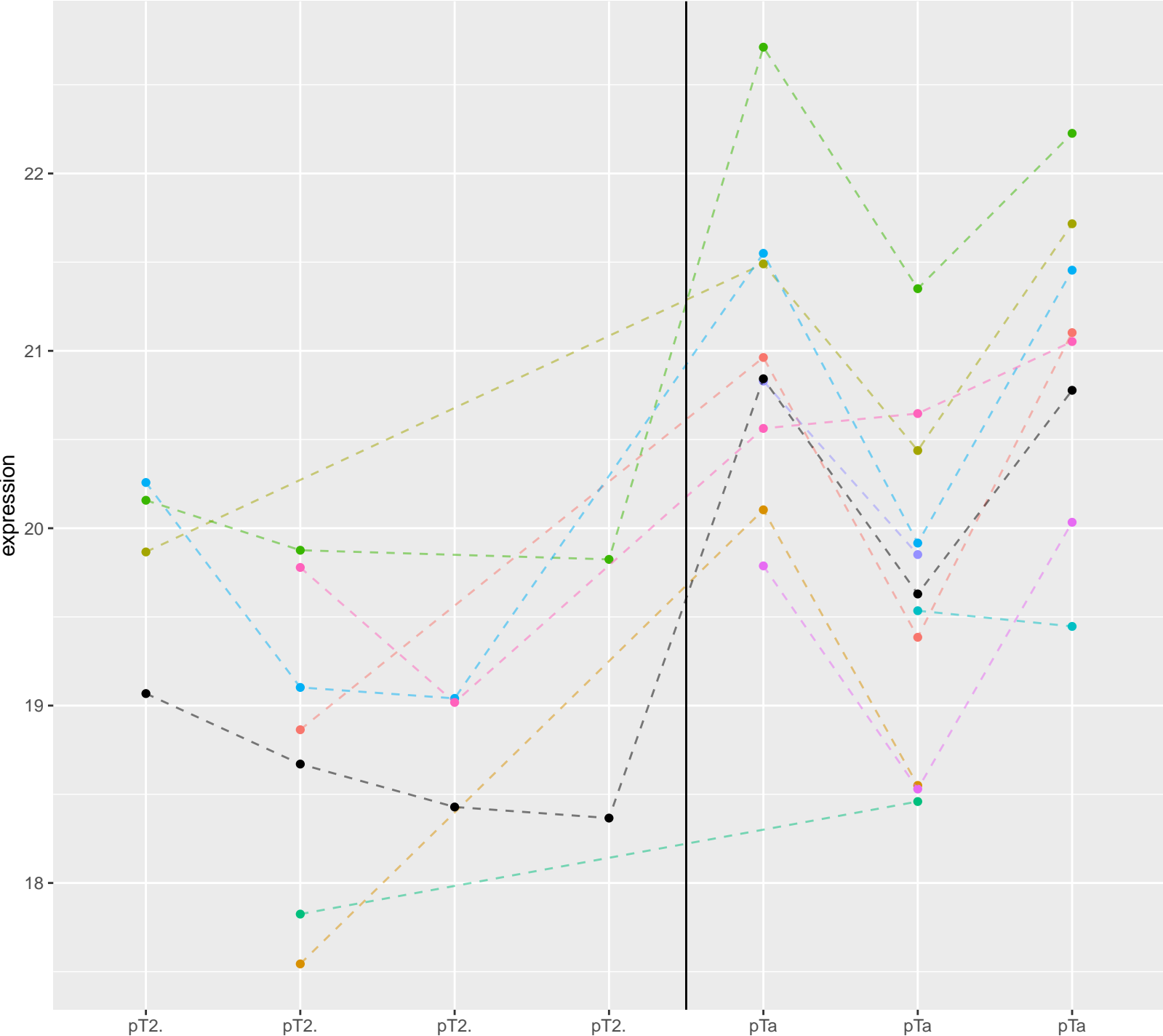


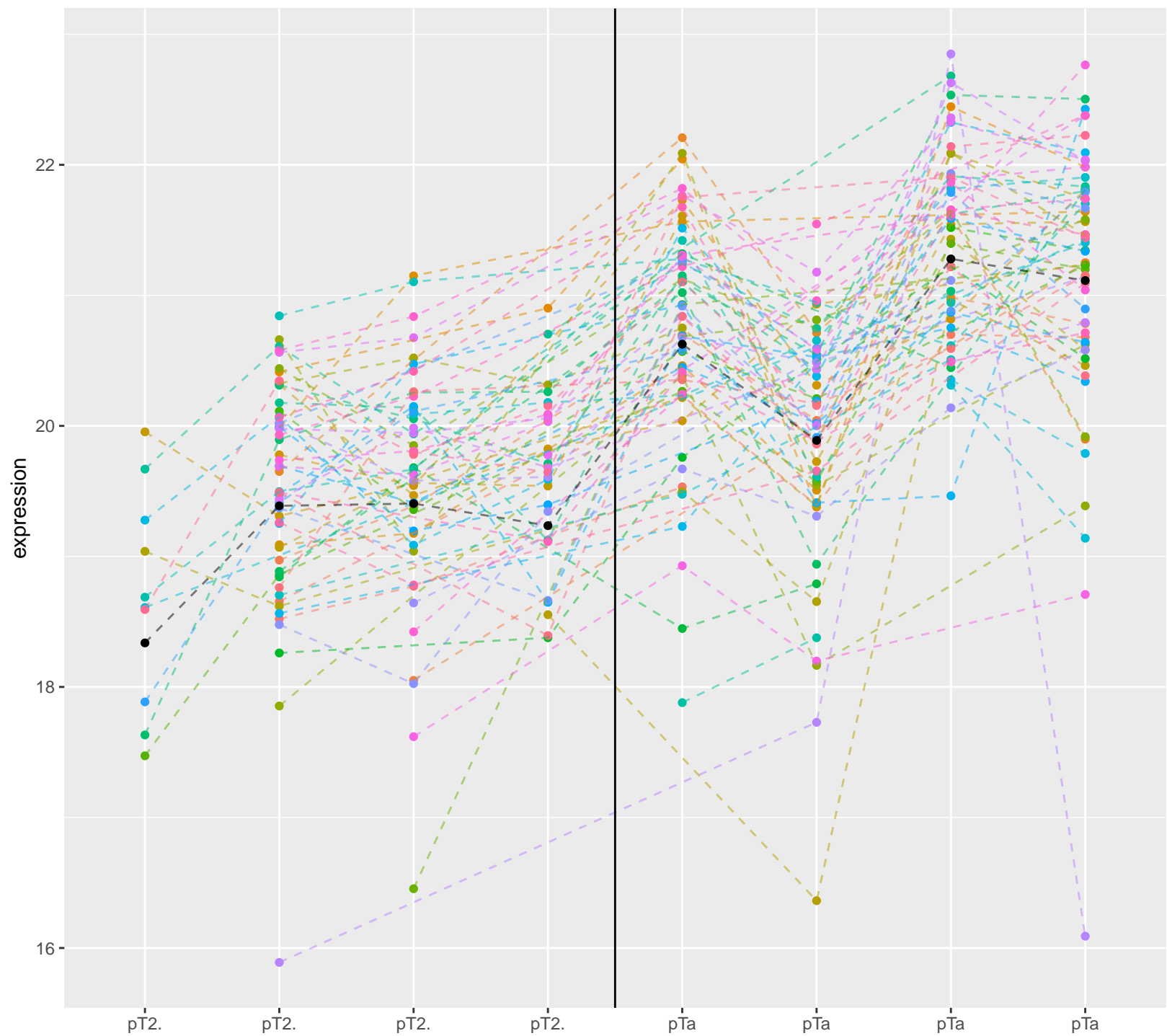
sp|O15382|BCAT2_HUMANBranched-chain-amino-acidaminotransferase,mitochondrial

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



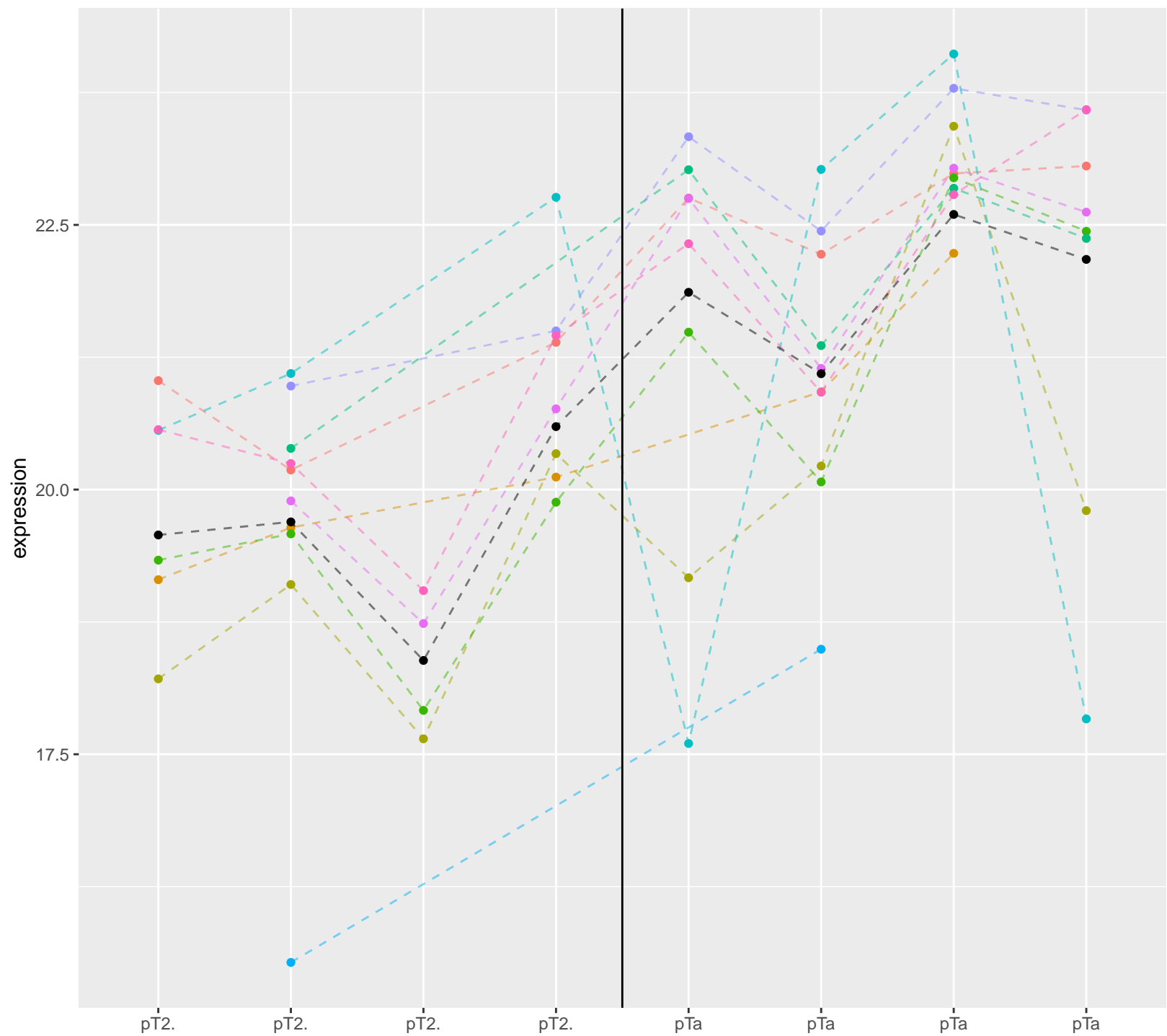
sp|O75369|FLNB_HUMANFilamin-B

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



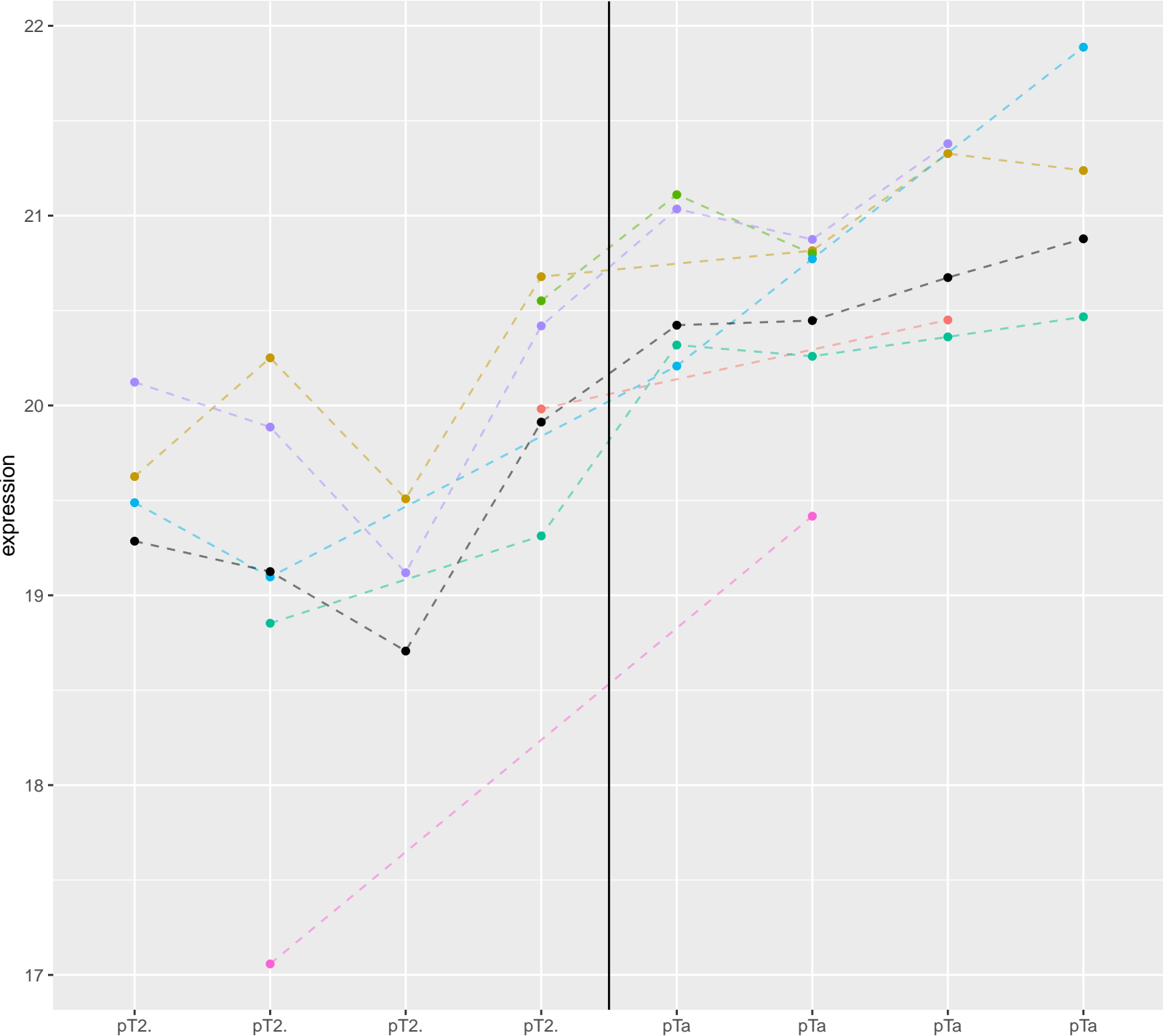
sp|O76070|SYUG_HUMANGamma-synuclein

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



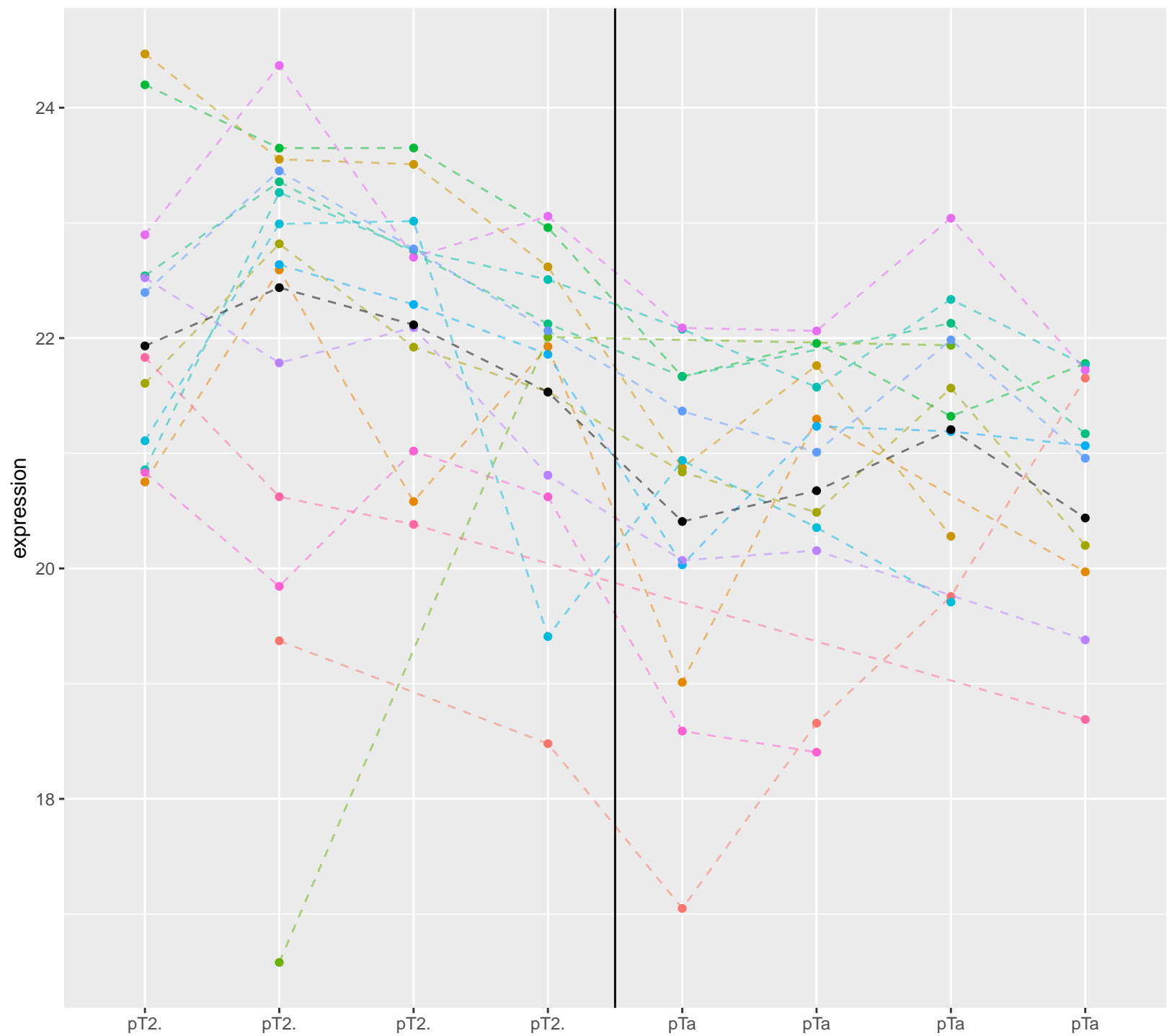
sp|P00390|GSHR_HUMANGlutathionereductase,mitochondrial

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



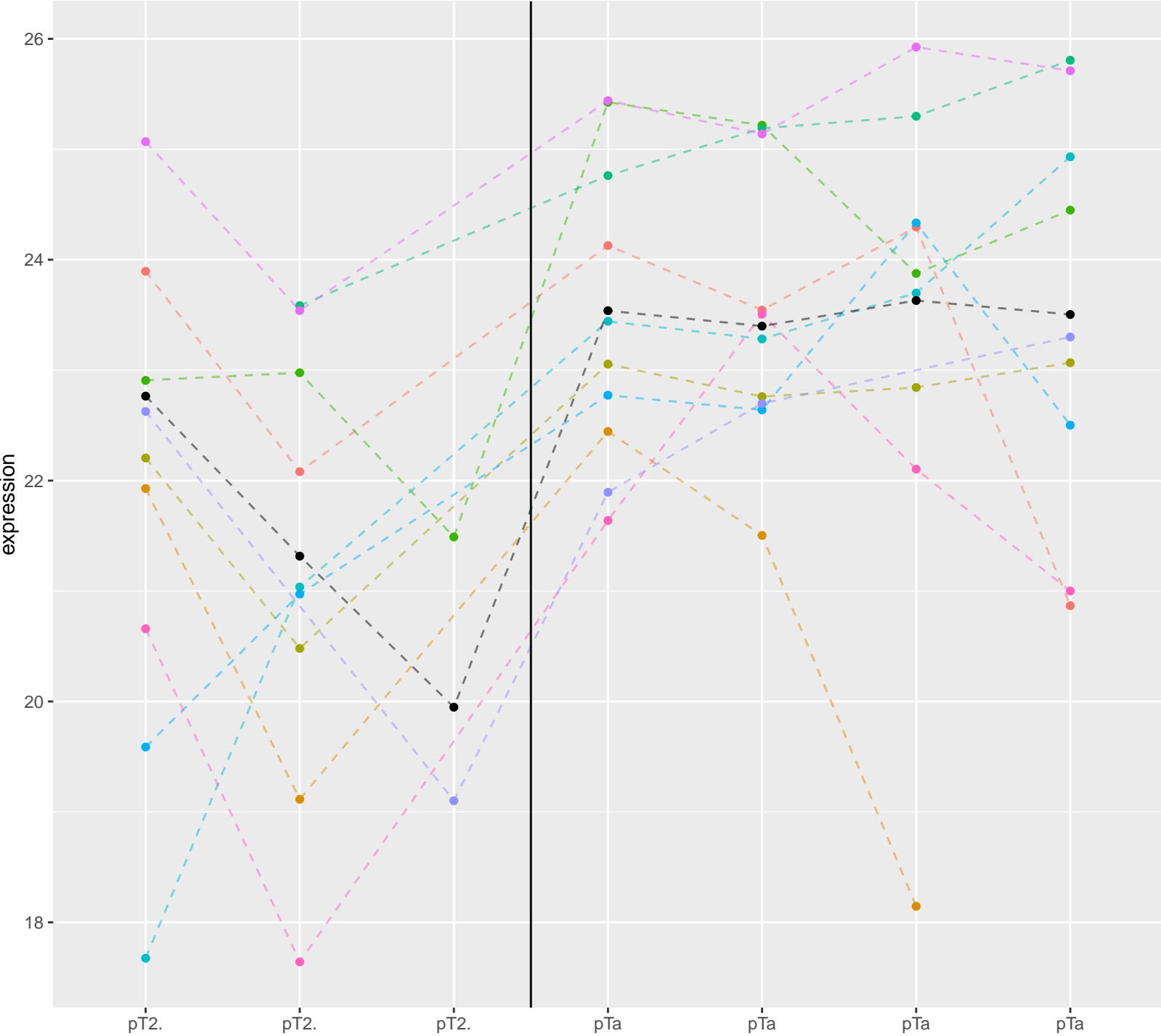
sp|P08758|ANXA5_HUMANAnnexinA5

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



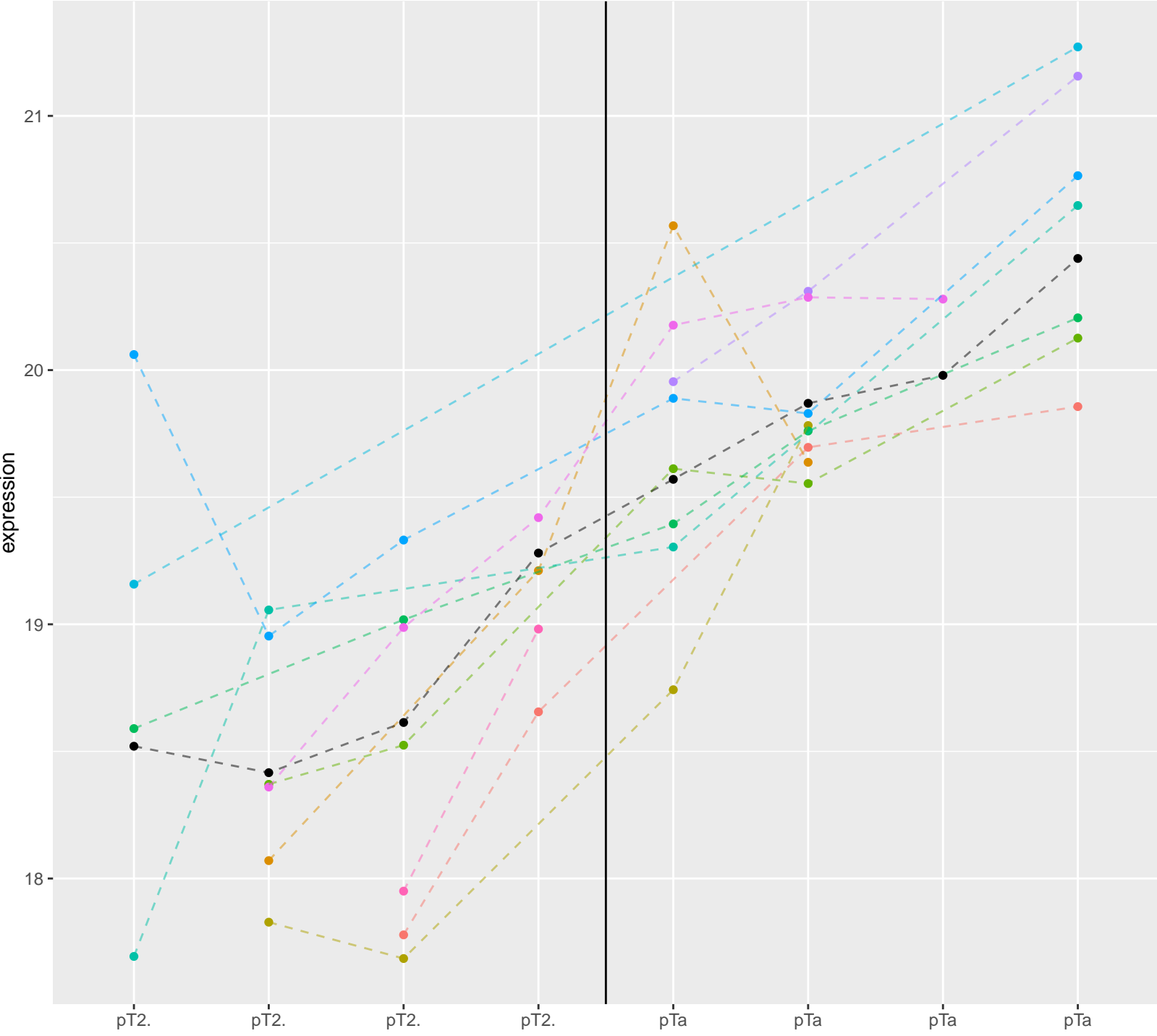
sp|P09488|GSTM1_HUMANGlutathioneS-transferaseMu1

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



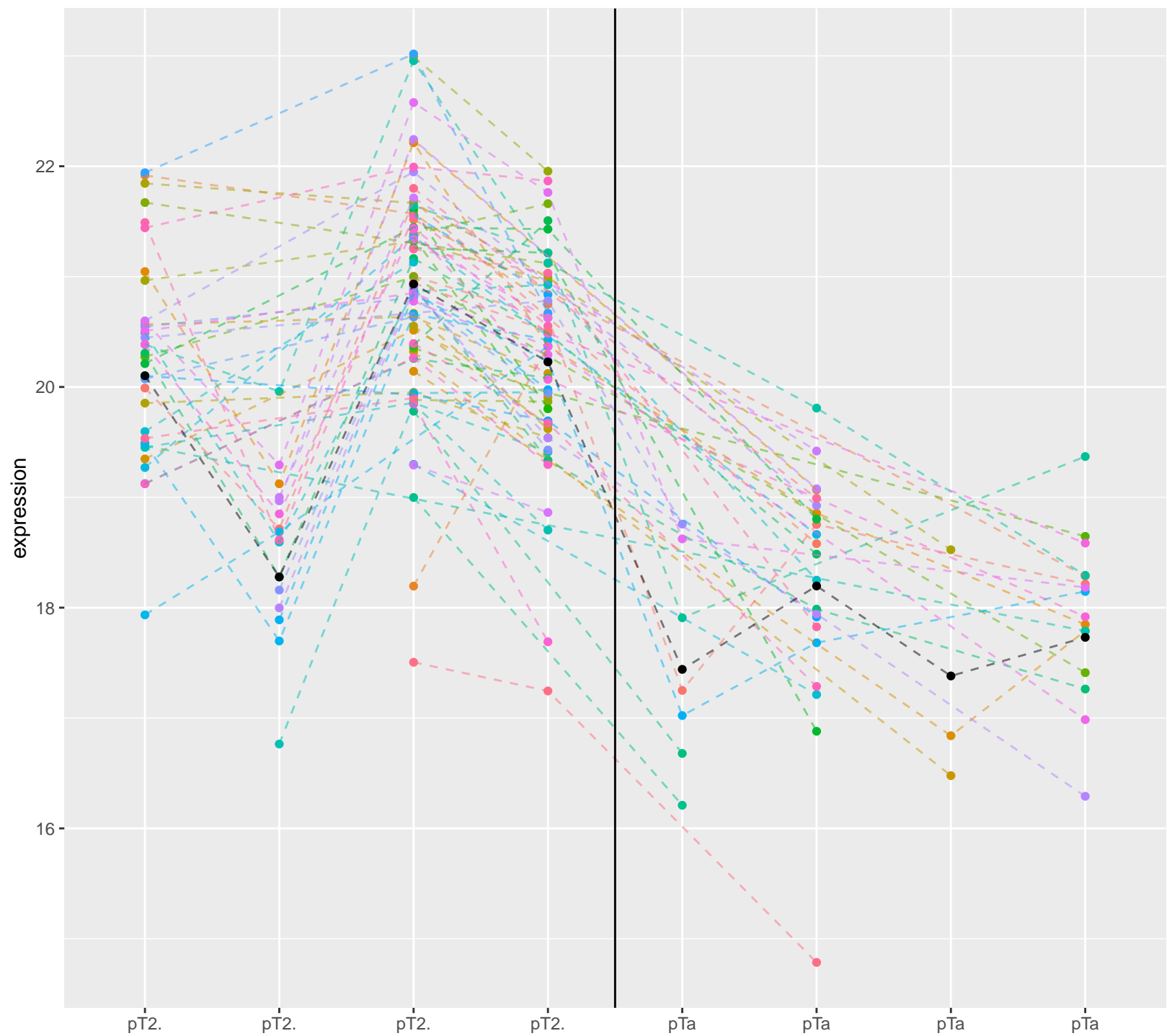
sp|P13798|ACPH_HUMANAcylamino-acid-releasingenzyme

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



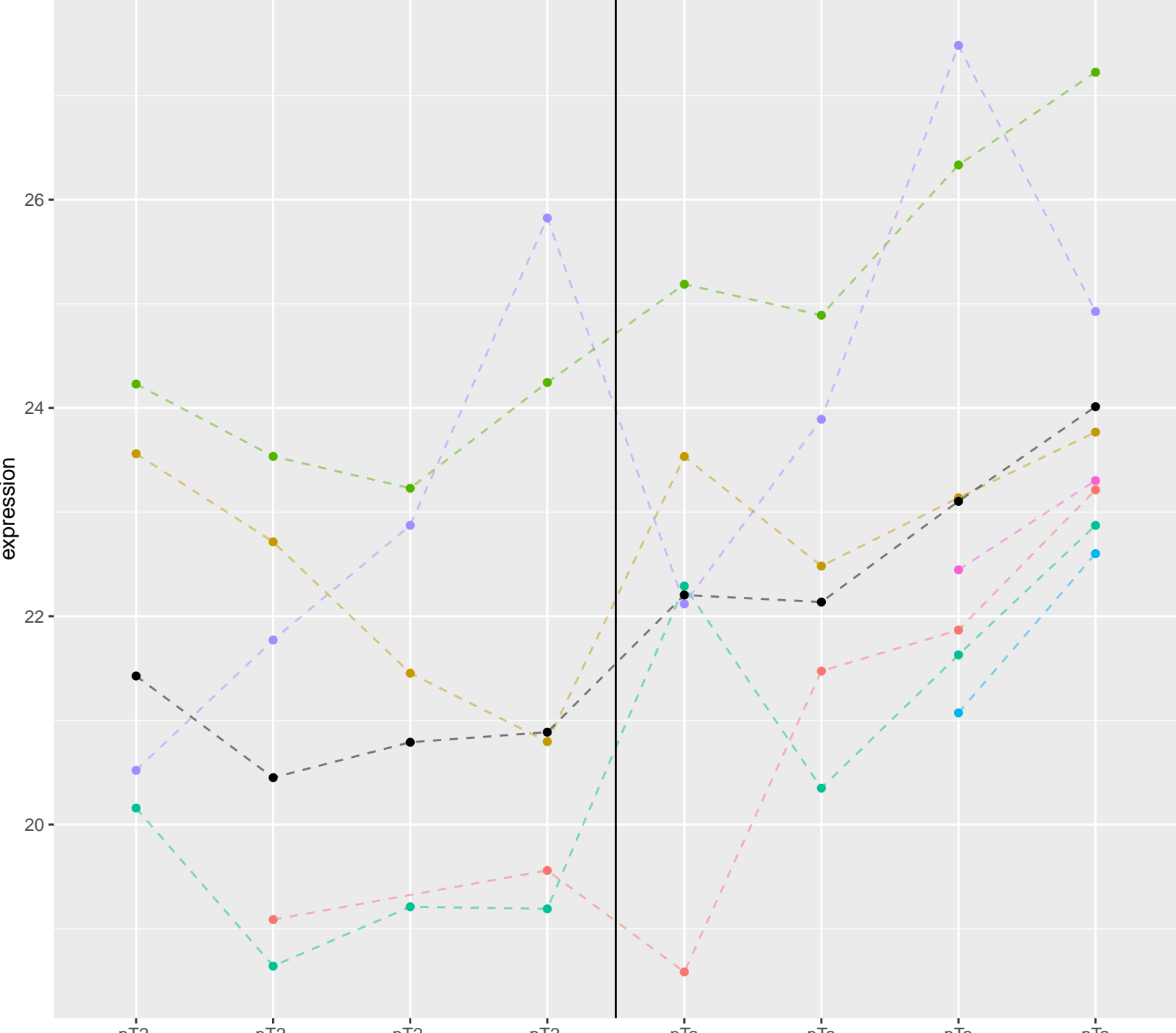
sp|P15924|DESP_HUMANDesmoplakin

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



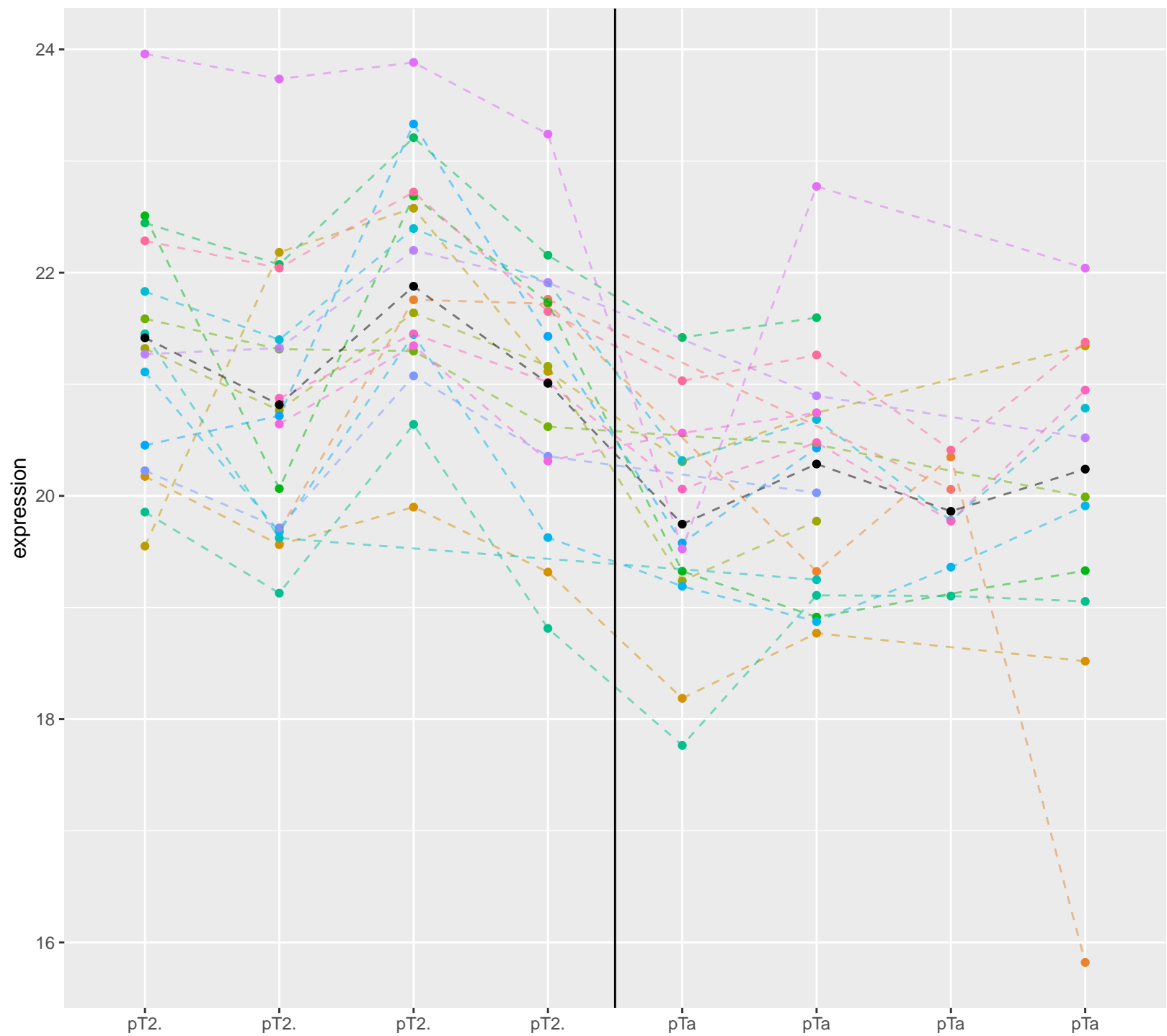
sp|P25815|S100P_HUMANProteinS100-P

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



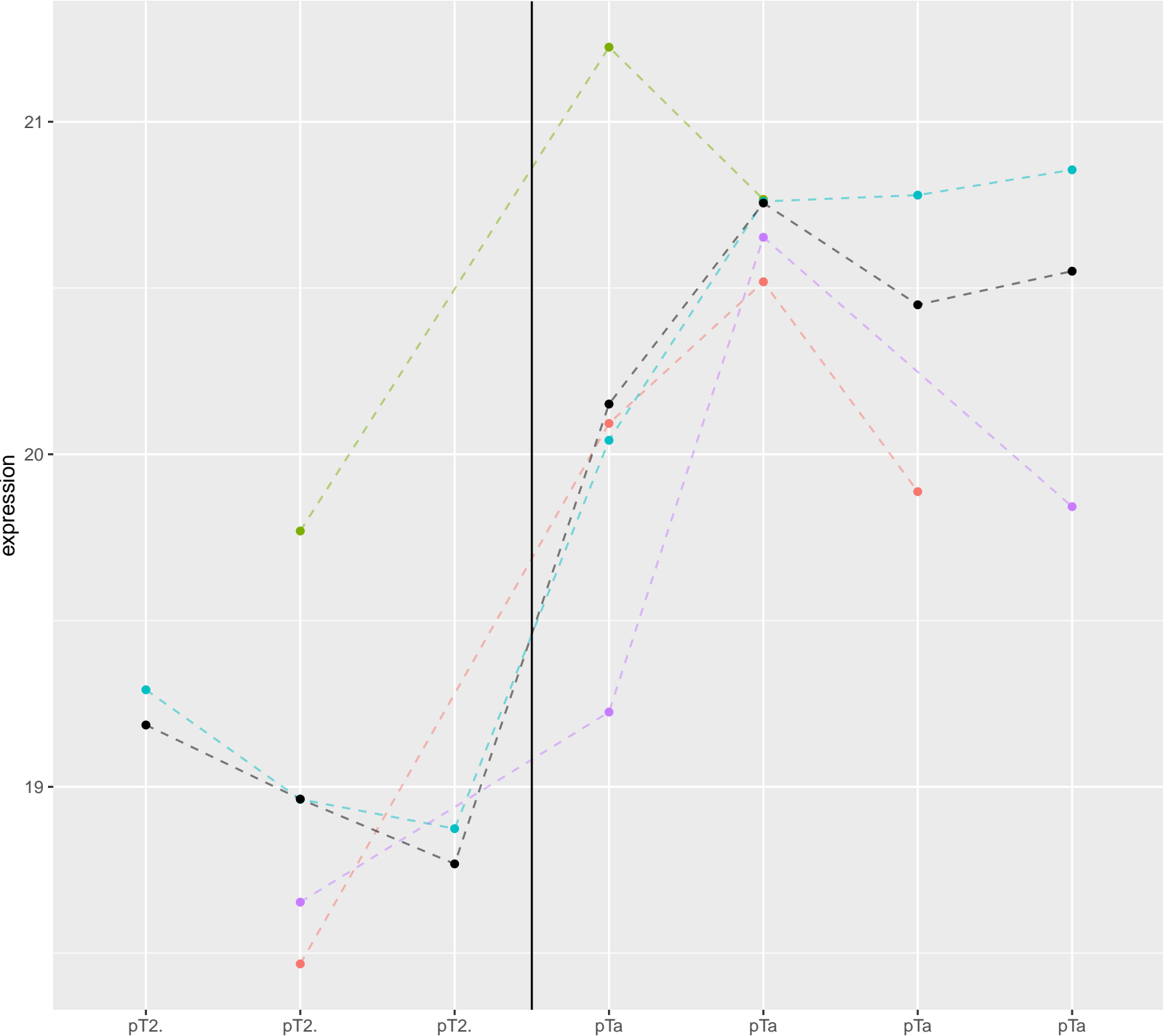
sp|P48735|IDHP_HUMAN|isocitrate dehydrogenase[NADP],mitochondrial

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|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|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

