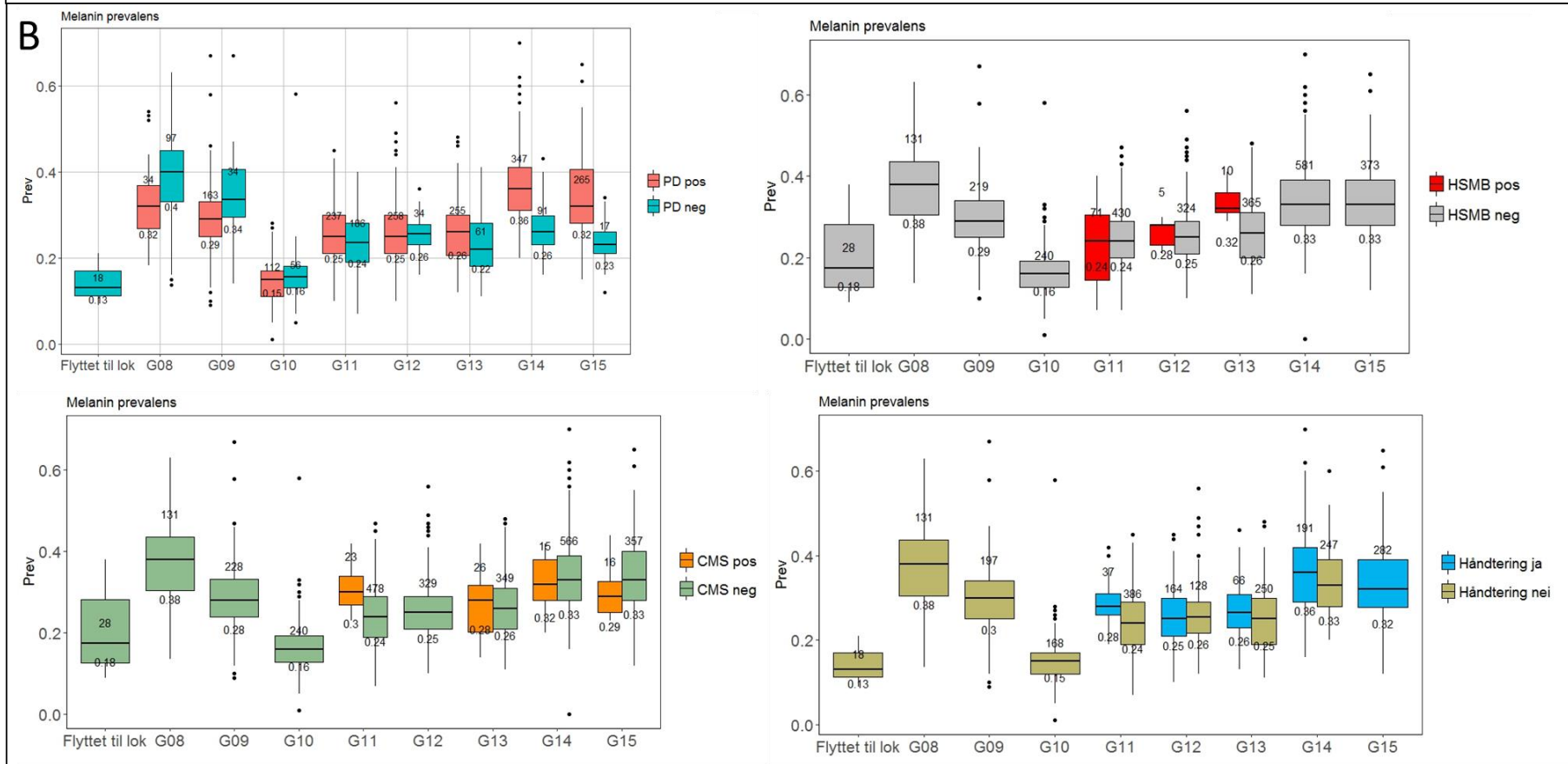
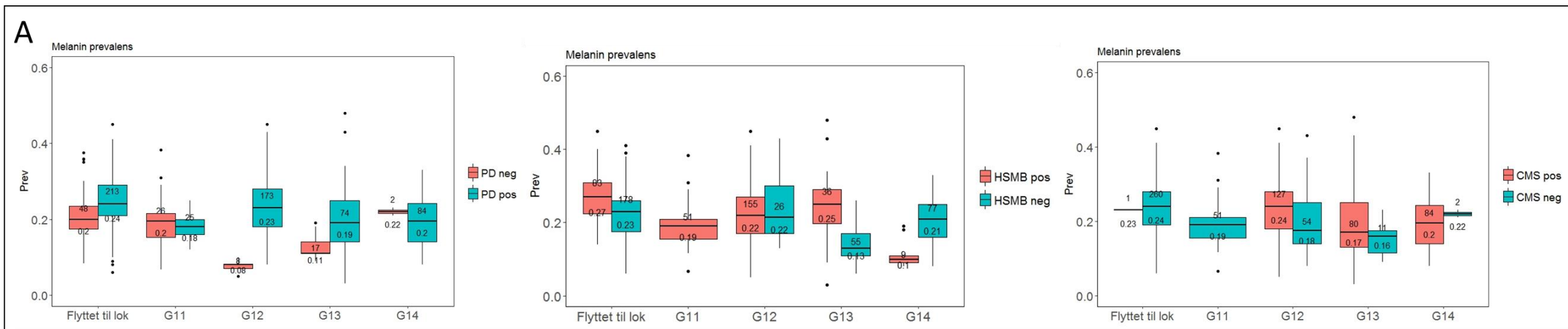


Vedlegg

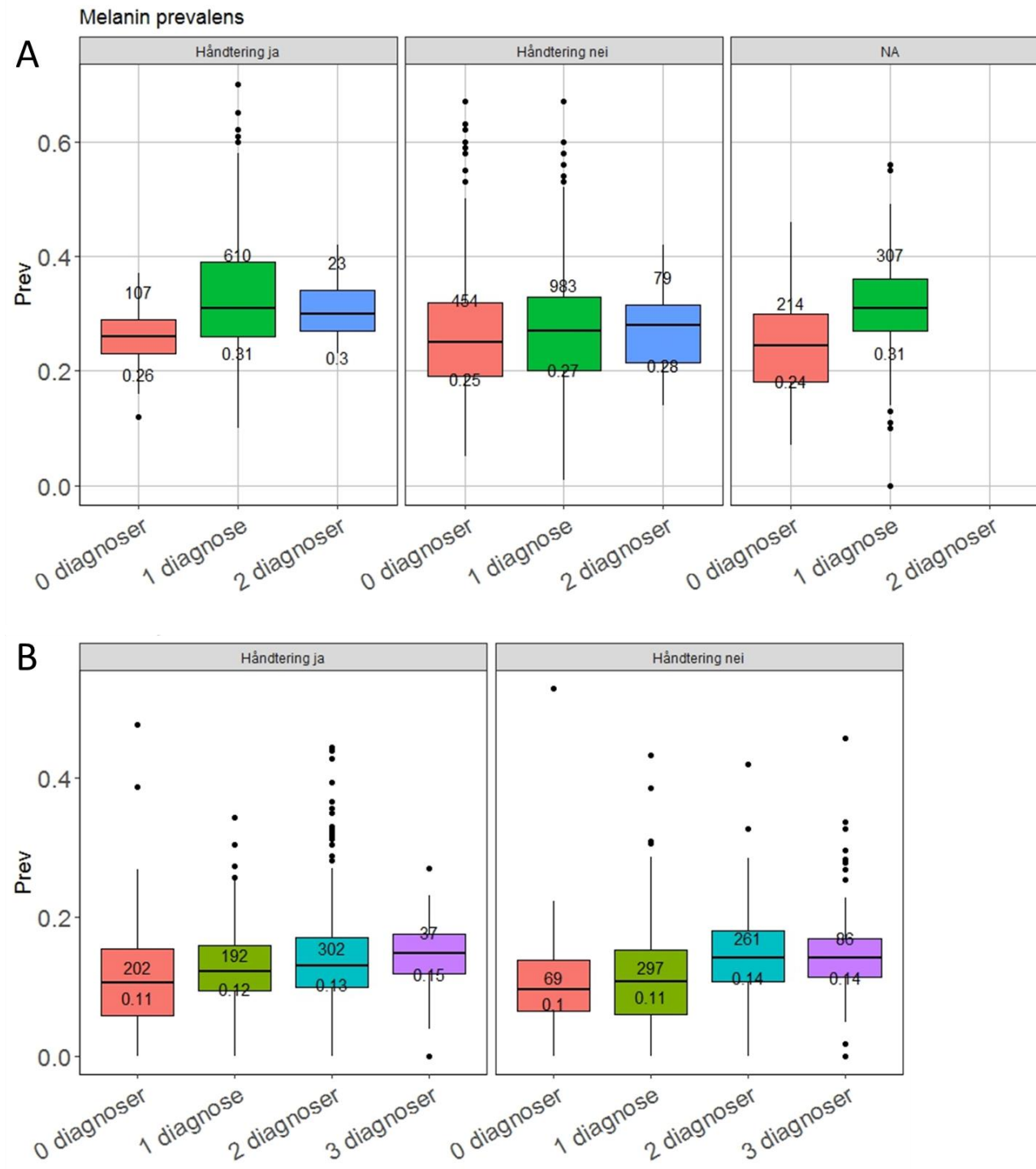
Epi-melaninrapporten

FHF#901256

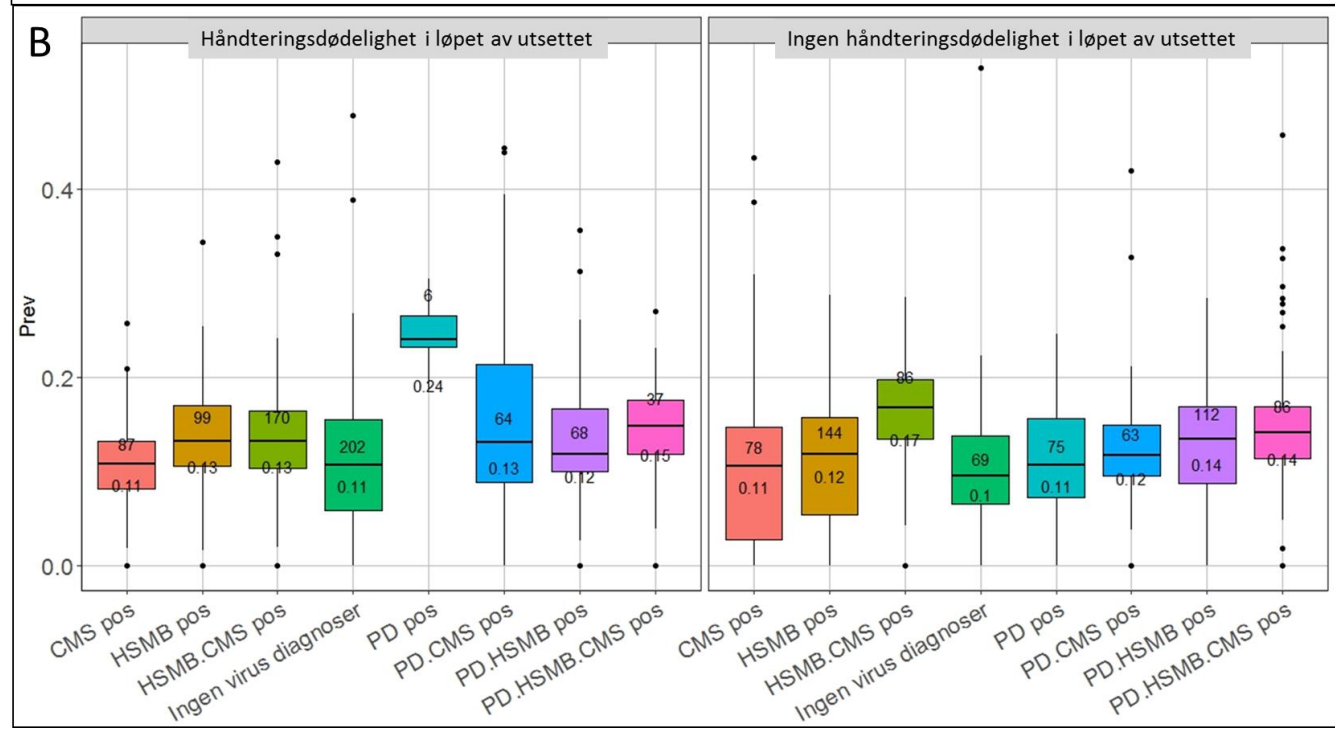
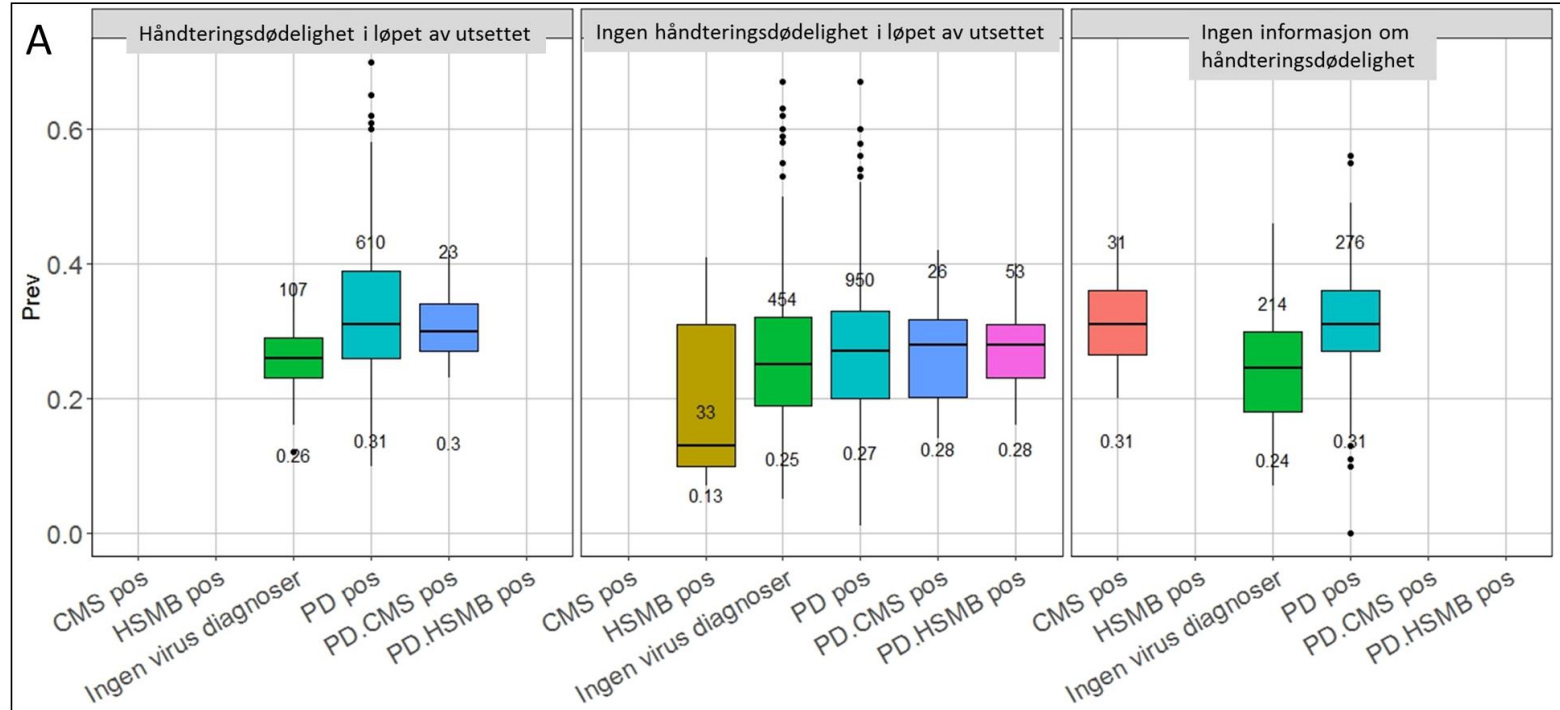
Figur S1



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