Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 02:49:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053672.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_SRR053672 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053672.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 02:49:05 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053672.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,264,175
Mapped reads	5,674,824 / 78.12%
Unmapped reads	1,589,351 / 21.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	167 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,093,412 / 15.05%
Duplication rate	13.43%
Clipped reads	787,775 / 10.84%

2.2. ACGT Content

Number/percentage of A's	79,246,905 / 29.9%
Number/percentage of C's	54,160,711 / 20.44%
Number/percentage of T's	75,562,488 / 28.51%
Number/percentage of G's	55,903,215 / 21.09%
Number/percentage of N's	163,613 / 0.06%
GC Percentage	41.53%

2.3. Coverage

Mean	0.0856

Standard Deviation	0.6753

2.4. Mapping Quality

Mean Mapping Quality	44.4

2.5. Mismatches and indels

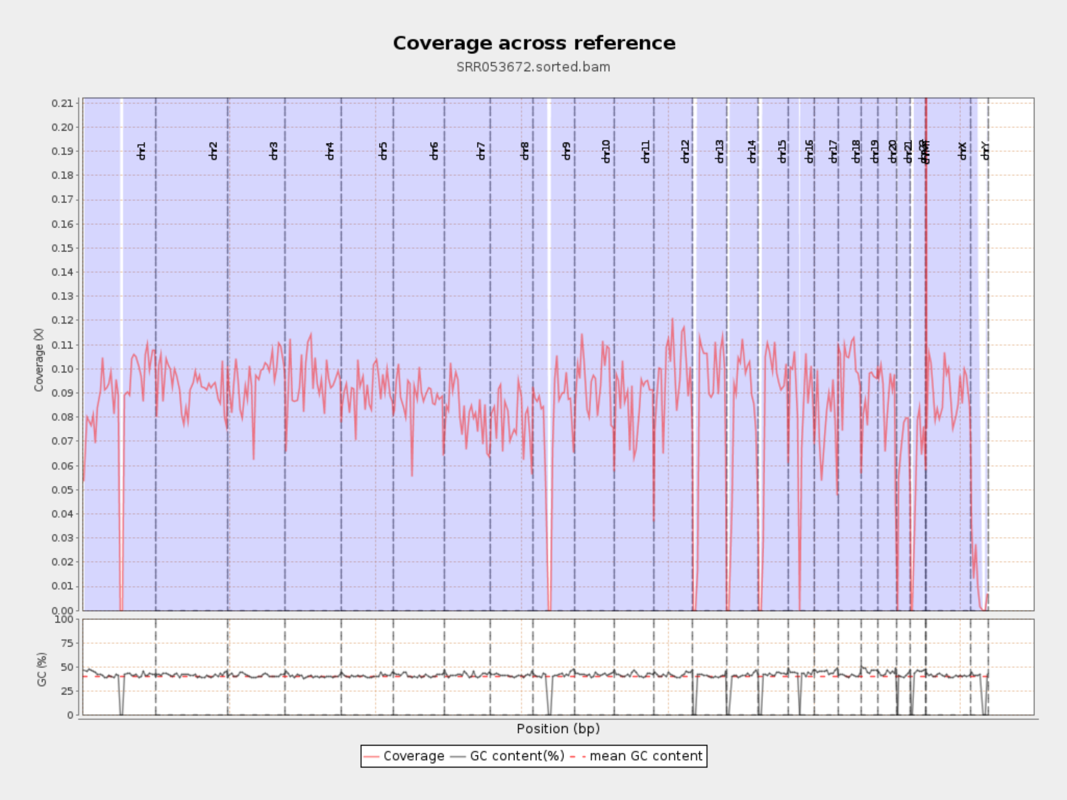
General error rate	0.71%
Mismatches	1,872,830
Insertions	12,544
Mapped reads with at least one insertion	0.22%
Deletions	36,433
Mapped reads with at least one deletion	0.64%
Homopolymer indels	44.28%

