SUPPLEMENTAL MATERIALS

Supplemental Table 1. NTFM Model Fit Statistics for Analyses in Combined MSUTR and MTFS Samples with Age and BMI not regressed out (N=547 twin families)

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sx | Model | -2lnL | df | Δ -2lnL (Δdf) | p | | AIC | BIC | SABIC | DIC |
| Total | Baseline | 5542.24 | 1992 |  |  | |  |  |  |  |
| ADSE | 5571.70 | 2014 | 29.46 (22) | | .13 | 1543.70 | -3562.73 | -366.10 | -1711.99 |
| ADFE | 5596.73 | 2014 | 54.49 (22) | | <.01 | 1568.73 | -3550.22 | -353.59 | -1699.47 |
| AFSE | 5570.28 | 2014 | 28.04 (22) | | .17 | 1542.28 | -3563.44 | -366.82 | -1712.70 |
| **ASE** | **5571.70** | **2015** | 29.46 (23) | | **.17** | **1541.70** | **-3565.88** | **-367.67** | **-1714.22** |
| ADE | 5596.73 | 2015 | 54.49 (23) | | <.01 | 1566.73 | -3553.37 | -355.16 | -1701.71 |
| AFE | 5594.63 | 2015 | 52.39 (23) | | <.01 | 1564.63 | -3554.42 | -356.21 | -1702.76 |
| AE | 5625.97 | 2016 | 83.73 (24) | | <.01 | 1593.97 | -3541.90 | -342.10 | -1689.32 |
| WP | Baseline | 5554.15 | 1988 |  |  | |  |  |  |  |
| ADSE | 5584.45 | 2010 | 30.30 (22) | | .11 | 1564.45 | -3543.75 | -353.47 | -1696.68 |
| ADFE | 5603.72 | 2010 | 49.57 (22) | | <.01 | 1583.72 | -3534.11 | -343.84 | -1687.05 |
| AFSE | 5583.50 | 2010 | 29.35 (22) | | .14 | 1563.50 | -3544.22 | -353.94 | -1697.15 |
| **ASE** | **5584.45** | **2011** | 30.30 (23) | | **.14** | **1562.45** | **-3546.90** | **-355.04** | **-1698.92** |
| ADE | 5607.60 | 2011 | 53.45 (23) | | <.01 | 1585.60 | -3535.33 | -343.46 | -1687.34 |
| AFE | 5603.72 | 2011 | 49.57 (23) | | <.01 | 1581.72 | -3537.27 | -345.40 | -1689.28 |
| AE | 5639.20 | 2012 | 85.05 (24) | | <.01 | 1615.20 | -3522.68 | -329.23 | -1673.77 |
| BE | Baseline | 5636.80 | 1989 |  |  | |  |  |  |  |
| ADSE | 5658.74 | 2011 | 21.94 (22) | | .46 | 1636.74 | -3509.75 | -317.89 | -1661.77 |
| ADFE | 5663.34 | 2011 | 26.54 (22) | | .23 | 1641.34 | -3507.46 | -315.59 | -1659.47 |
| AFSE | 5658.72 | 2011 | 21.92 (22) | | .46 | 1636.72 | -3509.77 | -317.90 | -1661.78 |
| **ASE** | **5658.74** | **2012** | 21.94 (23) | | **.52** | **1634.74** | **-3512.90** | **-319.45** | **-1664.00** |
| ADE | 5664.91 | 2012 | 28.11 (23) | | .21 | 1640.91 | -3509.82 | -316.37 | -1660.92 |
| AFE | 5663.34 | 2012 | 26.54 (23) | | .28 | 1639.34 | -3510.61 | -317.16 | -1661.70 |
| AE | 5674.70 | 2013 | 37.90 (24) | | .04 | 1648.70 | -3508.08 | -313.04 | -1658.25 |
| BD | Baseline | 5587.60 | 1989 |  |  | |  |  |  |  |
| ADSE | 5610.25 | 2011 | 22.65 (22) | | .42 | 1588.25 | -3534.00 | -342.14 | -1686.02 |
| ADFE | 5611.98 | 2011 | 24.38 (22) | | .33 | 1589.98 | -3533.14 | -341.27 | -1685.15 |
| AFSE | 5610.25 | 2011 | 22.65 (22) | | .42 | 1588.25 | -3534.00 | -342.14 | -1686.02 |
| ASE | 5612.98 | 2012 | 25.38 (23) | | .33 | 1588.98 | -3535.78 | -342.33 | -1686.88 |
| ADE | 5612.83 | 2012 | 25.23 (23) | | .34 | 1588.83 | -3535.86 | -342.41 | -1686.96 |
| **AFE** | **5612.01** | **2012** | 24.41 (23) | | **.38** | **1588.01** | **-3536.27** | **-342.82** | **-1687.37** |
| AE | 5639.02 | 2013 | 51.42 (24) | | <.01 | 1613.02 | -3525.92 | -330.88 | -1676.09 |

