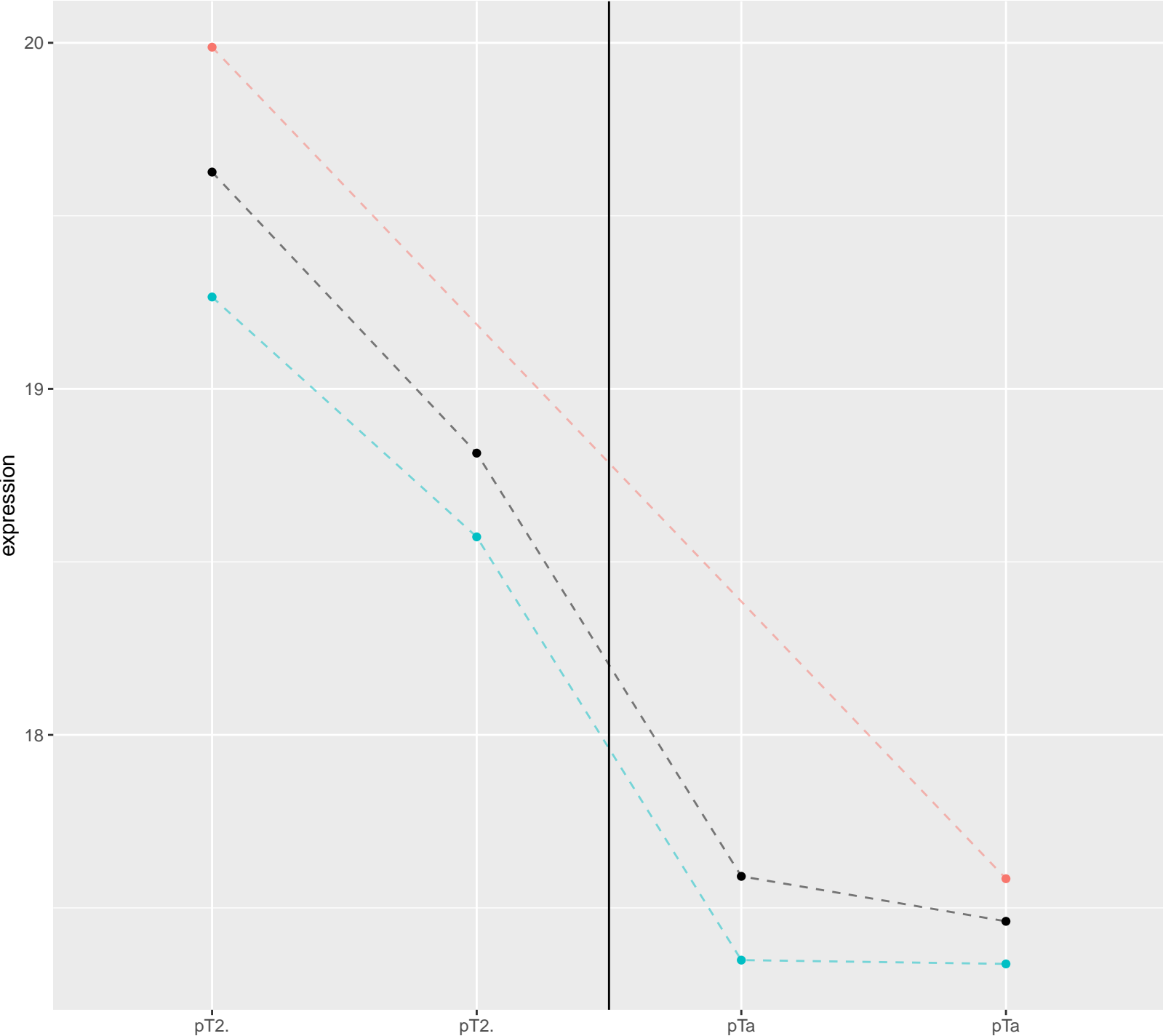


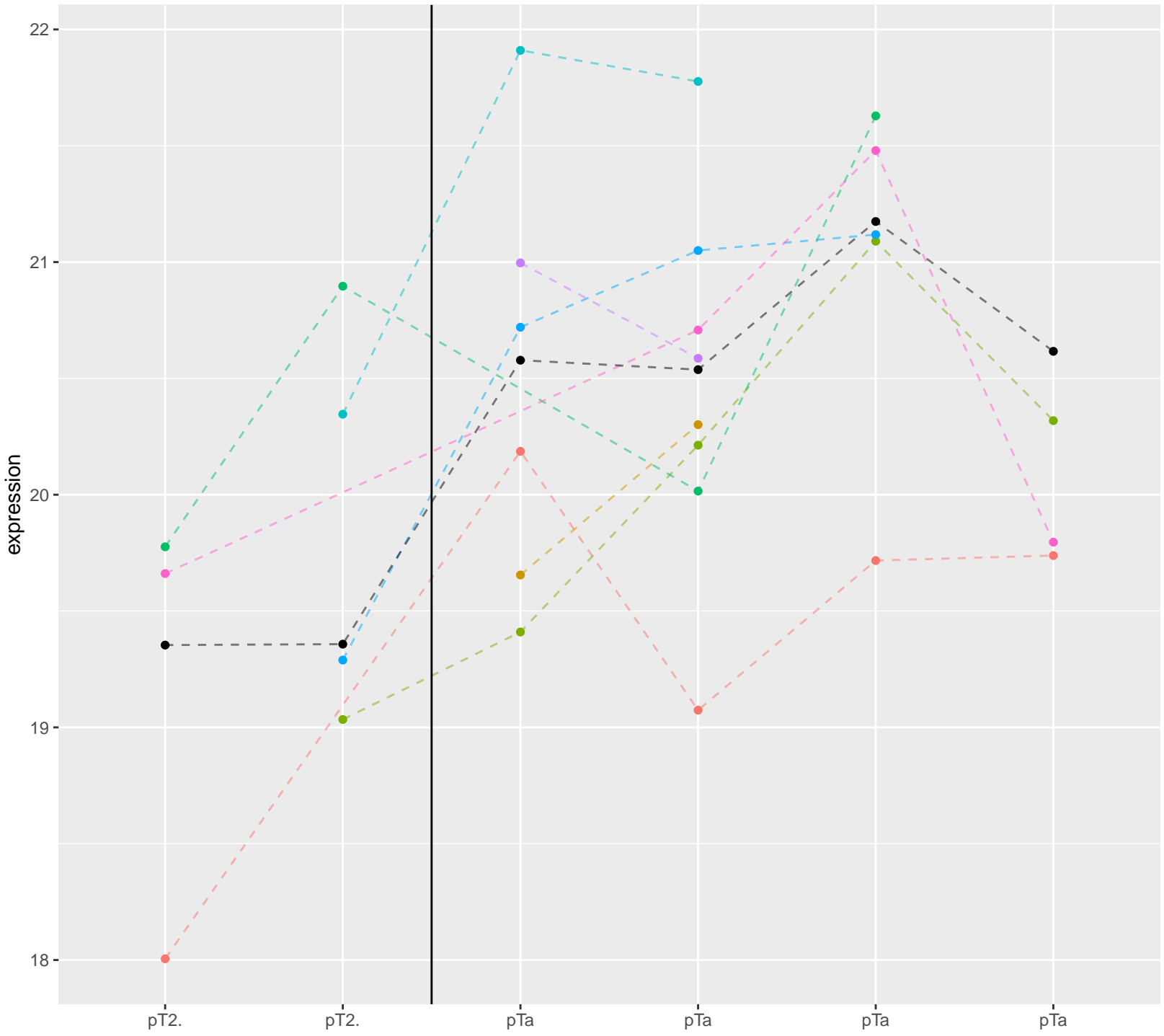
sp|O00154|BACH_HUMANCytosolicacylcoenzymeAthioesterhydrolase

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



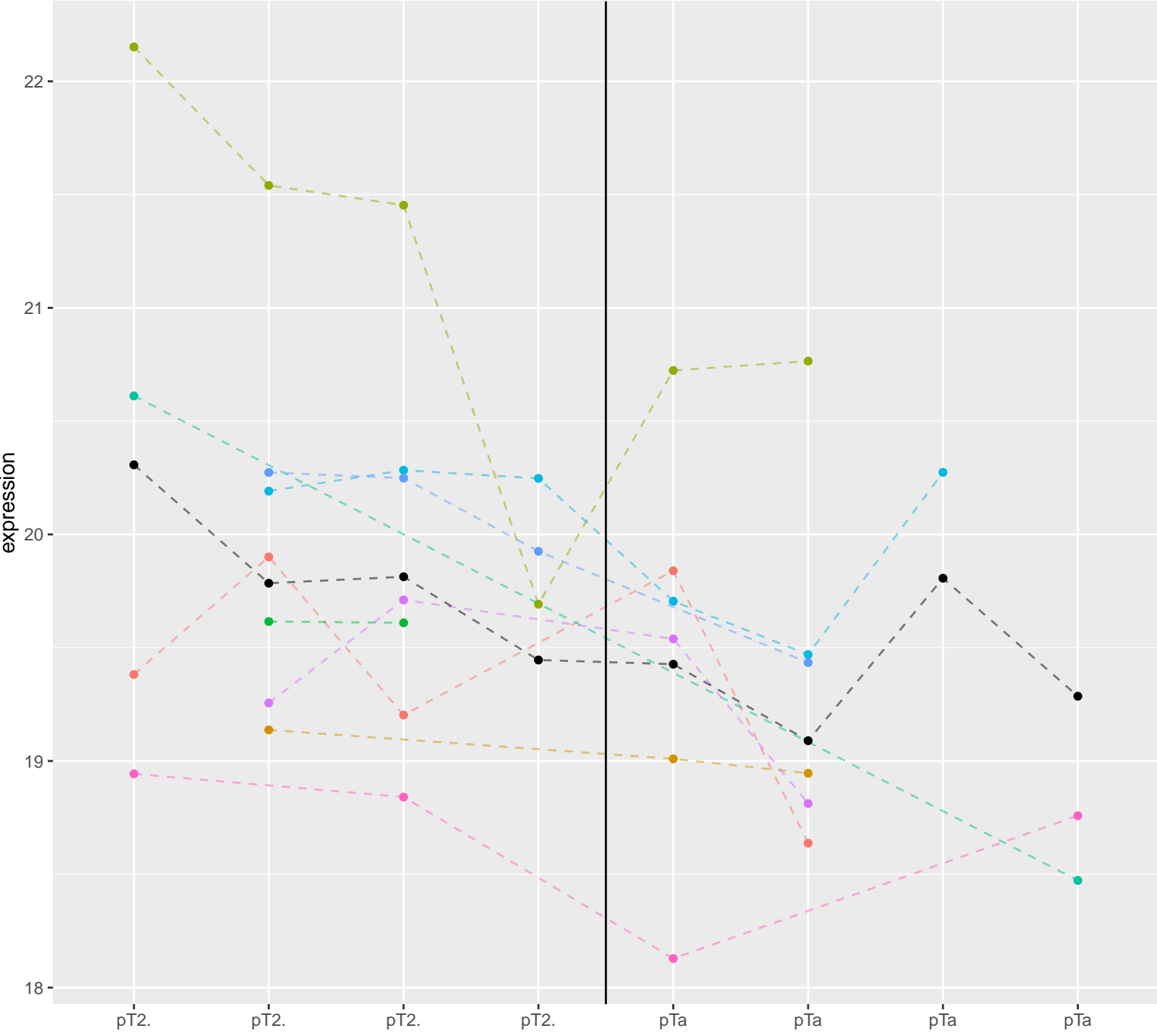
sp|O00515|LAD1_HUMANLadinin-1

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



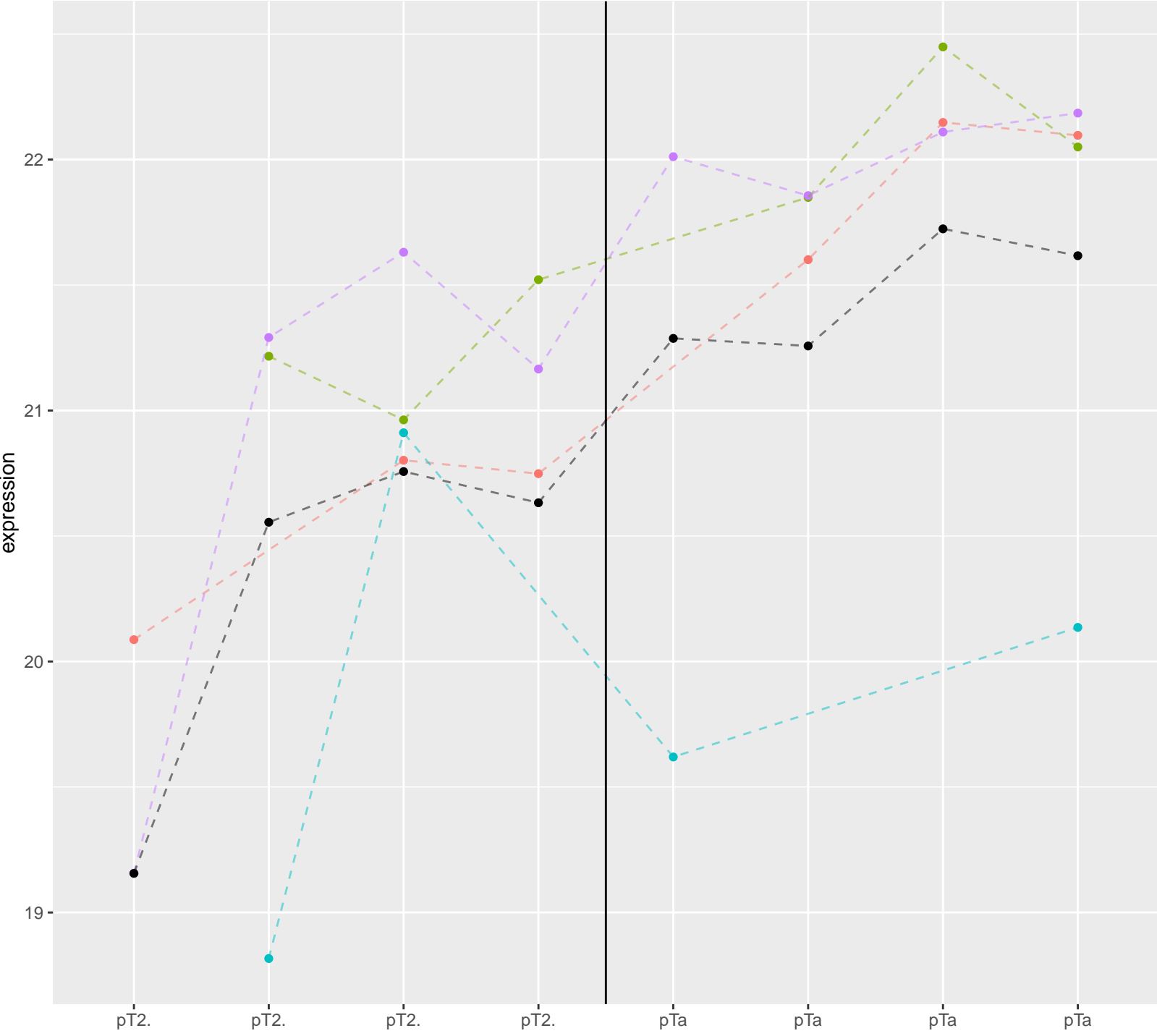
sp|O75131|CPNE3_HUMANCopine-3

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



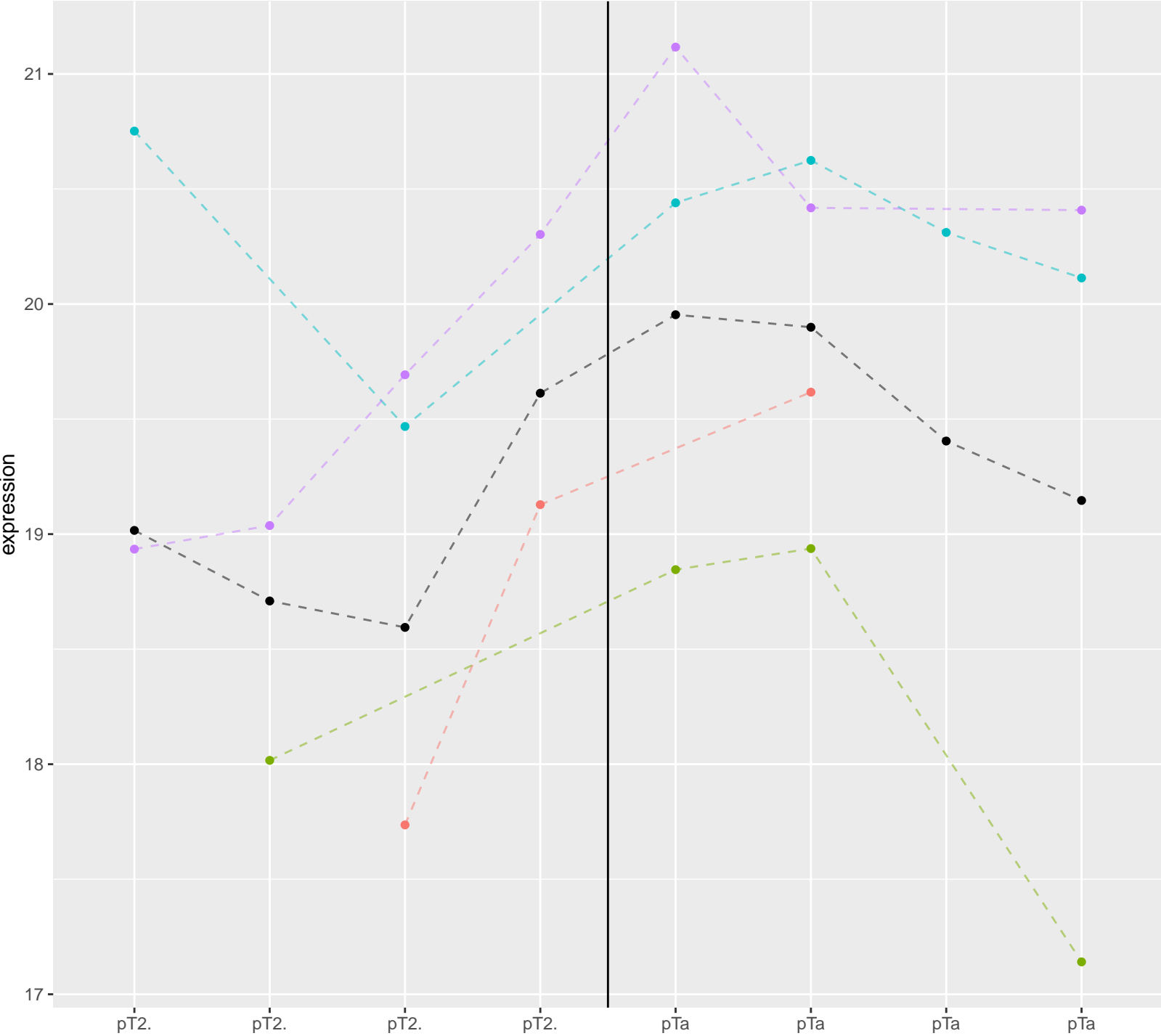
sp|O75608|LYPA1_HUMANAcyl-proteinthioesterase1

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



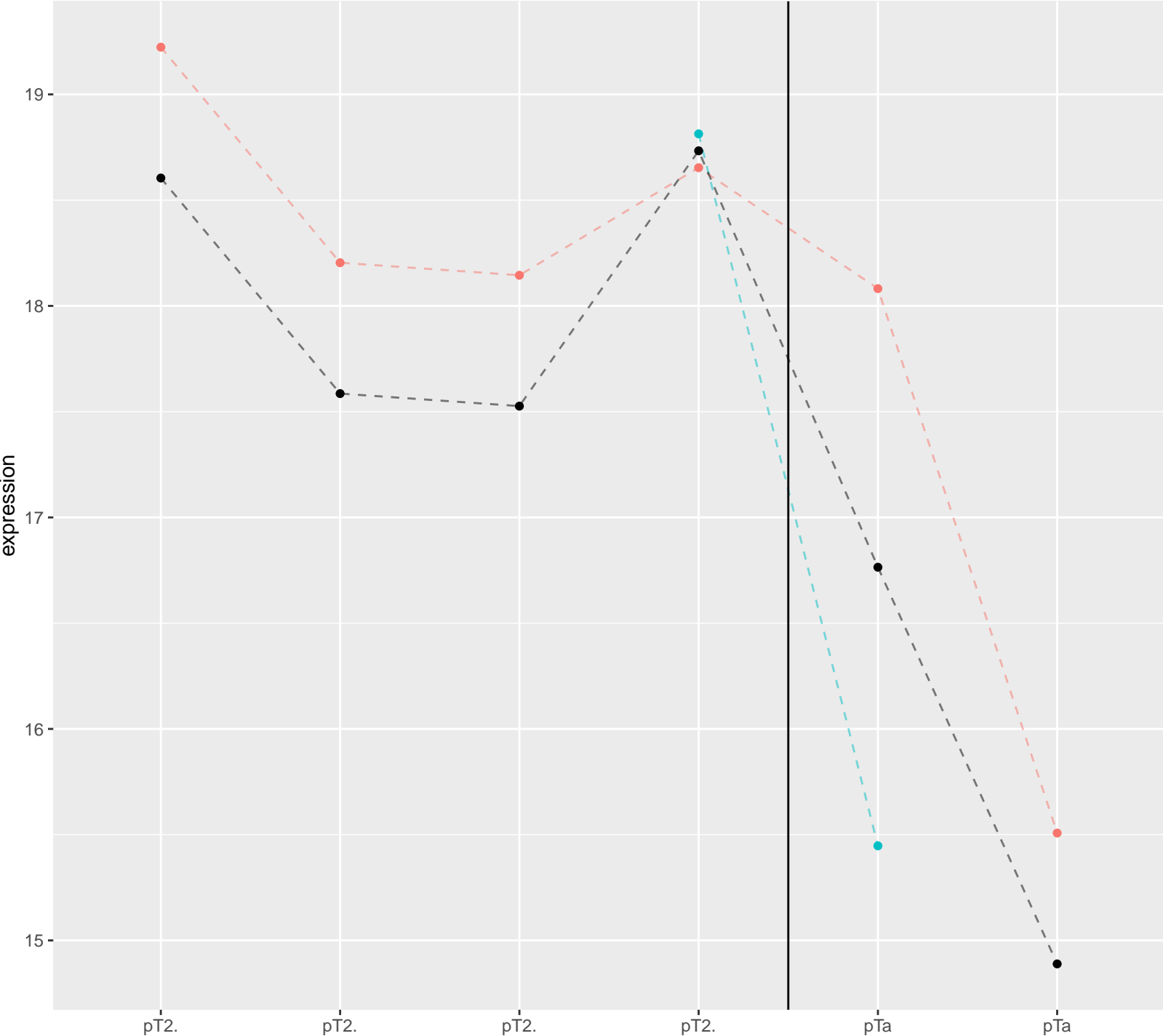
sp|O94905|ERLN2_HUMANErln-2

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



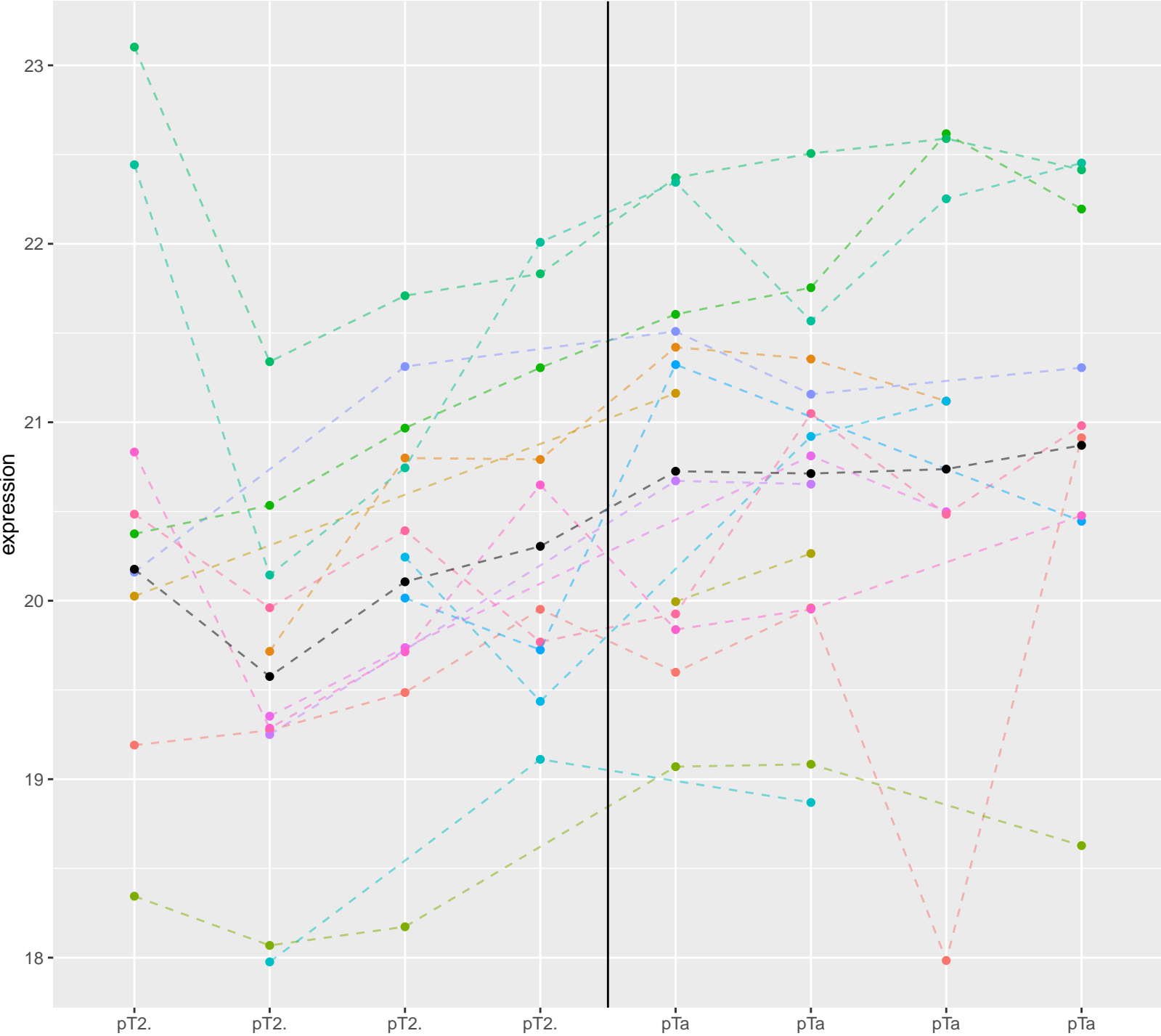
sp|O96005|CLPT1_HUMANClleftlipandpalatetransmembraneprotein1

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



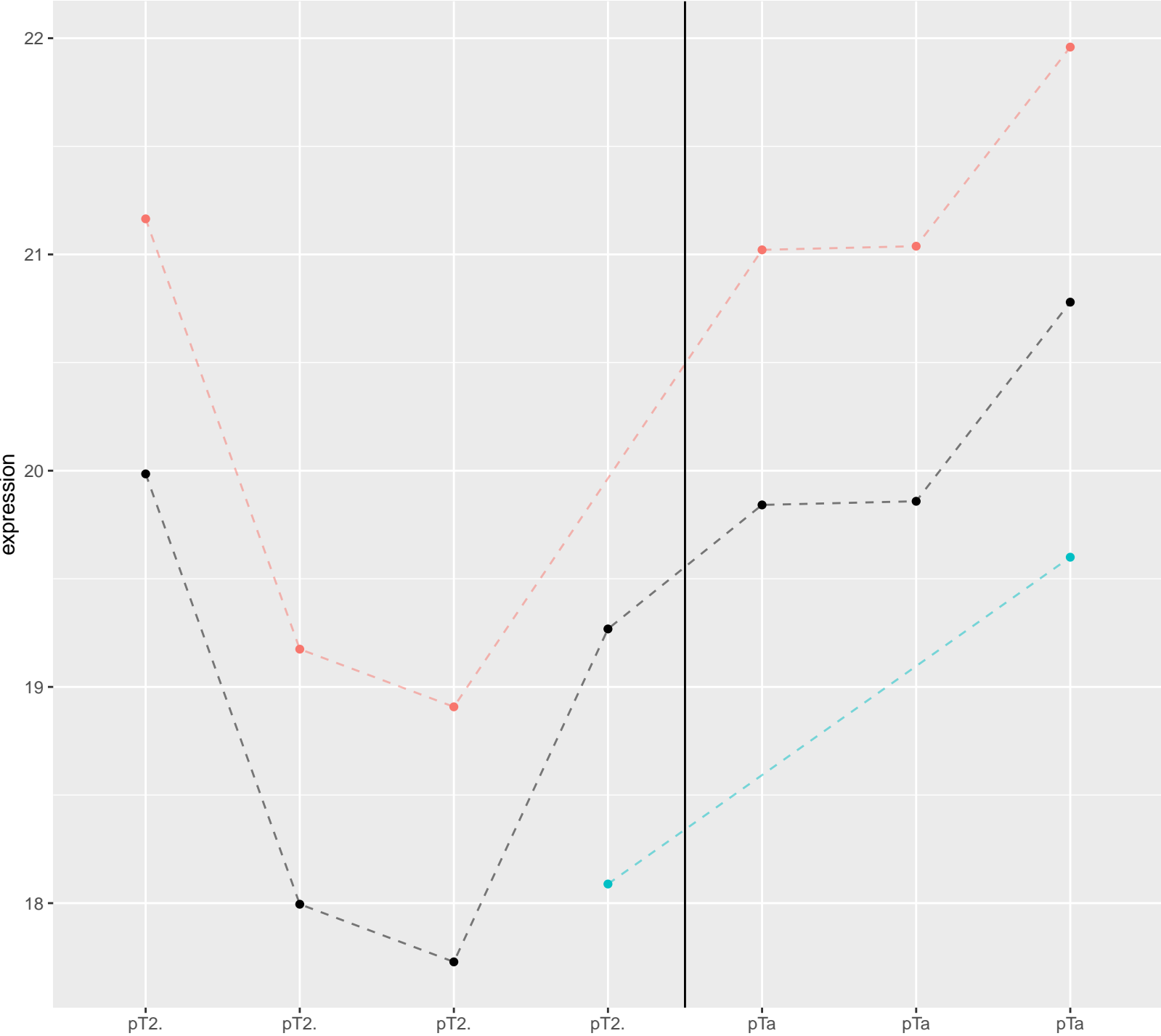
sp|P00505|AATM_HUMANAspartateaminotransferase,mitochondrial

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|P02656|APOC3_HUMANApolipoproteinC-III

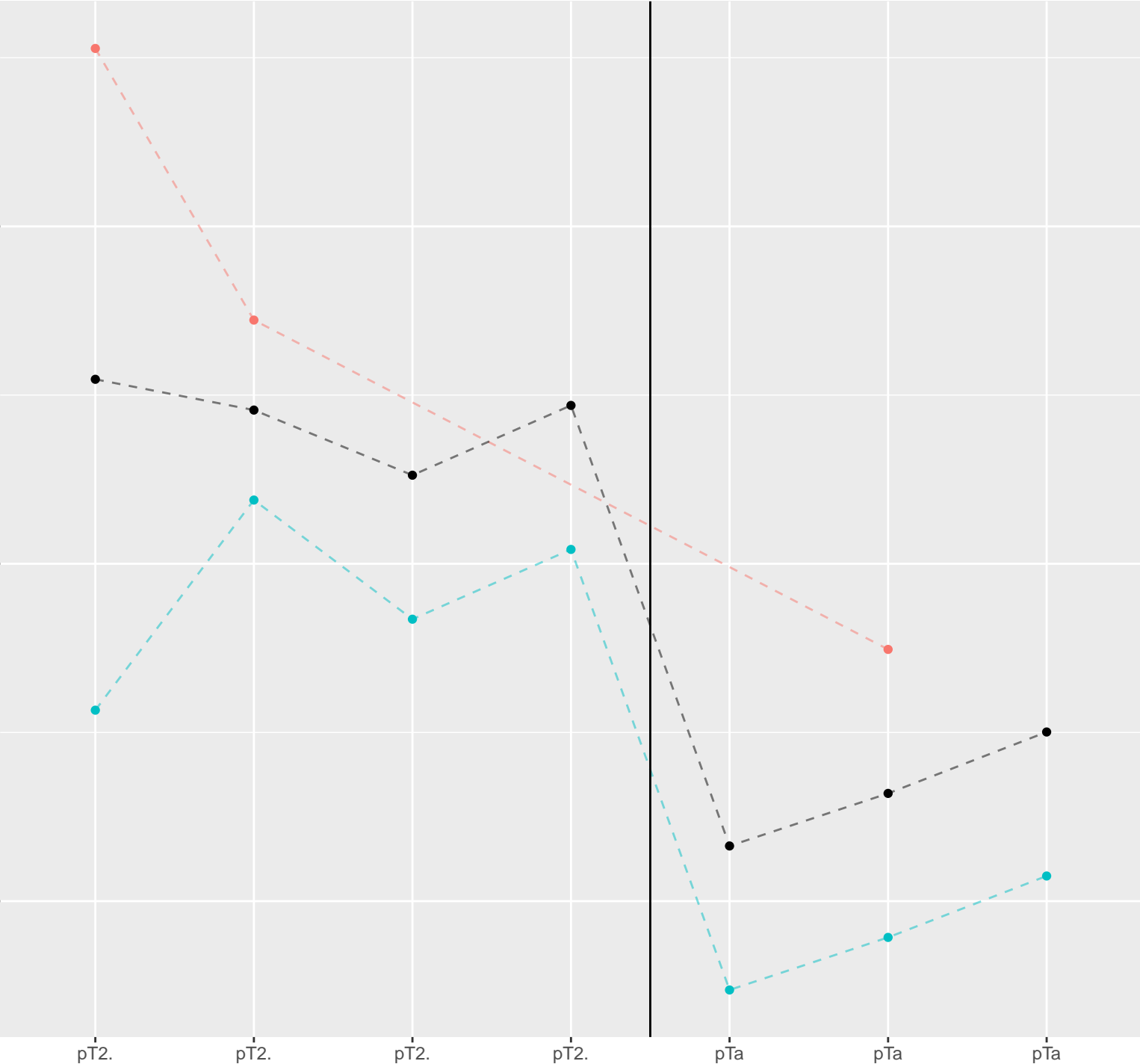
method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	2.9	1.71	5.63	7.52	0.304		0
msqrobsum	65.5	1.09	2.13	8.85	0.511		NA



sp|P08195|4F2_HUMAN4F2cell-surfaceantigenheavychain

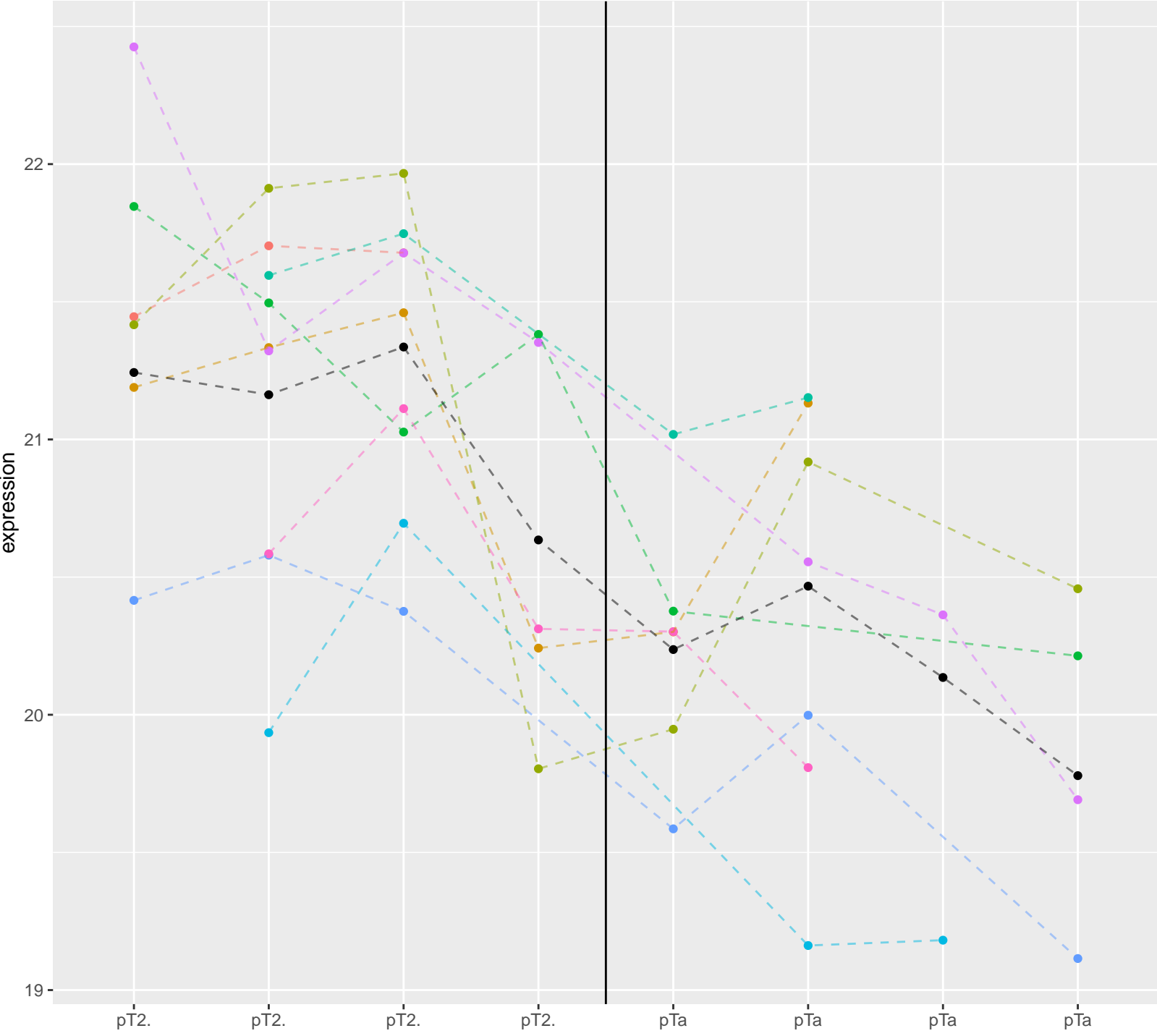
method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	1.5	-1.05	-5.61	9.57	0.187		0
msqrobsum	23.8	-1.09	-4.06	8.63	0.269		NA

expression



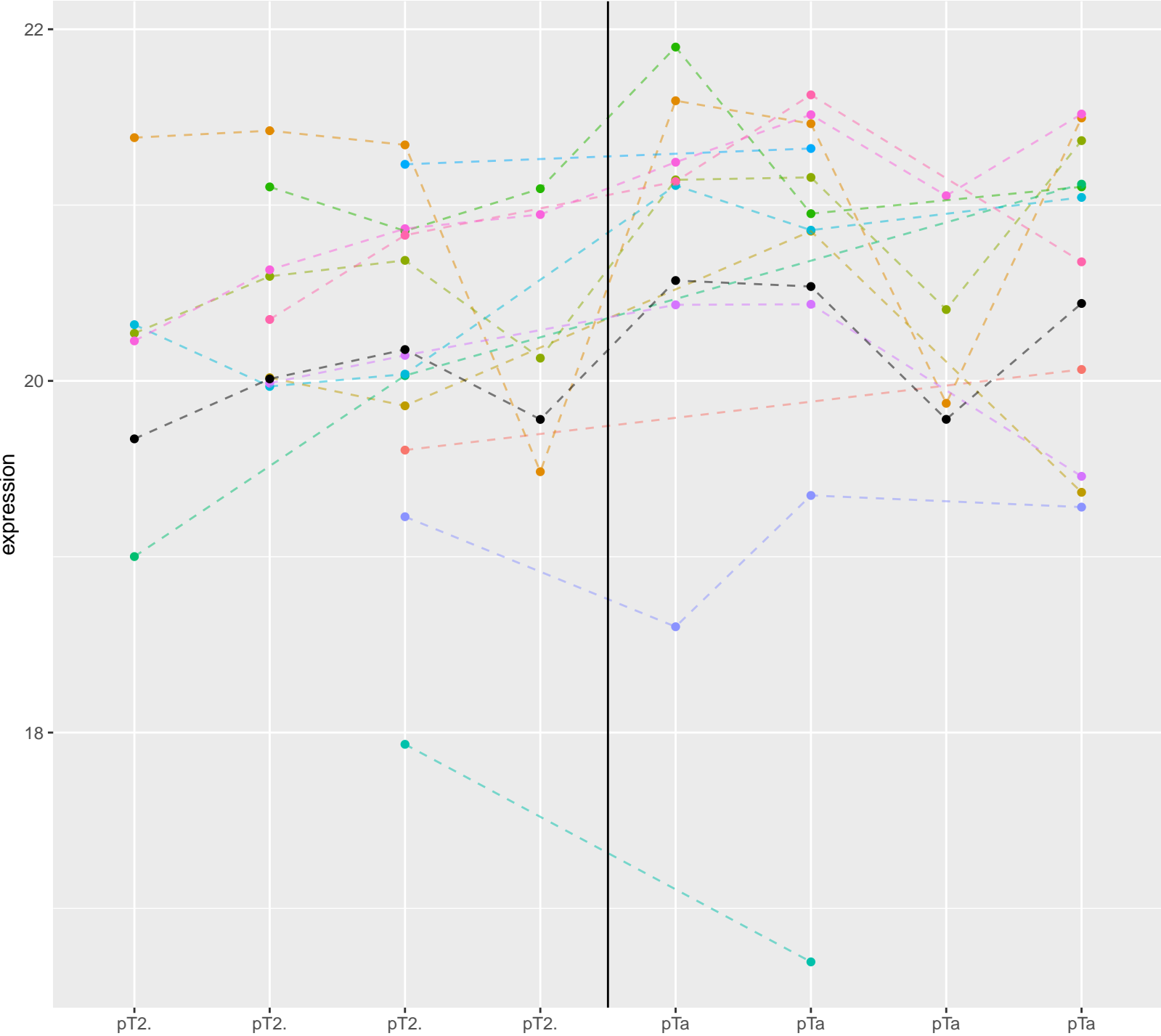
sp|P12004|PCNA_HUMANProliferatingcellnuclearantigen

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



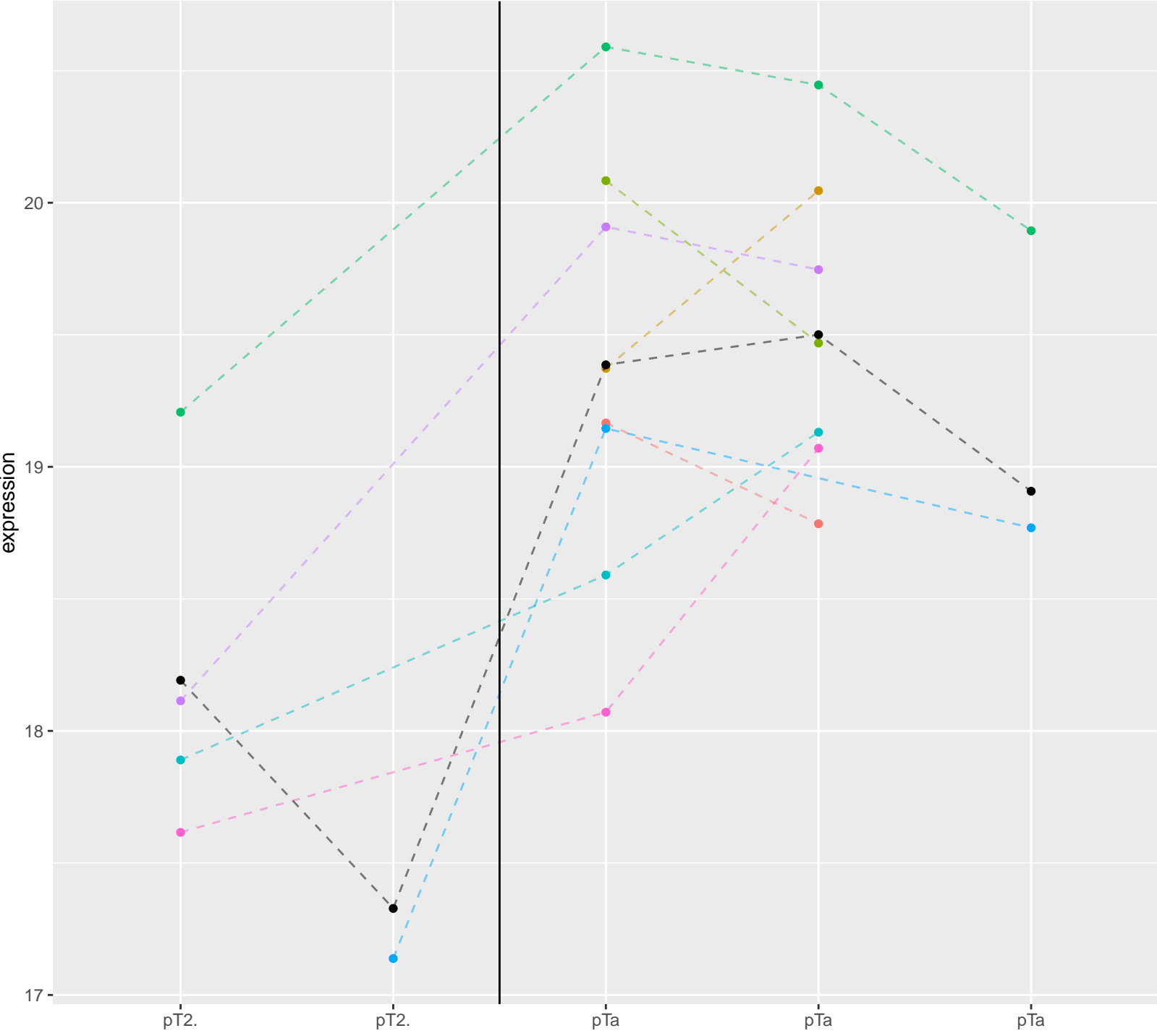
sp|P13489|RINI_HUMANRibonucleaseinhibitor

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



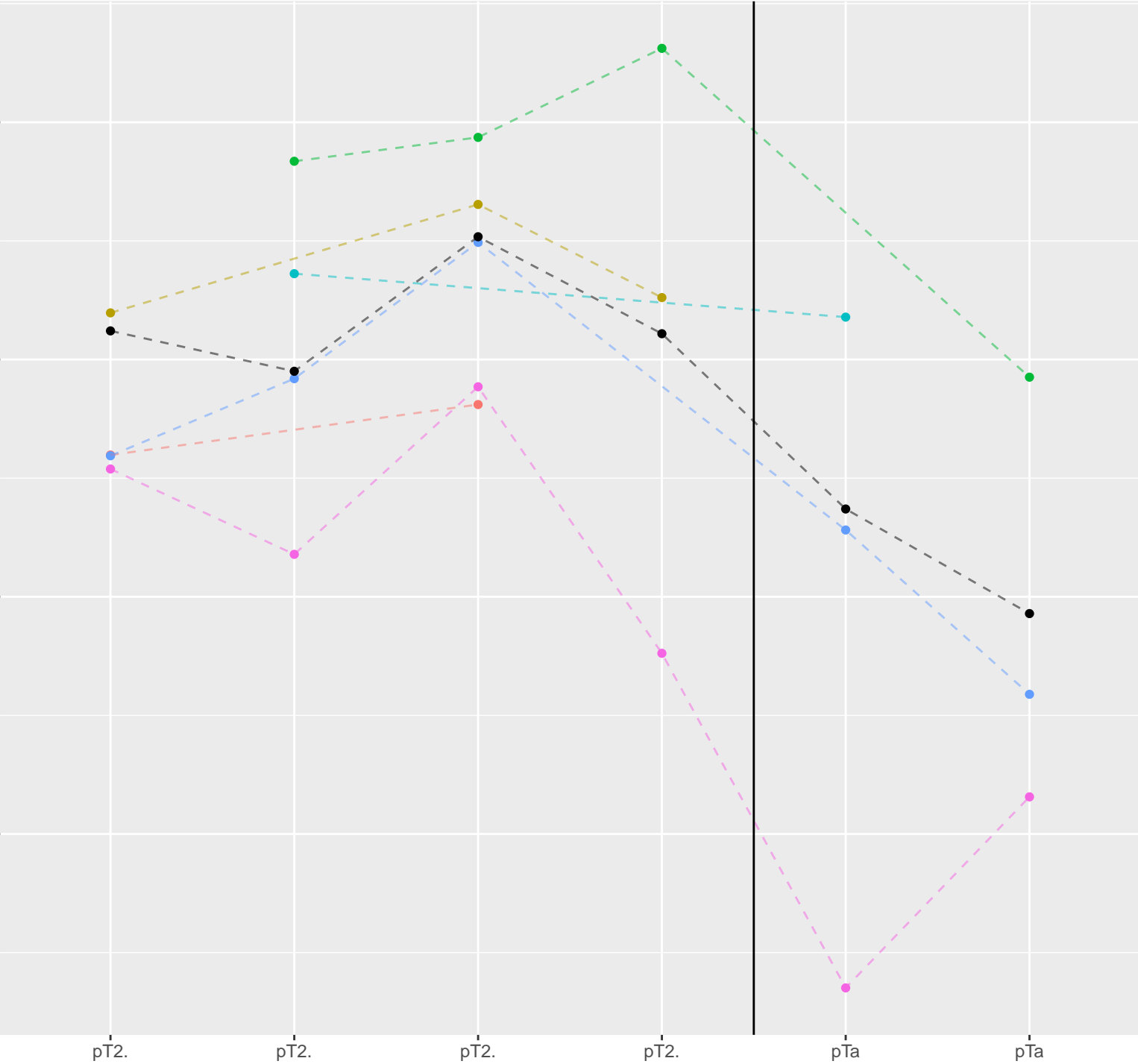
sp|P16144|ITB4_HUMANIntegrinbeta-4

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



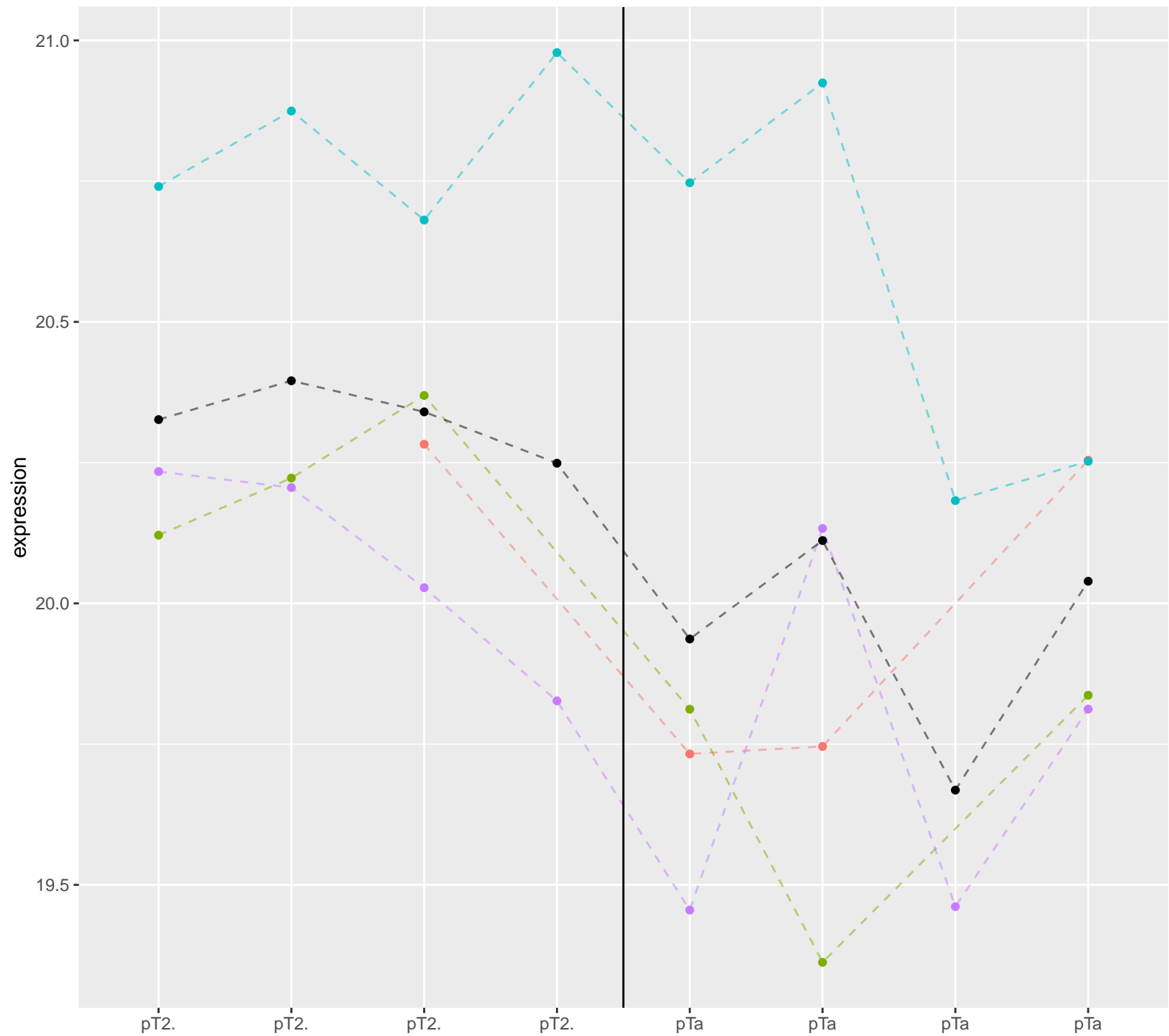
sp|P25205|MCM3_HUMAN|DNA replication licensing factor MCM3

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



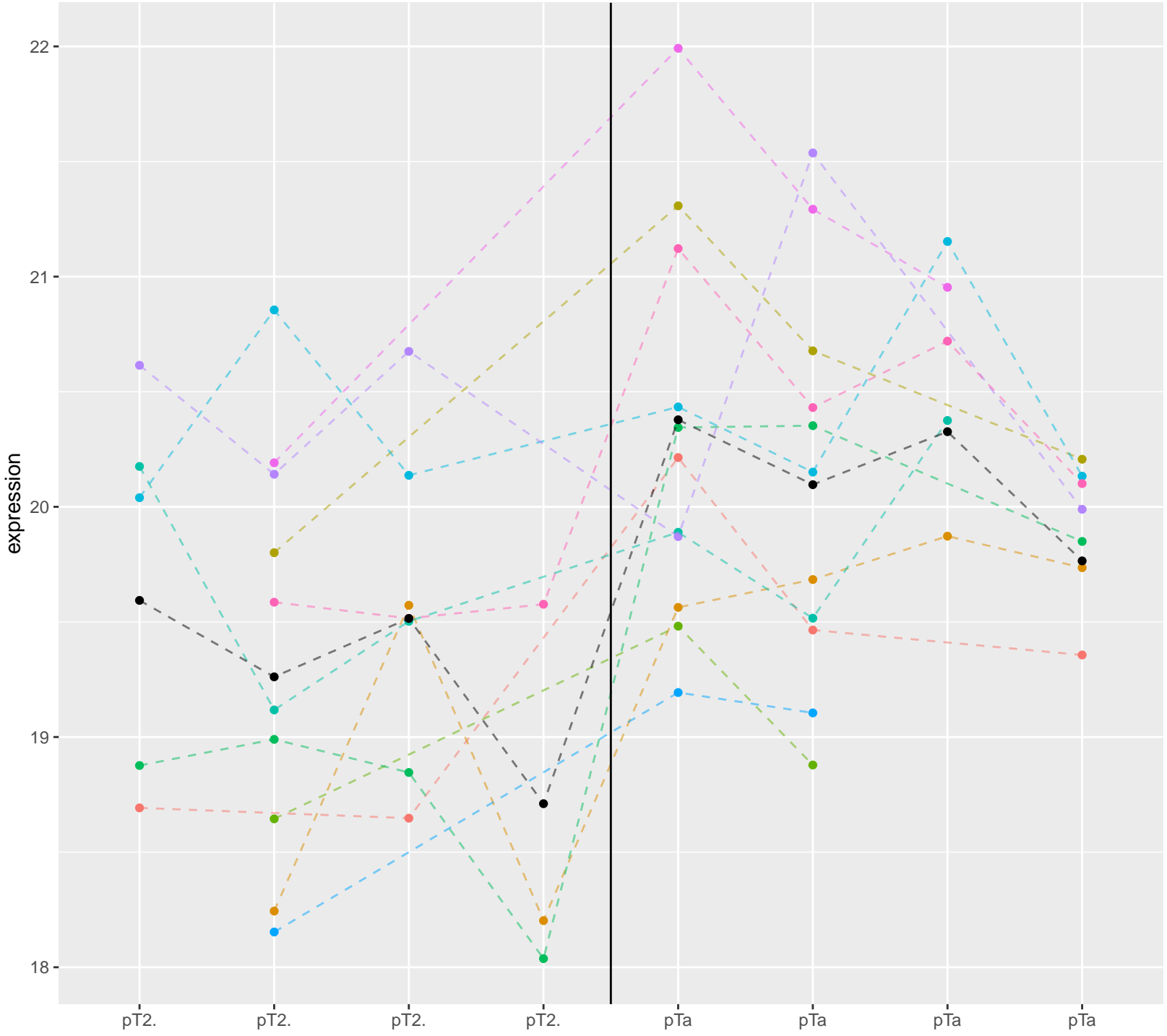
sp|P49720|PSB3_HUMANProteasomesubunitbetatype-3

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



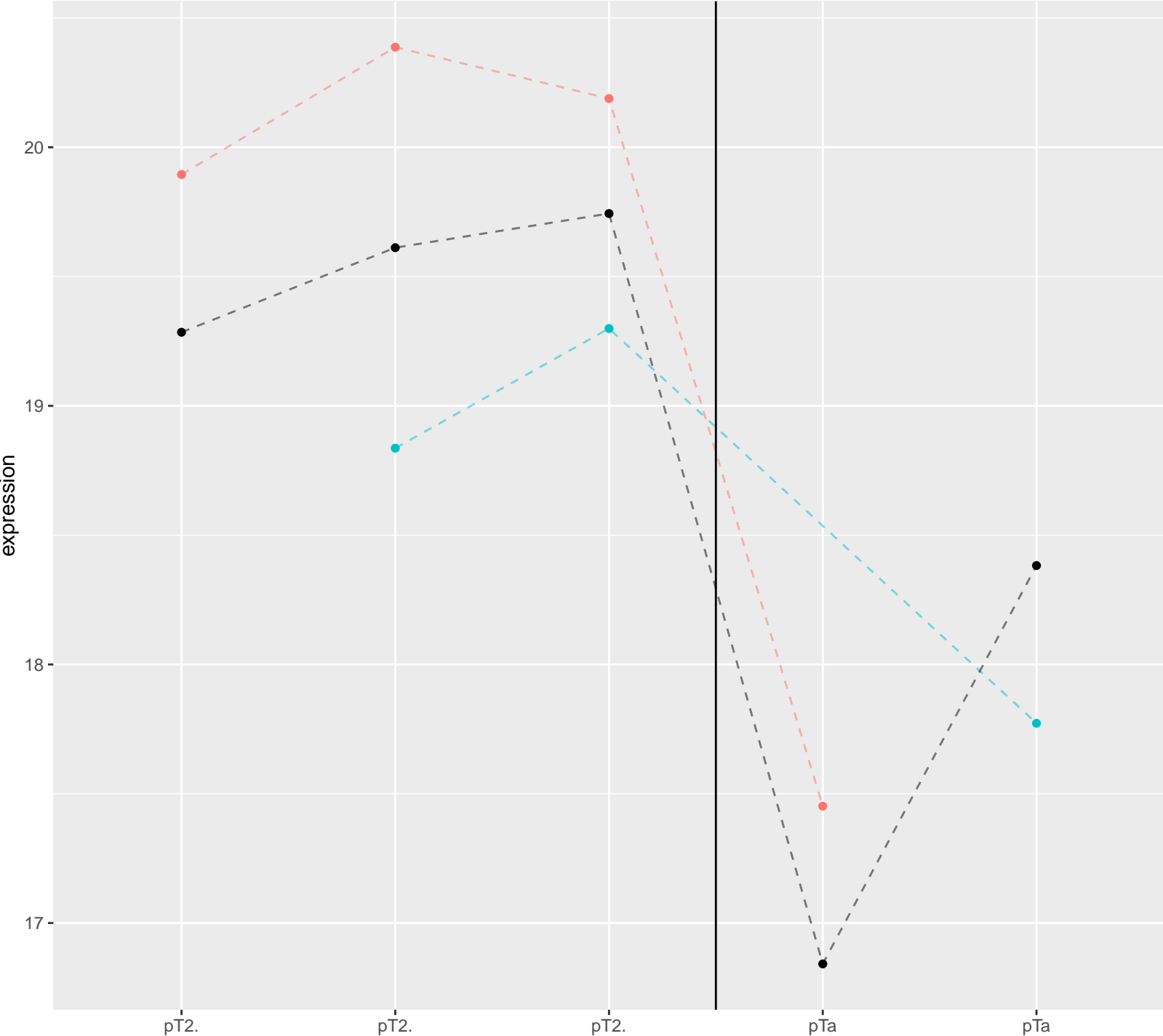
sp|P50570|DYN2_HUMANDynammin-2

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



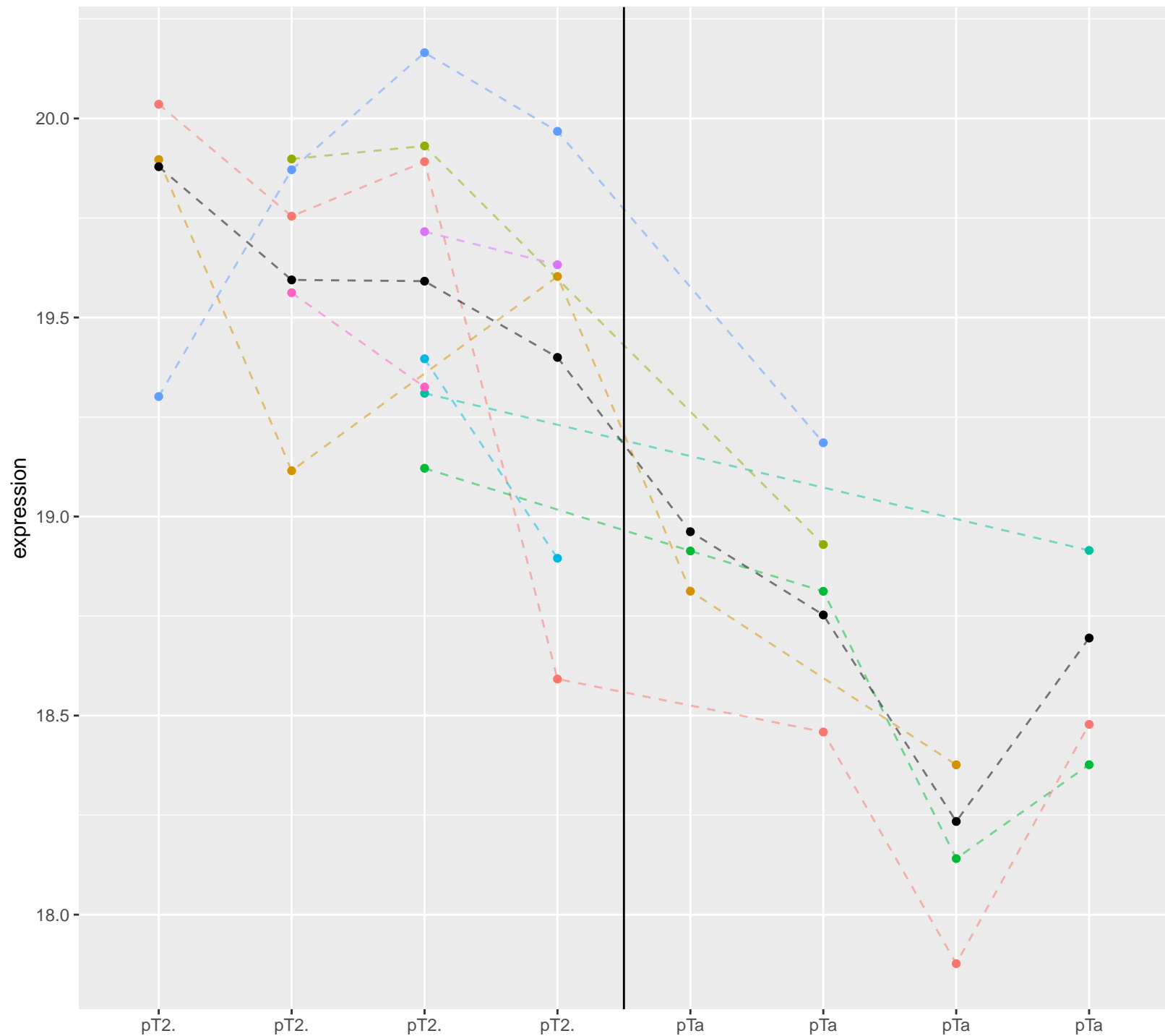
sp|P52292|HMA1_HUMANImportinsubunitalpha-1

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



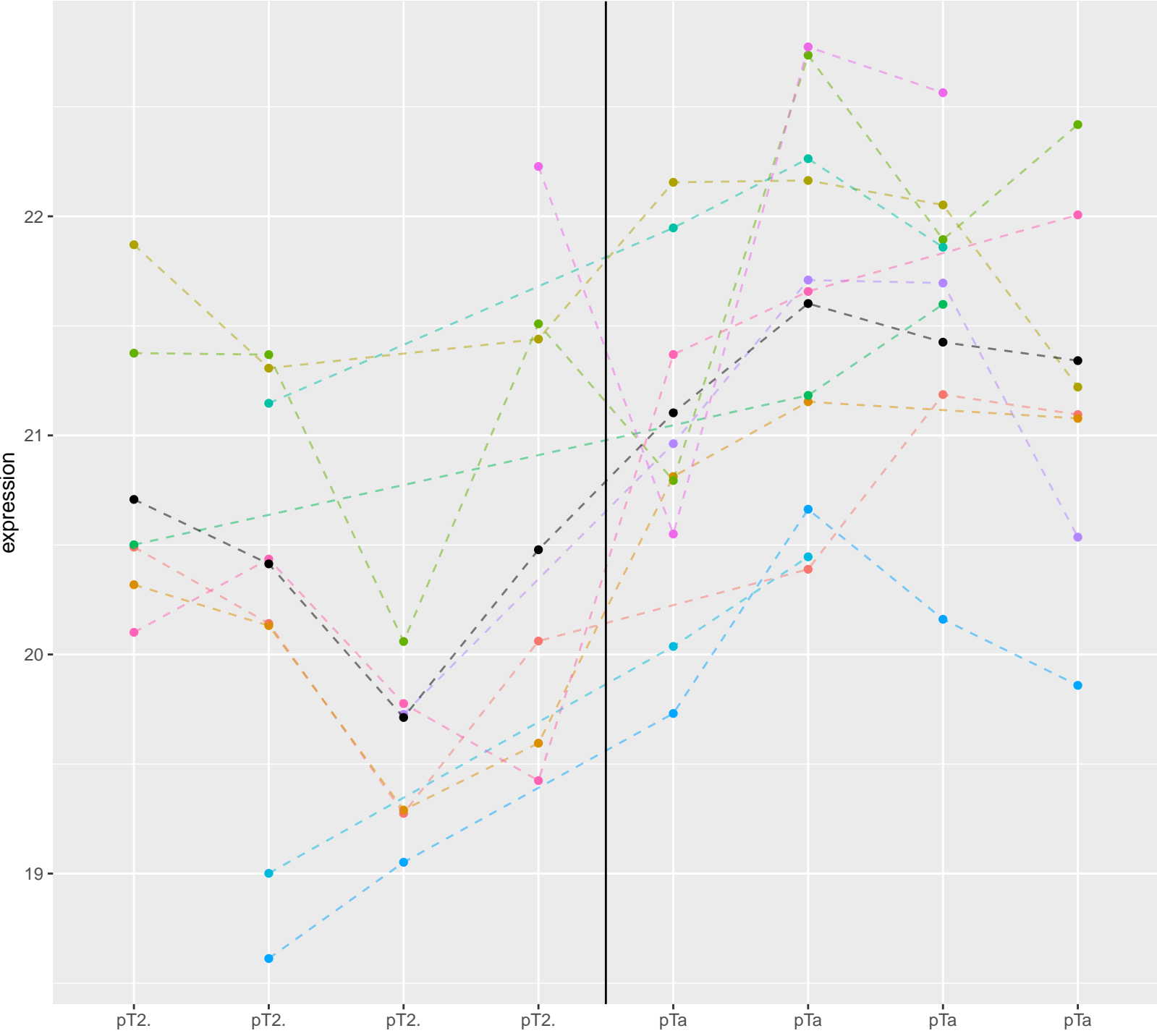
sp|P54577|SYYC_HUMANTyrosine--tRNA ligase, cytoplasmic

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|P78417|GSTO1_HUMANGlutathioneS-transferaseomega-1

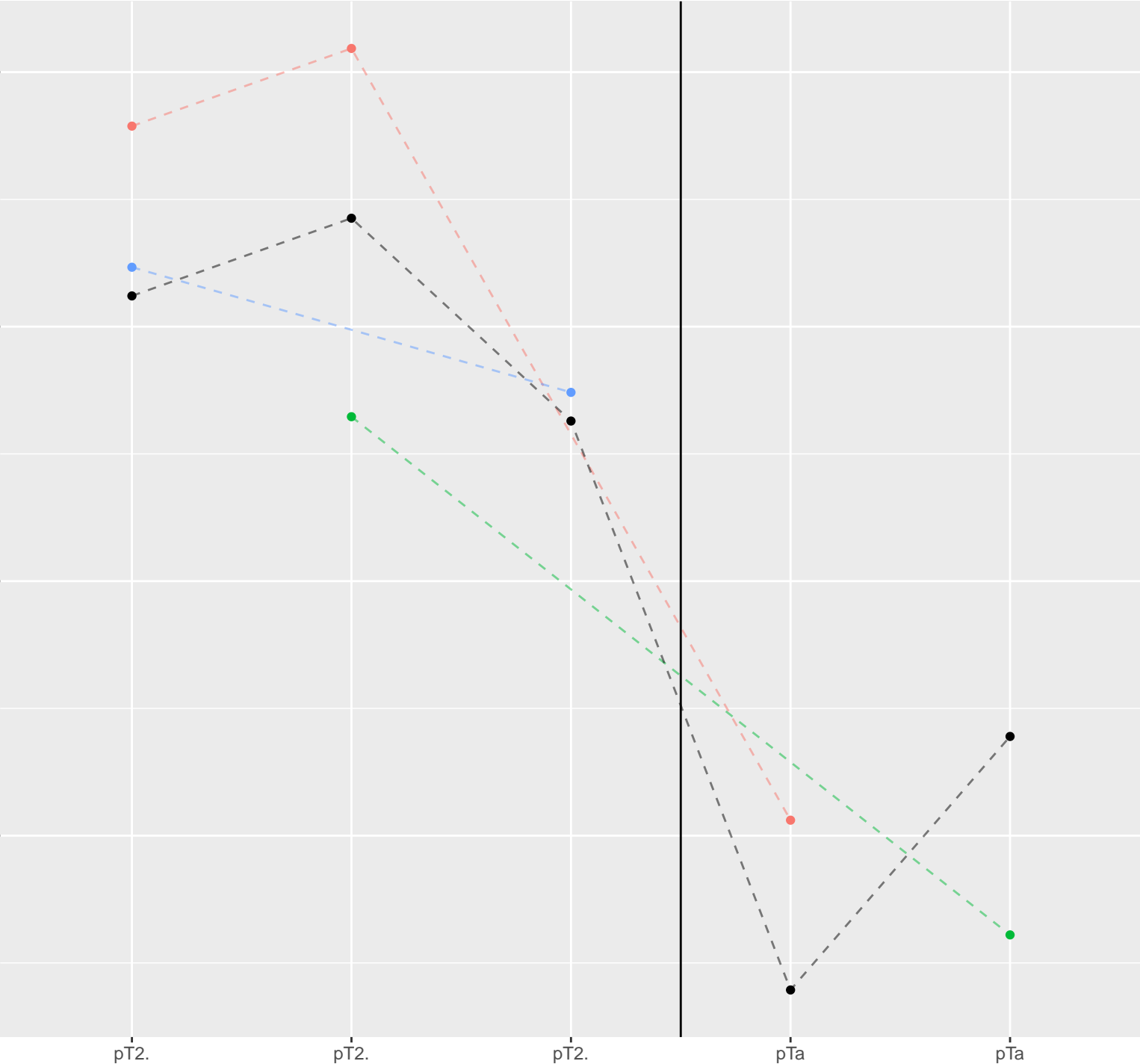
method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	0.3	0.997	4.75	47.4	0.21		0.715
msqrobsum	36	0.918	3.39	9.67	0.271		NA



sp|Q06828|FMOD_HUMANFibromodulin

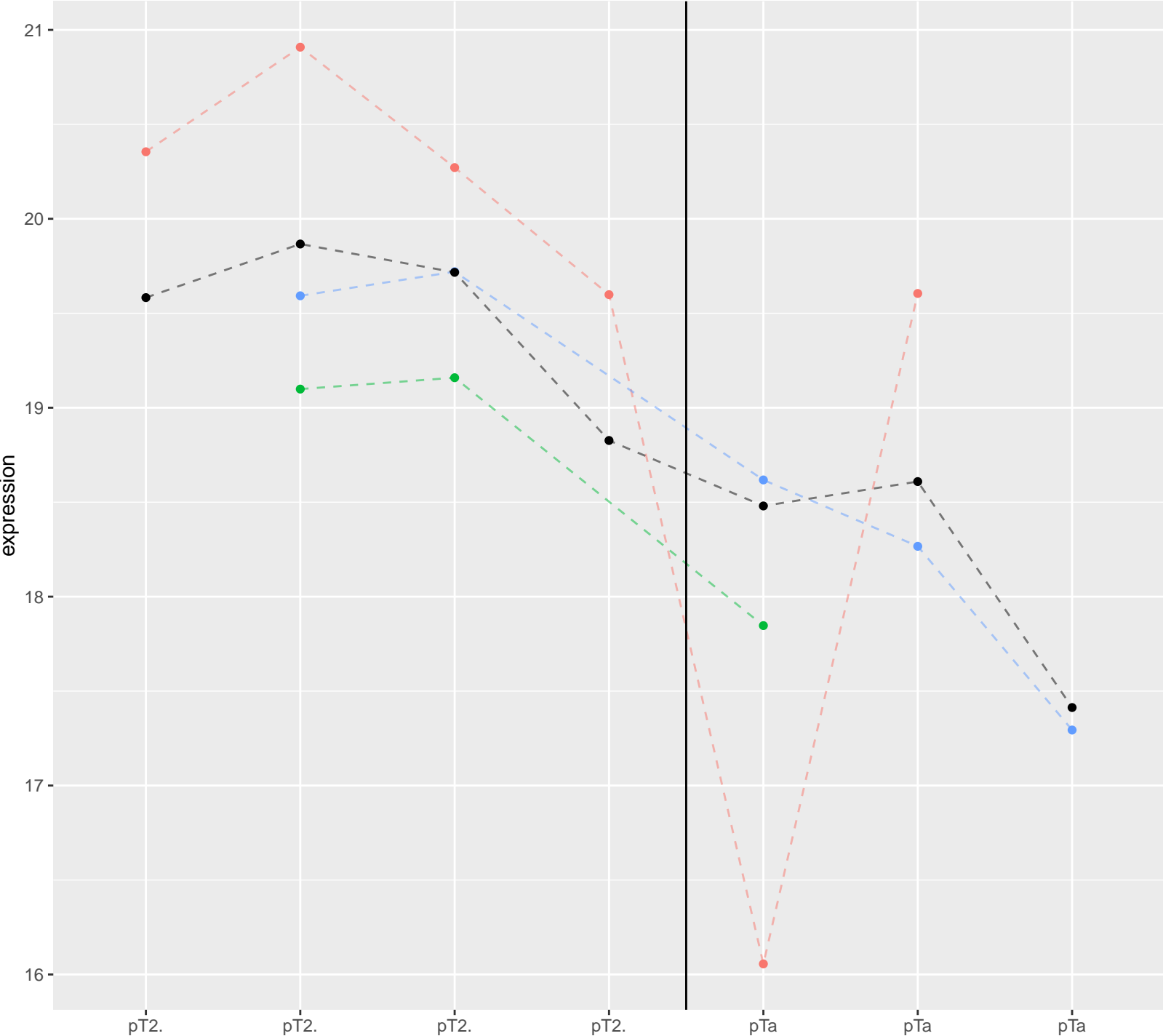
method	q-value	log fold change	t-value	df	se	theta	sample
msqrob	1.4	-2.47	-7.8	5.94	0.317		0
msqrobsum	24	-2.06	-4.44	6.67	0.465		NA

expression



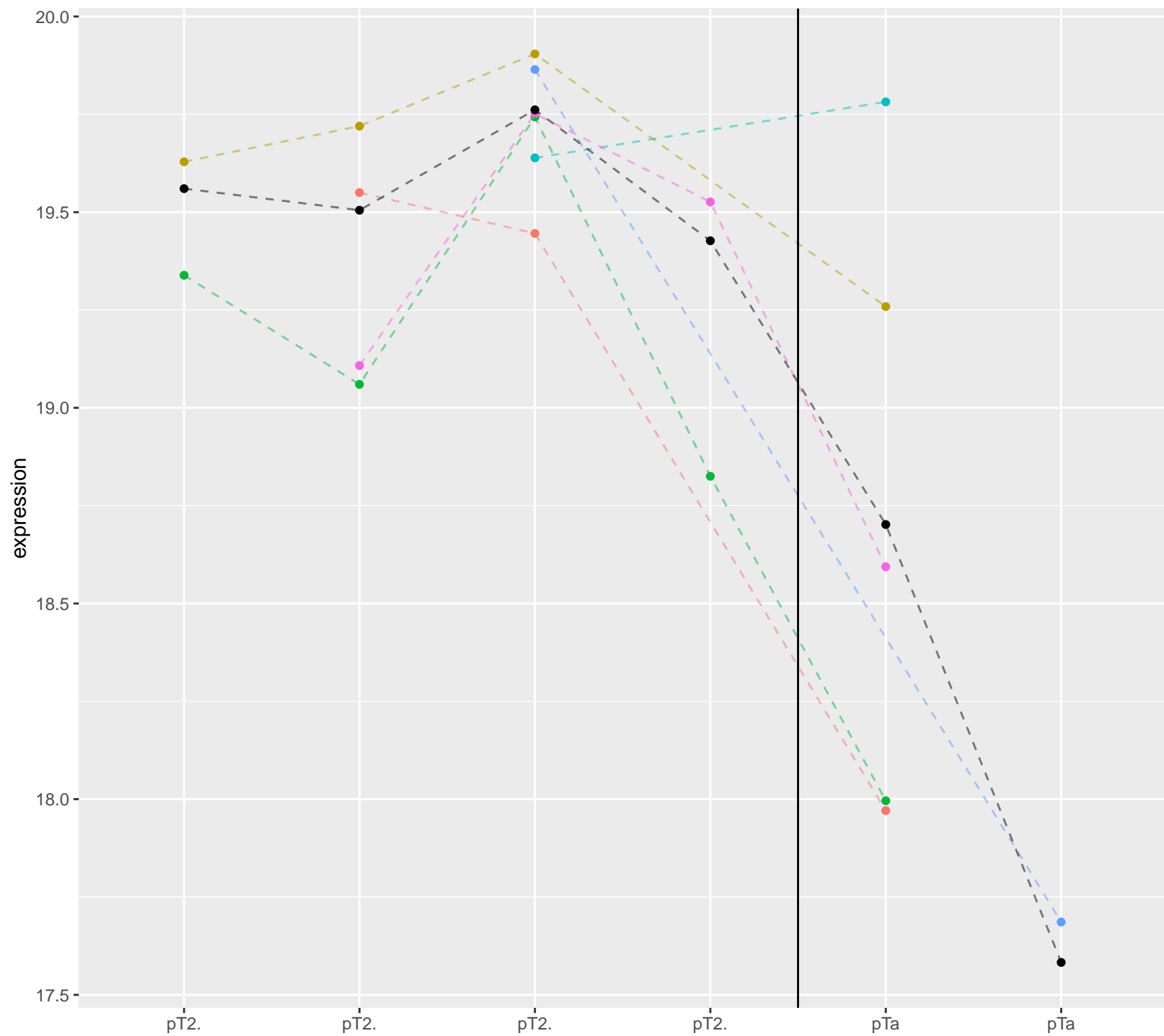
sp|Q13057|COASY_HUMANBifunctionalcoenzymeAsynthase

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



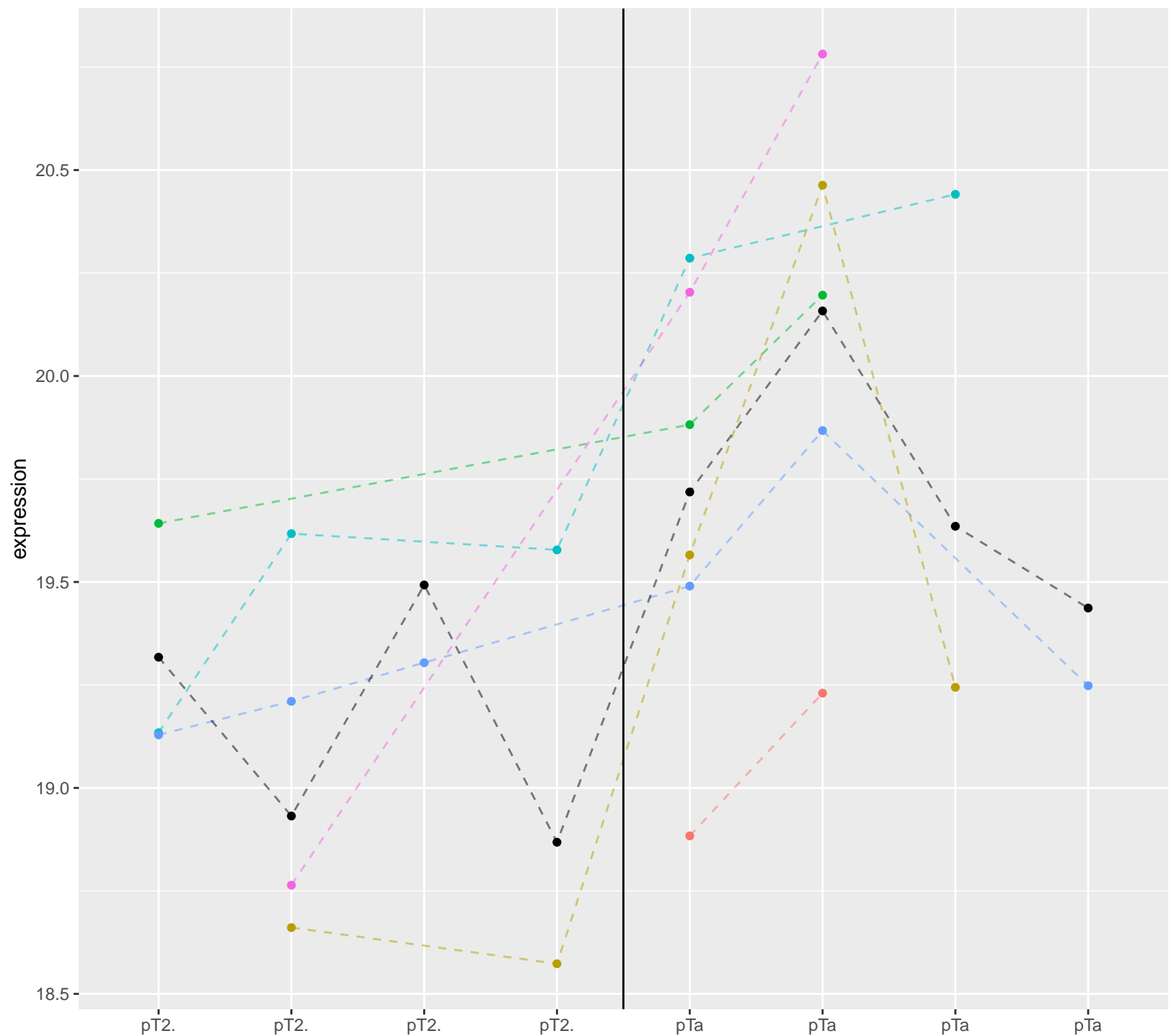
sp|Q14566|MCM6_HUMANDNAreplicationlicensingfactorMCM6

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



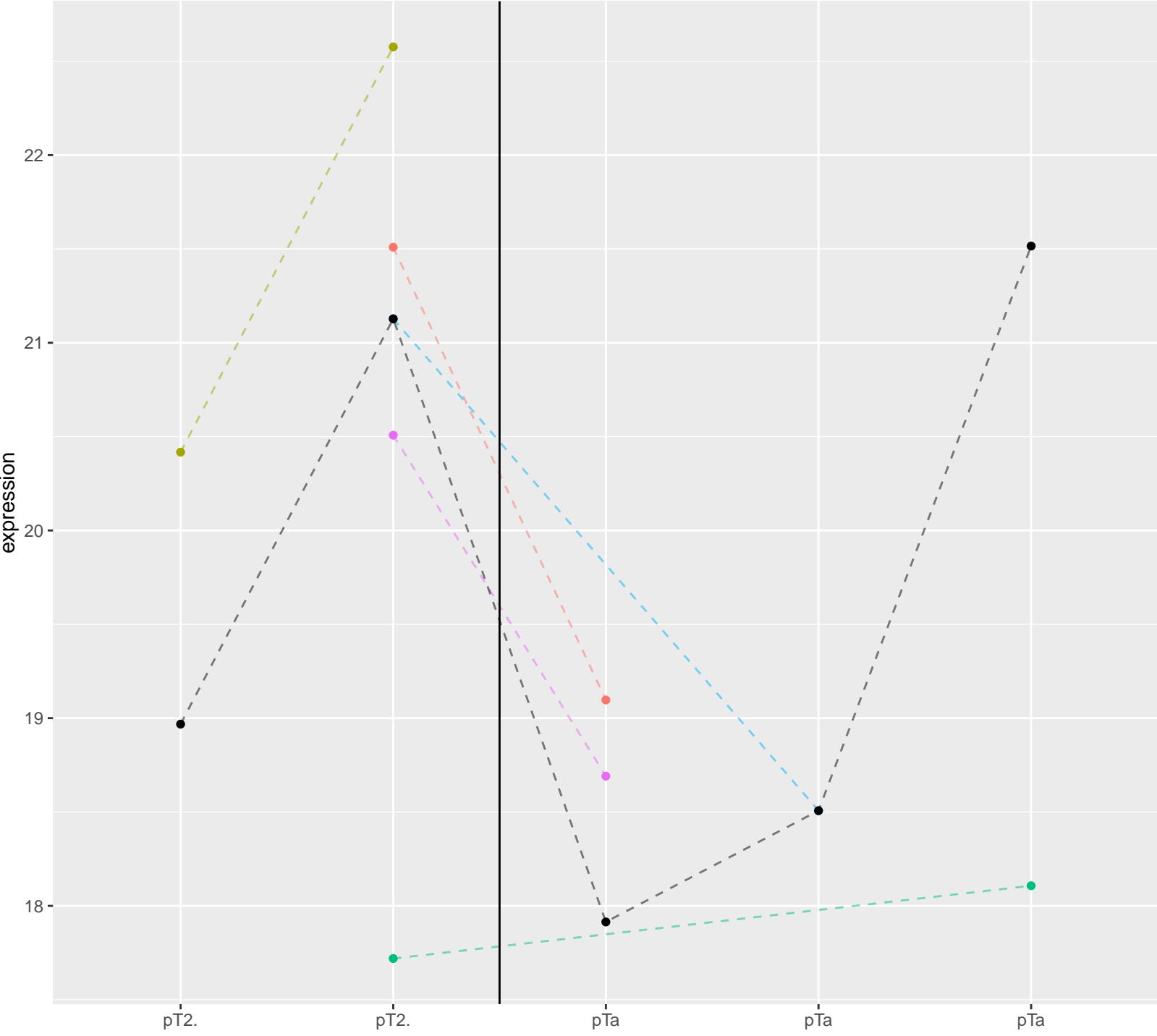
sp|Q5JTV8|TOIP1_HUMAN Torsin-1A-interacting protein1

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



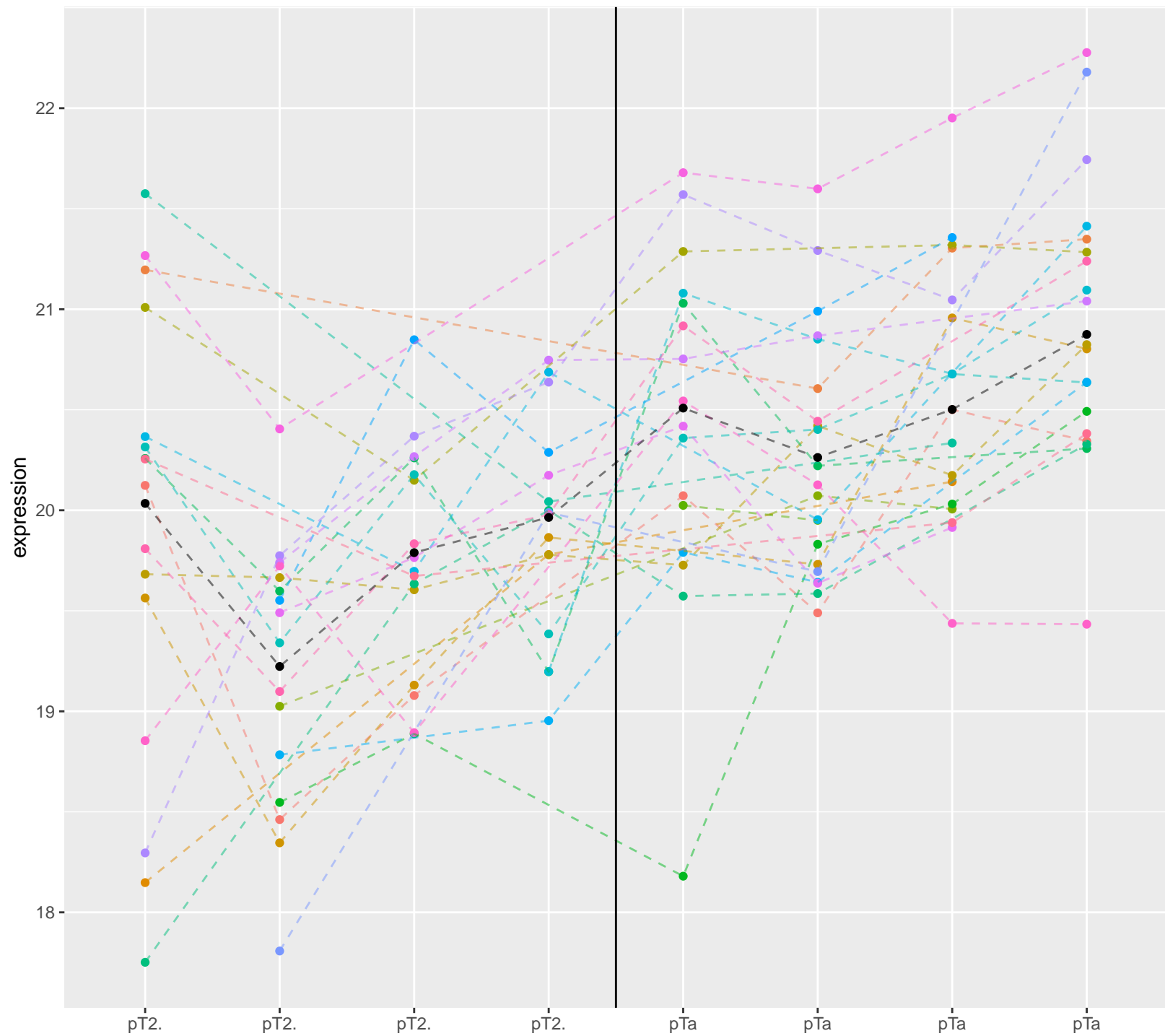
sp|Q7L5L3|GDPD3_HUMANGlycerophosphodiesterphosphodiesterasedomain-containingprotein3

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



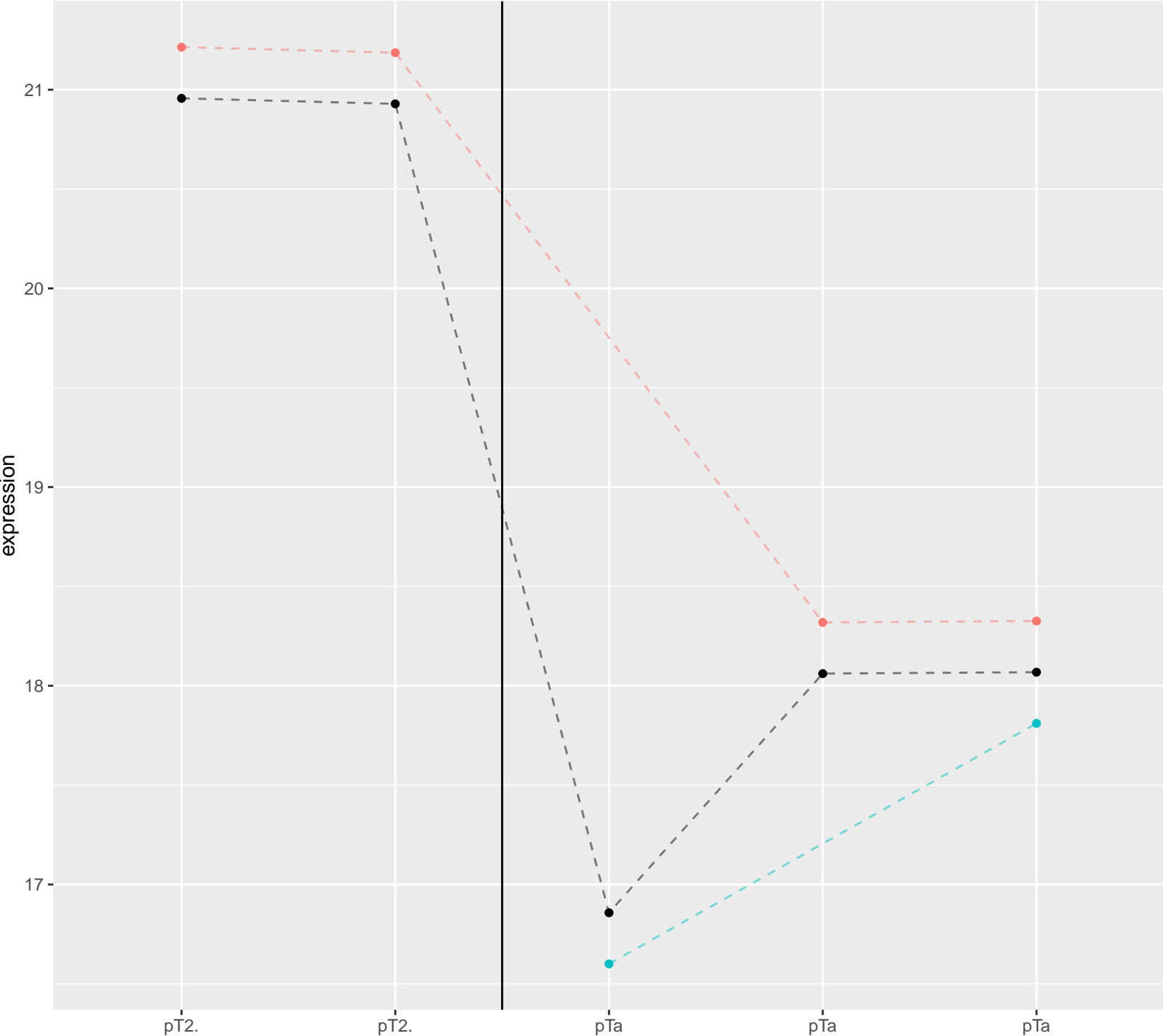
sp|Q8WUM4|PDC6I_HUMANProgrammedcelldeath6-interactingprotein

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



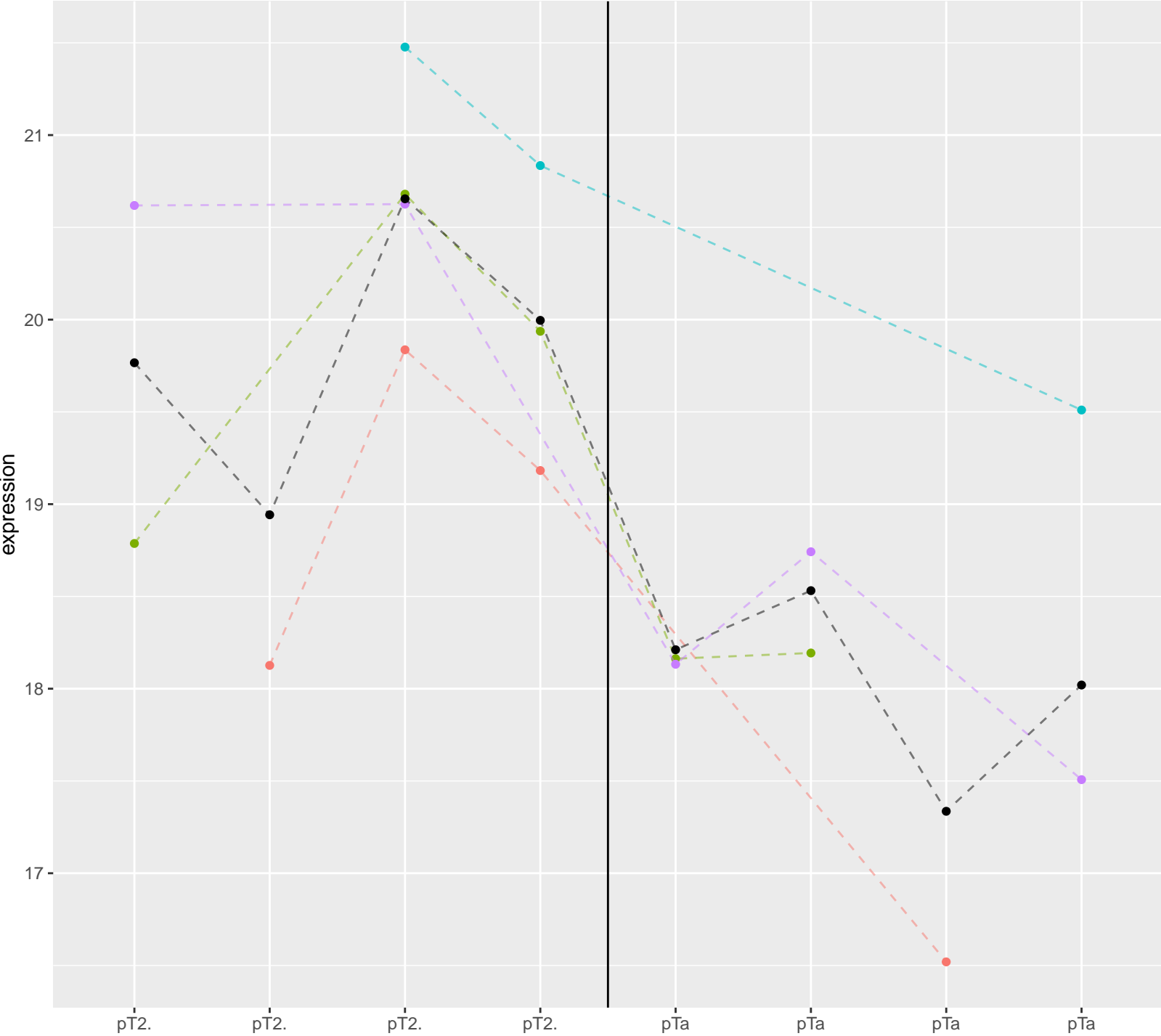
sp|Q8WWI1|LMO7_HUMANLIMdomainonlyprotein7

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



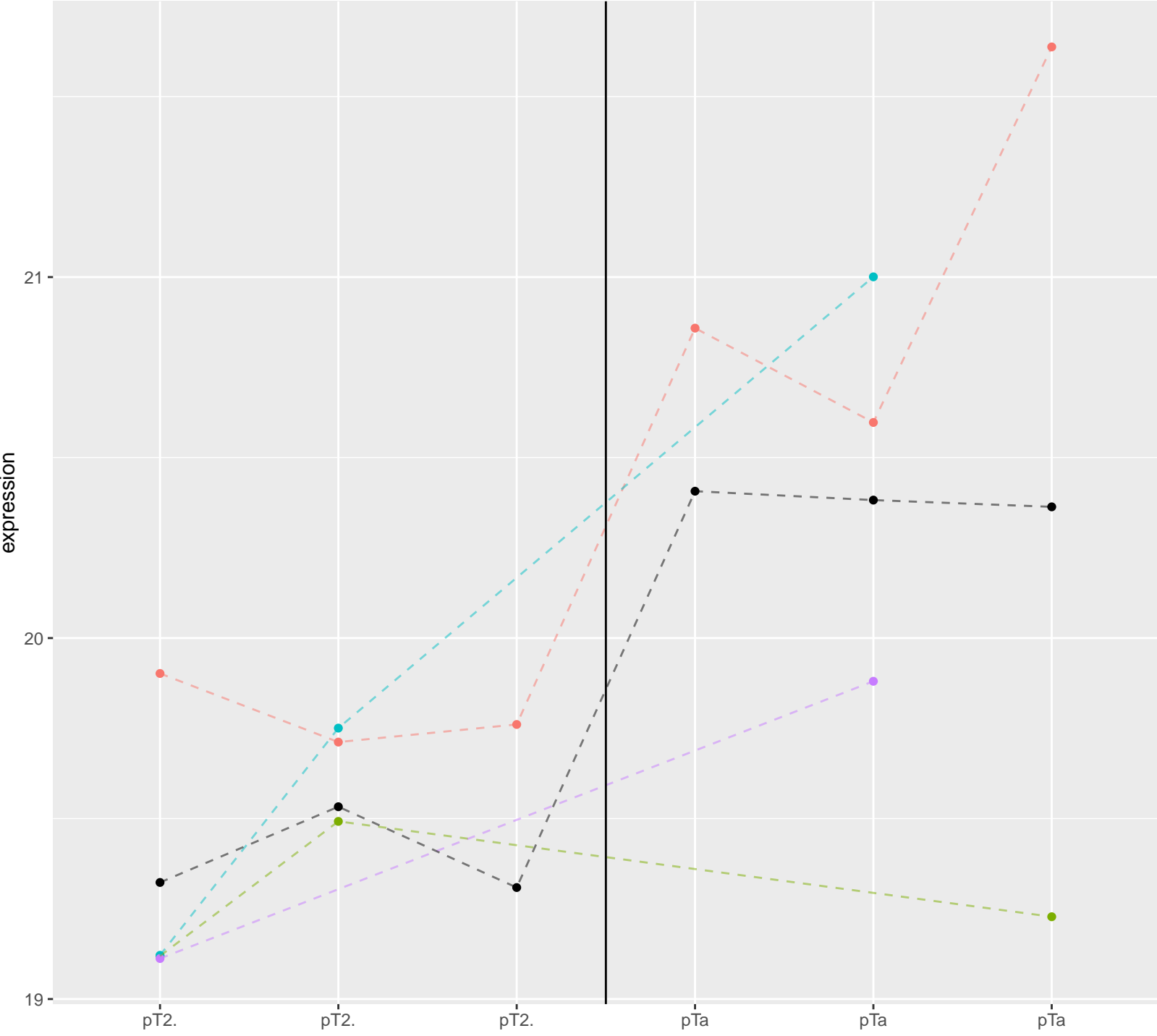
sp|Q92820|GGH_HUMANGamma-glutamylhydrolase

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



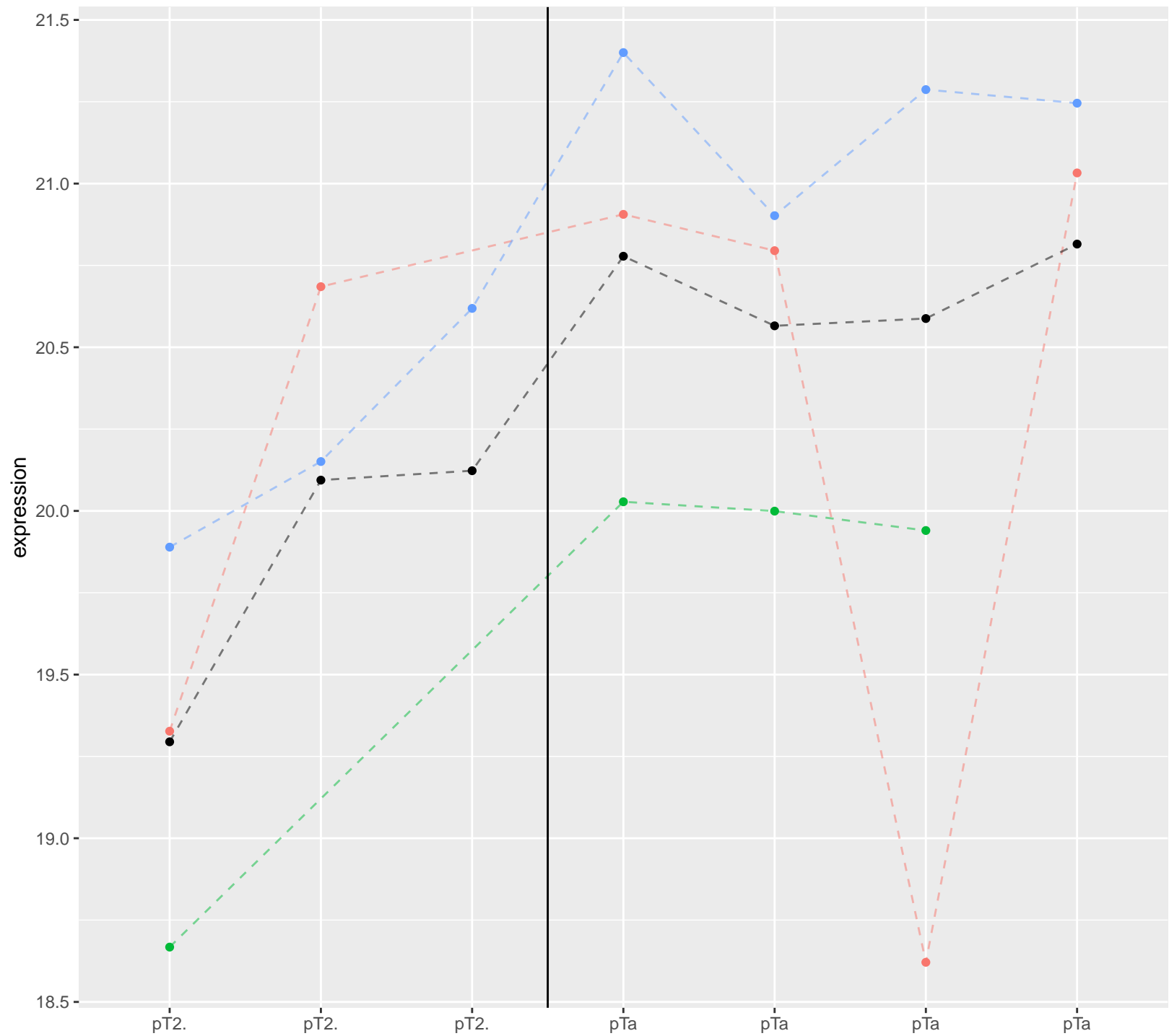
sp|Q99733|NP1L4_HUMANNucleosomeassemblyprotein1-like4

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|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|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

