Supplementary Information

"Wnt/β-catenin signaling induces MLL to create epigenetic changes in salivary gland tumors"

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Our **Supplementary Information** is submitted as merged pdf-file and includes:

- Seven Supplementary Figures and Legends
- Seven Supplementary Tables
- Supplemental References

Supplemental Figure Legends

Figure S1. *Co-expression of Keratin 10 and nuclear β-catenin in tumor cells at the invasive front of human salivary gland tumors. Anatomy and K14-Cre activity in mouse salivary glands. Scheme of breeding and verification of gene recombination.* **(A)** Sections of representative human salivary gland tumors (Tu1, Tu2) stained by immunofluorescence for cytokeratin 10 (in red) and β-catenin (in green, DAPI in blue). White dashed lines indicate tumor fronts. White arrow highlight cells co-expressing CK10 and nuclear β-catenin; white stars highlight CK10^{negative}/nuclear β-catenin cells. st; stroma, tu; tumor. **(B)** Structure of the salivary gland (AC; acinar cells, MEC; myoepithelial cells, IDC; intercalated duct cells, DC; ductal cells). **(C)** Keratin14-Cre-mediated expression of LacZ can be detected in ductal but not in acinar cells of the mouse salivary gland at P1. **(D,E)** Verification of K14 expression in salivary gland ducts by *in situ* hybridization. **(F)** Breeding scheme for the generation of compound mutant mice. **(G)** K14-Cre-mediated recombination of the BmpR1a and β-catenin genes was evaluated by recombination-specific PCR in wildtype, single mutant and double mutant (tumor) cells. Bars in A; 50 μm. Bars in C,D 200 μm.

Figure S2. *Wnt/β-catenin and Bmp signaling in the regulation of proliferation, apoptosis, and differentiation in mouse salivary glands at P90. Phenotypes in other K14-expressing tissues, and cytokeratin 10 expression in transplanted tumors.* **(A)** Histological analysis of wildtype, single (K14Cre;Bmpr1a^{LOF} or K14Cre;β-cat^{GOF}) and tumorigenic double mutant (K14Cre;β-cat^{GOF}:Bmpr1a^{LOF}) salivary glands as revealed by H&E staining and immunohistochemistry for cytokeratin 10 (marker for squamous cell carcinoma; insets) (Chu and Weiss, 2002). Bars; 250 μm. **(B)** Serial sections of double mutant mouse SG-SCC, as analyzed by immunohistochemistry for β-catenin (i) and pSmad1/5/8 (iii) and *in situ* hybridization for the Wnt/β-catenin target gene Axin2 (ii). Bars; 100 μm. At tumor fronts, β-catenin is located in nuclei and at cell junctions in central differentiated tumor areas (inset);

whereas phospho-Smad1/5/8 staining is low (inset shows nuclear pSmad1/5/8 staining in tubular cells from a differentiated, central area of the same tumor). **(C)** Left: quantification of apoptosis in salivary glands of wildtype and mutant mice, as determined by immunofluorescence for cleaved caspase 3. Middle and right: quantitative real-time PCR for the expression of genes important for proliferation (*c-myc* and *CK6*), apoptosis (*Fas*), and differentiation (*Loricrin*). Means and the standard deviations are shown (n=3, $*p < 0.05$, Student's t-test). P values are as compared with wildtype cells. **(D)** Sections of skin, esophagus and forestomach of wildtype and double mutant mice at P90, as analyzed by H&E staining. Bars; 250 µm.

Figure S3. *Characterization of expression patterns of CD24, CD29 and CD44 in salivary gland cells.* **(A,B)** FACS of wt and mutant salivary gland cells for the expression of CD24 (A) and CD29 (B), as indicated by the open histograms and the corresponding isotype controls (filled histograms). **(C)** Overlay of CD24 and CD29 signal intensities of wt and mutant salivary gland cells, as analyzed by FACS (single staining are shown in A,B). **(D,E)** FACS of CD44 expression in double mutant $CD24^{+}CD29^{+}$ tumor propagating cells. Note that $CD24^{+}CD29^{+}$ cells weakly express CD44. CT26 cells (a mouse colon carcinoma cell line) served as positive control for high CD44 expression.

Figure S4. *Proliferative activity in different subpopulations of double mutant salivary gland tumor cells, growth kinetics and cytokeratin expressions in transplanted tumors, and tumor propagating cells in secondary and tertiary tumor transplants.* **(A)** Freshly isolated tumor cells from double mutant mice were analyzed by FACS for the expression of CD24 and CD29 (profiles shown in black) and the proliferation marker Ki67 (profile indicated in red). **(B)** Quantification of proliferation in different CD24/CD29 subpopulations of double mutant tumor cells (of samples shown in A). Note that proliferation is highest in the high

$CD24^+CD29^+$ expressing tumor propagating cell population (P1) and in $CD24^{low}CD29^+$ cells (P4). **(C)** Tumor growth kinetics of transplants generated from different numbers of unsorted or sorted $CD24^+CD29^+$ salivary gland tumor cells after subcutaneous injection in the back skin of NOD/SCID mice (n=3). **(D)** Sections of tumors generated by injection of $CD24^+CD29^+$ tumor propagating cells of the salivary gland of double mutant mice into back skin of NOD/SCID mice. Cytokeratin 10 was highly expressed in differentiated but not in dedifferentiated parts of the tumors, as revealed by immunofluorescence analysis (CK10 in red, DAPI nuclei staining in blue). **(E)** Sections of tumors generated by injection of $CD24^+CD29^+$ tumor propagating cells of the salivary gland of double mutant mice into back skin of NOD/SCID mice. CK10 and CK14 are co-expressed by the tumor cells as revealed by immunofluorescence analysis (CK10 in red, CK14 in green, DAPI nuclear staining in blue). **(F)** FACS of salivary gland tumor cells from double mutant mice from secondary (2nd) and tertiary (3rd) transplanted tumors. High $CD24^+CD29^+$ expressing cells are marked by squares (insets), and quantification is shown above the squares (details on isotype control staining are shown in Supplementary Fig. 3). **(G)** Tumor outgrowths produced from subcutaneous injections of different cell numbers of unsorted or sorted $CD24^+CD29^+$ cells from secondary and tertiary tumors from double mutant glands into the back skin of NOD/SCID mice (each group n=3). Bar in D,E; 100 µm.

Figure S5. *Salivary gland $CD24^+CD29^+$ tumor propagating cells show increased expression of genes associated with maintenance of pluripotency and exhibit an increase in permissive and a decrease in repressive chromatin marks.* **(A)** Determination of active Bmp signaling by immunofluorescence for phospho-Smad 1/5/8 (in red; DAPI in blue) of cytospins of unsorted and $CD24^+CD29^+$ double-mutant mouse salivary gland squamous cell carcinoma cells (SG-SCC). Images from the analysis of two representative SG-SCC are shown. Quantifications are shown in **(B)**. Means and the standard deviations are shown and the P value is depicted (n=3, Student's t-test). **(C)** qRT-PCR of sorted $CD24^+CD29^+$ salivary gland cells from single mutant and double mutant mice at P80 to validate the salivary gland tumor propagating cell gene signature shown in Fig. 3C, which was identified by Affymetrix microarray analysis (n=3, $^*p < 0.05$, ANOVA, P values are as indicated by brackets, details shown in Supplementary Fig. 5D and Table S4). **(D)** Gene signature enriched in salivary gland tumor propagating cells of double mutant mice as determined by microarray profiling. Detailed expression is shown in Tables S2 and S4. **(E)** Immunofluorescence analysis for H3K9me3 of $CD24^+CD29^+$ salivary gland cells (red, DAPI in blue) from wt, single mutant ($Bmpr1a^{LOF}$ or $\beta\text{-}cat^{GOF}$) and double mutant mice. **(F)** Western blot analyses of tri-methylated H3K4, H3K27 and H3K9 from wt, single and double mutant mice (dm1, dm2) and from transplanted tumors (T1, T2). Histone 3 (H3) served as loading control. **(G)** Section of human salivary gland squamous cell carcinoma (SG-SCC) stained by immunofluorescence for H3K4me3 (in red) and β-catenin (in green, DAPI in blue). H3K4me3 co-localizes with nuclear β-catenin at the tumor fronts (white dotted line). Bars in A,D,F; 50 µm.

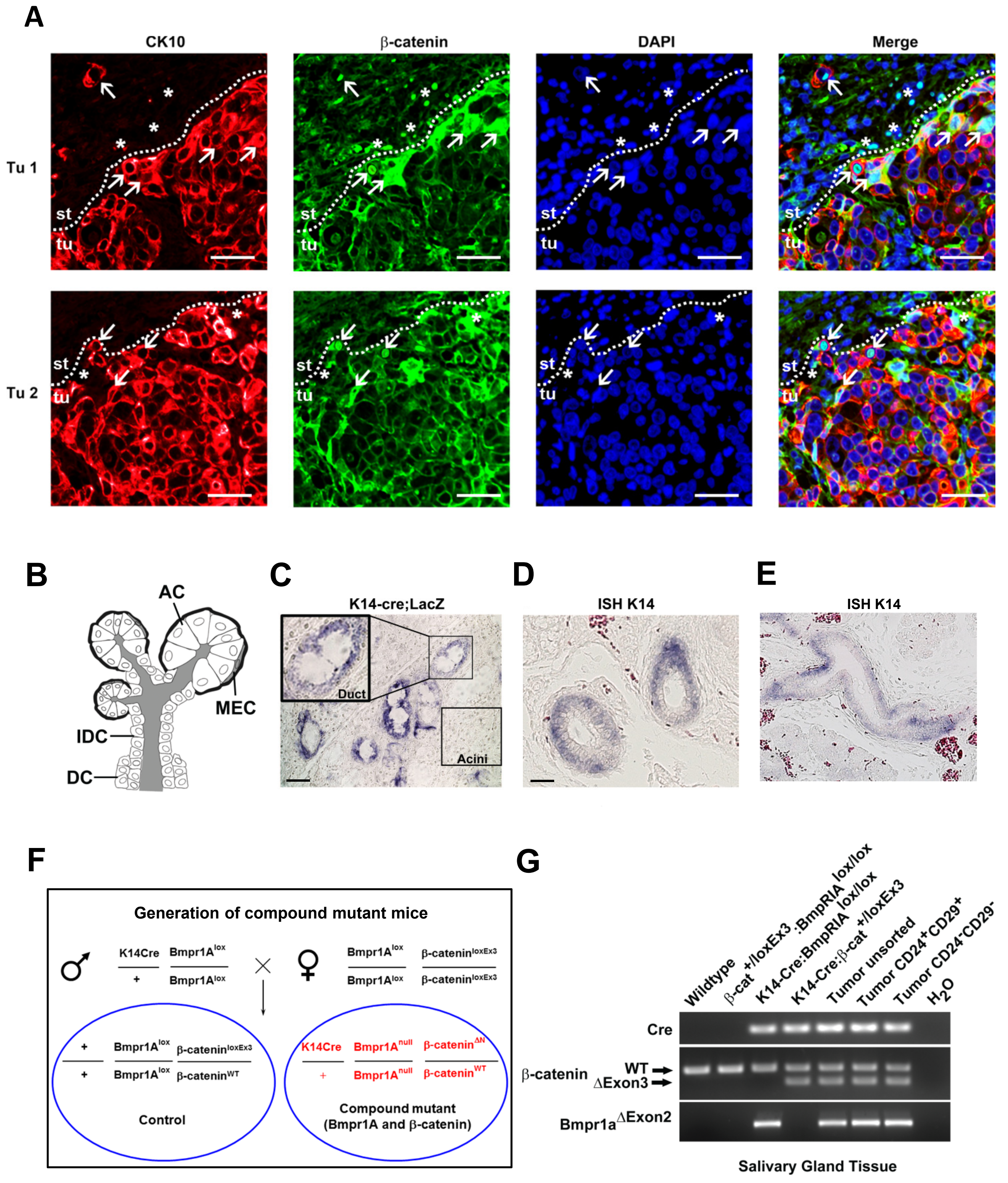
Figure S6. *The impact of high Wnt/β-catenin and low Bmp signaling on the expression of stem cell markers and self-renewal in human head and neck cancer. Salispheres of mouse tumor propagating cells respond to Wnt/β-catenin, HDAC and DNA methylation inhibitors.* **(A)** Human head and neck SCC cells (HNSCCUM-03T and HNSCCUM-02T) were analyzed by Western blotting for the expression of Axin2, pSmad1/5/8 and CD44. α-Tubulin served as a loading control. **(B)** Confirmation of the salivary gland tumor propagating cell-gene signature in human head and neck cancer cells, and effects on gene expression following treatment with either the Wnt/β-catenin activator CHIR or with the inhibitor ICG-001, as determined by qRT PCR. **(C)** Quantification of $CD24^+CD44^+$ cell populations in 03T and 02T cells treated with ICG-001 or CHIR, as determined by FACS. **(D)** Quantification of sphere formation of 03T and 02T cells treated with ICG-001 or CHIR. **(E)** H&E staining of a differentiated salisphere; inset shows magnified duct-like structures. **(F)** Differentiated salispheres show lumen formation in electron microscopy. The magnification highlights secretory granules (asterisk) and tight junctions (arrow). **(G)** Induction of *Amylase 1* (*Amy1*) expression in differentiated salispheres, as detected by qRT PCR (n=3). **(H)** Phase-contrast images of salispheres in Matrigel cultures treated with valproic acid (VPA) and 5-azacytidine (Aza). In B,C,D and G, the means and the standard deviations are shown (n=3, $*p < 0.05$, Student's t-test). P values are as compared with controls. Bars in E,H; 100 µm, in F; 5 µm.

Figure S7. *High Wnt/β-catenin signals correlate with increased expression of HELLS, NR5A2 and MLL in both salivary gland tumor propagating cells of double-mutant mice and high grade human head and neck tumors.* **(A)** Western blot analyses of HELLS and NR5A2 from salivary gland tumor propagating cells from double mutant mice after treatment with ICG-001. Tubulin served as loading control. **(B)** Human head and neck SCC cells (03T and 02T) were analyzed by immunofluorescence for nuclear β-catenin (in green, DAPI in blue) and changes in β-catenin localization were determined upon treatment with the Wnt/β-catenin inhibitor ICG-001 at 25µM. **(C)** Quantification of H3K4me3-positive tumor propagating cells upon siRNA-induced knockdown of *Mll*, *β-catenin, CBP* and *Ash1* or treatment with the Wnt/β-catenin inhibitor ICG-001 at 25µM, as analyzed by immunofluorescence in Figure 6C. The means and the standard deviations (SD) are specified (n=3). **(D)** siRNA efficacy in double mutant ($\beta\text{-}cat^{GOF};Bmpr1a^{LOF}$) salivary gland tumor propagating cells. The effect of transiently transfected siRNA pools was analyzed by qPCR. Results are normalized for β-actin. **(E)** Immunofluorescence analysis for CD24 (in green) and MLL (in red, DAPI in blue) in salivary glands from wt, single mutant ($Bmpr1a^{LOF}$ or $\beta\text{-}cat^{GOF}$) and double mutant mice. High power insets and separate channels are shown. **(F,G)** Associations between nuclear β-catenin, nuclear MLL and the clinical parameter "tumor grade" were measured on an ordinal scale and evaluated using Kendall's Tau (for τ and p-values see Figure 6F,G, further details are shown in Supplementary Table 1 and Materials and Methods). β-catenin and MLL expressions were determined by immunofluorescence analysis of human SG-SCC (n=13). **(H)** Quantification of NR5A2 expression in human head and neck cancer revealed increased levels in high grade tumors, as determined by immunohistochemistry (n=29, and data not shown). The bars give the means and standard deviations (***p <0.001, *p < 0.05, Student's t-test). P values are as compared with siCtr-transfected cells (D) or grade 2 tumors (H). Bars in B, E; 25 μm.

Supplemental Reference

Chu, P. G., and Weiss, L. M. (2002). Keratin expression in human tissues and neoplasms. Histopathology 40, 403-439.

Wend *et al.*, Suppl. Fig. 1



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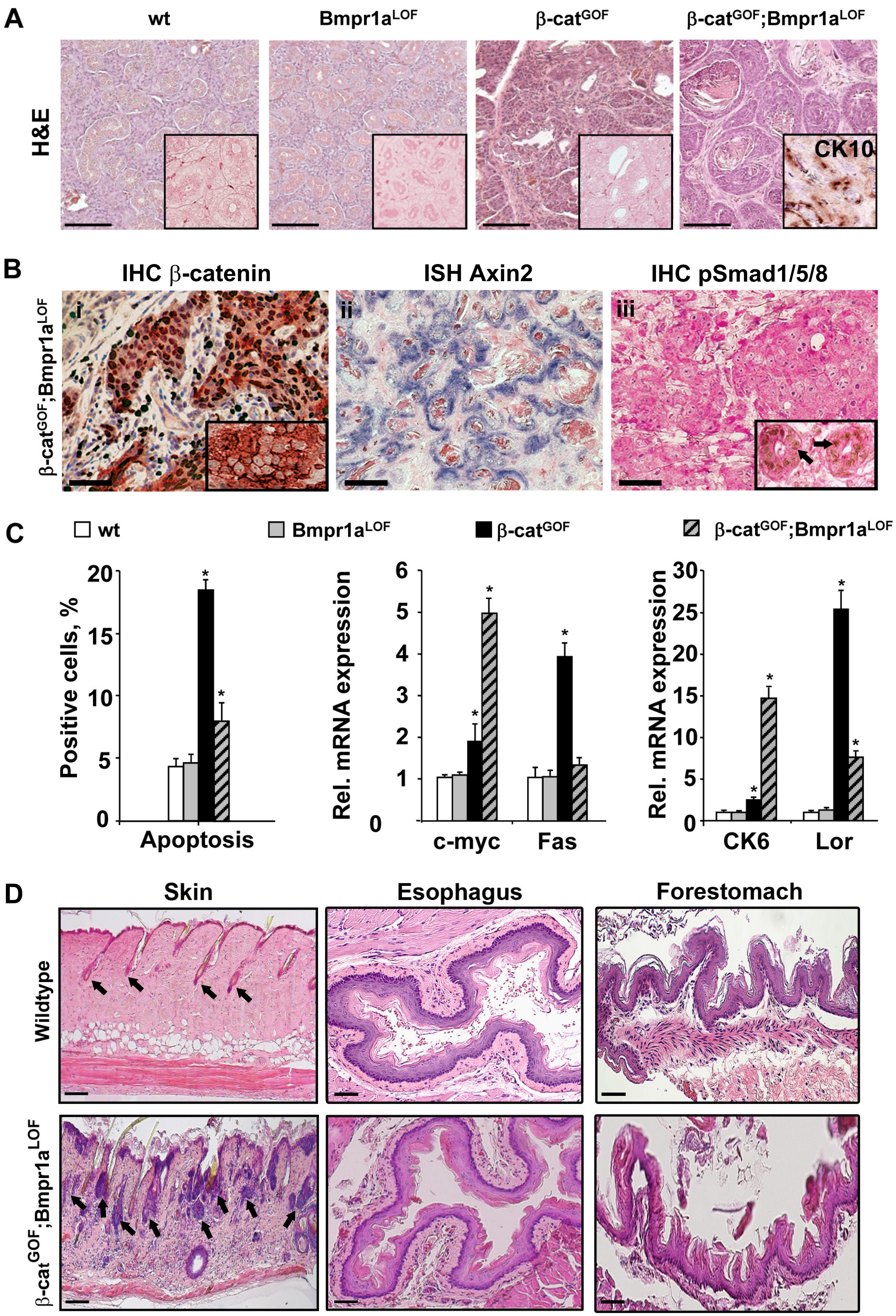

