Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 08:47:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054626.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_SRR054626 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054626.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 08:47:51 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054626.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,922,274
Mapped reads	3,614,568 / 73.43%
Unmapped reads	1,307,706 / 26.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	123 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	760,157 / 15.44%
Duplication rate	15.44%
Clipped reads	644,628 / 13.1%

2.2. ACGT Content

Number/percentage of A's	51,245,121 / 30.61%
Number/percentage of C's	34,622,176 / 20.68%
Number/percentage of T's	48,168,064 / 28.77%
Number/percentage of G's	33,390,849 / 19.94%
Number/percentage of N's	7,675 / 0%
GC Percentage	40.62%

2.3. Coverage

Mean	0.0541

Standard Deviation	0.5303

2.4. Mapping Quality

Mean Mapping Quality	43.91

2.5. Mismatches and indels

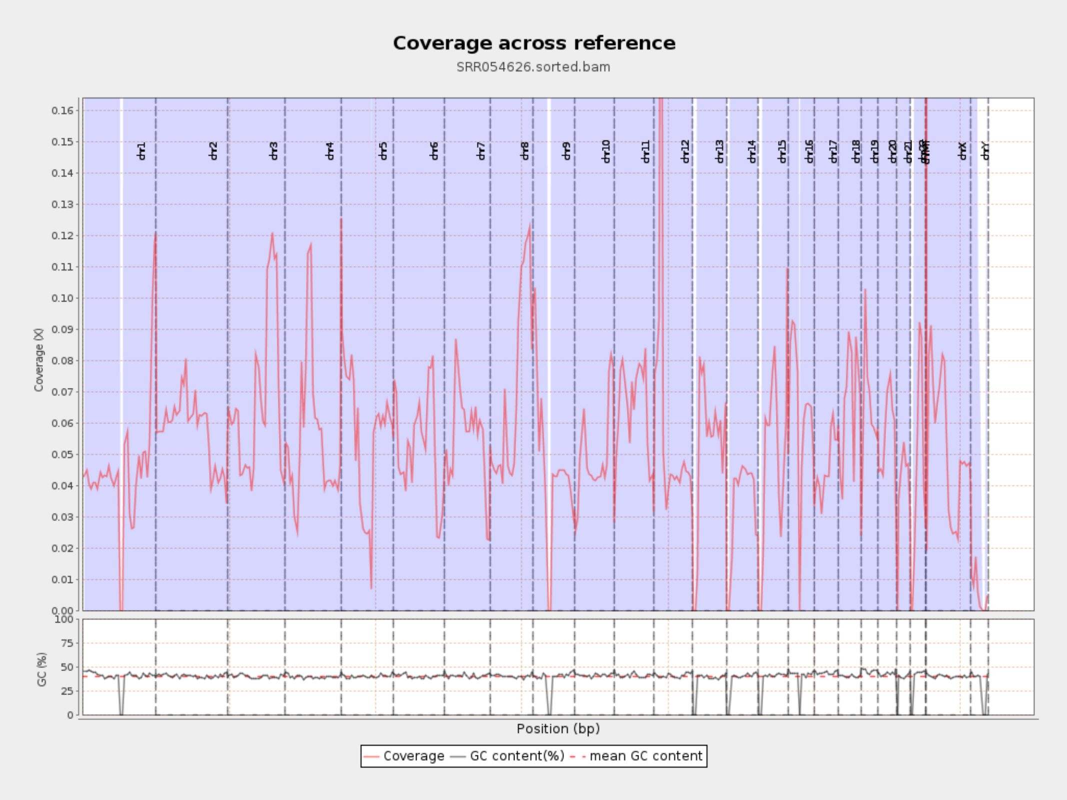
General error rate	0.69%
Mismatches	1,144,084
Insertions	7,833
Mapped reads with at least one insertion	0.22%
Deletions	25,033
Mapped reads with at least one deletion	0.69%
Homopolymer indels	43.72%

2.6. Chromosome stats

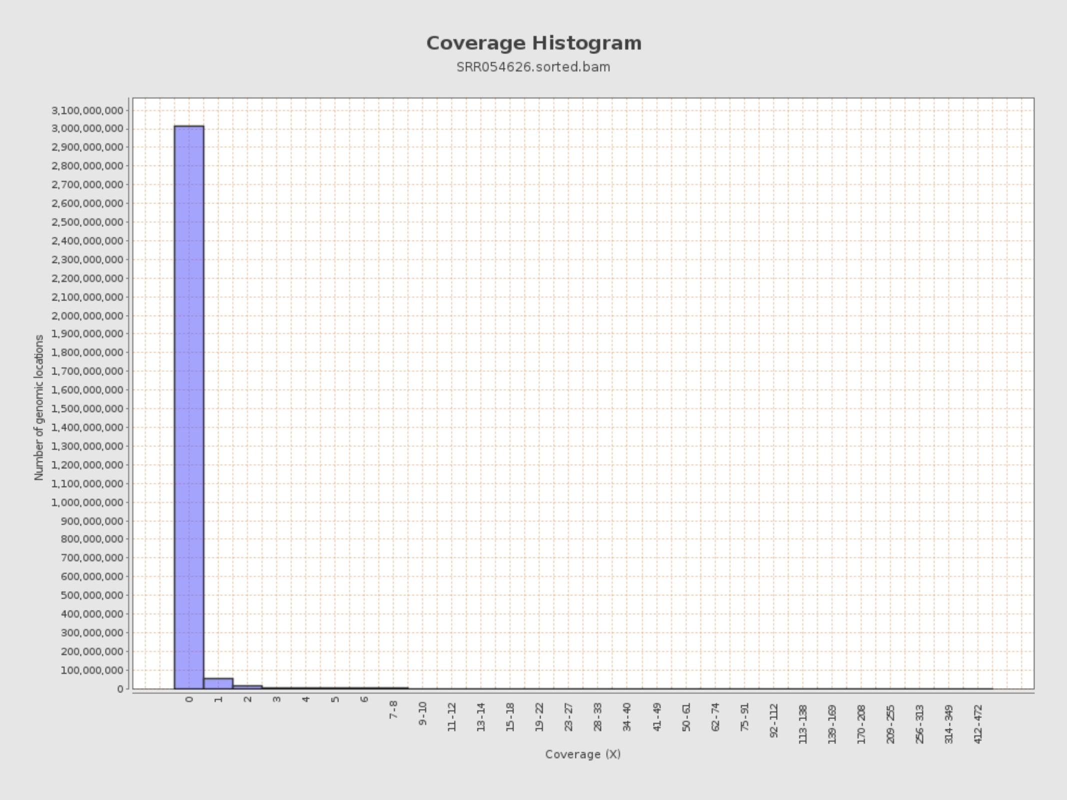
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11187350	0.0449	0.4988
chr2	243199373	14095581	0.058	0.574
chr3	198022430	13354859	0.0674	0.5716
chr4	191154276	10537870	0.0551	0.5156
chr5	180915260	10112329	0.0559	0.4992
chr6	171115067	9087954	0.0531	0.5195
chr7	159138663	8790159	0.0552	0.563

chr8	146364022	10337982	0.0706	0.6211
chr9	141213431	6388790	0.0452	0.4698
chr10	135534747	6711645	0.0495	0.4746
chr11	135006516	8805804	0.0652	0.6107
chr12	133851895	8536358	0.0638	0.6506
chr13	115169878	6013385	0.0522	0.4892
chr14	107349540	3697520	0.0344	0.4299
chr15	102531392	4921045	0.048	0.4597
chr16	90354753	5690196	0.063	0.5684
chr17	81195210	3747401	0.0462	0.4365
chr18	78077248	5171566	0.0662	0.5797
chr19	59128983	3907541	0.0661	0.653
chr20	63025520	3607544	0.0572	0.5109
chr21	48129895	1911550	0.0397	0.4634
chr22	51304566	2320800	0.0452	0.4546
chrMT	16571	24179	1.4591	3.1834
chrX	155270560	8165349	0.0526	0.5171
chrY	59373566	345423	0.0058	0.1496

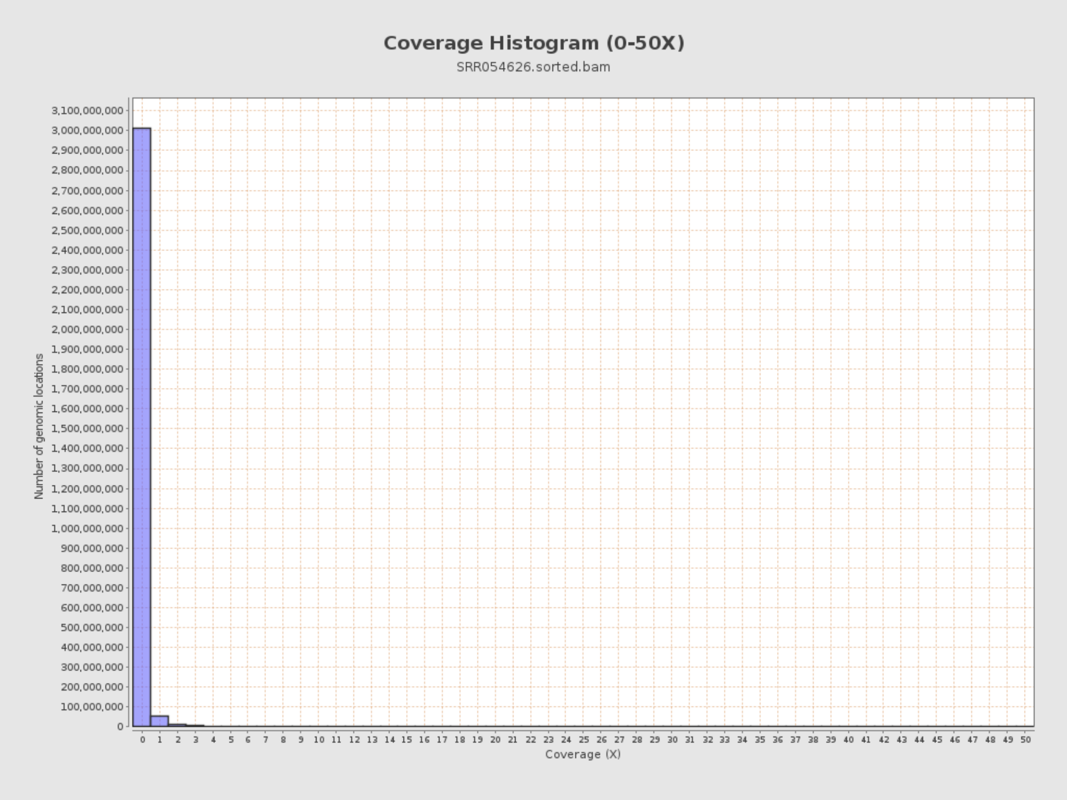
3. Results : Coverage across reference



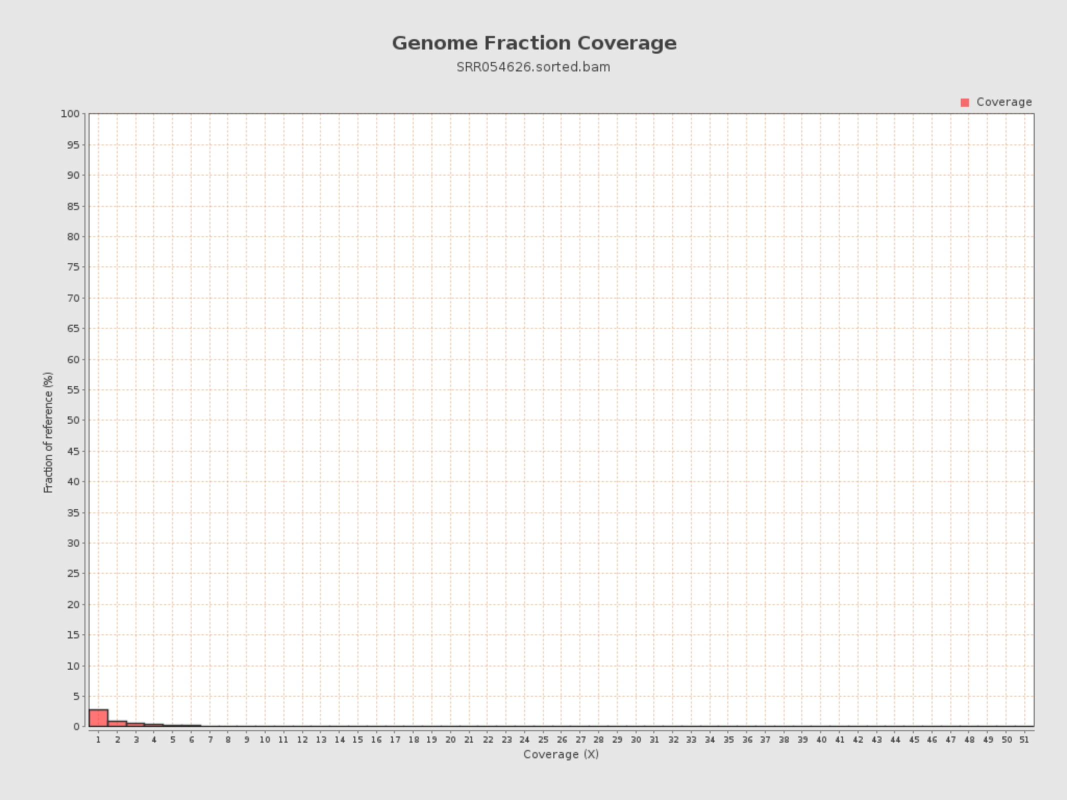
4. Results : Coverage Histogram



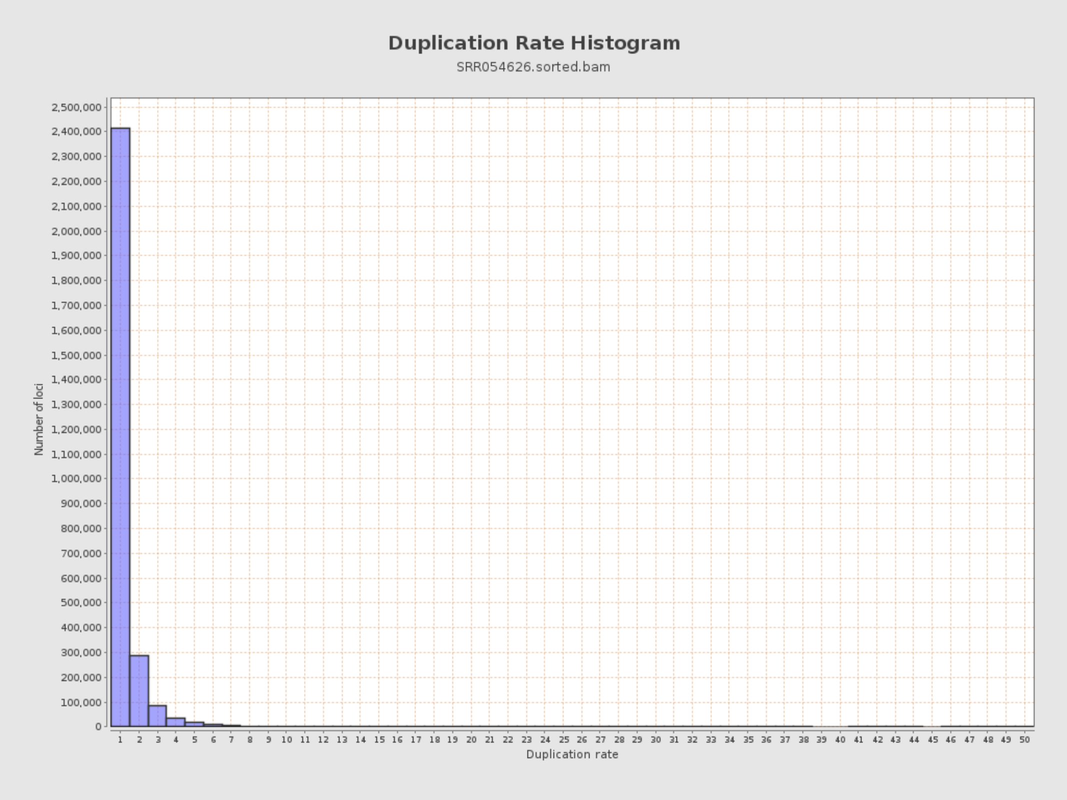
5. Results : Coverage Histogram (0-50X)



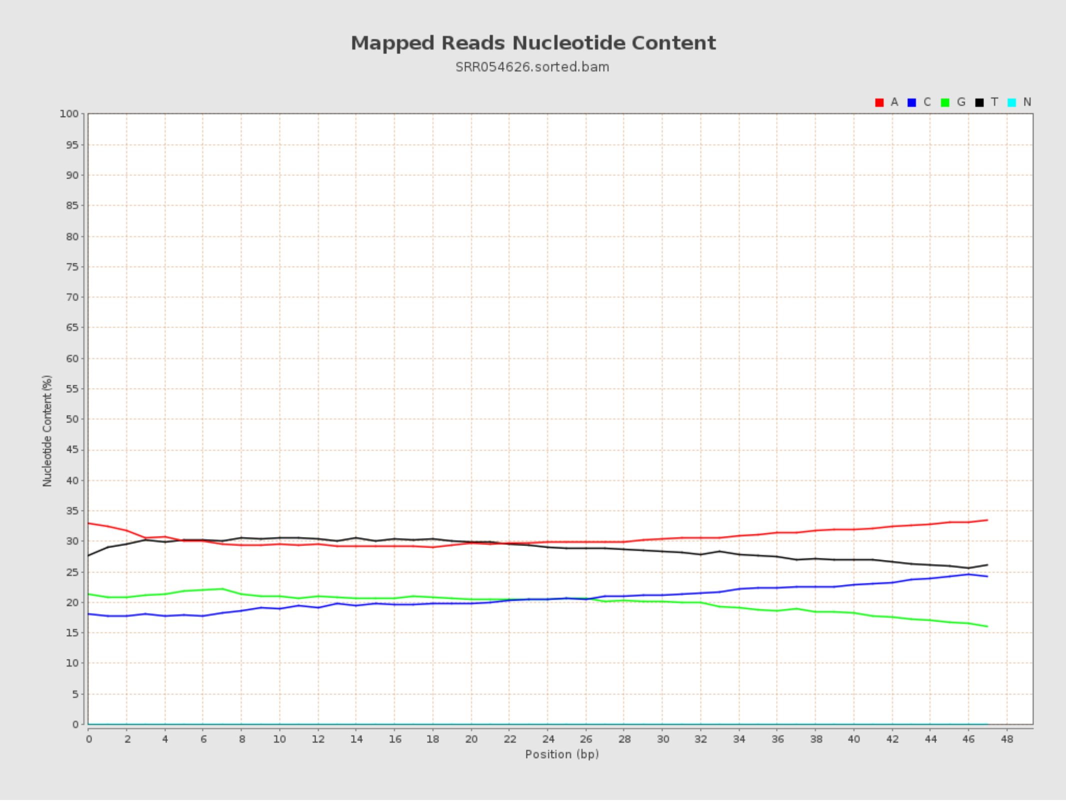
6. Results : Genome Fraction Coverage



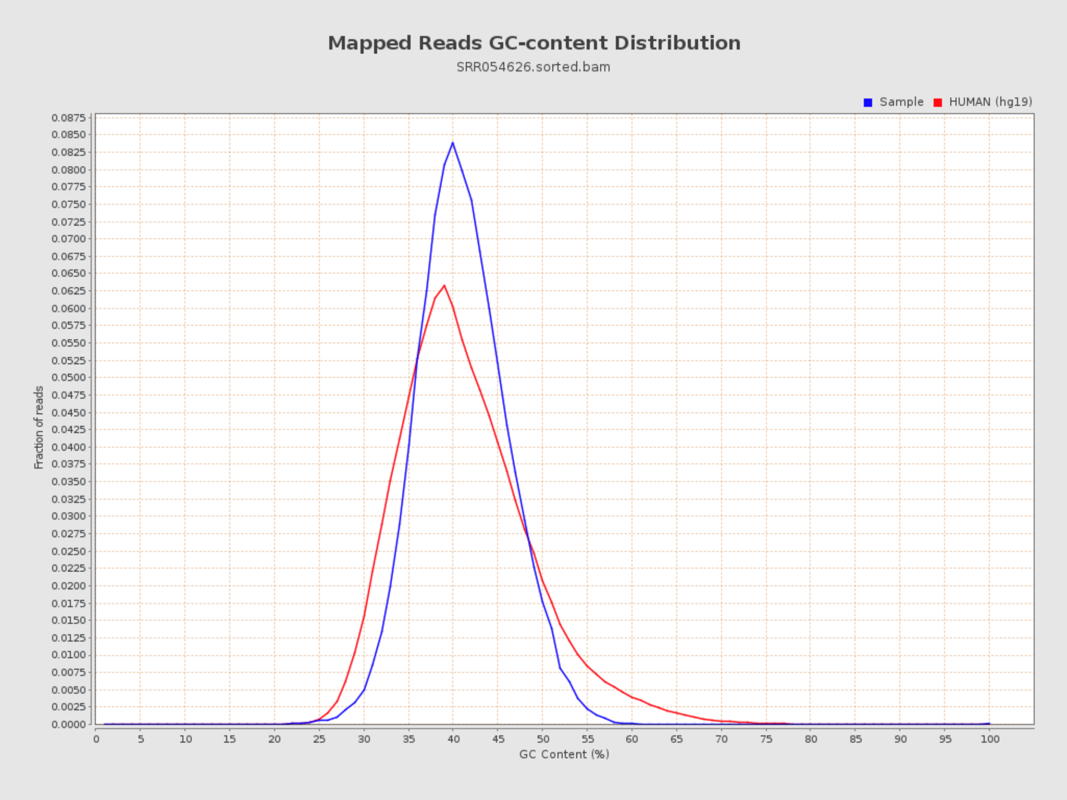
7. Results : Duplication Rate Histogram



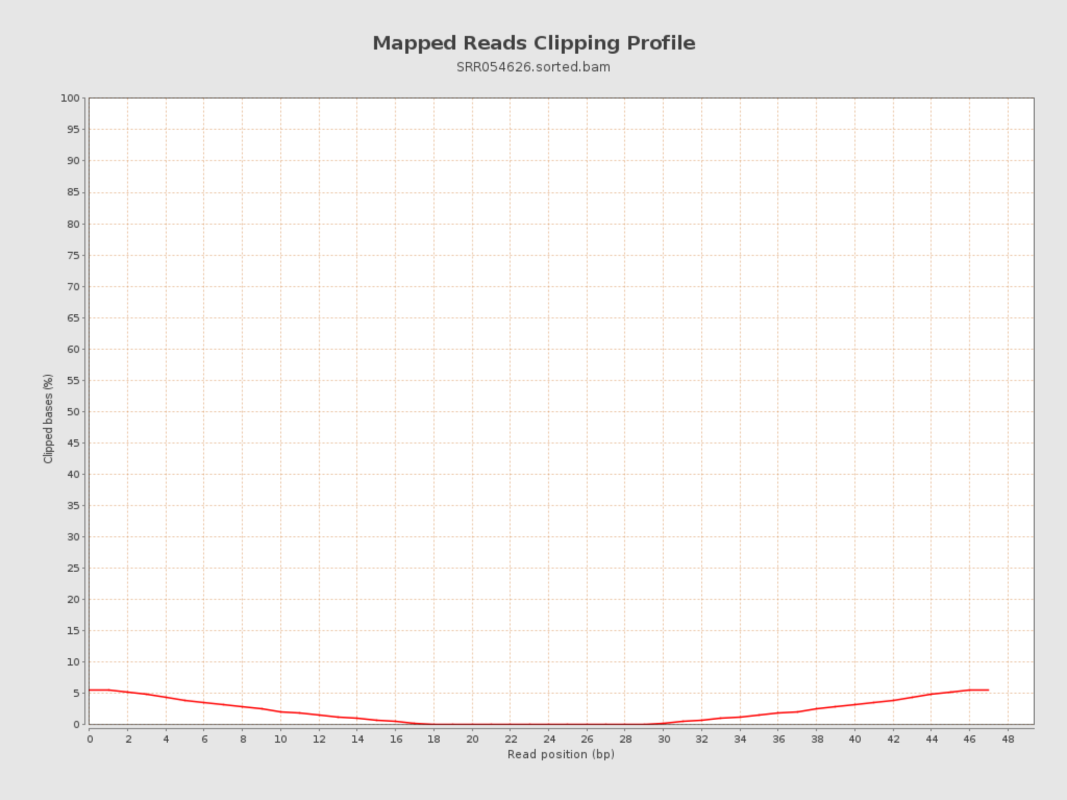
8. Results : Mapped Reads Nucleotide Content



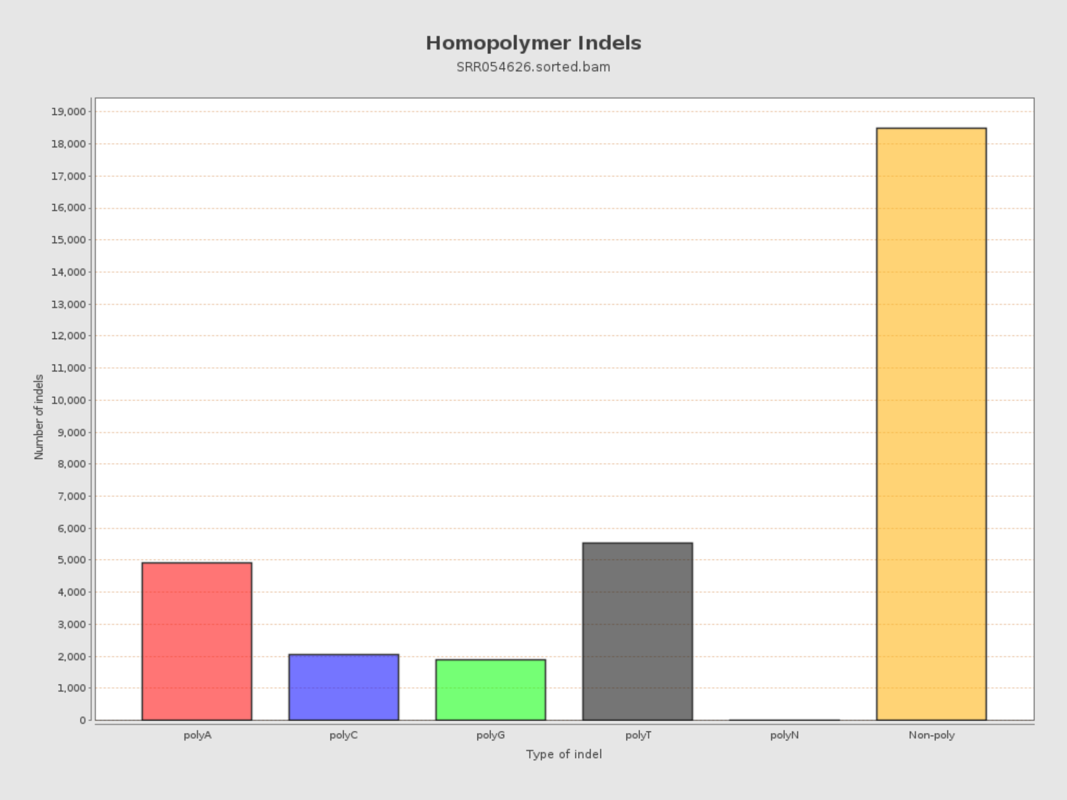
9. Results : Mapped Reads GC-content Distribution



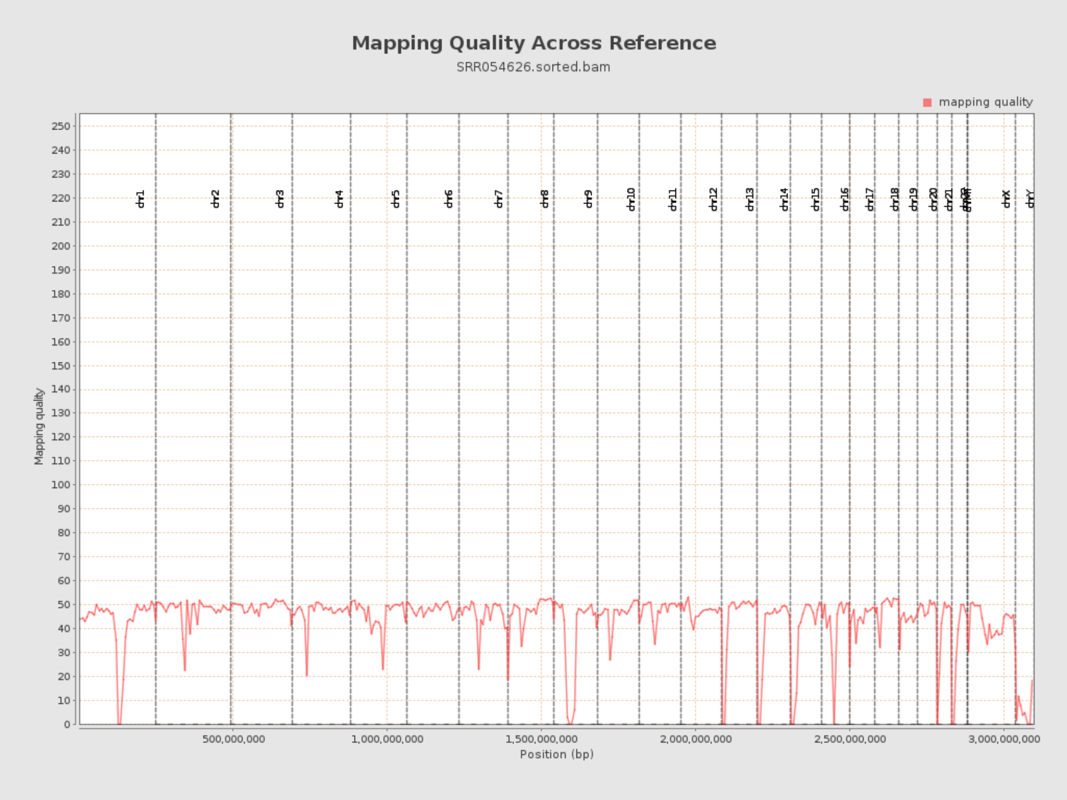
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram