Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 06:28:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054604.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_SRR054604 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054604.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 06:28:05 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054604.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,347,881
Mapped reads	3,244,785 / 74.63%
Unmapped reads	1,103,096 / 25.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	115 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	429,065 / 9.87%
Duplication rate	10.64%
Clipped reads	459,890 / 10.58%

2.2. ACGT Content

Number/percentage of A's	46,499,819 / 30.69%
Number/percentage of C's	29,797,736 / 19.67%
Number/percentage of T's	44,892,657 / 29.63%
Number/percentage of G's	30,283,373 / 19.99%
Number/percentage of N's	34,603 / 0.02%
GC Percentage	39.66%

2.3. Coverage

Mean	0.049

Standard Deviation	0.4433

2.4. Mapping Quality

Mean Mapping Quality	44.73

2.5. Mismatches and indels

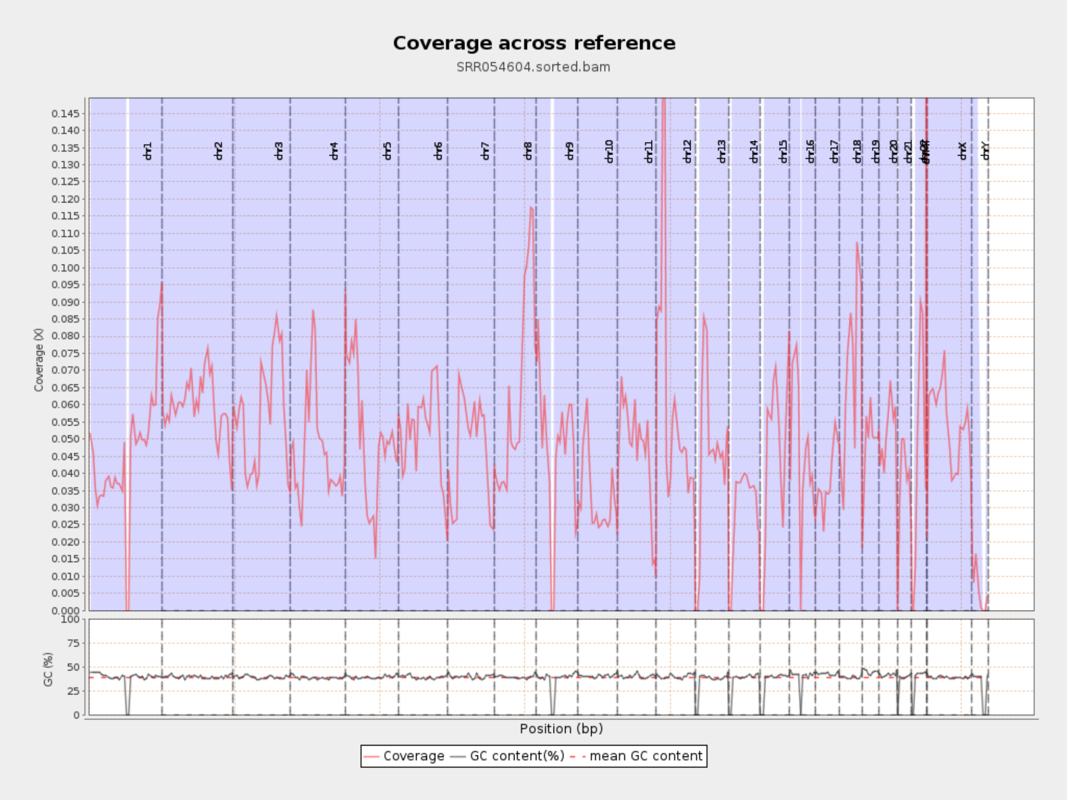
General error rate	0.75%
Mismatches	1,120,048
Insertions	7,151
Mapped reads with at least one insertion	0.22%
Deletions	22,445
Mapped reads with at least one deletion	0.69%
Homopolymer indels	44.55%

2.6. Chromosome stats

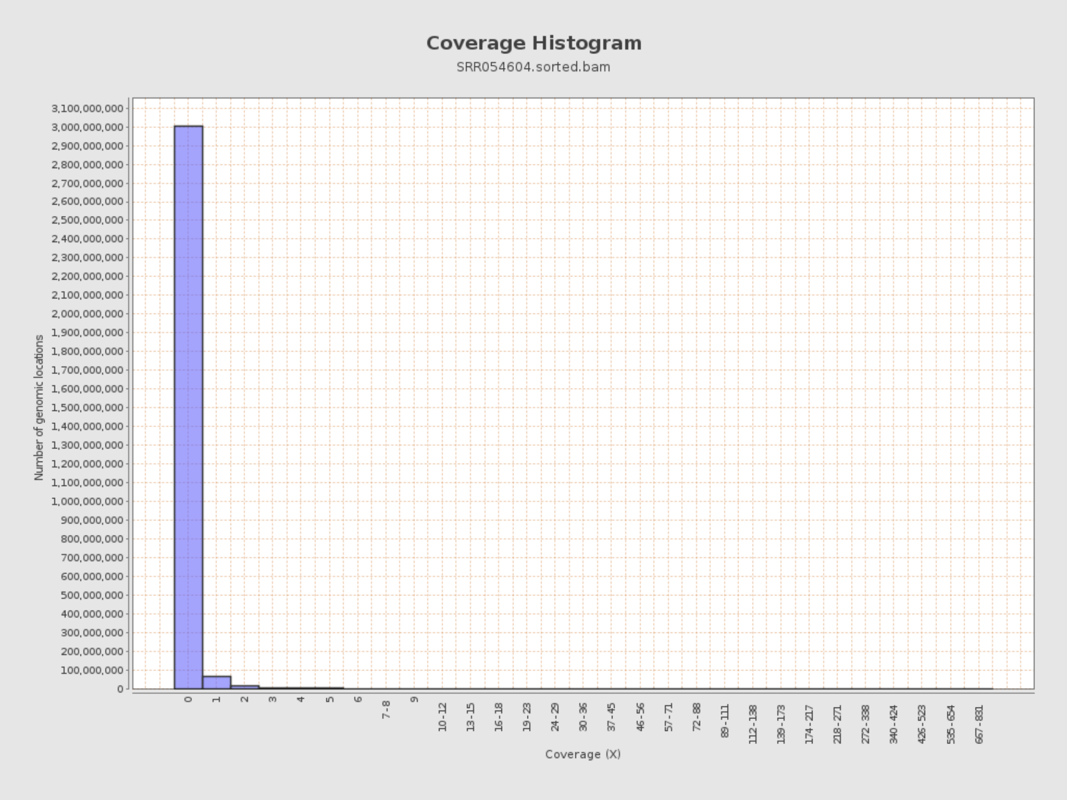
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11187634	0.0449	0.422
chr2	243199373	14553978	0.0598	0.5276
chr3	198022430	11345941	0.0573	0.4446
chr4	191154276	8988891	0.047	0.4074
chr5	180915260	9146745	0.0506	0.3851
chr6	171115067	8911875	0.0521	0.4467
chr7	159138663	7471384	0.0469	0.4272

chr8	146364022	9418415	0.0643	0.4824
chr9	141213431	6631235	0.047	0.4177
chr10	135534747	4573002	0.0337	0.3376
chr11	135006516	6316094	0.0468	0.6498
chr12	133851895	8183705	0.0611	0.4714
chr13	115169878	5137570	0.0446	0.4944
chr14	107349540	3215728	0.03	0.3202
chr15	102531392	4573056	0.0446	0.3482
chr16	90354753	4288271	0.0475	0.4101
chr17	81195210	3105791	0.0383	0.3416
chr18	78077248	5468193	0.07	0.5391
chr19	59128983	2939801	0.0497	0.4502
chr20	63025520	3260320	0.0517	0.4205
chr21	48129895	1756929	0.0365	0.3399
chr22	51304566	2300791	0.0448	0.3845
chrMT	16571	11328	0.6836	1.512
chrX	155270560	8411430	0.0542	0.4928
chrY	59373566	342443	0.0058	0.1321

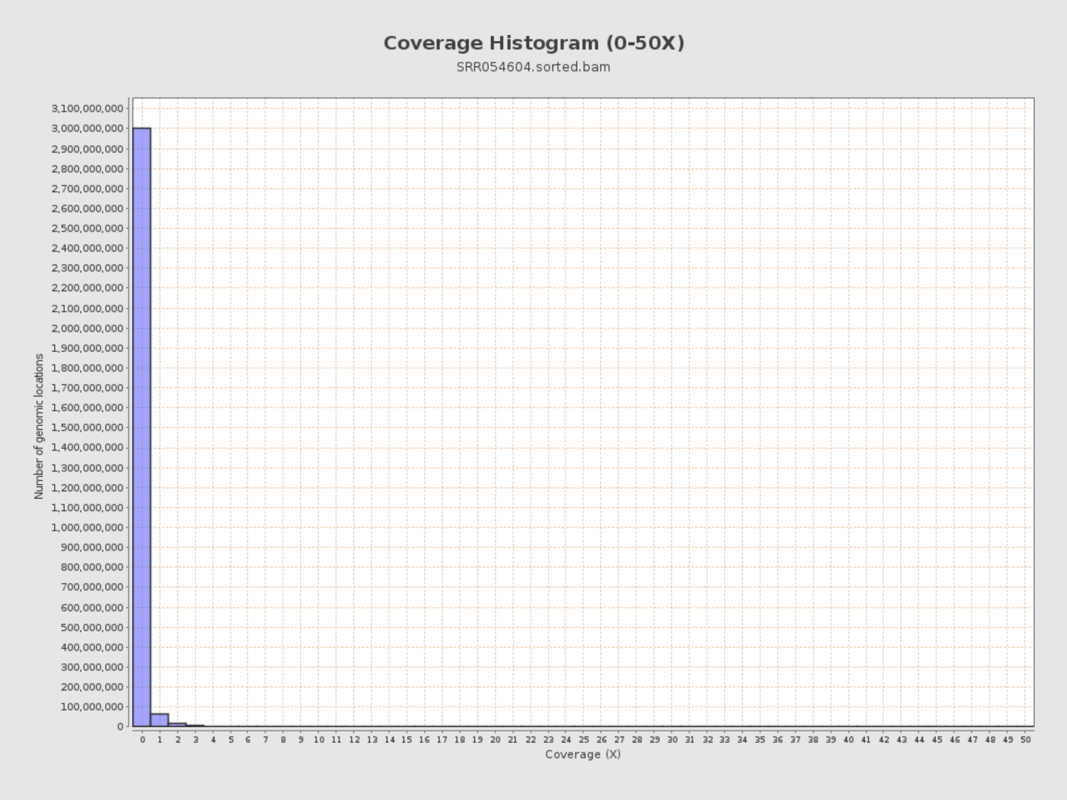
3. Results : Coverage across reference



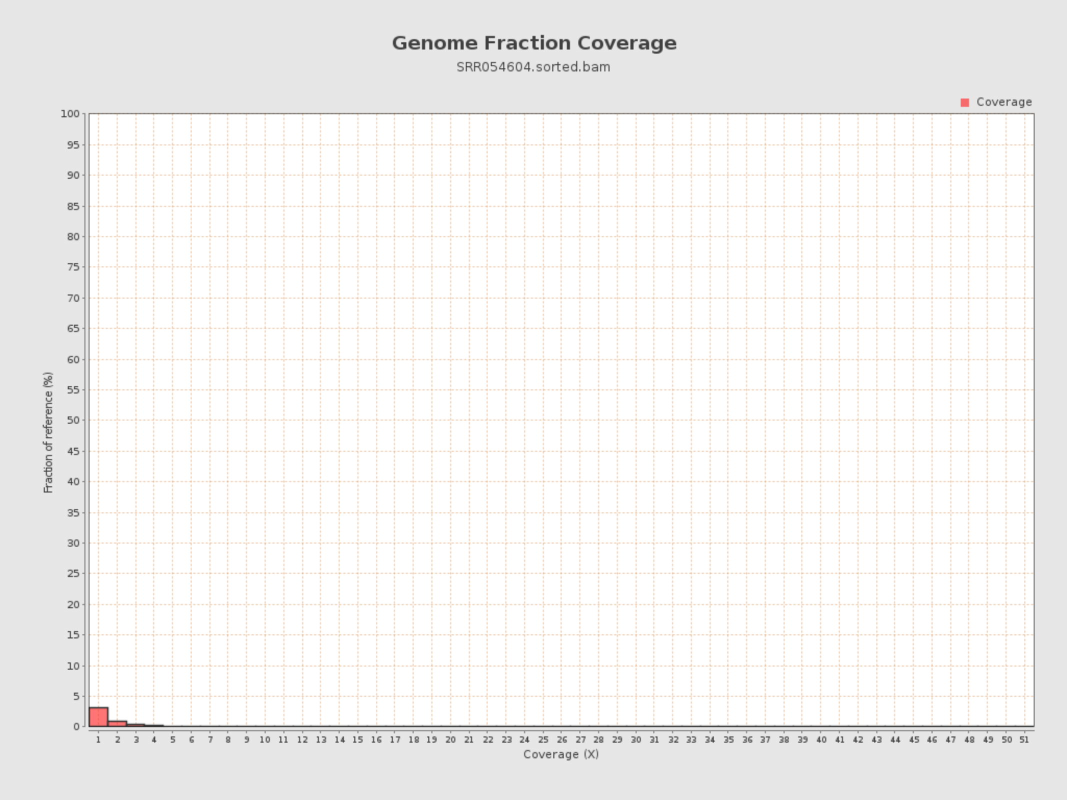