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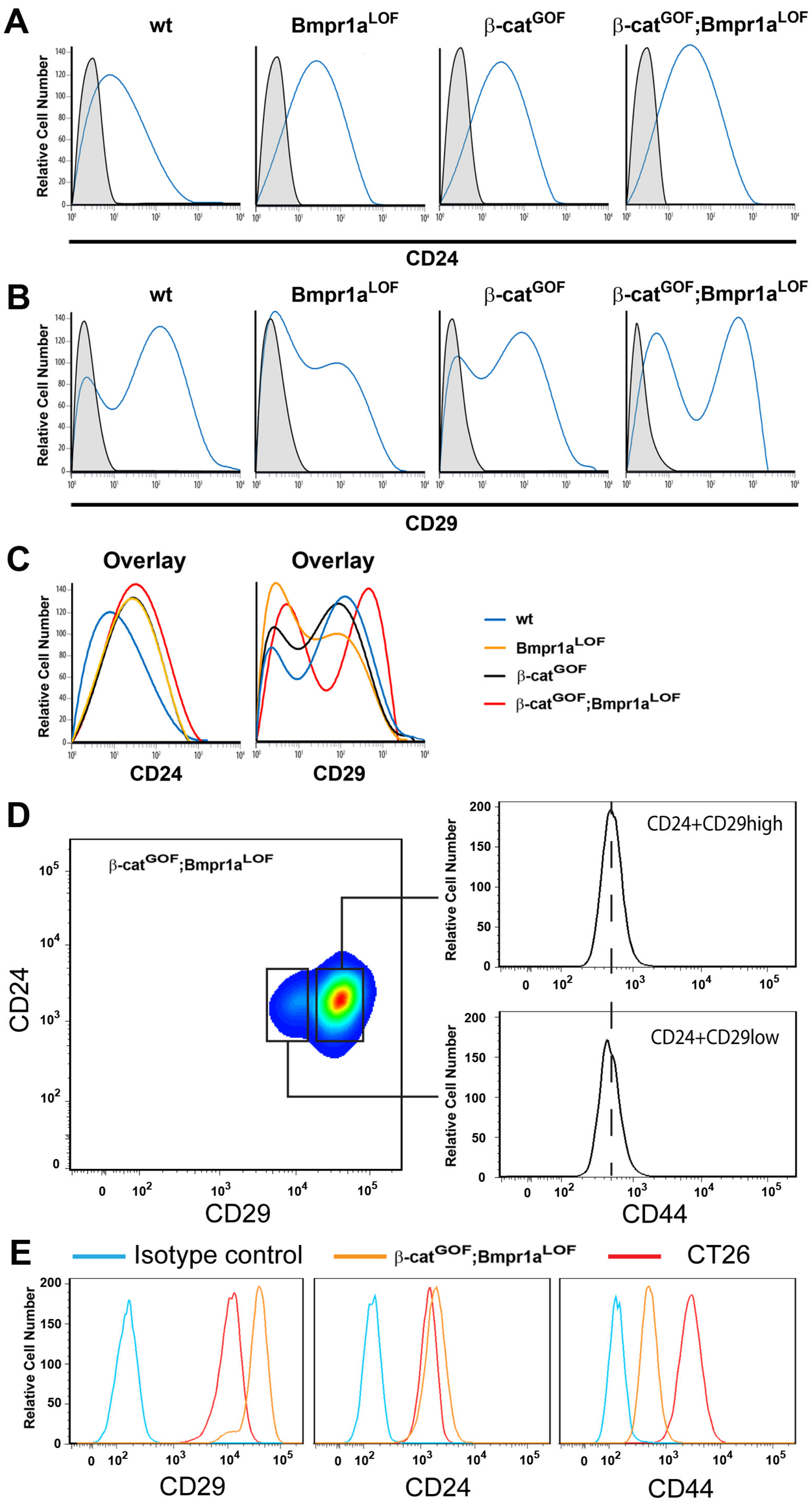

