

Supplementary Tables

Supplementary Table S1: Gene expression profile data used for depicting the GRN-space landscape.

To depict the GRN-space landscape in the vicinity of epithelial and mesenchymal cellular states, we collected the gene expression profile data for both epithelial cell types and mesenchymal cell types from both the GEO database of NCBI and the ArrayExpress database of EBI, as follows.

Database	Dataset ID	Sample ID
NCBI GEO	GSE32474	GSM803648,GSM803707,GSM803765
NCBI GEO	GSE58605	GSM1414981,GSM1414982,GSM1414983
NCBI GEO	GSE50832	GSM1230054,GSM1230055,GSM1230056
NCBI GEO	GSE57083	GSM1374389,GSM1374390
NCBI GEO	GSE25146	GSM618009,GSM618010
NCBI GEO	GSE50832	GSM1230782,GSM1230783,GSM1230784,GSM1230728,GSM1230729,GSM1230730,GSM1230701,GSM1230702,GSM1230703,GSM1230045,GSM1230046,GSM1230047
NCBI GEO	GSE12548	GSM315430,GSM315431,GSM315432 (Takahashi et al. 0h hour data for epithelium)
NCBI GEO	GSE10315	GSM260657,GSM260658,GSM260659,GSM260660,GSM260661,GSM260662
EBI ArrayExpress	E-MEXP-858	31mOhC,CW31M0hA,CW31M0hB
NCBI GEO	GSE24612	GSM606843,GSM606844
NCBI GEO	GSE9440	GSM239829,GSM239830,GSM239831
NCBI GEO	GSE9832	GSM248201,GSM248202,GSM248204,GSM248209,GSM248210,GSM248213,GSM248214
NCBI GEO	GSE9865	GSM249026,GSM249027
NCBI GEO	GSE12583	GSM315617,GSM315618
NCBI GEO	GSE14897	GSM372142,GSM372144,GSM372146
NCBI GEO	GSE18226	GSM452726,GSM452730,GSM452734,GSM452735,GSM452736,GSM452737
NCBI GEO	GSE23583	GSM579884,GSM579885,GSM579886,GSM579887,GSM579888,GSM579889,GSM579916,GSM579917,GSM579918
NCBI GEO	GSE12548	GSM315446,GSM315447,GSM315448 (Takahashi et al. 60h hour data for mesenchyme)

Supplementary Table S2: Selected genes as coordinate variables of the GRN subspace for EMT representation.

The 61 genes selected as coordinate variables of the GRN subspace for EMT are shown with gene symbols, gene IDs, medians of gene expression in the epithelial and mesenchymal states, as well as in Takahashi et al.'s experiment, together with gene descriptions by GENE of NCBI.

Gene symbol	gene ID	Probeset ID	medians of gene expression				gene description by NCBI-GENE
			Epithelial cells	Mesenchymal cells	Epithelial cells in Takahashi's data	Mesenchymal cells in Takahashi's data	
ANXA6	309	200982_s_at	37.4260	52.8347	46.8544	48.2881	annexin A6
AP1S3	130340	1555733_s_at	8.5412	5.3509	7.4116	7.5455	adaptor-related protein complex 1, sigma 3 subunit
ARHGAP24	83478	223422_s_at	281.7597	346.3200	309.6101	304.9180	Rho GTPase activating protein 24
ARHGEF6	9459	209539_at	161.6140	188.2597	164.0138	157.3823	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6
ARMCX1	51309	218694_at	235.0235	279.9637	252.6424	248.1394	armadillo repeat containing, X-linked 1
ASPM	259266	219918_s_at	271.3147	326.8425	293.1746	287.3387	asp (abnormal spindle) homolog, microcephaly associated
BAALC	79870	218899_s_at	237.9350	287.6153	256.1527	251.9426	brain and acute leukemia, cytoplasmic
BRI3BP	140707	225716_at	319.1979	394.3695	346.7931	344.0013	BRI3 binding protein
C1QBP	708	208910_s_at	154.8503	178.9144	155.1959	148.5080	complement component 1, q subcomponent binding protein
CBX5	23468	242069_at	419.2092	520.7431	474.5275	469.8778	chromobox homolog 5
CCDC8	83987	223495_at	288.1611	355.8931	315.2254	310.4508	coiled-coil domain containing 8
CCNB1	891	228729_at	346.4732	418.0904	375.6899	371.5474	cyclin B1
CKMT1A CKMT1B	548596 1159	202712_s_at	58.0337	71.7168	64.1883	64.7344	creatine kinase, mitochondrial 1A/1B
CLIP3	25999	235243_at	389.4957	475.4569	430.2769	428.4836	CAP-GLY domain containing linker protein 3
CNN1	1264	203951_at	101.6034	118.0456	105.0715	101.6708	calponin 1, basic, smooth muscle

COL13A1	1305	211343_s_at	166.2316	197.73946	171.25018	166.4525	collagen, type XIII, alpha 1
COL1A1	1277	1556499_s_at	23.58415	28.831247	29.506765	27.679142	collagen, type I, alpha 1
DLC1	10395	224822_at	301.3462	376.18973	331.5045	327.61805	DLC1 Rho GTPase activating protein
DSC2	1824	226817_at	334.9343	409.01804	366.38086	362.66517	desmocollin 2
ELTD1	535066	219134_at	246.4709	307.52796	272.82244	267.64738	EGF, latrophilin and seven transmembrane domain containing 1 [<i>Bos taurus</i> (cattle)]
ENPP1	5167	229088_at	361.0692	434.78203	389.13483	386.39138	ectonucleotide pyrophosphatase/phosphodiesterase 1
EVI2A	2123	204774_at	109.0613	132.74119	111.56038	107.54172	ecotropic viral integration site 2A
FBN1	2200	235318_at	394.9006	485.97115	441.90635	439.11597	fibrillin 1
FN1	2335	212464_s_at	205.7143	240.9104	216.30998	212.40252	fibronectin 1
GABARAPL	23710	211458_s_at	175.608	209.51139	181.68873	177.50342	GABA(A) receptor-associated protein like 1
GAP43	2596	204471_at	104.3506	125.56808	107.27773	102.60365	growth associated protein 43
HMMR	3161	207165_at	132.335	152.47542	133.4285	126.61648	hyaluronan-mediated motility receptor (RHAMM)
HPS3	84343	231121_at	386.1525	469.02192	424.8547	422.46928	Hermansky-Pudlak syndrome 3
IFNLR1	163702	244261_at	426.0665	524.33658	482.47325	477.07232	interferon, lambda receptor 1
KCND3	3752	213832_at	228.8653	268.37467	241.77789	236.72177	potassium channel, voltage gated Shal related subfamily D, member 3
LIMS1	3987						LIM and senescent cell antigen-like domains1/3/ 3-like
LIMS3	96626						
LIMS3L	100288695	223800_s_at	293.3617	364.48957	320.11373	316.37079	
LRPPRC	10128	211971_s_at	188.8315	220.7098	193.52489	189.2244	leucine-rich pentatricopeptide repeat containing
LRRN4CL	221091	1556427_s_at	14.54448	13.945574	14.961288	13.507702	LRRN4 C-terminal like
MAD2L1	4085	203362_s_at	92.11715	98.64707	91.755737	91.964449	MAD2 mitotic arrest deficient-like 1
MIR222HG	104457406	230127_at	377.4735	462.79759	418.01818	415.13376	mir222 host gene
NEGR1	257194	229461_x_at	371.3654	453.71036	411.15057	406.95643	neuronal growth regulator 1

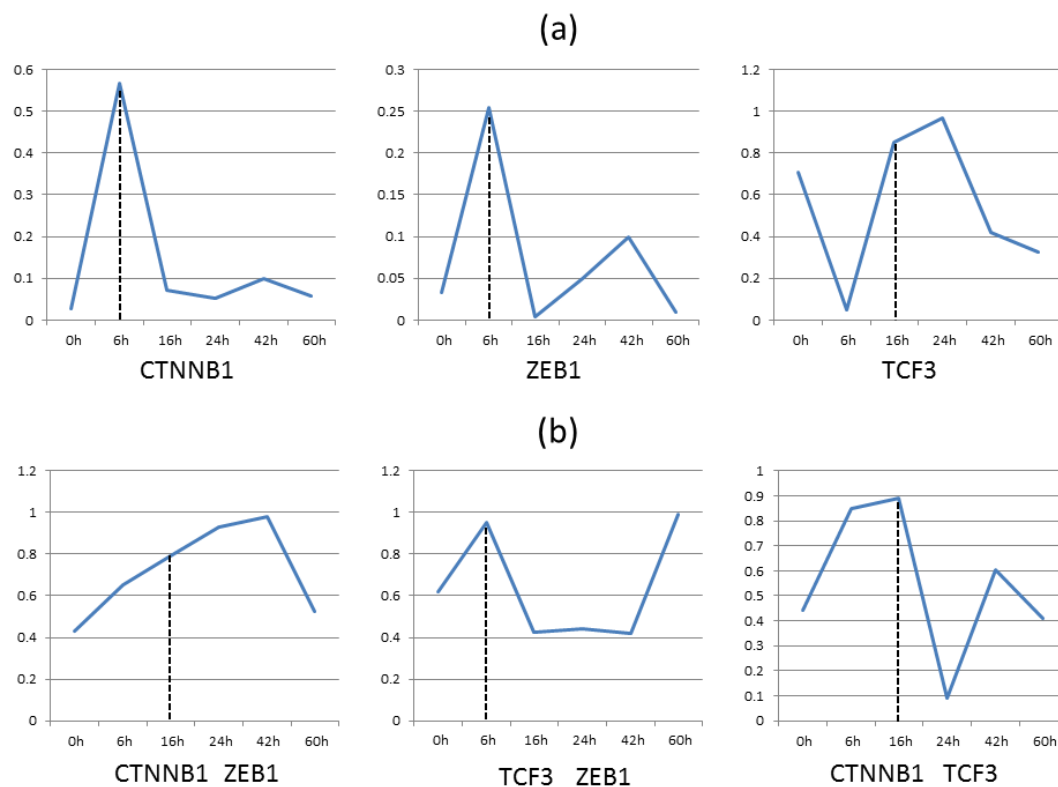
NFATC4	4776	236270_at	404.1241	500.35345	453.97249	449.54891	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4
NUP210	23225	212316_at	197.4709	226.28646	201.80165	197.0098	nucleoporin 210kDa
PAXIP1	22976	212825_at	216.6102	250.06231	225.97912	221.72788	PAX interacting (with transcription-activation domain) protein 1
PBK	55872	219148_at	259.0917	317.4496	282.78675	277.63484	PDZ binding kinase
PLSCR4	57088	218901_at	244.5695	298.12318	266.43027	261.34157	scramblase 4
PRKG1	19091	207119_at	120.0464	142.98307	123.34144	116.5139	protein kinase, cGMP-dependent, type I
PTGER1	5731	207650_x_at	136.9467	159.39237	137.61208	131.2176	prostaglandin E receptor 1 (subtype EP1), 42kDa
PVRL3	25945	213325_at	223.8796	260.93221	236.71967	231.87038	poliovirus receptor-related 3
RCAN2	53901	203498_at	97.24311	107.70898	97.322378	95.658324	regulator of calcineurin 2
RHOJ	57381	238905_at	411.0583	514.92339	468.05213	463.27683	ras homolog family member J
SEPT11	55752	201307_at	48.74439	65.91386	58.23728	60.421052	septin 11
SESN3	143686	235684_s_at	398.502	492.24572	446.11732	442.52997	sestrin 3
SH3PXD2A	9644	207661_s_at	141.1119	167.03443	143.62843	136.77832	SH3 and PX domains 2A
SLC25A13	10165	229061_s_at	356.4658	426.01638	383.78231	379.71565	solute carrier family 25 (aspartate/glutamate carrier), member 13
ST3GAL1	6482	225033_at	307.2061	385.22796	337.46985	335.02797	ST3 beta-galactoside alpha-2,3-sialyltransferase 1
SYNE2	23124	202761_s_at	68.01389	78.95854	72.358136	72.459103	spectrin repeat containing, nuclear envelope 2
TCEA3		226388_at	325.2317	403.39433	354.17747	351.01143	transcription elongation factor A (SII), 3
TIMELESS	8914	203046_s_at	79.00754	87.86439	80.795204	80.795945	timeless circadian clock
TNC	3371	237169_at	406.5662	506.68457	457.12012	453.81697	tenascin C
WNT5B	81029	221029_s_at	275.8283	336.69402	303.20107	297.88832	wingless-type MMTV integration site family, member 5B
XK	7504	206698_at	117.573	136.50863	117.92368	114.04674	X-linked Kx blood group

Remarks

1. Probe 202712_s_at corresponds to the two genes of CKMT1A and CKMT1B, together.

2. Probe223800_s_at corresponds to the three genes of LIMS1, LIMS3 and LIMS3L, together.
3. The gene expressions of several probes without gene symbols are eliminated (1560208_at, 1560526_at, 229456_s_at.) from the above list.
4. Gene IDs are those of Homo sapiens (human), except for the ELD1, which has no gene ID for Homo sapiens. Thus, we used the gene ID for Bos taurus (cattle) in the list.

Supplementary Figure



Supplementary Figure S1

(a) The standard deviations and (b) absolute values of correlation coefficients among the expressions of TCF3, ZEB1, and CTNNB1.