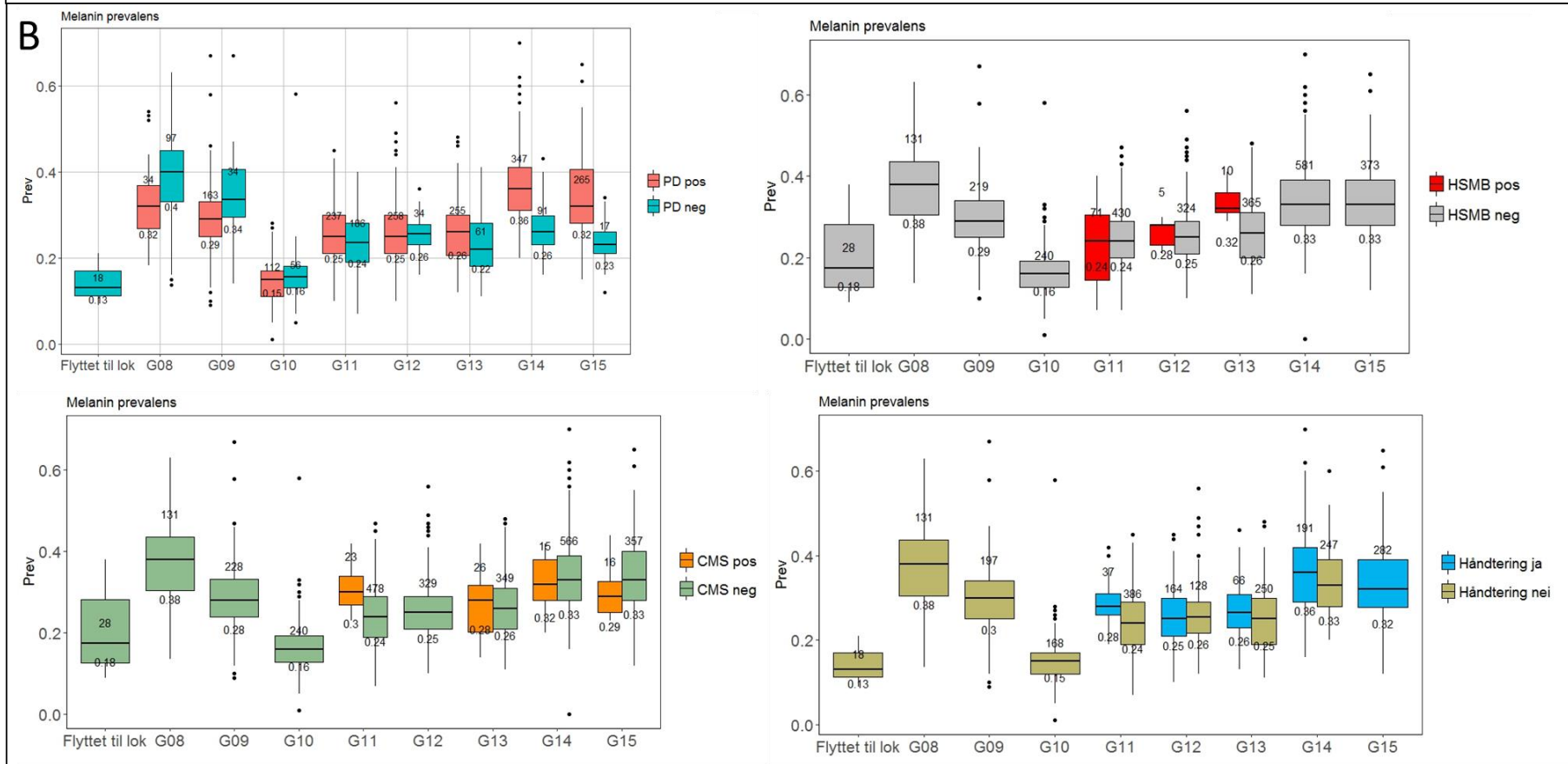
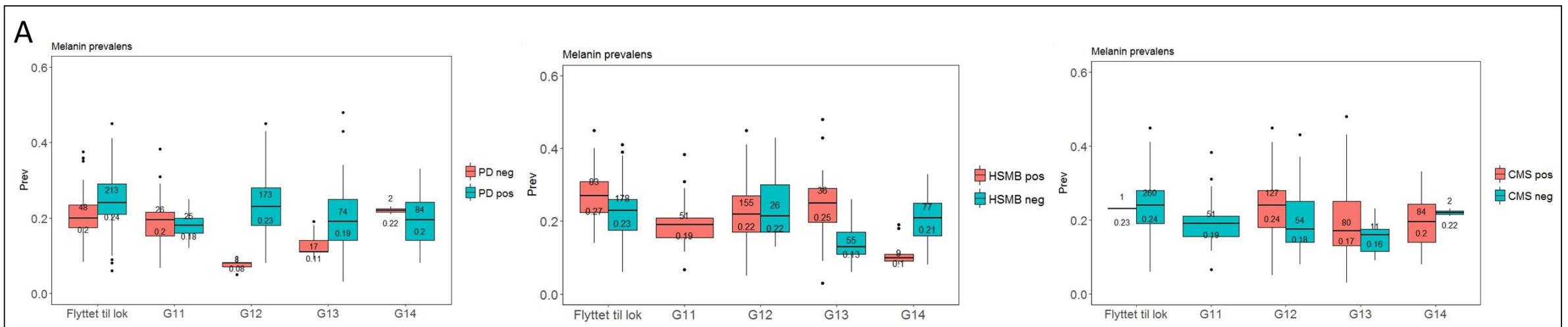


Vedlegg

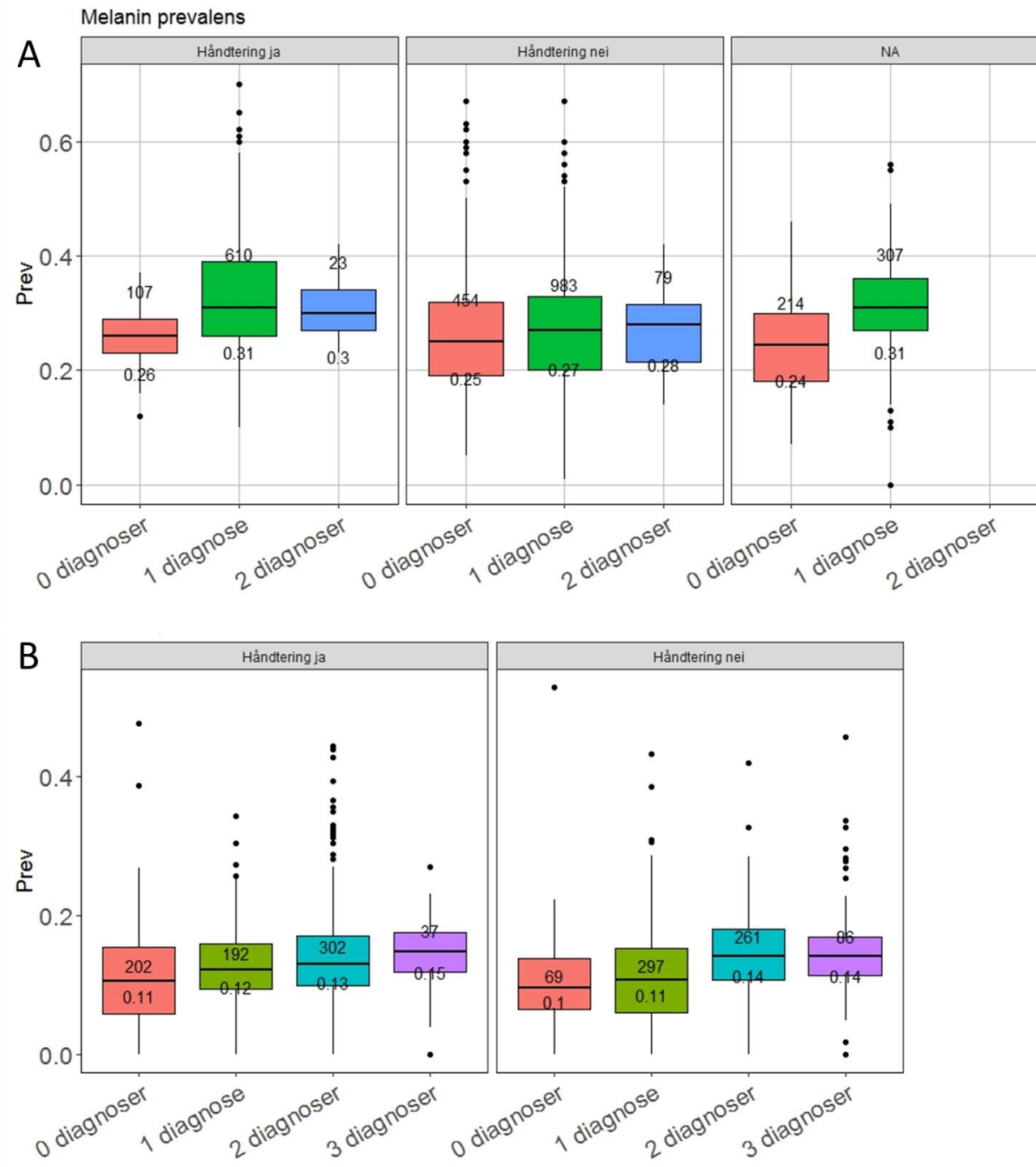
Epi-melaninrapporten

FHF#901256

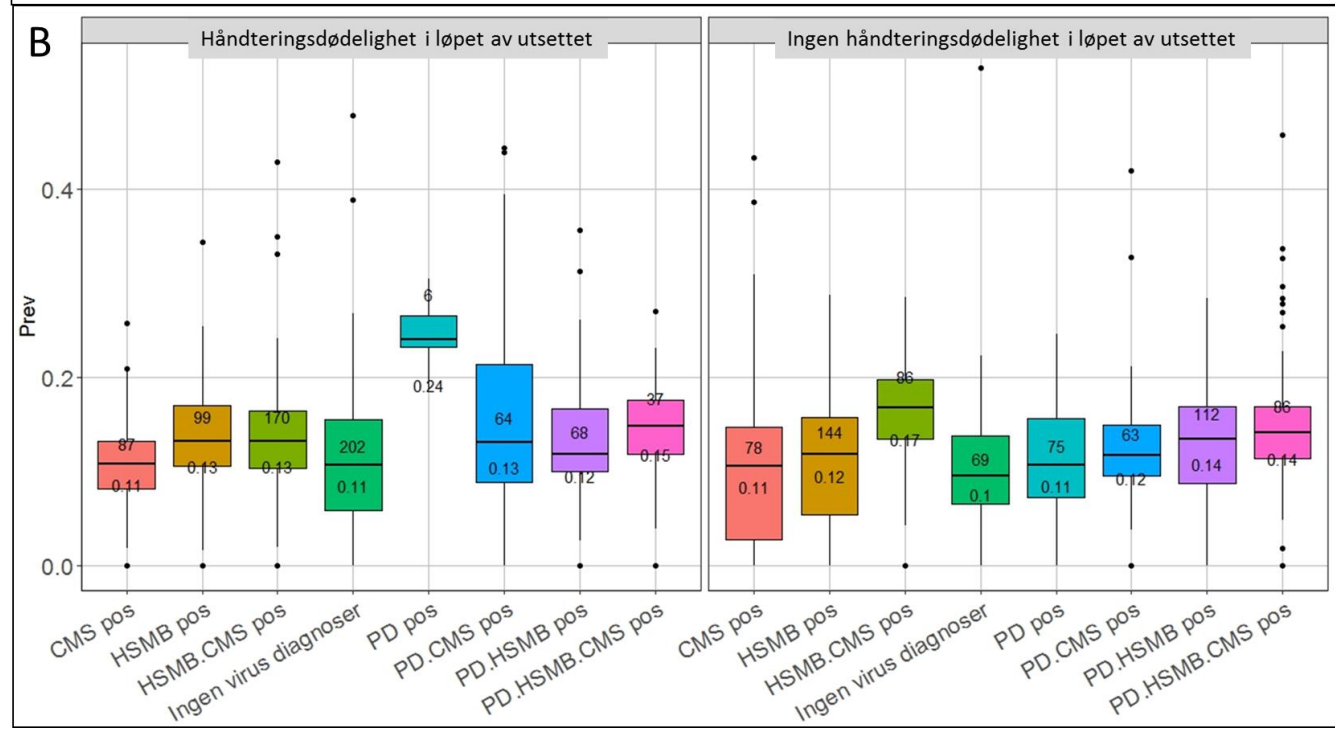
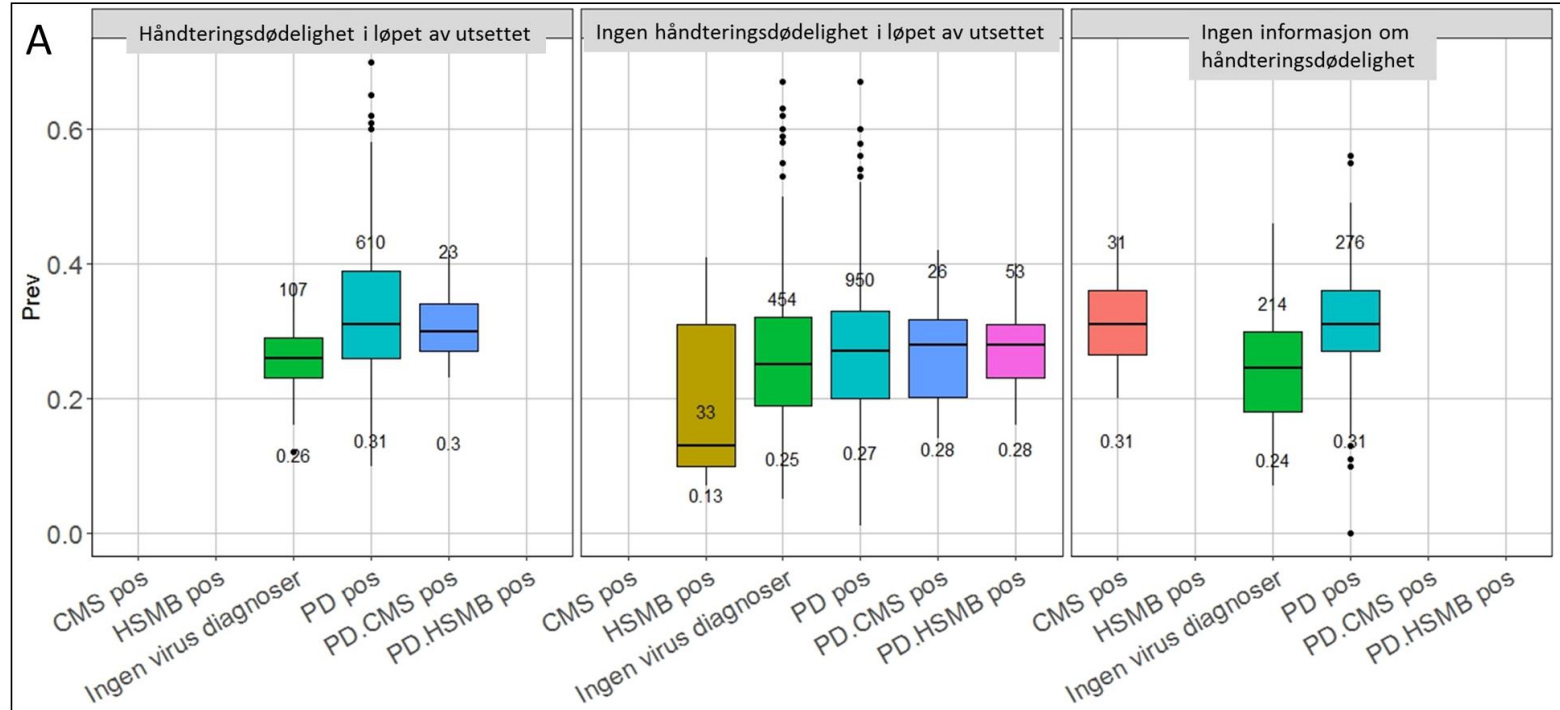
Figur S1



Figur S2



Figur S3



## Figur S4

Linear mixed model fit by REML ['lmerMod']  
Formula: Frekvens\_alle ~ 1 + (1 | Generasjon)  
Data: df.7

REML criterion at convergence: -815

Scaled residuals:

| Min     | 1Q      | Median  | 3Q     | Max    |
|---------|---------|---------|--------|--------|
| -2.1699 | -0.7824 | -0.0927 | 0.6637 | 3.9020 |

Random effects:

| Groups     | Name        | Variance  | Std.Dev. |
|------------|-------------|-----------|----------|
| Generasjon | (Intercept) | 0.0004083 | 0.02021  |
|            | Residual    | 0.0054927 | 0.07411  |

Number of obs: 350, groups: Generasjon, 4

Fixed effects:

|             | Estimate | Std. Error | t value |
|-------------|----------|------------|---------|
| (Intercept) | 0.20432  | 0.01144    | 17.86   |

AIC(fitAlle0) # -808

BIC(fitAlle0) # -797

r.squaredGLMM(fitAlle0)# R2m: 0.00 | R2c: 0.069

Intraclass correlation coefficient (ICC): 0.046

# Figur S5

Linear mixed model fit by REML ["lmerMod"]

Formula: Frekvens\_alle ~ diagn.count + Utsett.cat + Pond.gj.sn.vekt.g. + month.at.sea + (1 | Generasjon)

Data: df.7

REML criterion at convergence: -866.5

Scaled residuals:

| Min     | 1Q      | Median  | 3Q     | Max    |
|---------|---------|---------|--------|--------|
| -2.8465 | -0.6190 | -0.1062 | 0.5492 | 3.5837 |

Random effects:

| Groups     | Name        | Variance  | Std.Dev. |
|------------|-------------|-----------|----------|
| Generasjon | (Intercept) | 0.0002519 | 0.01587  |
| Residual   |             | 0.0041976 | 0.06479  |

Number of obs: 350, groups: Generasjon, 4

Fixed effects:

|                        | Estimate   | Std. Error | t value |
|------------------------|------------|------------|---------|
| (Intercept)            | -0.2428361 | 0.0562196  | -4.319  |
| diagn.count2 diagnoser | -0.0322778 | 0.0129781  | -2.487  |
| diagn.count3 diagnoser | -0.0171674 | 0.0138771  | -1.237  |
| Utsett.catHøst         | -0.1221974 | 0.0199567  | -6.123  |
| Pond.gj.sn.vekt.g.     | 0.0018072  | 0.0002422  | 7.463   |
| month.at.sea           | 0.0166967  | 0.0026144  | 6.386   |

Correlation of Fixed Effects:

|             | (Intr) | dgn.2d | dgn.3d | UtsttH | P.... |
|-------------|--------|--------|--------|--------|-------|
| dgn.cnt2dgn | 0.150  |        |        |        |       |
| dgn.cnt3dgn | 0.483  | 0.719  |        |        |       |
| UtsettctHst | 0.561  | 0.474  | 0.555  |        |       |
| Pnd.gj.s... | -0.600 | -0.410 | -0.498 | -0.911 |       |
| month.at.se | -0.937 | -0.202 | -0.544 | -0.416 | 0.383 |

```
AIC(fitAlle7) # -850
BIC(fitAlle7) # -819
r.squaredGLMM(fitAlle7)# R2m: 0.30 | R2c: 0.287
sem.model.fits(fitAlle7)
confint(fitAlle7, level = 0.95)
# p-values #
2*pt(-abs(summary(fitAlle7)$coefficients[2,3]),df=350-1)# p=0.013 # 2 diagnoser
2*pt(-abs(summary(fitAlle7)$coefficients[3,3]),df=350-1)# p=0.21 # 3 diagnoser
2*pt(-abs(summary(fitAlle7)$coefficients[4,3]),df=350-1)# p=0.0000000001 # utsett
2*pt(-abs(summary(fitAlle7)$coefficients[5,3]),df=350-1)# p=0.0000001 # Pond gj snitt vekt
2*pt(-abs(summary(fitAlle7)$coefficients[6,3]),df=350-1)# p=0.0000000001 # ant mndr i sjø
# #####
```

Intracluster correlation coefficient (ICC): 0.056

## Figur S6

Linear mixed model fit by REML ['lmerMod']  
Formula: Melanin.blod.prev ~ 1 + (1 | Generasjon)  
Data: tot.mod.df

AIC(fitAlle0) # -4827  
BIC(fitAlle0) # -4810  
r.squaredGLMM(fitAlle0)# R2m: 0.00 | R2c: 0.449

REML criterion at convergence: -4833.5

Intraclass correlation coefficient (ICC): 0.449

Scaled residuals:

| Min     | 1Q      | Median  | 3Q     | Max    |
|---------|---------|---------|--------|--------|
| -3.0164 | -0.6742 | -0.0736 | 0.6037 | 5.4823 |

Random effects:

| Groups     | Name        | Variance | Std.Dev. |
|------------|-------------|----------|----------|
| Generasjon | (Intercept) | 0.004954 | 0.07039  |
|            | Residual    | 0.006062 | 0.07786  |

Number of obs: 2152, groups: Generasjon, 8

Fixed effects:

|             | Estimate | Std. Error | t value |
|-------------|----------|------------|---------|
| (Intercept) | 0.28162  | 0.02495    | 11.29   |

# Figur S7

Linear mixed model fit by REML ['lmerMod']

Formula: Melanin.blod.prev ~ handl.cat\_new + sup.int.andel.tot.1 + month.at.sea + (1 | Generasjon)

Data: tot.mod.df

REML criterion at convergence: -5099.5

Scaled residuals:

| Min     | 1Q      | Median  | 3Q     | Max    |
|---------|---------|---------|--------|--------|
| -3.0998 | -0.6736 | -0.0803 | 0.5730 | 5.2180 |

Random effects:

| Groups     | Name        | Variance | Std.Dev. |
|------------|-------------|----------|----------|
| Generasjon | (Intercept) | 0.003547 | 0.05956  |
| Residual   |             | 0.005299 | 0.07279  |

Number of obs: 2152, groups: Generasjon, 8

Fixed effects:

|                             | Estimate  | Std. Error | t value |
|-----------------------------|-----------|------------|---------|
| (Intercept)                 | 0.105902  | 0.029495   | 3.59    |
| handl.cat_newHåndtering nei | -0.017608 | 0.004492   | -3.92   |
| sup.int.andel.tot.1         | -0.155723 | 0.012789   | -12.18  |
| month.at.sea                | 0.011689  | 0.001077   | 10.85   |

Correlation of Fixed Effects:

|                      |                    |
|----------------------|--------------------|
| (Intr) hnd_Hn s....1 |                    |
| hndlct_nwHn          | -0.112             |
| sp.nt.nd..1          | -0.139 -0.037      |
| month.at.se          | -0.685 0.009 0.096 |

```
AIC(fitAlle4) # -5187
BIC(fitAlle4) # -5053
r.squaredGLMM(fitAlle4)# R2m: 0.104 | R2c: 0.464
confint(fitAlle4, level = 0.95)
# p-values #
2*pt(-abs(summary(fitAlle4)$coefficients[2,3]),df=2152-1)# p=0.000001 # handling ja/nei
2*pt(-abs(summary(fitAlle4)$coefficients[3,3]),df=2152-1)# p= 0.00000000000000001 # sup.int.andel.tot
2*pt(-abs(summary(fitAlle4)$coefficients[4,3]),df=2152-1)# p=0.00000000001 # ant mndr i sjø
# ####
```

```
ANOVA test:
Data: tot.mod.df
Models:
fitAlle0: Melanin.blod.prev ~ 1 + (1 | Generasjon)
fitAlle4: Melanin.blod.prev ~ handl.cat_new + sup.int.andel.tot.1 + month.at.sea +
fitAlle4: (1 | Generasjon)
      Df  AIC   BIC logLik deviance Chisq Chi Df Pr(>Chisq)
fitAlle0 3 -4833.1 -4816.1 2419.6 -4839.1
fitAlle4 6 -5121.2 -5087.1 2566.6 -5133.2 294.07 3 < 2.2e-16 ***
```

Intracluster correlation coefficient (ICC): 0.40



## Figur S8

Linear mixed model fit by REML ['lmerMod']  
Formula: Mel.blod.prev ~ 1 + (1 | Generation)  
Data: tot.mod.df

REML criterion at convergence: -3594.3

Scaled residuals:

| Min     | 1Q      | Median  | 3Q     | Max    |
|---------|---------|---------|--------|--------|
| -2.1820 | -0.5545 | -0.0032 | 0.5545 | 5.9630 |

Random effects:

| Groups     | Name        | Variance  | Std.Dev. |
|------------|-------------|-----------|----------|
| Generation | (Intercept) | 0.0005025 | 0.02242  |
| Residual   |             | 0.0047099 | 0.06863  |

Number of obs: 1433, groups: Generation, 3

Fixed effects:

|             | Estimate | Std. Error | t value |
|-------------|----------|------------|---------|
| (Intercept) | 0.12507  | 0.01312    | 9.532   |

AIC(fitAlle0) # -3588

BIC(fitAlle0) # -3572

r.squaredGLMM(fitAlle0)# R2m: 0.00 | R2c: 0.09

Intraclass correlation coefficient (ICC): 0.096

# Figur S9

Linear mixed model fit by REML ['lmerMod']  
Formula: Mel.blod.prev ~ siteLong + diagn.count + TransferPeriod +  
(1 | Generation)  
Data: tot.mod.df

REML criterion at convergence: -3640.4

Scaled residuals:

|         |         |         |        |        |
|---------|---------|---------|--------|--------|
| Min     | 1Q      | Median  | 3Q     | Max    |
| -2.4717 | -0.5745 | -0.0116 | 0.5536 | 6.2300 |

Random effects:

| Groups     | Name        | Variance  | Std.Dev. |
|------------|-------------|-----------|----------|
| Generation | (Intercept) | 0.0002322 | 0.01524  |
| Residual   |             | 0.0044326 | 0.06658  |

Number of obs: 1433, groups: Generation, 3

Fixed effects:

|                        | Estimate | Std. Error | t value |
|------------------------|----------|------------|---------|
| (Intercept)            | 0.075323 | 0.011516   | 6.541   |
| siteLong               | 0.003864 | 0.001068   | 3.618   |
| diagn.count1 diagnose  | 0.009852 | 0.005344   | 1.844   |
| diagn.count2 diagnoser | 0.023843 | 0.005139   | 4.639   |
| diagn.count3 diagnoser | 0.001999 | 0.008015   | 0.249   |
| TransferPeriodQ3       | 0.025712 | 0.004205   | 6.114   |

Correlation of Fixed Effects:

| (Intr)      | sitLng | dgn.1d | dgn.2d | dgn.3d |
|-------------|--------|--------|--------|--------|
| siteLong    | -0.513 |        |        |        |
| dgn.cnt1dgn | -0.156 | -0.240 |        |        |
| dgn.cnt2dgn | -0.149 | -0.210 | 0.670  |        |
| dgn.cnt3dgn | -0.016 | -0.244 | 0.435  | 0.486  |
| TrnsfrPrdQ3 | -0.135 | -0.069 | 0.117  | -0.062 |
|             |        |        | -0.161 |        |

```
AIC(fitAlle3) # -3624
BIC(fitAlle3) # -3582
r.squaredGLMM(fitAlle3)# R2m: 0.08 | R2c: 0.115
confint(fitAlle3, level = 0.95)
# p-values #
2*pt(-abs(summary(fitAlle3)$coefficients[2,3]),df=1433-1)# p=0.0003 # Long
2*pt(-abs(summary(fitAlle3)$coefficients[3,3]),df=1433-1)# p= 0.06 # 1 diagnose
2*pt(-abs(summary(fitAlle3)$coefficients[4,3]),df=1433-1)# p=0.00001 # 2 diagnoser
2*pt(-abs(summary(fitAlle3)$coefficients[5,3]),df=1433-1)# p=0.80 # 3 diagnoser
2*pt(-abs(summary(fitAlle3)$coefficients[6,3]),df=1433-1)# p=0.000001 # TransferPeriodQ3
####
```

ANOVA test:

Data: tot.mod.df

Models:

fitAlle0: Mel.blod.prev ~ 1 + (1 | Generation)

fitAlle3: Mel.blod.prev ~ siteLong + diagn.count + TransferPeriod + (1 |

fitAlle3: Generation)

|          | Df | AIC     | BIC     | logLik | deviance | Chisq  | Chi | Df        | Pr(>Chisq) |
|----------|----|---------|---------|--------|----------|--------|-----|-----------|------------|
| fitAlle0 | 3  | -3595.3 | -3579.5 | 1800.7 | -3601.3  |        |     |           |            |
| fitAlle3 | 8  | -3679.4 | -3637.2 | 1847.7 | -3695.4  | 94.023 | 5   | < 2.2e-16 | ***        |

Intracluster correlation coefficient (ICC): 0.049