Note: Total= Minnesota Eating Behavior Survey Total Score; WP= Weight Preoccupation; BE= Binge Eating: BD= Body Dissatisfaction;, A= additive genetic, D= dominant genetic, S= environmental influences shared by siblings, F= environmental influences shared by all family members, and E= non-shared environmental influences. The best fitting model for each sample is highlighted in bold font, and is indicated by lowest AIC = Akaike’s Information Criterion, BIC = Bayesian Information Criterion, SABIC= sample size adjusted Bayesian Information Criterion, and DIC = Deviance Information Criterion values and a non-significant change in chi-square (-2lnL). If fit statistics identify more than one model as best fitting, the model with the most model fit statistic indicating best fit was selected.

Supplemental Table 2. Standardized and Unstandardized Parameter Estimates for the Best-Fitting Nuclear Twin Family Model for each Disordered Eating Symptom in MTFS + MSUTR Combined Sample with Age and BMI not regressed out (N=547 twin families)

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Model |  | A | E | D | S | F | passrGE |
| Total | AFSE  (full) | Std. | .036 (.000, .286) | **.498 (.428, .570)** | **-** | **.444 (.260, .550)** | .013 (.000, .047) |  |
| Unstd | .190 (-.530, .530) | **.706 (.654, .754)** | **-** | **.667 (.510, .742)** | .079 (-.047, .079) | .017 (-.035, .035) |
| ASE  (best) | Std. | **.173 (.075, .271)** | **.474 (.417, .540)** | **-** | **.350 (.250, .457)** | **-** | - |
| Unstd. | **.414 (.274, .517)** | **.689 (.646, .735)** | **-** | **.591 (.500, .676)** | **-** | - |
| WP | AFSE  (full) | Std. | .000 (.000, .263) | **.539 (.465, .607)** | **-** | **.450 (.248, .530)** | .010 (.000, .030) |  |
| Unstd. | .000 (-.506, .506) | **.734 (.682, .779)** | **-** | **.671 (.498, .728)** | .066 (-.065, .116) | .000 (-.025, .025) |
| ASE  (best) | Std. | .115 (.019, .211) | **.518 (.457, .588)** | **-** | **.364 (.261, .475)** | **-** | - |
| Unstd. | .336 (.136, .455) | **.720 (.676, .767)** | **-** | **.603 (.511, .689)** | **-** | - |
| BE | AFSE  (full) | Std. | .115 (.000, .424) | **.660 (.569, .763)** | **-** | .220 (.018, .373) | .000 (.000, .028) |  |
| Unstd. | .339 (-.649, .649) | **.813 (.754, .874)** | **-** | .469 (-.616, .616) | .013 (-.124, .116) | .004 (-.072, .024) |
| ASE  (best) | Std. | **.139 (.042, .238)** | **.655 (.579, .742)** | **-** | **.204 (.102, .312)** | **-** | - |
| Unstd. | **.373 (.205, .487)** | **.810 (.761, .861)** | **-** | **.451 (.319, .559)** | **-** | - |
| BD | AFE  (best) | Std. | **.620 (.482, .762)** | **.503 (.433, .586)** | - | **-** | **.062 (.025, .112)** |  |
| Unstd. | **.780 (.688, .862)** | **.709 (.658, .766)** | - | **-** | **-.172 (-.229, -.111)** | **-.121 (-.170, -.074)** |

Note: Total= Minnesota Eating Behavior Survey Total Score; WP= Weight Preoccupation; BE= Binge Eating; BD= Body Dissatisfaction; Std.= Standardized; Unstd.= Unstandardized; A= Additive genetic, E= non-shared environmental influences, D= dominant genetic, S= environmental influences shared by siblings, F= environmental influences shared by all family members, passrGE = passive rGE, 95% Confidence intervals are present below each estimate. Any intervals that include zero are non-significant. Significant parameter estimates are in bold. The best-fitting models are indicated by “best” under the model name. If the best fitting model does not include the “F” parameter and thus, does not compute passive rGE, the full model was also included (i.e., “full” listed under the model name).

Supplemental Table 3. NTFM Model Fit Statistics for Analyses in Combined MSUTR and MTFS Samples with Divorced Families Removed (N=397 twin families)

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sx | Model | -2lnL | df | Δ -2lnL (Δdf) | p | AIC | BIC | SABIC | DIC |
| Total | Baseline | 4096.47 | 1466 |  |  |  |  |  |  |
| ADSE | 4128.50 | 1488 | 32.03 (22) | .08 | 1152.50 | -2387.80 | -27.07 | -1020.42 |
| ADFE | 4145.86 | 1488 | 49.39 (22) | <.01 | 1169.86 | -2379.12 | -18.38 | -1011.74 |
| AFSE | 4126.46 | 1488 | 29.99 (22) | .12 | 1150.46 | -2388.82 | -28.09 | -1021.44 |
| **ASE** | **4128.50** | **1489** | **32.03 (23)** | **.10** | **1150.50** | **-2390.79** | **-28.47** | **-1022.49** |
| ADE | 4148.10 | 1489 | 51.63 (23) | <.01 | 1170.10 | -2380.99 | -18.67 | -1012.69 |
| AFE | 4145.88 | 1489 | 49.41 (23) | .001 | 1167.88 | -2382.10 | -19.78 | -1013.80 |
| AE | 4169.57 | 1490 | 73.10 (24) | <.01 | 1189.67 | -2373.20 | -9.29 | -1003.98 |
| WP | Baseline | 4138.64 | 1464 |  |  |  |  |  |  |
| ADSE | 4162.76 | 1486 | 24.12 (22) | .34 | 1190.76 | -2364.69 | -7.13 | -999.14 |
| ADFE | 4170.62 | 1486 | 31.98 (22) | .08 | 1198.62 | -2360.76 | -3.20 | -995.21 |
| AFSE | 4162.64 | 1486 | 24.00 (22) | .35 | 1190.64 | -2364.75 | -7.19 | -999.20 |
| **ASE** | **4162.76** | **1487** | **24.12 (23)** | **.40** | **1188.76** | **-2367.68** | **-8.53** | **-1001.22** |
| ADE | 4173.02 | 1487 | 34.38 (23) | .06 | 1199.02 | -2362.55 | -3.40 | -996.08 |
| AFE | 4170.62 | 1487 | 31.98 (23) | .10 | 1196.62 | -2363.75 | -4.60 | -997.29 |
| AE | 4189.79 | 1488 | 51.15 (24) | <.01 | 1213.79 | -2357.15 | 3.58 | -989.77 |
| BE | Baseline | 4169.38 | 1465 |  |  |  |  |  |  |
| ADSE | 4188.19 | 1487 | 18.81 (22) | .66 | 1214.19 | -2354.96 | 4.19 | -988.50 |
| ADFE | 4191.40 | 1487 | 22.02 (22) | .46 | 1217.40 | -2353.36 | 5.79 | -986.90 |
| AFSE | 4188.19 | 1487 | 18.81 (22) | .66 | 1214.19 | -2354.96 | 4.19 | -988.50 |
| **ASE** | **4188.24** | **1488** | **18.86 (23)** | **.71** | **1212.24** | **-2357.93** | **2.80** | **-990.55** |
| ADE | 4192.59 | 1488 | 23.21 (23) | .45 | 1216.59 | -2355.75 | 4.98 | -988.37 |
| AFE | 4191.40 | 1488 | 22.02 (23) | .52 | 1215.40 | -2356.35 | 4.38 | -988.97 |
| AE | 4203.55 | 1489 | 34.17 (24) | .08 | 1225.55 | -2353.27 | 9.06 | -984.97 |
| BD | Baseline | 4144.05 | 1463 |  |  |  |  |  |  |
| ADSE | 4164.91 | 1485 | 20.86 (22) | .53 | 1194.91 | -2360.62 | -4.64 | -995.99 |
| ADFE | 4165.94 | 1485 | 21.89 (22) | .47 | 1195.94 | -2360.10 | -4.13 | -995.48 |
| AFSE | 4164.91 | 1485 | 20.86 (22) | .53 | 1194.91 | -2360.62 | -4.64 | -995.99 |
| ASE | 4167.77 | 1486 | 23.72 (23) | .42 | 1195.77 | -2362.18 | -4.62 | -996.64 |
| ADE | 4167.18 | 1486 | 23.13 (23) | .45 | 1195.18 | -2362.47 | -4.91 | -996.93 |
| **AFE** | **4165.94** | **1486** | **21.89 (23)** | **.53** | **1193.94** | **-2363.10** | **-5.54** | **-997.55** |
| AE | 4190.58 | 1487 | 46.53 (24) | <.01 | 1216.58 | -2353.77 | 5.38 | -987.30 |

Note: Total= Minnesota Eating Behavior Survey Total Score; WP= Weight Preoccupation; BE= Binge Eating: BD= Body Dissatisfaction;, A= additive genetic, D= dominant genetic, S= environmental influences shared by siblings, F= environmental influences shared by all family members, and E= non-shared environmental influences. The best fitting model for each sample is highlighted in bold font, and is indicated by lowest AIC = Akaike’s Information Criterion, BIC = Bayesian Information Criterion, SABIC= sample size adjusted Bayesian Information Criterion, and DIC = Deviance Information Criterion values and a non-significant change in -2lnL. If fit statistics identify more than one model as best fitting, the model with the most model fit statistic indicating best fit was selected

Supplemental Table 4. Standardized and Unstandardized Parameter Estimates for the Best-Fitting Nuclear Twin Family Model for each Disordered Eating Symptom using Combined MTFS + MSUTR Sample with Divorced Families Removed (N=397 twin families)

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Model |  | A | E | D | S | F | passrGE |
| Total | AFSE  (full) | Std. | .000 (.000, .256) | **.510 (.435, .588)** | **-** | **.474 (.274, .567)** | .019 (.000, .051) |  |
| Unstd. | .000 (-.498, .498) | **.714 (.660, .767)** | **-** | **.689 (.523, .753)** | .092 (-.040, .149) | .000 (-.036, .036) |
| ASE  (best) | Std. | **.155 (.044, .267)** | **.485 (.418-.564)** | **-** | **.360 (.243-.488)** | **-** | - |
| Unstd. | **.390 (.210, .509)** | **.697 (.647, .751)** | **-** | **.600 (.493-.699)** | **-** | - |
| WP | AFSE  (full) | Std. | .057 (.000, .408) | **.597 (.501, .698)** | **-** | **.339 (.098 .476)** | .002 (.000, .029) |  |
| Unstd. | .238 (-.627, .627) | **.773 (.708, .835)** | **-** | **.583 (.313, .690)** | .029 (-.126, .113) | .008 (-.079, .025) |
| ASE  (best) | Std. | **.112 (.002, .223)** | **.587 (.508, .679)** | **-** | **.300 (.183, .427)** | **-** | - |
| Unstd. | .332 (-.466, .466) | **.766 (.713, .824)** | **-** | **.548 (.428, .653)** | **-** | - |
| BE | AFSE  (full) | Std. | .170 (.000, .529) | **.626 (.526, .745)** | **-** | .211(.000, .417) | .001 (.000, .057) |  |
| Unstd. | .413 (-.730, .730) | **.791(.725, .863)** | **-** | .460 (-.645, .460) | **-.018 (-**.**170, -.018)** | -.007 (-.102, .024) |
| ASE  (best) | Std. | **.134 (.019, .252)** | **.632 (.547, .732)** | **-** | **.235 (.115, .365)** | **-** | - |
| Unstd. | **.367 (.135, .504)** | **.795 (.740, .856)** | **-** | **.485 (.339, .604)** | **-** | - |
| BD | AFE  (best) | Std. | **.566(.408, .730)** | **.540 (.454 .645)** | - | **-** | **.077 (.030, .141)** | **-** |
| Unstd. | **.746(.635, .845)** | **.735 (.674, .803)** | - | **-** | **-.192 (-.257, -.121)** | **-.127 (-.182, -.074)** |

Note: Total= Minnesota Eating Behavior Survey Total Score; WP= Weight Preoccupation; BE= Binge Eating; BD= Body Dissatisfaction; Std.= Standardized; Unstd.= Unstandardized; A= additive genetic, E= non-shared environmental influences, D= dominant genetic, S= environmental influences shared by siblings, F= environmental influences shared by all family members, passrGE = passive rGE, 95% Confidence intervals are present below each estimate. Any intervals that include zero are non-significant. Significant parameter estimates are in bold. The best-fitting models are indicated by “best” under the model name. If the best fitting model does not include the “F” parameter and thus, does not compute passive rGE, the full model was also included (i.e., “full” listed under the model name).

Supplemental Table 5. Model Fit Statistics for NTFM Conducted Separately in MSUTR and MTFS Samples (MSUTR n= 279 twin families; MTFS n=268 twin families)

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sx | Model | -2lnL | df | Δ -2lnL (Δdf) | p | AIC | BIC | SABIC | DIC |
| WP  (MSUTR only) | Baseline | 2674.00 | 981 |  |  |  |  |  |  |
| ADSE | 2728.64 | 1003 | 54.64 (22) | <.01 | 722.64 | -1459.74 | 130.48 | -538.04 |
| ADFE | 2740.79 | 1003 | 66.79 (22) | <.01 | 734.79 | -1453.70 | 136.55 | -531.96 |
| AFSE | 2727.67 | 1003 | 53.67 (22) | <.01 | 721.67 | -1460.21 | 129.99 | -538.52 |
| **ASE** | **2728.64** | **1004** | **54.64 (23)** | **<.01** | **720.64** | **-1462.55** | **129.25** | **-539.94** |
| ADE | 2743.05 | 1004 | 69.05 (23) | <.01 | 735.05 | -1455.34 | 136.45 | -532.73 |
| AFE | 2740.79 | 1004 | 66.79 (23) | <.01 | 732.79 | -1456.48 | 135.32 | -533.86 |
| AE | 2754.74 | 1005 | 80.74 (24) | <.01 | 744.74 | -1452.31 | 141.07 | -528.78 |
| WP  (MTFS only) | Baseline | 2817.63 | 970 |  |  |  |  |  |  |
| ADSE | 2862.81 | 992 | 45.18 (22) | <.01 | 878.81 | -1341.73 | 230.90 | -430.14 |
| ADFE | 2864.32 | 992 | 46.69 (22) | <.01 | 880.32 | -1340.97 | 231.66 | -429.38 |
| AFSE | 2862.81 | 992 | 45.18 (22) | <.01 | 878.81 | -1341.73 | 230.90 | -430.14 |
| **ASE** | **2862.84** | **993** | **45.21 (22)** | **<.01** | **876.84** | **-1344.50** | **229.71** | **-432.00** |
| ADE | 2865.28 | 993 | 47.65 (23) | <.01 | 879.28 | -1343.28 | 230.93 | -430.78 |
| AFE | 2864.32 | 993 | 46.69 (23) | <.01 | 878.32 | -1343.77 | 230.45 | -431.26 |
| AE | 2873.12 | 994 | 55.49 (24) | <.01 | 885.12 | -1342.16 | 233.64 | -428.74 |

Note: WP= Weight Preoccupation. A= Additive genetic, D= dominant genetic, S= environmental influences shared by siblings, F= environmental influences shared by all family members, and E= non-shared environmental influences. The best fitting model for each sample is highlighted in bold font, and is indicated by lowest AIC = Akaike’s Information Criterion, BIC = Bayesian Information Criterion, SABIC= sample size adjusted Bayesian Information Criterion, and DIC = Deviance Information Criterion values and a non-significant change in -2lnL. If fit statistics identify more than one model as best fitting, the model with the most model fit statistic indicating best fit was selected (bolded).

Supplemental Table 6. Standardized and Unstandardized Parameter Estimates for the Best-Fitting Nuclear Twin Family Model Separately in MTFS + MSUTR Samples (MSUTR n= 279 twin families; MTFS n=268 twin families)

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Model |  | A | E | D | S | F | passrGE |
| WP  (MSUTR only) | AFSE  (full) | Std. | .000 (.000, .240) | **.517 (.430, .614)** | **-** | **.405 (.203, .515)** | .007 (.000, .035) |  |
| Unstd. | .000 (-.506, .506) | **.719 (.656, .784)** | **-** | **.637 (.451, .717)** | .060 (-.084, .135) | .000 (-.026, .026) |
| ASE  (best) | Std. | .079 (.000, .211) | **.502 (.420, .602)** | **-** | **.347 (.208, .499)** | **-** | - |
| Unstd. | .280 (-.459, .459) | **.709 (.648, .776)** | **-** | **.589 (.456, .706)** | **-** | - |
| WP  (MTFS only) | AFSE  (full) | Std. | .156 (.000, .614) | **.707 (.583, .856)** | **-** | .211 (.000, .443) | .001 (.000, .098) |  |
| Unstd. | .389 (-.755, .755) | **.841 (.764, .925)** | **-** | .459 (-.665, .665) | -.021 (-.195, .111) | -.010 (-.150, .000) |
| ASE  (best) | Std. | .111 (.000, .250) | **.715 (.605, .846)** | **-** | **.243 (.092, .408)** | - | - |
| Unstd. | .329 (-.490, .490) | **.845 (.778, .920)** | **-** | **.493 (.303, .638)** | - | - |

Note: WP= Weight Preoccupation; Std.= Standardized; Unstd. = Unstandardized; A= Additive genetic, E= non-shared environmental influences, D= dominant genetic, S= environmental influences shared by siblings, F= environmental influences shared by all family members, passrGE = passive rGE, 95% Confidence intervals are present below each estimate. Any intervals that include zero are non-significant. Significant parameter estimates are in bold. The best-fitting models are indicated by “best” under the model name. If the best fitting model does not include the “F” parameter and thus, does not compute passive rGE, the full model was also included (i.e., “full” listed under the model name).

Supplemental Table 7. Model Fit Statistics for Analyses in Combined MSUTR and MTFS Sample with parents from follow-up data collection removed (N=547 twin families)

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sx | Model | -2lnL | df | Δ -2lnL (Δdf) | p | AIC | BIC | SABIC | DIC |
| Total | Baseline | 5296.15 | 1894 |  |  |  |  |  |  |
| ADSE | 5322.53 | 1916 | 26.38 (22) | .24 | 1490.53 | -3378.40 | -337.32 | -1617.71 |
| ADFE | 5337.21 | 1916 | 41.06 (22) | <.01 | 1505.21 | -3371.06 | -329.98 | -1610.37 |
| AFSE | 5322.14 | 1916 | 25.99 (22) | .25 | 1490.14 | -3378.59 | -337.51 | -1617.90 |
| **ASE** | **5322.53** | **1917** | **26.38 (23)** | **.28** | **1488.53** | **-3381.55** | **-338.88** | **-1619.94** |
| ADE | 5340.42 | 1917 | 44.27 (23) | <.01 | 1506.42 | -3372.61 | -329.94 | -1611.00 |
| AFE | 5337.21 | 1917 | 41.06 (23) | .01 | 1503.21 | -3374.21 | -331.54 | -1612.60 |
| AE | 5363.85 | 1918 | 67.70 (24) | <.01 | 1527.85 | -3364.04 | -319.79 | -1601.52 |
| WP | Baseline | 5333.96 | 1891 |  |  |  |  |  |  |
| ADSE | 5355.46 | 1913 | 21.50 (22) | .49 | 1529.46 | -3352.47 | -316.16 | -1594.55 |
| ADFE | 5365.89 | 1913 | 31.93 (22) | .08 | 1539.89 | -3347.26 | -310.94 | -1589.33 |
| AFSE | 5354.91 | 1913 | 20.95 (22) | .52 | 1528.91 | -3352.75 | -316.43 | -1594.82 |
| **ASE** | **5355.46** | **1914** | **21.50 (23)** | **.55** | **1527.46** | **-3355.63** | **-317.72** | **-1596.78** |
| ADE | 5369.46 | 1914 | 35.50 (23) | .05 | 1541.46 | -3348.63 | -310.72 | -1589.78 |
| AFE | 5365.89 | 1914 | 31.93 (23) | .10 | 1537.89 | -3350.41 | -312.51 | -1591.57 |
| AE | 5387.74 | 1915 | 53.78 (24) | <.01 | 1557.74 | -3342.64 | -303.15 | -1582.87 |
| BE | Baseline | 5370.31 | 1892 |  |  |  |  |  |  |
| ADSE | 5389.40 | 1914 | 19.09 (22) | .64 | 1561.40 | -3338.66 | -300.75 | -1579.81 |
| ADFE | 5393.05 | 1914 | 22.74 (22) | .42 | 1565.05 | -3336.83 | -298.93 | -1577.98 |
| AFSE | 5389.40 | 1914 | 19.09 (22) | .64 | 1561.40 | -3338.66 | -300.75 | -1579.81 |
| **ASE** | **5389.45** | **1915** | **19.14 (23)** | **.69** | **1559.45** | **-3341.78** | **-302.29** | **-1582.02** |
| ADE | 5395.02 | 1915 | 24.71 (23) | .37 | 1565.02 | -3339.00 | -299.51 | -1579.24 |
| AFE | 5393.05 | 1915 | 22.74 (23) | .48 | 1563.05 | -3339.98 | -300.49 | -1580.22 |
| AE | 5406.99 | 1916 | 36.68 (24) | .05 | 1574.99 | -3336.17 | -295.09 | -1575.48 |
| BD | Baseline | 5359.91 | 1891 |  |  |  |  |  |  |
| ADSE | 5382.06 | 1913 | 22.15 (22) | .45 | 1556.06 | -3339.18 | -302.86 | -1581.25 |
| ADFE | 5382.26 | 1913 | 22.35 (22) | .44 | 1556.26 | -3339.08 | -302.76 | -1581.15 |
| AFSE | 5382.06 | 1913 | 22.15 (22) | .45 | 1556.06 | -3339.18 | -302.86 | -1581.25 |
| ASE | 5384.92 | 1914 | 25.01 (23) | .35 | 1556.92 | -3340.90 | -303.00 | -1582.05 |
| ADE | 5382.90 | 1914 | 22.99 (23) | .46 | 1554.90 | -3341.91 | -304.00 | -1583.06 |
| **AFE** | **5382.26** | **1914** | **22.35 (23)** | **.50** | **1554.26** | **-3342.23** | **-304.32** | **-1583.38** |
| AE | 5399.55 | 1915 | 39.64 (24) | .02 | 1569.55 | -3336.74 | -297.25 | -1576.97 |

Note: Total= Minnesota Eating Behavior Survey Total Score; WP= Weight Preoccupation; BE= Binge Eating: BD= Body Dissatisfaction; A= additive genetic, D= dominant genetic, S= environmental influences shared by siblings, F= environmental influences shared by all family members, and E= non-shared environmental influences. The best fitting model for each sample is highlighted in bold font, and is indicated by lowest AIC = Akaike’s Information Criterion, BIC = Bayesian Information Criterion, SABIC= sample size adjusted Bayesian Information Criterion, and DIC = Deviance Information Criterion values and a non-significant change in chi-square (-2lnL). If fit statistics identify more than one model as best fitting, the model with the most model fit statistic indicating best fit was selected.

Supplemental Table 8. Standardized and Unstandardized Parameter Estimates for the Best-Fitting Nuclear Twin Family Model for each Disordered Eating Symptom in MTFS + MSUTR Combined Sample with Parents from Follow-Up Data Collection Removed (N=547 twin families)

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Model |  | A | E | D | S | F | passrGE |
| Total | AFSE  (full) | Std. | .053 (.000, .330) | **.554 (.477, .635)** | **-** | **.375 (.179, .495)** | .004 (.000, .033) |  |
| Unstd | .230 (-.566, .566) | **.744 (.690, .797)** | **-** | **.613 (.423 .703)** | .044 (-.088, .044) | **.012 (-.051, .028)** |
| ASE  (best) | Std. | **.132 (.032, .233)** | **.539 (.476-.613)** | **-** | **.320 (.217-.431)** | **-** | - |
| Unstd. | **.360 (.178, .477)** | **.734 (.690, .783)** | **-** | **.566 (.466-.656)** | **-** | - |
| WP | AFSE  (full) | Std. | .000 (.000, .290) | **.631 (.548, .710)** | **-** | **.361 (.145, .444)** | .006 (.000, .018) |  |
| Unstd. | .000 (-.528, .528) | **.794 (.740, .843)** | **-** | **.601 (.380, .601)** | .050(-.088, .100) | .000 (-.021, .021) |
| ASE  (best) | Std. | .089 (.000, .186) | **.615 (.544, .696)** | **-** | **.293 (.188, .406)** | **-** | - |
| Unstd. | .297 (-.425, .425) | **.784 (.738, .834)** | **-** | **.541 (.433, .637)** | **-** | - |
| BE | AFSE  (full) | Std. | .130 (.000, .445) | **.670 (.577, .776)** | **-** | .201 (.000, .370) | .001 (.000, .048) |  |
| Unstd. | .360 (-.665, .665) | **.819 (.760, .881)** | **-** | .448 (-.608, .608) | -.018 (-.154, .094) | -.006 (-.089, .018) |
| ASE  (best) | Std. | **.096 (.000, .199)** | **.677 (.599, .766)** | **-** | **.224 (.117, .338)** | **-** | - |
| Unstd. | **.310 (-.446, .446)** | **.823 (.774, .875)** | **-** | **.473 (.341, .581)** | **-** | - |
| BD | AFE  (best) | Std. | **.448 (.315, .586)** | **.619 (.535, .716)** | - | **-** | **.043 (.013, .089)** |  |
| Unstd. | **.669 (.562, .766)** | **.787 (.732, .846)** | - | **-** | **-.147 (-.209, -.080)** | **-.086 (-.131, -.043)** |

Note: Total= Minnesota Eating Behavior Survey Total Score; WP= Weight Preoccupation; BE= Binge Eating; BD= Body Dissatisfaction; Std.= Standardized; Unstd.= Unstandardized; A= additive genetic, E= non-shared environmental influences, D= dominant genetic, S= environmental influences shared by siblings, F= environmental influences shared by all family members, passrGE = passive rGE, 95% Confidence intervals are present below each estimate. Any intervals that include zero are non-significant. Significant parameter estimates are in bold. The best-fitting models are indicated by “best” under the model name. If the best fitting model does not include the “F” parameter and thus, does not compute passive rGE, the full model was also included (i.e., “full” listed under the model name).