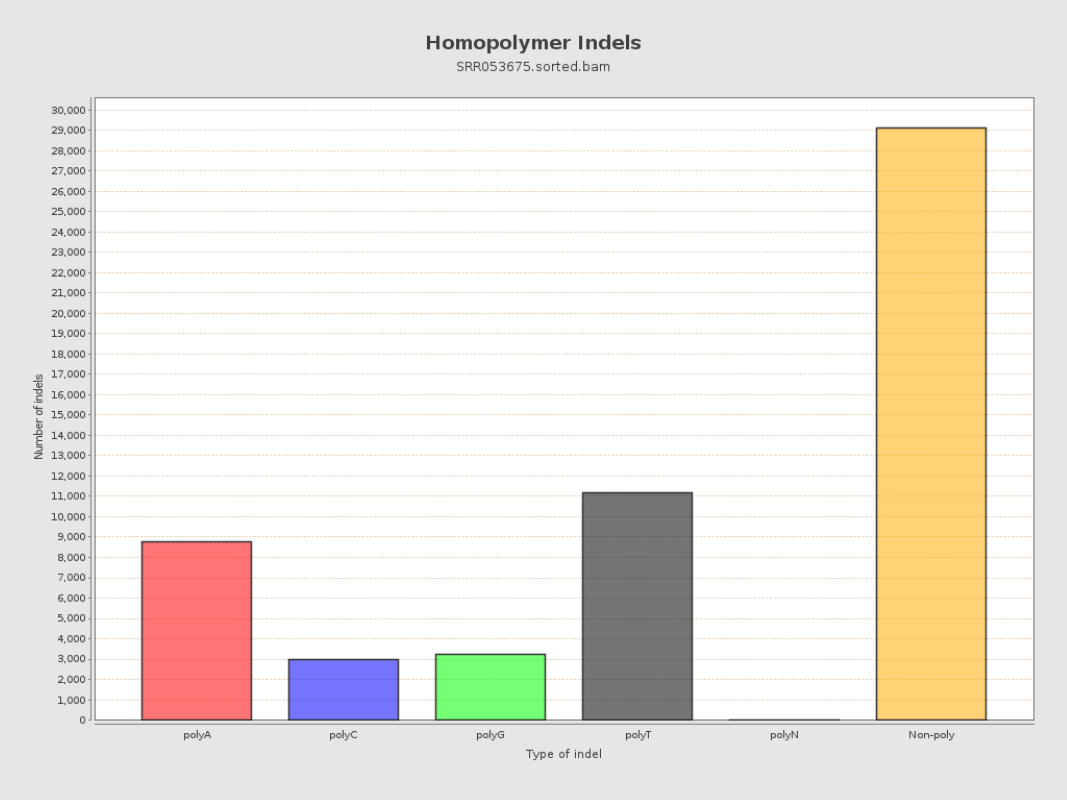
9. Results : Mapped Reads GC-content Distribution



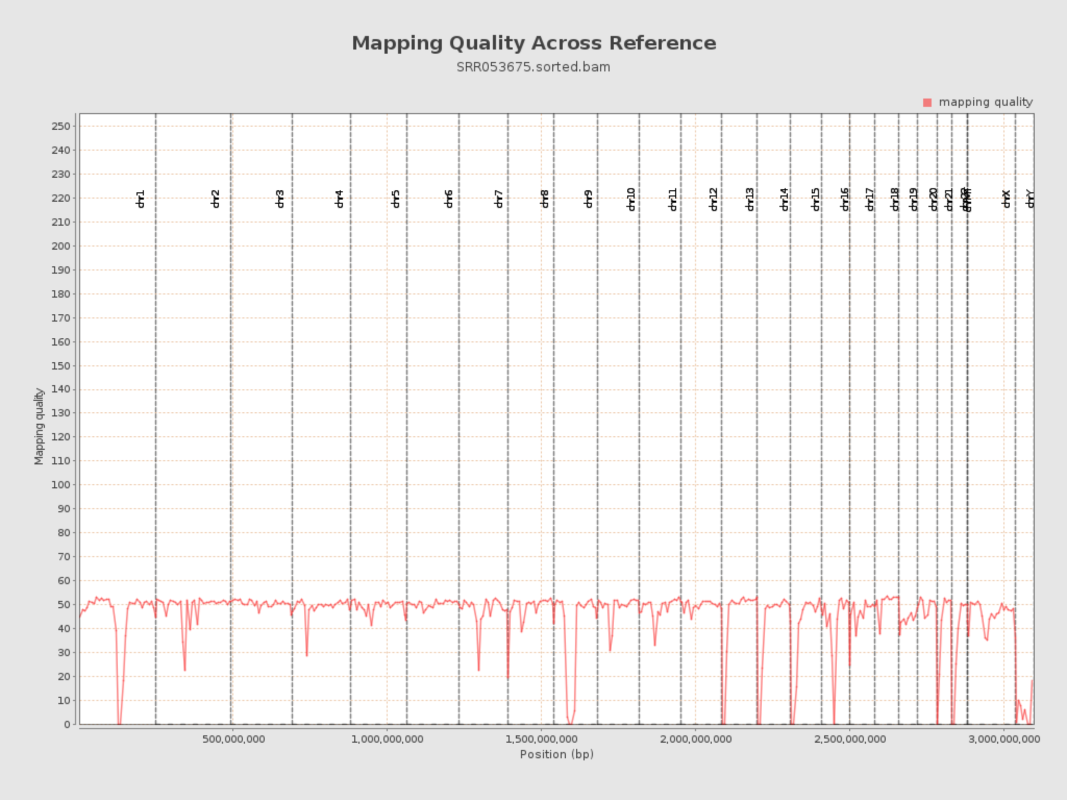
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram