Combined Model-Based Prediction for Non-Invasive Prenatal Screening

So-Yun Yang [1, †], Kyung Min Kang [2, †], Sook-Young Kim [3], Seo Young Lim [4], Hee Yeon Jang [1,2], Kirim Hong [5], Dong Hyun Cha [2,5], Sung Han Shim [1,2,*] and Je-Gun Joung [1,3,6*]

[1] Department of Biomedical Science, College of Life Science, CHA University, Seongnam, Gyunggi-do 13488, Korea
[2] Center for Genome Diagnostics, CHA Biotech Inc, Seoul 06135, Korea
[3] CHA Future Medicine Research Institute, CHA Bundang Medical Center, Seongnam, Gyunggi-do 13520, Korea
[4] Department of Biomedical Engineering, Hankuk University of Foreign Studies, Seoul, Korea
[5] Department of Obstetrics and Gynecology, CHA Gangnam Medical Center, CHA University, Seoul 06135, Korea
[6] Institute for Biomedical Informatics, CHA University School of Medicine, CHA University, Seongnam, Republic of Korea.
* Correspondence: e-mail@e-mail.com; Tel.:
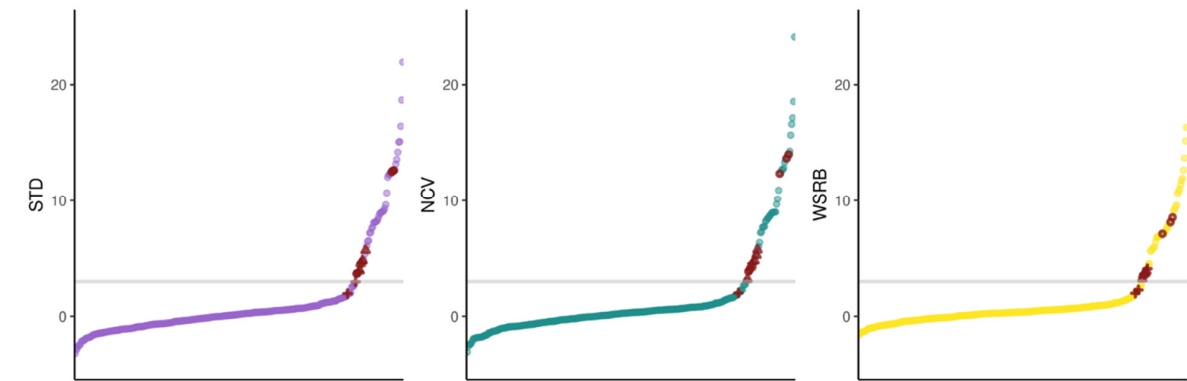† These authors contributed equally to this work

Figure S1. Z-scores of chromosomes 13, 18, and 21 calculated using three different methods.

Table S1. Number of trisomies predicted using three different methods.

	STD	NCV	WSRB	Confirmation
Trisomy 13	5	5	3	0
Trisomy 18	9	10	9	5
Trisomy 21	33	34	33	33
Total	47	49	45	38