Table S1. A description of TRACEvar features.

Table S1A. A description of TRACEvar tissue-specific features.

Feature Group	Data Source	Number of Features	Feature Name[1]	Description	Links
Adult Expression	Ref[41], Ref[42]	65	t_expression, t_age_Development	Gene expression level in adult tissues	https://gtexportal.org/home/, https://apps.kaessmannlab.org/evodevoapp/
Young Expression	Ref[42]	33	t_age_Development	Gene expression level in newborn to young adult tissues	https://apps.kaessmannlab.org/evodevoapp/
Preferential Expression	Ref[40]	54	t_preferential_expression	Preferential expression of the gene in adult tissue samples	
Process Activity	Ref[47]	112	t_max_tipa_pathways, t_min_tipa_pathways, t_median_tipa_pathways, t_mean_tipa_pathways	Activity of GO processes that include the gene in adult tissues	https://netbio.bgu.ac.il/tipa2/
Differential PPIs	Ref[50]	176	t_diff_net_max, t_diff_net_min, t_diff_net_med, t_mean, t_diff_net_max, t_diff_net_min, t_diff_net_med	Differential protein-protein interation (PPIs) scores of the gene in adult tissues	https://netbio.bgu.ac.il/diffnet/
PPIs	Ref[6]	486	t_num_interactors, t_num_interactors_dif_med, t_num_interactors_dif_mean, t_num_elevated_interactors,t _num_elevated_interactors_dif_median,t _num_elevated_interactors_dif_mean, t_num_specific_interactions ,t _num_specific_interactions_dif_median, t_num_specific_interactions_dif_mean	The number of PPIs o the gene in adult tissues	https://netbio.bgu.ac.il/myproteinnet2/
Paralog Relationships	Ref[31]	106	t_paralogs_ratio_highest_identity, t_paralogs_ratio_all	The ratio between the expression levels of the gene and its paralog(s) in adult tissues	
eQTL	Ref[41]	48	t_egene	eQTL involving the gene in adult tissues	GTEx Portal
Expression Variability	Ref[40]	19	t_LCV	Gene expression variability between individuals in adult tissues	
Embryonic Expression	Ref[42]	90	t_wpc_Development	Gene expression level in embrionic samples	https://apps.kaessmannlab.org/evodevoapp/
Expression Variability Across Ages	Ref[40]	7	t_CV	Time point specificity of gene expression level across age	

[1] t stands for the name of the relevant tissue; age stands for age of the sample donor; wpc stands for weeks post conception.

Table S1B. A description of variant-specific features from CADD.

Feature Group	Number of Features	Feature Name[1]
Conservation, Evolution	11	priPhCons, mamPhCons, verPhCons, priPhyloP, mamPhyloP, verPhyloP, GerpRS, GerpRSpval, GerpN, GerpS, Grantham
Variation Frequency	10	Freq100bp, Rare100bp, Sngl100bp, Freq1000bp, Rare1000bp, Sngl1000bp, Freq10000bp, Rare10000bp, Sngl10000bp, Dist2Mutation
Variation Consequence	8	Consequence_
Pathogenicity Scores	5	RawScore, PHRED, SIFTval, PolyPhenVal, ConsScore
micro-RNA	3	mirSVR-Score, mirSVR-E, mirSVR-Aln
Domain	5	Domain_
Variation Type	4	Length, Type_
Variation location	13	cDNApos, relcDNApos, CDSpos, relCDSpos, protPos, relProtPos, minDistTSS, AnnoType_CodingTranscript, AnnoType_Intergenic, AnnoType_NonCodingTranscript, AnnoType_Transcript, Consequence_3PRIME_UTR, Consequence_5PRIME_UTR
TF Binding Motif	9	motifECount, motifEHIPos, motifEScoreChng, motifDist, minDistTSE, TFBS, TFBSPeaks, TFBSPeaksMax, tOverlapMotifs
Chromatin State	32	cHmm, Enc
Splicing	15	MMSp_acceptorIntron, MMSp_acceptor, MMSp_exon, MMSp_donor, MMSp_donorIntron, Consequence_SPLICE_SITE, Dst2Splice, SpliceAI-acc-gain, SpliceAI-acc-loss, SpliceAI-don-gain, SpliceAI-don-loss, Dst2SplType_ACCEPTOR, Dst2SplType_DONOR, Consequence_CANONICAL_SPLICE, dbscSNV-ada_score
GC Content	2	GC, CpG

[1] Missing values were generally replaced by 0. Missing values for the following features appear in parenthesis: Chromatin State features (0.067), SIFTval(1), GC(0.42), CqG(0.02), priPhCons(0.115), mamPhCons(0.079), verPhCons(0.094),priPhyloP(-0.033), mamPhyloP(-0.038), verPhyloP(0.017), GerpN(1.91), GerpS(-0.2).

Table S2. Number of variants per tissue in the dataset.

Tissue	Causal Genes[1]	Benign Genes	Pathogenic Variants	Benign Variants	Fraction of Pathogenic Variants
Pituitary	27	9095	272	67661	0.004003945
Ovary	44	9078	280	67653	0.004121708
Liver	53	9069	484	67449	0.007124667
Brain basal ganglia	51	9071	488	67445	0.007183548
Blood	72	9050	536	67397	0.007890127
Tibial nerve	73	9049	563	67370	0.008287577
Artery	22	9100	585	67348	0.008611426
Lung	47	9075	633	67300	0.009318005
Brain spinal cord	58	9064	676	67257	0.009950981
Testis	111	9011	775	67158	0.011408299
Skin	115	9007	1337	66596	0.019681156
Brain Cerebellum	175	8947	1706	66227	0.025112979
Skeletal muscle	113	9009	1771	66162	0.026069804
Brain Cortex	128	8994	1811	66122	0.02665862
Heart	131	8991	1946	65987	0.028645872
Kidney	91	9031	2051	65882	0.030191512
General brain	515	8607	5892	62041	0.086732516

[1] Causal Genes refers to genes that contain pathogenic variants.

Table S3. A summary of patient cases and the rank of the pathogenic variant by different methods.

Table S3A. Patient cases metadata.

Case	Patient ID	Tissue	Disease Name	Number of Candidate Variants
AFOtB1305_Heart - Left Ventricle	OtB1305	Heart	Atrial fibrillation	542
AgenesisOfCC16550_brain	16550	Brain	AGENESIS OF CORPUS CALLOSUM	111
Ataxia13863_brain	13863	Brain	Ataxia	127
AtaxiaOtB0926_brain	OtB0926	Brain	Ataxia	145
ATLDOt4998_brain	Ot4998	Brain	Ataxia telangiectasia like disorder - ATLD	1528
Autism13498_brain	13498	Brain	Autism	241
AzoospermiaPMRRP28085_brain	28085	Brain	Azoospermia + PMR + RP	152
AzoospermiaPMRRP28085_Testis	28085	Brain	Azoospermia + PMR + RP	152
CardiacNeuralSyndrome41621_brain	41621	Brain	Cardiac Neural Syndrome	115
CardiacNeuralSyndrome41621_Heart - Left Ventricle	41621	Brain	Cardiac Neural Syndrome	115
CardiacNeuralsyndromeOtA46052_brain	OtA4605	Brain	PMR+Hypotonia	321
CardiomyopathyOtB0551_Heart - Left Ventricle	OtB0551	Heart	Cardiomyopathy	195
ComplexVDefOB13_brain	OB13	Brain	Complex V deficiency	310
ComplexVDefOB13_Muscle - Skeletal	OB13	Brain	Complex V deficiency	310
DevDelay5148_brain	5148	Brain	Developmental delay	187
diaphragmaticherniaOt2822_Muscle - Skeletal	Ot2822	Muscle - Skeletal	diaphragmatic hernia	358
EctodermalOtB0548_Skin - Not Sun Exposed	OtB0548	Skin	Ectodermal dysplasia	526
EctodermalOtB0549_Skin - Not Sun Exposed	OtB0549	Skin	Ectodermal dysplasia	511
EctodermalOtB0550_Skin - Not Sun Exposed	OtB0550	Skin	Ectodermal dysplasia	565
HSP13393_Muscle - Skeletal	13393	Muscle - Skeletal	Hereditary Spastic Paraparesis (HSP)	152
HSP16390_Muscle - Skeletal	16390	Muscle - Skeletal	HSP	137
HSP5199_brain	5199	Brain	Int disability+epilepsy+spastic q-plegia	700
HypotoniadevdelayOtA8152_brain	OtA8152	Brain	hypotonia and global neuro-developmental delay	192
HypotoniadevdelayOtA8152_Muscle - Skeletal	OtA8152	Brain	hypotonia and global neuro-developmental delay	192
HypotoniaOt2812_Muscle - Skeletal	Ot2812	Muscle - Skeletal	Hypotonia	1715

Leighsyndrome766M_brain	766M	Brain	Leigh syndrome	163
Metabolic16028_brain	16028	Brain	Metabolic-Neurologic disease	998
Microcephaly2922_brain	2922	Brain	microcephaly and epilepsy	206
MicrocephalyOB2_brain	OB2	Brain	Microcephaly + PMR	348
MicrocephalyOB3_brain	OB3	Brain	Microcephaly + PMR	309
MicrocephalyOB43_brain	OB43	Brain	microcephaly	272
MicrocephalyOt1097_brain	Ot1097	Brain	Microcephaly	1071
MicrocephalyOt5010_brain	Ot5010	Brain	microcephaly	376
MicrocephalyOtB0918_brain	OtB0918	Brain	Microcephaly + PMR	173
Migrane13859_brain	13859	Brain	Complicated migraine	134
Moyamoya13700_brain	13700	Brain	Moyamoya	178
Musculardystrophy13879_Muscle - Skeletal	13879	Muscle - Skeletal	Muscular dystrophy	203
Myopathy13786_Muscle - Skeletal	13786	Muscle - Skeletal	Myopathy	130
NPHPOB10_brain	OB10	Brain	NPHP	284
NPHPOt1114_brain	Ot1114	Brain	NPHP	330
NPHPOt1114_kidney	Ot1114	Brain	NPHP	330
NTDOtA4611_brain	OtA4611	Brain	NTD	799
OpticAtrophy16012_brain	16012	Brain	Optic atrophy plus	648
PCCAOt1103_brain	Ot1103	Brain	PCCA	364
PCCAOt1104_brain	Ot1104	Brain	PCCA	329
PMR1055M_brain	1055M	Brain	Severe Retardation	129
PMR13595_brain	13595	Brain	PMR	998
PMR16009_brain	16009	Brain	Mental retardation syndrome	1052
PMROt2823_brain	Ot2823	Brain	Mental Retardation	345
SeckelSyndromeSS2_brain	S2	Brain	Seckel Syndrome	182
Skin16264_Skin - Not Sun Exposed	16264	Skin	Ectodermal Dysplasia	102
SpasticParaparesisOt5005_Muscle - Skeletal	Ot5005	Muscle - Skeletal	Hereditary Spastic Paraparesis (HSP)	1052
Strabismus13556_brain	13556	Brain	strabismus, mental retardation, short stature	120
Strabismus13566_brain	13566	Brain	strabismus, mental retardation, short stature	132
Usher16032_brain	16032	Brain	Usher syndrome	179

Zellweger16114_brain	16114	Brain	Zellweger syndrome	134
Zellwegersyndrome13414_brain	13414	Brain	Zellweger syndrome	241

Table S3B. Description of Pathogenic variants.

Case	ACMG[1] Classification	Gene Name	Gene ID	Chromosome	Position	Reference	Alternative	Type
AFOtB1305_Heart - Left Ventricle	PM2 PP3 PS3 PP1	KCND2	ENSG00000184408	7	120381650	C	G	SNV
AgenesisOfCC16550_brain	PM2 PP3 PP1	L1CAM	ENSG00000198910	X	153135948	C	T	SNV
Ataxia13863_brain	PM2 PP3 PVS1 PP1	SACS	ENSG00000151835	13	23928836	ACA	A	DEL
AtaxiaOtB0926_brain	PM2 PP3 PP2 PP1	ATM	ENSG00000149311	11	108121706	T	C	SNV
ATLDOt4998_brain	PM2 PP3 PP1	MRE11A	ENSG00000020922	11	94219114	T	C	SNV
Autism13498_brain	PM2 PP3 PS3 PP1	PAK3	ENSG00000077264	X	110385360	C	G	SNV
AzoospermiaPMRRP28085_brain	PM2 PP3 PM4 PS3 PP1	SCAPER	ENSG00000140386	15	76866531	AG	A	DEL
AzoospermiaPMRRP28085_Testis	PM2 PP3 PM4 PS3 PP1	SCAPER	ENSG00000140386	15	76866531	AG	A	DEL
CardiacNeuralSyndrome41621_brain	PM2 PP3 PM4 PP1	RECQL4	ENSG00000160957	8	145738492	AAT	A	DEL
CardiacNeuralSyndrome41621_Heart - Left Ventricle	PM2 PP3 PM4 PP1	RECQL4	ENSG00000160957	8	145738492	AAT	A	DEL
CardiacNeuralsyndromeOtA46052_brain	PM2 PP3 PM4 PS3 PP1	RSRC1	ENSG00000174891	3	157841665	C	T	SNV
CardiomyopathyOtB0551_Heart - Left Ventricle	PM2 PP3 PS3 PP1	PLEKHM2	ENSG00000116786	1	16055171	AAG	A	DEL
ComplexVDefOB13_brain	PM2 PP3 PP2 PP1	SLC25A1	ENSG00000100075	22	19164125	T	C	SNV
ComplexVDefOB13_Muscle - Skeletal	PM2 PP3 PP2 PP1	SLC25A1	ENSG00000100075	22	19164125	T	C	SNV
DevDelay5148_brain	PM2 PP3 PP1 PP5	TBCD	ENSG00000141556	17	80828204	G	A	SNV

diaphragmaticherniaOt2822_Muscle - Skeletal	PM2 PP3 PP1	SYNM	ENSG00000182253	15	99670425	G	T	SNV
EctodermalOtB0548_Skin - Not Sun Exposed	PM2 PP3 PP1 PP5	TP63	ENSG00000073282	3	189584501	G	A	SNV
EctodermalOtB0549_Skin - Not Sun Exposed	PM2 PP3 PP1 PP5	TP63	ENSG00000073282	3	189584501	G	A	SNV
EctodermalOtB0550_Skin - Not Sun Exposed	PM2 PP3 PP1 PP5	TP63	ENSG00000073282	3	189584501	G	A	SNV
HSP13393_Muscle - Skeletal	PM2 PP3 PM4 PS3 PP1	KY	ENSG00000174611	3	134369751	A	AATGTCGATAGATACAGCACATGTCGATA	INS
HSP16390_Muscle - Skeletal	PM2 PP3 PP1	DSTYK	ENSG00000133059	1	205130494	G	A	SNV
HSP5199_brain	PM2 PP3 PS3 PP1	DEGS1	ENSG00000143753	1	224377960	A	G	SNV
HypotoniadevdelayOtA8152_brain	PM2 PP3 PM4 PS3 PP1	PAX7	ENSG00000009709	1	19071306	A	G	SNV
HypotoniadevdelayOtA8152_Muscle - Skeletal	PM2 PP3 PM4 PS3 PP1	PAX7	ENSG00000009709	1	19071306	A	G	SNV
HypotoniaOt2812_Muscle - Skeletal	PM2 PP3 PS3 PP1	CCDC174	ENSG00000154781	3	14712701	A	G	SNV
Leighsyndrome766M_brain	PM2 PS1 PM1 PP1 PP5	COX15	ENSG00000014919	10	101483814	G	A	SNV
Metabolic16028_brain	PM2 PP3 PVS1 PP1	TMEM70	ENSG00000175606	8	74888621	A	AT	INS
Microcephaly2922_brain	PM2 PP3 PVS1 PP1	AIMP2	ENSG00000106305	7	6063012	ATC	A	DEL
MicrocephalyOB2_brain	PM2 PP3 PM4 PS3 PP1	UNC80	ENSG00000144406	2	210640622	C	T	SNV
MicrocephalyOB3_brain	PM2 PP3 PM4 PS3 PP1	UNC80	ENSG00000144406	2	210640622	C	T	SNV
MicrocephalyOB43_brain	PM2 PP3 PP2 PP1	SBF1	ENSG00000100241	22	50902962	C	T	SNV
MicrocephalyOt1097_brain	PM2 PP3 PS3 PP1	WDFY3	ENSG00000163625	4	85636503	G	A	SNV
MicrocephalyOt5010_brain	PM2 PP3 PP1	STIL	ENSG00000123473	1	47716848	AA	A	DEL
MicrocephalyOtB0918_brain	PM2 PP3 PM4 PS3 PP1	UNC80	ENSG00000144406	2	210640622	C	T	SNV
Migrane13859_brain	PM2 PP3 PP1	CACNA1A	ENSG00000141837	19	13414691	G	A	SNV

Moyamoya13700_brain	PM2 PP3 PP2 PP1 PP5	RNF213	ENSG00000173821	17	78343601	T	A	SNV
Musculardystrophy13879_Muscle - Skeletal	PM2 PS1 PS3 PP1 PP5	MPV17	ENSG00000115204	2	27535925	C	T	SNV
Myopathy13786_Muscle - Skeletal	PM2 PP3 PVS1 PP1	SGCG	ENSG00000102683	13	23898506	G	A	SNV
NPHPOB10_brain	PM2 PP3 PS3 PP1	SLC30A9	ENSG00000014824	4	42067341	AAGC	A	DEL
NPHPOt1114_brain	PM2 PP3 PS3 PP1	SLC30A9	ENSG00000014824	4	42067341	AAGC	A	DEL
NPHPOt1114_kidney	PM2 PP3 PS3 PP1	SLC30A9	ENSG00000014824	4	42067341	AAGC	A	DEL
NTDOtA4611_brain	PM2 PP3 PVS1 PP1 PP5	FKTN	ENSG00000106692	9	108382330	A	AA	INS
OpticAtrophy16012_brain	PM2 PP3 PM1 PP1	OPA1	ENSG00000198836	3	193360578	C	G	SNV
PCCAOt1103_brain	PM2 PP3 PS3 PP1	VPS53	ENSG00000141252	17	465738	C	T	SNV
PCCAOt1104_brain	PM2 PP3 PS3 PP1	VPS53	ENSG00000141252	17	465738	C	T	SNV
PMR1055M_brain	PM2 PP3 PM4 PS3 PP1	SEC31A	ENSG00000138674	4	83763483	A	ATA	INS
PMR13595_brain	PM2 PP3 PM1 PP1	PGAP2	ENSG00000148985	11	3846278	G	A	SNV
PMR16009_brain	PM2 PP3 PP2 PP1 PP5	ZC4H2	ENSG00000126970	X	64137701	G	A	SNV
PMROt2823_brain	PM2 PP3 PM4 PP1	UBE3B	ENSG00000151148	12	109928849	G	A	SNV
SeckelSyndromeSS2_brain	PM2 PP3 PVS1 PS3 PP1	CENPJ	ENSG00000151849	13	25459823	T	C	SNV
Skin16264_Skin - Not Sun Exposed	PM2 PP3 PVS1 PP1	EOGT	ENSG00000163378	3	69037455	AT	A	DEL
SpasticParaparesisOt5005_Muscle - Skeletal	PM2 PP3 PM4 PS3 PP1	KY	ENSG00000174611	3	134369751	ACGATCAGCAG	A	DEL
Strabismus13556_brain	PM2 PP3 PP2 PP1	NF1	ENSG00000196712	17	29559867	C	A	SNV
Strabismus13566_brain	PM2 PP3 PP2 PP1	NF1	ENSG00000196712	17	29559867	C	A	SNV

Usher16032_brain	PM2 PP3 PVS1 PP1	GPR98	ENSG00000164199	5	90059126	AT	A	DEL
Zellweger16114_brain	PM2 PP3 PVS1 PP1	PEX6	ENSG00000124587	6	42934534	AC	A	DEL
Zellwegersyndrome13414_brain	PM2 PP3 PM1 PP1	HSD17B4	ENSG00000133835	5	118814660	A	AT	INS

[1] The American College of Medical Genetics and Genomics (ACMG).

Table S3C. The rank of pathogenic variants by different methods.

Case	TRACE Rank	CAPICE Rank	CADD Rank	Sift Rank	PolyPhen Rank
AFOtB1305_Heart - Left Ventricle	168	210	243	349	276
AgenesisOfCC16550_brain	32	77	44	36	49.5
Ataxia13863_brain	13	1	56		NA
AtaxiaOtB0926_brain	4	9	6	12	26
ATLDOt4998_brain	352	656	359.5	261	171
Autism13498_brain	5	1	47	20.5	5.5
AzoospermiaPMRRP28085_brain	1	1	24.5	NA	NA
AzoospermiaPMRRP28085_Testis	62	1	24.5	NA	NA
CardiacNeuralSyndrome41621_brain	6	1	12.5	NA	NA
CardiacNeuralSyndrome41621_Heart - Left Ventricle	38.5	1	12.5	NA	NA
CardiacNeuralsyndromeOtA46052_brain	1	1	2	NA	NA
CardiomyopathyOtB0551_Heart - Left Ventricle	43	2	1	NA	NA
ComplexVDefOB13_brain	118	69	95.5	30	42
ComplexVDefOB13_Muscle - Skeletal	80	69	95.5	30	42
DevDelay5148_brain	15	3	31	12.5	19.5
diaphragmaticherniaOt2822_Muscle - Skeletal	12	330	170	74.5	26

EctodermalOtB0548_Skin - Not Sun Exposed	1	24	15	94.5	74
EctodermalOtB0549_Skin - Not Sun Exposed	4	26	19.5	114.5	73.5
EctodermalOtB0550_Skin - Not Sun Exposed	3	26	18.5	104.5	82.5
HSP13393_Muscle - Skeletal	51	NA	15	NA	NA
HSP16390_Muscle - Skeletal	32	20	5.5	17	9.5
HSP5199_brain	154	248	205	166.5	141
HypotoniadevdelayOtA8152_brain	61	27	2	NA	NA
HypotoniadevdelayOtA8152_Muscle - Skeletal	1	27	2	NA	NA
HypotoniaOt2812_Muscle - Skeletal	687	113	1227.5	NA	NA
Leighsyndrome766M_brain	6	5	9	15	3
Metabolic16028_brain	133	195	424.5	NA	NA
Microcephaly2922_brain	38	15	31.5	NA	NA
MicrocephalyOB2_brain	15	20	1.5	NA	NA
MicrocephalyOB3_brain	12	12	2	NA	NA
MicrocephalyOB43_brain	13	14	8	NA	NA
MicrocephalyOt1097_brain	84	215	104	65.5	34.5
MicrocephalyOt5010_brain	173	60	18.5	NA	NA
MicrocephalyOtB0918_brain	1	3	2	NA	NA
Migrane13859_brain	1	1	22	10.5	2
Moyamoya13700_brain	32	64	49	10.5	26
Musculardystrophy13879_Muscle - Skeletal	112	21	55	64.5	58
Myopathy13786_Muscle - Skeletal	2	12	3	NA	NA
NPHPOB10_brain	34	39	116.5	NA	NA
NPHPOt1114_brain	44	47	138	NA	NA
NPHPOt1114_kidney	172	47	138	NA	NA
NTDOtA4611_brain	9	NA	9	NA	NA
OpticAtrophy16012_brain	22	49	78	17.5	13.5
PCCAOt1103_brain	33	21	82.5	NA	NA
PCCAOt1104_brain	29	25	85.5	NA	NA
PMR1055M_brain	2	4	7	NA	NA

PMR13595_brain	169	397	197	178.5	136
PMR16009_brain	83	101	109	35	28
PMROt2823_brain	15	5	11	NA	NA
SeckelSyndromeSS2_brain	62	130	68	NA	NA
Skin16264_Skin - Not Sun Exposed	55	28	52	NA	NA
SpasticParaparesisOt5005_Muscle - Skeletal	260	105	85.5	NA	NA
Strabismus13556_brain	2	3	8	10	14
Strabismus13566_brain	11	1	15	9.5	14.5
Usher16032_brain	1	8	5	NA	NA
Zellweger16114_brain	1	2	5.5	NA	NA
Zellwegersyndrome13414_brain	4	14	9	NA	NA

Table S4. Tissue-specific features used by the TRACEvar multi-tissue model.

Feature Group	Number of Features	Feature Name
Adult Expression	1	t[1]_expression
Preferential Expression	1	t_preferential_expression
Process Activity	5	t_max_tipa_pathways, t_min_tipa_pathways, t_median_tipa_pathways, t_mean_tipa_pathways
PPIs	9	t_num_interactors, t_num_interactors_dif_med, t_num_interactors_dif_mean, t_num_elevated_interactors,t _num_elevated_interactors_dif_median,t _num_elevated_interactors_dif_mean, t_num_specific_interactions ,t _num_specific_interactions_dif_median, t_num_specific_interactions_dif_mean
Paralog Relationships	2	t_paralogs_ratio_highest_identity, t_paralogs_ratio_all

[1]_ t stands for the name of the relevant tissue.