



**Supplementary Fig. S1.** Gene expression analysis of *SIX1* in human cancer samples. Cancer names in black color means no significant difference. Cancer names in red means highly expressed compare with normal control. Cancer names in green indicate lower expression in cancer samples ( $p < 0.05$ ). T: tumor, N: normal, ACC: adrenocortical carcinoma, BLCA: bladder urothelial carcinoma, BRCA: breast invasive carcinoma, CESC: cervical squamous cell carcinoma and endocervical adenocarcinoma, CHOL: cholangiocarcinoma, COAD: colon adenocarcinoma, DLBC: lymphoid neoplasm diffuse large B-cell lymphoma, ESCA: esophageal carcinoma, GBM: glioblastoma multiforme, HNSC: head and neck squamous cell carcinoma, KICH: kidney chromophobe, KIRC: kidney renal clear cell carcinoma, KIRP: kidney renal papillary cell carcinoma, LAML: acute myeloid leukemia, LGG: brain lower grade glioma, LIHC: liver hepatocellular carcinoma, LUAD: lung adenocarcinoma, LUSC: lung squamous cell carcinoma, MESO: mesothelioma, OV: ovarian serous cystadenocarcinoma, PAAD: pancreatic adenocarcinoma, PCPG: pheochromocytoma and paraganglioma, PRAD: prostate adenocarcinoma, READ: rectum adenocarcinoma, SARC: sarcoma, SKCM: skin cutaneous melanoma, STAD: stomach adenocarcinoma, TGCT: testicular germ cell tumor, THCA: thyroid carcinoma, THYM: thymoma, UCEC: uterine corpus endometrial carcinoma, UCS: uterine carcinosarcoma, UVM: uveal melanoma.

**Supplementary Table S1.** Human\_GO\_Cellular\_Component\_2021

Term	Overlap	p-value	Adjusted p-value	Odds ratio	Combined score	Genes
Nucleus (GO:0005634)	33/4,484	5.3E-11	1.60E-09	6.76	159.88	<i>FOXC2;FOXC1;FOXC1;TWIST2;TWIST1;GATA3;SOX2;NEUROD1;DACH1;SALL1;GBX2;OTX2;MSX1;PITX2;ATOH1;MYOG;SMAD2;MSX2;EYA1;PRRX1;EYA2;PAX6;SOX10;PAX2;SMARCA4;PAX8;WT1;MYOD1;SNAI1;CTNNB1;SNAI2;NEUROG1;FGF10</i>
Intracellular membrane-bounded organelle (GO:0043231)	33/5,192	3.2E-09	4.81E-08	5.57	108.85	<i>FOXC2;FOXC1;FOXC1;TWIST2;TWIST1;GATA3;SOX2;NEUROD1;DACH1;SALL1;GBX2;OTX2;MSX1;PITX2;ATOH1;MYOG;SMAD2;MSX2;EYA1;PRRX1;EYA2;PAX6;SOX10;PAX2;SMARCA4;PAX8;WT1;MYOD1;SNAI1;CTNNB1;SNAI2;NEUROG1;FGF10</i>
Catenin complex (GO:0016342)	2/31	2.7E-03	2.72E-02	28.62	169.08	<i>CDH1;CTNNB1</i>
Flotillin complex (GO:0016600)	1/5	1.2E-02	8.94E-02	101.77	446.44	<i>CDH1</i>
Chromocenter (GO:0010369)	1/6	1.5E-02	8.94E-02	81.41	342.39	<i>SALL1</i>
npBAF complex (GO:0071564)	1/11	2.7E-02	1.15E-01	40.69	146.73	<i>SMARCA4</i>
Beta-catenin-TCF complex (GO:1990907)	1/13	3.2E-02	1.15E-01	33.91	116.68	<i>CTNNB1</i>
Pericentric heterochromatin (GO:0005721)	1/14	3.4E-02	1.15E-01	31.30	105.42	<i>SNAI1</i>
nBAF complex (GO:0071565)	1/14	3.4E-02	1.15E-01	31.30	105.42	<i>SMARCA4</i>
Adherens junction (GO:0005912)	2/132	4.3E-02	1.27E-01	6.35	19.97	<i>CDH1;CTNNB1</i>
SWI/SNF complex (GO:0016514)	1/19	4.6E-02	1.27E-01	22.60	69.36	<i>SMARCA4</i>
Cortical actin cytoskeleton (GO:0030864)	1/42	1.0E-01	2.50E-01	9.91	22.83	<i>CDH1</i>
Cytoplasmic side of plasma membrane (GO:0009898)	1/55	1.3E-01	2.76E-01	7.52	15.41	<i>CDH1</i>
Cortical cytoskeleton (GO:0030863)	1/58	1.4E-01	2.76E-01	7.12	14.25	<i>CDH1</i>
Caveola (GO:0005901)	1/60	1.4E-01	2.76E-01	6.88	13.54	<i>CDH1</i>
Cell-cell junction (GO:0005911)	2/271	1.5E-01	2.76E-01	3.05	5.84	<i>CDH1;CTNNB1</i>
Endoplasmic reticulum lumen (GO:0005788)	2/285	1.6E-01	2.81E-01	2.90	5.32	<i>BMP4;SHH</i>
Apical junction complex (GO:0043296)	1/98	2.2E-01	3.63E-01	4.18	6.36	<i>CDH1</i>
Collagen-containing extracellular matrix (GO:0062023)	2/380	2.5E-01	3.88E-01	2.16	3.03	<i>SHH;FGF10</i>
Basolateral plasma membrane (GO:0016323)	1/151	3.2E-01	4.74E-01	2.69	3.11	<i>CTNNB1</i>
Membrane raft (GO:0045121)	1/163	3.4E-01	4.80E-01	2.49	2.72	<i>SHH</i>
Trans-Golgi network (GO:0005802)	1/239	4.5E-01	6.17E-01	1.69	1.34	<i>CDH1</i>
Actin cytoskeleton (GO:0015629)	1/316	5.5E-01	6.47E-01	1.27	0.76	<i>CDH1</i>
Nucleolus (GO:0005730)	2/733	5.5E-01	6.47E-01	1.10	0.65	<i>TWIST2;SMARCA4</i>
Intracellular membrane-bounded organelle (GO:0043232)	3/1,158	5.6E-01	6.47E-01	1.04	0.60	<i>SALL1;TWIST2;SMARCA4</i>
Nuclear lumen (GO:0031981)	2/745	5.6E-01	6.47E-01	1.08	0.62	<i>TWIST2;SMARCA4</i>
Focal adhesion (GO:0005925)	1/387	6.2E-01	6.54E-01	1.03	0.49	<i>CTNNB1</i>
Cell-substrate junction (GO:0030055)	1/394	6.3E-01	6.54E-01	1.02	0.47	<i>CTNNB1</i>
Intracellular organelle lumen (GO:0070013)	2/848	6.3E-01	6.54E-01	0.94	0.43	<i>BMP4;SHH</i>
Cytoskeleton (GO:0005856)	1/600	7.8E-01	7.82E-01	0.66	0.16	<i>CDH1</i>

GO: gene ontology.

Supplementary Table S2. Human\_KEGG\_2021

Term	Overlap	p-value	Adjusted p-value	Odds ratio	Combined score	Genes
Signaling pathways regulating pluripotency of stem cells	9/143	7.40E-11	4.73E-09	32.46159447	757.2451661	SOX2;SMAD2;BMP4;DLX5;WNT9B;CTNNB1;PAX6;NEUROG1;MYF5
Gastric cancer	8/149	3.24E-09	1.04E-07	26.75987842	523.126977	SMAD2;SHH;FGF8;CDH1;WNT9B;CTNNB1;FGF3;FGF10
Hippo signaling pathway	7/163	1.56E-07	3.33E-06	20.65563506	323.724592	SOX2;SMAD2;BMP4;CDH1;WNT9B;CTNNB1;SNAI2
Pathways in cancer	10/531	6.32E-07	1.01E-05	9.32293666	133.072429	SMAD2;BMP4;SHH;FGF8;PAX8;CDH1;WNT9B;CTNNB1;FGF3;FGF10
Proteoglycans in cancer	6/205	1.18E-05	1.51E-04	13.53426222	153.622109	SMAD2;SHH;WNT9B;TWIST2;TWIST1;CTNNB1
Basal cell carcinoma	4/63	1.85E-05	1.97E-04	29.31613854	319.5356769	BMP4;SHH;WNT9B;CTNNB1
Adherens junction	4/71	2.97E-05	2.31E-04	25.80532122	269.0216933	CDH1;SNAI1;CTNNB1;SNAI2
Melanoma	4/72	3.14E-05	2.31E-04	25.42455243	263.6456386	FGF8;CDH1;FGF3;FGF10
Breast cancer	5/147	3.25E-05	2.31E-04	15.49921753	160.1620314	FGF8;WNT9B;CTNNB1;FGF3;FGF10
Thyroid cancer	3/37	1.08E-04	6.72E-04	37.38923655	341.6326661	PAX8;CDH1;CTNNB1
Transcriptional misregulation in cancer	5/192	1.15E-04	6.72E-04	11.74272133	106.46286	PAX8;EYA1;PAX7;WT1;PAX3
Rap1 signaling pathway	5/210	1.76E-04	9.36E-04	10.70189702	92.54345771	FGF8;CDH1;CTNNB1;FGF3;FGF10
Hepatocellular carcinoma	4/168	8.19E-04	0.004030412	10.49098621	74.56804705	SMAD2;WNT9B;CTNNB1;SMARCA4
TGF-beta signaling pathway	3/94	0.00167936	0.007677073	13.92962357	89.00113745	SMAD2;BMP4;PITX2
Maturity onset diabetes of the young	2/26	0.001915765	0.008173931	34.59375	216.4751734	NEUROD1;PAX6
Calcium signaling pathway	4/240	0.003021962	0.012087848	7.263817244	42.14357077	FGF8;GDNF;FGF3;FGF10
Endometrial cancer	2/58	0.009260283	0.034862242	14.80208333	69.30366021	CDH1;CTNNB1
Inflammatory bowel disease	2/65	0.011523762	0.040973376	13.15277778	58.70537344	SMAD2;GATA3
Bacterial invasion of epithelial cells	2/77	0.015905777	0.053028749	11.04166667	45.72434655	CDH1;CTNNB1
Regulation of actin cytoskeleton	3/218	0.017191451	0.053028749	5.858980703	23.80704846	FGF8;FGF3;FGF10
Human T-cell leukemia virus 1 infection	3/219	0.017400058	0.053028749	5.831560284	23.62529361	SMAD2;MSX2;MSX1
Colorectal cancer	2/86	0.019588053	0.056324603	9.854166667	38.75481587	SMAD2;CTNNB1
Ras signaling pathway	3/232	0.020241654	0.056324603	5.496887485	21.43793103	FGF8;FGF3;FGF10
Chemical carcinogenesis	3/239	0.021871797	0.058324792	5.331950956	20.3816879	FGF8;FGF3;FGF10
Melanogenesis	2/101	0.026431519	0.067664689	8.35479798	30.35463591	WNT9B;CTNNB1
Th17 cell differentiation	2/107	0.029402797	0.072376117	7.875	27.77249048	SMAD2;GATA3
Thyroid hormone signaling pathway	2/121	0.036822368	0.084839973	6.943627451	22.92542615	BMP4;CTNNB1
MAPK signaling pathway	3/294	0.037117488	0.084839973	4.312129853	14.20271999	FGF8;FGF3;FGF10

Supplementary Table S2. Continued

Term	Overlap	p-value	Adjusted p-value	Odds ratio	Combined score	Genes
Apelin signaling pathway	2/137	0.046080253	0.100890196	6.115740741	18.82040176	<i>SMAD2;CDH1</i>
Fluid shear stress and atherosclerosis	2/139	0.047292279	0.100890196	6.025851582	18.38733307	<i>BMP4;CTNNB1</i>
Cushing syndrome	2/155	0.057397668	0.117129396	5.391339869	15.4071102	<i>WNT9B;CTNNB1</i>
PI3K-Akt signaling pathway	3/354	0.058564698	0.117129396	3.564102564	10.11358009	<i>FGF8;FGF3;FGF10</i>
Wnt signaling pathway	2/166	0.064742529	0.125561268	5.026930894	13.76040377	<i>WNT9B;CTNNB1</i>
Bladder cancer	1/41	0.097630215	0.183774522	10.15816327	23.6336602	<i>CDH1</i>
Hedgehog signaling pathway	1/56	0.13096182	0.239473042	7.382189239	15.00687934	<i>SHH</i>
Thyroid hormone synthesis	1/75	0.171453976	0.295759463	5.481522339	9.666337986	<i>PAX8</i>
Pancreatic cancer	1/76	0.173533135	0.295759463	5.408163265	9.4717853	<i>SMAD2</i>
Arrhythmogenic right ventricular cardiomyopathy	1/77	0.175607181	0.295759463	5.336734694	9.283280446	<i>CTNNB1</i>
Human papillomavirus infection	2/331	0.200505172	0.329034128	2.484929078	3.993070404	<i>WNT9B;CTNNB1</i>
Th1 and Th2 cell differentiation	1/92	0.206112569	0.329780111	4.453689168	7.03385741	<i>GATA3</i>
Prostate cancer	1/97	0.216033047	0.334844419	4.220663265	6.467423138	<i>CTNNB1</i>
AGE-RAGE signaling pathway in diabetic complications	1/100	0.221926912	0.334844419	4.092145949	6.160345888	<i>SMAD2</i>
Chagas disease	1/102	0.225832007	0.334844419	4.010709234	5.967790506	<i>SMAD2</i>
Parathyroid hormone synthesis, secretion and action	1/106	0.233584662	0.334844419	3.857142857	5.609098368	<i>GATA3</i>
Alzheimer disease	2/369	0.235437482	0.334844419	2.223319709	3.215609236	<i>WNT9B;CTNNB1</i>
Leukocyte transendothelial migration	1/114	0.248862408	0.34624335	3.582625971	4.982913653	<i>CTNNB1</i>
Cell cycle	1/124	0.26754039	0.364310319	3.289696366	4.337414433	<i>SMAD2</i>
Relaxin signaling pathway	1/129	0.276707924	0.366162767	3.160395408	4.060453122	<i>SMAD2</i>
FoxO signaling pathway	1/131	0.280343368	0.366162767	3.111459969	3.956968446	<i>FOXP1</i>
Spinocerebellar ataxia	1/143	0.301782956	0.386282184	2.846795056	3.410594866	<i>MYOD1</i>
Cell adhesion molecules	1/148	0.310530227	0.386376867	2.749271137	3.215201204	<i>CDH1</i>
mTOR signaling pathway	1/154	0.32088527	0.386376867	2.640656263	3.001559072	<i>WNT9B</i>
Cellular senescence	1/156	0.324302962	0.386376867	2.606319947	2.934917292	<i>SMAD2</i>
Hepatitis C	1/157	0.326005482	0.386376867	2.589481947	2.90239775	<i>CTNNB1</i>
Pathways of neurodegeneration	2/475	0.333730552	0.388341006	1.715732911	1.882881912	<i>WNT9B;CTNNB1</i>
Axon guidance	1/182	0.367228199	0.41968937	2.228999887	2.232949294	<i>SHH</i>

Supplementary Table S2. Continued

Term	Overlap	p-value	Adjusted p-value	Odds ratio	Combined score	Genes
Kaposi sarcoma-associated herpesvirus infection	1/193	0.38457366	0.431802004	2.100127551	2.006923756	<i>CTNNB1</i>
Focal adhesion	1/201	0.396895001	0.433830362	2.015306122	1.862311164	<i>CTNNB1</i>
Diabetic cardiomyopathy	1/203	0.399937365	0.433830362	1.995150535	1.828450387	<i>SMAD2</i>
Human cytomegalovirus infection	1/225	0.432426462	0.461254893	1.797193878	1.5066649	<i>CTNNB1</i>
Thermogenesis	1/232	0.442397615	0.464154874	1.742115028	1.420775327	<i>SMARCA4</i>
Salmonella infection	1/249	0.465904045	0.477409727	1.621296906	1.238306983	<i>CTNNB1</i>
Endocytosis	1/252	0.4699502	0.477409727	1.601674933	1.209470465	<i>SMAD2</i>
Cytokine-cytokine receptor interaction	1/295	0.524748024	0.524748024	1.364431487	0.879836023	<i>BMP4</i>

KEGG: Kyoto Encyclopedia of Genes and Genomes.

**Supplementary Table S3.** Mouse\_GO\_Cellular\_Component\_2021

Term	Overlap	p-value	Adjusted p-value	Odds ratio	Combined score	Genes
Nucleus (GO:0005634)	36/4,484	1.16E-13	2.89E-12	8.96184481	266.9494703	<i>DLX1;SETD2;FOXG1;FOXI1;GATA3;DACH2;SOX2;NEUROD1;DACH1;GBX2;ZIC1;OTX2;MSX1;PITX2;ATOH1;MYOG;TLE4;FOXD1;EYA1;EYA2;EYA3;EYA4;PAX6;LBX1;PAX2;TBX18;POU4F3;SMARCA4;CCNA1;PAX8;WT1;MYOD1;TLX1;MYF6;SNAI2;NEUROG1</i>
Intracellular membrane-bounded organelle (GO:0043231)	36/5,192	1.23E-11	1.54E-10	7.378144741	185.3289168	<i>DLX1;SETD2;FOXG1;FOXI1;GATA3;DACH2;SOX2;NEUROD1;DACH1;GBX2;ZIC1;OTX2;MSX1;PITX2;ATOH1;MYOG;TLE4;FOXD1;EYA1;EYA2;EYA3;EYA4;PAX6;LBX1;PAX2;TBX18;POU4F3;SMARCA4;CCNA1;PAX8;WT1;MYOD1;TLX1;MYF6;SNAI2;NEUROG1</i>
Bleb (GO:0032059)	1/5	0.012438777	0.077742357	101.7653061	446.4379351	<i>ANLN</i>
Cyclin A2-CDK2 complex (GO:0097124)	1/6	0.012438777	0.077742357	101.7653061	446.4379351	<i>CCNA1</i>
npBAF complex (GO:0071564)	1/11	0.027165345	0.107649107	40.69387755	146.734521	<i>SMARCA4</i>
Cell cortex region (GO:0099738)	1/12	0.027165345	0.107649107	40.69387755	146.734521	<i>ANLN</i>
Beta-catenin-TCF complex (GO:1990907)	1/13	0.032026213	0.107649107	33.90816327	116.68479	<i>TLE4</i>
nBAF complex (GO:0071565)	1/14	0.034447714	0.107649107	31.29827316	105.4223689	<i>SMARCA4</i>
SWI/SNF complex (GO:0016514)	1/19	0.046466455	0.129073487	22.59863946	69.35578083	<i>SMARCA4</i>
Cyclin-dependent protein kinase holoenzyme complex (GO:0000307)	1/30	0.072393966	0.180984914	14.0190007	36.80874148	<i>CCNA1</i>

Supplementary Table S3. Continued

Term	Overlap	p-value	Adjusted p-value	Odds ratio	Combined score	Genes
Serine/threonine protein kinase complex (GO:1902554)	1/37	0.088532228	0.201209609	11.28911565	27.36920369	<i>CCNA1</i>
Endoplasmic reticulum lumen (GO:0005788)	2/285	0.159296282	0.331867254	2.895612485	5.319209445	<i>BMP4;SHH</i>
Intrinsic component of endoplasmic reticulum membrane (GO:0031227)	1/121	0.261985313	0.50381791	3.37244898	4.517283553	<i>TMCO1</i>
Integral component of endoplasmic reticulum membrane (GO:0030176)	1/142	0.300020497	0.525207291	2.867129831	3.451750458	<i>TMCO1</i>
Chromosome (GO:0005694)	1/160	0.331087856	0.525207291	2.540238737	2.807907538	<i>SETD2</i>
Membrane raft (GO:0045121)	1/163	0.336132666	0.525207291	2.49281935	2.717794694	<i>SHH</i>
Integral component of organelle membrane (GO:0031301)	1/214	0.416403437	0.612357995	1.89106065	1.656759537	<i>TMCO1</i>
Cytoskeleton (GO:0005856)	2/600	0.444919634	0.615568257	1.348383501	1.092004034	<i>CCNA1;ANLN</i>

Supplementary Table S3. Continued

Term	Overlap	p-value	Adjusted p-value	Odds ratio	Combined score	Genes
Actin cytoskeleton (GO:0015629)	1/316	0.549452072	0.615568257	1.272108844	0.761781684	<i>ANLN</i>
Nucleolus (GO:0005730)	2/733	0.551618901	0.615568257	1.095474236	0.651695287	<i>FOXI1;SMARCA4</i>
Intracellular non-membrane-bounded organelle (GO:0043232)	3/1,158	0.559323487	0.615568257	1.03868472	0.603504163	<i>SETD2;FOXI1;SMARCA4</i>
Nuclear lumen (GO:0031981)	2/745	0.560539735	0.615568257	1.077108569	0.62348984	<i>FOXI1;SMARCA4</i>
Microtubule cytoskeleton (GO:0015630)	1/331	0.566322796	0.615568257	1.213358071	0.689904542	<i>CCNA1</i>
Collagen-containing extracellular matrix (GO:0062023)	1/380	0.617232346	0.632020918	1.053847396	0.508491647	<i>SHH</i>
Intracellular organelle lumen (GO:0070013)	2/848	0.632020918	0.632020918	0.940898345	0.43171501	<i>BMP4;SHH</i>

GO: gene ontology.



**Supplementary Table S4.** Mouse\_KEGG\_2021

Term	Overlap	p-value	Adjusted p-value	Odds ratio	Combined score	Genes
Transcriptional misregulation in cancer	7/192	4.74E-07	2.23E-05	17.39220616	253.2483825	<i>CCNA1;PAX8;EYA1;PAX7;WT1;TLX1;PAX3</i>
Signaling pathways regulating pluripotency of stem cells	6/143	1.47E-06	3.47E-05	19.72096881	264.7923377	<i>SOX2;BMP4;DLX5;PAX6;NEUROG1;MYF5</i>
Maturity onset diabetes of the young	2/26	0.001915765	0.030013652	34.59375	216.4751734	<i>NEUROD1;PAX6</i>
Hippo signaling pathway	3/163	0.007869541	0.085026928	7.894946809	38.24908702	<i>SOX2;BMP4;SNAI2</i>
Pathways in cancer	5/531	0.010266135	0.085026928	4.103084073	18.78763091	<i>BMP4;CCNA1;SHH;FGF8;PAX8</i>
Basal cell carcinoma	2/63	0.010854501	0.085026928	13.58538251	61.44906813	<i>BMP4;SHH</i>
TGF-beta signaling pathway	2/94	0.023131423	0.155310985	8.99365942	33.87518721	<i>BMP4;PITX2</i>
Gastric cancer	2/149	0.053524988	0.314459302	5.613095238	16.43293509	<i>SHH;FGF8</i>
Thyroid cancer	1/37	0.088532228	0.424122994	11.28911565	27.36920369	<i>PAX8</i>
Human T-cell leukemia virus 1 infection	2/219	0.10395435	0.424122994	3.788978495	8.577502458	<i>CCNA1;MSX1</i>
Calcium signaling pathway	2/240	0.120926656	0.424122994	3.450980392	7.290441319	<i>FGF8;GDNF</i>
Hedgehog signaling pathway	1/56	0.13096182	0.424122994	7.382189239	15.00687934	<i>SHH</i>
Notch signaling pathway	1/59	0.137481851	0.424122994	6.99929627	13.88844716	<i>TLE4</i>
Lysine degradation	1/63	0.146100703	0.424122994	6.546412113	12.59175625	<i>SETD2</i>
Inflammatory bowel disease	1/65	0.150378421	0.424122994	6.34119898	12.01403782	<i>GATA3</i>
Acute myeloid leukemia	1/67	0.154635136	0.424122994	6.148423006	11.47718066	<i>CCNA1</i>
Adherens junction	1/71	0.16308596	0.424122994	5.795918367	10.51076962	<i>SNAI2</i>
Melanoma	1/72	0.165185696	0.424122994	5.713998275	10.28911103	<i>FGF8</i>
Thyroid hormone synthesis	1/75	0.171453976	0.424122994	5.481522339	9.666337986	<i>PAX8</i>
Th1 and Th2 cell differentiation	1/92	0.206112569	0.476162455	4.453689168	7.03385741	<i>GATA3</i>
Progesterone-mediated oocyte maturation	1/100	0.221926912	0.476162455	4.092145949	6.160345888	<i>CCNA1</i>
Parathyroid hormone synthesis, secretion and action	1/106	0.233584662	0.476162455	3.857142857	5.609098368	<i>GATA3</i>
Th17 cell differentiation	1/107	0.235510907	0.476162455	3.820562187	5.524525481	<i>GATA3</i>
AMPK signaling pathway	1/120	0.260124462	0.476162455	3.400960384	4.579716459	<i>CCNA1</i>
Thyroid hormone signaling pathway	1/121	0.261985313	0.476162455	3.37244898	4.517283553	<i>BMP4</i>
Cell cycle	1/124	0.26754039	0.476162455	3.289696366	4.337414433	<i>CCNA1</i>
FoxO signaling pathway	1/131	0.280343368	0.476162455	3.111459969	3.956968446	<i>FOXG1</i>

Supplementary Table S4. Continued

Term	Overlap	p-value	Adjusted p-value	Odds ratio	Combined score	Genes
Fluid shear stress and atherosclerosis	1/139	0.294706918	0.476162455	2.929902396	3.579678318	<i>BMP4</i>
Spinocerebellar ataxia	1/143	0.301782956	0.476162455	2.846795056	3.410594866	<i>MYOD1</i>
Breast cancer	1/147	0.308789408	0.476162455	2.768241543	3.252948903	<i>FGF8</i>
Cellular senescence	1/156	0.324302962	0.476162455	2.606319947	2.934917292	<i>CCNA1</i>
Hepatitis B	1/162	0.33445522	0.476162455	2.508429459	2.747363087	<i>CCNA1</i>
Wnt signaling pathway	1/166	0.341140185	0.476162455	2.447124304	2.631788678	<i>TLE4</i>
Hepatocellular carcinoma	1/168	0.344457946	0.476162455	2.417573017	2.576608871	<i>SMARCA4</i>
Axon guidance	1/182	0.367228199	0.49313501	2.228999887	2.232949294	<i>SHH</i>
Epstein-Barr virus infection	1/202	0.398418068	0.494261877	2.005178191	1.845272055	<i>CCNA1</i>
Viral carcinogenesis	1/203	0.399937365	0.494261877	1.995150535	1.828450387	<i>CCNA1</i>
Proteoglycans in cancer	1/205	0.402964686	0.494261877	1.975390156	1.795444653	<i>SHH</i>
Rap1 signaling pathway	1/210	0.41046766	0.494261877	1.927643785	1.716486091	<i>FGF8</i>
Regulation of actin cytoskeleton	1/218	0.422280632	0.494261877	1.855826201	1.599880267	<i>FGF8</i>
Thermogenesis	1/232	0.442397615	0.494261877	1.742115028	1.420775327	<i>SMARCA4</i>
Ras signaling pathway	1/232	0.442397615	0.494261877	1.742115028	1.420775327	<i>FGF8</i>
Chemical carcinogenesis	1/239	0.452197036	0.494261877	1.69027611	1.341466124	<i>FGF8</i>
MAPK signaling pathway	1/294	0.523539104	0.548070159	1.369157902	0.886041712	<i>FGF8</i>
Cytokine-cytokine receptor interaction	1/295	0.524748024	0.548070159	1.364431487	0.879836023	<i>BMP4</i>
Human papillomavirus infection	1/331	0.566322796	0.578634161	1.213358071	0.689904542	<i>CCNA1</i>
PI3K-Akt signaling pathway	1/354	0.590995658	0.590995658	1.132971035	0.595882274	<i>FGF8</i>

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