Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 04:20:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054568.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_SRR054568 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054568.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 04:20:39 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054568.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,437,964
Mapped reads	10,664,492 / 73.86%
Unmapped reads	3,773,472 / 26.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	276 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	3,677,445 / 25.47%
Duplication rate	22.76%
Clipped reads	988,820 / 6.85%

2.2. ACGT Content

Number/percentage of A's	152,393,210 / 30.28%
Number/percentage of C's	98,177,327 / 19.51%
Number/percentage of T's	148,641,740 / 29.54%
Number/percentage of G's	103,896,276 / 20.65%
Number/percentage of N's	122,133 / 0.02%
GC Percentage	40.16%

2.3. Coverage

Mean	0.1626

Standard Deviation	1.4829

2.4. Mapping Quality

Mean Mapping Quality	44.65

2.5. Mismatches and indels

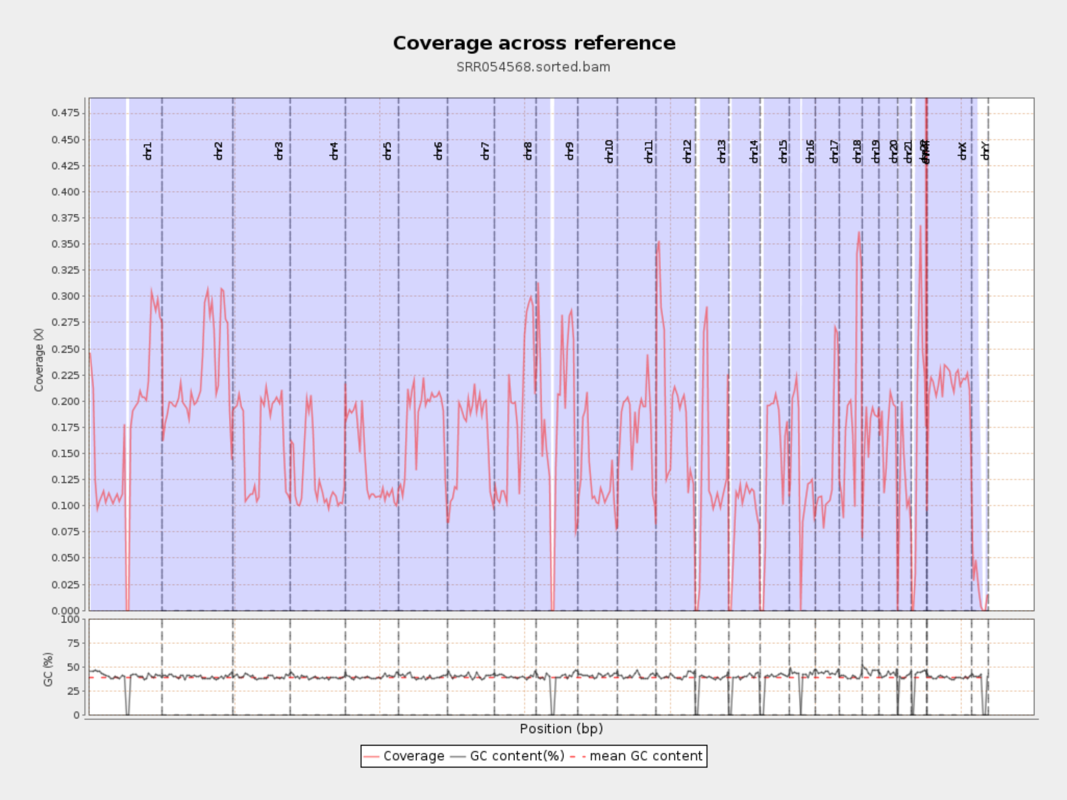
General error rate	0.56%
Mismatches	2,786,499
Insertions	22,603
Mapped reads with at least one insertion	0.21%
Deletions	71,367
Mapped reads with at least one deletion	0.67%
Homopolymer indels	47.45%

2.6. Chromosome stats

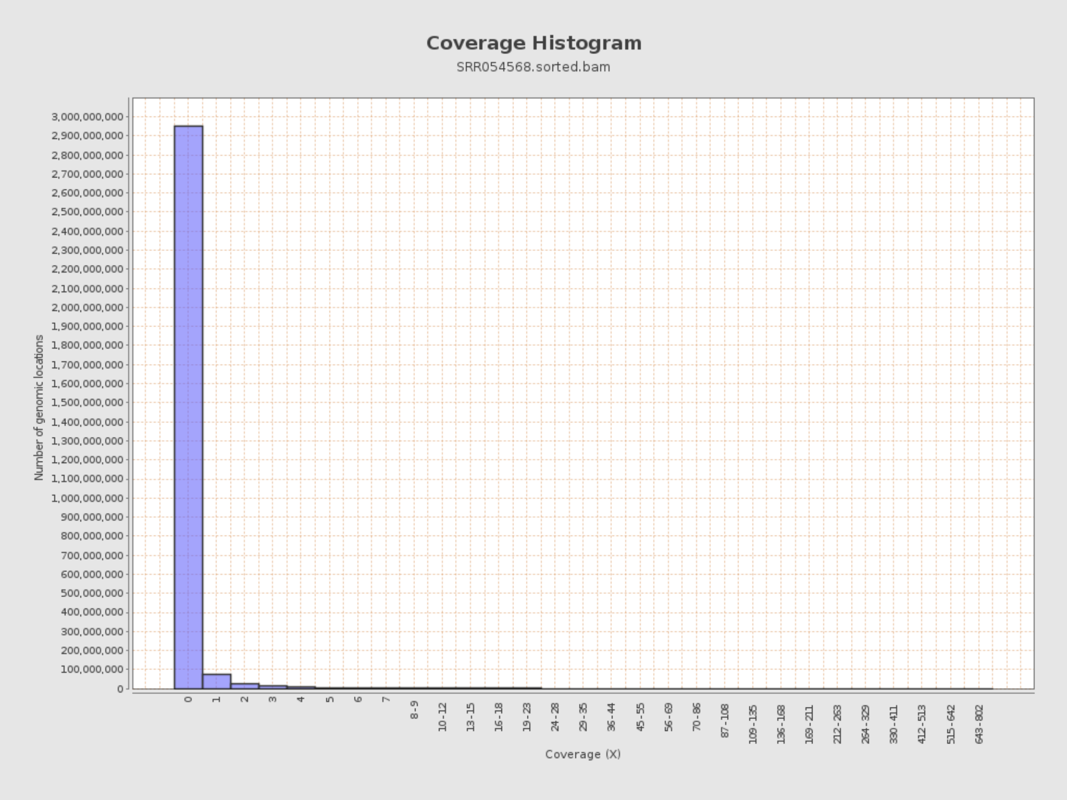
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	41499950	0.1665	1.5429
chr2	243199373	54529387	0.2242	1.791
chr3	198022430	32700599	0.1651	1.4545
chr4	191154276	24220717	0.1267	1.2819
chr5	180915260	24818423	0.1372	1.2654
chr6	171115067	30929176	0.1808	1.5912
chr7	159138663	26383721	0.1658	1.5427

chr8	146364022	27720907	0.1894	1.6412
chr9	141213431	26197856	0.1855	1.5895
chr10	135534747	17185998	0.1268	1.2746
chr11	135006516	23781616	0.1762	1.5158
chr12	133851895	26499496	0.198	1.6059
chr13	115169878	13641585	0.1184	1.1952
chr14	107349540	9723539	0.0906	1.0957
chr15	102531392	14611499	0.1425	1.3046
chr16	90354753	12061737	0.1335	1.2805
chr17	81195210	11488160	0.1415	1.2952
chr18	78077248	15512459	0.1987	1.7551
chr19	59128983	10199091	0.1725	1.5439
chr20	63025520	10757921	0.1707	1.4907
chr21	48129895	5521118	0.1147	1.2811
chr22	51304566	8811538	0.1717	1.5218
chrMT	16571	65492	3.9522	8.0417
chrX	155270560	33282806	0.2144	1.7634
chrY	59373566	1192342	0.0201	0.4479

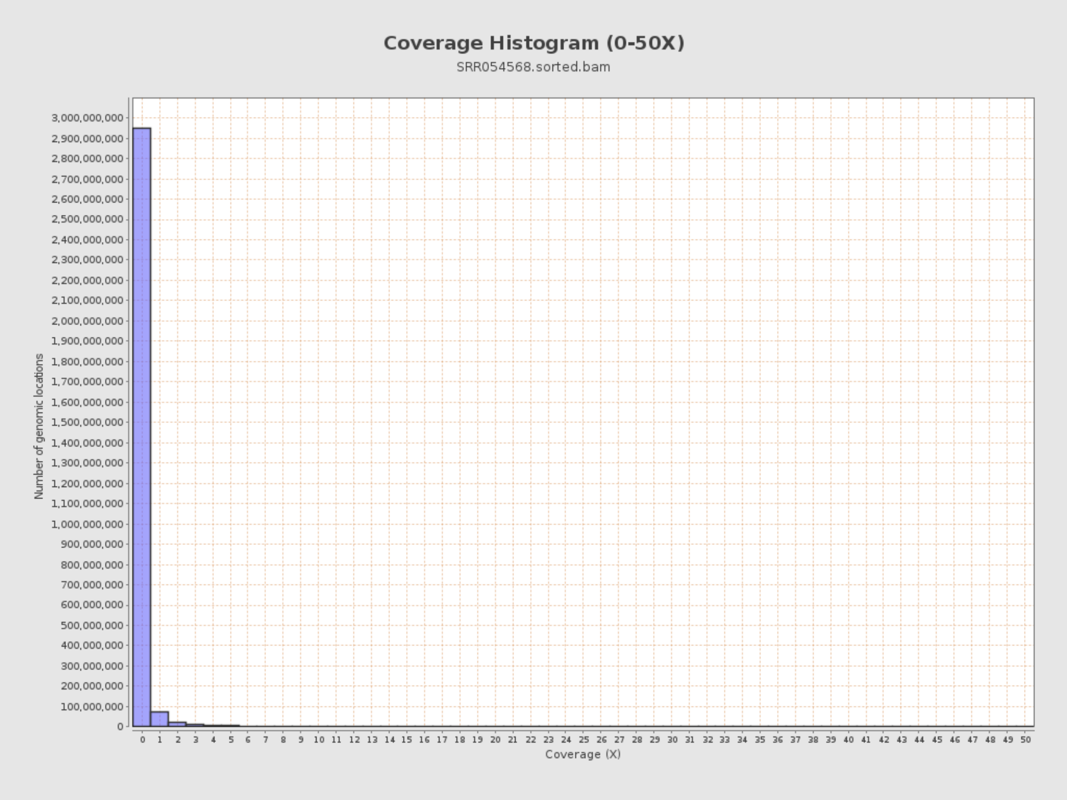
3. Results : Coverage across reference



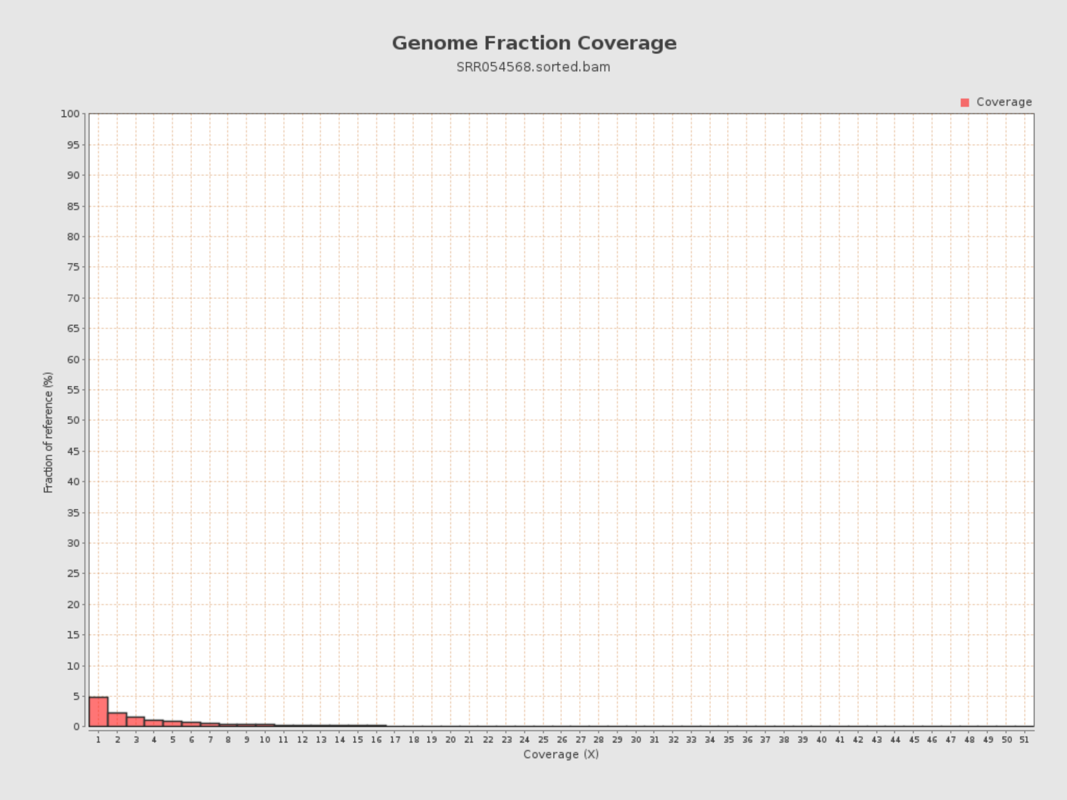
4. Results : Coverage Histogram



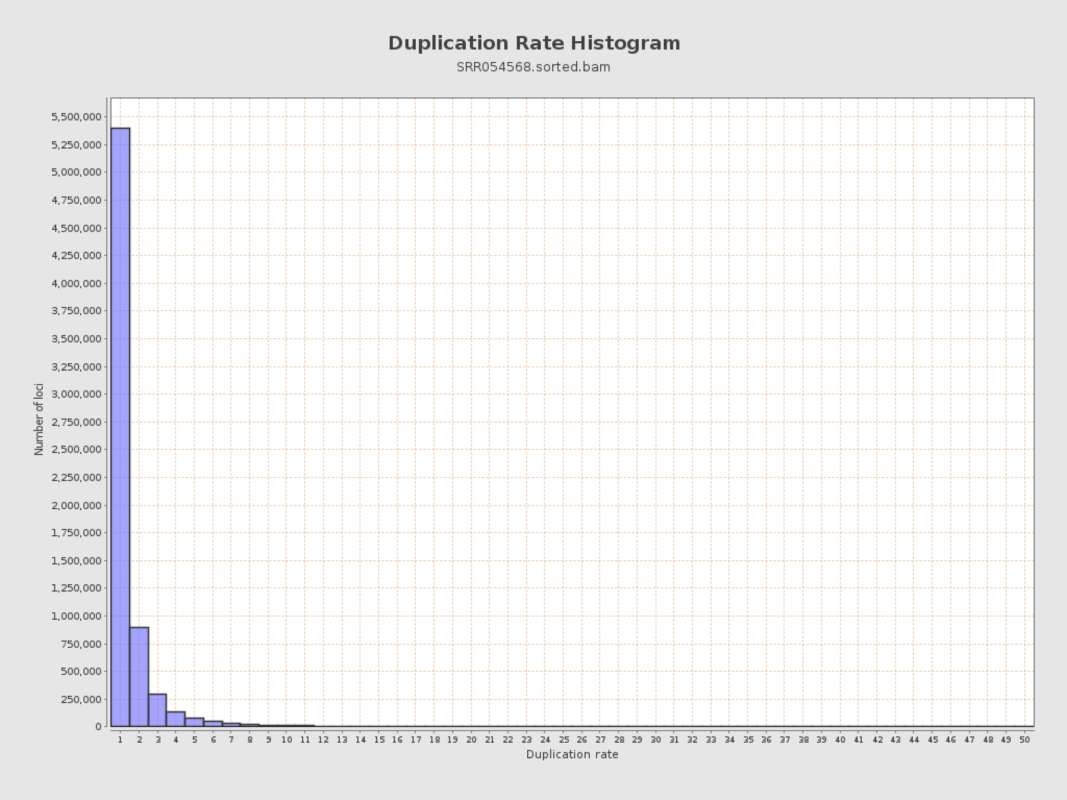
5. Results : Coverage Histogram (0-50X)



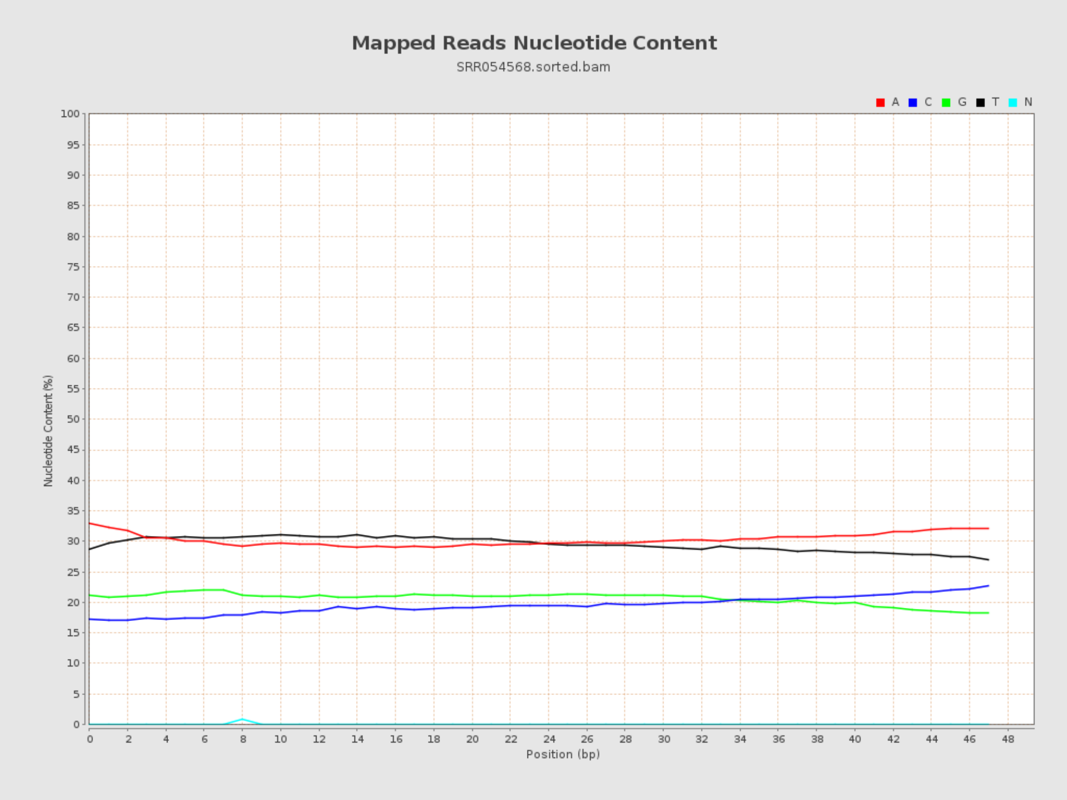
6. Results : Genome Fraction Coverage



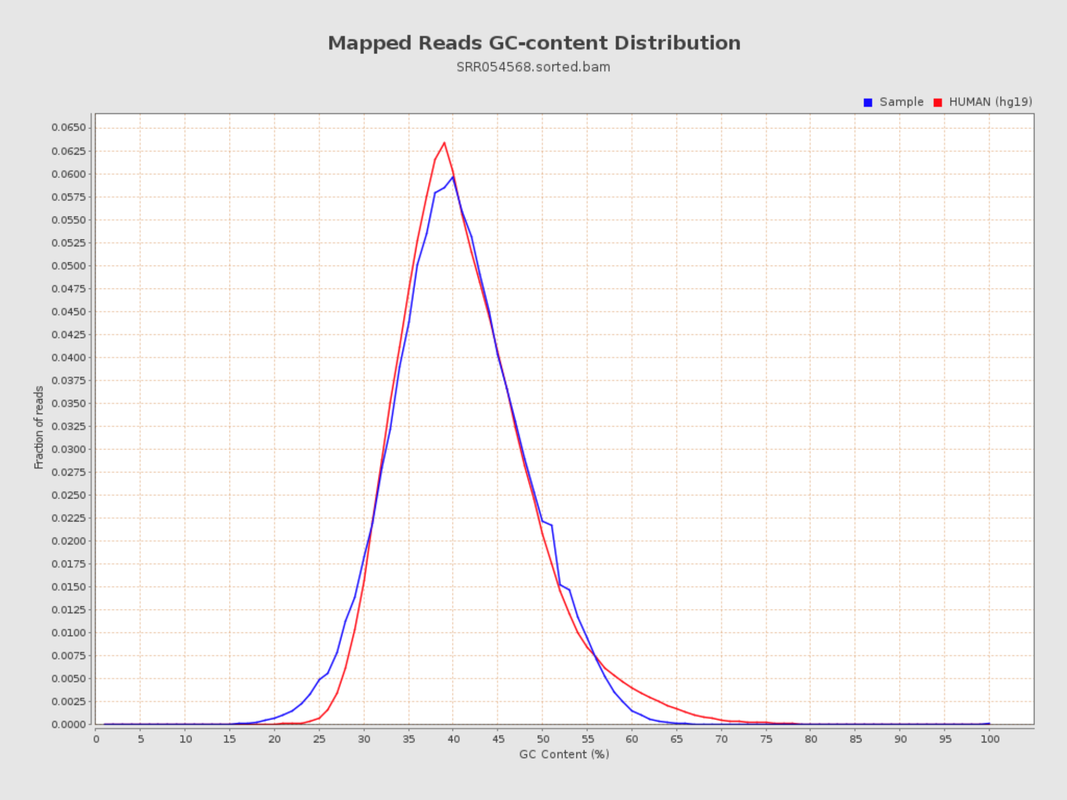
7. Results : Duplication Rate Histogram



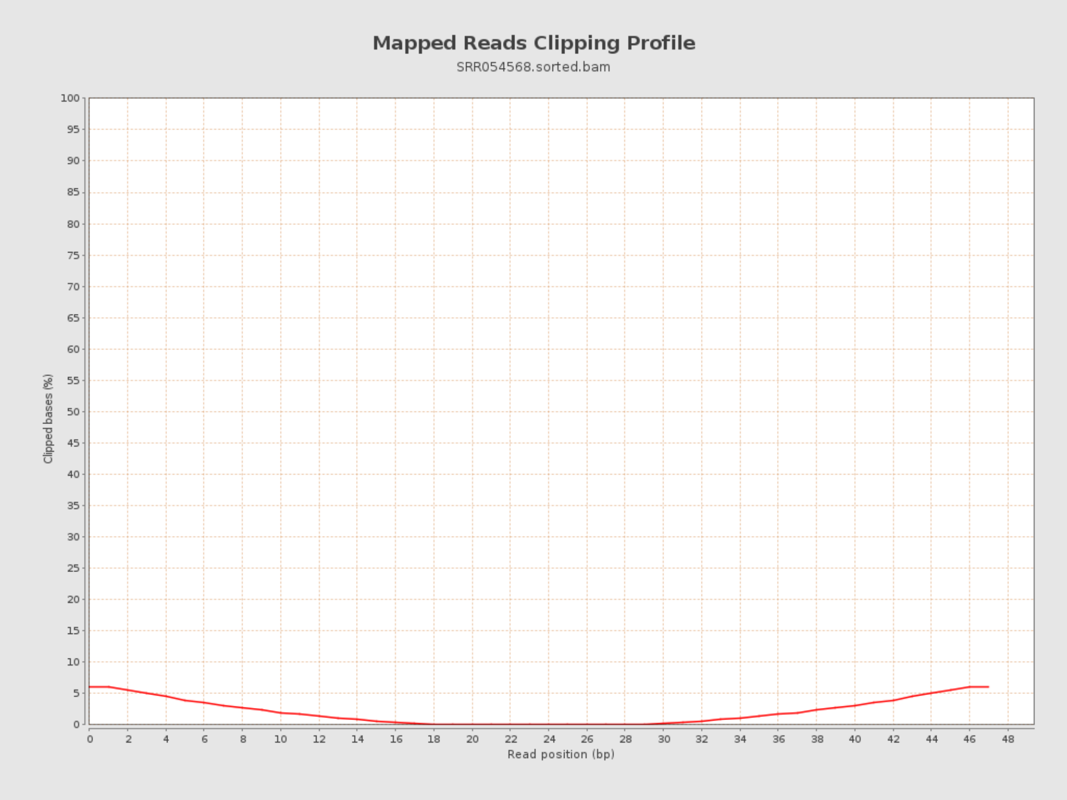
8. Results : Mapped Reads Nucleotide Content



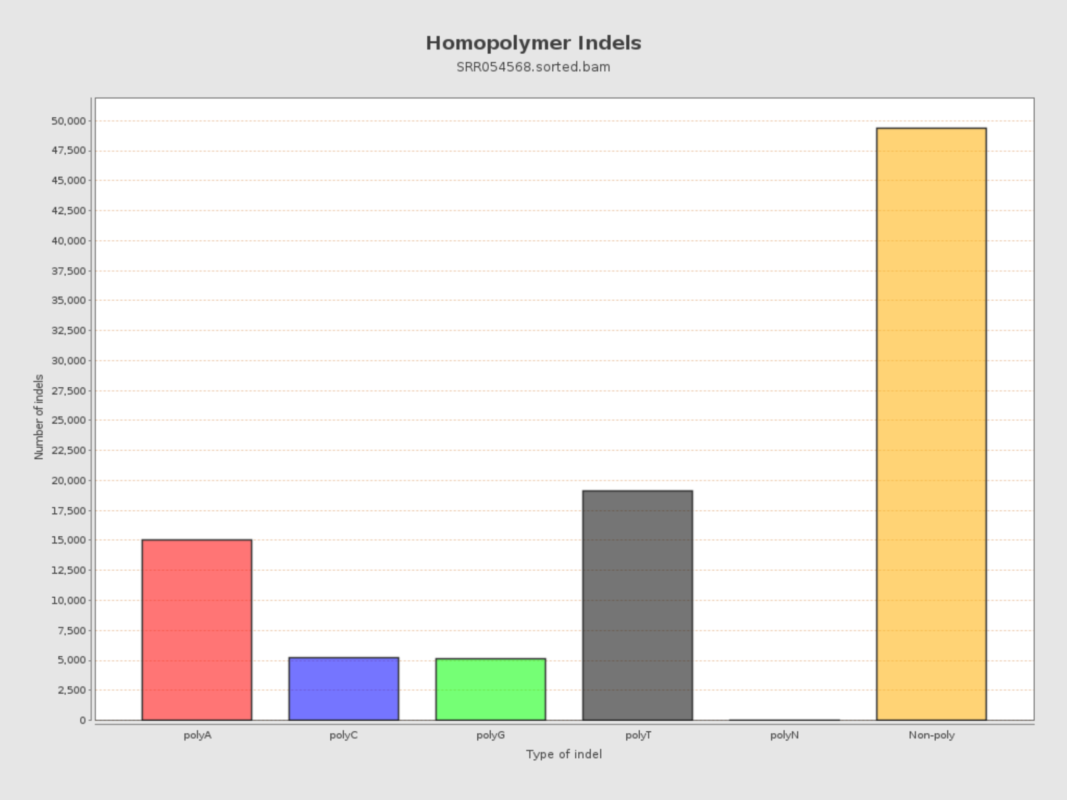
9. Results : Mapped Reads GC-content Distribution



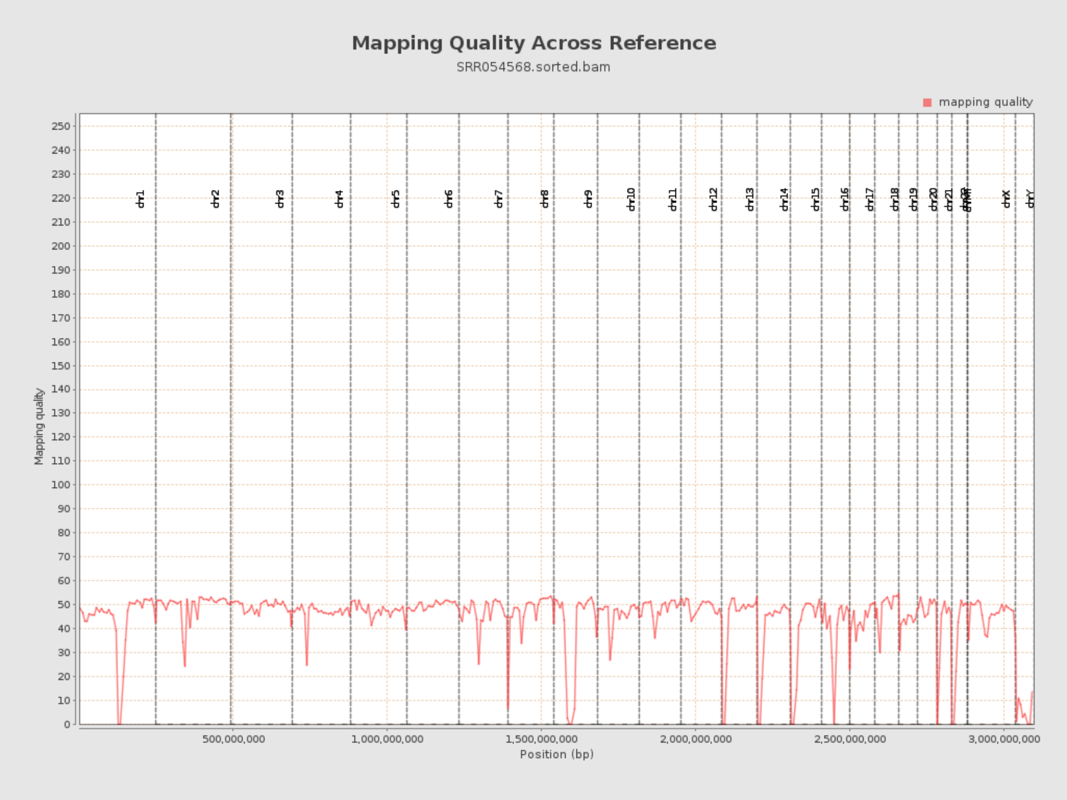
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram