Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 05:25:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054576.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_SRR054576 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054576.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 05:25:02 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054576.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,086,802
Mapped reads	6,460,828 / 71.1%
Unmapped reads	2,625,974 / 28.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	189 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,511,984 / 16.64%
Duplication rate	18.93%
Clipped reads	541,678 / 5.96%

2.2. ACGT Content

Number/percentage of A's	88,838,211 / 29.11%
Number/percentage of C's	59,564,646 / 19.52%
Number/percentage of T's	90,700,255 / 29.72%
Number/percentage of G's	65,940,786 / 21.61%
Number/percentage of N's	105,905 / 0.03%
GC Percentage	41.13%

2.3. Coverage

Mean	0.0986

Standard Deviation	0.7404

2.4. Mapping Quality

Mean Mapping Quality	44.6

2.5. Mismatches and indels

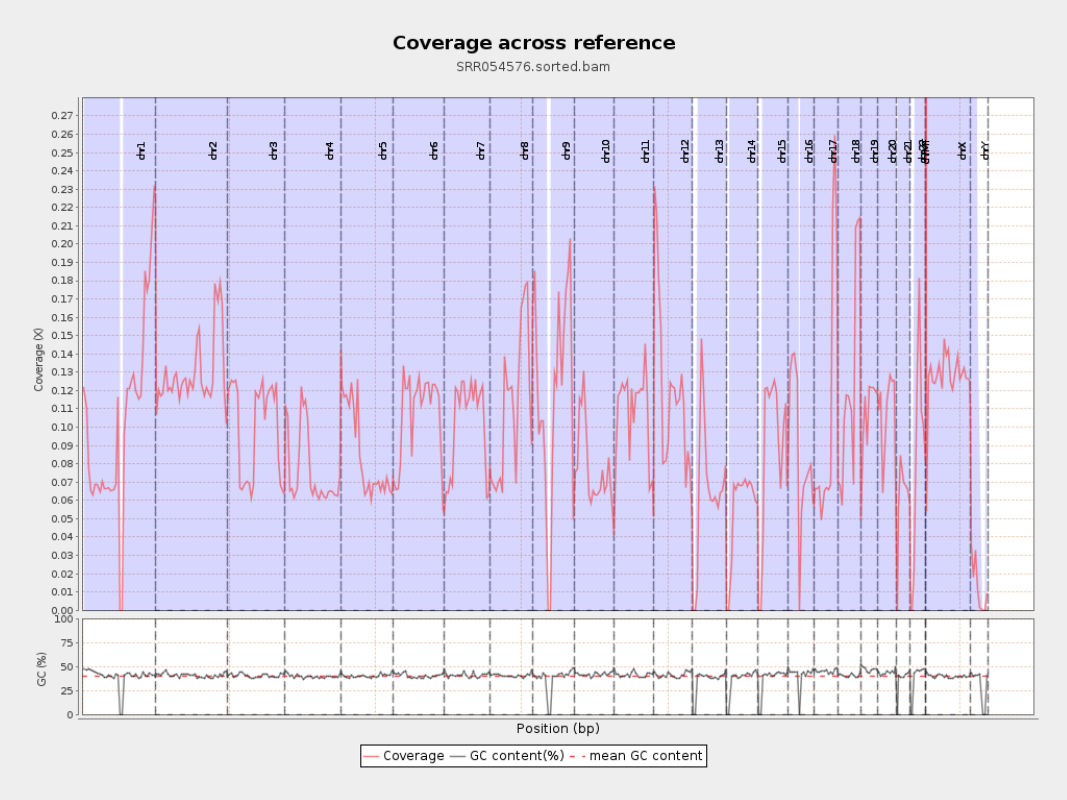
General error rate	0.59%
Mismatches	1,793,263
Insertions	12,757
Mapped reads with at least one insertion	0.2%
Deletions	42,105
Mapped reads with at least one deletion	0.65%
Homopolymer indels	47.71%

2.6. Chromosome stats

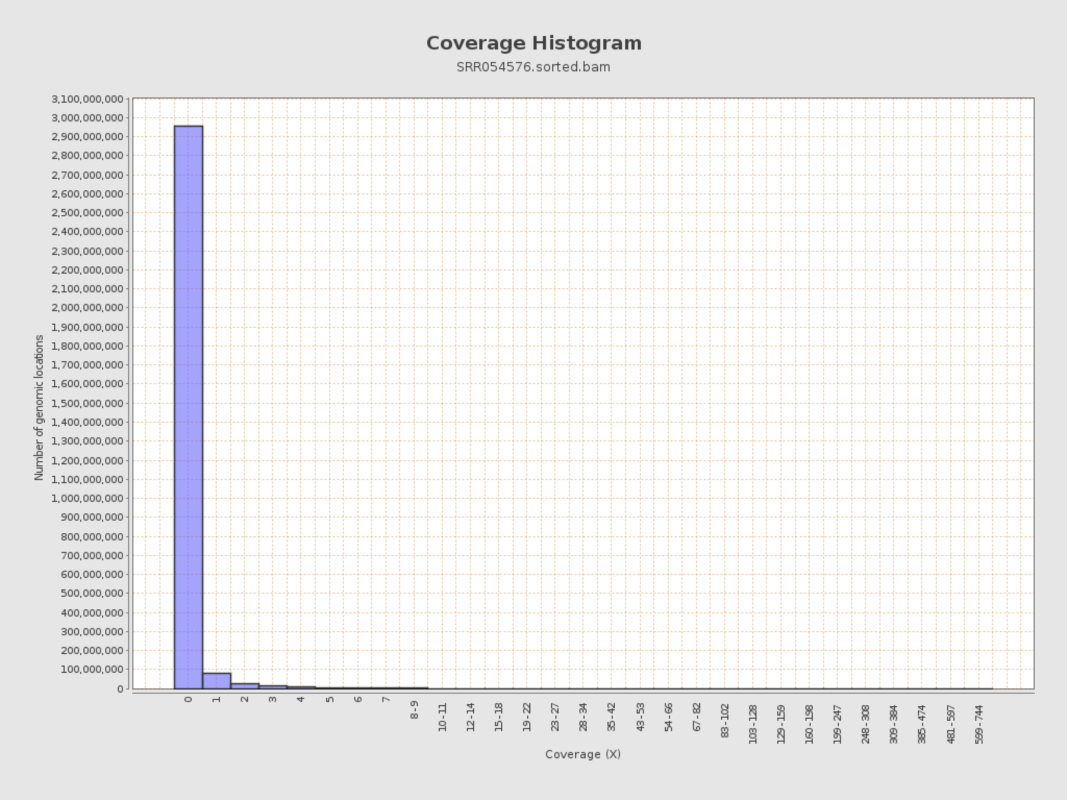
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25884432	0.1038	0.7939
chr2	243199373	31589213	0.1299	1.0498
chr3	198022430	19668975	0.0993	0.6825
chr4	191154276	14635469	0.0766	0.5848
chr5	180915260	15365128	0.0849	0.6036
chr6	171115067	18428099	0.1077	0.7506
chr7	159138663	15955949	0.1003	0.869

chr8	146364022	16270196	0.1112	0.7587
chr9	141213431	16474760	0.1167	0.7737
chr10	135534747	10571190	0.078	0.6516
chr11	135006516	14671065	0.1087	0.746
chr12	133851895	16317732	0.1219	0.7632
chr13	115169878	7499176	0.0651	0.5289
chr14	107349540	6004214	0.0559	0.5981
chr15	102531392	8999059	0.0878	0.6148
chr16	90354753	7688115	0.0851	0.6276
chr17	81195210	8520846	0.1049	0.708
chr18	78077248	9537872	0.1222	0.8595
chr19	59128983	6470176	0.1094	0.795
chr20	63025520	6793688	0.1078	0.7079
chr21	48129895	2942236	0.0611	0.5366
chr22	51304566	4350017	0.0848	0.6063
chrMT	16571	30825	1.8602	3.674
chrX	155270560	19787453	0.1274	0.8122
chrY	59373566	756965	0.0127	0.2309

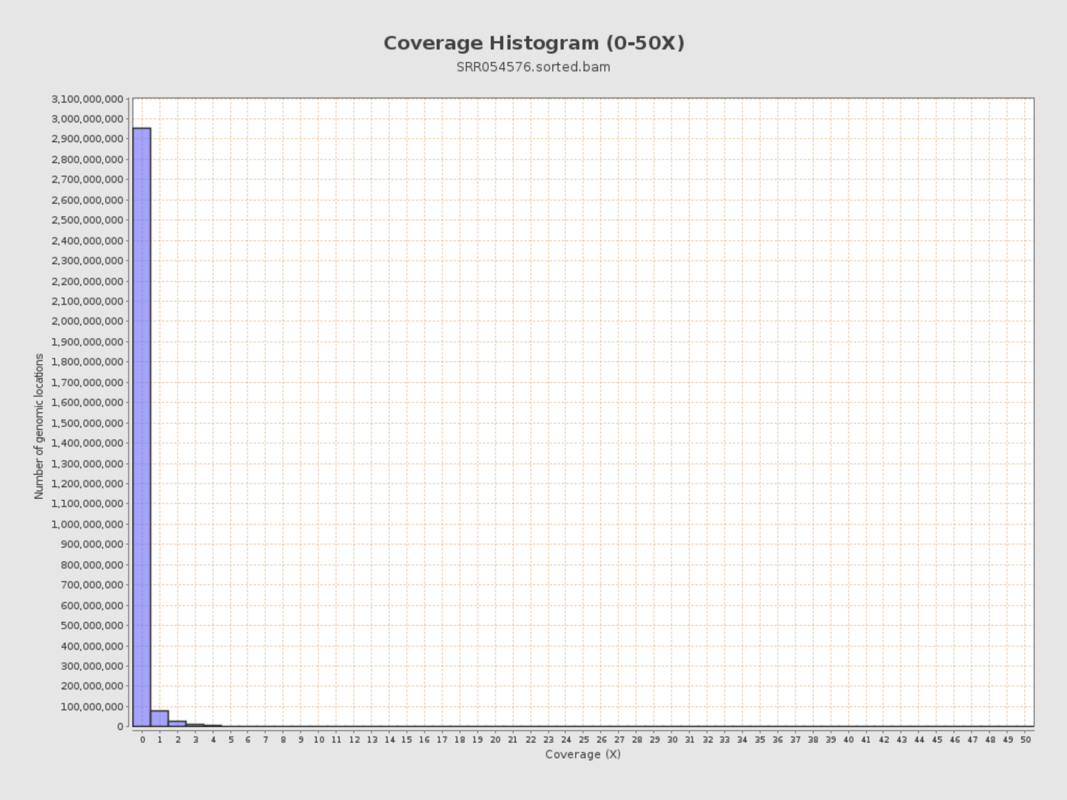
3. Results : Coverage across reference



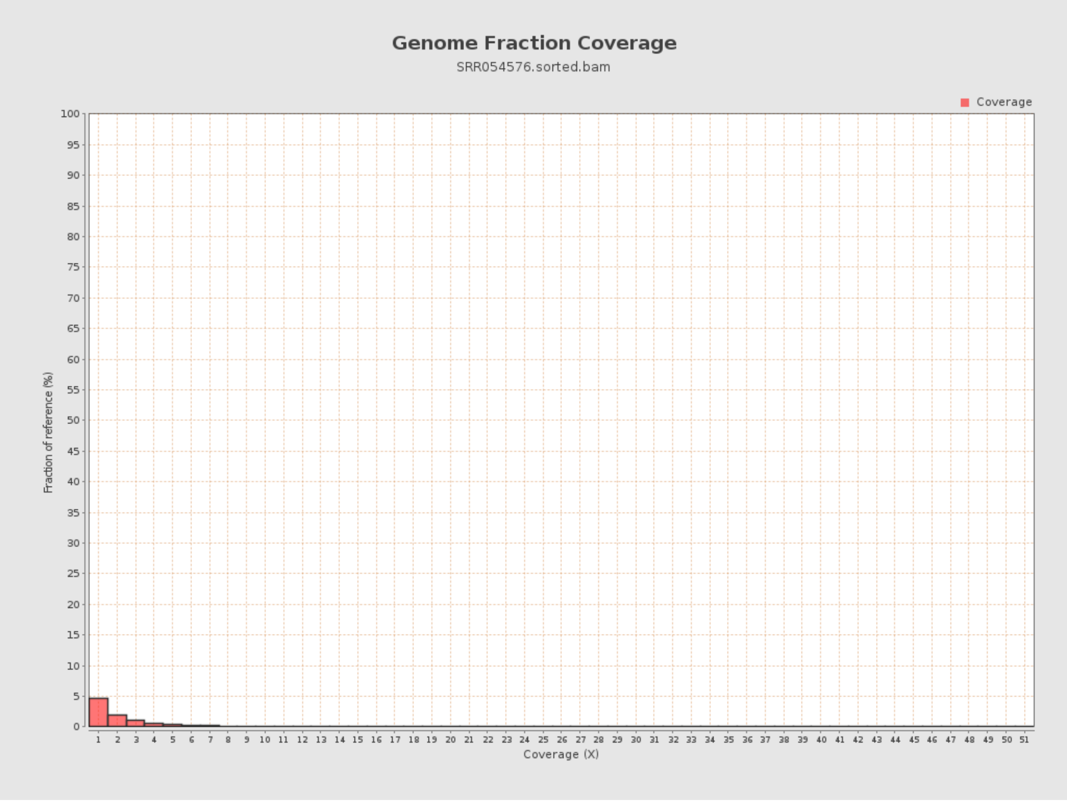
4. Results : Coverage Histogram



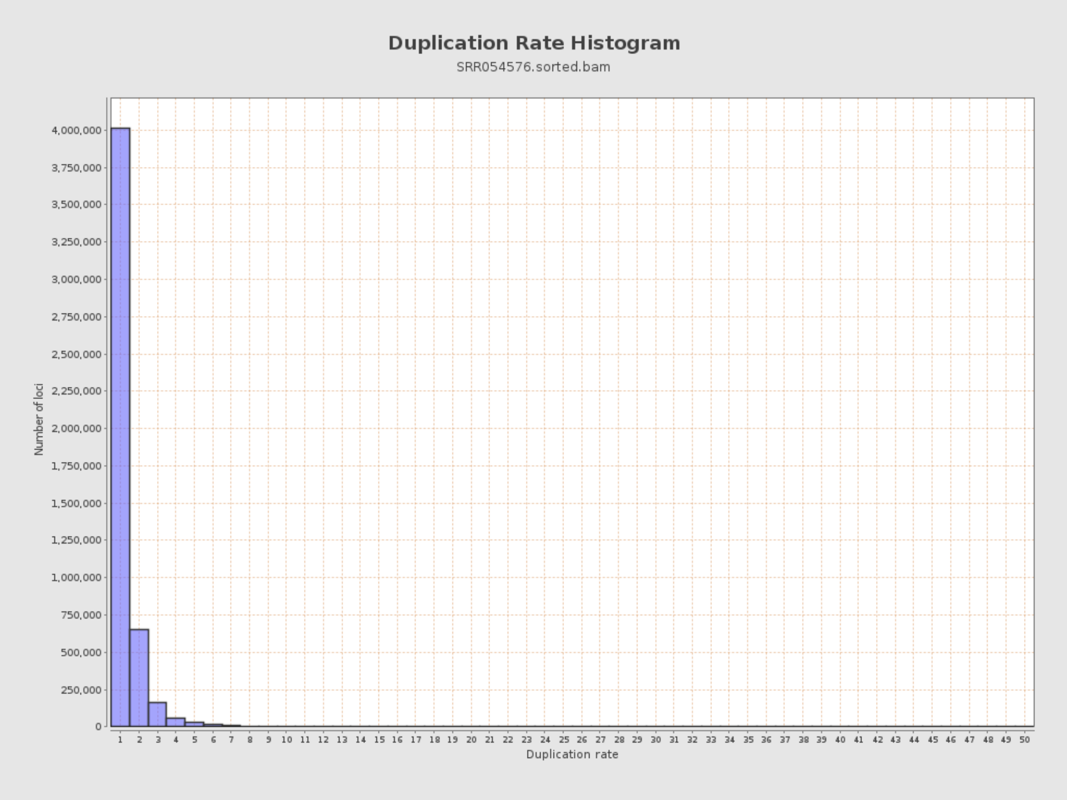
5. Results : Coverage Histogram (0-50X)



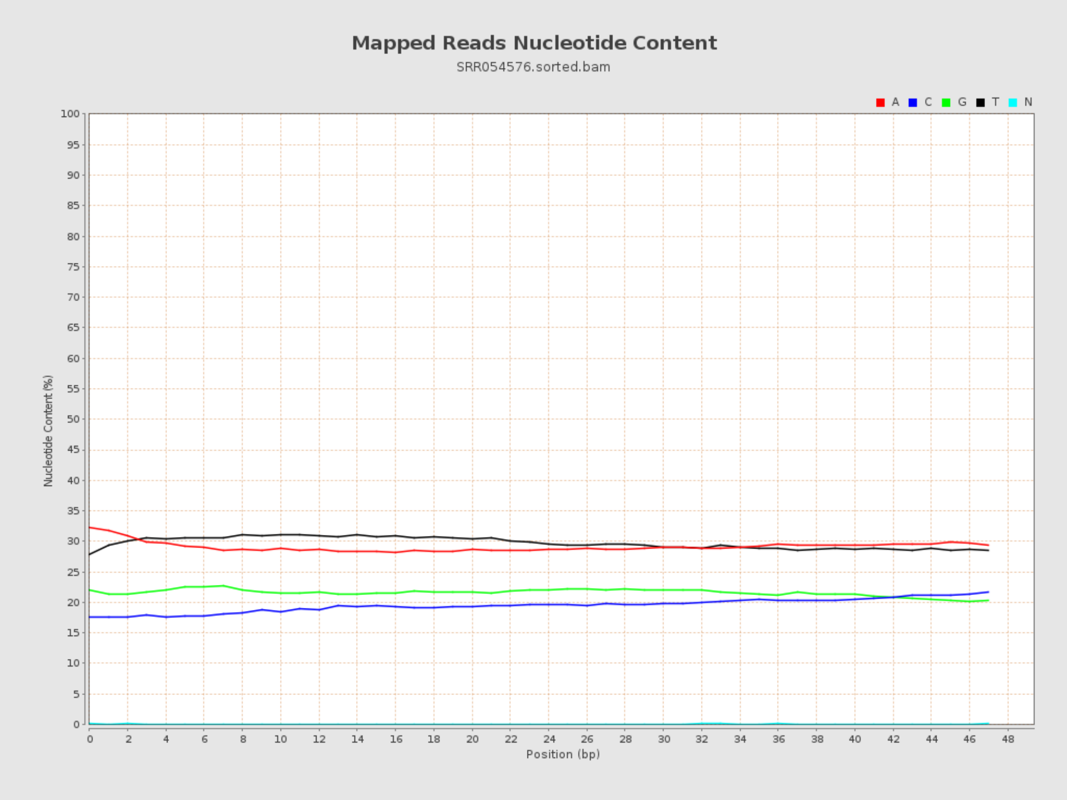
6. Results : Genome Fraction Coverage



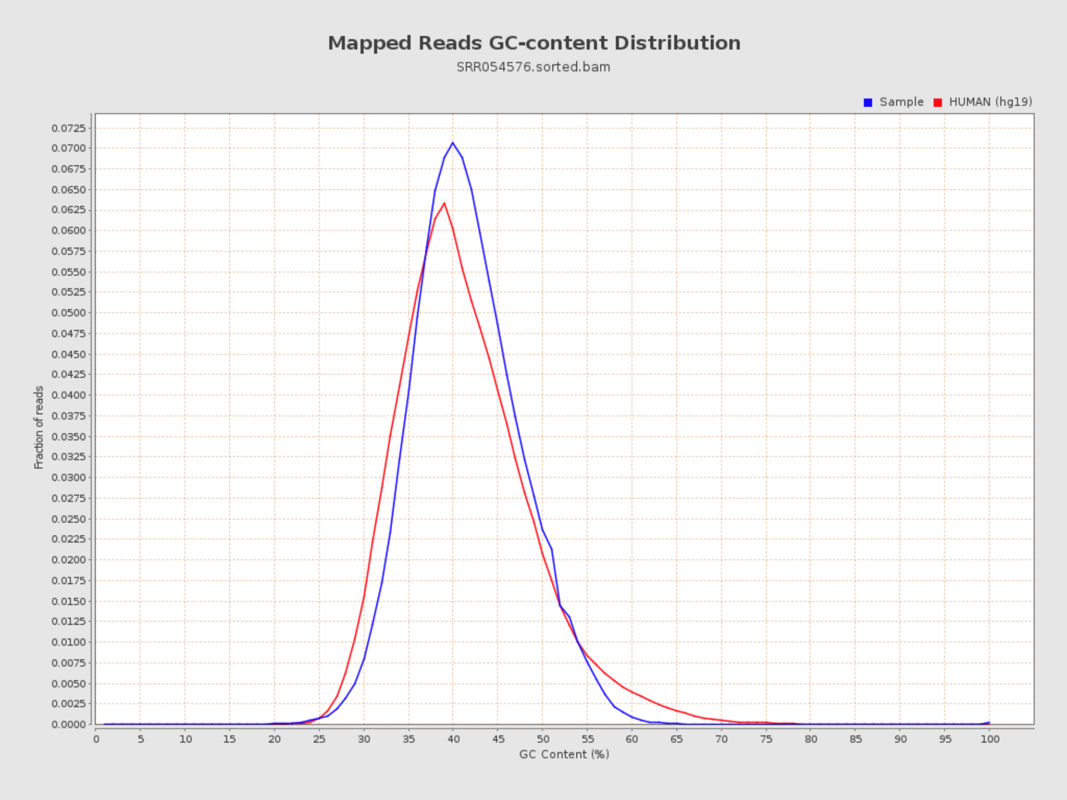
7. Results : Duplication Rate Histogram



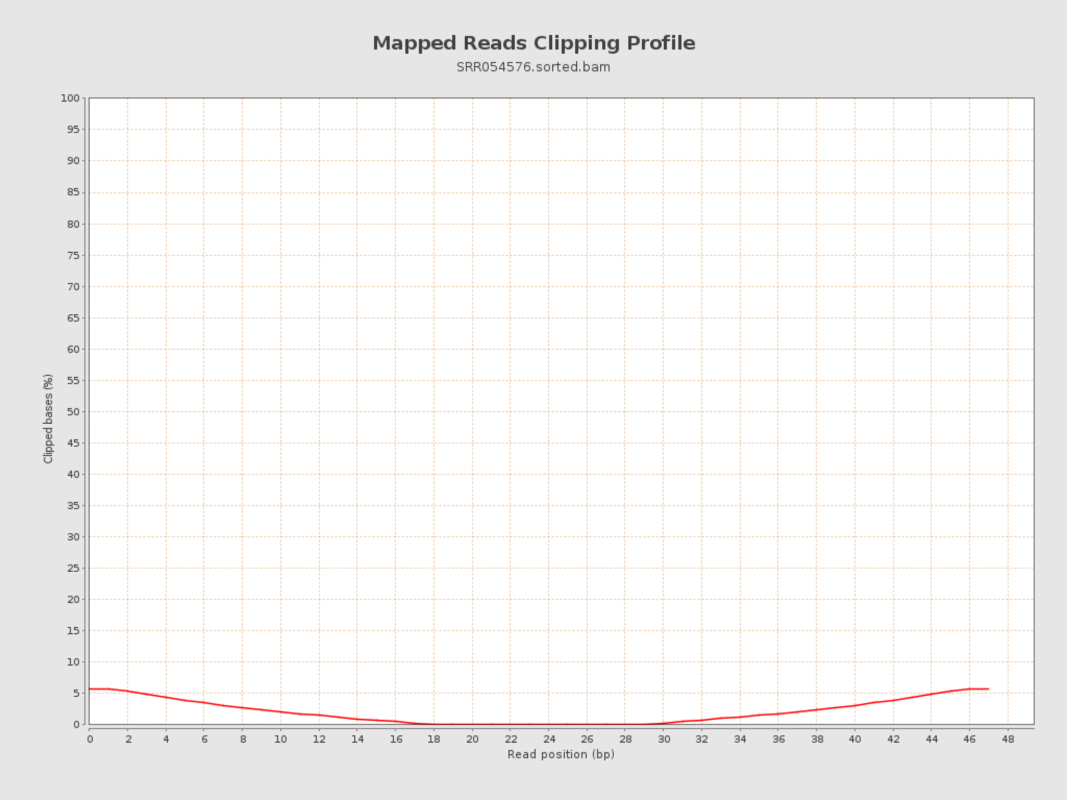
8. Results : Mapped Reads Nucleotide Content



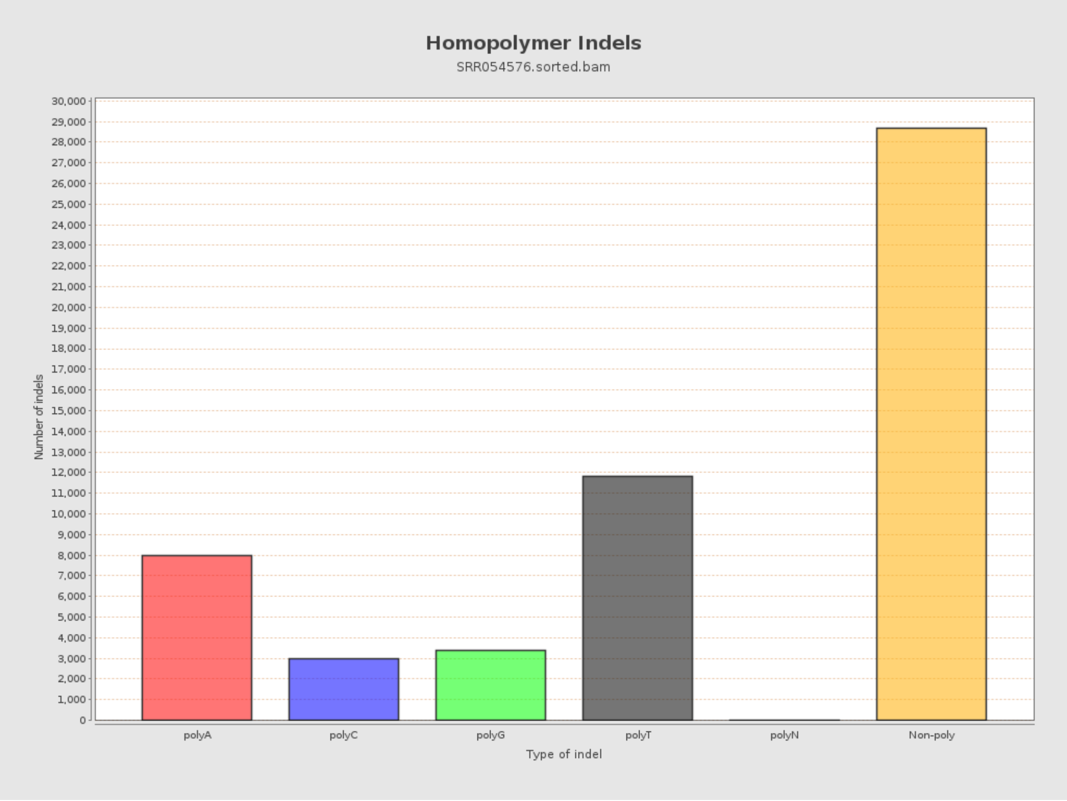
9. Results : Mapped Reads GC-content Distribution



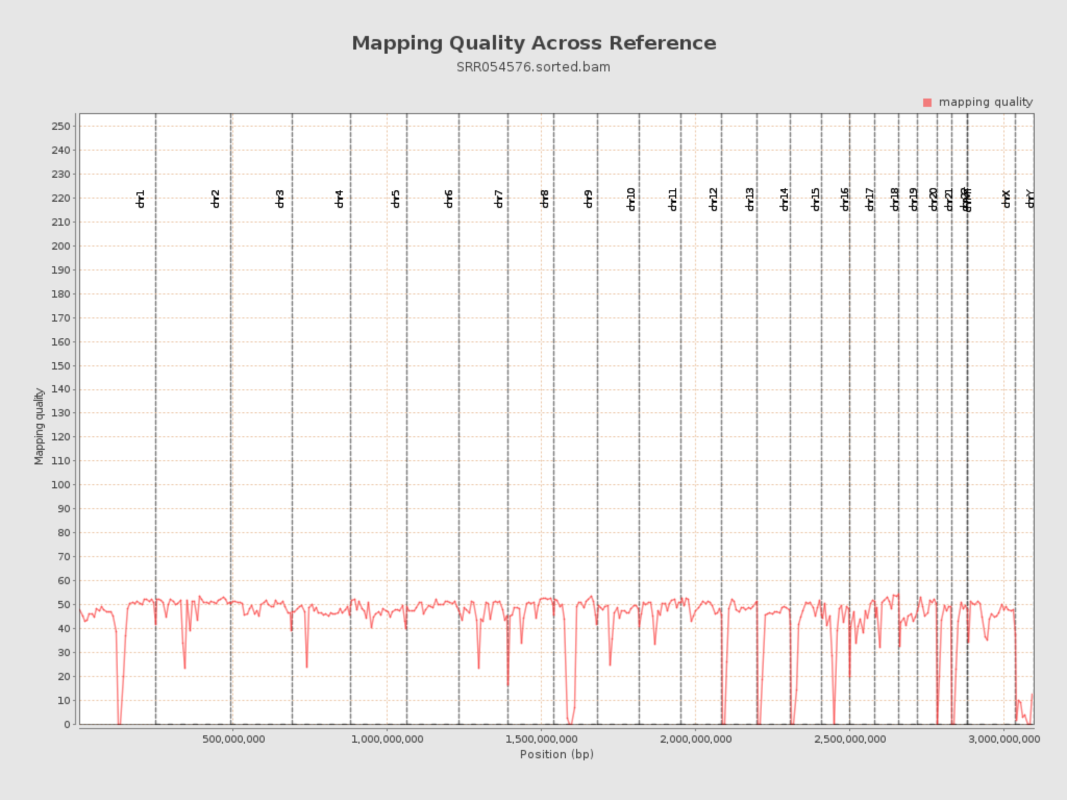
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram