Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 02:43:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053671.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_SRR053671 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053671.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 02:43:17 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053671.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,711,010
Mapped reads	6,588,710 / 61.51%
Unmapped reads	4,122,300 / 38.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	118 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,521,451 / 14.2%
Duplication rate	17.34%
Clipped reads	1,436,389 / 13.41%

2.2. ACGT Content

Number/percentage of A's	89,153,158 / 29.41%
Number/percentage of C's	61,922,513 / 20.42%
Number/percentage of T's	90,031,205 / 29.7%
Number/percentage of G's	61,859,855 / 20.4%
Number/percentage of N's	206,707 / 0.07%
GC Percentage	40.83%

2.3. Coverage

Mean	0.098

Standard Deviation	0.7873

2.4. Mapping Quality

Mean Mapping Quality	42.19

2.5. Mismatches and indels

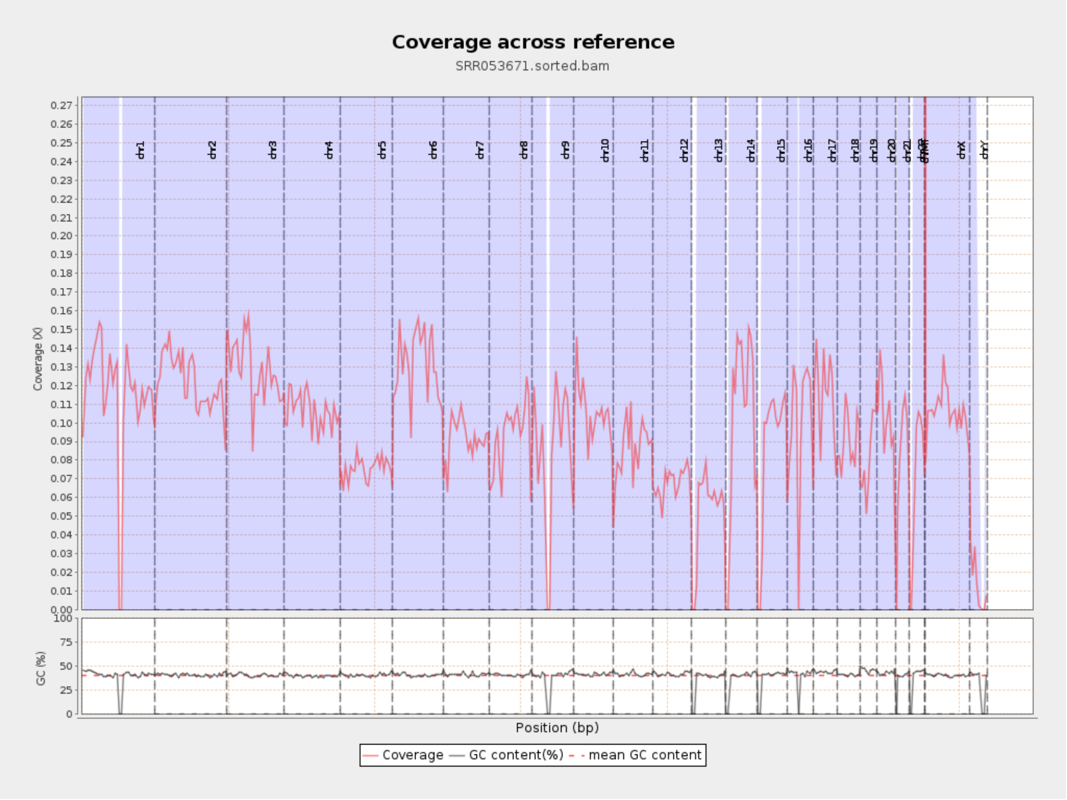
General error rate	1.55%
Mismatches	4,691,823
Insertions	16,728
Mapped reads with at least one insertion	0.25%
Deletions	39,362
Mapped reads with at least one deletion	0.6%
Homopolymer indels	37.4%

2.6. Chromosome stats

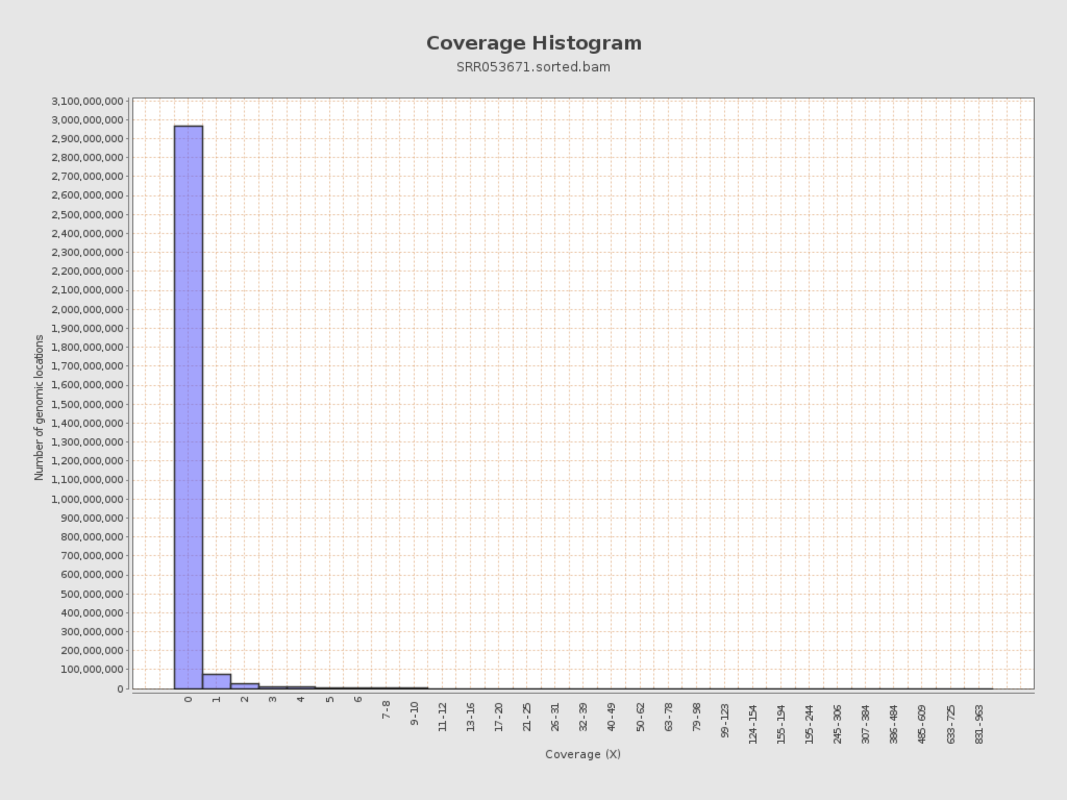
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28539761	0.1145	0.911
chr2	243199373	29662005	0.122	0.921
chr3	198022430	25536452	0.129	0.8457
chr4	191154276	20337419	0.1064	0.7651
chr5	180915260	13666991	0.0755	0.6524
chr6	171115067	22627287	0.1322	0.9562
chr7	159138663	14567917	0.0915	0.8631

chr8	146364022	13640193	0.0932	0.7606
chr9	141213431	12057307	0.0854	0.7269
chr10	135534747	14314650	0.1056	0.7974
chr11	135006516	11695099	0.0866	0.8493
chr12	133851895	9107494	0.068	0.6155
chr13	115169878	6071283	0.0527	0.5003
chr14	107349540	11314534	0.1054	0.83
chr15	102531392	8725901	0.0851	0.6562
chr16	90354753	8778978	0.0972	0.7398
chr17	81195210	9486366	0.1168	0.7929
chr18	78077248	7043924	0.0902	0.7714
chr19	59128983	4812118	0.0814	0.753
chr20	63025520	6504454	0.1032	0.7321
chr21	48129895	3870926	0.0804	0.6785
chr22	51304566	3541199	0.069	0.576
chrMT	16571	57275	3.4563	6.3605
chrX	155270560	16497989	0.1063	0.8044
chrY	59373566	771595	0.013	0.2356

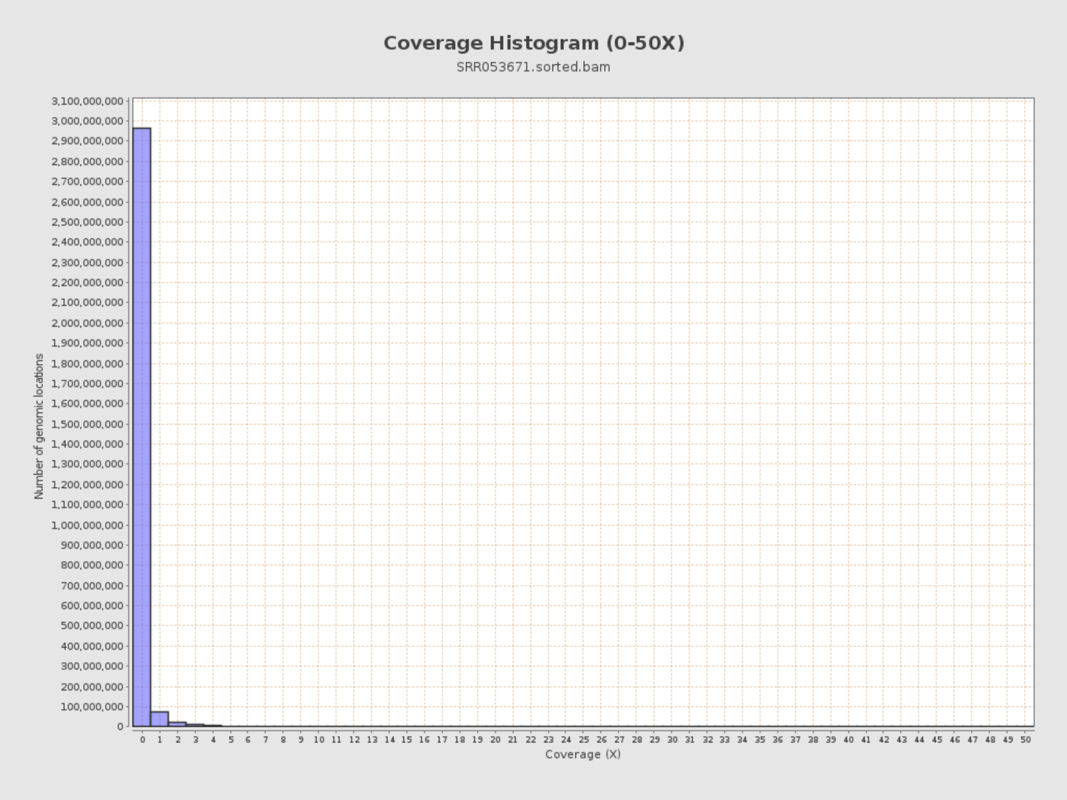
3. Results : Coverage across reference



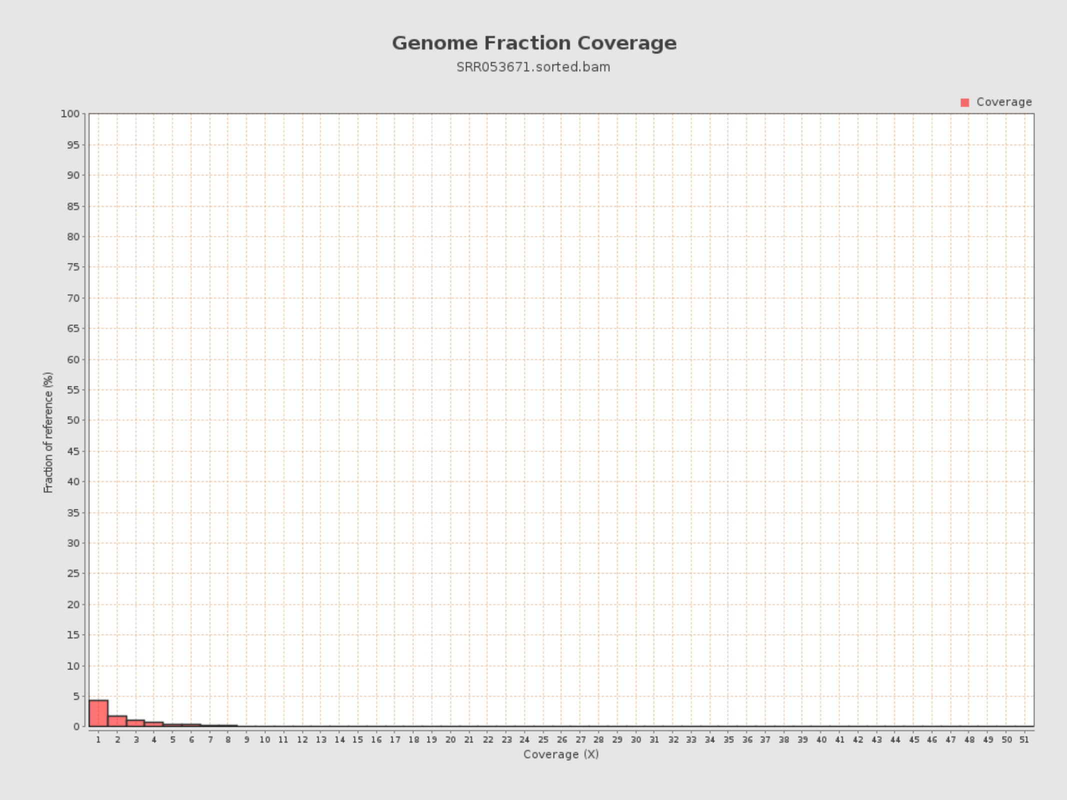
