

TFSEARCH Search Result

** TFSEARCH ver.1.3 ** (c)1995 Yutaka Akiyama (Kyoto Univ.)

This simple routine searches highly correlated sequence fragments versus TFMATRIX transcription factor binding site profile database by E.Wingender, R.Knueppel, P.Dietze, H.Karas (GBF-Braunschweig).

<Warning> Scoring scheme is so straightforward in this version.
 $\text{score} = 100.0 * (\text{'weighted sum'} - \text{min}) / (\text{max} - \text{min})$
 The score does not properly reflect statistical significance!

Database: TRANSFAC MATRIX TABLE, Rel.3.3 06-01-1998
 Query: M150bpTFSearch (150 bases)
 Taxonomy: Vertebrate
 Threshold: 85.0 point

TFMATRIX entries with High-scoring:

1	GCCTCCTGTT TCACGTAGAA TAAGCTCCTT CATAAAGTCA CAGACCAGTC	entry	score
	<-----	M00100	CdxA 96.2
	<-----	M00041	CRE-BP 87.2
	<-----	M00101	CdxA 87.1
	<-----	M00101	CdxA 85.7
51	AGGCTGAACA GCTCCGAGGA AACACCCAGA ATAAAAATAG TTTAATACAC	entry	score
	<-----	M00101	CdxA 92.9
	<-----	M00053	c-Rel 91.7
	<-----	M00099	S8 90.4
	<-----	M00148	SRY 89.1
	<-----	M00052	NF-kap 88.1
	<-----	M00101	CdxA 85.7
	<-----	M00054	NF-kap 85.4
	<-----	M00101	CdxA 85.0
101	ACAATTAGGT GTGGGTGTGG CCAGCAAATA CTCTGATTCT ACAATCTGTT	entry	score
	<-----	M00241	Nkx-2. 91.2
	<-----	M00099	S8 90.4
	<-----	M00073	deltaE 87.4
	<-----	M00131	HNF-3b 86.7

Total 15 high-scoring sites found.
 Max score: 96.2 point, Min score: 85.0 point

[TRANSFAC database document \(Notice to users\)](#)

[TFMATRIX: binding site distribution matrix](#)

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Transcription factor Affinity Prediction (TRAP) Web Tools

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TRAP (single sequence)

calculating... please wait...the results will appear below

Sequence: **MCoIX_150**

* The table is ranked from the lowest to the highest p-value.

Results are displayed in the table below [\[save table\]](#).

Affinity-based ranking of transcription factors

Rank	P-value	Corrected p-value	Matrix ID	Matrix name	Affinity Plot	Binding Sites
1	0.00153	0.737	M00395	V\$HOXA3_01	Graph	Sites
2	0.00317	0.737	M01440	V\$LHX8_01	Graph	Sites
3	0.00327	0.737	M01331	V\$ISX_01	Graph	Sites
4	0.00406	0.737	M01421	V\$LHX4_01	Graph	Sites
5	0.00526	0.737	M00403	V\$AMEF2_Q6	Graph	Sites
6	0.00646	0.737	M00150	V\$BRACH_01	Graph	Sites
7	0.00675	0.737	M01386	V\$EVX2_01	Graph	Sites
8	0.0083	0.737	M01371	V\$GBX1_01	Graph	Sites
9	0.00981	0.737	M01113	V\$CACD_01	Graph	Sites
10	0.0142	0.737	M01162	V\$OG2_01	Graph	Sites
11	0.0144	0.737	M00640	V\$HOXA4_Q2	Graph	Sites
12	0.0158	0.737	M01339	V\$PAX7_01	Graph	Sites
13	0.0175	0.737	M01388	V\$DLX5_01	Graph	Sites
14	0.018	0.737	M00415	V\$AREB6_04	Graph	Sites
15	0.019	0.737	M00423	V\$FOXJ2_Q2	Graph	Sites
16	0.0203	0.737	M00133	V\$TST1_01	Graph	Sites
17	0.0206	0.737	M01019	V\$TBX5_01	Graph	Sites
18	0.0213	0.737	M01020	V\$TBX5_Q2	Graph	Sites
19	0.0236	0.737	M00100	V\$CDXA_01	Graph	Sites
20	0.0236	0.737	M00935	V\$NFAT_Q4_Q1	Graph	Sites
21	0.0249	0.737	M01037	V\$GLI_Q2	Graph	Sites
22	0.0257	0.737	M00821	V\$NRF2_Q4	Graph	Sites
23	0.0265	0.737	M00053	V\$CREL_01	Graph	Sites
24	0.0272	0.737	M00099	V\$S8_01	Graph	Sites
25	0.0274	0.737	M00250	V\$GF1_01	Graph	Sites
26	0.0277	0.737	M00486	V\$PAX2_Q2	Graph	Sites
27	0.028	0.737	M00231	V\$MEF2_Q2	Graph	Sites
28	0.0329	0.737	M01431	V\$BARX2_01	Graph	Sites
29	0.0329	0.737	M01301	V\$MEF2_Q5	Graph	Sites

30	0.0348	0.737	M01023	V\$HSF1_Q6	Graph	Sites
31	0.0357	0.737	M00246	V\$EGR2_01	Graph	Sites
32	0.0365	0.737	M00407	V\$RSRFC4_Q2	Graph	Sites
33	0.037	0.737	M01462	V\$POU6F1_02	Graph	Sites
34	0.0374	0.737	M01044	V\$TBX5_Q5	Graph	Sites
35	0.0382	0.737	M01349	V\$HB9_01	Graph	Sites
36	0.0386	0.737	M01446	V\$BARHL2_01	Graph	Sites
37	0.0387	0.737	M00026	V\$RSRFC4_01	Graph	Sites
38	0.0388	0.737	M00405	V\$MMEF2_Q6	Graph	Sites
39	0.0403	0.737	M01588	V\$GKLF_02	Graph	Sites
40	0.041	0.737	M01657	V\$GLI3_Q5_01	Graph	Sites
41	0.0415	0.737	M01292	V\$HOXA13_01	Graph	Sites
42	0.0426	0.737	M01422	V\$LHX61_02	Graph	Sites
43	0.044	0.737	M00991	V\$CDX_Q5	Graph	Sites
44	0.0452	0.737	M01332	V\$BARHL1_01	Graph	Sites
45	0.046	0.737	M01016	V\$SOX17_01	Graph	Sites
46	0.0477	0.737	M01436	V\$CRX_02	Graph	Sites
47	0.0481	0.737	M00292	V\$FREAC4_01	Graph	Sites
48	0.0489	0.737	M01212	V\$STAT1STAT1_Q3	Graph	Sites
49	0.0509	0.737	M00641	V\$HSF_Q6	Graph	Sites
50	0.0518	0.737	M01429	V\$HOMEZ_01	Graph	Sites
51	0.0556	0.737	M01239	V\$RELB52_01	Graph	Sites
52	0.0559	0.737	M01365	V\$EN1_02	Graph	Sites
53	0.0566	0.737	M00774	V\$NFKB_Q6_01	Graph	Sites
54	0.0569	0.737	M00052	V\$NFKAPPAB65_01	Graph	Sites
55	0.0589	0.737	M01455	V\$EN2_01	Graph	Sites
56	0.061	0.737	M00105	V\$CDPCR3_01	Graph	Sites
57	0.0613	0.737	M01399	V\$HB24_01	Graph	Sites
58	0.0614	0.737	M01325	V\$LH2_01	Graph	Sites
59	0.063	0.737	M01403	V\$OTX3_01	Graph	Sites
60	0.063	0.737	M01448	V\$HOXD1_01	Graph	Sites
61	0.0631	0.737	M01382	V\$GBX2_01	Graph	Sites
62	0.0631	0.737	M01355	V\$ALX3_01	Graph	Sites
63	0.0633	0.737	M00081	V\$EVI1_04	Graph	Sites
64	0.0639	0.737	M01384	V\$RHGX11_02	Graph	Sites
65	0.0641	0.737	M01330	V\$HOXB3_01	Graph	Sites
66	0.0653	0.737	M00251	V\$XBP1_01	Graph	Sites
67	0.0659	0.737	M00420	V\$MEIS1AHOX9_01	Graph	Sites
68	0.0664	0.737	M01458	V\$CDX_Q5_01	Graph	Sites

Result [what is this?](#)[Return to Match](#)Match results filename :

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Matrix library : TRANSFAC MATRIX TABLE, Release 2013.1

Sequence file : 150.seq

Profile : vertebrate_non_redundant_minFP.prf

Only high-quality matrices : YES

Cut-offs : Minimize false positives

Total sequence length : 150

Total sites number : 6

Frequency of sites : 0.040000

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Scanning sequence ID: 150.seq_0 - View a [graphical output](#) of the following search resultShow entries

Matrix Id	Position(Strand)	Core Score	Matrix Score	Sequence	Factor Name
V\$TST1_01	76 (+)	0.929	0.903	ccaGAATAaaaatag	Tst-1
V\$RSRFC4_Q2	78 (+)	1	0.905	agaataaaAATAGtta	RSRFC4
V\$FOXJ2_02	81 (+)	0.897	0.905	ataAAAATagttta	FOXJ2
V\$OG2_01	102 (-)	1	1	cAATTA	OG-2
V\$TBX5_01	105 (+)	1	0.972	ttaGGTGTgggt	TBX5
V\$CACD_01	113 (-)	1	1	GGGTGtgg	CACD



Mascot Search Results

User : Praneeth Edirisinghe
Email :
Search title : Ced 2
MS data file : Ced_new2.mgf
Database : SwissProt 51.6 (257964 sequences; 93947433 residues)
Taxonomy : Rodentia (Rodents) (19706 sequences)
Timestamp : 10 Mar 2011 at 21:00:36 GMT
Enzyme : Trypsin
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 2 Da
Fragment Mass Tolerance : ± 1.5 Da
Max Missed Cleavages : 3
Instrument type : Default
Number of queries : 9192
Protein hits :

- [GDF7_MOUSE](#) Growth/differentiation factor 7 precursor (GDF-7) - Mus musculus (Mouse)
- [ALBU_MOUSE](#) Serum albumin precursor - Mus musculus (Mouse)
- [K2C1_MOUSE](#) Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1)
- [RALY_MOUSE](#) RNA-binding protein Raly (hnRNP associated with lethal yellow protein) (1
- [HRBL_MOUSE](#) HIV-1 Rev-binding protein-like protein (Rev/Rex activation domain-binding
- [ODPAT_RAT](#) Pyruvate dehydrogenase E1 component alpha subunit, testis-specific form,
- [ODPAT_MOUSE](#) Pyruvate dehydrogenase E1 component alpha subunit, testis-specific form,
- [FUS_MOUSE](#) RNA-binding protein FUS (Pigpen protein) - Mus musculus (Mouse)
- [SCN3A_RAT](#) Sodium channel protein type 3 subunit alpha (Sodium channel protein type
- [THNSL_MOUSE](#) Threonine synthase-like 1 - Mus musculus (Mouse)
- [SCRT2_MOUSE](#) Transcriptional repressor scratch 2 (Scratch homolog 2 zinc finger prote.
- [ADR1_MOUSE](#) Adiponectin receptor protein 1 - Mus musculus (Mouse)
- [NDUV2_MOUSE](#) NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial precursor
- [PTN21_RAT](#) Tyrosine-protein phosphatase non-receptor type 21 (EC 3.1.3.48) (Protein-
- [DC1L1_RAT](#) Cytoplasmic dynein 1 light intermediate chain 1 (Dynein light intermedia
- [PHX2A_MOUSE](#) Paired mesoderm homeobox protein 2A (Paired-like homeobox 2A) (PHOX2A ho
- [KT3K_MOUSE](#) Ketosamine-3-kinase (EC 2.7.1.-) (Fructosamine-3-kinase-related protein)
- [CONA1_MOUSE](#) Collagen alpha-1(XXIII) chain - Mus musculus (Mouse)
- [NFH_RAT](#) Neurofilament triplet H protein (200 kDa neurofilament protein) (Neurofi.
- [NEUG_MOUSE](#) Neurogranin (Ng) (RC3) - Mus musculus (Mouse)
- [SEM5A_MOUSE](#) Semaphorin-5A precursor (Semaphorin F) (Sema F) - Mus musculus (Mouse)
- [CD2L5_MOUSE](#) Cell division cycle 2-like protein kinase 5 (EC 2.7.11.22) (CDC2-related
- [CAC1H_RAT](#) Voltage-dependent T-type calcium channel subunit alpha-1H (Voltage-gated
- [MPIP1_RAT](#) M-phase inducer phosphatase 1 (EC 3.1.3.48) (Dual specificity phosphatas
- [RL14_MOUSE](#) 60S ribosomal protein L14 - Mus musculus (Mouse)
- [CAC1H_MOUSE](#) Voltage-dependent T-type calcium channel subunit alpha-1H (Voltage-gated
- [DPOD1_RAT](#) DNA polymerase delta catalytic subunit (EC 2.7.7.7) - Rattus norvegicus
- [BOREA_MOUSE](#) Borealin (Cell division cycle-associated protein 8) (MESrg) - Mus musculi
- [CBX6_MOUSE](#) Chromobox protein homolog 6 - Mus musculus (Mouse)
- [DOCK9_MOUSE](#) Dedicator of cytokinesis protein 9 (Cdc42 guanine nucleotide exchange fa
- [IL33_RAT](#) Interleukin-33 precursor (IL-33) - Rattus norvegicus (Rat)
- [RM36_MOUSE](#) 39S ribosomal protein L36, mitochondrial precursor (L36mt) (MRP-L36) - M
- [COBA1_MOUSE](#) Collagen alpha-1(XI) chain precursor - Mus musculus (Mouse)
- [EP15_MOUSE](#) Epidermal growth factor receptor substrate 15 (Protein Eps15) (AF-1p pro
- [PRP8_MOUSE](#) Pre-mRNA-processing-splicing factor 8 (Splicing factor Prp8) - Mus muscu
- [ALBU_RAT](#) Serum albumin precursor - Rattus norvegicus (Rat)
- [STAB1_MOUSE](#) Stabilin-1 precursor (FEEL-1 protein) - Mus musculus (Mouse)
- [HNF3A_MOUSE](#) Hepatocyte nuclear factor 3-alpha (HNF-3A) (Forkhead box protein A1) - M
- [TUB_MOUSE](#) Tubby protein - Mus musculus (Mouse)
- [TUB_RAT](#) Tubby protein homolog - Rattus norvegicus (Rat)
- [K0515_MOUSE](#) Uncharacterized protein KIAA0515 - Mus musculus (Mouse)
- [EPS8_MOUSE](#) Epidermal growth factor receptor kinase substrate 8 - Mus musculus (Mous
- [BAT2_RAT](#) Large proline-rich protein BAT2 (HLA-B-associated transcript 2) - Rattus
- [FZD8_MOUSE](#) Frizzled-8 precursor (Fz-8) (mFz8) - Mus musculus (Mouse)
- [FGRL1_MOUSE](#) Fibroblast growth factor receptor-like 1 precursor (FGF receptor-like pr
- [HRSL3_MOUSE](#) HRAS-like suppressor 3 (H-rev 107 protein) - Mus musculus (Mouse)
- [COBA2_MOUSE](#) Collagen alpha-2(XI) chain precursor - Mus musculus (Mouse)
- [3BHS1_MOUSE](#) 3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type I (3-beta-

3BHS6_MOUSE	3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type VI (3-beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type VI)
3BHS2_MOUSE	3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type II (3-beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type II)
CC45L_MOUSE	CDC45-related protein (PORC-PI-1) - Mus musculus (Mouse)
RAIN_MOUSE	Ras-interacting protein 1 (Rain) - Mus musculus (Mouse)
SFRP4_MOUSE	Secreted frizzled-related sequence protein 4 precursor (sFRP-4) (Frizzled-related protein 4)
PRAM_MOUSE	PML-RARA-regulated adapter molecule 1 (PRAM-1) - Mus musculus (Mouse)
AKA11_RAT	A-kinase anchor protein 11 (Protein kinase A-anchoring protein 11) (PRKAA11) - Rattus norvegicus (Rat)
GPR27_MOUSE	Probable G-protein coupled receptor 27 (Super conserved receptor expressed by random cloning) (GPR27) - Mus musculus (Mouse)
FOXK2_MOUSE	Forkhead box protein K2 (Interleukin enhancer-binding factor 1) (Cellular leukemia factor 1) - Mus musculus (Mouse)
RB_RAT	Retinoblastoma-associated protein (PP105) (RB) (Fragment) - Rattus norvegicus (Rat)
LPHN1_RAT	Latrophilin-1 precursor (Calcium-independent alpha-latrotoxin receptor 1) - Rattus norvegicus (Rat)
SUCA_MOUSE	Succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial precursor (SUCA) - Mus musculus (Mouse)
ARMX2_MOUSE	Armadillo repeat-containing X-linked protein 2 - Mus musculus (Mouse)
DDEF2_MOUSE	Development and differentiation-enhancing factor 2 (Pyk2 C-terminus-associated protein 2) - Mus musculus (Mouse)
NFH_MOUSE	Neurofilament triplet H protein (200 kDa neurofilament protein) (Neurofilament H) - Mus musculus (Mouse)
FCN1_RAT	Ficolin-1 precursor (Ficolin-A) (Ficolin-alpha) (M-ficolin) (Collagen/fibrinolytic system) - Rattus norvegicus (Rat)
MYG_RAT	Myoglobin - Rattus norvegicus (Rat)
LRC8E_MOUSE	Leucine-rich repeat-containing protein 8E - Mus musculus (Mouse)
GPR27_RAT	Probable G-protein coupled receptor 27 (Super conserved receptor expressed by random cloning) (GPR27) - Rattus norvegicus (Rat)
RM12_MOUSE	39S ribosomal protein L12, mitochondrial precursor (L12mt) (MRP-L12) - Mus musculus (Mouse)
ADH1_RAT	Alcohol dehydrogenase 1 (EC 1.1.1.1) (Alcohol dehydrogenase A subunit) - Rattus norvegicus (Rat)
LTBP3_MOUSE	Latent-transforming growth factor beta-binding protein 3 precursor (LTBP3) - Mus musculus (Mouse)
AT10D_MOUSE	Probable phospholipid-transporting ATPase VD (EC 3.6.3.1) (ATPVD) - Mus musculus (Mouse)
N4BP3_MOUSE	NEDD4-binding protein 3 (N4BP3) - Mus musculus (Mouse)
CUL7_MOUSE	Cullin-7 (CUL-7) (p185) (p193) - Mus musculus (Mouse)
CHMP6_MOUSE	Charged multivesicular body protein 6 (Chromatin-modifying protein 6) - Mus musculus (Mouse)
MAST2_MOUSE	Microtubule-associated serine/threonine-protein kinase 2 (EC 2.7.11.1) - Mus musculus (Mouse)
CK060_MOUSE	UPF0360 protein C11orf60 homolog - Mus musculus (Mouse)
S11L1_RAT	Signal-induced proliferation-associated 1-like protein 1 (SPA-1-like protein 1) - Rattus norvegicus (Rat)
S11L1_MOUSE	Signal-induced proliferation-associated 1-like protein 1 - Mus musculus (Mouse)
THIM_MOUSE	3-ketoacyl-CoA thiolase, mitochondrial (EC 2.3.1.16) (Beta-ketothiolase) - Mus musculus (Mouse)
ATX2_MOUSE	Ataxin-2 (Spinocerebellar ataxia type 2 protein homolog) - Mus musculus (Mouse)
TGM1_RAT	Protein-glutamine gamma-glutamyltransferase K (EC 2.3.2.13) (Transglutaminase 1) - Rattus norvegicus (Rat)
TGM1_MOUSE	Protein-glutamine gamma-glutamyltransferase K (EC 2.3.2.13) (Transglutaminase 1) - Mus musculus (Mouse)
WISP1_RAT	WNT1-inducible-signaling pathway protein 1 precursor (WISP-1) (ELM-1) - Rattus norvegicus (Rat)
MEPD_RAT	Thimet oligopeptidase (EC 3.4.24.15) (Endo-oligopeptidase A) (Endopeptidase) - Rattus norvegicus (Rat)
LZTS2_MOUSE	Leucine zipper putative tumor suppressor 2 - Mus musculus (Mouse)
SHE_MOUSE	SH2 domain-containing adapter protein E - Mus musculus (Mouse)
3BHS7_MOUSE	3 beta-hydroxysteroid dehydrogenase type 7 (3 beta-hydroxysteroid dehydrogenase type 7)
TLN2_MOUSE	Talin-2 - Mus musculus (Mouse)
ACES_MOUSE	Acetylcholinesterase precursor (EC 3.1.1.7) (AChE) - Mus musculus (Mouse)
OSBL1_RAT	Oxysterol-binding protein-related protein 1 (OSBP-related protein 1) (ORP1) - Rattus norvegicus (Rat)
OSBL1_MOUSE	Oxysterol-binding protein-related protein 1 (OSBP-related protein 1) (ORP1) - Mus musculus (Mouse)
RAB28_MOUSE	Ras-related protein Rab-28 - Mus musculus (Mouse)
PRC1_MOUSE	Protein regulator of cytokinesis 1 - Mus musculus (Mouse)

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Significance threshold p<
 Max. number of hits

Standard scoring MudPIT scoring Ions score or expect cut-off Show sub-sets

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1. [GDF7_MOUSE](#) Mass: 47861 Score: 53 Queries matched: 73 emPAI: 0.16
 Growth/differentiation factor 7 precursor (GDF-7) - Mus musculus (Mouse)

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
457	841.5600	840.5527	842.4722	-1.9195	1	16	5.2	10	R.EIRAQAR.A
2744	650.9300	1299.8454	1300.6987	-0.8532	0	15	7.6	1	R.AVTASESSPLALR.R
3358	462.2000	1383.5782	1381.6487	1.9294	0	27	0.38	1	R.AAGAGPAWSPGGGGGGR.T 3356
5812	596.4800	1786.4182	1785.0009	1.4172	1	15	5.6	5	R.APGPSALQAAAVPGPRAVR.R
5832	597.4000	1789.1782	1789.8020	-0.6238	0	22	1	3	R.LGFGWPGGGDGGGTAAEER.A 5831

Table 1. Primers for predictive candidate genes

Name	RefSeq ID	Sense primer (5'-3')	Anti-sense primer (5'-3')	Amplicon (bp)
<i>Foxj2</i>	NM_021899.3	CTCTTGAAGTCCCTGTCCGGT	CTGCGCCCTGTCTCTGTATA	106
<i>Klf3</i>	NM_008453.5	CCAAAGGAAGCGCAGGATAC	CAGGTGCATTTGTACGGCTT	123
<i>Mef2a</i>	NM_001033713.3	GGGGTGACTIONCCATTCTCCA	CATGTGTCCATCCTCATGCG	94
<i>Nobox</i>	NM_130869.3	GCCAACCTTCCTCTTCCTCT	TATGCTGTCACTGCCAGGAA	84
<i>Pou3f1</i>	NM_011141.2	CAAATTTGGGGTGAGGTGGG	TAGGATGGGGAGGGAGAACA	127
<i>Gapdh</i>	NM_008084	ACCCAGAAGACTGTGGATGG	CACATTGGGGGTAGGAACAC	171
<i>Col10a1</i>	NM_009925.4	GCAGCATTACGACCCAAGATC	TCTGTGAGCTCCATGATTGC	201
<i>Runx2</i>	NM_001145920	ACCCAGCCACCTTTACCTAC	TATGGAGTGCTGCTGGTCTG	150

Foxj2: forkhead box J2; **Klf3/Tef2**: Kruppel-like factor 3; **Mef2a**: myocyte enhancer factor 2A; **Nobox/OG2**: NOBOX oogenesis homeobox; **Pou3f1/Tst-1**: POU domain, class 3, transcription factor 1; **Gapdh**: glyceraldehydes-3-phosphate dehydrogenase; **Col10a1**: type X collagen, alpha 1; **Runx2** : runt-related transcription factor 2;

Table 2. Primers for candidate genes identified by Y1H

Name	RefSeq ID	Sense primer (5'-3')	Anti-sense primer (5'-3')	Amplicon (bp)
<i>Anxa2</i>	NM_007585.3	CTTCCGAAAGCTGATGGTCTG	CACGTCGGTTCCTTTCCTCTT	132
<i fn1<="" i=""></i>	NM_001276408.1	TACCCTTCCACACCCCAATC	TGCCAGGAAGCTGAATACCA	122
<i>Hspa5</i>	NM_001163434.1	CCTTGTGTTTGACCTGGGTG	CCATGACCCGCTGATCAAAG	131
<i>Nedd4</i>	NM_010890	CATGTGTGGTCTGGGAGATG	CCAGAACCAGTGGATGACCT	100
<i>Psmb1</i>	NM_011185.3	AGAATGTAGAGCACGTCCCC	ATACACATCCCTCTCGGCTG	89
<i>Ptgs2</i>	NM_011198.3	TGCAGAATTGAAAGCCCTCT	CCCCAAAGATAGCATCTGGA	95
<i>Rab1</i>	NM_008996.3	GCCCTTGAACCTCCTGATCCT	GGGCAATCACATTTCTGCT	123
<i>Rela</i>	NM_009045.4	CACCGGATTGAAGAGAAGCG	AGTTGAGTTTCGGGTAGGCA	132
<i>Rpl35</i>	NM_025592.3	CCTGCGACCCAAGAAGACTA	TCGTTGTCATCTCAGGCCTT	138
<i>Rps28</i>	NM_016844.2	AAATGTCAAAGGCCCCGTTT	TTCCGTGGGCTAAGTAGTGG	122

Anxa2: annexin A2; ***Fn1***: fibronectin 1; ***Hspa5***: heat shock protein 5; ***Nedd4***: neural precursor cell expressed, developmentally down-regulated 4; ***Psmb1***: proteasome (prosome, macropain) subunit, beta type 1; ***Ptgs2***: prostaglandin-endoperoxide synthase 2; ***Rab1***: member RAS oncogene family; ***Rela***: v-rel reticuloendotheliosis viral oncogene homolog A (avian); ***Rpl35***: ribosomal protein L35; ***Rps28***: ribosomal protein S28.

Table 3. Primers for candidate genes identified by MS

Name	RefSeq ID	Sense primer (5'-3')	Anti-sense primer (5'-3')	Amplicon (bp)
<i>Ddef2</i>	NM_001004364.2	ATCAAACAGGCCCCAGGATGA	TTCCCGTTCCTCTCTGTTCC	179
<i>Foxk2</i>	NM_001080932.2	TGTGCACTTTCAGGTTTCCG	GTTGATGGTCAGGGGTGAGA	137
<i>Fus</i>	NM_139149.2	GAGCTGGAGACTGGAAGTGT	CCCATATGAGAGCCTCCTGG	130
<i>Gdf7</i>	NM_013527.1	ATCGCGCCATTAGACTACGA	GAATGCTGATGGGACTGAGC	175
<i>Hnf3a</i>	NM_008259.3	CTCTCTACCCACCTACGCTG	ACCTCAGCATGACATGACCA	105
<i>N4bp3</i>	NM_145974.3	TATGAGTTCTCCTGCCCCAC	GTCGTTCCACATACAGACGC	169
<i>Rab28</i>	NM_027295.2	TCACACTTCCTCCTGCTCTG	GTGTGGTTCCAAATCGCACT	93
<i>Scrt2</i>	NM_001160410.1	AGCAATTTTGGAGGGTGCTG	TACTGCTGAAGGTGGGGAAG	142
<i>Sfrp4</i>	NM_016687.3	GGAGTGGTTGCAATGAGGTC	TGGCAGGAGGAATTGGTGAT	109
<i>Tgm1</i>	NM_001161714.1	AACAGAAGCACAGATTGGCG	AACCCGAGAGACACTGACTG	139

Ddef2: Asap2, ArfGAP with SH3 domain, ankyrin repeat and PH domain 2; ***Foxk2***: forkhead box K2; ***Fus***: fused in sarcoma, RNA-binding protein; ***Gdf7***: growth differentiation factor 7; ***Hnf3a (Foxa1)***: forkhead box A1; ***N4bp3***: NEDD4 binding protein 3; ***Rab28***: member RAS oncogene family; ***Scrt2***: scratch homolog 2, zinc finger protein (Drosophila); ***Sfrp4***: secreted frizzled-related protein 4; ***Tgm1***: transglutaminase 1, K polypeptide;