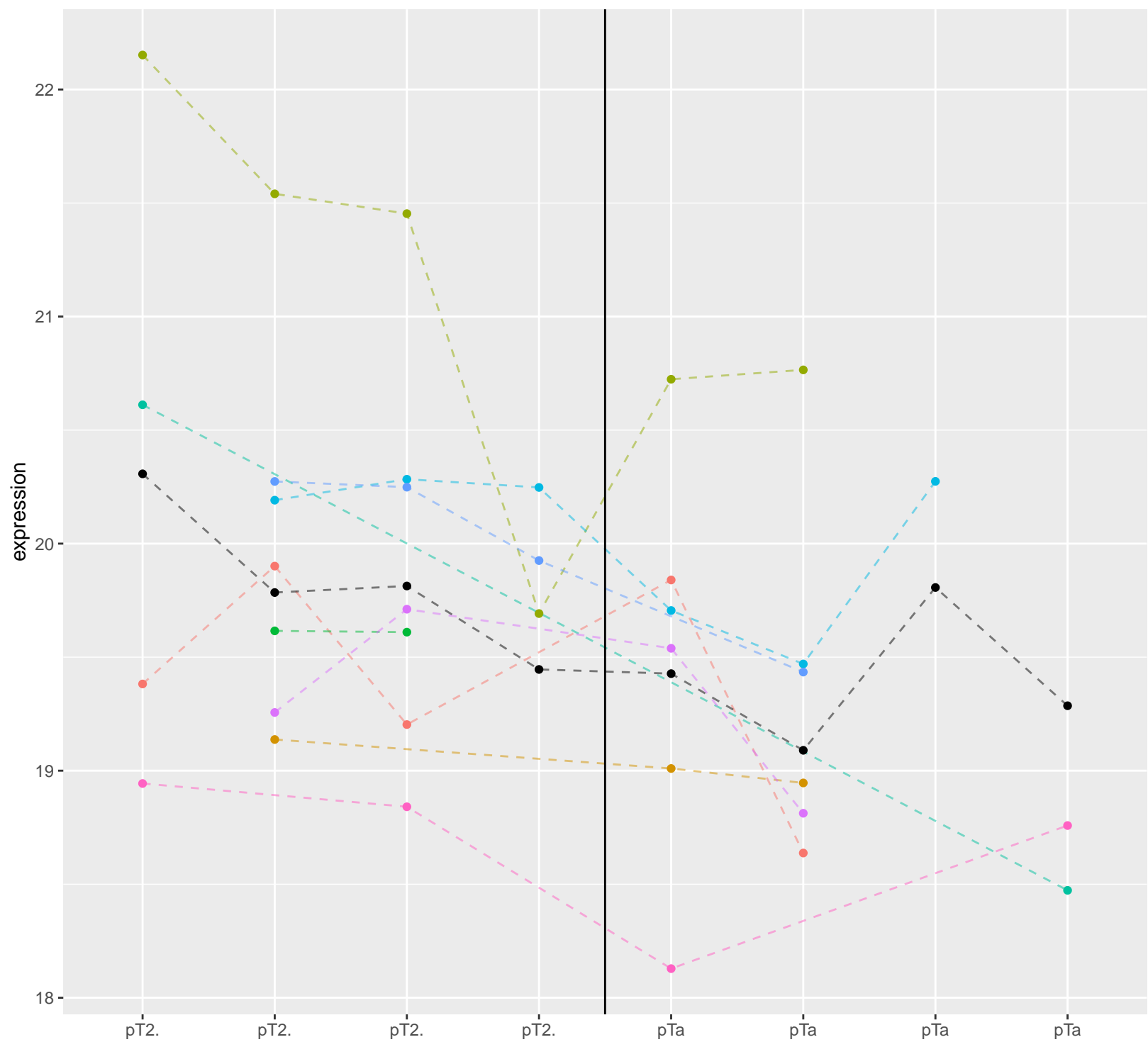


sp|O75131|CPNE3_HUMANCopine-3

MSqRob: q-value: 1.2% log fold change: -0.51 t-value: -4.25 df: 29.2 se: 0.12

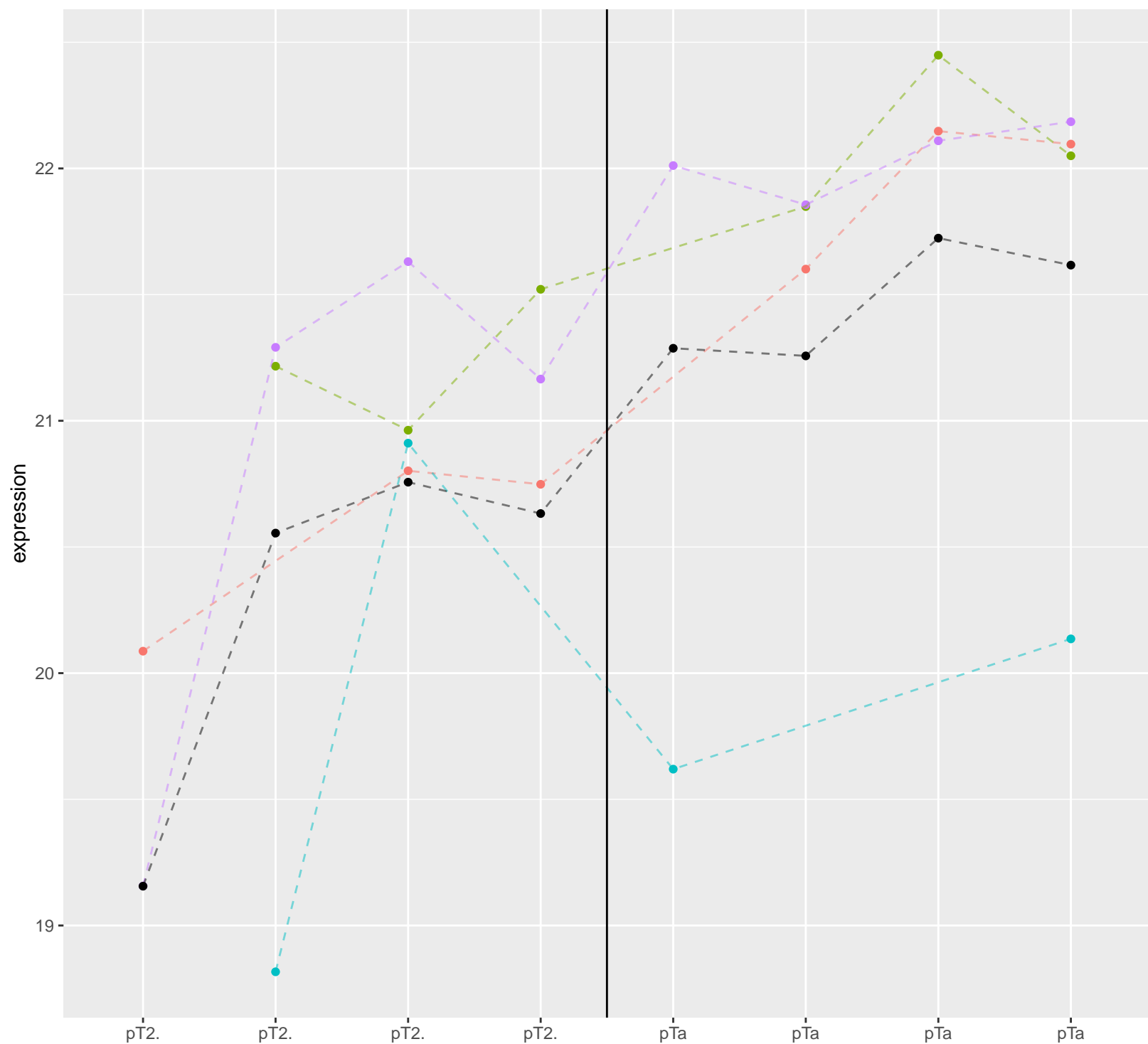
MSqRobSum: q-value: 100% log fold change: -0.3 t-value: -1.25 df: 9.9 se: 0.24



sp|O75608|LYPA1_HUMANAcyl-proteinthioesterase1

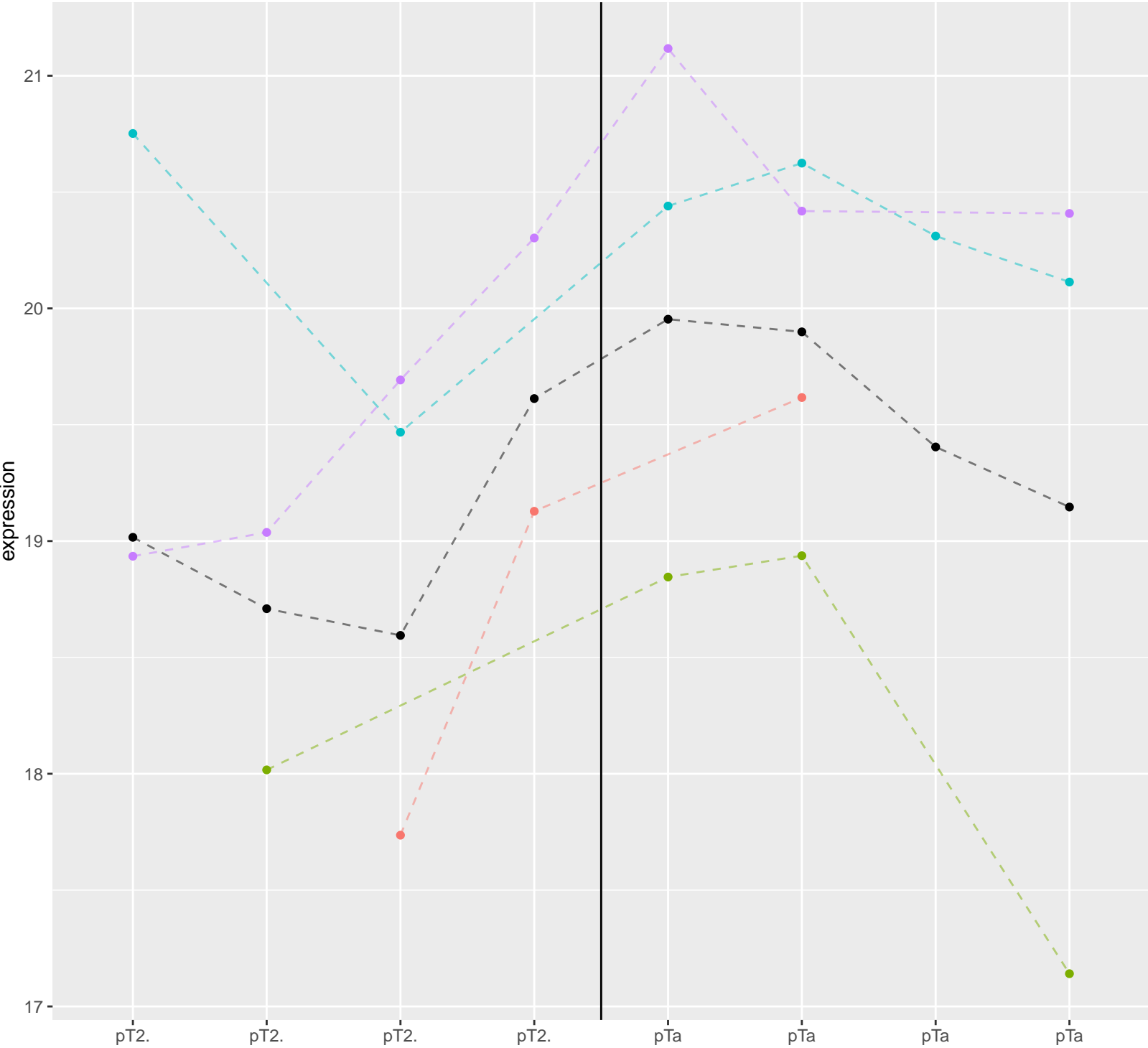
MSqRob: q-value: 0.3% log fold change: 0.92 t-value: 5.41 df: 20.8 se: 0.17

MSqRobSum: q-value: 41.2% log fold change: 0.92 t-value: 2.98 df: 9.7 se: 0.31



sp|O94905|ERLN2_HUMANErln-2

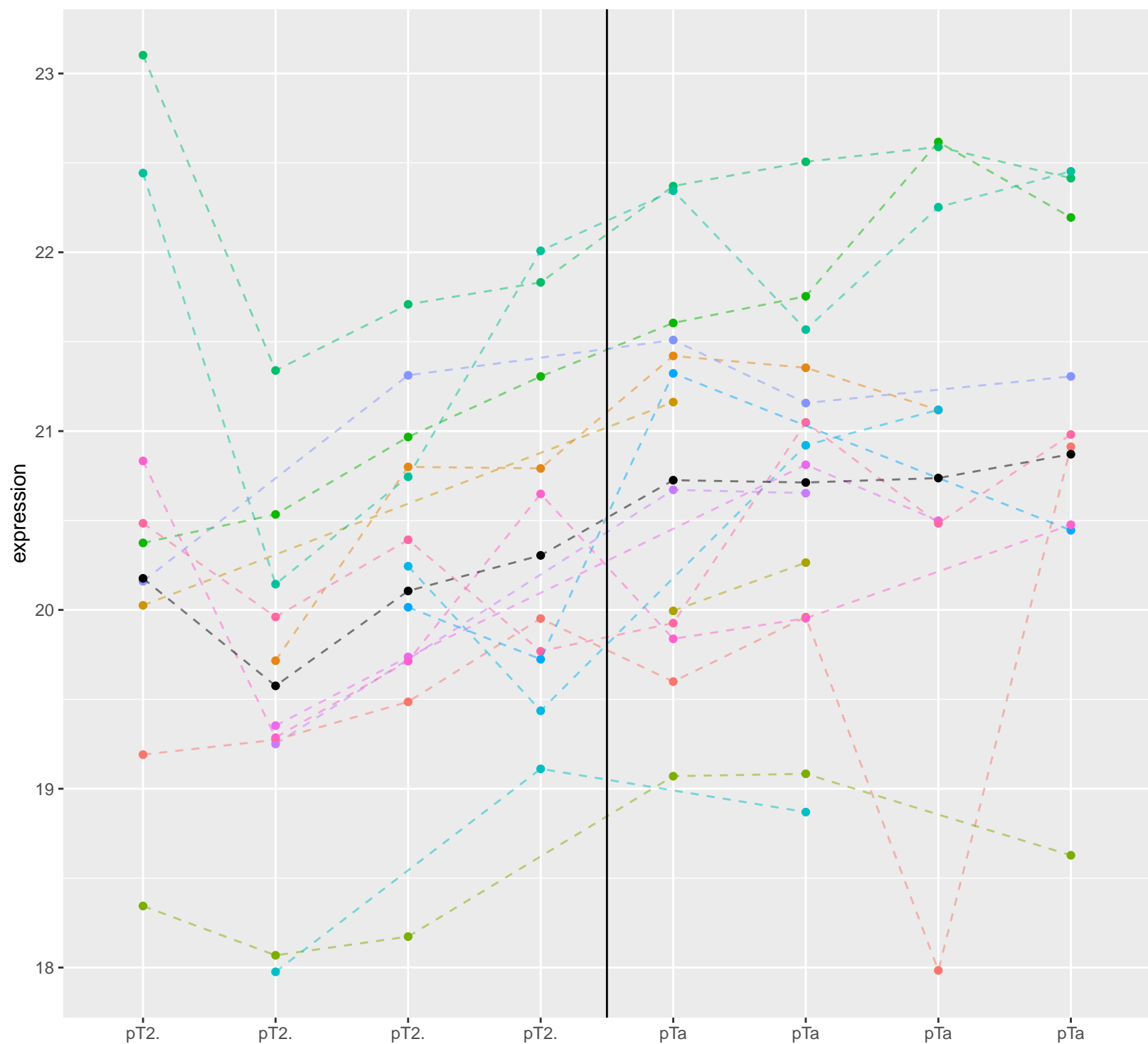
MSqRob: q-value: 5% log fold change: 0.75 t-value: 3.84 df: 17.8 se: 0.2
MSqRobSum: q-value: 86.9% log fold change: 0.47 t-value: 1.65 df: 9.9 se: 0.29



sp|P00505|AATM_HUMANAspartateaminotransferase,mitochondrial

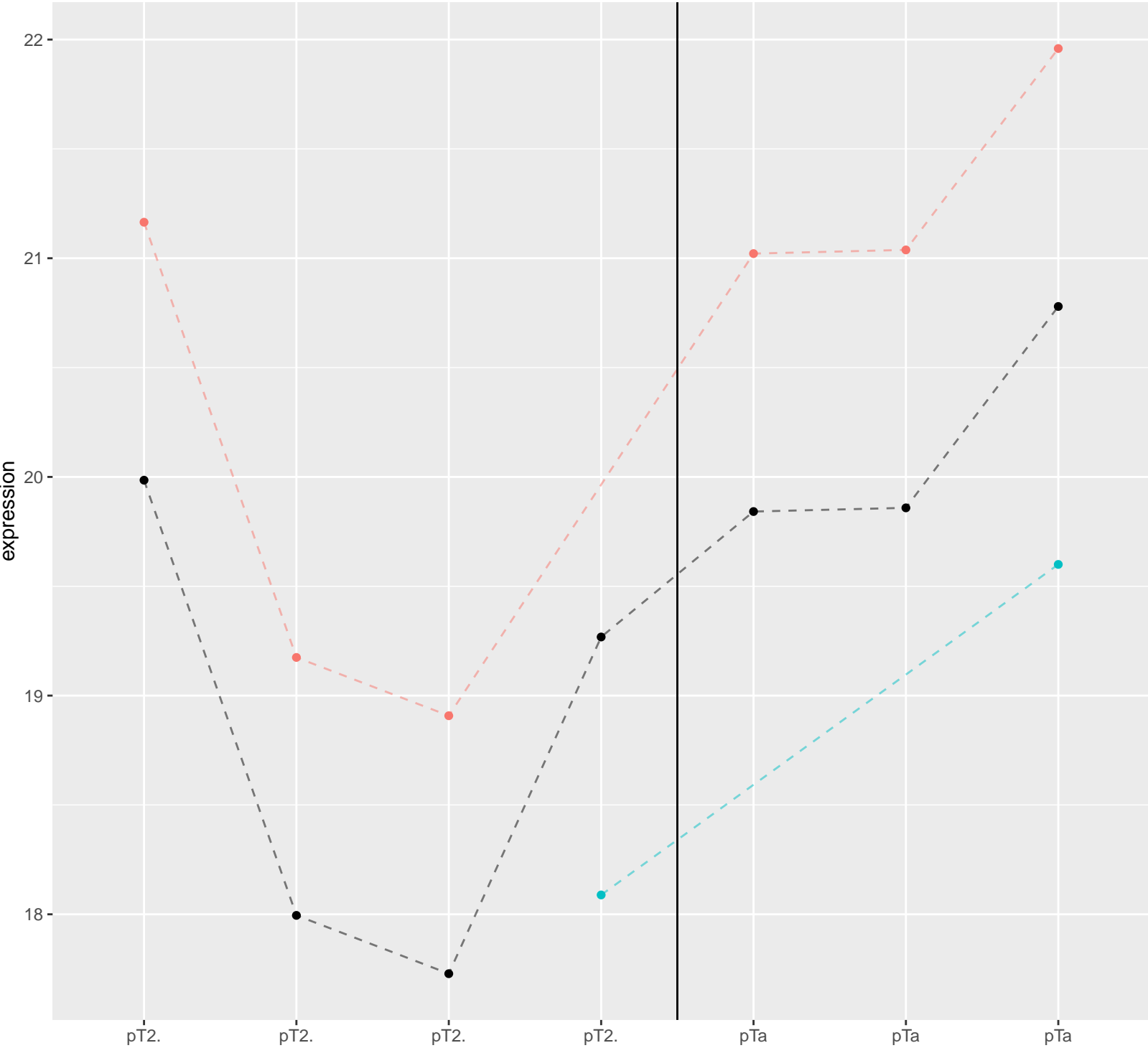
MSqRob: q-value: 0.3% log fold change: 0.72 t-value: 4.63 df: 68.3 se: 0.15

MSqRobSum: q-value: 54.1% log fold change: 0.63 t-value: 2.63 df: 9.7 se: 0.24



sp|P02656|APOC3_HUMANApolipoproteinC-III

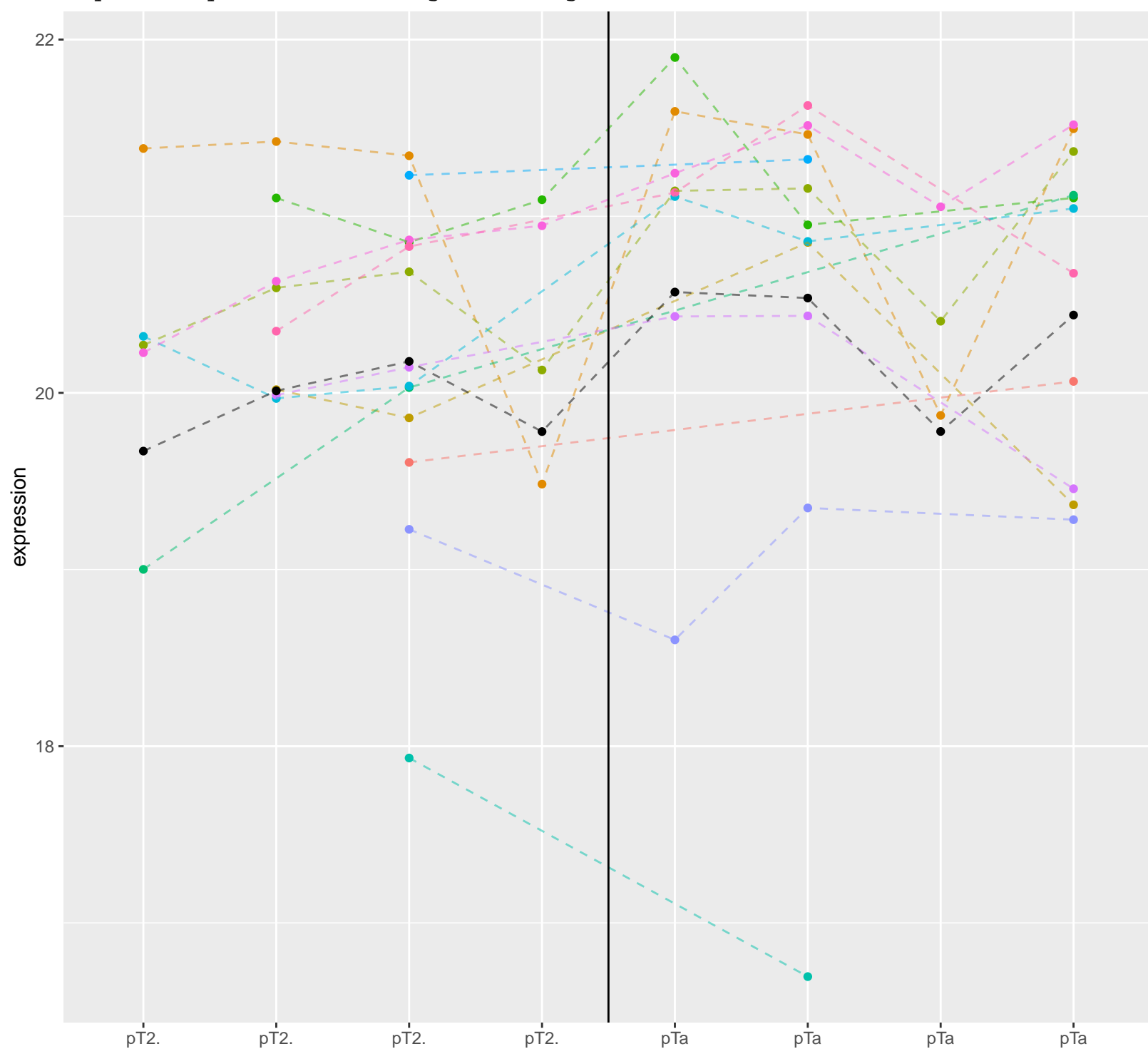
MSqRob: q-value: 2.9% log fold change: 1.71 t-value: 5.63 df: 7.5 se: 0.3
MSqRobSum: q-value: 65.5% log fold change: 1.09 t-value: 2.13 df: 8.9 se: 0.51



sp|P13489|RINI_HUMANRibonucleaseinhibitor

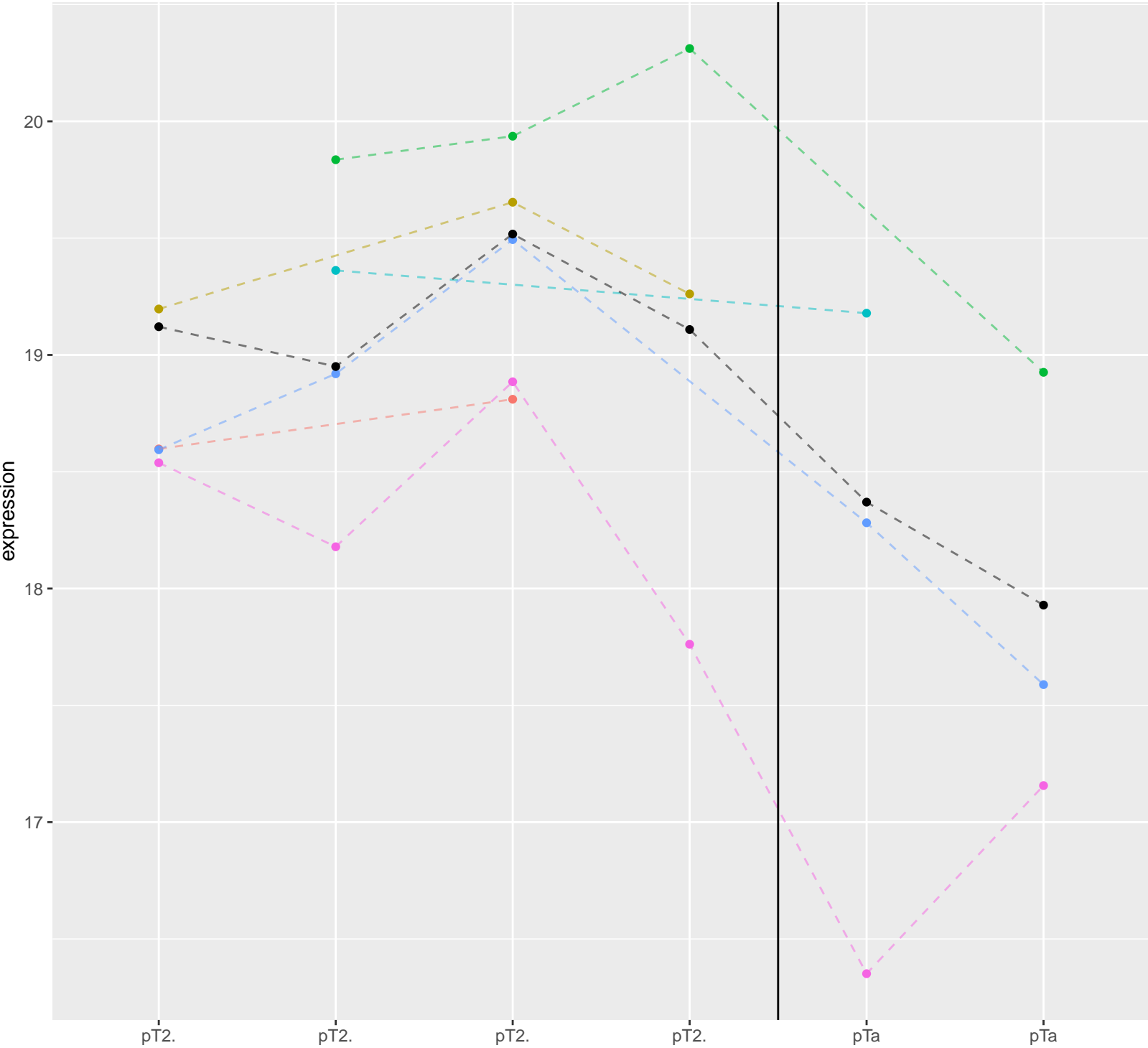
MSqRob: q-value: 0.6% log fold change: 0.42 t-value: 4.35 df: 52.1 se: 0.1

MSqRobSum: q-value: 100% log fold change: 0.32 t-value: 1.32 df: 9.9 se: 0.24



sp|P25205|MCM3_HUMANDNAreplicationlicensingfactorMCM3

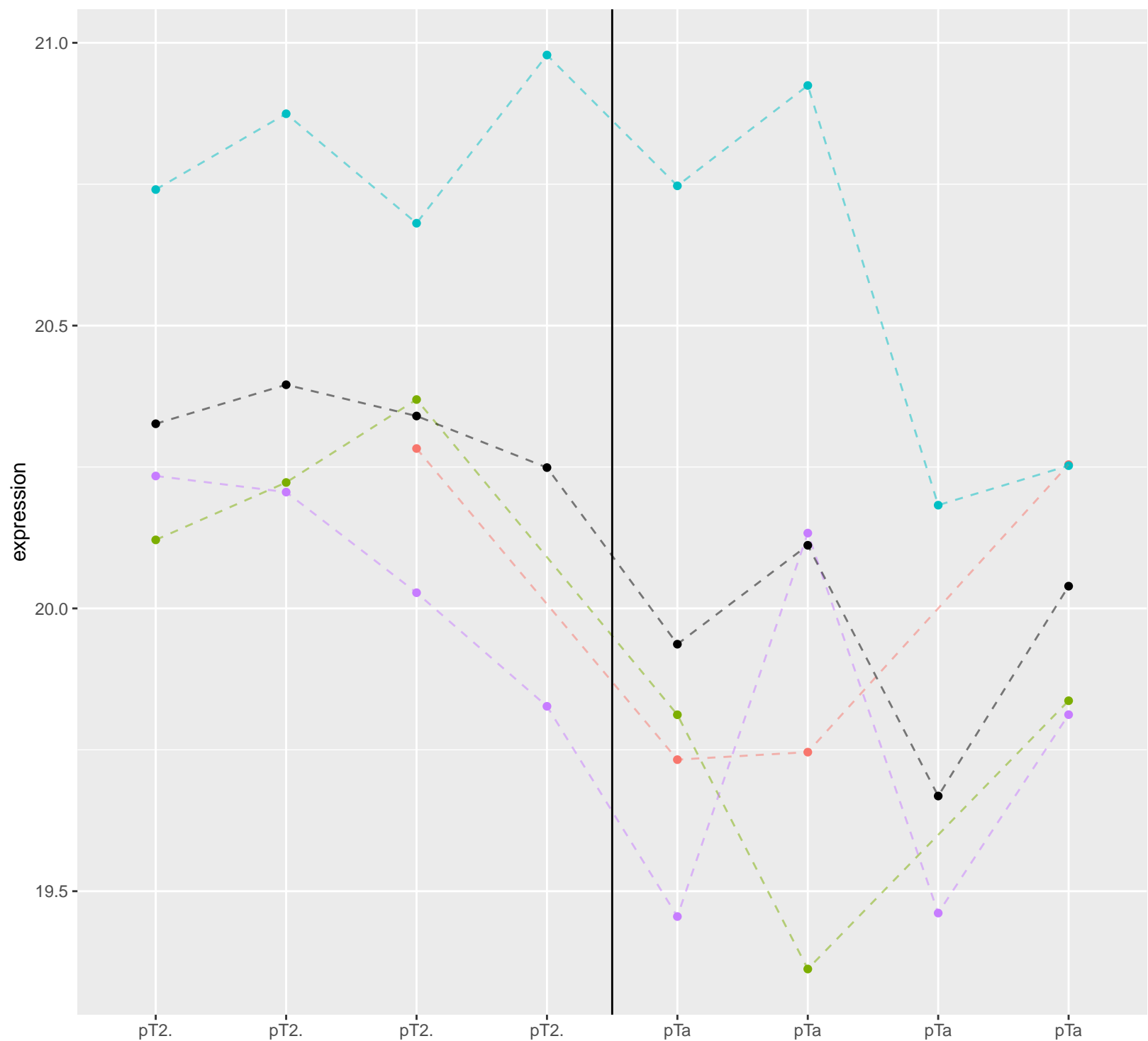
MSqRob: q-value: 1.5% log fold change: -1 t-value: -4.57 df: 16.8 se: 0.22
MSqRobSum: q-value: 52.3% log fold change: -0.98 t-value: -2.85 df: 7.7 se: 0.34



sp|P49720|PSB3_HUMANProteasomesubunitbetatype-3

MSqRob: q-value: 2.9% log fold change: -0.38 t-value: -3.96 df: 23.8 se: 0.1

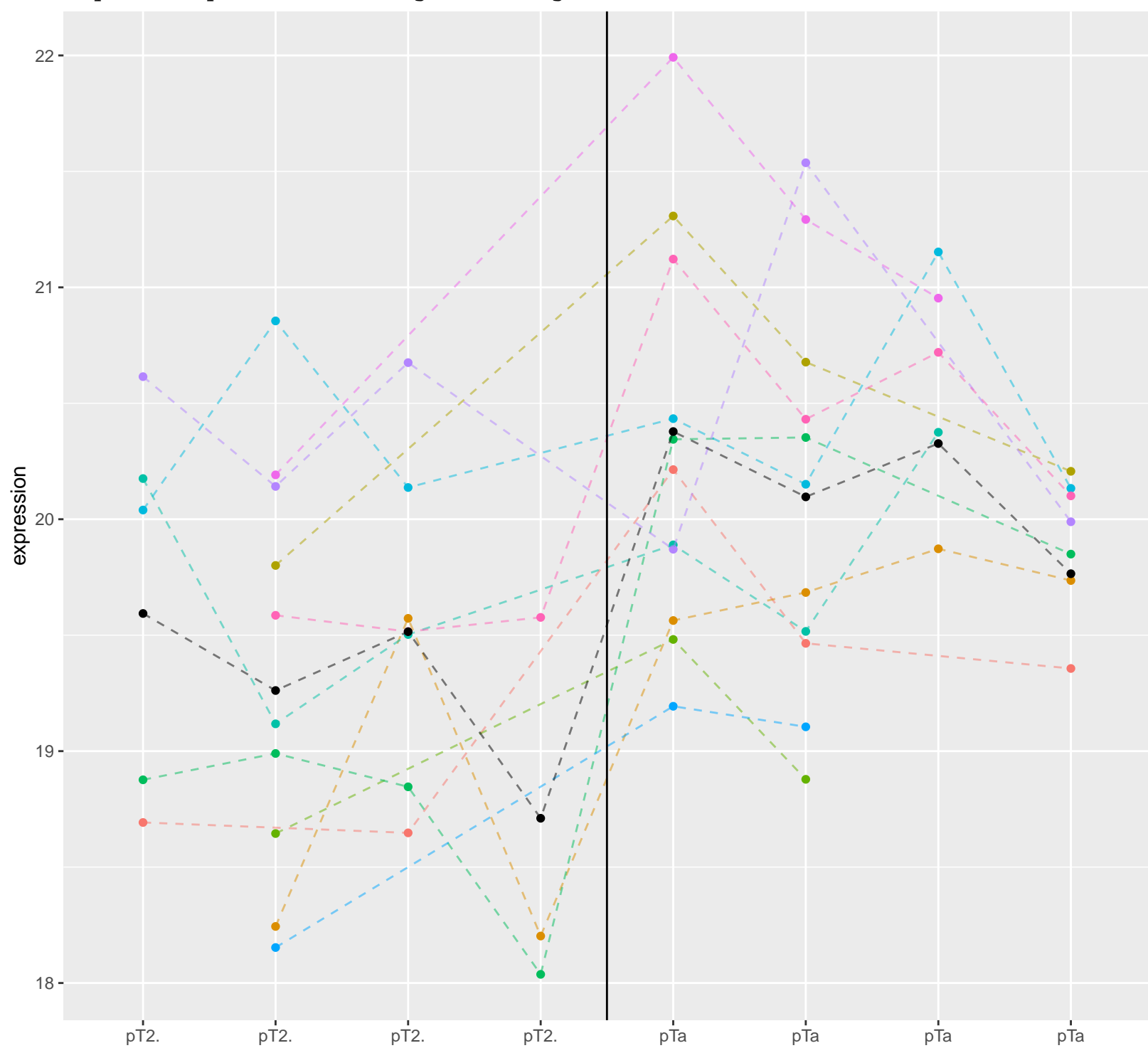
MSqRobSum: q-value: 99% log fold change: -0.33 t-value: -1.46 df: 9.7 se: 0.23



sp|P50570|DYN2_HUMANDynamlin-2

MSqRob: q-value: 0.9% log fold change: 0.79 t-value: 4.22 df: 46.5 se: 0.19

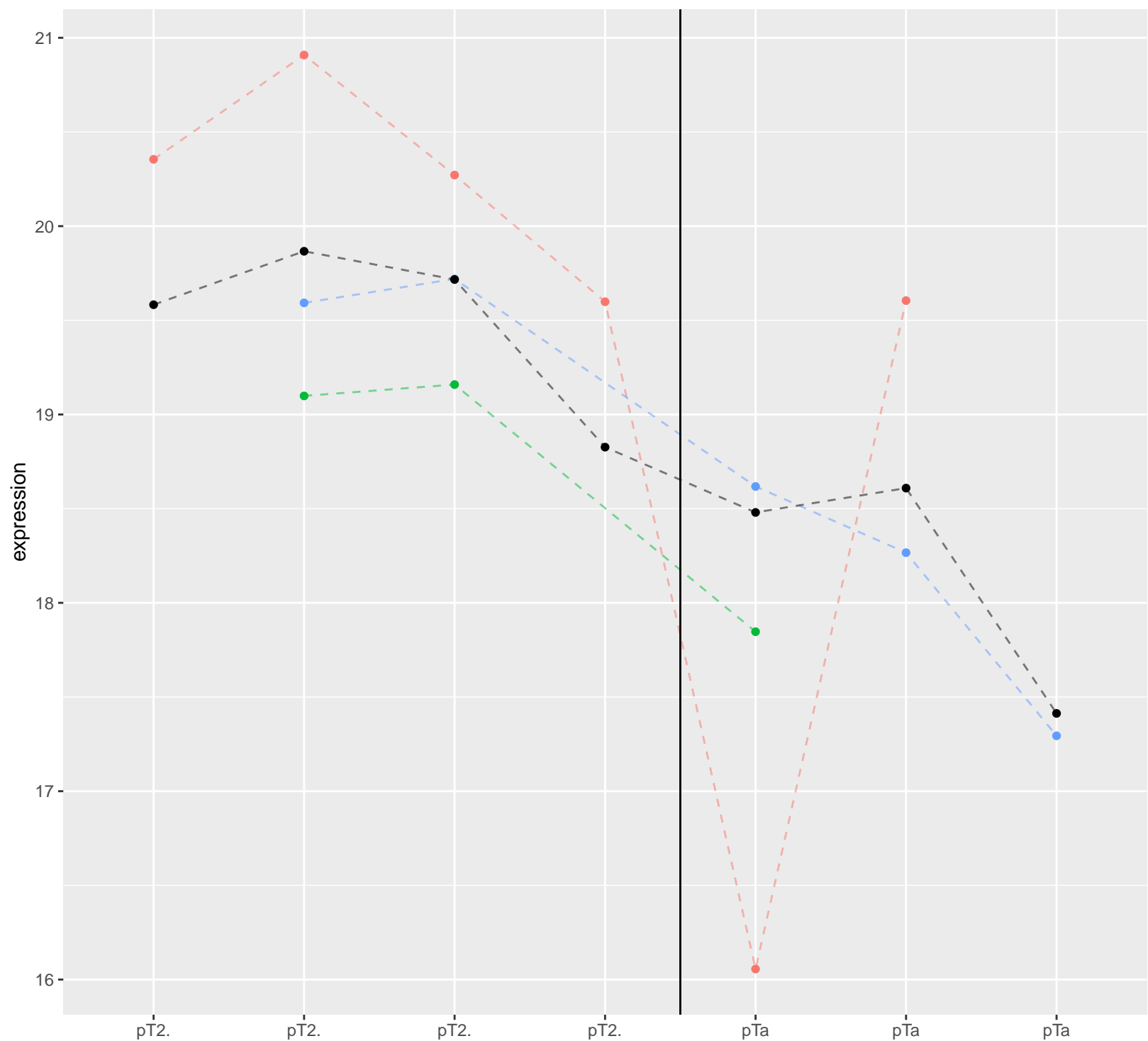
MSqRobSum: q-value: 50% log fold change: 0.78 t-value: 2.78 df: 9.7 se: 0.28



sp|Q13057|COASY_HUMANBifunctionalcoenzymeAsynthase

MSqRob: q-value: 2.6% log fold change: -1.58 t-value: -4.51 df: 13.6 se: 0.35

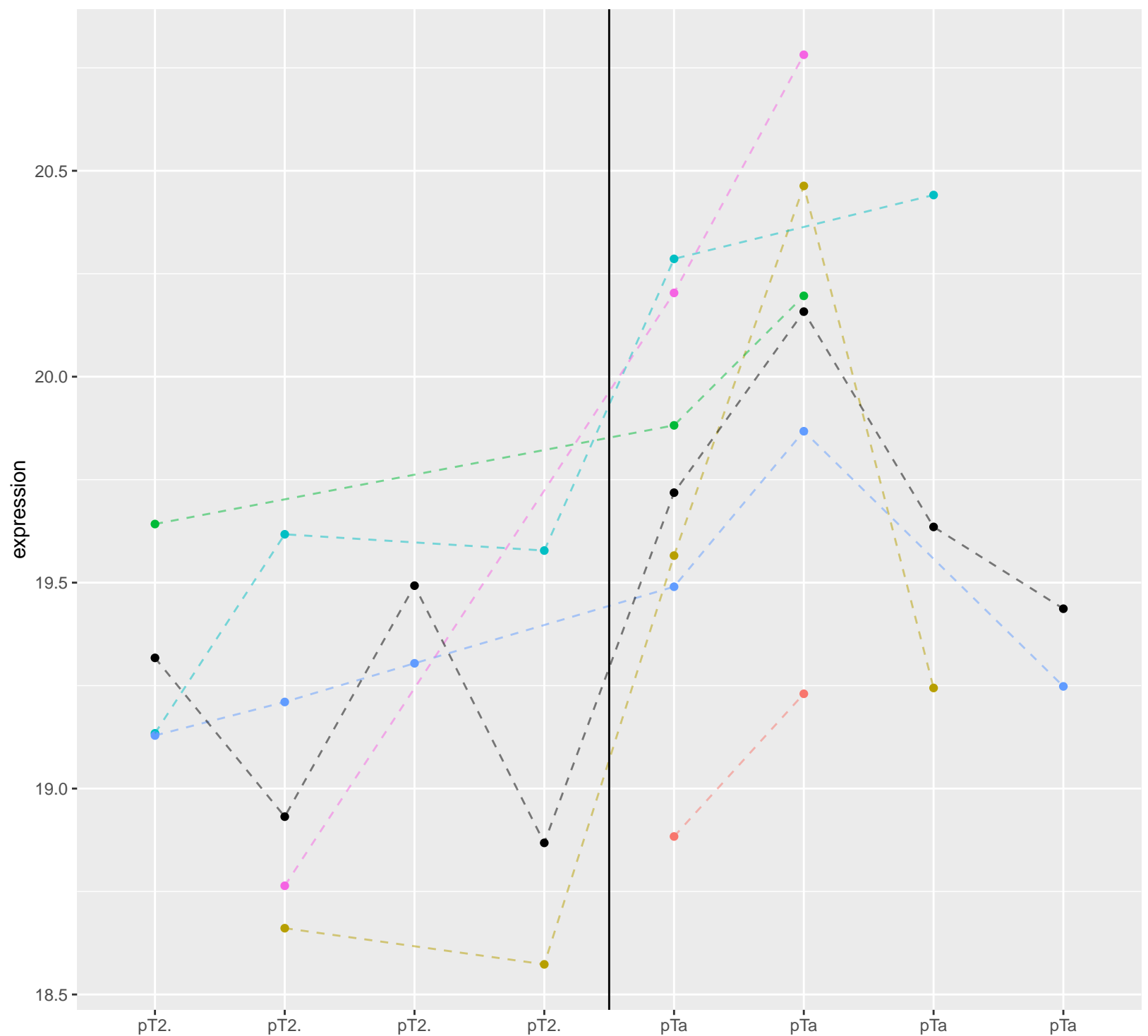
MSqRobSum: q-value: 41.2% log fold change: -1.17 t-value: -3.04 df: 8.7 se: 0.38



sp|Q5JTV8|TOIP1_HUMAN Torsin-1A-interacting protein1

MSqRob: q-value: 1.1% log fold change: 0.69 t-value: 4.63 df: 19.9 se: 0.15

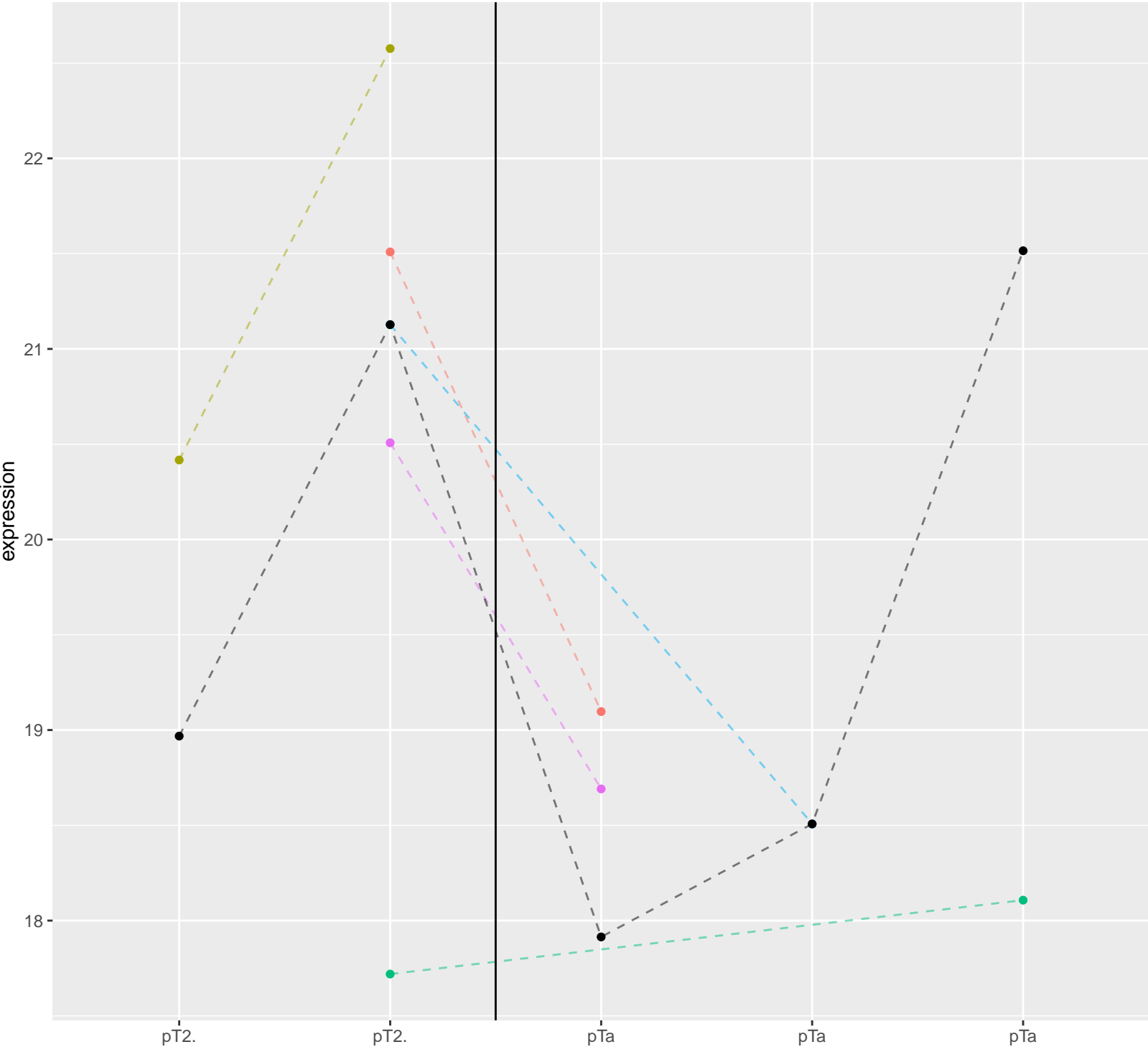
MSqRobSum: q-value: 74.5% log fold change: 0.51 t-value: 1.93 df: 9.8 se: 0.26



sp|Q7L5L3|GDPD3_HUMANGlycerophosphodiesterphosphodiesterasedomain-containingprotein3

MSqRob: q-value: 3.4% log fold change: -2.15 t-value: -4.66 df: 10.6 se: 0.46

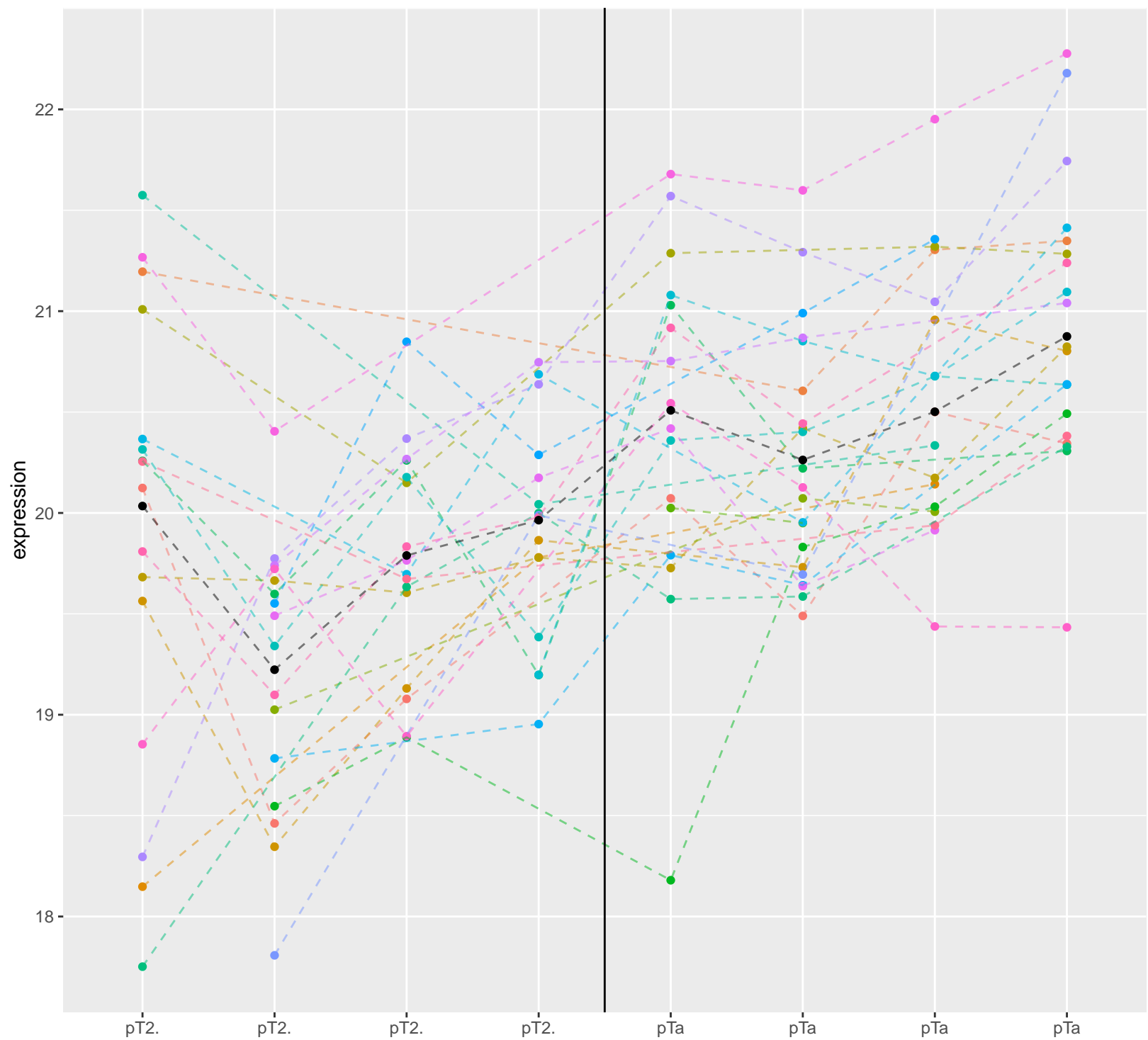
MSqRobSum: q-value: 100% log fold change: 0 t-value: 0 df: 7.6 se: 0



sp|Q8WUM4|PDC6I_HUMANProgrammedcelldeath6-interactingprotein

MSqRob: q-value: 3.2% log fold change: 0.73 t-value: 3.49 df: 111.9 se: 0.21

MSqRobSum: q-value: 54.8% log fold change: 0.69 t-value: 2.57 df: 9.7 se: 0.27



sp|Q9BRA2|TXD17_HUMANThioredoxin domain-containing protein17

MSqRob: q-value: 1.4% log fold change: 1 t-value: 4.81 df: 14.8 se: 0.21
MSqRobSum: q-value: 60.9% log fold change: 0.69 t-value: 2.42 df: 8.7 se: 0.29

