Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 04:30:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054569.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_SRR054569 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054569.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 04:30:21 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054569.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,742,501
Mapped reads	11,787,695 / 74.88%
Unmapped reads	3,954,806 / 25.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	363 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	4,060,271 / 25.79%
Duplication rate	22.4%
Clipped reads	1,320,131 / 8.39%

2.2. ACGT Content

Number/percentage of A's	167,405,593 / 30.22%
Number/percentage of C's	110,608,492 / 19.97%
Number/percentage of T's	160,879,599 / 29.04%
Number/percentage of G's	114,969,231 / 20.75%
Number/percentage of N's	116,913 / 0.02%
GC Percentage	40.72%

2.3. Coverage

Mean	0.179

Standard Deviation	1.611

2.4. Mapping Quality

Mean Mapping Quality	44.44

2.5. Mismatches and indels

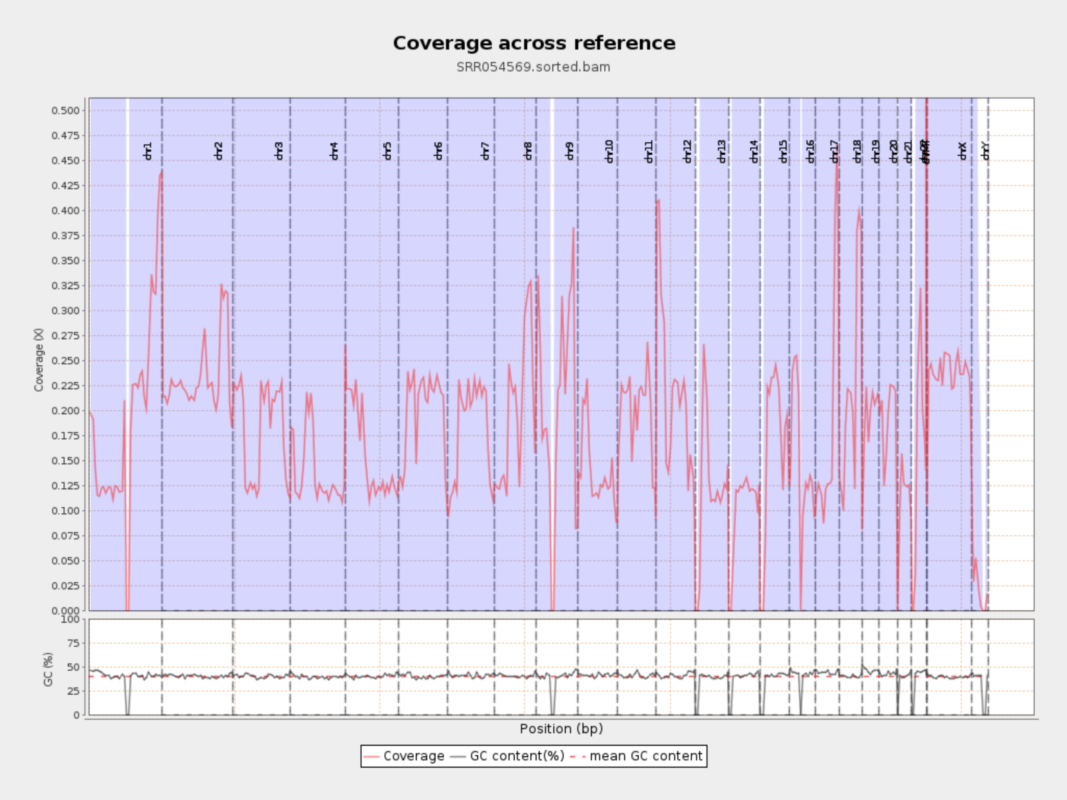
General error rate	0.55%
Mismatches	3,003,808
Insertions	24,747
Mapped reads with at least one insertion	0.21%
Deletions	77,964
Mapped reads with at least one deletion	0.66%
Homopolymer indels	46.67%

2.6. Chromosome stats

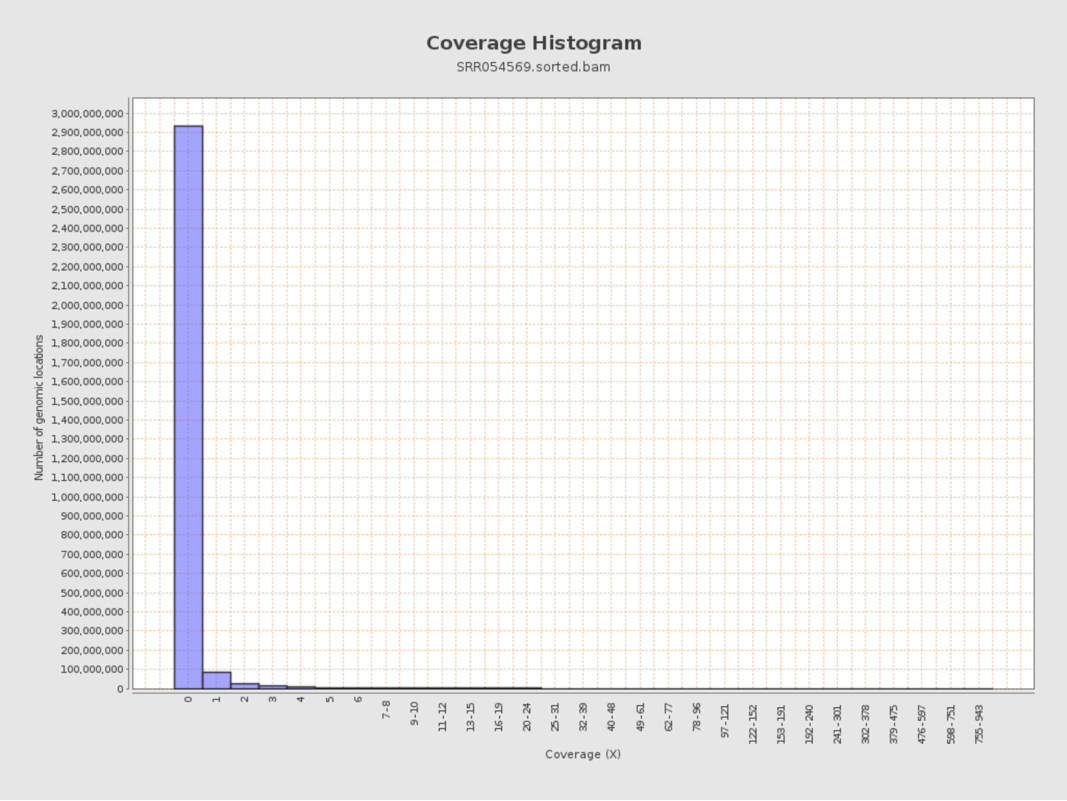
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	46982138	0.1885	1.7192
chr2	243199373	56999432	0.2344	1.9313
chr3	198022430	35932364	0.1815	1.5395
chr4	191154276	26465360	0.1385	1.3291
chr5	180915260	28011657	0.1548	1.3982
chr6	171115067	34089506	0.1992	1.7511
chr7	159138663	29045762	0.1825	1.6704

chr8	146364022	29727866	0.2031	1.7751
chr9	141213431	29570960	0.2094	1.7378
chr10	135534747	19126683	0.1411	1.3799
chr11	135006516	26690998	0.1977	1.7097
chr12	133851895	29592561	0.2211	1.7643
chr13	115169878	13542103	0.1176	1.2054
chr14	107349540	10740828	0.1001	1.2274
chr15	102531392	16723737	0.1631	1.4868
chr16	90354753	13562489	0.1501	1.389
chr17	81195210	15465423	0.1905	1.6656
chr18	78077248	17359879	0.2223	1.8637
chr19	59128983	11559931	0.1955	1.732
chr20	63025520	11993105	0.1903	1.5968
chr21	48129895	5341451	0.111	1.2341
chr22	51304566	7681952	0.1497	1.3925
chrMT	16571	26815	1.6182	4.6913
chrX	155270560	36572550	0.2355	1.8797
chrY	59373566	1290516	0.0217	0.4587

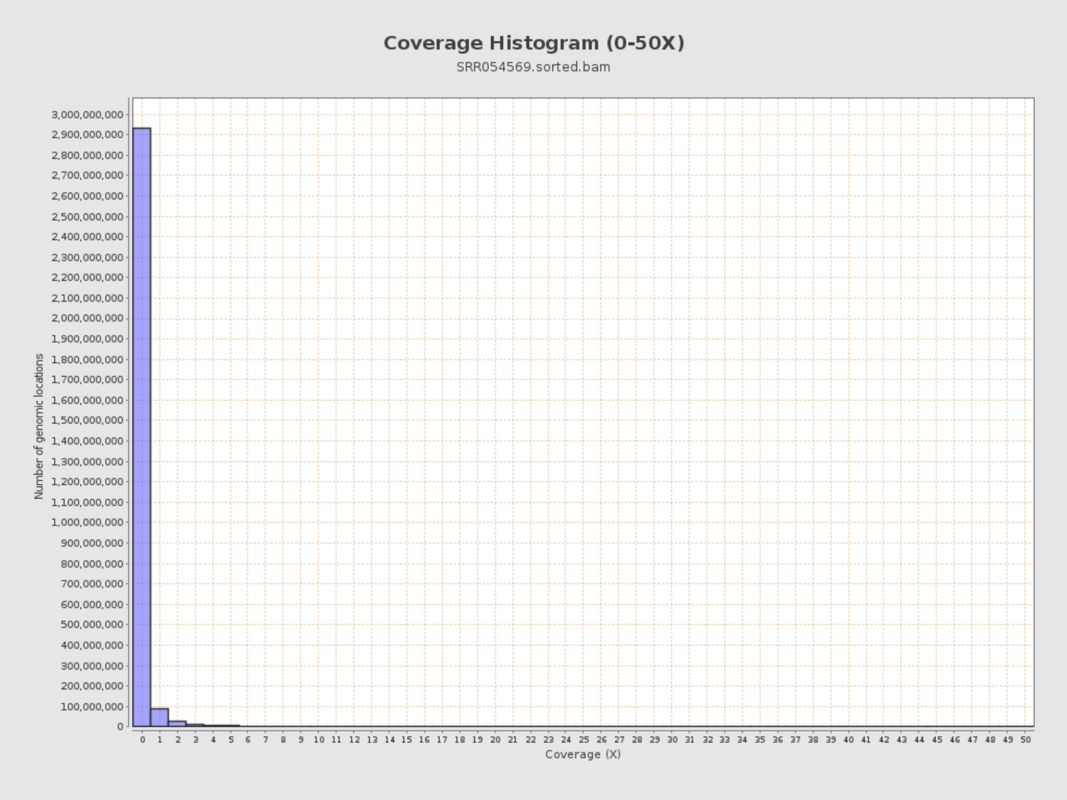
3. Results : Coverage across reference



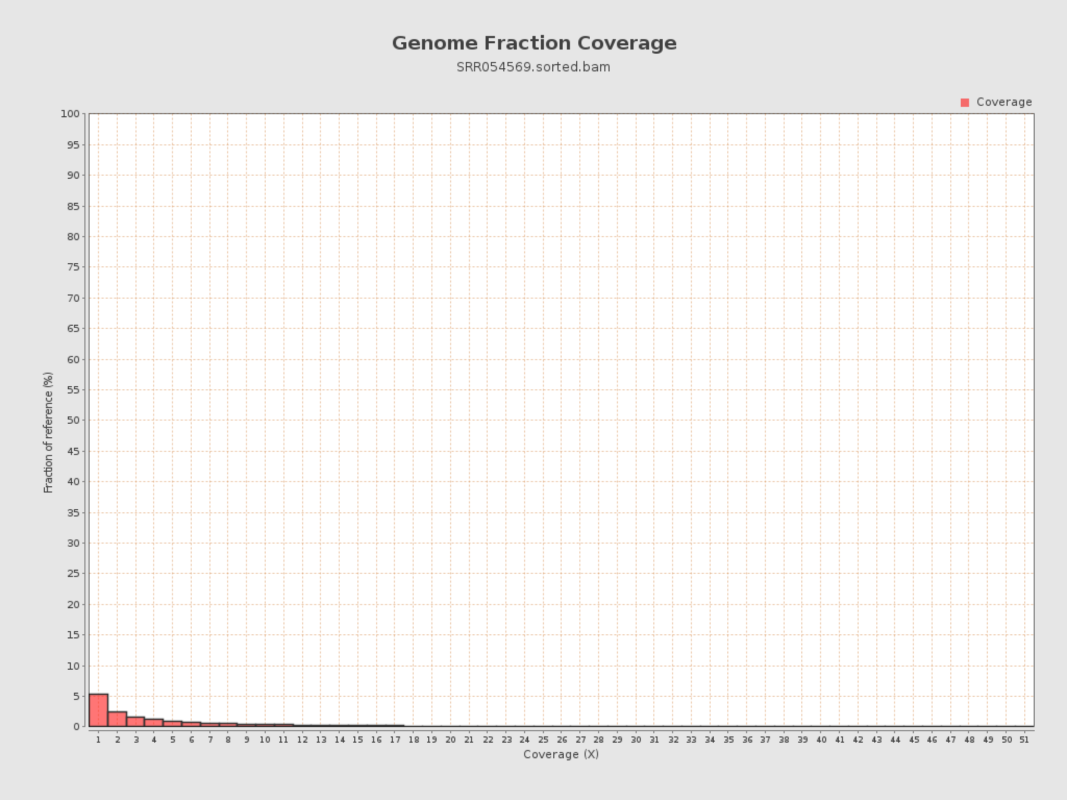
4. Results : Coverage Histogram



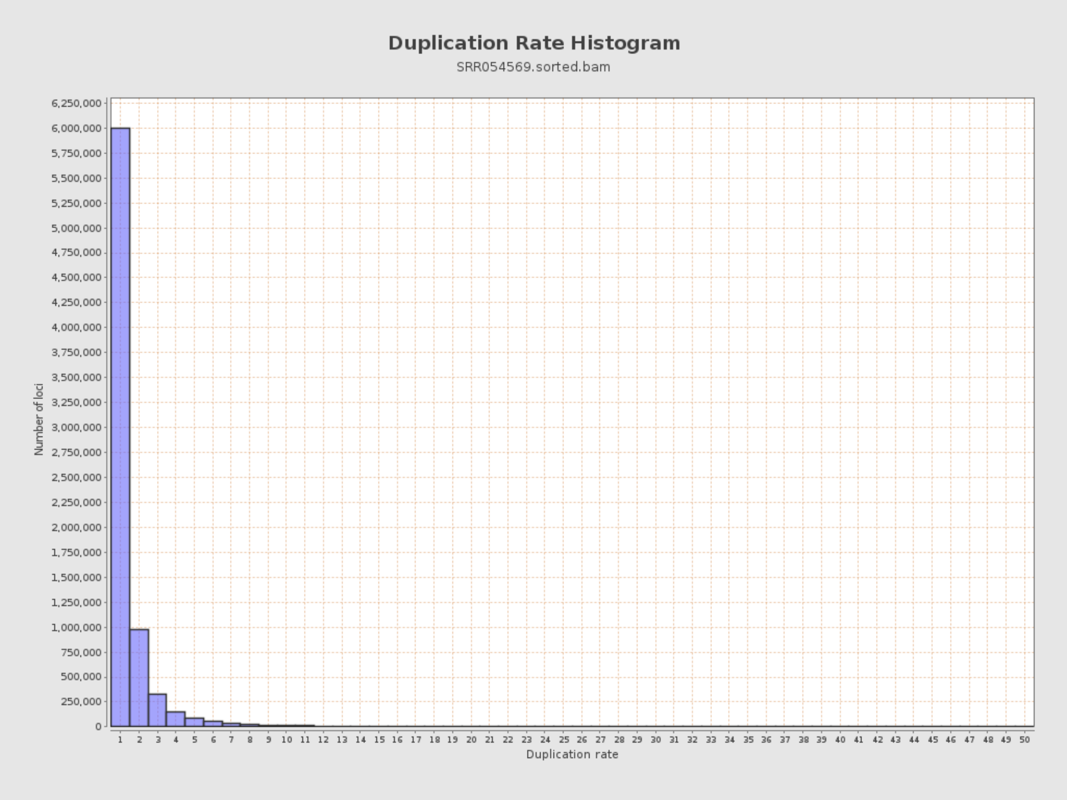
5. Results : Coverage Histogram (0-50X)



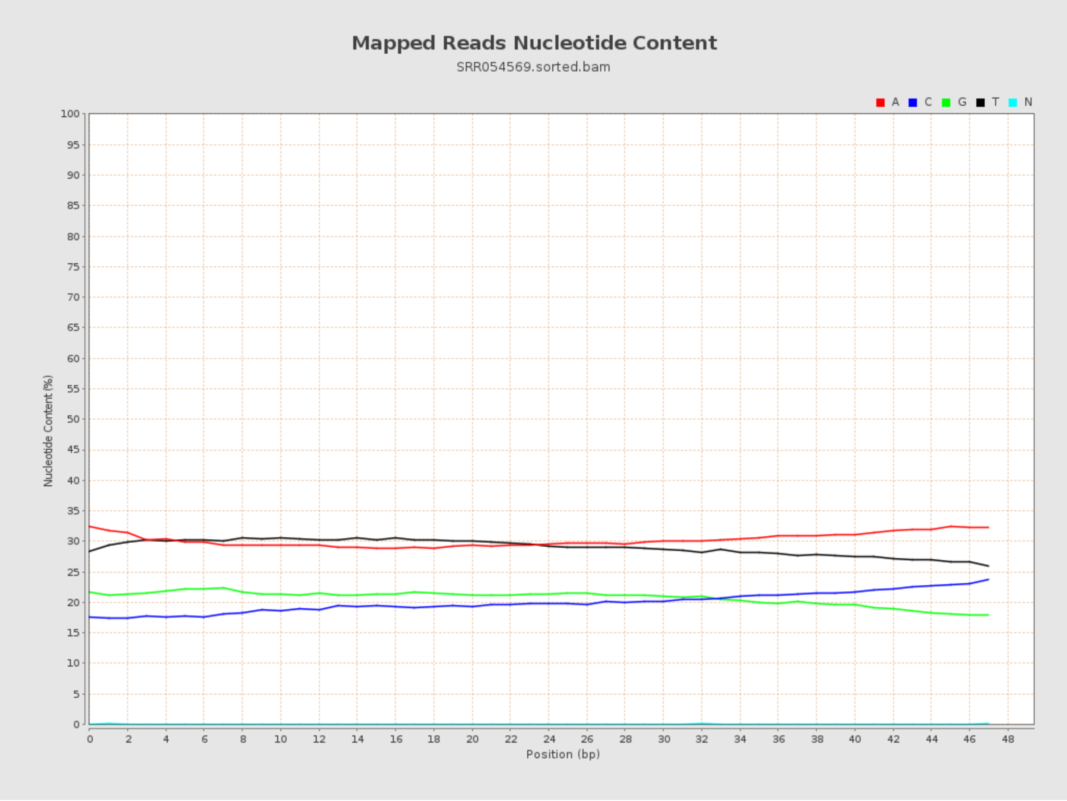
6. Results : Genome Fraction Coverage



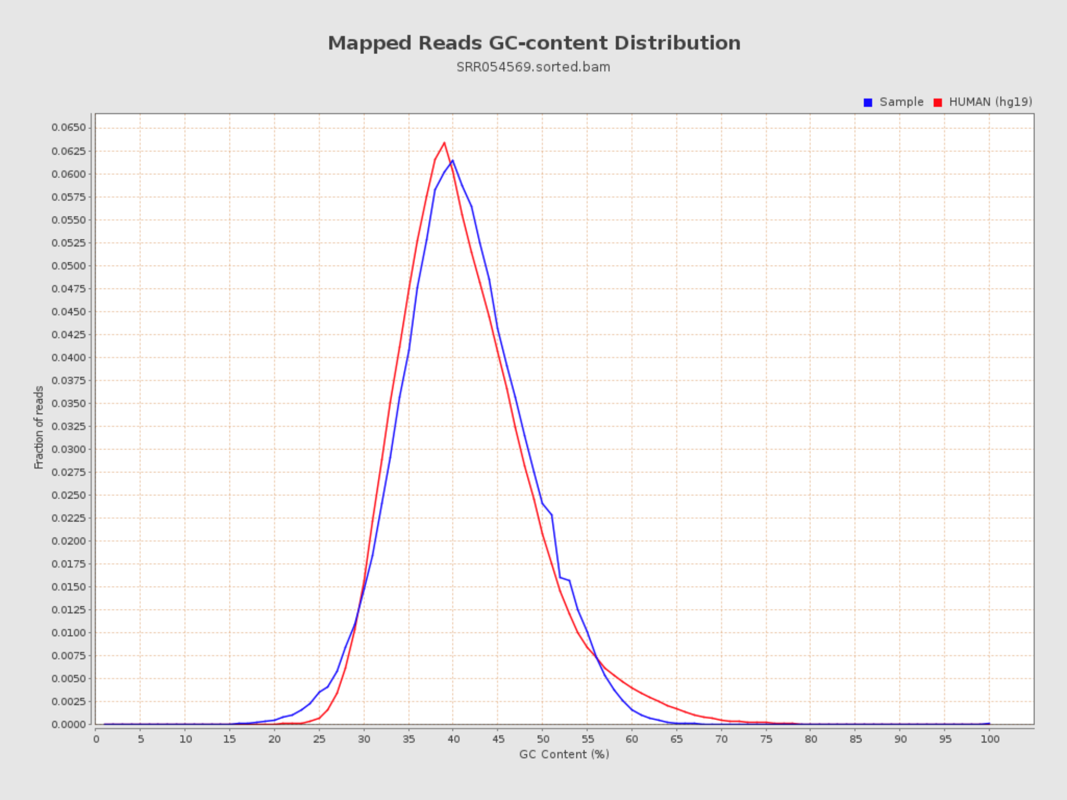
7. Results : Duplication Rate Histogram



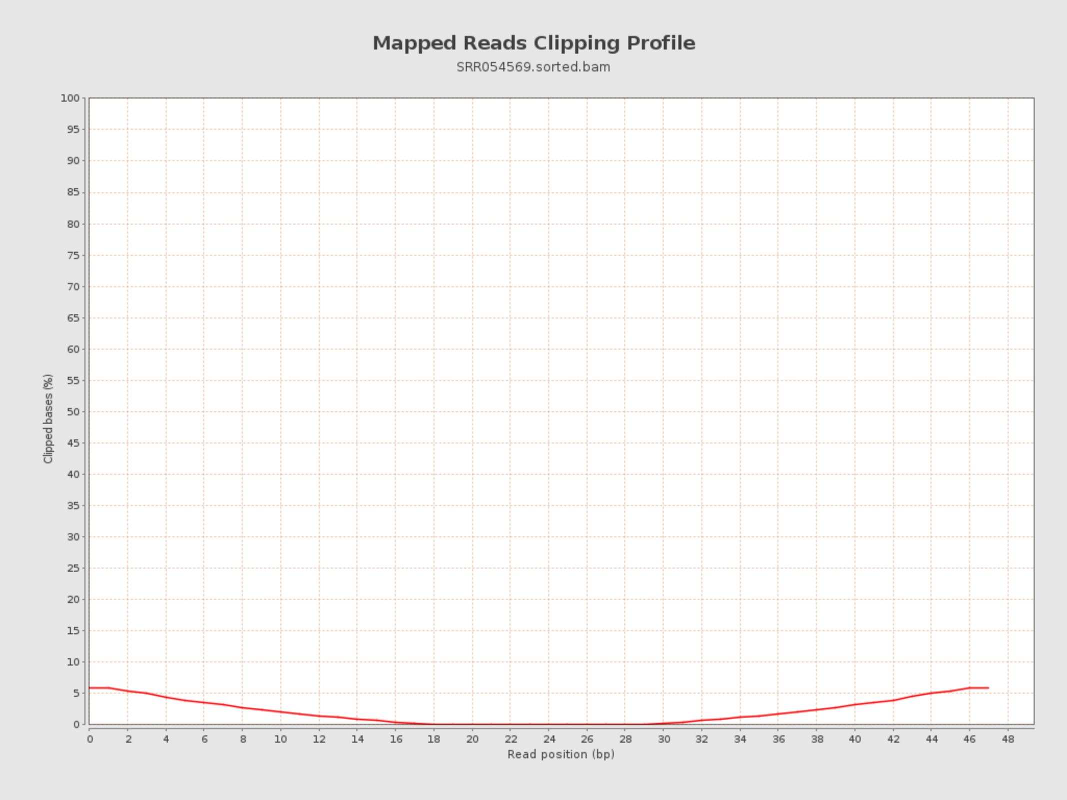
8. Results : Mapped Reads Nucleotide Content



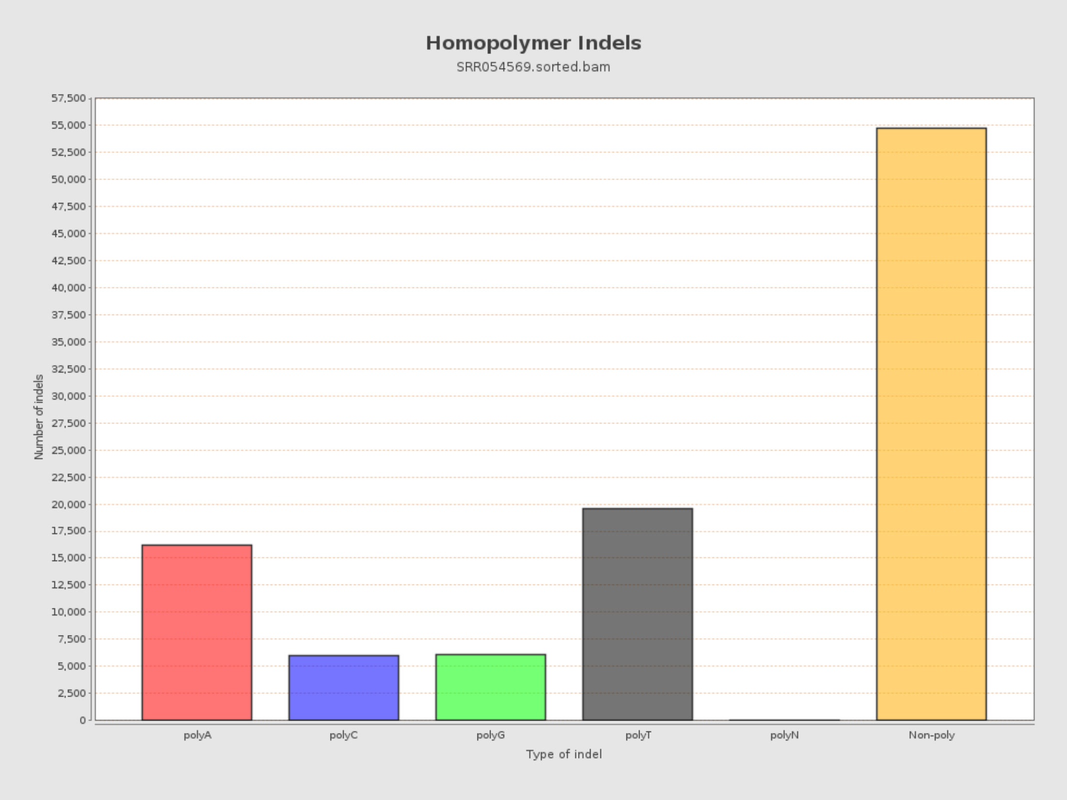
9. Results : Mapped Reads GC-content Distribution



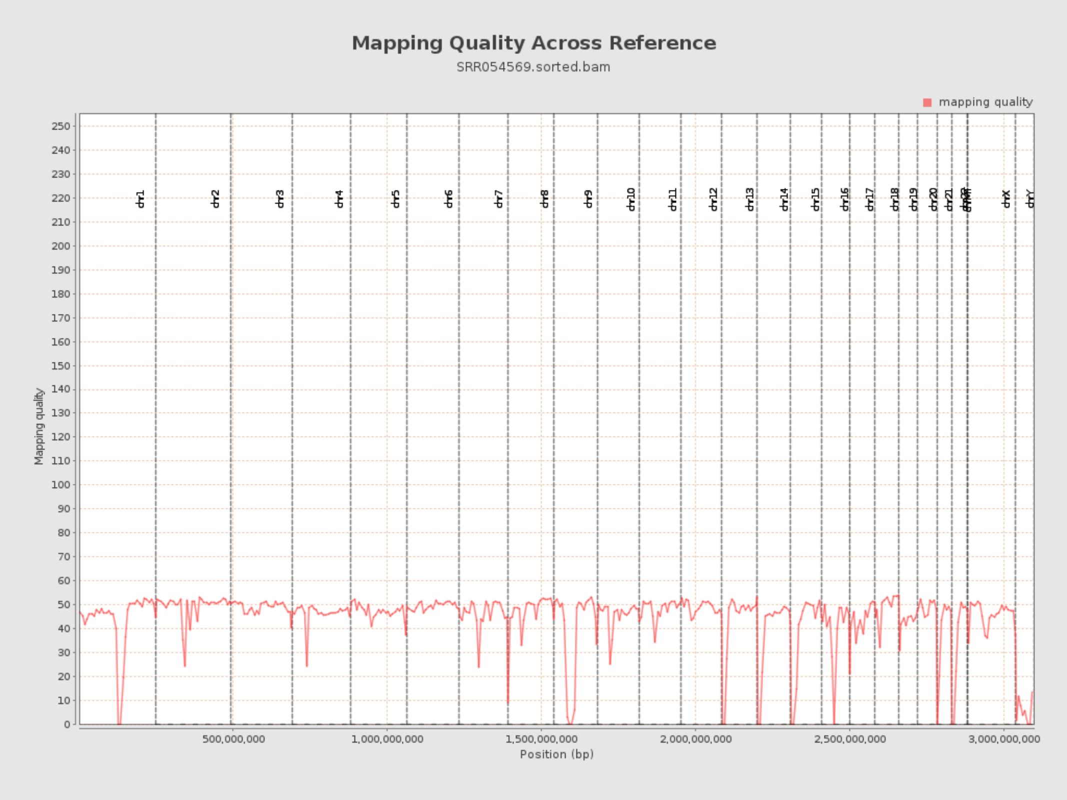
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram