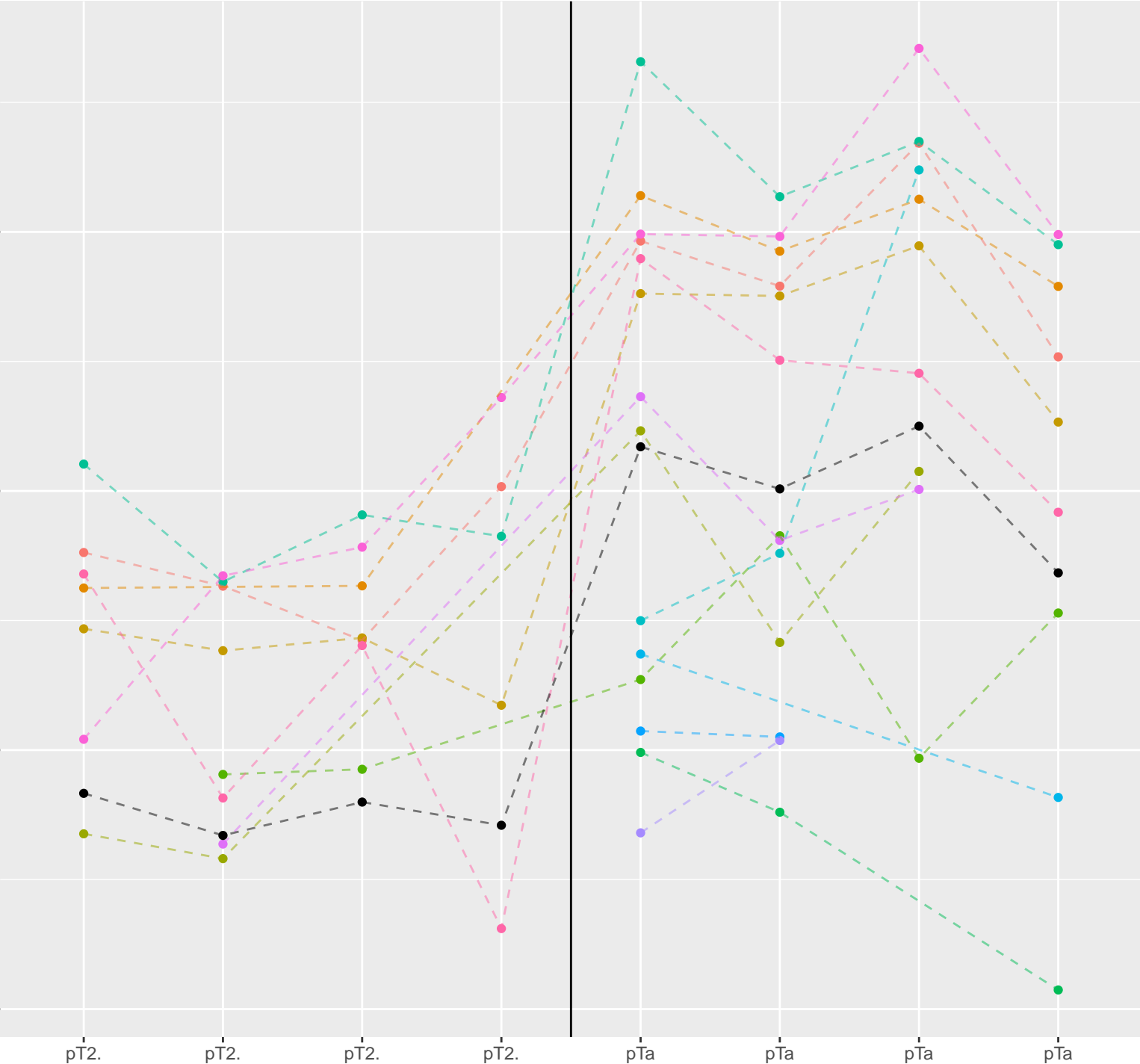


sp|Q04695|K1C17_HUMANKeratin,typeIcytoskeletal17

method	q-value	log fold change	t-value	df	se	theta	sample
msgrob	0	2.48	9.72	56.4	0.255		0.642
msgrobsum	0.7	2.60	9.40	9.63	0.277		NA

expression



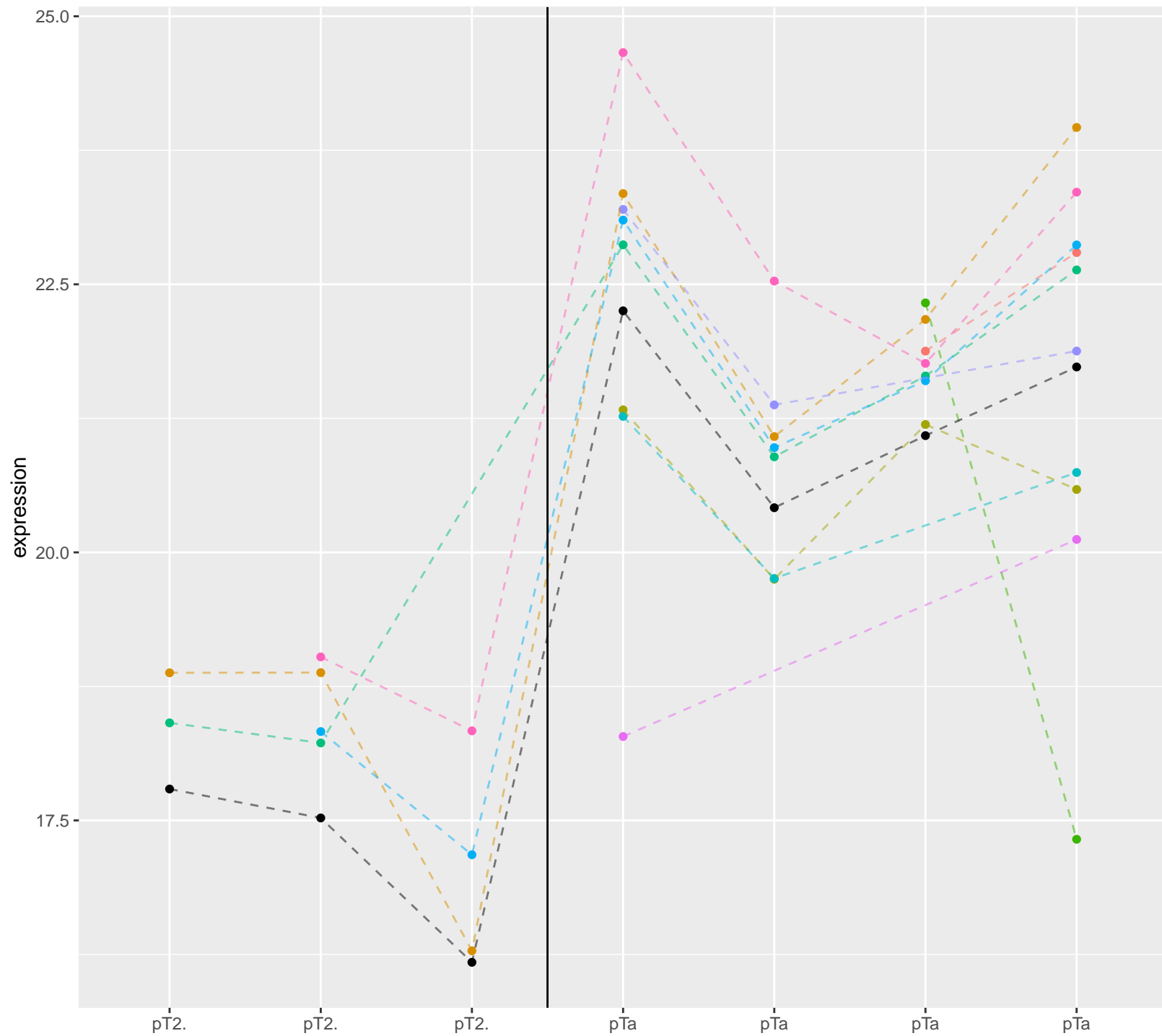
sp|O43175|SERA_HUMAND-3-phosphoglyceratedehydrogenase

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	0	-2.76	-6.81	54.3	0.405		1.25
msqrobsum	1.6	-2.66	-7.85	9.64	0.339		NA



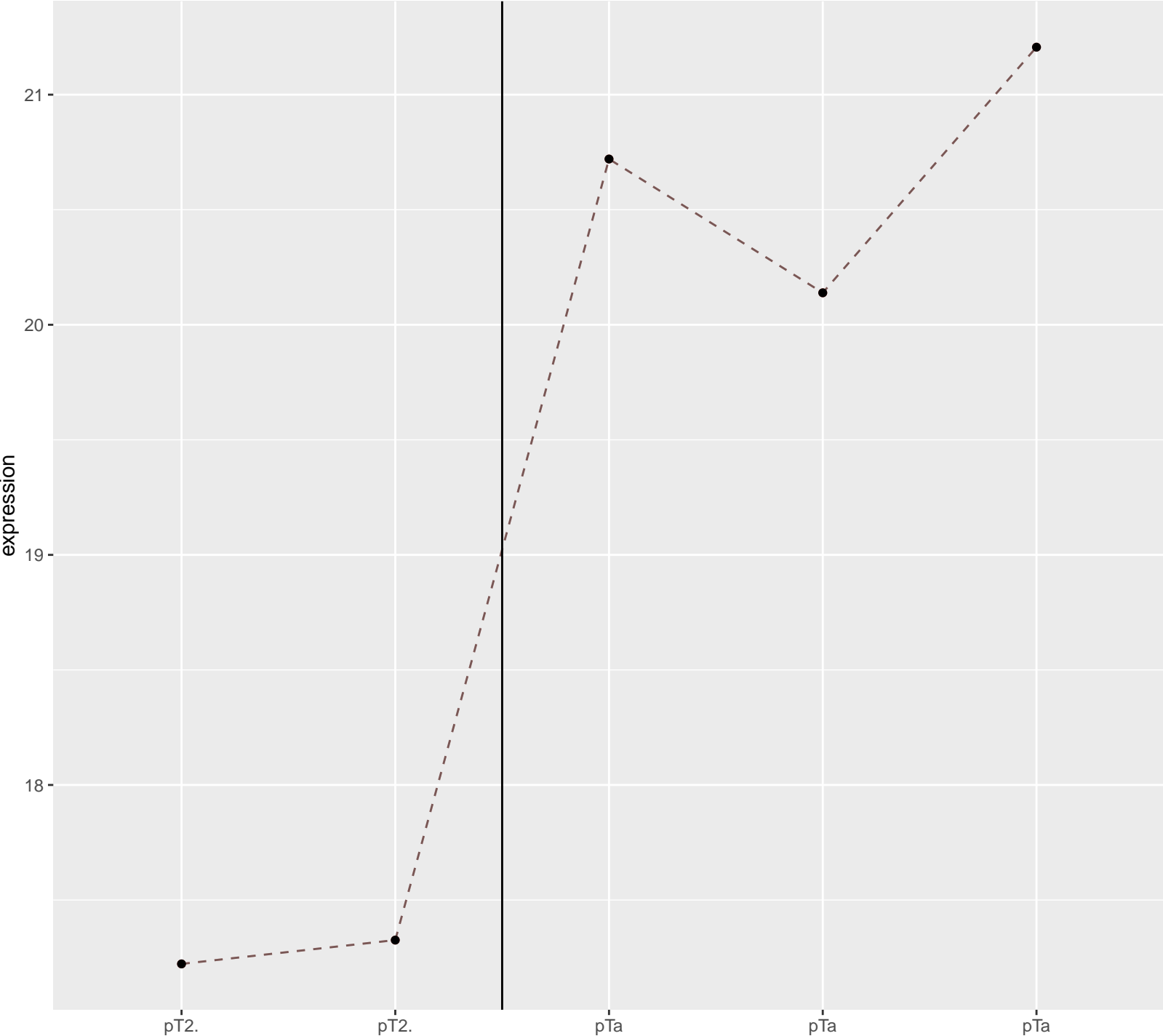
sp|P15428|PGDH_HUMAN15-hydroxyprostaglandin dehydrogenase[NAD(+)]

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	0	4.00	6.94	29.2	0.577		1.34
msqrobsum	2.4	4.11	7.64	8.64	0.538		NA



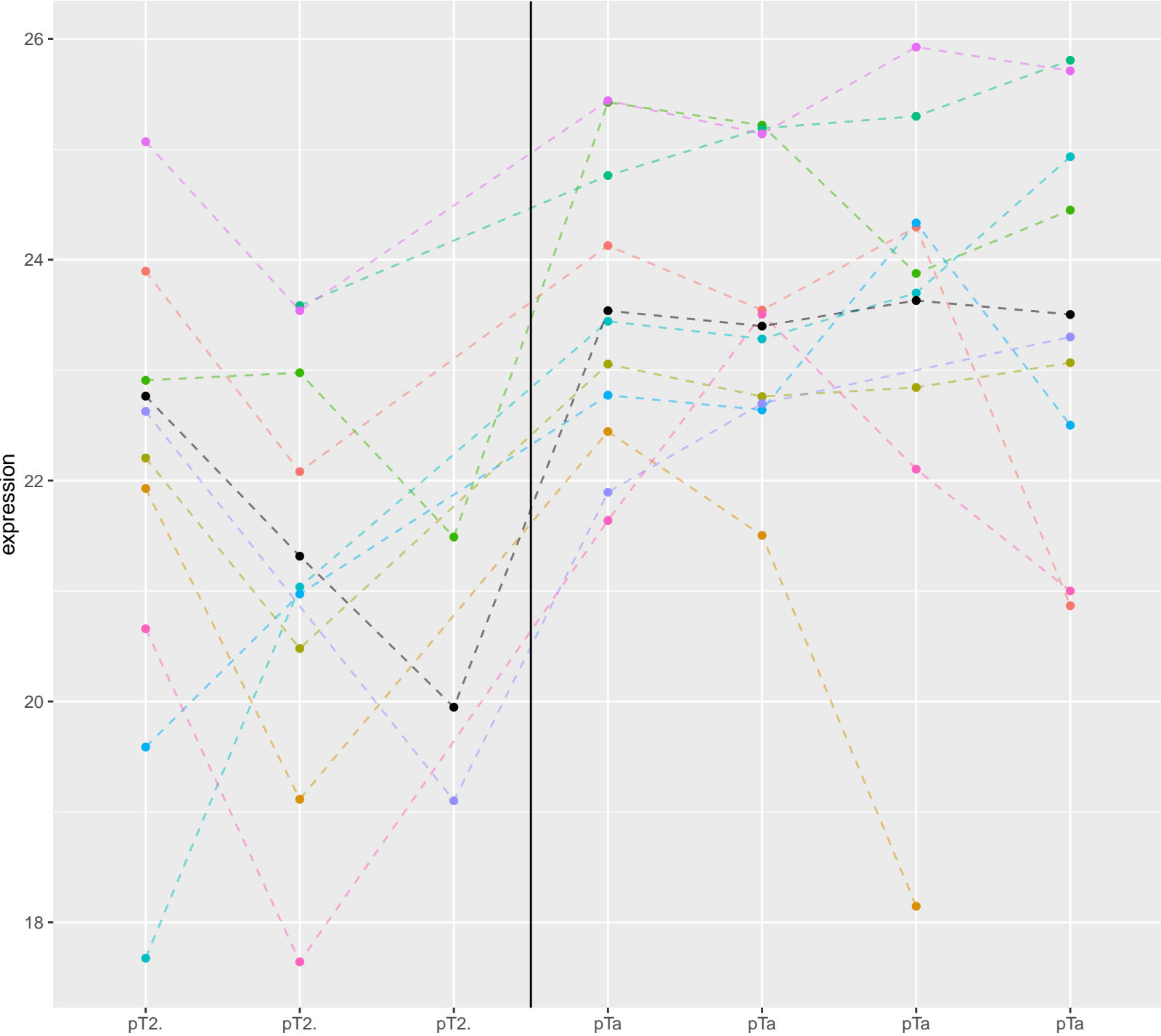
sp|Q9Y623|MYH4_HUMANMyosin-4

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	0.3	3.43	13.1	5.51	0.262		NA
msqrobsum	2.8	3.41	8.94	6.63	0.381		NA



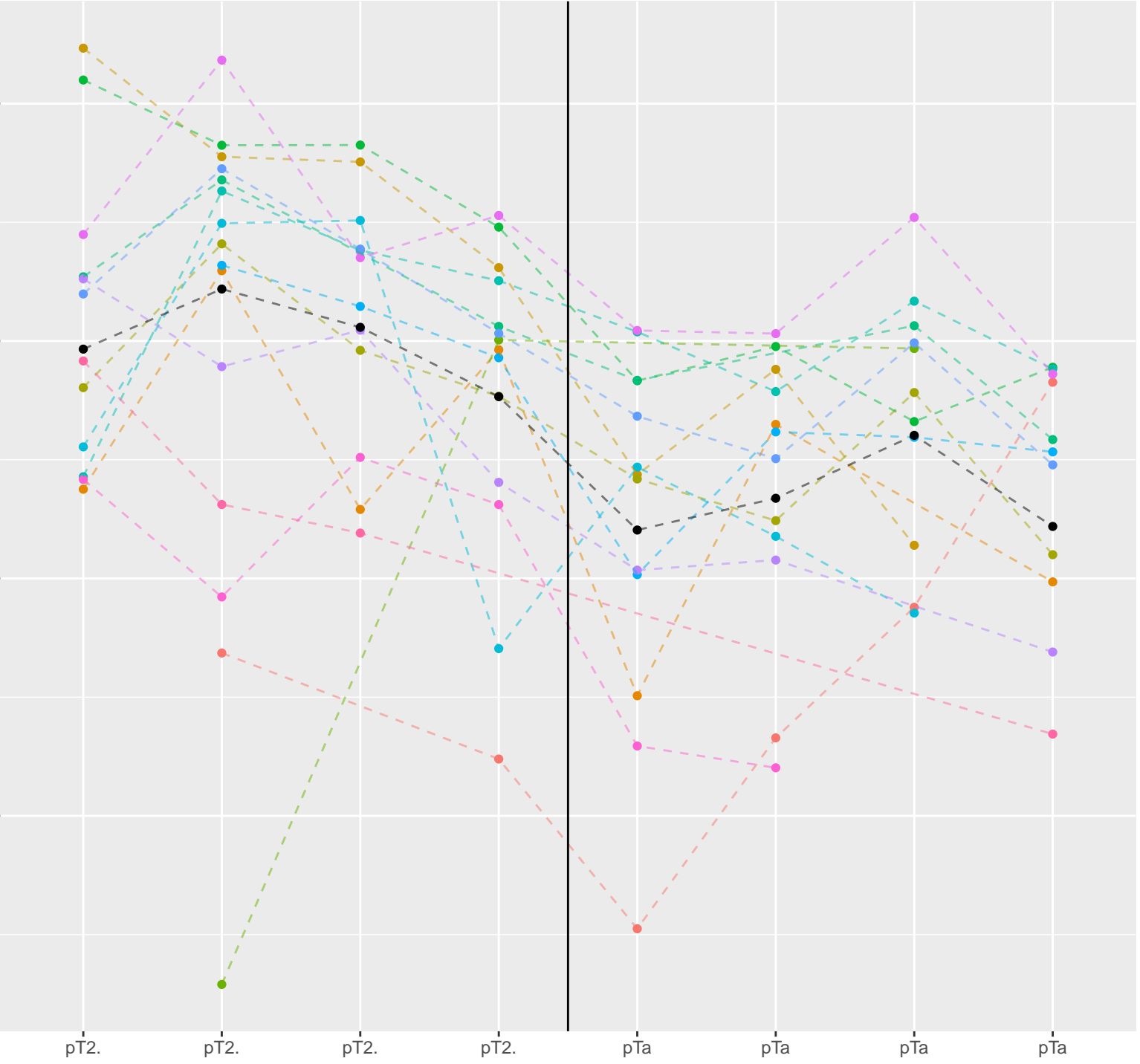
sp|P09488|GSTM1_HUMANGlutathioneS-transferaseMu1

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	0	1.91	8.69	50.2	0.22		0
msqrobsum	9.4	2.08	5.94	8.66	0.35		NA



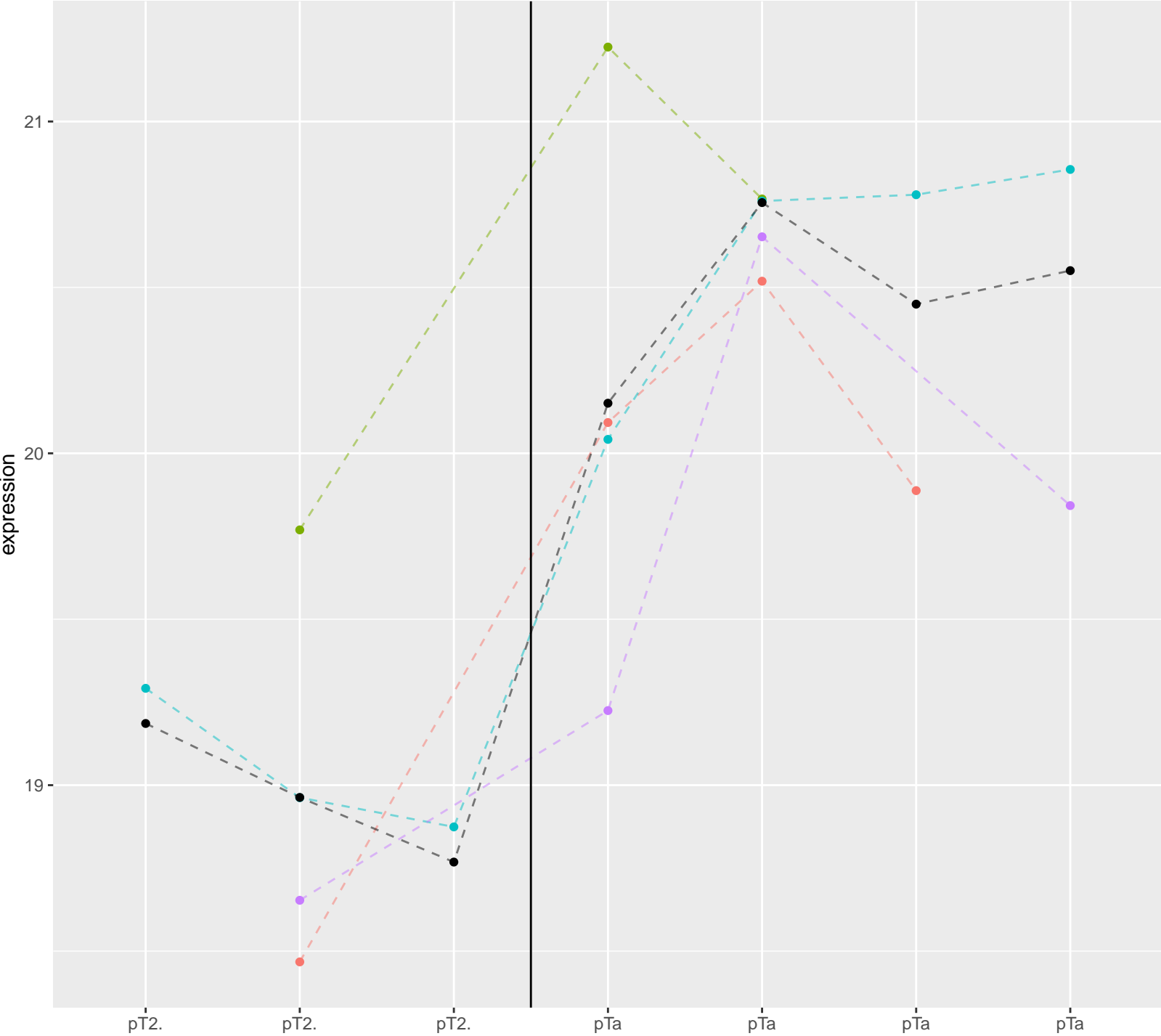
sp|P08758|ANXA5_HUMANAnnexinA5

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	0	-1.29	-5.50	83.5	0.235		0.427
msqrobsum	20.7	-1.27	-4.21	9.66	0.301		NA



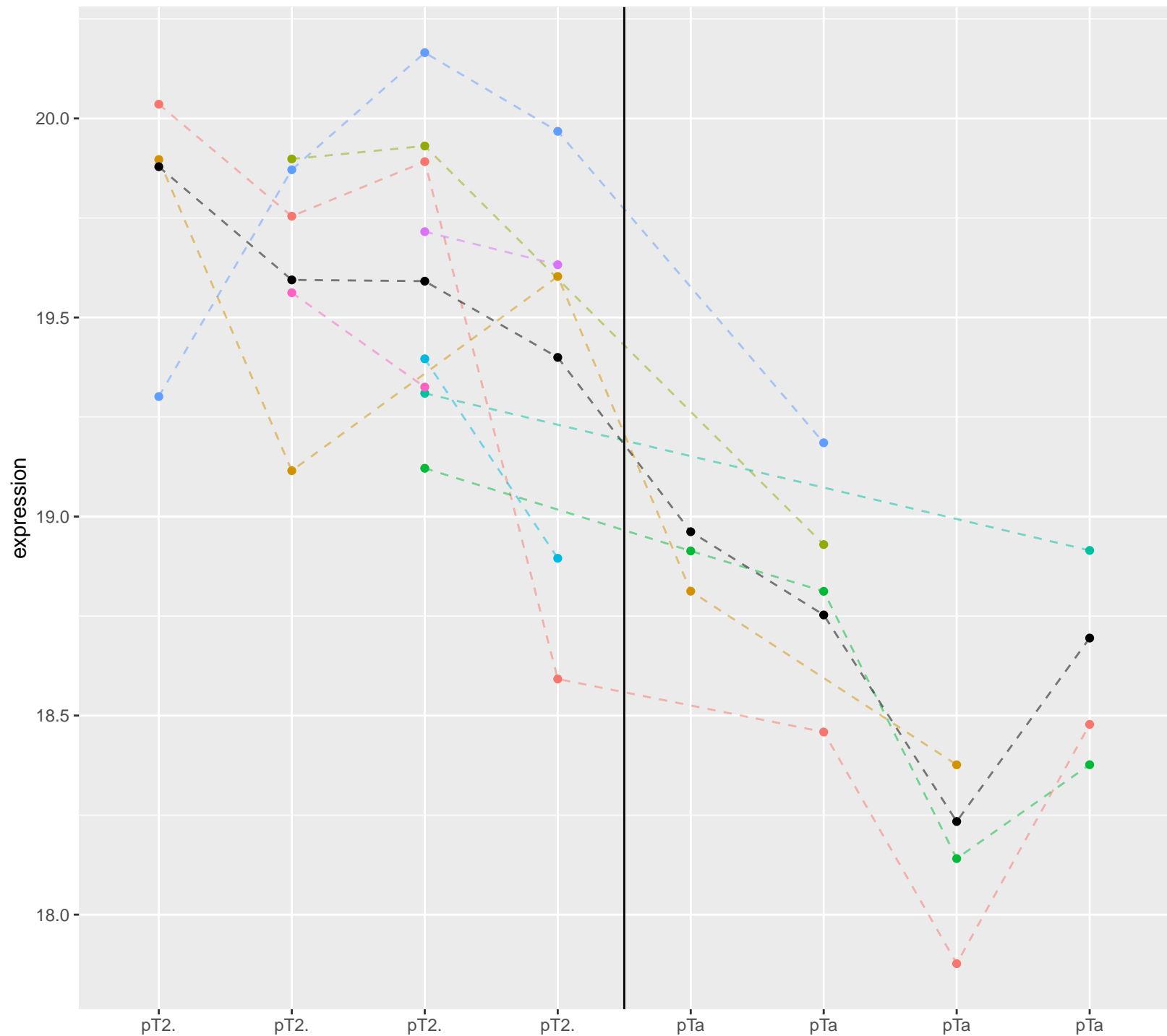
sp|Q5VW32|BROX_HUMANBRO1domain-containingproteinBROX

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	0	1.46	7.99	15.8	0.183		0.108
msqrobsum	14.1	1.48	5.12	8.63	0.290		NA



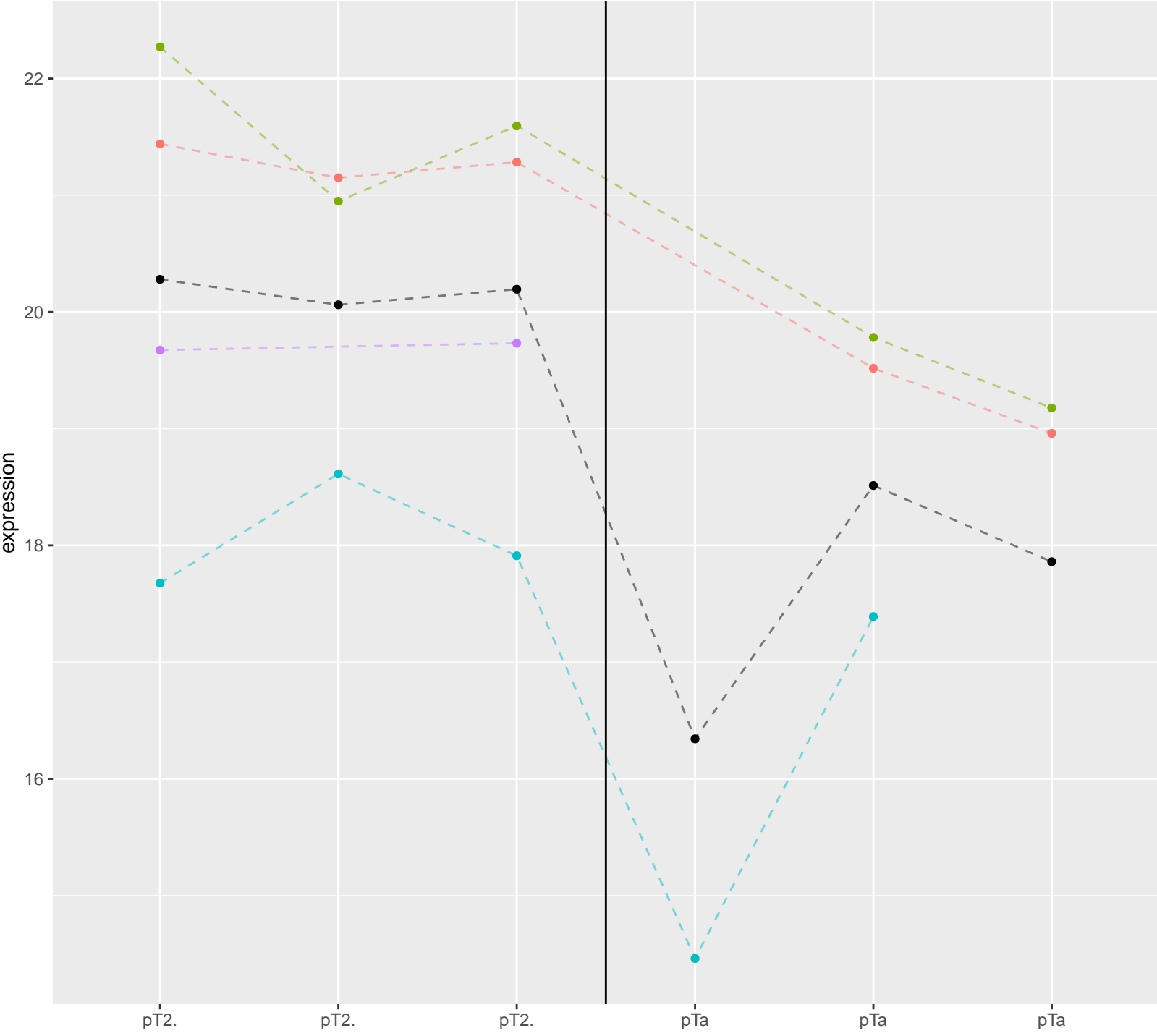
sp|P54577|SYYC_HUMANTyrosine--tRNA ligase, cytoplasmic

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	0	-0.930	-6.05	30.0	0.154		0.309
msqrobsum	36	-0.880	-3.44	9.65	0.255		NA



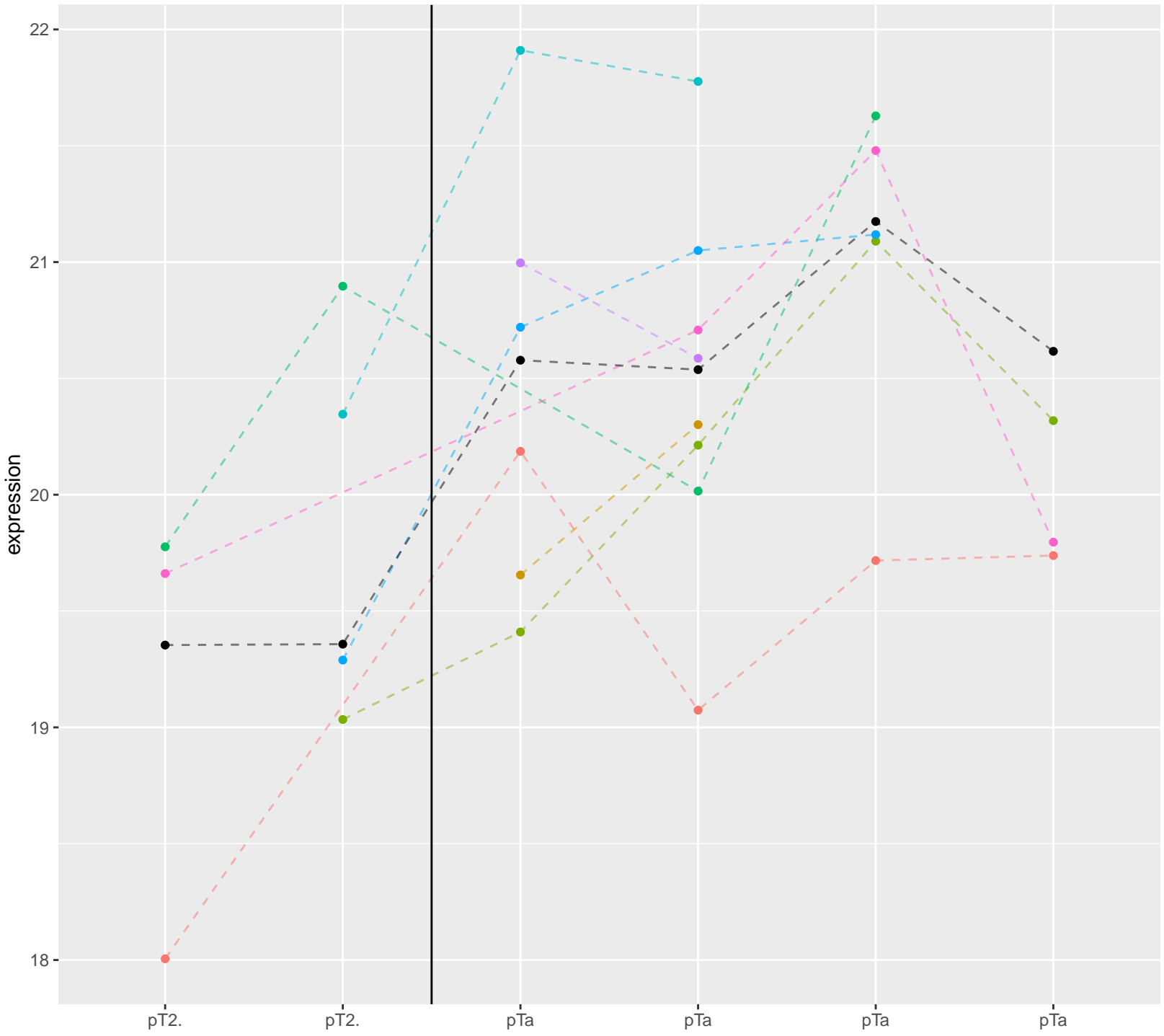
sp|Q6ZVX7|FBX50_HUMANF-boxonlyprotein50

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	0	-1.94	-7.56	14.6	0.257		0
msqrobsum	10.7	-2.32	-5.82	7.65	0.399		NA



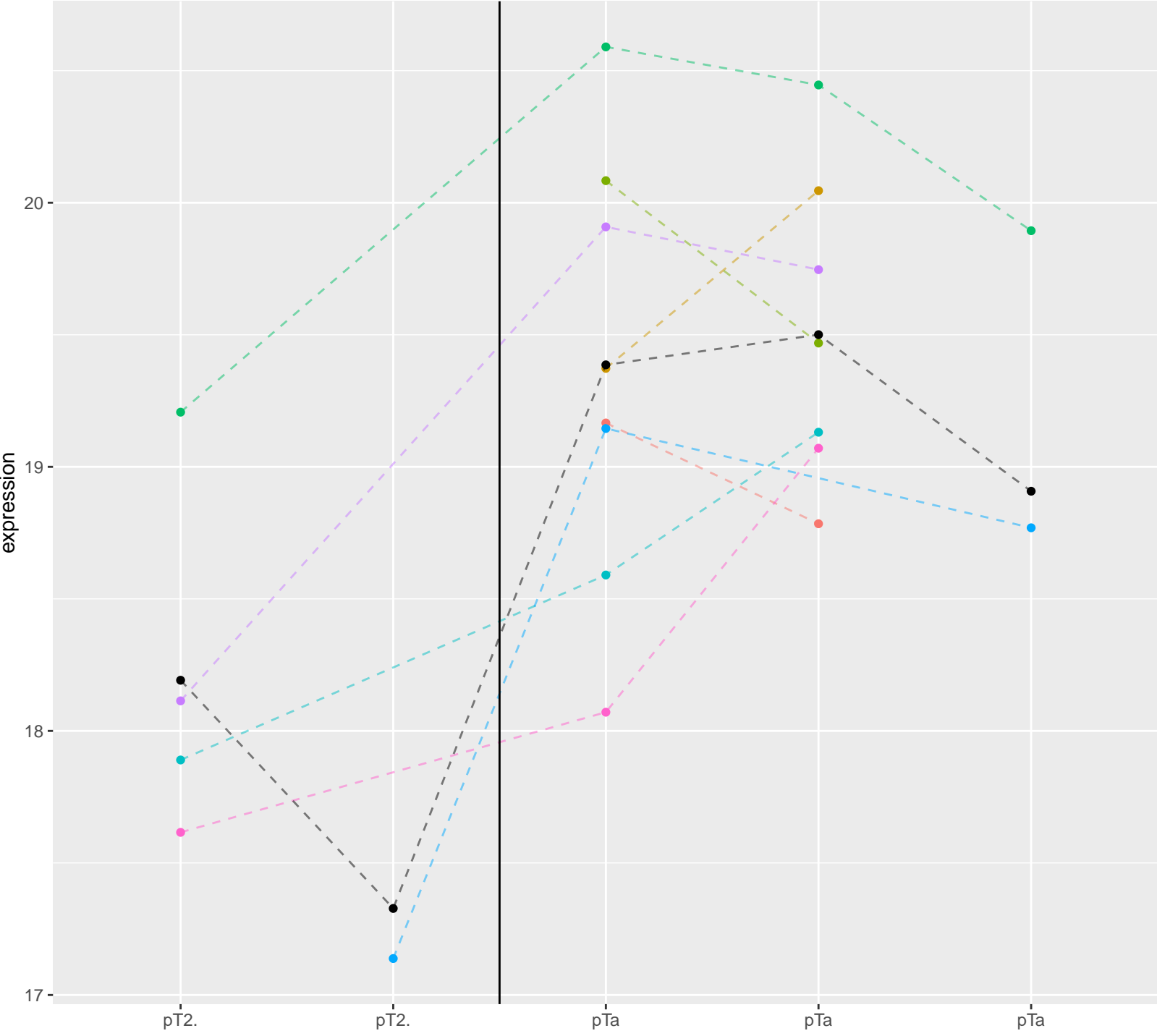
sp|O00515|LAD1_HUMANLadinin-1

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	0.1	1.34	6.19	22.2	0.217		0.347
msqrobsum	30.7	1.28	3.87	7.64	0.332		NA



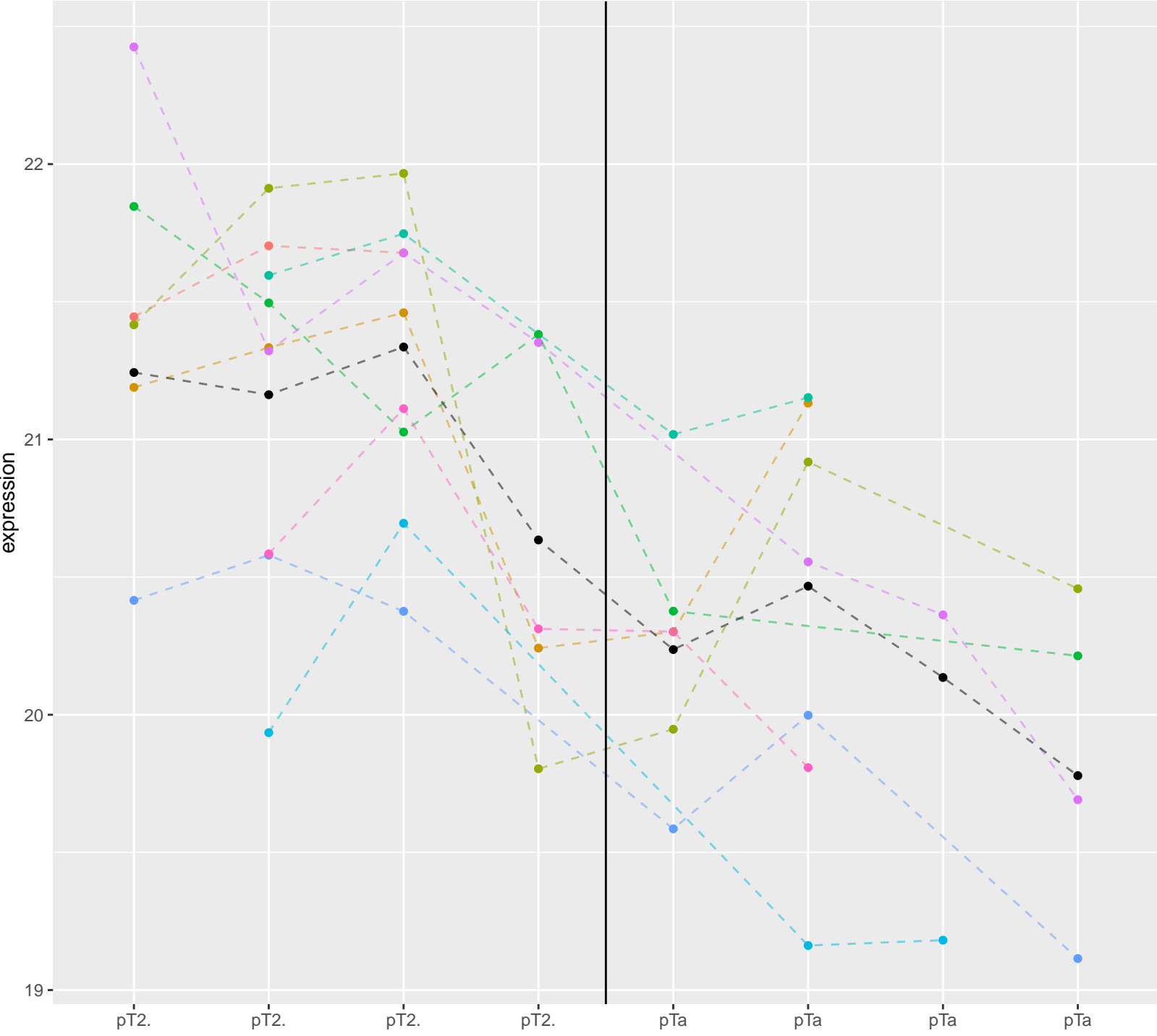
sp|P16144|ITB4_HUMANIntegrinbeta-4

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	0.1	1.33	6.79	16.6	0.195		0
msqrobsum	41.2	1.40	3.28	6.69	0.426		NA



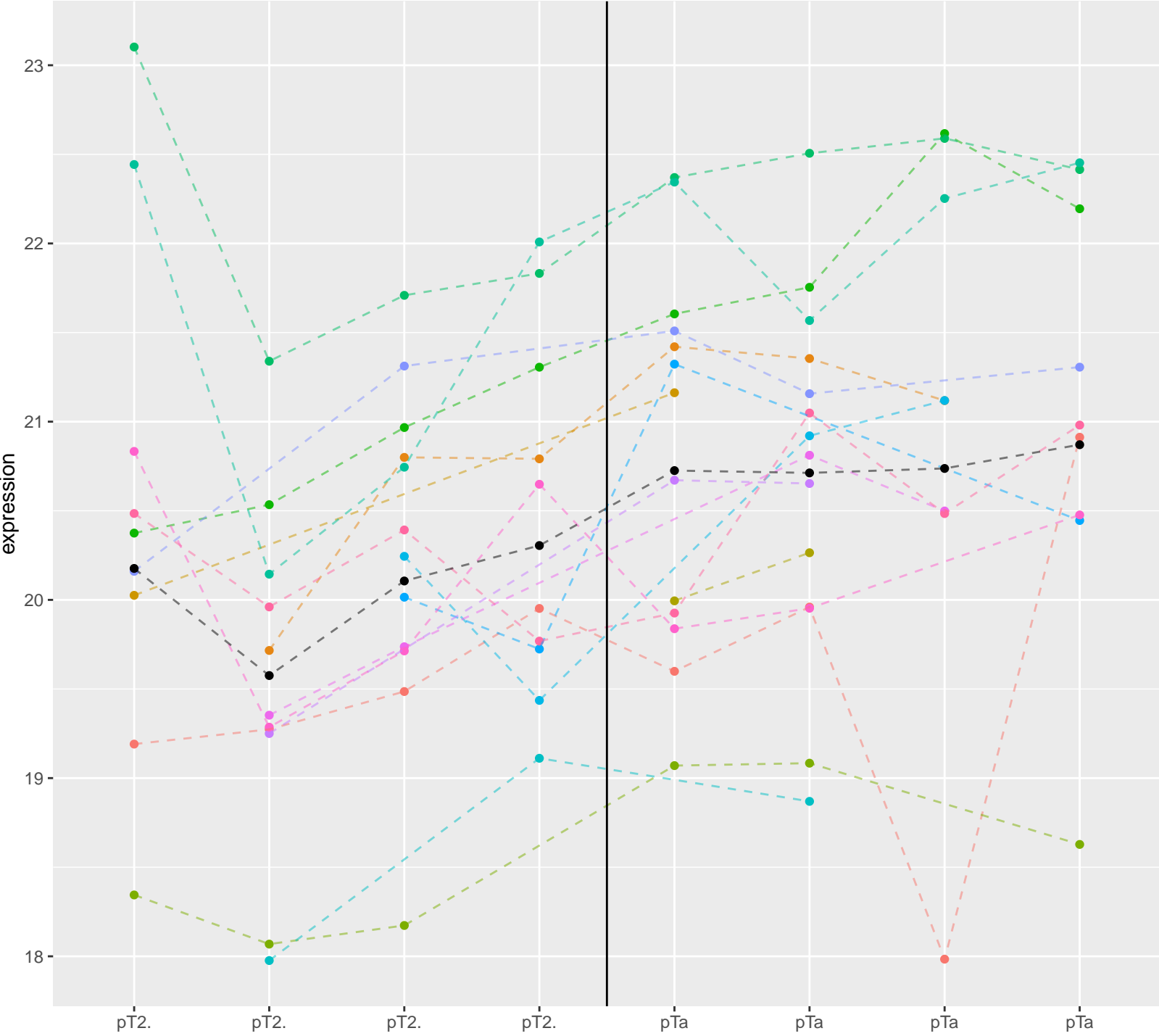
sp|P12004|PCNA_HUMANProliferatingcellnuclearantigen

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	0.2	-0.921	-5.08	37.4	0.181		0.623
msqrobsum	37.3	-0.891	-3.25	9.67	0.274		NA



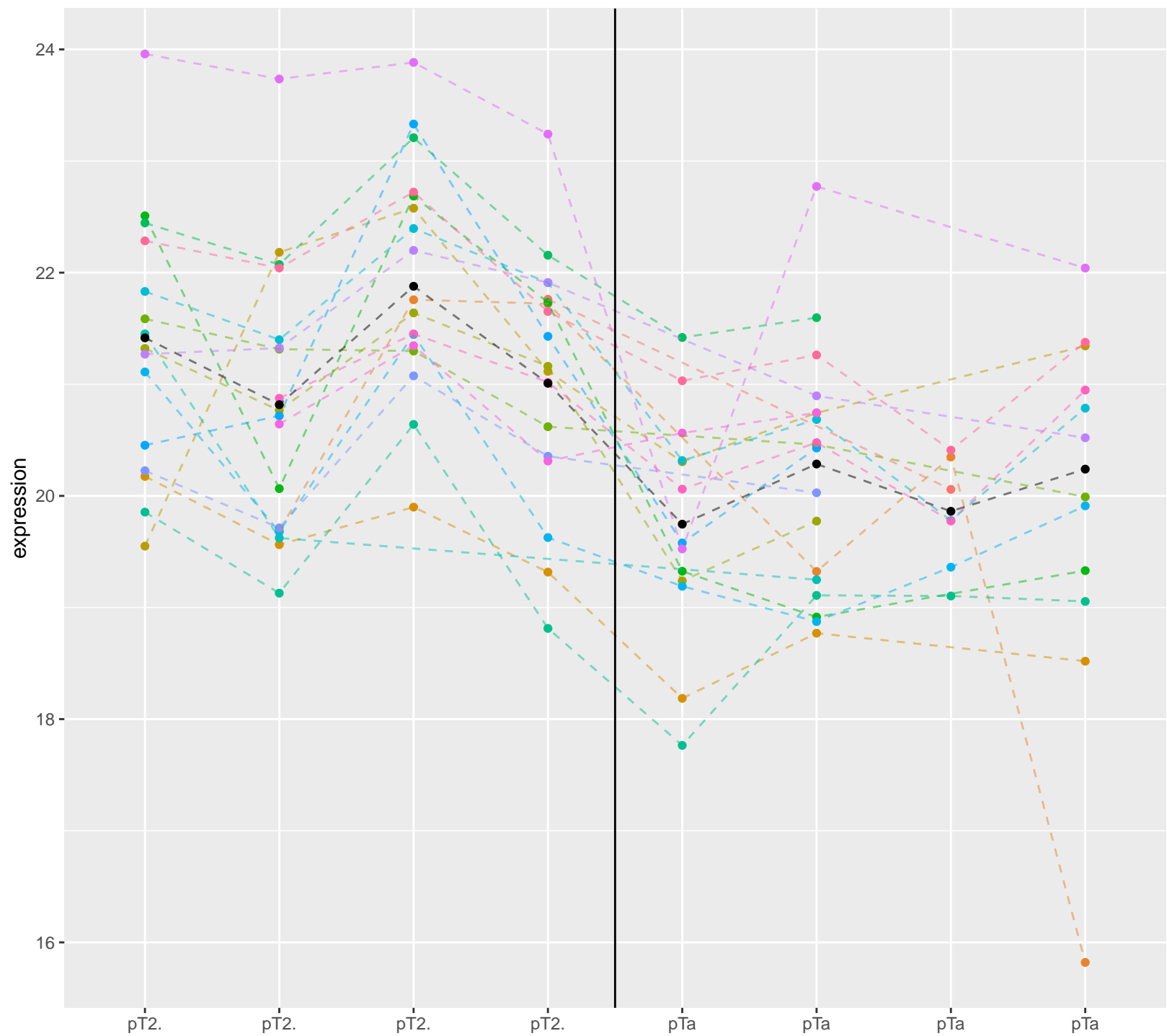
sp|P00505|AATM_HUMANAspartateaminotransferase,mitochondrial

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	0.3	0.716	4.63	68.3	0.155		0.461
msqrobsum	54.1	0.626	2.63	9.65	0.238		NA



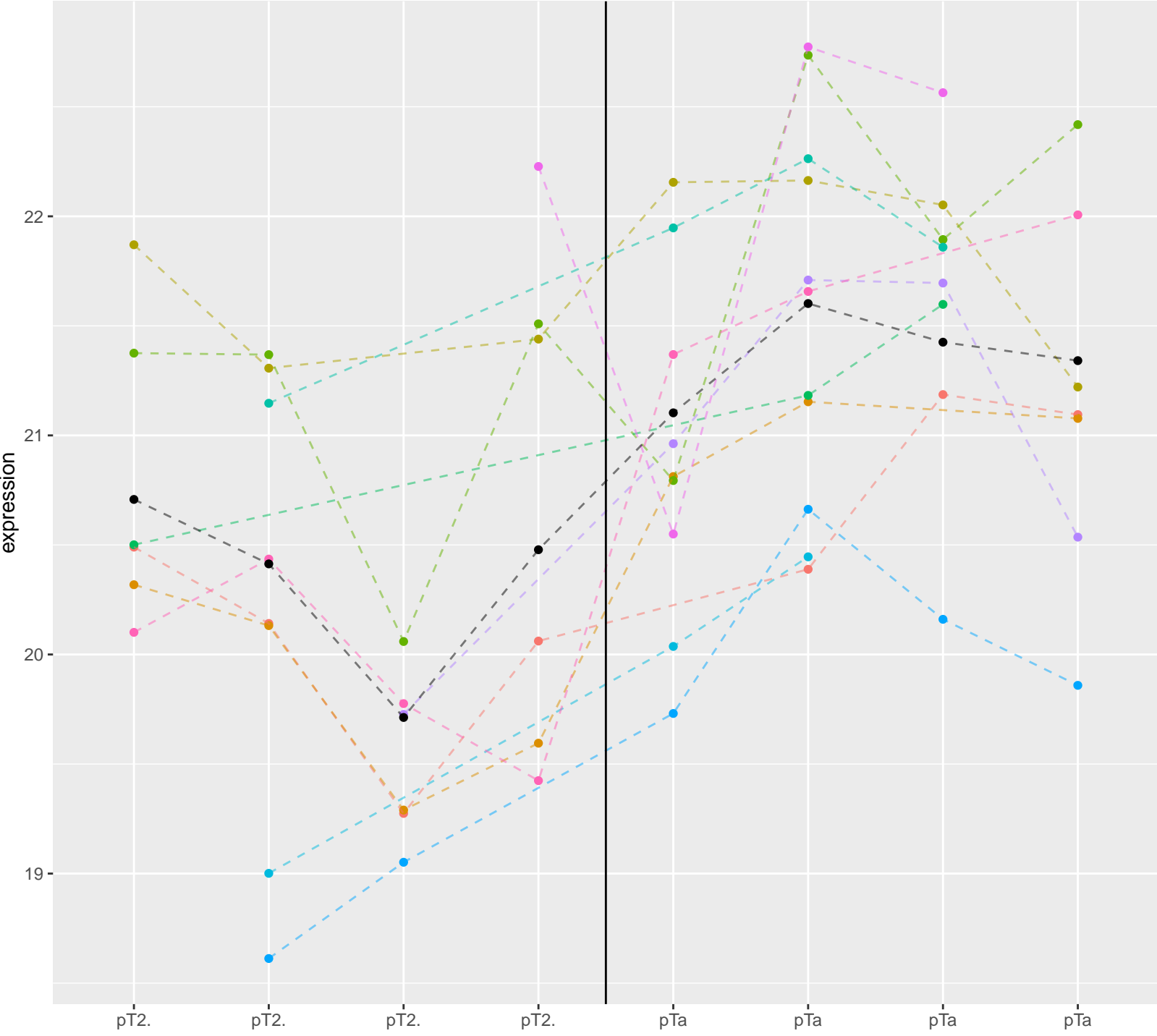
sp|P48735|IDHP_HUMAN|isocitrate dehydrogenase[NADP],mitochondrial

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	0.3	-1.17	-4.48	96.5	0.261		0.693
msqrobsum	23.8	-1.15	-3.88	9.67	0.296		NA



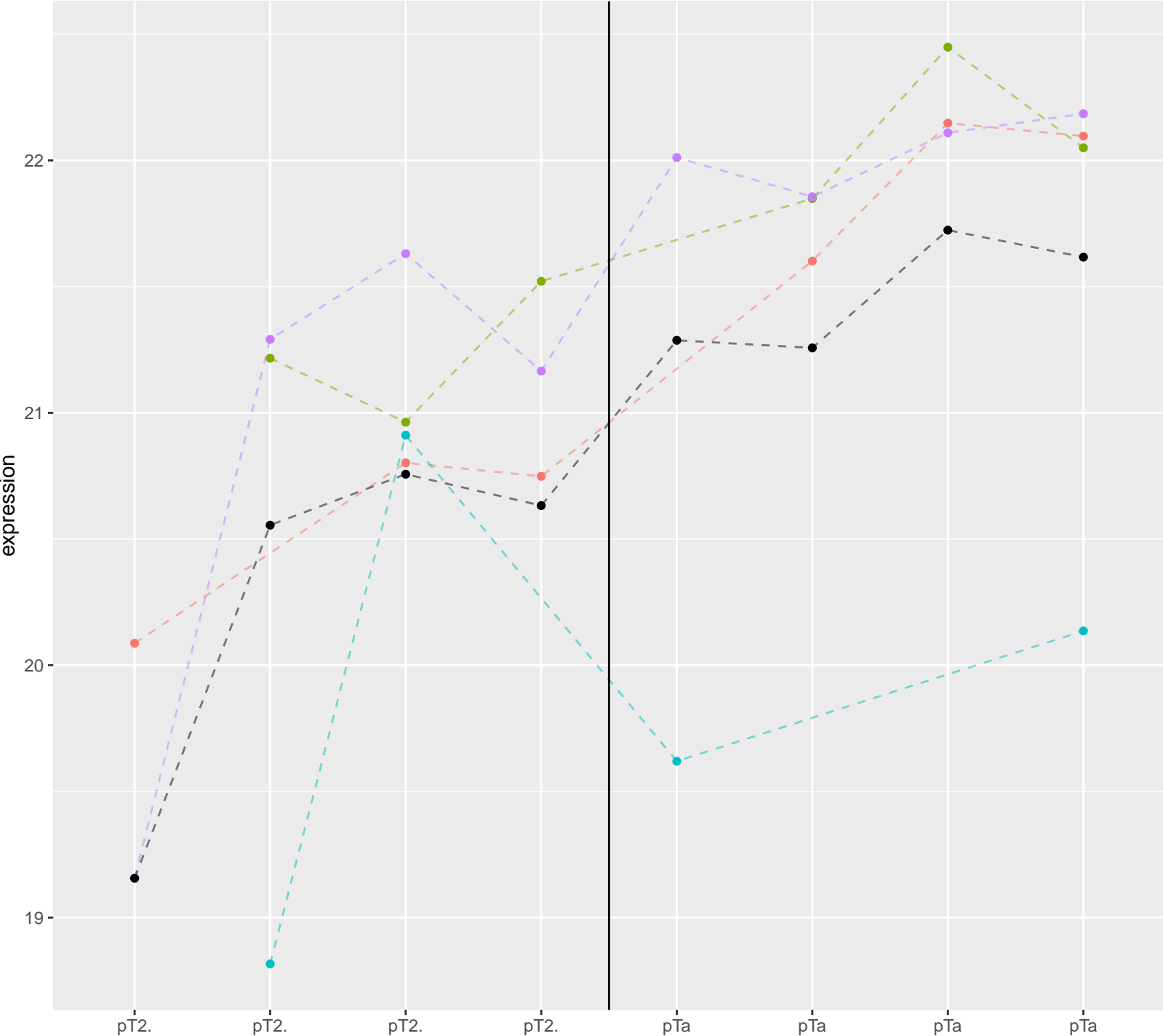
sp|P78417|GSTO1_HUMANGlutathioneS-transferaseomega-1

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	0.3	0.997	4.75	47.4	0.21		0.715
msqrobsum	36	0.918	3.39	9.67	0.271		NA



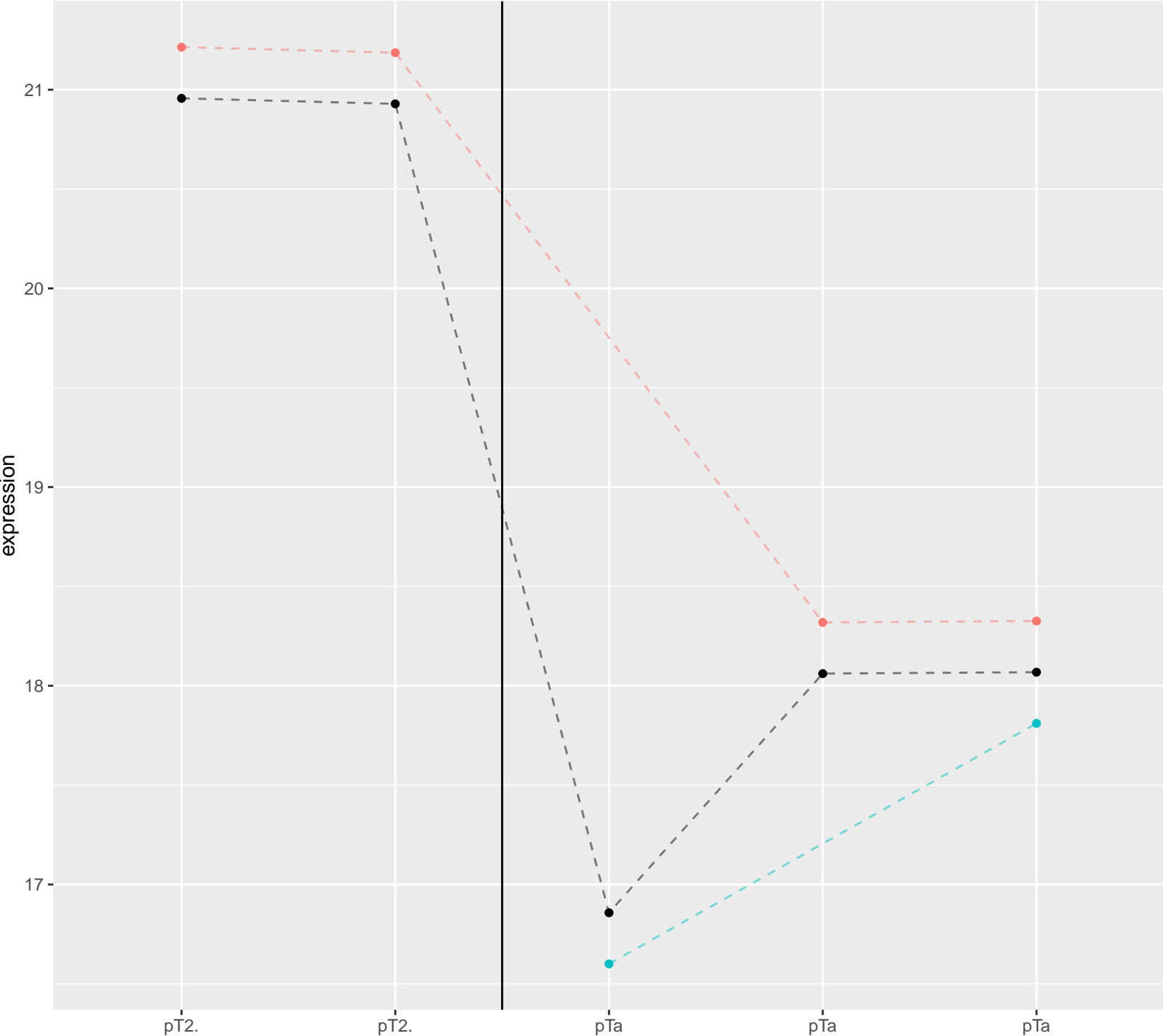
sp|O75608|LYPA1_HUMANAcyl-proteinthioesterase1

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	0.3	0.922	5.41	20.8	0.171		0.26
msqrobsum	41.2	0.918	2.98	9.71	0.308		NA



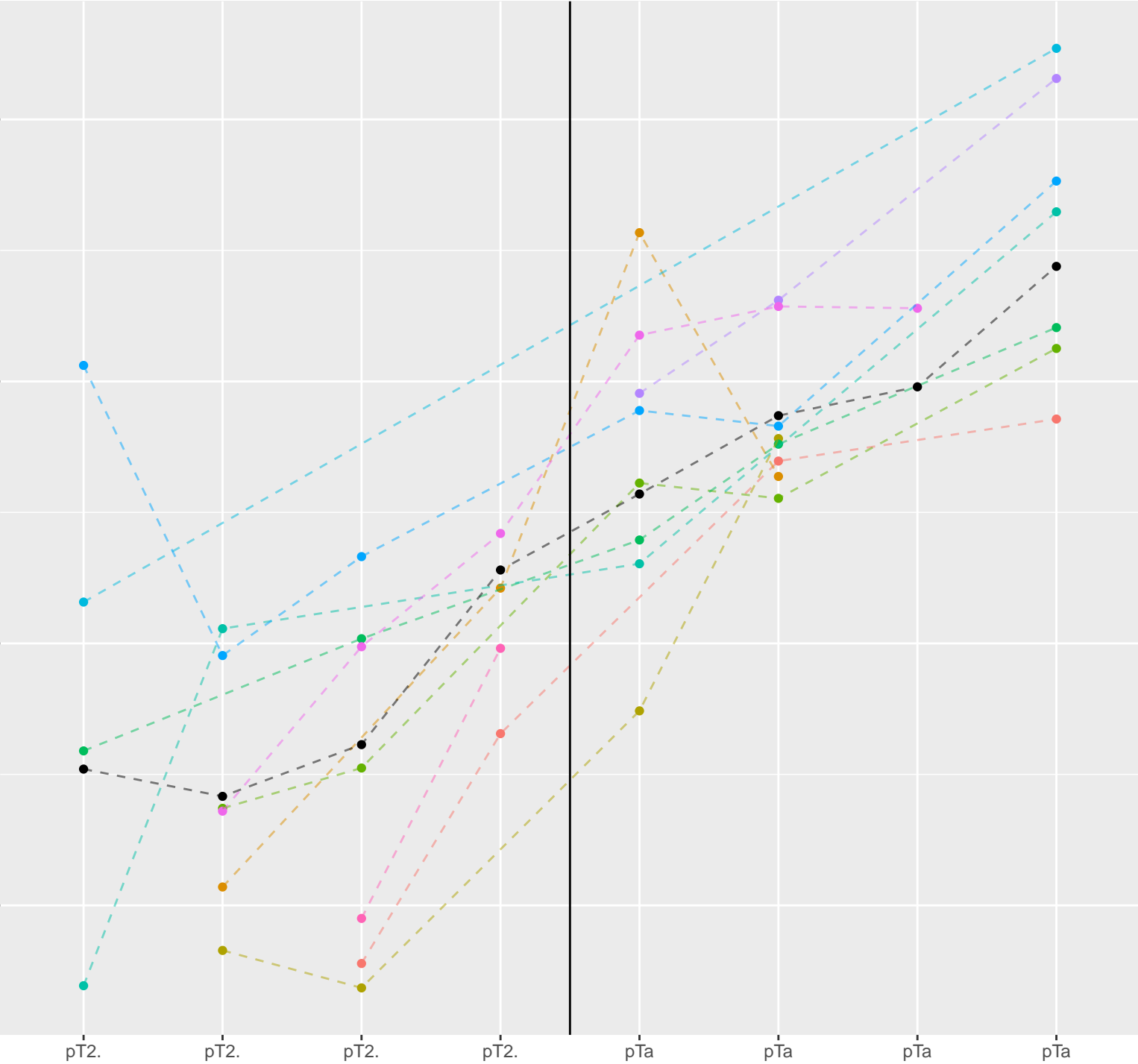
sp|Q8WWI1|LMO7_HUMANLIMdomainonlyprotein7

method	q-value	log fold change	t-value	df	se	theta	sample
msgrob	0.5	-2.88	-11.5	5.56	0.251		0
msgrobsum	10.7	-3.17	-6.61	6.64	0.479		NA



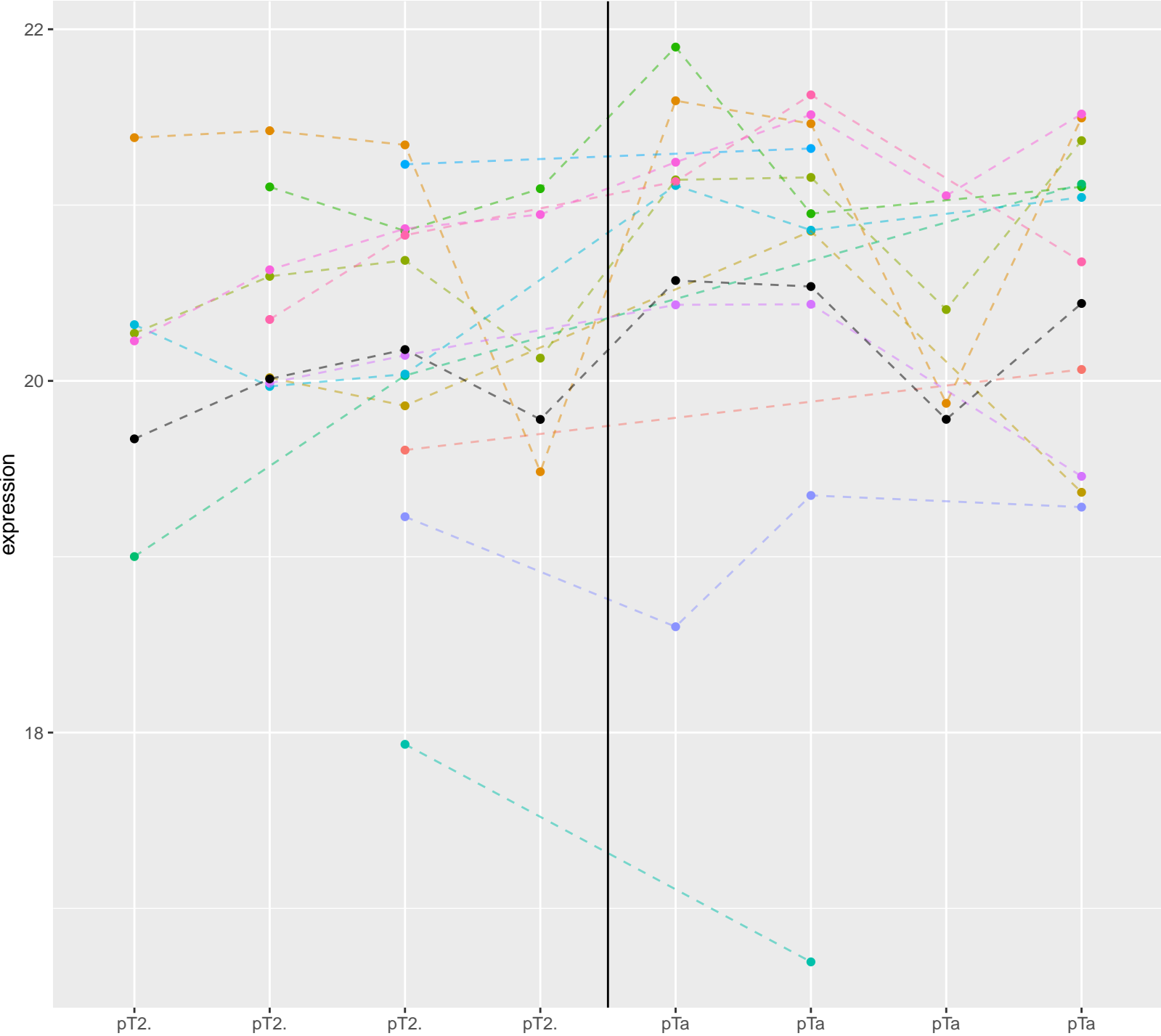
sp|P13798|ACPH_HUMANAcylamino-acid-releasingenzyme

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	0.5	1.23	4.65	33.0	0.265		1.01
msqrobsum	23.8	1.20	4.00	9.66	0.301		NA



sp|P13489|RINI_HUMANRibonucleaseinhibitor

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	0.6	0.423	4.35	52.1	0.097		0
msqrobsum	100	0.320	1.32	9.87	0.243		NA



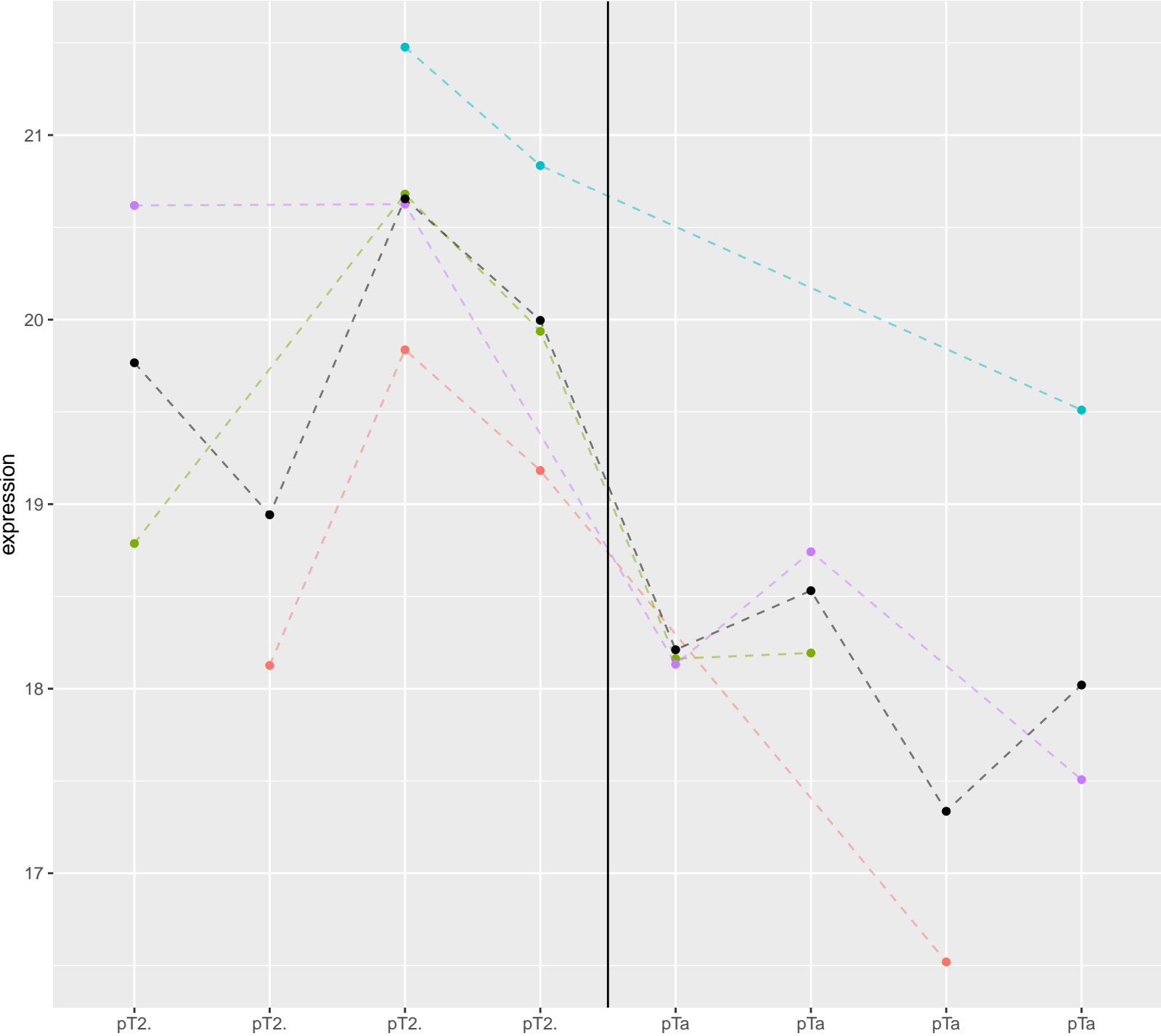
sp|P25815|S100P_HUMANProteinS100-P

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	0.7	1.91	4.49	33.2	0.425		0.614
msqrobsum	18.9	1.80	4.32	9.68	0.417		NA



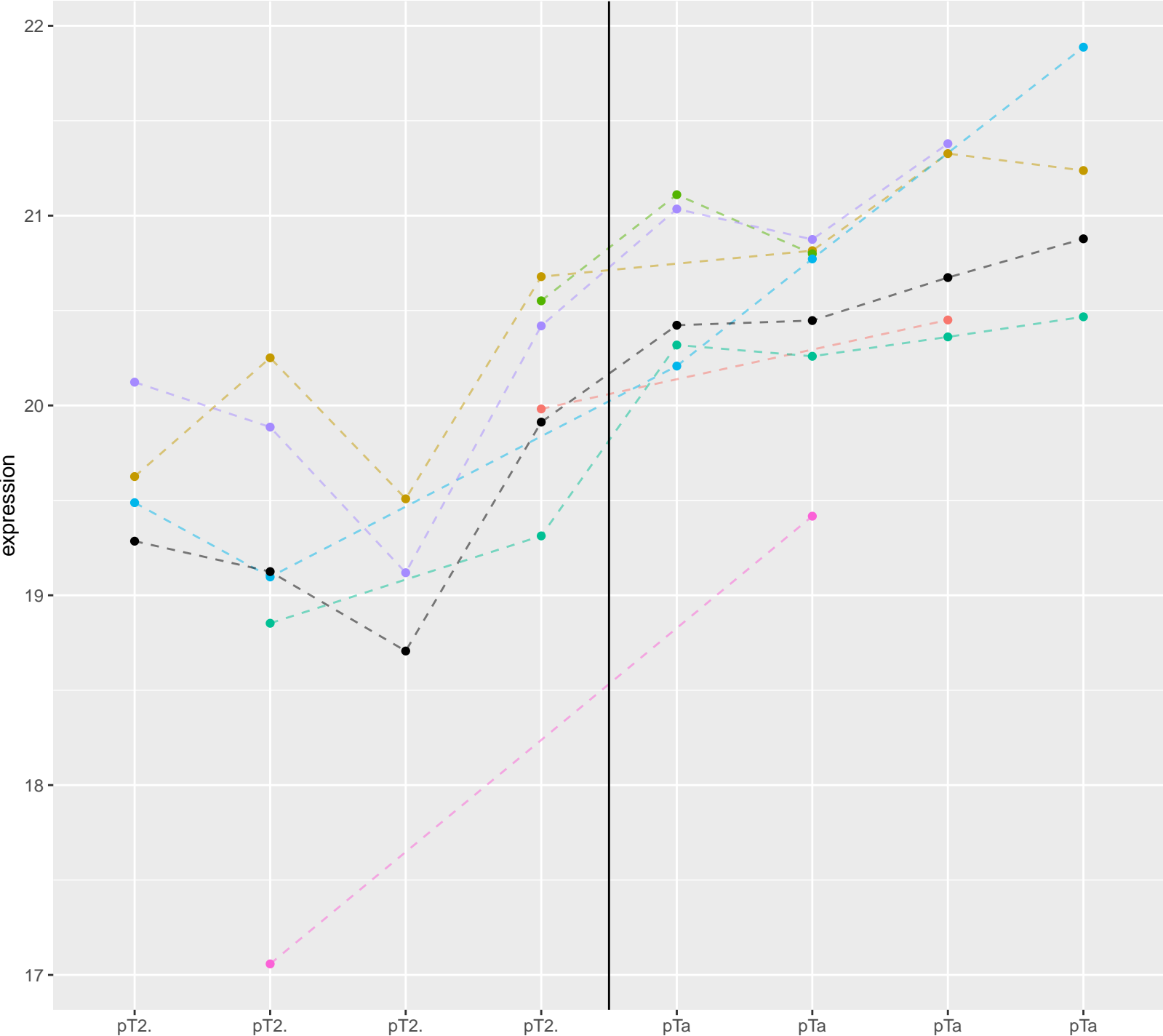
sp|Q92820|GGH_HUMANGamma-glutamylhydrolase

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	0.7	-1.94	-5.76	12.4	0.338		0.638
msqrobsum	16.9	-1.70	-4.53	9.67	0.376		NA



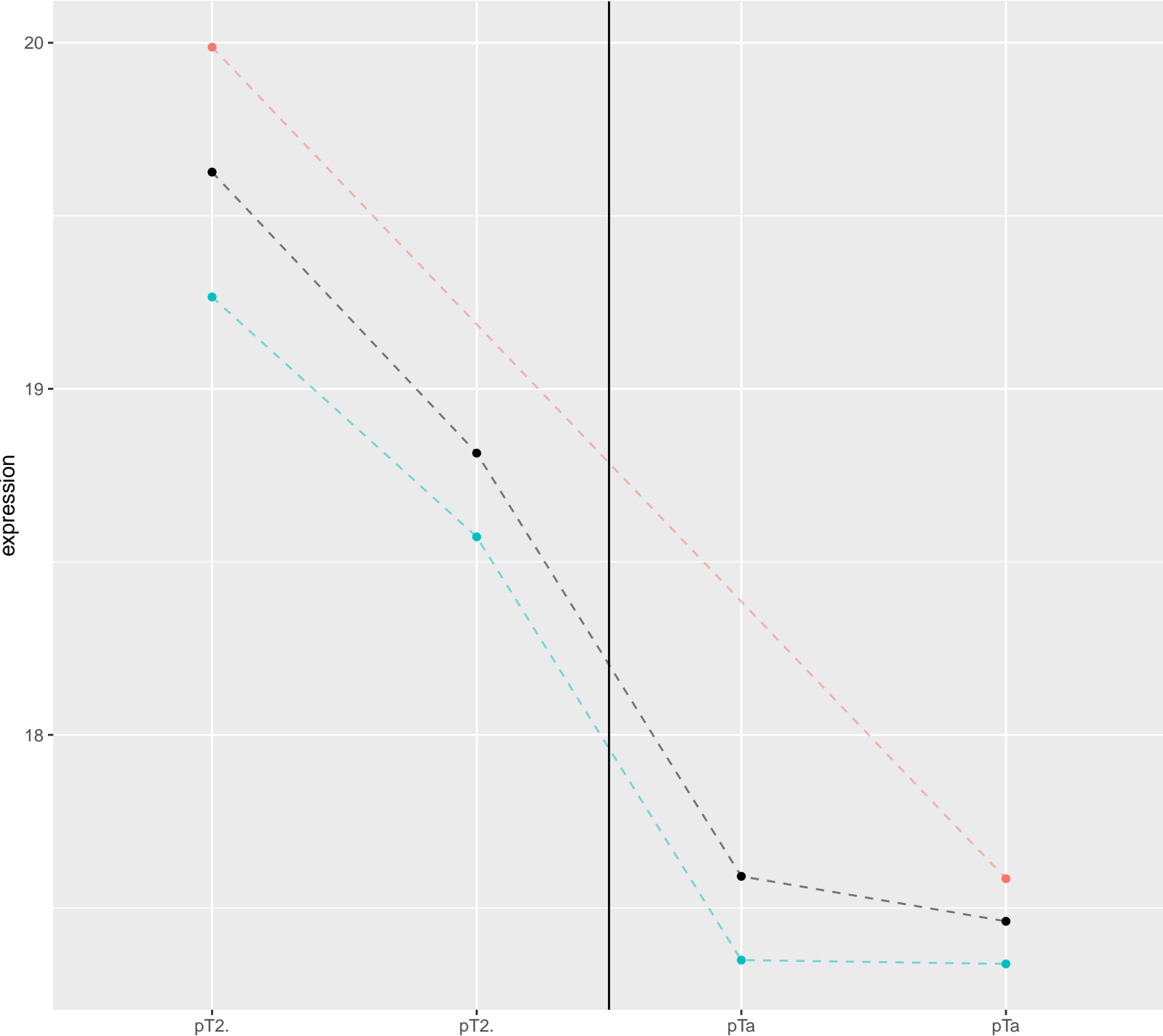
sp|P00390|GSHR_HUMANGlutathionereductase,mitochondrial

method	q-value	log fold change	t-value	df	se	theta	sample
msgrob	0.900	1.22	4.70	22.2	0.26		1.11
msgrobsum	14.1	1.34	4.82	9.65	0.277		NA



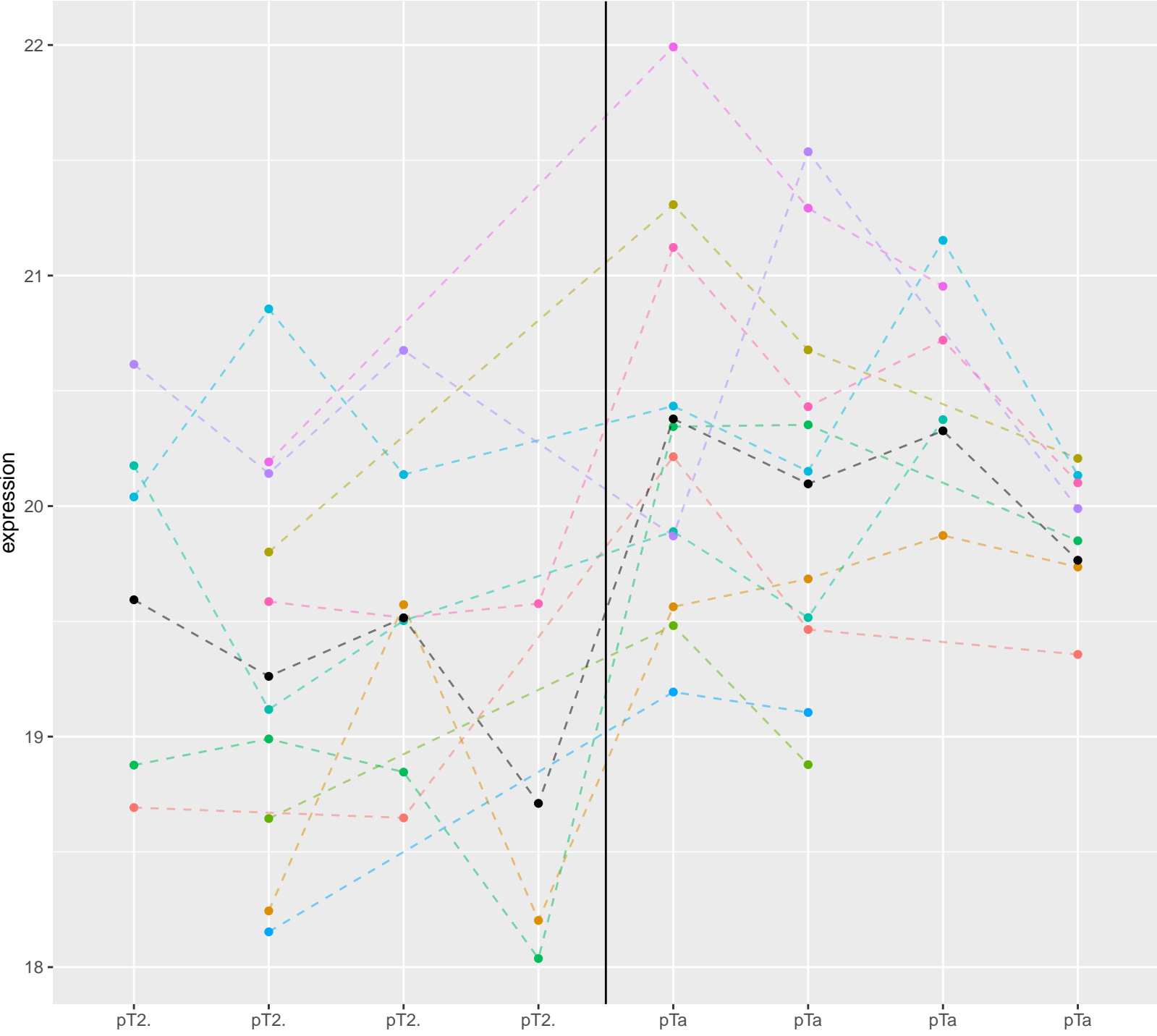
sp|O00154|BACH_HUMANCytosolicacylcoenzymeAthioesterhydrolase

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	0.900	-1.91	-9.27	5.72	0.206		0
msqrobsum	43	-1.59	-3.39	5.68	0.47		NA



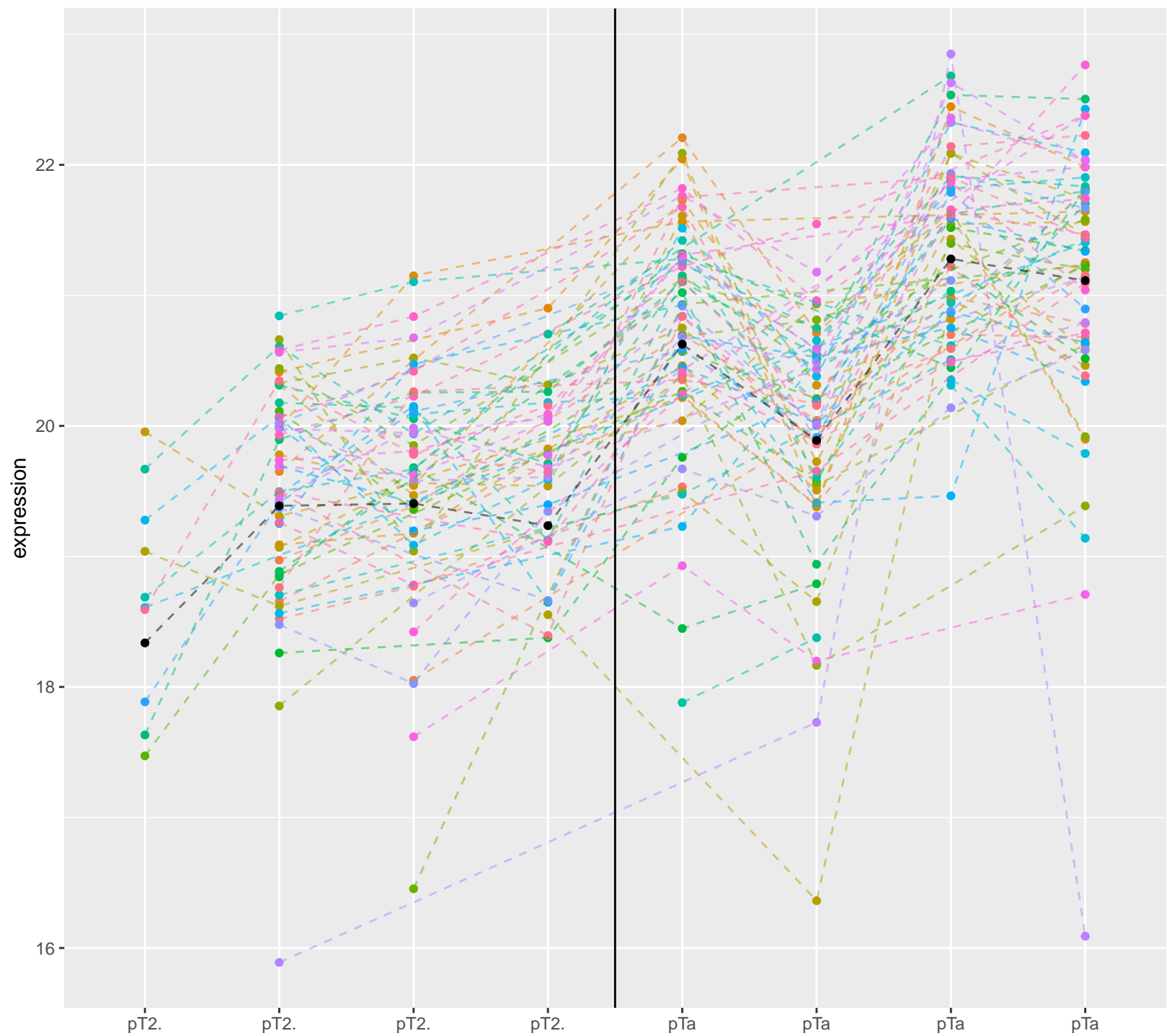
sp|P50570|DYN2_HUMANDynammin-2

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	0.900	0.791	4.22	46.5	0.188		0.53
msqrobsum	50	0.779	2.78	9.70	0.28		NA



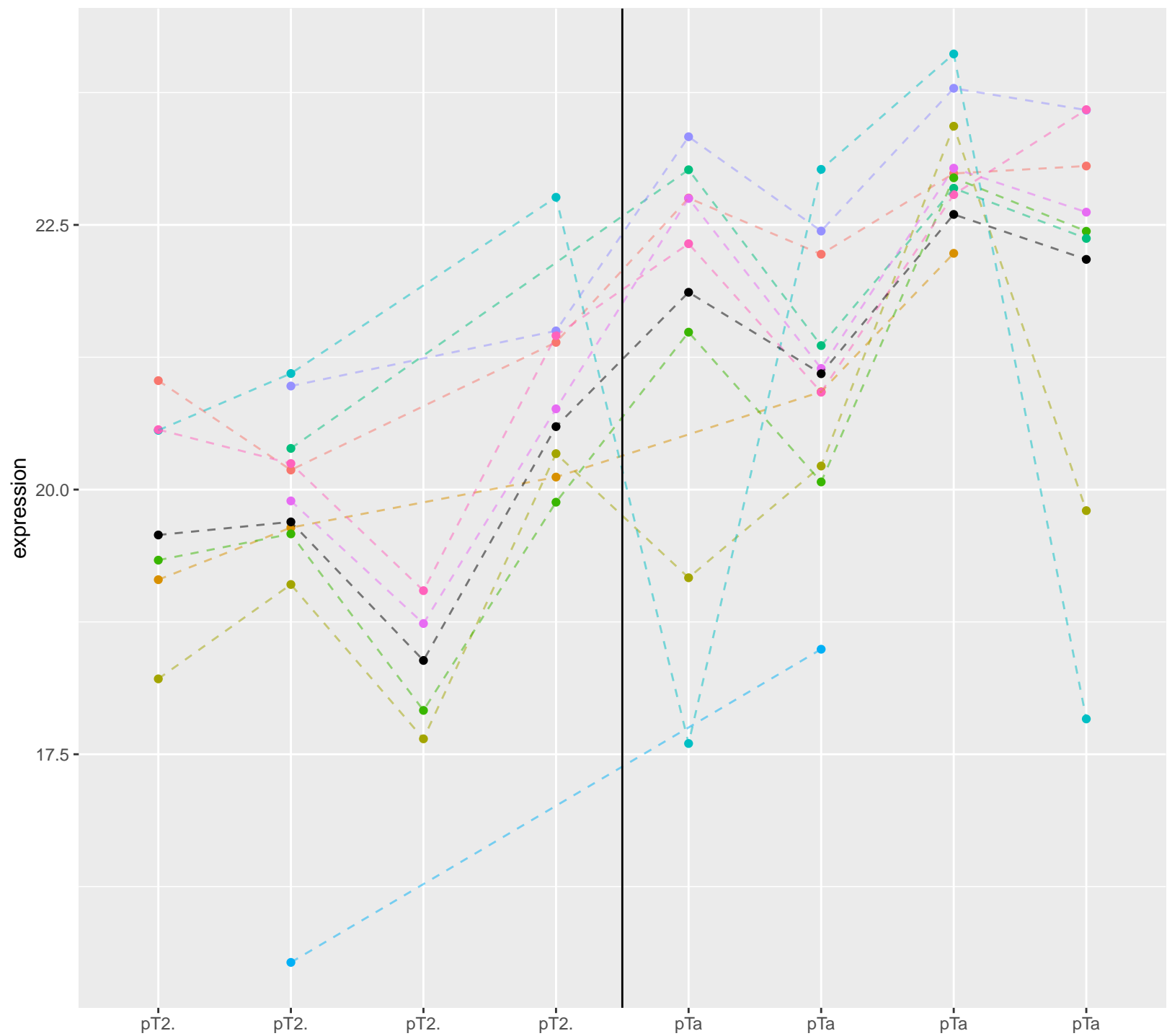
sp|O75369|FLNB_HUMANFilamin-B

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	0.900	1.48	3.89	287.	0.379		1.19
msqrobsum	20.7	1.54	4.18	9.68	0.368		NA



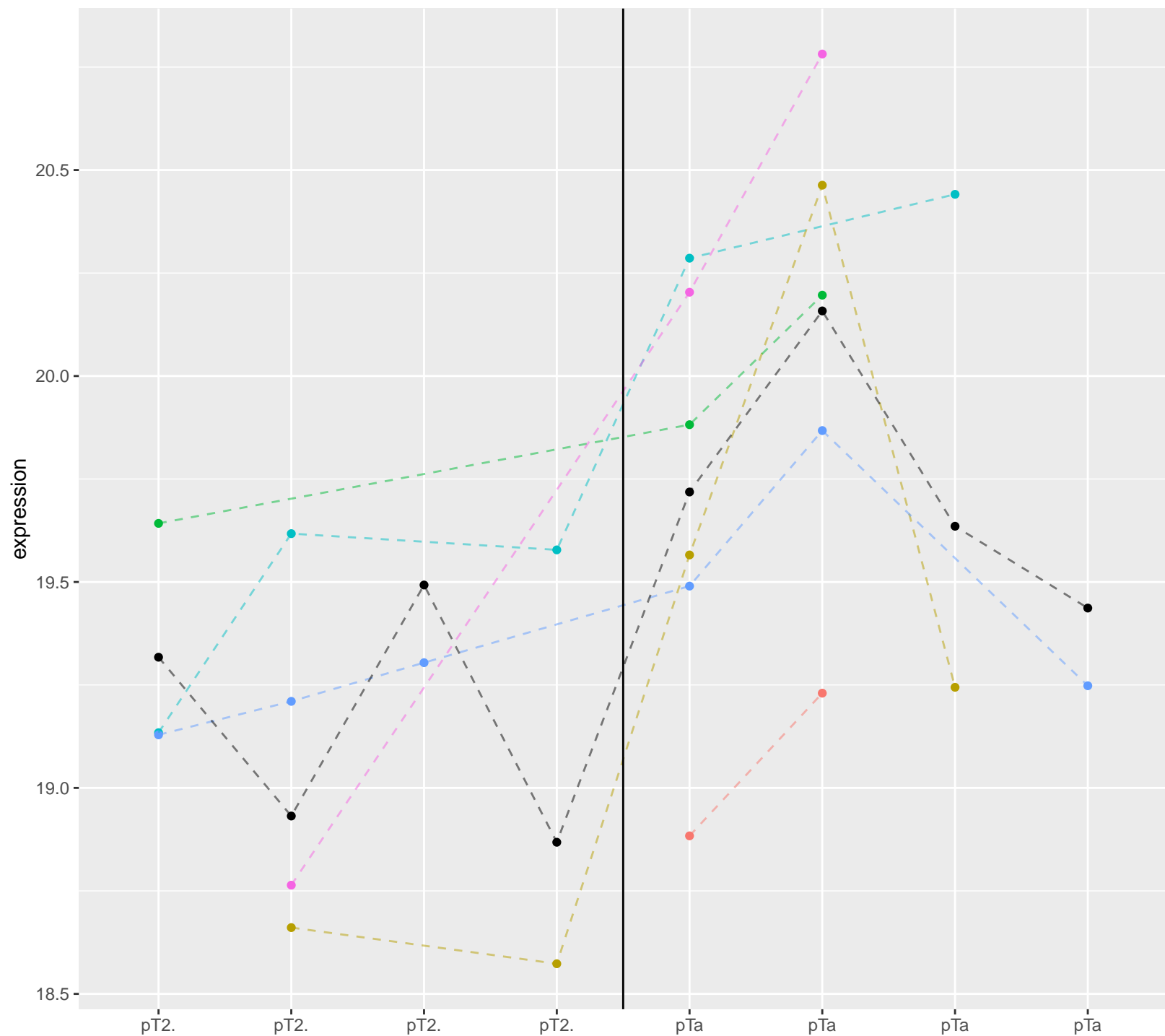
sp|O76070|SYUG_HUMANGamma-synuclein

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	1	2.19	4.11	49.5	0.533		1.36
msqrobsum	14.1	2.19	4.70	9.67	0.467		NA



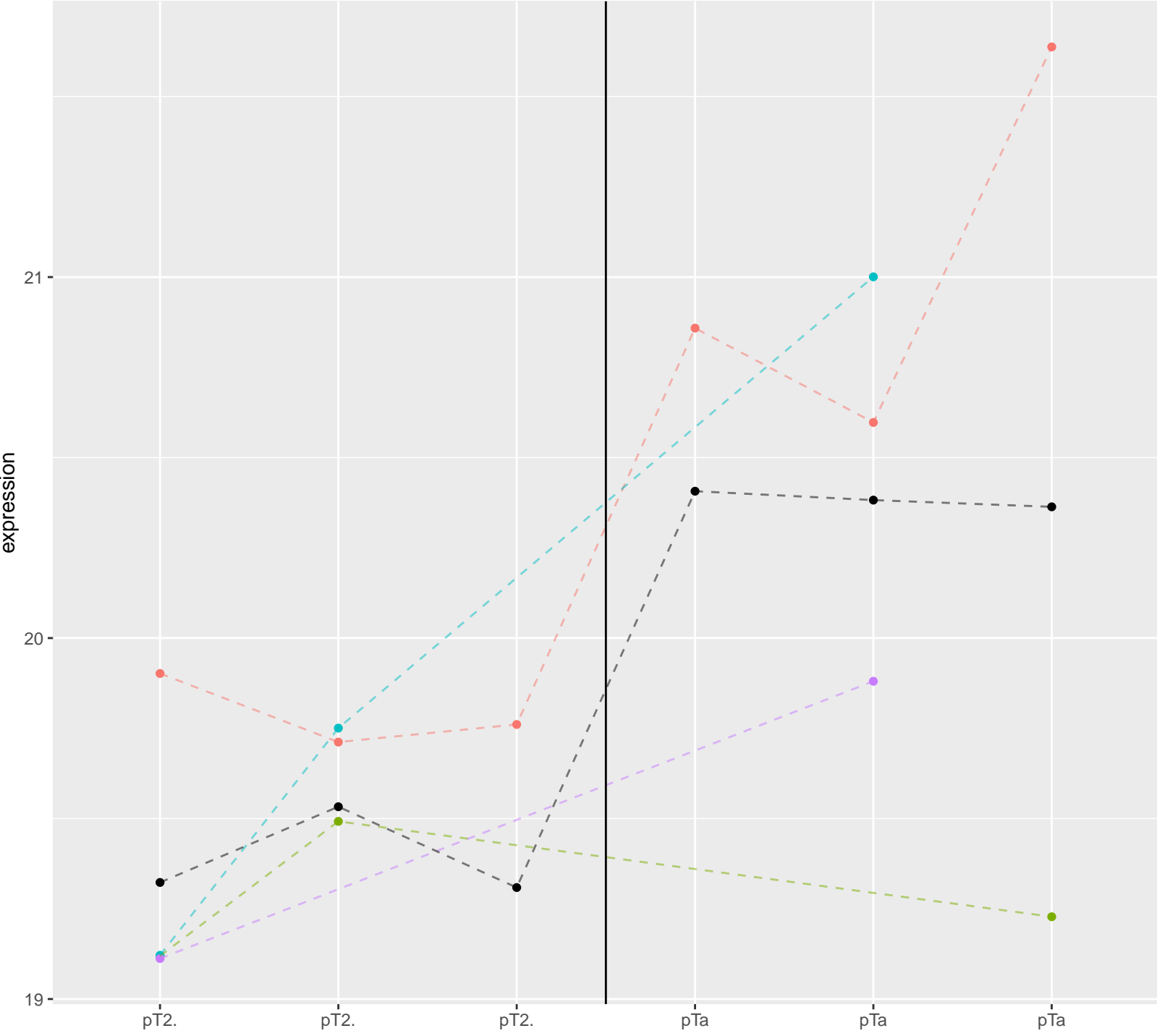
sp|Q5JTV8|TOIP1_HUMAN Torsin-1A-interacting protein1

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	1.10	0.694	4.63	19.9	0.15		0.2
msqrobsum	74.5	0.506	1.93	9.75	0.262		NA



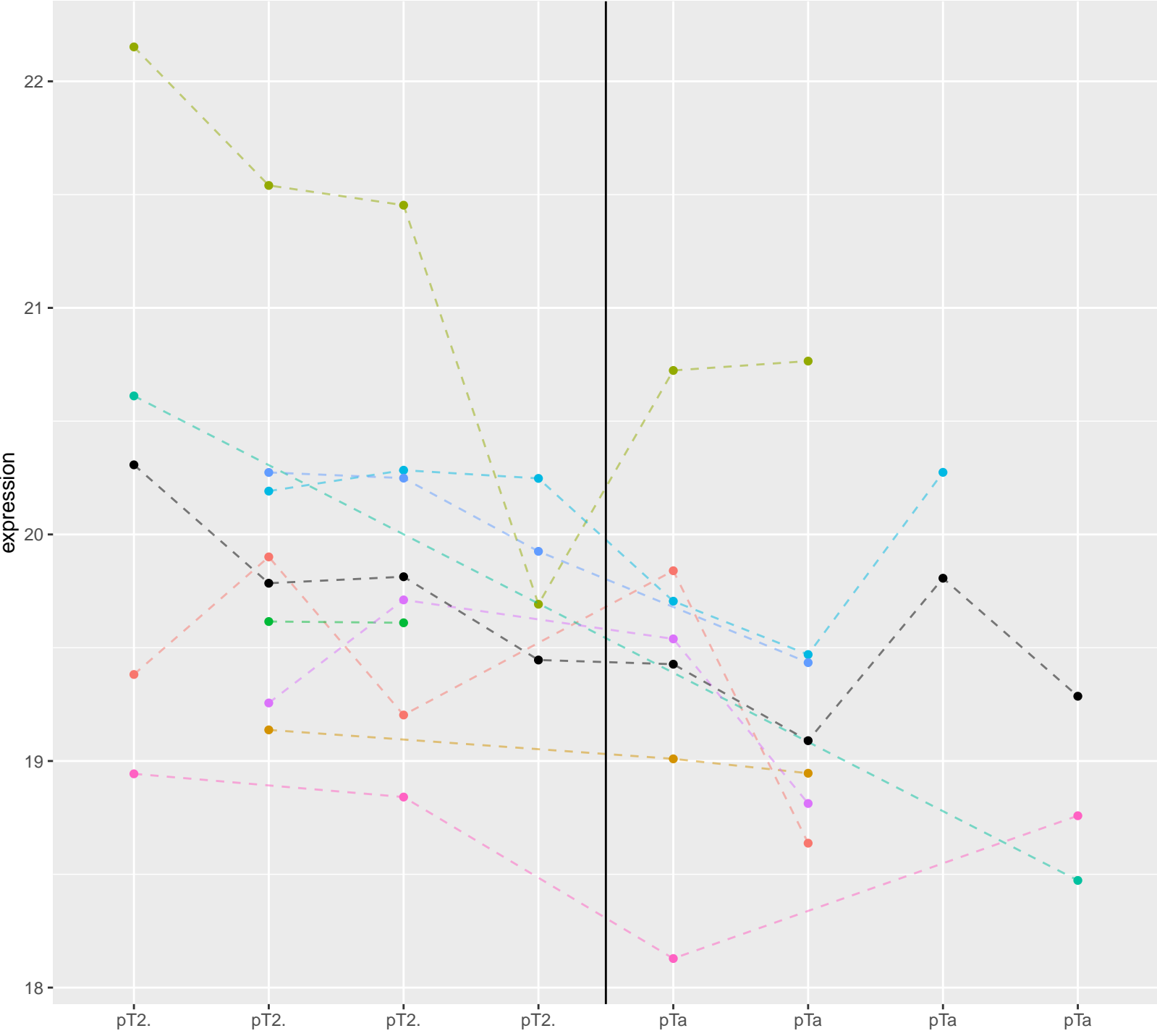
sp|Q99733|NP1L4_HUMANNucleosomeassemblyprotein1-like4

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	1.2	0.917	5.25	12.3	0.175		0
msqrobsum	37.3	1.01	3.41	7.62	0.296		NA



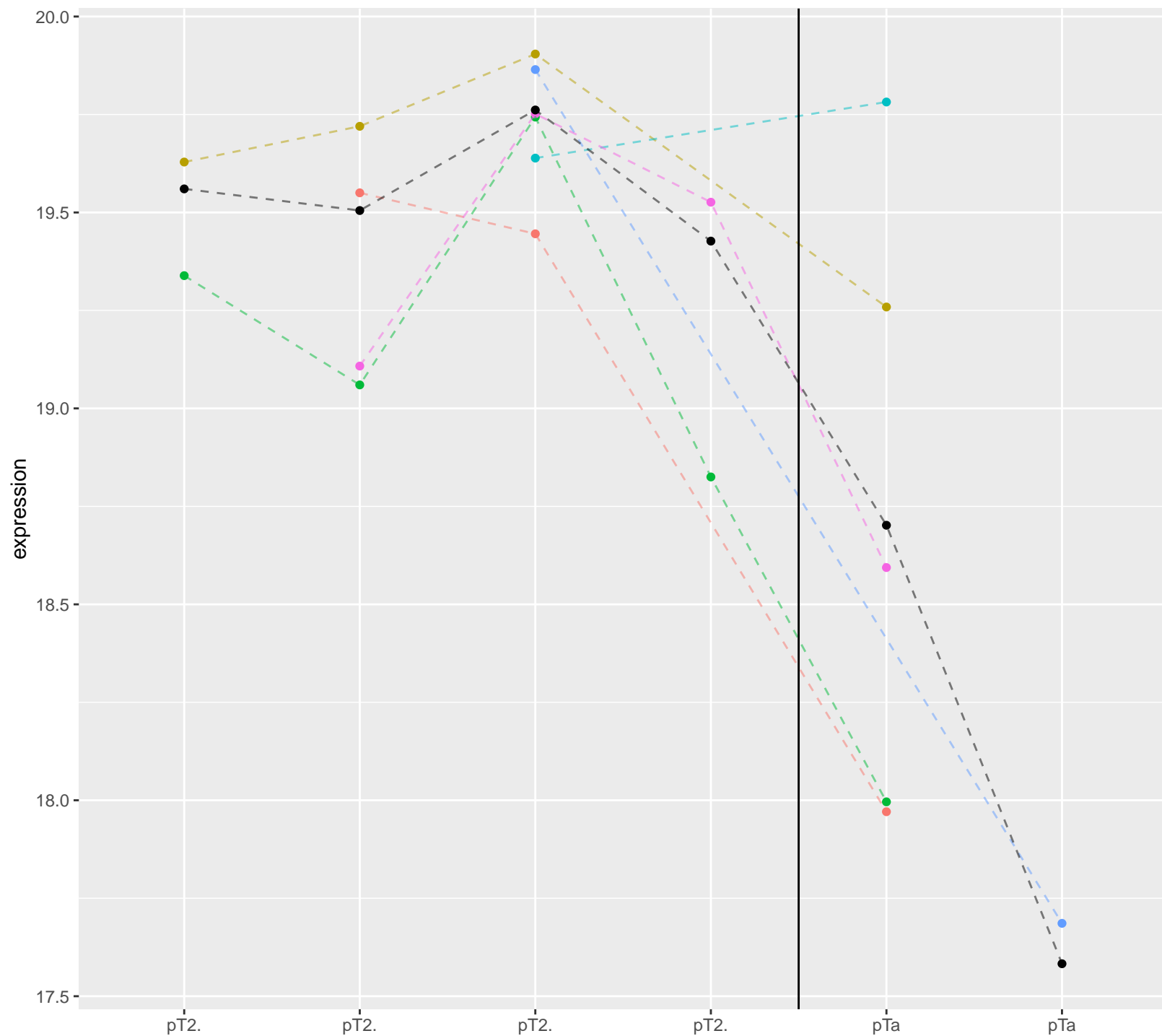
sp|O75131|CPNE3_HUMANCopine-3

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	1.2	-0.514	-4.26	29.2	0.121		0
msqrobsum	100	-0.304	-1.25	9.91	0.244		NA



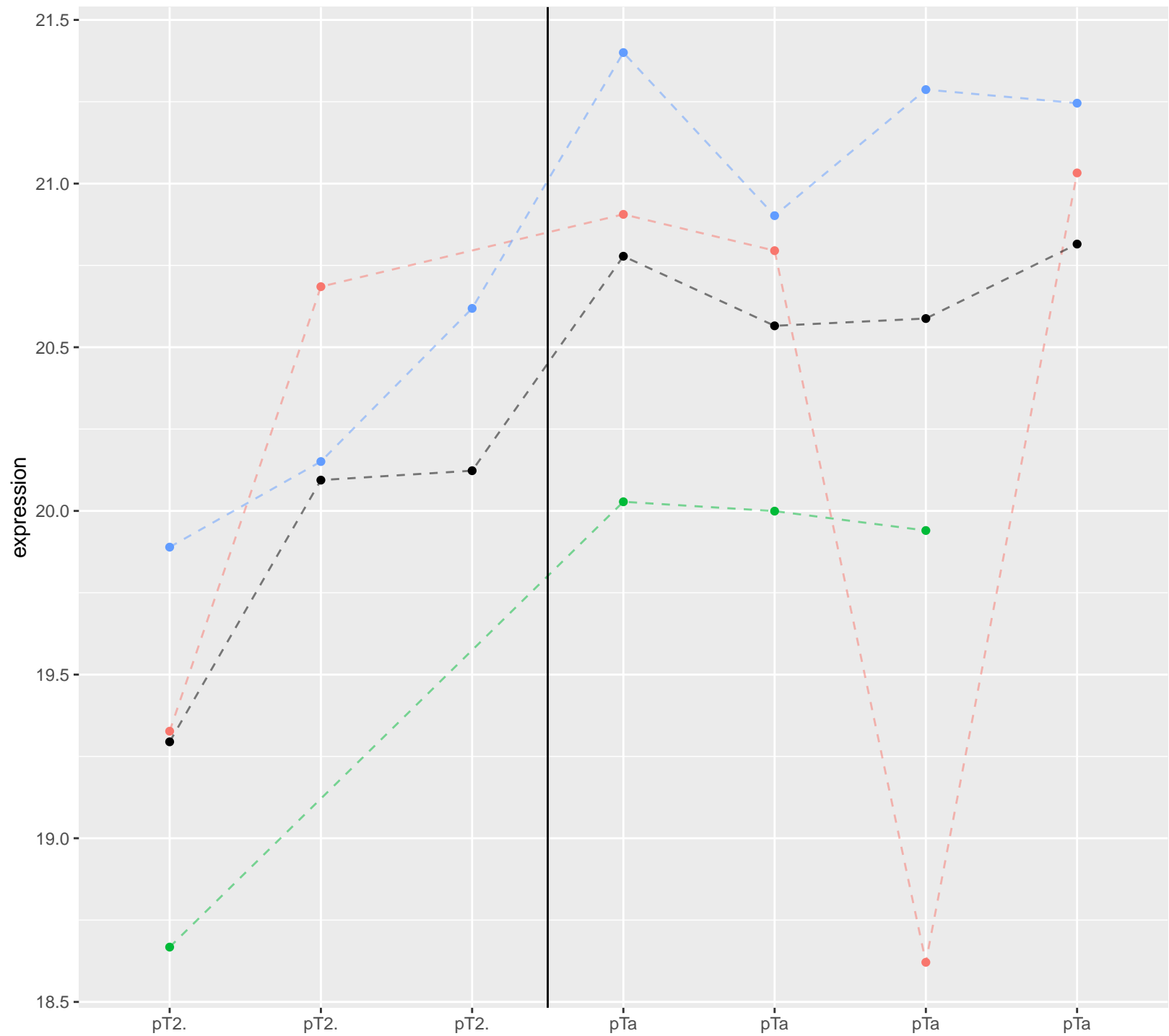
sp|Q14566|MCM6_HUMANDNAreplicationlicensingfactorMCM6

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	1.4	-1.12	-4.65	17.1	0.24		0.485
msqrobsum	37.3	-1.27	-3.50	7.68	0.364		NA



sp|Q9BRA2|TXD17_HUMANThioredoxin domain-containing protein17

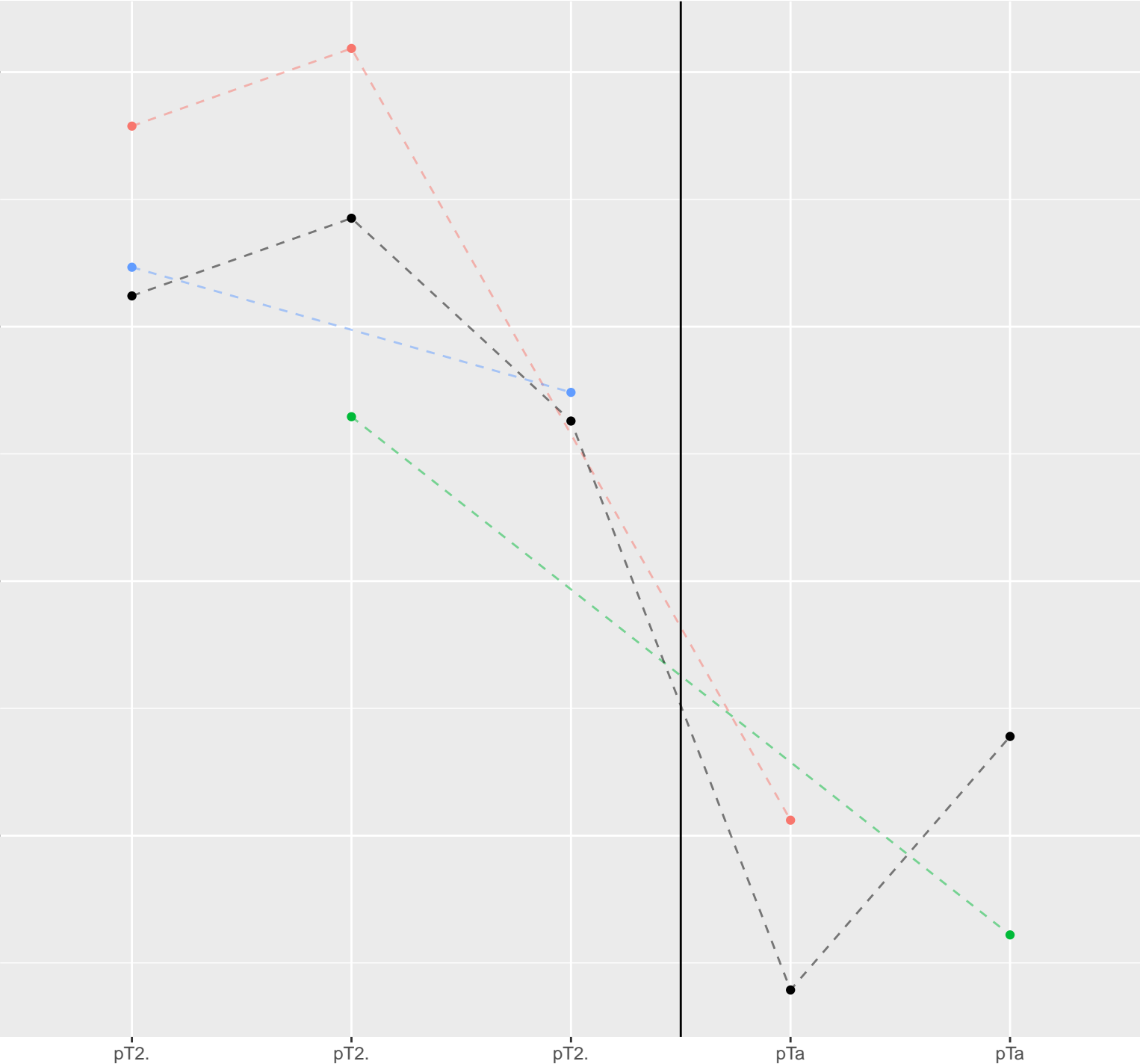
method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	1.4	0.997	4.81	14.8	0.207		0.316
msqrobsum	60.9	0.695	2.42	8.70	0.287		NA



sp|Q06828|FMOD_HUMANFibromodulin

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	1.4	-2.47	-7.8	5.94	0.317		0
msqrobsum	24	-2.06	-4.44	6.67	0.465		NA

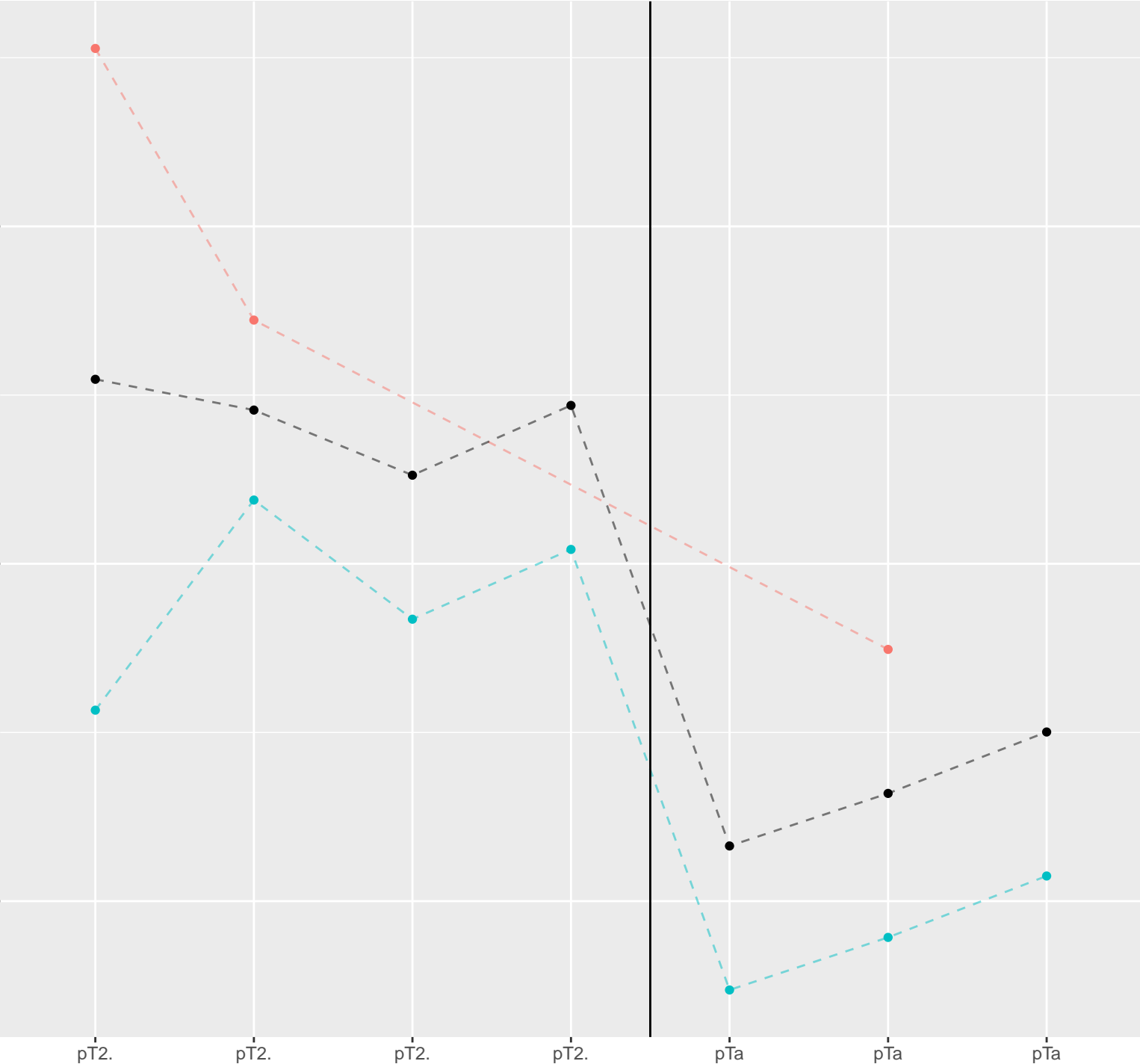
expression



sp|P08195|4F2_HUMAN4F2cell-surfaceantigenheavychain

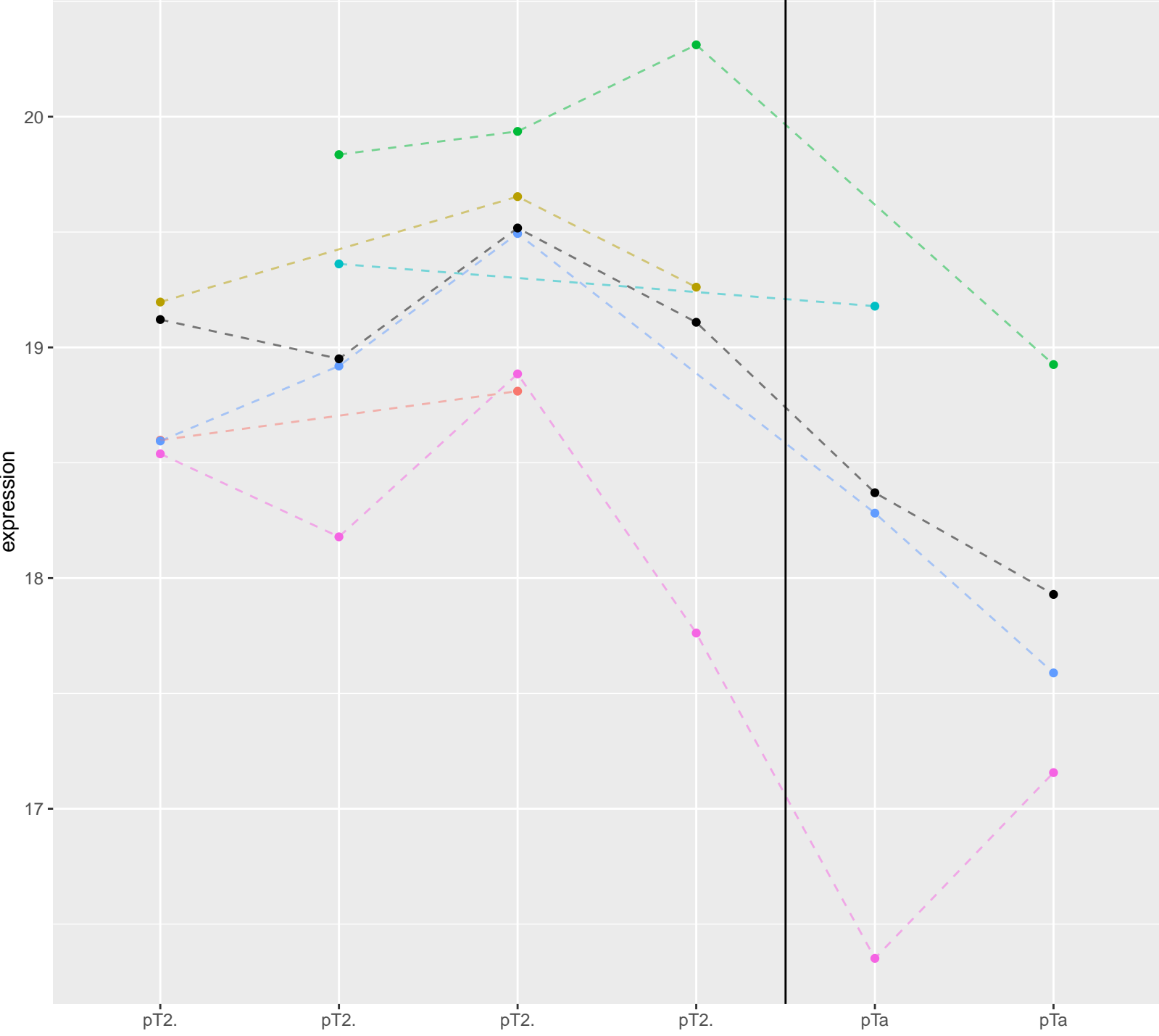
method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	1.5	-1.05	-5.61	9.57	0.187		0
msqrobsum	23.8	-1.09	-4.06	8.63	0.269		NA

expression



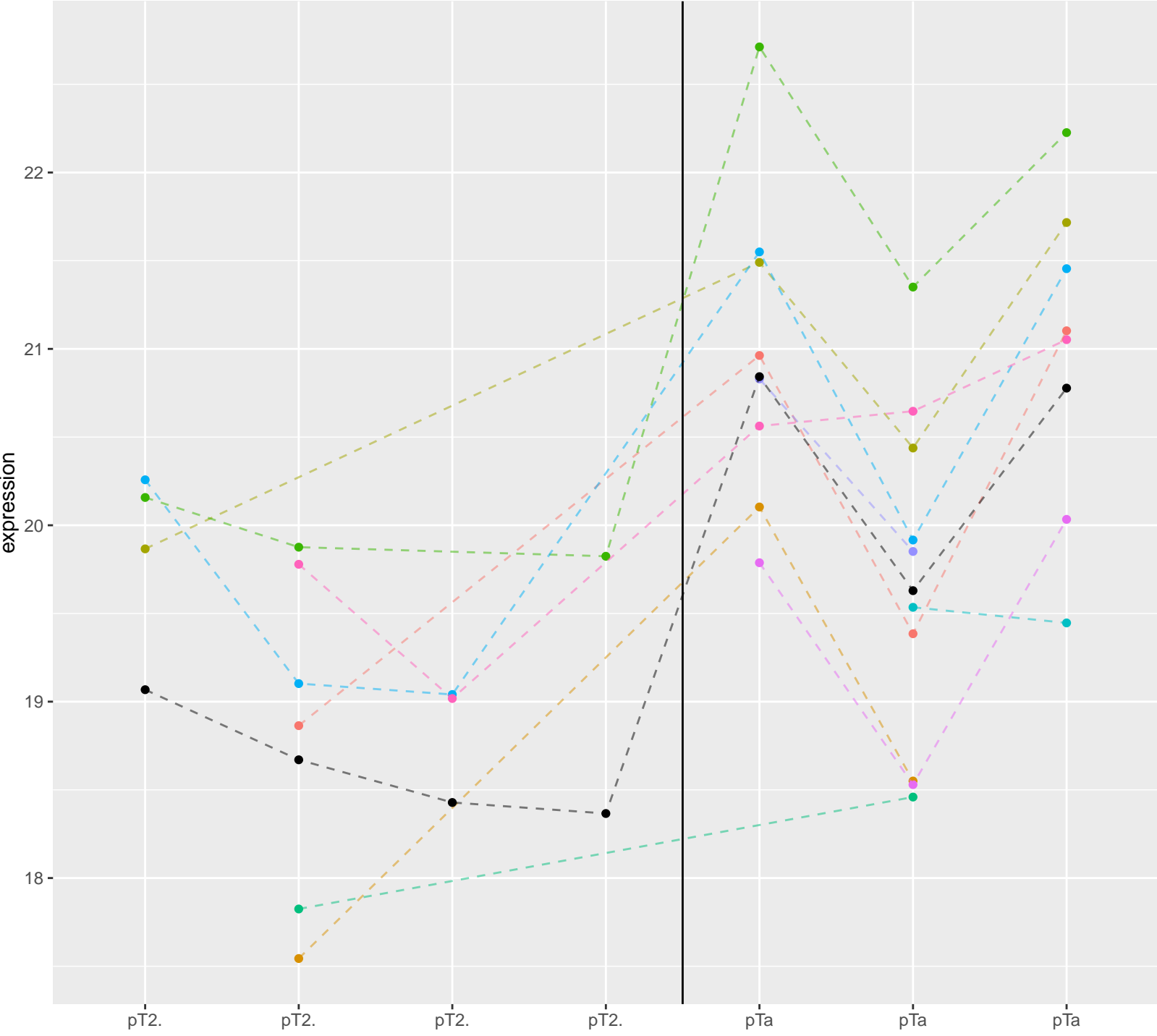
sp|P25205|MCM3_HUMAN|DNA replication licensing factor|MCM3

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	1.5	-0.997	-4.57	16.8	0.218		0.37
msqrobsum	52.3	-0.975	-2.85	7.67	0.342		NA



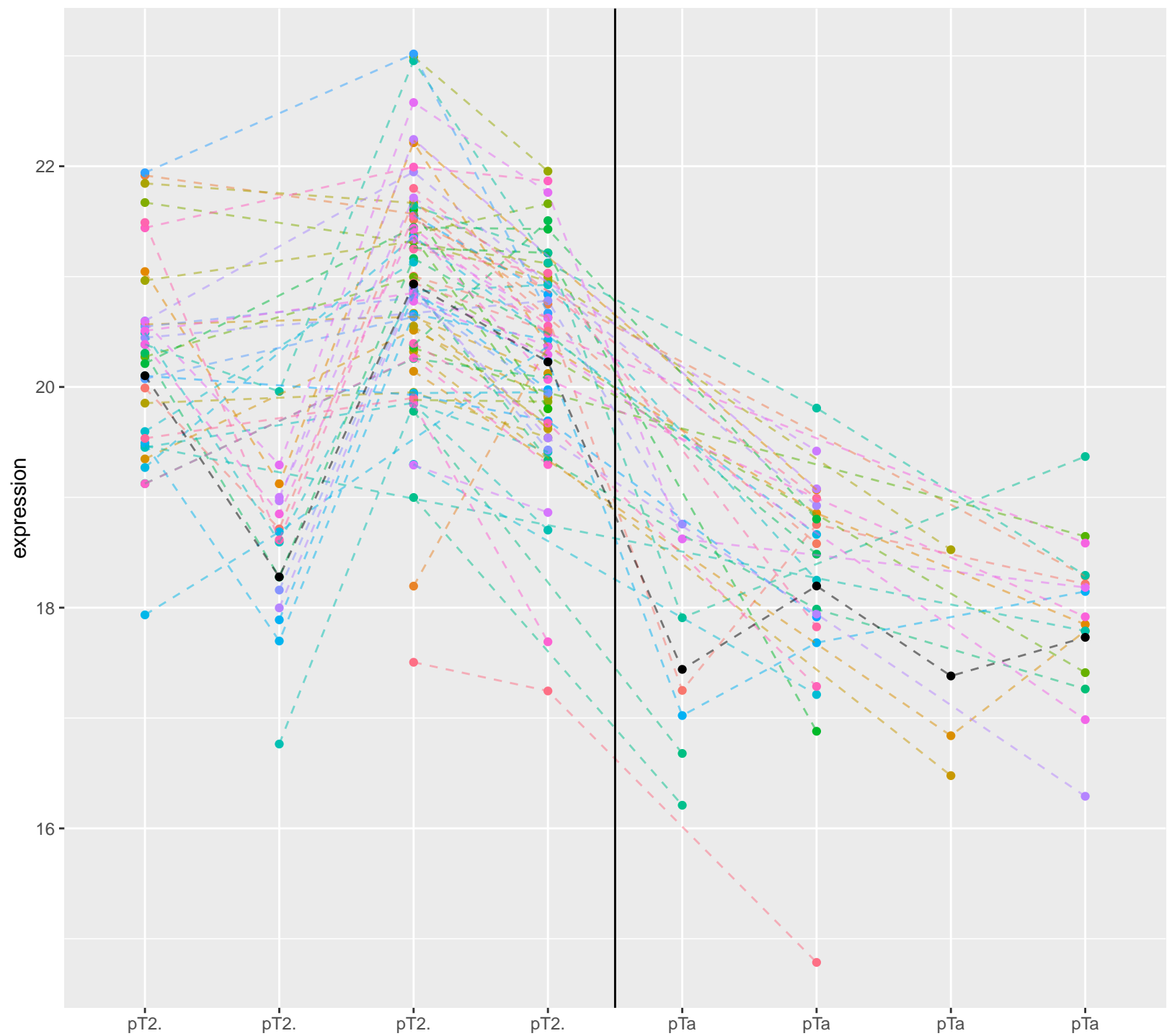
sp|O15382|BCAT2_HUMANBranched-chain-amino-acidaminotransferase,mitochondrial

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	1.7	1.63	4.18	24.8	0.391		1.44
msqrobsum	18.9	1.70	4.50	8.67	0.379		NA



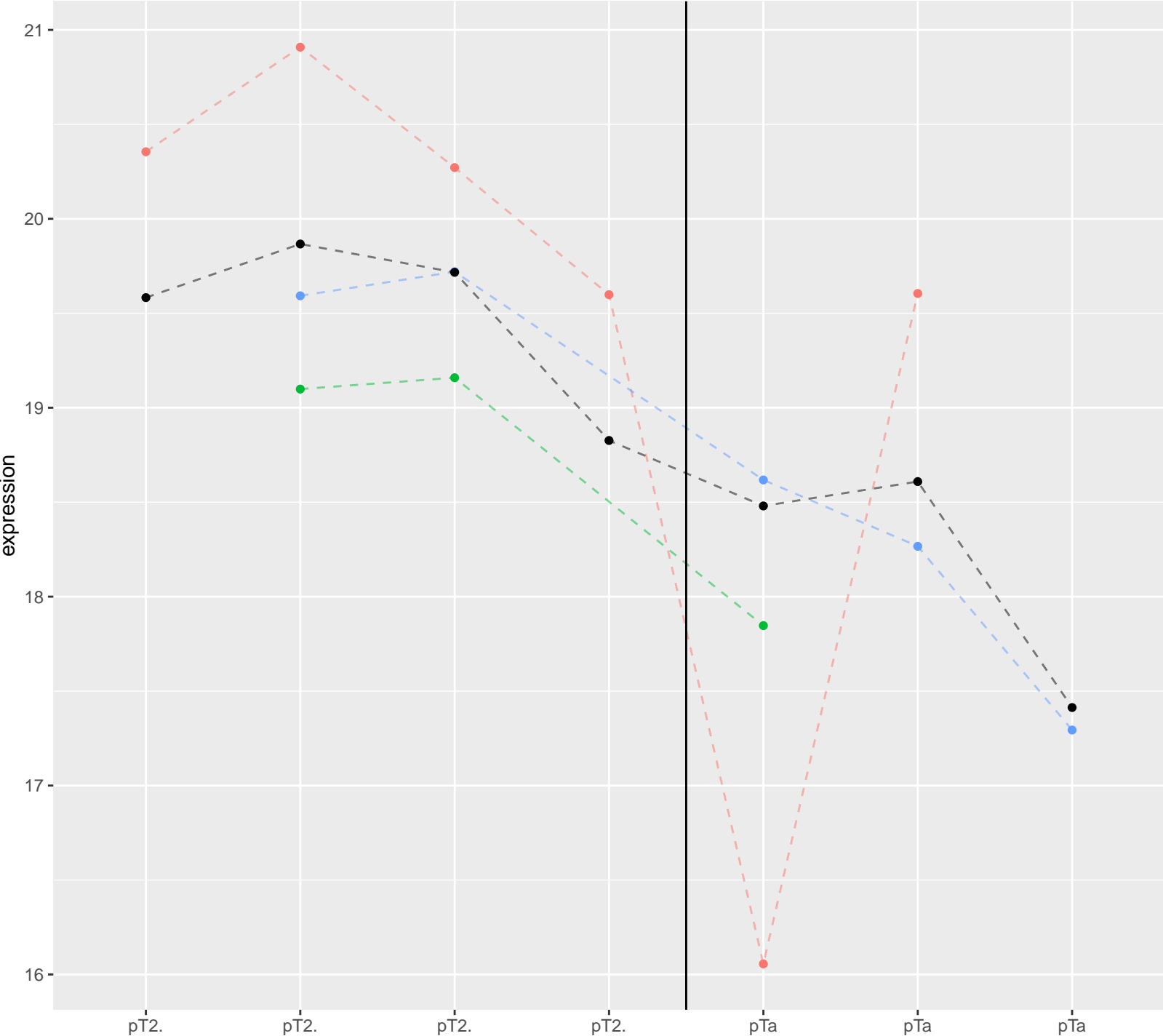
sp|P15924|DESP_HUMANDesmoplakin

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	2.5	-2.05	-3.57	155.	0.576		1.93
msqrobsum	10.7	-2.23	-5.23	9.67	0.427		NA



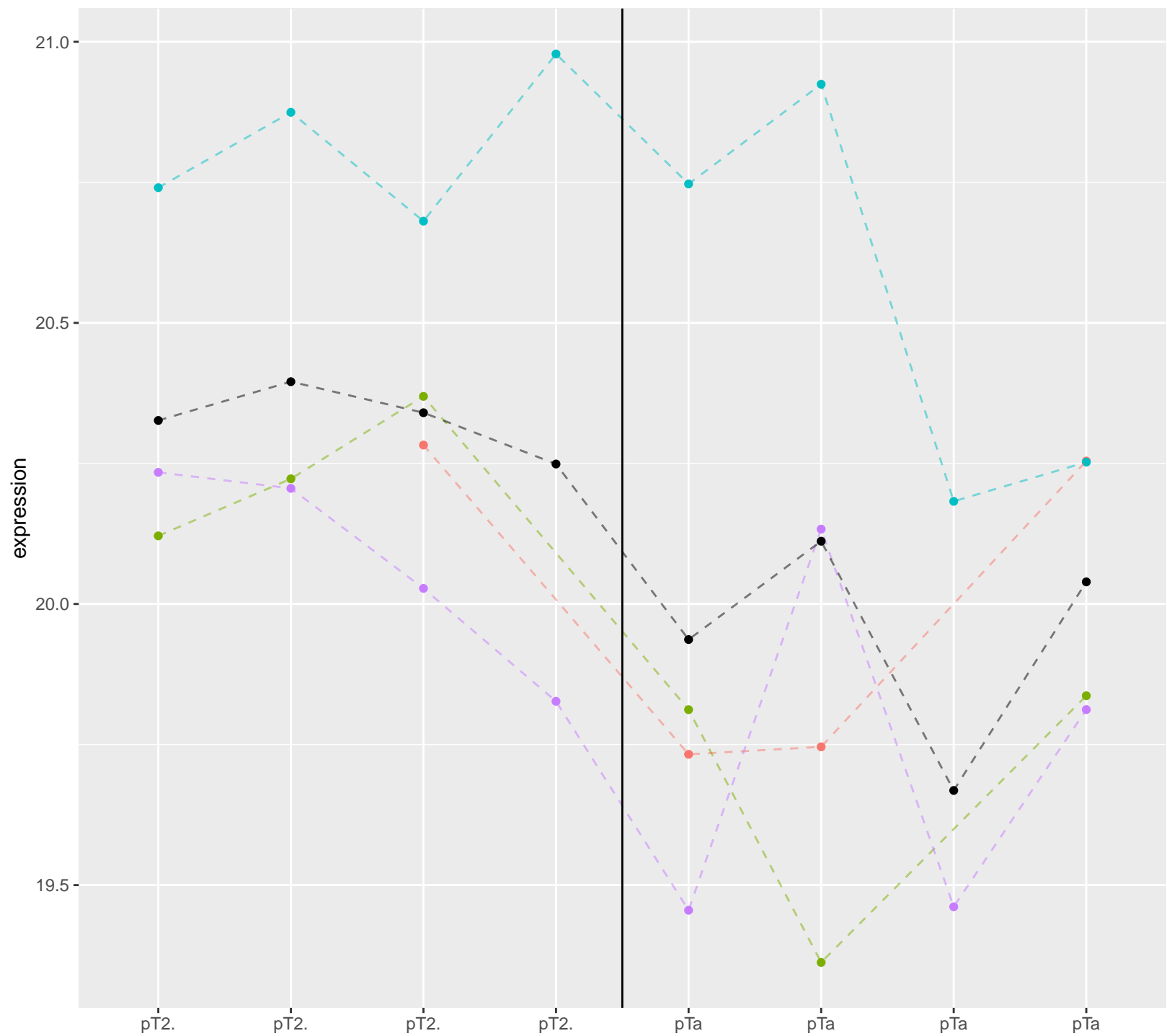
sp|Q13057|COASY_HUMANBifunctionalcoenzymeAsynthase

method	q-value	log fold change	t-value	df	se	theta	sample
msgrob	2.6	-1.58	-4.51	13.6	0.349		0
msgrobsum	41.2	-1.17	-3.04	8.72	0.384		NA



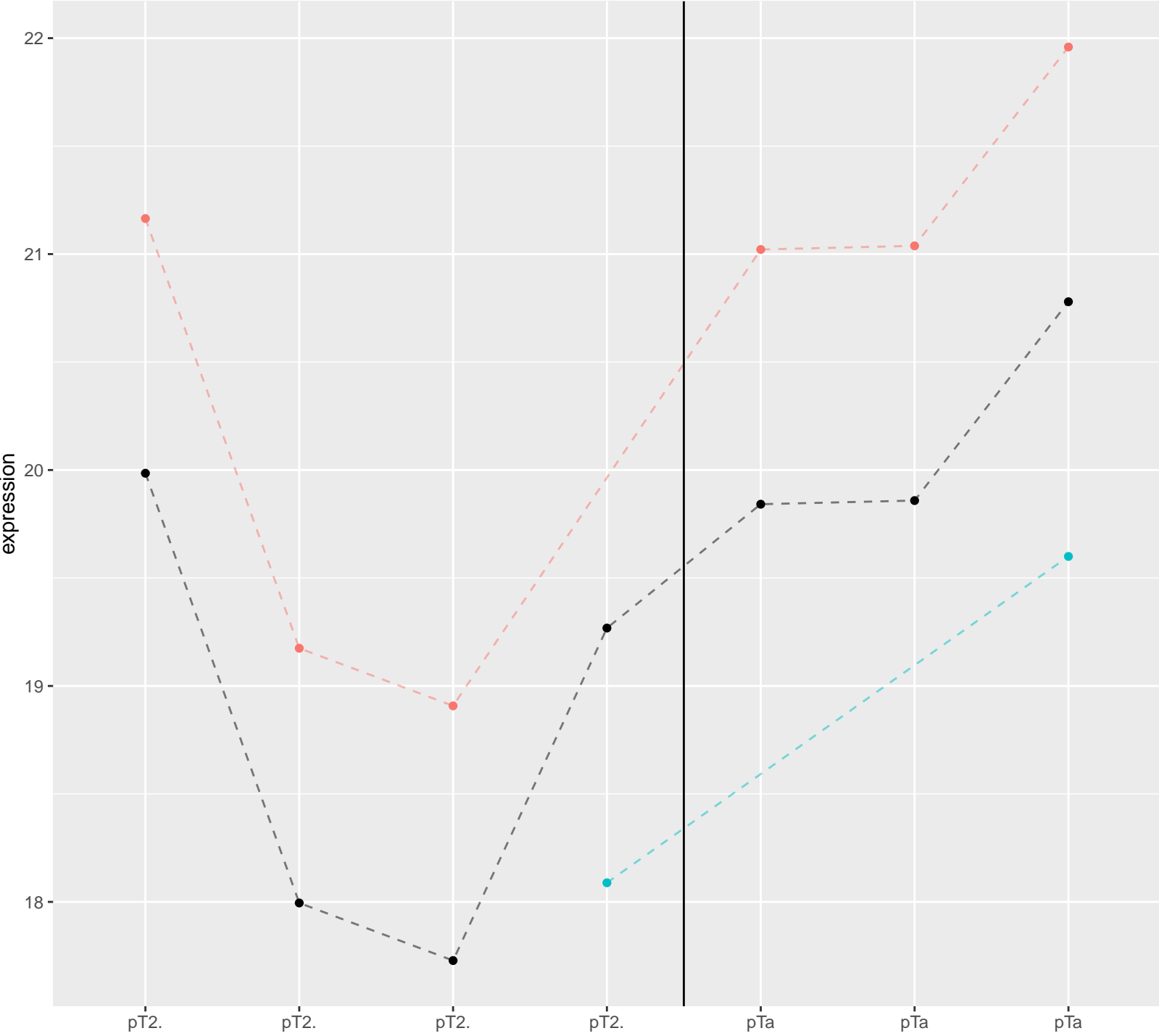
sp|P49720|PSB3_HUMANProteasomesubunitbetatype-3

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	2.9	-0.382	-3.96	23.8	0.097		0
msqrobsum	99	-0.334	-1.46	9.68	0.228		NA



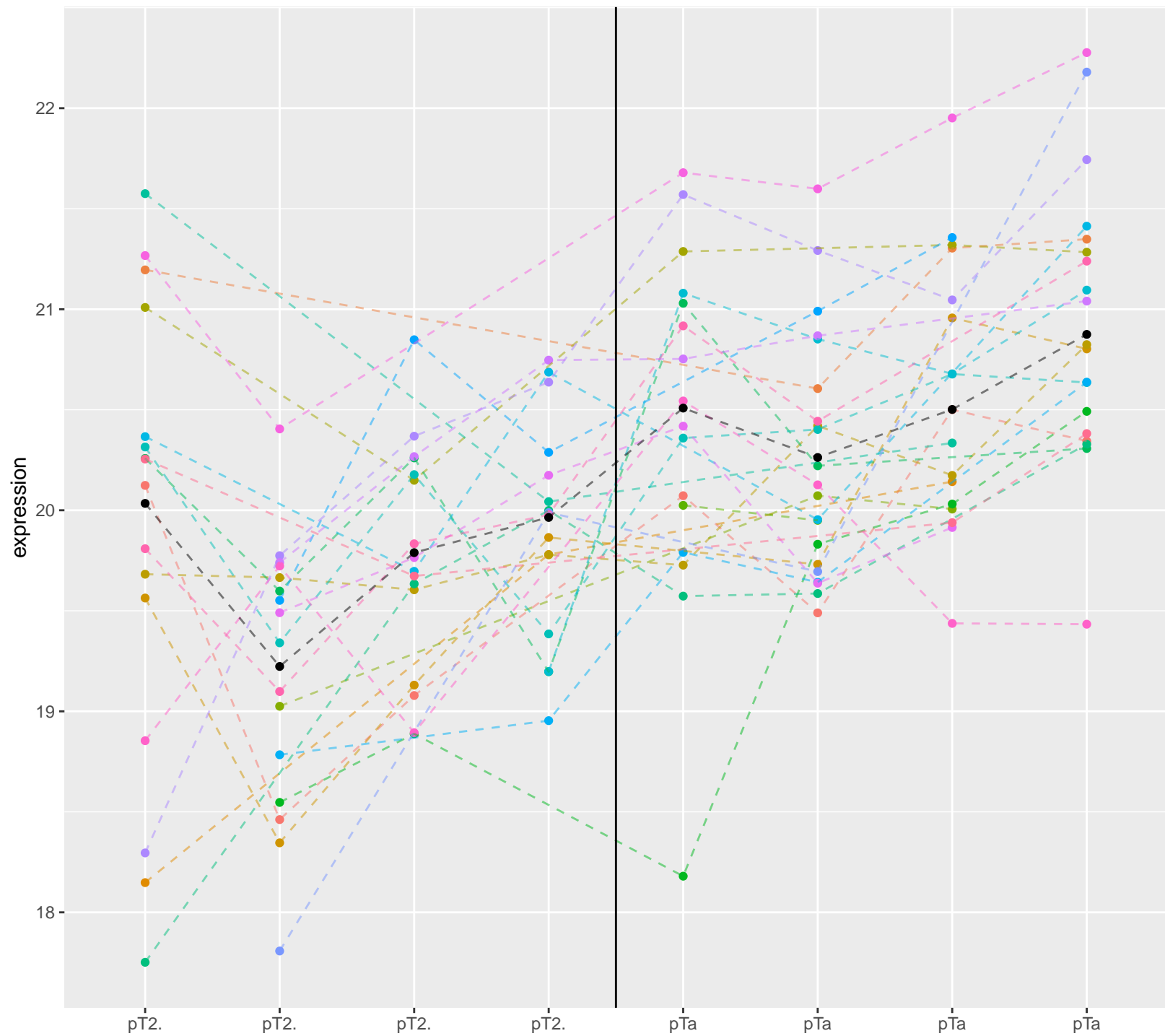
sp|P02656|APOC3_HUMANApolipoproteinC-III

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	2.9	1.71	5.63	7.52	0.304		0
msqrobsum	65.5	1.09	2.13	8.85	0.511		NA



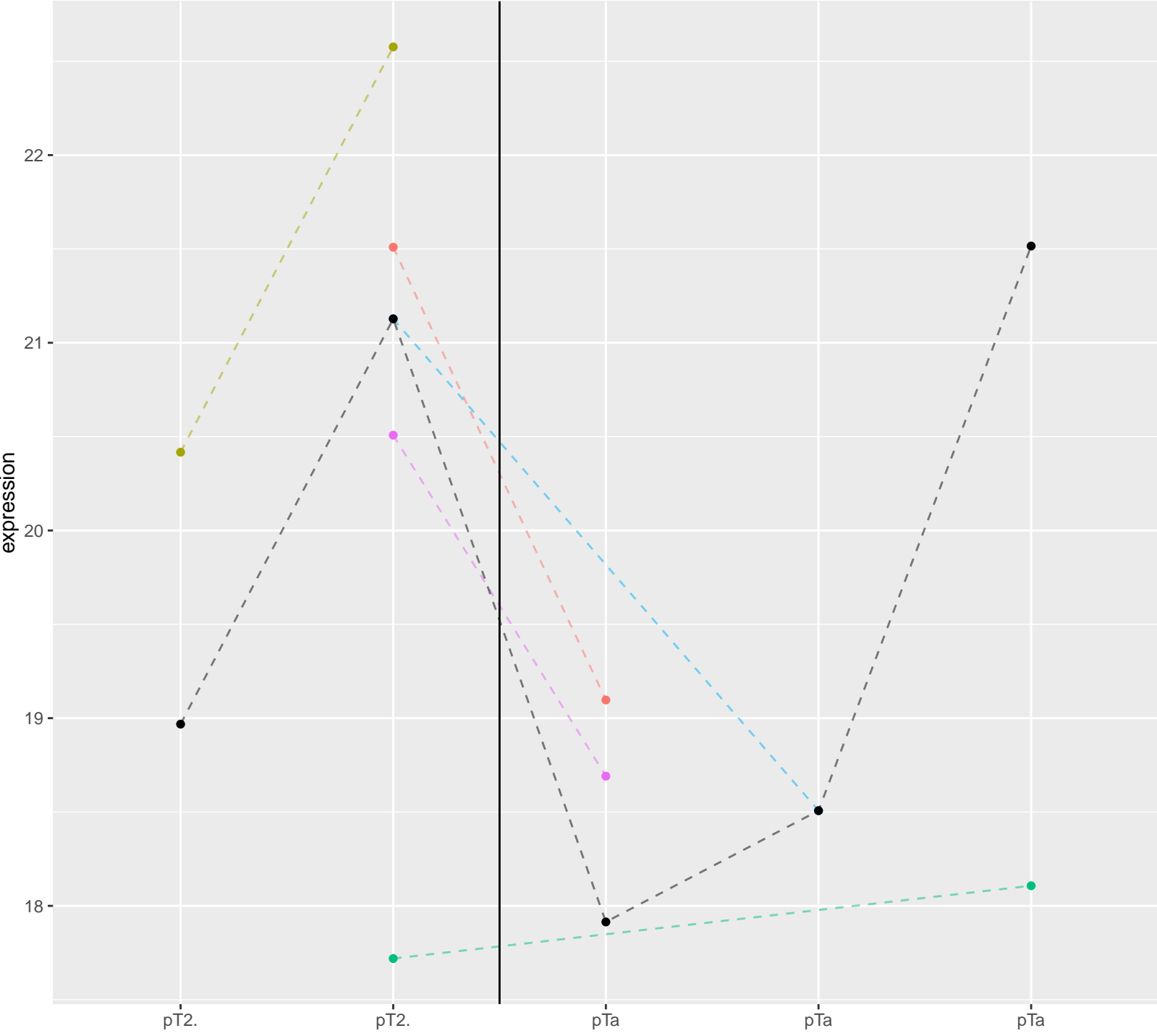
sp|Q8WUM4|PDC6I_HUMANProgrammedcelldeath6-interactingprotein

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	3.2	0.726	3.49	112.	0.208		0.671
msqrobsum	54.8	0.689	2.57	9.70	0.268		NA



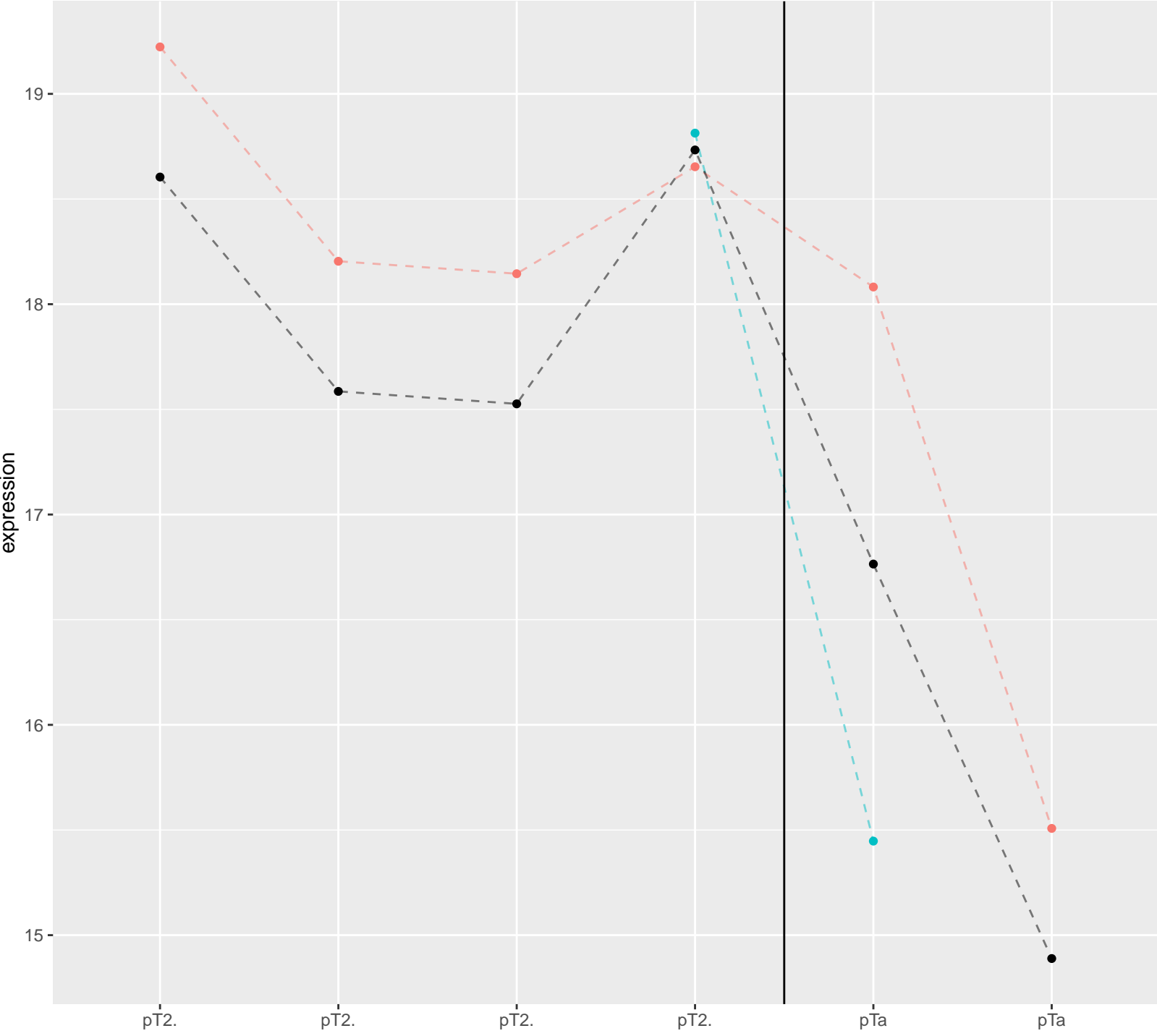
sp|Q7L5L3|GDPD3_HUMANGlycerophosphodiesterphosphodiesterasedomain-containingprotein3

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	3.4	-2.15	-4.66	10.6	0.461		0
msqrobsum	100	0	0	7.62	0		NA



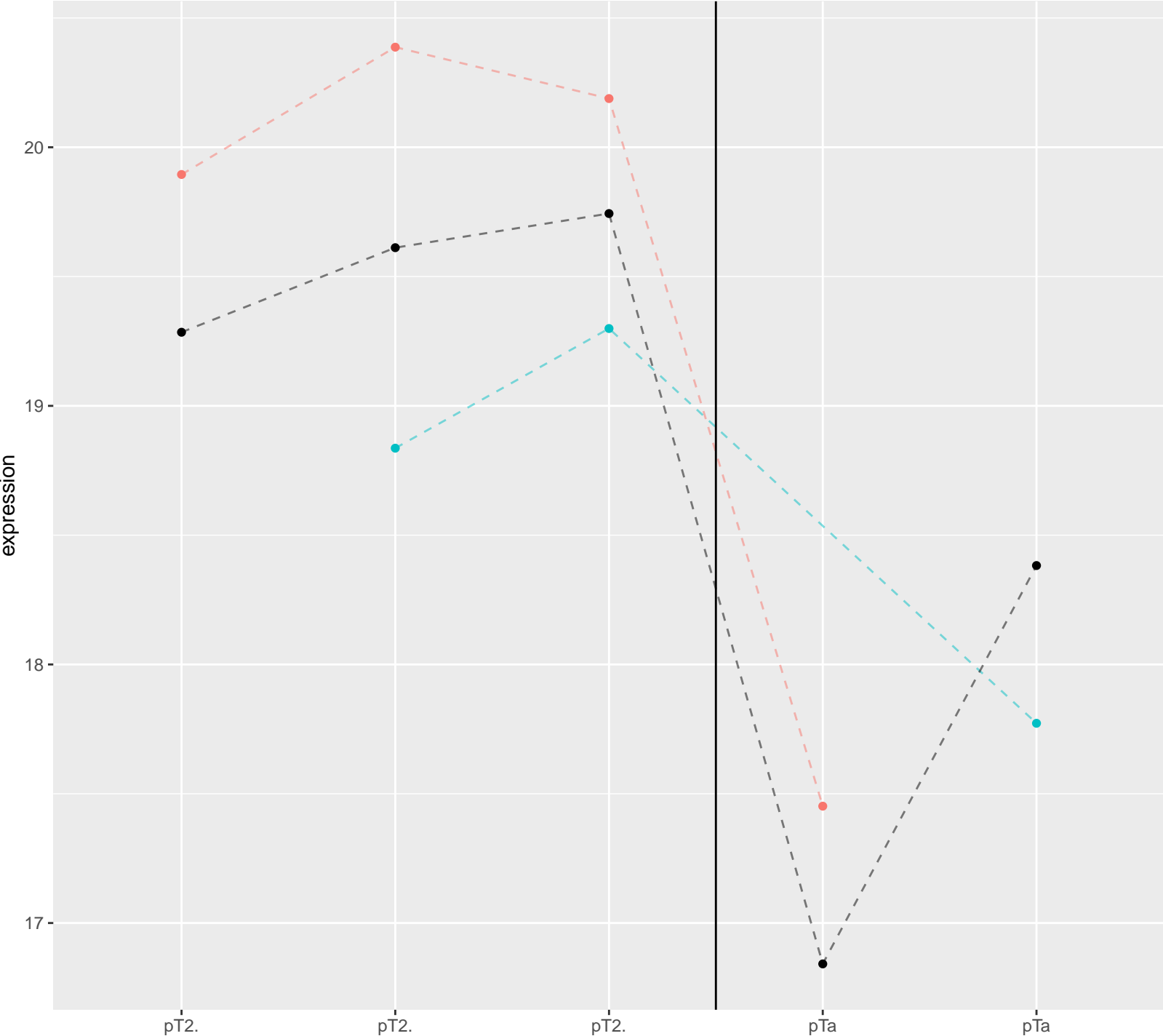
sp|O96005|CLPT1_HUMANClleftlipandpalatetransmembraneprotein1

method	q-value	log fold change	t-value	df	se	theta	sample
msgrob	4.40	-2.41	-4.90	8.39	0.491		0
msgrobsum	37.3	-2.04	-3.43	7.73	0.594		NA



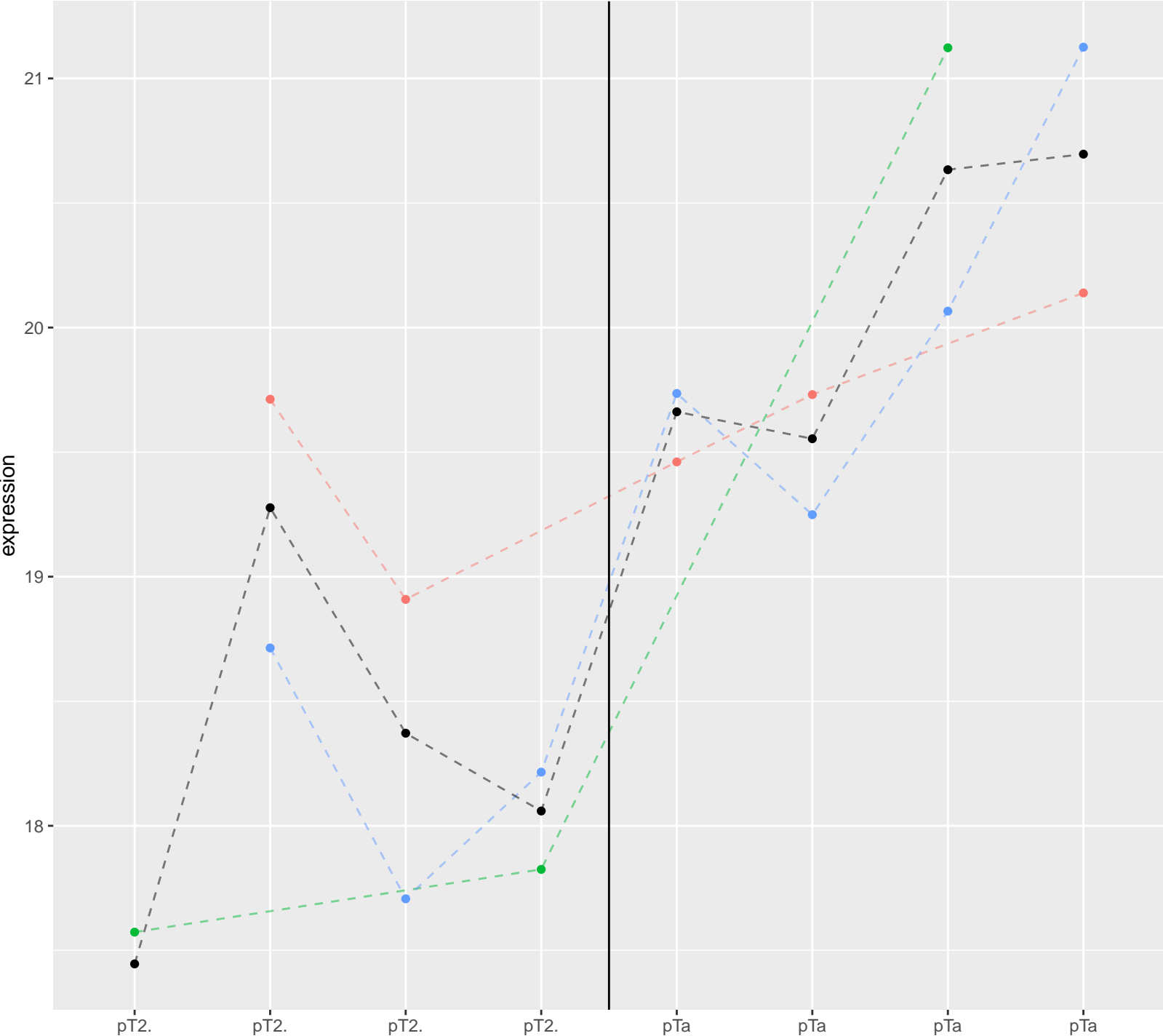
sp|P52292|HMA1_HUMANImportinsubunitalpha-1

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	4.40	-1.98	-5.46	6.84	0.363		0
msqrobsum	39.1	-1.64	-3.48	6.72	0.473		NA



sp|Q9Y371|SHLB1_HUMANEndophilin-B1

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	4.5	1.64	4.21	12.7	0.388		0.728
msqrobsum	23.8	1.72	3.98	9.69	0.432		NA



sp|O94905|ERLN2_HUMANErln-2

method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	5	0.751	3.84	17.8	0.195		0
msqrobsum	86.9	0.472	1.65	9.86	0.286		NA

