Supplemental Table S8. QUAST (Gurevich et al. 2013) analysis of *de novo* assemblies of NA12878 from different linked read methods (Zheng et al. 2016; Zhang et al. 2017; Wang et al. 2019) and nanopore method (Jain et al. 2018). Assembly results from other linked read methods and nanopore long read method were cited from Supplemental Table S5 in Wang et al, 2019.

Assembly	**TELL-Seq**	**stLFR-1***	**stLFR-2***	**10x***	**Nanopore***
# contigs (>= 0 bp)	34,085	18,102	18,905	17,016	2,337
# contigs (>= 25000 bp)	1,181	965	948	697	1,819
# contigs (>= 50000 bp)	542	500	500	351	1,332
Total length (>= 0 bp)	2,979,445,840	2,899,386,838	2,893,558,199	2,867,683,417	2,866,880,913
Total length (>= 25000 bp)	2,794,100,219	2,816,263,478	2,812,836,296	2,804,290,035	2,858,326,432
Total length (>= 50000 bp)	2,772,210,571	2,800,220,687	2,797,538,549	2,792,294,955	2,840,893,649
Largest contig	109,183,970	104,958,599	86,747,726	109,375,584	50,410,306
Total length	2,979,445,840	2,848,642,889	2,836,789,635	2,824,111,036	2,866,386,869
Reference length	3,099,922,541	3,099,922,541	3,099,922,541	3,099,922,541	3,099,922,541
GC (%)	40.91	40.88	40.82	40.84	40.86
Reference GC (%)	40.87	40.87	40.87	40.87	40.87
N50	31,462,027	28,877,588	26,308,501	45,263,628	7,667,013
# misassemblies	1,987	4,096	3,824	2,750	6,938
Genome fraction (%)	93.732	92.976	92.628	93.776	94.611
# N's per 100 kbp	6419.8	3039.36	2852.41	1085.71	0
# mismatches per 100 kbp	114.07	106.08	105.01	104.98	168.00
# indels per 100 kbp	25.61	25.64	25.56	28.32	165.25
Largest alignment	23,573,913	10,614,129	9,113,736	16,615,675	6,837,121
NA50	4,302,918	1,863,160	1,983,491	2,863,578	906,345

***** Wang et al, 2019.