2.6. Chromosome stats

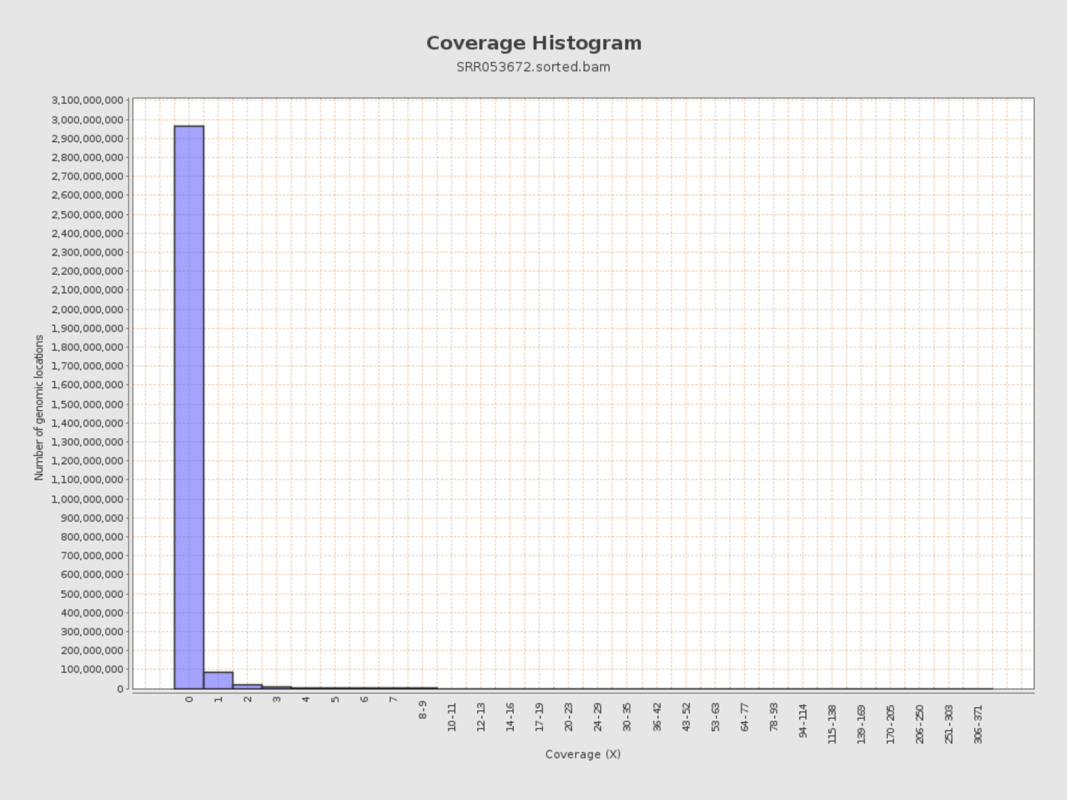
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21520189	0.0863	0.7118
chr2	243199373	22420553	0.0922	0.7351
chr3	198022430	18951068	0.0957	0.6953
chr4	191154276	18155337	0.095	0.7132
chr5	180915260	16470882	0.091	0.6718
chr6	171115067	15074989	0.0881	0.6739
chr7	159138663	12937481	0.0813	0.6711

chr8	146364022	11487142	0.0785	0.6429
chr9	141213431	10700747	0.0758	0.6248
chr10	135534747	12953123	0.0956	0.6995
chr11	135006516	11714624	0.0868	0.6901
chr12	133851895	13164675	0.0984	0.7099
chr13	115169878	9726298	0.0845	0.6504
chr14	107349540	8535909	0.0795	0.6811
chr15	102531392	8312087	0.0811	0.6238
chr16	90354753	7438404	0.0823	0.6599
chr17	81195210	6378692	0.0786	0.5966
chr18	78077248	7977966	0.1022	0.7649
chr19	59128983	5289928	0.0895	0.7035
chr20	63025520	5552393	0.0881	0.6678
chr21	48129895	3018776	0.0627	0.5963
chr22	51304566	2691467	0.0525	0.5001
chrMT	16571	10575	0.6382	1.883
chrX	155270560	13968441	0.09	0.686
chrY	59373566	636843	0.0107	0.223

