Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 23:58:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053618.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_SRR053618 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053618.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 23:58:27 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053618.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,938,923
Mapped reads	6,670,765 / 84.03%
Unmapped reads	1,268,158 / 15.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	189 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,289,646 / 16.24%
Duplication rate	14.42%
Clipped reads	523,913 / 6.6%

2.2. ACGT Content

Number/percentage of A's	92,151,519 / 29.21%
Number/percentage of C's	62,087,930 / 19.68%
Number/percentage of T's	92,775,229 / 29.41%
Number/percentage of G's	68,464,507 / 21.7%
Number/percentage of N's	6,279 / 0%
GC Percentage	41.38%

2.3. Coverage

Mean	0.1019

Standard Deviation	0.7373

2.4. Mapping Quality

Mean Mapping Quality	46.09

2.5. Mismatches and indels

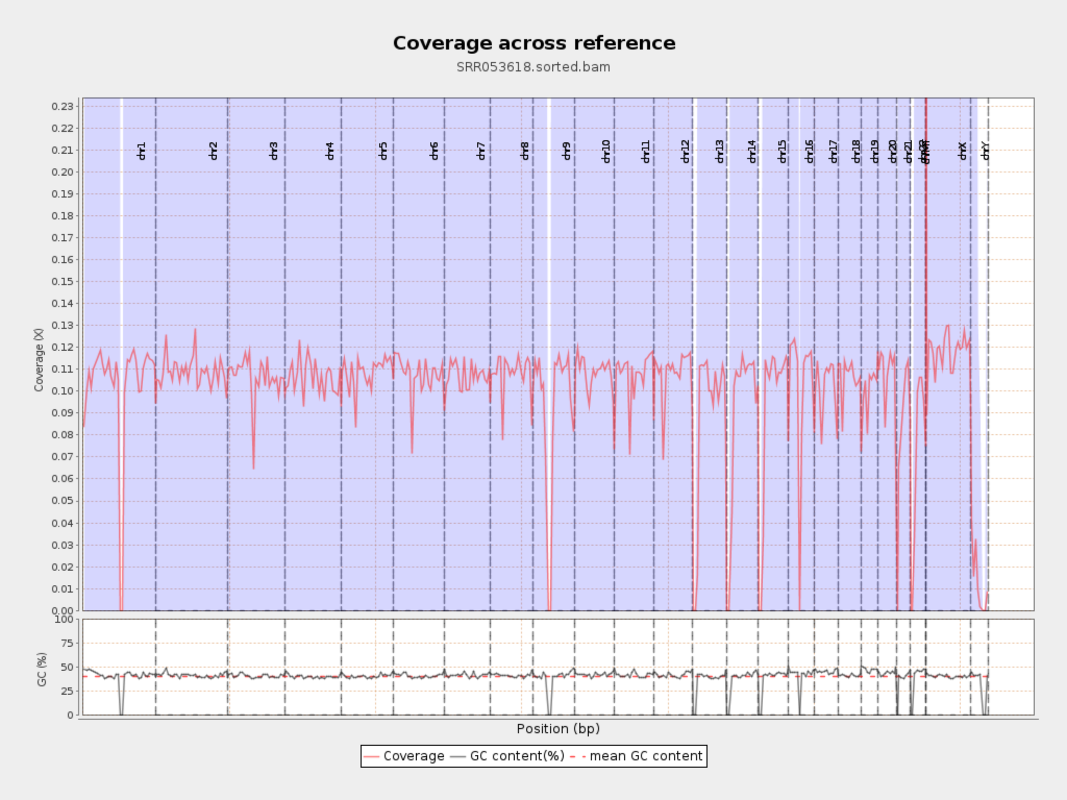
General error rate	0.52%
Mismatches	1,626,728
Insertions	12,042
Mapped reads with at least one insertion	0.18%
Deletions	42,548
Mapped reads with at least one deletion	0.64%
Homopolymer indels	47.27%

2.6. Chromosome stats

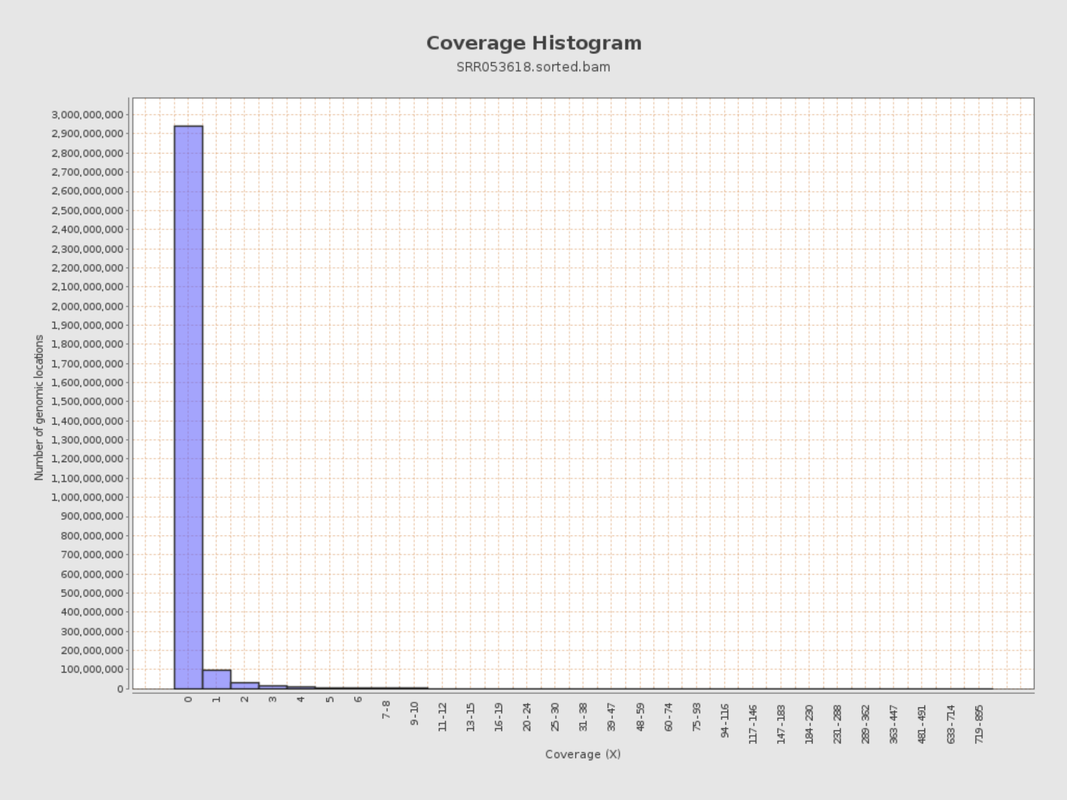
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25581320	0.1026	0.789
chr2	243199373	26510545	0.109	0.9953
chr3	198022430	21061603	0.1064	0.679
chr4	191154276	20404695	0.1067	0.7159
chr5	180915260	19646491	0.1086	0.6938
chr6	171115067	18400734	0.1075	0.727
chr7	159138663	17030015	0.107	0.7698

chr8	146364022	15818679	0.1081	0.7359
chr9	141213431	13035118	0.0923	0.6533
chr10	135534747	14785962	0.1091	0.7668
chr11	135006516	14509948	0.1075	0.7532
chr12	133851895	14634313	0.1093	0.7048
chr13	115169878	10119219	0.0879	0.6392
chr14	107349540	9684103	0.0902	0.678
chr15	102531392	9171693	0.0895	0.6287
chr16	90354753	9089604	0.1006	0.6874
chr17	81195210	8328517	0.1026	0.6776
chr18	78077248	8302308	0.1063	0.7639
chr19	59128983	5930627	0.1003	0.7541
chr20	63025520	6812899	0.1081	0.7139
chr21	48129895	4052102	0.0842	0.6821
chr22	51304566	3553035	0.0693	0.5412
chrMT	16571	14543	0.8776	2.0506
chrX	155270560	18332175	0.1181	0.7728
chrY	59373566	739169	0.0124	0.2686

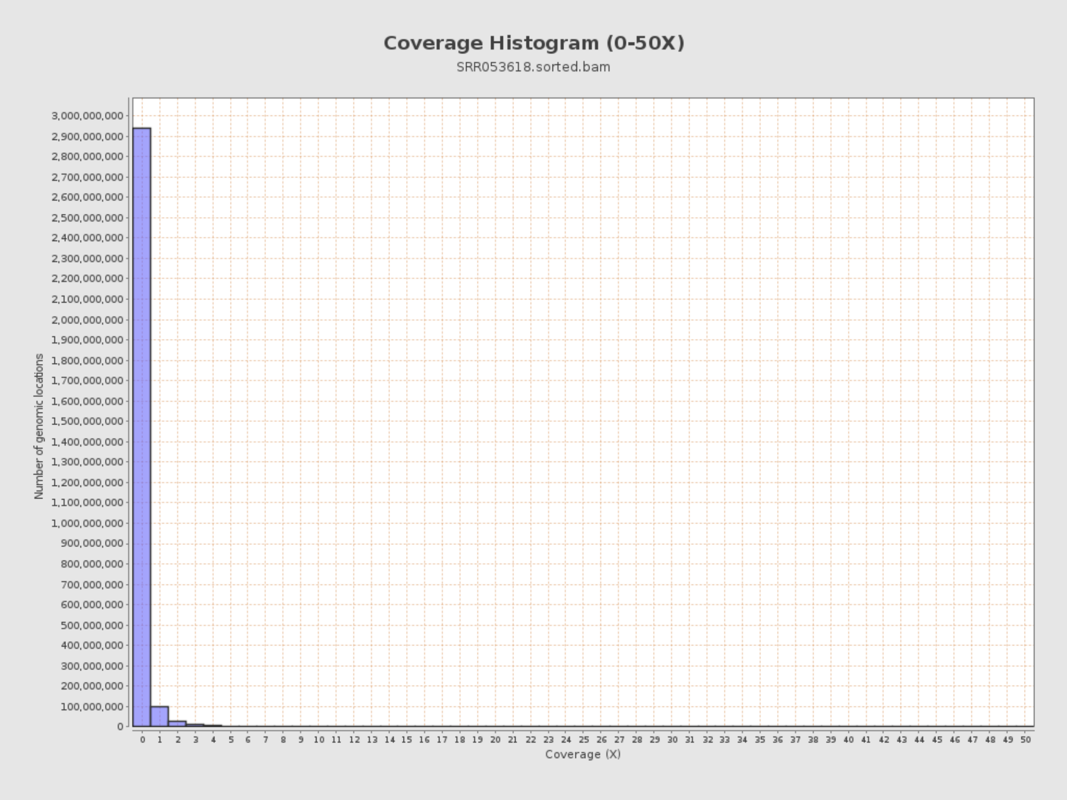
3. Results : Coverage across reference



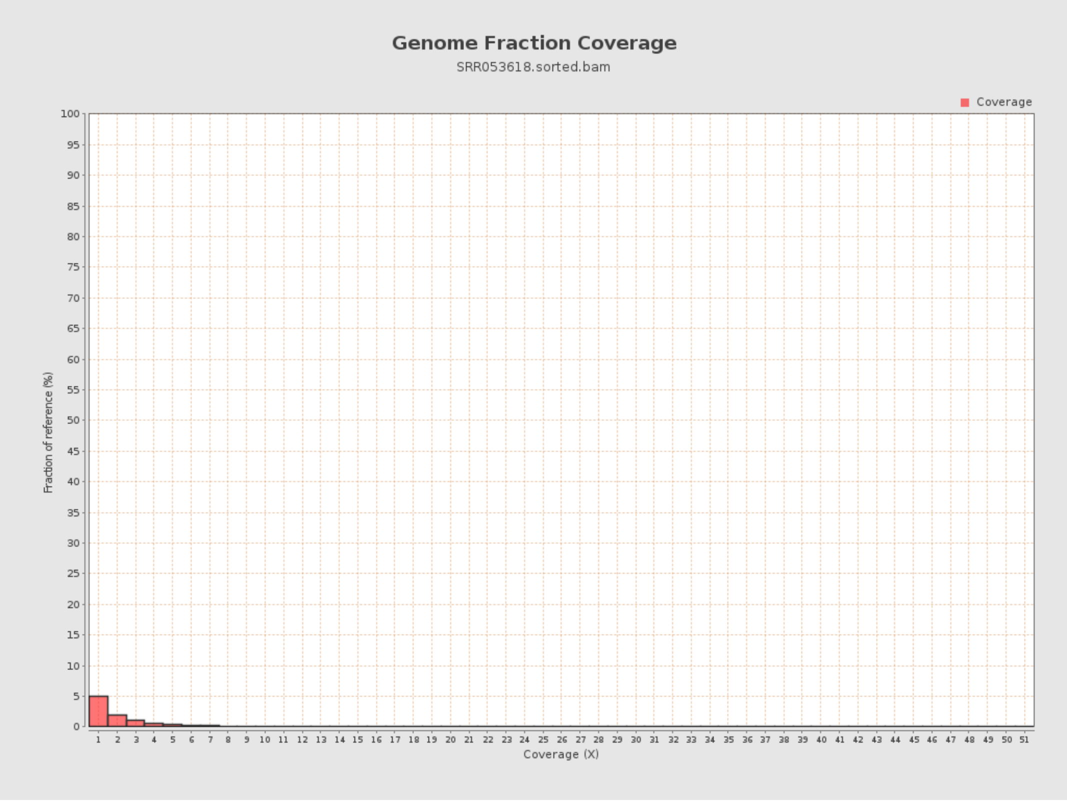
4. Results : Coverage Histogram



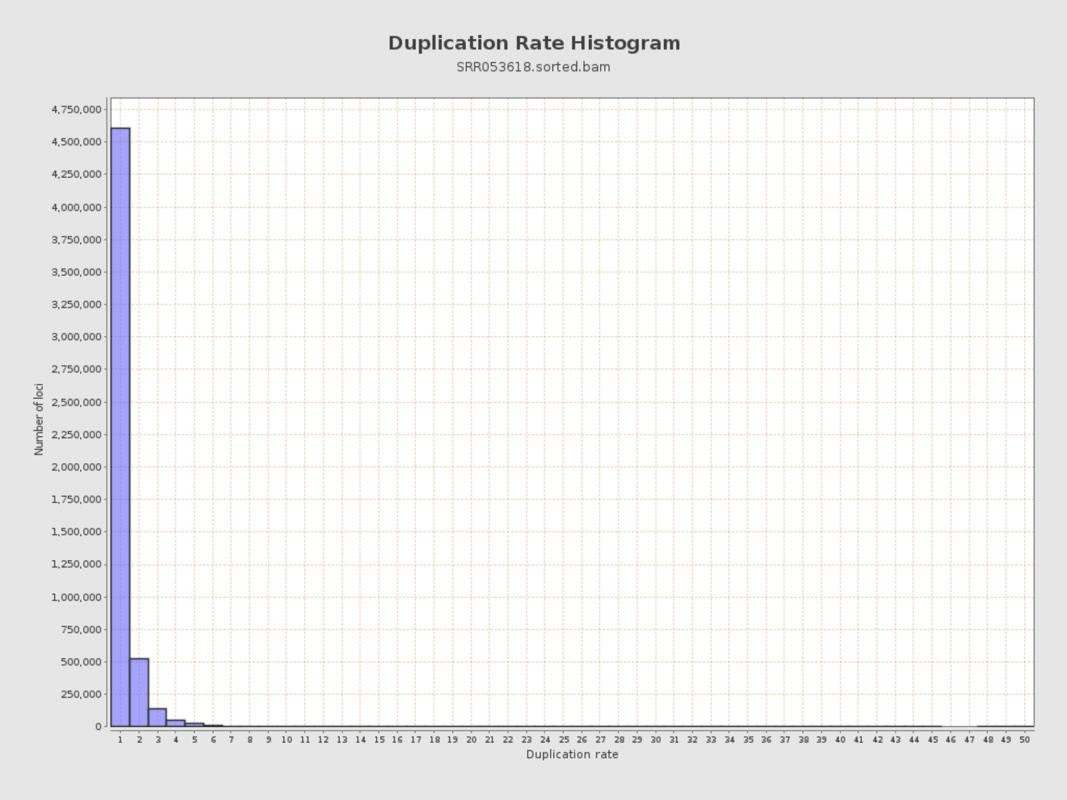
5. Results : Coverage Histogram (0-50X)



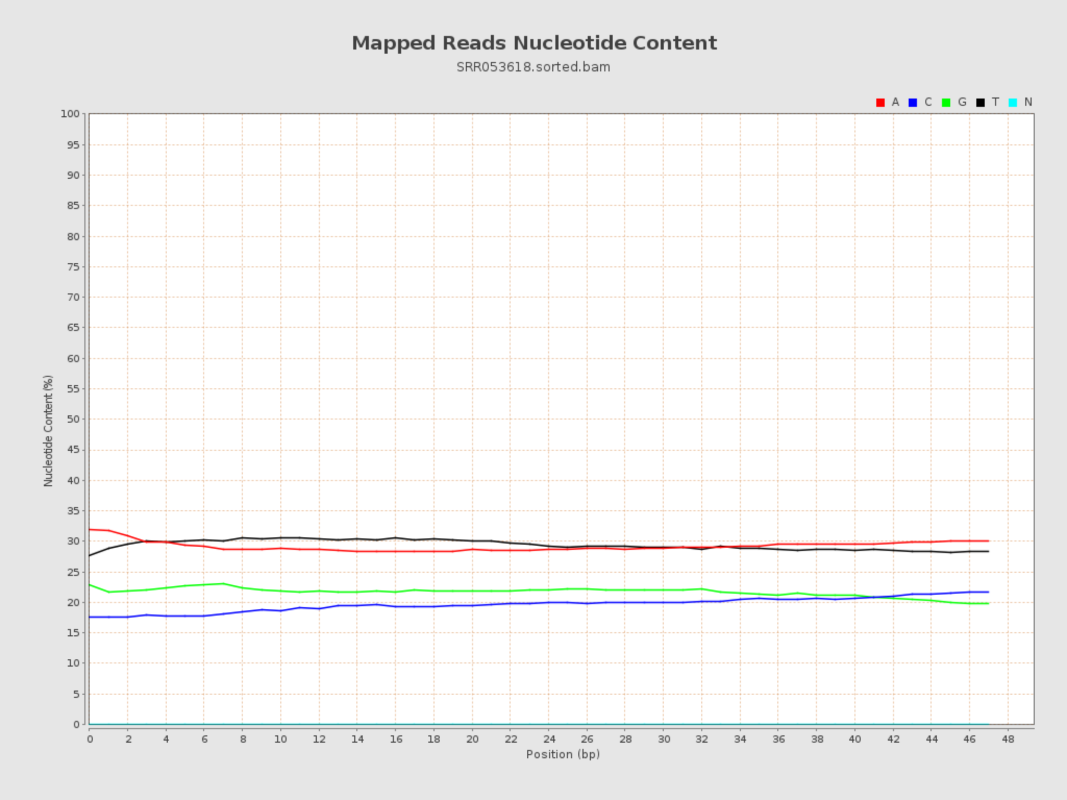
6. Results : Genome Fraction Coverage



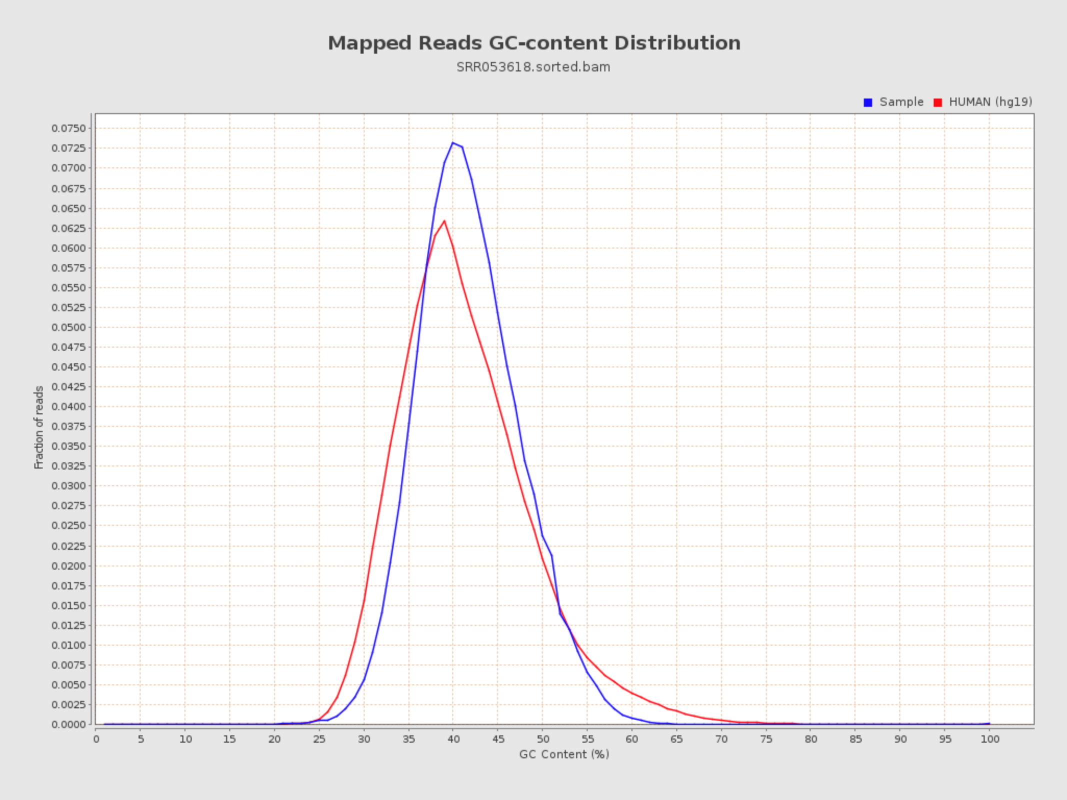
7. Results : Duplication Rate Histogram



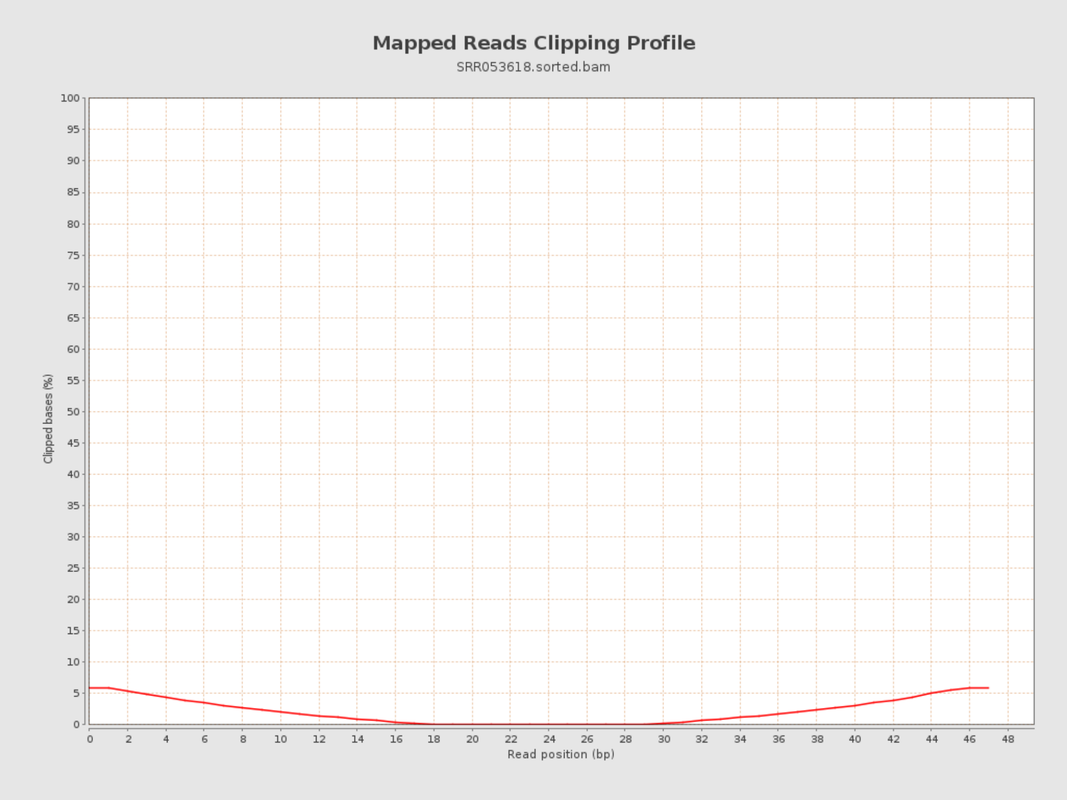
8. Results : Mapped Reads Nucleotide Content



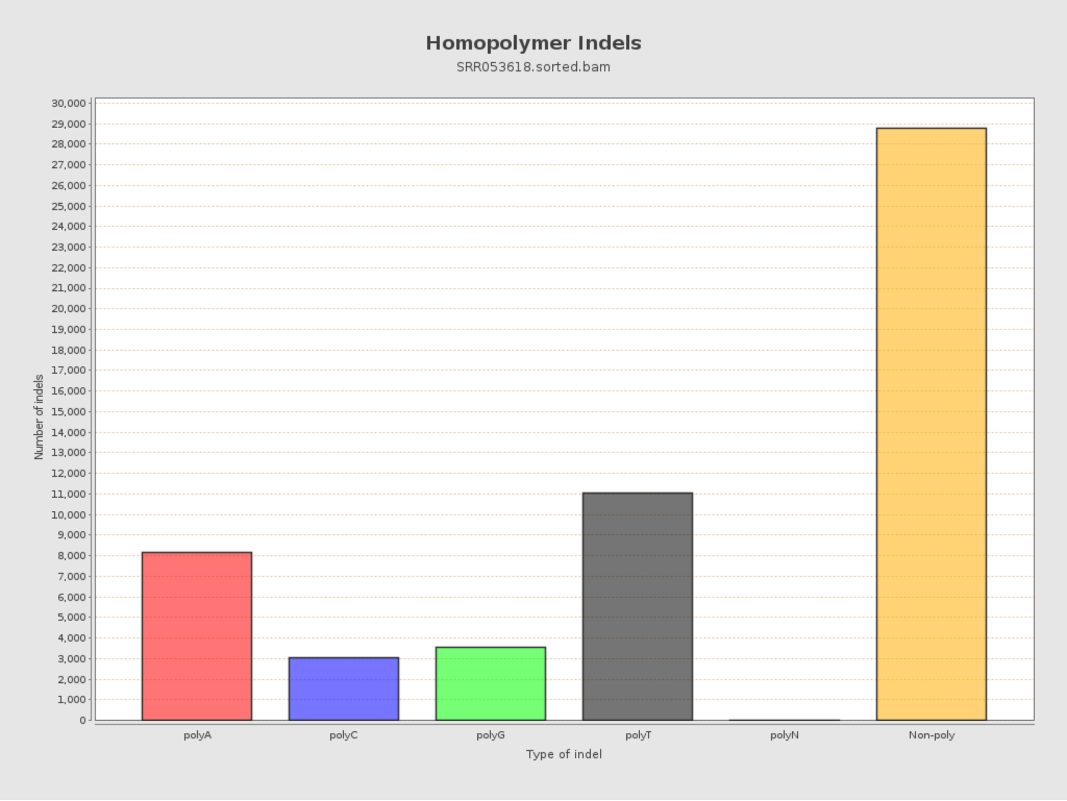
9. Results : Mapped Reads GC-content Distribution



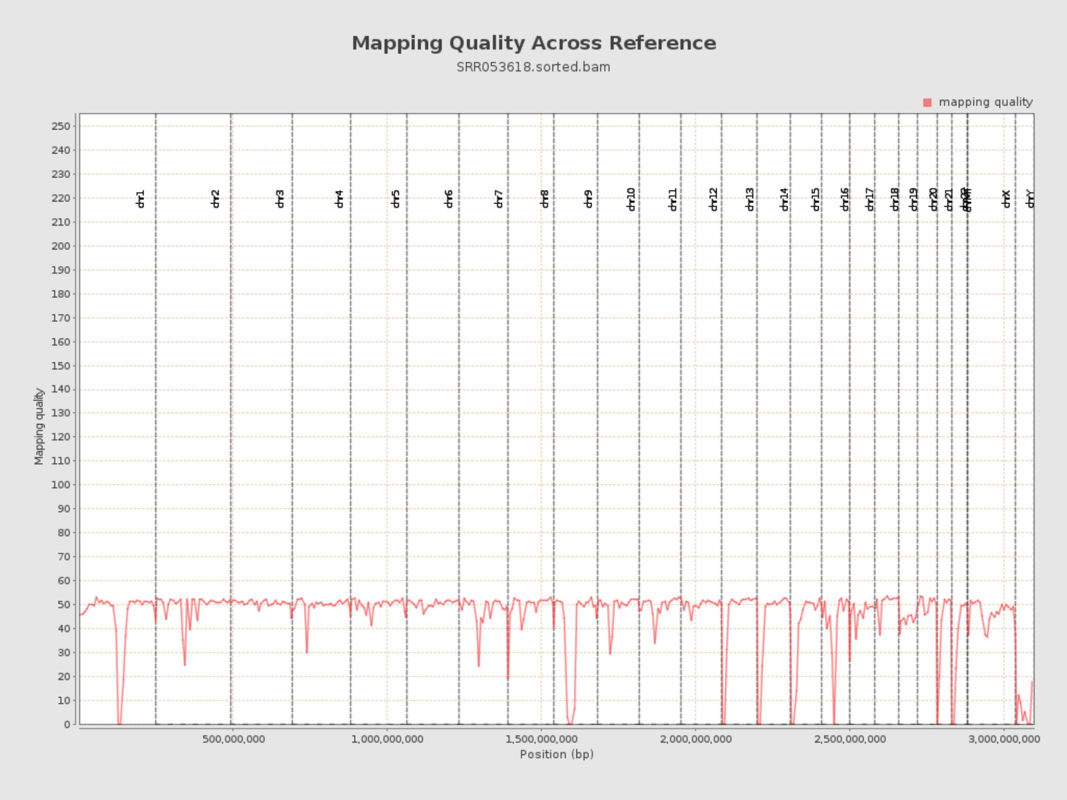
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram