Vaccinia screen results summary.

Converged = TM-align & FATCAT agreement **Excess Hits** = Large quantity of nonspec

Proteins with <16 secondary structural motifs (as determined by STRIDE) are highlighte

%ID was calculated based on a clustal omega alignment of the indicated uniprot identifi

Some proteins with hits have other hits that are extrememly close to the annotated hit.

Uniprot ID	Orf Name	pLDDT	Length (AA)	ssMotifs	Converged	Excess Hits
P21113	7kDaAtIP	68.74233	65	**9**	N	
P20982	A1	87.2308	150	22	N	
P20642	A10	77.11623	891	122	N	
P20988	A11	56.09341	318	25	N	
P20989	A12	62.00416	192	19	N	
P20990	A13	70.54972	70	**4**	Y	
P20991	A14	69.03298	90	**2**	Y	Y
p0ck28	A14p5	89.63571	53	**2**	Y	Y
P20992	A15	89.0949	94	**15**	N	
P20993	A16	81.98536	378	64	N	
P68592	A17	71.33835	203	22	N	
p20534	A18	86.7	493	74	Y	
P20994	A19	66.21313	77	**15**	N	
P68318	A2	77.66306	224	23	N	
P20995	A20	90.89355	426	58	N	
P20996	A21	85.92326	117	19	N	
P20997	A22	88.70113	176	23	Y	
P20998	A23	91.58571	382	60	N	
P68694	A24	91.11326	1164	213	Y	
P21114	A26	77.11563	322	34	N	
p20535	A27	78.05599	110	**15**	Y	Y
P68632	A28	81.33939	146	25	N	
P21087	A29	95.74789	305	51	N	
p0ck20	A2p5	69.70142	76	**7**	N	
P20643	A3	77.41739	644	97	N	
P68595	A30	78.62309	77	**6**	Y	Y
P21096	A31	80.39635	124	24	N	
P68614	A32	89.23297	270	42	N	
P68616	A33	74.04233	185	20	Y	
P21057	A34	90.60423	168	25	Y	
P21058	A35	88.00402	176	38	N	
P68618	A36	50.56892	221	18	N	
P21060	A37	87.80005	263	50	N	
P21061	A38	87.01837	277	36	Y	
P21062	A39	94.25722	403	85	Y	
P20983	A4	52.38249	281	28	N	
P21063	A40	66.87082	168	27	Y	
P21064	A41	89.74088	219	36	N	
P68695	A42	96.85205	133	25	Y	
P21065	A43	67.30829	194	24	N	
P21097	A44	95.30341	346	50	Y	

P21132	A45	93.24252	125	22	Y	
P21066	A46	71.92699	214	37	N	
P21067	A47	75.06809	244	24	Y	
P68693	A48	96.80824	204	27	Y	
P21068	A49	91.49097	162	18	N	
P68610	A5	76.81659	164	17	N	
p20492	A50	90.70989	552	91	Y	
P21069	A51	83.25104	334	56	N	
P21070	A52	88.23601	190	17	N	
P21071	A53	66.26683	103	20	N	
P68620	A54	58.26713	90	**5**	N	Y
P21073	A55	87.92701	564	106	Y	
P20978	A56	64.19411	315	35	N	
P21074	A57	91.44574	151	20	Y	
P20985	A6	91.34894	372	30	N	
p20635	A7	84.76429	710	134	N	
P20986	A8	79.39829	288	35	N	
P20987	A9	65.02727	99	**4**	Y	
p20510	AorfA	60.24153	119	26	n	
p20511	AorfB	75.7881	86	**1**	N	Y
p20512	AorfC	40.40304	128	**12**	N	
p20513	AorfD	49.14148	88	**10**	Y	
p20514	AorfE	42.43184	166	**13**	N	
p20515	AorfF	65.75827	75	**12**	N	
p20516	AorfG	59.32088	75	**12**	N	
p20517	AorfH	36.84384	128	**13**	N	
p20518	AorfI	55.97135	73	**6**	Y	Y
p20519	AorfJ	48.84006	73	**9**	N	
p20520	AorfK	39.61527	70	**11**	N	
P68624	AorfL	54.92525	88	**7**	Y	
P68626	AorfM	58.78473	76	**3**	Y	Y
p20523	AorfN	70.84175	70	**1**	Y	Y
p20524	AorfO	40.7194	83	**12**	N	
p20525	AorfP	35.78624	89	**14**	N	
p20526	AorfQ	44.01094	77	**7**	N	
p20527	AorfR	61.5128	66	**4**	Y	Y
P68628	AorfS	57.68266	67	**11**	N	
P68630	AorfT	52.02503	81	**8**	N	
p20530	AorfU	63.18684	72	**3**	Y	
p20505	B1	95.97757	300	49	Y	
P68687	B10	89.35938	166	40	Y	
P21007	B11	69.78397	88	**5**	Y	
P21098	B12	94.05945	283	42	Y	
P20841	B13	87.6357	116	20	Y	
P20842	B14	85.83112	222	34	Y	
P21089	B15	93.55426	149	16	Y	
P21116	B16	81.66437	30	**1**	Y	Y
P21075	B17	45.73089	340	61	N	

P21076	B18	87.10394	574	87	Y	
P21077	B19	93.77266	353	70	N	
P20999	B2	91.24447	219	42	N	
P21078	B20	49.01911	127	32	N	
P21099	B21	64.58082	91	**13**	Y	
P21100	B22	80.37308	181	21	N	
P21101	B23	73.59851	386	63	Y	
P21102	B24	81.14964	150	24	Y	
P21103	B25	76.88415	259	33	Y	
P21104	B26	67.3626	103	**10**	Y	
P21105	B27	77.64603	113	**15**	N	
P21106	B28	66.49728	122	24	N	
P21000	B3	75.25853	124	20	Y	
P21001	B4	74.79937	558	67	N	
P21115	B5	85.58255	317	62	N	
P68443	B6	80.86823	173	**11**	Y	
P68445	B7	69.05378	182	32	N	
P21004	B8	92.88861	272	45	N	
P21005	B9	81.06937	77	**9**	N	
P68473	BorfA	46.51293	107	**9**	N	
p20542	BorfB	59.96655	66	**9**	N	
p20543	BorfC	36.44316	95	16	N	
P68475	BorfD	59.85997	71	**5**	Y	
P68477	BorfE	40.35753	91	**13**	N	
p20546	BorfF	50.60222	75	**10**	N	
p20547	BorfG	65.03501	91	**2**	Y	Y
p20548	BorfH	43.73027	70	**13**	N	
p20549	BorfI	56.48816	67	**10**	N	
P21036	C1	82.9674	224	20	N	
P21043	C10	85.73095	331	53	N	
p20494	c11	72.89068	142	24	N	
p20531	C12	86.81473	353	57	Y	
P21044	C13	64.16698	65	**9**	N	
P21045	C14	81.71396	82	**12**	N	
P21037	C2	85.64696	512	93	Y	
P21090	C23	88.57905	244	40	N	
P68639	C3	90.06353	263	56	Y	
P21038	C4	81.96497	316	51	N	
P21039	C5	89.17651	204	20	Y	
P21040	C6	92.6986	151	16	N	
P68599	C7	93.20519	150	29	N	
P21041	C8	83.61364	184	28	N	
P21042	C9	86.34565	634	85	N	
P21119	CorfA	50.19871	69	**12**	N	
P21120	CorfB	60.48731	72	**6**	Y	Y
P21121	CorfC	71.63799	82	**6**	Y	Y
P21122	CorfD	66.64765	70	**3**	Y	Y
P21123	CorfE	84.93081	65	**2**	Y	Y

P20979	D1	90.48484	844	140	N	
P21012	D10	94.27866	248	34	N	
P20637	D11	91.01643	631	100	Y	
P20980	D12	96.66837	287	34	Y	
P68441	D13	95.34617	551	105	N	
P21008	D2	84.00116	146	21	N	
P21009	D3	87.61361	237	38	N	
p20536	D4	96.6796	218	45	Y	
P21010	D5	89.58724	785	147	N	
p20634	D6	86.64423	637	112	Y	
P21034	D7	91.4259	161	34	Y	
p20508	D8	89.6699	304	45	Y	
P21011	D9	91.26687	213	32	N	
p20550	DorfA	59.06901	84	**4**	Y	Y
p20551	DorfB	52.66891	80	**15**	N	
p20552	DorfC	41.73074	69	**10**	N	
P68479	DorfD	55.33893	72	**8**	N	
P68481	DorfE	48.15648	80	17	N	
P68483	DorfF	65.46633	69	**12**	Y	
P68485	DorfG	55.62048	90	**5**	Y	Y
P68487	DorfH	69.0556	61	**1**	Y	Y
p20553	DorfI	72.22042	74	**2**	N	
P21079	E1	94.07629	479	70	N	
P21050	E10	95.66748	95	**10**	Y	
P68449	E11	84.83324	129	22	N	
P21080	E2	89.72825	737	95	N	
P21081	E3	78.20192	190	27	N	
P21082	E4	68.36226	259	29	N	
P21046	E5	74.01381	341	34	N	
P21047	E6	84.78101	567	62	N	
P68447	E7	44.55575	166	20	N	
P21049	E8	80.53922	273	42	N	
p20509	E9	91.44555	1006	146	Y	
P21085	EorfA	49.13843	71	**9**	n	
p20554	EorfB	42.55432	106	**9**	Y	
p20555	EorfC	42.52227	70	**11**	N	
p20556	EorfD	53.83275	66	**15**	N	
p20557	EorfE	63.04056	65	**4**	Y	Y
p20558	EorfF	51.66814	115	**11**	Y	
P68450	F1	68.00448	226	21	N	
P21095	F10	89.65752	439	65	N	
P21052	F11	79.95733	354	45	N	
P21053	F12	88.68075	635	95	N	
P20638	F13	91.70991	372	71	Y	
P21019	F14	65.32265	73	**6**	N	
P21020	F15	81.8579	158	37	N	
P21021	F16	84.14321	231	25	N	
P68454	F17	70.68404	101	21	N	

P68634	F2	94.15347	147	26	Y	
P21013	F3	89.12424	480	94	N	
p20493	F4	88.21558	319	27	Y	
P21014	F5	70.75118	321	51	N	
P68601	F6	66.58151	74	**10**	N	
P21016	F7	50.84788	92	**9**	N	
P21017	F8	68.05785	65	**5**	N	
P68452	F9	83.26356	212	21	N	
p20559	ForfA	59.44491	67	**5**	Y	Y
p20560	ForfB	65.59204	78	**7**	N	
p20561	ForfC	59.57557	96	**7**	Y	Y
p20562	ForfD	67.73666	85	**5**	Y	
p20563	ForfE	58.68662	71	**5**	Y	Y
p20564	ForfF	66.70897	74	**4**	Y	Y
P21022	G1	87.26159	591	85	Y	
P68457	G2	93.47739	220	30	N	
P68459	G3	84.01472	111	**14**	N	
P68461	G4	91.5997	124	22	N	
P21026	G5	93.24123	434	65	N	
P68315	G5p5	77.45979	63	**10**	N	
P21027	G6	90.72357	165	36	N	
P21028	G7	64.33256	371	33	N	
P68612	G8	89.59898	260	50	Y	
P21030	G9	86.37393	340	51	N	
p20565	GorfA	32.24285	132	**13**	N	
p20566	GorfB	72.70645	72	**1**	Y	Y
P20495	H1	97.21163	171	21	Y	
p20496	H2	84.26683	189	28	N	
p20497	H3	86.44234	324	50	N	
P68439	H4	71.77599	795	107	N	
p20538	H5	65.45242	203	**10**	N	
P68697	H6	94.36452	314	41	Y	
p20539	H7	93.55347	146	16	N	
p20567	HorfA	77.6054	71	**2**	Y	Y
p20498	I1	83.96295	312	50	N	
P68604	I2	67.87248	73	**6**	Y	
p20499	I3	81.56212	269	45	N	
P20503	I4	93.1913	771	112	Y	
p20500	I5	83.24622	79	**8**	Y	Y
P68463	I6	85.76244	382	60	N	
p20501	I7	91.60765	423	55	N	
p20502	I8	91.6925	676	120	Y	
p20568	IorfA	57.44336	77	**8**	Y	Y
P21032	J1	73.72111	153	**11**	N	
P68564	J2	92.61234	177	38	Y	
P21033	J3	89.63018	333	37	Y	
P68608	J4	92.21356	185	33	Y	
P21083	J5	80.47185	133	20	N	

p20504	J6	93.89595	1286	208	Y	
p20632	K1	95.64797	284	47	Y	
p20532	K2	89.54373	369	65	Y	
P20639	K3	92.30271	88	18	Y	
p20537	K4	92.23112	424	72	Y	
P21084	K5	73.44188	136	20	Y	
P68465	K6	88.78416	81	**13**	Y	
P68467	K7	88.34052	149	16	Y	
p20569	KorfA	44.21513	81	**12**	N	
p20570	KorfB	61.64135	79	**6**	Y	Y
p20540	L1	78.59391	250	34	N	
P20843	L2	74.66685	87	**2**	Y	
P21031	L3	79.56406	350	43	N	
P20981	L4	79.44113	251	45	N	
P68622	L5	77.47556	128	18	N	
P20640	M1	86.22016	472	59	Y	
P21092	M2	75.51065	220	39	N	
P21054	N1	95.31486	117	**12**	Y	
P20641	N2	75.03608	175	**13**	N	
P21093	O1	82.19695	666	77	N	
P68690	O2	97.4889	108	17	Y	
p0ck22	O3	80.35554	35	**1**	Y	Y
P68489	U7kDa	73.8132	62	**3**	Y	Y
P68491	U8p7kDa	84.77117	72	**2**	Y	Y

ific (such as groups of unrelated proteins, not a large protein family) observed. This commonly overlaps with va
d in yellow and excluded as hits. Some select proteins in this category were still further annotated and may be o
ers
While these are often orthologs of the same gene/protein, they may be of interest. See supplemental figures.

Hit	Hit ID	%ID (Top Hit)
Helicases (top: HELLS)	Q9NRZ9	20.55
Mitochondrial resolvase tefm	Q0P4D6	21.34
Polymerases (Polr2b)	Q8CFI7	24.44
Klrh1	Q3UU75	23.87
Klrb1c	P27814	20.75
CD47	Q61735	27.08
Semaphorin Sema7a	Q9QUR8	27.23
Klra1	P20937	24.2
Profilin (Pfn2)	A0A0R4IPL1	27.27
Steroid dehydrogenases (Top: Hsd3b2)	P26149	32.46

sod1	O73872	18.55	
GSDMD	P57764	20.09	
DTYMK	P23919	18.01	
Ligases (Lig3)	P97386	55.43	
TNFRSF1B	P20333	24	
Kelch proteins (diablo is top)	Q9VUU5	23.49	
Guk1	Q64520	46.36	
Serinc1/drosophila ND-15			
PSME1	Q06323	19.72	
K7DYB1			
Kinases (top: VRK1)	Q99986	40.6	
Kelch proteins (top: Danio kelch-like protein 12)	A0A2R8Q6R0	28.57	
ambiguous			
Kinases (top: VRK1)	Q99986	33.33	
Serpins (top: Fly Spn42Dc)	A1Z6R4	33.04	*B13/B14 are fragment
Serpins (top: Serpina3j)	D3Z451	29.03	
Bcl2l2	P70345	13.86	

Ankyrin repeat and SOCS box-containing 15a	A0A2R8PZ70	20.53
Below threshhold: IL1r2		
Ankrd37		
ASB4	Q9Y574	20
Ankyrin proteins (top: ANKRD22)	Q5VYY1	22.76
Ankyrin proteins (top: Danio Ankyrin repeat and SOCS box pr	Q7T386	23.67
ambiguous - ankyrin or protein phosphatase 1?		
Slfn1	Q3UU73	25.21
Buffy	Q8T8Y5	20.96
F3/IFNGR1 (below threshold)		
Tmem91, KANTR		
Strong pyrin domain hits w/ FATCAT alone, some BCL2 domains with TM-align. See main text.		
Serpins (top: Serpinb1c)	Q5SV42	34.2
Keap1	Q14145	22.2
C4BPA	P04003	37.45
Kelch proteins(top: KLHL8)	Q9P2G9	21.03
below thresshold: bcl2l15		

just under thresshold: Nudt2			
Chd3, HELLS, smarcad1 - helicases	O16102	19.44	
Cmtr1, 2 (methyltransferase)	Q9W4N2	19.79	
UNG1 (danio)	A2BIQ2	19.81	
smarcad1b (danio)	E7F1C4	21.98	**look back
POL2RG	P62487	17.39	
Ca5b	Q9QZA0	33.33	
just under thresshold: NudT15, 16, etc			
	A1A750, weak		
lots, ambiguous			
lots, ambiguous			
GFER			
PolD1	P54358	24.26	
TMEM18			
CHIC1	Q5VXU3	18.18	
PLD4	Q96BZ4	25.62	

Dut	Q9CQ43	59.86
Rrm2b	Q6PEE3	75.24
Ifitm10?	Q8BR26	17.11
Ide	P22817	17.9
just below threshhold: FEN1/XRN2/XRN1 nucleases		
just below threshhold: polr2l		
just below threshhold: Plaat1, tmem222 - previously shown to have similarity to bacterial peptidase, NLPC/P6		
PCNA	Q9VIT0	20.4
Phosphatases (top: Danio tyrosine phosphatase Q0P4E3)	Q0P4E3	27.03
top1	E7FE49	19.59
mt-co3		
Rrm1	P07742	76.01
ambiguous, maybe odorant receptors/olfactory receptors?		
helicases (top: DHX35)	Q9H5Z1	20.5
TK1	P04184	66.67
cmtr2	Q9UAS6	19.75
POLR2E	P19388	21.88

POLR2A	P24928	24.07
Ankyrin proteins (top: Nfkbid)	Q2TB02	19.03
Serpins (top: SERPINA3	P01011	24.59
polr2g	P62488	20.48
PLD3	O35405	47.73
Mgll	O35678	32.35
Mgll		
BCL2L10	Q9Z0F3	18.8
ambiguous		
ASB2, other ankyrin	Q96Q27	23.94
MCL1		
Glrx	P35754	46.23

ccinia proteins with few structural motifs.
f interest.

s of a Serpin present as a single ORF in vaccinia strain WR

family, Plaat is a phospholipase/acyltransferase within this family

Synteny Analysis

Genome	Accession
Vaccinia virus	NC_006998
Skunkpox virus	NC_031038
NY014 poxvirus	NC_035469.1
Myxoma virus	NC_001132.2
Eptesipox virus	NC_035460.1

Poxvirus BLAST Database

Genome	Accession
Cotia virus	HQ646181.2
Saltwater crocodilepox	MK903858.1
Deerpox virus	AY689437.1
Fowlpox virus	MH706124.1
Eastern grey kangaroopox virus	MF661791.2
Lumpy skin disease virus	NC_003027.1
Molluscum contagiosum virus	MH320554.1
Orf virus	MG716417.1
Pteropox virus	KU980965.1
Sea otter poxvirus	MH427217.1
Sheeppox virus	MN072631.1
Squirrel poxvirus	HE601899.1
Swinepox virus	MZ682626.1
Yaba monkey tumor virus	AY386371.1

Viral gasdermins

Protein	Accession
Vaccinia virus gasdermin (COP)	M35027.1:c153690-152956
Rabbitpox virus gasdermin	AY484669.1:c159516-158782
Horsepox virus gasdermin	KY349117.1:c166272-165538
Buffalopox virus gasdermin	MG599038.1:c157906-157148
Vaccinia virus gasdermin (WR)	AY243312.1:c154675-153917
Cowpox virus gasdermin	KC813500.1:c153312-152578
Orthopoxvirus abatino gasdermin	NC 055231.1:c163765-163031
Ectromelia virus gasdermin	MN912466.1:c156293-155559
Akhmeta virus gasdermin	MH607143.1:c167386-166652
Taterapox virus gasdermin	DQ437594.1:c153307-152573
Variola virus gasdermin (17CE)	KY358055.1:c145385-144651
Variola virus gasdermin (1947)	DQ441432.1:c146026-145292
Variola virus gasdermin (1969)	DQ441437.1:c146904-146170
Alaskapox virus gasdermin	MN240300.1:c166555-165827
Skunkpox virus gasdermin	KU749310.1:c167631-166873
Volepox virus gasdermin	KU749311.1:c169057-168281
Raccoonpox virus gasdermin	KU749309.1:c145369-144644
Camelpox virus gasdermin (CMS, truncated)	AY009089.1:c154402-154034
Camelpox virus gasdermin (truncated)	MK910851.1:c154204-153836
NY014 poxvirus gasdermin	MF001305.1:c159640-158771
Murmansk poxxvirus gasdermin	MF001304.1:c160603-159728
Yoka poxvirus gasdermin	HQ849551.1:c134784-134035
Skunkpox virus gasdermin (short)	KU749310.1:172437-172985
Racconpox virus gasdermin (short)	KU749309.1:150174-150722
Volepox virus gasdermin (short)	KU749311.1:173861-174445
Murmansk poxxvirus gasdermin (short)	MF001304.1:c165763-165224
NY014 poxvirus gasdermin (short)	MF001305.1:c164808-164269
Myxoma virus gasdermin	NP_051846.1
Rabbit fibroma virus gasdermin	NP_052021.1
Eptesipox virus gasdermin	YP_009408097.1

Vertebrate gasdermins

Protein	Accession
Human gasdermin a	NP_835465.2
Chicken gasdermin a	NP_001026532.1
Bos taurus gasdermin a	NP_001071558.1
Macaca mulatta gasdermin a	XP_014975037.1
Pan troglodytes gasdermin a	XP_001171222.1
Desmodus rotundus gasdermin a	XP_024429158.1
Rousettus aegyptiacus gasdermin a	XP_016020091.2
Pteropus alecto gasdermin a	XP_006924750.1
Halichoerus grypus gasdermin a	XP_035935879.1
Octodon degus gasdermin a	XP_004633937.1
Rhinatrema bivittatum gasdermin a	XP_029428328.1
Amblyraja radiata gasdermin a	XP_032891479.1
Mouse gasdermin a3	Q5Y4Y6
Mouse gasdermin a3	Q9EST1

Mouse gasdermin a2	Q32M21
Human gasdermin b	NP_001159430.1
Bos taurus gasdermin b	NP_001231146.1
Pan troglodytes gasdermin b	XP_009430521.1
Sarcophilus harrisii gasdermin b	XP_023358160.1
Pteropus alecto gasdermin b	XP_024897515.1
Rousettus aegyptiacus gasdermin b	XP_036078993.1
Desmodus rotundus gasdermin b	XP_024429114.1
Macaca mulatta gasdermin b	XP_014975035.1
Halichoerus grypus gasdermin b	XP_035935913.1
Human gasdermin c	NP_113603.1
Macaca mulatta gasdermin c	XP_28708741.1
Bos taurus gasdermin c	NP_001039469.1
Sarcophilus harrisii gasdermin c	XP_31803207.1
Rousettus aegyptiacus gasdermin c	XP_036088919.1
Desmodus rotundus gasdermin c	XP_024427836.1
Felis catus gasdermin c	XP_019678683.1
Pan troglodytes gasdermin c	XP_001153860.1
Mus pahari gasdermin c	XP_021073018.1
Human gasdermin d	NP_079012.3
Mouse gasdermin d	NP_081236.1
Bos taurus gasdermin d	NP_001039625.1
Macaca mulatta gasdermin d	XP_015001615.2
Pteropus alecto gasdermin d	XP_006913014.1
Rousettus aegyptiacus gasdermin d	XP_036089037.1
Desmodus rotundus gasdermin d	XP_024428237.1
Pan troglodytes gasdermin d	XP_009454389.2
Felis catus gasdermin d	XP_023104116.1
Human gasdermin e	NP_001120925.1
Mouse gasdermin e	NP_061239.1
Chicken gasdermin e	NP_001006361.1
Bos taurus gasdermin e	NP_001180041.1
Xenopus tropicalis gasdermin e	XP_002933445.2
Macaca mulatta gasdermin e	XP_001096213.2
Pteropus alecto gasdermin e	XP_006912063.1
Sarcophilus harrisii gasdermin e	XP_031796450.1
Chelonia mydas gasdermin e	XP_027689547.1
Rana temporaria gasdermin e	XP_040208817.1
Chrysemys picta bellii gasdermin e	XP_023962559.1
Rhinatrema bivittatum gasdermin e	XP_029444983.1
Octodon degus gasdermin e	XP_004626528.1
Mus pahari gasdermin e	XP_021046698.1
Pygosceli adeliae gasdermin e	XP_009324004.1
Desmodus rotundus gasdermin e	XP_024418892.1
Rousettus aegyptiacus gasdermin e	XP_016015046.2
Amblyraja radiata gasdermin e	XP_032903802.1
Pan troglodytes gasdermin e	XP_001159685.3

Omitted from tree (severe truncation)

Hypsugopox virus gasdermin (pseudogene)	MK860688.1:c133573-132651

Vertebrate pyrin domain containing proteins

Protein	Accession
POP1 (Human)	NP_690865.1
ASC (Human)	NP_660183.1
Danio PYD protein	NP_001104231.1
ASC (Danio)	Q9I9N6.1
PYDC2 (Human)	NP_001076777.1
AIM2 (Mouse)	NP_001013801.2
IFI203 (Mouse)	BAE43039.1
Danio CASPb	NP_690840.2
Danio CASPa	NP_571580.1

M013L family

Protein	Accession
M013L	NP_051727.1
S013L	NP_051902.1
Deerpox M013L homolog	YP_227401.1
Yaba M013L homolog	NP_073403.1
Tanapox M013L homolog	ABQ43490.1
Swinepox m013L homolog	NP_570174.1

C1L family

Protein	Accession
Vaccinia C1 protein	P21036.1
Buffalopox C1 homolog	QCY53926.1
Cowpox C1 homolog	AGY97559.1
Rabbitpox C1 homolog	AAS49732.1
Horsepox C1 homolog	YP_010509239.1
Orthopox abatino C1 homolog	YP_010085697.1
Akhmeta virus C1 homolog	YP_010085480.1
Variola B22L (C1 homolog)	AAA69361.1
Monkeypox C1 homolog	YP_010377017.1
Alaskapox C1 homolog	QED21215.1
Volepox C1 homolog	YP_009281774.1
Skunkpox C1 homolog	YP_009282720.1
Raccoonpox C1 homolog	YP_009143336.1
NY014 poxvirus C1 homolog	YP_009408409.1
Murmansk poxvirus C1 homolog	YP_009408207.1
Yoka poxvirus C1 homolog	YP_004821365.1

Cloning

OLIGO
pCMV_hsGSDMD_N_R
pCMV_hsGSDMD_C_F
pCMV_hsGSDMD_C_R
pEF-Flag_F
pEF-C1_R
C1_PYD_r
C1_bcl2_fwd1
C1_bcl2_fwd2
cop_donor_c1_5pF
cop_donor_c1_5pR
cop_donor_c1_3pF
cop_donor_c1_3pR

PCR Genotyping for Recombinant Virus

OLIGO
a47_5p_flank_PCRfwd
a47_5p_flank_PCRrev_rec
a47_5p_flank_PCRrev_wt
a47_3p_flank_PCRfwd_rec
a47_3p_flank_PCRfwd_wt
a47_3p_flank_PCRrev
c1_5p_flank_PCRfwd
c1_5p_flank_PCRrev_wt
c1_3p_flank_PCRfwd_wt
c1_3p_flank_PCRrev

SEQUENCE
CGTCAActcgagctaATCTGTCAAGAAATTGTGGAG
gacctctagaaccATGGAACAAAAACTCATCTCAGAAGAGGATCTGggttctGGGGTCCCCGCTGAAG
CGTCAACTCGAGctaATGGGGTTCTTGGCTAAGACCGGAC
gaatCCCGGGaccatggactacaaagacg
CCACTAgcggccgcctaTTTGCTCATAAGTTCCTTC
CATAgcggccgcctaGAGTATAGCAAATCTGACTGCTG
gacgacaagGGTGGAGGTGGTACCatgGACAAAATGACCGAGGATATTAAGC
gacctctagaaccatggactacaaagacgatgacgacaagGGTGGAGG
gctcaagcttttcatcctttgataattttccaaattc
gctaCAATTGtttttttataaaaaatattgaatatatataaacctttac
gcttCTCGAGttatttatttttcaccatatagatcaatcattagatc
gctaGAGCTCttcaaatgtttcattaactacgtg

SEQUENCE
cgattaatgccccacgagac
GTGACCGTTTACGTCGCC
gagcttagtccgtttgtccac
GAGGACGTGACGGCTG
ctgagaggtcaatacctaactcc
cgtctacatgttctgccgtaac
cggagacgccgtaataatttcc
cctacgataggacacgtaaaagc
catcatctgtaagatttttgagatgtc
cgctaagcgaatgatcgc

NOTES
PCR off of gBlock for full-length GSDMD
PCR off of gBlock for full-length GSDMD
PCR off of gBlock for full-length GSDMD
For all FLAG-tagged constructs (C1)
For C1 full length and C1 BCL2 domain
used with pEF-Flag_F
first PCR for BCL2 domain cloning: used with with pEF_C1_R
second PCR for BCL2 domain cloning: used with pEF_C1_R, had to add a third PCR round (pEF_C1_
Used VC2 DNA as template to paste into cut pUC19_muGFP_A47_donor vector
Used VC2 DNA as template to paste into cut pUC19_muGFP_A47_donor vector
Used VC2 DNA as template to paste into cut pUC19_muGFP_A47_donor vector
Used VC2 DNA as template to paste into cut pUC19_muGFP_A47_donor vector

NOTES

expect:250bp
expect: 380bp

expect: 287bp
expect: 191
TM 57, for recomb: use with a47_5p_flank_PCRrev_rec: expect 270bp product, for WT use with c1_5
TM56
TM 54
TM 55, for rec use with a47_5p_flank_PCRrev_wt, expect 220bp product, for WT expect 240 (with c1_

R) to add correct cut site due to mistake in cloning design

p_flank_PCRfwd, expect 240bp product

_5p_flank_PCRrev_wt)

pCMV_vvGSDM	This Study
pCMV_GSDMD_CTD	This Study
pEF1α_C1	This Study
pEF1α_C1_PYD	This Study
pEF1α_C1_BCL2	This Study
pUC19_muGFP_Donor_A47	This Study
pUC19_muGFP_Donor_C1	This Study
pET_SUMO_eptvGSDM	This Study

pLEX-MCS-ASC-GFP was a gift from Christian Stehlik (Addgene, catalog number: 73957)
pCMV-pro-IL1β-C-Flag was a kind gift from Bruce Beutler (Addgene, catalog number: 75131)
pcDNA3-N-Flag-NLRP3 was a kind gift from Bruce Beutler (Addgene, catalog number: 75127)
pcDNA3-N-Flag-ASC1 was a kind gift from Bruce Beutler (Addgene, catalog number: 75134)
pcDNA3-N-Flag-Caspase-1 was a kind gift from Bruce Beutler (Addgene, catalog number: 75128)
pcDNA3-N-HA-NEK7 was a kind gift from Bruce Beutler (Addgene, catalog number: 75142)

Table S1. Crystallographic statistics, Related to Figure 2 and Figure NN

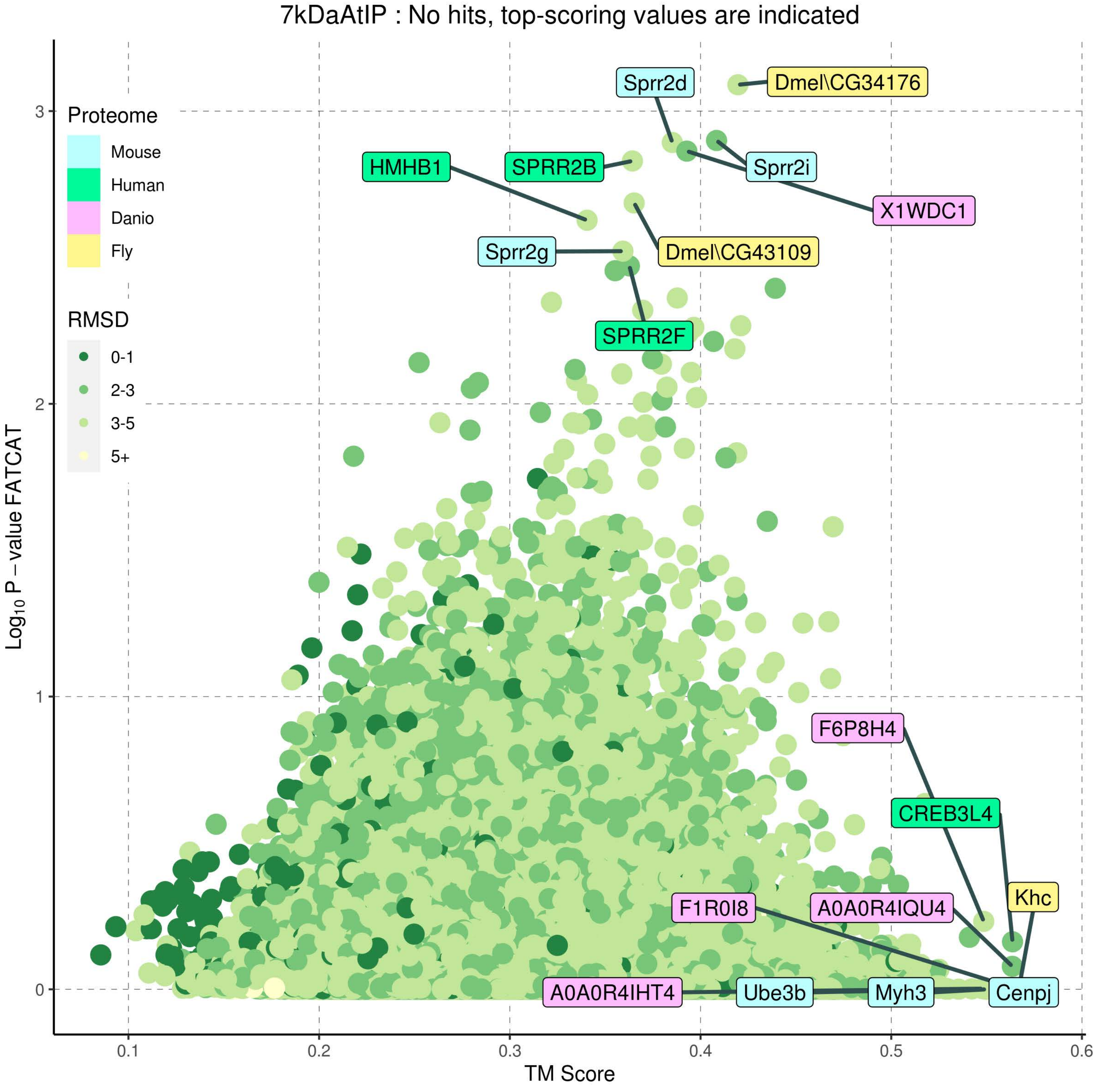
	EPTV A47L	EPTV A47L (SeMet)
Data Collection		
Resolution (Å)[a]	48.65–1.46 (1.48–1.46)	48.39–1.54 (1.57–1.54)
Wavelength (Å)	0.9792	0.9792
Space group	C 2 2 2_1	C 2 2 2_1
Unit cell: a, b, c (Å)	64.46 74.14 95.60	63.51, 74.71, 95.29
Unit cell: α, β, γ (°)	90.00 90.00 90.00	90.00, 90.00, 90.00
Molecules per ASU	1	1
Total reflections	543256	920245
Unique reflections	40114	33934
Completeness (%)[a]	100.0 (99.6)	100.0 (99.9)
Multiplicity[a]	13.5 (13.2)	27.1 (23.4)
I/σI[a]	18.3 (1.6)	15.7 (2.1)
CC(1/2)[b] (%)[a]	99.9 (50.5)	99.9 (88.8)
Rpim[c] (%)[a]	1.9 (71.8)	3.0 (68.9)
Sites		5
Refinement		
Resolution (Å)	48.65–1.46	
Free reflections	40033	
R-factor / R-free	19.0 / 21.2	
Bond distance (RMS Å)	0.01	
Bond angles (RMS °)	1.10	
Structure/Stereochemistry		
No. atoms: protein	1658	
No. atoms: water	85	
Average B-factor: protein	32.8	
Average B-factor: water	43.1	
Ramachandran plot: favored	99.01%	
Ramachandran plot: allowed	0.99%	
Ramachandran plot: outliers	0.00%	
Rotamer outliers	0.52%	
MolProbity[d] score	1.05	
Protein Data Bank ID	**TBD**	

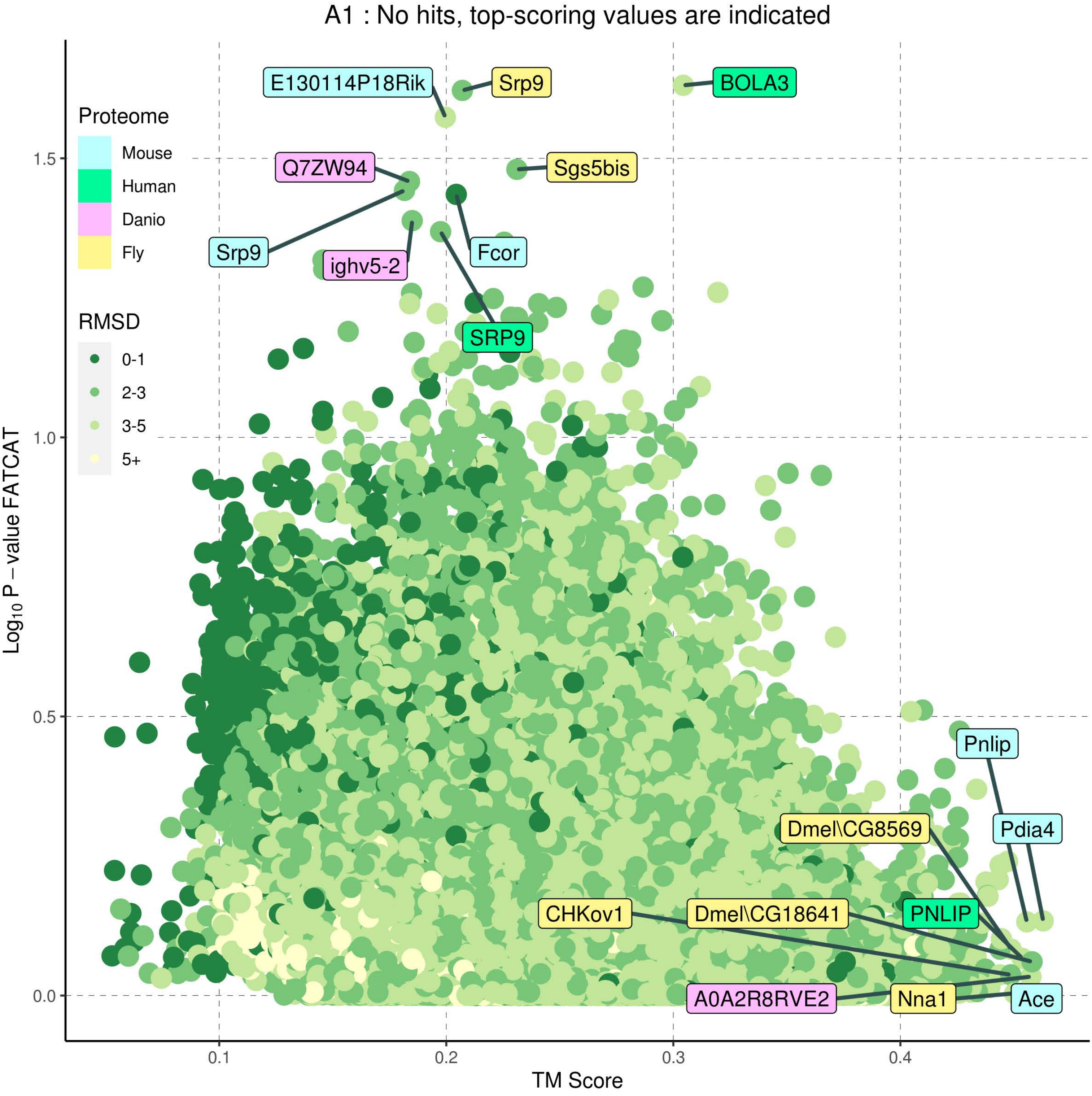
[a] Highest resolution shell values in parentheses

[b] (Karplus and Diederichs, 2012)

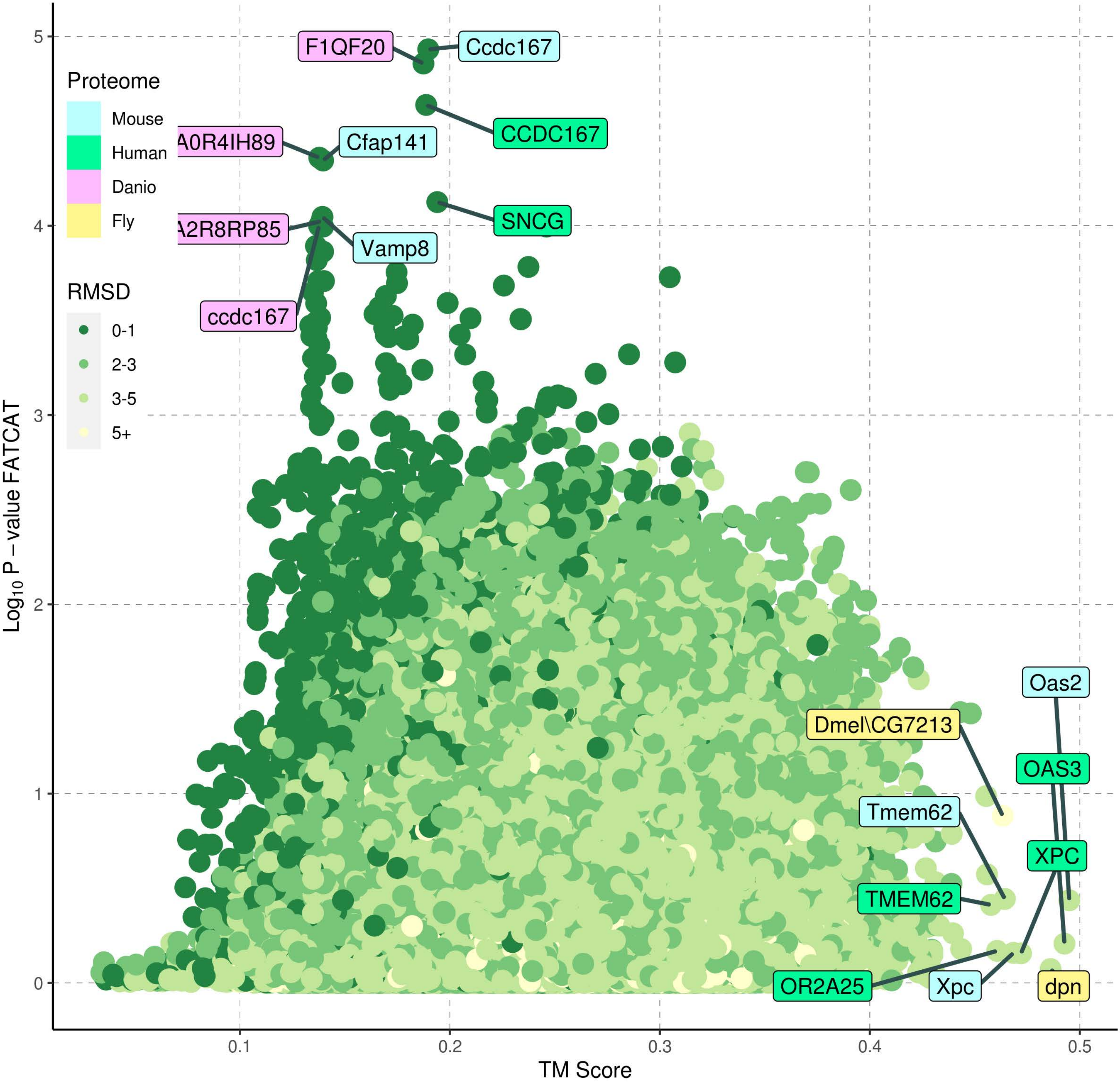
[c] (Weiss, 2001)

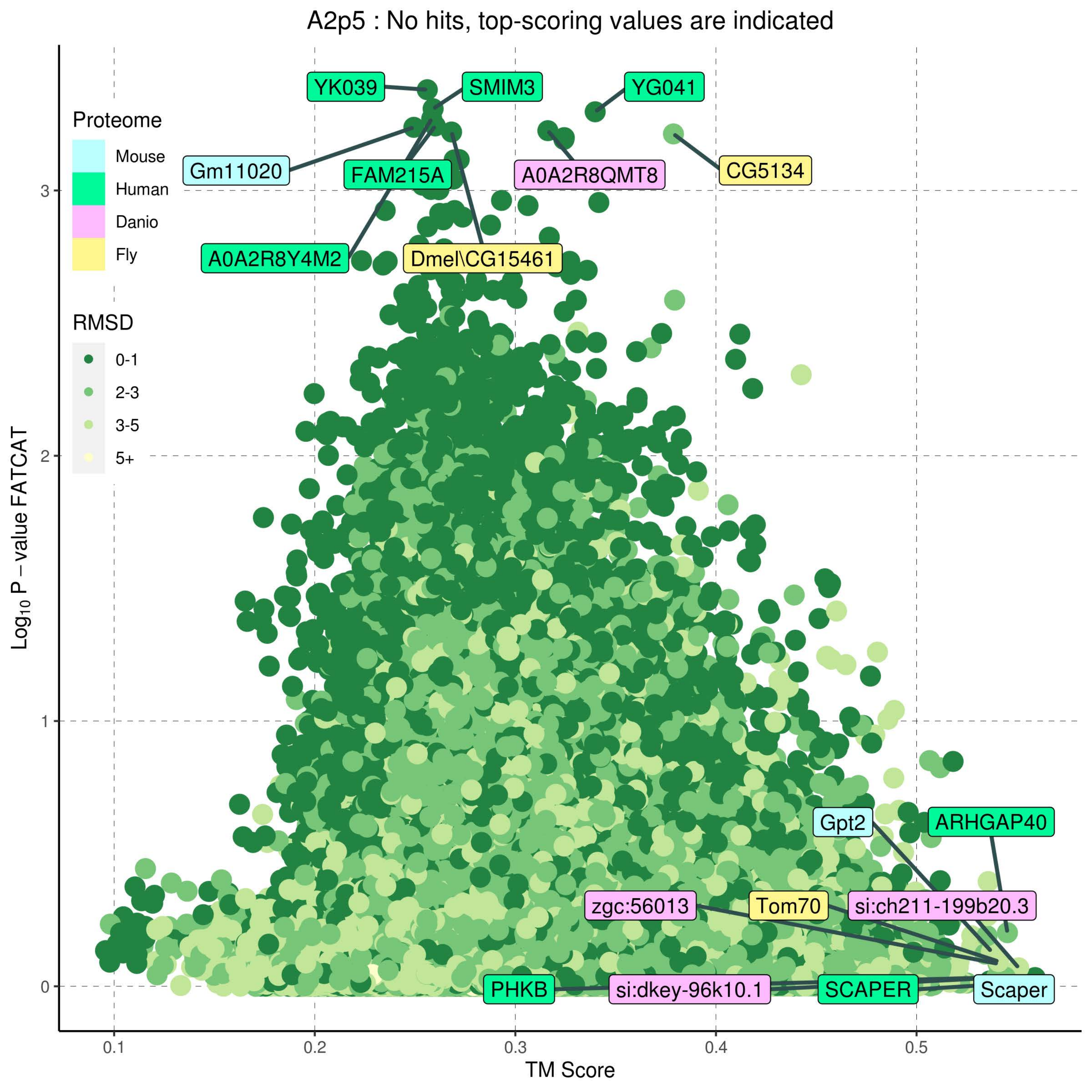
[d] (Chen et al., 2010)

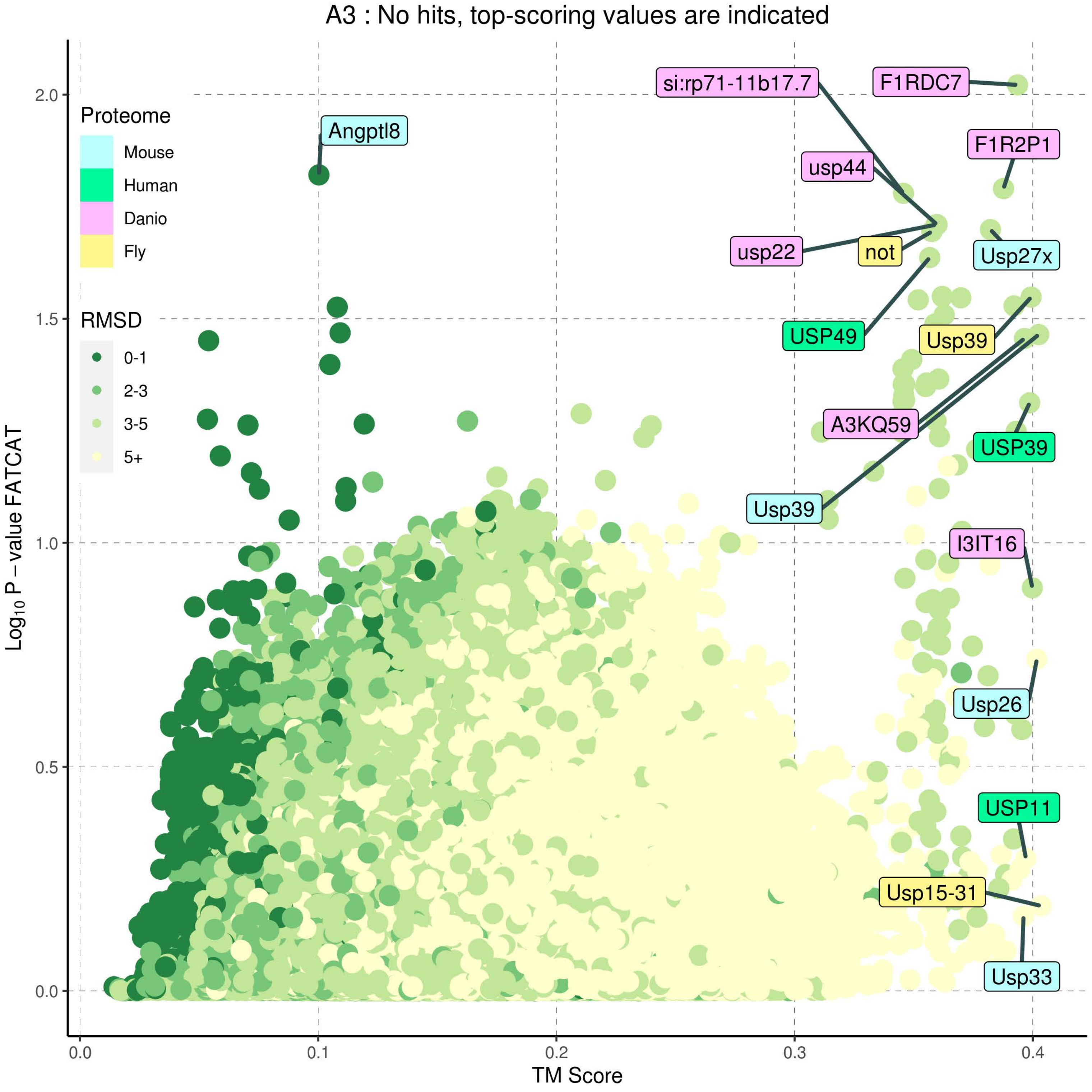

7kDaAtIP : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Sprr2d
Dmel\CG34176
HMHB1
SPRR2B
Sprr2i
X1WDC1
Sprr2g
Dmel\CG43109
SPRR2F
F6P8H4
CREB3L4
Khc
F1R0I8
A0A0R4IQU4
A0A0R4IHT4
Ube3b
Myh3
Cenpj
Log10 P – value FATCAT
0
1
2
3
TM Score
0.1
0.2
0.3
0.4
0.5
0.6

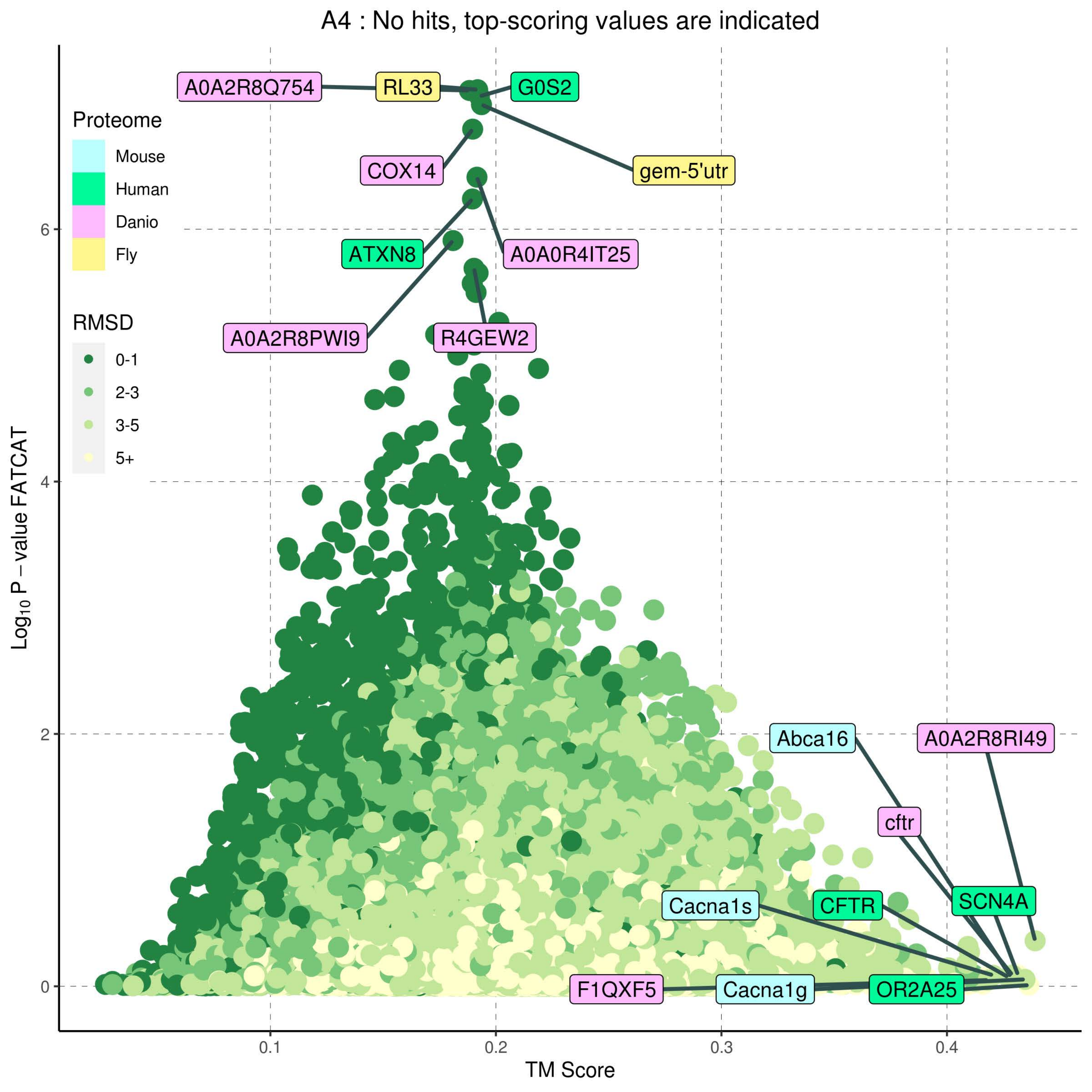

A1 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
E130114P18Rik
Srp9
BOLA3
Q7ZW94
Sgs5bis
Srp9
ighv5-2
Fcor
SRP9
Pnlip
Pdia4
Dmel\CG8569
CHKov1
Dmel\CG18641
PNLIP
A0A2R8RVE2
Nna1
Ace
Log10 P – value FATCAT
1.5
1.0
0.5
0.0
0.1
0.2
0.3
0.4
TM Score

A2 : No hits, top-scoring values are indicated

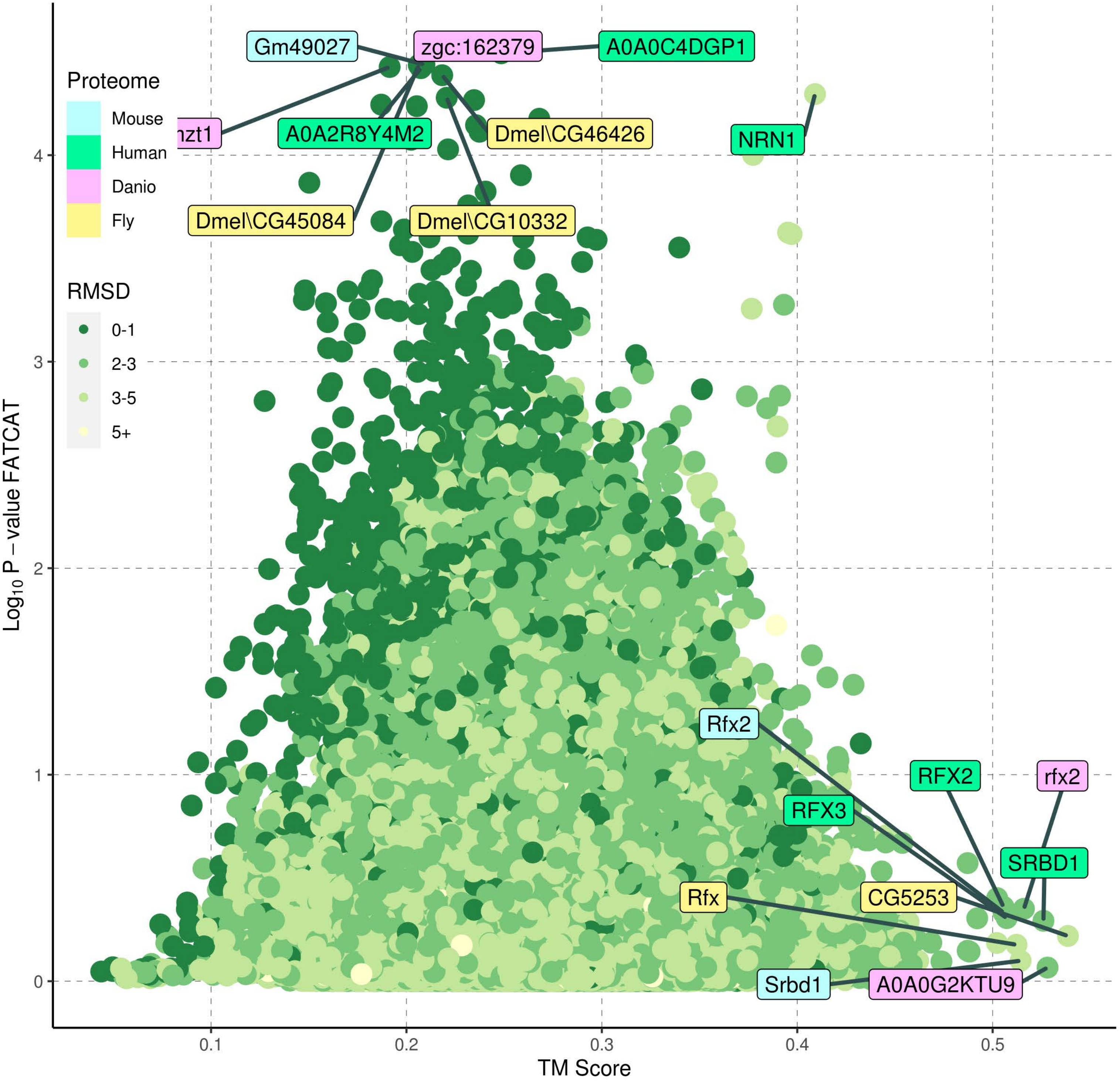



A2p5 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
YK039
SMIM3
YG041
Gm11020
FAM215A
A0A2R8QMT8
CG5134
A0A2R8Y4M2
Dmel\CG15461
Gpt2
ARHGAP40
zgc:56013
Tom70
si:ch211-199b20.3
PHKB
si:dkey-96k10.1
SCAPER
Scaper
Log10 P − value FATCAT
TM Score
0
1
2
3
0.1
0.2
0.3
0.4
0.5

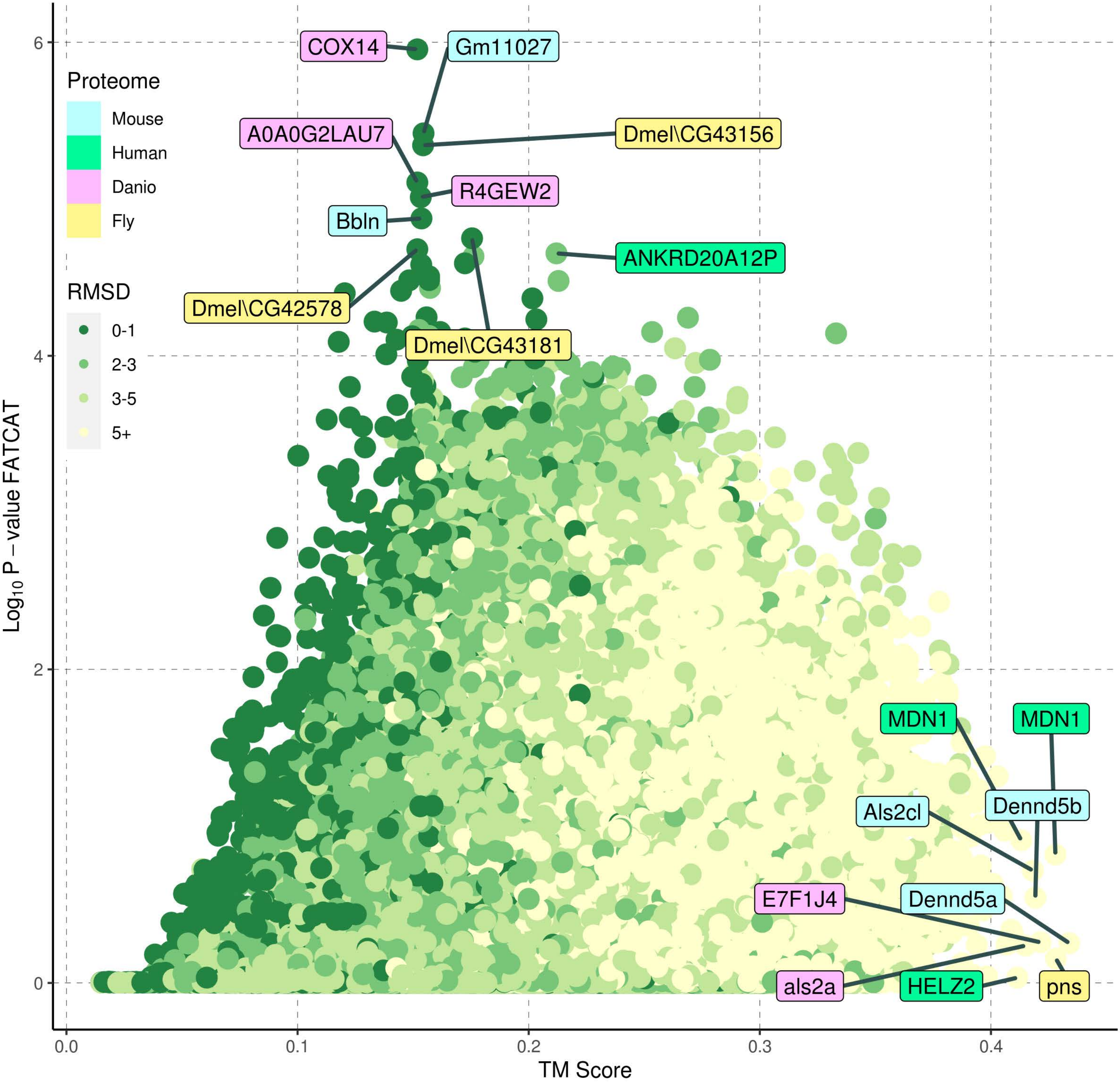

A3 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log₁₀ P − value FATCAT
TM Score
0.0
0.5
1.0
1.5
2.0
0.0
0.1
0.2
0.3
0.4
Angptl8
si:rp71-11b17.7
F1RDC7
F1R2P1
usp44
usp22
not
Usp27x
USP49
Usp39
A3KQ59
USP39
Usp39
I3IT16
Usp26
USP11
Usp15-31
Usp33

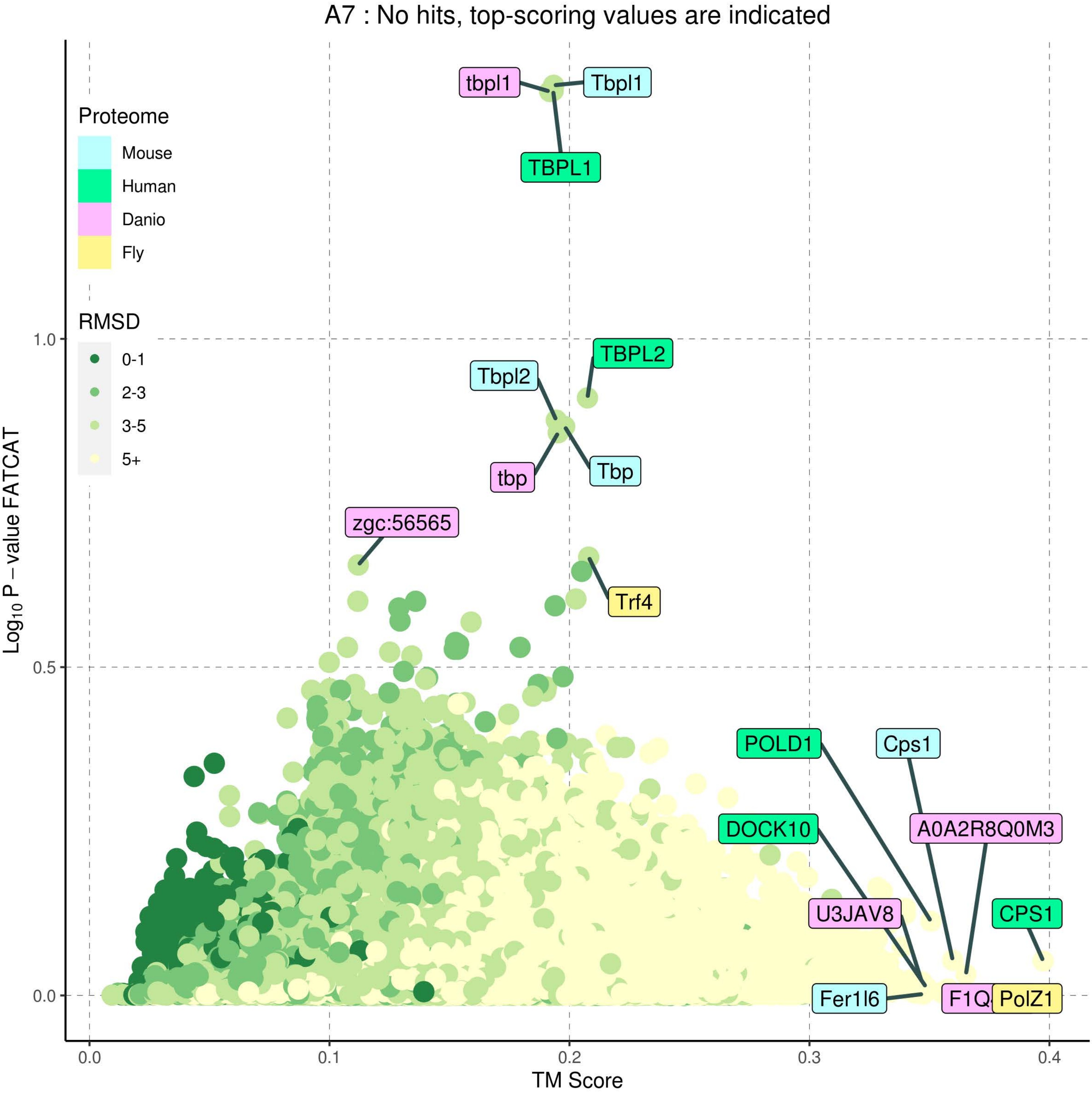

A4 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
TM Score
0
2
4
6
0.1
0.2
0.3
0.4
A0A2R8Q754
RL33
G0S2
COX14
gem-5'utr
ATXN8
A0A0R4IT25
A0A2R8PWI9
R4GEW2
Abca16
A0A2R8RI49
cftr
SCN4A
Cacna1s
CFTR
F1QXF5
Cacna1g
OR2A25

A5 : No hits, top-scoring values are indicated



A6 : No hits, top-scoring values are indicated




A7 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log$_{10}$ P − value FATCAT
TM Score
0.0
0.5
1.0
0.0
0.1
0.2
0.3
0.4
tbpl1
Tbpl1
TBPL1
TBPL2
Tbpl2
tbp
Tbp
zgc:56565
Trf4
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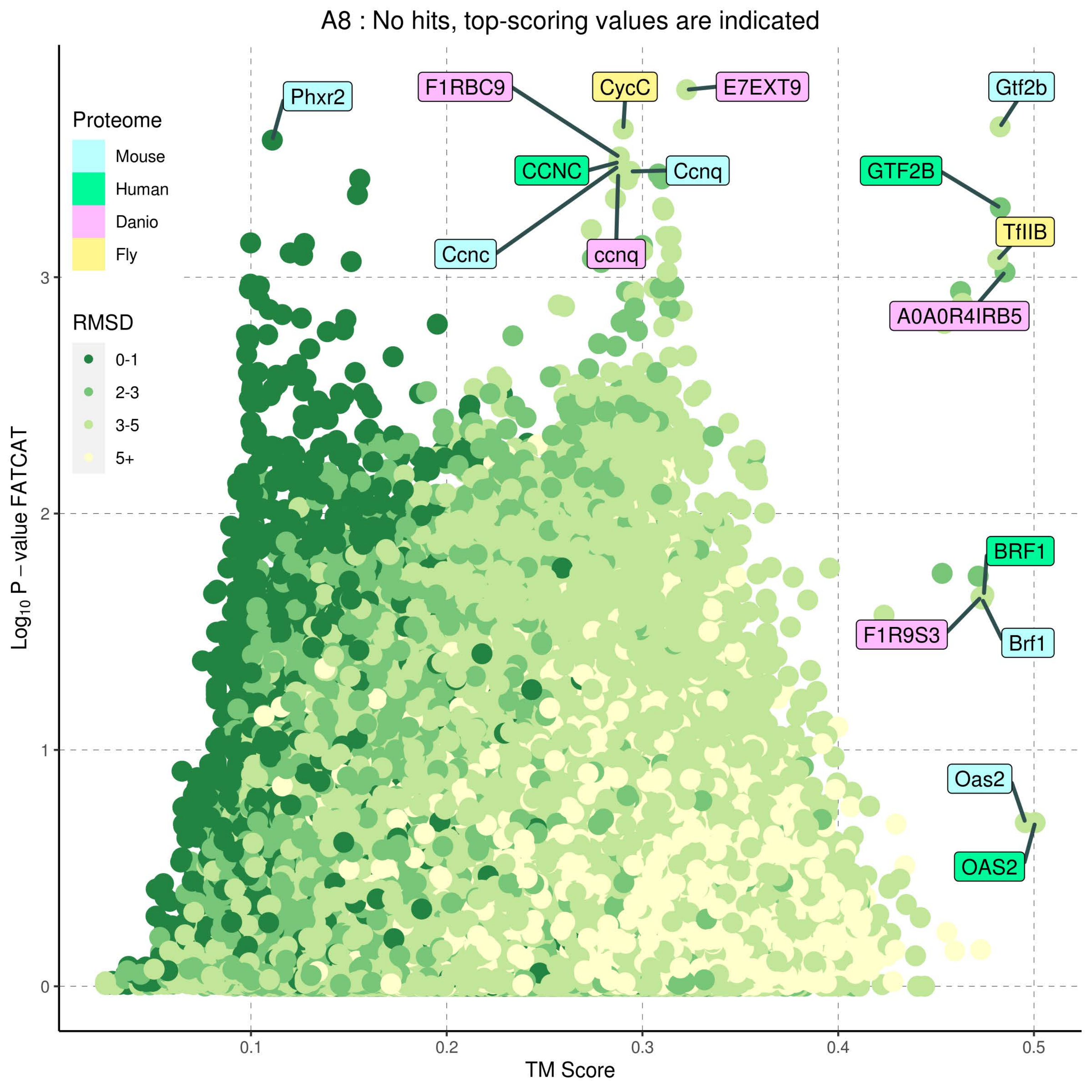
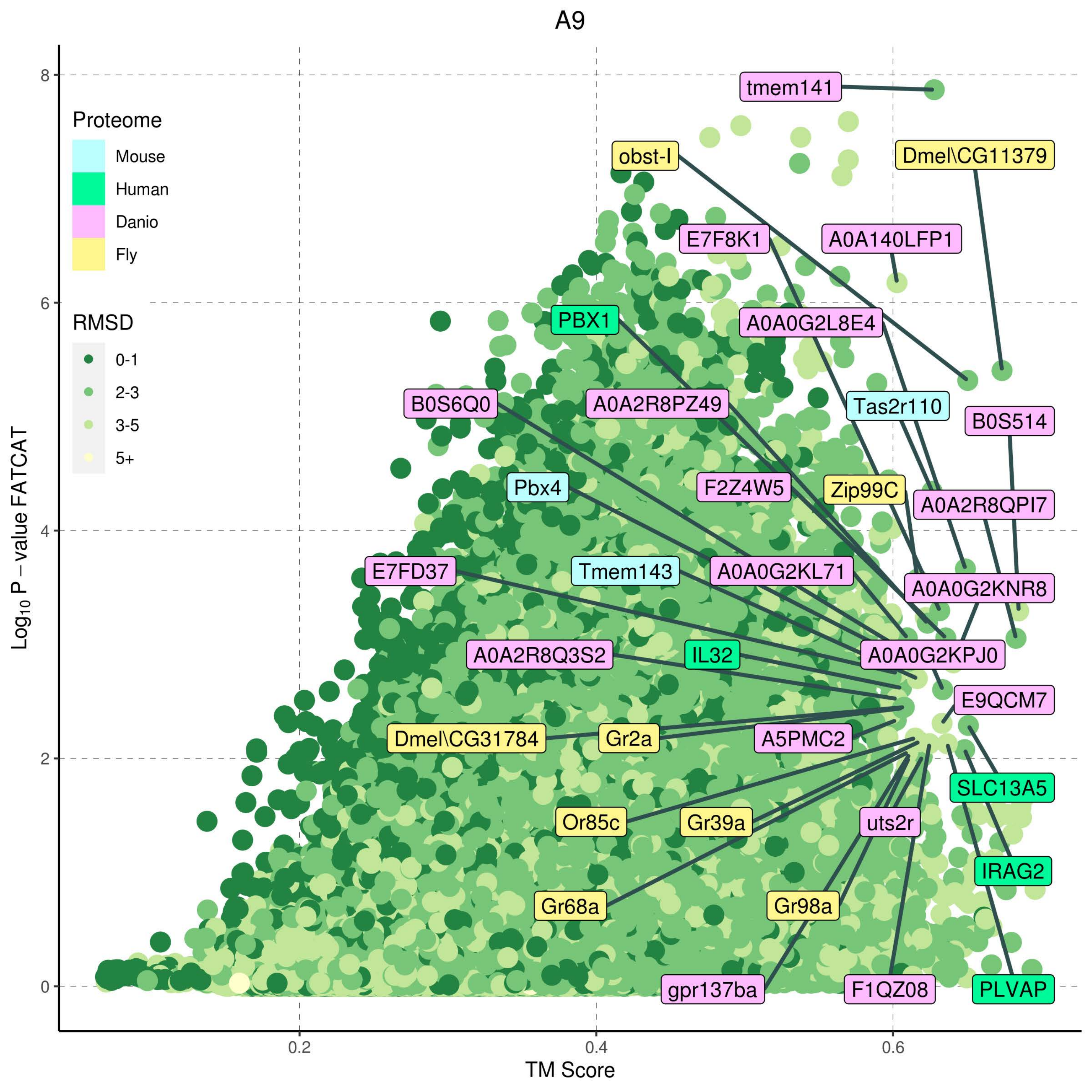
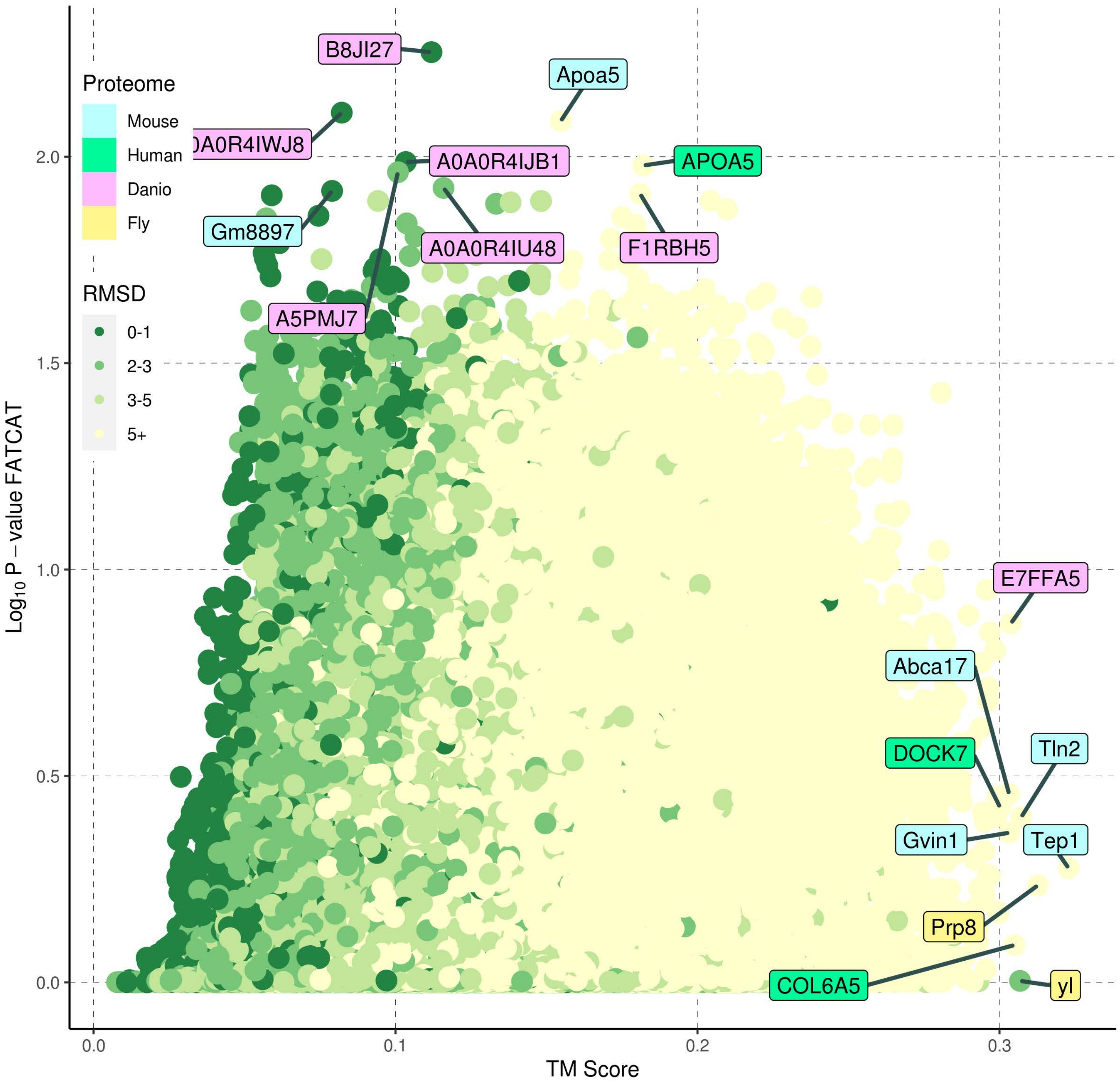
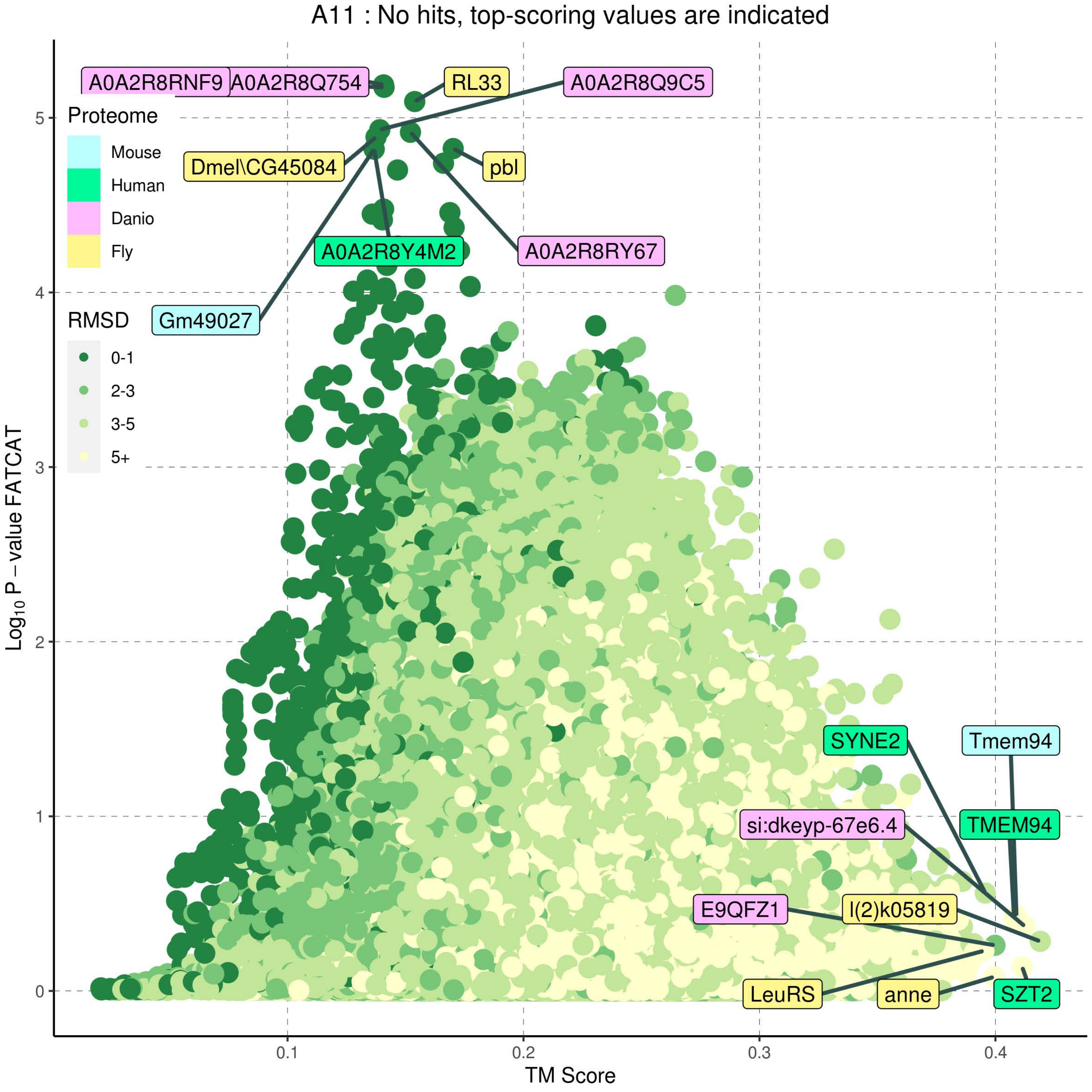
Fer1l6
F1Q
PolZ1


A8 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Phxr2
F1RBC9
CycC
E7EXT9
Gtf2b
CCNC
Ccnq
GTF2B
Ccnc
ccnq
TfIIB
A0A0R4IRB5
BRF1
F1R9S3
Brf1
Oas2
OAS2
Log10 P − value FATCAT
0
1
2
3
0.1
0.2
0.3
0.4
0.5
TM Score


A9
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
tmem141
obst-I
Dmel\CG11379
E7F8K1
A0A140LFP1
PBX1
A0A0G2L8E4
B0S6Q0
A0A2R8PZ49
Tas2r110
B0S514
Pbx4
F2Z4W5
Zip99C
A0A2R8QPI7
E7FD37
Tmem143
A0A0G2KL71
A0A0G2KNR8
A0A2R8Q3S2
IL32
A0A0G2KPJ0
E9QCM7
Dmel\CG31784
Gr2a
A5PMC2
SLC13A5
Or85c
Gr39a
uts2r
IRAG2
Gr68a
Gr98a
gpr137ba
F1QZ08
PLVAP
Log$_{10}$ P − value FATCAT
8
6
4
2
0
TM Score
0.2
0.4
0.6



A10 : No hits, top-scoring values are indicated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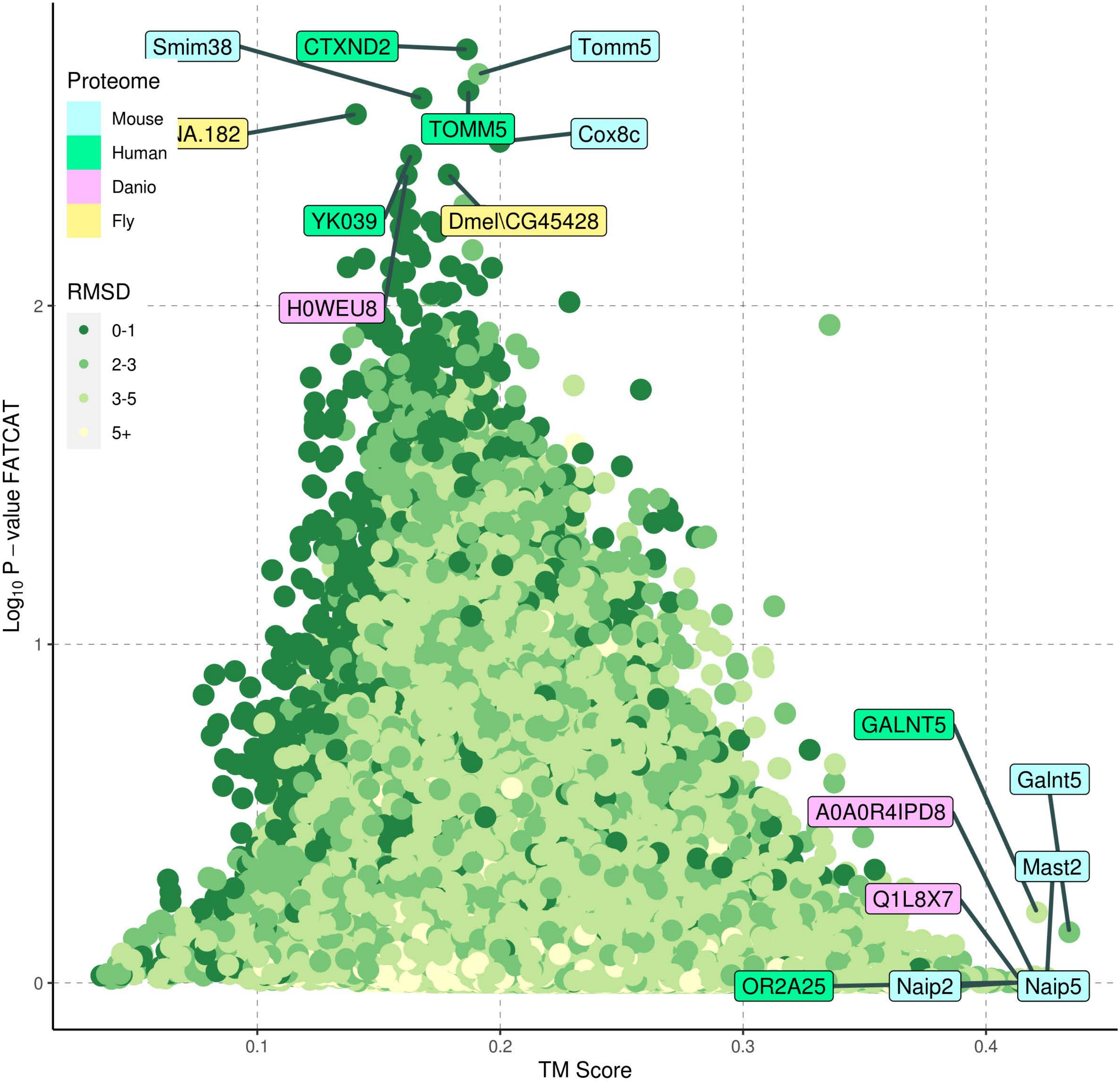
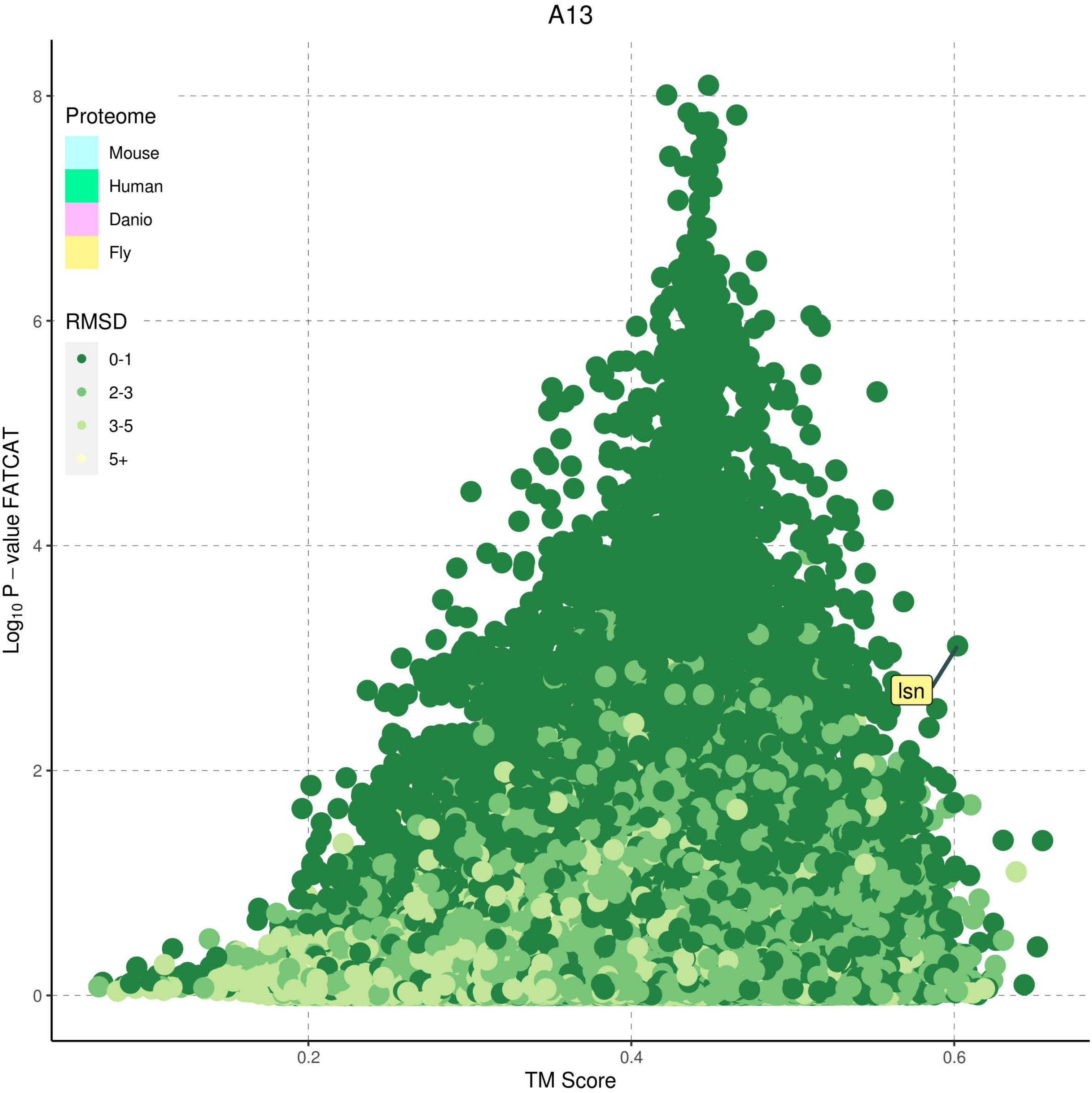
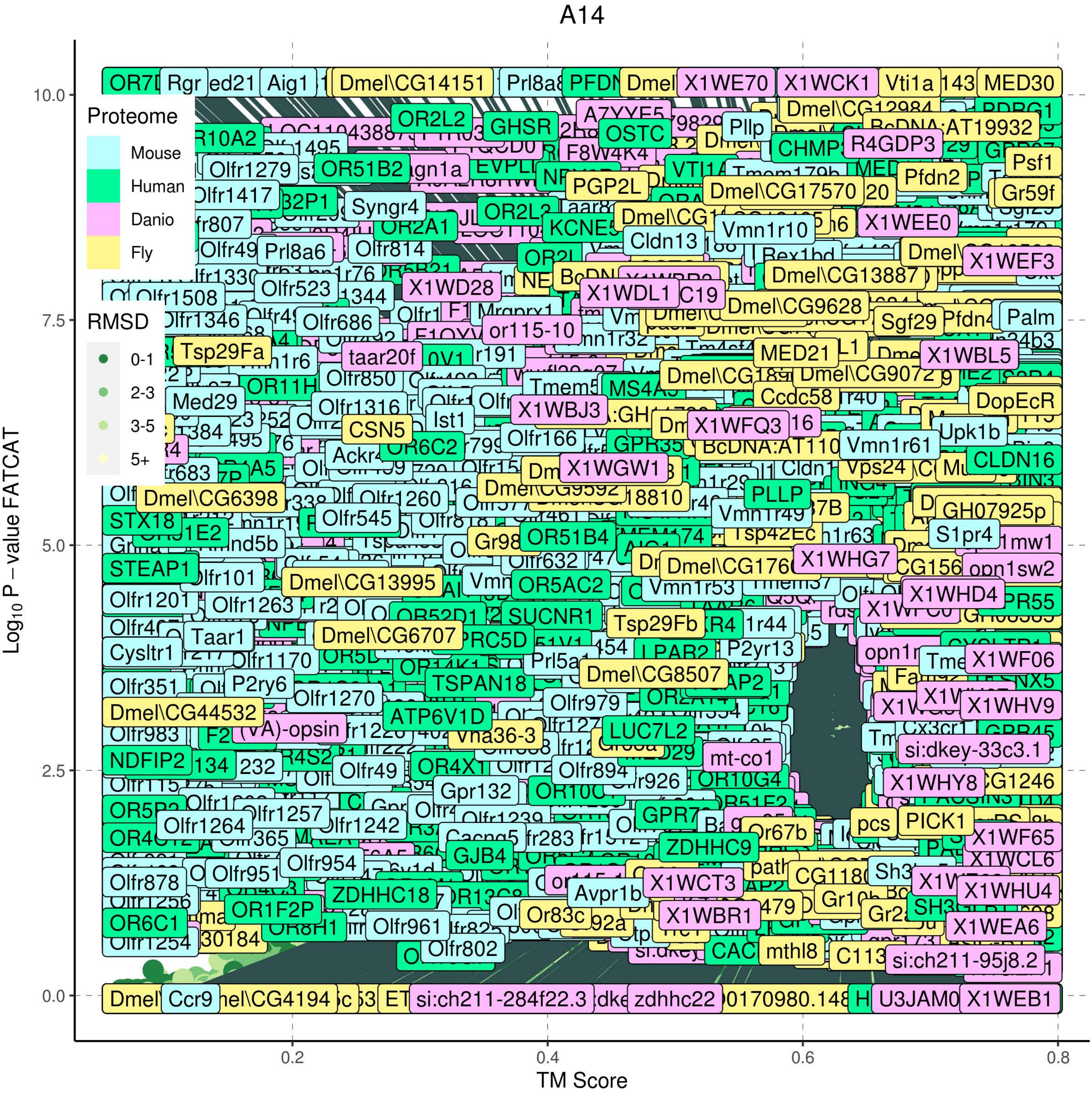
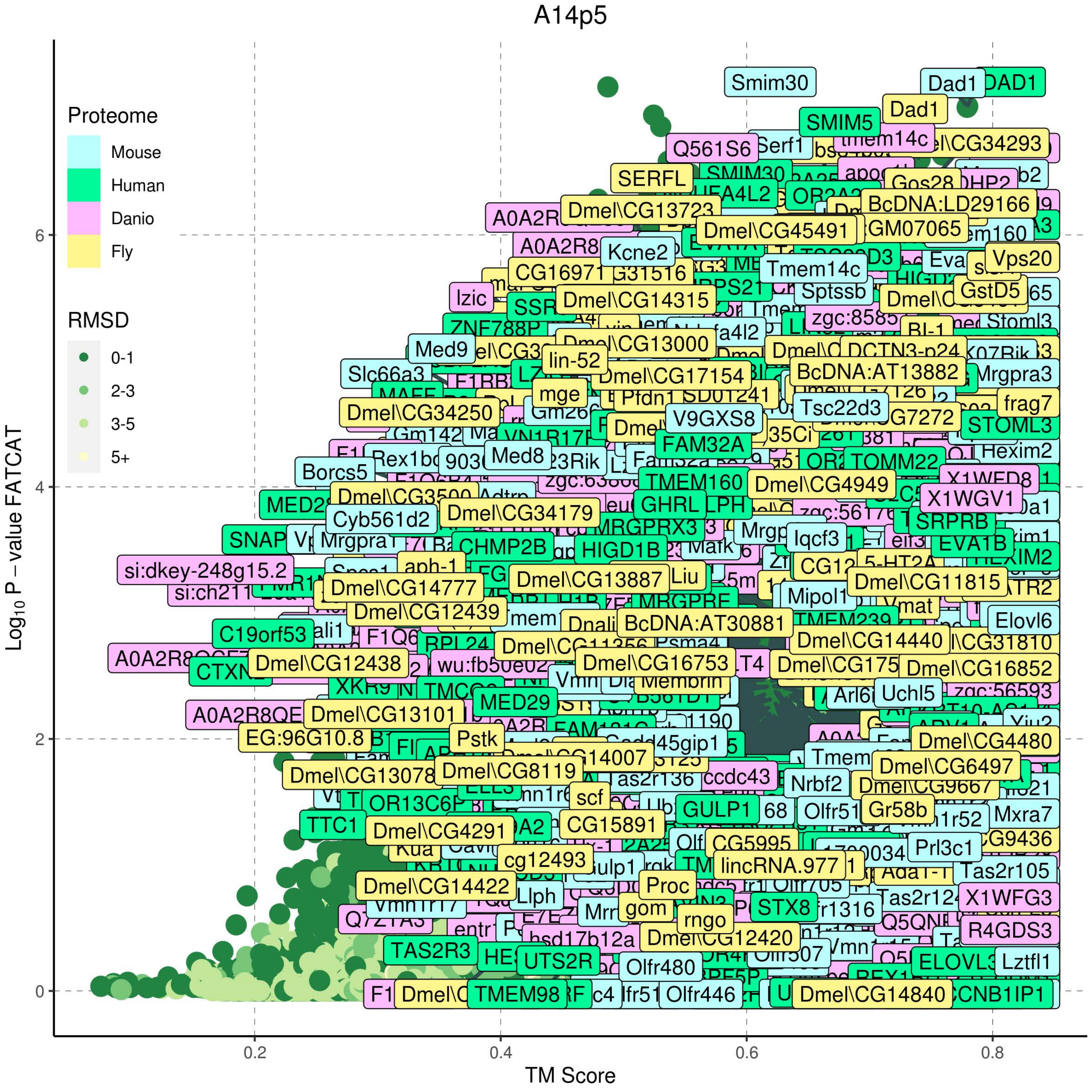
RL33
A0A2R8Q9C5
Dmel\CG45084
pbl
A0A2R8Y4M2
A0A2R8RY67
Gm49027
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
SYNE2
Tmem94
si:dkeyp-67e6.4
TMEM94
E9QFZ1
l(2)k05819
LeuRS
anne
SZT2
Log10 P − value FATCAT
0
1
2
3
4
5
TM Score
0.1
0.2
0.3
0.4

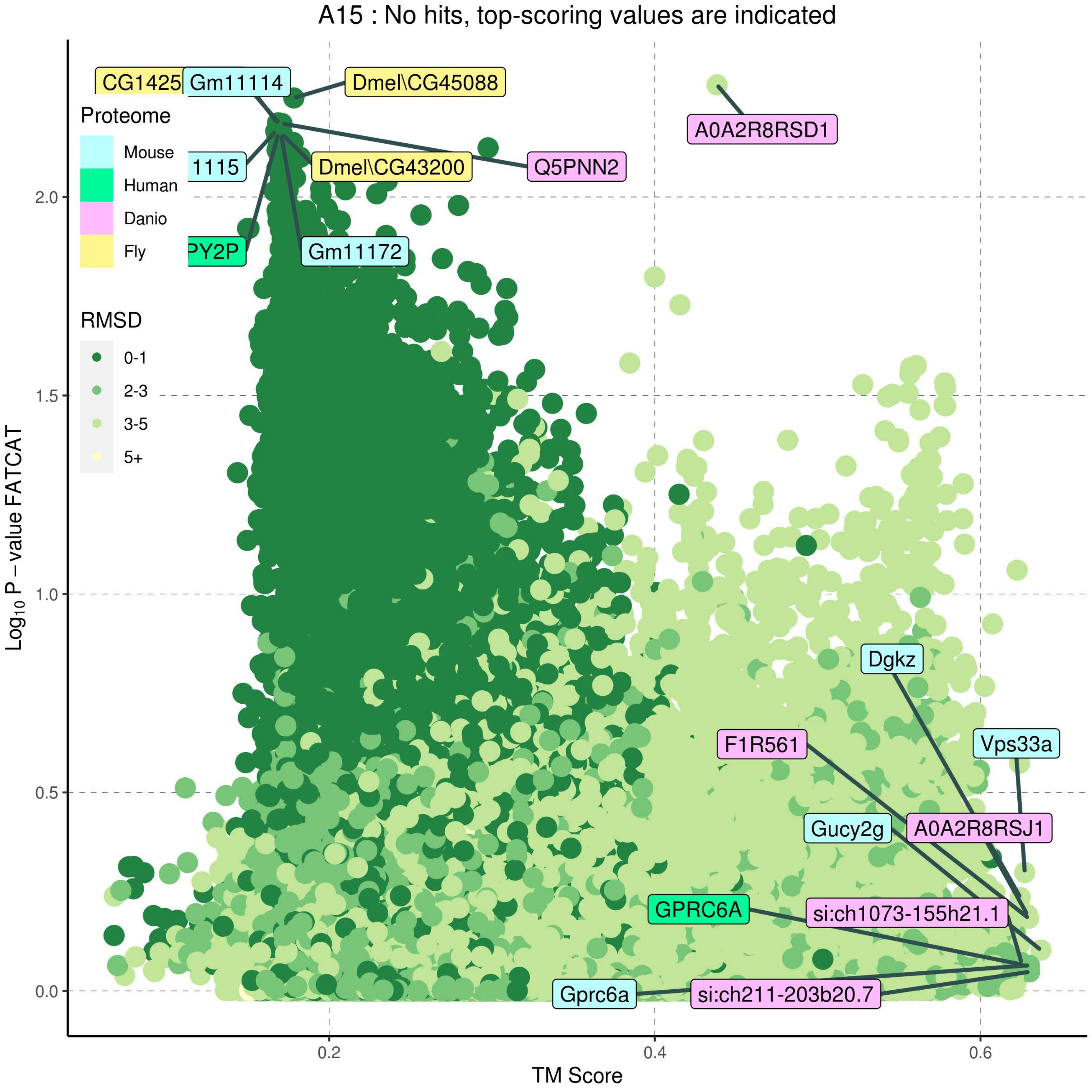
A12 : No hits, top-scoring values are indicated



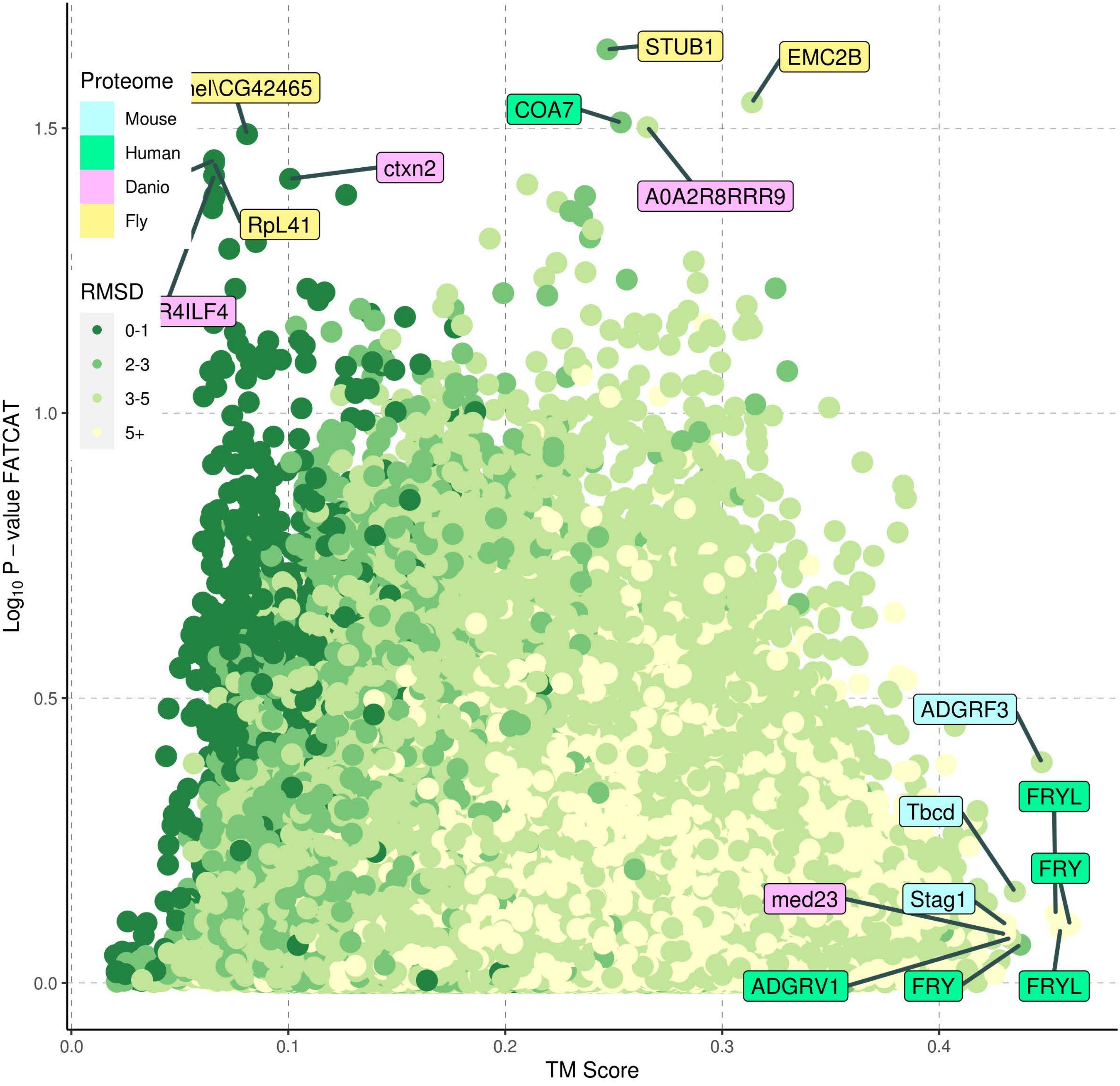

A13
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Isn
Log10 P – value FATCAT
0
2
4
6
8
TM Score
0.2
0.4
0.6


A14
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log$_{10}$ P − value FATCAT
10.0
7.5
5.0
2.5
0.0
TM Score
0.2
0.4
0.6
0.8

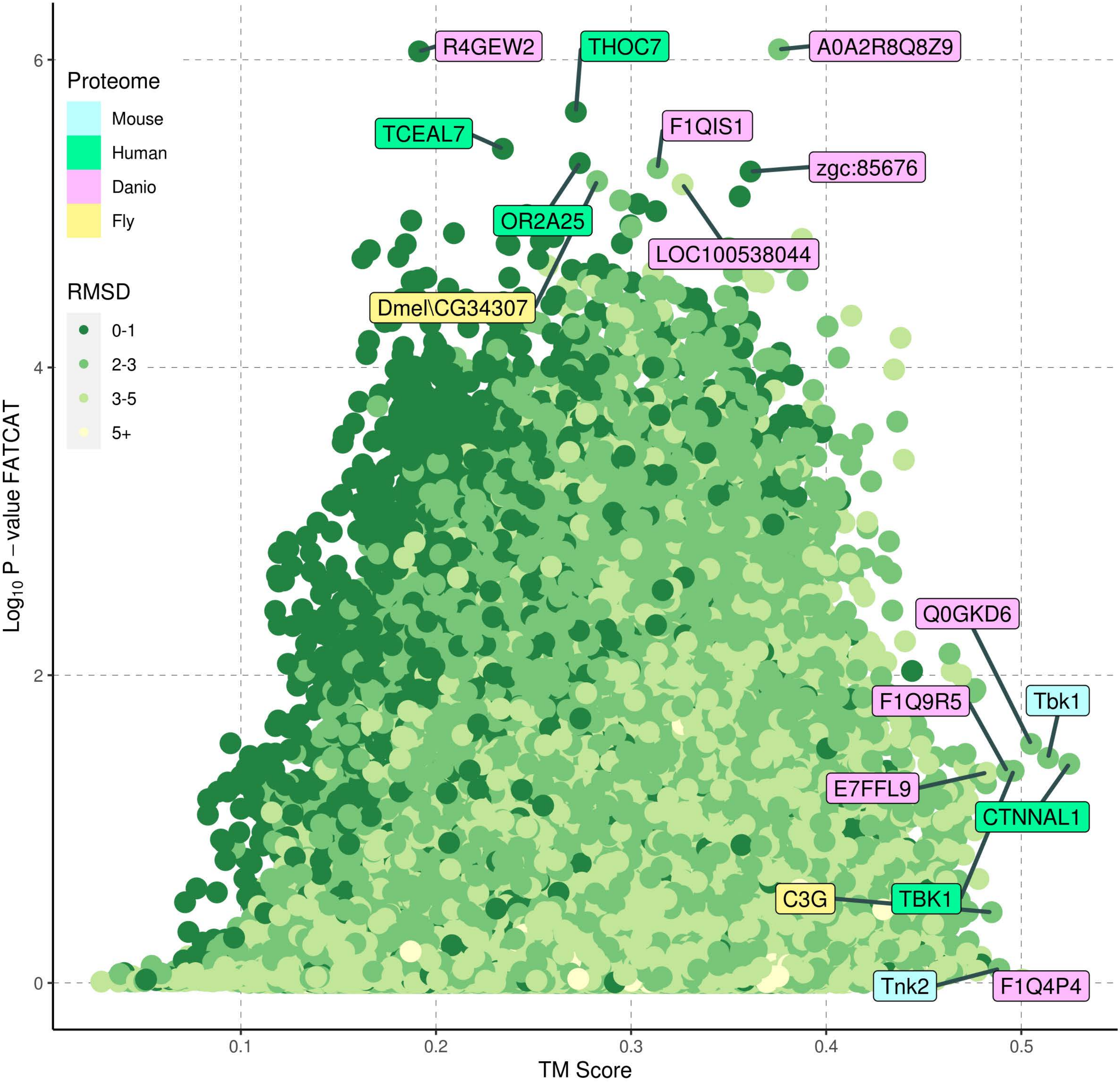

A14p5
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
TM Score
0
2
4
6
0.2
0.4
0.6
0.8
Smim30
Dad1
DAD1
SMIM5
Q561S6
SERFL
Kcne2
Tmem14c
Vps20
Med9
Slc66a3
Dmel\CG34250
Borcs5
Cyb561d2
si:dkey-248g15.2
C19orf53
CTXN2
TTC1
Elovl6
Mxra7
Lztfl1
CCNB1IP1
Dmel\CG14840

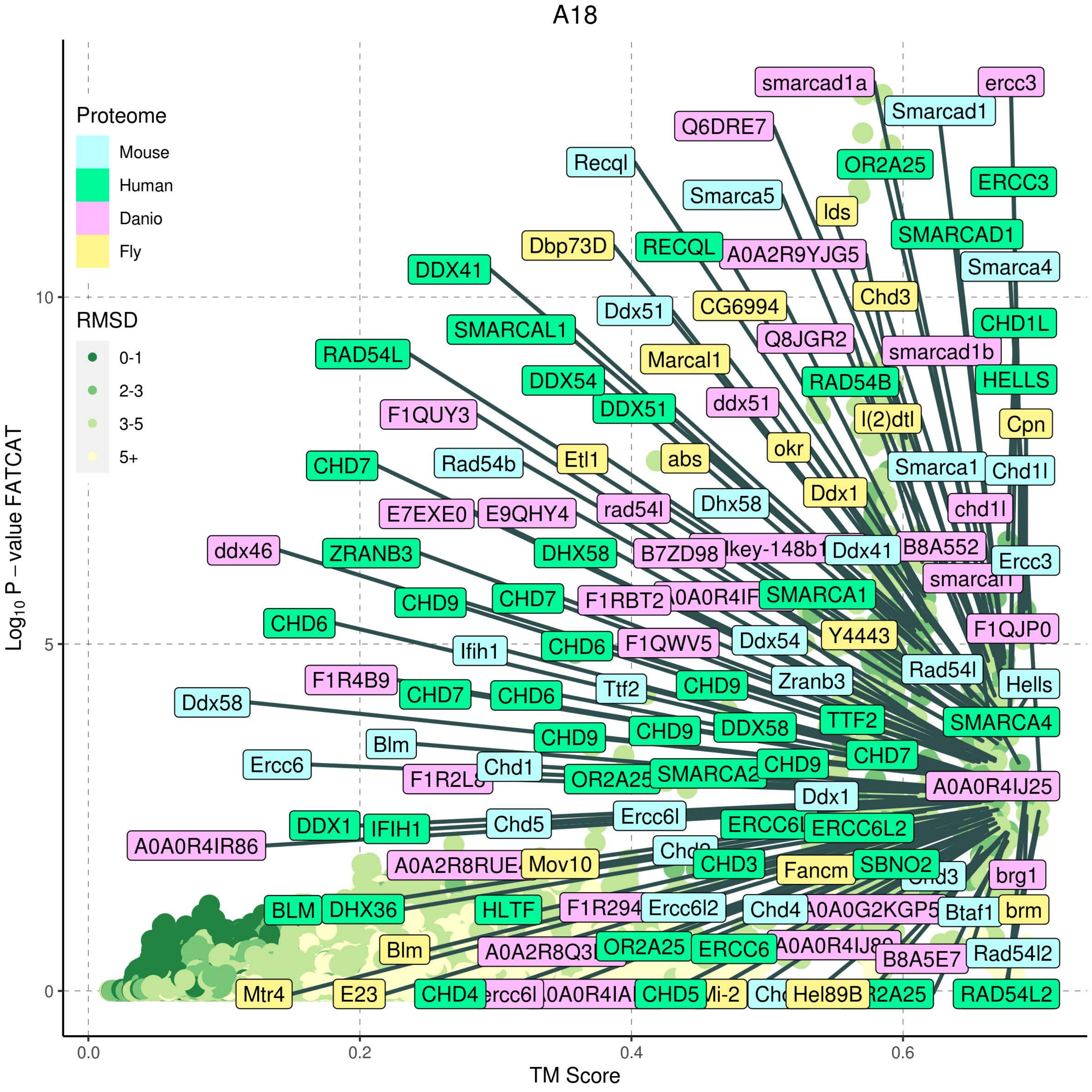

A15 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
CG1425
Gm11114
Dmel\CG45088
A0A2R8RSD1
1115
Dmel\CG43200
Q5PNN2
PY2P
Gm11172
Dgkz
F1R561
Vps33a
Gucy2g
A0A2R8RSJ1
GPRC6A
si:ch1073-155h21.1
Gprc6a
si:ch211-203b20.7
Log10 P − value FATCAT
TM Score
0.0
0.5
1.0
1.5
2.0
0.2
0.4
0.6

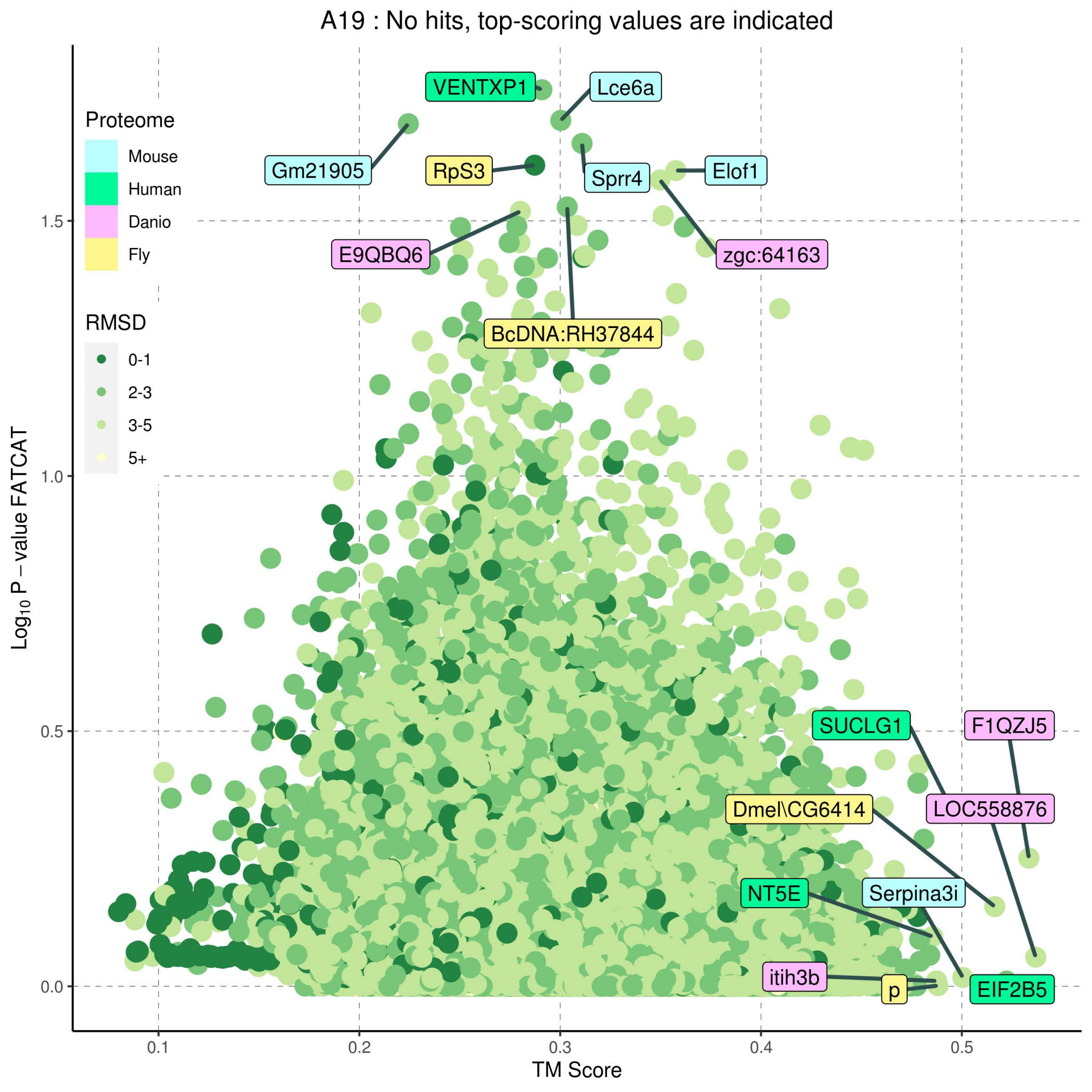
A16 : No hits, top-scoring values are indicated

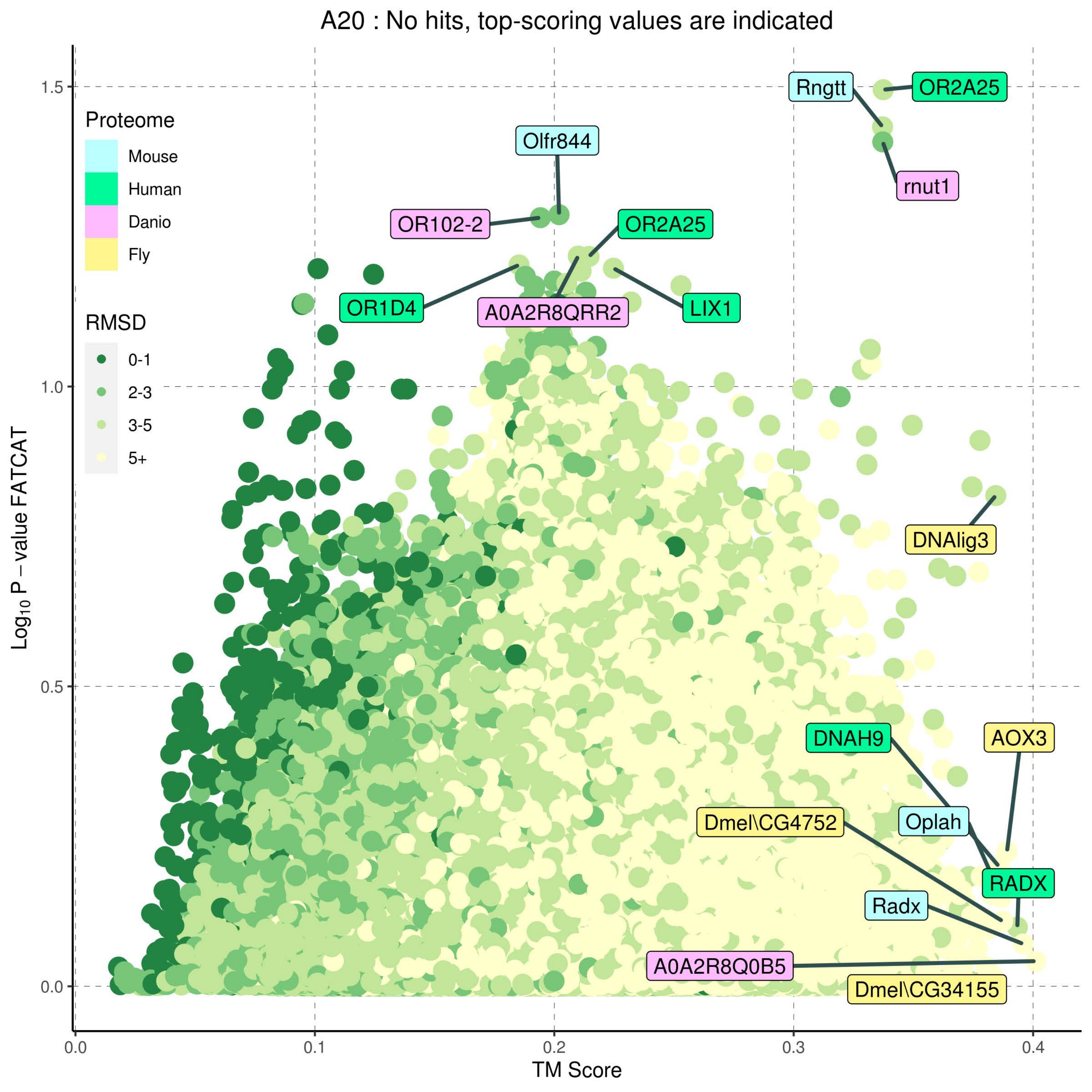


A17 : No hits, top-scoring values are indicated

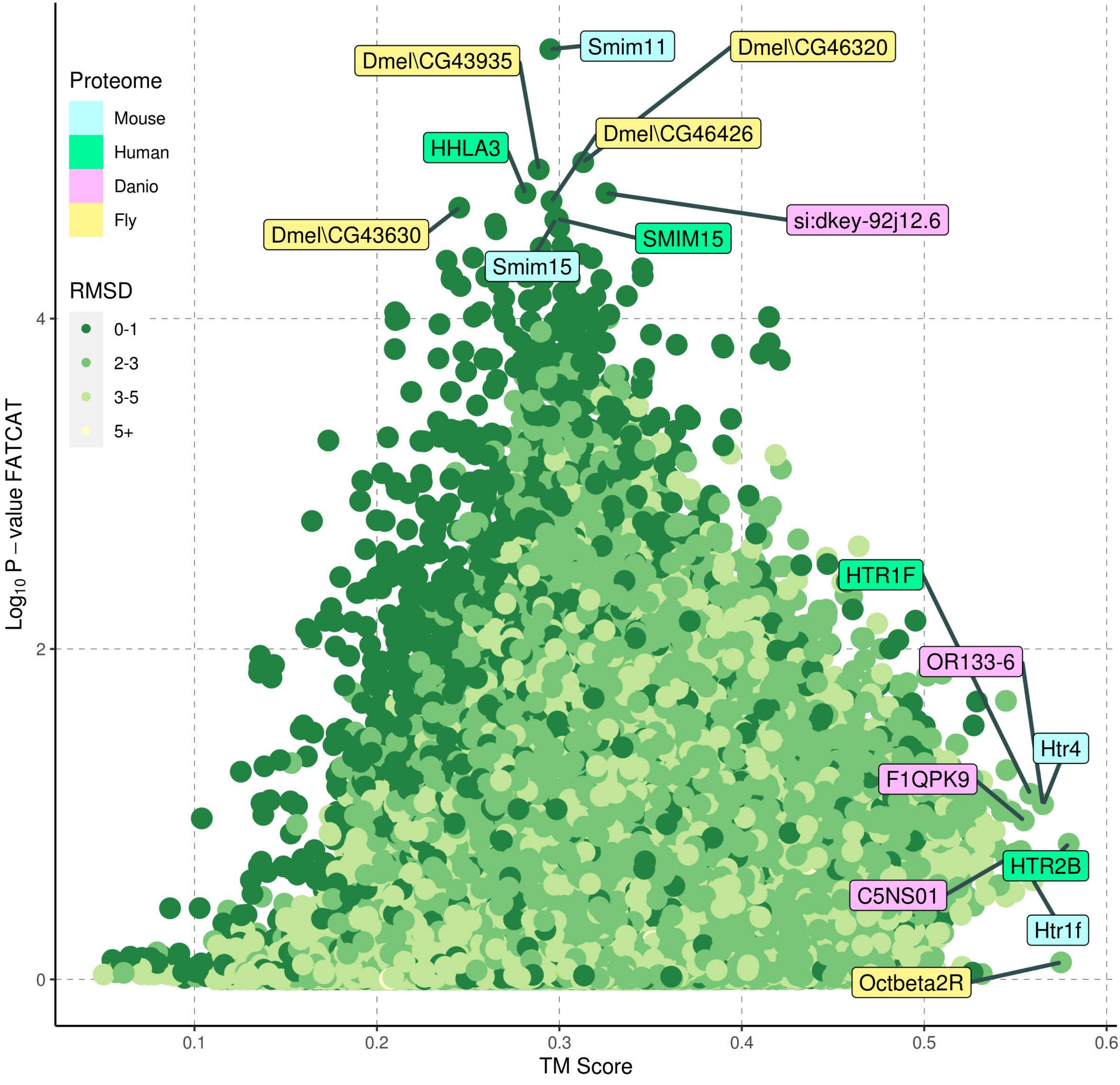


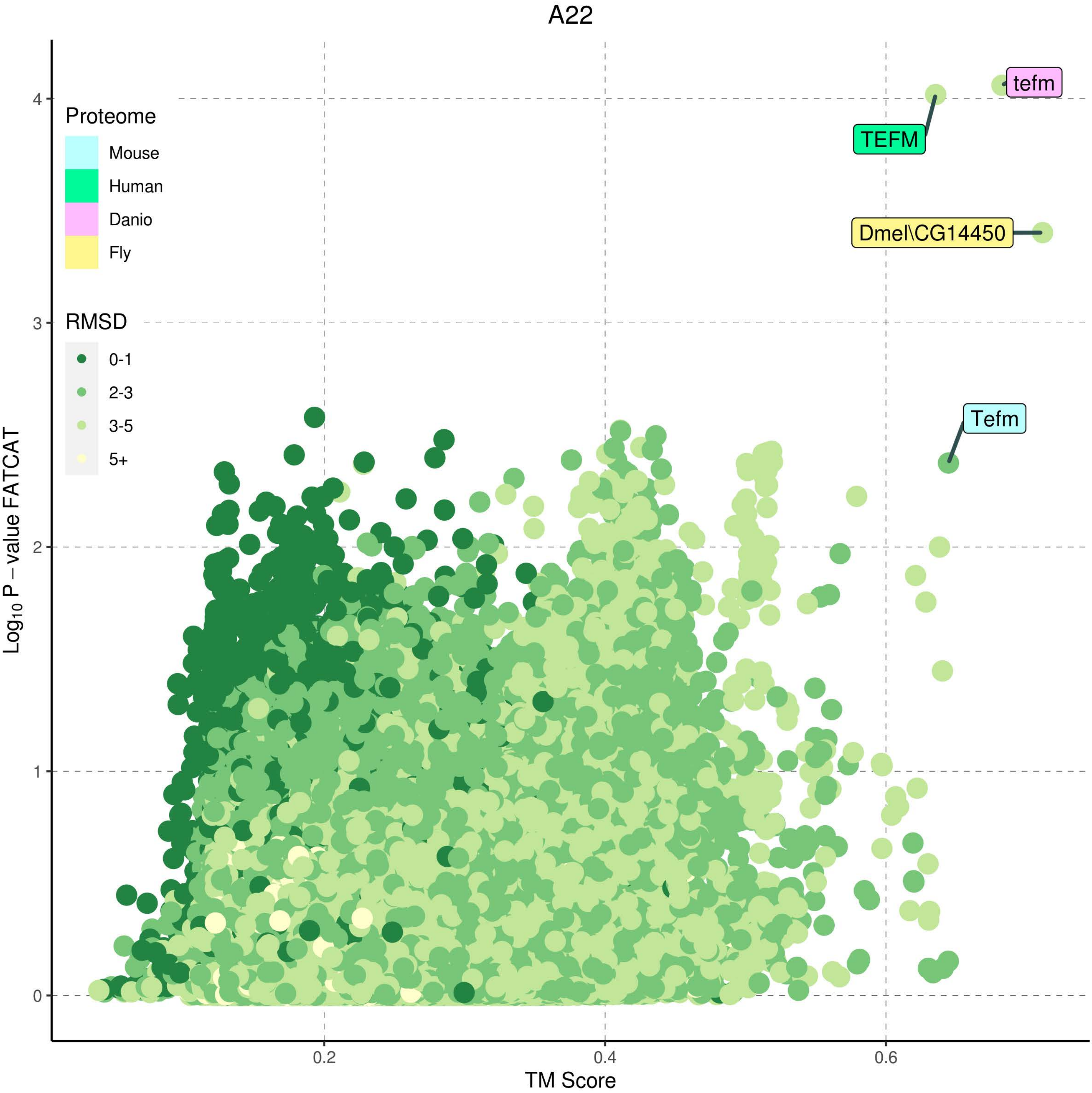

A18
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
TM Score
0.0
0.2
0.4
0.6
0
5
10
smarcad1a
ercc3
Smarcad1
Q6DRE7
Recql
OR2A25
ERCC3
Smarca5
lds
SMARCAD1
Dbp73D
RECQL
A0A2R9YJG5
Smarca4
DDX41
Chd3
Ddx51
CG6994
CHD1L
SMARCAL1
Q8JGR2
smarcad1b
RAD54L
Marcal1
HELLS
DDX54
RAD54B
ddx51
DDX51
l(2)dtl
Cpn
F1QUY3
okr
CHD7
Rad54b
Etl1
abs
Smarca1
Chd1l
Dhx58
Ddx1
E7EXE0
E9QHY4
rad54l
chd1l
ddx46
ZRANB3
DHX58
B7ZD98
Ddx41
B8A552
Ercc3
smarcal1
CHD9
CHD7
F1RBT2
SMARCA1
CHD6
F1QJP0
Ifih1
CHD6
F1QWV5
Ddx54
Y4443
F1R4B9
Rad54l
CHD7
CHD6
Ttf2
CHD9
Zranb3
Hells
Ddx58
TTF2
SMARCA4
Blm
CHD9
CHD9
DDX58
CHD7
Ercc6
Chd1
CHD9
OR2A25
SMARCA2
A0A0R4IJ25
Ddx1
Ercc6l
DDX1
IFIH1
Chd5
ERCC6L
ERCC6L2
A0A0R4IR86
CHD3
Mov10
Fancm
SBNO2
brg1
BLM
DHX36
HLTF
Ercc6l2
Chd4
A0A0G2KGP5
Btaf1
brm
Blm
OR2A25
ERCC6
B8A5E7
Rad54l2
Mtr4
E23
CHD4
CHD5
Hel89B
RAD54L2


A19 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P − value FATCAT
TM Score
0.0
0.5
1.0
1.5
0.1
0.2
0.3
0.4
0.5
VENTXP1
Lce6a
Gm21905
RpS3
Sprr4
Elof1
E9QBQ6
zgc:64163
BcDNA:RH37844
SUCLG1
F1QZJ5
Dmel\CG6414
LOC558876
NT5E
Serpina3i
itih3b
p
EIF2B5

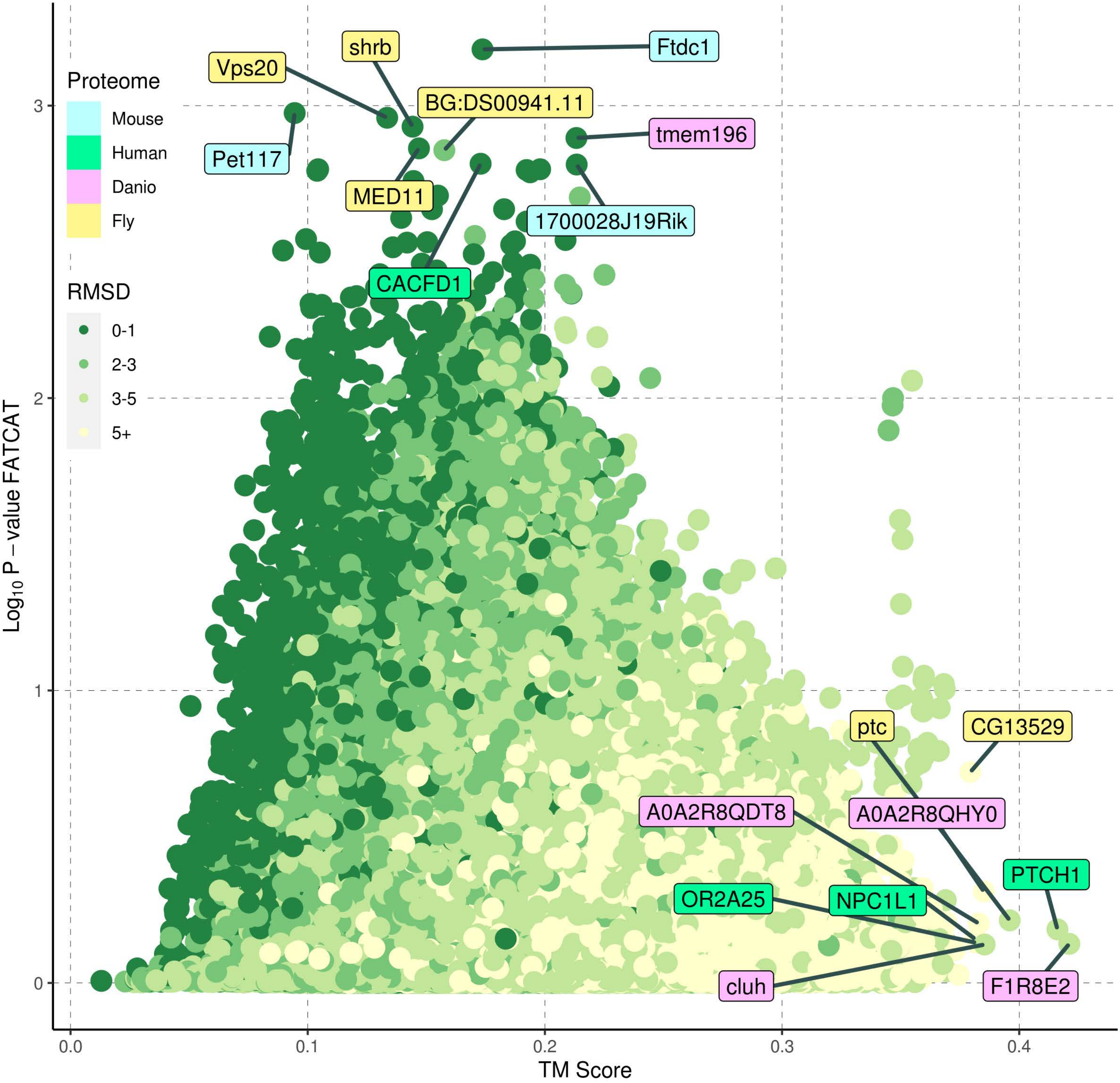

A20 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
TM Score
0.0
0.5
1.0
1.5
0.0
0.1
0.2
0.3
0.4
Rngtt
OR2A25
rnut1
Olfr844
OR102-2
OR2A25
OR1D4
A0A2R8QRR2
LIX1
DNAlig3
DNAH9
AOX3
Oplah
Dmel\CG4752
RADX
Radx
A0A2R8Q0B5
Dmel\CG34155

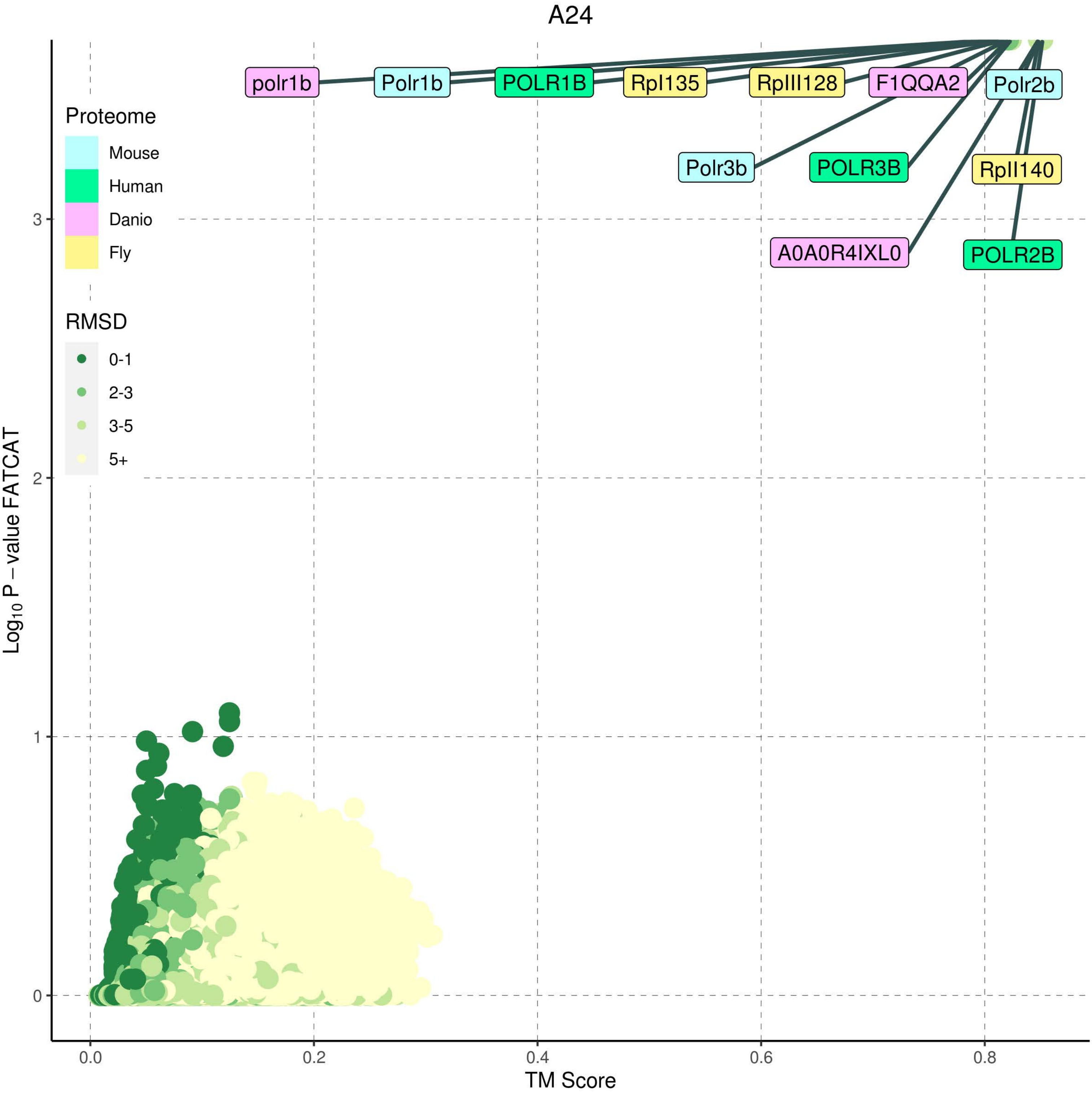
A21 : No hits, top-scoring values are indicated



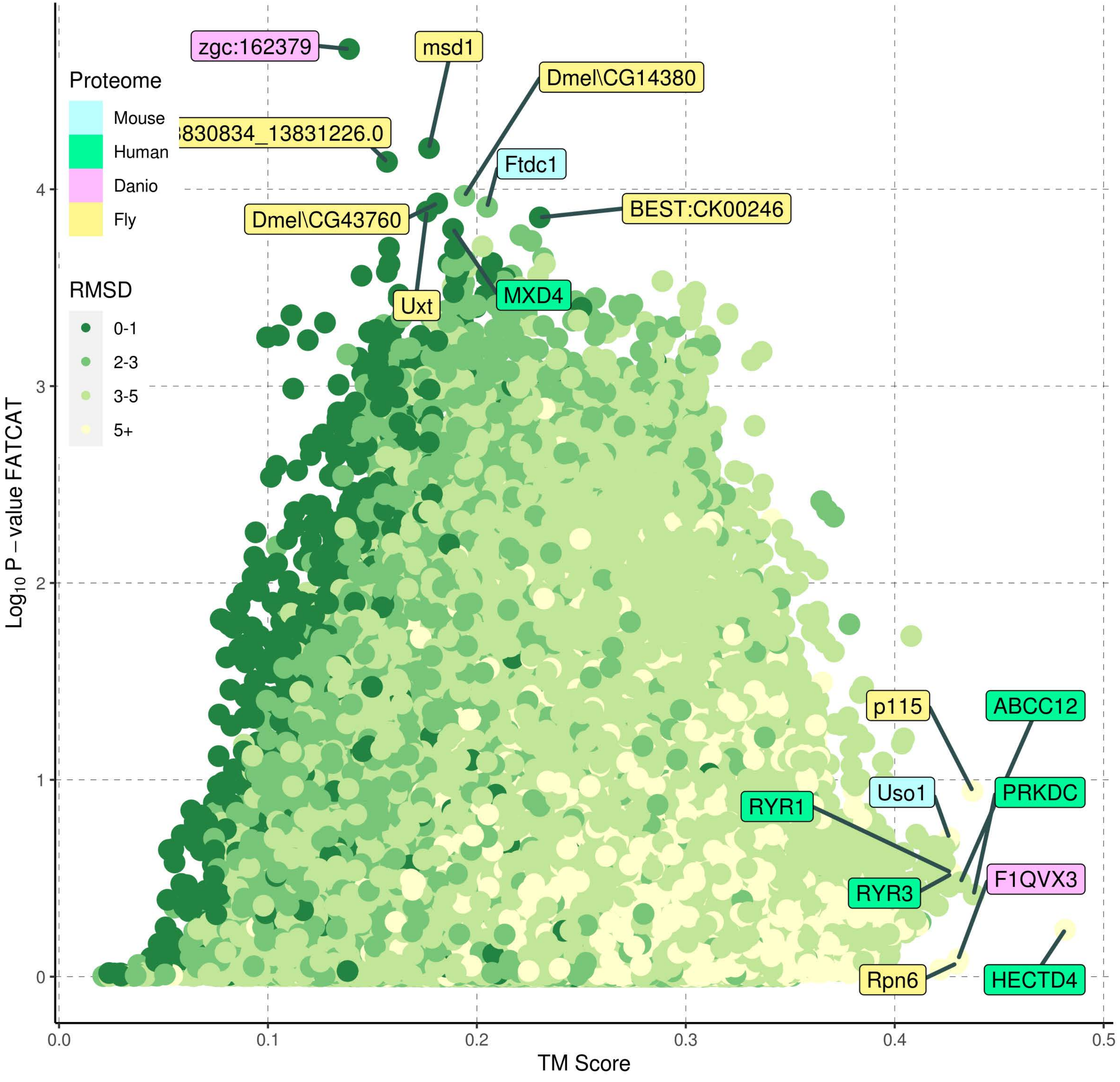

A22
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
tefm
TEFM
Dmel\CG14450
Tefm
Log₁₀ P – value FATCAT
0
1
2
3
4
TM Score
0.2
0.4
0.6

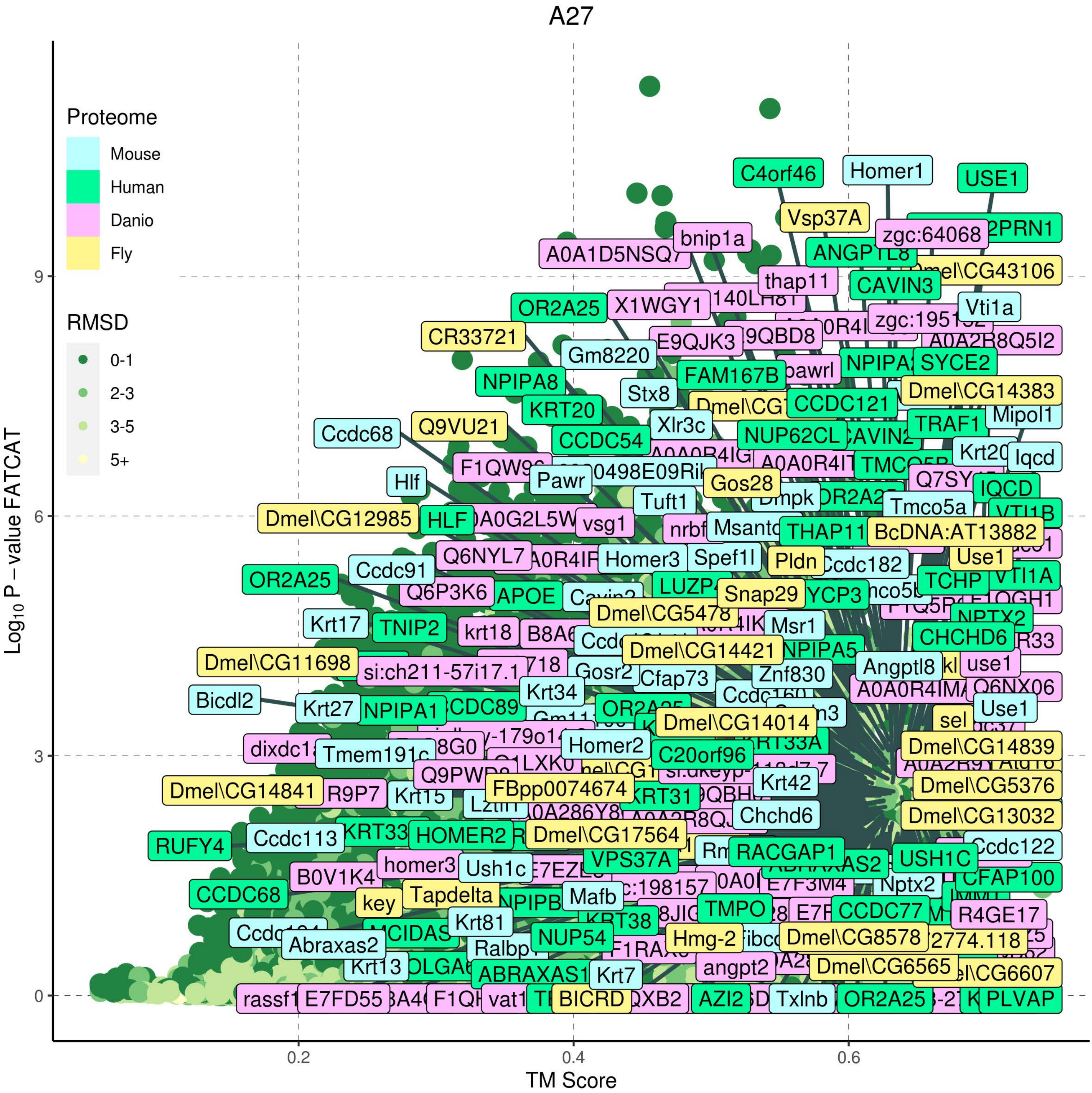
A23 : No hits, top-scoring values are indicated



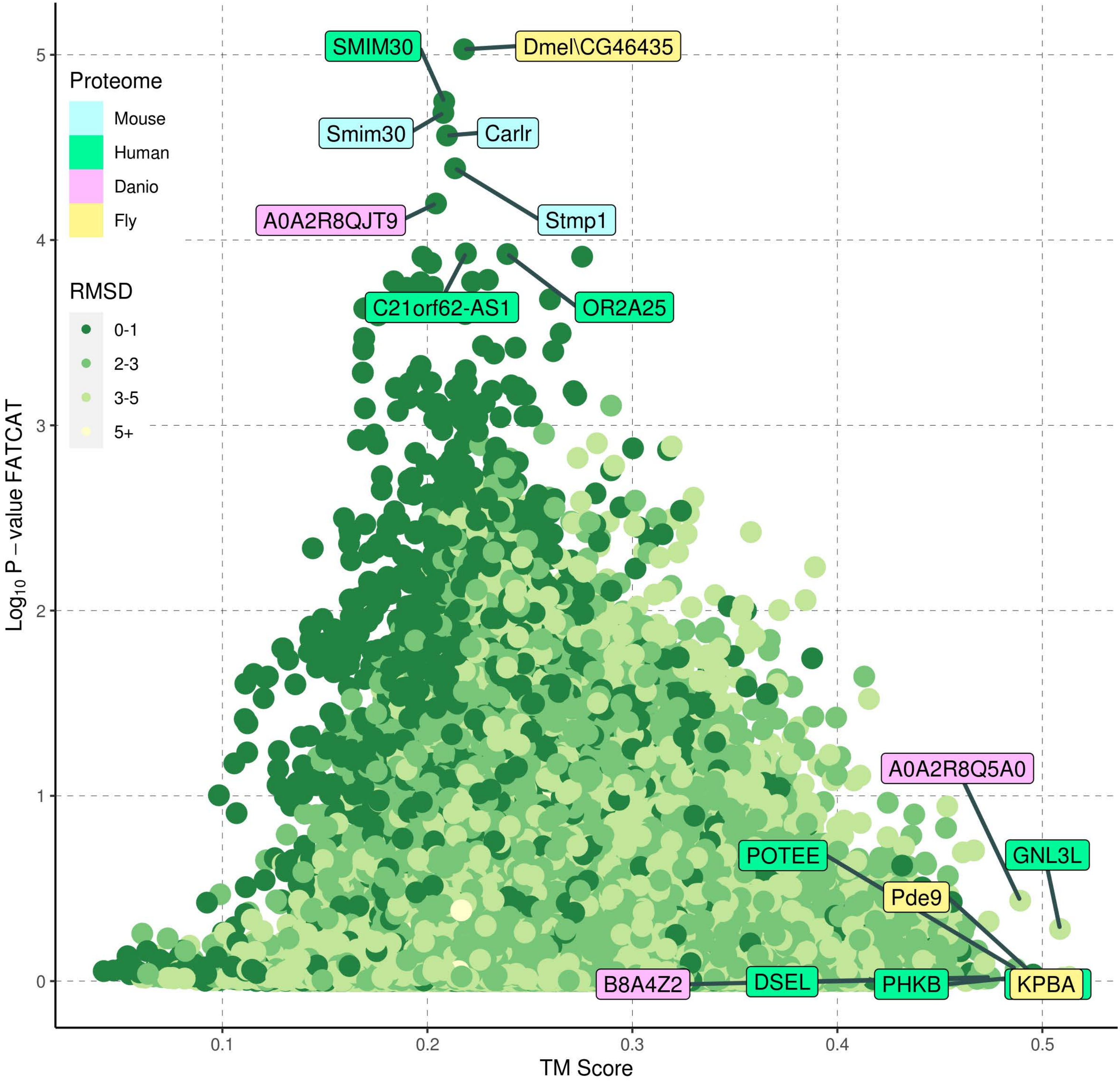

A24
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
polr1b
Polr1b
POLR1B
Rpl135
RpIII128
F1QQA2
Polr2b
Polr3b
POLR3B
RpII140
A0A0R4IXL0
POLR2B
Log₁₀ P − value FATCAT
3
2
1
0
TM Score
0.0
0.2
0.4
0.6
0.8

A26 : No hits, top-scoring values are indicated

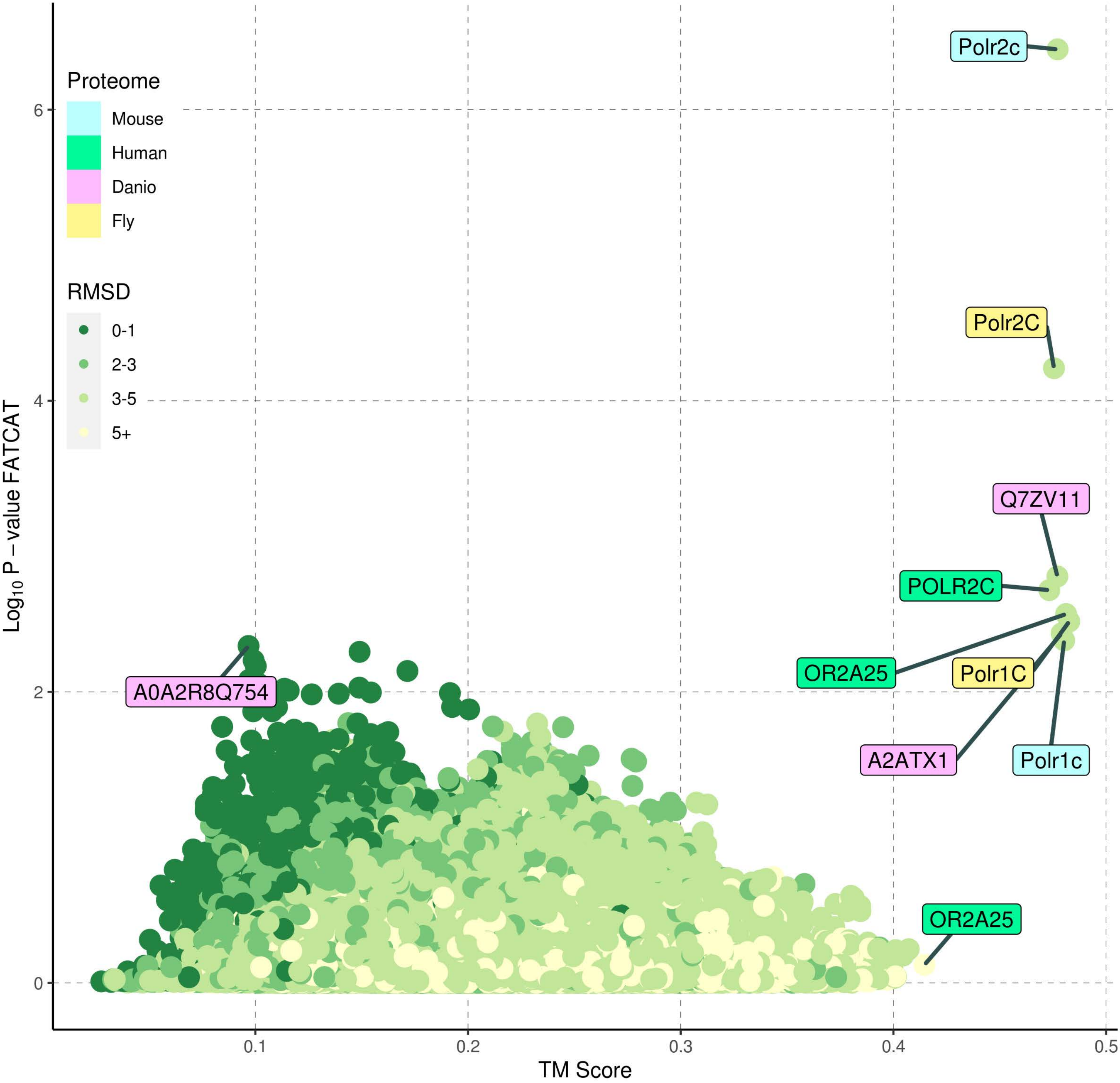


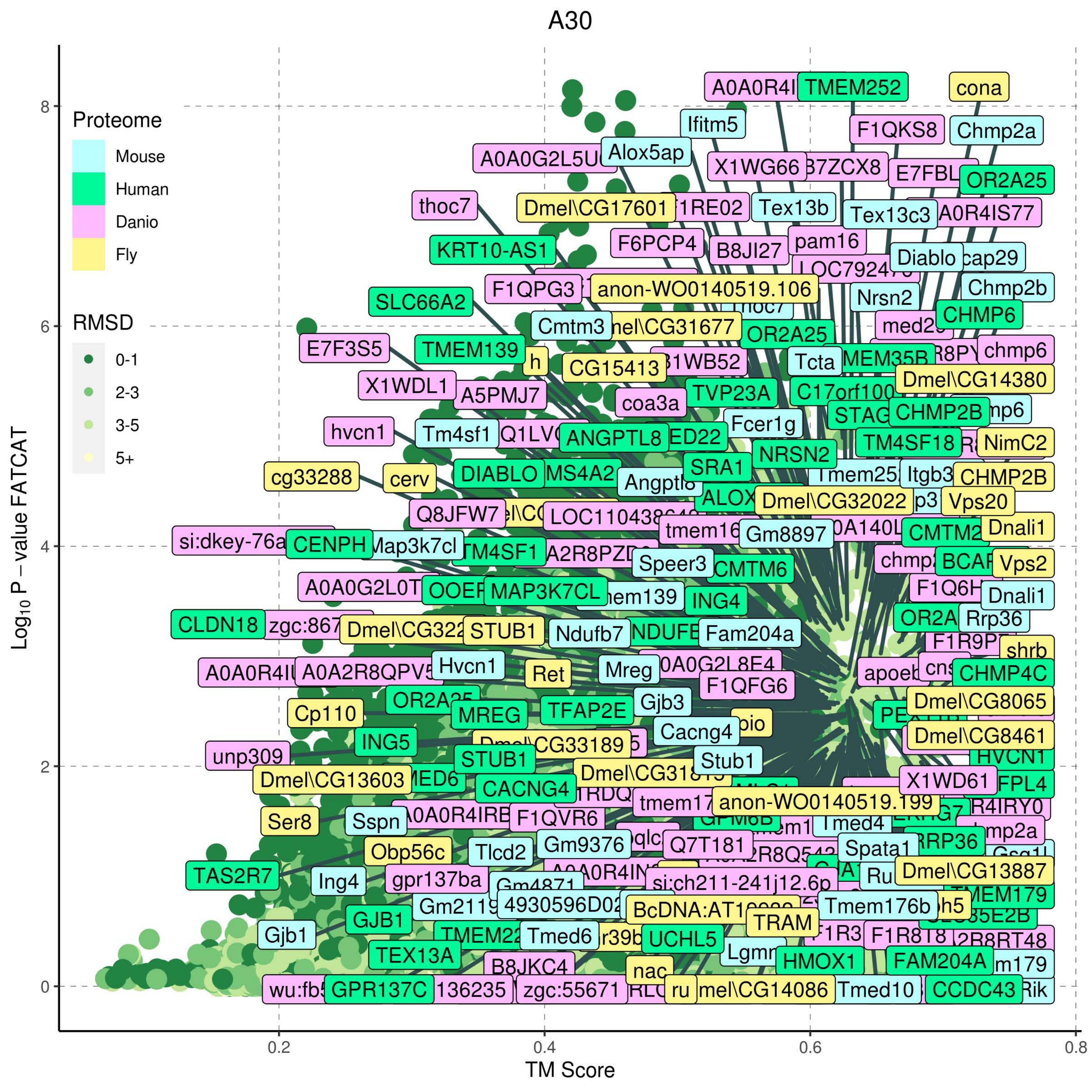

A27
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P − value FATCAT
TM Score
0
3
6
9
0.2
0.4
0.6
C4orf46
Homer1
USE1
Vsp37A
bnip1a
zgc:64068
A0A1D5NSQ7
ANGPTL8
Dmel\CG43106
thap11
CAVIN3
OR2A25
X1WGY1
zgc:1951
Vti1a
CR33721
E9QJK3
A0A2R8Q5I2
Gm8220
NPIPA8
FAM167B
pawrl
SYCE2
Stx8
Dmel\CG14383
KRT20
CCDC121
Mipol1
Ccdc68
Q9VU21
CCDC54
Xlr3c
NUP62CL
TRAF1
Krt20
Iqcd
F1QW9
0498E09Rik
TMCO5B
Hlf
Pawr
Gos28
Q7SY
IQCD
Tuft1
Tmco5a
Dmel\CG12985
HLF
A0G2L5W
vsg1
nrbf
Msantd
THAP11
BcDNA:AT13882
Q6NYL7
Homer3
Spef1l
Pldn
Ccdc182
Use1
OR2A25
Ccdc91
LUZP
TCHP
VTI1A
Q6P3K6
APOE
Snap29
SYCP3
Dmel\CG5478
Krt17
TNIP2
krt18
Msr1
NPTX2
CHCHD6
Dmel\CG14421
NPIPA5
Dmel\CG11698
si:ch211-57i17.1
Gosr2
Cfap73
Znf830
Angptl8
use1
A0A0R4IMA
Q6NX06
Bicdl2
Krt34
Krt27
NPIPA1
CCDC89
Dmel\CG14014
sel
Use1
dixdc1
Tmem191c
Homer2
C20orf96
Dmel\CG14839
Q9PWD
Krt42
Dmel\CG5376
Dmel\CG14841
R9P7
Krt15
FBpp0074674
KRT31
Chchd6
Dmel\CG13032
KRT33
HOMER2
Dmel\CG17564
RUFY4
Ccdc113
RACGAP1
Ccdc122
VPS37A
USH1C
homer3
Ush1c
B0V1K4
Nptx2
CFAP100
CCDC68
Tapdelta
Mafb
key
TMPO
CCDC77
R4GE17
Krt81
MCIDAS
Dmel\CG8578
Abraxas2
NUP54
Hmg-2
Ralbp1
Krt13
OLGA
ABRAXAS1
Krt7
angpt2
Dmel\CG6565
rassf1
E7FD55
F1QH
vat1
BICRD
AZI2
Txlnb
OR2A25
PLVAP

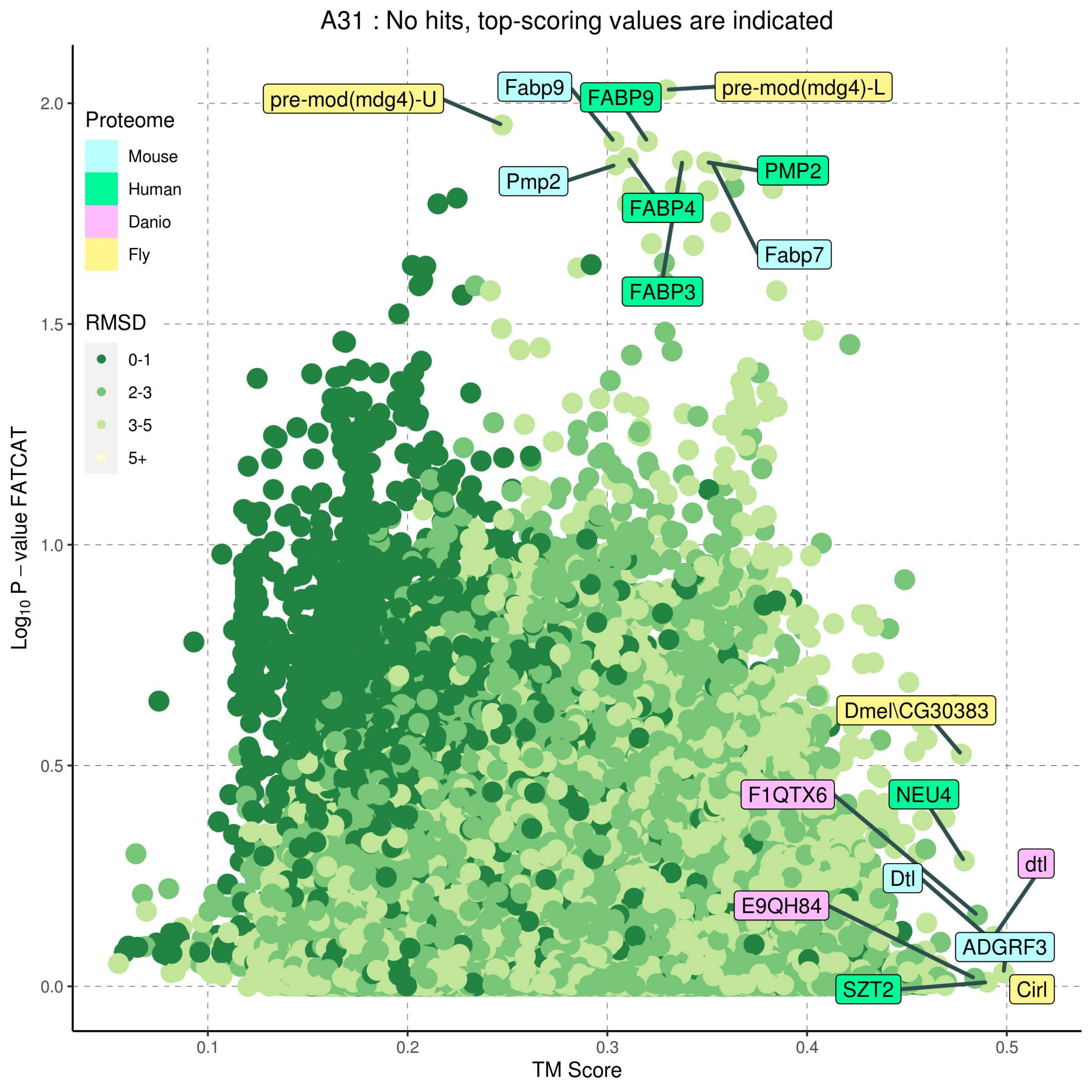
A28 : No hits, top-scoring values are indicated



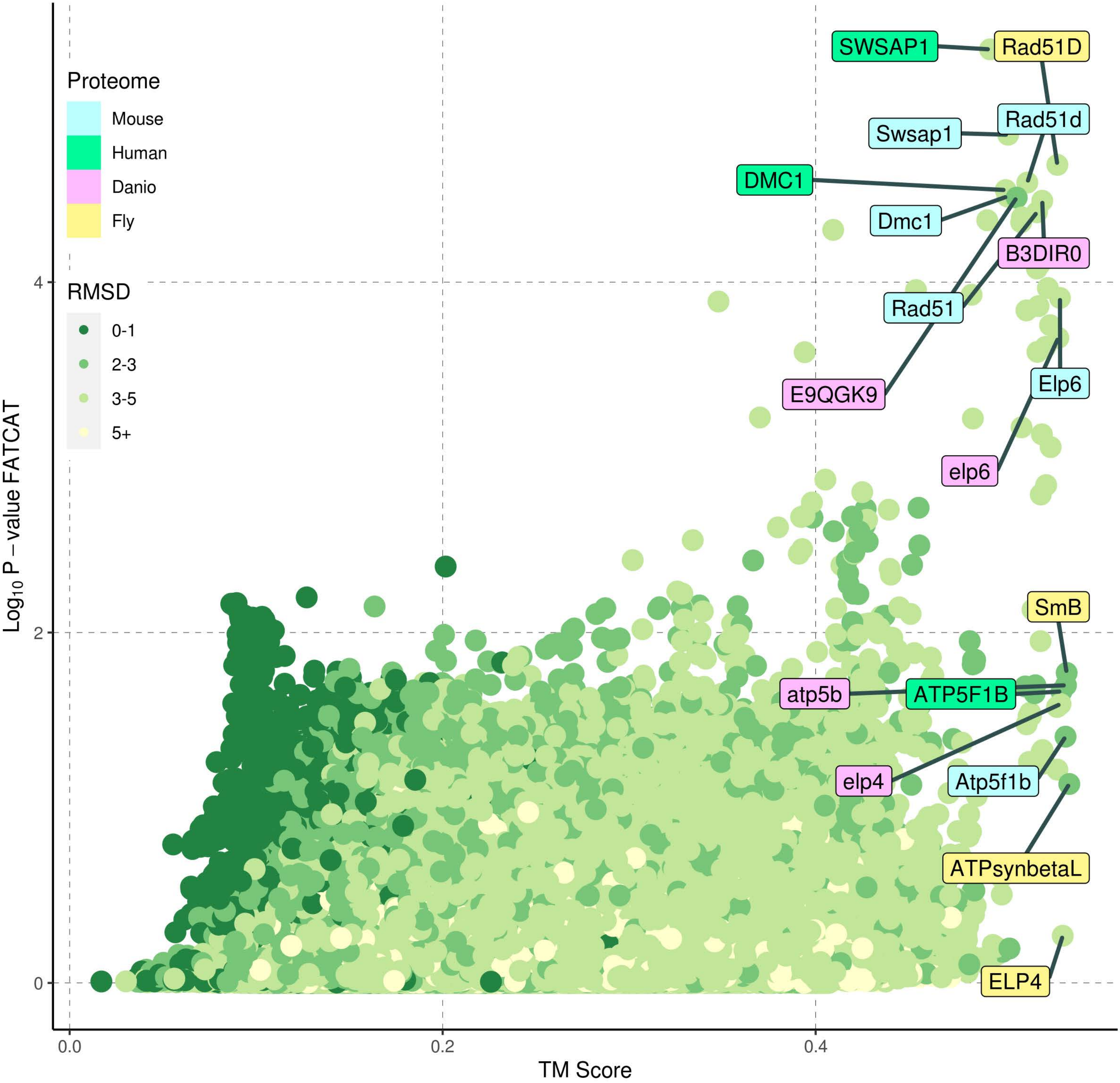
A29 : No hits, top-scoring values are indicated

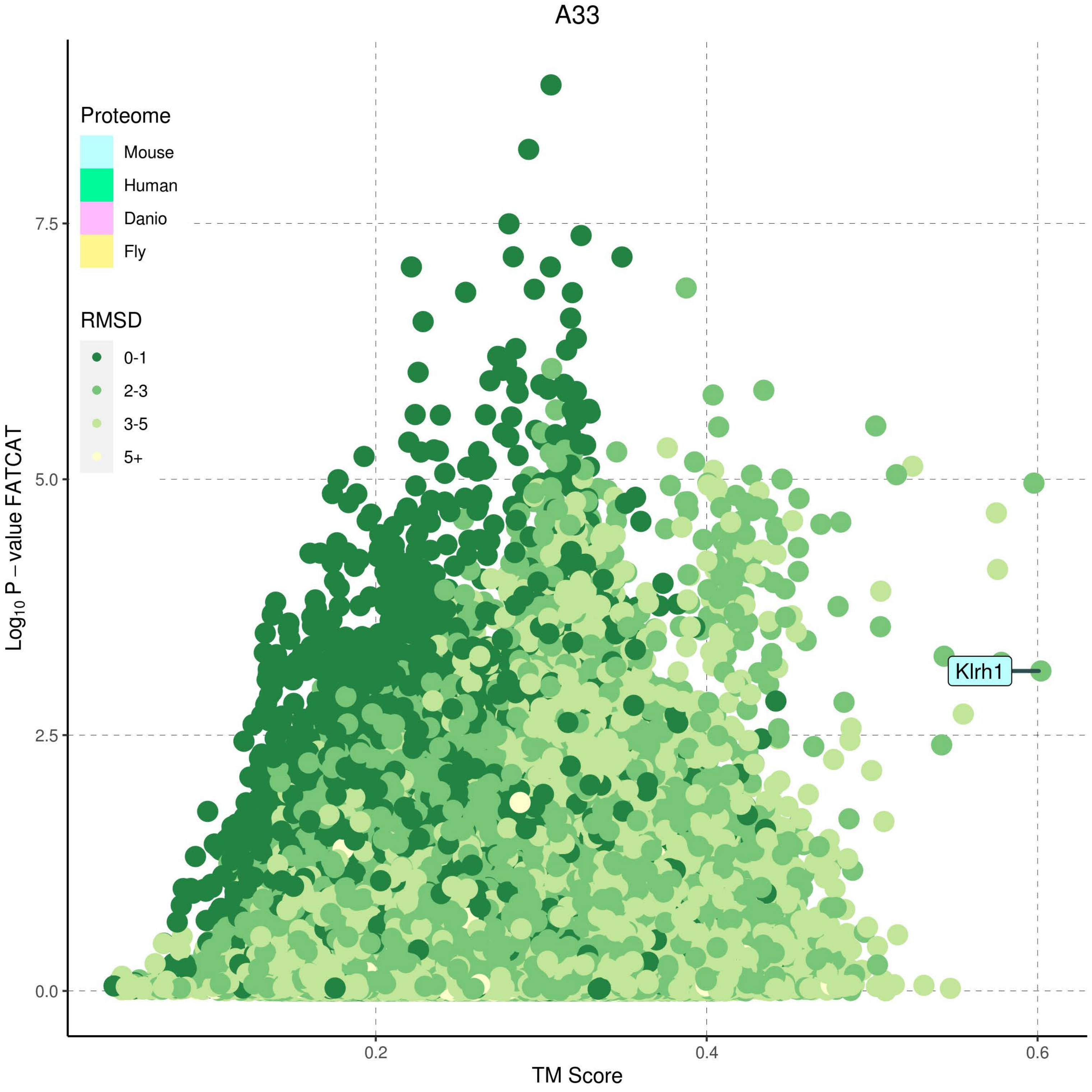


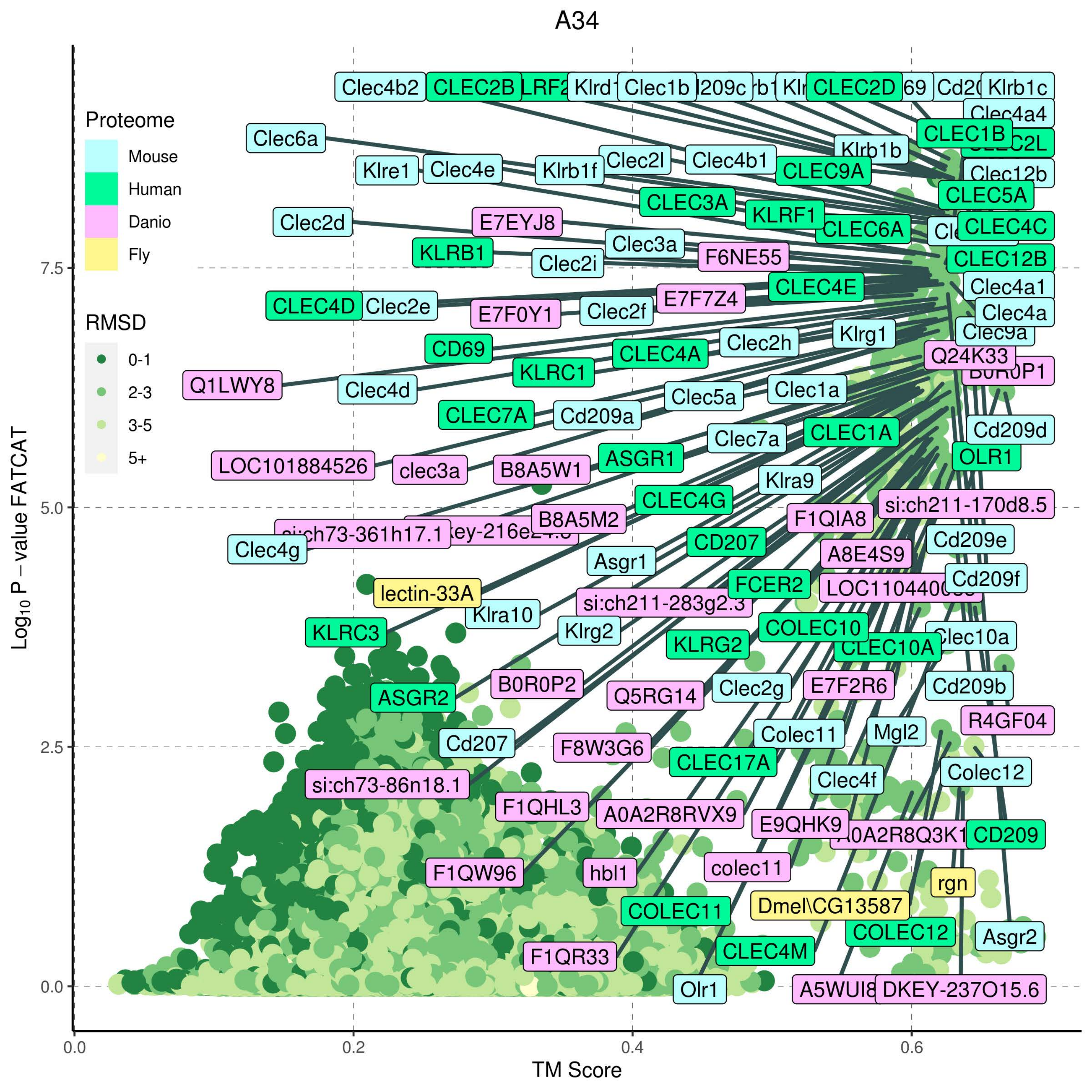

A30
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
TM Score
0
2
4
6
8
0.2
0.4
0.6
0.8
A0A0R4I
TMEM252
cona
Ifitm5
F1QKS8
Chmp2a
A0A0G2L5U
Alox5ap
X1WG66
B7ZCX8
E7FBL
OR2A25
thoc7
Dmel\CG17601
F1RE02
Tex13b
Tex13c3
A0R4IS77
KRT10-AS1
F6PCP4
B8JI27
pam16
Diablo
cap29
LOC7924
F1QPG3
anon-WO0140519.106
Chmp2b
SLC66A2
thoc7
Nrsn2
Cmtm3
Dmel\CG31677
OR2A25
med2
CHMP6
E7F3S5
TMEM139
h
CG15413
B1WB52
Tcta
TMEM35B
R8PY
chmp6
X1WDL1
A5PMJ7
coa3a
TVP23A
C17orf100
Dmel\CG14380
STAG
CHMP2B
mp6
hvcn1
Tm4sf1
Q1LV
ANGPTL8
MED22
Fcer1g
TM4SF18
NimC2
cg33288
cerv
DIABLO
MS4A2
Angptl8
SRA1
NRSN2
Tmem25
Itgb3
CHMP2B
Q8JFW7
Dmel\CG
LOC110438
ALOX
Dmel\CG32022
p3
Vps20
si:dkey-76a
CENPH
Map3k7cl
TM4SF1
A2R8PZD
tmem16
Gm8897
A0A140L
CMTM2
Dnali1
Speer3
CMTM6
chmp
BCAF
Vps2
A0A0G2L0T
OOEP
MAP3K7CL
tmem139
ING4
F1Q6H
Dnali1
CLDN18
zgc:867
Dmel\CG322
STUB1
Ndufb7
NDUFB
Fam204a
OR2A
Rrp36
F1R9P
shrb
A0A0R4I
A0A2R8QPV5
Hvcn1
Ret
Mreg
A0A0G2L8E4
F1QFG6
apoeb
cns
CHMP4C
OR2A25
Cp110
MREG
TFAP2E
Gjb3
PEX
Dmel\CG8065
pio
ING5
Dmel\CG33189
Cacng4
Dmel\CG8461
unp309
STUB1
Stub1
HVCN1
Dmel\CG13603
MED6
CACNG4
Dmel\CG318
X1WD61
FPL4
TRDQ
tmem17
anon-WO0140519.199
R4IRY0
Ser8
Sspn
A0A0R4IRE
F1QVR6
GPM6B
Tmed4
ERFG7
mp2a
Obp56c
Tlcd2
Gm9376
Q7T181
A2R8Q54
Spata1
RRP36
TAS2R7
Ing4
gpr137ba
Gm4871
A0A0R4IN
si:ch211-241j12.6p
Ru
Dmel\CG13887
Gm2119
4930596D02
BcDNA:AT1
Tmem176b
h5
TMEM179
GJB1
TRAM
Gjb1
TMEM22
Tmed6
r39b
UCHL5
F1R3
F1R8T8
2R8RT48
TEX13A
Lgmn
HMOX1
FAM204A
m179
B8JKC4
nac
wu:fb5
GPR137C
136235
zgc:55671
RLC
ru
Dmel\CG14086
Tmed10
CCDC43
Rik

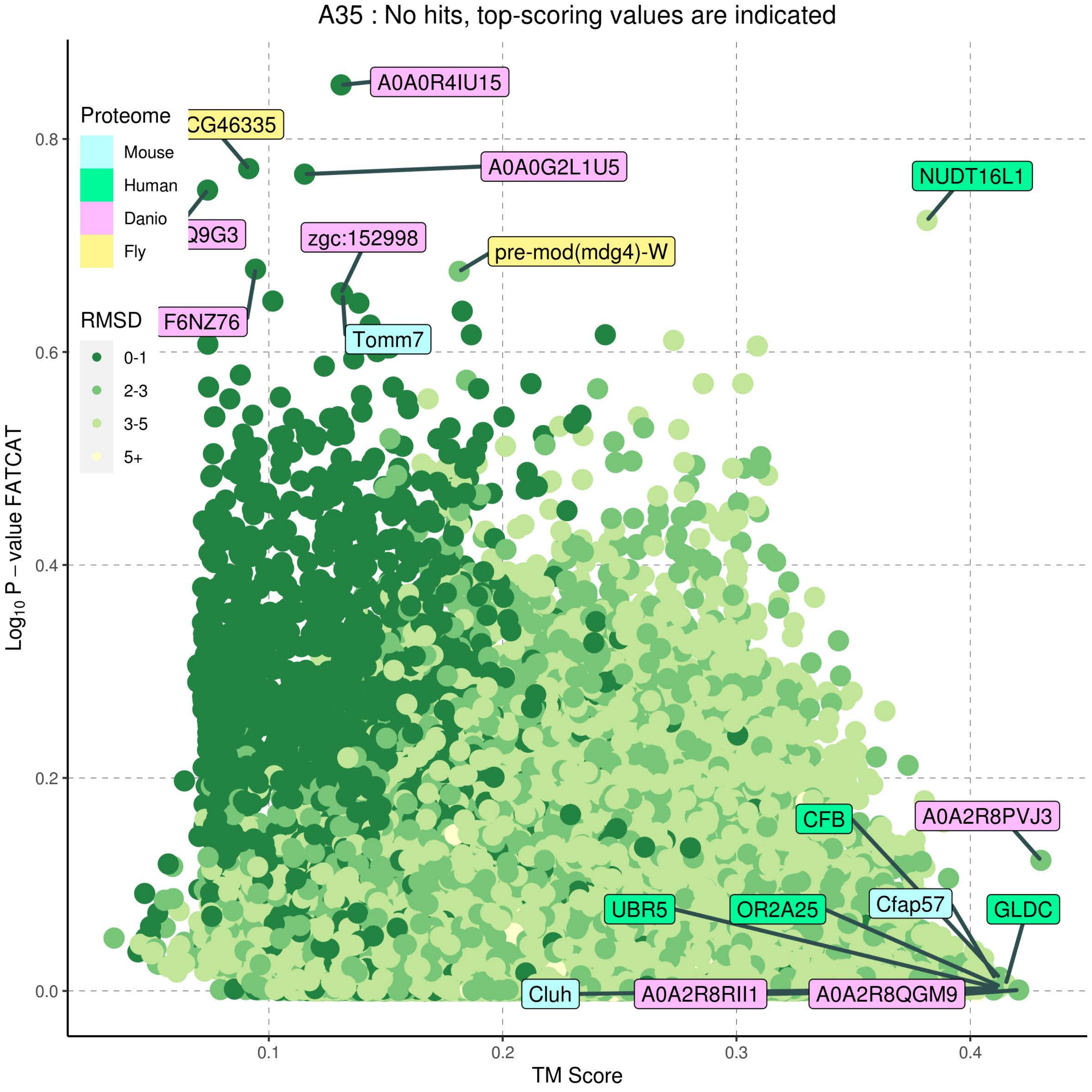

A31 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
TM Score
0.0
0.5
1.0
1.5
2.0
0.1
0.2
0.3
0.4
0.5
pre-mod(mdg4)-U
Fabp9
FABP9
pre-mod(mdg4)-L
Pmp2
PMP2
FABP4
Fabp7
FABP3
Dmel\CG30383
F1QTX6
NEU4
dtl
Dtl
E9QH84
ADGRF3
SZT2
Cirl

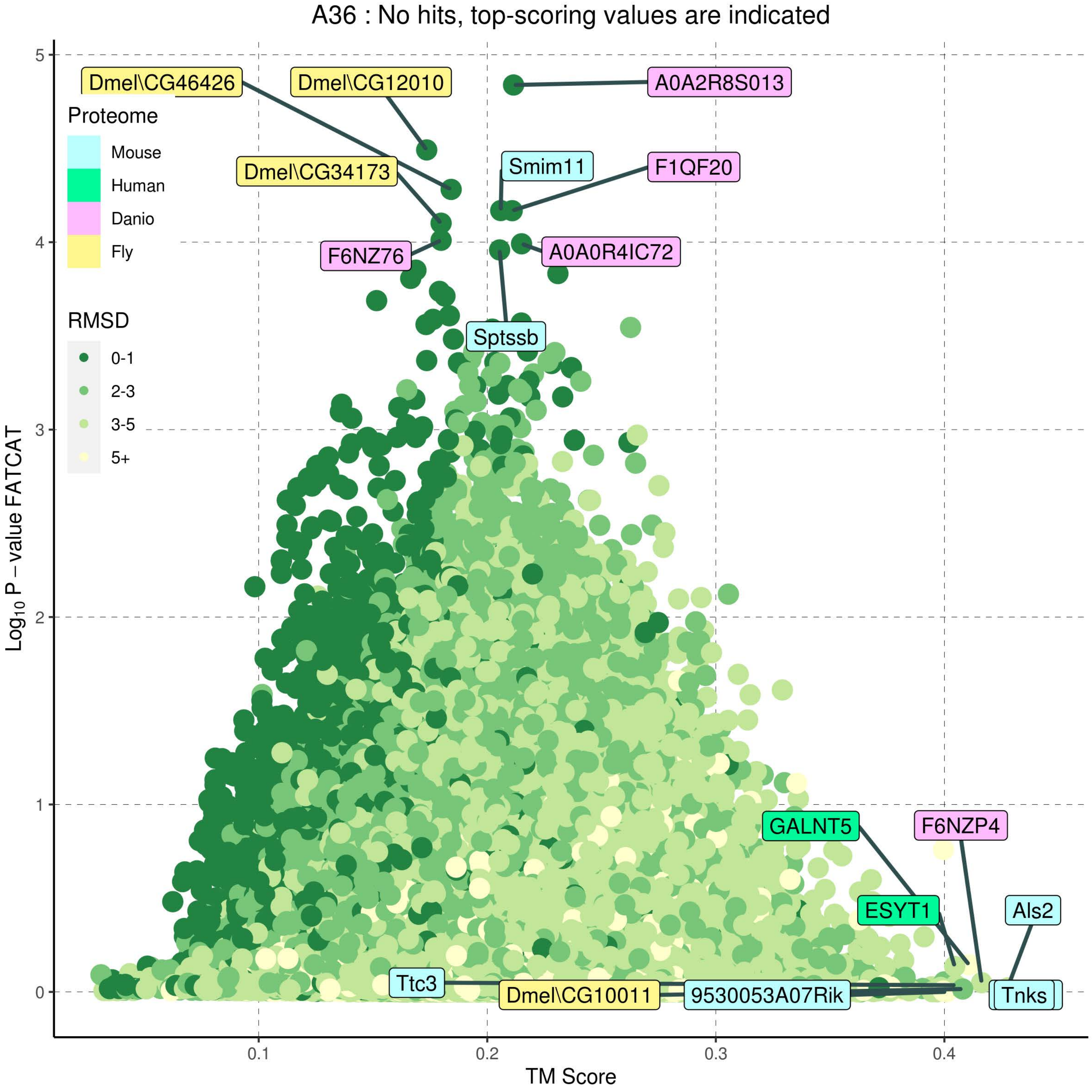
A32 : No hits, top-scoring values are indicated

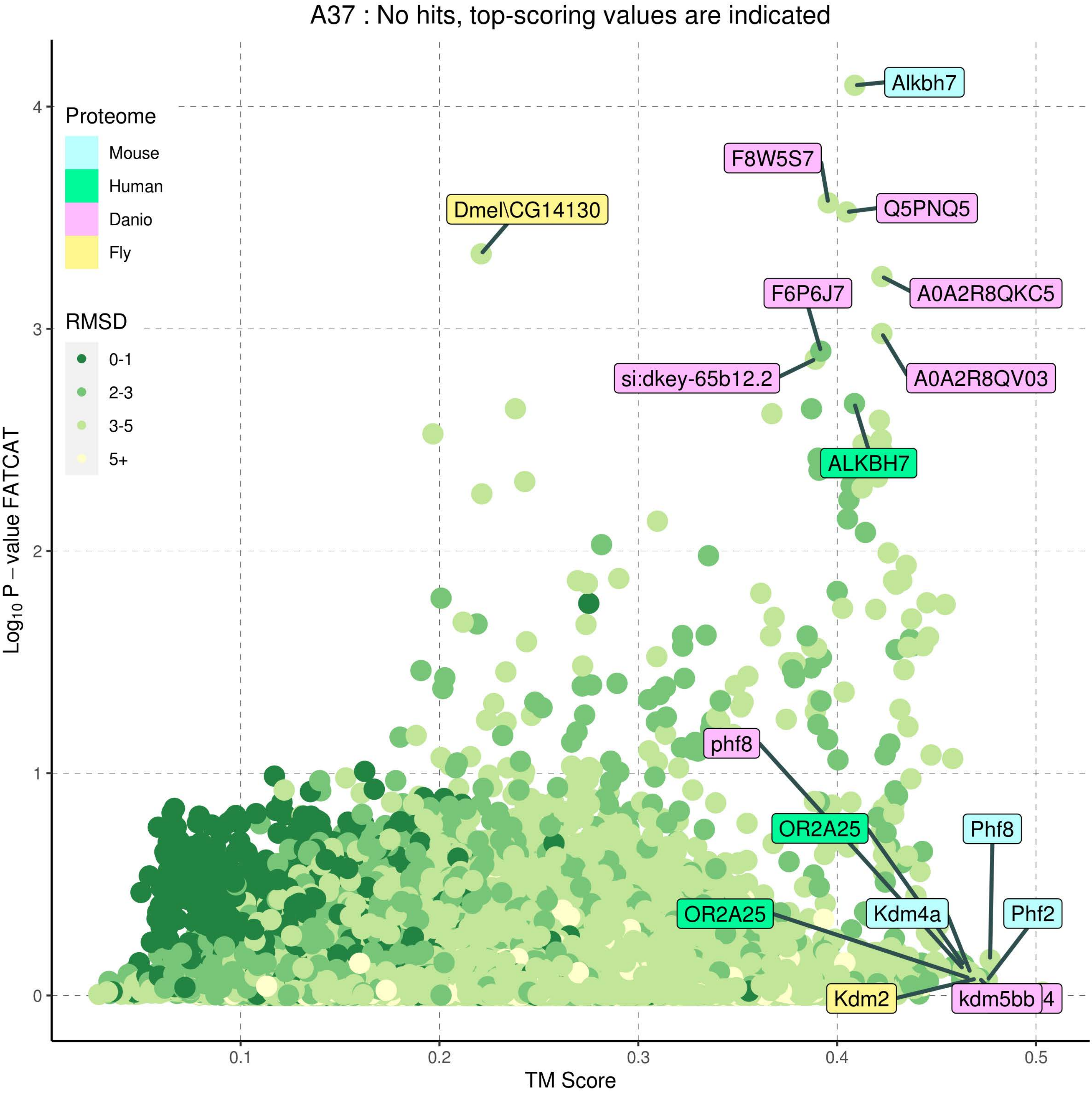


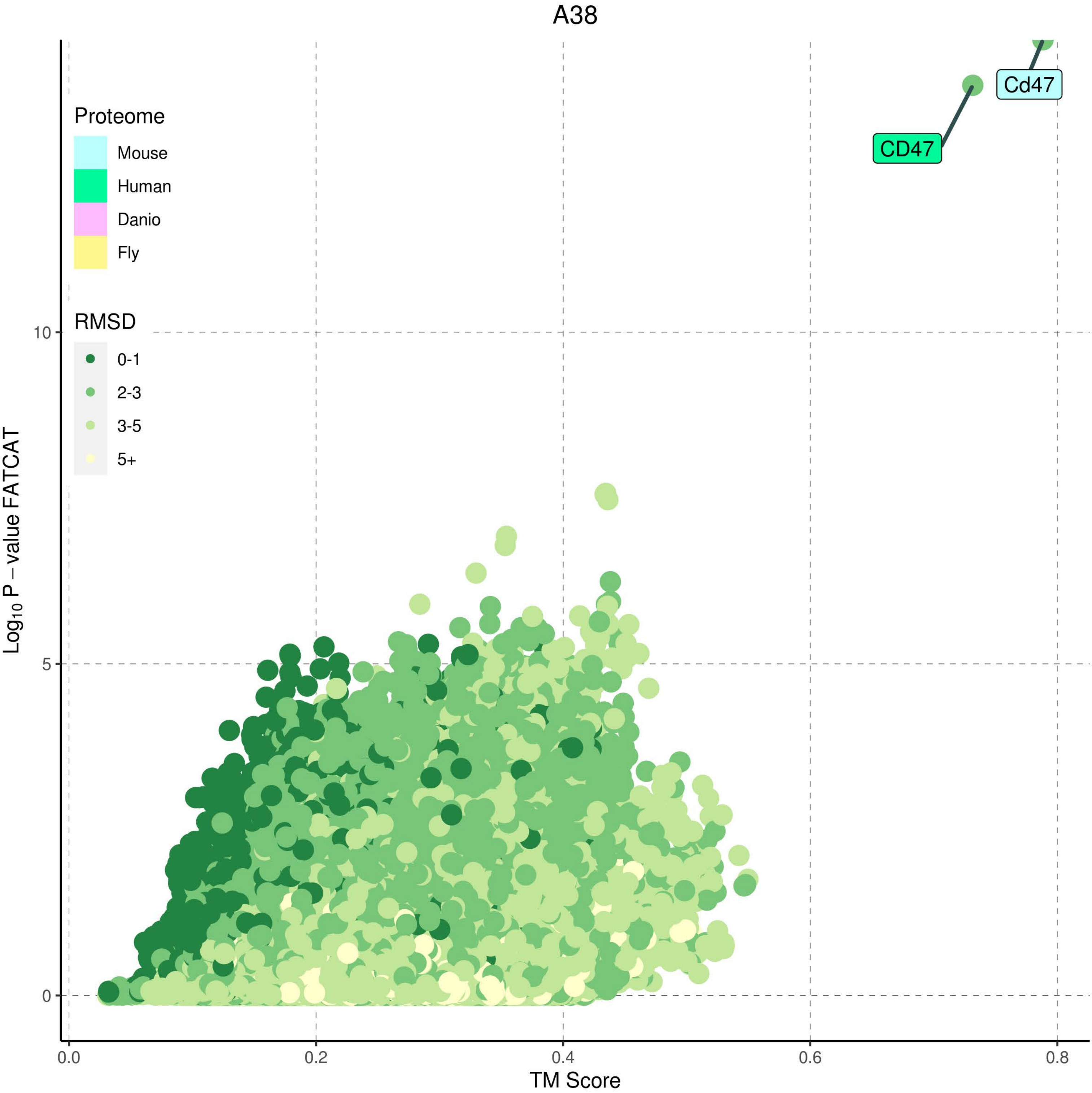

A33
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Klrh1
Log10 P – value FATCAT
7.5
5.0
2.5
0.0
0.2
0.4
0.6
TM Score

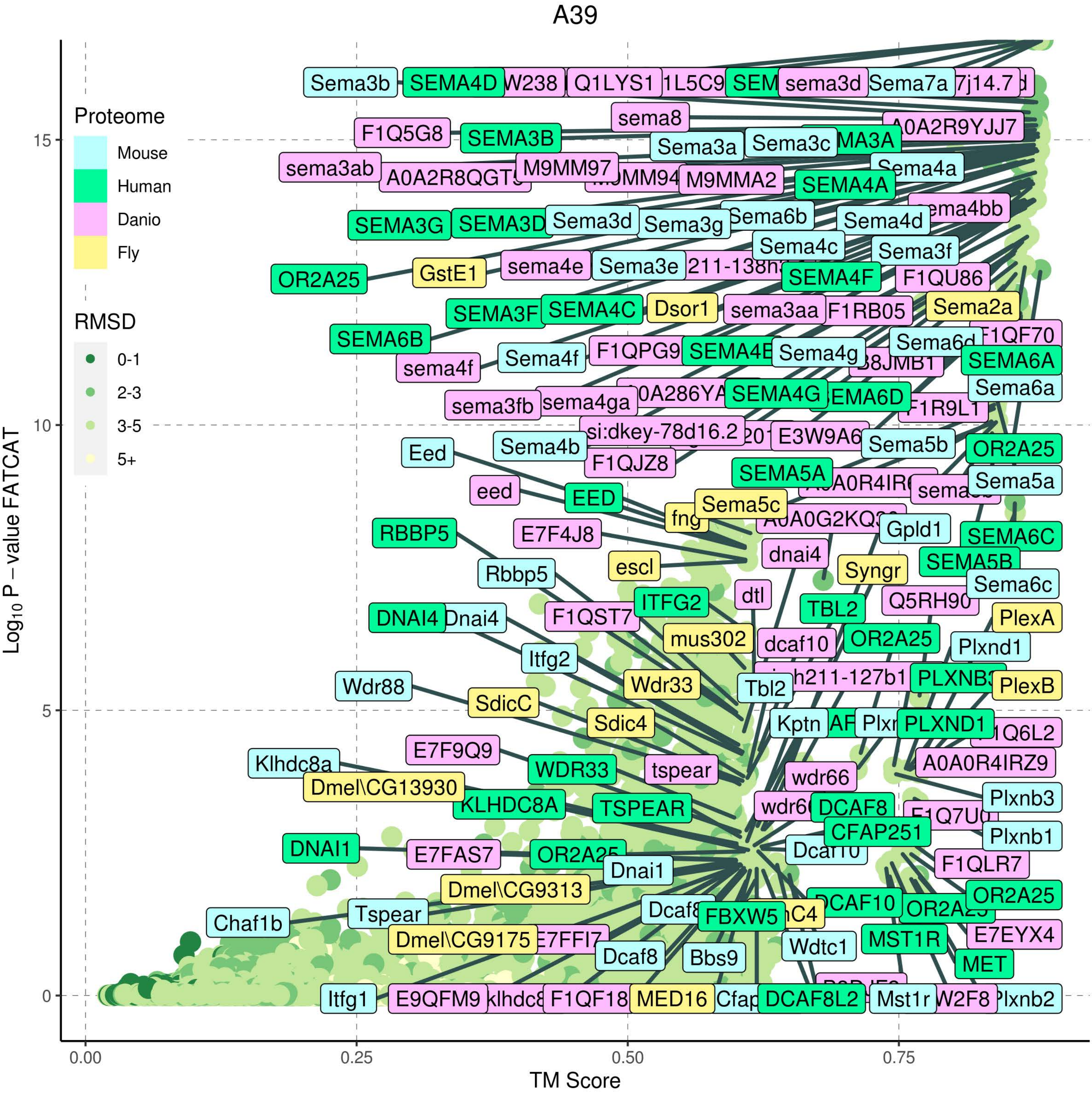

A34
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log₁₀ P − value FATCAT
TM Score
0.0
2.5
5.0
7.5
0.0
0.2
0.4
0.6
Clec4b2
CLEC2B
LRF2
Klrd1
Clec1b
l209c
rb1
Klr
CLEC2D
69
Cd20
Klrb1c
Clec4a4
CLEC1B
Clec6a
Klrb1b
CLEC2L
Klre1
Clec4e
Klrb1f
Clec2l
Clec4b1
CLEC9A
Clec12b
CLEC5A
CLEC3A
Clec2d
E7EYJ8
KLRF1
CLEC6A
Cl
CLEC4C
Clec3a
KLRB1
F6NE55
Clec2i
CLEC12B
CLEC4E
Clec4a1
E7F7Z4
CLEC4D
Clec2e
E7F0Y1
Clec2f
Clec4a
Klrg1
Clec9a
CD69
Clec2h
CLEC4A
Q24K33
KLRC1
B0R0P1
Q1LWY8
Clec4d
Clec1a
Clec5a
CLEC7A
Cd209a
Cd209d
Clec7a
CLEC1A
ASGR1
OLR1
LOC101884526
clec3a
B8A5W1
Klra9
CLEC4G
si:ch211-170d8.5
F1QIA8
B8A5M2
si:ch73-361h17.1
key-216e
CD207
Cd209e
Clec4g
A8E4S9
Asgr1
FCER2
Cd209f
LOC1104400
lectin-33A
si:ch211-283g2.3
Klra10
KLRC3
Klrg2
COLEC10
KLRG2
Clec10a
CLEC10A
B0R0P2
ASGR2
Q5RG14
Clec2g
E7F2R6
Cd209b
R4GF04
Mgl2
Colec11
Cd207
F8W3G6
CLEC17A
Colec12
Clec4f
si:ch73-86n18.1
F1QHL3
A0A2R8RVX9
E9QHK9
A0A2R8Q3K1
CD209
F1QW96
hbl1
colec11
rgn
Dmel\CG13587
COLEC11
COLEC12
Asgr2
F1QR33
CLEC4M
Olr1
A5WUI8
DKEY-237O15.6


A35 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
A0A0R4IU15
CG46335
A0A0G2L1U5
NUDT16L1
Q9G3
zgc:152998
pre-mod(mdg4)-W
F6NZ76
Tomm7
CFB
A0A2R8PVJ3
UBR5
OR2A25
Cfap57
GLDC
Cluh
A0A2R8RII1
A0A2R8QGM9
Log10 P – value FATCAT
0.8
0.6
0.4
0.2
0.0
TM Score
0.1
0.2
0.3
0.4

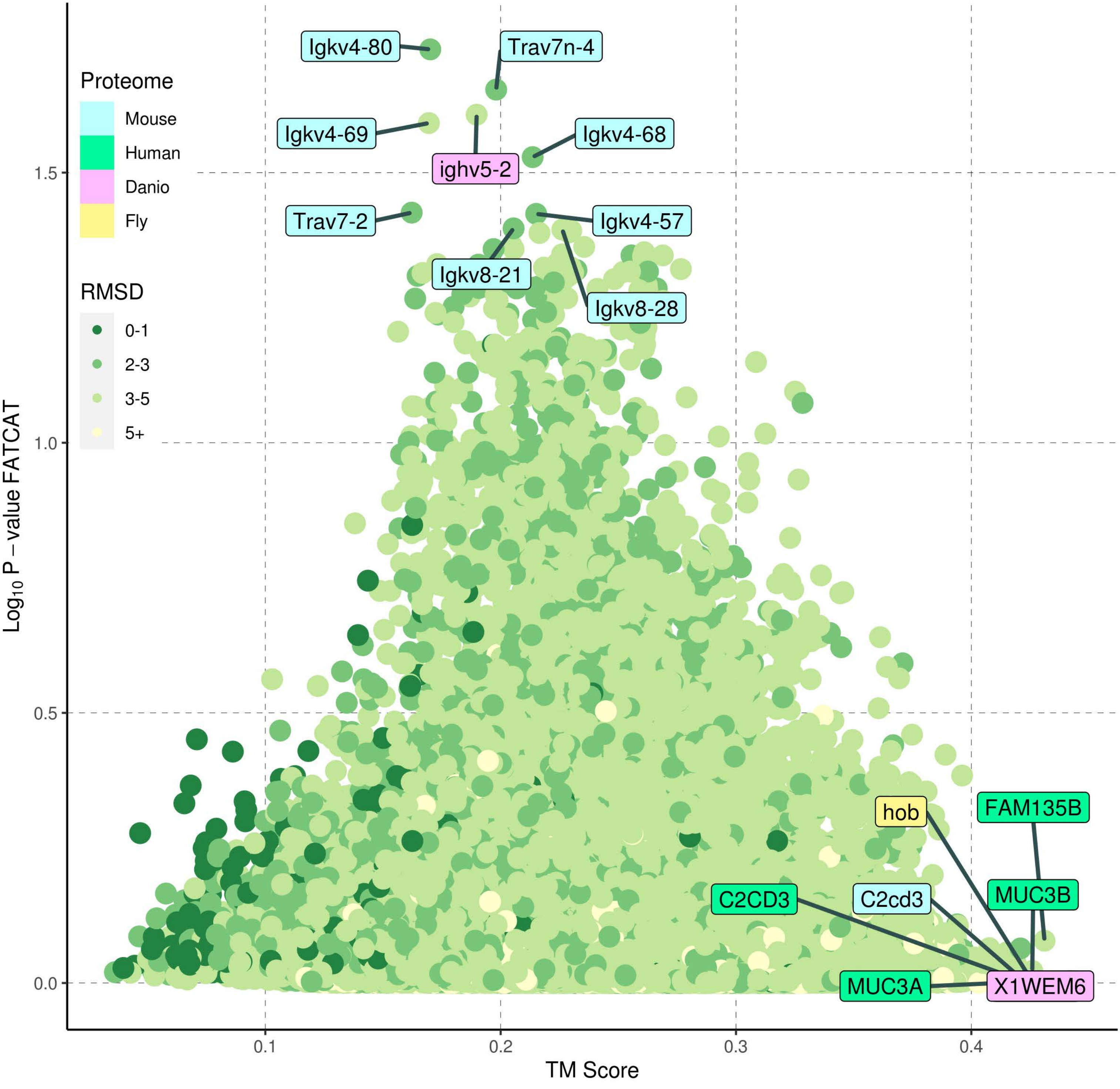

A36 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Dmel\CG46426
Dmel\CG12010
A0A2R8S013
Smim11
F1QF20
Dmel\CG34173
F6NZ76
A0A0R4IC72
Sptssb
GALNT5
F6NZP4
ESYT1
Als2
Ttc3
Dmel\CG10011
9530053A07Rik
Tnks
5
4
3
2
1
0
Log10 P – value FATCAT
0.1
0.2
0.3
0.4
TM Score


A37 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log₁₀ P – value FATCAT
TM Score
0
1
2
3
4
0.1
0.2
0.3
0.4
0.5
Alkbh7
F8W5S7
Q5PNQ5
Dmel\CG14130
F6P6J7
A0A2R8QKC5
si:dkey-65b12.2
A0A2R8QV03
ALKBH7
phf8
OR2A25
Phf8
OR2A25
Kdm4a
Phf2
Kdm2
kdm5bb
4

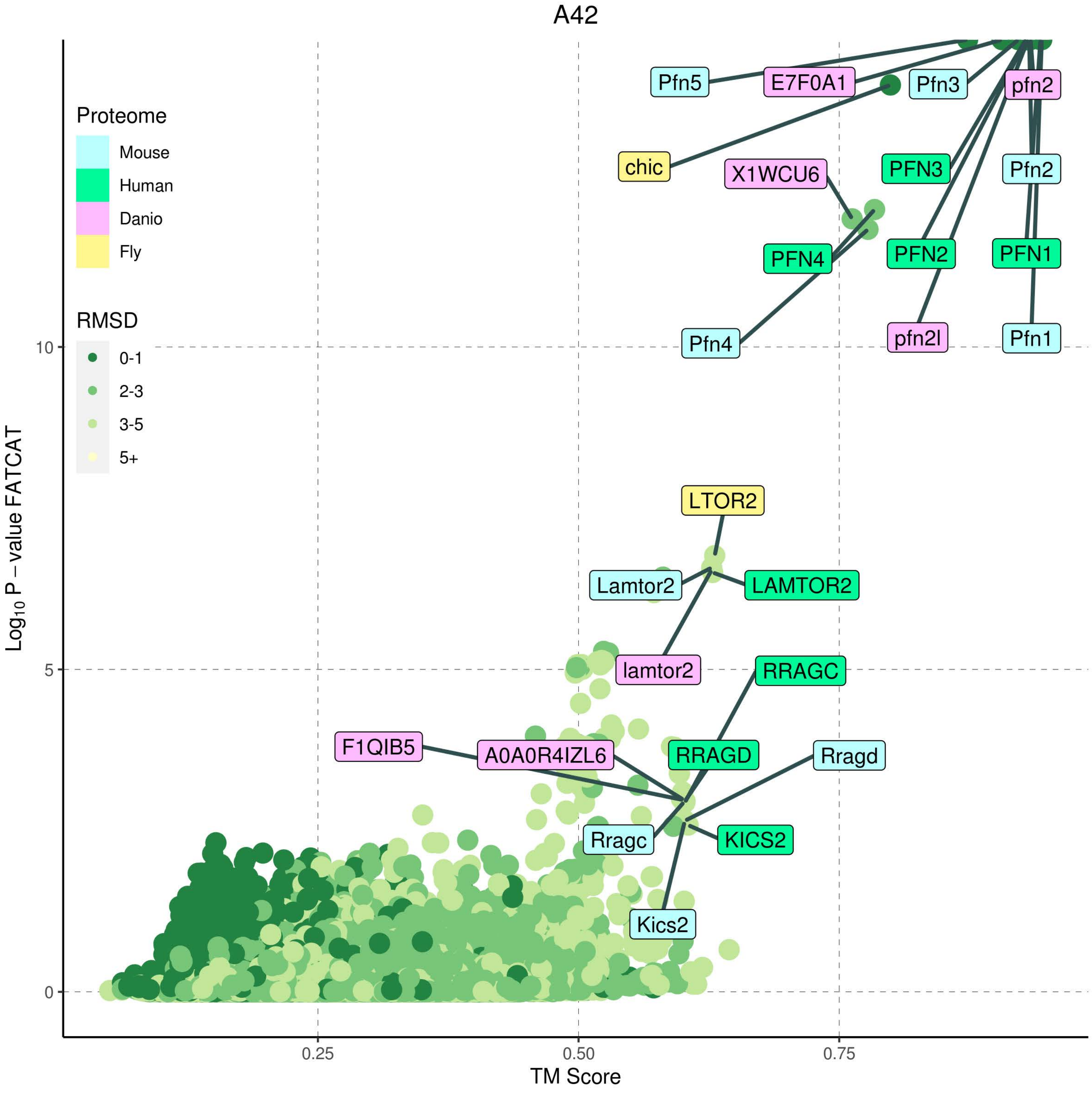

A38
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Cd47
CD47
Log10 P −value FATCAT
TM Score
0
5
10
0.0
0.2
0.4
0.6
0.8

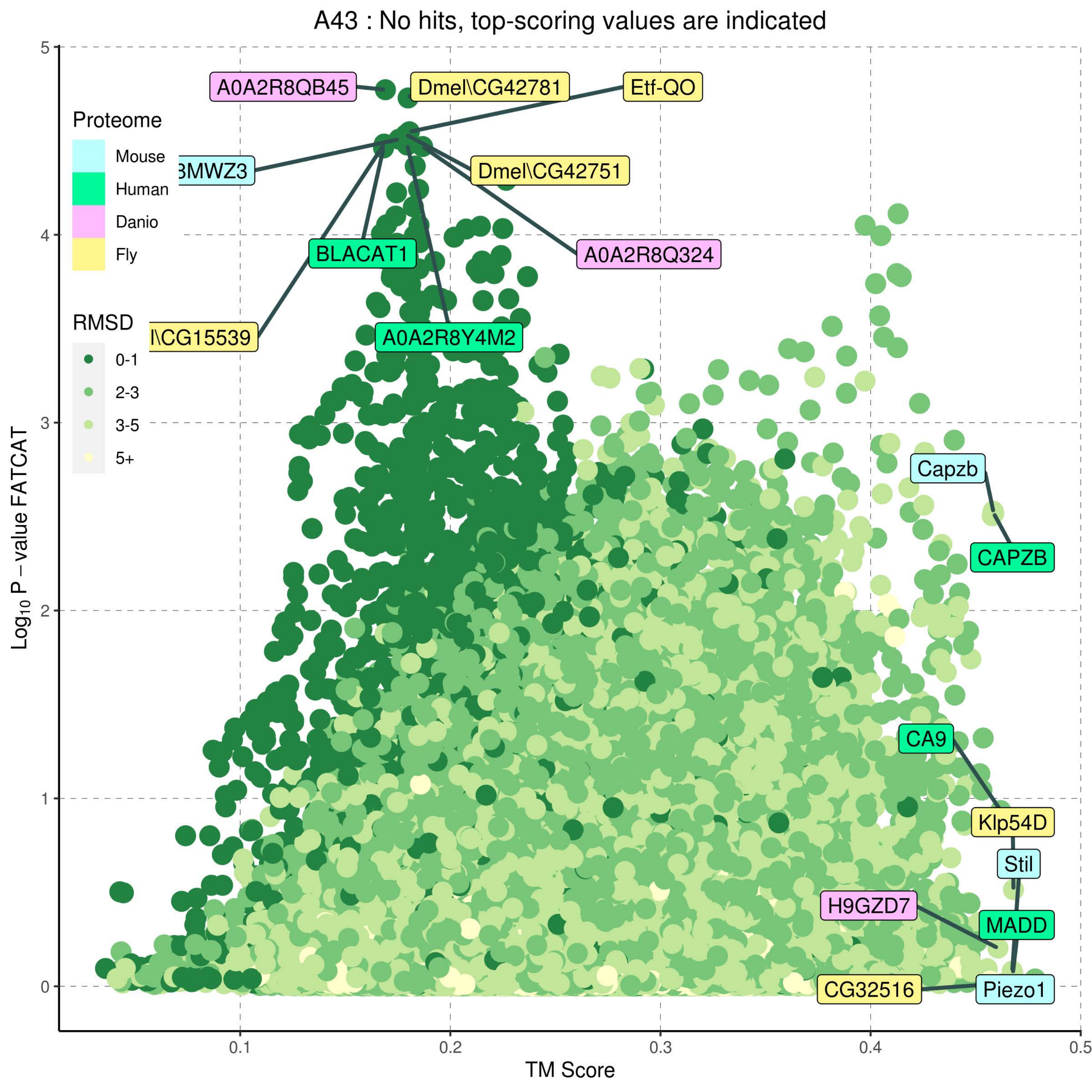

A39
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
TM Score
0.00
0.25
0.50
0.75
0
5
10
15
Sema3b
SEMA4D
W238
Q1LYS1
1L5C9
SEM
sema3d
Sema7a
7j14.7
sema8
F1Q5G8
SEMA3B
A0A2R9YJJ7
Sema3a
Sema3c
MA3A
sema3ab
A0A2R8QGT
M9MM97
M9MM94
M9MMA2
Sema4a
SEMA4A
sema4bb
SEMA3G
SEMA3D
Sema3d
Sema3g
Sema6b
Sema4d
Sema4c
Sema3f
OR2A25
GstE1
sema4e
Sema3e
211-138h
SEMA4F
F1QU86
SEMA3F
SEMA4C
Dsor1
sema3aa
F1RB05
Sema2a
SEMA6B
Sema6d
F1QF70
sema4f
Sema4f
F1QPG9
SEMA4E
Sema4g
B8JMB1
SEMA6A
A0A286YA
SEMA4G
SEMA6D
Sema6a
sema3fb
sema4ga
F1R9L1
si:dkey-78d16.2
E3W9A6
Eed
Sema4b
Sema5b
OR2A25
F1QJZ8
SEMA5A
A0A0R4IR
Sema5a
eed
EED
fng
Sema5c
A0A0G2KQ
RBBP5
E7F4J8
Gpld1
SEMA6C
dnai4
escl
Syngr
SEMA5B
Rbbp5
dtl
Sema6c
ITFG2
TBL2
Q5RH90
DNAI4
Dnai4
F1QST7
PlexA
mus302
dcaf10
OR2A25
Itfg2
Plxnd1
h211-127b1
PLXNB
Wdr88
SdicC
Wdr33
Tbl2
PlexB
Sdic4
Kptn
Plx
PLXND1
F1Q6L2
E7F9Q9
Klhdc8a
WDR33
tspear
A0A0R4IRZ9
wdr66
Dmel\CG13930
Plxnb3
KLHDC8A
TSPEAR
wdr6
DCAF8
F1Q7U
CFAP251
DNAI1
Plxnb1
E7FAS7
OR2A25
Dcaf10
Dnai1
F1QLR7
Dmel\CG9313
DCAF10
OR2A25
Chaf1b
Tspear
Dcaf8
FBXW5
C4
OR2A25
Dmel\CG9175
E7FFI7
MST1R
E7EYX4
Wdtc1
Dcaf8
Bbs9
MET
Itfg1
E9QFM9
klhdc
F1QF18
MED16
Cfap
DCAF8L2
Mst1r
W2F8
Plxnb2

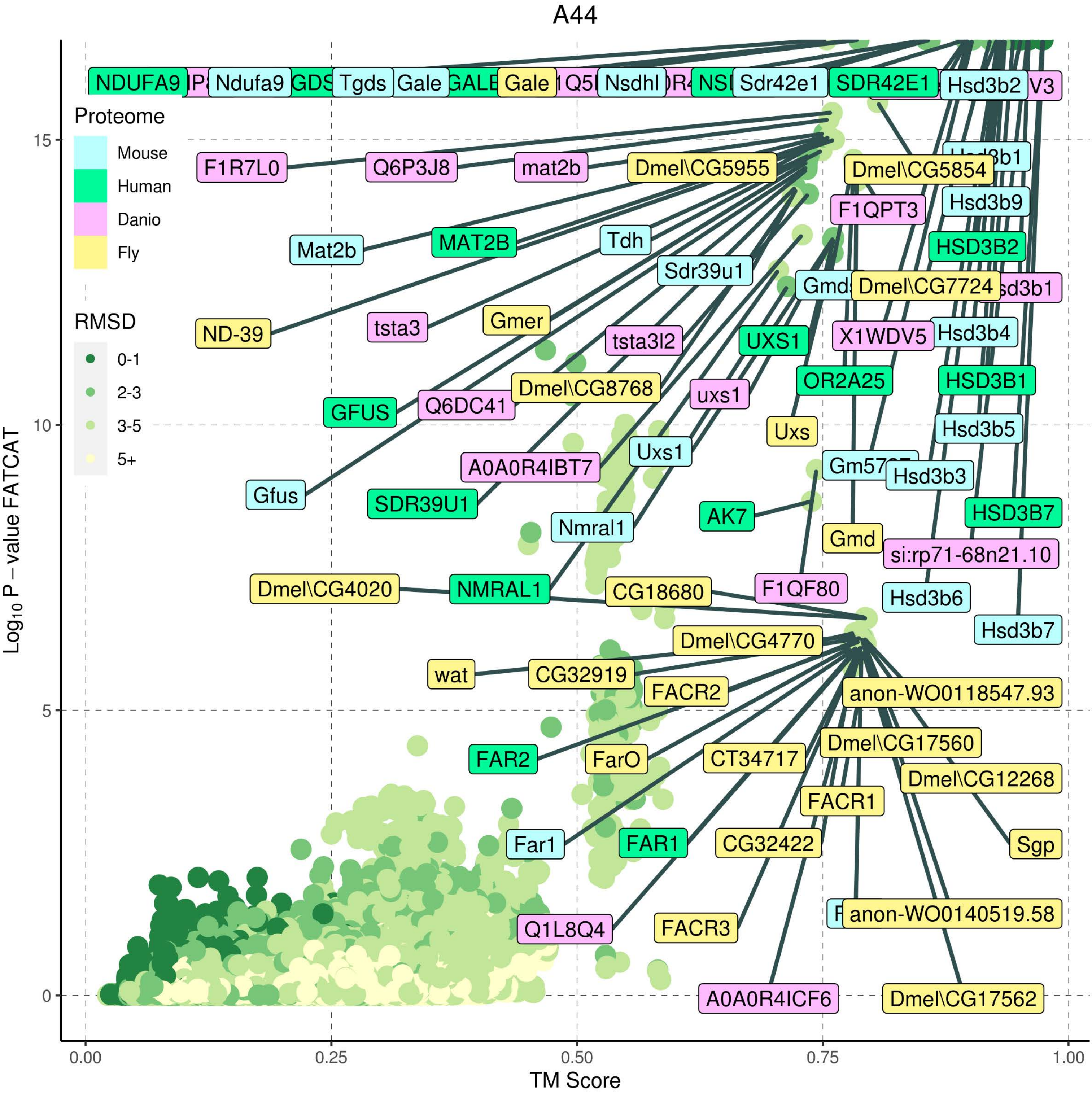

A40
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Klra1
6
4
2
0
0.2
0.4
0.6
TM Score
Log$_{10}$ P − value FATCAT

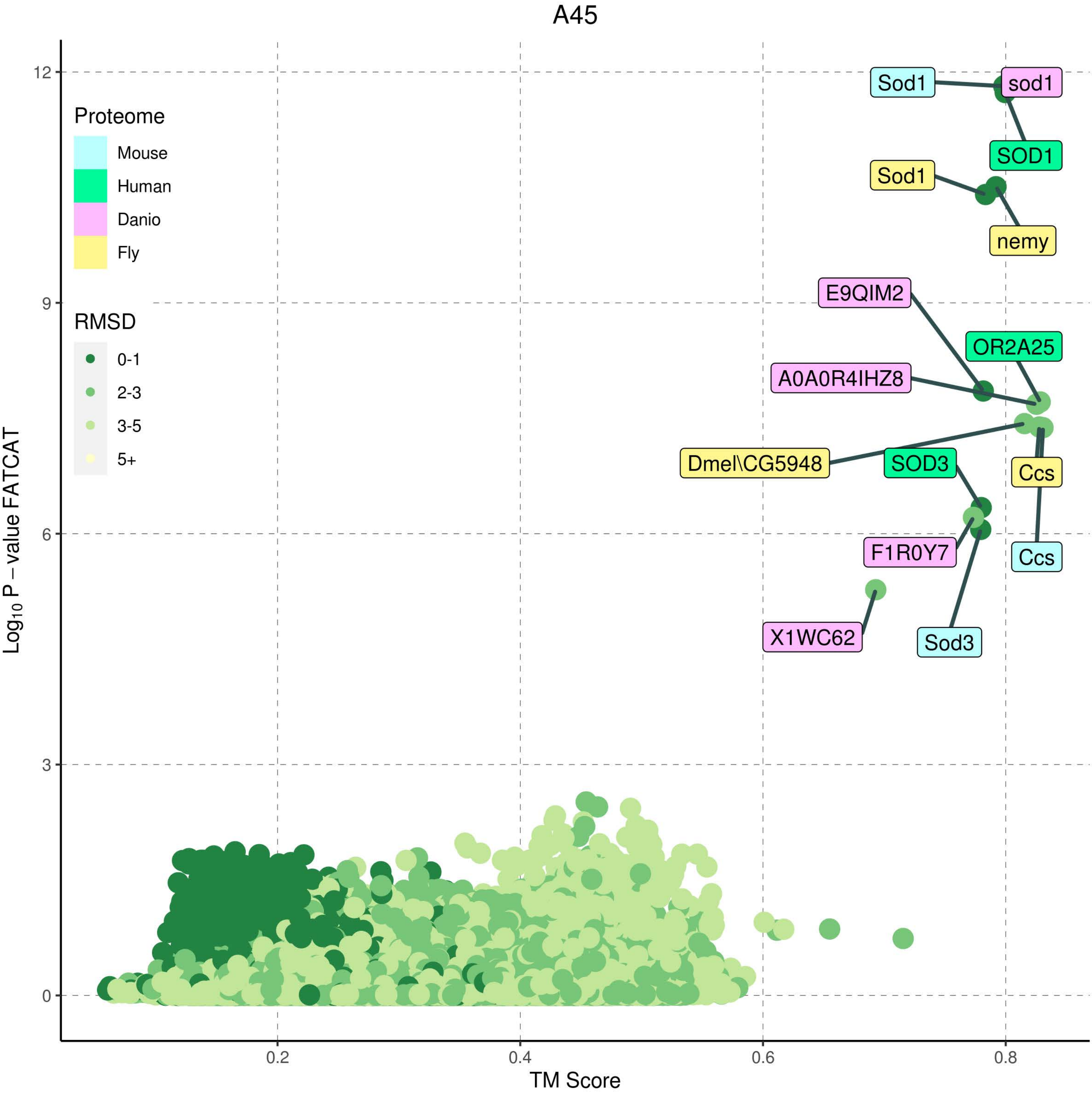


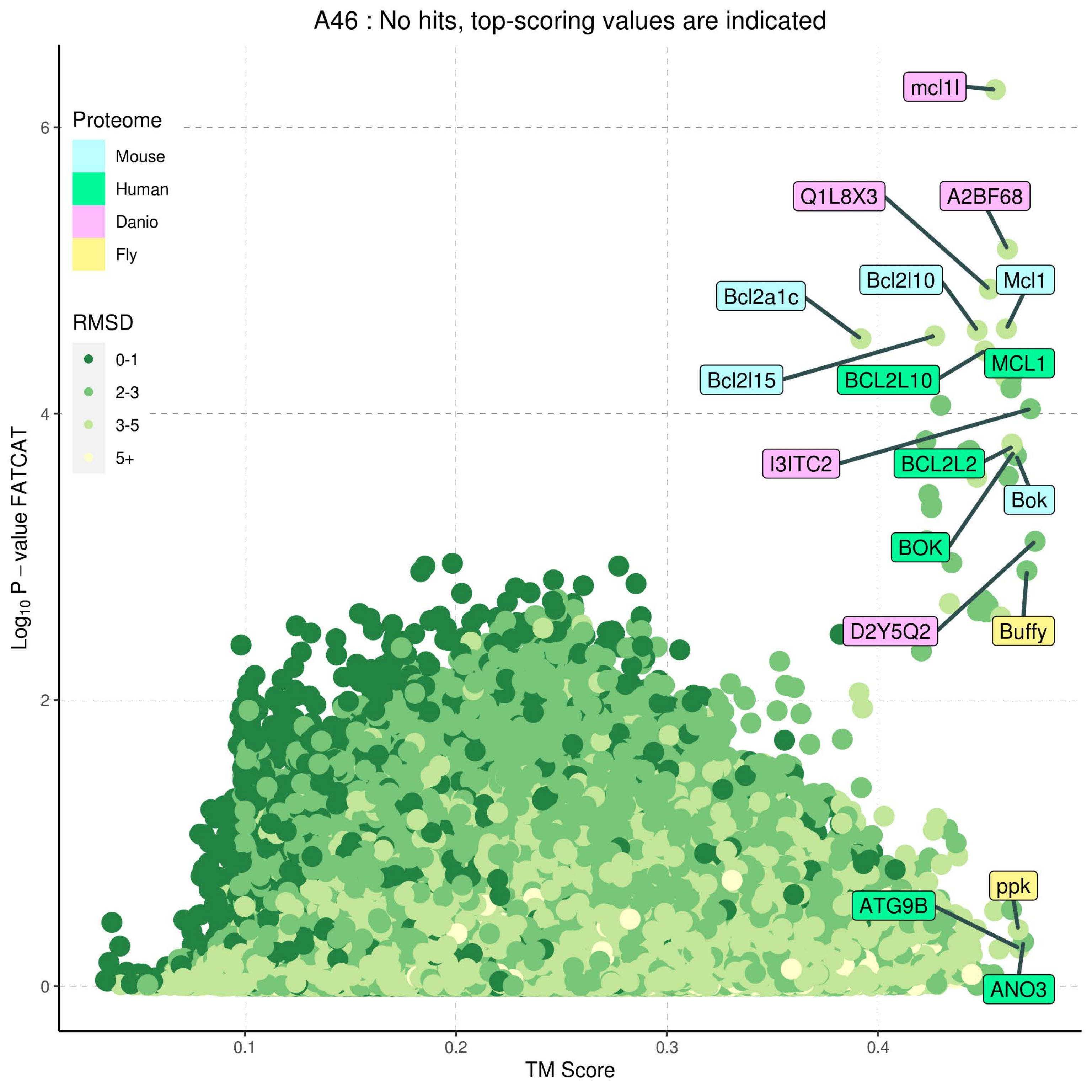
A41 : No hits, top-scoring values are indicated

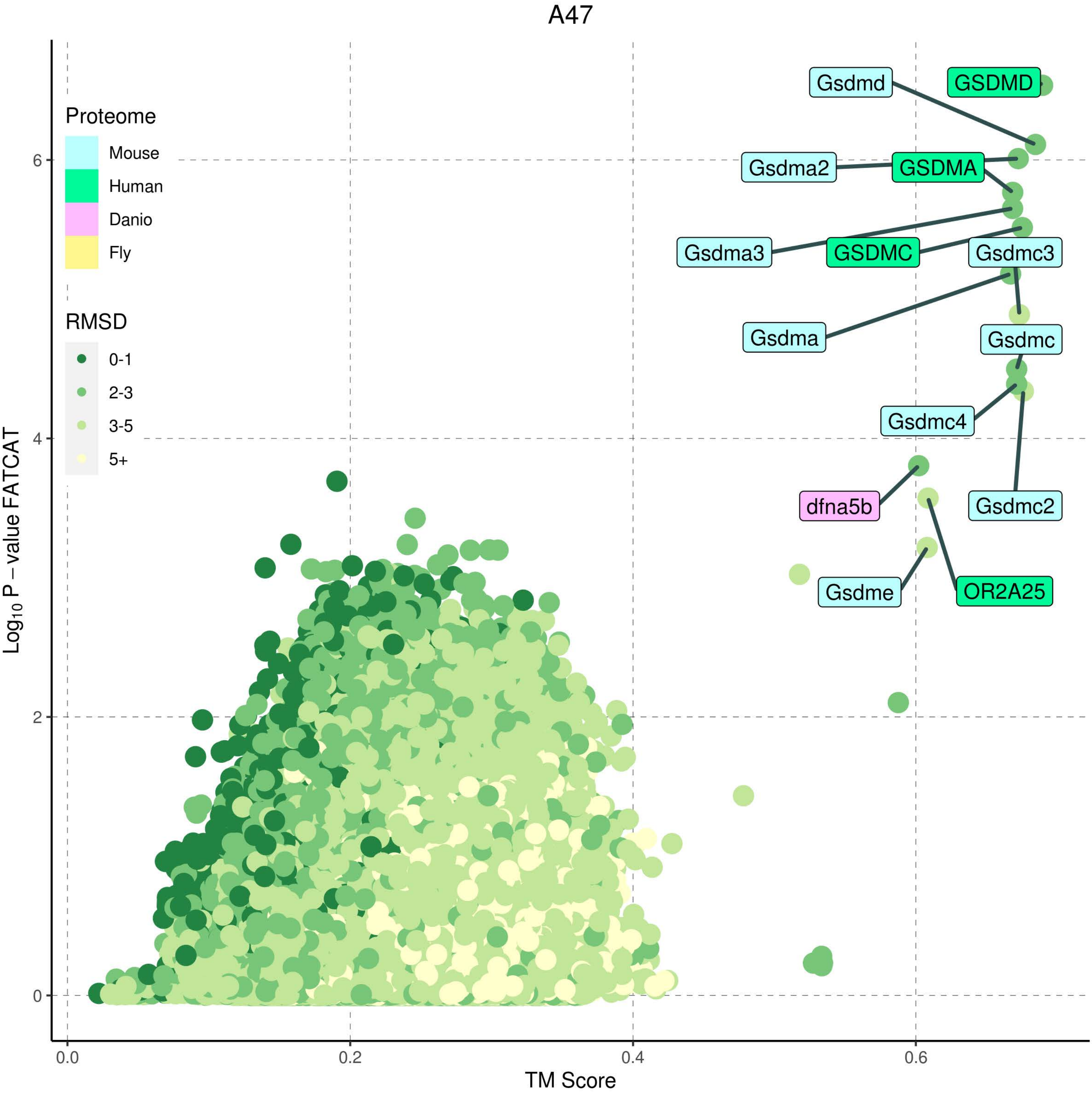

A42
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Pfn5
E7F0A1
Pfn3
pfn2
chic
X1WCU6
PFN3
Pfn2
PFN4
PFN2
PFN1
Pfn4
pfn2l
Pfn1
LTOR2
Lamtor2
LAMTOR2
lamtor2
RRAGC
F1QIB5
A0A0R4IZL6
RRAGD
Rragd
Rragc
KICS2
Kics2
Log₁₀ P – value FATCAT
10
5
0
0.25
0.50
0.75
TM Score

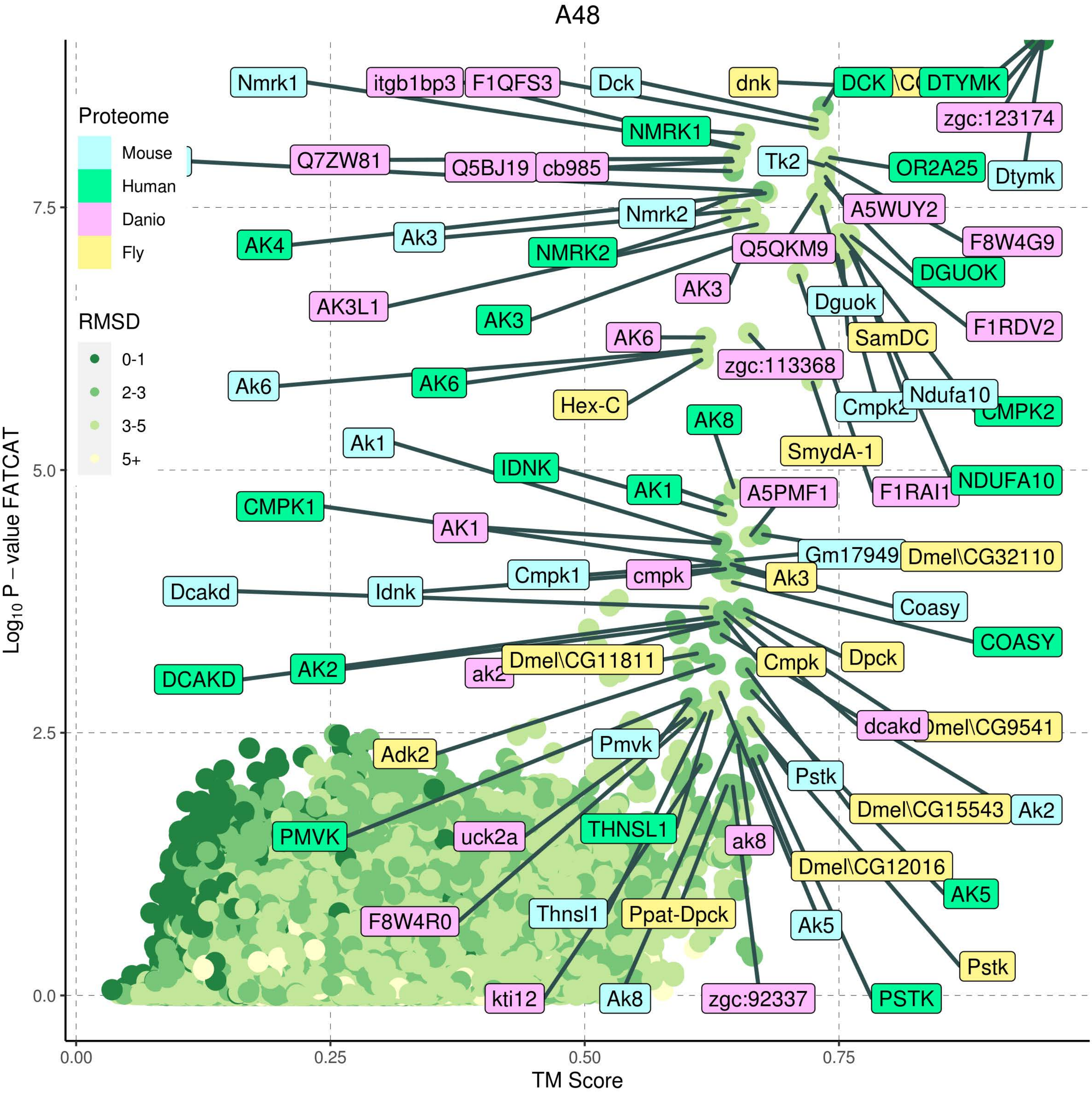

A43 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log$_{10}$ P – value FATCAT
TM Score
0
1
2
3
4
5
0.1
0.2
0.3
0.4
0.5
A0A2R8QB45
Dmel\CG42781
Etf-QO
3MWZ3
Dmel\CG42751
A0A2R8Q324
BLACAT1
l\CG15539
A0A2R8Y4M2
Capzb
CAPZB
CA9
Klp54D
Stil
H9GZD7
MADD
CG32516
Piezo1

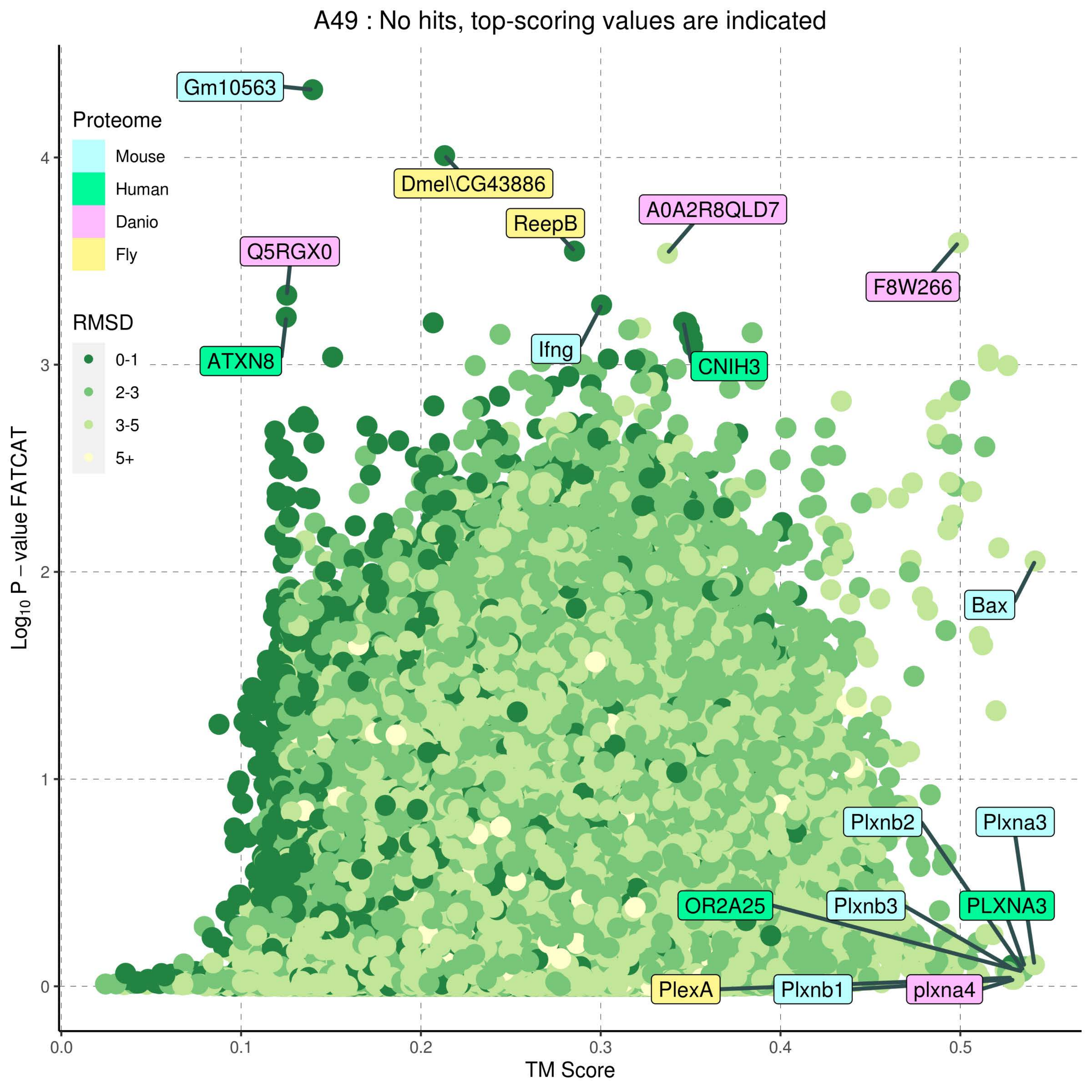

A44
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
TM Score
0.00
0.25
0.50
0.75
1.00
0
5
10
15
NDUFA9
Ndufa9
Tgds
Gale
Gale
Nsdhl
Sdr42e1
SDR42E1
Hsd3b2
F1R7L0
Q6P3J8
mat2b
Dmel\CG5955
Dmel\CG5854
Hsd3b9
F1QPT3
Mat2b
MAT2B
Tdh
HSD3B2
Sdr39u1
Dmel\CG7724
ND-39
tsta3
Gmer
tsta3l2
UXS1
X1WDV5
Hsd3b4
GFUS
Q6DC41
Dmel\CG8768
uxs1
OR2A25
HSD3B1
Uxs
Hsd3b5
Uxs1
A0A0R4IBT7
Hsd3b3
Gfus
SDR39U1
AK7
HSD3B7
Nmral1
Gmd
si:rp71-68n21.10
Dmel\CG4020
NMRAL1
CG18680
F1QF80
Hsd3b6
Hsd3b7
Dmel\CG4770
wat
CG32919
FACR2
anon-WO0118547.93
FAR2
FarO
CT34717
Dmel\CG17560
Dmel\CG12268
FACR1
Far1
FAR1
CG32422
Sgp
anon-WO0140519.58
Q1L8Q4
FACR3
A0A0R4ICF6
Dmel\CG17562

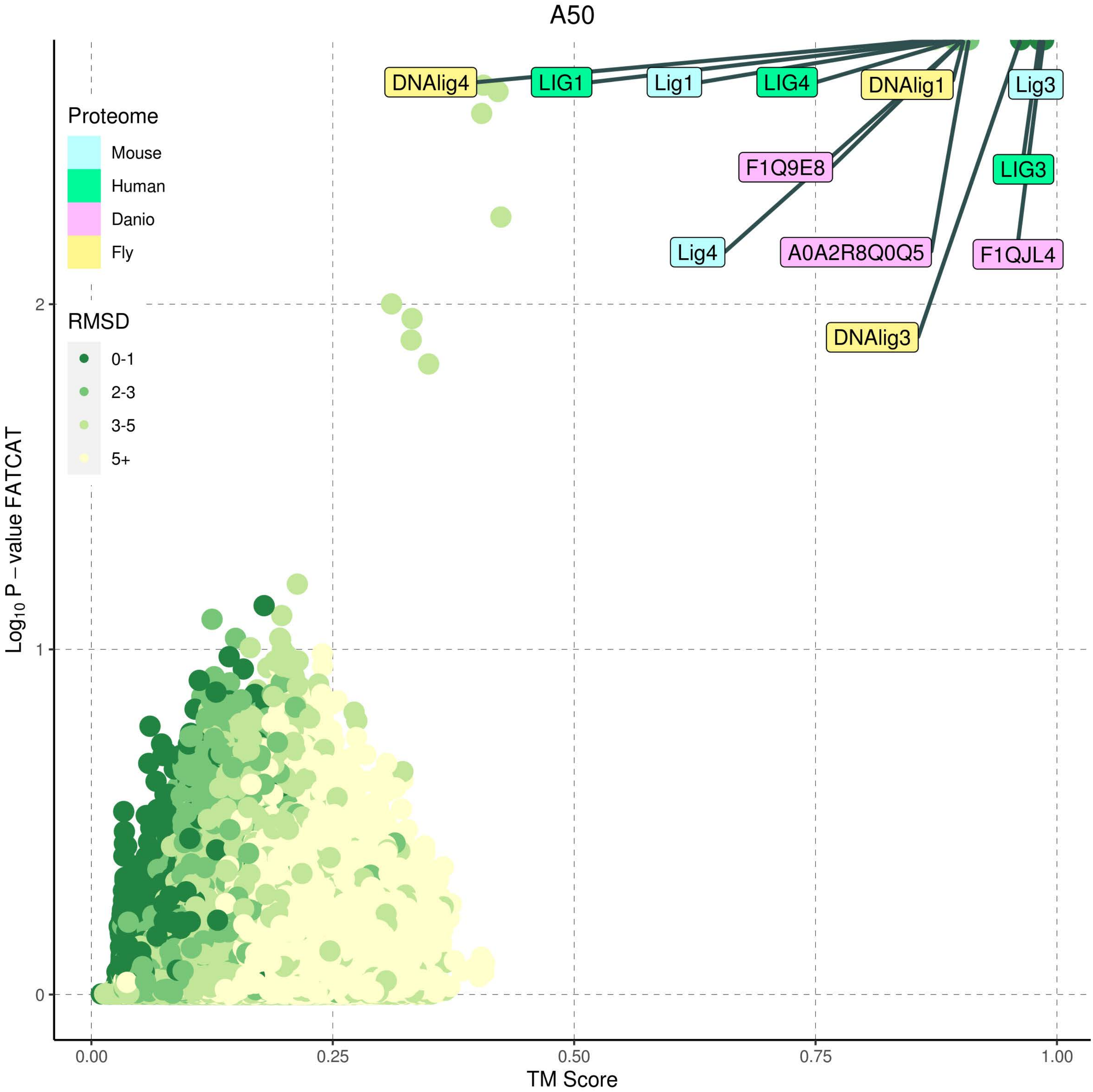

A45
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Sod1
sod1
SOD1
Sod1
nemy
E9QIM2
OR2A25
A0A0R4IHZ8
Dmel\CG5948
SOD3
Ccs
F1R0Y7
Ccs
X1WC62
Sod3
Log10 P – value FATCAT
TM Score
12
9
6
3
0
0.2
0.4
0.6
0.8

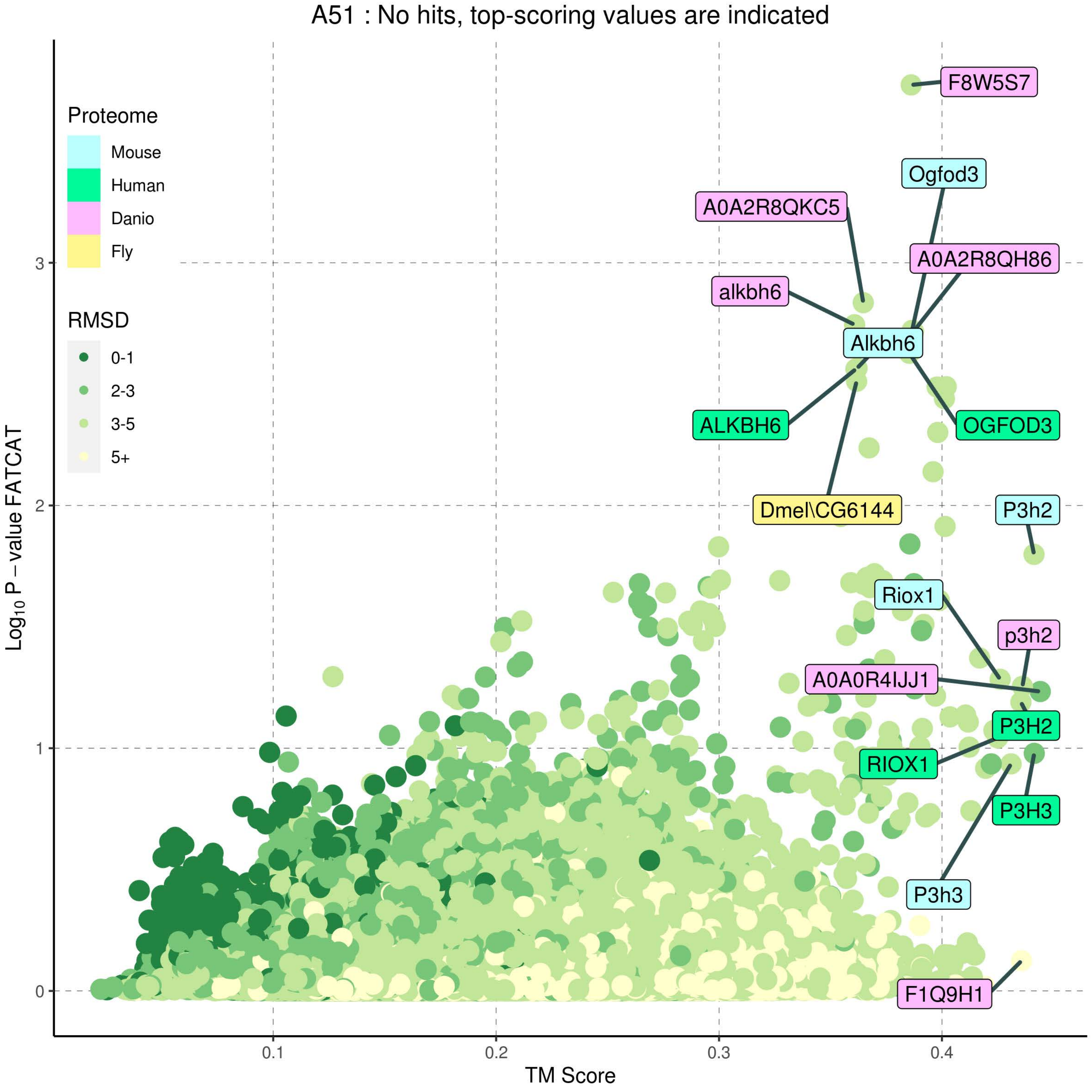

A46 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P − value FATCAT
TM Score
0
2
4
6
0.1
0.2
0.3
0.4
mcl1l
Q1L8X3
A2BF68
Bcl2l10
Mcl1
Bcl2a1c
Bcl2l15
BCL2L10
MCL1
I3ITC2
BCL2L2
Bok
BOK
D2Y5Q2
Buffy
ppk
ATG9B
ANO3


A47
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Gsdmd
GSDMD
Gsdma2
GSDMA
Gsdma3
GSDMC
Gsdmc3
Gsdma
Gsdmc
Gsdmc4
dfna5b
Gsdmc2
Gsdme
OR2A25
Log_{10} P − value FATCAT
0
2
4
6
0.0
0.2
0.4
0.6
TM Score

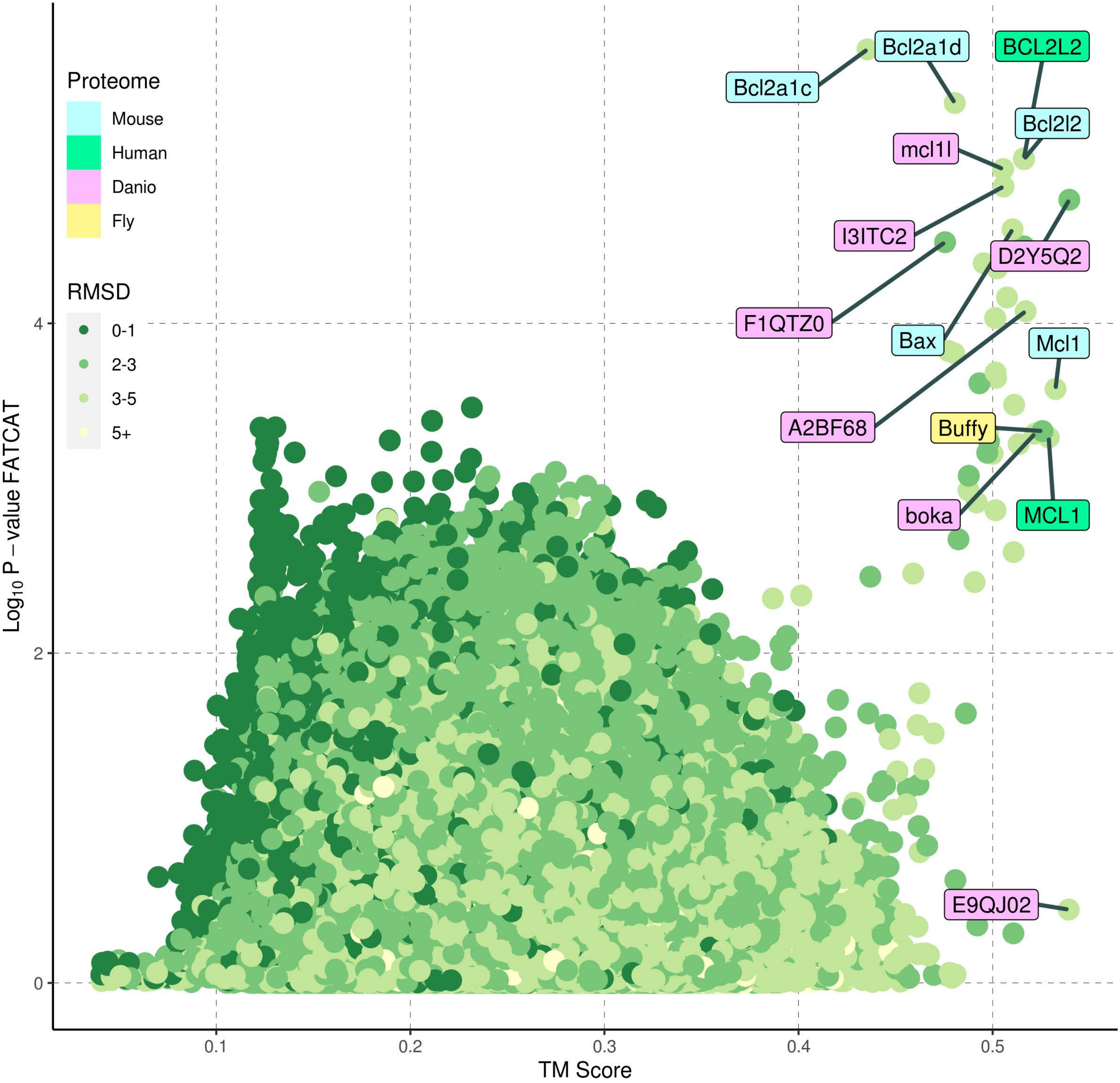

A48
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P − value FATCAT
TM Score
0.00
0.25
0.50
0.75
0.0
2.5
5.0
7.5
Nmrk1
itgb1bp3
F1QFS3
Dck
dnk
DCK
\C
DTYMK
zgc:123174
NMRK1
Q7ZW81
Q5BJ19
cb985
Tk2
OR2A25
Dtymk
Nmrk2
A5WUY2
F8W4G9
AK4
Ak3
NMRK2
Q5QKM9
DGUOK
AK3
AK3L1
AK3
Dguok
F1RDV2
SamDC
AK6
zgc:113368
Ak6
AK6
Hex-C
Cmpk2
Ndufa10
CMPK2
AK8
Ak1
SmydA-1
IDNK
NDUFA10
AK1
A5PMF1
F1RAI1
CMPK1
AK1
Gm17949
Dmel\CG32110
Cmpk1
cmpk
Ak3
Dcakd
Idnk
Coasy
COASY
Dmel\CG11811
Dpck
ak2
Cmpk
DCAKD
AK2
dcakd
Dmel\CG9541
Adk2
Pmvk
Pstk
Dmel\CG15543
Ak2
PMVK
uck2a
THNSL1
ak8
Dmel\CG12016
AK5
F8W4R0
Thnsl1
Ppat-Dpck
Ak5
Pstk
kti12
Ak8
zgc:92337
PSTK


A49 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Gm10563
Dmel\CG43886
A0A2R8QLD7
ReepB
Q5RGX0
F8W266
Ifng
ATXN8
CNIH3
Bax
Plxnb2
Plxna3
OR2A25
Plxnb3
PLXNA3
PlexA
Plxnb1
plxna4
Log_{10} P − value FATCAT
TM Score
0
1
2
3
4
0.0
0.1
0.2
0.3
0.4
0.5

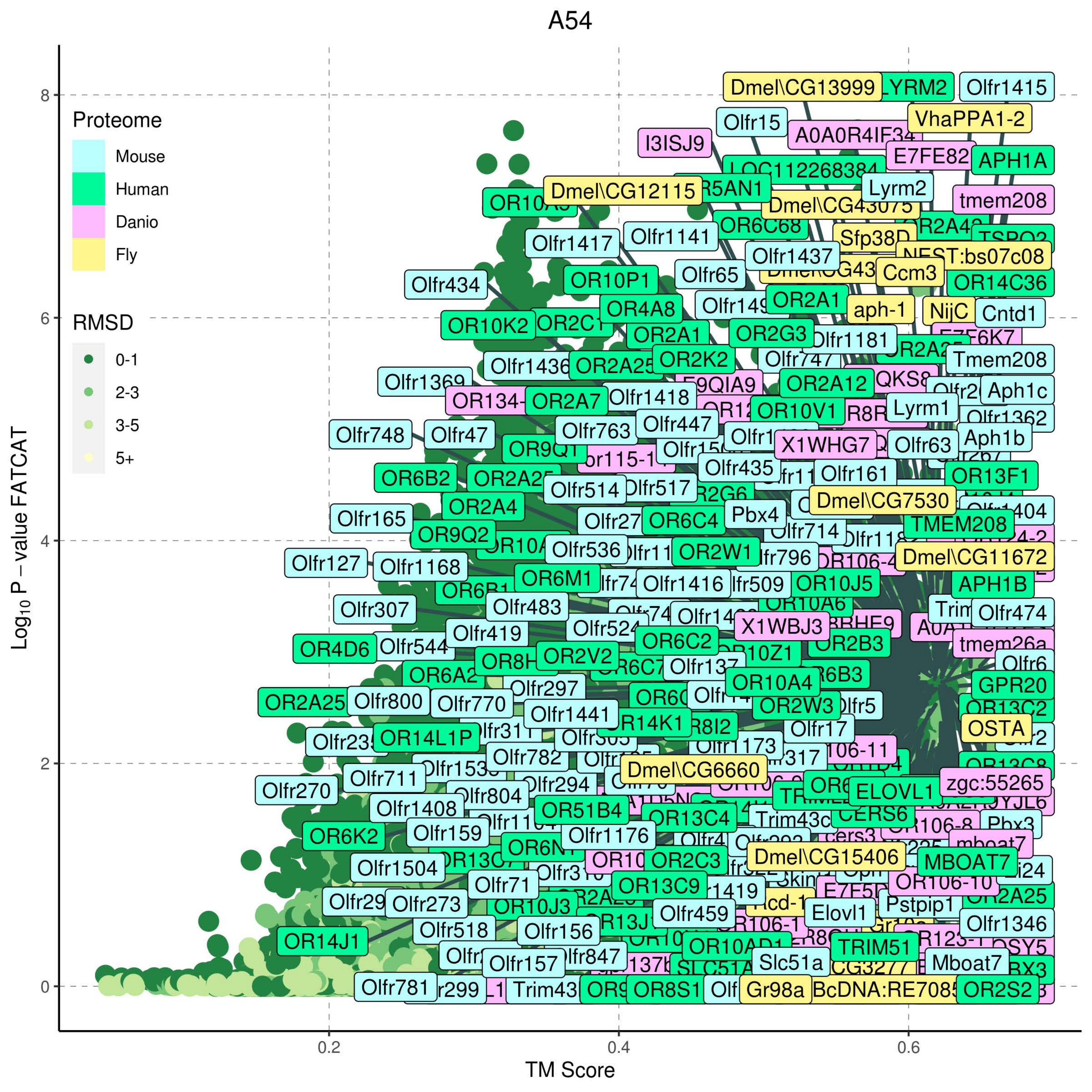

A50
DNAlig4
LIG1
Lig1
LIG4
DNAlig1
Lig3
F1Q9E8
LIG3
Lig4
A0A2R8Q0Q5
F1QJL4
DNAlig3
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log_{10} P – value FATCAT
TM Score
0
1
2
0.00
0.25
0.50
0.75
1.00

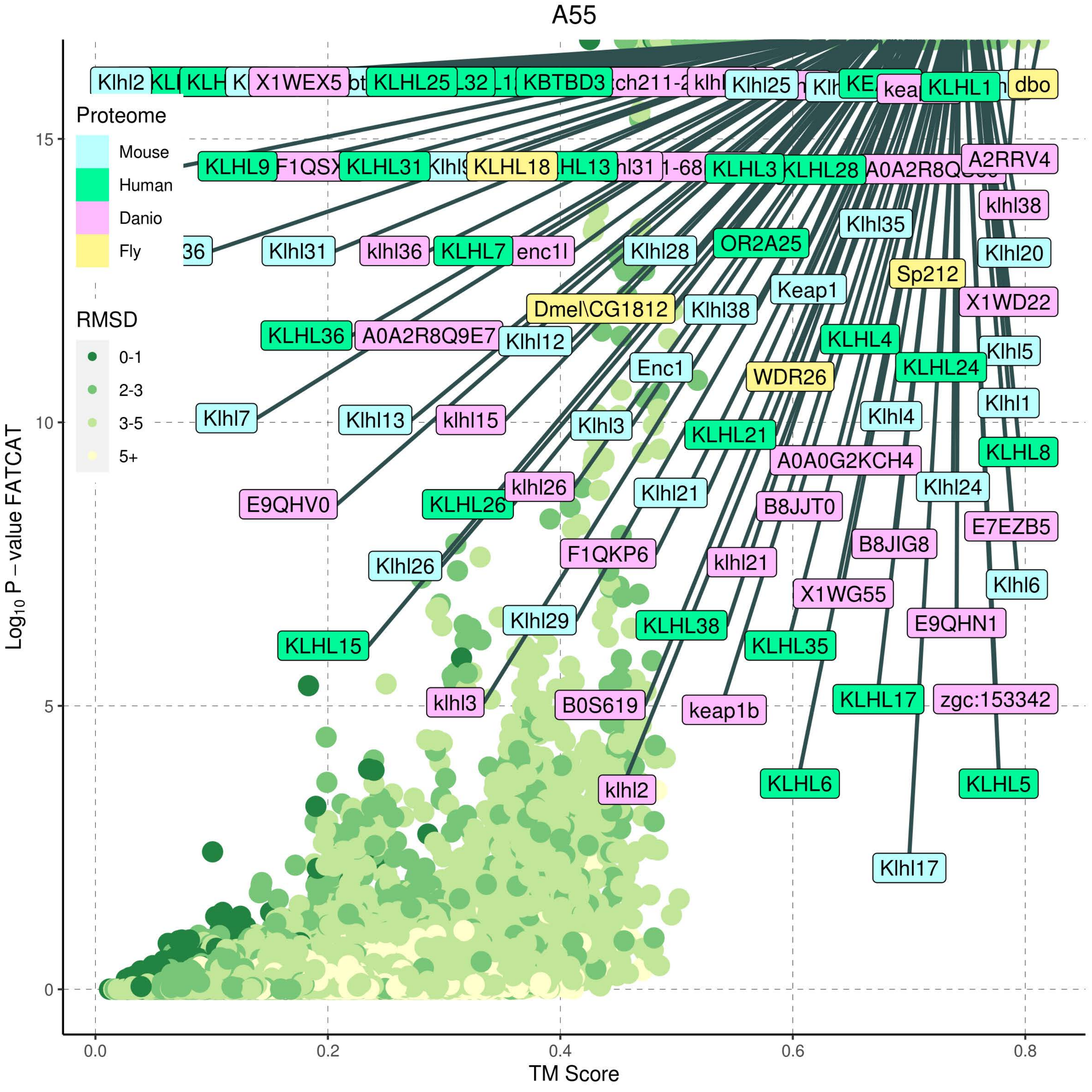

A51 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log$_{10}$ P − value FATCAT
TM Score
0
1
2
3
0.1
0.2
0.3
0.4
F8W5S7
Ogfod3
A0A2R8QKC5
A0A2R8QH86
alkbh6
Alkbh6
ALKBH6
OGFOD3
Dmel\CG6144
P3h2
Riox1
p3h2
A0A0R4IJJ1
P3H2
RIOX1
P3H3
P3h3
F1Q9H1

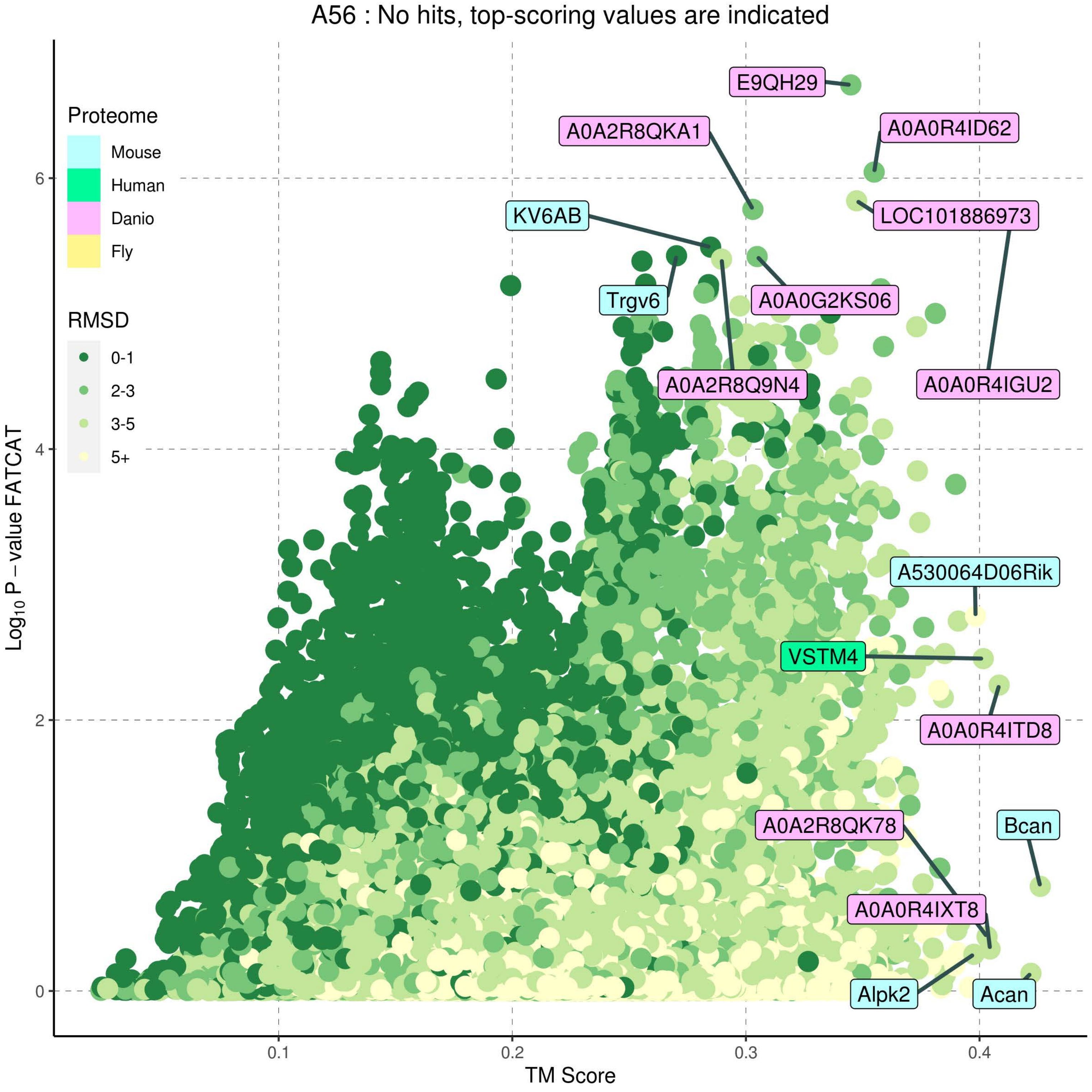
A52 : No hits, top-scoring values are indicated

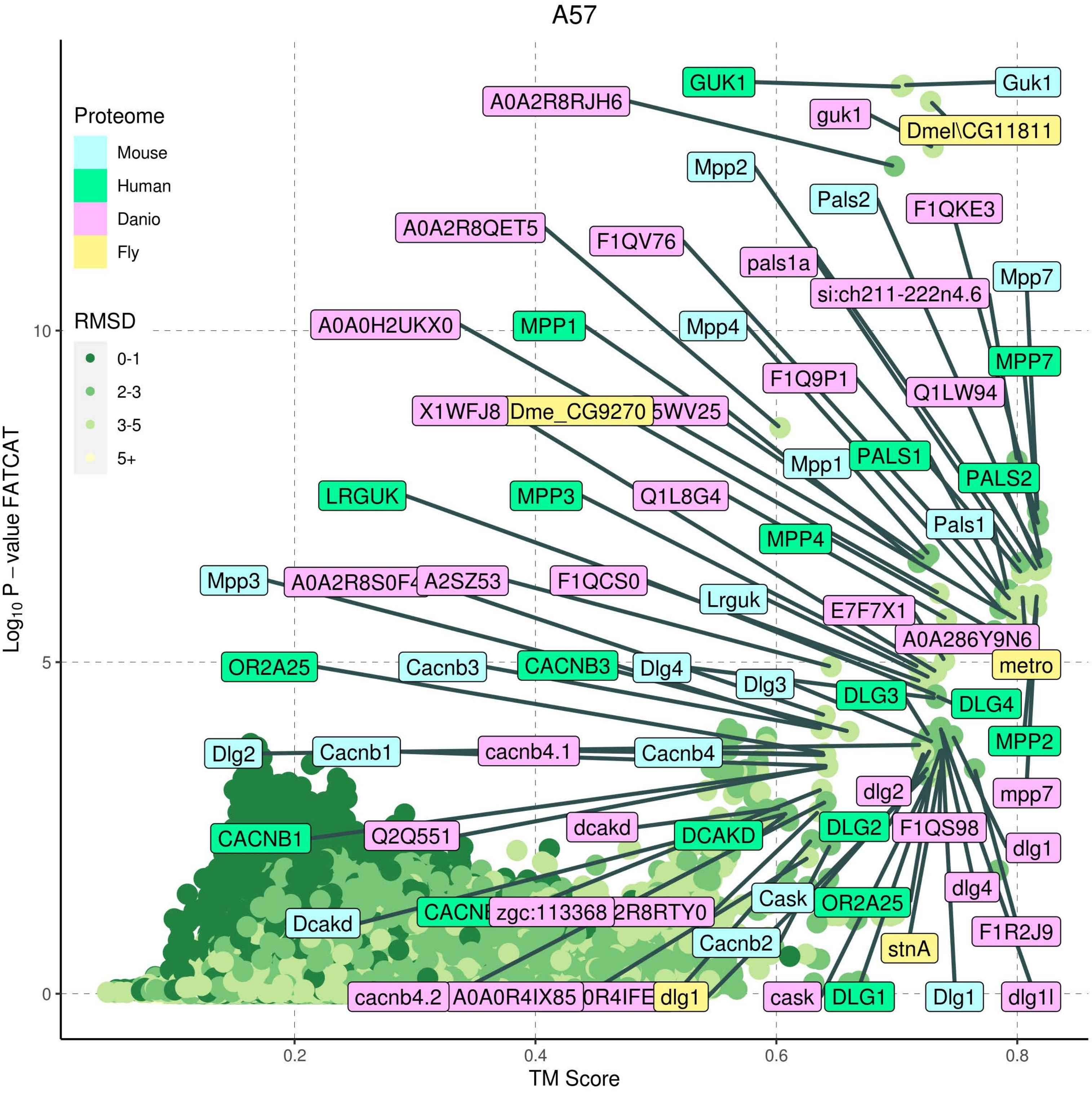


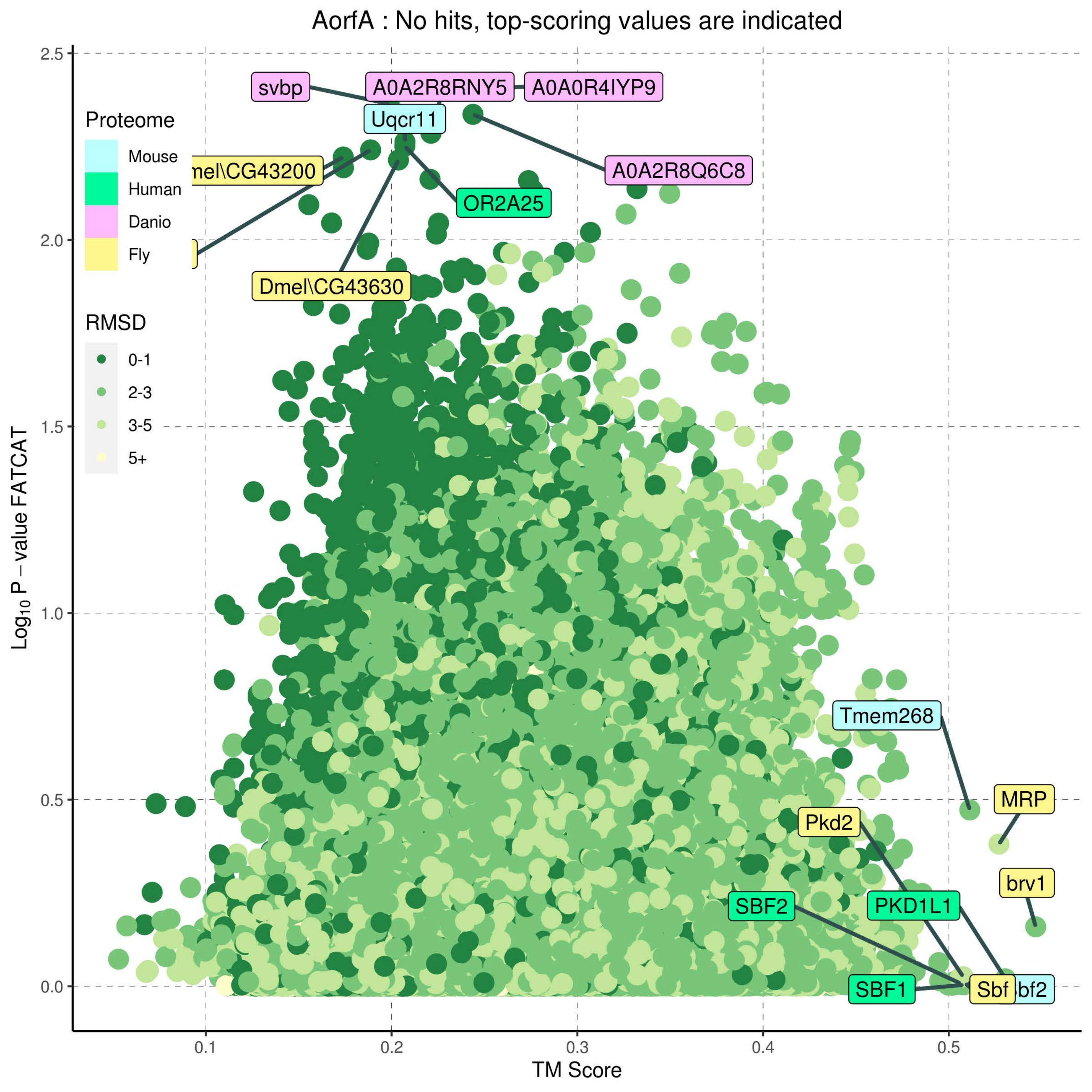

A53
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
TNFRSF1B
LTBR
Tnfrsf1b
Log_{10} P − value FATCAT
0
1
2
3
4
0.2
0.4
0.6
TM Score

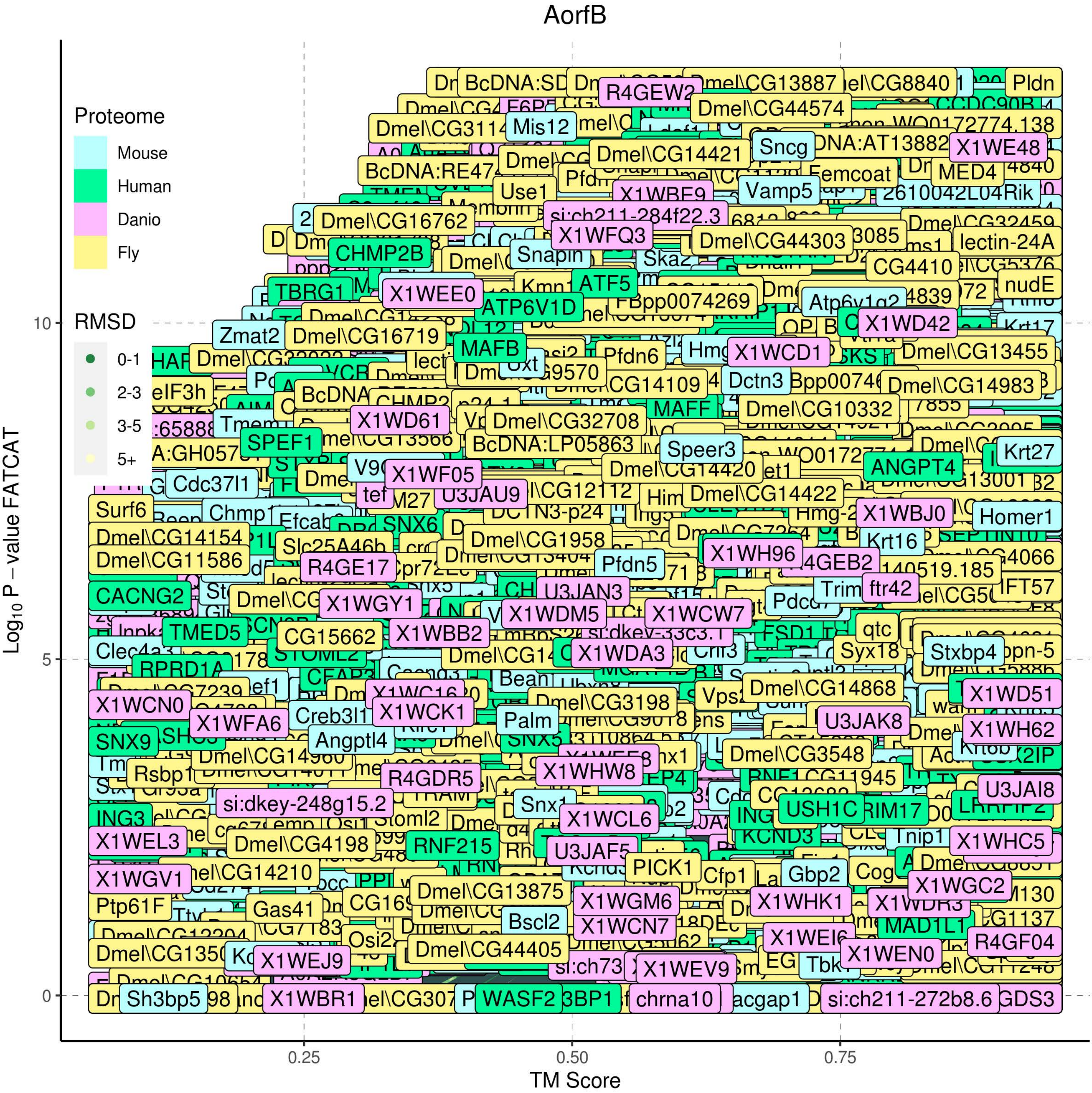

A54
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
TM Score
0
2
4
6
8
0.2
0.4
0.6
Dmel\CG13999
LYRM2
Olfr1415
Olfr15
A0A0R4IF34
VhaPPA1-2
I3ISJ9
E7FE82
APH1A
LOC112268384
Lyrm2
Dmel\CG12115
R5AN1
OR10A3
Dmel\CG43075
tmem208
OR6C68
OR2A42
Olfr1417
Olfr1141
Sfp38D
TSPO2
Olfr1437
NEST:bs07c08
Olfr65
Ccm3
Olfr434
OR10P1
OR14C36
OR4A8
Olfr149
OR2A1
aph-1
NijC
Cntd1
OR10K2
OR2C1
OR2A1
OR2G3
Olfr1181
Olfr1436
OR2A25
OR2K2
Olfr747
Tmem208
F9QIA9
OR2A12
QKS8
Olfr1369
Aph1c
OR134-
OR2A7
Olfr1418
OR10V1
Lyrm1
Olfr1362
Olfr748
Olfr47
Olfr763
Olfr447
X1WHG7
Olfr63
Aph1b
OR9Q1
or115-1
Olfr435
Olfr161
OR13F1
OR6B2
OR2A25
Olfr514
Olfr517
Dmel\CG7530
OR2A4
Olfr165
Olfr27
OR6C4
Pbx4
Olfr1404
Olfr714
TMEM208
OR9Q2
Olfr536
OR2W1
Olfr796
Dmel\CG11672
Olfr127
Olfr1168
OR6M1
Olfr1416
OR10J5
APH1B
Olfr483
Olfr307
OR10A6
Olfr474
Olfr524
X1WBJ3
Olfr419
OR4D6
Olfr544
OR6C2
OR2B3
tmem26a
OR2V2
OR10Z1
Olfr6
OR6A2
Olfr137
OR6B3
Olfr297
OR10A4
GPR20
OR2A25
Olfr800
Olfr770
OR2W3
Olfr5
OR13C2
Olfr1441
OR14K1
OSTA
Olfr17
OR14L1P
Olfr1173
Olfr782
Olfr317
Dmel\CG6660
Olfr711
Olfr294
Olfr270
ELOVL1
zgc:55265
Olfr804
OR51B4
Olfr1408
OR13C4
Trim43c
CERS6
Pbx3
OR6K2
Olfr159
Olfr1176
mboat7
OR6N1
Dmel\CG15406
MBOAT7
OR2C3
Olfr1504
OR106-10
OR13C9
Olfr71
Olfr1419
Olfr29
Olfr273
OR10J3
Elovl1
Pstpip1
OR2A25
Olfr459
Olfr1346
Olfr518
Olfr156
OR14J1
OR10AD1
TRIM51
Olfr847
Olfr157
Slc51a
Mboat7
Olfr781
Trim43
OR8S1
Gr98a
BcDNA:RE7085
OR2S2

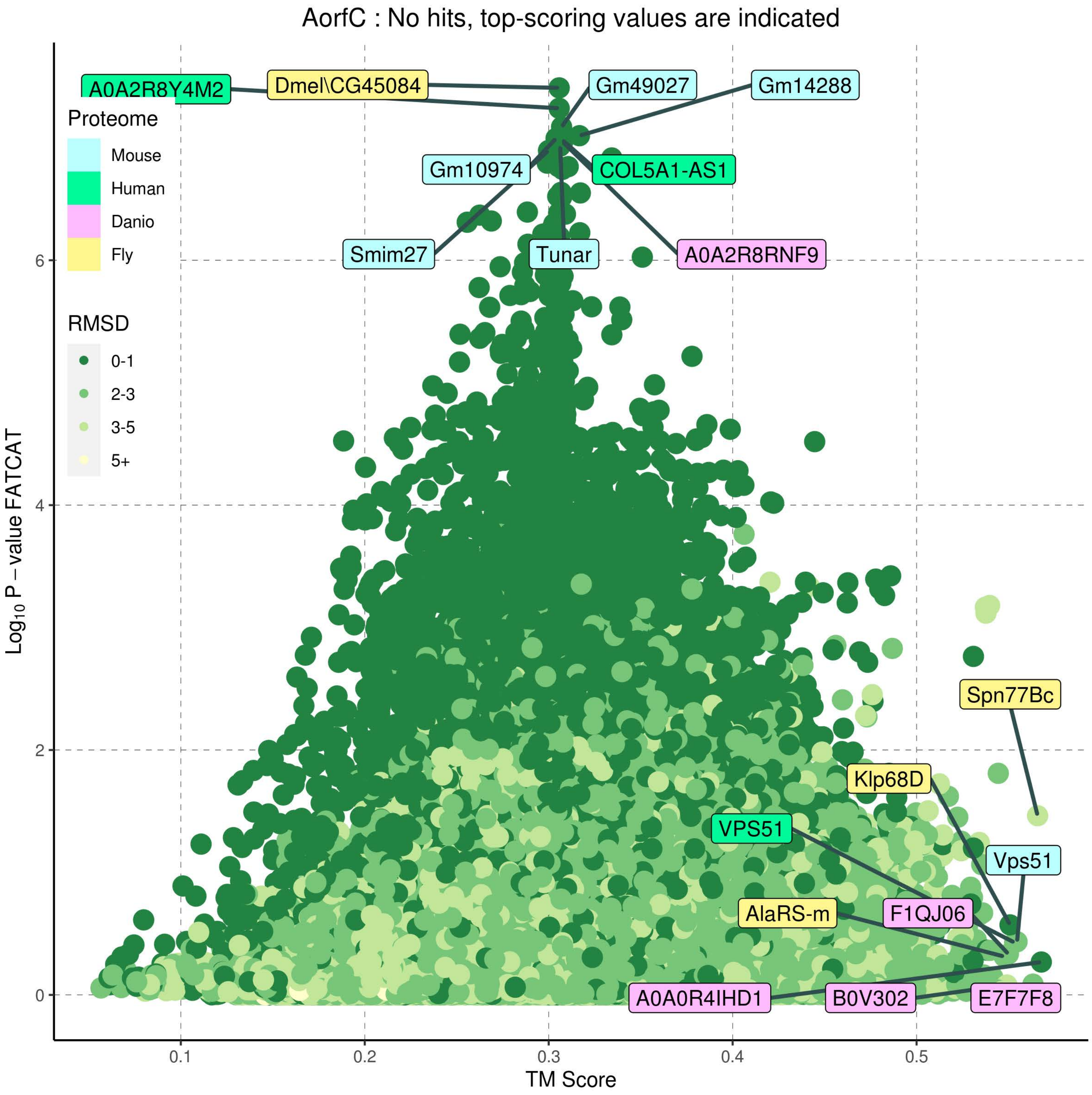

A55
Log₁₀ P − value FATCAT
TM Score
0.0
0.2
0.4
0.6
0.8
0
5
10
15
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Klhl2
X1WEX5
KLHL25
KBTBD3
Klhl25
keap
KLHL1
dbo
KLHL9
KLHL31
KLHL18
KLHL3
KLHL28
A2RRV4
klhl38
Klhl35
Klhl31
klhl36
KLHL7
enc1l
Klhl28
OR2A25
Klhl20
Sp212
Keap1
X1WD22
Dmel\CG1812
Klhl38
KLHL36
A0A2R8Q9E7
Klhl12
KLHL4
Klhl5
Enc1
WDR26
KLHL24
Klhl7
Klhl13
klhl15
Klhl3
KLHL21
Klhl4
Klhl1
A0A0G2KCH4
KLHL8
klhl26
Klhl21
Klhl24
E9QHV0
KLHL26
B8JJT0
E7EZB5
B8JIG8
F1QKP6
klhl21
Klhl26
X1WG55
Klhl6
Klhl29
KLHL38
E9QHN1
KLHL15
KLHL35
klhl3
B0S619
keap1b
KLHL17
zgc:153342
klhl2
KLHL6
KLHL5
Klhl17


A56 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
E9QH29
A0A2R8QKA1
A0A0R4ID62
KV6AB
LOC101886973
Trgv6
A0A0G2KS06
A0A2R8Q9N4
A0A0R4IGU2
A530064D06Rik
VSTM4
A0A0R4ITD8
A0A2R8QK78
Bcan
A0A0R4IXT8
Alpk2
Acan
6
4
2
0
0.1
0.2
0.3
0.4
TM Score
Log_{10} P – value FATCAT

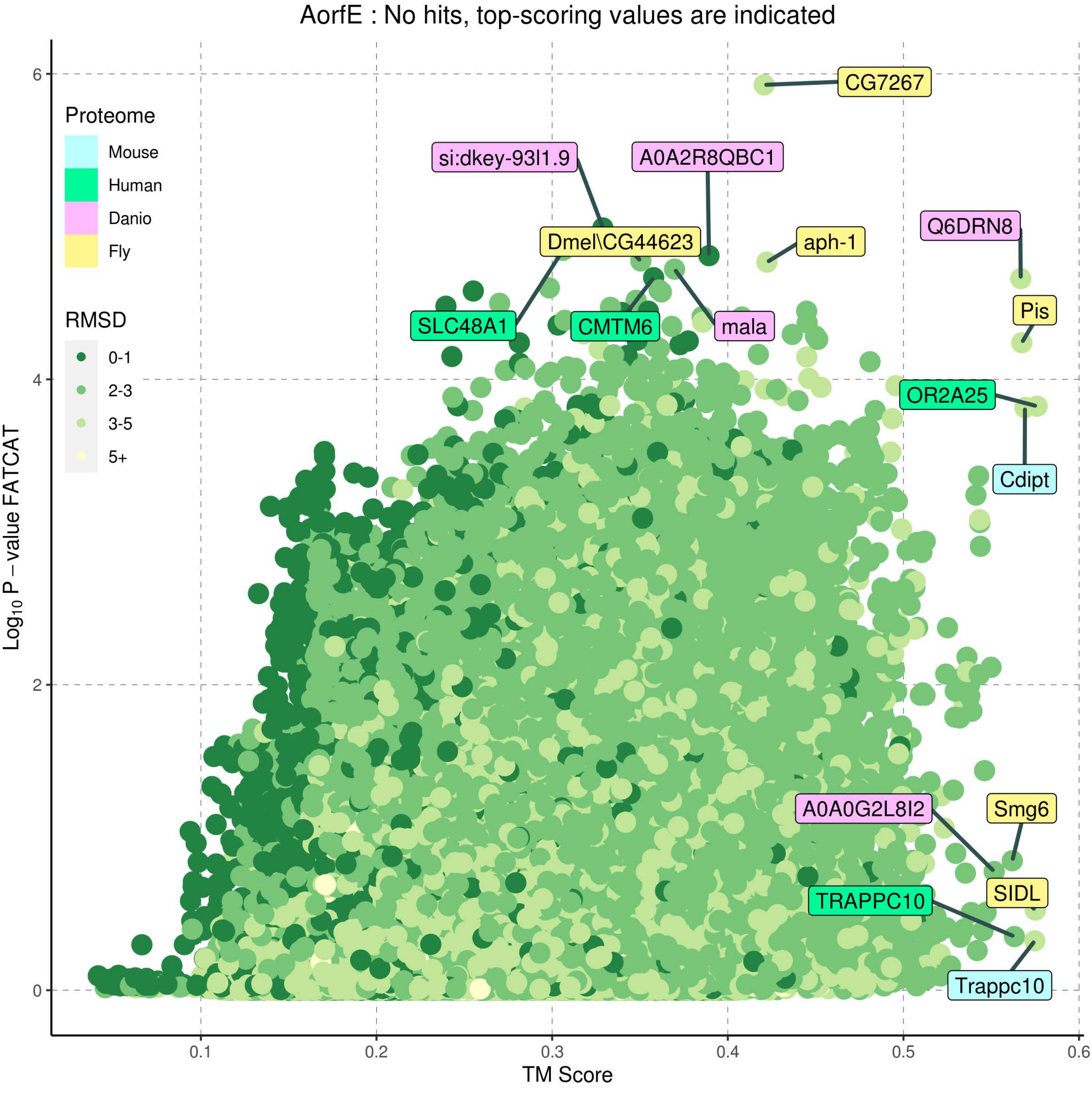

A57
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log₁₀ P – value FATCAT
TM Score
0
5
10
0.2
0.4
0.6
0.8
GUK1
Guk1
A0A2R8RJH6
guk1
Dmel\CG11811
Mpp2
Pals2
F1QKE3
A0A2R8QET5
F1QV76
pals1a
Mpp7
si:ch211-222n4.6
A0A0H2UKX0
MPP1
Mpp4
MPP7
F1Q9P1
Q1LW94
X1WFJ8
Dme_CG9270
5WV25
Mpp1
PALS1
PALS2
LRGUK
MPP3
Q1L8G4
Pals1
MPP4
Mpp3
A0A2R8S0F4
A2SZ53
F1QCS0
Lrguk
E7F7X1
A0A286Y9N6
OR2A25
Cacnb3
CACNB3
Dlg4
metro
Dlg3
DLG3
DLG4
MPP2
Dlg2
Cacnb1
cacnb4.1
Cacnb4
dlg2
mpp7
CACNB1
Q2Q551
dcakd
DCAKD
DLG2
F1QS98
dlg1
dlg4
Cask
OR2A25
Dcakd
CACNE
zgc:113368
2R8RTY0
Cacnb2
F1R2J9
stnA
cacnb4.2
A0A0R4IX85
0R4IFE
dlg1
cask
DLG1
Dlg1
dlg1l

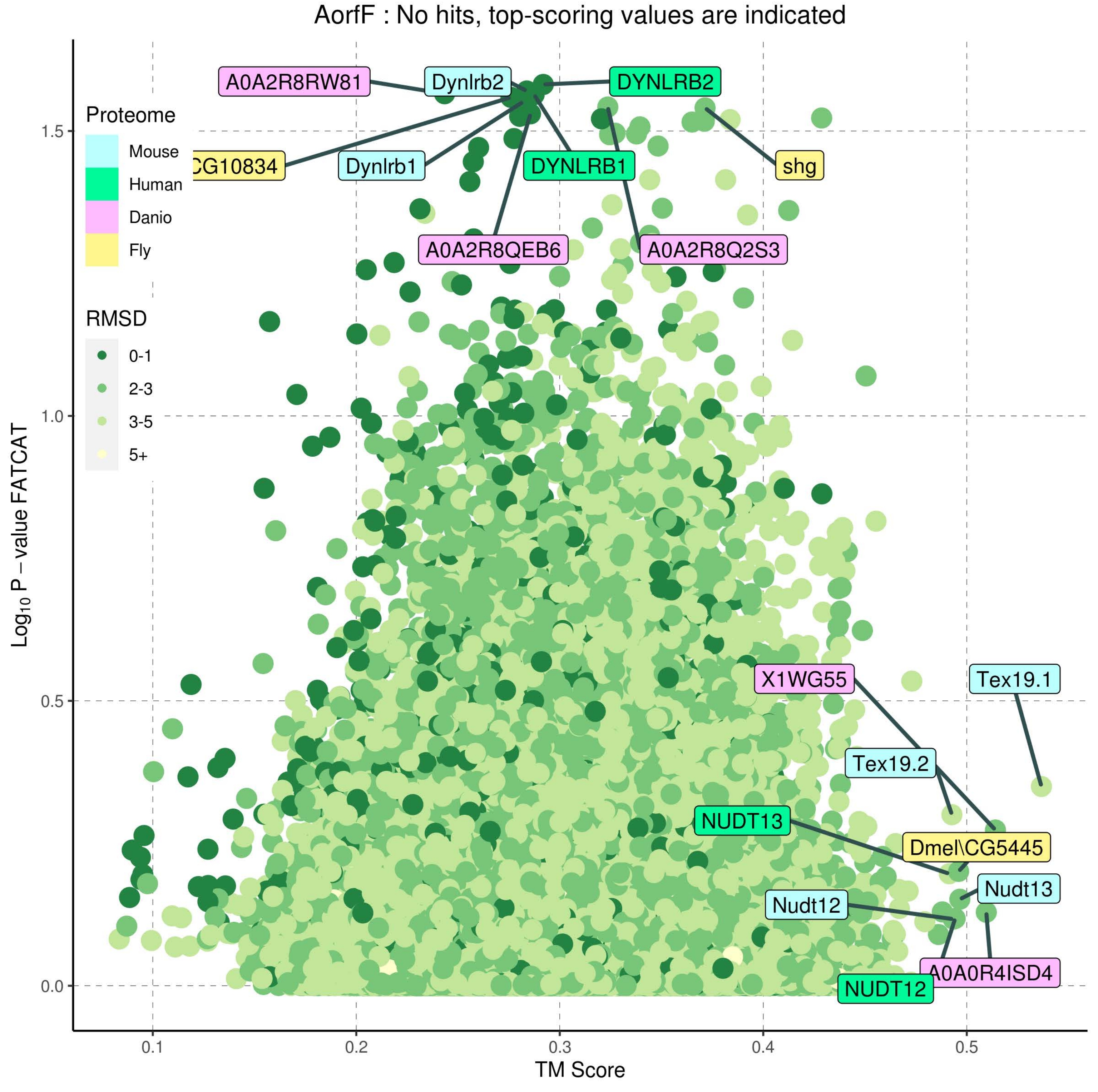

AorfA : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
TM Score
0.0
0.5
1.0
1.5
2.0
2.5
0.1
0.2
0.3
0.4
0.5
svbp
A0A2R8RNY5
A0A0R4IYP9
Uqcr11
A0A2R8Q6C8
OR2A25
Dmel\CG43630
Tmem268
MRP
Pkd2
brv1
SBF2
PKD1L1
SBF1
Sbf

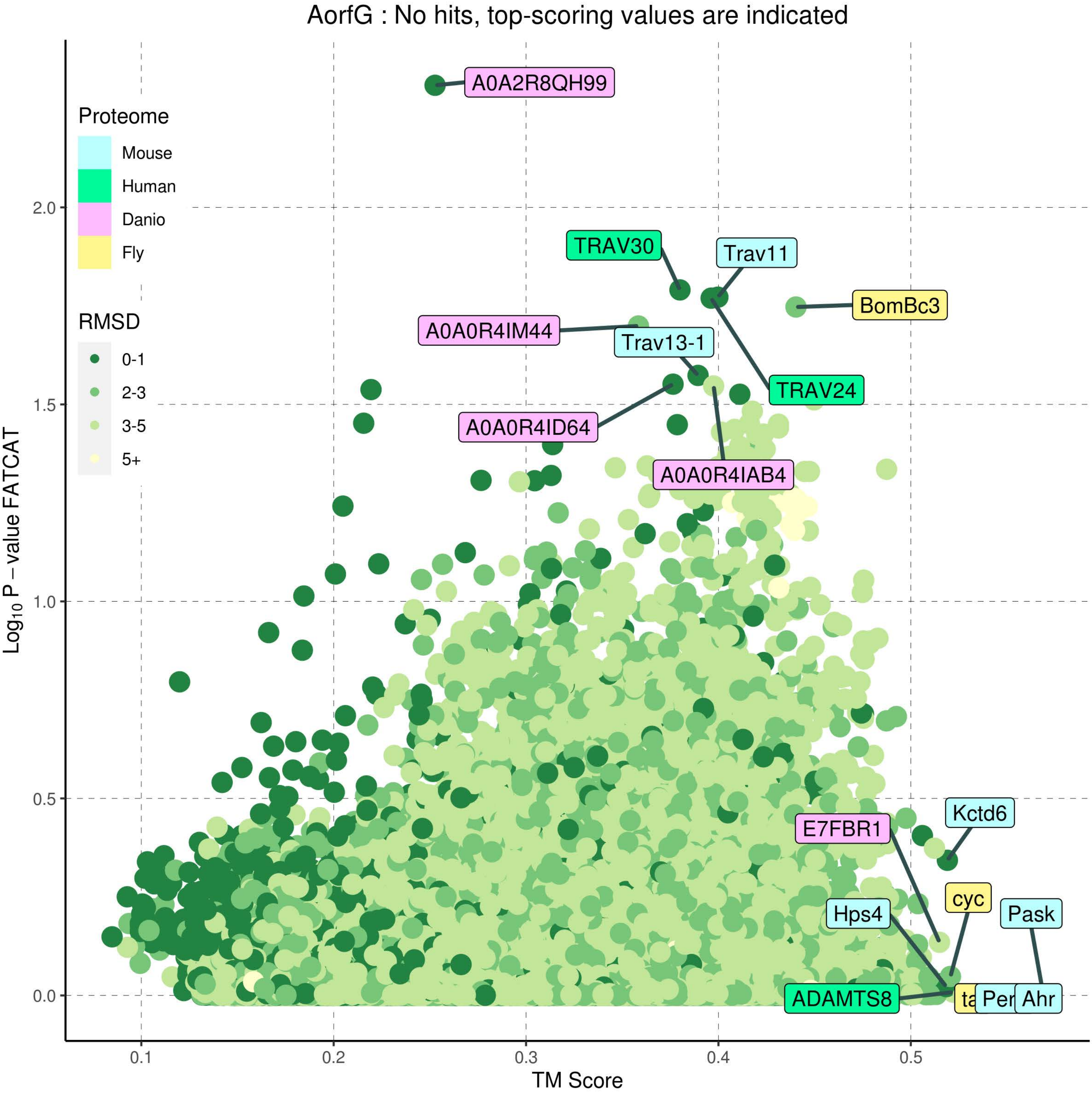

AorfB
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P − value FATCAT
TM Score
0
5
10
0.25
0.50
0.75
R4GEW2
Dmel\CG13887
Dmel\CG8840
Pldn
Dmel\CG44574
Mis12
Dmel\CG14421
Sncg
X1WE48
BcDNA:AT13882
MED4
Femcoat
Use1
Vamp5
2610042L04Rik
X1WBF9
si:ch211-284f22.3
Dmel\CG16762
X1WFQ3
Dmel\CG44303
lectin-24A
CHMP2B
Snapin
CG4410
TBRG1
X1WEE0
ATF5
FBpp0074269
nudE
ATP6V1D
X1WD42
Zmat2
Dmel\CG16719
MAFB
Pfdn6
X1WCD1
Dmel\CG13455
eIF3h
Dmel\CG14109
Dctn3
Dmel\CG14983
X1WD61
MAFF
Dmel\CG10332
Dmel\CG32708
SPEF1
BcDNA:LP05863
Speer3
Krt27
Cdc37l1
X1WF05
ANGPT4
Dmel\CG14420
U3JAU9
Dmel\CG14422
Surf6
X1WBJ0
Homer1
SNX6
Dmel\CG14154
Dmel\CG1958
Krt16
Dmel\CG11586
R4GE17
X1WH96
Pfdn5
CACNG2
U3JAN3
X1WGY1
X1WDM5
X1WCW7
TMED5
CG15662
X1WBB2
X1WDA3
qtc
Syx18
Stxbp4
RPRD1A
X1WCN0
Dmel\CG14868
X1WD51
X1WFA6
X1WCK1
Creb3l1
Palm
Dmel\CG3198
U3JAK8
X1WH62
SNX9
Angptl4
Dmel\CG14960
Dmel\CG3548
Rsbp1
R4GDR5
X1WHW8
U3JAI8
si:dkey-248g15.2
USH1C
ING3
X1WCL6
X1WEL3
Dmel\CG4198
RNF215
U3JAF5
Tnip1
X1WHC5
X1WGV1
PICK1
Cfp1
Gbp2
X1WGC2
Ptp61F
Dmel\CG13875
X1WGM6
X1WHK1
Gas41
Bscl2
X1WCN7
MAD1L1
Osi2
X1WEI6
R4GF04
Dmel\CG44405
X1WEJ9
X1WEN0
X1WEV9
Sh3bp5
X1WBR1
WASF2
chrna10
si:ch211-272b8.6

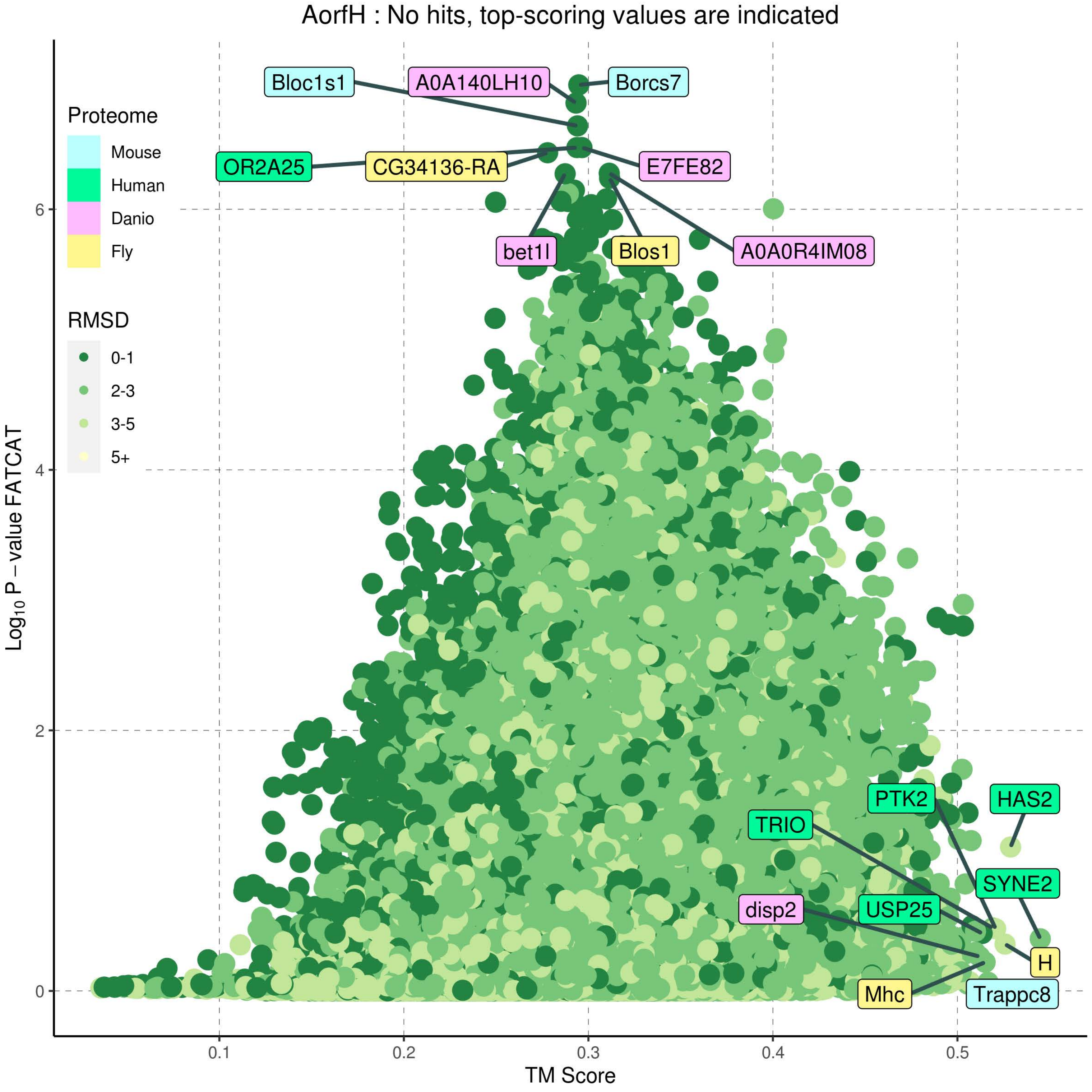

AorfC : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
A0A2R8Y4M2
Dmel\CG45084
Gm49027
Gm14288
Gm10974
COL5A1-AS1
Smim27
Tunar
A0A2R8RNF9
Spn77Bc
Klp68D
VPS51
Vps51
AlaRS-m
F1QJ06
A0A0R4IHD1
B0V302
E7F7F8
Log_{10} P − value FATCAT
6
4
2
0
0.1
0.2
0.3
0.4
0.5
TM Score

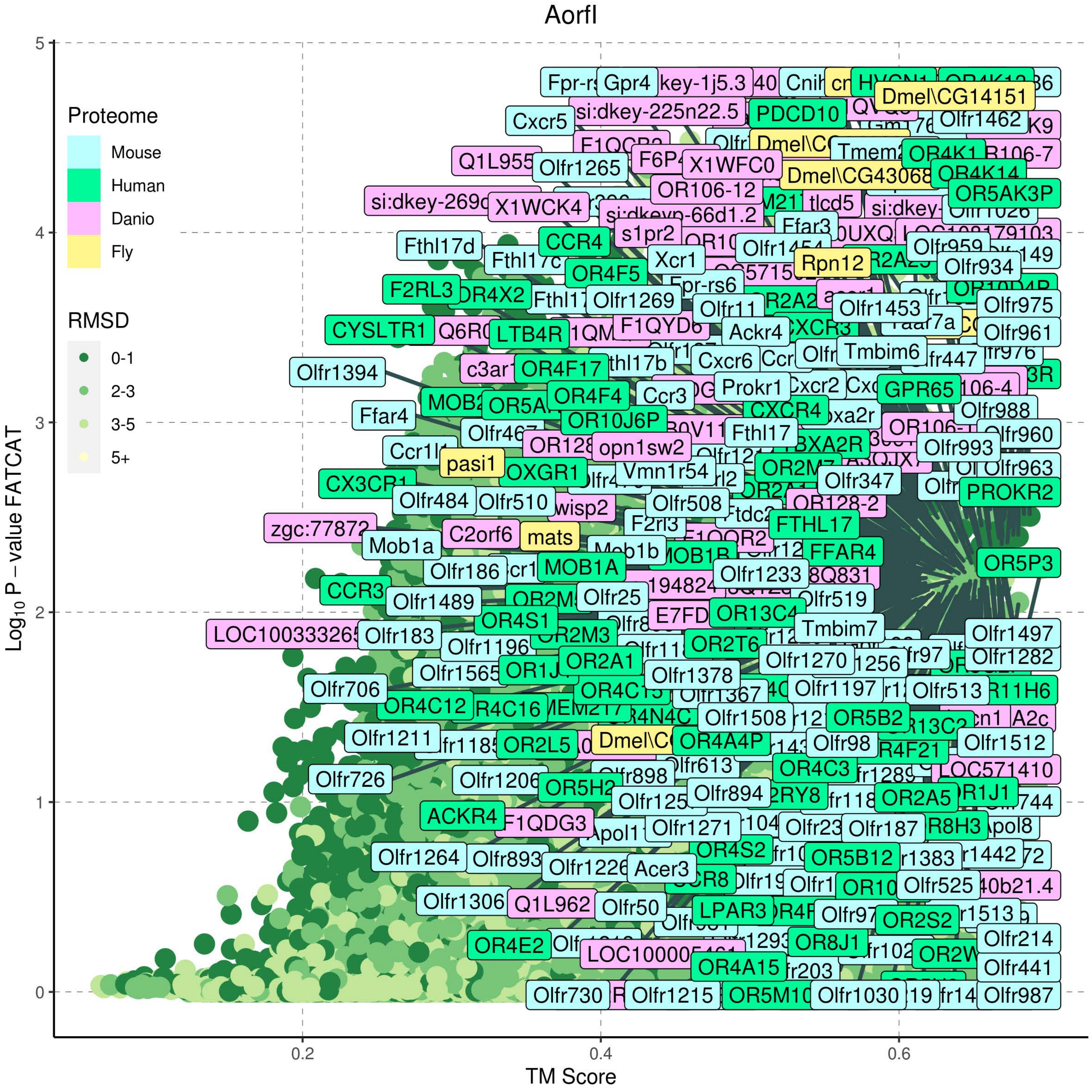

AorfD
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
ND-15
SERINC1
Serinc1
$\mathrm{Log_{10}}$ P − value FATCAT
4
3
2
1
0
0.2
0.4
0.6
TM Score

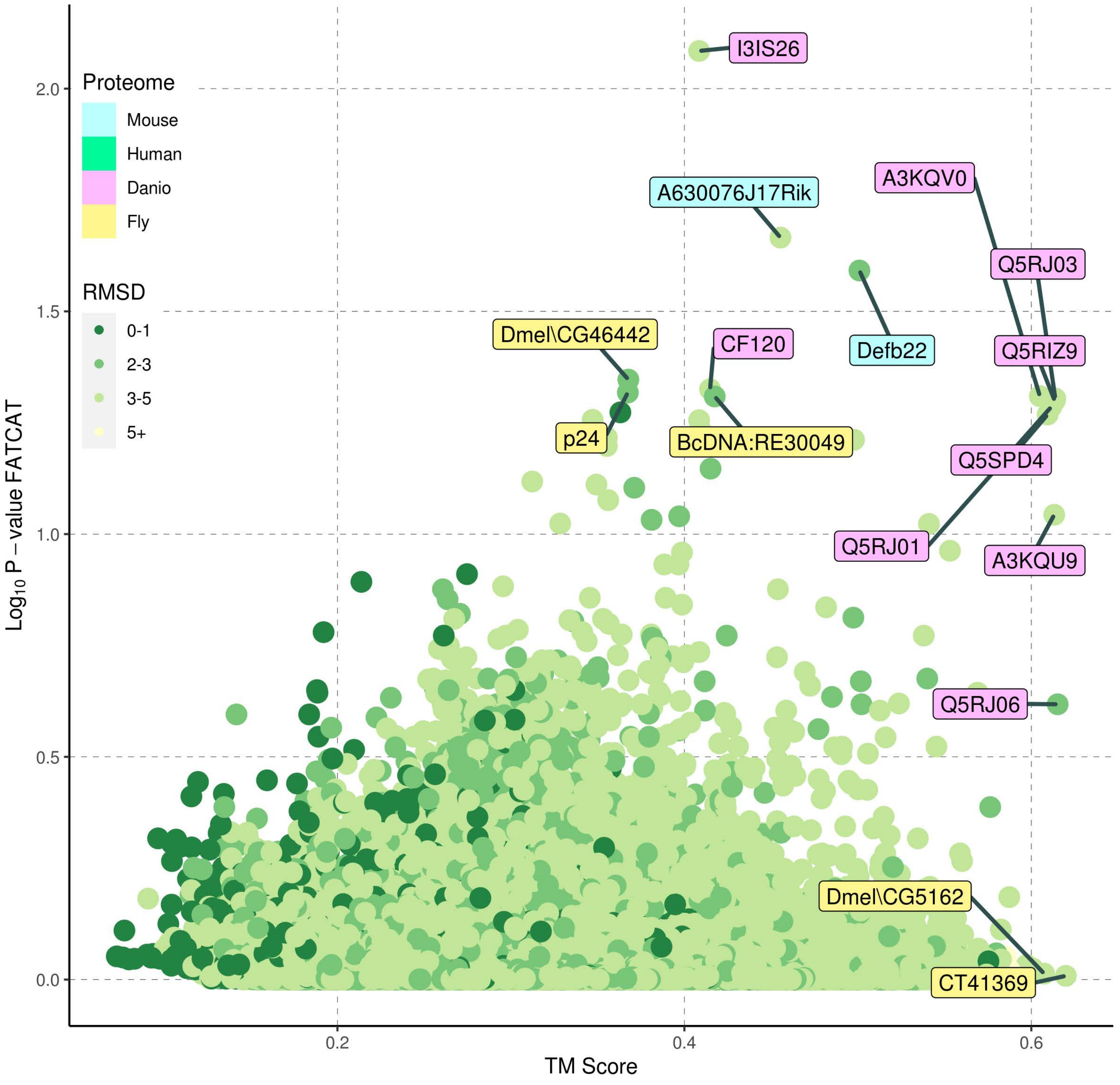

AorfE : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
CG7267
si:dkey-93l1.9
A0A2R8QBC1
Dmel\CG44623
aph-1
Q6DRN8
SLC48A1
CMTM6
mala
Pis
OR2A25
Cdipt
A0A0G2L8I2
Smg6
SIDL
TRAPPC10
Trappc10
Log10 P – value FATCAT
TM Score
0
2
4
6
0.1
0.2
0.3
0.4
0.5
0.6


AorfF : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
A0A2R8RW81
Dynlrb2
DYNLRB2
CG10834
Dynlrb1
DYNLRB1
shg
A0A2R8QEB6
A0A2R8Q2S3
X1WG55
Tex19.1
Tex19.2
NUDT13
Dmel\CG5445
Nudt13
Nudt12
A0A0R4ISD4
NUDT12
Log10 P − value FATCAT
TM Score
0.0
0.5
1.0
1.5
0.1
0.2
0.3
0.4
0.5

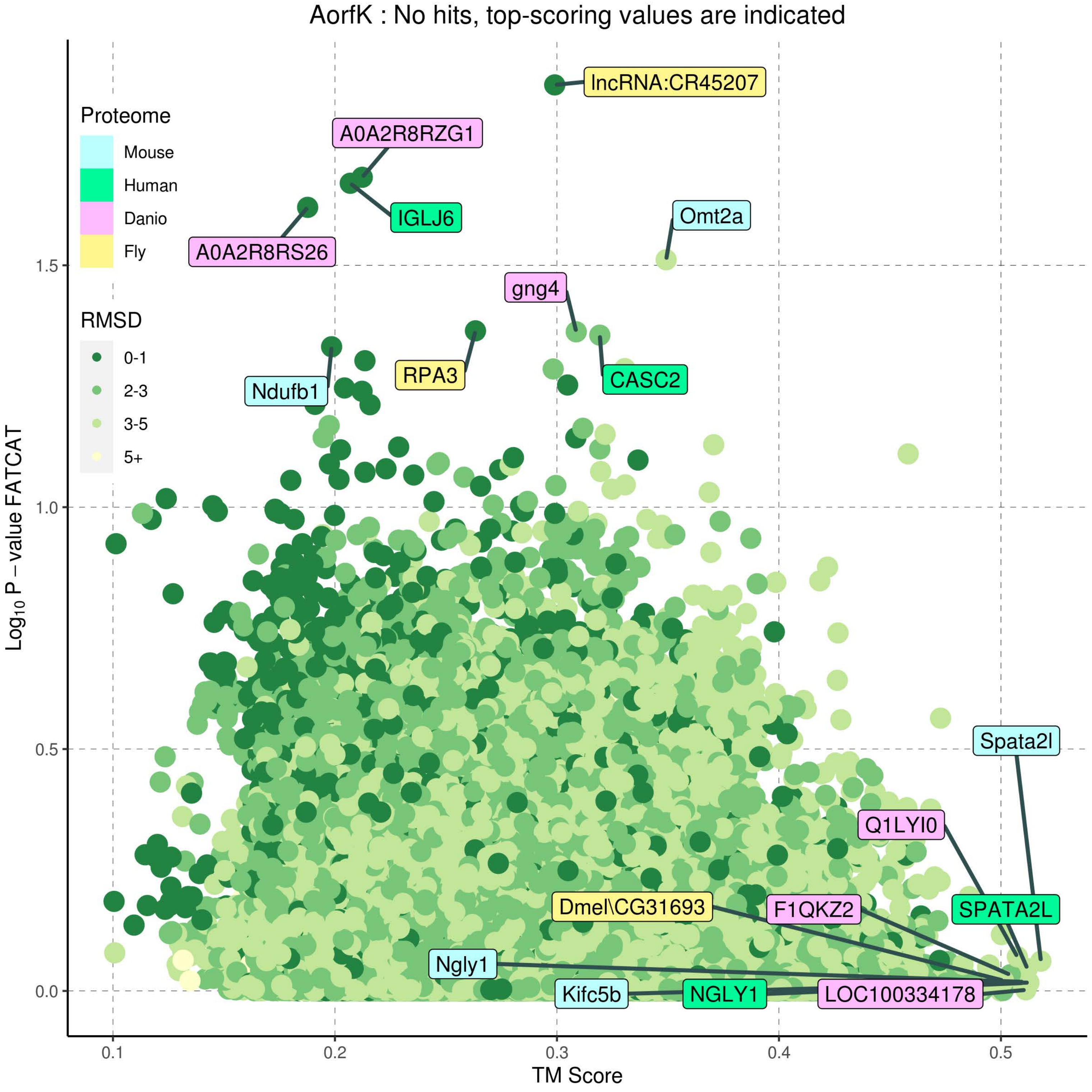

AorfG : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log$_{10}$ P – value FATCAT
TM Score
0.0
0.5
1.0
1.5
2.0
0.1
0.2
0.3
0.4
0.5
A0A2R8QH99
TRAV30
Trav11
BomBc3
A0A0R4IM44
Trav13-1
TRAV24
A0A0R4ID64
A0A0R4IAB4
Kctd6
E7FBR1
cyc
Hps4
Pask
ADAMTS8
ta
Per
Ahr

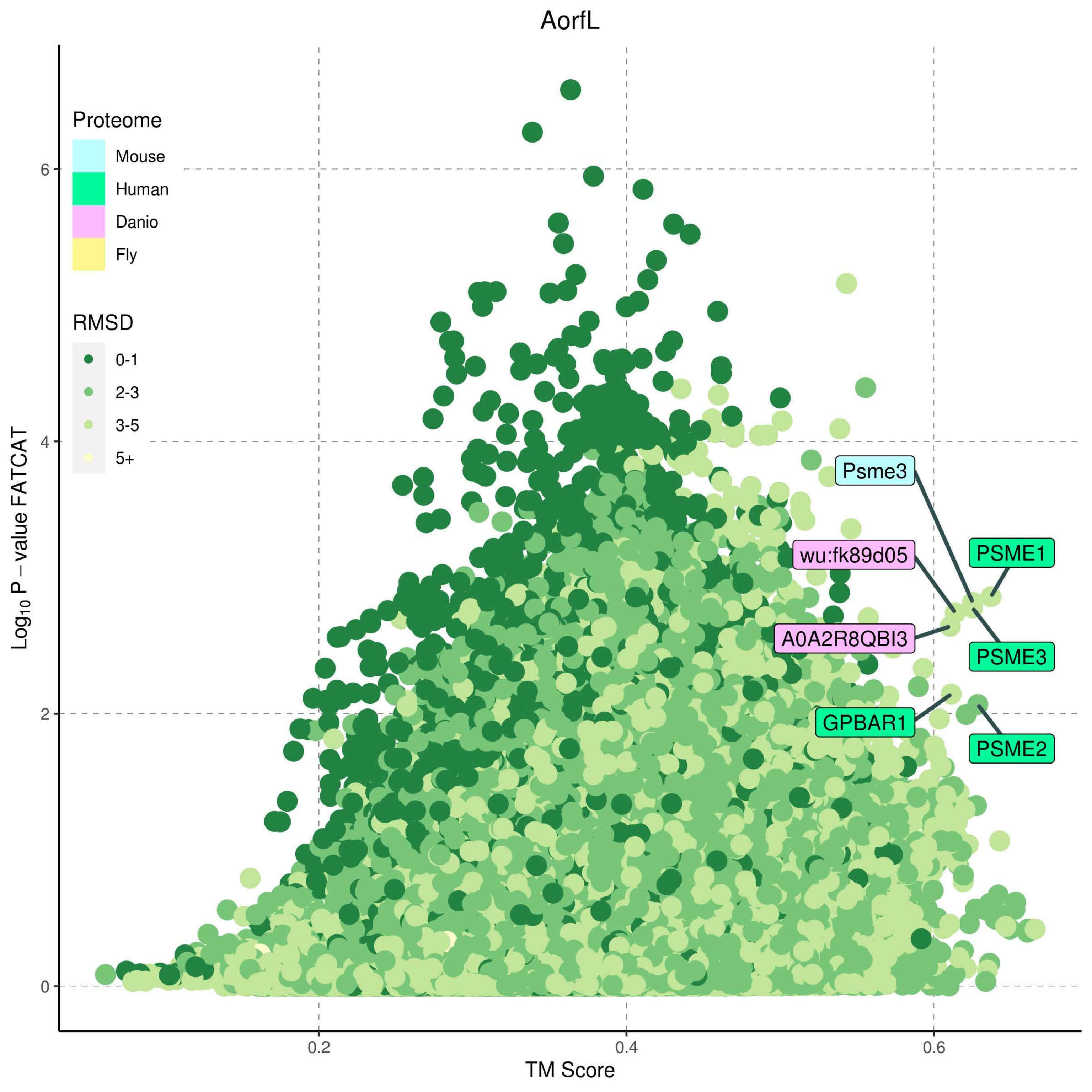

AorfH : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Bloc1s1
A0A140LH10
Borcs7
OR2A25
CG34136-RA
E7FE82
bet1l
Blos1
A0A0R4IM08
PTK2
HAS2
TRIO
SYNE2
disp2
USP25
H
Mhc
Trappc8
Log10 P − value FATCAT
TM Score
0
2
4
6
0.1
0.2
0.3
0.4
0.5

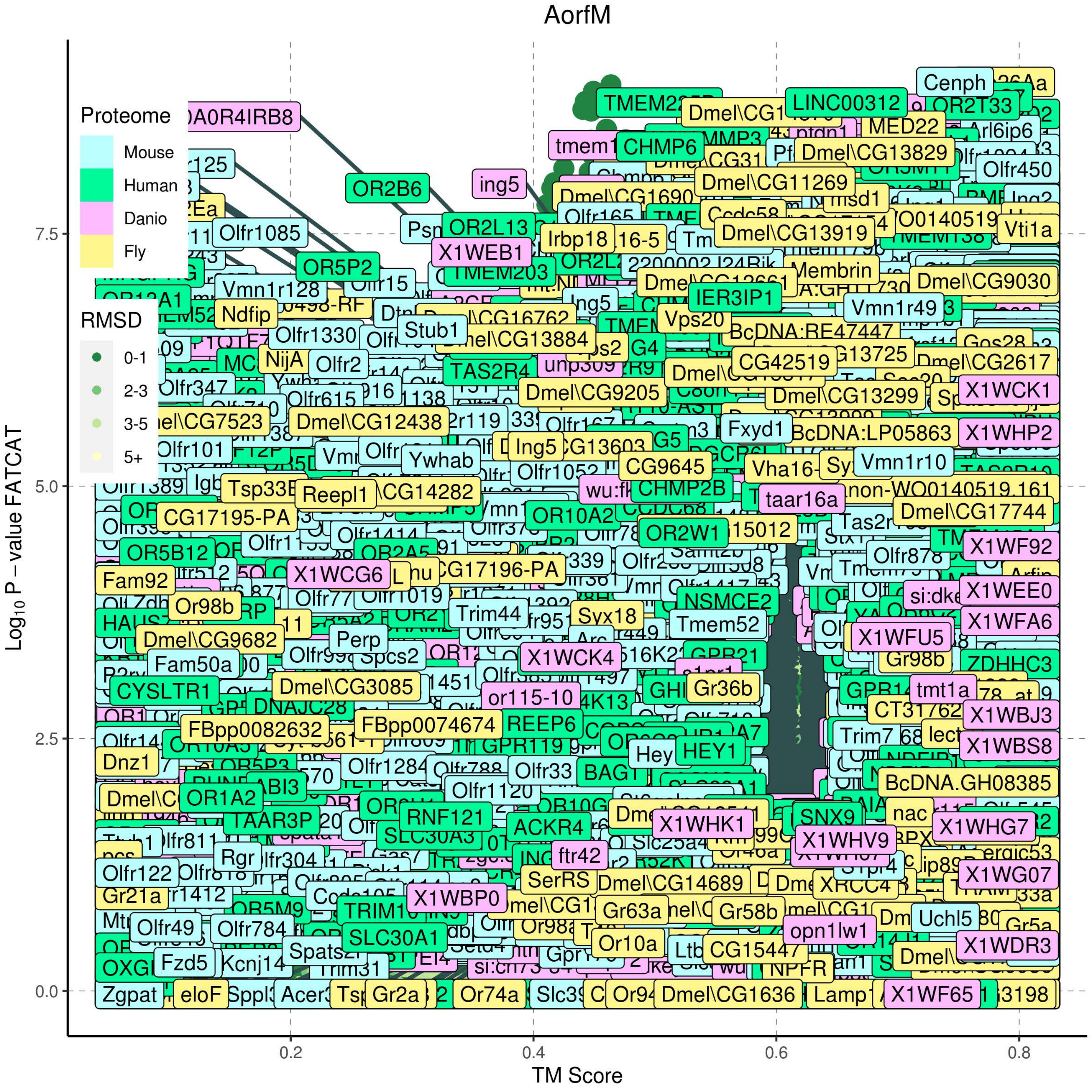

Aorfl
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P − value FATCAT
TM Score
0
1
2
3
4
5
0.2
0.4
0.6
Gpr4
key-1j5.3
Dmel\CG14151
si:dkey-225n22.5
PDCD10
Cxcr5
Olfr1462
Q1L955
Olfr1265
X1WFC0
Dmel\CG43068
OR4K14
OR106-12
OR5AK3P
si:dkey-269c
X1WCK4
tlcd5
Ffar3
Fthl17d
CCR4
s1pr2
Fthl17c
Xcr1
Olfr959
Rpn12
Olfr934
OR4F5
Fpr-rs6
F2RL3
OR4X2
Olfr1269
Olfr1453
Olfr975
CYSLTR1
LTB4R
F1QYD6
Ackr4
Olfr961
Cxcr6
Tmbim6
Olfr1394
c3ar1
OR4F17
Prokr1
Cxcr2
GPR65
OR4F4
Ccr3
CXCR4
Olfr988
Ffar4
OR10J6P
Fthl17
TBXA2R
Olfr960
pasi1
opn1sw2
Olfr993
OXGR1
Vmn1r54
Olfr963
Olfr347
PROKR2
Olfr484
Olfr510
wisp2
Olfr508
OR128-2
zgc:77872
C2orf6
mats
F2rl3
FTHL17
Mob1a
Mob1b
FFAR4
OR5P3
Olfr186
MOB1A
Olfr1233
CCR3
Olfr1489
Olfr25
Olfr519
OR4S1
OR13C4
Tmbim7
LOC100333265
Olfr183
OR2M3
OR2T6
Olfr1497
Olfr1196
OR2A1
Olfr1270
Olfr1282
Olfr1565
Olfr1378
Olfr706
Olfr1197
Olfr513
OR4C12
Olfr1367
Olfr1508
OR5B2
Olfr1211
OR2L5
OR4A4P
Olfr98
Olfr1512
Olfr726
Olfr1206
OR5H2
Olfr898
Olfr613
OR4C3
LOC571410
Olfr894
OR2A5
ACKR4
F1QDG3
Olfr1271
Olfr187
Olfr1264
Olfr893
OR4S2
OR5B12
Olfr1226
Acer3
Olfr525
Olfr1306
Q1L962
Olfr50
LPAR3
OR2S2
OR4E2
OR8J1
Olfr214
OR4A15
Olfr441
Olfr730
Olfr1215
Olfr1030
Olfr987

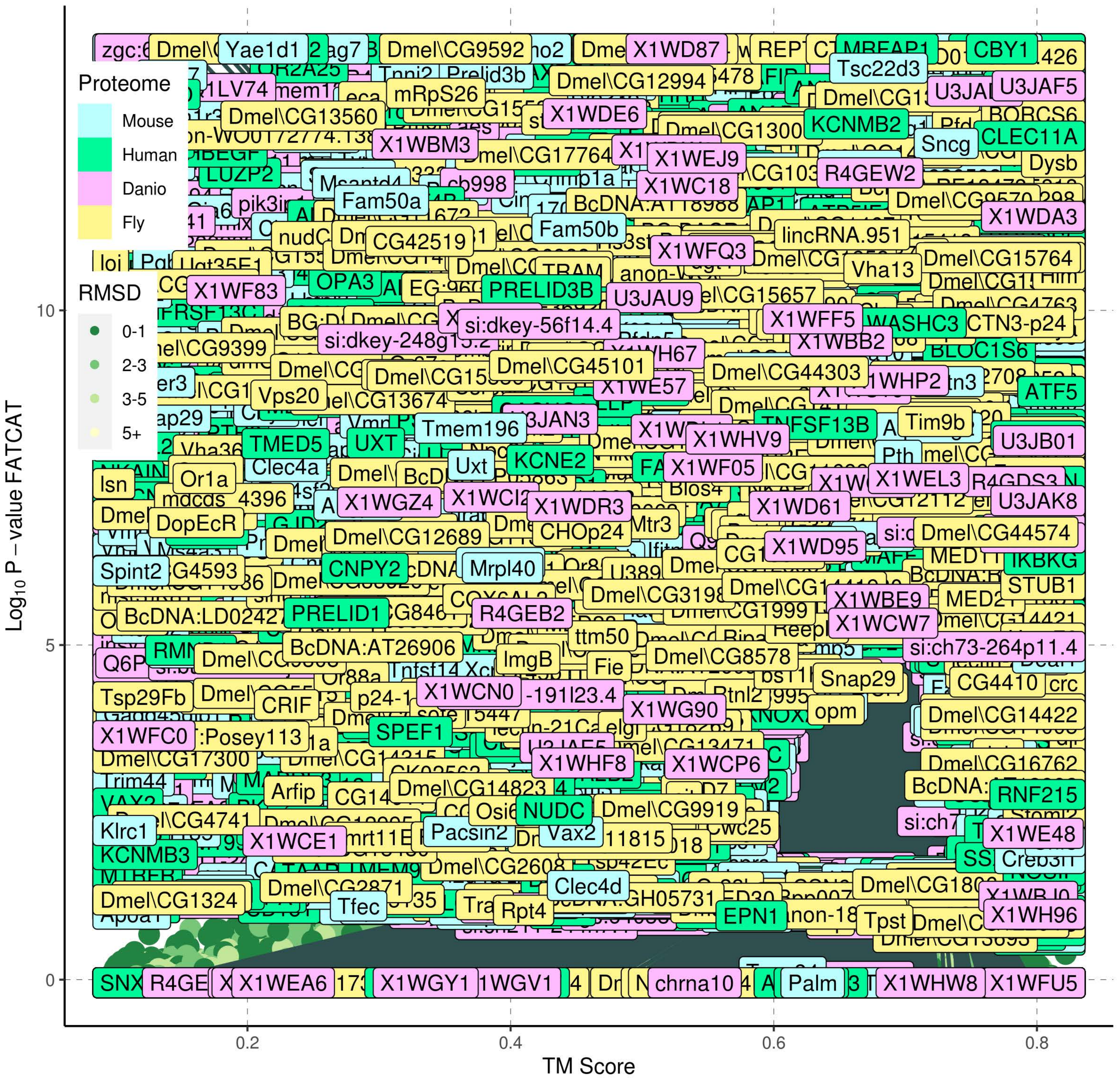


AorfJ : No hits, top-scoring values are indicated


AorfK : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
lncRNA:CR45207
A0A2R8RZG1
IGLJ6
A0A2R8RS26
Omt2a
gng4
RPA3
CASC2
Ndufb1
Spata2l
Q1LYI0
SPATA2L
F1QKZ2
Dmel\CG31693
Ngly1
Kifc5b
NGLY1
LOC100334178
Log10 P – value FATCAT
1.5
1.0
0.5
0.0
0.1
0.2
0.3
0.4
0.5
TM Score


AorfL
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log₁₀ P − value FATCAT
TM Score
0
2
4
6
0.2
0.4
0.6
Psme3
wu:fk89d05
PSME1
A0A2R8QBI3
PSME3
GPBAR1
PSME2

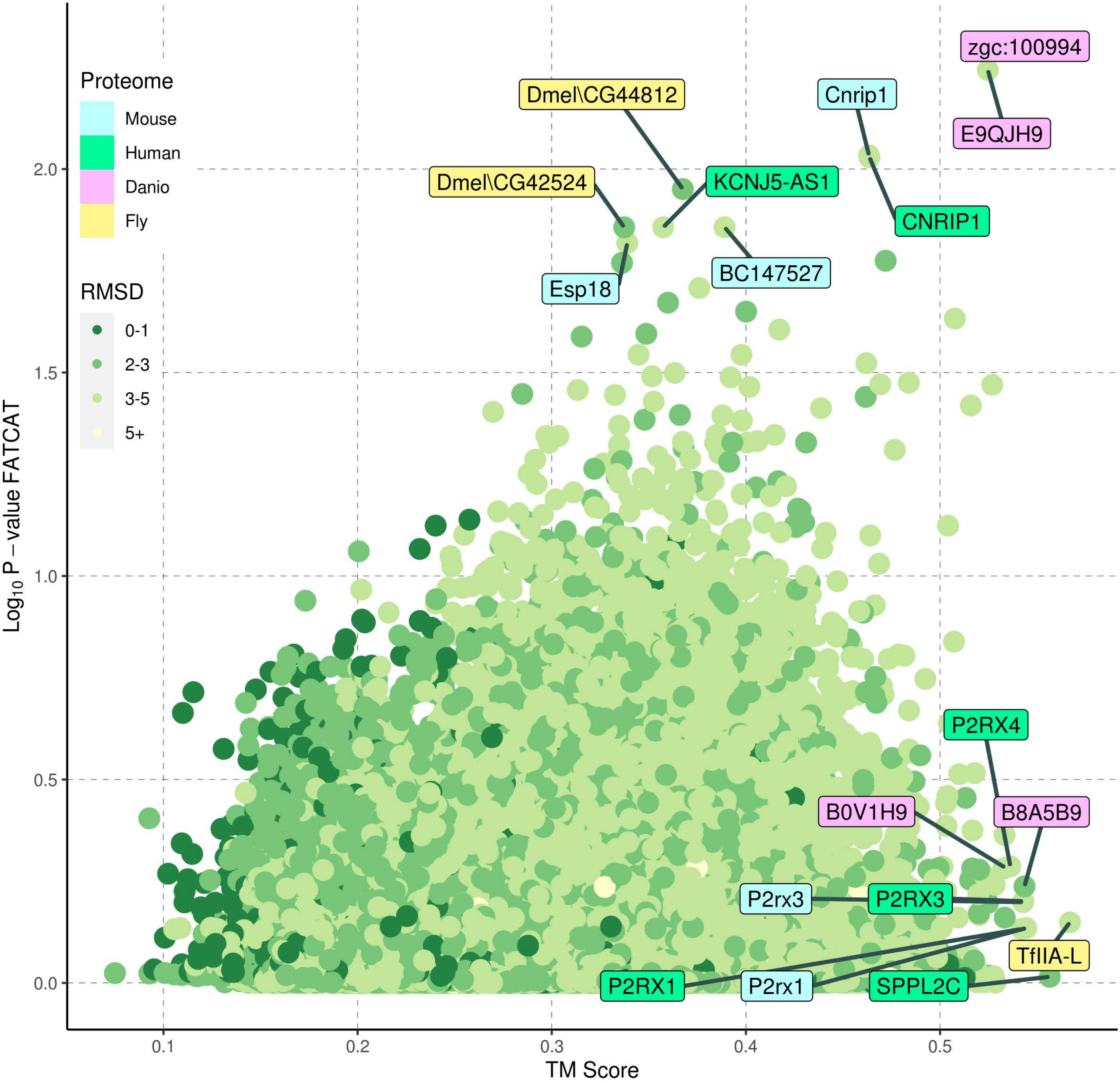

AorfM
Log₁₀ P − value FATCAT
TM Score
0.0
2.5
5.0
7.5
0.2
0.4
0.6
0.8
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Cenph
LINC00312
OR2T33
MED22
Arl6ip6
Dmel\CG13829
Olfr450
CHMP6
Dmel\CG11269
OR2B6
ing5
Psm
OR2L13
X1WEB1
Irbp18
Dmel\CG13919
Vti1a
Olfr1085
OR5P2
Olfr15
TMEM203
Membrin
Dmel\CG9030
Vmn1r128
IER3IP1
Vmn1r49
Ndfip
Stub1
Dmel\CG16762
Vps20
Olfr1330
Dmel\CG13884
CG42519
Dmel\CG2617
NijA
Olfr2
TAS2R4
unp309
X1WCK1
Olfr347
Olfr615
Dmel\CG9205
Dmel\CG13299
Dmel\CG12438
Fxyd1
BcDNA:LP05863
X1WHP2
Olfr101
Ywhab
Ing5
Vmn1r10
Olfr1052
CG9645
Tsp33B
Reepl1
CHMP2B
taar16a
CG17195-PA
OR10A2
OR2W1
Dmel\CG17744
OR5B12
X1WF92
Fam92
X1WCG6
CG17196-PA
Olfr1019
NSMCE2
X1WEE0
Or98b
Trim44
Syx18
Tmem52
X1WFA6
Dmel\CG9682
Perp
X1WFU5
X1WCK4
Gr98b
ZDHHC3
Fam50a
CYSLTR1
Dmel\CG3085
or115-10
Gr36b
tmt1a
DNAJC28
X1WBJ3
FBpp0082632
FBpp0074674
REEP6
GPR119
HEY1
Trim7
X1WBS8
Dnz1
Olfr1284
Olfr33
BAG1
Olfr1120
BcDNA.GH08385
OR1A2
TAAR3P
RNF121
ACKR4
X1WHK1
SNX9
nac
X1WHG7
SLC30A3
X1WHV9
Rgr
ftr42
Olfr122
SerRS
Dmel\CG14689
XRCC4
X1WG07
Gr21a
X1WBP0
Olfr49
Olfr784
Gr63a
Gr58b
Uchl5
opn1lw1
SLC30A1
Spats2l
Or10a
CG15447
X1WDR3
Fzd5
Kcnj14
Trim31
NPFR
Zgpat
eloF
Gr2a
Or74a
Dmel\CG1636
Lamp1
X1WF65

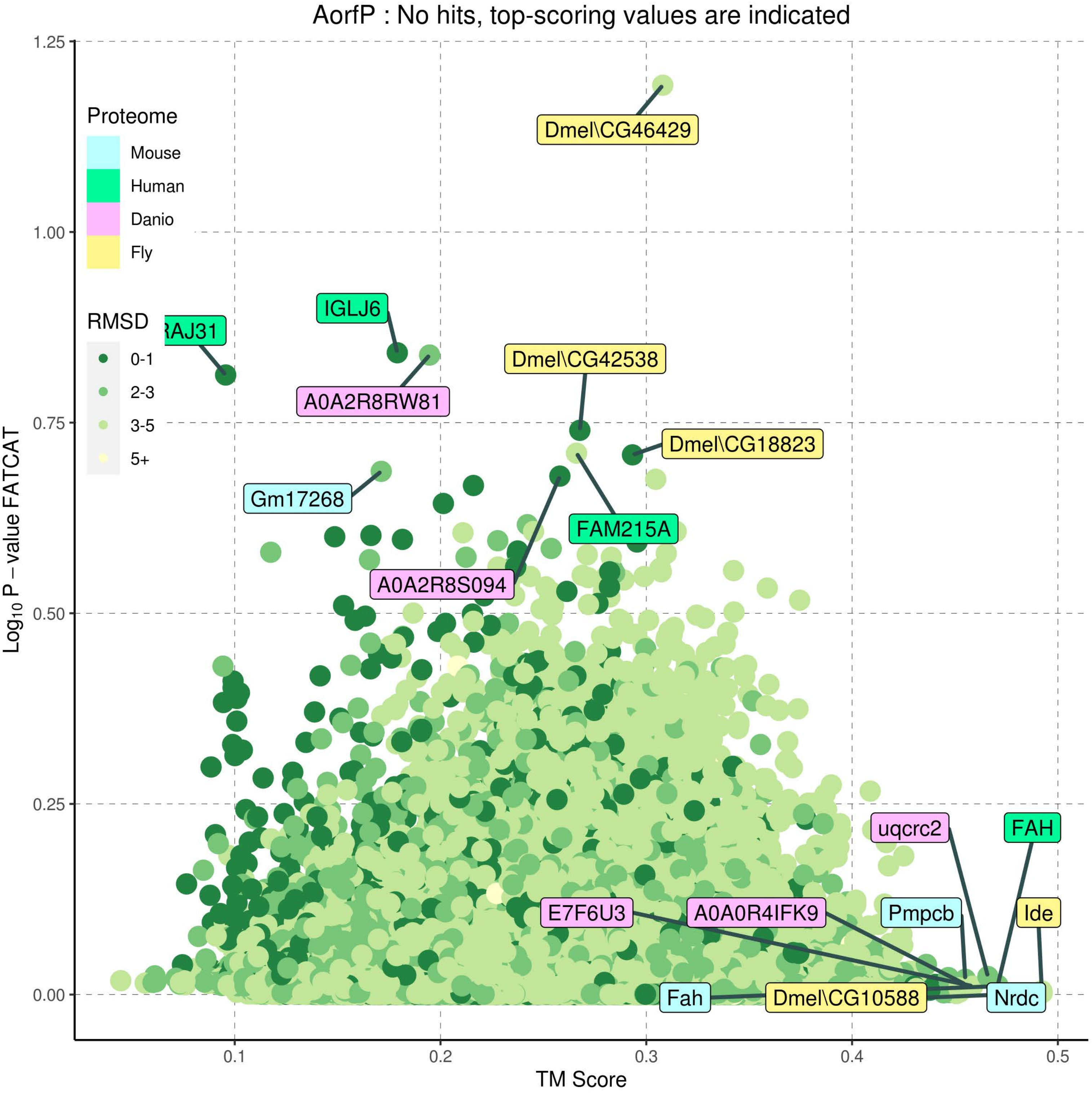


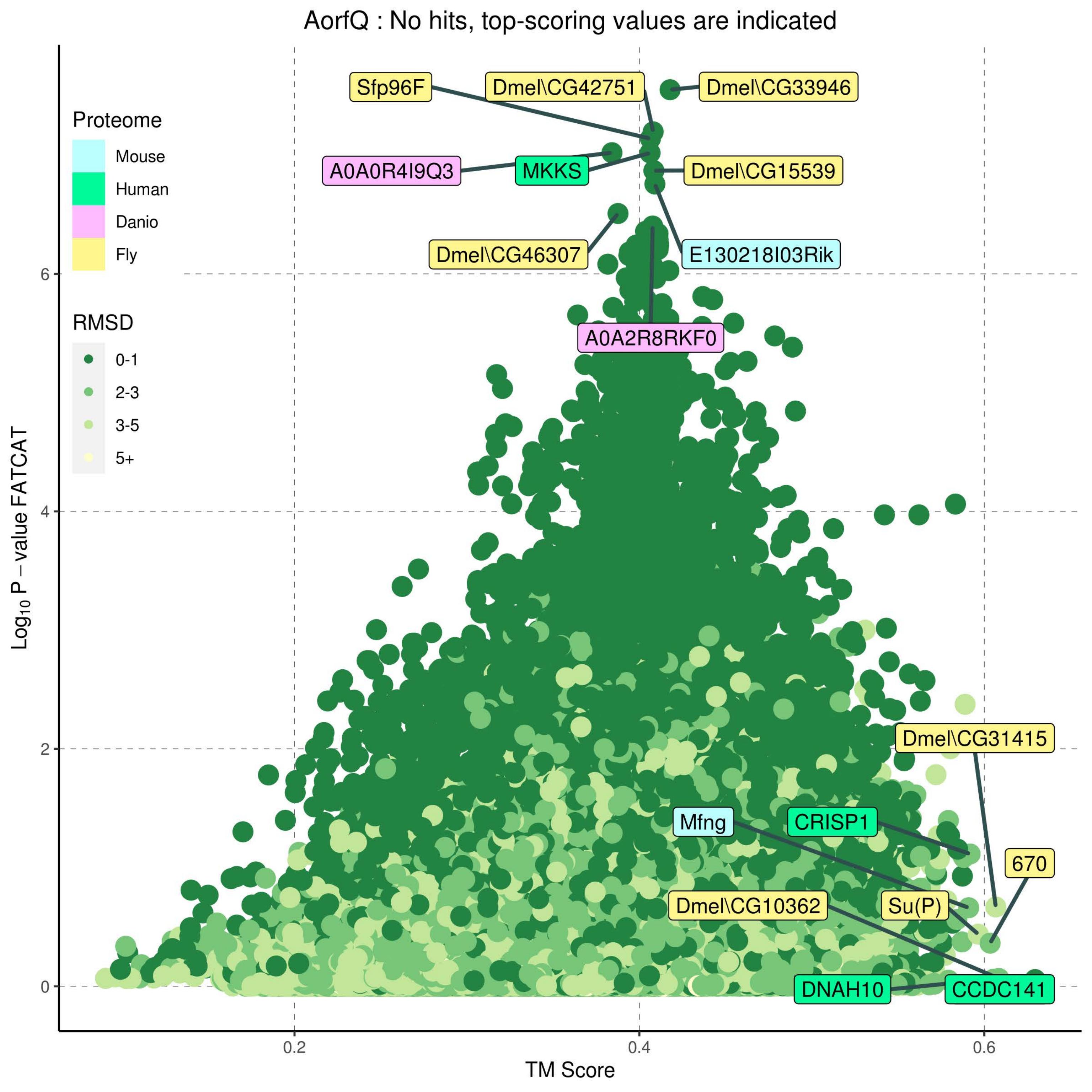
AorfN

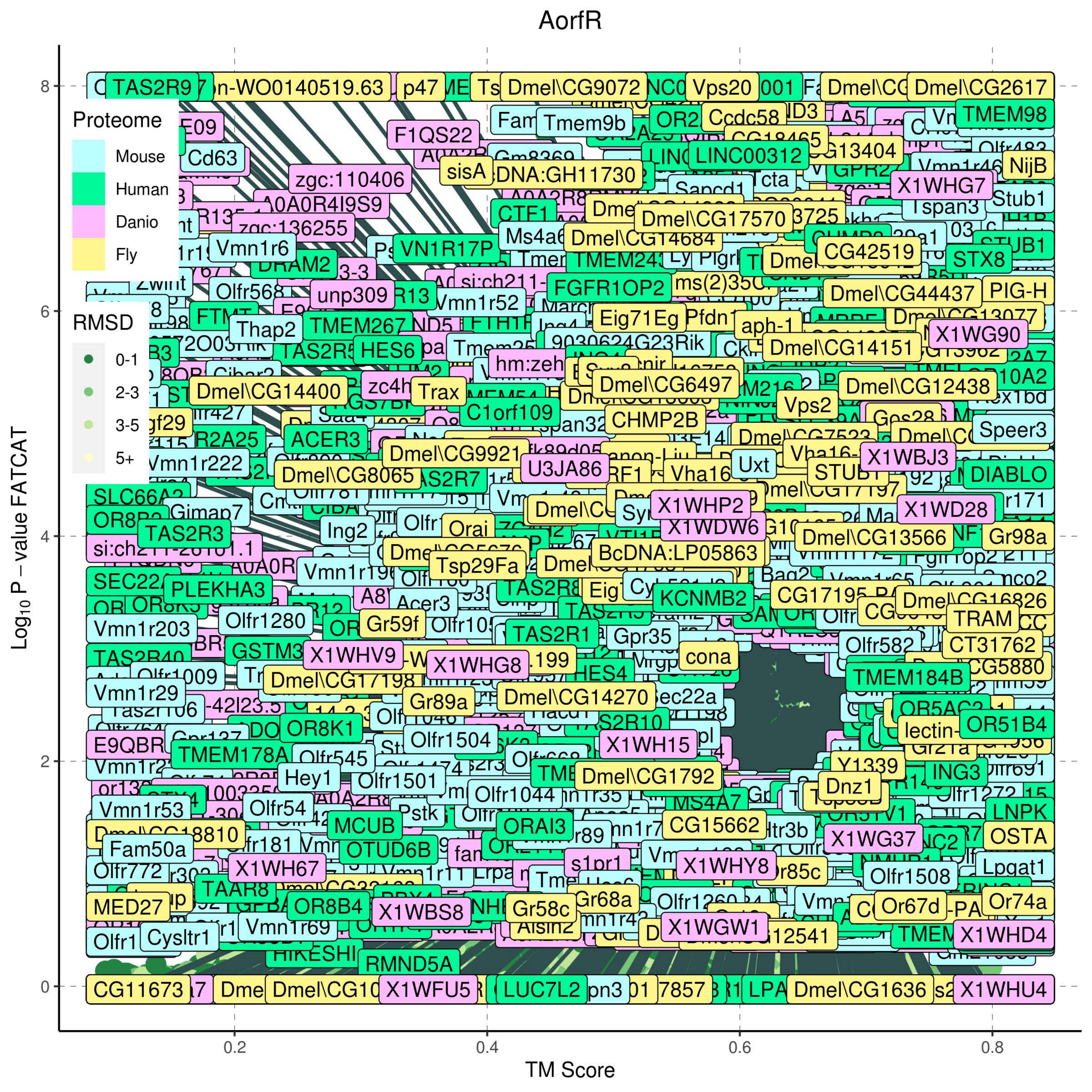
Log$_{10}$ P – value FATCAT
TM Score
0
5
10
0.2
0.4
0.6
0.8
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+

AorfO : No hits, top-scoring values are indicated

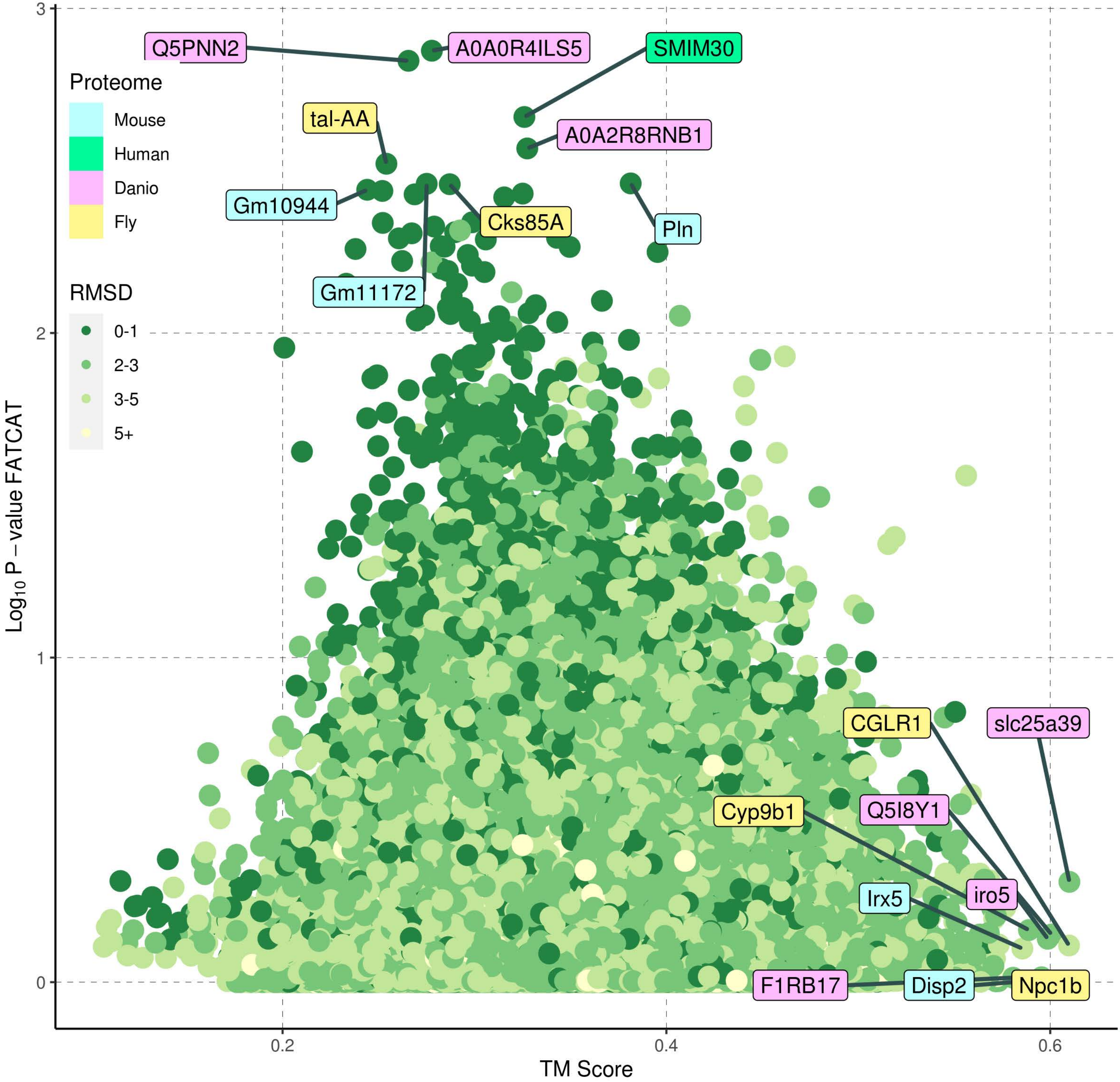


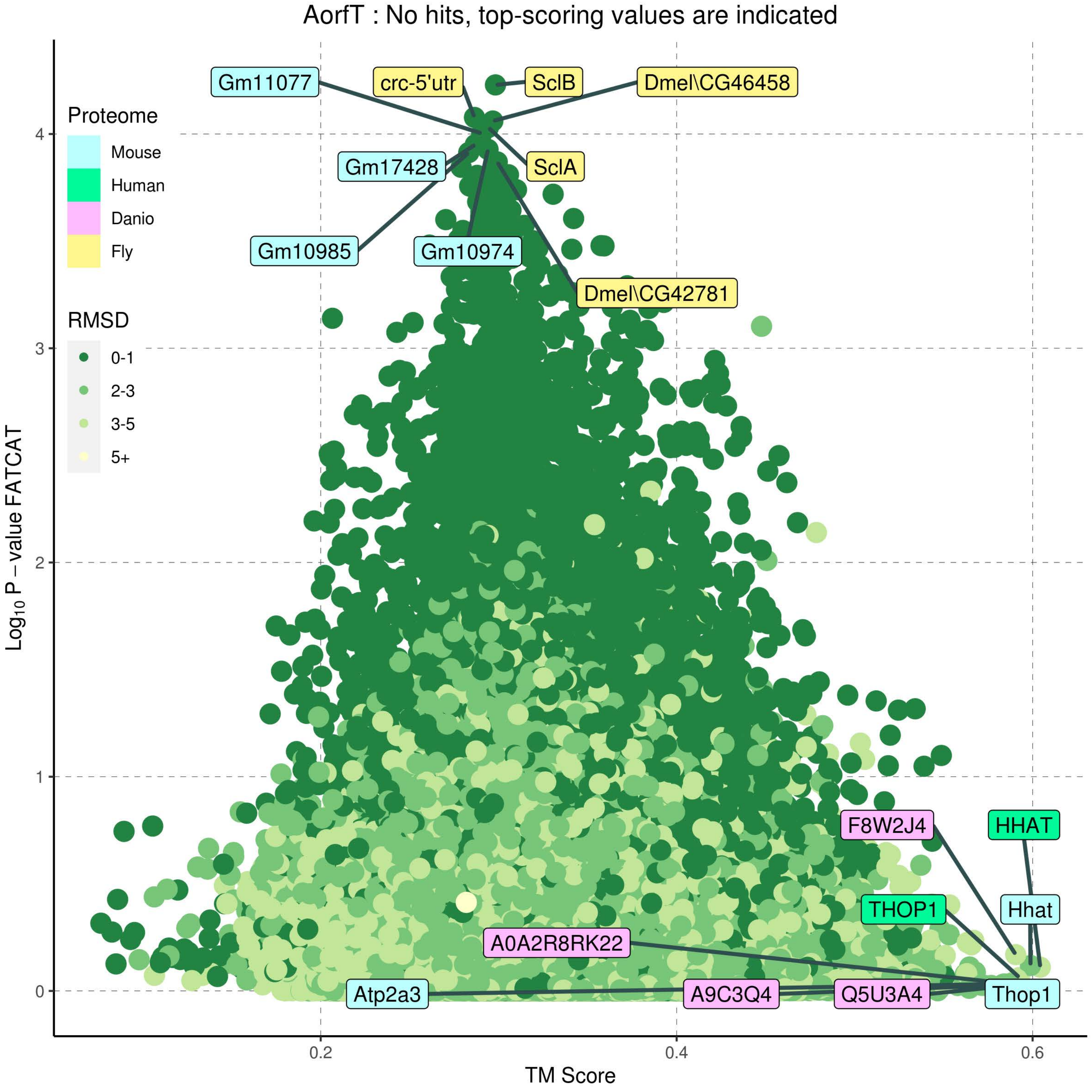

AorfP : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Dmel\CG46429
RAJ31
IGLJ6
A0A2R8RW81
Dmel\CG42538
Dmel\CG18823
Gm17268
FAM215A
A0A2R8S094
uqcrc2
FAH
E7F6U3
A0A0R4IFK9
Pmpcb
Ide
Fah
Dmel\CG10588
Nrdc
Log10 P – value FATCAT
1.25
1.00
0.75
0.50
0.25
0.00
0.1
0.2
0.3
0.4
0.5
TM Score

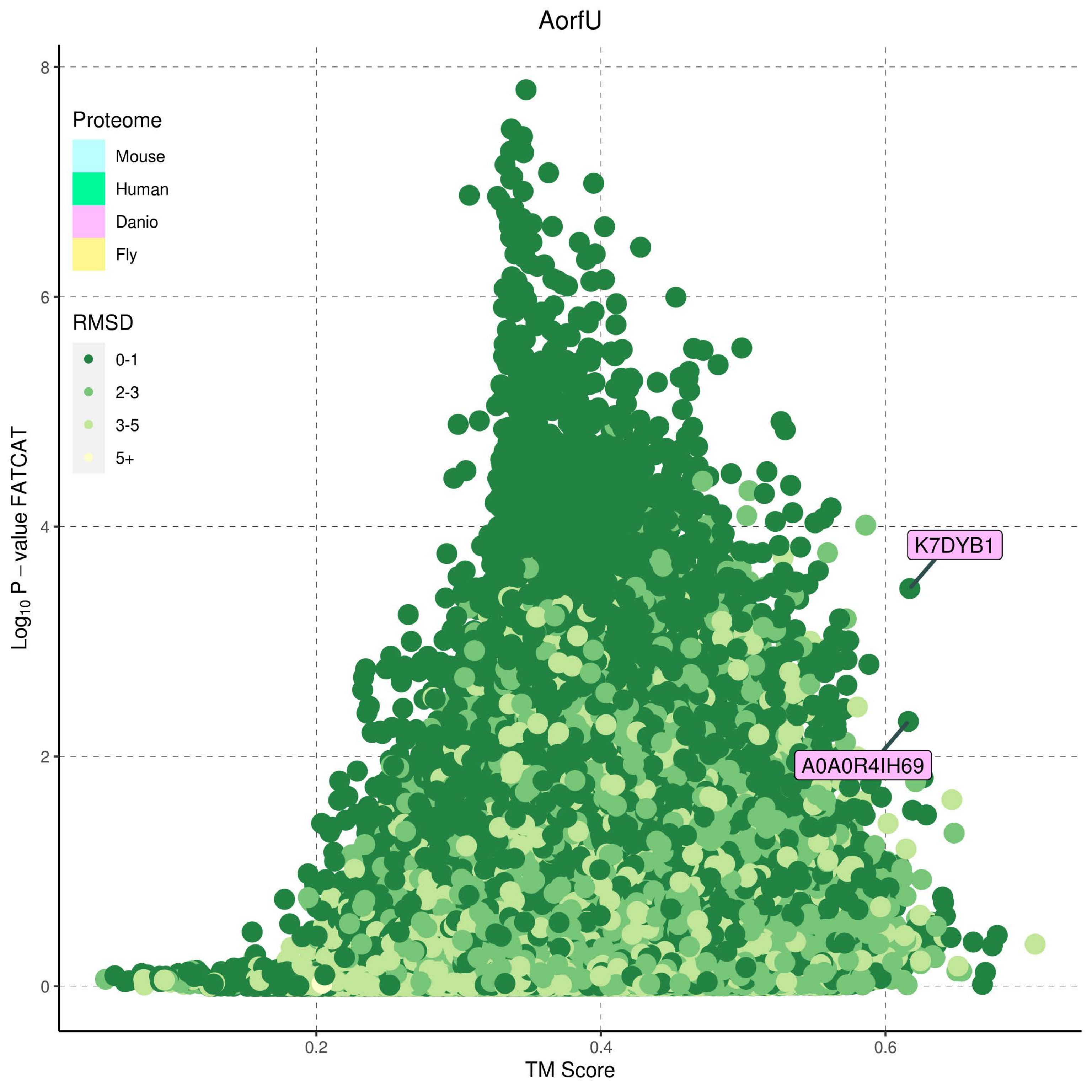

AorfQ : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Sfp96F
Dmel\CG42751
Dmel\CG33946
A0A0R4I9Q3
MKKS
Dmel\CG15539
Dmel\CG46307
E130218I03Rik
A0A2R8RKF0
Dmel\CG31415
Mfng
CRISP1
670
Dmel\CG10362
Su(P)
DNAH10
CCDC141
Log10 P − value FATCAT
6
4
2
0
0.2
0.4
0.6
TM Score

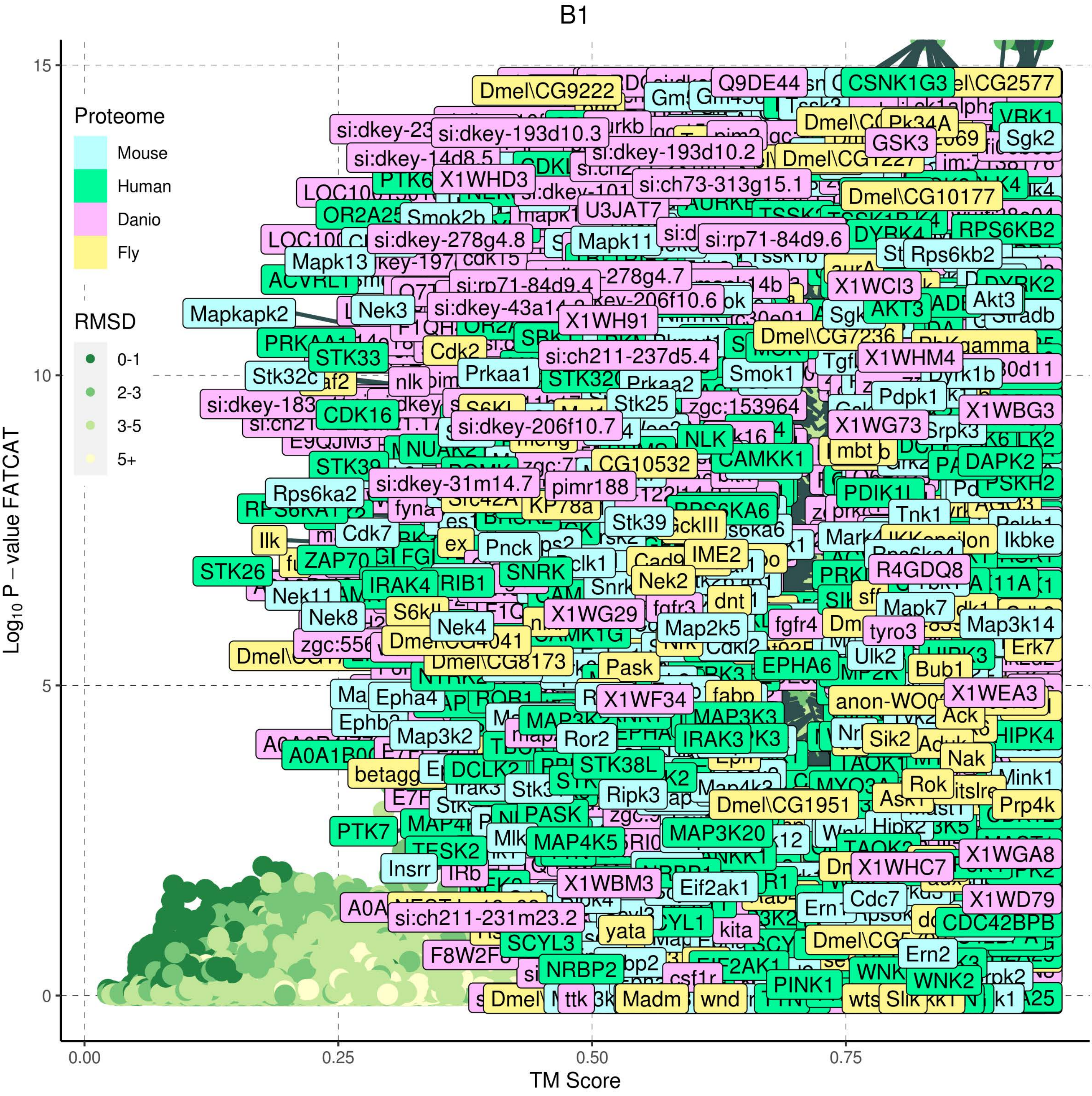

AorfR
Proteome
🟦 Mouse
🟩 Human
🟪 Danio
🟨 Fly
RMSD
● 0-1
● 2-3
● 3-5
● 5+
Log10 P − value FATCAT
TM Score
0
2
4
6
8
0.2
0.4
0.6
0.8
TAS2R9
p47
Dmel\CG9072
Vps20
Dmel\CG2617
Tmem9b
OR2
Ccdc58
TMEM98
F1QS22
Cd63
LINC00312
zgc:110406
sisA
NijB
X1WHG7
Stub1
A0A0R4I9S9
CTF1
Dmel\CG17570
zgc:136255
Vmn1r6
VN1R17P
Ms4a6
Dmel\CG14684
CG42519
STX8
STUB1
DRAM2
Zwint
Olfr568
unp309
Vmn1r52
FGFR1OP2
Dmel\CG44437
PIG-H
FTMT
Thap2
TMEM267
TAS2R5
HES6
Eig71Eg
aph-1
X1WG90
Dmel\CG14151
9030624G23Rik
hm:zeh
Dmel\CG6497
Dmel\CG12438
Dmel\CG14400
zc4h
Trax
C1orf109
Vps2
CHMP2B
ACER3
Speer3
Vmn1r222
Dmel\CG9921
U3JA86
Uxt
X1WBJ3
Dmel\CG8065
STUB1
DIABLO
SLC66A2
Gimap7
X1WHP2
X1WD28
TAS2R3
Ing2
Orai
X1WDW6
Dmel\CG13566
Gr98a
si:ch211-261d1.1
BcDNA:LP05863
Tsp29Fa
SEC22
PLEKHA3
Vmn1r196
KCNMB2
Dmel\CG16826
Acer3
TRAM
Vmn1r203
Olfr1280
Gr59f
TAS2R1
Gpr35
CT31762
X1WHV9
X1WHG8
cona
GSTM3
Olfr1009
Dmel\CG17198
Vmn1r29
TMEM184B
Gr89a
Dmel\CG14270
Sec22a
OR8K1
OR51B4
E9QBR
Olfr1504
X1WH15
TMEM178A
Olfr545
Hey1
Olfr1501
Dmel\CG1792
Y1339
Dnz1
ING3
Vmn1r53
Olfr54
Olfr1044
MCUB
ORAI3
CG15662
X1WG37
OSTA
LNPK
Dmel\CG18810
Fam50a
OTUD6B
X1WH67
s1pr1
X1WHY8
Olfr1508
Lpgat1
Olfr772
TAAR8
MED27
OR8B4
X1WBS8
Gr58c
Gr68a
Or67d
Or74a
Cysltr1
Vmn1r69
X1WGW1
X1WHD4
HIKESHI
RMND5A
CG11673
Dmel\CG1636
X1WFU5
LUC7L2
X1WHU4

AorfS : No hits, top-scoring values are indicated

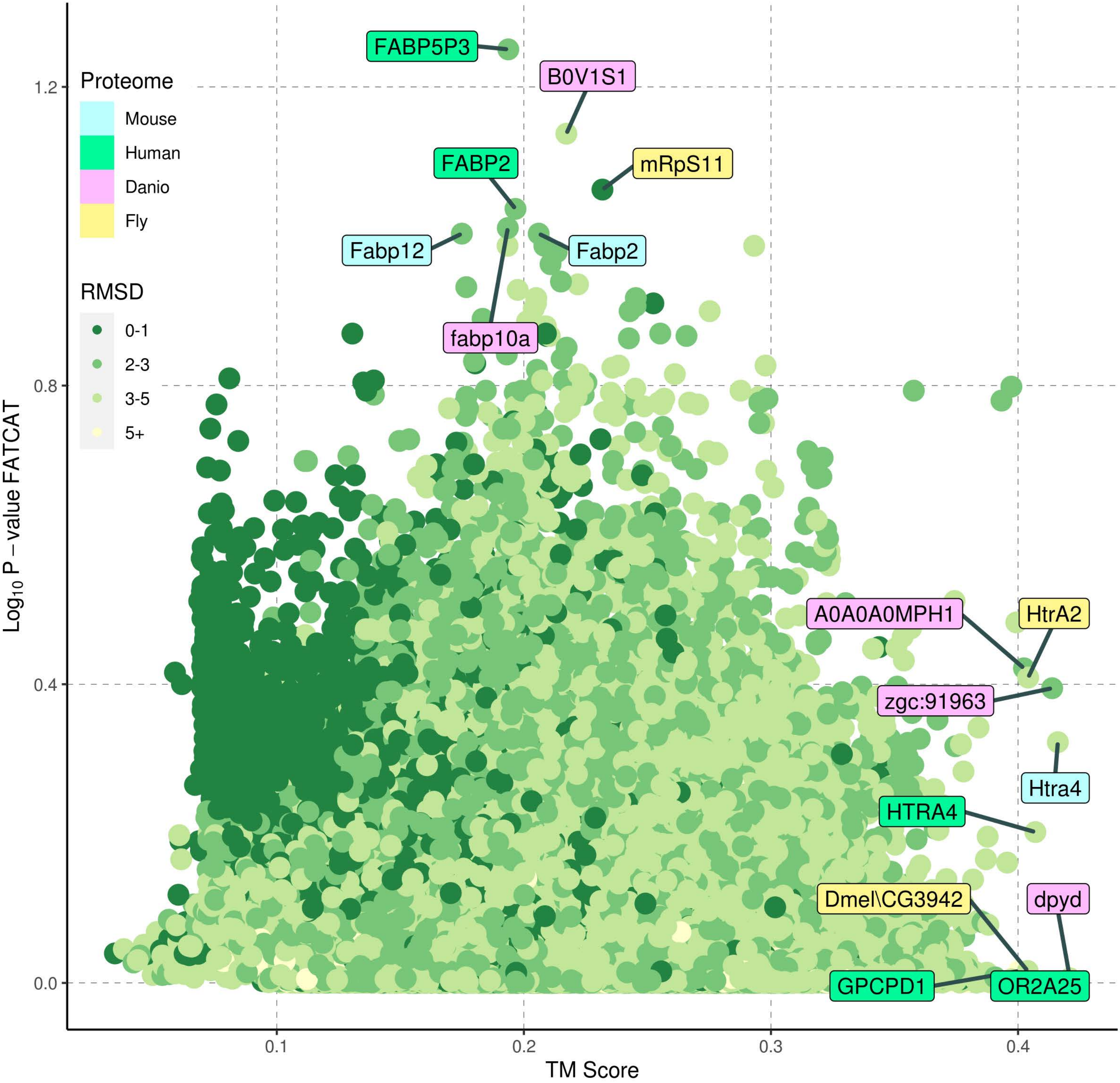


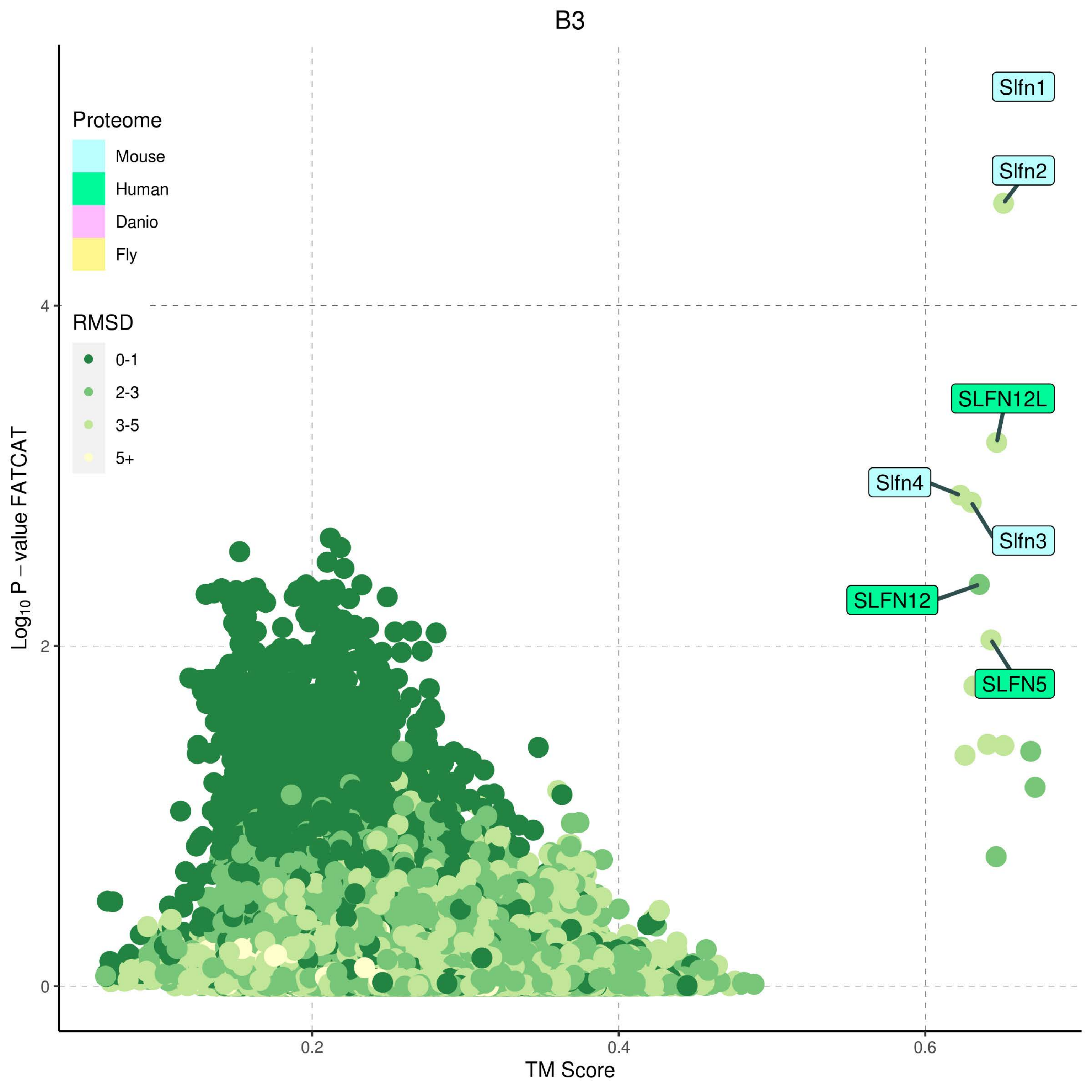

AorfT : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log₁₀ P – value FATCAT
TM Score
0
1
2
3
4
0.2
0.4
0.6
Gm11077
crc-5'utr
SclB
Dmel\CG46458
Gm17428
SclA
Gm10985
Gm10974
Dmel\CG42781
F8W2J4
HHAT
THOP1
Hhat
A0A2R8RK22
Atp2a3
A9C3Q4
Q5U3A4
Thop1

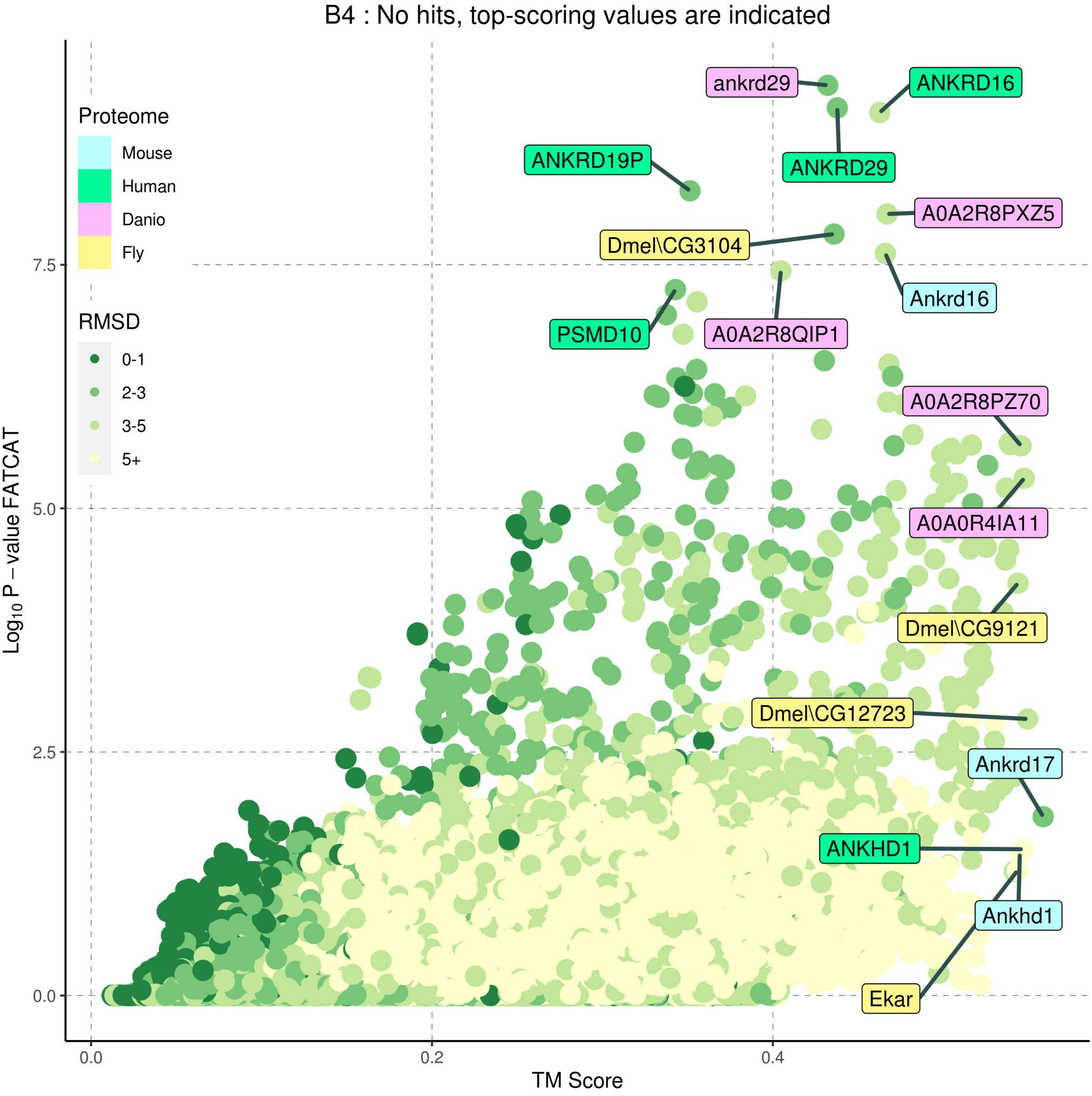

AorfU
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
K7DYB1
A0A0R4IH69
Log₁₀ P – value FATCAT
8
6
4
2
0
TM Score
0.2
0.4
0.6

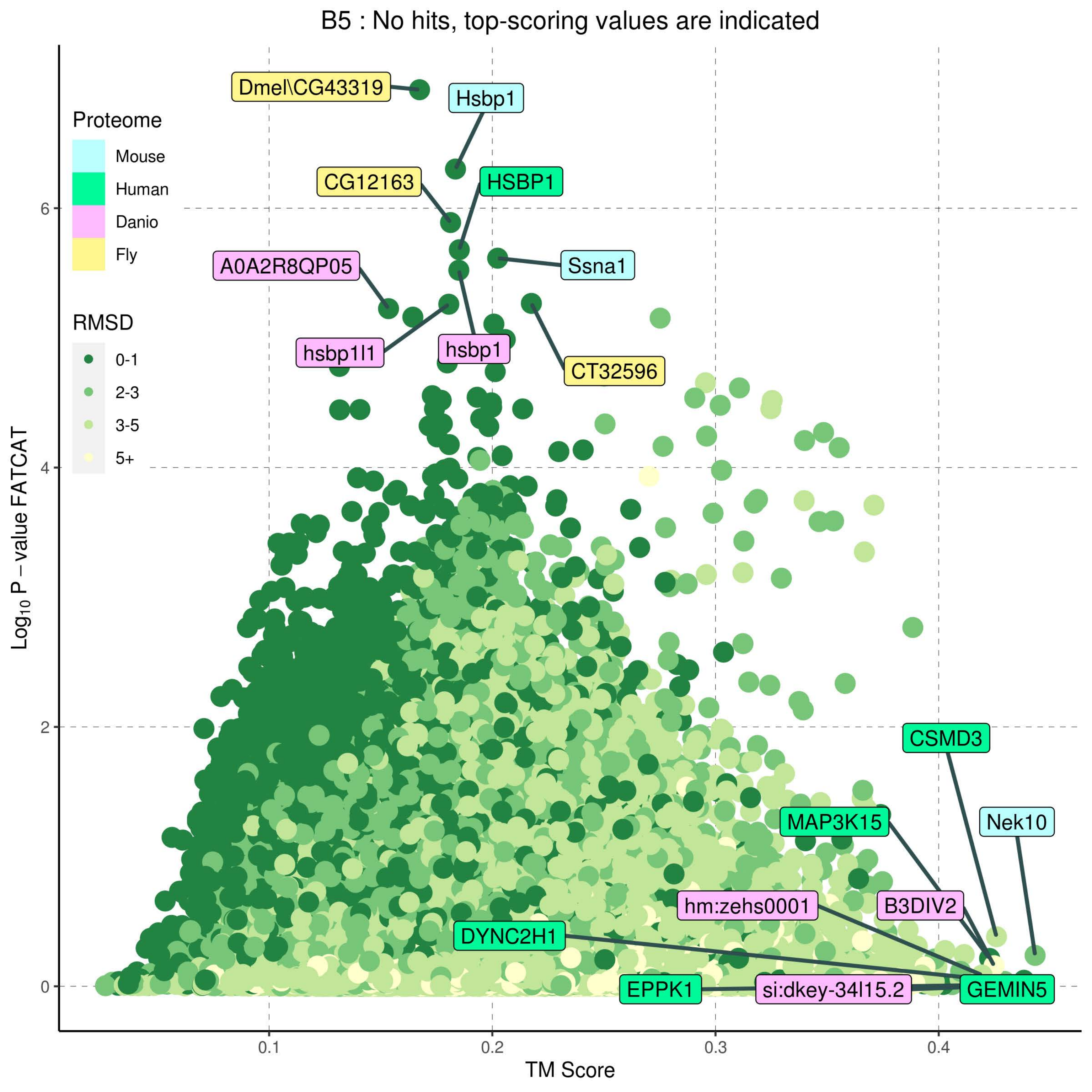

B1
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P − value FATCAT
TM Score
0.00
0.25
0.50
0.75
0
5
10
15
Dmel\CG9222
Q9DE44
CSNK1G3
Dmel\CG2577
VRK1
Pk34A
Sgk2
GSK3
si:dkey-193d10.3
si:dkey-14d8.5
si:dkey-193d10.2
Dmel\CG1227
si:ch73-313g15.1
PTK6
X1WHD3
Dmel\CG10177
OR2A25
Smok2b
U3JAT7
RPS6KB2
si:dkey-278g4.8
Mapk11
si:rp71-84d9.6
Mapk13
Rps6kb2
ACVRL1
si:rp71-84d9.4
X1WCI3
DYRK2
Mapkapk2
Nek3
si:dkey-43a14.9
X1WH91
AKT3
Akt3
Stradb
PRKAA1
STK33
Cdk2
si:ch211-237d5.4
Dmel\CG7236
X1WHM4
Stk32c
nlk
Prkaa1
Prkaa2
Smok1
Dyrk1b
Pdpk1
si:dkey-183
CDK16
Stk25
zgc:153964
X1WBG3
si:dkey-206f10.7
NLK
X1WG73
Srpk3
NUAK2
CAMKK1
mbt
DAPK2
CG10532
STK39
si:dkey-31m14.7
pimr188
PDIK1L
PSKH2
Rps6ka2
KP78a
fyna
RPS6KA6
Stk39
GckIII
Tnk1
Ilk
Cdk7
ex
Pnck
Mark4
IKKepsilon
Ikbke
ZAP70
IME2
STK26
IRAK4
RIB1
SNRK
R4GDQ8
Nek11
Nek2
dnt
Nek8
S6kII
X1WG29
Mapk7
Nek4
Map2k5
fgfr4
tyro3
Map3k14
Dmel\CG4041
Ulk2
Erk7
Dmel\CG8173
Pask
EPHA6
Bub1
Epha4
X1WEA3
X1WF34
fabp
Ephb2
MAP3K3
Ack
Map3k2
Ror2
IRAK3
Sik2
HIPK4
A0A1B0
betagg
DCLK2
STK38L
Nak
Ripk3
Rok
Mink1
Dmel\CG1951
Prp4k
PTK7
PASK
TESK2
MAP4K5
MAP3K20
Hipk2
X1WGA8
Insrr
IRb
X1WBM3
Eif2ak1
X1WHC7
Cdc7
X1WD79
si:ch211-231m23.2
yata
kita
Ern1
CDC42BPB
SCYL3
Ern2
F8W2F0
NRBP2
PINK1
WNK2
Madm
wnd
Slik
ttk
Dmel\

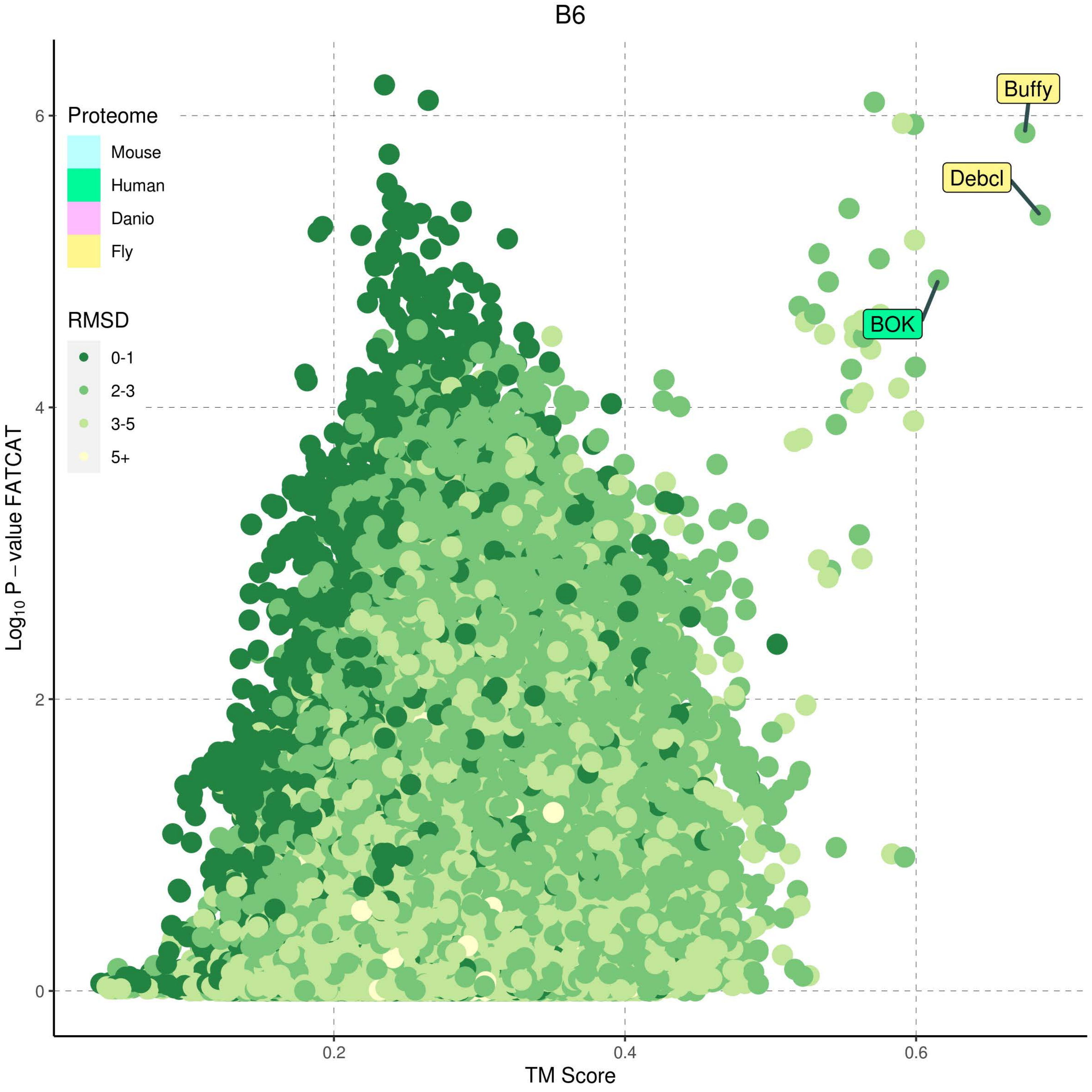
B2 : No hits, top-scoring values are indicated

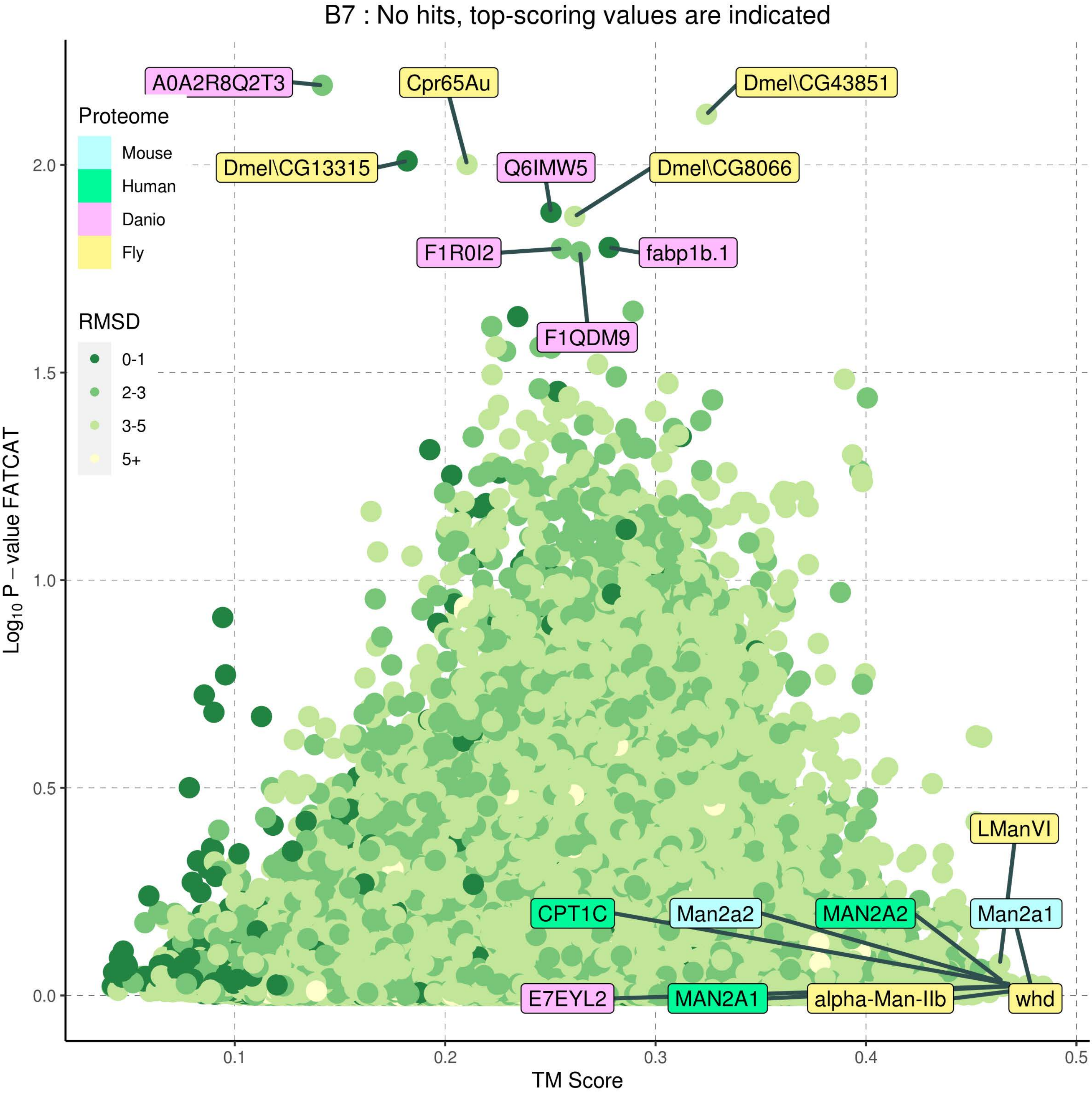


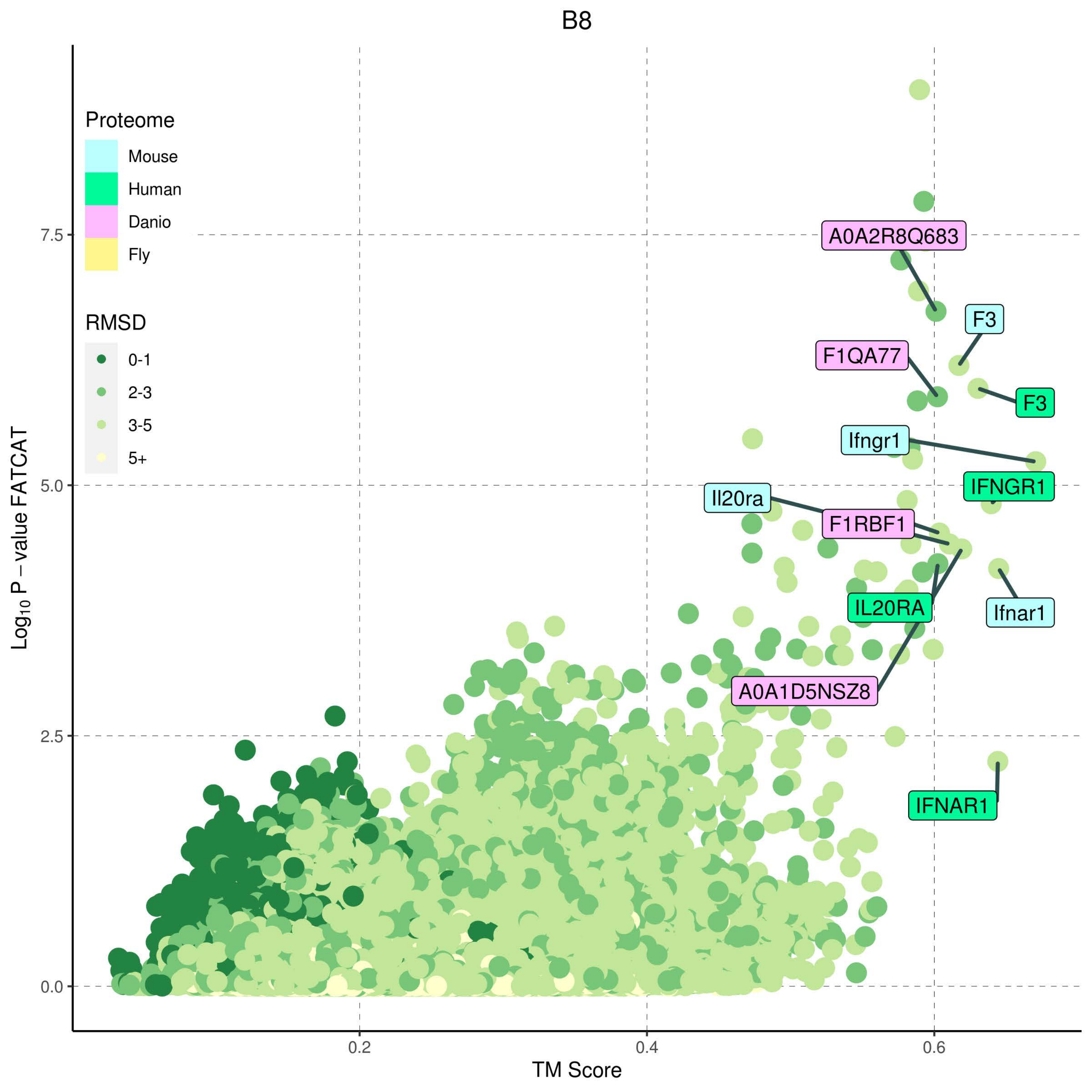

B3
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Slfn1
Slfn2
SLFN12L
Slfn4
Slfn3
SLFN12
SLFN5
4
2
0
0.2
0.4
0.6
TM Score
Log10 P – value FATCAT

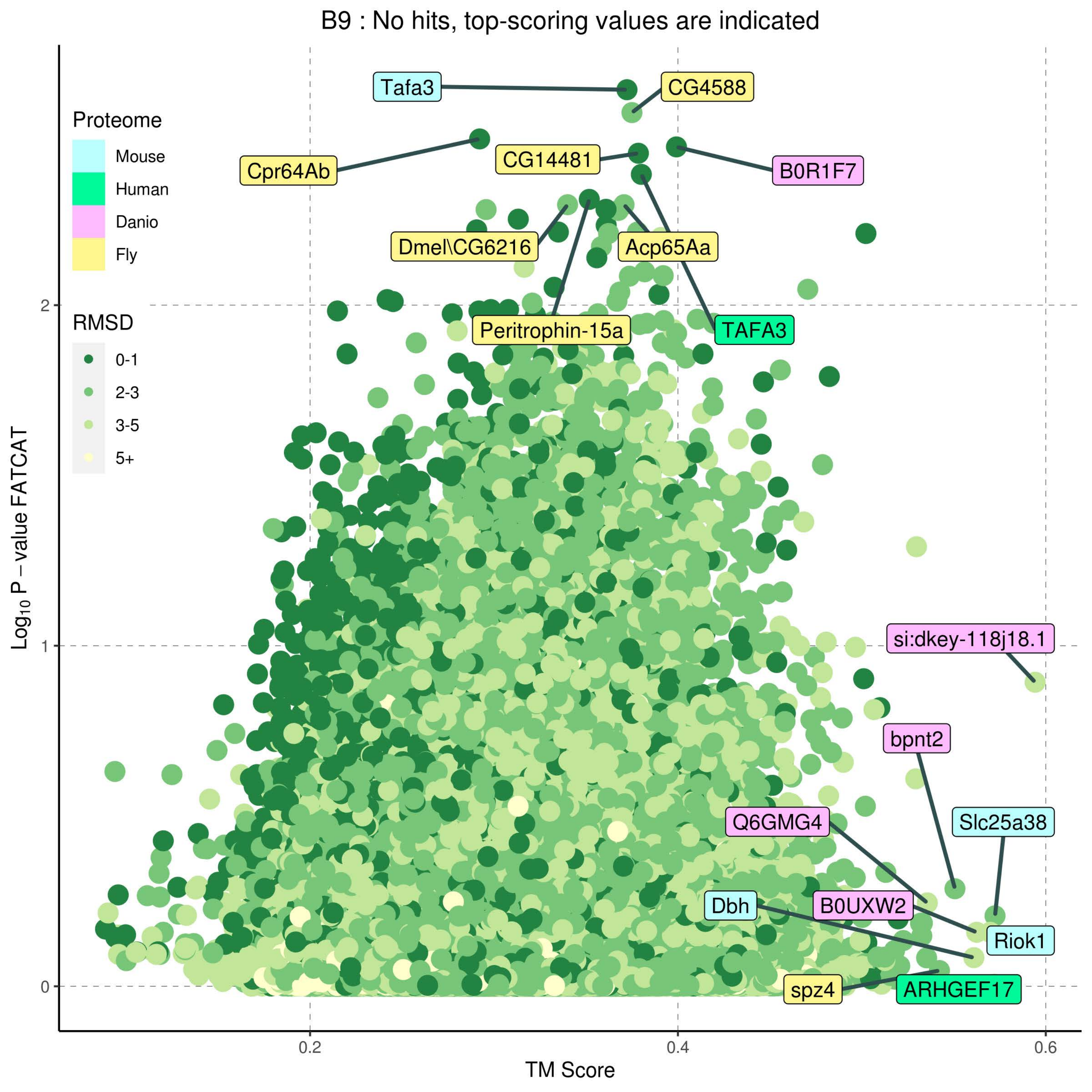

B4 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
ankrd29
ANKRD16
ANKRD29
ANKRD19P
A0A2R8PXZ5
Dmel\CG3104
Ankrd16
PSMD10
A0A2R8QIP1
A0A2R8PZ70
A0A0R4IA11
Dmel\CG9121
Dmel\CG12723
Ankrd17
ANKHD1
Ankhd1
Ekar
Log10 P – value FATCAT
7.5
5.0
2.5
0.0
0.0
0.2
0.4
TM Score

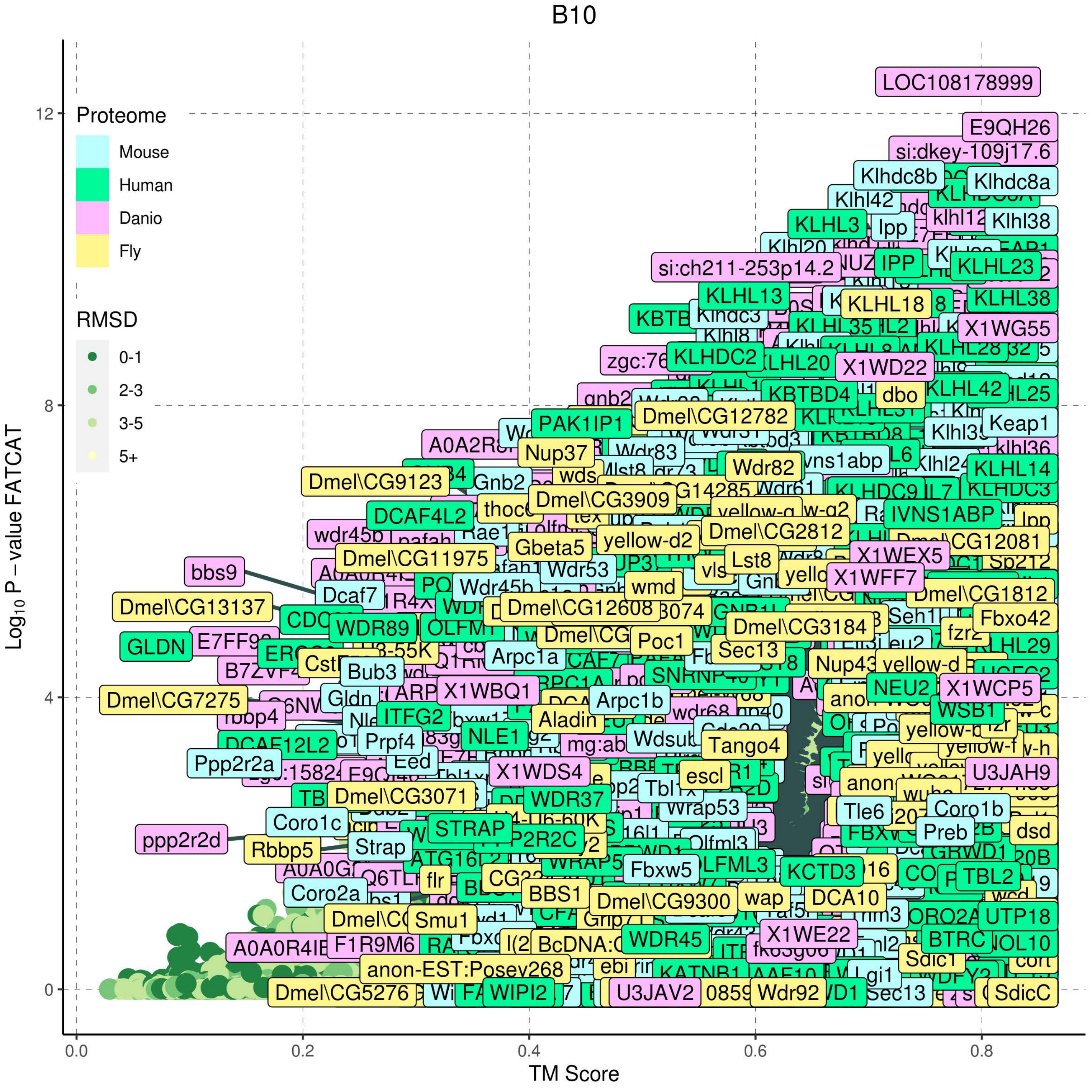

B5 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
TM Score
0
2
4
6
0.1
0.2
0.3
0.4
Dmel\CG43319
Hsbp1
CG12163
HSBP1
Ssna1
A0A2R8QP05
hsbp1l1
hsbp1
CT32596
CSMD3
Nek10
MAP3K15
hm:zehs0001
B3DIV2
DYNC2H1
EPPK1
si:dkey-34l15.2
GEMIN5

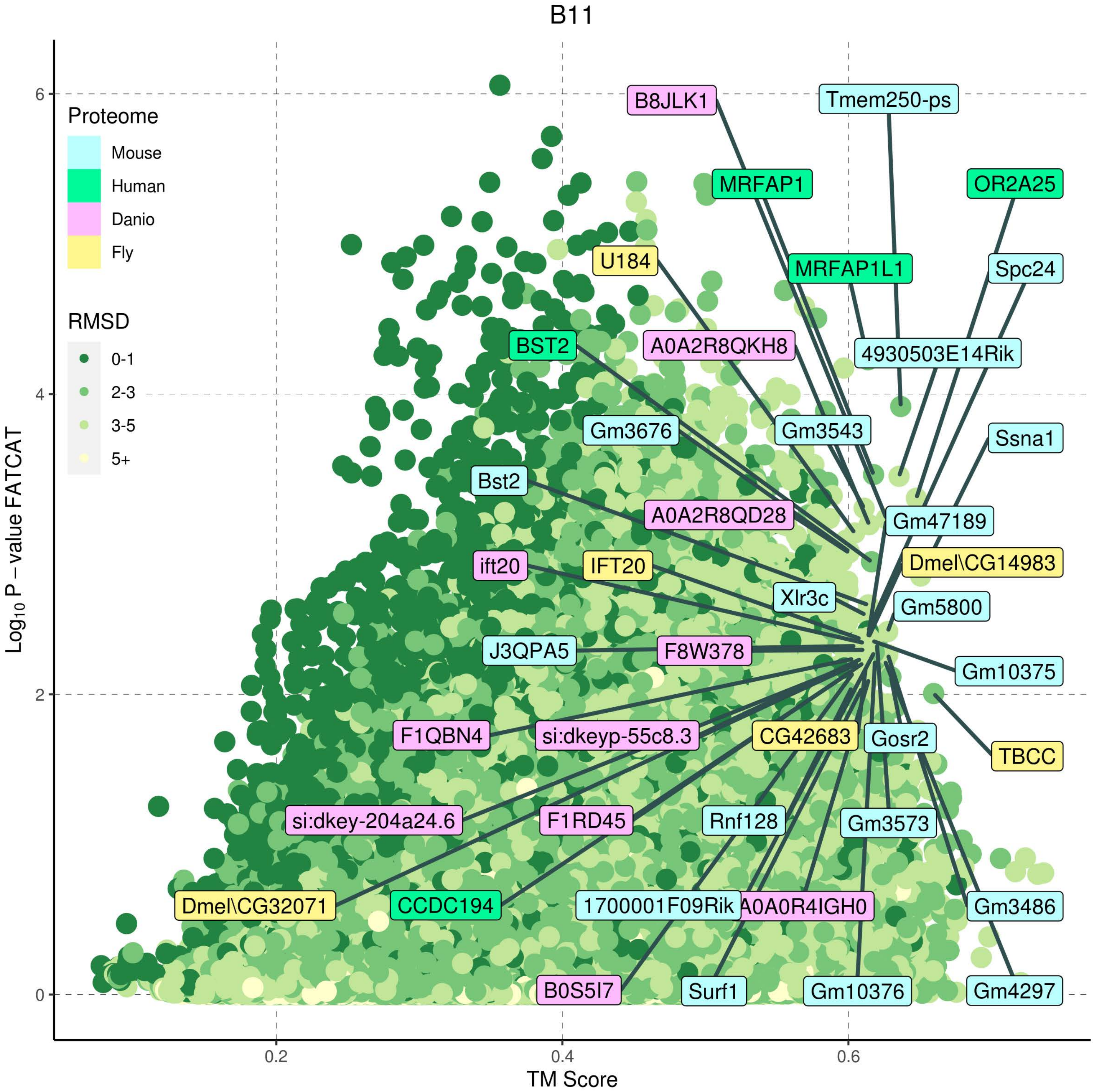

B6
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Buffy
Debcl
BOK
Log$_{10}$ P − value FATCAT
TM Score
0
2
4
6
0.2
0.4
0.6

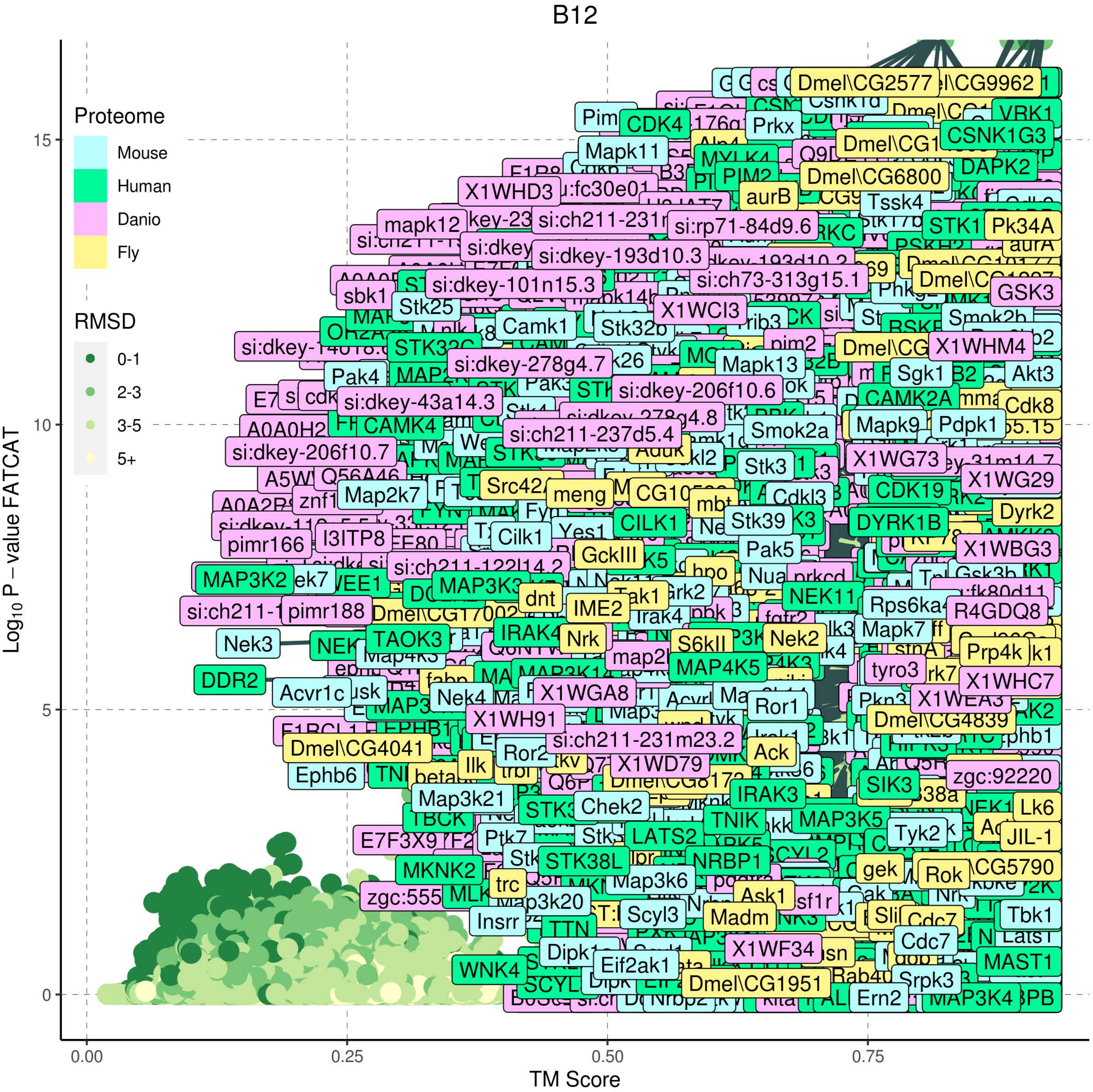

B7 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
A0A2R8Q2T3
Cpr65Au
Dmel\CG43851
Dmel\CG13315
Q6IMW5
Dmel\CG8066
F1R0I2
fabp1b.1
F1QDM9
LManVI
CPT1C
Man2a2
MAN2A2
Man2a1
E7EYL2
MAN2A1
alpha-Man-IIb
whd
Log10 P – value FATCAT
2.0
1.5
1.0
0.5
0.0
TM Score
0.1
0.2
0.3
0.4
0.5

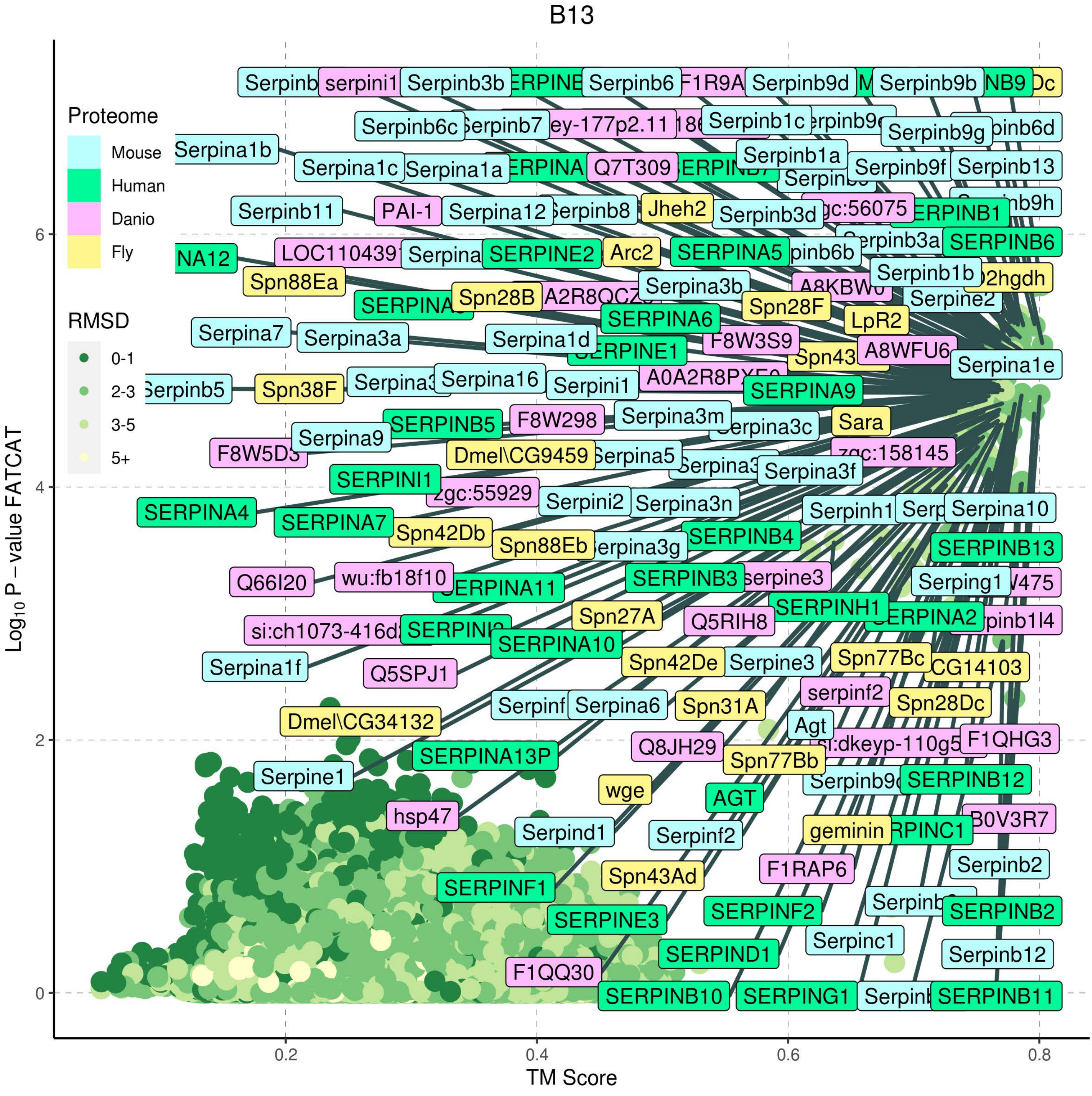

B8
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log₁₀ P − value FATCAT
7.5
5.0
2.5
0.0
TM Score
0.2
0.4
0.6
A0A2R8Q683
F3
F1QA77
F3
Ifngr1
IFNGR1
Il20ra
F1RBF1
IL20RA
Ifnar1
A0A1D5NSZ8
IFNAR1

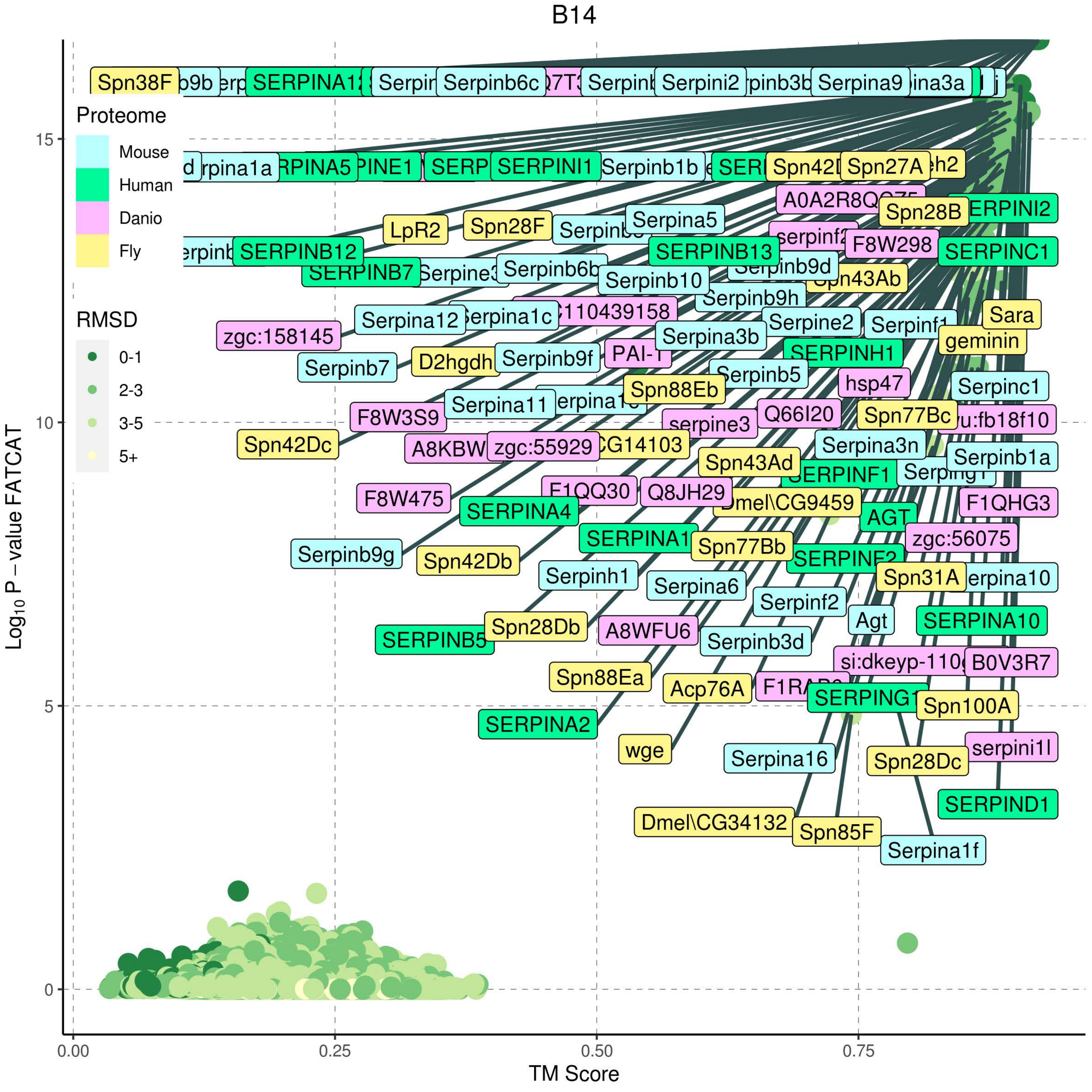

B9 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Tafa3
CG4588
Cpr64Ab
CG14481
B0R1F7
Dmel\CG6216
Acp65Aa
Peritrophin-15a
TAFA3
si:dkey-118j18.1
bpnt2
Q6GMG4
Slc25a38
Dbh
B0UXW2
Riok1
spz4
ARHGEF17
Log$_{10}$ P − value FATCAT
2
1
0
TM Score
0.2
0.4
0.6

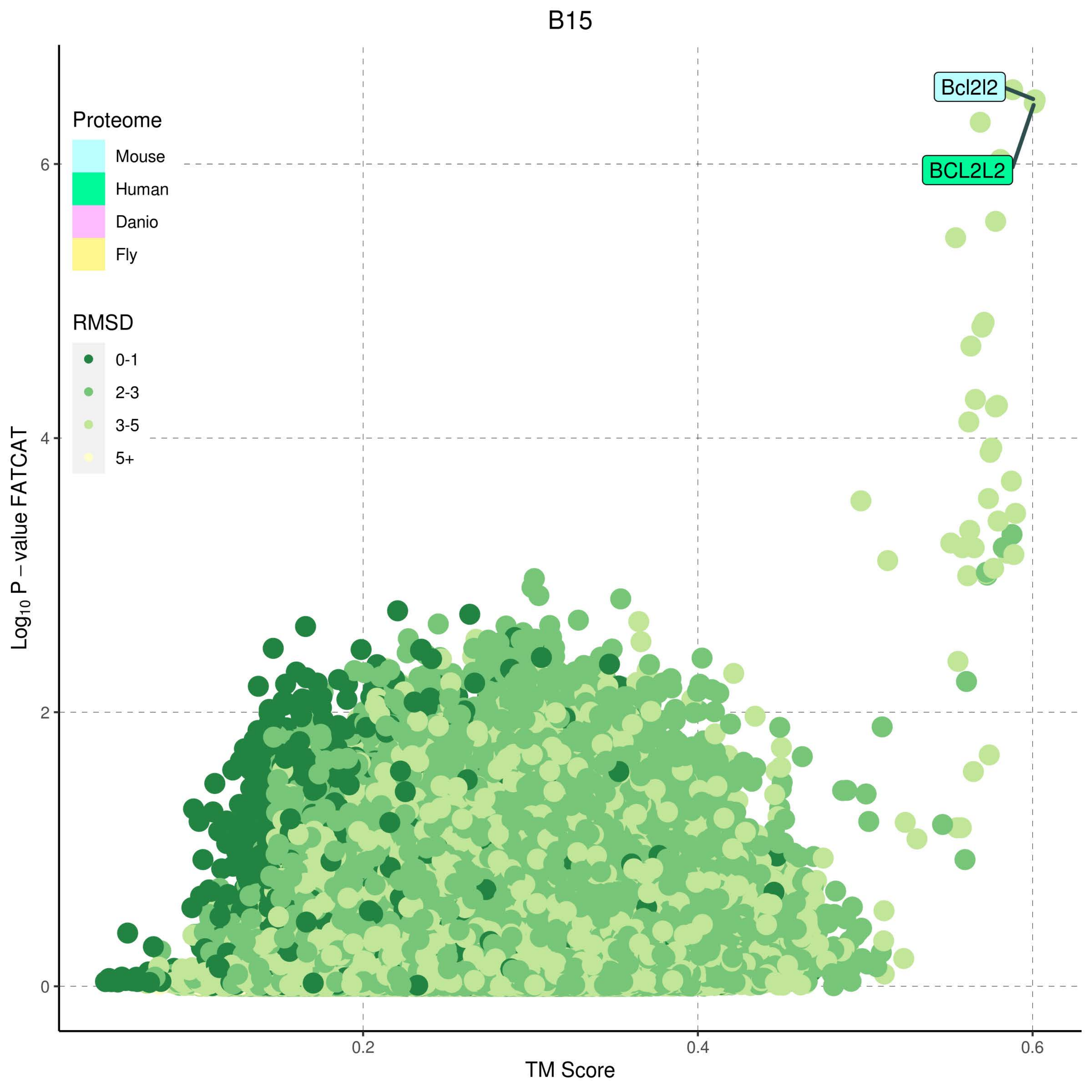

B10
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P − value FATCAT
TM Score
0
4
8
12
0.0
0.2
0.4
0.6
0.8
LOC108178999
E9QH26
si:dkey-109j17.6
Klhdc8b
Klhdc8a
Klhl42
KLHL3
Ipp
klhl12
Klhl38
si:ch211-253p14.2
IPP
KLHL23
KLHL13
KLHL18
KLHL38
KBTB
Klhdc3
KLHL35
X1WG55
zgc:76
KLHDC2
KLHL20
X1WD22
KLHL28
KBTBD4
dbo
KLHL42
gnb2
Dmel\CG12782
Keap1
PAK1IP1
Klhl35
A0A2R
Nup37
Wdr83
Wdr82
vns1abp
Klhl24
KLHL14
Dmel\CG9123
Gnb2
wds
KLHDC9
KLHDC3
Dmel\CG3909
Dmel\CG14285
Wdr61
DCAF4L2
yellow-g
IVNS1ABP
Ipp
wdr45b
Dmel\CG2812
yellow-d2
Dmel\CG12081
Gbeta5
Dmel\CG11975
X1WEX5
bbs9
Wdr53
Lst8
Sp212
X1WFF7
Wdr45b
wmd
Dcaf7
Dmel\CG1812
Dmel\CG13137
Dmel\CG12608
Fbxo42
WDR89
Dmel\CG3184
GLDN
Poc1
E7FF9
Arpc1a
Sec13
fzr2
Bub3
Nup43
yellow-d
X1WBQ1
NEU2
X1WCP5
Dmel\CG7275
Arpc1b
wdr68
Gldn
ITFG2
Aladin
WSB1
rbbp4
Prpf4
NLE1
Tango4
yellow-f
Wdsub
Ppp2r2a
Eed
X1WDS4
escl
U3JAH9
Dmel\CG3071
WDR37
Tbl1x
Coro1c
Wrap53
Tle6
Coro1b
STRAP
Preb
dsd
ppp2r2d
Rbbp5
Strap
Olfml3
Fbxw5
KCTD3
TBL2
flr
BBS1
Coro2a
Dmel\CG9300
wap
DCA10
Smu1
UTP18
X1WE22
A0A0R4IE
F1R9M6
WDR45
BTRC
Sdic1
anon-EST:Posev268
Lgi1
U3JAV2
Wdr92
Sec13
SdicC
Dmel\CG5276
WIPI2

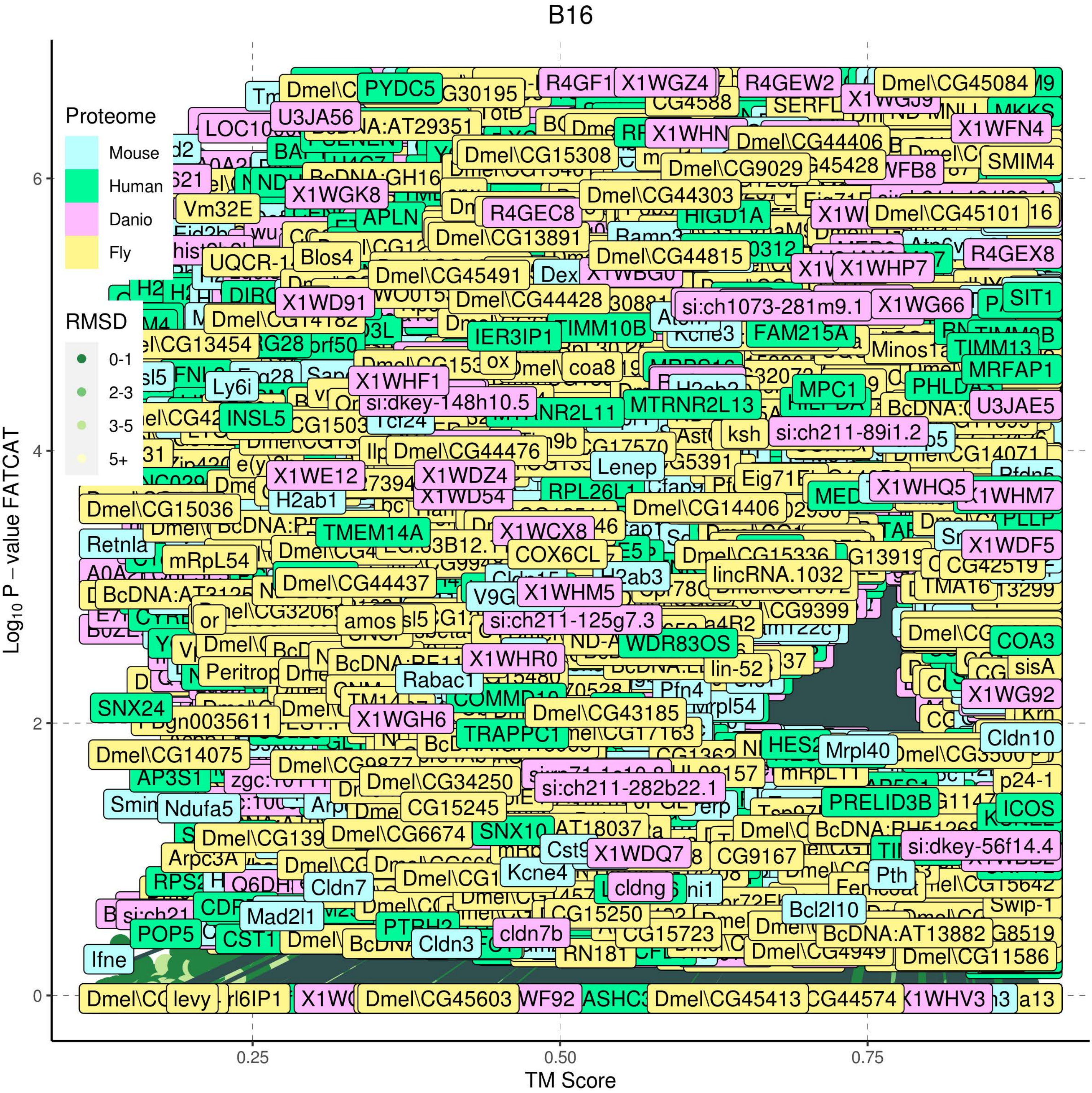

B11
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
B8JLK1
Tmem250-ps
MRFAP1
OR2A25
U184
MRFAP1L1
Spc24
BST2
A0A2R8QKH8
4930503E14Rik
Gm3676
Gm3543
Ssna1
Bst2
A0A2R8QD28
Gm47189
ift20
IFT20
Dmel\CG14983
Xlr3c
Gm5800
J3QPA5
F8W378
Gm10375
F1QBN4
si:dkeyp-55c8.3
CG42683
Gosr2
TBCC
si:dkey-204a24.6
F1RD45
Rnf128
Gm3573
Dmel\CG32071
CCDC194
1700001F09Rik
A0A0R4IGH0
Gm3486
B0S5I7
Surf1
Gm10376
Gm4297
6
4
2
0
0.2
0.4
0.6
TM Score
Log_{10} P − value FATCAT

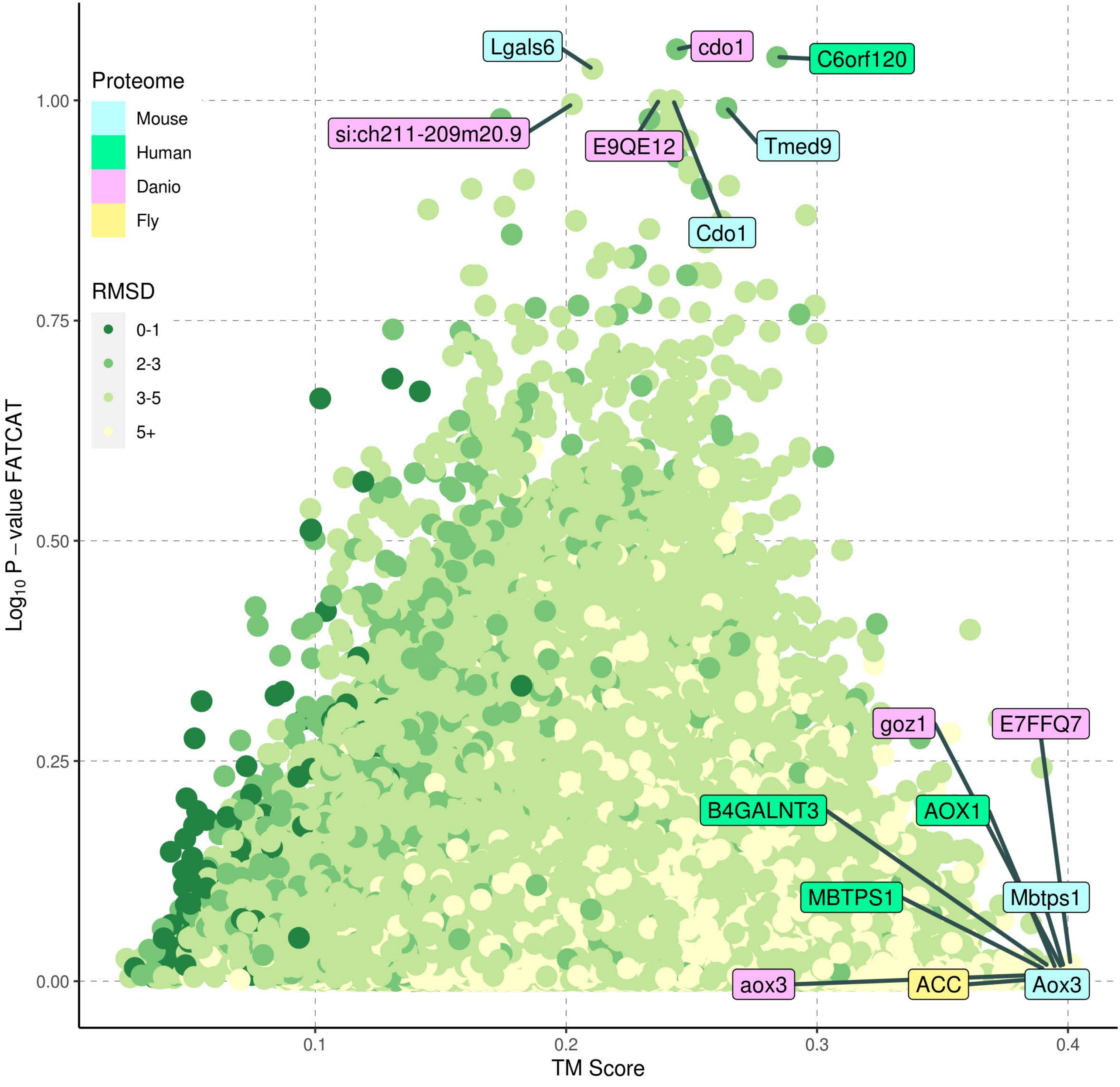

B12
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P − value FATCAT
TM Score
0.00
0.25
0.50
0.75
0
5
10
15
Dmel\CG2577
Dmel\CG9962
VRK1
CSNK1G3
Pim
CDK4
Prkx
Mapk11
PIM2
Dmel\CG6800
DAPK2
X1WHD3
aurB
Tssk4
mapk12
si:rp71-84d9.6
Pk34A
aurA
si:dkey-193d10.3
si:ch73-313g15.1
sbk1
si:dkey-101n15.3
GSK3
Stk25
X1WCI3
Camk1
Stk32b
Smok2b
STK32C
si:dkey-278g4.7
pim2
X1WHM4
Pak4
Mapk13
Sgk1
Akt3
si:dkey-206f10.6
si:dkey-43a14.3
CAMK2A
Cdk8
CAMK4
si:ch211-237d5.4
Smok2a
Mapk9
Pdpk1
si:dkey-206f10.7
Stk3
X1WG73
X1WG29
Src42A
meng
Map2k7
Cdkl3
CDK19
Dyrk2
pimr166
I3ITP8
Cilk1
Yes1
CILK1
Stk39
DYRK1B
X1WBG3
GckIII
Pak5
MAP3K2
WEE1
hpo
Nua
dnt
IME2
Tak1
NEK11
Rps6ka
R4GDQ8
pimr188
Nek3
TAOK3
IRAK4
Nrk
S6kII
Nek2
Mapk7
Prp4k
tyro3
X1WHC7
DDR2
MAP4K5
Acvr1c
Nek4
X1WGA8
Ror1
X1WH91
Dmel\CG4839
si:ch211-231m23.2
Dmel\CG4041
Ror2
X1WD79
Ack
Ephb6
Ilk
zgc:92220
Map3k21
Chek2
IRAK3
SIK3
TBCK
TNIK
MAP3K5
Lk6
Tyk2
JIL-1
E7F3X9
LATS2
MKNK2
STK38L
NRBP1
gek
Rok
Dmel\CG5790
trc
Map3k6
zgc:555
Map3k20
Ask1
Insrr
Scyl3
Madm
Cdc7
Tbk1
TTN
X1WF34
Dipk
Eif2ak1
MAST1
WNK4
Dmel\CG1951
Srpk3
Ern2
MAP3K4

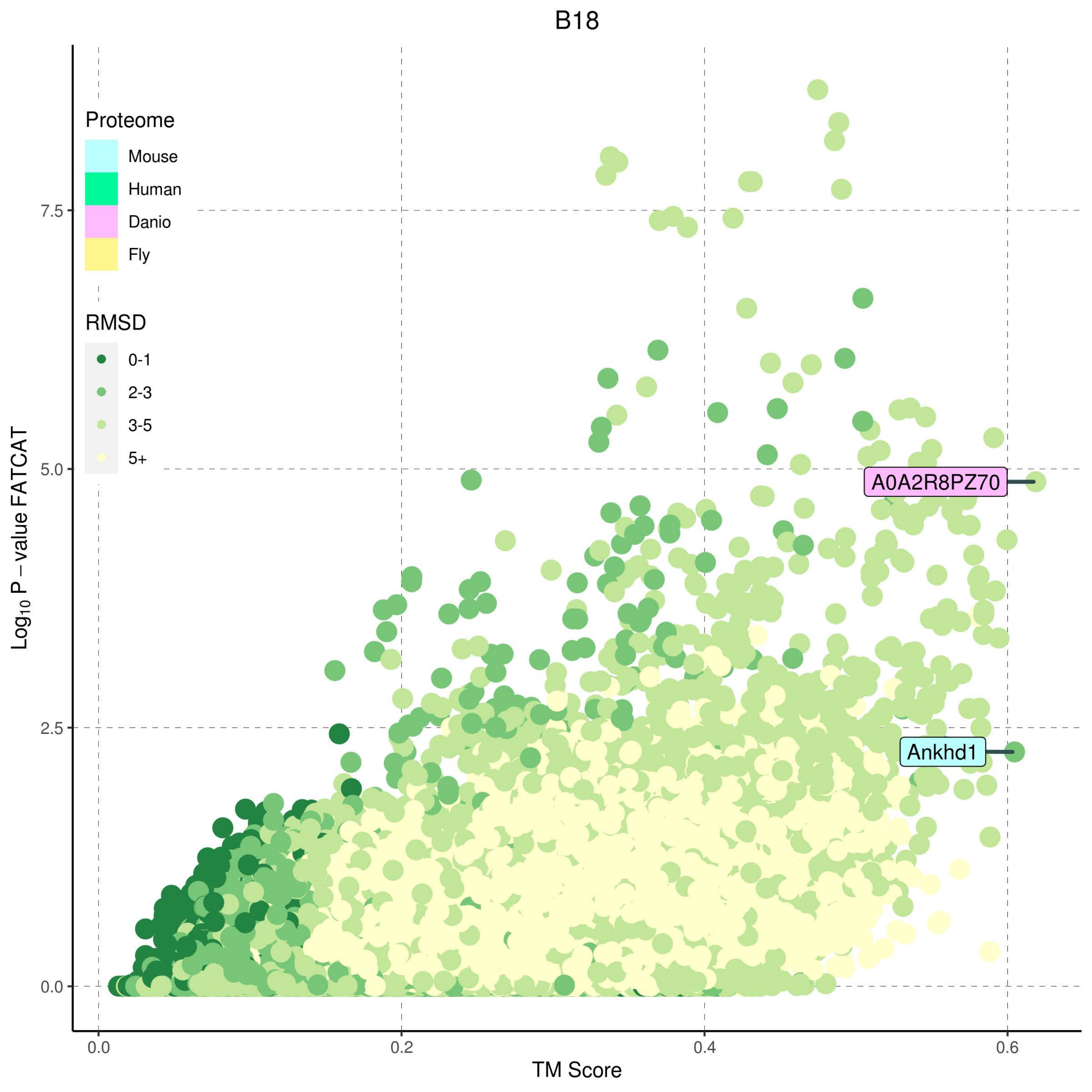

B13
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P - value FATCAT
TM Score
0
2
4
6
0.2
0.4
0.6
0.8
Serpinb
serpini1
Serpinb3b
Serpinb6
Serpinb9d
Serpinb9b
NB9
Serpinb6c
Serpinb7
Serpinb1c
Serpinb9g
Serpina1b
Serpina1c
Serpina1a
Q7T309
Serpinb1a
Serpinb9f
Serpinb13
Serpinb11
PAI-1
Serpina12
Serpinb8
Jheh2
Serpinb3d
SERPINB1
NA12
LOC110439
SERPINE2
Arc2
SERPINA5
Serpinb3a
SERPINB6
Spn88Ea
Serpinb1b
Spn28B
Serpina3b
Spn28F
Serpine2
SERPINA6
LpR2
Serpina7
Serpina3a
Serpina1d
SERPINE1
F8W3S9
A8WFU6
Serpina1e
Serpinb5
Spn38F
Serpina16
Serpini1
SERPINA9
SERPINB5
F8W298
Serpina3m
Sara
Serpina9
F8W5D3
Dmel\CG9459
Serpina5
Serpina3f
SERPINI1
Zgc:55929
Serpini2
Serpina3n
Serpinh1
Serpina10
SERPINA4
SERPINA7
Spn42Db
Spn88Eb
SERPINB4
SERPINB13
Q66I20
wu:fb18f10
SERPINA11
SERPINB3
serpine3
Serping1
SERPINH1
Spn27A
Q5RIH8
SERPINA2
SERPINA10
Serpina1f
Q5SPJ1
Spn42De
Serpine3
Spn77Bc
CG14103
serpinf2
Serpina6
Spn31A
Spn28Dc
Dmel\CG34132
Agt
Q8JH29
F1QHG3
SERPINA13P
Spn77Bb
Serpine1
wge
SERPINB12
AGT
hsp47
Serpind1
Serpinf2
geminin
B0V3R7
F1RAP6
Serpinb2
SERPINF1
Spn43Ad
SERPINF2
SERPINB2
SERPINE3
Serpinc1
SERPIND1
Serpinb12
F1QQ30
SERPINB10
SERPING1
SERPINB11


B14
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log$_{10}$ P – value FATCAT
TM Score
0.00
0.25
0.50
0.75
0
5
10
15
Spn38F
Serpinb6c
Serpini2
Serpina9
SERPINA5
Serpina1a
SERPINI1
Serpinb1b
Spn27A
Spn42D
A0A2R8Q
Spn28B
SERPINI2
LpR2
Spn28F
Serpina5
SERPINB12
SERPINB13
F8W298
SERPINC1
SERPINB7
Serpinb6b
Serpinb10
Serpinb9d
Serpinb9h
Serpina12
Serpina1c
110439158
Serpine2
Serpinf1
Sara
zgc:158145
Serpina3b
geminin
Serpinb7
D2hgdh
Serpinb9f
PAI-1
SERPINH1
Serpinb5
hsp47
Serpinc1
F8W3S9
Serpina11
Spn88Eb
Q66I20
Spn77Bc
serpine3
Spn42Dc
A8KBW
zgc:55929
CG14103
Serpina3n
Serpinb1a
Spn43Ad
SERPINF1
F8W475
F1QQ30
Q8JH29
Dmel\CG9459
F1QHG3
SERPINA4
AGT
zgc:56075
SERPINA1
Spn77Bb
Serpinb9g
Spn42Db
SERPINF2
Serpinh1
Serpina6
Spn31A
Serpina10
Serpinf2
Agt
SERPINA10
Spn28Db
SERPINB5
A8WFU6
Serpinb3d
B0V3R7
Spn88Ea
Acp76A
SERPING1
Spn100A
SERPINA2
wge
serpini1l
Serpina16
Spn28Dc
SERPIND1
Dmel\CG34132
Spn85F
Serpina1f

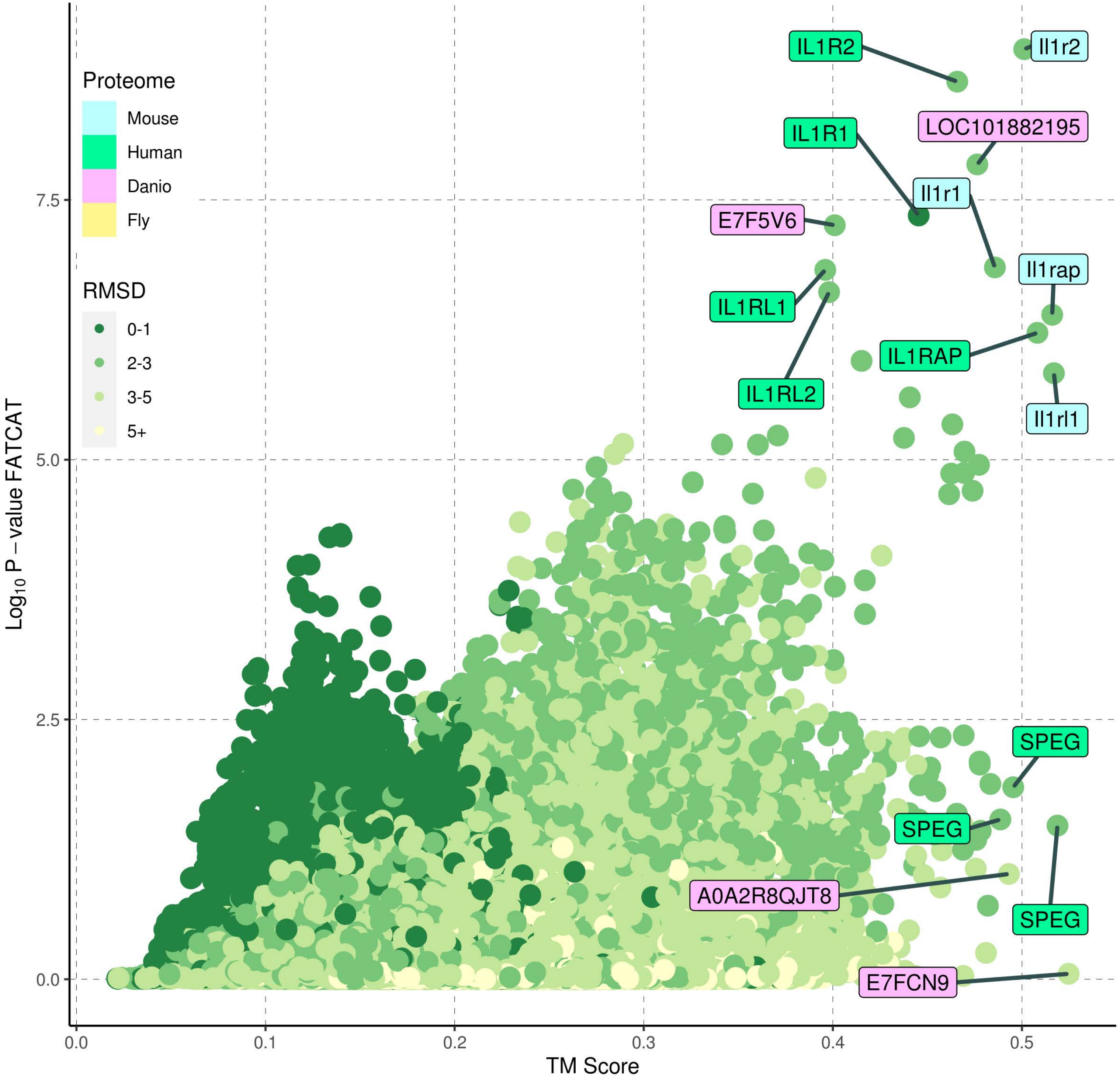

B15
Bcl2l2
BCL2L2
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log_{10} P − value FATCAT
6
4
2
0
TM Score
0.2
0.4
0.6

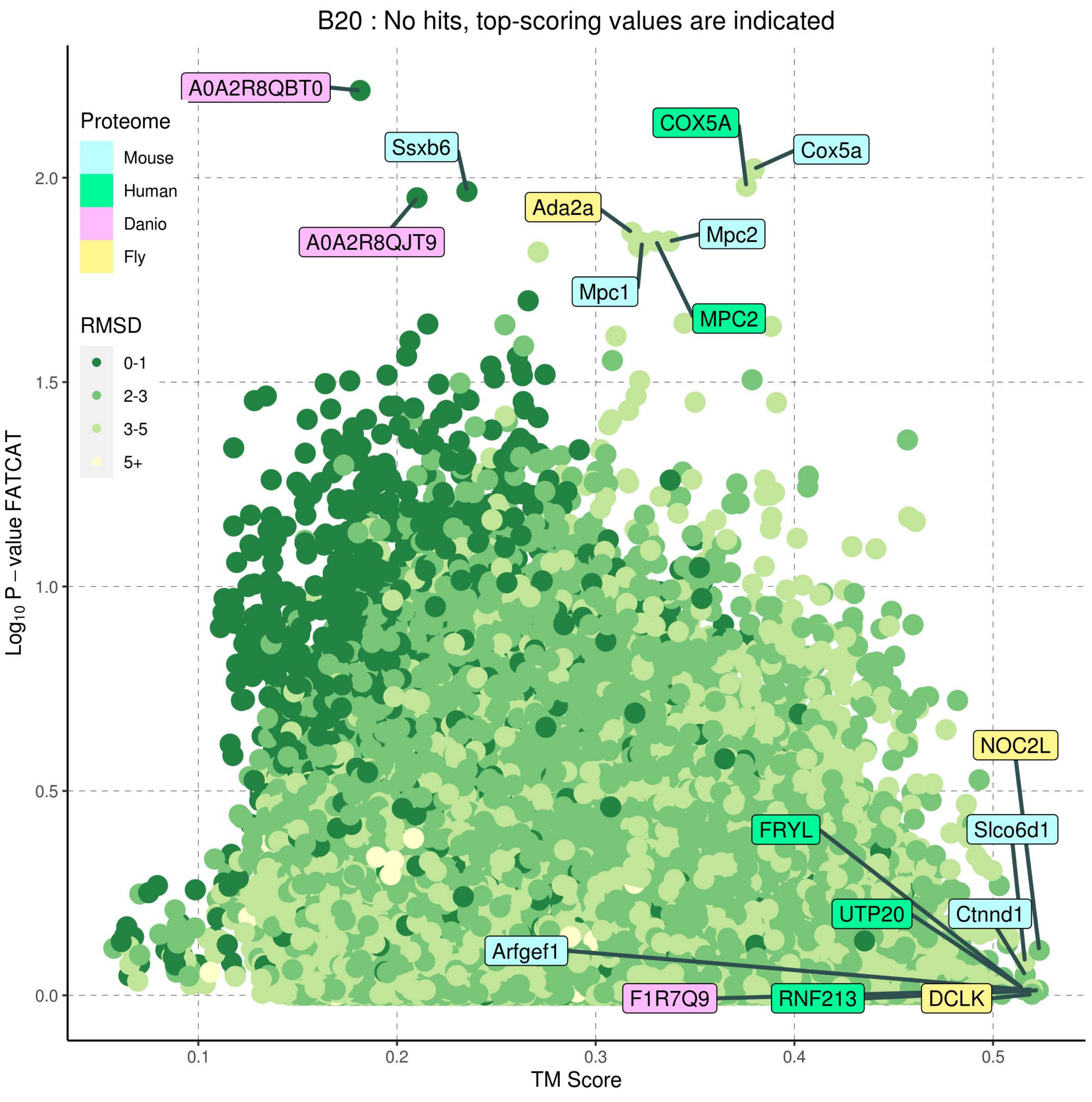

B16
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log$_{10}$ P − value FATCAT
0
2
4
6
TM Score
0.25
0.50
0.75

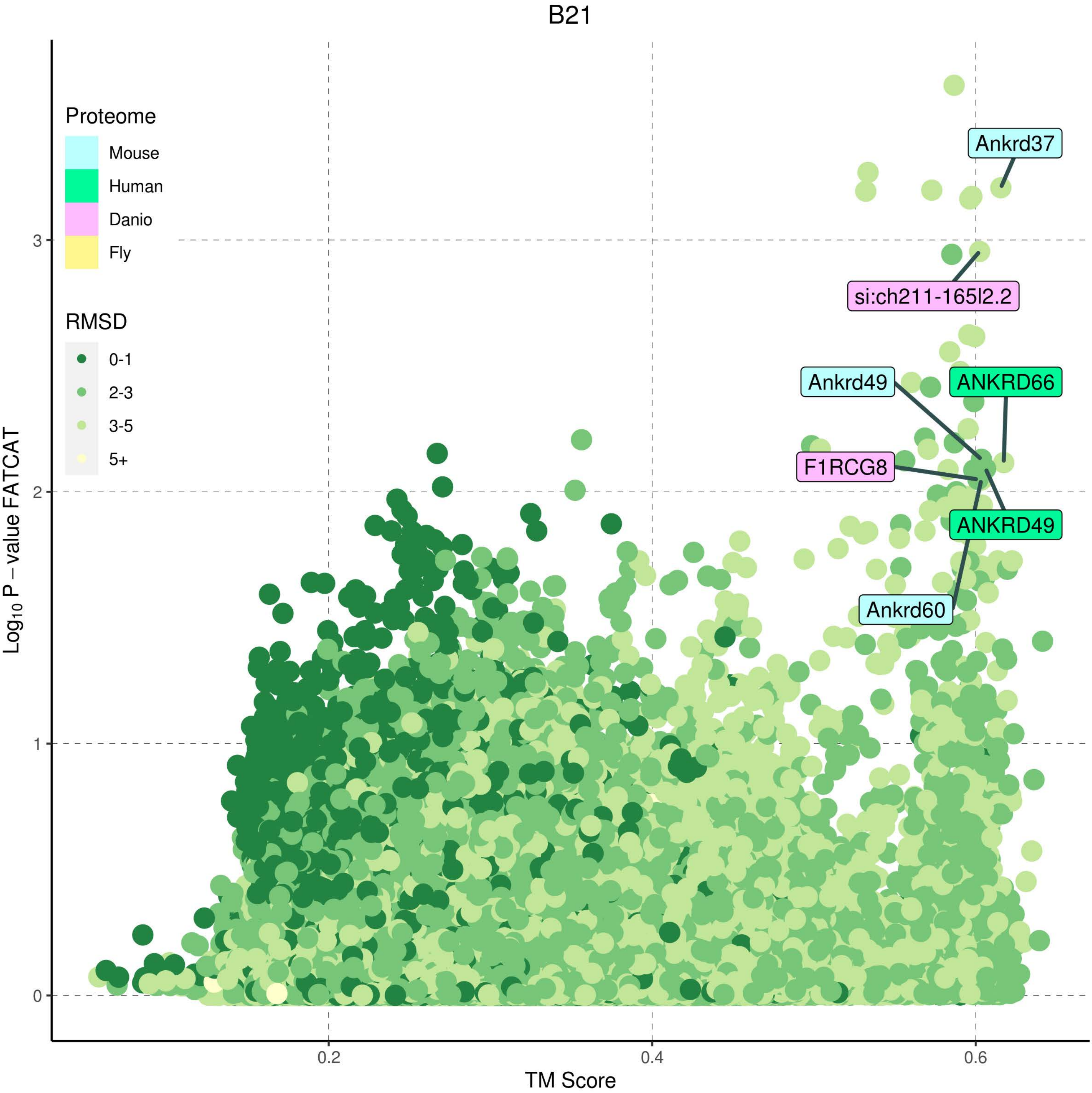

B17 : No hits, top-scoring values are indicated

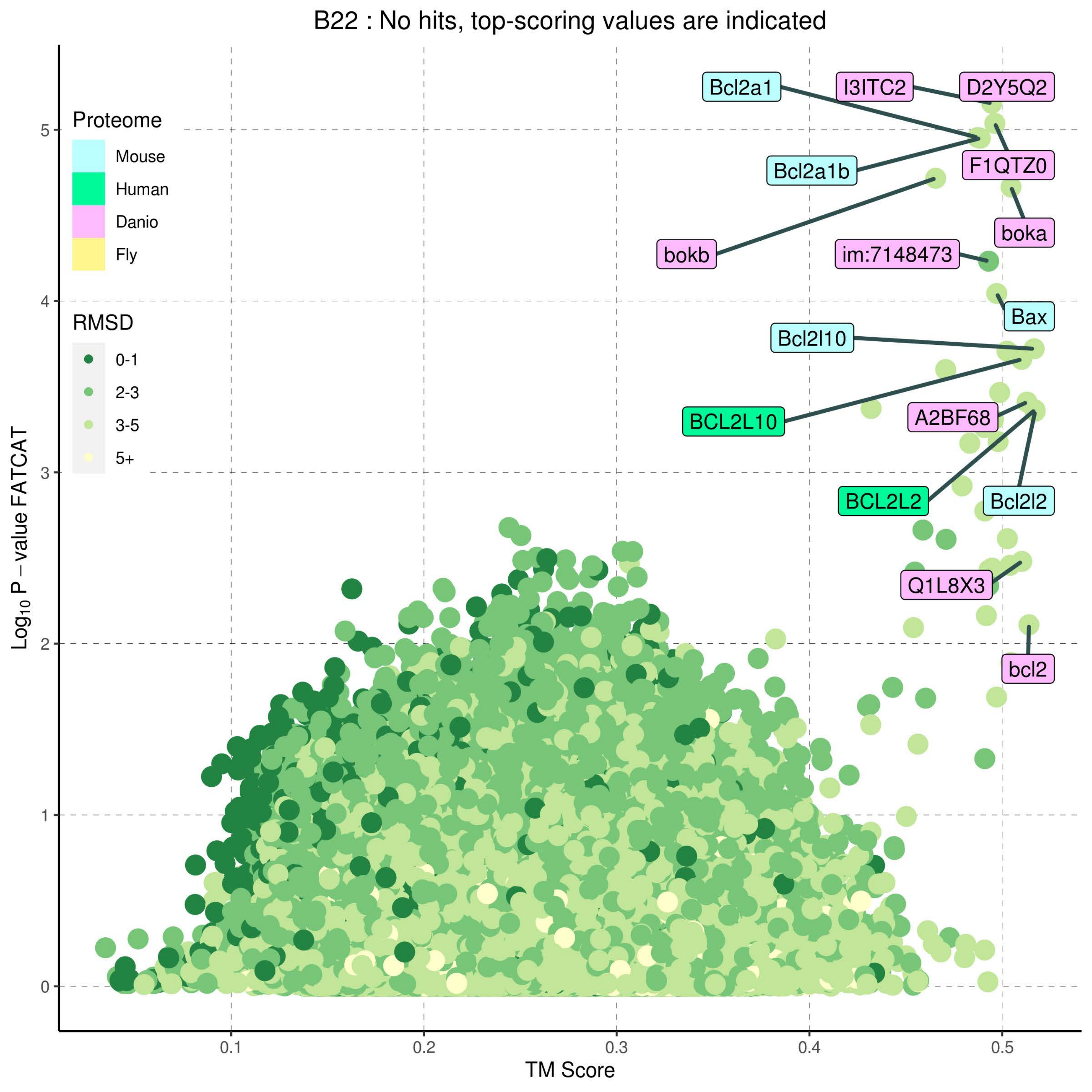

B18
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
A0A2R8PZ70
Ankhd1
Log₁₀ P − value FATCAT
7.5
5.0
2.5
0.0
0.0
0.2
0.4
0.6
TM Score

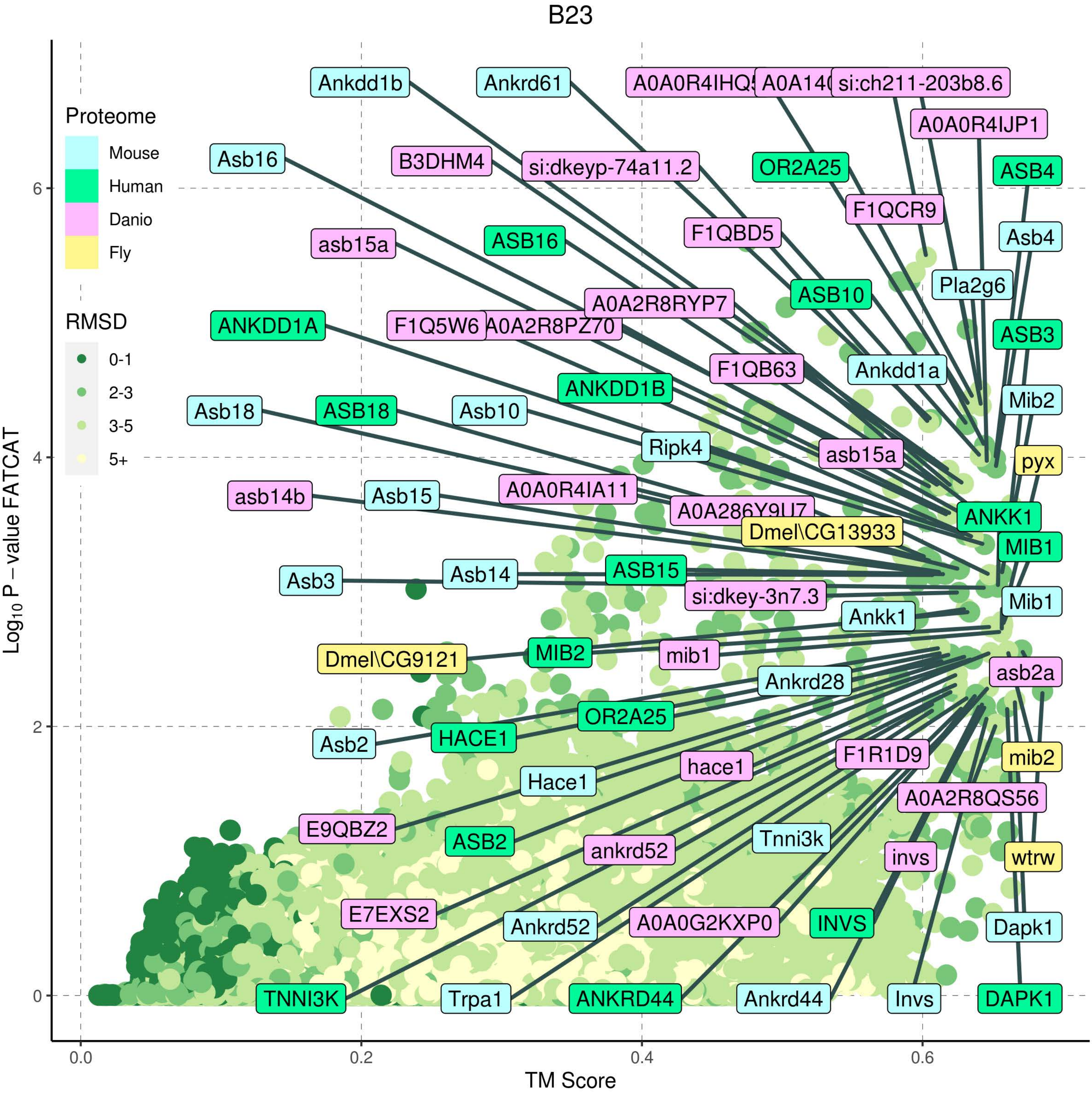
B19 : No hits, top-scoring values are indicated

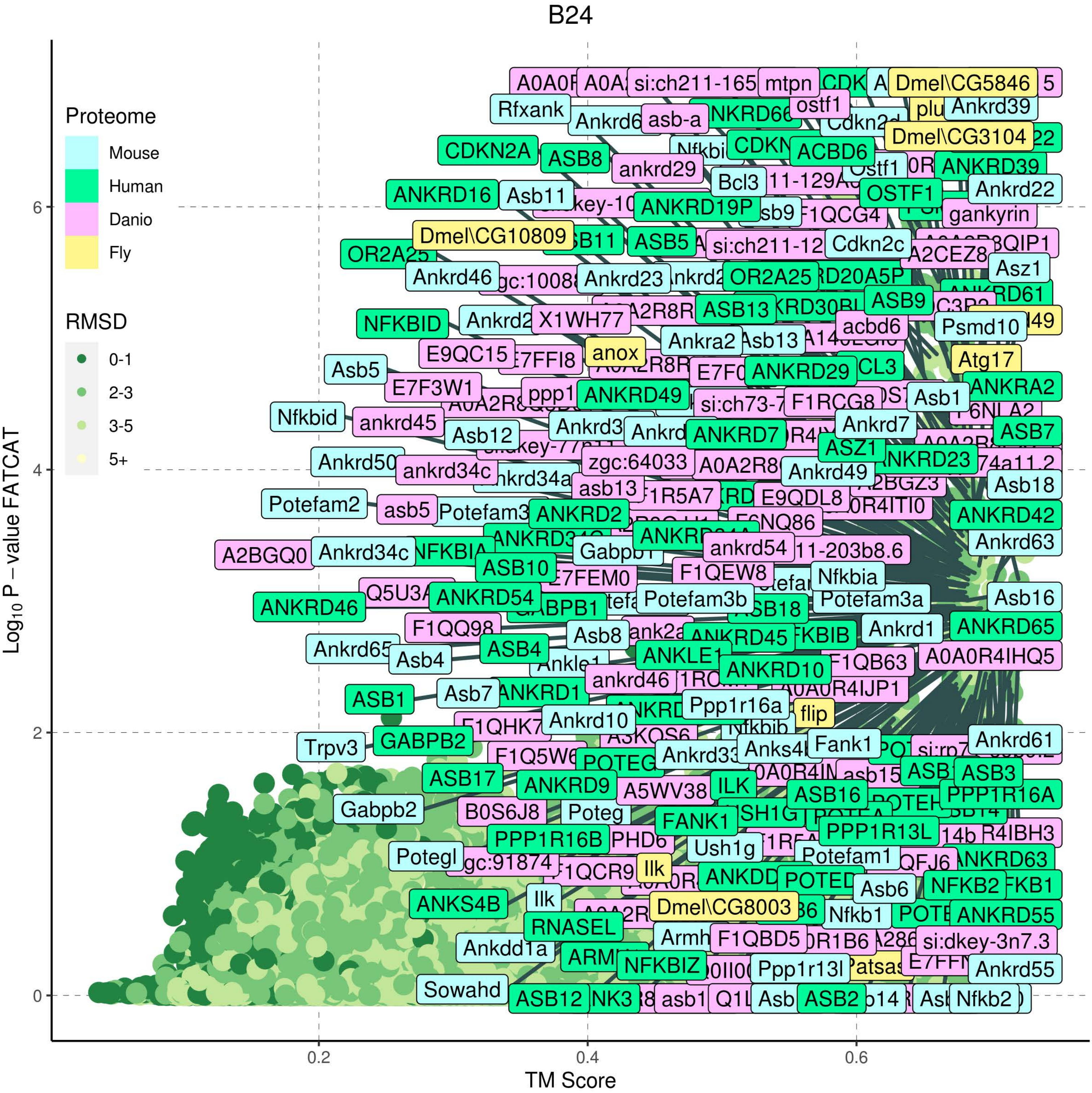


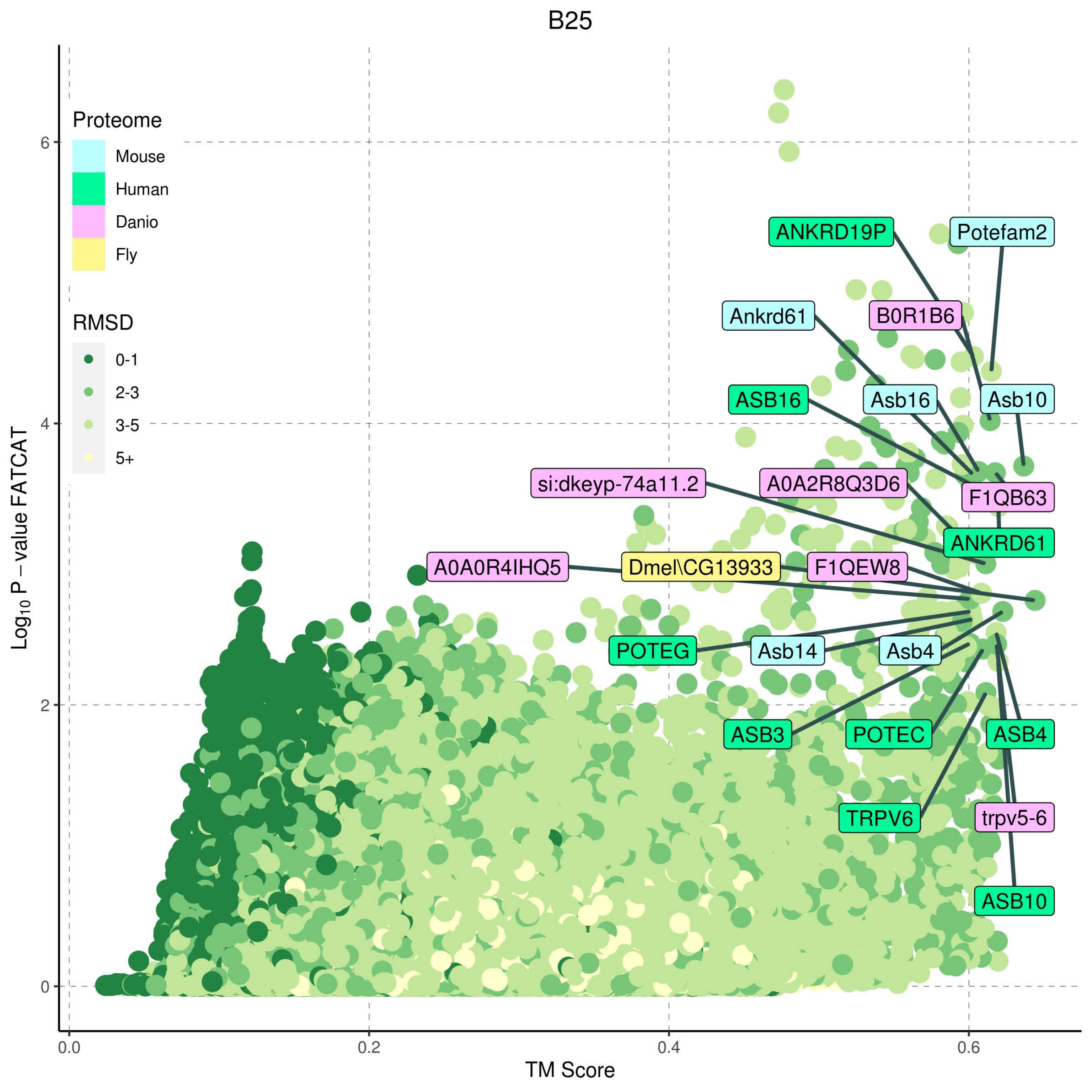

B20 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
A0A2R8QBT0
Ssxb6
COX5A
Cox5a
A0A2R8QJT9
Ada2a
Mpc2
Mpc1
MPC2
NOC2L
FRYL
Slco6d1
UTP20
Ctnnd1
Arfgef1
F1R7Q9
RNF213
DCLK
Log10 P − value FATCAT
2.0
1.5
1.0
0.5
0.0
0.1
0.2
0.3
0.4
0.5
TM Score

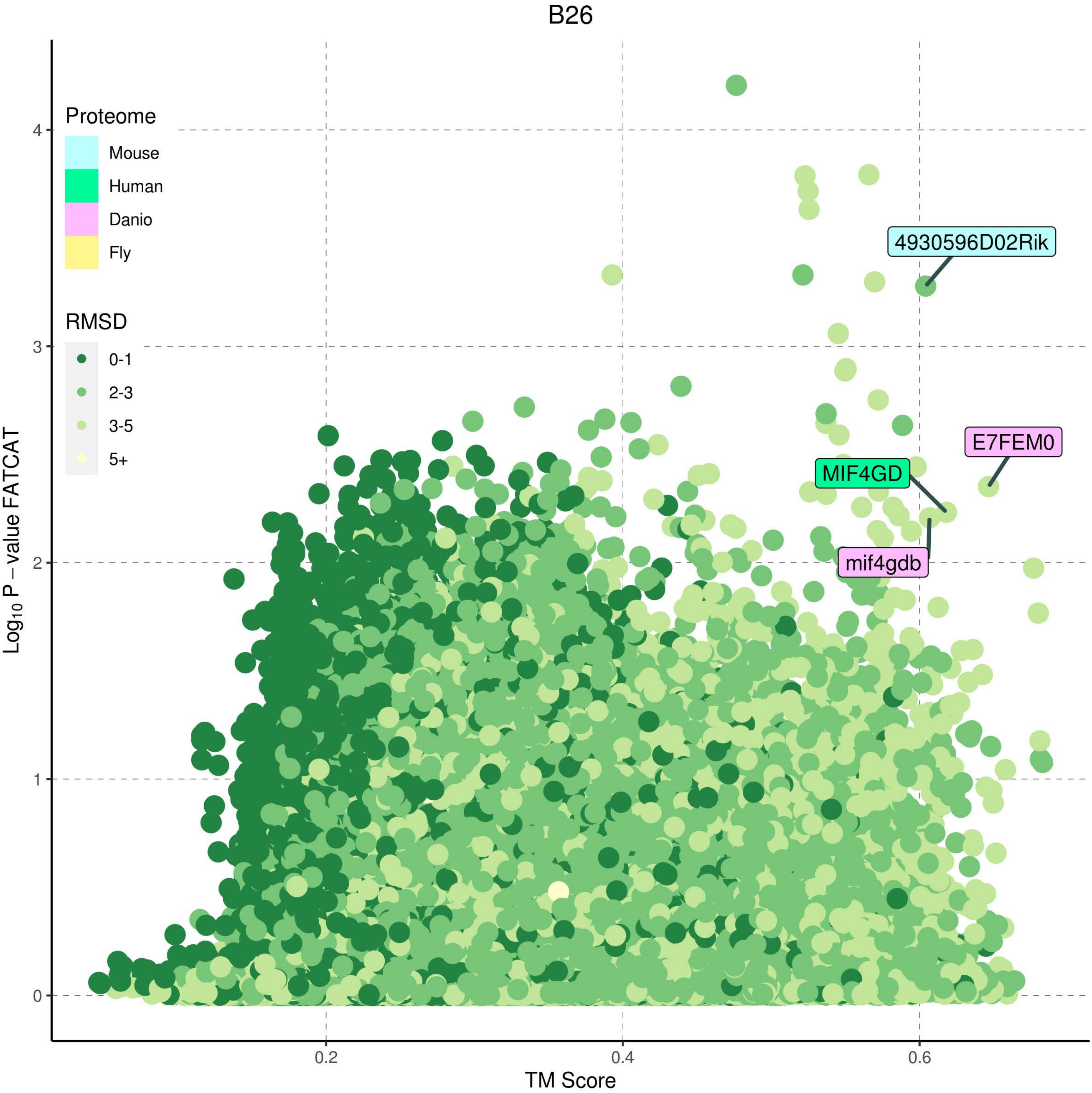

B21
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Ankrd37
si:ch211-165l2.2
Ankrd49
ANKRD66
F1RCG8
ANKRD49
Ankrd60
Log10 P − value FATCAT
3
2
1
0
0.2
0.4
0.6
TM Score

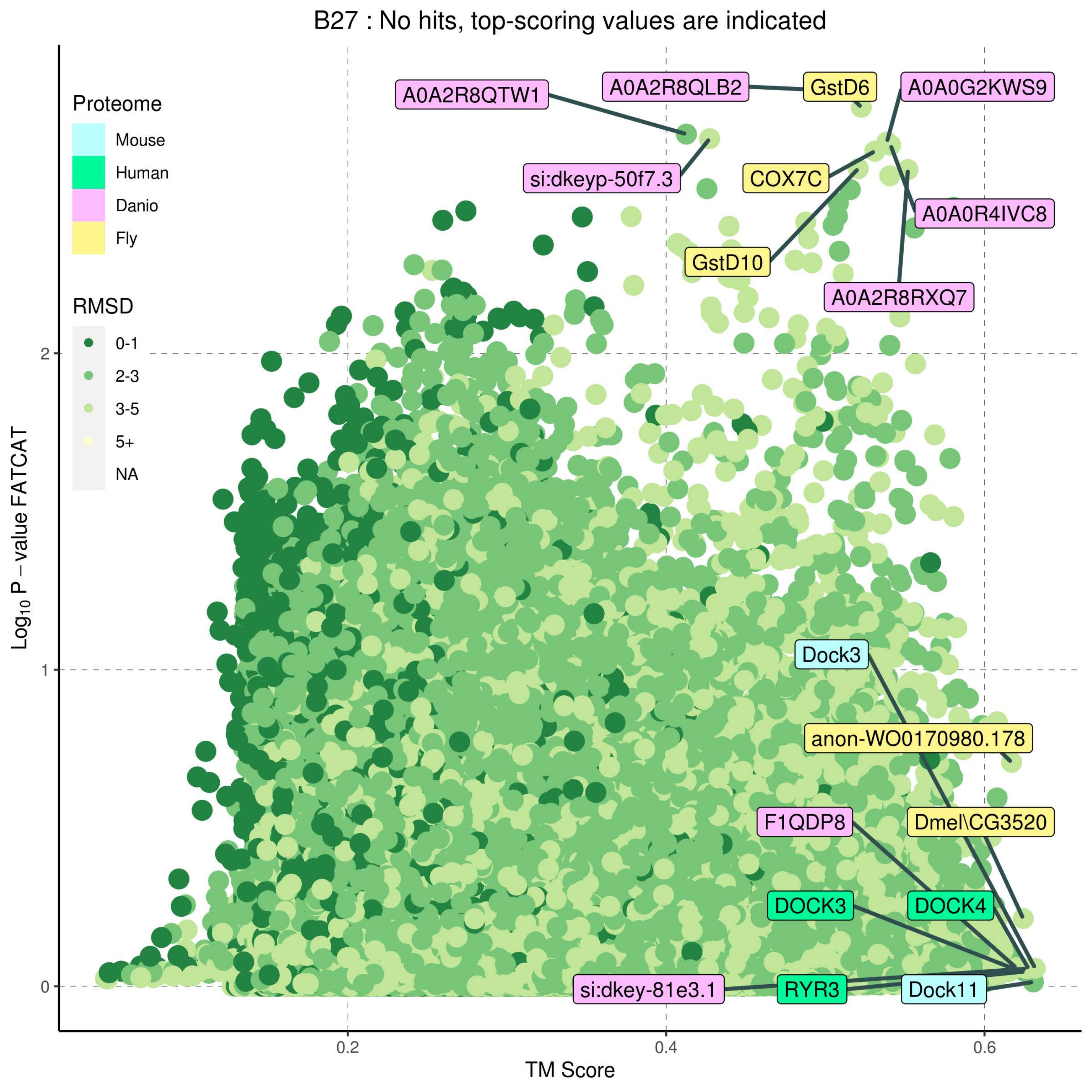

B22 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Bcl2a1
I3ITC2
D2Y5Q2
F1QTZ0
Bcl2a1b
boka
bokb
im:7148473
Bax
Bcl2l10
BCL2L10
A2BF68
BCL2L2
Bcl2l2
Q1L8X3
bcl2
Log_{10} P − value FATCAT
0
1
2
3
4
5
TM Score
0.1
0.2
0.3
0.4
0.5


B23
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log₁₀ P – value FATCAT
TM Score
0
2
4
6
0.0
0.2
0.4
0.6
Ankdd1b
Ankrd61
A0A0R4IHQ5
A0A14
si:ch211-203b8.6
A0A0R4IJP1
Asb16
B3DHM4
si:dkeyp-74a11.2
OR2A25
ASB4
F1QCR9
asb15a
ASB16
F1QBD5
Asb4
Pla2g6
ASB10
A0A2R8RYP7
ANKDD1A
F1Q5W6
A0A2R8PZ70
ASB3
F1QB63
Ankdd1a
ANKDD1B
Mib2
Asb18
ASB18
Asb10
Ripk4
asb15a
pyx
asb14b
Asb15
A0A0R4IA11
A0A286Y9U7
ANKK1
Dmel\CG13933
MIB1
Asb3
Asb14
ASB15
si:dkey-3n7.3
Mib1
Ankk1
Dmel\CG9121
MIB2
mib1
asb2a
Ankrd28
OR2A25
Asb2
HACE1
mib2
F1R1D9
hace1
Hace1
A0A2R8QS56
E9QBZ2
ASB2
ankrd52
Tnni3k
invs
wtrw
E7EXS2
Ankrd52
A0A0G2KXP0
INVS
Dapk1
TNNI3K
Trpa1
ANKRD44
Ankrd44
Invs
DAPK1

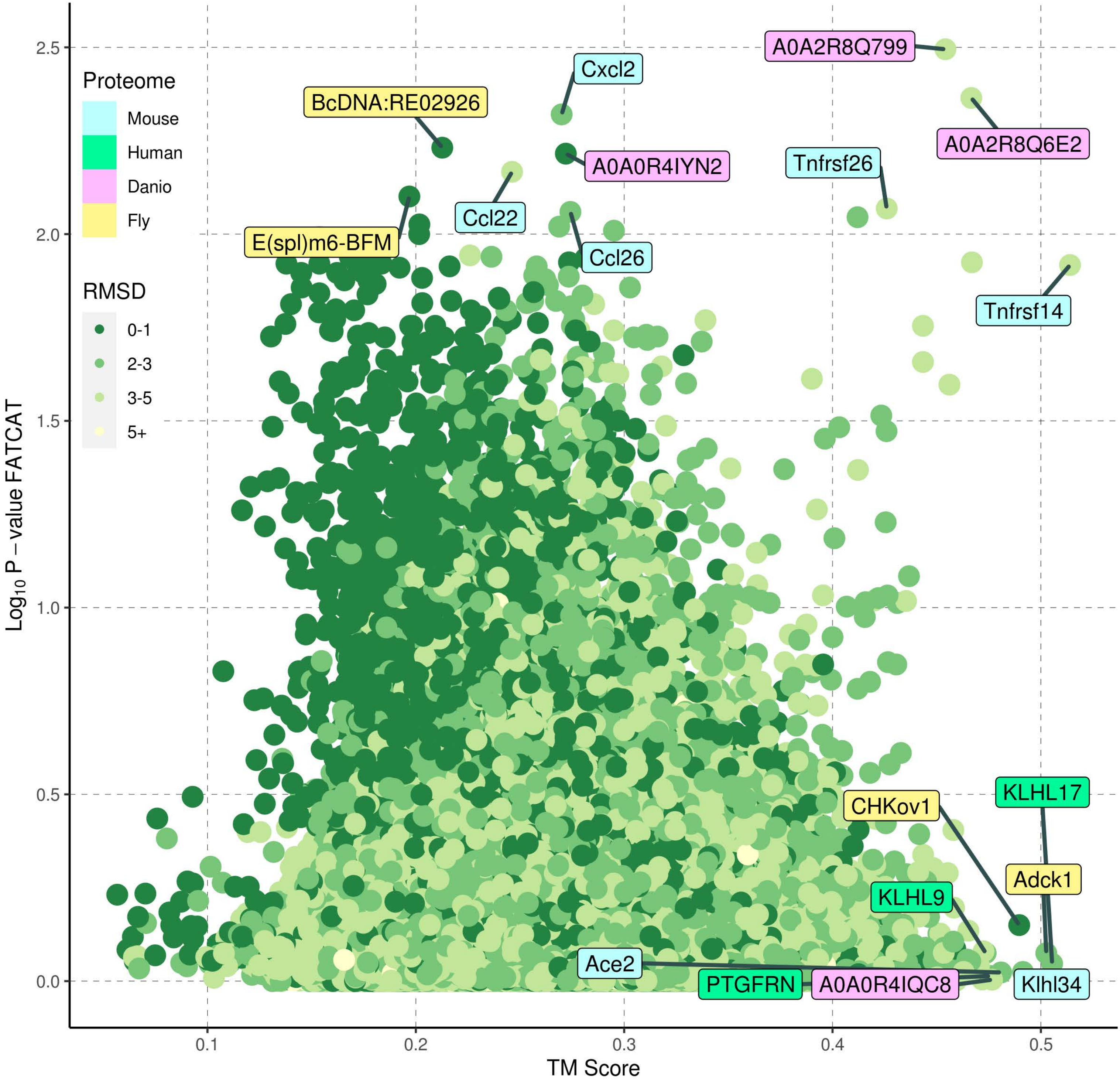

B24
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P − value FATCAT
TM Score
0
2
4
6
0.2
0.4
0.6
Dmel\CG5846
mtpn
Rfxank
Ankrd39
ostf1
asb-a
Dmel\CG3104
CDKN2A
ASB8
ACBD6
ankrd29
Bcl3
ANKRD39
ANKRD16
Asb11
OSTF1
Ankrd22
ANKRD19P
gankyrin
Dmel\CG10809
ASB5
Cdkn2c
OR2A25
A2CEZ8
Asz1
Ankrd46
Ankrd23
ASB9
ASB13
NFKBID
X1WH77
acbd6
Psmd10
anox
Ankra2
Atg17
E9QC15
Asb5
ANKRD29
ANKRA2
E7F3W1
ANKRD49
Asb1
Nfkbid
ankrd45
F1RCG8
Ankrd7
ANKRD7
ASB7
Asb12
ASZ1
Ankrd50
ankrd34c
zgc:64033
Ankrd49
ANKRD23
Asb18
Potefam2
asb5
ANKRD2
E9QDL8
ANKRD42
Ankrd63
A2BGQ0
Ankrd34c
ankrd54
ASB10
F1QEW8
E7FEM0
Nfkbia
ANKRD46
ANKRD54
Potefam3b
Potefam3a
Asb16
F1QQ98
Asb8
ASB18
Ankrd1
ANKRD65
Ankrd65
Asb4
ASB4
ANKRD45
ANKLE1
F1QB63
A0A0R4IHQ5
ankrd46
ANKRD10
A0A0R4IJP1
ASB1
Asb7
ANKRD1
Ppp1r16a
flip
Ankrd10
Trpv3
GABPB2
Fank1
Ankrd61
Ankrd33
ASB3
ASB17
ANKRD9
A5WV38
ILK
ASB16
PPP1R16A
Gabpb2
B0S6J8
Poteg
FANK1
PPP1R16B
PPP1R13L
Ush1g
Potefam1
Potegl
Ilk
POTED
NFKB2
ANKS4B
Asb6
Dmel\CG8003
Nfkb1
ANKRD55
RNASEL
F1QBD5
si:dkey-3n7.3
Ankdd1a
NFKBIZ
Ppp1r13l
Ankrd55
Sowahd
ASB12
ASB2
Nfkb2

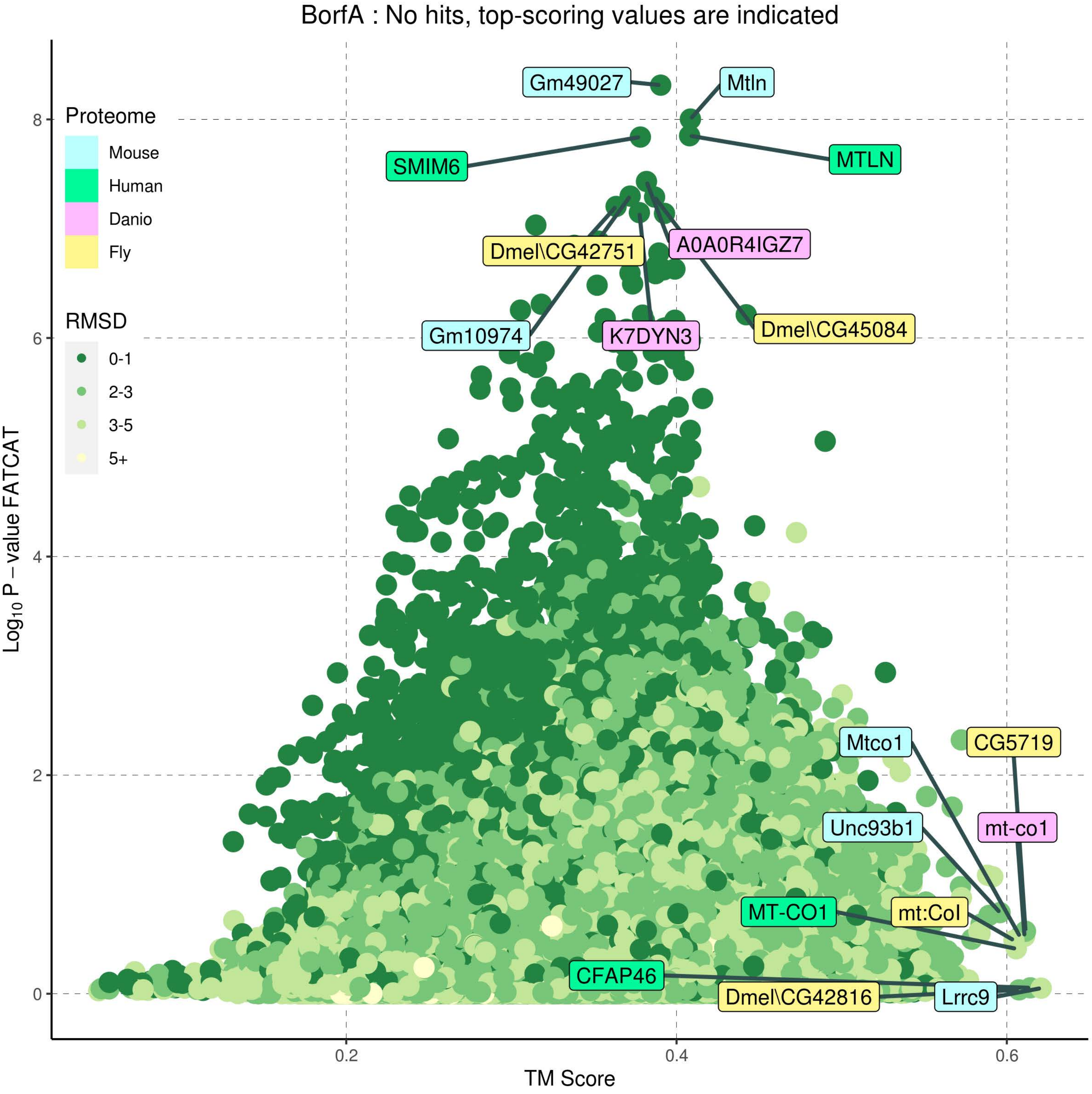

B25
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
ANKRD19P
Potefam2
Ankrd61
B0R1B6
ASB16
Asb16
Asb10
si:dkeyp-74a11.2
A0A2R8Q3D6
F1QB63
ANKRD61
A0A0R4IHQ5
Dmel\CG13933
F1QEW8
POTEG
Asb14
Asb4
ASB3
POTEC
ASB4
TRPV6
trpv5-6
ASB10
Log₁₀ P − value FATCAT
6
4
2
0
0.0
0.2
0.4
0.6
TM Score

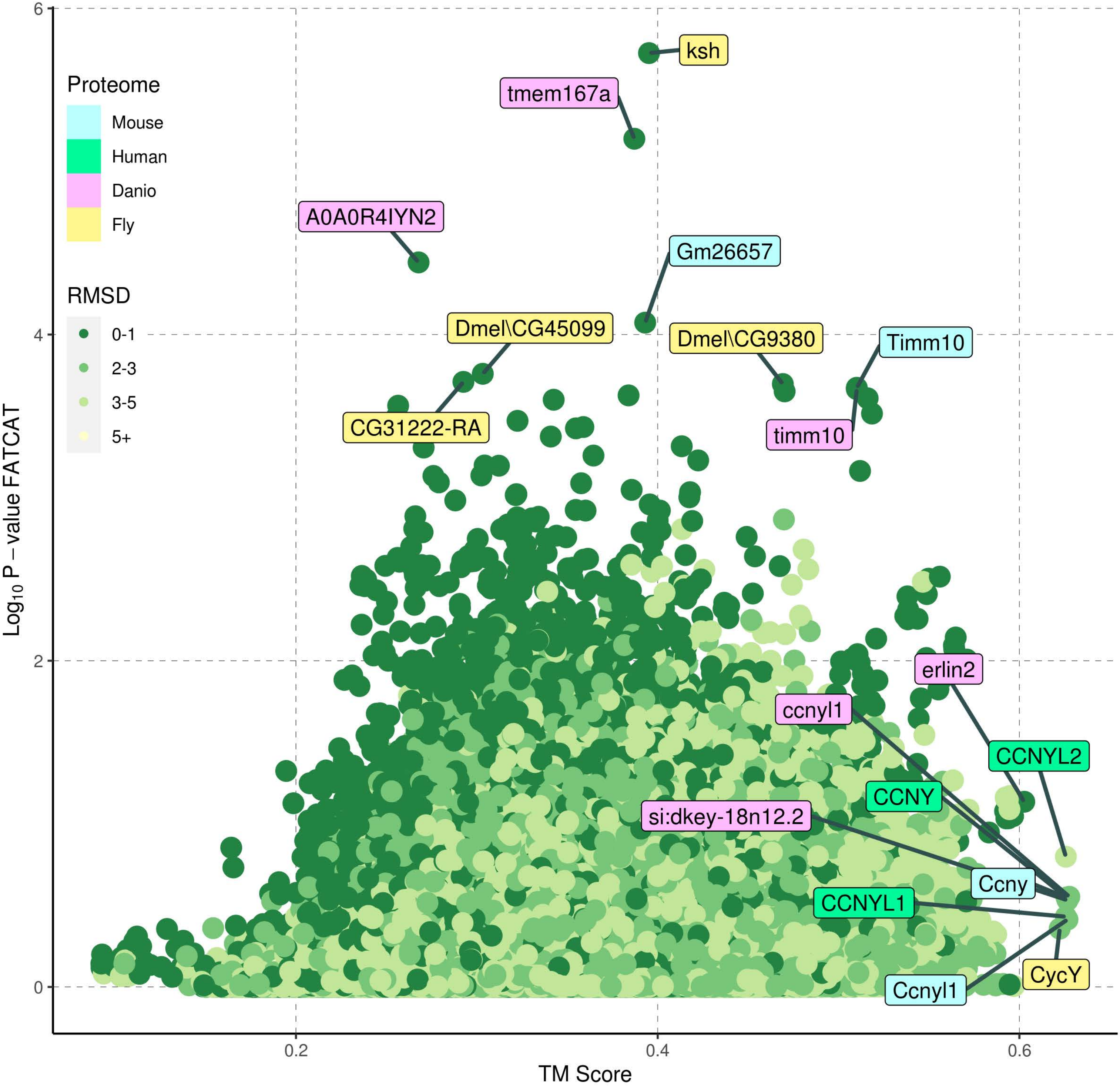

B26
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
4930596D02Rik
E7FEM0
MIF4GD
mif4gdb
Log₁₀ P − value FATCAT
0
1
2
3
4
0.2
0.4
0.6
TM Score


B27 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
NA
A0A2R8QTW1
A0A2R8QLB2
GstD6
A0A0G2KWS9
si:dkeyp-50f7.3
COX7C
A0A0R4IVC8
GstD10
A0A2R8RXQ7
Dock3
anon-WO0170980.178
F1QDP8
Dmel\CG3520
DOCK3
DOCK4
si:dkey-81e3.1
RYR3
Dock11
Log_{10} P – value FATCAT
2
1
0
TM Score
0.2
0.4
0.6

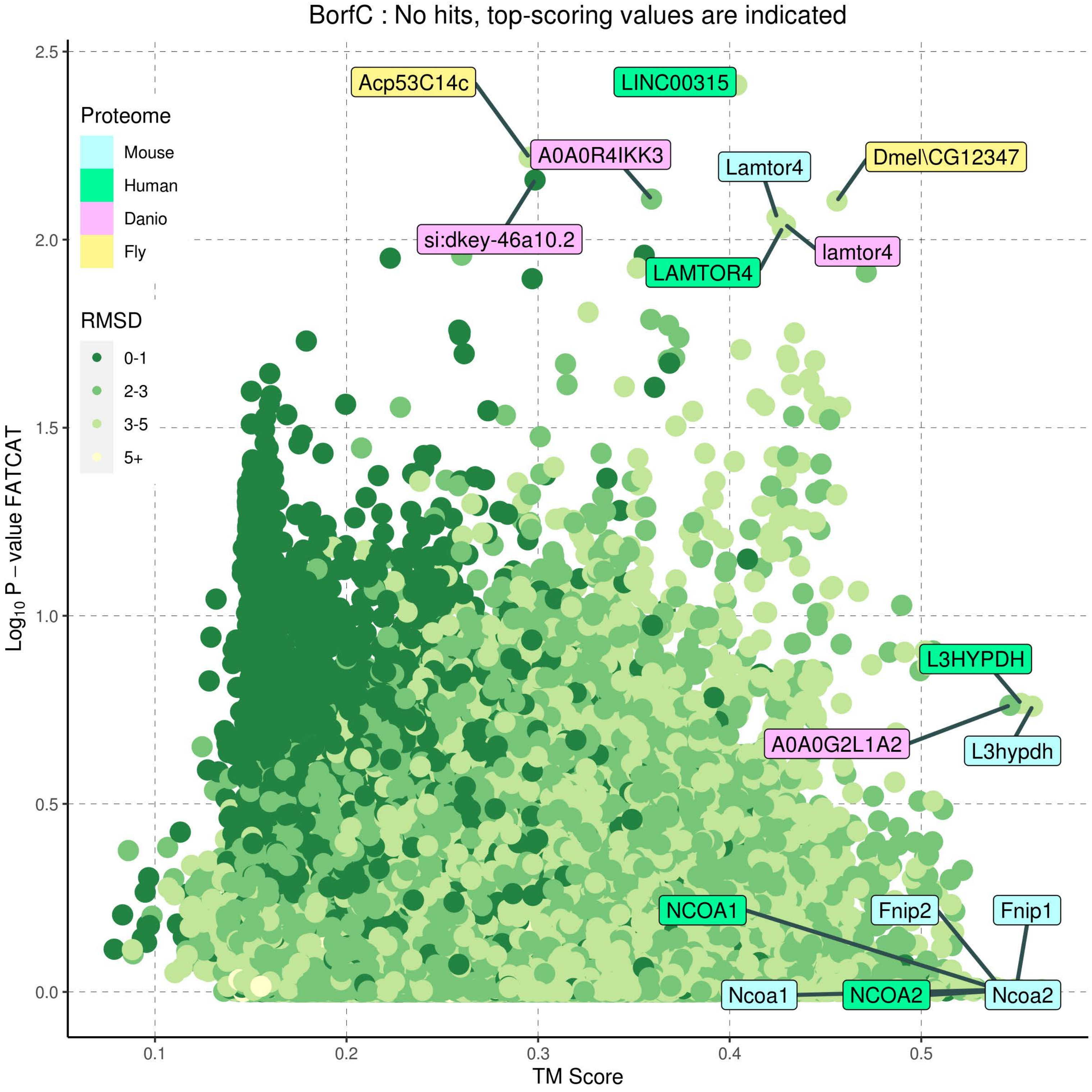
B28 : No hits, top-scoring values are indicated

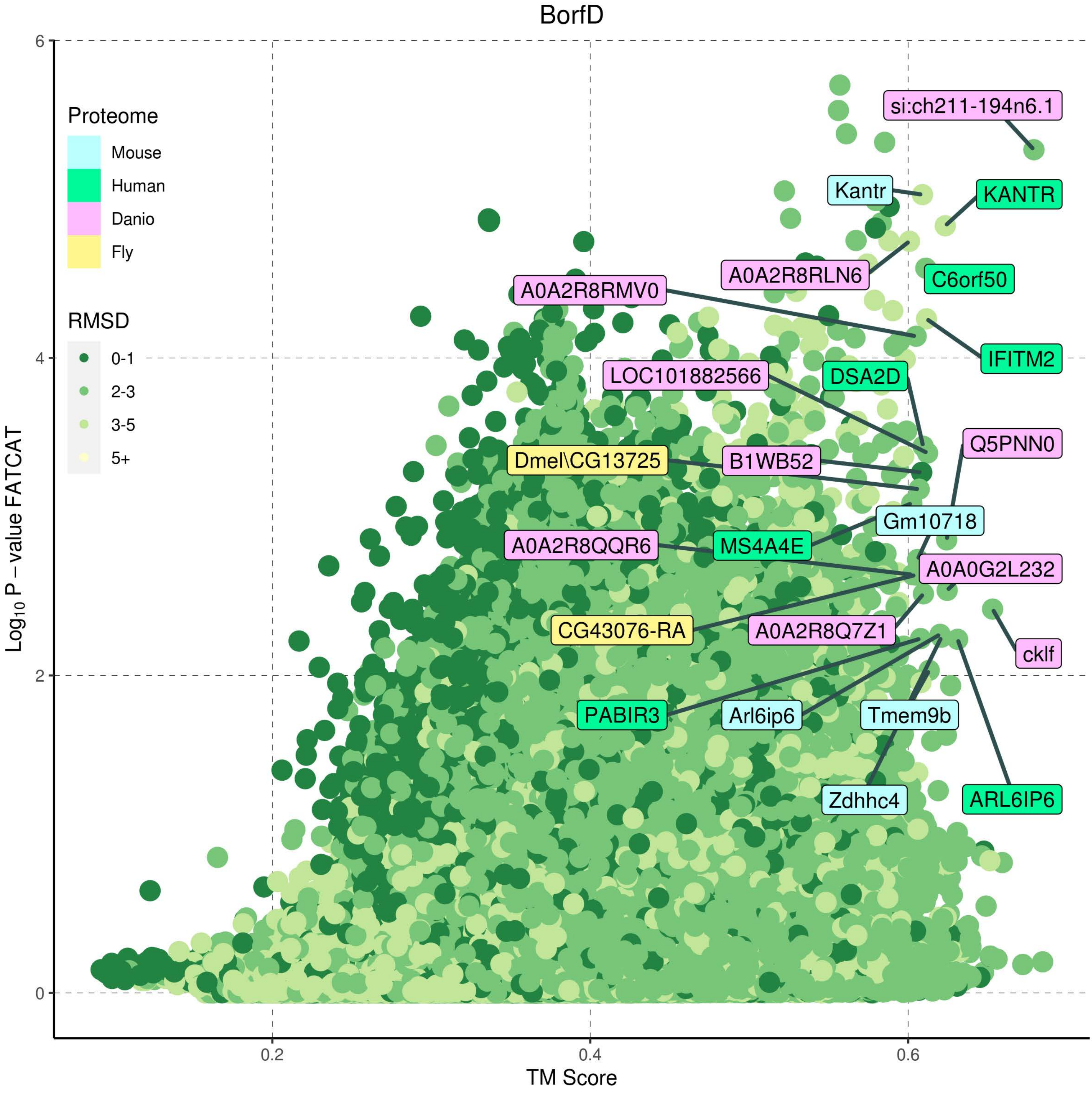


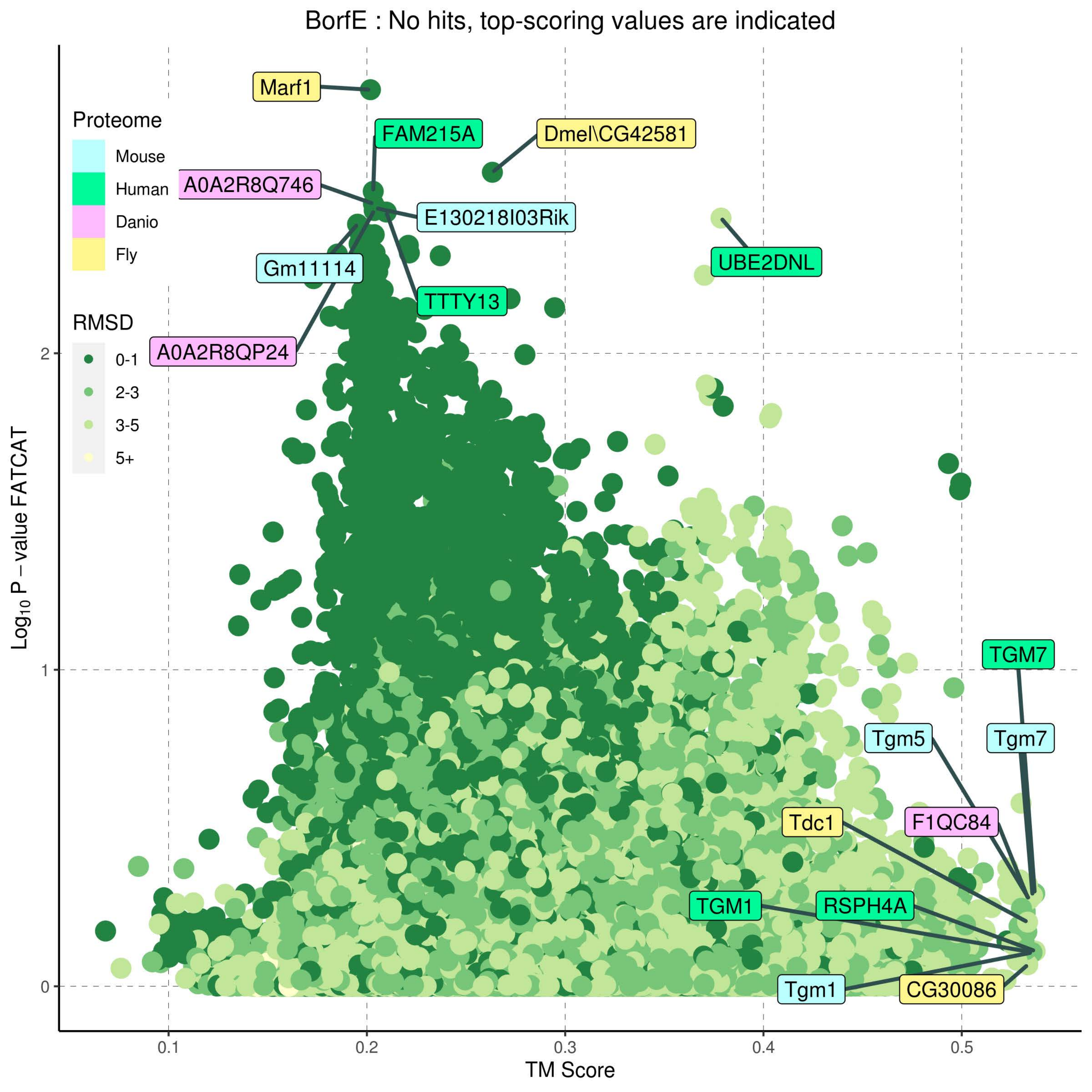

BorfA : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log₁₀ P − value FATCAT
TM Score
0
2
4
6
8
0.2
0.4
0.6
Gm49027
Mtln
SMIM6
MTLN
Dmel\CG42751
A0A0R4IGZ7
Gm10974
K7DYN3
Dmel\CG45084
Mtco1
CG5719
Unc93b1
mt-co1
MT-CO1
mt:CoI
CFAP46
Dmel\CG42816
Lrrc9

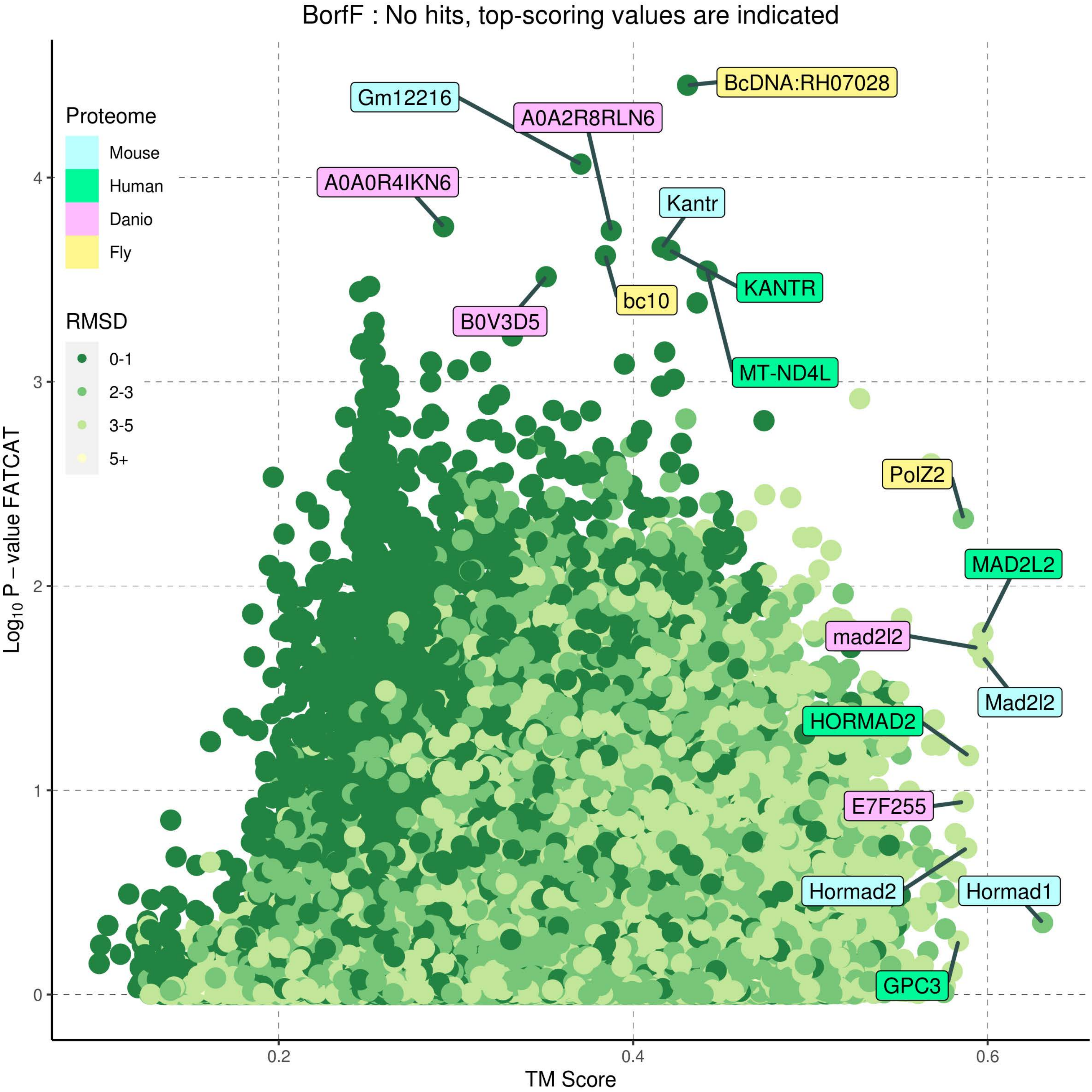


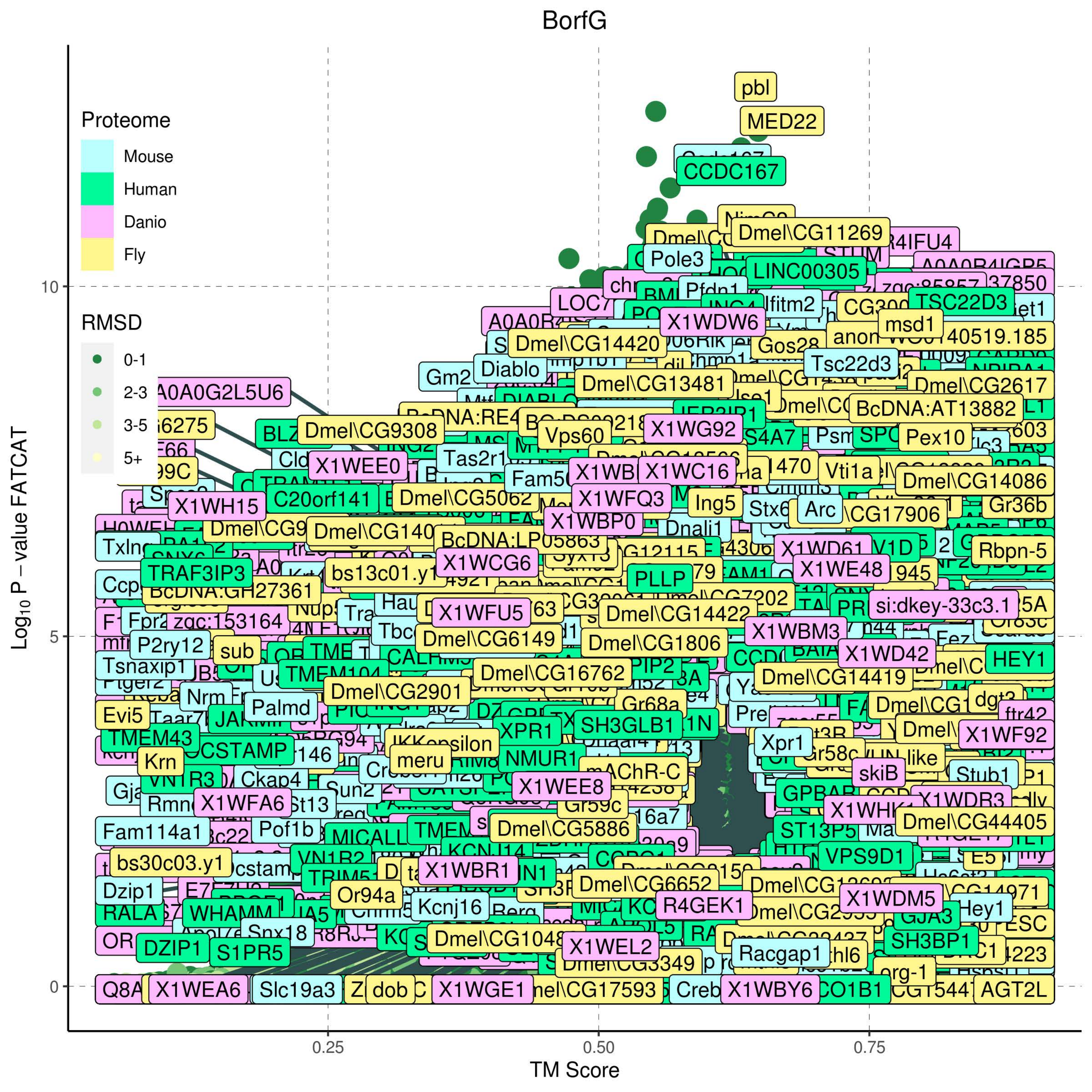
BorfB : No hits, top-scoring values are indicated

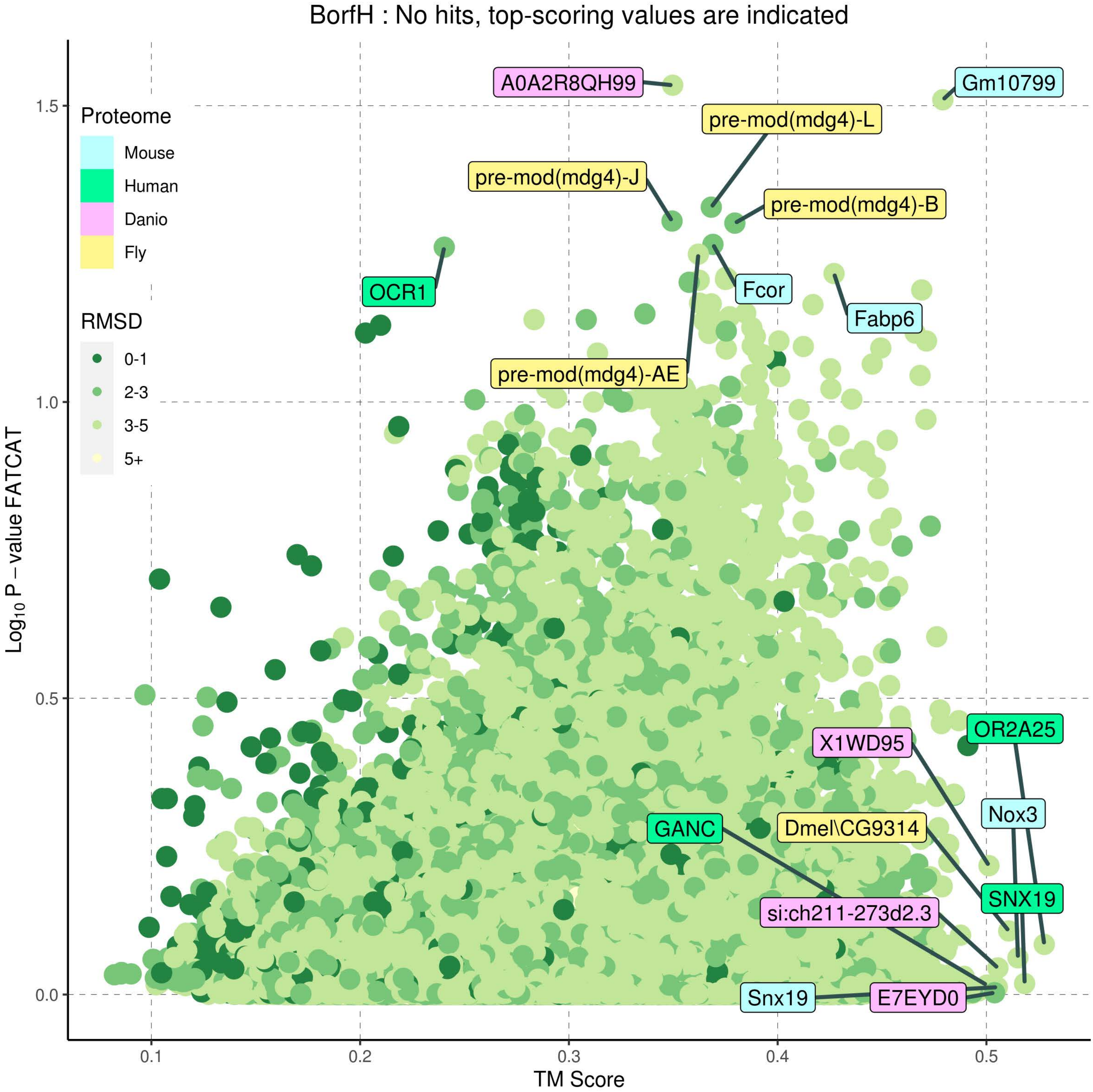

BorfC : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Acp53C14c
LINC00315
A0A0R4IKK3
Lamtor4
Dmel\CG12347
si:dkey-46a10.2
lamtor4
LAMTOR4
L3HYPDH
A0A0G2L1A2
L3hypdh
NCOA1
Fnip2
Fnip1
Ncoa1
NCOA2
Ncoa2
Log$_{10}$ P − value FATCAT
2.5
2.0
1.5
1.0
0.5
0.0
TM Score
0.1
0.2
0.3
0.4
0.5

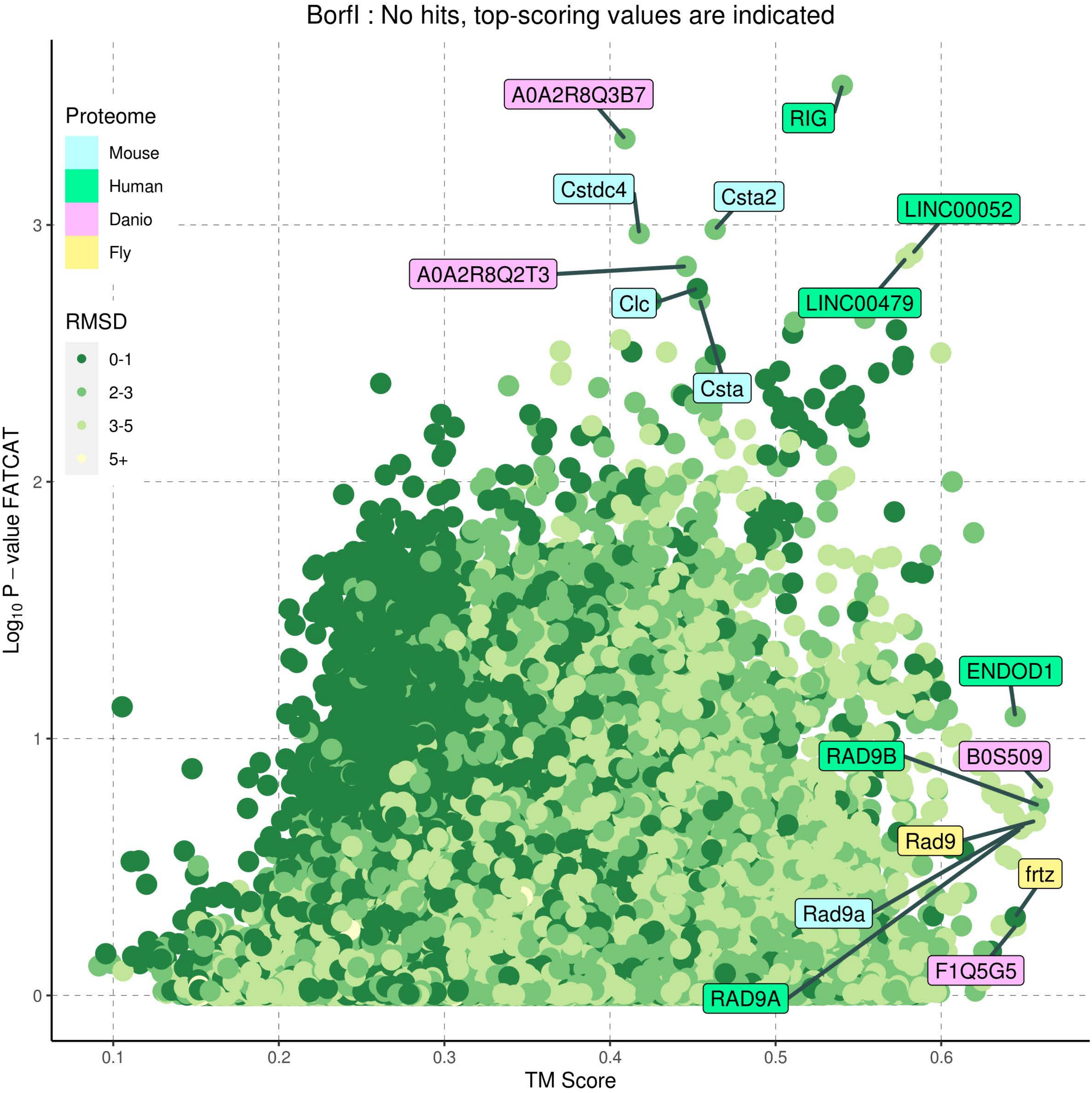

BorfD
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
si:ch211-194n6.1
Kantr
KANTR
A0A2R8RLN6
C6orf50
A0A2R8RMV0
IFITM2
LOC101882566
DSA2D
Q5PNN0
Dmel\CG13725
B1WB52
Gm10718
A0A2R8QQR6
MS4A4E
A0A0G2L232
CG43076-RA
A0A2R8Q7Z1
ckIf
PABIR3
Arl6ip6
Tmem9b
Zdhhc4
ARL6IP6
Log₁₀ P – value FATCAT
TM Score
0
2
4
6
0.2
0.4
0.6

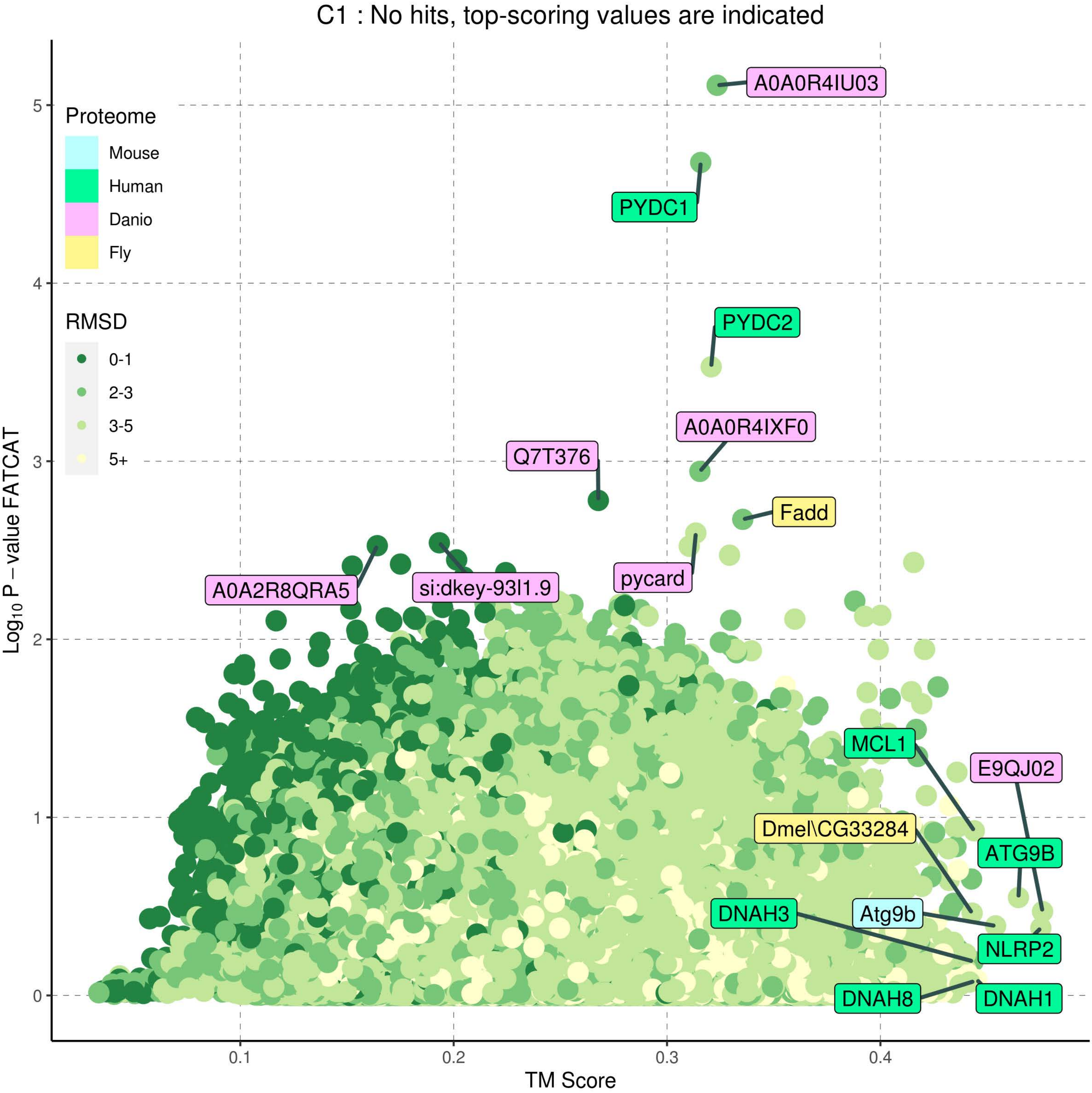

BorfE : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Marf1
FAM215A
Dmel\CG42581
A0A2R8Q746
E130218I03Rik
Gm11114
UBE2DNL
TTTY13
A0A2R8QP24
TGM7
Tgm5
Tgm7
Tdc1
F1QC84
TGM1
RSPH4A
Tgm1
CG30086
Log₁₀ P – value FATCAT
0
1
2
TM Score
0.1
0.2
0.3
0.4
0.5

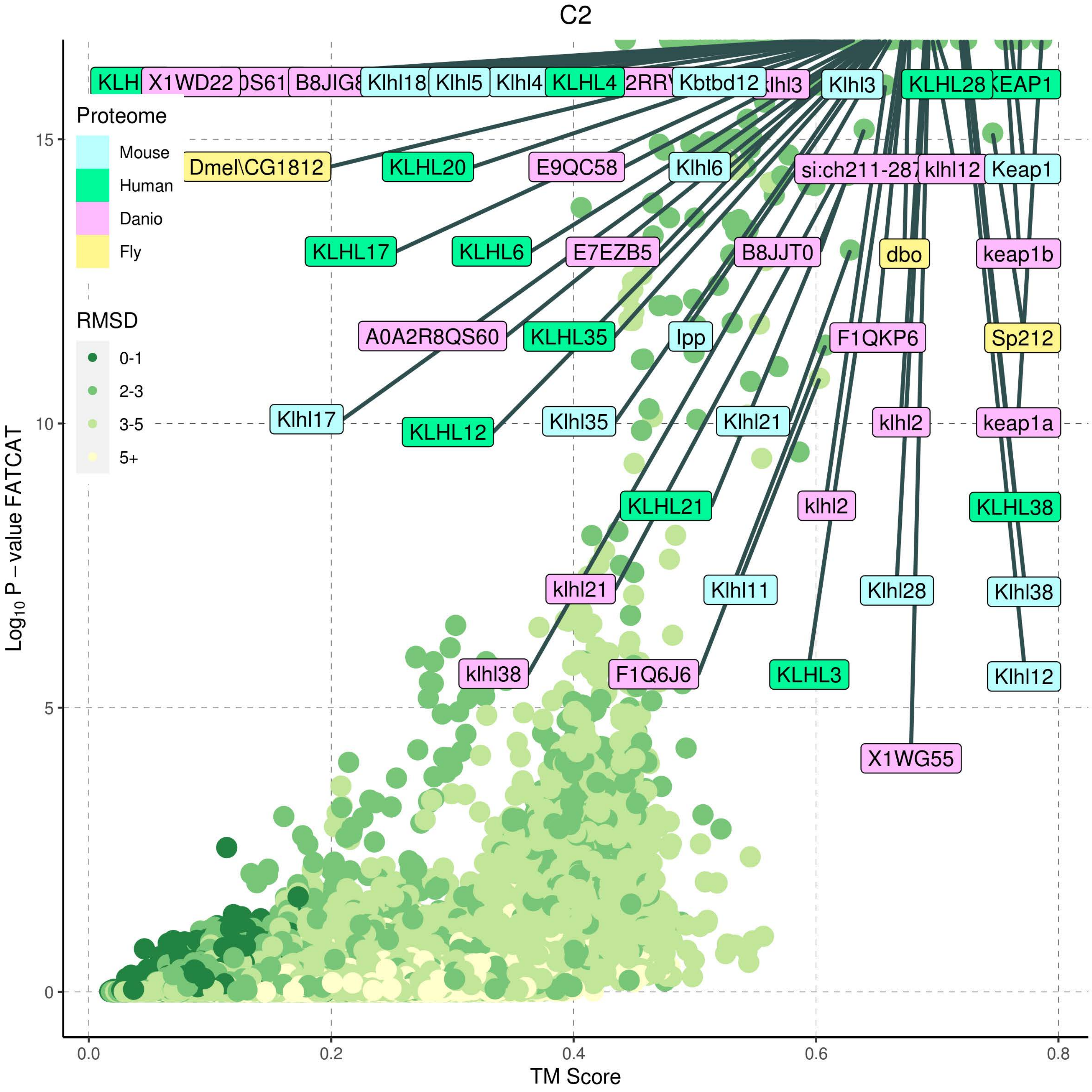

BorfF : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
BcDNA:RH07028
Gm12216
A0A2R8RLN6
A0A0R4IKN6
Kantr
KANTR
bc10
B0V3D5
MT-ND4L
PolZ2
MAD2L2
mad2l2
Mad2l2
HORMAD2
E7F255
Hormad2
Hormad1
GPC3
Log₁₀ P – value FATCAT
0
1
2
3
4
TM Score
0.2
0.4
0.6

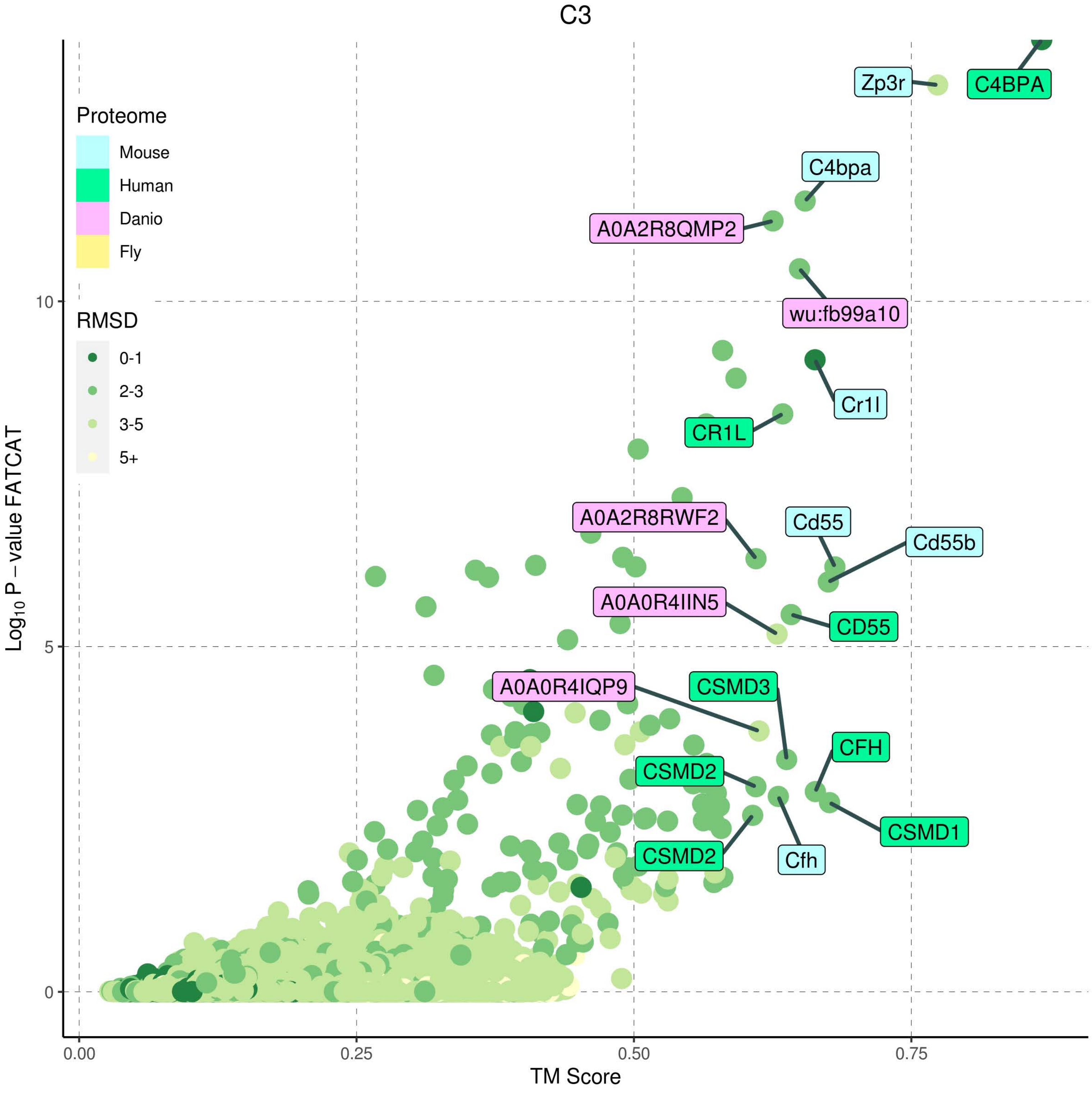

BorfG
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
TM Score
0
5
10
0.25
0.50
0.75
pbl
MED22
CCDC167
Dmel\CG11269
Pole3
LINC00305
Pfdn1
Ifitm2
TSC22D3
X1WDW6
msd1
Dmel\CG14420
Gos28
Tsc22d3
Diablo
Dmel\CG13481
Dmel\CG2617
BcDNA:AT13882
A0A0G2L5U6
Dmel\CG9308
X1WG92
Vps60
Pex10
X1WEE0
X1WC16
Vti1a
Dmel\CG14086
C20orf141
Dmel\CG5062
X1WFQ3
Ing5
Arc
Gr36b
X1WBP0
BcDNA:LP05863
X1WCG6
TRAF3IP3
bs13c01.y1
PLLP
X1WE48
Rbpn-5
zgc:153164
X1WFU5
Dmel\CG14422
si:dkey-33c3.1
P2ry12
sub
Dmel\CG6149
Dmel\CG1806
X1WBM3
X1WD42
HEY1
Tsnaxip1
Dmel\CG16762
Dmel\CG14419
Dmel\CG2901
Palmd
Evi5
SH3GLB1
XPR1
TMEM43
Xpr1
X1WF92
Krn
meru
NMUR1
mAChR-C
skiB
Stub1
Ckap4
X1WEE8
X1WFA6
GPBAR
X1WDR3
Pof1b
Dmel\CG5886
Dmel\CG44405
Fam114a1
ST13P5
bs30c03.y1
VPS9D1
X1WBR1
Dzip1
Dmel\CG6652
Or94a
Kcnj16
R4GEK1
X1WDM5
Hey1
RALA
WHAMM
Snx18
SH3BP1
DZIP1
S1PR5
X1WEL2
Racgap1
org-1
Q8A
X1WEA6
Slc19a3
dob
X1WGE1
X1WBY6
AGT2L

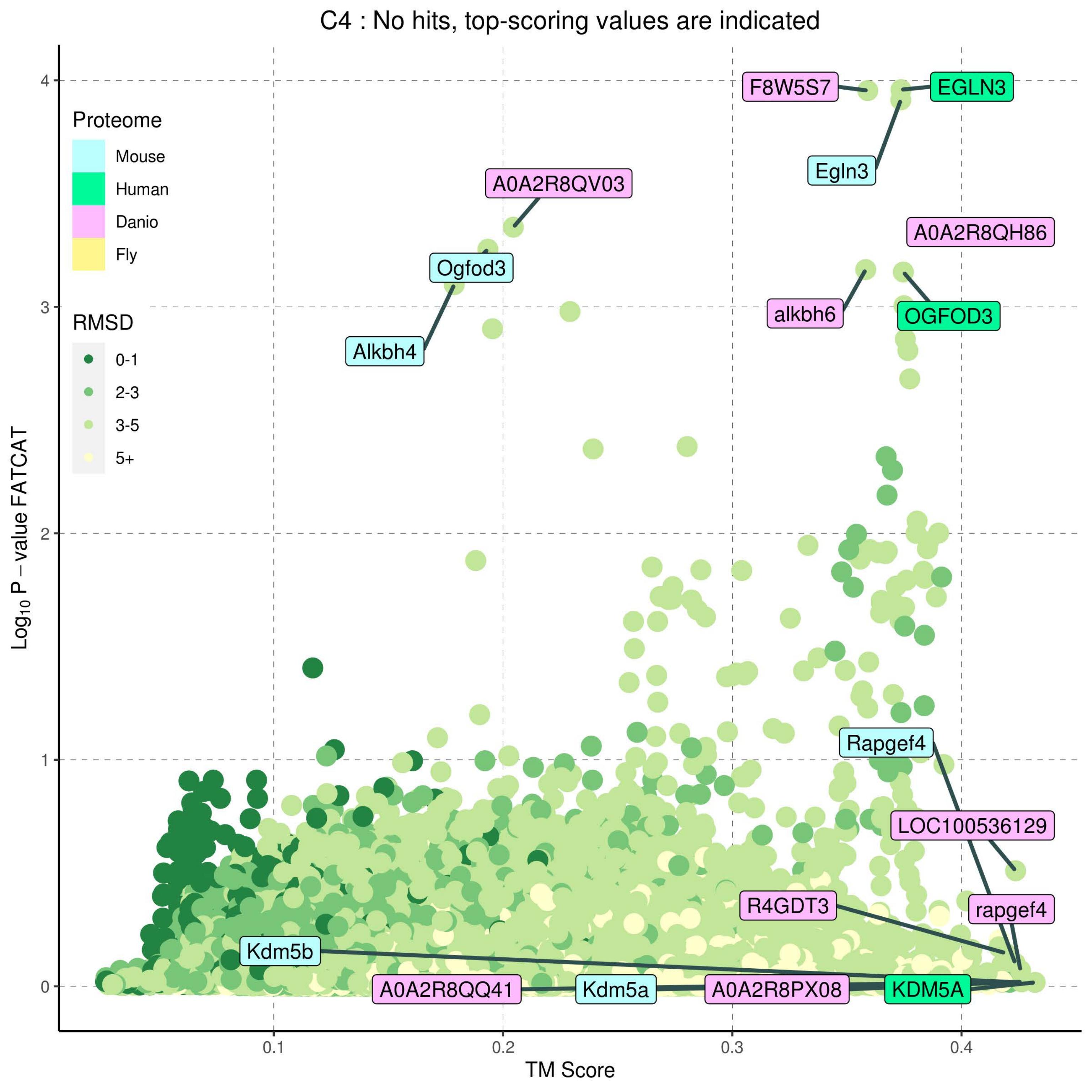

BorfH : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P − value FATCAT
TM Score
1.5
1.0
0.5
0.0
0.1
0.2
0.3
0.4
0.5
A0A2R8QH99
Gm10799
pre-mod(mdg4)-L
pre-mod(mdg4)-J
pre-mod(mdg4)-B
OCR1
Fcor
Fabp6
pre-mod(mdg4)-AE
OR2A25
X1WD95
Nox3
GANC
Dmel\CG9314
SNX19
si:ch211-273d2.3
Snx19
E7EYD0

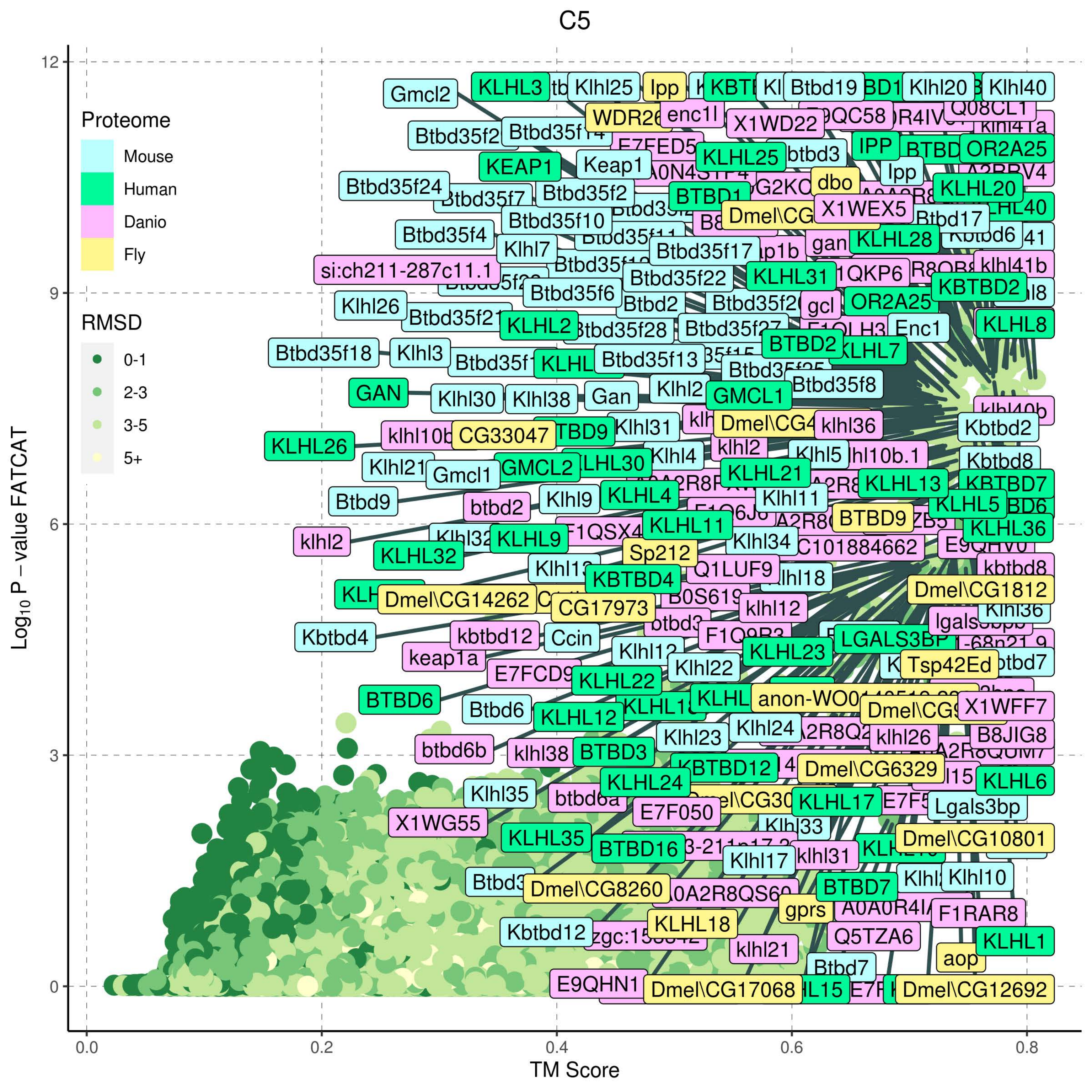

BorfI : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
A0A2R8Q3B7
RIG
Cstdc4
Csta2
LINC00052
A0A2R8Q2T3
Clc
LINC00479
Csta
ENDOD1
RAD9B
B0S509
Rad9
frtz
Rad9a
F1Q5G5
RAD9A
Log10 P − value FATCAT
0
1
2
3
TM Score
0.1
0.2
0.3
0.4
0.5
0.6

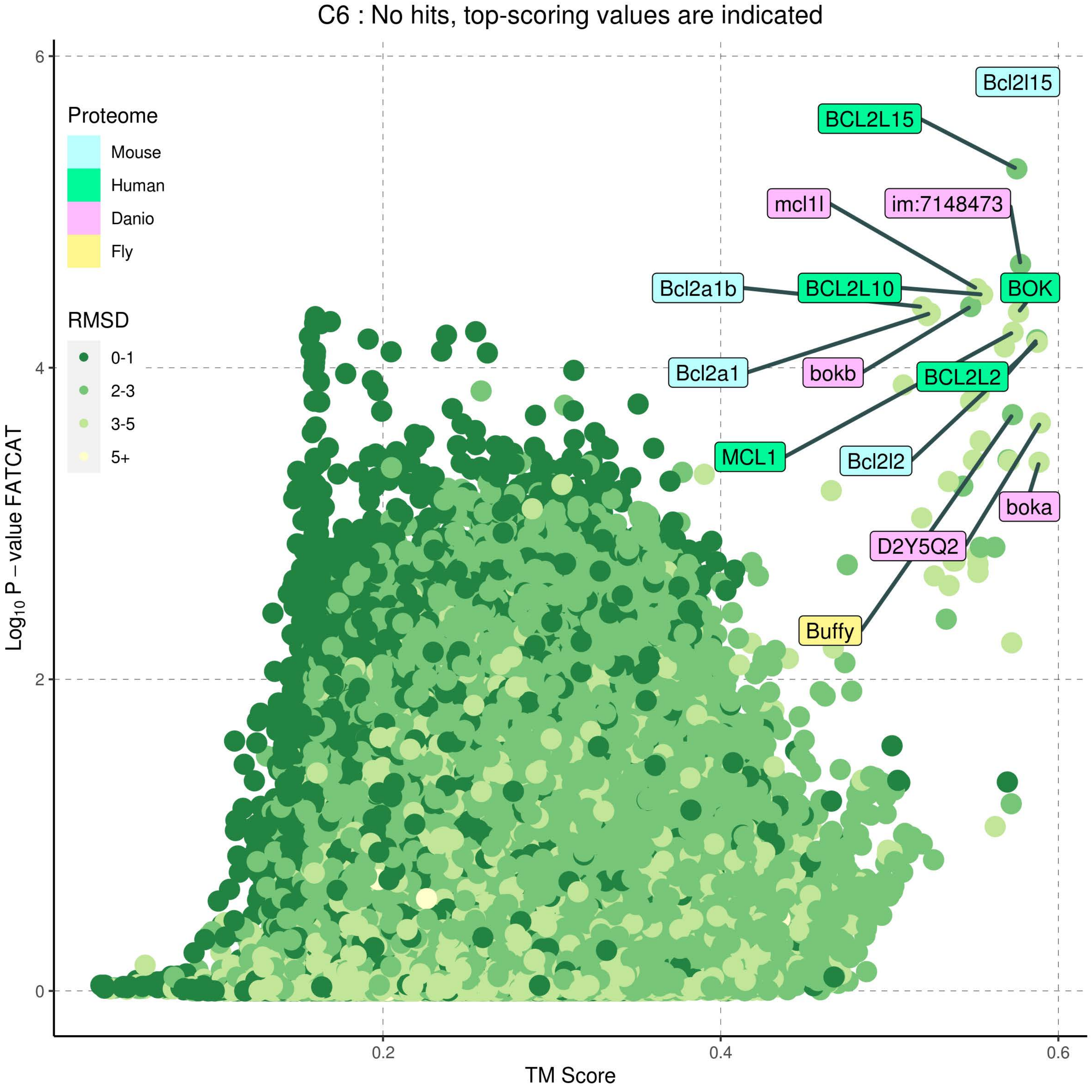

C1 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
A0A0R4IU03
PYDC1
PYDC2
A0A0R4IXF0
Q7T376
Fadd
pycard
A0A2R8QRA5
si:dkey-93l1.9
MCL1
E9QJ02
Dmel\CG33284
ATG9B
Atg9b
DNAH3
NLRP2
DNAH8
DNAH1
Log10 P – value FATCAT
0
1
2
3
4
5
TM Score
0.1
0.2
0.3
0.4

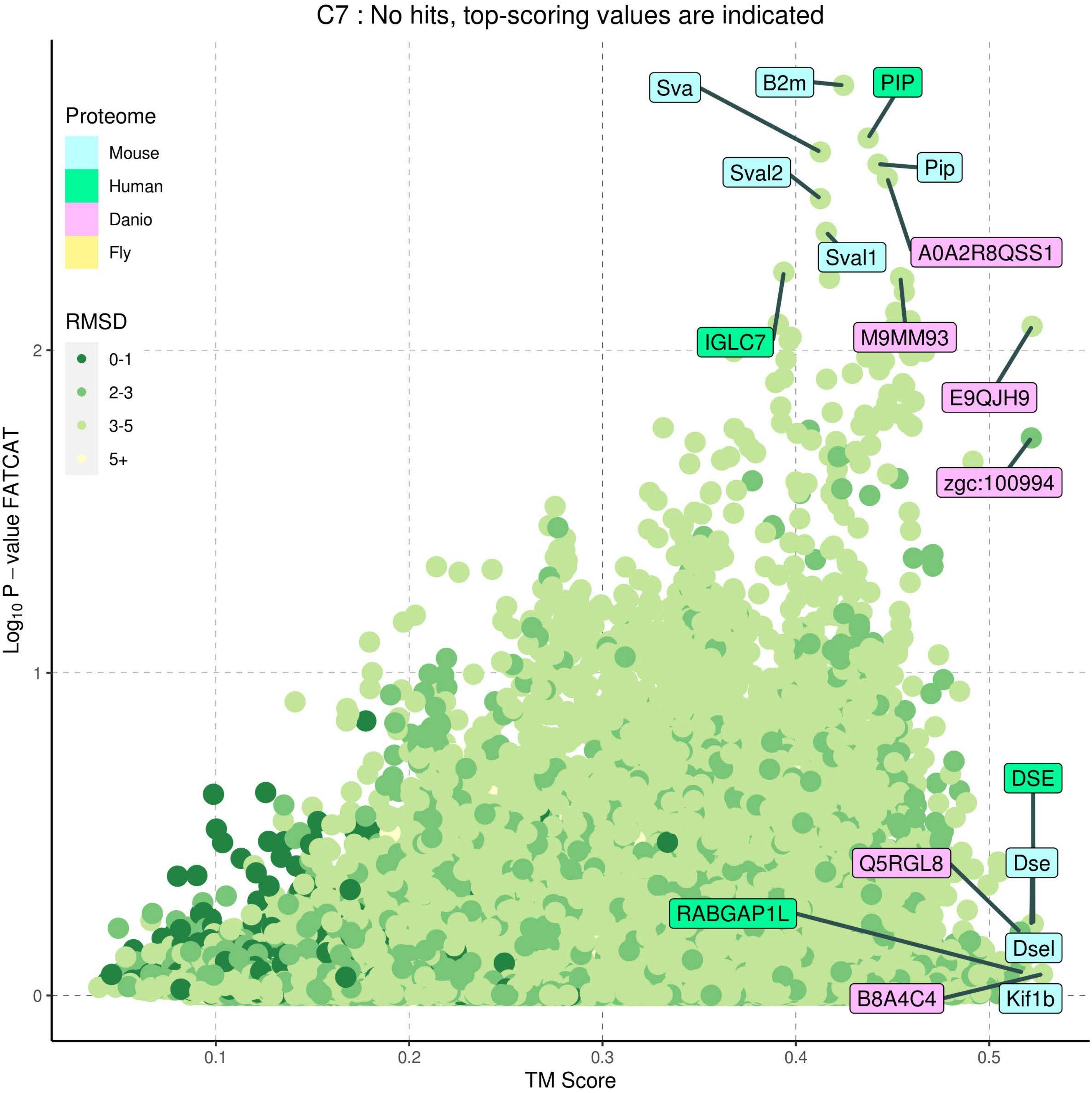

C2
KLH
X1WD22
0S61
B8JIG8
Klhl18
Klhl5
Klhl4
KLHL4
2RRY
Kbtbd12
klhl3
Klhl3
KLHL28
KEAP1
Proteome
Mouse
Human
Danio
Fly
Dmel\CG1812
KLHL20
E9QC58
Klhl6
si:ch211-287
klhl12
Keap1
KLHL17
KLHL6
E7EZB5
B8JJT0
dbo
keap1b
RMSD
0-1
2-3
3-5
5+
A0A2R8QS60
KLHL35
lpp
F1QKP6
Sp212
Klhl17
KLHL12
Klhl35
Klhl21
klhl2
keap1a
KLHL21
klhl2
KLHL38
klhl21
Klhl11
Klhl28
Klhl38
klhl38
F1Q6J6
KLHL3
Klhl12
X1WG55
15
10
5
0
0.0
0.2
0.4
0.6
0.8
Log_{10} P − value FATCAT
TM Score


C3
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log₁₀ P – value FATCAT
TM Score
0
5
10
0.00
0.25
0.50
0.75
Zp3r
C4BPA
C4bpa
A0A2R8QMP2
wu:fb99a10
Cr1l
CR1L
A0A2R8RWF2
Cd55
Cd55b
A0A0R4IIN5
CD55
A0A0R4IQP9
CSMD3
CFH
CSMD2
CSMD1
CSMD2
Cfh

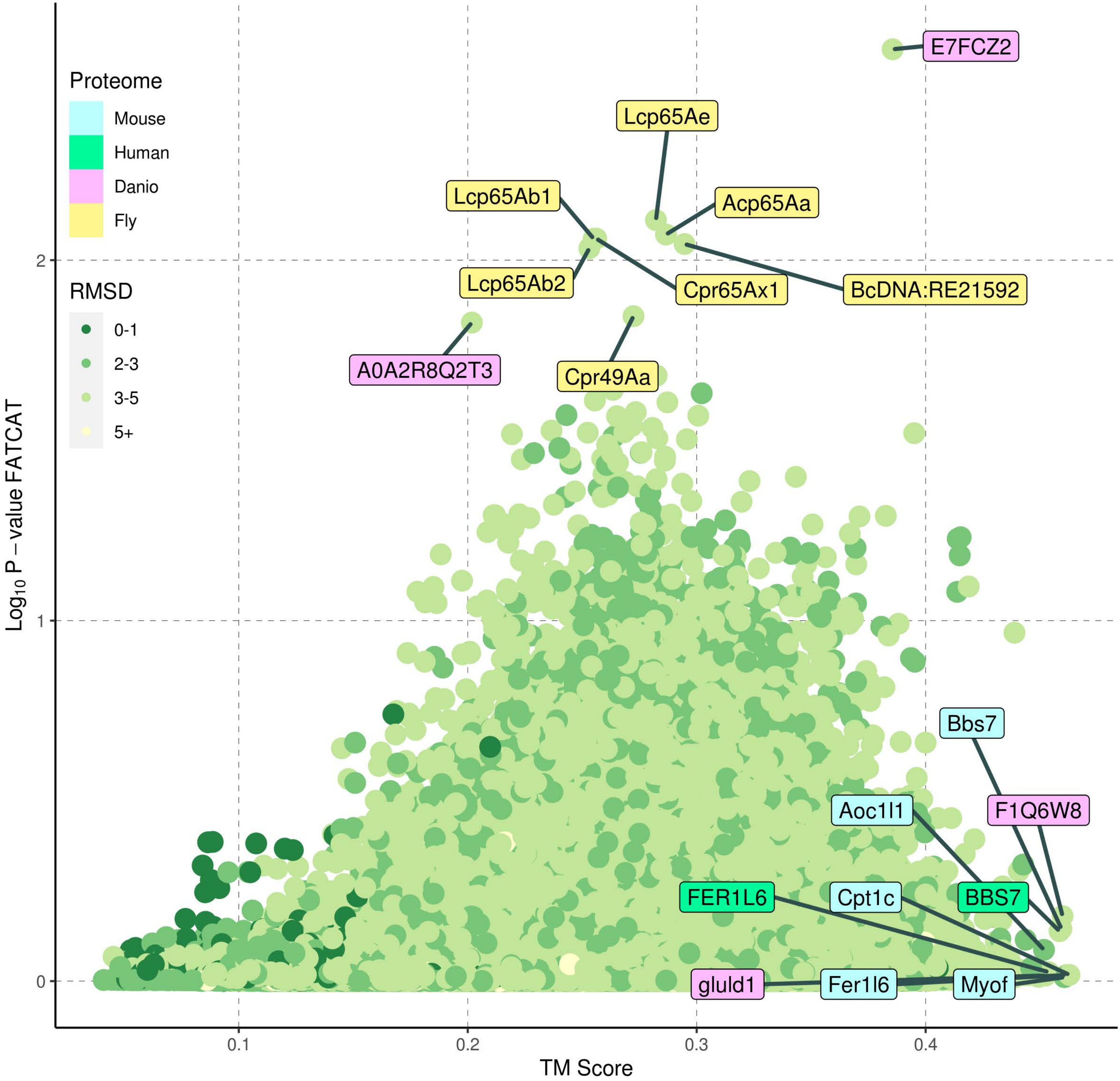

C4 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
F8W5S7
EGLN3
Egln3
A0A2R8QV03
A0A2R8QH86
Ogfod3
alkbh6
OGFOD3
Alkbh4
Rapgef4
LOC100536129
R4GDT3
rapgef4
Kdm5b
A0A2R8QQ41
Kdm5a
A0A2R8PX08
KDM5A
Log10 P − value FATCAT
TM Score
0
1
2
3
4
0.1
0.2
0.3
0.4

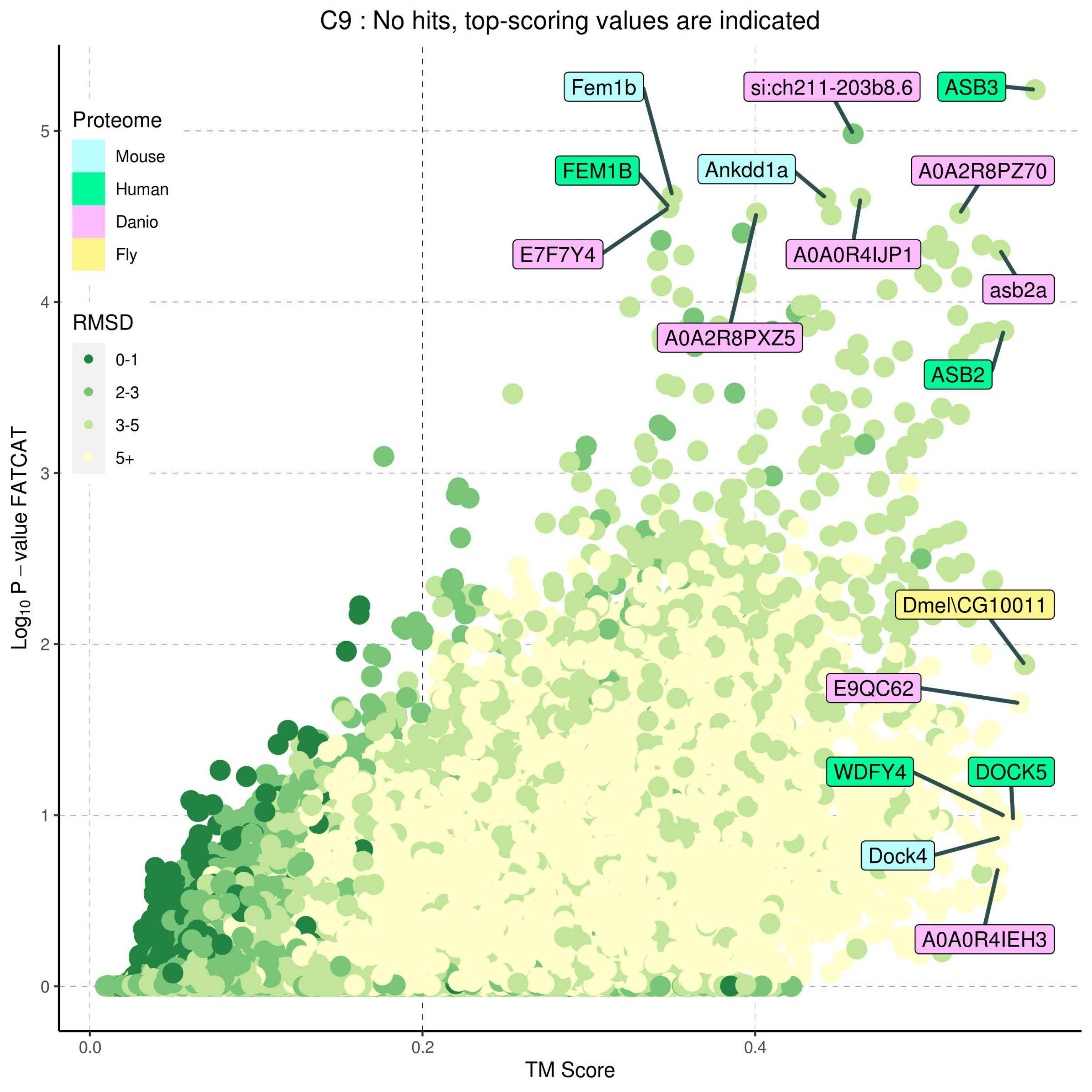

C5
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P − value FATCAT
TM Score
0.0
0.2
0.4
0.6
0.8
0
3
6
9
12
Gmcl2
KLHL3
Klhl25
Ipp
Btbd19
Klhl20
Klhl40
WDR26
enc1l
X1WD22
Q08CL1
Btbd35f2
Btbd35f14
E7FED5
KLHL25
btbd3
IPP
OR2A25
KEAP1
Keap1
Ipp
Btbd35f24
Btbd35f7
Btbd35f2
BTBD1
dbo
KLHL20
Btbd35f10
X1WEX5
Btbd17
Btbd35f4
Klhl7
gan
KLHL28
Btbd35f17
si:ch211-287c11.1
Btbd35f22
KLHL31
klhl41b
KBTBD2
Btbd35f6
Klhl26
Btbd2
gcl
OR2A25
Btbd35f21
KLHL2
Btbd35f28
Enc1
KLHL8
Btbd35f18
Klhl3
BTBD2
KLHL7
Btbd35f13
Btbd35f8
GAN
Klhl30
Klhl38
Gan
Klhl2
GMCL1
klhl40b
klhl10b
CG33047
Klhl31
klhl36
Kbtbd2
KLHL26
klhl2
Klhl5
Kbtbd8
Klhl21
Gmcl1
GMCL2
KLHL30
Klhl4
KLHL21
KLHL13
KBTBD7
Btbd9
btbd2
Klhl9
KLHL4
Klhl11
BTBD9
KLHL5
klhl2
KLHL9
KLHL11
KLHL36
KLHL32
Klhl34
Sp212
Q1LUF9
kbtbd8
KBTBD4
Dmel\CG1812
Dmel\CG14262
CG17973
klhl12
Klhl36
Kbtbd4
kbtbd12
Ccin
LGALS3BP
keap1a
E7FCD9
Klhl22
KLHL23
Tsp42Ed
KLHL22
BTBD6
Btbd6
KLHL12
X1WFF7
btbd6b
klhl38
BTBD3
Klhl23
Klhl24
klhl26
B8JIG8
KBTBD12
Dmel\CG6329
KLHL24
KLHL6
Klhl35
btbd6a
E7F050
KLHL17
Lgals3bp
X1WG55
Klhl33
KLHL35
BTBD16
Klhl17
klhl31
Dmel\CG10801
Dmel\CG8260
BTBD7
Klhl10
gprs
F1RAR8
Kbtbd12
KLHL18
Q5TZA6
klhl21
KLHL1
aop
Btbd7
E9QHN1
Dmel\CG17068
Dmel\CG12692

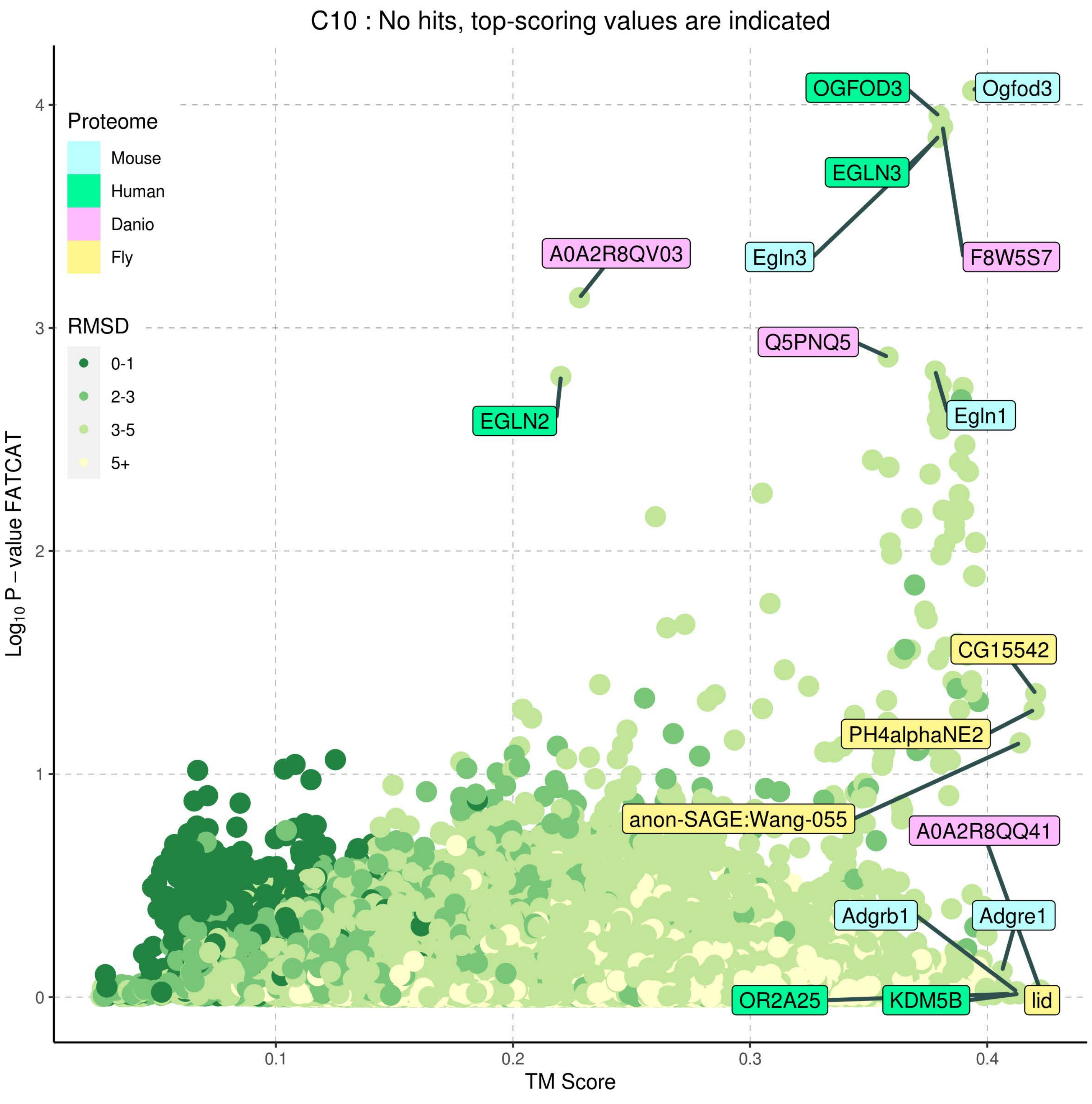

C6 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Bcl2l15
BCL2L15
mcl1l
im:7148473
Bcl2a1b
BCL2L10
BOK
Bcl2a1
bokb
BCL2L2
MCL1
Bcl2l2
boka
D2Y5Q2
Buffy
6
4
2
0
0.2
0.4
0.6
Log10 P − value FATCAT
TM Score

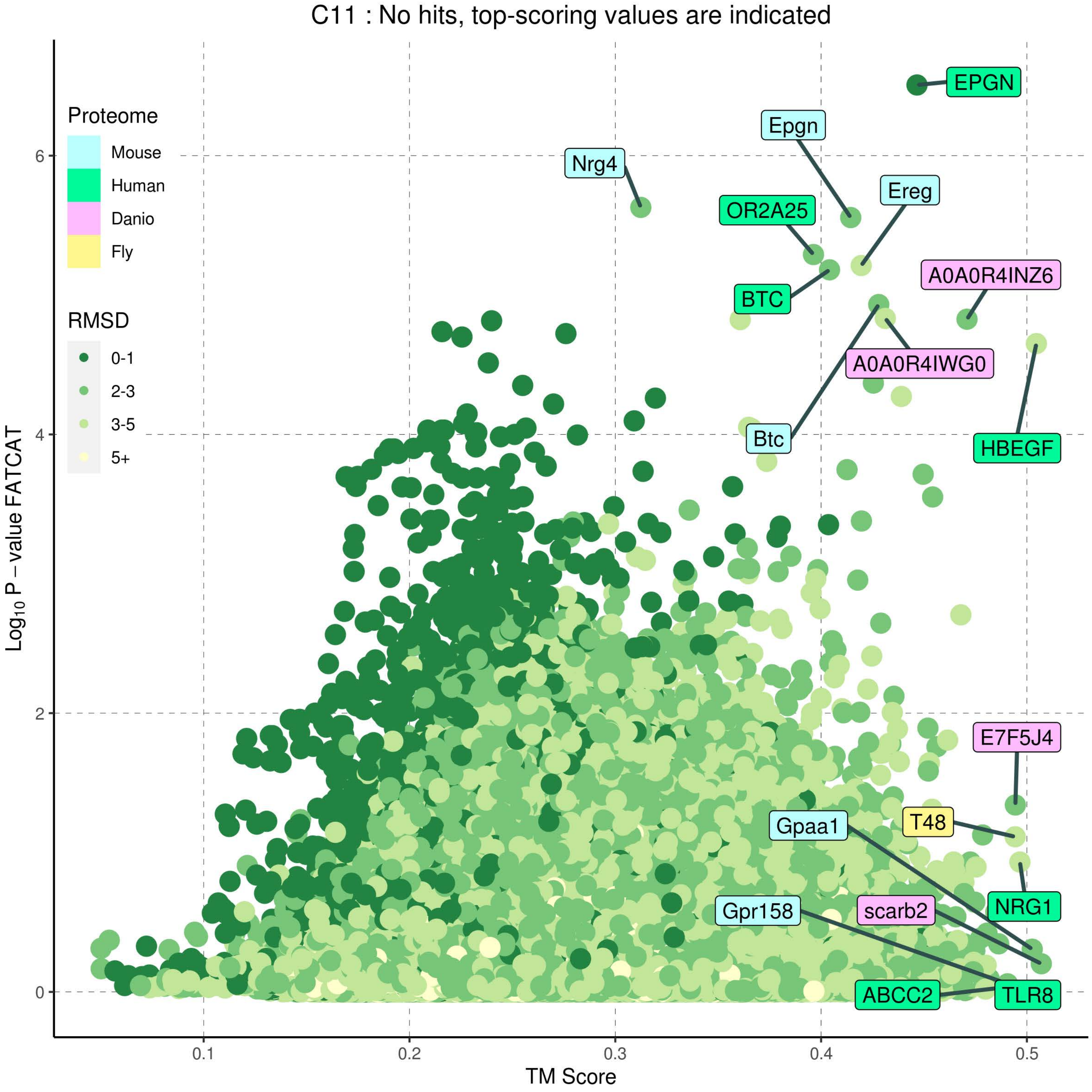

C7 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
TM Score
0
1
2
0.1
0.2
0.3
0.4
0.5
Sva
B2m
PIP
Pip
Sval2
Sval1
A0A2R8QSS1
IGLC7
M9MM93
E9QJH9
zgc:100994
DSE
Dse
Q5RGL8
RABGAP1L
Dsel
B8A4C4
Kif1b

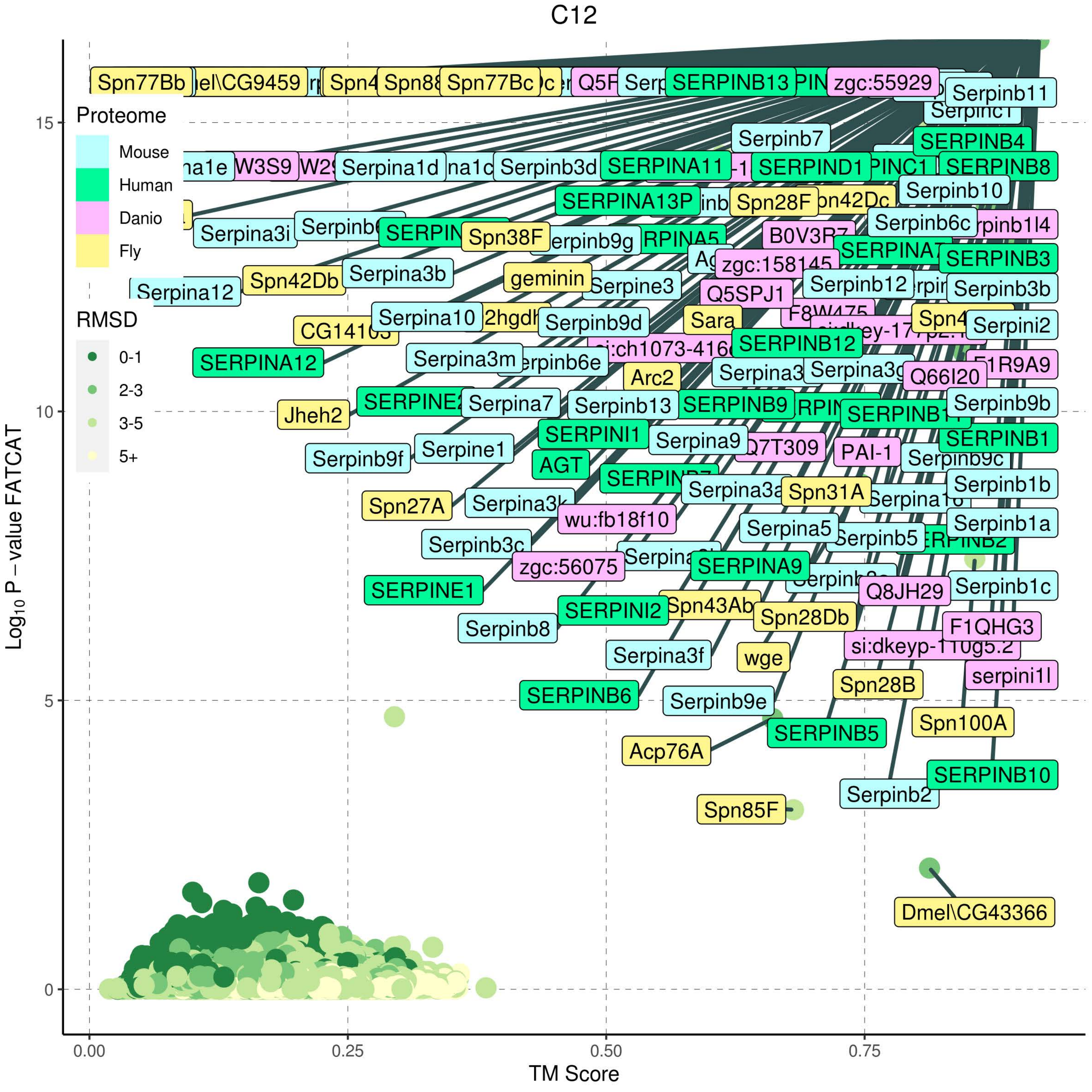
C8 : No hits, top-scoring values are indicated

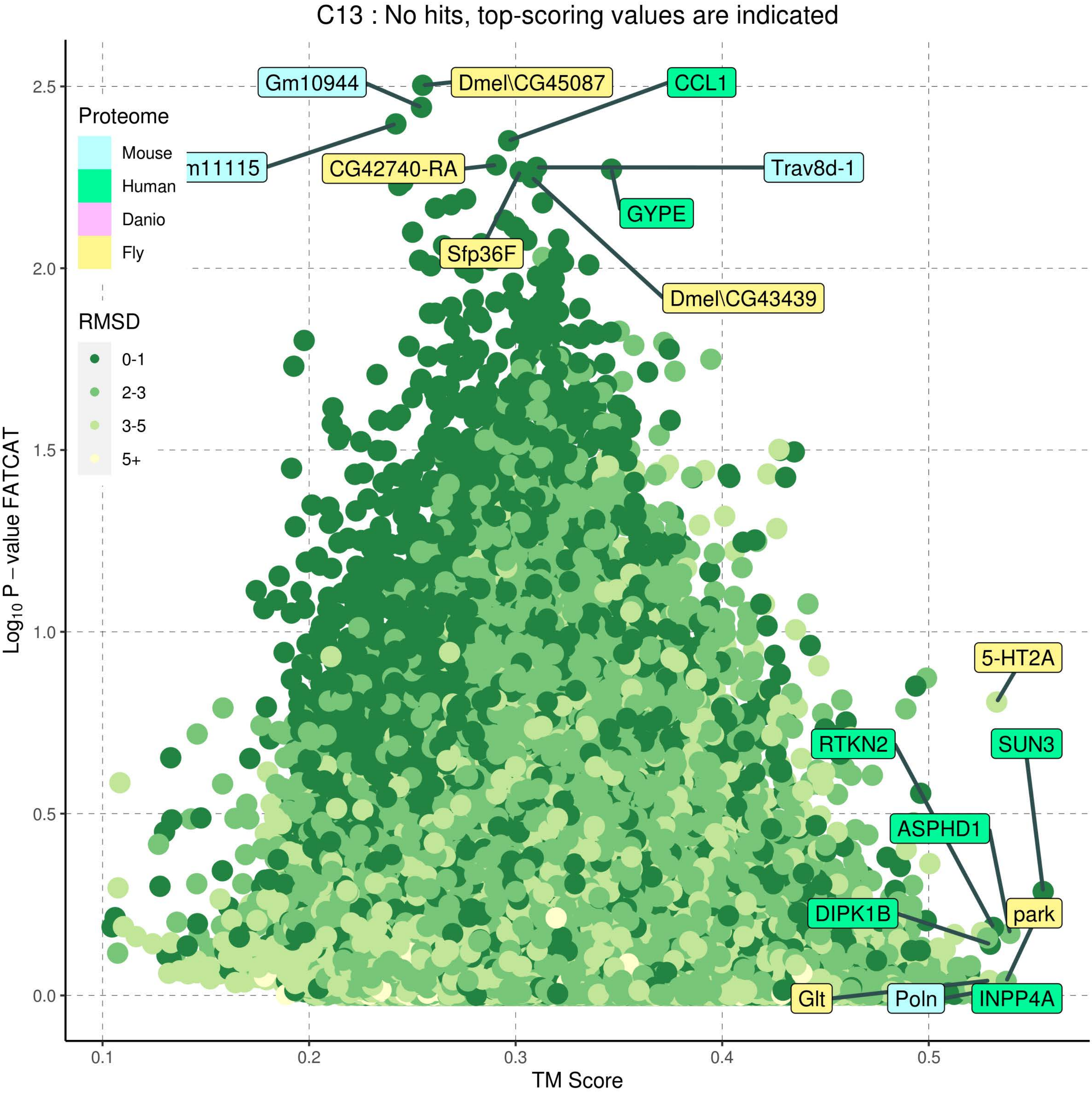



C9 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Fem1b
si:ch211-203b8.6
ASB3
FEM1B
Ankdd1a
A0A2R8PZ70
E7F7Y4
A0A0R4IJP1
asb2a
A0A2R8PXZ5
ASB2
Dmel\CG10011
E9QC62
WDFY4
DOCK5
Dock4
A0A0R4IEH3
Log_{10} P − value FATCAT
TM Score
0
1
2
3
4
5
0.0
0.2
0.4

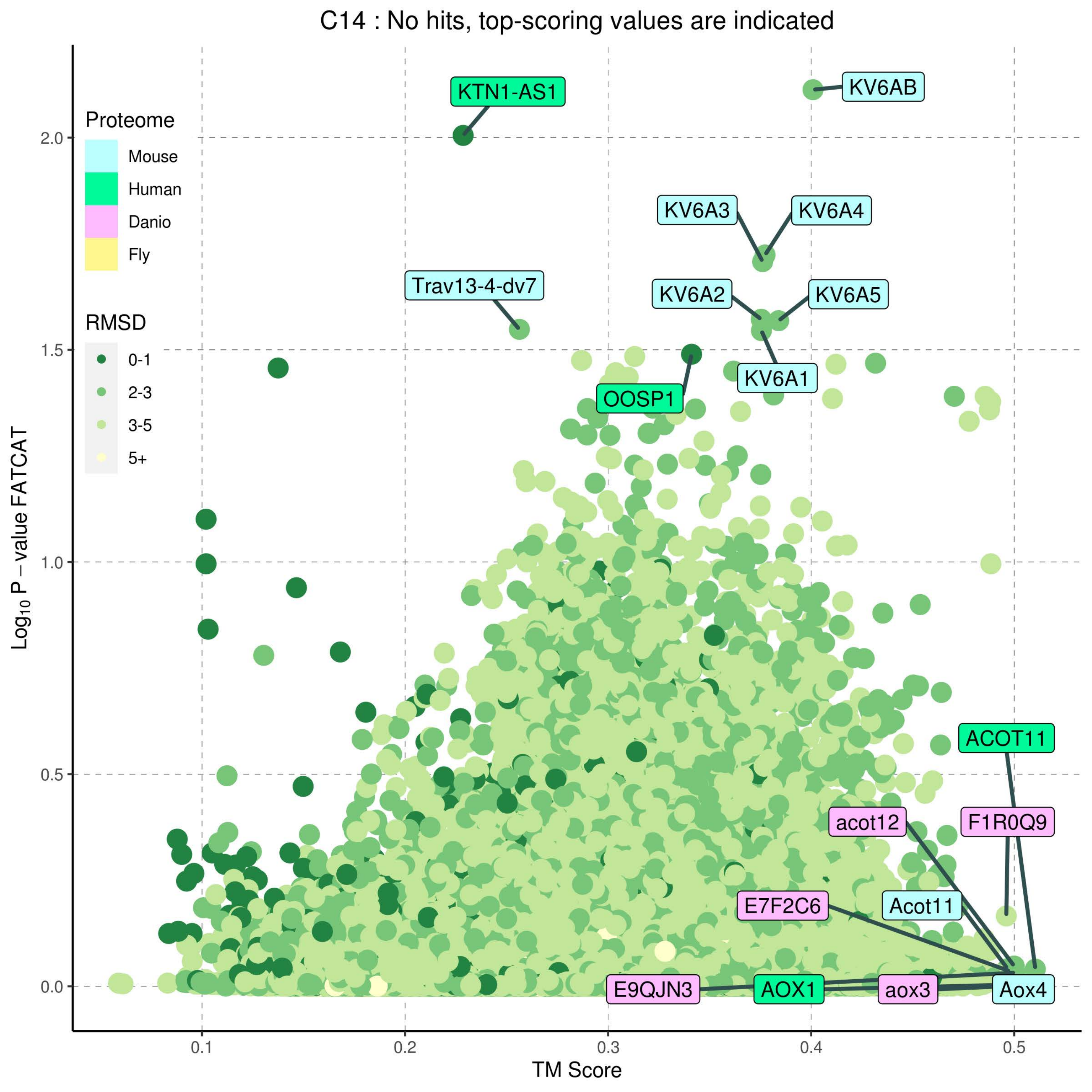

C10 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
TM Score
0
1
2
3
4
0.1
0.2
0.3
0.4
OGFOD3
Ogfod3
EGLN3
Egln3
F8W5S7
A0A2R8QV03
Q5PNQ5
EGLN2
Egln1
CG15542
PH4alphaNE2
anon-SAGE:Wang-055
A0A2R8QQ41
Adgrb1
Adgre1
OR2A25
KDM5B
lid

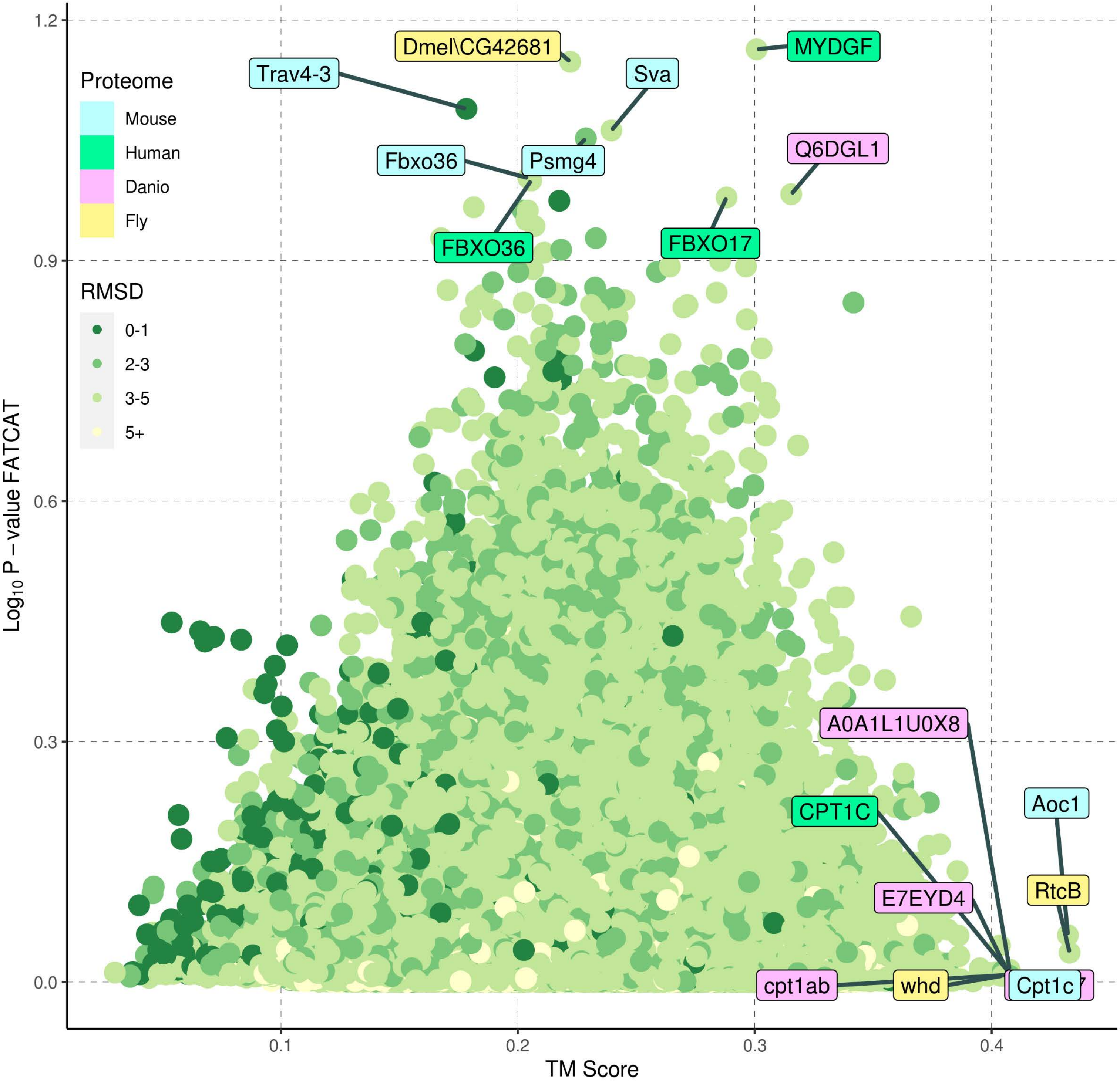

C11 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log₁₀ P – value FATCAT
TM Score
0
2
4
6
0.1
0.2
0.3
0.4
0.5
EPGN
Epgn
Nrg4
Ereg
OR2A25
BTC
A0A0R4INZ6
A0A0R4IWG0
Btc
HBEGF
E7F5J4
T48
Gpaa1
NRG1
Gpr158
scarb2
ABCC2
TLR8


C12
Spn77Bb
el\CG9459
Spn4
Spn88
Spn77Bc
Q5F
Serp
SERPINB13
zgc:55929
Serpinb11
Serpinc1
Proteome
Mouse
Human
Danio
Fly
Serpinb7
SERPINB4
a1e
W3S9
W2
Serpina1d
na1c
Serpinb3d
SERPINA11
SERPIND1
PINC1
SERPINB8
Serpinb10
SERPINA13P
inb
Spn28F
n42Dc
Serpina3i
Serpinb
SERPIN
Spn38F
erpinb9g
RPINA5
B0V3R7
Serpinb6c
rpinb1l4
Ag
zgc:158145
SERPINA7
SERPINB3
Serpina12
Spn42Db
Serpina3b
geminin
Serpine3
Q5SPJ1
Serpinb12
rpi
Serpinb3b
RMSD
0-1
2-3
3-5
5+
CG14103
Serpina10
2hgdh
Serpinb9d
Sara
F8W475
si:dkey-17
Spn4
Serpini2
SERPINA12
si:ch1073-416
SERPINB12
Serpina3m
erpinb6e
Arc2
Serpina3
Serpina3g
Q66I20
F1R9A9
SERPINE2
Serpina7
Serpinb13
SERPINB9
RPIN
SERPINB11
Serpinb9b
Jheh2
SERPINI1
Serpina9
Q7T309
PAI-1
SERPINB1
Serpinb9f
Serpine1
AGT
Serpinb9c
SERPINB7
Serpina3a
Spn31A
Serpina1b
Serpinb1b
Spn27A
Serpina3k
wu:fb18f10
Serpina5
Serpinb5
ERPINB2
Serpinb1a
Serpinb3c
zgc:56075
Serpina3
SERPINA9
erpinb
SERPINE1
Q8JH29
Serpinb1c
SERPINI2
Spn43Ab
Spn28Db
F1QHG3
Serpinb8
si:dkeyp-110g5.2
Serpina3f
wge
serpini1l
Spn28B
SERPINB6
Serpinb9e
Spn100A
SERPINB5
Acp76A
SERPINB10
Serpinb2
Spn85F
Dmel\CG43366
15
10
5
0
0.00
0.25
0.50
0.75
TM Score
Log_{10} P – value FATCAT

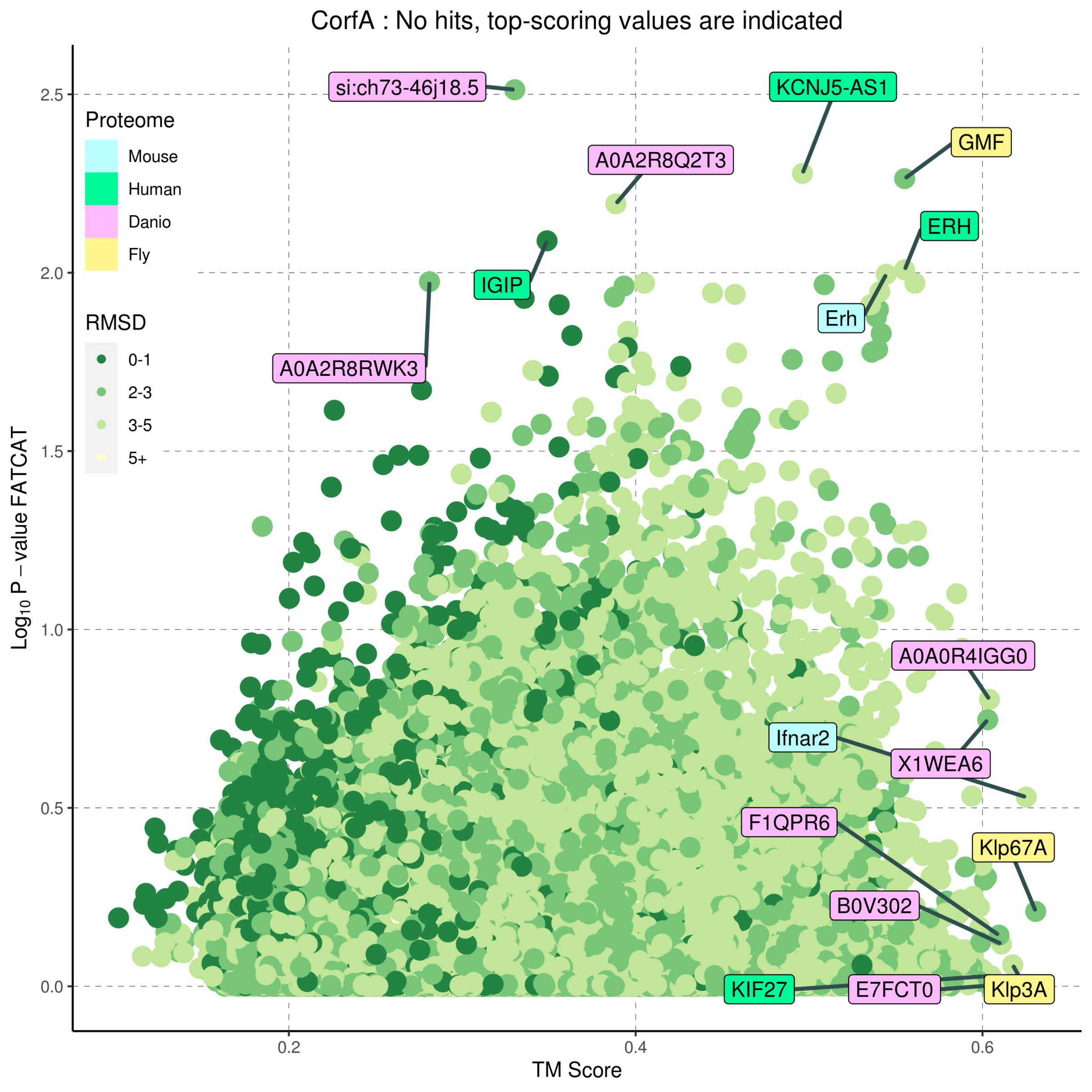


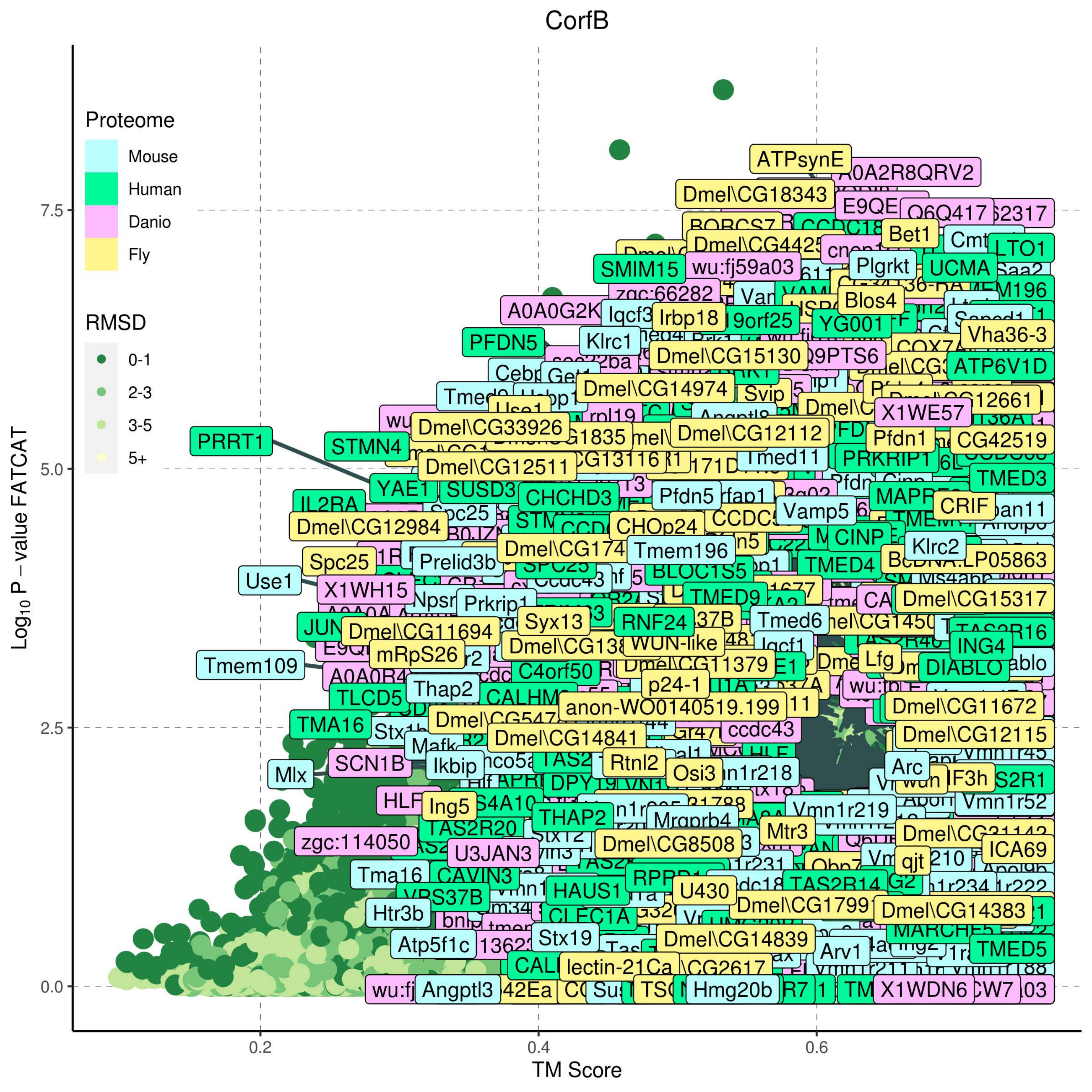
C13 : No hits, top-scoring values are indicated

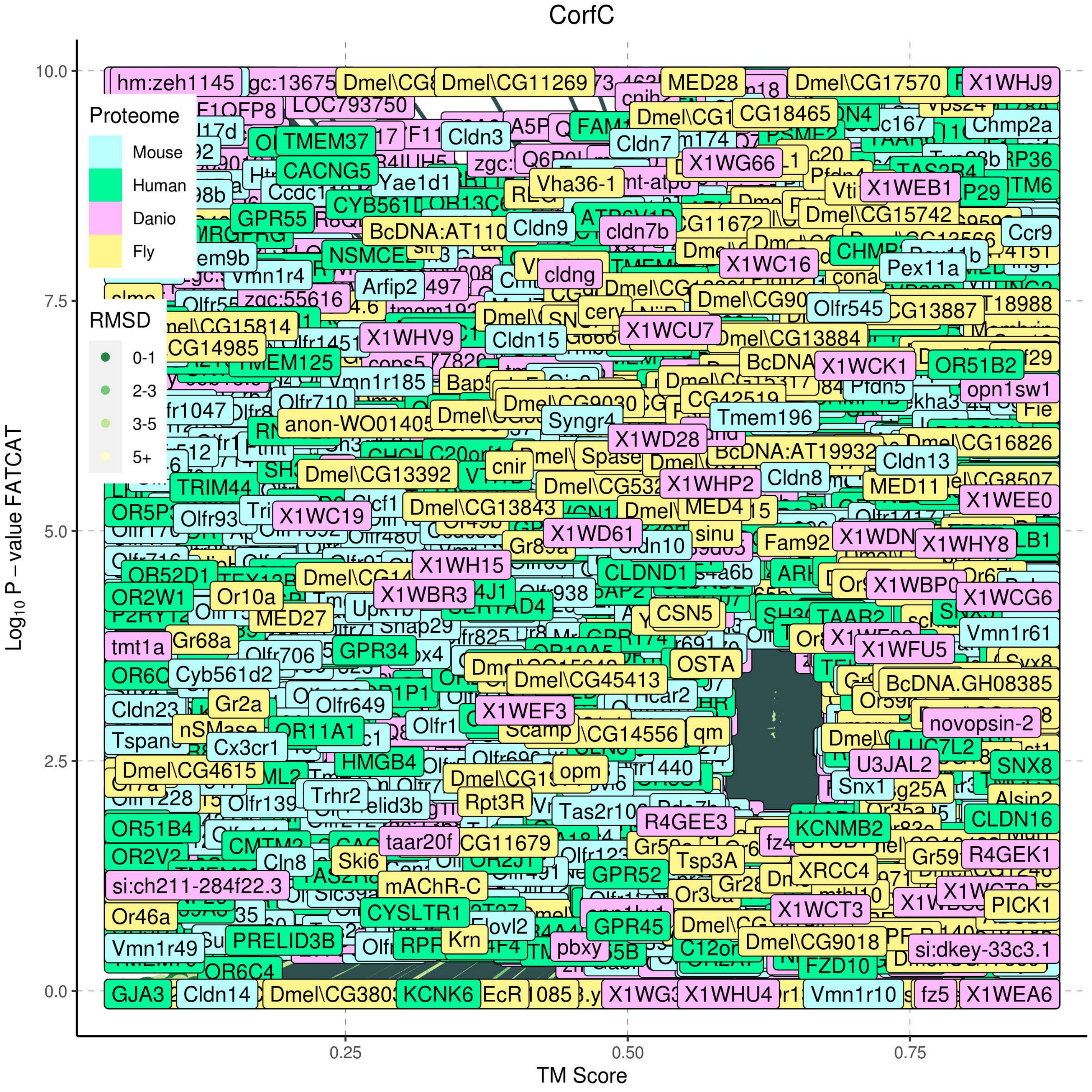

C14 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log_{10} P − value FATCAT
TM Score
0.0
0.5
1.0
1.5
2.0
0.1
0.2
0.3
0.4
0.5
KTN1-AS1
KV6AB
KV6A3
KV6A4
Trav13-4-dv7
KV6A2
KV6A5
KV6A1
OOSP1
ACOT11
acot12
F1R0Q9
E7F2C6
Acot11
E9QJN3
AOX1
aox3
Aox4

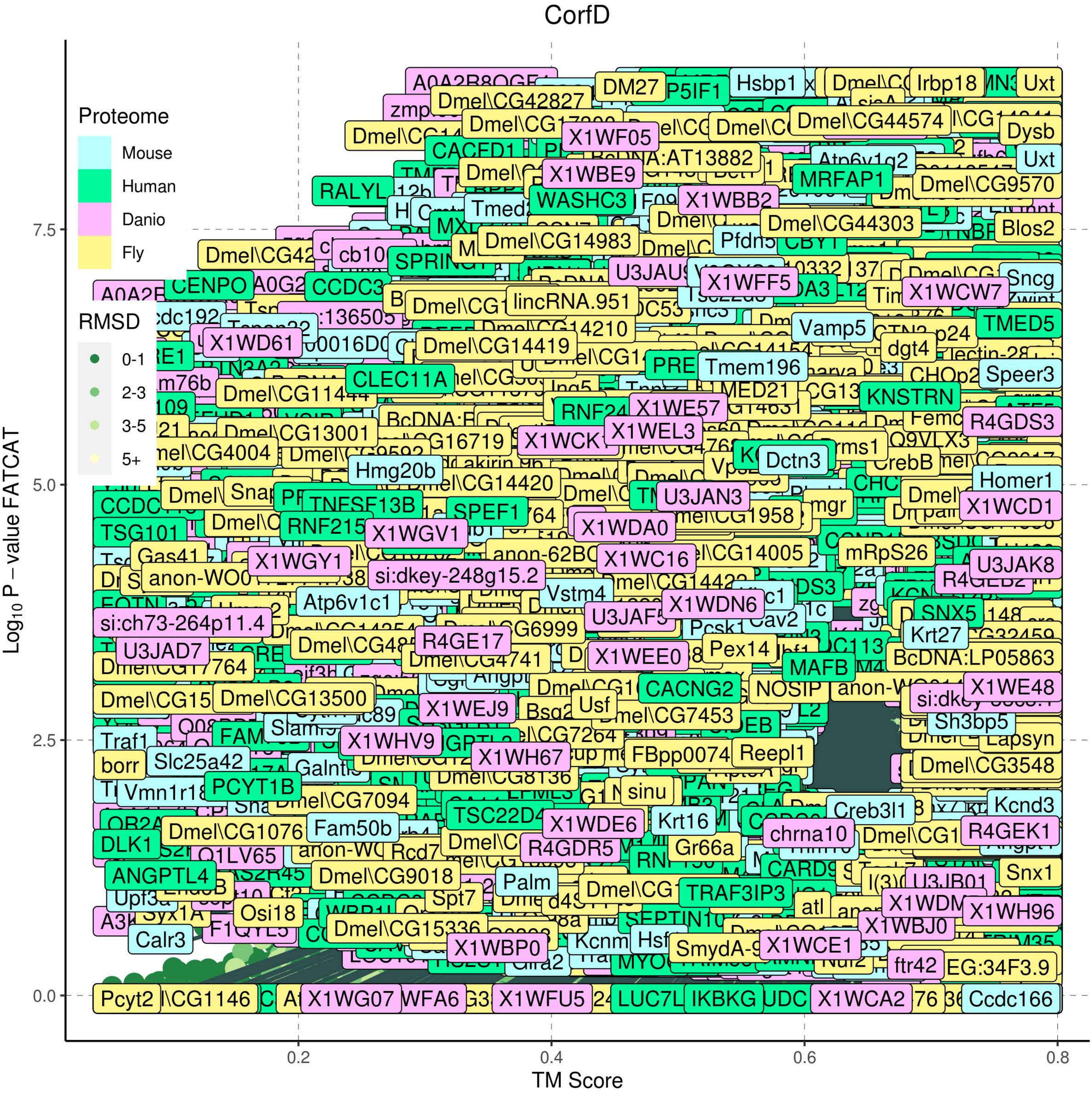


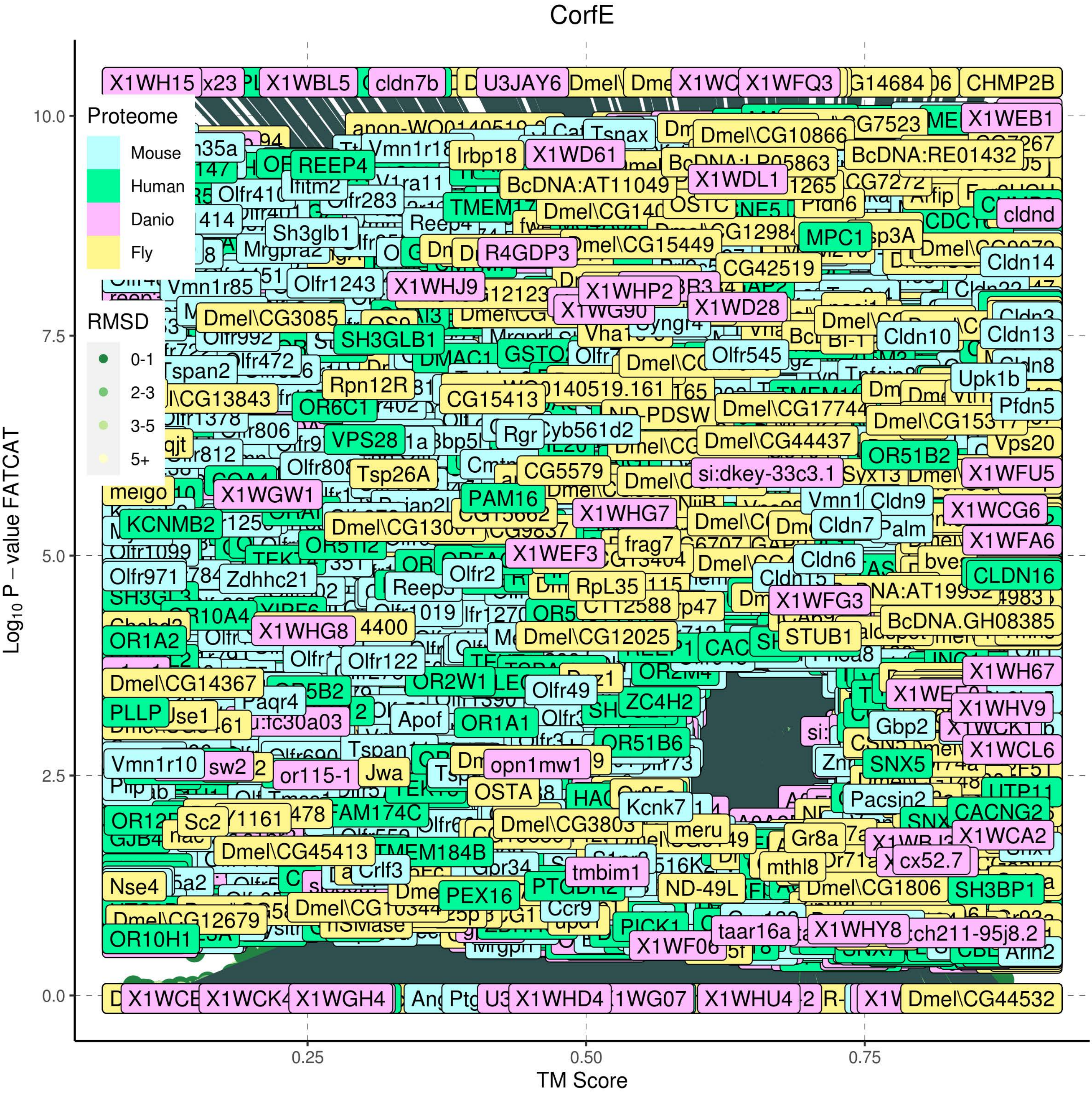
C23 : No hits, top-scoring values are indicated

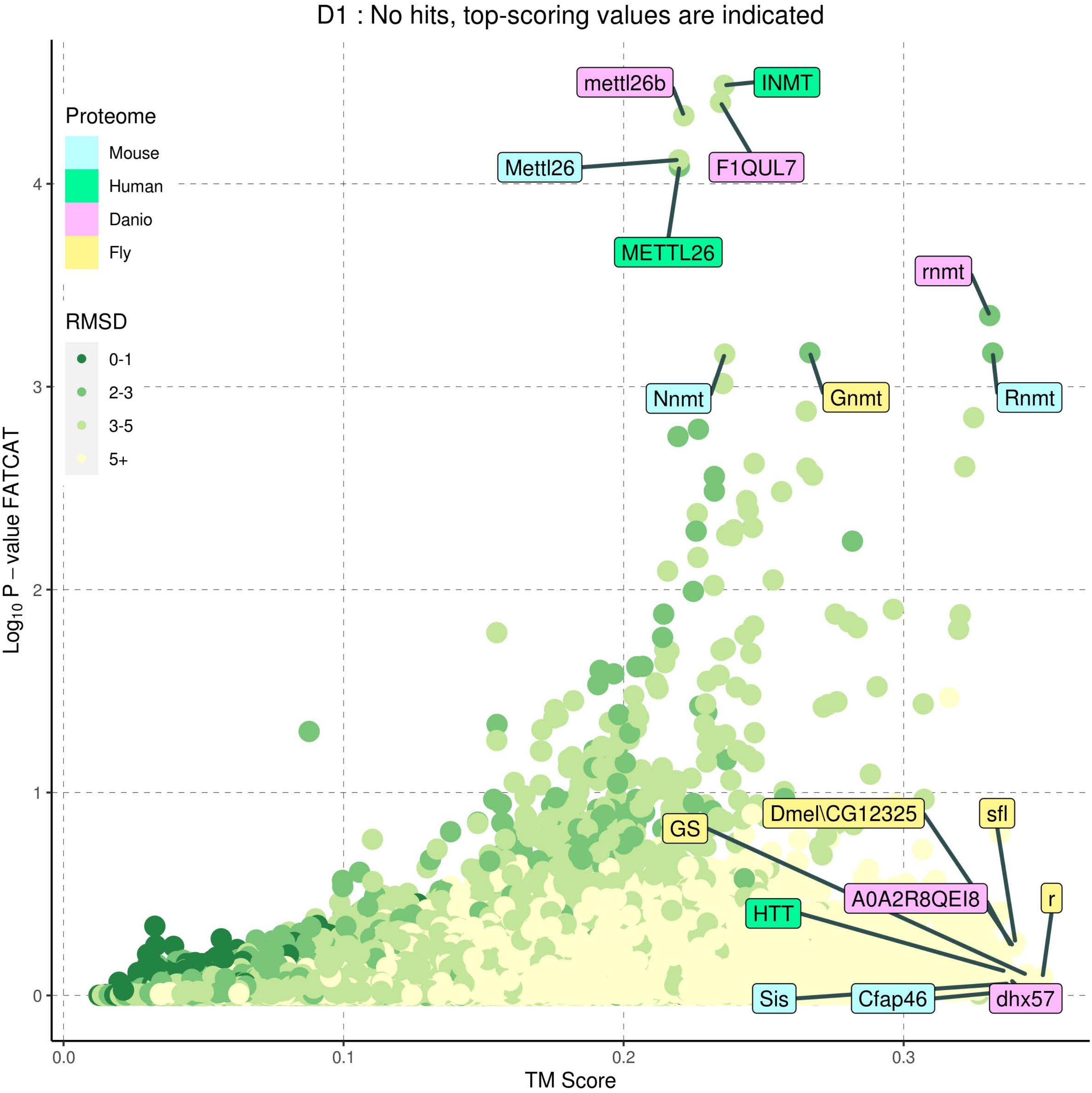

CorfA : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
TM Score
0.0
0.5
1.0
1.5
2.0
2.5
0.2
0.4
0.6
si:ch73-46j18.5
KCNJ5-AS1
GMF
A0A2R8Q2T3
ERH
IGIP
Erh
A0A2R8RWK3
A0A0R4IGG0
Ifnar2
X1WEA6
F1QPR6
Klp67A
B0V302
KIF27
E7FCT0
Klp3A

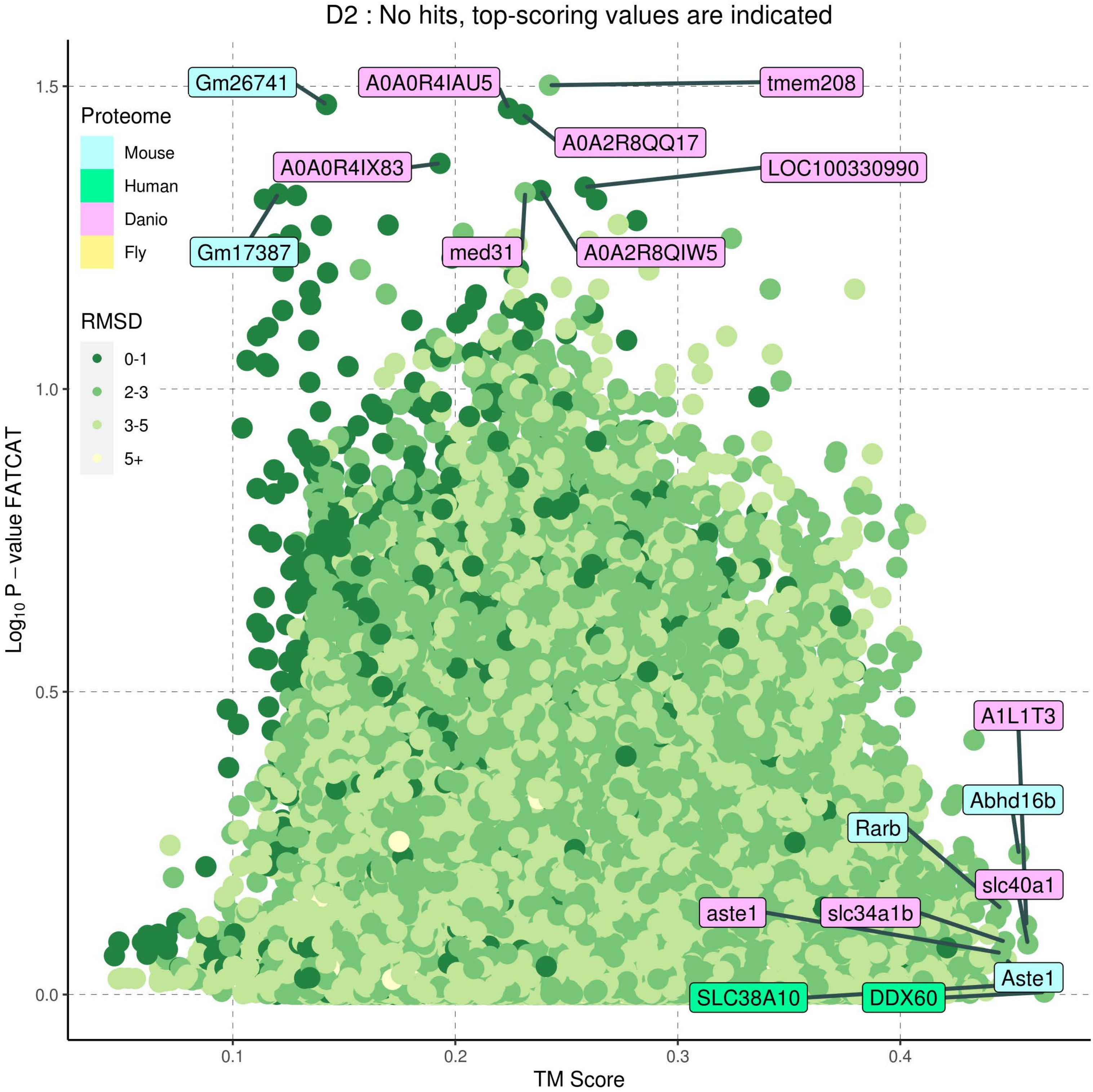

CorfB
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log$_{10}$ P − value FATCAT
TM Score
7.5
5.0
2.5
0.0
0.2
0.4
0.6
ATPsynE
A0A2R8QRV2
Dmel\CG18343
E9QE
Q6Q417
Bet1
Cmt
LTO1
SMIM15
wu:fj59a03
Plgrkt
UCMA
zgc:66282
Blos4
A0A0G2K
Iqcf3
Irbp18
9orf25
YG001
PFDN5
Klrc1
Dmel\CG15130
Q9PTS6
Vha36-3
ATP6V1D
Dmel\CG14974
Svip
Dmel\CG12661
X1WE57
Dmel\CG33926
Dmel\CG12112
Pfdn1
CG42519
PRRT1
STMN4
Dmel\CG12511
Tmed11
PRKRIP1
TMED3
YAE1
SUSD3
CHCHD3
Pfdn5
MAPRE
CRIF
IL2RA
Spc25
Vamp5
Dmel\CG12984
CHOp24
CINP
Dmel\CG174
Tmem196
Klrc2
Spc25
Prelid3b
TMED4
BcDNA:LP05863
Use1
X1WH15
BLOC1S5
TMED9
Dmel\CG15317
Npsr
Prkrip1
Syx13
RNF24
Tmed6
JUN
Dmel\CG11694
TAS2R16
ING4
mRpS26
WUN-like
Tmem109
Dmel\CG11379
Lfg
DIABLO
C4orf50
p24-1
TLCD5
Thap2
CALHM
anon-WO0140519.199
Dmel\CG11672
TMA16
Dmel\CG14841
ccdc43
Dmel\CG12115
Mafk
Mlx
SCN1B
Ikbip
Rtnl2
Osi3
Arc
HLF
Ing5
THAP2
Mrgprb4
Vmn1r219
Vmn1r52
TAS2R20
Mtr3
Dmel\CG8508
ICA69
zgc:114050
U3JAN3
qjt
Tma16
CAVIN3
HAUS1
U430
TAS2R14
VPS37B
Htr3b
CLEC1A
Dmel\CG1799
Dmel\CG14383
Stx19
Dmel\CG14839
Atp5f1c
Arv1
TMED5
lectin-21Ca
Angptl3
Hmg20b
X1WDN6

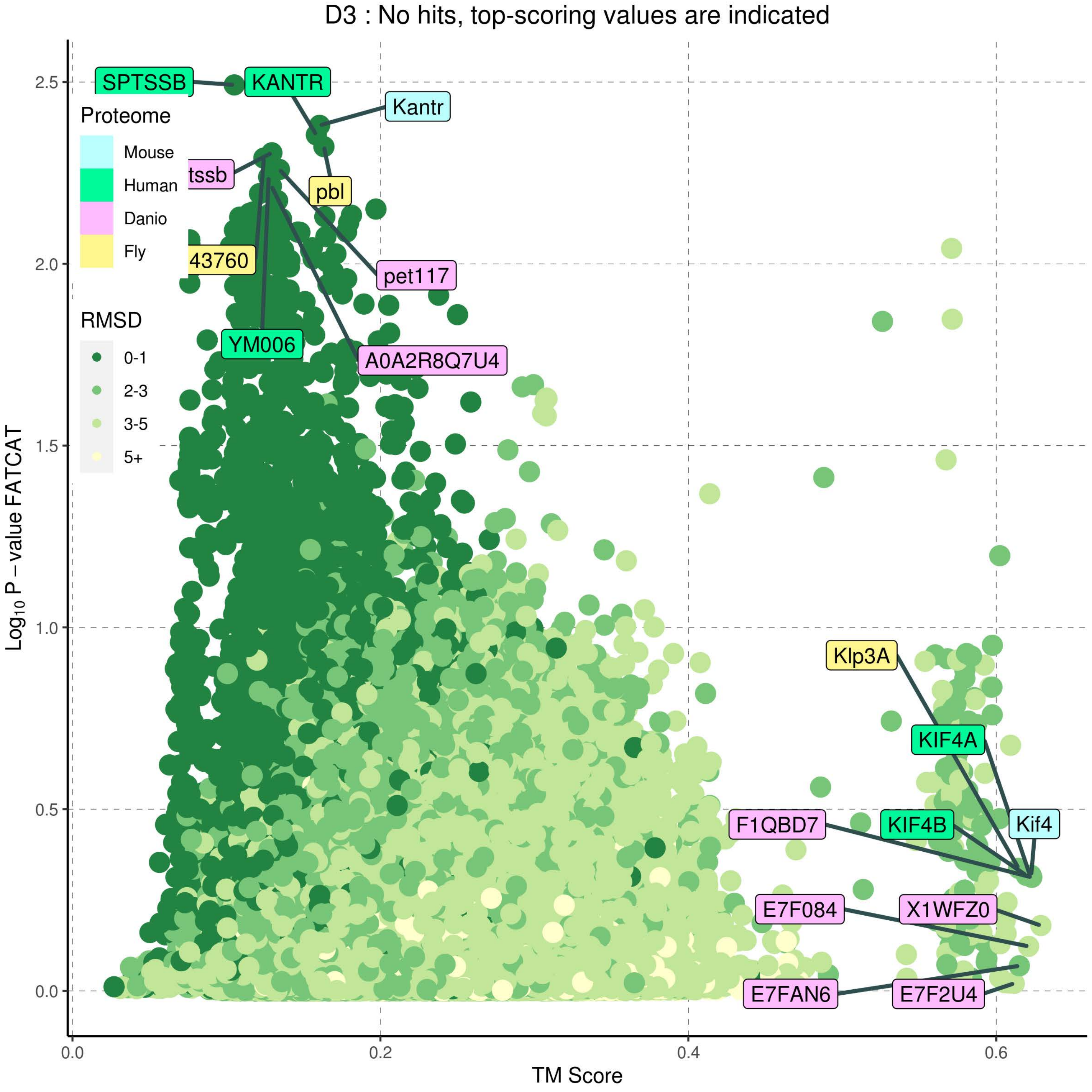

CorfC
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log$_{10}$ P − value FATCAT
TM Score
10.0
7.5
5.0
2.5
0.0
0.25
0.50
0.75
hm:zeh1145
Dmel\CG11269
MED28
Dmel\CG17570
X1WHJ9
LOC793750
CG18465
Chmp2a
TMEM37
Cldn3
Cldn7
CACNG5
X1WG66
Yae1d1
Vha36-1
X1WEB1
GPR55
BcDNA:AT110
Cldn9
cldn7b
Ccr9
NSMCE
X1WC16
Pex11a
Vmn1r4
Arfip2
cldng
zgc:55616
Olfr545
CG13887
X1WHV9
Cldn15
X1WCU7
Dmel\CG13884
CG14985
TMEM125
X1WCK1
OR51B2
Vmn1r185
opn1sw1
anon-WO01405
Syngr4
Tmem196
X1WD28
BcDNA:AT19932
Dmel\CG16826
Cldn13
TRIM44
Dmel\CG13392
cnir
X1WHP2
Cldn8
MED11
X1WEE0
X1WC19
Dmel\CG13843
MED4
X1WD61
sinu
Fam92
X1WHY8
X1WH15
CLDND1
X1WBR3
OR2W1
Or10a
MED27
CSN5
X1WCG6
Vmn1r61
tmt1a
Gr68a
GPR34
X1WFU5
OSTA
Cyb561d2
Dmel\CG45413
BcDNA.GH08385
Cldn23
Gr2a
Olfr649
X1WEF3
novopsin-2
OR11A1
Cx3cr1
qm
HMGB4
SNX8
Dmel\CG4615
opm
U3JAL2
Trhr2
Rpt3R
Snx1
OR51B4
R4GEE3
KCNMB2
CLDN16
taar20f
CG11679
R4GEK1
Ski6
Cln8
Tsp3A
XRCC4
GPR52
si:ch211-284f22.3
mAChR-C
X1WCT3
PICK1
Or46a
CYSLTR1
Vmn1r49
PRELID3B
Krn
pbxy
GPR45
Dmel\CG9018
si:dkey-33c3.1
OR6C4
FZD10
GJA3
Cldn14
KCNK6
EcR
X1WHU4
Vmn1r10
fz5
X1WEA6

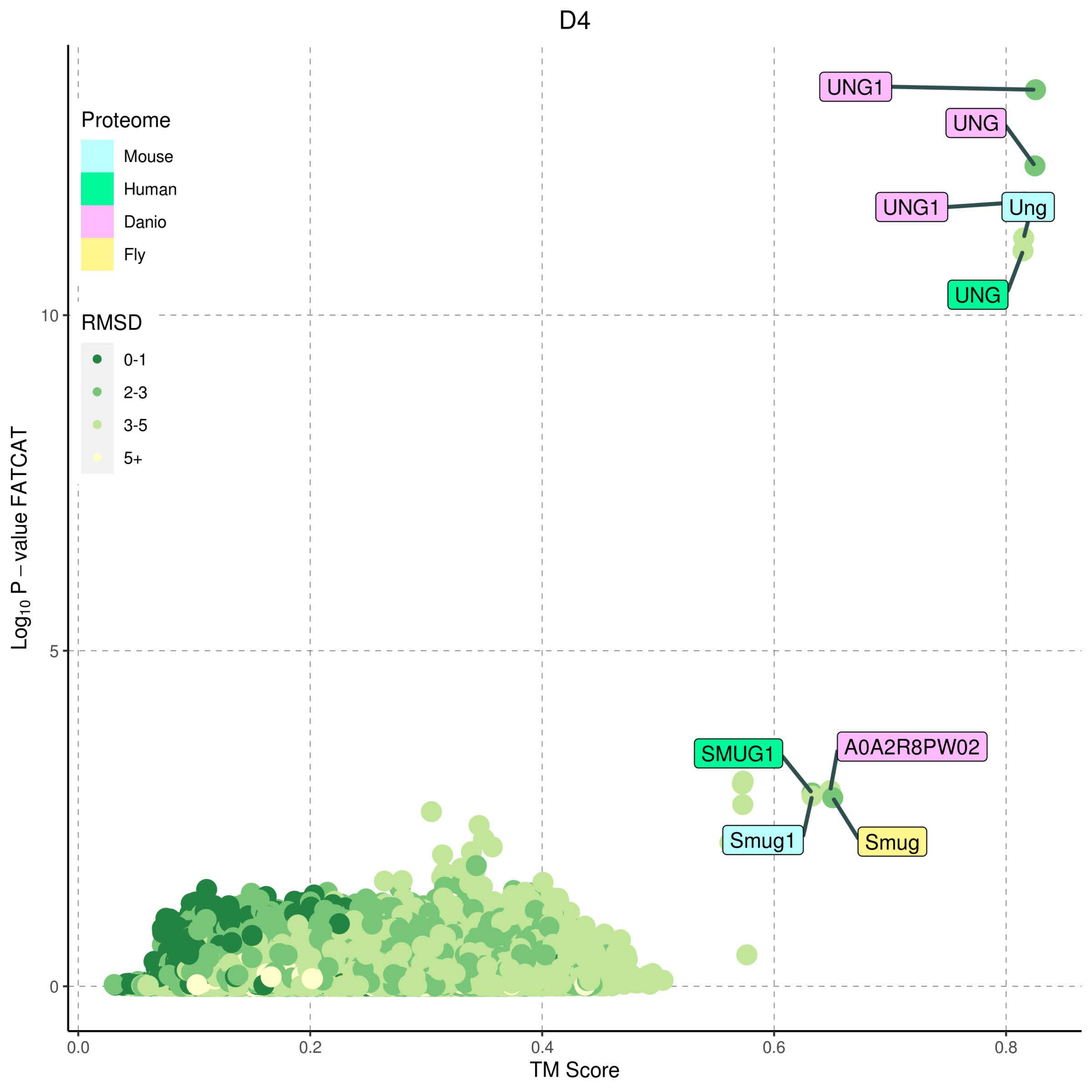

CorfD
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log$_{10}$ P – value FATCAT
7.5
5.0
2.5
0.0
TM Score
0.2
0.4
0.6
0.8
DM27
Hsbp1
Irbp18
Uxt
Dmel\CG42827
Dmel\CG44574
Dysb
X1WF05
CACFD1
Atp6v1g2
X1WBE9
MRFAP1
Dmel\CG9570
RALYL
WASHC3
X1WBB2
Tmed2
Dmel\CG44303
Blos2
Dmel\CG14983
Pfdn5
X1WFF5
X1WCW7
Sncg
CENPO
CCDC3
lincRNA.951
Vamp5
TMED5
X1WD61
Dmel\CG14419
Tmem196
dgt4
CLEC11A
Speer3
Dmel\CG11444
KNSTRN
X1WE57
X1WEL3
R4GDS3
Dmel\CG13001
Dctn3
Hmg20b
Homer1
Dmel\CG14420
U3JAN3
TNFSF13B
SPEF1
X1WCD1
TSG101
RNF215
X1WGV1
X1WDA0
Gas41
X1WGY1
X1WC16
mRpS26
U3JAK8
si:dkey-248g15.2
Vstm4
Atp6v1c1
X1WDN6
SNX5
si:ch73-264p11.4
Krt27
R4GE17
U3JAD7
X1WEE0
Pex14
MAFB
BcDNA:LP05863
Dmel\CG13500
CACNG2
NOSIP
X1WE48
X1WEJ9
Usf
Dmel\CG7453
Sh3bp5
X1WHV9
X1WH67
Reepl1
Lapsyn
borr
Slc25a42
PCYT1B
Dmel\CG3548
Dmel\CG8136
sinu
Dmel\CG7094
TSC22D4
X1WDE6
Krt16
Creb3l1
Kcnd3
Fam50b
chrna10
R4GEK1
DLK1
Q1LV65
R4GDR5
Gr66a
ANGPTL4
Dmel\CG9018
Palm
TRAF3IP3
Snx1
Osi18
Spt7
atl
X1WH96
Calr3
Dmel\CG15336
X1WBJ0
X1WBP0
X1WCE1
ftr42
EG:34F3.9
Pcyt2
X1WG07
X1WFU5
IKBKG
X1WCA2
Ccdc166

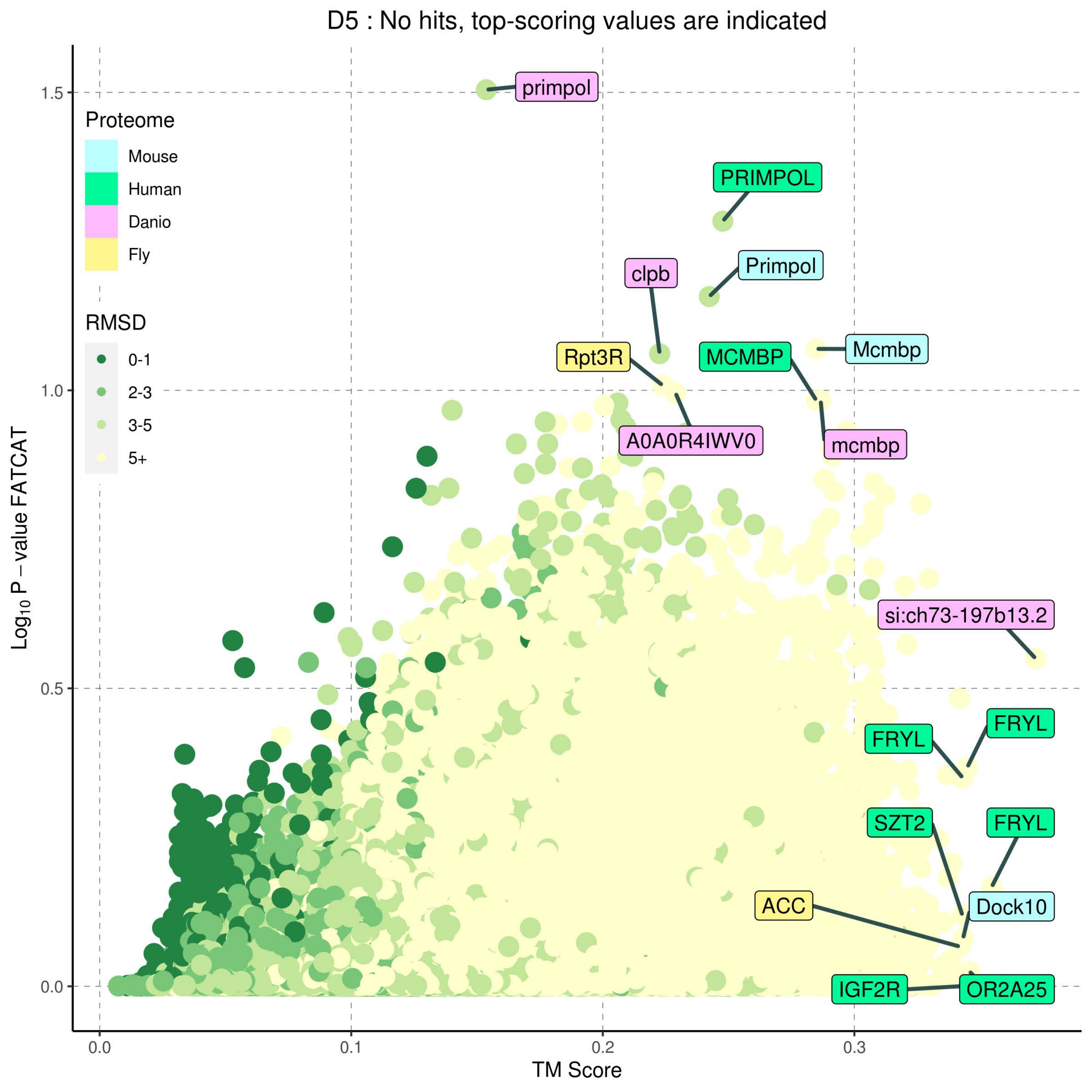

CorfE
Log10 P – value FATCAT
TM Score
0.0
2.5
5.0
7.5
10.0
0.25
0.50
0.75
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
X1WH15
X1WBL5
cldn7b
U3JAY6
X1WFQ3
CHMP2B
X1WEB1
Tsnax
Dmel\CG10866
Irbp18
X1WD61
BcDNA:RE01432
REEP4
Ifitm2
BcDNA:AT11049
X1WDL1
Olfr283
Sh3glb1
MPC1
cldnd
Mrgpra2
R4GDP3
CG42519
Cldn14
Olfr1243
X1WHJ9
X1WHP2
Vmn1r85
X1WD28
X1WG90
Dmel\CG3085
Olfr992
SH3GLB1
Cldn10
Cldn13
Olfr472
Olfr545
Tspan2
Rpn12R
Upk1b
Pfdn5
CG15413
OR6C1
ND-PDSW
Dmel\CG17744
Olfr1378
Olfr806
VPS28
Rgr
Cyb561d2
Dmel\CG44437
Vps20
OR51B2
Olfr808
Tsp26A
CG5579
si:dkey-33c3.1
X1WFU5
X1WGW1
PAM16
X1WHG7
Cldn9
X1WCG6
KCNMB2
Dmel\CG13001
Cldn7
Palm
X1WFA6
Olfr1099
X1WEF3
frag7
Cldn6
Olfr971
Zdhhc21
Olfr2
RpL35
CLDN16
X1WFG3
OR10A4
BcDNA.GH08385
X1WHG8
OR1A2
Dmel\CG12025
STUB1
Olfr122
X1WH67
Dmel\CG14367
OR2W1
Olfr49
ZC4H2
Paqr4
X1WHV9
PLLP
Apof
OR1A1
Gbp2
OR51B6
X1WCL6
Vmn1r10
sw2
or115-1
Jwa
opn1mw1
SNX5
OSTA
Kcnk7
Pacsin2
UTP11
OR12
Sc2
FAM174C
CACNG2
Dmel\CG3803
meru
Gr8a
X1WCA2
Dmel\CG45413
TMEM184B
cx52.7
Crlf3
tmbim1
mthl8
Nse4
ND-49L
Dmel\CG1806
SH3BP1
PEX16
Dmel\CG12679
Dmel\CG10344
Ccr9
PICK1
taar16a
X1WHY8
OR10H1
X1WF06
Arln2
X1WCK4
X1WGH4
X1WHD4
X1WHU4
Dmel\CG44532

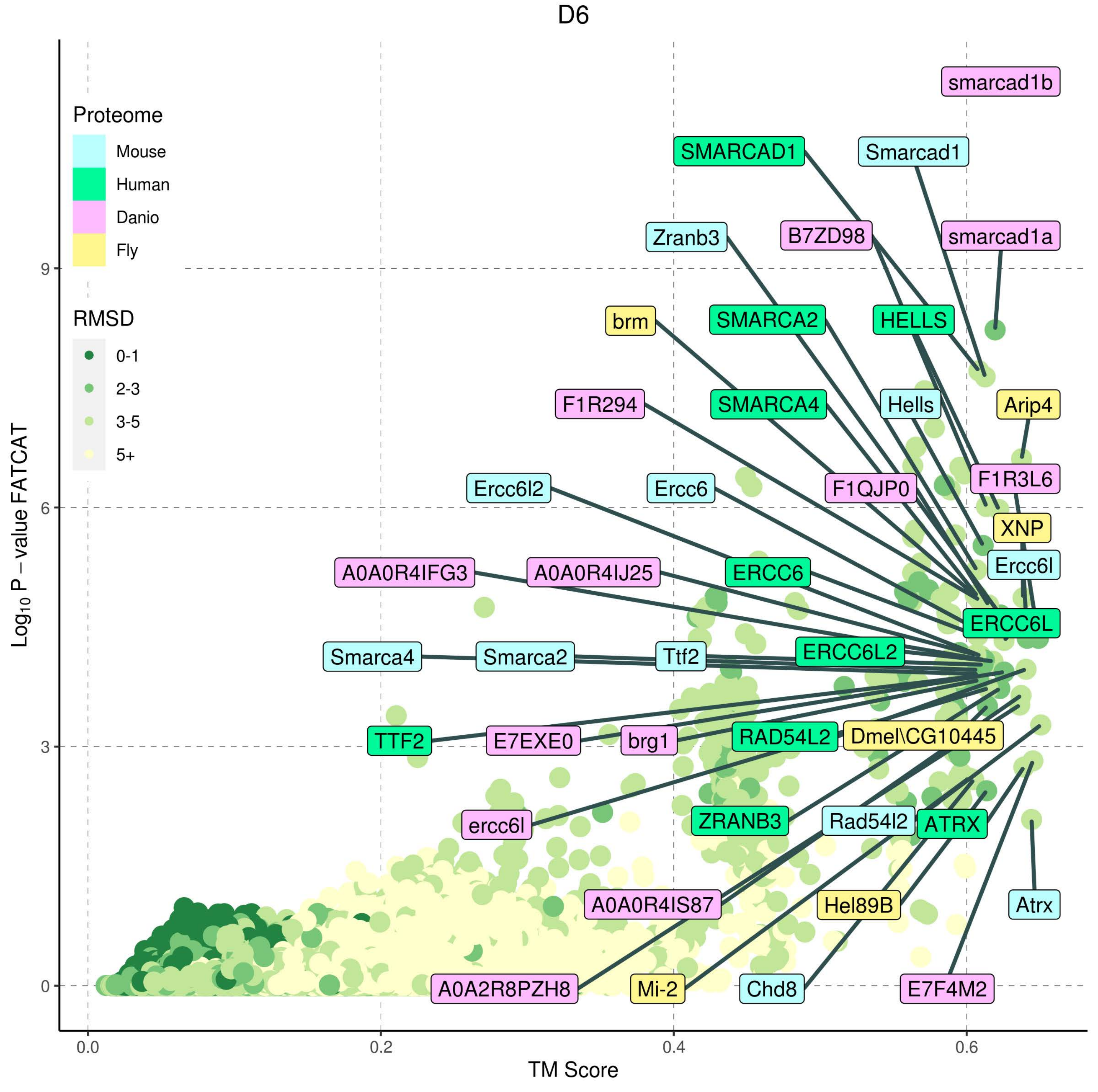

D1 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
mettl26b
INMT
F1QUL7
Mettl26
METTL26
rnmt
Nnmt
Gnmt
Rnmt
Dmel\CG12325
sfl
GS
A0A2R8QEI8
r
HTT
Sis
Cfap46
dhx57
Log₁₀ P – value FATCAT
0
1
2
3
4
TM Score
0.0
0.1
0.2
0.3

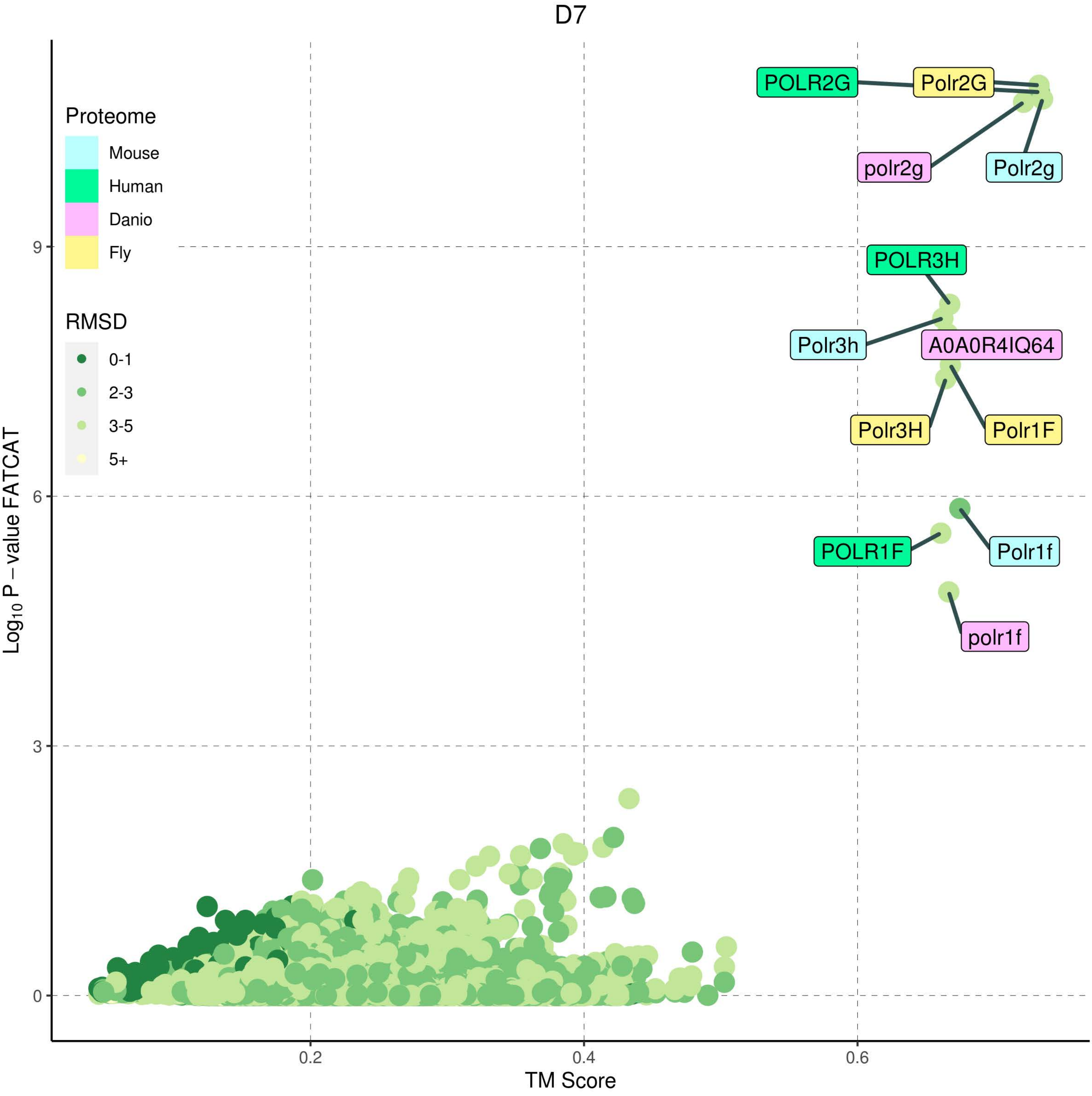

D2 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P − value FATCAT
TM Score
0.0
0.5
1.0
1.5
0.1
0.2
0.3
0.4
Gm26741
A0A0R4IAU5
tmem208
A0A2R8QQ17
A0A0R4IX83
LOC100330990
Gm17387
med31
A0A2R8QIW5
A1L1T3
Abhd16b
Rarb
slc40a1
aste1
slc34a1b
Aste1
SLC38A10
DDX60

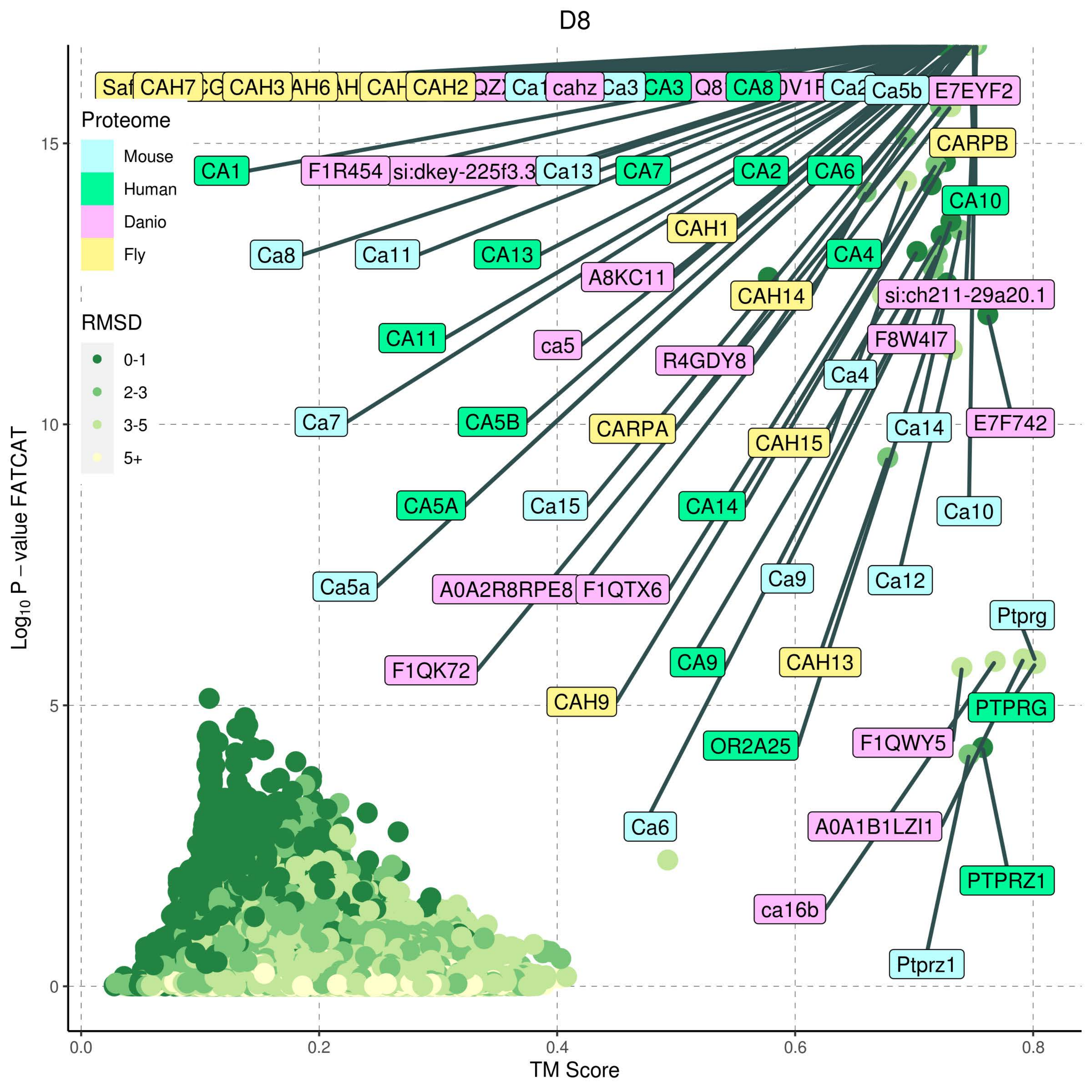

D3 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
SPTSSB
KANTR
Kantr
tssb
pbl
43760
pet117
YM006
A0A2R8Q7U4
Klp3A
KIF4A
F1QBD7
KIF4B
Kif4
E7F084
X1WFZ0
E7FAN6
E7F2U4
Log10 P - value FATCAT
2.5
2.0
1.5
1.0
0.5
0.0
TM Score
0.0
0.2
0.4
0.6


D4
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
UNG1
UNG
UNG1
Ung
UNG
SMUG1
A0A2R8PW02
Smug1
Smug
Log10 P − value FATCAT
10
5
0
0.0
0.2
0.4
0.6
0.8
TM Score

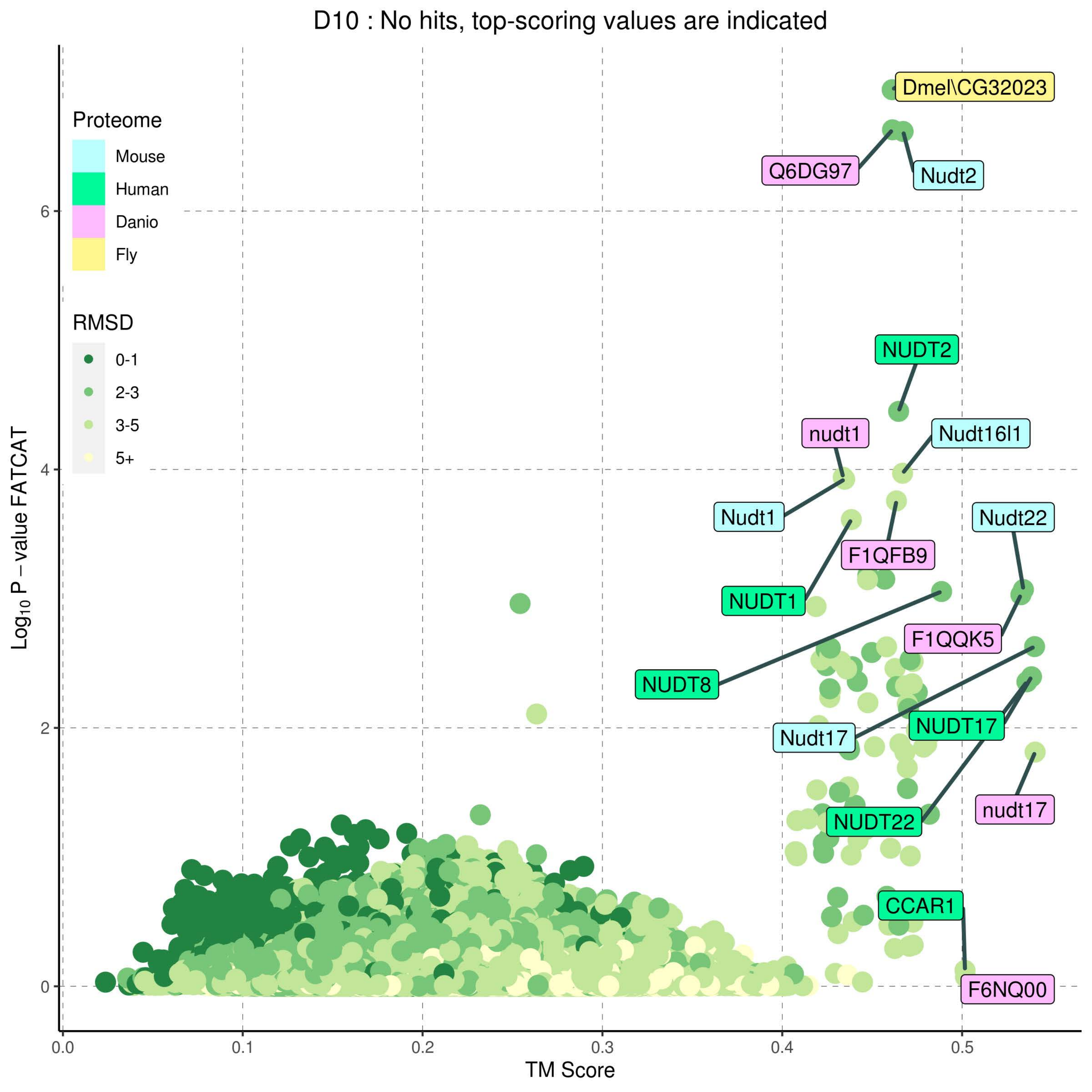

D5 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
1.5
1.0
0.5
0.0
TM Score
0.0
0.1
0.2
0.3
primpol
PRIMPOL
Primpol
clpb
Rpt3R
MCMBP
Mcmbp
A0A0R4IWV0
mcmbp
si:ch73-197b13.2
FRYL
FRYL
SZT2
FRYL
ACC
Dock10
IGF2R
OR2A25

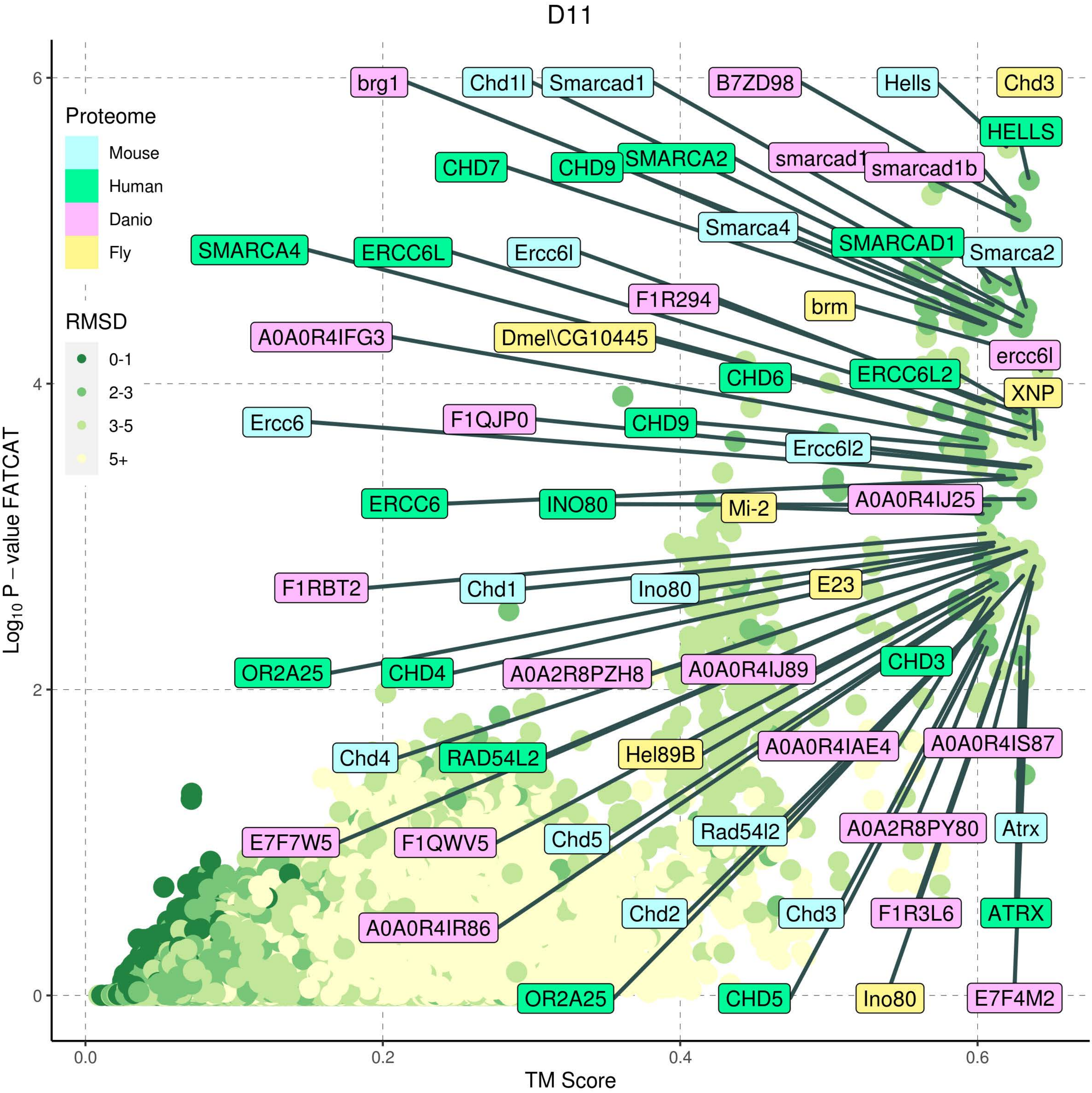

D6
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log₁₀ P – value FATCAT
TM Score
0
3
6
9
0.0
0.2
0.4
0.6
smarcad1b
SMARCAD1
Smarcad1
Zranb3
B7ZD98
smarcad1a
brm
SMARCA2
HELLS
F1R294
SMARCA4
Hells
Arip4
Ercc6l2
Ercc6
F1QJP0
F1R3L6
XNP
A0A0R4IFG3
A0A0R4IJ25
ERCC6
Ercc6l
ERCC6L
Smarca4
Smarca2
Ttf2
ERCC6L2
TTF2
E7EXE0
brg1
RAD54L2
Dmel\CG10445
ercc6l
ZRANB3
Rad54l2
ATRX
A0A0R4IS87
Hel89B
Atrx
A0A2R8PZH8
Mi-2
Chd8
E7F4M2

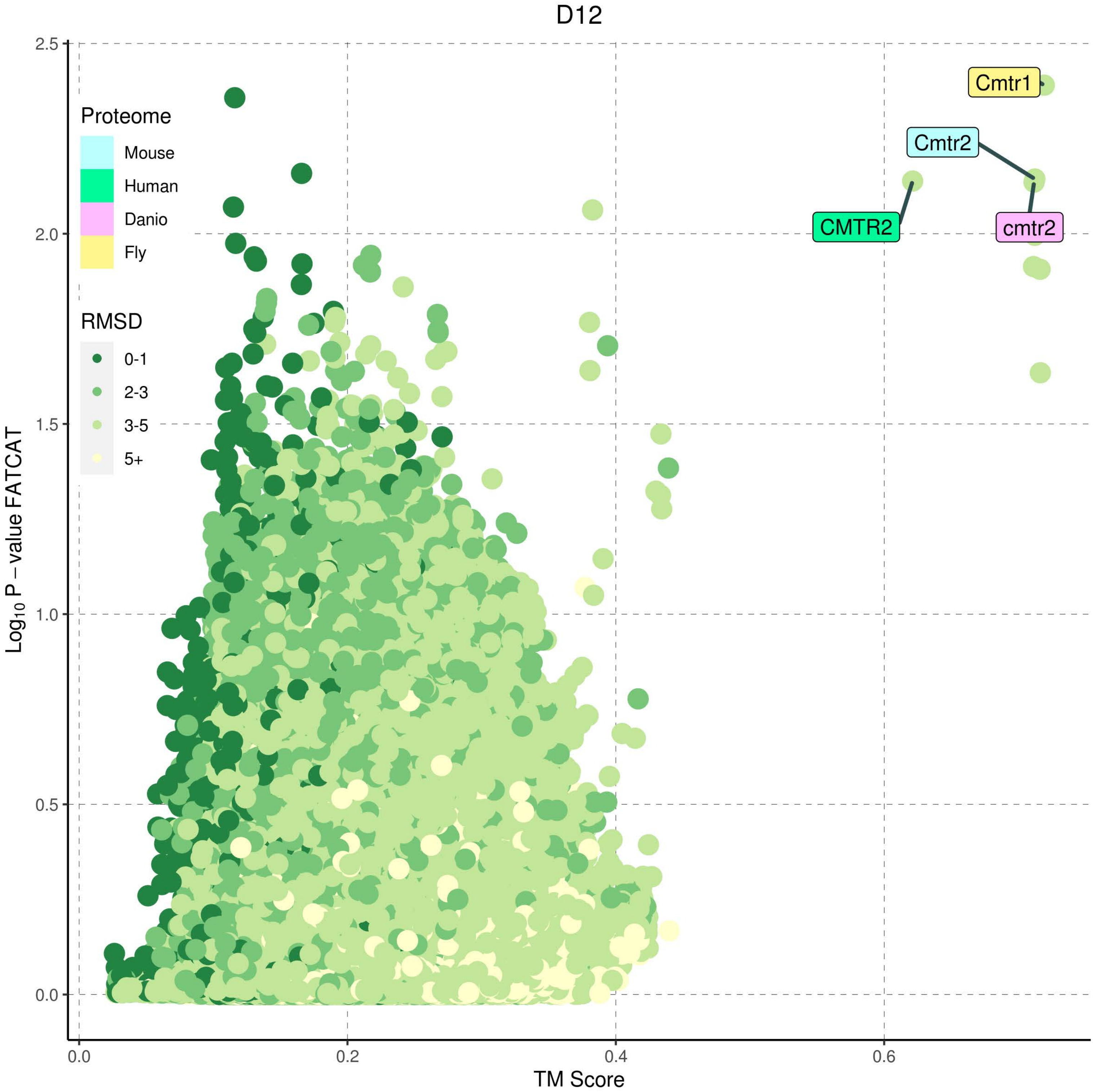

D7
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
POLR2G
Polr2G
polr2g
Polr2g
POLR3H
Polr3h
A0A0R4IQ64
Polr3H
Polr1F
POLR1F
Polr1f
polr1f
Log10 P − value FATCAT
0
3
6
9
TM Score
0.2
0.4
0.6


D8
Saf
CAH7
CG
CAH3
AH6
AH
CAH
CAH2
QZ
Ca1
cahz
Ca3
CA3
Q8
CA8
0V1F
Ca2
Ca5b
E7EYF2
Proteome
Mouse
Human
Danio
Fly
CARPB
CA1
F1R454
si:dkey-225f3.3
Ca13
CA7
CA2
CA6
CA10
CAH1
Ca8
Ca11
CA13
CA4
A8KC11
CAH14
si:ch211-29a20.1
RMSD
0-1
2-3
3-5
5+
CA11
ca5
F8W4I7
R4GDY8
Ca4
Ca7
CA5B
CARPA
Ca14
E7F742
CAH15
CA5A
Ca15
CA14
Ca10
Ca5a
A0A2R8RPE8
F1QTX6
Ca9
Ca12
Ptprg
F1QK72
CA9
CAH13
CAH9
PTPRG
OR2A25
F1QWY5
Ca6
A0A1B1LZI1
PTPRZ1
ca16b
Ptprz1
Log₁₀ P – value FATCAT
15
10
5
0
0.0
0.2
0.4
0.6
0.8
TM Score

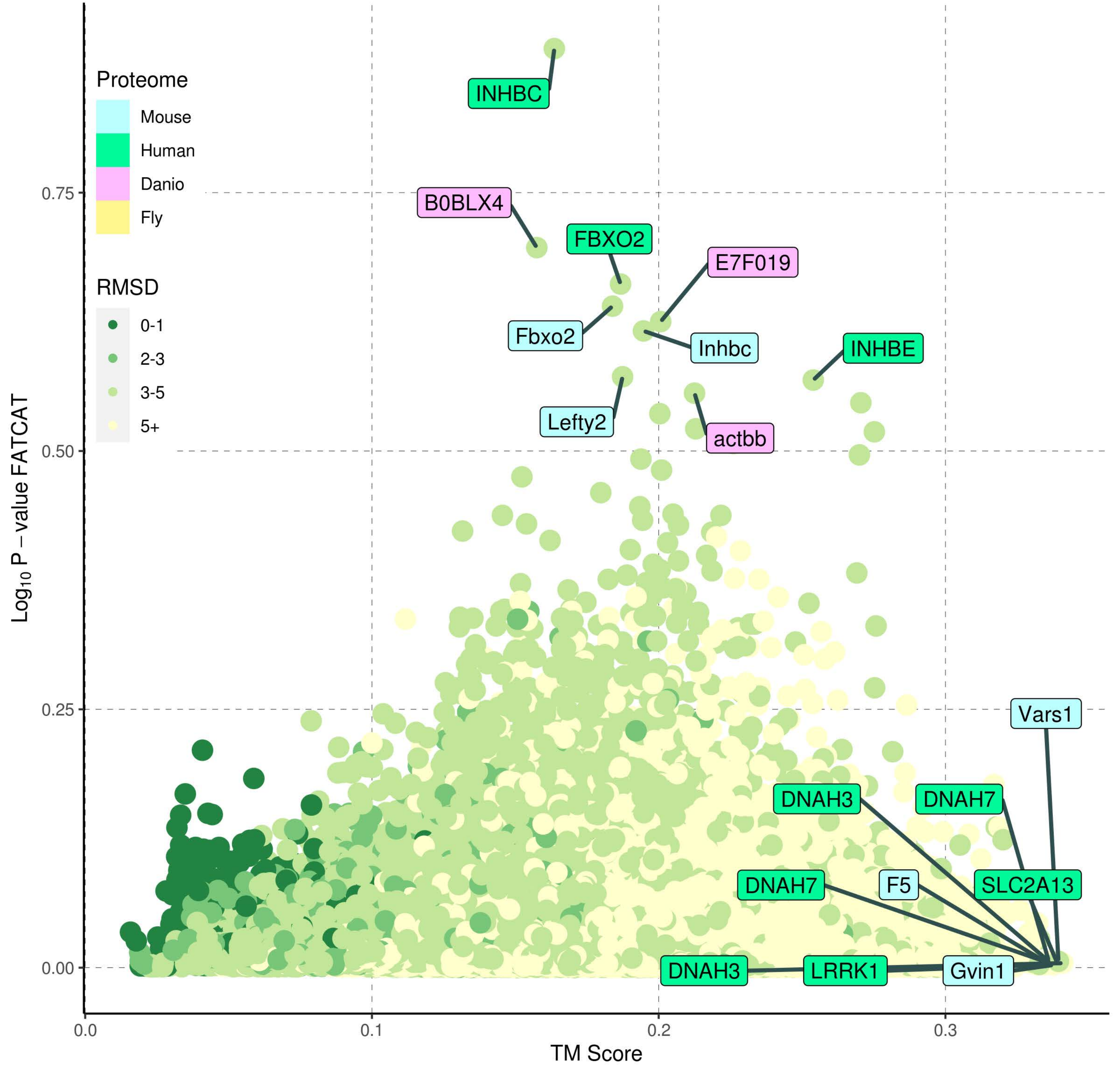

D9 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
NUDT15
Nudt15
nudt1
Nudt16
IDI2
Nudt1
Idi2
IDI1
Idi1
Nudt22
F1QQK5
NUDT22
NUDT16
Nudt17
NUDT17
nudt17
CCAR1
F6NQ00
Log$_{10}$ P − value FATCAT
4
3
2
1
0
0.2
0.4
0.6
TM Score

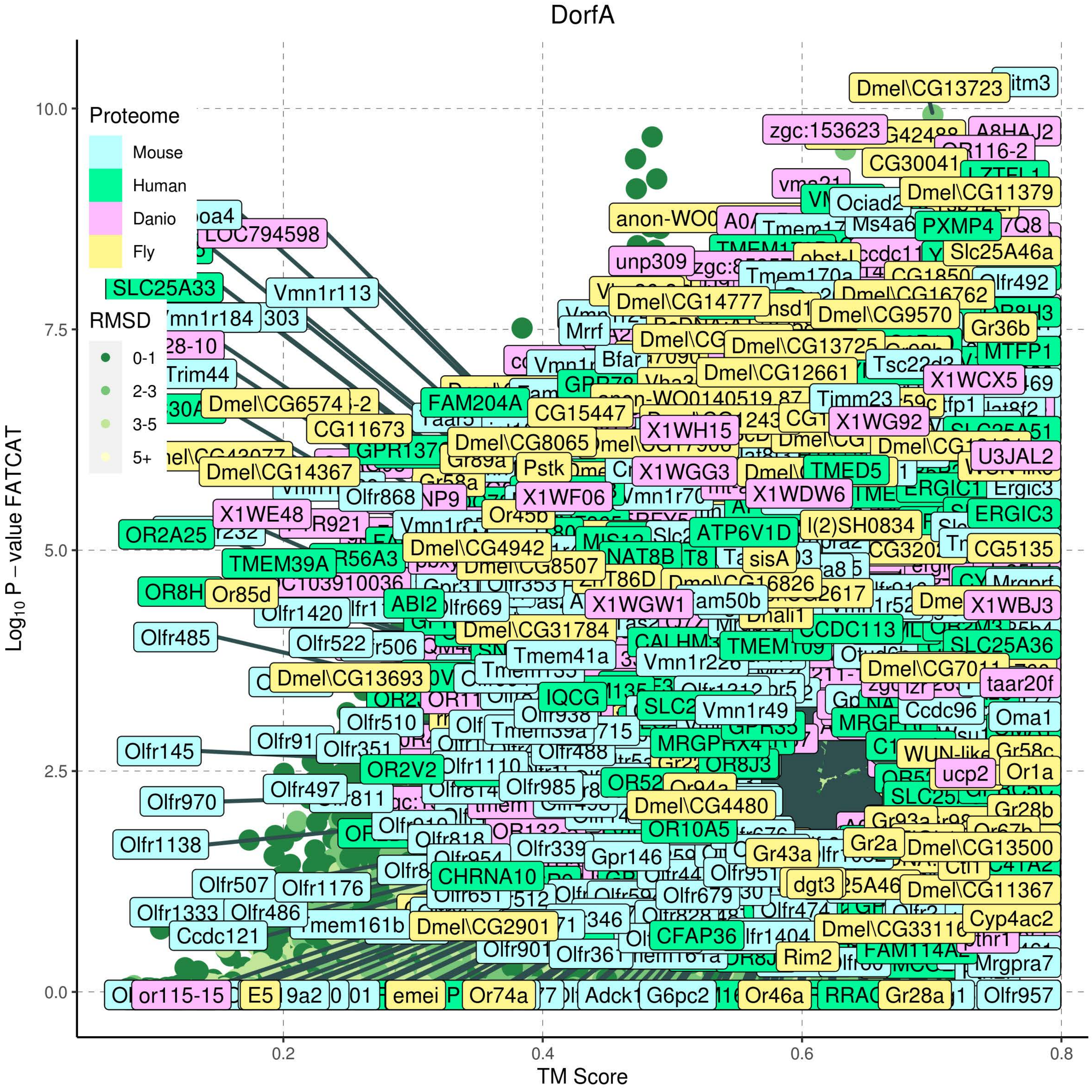

D10 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Dmel\CG32023
Q6DG97
Nudt2
NUDT2
nudt1
Nudt16l1
Nudt1
F1QFB9
Nudt22
NUDT1
NUDT8
F1QQK5
Nudt17
NUDT17
nudt17
NUDT22
CCAR1
F6NQ00
Log10 P − value FATCAT
6
4
2
0
0.0
0.1
0.2
0.3
0.4
0.5
TM Score

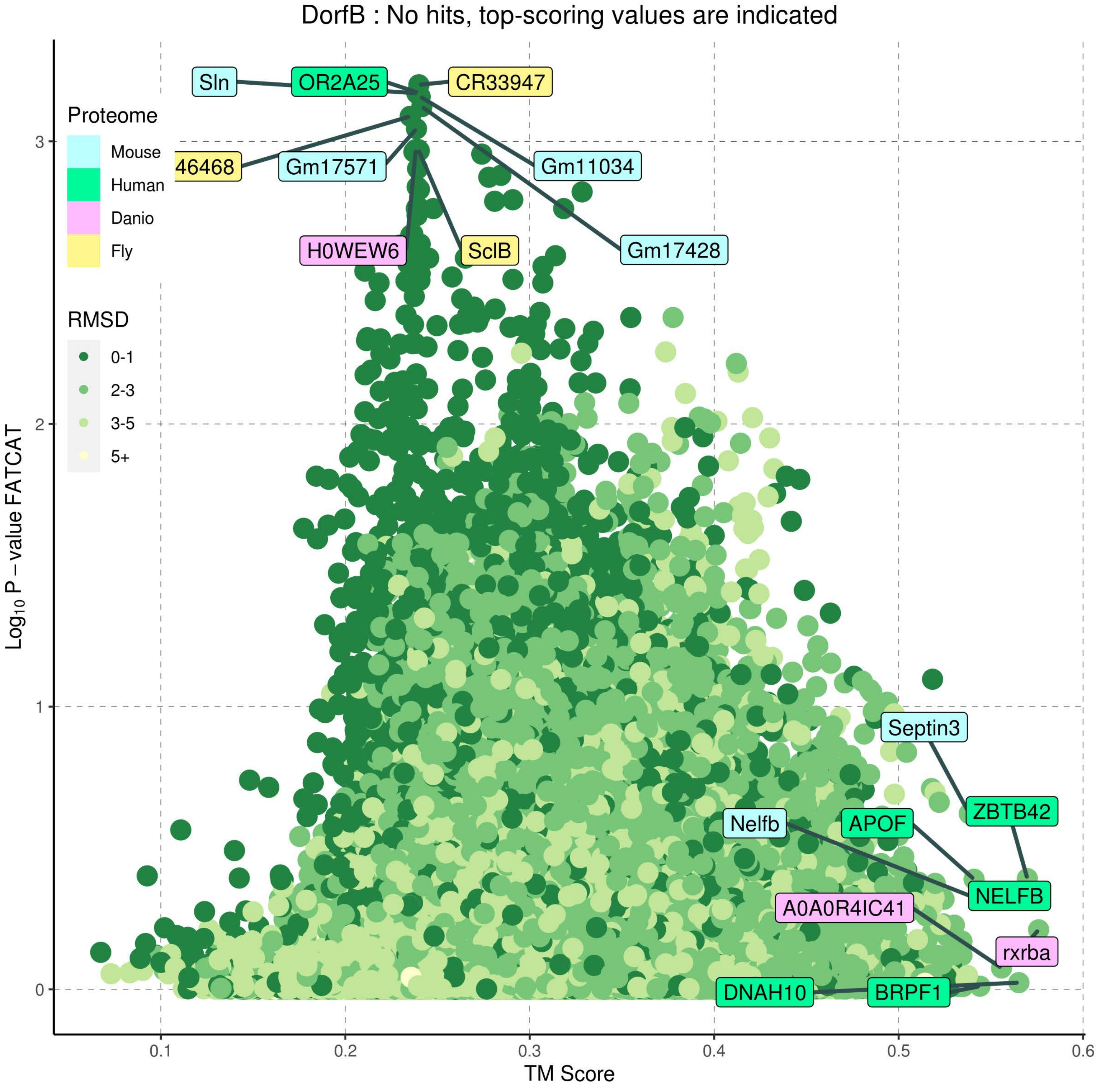

D11
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
brg1
Chd1l
Smarcad1
B7ZD98
Hells
Chd3
HELLS
CHD7
CHD9
SMARCA2
smarcad1
smarcad1b
Smarca4
SMARCAD1
Smarca2
SMARCA4
ERCC6L
Ercc6l
F1R294
brm
A0A0R4IFG3
Dmel\CG10445
ercc6l
CHD6
ERCC6L2
XNP
Ercc6
F1QJP0
CHD9
Ercc6l2
ERCC6
INO80
Mi-2
A0A0R4IJ25
F1RBT2
Chd1
Ino80
E23
OR2A25
CHD4
A0A2R8PZH8
A0A0R4IJ89
CHD3
Chd4
RAD54L2
Hel89B
A0A0R4IAE4
A0A0R4IS87
E7F7W5
F1QWV5
Chd5
Rad54l2
A0A2R8PY80
Atrx
A0A0R4IR86
Chd2
Chd3
F1R3L6
ATRX
OR2A25
CHD5
Ino80
E7F4M2
0
2
4
6
0.0
0.2
0.4
0.6
TM Score
Log_{10} P – value FATCAT

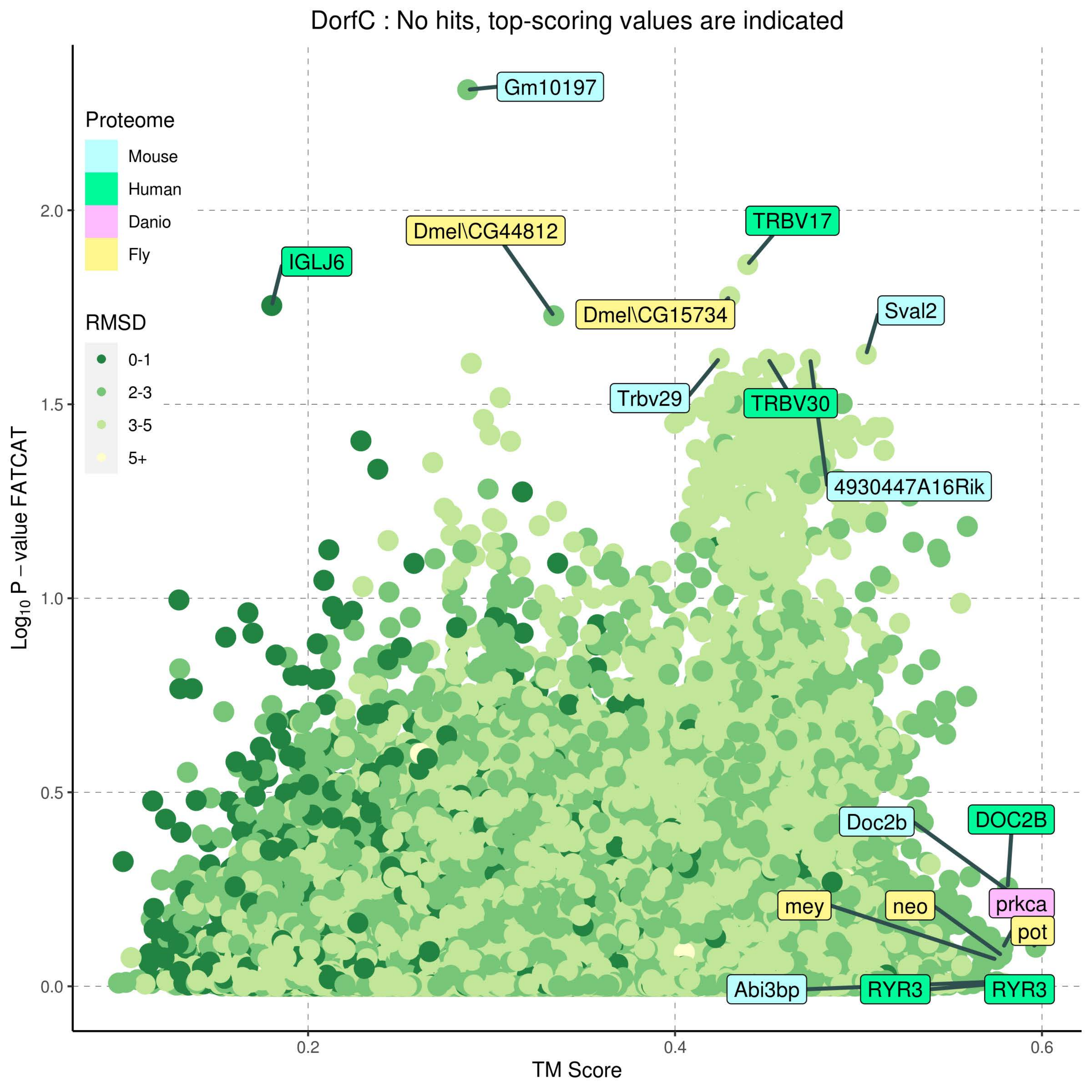

D12
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Cmtr1
Cmtr2
CMTR2
cmtr2
Log10 P − value FATCAT
TM Score
0.0
0.5
1.0
1.5
2.0
2.5
0.0
0.2
0.4
0.6

D13 : No hits, top-scoring values are indicated

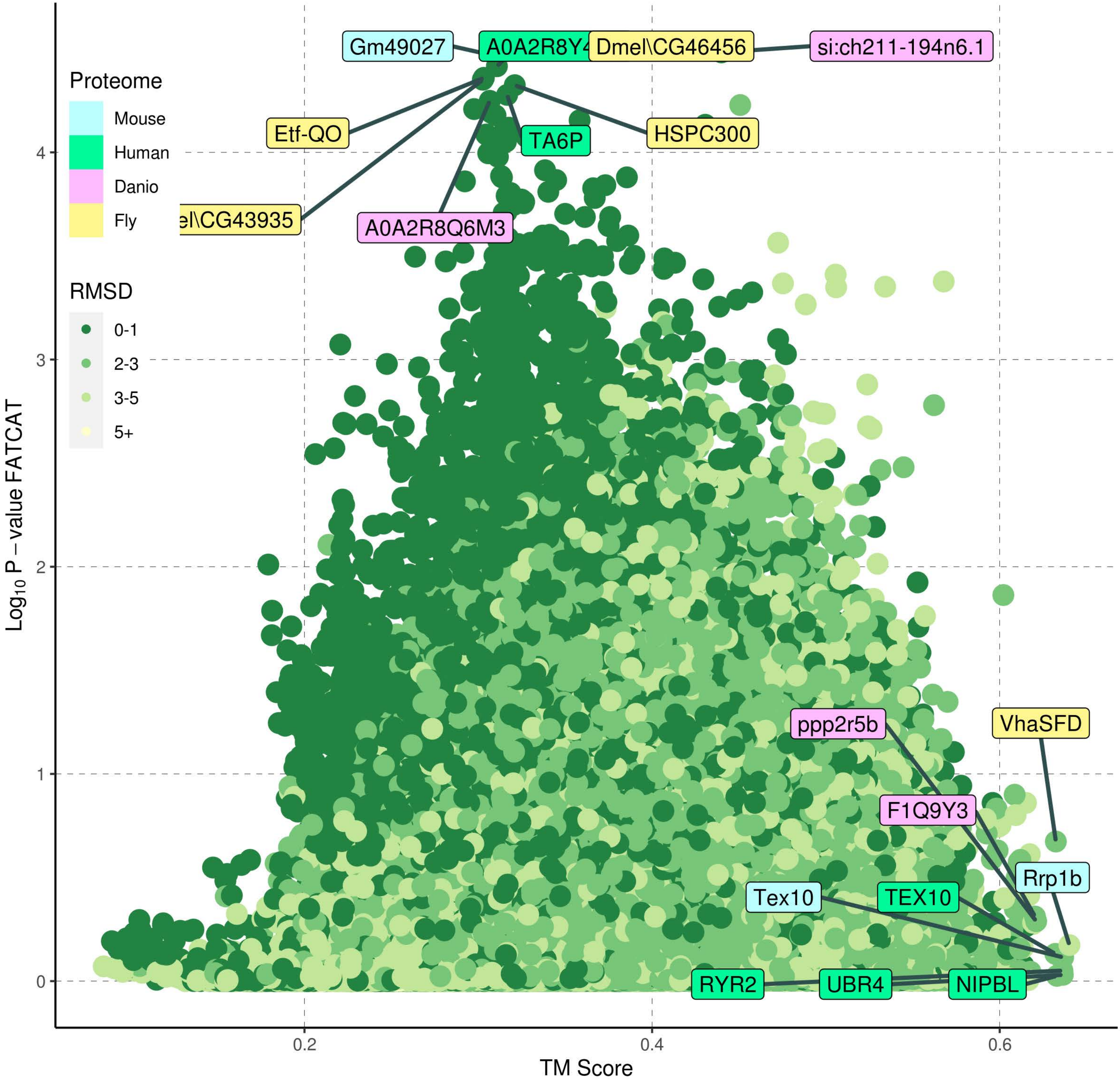


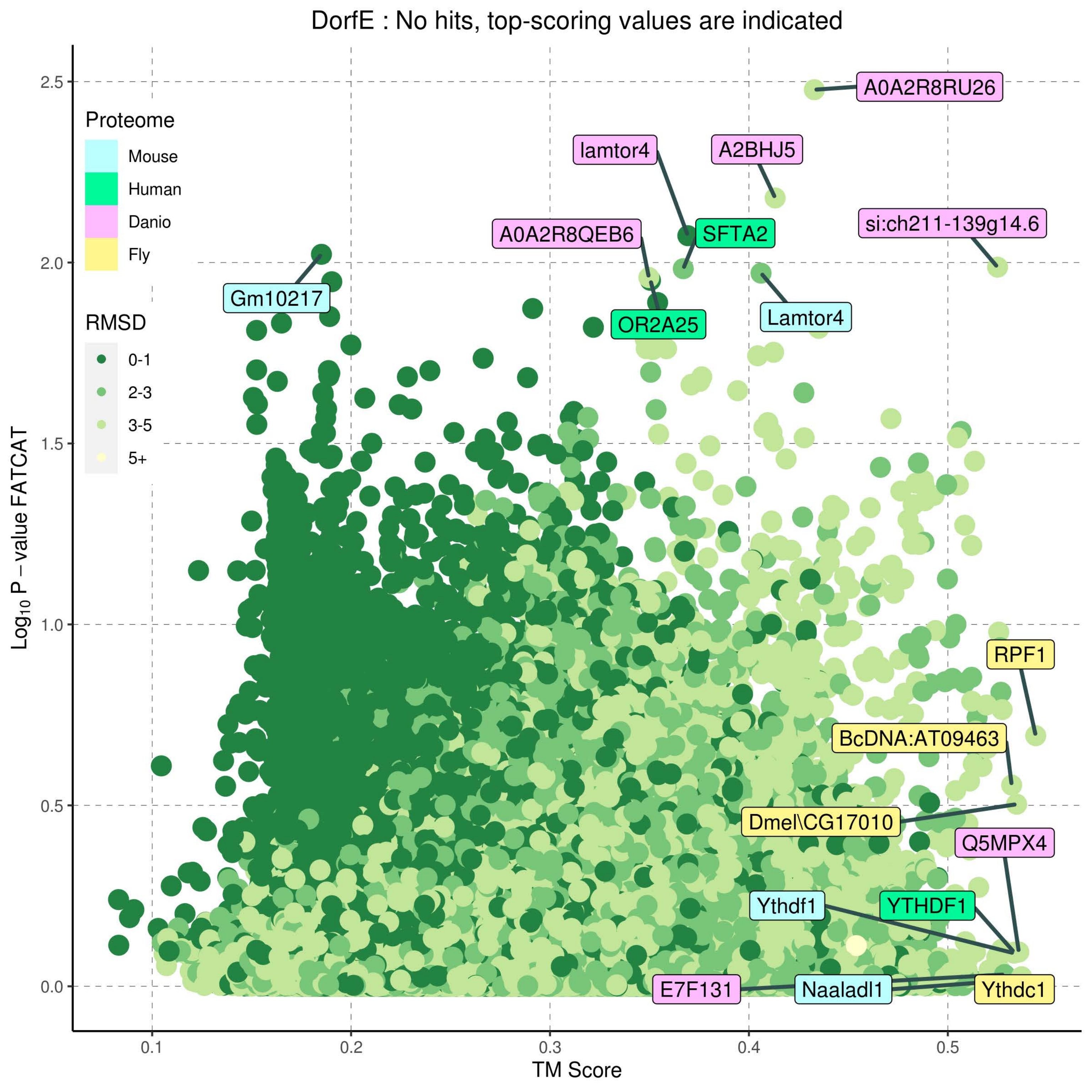

DorfA
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
TM Score
0.2
0.4
0.6
0.8
Log10 P − value FATCAT
0.0
2.5
5.0
7.5
10.0
Dmel\CG13723
itm3
zgc:153623
A8HAJ2
CG30041
Dmel\CG11379
Ociad2
PXMP4
Slc25A46a
Olfr492
Dmel\CG16762
Dmel\CG9570
Gr36b
MTFP1
X1WCX5
Timm23
X1WG92
U3JAL2
Ergic3
ERGIC3
CG5135
X1WBJ3
SLC25A36
taar20f
Oma1
Gr58c
Or1a
ucp2
Gr28b
Dmel\CG13500
Dmel\CG11367
Cyp4ac2
Mrgpra7
Olfr957
LOC794598
SLC25A33
Vmn1r113
Vmn1r184
Trim44
Dmel\CG6574
CG11673
Dmel\CG14367
X1WE48
OR2A25
TMEM39A
OR8H
Or85d
Olfr1420
Olfr485
Olfr522
Dmel\CG13693
Olfr510
Olfr145
Olfr970
Olfr497
Olfr1138
Olfr507
Olfr1176
Olfr1333
Olfr486
Ccdc121
or115-15
emei
Or74a
Adck1
G6pc2
Or46a
Gr28a
unp309
Dmel\CG14777
Mrrf
Bfar
Dmel\CG13725
Dmel\CG12661
Tsc22d3
FAM204A
CG15447
X1WH15
Dmel\CG8065
GPR137
Pstk
X1WGG3
TMED5
ERGIC1
X1WDW6
X1WF06
Olfr868
Or45b
ATP6V1D
l(2)SH0834
Dmel\CG4942
Dmel\CG8507
NAT8B
sisA
X1WGW1
ABI2
Olfr669
Dmel\CG31784
CCDC113
TMEM109
Tmem41a
Vmn1r226
Dmel\CG7011
IQCG
Vmn1r49
Ccdc96
MRGPRX4
OR8J3
OR2V2
Olfr488
Olfr985
Dmel\CG4480
OR10A5
Gr2a
Gr43a
Olfr339
Gpr146
CHRNA10
Olfr951
dgt3
Olfr679
Dmel\CG2901
CFAP36
Dmel\CG33116
Rim2
Olfr361
Olfr901
anon-WO0140519.87

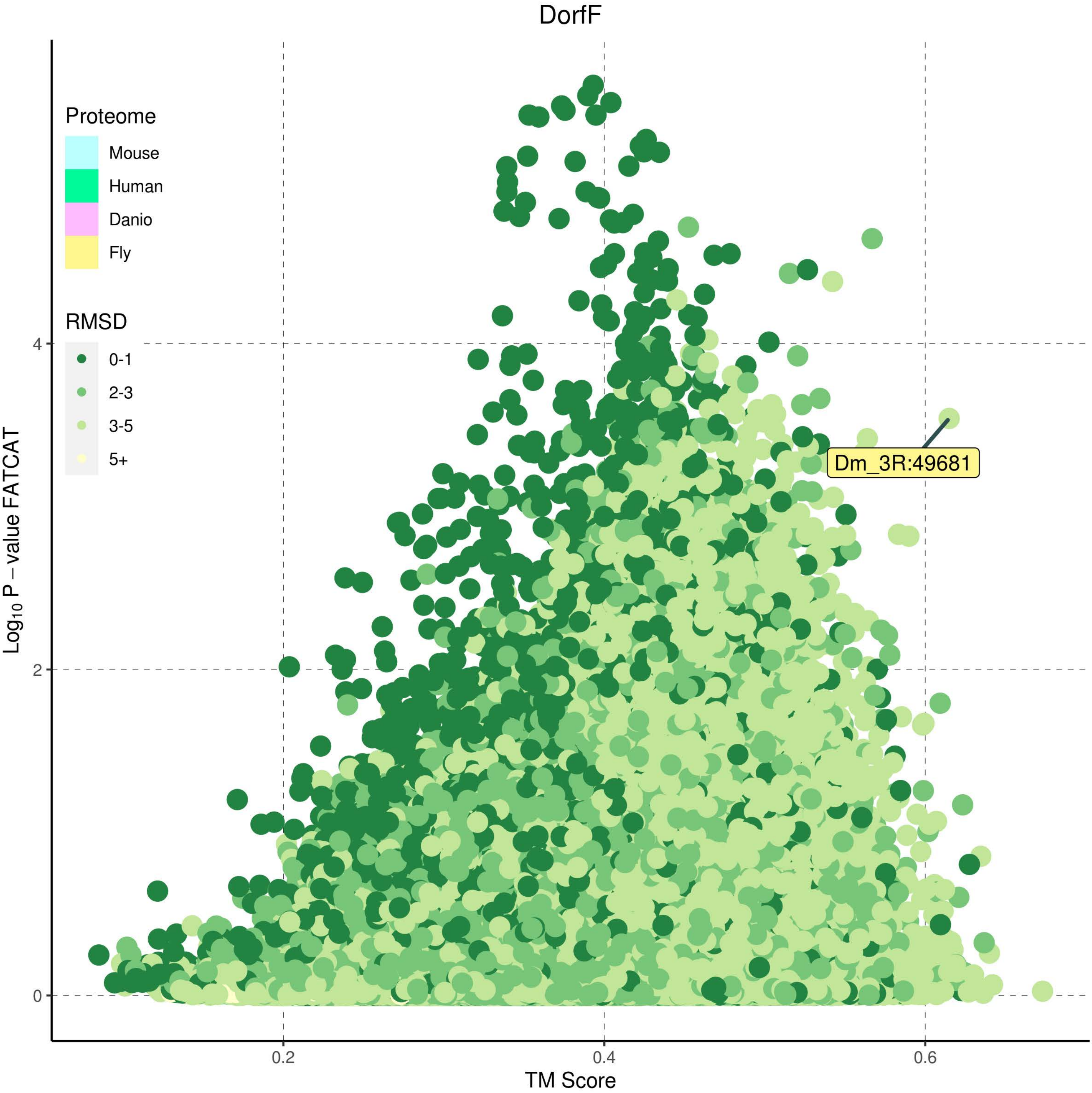

DorfB : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P − value FATCAT
TM Score
0
1
2
3
0.1
0.2
0.3
0.4
0.5
0.6
Sln
OR2A25
CR33947
46468
Gm17571
Gm11034
H0WEW6
SclB
Gm17428
Septin3
ZBTB42
Nelfb
APOF
NELFB
A0A0R4IC41
rxrba
DNAH10
BRPF1

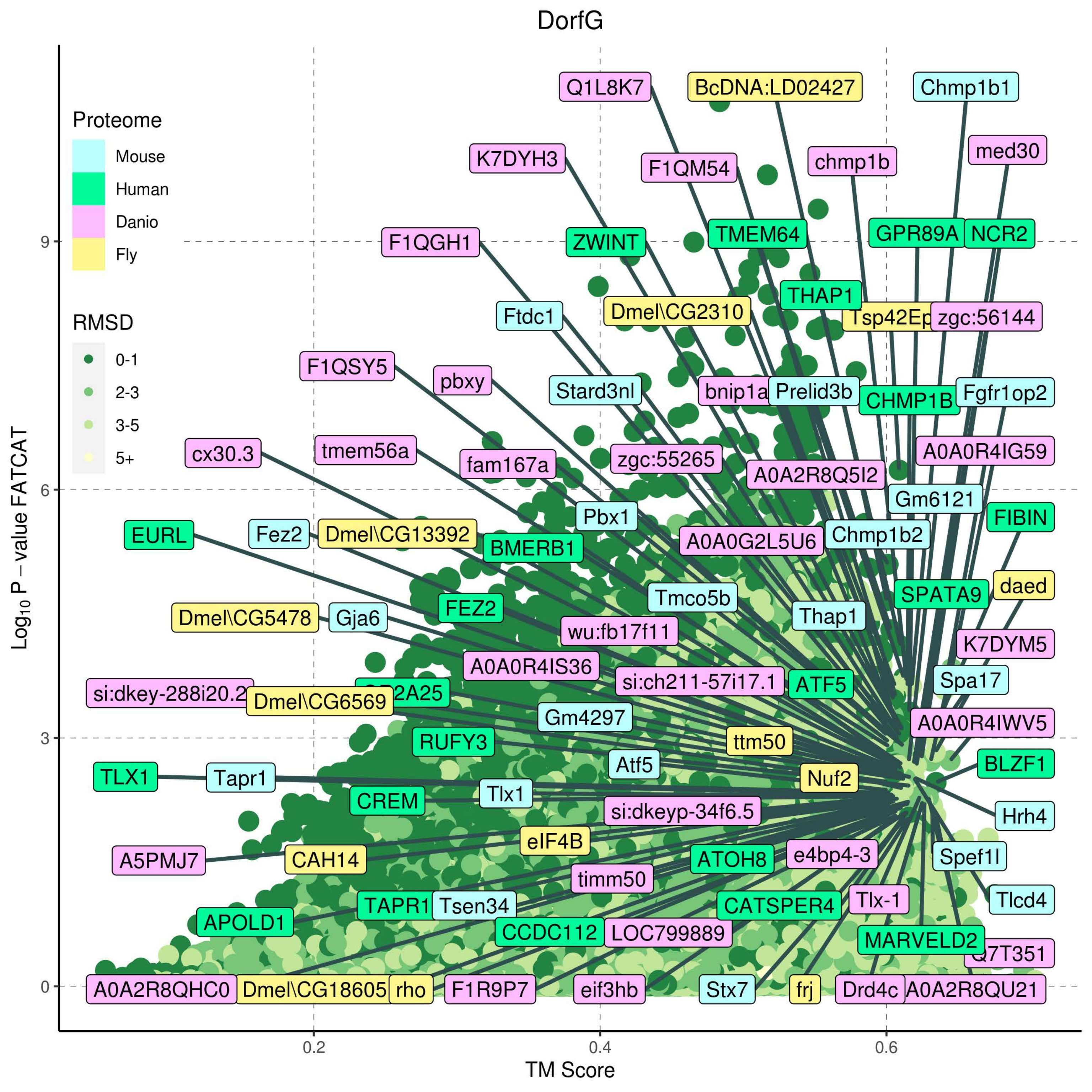

DorfC : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P − value FATCAT
2.0
1.5
1.0
0.5
0.0
TM Score
0.2
0.4
0.6
Gm10197
Dmel\CG44812
IGLJ6
TRBV17
Dmel\CG15734
Sval2
Trbv29
TRBV30
4930447A16Rik
Doc2b
DOC2B
mey
neo
prkca
pot
Abi3bp
RYR3
RYR3

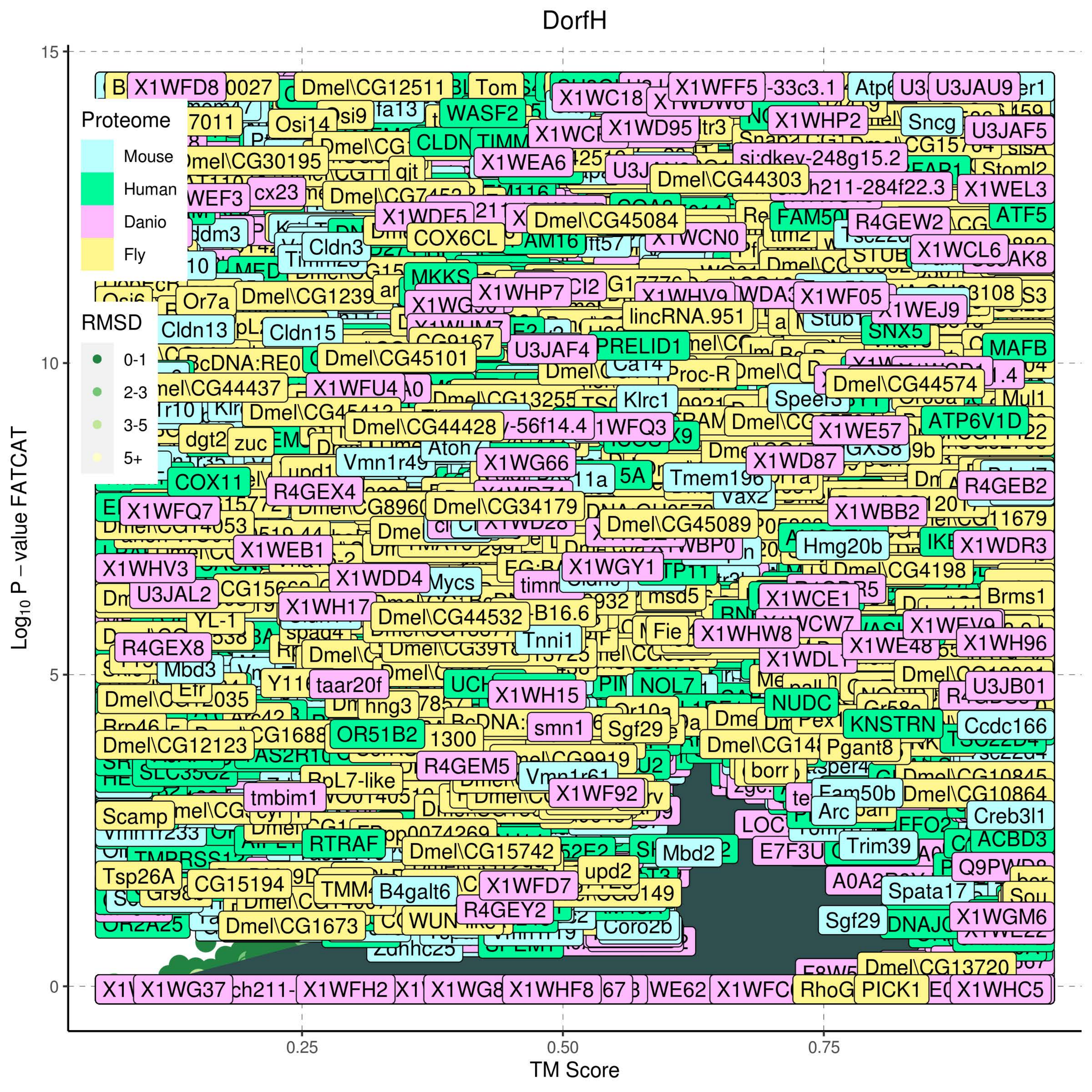
DorfD : No hits, top-scoring values are indicated

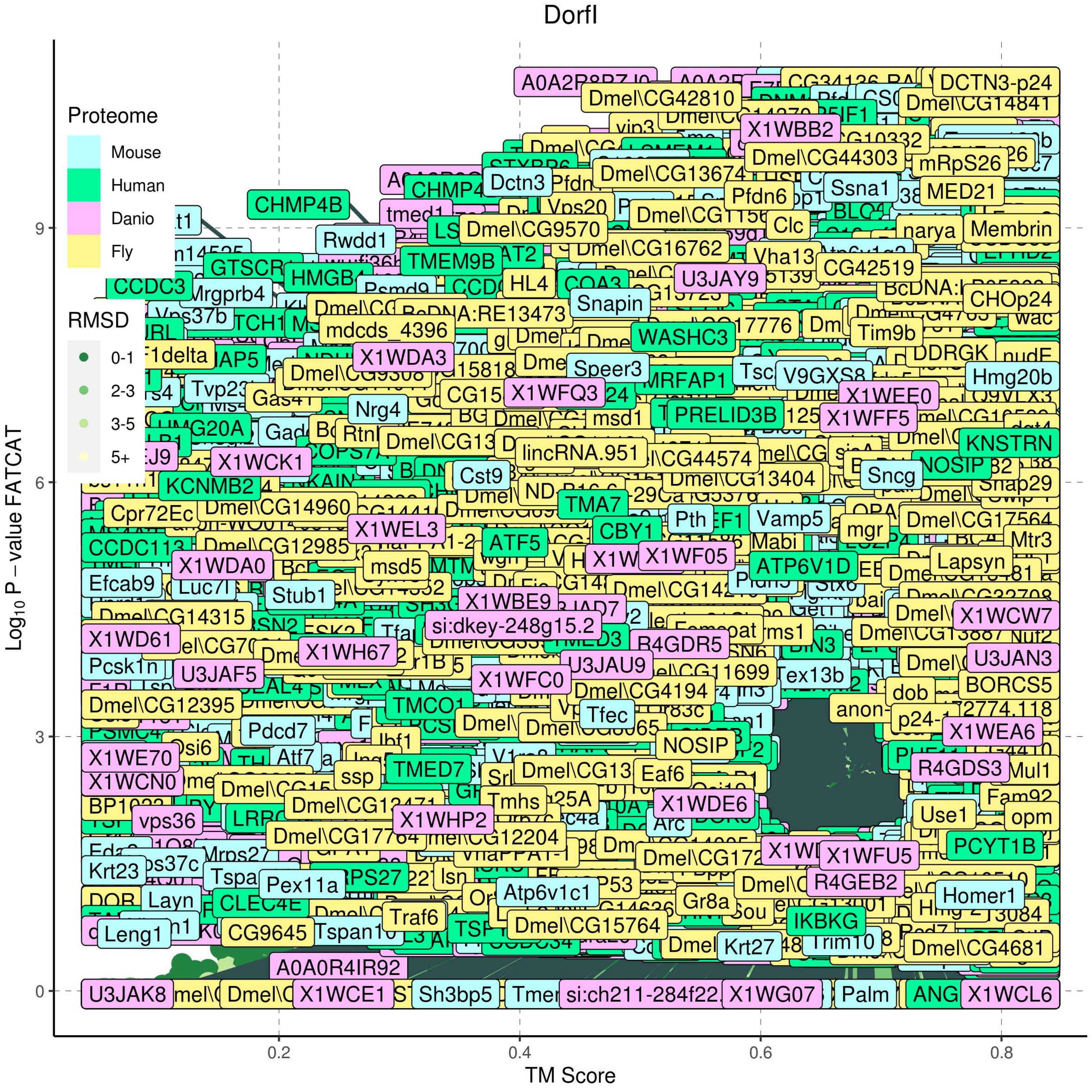


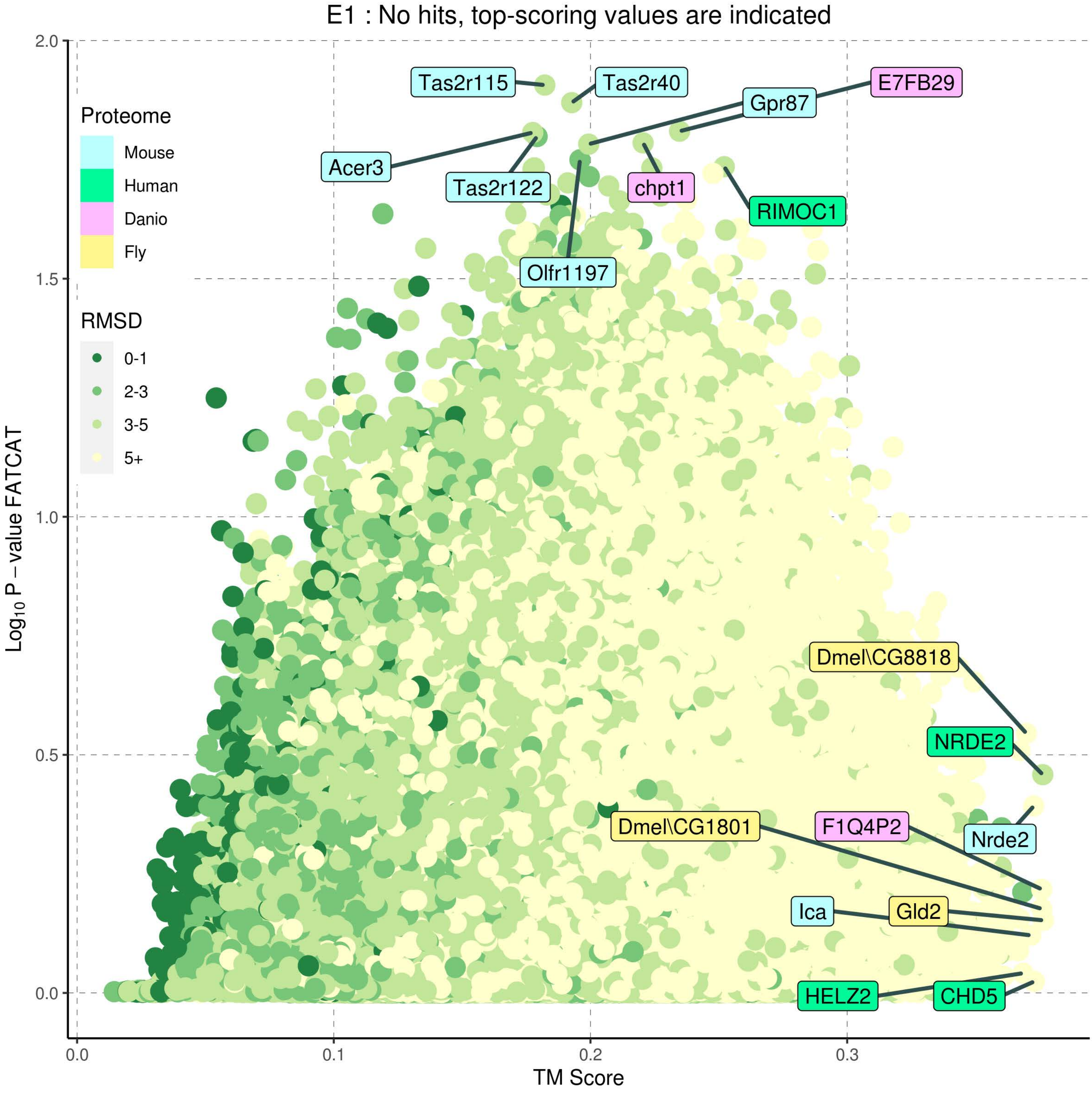

DorfE : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log$_{10}$ P – value FATCAT
TM Score
0.1
0.2
0.3
0.4
0.5
0.0
0.5
1.0
1.5
2.0
2.5
A0A2R8RU26
lamtor4
A2BHJ5
SFTA2
A0A2R8QEB6
si:ch211-139g14.6
Gm10217
OR2A25
Lamtor4
RPF1
BcDNA:AT09463
Dmel\CG17010
Q5MPX4
Ythdf1
YTHDF1
E7F131
Naaladl1
Ythdc1

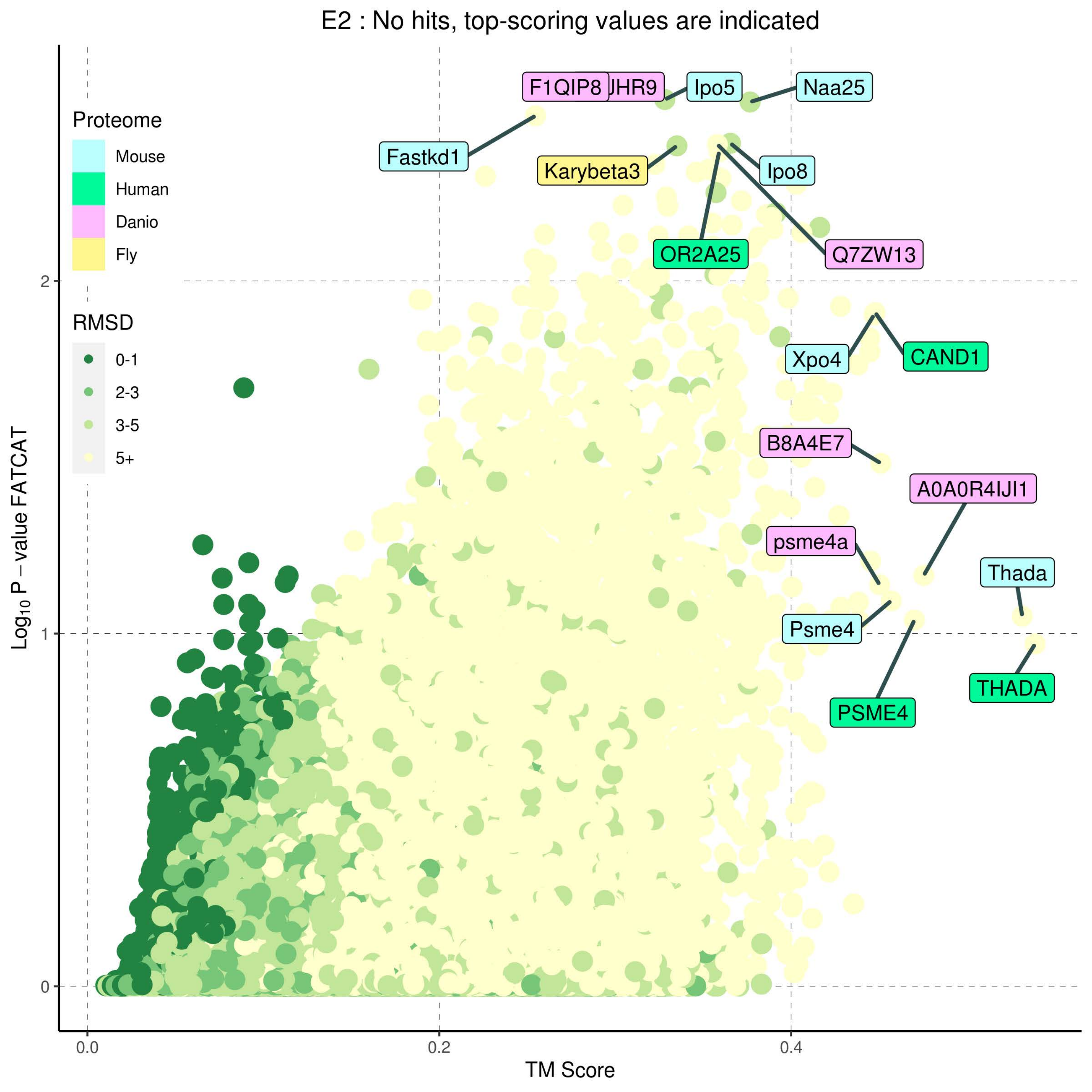

DorfF
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Dm_3R:49681
Log$_{10}$ P − value FATCAT
0
2
4
TM Score
0.2
0.4
0.6

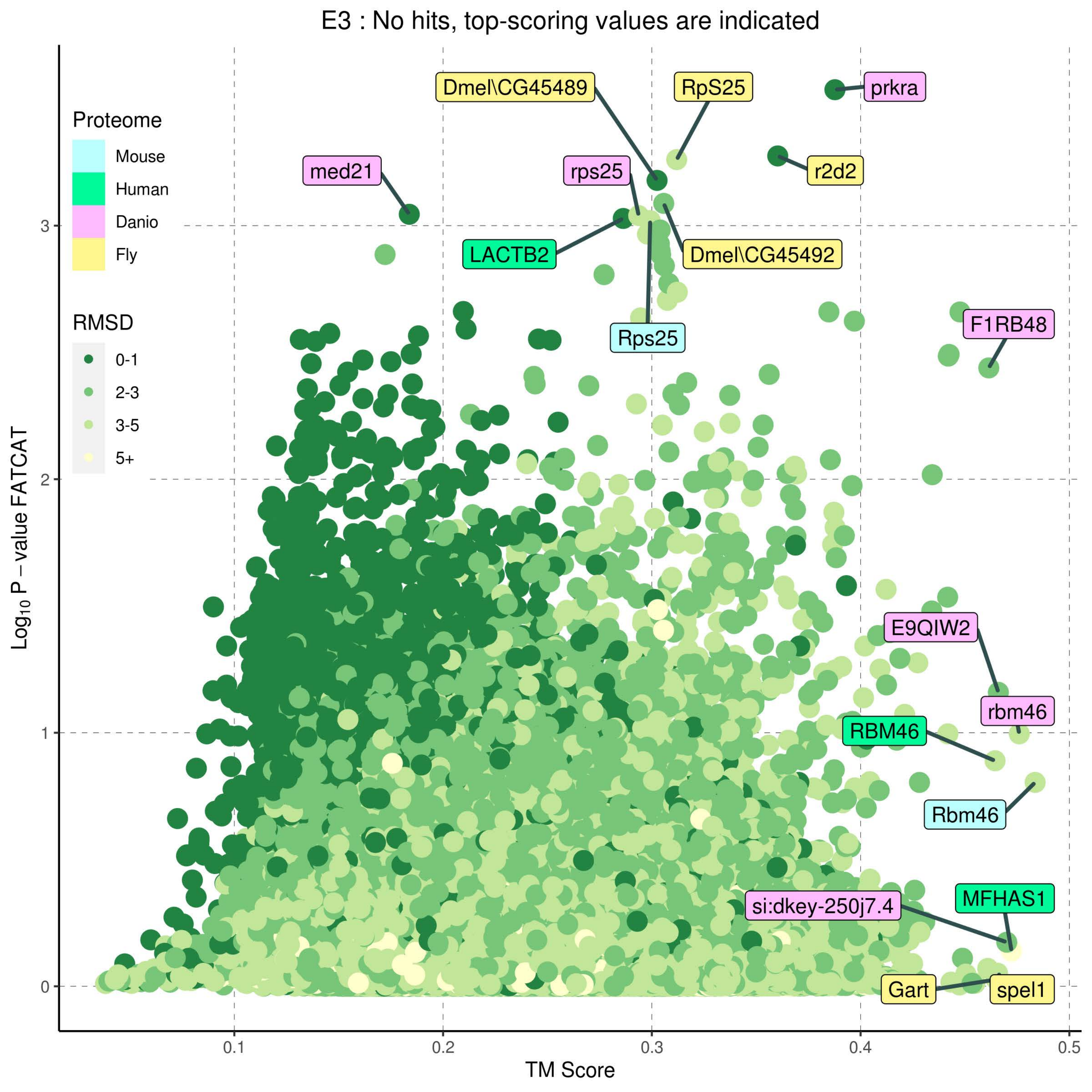

DorfG
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Q1L8K7
BcDNA:LD02427
Chmp1b1
K7DYH3
F1QM54
chmp1b
med30
F1QGH1
ZWINT
TMEM64
GPR89A
NCR2
THAP1
Ftdc1
Dmel\CG2310
Tsp42Ep
zgc:56144
F1QSY5
pbxy
Stard3nl
bnip1a
Prelid3b
CHMP1B
Fgfr1op2
cx30.3
tmem56a
fam167a
zgc:55265
A0A2R8Q5I2
A0A0R4IG59
Gm6121
EURL
Fez2
Dmel\CG13392
BMERB1
Pbx1
A0A0G2L5U6
Chmp1b2
FIBIN
Tmco5b
SPATA9
daed
Dmel\CG5478
Gja6
FEZ2
wu:fb17f11
Thap1
K7DYM5
A0A0R4IS36
si:ch211-57i17.1
ATF5
Spa17
si:dkey-288i20.2
R2A25
Dmel\CG6569
Gm4297
A0A0R4IWV5
RUFY3
ttm50
Atf5
BLZF1
TLX1
Tapr1
Nuf2
CREM
Tlx1
si:dkeyp-34f6.5
Hrh4
eIF4B
A5PMJ7
CAH14
ATOH8
e4bp4-3
Spef1l
timm50
TAPR1
Tsen34
CATSPER4
Tlx-1
Tlcd4
APOLD1
CCDC112
LOC799889
MARVELD2
Q7T351
A0A2R8QHC0
Dmel\CG18605
rho
F1R9P7
eif3hb
Stx7
frj
Drd4c
A0A2R8QU21
9
6
3
0
Log10 P − value FATCAT
0.2
0.4
0.6
TM Score

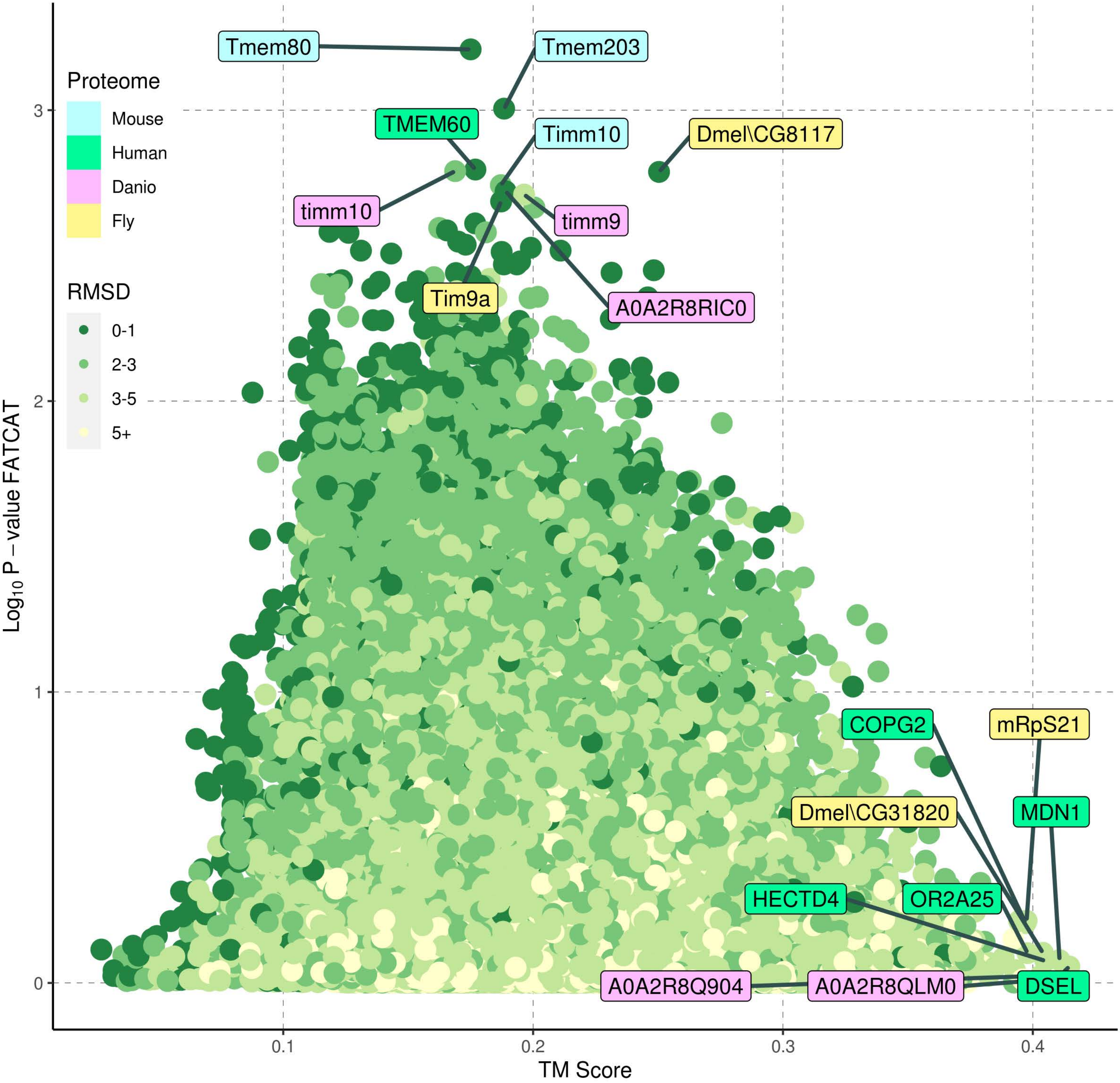

DorfH
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log$_{10}$ P – value FATCAT
15
10
5
0
TM Score
0.25
0.50
0.75


Dorfl
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
TM Score
0
3
6
9
0.2
0.4
0.6
0.8
DCTN3-p24
Dmel\CG42810
Dmel\CG14841
X1WBB2
Dmel\CG44303
mRpS26
CHMP4B
Dctn3
Dmel\CG13674
Ssna1
MED21
Pfdn6
Rwdd1
Dmel\CG9570
Clc
narya
Membrin
Dmel\CG16762
Vha13
TMEM9B
GTSCR
HMGB
U3JAY9
CG42519
CCDC3
HL4
Mrgprb4
Snapin
CHOp24
Vps37b
BcDNA:RE13473
mdcds_4396
WASHC3
Tim9b
X1WDA3
DDRGK
Dmel\CG9308
Speer3
Hmg20b
Tvp23
X1WFQ3
MRFAP1
V9GXS8
X1WEE0
Gas41
Nrg4
PRELID3B
X1WFF5
HMG20A
msd1
KNSTRN
Dmel\CG13
lincRNA.951
X1WCK1
Cst9
Dmel\CG13404
Sncg
NOSIP
Snap29
KCNMB2
TMA7
Cpr72Ec
Dmel\CG14960
Pth
Vamp5
mgr
Dmel\CG17564
X1WEL3
CBY1
CCDC113
Dmel\CG12985
ATF5
Mtr3
X1WDA0
X1WF05
msd5
ATP6V1D
Lapsyn
Efcab9
Luc7l
Stub1
X1WBE9
Dmel\CG14315
si:dkey-248g15.2
X1WCW7
X1WD61
X1WH67
R4GDR5
Pcsk1n
U3JAF5
U3JAU9
X1WFC0
Tex13b
U3JAN3
Dmel\CG4194
BORCS5
Dmel\CG12395
TMCO1
dob
Tfec
Pdcd7
NOSIP
X1WEA6
X1WE70
Osi6
Atf7
TMED7
Dmel\CG13
Eaf6
R4GDS3
Mul1
X1WCN0
ssp
X1WDE6
vps36
Tmhs
X1WHP2
Use1
opm
Dmel\CG17764
PCYT1B
Krt23
X1WFU5
Pex11a
R4GEB2
Tspan
Isn
Atp6v1c1
Homer1
Layn
CLEC4E
Gr8a
Traf6
Dmel\CG15764
IKBKG
Leng1
CG9645
Krt27
Trim10
Dmel\CG4681
A0A0R4IR92
U3JAK8
X1WCE1
Sh3bp5
si:ch211-284f22
X1WG07
Palm
ANG
X1WCL6

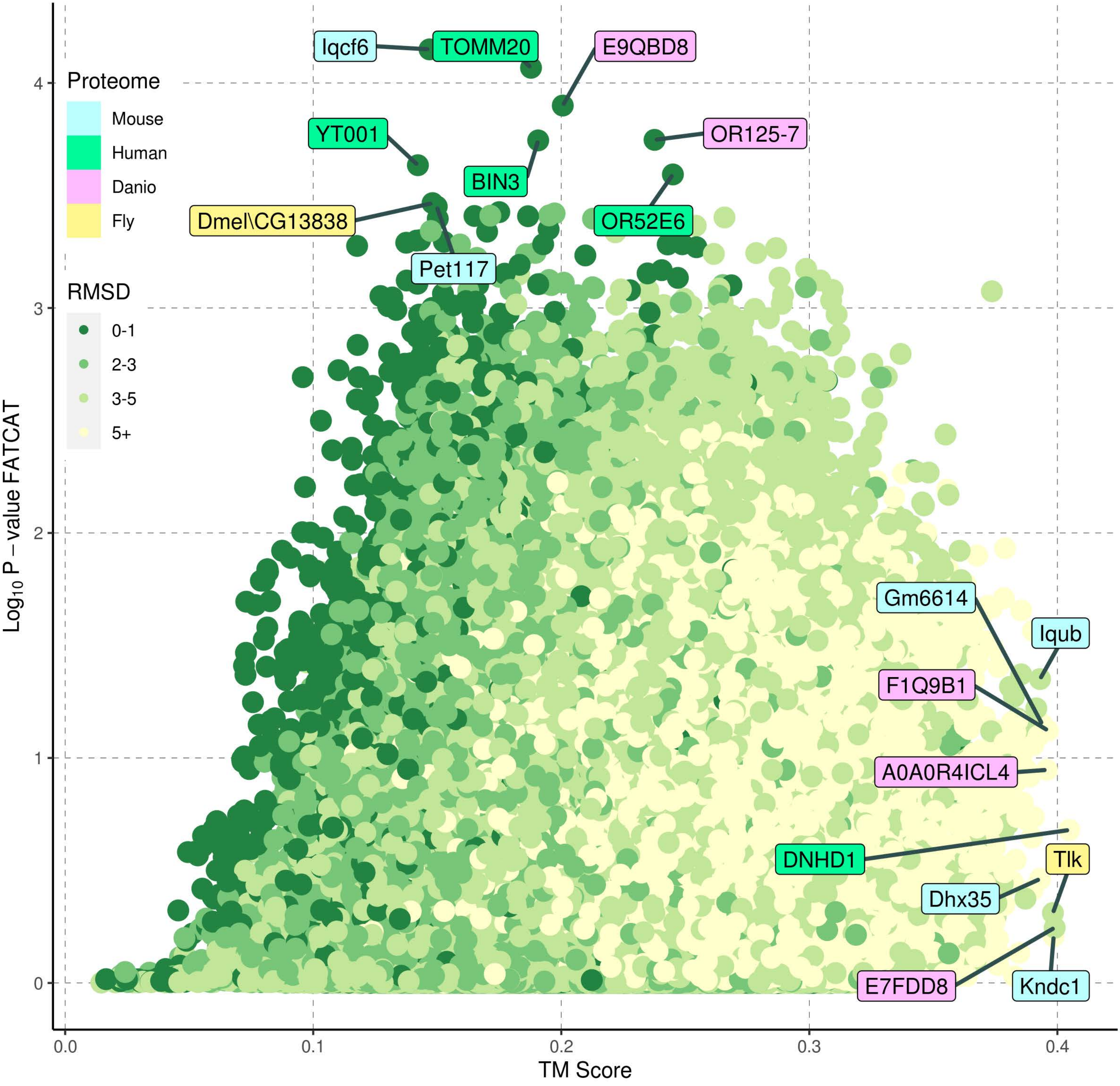

E1 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P − value FATCAT
TM Score
2.0
1.5
1.0
0.5
0.0
0.0
0.1
0.2
0.3
Tas2r115
Tas2r40
E7FB29
Gpr87
Acer3
Tas2r122
chpt1
RIMOC1
Olfr1197
Dmel\CG8818
NRDE2
Dmel\CG1801
F1Q4P2
Nrde2
Ica
Gld2
HELZ2
CHD5

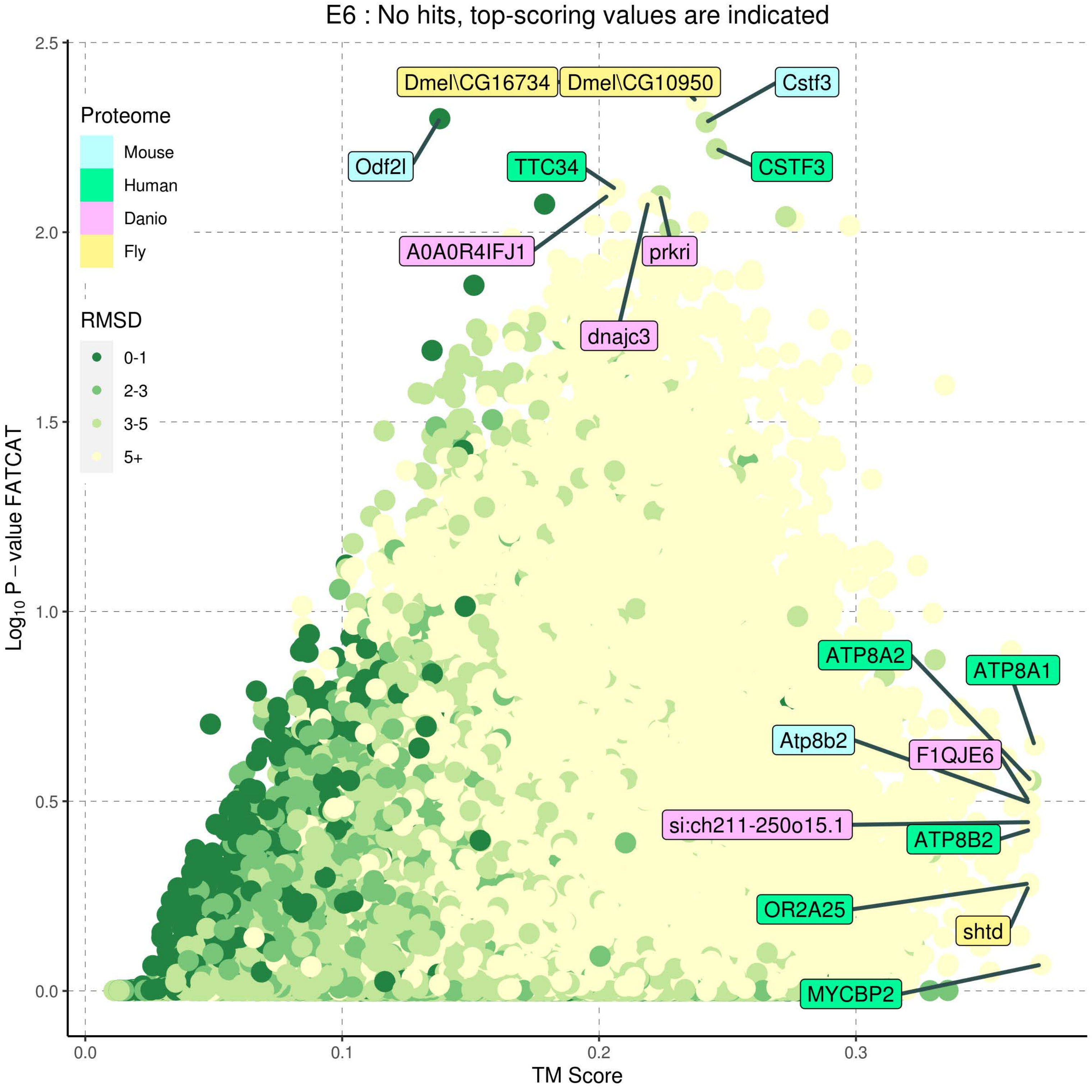

E2 : No hits, top-scoring values are indicated

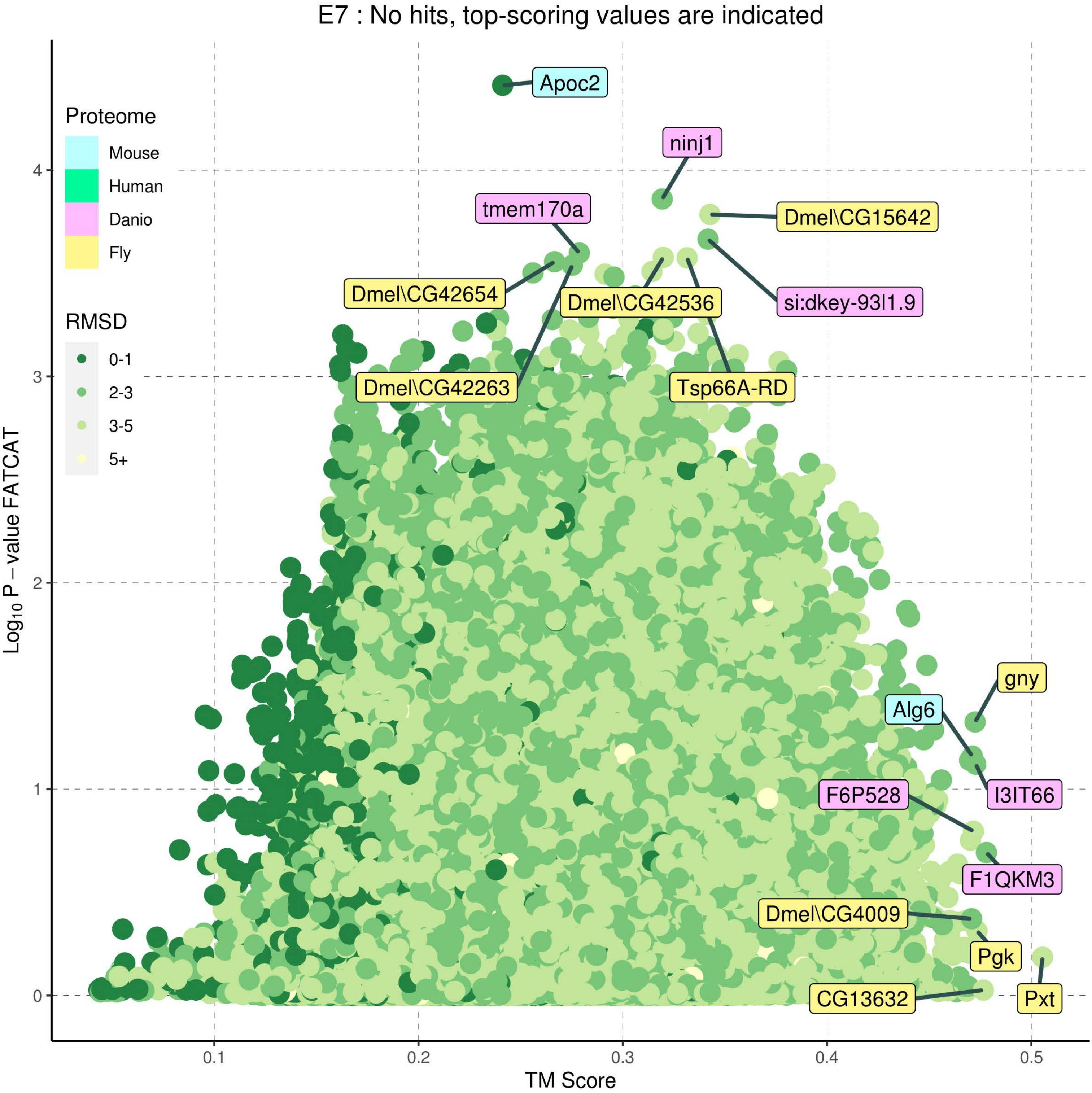

E3 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log₁₀ P − value FATCAT
TM Score
0
1
2
3
0.1
0.2
0.3
0.4
0.5
Dmel\CG45489
RpS25
prkra
med21
rps25
r2d2
LACTB2
Dmel\CG45492
Rps25
F1RB48
E9QIW2
rbm46
RBM46
Rbm46
MFHAS1
si:dkey-250j7.4
Gart
spel1

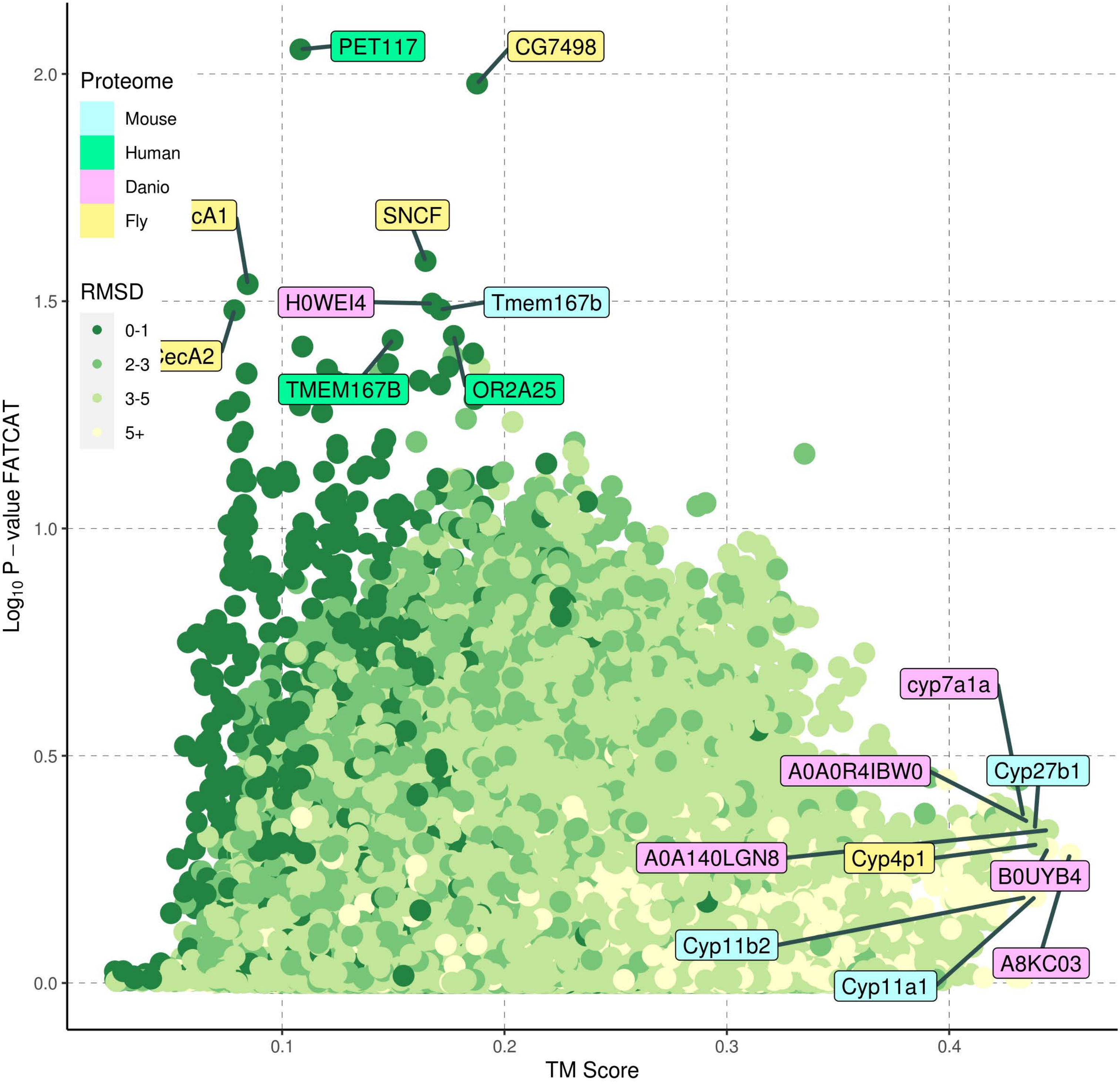

E4 : No hits, top-scoring values are indicated

E5 : No hits, top-scoring values are indicated

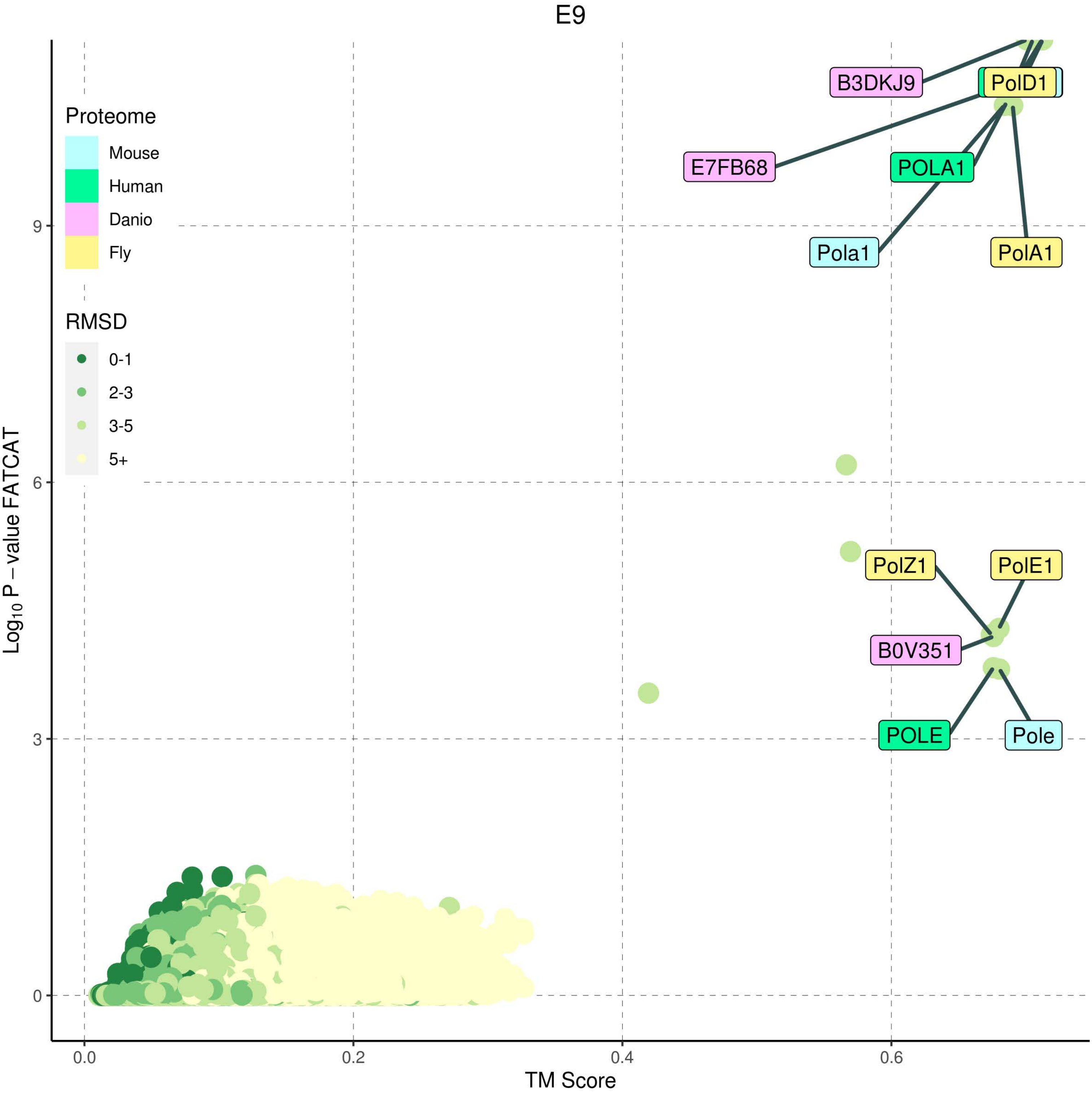


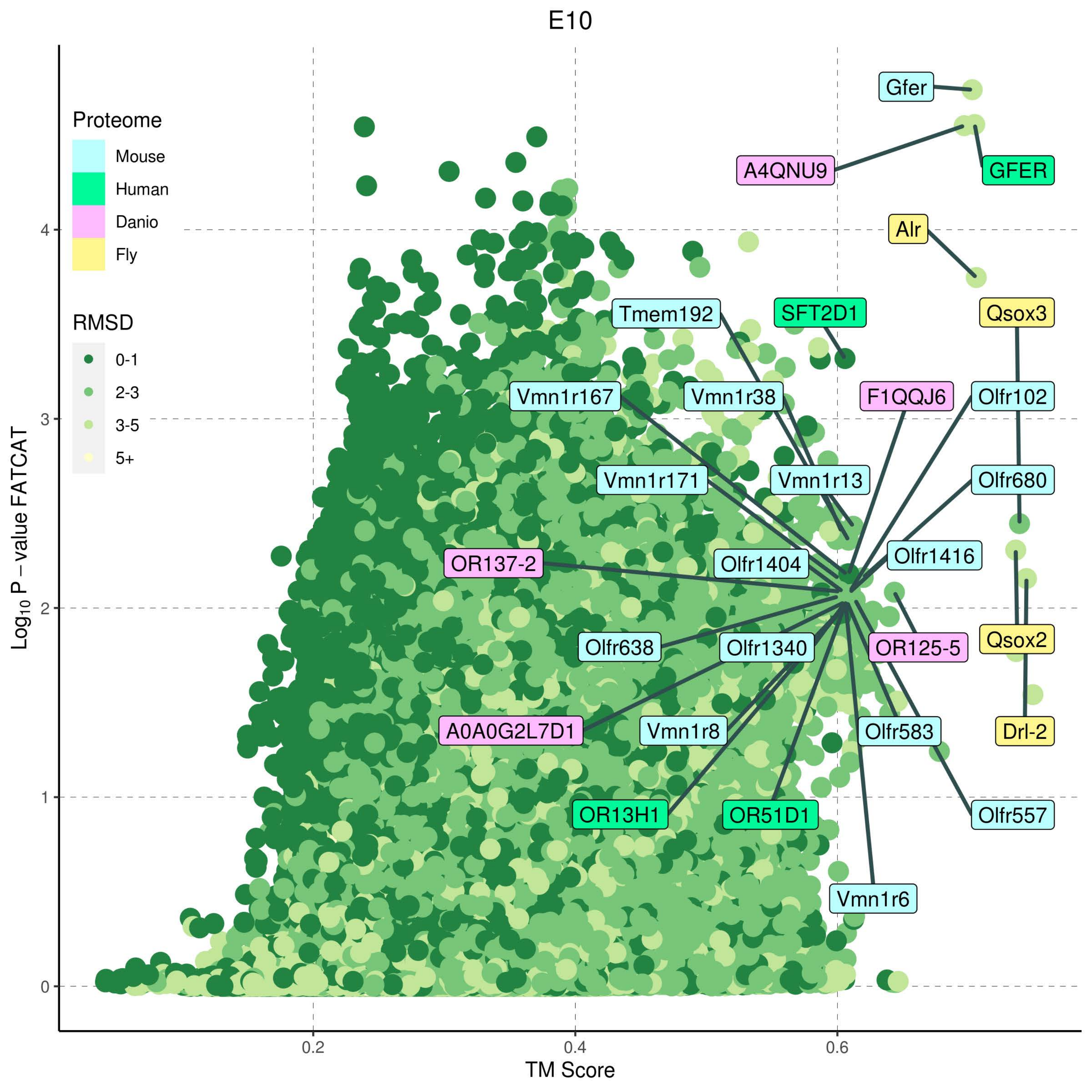

E6 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Dmel\CG16734
Dmel\CG10950
Cstf3
Odf2l
TTC34
CSTF3
A0A0R4IFJ1
prkri
dnajc3
ATP8A2
ATP8A1
Atp8b2
F1QJE6
si:ch211-250o15.1
ATP8B2
OR2A25
shtd
MYCBP2
Log10 P − value FATCAT
TM Score
0.0
0.5
1.0
1.5
2.0
2.5
0.0
0.1
0.2
0.3

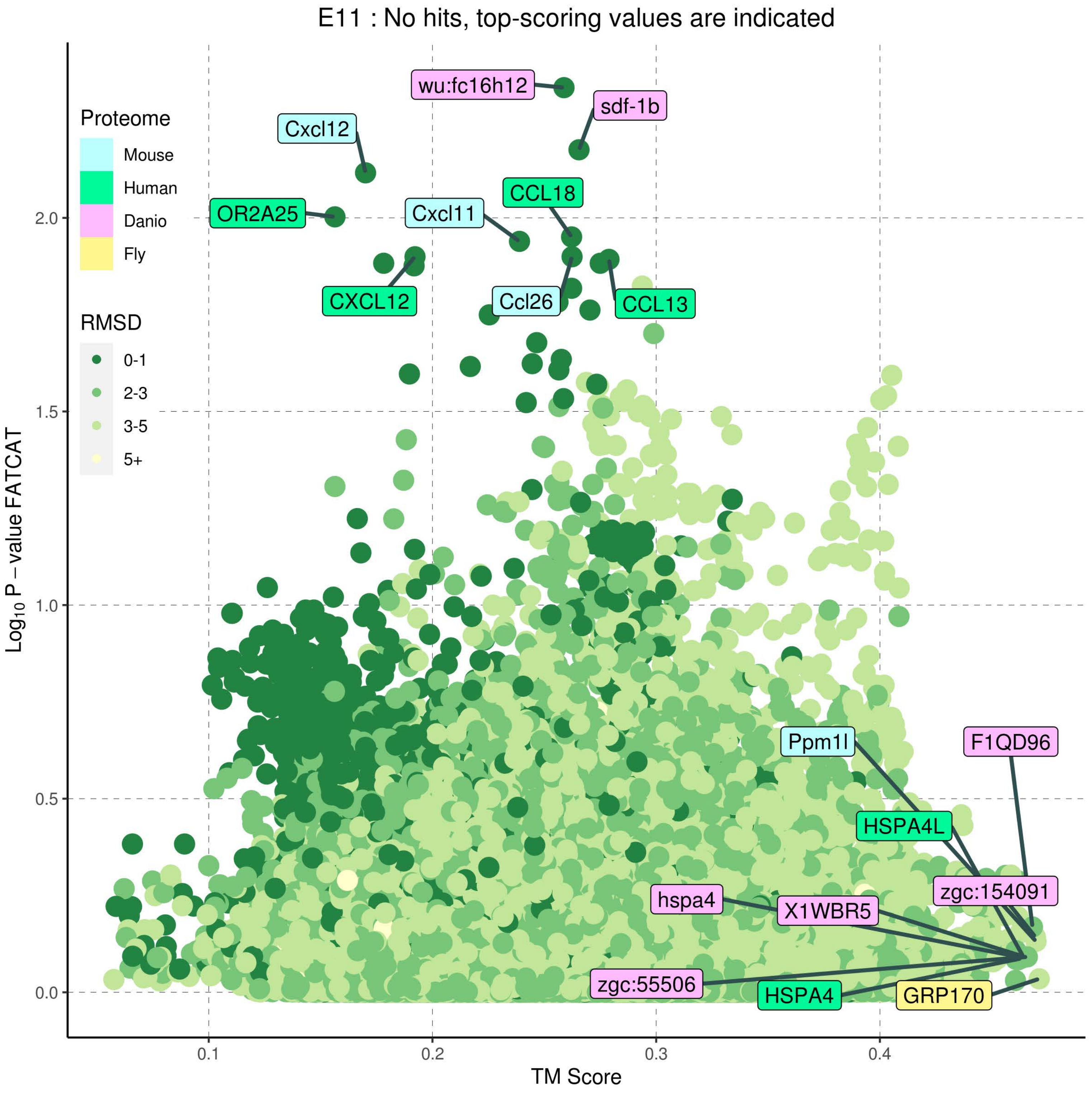

E7 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Apoc2
ninj1
tmem170a
Dmel\CG15642
Dmel\CG42654
Dmel\CG42536
si:dkey-93l1.9
Dmel\CG42263
Tsp66A-RD
gny
Alg6
I3IT66
F6P528
F1QKM3
Dmel\CG4009
Pgk
CG13632
Pxt
Log10 P – value FATCAT
0
1
2
3
4
TM Score
0.1
0.2
0.3
0.4
0.5

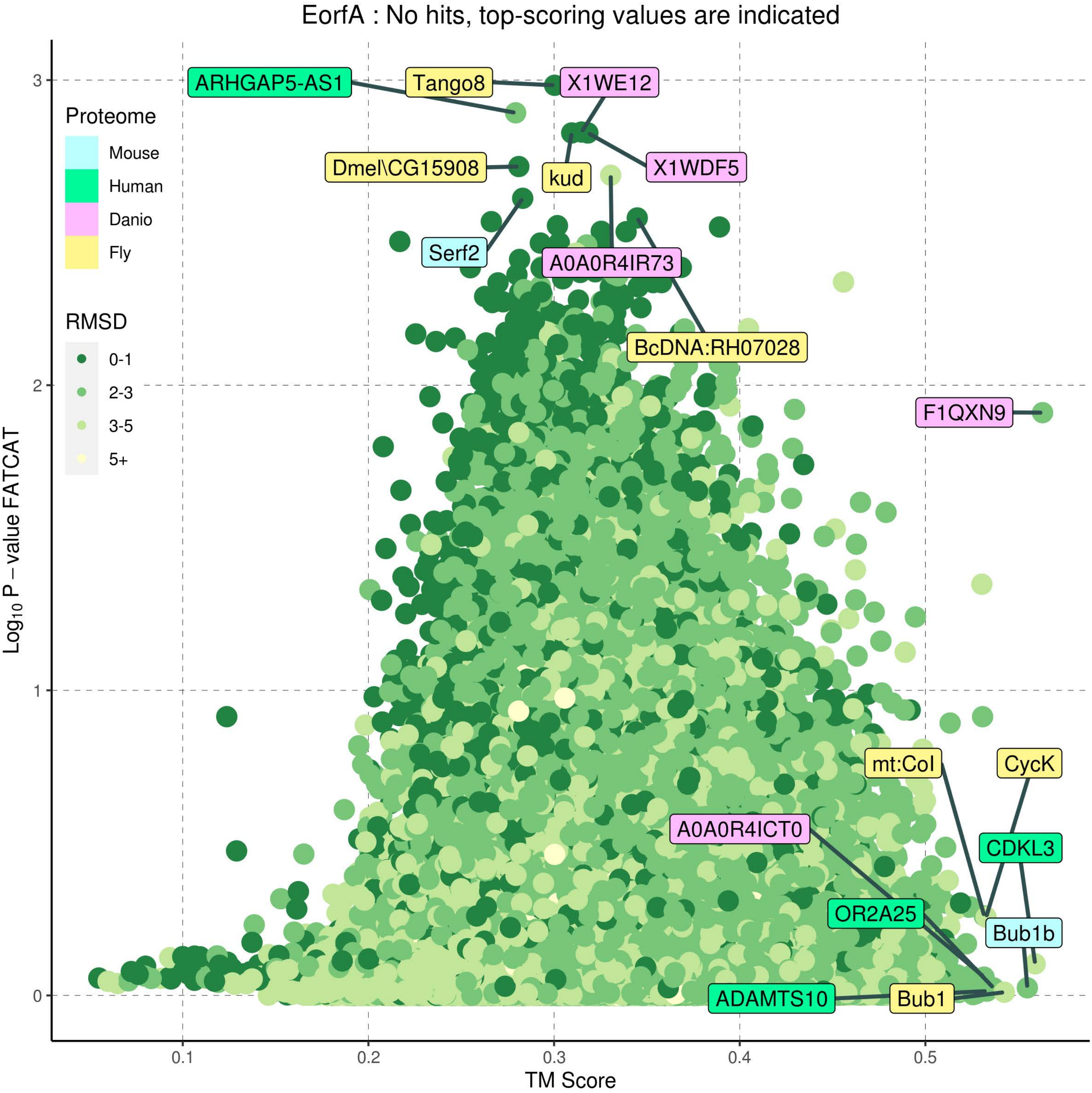


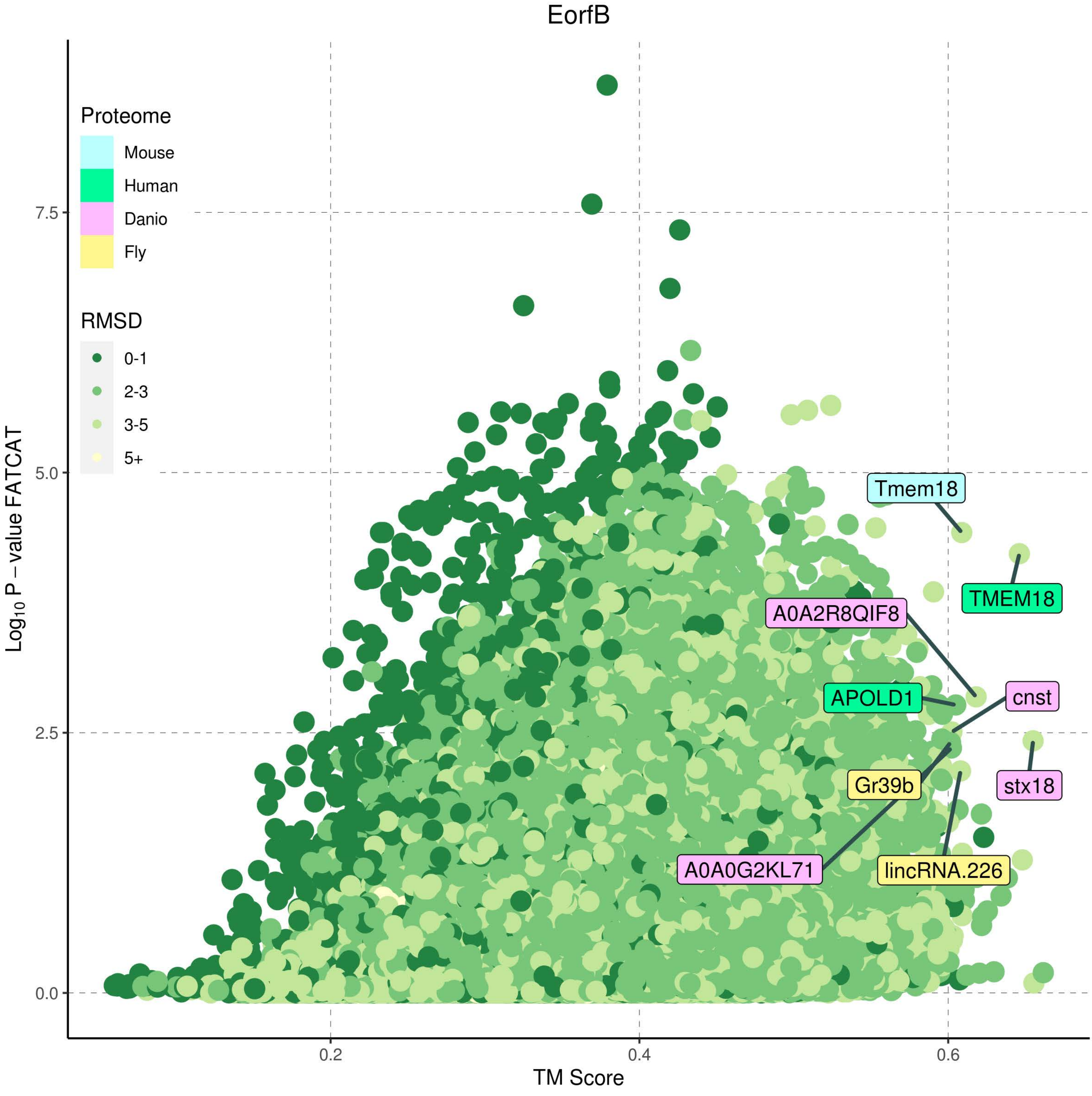
E8 : No hits, top-scoring values are indicated

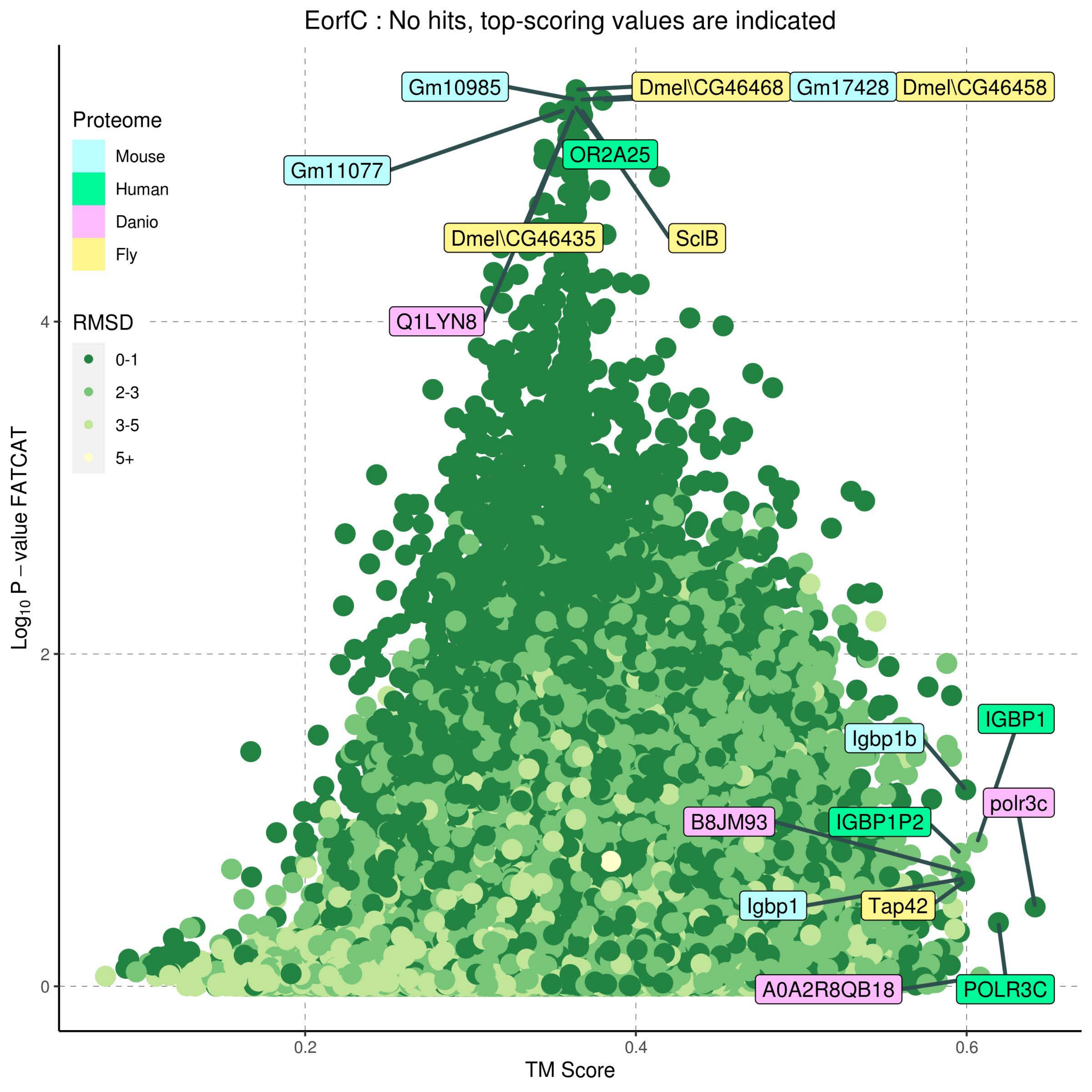

E9
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
B3DKJ9
PolD1
E7FB68
POLA1
Pola1
PolA1
PolZ1
PolE1
B0V351
POLE
Pole
Log10 P – value FATCAT
0
3
6
9
TM Score
0.0
0.2
0.4
0.6

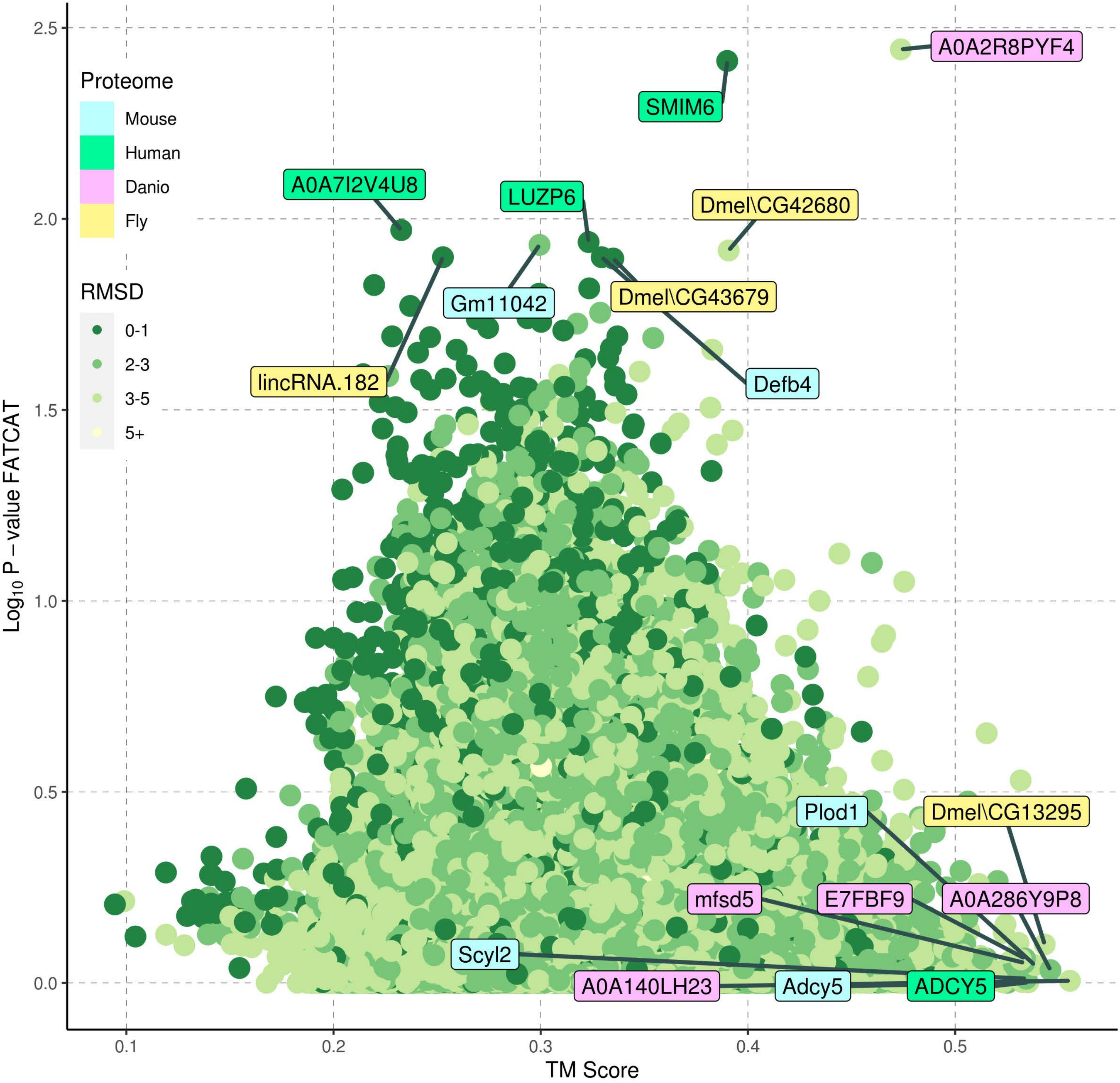

E10
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Gfer
A4QNU9
GFER
Alr
Tmem192
SFT2D1
Qsox3
Vmn1r167
Vmn1r38
F1QQJ6
Olfr102
Vmn1r171
Vmn1r13
Olfr680
OR137-2
Olfr1404
Olfr1416
Olfr638
Olfr1340
OR125-5
Qsox2
A0A0G2L7D1
Vmn1r8
Olfr583
Drl-2
OR13H1
OR51D1
Olfr557
Vmn1r6
Log_{10} P − value FATCAT
TM Score
0
1
2
3
4
0.2
0.4
0.6


E11 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
wu:fc16h12
sdf-1b
Cxcl12
OR2A25
Cxcl11
CCL18
CXCL12
Ccl26
CCL13
Ppm1l
F1QD96
HSPA4L
zgc:154091
hspa4
X1WBR5
zgc:55506
HSPA4
GRP170
Log$_{10}$ P – value FATCAT
0.0
0.5
1.0
1.5
2.0
TM Score
0.1
0.2
0.3
0.4

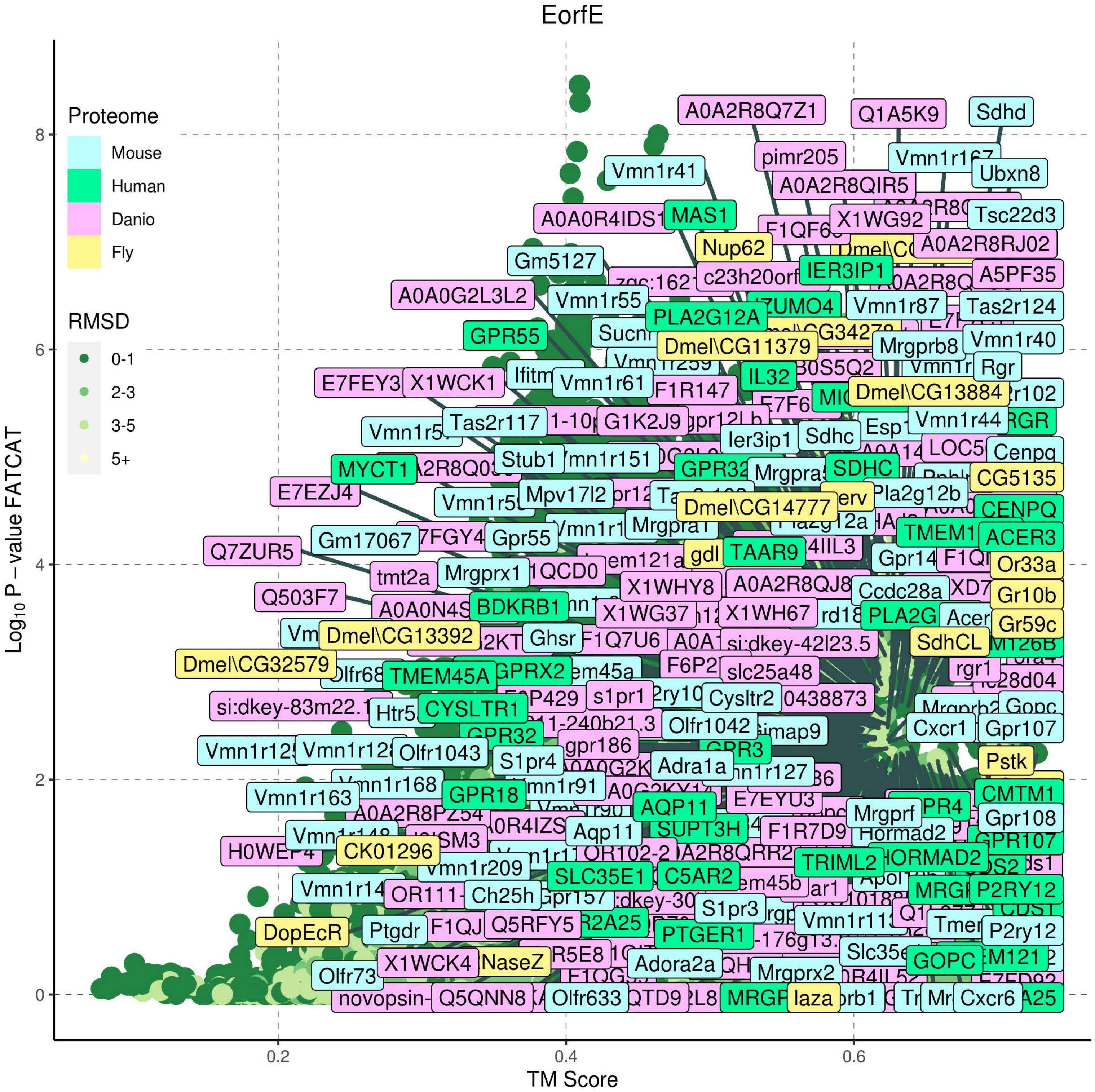

EorfA : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
ARHGAP5-AS1
Tango8
X1WE12
X1WDF5
kud
Dmel\CG15908
Serf2
A0A0R4IR73
BcDNA:RH07028
F1QXN9
mt:CoI
CycK
CDKL3
A0A0R4ICT0
OR2A25
Bub1b
ADAMTS10
Bub1
Log10 P – value FATCAT
TM Score
0
1
2
3
0.1
0.2
0.3
0.4
0.5

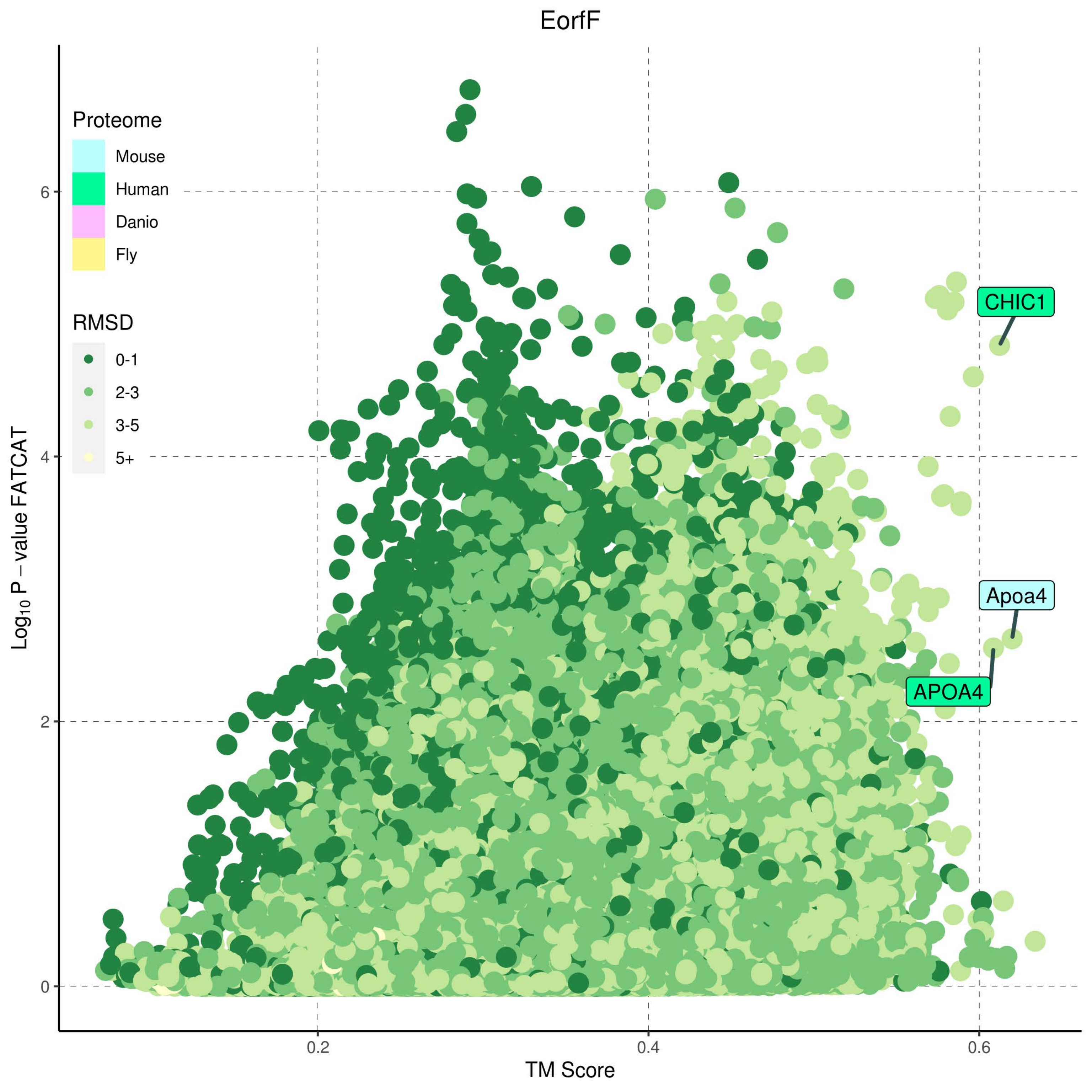

EorfB
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log$_{10}$ P − value FATCAT
7.5
5.0
2.5
0.0
0.2
0.4
0.6
TM Score
Tmem18
TMEM18
A0A2R8QIF8
APOLD1
cnst
Gr39b
stx18
A0A0G2KL71
lincRNA.226


EorfC : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P − value FATCAT
TM Score
0
2
4
0.2
0.4
0.6
Gm10985
Dmel\CG46468
Gm17428
Dmel\CG46458
OR2A25
Gm11077
Dmel\CG46435
SclB
Q1LYN8
IGBP1
Igbp1b
polr3c
B8JM93
IGBP1P2
Igbp1
Tap42
A0A2R8QB18
POLR3C

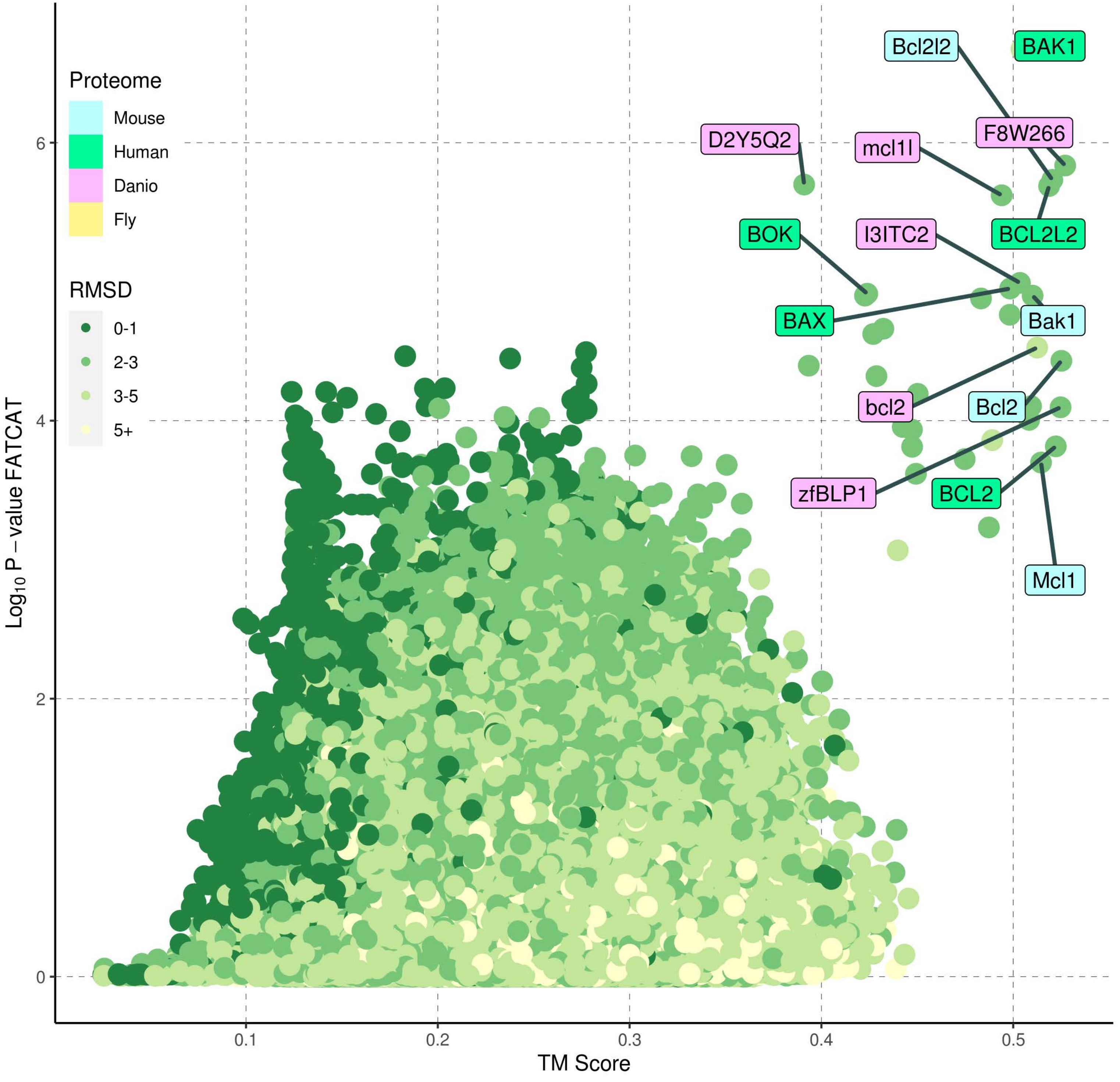


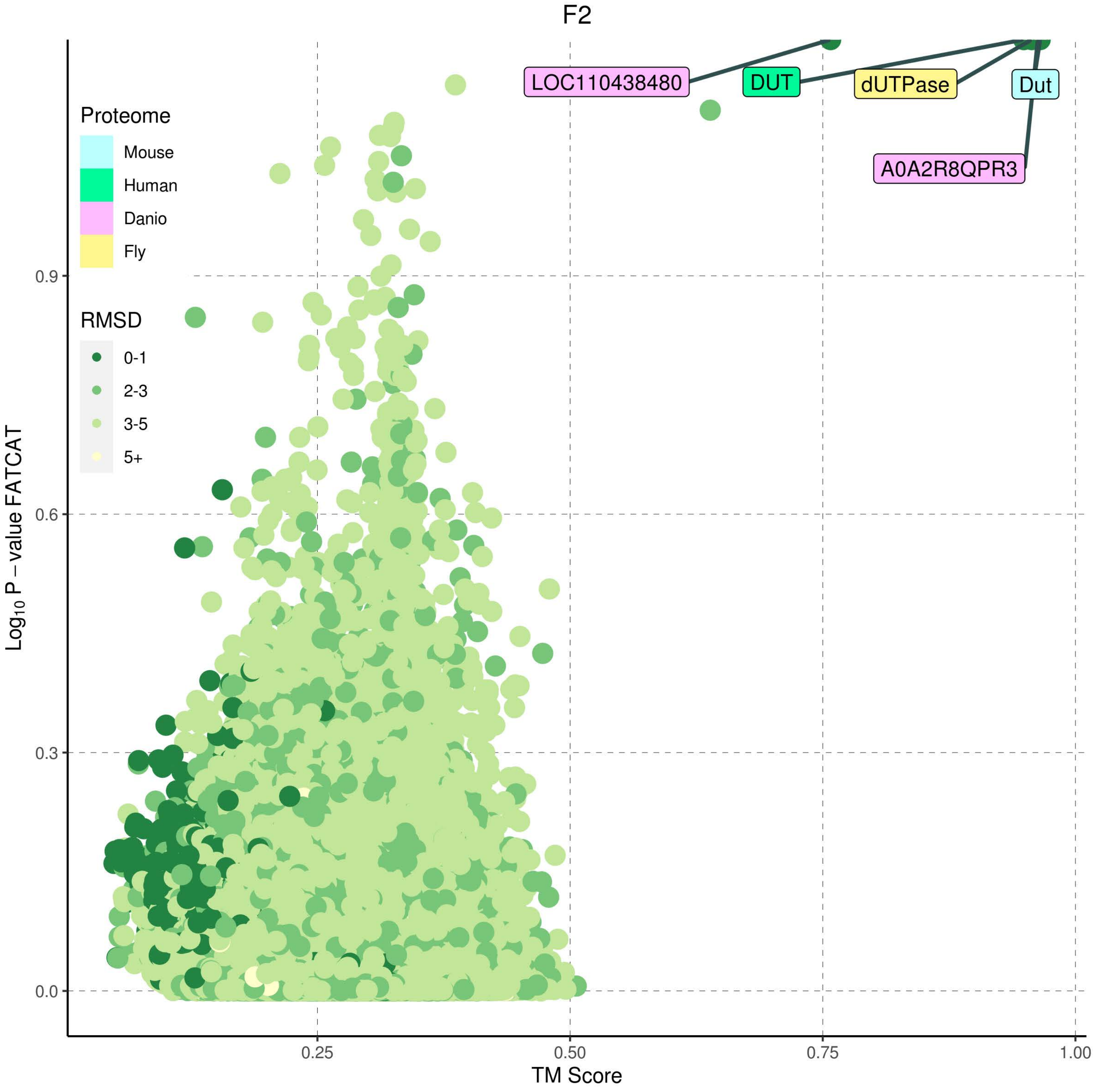
EorfD : No hits, top-scoring values are indicated

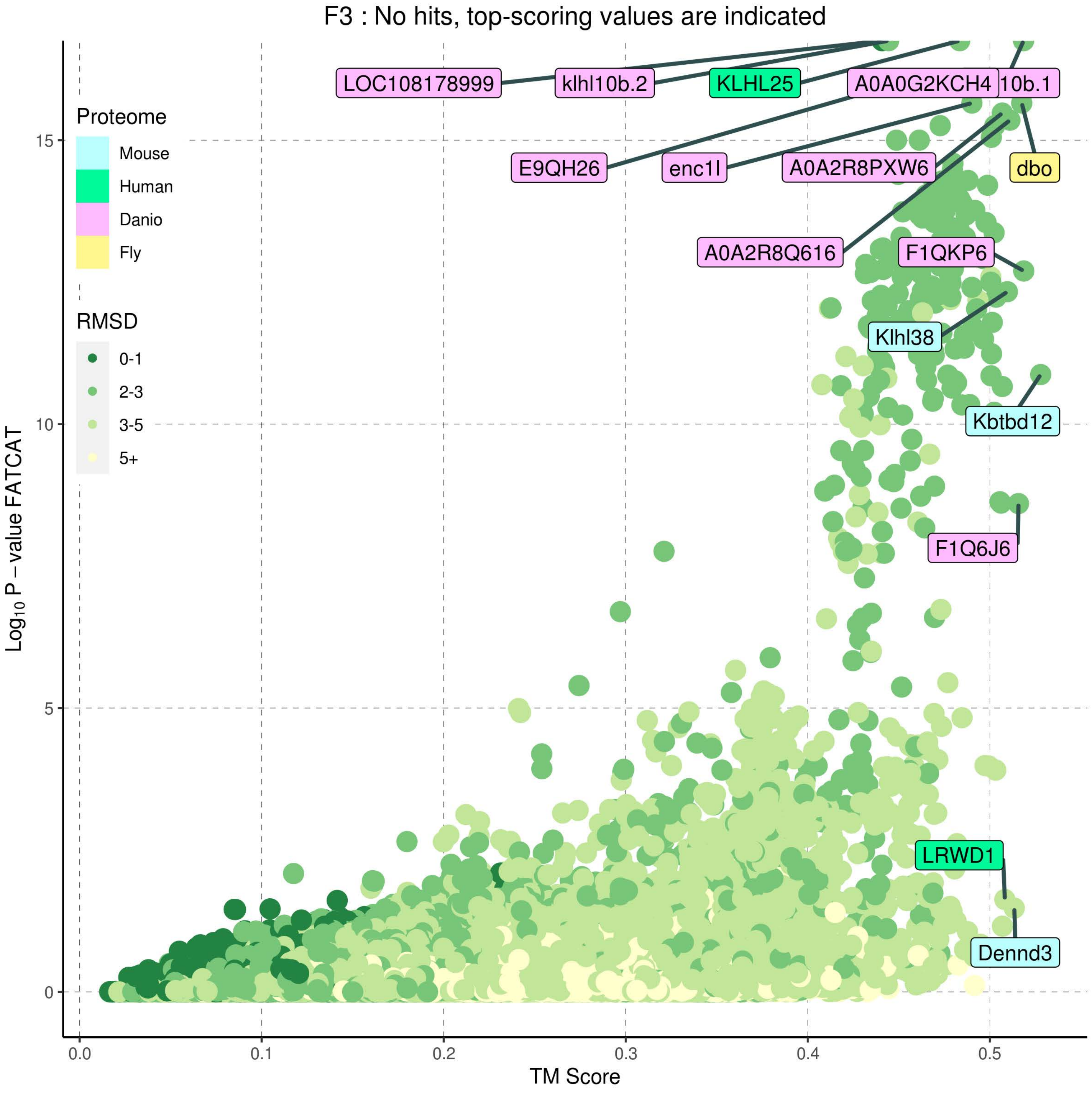

EorfE
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log₁₀ P − value FATCAT
TM Score
0
2
4
6
8
0.2
0.4
0.6
A0A2R8Q7Z1
Q1A5K9
Sdhd
pimr205
Vmn1r167
Ubxn8
Vmn1r41
A0A2R8QIR5
Tsc22d3
A0A0R4IDS1
MAS1
F1QF63
X1WG92
Nup62
A0A2R8RJ02
Gm5127
c23h20orf
IER3IP1
A5PF35
A0A0G2L3L2
Vmn1r55
IZUMO4
Vmn1r87
Tas2r124
PLA2G12A
GPR55
Sucnr
Dmel\CG34278
Dmel\CG11379
Mrgprb8
Vmn1r40
Vmn1r259
IL32
Rgr
E7FEY3
X1WCK1
Ifitm
Vmn1r61
F1R147
Dmel\CG13884
Vmn1r5
Tas2r117
G1K2J9
Vmn1r44
RGR
Ier3ip1
Sdhc
Esp
LOC5
Cenpq
MYCT1
Stub1
Vmn1r151
GPR32
Mrgpra
SDHC
CG5135
E7EZJ4
Mpv17l2
Pla2g12b
Vmn1r5
Dmel\CG14777
Serv
CENPQ
Mrgpra1
Pla2g12a
TMEM1
ACER3
Q7ZUR5
Gm17067
E7FGY4
Gpr55
Vmn1r1
gdl
TAARr9
Gpr14
F1Q
Or33a
tmt2a
Mrgprx1
F1QCD0
X1WHY8
A0A2R8QJ8
Ccdc28a
XD7
Gr10b
Q503F7
A0A0N4S
BDKRB1
X1WG37
X1WH67
PLA2G
Acer
Gr59c
Dmel\CG13392
Ghsr
F1Q7U6
si:dkey-42l23.5
SdhCL
Dmel\CG32579
Olfr68
TMEM45A
GPRX2
F6P2
slc25a48
rgr1
si:dkey-83m22.1
Htr5
CYSLTR1
F1P429
s1pr1
Cysltr2
Gopc
GPR32
Olfr1042
Cxcr1
Gpr107
Vmn1r12
Vmn1r12
Olfr1043
gpr186
S1pr4
GPR3
Adra1a
Vmn1r127
Pstk
Vmn1r168
Vmn1r163
Vmn1r91
GPR18
A0A2R8PZ54
AQP11
E7EYU3
CMTM1
Mrgprf
Gpr108
Vmn1r148
A0R4IZS
Aqp11
SUPT3H
F1R7D9
Hormad2
GPR107
H0WEF4
CK01296
OR102-2
A0A2R8QRR2
TRIML2
HORMAD2
Vmn1r209
SLC35E1
C5AR2
Vmn1r14
OR111-
Ch25h
Gpr157
MRGP
P2RY12
S1pr3
Vmn1r11
DopEcR
Ptgdr
F1QJ
Q5RFY5
PTGER1
Tmem
P2ry12
X1WCK4
NaseZ
Adora2a
Slc35e
GOPC
Olfr73
Mrgprx2
novopsin-
Q5QNN8
Olfr633
QTD9
MRGP
laza
Tr
Mr
Cxcr6

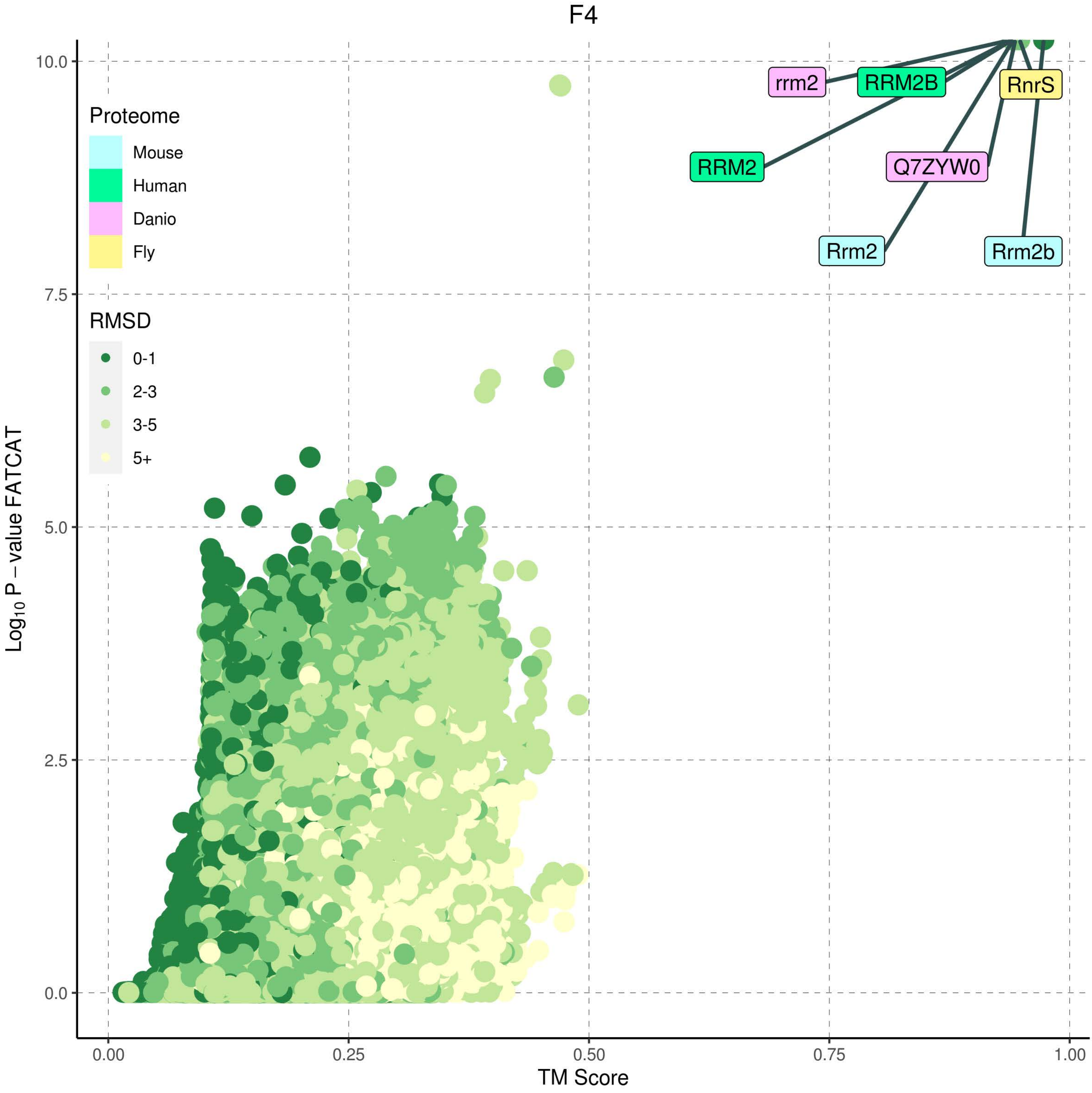

EorfF
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
CHIC1
Apoa4
APOA4
Log₁₀ P – value FATCAT
6
4
2
0
0.2
0.4
0.6
TM Score

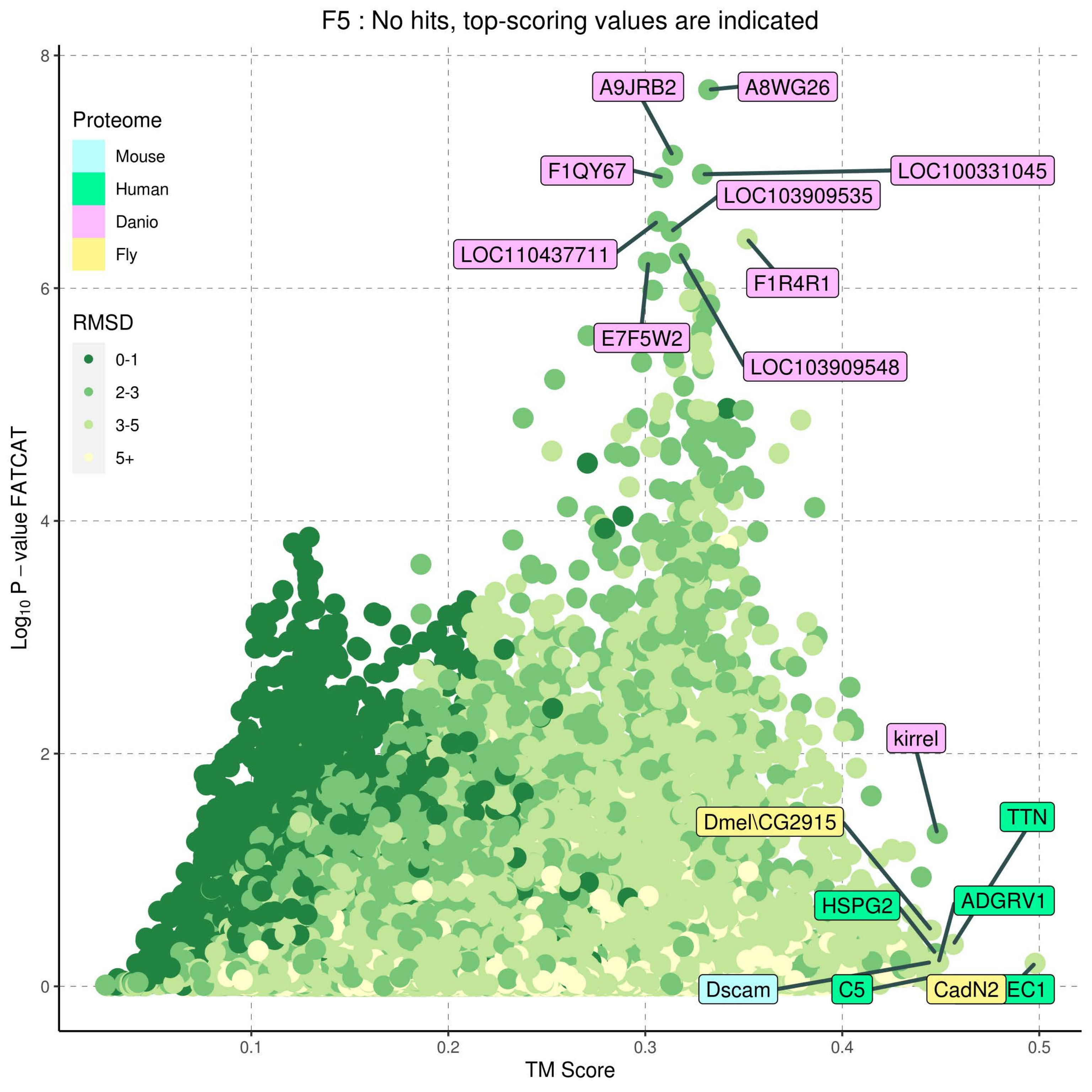
F1 : No hits, top-scoring values are indicated



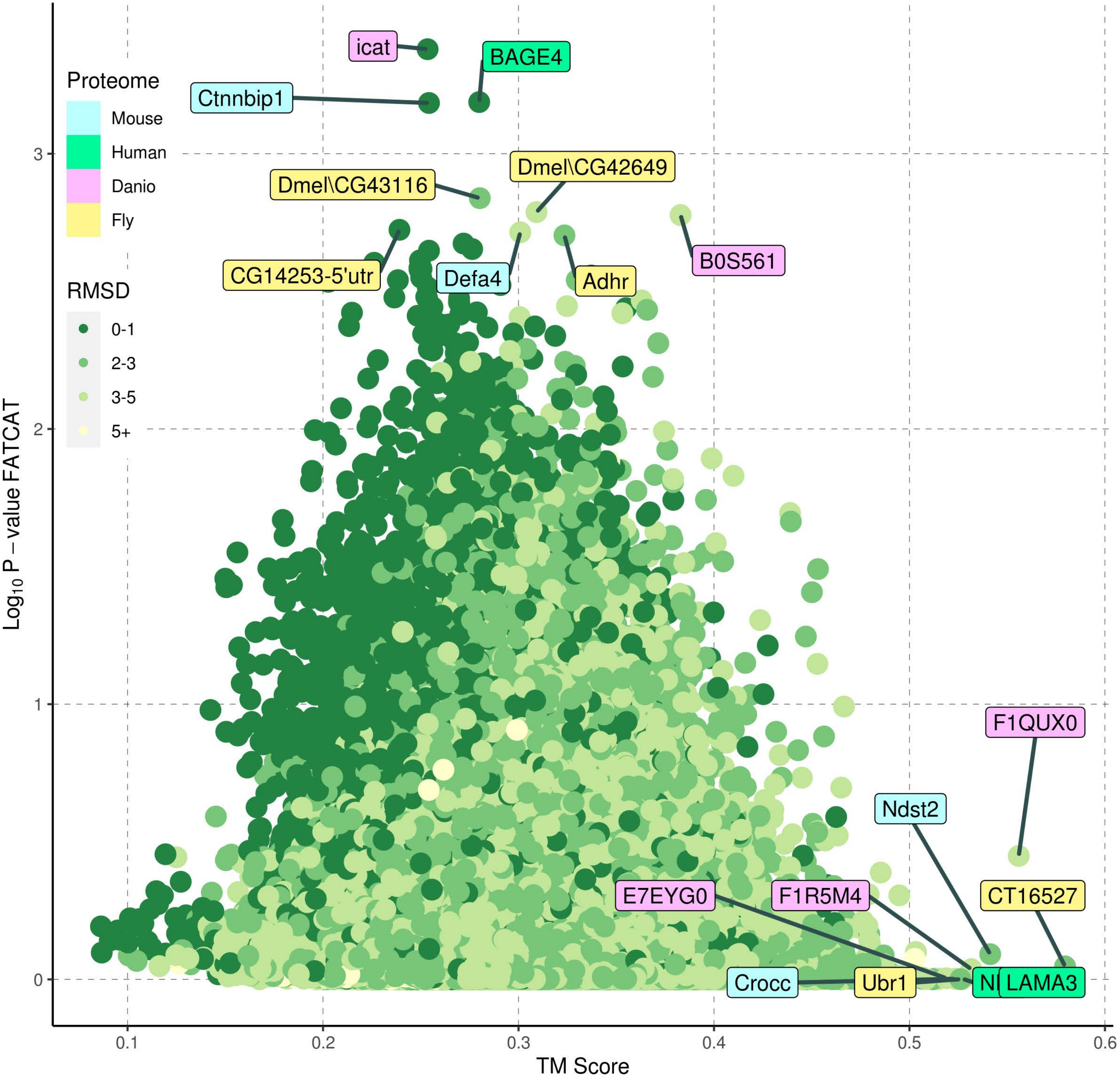

F2
LOC110438480
DUT
dUTPase
Dut
A0A2R8QPR3
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
0.9
0.6
0.3
0.0
0.25
0.50
0.75
1.00
TM Score

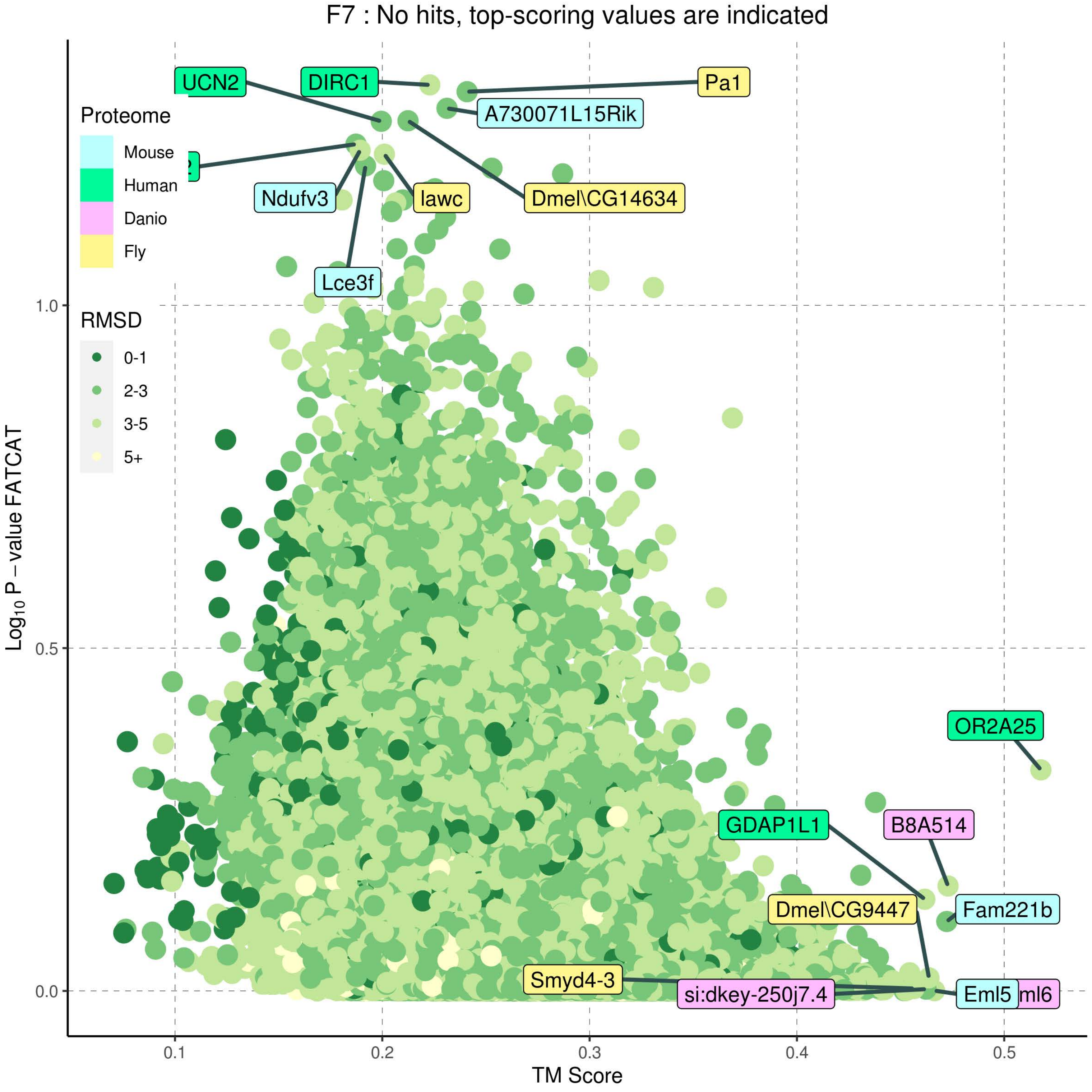

F3 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
LOC108178999
klhl10b.2
KLHL25
A0A0G2KCH4
10b.1
E9QH26
enc1l
A0A2R8PXW6
dbo
A0A2R8Q616
F1QKP6
Klhl38
Kbtbd12
F1Q6J6
LRWD1
Dennd3
Log$_{10}$ P – value FATCAT
TM Score
0
5
10
15
0.0
0.1
0.2
0.3
0.4
0.5

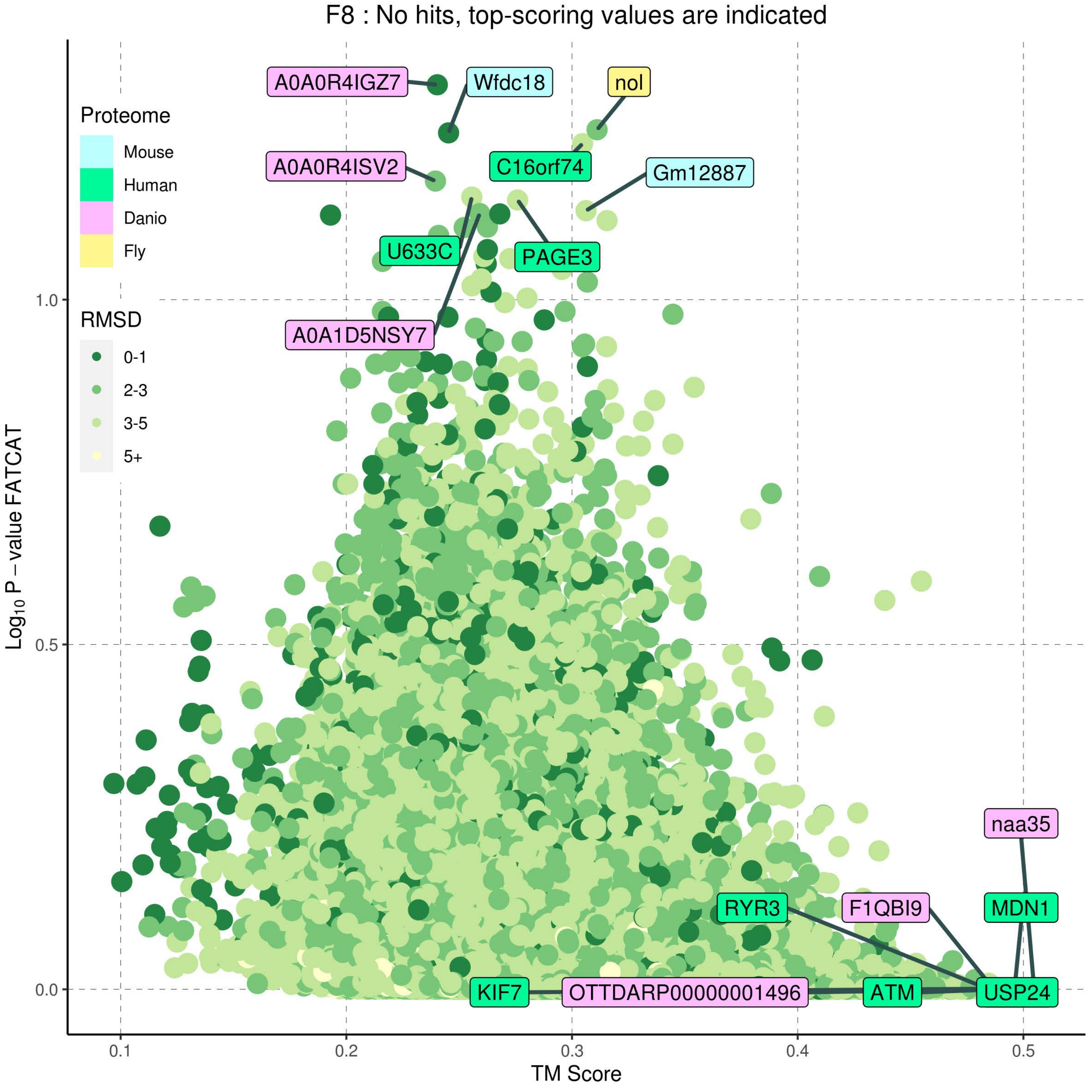

F4
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
rrm2
RRM2B
RnrS
RRM2
Q7ZYW0
Rrm2
Rrm2b
10.0
7.5
5.0
2.5
0.0
Log_{10} P − value FATCAT
0.00
0.25
0.50
0.75
1.00
TM Score

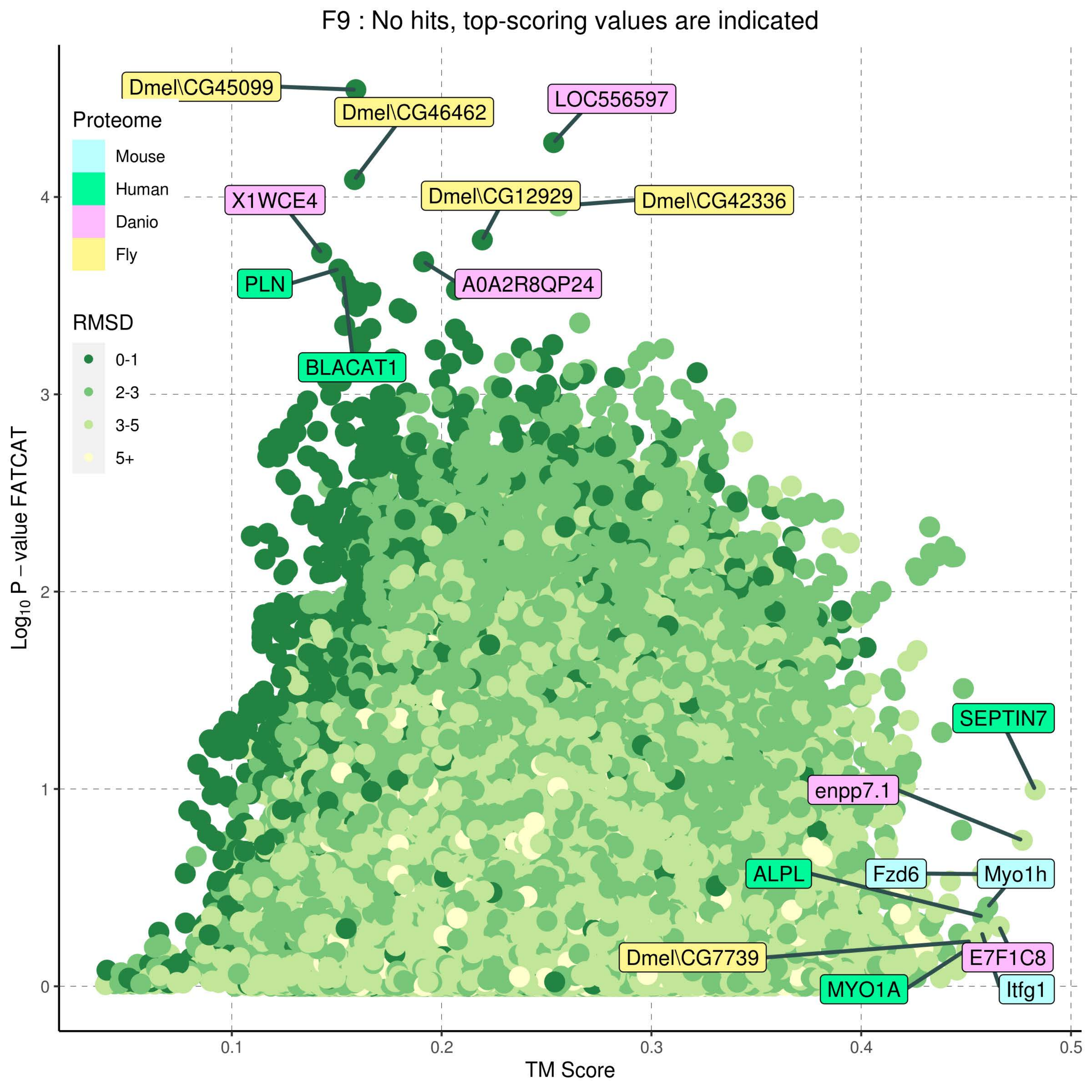

F5 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
A9JRB2
A8WG26
F1QY67
LOC100331045
LOC103909535
LOC110437711
F1R4R1
E7F5W2
LOC103909548
kirrel
Dmel\CG2915
TTN
HSPG2
ADGRV1
Dscam
C5
CadN2
EC1
8
6
4
2
0
Log10 P − value FATCAT
0.1
0.2
0.3
0.4
0.5
TM Score

F6 : No hits, top-scoring values are indicated

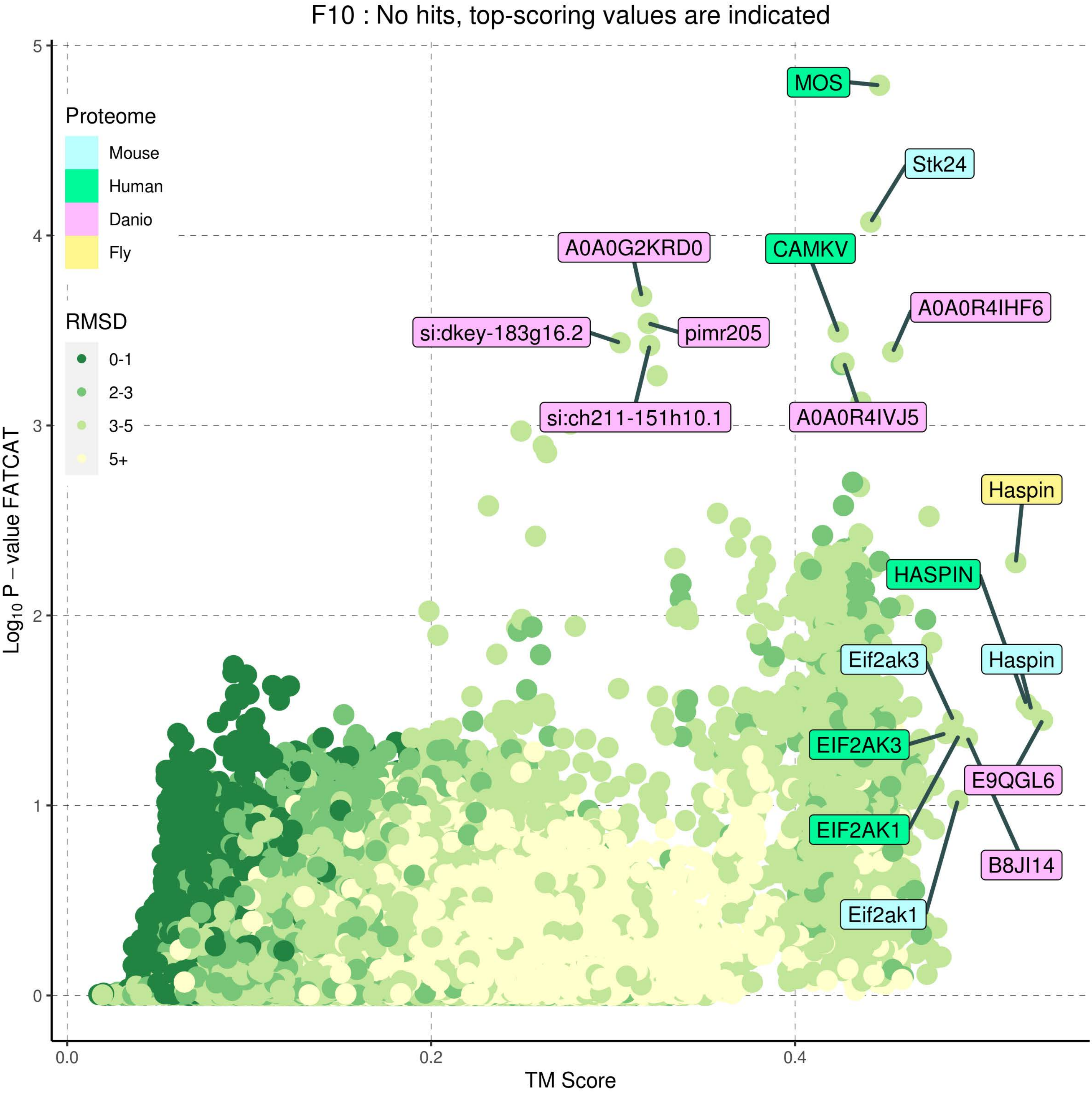


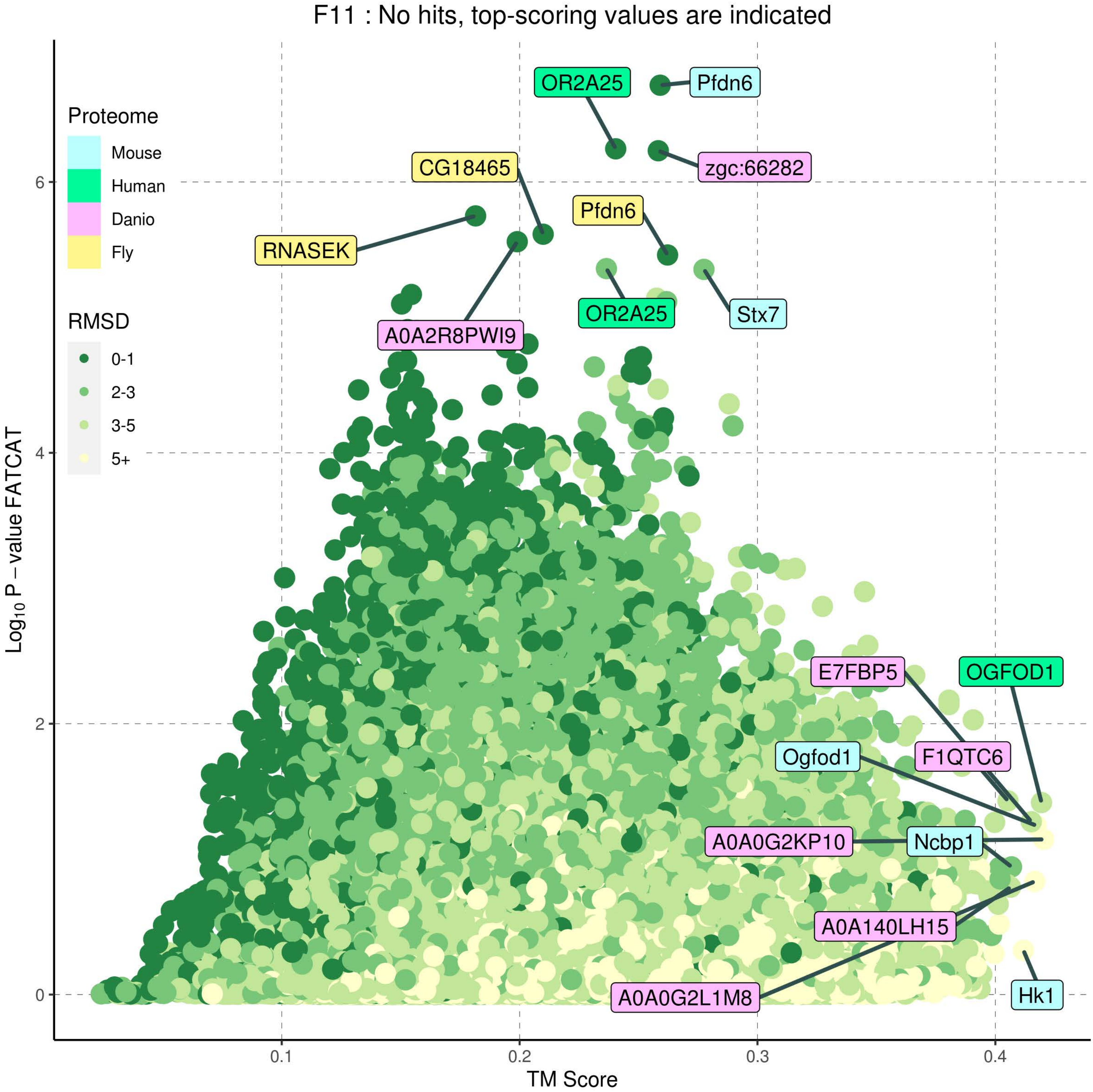

F7 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
UCN2
DIRC1
Pa1
A730071L15Rik
2
Ndufv3
lawc
Dmel\CG14634
Lce3f
OR2A25
GDAP1L1
B8A514
Fam221b
Dmel\CG9447
Smyd4-3
si:dkey-250j7.4
Eml5
ml6
Log₁₀ P − value FATCAT
1.0
0.5
0.0
0.1
0.2
0.3
0.4
0.5
TM Score

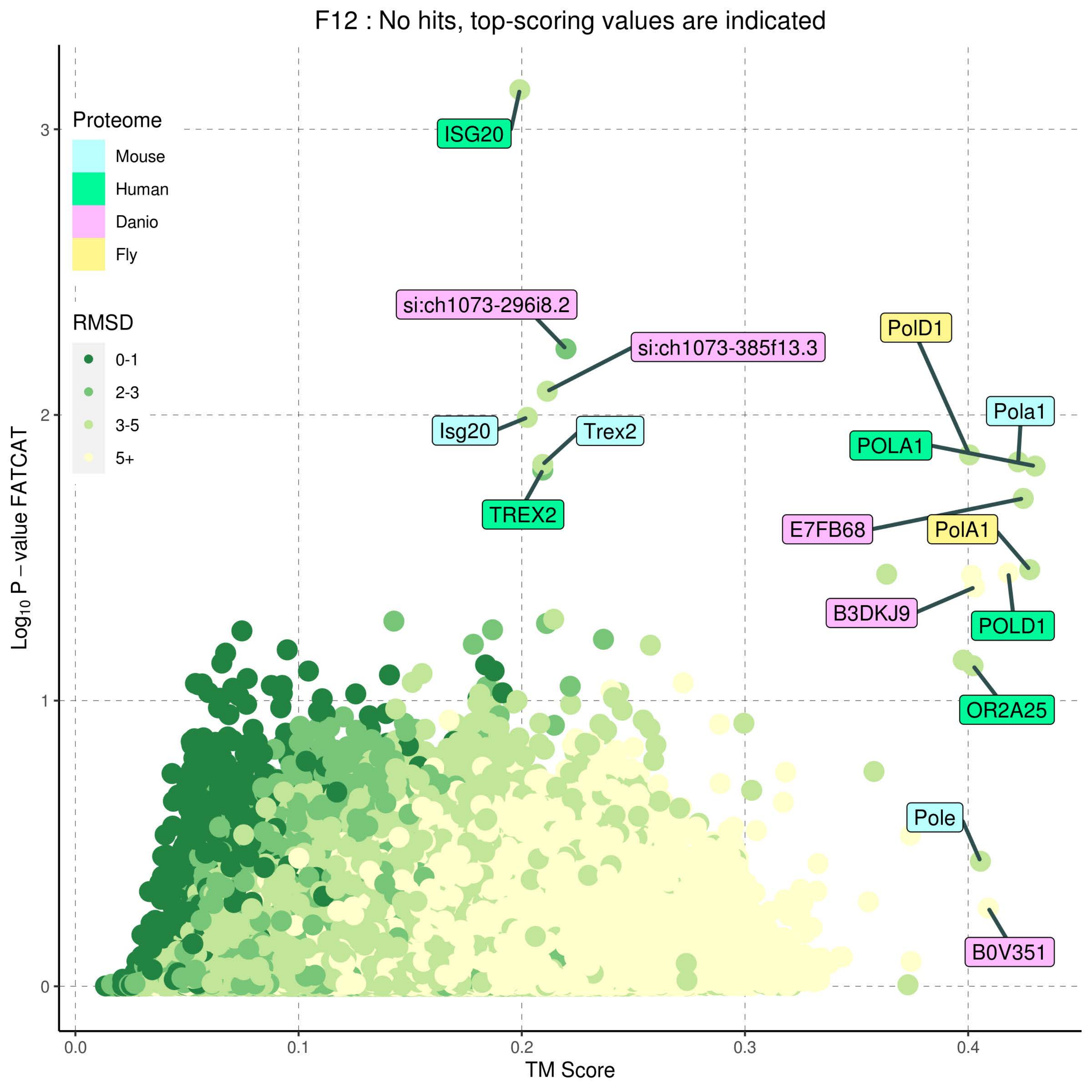

F8 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
A0A0R4IGZ7
Wfdc18
nol
A0A0R4ISV2
C16orf74
Gm12887
U633C
PAGE3
A0A1D5NSY7
naa35
RYR3
F1QBI9
MDN1
KIF7
OTTDARP00000001496
ATM
USP24
Log_{10} P − value FATCAT
1.0
0.5
0.0
0.1
0.2
0.3
0.4
0.5
TM Score

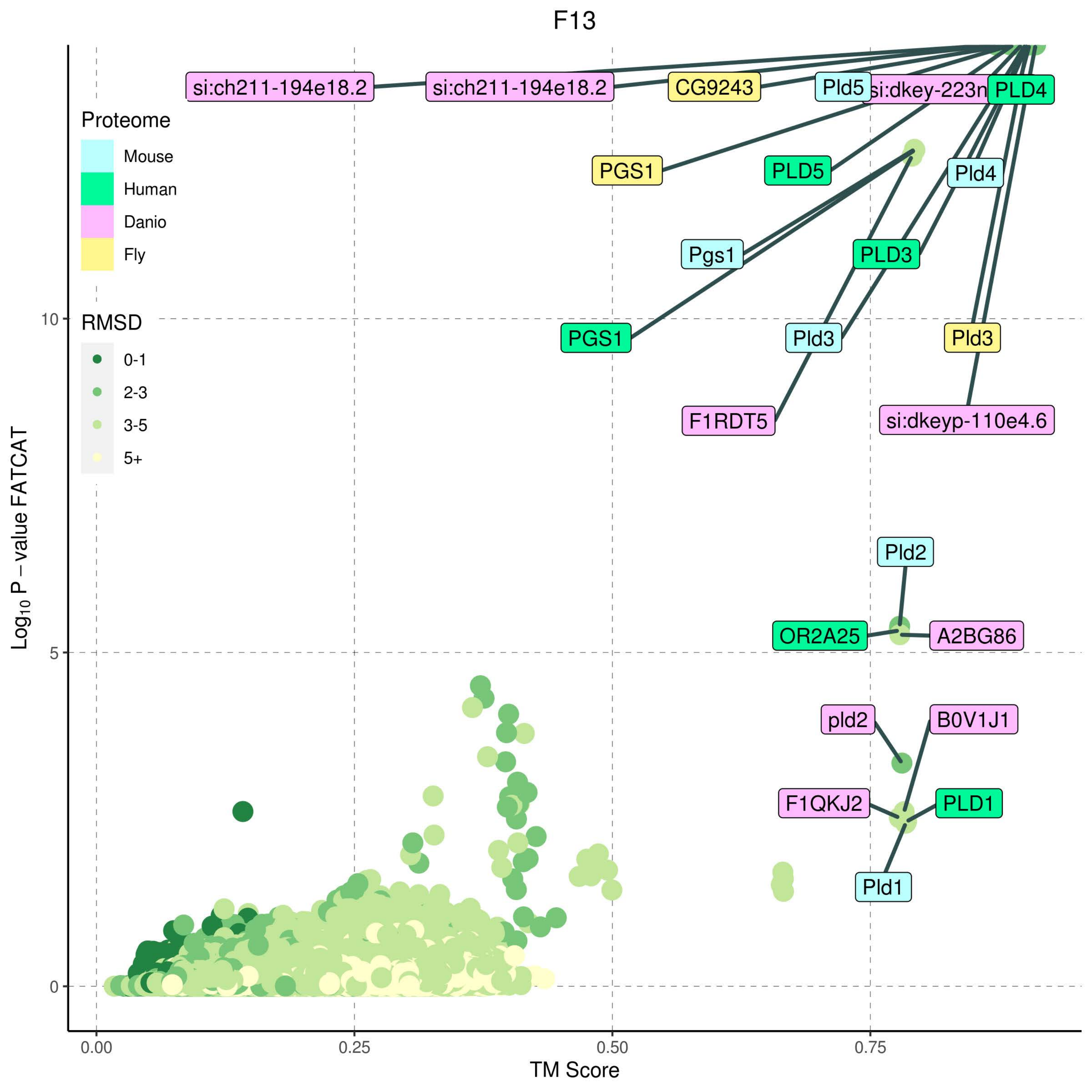


F9 : No hits, top-scoring values are indicated

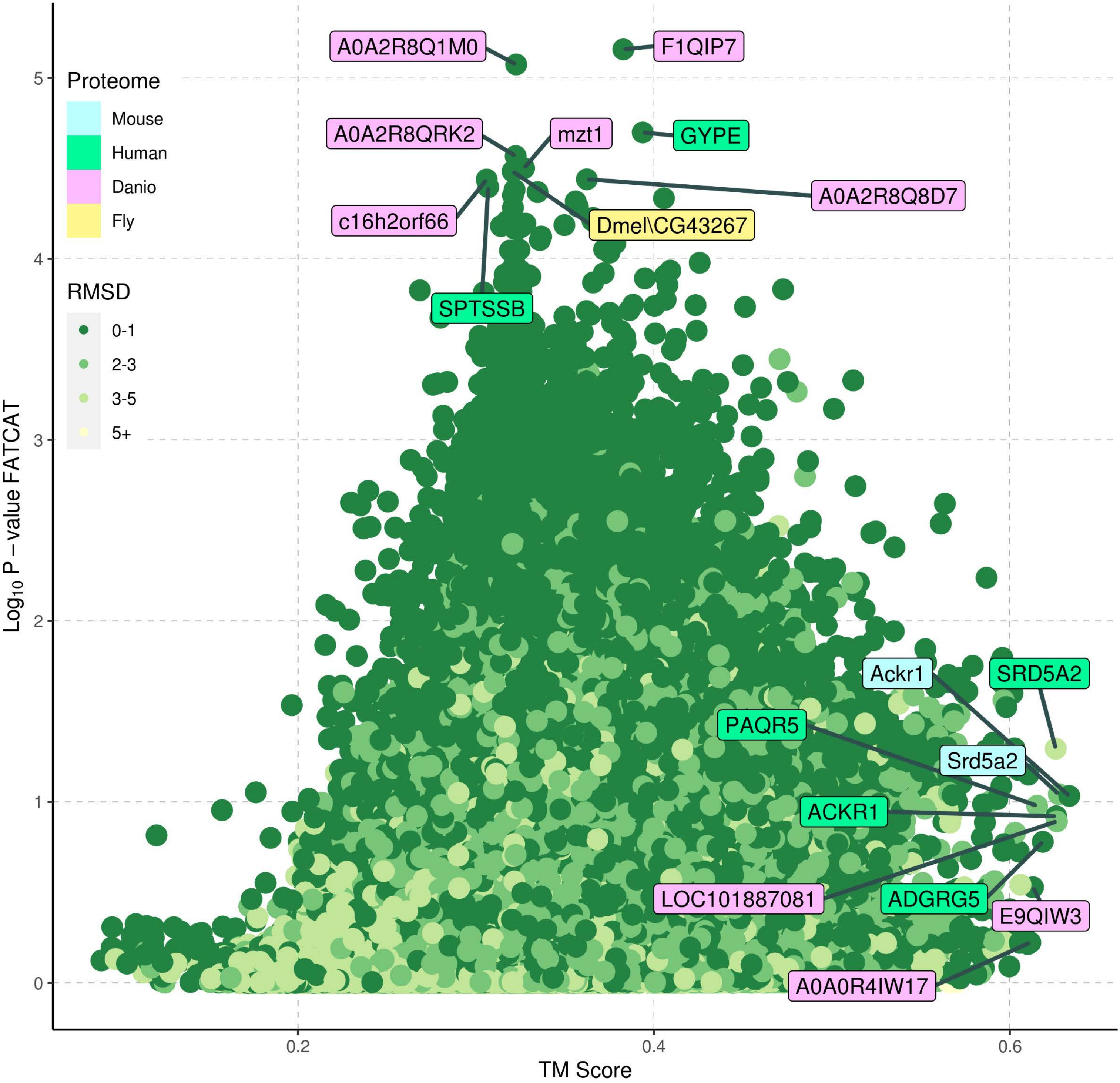

F10 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
MOS
Stk24
A0A0G2KRD0
CAMKV
A0A0R4IHF6
si:dkey-183g16.2
pimr205
si:ch211-151h10.1
A0A0R4IVJ5
Haspin
HASPIN
Eif2ak3
Haspin
EIF2AK3
E9QGL6
EIF2AK1
B8JI14
Eif2ak1
Log_{10} P – value FATCAT
0
1
2
3
4
5
TM Score
0.0
0.2
0.4

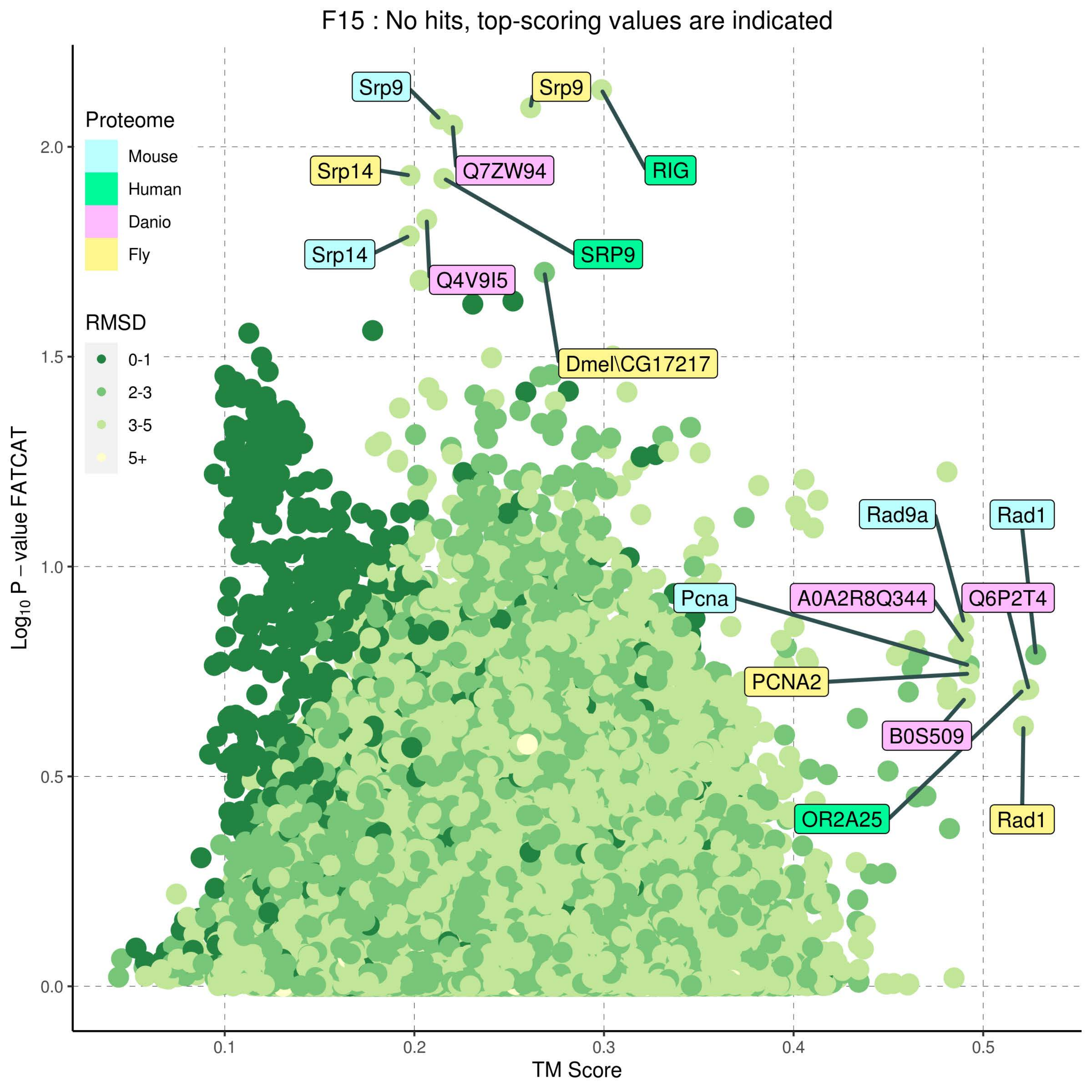

F11 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
TM Score
0
2
4
6
0.1
0.2
0.3
0.4
OR2A25
Pfdn6
zgc:66282
CG18465
Pfdn6
RNASEK
A0A2R8PWI9
OR2A25
Stx7
E7FBP5
OGFOD1
Ogfod1
F1QTC6
A0A0G2KP10
Ncbp1
A0A140LH15
A0A0G2L1M8
Hk1

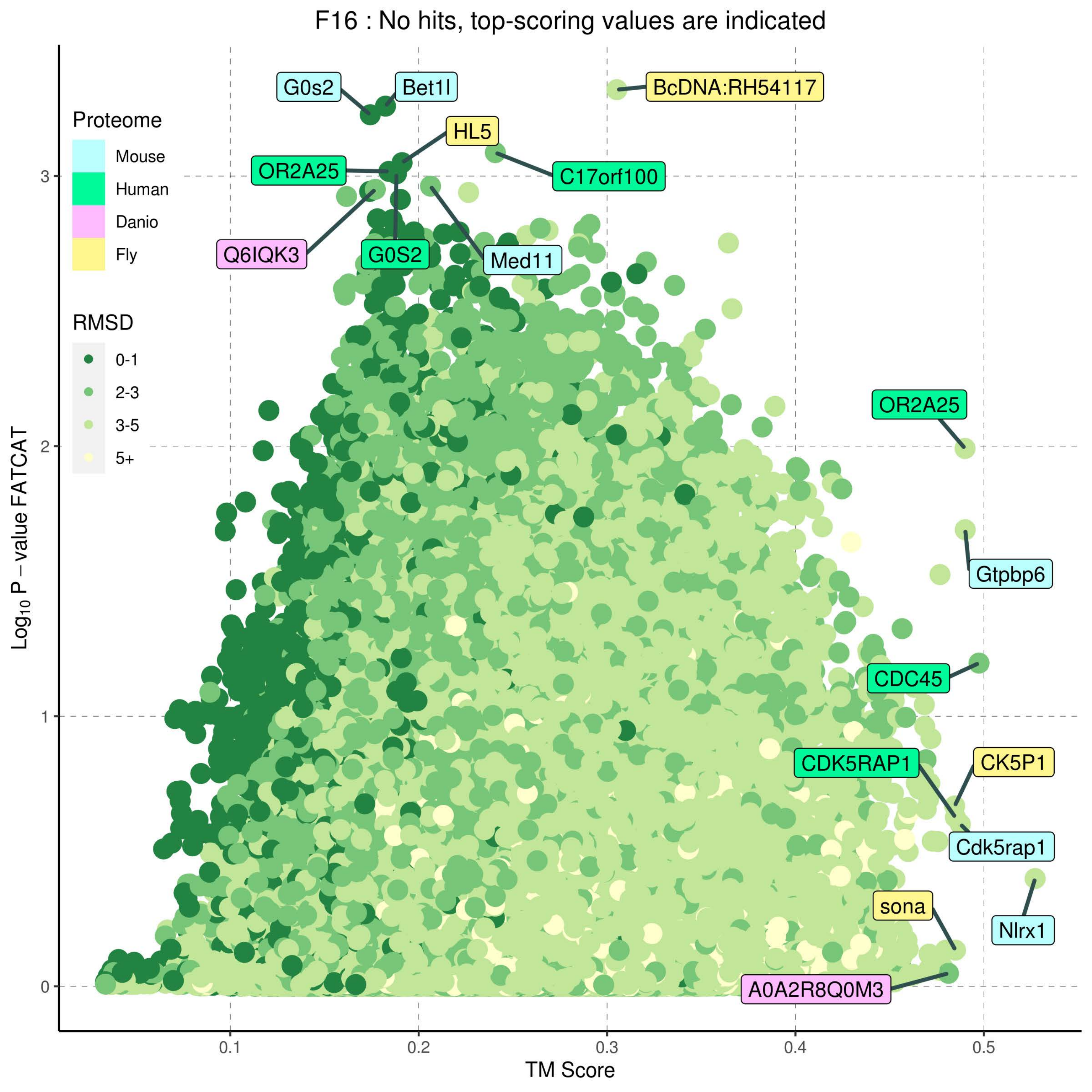

F12 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
ISG20
si:ch1073-296i8.2
si:ch1073-385f13.3
Isg20
Trex2
TREX2
PolD1
Pola1
POLA1
E7FB68
PolA1
B3DKJ9
POLD1
OR2A25
Pole
B0V351
Log10 P – value FATCAT
0
1
2
3
0.0
0.1
0.2
0.3
0.4
TM Score

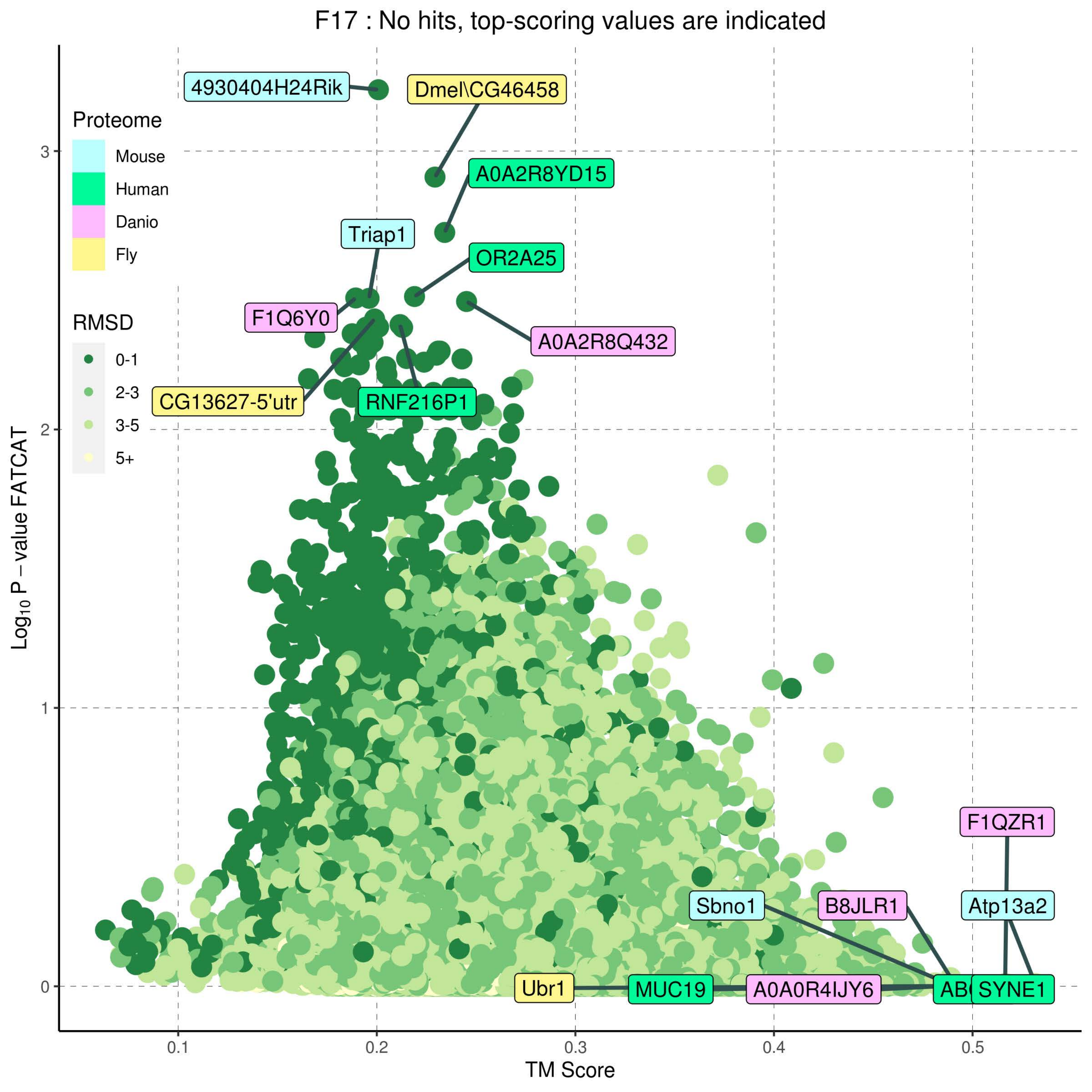

F13
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
si:ch211-194e18.2
si:ch211-194e18.2
CG9243
Pld5
si:dkey-223n
PLD4
PGS1
PLD5
Pld4
Pgs1
PLD3
PGS1
Pld3
Pld3
F1RDT5
si:dkeyp-110e4.6
Pld2
OR2A25
A2BG86
pld2
B0V1J1
F1QKJ2
PLD1
Pld1
10
5
0
0.00
0.25
0.50
0.75
TM Score
Log10 P – value FATCAT

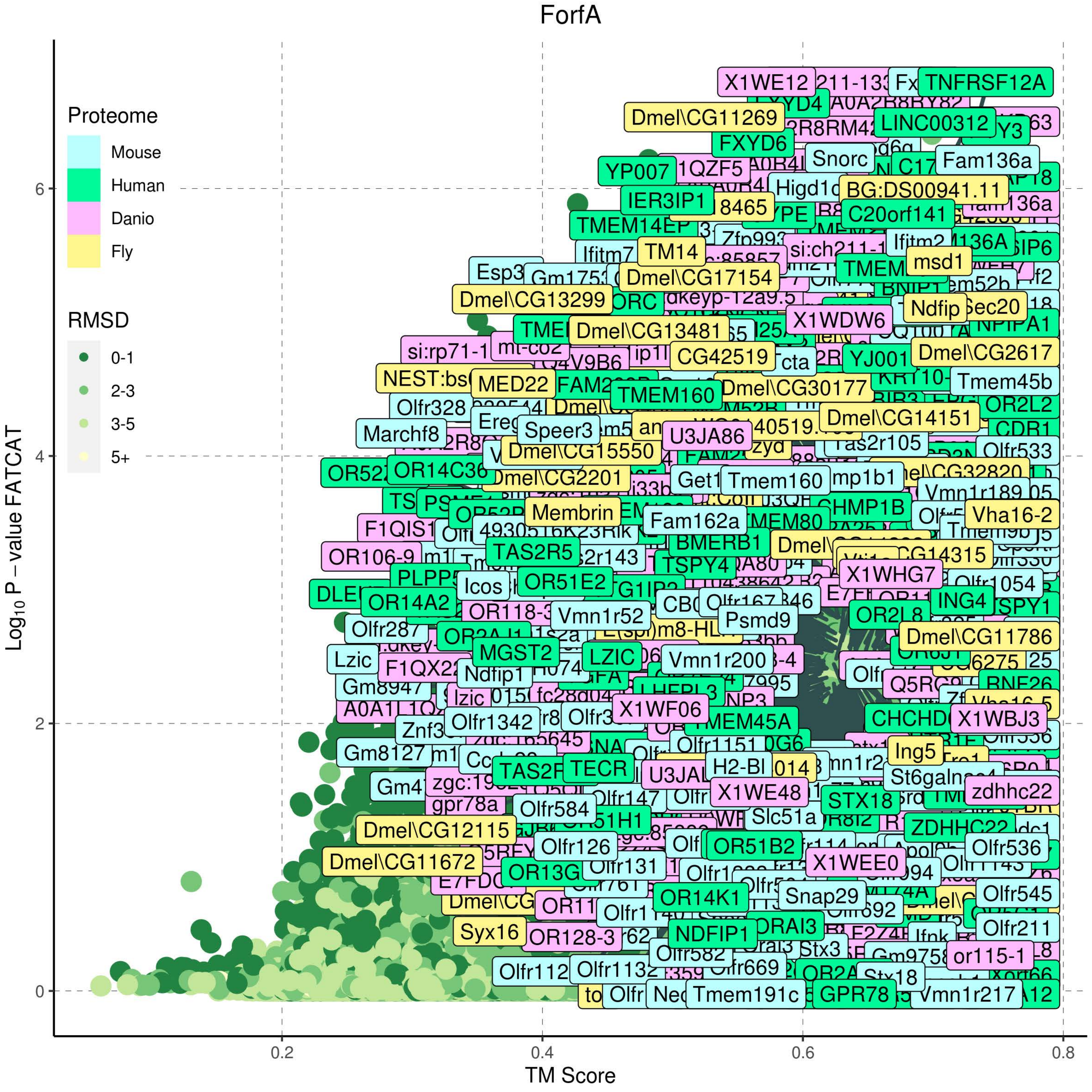
F14 : No hits, top-scoring values are indicated



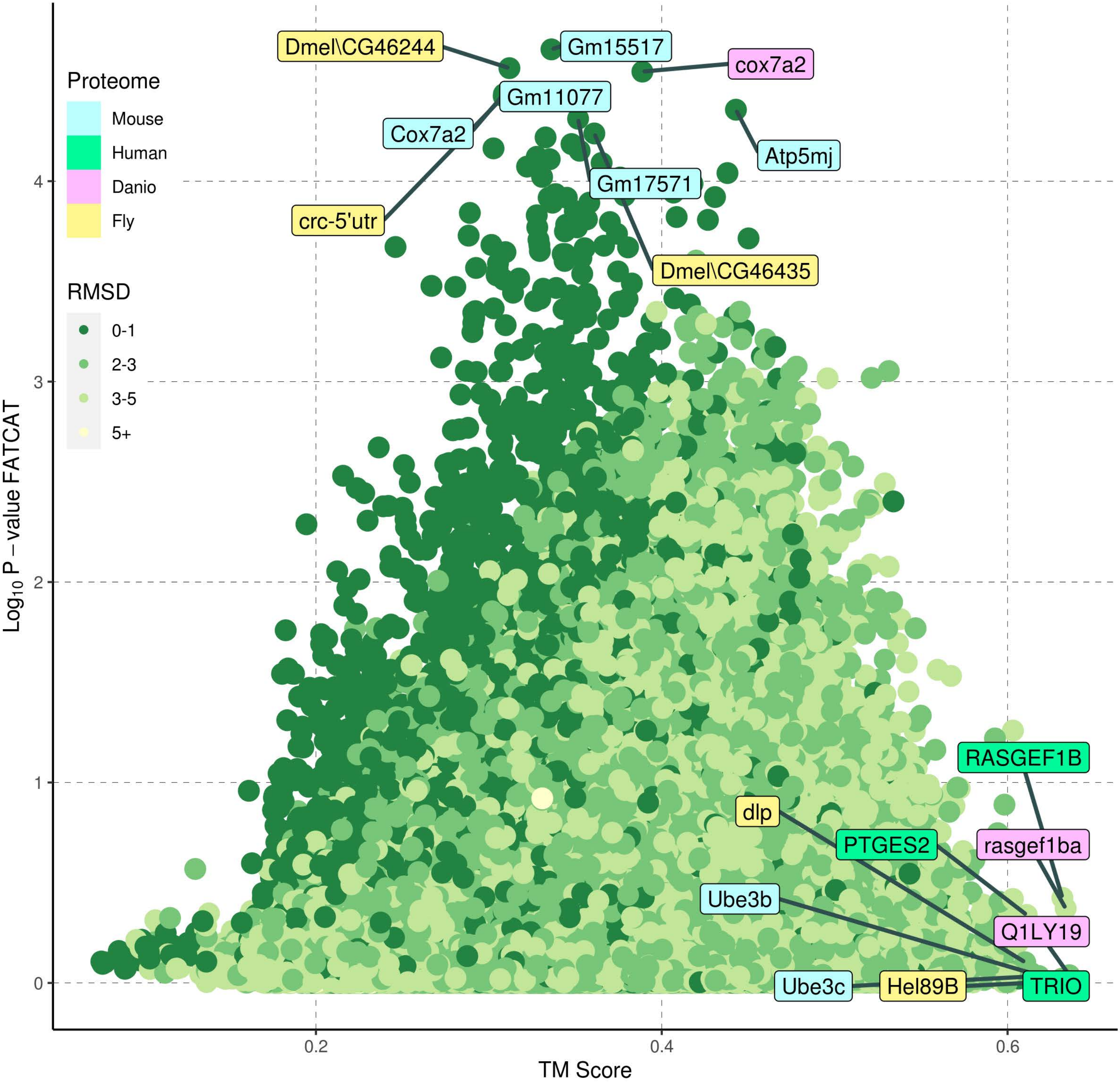

F15 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Srp9
Srp9
Q7ZW94
RIG
Srp14
SRP9
Srp14
Q4V9I5
Dmel\CG17217
Rad9a
Rad1
Pcna
A0A2R8Q344
Q6P2T4
PCNA2
B0S509
OR2A25
Rad1
Log10 P – value FATCAT
2.0
1.5
1.0
0.5
0.0
TM Score
0.1
0.2
0.3
0.4
0.5

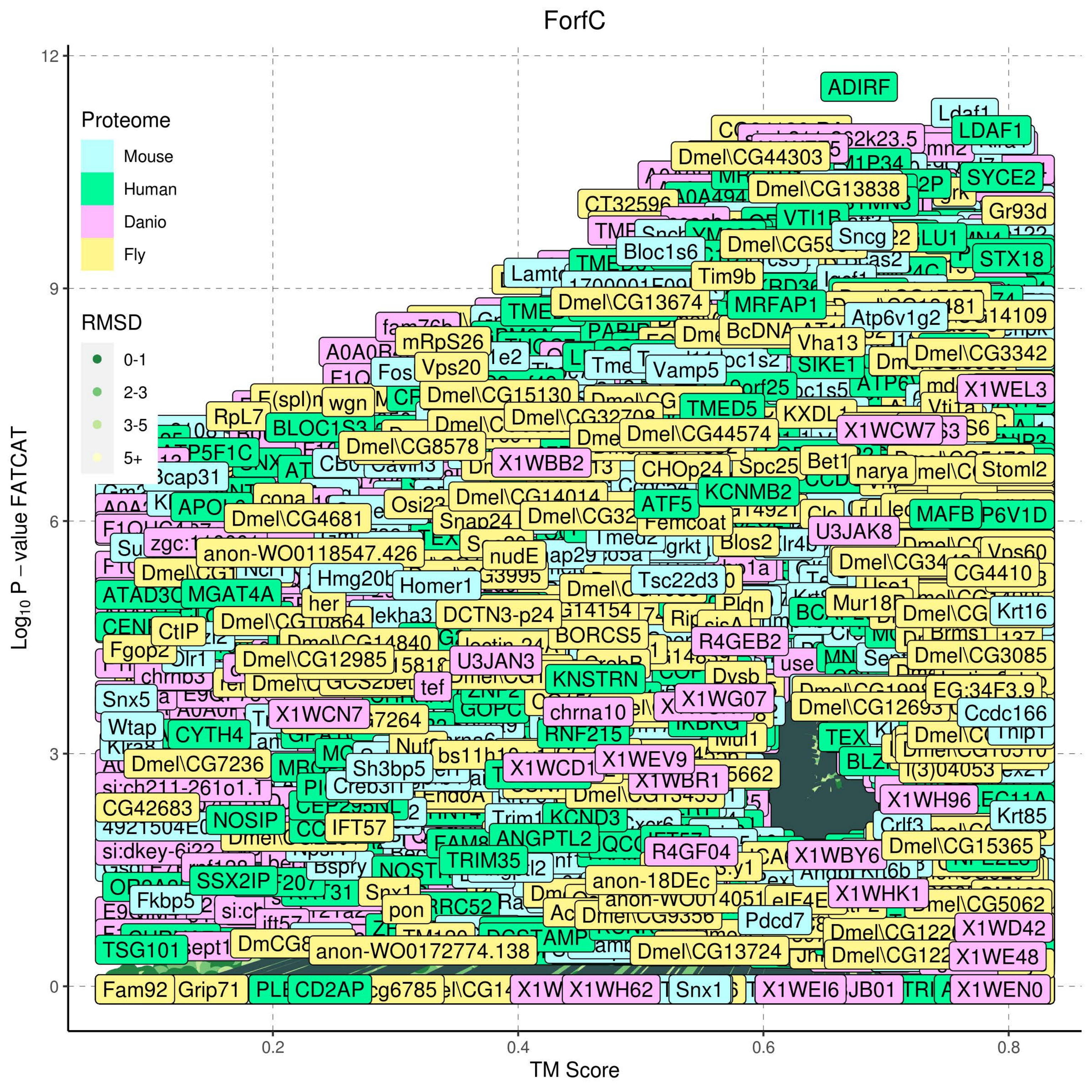

F16 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
G0s2
Bet1l
BcDNA:RH54117
HL5
OR2A25
C17orf100
Q6IQK3
G0S2
Med11
OR2A25
Gtpbp6
CDC45
CDK5RAP1
CK5P1
Cdk5rap1
sona
Nlrx1
A0A2R8Q0M3
Log10 P − value FATCAT
0
1
2
3
0.1
0.2
0.3
0.4
0.5
TM Score

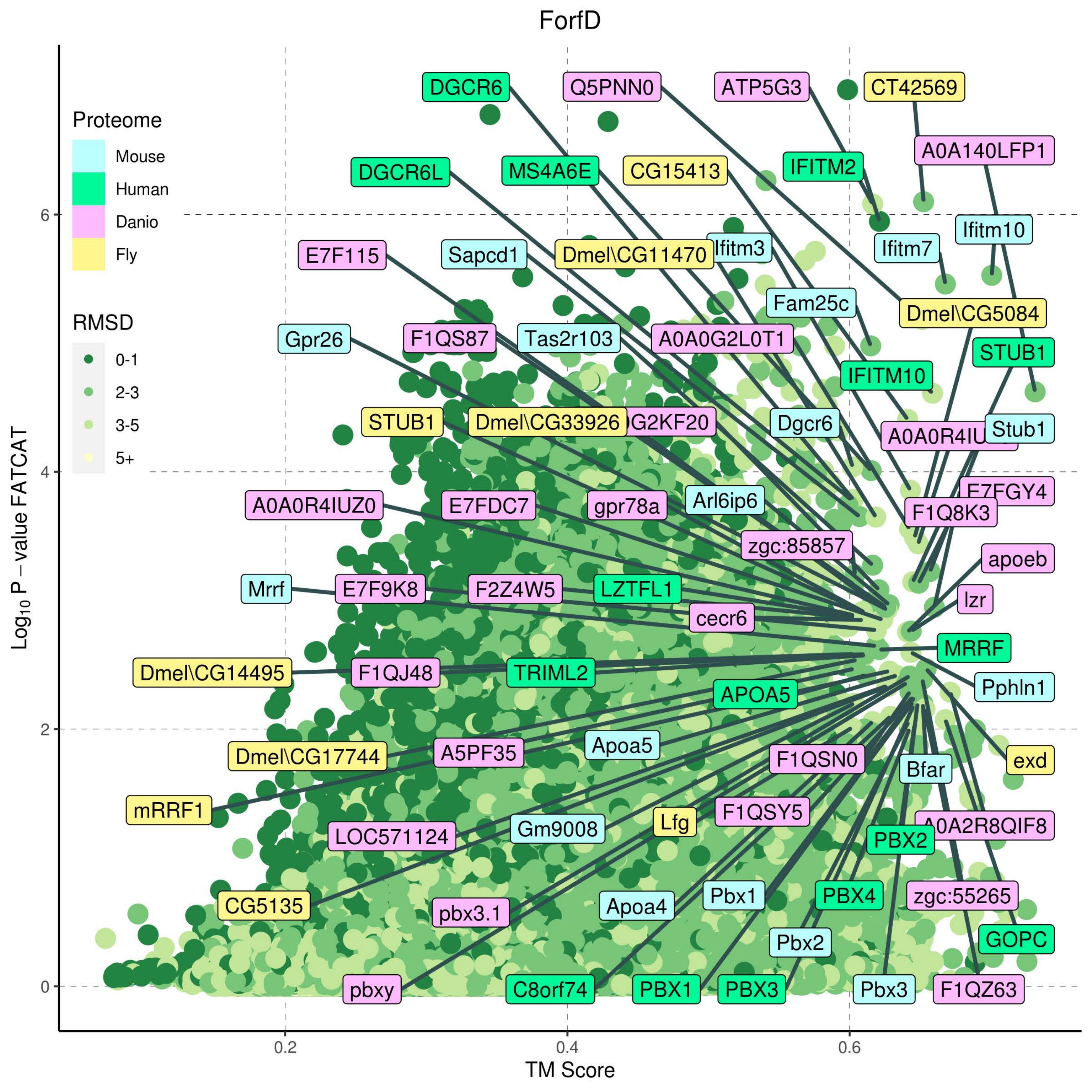

F17 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log₁₀ P − value FATCAT
TM Score
0
1
2
3
0.1
0.2
0.3
0.4
0.5
4930404H24Rik
Dmel\CG46458
A0A2R8YD15
Triap1
OR2A25
F1Q6Y0
A0A2R8Q432
CG13627-5'utr
RNF216P1
F1QZR1
Sbno1
B8JLR1
Atp13a2
Ubr1
MUC19
A0A0R4IJY6
AB
SYNE1

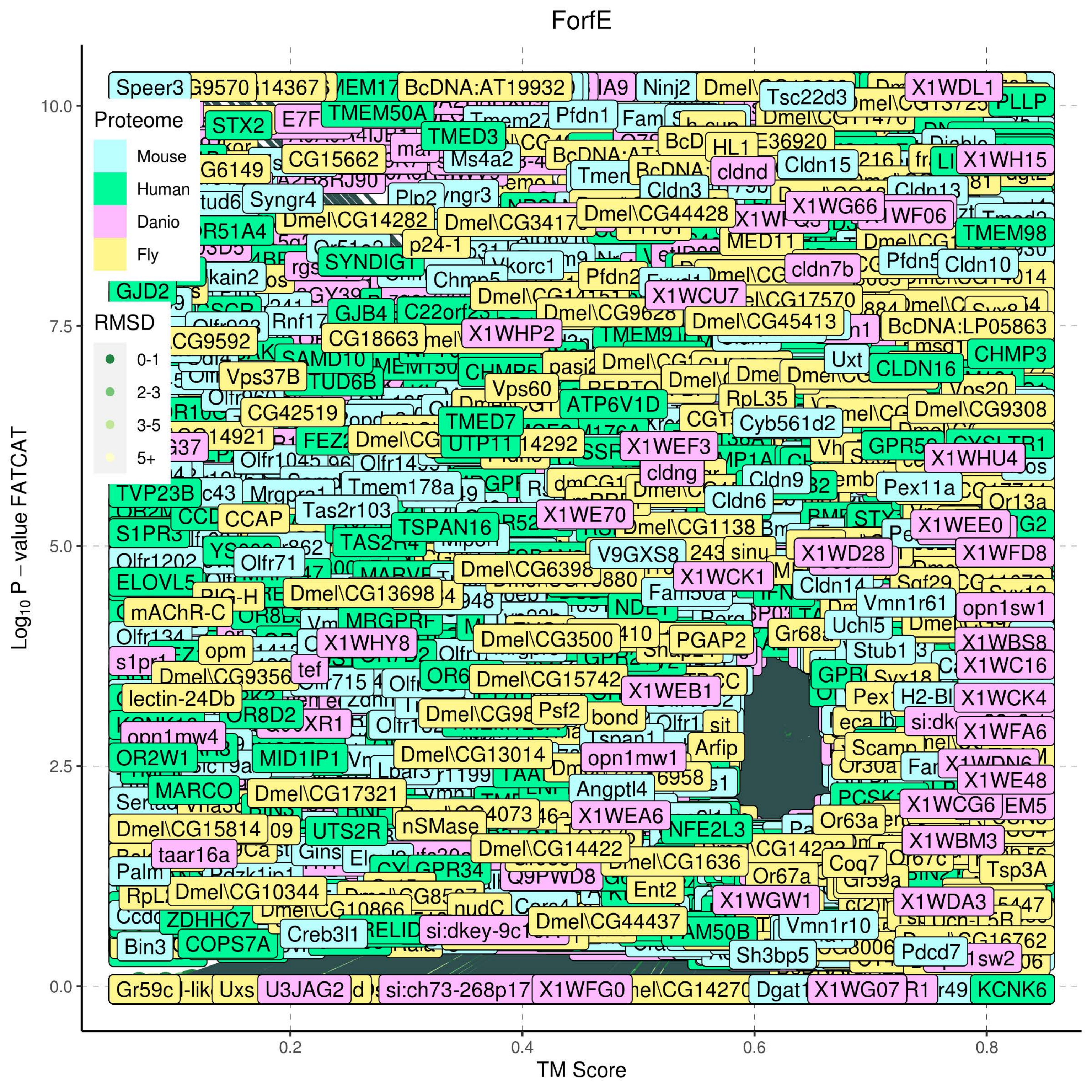

ForfA
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P − value FATCAT
TM Score
0
2
4
6
0.2
0.4
0.6
0.8
X1WE12
TNFRSF12A
FXYD4
Dmel\CG11269
LINC00312
FXYD6
Snorc
Fam136a
YP007
1QZF5
Higd1c
BG:DS00941.11
IER3IP1
8465
C20orf141
TMEM14EP
Ifitm7
TM14
Ifitm2
msd1
Esp3
Dmel\CG17154
Dmel\CG13299
X1WDW6
Ndfip
Sec20
Dmel\CG13481
NPIPA1
si:rp71-1
mt-co2
CG42519
YJ001
Dmel\CG2617
NEST:bs
MED22
TMEM160
Dmel\CG30177
Tmem45b
Olfr328
OR2L2
Speer3
Dmel\CG14151
Marchf8
U3JA86
CDR1
Dmel\CG15550
Olfr533
OR14C36
Dmel\CG2201
Tmem160
CHMP1B
Vmn1r189
Membrin
Vha16-2
Fam162a
TMEM80
F1QIS1
4930516K23Rik
TAS2R5
BMERB1
OR106-9
TSPY4
X1WHG7
PLPP5
Icos
OR51E2
Olfr1054
OR14A2
Psmd9
ING4
OR2L8
Vmn1r52
Olfr287
Dmel\CG11786
MGST2
LZIC
Vmn1r200
Lzic
F1QX22
Ndfip1
Gm8947
X1WF06
LHFPL3
CHCHD
X1WBJ3
Olfr1342
TMEM45A
Gm8127
Olfr1151
Ing5
TAS2R
TECR
H2-Bl
St6galnac4
X1WE48
STX18
zdhhc22
gpr78a
Olfr584
Slc51a
Dmel\CG12115
ZDHHC22
Olfr126
OR51B2
Olfr536
Dmel\CG11672
Olfr131
X1WEE0
Olfr545
OR14K1
Snap29
Syx16
OR128-3
NDFIP1
ORAI3
Olfr211
Olfr582
or115-1
Olfr112
Olfr1132
Olfr669
Stx18
Tmem191c
GPR78
Vmn1r217

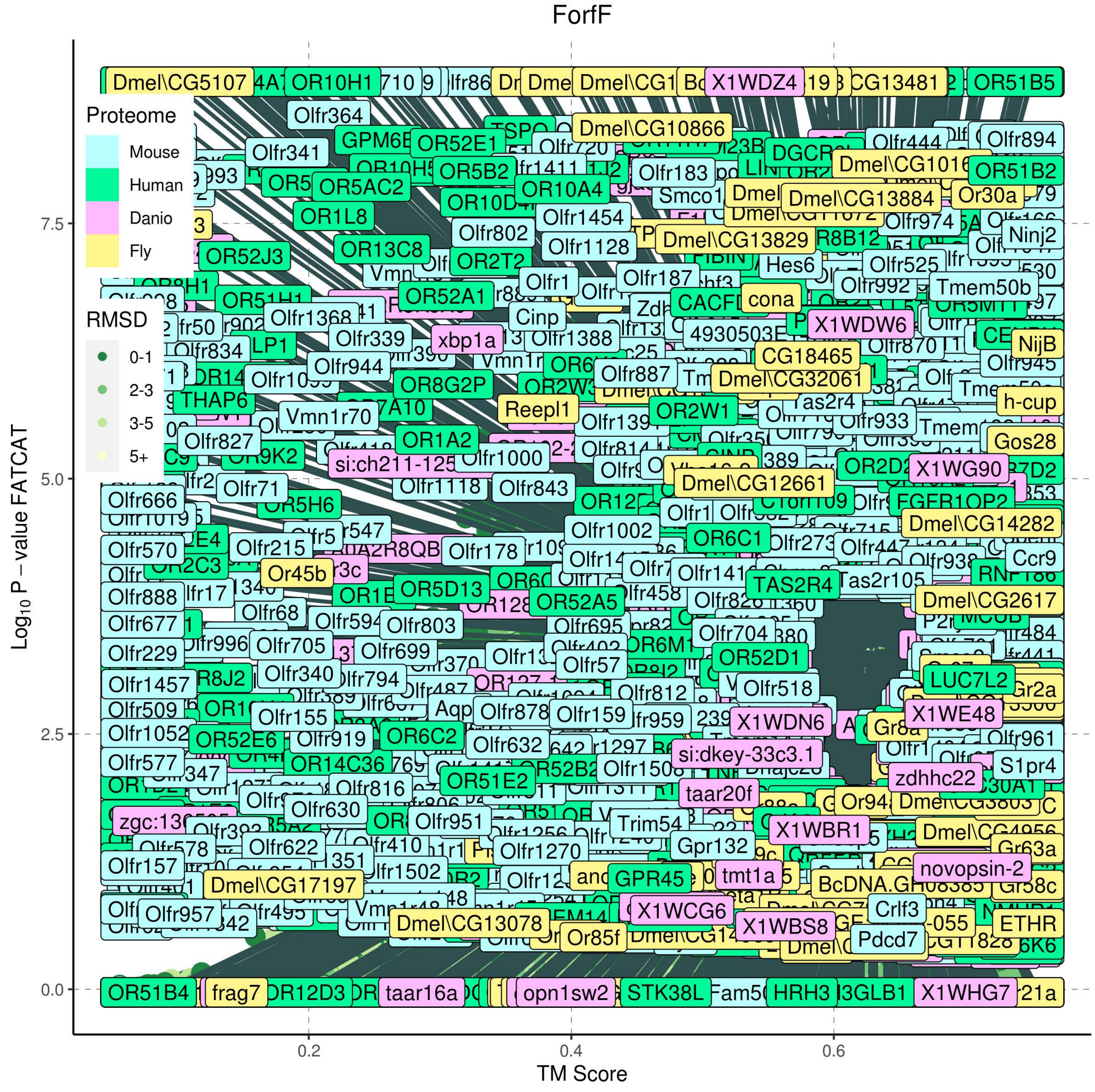
ForfB : No hits, top-scoring values are indicated

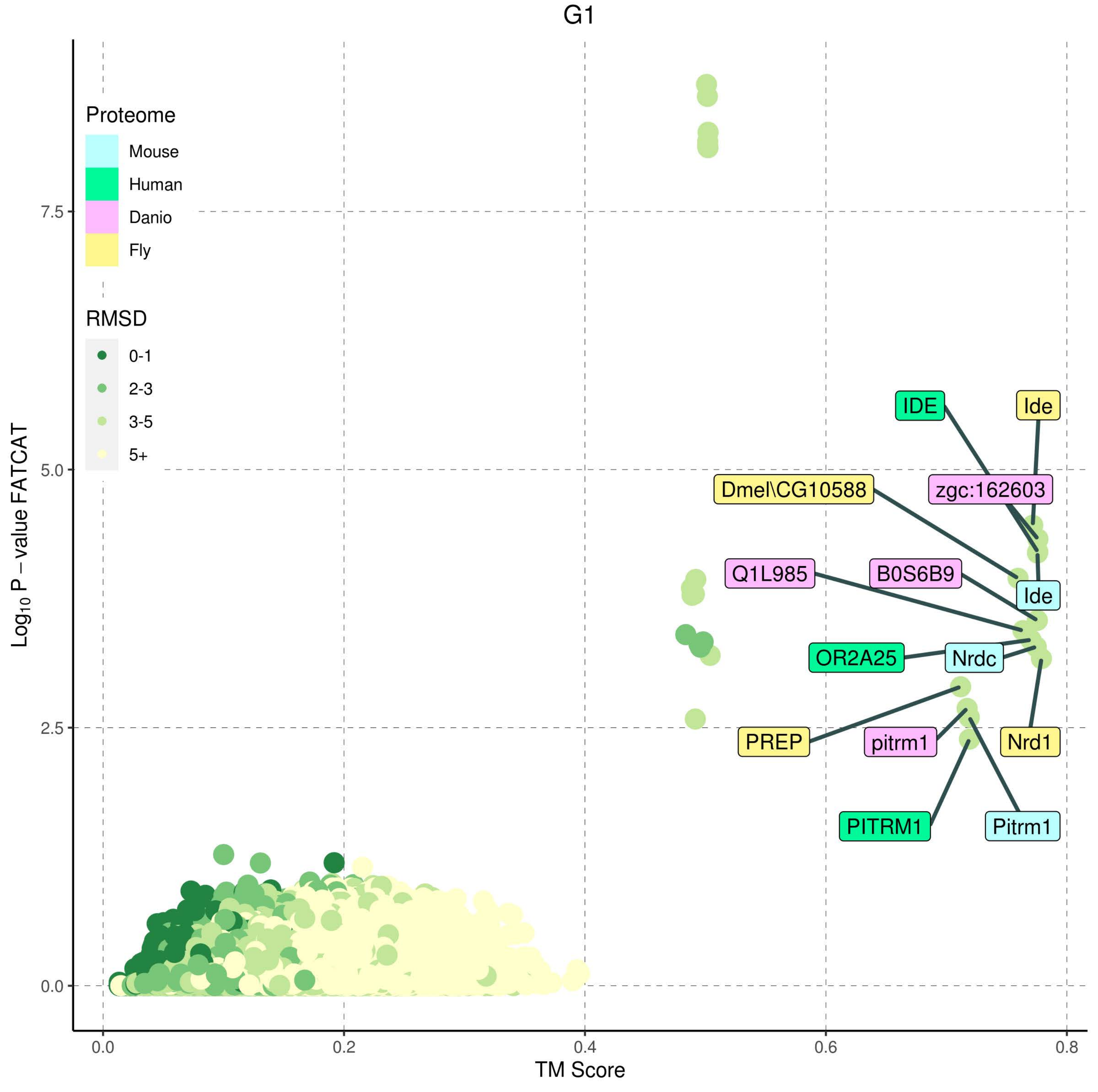


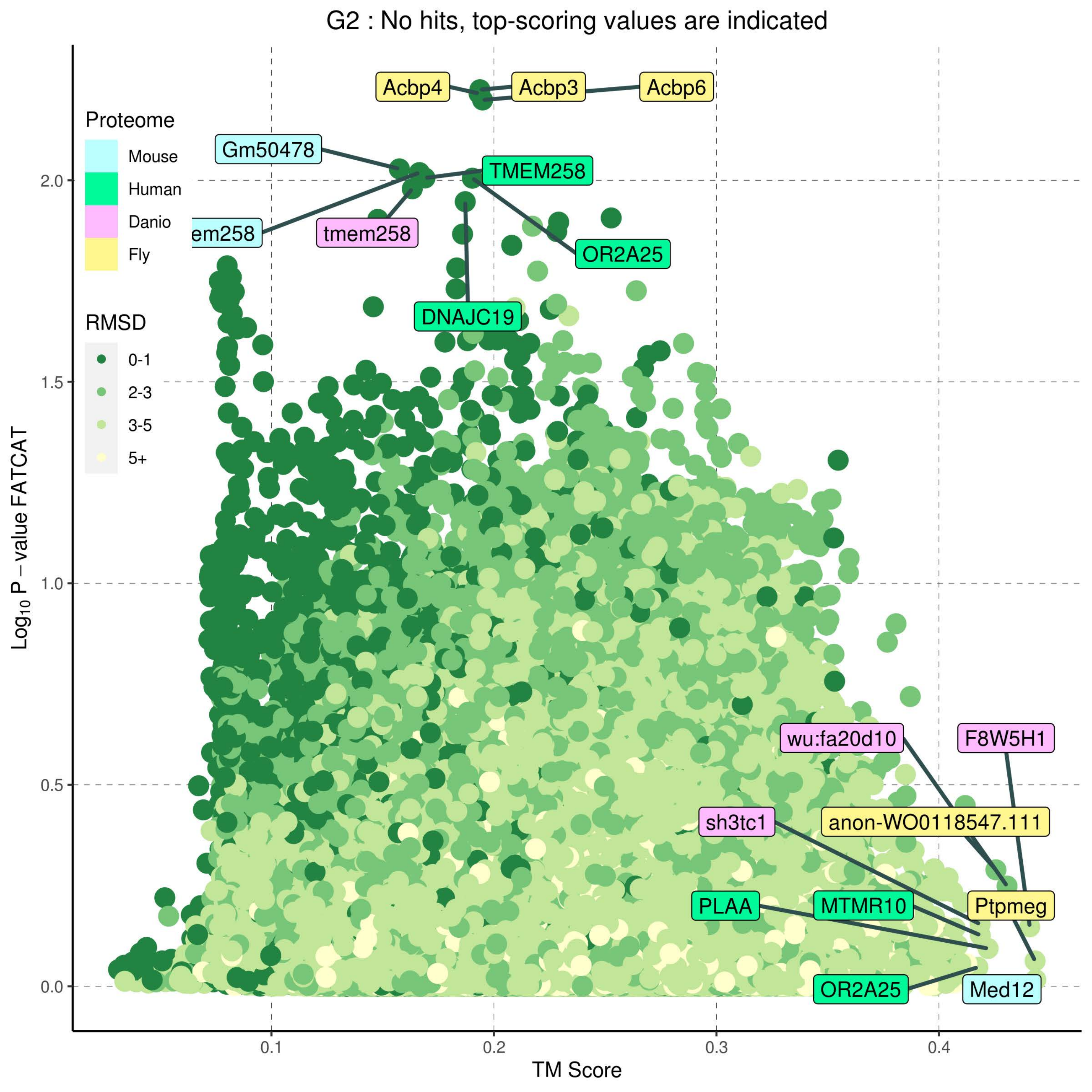

ForfC
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
TM Score
12
9
6
3
0
0.2
0.4
0.6
0.8
ADIRF
Ldaf1
LDAF1
Dmel\CG44303
SYCE2
Dmel\CG13838
CT32596
VTI1B
Gr93d
Sncg
Bloc1s6
STX18
Tim9b
Dmel\CG13674
MRFAP1
Atp6v1g2
mRpS26
Vha13
Dmel\CG3342
Vps20
Vamp5
SIKE1
X1WEL3
Dmel\CG15130
TMED5
KXDL1
RpL7
wgn
BLOC1S3
Dmel\CG44574
X1WCW7
Dmel\CG8578
ATP5F1C
X1WBB2
CHOp24
Spc25
Bet1
narya
Stoml2
KCNMB2
Dmel\CG14014
ATF5
Dmel\CG4681
Osi23
Femcoat
MAFB
P6V1D
Snap24
U3JAK8
anon-WO0118547.426
nudE
Blos2
Dmel\CG34
Vps60
CG4410
Hmg20b
Homer1
Tsc22d3
ATAD3C
MGAT4A
her
Mur18B
Pldn
Krt16
Dmel\CG10864
DCTN3-p24
CtIP
BORCS5
R4GEB2
Fgop2
Dmel\CG12985
U3JAN3
Dmel\CG3085
KNSTRN
Dysb
tef
EG:34F3.9
Snx5
X1WG07
X1WCN7
chrna10
Dmel\CG12693
Ccdc166
Wtap
CYTH4
RNF215
Dmel\CG7236
X1WEV9
Sh3bp5
X1WCD1
X1WBR1
I(3)04053
si:ch211-261o1.1
X1WH96
CG42683
NOSIP
IFT57
KCND3
Krt85
Crlf3
ANGPTL2
Dmel\CG15365
TRIM35
R4GF04
X1WBY6
SSX2IP
anon-18DEc
Fkbp5
X1WHK1
Dmel\CG5062
pon
Pdcd7
X1WD42
TSG101
anon-WO0172774.138
Dmel\CG13724
X1WE48
Fam92
Grip71
CD2AP
cg6785
X1WH62
Snx1
X1WEI6
X1WEN0

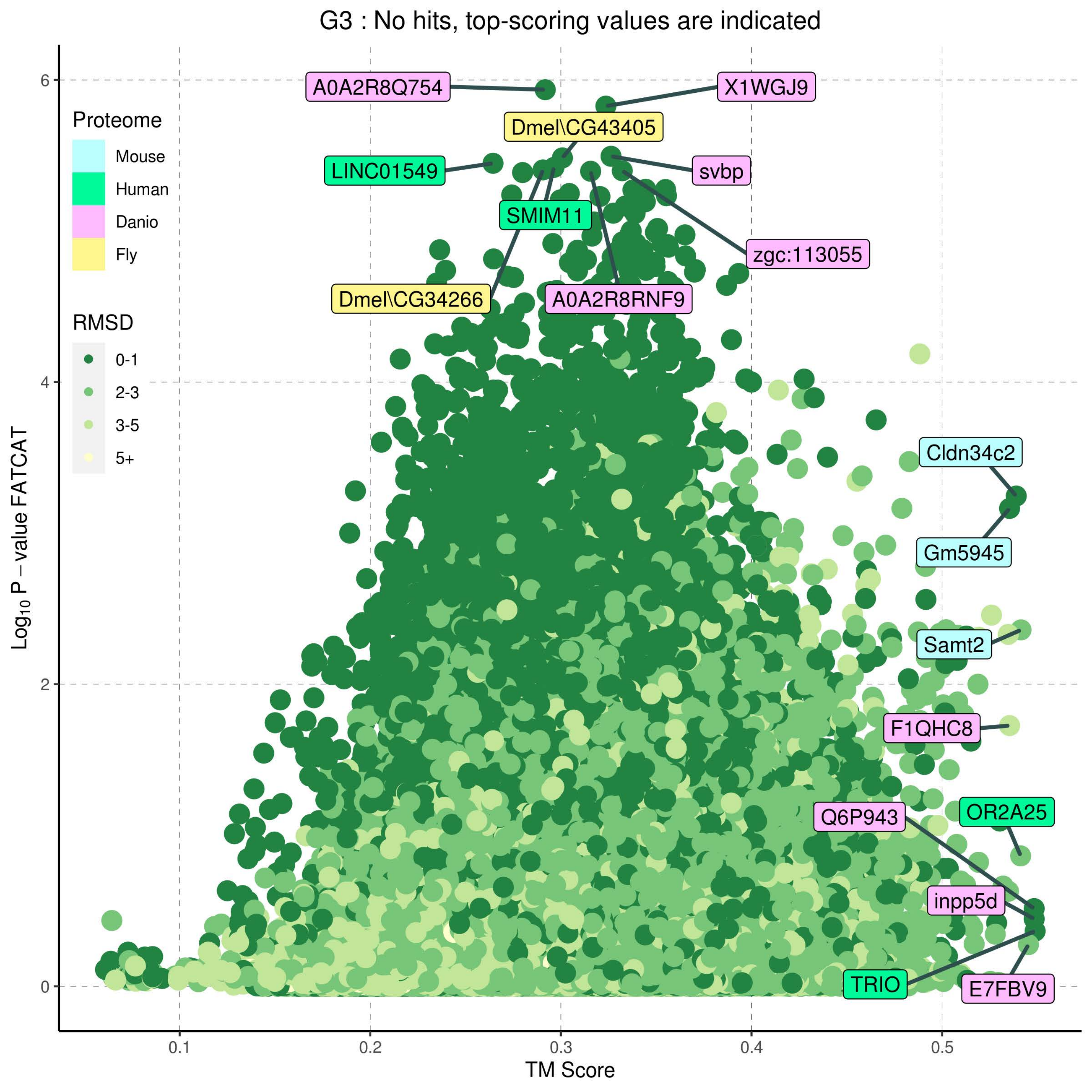

ForfD
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log₁₀ P − value FATCAT
TM Score
0
2
4
6
0.2
0.4
0.6
DGCR6
Q5PNN0
ATP5G3
CT42569
A0A140LFP1
DGCR6L
MS4A6E
CG15413
IFITM2
Ifitm10
Ifitm3
Ifitm7
E7F115
Sapcd1
Dmel\CG11470
Fam25c
Dmel\CG5084
Gpr26
F1QS87
Tas2r103
A0A0G2L0T1
STUB1
IFITM10
STUB1
Dmel\CG33926
G2KF20
Dgcr6
A0A0R4IU
Stub1
E7FGY4
A0A0R4IUZ0
E7FDC7
gpr78a
Arl6ip6
F1Q8K3
zgc:85857
apoeb
Mrrf
E7F9K8
F2Z4W5
LZTFL1
lzr
cecr6
MRRF
Dmel\CG14495
F1QJ48
TRIML2
Pphln1
APOA5
Dmel\CG17744
A5PF35
Apoa5
F1QSN0
Bfar
exd
mRRF1
F1QSY5
Lfg
Gm9008
LOC571124
A0A2R8QIF8
PBX2
CG5135
pbx3.1
Apoa4
Pbx1
PBX4
zgc:55265
GOPC
Pbx2
pbxy
C8orf74
PBX1
PBX3
Pbx3
F1QZ63

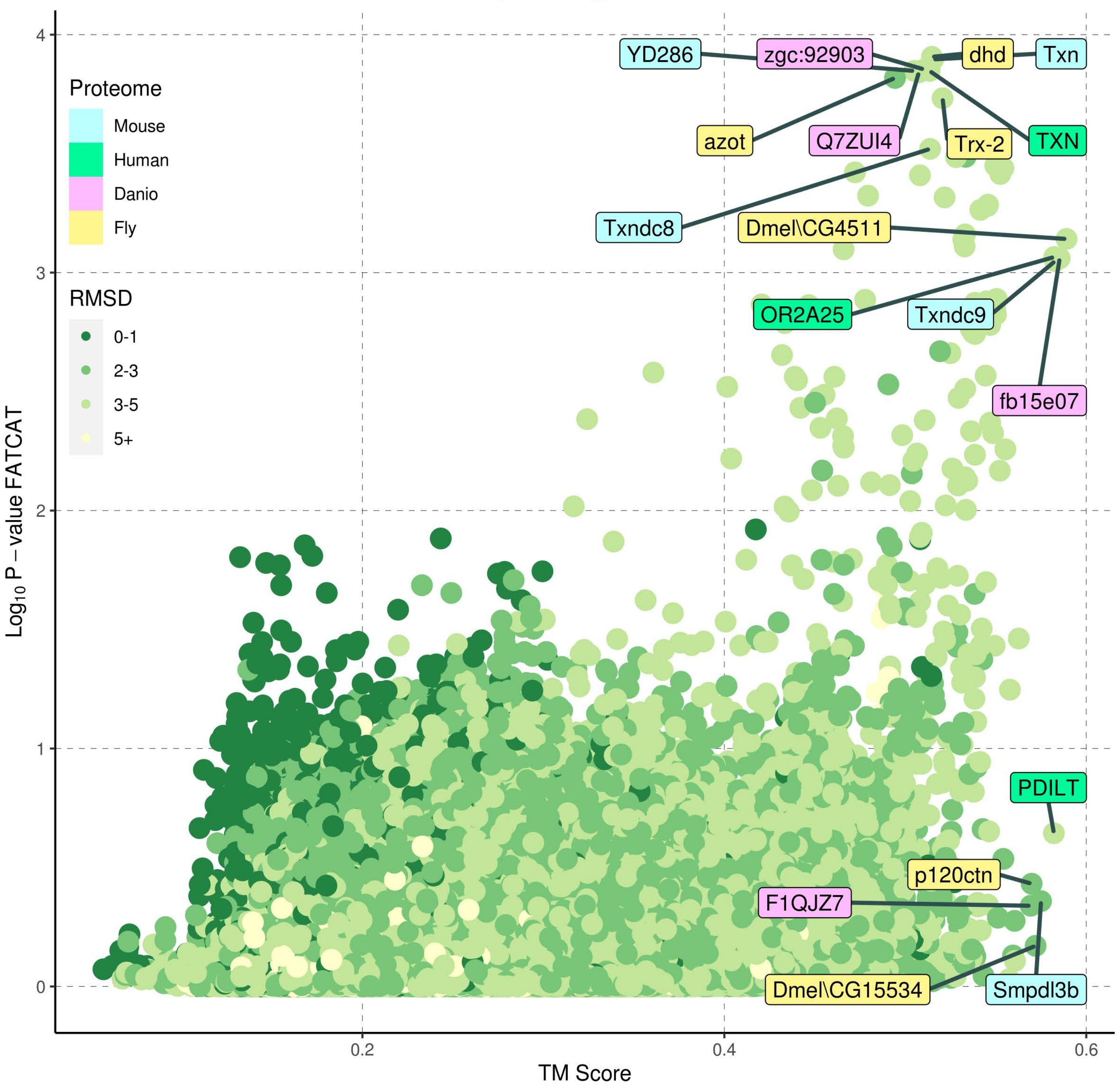

ForfE
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
TM Score
10.0
7.5
5.0
2.5
0.0
0.2
0.4
0.6
0.8
Speer3
BcDNA:AT19932
Ninj2
Tsc22d3
X1WDL1
PLLP
STX2
TMEM50A
Pfdn1
TMED3
CG15662
Ms4a2
HL1
Cldn15
X1WH15
cldnd
Cldn3
Syngr4
X1WG66
Dmel\CG14282
Dmel\CG44428
TMEM98
MED11
p24-1
SYNDIG1
Vkorc1
Pfdn2
cldn7b
Cldn10
GJD2
X1WCU7
Dmel\CG9628
Dmel\CG45413
BcDNA:LP05863
GJB4
X1WHP2
CG18663
CG9592
Uxt
CHMP3
CLDN16
Vps37B
TUD6B
Vps60
ATP6V1D
RpL35
Dmel\CG9308
CG42519
TMED7
UTP11
Cyb561d2
X1WEF3
X1WHU4
cldng
Cldn9
TVP23B
Tmem178a
Pex11a
Tas2r103
CCAP
TSPAN16
X1WE70
Dmel\CG1138
Cldn6
Or13a
X1WEE0
S1PR3
Olfr71
V9GXS8
X1WD28
X1WFD8
ELOVL5
Dmel\CG6398
X1WCK1
Cldn14
Dmel\CG13698
mAChR-C
Vmn1r61
opn1sw1
Dmel\CG3500
PGAP2
X1WHY8
Uchl5
X1WBS8
Stub1
X1WC16
Dmel\CG9356
tef
Dmel\CG15742
X1WEB1
X1WCK4
lectin-24Db
OR8D2
Psf2
X1WFA6
opn1mw4
OR2W1
MID1IP1
Dmel\CG13014
opn1mw1
Arfip
Scamp
X1WE48
MARCO
Dmel\CG17321
Angptl4
X1WCG6
Dmel\CG15814
UTS2R
nSMase
X1WEA6
NFE2L3
Or63a
X1WBM3
taar16a
Dmel\CG14422
Dmel\CG1636
Coq7
Tsp3A
Palm
GPR34
Q9PWD8
Or67a
Dmel\CG10344
Ent2
X1WGW1
X1WDA3
ZDHHC7
nudC
Dmel\CG44437
Creb3l1
Vmn1r10
Bin3
COPS7A
Sh3bp5
Pdcd7
Gr59c
Uxs
U3JAG2
X1WFG0
Dgat1
X1WG07
KCNK6

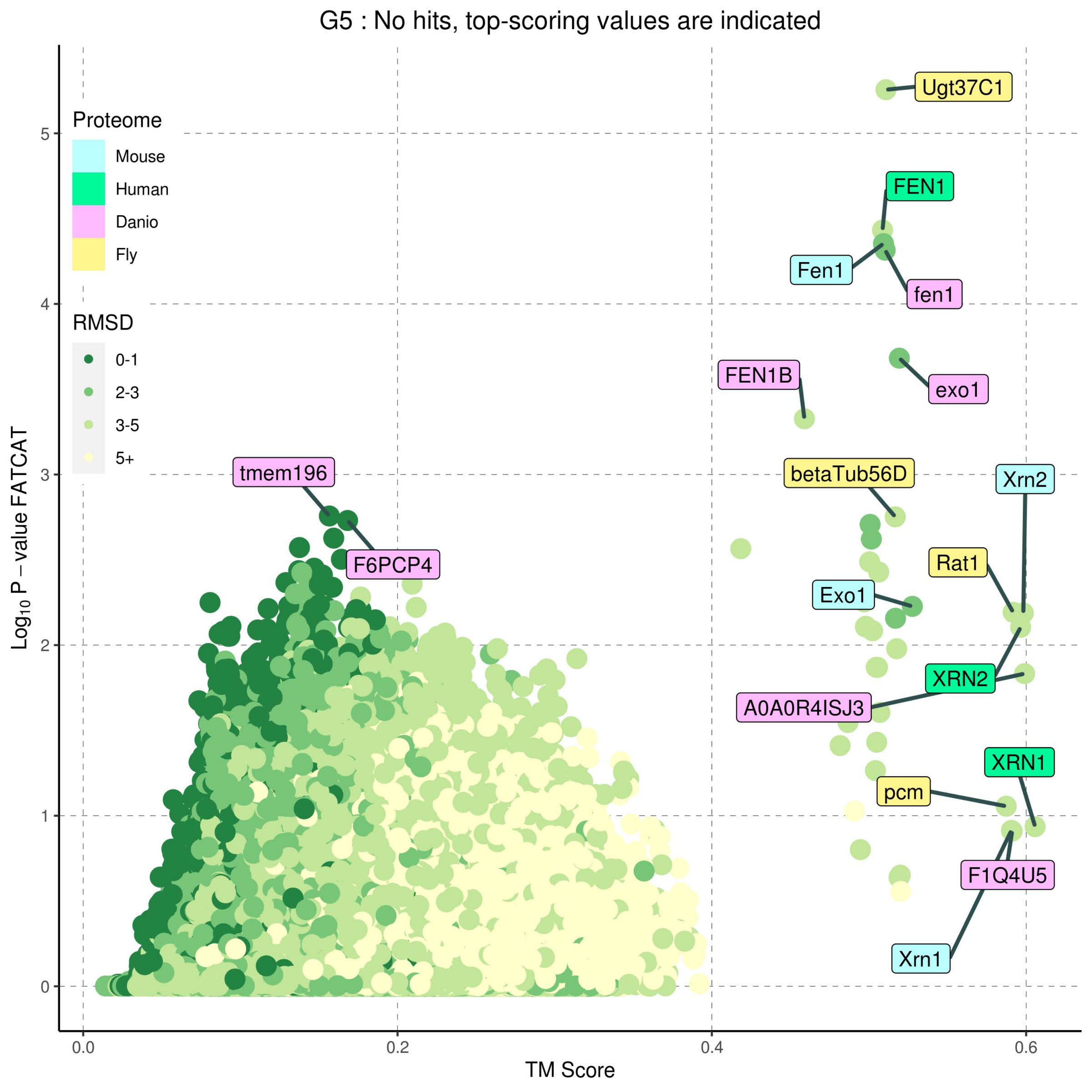

ForfF
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
7.5
5.0
2.5
0.0
0.2
0.4
0.6
TM Score
Dmel\CG5107
OR10H1
Dmel\CG1
X1WDZ4
CG13481
OR51B5
Olfr364
Dmel\CG10866
GPM6E
OR52E1
Olfr341
Olfr444
Olfr894
Olfr720
DGCR
Dmel\CG1016
OR51B2
OR5AC2
OR5B2
OR10A4
Olfr183
Smco1
Dmel\CG13884
Or30a
OR1L8
OR10D4
Olfr1454
Olfr974
Olfr802
Ninj2
OR13C8
Olfr1128
Dmel\CG13829
OR8B12
OR52J3
OR2T2
Hes6
Olfr525
OR8H1
Olfr1
Olfr187
Olfr992
Tmem50b
OR51H1
OR52A1
CACFD
cona
Olfr1368
Cinp
X1WDW6
xbp1a
Olfr339
Olfr1388
4930503E
Olfr870
NijB
Olfr834
LP1
Olfr944
CG18465
Olfr945
OR14
OR8G2P
Olfr887
Dmel\CG32061
THAP6
Reepl1
OR2W1
Tas2r4
h-cup
Vmn1r70
OR7A10
Olfr933
Olfr827
OR1A2
Gos28
OR9K2
si:ch211-125
Olfr1000
OR2D2
X1WG90
OR7D2
Olfr71
Olfr1118
Olfr843
Dmel\CG12661
Olfr666
OR5H6
OR12
FGFR1OP2
Dmel\CG14282
Olfr1002
OR6C1
Olfr570
Olfr215
Olfr178
Olfr273
Olfr447
Olfr938
Ccr9
OR2C3
Or45b
Olfr141
TAS2R4
Tas2r105
Olfr888
OR5D13
OR52A5
Olfr458
Olfr826
Dmel\CG2617
Olfr68
Olfr677
Olfr594
Olfr803
Olfr695
Olfr704
Olfr229
Olfr996
Olfr705
Olfr699
OR6M1
OR52D1
Olfr57
Olfr1457
OR8J2
Olfr340
Olfr794
Olfr518
LUC7L2
Gr2a
Olfr509
Olfr155
Olfr878
Olfr159
Olfr812
Olfr959
X1WDN6
X1WE48
Gr8a
Olfr1052
OR52E6
Olfr919
OR6C2
Olfr632
Olfr961
Olfr577
OR14C36
si:dkey-33c3.1
S1pr4
Olfr347
OR51E2
OR52B2
Olfr1508
zdhhc22
Olfr816
Olfr630
taar20f
Or94
Dmel\CG3803
zgc:13
Olfr951
Trim54
X1WBR1
Dmel\CG4956
Olfr578
Olfr622
Olfr410
Olfr1270
Gpr132
Gr63a
Olfr157
Olfr1502
novopsin-2
Dmel\CG17197
GPR45
tmt1a
BcDNA.GH08385
Gr58c
Olfr957
X1WCG6
Crlf3
Dmel\CG13078
X1WBS8
ETHR
Or85f
Pdcd7
OR51B4
frag7
OR12D3
taar16a
opn1sw2
STK38L
HRH3
X1WHG7

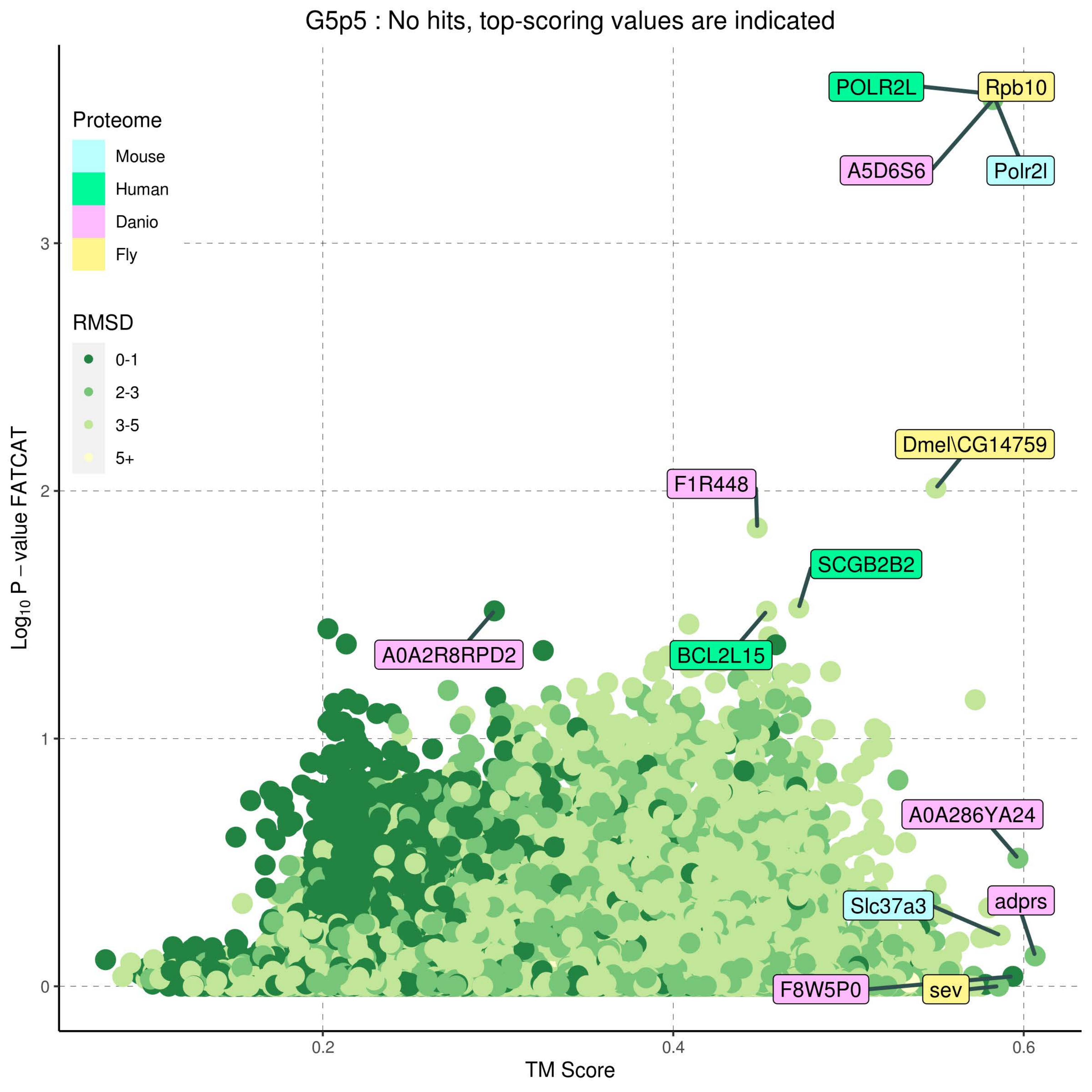

G1
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P − value FATCAT
TM Score
0.0
2.5
5.0
7.5
0.0
0.2
0.4
0.6
0.8
IDE
Ide
Dmel\CG10588
zgc:162603
Q1L985
B0S6B9
Ide
OR2A25
Nrdc
PREP
pitrm1
Nrd1
PITRM1
Pitrm1

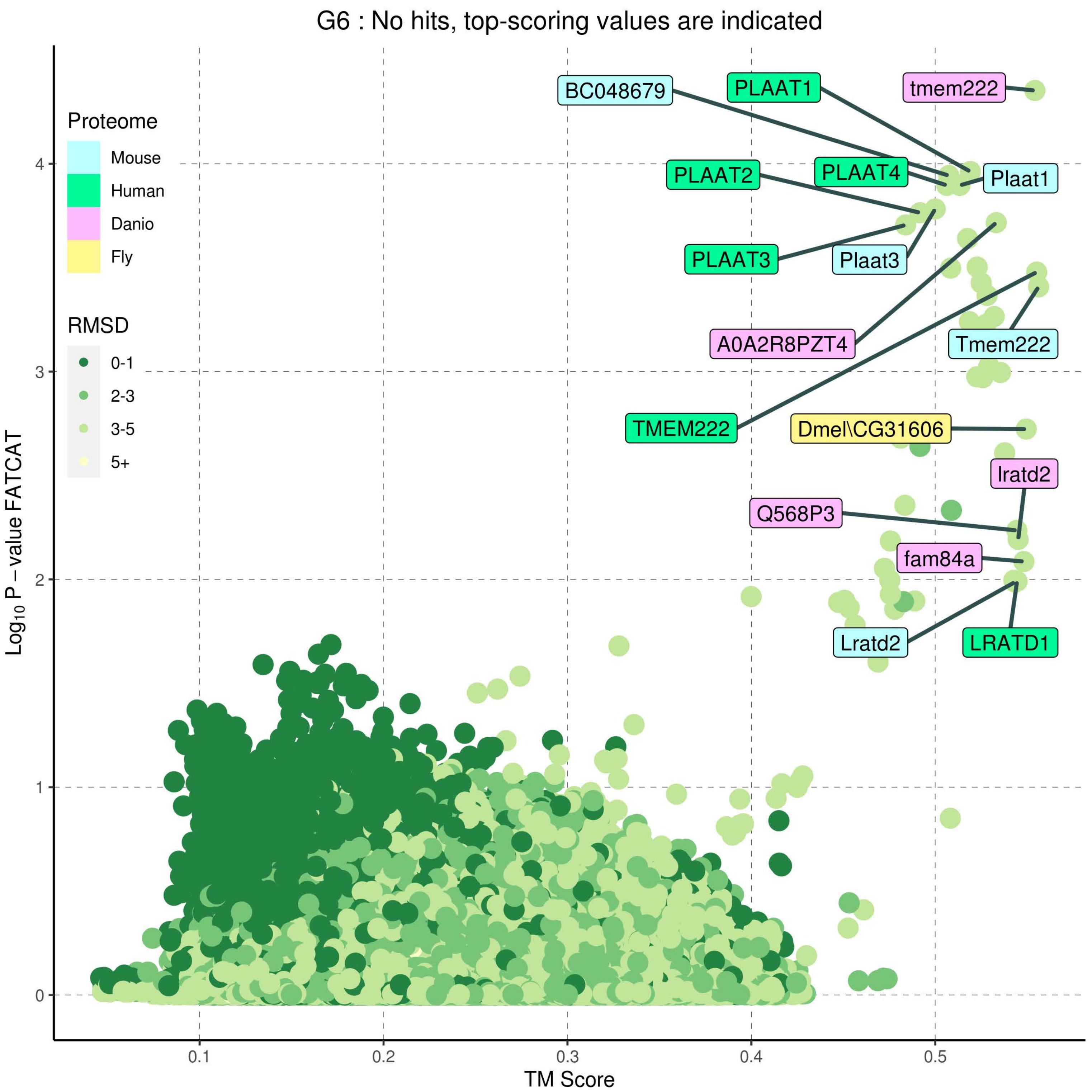

G2 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Acbp4
Acbp3
Acbp6
Gm50478
TMEM258
em258
tmem258
OR2A25
DNAJC19
wu:fa20d10
F8W5H1
sh3tc1
anon-WO0118547.111
PLAA
MTMR10
Ptpmeg
OR2A25
Med12
Log10 P – value FATCAT
2.0
1.5
1.0
0.5
0.0
0.1
0.2
0.3
0.4
TM Score

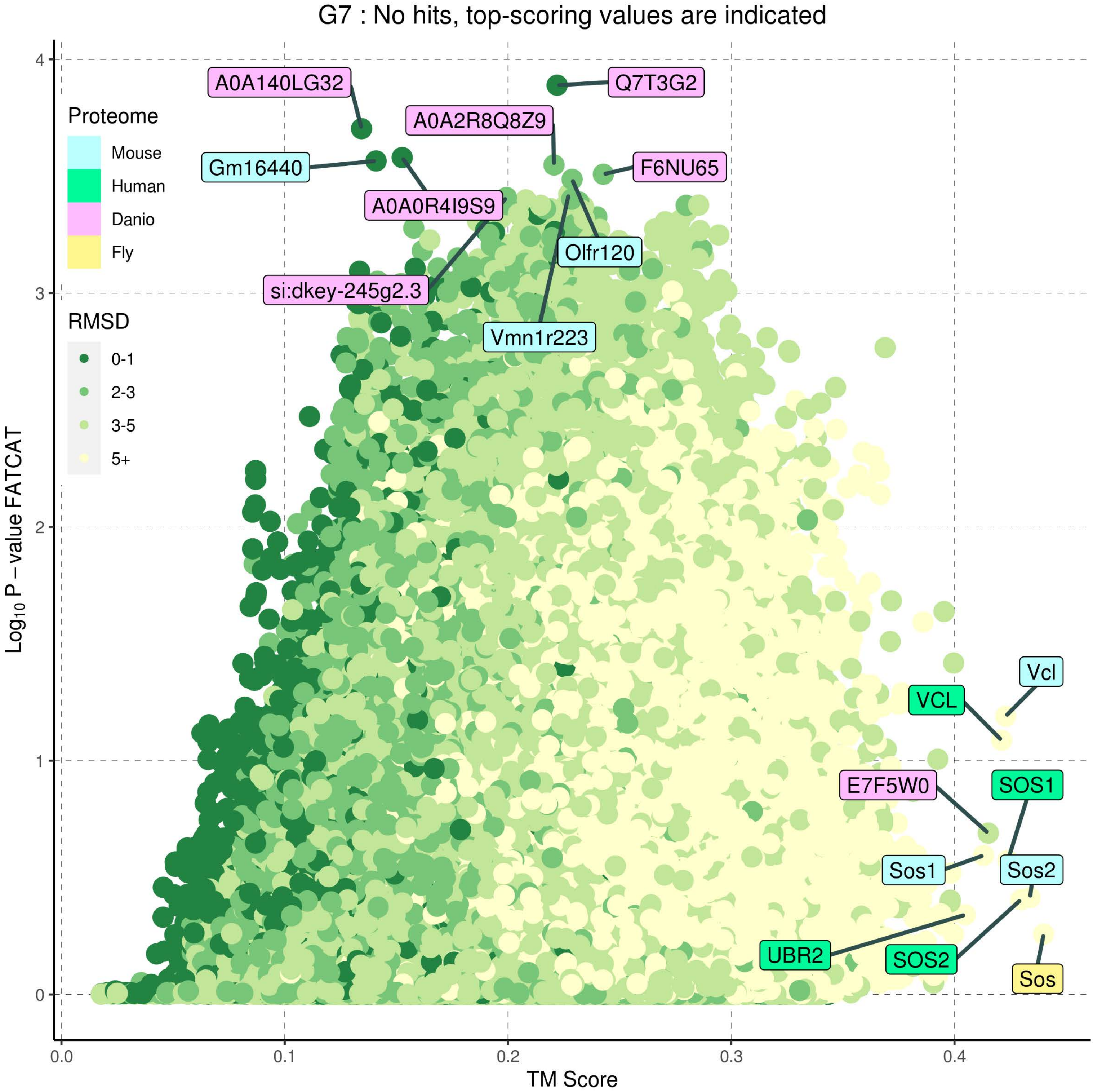

G3 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
A0A2R8Q754
X1WGJ9
Dmel\CG43405
LINC01549
svbp
SMIM11
zgc:113055
Dmel\CG34266
A0A2R8RNF9
Cldn34c2
Gm5945
Samt2
F1QHC8
OR2A25
Q6P943
inpp5d
TRIO
E7FBV9
Log_{10} P − value FATCAT
0
2
4
6
0.1
0.2
0.3
0.4
0.5
TM Score

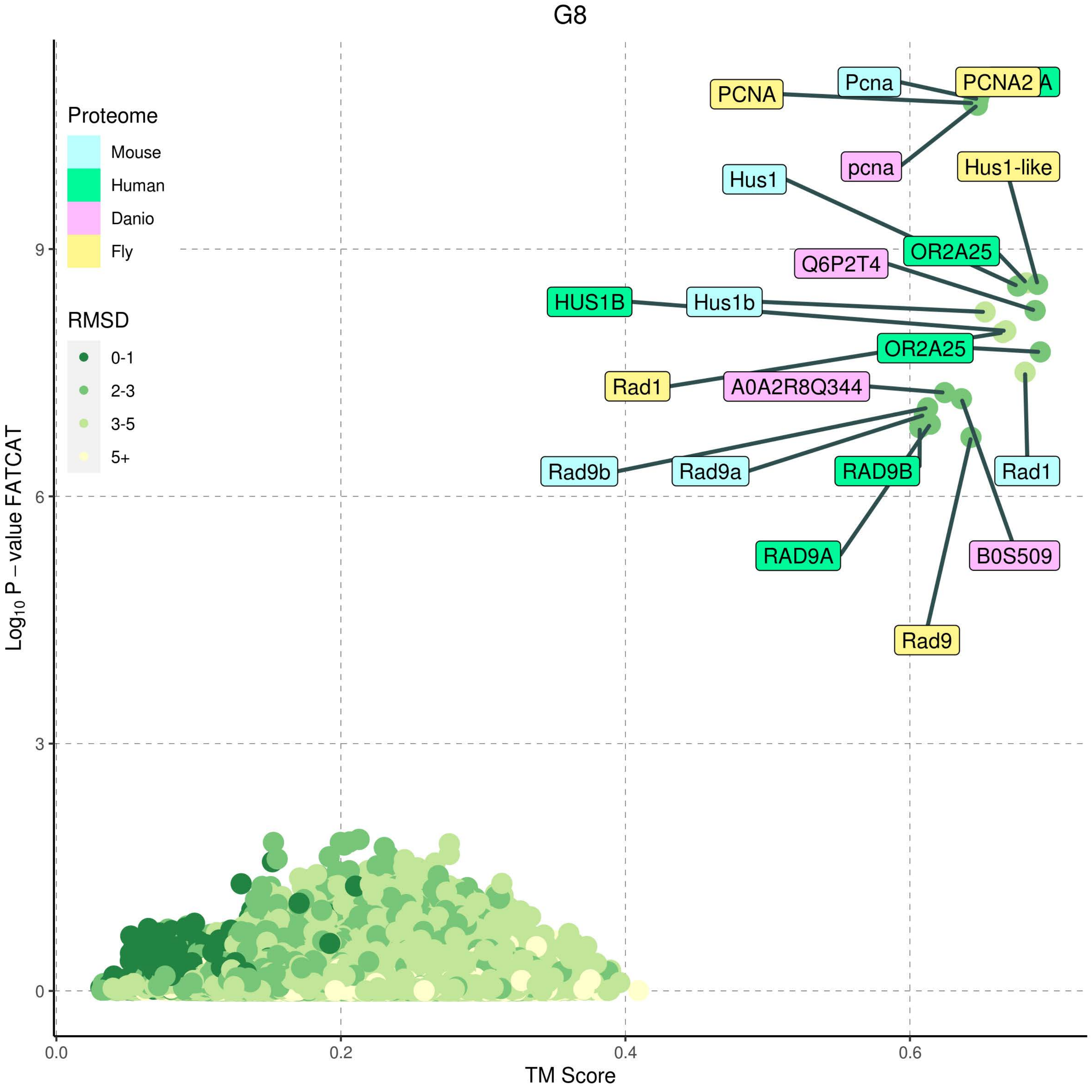

G4 : No hits, top-scoring values are indicated

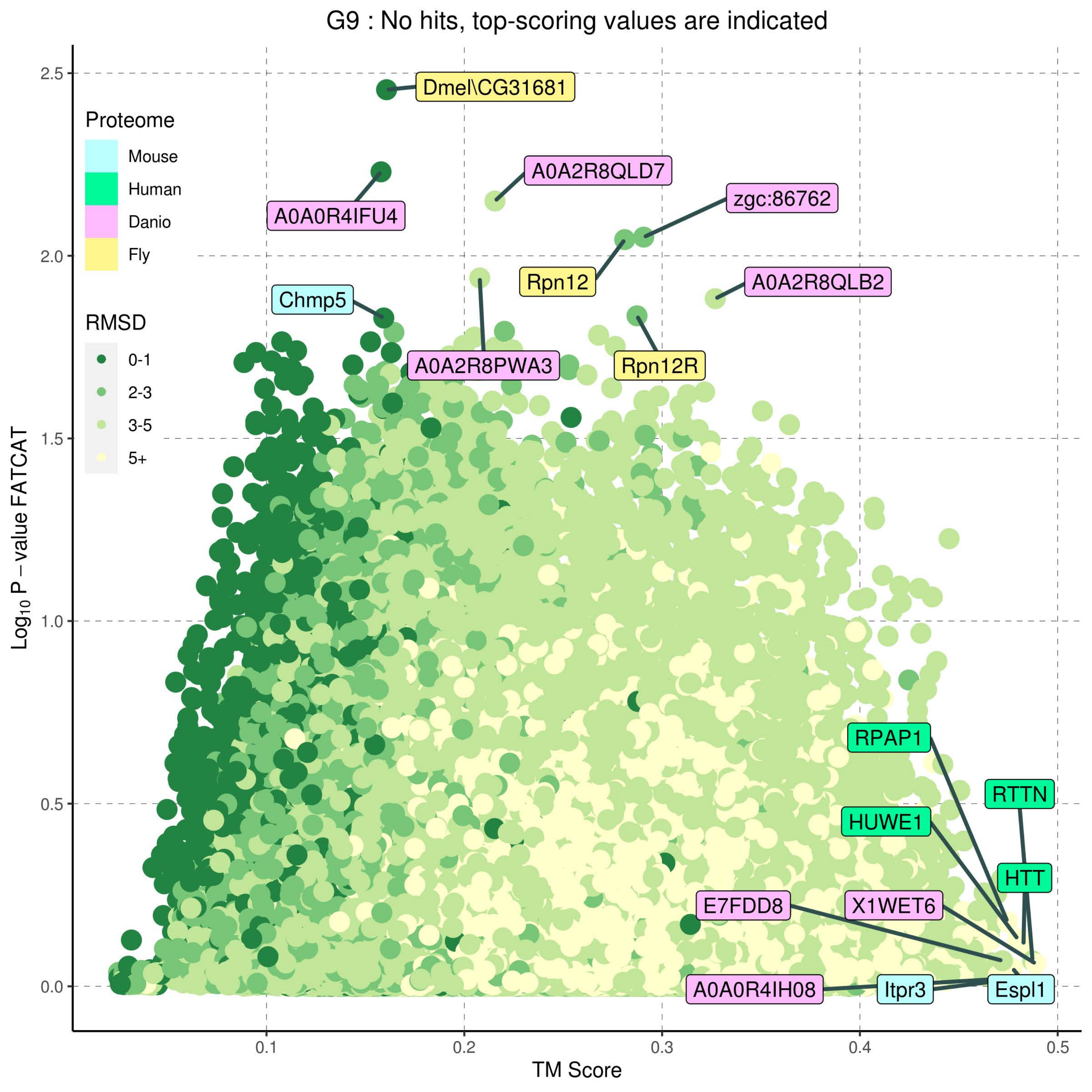

G5 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log$_{10}$ P – value FATCAT
TM Score
0
1
2
3
4
5
0.0
0.2
0.4
0.6
Ugt37C1
FEN1
Fen1
fen1
FEN1B
exo1
tmem196
F6PCP4
betaTub56D
Xrn2
Rat1
Exo1
XRN2
A0A0R4ISJ3
XRN1
pcm
F1Q4U5
Xrn1

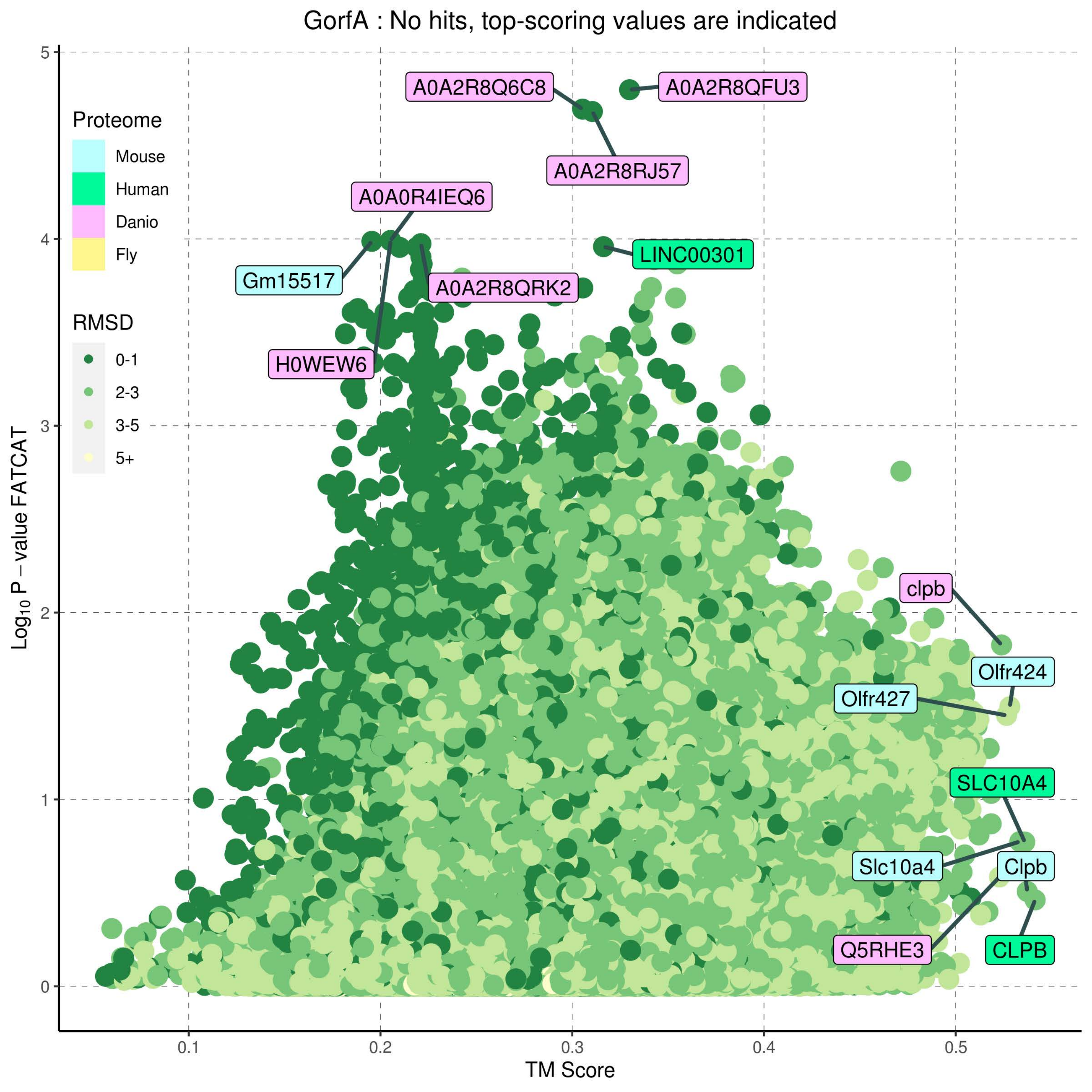

G5p5 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
POLR2L
Rpb10
A5D6S6
Polr2l
Dmel\CG14759
F1R448
SCGB2B2
A0A2R8RPD2
BCL2L15
A0A286YA24
adprs
Slc37a3
F8W5P0
sev
Log10 P − value FATCAT
3
2
1
0
0.2
0.4
0.6
TM Score

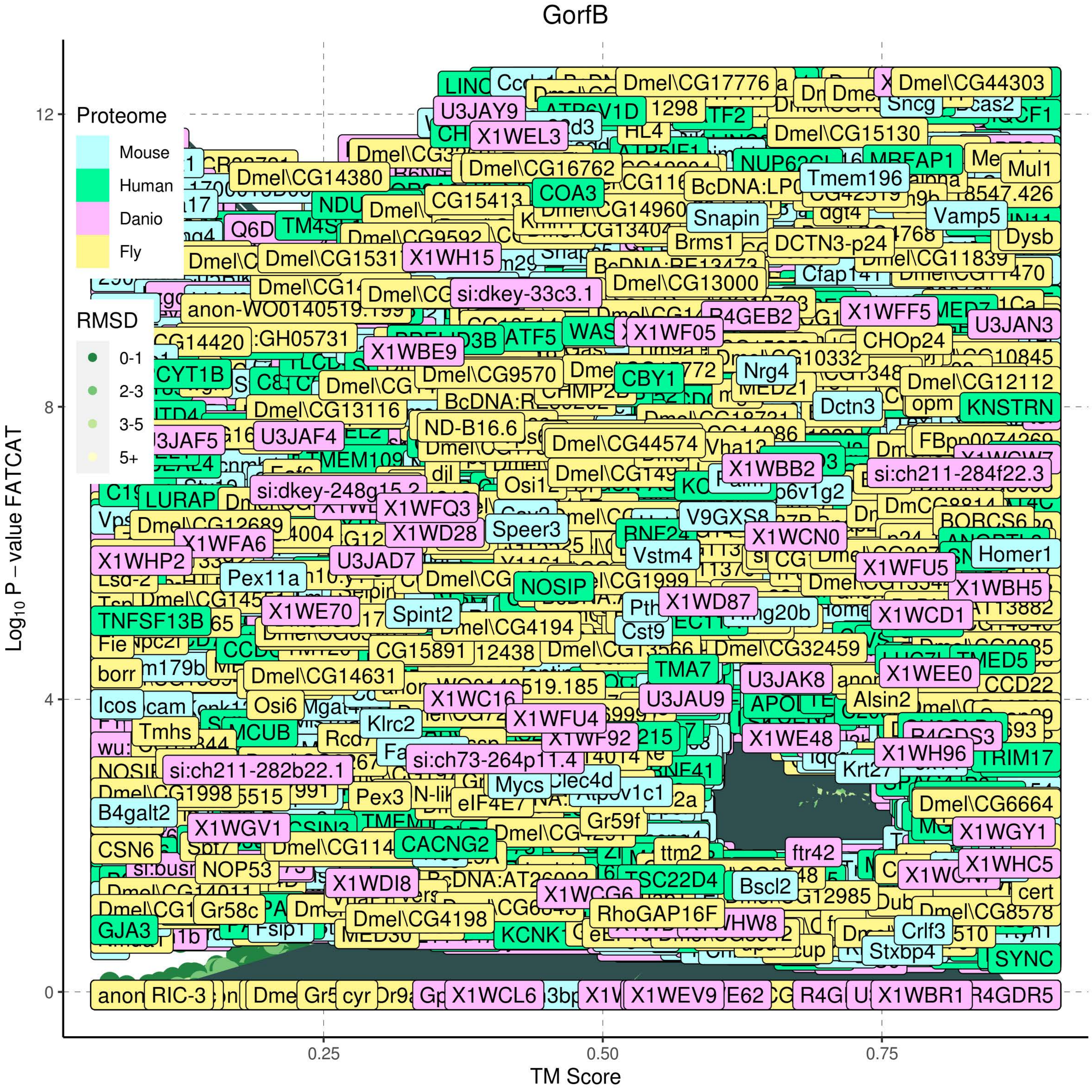

G6 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
BC048679
PLAAT1
tmem222
PLAAT2
PLAAT4
Plaat1
PLAAT3
Plaat3
A0A2R8PZT4
Tmem222
TMEM222
Dmel\CG31606
lratd2
Q568P3
fam84a
Lratd2
LRATD1
Log10 P − value FATCAT
0
1
2
3
4
TM Score
0.1
0.2
0.3
0.4
0.5

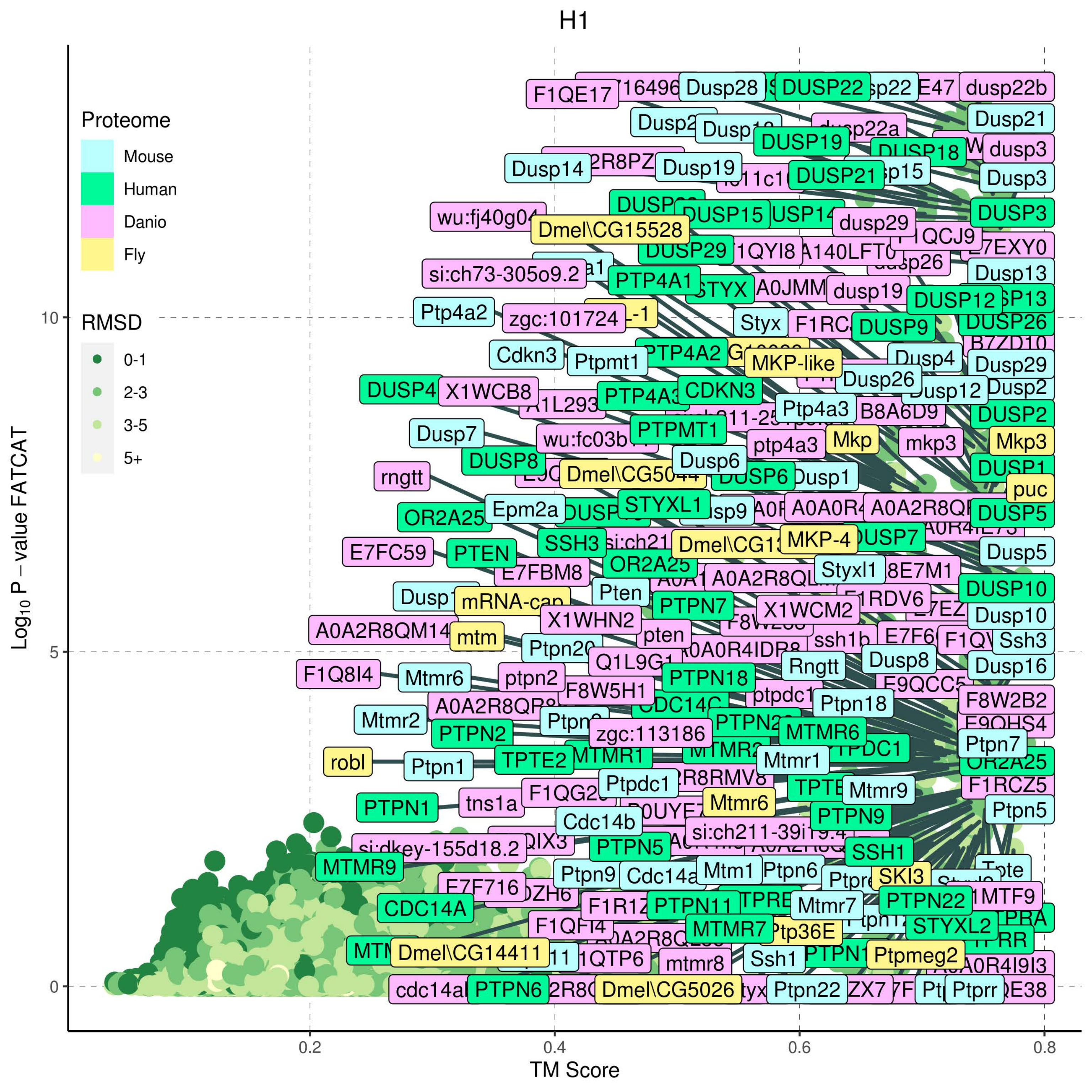

G7 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
A0A140LG32
Q7T3G2
A0A2R8Q8Z9
Gm16440
F6NU65
A0A0R4I9S9
Olfr120
si:dkey-245g2.3
Vmn1r223
Vcl
VCL
E7F5W0
SOS1
Sos1
Sos2
UBR2
SOS2
Sos
Log$_{10}$ P − value FATCAT
4
3
2
1
0
TM Score
0.0
0.1
0.2
0.3
0.4

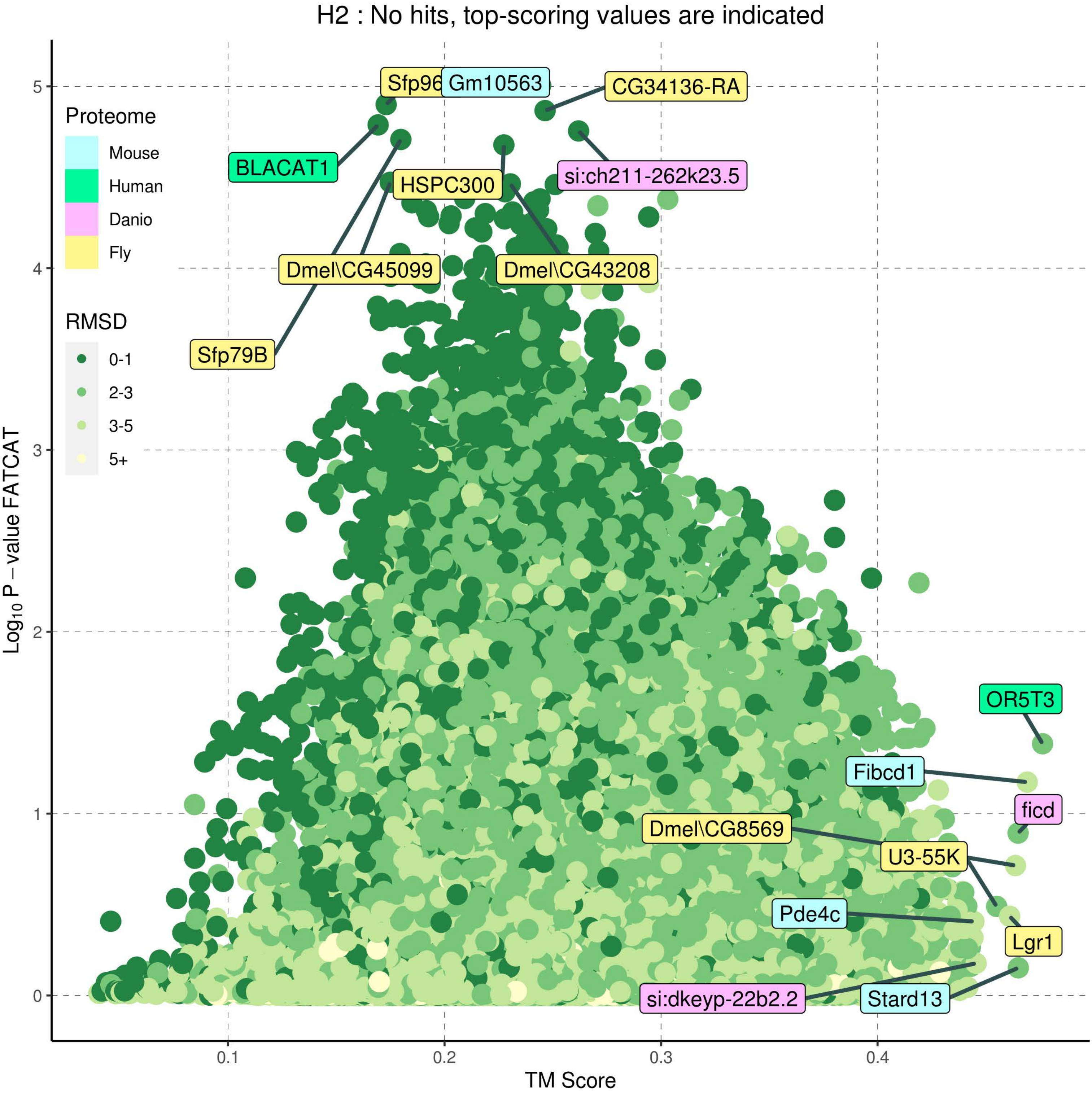

G8
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
TM Score
0
3
6
9
0.0
0.2
0.4
0.6
Pcna
PCNA2
A
PCNA
pcna
Hus1
Hus1-like
OR2A25
Q6P2T4
HUS1B
Hus1b
OR2A25
Rad1
A0A2R8Q344
Rad9b
Rad9a
RAD9B
Rad1
RAD9A
B0S509
Rad9

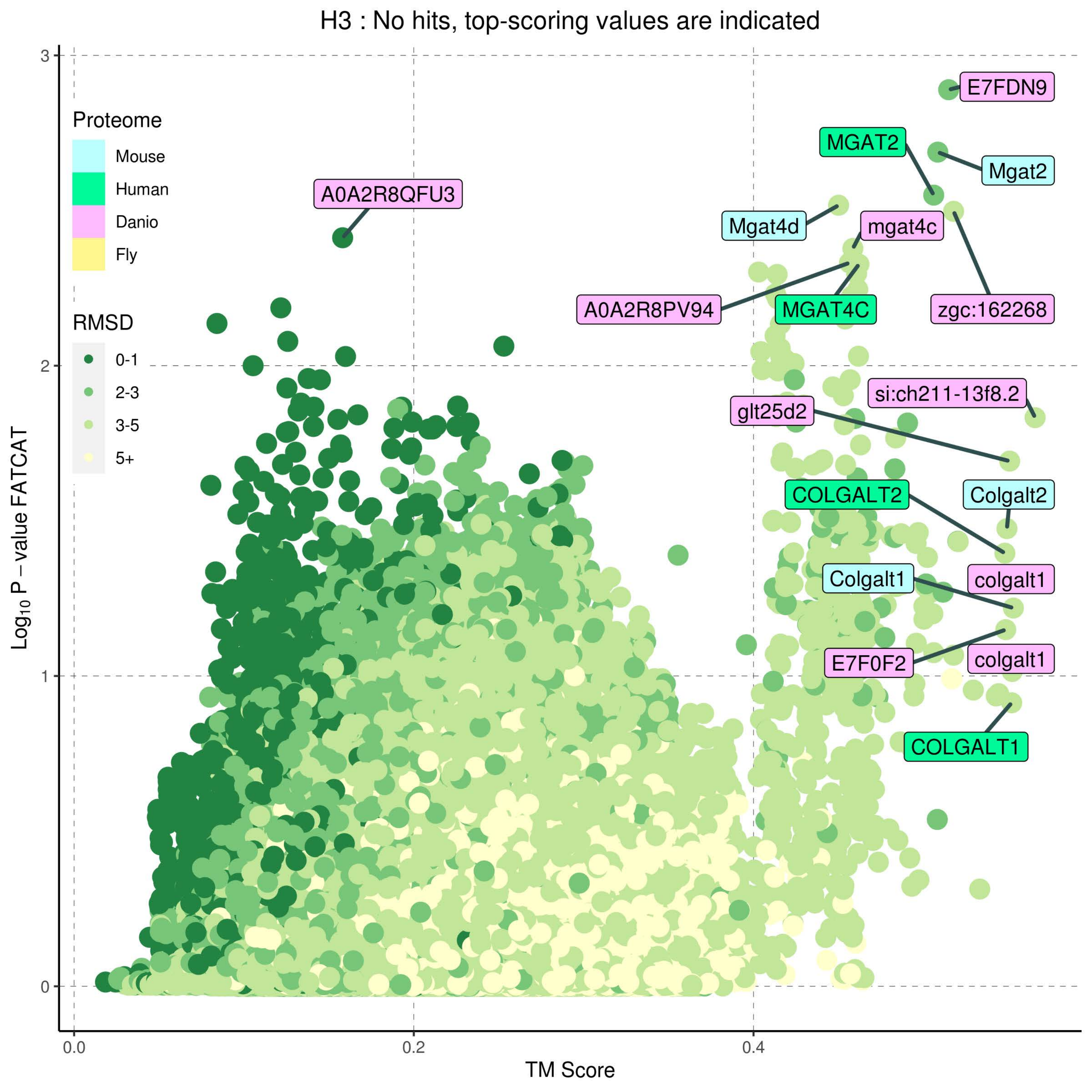

G9 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log$_{10}$ P − value FATCAT
TM Score
2.5
2.0
1.5
1.0
0.5
0.0
0.1
0.2
0.3
0.4
0.5
Dmel\CG31681
A0A2R8QLD7
A0A0R4IFU4
zgc:86762
Rpn12
A0A2R8QLB2
Chmp5
A0A2R8PWA3
Rpn12R
RPAP1
RTTN
HUWE1
HTT
E7FDD8
X1WET6
A0A0R4IH08
Itpr3
Espl1

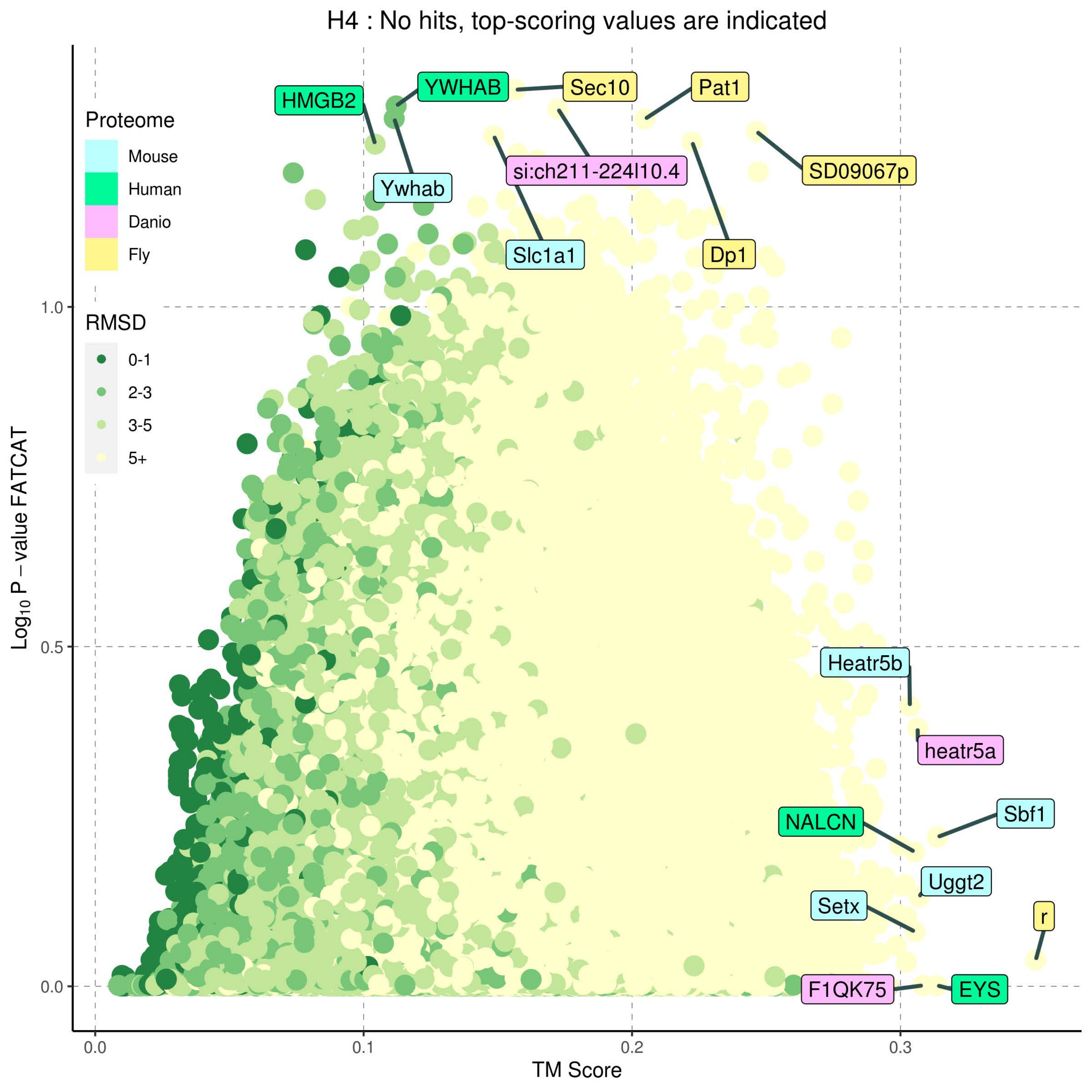

GorfA : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
TM Score
0
1
2
3
4
5
0.1
0.2
0.3
0.4
0.5
A0A2R8Q6C8
A0A2R8QFU3
A0A2R8RJ57
A0A0R4IEQ6
Gm15517
LINC00301
A0A2R8QRK2
H0WEW6
clpb
Olfr424
Olfr427
SLC10A4
Slc10a4
Clpb
Q5RHE3
CLPB

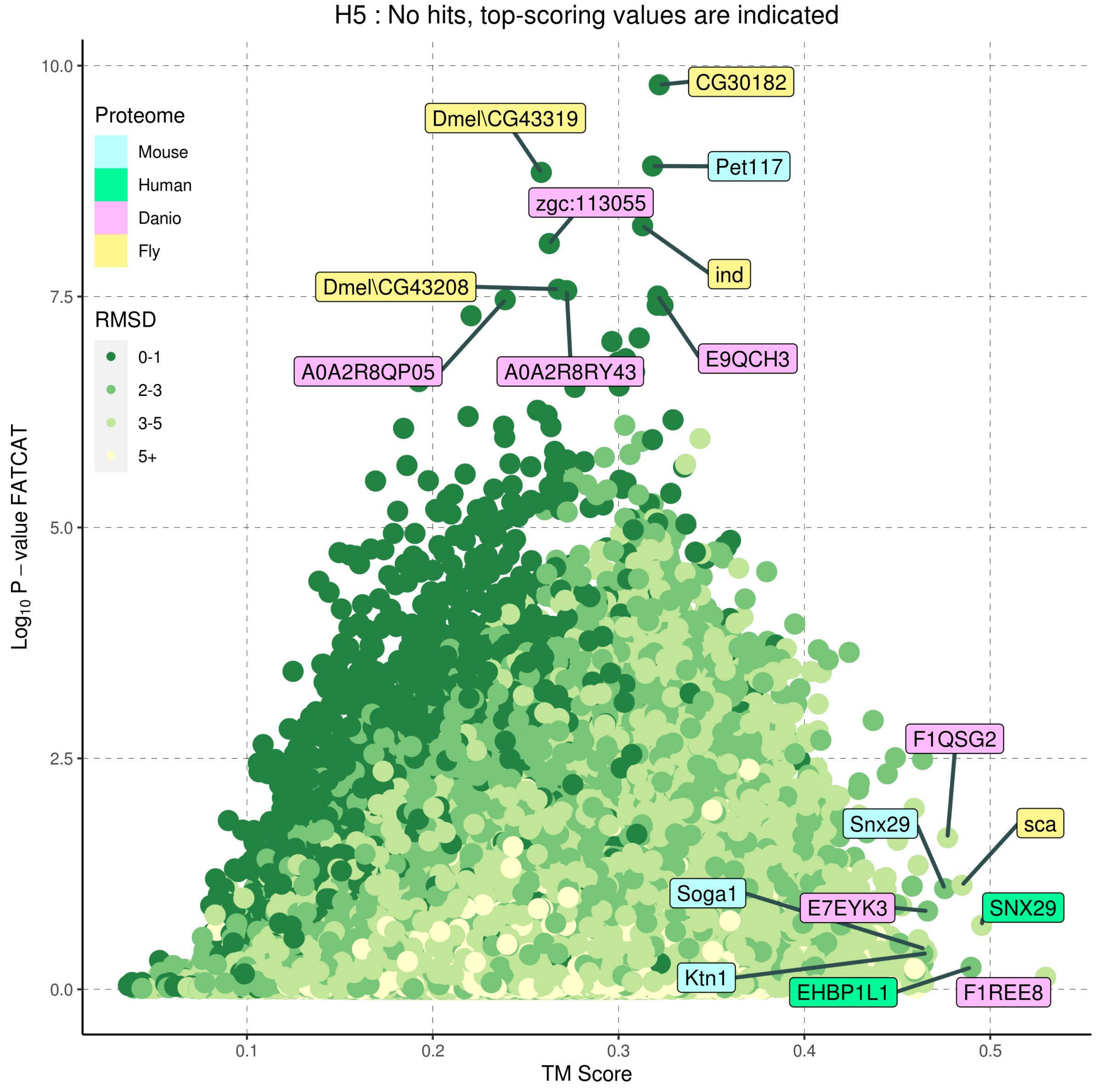

GorfB
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
0
4
8
12
TM Score
0.25
0.50
0.75
Dmel\CG17776
Dmel\CG44303
Dmel\CG15130
Dmel\CG14380
Dmel\CG16762
Snapin
Vamp5
DCTN3-p24
Dmel\CG13000
si:dkey-33c3.1
X1WFF5
U3JAN3
X1WBE9
CHOp24
Dmel\CG9570
Nrg4
Dmel\CG12112
KNSTRN
Dctn3
Dmel\CG44574
X1WBB2
si:ch211-284f22.3
si:dkey-248g15.2
X1WFQ3
X1WD28
Speer3
X1WCN0
Homer1
X1WHP2
X1WFA6
U3JAD7
Pex11a
NOSIP
X1WFU5
X1WBH5
TNFSF13B
X1WE70
Spint2
X1WD87
X1WCD1
Dmel\CG32459
Dmel\CG4194
CG15891
TMA7
U3JAK8
X1WEE0
Dmel\CG14631
X1WC16
X1WFU4
U3JAU9
Alsin2
Icos
Osi6
Klrc2
MCUB
X1WE48
X1WH96
TRIM17
si:ch211-282b22.1
si:ch73-264p11.4
Mycs
B4galt2
X1WGV1
Dmel\CG6664
X1WGY1
CSN6
CACNG2
ftr42
X1WHC5
X1WDI8
X1WCG6
TSC22D4
Bscl2
RhoGAP16F
Dmel\CG4198
Dmel\CG8578
GJA3
Crlf3
Stxbp4
SYNC
RIC-3
X1WCL6
X1WEV9
X1WBR1
R4GDR5

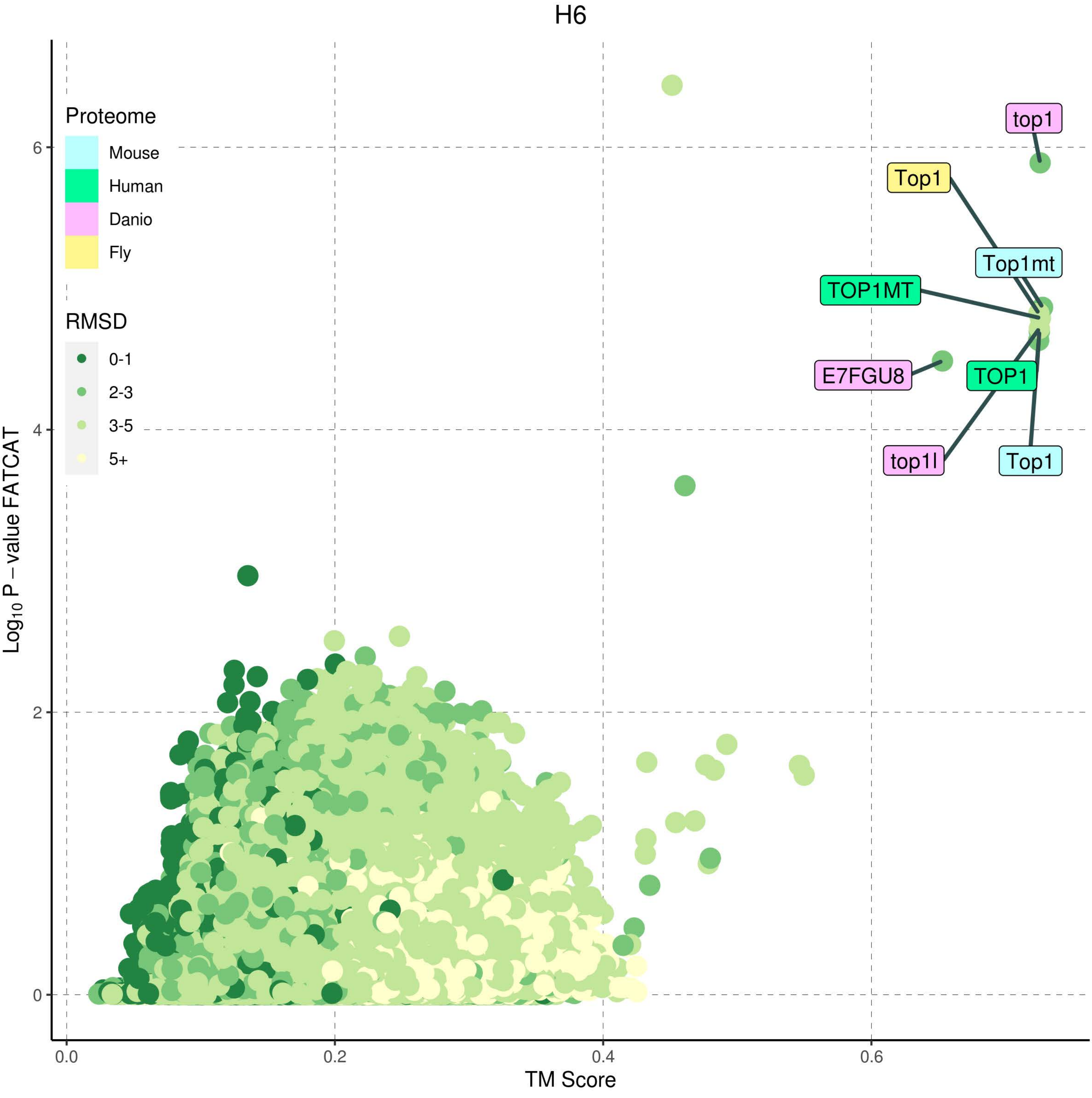

H1
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P − value FATCAT
TM Score
0
5
10
0.2
0.4
0.6
0.8
F1QE17
Dusp28
DUSP22
E47
dusp22b
Dusp21
dusp22a
DUSP19
DUSP18
dusp3
Dusp14
Dusp19
DUSP21
Dusp3
wu:fj40g04
DUSP15
dusp29
DUSP3
Dmel\CG15528
DUSP29
F1QCJ9
si:ch73-305o9.2
PTP4A1
STYX
dusp19
Dusp13
DUSP12
Ptp4a2
zgc:101724
Styx
DUSP9
DUSP26
Cdkn3
Ptpmt1
PTP4A2
MKP-like
Dusp4
Dusp29
DUSP4
X1WCB8
PTP4A3
CDKN3
Dusp26
Dusp12
Dusp2
Ptp4a3
B8A6D9
DUSP2
Dusp7
wu:fc03b
PTPMT1
ptp4a3
Mkp
mkp3
Mkp3
DUSP8
Dusp6
Dmel\CG5044
DUSP6
Dusp1
DUSP1
rngtt
puc
Epm2a
STYXL1
OR2A25
A0A2R8QF
DUSP5
SSH3
MKP-4
DUSP7
E7FC59
PTEN
Dusp5
E7FBM8
OR2A25
Styxl1
A0A2R8QL
Pten
DUSP10
mRNA-cap
PTPN7
X1WCM2
X1WHN2
Dusp10
A0A2R8QM14
mtm
pten
ssh1b
Ssh3
Ptpn20
A0A0R4IDR8
Q1L9G1
Dusp8
F1Q8I4
Mtmr6
ptpn2
PTPN18
Rngtt
Dusp16
F8W5H1
F9QCC5
A0A2R8QR8
ptpdc1
Ptpn18
F8W2B2
Mtmr2
zgc:113186
MTMR6
PTPN2
Ptpn7
robl
Ptpn1
TPTE2
MTMR1
Mtmr1
OR2A25
Ptpdc1
F1RCZ5
PTPN1
tns1a
Mtmr9
Mtmr6
Ptpn5
Cdc14b
PTPN9
si:ch211-39i19.4
si:dkey-155d18.2
PTPN5
SSH1
MTMR9
Ptpn9
Cdc14a
Mtm1
Ptpn6
SKI3
Tpte
E7F716
PTPN11
Mtmr7
PTPN22
CDC14A
MTMR7
Ptp36E
STYXL2
Dmel\CG14411
1QTP6
mtmr8
Ssh1
Ptpmeg2
cdc14al
PTPN6
Dmel\CG5026
Ptpn22
Ptprr

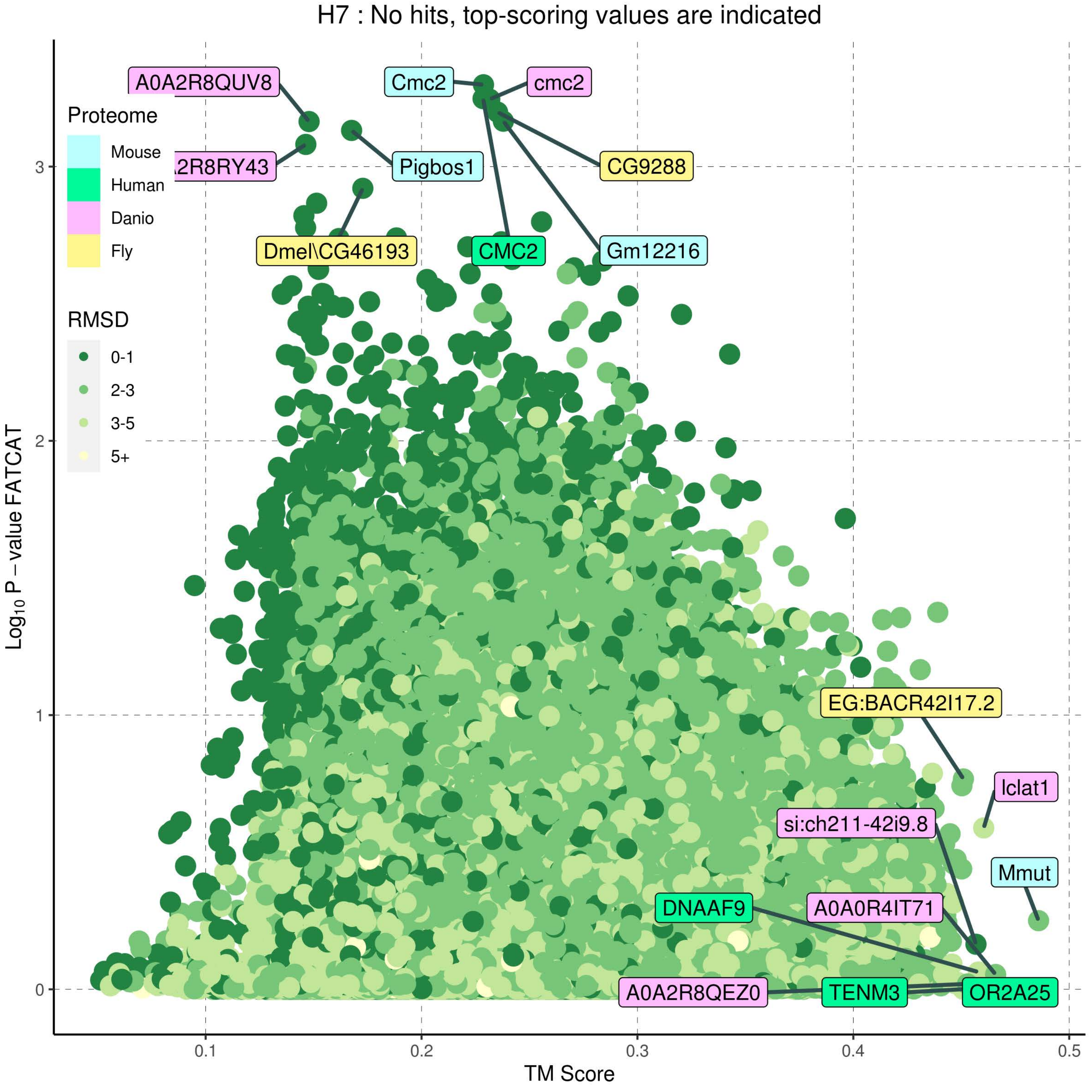

H2 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log$_{10}$ P – value FATCAT
TM Score
0
1
2
3
4
5
0.1
0.2
0.3
0.4
Sfp96
Gm10563
CG34136-RA
BLACAT1
si:ch211-262k23.5
HSPC300
Dmel\CG45099
Dmel\CG43208
Sfp79B
OR5T3
Fibcd1
ficd
Dmel\CG8569
U3-55K
Pde4c
Lgr1
si:dkeyp-22b2.2
Stard13

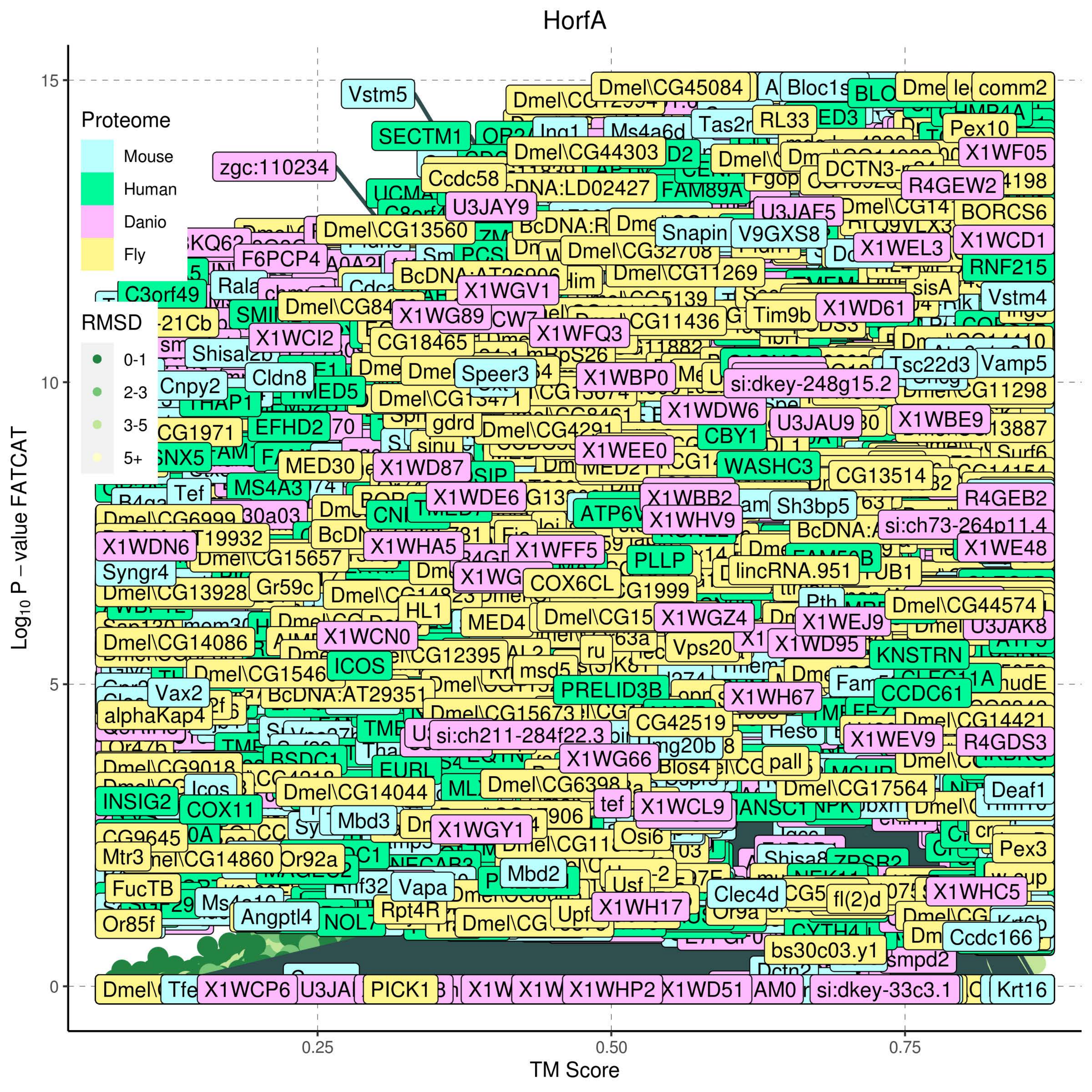

H3 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
E7FDN9
MGAT2
Mgat2
A0A2R8QFU3
Mgat4d
mgat4c
A0A2R8PV94
MGAT4C
zgc:162268
si:ch211-13f8.2
glt25d2
COLGALT2
Colgalt2
Colgalt1
colgalt1
E7F0F2
colgalt1
COLGALT1
Log₁₀ P – value FATCAT
3
2
1
0
0.0
0.2
0.4
TM Score

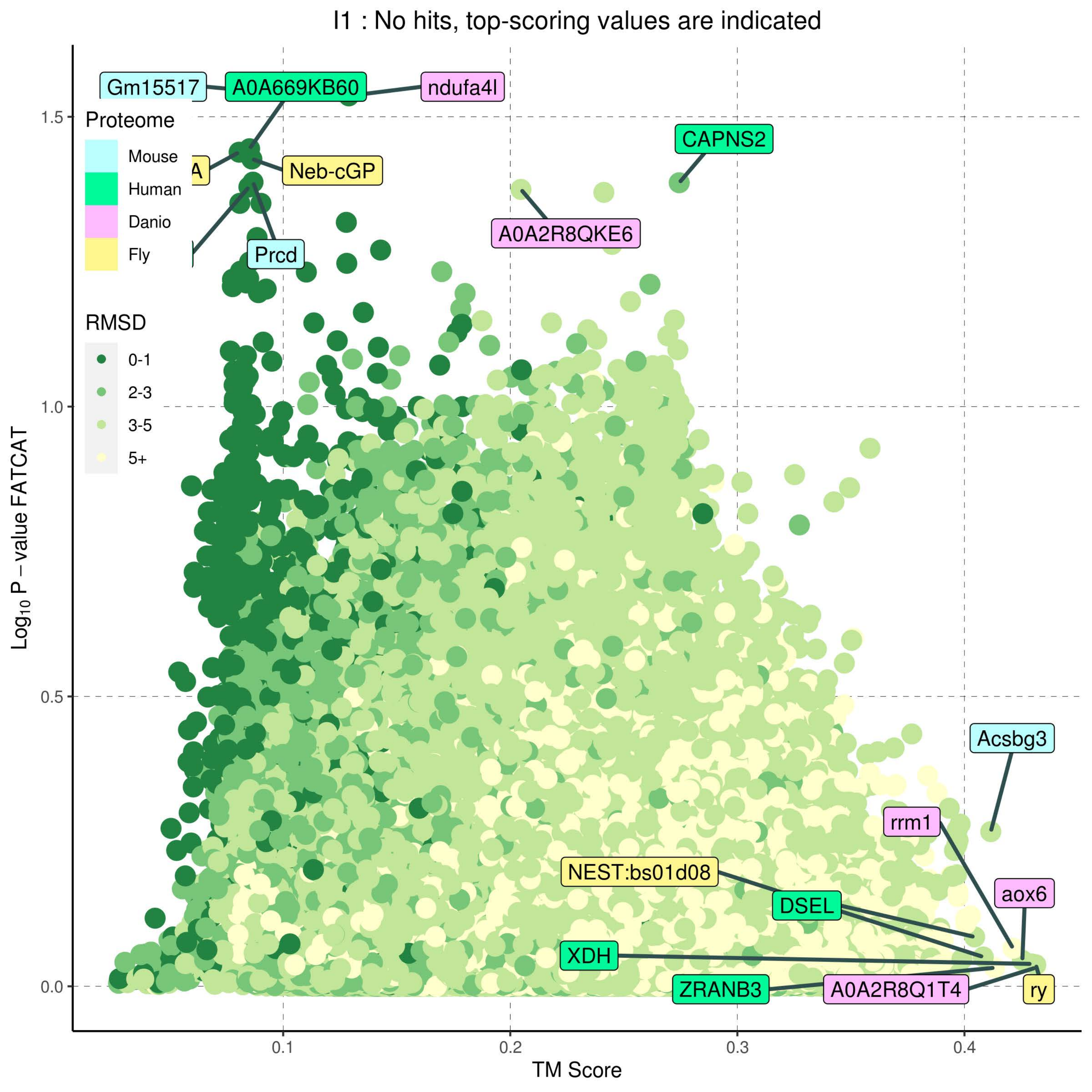

H4 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
HMGB2
YWHAB
Sec10
Pat1
Ywhab
si:ch211-224l10.4
SD09067p
Slc1a1
Dp1
Heatr5b
heatr5a
NALCN
Sbf1
Uggt2
Setx
r
F1QK75
EYS
Log10 P − value FATCAT
1.0
0.5
0.0
0.0
0.1
0.2
0.3
TM Score

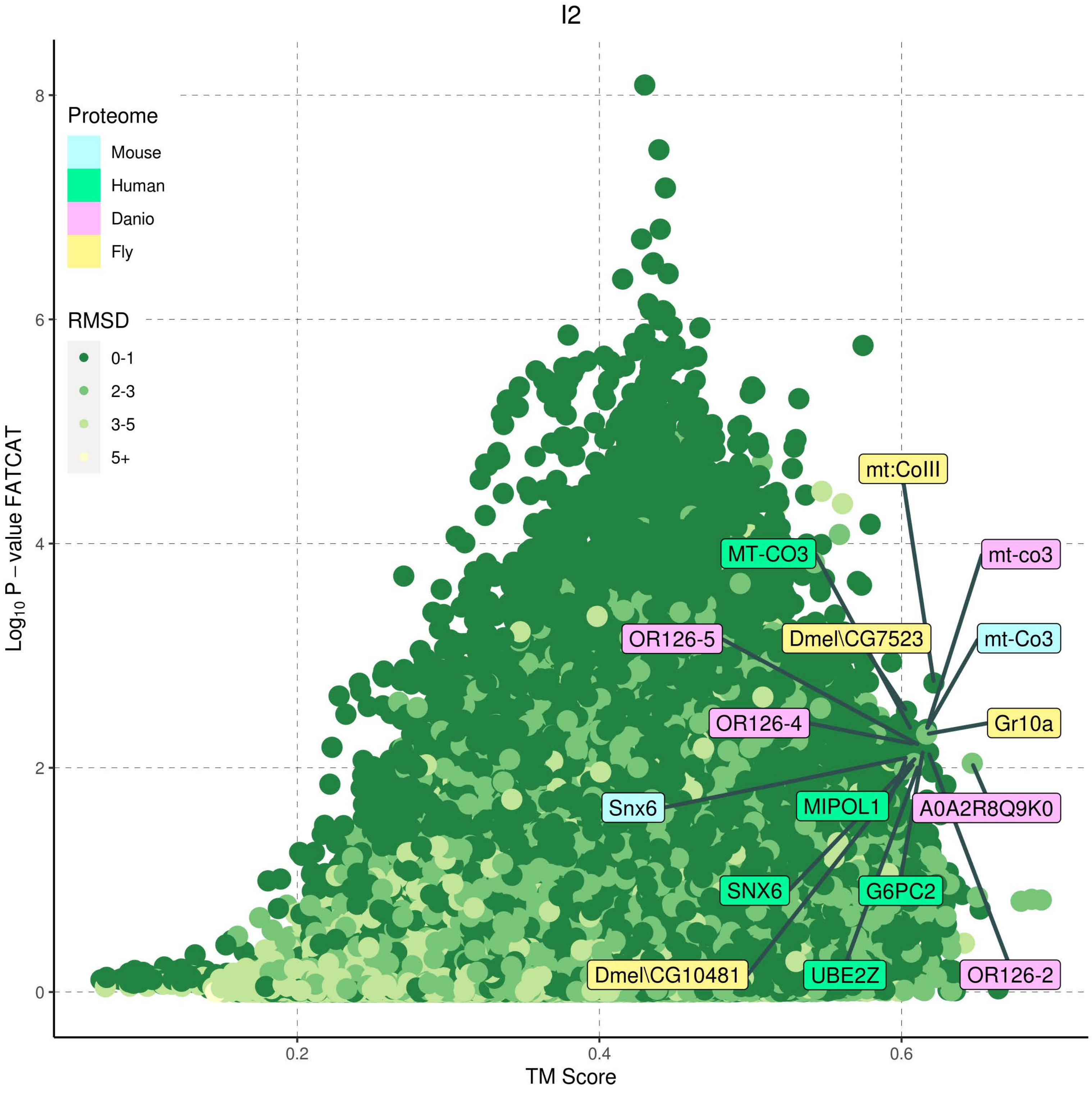

H5 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
CG30182
Dmel\CG43319
Pet117
zgc:113055
ind
Dmel\CG43208
E9QCH3
A0A2R8QP05
A0A2R8RY43
F1QSG2
Snx29
sca
Soga1
E7EYK3
SNX29
Ktn1
EHBP1L1
F1REE8
10.0
7.5
5.0
2.5
0.0
0.1
0.2
0.3
0.4
0.5
TM Score
Log10 P – value FATCAT


H6
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
top1
Top1
Top1mt
TOP1MT
E7FGU8
TOP1
top1l
Top1
Log10 P – value FATCAT
TM Score
0
2
4
6
0.0
0.2
0.4
0.6

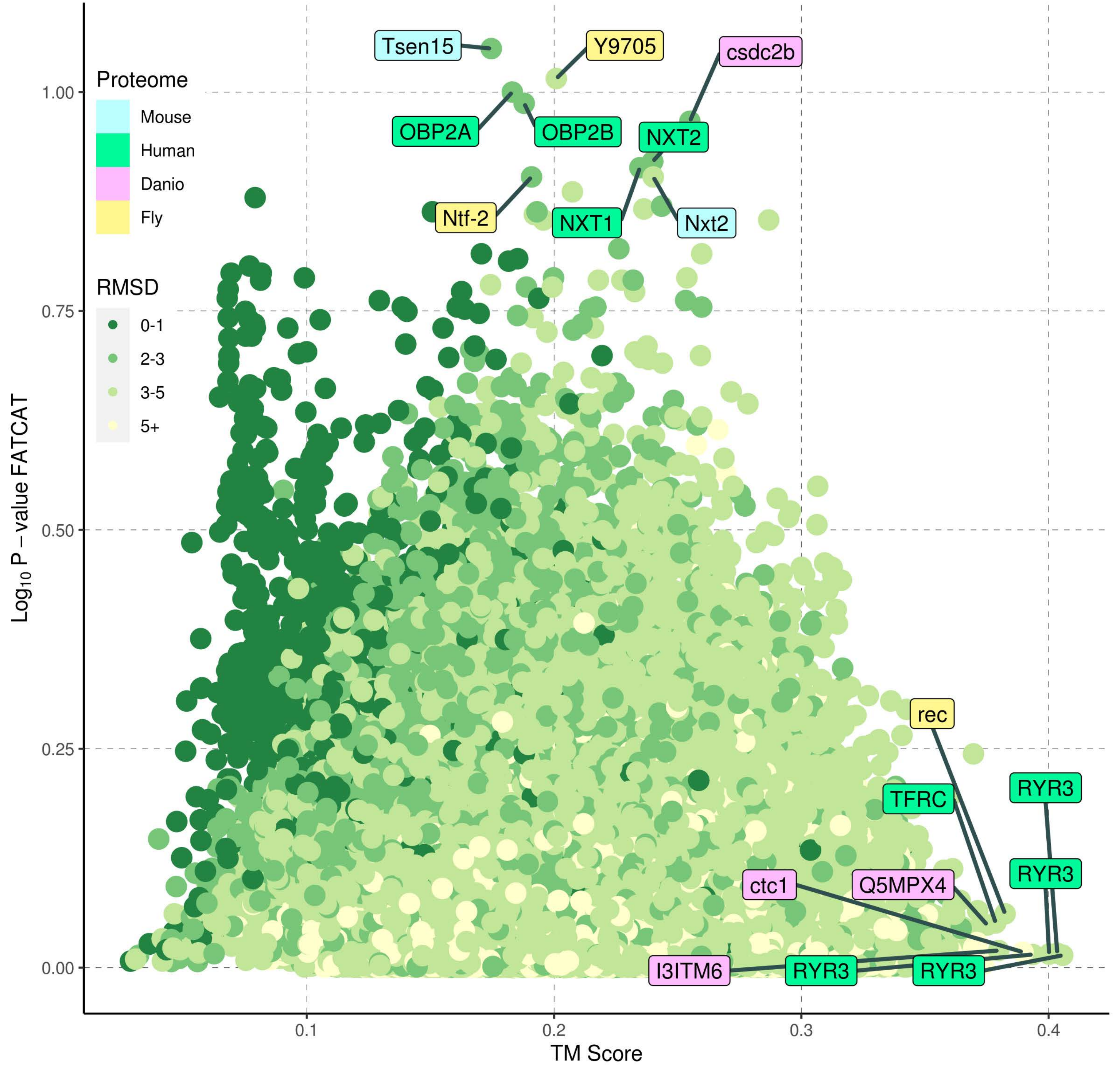

H7 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
A0A2R8QUV8
Cmc2
cmc2
2R8RY43
Pigbos1
CG9288
Dmel\CG46193
CMC2
Gm12216
EG:BACR42I17.2
lclat1
si:ch211-42i9.8
Mmut
DNAAF9
A0A0R4IT71
A0A2R8QEZ0
TENM3
OR2A25
Log10 P − value FATCAT
3
2
1
0
TM Score
0.1
0.2
0.3
0.4
0.5

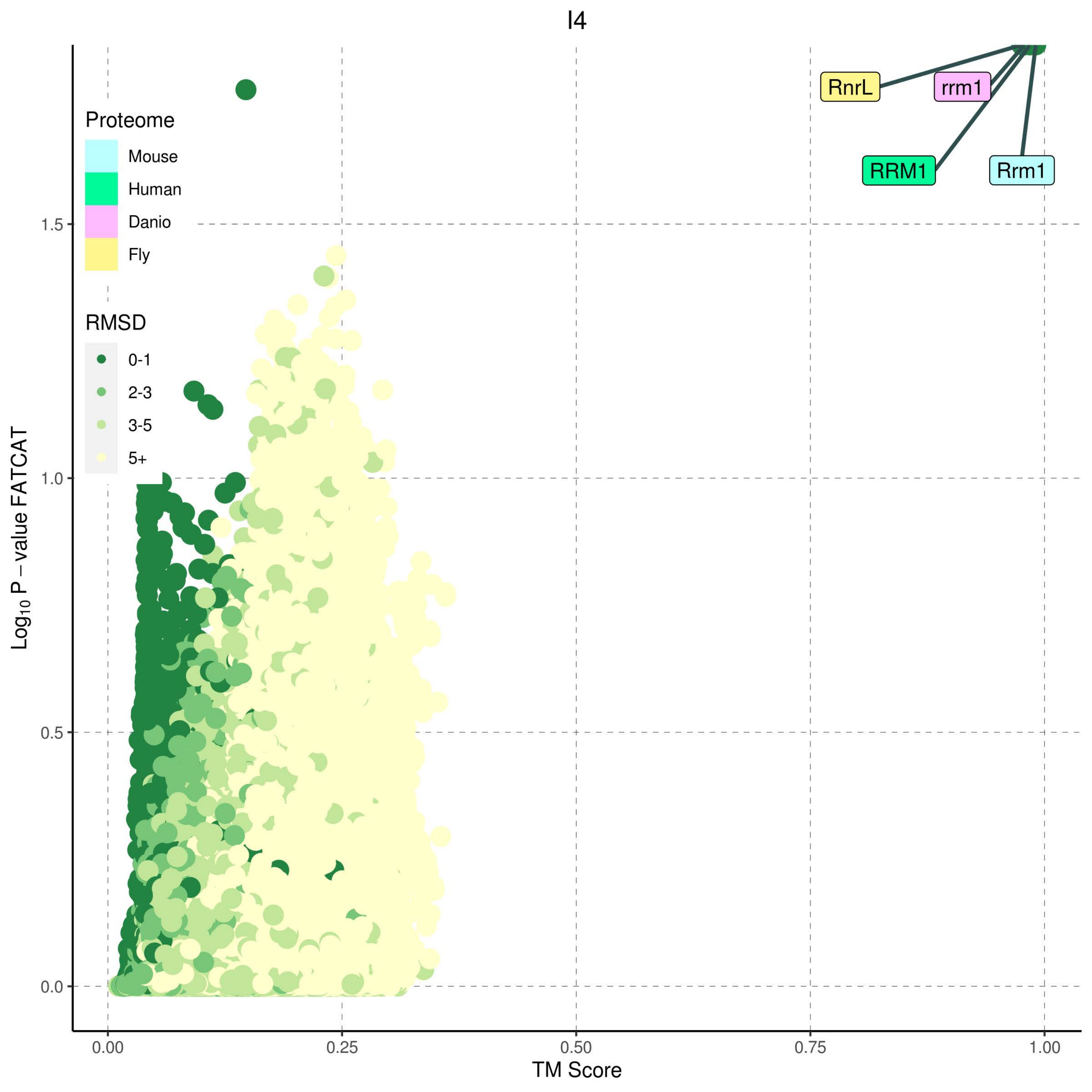

HorfA
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log$_{10}$ P − value FATCAT
TM Score
0
5
10
15
0.25
0.50
0.75
Vstm5
SECTM1
zgc:110234
Dmel\CG45084
Bloc1s
comm2
Tas2r
RL33
Ms4a6d
Ing1
Pex10
Dmel\CG44303
X1WF05
Ccdc58
cDNA:LD02427
FAM89A
DCTN3
R4GEW2
U3JAY9
U3JAF5
BORCS6
Dmel\CG13560
F6PCP4
Snapin
V9GXS8
X1WEL3
X1WCD1
Dmel\CG32708
Dmel\CG11269
RNF215
C3orf49
X1WGV1
sisA
Vstm4
X1WG89
Dmel\CG11436
Tim9b
X1WD61
X1WCI2
X1WFQ3
CG18465
Shisal2b
Cldn8
Cnpy2
Speer3
X1WBP0
Tsc22d3
Vamp5
si:dkey-248g15.2
Dmel\CG11298
THAP1
TMED5
Dmel\CG13471
X1WDW6
U3JAU9
X1WBE9
CG1971
EFHD2
gdrd
Dmel\CG4291
CBY1
SNX5
X1WEE0
WASHC3
MED30
X1WD87
CG13514
MS4A3
Tef
X1WDE6
X1WBB2
Sh3bp5
R4GEB2
Dmel\CG6999
X1WHV9
si:ch73-264p11.4
X1WDN6
Dmel\CG15657
X1WHA5
X1WFF5
PLLP
X1WE48
Syngr4
lincRNA.951
Dmel\CG13928
Gr59c
COX6CL
Dmel\CG44574
HL1
MED4
X1WGZ4
X1WEJ9
U3JAK8
Dmel\CG14086
X1WCN0
Dmel\CG12395
Vps20
X1WD95
KNSTRN
ICOS
msd5
Vax2
BcDNA:AT29351
PRELID3B
X1WH67
CCDC61
alphaKap4
Dmel\CG15673
si:ch211-284f22.3
CG42519
Dmel\CG14421
X1WEV9
R4GDS3
X1WG66
pall
Dmel\CG9018
Dmel\CG14044
Dmel\CG6398
Dmel\CG17564
Deaf1
INSIG2
COX11
tef
X1WCL9
Mbd3
X1WGY1
Osi6
CG9645
Mtr3
Dmel\CG14860
Or92a
Pex3
Mbd2
Usf
X1WHC5
FucTB
Vapa
Clec4d
fl(2)d
Angptl4
NOL7
Rpt4R
X1WH17
Or85f
Ccdc166
bs30c03.y1
smpd2
Tfe
X1WCP6
PICK1
X1WHP2
X1WD51
si:dkey-33c3.1
Krt16

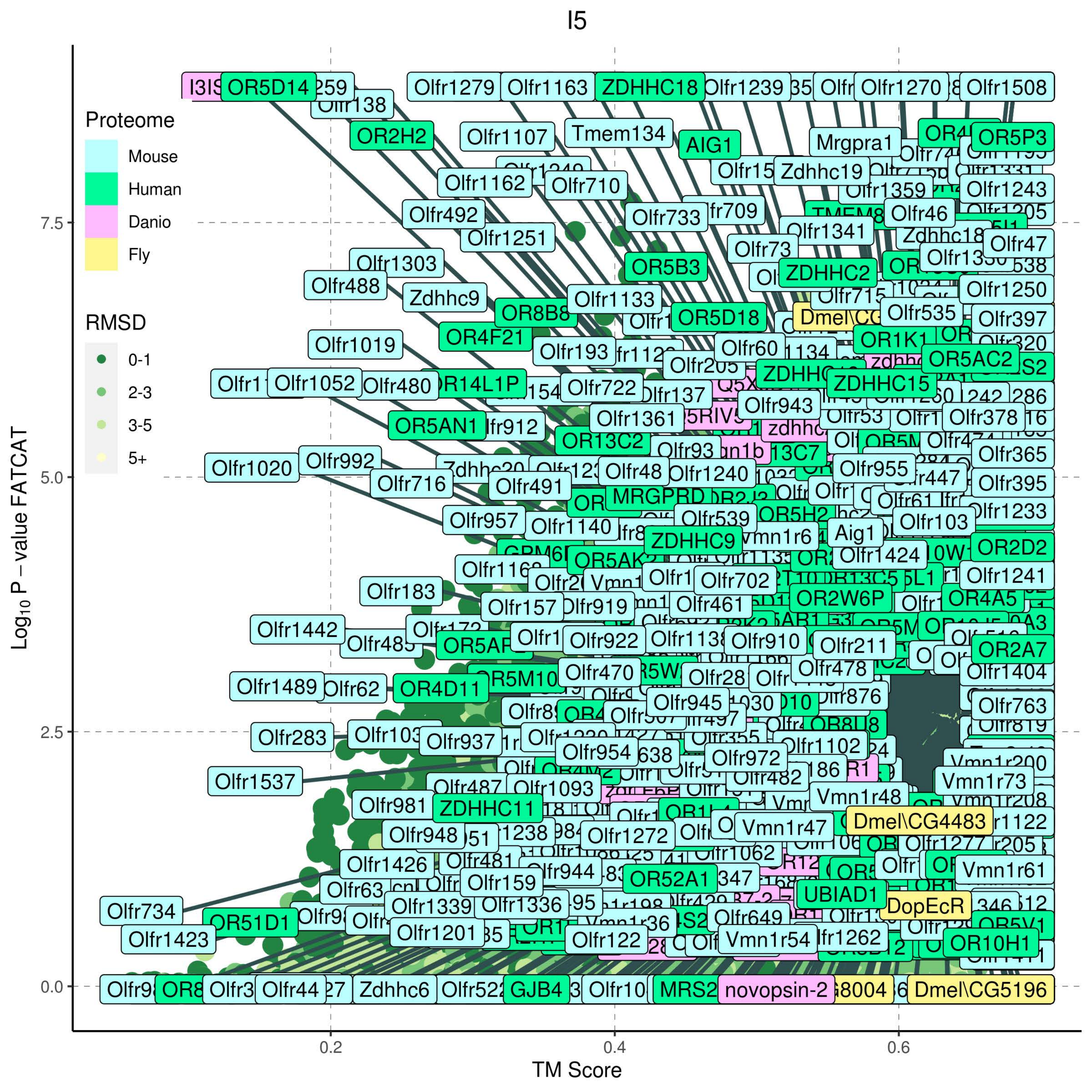

I1 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Gm15517
A0A669KB60
ndufa4l
CAPNS2
Neb-cGP
A0A2R8QKE6
Prcd
Acsbg3
rrm1
NEST:bs01d08
DSEL
aox6
XDH
ZRANB3
A0A2R8Q1T4
ry
Log$_{10}$ P − value FATCAT
TM Score
0.0
0.5
1.0
1.5
0.1
0.2
0.3
0.4

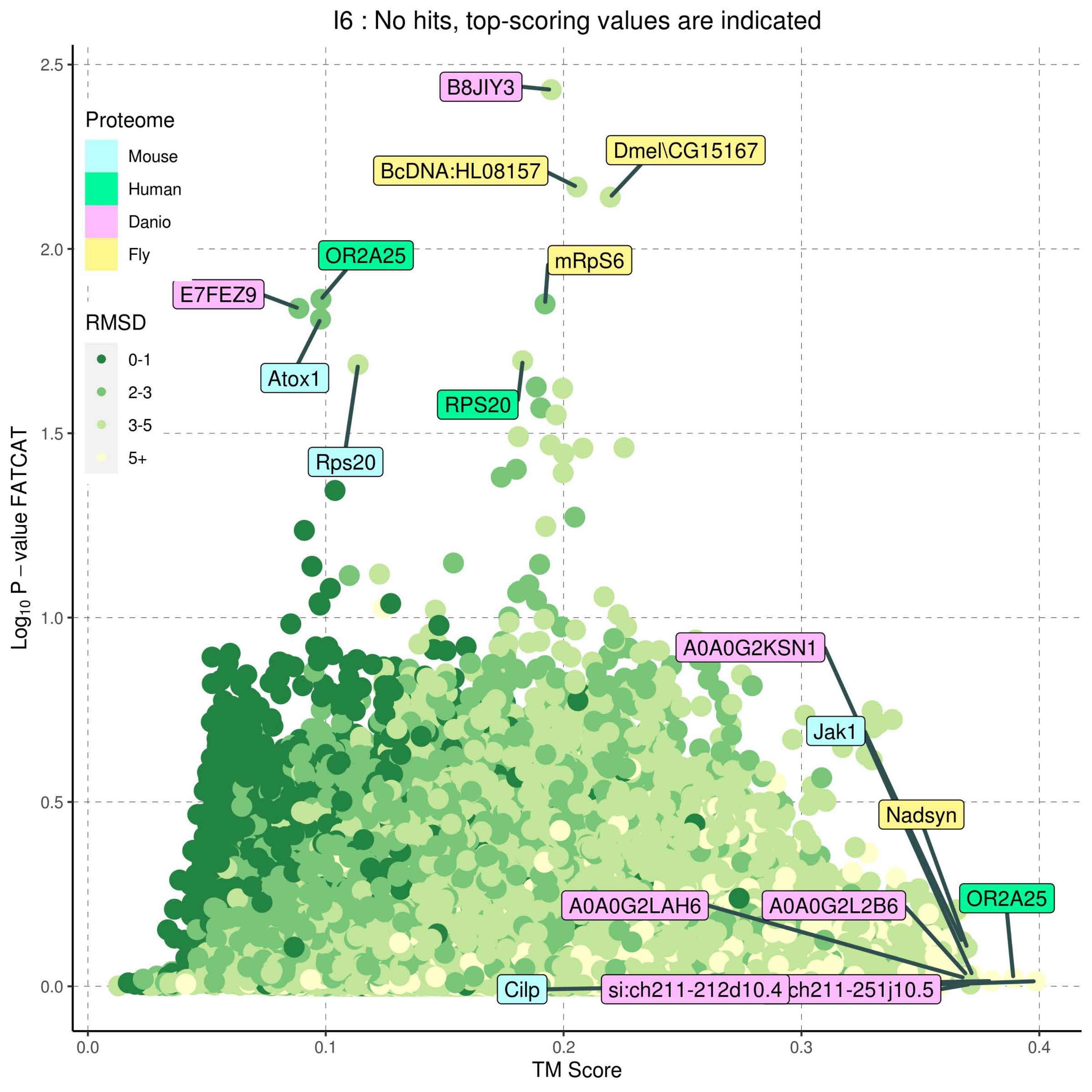

I2
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
8
6
4
2
0
TM Score
0.2
0.4
0.6
mt:CoIII
MT-CO3
mt-co3
OR126-5
Dmel\CG7523
mt-Co3
OR126-4
Gr10a
Snx6
MIPOL1
A0A2R8Q9K0
SNX6
G6PC2
Dmel\CG10481
UBE2Z
OR126-2

I3 : No hits, top-scoring values are indicated

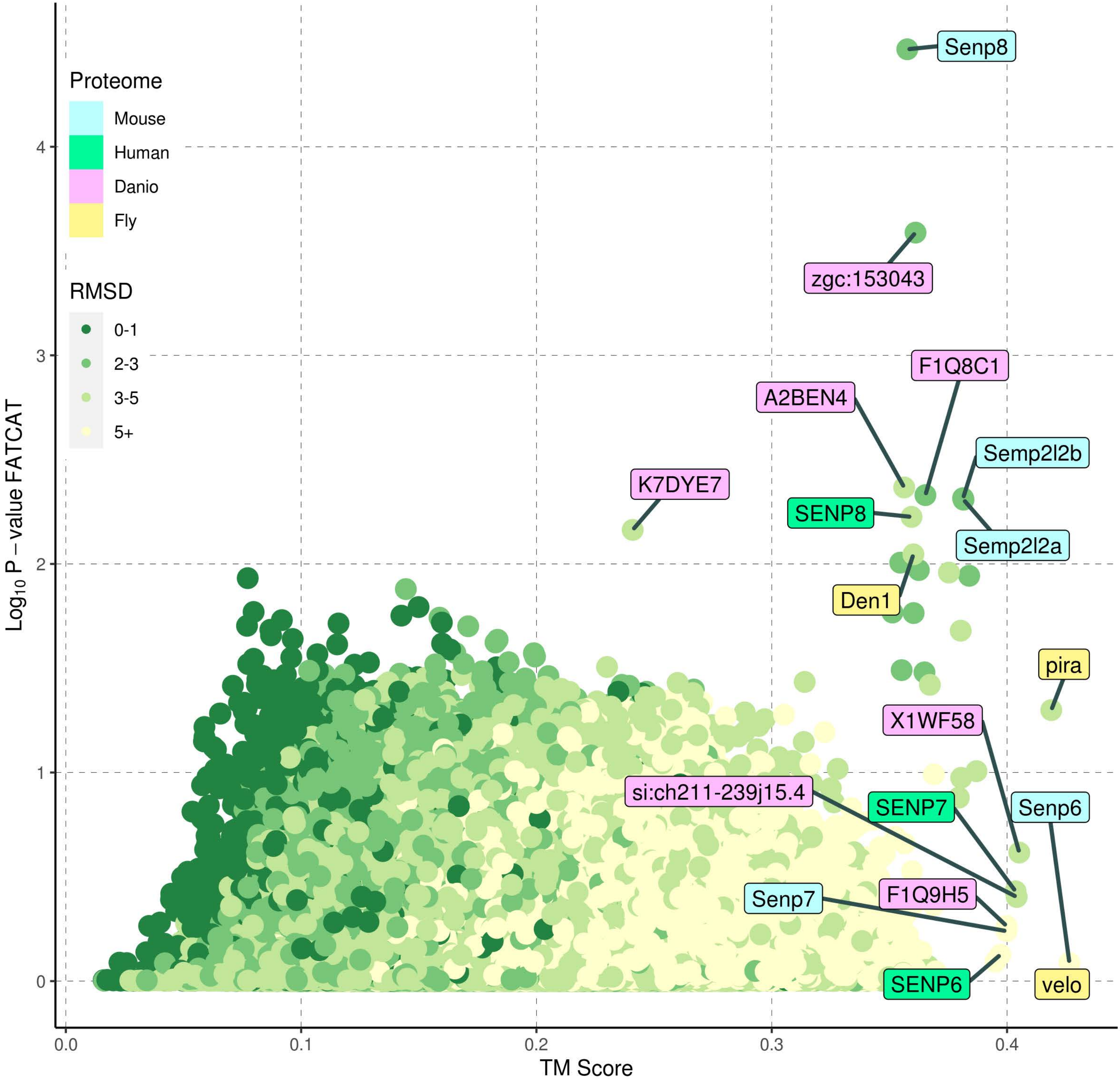


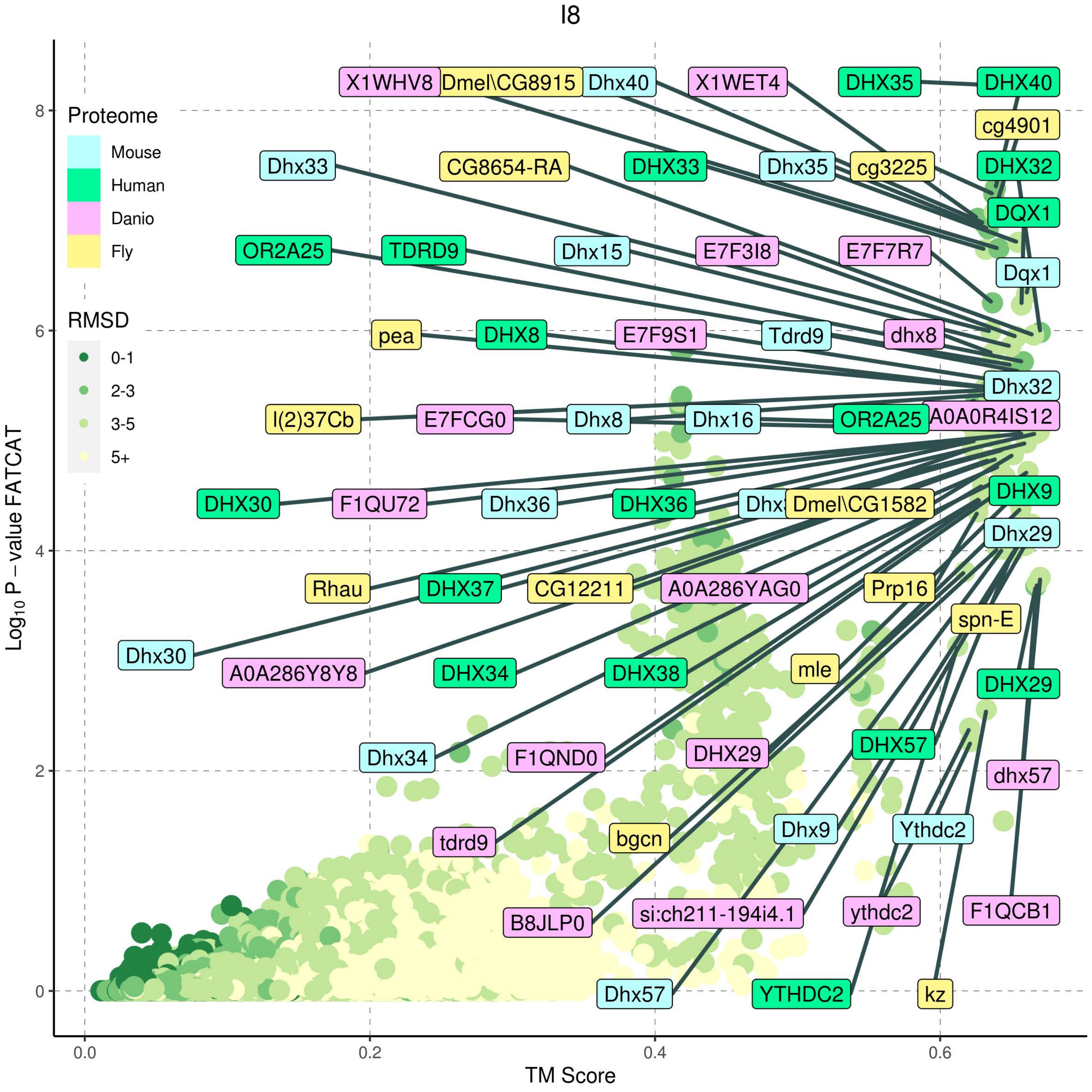

I4
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
RnrL
rrm1
RRM1
Rrm1
Log₁₀ P – value FATCAT
TM Score
0.0
0.5
1.0
1.5
0.00
0.25
0.50
0.75
1.00

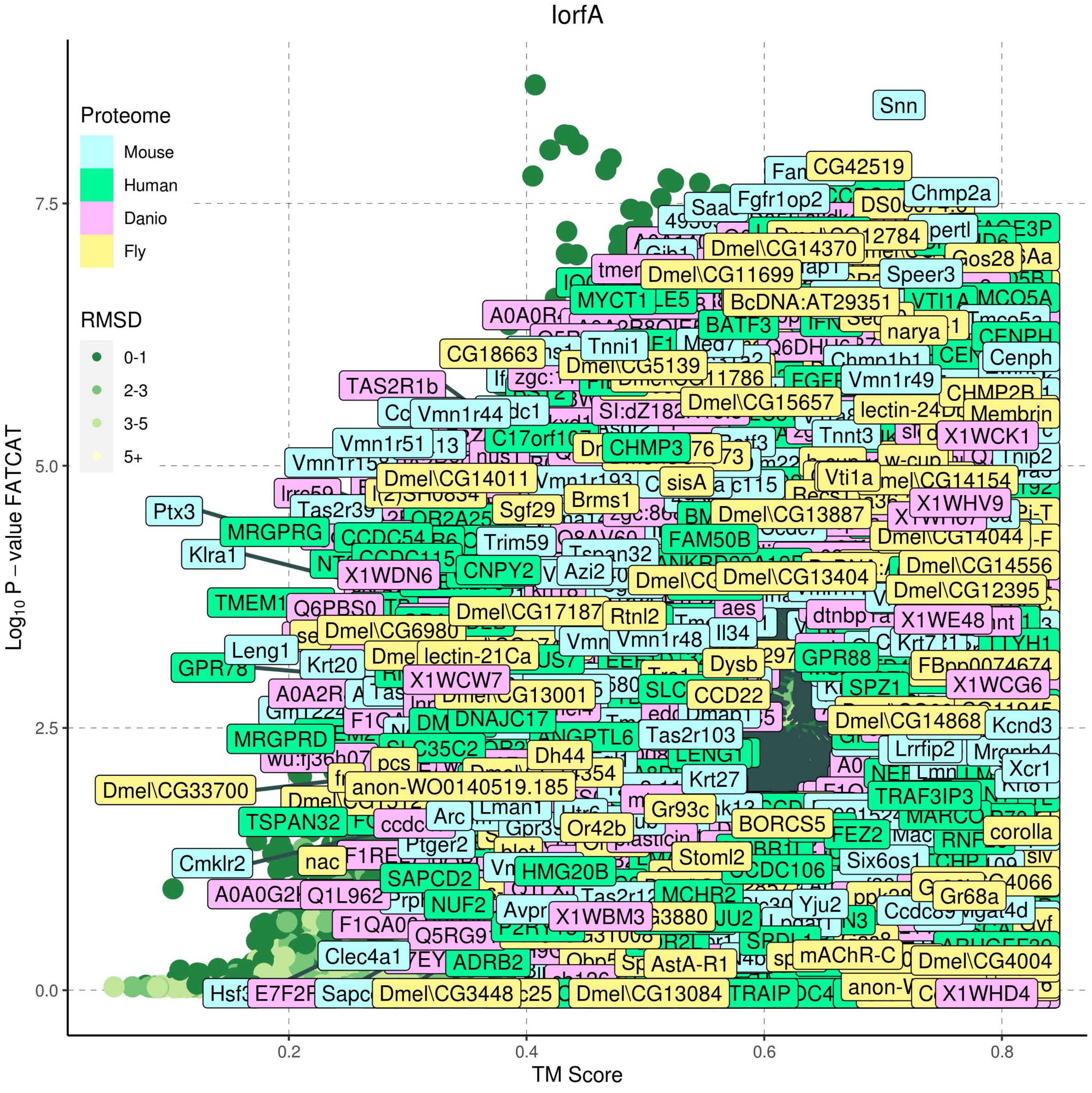

I5
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log₁₀ P − value FATCAT
TM Score
7.5
5.0
2.5
0.0
0.2
0.4
0.6
OR5D14
Olfr138
Olfr1279
Olfr1163
ZDHHC18
Olfr1239
Olfr1270
Olfr1508
OR2H2
Olfr1107
Tmem134
AIG1
Mrgpra1
OR5P3
Zdhhc19
Olfr1162
Olfr710
Olfr1359
Olfr1243
Olfr492
Olfr733
Olfr46
Olfr1251
Olfr1341
Olfr47
Olfr1303
OR5B3
Olfr73
ZDHHC2
Olfr488
Zdhhc9
Olfr1133
OR8B8
OR5D18
Olfr1250
Olfr535
Olfr397
OR4F21
Olfr1019
Olfr193
Olfr60
OR1K1
OR5AC2
Olfr205
ZDHHC15
Olfr1052
Olfr480
OR14L1P
Olfr722
Olfr137
Olfr943
Olfr378
OR5AN1
Olfr1361
OR13C2
Olfr53
Olfr365
Olfr1020
Olfr992
Olfr93
Olfr48
Olfr1240
Olfr955
Olfr447
Olfr716
Olfr491
Olfr395
MRGPRD
Olfr539
OR5H2
Olfr103
Olfr1233
Olfr957
Olfr1140
ZDHHC9
Aig1
OR2D2
Olfr1424
OR5AK2
Olfr183
Olfr702
Olfr1241
Olfr157
Olfr919
Olfr461
OR2W6P
OR4A5
Olfr1442
Olfr485
OR5AP2
Olfr922
Olfr910
Olfr211
OR2A7
Olfr470
Olfr478
Olfr1404
Olfr1489
Olfr62
OR4D11
OR5M10
Olfr945
Olfr876
Olfr763
Olfr283
Olfr937
Olfr954
Olfr972
Olfr1102
Olfr819
Olfr1537
Olfr482
Vmn1r200
Vmn1r73
Olfr487
Olfr1093
Olfr981
ZDHHC11
Vmn1r48
Dmel\CG4483
Olfr948
Olfr1272
Vmn1r47
Olfr1062
Olfr1277
Olfr1426
Olfr481
Olfr944
OR52A1
Vmn1r61
Olfr159
Olfr63
UBIAD1
Olfr1339
Olfr1336
DopEcR
Olfr734
OR51D1
Olfr649
Olfr1201
Vmn1r36
OR10H1
Olfr1423
Olfr122
Vmn1r54
Zdhhc6
GJB4
MRS2
novopsin-2
Dmel\CG5196
Olfr44

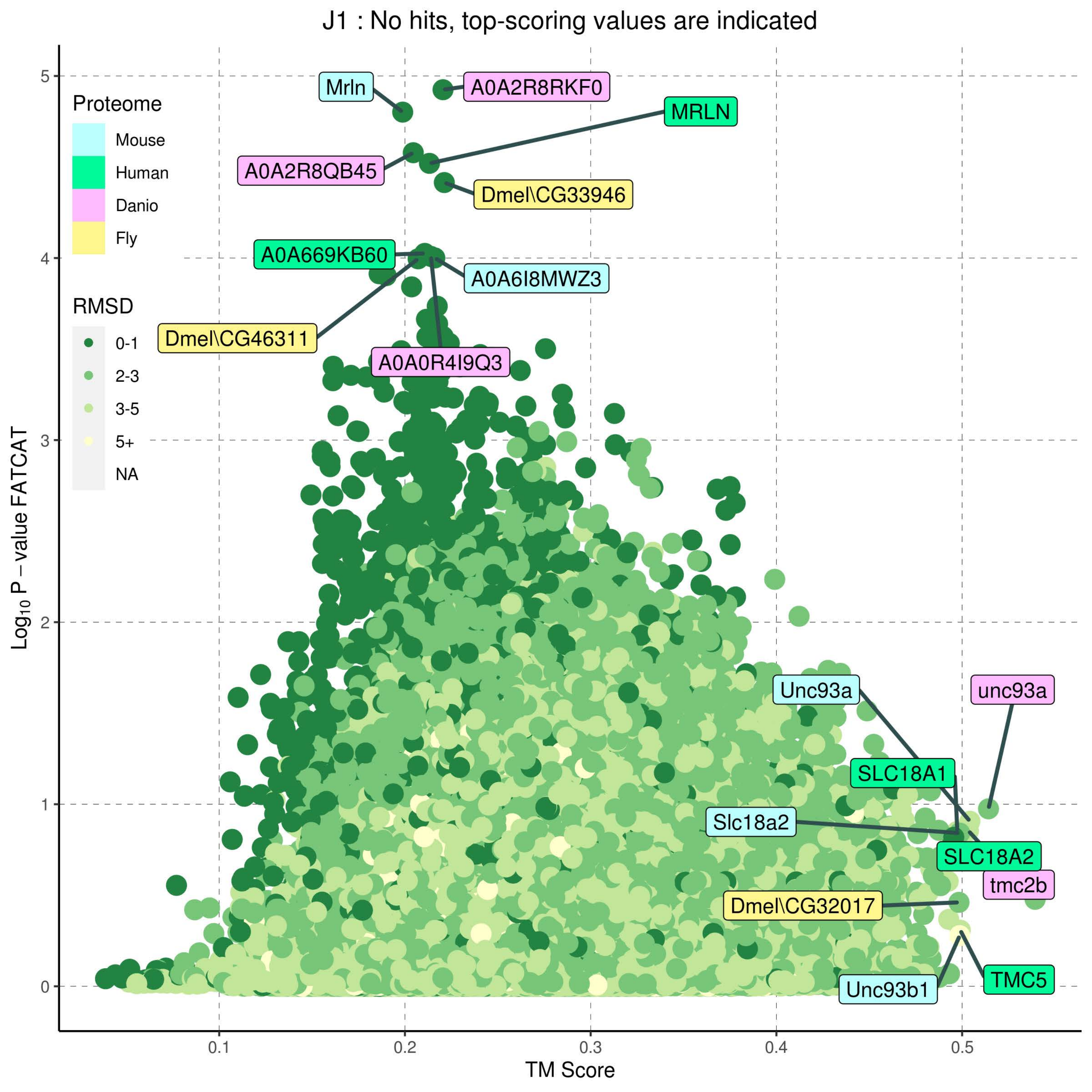

I6 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
B8JIY3
Dmel\CG15167
BcDNA:HL08157
OR2A25
mRpS6
E7FEZ9
Atox1
RPS20
Rps20
A0A0G2KSN1
Jak1
Nadsyn
OR2A25
A0A0G2LAH6
A0A0G2L2B6
Cilp
si:ch211-212d10.4
ch211-251j10.5
Log$_{10}$ P – value FATCAT
TM Score
0.0
0.5
1.0
1.5
2.0
2.5
0.0
0.1
0.2
0.3
0.4

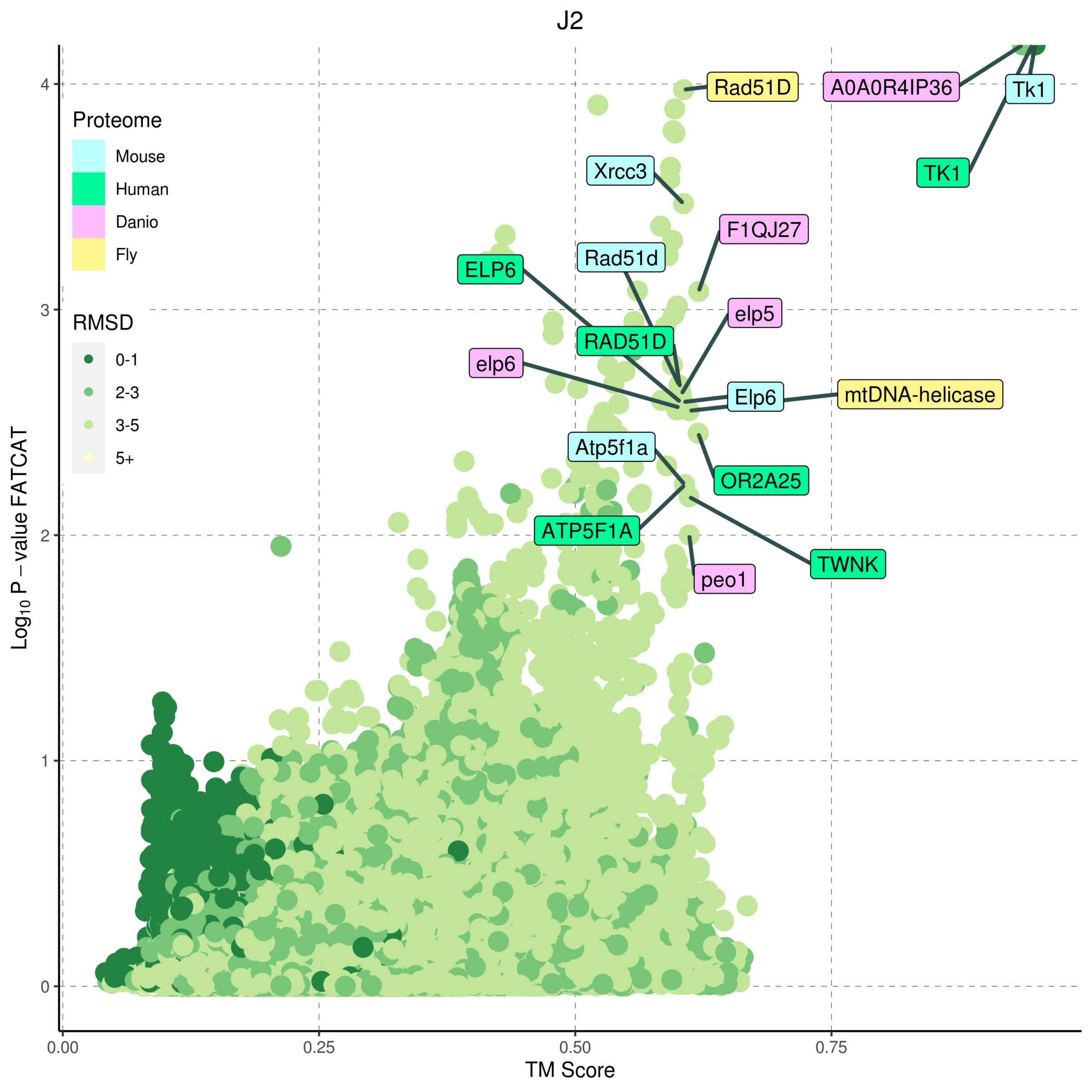
I7 : No hits, top-scoring values are indicated

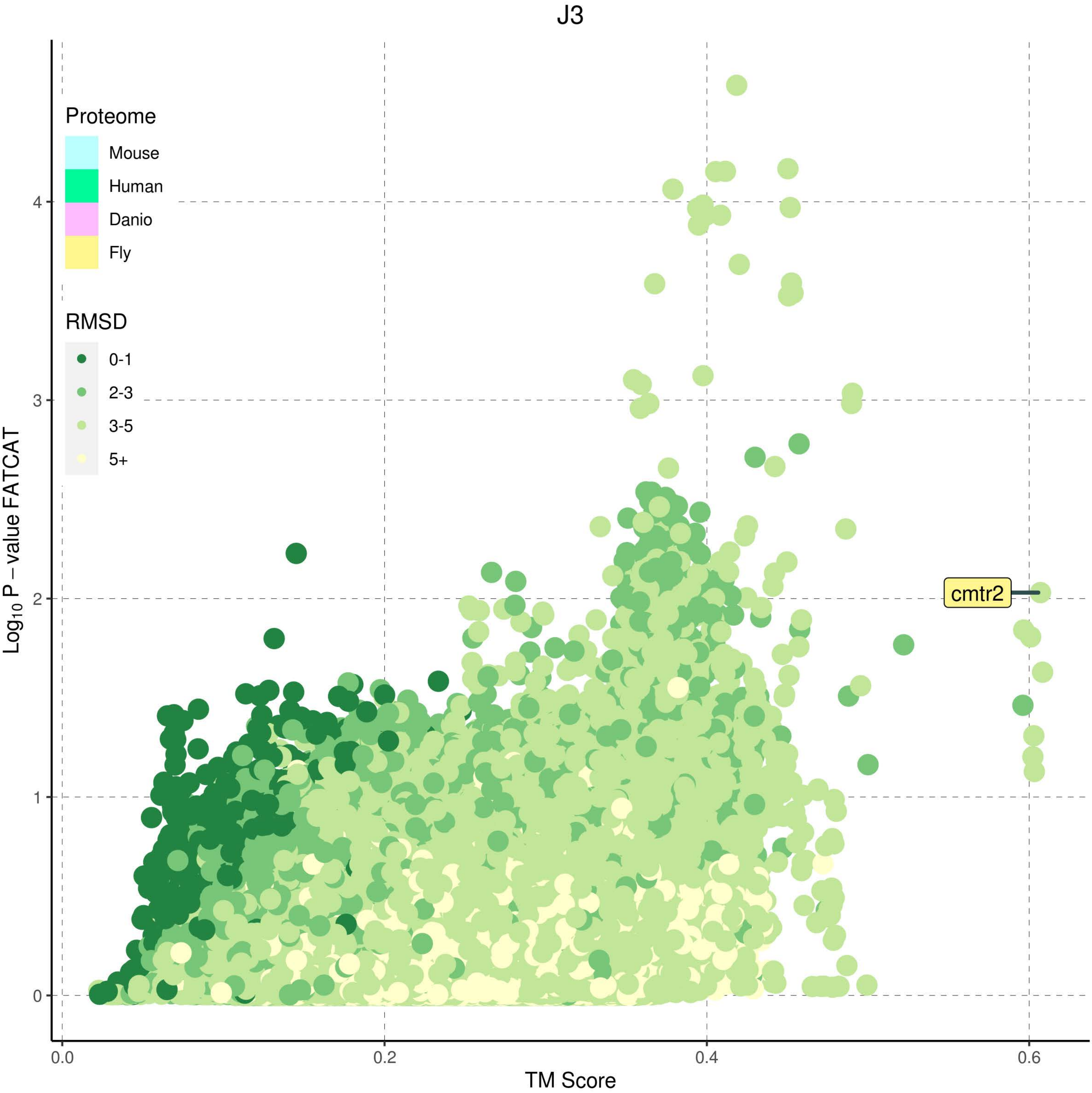



I8
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log₁₀ P − value FATCAT
TM Score
0.0
0.2
0.4
0.6
0
2
4
6
8
X1WHV8
Dmel\CG8915
Dhx40
X1WET4
DHX35
DHX40
cg4901
Dhx33
CG8654-RA
DHX33
Dhx35
cg3225
DHX32
DQX1
OR2A25
TDRD9
Dhx15
E7F3I8
E7F7R7
Dqx1
pea
DHX8
E7F9S1
Tdrd9
dhx8
Dhx32
l(2)37Cb
E7FCG0
Dhx8
Dhx16
OR2A25
A0A0R4IS12
DHX30
F1QU72
Dhx36
DHX36
Dhx
Dmel\CG1582
DHX9
Dhx29
Rhau
DHX37
CG12211
A0A286YAG0
Prp16
spn-E
Dhx30
A0A286Y8Y8
DHX34
DHX38
mle
DHX29
Dhx34
F1QND0
DHX29
DHX57
dhx57
tdrd9
bgcn
Dhx9
Ythdc2
B8JLP0
si:ch211-194i4.1
ythdc2
F1QCB1
Dhx57
YTHDC2
kz

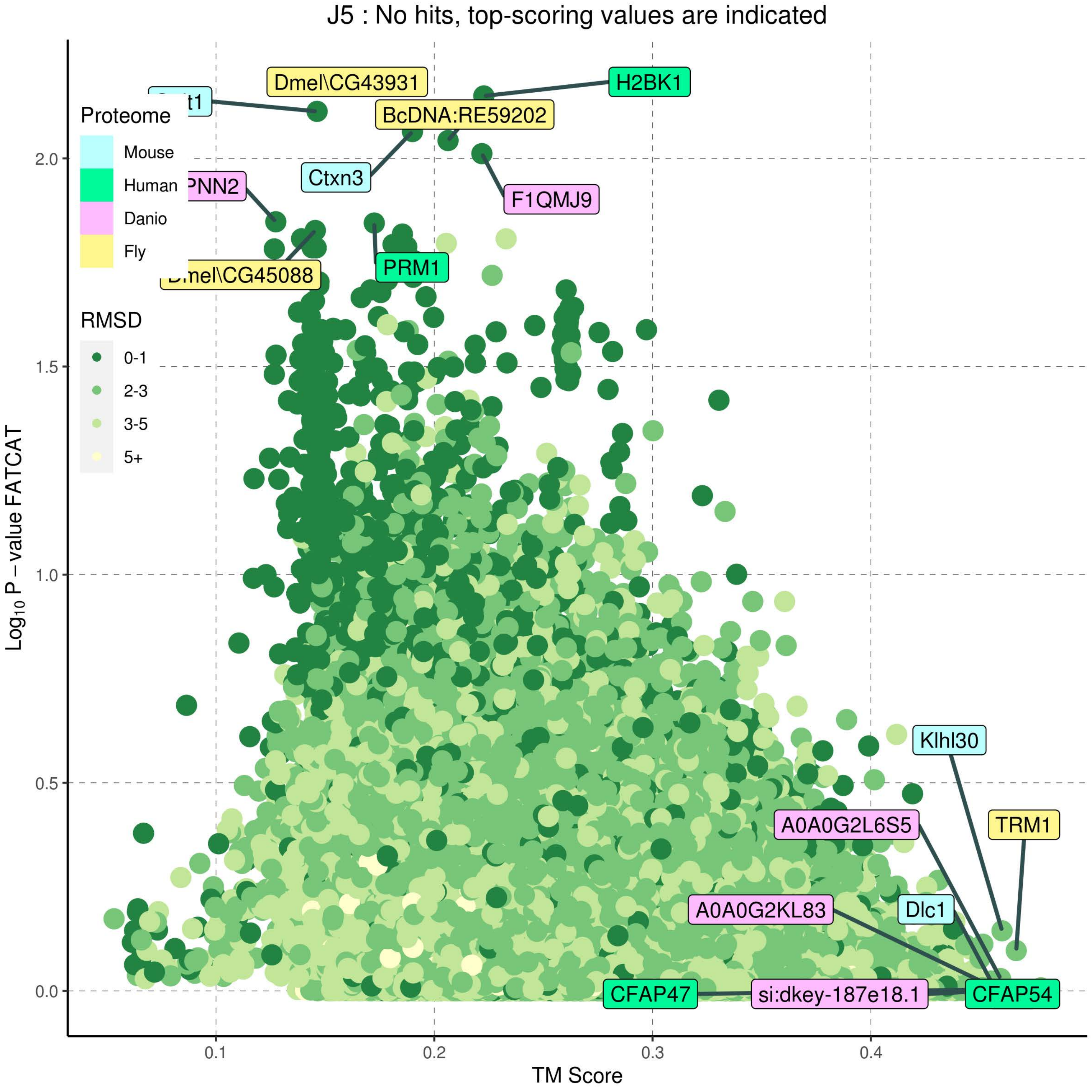

lorfA
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log$_{10}$ P − value FATCAT
TM Score
0.0
2.5
5.0
7.5
0.2
0.4
0.6
0.8
Snn
CG42519
Chmp2a
Fgfr1op2
Dmel\CG12784
Dmel\CG14370
Gos28
Dmel\CG11699
Speer3
MYCT1
BcDNA:AT29351
VTI1A
BATF3
narya
CENPH
Tnni1
Cenph
CG18663
Dmel\CG5139
Vmn1r49
TAS2R1b
CHMP2B
Dmel\CG15657
Vmn1r44
lectin-24Db
Membrin
C17orf107
Tnnt3
X1WCK1
Vmn1r51
CHMP3
Dmel\CG14011
sisA
Vti1a
Ptx3
Brms1
Sgf29
Dmel\CG13887
X1WHV9
MRGPRG
Trim59
FAM50B
Dmel\CG14044
Klra1
CNPY2
Azi2
Dmel\CG14556
X1WDN6
Dmel\CG13404
Dmel\CG12395
Q6PBS0
Dmel\CG17187
Rtnl2
aes
dtnbp1a
X1WE48
Dmel\CG6980
Vmn1r48
Il34
Leng1
lectin-21Ca
Dysb
GPR88
FBpp0074674
GPR78
Krt20
X1WCW7
SPZ1
X1WCG6
Dmel\CG13001
CCD22
DNAJC17
Dmel\CG14868
Kcnd3
MRGPRD
ANGPTL6
Tas2r103
Lrrfip2
Dh44
Xcr1
Dmel\CG33700
anon-WO0140519.185
Krt27
TRAF3IP3
TSPAN32
Arc
Gr93c
BORCS5
Or42b
corolla
FEZ2
Ptger2
Cmklr2
nac
Stoml2
Six6os1
SAPCD2
HMG20B
CCDC106
Gr68a
Q1L962
MCHR2
NUF2
X1WBM3
Yju2
F1QA06
Q5RG91
Clec4a1
ADRB2
AstA-R1
mACHR-C
Dmel\CG4004
Dmel\CG3448
Dmel\CG13084
TRAIP
X1WHD4

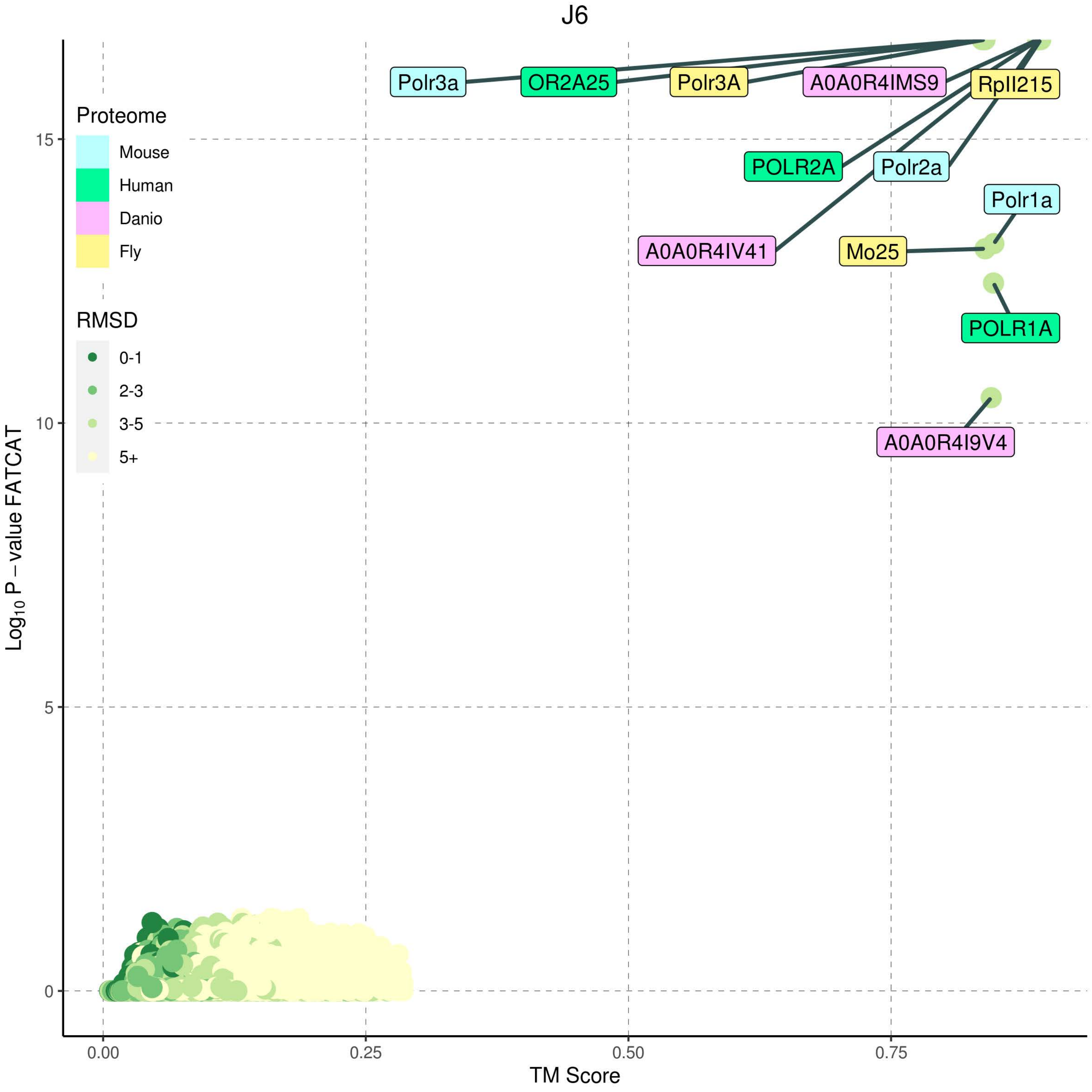

J1 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
NA
Log10 P − value FATCAT
TM Score
0
1
2
3
4
5
0.1
0.2
0.3
0.4
0.5
Mrln
A0A2R8RKF0
MRLN
A0A2R8QB45
Dmel\CG33946
A0A669KB60
A0A6I8MWZ3
Dmel\CG46311
A0A0R4I9Q3
Unc93a
unc93a
SLC18A1
Slc18a2
SLC18A2
tmc2b
Dmel\CG32017
TMC5
Unc93b1

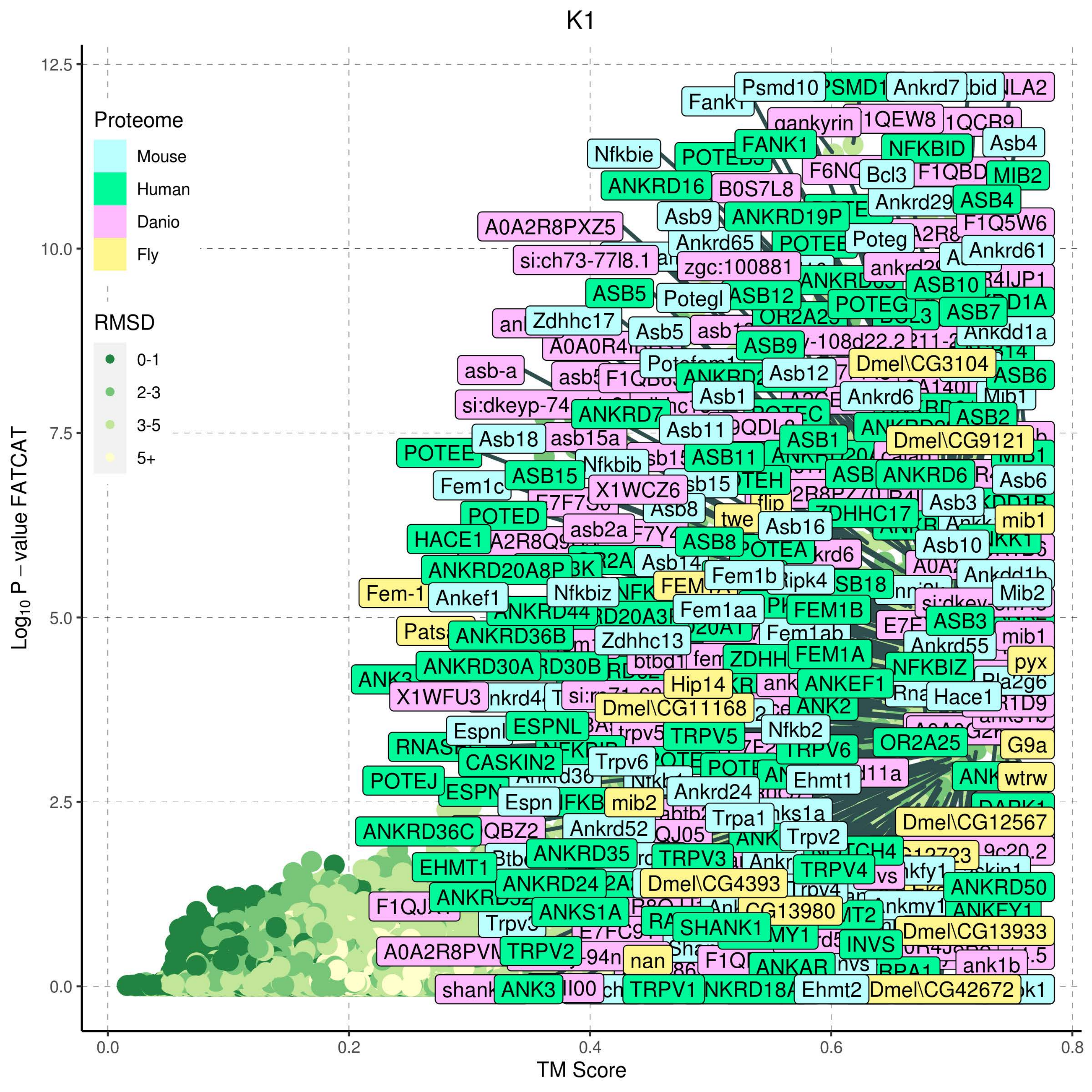

J2
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Rad51D
A0A0R4IP36
Tk1
TK1
Xrcc3
F1QJ27
Rad51d
ELP6
elp5
RAD51D
elp6
Elp6
mtDNA-helicase
Atp5f1a
OR2A25
ATP5F1A
TWNK
peo1
Log10 P − value FATCAT
0
1
2
3
4
TM Score
0.00
0.25
0.50
0.75

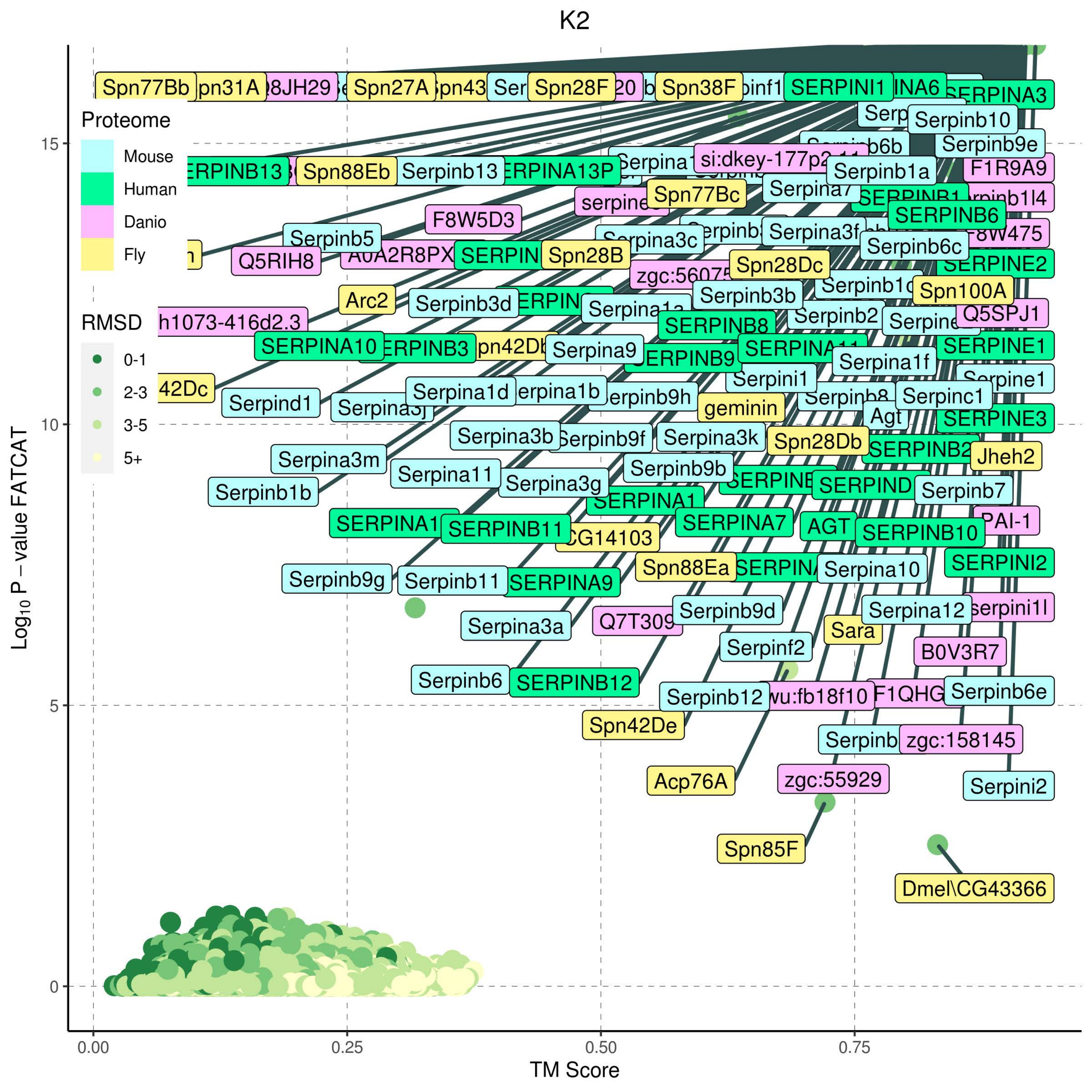

J3
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
cmtr2
Log$_{10}$ P − value FATCAT
TM Score
0
1
2
3
4
0.0
0.2
0.4
0.6

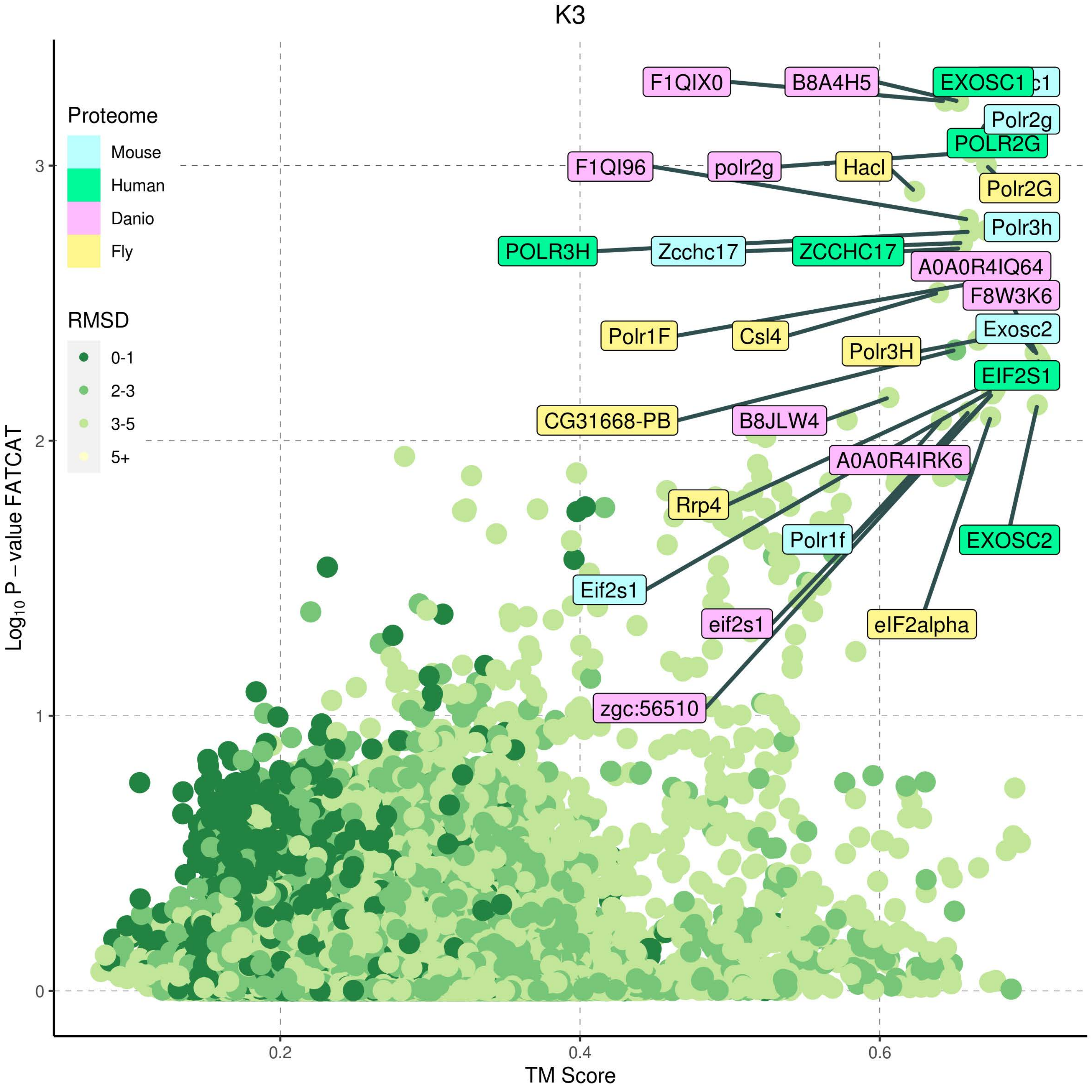

J4
POLR2E
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log$_{10}$ P − value FATCAT
0
1
2
3
4
5
TM Score
0.2
0.4
0.6

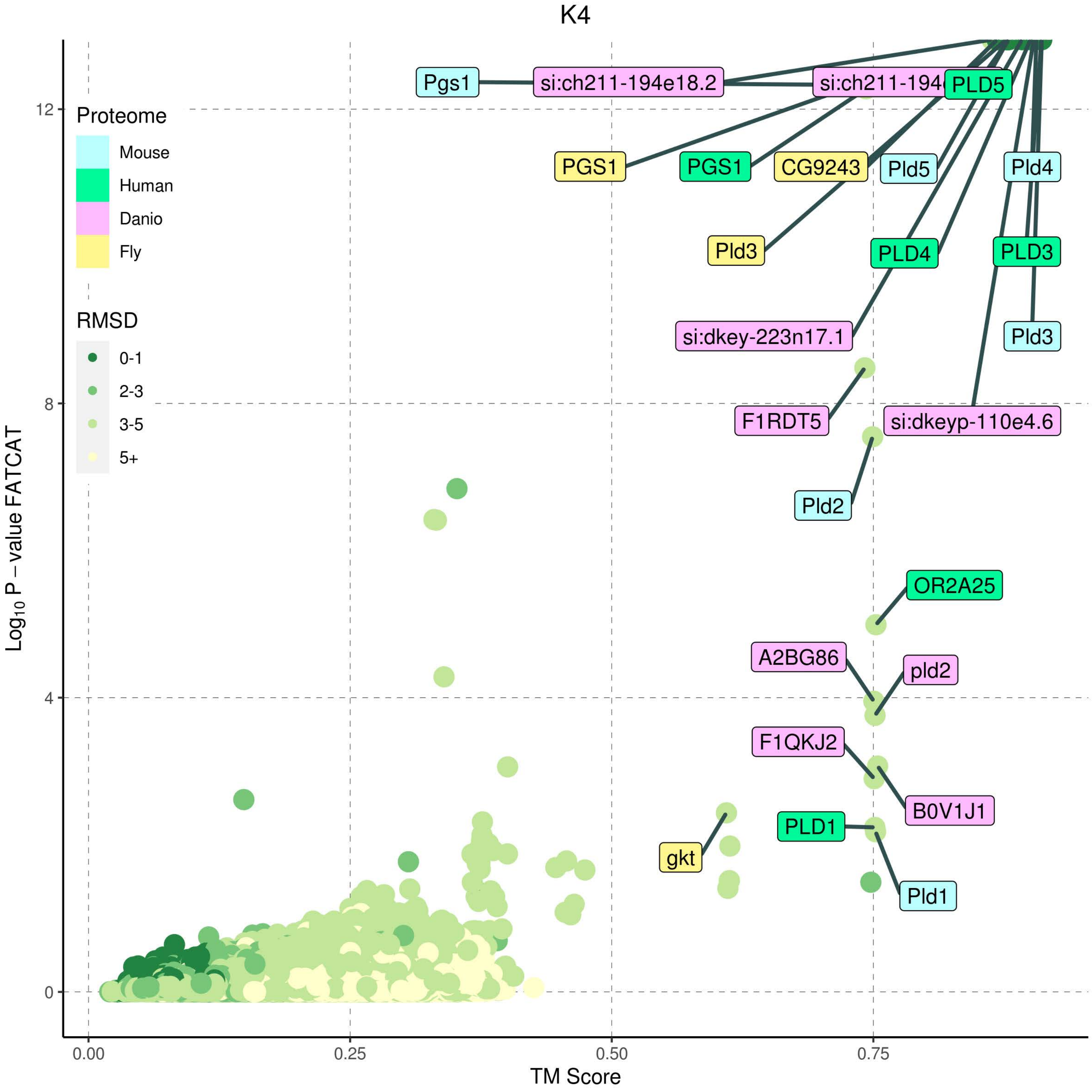

J5 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
t1
Dmel\CG43931
H2BK1
BcDNA:RE59202
Ctxn3
PNN2
F1QMJ9
PRM1
mel\CG45088
Klhl30
TRM1
A0A0G2L6S5
A0A0G2KL83
Dlc1
CFAP47
si:dkey-187e18.1
CFAP54
2.0
1.5
1.0
0.5
0.0
Log10 P – value FATCAT
0.1
0.2
0.3
0.4
TM Score

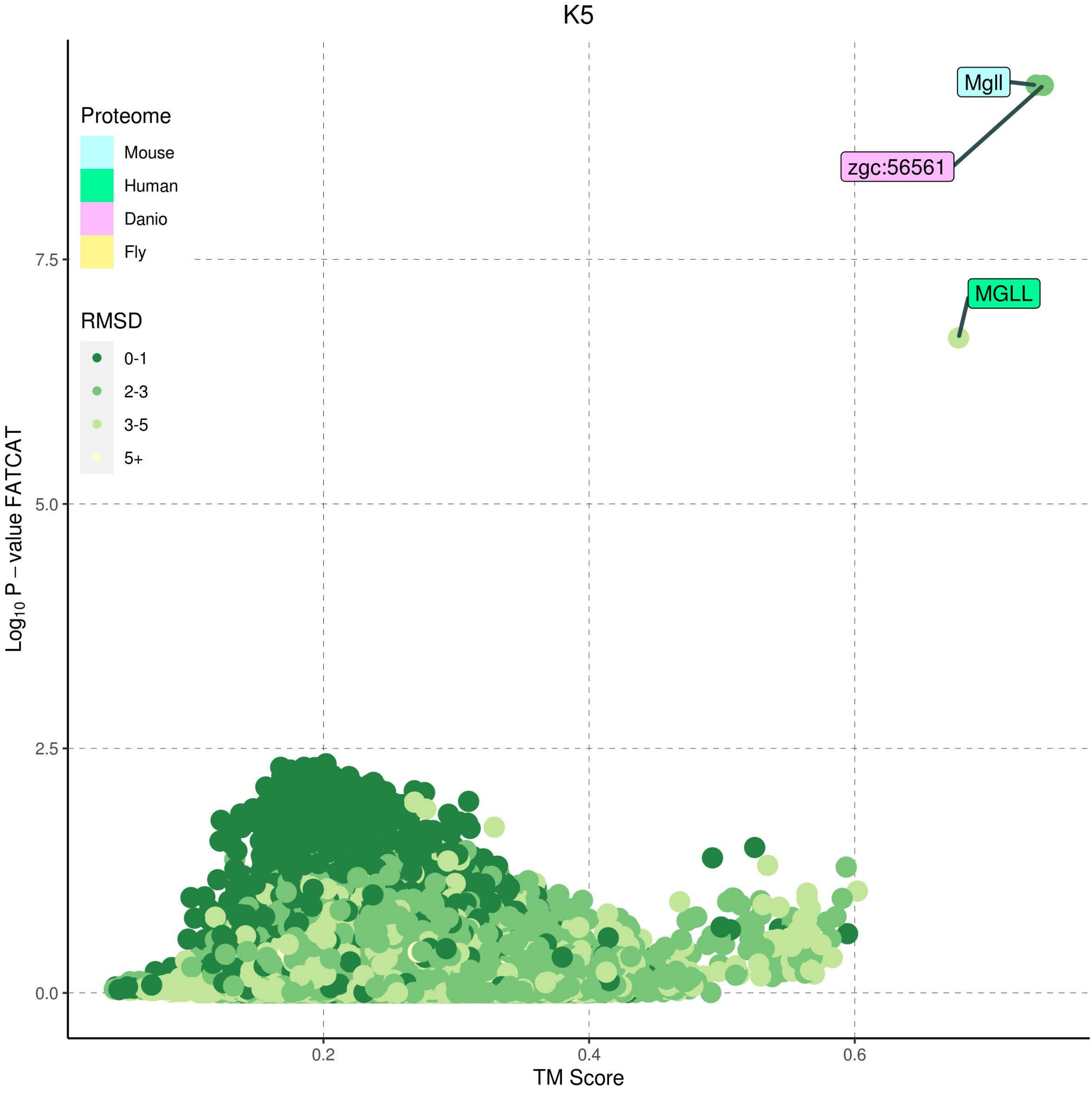

J6
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Polr3a
OR2A25
Polr3A
A0A0R4IMS9
RpII215
POLR2A
Polr2a
Polr1a
A0A0R4IV41
Mo25
POLR1A
A0A0R4I9V4
15
10
5
0
0.00
0.25
0.50
0.75
TM Score
Log$_{10}$ P − value FATCAT

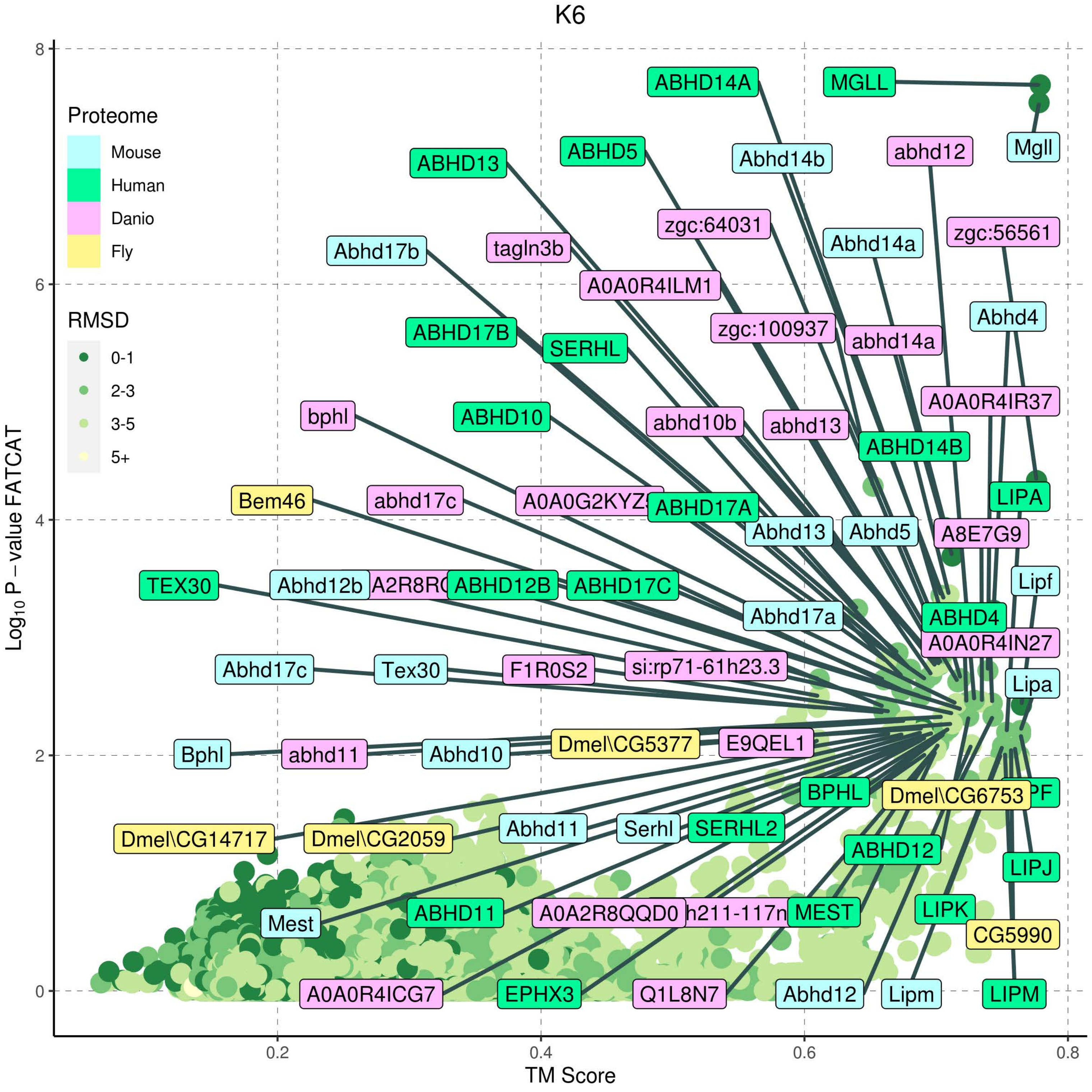

K1
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log$_{10}$ P − value FATCAT
TM Score
0.0
2.5
5.0
7.5
10.0
12.5
0.0
0.2
0.4
0.6
0.8
Psmd10
Ankrd7
Fank1
gankyrin
FANK1
NFKBID
Asb4
Nfkbie
F6NC
Bcl3
F1QBD
MIB2
ANKRD16
B0S7L8
Ankrd29
ASB4
A0A2R8PXZ5
Asb9
ANKRD19P
F1Q5W6
Ankrd65
POTEE
Poteg
Ankrd61
si:ch73-77l8.1
zgc:100881
ASB5
Potegl
ASB12
ASB10
POTEG
ASB7
Zdhhc17
Asb5
Ankdd1a
A0A0R4
ASB9
asb-a
Potefam1
Asb12
Dmel\CG3104
ASB6
asb5
ANKRD2
Asb1
Ankrd6
Mib1
si:dkeyp-74
ANKRD7
Asb11
ASB2
Asb18
asb15a
ASB1
Dmel\CG9121
POTEE
Nfkbib
ASB11
ASB15
ANKRD6
Asb6
Fem1c
X1WCZ6
flip
Asb8
Asb3
POTED
twe
Asb16
ZDHHC17
mib1
HACE1
asb2a
ASB8
POTEA
Asb10
ANKRD20A8P
Asb14
Fem1b
Ripk4
Ankdd1b
Fem-1
Ankef1
Nfkbiz
FEM1B
Mib2
ANKRD44
Fem1aa
Patsas
ANKRD36B
Zdhhc13
Fem1ab
ASB3
mib1
FEM1A
Ankrd55
pyx
ANKRD30A
NFKBIZ
ANK3
ANKEF1
X1WFU3
Hip14
Hace1
Dmel\CG11168
ANK2
Espnl
ESPNL
Nfkb2
TRPV5
RNASE
TRPV6
OR2A25
G9a
CASKIN2
Trpv6
POTEJ
Ehmt1
wtrw
ESPN
Espn
mib2
Ankrd24
Trpa1
Dmel\CG12567
ANKRD36C
Ankrd52
Trpv2
EHMT1
ANKRD35
TRPV3
TRPV4
ANKRD24
Dmel\CG4393
ANKRD50
F1QJ
ANKS1A
CG13980
Trpv3
SHANK1
Dmel\CG13933
A0A2R8PVM
TRPV2
INVS
nan
ANKAR
ank1b
ANK3
TRPV1
Ehmt2
Dmel\CG42672

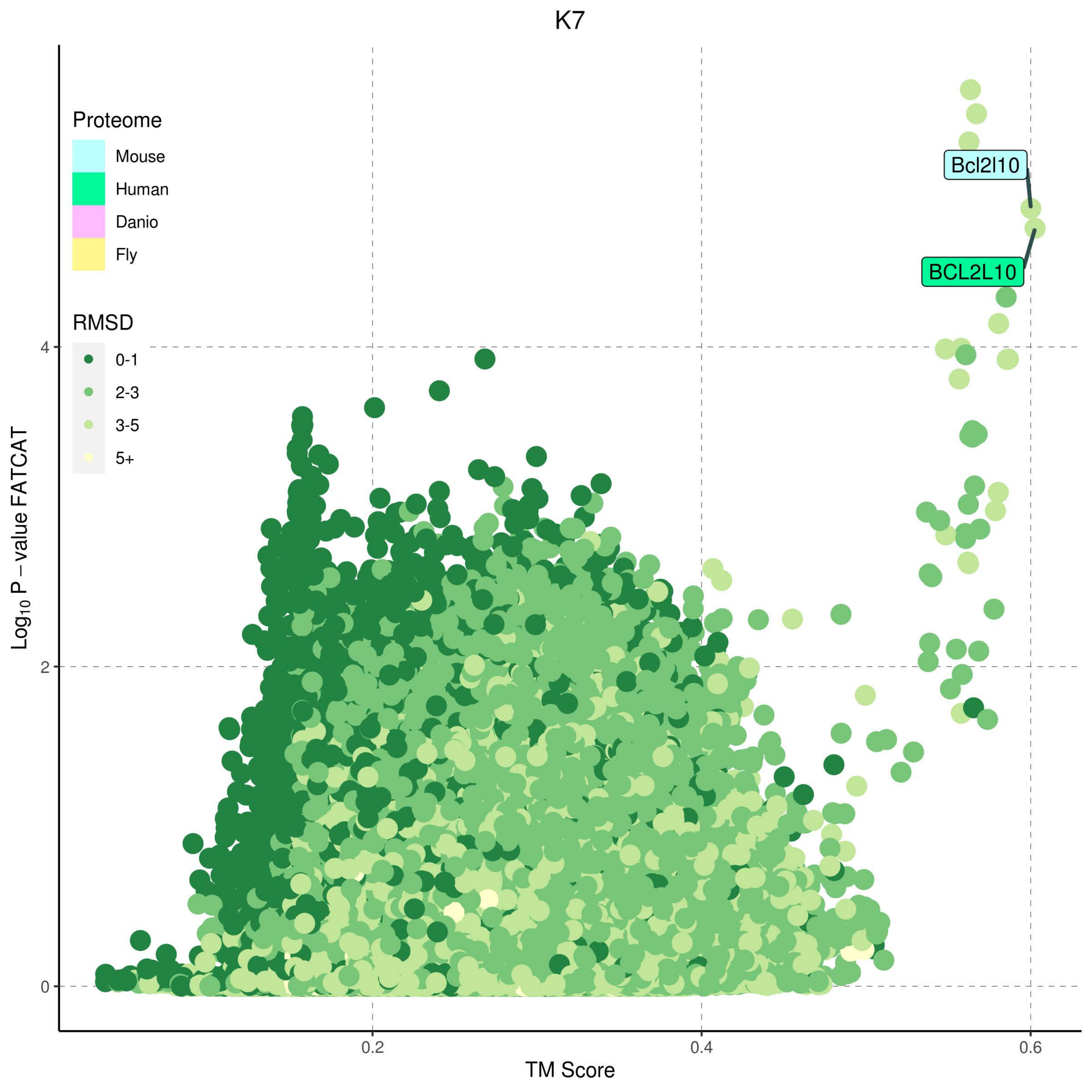

K2
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P − value FATCAT
TM Score
0.00
0.25
0.50
0.75
0
5
10
15
Spn77Bb
Spn27A
Spn28F
Spn38F
SERPINI1
SERPINA3
Serpinb10
Serpinb9e
F1R9A9
Spn88Eb
Serpinb13
si:dkey-177p2
Serpinb1a
Spn77Bc
Serpina7
SERPINB6
F8W5D3
Serpinb5
Serpina3c
Serpina3f
Serpinb6c
Q5RIH8
SERPINE2
Spn28B
Spn28Dc
Arc2
Serpinb3d
Serpinb3b
Spn100A
Serpinb2
Q5SPJ1
SERPINB8
SERPINA10
SERPINB3
Serpina9
SERPINB9
Serpina1f
SERPINE1
Serpini1
Serpine1
Serpind1
Serpina1d
Serpinc1
geminin
Agt
SERPINE3
Serpina3b
Serpinb9f
Serpina3k
Spn28Db
Jheh2
Serpina3m
Serpina11
Serpina3g
Serpinb9b
Serpinb7
Serpinb1b
SERPINB11
SERPINA7
AGT
SERPINB10
PAI-1
CG14103
Spn88Ea
Serpina10
SERPINI2
Serpinb9g
Serpinb11
SERPINA9
Serpinb9d
Serpina12
Serpina3a
Sara
Serpinf2
B0V3R7
Serpinb6
SERPINB12
Serpinb12
wu:fb18f10
Serpinb6e
Spn42De
zgc:158145
Acp76A
zgc:55929
Serpini2
Spn85F
Dmel\CG43366

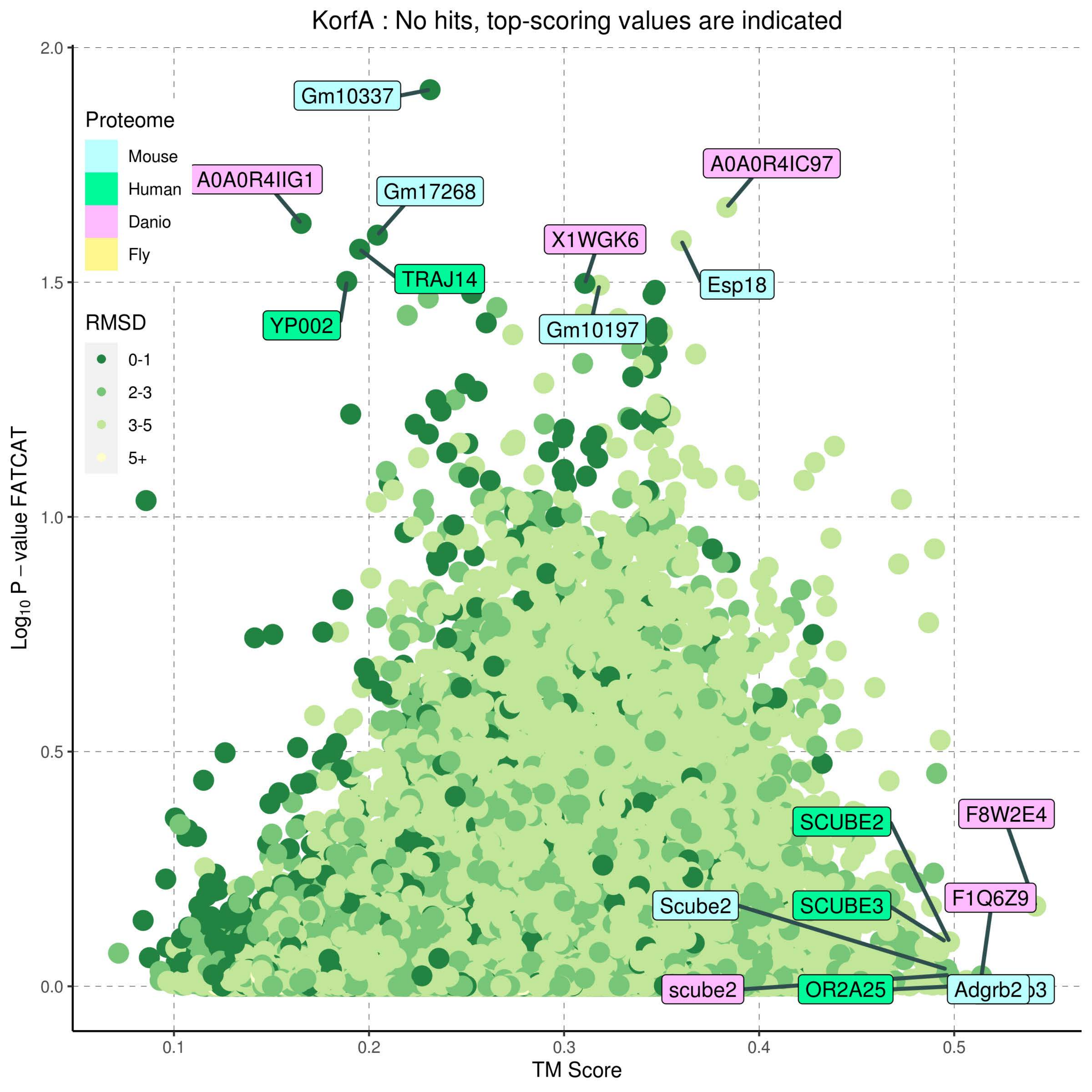

K3
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log₁₀ P – value FATCAT
3
2
1
0
TM Score
0.2
0.4
0.6
F1QIX0
B8A4H5
EXOSC1
c1
Polr2g
POLR2G
F1QI96
polr2g
Hacl
Polr2G
Polr3h
POLR3H
Zcchc17
ZCCHC17
A0A0R4IQ64
F8W3K6
Polr1F
Csl4
Exosc2
Polr3H
EIF2S1
CG31668-PB
B8JLW4
A0A0R4IRK6
Rrp4
Polr1f
EXOSC2
Eif2s1
eif2s1
eIF2alpha
zgc:56510

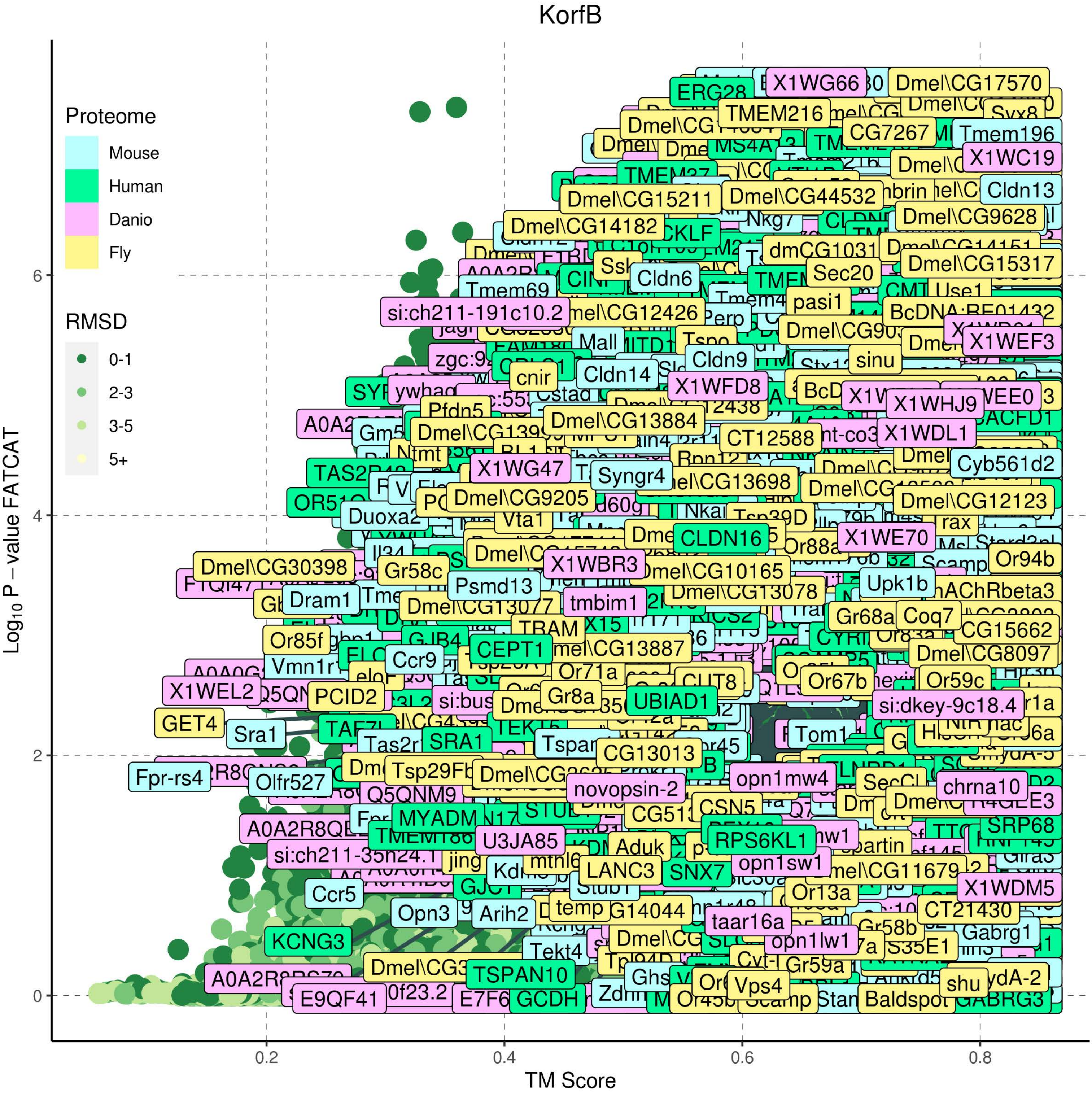

K4
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Pgs1
si:ch211-194e18.2
si:ch211-194
PLD5
PGS1
PGS1
CG9243
Pld5
Pld4
Pld3
PLD4
PLD3
si:dkey-223n17.1
Pld3
F1RDT5
si:dkeyp-110e4.6
Pld2
OR2A25
A2BG86
pld2
F1QKJ2
B0V1J1
PLD1
gkt
Pld1
Log10 P – value FATCAT
12
8
4
0
0.00
0.25
0.50
0.75
TM Score

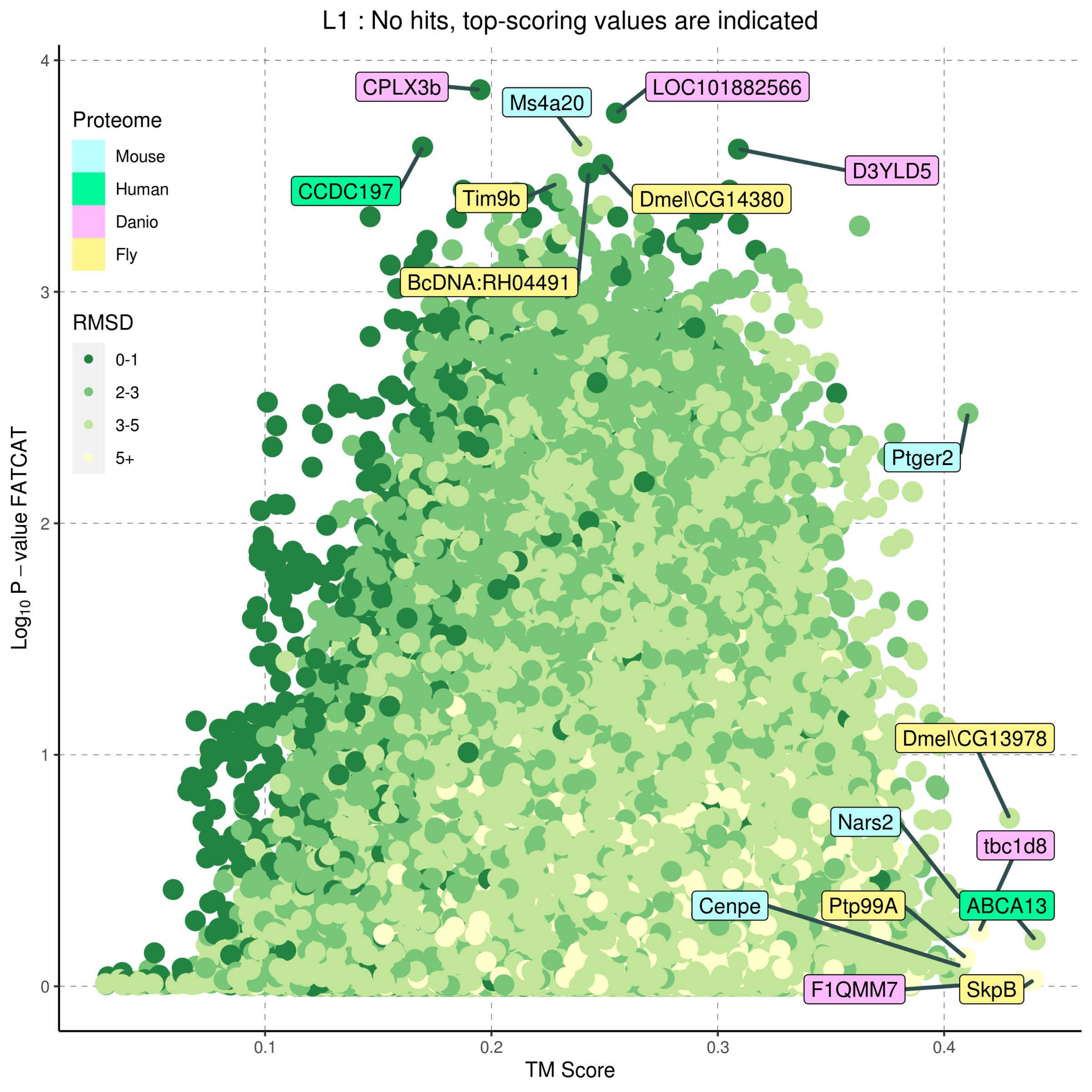

K5
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Mgll
zgc:56561
MGLL
7.5
5.0
2.5
0.0
0.2
0.4
0.6
Log10 P – value FATCAT
TM Score

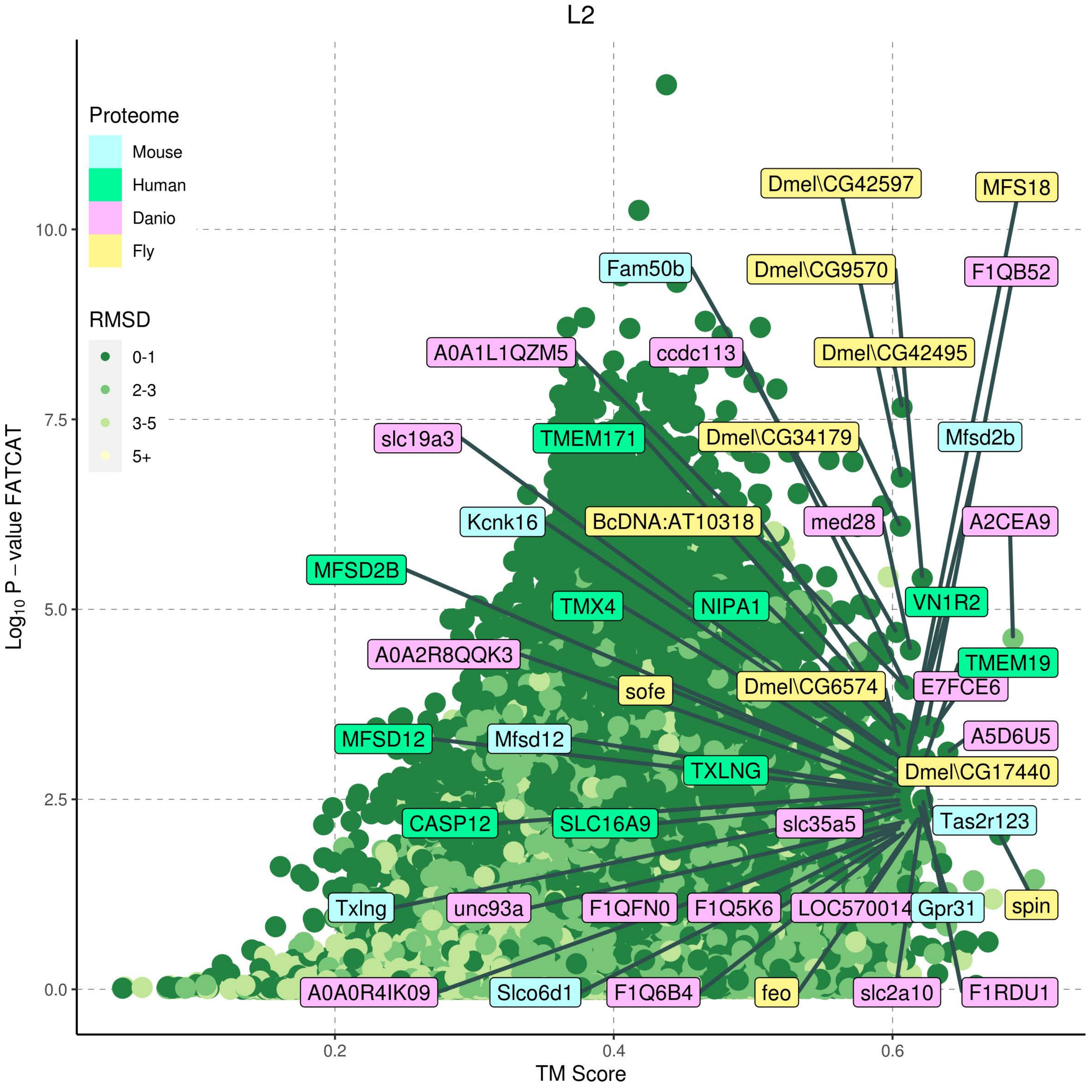

K6
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log₁₀ P – value FATCAT
TM Score
0
2
4
6
8
0.2
0.4
0.6
0.8
ABHD14A
MGLL
Mgll
ABHD13
ABHD5
Abhd14b
abhd12
zgc:64031
Abhd14a
zgc:56561
Abhd17b
tagln3b
A0A0R4ILM1
zgc:100937
abhd14a
Abhd4
ABHD17B
SERHL
A0A0R4IR37
bphl
ABHD10
abhd10b
abhd13
ABHD14B
Bem46
abhd17c
A0A0G2KYZ
ABHD17A
LIPA
Abhd13
Abhd5
A8E7G9
TEX30
Abhd12b
A2R8RC
ABHD12B
ABHD17C
Lipf
Abhd17a
ABHD4
A0A0R4IN27
Abhd17c
Tex30
F1R0S2
si:rp71-61h23.3
Lipa
Bphl
abhd11
Abhd10
Dmel\CG5377
E9QEL1
BPHL
Dmel\CG6753
PF
Dmel\CG14717
Dmel\CG2059
Abhd11
Serhl
SERHL2
ABHD12
LIPJ
Mest
ABHD11
A0A2R8QQD0
h211-117n
MEST
LIPK
CG5990
A0A0R4ICG7
EPHX3
Q1L8N7
Abhd12
Lipm
LIPM

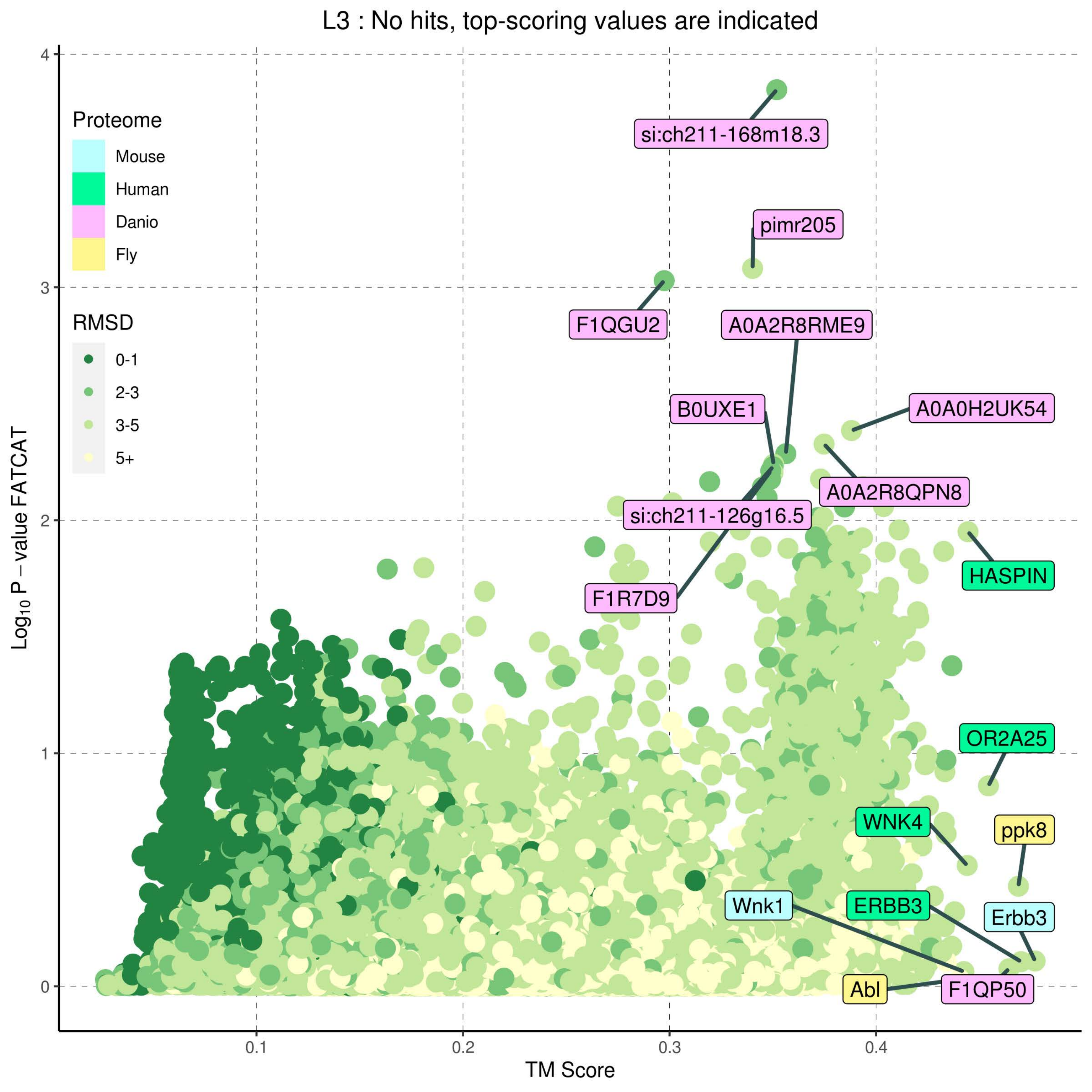

K7
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Bcl2l10
BCL2L10
Log₁₀ P − value FATCAT
TM Score
0
2
4
0.2
0.4
0.6

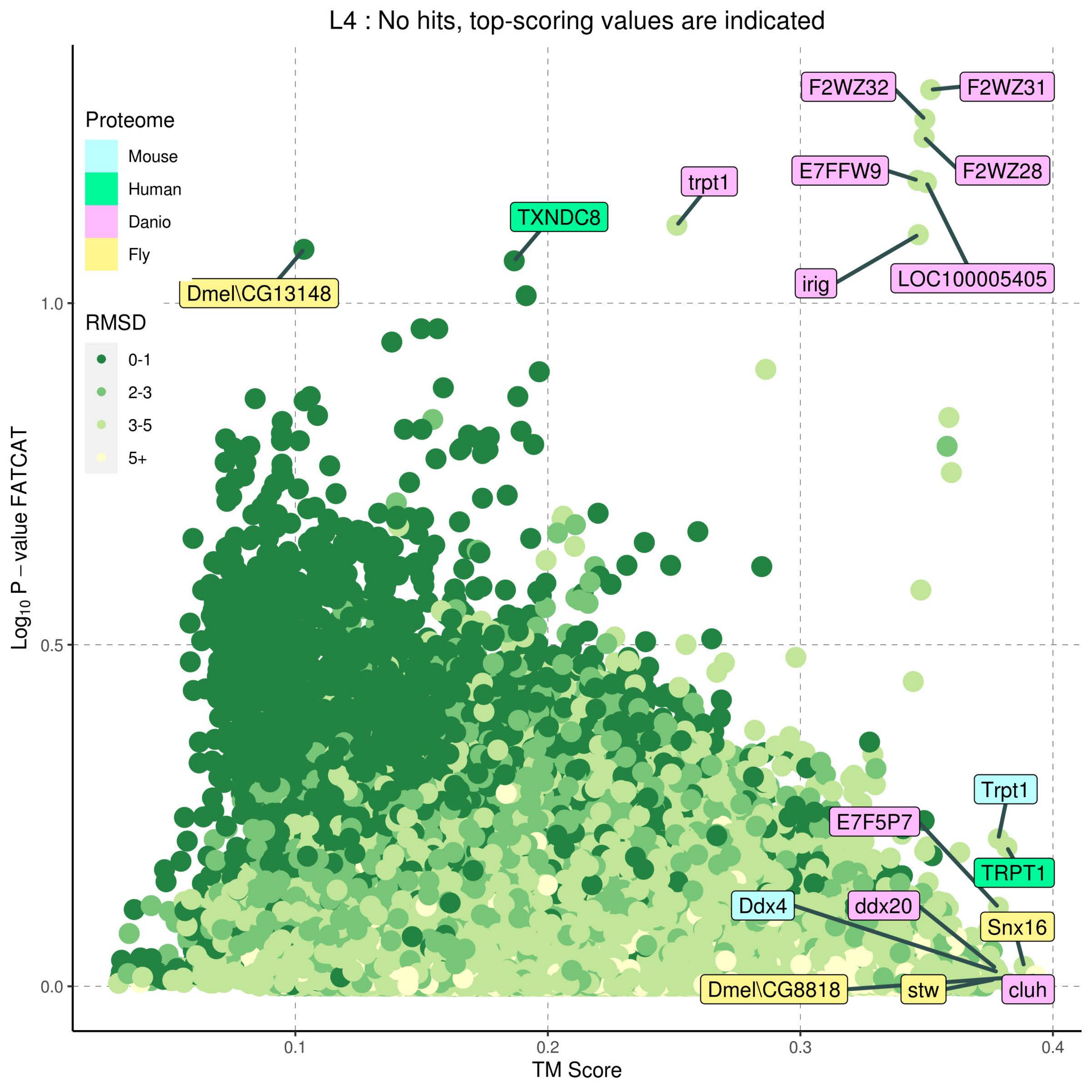

KorfA : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Gm10337
A0A0R4IIG1
Gm17268
TRAJ14
YP002
X1WGK6
Gm10197
A0A0R4IC97
Esp18
SCUBE2
F8W2E4
Scube2
SCUBE3
F1Q6Z9
scube2
OR2A25
Adgrb2
2.0
1.5
1.0
0.5
0.0
0.1
0.2
0.3
0.4
0.5
Log₁₀ P – value FATCAT
TM Score

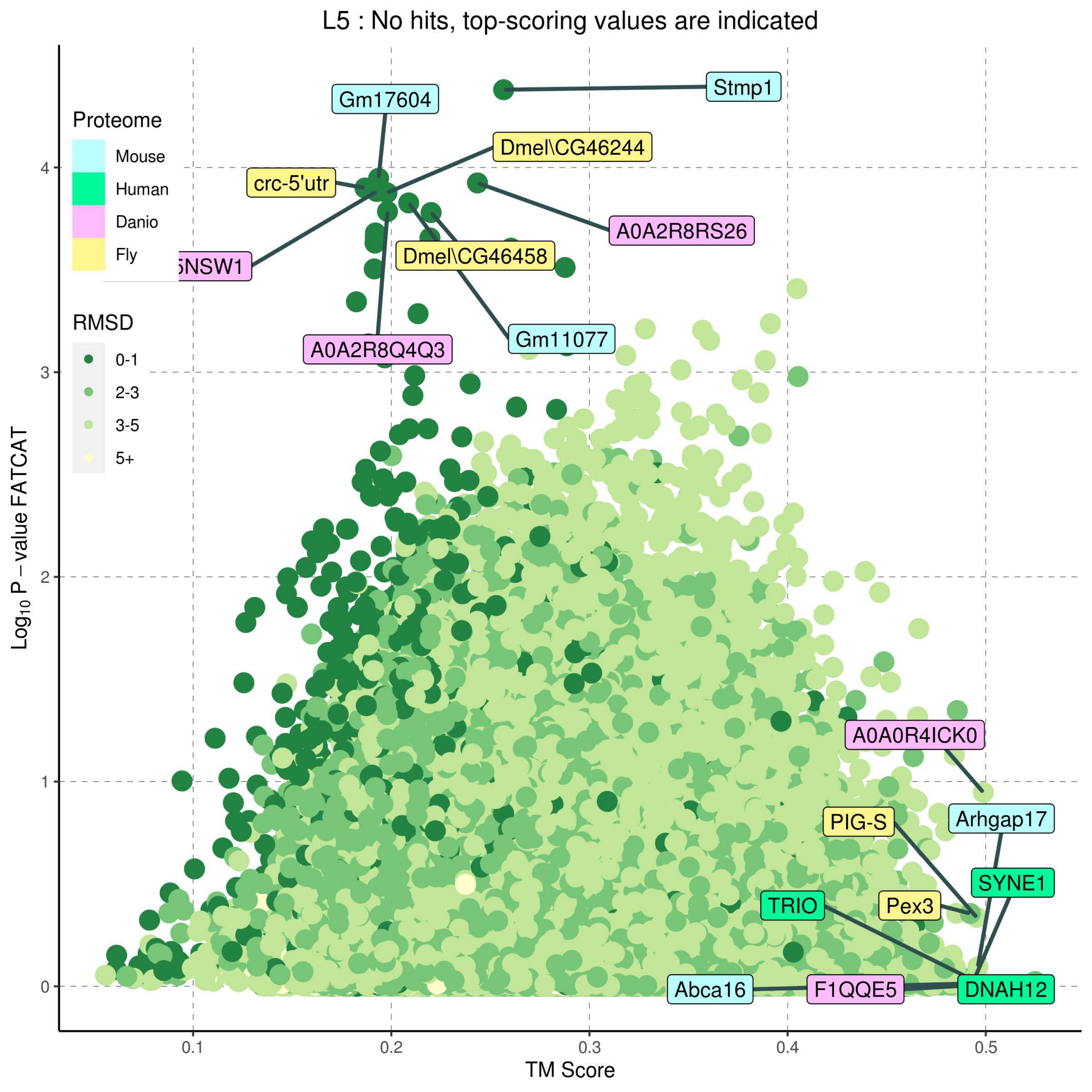

KorfB
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
TM Score
0
2
4
6
0.2
0.4
0.6
0.8
X1WG66
Dmel\CG17570
ERG28
TMEM216
CG7267
Tmem196
X1WC19
TMEM37
Dmel\CG15211
Dmel\CG44532
Cldn13
Dmel\CG9628
Dmel\CG14182
CKLF
Nkg7
dmCG1031
Dmel\CG15317
Ssk
Cldn6
Sec20
Tmem69
pasi1
si:ch211-191c10.2
Perp
Mall
X1WEF3
zgc:9
Cldn9
sinu
cnir
Cldn14
X1WFD8
X1WHJ9
Pfdn5
Dmel\CG13884
A0A2
X1WDL1
CT12588
Ntmt
Cyb561d2
X1WG47
Syngr4
TAS2R
Dmel\CG9205
Dmel\CG12123
Duoxa2
Vta1
Tsp39D
CLDN16
X1WE70
rax
Or88a
X1WBR3
Dmel\CG30398
Gr58c
Dmel\CG10165
Or94b
Psmd13
Upk1b
Dram1
Dmel\CG13078
nAChRbeta3
Dmel\CG13077
tmbim1
Gr68a
Coq7
TRAM
CG15662
Or85f
CEPT1
Dmel\CG13887
Dmel\CG8097
Ccr9
Vmn1r1
Or71a
CUT8
Or67b
Or59c
X1WEL2
PCID2
Gr8a
UBIAD1
si:dkey-9c18.4
GET4
Sra1
Tom1
Tas2r
SRA1
Tspan
CG13013
Fpr-rs4
Olfr527
Tsp29Fb
opn1mw4
Q5QNM9
novopsin-2
chrna10
MYADM
CSN5
SRP68
A0A2R8QE
U3JA85
RPS6KL1
si:ch211-35n24.1
Aduk
LANC3
SNX7
opn1sw1
Dmel\CG11679
X1WDM5
Ccr5
GJC1
Or13a
Opn3
Arih2
temp
G14044
CT21430
KCNG3
taar16a
Gr58b
Gabrg1
Tekt4
opn1lw1
S35E1
Dmel\CG3
TSPAN10
Gr59a
A0A2R8RS70
shu
Vps4
E9QF41
0f23.2
GCDH
Scamp
Baldspot
GABRG3

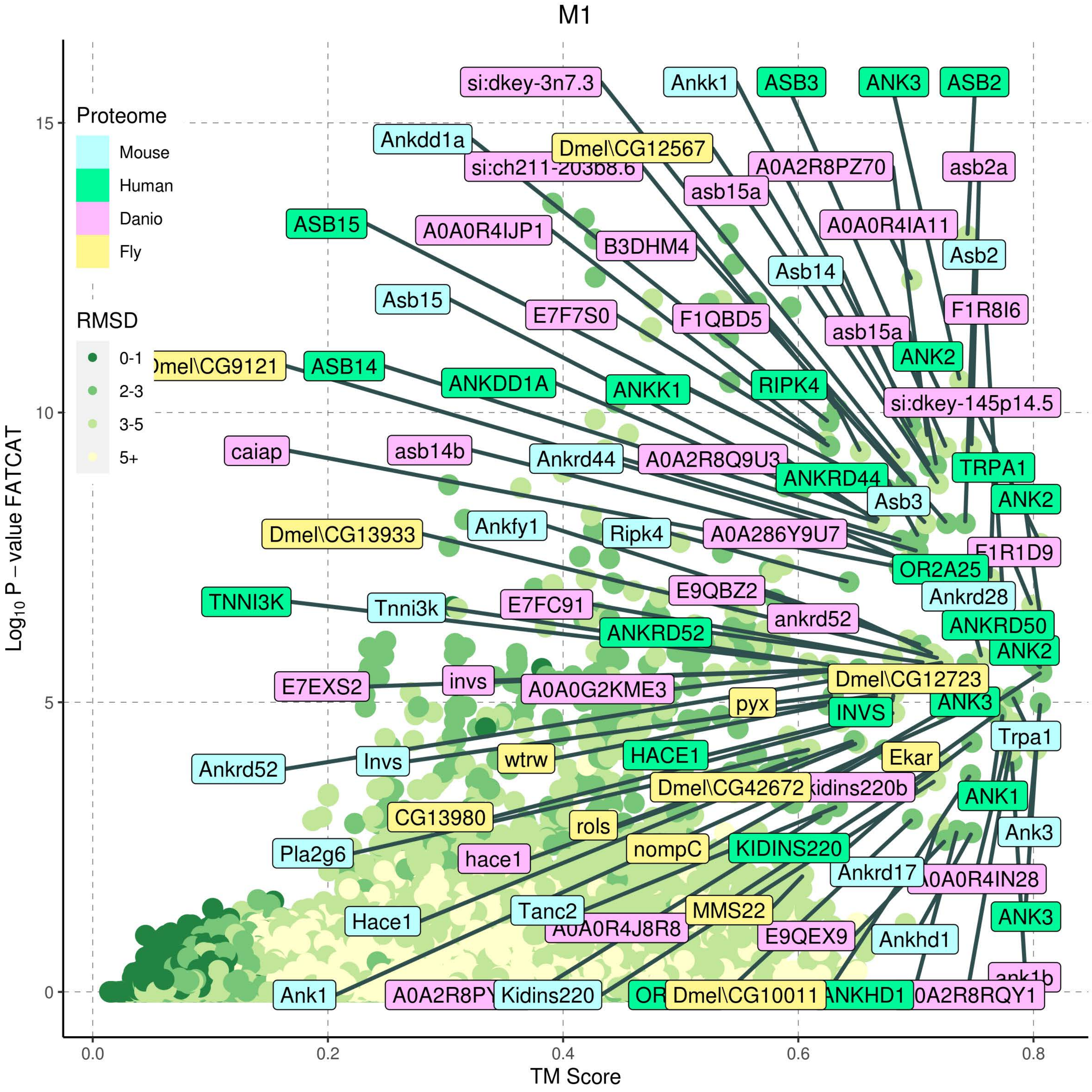

L1 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
CPLX3b
Ms4a20
LOC101882566
CCDC197
Tim9b
Dmel\CG14380
D3YLD5
BcDNA:RH04491
Ptger2
Dmel\CG13978
Nars2
tbc1d8
ABCA13
Cenpe
Ptp99A
F1QMM7
SkpB
Log10 P − value FATCAT
TM Score
0
1
2
3
4
0.1
0.2
0.3
0.4

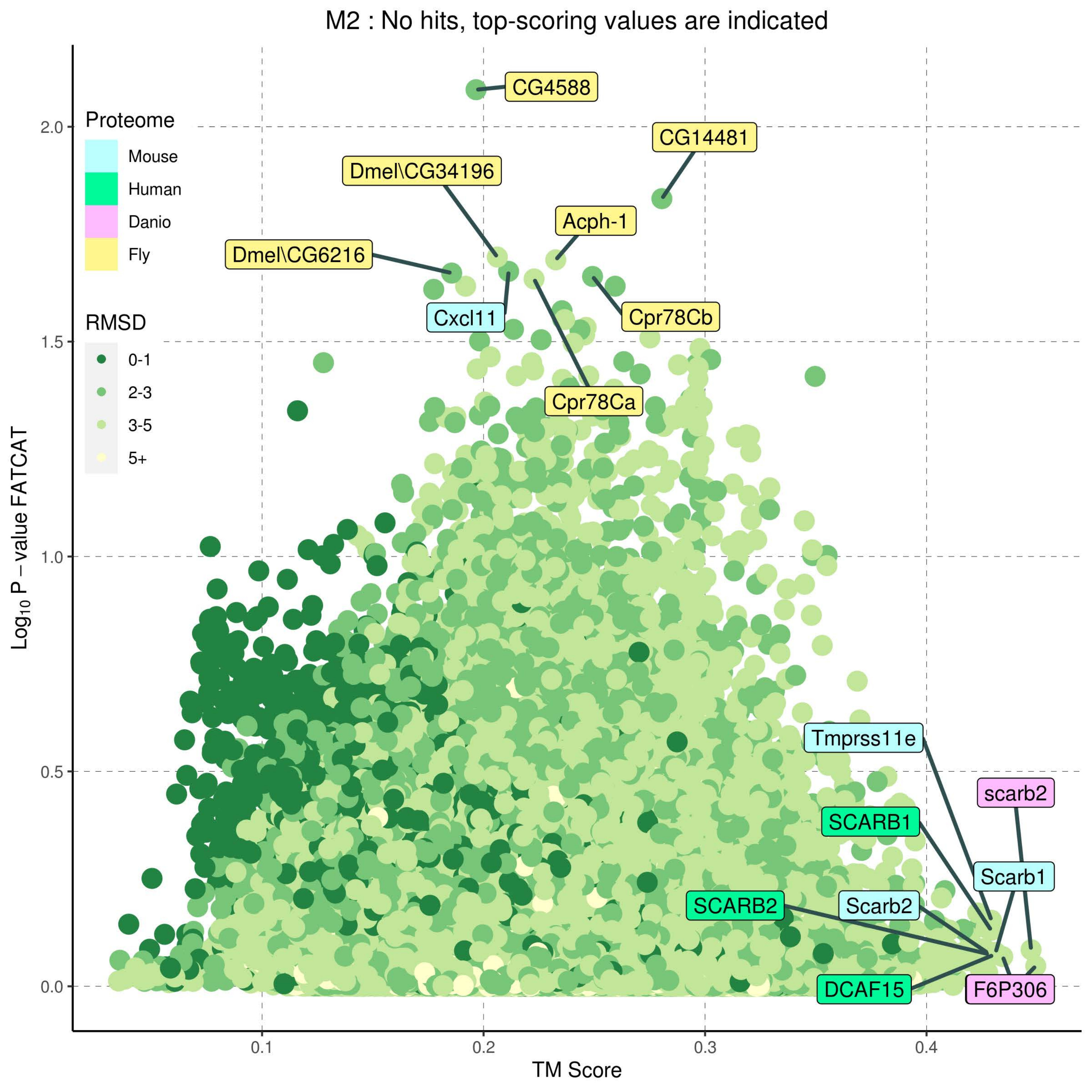

L2
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log₁₀ P − value FATCAT
TM Score
10.0
7.5
5.0
2.5
0.0
0.2
0.4
0.6
Dmel\CG42597
MFS18
Fam50b
Dmel\CG9570
F1QB52
A0A1L1QZM5
ccdc113
Dmel\CG42495
slc19a3
TMEM171
Dmel\CG34179
Mfsd2b
Kcnk16
BcDNA:AT10318
med28
A2CEA9
MFSD2B
TMX4
NIPA1
VN1R2
A0A2R8QQK3
TMEM19
sofe
Dmel\CG6574
E7FCE6
A5D6U5
MFSD12
Mfsd12
TXLNG
Dmel\CG17440
CASP12
SLC16A9
slc35a5
Tas2r123
Txlng
unc93a
F1QFN0
F1Q5K6
LOC570014
Gpr31
spin
A0A0R4IK09
Slco6d1
F1Q6B4
feo
slc2a10
F1RDU1

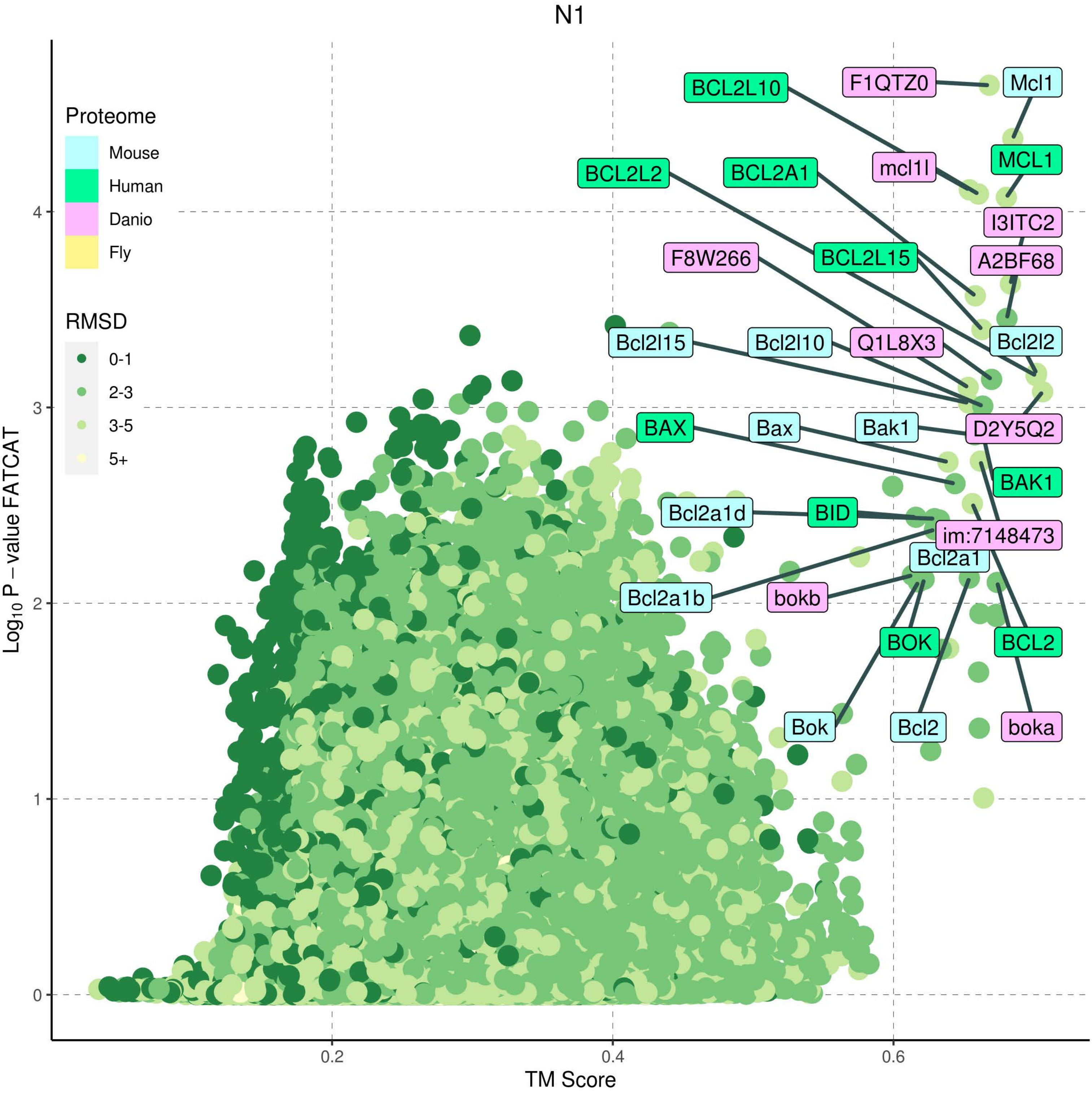

L3 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
si:ch211-168m18.3
pimr205
F1QGU2
A0A2R8RME9
B0UXE1
A0A0H2UK54
A0A2R8QPN8
si:ch211-126g16.5
HASPIN
F1R7D9
OR2A25
WNK4
ppk8
Wnk1
ERBB3
Erbb3
Abl
F1QP50
Log_{10} P − value FATCAT
TM Score
0
1
2
3
4
0.1
0.2
0.3
0.4


L4 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log10 P – value FATCAT
TM Score
1.0
0.5
0.0
0.1
0.2
0.3
0.4
F2WZ32
F2WZ31
F2WZ28
E7FFW9
trpt1
TXNDC8
irig
LOC100005405
Dmel\CG13148
Trpt1
E7F5P7
TRPT1
Ddx4
ddx20
Snx16
Dmel\CG8818
stw
cluh

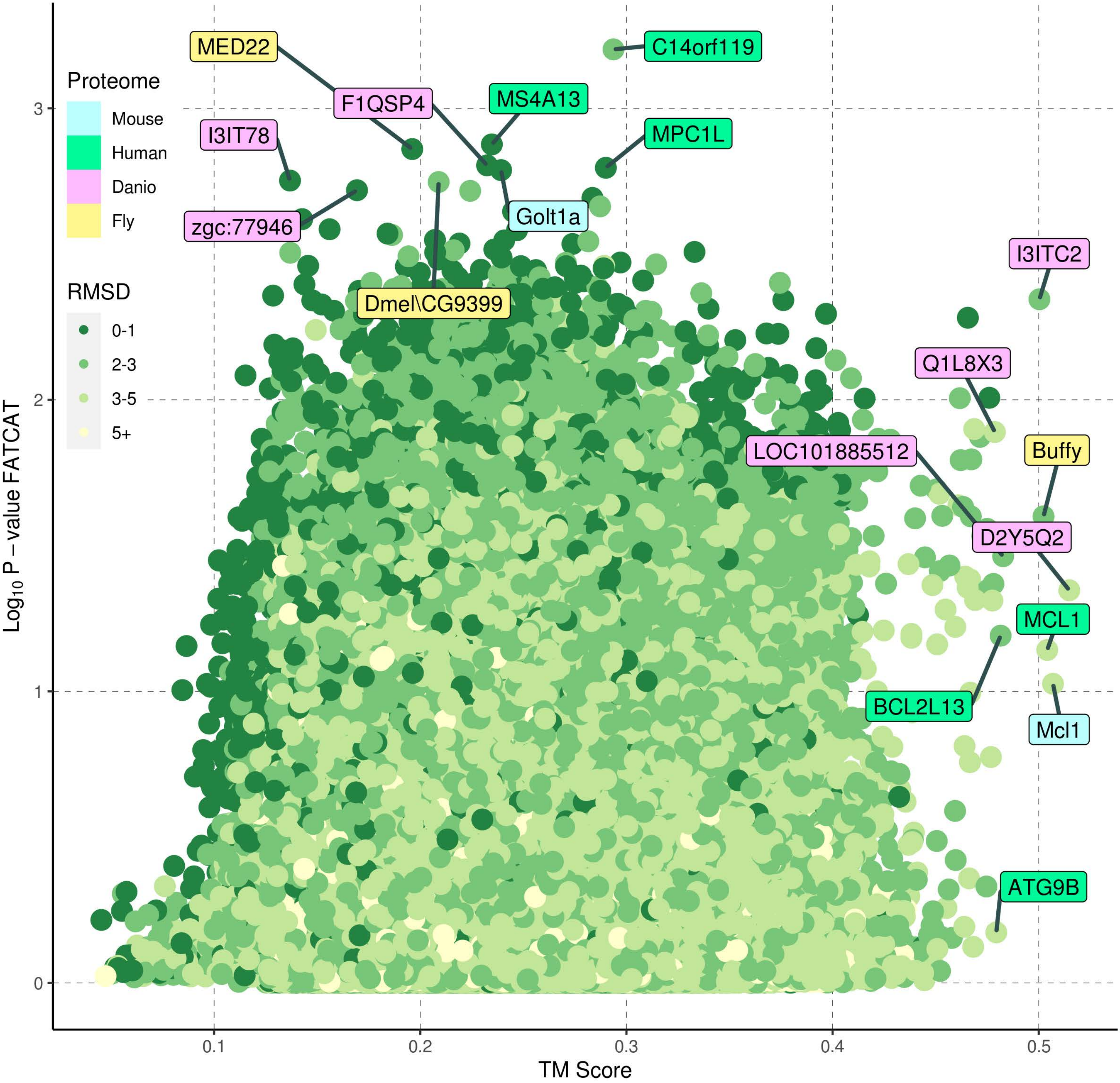

L5 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Stmp1
Gm17604
Dmel\CG46244
crc-5'utr
A0A2R8RS26
5NSW1
Dmel\CG46458
Gm11077
A0A2R8Q4Q3
A0A0R4ICK0
PIG-S
Arhgap17
SYNE1
TRIO
Pex3
Abca16
F1QQE5
DNAH12
Log$_{10}$ P – value FATCAT
4
3
2
1
0
TM Score
0.1
0.2
0.3
0.4
0.5

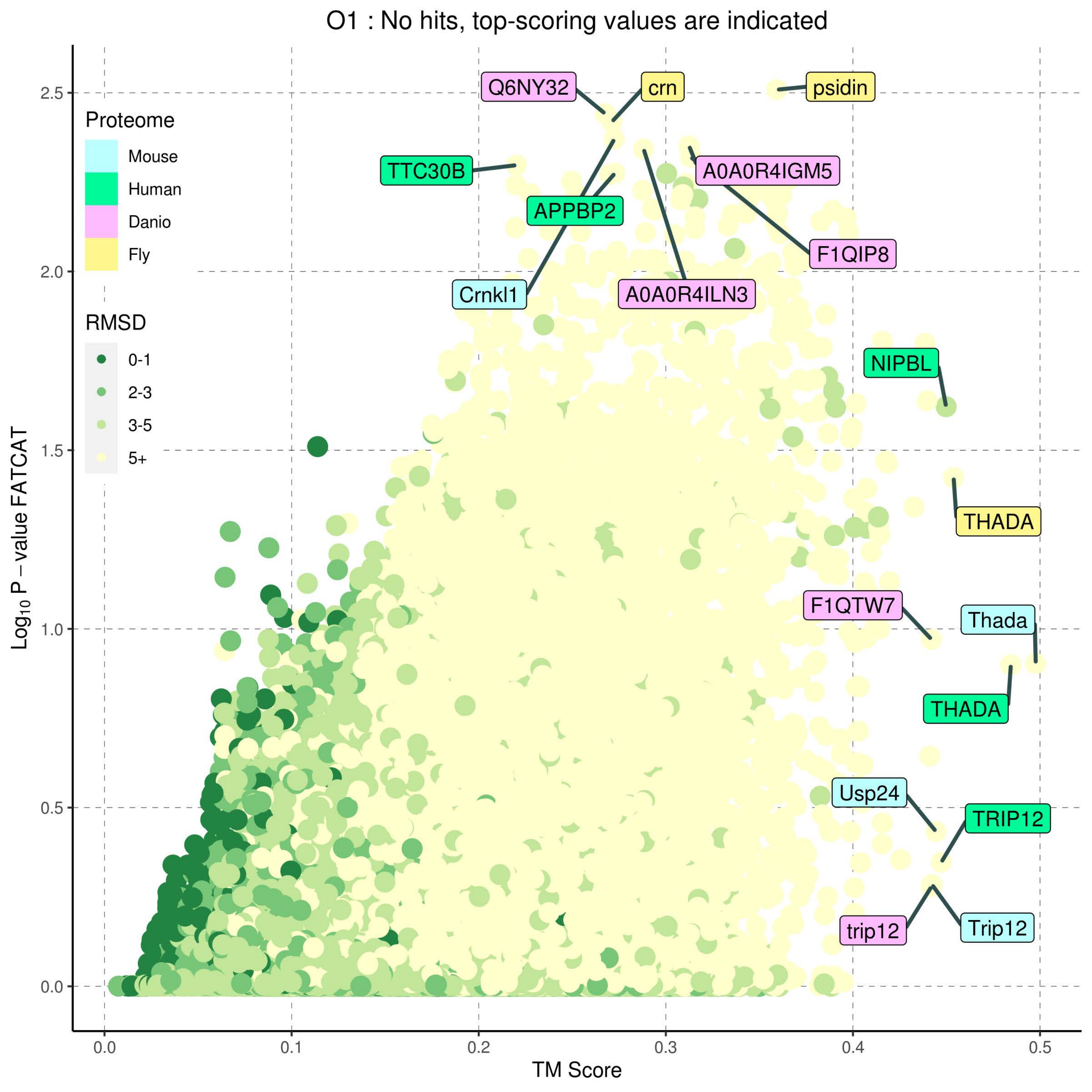

M1
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log₁₀ P − value FATCAT
TM Score
0
5
10
15
0.0
0.2
0.4
0.6
0.8
si:dkey-3n7.3
Ankk1
ASB3
ANK3
ASB2
Ankdd1a
Dmel\CG12567
si:ch211-203b8.6
A0A2R8PZ70
asb2a
asb15a
ASB15
A0A0R4IJP1
B3DHM4
A0A0R4IA11
Asb2
Asb14
Asb15
E7F7S0
F1QBD5
asb15a
F1R8I6
ANK2
mel\CG9121
ASB14
ANKDD1A
ANKK1
RIPK4
si:dkey-145p14.5
caiap
asb14b
Ankrd44
A0A2R8Q9U3
TRPA1
ANKRD44
Asb3
ANK2
Dmel\CG13933
Ankfy1
Ripk4
A0A286Y9U7
F1R1D9
OR2A25
E9QBZ2
Ankrd28
TNNI3K
Tnni3k
E7FC91
ankrd52
ANKRD50
ANKRD52
ANK2
E7EXS2
invs
A0A0G2KME3
Dmel\CG12723
pyx
ANK3
INVS
Trpa1
Ankrd52
Invs
wtrw
HACE1
Ekar
Dmel\CG42672
kidins220b
ANK1
CG13980
rols
Ank3
Pla2g6
hace1
nompC
KIDINS220
Ankrd17
0A0R4IN28
Tanc2
MMS22
Hace1
A0A0R4J8R8
E9QEX9
Ankhd1
ANK3
ank1b
Ank1
A0A2R8PY
Kidins220
OR
Dmel\CG10011
ANKHD1
0A2R8RQY1

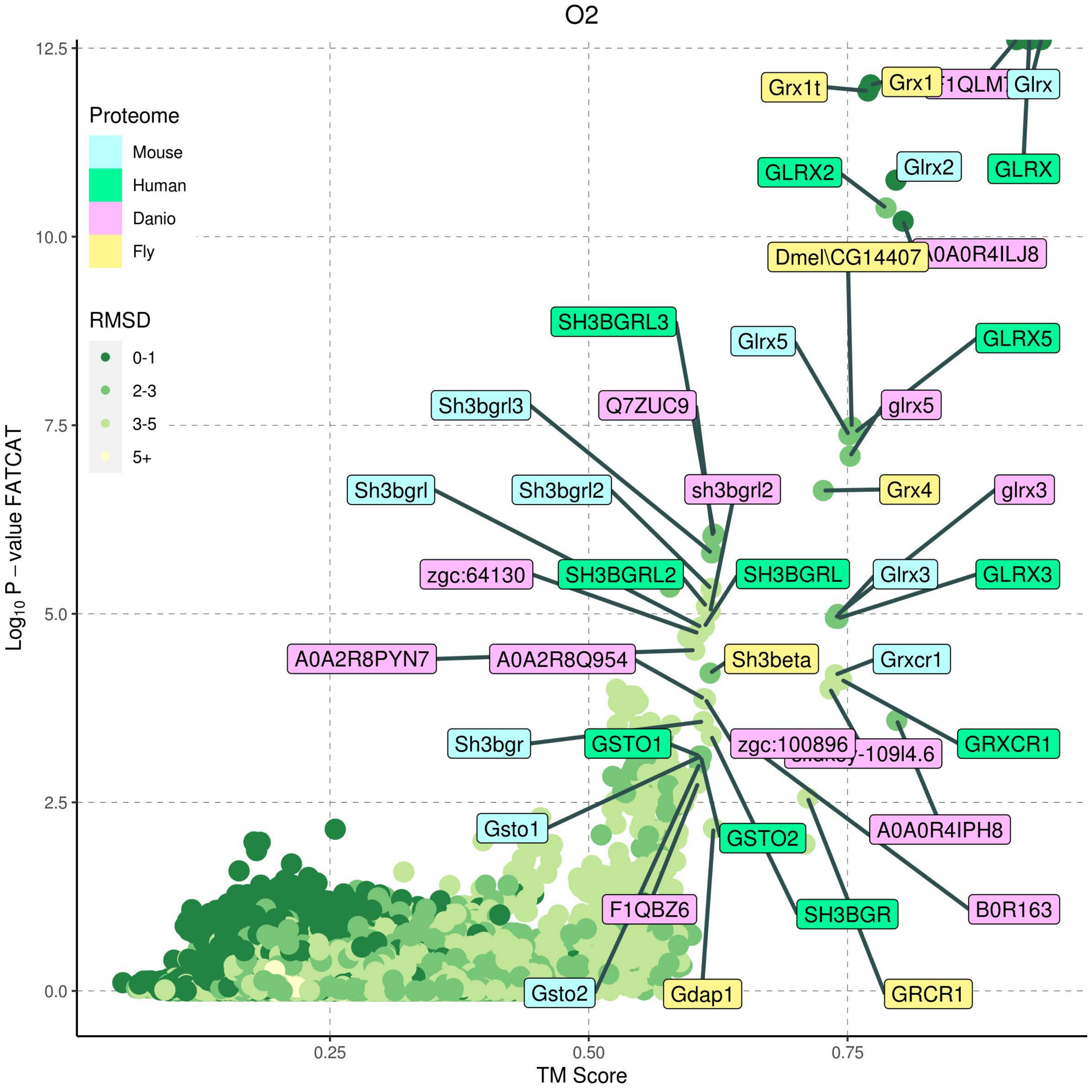

M2 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
CG4588
CG14481
Dmel\CG34196
Acph-1
Dmel\CG6216
Cxcl11
Cpr78Cb
Cpr78Ca
Tmprss11e
scarb2
SCARB1
Scarb1
SCARB2
Scarb2
DCAF15
F6P306
Log₁₀ P – value FATCAT
2.0
1.5
1.0
0.5
0.0
0.1
0.2
0.3
0.4
TM Score


N1
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Log$_{10}$ P – value FATCAT
TM Score
0
1
2
3
4
0.2
0.4
0.6
BCL2L10
F1QTZ0
Mcl1
mcl1l
MCL1
BCL2L2
BCL2A1
I3ITC2
F8W266
BCL2L15
A2BF68
Bcl2l15
Bcl2l10
Q1L8X3
Bcl2l2
BAX
Bax
Bak1
D2Y5Q2
BAK1
Bcl2a1d
BID
im:7148473
Bcl2a1
Bcl2a1b
bokb
BOK
BCL2
Bok
Bcl2
boka

N2 : No hits, top-scoring values are indicated




O1 : No hits, top-scoring values are indicated
Proteome
Mouse
Human
Danio
Fly
RMSD
0-1
2-3
3-5
5+
Q6NY32
crn
psidin
TTC30B
A0A0R4IGM5
APPBP2
F1QIP8
Crnkl1
A0A0R4ILN3
NIPBL
THADA
F1QTW7
Thada
THADA
Usp24
TRIP12
trip12
Trip12
Log10 P − value FATCAT
TM Score
0.0
0.5
1.0
1.5
2.0
2.5
0.0
0.1
0.2
0.3
0.4
0.5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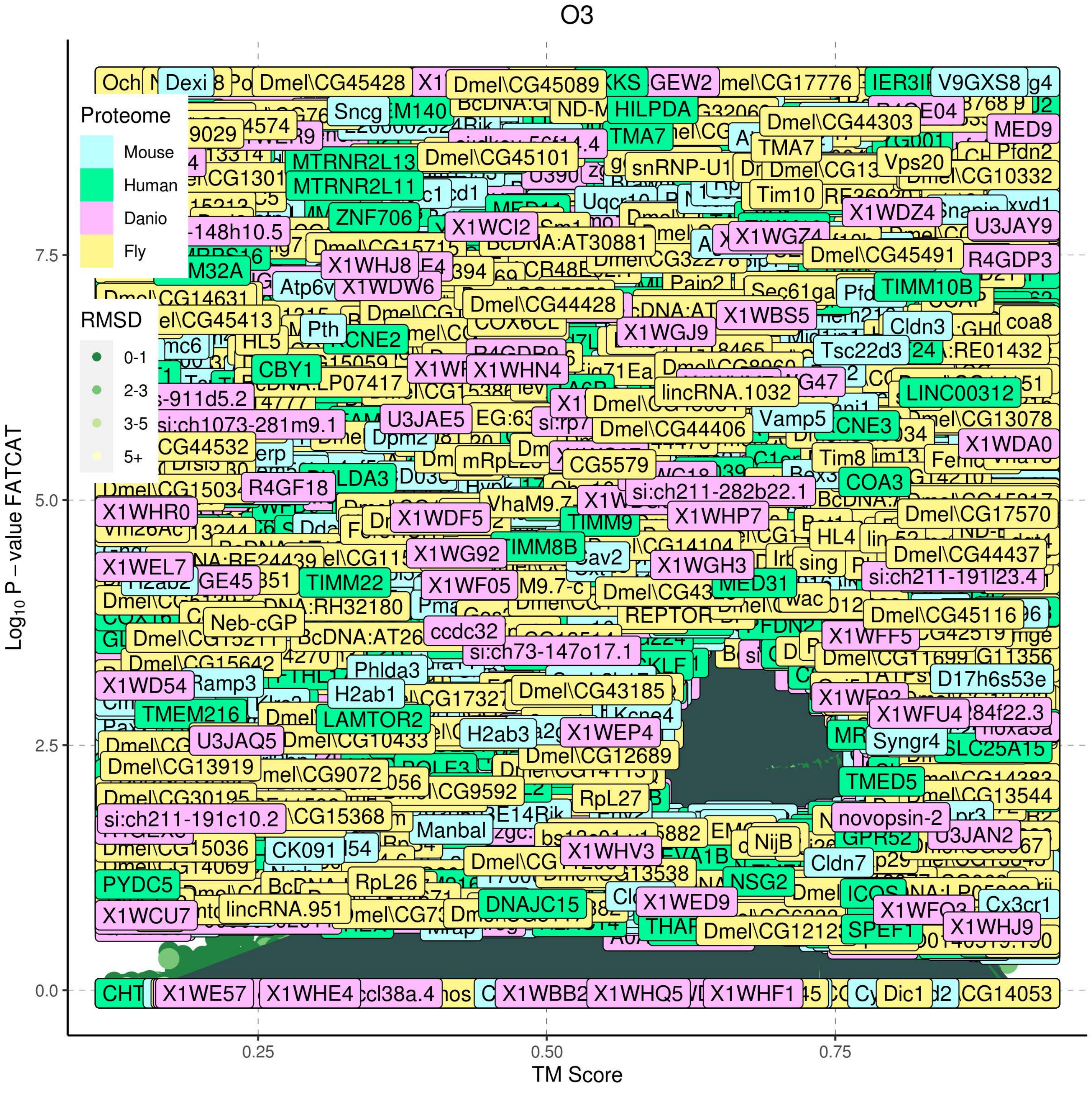
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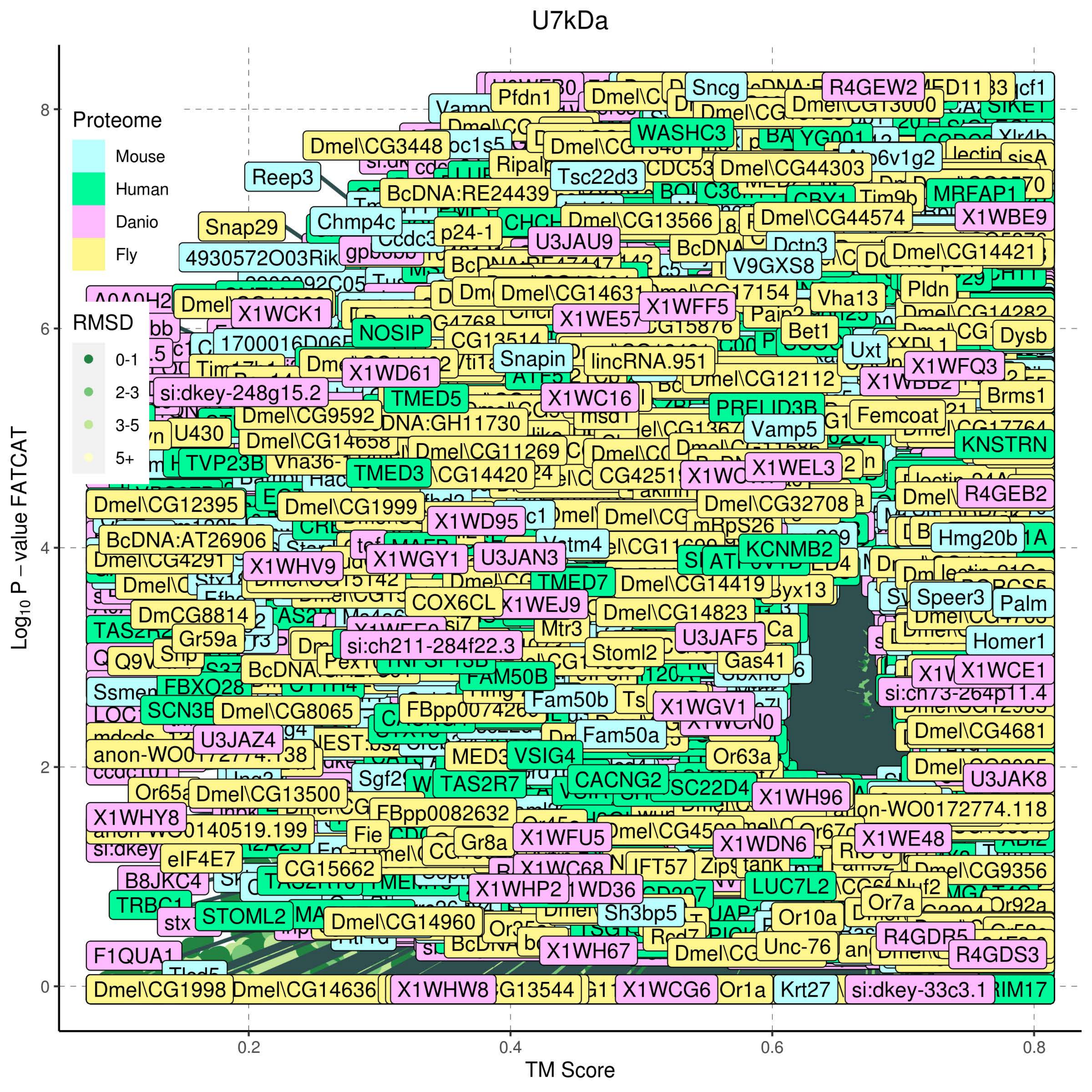
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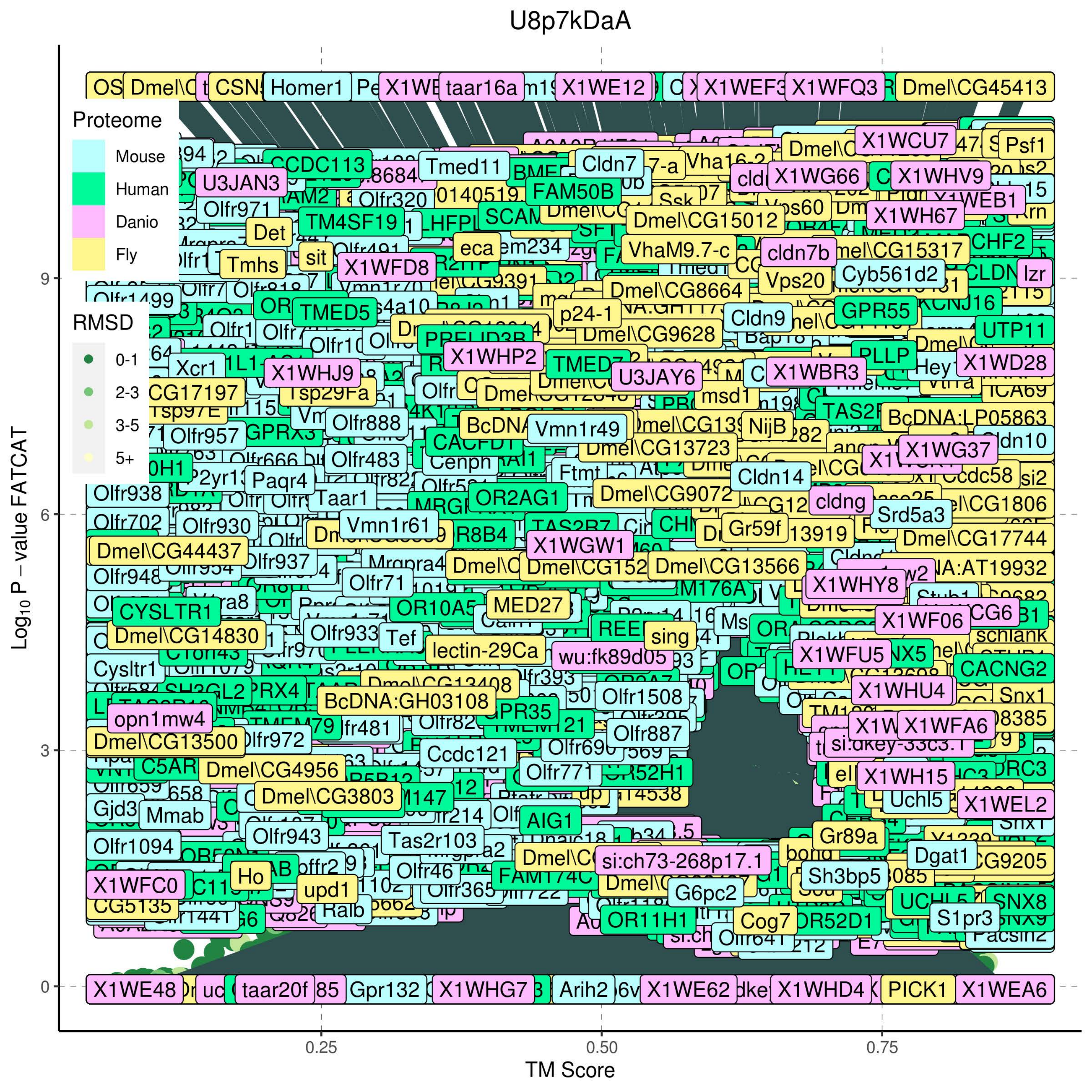
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5+
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>MF001305.1:c159640-158771 NY 014 poxvirus strain 2013 complete genome
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RDAITELTDIANEIDNT---------------DVKLITTFIISSIYKITRFQSFLVELAM-YHKVLDKIQHI---
MEYIIDNHSRIDNNGFTPYSDNDPDFNQVIA--
CIIYNLLRSSGMEINYSKYKAWWNPRHDYVDTFGLLYVIFTILSIIDDNX-------------------------------------------
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>KU749309.1:150174-150722 Raccoonpox virus strain 85A complete genome
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-------------------------------------------------------------------------------------------------------------------------------
MLNDYIGQIYIRCRAILSIPDDYKHKFIKSLTHLI--RYNGRTYNRCT------------------------
RDAITELSDIANNIGNN---------------DVKIITTFIISSIYKITRFQSFLVELAM-YHKVLDKIQHI---
MEYIIENHSHNDTNGFTPYSTDDTNFNQVIA--
CIIYNLLKSSGMEINYSECKAWWNPRHDYVDTFGLLYIIVTILLIIDGDQYNFYNKLEKNKX---------------------------
----------------------------------------------------------------------------------
>MF001304.1:c165763-165224 Murmansk poxvirus strain LEIV-11411 complete genome
--------------------------------------------------------------------------------------------------------------------------M--
LSVPSQYKDLLQEYYDIITSVPDEYRDIFVEYLIYLI--EYDGRISNKRT------------------------
RDIKKELINIVGKVSDKT--------------RLMNFISFITESICRLTRFQSFLLELAS-YHNVLDEVQEI---
MGDIIENHCRMEIIGFTTYDINSIVL-------SIIYNMLKTSGMRVDYDTSKAWWNP--
EYRDMFGSLYMIVTTLTILKNIX----------------------------------------------------------------------------------------------------------
--------------
>MF001305.1:c164808-164269 NY 014 poxvirus strain 2013 complete genome
----------------------------------------------------------------------------------------------------------------------------
MLSVPSKYKDLLQEYYDIITSVPDEYRDIFVQYLIYLI--EYDGRISN---------------------------
KRTRDIKKELINIVGKVSDKT-----------RLMNFISFITESICRLTRFQSFLLELAS-YHDVLDEVQEI---
MGDIIKNHCRMEIIGFTAYDINSIVL-------SIIYNMLKTSGMRVDYDTSKVWWNP--
EYSDMFGSLYMIVTTLTILKNIX----------------------------------------------------------------------------------------------------------
--------------
>NP 051846.1 m132L Myxoma virus
-------------------------------------------------------------------------------------------------------------MGNLLYCCFTV--
EKTVPSIQRYVNGQVNLDNFLARHRKRSILLYLLKVI--RDDKLLNEVC----------------------------
RVKKKYSVYLYGCKNPNA-----------EVVNFINYILVYLNALSCTQKRLLYIII-AENMISSFIGY---
INTVFTSNAVKFKDSE-----------------RCIEELFIETGLYI---SPQGSYKKHTEVMEELIYLYILARLFKQLL-----------
------------------------------------------------------------------------------------------------------------------
>NP 052021.1 gp132L Rabbit fibroma virus
-------------------------------------------------------------------------------------------------------------MGNLLYCCFVV--
DVTTPSIQRYVNEQVNLDKFLSRRKKKSILLYLLKVI--RNDKLLTEVYC------------------------------
SKKYSELYGCKNPNT-----------EVVNFINYILIYLNALSYTQKRLLYIII-AENMITSFIEY---
INAVFTSSSTVKFKDSE----------------RCIEELFIETGLYISSSQGYNKQHT--EVMEELIYLYILAKLFKQLL---------
--------------------------------------------------------------------------------------------------------------------
>YP 009408097.1 Immunoprevalent protein Eptesipox virus
-----------------------------------------------------------------------------------------MGNSTSVSKSCNNAVTHVSANSIRQHIL--
FNNFETLHKDIQSKIDLVNTFTPQTKNLIFRNLLIVI--TNSYHLQNLLDALE----------------
QLEPMYVTDAYSEAILNEIGLCDKGIPNL--------SSIHFMIYLVSGLTKLTTKQSKILMEIVTDAKIFCHHVNV---
LEYIIKKNVEKLETVTSTLLEKYTKL-------PLEVTLFKESGLKIQ--GNTYIWDP--EHKKSICNLYTVIKIMSYIM----
---------------------------------------------------------------------------------------------------------------------------
```

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>ref|NP 835465.2| chromosome 17 organism Homo sapiens gcode 1 chromosome 17 map
17q21.1 gasdermin-A Homo sapiens
---------------------------------------------------------------------------------------------------GDV--
HEGFRTLKEEVQRETQQVEKLSRVGQSSLLSSLSKLL--GKKKELQDLELALEG----------------ALD--
KGHEVTLEALPKDVLLSK--------------EAVGAILYFVGALTELSEAQQKLLVKSM-EKKILPVQLKL---
VESTMEQNFLLDKEGVFPLQPELLSSLGDEEL-TLTEALVGLSGLEVQRSGPQYMWDP--
DTLPRLCALYAGLSLLQQLTKAS----------------------------------------------------------------------------------------
----------------
>ref|XP 015154998.2| location chromosome chromosome 27 completeness complete organism
Gallus gallus isolate bGalGal1 gcode 1 chromosome 27 sex female tissue type blood country
USA: Fayetteville lat ls
--------------------------------------------------------------------------------------------------DGFA--
HTEVEALEEEVKEKCGILCQLAGELNAIVLKTIKAVM--RDRNLLEELSGKMEAVLD-DPDNCE------
LTTQSPDLEVLLSTLKGSPRCDLL-------------SLTEAISYTLDAFSELTEDQLLLLLESL-EVEIVPQQLKL---
VRSILEQSAELGAA------AGLLSSFSEQQQQLTTAVLELSGVELQGSGAAVCTE---
ESFPSLSALYAALHALHCLVGAGGRSARAD---------------------------------------------------------------------------
----------------------
>ref|XP 024836266.1| location chromosome chromosome 19 completeness complete organism
Bos taurus isolate L1 Dominette 01449 registration number 42190680 breed Hereford gcode 1
chromosome 19 sex fem...
---------------------------------------------------------------------------------------------------GAV--
HEDFRTLKEEVQRETQEVEKLSPEGKSSLLSSLSKLL--GKKKELQDLELTLEE----------------ALG--
KGHEETLEALPKNVLLSK--------------GAMDAILYFLGALAELSEAQQKLLVKSM-EKKILPVQLKL---
VESTMEQNFLQDKEGVFPLRPELLSSLGEEEL-TLTEALVGLSGLEVQRSGPQYTWDP--
DTLPRLCALYAGLSLLRLLTKAS------------------------------------------------------------------------------------------
--------------
>ref|XP 014975037.1| location chromosome chromosome 16 completeness complete organism
Macaca mulatta isolate AG07107 bio material Coriell:AG07107 gcode 1 chromosome 16 sex
female tissue type fibroblaa
---------------------------------------------------------------------------------------------------GDV--
HEGFGTLKEEVQRETQQVERLSQAGQSSLLSSLSKLL--GKKKELQDLELALEG----------------ALD--
KGHEVTLEALPKDVLLSK--------------EAVGAILYFVGALTELSEVQQKLLVKSM-EKKILPVQLKL---
VESTMEQNFLQDKEGVFPLHPELLSSLGEEEL-TLTEALVGLSGLEVQRSGPQYMWDP--
DTLPRLCALYAGLSLLQQLTKAS----------------------------------------------------------------------------------------
----------------
>ref|XP 001171222.1| location chromosome chromosome 17 completeness complete organism
Pan troglodytes isolate Yerkes chimp pedigree *C0471 (Clint) gcode 1 chromosome 17 sex male
tissue type blood devs
---------------------------------------------------------------------------------------------------GDV--
HEGFRTLKEEVQRETQQVEKLSRVGQSSLLSSLSKLL--GKKKELQDLELALEG----------------ALD--
KGHEVTLEALPKDVLLSK--------------EAMGAILYFVGALTELSEAQQKLLVKSM-EKKILPVQLKL---
VESTMEQNFLLDKEGVFPLQPELLSSLGDEEL-TLTEALVGLSGLEVQRSGPQYMWDP--
DTLPRLCALYAGLSLLQQLTKAS----------------------------------------------------------------------------------------
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>ref|XP 024429158.1| chromosome Unknown completeness complete organism Desmodus
rotundus isolate DRU21DN04 gcode 1 chromosome Unknown sex male tissue type muscle/skin
sample dev stage adult country Us
--------------------------------------------------------------------------------------------------------------------GEV--
HQDFRMLKEEIQRETQEVEKLSRMGQSSLLTSLSKLL--GKKKELQDLELTLEG----------------ALD--
KGHEVALEALPKDVLLSK--------------EVVGAILYFLGALTELSEAQQKLLVKSM-EKKILPVQLKL---
VESIMEQNFLLDKEGVFPLQPNLLSCLGEEEL-TFTEALVGLSGLEVQRSGPQYMWDP--
DTLPDLCALYAGLSFLQLLTKAS--------------------------------------------------------------------------------------------------------
---------------
>ref|XP 016020091.2| chromosome Unknown completeness complete organism Rousettus
aegyptiacus isolate mRouAeg1 gcode 1 chromosome Unknown sex male tissue type muscle dev
stage adult country USA: Berkes
--------------------------------------------------------------------------------------------------------------------GEV--
HEDFRTLKEEIQRETQEVEKLSHLGQSSLLTSLSKLL--GNRKELQDLELTLEG----------------ALG--
KGHEVTLEALPKDVLLSK--------------EALGAILYFLGALTELSEVQQKLLVKSM-EKKILPVQLKL---
VESTMEQNFLQDKEGVFPLQPDLLSSLGEEDL-TLTEALVGLSGLEVQRSGPQYTWDP--
DTLPHLCALYAGLSFLQLLTKAS--------------------------------------------------------------------------------------------------------
---------------
>ref|XP 006924750.1| chromosome Unknown completeness complete organism Pteropus
alecto gcode 1 chromosome Unknown sex male tissue type kidney country Australia: Anglican
Church Grammar School East Bro
--------------------------------------------------------------------------------------------------------------------GEV--
HEDFRTLKEEIQRETQEVEKLSHVGRSSLLTSLSKLL--GNRKELQDLELTLEG----------------ALG--
KGHEVTLEALPKDVLLSK--------------EALGAILYFLGALTELSEVQQKLLVKSM-EKKILPVQLKL---
VESTMEQNFLQDKESVFPLQPDLLSSLGEEDL-TLTEALVGLSGLEVQRSGPQYTWDP--
DTLPCLCALYAGLSLLQLLTKAS--------------------------------------------------------------------------------------------------------
---------------
>ref|XP 035935879.1| chromosome Unknown completeness complete organism Halichoerus
grypus isolate 241Hg ecotype Northwest Atlantic gcode 1 chromosome Unknown sex male
tissue type blood dev stage molts
--------------------------------------------------------------------------------------------------------------------KEE--
HGDFKTLKEEVQREIQEVKKLSRVGQSSLLTSLSKLL--GKKKELQDLELMLEG----------------ALD--
KGHEVTPEALPKDVLVSK--------------EAMGGILYFLGALIELSEAQQKLLIKSV-EKKILPMQLKL---
VESTMEQSFLQDKDGVFPLQPDLLSSLGEEEL-TLTEALVGLSGLEVQRSGPQYTWDP--
DTLPRLCALYAGLSLLQLLTKAS--------------------------------------------------------------------------------------------------------
---------------
>ref|XP 004633937.1| chromosome Unknown completeness complete organism Octodon
degus isolate 3935 gcode 1 chromosome Unknown sex female gasdermin-A Octodon degus
--------------------------------------------------------------------------------------------------------------------GEV--
HEDFKTLKEEVRRETQEVDKLSRAGQGSLLSSLSNLL--GKKKELQDLELTLEG----------------ALD--
KGHEVTLEALPKDVLLSK--------------ESMGAILYFLGALTVLSEAQQKLLVKSV-EKKLLPVQLKL---
VESTLEQNFLQDKEGVFPLRPDLLSSLGEEEL-TLTEALVGLSGLEVQRSGPQYTWDP--
DTLPRLCALYASLSLLQLLARSP--------------------------------------------------------------------------------------------------------
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>ref|XP 029428328.1| location chromosome chromosome 12 completeness complete organism
Rhinatrema bivittatum gcode 1 chromosome 12 gasdermin-A Rhinatrema bivittatum
--------------------------------------------------------------------------------------------DYLRILENF----
QEGFPAVMAQIEKECVEFTLLSPEVAEQFLAAFLLLI--KDPKTSADVESRLEQSLY-C-SARESKA---HPE--
PSIARLLGYLGLSSRPVVI-------------PLVRAVLFFLDAVSELDEDGTSLLVESV-ERQDTGQQLKR---
VQKVLEEELFSVRQGSL-------------------------AGDEAAGGVSPEGWSP--AVQSCAMALYAALYALHVLSSC--
-------------------------------------------------------------------------------------------------------
>XP 032891479.1 gasdermin-A Amblyraja radiata
--------------------------------------------------------------------------------------------------SLFC--
QDTANVNGDEVFEICCELQCLDKGLKQRLLGLVCQII--EDSELLSILSDVLCEA-C-A-GTDYTLSELEKLD--
KKRRECGENLLAIWSEDQLKNAVED-------NLLKAVSILFAALEDLPPTTLPVLIQSL-KMQILPQQLTL---
VTGILKDLDHSQVDQALKVETE---SFTEDAF-GITAEMLTDVGLHLERDSVQKTREP--S----
LHELSVALYCLNALSSN----------------------------------------------------------------------------------------------------
------
>sp|Q5Y4Y6|GSDA3 MOUSE Gasdermin-A3 OS Mus musculus OX 10090 GN Gsdma3 PE 1 SV 1
-----------------------------------------------------------------------------------------------------GEM--
HEDFKTLKEEVQRETQEVEKLSPVGRSSLLTSLSHLL--GKKKELQDLEQKLEG----------------ALD--
KGQKVTLEALPKDVLLSK--------------DAMDAILYFLGALTELTEEQLKILVKSL-EKKILPVQLKL---
VESTLEQNFLQDKEGVFPLQPDLLSSLGEEEL-TLTEALVGLSGLEVQRSGPQYAWDP--
DTRHNLCALYAGLSLLHLLSRKSNALTYCALS---------------------------------------------------------------------------
---------------------
>sp|Q9EST1|GSDMA MOUSE Gasdermin-A OS Mus musculus OX 10090 GN Gsdma PE 2 SV 1
-----------------------------------------------------------------------------------------------------GEM--
HEDFKTLKEEVQRETQEVEKLSPVGRSSLLTSLSHLL--GKKKELQDLEQTLEG----------------ALD--
KGHEVTLEALPKDVLLSK--------------DAMDAILYFLGALTVLSEAQQKLLVKSL-EKKILPVQLKL---
VESTMEKNFLQDKEGVFPLQPDLLSSLGEEEL-ILTEALVGLSGLEVQRSGPQYTWDP--
DTLPHLCALYAGLSLLQLLSKNS------------------------------------------------------------------------------------------
---------------
>sp|Q32M21|GSDA2 MOUSE Gasdermin-A2 OS Mus musculus OX 10090 GN Gsdma2 PE 2 SV 1
-----------------------------------------------------------------------------------------------------GEM--
HEDFKTLKKEVQQETQEVEKLSPVGRSSLLTSLSHLL--GKKKELQDLEQMLEG----------------ALD--
KGHEVTLEALPKDVLLLK--------------DAMDAILYFLGALTELSEEQLKILVKSL-ENKVLPVQLKL---
VESILEQNFLQDKEDVFPLRPDLLSSLGEEDQ-ILTEALVGLSGLEVQRSGPQYTWNP--
DTCHNLCALYAGLSLLHLLSRDS-----------------------------------------------------------------------------------------
----------------
>ref|NP 001159430.1| chromosome 17 organism Homo sapiens gcode 1 chromosome 17 map
17q21.1 gasdermin-B isoform 3 Homo sapiens
------------------------------------------------------------------------------------------------------------------------------
-----DVLNSLAKCL--GKEDIRQDLEQRVSEVLI-S-G---------ELHMEDPDKPLLSSLFNAAGVLVE-------------
ARAKAILDFLDALLELSEEQQ-FVAEAL-EKGTLPLLKDQ---VKSVMEQNWD-----------------------------------
ELASSPPDMDYDP---EARILCALYVVVSILLELAEGPTSVSS---------------------------------------------------------
-----------------------------------------
>ref|NP 001231146.1| chromosome 19 organism Bos taurus gcode 1 chromosome 19 map 19
gasdermin-B Bos taurus
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-----EALNCFTKCL--SSEEELQDLEQRVSEVQC-S-G---------ELQMNSPANSLISSLFNAAGALIE------------
ARAETIWDVLDALMELSEYRQ-FVAEVL-DKGELRPVKDK---VESILEEN------------------------
RCEGPLDVSCD---------------PEARTLCALYVVVSILLQLSEKPTSVSS----------------------------------------------
------------------------------------------------------
>ref|XP 009430521.1| location chromosome chromosome 17 completeness complete organism
Pan troglodytes isolate Yerkes chimp pedigree *C0471 (Clint) gcode 1 chromosome 17 sex male
tissue type blood devs
---------------------------------------------------------------------------------------------------------------------------------
-----DVLNSLAKCL--GKEEIRQDLEQRVSEVLISR-----------ELHMEDPDKPLLSSLFNAAGVLVE------------
VRAKAILDFLDALLELSEEQQ-FVAEAL-EKGTLPLLKDQ---VKSVMEQNWD---------------------------------
ELASSPPDMDCDP---EARILCALYVVVSVLLELAEGPTSVSS-----------------------------------------------------
-------------------------------------------
>ref|XP 023358160.1| location chromosome chromosome 4 completeness complete organism
Sarcophilus harrisii gcode 1 chromosome 4 cell line 91H gasdermin-B Sarcophilus harrisii
---------------------------------------------------------------------------------------------------------------------------------
-----AVLDLLTRLL---QDEALGEMEGKVAMALF-T-E---------ELS--DPENPLLSVLFDASGSSMQ------------
NQAEGILDFLEALTELKEEQQKILPKVV-EKGLLSETMKL---VEDLLRQSETFSLKAD----------------
SITHTLVGICDPEGKLEQP-VTWDS--ETCHSLCALYTVLSVLMLLAQGSVSVP------------------------------------
---------------------------------------------------------------
>ref|XP 024897515.1| chromosome Unknown completeness complete organism Pteropus
alecto gcode 1 chromosome Unknown sex male tissue type kidney country Australia: Anglican
Church Grammar School East Bro
---------------------------------------------------------------------------------------------------------------------------------
-----DALSCLTKCL--TKDEQLQDLEQRMSEVLISG-----------ELQMDSPAGPLISSLFNAAGILVE------------
TRTEAIMDFLDAVMELFE-EKELVGEAL-EKGTLPLLKEQ---VESVLDQNGGEQPE------------------------------
-------CVGCDP---EAQILHALYVAVSILLQLSEKPASASS------------------------------------------------------
-------------------------------------
>ref|XP 036078993.1| chromosome Unknown completeness complete organism Rousettus
aegyptiacus isolate mRouAeg1 gcode 1 chromosome Unknown sex male tissue type muscle dev
stage adult country USA: Berkes
---------------------------------------------------------------------------------------------------------------------------------
-----DALSCLSKCL--TKDEQLQDLEQRVSEILISG-----------ELQMDSPAGLLINSLFNASGILVE------------
TRTEAIMDFLDALMELSE-EKELVAEAL-EKGTLPLLKE----------QNCGEQPE-----------------------------------
YVGWDP---EAQVLRTIYAAVSILLLLSEKPASVSC----------------------------------------------------------------
-----------------------------
>ref|XP 024429114.1| chromosome Unknown completeness complete organism Desmodus
rotundus isolate DRU21DN04 gcode 1 chromosome Unknown sex male tissue type muscle/skin
sample dev stage adult country Us
---------------------------------------------------------------------------------------------------------------------------------
-----NVLSCLTKCL--TSDGELQALEERVSEVLV-S-E---------ELQVEGPADPLISSLFNAAGILVE------------
ACIEAILDFLDALKELSEEKE-LVAETL-EKGTLPLLKDQSGGLKSVLEQEWGEQPRG------------------------------
-------VGRDP---EAQTVCTLYLVVSILLQLSEKPAPASSC-------------------------------------------------------
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>ref|XP 014975035.1| location chromosome chromosome 16 completeness complete organism
Macaca mulatta isolate AG07107 bio material Coriell:AG07107 gcode 1 chromosome 16 sex
female tissue type fibroblaa
-------------------------------------------------------------------------------------------------------------------------------
-----DVLNFLTKCL--GREELWQDLEQKISEVLI-F-G---------ELQMEDPVNPLLSSLFNAAGILVG-------------
ARAEAILDFLDALLELSEEQH-LVAEAL-EKGTLPLLKDQ---VKPIMEQNWD-----------------------------------
ELASSPHDMDCDP---EARIPCALYVVVSVLLELAEGTTSVSS--------------------------------------------------------
-------------------------------------------
>ref|XP 035935913.1| chromosome Unknown completeness complete organism Halichoerus
grypus isolate 241Hg ecotype Northwest Atlantic gcode 1 chromosome Unknown sex male
tissue type blood dev stage molts
---------------------------------------------------------------------------------------------------------------
DVLSCLRGQLPLSAKVFEVLISGSRHLEMEGLVGLL----------------------------------------------ISSLFNAAGFLVK-
------------AHTESILDVLDAL--ITSEEQHLVAEAL-EKGTLPLLKDQ---VRSVLEQNWSEQPH----------------------
------------------DVGWDP---DAXLLCALYVALSLLLQLGEKPTSVPS----------------------------------------------------
---------------------------------------------------
>ref|NP 113603.1| chromosome 8 organism Homo sapiens gcode 1 chromosome 8 map
8q24.21 gasdermin-C Homo sapiens
-----------------------------------------------
LLPSFHTISPTLFNASSNDMKLKPELFLTQQFLSGHLPKYEQVHILPVG-RIEEPF----
WQNFKHLQEEVFQKIKTLAQLSKDVQDVMFYSILAML--RDRGALQDLMNMLELDSS-G-----------HLD--
GPGGAILKKLQQDSNHAWF-------------NPKDPILYLLEAIMVLSDFQHDLLACSM-EKRILLQQQEL---
VRSILEPNFRYPWSIPFTLKPELLAPLQSEGL-AITYGLLEECGLRMELDNPRSTWDV--
EAKMPLSALYGTLSLLQQLAEA---------------------------------------------------------------------------------------------
----------------
>ref|XP 028708741.1| location chromosome chromosome 8 completeness complete organism
Macaca mulatta isolate AG07107 bio material Coriell:AG07107 gcode 1 chromosome 8 sex
female tissue type fibroblasta
-----------------------------------------------
WLPSFHTISPTLFNASPKDMKLKPELFLKPKFLRGHLPKYEQVCILPVG-RIEEPF----
WQNFKHLQEEVFQKIKTLAQLSKDVQDVVFYSILAML--GDRGALQDLMDMLELDSS-G-----------HLD--
GPGGAILKKLQQYSNRAWF-------------NPKDPILYLLEAIMVLNDIQHDLLACSV-EMRILLQQQEL---
VRSILEPNFRYPWSIPFTLKPELLAPLQSEGL-AITYGLLEECGLRMELDNPRSTWDL--
EAKIPLSALYGTLSLLQQLAEA-----------------------------------------------------------------------------------------------
--------------
>ref|NP 001039469.1| chromosome 14 organism Bos taurus breed L1 Hereford gcode 1
chromosome 14 map 14 gasdermin-C Bos taurus
-----------------------------------------------------------------
ILSISDDNKRKAFFVGKVQRQSAMGTKRRPILPIGRIQEPI--
SRDFKSLQNEVSREIEAVAELPRDIRDALFHTILAKL--KDQGALQDLTDMLDGNLW-------------------
DHTGSFLSEMREDSRNVWL-------------ESRPCVIYLLEALLVLSDIQHELLAWSM-EKRILPQQREL---
VESILEPNFRYPWNIPFTLDPKLLASLQDEGL-AVTFGLLQECGLRVAPDNPKGTWDL--
EAKKPLSALYGSLSVLQQLAEA----------------------------------------------------------------------------------------------
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>ref|XP 031803207.1| location chromosome chromosome 1 completeness complete organism
Sarcophilus harrisii gcode 1 chromosome 1 cell line 91H gasdermin-C Sarcophilus harrisii
--------------------------------------------------
HTEIGLGSMRGMEEKLEWKDYPKLSLFLETIEETQQGFGWKQQDRNNCQR--
VRDFQRLLEEVTFQKKDLVRMPGKQRTTLLCALHDLL--GNRTALQDLEDKLLHVLD-SGIWG-------KME--
GPGNTILSNLQDSSDSPVN-------------GYITGFLYLLEALAALSDNQHDLLAQSL-EKKILSQQLKL---
VKSILETNFNQFHS-TFILPPEILSLIDEEL--NLSLELVEDCGLQLQRTEQMLILDP--
EGKNPLCALYGALSCLLSLSED-------------------------------------------------------------------------------------
--------------
>ref|XP 036088919.1| chromosome Unknown completeness complete organism Rousettus
aegyptiacus isolate mRouAeg1 gcode 1 chromosome Unknown sex male tissue type muscle dev
stage adult country USA: Berkes
-----------------------------------------------------------------FRLQLQSFTGGREIQPKSGECEIQILSGRAQRSC-
-WLDFGRLQEEVS-WYVKKAQLLEDMGAVVFSSILAML--GDWEALEGLEDKLEQKPL-G-----------HLD--
GPGGVILNALRESSSYQWF-------------NSEDSILYLLEAINGLSDLQHDLLAWSM-EKKVLLQQRDL---
VRSILEPNFKYPWNIPFTMKPELLAPLRGEAL-AITYGLLEECGLTMEPNSPRSTWDL--
EAKKPLSALYAALSVLQQLAEA-------------------------------------------------------------------------------------
--------------
>ref|XP 024427836.1| chromosome Unknown completeness complete organism Desmodus
rotundus isolate DRU21DN04 gcode 1 chromosome Unknown sex male tissue type muscle/skin
sample dev stage adult country Us
----------------------------------------------------------------------------------------------------
DFKRLHEEVSKRVIAAAELSKDIKGVVFSNILAML--GDRGALQDLVHMLEQEPLKG-----------HLN--
GPGGTILNELQKDSSFAWN-------------GSQYLILYLLEAMMVLSDVQLCLLAPSM-EKKILSQQRDL---
VRSILEPNFKYPWSIPFTLKPELLAPLQGEGL-AITYGLLDECGLKMELHSPRSTWDL--
EAKKPLSALYGTLSVLQQLAEA-------------------------------------------------------------------------------------
--------------
>ref|XP 019678683.1| location chromosome chromosome F2 completeness complete organism
Felis catus isolate Cinnamon breed Abyssinian gcode 1 chromosome F2 sex female gasdermin-C
Felis catus
------------------------------------------------------------------
AVNNGPLYTMSVSDVRKPLDLVLHSPGRIQRVL--WQDFKQLHEEIFQEMEALAQLSKDTQDSIFHTILNML--
GNREALQDLTDTLDGSPL-D-----------LLD--DFGGTILNEMQPDTRDLWI------------
QARFHIIYLLEVIMVLSDTQHDLLAQSM-EKRILLQQQKL---VRSILEPNFKYCWDIPFTLKPELLAPLQGEDL-
AITYGLLEECGLKMELNSPRSTWDL--ETKQPLSALYGTLSLLQQLTGSPERPGPTPVYAESVPDELGGV---------
-----------------------------------------------------------------------
>ref|XP 001153860.1| location chromosome chromosome 8 completeness complete organism
Pan troglodytes isolate Yerkes chimp pedigree *C0471 (Clint) gcode 1 chromosome 8 sex male
tissue type blood dev ss
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LLPSFHTISPTLFNASSNDMKLKPELFLTQQFLSGHLPKYEQVHILPVG-RIEERF----
WQNFKHLQEEVFQKIKTLAQLSKDVQNVVFYSILAML--RDRGALQDLMNMLELDSS-G-----------HLD--
GPGGAILKKLQQDSNHAWF-------------NPKDPILYLLEAIMVLSDFQHDLLACSV-EKRILLQQQEL---
VRSILEPNFRYPWSIPFTLKPELLAPLQSEGL-AITYGLLEECGLRMELDNPRSTWDV--
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EAKMPLSALYGTLSLLQQLAEA-----------------------------------------------------------------------------------------
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>ref|XP 021073018.1| location chromosome chromosome 17 completeness complete organism
Mus pahari gcode 1 chromosome 17 sex female tissue type tail gasdermin-C Mus pahari
-----------------------------------------------------------------RPMYLSGHFEILRHHEEIIRIGSRIEYISPIGTIEEPT--
HLDFQCLQNEVSQKTMLLAELSKDVQEVVFSSFLHMLCEGDSEVLYDLMKMLELNQL-E-----------HMD--
GPGGKILEELQKDRSPSWI-------------DLKDLILNLLQALMVLSNTQLSLLAQSV-EMRLLLQQQEL---
VKSILQPNYKYPWHIPFTLQPQLLAPLQGEGL-AITYELLEECGLKMELNNPRSTWHL--
EVKMPLSALYASLSLLQQLSEA------------------------------------------------------------------------------------------
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>ref|NP 081236.1| chromosome 15 organism Mus musculus strain C57BL/6 gcode 1
chromosome 15 map 15 gasdermin-D Mus musculus
--------------------------------------------------------------------------------------------DG-IDEEELIE--
AADFQGLYAEVKACSSELESLEMELRQQILVNIGKIL--QDQPSMEALEASLGQGLC-SGGQVE------PLD--
GPAGCILECLVLDSGELVP-------------ELAAPIFYLLGALAVLSETQQQLLAKAL-ETTVLSKQLEL---
VKHVLEQSTPWQEQSSVSLPTVLLGDCWDEK--NPTWVLLEECGLRLQVESPQVHWEP--
TSLIPTSALYASLFLLSSLGQKPC-----------------------------------------------------------------------------------------
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>ref|NP 079012.3| chromosome 8 organism Homo sapiens gcode 1 chromosome 8 map 8q24.3
gasdermin-D Homo sapiens
--------------------------------------------------------------------------------------------DGVPAEGAF----
TEDFQGLRAEVETISKELELLDRELCQLLLEGLEGVL--RDQLALRALEEALEQGQS-L-GPVE------PLD--
GPAGAVLECLVLSSGMLVP-------------ELAIPVVYLLGALTMLSETQHKLLAEAL-ESQTLLGPLEL---
VGSLLEQSAPWQERSTMSLPPGLLGNSWGEG--APAWVLLDECGLELGEDTPHVCWEP--
QAQGRMCALYASLALLSGLSQEPH------------------------------------------------------------------------------------
-------------------
>ref|NP 001039625.1| chromosome 14 organism Bos taurus breed Hereford gcode 1
chromosome 14 map 14 gasdermin-D Bos taurus
--------------------------------------------------------------------------------------------DG-STEHWLAT--
TDDYQGLRAEVKAWAMGLEGLSKGLCGQLLGGLGQVL--RDEPALQALEDSLEQGLC-S-GPVE------PRD--
GPVGAILESLVLPSGQLET-------------ELAGPVFYLLQALAVLSEAQHVLLAEVL-EMGALSGTFWL---
VESLVEQSSPWQEHRAVSLPPERLGDSWGSE--APGWALLEACGLEPQVGTPQVCWEP--
GARGCACALYACLALLLRLSQLC----------------------------------------------------------------------------------------
----------------
>ref|XP 015001615.2| location chromosome chromosome 8 completeness complete organism
Macaca mulatta isolate AG07107 bio material Coriell:AG07107 gcode 1 chromosome 8 sex
female tissue type fibroblasta
--------------------------------------------------------------------------------------------DGVPAEGTF----
TEDFQGLREEVEAISKELELLDRELCQLLLEGLEGVL--RDQLALRALEEALEQGLS-L-GPVE------SLD--
GPAGAVLECLVLESRMLVP-------------ELAVPVVYLLGALTMLSETQHKLLAEAL-ESQTLLGPLEL---
VGSLLEQSAPWQERSTVSLPPGLLGSSWGEG--APAWVLLEECGLELGEDTPHVCWEP--
QAQGRMCALYASLALLSGLSQEPH------------------------------------------------------------------------------------
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>ref|XP 006913014.1| chromosome Unknown completeness complete organism Pteropus alecto gcode 1 chromosome Unknown sex male tissue type kidney country Australia: Anglican Church Grammar School East Bro
--------------------------------------------------------------------------------------------DG-PTENCLVP--
TEDFQGLQVEVKAWASALENGSATLCGQLLGGLGQVL--RDEPALQALEESLEQGLC-S-GRAE------PLH--
GPAGAVLECLVLHCRTLVE-------------ELARPVFYLLEALAALSETQHMLLAEVL-ETGALPESVEL---
VETLLEQSTPWQEREAISLSPRLLGSNWGSE--APAWVLLEECGLKLQVGAPQVCWEP--
EAQGPTCALYACLALLLKLSQLR----------------------------------------------------------------------------------------
----------------
>ref|XP 036089037.1| chromosome Unknown completeness complete organism Rousettus aegyptiacus isolate mRouAeg1 gcode 1 chromosome Unknown sex male tissue type muscle dev stage adult country USA: Berkes
--------------------------------------------------------------------------------------------DG-PAEHWLVP--
TEDFQGLQMEVRAWARALEDASATLCGQLLGALGQVL--WDEPALQALEESLEQGLC-S-GRAE------PLH--
GPAGAVLECLVLRCGTLVE-------------ELAGPVFYLLGALAALSETQHVLLAKAL-ETGALPEWVKL---
VETLLEQSTPWQEREAISLPSELLESSWGSE--APAWVLLEECGLKLQVGAPQVCWEP--
EAQGPTCALYACLALLLRLSQLR----------------------------------------------------------------------------------------
----------------
>ref|XP 024428237.1| chromosome Unknown completeness complete organism Desmodus rotundus isolate DRU21DN04 gcode 1 chromosome Unknown sex male tissue type muscle/skin sample dev stage adult country Us
--------------------------------------------------------------------------------------------DG-LDEDQVVP--
TEDFQGLQAEVQVWAGPLESLSKTLCEQLLRGLAQVL--RDELALQTLEGSLEQGLC-C-GRAE------PLQ--
GPAGHVLECLVLPCRTLVN-------------ELAGPVTYLLGALAALSEAQRMLLAEVL-EASALPEPFKL---
VEKLLEQSSPWQECRALSLPPGLLGGSWGPE--VPAWILLEACGLELQVDAPQVSWKP--
EAQGCTCALYACLALLSKLSQLC----------------------------------------------------------------------------------------
----------------
>ref|XP 009454389.2| location chromosome chromosome 8 completeness complete organism Pan troglodytes isolate Yerkes chimp pedigree *C0471 (Clint) gcode 1 chromosome 8 sex male tissue type blood dev ss
--------------------------------------------------------------------------------------------DGVPAEGAF----
TEDFQGLRVEVETISKELERLDRELCQLLLKGLEGVL--RDQLALRALEEALEQGQS-L-GPVE------PLD--
GPAGAVLECLVFSSGVLVL-------------ELAIPVVYLLGALTMLSETQHKLLAEAL-ESQTLLGPLEL---
VGSLLEQSAPWQERSTMSLPPGLLGSSWGEG--APAWVLLDECGLELGEDTPHVCWEP--
QAQGRMCALYASLALLSGLSQEPH------------------------------------------------------------------------------------
-------------------
>ref|XP 023104116.1| location chromosome chromosome F2 completeness complete organism Felis catus isolate Cinnamon breed Abyssinian gcode 1 chromosome F2 sex female gasdermin-D Felis catus
--------------------------------------------------------------------------------------------DG-DIEDQMPV--
TEDFQGLKVEVSVHADGLKGLSGELCGQILAGLMKVL--REEPALESLQEELEQGLC-C-GWVA------SPD--
APGGAILECLVQSSGKVEE-------------ELARPILYLVQALTELNETQRVLLAEAL-ETGDLSGQSRL---
VQSVLEQSSPWKEHRAVSLPQELLGSSWDSE--APAWVLLEECGLELRVDVPQVHWQP--
```

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DAQGRTSALYACLVLLPHLSQDQLNETQRVLLAEALETGDLSGQSRLVQSVLEQSSPWKEHRAVSLPQELLGS
SWDSEAPAWVLLEECGLELRVDVPQVHWQPDAQGRTSALYACLVLLPHLSQDRA
>ref|NP 001120925.1| chromosome 7 organism Homo sapiens gcode 1 chromosome 7 map
7p15.3 gasdermin-E isoform a Homo sapiens
---------------------------------------------------------------------------------------DAAHGISSQDGP--
LSVLKQATLLLERNFHPFAELPEPQQTALSDIFQAVL--FDDELLMVLEPVCDDLVS-GLSPTVAVLG--ELK--
PRQQQDLVAFLQLVGCSLQGGCPGPED-AGSKQLFMTAYFLVSALAEMPDSAAALLGTCC-KLQIIPTLCHL--
-LRALSDDGVSDLED------PTLTPLKDTERF-
GIVQRLFASADISLERLKSSVKAVILKDSKVFPLLLCITLNGLCALGREHS------------------------------------------
--------------------------------------------------------
>ref|NP 061239.1| chromosome 6 organism Mus musculus strain C57BL/6 gcode 1
chromosome 6 map 6 gasdermin-E precursor Mus musculus
---------------------------------------------------------------------------------------DGGQGISSQDGP--
LRVVKQATLHLERSFHPFAVLPAQQQRALFCVLQKIL--FDEELLRALEQVCDDVAG-GLWSSQAVLAMEELT-
-DSQQQDLTAFLQLVGYRIQGEHPGPQDEVSNQKLFATAYFLVSALAEMPDNATVFLGTCC-KLHVISSLCCL-
--LHALSDDSVCDFHN------PTLAPLRDTERF-
GIVQRLFASADIALERMQFSAKATILKDSCIFPLILHITLSGLSTLSKEHEEELCQSGHATGQD--------------------
------------------------------------------------------------------
>ref|NP 001006361.1| chromosome 2 organism Gallus gallus breed Leghorn gcode 1
chromosome 2 map 2 gasdermin-E Gallus gallus
---------------------------------------------------------------------------FLFHPDAVDNGMYSGAENPVPSHAS--
LSVLKKDLSQLKAQFQPFVKLPEDKQRALYKSLCELL--LHEETLTALEDVLDALCT-GDKPDLK-----ELK--
PAQQQDLADFLQLVGCRVQDELLLQNYHLQDEELLSAAHLLISAISELSDYTLVLLRACS-DLQVVPALCCL---
PYIASADGTLALSS------PSVATLTDRRRF-
DVAQRLFASANINLEKTETSVKAVTMREPRFFPLVLYVALCGLHSLGGTVEELF---------------------------------
--------------------------------------------------------------
>ref|NP 001180041.1| chromosome 4 organism Bos taurus breed Hereford gcode 1
chromosome 4 map 4 gasdermin-E Bos taurus
---------------------------------------------------------------------------------------DAGQGLPAQDKP--
LSVLKQATLLLERNFHPFMELPEQQQIALNDVLQAVL--LDEELLVVLEQVCDDIVS-SLSPSLVALG--ELK--
PSQKHNLTTFLRLVGCSVQGERLGSQDVVDNQKLFSTAFFLVSALAEMPDNAAALLGTCC-KLQIIPLLYHL---
LRALSHDGVSDLED------PALAPLKDREKF-
GIVQRLFAATDINLERMQSSVKAASREDPNVLPLILYISLSGLCALGRAQ----------------------------------------
----------------------------------------------------------
>ref|XP 002933445.2| location chromosome chromosome 6 completeness complete organism
Xenopus tropicalis strain Nigerian gcode 1 chromosome 6 sex female tissue type liver and blood
dev stage adult nots
---------------------------------------------------------------------------VLFDWDVVDGSKEAFVRKCILRSAP--
LCLLREGIAAHEKHFSAWKQLPDVQCLELYTLLCQIL--YDGQALSKLHAVVEDLCS-KRKPTQAAFD--ELM--
PSQRIIAENILYLSGYDMPNGKFLHAANR---ELLVALHILTSALNELSDSALAVLGTCC-ELQLLPVFSAL---
MNMSSDEGLCSTTE------PALMDFLDQERF-
YVSQKLFALFNIELEIKEDFIYAATAEDPGFLPLILFIVITGLQLLKRD------------------------------------------------
----------------------------------------------------
```

```
>ref|XP 001096213.2| location chromosome chromosome 3 completeness complete organism
Macaca mulatta isolate AG07107 bio material Coriell:AG07107 gcode 1 chromosome 3 sex
female tissue type fibroblasta
---------------------------------------------------------------------------------------------------DAAHGISSQDGP--
LSVLKQVTPLLERNFHPFVELPEPQQTALSDIFQAVL--FDDELLMVLEPVCDDLVS-GLSPPMAVLG--ELK--
LQQQQDLEAFLQLVGCSLHGGCPGPED-TGSKQLFMTAYFLVSALSEMPDNAAALLGTCC-KLQIIPTLCHL---
LRVLSDDGVSDLED------PTLAPLKDTERF-GIVQRLFASADISLERLKSSVKAVILKDSKVFP-
LLCIALNGLCALGREHS------------------------------------------------------------------------------------------------------------
----
>ref|XP 006912063.1| chromosome Unknown completeness complete organism Pteropus
alecto gcode 1 chromosome Unknown sex male tissue type kidney country Australia: Anglican
Church Grammar School East Bro
---------------------------------------------------------------------------------------------------DAWQGPPASDKP--
LSVLKEVTLPLEKSFRPFAELPEQQQTALSGILQAVL--FDDELLLALEQVCDDVFS-DLSPPRVIPG--ELK--
PSQQQDLMAFLHLVGYSMQSGCPGPEDAVSNQKLFSTAYFLVSALAEMPDNAAALLGTCC-KLQIIPTLCHL-
--LHVLSADGESDLED------AALAPLRDTERF-
EIVQRLLAAADINLERQQSSVKAVTCQVPNVSPLVLYISLNGLWALGRMHQ----------------------------------------
------------------------------------------------------------------------
>ref|XP 031796450.1| location chromosome chromosome 5 completeness complete organism
Sarcophilus harrisii gcode 1 chromosome 5 cell line 91H gasdermin-E Sarcophilus harrisii
--------------------------------------------------------------------------------------------DSVDGKSEAVKLTPVEGP--
LSALKHGMLVLERNFRPFVELSGHHRAALCEILWEVL--LDDELVVALDTVLSDVLAGGRPRLWALP---GLS--
PGQQQQLAAFLGLAGLHVQEDSRVRRDARAPRELLSTAHFLVSALAEMPDDTVALMGVCC-
QLHLIPTLCHL---PQVTSADGVSELGD------PSLAPLSDAGSF-
EVVQKLFALSHISLERREAHVEAVIMKRPQYLPLVLYITLHGLCALEGKAE---------------------------------------------
------------------------------------------------------------------
>ref|XP 027689547.1| location chromosome chromosome 2 completeness complete organism
Chelonia mydas isolate rCheMyd1 gcode 1 chromosome 2 sex male tissue type blood dev stage
adult country Israel: Mes
-------------------------------------------------------------------------------------FLYQPDAVDSDRRSGDRNIVPSDAS--
LSVLKQDLLLLKMQFQPFVKLPEDKQGALNKIFYELL--HHEEIVIALEEVLDSIFT-GEEPDFTDLK--ELK--
PPQQQNITDFLQLVGYSLQNELLQKDQLHYT-GLFSAAHILISAVAELSDYTLALLRACC-DIQIVPILCYL---
PNVASADGTLTLRD------PALAPLTDTGRF-
HIVQRLFALSNINLEMMESSMKAVTMKEPSFFPFILYIALYGFYALGGTI-----------------------------------------------
------------------------------------------------------------------
>ref|XP 040208817.1| location chromosome chromosome 5 completeness complete organism
Rana temporaria gcode 1 chromosome 5 gasdermin-E Rana temporaria
--------------------------------------------------------------------------------------FDWDMVDLSRNISVDGKAVPSNYS--
LSAIKSDILEITKPFSVLQDLPEAHRGEIYNGLFEIL--HDGQTVTQLQAVVEEICL-EKRPGLTFLS--ELK--
SPERAWVQKILHLIGYDMLNQKLIEPFKK---DLLSAVHLLTSALDEMPDTALAILGACC-KLHLLPALWAL---
TNITSDEGLCSRTE------PALTDLIHQGRF-QIAQSLFSFFNMRLELNEKNIAVTS-
EDPSLLPHILYIAISGFHALKNNLKI----------------------------------------------------------------------------------------------
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```

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>ref|XP 023962559.1| location chromosome chromosome 2 completeness complete organism
Chrysemys picta bellii isolate RCT428 sub species bellii gcode 1 chromosome 2 sex female
country USA: Grant Co. ...
---------------------------------------------------------------------------------------------FLYQPDAVDSDRHSGDRNIIPSGAS--
LSVLKQDLLLLKMQFQPFVKLPEDKQGALNKIFYEFL--HHEEMVTALEEVLDSICT-GEEPDFTDLK--ELK--
PPQQQNITDFLQLVGYSLQNELLLQNDQLHYKGLFSAAHILISAVAELSDYTLALLRACC-DIQIIPALCCL---
PNVASADGTLTLRD------PALAPLTDTGRF-
DIVQRLFALSNINLEMMESSVKAVTMKEPSFFPFILYIALYGFYALGGTI----------------------------------------------------
------------------------------------------------------------------------
>ref|XP 029444983.1| location chromosome chromosome 2 completeness complete organism
Rhinatrema bivittatum gcode 1 chromosome 2 gasdermin-E isoform X1 Rhinatrema bivittatum
----------------------------------------------------------------------------------------------YSWDVVDSGDRSMMNRNVVPSDAP-
-LSLLKQDVLQQTKIFQSFLELPEEKRSVLNKLLCEIL--SHGETLTLLEDVLDDICT-EHKPNLTALN--ELK--
VEQQQNIKDLWPLLGLGLENELLLQPEKLQEKELLLATHVLVSALEEMGDSPLAILRACC-ELHLMPVLCHL---
LNSLSDDGTSMRDS--------
LLSIFNDKGRFQIAQKLFSLSNISLELTEDNIRAVTKSEPGFLPLILSIILSGFHVLAGTF-------------------------------------
---------------------------------------------------------------------------------------
>ref|XP 004626528.1| chromosome Unknown completeness complete organism Octodon
degus isolate 3935 gcode 1 chromosome Unknown sex female gasdermin-E Octodon degus
------------------------------------------------------------------------------------------------------------DAKHGMLSKDGL--
LSVLKQATLPLERNFHPFVELPAQQQQALHNLLQAVL--LDEELLVVLEQVCDDMAG-
SVWSPQTALAMRALK--
APQQQDLTAFLQLVGCSIQGECPSPEDEVSNQKLFATAYFLVSALAEMPDNAAALLGICC-KLQIIPTLYHM---
LRALSDDGVCDLED------PTLAPLRDTERF-
GIVQRLFVATDINLEQEQASVKAVILKDPHIFPLILYITLNGLCALGREH------------------------------------------------------
----------------------------------------------------------------------
>ref|XP 021046698.1| location chromosome chromosome 2 completeness complete organism
Mus pahari gcode 1 chromosome 2 sex female tissue type tail gasdermin-E Mus pahari
------------------------------------------------------------------------------------------------------------DGGQGISSQDGP--
LRVVKQATLHLERSFHPFAVLPAQQQRALFCVLQKIL--FDEELLRALEQVCDDVAG-GLWSSQAISAMEELT--
DSQQQDLTAFLQLVGYRIQGEHPGPQDAVSNQKLFATAYFLVSALAEMPDNATVFLGTCC-KLHVISSLCCL--
-LHALSDDSVCDFQD------PALAPLRDTERF-
GIVQRLFASADIALERMQFSAKATILKDSCIFPLILHITLSGLSTLSKEHEEQLCQSEGHATGQD-----------------------
-----------------------------------------------------------------------------------
>ref|XP 009324004.1| chromosome Unknown completeness complete organism Pygoscelis
adeliae isolate BGI AS28 gcode 1 sex male country Antarctica chromosome Unknown
PREDICTED: non-syndromic hearing impae
---------------------------------------------------------------------------------------------FLYQPDAVDNEMYSGAKNRIPSDAS--
LSVLKQDLSWLKTQFQPFVKLPEDKQRALYKTLCELL--LHEEMVAALEDLLDDICT-GDKPDLK-----ELK--
PAQQQDLLGFLQLLGCSLQSELLLQKYQPQDEELLSAAHLLISAISELPDYTLVLLRACC-DLQVVPALCCL---
PNIASADGTLALSS------PLVATLTDRGRF-
DVVQRLFASSNITLEMTVSSVKAVTMKEPRFFPLVLYVALYGFYALGGNV------------------------------------------------
----------------------------------------------------------------------------
```

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>ref|XP 024418892.1| chromosome Unknown completeness complete organism Desmodus
rotundus isolate DRU21DN04 gcode 1 chromosome Unknown sex male tissue type muscle/skin
sample dev stage adult country Us
-------------------------------------------------------------------------------------------DAGQGPSAPDEP--
LSVLKQATLPLERAFHPFGQLPEQEQTALSGVLQVVL--FDEELLVVLEQVCDDMVG-GLPPSLAVLG--ELK--
PPQKQNLMAFLQLVGCSMQGECLGPQGVVSNQKLFSTAYFLVSALAEMPDNAAALLGTCC-
KLQIIPALCHL---LRALSAGGEPDLED------TALAPLRDTERF-
GIVQCLLATASLDLERRQSSVKAVTCQVPNVSPLVLYVSLSGLHALGRAHQ---------------------------------------
----------------------------------------------------------------
>ref|XP 016015046.2| chromosome Unknown completeness complete organism Rousettus
aegyptiacus isolate mRouAeg1 gcode 1 chromosome Unknown sex male tissue type muscle dev
stage adult country USA: Berkes
-------------------------------------------------------------------------------------------DAWQRPSASDKP--
LSVLKQVSLPLERSFRPFAELPQQQQTALSGILQAVL--FDEELLLALEQVCDDVFS-GLSPPRAMPG--ELK--
PSQQQDLAAFLRLVGYSVQSGCPGPEDAVSNQKLFSTAYFLVSALAEMPDNAAALLGTCC-KLQMIPTLCHL-
--LRALSADGESDLED------AALAPLRDTERF-
EIVQRLLAAADIRLERRQSSVKAVTYPVPDVSQLVLYVSLNGLWALARMHQ-------------------------------------
------------------------------------------------------------------
>ref|XP 032903802.1| location chromosome chromosome 2 completeness complete organism
Amblyraja radiata isolate CabotCenter1 gcode 1 chromosome 2 sex male tissue type testis liver
country USA: Gulf ofa
------------------------------------------------------------------------------PLSCVDGAHKCQLSALEMDVPSETS--
LIILKPAIEEANQQFQPFHELAEEKCLQLFRLYCEFL--YHEEVISFLENALDELSS-TEQPNLLGLQ--ELD--
STQAQRVKELLQILGYSCPNEQGSLKKDITTPEILTAAFYLVSALAGMSEESLAVLGICC-ETQILPTLHYL---
INNVPDDGIVPVDN------PNMLPLQEEDNF-
YIAHRLFALSNICLEVRETAIKVITDDQPGMAPVLLCIVLQGFAILSGIKRNTSDPKTQT----------------------------
------------------------------------------------------------------
>ref|XP 001159685.3| location chromosome chromosome 7 completeness complete organism
Pan troglodytes isolate Yerkes chimp pedigree *C0471 (Clint) gcode 1 chromosome 7 sex male
tissue type blood dev ss
-------------------------------------------------------------------------------------------DAAHGISSQDGP--
LSVLKQATLLLERNFHPFAELPEPQQTALSDIFQAVL--FDDELLMVLEPVCDDLVS-GLPSTVAVLG--ELK--
PRQQQDLVAFLQLVGCSLQGGCPGPED-AGSKQLFMTAYFLVSALAEMPDNAAALLGTCC-KLQIIPTLCHL--
-LRALSDDGVSDLED------PILTPLKDAERF-
GIVQRLFASADISLERLKSSVKAVILKDSKVFPLLLCITLNGLCALGREHS--------------------------------------------
-----------------------------------------------------------
```

PYD Alignment

```
>sp|Q8WXC3|PYDC1 HUMAN Pyrin domain-containing protein 1 OS=Homo sapiens OX=9606
GN=PYDC1 PE=1 SV=1
--------------------MGTKREAIL-KVLENLTPEELKKFKMKLGTVPLREGFE----RIPRGALGQLDIV-DLTDKLVAS-
-YYEDYAAELVVAVLRDMR-----------MLEEAAR-LQRAA-----------
>NP 660183.1:1-88 apoptosis-associated speck-like protein containing a CARD isoform b Homo
sapiens
```

```
--------------------MGRARDAIL-DALENLTAEELKKFKLKLLSVPLREGYG----RIPRGALLSMDAL-DLTDKLVSF-
-YLETYGAE-LTANVLRDM-----------GLQEMAG-QLQAA-----------
>NP 001104231.1 uncharacterized protein LOC796649 Danio rerio
--------------------MASTKTEIL-DVLDELRERE---FKD---FKWRLSNKETLENSIPRGKLENADRQ-
DVVDYMEQH--FGTSEAGK-VAVRL--LH-----------SMNQNNL-AEQLKKTLAVVSKV--
>q919n6 danio asc
-------------------MAESFKEHLQ-EAFEDLGADN---LRK---FKSKLGDRRQEP-
RVTKSAIEKLKDEIDLADLMVGV--FTSKDAVS-VTVEI--LR-----------AIKCNAV-ADDLLRNTGQS-----
>q56p42 pydc2 human
-----------------MASSAELDFNLQ-ALLEQLSQDELSKFKS---LIRTISLGK----ELQTVPQTEVDKA-N-GKQLVEI--
FTSHSCS--YWAGMAAIQ-----------VFEKMNQ-THLSGRADEHCVM---
>q91vj1 pycard mouse
-------------------MESEYREMLLLTGLDHITEEE---LKR---FKYFALTEF----QIARSTLDVADRT-ELADHLIQS--
AGAASAVTKAINIFQKLN-----------YMHIANA-LEEKKKE---------
>o35368 ifi203 mouse
--------------------MAEYKNIVLLKGLENMEDYQ---FRT---VKSLLRKEL----KLTKKMQEDYDRI-
QLADWMEDK--FPK---DA-GLDKL--IK-----------VCEHIKD-LKDLAKKLKTEKAK--
>q504j1 caspb danio
---------------------------LS-DVLEDLVESELKQFTR---QLWIGVKPGVE--PIPRGKLENKDRQ-DVVDSMVQQ--
YSED-AGTITVQTL--RK-----------IKQNERA-----------------
>q919l7 caspa danio
--------------------------HLQ-DALSNIGADN---LRR---FQSRLGDRKQEP-RVRKSTIEKLKDEIDLVDLLVNT--
FTSD-AVS-VTVDI--LR-----------GIKCNAV-AE--------------
>tr|B2CWB9|B2CWB9 9POXV M013 OS=Myxoma virus OX=10273 GN=m013L PE=4 SV=1
---------------------MEHRGVII-TVLENLSDYQ---FKM---FIYLAMEDL----YIERAEKEKIDRI-DLAHKISEQ--
YLGTDYIE-FMKRV--TD-----------FIPNKVY-VDSLLARAEADA----
>NP 051902.1 Hypothetical protein SFV s013L Rabbit fibroma virus
---------------------MEHRGVII-TVLENLTDYQ---FKM---FLYLVTEDL----RINPVEKEKIDRI-DLAYKISEL--
YPGHSYIE-FMKQV--TG-----------YIPNKVY-VDSLLKNAEENT----
>YP 227401.1 hypothetical protein DpV83gp024 Deerpox virus W-848-83
---------------------MELRSAII-AVLENINRYQ---FKM---VIFIVQDEL----YIEEEEKLTMDRI-DLAEKLIKK--YKD--
-IR-SLYFL--LN-----------IFKEMPD-TEFVKKQLSDYIKRF-
>NP 073403.1 18L protein Yaba-like disease virus
-----------------MLYTMRIKSAII-FSLEDVTHYQ---FKI---LIFLTKDEL----NISDEEKQILDRV-DFAEKLFQT--
YPG---IK-SLYFL--EK-----------AISMVPN-AKYARSNINRLISDL-
>ABQ43490.1 pyrin domain Tanapox virus
-----------------MLYNMRIKSAII-FSLEDVTHYQ---FKI---LIFLTKDEL----NINDEEKQILDRV-DFAEKLFQA--
YPG---IK-SLYFL--EK-----------AISMVPN-AKYARSNINRLISDL-
>NP 570174.1 Hypothetical protein SWPVgp014 Swinepox virus
---------------------MELRYTII-SVLERLTPYQ---FKT---LLFLIQDDI----NISNDDINVLDRV-DLAIKIMNK--YNN-
--YR-AIYFL--YK-----------VILRIHN-TEYISGTLQRSIQNI-
>Vaccinia
-----MVKNNKISNSCRMIMSTNPNNILM-RHLKNLTDDE---FKC---IIHRSSDFL----YLSDSDYTSITKE-
TLVSEIVEE--YPDD-CNK-ILAII--FL-----------VLDKDID-VDIET-----------
```

```
>Buffalopox
-----MVKNNKISNSCLMIMSTNPNNILM-RHLKNLTDDE---FKC---IIHRSSDFL----YLSDSDYTSITKE-
TLVSEIVEE--YPDD-CNK-ILAII--FL-----------VLDKDID-VDIET-----------
>Cowpox
MVKSNKIQKNKISNSCRMIMSTNPNNILM-RHLKNLTDDE---FKC---IIHRSSDFL----YLSDRDYTSITKE-
TLVSEIVEE--YPDD-CNK-ILAII--FL-----------VLDKDID-VDIET-----------
>Rabbitpox
-----MVKNNKISNSCLMIMSTDPNNILM-RHLKNLTDDE---FKC---IIHRSSDFL----YLSDRDYTSITKE-
TLVSEIVEE--YPDD-CNK-ILAII--FL-----------VLDKDID-VDIET-----------
>Horsepox
------MVKNKISNSCLMIMSTDPNNILM-RHLKNLTDDE---FKC---IIHRSSDFL----YLSNRDYTSITKE-
TLVSEIVEE--YPDD-CNK-ILAII--FL-----------VLDKDID-VDIKT-----------
>Orthopox abatino
MVKNNKIQKIKTSNSYRDVIMTNPNNILM-RHLKNLTDDE---FKC---IVNRSSDFI----YLSDRDYTSITKE-
TLVSEIVEE--YPDD-CNK-ILAII--FL-----------VLGKDVD-IETET-----------
>Akhmeta virus
MVKSNKIQKNKISNSCRYMIMNTNTNILM-RHLKNLTDDE---FKC---IIHRSSDFL----YLSDRDYTSITKE-
TLVSEIVEE--YQDD-CNK-ILAII--FL-----------VLDKDID-VDIET-----------
>Variola Virus
-----------------MIMSTDPNNILM-RYLKNLTDDK---FKC---IIHQSSDFL----YLSDRDYTSITKE-TLVSEIVEE--
YPDD-CNK-ILAII--FL-----------VLDKDID-VDIET-----------
>Monkeypox
-----------------MIMRTDTNNILM-RHLKNLTDDE---FKC---IIHRSSDFL----YLSDRDYTSITKE-TLVSEIVEE--
YPDD-CNK-ILAII--FL-----------VLDKDID-VDIET-----------
>Alaskapox
-----------------------MNTILM-RHFKNLTDDE---FKC---IIHRSSDFI----YLSDRDYTSITKE-TLVSEIVEE--YPDD-
CDK-ILAII--FL-----------VLGKDIE-VDVKT-----------
>Volepox
---------------------MANKNRLV-SYLKNLTDDE---FKC---IIYRSSDFI----YLSDSDHDTITKE-KLVKEIIEE--
YPDD-CNK-ILAII--FL-----------VLDKDID-IDIET-----------
>Skunkpox
----------------------MNKNRLV-KYLKNLTDDE---FKC---IIYRSSDFI----YLSDSDHDNITRE-TLVKEIMEE--
YPDD-CNK-ILAII--FL-----------VLDKDID-LDIET-----------
>Raccoonpox
---------------------MDVKNRIV-KYLKNLTDDE---FRY---IIYRSSDFI----YLSDGDHNTITKE-TLVNEIIEE--
YPDD-CNK-IFAII--FL-----------VLDIDID-LDTET-----------
>NY 014 poxvirus
------------------------MDKIM-CYLNNITDEE---FET---VIDRSSNFL----YLSDDDHTNITRE-SLALEIVEE--
YPND-CER-ILAII--LL-----------SLDKYIS-FESTI-----------
>Murmansk poxvirus
------------------------MDKIT-HYLNNITDGE---FET---VIDRSSNFL----YLSDDDHTNITRE-SLALEIVEE--YPND-
CER-ILAIL--LL-----------SLDKYIS-FESTI-----------
>Yoka poxvirus
```

```
-----------------------MNKIL-NYFNSITDDE---FKT---IISISSDFL----YLSDNDNINITKE-SLALEILEQYPYPND-
YEK-ILSML--LL-----------ALGKYVF-FETII-----------
>QDJ94995.1 IFN-inducible protein Hypsugopox virus
------------------MDSYTKGSIL-YALKNLTFQQ---LKE---FMFISSEQL----YLSNKDRLNFDVV-DLADRIIIV--
CHDN-ALK-AFKLI--KE-----------ILTMMES-VDFVINYMNKCIENTC
>QHG62576.1 hypothetical protein Cetacean poxvirus 1
----------MIDSKSLNVEIEVKIALM-RALDELSSYQ---LKV---LAFLTSNRV----CVIHRSMSNVDRV-
DIAKRINTT--LP---CVC-SLTYLRDLLKNVKHTESVRDILCEDINYIESIMRNNNEIKRFTC
>YP 009407969.1 IFN-inducible protein Eptesipox virus
------------------MDAFTKGSTL-YALKNLTFNQ---LKE---FMFISSDGL----YLTHKNRLEFDVV-DLADRIIIV--
NNNN-PLK-VFKHI--KE-----------TLCLMDD-VEFVLKYIDKCIENCA
```

GSDM Tree

```
(((((((((((((('AY484669.1:c159516-158782 Rabbitpox virus complete
genome':0.00000632,'KY349117.1:c166272-165538 Horsepox virus strain MNR complete
genome':0.00396044)0.5300:0.00000632,'M35027.1:c153690-152956 Vaccinia virus
Copenhagen complete genome':0.00396094)0.6900:0.00396040,('MG599038.1:c157906-
157148 Buffalopox virus isolate Karachi 2005 complete
genome':0.00000632,'AY243312.1:c154675-153917 Vaccinia virus WR complete
genome':0.00384602)0.7600:0.00398762)0.8500:0.01196656,'KC813500.1:c153312-152578
Cowpox virus strain MonKre08/4 complete
genome':0.00000632)0.2000:0.00001264,'MN912466.1:c156293-155559 Ectromelia virus WH
complete genome':0.01989595)0.6200:0.00395345,'NC 055231.1:c163765-163031
Orthopoxvirus Abatino complete
genome':0.00793905)0.5300:0.00641072,('MH607143.1:c167386-166652 Akhmeta virus isolate
Vani 2010 complete genome':0.02387728,((('AY009089.1:c154402-154034 Camelpox virus CMS
complete genome':0.00000632,'MK910851.1:c154204-153836 Camelpox virus strain
Negev2016 complete genome':0.00808054)0.9200:0.02440740,'DQ437594.1:c153307-152573
Taterapox virus strain Dahomey 1968 complete
genome':0.01191498)0.3300:0.00000632,('KY358055.1:c145385-144651 Variola virus strain
VD21 17th century complete genome':0.00000632,('DQ441432.1:c146026-145292 Variola virus
strain Korea 1947 (Lee Masterseed) complete genome':0.00395560,'DQ441437.1:c146904-
146170 Variola virus strain Sierra Leone 1969 (V68-258) complete
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54384)0.5300:0.03253804,'MN240300.1:c166555-165827 Alaskapox virus complete
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strain 85A complete genome':0.10647955,('KU749310.1:c167631-166873 Skunkpox virus strain
WA complete genome':0.07403330,'KU749311.1:c169057-168281 Volepox virus strain CA
complete
genome':0.09493255)0.5900:0.02370722)0.4600:0.07236375)1.0000:0.50096918,('HQ849551.
1:c134784-134035 Yoka poxvirus strain DakArB 4268 complete
genome':0.41854758,('MF001305.1:c159640-158771 NY 014 poxvirus strain 2013 complete
genome':0.10644996,'MF001304.1:c160603-159728 Murmansk poxvirus strain LEIV-11411
```

complete genome':0.06453801)0.8000:0.16035801)0.4100:0.07538004)1.0000:1.10608085,YP_009408097.1_Immunoprevalent_protein_Eptesipox_virus:0.88065310)0.5900:0.32061200,((NP_051846.1_m132L_Myxoma_virus:0.09720761,NP_052021.1_gp132L_Rabbit_fibroma_virus:0.24063256)1.0000:1.72365406,(('MF001304.1:c165763-165224 Murmansk poxvirus strain LEIV-11411 complete genome':0.04040716,'MF001305.1:c164808-164269 NY 014 poxvirus strain 2013 complete genome':0.11589372)0.8900:0.43947697,('KU749311.1:173861-174445 Volepox virus strain CA complete genome':0.03751514,('KU749310.1:172437-172985 Skunkpox virus strain WA complete genome':0.06828167,'KU749309.1:150174-150722 Raccoonpox virus strain 85A complete genome':0.09772203)0.6700:0.06086908)0.9400:0.42301996)1.0000:1.32178979)0.4300:0.41793913)0.6600:0.74188710,((((((((ref|NP_113603.1|_chromosome_8_organism_Homo_sapiens_gcode_1_chromosome_8_map_8q24.21_gasdermin-C_Homo_sapiens:0.00648950,'ref|XP 001153860.1| location chromosome chromosome 8 completeness complete organism Pan troglodytes isolate Yerkes chimp pedigree *C0471 (Clint) gcode 1 chromosome 8 sex male tissue type blood dev ss':0.01016408)0.7300:0.02356312,'ref|XP 028708741.1| location chromosome chromosome 8 completeness complete organism Macaca mulatta isolate AG07107 bio material Coriell:AG07107 gcode 1 chromosome 8 sex female tissue type fibroblasta':0.05208806)1.0000:0.26393153,ref|XP_019678683.1|_location_chromosome_chromosome_F2_completeness_complete_organism_Felis_catus_isolate_Cinnamon_breed_Abyssinian_gcode_1_chromosome_F2_sex_female_gasdermin-C_Felis_catus:0.41823708)0.1300:0.05011136,('ref|XP 036088919.1| chromosome Unknown completeness complete organism Rousettus aegyptiacus isolate mRouAeg1 gcode 1 chromosome Unknown sex male tissue type muscle dev stage adult country USA: Berkes':0.32082568,ref|XP_024427836.1|_chromosome_Unknown_completeness_complete_organism_Desmodus_rotundus_isolate_DRU21DN04_gcode_1_chromosome_Unknown_sex_male_tissue_type_muscle/skin_sample_dev_stage_adult_country_Us:0.13881323)0.6000:0.09111937)0.1400:0.07902331,ref|NP_001039469.1|_chromosome_14_organism_Bos_taurus_breed_L1_Hereford_gcode_1_chromosome_14_map_14_gasdermin-C_Bos_taurus:0.55125872)0.3600:0.07430343,ref|XP_021073018.1|_location_chromosome_chromosome_17_completeness_complete_organism_Mus_pahari_gcode_1_chromosome_17_sex_female_tissue_type_tail_gasdermin-C_Mus_pahari:0.36366499)0.9800:0.59858814,ref|XP_031803207.1|_location_chromosome_chromosome_1_completeness_complete_organism_Sarcophilus_harrisii_gcode_1_chromosome_1_cell_line_91H_gasdermin-C_Sarcophilus_harrisii:0.73800521)0.4200:0.14672251,((('ref|XP 015154998.2| location chromosome chromosome 27 completeness complete organism Gallus gallus isolate bGalGal1 gcode 1 chromosome 27 sex female tissue type blood country USA: Fayetteville lat ls':0.89302167,ref|XP_029428328.1|_location_chromosome_chromosome_12_completeness_complete_organism_Rhinatrema_bivittatum_gcode_1_chromosome_12_gasdermin-A_Rhinatrema_bivittatum:1.13451927)0.3600:0.10801623,XP_032891479.1_gasdermin-A_Amblyraja_radiata:1.35621246)0.1500:0.21106408,(ref|NP_081236.1|_chromosome_15_organism_Mus_musculus_strain_C57BL/6_gcode_1_chromosome_15_map_15_gasdermin-D_Mus_musculus:0.37973081,(((ref|NP_079012.3|_chromosome_8_organism_Homo_sapiens

```
_gcode_1_chromosome_8_map_8q24.3_gasdermin-D_Homo_sapiens:0.00490946,'ref|XP
009454389.2| location chromosome chromosome 8 completeness complete organism Pan
troglodytes isolate Yerkes chimp pedigree *C0471 (Clint) gcode 1 chromosome 8 sex male
tissue type blood dev ss':0.03154543)0.9800:0.02755997,'ref|XP 015001615.2| location
chromosome chromosome 8 completeness complete organism Macaca mulatta isolate
AG07107 bio material Coriell:AG07107 gcode 1 chromosome 8 sex female tissue type
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D_Felis_catus:0.38688835,(ref|NP_001039625.1|_chromosome_14_organism_Bos_taurus_bre
ed_Hereford_gcode_1_chromosome_14_map_14_gasdermin-
D_Bos_taurus:0.18906395,(ref|XP_024428237.1|_chromosome_Unknown_completeness_com
plete_organism_Desmodus_rotundus_isolate_DRU21DN04_gcode_1_chromosome_Unknown_
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006913014.1| chromosome Unknown completeness complete organism Pteropus alecto gcode
1 chromosome Unknown sex male tissue type kidney country Australia: Anglican Church
Grammar School East Bro':0.05855083,'ref|XP 036089037.1| chromosome Unknown
completeness complete organism Rousettus aegyptiacus isolate mRouAeg1 gcode 1
chromosome Unknown sex male tissue type muscle dev stage adult country USA:
Berkes':0.07916446)0.9600:0.08309248)0.6600:0.09456772)0.6500:0.07865023)0.8200:0.1148
4867)0.5700:0.05693998)1.0000:0.51206201)0.1000:0.19500033)0.0200:0.03306529)0.0000:0.
15081324,((sp|Q5Y4Y6|GSDA3_MOUSE_Gasdermin-
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MOUSE_Gasdermin-
A2_OS_Mus_musculus_OX_10090_GN_Gsdma2_PE_2_SV_1:0.08079961)0.5000:0.01350323,(s
p|Q9EST1|GSDMA_MOUSE_Gasdermin-
A_OS_Mus_musculus_OX_10090_GN_Gsdma_PE_2_SV_1:0.01547699,((('ref|XP 016020091.2|
chromosome Unknown completeness complete organism Rousettus aegyptiacus isolate
mRouAeg1 gcode 1 chromosome Unknown sex male tissue type muscle dev stage adult country
USA: Berkes':0.00923641,'ref|XP 006924750.1| chromosome Unknown completeness complete
organism Pteropus alecto gcode 1 chromosome Unknown sex male tissue type kidney country
Australia: Anglican Church Grammar School East
Bro':0.01784865)0.9500:0.03854298,ref|XP_024429158.1|_chromosome_Unknown_complete
ness_complete_organism_Desmodus_rotundus_isolate_DRU21DN04_gcode_1_chromosome_
Unknown_sex_male_tissue_type_muscle/skin_sample_dev_stage_adult_country_Us:0.077303
13)0.4600:0.00685917,(ref|XP_035935879.1|_chromosome_Unknown_completeness_complet
e_organism_Halichoerus_grypus_isolate_241Hg_ecotype_Northwest_Atlantic_gcode_1_chrom
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6266.1|_location_chromosome_chromosome_19_completeness_complete_organism_Bos_tau
rus_isolate_L1_Dominette_01449_registration_number_42190680_breed_Hereford_gcode_1_
chromosome_19_sex_fem...:0.07277097,ref|XP_004633937.1|_chromosome_Unknown_comp
leteness_complete_organism_Octodon_degus_isolate_3935_gcode_1_chromosome_Unknown
_sex_female_gasdermin-A_Octodon_degus:0.08986357)0.0600:0.00538989,('ref|XP
014975037.1| location chromosome chromosome 16 completeness complete organism Macaca
```

```
mulatta isolate AG07107 bio material Coriell:AG07107 gcode 1 chromosome 16 sex female
tissue type
fibroblaa':0.03818418,(ref|NP_835465.2|_chromosome_17_organism_Homo_sapiens_gcode_
1_chromosome_17_map_17q21.1_gasdermin-A_Homo_sapiens:0.00536674,'ref|XP
001171222.1| location chromosome chromosome 17 completeness complete organism Pan
troglodytes isolate Yerkes chimp pedigree *C0471 (Clint) gcode 1 chromosome 17 sex male
tissue type blood
devs':0.00000632)0.5100:0.01070020)0.9800:0.04354841)0.1500:0.00623461)0.1800:0.005534
76)0.8000:0.06299807)0.7900:0.04239040)0.9900:0.44258489,((((((('ref|XP 024897515.1|
chromosome Unknown completeness complete organism Pteropus alecto gcode 1
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completeness complete organism Rousettus aegyptiacus isolate mRouAeg1 gcode 1
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3352)0.4000:0.02806263,ref|XP_035935913.1|_chromosome_Unknown_completeness_compl
ete_organism_Halichoerus_grypus_isolate_241Hg_ecotype_Northwest_Atlantic_gcode_1_chro
mosome_Unknown_sex_male_tissue_type_blood_dev_stage_molts:0.34581838)0.2500:0.0300
4080,ref|NP_001231146.1|_chromosome_19_organism_Bos_taurus_gcode_1_chromosome_1
9_map_19_gasdermin-B_Bos_taurus:0.26530564)0.4800:0.09159899,('ref|XP 014975035.1|
location chromosome chromosome 16 completeness complete organism Macaca mulatta
isolate AG07107 bio material Coriell:AG07107 gcode 1 chromosome 16 sex female tissue type
fibroblaa':0.11006455,(ref|NP_001159430.1|_chromosome_17_organism_Homo_sapiens_gco
de_1_chromosome_17_map_17q21.1_gasdermin-
B_isoform_3_Homo_sapiens:0.01869987,'ref|XP 009430521.1| location chromosome
chromosome 17 completeness complete organism Pan troglodytes isolate Yerkes chimp
pedigree *C0471 (Clint) gcode 1 chromosome 17 sex male tissue type blood
devs':0.01689996)0.9400:0.05518121)1.0000:0.07184298)1.0000:0.50473782,ref|XP_0233581
60.1|_location_chromosome_chromosome_4_completeness_complete_organism_Sarcophilus
_harrisii_gcode_1_chromosome_4_cell_line_91H_gasdermin-
B_Sarcophilus_harrisii:0.56088280)0.9600:0.33170458,('ref|XP 032903802.1| location
chromosome chromosome 2 completeness complete organism Amblyraja radiata isolate
CabotCenter1 gcode 1 chromosome 2 sex male tissue type testis liver country USA: Gulf
ofa':0.57159834,(((ref|XP_002933445.2|_location_chromosome_chromosome_6_completenes
s_complete_organism_Xenopus_tropicalis_strain_Nigerian_gcode_1_chromosome_6_sex_fem
ale_tissue_type_liver_and_blood_dev_stage_adult_nots:0.58041056,ref|XP_040208817.1|_loc
ation_chromosome_chromosome_5_completeness_complete_organism_Rana_temporaria_gc
ode_1_chromosome_5_gasdermin-
E_Rana_temporaria:0.43530056)0.7400:0.37086991,ref|XP_029444983.1|_location_chromoso
me_chromosome_2_completeness_complete_organism_Rhinatrema_bivittatum_gcode_1_chr
omosome_2_gasdermin-
E_isoform_X1_Rhinatrema_bivittatum:0.30113784)0.5100:0.13675007,(((ref|NP_001006361.1
```

|_chromosome_2_organism_Gallus_gallus_breed_Leghorn_gcode_1_chromosome_2_map_2_gasdermin-E_Gallus_gallus:0.14607108,'ref|XP 009324004.1| chromosome Unknown completeness complete organism Pygoscelis adeliae isolate BGI AS28 gcode 1 sex male country Antarctica chromosome Unknown PREDICTED: non-syndromic hearing impae':0.06555493)1.0000:0.18747693,('ref|XP 027689547.1| location chromosome chromosome 2 completeness complete organism Chelonia mydas isolate rCheMyd1 gcode 1 chromosome 2 sex male tissue type blood dev stage adult country Israel: Mes':0.07982534,'ref|XP 023962559.1| location chromosome chromosome 2 completeness complete organism Chrysemys picta bellii isolate RCT428 sub species bellii gcode 1 chromosome 2 sex female country USA: Grant Co. ...':0.01125944)0.9900:0.09327687)0.9600:0.15059215,(ref|XP_031796450.1|_location_chromosome_chromosome_5_completeness_complete_organism_Sarcophilus_harrisii_gcode_1_chromosome_5_cell_line_91H_gasdermin-E_Sarcophilus_harrisii:0.49835971,(((('ref|XP 006912063.1| chromosome Unknown completeness complete organism Pteropus alecto gcode 1 chromosome Unknown sex male tissue type kidney country Australia: Anglican Church Grammar School East Bro':0.04540917,'ref|XP 016015046.2| chromosome Unknown completeness complete organism Rousettus aegyptiacus isolate mRouAeg1 gcode 1 chromosome Unknown sex male tissue type muscle dev stage adult country USA: Berkes':0.06765941)1.0000:0.10802648,ref|XP_024418892.1|_chromosome_Unknown_completeness_complete_organism_Desmodus_rotundus_isolate_DRU21DN04_gcode_1_chromosome_Unknown_sex_male_tissue_type_muscle/skin_sample_dev_stage_adult_country_Us:0.12144140)0.9300:0.07802127,ref|NP_001180041.1|_chromosome_4_organism_Bos_taurus_breed_Hereford_gcode_1_chromosome_4_map_4_gasdermin-E_Bos_taurus:0.16311047)0.7200:0.04030548,(((ref|NP_001120925.1|_chromosome_7_organism_Homo_sapiens_gcode_1_chromosome_7_map_7p15.3_gasdermin-E_isoform_a_Homo_sapiens:0.00453124,'ref|XP 001159685.3| location chromosome chromosome 7 completeness complete organism Pan troglodytes isolate Yerkes chimp pedigree *C0471 (Clint) gcode 1 chromosome 7 sex male tissue type blood dev ss':0.00911979)0.9900:0.01107332,'ref|XP 001096213.2| location chromosome chromosome 3 completeness complete organism Macaca mulatta isolate AG07107 bio material Coriell:AG07107 gcode 1 chromosome 3 sex female tissue type fibroblasta':0.05555503)1.0000:0.14905206,(ref|XP_004626528.1|_chromosome_Unknown_completeness_complete_organism_Octodon_degus_isolate_3935_gcode_1_chromosome_Unknown_sex_female_gasdermin-E_Octodon_degus:0.14112392,(ref|NP_061239.1|_chromosome_6_organism_Mus_musculus_strain_C57BL/6_gcode_1_chromosome_6_map_6_gasdermin-E_precursor_Mus_musculus:0.01643603,ref|XP_021046698.1|_location_chromosome_chromosome_2_completeness_complete_organism_Mus_pahari_gcode_1_chromosome_2_sex_female_tissue_type_tail_gasdermin-E_Mus_pahari:0.04506946)1.0000:0.24424411)0.8800:0.06822000)0.6100:0.02349932)1.0000:0.29867710)1.0000:0.32476703)0.9400:0.23585091)0.6400:0.34461861)1.0000:1.77119903)0.0100:0.08220955);

PYD Tree

```
(sp_Q8WXC3_PYDC1_HUMAN:0.0000021986,NP_660183.1_1-
88:0.8189957255,((((NP_001104231.1:0.5582152076,(q919n6_danio:0.1596274241,q919l7_cas
pa:0.1464068014)100:1.6604787690)78:0.3649286491,q504j1_caspb:0.8779213839)75:0.3248
494404,q91vj1_pycard:1.3275505794)53:0.3488003785,(q56p42_pydc2:2.4248812488,((((o353
68_ifi203:1.9252008714,(tr_B2CWB9_B2CWB9_9POXV:0.1873719086,NP_051902.1:0.1151924
580)98:0.8588394249)30:0.1685723872,QHG62576.1_hypothetical:1.3381578798)25:0.020581
3423,((YP_227401.1:0.4922697513,((NP_073403.1:0.0000024848,ABQ43490.1_pyrin:0.032263
9322)100:0.5536693021,NP_570174.1:0.6631629338)89:0.1050133382)91:0.2980680604,(QDJ
94995.1_IFN-
inducible:0.0322861746,YP_009407969.1:0.3451439803)100:1.1424169120)56:0.1652826846)
38:0.2909839033,((((((Vaccinia:0.0000024478,(Cowpox:0.0000024085,((Orthopox_abatino:0.10
55672911,Alaskapox:0.0953186299)96:0.0427250561,Akhmeta_virus:0.0648530371)92:0.0274
133695)92:0.0511067176)53:0.0098506539,Buffalopox:0.0000023745)51:0.0083698252,(Rabbi
tpox:0.0000027502,((Horsepox:0.0531890168,Variola_Virus:0.0358970206)28:0.0000020161,
Monkeypox:0.0242749897)26:0.0000027502)32:0.0115162760)97:0.2153206803,(Volepox:0.0
403124363,Skunkpox:0.0547150846)81:0.0431585044)36:0.0492731175,Raccoonpox:0.084855
2751)84:0.2158394416,((NY_014:0.0278797725,Murmansk_poxvirus:0.0311930000)97:0.1567
232511,Yoka_poxvirus:0.3046051547)97:0.3533709024)96:0.7863255573)26:0.1931065783)79
:0.4863747229)100:0.9712551055);
```

```
#!/bin/bash

#checks to ensure that matching files are present in both folders

for tmfile in TM/*; do
	name=${tmfile##*/}

	if [ -f "FATCAT/$name" ]; then
		echo "$name"
	else
		echo "$name is MISSING in FATCAT folder"
	fi
done


for fatfile in FATCAT/*; do
	name=${fatfile##*/}

	if [ -f "TM/$name" ]; then
		echo "$name"
	else
		echo "$name is MISSING in TM folder"
	fi
done
```

AlphaFold parameters

```
# explicit run of run_alphafold pointing to the appropriate databases on the RAM disk, for file
passed in as $1
singularity exec --nv /uufs/chpc.utah.edu/sys/installdir/alphafold/2.1.2/alphafold_2.1.2.sif
/app/run_alphafold.sh --data_dir=/scratch/general/lustre/app-repo/alphafold --
uniref90_database_path=/scratch/general/lustre/app-repo/alphafold/uniref90/uniref90.fasta -
-mgnify_database_path=/scratch/general/lustre/app-
repo/alphafold/mgnify/mgy_clusters_2018_12.fa --
uniclust30_database_path=/dev/shm/af/uniclust30_2018_08 --
bfd_database_path=/dev/shm/af/bfd_metaclust_clu_complete_id30_c90_final_seq.sorted_opt
--pdb70_database_path=/dev/shm/af/pdb70 --
template_mmcif_dir=/scratch/general/nfs1/app-repo/alphafold/pdb_mmcif/mmcif_files --
obsolete_pdbs_path=/scratch/general/nfs1/app-repo/alphafold/pdb_mmcif/obsolete.dat --
fasta_paths=$1 --max_template_date=2020-05-14 --output_dir=temp_module --use_gpu_relax
```

Example FATCAT call for file passed in as $1

```
FATCATSearch.pl $1 /scratch/general/vast/user_directory/drome_v2/chain_list-drome-fatcat  -i
/scratch/general/vast/user_directory/drome_v2/ -q > $1.drosophila.FATCAT.txt &
```

Example TM-align call for file passed in as $FILE

```
TMalign -dir1 /home/ian/AlphaDat/Proteomes/human_v2/
/home/ian/AlphaDat/Proteomes/human_v2/chain_list $FILE -outfmt 2 -fast > $FILE.human.txt
&
```

```
#!/bin/bash

#this file extracts hit name, score, opt-rmsd, align-len, and P-value from a fatcat file in a format
suitable for further processing
#IB 3.21.2022

for FILE in *FATCAT.txt
do
	outfile="$FILE.scores.txt"
	echo "Model Score RMSD Aligned P-value" >> $outfile
	reading=0 #0 before read, 1 when alignment found
	while read line
	do
		if [[ ${line:0:5} == "Align" ]] #we found a new entry
		then
			reading=1
			string="${line#*with *}"
			desired="${string%.pdb*}"
			echo -n $desired >> $outfile
		else
			if ((reading == 1))
			then
				string="${line#*Score *}"
				desired="${string% align*}"
				echo -n " $desired" >> $outfile

				string="${line#*opt-rmsd *}"
				desired="${string% chain*}"
				echo -n " $desired" >> $outfile
```

```
                                        string="${line#*align-len *}"
                                        desired="${string% gaps*}"
                                        echo -n " $desired" >> $outfile
                                        reading=2
                    else
                              if ((reading == 2))
                              then
                                        string="${line#*P-value *}"
                                        desired="${string% Afp*}"
                                        echo " $desired" >> $outfile
                                        reading=0
                              fi
                              fi
                    fi
          done < $FILE
done
```

```
#FATCAT and TMalign data visualization v0.2
#IB 11.28.2022
#Requires properly-formatted TM-align + FATCAT datafiles
#Requires a "working_prot.txt" list of input files
#change working directory as appropriate
#This script has been adapted to produce a figure suitable for import into illustrator as an SVG

#next: work on limiting "too many hit" plots

library(ggplot2)
library(ggimage)
library(ggrepel)
library(ggnewscale)
library(svglite)


protList <-read.table("/home/ian/homology_search/fcresults/working_prot.txt")
protList <- unlist(protList)

cols <- c("Mouse" = "paleturquoise1", "Human" = "mediumspringgreen", "Danio" = "plum1",
"Fly" = "khaki1")

for (protein in protList) {
  setwd("/home/ian/homology_search/fcresults/fat_tm_merge/converted")
  hasHits <- 0
```

```
  mouseData <- read.table(header = TRUE, text=gsub(" ", "\t",
readLines(paste(protein,".pdb.mouse.txt",sep=""))))
  humanData <- read.table(header = TRUE, text=gsub(" ", "\t",
readLines(paste(protein,".pdb.human.txt",sep=""))))
  danioData <- read.table(header = TRUE, text=gsub(" ", "\t",
readLines(paste(protein,".pdb.danio.txt",sep=""))))
  flyData   <- read.table(header = TRUE, text=gsub(" ", "\t",
readLines(paste(protein,".pdb.drosophila.txt",sep=""))))

  #append source genome name - used later when annotating graphs
  mouseData$Proteome <- "Mouse"
  humanData$Proteome <- "Human"
  danioData$Proteome <- "Danio"
  flyData$Proteome <- "Fly"

  testData <- merge(humanData, mouseData, all = TRUE)
  testData <- merge(testData, danioData, all = TRUE)
  testData <- merge(testData, flyData, all = TRUE)

  #Hits defined as TM score > 0.6 AND FATCAT P-value < 0.01
  hits <- testData[testData$TM2 > 0.6, ]
  hits <- hits[-log10(hits$P.value)>2, ]

  #if no hits, instead label the top .01% of results from each tool
  if (nrow(hits)>0){
    finalLabel <- hits
    hasHits <- 1
  } else {
    topP <- quantile(-log10(testData$P.value), probs = .9999)
    topTM <- quantile(testData$TM2, probs = .9999)
    toLabel <- testData[testData$TM2>topTM, ]
    toLabel2 <- testData[-log10(testData$P.value)>topP, ]
    toLabel3 <- rbind(toLabel, toLabel2)
    finalLabel <- unique(toLabel3)
  }

  if(hasHits) {
    graphTitle<-protein
  } else {
    graphTitle<-paste(protein, ": No hits, top-scoring values are indicated")
  }


  p <- ggplot(testData, aes(x=TM2, y=(-log10(P.value)))) +
```

```
   ggtitle(graphTitle) +
   xlab("TM Score") +
   ylab(bquote(Log[10]~P-value~FATCAT)) +
   geom_point(data = humanData, aes(x=TM2, y=(-log10(P.value)), size=1,
color=factor(cut(RMSD.1, c(0,2,3,5,Inf))))) +
   geom_point(data = mouseData, aes(x=TM2, y=(-log10(P.value)), size=1,
color=factor(cut(RMSD.1, c(0,2,3,5,Inf))))) +
   geom_point(data = danioData, aes(x=TM2, y=(-log10(P.value)), size=1,
color=factor(cut(RMSD.1, c(0,2,3,5,Inf))))) +
   geom_point(data = flyData,   aes(x=TM2, y=(-log10(P.value)), size=1,
color=factor(cut(RMSD.1, c(0,2,3,5,Inf))))) +
   labs(color="RMSD")+
   scale_color_brewer(palette="YlGn", labels = c("0-1","2-3","3-5","5+"), direction=-1,
drop=FALSE) +
   new_scale_color() +
   new_scale_fill() +
   geom_label_repel(data = finalLabel, aes(label=Gene, fill=Proteome),
                #color = rep(c("green","red","yellow","blue")[as.factor(finalLabel$Proteome)],times
= 2),
                size = 6,
                seed = 2, box.padding = 1, nudge_x = 0, min.segment.length = 0, segment.size = 1,
segment.color="darkslategrey", max.overlaps = Inf)+ #Inf overlaps leads to issues
   scale_fill_manual(values = cols,
                 labels = c("Mouse", "Human", "Danio", "Fly")) +

   guides(fill = guide_legend(override.aes = aes(color = NA))) +
   guides(size = "none") +

   theme(
          panel.background = element_blank(),
          panel.border = element_blank(),
          panel.grid.major = element_line(size = 0.1, color = "black", linetype = "dashed"),
          panel.grid.minor = element_blank(),
          axis.line = element_line(color="black"),
          axis.text = element_text(size = 22),
          axis.title = element_text(size = 30),
          plot.title = element_text(hjust = 0.5, size = 30),
          legend.text = element_text(size = 22),
          legend.title = element_text(size = 22),
          legend.position = c(0.15, 0.8)
      )

 setwd("/home/ian/homology_search/fcresults")
 #change to SVG to import into illustrator, etc
```

```
  ggsave(filename = paste(protein,".png",sep=""), plot = p, width = 8, height = 8)
}
```

```
#FATCAT and TMalign data visualization v0.2
#IB 12.14.22
#Requires properly-formatted TM-align + FATCAT datafiles
#Requires a "working_prot.txt" list of input files
#change working directory as appropriate

#next: work on limiting "too many hit" plots

library(ggplot2)
library(ggimage)
library(ggrepel)
library(ggnewscale)


protList <-read.table("/home/ian/homology_search/fcresults/working_prot.txt")
protList <- unlist(protList)

cols <- c("Mouse" = "paleturquoise1", "Human" = "mediumspringgreen", "Danio" = "plum1",
"Fly" = "khaki1")

for (protein in protList) {
  setwd("/home/ian/homology_search/fcresults/fat_tm_merge/converted")
  hasHits <- 0
  mouseData <- read.table(header = TRUE, text=gsub(" ", "\t",
readLines(paste(protein,".pdb.mouse.txt",sep=""))))
  humanData <- read.table(header = TRUE, text=gsub(" ", "\t",
readLines(paste(protein,".pdb.human.txt",sep=""))))
  danioData <- read.table(header = TRUE, text=gsub(" ", "\t",
readLines(paste(protein,".pdb.danio.txt",sep=""))))
  flyData   <- read.table(header = TRUE, text=gsub(" ", "\t",
readLines(paste(protein,".pdb.drosophila.txt",sep=""))))

  #append source genome name - used later when annotating graphs
  mouseData$Proteome <- "Mouse"
  humanData$Proteome <- "Human"
  danioData$Proteome <- "Danio"
  flyData$Proteome <- "Fly"

  testData <- merge(humanData, mouseData, all = TRUE)
  testData <- merge(testData, danioData, all = TRUE)
```

```
  testData <- merge(testData, flyData, all = TRUE)

  #Hits defined as TM score > 0.6 AND FATCAT P-value < 0.01
  hits <- testData[testData$TM2 > 0.6, ]
  hits <- hits[-log10(hits$P.value)>2, ]

  #if no hits, instead label the top .01% of results from each tool

    topP <- quantile(-log10(testData$P.value), probs = .9999)
    topTM <- quantile(testData$TM2, probs = .9999)
    toLabel <- testData[testData$TM2>topTM, ]
    toLabel2 <- testData[-log10(testData$P.value)>topP, ]
    toLabel3 <- rbind(toLabel, toLabel2)
    finalLabel <- unique(toLabel3)

  if(hasHits) {
    graphTitle<-protein
  } else {
    graphTitle<-paste(protein, ": No hits, top-scoring values are indicated")
  }



  p <- ggplot(testData, aes(x=TM2, y=(-log10(P.value)))) +
    ggtitle(graphTitle) +
    xlab("TM Score") +
    ylab(bquote(Log[10]~P-value~FATCAT)) +
    geom_point(data = humanData, aes(x=TM2, y=(-log10(P.value)), size=1,
color=factor(cut(RMSD.1, c(0,2,3,5,Inf))))) +
    geom_point(data = mouseData, aes(x=TM2, y=(-log10(P.value)), size=1,
color=factor(cut(RMSD.1, c(0,2,3,5,Inf))))) +
    geom_point(data = danioData, aes(x=TM2, y=(-log10(P.value)), size=1,
color=factor(cut(RMSD.1, c(0,2,3,5,Inf))))) +
    geom_point(data = flyData,   aes(x=TM2, y=(-log10(P.value)), size=1,
color=factor(cut(RMSD.1, c(0,2,3,5,Inf))))) +
    labs(color="RMSD")+
    scale_color_brewer(palette="YlGn", labels = c("0-1","2-3","3-5","5+"), direction=-1,
drop=FALSE) +
    new_scale_color() +
    new_scale_fill() +
    geom_label_repel(data = finalLabel, aes(label=Entry, fill=Proteome),
                  #color = rep(c("green","red","yellow","blue")[as.factor(finalLabel$Proteome)],times
= 2),
                  seed = 2, box.padding = 1, nudge_x = 0, min.segment.length = 0, segment.size = 1,
segment.color="darkslategrey", max.overlaps = Inf)+ #Inf overlaps leads to issues
```

```
    scale_fill_manual(values = cols,
                labels = c("Mouse", "Human", "Danio", "Fly")) +

    guides(fill = guide_legend(override.aes = aes(color = NA))) +
    guides(size = "none") +

    theme(
          panel.background = element_blank(),
          panel.border = element_blank(),
          panel.grid.major = element_line(size = 0.1, color = "black", linetype = "dashed"),
          panel.grid.minor = element_blank(),
          axis.line = element_line(color="black"),

          plot.title = element_text(hjust = 0.5),
          legend.position = c(0.06, 0.75)
      )

  setwd("/home/ian/homology_search/fcresults")
  ggsave(filename = paste(protein,"_toponly_uniprot.png",sep=""), plot = p, width = 8, height =
8)
}
```

```
#FATCAT and TMalign data visualization v0.2
#IB 10.11.2022
#Requires properly-formatted TM-align + FATCAT datafiles
#Requires a "working_prot.txt" list of input files
#change working directory as appropriate

library(ggplot2)
library(ggimage)
library(ggrepel)
library(ggnewscale)


protList <-read.table("/home/ian/homology_search/fcresults/working_prot.txt")
protList <- unlist(protList)

cols <- c("Mouse" = "paleturquoise1", "Human" = "mediumspringgreen", "Danio" = "plum1",
"Fly" = "khaki1")

for (protein in protList) {
```

```
  setwd("/home/ian/homology_search/fcresults/fat_tm_merge/converted")
  hasHits <- 0
  mouseData <- read.table(header = TRUE, text=gsub(" ", "\t",
readLines(paste(protein,".pdb.mouse.txt",sep=""))))
  humanData <- read.table(header = TRUE, text=gsub(" ", "\t",
readLines(paste(protein,".pdb.human.txt",sep=""))))
  danioData <- read.table(header = TRUE, text=gsub(" ", "\t",
readLines(paste(protein,".pdb.danio.txt",sep=""))))
  flyData   <- read.table(header = TRUE, text=gsub(" ", "\t",
readLines(paste(protein,".pdb.drosophila.txt",sep=""))))

  #append source genome name - used later when annotating graphs
  mouseData$Proteome <- "Mouse"
  humanData$Proteome <- "Human"
  danioData$Proteome <- "Danio"
  flyData$Proteome <- "Fly"

  testData <- merge(humanData, mouseData, all = TRUE)
  testData <- merge(testData, danioData, all = TRUE)
  testData <- merge(testData, flyData, all = TRUE)

  #Hits defined as TM score > 0.6 AND FATCAT P-value < 0.01
  hits <- testData[testData$TM2 > 0.6, ]
  hits <- hits[-log10(hits$P.value)>2, ]

  #if no hits, instead label the top .01% of results from each tool
  if (nrow(hits)>0){
    finalLabel <- hits
    hasHits <- 1
  } else {
    topP <- quantile(-log10(testData$P.value), probs = .9999)
    topTM <- quantile(testData$TM2, probs = .9999)
    toLabel <- testData[testData$TM2>topTM, ]
    toLabel2 <- testData[-log10(testData$P.value)>topP, ]
    toLabel3 <- rbind(toLabel, toLabel2)
    finalLabel <- unique(toLabel3)
  }

  if(hasHits) {
    graphTitle<-protein
  } else {
    graphTitle<-paste(protein, ": No hits, top-scoring values are indicated")
  }
```

```
  p <- ggplot(testData, aes(x=TM2, y=(-log10(P.value)))) +
    ggtitle(graphTitle) +
    xlab("TM Score") +
    ylab(bquote(Log[10]~P-value~FATCAT)) +
    geom_point(data = humanData, aes(x=TM2, y=(-log10(P.value)), size=1,
color=factor(cut(RMSD.1, c(0,2,3,5,Inf))))) +
    geom_point(data = mouseData, aes(x=TM2, y=(-log10(P.value)), size=1,
color=factor(cut(RMSD.1, c(0,2,3,5,Inf))))) +
    geom_point(data = danioData, aes(x=TM2, y=(-log10(P.value)), size=1,
color=factor(cut(RMSD.1, c(0,2,3,5,Inf))))) +
    geom_point(data = flyData,   aes(x=TM2, y=(-log10(P.value)), size=1,
color=factor(cut(RMSD.1, c(0,2,3,5,Inf))))) +
    labs(color="RMSD")+
    scale_color_brewer(palette="YlGn", labels = c("0-1","2-3","3-5","5+"), direction=-1,
drop=FALSE) +
    new_scale_color() +
    new_scale_fill() +
    geom_label_repel(data = finalLabel, aes(label=Gene, fill=Proteome),
                #color = rep(c("green","red","yellow","blue")[as.factor(finalLabel$Proteome)],times
= 2),
                seed = 2, box.padding = 1, nudge_x = 0, min.segment.length = 0, segment.size = 1,
segment.color="darkslategrey", max.overlaps = Inf)+ #Inf overlaps leads to issues
    scale_fill_manual(values = cols,
                 labels = c("Mouse", "Human", "Danio", "Fly")) +

    guides(fill = guide_legend(override.aes = aes(color = NA))) +
    guides(size = "none") +

    theme(
          panel.background = element_blank(),
          panel.border = element_blank(),
          panel.grid.major = element_line(size = 0.1, color = "black", linetype = "dashed"),
          panel.grid.minor = element_blank(),
          axis.line = element_line(color="black"),

          plot.title = element_text(hjust = 0.5),
          legend.position = c(0.06, 0.75)
       )

  setwd("/home/ian/homology_search/fcresults")
  ggsave(filename = paste(protein,".png",sep=""), plot = p, width = 8, height = 8)
}
```

```bash
#!/bin/bash
#Finalized by Ian Boys ~10.2022
#Merges FATCAT and TM-align search results for visualization and analysis in R
#Make sure to QC FATCAT files first to ensure that runs completed
#Requires FATCAT and TM-align search results in separate "FATCAT" and "TM" folders in root directory
#Requires UNIPROT gene name/accession ID conversion lists under "IDs" in root directory
#Naming conventions are those used in FATCAT CHPC scripts and local TM-align scripts. Modify below if required

#set up directories
#rootdir=$(pwd)
rootdir="$( cd -- "$(dirname "$0")" >/dev/null 2>&1 ; pwd -P )"
mkdir TM/TMconvert
mkdir res
mkdir final
mkdir final/converted
echo $rootdir

#remove "pound" and CPU time report from TMalign results
cd "$rootdir/TM"
for file in *.txt; do
	#sed -i '$ d' $file #remove the last line
	sed '1s/^.//' $file > TMconvert/$file #get rid of the first character (#)
done
cd $rootdir

#rename FATCAT files to use same naming as TMalign
for fatfile in FATCAT/*.FATCAT.txt.scores.txt; do
	mv -- "$fatfile" "${fatfile%.FATCAT.txt.scores.txt}.txt"
done
cd $rootdir

#join FATCAT and TMalign files
for file in TM/TMconvert/*; do
	name=${file##*/}

	if [ -f "FATCAT/$name" ]; then
		paste "$file" "FATCAT/$name" > "res/$name"
	fi
done
cd $rootdir
```

```
#append gene names to existing tables
for file in res/*; do
	name=${file##*/}

	case $name in
		*"human"*)
			paste "IDs/humanIDs.tsv" "res/$name" > "final/$name";;
		*"drosophila"*)
			paste "IDs/flyIDs.tsv" "res/$name" > "final/$name";;
		*"danio"*)
			paste "IDs/danioIDs.tsv" "res/$name" > "final/$name";;
		*"mouse"*)
			paste "IDs/mouseIDs.tsv" "res/$name" > "final/$name";;

	esac
done

#removes "short match" (ie failed) TM-align results, as these interfere w/ downstream analysis
cd $rootdir/final
for file in *.txt; do
	grep -v "Short match" $file > converted/$file
done
```

```
#!/bin/bash
#check for expected last ID within fatcat file, echo problem files to log.txt

for file in *.txt; do
	name=${file##*/}

	case $name in
		*"human"*)
			if ! grep -q "X6R8D5" $file; then echo $file >> log.txt ; fi ;;
		*"drosophila"*)
			if ! grep -q "X4YX01" $file; then echo $file >> log.txt ; fi ;;
		*"danio"*)
			if ! grep -q "Z4YHZ5" $file; then echo $file >> log.txt ; fi ;;
		*"mouse"*)
			if ! grep -q "W8DXL4" $file; then echo $file >> log.txt ; fi ;;
	esac
done
```

```
#!/bin/bash

outfile="secondary_structures.txt"
numss=0

for FILE in *.pdb
do
	stride $FILE > $FILE.stride
done

for FILE in *.stride
do
	echo -n $FILE >> $outfile
	while read line
	do
		if [[ ${line:0:3} == 'LOC' ]]
		then
			((numss++))
		fi
	done < $FILE
	echo -n " " >> $outfile
	echo $numss >> $outfile
	numss=0
done
```