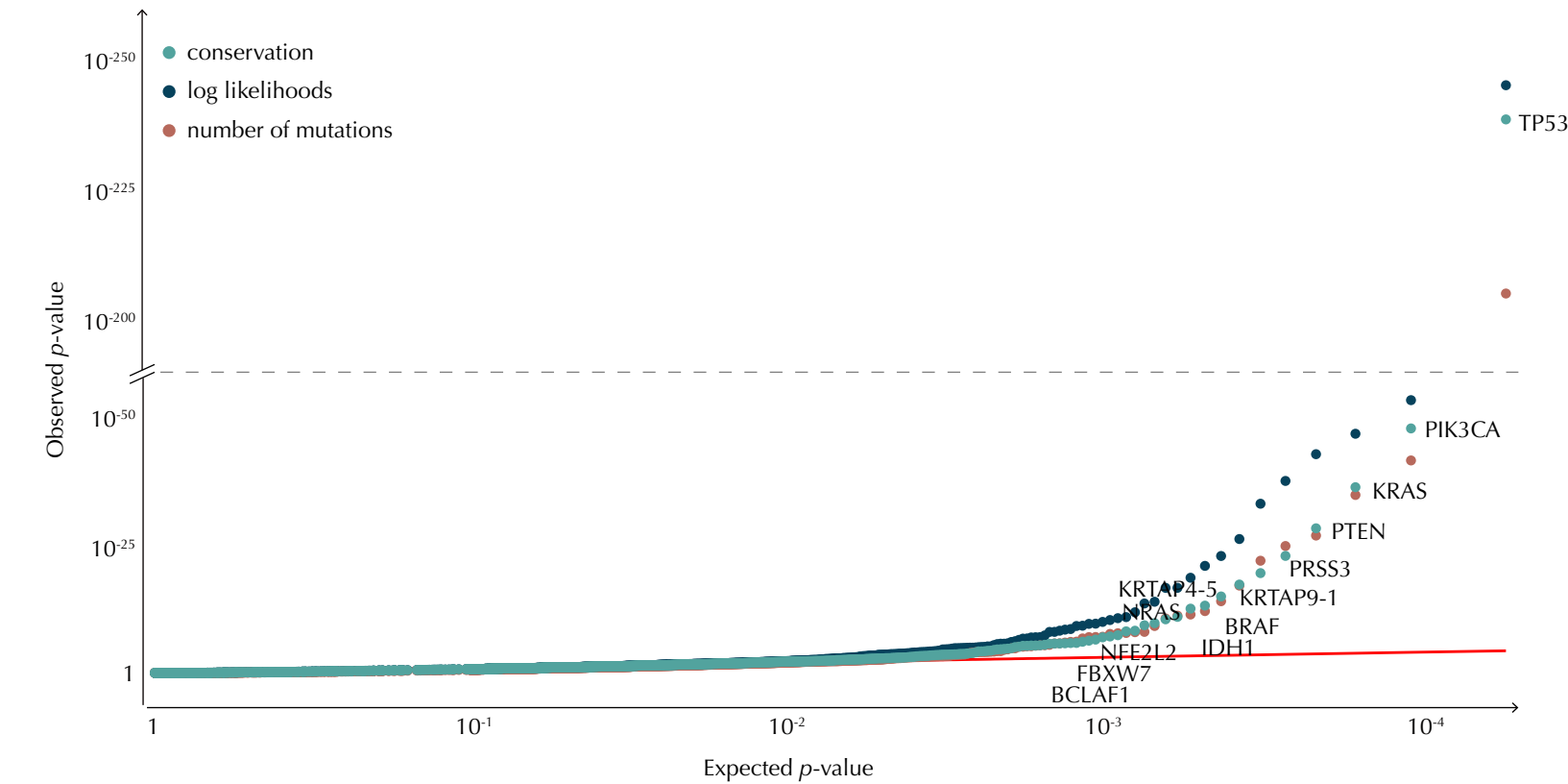
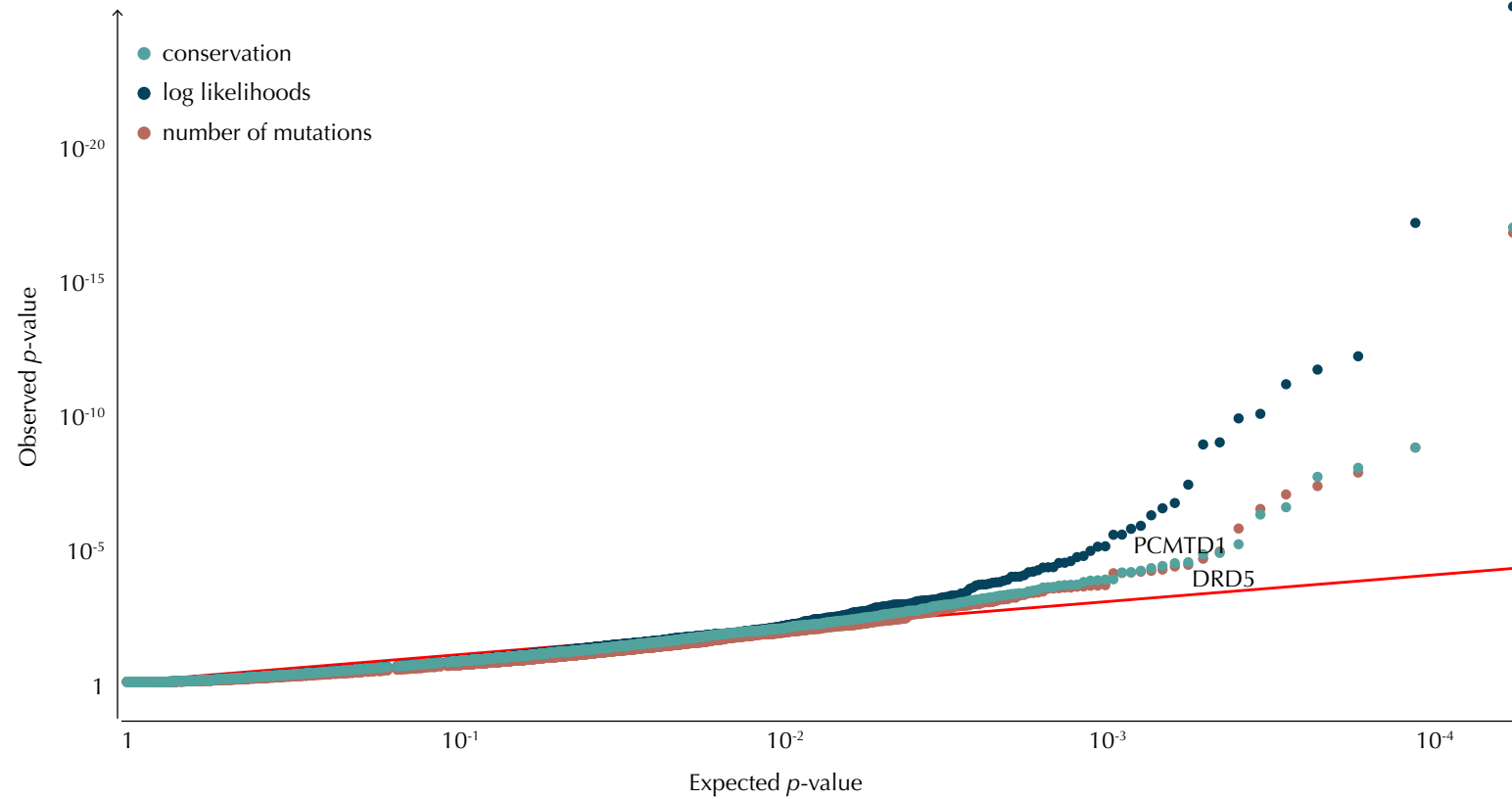


A protein-coding genes ($n = 19,256$)

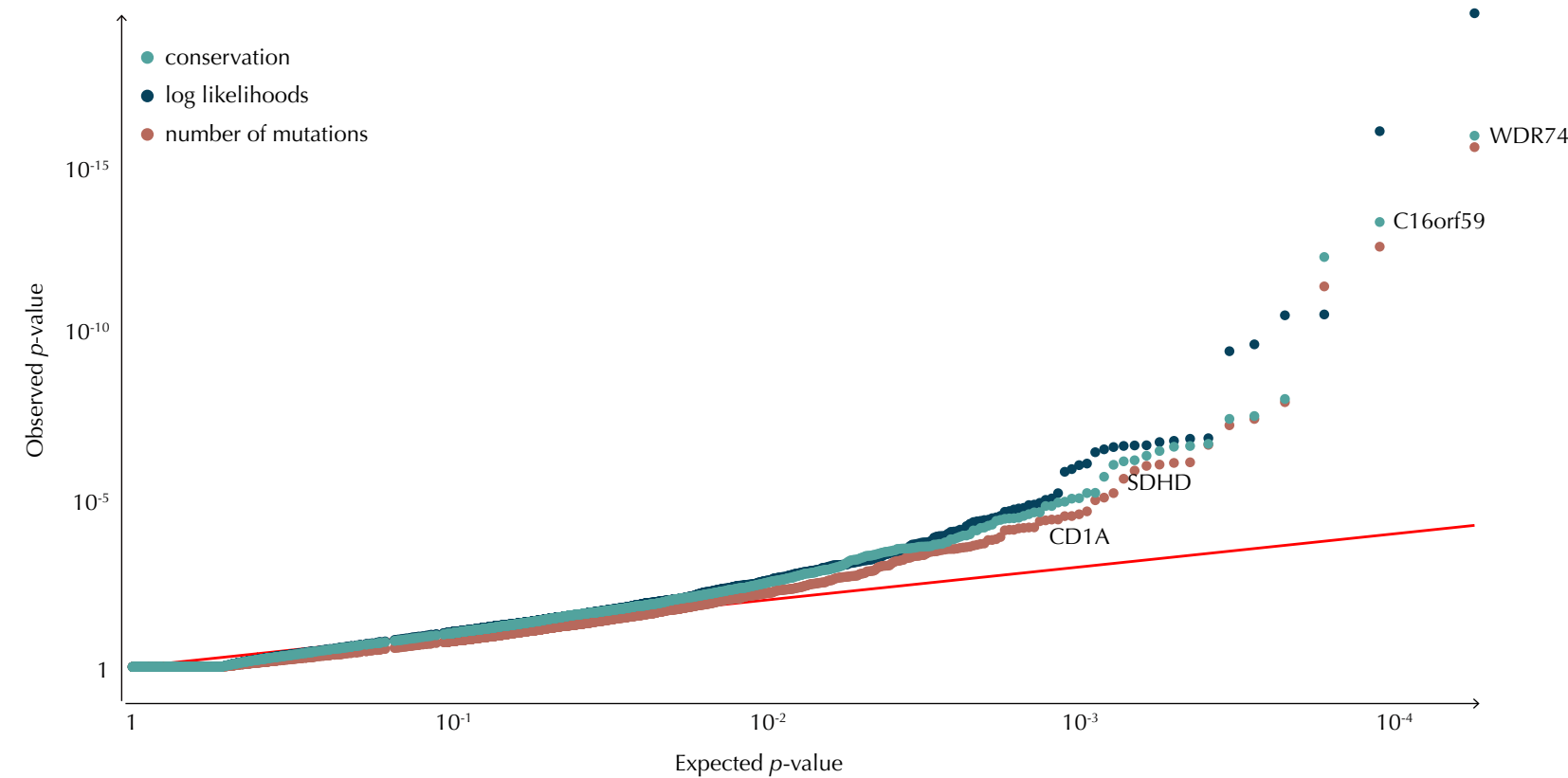
rank	conservation		log likelihoods		number of mutations	
	gene name	q-value	gene name	q-value	gene name	q-value
1	TP53	1.15×10^{-235}	TP53	2.65×10^{-242}	TP53	8.21×10^{-202}
2	PIK3CA	2.82×10^{-44}	PIK3CA	8.90×10^{-50}	PIK3CA	4.69×10^{-38}
3	KRAS	4.93×10^{-33}	MUC4	2.01×10^{-43}	KRAS	1.61×10^{-31}
4	PTEN	3.70×10^{-25}	KRAS	1.42×10^{-39}	PTEN	9.30×10^{-24}
5	PRSS3	6.80×10^{-20}	PRSS3	1.79×10^{-34}	PRSS3	8.07×10^{-22}
6	MUC4	1.26×10^{-16}	PTEN	4.07×10^{-30}	MUC4	4.95×10^{-19}
7	KRTAP9-1	1.77×10^{-14}	KRTAP9-1	2.51×10^{-23}	KRTAP9-1	2.83×10^{-14}
8	BRAF	3.25×10^{-12}	KRTAP4-5	4.42×10^{-20}	KRTAP4-5	2.71×10^{-11}
9	IDH1	1.76×10^{-10}	BRAF	3.28×10^{-18}	BRAF	2.04×10^{-9}
10	KRTAP4-5	6.11×10^{-10}	AL390778.1	5.96×10^{-16}	IDH1	8.41×10^{-9}

gene name	TP53	PIK3CA	KRAS	PTEN	PRSS3	MUC4	KRTAP9-1	BRAF	IDH1	KRTAP4-5	AL390778.1
region size (bp)	1,378	3,207	708	1,212	1,056	16,239	770	2,301	1,245	546	735
observed mutations	169	95	42	38	51	244	87	44	25	47	33
expected mutations	3.3	12.0	2.2	2.5	3.5	74.1	2.8	9.5	3.5	2.4	5.2

B 3' UTRs ($n = 18,481$)

rank	conservation		log likelihoods		number of mutations	
	gene name	q-value	gene name	q-value	gene name	q-value
1	MYO5B	1.46×10^{-13}	MYO5B	7.03×10^{-22}	MYO5B	2.33×10^{-13}
2	PRSS3	1.41×10^{-5}	VPS53	4.95×10^{-14}	PRSS3	1.41×10^{-5}
3	ADD2	5.44×10^{-5}	PRSS3	3.44×10^{-9}	ADD2	8.21×10^{-5}
4	SEC14L1	8.87×10^{-5}	SEC14L1	8.18×10^{-9}	SEC14L1	1.98×10^{-4}
5	FAHD2B	9.92×10^{-4}	TBC1D22A	2.33×10^{-8}	FAHD2B	3.27×10^{-4}
6	VPS53	1.55×10^{-3}	FAHD2B	2.53×10^{-7}	VPS53	9.61×10^{-4}
7	LRTM1	1.75×10^{-2}	ADD2	3.21×10^{-7}	TBC1D22A	4.48×10^{-3}
8	SGCZ	3.23×10^{-2}	FAM101B	2.24×10^{-6}	LRTM1	2.89×10^{-2}
9	ELOVL3	3.23×10^{-2}	MUC19	2.40×10^{-6}	SGCZ	4.77×10^{-2}
10	DRD5	5.76×10^{-2}	LRTM1	7.01×10^{-5}	C7	7.25×10^{-2}

gene name	MYO5B	PRSS3	ADD2	SEC14L1	FAHD2B	VPS53	LRTM1	SGCZ	ELOVL3	DRD5	C7	TBC1D22A	FAM101B	MUC19
region size (bp)	3,658	52	8,257	3,052	172	11,085	222	579	337	545	1,366	2,067	3,186	8,002
observed mutations	78	7	50	31	10	56	9	19	8	22	22	37	19	126
expected mutations	10.1	0.2	12.4	7.9	0.8	19.0	1.1	5.0	1.0	3.5	6.1	9.9	4.6	61.6

C 5' UTRs ($n = 18,220$)

rank	conservation		log likelihoods		number of mutations	
	gene name	q-value	gene name	q-value	gene name	q-value
1	WDR74	1.84×10^{-12}	WDR74	3.79×10^{-16}	WDR74	4.07×10^{-12}
2	C16orf59	3.66×10^{-10}	MRPL36	6.74×10^{-13}	MRPL36	2.02×10^{-9}
3	MRPL36	2.76×10^{-9}	MTG2	1.18×10^{-7}	C16orf59	2.12×10^{-8}
4	MTRNR2L13	3.89×10^{-5}	HLA-F	1.18×10^{-7}	MTRNR2L13	4.86×10^{-5}
5	HLA-F	1.02×10^{-4}	C16orf59	7.07×10^{-7}	MTG2	1.24×10^{-4}
6	MTG2	1.03×10^{-4}	ZNF717	9.47×10^{-7}	HLA-F	1.61×10^{-4}
7	NDUFB9	4.75×10^{-4}	NDUFB9	3.08×10^{-4}	EVI2A	5.34×10^{-4}
8	PRKAG1	4.75×10^{-4}	TBC1D12	3.08×10^{-4}	DHX16	1.46×10^{-3}
9	EVI2A	4.75×10^{-4}	MTRNR2L13	3.10×10^{-4}	ZNF717	1.46×10^{-3}
10	TBC1D12	5.74×10^{-4}	EVI2A	3.10×10^{-4}	PRKAG1	1.46×10^{-3}

gene name	WDR74	C16orf59	MRPL36	MTRNR2L13	HLA-F	MTG2	NDUFB9	PRKAG1	EVI2A	TBC1D12	DHX16	ZNF717
region size (bp)	839	173	166	941	384	26	84	487	548	110	323	600
observed mutations	30	12	18	20	19	5	6	11	9	6	10	27
expected mutations	2.4	0.6	0.9	3.7	2.2	0.1	0.3	1.4	0.7	0.3	1.1	4.4