

**Supplemental Table S7.** QCAST (Gurevich et al. 2013) analysis of *de novo* assembly of NA12878 from TELL-Seq data.

Assembly	TELL-Seq*
# contigs (>= 0 bp)	34,085
# contigs (>= 1000 bp)	34,085
# contigs (>= 5000 bp)	13,584
# contigs (>= 10000 bp)	7,508
# contigs (>= 25000 bp)	1,181
# contigs (>= 50000 bp)	542
Total length (>= 0 bp)	2,979,445,840
Total length (>= 1000 bp)	2,979,445,840
Total length (>= 5000 bp)	2,929,255,010
Total length (>= 10000 bp)	2,886,528,456
Total length (>= 25000 bp)	2,794,100,219
Total length (>= 50000 bp)	2,772,210,571
# contigs	34,085
Largest contig	109,183,970
Total length	2,979,445,840
Reference length	3,099,922,541
GC (%)	40.91
Reference GC (%)	40.87
N50	31,462,027
NG50	29,617,959
N75	12,845,396
NG75	10,385,879
L50	28
LG50	30
L75	65
LG75	73
# misassemblies	1,987
# misassembled contigs	939
Misassembled contigs length	2,677,809,708
# local misassemblies	1,549
# scaffold gap ext. mis.	9,216
# scaffold gap loc. mis.	20,150
# unaligned mis. contigs	74
# unaligned contigs	4158 + 1220 part
Unaligned length	23,049,908
Genome fraction (%)	93.732
Duplication ratio	1.075
# N's per 100 kbp	6419.8
# mismatches per 100 kbp	114.07
# indels per 100 kbp	25.61
Largest alignment	23,573,913
Total aligned length	2,771,334,486
NA50	4,302,918
NGA50	4,086,890
NA75	1,495,528
NGA75	1,123,338
LA50	196
LGA50	211
LA75	473
LGA75	543

\*All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Gurevich A, Saveliev V, Vyahhi N, Tesler G. 2013. QCAST: quality assessment tool for genome assemblies. *Bioinformatics* **29**: 1072–1075. doi:10.1093/bioinformatics/btt086