

Table S1 The expression of AURKA is shown using a H-score and compared to the expression of the master genes given as percentages of stained nuclei (no H-score was built because staining intensity was 3+ in all cases). The cases were ordered according to the expression score for AURKA into three blocks, H-score low 10-49 (green), median 50-100 (yellow), high 101-300 (red)

AURKA	ASCL1	NeuroD	POU2F3
10	45	0	0
10	0	100	0
15	6	13	0
15	0	0	0
17	100	10	0
20	50	5	0
20	0	0	0
20	0	0	0
25	10	0	0
25	10	0	0
25	40	15	0
25	0	30	0
30	0	0	80
30	20	40	90
30	0	0	60
30	0	20	0
40	50	100	2
40	0	40	0
44	30	0	0
50	0	10	0
55	30	50	0
56	20	20	0
60	0	14	0
64	0	60	0
66	0	50	0
80	0	0	0
80	0	16	0
83	5	70	0
85	0	0	0
100	10	70	0
100	50	35	0
100	0	30	0

Table S1 (continued)

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AURKA	ASCL1	NeuroD	POU2F3
106	23	50	0
120	35	40	22
120	0	10	100
120	60	50	0
130	90	80	0
130	10	60	0
130	10	12	0
140	60	50	0
140	0	60	0
140	0	0	0
140	0	50	0
140	0	0	0
140	0	0	0
145	35	30	0
145	0	15	90
160	10	50	0
160	0	10	0
160	3	40	100
160	10	60	0
170	10	50	0
180	50	35	0
200	90	40	0
260	90	80	0
280	90	80	0
290	30	0	0
290	10	70	0
290	50	35	0
290	35	30	0
300	0	30	0

ASCL1, achaete scute family BHLH transcription factor 1; POU2F3, POU class 2 homeobox 3; AURKA, aurora kinase A.