4. Results : Coverage Histogram



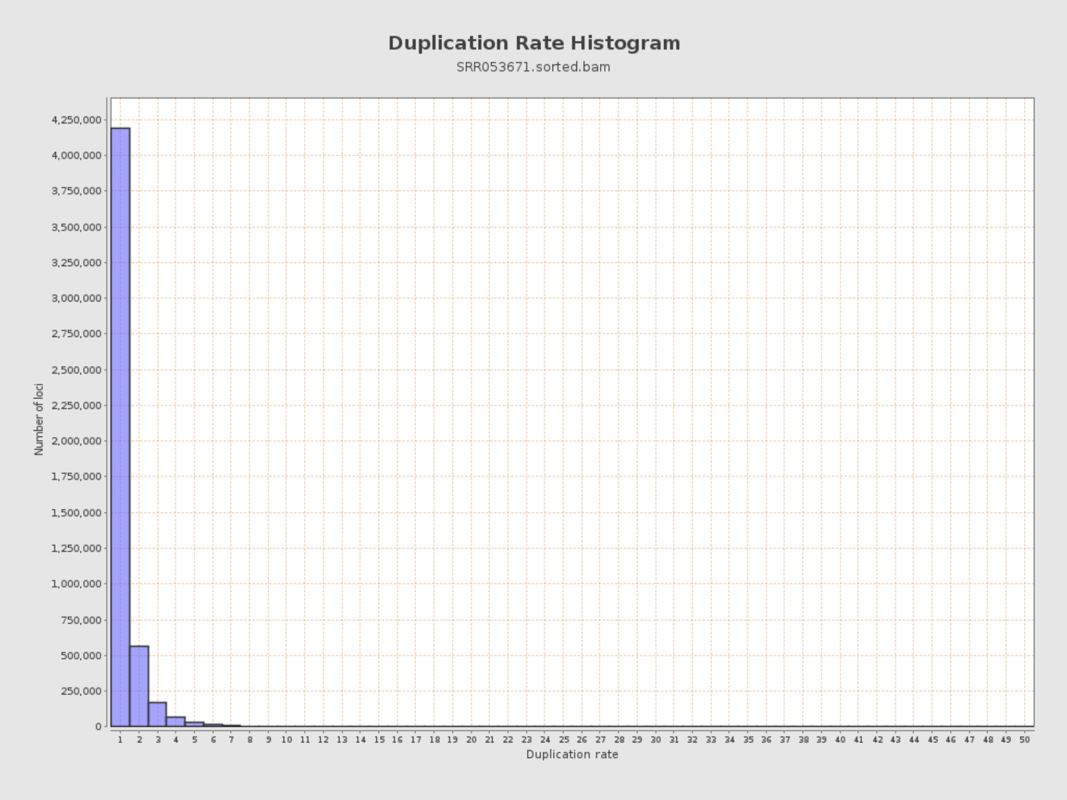
5. Results : Coverage Histogram (0-50X)



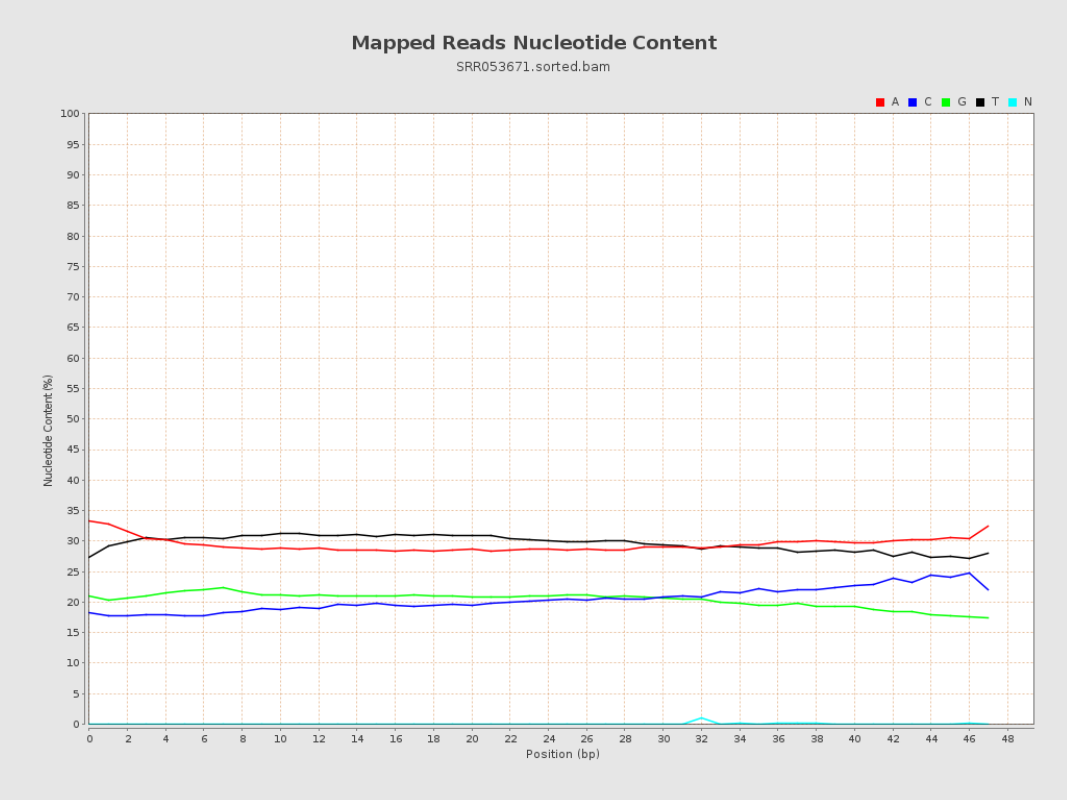
6. Results : Genome Fraction Coverage



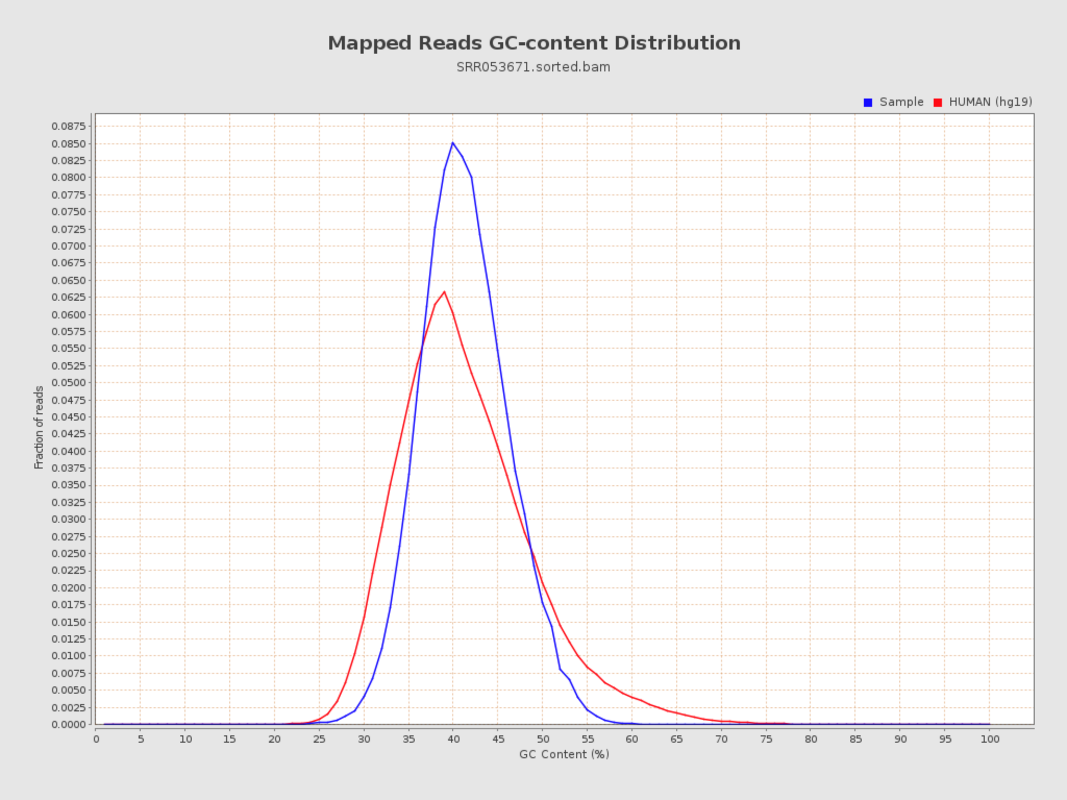
7. Results : Duplication Rate Histogram



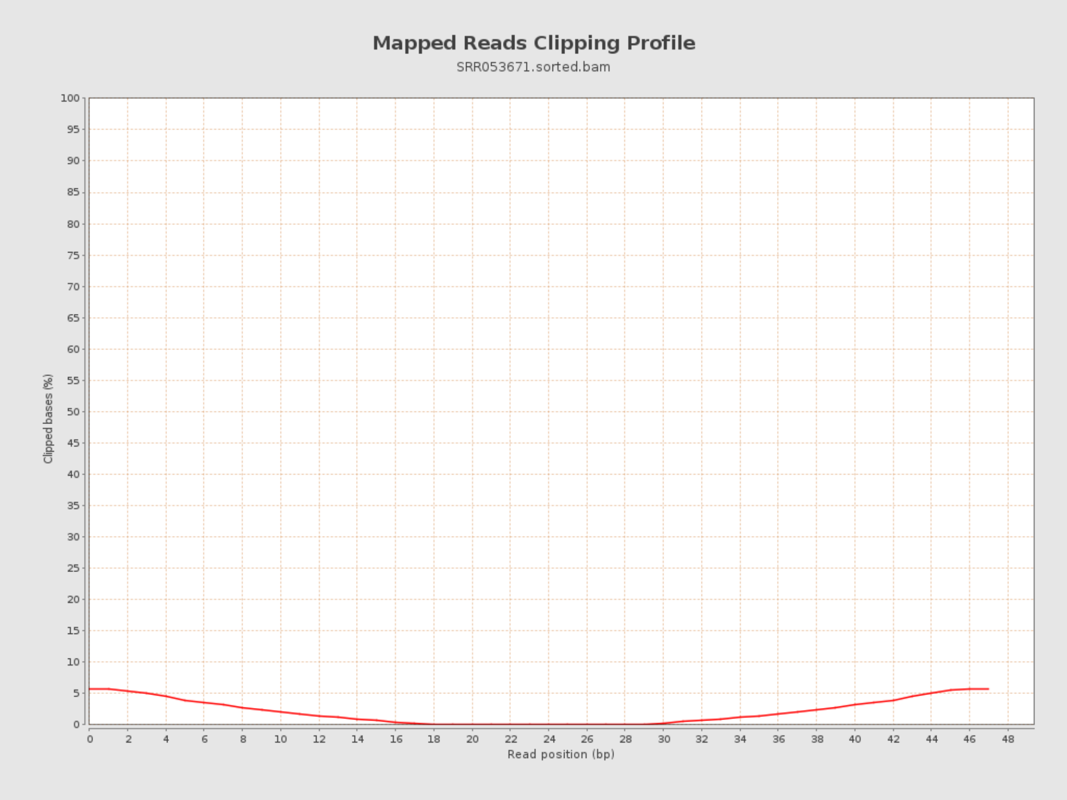
8. Results : Mapped Reads Nucleotide Content



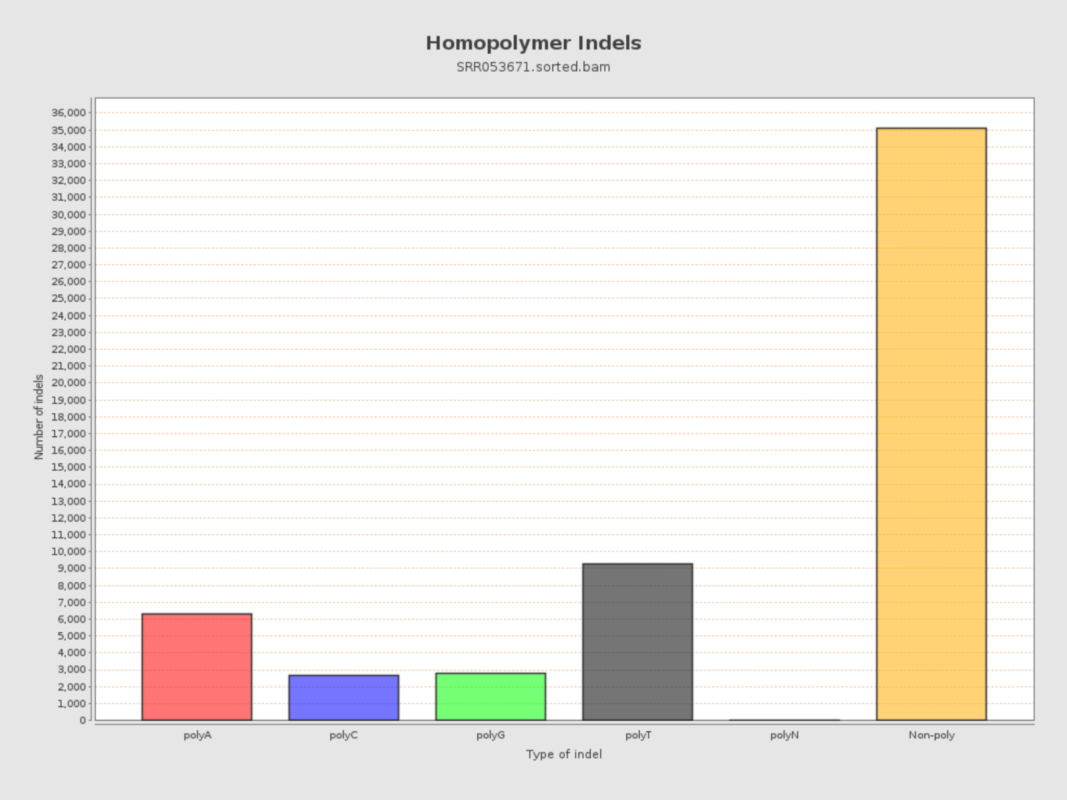
9. Results : Mapped Reads GC-content Distribution



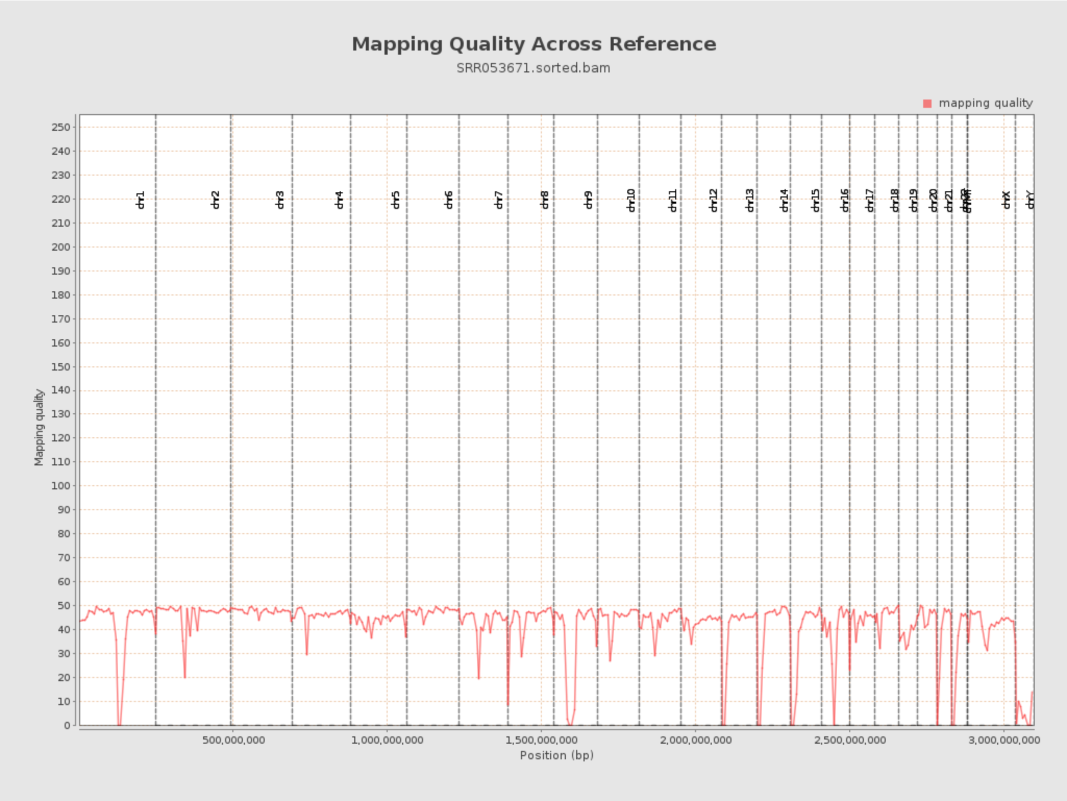
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram