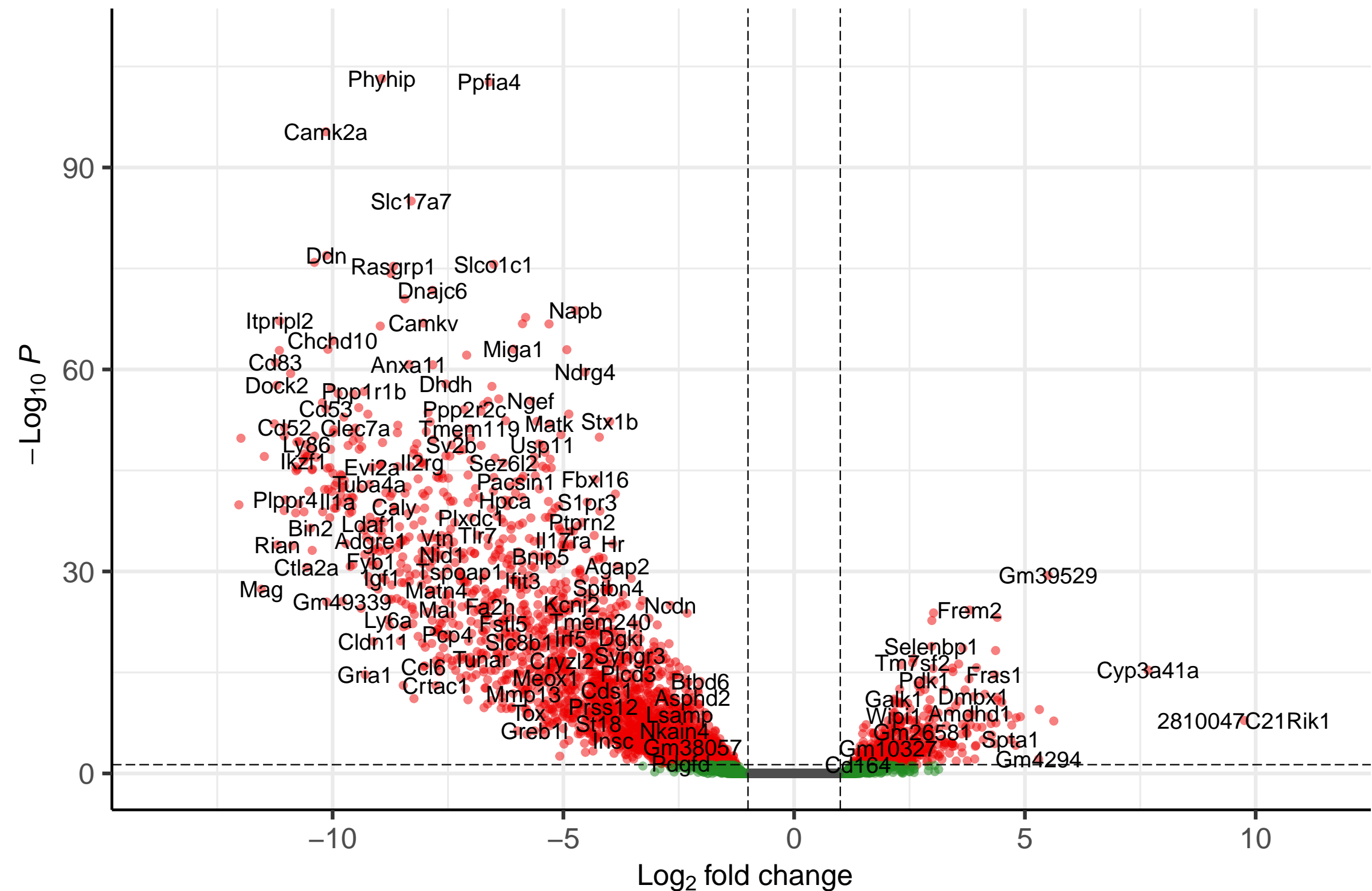


# Full\_Dataset\_all\_genes\_additive\_Model\_NS1\_vs\_Tumor

Full\_Dataset\_all\_genes\_additive

● NS ● Log<sub>2</sub> FC ● p-value and log<sub>2</sub> FC



total = 17322 variables