4. Results : Coverage Histogram



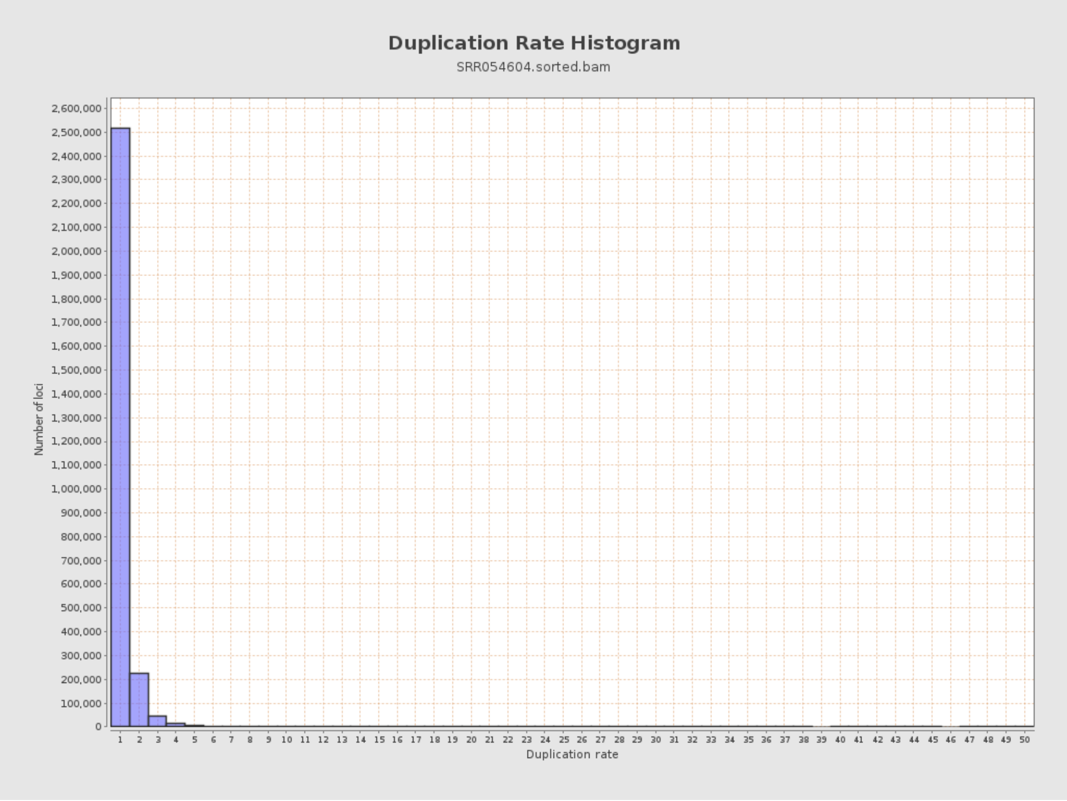
5. Results : Coverage Histogram (0-50X)



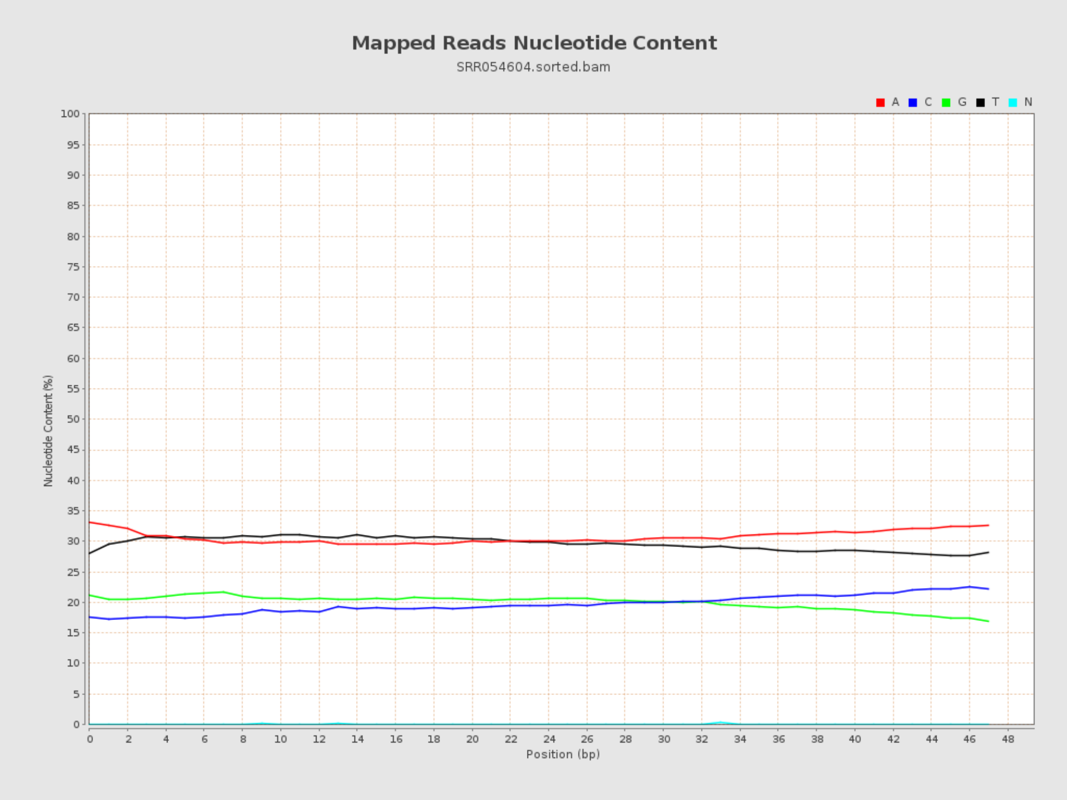
6. Results : Genome Fraction Coverage



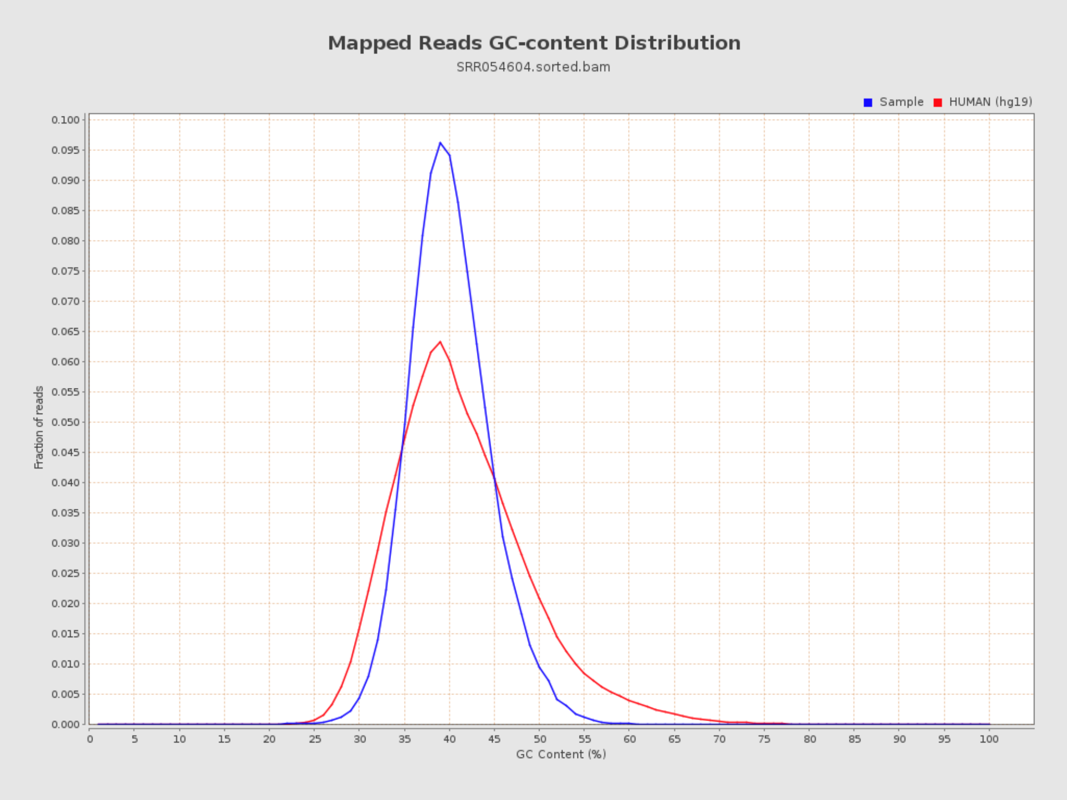
7. Results : Duplication Rate Histogram



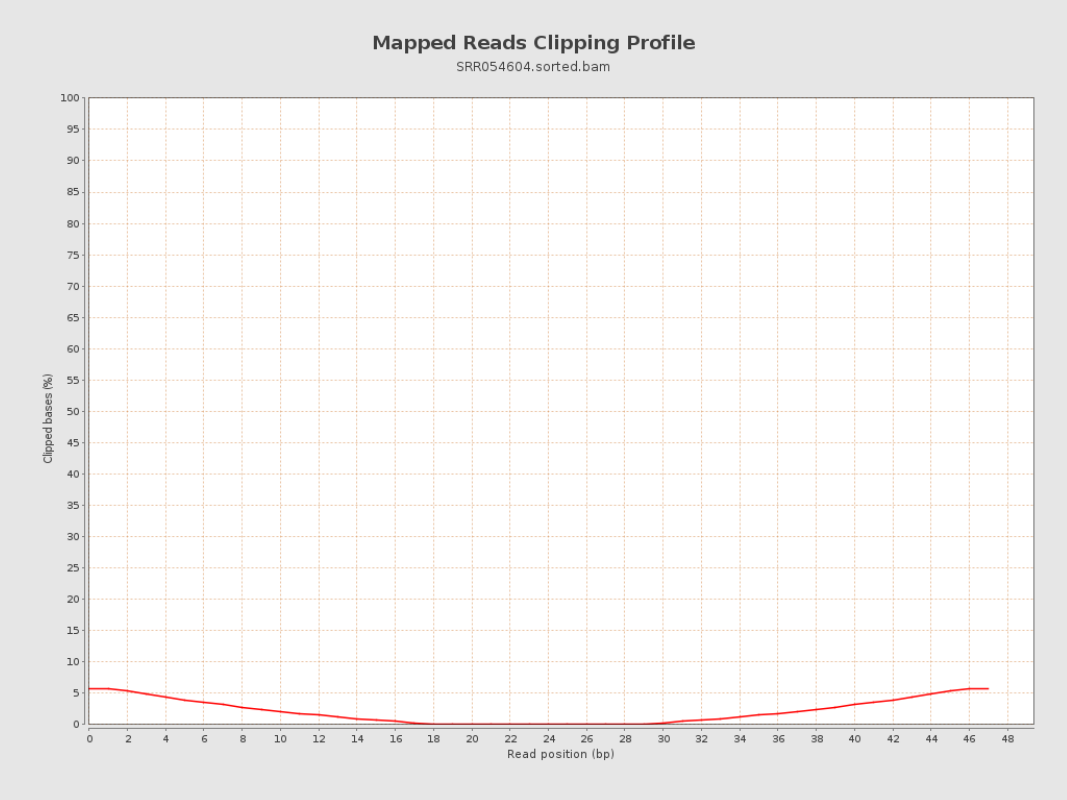
8. Results : Mapped Reads Nucleotide Content



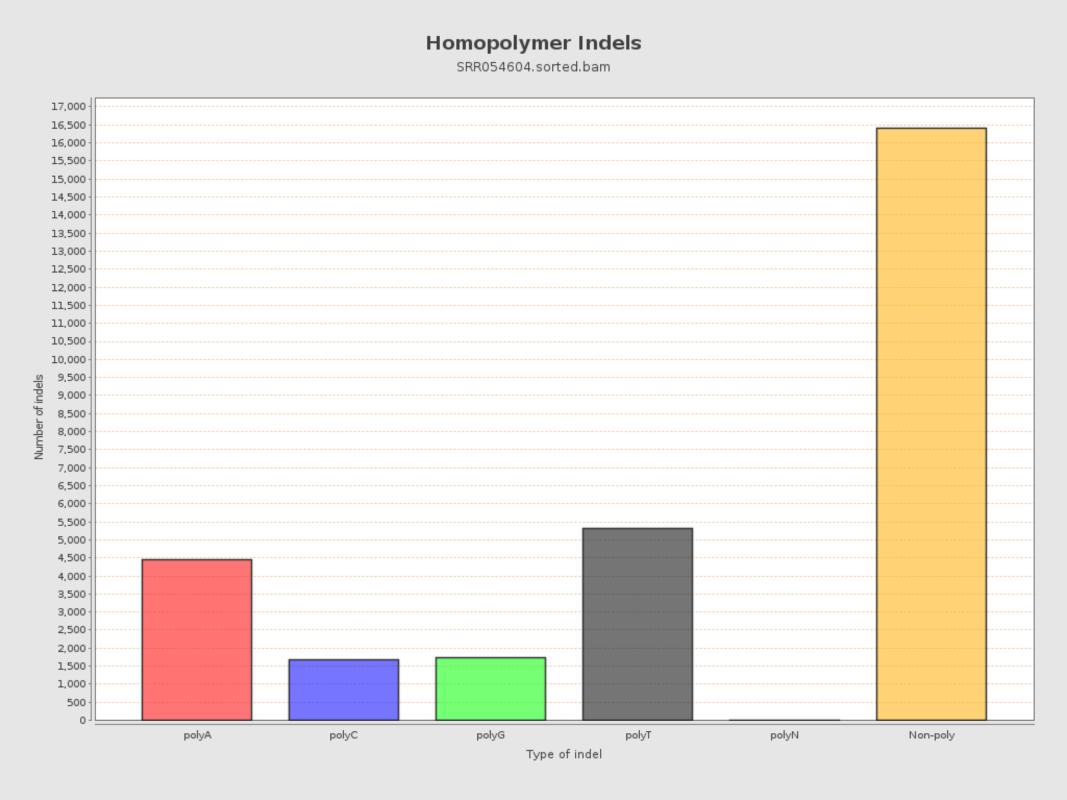
9. Results : Mapped Reads GC-content Distribution



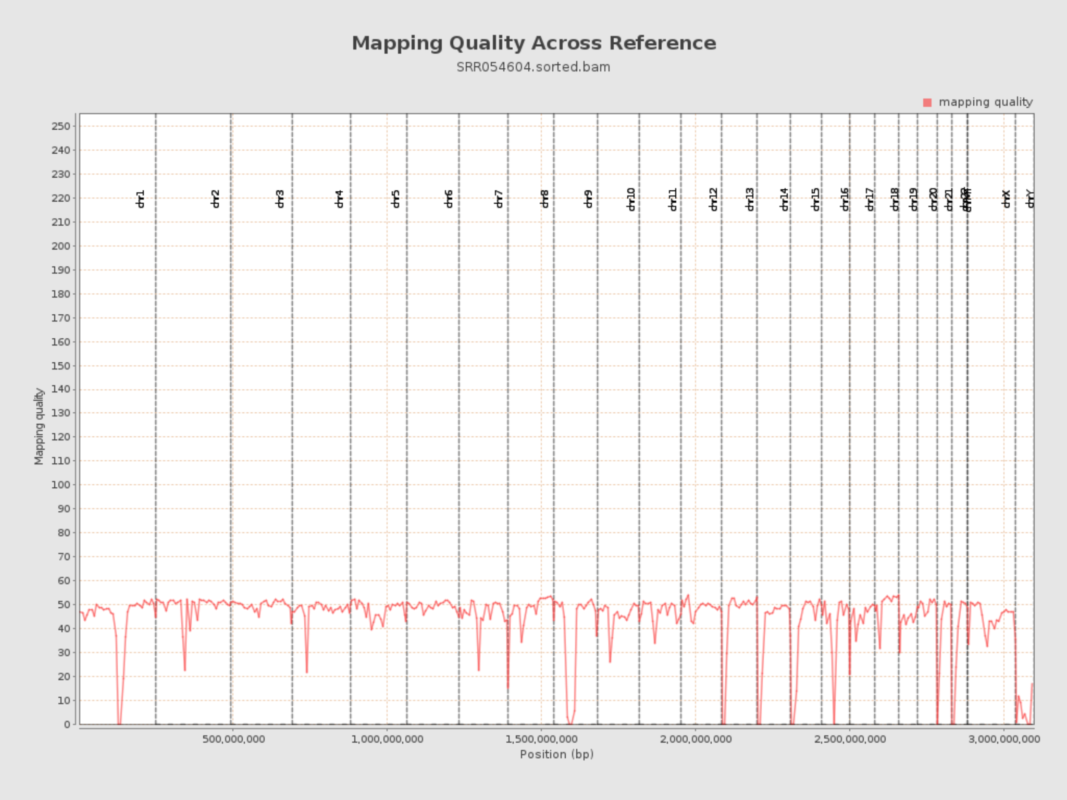
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram