Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 22:43:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053437.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_SRR053437 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053437.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 22:43:59 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053437.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,420,796
Mapped reads	5,377,627 / 63.86%
Unmapped reads	3,043,169 / 36.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	175 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,143,402 / 13.58%
Duplication rate	15.63%
Clipped reads	849,013 / 10.08%

2.2. ACGT Content

Number/percentage of A's	74,935,540 / 29.94%
Number/percentage of C's	48,728,826 / 19.47%
Number/percentage of T's	74,641,094 / 29.82%
Number/percentage of G's	51,678,116 / 20.65%
Number/percentage of N's	301,457 / 0.12%
GC Percentage	40.12%

2.3. Coverage

Mean	0.0809

Standard Deviation	1.1532

2.4. Mapping Quality

Mean Mapping Quality	43.27

2.5. Mismatches and indels

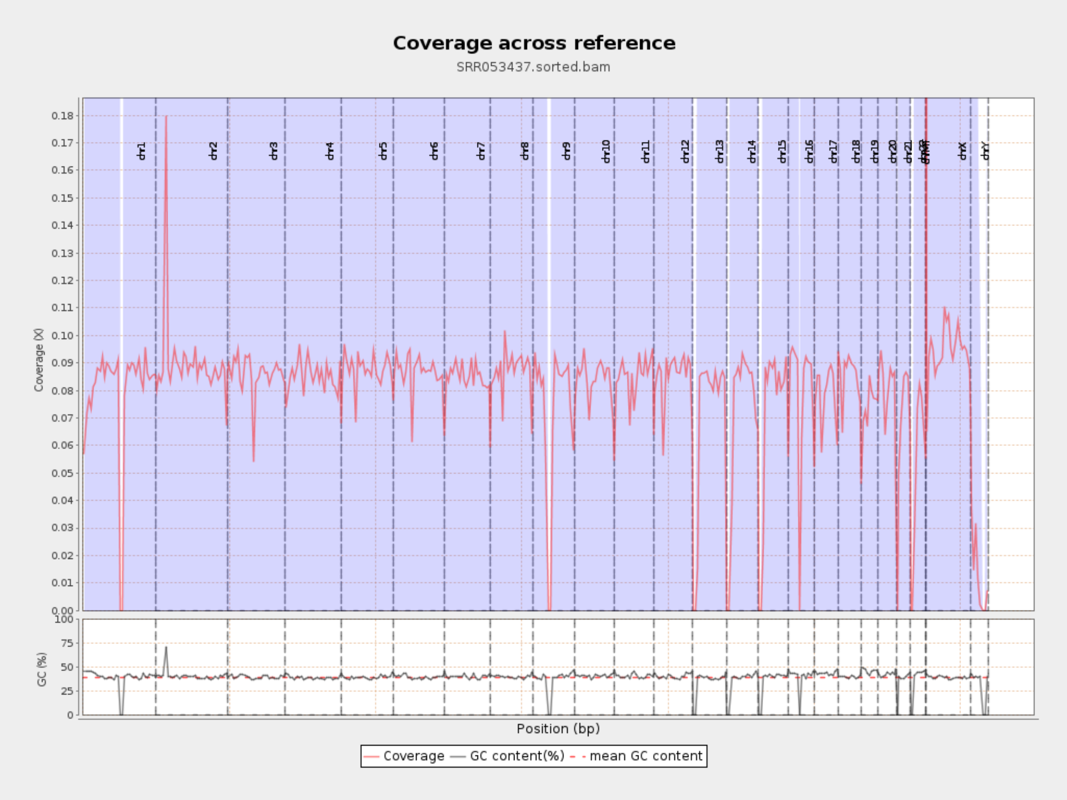
General error rate	1.3%
Mismatches	3,227,036
Insertions	16,807
Mapped reads with at least one insertion	0.31%
Deletions	36,289
Mapped reads with at least one deletion	0.67%
Homopolymer indels	42.05%

2.6. Chromosome stats

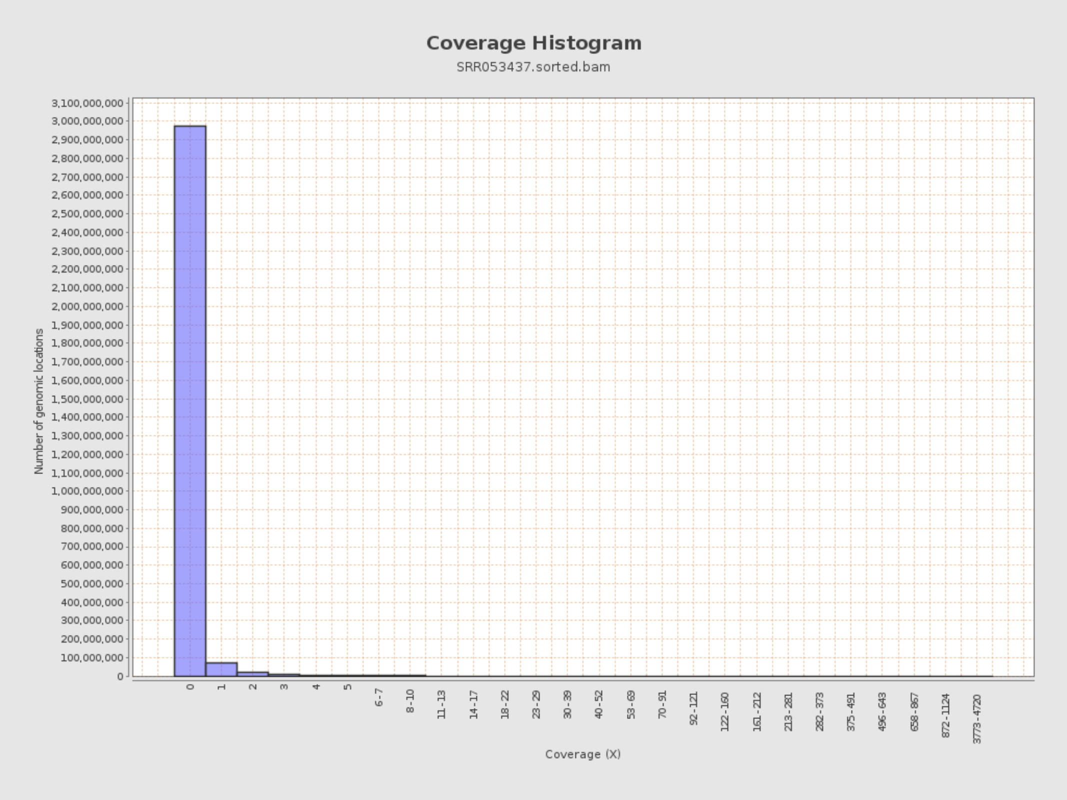
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19790301	0.0794	0.7044
chr2	243199373	21941333	0.0902	3.4914
chr3	198022430	17057515	0.0861	0.6189
chr4	191154276	16326643	0.0854	0.6379
chr5	180915260	15794691	0.0873	0.6208
chr6	171115067	14855419	0.0868	0.662
chr7	159138663	13510148	0.0849	0.7164

chr8	146364022	12738338	0.087	0.6602
chr9	141213431	10254623	0.0726	0.5838
chr10	135534747	11424892	0.0843	0.6639
chr11	135006516	11450761	0.0848	0.6739
chr12	133851895	11506114	0.086	0.618
chr13	115169878	8053548	0.0699	0.5471
chr14	107349540	7617460	0.071	0.6629
chr15	102531392	7101570	0.0693	0.5652
chr16	90354753	6999208	0.0775	0.6051
chr17	81195210	6424289	0.0791	0.5763
chr18	78077248	6670438	0.0854	0.6927
chr19	59128983	4370311	0.0739	0.654
chr20	63025520	5138875	0.0815	0.607
chr21	48129895	3205703	0.0666	0.5827
chr22	51304566	2643304	0.0515	0.4647
chrMT	16571	43876	2.6478	4.5014
chrX	155270560	14705628	0.0947	0.6835
chrY	59373566	711020	0.012	0.237

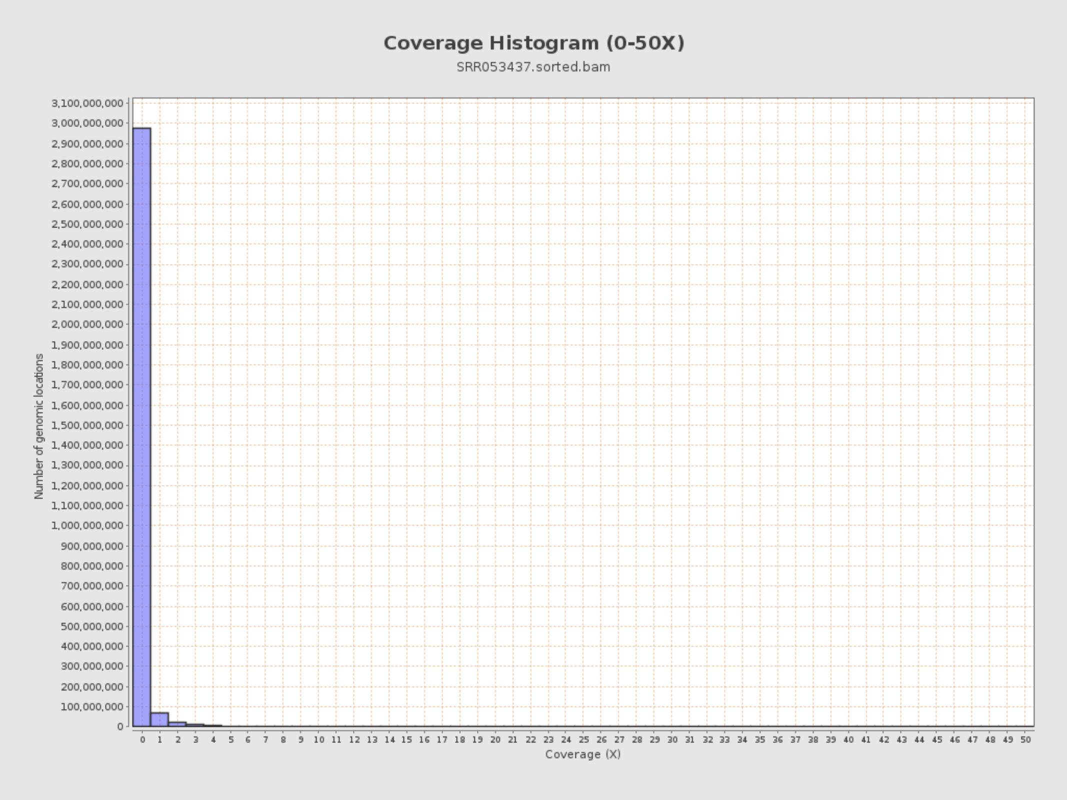
3. Results : Coverage across reference



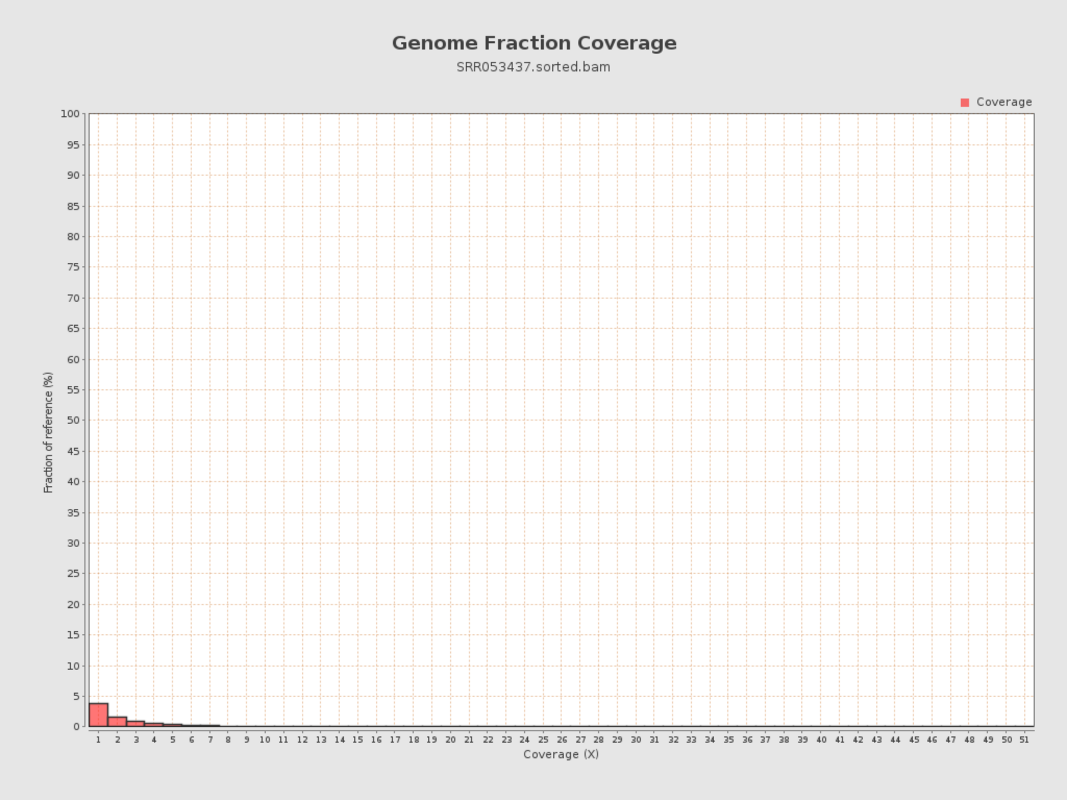
4. Results : Coverage Histogram



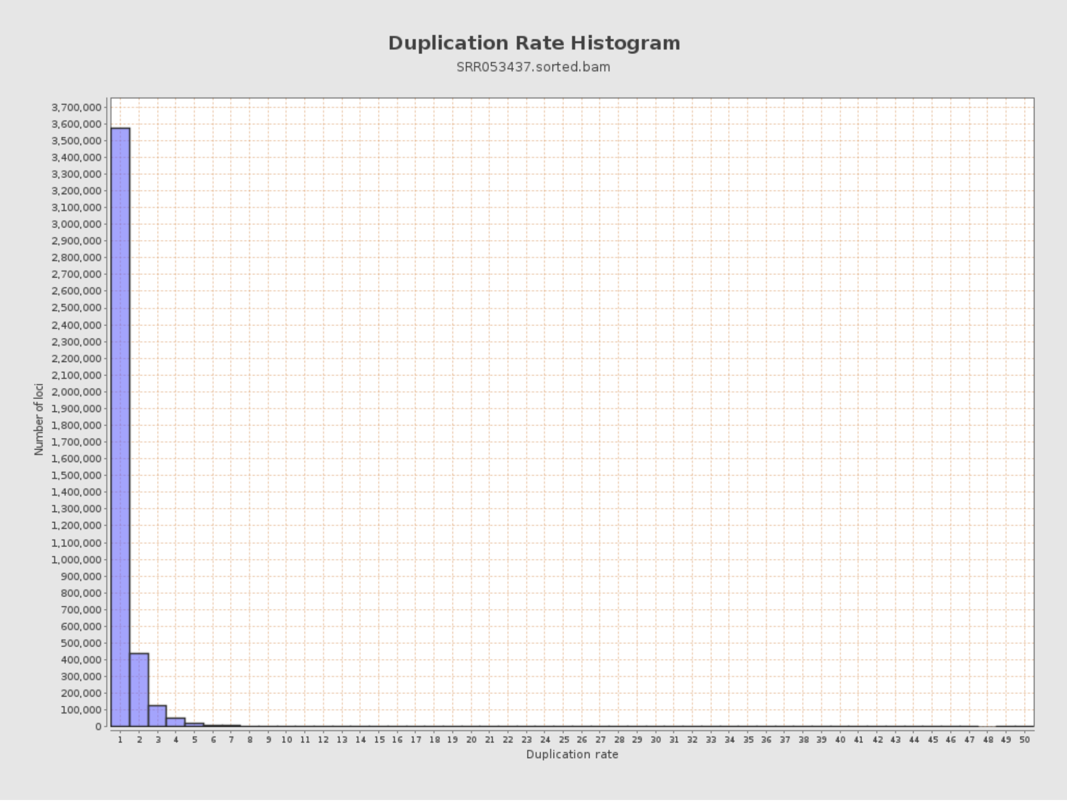
5. Results : Coverage Histogram (0-50X)



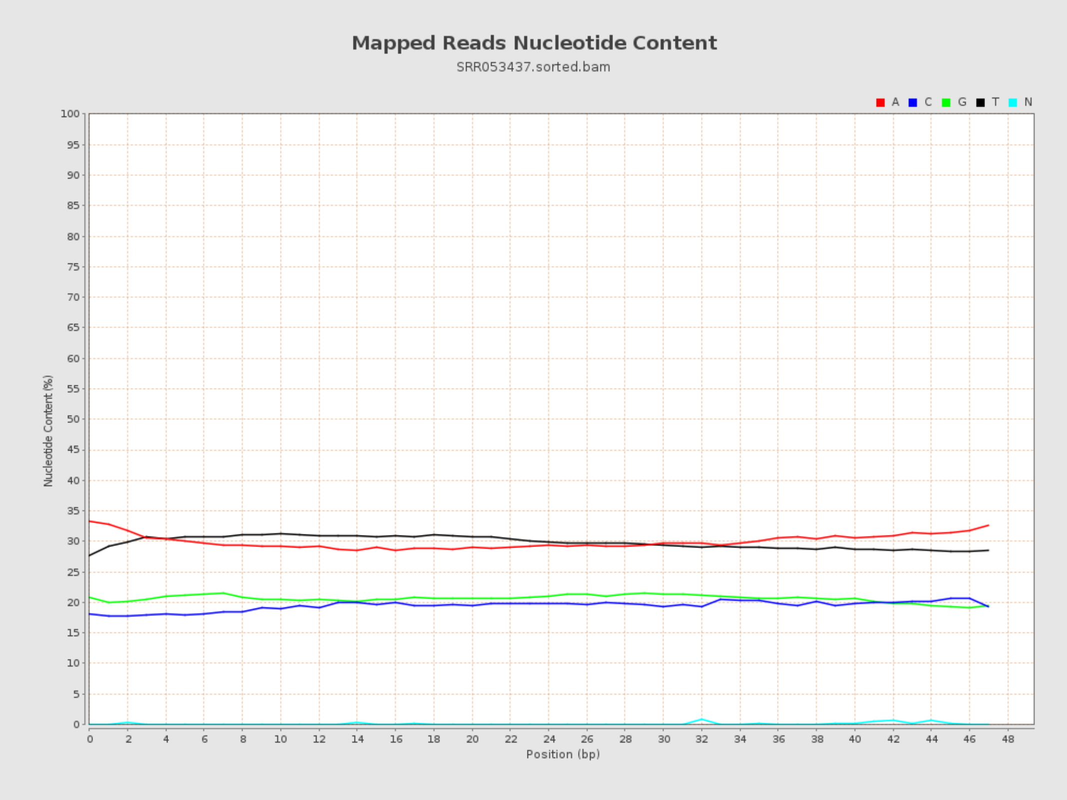
6. Results : Genome Fraction Coverage



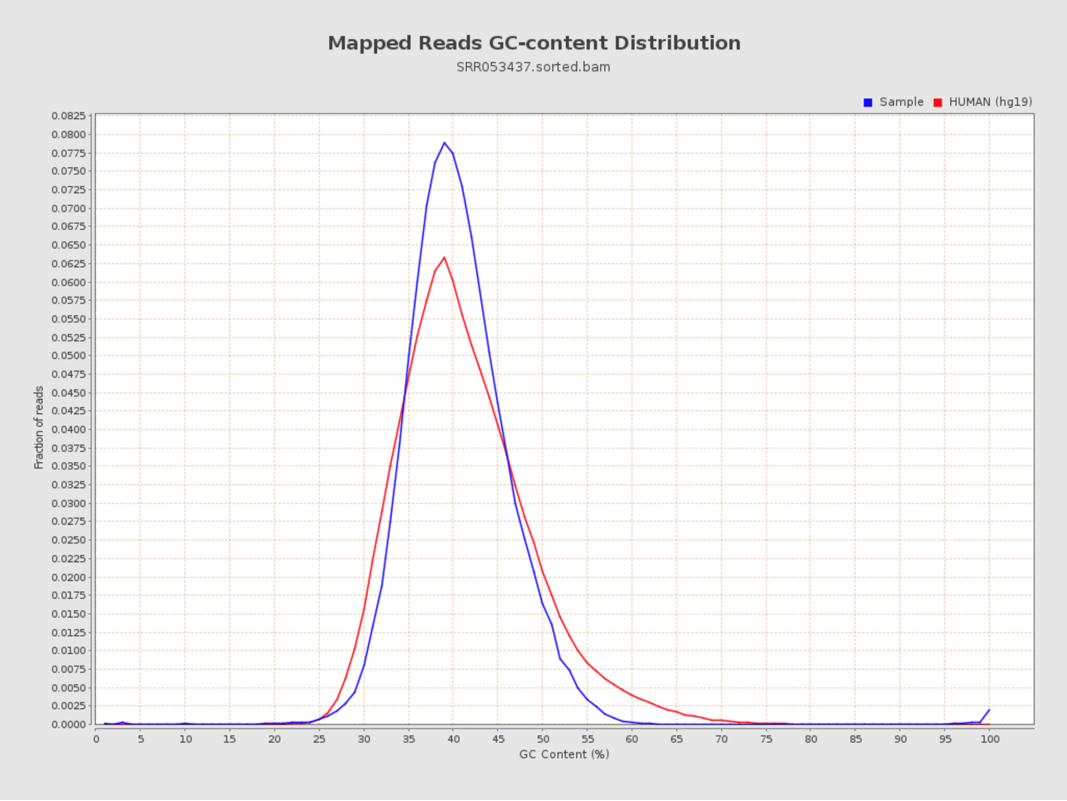
7. Results : Duplication Rate Histogram



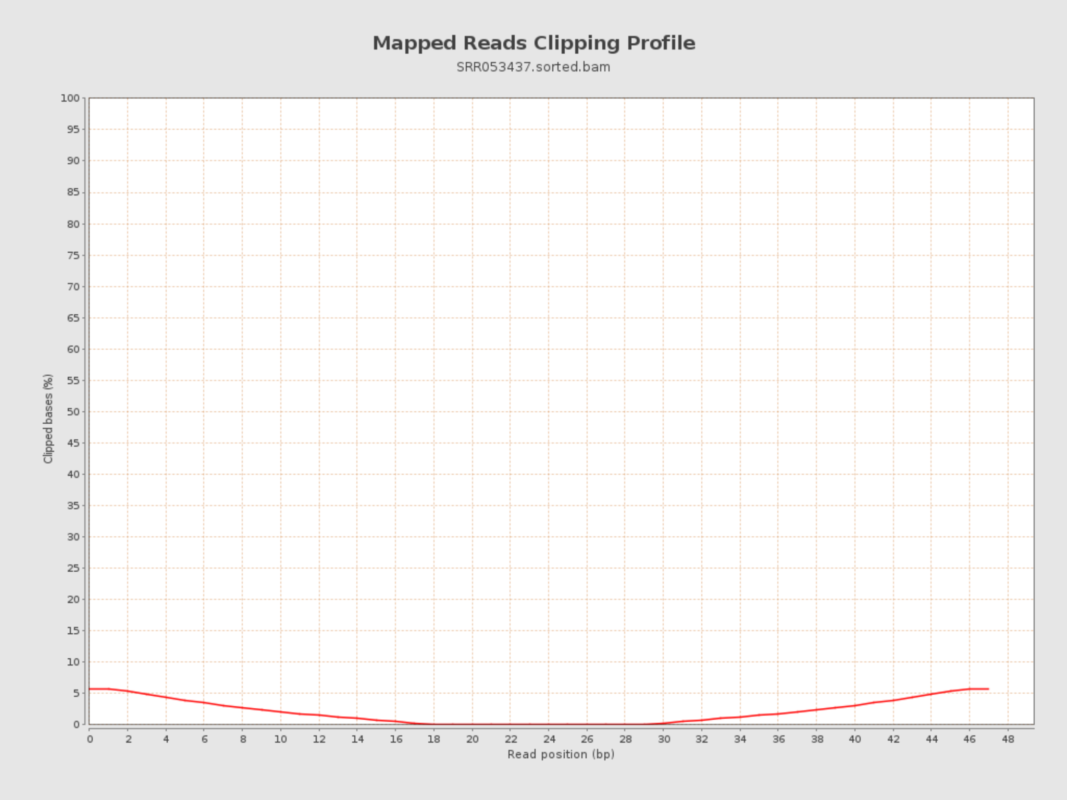
8. Results : Mapped Reads Nucleotide Content



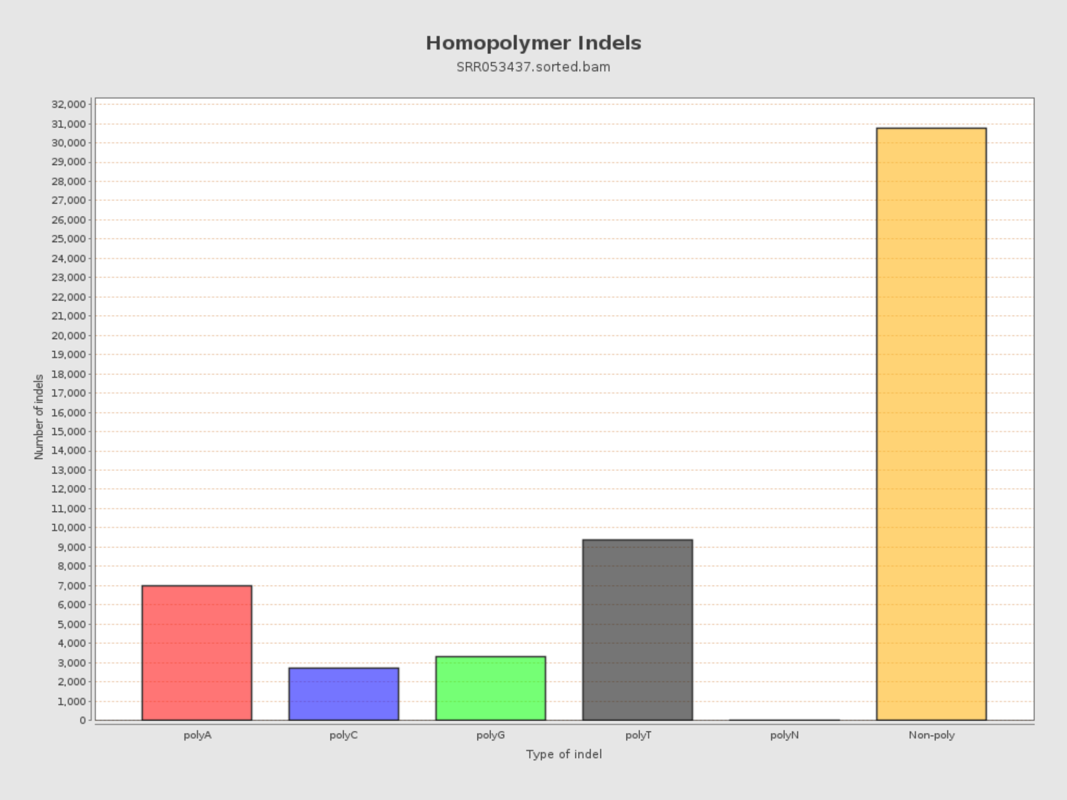
9. Results : Mapped Reads GC-content Distribution



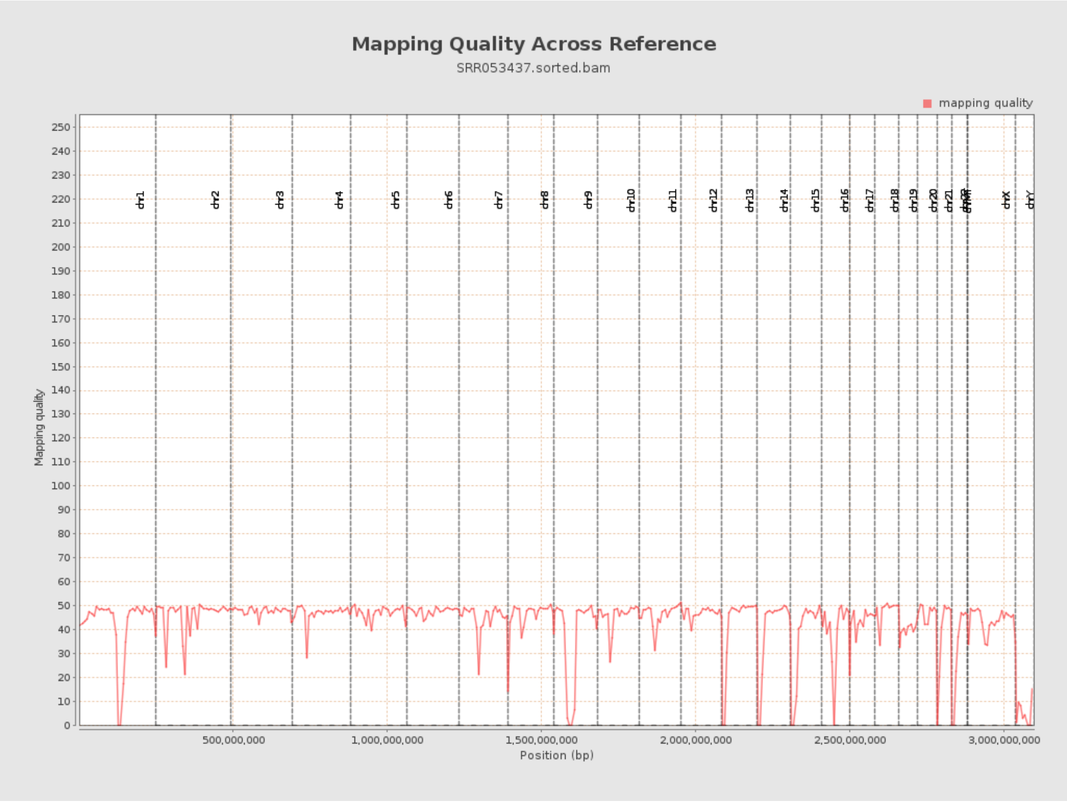
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram