

Extended Data Table 1 | Trypsin and chymotrypsin activities of snFPITE.

Parameter	point 1	point 2	Time (min)	ΔA_{253}	Concentration (mg/mL)	Activity (U/mg)
A253 (nm)	0.408	0.411	3	0.003	0.56	535.71
A256 (nm)	0.230	0.279	8	0.049	0.56	0.12

Extended Data Table 2 | The degradation of snFPITE on D-dimer.

Samples ID	+Saline	+snFPITE
	(D-dimer concentration, mg/L)	(D-dimer concentration, mg/L)
319	3.19	1.32
316	15.17	--
305	250	0
293	4.4	0
289	6.06	0.23

Note: "--" represents undetectable.

Extended Data Table 3 | The cleavage sites involved in the process of plasminogen activated by snFPITE

Steps	Sites
Step one	96K/97K, 97K/98V, 99Y/100L, 104K/105T, 111Y/112R, 343R/344W, 344W/345E, 346Y/347C, 348K/349I, 352C/353D, 359T/360E
Step two	120N/121G, 126K/127W, 127W/128S, 575K/576K, 580R/581V
Step three	479E/480D, 489Y/490R, 492K/493R, 493R/494A
Step four	565F/566D, 569K/570P

Note: Sites were the cleavage sites on the plasminogen (AAA60113.1); Steps were the mainly steps involved in the plasminogen activation.

Extended Data Table 4 | Statistics of data collection and refinement for molecular replacement.

Category	snFPITE-n1	snFPITE-n2
Data collection		
Space group	P 21 2 21	P 21 21 21
Cell dimensions		
<i>a</i> , <i>b</i> , <i>c</i> (Å)	40.315, 43.73, 121.59	39.262, 59.738, 193.702
α , β , γ (°)	90, 90, 90	90, 90, 90
Resolution (Å)	43.73 - 1.99 (2.04 - 1.99)	96.85 - 1.50 (1.53 - 1.50)
<i>R</i> _{merge}	0.021 (0.025)	0.077 (0.628)
<i>I</i> / σI	24.6 (14.9)	12.6 (2.6)
Completeness (%)	99.2 (95.9)	96.0 (99.9)
Redundancy	3.2 (2.5)	5.7 (5.7)
Refinement		
Resolution (Å)	1.99	1.50
No. reflections	15312	71213
<i>R</i> _{work} / <i>R</i> _{free}	0.1563 / 0.2047	0.1632 / 0.1864
No. atoms	2002	4045
Protein	1749	3520
Ligand/ion	15	80
Solvent	238	445
<i>B</i> -factors	24.10	20.28
Protein	22.89	18.57
Ligand/ion	43.32	41.15
Solvent	31.79	30.05
R.m.s. deviations		
Bond lengths (Å)	0.002	0.012
Bond angles (°)	0.50	1.14

*Values in parentheses are for the highest-resolution shell.

Extended Data Table 5 | *snFPITE* genes identified from *S. nudus*.

No.	ID	Identification methods	Notes
1	snFPITE-c1	Cloning, based on conserved sequences	Functionally verified with Pichia pastoris system
2	snFPITE-c2	Cloning, based on the transcriptome sequence	Protein sequence is identical to snFPITE-n1
3	snFPITE-c3	Cloning, based on the transcriptome sequence	
4	snFPITE-c4	Cloning, based on the transcriptome sequence	
5	snFPITE-c5	Cloning, based on the transcriptome sequence	
6	snFPITE-c6	Cloning, based on the transcriptome sequence	
7	snFPITE-c7	Cloning, based on the transcriptome sequence	
8	snFPITE-c8	Cloning, based on the transcriptome sequence	
9	snFPITE-c9	Cloning, based on the transcriptome sequence	
10	snFPITE-c10	Cloning, based on the transcriptome sequence	
11	snFPITE-n1	Mass spectroscopy	
12	snFPITE-n2	Mass spectroscopy	Contain A and B subunit, sequence of B is identical to snFPITE-n1.
13	snFPITE1	Genome sequencing	Functionally verified with HEK293 system
14	snFPITE2	Genome sequencing	
15	snFPITE3	Genome sequencing	
16	snFPITE4	Genome sequencing	
17	snFPITE5	Genome sequencing	Functionally verified with HEK293 system
18	snFPITE6	Genome sequencing	
19	snFPITE7	Genome sequencing	
20	snFPITE8	Genome sequencing	
21	snFPITE9	Genome sequencing	
22	snFPITE10	Genome sequencing	
23	snFPITE11	Genome sequencing	
24	snFPITE12	Genome sequencing	

25	snFPITE13	Genome sequencing	Functionally verified with HEK293 system
26	snFPITE14	Genome sequencing	
27	snFPITE15	Genome sequencing	Functionally verified with HEK293 system
28	snFPITE-p1	Genome sequencing	Functionally verified with HEK293 system
29	snFPITE-p2	Genome sequencing	

Extended Data Table 6 | Statistics of sequencing data using the Illumina sequencing platform.

Paired-end libraries	Insert size (kb)	Reads length (bp) (Raw / Clean)	Raw data (Gb)	Clean data (Gb)	Sequence depth (×) of clean data
Solexa Reads	0.45	250 / 248	181.89	158.75	95.06
	0.8	125 / 123	118.90	107.48	64.36
	2	49 / 47	65.35	21.21	12.70
	5	49 / 47	66.75	14.50	8.68
	10	49 / 47	60.00	13.86	8.30
	20	49 / 47	30.23	7.45	4.46
	40	49 / 47	28.67	8.25	4.94
Total	/	/	551.81	331.50	198.50

Note: We constructed two short libraries with insert size of 450 bp and 800 bp, respectively. The calculation of sequence depth was based on the assembled genome size of 1.67 Gb.

Extended Data Table 7 | Genome size estimation by the *k*-mer method with K=31.

K	Total <i>k</i>-mer Number	Peak depth	Genome size (Gb)	Used bases (bp)	Used reads
31	127,777,276,942	78	1.64	158,753,478,016	6,401,349,926

Note: The genome size was estimated according to the following formula: Genome size = (Total *k*-mer Number /Peak Depth).

Extended Data Table 8 | Statistics of the PacBio RS sequencing.

Libraries	Insert size (kb)	Cell number	Total subread length (Gb)	Sequence depth (×) *
PacBio Reads	20	43	36.17	21.23

Note: *The calculation of sequence depth was based on the assembled genome size of 1.67 Gb.

Extended Data Table 9 | Statistics of the *S. nudus* genome assembly.

Parameter	Contig		Scaffold	
	Size (bp)	Number	Size (bp)	Number
N90	7,957	47,150	160,856	2,652
N80	15,062	32,816	327,786	1,955
N70	21,880	24,025	441,155	1,504
N60	28,900	17,664	539,685	1,151
N50	36,759	12,733	651,131	858
Longest	477,862	/	3,350,528	/
Total Size	1,604,860,243	/	1,727,737,036	/
Total Number (≥ 100 bp)	/	136948	/	72,674
Total Number (≥ 2 kb)	/	72565	/	16,494

Extended Data Table 10 | Statistics of repetitive elements in the *S. nudus* genome.

Category	RepBase TEs		TE Proteins		De novo		Combined TEs	
	Length (bp)	% of Genome	Length (bp)	% of Genome	Length (bp)	% of Genome	Length (bp)	% of Genome
DNA	35,872,627	2.0763	3,438,284	0.1990	319,700,441	18.5040	337,391,276	19.5279
LINE	16,896,351	0.9779	26,899,754	1.5569	98,988,484	5.7294	119,072,992	6.8918
SINE	432,076	0.0250	0	0	3,639,846	0.2107	4,023,736	0.2329
LTR	20,314,925	1.1758	22,659,547	1.3115	206,789,208	11.9688	215,881,769	12.4951
Other	34,630	0.0020	0	0	85,675	0.0050	120,305	0.0070
Unknown	0	0	0	0	42,935,874	2.4851	42,935,874	2.4851
Total	66,108,479	3.8263	52,971,231	3.0659	614,147,574	35.5464	641,450,808	37.1267

Note: Repeat elements were identified by different methods and then combined into the final repeat set.

Extended Data Table 11 | Gene annotation of the *S. nudus* genome.

Gene set	Number	Average gene length (bp)	Average CDS length (bp)	Average exon per gene	Average exon length (bp)	Average intron length (bp)
<i>C. teleta</i>	33,866	19,937.37	554.32	2.74	202.31	11,140.22
<i>C. gigas</i>	19,459	22,357.16	588.24	3.24	181.29	9,697.84
<i>D. rerio</i>	18,722	40,116.89	634.71	3.21	198.00	17,900.99
<i>O. bimaculoides</i>	27,847	24,794.96	550.73	2.54	216.76	15,735.80
<i>P. caudatus</i>	17,986	22,616.73	552.79	2.90	190.34	11,586.63
RNA-Seq(transcripts)	70,689	12,633.40	1,793.49	5.18	346.54	2,596.09
Iso-Seq	14,085	15,796.82	2,493.06	5.56	448.35	2,917.20
Maker (Final set)	45,896	13,850.23	1,021.62	5.81	269.59	2,548.85

Note: Those genes with previous stop codons or ambiguous bases were filtered in the final gene set.

Extended Data Table 12 | Gene function annotation of *S. nudus*.

Classification		Number	Percentage (%)
Total genes		45,896	/
Annotated	InterPro	33,098	72.12
	GO	20,899	45.54
	COG	11,282	24.58
	KEGG	28,313	61.69
	Swissprot	27,404	59.71
	TrEMBL	34,618	75.43
	Nr	34,743	75.70
All annotated		36,951	80.51

Extended Data Table 13 | Gene families clustered in 14 representative species.

Species	#Total genes	Unclustered genes	#Families	#Unique families	Average genes per family
<i>C. elegans</i>	20,184	6,830	4,983	1,268	2.68
<i>C. teleta</i>	32,173	5,573	13,824	1,410	1.92
<i>C. gigas</i>	26,088	6,701	10,547	1,230	1.84
<i>D. rerio</i>	24,700	2,674	8,306	1,042	2.65
<i>D. melanogaster</i>	13,866	4,466	5,131	521	1.83
<i>H. robusta</i>	23,432	7,928	7,705	802	2.01
<i>L. anatina</i>	34,075	5,636	13,960	2,704	2.04
<i>L. gigantea</i>	23,340	4,092	11,798	771	1.63
<i>M. lignano</i>	49,016	1,930	11,049	5,494	4.26
<i>N. vectensis</i>	24,773	5,310	9,656	1,160	2.02
<i>O. bimaculoides</i>	33,608	15,584	9,988	746	1.8
<i>P. caudatus</i>	13,719	3,154	7,313	271	1.44
<i>S. purpuratus</i>	21,854	4,483	7,989	823	2.17
<i>S. nudus</i>	45,896	13,527	15,607	1,941	2.07

Note: Unique families: the specific gene families of this species.

Unclustered genes: those genes that are not clustered into any known gene family.

Extended Data Table 14 | Significantly enriched KEGG pathways in *S. nudus* significant expansion gene families

Pathway	Sample (264)	Background (28,360)	Q-value	Pathway ID
Lipoic acid metabolism	30	36	3.73E-54	ko00785
Glioma	46	210	4.73E-48	ko05214
Thyroid cancer	35	97	4.47E-45	ko05216
Acute myeloid leukemia	35	98	5.18E-45	ko05221
Long-term potentiation	46	283	4.25E-42	ko04720
Melanoma	35	123	3.34E-41	ko05218
Chronic myeloid leukemia	35	123	3.34E-41	ko05220
Endometrial cancer	35	129	1.95E-40	ko05213
Pancreatic cancer	35	133	5.79E-40	ko05212
Non-small cell lung cancer	35	134	6.99E-40	ko05223
Bladder cancer	35	138	2.01E-39	ko05219
Colorectal cancer	35	139	2.45E-39	ko05210
Natural killer cell mediated cytotoxicity	35	143	6.83E-39	ko04650
Neurotrophin signaling pathway	46	340	9.00E-39	ko04722
Progesterone-mediated oocyte maturation	35	157	2.16E-37	ko04914
Renal cell carcinoma	35	167	2.09E-36	ko05211
Insulin signaling pathway	46	384	2.09E-36	ko04910
Alcoholism	46	395	7.23E-36	ko05034
ErbB signaling pathway	35	178	1.97E-35	ko04012
Long-term depression	35	187	1.18E-34	ko04730
Prostate cancer	35	194	4.37E-34	ko05215
Vascular smooth muscle contraction	46	436	5.30E-34	ko04270
Chemokine signaling pathway	35	214	1.46E-32	ko04062
Hepatitis C	35	224	7.35E-32	ko05160
FoxO signaling pathway	35	225	8.29E-32	ko04068
MAPK signaling pathway - fly	35	293	9.42E-28	ko04013
Rap1 signaling pathway	46	674	8.49E-26	ko04015
mTOR signaling pathway	35	341	1.65E-25	ko04150
Dorso-ventral axis formation	41	533	5.61E-25	ko04320
cAMP signaling pathway	46	744	4.88E-24	ko04024

Tyrosine metabolism	28	221	4.75E-23	ko00350
MAPK signaling pathway	35	450	1.56E-21	ko04010
Serotonergic synapse	35	478	1.08E-20	ko04726
Prion diseases	35	508	7.52E-20	ko05020
Regulation of actin cytoskeleton	35	513	1.00E-19	ko04810
Notch signaling pathway	35	546	7.13E-19	ko04330
Choline metabolism in cancer	29	347	7.94E-19	ko05231
Vitamin digestion and absorption	26	286	7.38E-18	ko04977
Proteoglycans in cancer	35	736	6.64E-15	ko05205
Metabolic pathways	97	4,748	8.26E-15	ko01100
Pathways in cancer	35	759	1.58E-14	ko05200
Transcriptional misregulation in cancer	27	440	2.76E-14	ko05202
Thyroid hormone signaling pathway	35	808	9.52E-14	ko04919
Focal adhesion	35	930	5.27E-12	ko04510
Ubiquinone and other terpenoid-quinone biosynthesis	13	98	1.63E-11	ko00130
MicroRNAs in cancer	35	1,056	1.68E-10	ko05206
Tuberculosis	36	1,204	1.42E-09	ko05152
Phenylalanine metabolism	13	145	2.23E-09	ko00360
Phototransduction	11	111	1.47E-08	ko04744
Phagosome	34	1,236	3.31E-08	ko04145
Peroxisome	18	411	1.31E-07	ko04146
Retinol metabolism	18	510	2.97E-06	ko00830
Phototransduction - fly	11	209	8.24E-06	ko04745
Melanogenesis	11	230	2.00E-05	ko04916
Olfactory transduction	11	234	2.31E-05	ko04740
Gastric acid secretion	11	238	2.66E-05	ko04971
Pertussis	11	243	3.16E-05	ko05133
Oocyte meiosis	11	261	5.99E-05	ko04114
Glucagon signaling pathway	11	274	9.14E-05	ko04922
Amphetamine addiction	11	280	1.09E-04	ko05031
Circadian entrainment	11	301	2.03E-04	ko04713
GnRH signaling pathway	11	303	2.12E-04	ko04912
Phosphatidylinositol signaling system	11	307	2.34E-04	ko04070

Aldosterone synthesis and secretion	11	311	2.57E-04	ko04925
Adrenergic signaling in cardiomyocytes	11	314	2.71E-04	ko04261
Renin secretion	11	314	2.71E-04	ko04924
Pathogenic Escherichia coli infection	9	228	4.29E-04	ko05130
Estrogen signaling pathway	11	349	6.45E-04	ko04915
Dopaminergic synapse	11	375	1.15E-03	ko04728
Pentose and glucuronate interconversions	8	212	1.18E-03	ko00040
Gap junction	9	278	1.66E-03	ko04540
Alzheimer's disease	11	427	3.07E-03	ko05010
Oxytocin signaling pathway	11	457	5.06E-03	ko04921
cGMP-PKG signaling pathway	11	464	5.59E-03	ko04022
Inflammatory mediator regulation of TRP channels	11	465	5.60E-03	ko04750
Salivary secretion	11	466	5.62E-03	ko04970

Extended Data Table 15 | Significantly enriched KEGG pathway of *S. nudus* genes in unique gene families.

Pathway	Sample (3,440)	Background (28,360)	Q-value	Pathway ID
Tuberculosis	457	1204	9.891591e-121	ko05152
Phagosome	455	1236	8.947428e-115	ko04145
NOD-like receptor signaling pathway	241	662	6.016923e-58	ko04621
Salmonella infection	146	316	1.480982e-49	ko05132
Legionellosis	156	367	3.042418e-47	ko05134
Hematopoietic cell lineage	175	446	3.136179e-47	ko04640
Thyroid hormone signaling pathway	205	808	3.733105e-24	ko04919
MicroRNAs in cancer	240	1,056	2.849148e-21	ko05206
Notch signaling pathway	150	546	3.278668e-21	ko04330
Prion diseases	132	508	1.840520e-16	ko05020
Cell adhesion molecules (CAMs)	111	403	8.054951e-16	ko04514
Epstein-Barr virus infection	175	779	4.986685e-15	ko05169
Dorso-ventral axis formation	132	533	9.304868e-15	ko04320
Malaria	72	232	3.506186e-13	ko05144
Staphylococcus aureus infection	83	309	2.506523e-11	ko05150
ECM-receptor interaction	124	576	1.807470e-09	ko04512
Complement and coagulation cascades	78	359	3.241786e-06	ko04610
Intestinal immune network for IgA production	14	27	1.003254e-05	ko04672
Protein digestion and absorption	124	695	9.379729e-05	ko04974
PI3K-Akt signaling pathway	161	989	8.065024e-04	ko04151
Focal adhesion	148	930	4.324576e-03	ko04510
Transcriptional misregulation in cancer	78	440	4.847655e-03	ko05202
Histidine metabolism	27	115	6.458731e-03	ko00340
TNF signaling pathway	50	259	6.982528e-03	ko04668

Extended Data Table 16 | Summary of the 17 *snFPITE* genes identified from the *S. nudus* genome.

Gene ID	Description	AA length	AA identity	Exon number
snFPITE1	partial CDS, without start, stop codon	164	52.727	3
snFPITE2	Complete CDS	269	99.582	6
snFPITE3	Complete CDS	268	57.261	6
snFPITE4	partial CDS, without start, stop codon	239	55.187	5
snFPITE5	partial CDS, without start codon	164	52.727	3
snFPITE6	partial CDS, without start, stop codon	164	52.121	3
snFPITE7	Complete CDS	258	53.556	5
snFPITE8	partial CDS, without start, stop codon	240	57.438	5
snFPITE9	partial CDS, without stop codon	281	51.867	6
snFPITE10	partial CDS, without start, stop codon	164	50.91%	3
snFPITE11	partial CDS, without start, stop codon	164	50.91%	3
snFPITE12	partial CDS, without start, stop codon	178	50.28%	4
snFPITE13	Complete CDS	277	55.187	6
snFPITE14	partial CDS, without start, stop codon	104	78.846	2
snFPITE15	Complete CDS	267	51.037	6
snFPITE-p1	With premature stop codon	240	/	5
snFPITE-p2	With premature stop codon	166	/	3

Note: aa identity was calculated by comparing with the sequence of snFPITE-c1

Extended Data Table 17 | The 223 plasminogen genes downloaded from the KEGG database.

Gene ID in KEGG	New Gene IDs	Species Latin name (common name)
hsa:5340	Mammals_human_hsa	<i>Homo sapiens</i> (human)
ptr:463117	Mammals_chimpanzee_ptr	<i>Pan troglodytes</i> (chimpanzee)
pps:100982214	Mammals_bonobo_pps	<i>Pan paniscus</i> (bonobo)
ggo:101150968	Mammals_gorilla_ggo	<i>Gorilla gorilla gorilla</i> (western lowland gorilla)
pon:100172984	Mammals_orangutan_pon	<i>Pongo abelii</i> (Sumatran orangutan)
nle:101177406	Mammals_gibbon_nle	<i>Nomascus leucogenys</i> (northern white-cheeked gibbon)
mcc:703891	Mammals_monkey_mcc	<i>Macaca mulatta</i> (rhesus monkey)
mcf:102145643	Mammals_macaque_mcf	<i>Macaca fascicularis</i> (crab-eating macaque)
csab:103240838	Mammals_monkey_csab	<i>Chlorocebus sabaeus</i> (green monkey)
caty:105594241	Mammals_mangabey_caty	<i>Cercocebus atys</i> (sooty mangabey)
panu:101008370	Mammals_baboon_panu	<i>Papio anubis</i> (olive baboon)
rro:104670000	Mammals_monkey_rro	<i>Rhinopithecus roxellana</i> (golden snub-nosed monkey)
rbb:108527991	Mammals_monkey_rbb	<i>Rhinopithecus bieti</i> (black snub-nosed monkey)
tfn:117096916	Mammals_langur_tfn	<i>Trachypithecus francoisi</i> (Francois's langur)
pteh:111550287	Mammals_Colobus_pteh	<i>Ptilocolobus tephrosceles</i> (Ugandan red Colobus)
sbq:101028314	Mammals_monkey_sbq	<i>Saimiri boliviensis boliviensis</i> (Bolivian squirrel monkey)
csyr:103270361	Mammals_tarsier_csyr	<i>Carlito syrichta</i> (Philippine tarsier)
mmur:105868601	Mammals_lemur_mmur	<i>Microcebus murinus</i> (gray mouse lemur)
mmu:18815	Mammals_mouse_mmu	<i>Mus musculus</i> (mouse)
mcal:110312566	Mammals_mouse_mcal	<i>Mus caroli</i> (Ryukyu mouse)
mpah:110338193	Mammals_mouse_mpah	<i>Mus pahari</i> (shrew mouse)
rno:85253	Mammals_rat_rno	<i>Rattus norvegicus</i> (rat)
mcoc:116077314	Mammals_mouse_mcoc	<i>Mastomys coucha</i> (southern multimammate mouse)
mun:110554863	Mammals_gerbil_mun	<i>Meriones unguiculatus</i> (Mongolian gerbil)
cge:100761455	Mammals_hamster_cge	<i>Cricetulus griseus</i> (Chinese hamster)
pleu:114691365	Mammals_mouse_pleu	<i>Peromyscus leucopus</i> (white-footed mouse)
hgl:101703481	Mammals_rat_hgl	<i>Heterocephalus glaber</i> (naked mole rat)
cpoc:100725098	Mammals_pig_cpoc	<i>Cavia porcellus</i> (domestic guinea pig)
dord:105991843	Mammals_rat_dord	<i>Dipodomys ordii</i> (Ord's kangaroo rat)
dsp:122116130	Mammals_rat_dsp	<i>Dipodomys spectabilis</i> (banner-tailed kangaroo)

ocu:100357844	Mammals_rabbit_ocu	rat)
tup:102500037	Mammals_shrew_tup	<i>Oryctolagus cuniculus</i> (rabbit)
cfa:403602	Mammals_dog_cfa	<i>Tupaia chinensis</i> (Chinese tree shrew)
vvp:112932977	Mammals_fox_vvp	<i>Canis lupus familiaris</i> (dog)
vlg:121482051	Mammals_fox_vlg	<i>Vulpes vulpes</i> (red fox)
umr:103660825	Mammals_bear_umr	<i>Vulpes lagopus</i> (Arctic fox)
uah:113259627	Mammals_horribilis_uah	<i>Ursus maritimus</i> (polar bear)
uar:123797541	Mammals_bear_uar	<i>Ursus arctos horribilis</i>
oro:101380010	Mammals_walrus_oro	<i>Ursus americanus</i> (American black bear)
elk:111158701	Mammals_otter_elk	<i>Odobenus rosmarus divergens</i> (Pacific walrus)
mpuf:101674016	Mammals_ferret_mpuf	<i>Enhydra lutris kenyoni</i> (northern sea otter)
eju:114209283	Mammals_lion_eju	<i>Mustela putorius furo</i> (domestic ferret)
zca:113927514	Mammals_lion_zca	<i>Eumetopias jubatus</i> (Steller sea lion)
mlx:118001788	Mammals_seal_mlx	<i>Zalophus californianus</i> (California sea lion)
fca:101095261	Mammals_cat_fca	<i>Mirounga leonina</i> (Southern elephant seal)
pyu:121013217	Mammals_jaguarundi_pyu	<i>Felis catus</i> (domestic cat)
pbg:122490155	Mammals_cat_pbg	<i>Puma yagouaroundi</i> (jaguarundi)
ptg:102963262	Mammals_tiger_ptg	<i>Prionailurus bengalensis</i> (leopard cat)
ppad:109245399	Mammals_leopard_ppad	<i>Panthera tigris altaica</i> (Amur tiger)
aju:106985023	Mammals_cheetah_aju	<i>Panthera pardus</i> (leopard)
hhv:120224270	Mammals_hyena_hhv	<i>Acinonyx jubatus</i> (cheetah)
bta:280897	Mammals_cow_bta	<i>Hyaena hyaena</i> (striped hyena)
bom:102279186	Mammals_yak_bom	<i>Bos taurus</i> (cow)
biu:109564099	Mammals_cattle_biu	<i>Bos mutus</i> (wild yak)
bbub:102410794	Mammals_buffalo_bbub	<i>Bos indicus</i> (zebu cattle)
chx:102184723	Mammals_goat_chx	<i>Bubalus bubalis</i> (water buffalo)
oas:101112066	Mammals_sheep_oas	<i>Capra hircus</i> (goat)
oda:120862822	Mammals_oryx_oda	<i>Ovis aries</i> (sheep)
ccad:122434049	Mammals_wapiti_ccad	<i>Oryx dammah</i> (scimitar-horned oryx)
ssc:733660	Mammals_pig_ssc	<i>Cervus canadensis</i> (wapiti)
cfr:102520339	Mammals_camel_cfr	<i>Sus scrofa</i> (pig)
cbai:105077372	Mammals_camel_cbai	<i>Camelus ferus</i> (Wild Bactrian camel)
cdk:105086291	Mammals_camel_cdk	<i>Camelus bactrianus</i> (Bactrian camel)
bacu:103006994	Mammals_whale_bacu	<i>Camelus dromedarius</i> (Arabian camel)
lve:103073034	Mammals_dolphin_lve	<i>Balaenoptera acutorostrata scammoni</i> (minke whale)
oor:101277612	Mammals_whale_oor	<i>Lipotes vexillifer</i> (Yangtze River dolphin)
		<i>Orcinus orca</i> (killer whale)

dle:111167658	Mammals_whale_dle	<i>Delphinapterus leucas</i> (beluga whale)
pcad:102979031	Mammals_whale_pcad	<i>Physeter catodon</i> (sperm whale)
psiu:116763519	Mammals_vaquita_psiu	<i>Phocoena sinus</i> (vaquita)
ecb:100050531	Mammals_horse_ecb	<i>Equus caballus</i> (horse)
epz:103556183	Mammals_horse_epz	<i>Equus przewalskii</i> (Przewalski's horse)
eai:106842046	Mammals_ass_eai	<i>Equus asinus</i> (ass)
myb:102260529	Mammals_bat_myb	<i>Myotis brandtii</i> (Brandt's bat)
myd:102774931	Mammals_davidii_myd	<i>Myotis davidii</i>
mmyo:118660444	Mammals_myotis_mmyo	<i>Myotis myotis</i>
mlf:102424999	Mammals_bat_mlf	<i>Myotis lucifugus</i> (little brown bat)
mna:107535735	Mammals_natalensis_mna	<i>Miniopterus natalensis</i>
pkl:118705887	Mammals_pipistrelle_pkl	<i>Pipistrellus kuhlii</i> (Kuhl's pipistrelle)
dro:112297415	Mammals_bat_dro	<i>Desmodus rotundus</i> (common vampire bat)
shon:118995861	Mammals_hondurensis_shon	<i>Sturnira hondurensis</i>
ajm:119034890	Mammals_bat_ajm	<i>Artibeus jamaicensis</i> (Jamaican fruit-eating bat)
pdic:114490103	Mammals_bat_pdic	<i>Phyllostomus discolor</i> (pale spear-nosed bat)
phas:123822005	Mammals_bat_phas	<i>Phyllostomus hastatus</i> (greater spear-nosed bat)
mmf:118621651	Mammals_bat_mmf	<i>Molossus molossus</i> (Pallas's mastiff bat)
rfq:117017320	Mammals_bat_rfq	<i>Rhinolophus ferrumequinum</i> (greater horseshoe bat)
pale:102888257	Mammals_fox_pale	<i>Pteropus alecto</i> (black flying fox)
pgig:120618261	Mammals_fox_pgig	<i>Pteropus giganteus</i> (Indian flying fox)
pvp:105305678	Mammals_fox_pvp	<i>Pteropus vampyrus</i> (large flying fox)
ray:107514737	Mammals_rousette_ray	<i>Rousettus aegyptiacus</i> (Egyptian rousette)
mjv:108403113	Mammals_pangolin_mjv	<i>Manis javanica</i> (Malayan pangolin)
tod:119253032	Mammals_mole_tod	<i>Talpa occidentalis</i> (Iberian mole)
sara:101557844	Mammals_shrew_sara	<i>Sorex araneus</i> (European shrew)
lav:100664589	Mammals_elephant_lav	<i>Loxodonta africana</i> (African savanna elephant)
tmu:101342891	Mammals_manatee_tmu	<i>Trichechus manatus latirostris</i> (Florida manatee)
dnm:101433356	Mammals_armadillo_dnm	<i>Dasypus novemcinctus</i> (nine-banded armadillo)
mdo:100028030	Mammals_opossum_mdo	<i>Monodelphis domestica</i> (opossum)
gas:123246662	Mammals_Opossum_gas	<i>Gracilinanus agilis</i> (Agile Gracile Mouse Opossum)
shr:100928828	Mammals_devil_shr	<i>Sarcophilus harrisii</i> (Tasmanian devil)
pcw:110208618	Mammals_koala_pcw	<i>Phascolarctos cinereus</i> (koala)
oaa:100088128	Mammals_platypus_oaa	<i>Ornithorhynchus anatinus</i> (platypus)
gga:421580	Birds_chicken_gga	<i>Gallus gallus</i> (chicken)

pcoc:116243040	Birds_pheasant_pcoc	<i>Phasianus colchicus</i> (Ring-necked pheasant)
mgp:100548534	Birds_turkey_mgp	<i>Meleagris gallopavo</i> (turkey)
cjo:107311524	Birds_quail_cjo	<i>Coturnix japonica</i> (Japanese quail)
nmel:110396056	Birds_guineafowl_nmel	<i>Numida meleagris</i> (helmeted guineafowl)
apla:113839591	Birds_mallard_apla	<i>Anas platyrhynchos</i> (mallard)
acyg:106039506	Birds_goose_acyg	<i>Anser cygnoides domesticus</i> (swan goose)
aful:116487806	Birds_duck_aful	<i>Aythya fuligula</i> (tufted duck)
tgu:100228354	Birds_finch_tgu	<i>Taeniopygia guttata</i> (zebra finch)
lsr:110476048	Birds_finch_lsr	<i>Lonchura striata domestica</i> (Bengalese finch)
scan:103820555	Birds_canary_scan	<i>Serinus canaria</i> (common canary)
pmoa:120501342	Birds_sparrow_pmoa	<i>Passer montanus</i> (Eurasian tree sparrow)
otc:121335915	Birds_snowfinch_otc	<i>Onychostruthus taczanowskii</i> (white-rumped snowfinch)
pruf:121354960	Birds_snowfinch_pruf	<i>Pyrgilauda ruficollis</i> (rufous-necked snowfinch)
gfr:102036598	Birds_ground-finch_gfr	<i>Geospiza fortis</i> (medium ground-finch)
fab:101812892	Birds_flycatcher_fab	<i>Ficedula albicollis</i> (collared flycatcher)
phi:102104141	Birds_ground-tit_phi	<i>Pseudopodoces humilis</i> (Tibetan ground-tit)
pmaj:107202233	Birds_Tit_pmaj	<i>Parus major</i> (Great Tit)
ccae:111927697	Birds_tit_ccae	<i>Cyanistes caeruleus</i> (blue tit)
ccw:104690418	Birds_crow_ccw	<i>Corvus cornix</i> (hooded crow)
etl:114055648	Birds_flycatcher_etl	<i>Empidonax traillii</i> (willow flycatcher)
zab:102061612	Birds_sparrow_zab	<i>Zonotrichia albicollis</i> (white-throated sparrow)
fpg:101922752	Birds_falcon_fpg	<i>Falco peregrinus</i> (peregrine falcon)
fch:102056450	Birds_falcon_fch	<i>Falco cherrug</i> (Saker falcon)
clv:102089195	Birds_pigeon_clv	<i>Columba livia</i> (rock pigeon)
egz:104124822	Birds_egret_egz	<i>Egretta garzetta</i> (little egret)
nni:104018086	Birds_ibis_nni	<i>Nipponia nippon</i> (crested ibis)
acun:113478285	Birds_owl_acun	<i>Athene cunicularia</i> (burrowing owl)
tala:104366057	Birds_owl_tala	<i>Tyto alba</i> (Barn owl)
padl:103918269	Birds_penguin_padl	<i>Pygoscelis adeliae</i> (Adelie penguin)
ache:115344328	Birds_chrysaetos_ache	<i>Aquila chrysaetos chrysaetos</i>
aam:106486812	Birds_kiwi_aam	<i>Apteryx mantelli mantelli</i> (brown kiwi)
arow:112966413	Birds_kiwi_arow	<i>Apteryx rowi</i> (Okarito brown kiwi)
asn:102377482	Reptiles_alligator_asn	<i>Alligator sinensis</i> (Chinese alligator)
amj:102574160	Reptiles_alligator_amj	<i>Alligator mississippiensis</i> (American alligator)
cpoo:109320064	Reptiles_crocodile_cpoo	<i>Crocodylus porosus</i> (Australian saltwater crocodile)
ggn:109304721	Reptiles_Gharial_ggn	<i>Gavialis gangeticus</i> (Gharial)

pss:102446422	Reptiles_turtle_pss	<i>Pelodiscus sinensis</i> (Chinese soft-shelled turtle)
cmy:102936450	Reptiles_turtle_cmy	<i>Chelonia mydas</i> (green sea turtle)
tst:117874784	Reptiles_elegans_tst	<i>Trachemys scripta elegans</i>
cabi:116832454	Reptiles_tortoise_cabi	<i>Chelonoidis abingdonii</i> (Abingdon island giant tortoise)
mrvt:120401576	Reptiles_turtle_mrv	<i>Mauremys reevesii</i> (Reeves's turtle)
acs:100554661	Reptiles_anole_acs	<i>Anolis carolinensis</i> (green anole)
pvt:110087374	Reptiles_dragon_pvt	<i>Pogona vitticeps</i> (central bearded dragon)
sund:121921892	Reptiles_lizard_sund	<i>Sceloporus undulatus</i> (fence lizard)
pbi:103048250	Reptiles_python_pbi	<i>Python bivittatus</i> (Burmese python)
pmur:107292070	Reptiles_habu_pmur	<i>Protobothrops mucrosquamatus</i> (Taiwan habu)
pgut:117672075	Reptiles_guttatus_pgut	<i>Pantherophis guttatus</i>
vko:123019113	Reptiles_dragon_vko	<i>Varanus komodoensis</i> (Komodo dragon)
pmua:114594312	Reptiles_lizard_pmua	<i>Podarcis muralis</i> (common wall lizard)
zvi:118081956	Reptiles_lizard_zvi	<i>Zootoca vivipara</i> (common lizard)
gja:107113336	Reptiles_japonicus_gja	<i>Gekko japonicus</i>
xla:108717414	Amphibians_frog_xla	<i>Xenopus laevis</i> (African clawed frog)
xtr:100496227	Amphibians_frog_xtr	<i>Xenopus tropicalis</i> (tropical clawed frog)
npr:108794574	Amphibians_parkeri_npr	<i>Nanorana parkeri</i>
rtem:120937406	Amphibians_frog_rtem	<i>Rana temporaria</i> (common frog)
bbuf:120998571	Amphibians_toad_bbuf	<i>Bufo bufo</i> (common toad)
bgar:122934628	Amphibians_toad_bgar	<i>Bufo gargarizans</i> (Asiatic toad)
dre:322691	Fishes_zebrafish_dre	<i>Danio rerio</i> (zebrafish)
srx:107727632	Fishes_rhinoceros_srx	<i>Sinocyclocheilus rhinoceros</i>
sanh:107678850	Fishes_anhuiensis_sanh	<i>Sinocyclocheilus anhuiensis</i>
sgb:107603092	Fishes_grahami_sgb	<i>Sinocyclocheilus grahami</i>
ccar:109066107	Fishes_carp_ccar	<i>Cyprinus carpio</i> (common carp)
caua:113073629	Fishes_goldfish_caua	<i>Carassius auratus</i> (goldfish)
smeo:124376532	Fishes_meridionalis_smeo	<i>Silurus meridionalis</i>
tru:101071971	Fishes_torafugu_tru	<i>Takifugu rubripes</i> (torafugu)
lco:104934222	Fishes_croaker_lco	<i>Larimichthys crocea</i> (large yellow croaker)
cgob:115003888	Fishes_gobio_cgob	<i>Cottoperca gobio</i>
ely:117270450	Fishes_grouper_ely	<i>Epinephelus lanceolatus</i> (giant grouper)
plep:121955536	Fishes_coralgrouper_plep	<i>Plectropomus leopardus</i> (leopard coralgrouper)
sluc:116060333	Fishes_pikeperch_sluc	<i>Sander lucioperca</i> (pikeperch)
ecra:117961189	Fishes_darter_ecra	<i>Etheostoma cragini</i> (Arkansas darter)
pflv:114573060	Fishes_perch_pflv	<i>Perca flavescens</i> (yellow perch)
gat:120807800	Fishes_stickleback_gat	<i>Gasterosteus aculeatus</i> (three-spined)

ppug:119194697	Fishes_stickleback_ppug	stickleback)
msam:119909229	Fishes_bass_msam	<i>Pungitius pungitius</i> (ninespine stickleback)
cud:121521715	Fishes_wrasse_cud	<i>Micropterus salmoides</i> (largemouth bass)
mze:101468078	Fishes_mbuna_mze	<i>Cheilinus undulatus</i> (humphead wrasse)
onl:100702671	Fishes_tilapia_onl	<i>Maylandia zebra</i> (zebra mbuna)
oau:116333129	Fishes_tilapia_oau	<i>Oreochromis niloticus</i> (Nile tilapia)
oml:112141006	Fishes_medaka_oml	<i>Oreochromis aureus</i> (blue tilapia)
xma:102220810	Fishes_platyfish_xma	<i>Oryzias melastigma</i> (Indian medaka)
xco:114158132	Fishes_platyfish_xco	<i>Xiphophorus maculatus</i> (southern platyfish)
xhe:116733665	Fishes_swordtail_xhe	<i>Xiphophorus couchianus</i> (Monterrey platyfish)
pret:103457236	Fishes_guppy_pret	<i>Xiphophorus hellerii</i> (green swordtail)
pmei:106931502	Fishes_molly_pmei	<i>Poecilia reticulata</i> (guppy)
gaf:122825218	Fishes_mosquitofish_gaf	<i>Poecilia mexicana</i> (shortfin molly)
cvg:107083516	Fishes_minnow_cvg	<i>Gambusia affinis</i> (western mosquitofish)
ctul:119774956	Fishes_tularosa_ctul	<i>Cyprinodon variegatus</i> (sheepshead minnow)
nfu:107377734	Fishes_killifish_nfu	<i>Cyprinodon tularosa</i>
kmr:108228558	Fishes_rivulus_kmr	<i>Nothobranchius furzeri</i> (turquoise killifish)
alim:106529618	Fishes_killifish_alim	<i>Kryptolebias marmoratus</i> (mangrove rivulus)
aoce:111565453	Fishes_anemonefish_aoce	<i>Austrofundulus limnaeus</i> (annual killifish)
csem:103381256	Fishes_sole_csem	<i>Amphiprion ocellaris</i> (clown anemonefish)
pov:109642575	Fishes_flounder_pov	<i>Cynoglossus semilaevis</i> (tongue sole)
ssen:122784031	Fishes_sole_ssen	<i>Paralichthys olivaceus</i> (Japanese flounder)
hhip:117758058	Fishes_halibut_hhip	<i>Solea senegalensis</i> (Senegalese sole)
lcf:108890445	Fishes_perch_lcf	<i>Hippoglossus hippoglossus</i> (Atlantic halibut)
sdu:111237002	Fishes_amberjack_sdu	<i>Lates calcarifer</i> (barramundi perch)
slal:111672494	Fishes_amberjack_slal	<i>Seriola dumerili</i> (greater amberjack)
xgl:120788844	Fishes_swordfish_xgl	<i>Seriola lalandi dorsalis</i> (Yellowtail amberjack)
bpec:110154232	Fishes_mudskipper_bpec	<i>Xiphias gladius</i> (swordfish)
omy:100136085	Fishes_trout_omy	<i>Boleophthalmus pectinirostris</i> (great blue-spotted mudskipper)
ogo:123995076	Fishes_salmon_ogo	<i>Oncorhynchus mykiss</i> (rainbow trout)
one:115107740	Fishes_salmon_one	<i>Oncorhynchus gorbuscha</i> (pink salmon)
snh:120024461	Fishes_trout_snh	<i>Oncorhynchus nerka</i> (sockeye salmon)
aang:118230680	Fishes_eel_aang	<i>Salvelinus namaycush</i> (lake trout)
loc:102691654	Fishes_gar_loc	<i>Anguilla anguilla</i> (European eel)
pspa:121317025	Fishes_paddlefish_pspa	<i>Lepisosteus oculatus</i> (spotted gar)
arut:117410584	Fishes_sterlet_arut	<i>Polyodon spathula</i> (Mississippi paddlefish)
		<i>Acipenser ruthenus</i> (sterlet)

lcm:102358032	Fishes_coelacanth_lcm	<i>Latimeria chalumnae</i> (coelacanth)
bfo:118425921	Lancelets_lancelet_bfo	<i>Branchiostoma floridae</i> (Florida lancelet)
bbel:109473926	Lancelets_lancelet_bbel	<i>Branchiostoma belcheri</i> (Belcher's lancelet)
cin:100182351	Ascidians_squirt_cin	<i>Ciona intestinalis</i> (sea squirt)
sclv:120329399	Ascidians_clava_sclv	<i>Styela clava</i>
gae:121366164	Mollusks_aegis_gae	<i>Gigantopelta aegis</i>
hrf:124124485	Mollusks_abalone_hrf	<i>Haliotis rufescens</i> (red abalone)
hrj:124285708	Mollusks_abalone_hrj	<i>Haliotis rubra</i> (blacklip abalone)
crg:105328831	Mollusks_oyster_crg	<i>Crassostrea gigas</i> (Pacific oyster)
pmax:117328445	Mollusks_maximus_pmax	<i>Pecten maximus</i>
mmer:123553903	Mollusks_quahog_mmer	<i>Mercenaria mercenaria</i> (northern quahog)
xen:124449513	Cnidarians_Carnegie-2017_xen	<i>Xenia sp. Carnegie-2017</i>
tad:TRIADDRAFT_10520	Placozoans_adhaerens_tad	<i>Trichoplax adhaerens</i>

Extended Data Table 18 | The 14 plasminogen genes downloaded from public databases.

Gene ID	New Gene ID	gene function	species Latin name	Protein sequence
P0CJ41.1	Trimeresurus_albolabris: P0CJ41.1	fibrinogenase albofibrinase	<i>Trimeresurus albolabris</i>	VVGGDECNINEHSLVAIFNSTGFFCSGTLINQEWV VTAAHCDSKNFKMKFGAHSKLLNEDEQIRNPKE KFICPNKKSNEILDKDIMLIKLDSPVSNSAHIAPLSLP SSPPSVGSVCRIMGWGSTTPIEVITYPDVPYCANINL LDDAECKPGYPELLPEYRTLCAIVQGGKDTCCGGD SGGPLICNEKLHGIVSYGGHPCGQSHKPGIYTNVFD YNDWIQSIHAGNTDATCLS VIGGTNASPGFEPWQLSQQRQSGSWSHSCGASLLSS TSALSASHCVDGVLNNIRVIAGLWQQSDTSGTQT ANVDSYTMHENYGAGTASYNDIAILHLATSISLGG NIQAAVLPANNNNDYAGTTCVISGWGRDGTNNL PDILQKSSIPVITTAQCTAAMVGVGGANIWDNHICV QDPAGNTGACNGDSGGPLNCPDGGTRVVGVTSWV VSSGLGACLPDYPVSVYTRVSAYLGWIGDNS IVGGIEARPYEFPWQVSVRRKSSDSHFCCGSIINDR WVCAAHCMQGEAPALVSLVVGHEHDSSAASTVRQ THDVDSIFVNENYDPATLENDVSVIKTAVAITFDIN VGPICAPDPANDYVYRKSQCSGWGTINSGGVCCPA VRLRYVTNLNITTNAFCDAVYTSDTIYDDMICATDNT GMTDRDSCQGDSGGPLSVKDGSGIFSLVGIVSWGIG GCASGYPGVYSRVGFHAGWITDITNN IVGGIEARPYEFPWQVSVRRKSSDSHFCCGSIINDR WVCAAHCMQGESPALVSLVVGHEHDSSAASTVRQ THDVDSIFVHEDYNGNTFENDVSVIKTVNAIAIDIN VGPICAPDPANDYVYRKSQCSGWGTVNSGGVCCP NVLRYVTNLNVTNNAFCDDIYSPLYTITSDMICATDN TGQNERDSCQGDSGGPLSVKDGSGIFSLIGIVSWGIG GCASGYPGVYARVGSQTGWITDIITNN VIGGTNASPGFEPWQLSQQRQSGSWSHSCGASLLSS TSALSASHCVDGVLNNIRVIAGLWQQSDTSGTQT ANVDSYTMHENYGAGTASYNDIAILHLATSISLGG NIQAAVLPANNNNDYAGTTCVISGWGRDGTNNL PDILQKSSIPVITTAQCTAAMVGVGGANIWDNHICV QDPAGNTGACNGDSGGPLNCPDGGTRVVGVTSWV VSSGLGACLPDYPVSVYTRVSAHLGWIGDNSR VVGGSDDTTIGQYPHQLSLRVTGSHSCGASLIGTTTRA VTAAHCTGSAIAVYSILGGTTDRTVTNCATCVLRD
1M9U_A	Eisenia_fetida:1M9U_A	fibrinolytic enzyme	<i>Eisenia fetida</i>	
1YM0_A	Eisenia_fetida:1YM0_A	fibrinolytic enzyme	<i>Eisenia fetida</i>	
AAR13224.1	Eisenia_fetida:AAR13224.1	fibrinolytic enzyme	<i>Eisenia fetida</i>	
AAW27919.1	Eisenia_fetida:AAW27919.1	fibrinolytic enzyme	<i>Eisenia fetida</i>	
ABG68022.1	Eisenia_fetida:ABG68022.1	fibrinolytic enzyme	<i>Eisenia fetida</i>	

22.1				LNFLNRHPAYDGNAPGYPNDAVIGFAAVATNTN LQAI SLATPSDGNFAGDSCVITGWGQTGSIGGLPDA LQLATMNVLTNADCTNTWGAVRINDGHICVSAAG RSACSGDSGGPLECSNRLAGATSWGEASCDPSYPS VYTRVSYFYTWIIAQ IVGGIEARPYEFPWQVSVRRKSSDSHFCCGSIINDR WVCAAHCMQGESPALVSLVVGEHDSSAASTVRQ THDVDSIFVHEDYNGNTFENDVSVIKTVNAIAIDIN VGPICAPDPANDYVYRKSQLCSGWGTINSGGVCCPN VRLRYVTLNVTTNAFCDIYSPLYTITSDMICATDNT GQNERDSCQGDSSGGLSVKDGSGIFSLIGIVSWGIG CASGYPGVYARVGSQTGWITDIITNN IVGGIEARPYEFPWQVSVRRKSSDSHFCCGSIINDR WVCAAHCMQGESPALVSLVVGEHDSSAASTVRQ THDVDSIFVNENYDPRTLNDVSVIKTAIAITFDINV GPICAPDPANDYVYRKSQLCSGWGTINSGGICCPAVL RYVTLNITTNAFCDVYTSDTIYDDMICATDNTGM TDRDSCQGDSSGGLSVKDGSGIFSLGGIVSWGIGCA SGYPGVYSRVGFHAGWITDTITNN IVGGIEARPYEFPWQVSVRRKSSDSHFCCGSIINDR WVCAAHCMQGEAPALVSLVVGEHDSRAASTVR QTHDVDSIFVHEDYNANTLNDVSVIKTSVAITFDI NVGPICAPDPANDYVYRKSQLCSGWGTINSGGICCP NVLRYVTLNVTTNQFCEDVYPLNSIYDDMICASDN TGGNDRDSCQGDSSGGLSVKDGSGIFSLIGIVSWGIG GCASGYPGVYSRVGFHAAWITDIITNN APIKGYSVTVXLYIFDCQKWSSNYPHKPNFSDATDP KGPWCYT TDYXGAASVTRSGLRGDEQTPHRHTFSP QSFAGLTACVKGTGEGYRGTAALT VSGKACQAW ASQTPGDVYSCQGLVSNYCRNPDGEKLPWCYTTE YCNVPSC TGGPTGSEYHEILTPAQDXYTGIVEDYRG KMSPDAGLEENFCRNPDQDPQGPWCYTXNPEAXP RYCDVLSVVGXEAQRNSXPRQISLQYGWQTVHV QSIHAEP RGV DIALVKIAPPAQLTACVITXWGETQG TGEDVQFCAGYPEGGTDPVSLVCLEPCVLAPVLVG VVILPXNDRXQ MPLIRVLASLLILQLSYGKSLDNGAKAITS LDRIIGG FECNPSEHRS LVYLYNSAGFFCSGTLNHEWVLTA AHCNREDIQIRLG VHN VHVHYEDEQIRVPKEKLCC LSTNNCTQFSQDIMLIRLNSPVNYSEHIAPLSLPSNP PSMGSVCCVMGWGTITSPEVTYPEVPHCVDINILHI
AAL28118.1	Lumbricus_rubellus:AA L28118.1	fibrinolytic enzyme	<i>Lumbricus rubellus</i>	
BAB40767.1	Lumbricus_rubellus:BA B40767.1	fibrinolytic enzyme	<i>Lumbricus rubellus</i>	
BAB40768.1	Lumbricus_rubellus:BA B40768.1	fibrinolytic enzyme	<i>Lumbricus rubellus</i>	
P33574.1	Petromyzon_marinus:P33574.1	plasminogen	<i>Petromyzon marinus</i>	
Q5MCS0.1	Hydrophis_hardwickii:Q5MCS0.1	fibrinogenase albofibrinase	<i>Hydrophis hardwickii</i>	

				PVCQAAYPTMSGKNILCAGILEGGKDSCKGDSGGP LICNGQIQGIVSWGRFPCAQFLEPGIYTKVFDYKDW IEGIIAGNSNVICP MDFCWKAALLLGAVICSASSSDVEGYSKTEGAWV LSLHRRQYSVNSVTDCAAKCNAETTFTCKSFAYVE KDQECWTAASNSKTEPVLRRQNSALYEKNDYLLE CVNGLGTDYRGTAKTKSGKVCQRWEARFPHRPN ITPQTHPRADLDSNFCRNPDGDSRGPWCYTTPETR WEHCNVTSCGEDCIHCNGEDYRGKASITENGYTCQ RWDSQSPHSHGYNPDAIPEKYLEENYCRNPDGDP PWCFTTSSSKRWDYCAIPRCTSEPPTIVPELTCASGE GQAYRGTVGVTVTGKACQMWSQTPHKHSRTPE NYPCKGLDNNYCRNPDEHEKMPWCYTTPETRWEF CRVPRCGDSPDPDEAVSPPEENNDCEGNGANYRG VTSETVSGKKCQMWSMSPHSHDKSPQNFPEAGLR RNFCRNPDGDRAPWCYTTPDKVRWEYCSLKKCSE PTKSPQPQDTQSPAEDCKIGNGESYRGPTSITVSG VTCQGWDRDQSPHSHSFTPTQTHPDKGLENECRNP DGDSNGPWCYTTPDRNKKWDYCIQPDCAEDLTCGT PVYKPRRCFGRIVGGCQSRPHSWPWQISLRTSSGIH FCGGTLIDPQWVLTAKHCLERSTRPSAYKVLMDI KERAIEPSKQERRLEKIVQGPVGDIALKLDRPADI NDKVLPAKLPEKDYTVPSDTGCVYVTGWGETQGTG GEGVLKETGFPVIENRVCNGPSYLNVRKSHEMCA GNRDGGHDSCQGDSSGGLVCFSSQNKYVVQGVTSW GLGCANAMKPGVYVRVSKFIDWIETTMKAG VIGGDECNINEHRFLALLYSERFQCGGTLINEEWVL TAAHCDMGMNMYIYLGVHNVSQYDDEQRRYPKK KYFCLSSRNYNQWDNDIMLIRLNRPVRNSAHAPLS LPSGPPSVGSVCRVMGWGTITSPNETYPDVPHCANI NILDYEVCRAYAGLPATSRITLCAGILEGGKDSCR GDSGGPLICNGEIQGIVSWGGNICAQPREPGLYTKV FDYIDWISIIAGNTTVNCP IVGGIEARPYEFPWQVSVRRKSSDSHFCCGSIINDR WVCAAHCMQGEAPALVSLVVGEDRSAASTVR QTHDVSIFVHEDYNTNTLENDVSVIKTSVAITFDI NVGPICAPDPANDYVYRKSCSGWGTINSGGICCP NVLRYVTLNDDTNQYCEDVYPLNSIYDDMICASDN TGGNDRDSCQGDSSGGLSVKDGSGIFSLIGIVSWG GCASGYPGVYSRVGFHAAWITDIITNN
NP_001098 315.1	Oryzias_lati pes:NP_001 098315.1	plasminog en precursor	<i>Oryzias latipes</i>	
CAB65936. 1	Gloydius_bl omhoffii:CA B65936.1	fibrinogen ase albofibras e	<i>Gloydius blomhoffii</i>	
AAP04532. 1	Lumbricus_ bimastus:A AP04532.1	fibrinolyti c enzyme	<i>Lumbricus bimastus</i>	

Extended Data Table 19 | Protein sequence alignment between full-length transcripts and *snFPITE* genes identified by mass spectroscopy and cloning methods.

Query id	Query length	Subject id	Subject length	% of identity	Alignment length
snFPITE-n2(A)	238	2k3k0.5to1kb_part0_c39_f1p4_863	863	84.937	239
snFPITE-n2(A)	238	1k2k0.5to1kb_part0_c13_f4p2_880	880	84.937	239
snFPITE-n1	239	2k3k0.5to1kb_part0_c39_f1p4_863	863	87.448	239
snFPITE-n1	239	1k2k0.5to1kb_part0_c13_f4p2_880	880	87.448	239
snFPITE-n1	239	1k2k0.5to1kb_part0_c123_f1p0_858	858	82.427	239
snFPITE-c3	237	2k3k0.5to1kb_part0_c5_f3p10_863	863	81.498	227
snFPITE-c3	237	1k2k0.5to1kb_part0_c0_f12p17_862	862	81.498	227
snFPITE-c3	237	5k10k0.5to1kb_part0_c5_f2p0_862	862	81.057	227
snFPITE-c3	237	1k2k1to1.5kb_part0_c65302_f1p24_1247	1247	81.498	227
snFPITE-c3	237	1k2k1to1.5kb_part0_c861_f7p19_1444	1444	81.498	227
snFPITE-c3	237	3k6k3.5to4kb_part0_c2516_f2p0_3884	3884	80.617	227
snFPITE-c4	232	1k2k0.5to1kb_part0_c14_f4p7_884	884	91.379	232
snFPITE-c4	232	2k3k0.5to1kb_part0_c49_f1p2_880	880	91.379	232
snFPITE-c4	232	5k10k0.5to1kb_part0_c32_f1p0_882	882	88.696	230
snFPITE-c5	232	2k3k0.5to1kb_part0_c49_f1p2_880	880	91.379	232
snFPITE-c5	232	1k2k0.5to1kb_part0_c14_f4p7_884	884	91.379	232
snFPITE-c5	232	5k10k0.5to1kb_part0_c32_f1p0_882	882	89.13	230
snFPITE-c6	242	1k2k0.5to1kb_part0_c24_f2p4_913	913	95.455	242
snFPITE-c7	242	1k2k0.5to1kb_part0_c24_f2p4_913	913	95.041	242
snFPITE-c9	238	2k3k0.5to1kb_part0_c5_f3p10_863	863	91.597	238
snFPITE-c9	238	1k2k0.5to1kb_part0_c0_f12p17_862	862	91.597	238
snFPITE-c9	238	5k10k0.5to1kb_part0_c5_f2p0_862	862	91.176	238
snFPITE-c9	238	1k2k1to1.5kb_part0_c65302_f1p24_1247	1247	91.597	238
snFPITE-c9	238	1k2k1to1.5kb_part0_c861_f7p19_1444	1444	91.597	238
snFPITE-c9	238	3k6k3.5to4kb_part0_c2516_f2p0_3884	3884	90.756	238
snFPITE-c10	239	2k3k0.5to1kb_part0_c39_f1p4_863	863	87.866	239
snFPITE-c10	239	1k2k0.5to1kb_part0_c13_f4p2_880	880	87.866	239
snFPITE-c10	239	1k2k0.5to1kb_part0_c123_f1p0_858	858	81.59	239

Extended Data Table 20 | Nucleotide sequence alignment between full-length transcripts and *snFPITE* genes identified by mass spectroscopy and cloning methods.

Query id	Query length (bp)	Subject ID	Subject length (bp)	% identity	Alignment length (bp)
snFPITE-n1	720	2k3k0.5to1kb_part0_c39_f1p4_863	863	87.639	720
snFPITE-n1	720	1k2k0.5to1kb_part0_c13_f4p2_880	880	87.639	720
snFPITE-n1	720	1k2k0.5to1kb_part0_c123_f1p0_858	858	85.635	717
snFPITE-c3	714	2k3k0.5to1kb_part0_c5_f3p10_863	863	90.336	714
snFPITE-c3	714	1k2k0.5to1kb_part0_c0_f12p17_862	862	90.336	714
snFPITE-c3	714	5k10k0.5to1kb_part0_c5_f2p0_862	862	90.196	714
snFPITE-c3	714	1k2k1to1.5kb_part0_c65302_f1p24_1247	1247	90.196	714
snFPITE-c3	714	1k2k1to1.5kb_part0_c861_f7p19_1444	1444	90.196	714
snFPITE-c3	714	3k6k3.5to4kb_part0_c2516_f2p0_3884	3884	89.776	714
snFPITE-c4	696	1k2k0.5to1kb_part0_c14_f4p7_884	884	92.098	696
snFPITE-c4	696	5k10k0.5to1kb_part0_c32_f1p0_882	882	91.954	696
snFPITE-c4	696	2k3k0.5to1kb_part0_c49_f1p2_880	880	91.81	696
snFPITE-c4	696	1k2k0.5to1kb_part0_c67_f1p1_860	860	85.441	680
snFPITE-c5	696	1k2k0.5to1kb_part0_c14_f4p7_884	884	91.81	696
snFPITE-c5	696	5k10k0.5to1kb_part0_c32_f1p0_882	882	91.667	696
snFPITE-c5	696	2k3k0.5to1kb_part0_c49_f1p2_880	880	91.523	696
snFPITE-c5	696	1k2k0.5to1kb_part0_c67_f1p1_860	860	85.147	680
snFPITE-c6	729	1k2k0.5to1kb_part0_c24_f2p4_913	913	92.72	728
snFPITE-c7	726	1k2k0.5to1kb_part0_c24_f2p4_913	913	92.562	726
snFPITE-c9	714	2k3k0.5to1kb_part0_c5_f3p10_863	863	89.496	714
snFPITE-c9	714	1k2k0.5to1kb_part0_c0_f12p17_862	862	89.496	714
snFPITE-c9	714	5k10k0.5to1kb_part0_c5_f2p0_862	862	89.356	714
snFPITE-c9	714	1k2k1to1.5kb_part0_c65302_f1p24_1247	1247	89.356	714
snFPITE-c9	714	1k2k1to1.5kb_part0_c861_f7p19_1444	1444	89.356	714
snFPITE-c9	714	3k6k3.5to4kb_part0_c2516_f2p0_3884	3884	89.076	714
snFPITE-c10	720	2k3k0.5to1kb_part0_c39_f1p4_863	863	87.917	720
snFPITE-c10	720	1k2k0.5to1kb_part0_c13_f4p2_880	880	87.917	720
snFPITE-c10	720	1k2k0.5to1kb_part0_c123_f1p0_858	858	85.216	717

Extended Data Table 21 | Alignment between 14 full-length transcripts and 17 *snFPITE* genes identified from the assembled *S. nudus* genome.

Query id	Query length (bp)	Subject id	Subject length (bp)	% identity	Alignment length (bp)
snFPITE4	717	2k3k0.5to1kb_part0_c39_f1p4_863	863	99.861	717
snFPITE4	717	1k2k0.5to1kb_part0_c13_f4p2_880	880	99.861	717
snFPITE4	717	1k2k0.5to1kb_part0_c123_f1p0_858	858	88.703	717
snFPITE3	807	2k3k0.5to1kb_part0_c39_f1p4_863	863	94.052	807
snFPITE3	807	1k2k0.5to1kb_part0_c13_f4p2_880	880	94.052	807
snFPITE3	807	1k2k0.5to1kb_part0_c123_f1p0_858	858	91.542	804
snFPITE7	777	2k3k0.5to1kb_part0_c5_f3p10_863	863	92.782	762
snFPITE7	777	1k2k0.5to1kb_part0_c0_f12p17_862	862	92.782	762
snFPITE7	777	5k10k0.5to1kb_part0_c5_f2p0_862	862	92.651	762
snFPITE7	777	1k2k1to1.5kb_part0_c65302_f1p24_1247	1247	92.651	762
snFPITE7	777	1k2k1to1.5kb_part0_c861_f7p19_1444	1444	92.651	762
snFPITE7	777	3k6k3.5to4kb_part0_c2516_f2p0_3884	3884	92.388	762
snFPITE9	843	5k10k0.5to1kb_part0_c5_f2p0_862	862	74.241	823
snFPITE9	843	2k3k0.5to1kb_part0_c5_f3p10_863	863	74.272	824
snFPITE9	843	1k2k1to1.5kb_part0_c65302_f1p24_1247	1247	74.272	824
snFPITE9	843	1k2k0.5to1kb_part0_c0_f12p17_862	862	74.272	824
snFPITE9	843	1k2k1to1.5kb_part0_c861_f7p19_1444	1444	74.272	824
snFPITE9	843	3k6k3.5to4kb_part0_c2516_f2p0_3884	3884	74.029	824

Extended Data Table 22 | Ten selected *snFPITEs* for the recombinant expression.

Gene ID	System	Notes
<i>snFPITE13</i>	HEK293	Containing X fragment
<i>snFPITE4</i>	HEK293	
<i>snFPITE3</i>	HEK293	Containing X fragment
<i>snFPITE8</i>	HEK293	
<i>snFPITE-p1</i>	HEK293	Containing premature stop codon
<i>snFPITE7</i>	HEK293	Containing X fragment
<i>snFPITE15</i>	HEK293	
<i>snFPITE9</i>	HEK293	
<i>snFPITE2</i>	HEK293	Containing X fragment
<i>snFPITE-c1</i>	<i>Pichia pastoris</i>	