

```

Linear mixed model fit by REML ['lmerModLmerTest']
Formula: Abundance ~ 0 + (1|BioFraction) + Genotype
  Data: subdat
REML criterion at convergence: 9.9247
Random effects:
 Groups      Name      Std.Dev.
BioFraction (Intercept) 0.1780
Residual          0.2259
Number of obs: 42, groups: BioFraction, 7
Fixed Effects:
GenotypeControl  GenotypeMutant
          7.133          5.616

```

Contrast:

GenotypeControl	GenotypeMutant
-1	1

Results:

Protein	P.value	Log2.FC	t.statistic	variance
Q3UMB9	0	-1.516927	-21.75455	0.0048622