Model 1 - full

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method [lmerModLmerTest]
Formula: MYR ~ abDCT(yes-no) + breed + parity + log10(SCCb) + log10(SCCa) + (1 | Herd) + (1 | Animal)
Data: dataopt1
REML criterion at convergence: -4046.1

Scaled residuals:
    Min       1Q        Median    3Q        Max
-4.3255   -0.5568     0.0124    0.5776    3.6922

Random effects:
 Groups Name              Variance         SD
 Animal   (Intercept)     0.0000000        0.00000
 Herd     (Intercept)     0.0003733        0.01932
 Residual                 0.0026955        0.05192
Number of observations: 1380, groups:  Animal, 1375; Herd, 237

Fixed effects:
                         Estimate    SE             df           T-value     Pr(>|t|)
(Intercept)              6.322e-02   8.007e-03      1.335e+03     7.896      5.98e-15 ***
abDCT(yes-no)1           6.886e-03   3.212e-03      1.240e+03     2.144      0.0322 *
Breed1                  -2.655e-03   6.268e-03      3.534e+02    -0.424      0.6721
Breed2                 -1.920e-02    2.395e-02      1.169e+03    -0.802      0.4229
Breed3                   5.305e-03   5.480e-03      5.363e+02     0.968      0.3334
Breed4                  -1.924e-02   1.169e-02      1.370e+03    -1.646      0.1000 .
Parity                  -1.311e-02   8.604e-04      1.359e+03   -15.238     < 2e-16 ***
log10(SCCb)              6.849e-03   3.759e-03      1.368e+03     1.822      0.0687 .
log10(SCCa)             -1.466e-02   2.639e-03      1.357e+03    -5.556      3.32e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Correlation of Fixed Effects:
                  (Intr)  abDCT   Breed1  Breed2  Breed3  Breed4  Parity  log10(SCCb)
abDCT(yes-no)1    -0.147
Breed1            -0.043  -0.065
Breed2            -0.035   0.029   0.019
Breed3            -0.002  -0.027   0.220   0.024
Breed4            -0.011  -0.005   0.071   0.009   0.123
Parity            -0.005  -0.003   0.032   0.027   0.107   0.046
log10(SCCb)       -0.751  -0.103  -0.014  -0.003  -0.087  -0.029  -0.274
log10(SCCa)       -0.374   0.124  -0.067   0.014  -0.075  -0.020  -0.079  -0.154
optimizer (nloptwrap) convergence code: 0 (OK)
boundary (singular) fit: see ?isSingular
```

MYR = milk yield ratio in 305 DIM from the milk recording data before and after dry cow therapy; abDCT(yes-no) = antibiotic or non-antibiotic dry cow therapy; log10(SCCb) = SCC from the last milk recording data before dry cow therapy; log10(SCCa) = SCC from the first milk recording data after calving; Breed1 = Brown Swiss; Breed2 = Pinzgauer; Breed3 = Holstein Friesian; Breed4 = Red Holsteins.

Model 1 – final

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method [lmerModLmerTest]
Formula: MYR ~ abDCT(yes-no) + parity + log10(SCCa) + (1 | Herd)
Data: dataopt1
REML criterion at convergence: -4076.5

Scaled residuals:
   Min          1Q            Median        3Q            Max
-4.3384       -0.5614       -0.0054       0.5750        3.6244

Random effects:
 Groups Name                 Variance              SD
 Herd     (Intercept)        0.0003634             0.01906
 Residual                    0.0027083             0.05204
Number of observations: 1380, groups:  Herd, 237

Fixed effects:
                             Estimate     SE                   df             T-value         Pr(>|t|)
(Intercept)                  7.408e-02    5.241e-03            1.279e+03      14.134          < 2e-16 ***
abDCT(yes-no)                7.547e-03    3.187e-03            1.229e+03       2.368             0.018 *
Parity                      -1.269e-02    8.251e-04            1.367e+03     -15.385          < 2e-16 ***
log10(SCCa)                 -1.378e-02    2.597e-03            1.373e+03      -5.306          1.3e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
                             (Intr)         abDCT          Parity
abDCT(yes-no)                -0.352
Parity                       -0.324        -0.030
lg10(SCCa)                   -0.776         0.105          -0.120
```

MYR = milk yield ratio in 305 DIM from the milk recording data before and after dry cow therapy; abDCT(yes-no) = antibiotic or non-antibiotic dry cow therapy; log10(SCCa) = SCC from the first milk recording data after calving.

Model 1a

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method [lmerModLmerTest]
Formula: MYR ~ abDCT(group) + parity + log10(SCCa) + (1 | Herd)
Data: dataopt1group
REML criterion at convergence: -4057

Scaled residuals:
    Min        1Q          Median      3Q          Max
-4.3311     -0.5652     -0.0083     0.5781      3.6634

Random effects:
 Groups Name              Variance        SD
 Herd     (Intercept)     0.0003626       0.01904
Residual                  0.0027088       0.05205
Number of observations: 1380, groups:  Herd, 237

Fixed effects:
                          Estimate    SE              df          T-value      Pr(>|t|)
(Intercept)               7.444e-02   5.257e-03       1.277e+03   14.161        < 2e-16 ***
penicillins               4.733e-03   5.801e-03       1.198e+03    0.816        0.4147
cloxacillin               6.921e-03   3.537e-03       1.171e+03    1.957        0.0506 .
cephalosporins            1.420e-02   8.783e-03       1.237e+03    1.617        0.1061
rifaximin                 2.993e-02   1.580e-02       1.321e+03    1.894        0.0584 .
Parity                   -1.279e-02   8.309e-04       1.363e+03  -15.399        < 2e-16 ***
log10(SCCa)              -1.384e-02   2.599e-03       1.371e+03   -5.327       1.17e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Correlation of Fixed Effects:

	(Intr)	penicillins	cloxacillin	cephalosporins	rifaximin	Parity
penicillins	-0.171					
cloxacillin	-0.328	0.215				
cephalosporins	-0.154	0.068	0.158			
rifaximin	-0.003	0.042	0.090	0.038		
Parity	-0.330	-0.015	-0.024	0.033	-0.113	
log10(SCCa)	-0.776	0.040	0.102	0.056	-0.011	-0.115

MYR = milk yield ratio in 305 DIM from the milk recording data before and after dry cow therapy; abDCT(group) = different antibiotic dry cow therapy groups; log10(SCCa) = SCC from the first milk recording data after calving.

Model 1b

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method [lmerModLmerTest]
Formula: MYR ~ pathogen(group):abDCT(yes-no) + parity + log10(SCCa) + (1 | Herd)
Data: dataopt1bac
REML criterion at convergence: -296.2

Scaled residuals:
   Min       1Q        Median    3Q        Max
-2.6420   -0.5686   -0.1326   0.6174    3.4951

Random effects:
 Groups Name              Variance         SD
 Herd   (Intercept)       0.000000         0.00000
 Residual                 0.002523         0.05023
Number of observations: 113, groups:  Herd, 51

Fixed effects:
                                  Estimate    SE         df            T-value    Pr(>|t|)
(Intercept)                       0.075492    0.024736   103.000000     3.052     0.00289 **
Parity                           -0.015004    0.002836   103.000000    -5.290     6.93e-07 ***
log10(SCCa)                      -0.023539    0.009178   103.000000    -2.565     0.01176 *
pathogen(group)0:abDCT(yes-no)0   0.027414    0.022032   103.000000     1.244     0.21622
pathogen(group)1:abDCT(yes-no)0   0.055080    0.036725   103.000000     1.500     0.13673
pathogen(group)2:abDCT(yes-no)0   0.026854    0.028068   103.000000     0.957     0.34093
pathogen(group)4:abDCT(yes-no)0   0.023742    0.030581   103.000000     0.776     0.43932
pathogen(group)0:abDCT(yes-no)1   0.035956    0.022705   103.000000     1.584     0.11634
pathogen(group)1:abDCT(yes-no)1   0.072322    0.025467   103.000000     2.840     0.00544 **
pathogen(group)2:abDCT(yes-no)1   0.060642    0.024918   103.000000     2.434     0.01667 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Correlation of Fixed Effects:
                (Intr)  Parity  log10(SCCa)  EVV10:abDCT  EVV11:abDCT  EVV12:abDCT  EVV14:abDCT  EVV10:abDCT  EVV11:abDCT
                                               (yes-no)0    (yes-no)0    (yes-no)0    (yes-no)0    (yes-no)1    (yes-no)1
Parity          -0.187
log10(SCCa)     -0.462  -0.253
EVV10:abDCT     -0.764  -0.012    -0.006
   (yes-no)0
EVV11:abDCT
   (yes-no)0    -0.325  -0.024    -0.239        0.523
EVV12:abDCT
   (yes-no)0    -0.558   0.007    -0.091        0.681        0.431
EVV14:abDCT
   (yes-no)0    -0.524   0.062    -0.096        0.624        0.394        0.498
EVV10:abDCT
   (yes-no)1    -0.699  -0.064    -0.053        0.842        0.524        0.666        0.608
EVV11:abDCT
   (yes-no)1    -0.581  -0.106    -0.096        0.752        0.484        0.599        0.544        0.743
EVV12:abDCT
   (yes-no)1    -0.653   0.063    -0.091        0.766        0.478        0.609        0.562        0.745        0.666
fit warnings:
fixed-effect model matrix is rank deficient so dropping 1 column / coefficient optimizer (nloptwrap) convergence code: 0 (OK)
boundary (singular) fit: see ?isSingular
```

MYR = milk yield ratio in 305 DIM from the milk recording data before and after dry cow therapy; pathogen(group) = results of bacteriological examinations classified in major pathogens, minor pathogens, other pathogens and negative test results; abDCT(yes-no) = antibiotic or non-antibiotic dry cow therapy; log10(SCCa) = SCC from the first milk recording data after calving; pathogen(group)0 = negative bacteriological test result; pathogen(group)1 = major pathogens group; pathogen(group)2 = minor pathogens group; pathogen(group)4 = other pathogens group.

Model 2 - full

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: CCR ~ abDCT(yes-no) + breed + parity + sqrt(milk yield before) + (1 | Herd) + (1 | Animal)
Data: dataopt1
REML criterion at convergence: 2677.6

Scaled residuals:
   Min        1Q         Median     3Q         Max
-2.12245   -0.41787   -0.02372   0.36835    2.80983

Random effects:
 Groups Name              Variance          SD
 Animal   (Intercept)     0.23265           0.4823
 Herd     (Intercept)     0.01147           0.1071
 Residual                 0.15588           0.3948
Number of observations: 1380, groups:  Animal, 1375; Herd, 237

Fixed effects:
                          Estimate     SE                df           T-value     Pr(>|t|)
 (Intercept)              -4.858e-01   1.640e-01         6.369e+02    -2.963      0.00316 **
abDCT(yes-no)1            -2.309e-01   3.524e-02         9.372e+02    -6.552      9.35e-11 ***
Breed1                     1.181e-01   6.153e-02         2.573e+02     1.919      0.05610 .
Breed2                    -1.025e-01   2.679e-01         1.018e+03    -0.383      0.70216
Breed3                     3.659e-02   5.725e-02         3.468e+02     0.639      0.52316
Breed4                    -1.028e-02   1.354e-01         1.323e+03    -0.076      0.93949
Parity                    -2.898e-02   9.937e-03         1.329e+03    -2.916      0.00361 **
sqrt(milk yield before)    2.878e-03   1.851e-03         5.738e+02     1.555      0.12058
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Correlation of Fixed Effects:

	(Intr)	abDCT(yes-no)1	Breed1	Breed2	Breed3	Breed4	Parity
abDCT(yes-no)1	-0.057						
Breed1	-0.056	-0.068					
Breed2	-0.153	0.028	0.025				
Breed3	0.198	-0.019	0.149	-0.009			
Breed4	0.065	-0.003	0.054	-0.002	0.104		
Parity	0.108	-0.014	0.017	-0.011	0.153	0.070	
sqrt(milk yield before)	-0.974	-0.035	0.014	0.139	-0.263	-0.093	-0.270

CCR = cell count ratio from the last milk recording data before dry cow therapy and the first SCC after calving; abDCT(yes-no) = antibiotic or non-antibiotic dry cow therapy; sqrt (milk yield before) = square root from the milk yield in 305 DIM from the milk recording data before dry cow therapy; Breed1 = Brown Swiss; Breed2 = Pinzgauer; Breed3 = Holstein Friesian; Breed4 = Red Holsteins.

Model 2 – final

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: CCR ~ abDCT(yes-no) + parity + sqrt(milk yield before) + (1 | Herd) + (1 | Animal)
Data: dataopt1
REML criterion at convergence: 2671

Scaled residuals:
   Min        1Q          Median      3Q          Max
-2.14716    -0.41438    -0.02513    0.36165     2.82431

Random effects:
 Groups Name              Variance          SD
 Animal   (Intercept)     0.23065           0.4803
 Herd     (Intercept)     0.01199           0.1095
 Residual                 0.15746           0.3968
Number of observations: 1380, groups:  Animal, 1375; Herd, 237

Fixed effects:
                          Estimate     SE              df          T-value     Pr(>|t|)
 (Intercept)              -4.898e-01   1.583e-01       5.768e+02   -3.094      0.00207 **
abDCT(yes-no)1            -2.254e-01   3.518e-02       9.487e+02   -6.406      2.34e-10 ***
Parity                    -2.982e-02   9.808e-03       1.322e+03   -3.040      0.00241 **
sqrt(milk yield before)    3.093e-03   1.765e-03       5.062e+02    1.753      0.08026 .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Correlation of Fixed Effects:

	(Intr)	abDCT	Parity
abDCT(yes-no)1	-0.057		
Parity	0.079	-0.011	
sqrt(milk yield before)	-0.975	-0.042	-0.241

CCR = cell count ratio from the last milk recording data before dry cow therapy and the first SCC after calving; abDCT(yes-no) = antibiotic or non-antibiotic dry cow therapy; sqrt (milk yield before) = square root from the milk yield in 305 DIM from the milk recording data before dry cow therapy.

Model 2a

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: CCR ~ abDCT(group) + parity + sqrt(milk yield before) + (1 | Herd) + (1 | Animal)
Data: dataopt1group
REML criterion at convergence: 2676.6

Scaled residuals:
    Min        1Q         Median     3Q         Max
-2.13675   -0.41811   -0.02762   0.36055    2.81706

Random effects:
 Groups Name           Variance       SD
 Animal   (Intercept)  0.23197        0.4816
 Herd     (Intercept)  0.01209        0.1100
 Residual              0.15625        0.3953
Number of observations: 1380, groups:  Animal, 1375; Herd, 237

Fixed effects:
                        Estimate    SE           df           T-value   Pr(>|t|)
 (Intercept)            -4.853e-01  1.593e-01    5.774e+02    -3.045    0.00243 **
penicillins             -1.693e-01  6.472e-02    9.757e+02    -2.616    0.00905 **
cloxacillin             -2.334e-01  3.882e-02    8.816e+02    -6.011    2.7e-09 ***
cephalosporins          -3.212e-01  9.738e-02    8.311e+02    -3.299    0.00101 **
rifaximin               -1.105e-01  1.800e-01    1.283e+03    -0.614    0.53929
Parity                  -3.112e-02  9.907e-03    1.320e+03    -3.141    0.00172 **
sqrt(milk yield before)  3.080e-03  1.778e-03    5.074e+02     1.732    0.08379 .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Correlation of Fixed Effects:

	(Intr)	penicillins	cloxacillin	cephalosporins	rifaximin	Parity
penicillins	0.044					
cloxacillin	-0.092	0.221				
cephalosporins	0.021	0.087	0.152			
rifaximin	-0.035	0.045	0.085	0.028		
Parity	0.085	0.005	-0.015	0.058	-0.125	
sqrt(milk yield before)	-0.975	-0.098	0.002	-0.065	0.034	-0.247

CCR = cell count ratio from the last milk recording data before dry cow therapy and the first SCC after calving; abDCT(group) = different antibiotic dry cow therapy groups; sqrt (milk yield before) = square root from the milk yield in 305 DIM from the milk recording data before dry cow therapy.

Model 2b

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']
Formula: CCR ~ pathogen(group):abDCT(yes-no) + parity + sqrt(milk yield before) + (1 | Herd)
Data: dataopt1bac
REML criterion at convergence: 229.6

Scaled residuals:
   Min        1Q         Median     3Q         Max
-1.80781   -0.73293   -0.03457   0.60539    2.98258

Random effects:
 Groups Name           Variance        SD
 Herd    (Intercept)   0.01477         0.1215
 Residual              0.37918         0.6158
Number of observations: 113, groups:  Herd, 51

Fixed effects:
                                  Estimate    SE          df           T-value    Pr(>|t|)
(Intercept)                       -2.212270   0.596005     71.689325   -3.712     0.000404 ***
Parity                             0.017222   0.034835     91.134744    0.494     0.622227
sqrt(milk yield before)            0.014286   0.005949     56.912216    2.401     0.019618 *
pathogen(group)0:abDCT(yes-no)0    0.268133   0.275406    102.990996    0.974     0.332541
pathogen(group)1:abDCT(yes-no)0    1.335544   0.450338    102.324496    2.966     0.003759 **
pathogen(group)2:abDCT(yes-no)0    0.601524   0.348809    102.215760    1.725     0.087639 .
pathogen(group)4:abDCT(yes-no)0    0.468256   0.380621    102.686368    1.230     0.221417
pathogen(group)0:abDCT(yes-no)1    0.269105   0.281608     99.667204    0.956     0.341585
pathogen(group)1:abDCT(yes-no)1    0.342448   0.320620     97.369703    1.068     0.288125
pathogen(group)2:abDCT(yes-no)1    0.359150   0.308427    101.532552    1.164     0.246967
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
Correlation of Fixed Effects:
                (Intr)  Parity  sqrt(milk     EVV10:abDCT  EVV11:abDCT  EVV12:abDCT  EVV14:abDCT  EVV10:abDCT  EVV11:abDCT
                               yield before)  (yes-no)0    (yes-no)0    (yes-no)0    (yes-no)0    (yes-no)1    (yes-no)1
Parity          -0.043
sqrt(milk       -0.887  -0.141
yield before)
EVV10:abDCT     -0.347   0.006  -0.055
  (yes-no)0
EVV11:abDCT     -0.365  -0.102   0.152         0.517
  (yes-no)0
EVV12:abDCT     -0.381  -0.017   0.078         0.673        0.427
  (yes-no)0
EVV14:abDCT     -0.254   0.059  -0.049         0.625        0.370        0.486
  (yes-no)0
EVV10:abDCT     -0.343  -0.069  -0.034         0.835        0.511        0.654        0.602
  (yes-no)1
EVV11:abDCT     -0.420  -0.147   0.113         0.732        0.480        0.590        0.522        0.725
  (yes-no)1
EVV12:abDCT     -0.352   0.052  -0.011         0.764        0.462        0.599        0.558        0.744        0.650
  (yes-no)1
fit warnings:
fixed-effect model matrix is rank deficient so dropping 1 column / coefficient
```

CCR = cell count ratio from the last milk recording data before dry cow therapy and the first SCC after calving; pathogen(group) = results of bacteriological examinations classified in major pathogens, minor pathogens, other pathogens and negative test results; abDCT(yes-no) = antibiotic or non-antibiotic dry cow therapy; sqrt (milk yield before) = square root from the milk yield in 305 DIM from the milk recording data before dry cow therapy; pathogen(group)0 = negative bacteriological test result; pathogen(group)1 = major pathogens group; pathogen(group)2 = minor pathogens group; pathogen(group)4 = other pathogens group.

Model 3

```
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
 Family: binomial (logit)
Formula: IMGa ~ IMGb * abDCT(yes-no) + (1 | herd)
Data: data

   AIC        BIC        logLik     deviance   df.resid
  2463.6      2494.3     -1226.8    2453.6     3457

Scaled residuals:
   Min        1Q         Median     3Q         Max
-0.6728     -0.3614     -0.3138    -0.2854     3.6450

Random effects:
 Groups Name        Variance   SD
 herd  (Intercept)  0.1858     0.4311
Number of observations: 3462, groups:  herd, 251

Fixed effects:
                         Estimate   SE              z value        Pr(>|z|)
(Intercept)              -2.2476    0.0972          -23.123          < 2e-16 ***
IMGb                      0.7887    0.1509            5.228        1.71e-07 ***
abDCT(yes-no)1           -0.1560    0.1410           -1.107        0.268
IMGb:abDCT(yes-no)1      -0.1031    0.2347           -0.439        0.661
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
Correlation of Fixed Effects:
                     (Intr)   IMGb     abDCT(yes-no)1
IMGb                 -0.424
abDCT(yes-no)1       -0.570    0.309
IMGb:abDCT(yes-no)1   0.285   -0.636   -0.563
```

IMGa = inflammation of the mammary gland after calving defined via SCC threshold of >200,000 cells/mL in the first milk recording data after calving; IMGb = inflammation of the mammary gland before dry-off defined via SCC threshold of >200,000 cells/mL in the last milk recording data before dry-off; abDCT(yes-no) = antibiotic or non-antibiotic dry cow therapy.

Model 3a

```
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
 Family: binomial (logit)
Formula: IMGa ~ IMGb * abDCT(group) + (1 | herd)
Data: data

   AIC       BIC       logLik     deviance   df.resid
  2467.9     2535.5    -1222.9    2445.9     3451

Scaled residuals:
   Min       1Q        Median     3Q         Max
-0.6687    -0.3681    -0.3163    -0.2777     4.4617

Random effects:
 Groups Name         Variance   SD
 herd  (Intercept)   0.183      0.4278
Number of observations: 3462, groups:  herd, 251

Fixed effects:
                       Estimate    SE          z value     Pr(>|z|)
(Intercept)            -2.24504    0.09703     -23.139     < 2e-16 ***
IMGb                    0.78989    0.15083       5.237     1.63e-07 ***
penicillins             0.27116    0.23175       1.170     0.2420
cloxacillin            -0.27815    0.16269      -1.710     0.0873 .
cephalosporins         -0.27375    0.48818      -0.561     0.5750
rifaximin              -0.85602    1.03750      -0.825     0.4093
IMGb:penicillins       -1.10060    0.54307      -2.027     0.0427 *
IMGb:cloxacillin        0.04559    0.26046       0.175     0.8611
IMGb:cephalosporins     0.15877    0.67276       0.236     0.8134
IMGb:rifaximin          1.27996    1.24328       1.030     0.3032
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

Correlation of Fixed Effects:

	(Intr)	IMGb	penicillins	cloxacillin	cephalosporins	rifaximin	IMGb:penicillins	IMGb:cloxacillins	IMGb:cephalosporins
IMGb	-0.425								
penicillins	-0.331	0.193							
cloxacillin	-0.493	0.267	0.187						
cephalosporins	-0.178	0.085	0.061	0.094					
rifaximin	-0.093	0.039	0.030	0.049	0.017				
IMGb:penicillins	0.130	-0.272	-0.407	-0.079	-0.026	-0.012			
IMGb:cloxacillin	0.257	-0.574	-0.112	-0.588	-0.048	-0.024	0.160		
IMGb:cephalosporins	0.108	-0.216	-0.044	-0.062	-0.693	-0.009	0.060	0.124	
IMGb:rifaximin	0.049	-0.122	-0.023	-0.032	-0.006	-0.823	0.033	0.070	0.027

IMGa = inflammation of the mammary gland after calving defined via SCC threshold of >200,000 cells/mL in the first milk recording data after calving; IMGb = inflammation of the mammary gland before dry-off defined via SCC threshold of >200,000 cells/mL in the last milk recording data before dry-off; abDCT(group) = different antibiotic dry cow therapy groups.

Model 3 reduced

```
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
 Family: binomial (logit)
Formula: IMGa ~ IMGb + (1 | herd)
Data: data

    AIC       BIC        logLik      deviance    df.resid
  2462.4    2480.9      -1228.2      2456.4      3459

Scaled residuals:
    Min       1Q         Median      3Q          Max
-0.6540    -0.3689      -0.3144     -0.2854      3.5356

Random effects:
 Groups Name         Variance     SD
 herd  (Intercept)   0.2125       0.461
Number of observations: 3462, groups:  herd, 251

Fixed effects:
                     Estimate     SE              z value         Pr(>|z|)
(Intercept)          -2.31821     0.08079         -28.694         < 2e-16 ***
IMGb                  0.72912     0.11614           6.278         3.43e-10 ***

---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation of Fixed Effects:
              (Intr)
IMGb          -0.430
```

IMGa = inflammation of the mammary gland after calving defined via SCC threshold of >200,000 cells/mL in the first milk recording data after calving; IMGb = inflammation of the mammary gland before dry-off defined via SCC threshold of >200,000 cells/mL in the last milk recording data before dry-off.

Model 4

```
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
 Family: binomial (logit)
Formula: CM30(yes-no) ~ IMGb * abDCT(yes-no) + (1 | herd)
Data: data

    AIC         BIC             logLik          deviance        df.resid
  1354.5        1385.2          -672.3          1344.5          3418

Scaled residuals:
    Min         1Q              Median          3Q              Max
-0.3666         -0.2320         -0.2081         -0.1954         5.1210


Random effects:
 Groups Name            Variance        SD
 herd  (Intercept)      0.2199          0.469
Number of observations: 3423, groups:  herd, 247


Fixed effects:
                                Estimate        SE                      z value                 Pr(>|z|)
(Intercept)                     -3.17797        0.14677                 -21.653                 <2e-16 ***
IMGb                             0.33216        0.24729                   1.343                 0.179
abDCT(yes-no)1                   0.04983        0.19502                   0.256                 0.798
IMGb:abDCT(yes-no)1              0.12549        0.35374                   0.355                 0.723
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
Correlation of Fixed Effects:
                          (Intr)     IMGb      abDCT(yes-no)1
IMGb                      -0.408
abDCT(yes-no)1            -0.535      0.317
IMGb:abDCT(yes-no)1        0.278     -0.697    -0.535
```

CM30(yes-no) = diagnosed clinical mastitis cases by veterinarians within 30 DIM; IMGb = inflammation of the mammary gland before dry-off defined via SCC threshold of >200,000 cells/mL in the last milk recording data before dry-off; abDCT(yes-no) = antibiotic or non-antibiotic dry cow therapy.

Model 5

```
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
 Family: binomial (logit)
Formula: CM90(yes-no) ~ IMGb * abDCT(yes-no) + (1 | herd)
Data: data

AIC         BIC         logLik      deviance    df.resid
1931.2      1961.8      -960.6      1921.2      3418

Scaled residuals:
   Min      1Q          Median      3Q          Max
-0.6445     -0.3082     -0.2653     -0.2331     4.3678

Random effects:
 Groups Name            Variance    SD
 herd  (Intercept)      0.3662      0.6052
Number of observations: 3423, groups:  herd, 247

Fixed effects:
                        Estimate    SE               z value          Pr(>|z|)
(Intercept)             -2.70495    0.11874          -22.780          <2e-16 ***
IMGb                     0.36494    0.20050            1.820          0.0687 .
abDCT(yes-no)1           0.08781    0.15888            0.553          0.5805
IMGb:abDCT(yes-no)1      0.10921    0.28496            0.383          0.7015
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
Correlation of Fixed Effects:
                      (Intr)   IMGb     abDCT(yes-no)1
IMGb                  -0.413
abDCT(yes-no)1        -0.554    0.314
IMGb:abDCT(yes-no)1    0.289   -0.698   -0.524
```

CM90(yes-no) = diagnosed clinical mastitis cases by veterinarians within 90 DIM; IMGb = inflammation of the mammary gland before dry-off defined via SCC threshold of >200,000 cells/mL in the last milk recording data before dry-off; abDCT(yes-no) = antibiotic or non-antibiotic dry cow therapy.