# Electronic supplementary materials for: Heritability and developmental plasticity of growth in an oviparous lizard

## Model fitting and selection of random effects structure

We fit different models to investigate what random effects structure was best suited for our dataset. Only the intercept was included as fixed effects in these models. Lizard identity was included twice to partition out permanent environmental effects (*PE*) given that we had repeated measures of the same individuals (Wilson et al., 2010). We also estimated maternal effects by including mother identity (M). We fit models that contained random intercepts and slopes (a linear and quadratic slope of age) at each of the three random effect levels. In all cases age was z-transformed. Our pedigree had lower levels of paternal half-sibs than we expected from our breeding design because of either sperm precedence or male mating monopolization that was outside our control (See Table S11). Decoupling genetic (G) and maternal effects (M) may therefore have been difficult. As such, we also fit the same models but excluding M to test if G and M were confounded. Given that we fit random slopes of age to estimate changes in variance across age, this meant decoupling G from PE effects might also be challenging. As such, we also fit models that only included G and M. The full list of models are provided in Table S1.

WAIC values are presented in Table S1. Model 1 has the highest WAIC value indicating that it is the least supported model. Model 3 was had the lowest WAIC value indicating that it is the best supported model. Between model 5 -6, model 6 had the highest DIC, indicating that *PE* should be included as a random intercept only. Model 7 was the second best supported model and improvement in WAIC value was marginal by including a quadratic slope for PE. To avoid overfitting, we selected the more parsimonious model (Model 7) and used this random effect structure for the remaining analysis unless stated otherwise.

**Table S1** WAIC of six intercept models with different combinations of random effects structures for additive genetic variance, maternal variance and permanent environmental variance. DIC was calculated by subtracting the DIC value of each model from the DIC value of model 1. *G M, PE* represents additive genetic variance, maternal variance and permanent environment variance, respectively.

|  |  |  |  |
| --- | --- | --- | --- |
| **Model** | **WAIC** |  | **Std. Error** |
| Model 3 - quadratic slopes for *G, M, PE* | -3258 | 0 | 0 |
| Model 7 - intercept for *PE*, quadratic slopes for *G, M* | -3261 | -1.122 | 3.245 |
| Model 4 - intercept for *G*, linear slopes for *M, PE* | -1382 | -939.4 | 38.91 |
| Model 2 - linear slopes for G, *M, PE* | -1381 | -939.5 | 39.03 |
| Model 6 - intercept for *PE*, linear slopes for *G, M* | -1382 | -940 | 38.94 |
| Model 5 - intercept for *M*, linear slopes for *G, PE* | -1370 | -945.4 | 40.3 |
| Model 1 - intercepts for *G*, *M, PE* | 4550 | -3905 | 49.91 |

## Does our data have heterogenous residual variance?

Residual variance may impact estimates of heritability if changes over time (heterogenous variance) are not properly accounted for. We therefore explicitly modelled residual variance to verify if this was the case comparing homogeneous and heterogenous models using LOO and WAIC values. We fitted two models, both of which had the same random effects structure as our top supported model described above (Table S1). The model with heterogenous variance was best supported (Table S2), we therefore modelled heterogenous variance in all subsequent models unless stated otherwise.

**Table S2** Comparisons of expected log predictive density values for LOO and WAIC values to test the importance of heterogenous and homogenous residual variance. Note that difference in values are calculated by subtracting values from the model with lowest LOO and WAIC values i.e. the heterogenous variance model

|  |  |  |  |
| --- | --- | --- | --- |
| **Model** | **WAIC** |  | **Std. Error** |
| Model 7 with heterogenous variance | -3280 | 0 | 0 |
| Model 7 with homogenous variance | -3261 | -9.783 | 6.429 |

## The influence of developmental temperature on genetic and non-genetic variance across age

We fitted random intercepts for , , and to estimate the overall estimate across age. In other words, the average variance across all age classes. We found that additive genetic variance, permanent environmental variance, and heritability of growth appears to be higher in the hot developmental temperature treatment however, there were no significant differences among treatment groups (Table S3).

**Table S3** Treatment comparisons of additive genetic variance, maternal variance, permanent environmental variance, residual variance and heritability. These are estimated from a model where random intercepts were fitted for all variance components. Bolded estimates are significantly different from zero. Hot treatment group nobs = 1892, cold treatment group nobs = 2036. Values with \* indicate very small values that were above zero.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | | **Hot developmental temperature  (nlizards = 125)** | | | | | | **Cold developmental temperature  (nlizards = 136)** | | | | | |
|  | | **Estimate** | | **Lower** | | **Upper** | | **Estimate** | | **Lower** | | **Upper** | |
| Vadditive genetic | | **0.028** | | **0.001** | | **0.056** | | **0.01** | | **0\*** | | **0.025** | |
| Vmaternal | | **0.006** | | **0\*** | | **0.024** | | **0.005** | | **0\*** | | **0.016** | |
| Vresidual | | **0.25** | | **0.23** | | **0.271** | | **0.274** | | **0.254** | | **0.294** | |
| Heritability (h2) | | **0.041** | | **0.002** | | **0.083** | | **0.013** | | **0\*** | | **0.033** | |

To test how variance components and heritability change with age in each treatment group, we fitted an intercept in our fixed effects and used the best supported random effect structure (Model 7) with heterogenous residual variance. There were no differences among treatment groups (Fig. 3). The and matrices for each treatment group are presented in Table S3-S4.

**Table S4.** *G* and *M* variance-covariance / correlation matrices between growth trajectory parameters(intercept, linear slope, and quadratic slope) for lizards from the hot developmental temperature treatment group (nlizards = 125, nobs = 1,330). Variances are represented along the diagonal, covariances are represented in the upper triangle and correlations are represented in the lower triangle. Values in the brackets represent the 95% credible intervals. Note that residual variance slope is in on log scale (i.e., for every 1 SD unit increase in age we expect a decrease in log(SD)).

|  |  |  |  |
| --- | --- | --- | --- |
| *G* | | | |
|  | Intercept | Linear Slope | Quadratic Slope |
| Intercept | 0.015  (0.009 - 0.024) | 0.00201  (-0.00339 - 0.0087) | -0.00663  (-0.0125 - -0.0022) |
| Linear Slope | 0.122  (-0.241 - 0.465) | 0.016  (0.008 - 0.027) | 0.00438  (3.9e-07 - 0.0101) |
| Quadratic Slope | -0.557  (-0.774 - -0.275) | 0.372  (4.04e-05 - 0.695) | 0.009  (0.004 - 0.015) |
| *M* | | | |
|  | Intercept | Linear Slope | Quadratic Slope |
| Intercept | 0.055  (0.001 - 0.161) | 0.101  (0.00258 - 0.218) | -0.0309  (-0.0677 - -0.000631) |
| Linear Slope | 0.889  (0.206 - 0.995) | 0.253  (0.17 - 0.373) | -0.0722  (-0.108 - -0.0456) |
| Quadratic Slope | -0.88  (-0.995 - -0.21) | -0.932  (-0.994 - -0.793) | 0.024  (0.013 - 0.041) |
|  | | *Residual* | *Residual Slope* |
|  | |  | |
|  | | 0.0169  (0.0155 - 0.0185) | -0.135  (-0.188 - -0.0808) |

**Table S5.** *G* and *M* variance-covariance / correlation matrices between growth trajectory parameters (intercept, linear slope and quadratic slope) for lizards from the cold developmental temperature treatment group (nlizards = 136, nobs = 1596). PE variance is also presented. Variances are represented along the diagonal, covariances are represented in the upper triangle and correlations are represented in the lower triangle. Bolded estimates are significantly different from zero. Values in the brackets represent the 95% credible intervals. Note that residual variance slope is in SD units.

|  |  |  |  |
| --- | --- | --- | --- |
| *G* | | | |
|  | Intercept | Linear Slope | Quadratic Slope |
| Intercept | **0.008  (0.001 to 0.018)** | **0.00132  (-0.00331 to 0.00704)** | **-0.00488  (-0.0104 to -0.000589)** |
| Linear Slope | **0.123  (-0.454 to 0.62)** | **0.014  (0.008 to 0.023)** | **0.00422  (0.000231 to 0.00917)** |
| Quadratic Slope | **-0.646  (-0.931 to -0.193)** | **0.411  (0.0231 to 0.731)** | **0.008  (0.004 to 0.013)** |
| *M* | | | |
|  | Intercept | Linear Slope | Quadratic Slope |
| Intercept | **0.032  (0 to 0.12)** | 0.0718  (-0.00275 **to** 0.183) | **-0.0227  (-0.0585 to 0.000568)** |
| Linear Slope | 0.78  (-0.327 **to** 0.991) | **0.267  (0.185 to 0.382)** | **-0.078  (-0.114 to -0.0517)** |
| Quadratic Slope | -0.794  (-0.992 **to** 0.244) | **-0.933  (-0.994 to -0.811)** | **0.026  (0.016 to 0.041)** |
| *PE* | | *Residual* | *Residual Slope (SD)* |
| **0.065 (6.55e-05 to 0.00938)** | | **4.15  (3.97 to 4.34)** | -0.135 (-0.184 **to** -0.075) |

## Accounting for scale-effects using coefficients of variation

As the mean body mass increases over time, the variance may also increase concurrently due to scale effects and potentially bias estimates of quantitative genetics parameters (Wilson, Kruuk, et al., 2005). We therefore calculated coefficients of variation (CV) across age for each variance component using the following equation:

where is the CV for a given variance component e.g. is the CV of maternal effects. The CV of maternal effects () and showed the same pattern as the raw variance estimates (Fig. S1-2). There were no treatment differences in , (Fig. S2). Both of which followed a quadratic relationship like the raw variance estimates in Fig. S1. We therefore conclude changes in mean mass did not affect estimation of variance components.

**Figure. S1** Scatterplot showing the relationship of the how the coefficient of variance of additive genetic variance (*G*) and maternal effects (*M*) changed with age for the hot developmental treatment (n = 125, red) and the cold developmental treatment (n = 136, blue). Points represent posterior means, thin lines represent the 95% credible intervals, thick lines represent the mean for each treatment group.

## Do growth trajectories differ among incubation treatments?

To test for treatment differences in growth trajectories, we fitted four models with different combinations of treatment interactions with the linear and quadratic age parameters and compared their WAIC values (Table 1). The best supported model was the full model (Table S5), its *G* and *M* matrix is presented in Table S6 below. Model coefficients for the other three models are presented in Table S7-S9)

**Table S6.** *G* and *M* variance-covariance / correlation matrices between growth trajectory parameters (intercept, linear slope and quadratic slope) for the overall population (nlizards = 261, nobs = 2926). *PE* and Residual variance is also presented. Variances are represented along the diagonal, covariances are represented in the upper triangle and correlations are represented in the lower triangle. Bolded estimates are significantly different from zero. Values in the brackets represent the 95% credible intervals. Note that residual variance slope is in SD units.

|  |  |  |  |
| --- | --- | --- | --- |
| *G* | | | |
|  | Intercept | Linear Slope | Quadratic Slope |
| Intercept | **0.012  (0.007 to 0.019)** | 5.82e-05  (-0.0030**9 to 0**.00311) | **-0.00724  (-0.0108 to -0.00416)** |
| Linear Slope | 0.00484  (-0.237 to 0.238) | **0.014  (0.01 to 0.019)** | **0.0096  (0.00645 to 0.0139)** |
| Quadratic Slope | **-0.559  (-0.751 to -0.362)** | **0.689  (0.549 to 0.81)** | **0.014  (0.01 to 0.019)** |
| *M* | | | |
|  | Intercept | Linear Slope | Quadratic Slope |
| Intercept | **0.001  (0 to 0.004)** | -5.11e-05  (-0.00175 to 0.00165) | -0.000196  (-0.00169 to 0.000277) |
| Linear Slope | -0.0555  (-0.844 to 0.773) | **0.005  (0.002 to 0.01)** | 5.78e-05  (-0.00114 to 0.00176) |
| Quadratic Slope | -0.181  (-0.937 to 0.799) | -0.0121  (-0.865 to 0.845) | **0  (0 to 0.002)** |
| *PE* | | *Residual* | *Residual Slope (SD)* |
| **0.00333 (0.000317- 0.00653)** | | **4.36  (4.23 - 4.48)** | **-0.0483 (-0.0852 - -0.0105)** |

|  |  |  |  |
| --- | --- | --- | --- |
| Table S7 Estimates from model with interaction between treatment and age (linear growth rate) only. Bolded estimates are significantly different from zero. \* indicates that value is above zero prior to rounding. nobs = 2926. Age measured in days was z-transformed (mean = 361.34, SD = 185.16) | | | |
| Parameter | Estimate | Lower | Upper |
| *Fixed effects* |  |  |  |
| Intercept | **-0.995** | **-1.014** | **-0.977** |
| Treatment | **-0.072** | **-0.101** | **-0.045** |
| Age | **0.507** | **0.482** | **0.531** |
| Age2 | **-0.186** | **-0.199** | **-0.173** |
| Treatment Age | -0.005 | -0.028 | 0.018 |
| *Random effects* |  |  |  |
| Maternal variance |  |  |  |
| Intercept | **0.024** | **0.001** | **0.064** |
| Slope | **0.069** | **0.04** | **0.099** |
| Quadratic | **0.016** | **0.001** | **0.044** |
| Cor intercept - slope | -0.058 | -0.845 | 0.776 |
| Cor intercept - quadratic | -0.157 | -0.921 | 0.849 |
| Cor slope - quadratic | -0.06 | -0.877 | 0.815 |
| Permanent Environment Variance | **0.055** | **0.017** | **0.08** |
| Additive Genetic Variance |  |  |  |
| Intercept | **0.109** | **0.08** | **0.137** |
| Slope | **0.116** | **0.1** | **0.135** |
| Quadratic | **0.117** | **0.101** | **0.137** |
| Cor intercept - slope | 0.014 | -0.233 | 0.242 |
| Cor intercept - quadratic | -0.549 | -0.742 | -0.356 |
| Cor slope - quadratic | **0.686** | **0.542** | **0.804** |
| Residual | **-2.087** | **-2.118** | **-2.057** |
| Residual x Age | -0.048 | -0.084 | -0.011 |

|  |  |  |  |
| --- | --- | --- | --- |
| Table S8Estimates from model with interaction between treatment and quadratic age parameter only. Bolded estimates are significantly different from zero. \* indicates that value is above zero prior to rounding. nobs = 2926. Age measured in days was z-transformed (mean = 361.34, SD = 185.16). Cor represents correlation | | | |
| Parameter | Estimate | Lower | Upper |
| *Fixed effects* |  |  |  |
| Intercept | **-0.99** | **-1.009** | **-0.97** |
| Age | **0.504** | **0.482** | **0.525** |
| Treatment | **-0.083** | **-0.116** | **-0.053** |
| Age2 | **-0.194** | **-0.212** | **-0.177** |
| Treatment x Age2 | 0.017 | -0.007 | 0.042 |
| *Random effects* |  |  |  |
| Maternal variance |  |  |  |
| Intercept | **0.025** | **0.001** | **0.064** |
| Slope | **0.069** | **0.041** | **0.098** |
| Quadratic | **0.016** | **0.001** | **0.047** |
| Cor intercept - slope | -0.091 | -0.868 | 0.765 |
| Cor intercept - quadratic | -0.175 | -0.929 | 0.826 |
| Cor slope - quadratic | -0.047 | -0.902 | 0.835 |
| Permanent Environment Variance | **0.056** | **0.02** | **0.081** |
| Additive Genetic Variance |  |  |  |
| Intercept | **0.109** | **0.077** | **0.135** |
| Slope | **0.116** | **0.099** | **0.135** |
| Quadratic | **0.118** | **0.102** | **0.135** |
| Cor intercept - slope | 0.006 | -0.233 | 0.249 |
| Cor intercept - quadratic | -0.559 | -0.755 | -0.352 |
| Cor slope - quadratic | **0.687** | **0.544** | **0.8** |
| Residual | **-2.087** | **-2.119** | **-2.055** |
| Residual x Age | **-0.047** | **-0.084** | **-0.01** |

|  |  |  |  |
| --- | --- | --- | --- |
| Table S9 Estimates from model with main effects of treatment and age only. Bolded estimates are significantly different from zero. \* indicates that value is above zero prior to rounding. nobs = 2926. G is the additive genetic variance, Age measured in days was z-transformed (mean = 361.34, SD = 185.16). | | | |
| Parameter | Estimate | Lower | Upper |
| *Fixed effects* |  |  |  |
| Intercept | **-0.997** | **-1.015** | **-0.979** |
| Treatment | **-0.069** | **-0.095** | **-0.046** |
| Age | **0.504** | **0.481** | **0.526** |
| Age2 | **-0.186** | **-0.198** | **-0.172** |
| *Random effects* |  |  |  |
| Maternal variance |  |  |  |
| Intercept | **0.025** | **0.001** | **0.064** |
| Slope | **0.07** | **0.042** | **0.099** |
| Quadratic | **0.017** | **0.001** | **0.047** |
| Cor intercept - slope | -0.057 | -0.871 | 0.811 |
| Cor intercept - quadratic | -0.163 | -0.924 | 0.84 |
| Cor slope - quadratic | -0.02 | -0.865 | 0.814 |
| Permanent Environment Variance | **0.055** | **0.017** | **0.081** |
| Additive Genetic Variance |  |  |  |
| Intercept | **0.109** | **0.077** | **0.136** |
| Slope | **0.115** | **0.098** | **0.134** |
| Quadratic | **0.117** | **0.101** | **0.134** |
| Cor intercept - slope | 0.021 | -0.218 | 0.265 |
| Cor intercept - quadratic | -0.552 | -0.737 | -0.357 |
| Cor slope - quadratic | **0.68** | **0.529** | **0.794** |
| Residual | **-2.087** | **-2.118** | **-2.057** |
| Residual x Age | **-0.048** | **-0.085** | **-0.013** |

|  |  |  |  |
| --- | --- | --- | --- |
| Table S10Estimates from model testing the effects of incubation treatment on changes in mass over age. Note that individual variation is not accounted for in random effects, only variation among different mothers to account for non-independence among siblings. Bolded estimates are significantly different from zero. \* indicates that value is above zero prior to rounding. nobs = 2926. Age measured in days was z-transformed (mean = 361.34, SD = 185.16). \* indicates that value is very small but does not overlap zero prior to rounding | | | |
|  | Estimate | Lower | Upper |
| *Fixed effects* |  |  |  |
| Intercept | **-0.77** | **-0.85** | **-0.68** |
| Treatment | **-0.01** | **-0.01** | **-0.01** |
| Age | 0.63 | 0.57 | 0.7 |
| Age2 | -0.05 | -0.1 | 0.01 |
| Treatment Age | **-0\*** | **-0.01** | **-0\*** |
| Treatment Age2 | **-0\*** | **-0\*** | **-0\*** |
| *Random effects* |  |  |  |
| Maternal variance |  |  |  |
| Intercept | **0.08** | **0.06** | **0.09** |
| Residual | **0.18** | **0.18** | **0.19** |

## Pedigree and Genomic Relatedness

We submitted a total of 437 tissues samples, five samples experienced problems during extraction and sequencing and were therefore excluded from the final dataset (n = 432). One individual was excluded from the dataset and may be related to contamination as this individual appeared to be unrelated to any other samples in the dataset.

DNA was extracted from tissue samples using a Qiagen DNeasy Blood and Tissue Kits following the manufacturer’s instructions. Diversity Arrays Technology (DArT) combines next generation sequencing platforms and genome complexity reduction methods (Kilian et al., 2012) to select the most appropriate method for *L.delicata.* Sequences were processed using DArT specific pipelines. The main pipeline filtered out poor quality sequences which resulted in a total of 185,963 SNPs for our final analysis.

**Table S11** Pedigree statistics for each treatment. The number of offspring and sires per dam (clutch) are provided for 23 and 29 C treatments. 'w' indicates a male not present within the breeding design resulting from mating or stored sperm from wild interactions.

| **Treatment** | **Dam** | **Sire** | **Number of Offspring** |
| --- | --- | --- | --- |
| **23** | ld0005 | ld0095 | 2 |
|  | - | ld0442 | 1 |
|  | ld0015 | ld0095 | 1 |
|  | ld0016 | ld0051 | 1 |
|  | ld0019 | ld0137 | 1 |
|  | ld0025 | ld0018 | 2 |
|  | ld0033 | ld0069 | 2 |
|  | ld0035 | ld0049 | 2 |
|  | ld0039 | ld0150 | 2 |
|  | ld0057 | ld0104 | 4 |
|  | ld0062 | ld0011 | 4 |
|  | - | ld0137 | 1 |
|  | ld0067 | ld0095 | 2 |
|  | - | ld0442 | 4 |
|  | ld0068 | ld0006 | 2 |
|  | ld0069 | ld0102 | 1 |
|  | ld0081 | ld0111 | 2 |
|  | ld0085 | ld0076 | 3 |
|  | - | ld0137 | 1 |
|  | ld0090 | ld0027 | 4 |
|  | ld0091 | ld0043 | 1 |
|  | ld0093 | ld0140 | 3 |
|  | ld0101 | ld0077 | 1 |
|  | ld0103 | ld0150 | 3 |
|  | ld0106 | ld0175 | 6 |
|  | ld0116 | ld0143 | 4 |
|  | ld0122 | ld0076 | 5 |
|  | ld0125 | ld0107 | 2 |
|  | ld0126 | ld0115 | 3 |
|  | ld0132 | ld0042 | 1 |
|  | ld0136 | ld0077 | 2 |
|  | ld0139 | ld0006 | 3 |
|  | ld0144 | ld0013 | 2 |
|  | ld0147 | ld0018 | 2 |
|  | ld0152 | ld0140 | 3 |
|  | ld0156 | w0001 | 2 |
|  | ld0157 | w0002 | 2 |
|  | ld0161 | w0004 | 2 |
|  | ld0163 | w0005 | 1 |
|  | ld0164 | w0006 | 1 |
|  | ld0165 | w0008 | 1 |
|  | ld0166 | w0009 | 2 |
|  | ld0168 | w0036 | 1 |
|  | ld0173 | w0011 | 2 |
|  | ld0182 | w0013 | 1 |
|  | ld0185 | w0014 | 1 |
|  | ld0186 | w0015 | 1 |
|  | ld0189 | w0016 | 2 |
|  | ld0190 | w0017 | 1 |
|  | ld0191 | w0018 | 3 |
|  | ld0193 | ld0020 | 1 |
|  | ld0194 | w0019 | 1 |
|  | ld0195 | w0020 | 1 |
|  | ld0198 | w0022 | 1 |
|  | ld0202 | w0023 | 1 |
|  | ld0203 | w0024 | 2 |
|  | ld0204 | w0025 | 1 |
|  | ld0207 | w0026 | 2 |
|  | ld0208 | w0028 | 2 |
|  | ld0209 | w0029 | 2 |
|  | ld0210 | w0030 | 2 |
|  | ld0215 | w0031 | 2 |
|  | ld0390 | w0032 | 1 |
|  | ld0402 | ld0138 | 1 |
|  | – | w0033 | 2 |
|  | ld0403 | w0034 | 1 |
|  | ld2015 | ld0049 | 2 |
|  | – | ld0075 | 3 |
|  | – | ld0104 | 1 |
| **29** | ld0005 | ld0095 | 1 |
|  | – | ld0442 | 5 |
|  | ld0015 | ld0069 | 1 |
|  | ld0016 | ld0051 | 1 |
|  | ld0025 | ld0018 | 2 |
|  | ld0033 | ld0069 | 1 |
|  | ld0035 | ld0049 | 3 |
|  | ld0039 | ld0150 | 2 |
|  | ld0057 | ld0075 | 1 |
|  | – | ld0104 | 1 |
|  | ld0062 | ld0011 | 4 |
|  | – | ld0137 | 2 |
|  | ld0067 | ld0095 | 1 |
|  | – | ld0442 | 3 |
|  | ld0068 | ld0006 | 4 |
|  | ld0069 | ld0102 | 2 |
|  | ld0072 | ld0119 | 1 |
|  | ld0081 | ld0111 | 2 |
|  | ld0085 | ld0076 | 3 |
|  | – | ld0137 | 1 |
|  | ld0090 | ld0027 | 4 |
|  | ld0091 | ld0043 | 2 |
|  | ld0093 | ld0140 | 3 |
|  | ld0103 | ld0150 | 2 |
|  | ld0106 | ld0175 | 3 |
|  | ld0116 | ld0143 | 5 |
|  | ld0121 | ld0146 | 2 |
|  | ld0122 | ld0076 | 4 |
|  | ld0125 | ld0107 | 2 |
|  | ld0126 | ld0115 | 2 |
|  | ld0132 | ld0042 | 1 |
|  | ld0136 | ld0077 | 2 |
|  | ld0139 | ld0006 | 3 |
|  | ld0144 | ld0013 | 2 |
|  | ld0147 | ld0018 | 1 |
|  | ld0152 | ld0140 | 3 |
|  | ld0156 | w0001 | 2 |
|  | ld0157 | w0002 | 1 |
|  | ld0160 | w0003 | 2 |
|  | ld0161 | w0004 | 2 |
|  | ld0163 | w0005 | 1 |
|  | ld0164 | w0006 | 1 |
|  | ld0169 | w0010 | 2 |
|  | ld0173 | w0011 | 1 |
|  | ld0181 | w0012 | 1 |
|  | ld0182 | w0013 | 2 |
|  | ld0185 | w0014 | 2 |
|  | ld0186 | w0015 | 2 |
|  | ld0189 | w0016 | 1 |
|  | ld0190 | w0017 | 1 |
|  | ld0191 | w0018 | 2 |
|  | ld0193 | ld0020 | 2 |
|  | ld0194 | w0019 | 1 |
|  | ld0195 | w0020 | 1 |
|  | ld0197 | w0021 | 1 |
|  | ld0198 | w0022 | 1 |
|  | ld0202 | w0023 | 2 |
|  | ld0203 | w0024 | 1 |
|  | ld0204 | w0025 | 1 |
|  | ld0208 | w0028 | 1 |
|  | ld0210 | w0030 | 2 |
|  | ld0402 | ld0138 | 2 |
|  | – | w0033 | 2 |
|  | ld0403 | w0034 | 1 |
|  | ld2015 | ld0049 | 1 |
|  | – | ld0075 | 2 |