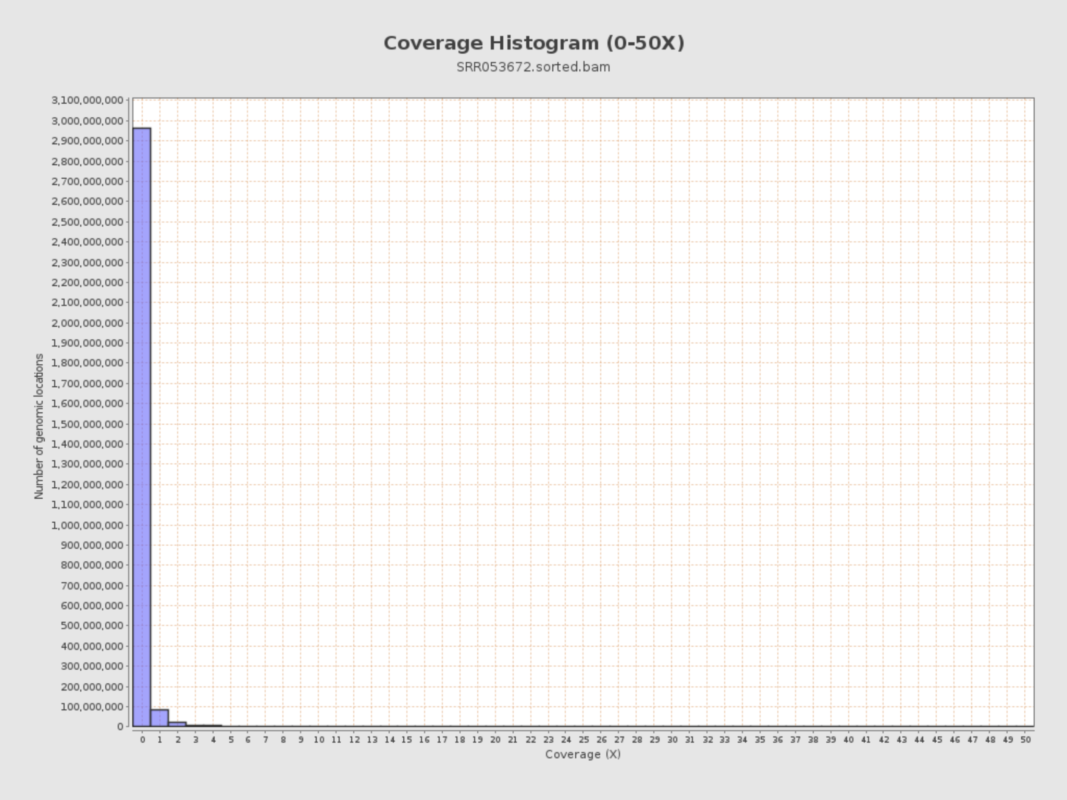
3. Results : Coverage across reference



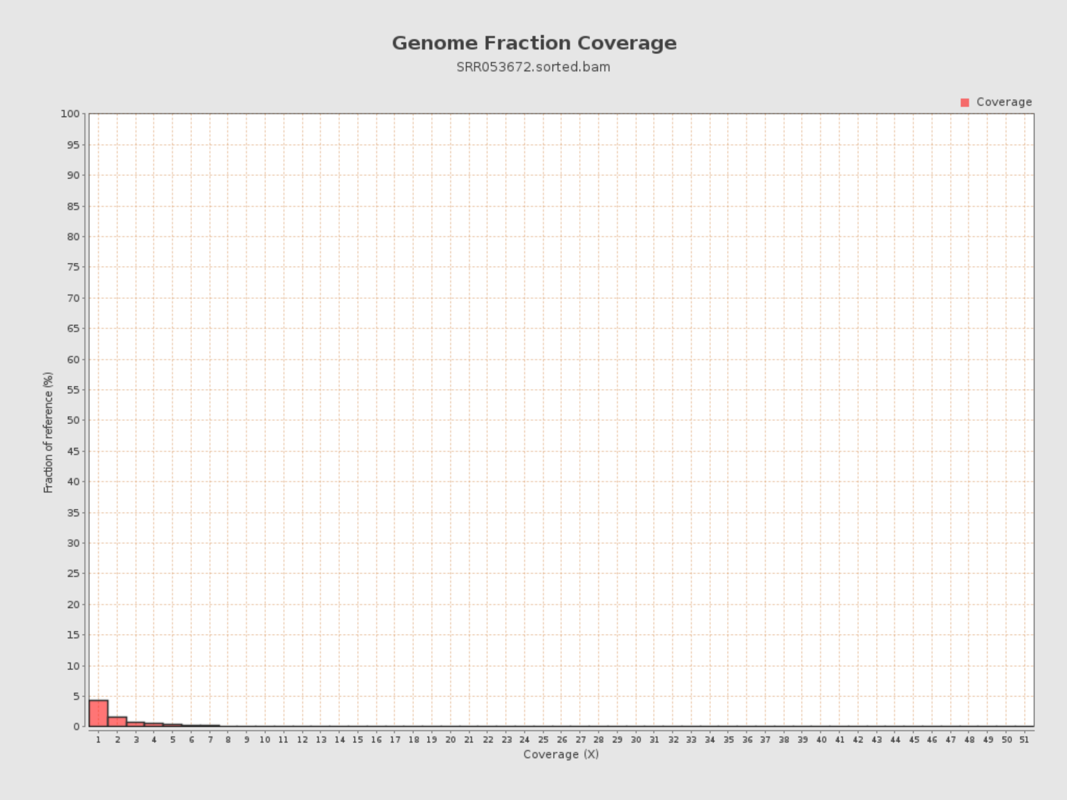
4. Results : Coverage Histogram



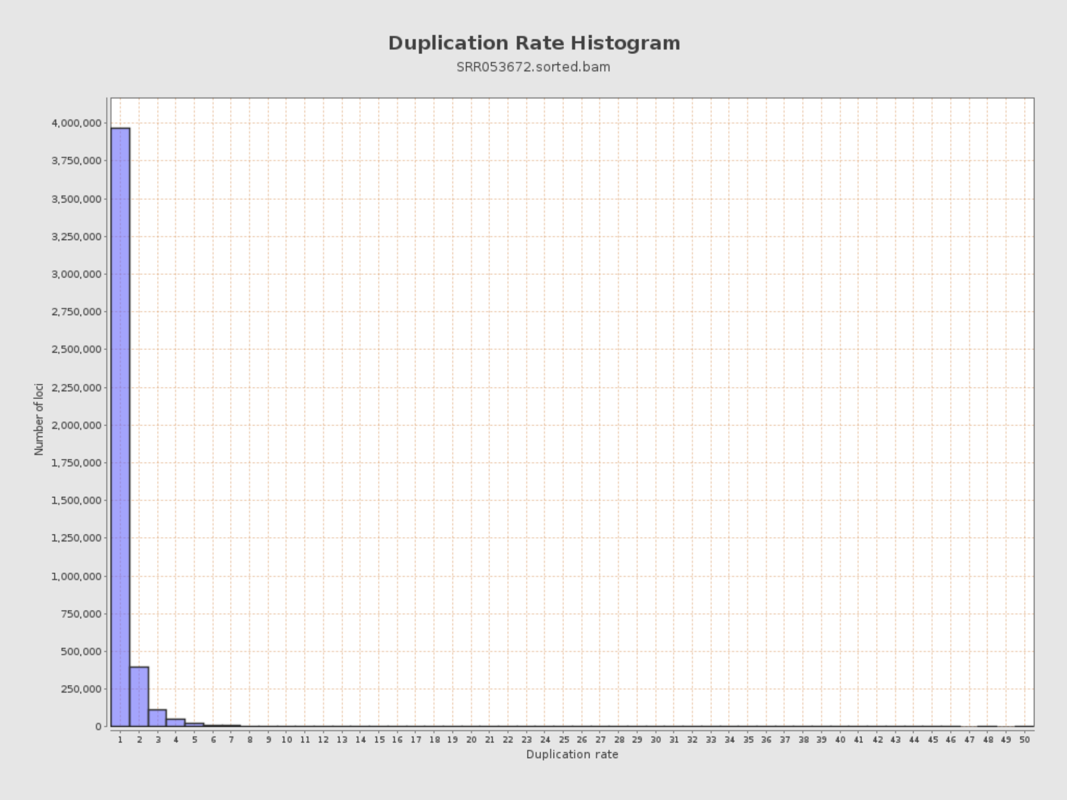
5. Results : Coverage Histogram (0-50X)



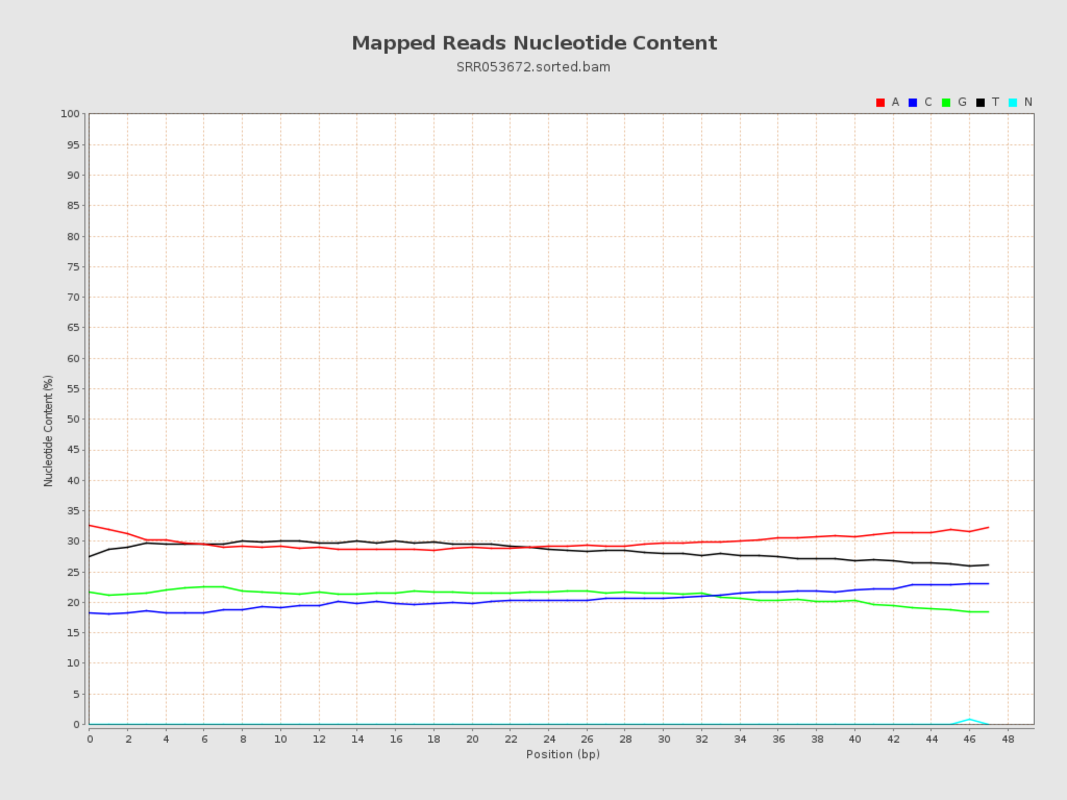
6. Results : Genome Fraction Coverage



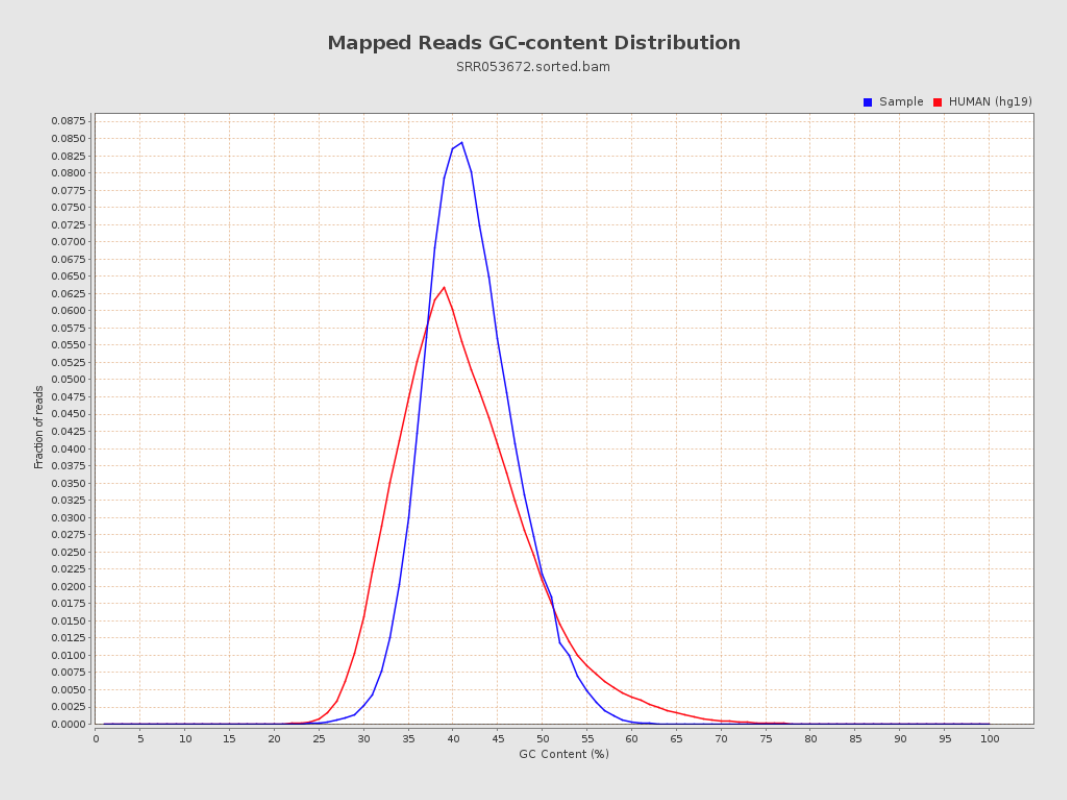
7. Results : Duplication Rate Histogram



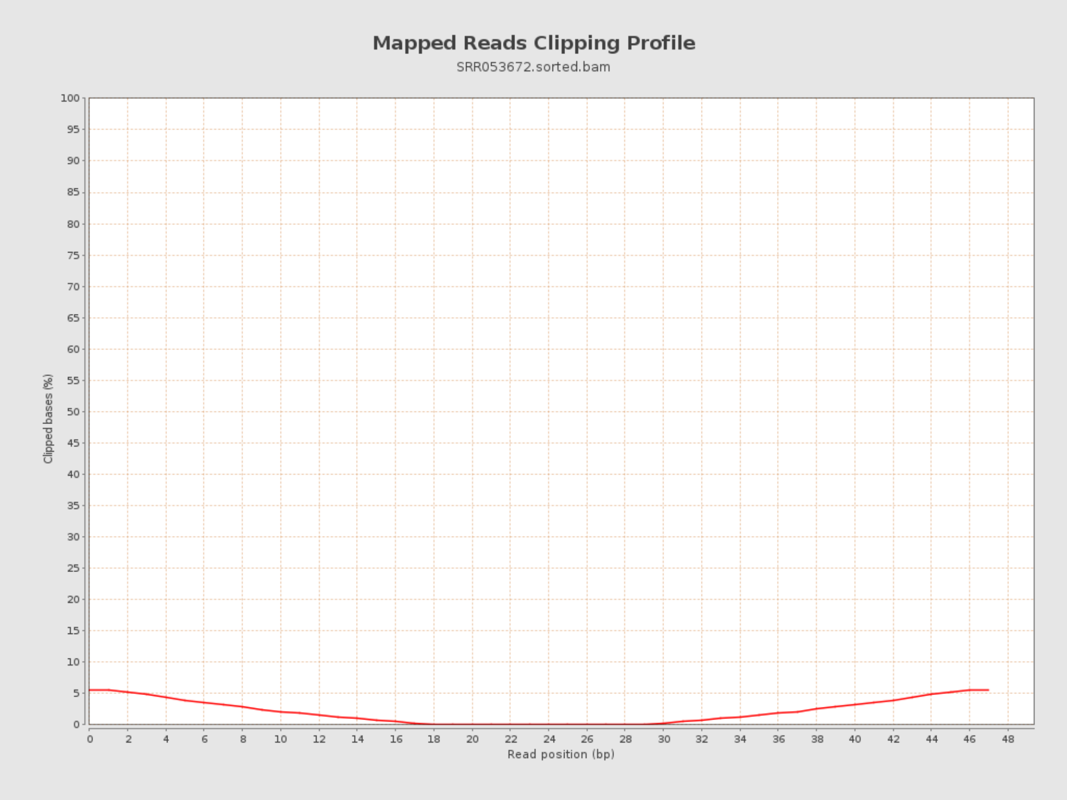
8. Results : Mapped Reads Nucleotide Content



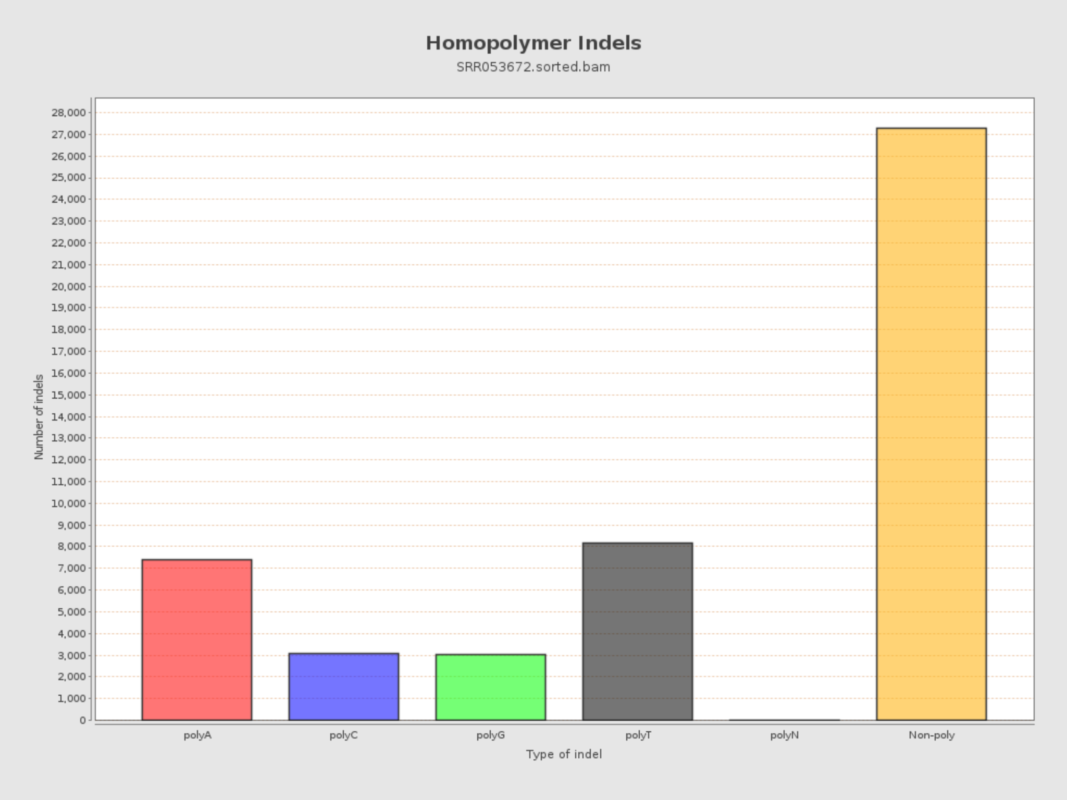
9. Results : Mapped Reads GC-content Distribution



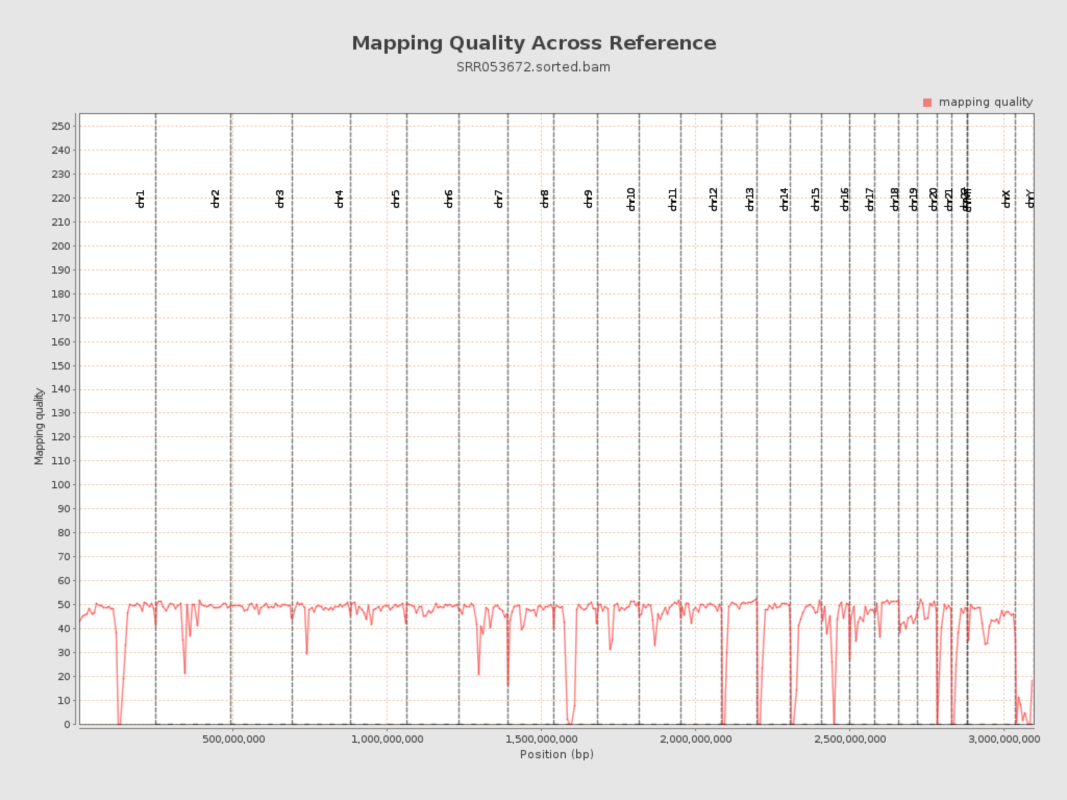
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram