

**B**

models	aic	deltaAIC	batch_p	e_p	sumVIF
~ 1	-215.3	NA	NA	NA	NA
~ Batch	-263.7	48.4	2.2e-12	NA	NA
~ Batch + Tissue	-263.8	48.5	1.3e-03	NA	7
~ Batch + Tissue + Status	-268.5	53.2	3.6e-03	1.5e-02	8
~ Batch + Tissue + Status + Tissue:Status	-260.1	44.8	8.3e-03	5.8e-02	12
~ Tissue + Status + Tissue:Status	-253.6	38.3	NA	3.1e-08	4
~ Tissue + Status	-261.0	45.7	NA	5.2e-03	2

C

paleturquoise~ Tissue + Status

	Sum Sq	Df	F value	Pr(>F)	eta^2
Batch	0.045	1	8.9	0.0036	0.079
Tissue	0.096	9	2.1	0.035	0.16
Status	0.031	1	6.2	0.015	0.057
Residuals	0.52	100	NA	NA	NA

D

BP GO terms enriched in paleturquoise module

ID	Description	GeneRatio	pvalue	p.adjust
GO:0036444	calcium import into the mitochondrion	4/571	0.0010	0.61
GO:0043484	regulation of RNA splicing	7/571	0.0017	0.61
GO:0030148	sphingolipid biosynthetic process	8/571	0.0023	0.61
GO:0006376	mRNA splice site selection	5/571	0.0025	0.61
GO:0044257	cellular protein catabolic process	4/571	0.0030	0.61
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	16/571	0.0030	0.61
GO:0006851	mitochondrial calcium ion transmembrane transport	5/571	0.0048	0.61
GO:0031398	positive regulation of protein ubiquitination	9/571	0.0052	0.61
GO:0002756	MyD88-independent toll-like receptor signaling pathway	4/571	0.0054	0.61
GO:0051560	mitochondrial calcium ion homeostasis	4/571	0.0069	0.61