

Supplementary Table 1 Correlation of DLX genes with clinical characteristics of COAD patients

DLX1

Characteristic	Low expression of	High expression of	p	statistic	method
	DLX1	DLX1			
n	239	239			
T stage, n (%)			0.09	6.5	Chisq.test
T1	7 (1.5%)	4 (0.8%)			
T2	39 (8.2%)	44 (9.2%)			
T3	171 (35.8%)	152 (31.9%)			
T4	22 (4.6%)	38 (8%)			
N stage, n (%)			0.1	4.61	Chisq.test
N0	148 (31%)	136 (28.5%)			
N1	57 (11.9%)	51 (10.7%)			
N2	34 (7.1%)	52 (10.9%)			
M stage, n (%)			0.703	0.15	Chisq.test
M0	176 (42.4%)	173 (41.7%)			
M1	31 (7.5%)	35 (8.4%)			
Pathologic stage, n (%)			0.519	2.27	Chisq.test
Stage I	38 (8.1%)	43 (9.2%)			
Stage II	102 (21.8%)	85 (18.2%)			
Stage III	64 (13.7%)	69 (14.8%)			
Stage IV	31 (6.6%)	35 (7.5%)			
Primary therapy outcome, n (%)			0.698		Fisher.test
PD	14 (5.6%)	11 (4.4%)			
SD	3 (1.2%)	1 (0.4%)			
PR	6 (2.4%)	7 (2.8%)			
CR	102 (40.8%)	106 (42.4%)			

Gender, n (%)			0.314	1.02	Chisq.test
Female	107 (22.4%)	119 (24.9%)			
Male	132 (27.6%)	120 (25.1%)			
Race, n (%)			0.589	1.06	Chisq.test
Asian	4 (1.3%)	7 (2.3%)			
Black or African American	31 (10.1%)	32 (10.5%)			
White	120 (39.2%)	112 (36.6%)			
Age, n (%)			0.226	1.47	Chisq.test
<=65	104 (21.8%)	90 (18.8%)			
>65	135 (28.2%)	149 (31.2%)			
Weight, n (%)			0.461	0.54	Chisq.test
<=90	95 (34.8%)	94 (34.4%)			
>90	47 (17.2%)	37 (13.6%)			
Height, n (%)			0.997	0	Chisq.test
<170	66 (25.8%)	61 (23.8%)			
>=170	66 (25.8%)	63 (24.6%)			
BMI, n (%)			0.533	0.39	Chisq.test
<25	42 (16.4%)	45 (17.6%)			
>=25	90 (35.2%)	79 (30.9%)			
Residual tumor, n (%)			0.179		Fisher.test
R0	171 (45.7%)	175 (46.8%)			
R1	0 (0%)	4 (1.1%)			
R2	11 (2.9%)	13 (3.5%)			
CEA level, n (%)			0.621	0.25	Chisq.test
<=5	97 (32%)	99 (32.7%)			
>5	49 (16.2%)	58 (19.1%)			
Perineural invasion, n (%)			0.763	0.09	Chisq.test

NO	65 (35.9%)	70 (38.7%)			
YES	24 (13.3%)	22 (12.2%)			
Lymphatic invasion, n (%)			0.758	0.1	Chisq.test
NO	134 (30.9%)	132 (30.4%)			
YES	88 (20.3%)	80 (18.4%)			
History of colon polyps, n (%)			0.302	1.07	Chisq.test
NO	132 (32.4%)	130 (31.9%)			
YES	65 (15.9%)	81 (19.9%)			
Neoplasm type, n (%)			1		Fisher.test
Colon adenocarcinoma	239 (50%)	239 (50%)			
Rectum adenocarcinoma	0 (0%)	0 (0%)			
Colon polyps present, n (%)			0.142	2.16	Chisq.test
NO	74 (29.7%)	88 (35.3%)			
YES	49 (19.7%)	38 (15.3%)			
Age, median (IQR)	68 (57.5, 75)	70 (60, 79)	0.021	25089.5	Wilcoxon

DLX2

Characteristic	Low expression of	High expression of	p	statistic	method
	DLX2	DLX2			
n	239	239			
T stage, n (%)			0.375	3.11	Chisq.test
T1	6 (1.3%)	5 (1%)			
T2	45 (9.4%)	38 (8%)			
T3	163 (34.2%)	160 (33.5%)			
T4	24 (5%)	36 (7.5%)			
N stage, n (%)			0.2	3.22	Chisq.test
N0	150 (31.4%)	134 (28%)			

N1	53 (11.1%)	55 (11.5%)			
N2	36 (7.5%)	50 (10.5%)			
M stage, n (%)			0.005	7.9	Chisq.test
M0	180 (43.4%)	169 (40.7%)			
M1	21 (5.1%)	45 (10.8%)			
Pathologic stage, n (%)			0.014	10.64	Chisq.test
Stage I	45 (9.6%)	36 (7.7%)			
Stage II	100 (21.4%)	87 (18.6%)			
Stage III	67 (14.3%)	66 (14.1%)			
Stage IV	21 (4.5%)	45 (9.6%)			
Primary therapy outcome, n (%)			0.036		Fisher.test
PD	12 (4.8%)	13 (5.2%)			
SD	3 (1.2%)	1 (0.4%)			
PR	2 (0.8%)	11 (4.4%)			
CR	110 (44%)	98 (39.2%)			
Gender, n (%)			0.927	0.01	Chisq.test
Female	112 (23.4%)	114 (23.8%)			
Male	127 (26.6%)	125 (26.2%)			
Race, n (%)			0.802	0.44	Chisq.test
Asian	5 (1.6%)	6 (2%)			
Black or African American	33 (10.8%)	30 (9.8%)			
White	127 (41.5%)	105 (34.3%)			
Age, n (%)			0.226	1.47	Chisq.test
<=65	104 (21.8%)	90 (18.8%)			
>65	135 (28.2%)	149 (31.2%)			
Weight, n (%)			0.094	2.8	Chisq.test
<=90	97 (35.5%)	92 (33.7%)			

>90	53 (19.4%)	31 (11.4%)			
Height, n (%)			0.812	0.06	Chisq.test
<170	69 (27%)	58 (22.7%)			
>=170	73 (28.5%)	56 (21.9%)			
BMI, n (%)			0.207	1.6	Chisq.test
<25	43 (16.8%)	44 (17.2%)			
>=25	99 (38.7%)	70 (27.3%)			
Residual tumor, n (%)			0.002		Fisher.test
R0	174 (46.5%)	172 (46%)			
R1	0 (0%)	4 (1.1%)			
R2	5 (1.3%)	19 (5.1%)			
CEA level, n (%)			0.252	1.31	Chisq.test
<=5	101 (33.3%)	95 (31.4%)			
>5	47 (15.5%)	60 (19.8%)			
Perineural invasion, n (%)			0.959	0	Chisq.test
NO	73 (40.3%)	62 (34.3%)			
YES	24 (13.3%)	22 (12.2%)			
Lymphatic invasion, n (%)			0.013	6.23	Chisq.test
NO	148 (34.1%)	118 (27.2%)			
YES	72 (16.6%)	96 (22.1%)			
History of colon polyps, n (%)			0.565	0.33	Chisq.test
NO	133 (32.6%)	129 (31.6%)			
YES	69 (16.9%)	77 (18.9%)			
Neoplasm type, n (%)			1		Fisher.test
Colon adenocarcinoma	239 (50%)	239 (50%)			
Rectum adenocarcinoma	0 (0%)	0 (0%)			

Colon polyps present, n					
(%)			1	0	Chisq.test
NO	87 (34.9%)	75 (30.1%)			
YES	47 (18.9%)	40 (16.1%)			
Age, median (IQR)	69 (57, 76)	69 (60, 78)	0.069	25817	Wilcoxon
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DLX3					
	Low expression of	High expression of			
Characteristic	DLX3	DLX3	p	statistic	method
n	239	239			
T stage, n (%)			0.618	1.79	Chisq.test
T1	5 (1%)	6 (1.3%)			
T2	40 (8.4%)	43 (9%)			
T3	168 (35.2%)	155 (32.5%)			
T4	26 (5.5%)	34 (7.1%)			
N stage, n (%)			< 0.001	14.27	Chisq.test
N0	160 (33.5%)	124 (25.9%)			
N1	50 (10.5%)	58 (12.1%)			
N2	29 (6.1%)	57 (11.9%)			
M stage, n (%)			< 0.001	14.77	Chisq.test
M0	183 (44.1%)	166 (40%)			
M1	17 (4.1%)	49 (11.8%)			
Pathologic stage, n (%)			< 0.001	26.91	Chisq.test
Stage I	41 (8.8%)	40 (8.6%)			
Stage II	116 (24.8%)	71 (15.2%)			
Stage III	62 (13.3%)	71 (15.2%)			
Stage IV	17 (3.6%)	49 (10.5%)			
Primary therapy					
outcome, n (%)			0.088		Fisher.test
PD	9 (3.6%)	16 (6.4%)			

SD	0 (0%)	4 (1.6%)			
PR	6 (2.4%)	7 (2.8%)			
CR	109 (43.6%)	99 (39.6%)			
Gender, n (%)			0.054	3.7	Chisq.test
Female	124 (25.9%)	102 (21.3%)			
Male	115 (24.1%)	137 (28.7%)			
Race, n (%)			0.971	0.06	Chisq.test
Asian	6 (2%)	5 (1.6%)			
Black or African American	32 (10.5%)	31 (10.1%)			
White	118 (38.6%)	114 (37.3%)			
Age, n (%)			0.05	3.83	Chisq.test
<=65	86 (18%)	108 (22.6%)			
>65	153 (32%)	131 (27.4%)			
Weight, n (%)			0.29	1.12	Chisq.test
<=90	91 (33.3%)	98 (35.9%)			
>90	47 (17.2%)	37 (13.6%)			
Height, n (%)			0.045	4.01	Chisq.test
<170	73 (28.5%)	54 (21.1%)			
>=170	57 (22.3%)	72 (28.1%)			
BMI, n (%)			0.658	0.2	Chisq.test
<25	42 (16.4%)	45 (17.6%)			
>=25	88 (34.4%)	81 (31.6%)			
Residual tumor, n (%)			< 0.001		Fisher.test
R0	182 (48.7%)	164 (43.9%)			
R1	2 (0.5%)	2 (0.5%)			
R2	3 (0.8%)	21 (5.6%)			
CEA level, n (%)			1	0	Chisq.test
<=5	94 (31%)	102 (33.7%)			

>5	51 (16.8%)	56 (18.5%)			
Perineural invasion, n (%)			0.968	0	Chisq.test
NO	67 (37%)	68 (37.6%)			
YES	22 (12.2%)	24 (13.3%)			
Lymphatic invasion, n (%)			0.365	0.82	Chisq.test
NO	143 (32.9%)	123 (28.3%)			
YES	82 (18.9%)	86 (19.8%)			
History of colon polyps, n (%)			0.616	0.25	Chisq.test
NO	130 (31.9%)	132 (32.4%)			
YES	77 (18.9%)	69 (16.9%)			
Neoplasm type, n (%)			1		Fisher.test
Colon adenocarcinoma	239 (50%)	239 (50%)			
Rectum adenocarcinoma	0 (0%)	0 (0%)			
Colon polyps present, n (%)			1	0	Chisq.test
NO	81 (32.5%)	81 (32.5%)			
YES	44 (17.7%)	43 (17.3%)			
Age, median (IQR)	69 (61, 78.5)	68 (55.5, 76)	0.012	32364	Wilcoxon

DLX4

Characteristic	Low expression of	High expression of	p	statistic	method
	DLX4	DLX4			
n	239	239			
T stage, n (%)			0.309	3.59	Chisq.test
T1	4 (0.8%)	7 (1.5%)			
T2	38 (8%)	45 (9.4%)			
T3	171 (35.8%)	152 (31.9%)			

T4	26 (5.5%)	34 (7.1%)			
N stage, n (%)			0.336	2.18	Chisq.test
N0	148 (31%)	136 (28.5%)			
N1	54 (11.3%)	54 (11.3%)			
N2	37 (7.7%)	49 (10.3%)			
M stage, n (%)			0.944	0	Chisq.test
M0	175 (42.2%)	174 (41.9%)			
M1	34 (8.2%)	32 (7.7%)			
Pathologic stage, n (%)			0.063	7.3	Chisq.test
Stage I	34 (7.3%)	47 (10.1%)			
Stage II	107 (22.9%)	80 (17.1%)			
Stage III	60 (12.8%)	73 (15.6%)			
Stage IV	34 (7.3%)	32 (6.9%)			
Primary therapy outcome, n (%)			0.618		Fisher.test
PD	12 (4.8%)	13 (5.2%)			
SD	1 (0.4%)	3 (1.2%)			
PR	5 (2%)	8 (3.2%)			
CR	107 (42.8%)	101 (40.4%)			
Gender, n (%)			0.647	0.21	Chisq.test
Female	110 (23%)	116 (24.3%)			
Male	129 (27%)	123 (25.7%)			
Race, n (%)			0.512	1.34	Chisq.test
Asian	4 (1.3%)	7 (2.3%)			
Black or African American	30 (9.8%)	33 (10.8%)			
White	121 (39.5%)	111 (36.3%)			
Age, n (%)			0.926	0.01	Chisq.test
<=65	98 (20.5%)	96 (20.1%)			

>65	141 (29.5%)	143 (29.9%)			
Weight, n (%)			0.77	0.09	Chisq.test
<=90	96 (35.2%)	93 (34.1%)			
>90	45 (16.5%)	39 (14.3%)			
Height, n (%)			0.315	1.01	Chisq.test
<170	70 (27.3%)	57 (22.3%)			
>=170	62 (24.2%)	67 (26.2%)			
BMI, n (%)			0.25	1.32	Chisq.test
<25	40 (15.6%)	47 (18.4%)			
>=25	92 (35.9%)	77 (30.1%)			
Residual tumor, n (%)			0.243		Fisher.test
R0	181 (48.4%)	165 (44.1%)			
R1	1 (0.3%)	3 (0.8%)			
R2	9 (2.4%)	15 (4%)			
CEA level, n (%)			0.55	0.36	Chisq.test
<=5	85 (28.1%)	111 (36.6%)			
>5	51 (16.8%)	56 (18.5%)			
Perineural invasion, n (%)			0.903	0.01	Chisq.test
NO	65 (35.9%)	70 (38.7%)			
YES	21 (11.6%)	25 (13.8%)			
Lymphatic invasion, n (%)			0.498	0.46	Chisq.test
NO	140 (32.3%)	126 (29%)			
YES	82 (18.9%)	86 (19.8%)			
History of colon polyps, n (%)			0.417	0.66	Chisq.test
NO	124 (30.4%)	138 (33.8%)			
YES	76 (18.6%)	70 (17.2%)			

Neoplasm type, n (%)			1		Fisher.test
Colon adenocarcinoma	239 (50%)	239 (50%)			
Rectum adenocarcinoma	0 (0%)	0 (0%)			
Colon polyps present, n (%)			0.963	0	Chisq.test
NO	80 (32.1%)	82 (32.9%)			
YES	44 (17.7%)	43 (17.3%)			
Age, median (IQR)	69 (58, 76)	68 (58.5, 78)	0.484	27503.5	Wilcoxon

DLX5

Characteristic	Low expression of	High expression of	p	statistic	method
	DLX5	DLX5			
n	239	239			
T stage, n (%)			< 0.001	17.26	Chisq.test
T1	6 (1.3%)	5 (1%)			
T2	56 (11.7%)	27 (5.7%)			
T3	156 (32.7%)	167 (35%)			
T4	20 (4.2%)	40 (8.4%)			
N stage, n (%)			< 0.001	21.17	Chisq.test
N0	165 (34.5%)	119 (24.9%)			
N1	47 (9.8%)	61 (12.8%)			
N2	27 (5.6%)	59 (12.3%)			
M stage, n (%)			0.005	7.83	Chisq.test
M0	185 (44.6%)	164 (39.5%)			
M1	22 (5.3%)	44 (10.6%)			
Pathologic stage, n (%)			< 0.001	24.08	Chisq.test
Stage I	56 (12%)	25 (5.4%)			
Stage II	100 (21.4%)	87 (18.6%)			
Stage III	55 (11.8%)	78 (16.7%)			
Stage IV	22 (4.7%)	44 (9.4%)			

Primary therapy					
outcome, n (%)			0.005		Fisher.test
PD	5 (2%)	20 (8%)			
SD	3 (1.2%)	1 (0.4%)			
PR	7 (2.8%)	6 (2.4%)			
CR	114 (45.6%)	94 (37.6%)			
Gender, n (%)			0.314	1.02	Chisq.test
Female	107 (22.4%)	119 (24.9%)			
Male	132 (27.6%)	120 (25.1%)			
Race, n (%)			0.3		Fisher.test
Asian	7 (2.3%)	4 (1.3%)			
Black or African American	24 (7.8%)	39 (12.7%)			
White	101 (33%)	131 (42.8%)			
Age, n (%)			< 0.001	13.2	Chisq.test
<=65	77 (16.1%)	117 (24.5%)			
>65	162 (33.9%)	122 (25.5%)			
Weight, n (%)			0.354	0.86	Chisq.test
<=90	85 (31.1%)	104 (38.1%)			
>90	32 (11.7%)	52 (19%)			
Height, n (%)			0.321	0.99	Chisq.test
<170	57 (22.3%)	70 (27.3%)			
>=170	49 (19.1%)	80 (31.2%)			
BMI, n (%)			0.898	0.02	Chisq.test
<25	37 (14.5%)	50 (19.5%)			
>=25	69 (27%)	100 (39.1%)			
Residual tumor, n (%)			0.533		Fisher.test
R0	177 (47.3%)	169 (45.2%)			
R1	1 (0.3%)	3 (0.8%)			

R2	11 (2.9%)	13 (3.5%)			
CEA level, n (%)			0.133	2.26	Chisq.test
<=5	96 (31.7%)	100 (33%)			
>5	42 (13.9%)	65 (21.5%)			
Perineural invasion, n (%)			0.023	5.17	Chisq.test
NO	63 (34.8%)	72 (39.8%)			
YES	12 (6.6%)	34 (18.8%)			
Lymphatic invasion, n (%)			< 0.001	14.88	Chisq.test
NO	150 (34.6%)	116 (26.7%)			
YES	62 (14.3%)	106 (24.4%)			
History of colon polyps, n (%)			0.009	6.9	Chisq.test
NO	121 (29.7%)	141 (34.6%)			
YES	88 (21.6%)	58 (14.2%)			
Neoplasm type, n (%)			1		Fisher.test
Colon adenocarcinoma	239 (50%)	239 (50%)			
Rectum adenocarcinoma	0 (0%)	0 (0%)			
Colon polyps present, n (%)			0.054	3.73	Chisq.test
NO	60 (24.1%)	102 (41%)			
YES	44 (17.7%)	43 (17.3%)			
Age, median (IQR)	71 (62.5, 78)	66 (54.5, 75.5)	< 0.001	34317.5	Wilcoxon

DLX6

Characteristic	Low expression of	High expression of	p	statistic	method
	DLX6	DLX6			
n	239	239			
T stage, n (%)			0.119	5.86	Chisq.test

T1	2 (0.4%)	9 (1.9%)			
T2	40 (8.4%)	43 (9%)			
T3	169 (35.4%)	154 (32.3%)			
T4	27 (5.7%)	33 (6.9%)			
N stage, n (%)			0.567	1.13	Chisq.test
N0	147 (30.8%)	137 (28.7%)			
N1	53 (11.1%)	55 (11.5%)			
N2	39 (8.2%)	47 (9.8%)			
M stage, n (%)			1	0	Chisq.test
M0	179 (43.1%)	170 (41%)			
M1	34 (8.2%)	32 (7.7%)			
Pathologic stage, n (%)			0.479	2.48	Chisq.test
Stage I	38 (8.1%)	43 (9.2%)			
Stage II	101 (21.6%)	86 (18.4%)			
Stage III	61 (13.1%)	72 (15.4%)			
Stage IV	34 (7.3%)	32 (6.9%)			
Primary therapy outcome, n (%)			0.892		Fisher.test
PD	12 (4.8%)	13 (5.2%)			
SD	2 (0.8%)	2 (0.8%)			
PR	7 (2.8%)	6 (2.4%)			
CR	92 (36.8%)	116 (46.4%)			
Gender, n (%)			0.647	0.21	Chisq.test
Female	110 (23%)	116 (24.3%)			
Male	129 (27%)	123 (25.7%)			
Race, n (%)			0.054	5.85	Chisq.test
Asian	8 (2.6%)	3 (1%)			
Black or African American	25 (8.2%)	38 (12.4%)			

White	124 (40.5%)	108 (35.3%)			
Age, n (%)			0.78	0.08	Chisq.test
<=65	95 (19.9%)	99 (20.7%)			
>65	144 (30.1%)	140 (29.3%)			
Weight, n (%)			0.299	1.08	Chisq.test
<=90	89 (32.6%)	100 (36.6%)			
>90	46 (16.8%)	38 (13.9%)			
Height, n (%)			0.104	2.64	Chisq.test
<170	70 (27.3%)	57 (22.3%)			
>=170	57 (22.3%)	72 (28.1%)			
BMI, n (%)			1	0	Chisq.test
<25	43 (16.8%)	44 (17.2%)			
>=25	84 (32.8%)	85 (33.2%)			
Residual tumor, n (%)			1		Fisher.test
R0	168 (44.9%)	178 (47.6%)			
R1	2 (0.5%)	2 (0.5%)			
R2	12 (3.2%)	12 (3.2%)			
CEA level, n (%)			0.412	0.67	Chisq.test
<=5	99 (32.7%)	97 (32%)			
>5	48 (15.8%)	59 (19.5%)			
Perineural invasion, n (%)			0.372	0.8	Chisq.test
NO	67 (37%)	68 (37.6%)			
YES	27 (14.9%)	19 (10.5%)			
Lymphatic invasion, n (%)			0.826	0.05	Chisq.test
NO	134 (30.9%)	132 (30.4%)			
YES	82 (18.9%)	86 (19.8%)			

History of colon polyps, n (%)			0.724	0.12	Chisq.test
NO	130 (31.9%)	132 (32.4%)			
YES	69 (16.9%)	77 (18.9%)			
Neoplasm type, n (%)			1		Fisher.test
Colon adenocarcinoma	239 (50%)	239 (50%)			
Rectum adenocarcinoma	0 (0%)	0 (0%)			
Colon polyps present, n (%)			0.963	0	Chisq.test
NO	80 (32.1%)	82 (32.9%)			
YES	44 (17.7%)	43 (17.3%)			
Age, median (IQR)	69 (59, 77)	68 (57, 77.5)	0.547	29470.5	Wilcoxon

Supplementary Table 2 The list of genes associated with DLX genes

Gene names	Gene names	Gene names
ABCC2	FGF19	PIP4K2B
ADAMTSL2	FGF20	PRDM11
AKAP7	FOXC2	PRR9
AL035425.2	FXYD1	PRSS56
AMBN	FZD7	PTP4A3
AMER3	GAL	QSOX2
APCDD1	HAVCR1	RASL11B
ARHGAP36	HCN4	RIMS4
ASPSCR1	HEY1	RTL5
ATOH8	HS3ST4	SATB2
ATXN7L2	ID4	SBK2
AXIN2	IGDCC3	SERPINI1
BCAM	IGF2BP1	SEZ6
BCORL1	ISM1	SH3GL2
BSX	IVL	SHISA7
C10orf82	KCNN1	SLC22A11
C1QL4	KLF14	SLC30A2
CAB39L	KRT23	SLC38A3
CACNG7	KRT31	SLC38A4
CDK5R1	KRT35	SLC38A8
CELSR2	KRT37	SLC46A1
CER1	KRTAP4-6	SLITRK1
CHRND	LHX3	SMAD7
CHST13	LMX1A	SP7
CILP2	LRRC43	SPATA31A5
CKB	LY6G6D	SRCIN1
CLDN19	MAFA	STK36

CNPY1	MAGEF1	STRIT1
COCH	METAP1D	SYT6
COMP	MFAP2	SYT7
CWH43	MGP	TCP11X1
DBF4B	MTARC1	TESMIN
DEFB106B	MYH7B	TFAP2B
DLX1	MYL3	TLCD3B
DLX2	NCAN	TNFAIP8L3
DLX3	NELL2	TNFRSF19
DLX4	NEUROD1	TRIM71
DLX5	NEUROD4	TTL4
DLX6	NKD1	TTPA
DMRT2	NOTUM	UNK
DNMT3A	NXF2B	VENTX
DNMT3B	NXPH3	VWA5B2
DYNC1I1	OGDHL	WNT3
EDC3	OLFML3	WNT6
ELAVL2	OR12D2	ZDHHC22
ETNK2	PABPC1L	ZNF385C
F10	PCSK2	ZNF620
FBXO17	PGBD5	
FGF1	PHF12	
FGF18	PHYHIPL	

Supplementary Table 3 GO and KEGG analysis of genes associated with DLX genes

ONT	ID	Description	GeneRatio	BgRatio	pvalue	padjust	qvalue	geneID	Count
BP	GO:0007389	pattern specification process	15/35	446/1867	8.352E-07	0.0016	0.0017	DLX1/DLX2/CELSR2/FGF1/FOXC2/NEUROD1/WNT3/WNT6/LHX3/AXIN2/CER1/DMRT2/SATB2/HEY1/NKD1	15
BP	GO:003002	regionalization	13/35	351/1867	1.632E-06	0.0016	0.0017	DLX1/DLX2/CELSR2/FGF1/FOXC2/NEUROD1/WNT3/LHX3/AXIN2/CER1/DMRT2/HEY1/NKD1	13
BP	GO:0048705	skeletal system morphogenesis	10/35	239/1867	9.526E-06	0.0061	0.0054	COMP/COCH/DLX2/DLX5/FOXC2/MGP/AXIN2/FGF18/CER1/SATB2	10

BP	GO:0060350	endocho ndral bone morpho genesis	6/13 5 0	73/1 8670 05	1.462 73E-05	0.007 17836 9	0.006 51686 7	COMP/COCH/DLX5/AXIN2/FGF18/CER1	6
BP	GO:0021766	hippoca mpus develop ment	6/13 5 6	81/1 8670 05	2.659 95E-05	0.007 62249 9	0.006 92006 9	DLX1/DLX2/ID4/LMX1A/NEUROD1/CDK5R1	6
BP	GO:0045165	cell fate commit ment	10/1 35 5	270/ 1867 0	2.729 95E-05	0.007 62249 9	0.006 92006 9	DLX1/DLX2/FOXC2/NEUROD1/WNT3/WNT6/LHX3/ FZD7/SATB2/NEUROD4	10
BP	GO:0061448	connecti ve tissue develop ment	10/1 35 8	273/ 1867 0	2.999 3E-05	0.007 62249 9	0.006 92006 9	COMP/COCH/DLX2/FOXC2/ID4/MGP/AXIN2/FGF18 /CER1/SATB2	10

BP	GO:0009952	anterior/posterior pattern specification	9/135	219/18670	3.10647E-05	0.007622499	0.006920069	CELSR2/FOXC2/NEUROD1/WNT3/AXIN2/CER1/DMRT2/HEY1/NKD1	9
BP	GO:0021877	forebrain neuron fate commitment	3/135	10/18670	4.27521E-05	0.009324714	0.008465421	DLX1/DLX2/SATB2	3
BP	GO:0043588	skin development	12/135	419/18670	5.36606E-05	0.010018817	0.009095561	COMP/IVL/KRT31/KRT35/TFAP2B/KRT37/KRT23/GAL/TNFRSF19/KRTAP4-6/APCDD1/PRR9	12

BP	GO:0021953	central nervous system neuron differentiation	8/13	183/5	5.614	0.010	0.009	DLX1/DLX2/DLX5/ID4/LMX1A/WNT3/LHX3/SATB2	8
				18670	21E-05	018817	095561		
BP	GO:0003407	neural retina development	5/13	62/1	8.531	0.013	0.012	DLX1/DLX2/NEUROD1/TFAP2B/NEUROD4	5
				8670	53E-05	956168	670077		
BP	GO:0048715	negative regulation of oligodendrocyte differentiation	3/13	13/1	0.000	0.015	0.013	DLX1/DLX2/ID4	3
				8670	100284	142889	747439		

BP	GO:0021761	limbic system development	6/13	109/5	0.000	0.018	0.016	DLX1/DLX2/ID4/LMX1A/NEUROD1/CDK5R1	6
				1867	14071	54076	83219		
				0		4	2		
BP	GO:0051216	cartilage development	8/13	209/5	0.000	0.018	0.016	COMP/COCH/DLX2/MGP/AXIN2/FGF18/CER1/SATB2	8
				1867	14167	54076	83219		
				0	7	4	2		
BP	GO:0001503	ossification	11/1	398/35	0.000	0.018	0.016	COMP/DLX5/FOXC2/ID4/MGP/WNT3/AXIN2/FGF18/CER1/SATB2/SP7	11
				1867	15155	59324	87983		
				0		7	8		
BP	GO:0060349	bone morphogenesis	6/13	114/5	0.000	0.020	0.018	COMP/COCH/DLX5/AXIN2/FGF18/CER1	6
				1867	17993	13240	27715		
				0	6	3	8		
BP	GO:0031214	biomineral tissue development	7/13	163/5	0.000	0.020	0.018	AMBN/COMP/MGP/WNT6/AXIN2/CER1/HEY1	7
				1867	18460	13240	27715		
				0	7	3	8		

BP	GO:0	artery	5/13	76/1	0.000	0.023	0.021	COMP/FOXC2/SMAD7/TFAP2B/HEY1	5
	04884	morpho	5	8670	22466	21132	07234		
	4	genesis			4	3	8		
BP	GO:0	pallium	7/13	172/	0.000	0.025	0.022	DLX1/DLX2/ID4/LMX1A/NEUROD1/CDK5R1/IGF2BP	7
	02154	develop	5	1867	25664	18971	86842	1	
	3	ment		0	5	2	5		
BP	GO:0	regulati	9/13	292/	0.000	0.025	0.023	DLX1/FGF1/SMAD7/TFAP2B/FGF18/CER1/ADAMTS	9
	09028	on of	5	1867	27720	91214	52428	L2/PTP4A3/RASL11B	
	7	cellular		0	6				
		response							
		to							
		growth							
		factor							
		stimulus							
BP	GO:0	eye	10/1	362/	0.000	0.027	0.024	DLX1/DLX2/FOXC2/MFAP2/NEUROD1/TFAP2B/WN	10
	00165	develop	35	1867	30560	26810	75528	T6/NEUROD4/NKD1/PRSS56	
	4	ment		0	3	3	8		

BP	GO:015006	visual system development	10/135	366/1867	0.000	0.028	0.025	DLX1/DLX2/FOXC2/MFAP2/NEUROD1/TFAP2B/WNT6/NEUROD4/NKD1/PRSS56	10
				0	5	1	2		
BP	GO:006035	cartilage development involved in endochondral bone morphogenesis	4/135	47/1867	0.000	0.028	0.026	COMP/COCH/AXIN2/CER1	4
				5	8670	36645	90314	23966	
				1		8	8		
BP	GO:004888	sensory system	10/135	371/1867	0.000	0.028	0.026	DLX1/DLX2/FOXC2/MFAP2/NEUROD1/TFAP2B/WNT6/NEUROD4/NKD1/PRSS56	10
				0	0	3	8		

		develop ment								
BP	GO:0	odontog	6/13	132/	0.000	0.028	0.026	AMBN/DLX1/DLX2/DLX3/WNT6/AXIN2		6
	04247	enesis	5	1867	39736	90314	23966			
	6			0	7	8				
BP	GO:0	chondro	4/13	48/1	0.000	0.028	0.026	COMP/COCH/AXIN2/FGF18		4
	00206	cyte	5	8670	39754	90314	23966			
	3	develop ment			7	8				
BP	GO:0	forebrai	10/1	381/	0.000	0.032	0.029	DLX1/DLX2/DLX5/ID4/LMX1A/NEUROD1/LHX3/CD	10	
	03090	n	35	1867	45697	03734	08503	K5R1/IGF2BP1/SATB2		
	0	develop ment		0	7	8	7			
BP	GO:0	telencep	8/13	251/	0.000	0.032	0.029	DLX1/DLX2/DLX5/ID4/LMX1A/NEUROD1/CDK5R1/	8	
	02153	halon	5	1867	48725	26031	28745	IGF2BP1		
	7	develop ment		0			2			

BP	GO:0042475	odontogenesis of dentin-containing tooth	5/13	90/1	0.000	0.032	0.029	AMBN/DLX1/DLX2/DLX3/WNT6	5
			5	8670	49302	26031	28745		
					6		2		
BP	GO:0072073	kidney epithelium development	6/13	140/5	0.000	0.034	0.031	FGF1/FOXC2/SMAD7/TFAP2B/WNT6/CER1	6
			5	1867	54326	40060	23051		
				0		2	2		
BP	GO:0021879	forebrain neuron differentiation	4/13	53/1	0.000	0.035	0.032	DLX1/DLX2/DLX5/SATB2	4
			5	8670	58181	69066	40169		
					4	8	5		

BP	GO:0	cerebral	3/13	24/1	0.000	0.039	0.036	DLX1/DLX2/ID4	3
	02189	cortex	5	8670	66956	67221	01633		
	5	neuron			6	9	7		
		different							
		iation							
BP	GO:0	ureteric	5/13	97/1	0.000	0.039	0.036	FGF1/FOXC2/SMAD7/WNT6/CER1	5
	00165	bud	5	8670	69442	67221	01633		
	7	develop			1	9	7		
		ment							
BP	GO:0	mesone	5/13	98/1	0.000	0.039	0.036	FGF1/FOXC2/SMAD7/WNT6/CER1	5
	07216	phric	5	8670	72756	67221	01633		
	3	epitheli				9	7		
		um							
		develop							
		ment							

BP	GO:007216	mesonephric tubule development	5/13	98/1	0.000	0.039	0.036	FGF1/FOXC2/SMAD7/WNT6/CER1	5
			5	8670	72756	67221	01633		
			4			9	7		
BP	GO:006084	artery development	5/13	100/0	0.000	0.042	0.038	COMP/FOXC2/SMAD7/TFAP2B/HEY1	5
			5	1867	79736	30361	40524		
			0	0	8	9	9		
BP	GO:005508	monovalent inorganic anion homeostasis	3/13	26/1	0.000	0.042	0.038	CKB/ABCC2/TFAP2B	3
			5	8670	85107	79626	85249		
			3		8		1		
BP	GO:000182	mesonephros	5/13	102/0	0.000	0.042	0.038	FGF1/FOXC2/SMAD7/WNT6/CER1	5
			5	1867	87205	79626	85249		
			3	0	8		1		

		develop ment								
BP	GO:0	cerebell	5/13	102/	0.000	0.042	0.038	CKB/LMX1A/NEUROD1/CDK5R1/SEZ6		5
	02154	um	5	1867	87205	79626	85249			
	9	develop ment		0	8		1			
BP	GO:0	negative	9/13	344/	0.000	0.043	0.039	DLX1/DLX2/ID4/LMX1A/TTPA/WNT3/CDK5R1/HEY	9	
	01072	regulati	5	1867	90165	16932	19117	1/GAL		
	1	on of cell develop ment		0	2	7	9			
BP	GO:0	drug	7/13	214/	0.000	0.044	0.040	ABCC2/SYT7/SLC38A3/FGF20/GAL/SLC46A1/SYT6		7
	01589	transpor	5	1867	94540	18630	11444			
	3	t		0	2	8	3			
BP	GO:0	BMP	6/13	157/	0.000	0.044	0.040	COMP/DLX1/DLX5/SMAD7/TFAP2B/CER1		6
	03050	signalin	5	1867	98967	50954	40789			
	9			0	9	2	1			

BP	GO:007026	cornification	5/13	112/1867	0.001	0.052	0.047	IVL/KRT31/KRT35/KRT37/KRT23	5
	8			0	9	2	2		
BP	GO:0021872	forebrain generation of neurons	4/13	66/1867	0.001	0.052	0.047	DLX1/DLX2/DLX5/SATB2	4
					4	2	2		
BP	GO:0008543	fibroblast growth factor receptor signaling pathway	5/13	114/1867	0.001	0.055	0.050	FGF1/FGF18/FGF19/FGF20/TRIM71	5
					0	1	2	8	

BP	GO:0071772	response to BMP	6/13	170/1867	0.001	0.055	0.050	COMP/DLX1/DLX5/SMAD7/TFAP2B/CER1	6
			5	0	48925	7	15869	07569	
						2		8	
BP	GO:0071773	cellular response to BMP stimulus	6/13	170/1867	0.001	0.055	0.050	COMP/DLX1/DLX5/SMAD7/TFAP2B/CER1	6
			5	0	48925	7	15869	07569	
						2		8	
BP	GO:0045666	positive regulation of neuron differentiation	9/13	371/1867	0.001	0.055	0.050	DLX1/DLX2/DNMT3B/NEUROD1/SERPINI1/WNT3/FGF20/CACNG7/SLITRK1	9
			5	0	52382	3	39379	28913	
						2		3	
BP	GO:0060560	developmental growth involved	7/13	235/1867	0.001	0.057	0.052	FGF1/SH3GL2/WNT3/CDK5R1/GAL/CACNG7/NKD1	7
			5	0	62154	2	87432	54107	
						2		7	

		in							
		morpho							
		genesis							
BP	GO:0	somitog	4/13	70/1	0.001	0.058	0.052	FOXC2/AXIN2/DMRT2/NKD1	4
	00175	enesis	5	8670	65730	09454	74100		
	6				7	2	3		
BP	GO:0	positive	6/13	176/	0.001	0.061	0.055	F10/FGF1/FGF18/FGF19/FGF20/TNFAIP8L3	6
	05189	regulati	5	1867	77599	16266	52639		
	7	on of		0	2	5	2		
		protein							
		kinase B							
		signalin							
		g							
BP	GO:0	cardiac	4/13	73/1	0.001	0.065	0.059	FOXC2/SMAD7/MYL3/HEY1	4
	00320	ventricle	5	8670	93485	48474	45018		
	8	morpho			2	7	5		
		genesis							

BP	GO:000854	epiderm is development	10/135	464/1867	0.00202449	0.06687335	0.06071083	IVL/KRT31/KRT35/KRT37/KRT23/GAL/TNFRSF19/KRTAP4-6/APCDD1/PRR9	10
BP	GO:004301	camera-type eye development	8/135	314/1867	0.00204922	0.06687335	0.06071083	DLX1/DLX2/FOXC2/NEUROD1/TFAP2B/WNT6/NEUROD4/PRSS56	8
BP	GO:000341	growth plate cartilage development	3/135	36/18670	0.00221719	0.06687335	0.06071083	COMP/COCH/CER1	3
BP	GO:004870	embryonic skeletal system	5/136	126/18670	0.00222813	0.06687335	0.06071083	DLX1/DLX2/FOXC2/DMRT2/SATB2	5

		develop ment								
BP	GO:0	negative	5/13	126/	0.002	0.066	0.060	DLX1/SMAD7/CER1/ADAMTSL2/RASL11B		5
	09010	regulati	5	1867	22813	87335	71083			
	1	on of		0	4	6				
		transme mbrane receptor protein serine/t reonine kinase signalin g pathway								

BP	GO:0	endothelial cell chemotaxis to fibroblast growth factor	2/13	10/1	0.002	0.066	0.060	FGF1/FGF18	2
	03576		5	8670	24841	87335	71083		
	8				6	6			
BP	GO:0	regulation of photoreceptor cell differentiation	2/13	10/1	0.002	0.066	0.060	DLX1/DLX2	2
	04653		5	8670	24841	87335	71083		
	2				6	6			
BP	GO:2	regulation of endothelial cell chemotaxis to fibroblast growth factor	2/13	10/1	0.002	0.066	0.060	FGF1/FGF18	2
	00054		5	8670	24841	87335	71083		
	4				6	6			

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BP	GO:0	dopami	3/13	37/1	0.002	0.070	0.063	LMX1A/WNT3/FGF20	3
	07154	nergic	5	8670	40016	32131	84104		
	2	neuron			7		8		
		different							
		iation							

BP	GO:0	cerebral	2/13	11/1	0.002	0.076	0.069	DLX1/DLX2	2
	02189	cortex	5	8670	73507	69919	63119		
	2	GABAer			1	2	4		
		gic							
		interneu							
		ron							

differentiation

BP	GO:003576	cell chemotaxis to fibroblast growth factor	2/13	11/1	0.002	0.076	0.069	FGF1/FGF18	2
	6		5	8670	73507	69919	63119		
					1	2	4		
BP	GO:190484	regulation of cell chemotaxis to fibroblast growth factor	2/13	11/1	0.002	0.076	0.069	FGF1/FGF18	2
	7		5	8670	73507	69919	63119		
					1	2	4		

BP	GO:004871	regulation of oligodendrocyte differentiation	3/13	39/1	0.002	0.076	0.069	DLX1/DLX2/ID4	3
			5	8670	79351	82135	7421		
					9	6			
BP	GO:007219	Notch signaling pathway	6/13	193/5	0.002	0.076	0.069	DLX1/DLX2/FOXC2/PTP4A3/HEY1/NEUROD4	6
				1867	81769	82135	7421		
				0	6	6			
BP	GO:0014046	dopamine secretion	3/13	40/1	0.003	0.079	0.072	SYT7/FGF20/SYT6	3
			5	8670	00418	69220	34839		
					9	2	1		
BP	GO:0014059	regulation of dopamine	3/13	40/1	0.003	0.079	0.072	SYT7/FGF20/SYT6	3
			5	8670	00418	69220	34839		
					9	2	1		

		ne								
		secretio								
		n								
BP	GO:1	negative	4/13	83/1	0.003	0.080	0.073	DLX1/SMAD7/ADAMTSL2/RASL11B		4
	90384	regulati	5	8670	09041	88648	43262			
	5	on of			6	9	2			
		cellular								
		response								
		to								
		transfor								
		ming								
		growth								
		factor								
		beta								
		stimulus								

BP	GO:0	cellular	2/13	12/1	0.003	0.083	0.075	CKB/ABCC2	2
	03000	anion	5	8670	26657	27643	60232		
	2	homeost			4	3	8		
		asis							
BP	GO:0	cellular	2/13	12/1	0.003	0.083	0.075	CKB/ABCC2	2
	03032	monoval	5	8670	26657	27643	60232		
	0	ent			4	3	8		
		inorgani							
		c anion							
		homeost							
		asis							
BP	GO:0	negative	3/13	43/1	0.003	0.092	0.084	DLX1/DLX2/HEY1	3
	04574	regulati	5	8670	69383	96149	39489		
	6	on of			4	5			
		Notch							
		signalin							

		g								
		pathway								
BP	GO:0	cellular	5/13	143/	0.003	0.093	0.085	FGF1/FGF18/FGF19/FGF20/TRIM71		5
	04434	response	5	1867	84364	94128	28438			
	4	to		0		3	9			
		fibroblas								
		t growth								
		factor								
		stimulus								
BP	GO:0	endocho	3/13	44/1	0.003	0.093	0.085	COMP/COCH/CER1		3
	00341	ndral	5	8670	94336	94128	28438			
	6	bone			2	3	9			
		growth								
BP	GO:0	retina	5/13	144/	0.003	0.093	0.085	DLX1/DLX2/NEUROD1/TFAP2B/NEUROD4		5
	06004	develop	5	1867	95922	94128	28438			
	1	ment in		0	8	3	9			

BP	GO:0030510	regulating BMP signaling pathway	4/13	91/18670	0.004	0.099	0.090	DLX1/SMAD7/TFAP2B/CER1	4
			5	6	30007	30645	15514		
					6		4		
CC	GO:0099699	integral component of synaptic membrane	6/13	152/1971	0.000	0.093	0.086	CHRND/SYT7/CACNG7/SLITRK1/SYT6/SHISA7	6
			8	7	70838	80697	40116		
					2	6	2		
CC	GO:0099240	intrinsic component of synaptic	6/13	164/1971	0.001	0.093	0.086	CHRND/SYT7/CACNG7/SLITRK1/SYT6/SHISA7	6
			8	7	05167	80697	40116		
					3	6	2		

		membrane							
		ne							
CC	GO:0	hippocampal mossy fiber to CA3 synapse	3/13	34/1	0.001	0.093	0.086	SH3GL2/SYT7/AKAP7	3
	09868	mpal	8	9717	71265	80697	40116		
	6	mossy			9	6	2		
		fiber to							
		CA3							
		synapse							
CC	GO:0	integral component of postsynaptic specialization membrane	4/13	74/1	0.001	0.093	0.086	CHRND/CACNG7/SLITRK1/SHISA7	4
	09906	compon	8	9717	80929	80697	40116		
	0	ent of			8	6	2		
		postsyn							
		aptic							
		specializ							
		ation							
		membra							
		ne							

CC	GO:009894	intrinsic component of postsynaptic specialization membrane	4/138	77/19717	0.00209390	0.09380697	0.08640116	CHRND/CACNG7/SLITRK1/SHISA7	4
CC	GO:004302	neuronal cell body	10/138	497/19717	0.00264135	0.09861047	0.09082544	CKB/KCNN1/PCSK2/SERPINI1/SH3GL2/CDK5R1/GAL/CACNG7/SRCIN1/SEZ6	10
MF	GO:000122	DNA-binding transcription activator	13/128	439/1769	1.79619E-05	0.00453608	0.00421853	DLX2/DLX3/DLX5/FOXC2/LMX1A/NEUROD1/TFAP2B/LHX3/SATB2/VENTX/SP7/KLF14/MAFA	13

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 ase II-
 specific

MF	GO:005104	fibroblast growth factor receptor binding	4/128	25/7697	2.93598E-05	0.00453608	0.00421853	FGF1/FGF18/FGF19/FGF20	4
KEGG	hsa05224	Breast cancer	9/54	147/8076	4.54381E-07	3.77136E-05	3.06109E-05	FGF1/WNT3/WNT6/AXIN2/FZD7/FGF18/FGF19/HEY1/FGF20	9
KEGG	hsa05226	Gastric cancer	8/54	149/8076	5.64326E-06	0.00023419	0.00019008	FGF1/WNT3/WNT6/AXIN2/FZD7/FGF18/FGF19/FGF20	8

KEGG	hsa04	Hippo	7/54	157/	7.549	0.001	0.001	FGF1/SMAD7/WNT3/WNT6/AXIN2/FZD7/NKD1	7
	390	signalin		8076	29E-	76566	43313		
		g			05	3	2		
		pathway							
KEGG	hsa04	Wnt	7/54	160/	8.509	0.001	0.001	WNT3/WNT6/AXIN2/FZD7/CER1/NKD1/NOTUM	7
	310	signalin		8076	22E-	76566	43313		
		g			05	3	2		
		pathway							
KEGG	hsa04	Signalin	6/54	143/	0.000	0.005	0.004	DLX5/ID4/WNT3/WNT6/AXIN2/FZD7	6
	550	g		8076	35609	91112	79787		
		pathway			2	7	1		
		s							
		regulati							
		ng							
		pluripot							
		ency of							

