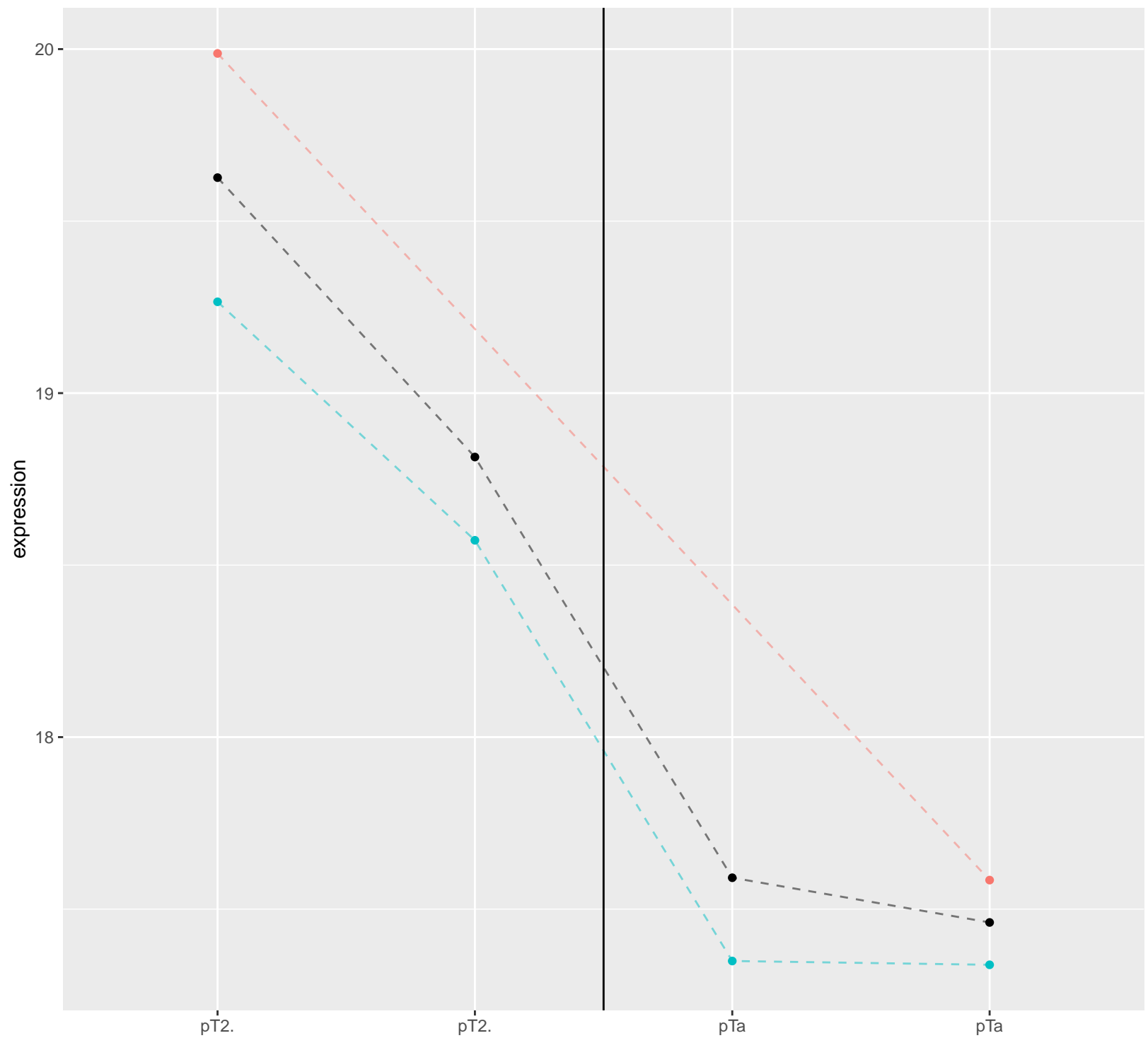


sp|O00154|BACH_HUMANCytosolicacylcoenzymeAthioesterhydrolase

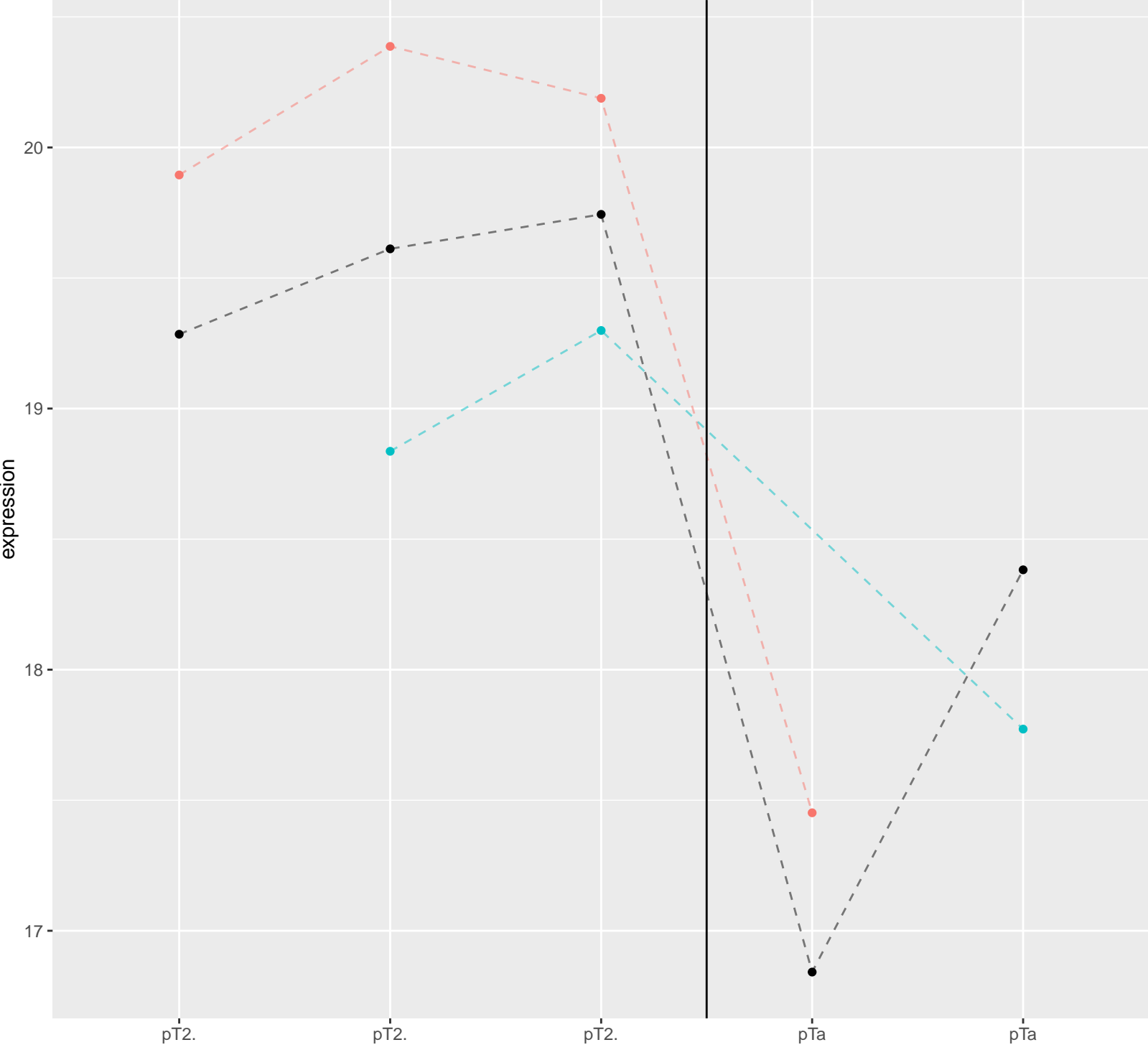
MSqRob: q-value: 0.9% log fold change: -1.91 t-value: -9.27 df: 5.7 se: 0.21

MSqRobSum: q-value: 43% log fold change: -1.59 t-value: -3.39 df: 5.7 se: 0.47



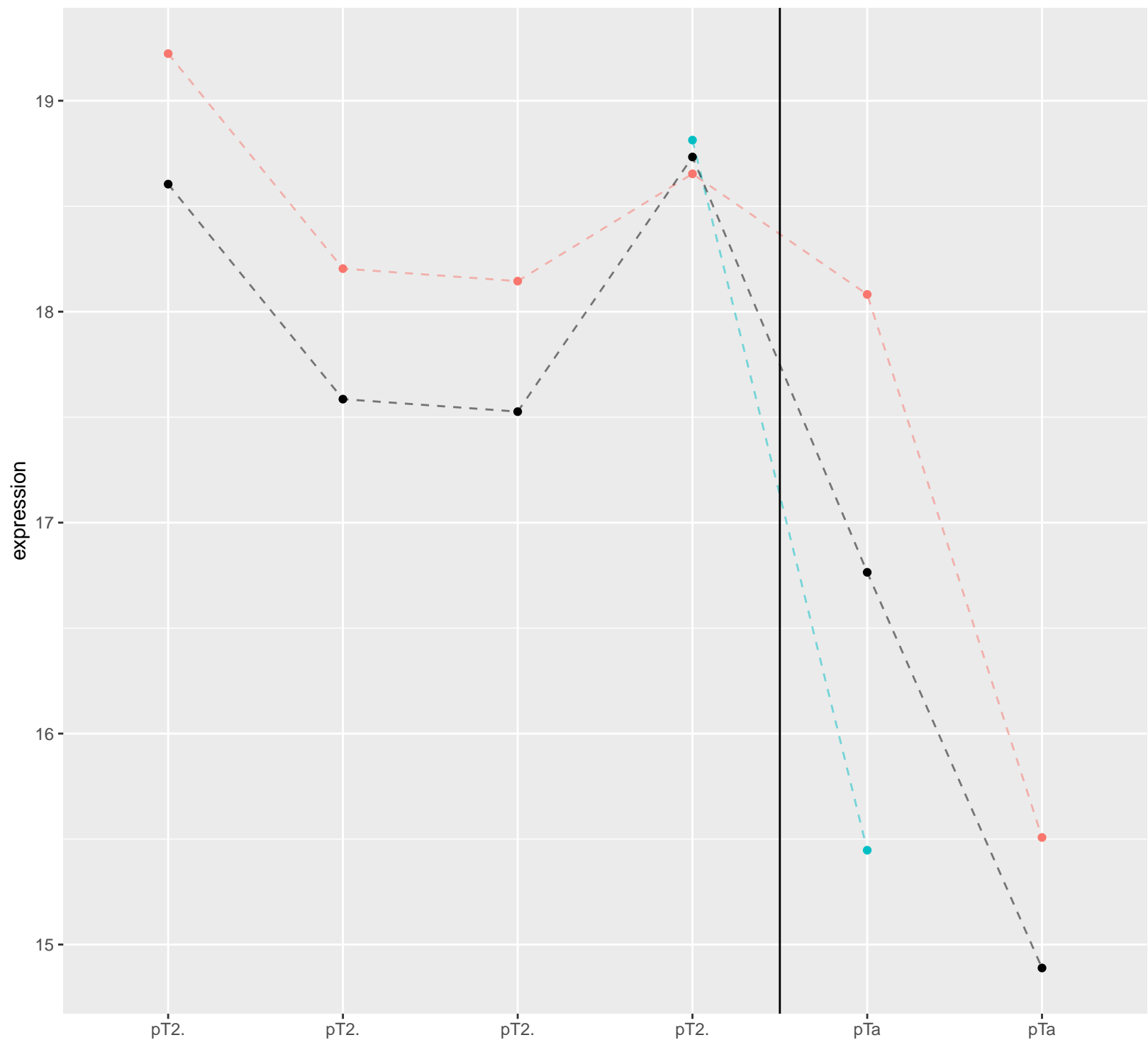
sp|P52292|IMA1_HUMANImportinsubunitalpha-1

MSqRob: q-value: 4.4% log fold change: -1.98 t-value: -5.46 df: 6.8 se: 0.36
MSqRobSum: q-value: 39.1% log fold change: -1.64 t-value: -3.48 df: 6.7 se: 0.47



sp|O96005|CLPT1_HUMANCleftlipandpalatetransmembraneprotein1

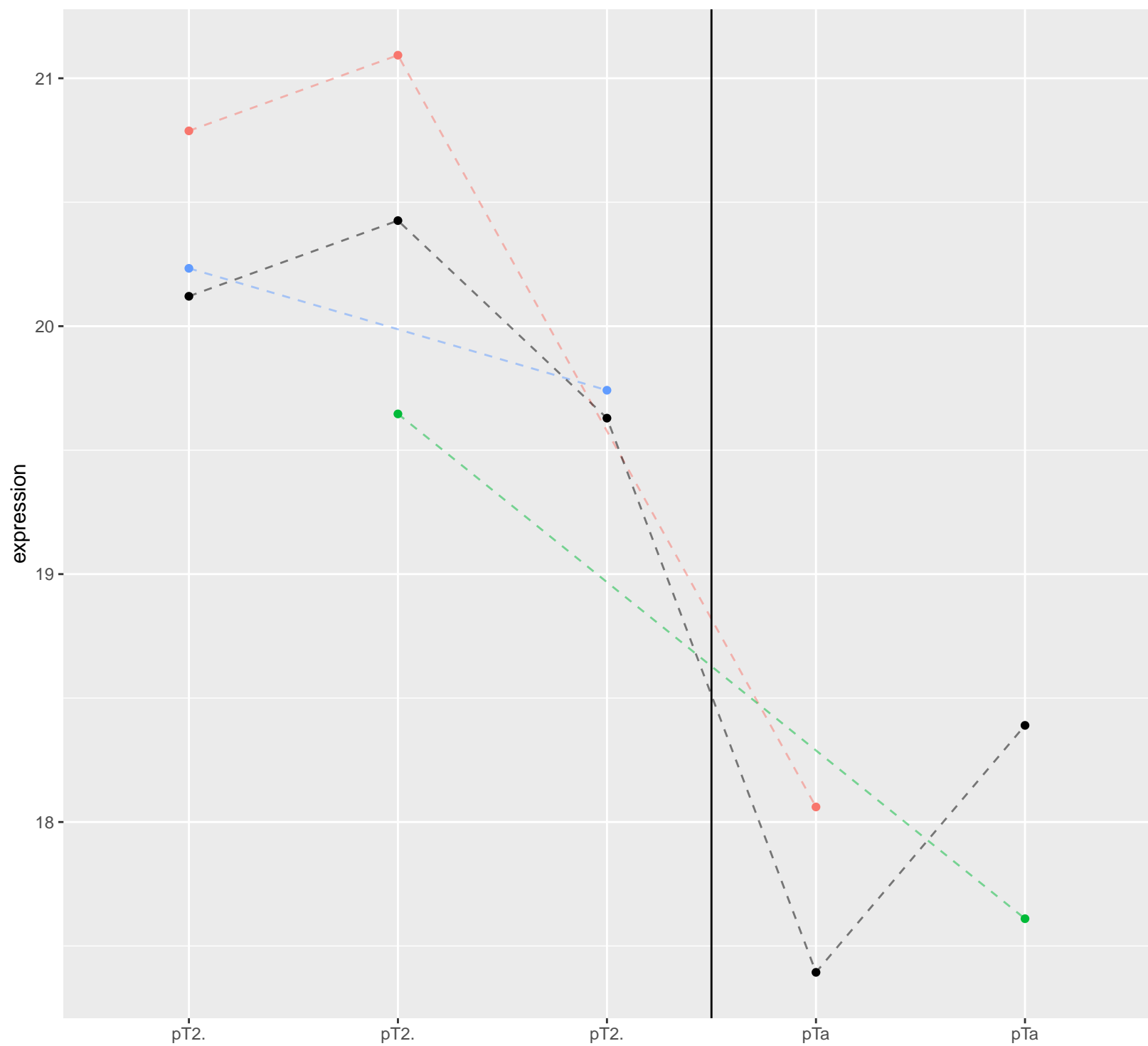
MSqRob: q-value: 4.4% log fold change: -2.41 t-value: -4.9 df: 8.4 se: 0.49
MSqRobSum: q-value: 37.3% log fold change: -2.04 t-value: -3.43 df: 7.7 se: 0.59



sp|Q06828|FMOD_HUMANFibromodulin

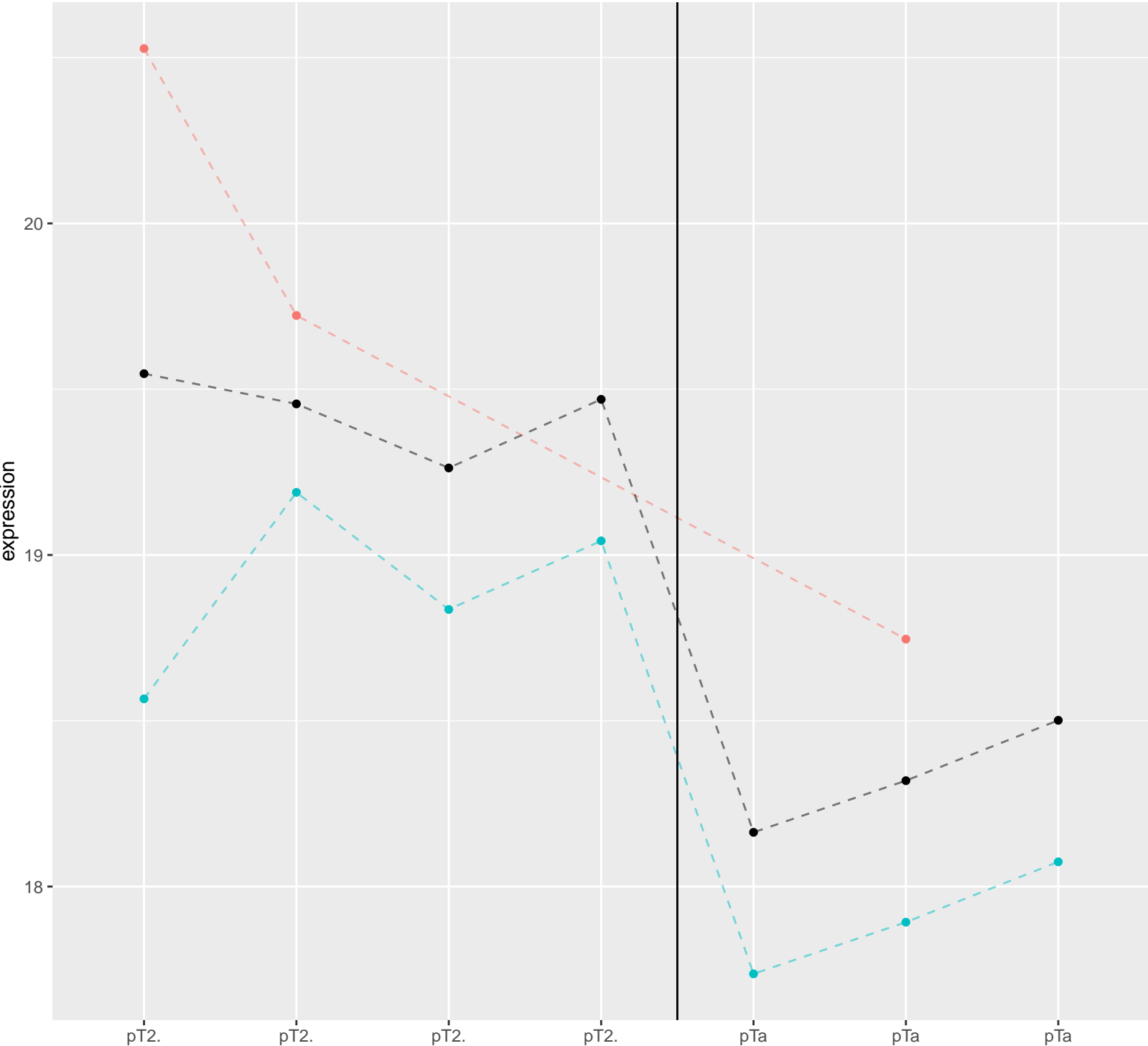
MSqRob: q-value: 1.4% log fold change: -2.47 t-value: -7.8 df: 5.9 se: 0.32

MSqRobSum: q-value: 24% log fold change: -2.06 t-value: -4.44 df: 6.7 se: 0.46



sp|P08195|4F2_HUMAN4F2cell-surfaceantigenheavychain

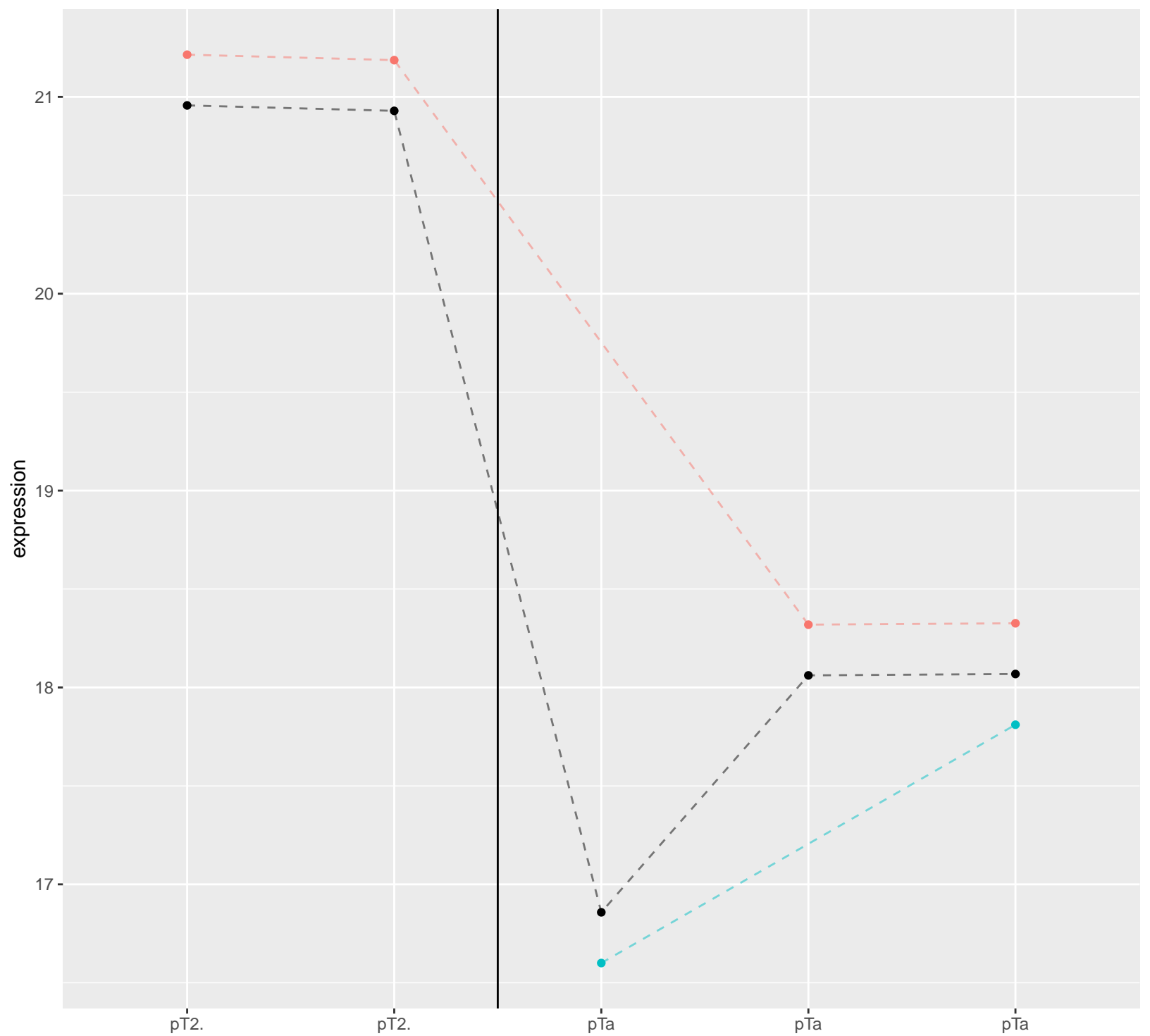
MSqRob: q-value: 1.5% log fold change: -1.05 t-value: -5.61 df: 9.6 se: 0.19
MSqRobSum: q-value: 23.8% log fold change: -1.09 t-value: -4.06 df: 8.6 se: 0.27



sp|Q8WWI1|LMO7_HUMANLIMdomainonlyprotein7

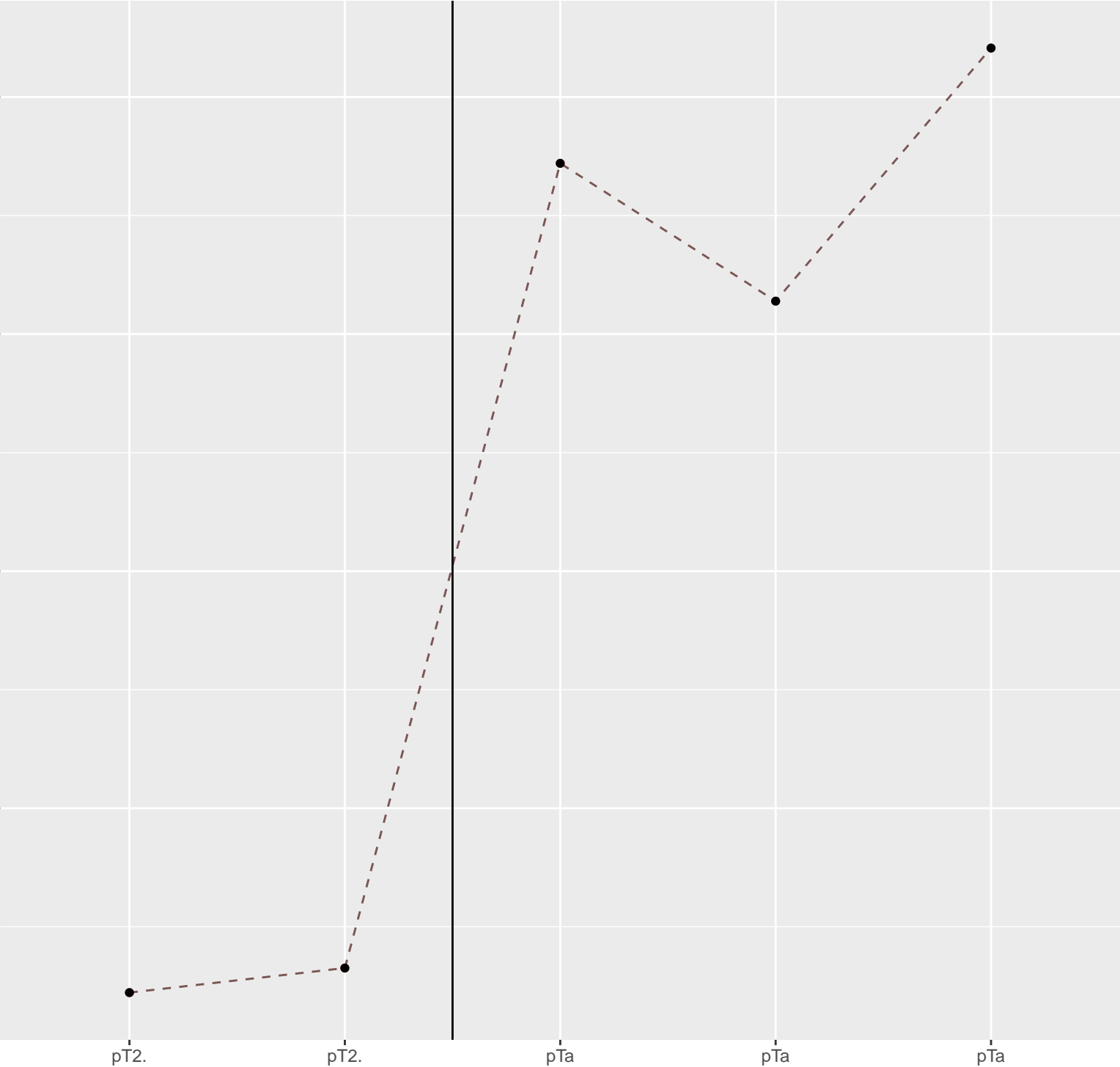
MSqRob: q-value: 0.5% log fold change: -2.88 t-value: -11.48 df: 5.6 se: 0.25

MSqRobSum: q-value: 10.7% log fold change: -3.17 t-value: -6.61 df: 6.6 se: 0.48



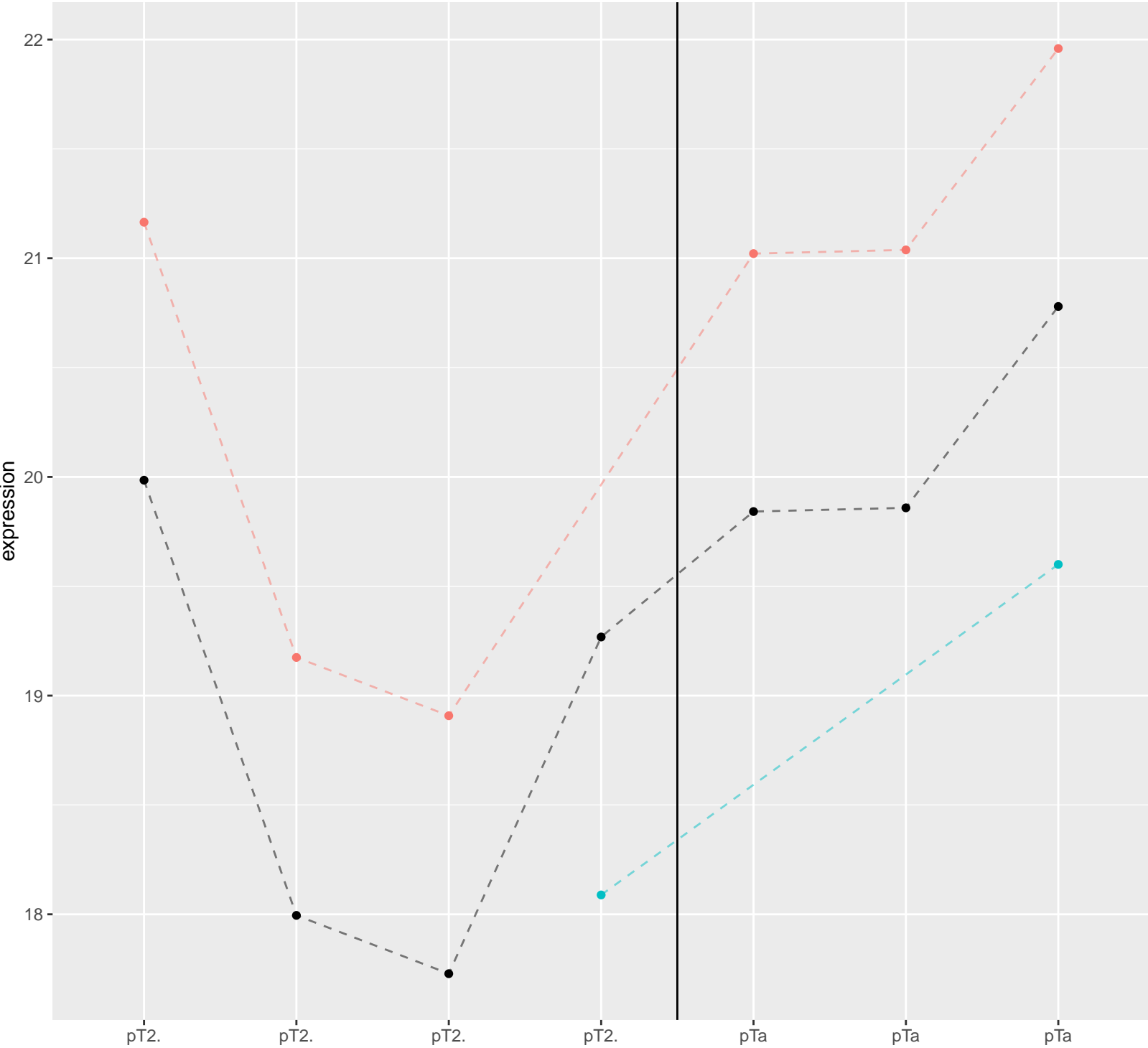
sp|Q9Y623|MYH4_HUMANMyosin-4

MSqRob: q-value: 0.3% log fold change: 3.43 t-value: 13.09 df: 5.5 se: 0.26
MSqRobSum: q-value: 2.8% log fold change: 3.41 t-value: 8.94 df: 6.6 se: 0.38



sp|P02656|APOC3_HUMANApolipoproteinC-III

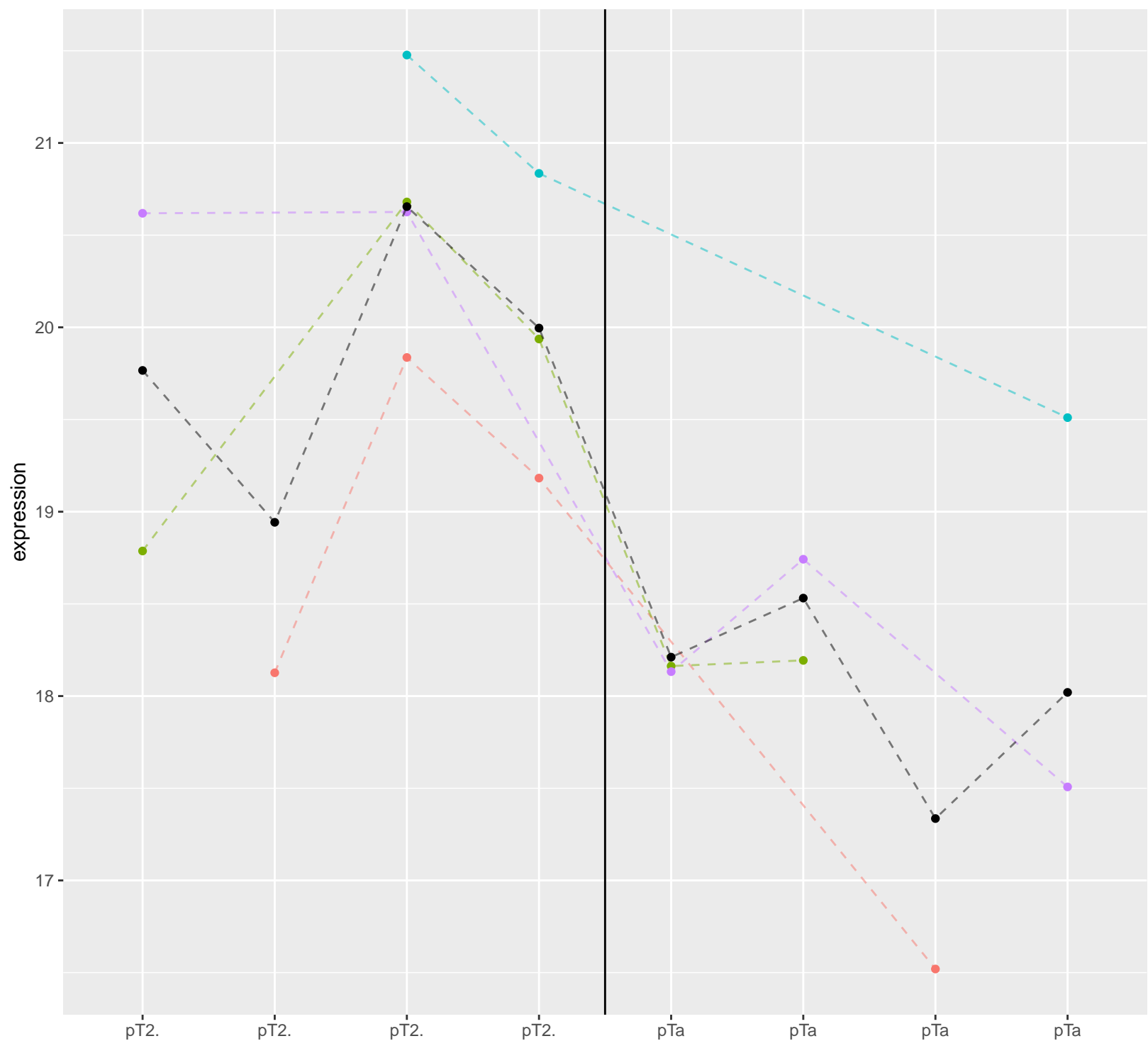
MSqRob: q-value: 2.9% log fold change: 1.71 t-value: 5.63 df: 7.5 se: 0.3
MSqRobSum: q-value: 65.5% log fold change: 1.09 t-value: 2.13 df: 8.9 se: 0.51



sp|Q92820|GGH_HUMANGamma-glutamylhydrolase

MSqRob: q-value: 0.7% log fold change: -1.94 t-value: -5.76 df: 12.4 se: 0.34

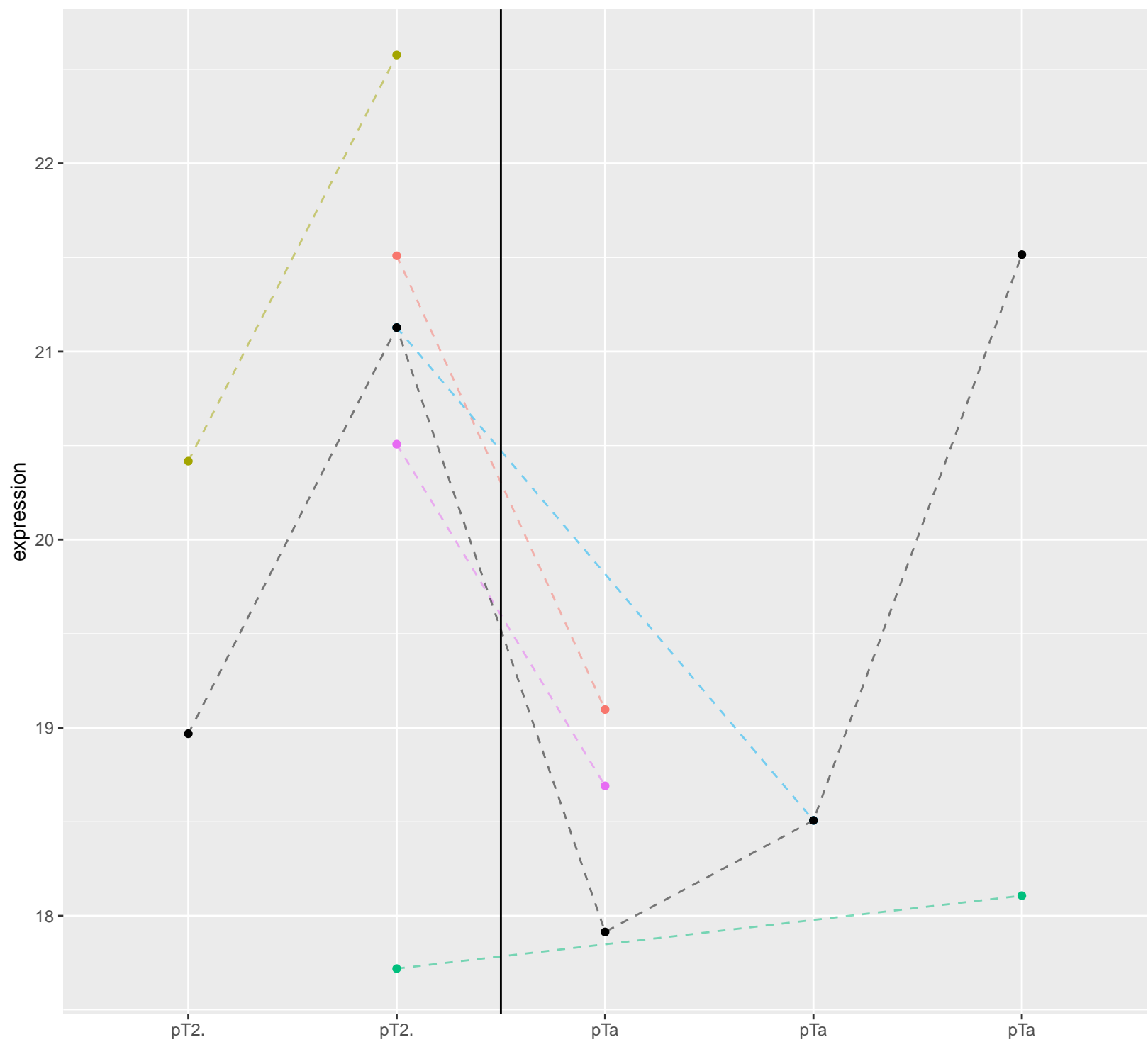
MSqRobSum: q-value: 16.9% log fold change: -1.7 t-value: -4.53 df: 9.7 se: 0.38



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

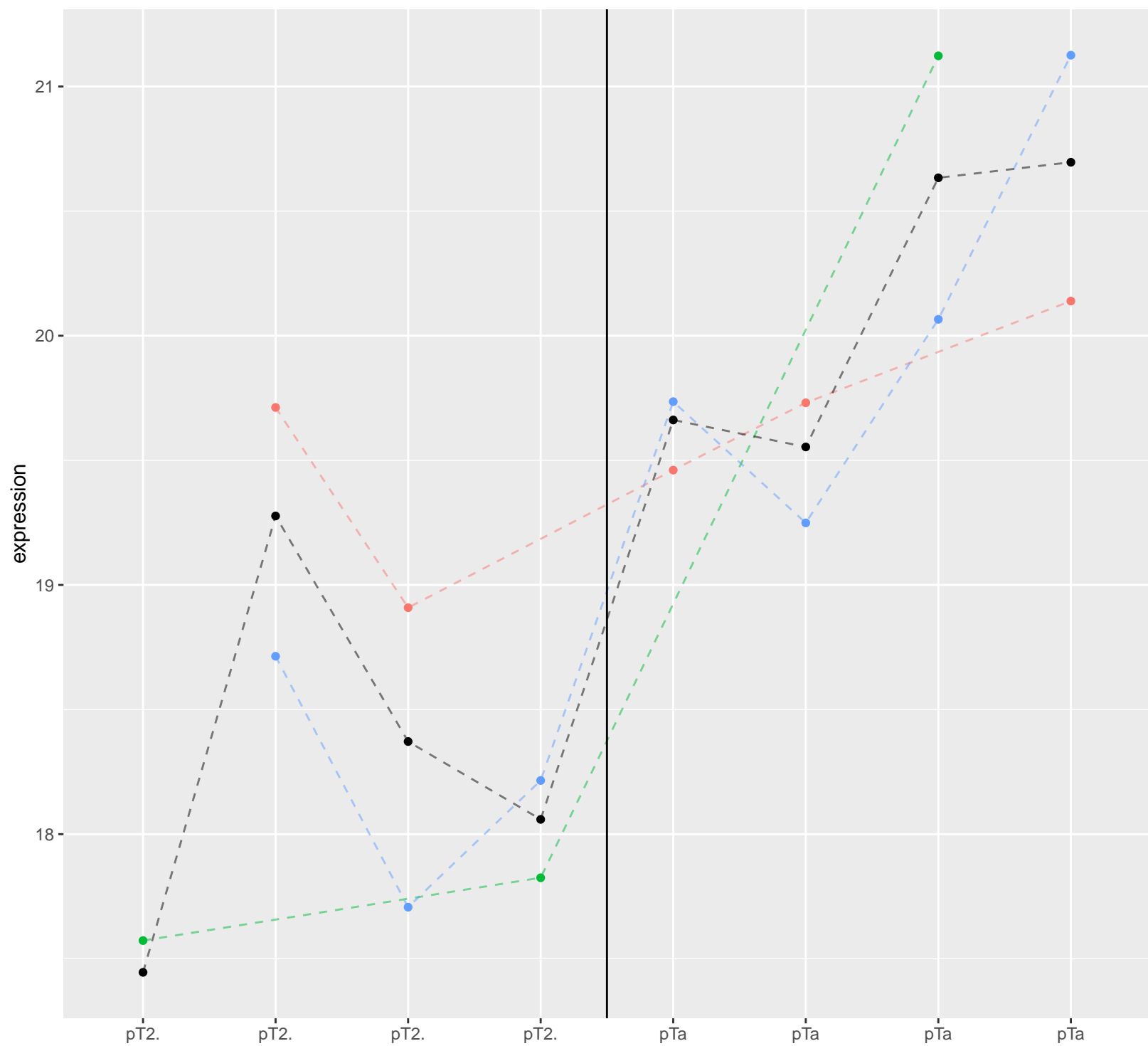
MSqRobSum: q-value: 100% log fold change: 0 t-value: 0 df: 7.6 se: 0



sp|Q9Y371|SHLB1_HUMANEndophilin-B1

MSqRob: q-value: 4.5% log fold change: 1.64 t-value: 4.21 df: 12.7 se: 0.39

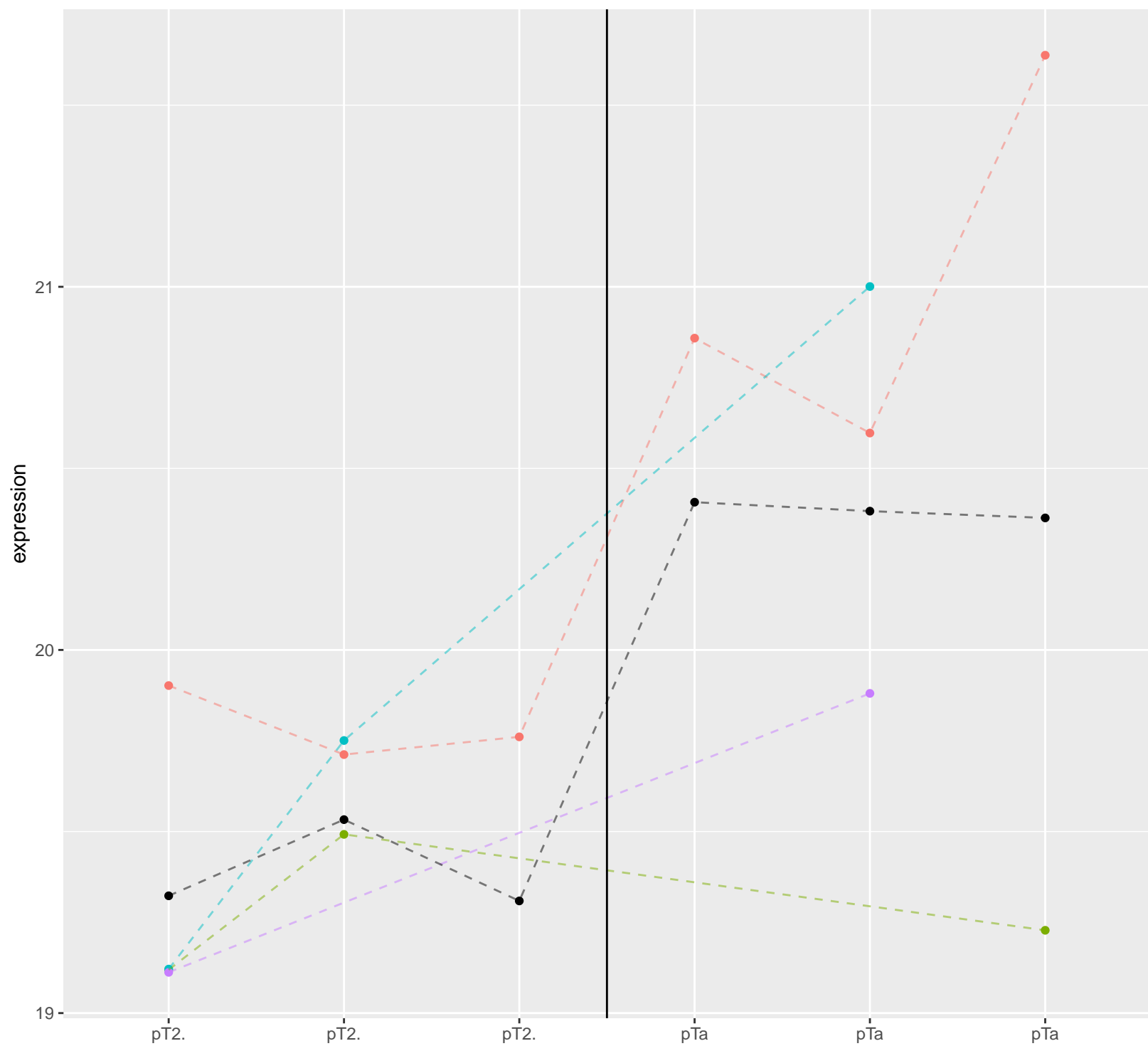
MSqRobSum: q-value: 23.8% log fold change: 1.72 t-value: 3.98 df: 9.7 se: 0.43



sp|Q99733|NP1L4_HUMANNucleosomeassemblyprotein1-like4

MSqRob: q-value: 1.2% log fold change: 0.92 t-value: 5.25 df: 12.3 se: 0.17

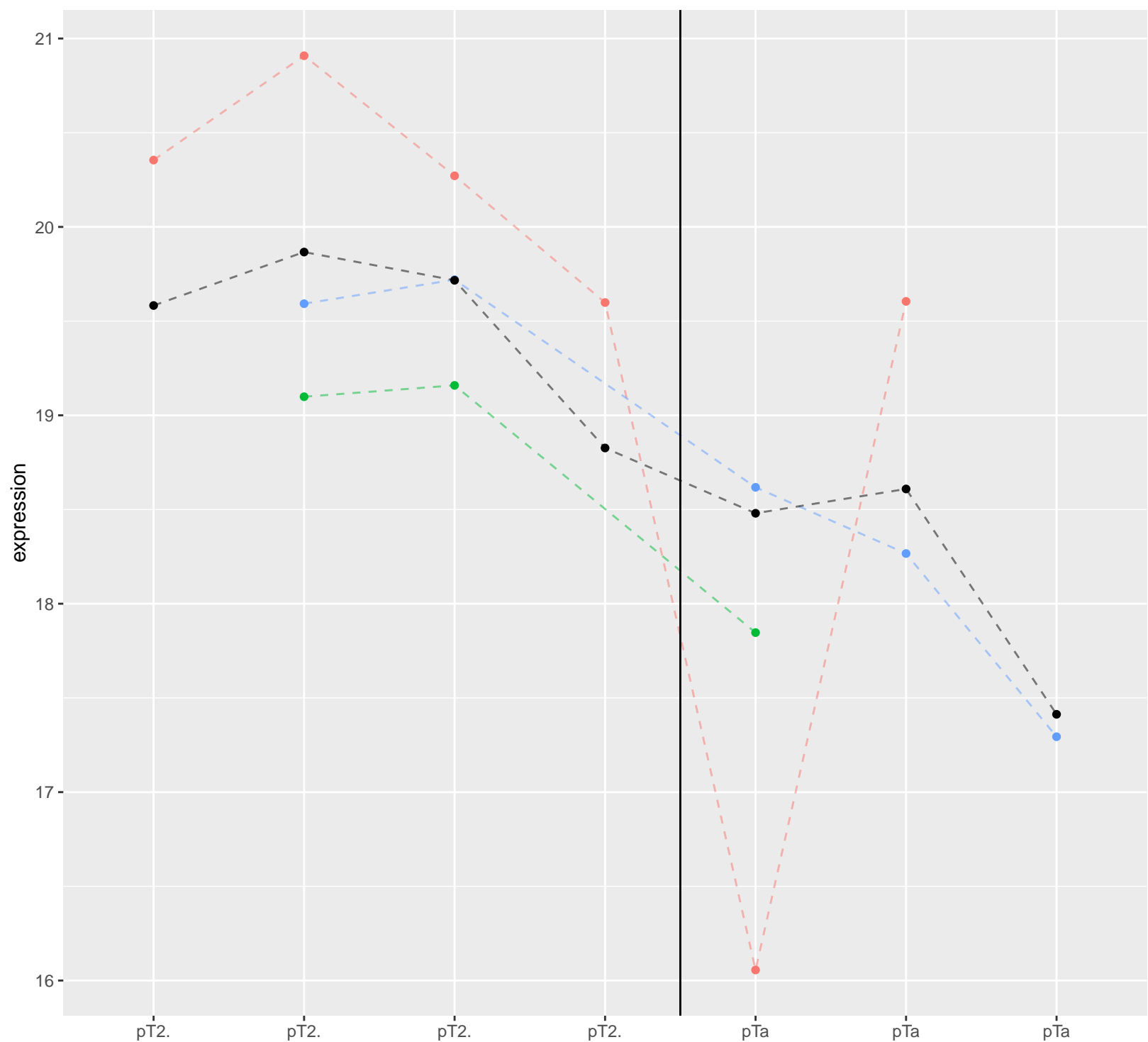
MSqRobSum: q-value: 37.3% log fold change: 1.01 t-value: 3.41 df: 7.6 se: 0.3



sp|Q13057|COASY_HUMANBifunctionalcoenzymeAsynthase

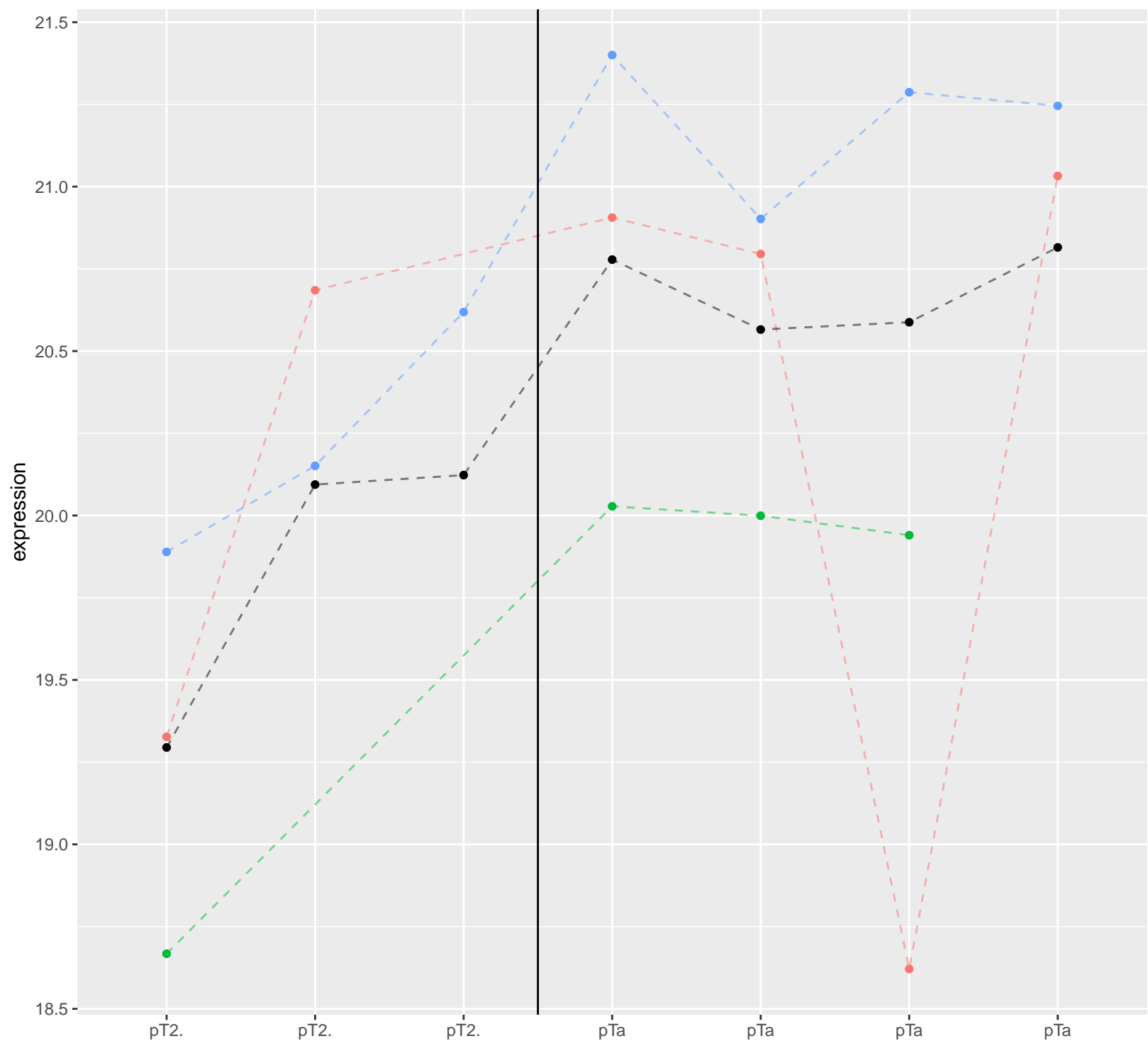
MSqRob: q-value: 2.6% log fold change: -1.58 t-value: -4.51 df: 13.6 se: 0.35

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



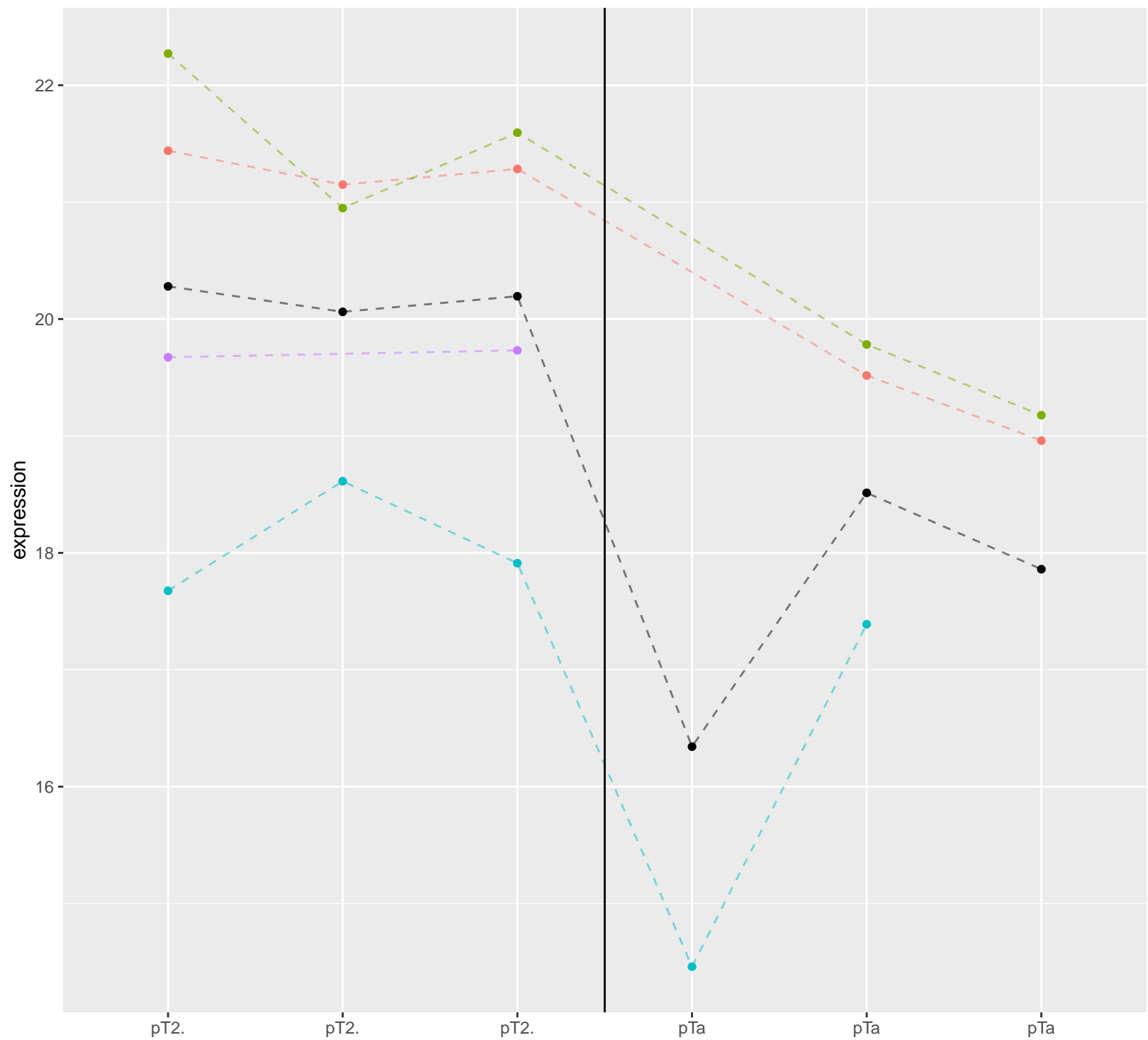
sp|Q9BRA2|TXD17_HUMANThioredoxin domain-containing protein17

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



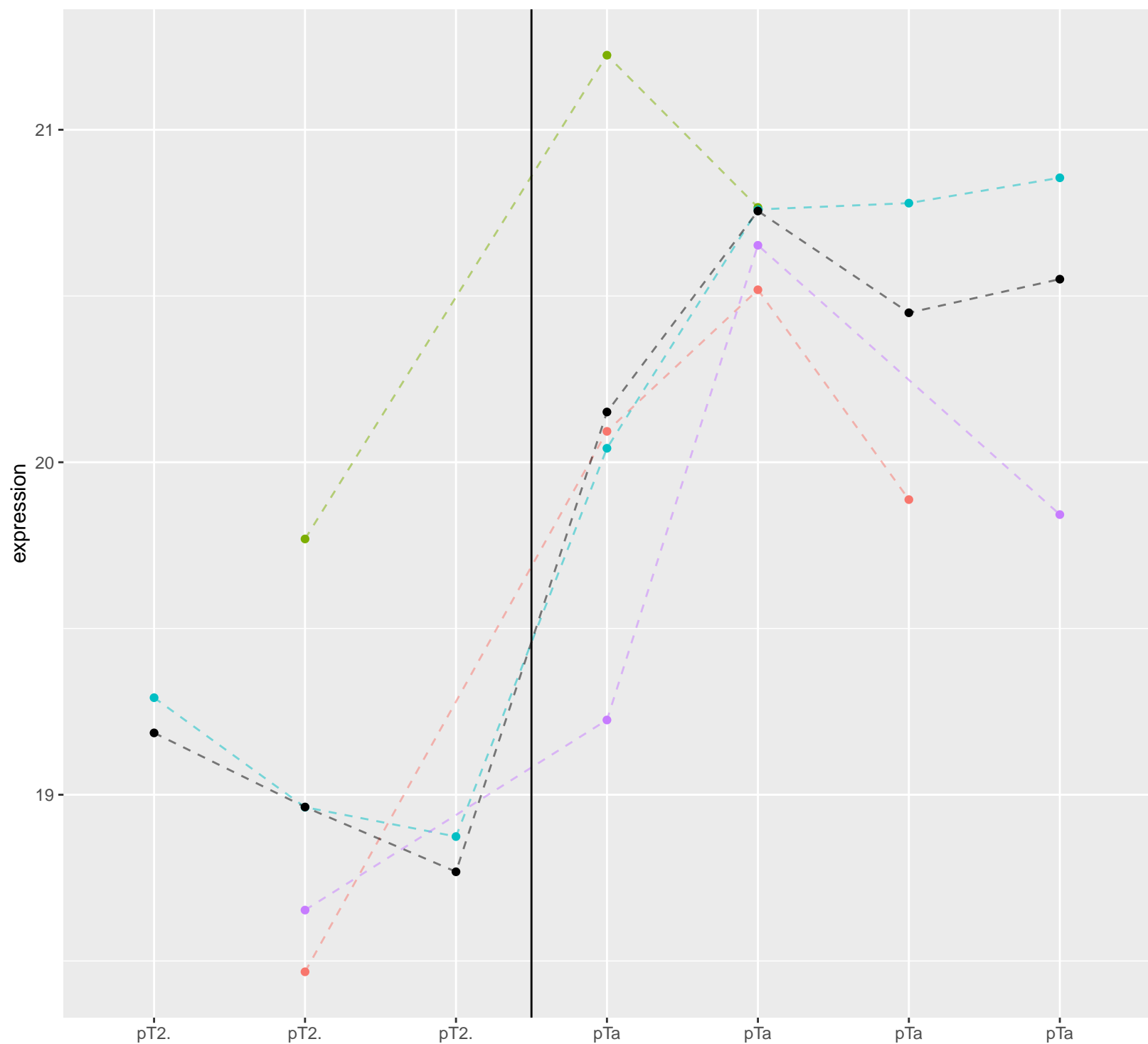
sp|Q6ZVX7|FBX50_HUMANF-boxonlyprotein50

MSqRob: q-value: 0% log fold change: -1.94 t-value: -7.56 df: 14.6 se: 0.26
MSqRobSum: q-value: 10.7% log fold change: -2.32 t-value: -5.83 df: 7.7 se: 0.4



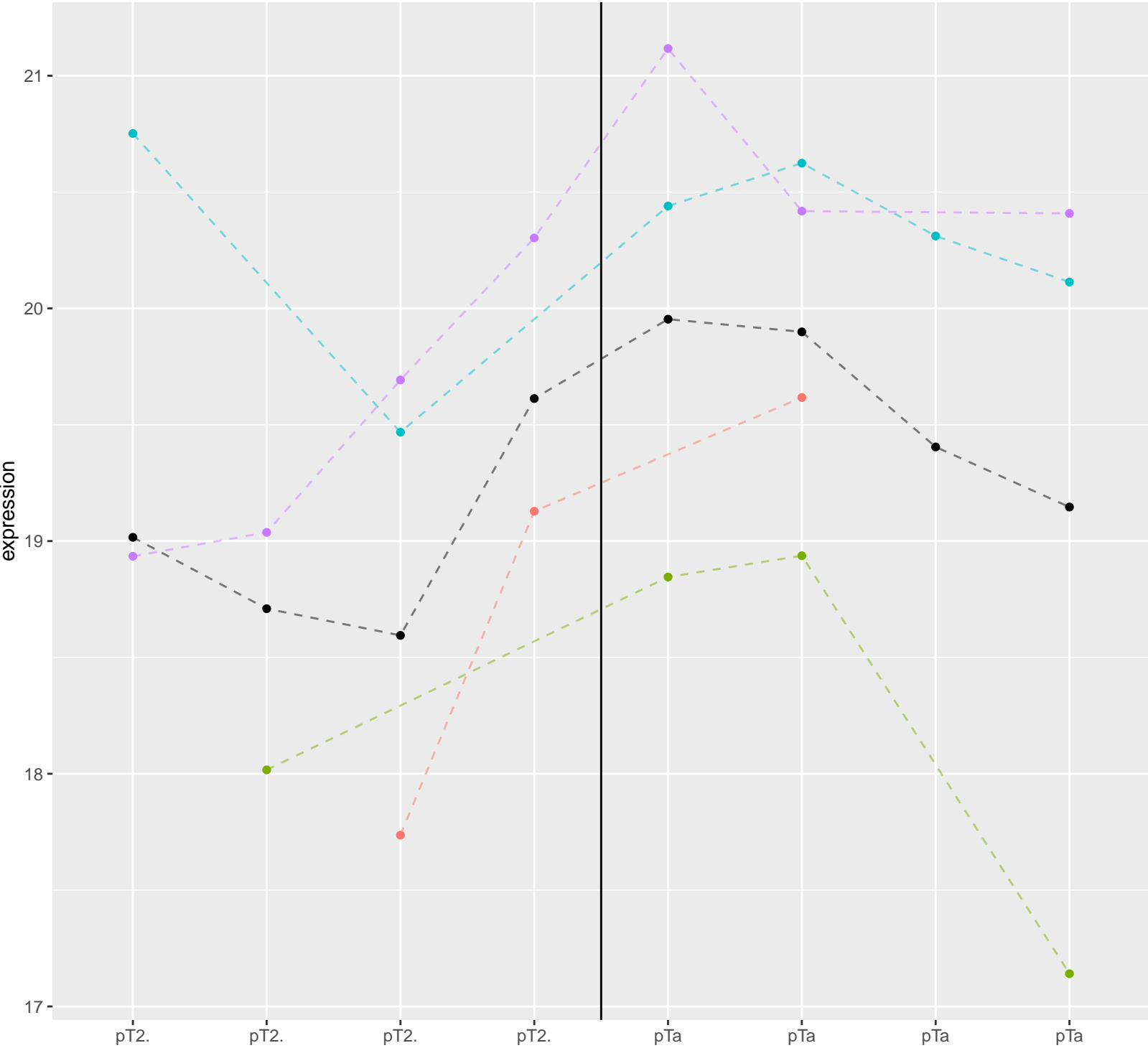
sp|Q5VW32|BROX_HUMANBRO1domain-containingproteinBROX

MSqRob: q-value: 0% log fold change: 1.46 t-value: 7.99 df: 15.8 se: 0.18
MSqRobSum: q-value: 14.1% log fold change: 1.48 t-value: 5.12 df: 8.6 se: 0.29



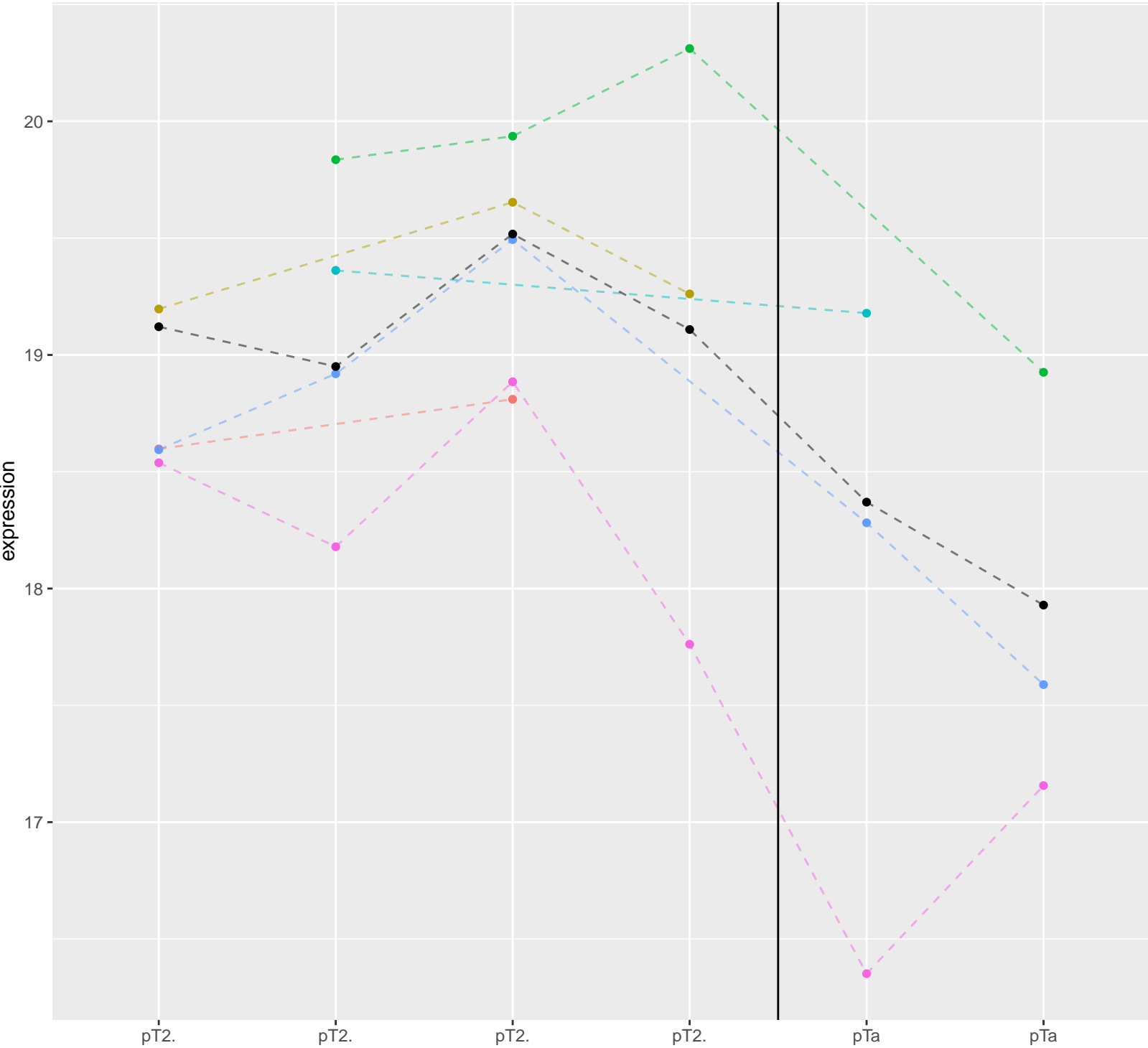
sp|O94905|ERLN2_HUMANErln-2

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



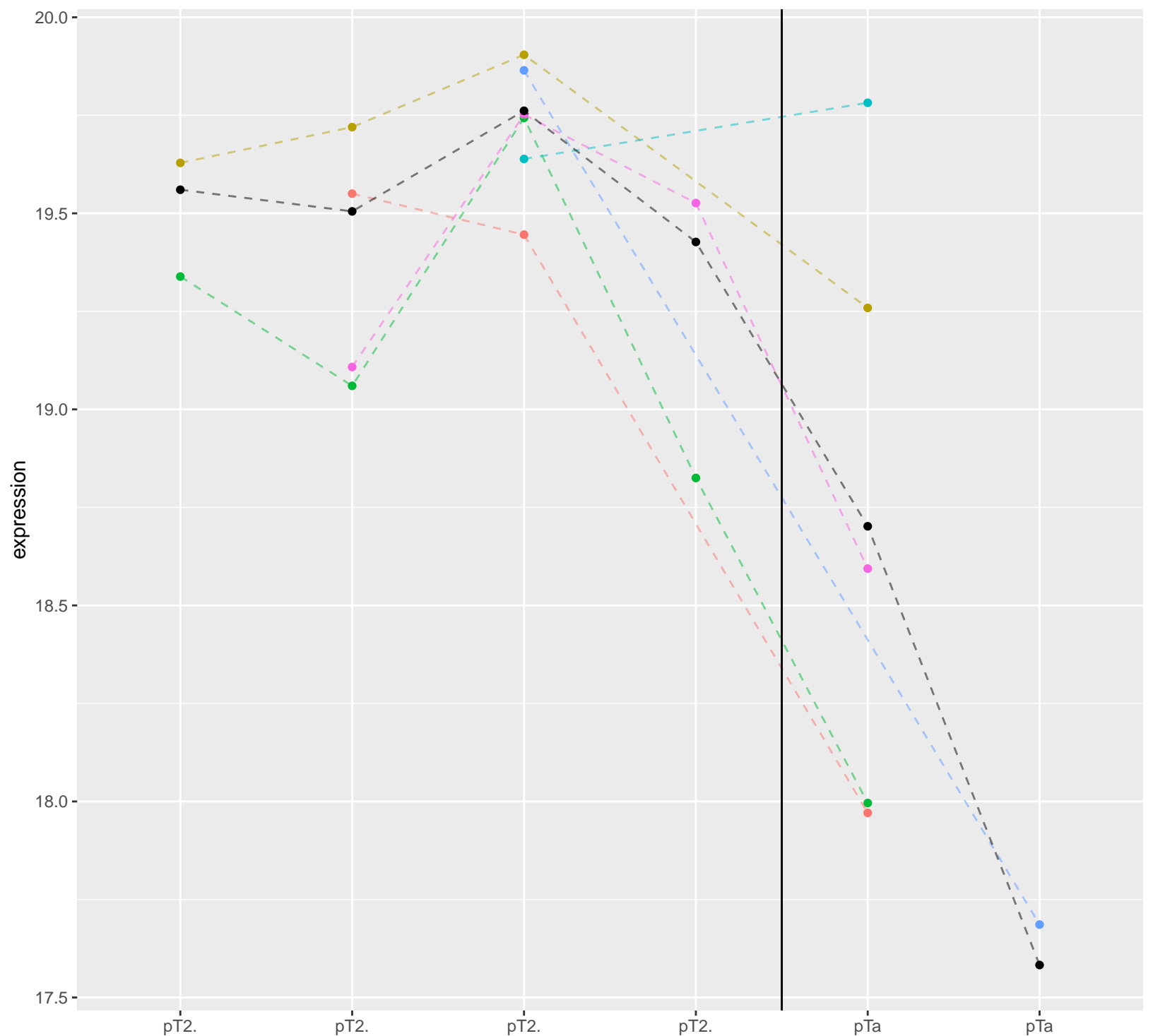
sp|P25205|MCM3_HUMAN|DNA replication licensing factor MCM3

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



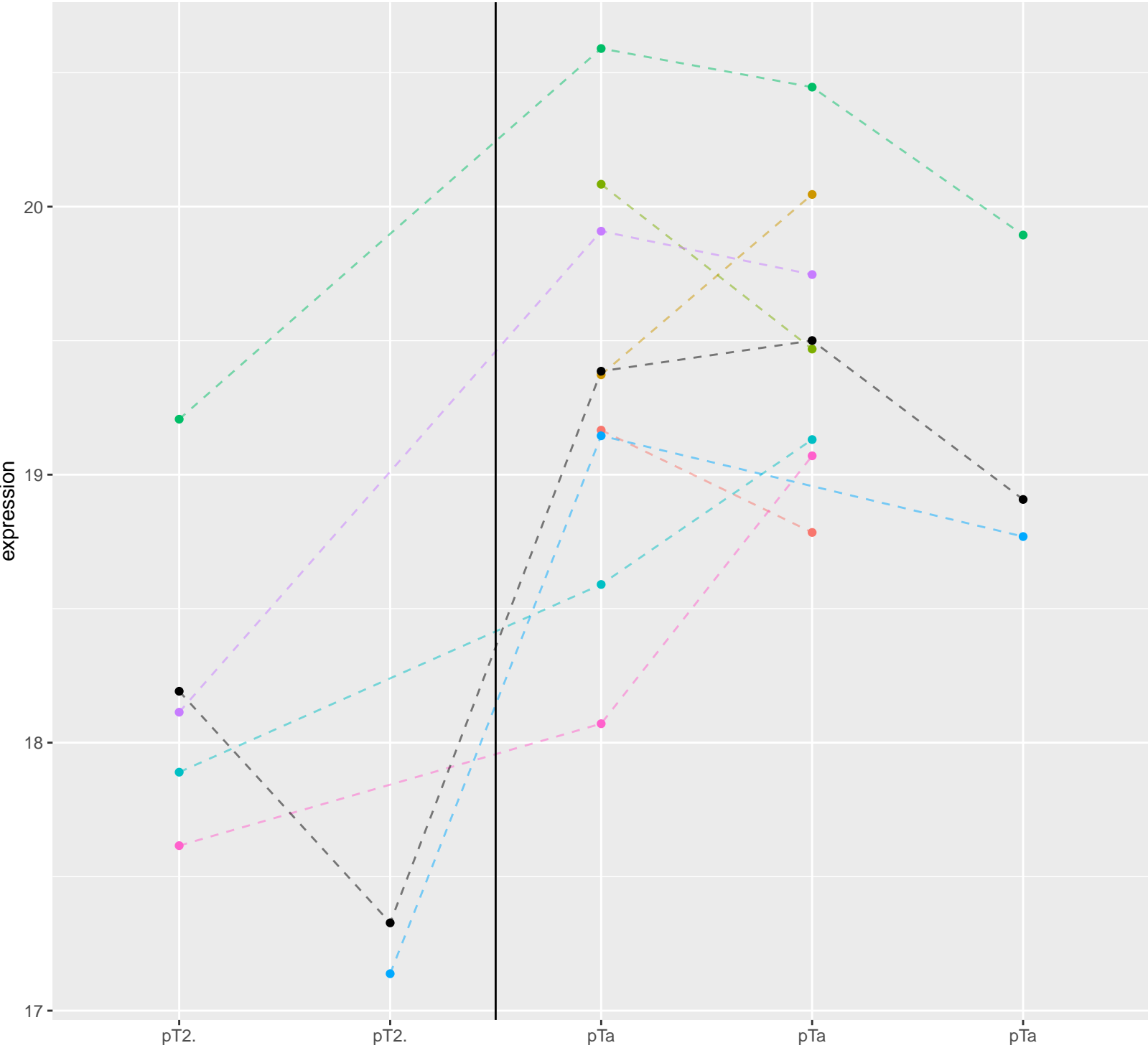
sp|Q14566|MCM6_HUMANDNAreplicationlicensingfactorMCM6

MSqRob: q-value: 1.4% log fold change: -1.12 t-value: -4.65 df: 17.1 se: 0.2
 MSqRobSum: q-value: 37.3% log fold change: -1.27 t-value: -3.5 df: 7.7 se: 0.36



sp|P16144|ITB4_HUMANIntegrinbeta-4

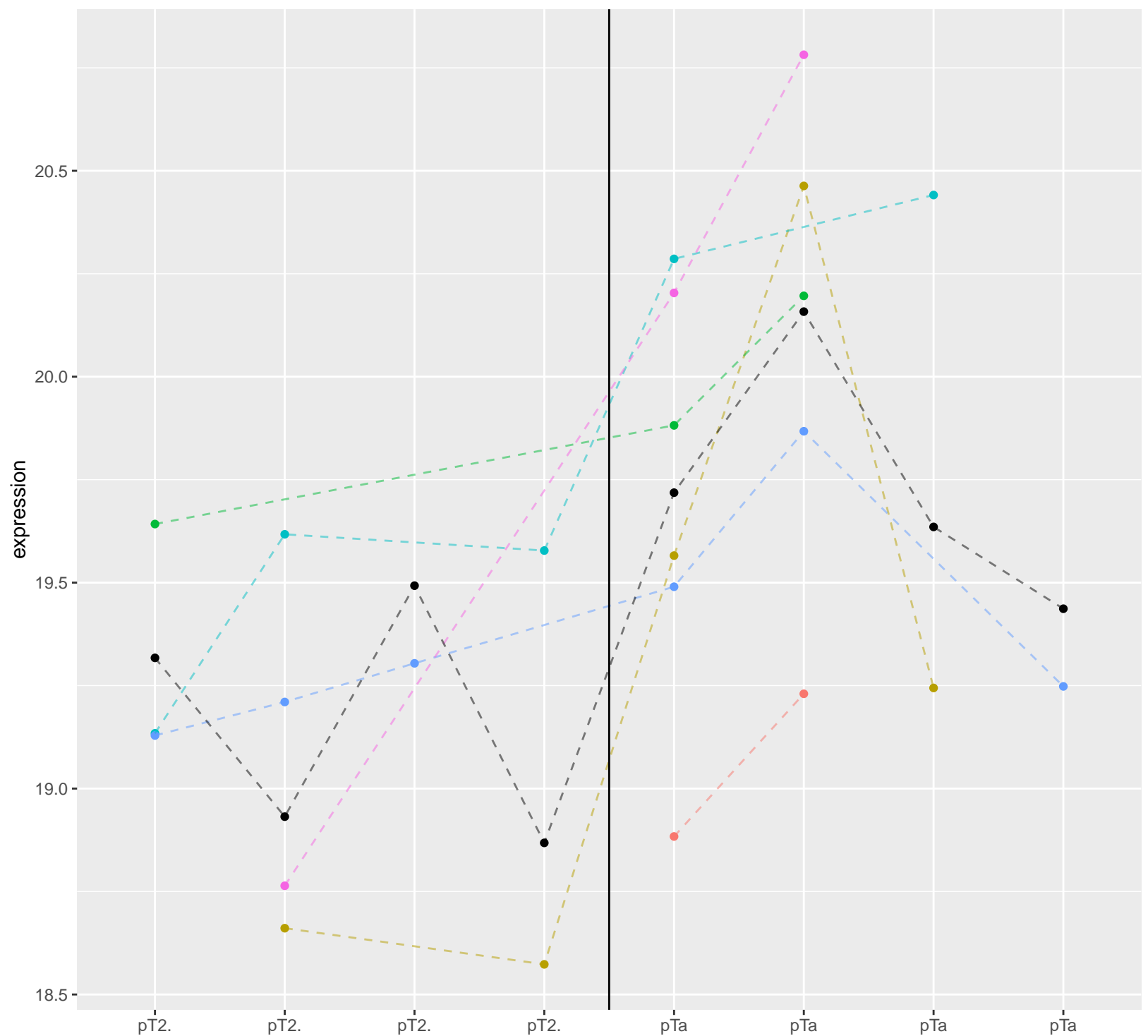
MSqRob: q-value: 0.1% log fold change: 1.33 t-value: 6.79 df: 16.6 se: 0.2
MSqRobSum: q-value: 41.2% log fold change: 1.4 t-value: 3.28 df: 6.7 se: 0.43



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

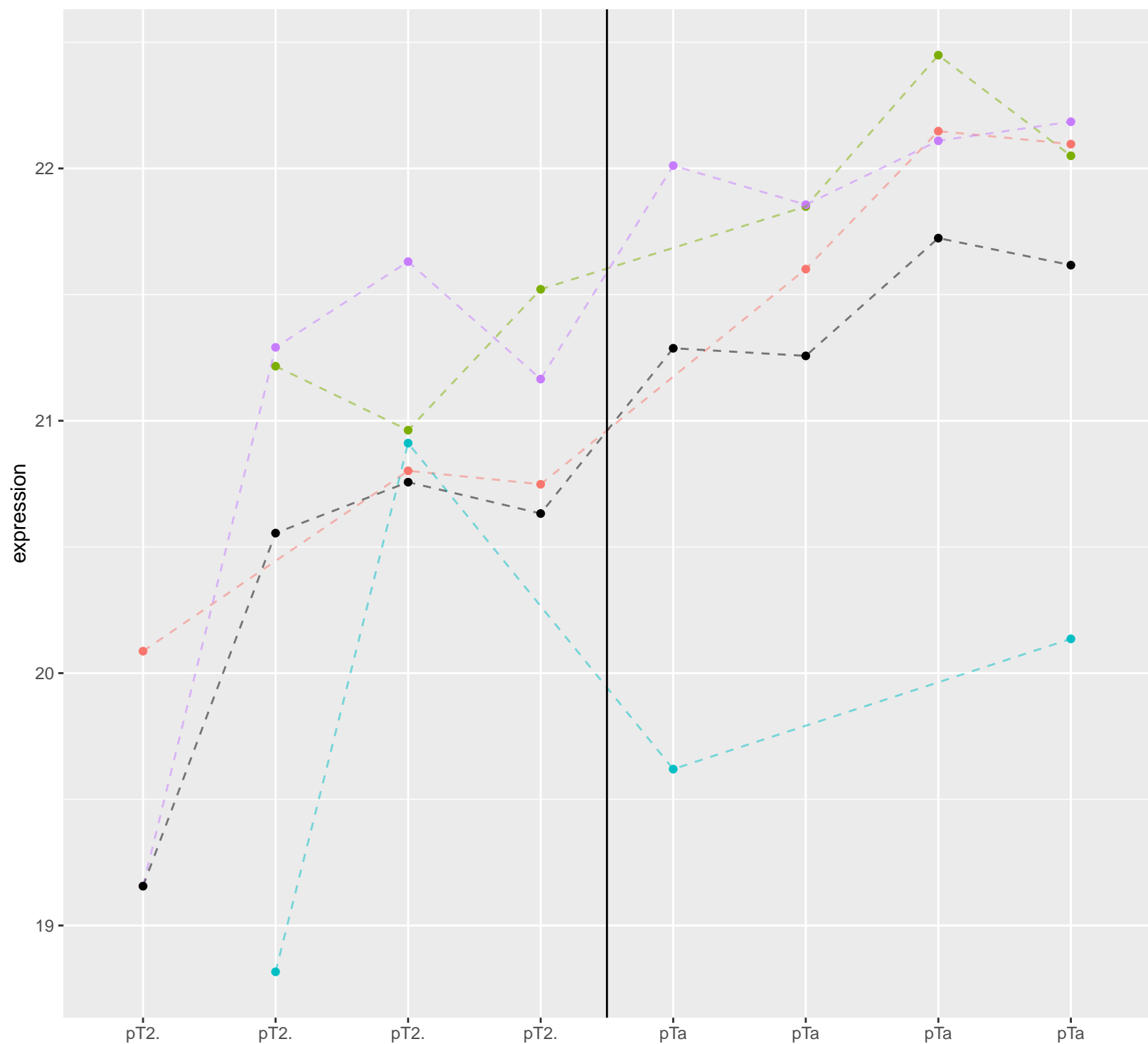
MSqRobSum: q-value: 74.5% log fold change: 0.51 t-value: 1.93 df: 9.8 se: 0.26



sp|O75608|LYPA1_HUMANAcyl-proteinthioesterase1

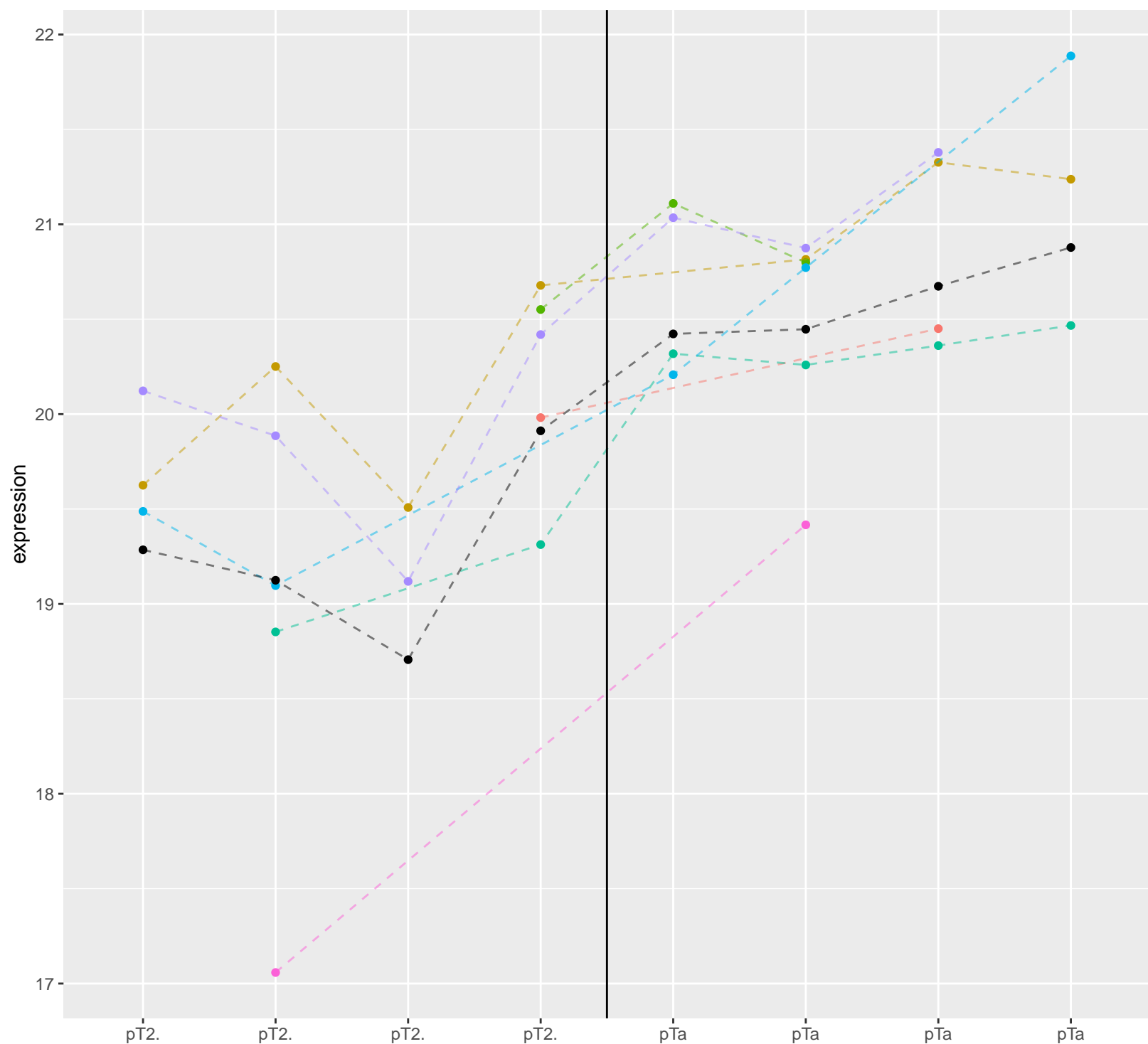
MSqRob: q-value: 0.3% log fold change: 0.92 t-value: 5.41 df: 20.8 se: 0.17

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



sp|P00390|GSHR_HUMANGlutathionereductase,mitochondrial

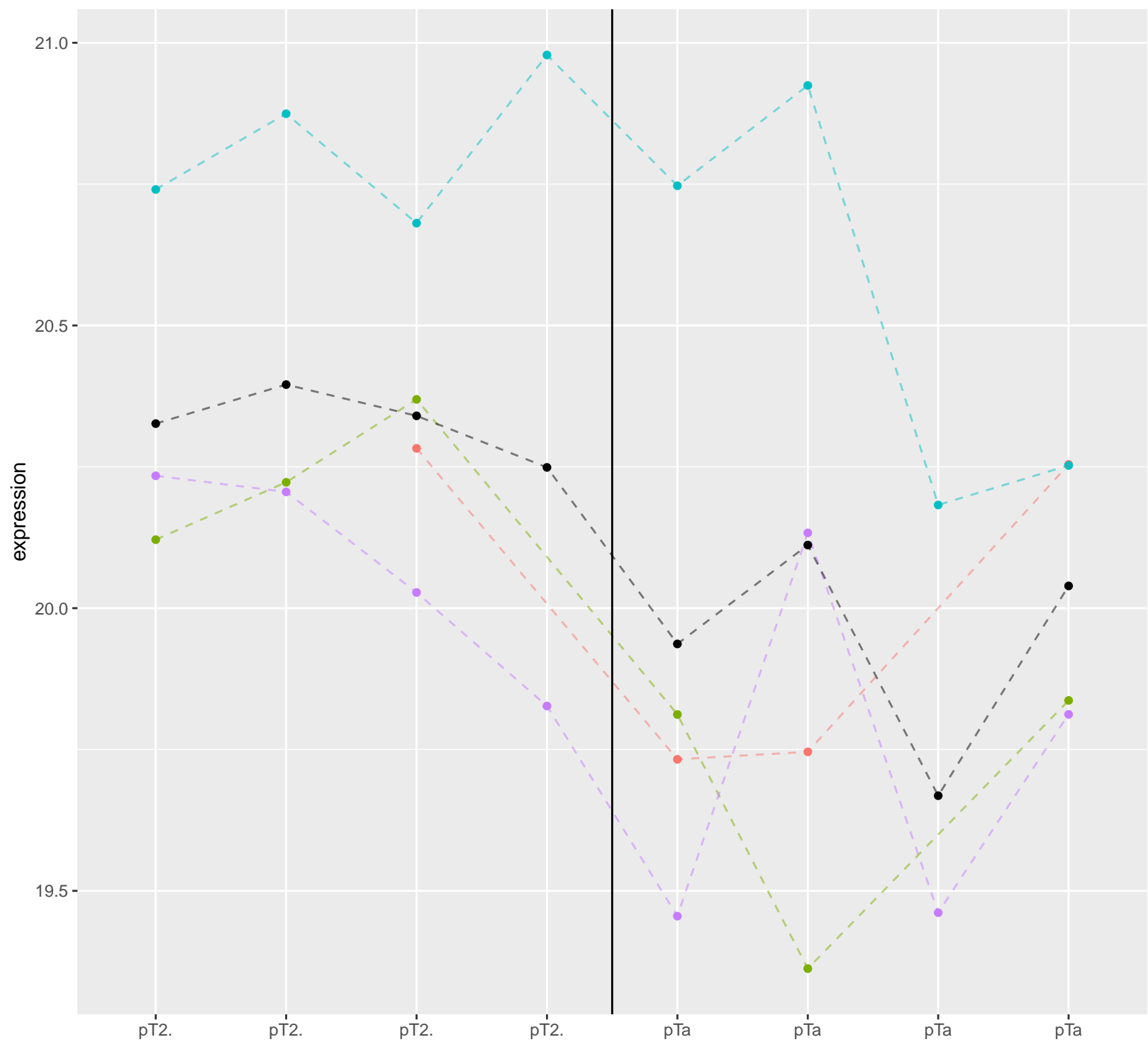
MSqRob: q-value: 0.9% log fold change: 1.22 t-value: 4.7 df: 22.2 se: 0.26
 MSqRobSum: q-value: 14.1% log fold change: 1.34 t-value: 4.82 df: 9.6 se: 0.28



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

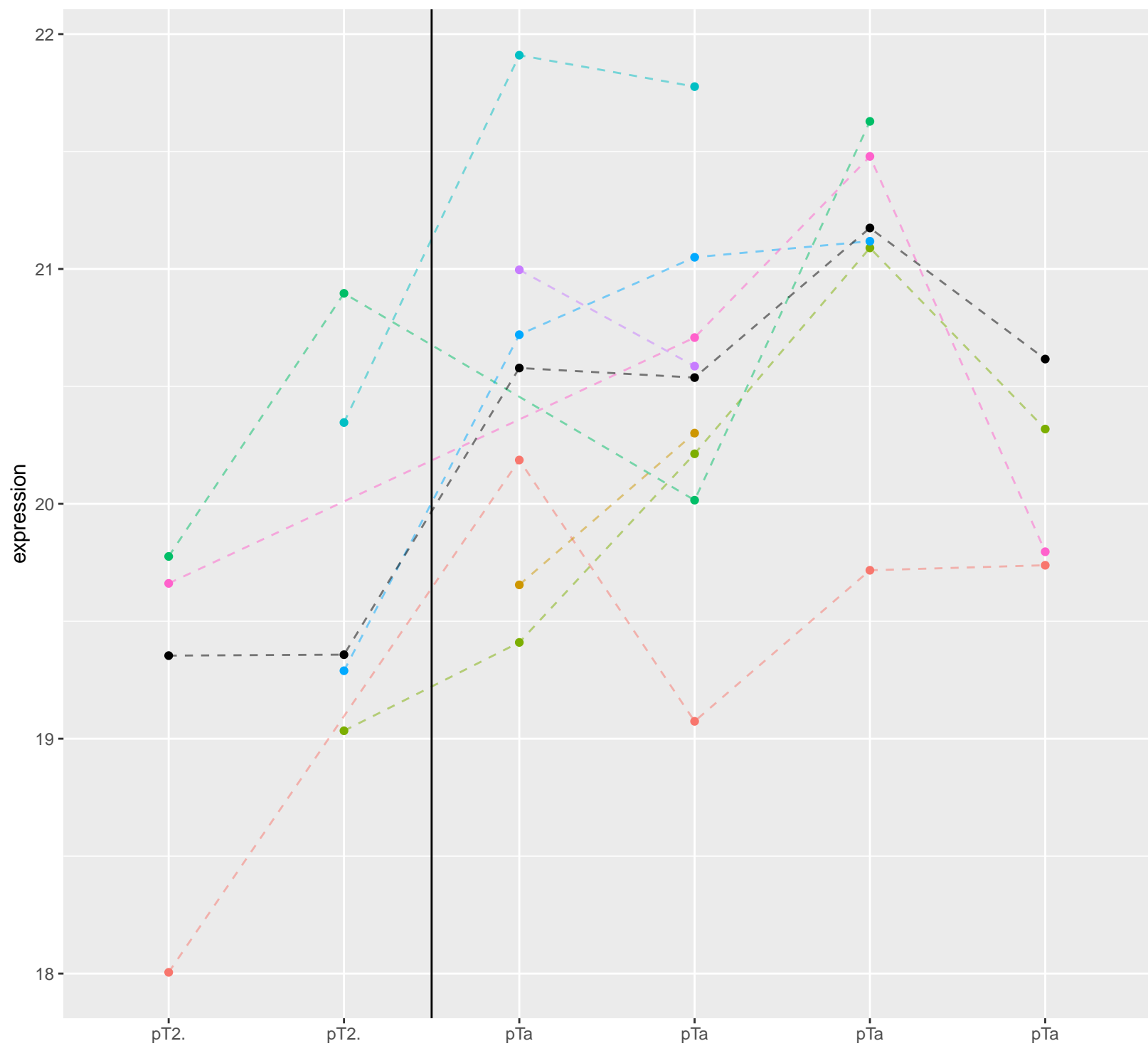
MSqRobSum: q-value: 99% log fold change: -0.33 t-value: -1.46 df: 9.7 se: 0.23



sp|O00515|LAD1_HUMANLadinin-1

MSqRob: q-value: 0.1% log fold change: 1.34 t-value: 6.19 df: 22.2 se: 0.22

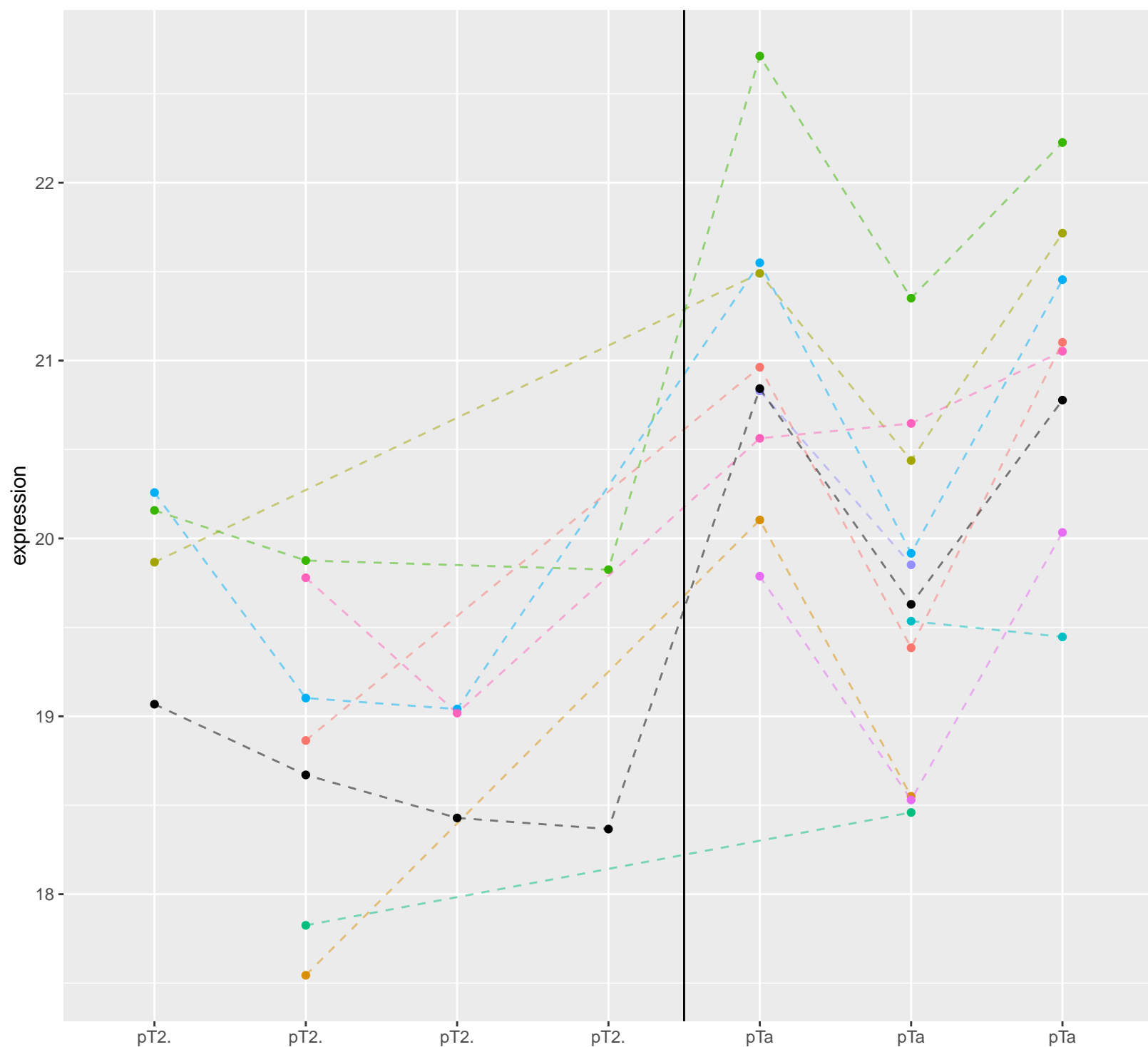
MSqRobSum: q-value: 30.7% log fold change: 1.28 t-value: 3.87 df: 7.6 se: 0.33



sp|O15382|BCAT2_HUMANBranched-chain-amino-acidaminotransferase,mitochondrial

MSqRob: q-value: 1.7% log fold change: 1.63 t-value: 4.18 df: 24.8 se: 0.39

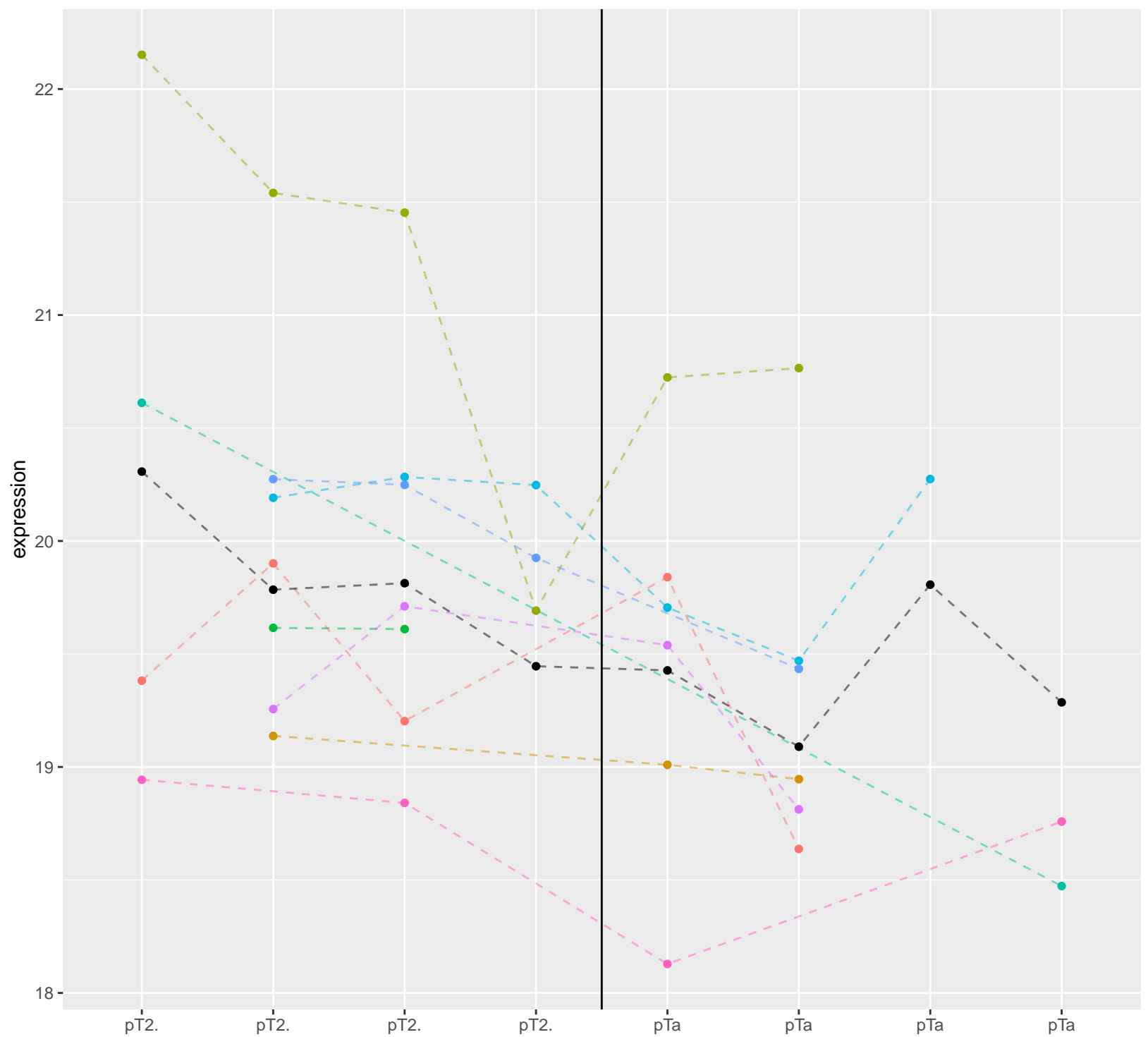
MSqRobSum: q-value: 18.9% log fold change: 1.7 t-value: 4.5 df: 8.7 se: 0.38



sp|O75131|CPNE3_HUMANCopine-3

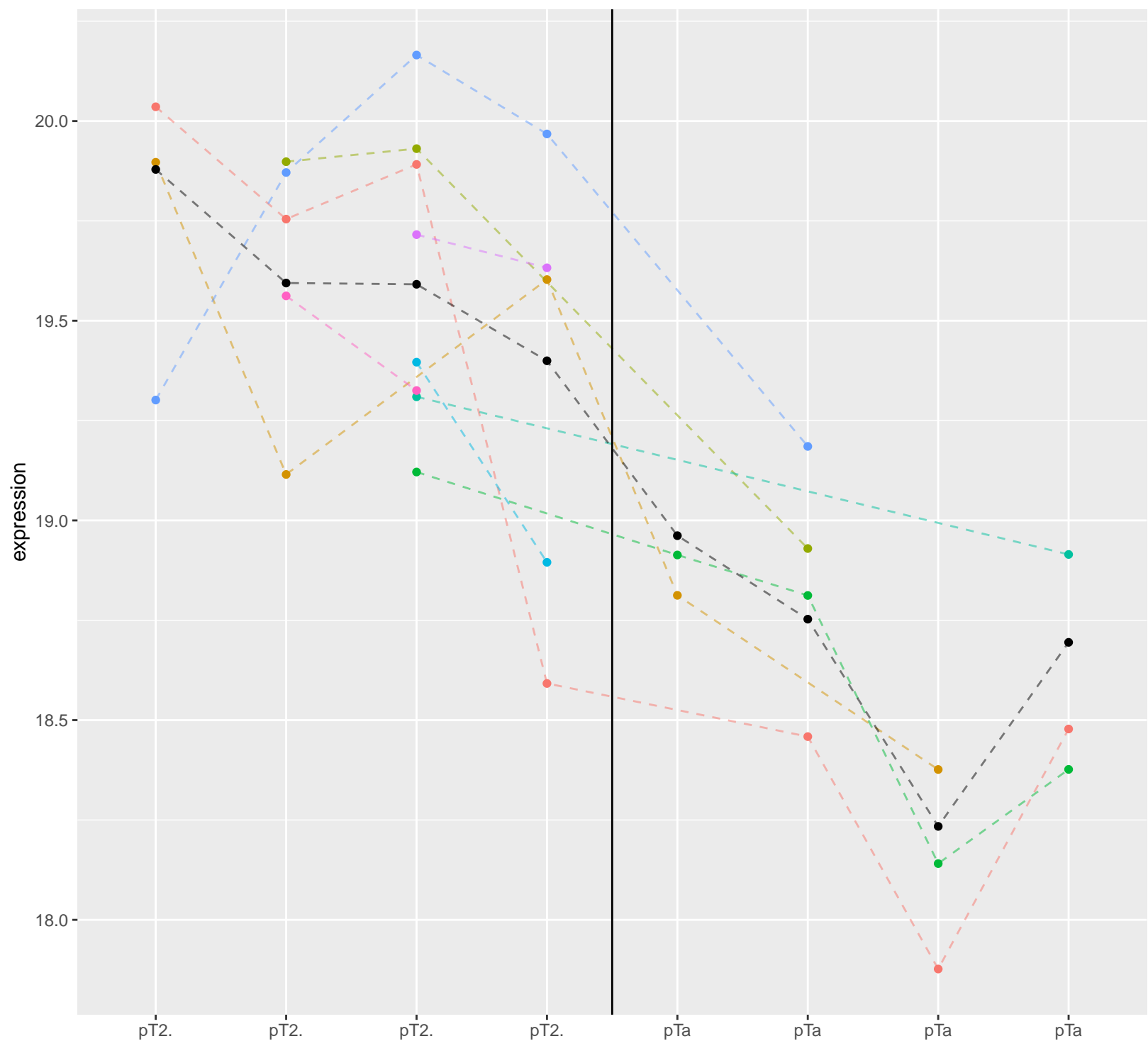
MSqRob: q-value: 1.2% log fold change: -0.51 t-value: -4.25 df: 29.2 se: 0.12

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



sp|P54577|SYYC_HUMANTyrosine--tRNA ligase, cytoplasmic

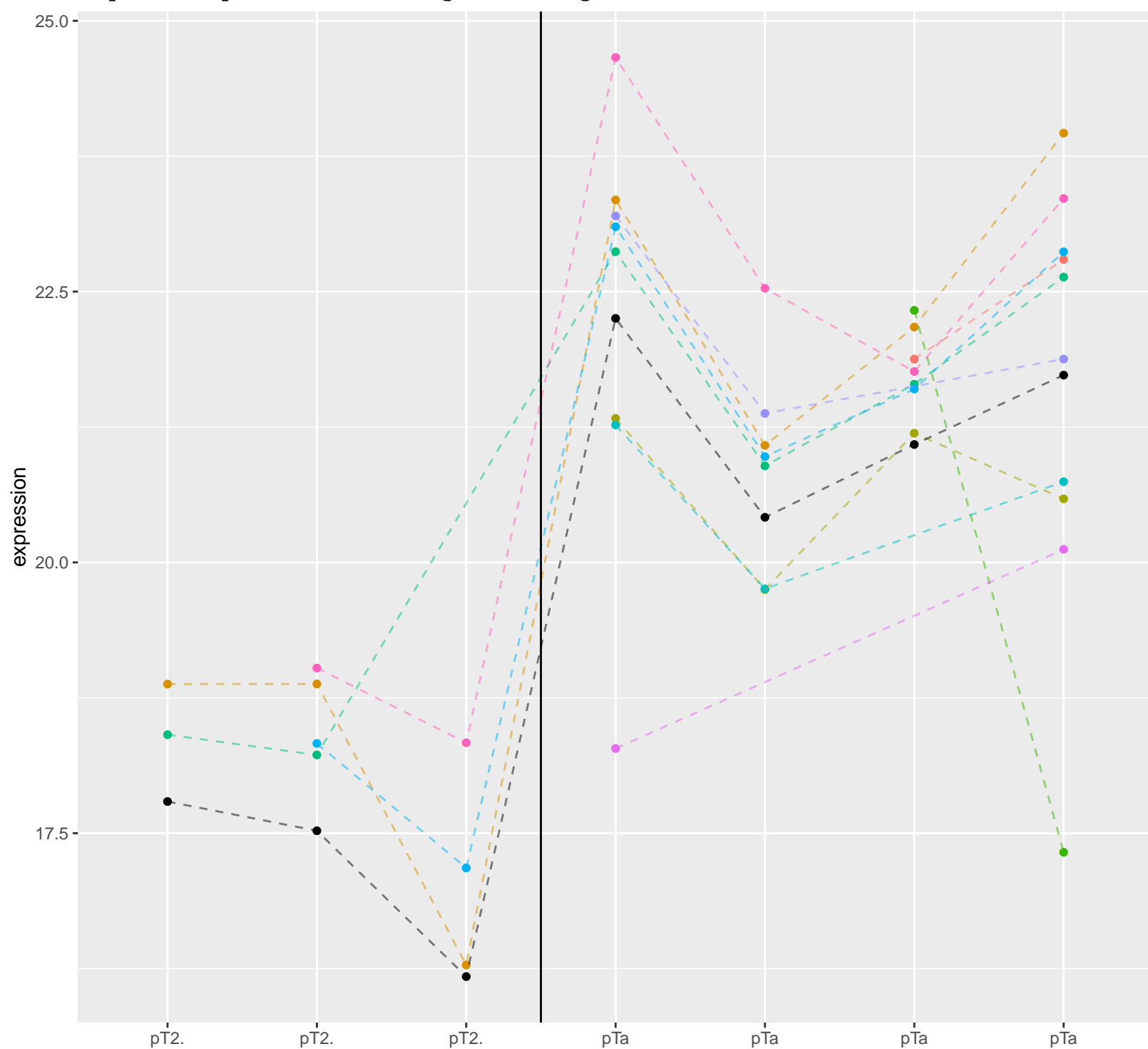
MSqRob: q-value: 0% log fold change: -0.93 t-value: -6.05 df: 30 se: 0.15
 MSqRobSum: q-value: 36% log fold change: -0.88 t-value: -3.44 df: 9.7 se: 0.26



sp|P15428|PGDH_HUMAN15-hydroxyprostaglandin dehydrogenase[NAD(+)]

MSqRob: q-value: 0% log fold change: 4 t-value: 6.94 df: 29.2 se: 0.58

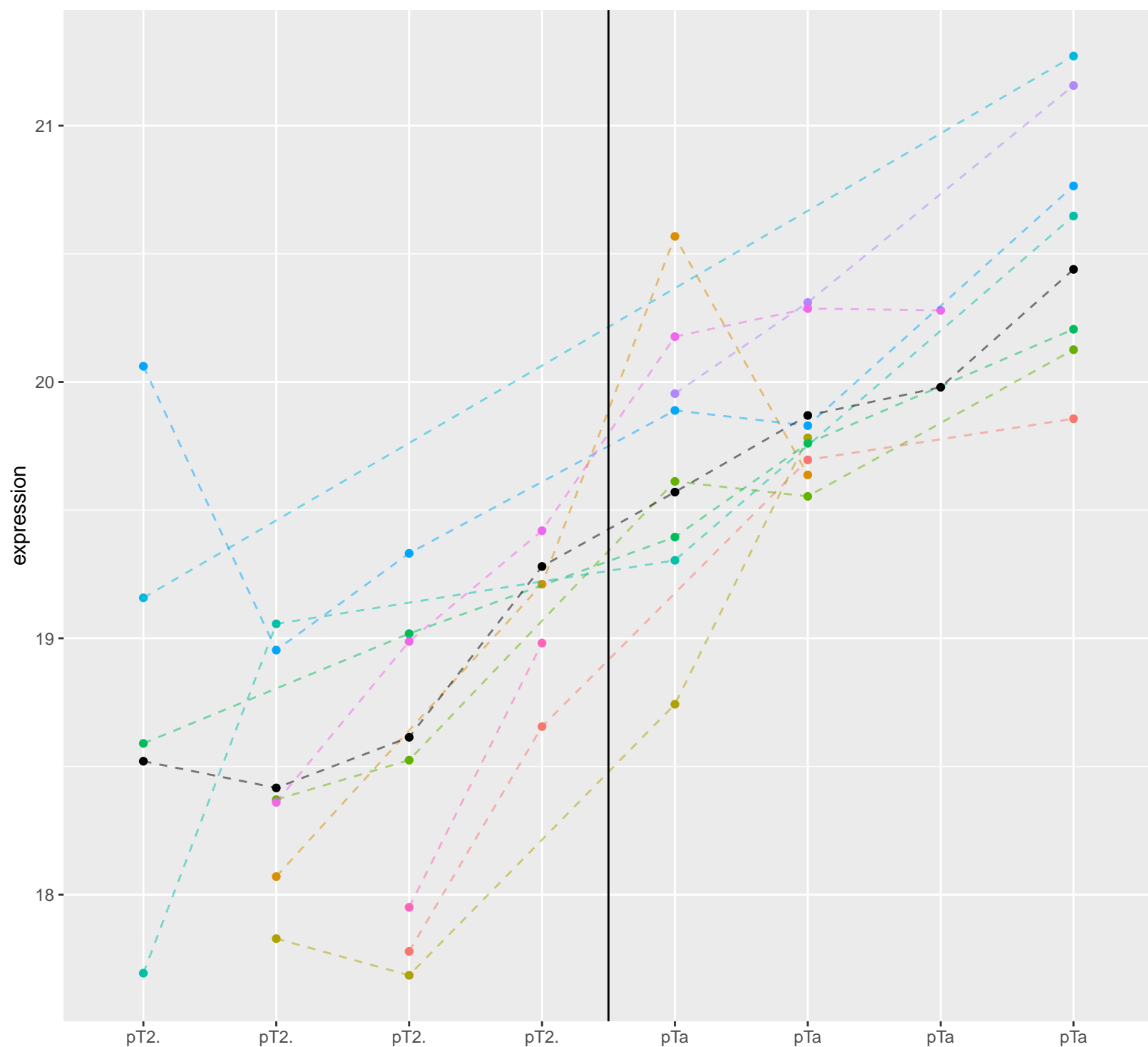
MSqRobSum: q-value: 2.4% log fold change: 4.11 t-value: 7.64 df: 8.6 se: 0.54



sp|P13798|ACPH_HUMANAcylamino-acid-releasingenzyme

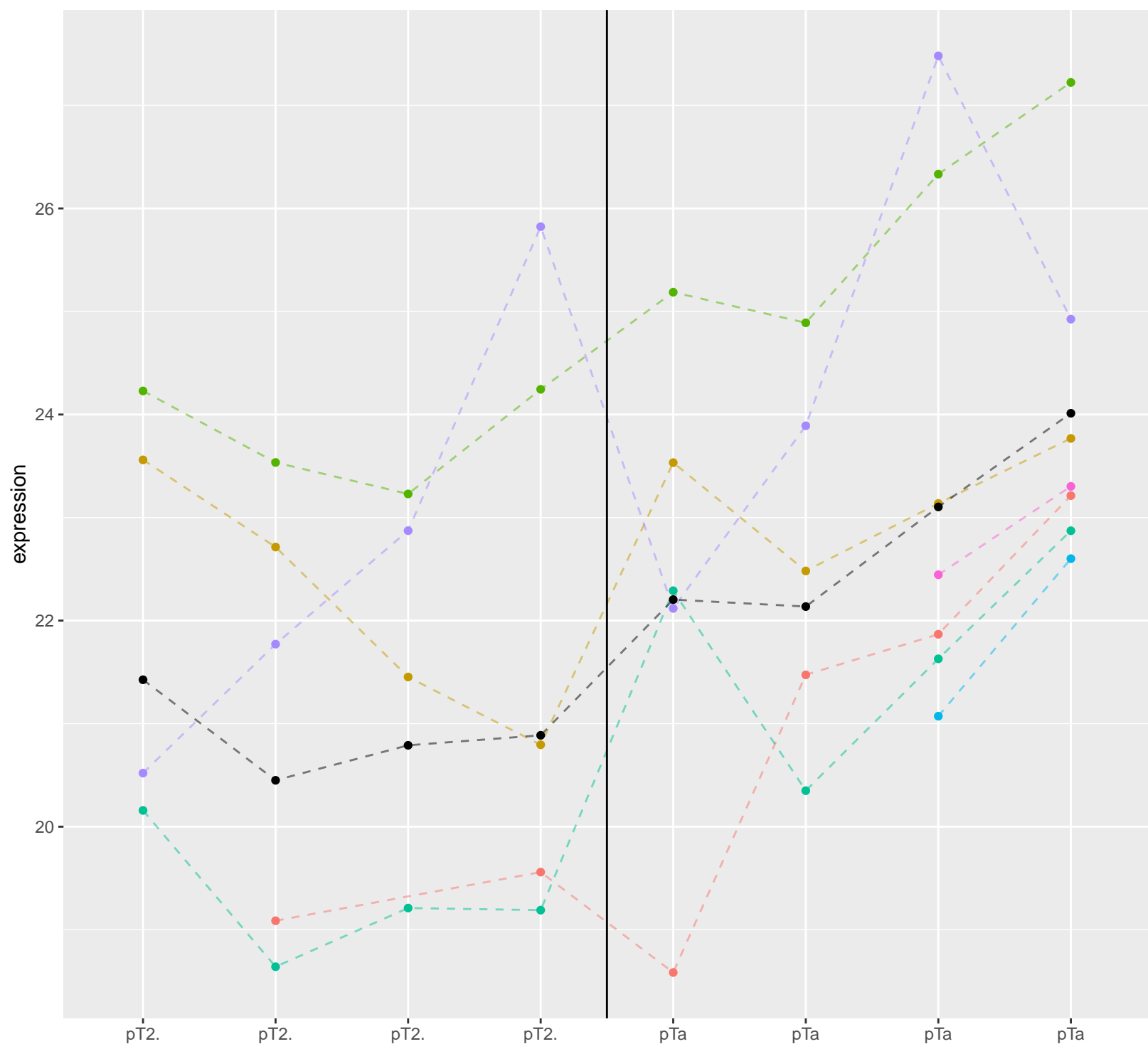
MSqRob: q-value: 0.5% log fold change: 1.23 t-value: 4.65 df: 33 se: 0.27

MSqRobSum: q-value: 23.8% log fold change: 1.2 t-value: 4 df: 9.7 se: 0.3



sp|P25815|S100P_HUMANProteinS100-P

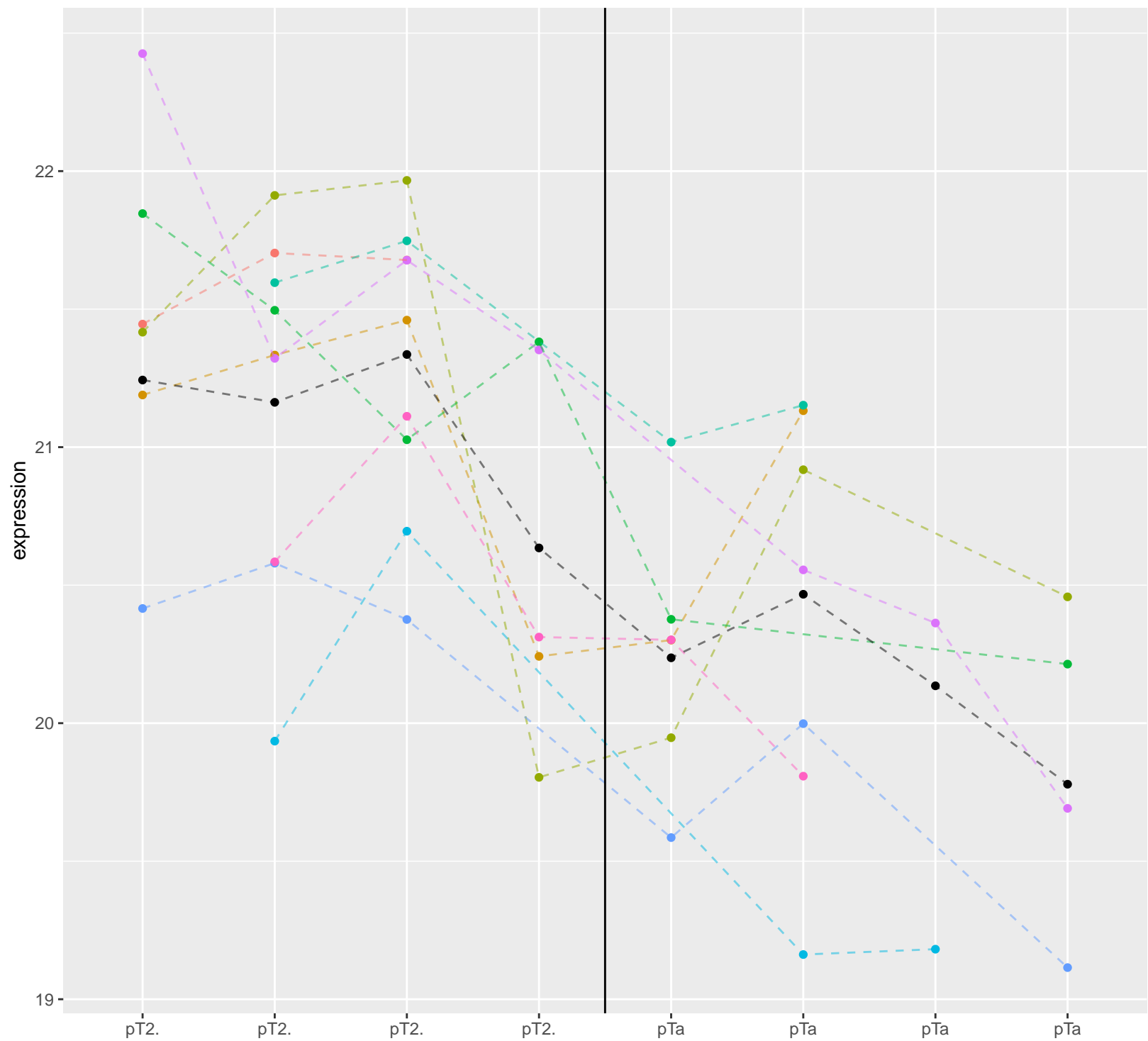
MSqRob: q-value: 0.7% log fold change: 1.91 t-value: 4.49 df: 33.2 se: 0.43
 MSqRobSum: q-value: 18.9% log fold change: 1.8 t-value: 4.33 df: 9.7 se: 0.42



sp|P12004|PCNA_HUMANProliferatingcellnuclearantigen

MSqRob: q-value: 0.2% log fold change: -0.92 t-value: -5.08 df: 37.4 se: 0.18

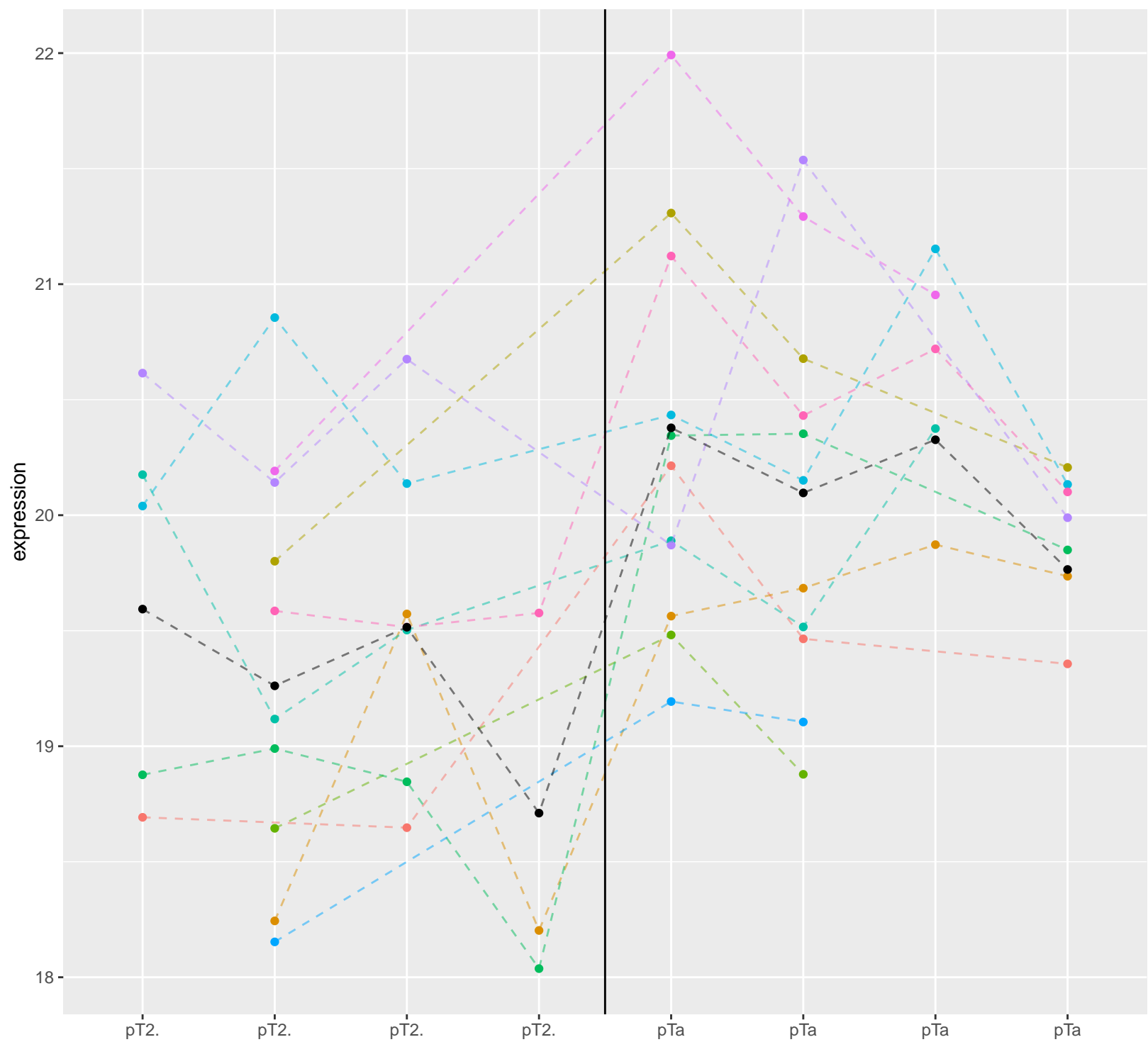
MSqRobSum: q-value: 37.3% log fold change: -0.89 t-value: -3.25 df: 9.7 se: 0.27



sp|P50570|DYN2_HUMANDynammin-2

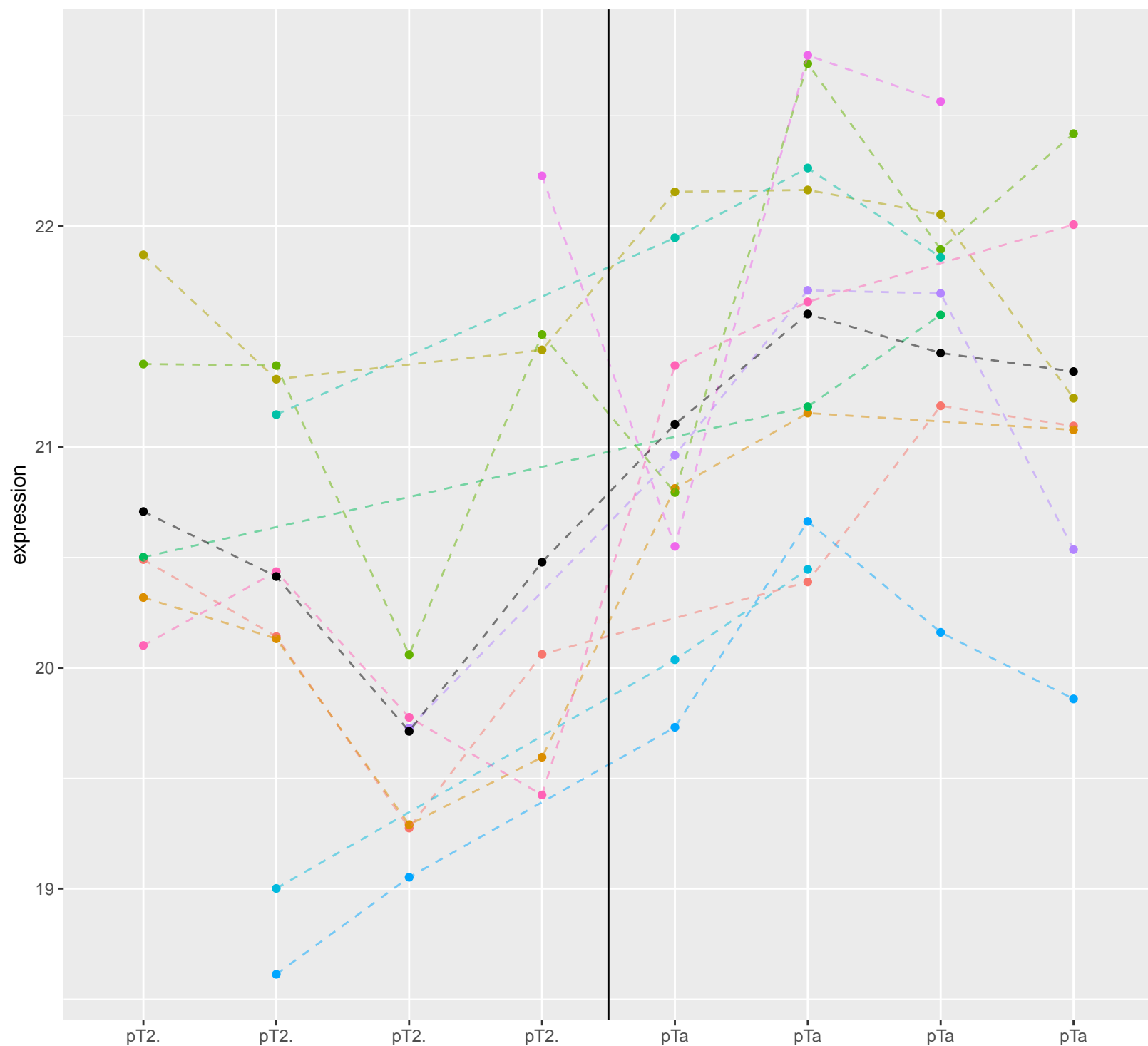
MSqRob: q-value: 0.9% log fold change: 0.79 t-value: 4.22 df: 46.5 se: 0.19

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



sp|P78417|GSTO1_HUMANGlutathioneS-transferaseomega-1

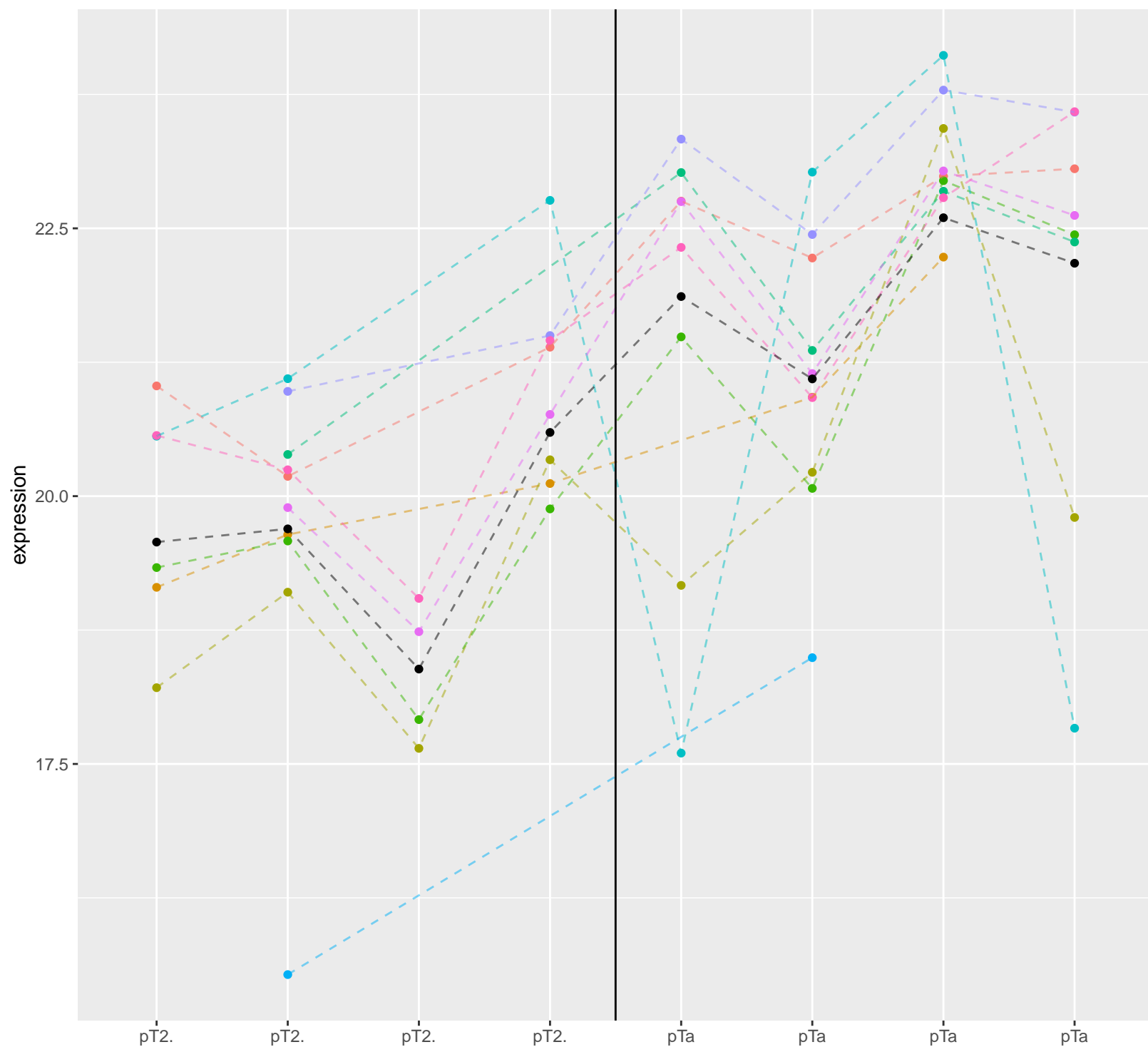
MSqRob: q-value: 0.3% log fold change: 1 t-value: 4.75 df: 47.4 se: 0.21
 MSqRobSum: q-value: 36% log fold change: 0.92 t-value: 3.39 df: 9.7 se: 0.27



sp|O76070|SYUG_HUMANGamma-synuclein

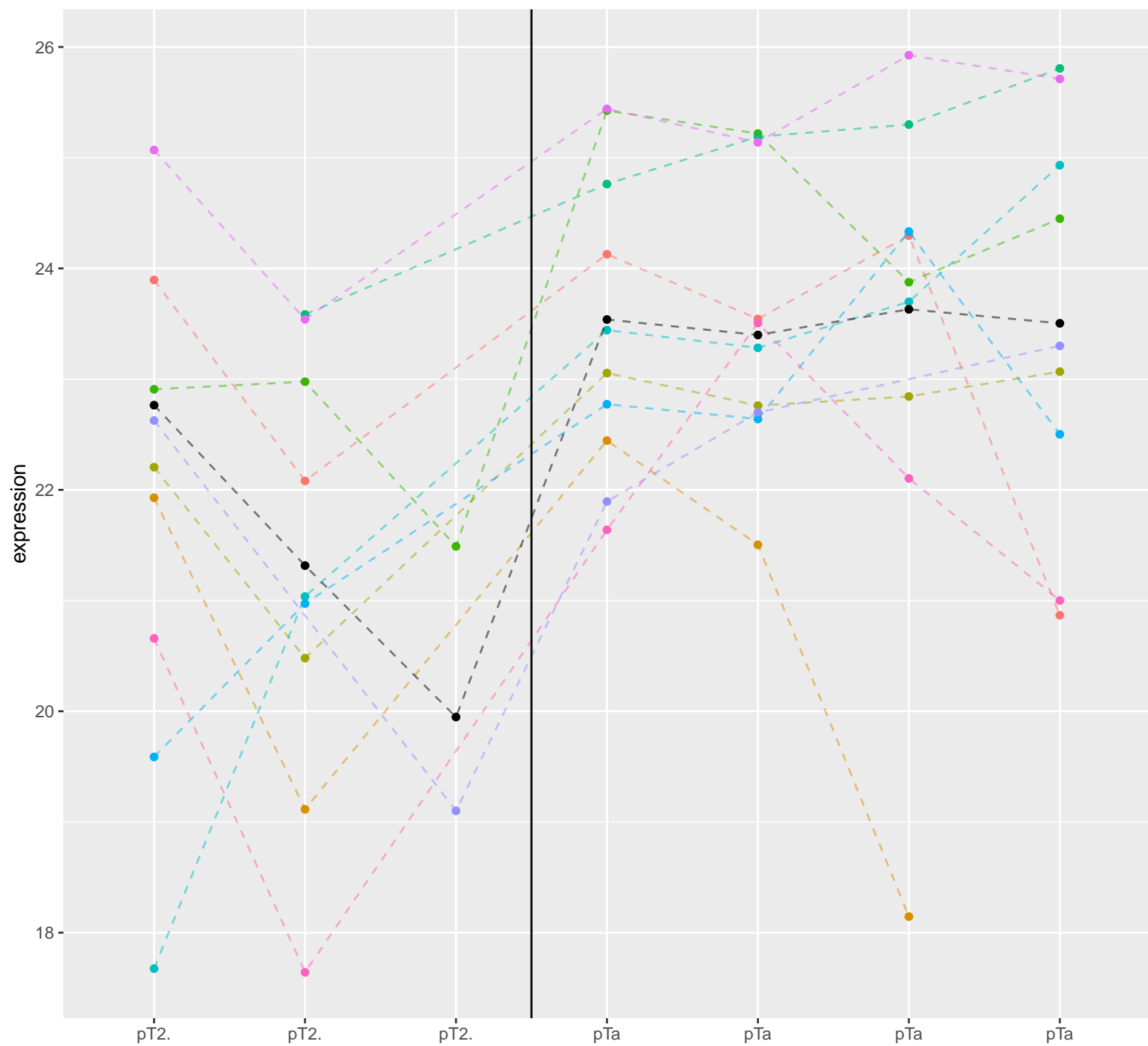
MSqRob: q-value: 1% log fold change: 2.19 t-value: 4.11 df: 49.5 se: 0.53

MSqRobSum: q-value: 14.1% log fold change: 2.19 t-value: 4.7 df: 9.7 se: 0.47



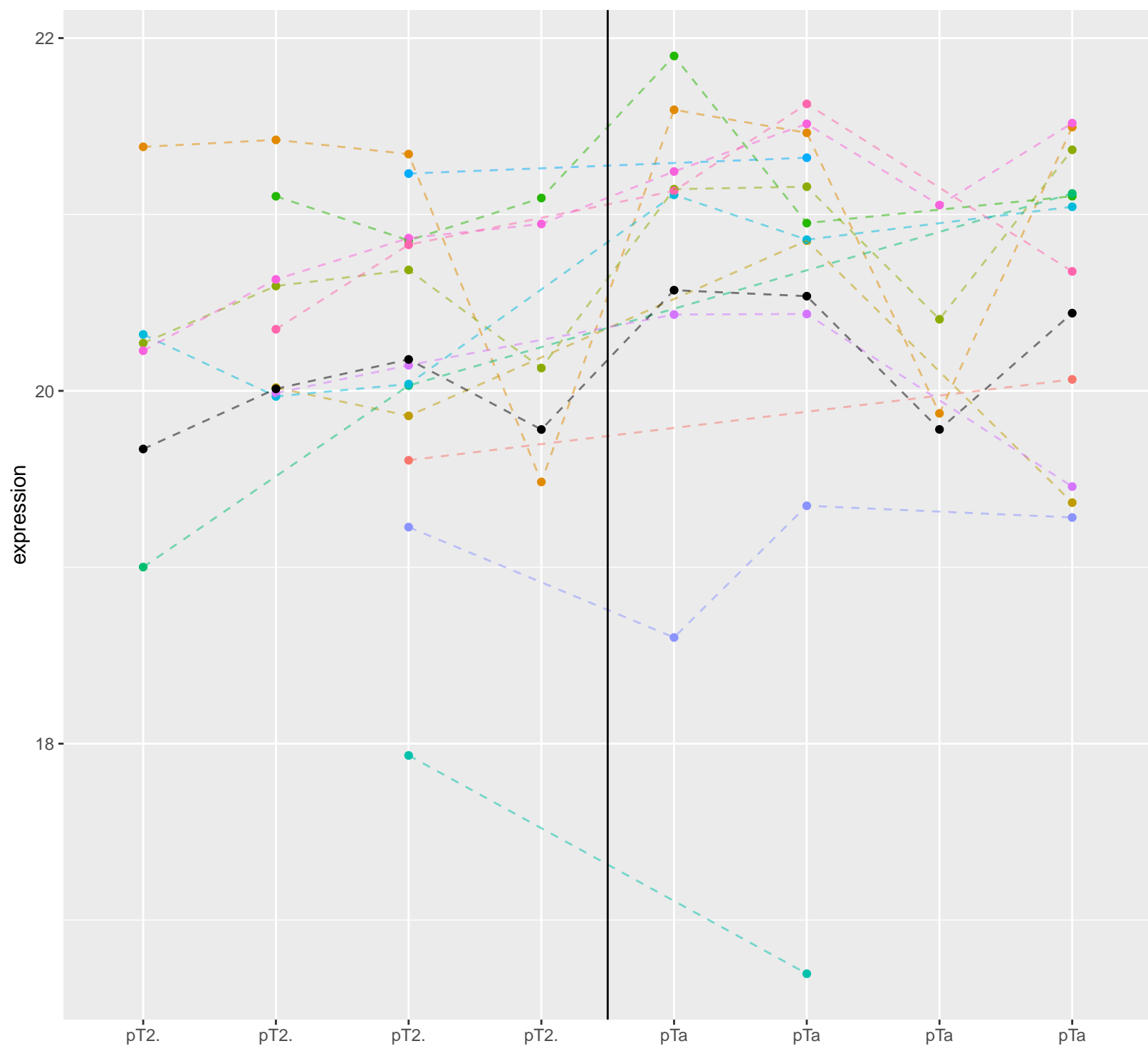
sp|P09488|GSTM1_HUMANGlutathioneS-transferaseMu1

MSqRob: q-value: 0% log fold change: 1.91 t-value: 8.69 df: 50.2 se: 0.22
 MSqRobSum: q-value: 9.4% log fold change: 2.08 t-value: 5.94 df: 8.7 se: 0.35



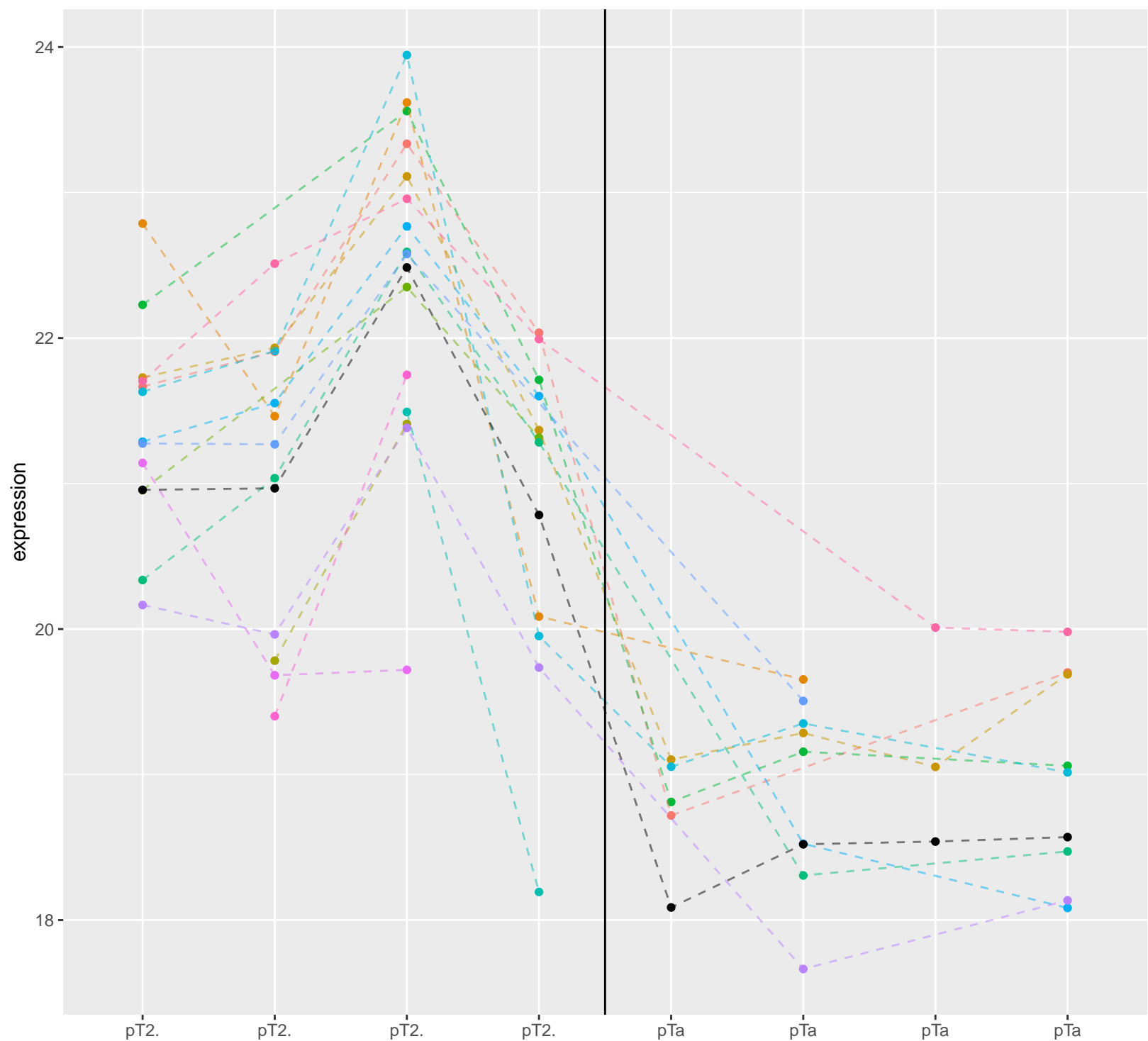
sp|P13489|RINI_HUMANRibonucleaseinhibitor

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|O43175|SERA_HUMAND-3-phosphoglyceratedehydrogenase

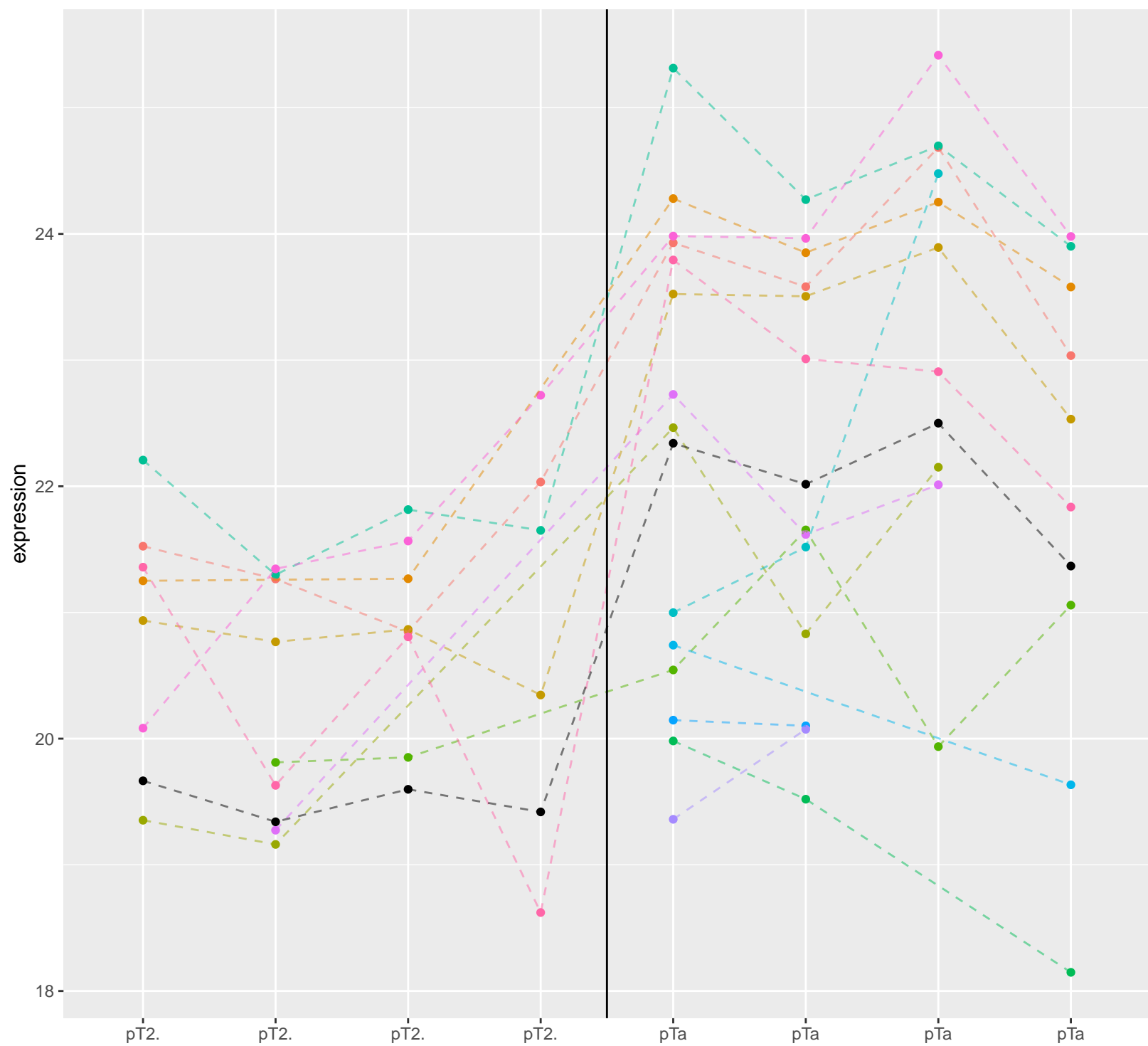
MSqRob: q-value: 0% log fold change: -2.76 t-value: -6.81 df: 54.3 se: 0.4
 MSqRobSum: q-value: 1.6% log fold change: -2.66 t-value: -7.85 df: 9.6 se: 0.34



sp|Q04695|K1C17_HUMANKeratin,typeIcytoskeletal17

MSqRob: q-value: 0% log fold change: 2.48 t-value: 9.71 df: 56.4 se: 0.25

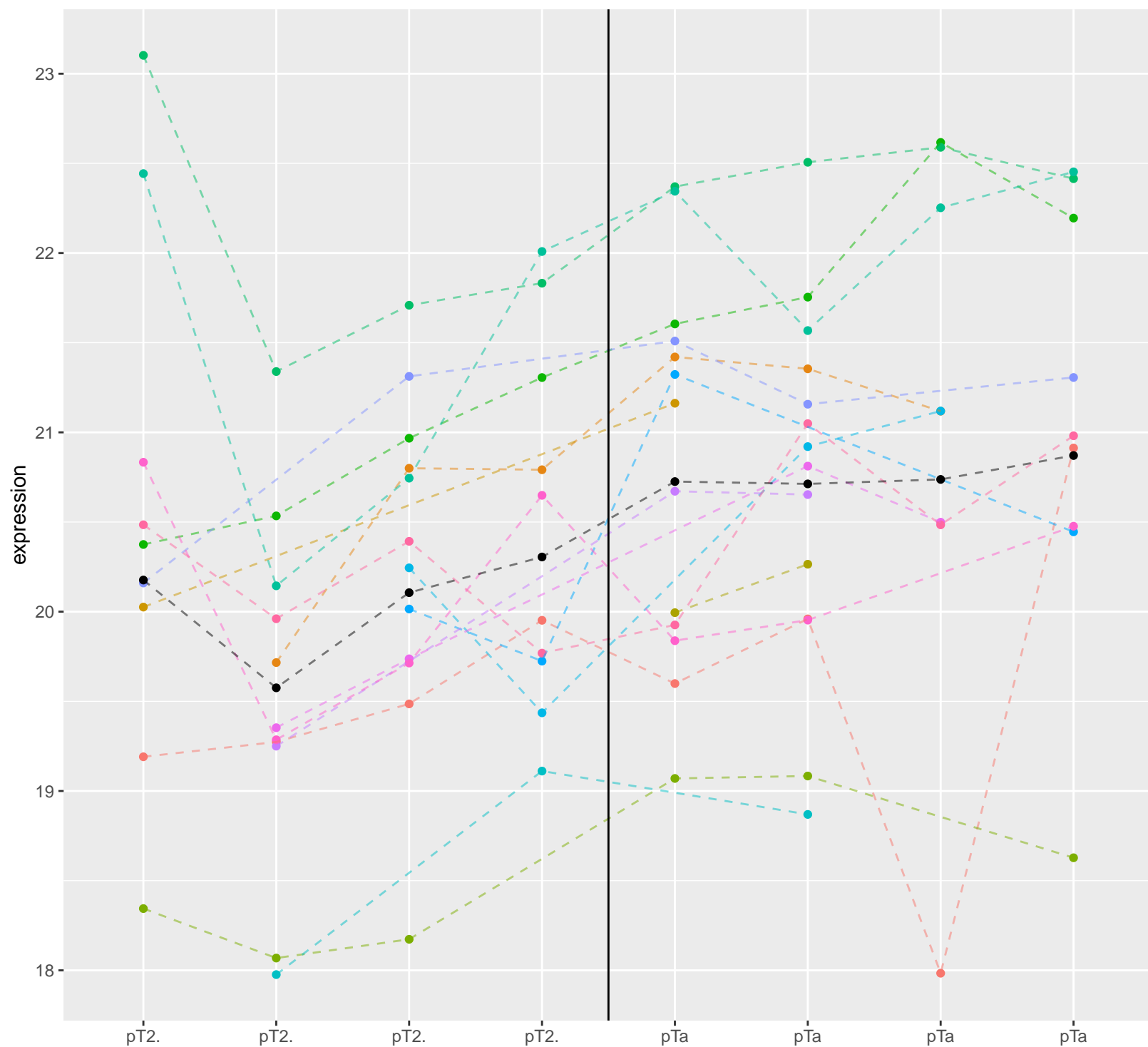
MSqRobSum: q-value: 0.7% log fold change: 2.6 t-value: 9.4 df: 9.6 se: 0.28



sp|P00505|AATM_HUMANAspartateaminotransferase,mitochondrial

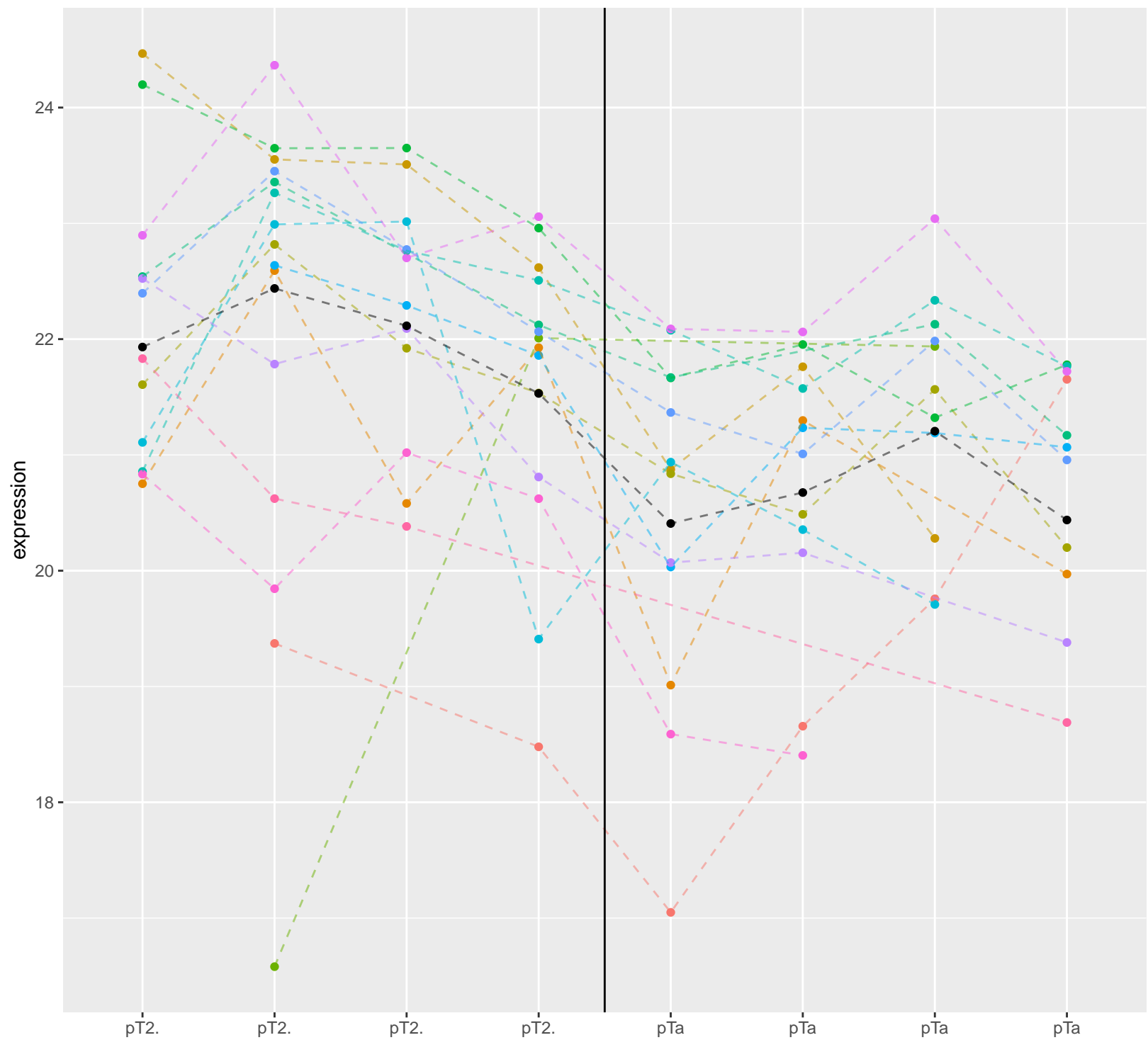
MSqRob: q-value: 0.3% log fold change: 0.72 t-value: 4.63 df: 68.3 se: 0.15

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



sp|P08758|ANXA5_HUMANAnnexinA5

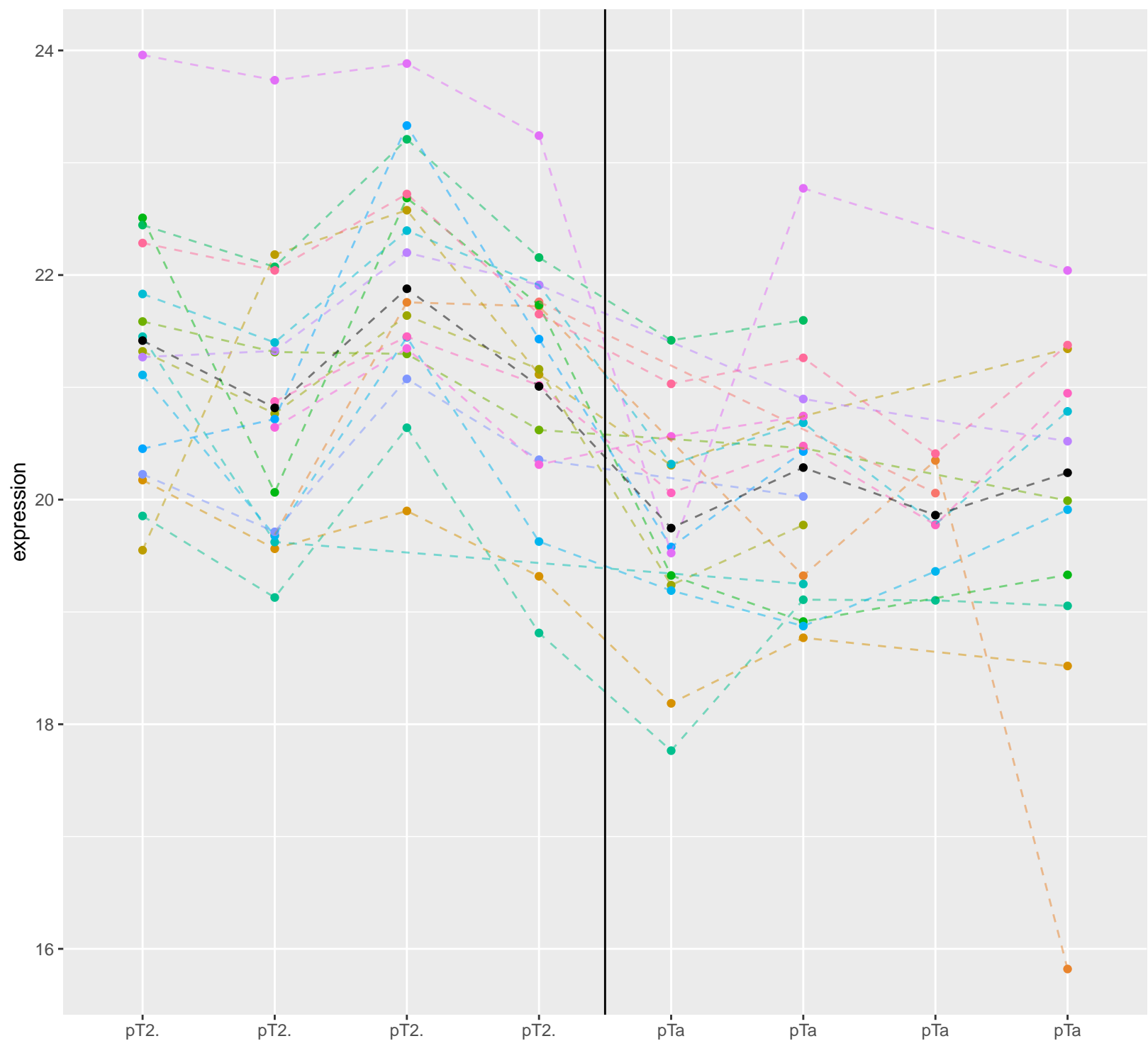
MSqRob: q-value: 0% log fold change: -1.29 t-value: -5.5 df: 83.5 se: 0.24
 MSqRobSum: q-value: 20.7% log fold change: -1.27 t-value: -4.21 df: 9.7 se: 0.3



sp|P48735|IDHP_HUMAN|isocitrate dehydrogenase[NADP],mitochondrial

MSqRob: q-value: 0.3% log fold change: -1.17 t-value: -4.48 df: 96.5 se: 0.26

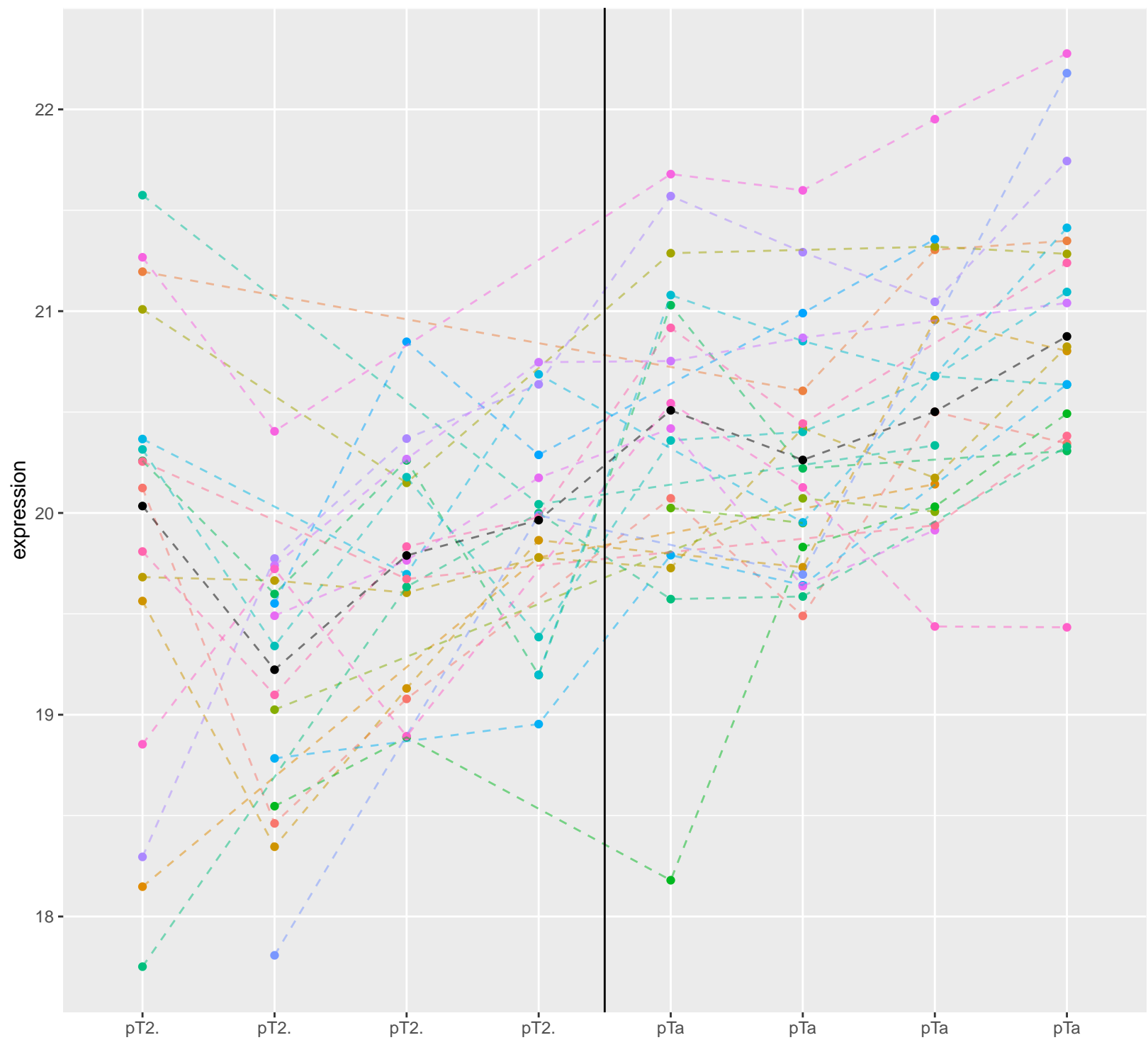
MSqRobSum: q-value: 23.8% log fold change: -1.15 t-value: -3.88 df: 9.7 se: 0.3



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

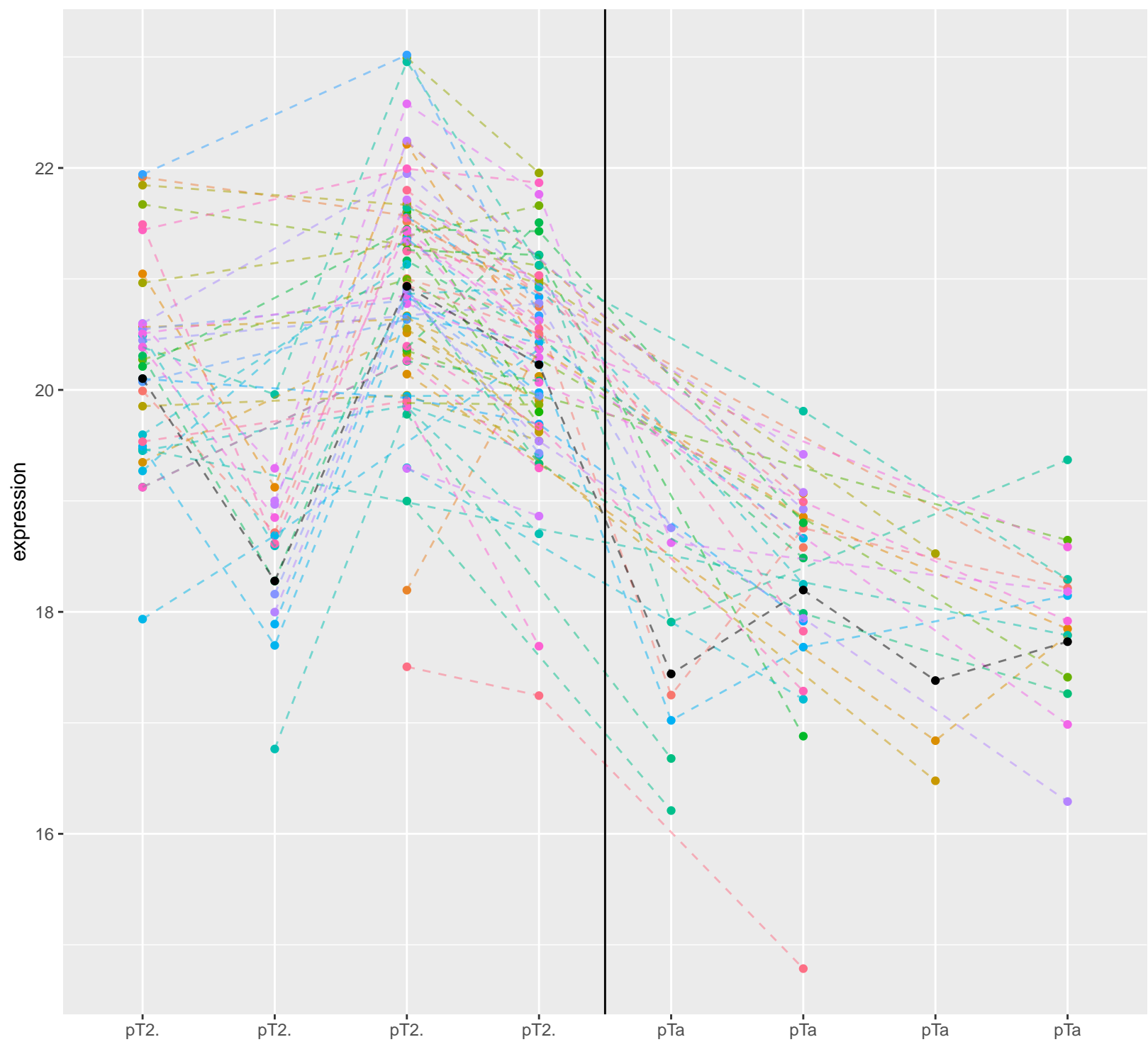
MSqRobSum: q-value: 54.8% log fold change: 0.69 t-value: 2.57 df: 9.7 se: 0.27



sp|P15924|DESP_HUMANDesmoplakin

MSqRob: q-value: 2.5% log fold change: -2.05 t-value: -3.57 df: 155.5 se: 0.5

MSqRobSum: q-value: 10.7% log fold change: -2.23 t-value: -5.23 df: 9.7 se: 0.43



sp|O75369|FLNB_HUMANFilamin-B

MSqRob: q-value: 0.9% log fold change: 1.48 t-value: 3.89 df: 287.3 se: 0.38

MSqRobSum: q-value: 20.7% log fold change: 1.54 t-value: 4.18 df: 9.7 se: 0.37

