Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 04:02:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054566.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_SRR054566 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054566.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 04:02:21 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054566.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,441,281
Mapped reads	9,809,568 / 72.98%
Unmapped reads	3,631,713 / 27.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	260 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	3,304,944 / 24.59%
Duplication rate	22.97%
Clipped reads	757,411 / 5.63%

2.2. ACGT Content

Number/percentage of A's	138,542,702 / 29.84%
Number/percentage of C's	90,551,195 / 19.5%
Number/percentage of T's	137,694,066 / 29.65%
Number/percentage of G's	97,314,394 / 20.96%
Number/percentage of N's	218,938 / 0.05%
GC Percentage	40.46%

2.3. Coverage

Mean	0.15

Standard Deviation	1.3691

2.4. Mapping Quality

Mean Mapping Quality	44.56

2.5. Mismatches and indels

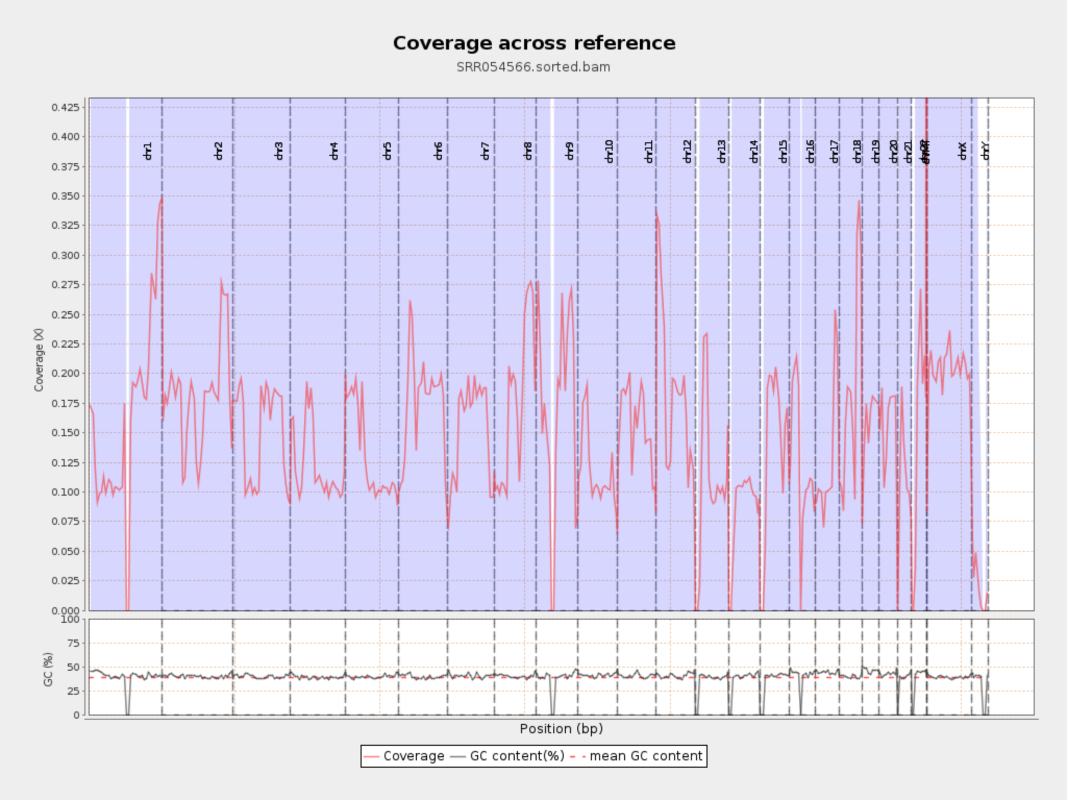
General error rate	0.66%
Mismatches	3,031,193
Insertions	20,370
Mapped reads with at least one insertion	0.21%
Deletions	64,677
Mapped reads with at least one deletion	0.66%
Homopolymer indels	47.8%

2.6. Chromosome stats

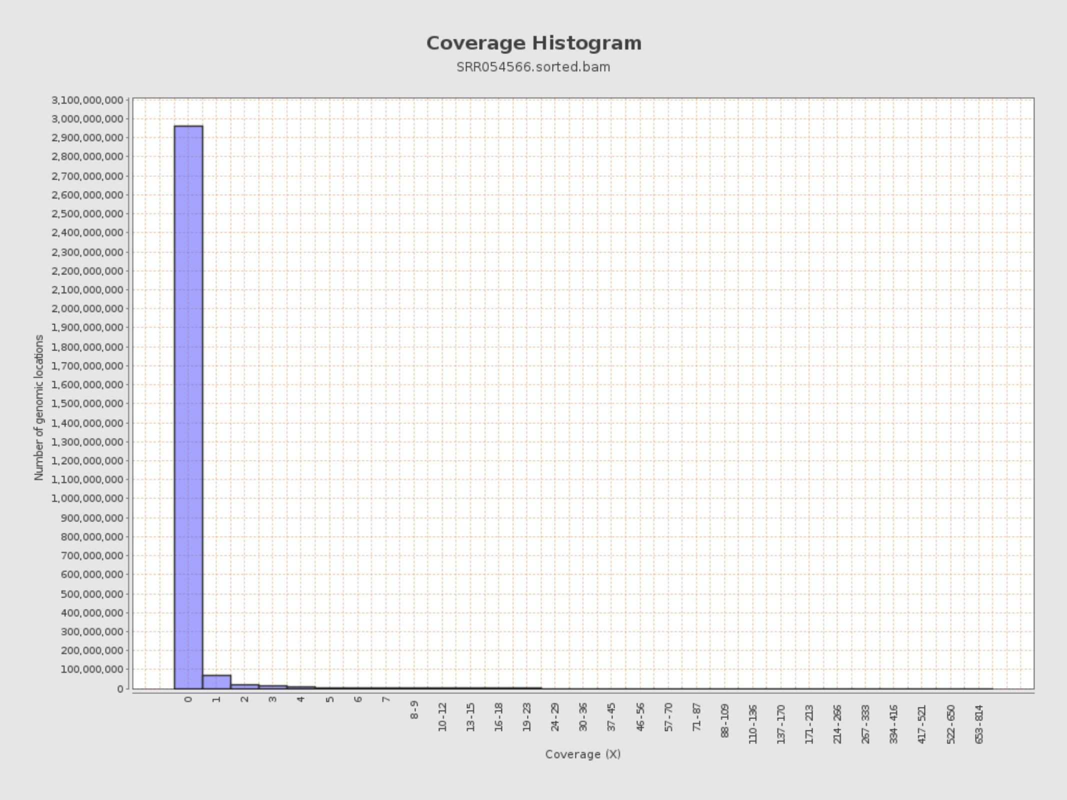
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	39694703	0.1593	1.5131
chr2	243199373	44044931	0.1811	1.5801
chr3	198022430	29796430	0.1505	1.2979
chr4	191154276	23392489	0.1224	1.1863
chr5	180915260	23622474	0.1306	1.2053
chr6	171115067	30033835	0.1755	1.5114
chr7	159138663	24595011	0.1546	1.3918

chr8	146364022	26090167	0.1783	1.5295
chr9	141213431	24617337	0.1743	1.4693
chr10	135534747	16194729	0.1195	1.2183
chr11	135006516	21205059	0.1571	1.4067
chr12	133851895	24894575	0.186	1.4777
chr13	115169878	12064023	0.1047	1.0868
chr14	107349540	9138719	0.0851	1.0395
chr15	102531392	14081065	0.1373	1.2255
chr16	90354753	11394629	0.1261	1.1865
chr17	81195210	10438476	0.1286	1.1654
chr18	78077248	14493453	0.1856	1.5907
chr19	59128983	9542754	0.1614	1.4369
chr20	63025520	9950006	0.1579	1.3643
chr21	48129895	5316409	0.1105	1.1792
chr22	51304566	7361765	0.1435	1.2841
chrMT	16571	28412	1.7146	4.8206
chrX	155270560	31270999	0.2014	1.6168
chrY	59373566	1155343	0.0195	0.4323

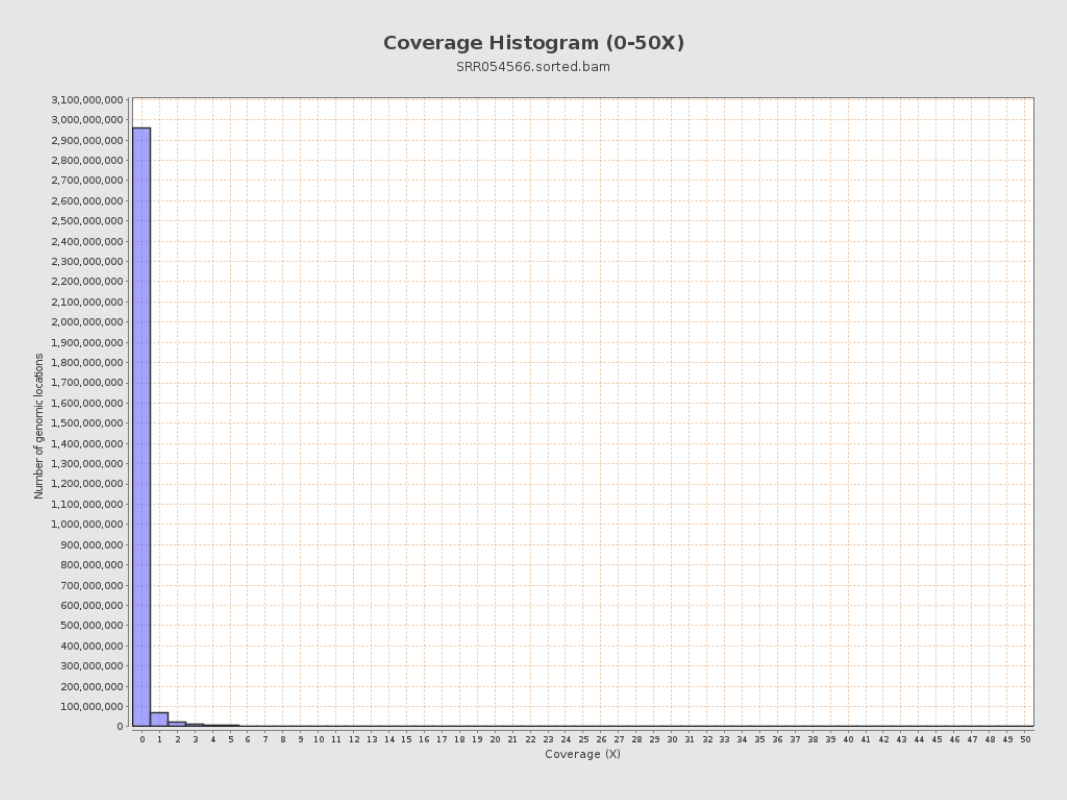
3. Results : Coverage across reference



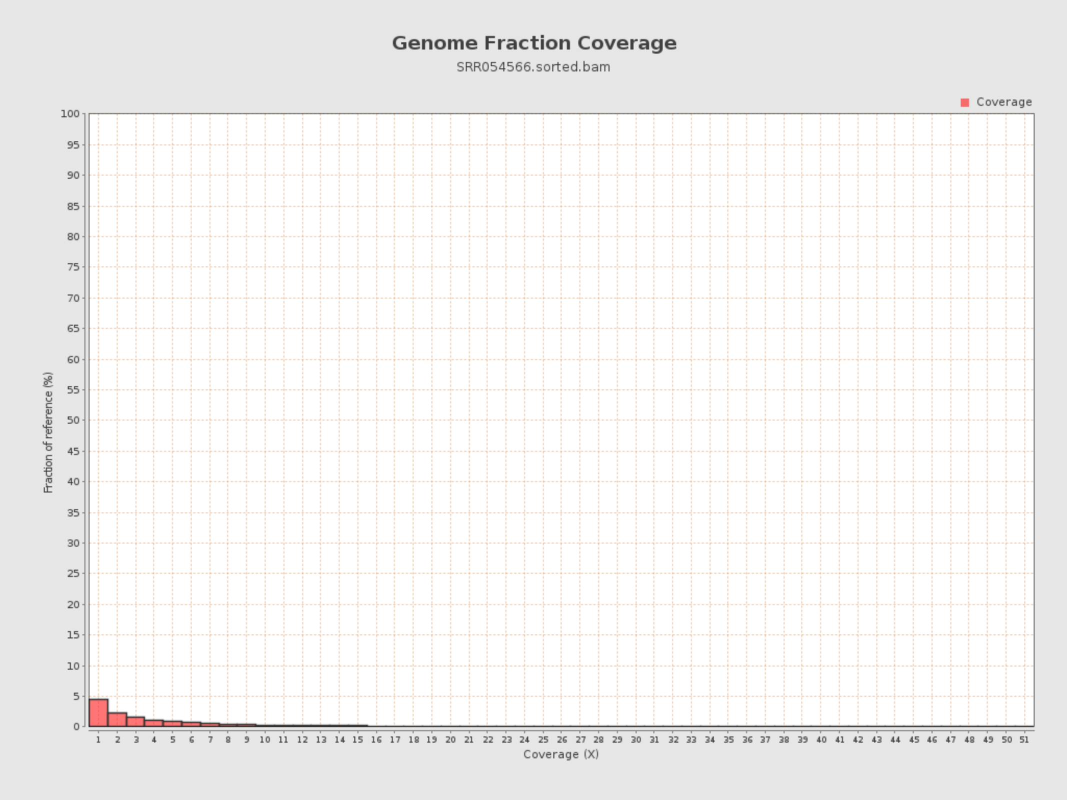
4. Results : Coverage Histogram



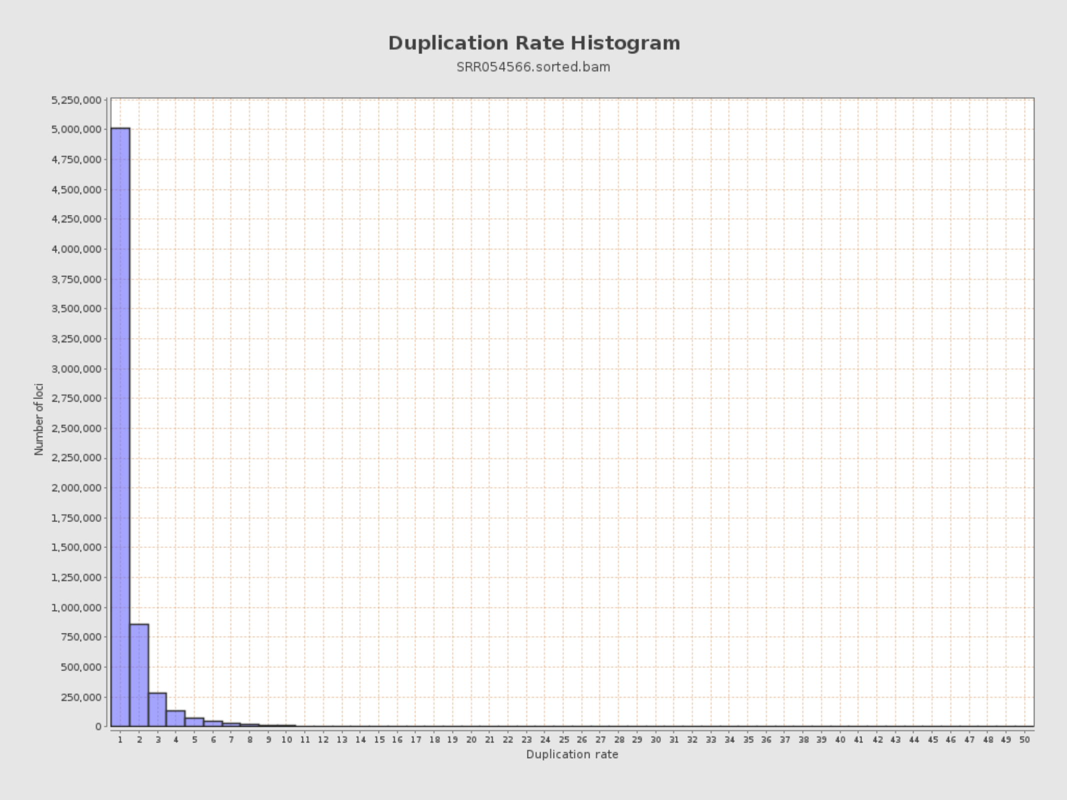
5. Results : Coverage Histogram (0-50X)



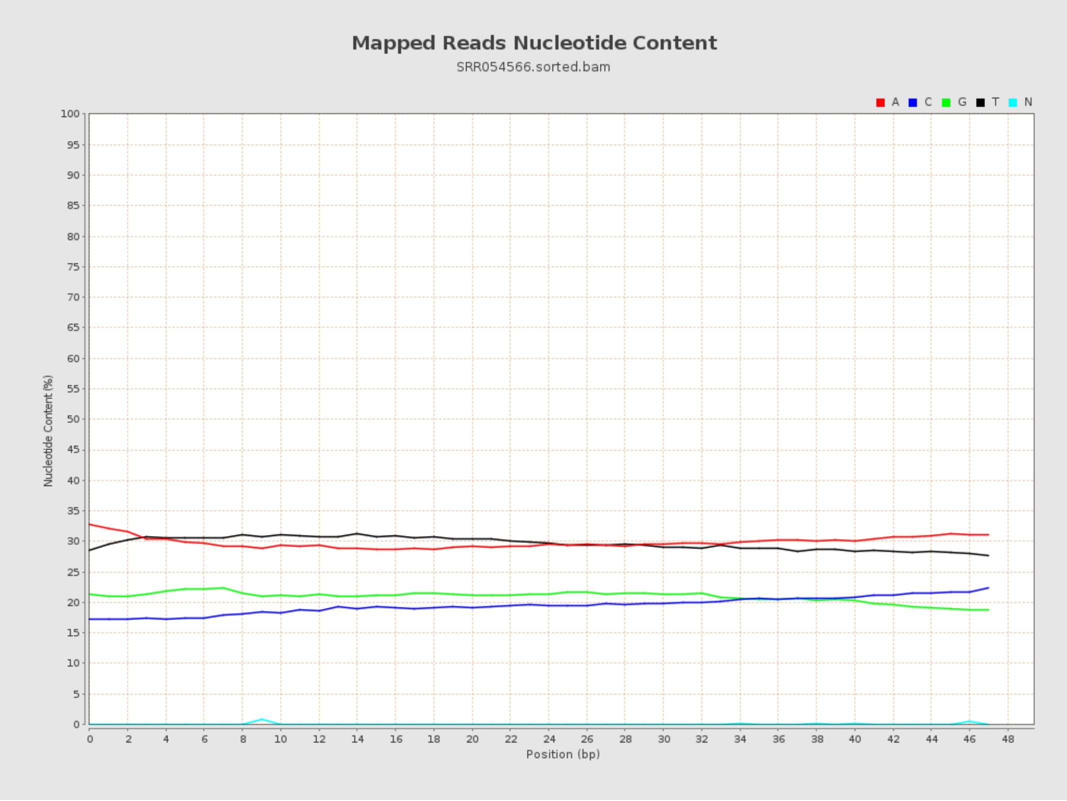
6. Results : Genome Fraction Coverage



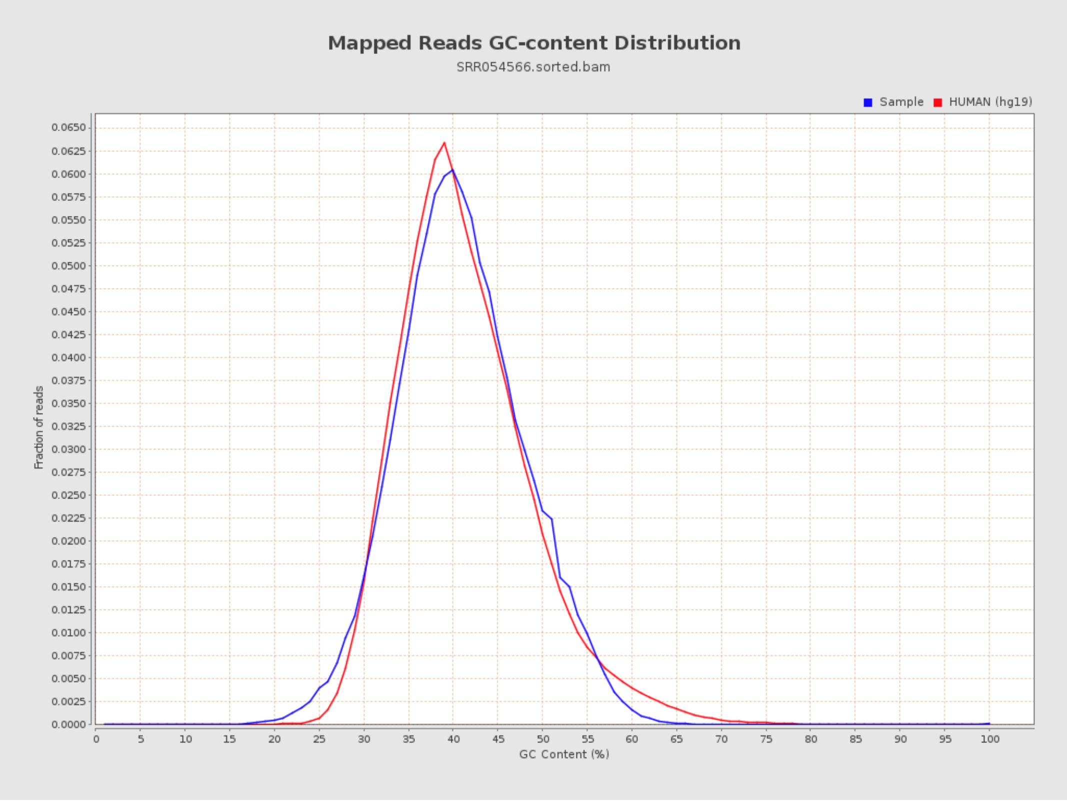
7. Results : Duplication Rate Histogram



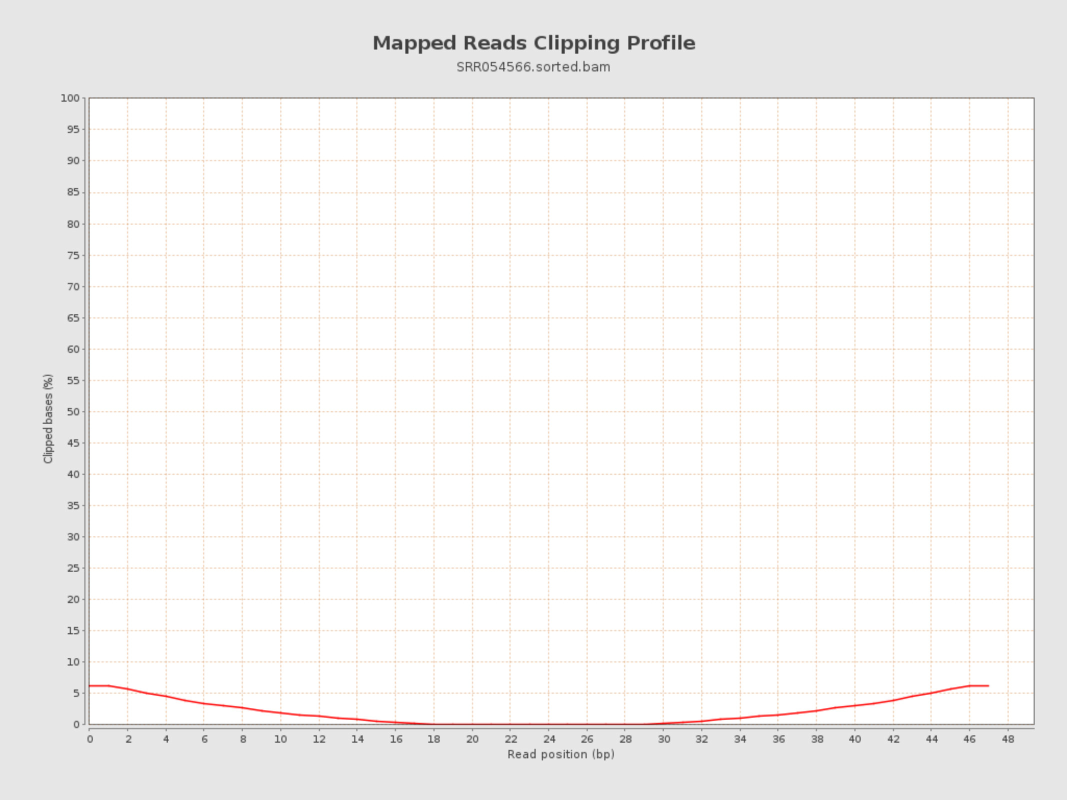
8. Results : Mapped Reads Nucleotide Content



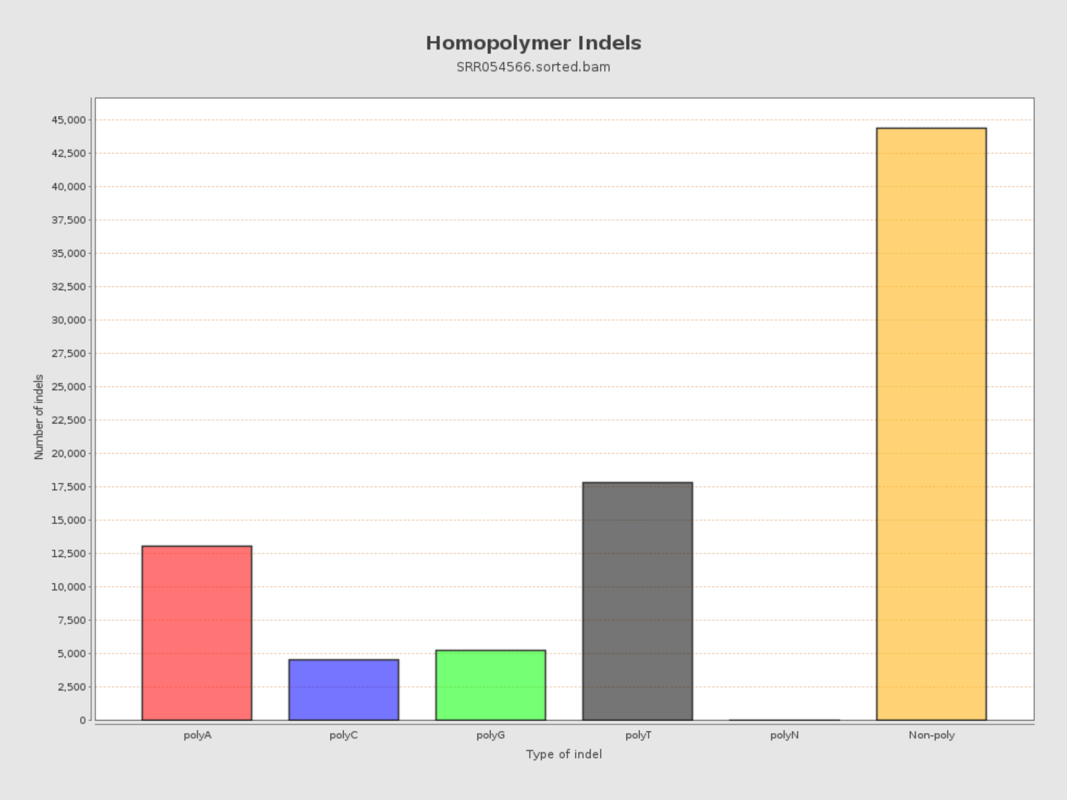
9. Results : Mapped Reads GC-content Distribution



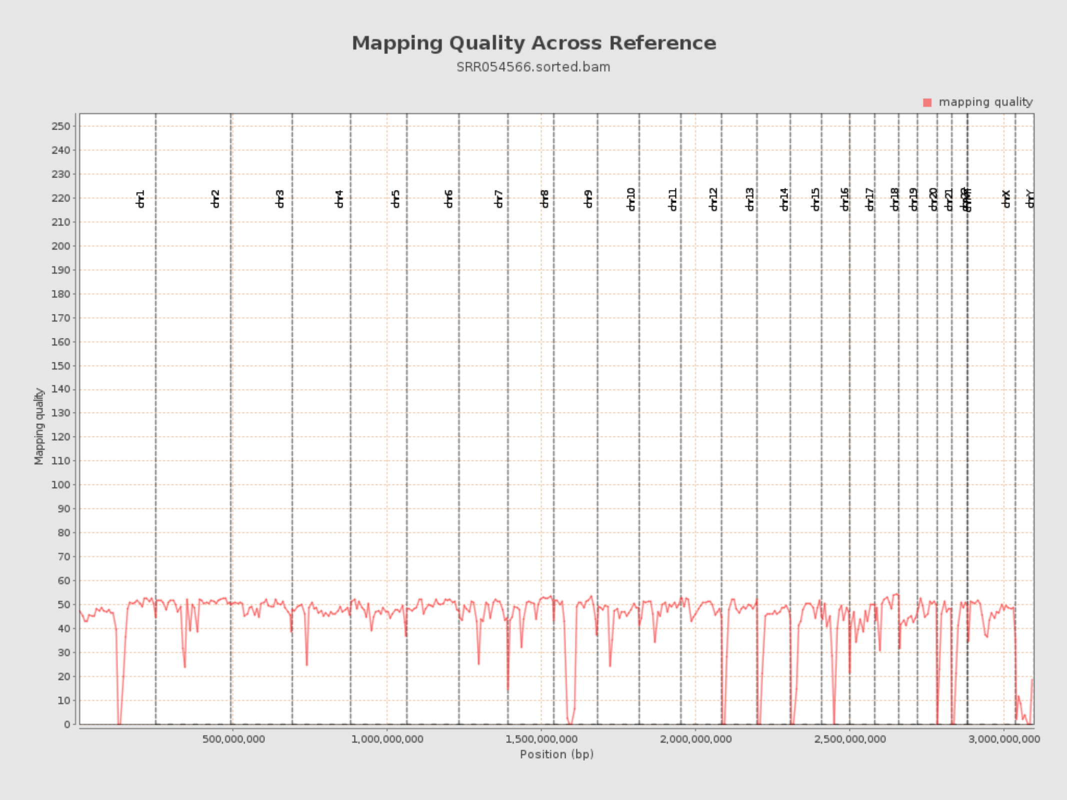
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram