Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 04:57:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054572.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_SRR054572 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054572.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 04:57:17 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054572.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,923,030
Mapped reads	10,155,512 / 72.94%
Unmapped reads	3,767,518 / 27.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	328 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	3,404,531 / 24.45%
Duplication rate	22.68%
Clipped reads	1,212,110 / 8.71%

2.2. ACGT Content

Number/percentage of A's	144,051,318 / 30.24%
Number/percentage of C's	94,701,609 / 19.88%
Number/percentage of T's	138,471,939 / 29.07%
Number/percentage of G's	98,905,536 / 20.76%
Number/percentage of N's	182,125 / 0.04%
GC Percentage	40.65%

2.3. Coverage

Mean	0.1539

Standard Deviation	1.3648

2.4. Mapping Quality

Mean Mapping Quality	44.14

2.5. Mismatches and indels

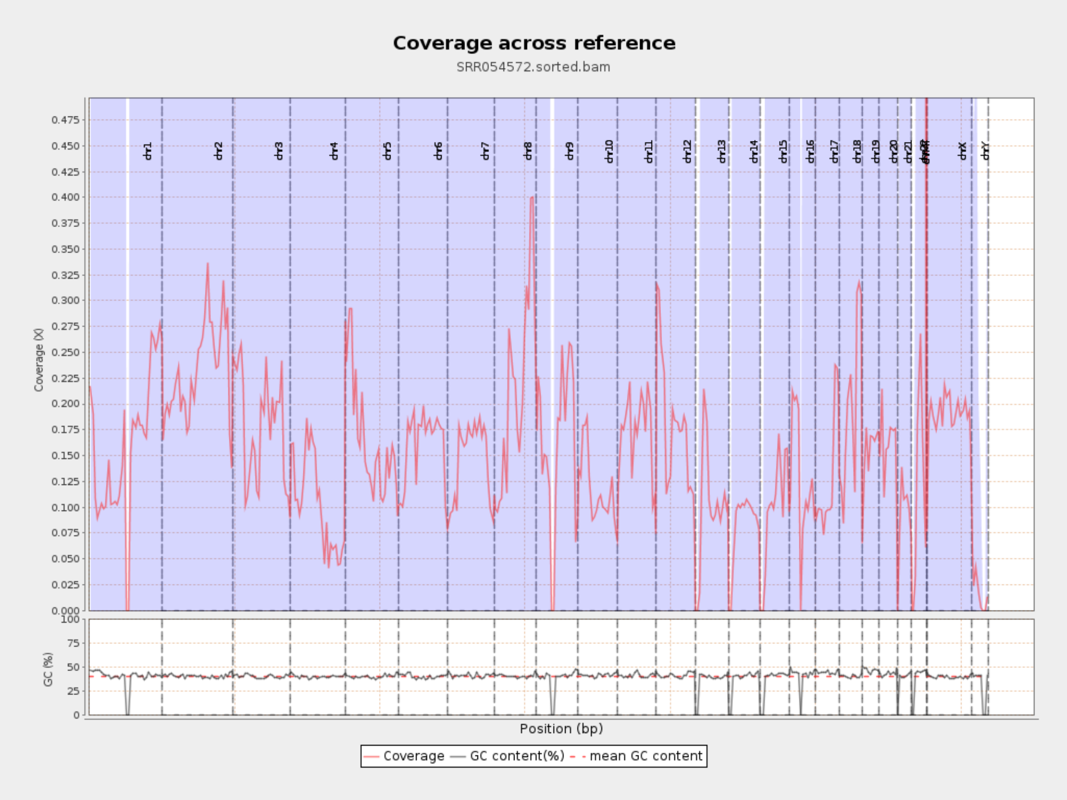
General error rate	0.58%
Mismatches	2,736,807
Insertions	20,985
Mapped reads with at least one insertion	0.21%
Deletions	65,771
Mapped reads with at least one deletion	0.65%
Homopolymer indels	46.73%

2.6. Chromosome stats

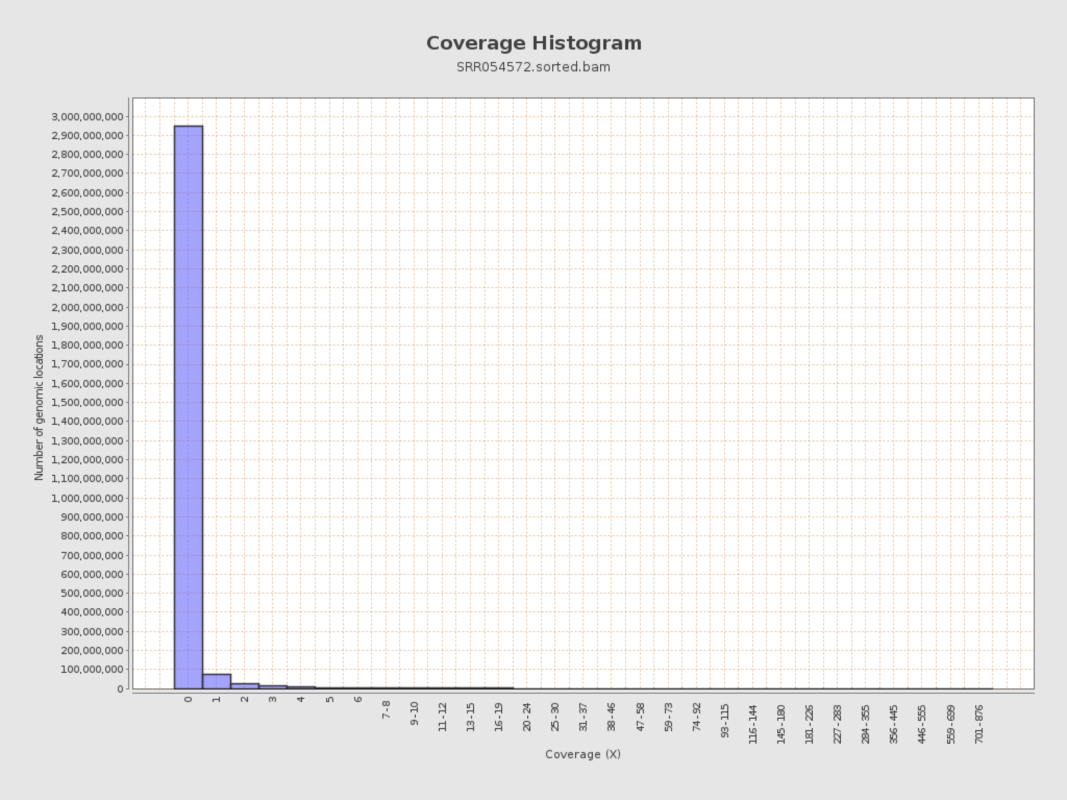
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	38690174	0.1552	1.41
chr2	243199373	56360864	0.2317	1.7994
chr3	198022430	35610963	0.1798	1.4325
chr4	191154276	19647001	0.1028	1.0459
chr5	180915260	29531686	0.1632	1.3664
chr6	171115067	27401717	0.1601	1.4083
chr7	159138663	23268063	0.1462	1.3427

chr8	146364022	31805882	0.2173	1.6996
chr9	141213431	23069943	0.1634	1.3613
chr10	135534747	16188528	0.1194	1.1859
chr11	135006516	23252583	0.1722	1.4538
chr12	133851895	24083038	0.1799	1.422
chr13	115169878	11204828	0.0973	0.9939
chr14	107349540	8790564	0.0819	1.0259
chr15	102531392	10009612	0.0976	0.9759
chr16	90354753	11672674	0.1292	1.1854
chr17	81195210	10369696	0.1277	1.1484
chr18	78077248	15179679	0.1944	1.5833
chr19	59128983	9259163	0.1566	1.4084
chr20	63025520	10197396	0.1618	1.3518
chr21	48129895	4496244	0.0934	1.0027
chr22	51304566	5855888	0.1141	1.101
chrMT	16571	90583	5.4664	11.9402
chrX	155270560	29340716	0.189	1.5207
chrY	59373566	1033078	0.0174	0.3612

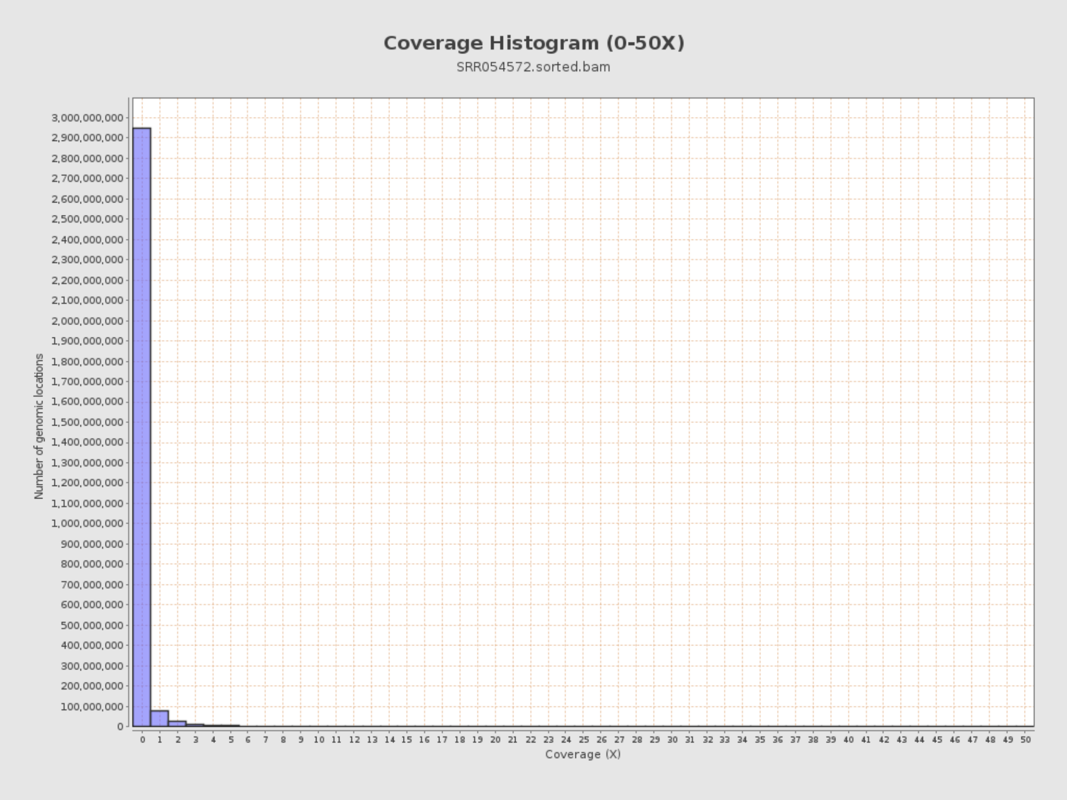
3. Results : Coverage across reference



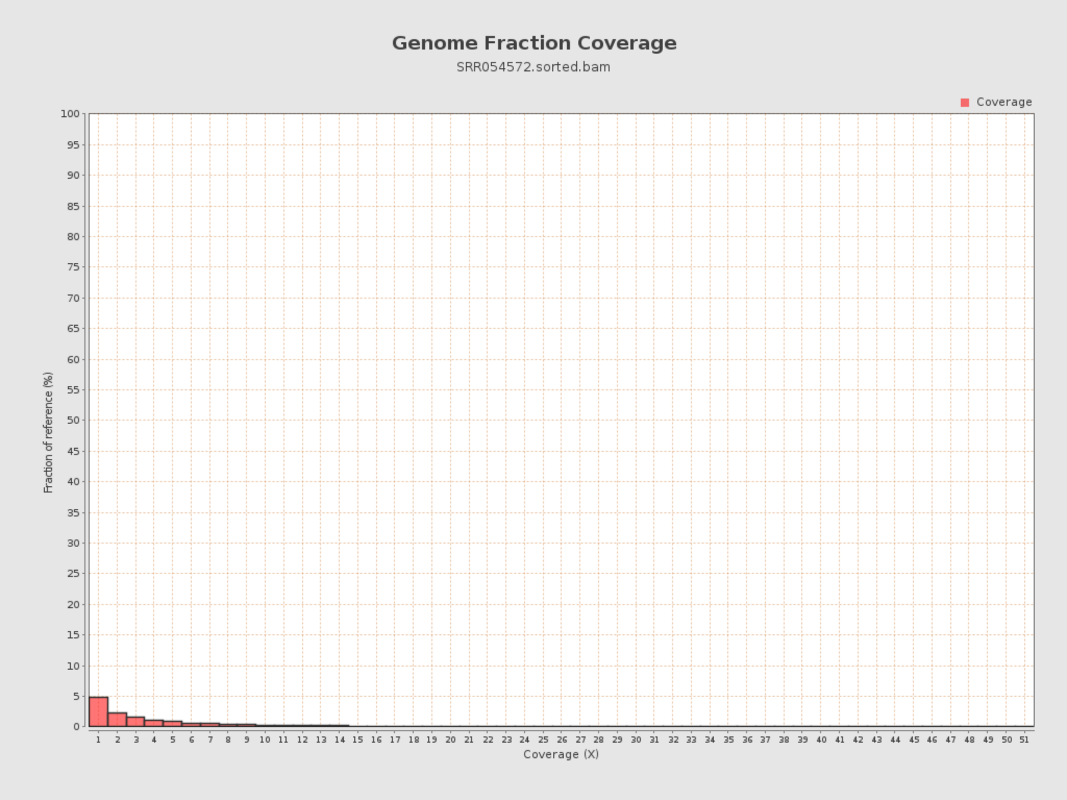
4. Results : Coverage Histogram



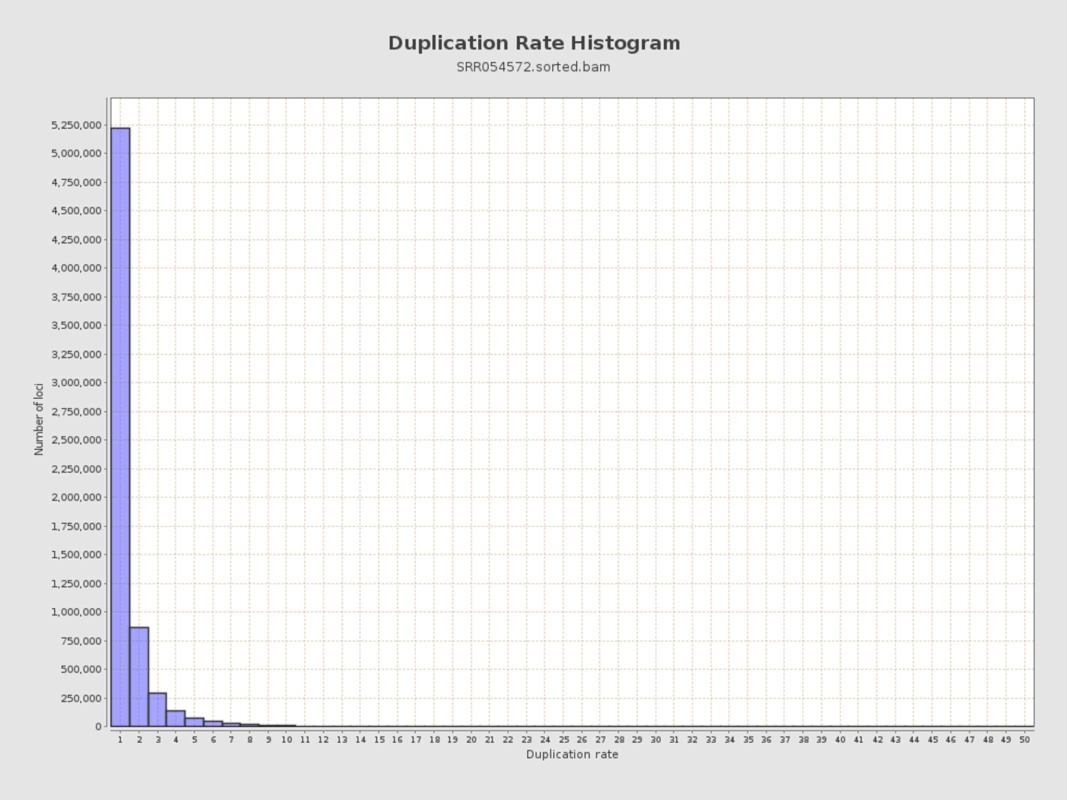
5. Results : Coverage Histogram (0-50X)



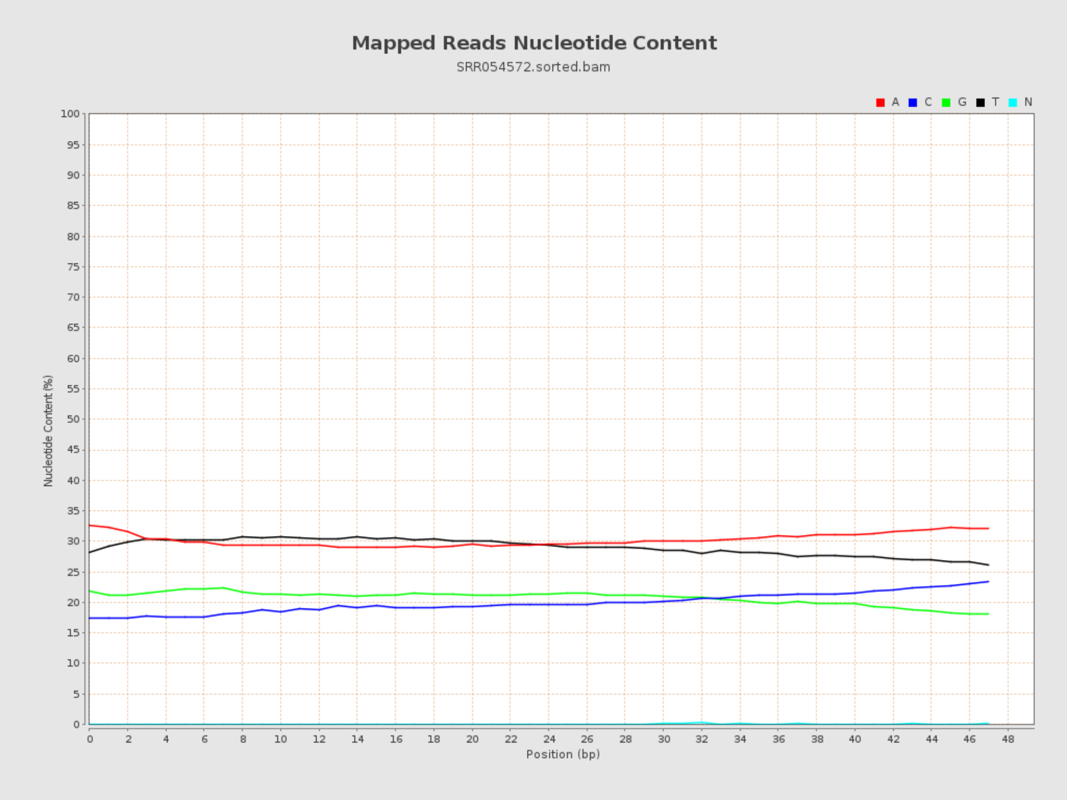
6. Results : Genome Fraction Coverage



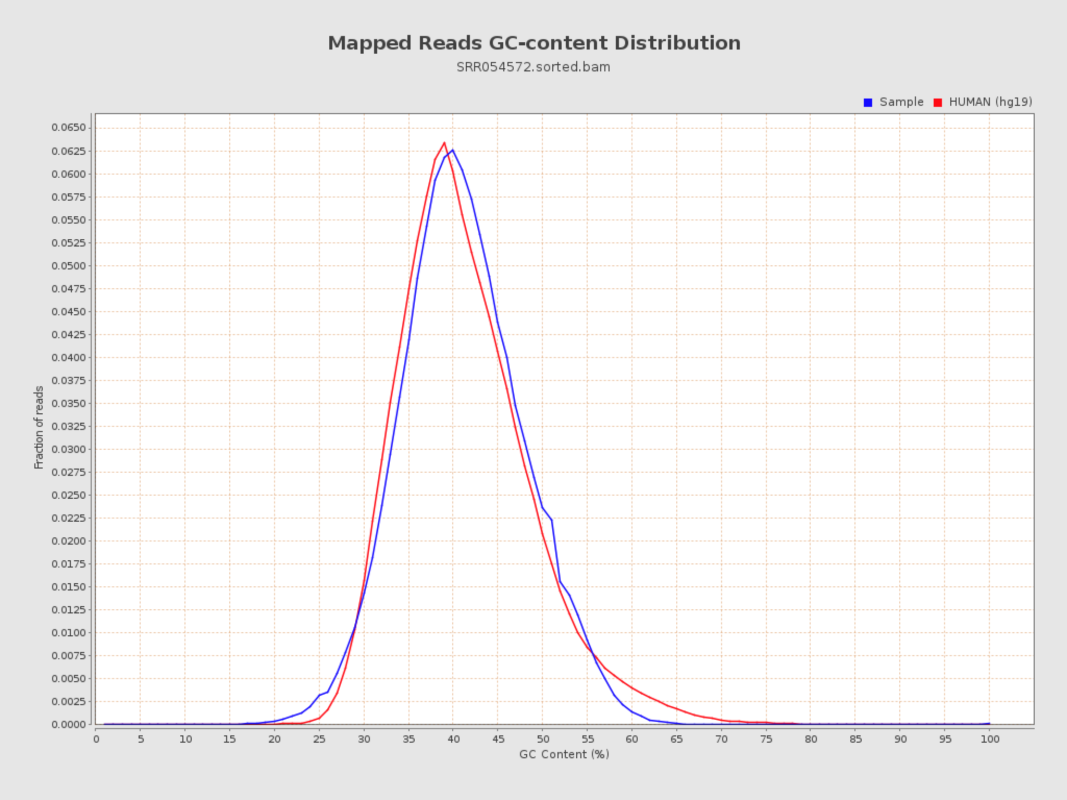
7. Results : Duplication Rate Histogram



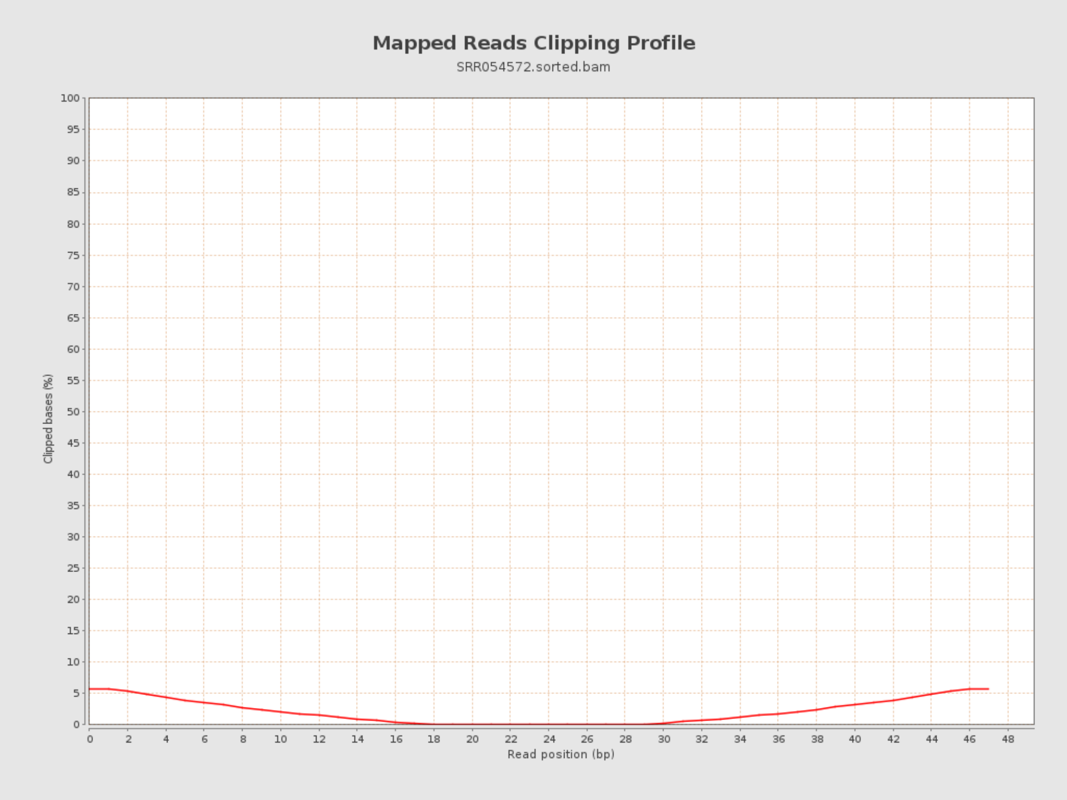
8. Results : Mapped Reads Nucleotide Content



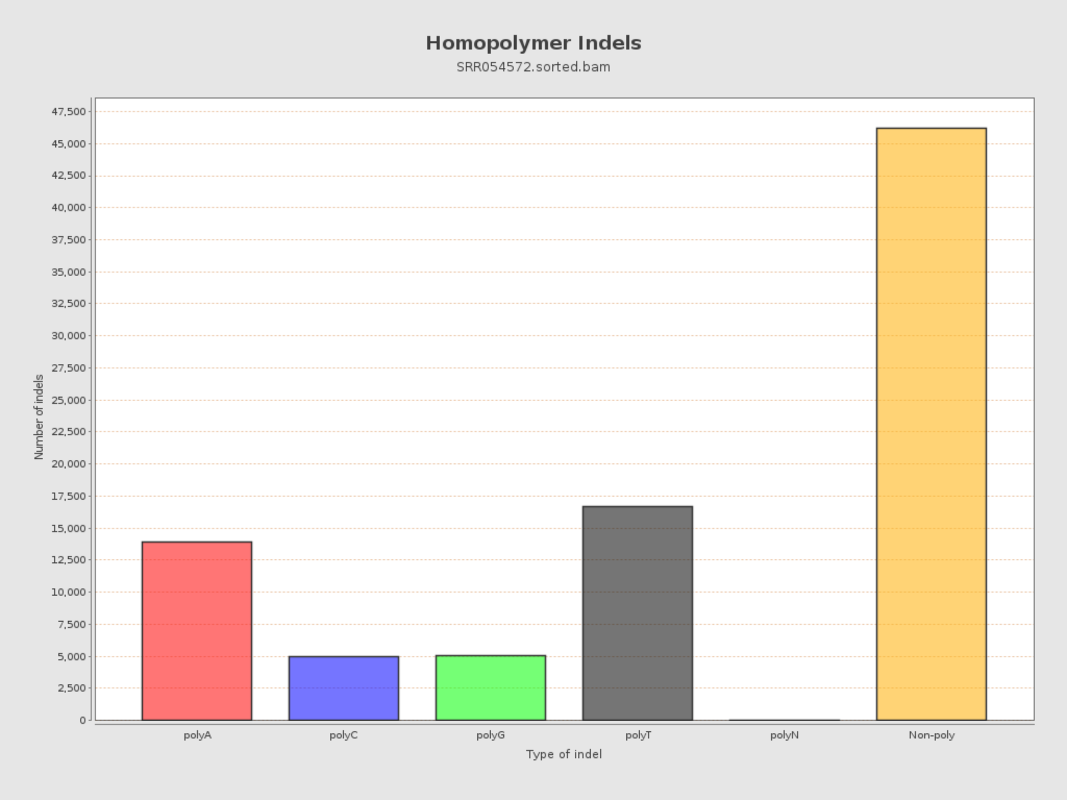
9. Results : Mapped Reads GC-content Distribution



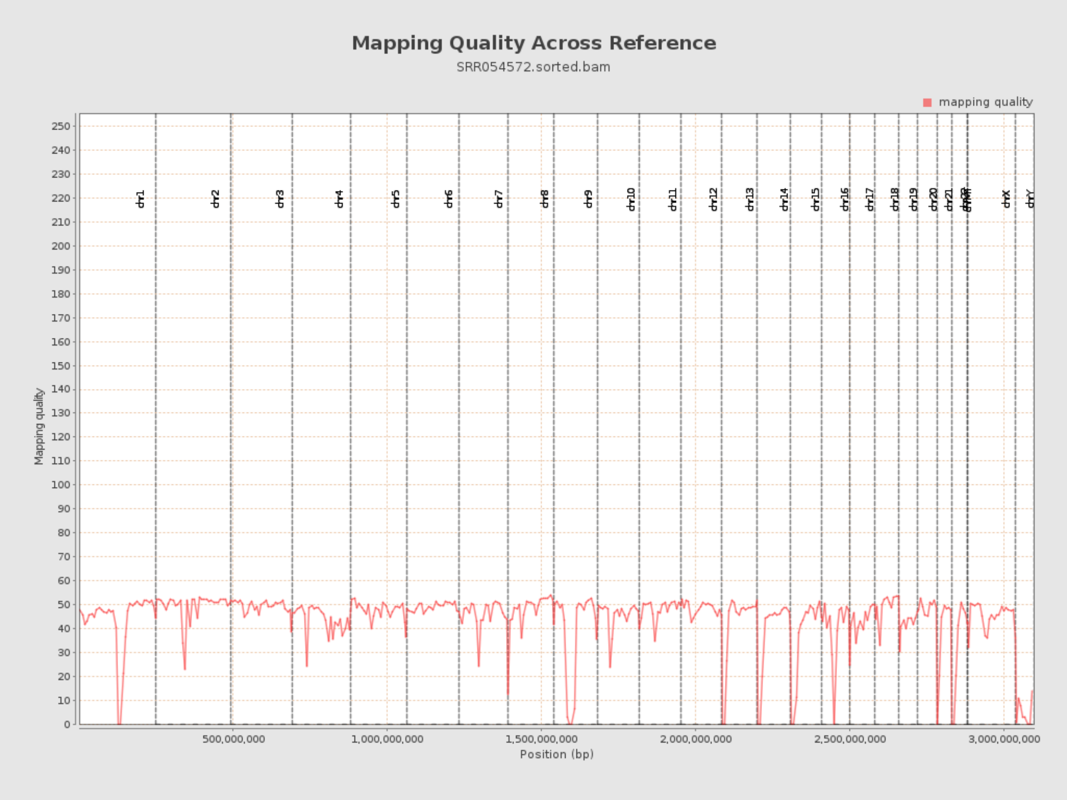
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram