Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 03:45:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054213.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_SRR054213 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054213.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 03:45:46 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054213.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,429,097
Mapped reads	6,005,563 / 80.84%
Unmapped reads	1,423,534 / 19.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	243 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,237,304 / 16.65%
Duplication rate	15.5%
Clipped reads	617,436 / 8.31%

2.2. ACGT Content

Number/percentage of A's	84,305,250 / 29.83%
Number/percentage of C's	55,297,816 / 19.57%
Number/percentage of T's	83,808,557 / 29.66%
Number/percentage of G's	59,133,229 / 20.92%
Number/percentage of N's	58,427 / 0.02%
GC Percentage	40.49%

2.3. Coverage

Mean	0.0913

Standard Deviation	0.736

2.4. Mapping Quality

Mean Mapping Quality	45.18

2.5. Mismatches and indels

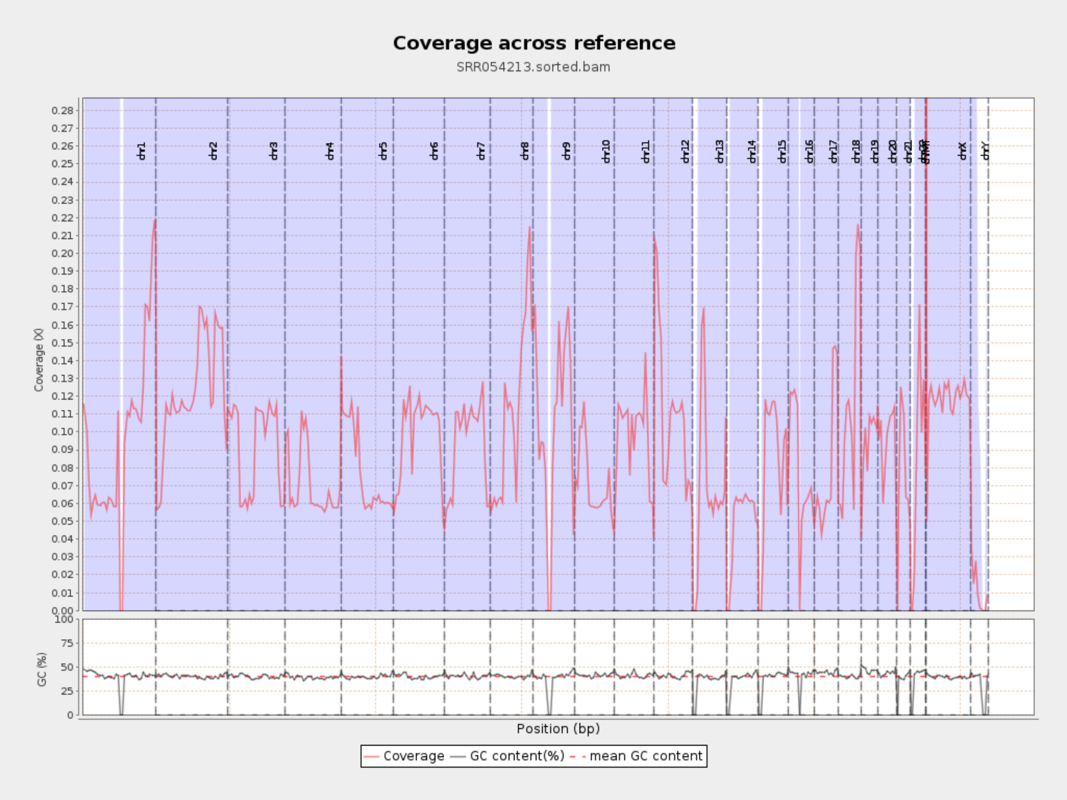
General error rate	0.53%
Mismatches	1,492,344
Insertions	11,721
Mapped reads with at least one insertion	0.19%
Deletions	39,656
Mapped reads with at least one deletion	0.66%
Homopolymer indels	46.68%

2.6. Chromosome stats

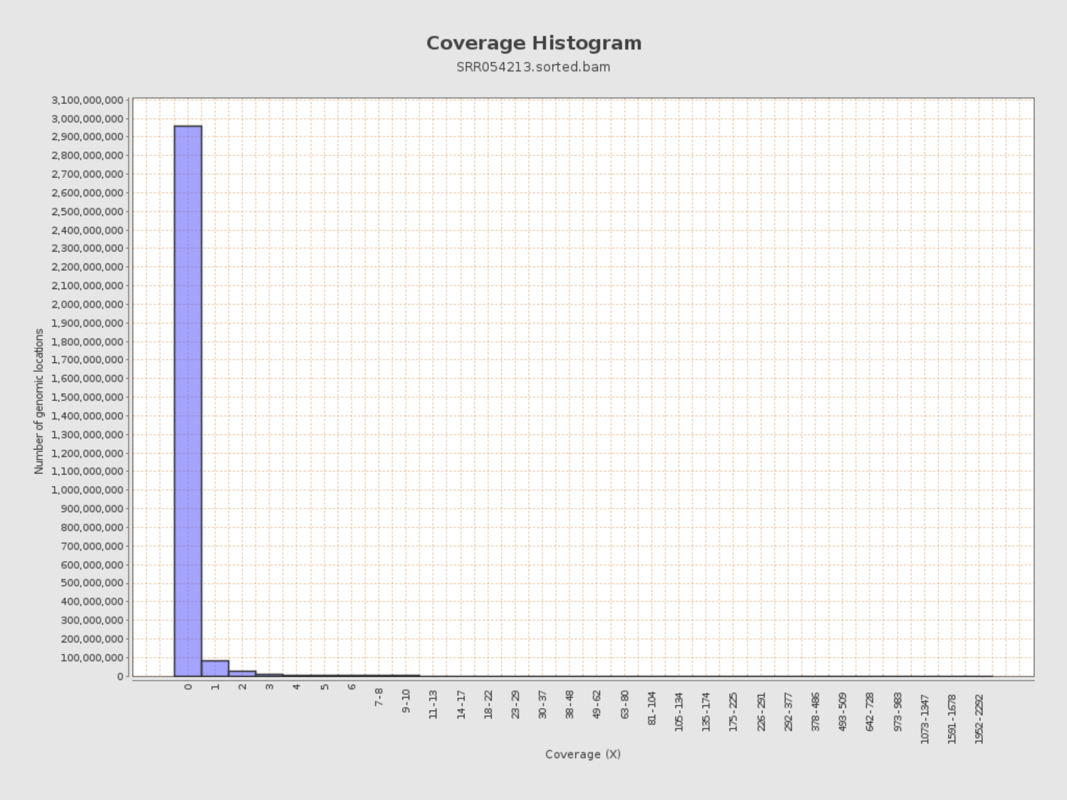
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23870903	0.0958	0.7889
chr2	243199373	29671102	0.122	0.831
chr3	198022430	18111574	0.0915	0.6329
chr4	191154276	13500146	0.0706	0.5701
chr5	180915260	14053278	0.0777	0.5774
chr6	171115067	17122643	0.1001	0.7364
chr7	159138663	14682873	0.0923	1.3613

chr8	146364022	16492995	0.1127	0.7751
chr9	141213431	14879833	0.1054	0.7572
chr10	135534747	9633344	0.0711	0.6186
chr11	135006516	13420572	0.0994	0.705
chr12	133851895	15122254	0.113	0.736
chr13	115169878	7698223	0.0668	0.5436
chr14	107349540	5394158	0.0502	0.5338
chr15	102531392	8272406	0.0807	0.5883
chr16	90354753	6882025	0.0762	0.6092
chr17	81195210	6414403	0.079	0.5803
chr18	78077248	9002424	0.1153	0.8054
chr19	59128983	5679079	0.096	0.736
chr20	63025520	6043962	0.0959	0.6693
chr21	48129895	3503781	0.0728	0.6258
chr22	51304566	4274435	0.0833	0.6249
chrMT	16571	33811	2.0404	3.7372
chrX	155270560	18253508	0.1176	0.7556
chrY	59373566	649195	0.0109	0.2154

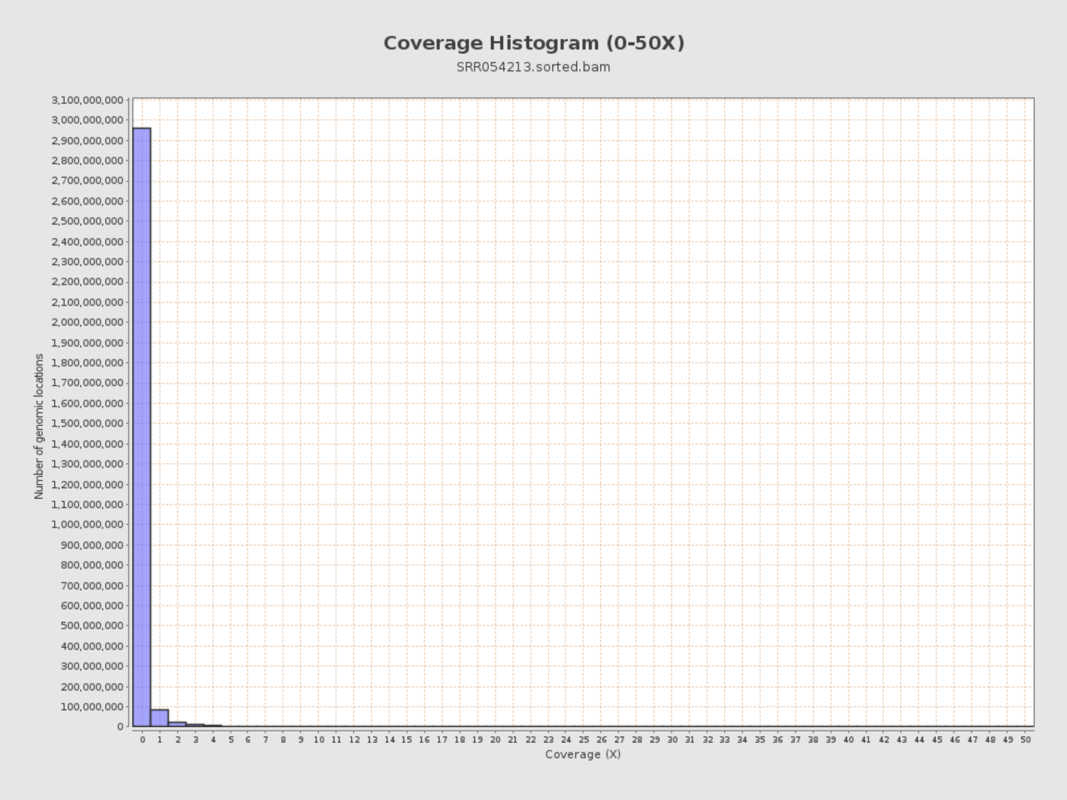
3. Results : Coverage across reference



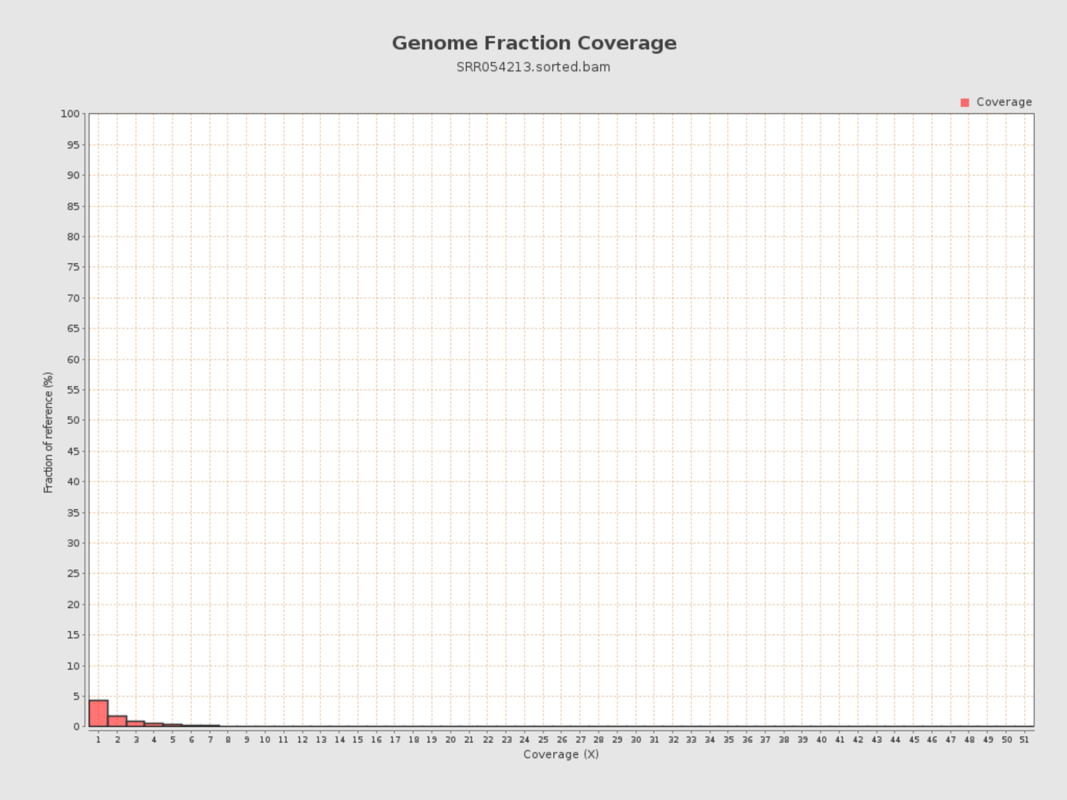
4. Results : Coverage Histogram



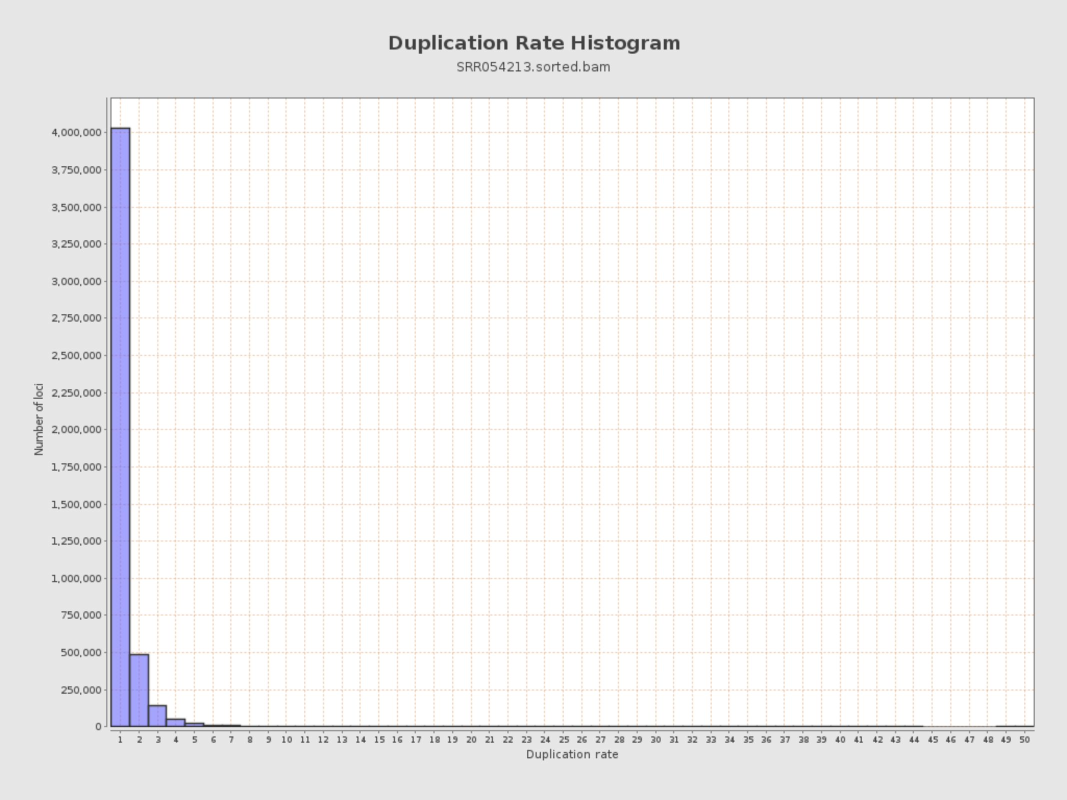
5. Results : Coverage Histogram (0-50X)



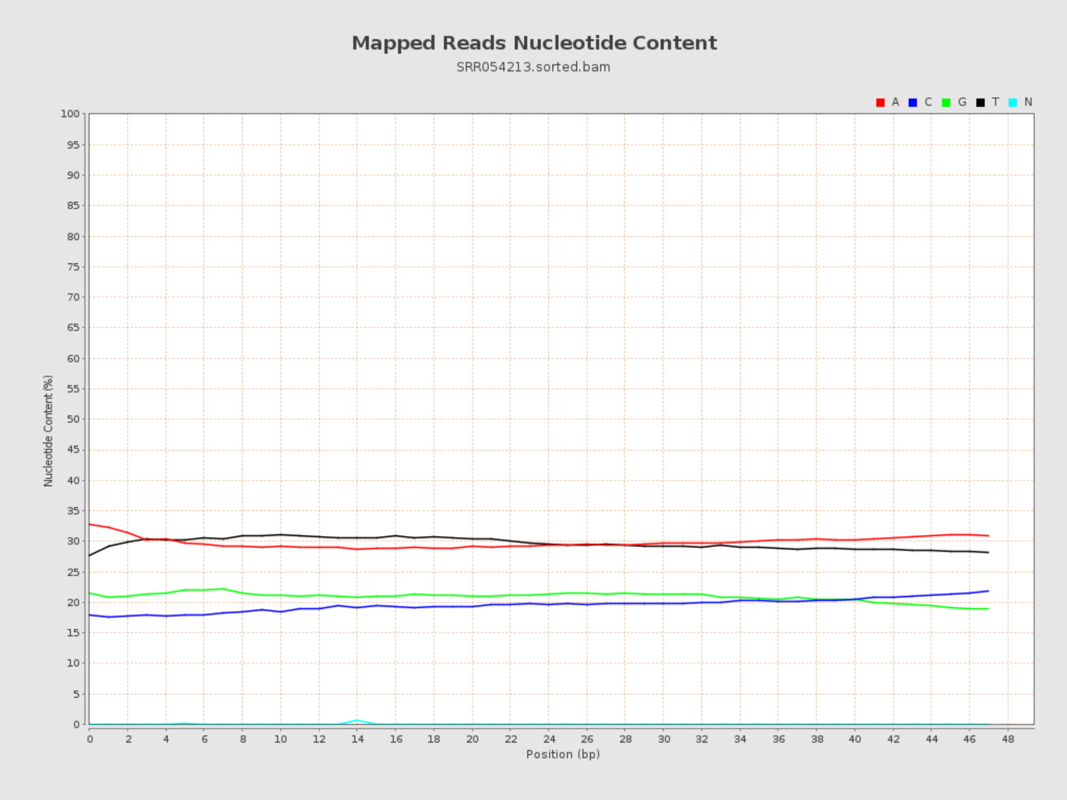
6. Results : Genome Fraction Coverage



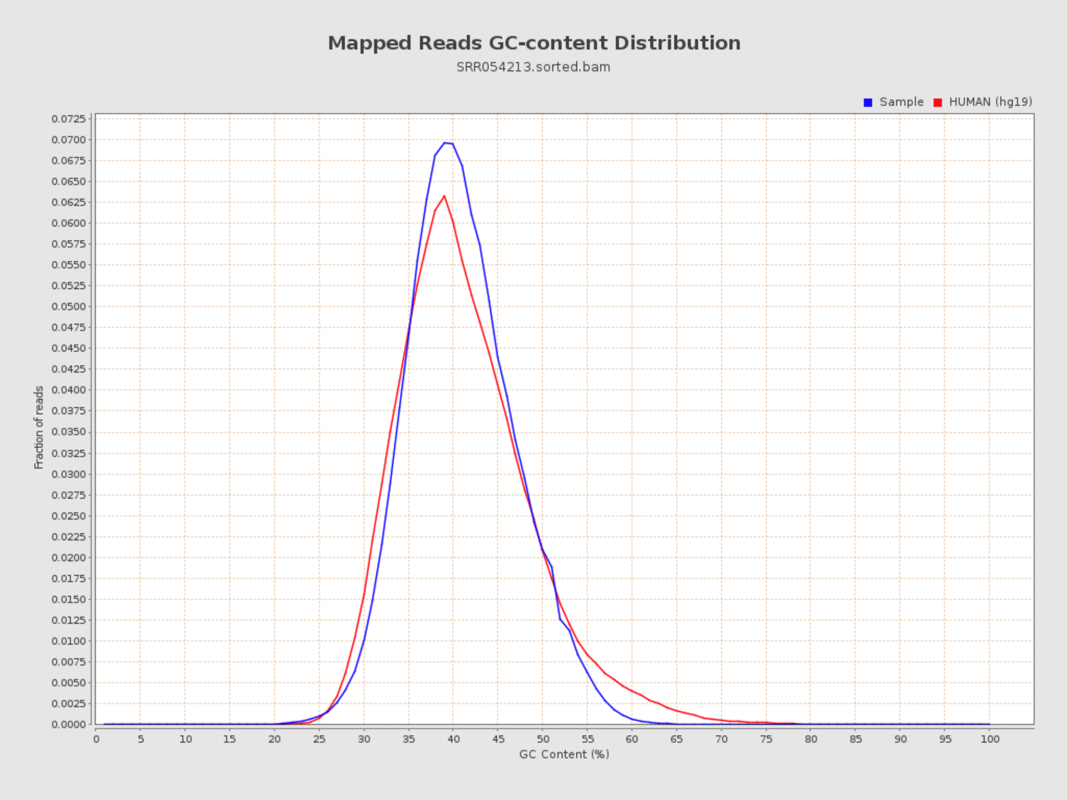
7. Results : Duplication Rate Histogram



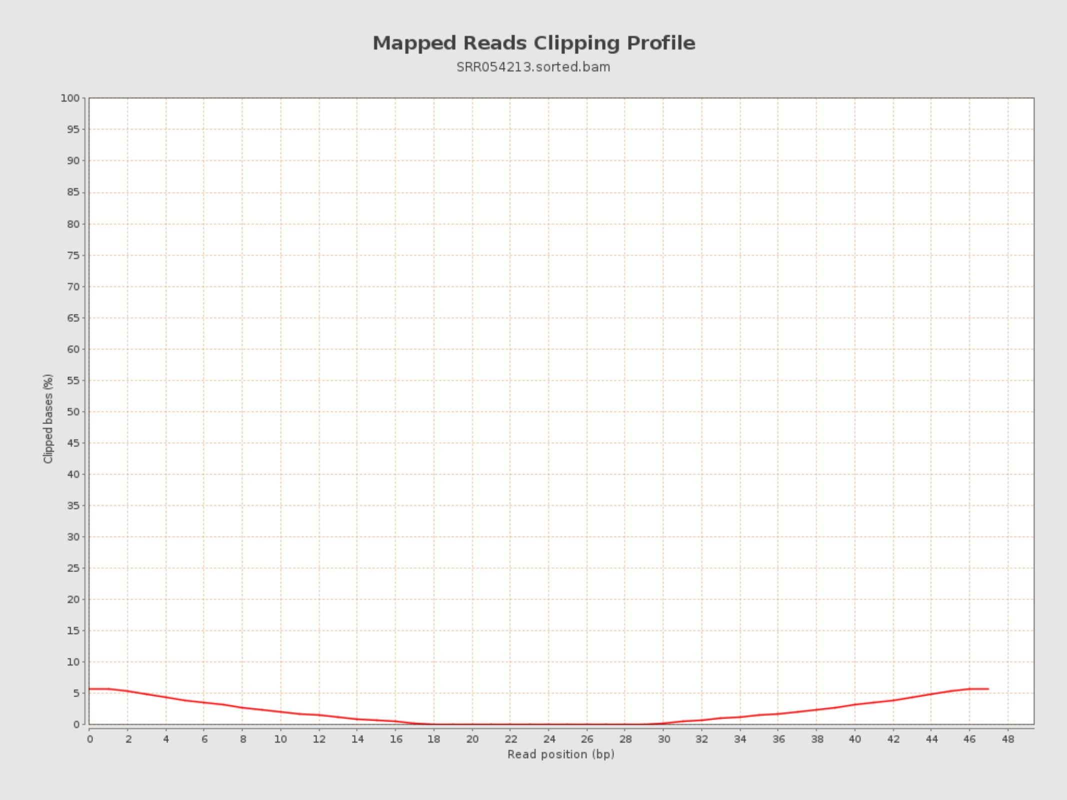
8. Results : Mapped Reads Nucleotide Content



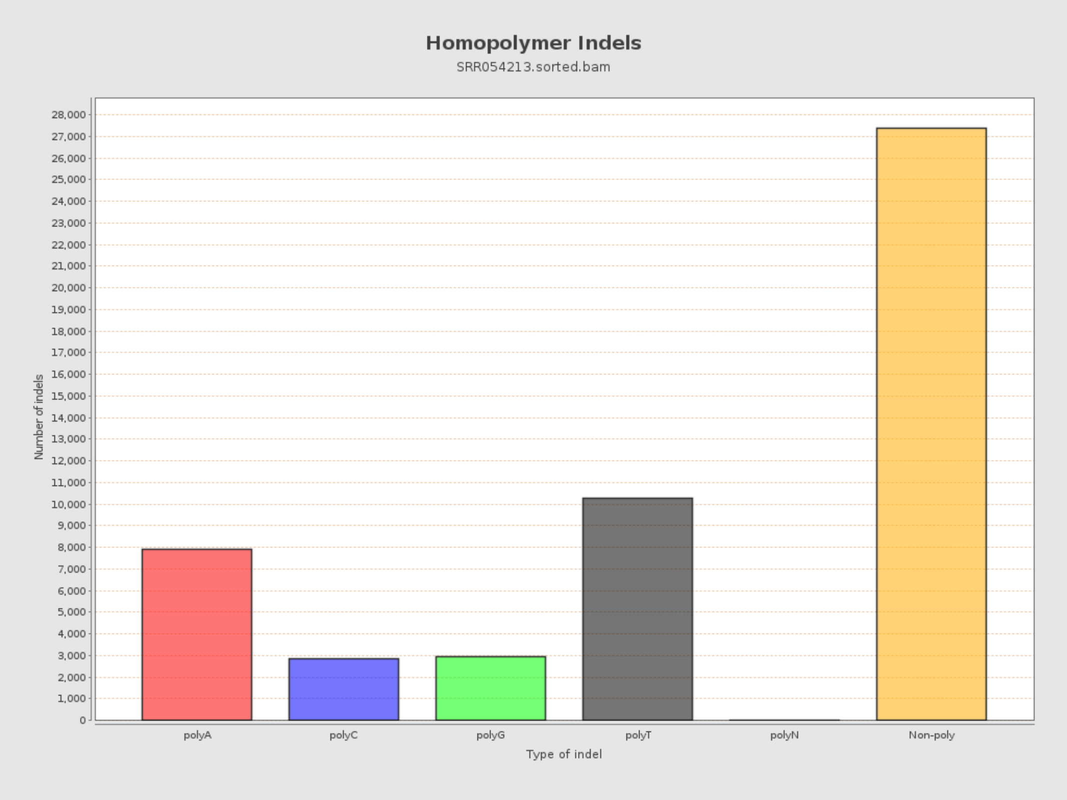
9. Results : Mapped Reads GC-content Distribution



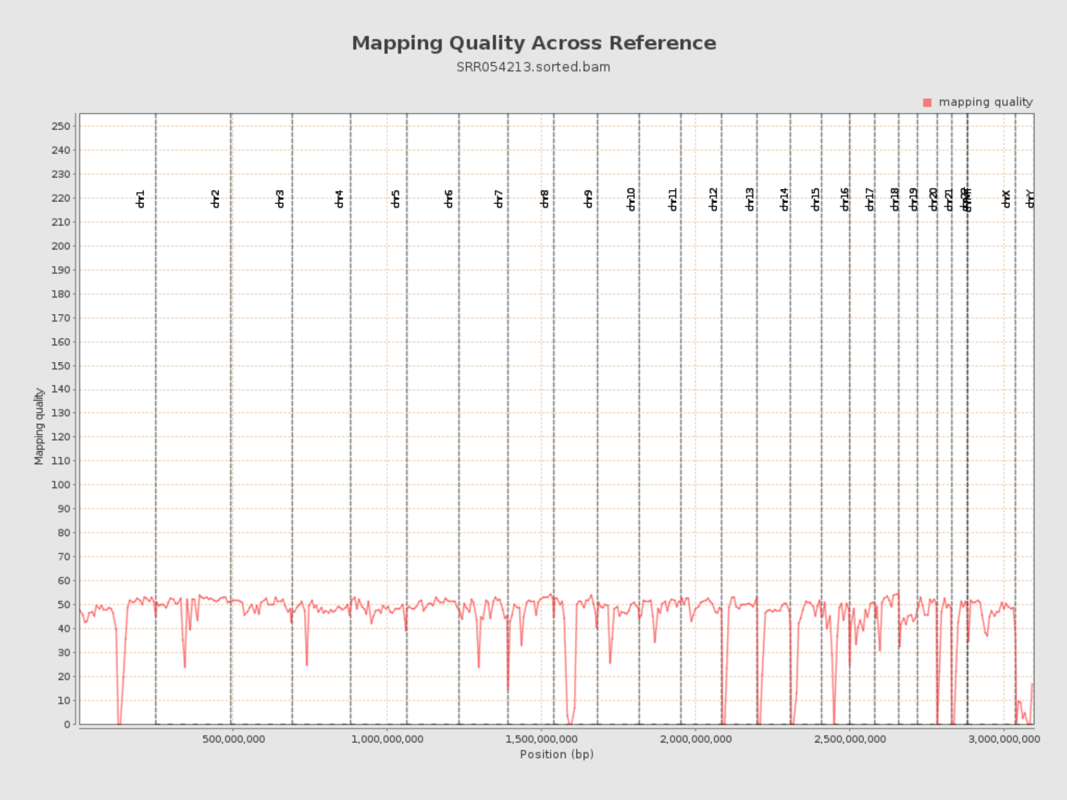
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram