Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 02:37:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053670.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_SRR053670 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053670.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 02:37:17 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053670.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,919,817
Mapped reads	5,581,231 / 56.26%
Unmapped reads	4,338,586 / 43.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	128 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,997,410 / 20.14%
Duplication rate	24.36%
Clipped reads	1,167,163 / 11.77%

2.2. ACGT Content

Number/percentage of A's	74,493,787 / 29%
Number/percentage of C's	51,635,145 / 20.1%
Number/percentage of T's	77,866,864 / 30.31%
Number/percentage of G's	52,781,433 / 20.54%
Number/percentage of N's	130,170 / 0.05%
GC Percentage	40.64%

2.3. Coverage

Mean	0.083

Standard Deviation	0.8647

2.4. Mapping Quality

Mean Mapping Quality	40.5

2.5. Mismatches and indels

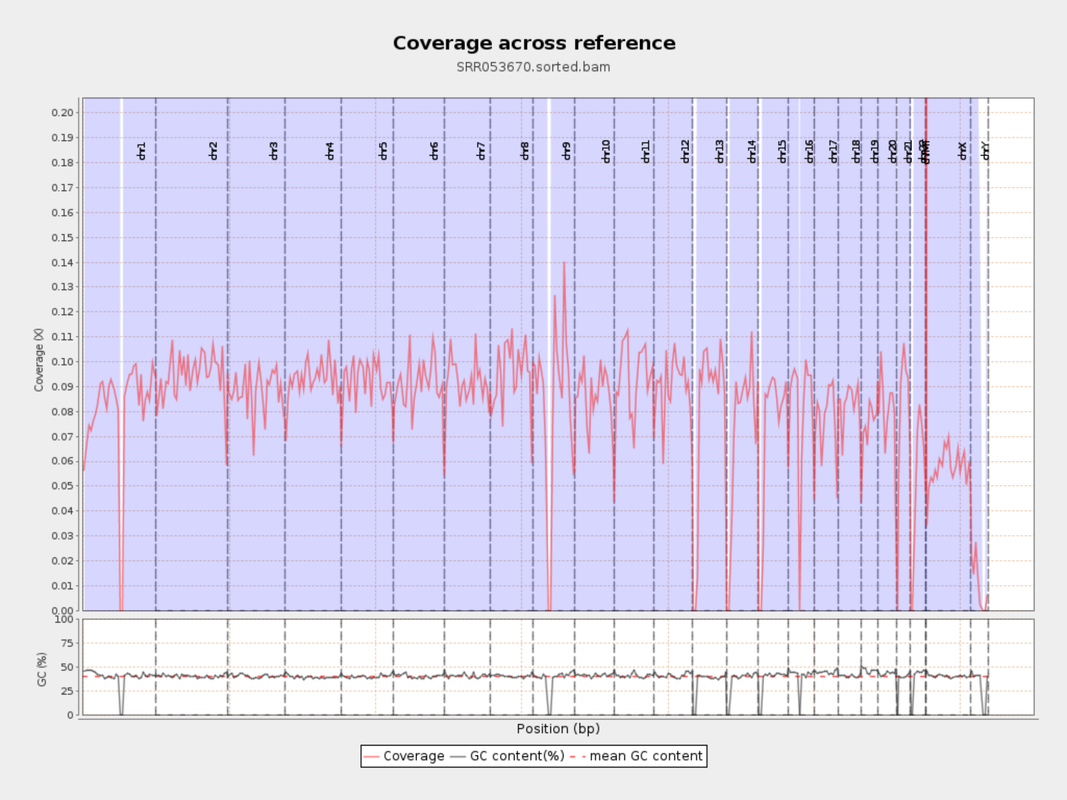
General error rate	1.65%
Mismatches	4,230,580
Insertions	15,534
Mapped reads with at least one insertion	0.28%
Deletions	32,473
Mapped reads with at least one deletion	0.58%
Homopolymer indels	38.08%

2.6. Chromosome stats

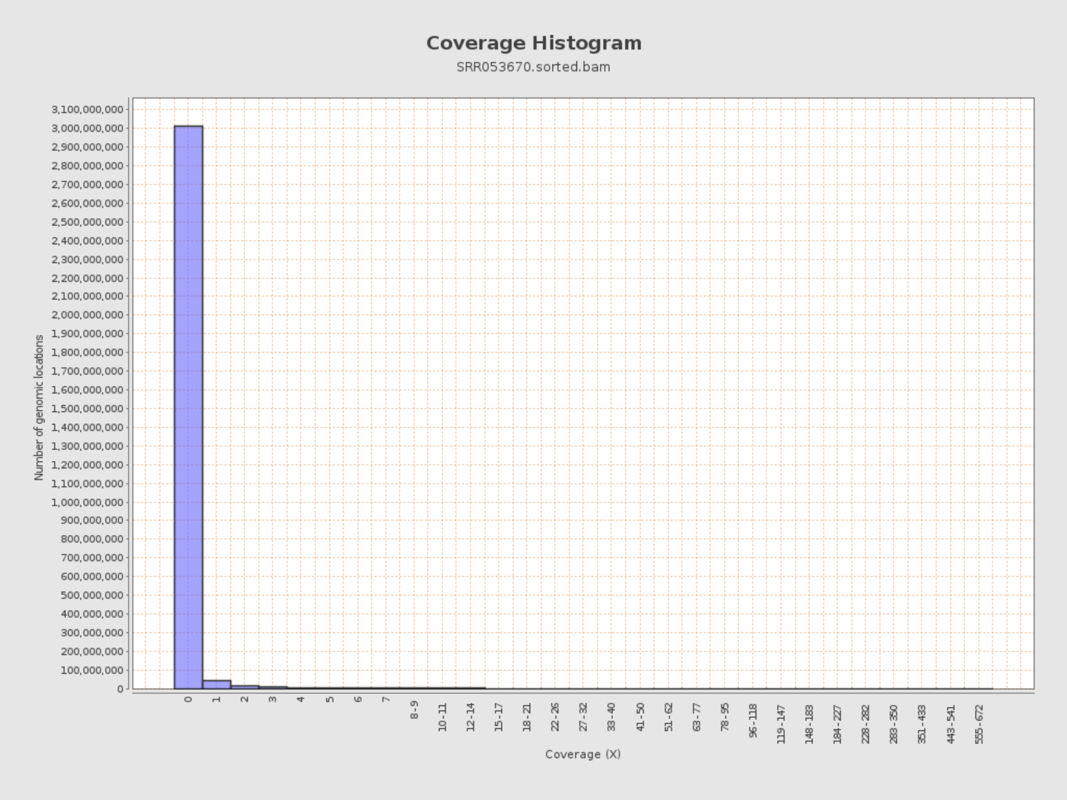
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20030586	0.0804	0.8697
chr2	243199373	23000641	0.0946	0.9499
chr3	198022430	17443254	0.0881	0.9205
chr4	191154276	17805236	0.0931	0.9124
chr5	180915260	16611971	0.0918	0.8845
chr6	171115067	15694799	0.0917	0.98
chr7	159138663	14559756	0.0915	0.9263

chr8	146364022	13915140	0.0951	0.9275
chr9	141213431	11803881	0.0836	0.8478
chr10	135534747	11785032	0.087	0.865
chr11	135006516	12644887	0.0937	0.9572
chr12	133851895	12116174	0.0905	0.8852
chr13	115169878	9179594	0.0797	0.8514
chr14	107349540	7746596	0.0722	0.8085
chr15	102531392	7176771	0.07	0.7547
chr16	90354753	7103173	0.0786	0.8007
chr17	81195210	6367921	0.0784	0.7486
chr18	78077248	6479926	0.083	0.8725
chr19	59128983	4452707	0.0753	0.7919
chr20	63025520	5112632	0.0811	0.8212
chr21	48129895	3754465	0.078	0.8177
chr22	51304566	2611355	0.0509	0.6059
chrMT	16571	29215	1.763	3.8208
chrX	155270560	8917609	0.0574	0.6739
chrY	59373566	609578	0.0103	0.223

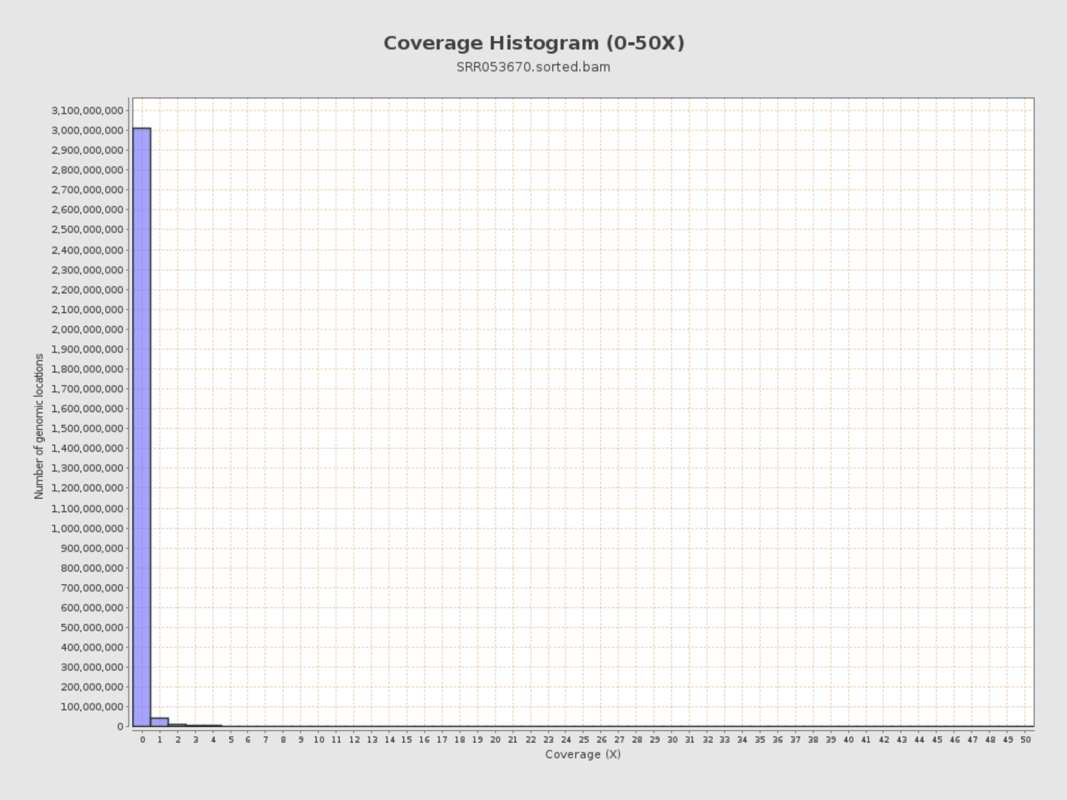
3. Results : Coverage across reference



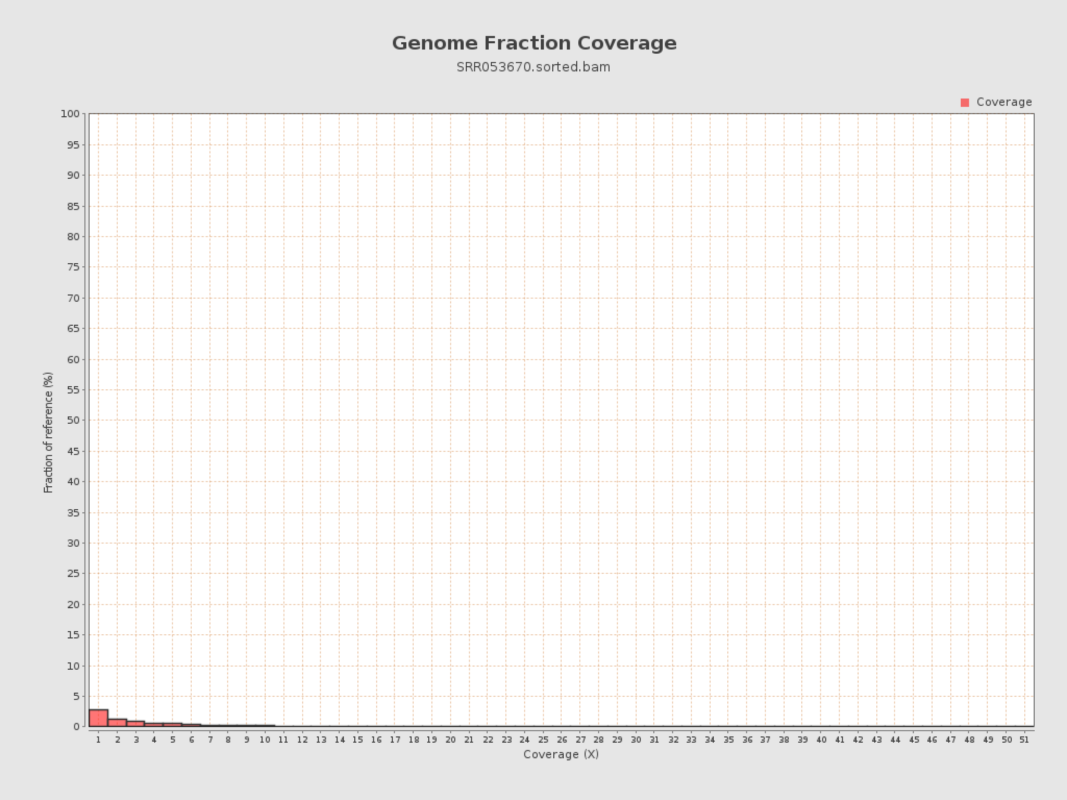
4. Results : Coverage Histogram



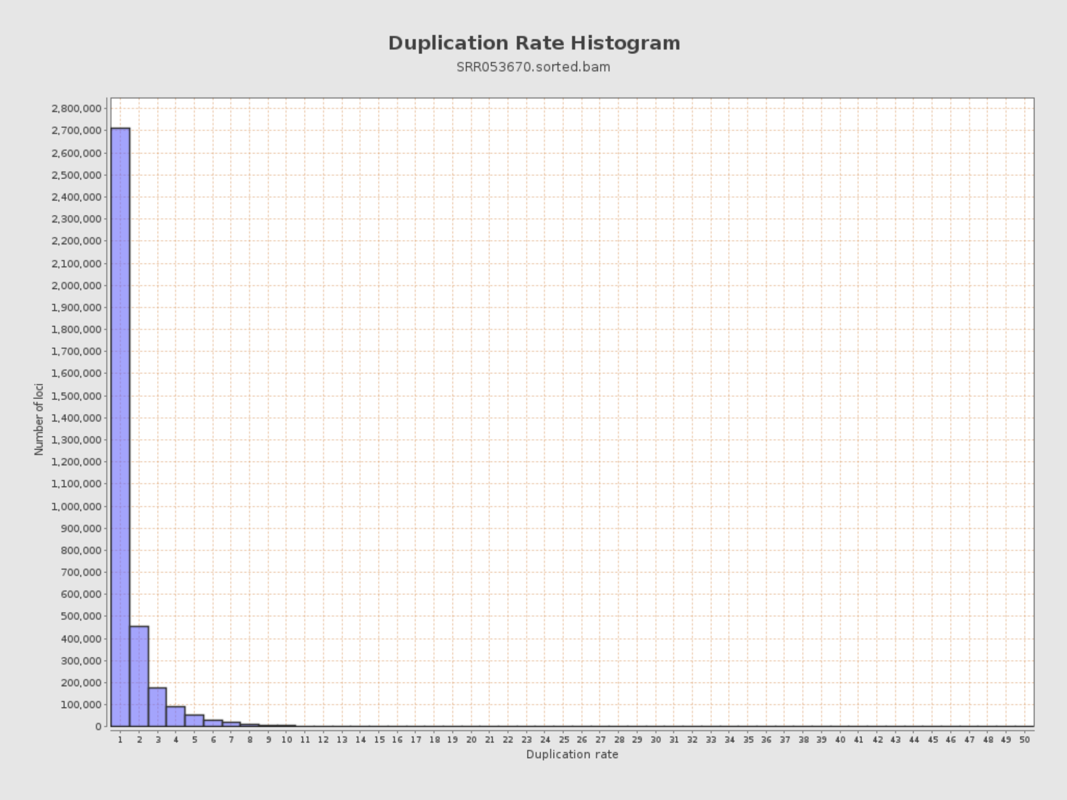
5. Results : Coverage Histogram (0-50X)



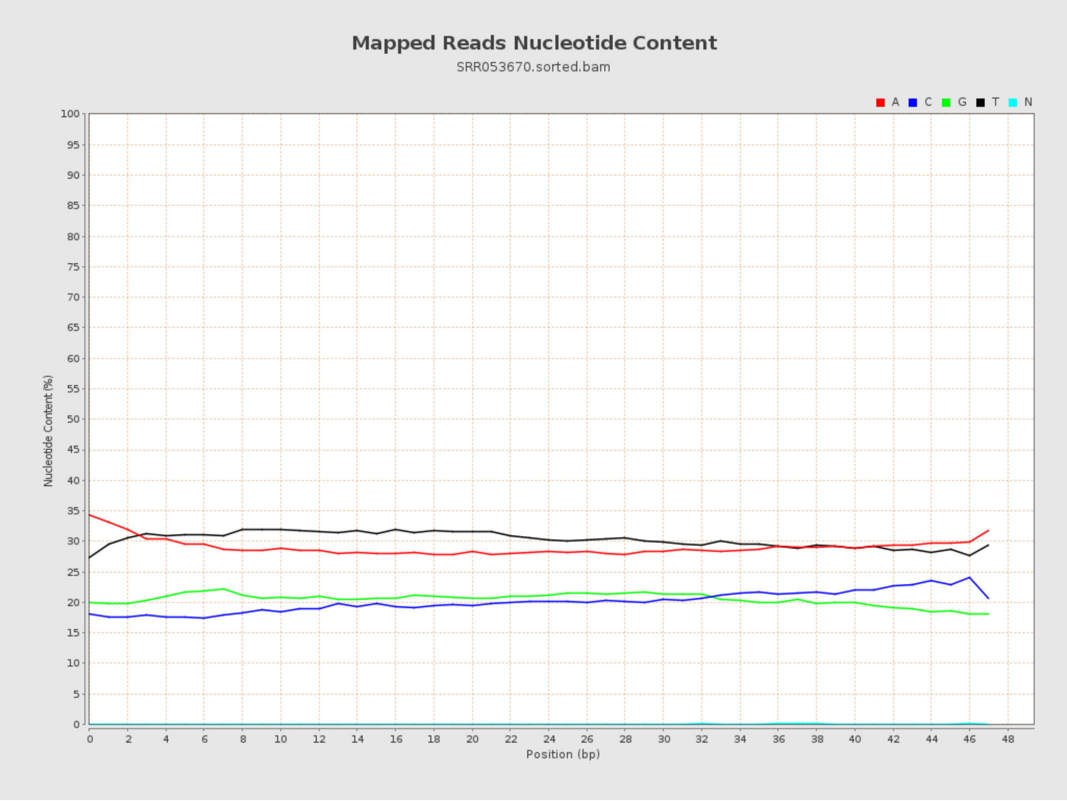
6. Results : Genome Fraction Coverage



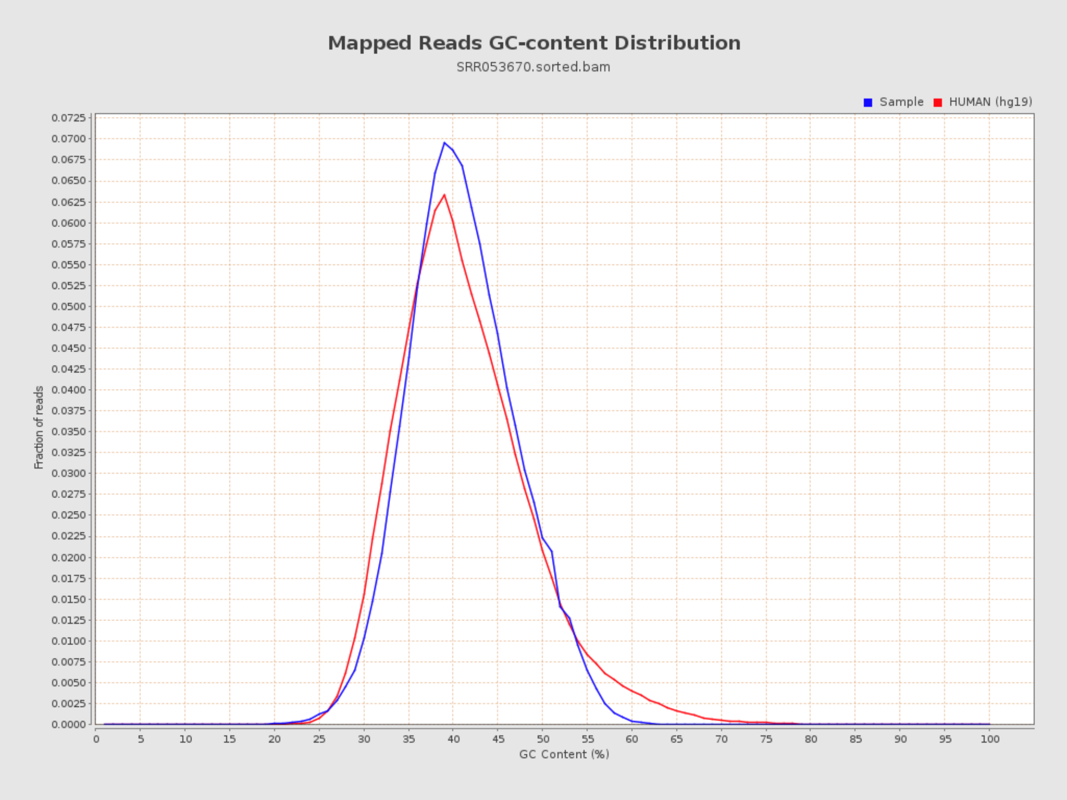
7. Results : Duplication Rate Histogram



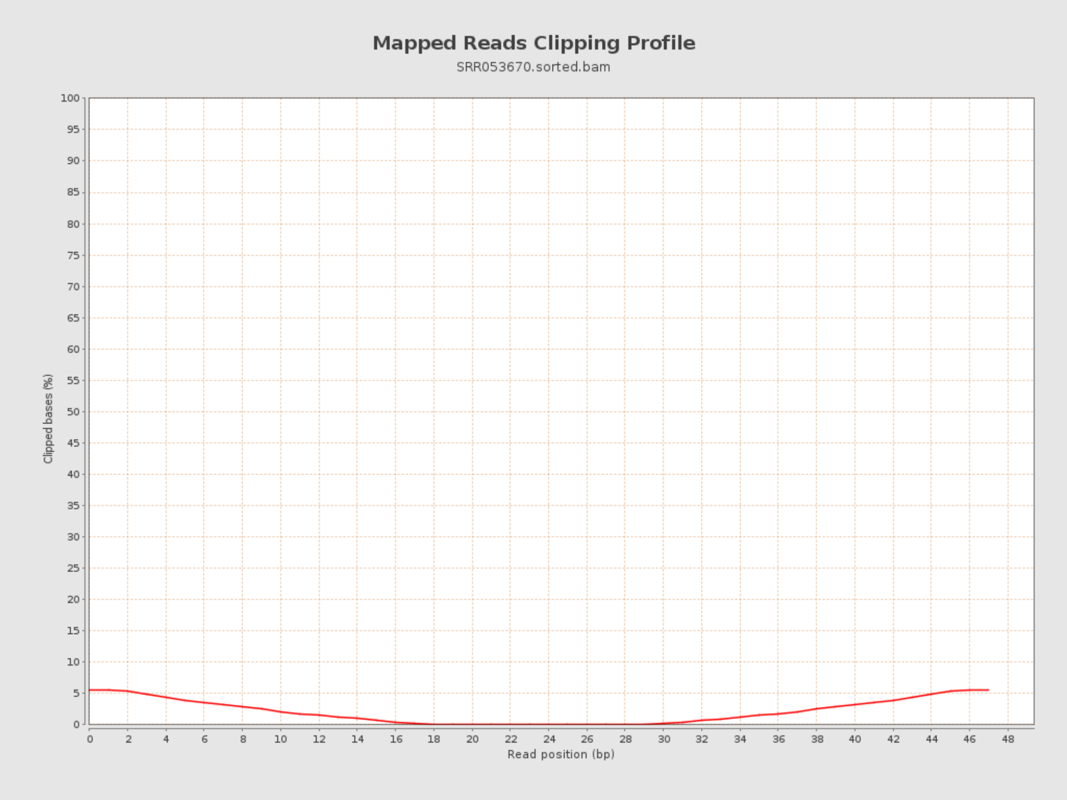
8. Results : Mapped Reads Nucleotide Content



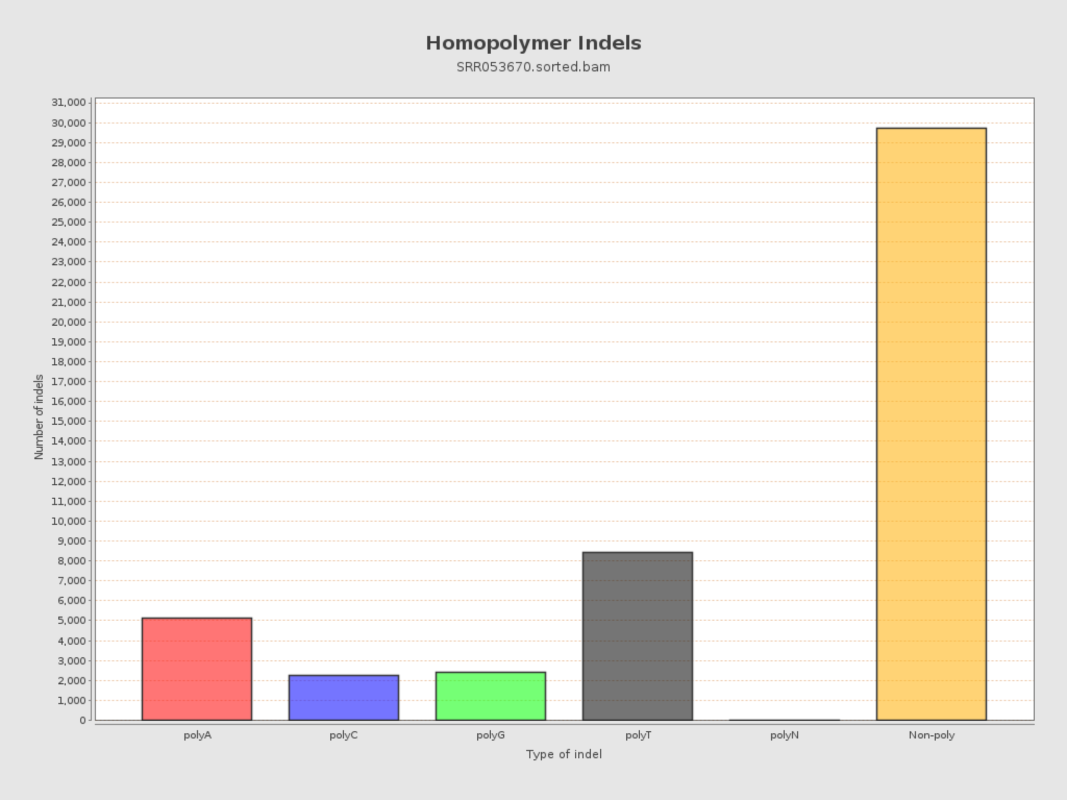
9. Results : Mapped Reads GC-content Distribution



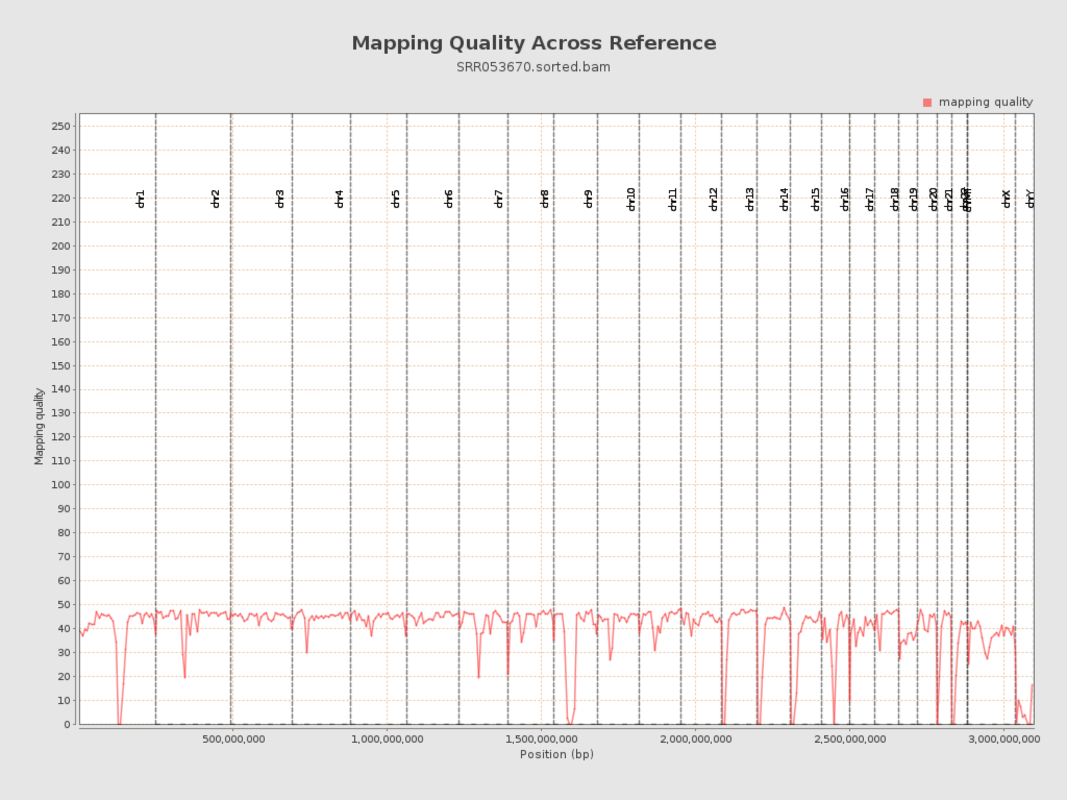
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram