Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 03:53:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054565.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_SRR054565 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054565.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 03:53:26 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054565.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,436,964
Mapped reads	10,557,169 / 78.57%
Unmapped reads	2,879,795 / 21.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	284 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,690,397 / 20.02%
Duplication rate	18.28%
Clipped reads	758,436 / 5.64%

2.2. ACGT Content

Number/percentage of A's	146,484,076 / 29.31%
Number/percentage of C's	95,880,736 / 19.18%
Number/percentage of T's	148,148,437 / 29.64%
Number/percentage of G's	109,339,679 / 21.87%
Number/percentage of N's	6,194 / 0%
GC Percentage	41.06%

2.3. Coverage

Mean	0.1615

Standard Deviation	1.1405

2.4. Mapping Quality

Mean Mapping Quality	45.47

2.5. Mismatches and indels

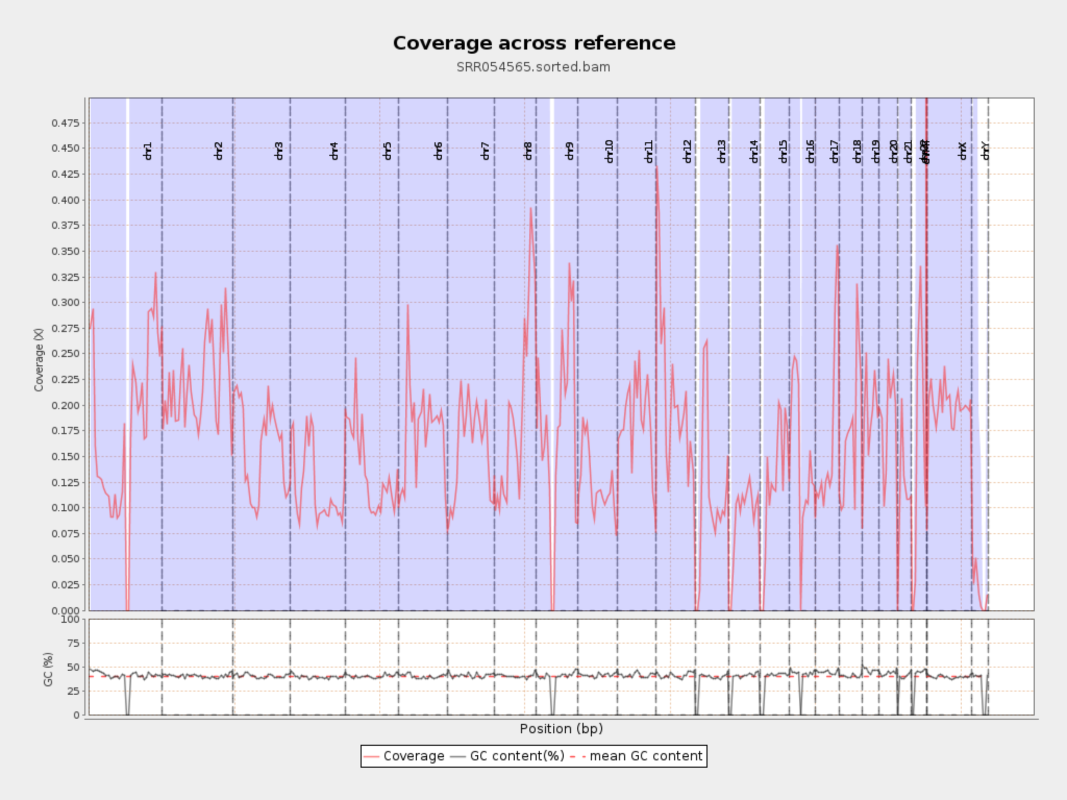
General error rate	0.48%
Mismatches	2,371,176
Insertions	20,176
Mapped reads with at least one insertion	0.19%
Deletions	67,305
Mapped reads with at least one deletion	0.64%
Homopolymer indels	48.43%

2.6. Chromosome stats

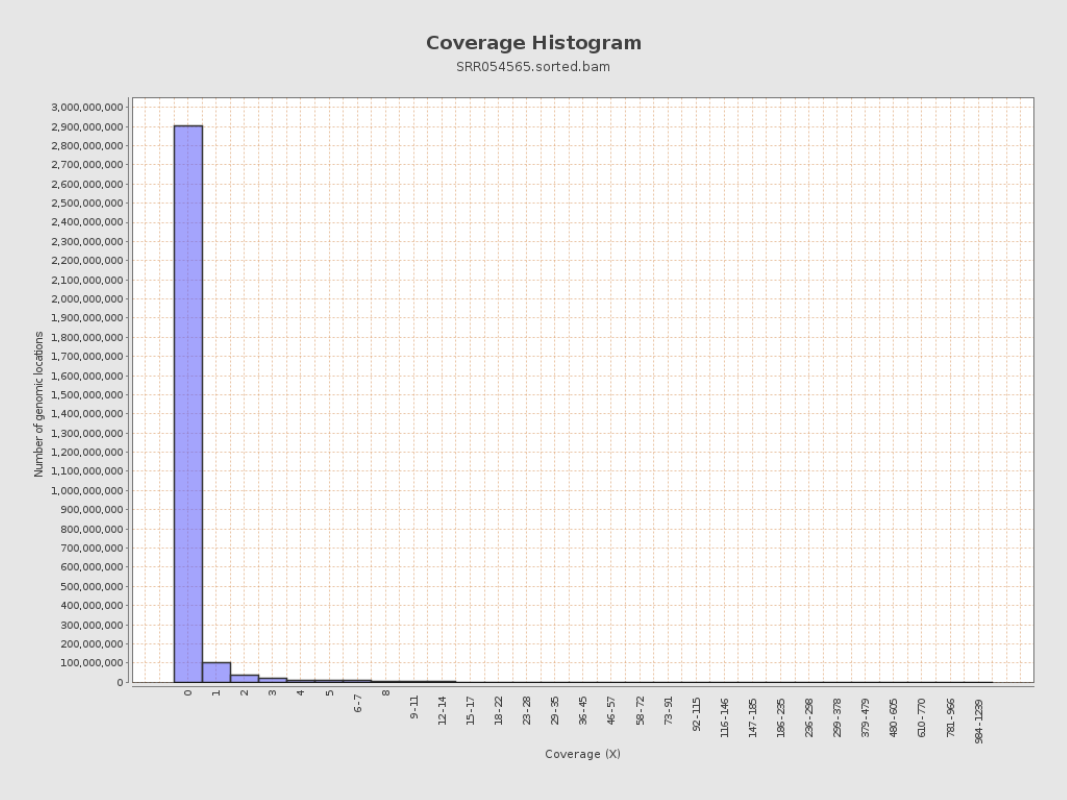
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	43326770	0.1738	1.2563
chr2	243199373	53886861	0.2216	1.4762
chr3	198022430	31576127	0.1595	1.0042
chr4	191154276	22784836	0.1192	0.8536
chr5	180915260	24529309	0.1356	0.9032
chr6	171115067	29712860	0.1736	1.1582
chr7	159138663	25543402	0.1605	1.4174

chr8	146364022	29103722	0.1988	1.2725
chr9	141213431	25843360	0.183	1.1823
chr10	135534747	16970447	0.1252	1.0222
chr11	135006516	24874806	0.1842	1.25
chr12	133851895	28160907	0.2104	1.2086
chr13	115169878	12168388	0.1057	0.8061
chr14	107349540	9553760	0.089	0.9098
chr15	102531392	12363188	0.1206	0.851
chr16	90354753	13644264	0.151	0.9951
chr17	81195210	13915078	0.1714	1.0825
chr18	78077248	13767870	0.1763	1.2573
chr19	59128983	11391485	0.1927	1.3144
chr20	63025520	11634008	0.1846	1.1324
chr21	48129895	5629489	0.117	0.9425
chr22	51304566	7765643	0.1514	0.9936
chrMT	16571	30018	1.8115	3.9536
chrX	155270560	30642106	0.1973	1.2648
chrY	59373566	1141139	0.0192	0.397

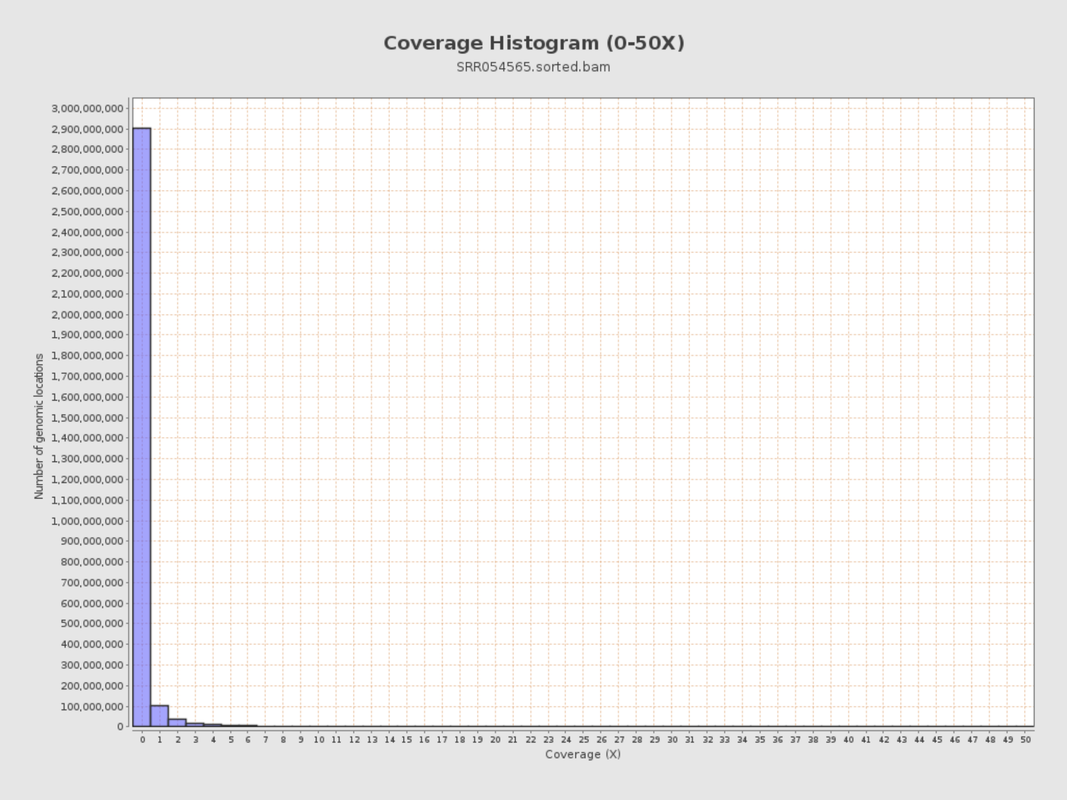
3. Results : Coverage across reference



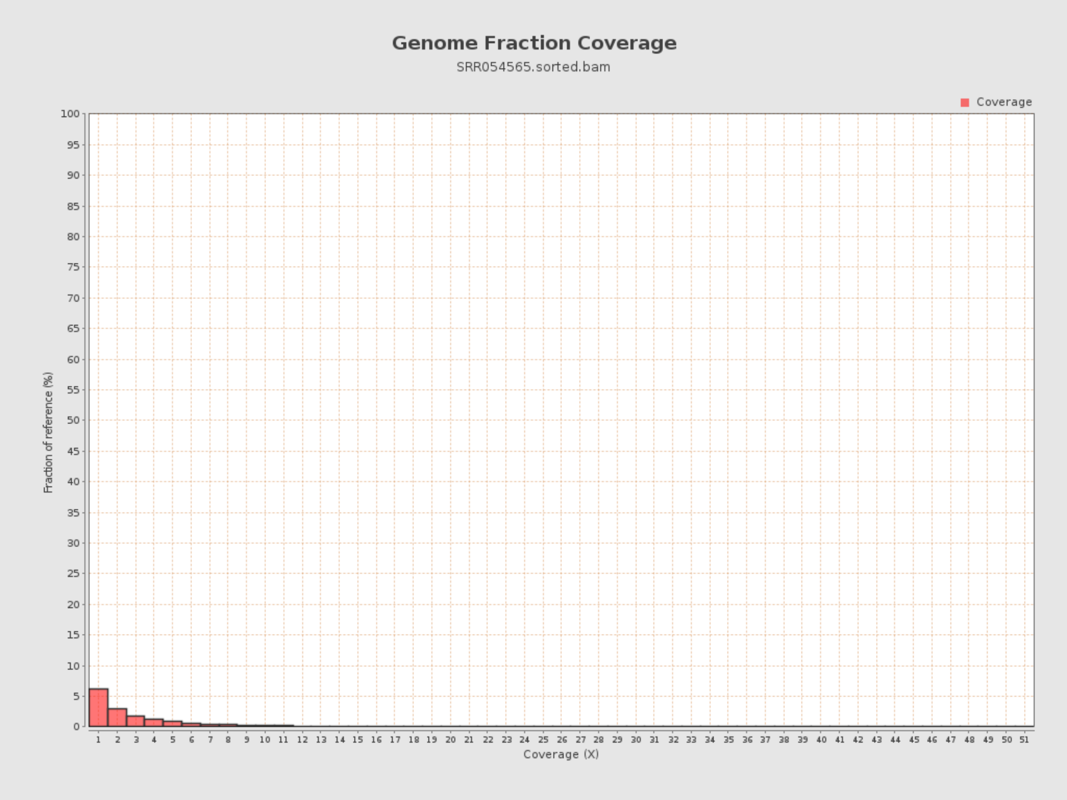
4. Results : Coverage Histogram



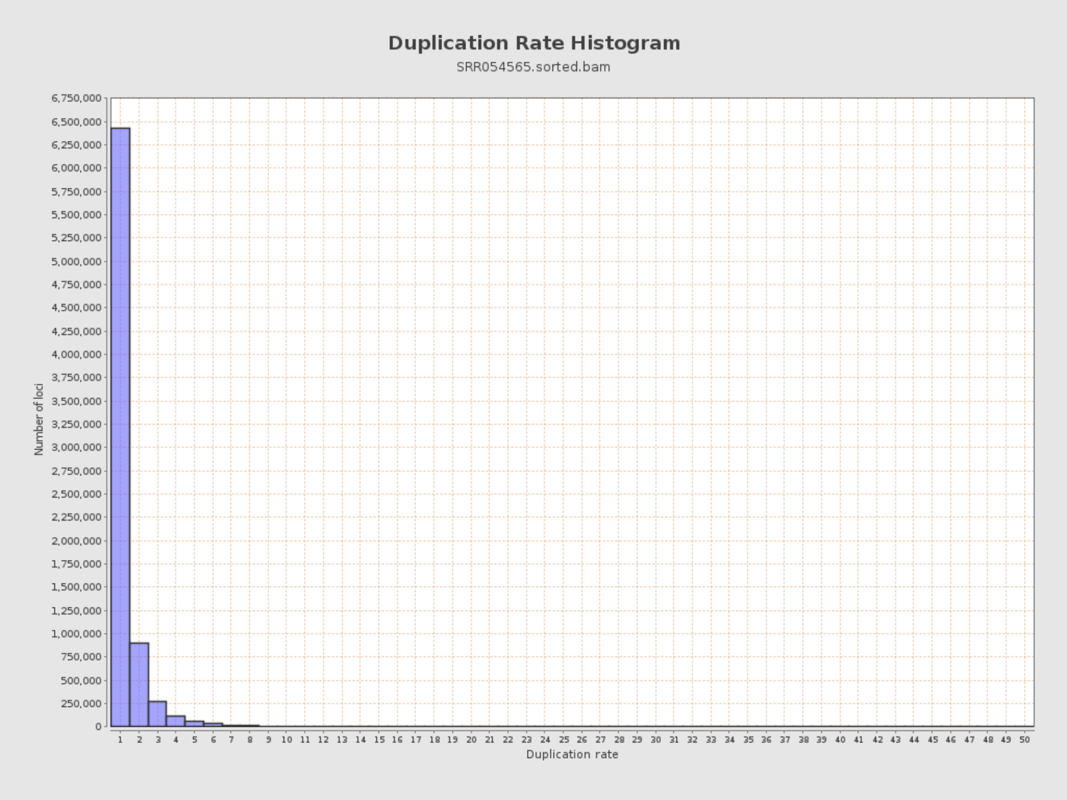
5. Results : Coverage Histogram (0-50X)



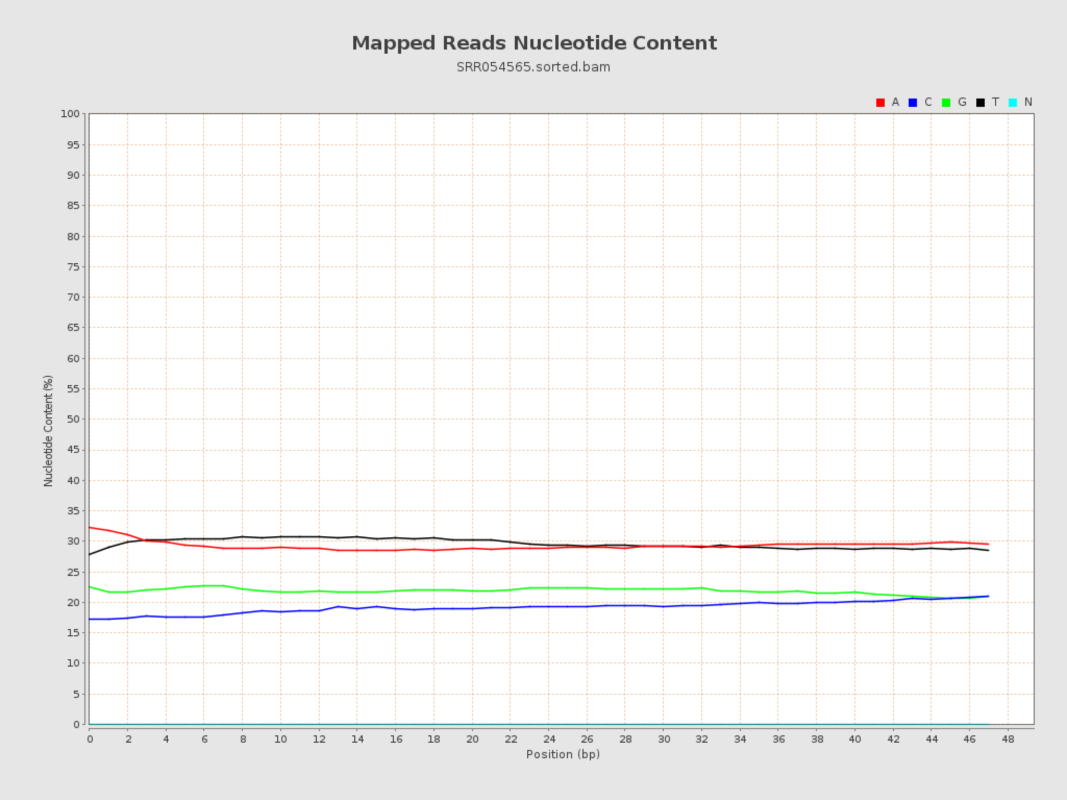
6. Results : Genome Fraction Coverage



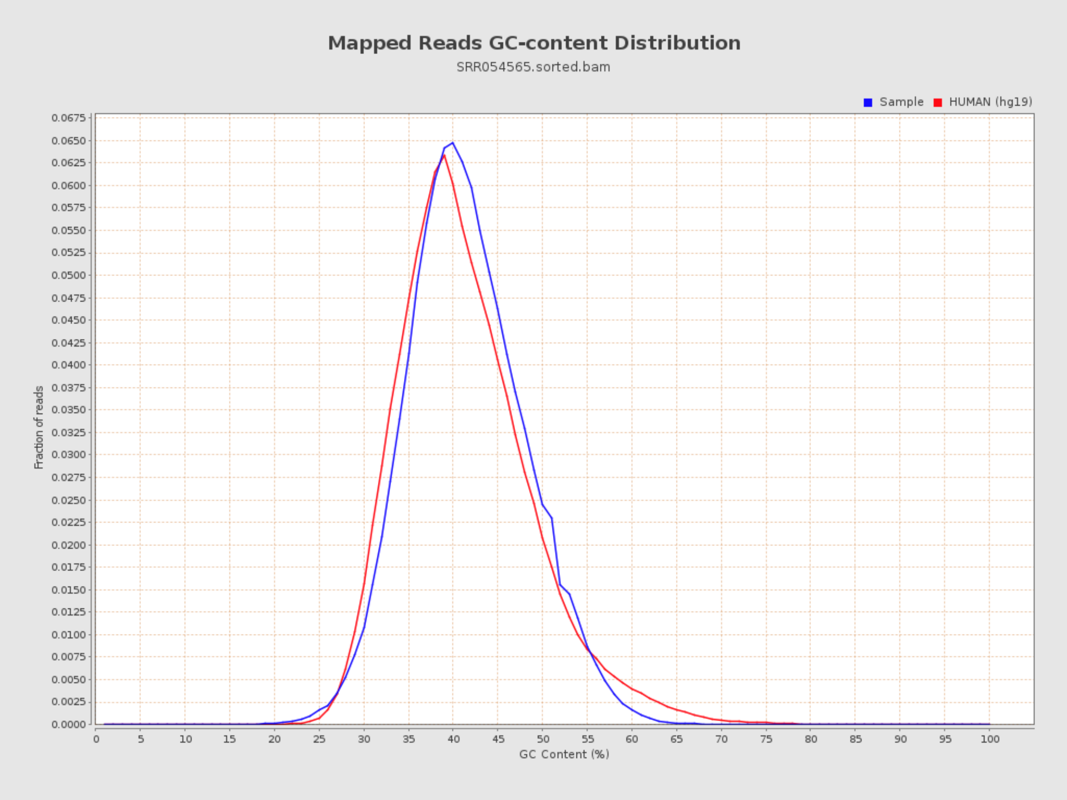
7. Results : Duplication Rate Histogram



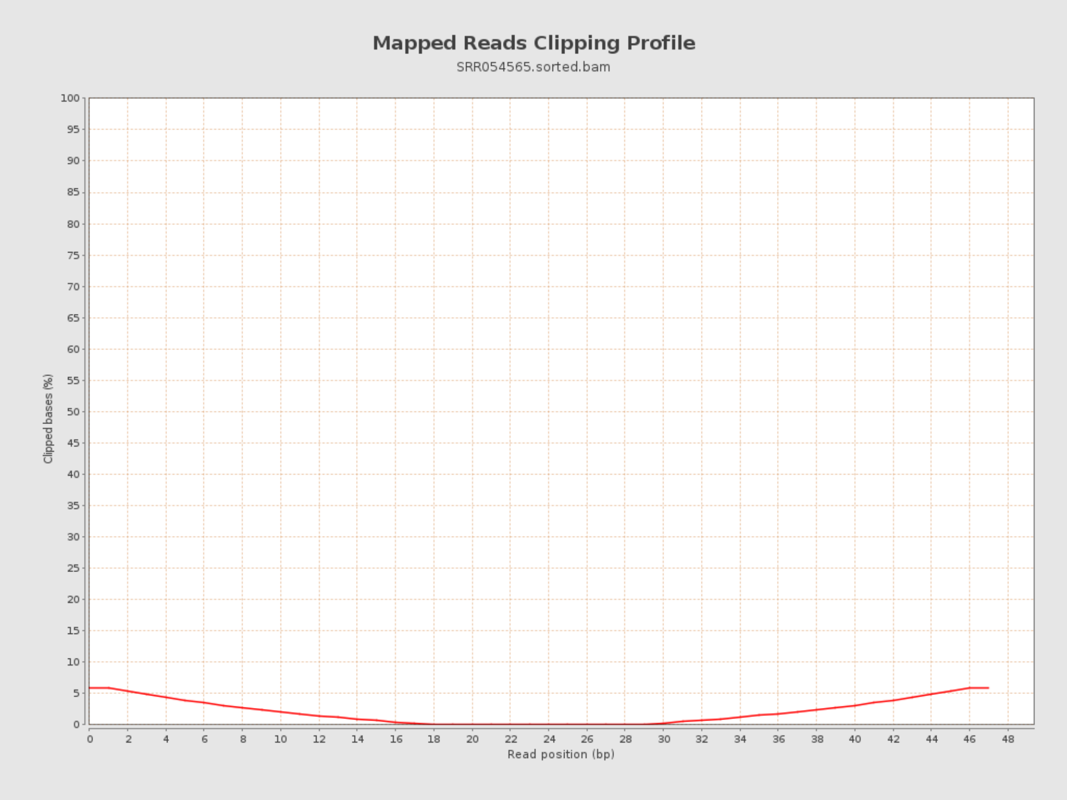
8. Results : Mapped Reads Nucleotide Content



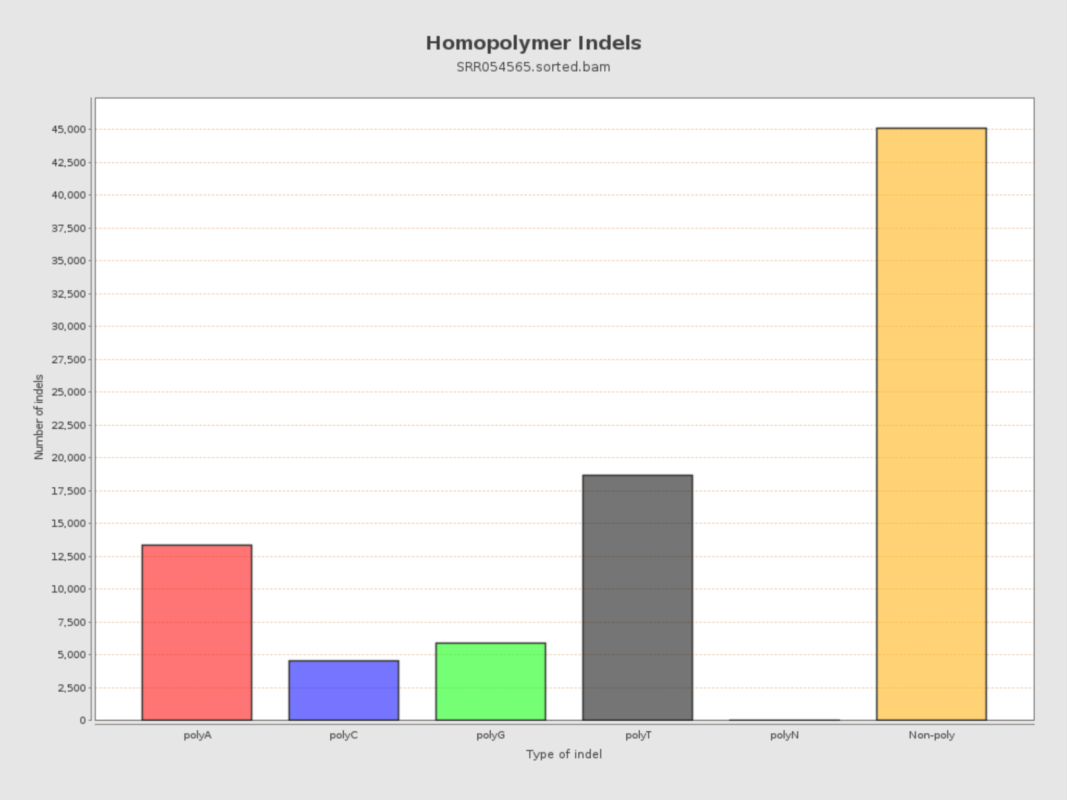
9. Results : Mapped Reads GC-content Distribution



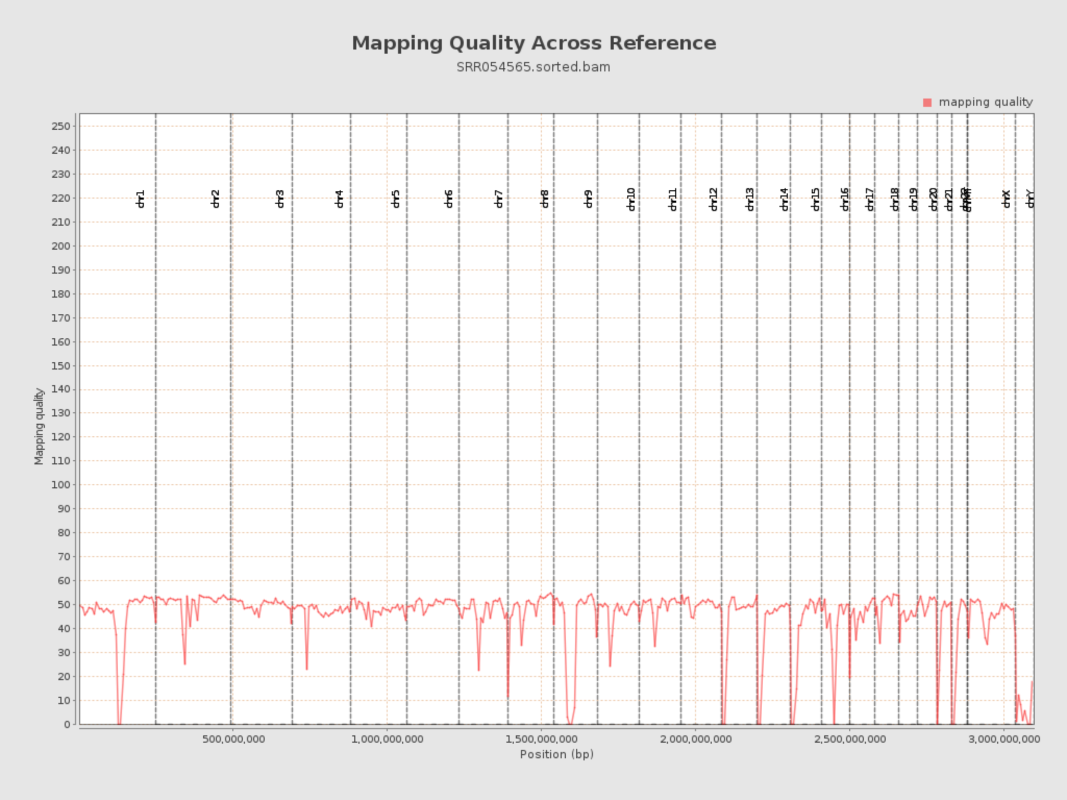
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram