

## Model0 – Intrafraction Comparisons

Linear mixed model fit by REML. t-tests use Satterthwaite's method

[lmerModLmerTest]

Formula: Abundance ~ 0 + Genotype.BioFraction + (1|Mixture)

Data: msstats\_prot %>% filter(Protein == swip)

REML criterion at convergence: 3.7

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.4998	-0.6099	-0.1471	0.7489	1.4237

Random effects:

Groups	Name	Variance	Std.Dev.
Mixture	(Intercept)	0.009667	0.09832
Residual		0.034474	0.18567

Number of obs: 42, groups: Mixture, 3

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t )
ConditionControl.F10	7.6192	0.1213	17.2481	62.81	<2e-16 ***
ConditionControl.F4	6.7117	0.1213	17.2481	55.33	<2e-16 ***
ConditionControl.F5	6.9462	0.1213	17.2481	57.26	<2e-16 ***
ConditionControl.F6	7.2407	0.1213	17.2481	59.69	<2e-16 ***
ConditionControl.F7	7.3216	0.1213	17.2481	60.36	<2e-16 ***
ConditionControl.F8	7.1298	0.1213	17.2481	58.78	<2e-16 ***
ConditionControl.F9	6.9549	0.1213	17.2481	57.34	<2e-16 ***
ConditionMutant.F10	5.7850	0.1213	17.2481	47.69	<2e-16 ***
ConditionMutant.F4	5.4051	0.1213	17.2481	44.56	<2e-16 ***
ConditionMutant.F5	5.5681	0.1213	17.2481	45.90	<2e-16 ***
ConditionMutant.F6	5.6415	0.1213	17.2481	46.51	<2e-16 ***
ConditionMutant.F7	5.6331	0.1213	17.2481	46.44	<2e-16 ***
ConditionMutant.F8	5.4930	0.1213	17.2481	45.28	<2e-16 ***
ConditionMutant.F9	5.7813	0.1213	17.2481	47.66	<2e-16 ***

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Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Goodness of fit

R2m	R2c
0.9351423	0.9493463

*Marginal and conditional R-squared for mixed effect model (Nakagawa et al., 2014).*

## Statistical Results

protein	contrast	log2FC	Pvalue	Tstatistic	SE	DF
Q3UMB9	Mutant.F7-Control.F7	-1.688576	0	-11.13831	0.1516008	25.99987

## Model1 – Mutant-Control Comparison

Linear mixed model fit by REML. t-tests use Satterthwaite's method  
[lmerModLmerTest]

Formula: Abundance ~ 0 + Genotype + BioFraction + (1|Subject)

Data: msstats\_prot %>% filter(Protein == swip)

REML criterion at convergence: -7.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.12532	-0.55464	-0.09399	0.58495	1.98324

Random effects:

Groups	Name	Variance	Std.Dev.
Subject	(Intercept)	0.03412	0.1847
Residual		0.02293	0.1514

Number of obs: 42, groups: Subject, 6

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t )	
GenotypeControl	6.81676	0.12546	6.32017	54.332	1.11e-09	***
GenotypeMutant	5.30003	0.12546	6.32017	42.243	5.44e-09	***
BioFractionF5	0.19875	0.08742	30.00000	2.273	0.030328	*
BioFractionF6	0.38272	0.08742	30.00000	4.378	0.000134	***
BioFractionF7	0.41895	0.08742	30.00000	4.792	4.19e-05	***
BioFractionF8	0.25304	0.08742	30.00000	2.894	0.007018	**
BioFractionF9	0.30969	0.08742	30.00000	3.542	0.001319	**
BioFractionF10	0.64373	0.08742	30.00000	7.363	3.34e-08	***

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Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

### Goodness of fit

R2m	R2c
0.9162647	0.9663459

### Statistical Results

protein	contrast	log2FC	Pvalue	Tstatistic	SE	DF
Q3UMB9	Mutant-Control	-1.516727	0.0006566	-9.605806	0.1578969	3.999999