Contrast:

Group	x
Control.F4	-1
Mutant.F4	1
Control.F5	0
Mutant.F5	0
Control.F6	0
Mutant.F6	0
Control.F7	0
Mutant.F7	0
Control.F8	0
Mutant.F8	0
Control.F9	0
Mutant.F9	0
Control.F10	0
Mutant.F10	0

Results:

Comparison	Protein	Log2 Fold Change	P-value	P-adjust	SE	DF
Mutant.F10-Control.F10	Q3UMB9	-1.835485	0	0	0.1513823	26.00002
Mutant.F4-Control.F4	Q3UMB9	-1.307498	0	0	0.1513823	26.00002
Mutant.F5-Control.F5	Q3UMB9	-1.377369	0	0	0.1513823	26.00002
Mutant.F6-Control.F6	Q3UMB9	-1.598311	0	0	0.1513823	26.00002
Mutant.F7-Control.F7	Q3UMB9	-1.688940	0	0	0.1513823	26.00002
Mutant.F8-Control.F8	Q3UMB9	-1.637331	0	0	0.1513823	26.00002
Mutant.F9-Control.F9	Q3UMB9	-1.173553	0	0	0.1513823	26.00002

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method
[lmerModLmerTest]
Formula: Abundance ~ 1 + (1|Mixture) + Condition
   Data: msstats_prot %>% filter(Protein == prot)

REML criterion at convergence: 3.7

Scaled residuals:
    Min      1Q  Median      3Q     Max
-1.5019 -0.6087 -0.1490  0.7500  1.4234

Random effects:
 Groups   Name        Variance Std.Dev.
 Mixture  (Intercept) 0.009755 0.09877
 Residual             0.034375 0.18540
Number of obs: 42, groups:  Mixture, 3

Fixed effects:
                   Estimate Std. Error      df t value Pr(>|t|)
(Intercept)          7.6219     0.1213 17.1227  62.843  < 2e-16 ***
ConditionControl.F4  -0.9095     0.1514 26.0000  -6.008 2.41e-06 ***
ConditionControl.F5  -0.6757     0.1514 26.0000  -4.464 0.000138 ***
ConditionControl.F6  -0.3812     0.1514 26.0000  -2.518 0.018302 *
ConditionControl.F7  -0.3003     0.1514 26.0000  -1.983 0.057978 .
ConditionControl.F8  -0.4917     0.1514 26.0000  -3.248 0.003198 **
ConditionControl.F9  -0.6658     0.1514 26.0000  -4.398 0.000165 ***
ConditionMutant.F10  -1.8355     0.1514 26.0000 -12.125 3.33e-12 ***
ConditionMutant.F4   -2.2170     0.1514 26.0000 -14.645 4.51e-14 ***
ConditionMutant.F5   -2.0531     0.1514 26.0000 -13.562 2.66e-13 ***
ConditionMutant.F6   -1.9795     0.1514 26.0000 -13.076 6.11e-13 ***
ConditionMutant.F7   -1.9892     0.1514 26.0000 -13.140 5.46e-13 ***
ConditionMutant.F8   -2.1290     0.1514 26.0000 -14.064 1.15e-13 ***
ConditionMutant.F9   -1.8394     0.1514 26.0000 -12.150 3.18e-12 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation matrix not shown by default, as p = 14 > 12.
Use print(summary(fit), correlation=TRUE)  or
    vcov(summary(fit))        if you need it
```