

Table S1. General data of patients with TIA.

Serum No.	Gender	Age	Height	Weight	BMI	Blood pressure	Smoking	Smoking period	Alcohol	Alcohol Freq.
Total 23	1: Male 2: Female	Average 67.09	(cm) 160.8	(kg) 64.3	(kg/m ²) 24.5	1: <120/80mmHg 2: ~139/89mmHg 3: ~159/99mmHg 4: ~179/109mmHg 5: >180/110mmHg	0: None 1: Yes	(year)	0: None 1: Yes	(time/w)
02108	1	55	172.0	76.5	26.0	3	1	40	0	0
02129	1	69	148.0	45.5	21.0	4	0	0	1	1
02135	2	69	141.0	50.0	25.1	5	0	0	0	0
02136	1	70		75.0		5	1	50	0	0
02180	1	53	170.0	68.0	23.5	3	1	33	1	7
02256	1	67	168.0	75.0	26.6	5	0	0	1	4
02265	1	92	150.0	60.0	26.7	5	1		1	7
02267	1	67	170.5	73.0	25.1	4	1		0	0
02269	2	80	137.0	38.0	20.2	3	1		1	0
02271	1	73	163.5	56.5	21.1	3	1		1	0
02272	1	71	165.0	81.0	29.8	3	1	51	0	0
02278	1	71	166.0	69.0	25.0	3	1		0	0
02280	1	64	160.0	78.0	30.5	5	1	30	0	0
02284	1	55	169.5	77.0	26.8	5	0	0	1	0
02291	1	73	164.0	56.0	20.8	3	1		1	1
02297	2	84	148.0	51.0	23.3	3	0	0	0	0
02304	1	55	172.0	78.0	26.4	5	0	0	1	1
02310	1	70	170.0	61.0	21.1	5	1	50	1	7
02322	1	59	188.0	75.0	21.2	3	0	0	1	7
05874	2	83	150.0	50.0	22.2	1	0	0	0	0
06150	2	49	152.0	53.0	22.9	3	0	0	0	0
07405	2	57				1	0	0	0	0
07366	2	57	153.0	67.0	28.6	3	0	0	0	0

This table describes the gender, age, height, weight, BMI, blood pressure, smoking habit and alcohol habit of a total of 23 TIA patients.

Table S2. Results of homology search using BLAST for monoclonal antigen by SEREX.

Clone No.	Gene full name (Homology)	Accession No.	Query cover	CDS	Start site of cloned region
108-C-F	Matrix Metalloproteinase 1 (Interstitial Collagenase) (MMP1)	NM_002421	99%	144..1553	90
108-E-F	Secreted Protein Acidic and Cysteine Rich (osteonectin) (SPARC)	NM_003118	99%	204..1115	578
108-G-F	5'-nucleotidase, ecto (CD73) (NT5E)	NM_002526	99%	557..2281	516
108-H-F	SEC14-like 1 (<i>S. cerevisiae</i>) (SEC14L1)	NM_003003	95%	268..2415	132
108-I-F	Eukaryotic Translation Elongation Factor 1 Alpha 1 (EEF1A1)	NM_001402	99%	64..1452	12
108-J-F	Ribosomal Modification Protein Rimk-Like Family Member B (RIMKLB)	NM_001297776	99%	455..1615	353
129-D-F	Vimentin (VIM)	NM_003380	99%	414..1814	279
135-A-F	Transmembrane Protein 57 (TMEM57)	NM_018202	99%	242..2236	72
135-B-F	Lysosomal-Associated Membrane Protein 1 (LAMP1)	NM_005561	99%	282..1535	803
135-H-F	Wnt Ligand Secretion Mediator (WLS)	NM_024911	95%	303..1928	108
135-M-F	Inhibitor of Growth Family, Member 3 (ING3)	NM_019071	99%	135..1391	37
135-Q-F	Signal Peptidase Complex Subunit 3 Homolog (<i>S. cerevisiae</i>) (SPCS3)	NM_021928	99%	139..681	51
135-T-F	V-Ral Simian Leukemia Viral Oncogene Homolog B (RALB)	NM_002881	95%	191..811	143
136-B-F	Zinc Finger, FYVE Domain Containing 16 (ZFYVE16)	NM_014733	99%	181..4800	34
136-C-F	Serpin Peptidase Inhibitor, Clade E (Nexin, Plasminogen Activator Inhibitor Type 1), Member 2 (SERPINE2)	NM_001136530	99%	138..1367	1070
256-C-F	Endothelial Cell Surface Expressed Chemotaxis and Apoptosis Regulator (ECSCR)	NM_001077693	95%	74..691	208
256-E-F	LIM and Senescent Cell Antigen-Like Domains 1 (LIMS1)	NM_001193485	95%	264..1427	130
256-J-F	Chaperonin Containing TCP1, Subunit 5 (Epsilon) (CCT5)	NM_012073	99%	172..1797	177
256-L-F	Deoxy Thymidylate Kinase (Thymidylate Kinase) (DTYMK)	NM_012145	99%	186..824	164
256-P-F	PHD Finger Protein 20 (PHF20)	NM_016436	99%	112..3150	48
256-Q-F	Aldolase A, Fructose-Bisphosphate (ALDOA)	NM_184041	96%	277..1371	236
256-S-F	Anillin, Actin Binding Protein (ANLN)	NM_018685	99%	225..3599	81

265-A-F	Poly(A) Binding Protein, Cytoplasmic 1 (PABPC1)	NM_002568	99%	505..2415	456
265-C-F	Fumarate Hydratase (FH)	NM_000143	99%	64..1596	98
265-D-F	Estrogen Receptor Binding Site Associated, Antigen, 9 (EBAG9)	NM_198120	100%	236..877	199
265-E-F	Ring Finger Protein 41, E3 Ubiquitin Protein Ligase (RNF41)	NM_005785	99%	381..1334	548
265-G-F	Zinc Finger, HIT-Type Containing 6 (ZNHIT6)	NM_017953	100%	150..1562	15
265-J-F	Histone Deacetylase 2 (HDAC2)	NM_001527	99%	288..1754	800
265-Q-F	Poly(A) Binding Protein, Cytoplasmic 4 (Inducible Form) (PABPC4)	NM_001135653	99%	899..2881	913
269-C-F	Aspartyl Aminopeptidase (DNPEP)	NM_012100	99%	147..1604	49
271-B-F	Retinoic Acid Induced 14 (RAI14)	NM_015577	100%	197..3139	116
271-F-F	Cyclin I (CCNI)	NM_006835	99%	545..1678	692
271-J-F	DEAH (Asp-Glu-Ala-His) Box Polypeptide 32 (DHX32)	NM_018180	96%	492..2723	243
272-A-F	Kinectin 1 (Kinesin Receptor) (KTN1)	NM_001079521	99%	179..4252	82
272-D-F	SAM and SH3 Domain Containing 1 (SASH1)	NM_015278	99%	476..4219	392
272-E-F	Prolyl 3-Hydroxylase Family Member 4 (Non-Enzymatic) (P3H4)	NM_006455	99%	285..1598	737
272-J-F	TBC1 Domain Family, Member 4 (TBC1D4)	NM_014832	99%	348..4244	1676
278-B-F	Kinesin Family Member 20B (KIF20B)	NM_001284259	95%	93..5555	2321
278-E-F	TBC1 Domain Family, Member 22B (TBC1D22B)	NM_017772	99%	215..1732	1381
278-F-F	Kinesin Light Chain 1 (Klc1)	NM_005552	99%	309..1991	42
278-I-F	Oxysterol Binding Protein-Like 9 (Osbp19)	NM_148904	93%	489..2165	34
278-J-F	Sec1 Family Domain Containing 1 (Scfd1)	NM_016106	99%	86..2014	74
278-K-F	Pyridoxal-Dependent Decarboxylase Domain Containing 1 (Pdxdc1)	NM_015027	100%	238..2604	477
278-L-F	Pds5 Cohesin Associated Factor B (Pds5b)	NM_015032	99%	187..4530	857
284-A-F	Unc-45 Homolog A (C. Elegans) (Unc45a)	NM_001039675	99%	836..3625	826
284-C-F	Connective Tissue Growth Factor (Ctgf)	NM_001901	99%	207..1256	32
291-E-F	Lysyl-Trna Synthetase (Kars)	NM_001130089	99%	145..2022	699
291-F-F	Eukaryotic Translation Elongation Factor 1 Gamma (Eef1g)	NM_001404	99%	147..1460	149
291-H-F	Aldehyde Dehydrogenase 3 Family,	NM_001031806	99%	222..1748	1145

	Member A2 (Aldh3a2)				
297-G-F	Chromobox Homolog 5 (CBX5)	NM_012117	100%	167..742	55
297-H-F	Interferon, Gamma-Inducible Protein 16 (IFI16)	NM_005531	99%	291..2480	21
297-K-F	Thioredoxin Reductase 1 (TXNRD1)	NM_003330	99%	656..2311	666
297-N-F	Enoyl-Coa Delta Isomerase 2 (ECI2)	NM_006117	99%	118..1212	35
297-Q-F	WD Repeat Domain 1 (WDR1)	NM_017491	100%	284..2104	1178
297-R-F	Chromobox Homolog 1 (CBX1)	NM_001127228	99%	292..849	99
297-T-F	Tumor Protein, Translationally-Controlled 1 (TPT1)	NM_001286272	99%	216..809	124
297-U-F	Ribosomal Protein S10 (RPS10)	NM_001203245	95%	247..744	245
297-Y-F	DEK Proto-Oncogene (DEK)	NM_003472	99%	194..1321	65
297-Z-F	Serpin Peptidase Inhibitor, Clade E (Nexin, Plasminogen Activator Inhibitor Type 1), Member 1 (SERPINE1)	NM_000602	99%	158..1366	671
304-H-F	Nuclear Export Mediator Factor (NEMF)	NM_004713	99%	321..3551	2837
310-A-F	Dihydrolipoamide Dehydrogenase (DLD)	NM_000108	99%	145..1674	88
310-C-F	Coiled-Coil Domain Containing 68 (CCDC68)	NM_025214	99%	276..1283	82
310-G-F	Thioredoxin Domain Containing 5 (Endoplasmic Reticulum) (TXNDC5)	NM_030810	99%	39..1337	45
310-I-F	DDB1 and CUL4 Associated Factor 8 (DCAF8)	NM_015726	99%	213..2006	187
310-J-F	Nuclear Receptor Binding SET Domain Protein 1 (NSD1)	NM_172349	99%	161..7444	1015
310-K-F	Microtubule-Actin Crosslinking Factor 1 (MACF1)	NM_012090	95%	53..16345	11522
310-M-F	Serologically Defined Colon Cancer Antigen 8 (SDCCAG8)	NM_006642	99%	170..2311	1251
310-N-F	Eukaryotic Translation Initiation Factor 3, Subunit M (EIF3M)	NM_006360	93%	122..1246	86
322-A-F	BRCA1-Associated ATM Activator 1 (BRAT1)	NM_152743	99%	289..2754	246
1A1a-3	COPI Coat Complex Subunit Beta 2 (COPB2)	NM_004766.3	96%	<1..>1582	782
2G1a-3	Scavenger Receptor Class B Member 2 (SCARB2)	NM_001204255.2	95%	282..1289	1358
2H2a-3	Triosephosphate Isomerase 1 (TPI1)	NM_000365.6	92%	37..786	9
3A1a-3	Von Willebrand Factor (VWF)	NM_000552.5	92%	<1..>917	5290
3B1a	Cerebellar Degeneration Related Protein 2 Like (CDR2L)	NM_014603.3	92%	413..1810	1698
3B5a-3	Cadherin 5 (CDH5)	AB035304.1	95%	88..2442	1973
3B7a-3	Homo Sapiens Yippee Like 2 (YPEL2)	NM_001005404.4	93%	252..611	3544

4G1a-3	Pan Paniscus ADP Dependent Glucokinase (ADPGK)	XM_008971902.2	93%	31..>887	604
4H1a-3	Serpin Family B Member 9 (SERPINB9)	XM_017010943.1	89%	584..1561	3538
4H3a-3	Activin A Receptor Like Type 1 (ACVRL1)	NM_001077401.2	93%	93..1604	2633
4H5a-3	ANTXR Cell Adhesion Molecule 2 (ANTXR2)	NM_001286781.2	91%		2200
4I2a-3	Integrin Subunit Beta 5 (ITGB5)	NM_002213.5	95%	366..2765	1
4I4a-3	Protein Phosphatase 2 Regulatory Subunit B'gamma (PPP2R5C)	NG_047069.1	92%		86910
4J2a-3	Ribonuclease P/MRP Subunit P25 Like (RPP25L)	NM_148178.3	91%	71..562	1

This table describes the gene full name (homology), accession No., query cover, CDS and start site of cloned region of total cDNA clones retrieved by NCBI BLAST. CDS is the abbreviation of coding sequence, which refers to the coding sequence region in mature mRNA that can be translated into protein, starting from the start codon and ending with the stop codon.