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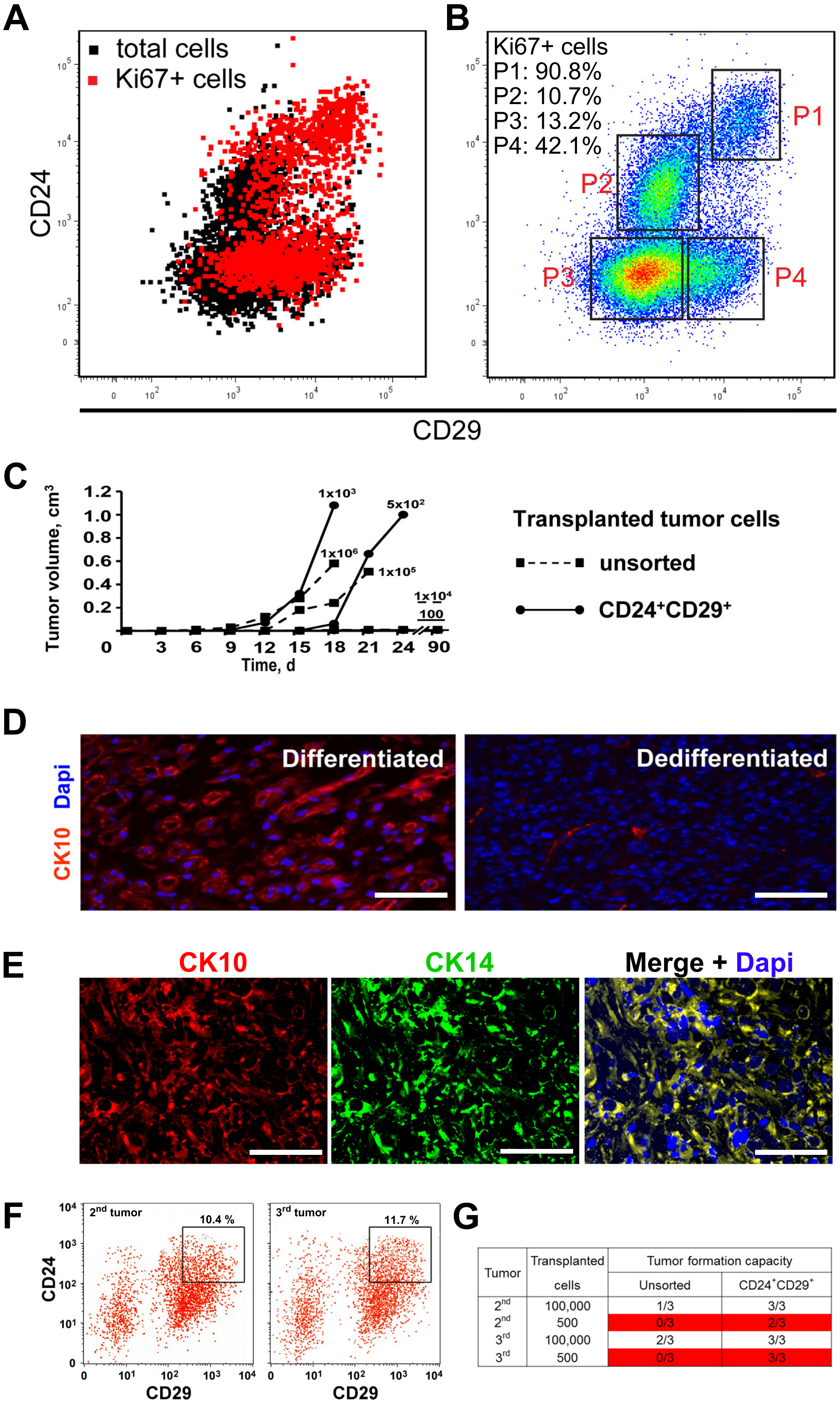
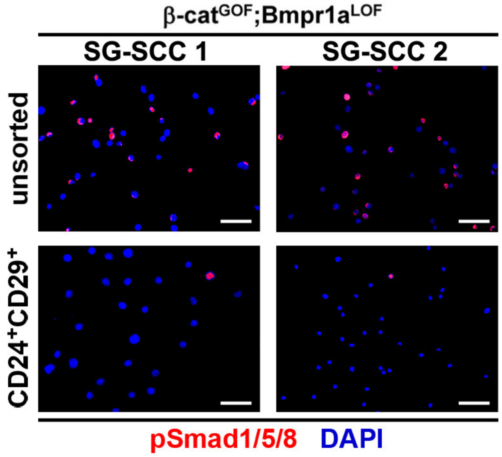


Tumor	Transplanted cells	Tumor formation capacity	
		Unsorted	$CD24^{+}CD29^{+}$
2nd	100,000	1/3	3/3
2nd	500	0/3	2/3
3rd	100,000	2/3	3/3
3rd	500	0/3	3/3

Wend *et al.*, Suppl. Fig. 5

A



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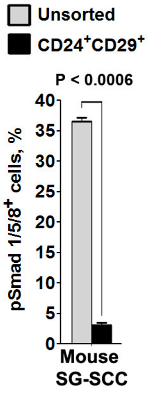

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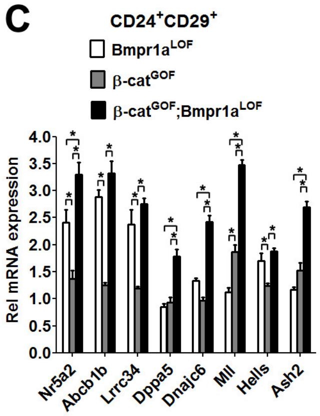

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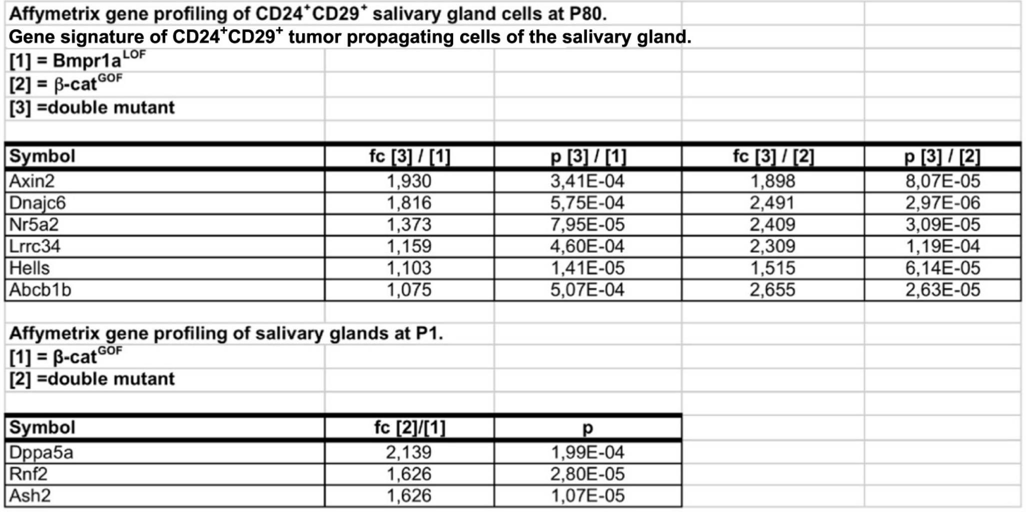


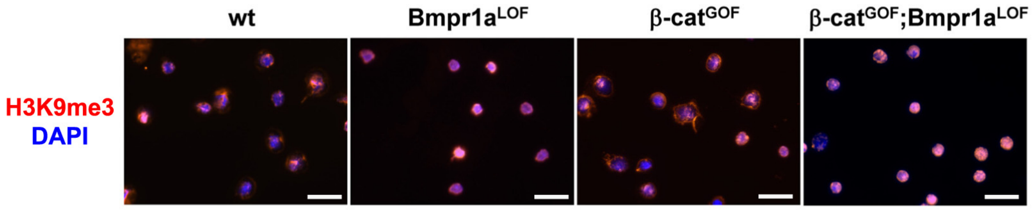
Affymetrix gene profiling of CD24^{+}CD29^{+} salivary gland cells at P80.
Gene signature of CD24^{+}CD29^{+} tumor propagating cells of the salivary gland.
[1] = Bmpr1a^{LOF}
[2] = β-cat^{GOF}
[3] =double mutant

Symbol	fc [3] / [1]	p [3] / [1]	fc [3] / [2]	p [3] / [2]
Axin2	1,930	3,41E-04	1,898	8,07E-05
Dnajc6	1,816	5,75E-04	2,491	2,97E-06
Nr5a2	1,373	7,95E-05	2,409	3,09E-05
Lrrc34	1,159	4,60E-04	2,309	1,19E-04
Hells	1,103	1,41E-05	1,515	6,14E-05
Abcb1b	1,075	5,07E-04	2,655	2,63E-05

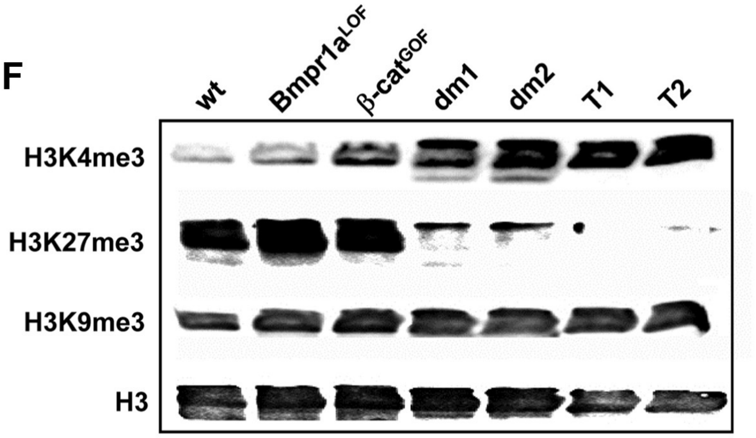
Affymetrix gene profiling of salivary glands at P1.
[1] = β-cat^{GOF}
[2] =double mutant

Symbol	fc [2]/[1]	p
Dppa5a	2,139	1,99E-04
Rnf2	1,626	2,80E-05
Ash2	1,626	1,07E-05

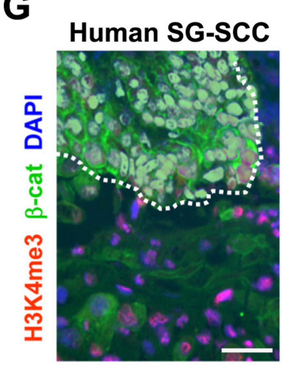
E



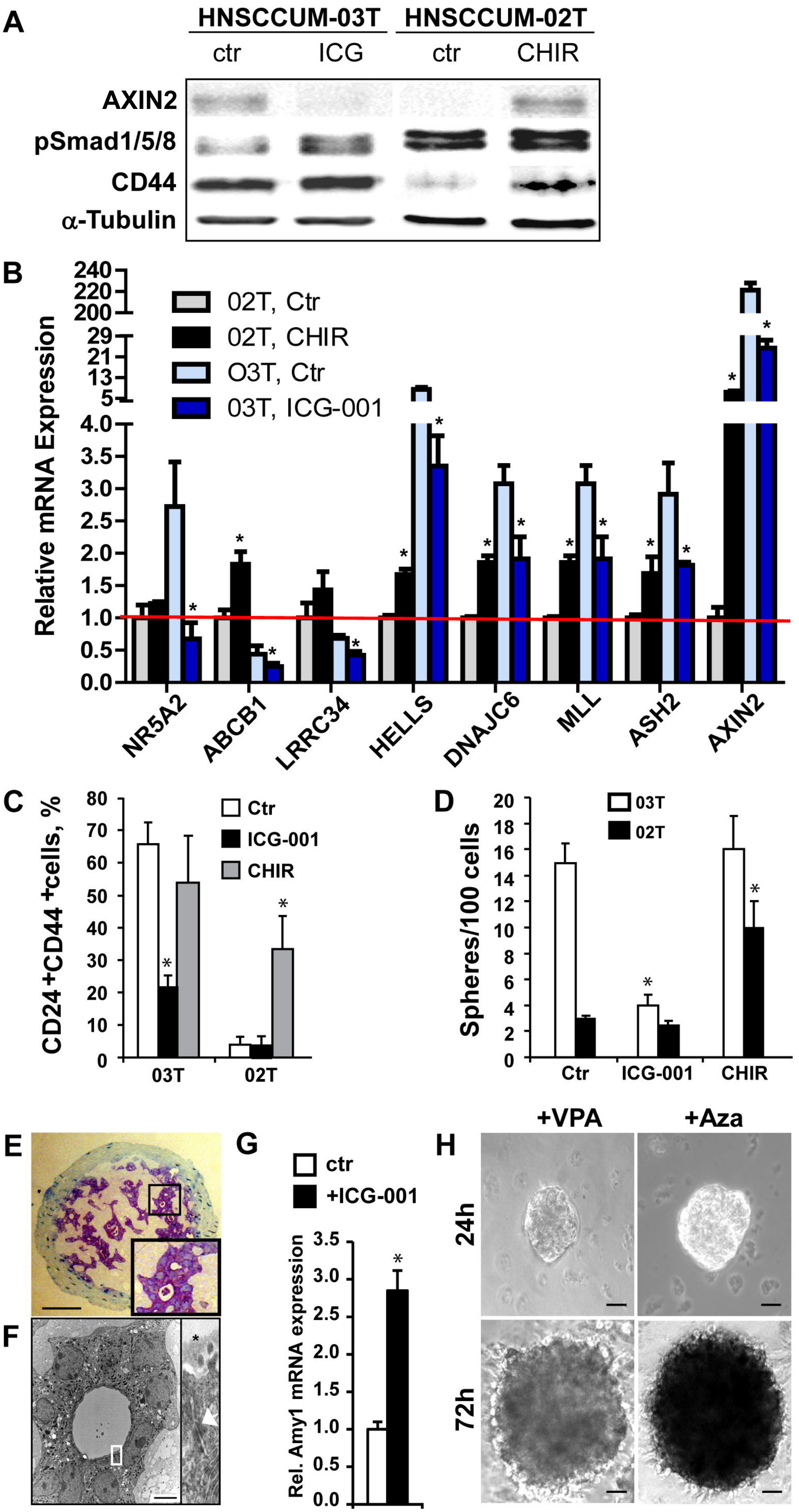
F



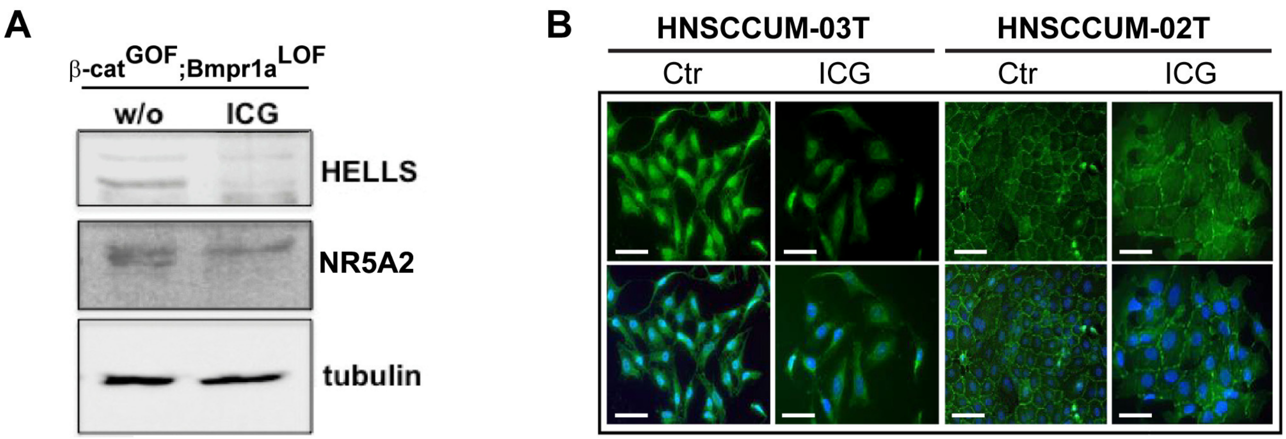
G



Wend *et al.*, Suppl. Fig. 6

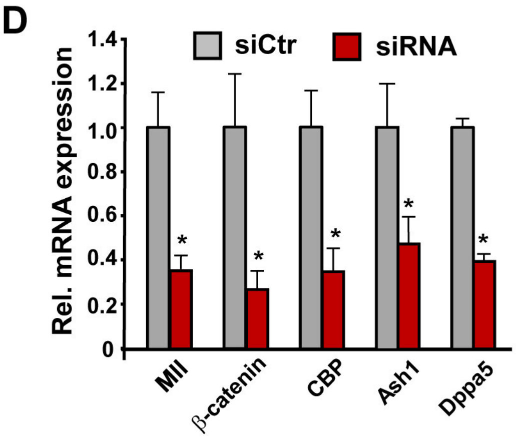


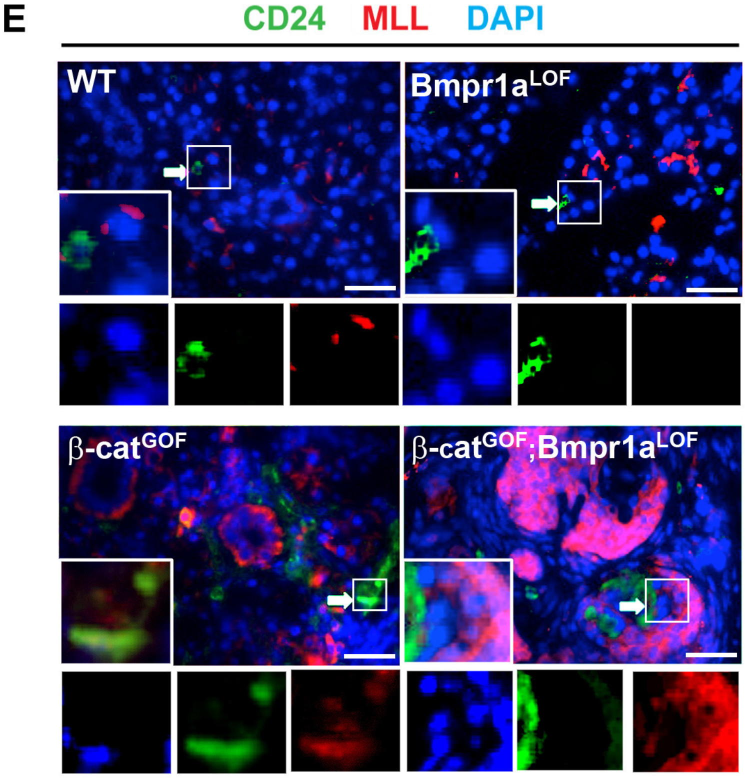
Wend *et al.*, Suppl. Fig. 7



C

	H3K4me3$^+$ cells	
Treatment	Mean (%)	SD (%)
siCtr	97.6	5.9
ICG-001	29.1	4.3
siMll	52.4	5.1
siβ-catenin	61.9	5.8
siCBP	63.2	4.7
siAsh1	95.3	7.6





F

Nuclear β-catenin	Nuclear MLL low	med	high	Total (n) (n)
low	2	2	0	4
med	0	3	2	5
high	0	0	4	4
Total (n)	2	5	6	13

G

	Marker expression						Total
	low		medium		high		(n)
Tumor Grade	β-cat	MLL	β-cat	MLL	β-cat	MLL	β-cat/MLL
2	3	2	1	2	0	0	4/4
3	1	0	4	3	4	6	9/9
Total (n)	4	2	5	5	4	6	13/13

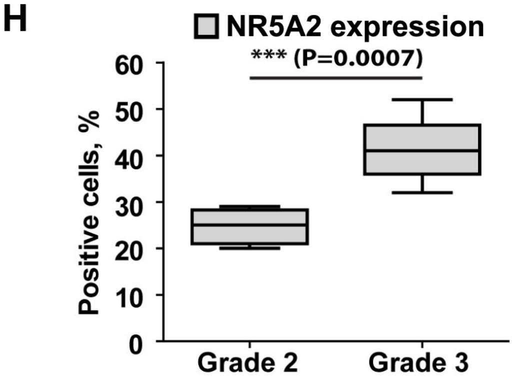


Table S1: Characteristics of human salivary gland and head and neck SCCs.[1]

#	Origin	SG-SCC[2] #	Sex	Age at diagnosis (years)	Site	Grade	IHC β-catenin[3]	IHC pS1/5/8[3]	IHC MLL[3]
1	Ch Berlin[4]	1	M	32	parotid	3	n (n-high)	-	high
2	Ch Berlin	2	M	55	parotid	2	n (n-med)	-	med
3	Ch Berlin	3	F	64	parotid	3	n (n-med)	-	med
4	Ch Berlin	4	F	71	parotid	3	n (n-high)	-	high
5	Ch Berlin	5	F	74	parotid	3	n (n-med)	-	high
6	Ch Berlin	6	M	76	parotid	3	n (n-med)	-	high
7	Ch Berlin	7	F	76	parotid	2	m (n-low)	+	med
8	Ch Berlin	8	F	76	parotid	3	n (n-med)	-	med
9	Ch Berlin	9	M	76	parotid	3	n (n-high)	-	high
10	Ch Berlin	10	F	79	sublingual	3	m (n-low)	+	med
11	Ch Berlin	11	M	80	parotid	3	n (n-high)	-	high
12	Ch Berlin	12	F	83	parotid	2	m (n-low)	+	low
13	Ch Berlin	13	F	94	parotid	2	m (n-low)	+	low
14	UH Düss[5]	14	M	61	parotid	2	n	-	n.d.
15	UH Düss	15	F	74	parotid	2	m	+	n.d.
16	UH Düss	16	M	76	parotid	2	m	+	n.d.
17	UH Düss	17	M	84	parotid	2	m	+	n.d.
18	UH Düss	18	F	90	parotid	3	m	+	n.d.
				Ø 73.4 ØF 78.1 ØM 67.5					
		HN-SCC[6] #							
19	UH Düss	1	M	47	mandible	2	n	-	n.d.
20	UH Düss	2	M	49	pharynx	2	m	+	n.d.
21	UH Düss	3	F	49	tongue	2	n	-	n.d.
22	UH Düss	4	M	51	tongue	3	n	-	n.d.
23	UH Düss	5	F	52	larynx	3	m	+	n.d.
24	UH Düss	6	M	54	mouth floor	3	n	-	n.d.
25	UH Düss	7	M	57	glottis	2	n	-	n.d.
26	UH Düss	8	M	58	pharynx	1	m	+	n.d.
27	UH Düss	9	M	58	pharynx	2	m	+	n.d.
28	UH Düss	10	M	58	tonsil	2	m	+	n.d.
29	UH Düss	11	M	59	larynx	2	m	+	n.d.
30	UH Düss	12	M	59	larynx	2	n	-	n.d.
31	UH Düss	13	M	60	pharynx	2	n	-	n.d.
32	UH Düss	14	F	60	pharynx	2	m	+	n.d.
33	UH Düss	15	M	61	pharynx	2	n	-	n.d.
34	UH Düss	16	M	61	tongue	2	m	+	n.d.
35	UH Düss	17	M	65	larynx	1	m	-	n.d.
36	UH Düss	18	M	65	mouth floor	2	m	+	n.d.
37	UH Düss	19	M	66	larynx	2	m	+	n.d.
38	UH Düss	20	M	68	pharynx	2	n	-	n.d.
39	UH Düss	21	M	68	mouth floor/tongue	2	n	-	n.d.
40	UH Düss	22	M	71	pharynx	2	m	+	n.d.
41	UH Düss	23	M	73	tonsil	2	m	+	n.d.
42	UH Düss	24	M	73	larynx	2	m	+	n.d.
43	UH Düss	25	M	73	tongue	2	m	+	n.d.
44	UH Düss	26	M	74	glottis/larynx	2	n	-	n.d.
45	UH Düss	27	M	77	pharynx	2	m	+	n.d.
46	UH Düss	28	M	78	pharynx	2	m	+	n.d.
47	UH Düss	29	M	80	glottis	2	m	-	n.d.
				Ø 62.9 ØF 53.7 ØM 64.0					

[1] Tumor specimens from 47 patients with primary salivary gland and head and neck squamous cell carcinoma (SCC) were evaluated. Cases with possible metastatic origin were stringently excluded. Tumour staging and grading was performed according to current clinical and pathological classifications (Barnes et al, 2005).

[2] SG-SCC, salivary gland squamous cell carcinoma. Tumors with mucoepidermoid or adenoid origin were stringently excluded by our collaborating pathologists.

[3] Scoring was based on intensity and percentage of positively stained cells by immunohistochemistry (IHC) for β-catenin (intracellular localization as analyzed for Fig. 1A: n, nuclear in ≥ 20% of the cells; m, membrane; cp, cytoplasmic. Nuclear score "n" [in brackets] as analyzed for Fig. 6F,G: low; ≤5%, medium; 5-25%, high; ≥25%), p-Smad 1/5/8 (as analyzed for Fig. 1A: -/detectable in ≤ 10% of the cells; +/detectable in ≥ 10% of the cells), and MLL (Nuclear score as analyzed for Fig. 6F,G: low; ≤5%, medium; 5-20%, high; ≥20%). n.d.; not determined.

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[6] HN-SCC, head and neck squamous cell carcinoma.

Reference:

Barnes L, Eveson JW, Reichart P, Sidransky D (2005) World Health Organization Classification of Tumours, Pathology & Genetics of Head and Neck Tumours. *IARC Press, Lyon*

Suppl. Table 2: Affymetrix gene profiling of salivary glands at P1.*

[1] = β-cat^{GOF}
[2] =double mutant

Probe ID	Symbol/Description	fc [2]/[1]	p
1420347_at	palate, lung, and nasal epithelium carcinoma associated	66.667	8.22E-06
1447360_at	TSC22-related inducible leucine zipper 1b (Tilz1b)	35.211	6.87E-05
1425447_at	dickkopf homolog 4 (Xenopus laevis)	16.807	3.02E-06
1441172_at	AF4/FMR2 family, member 3 (Aff3), mRNA	12.594	5.09E-04
1437894_at	prospero-related homeobox 1	6.024	2.93E-04
1429856_at	tetraspanin 18	5.464	3.94E-04
1450781_at	high mobility group AT-hook 2	5.291	2.06E-04
1446269_at	high mobility group box transcription factor 1	5.291	6.53E-06
1423635_at	bone morphogenetic protein 2	4.505	4.22E-05
1422833_at	forkhead box A2	4.484	2.23E-04
1422912_at	bone morphogenetic protein 4	3.968	3.32E-07
1428816_a_at	GATA binding protein 2	3.953	2.18E-04
1416693_at	forkhead box C2	3.817	6.93E-05
1441165_s_at	calsyntenin 2	3.717	4.91E-05
1420085_at	fibroblast growth factor 4	3.717	5.74E-05
1448877_at	distal-less homeobox 2	3.676	6.14E-06
1427489_at	integrin alpha 8	3.676	4.72E-04
1417278_a_at	naked cuticle 1 homolog (Drosophila)	3.676	3.60E-05
1421299_a_at	lymphoid enhancer binding factor 1	3.623	1.99E-05
1416101_a_at	histone 1, H1c	3.584	5.13E-07
1445123_at	Chromobox homolog 1 (Drosophila HP1 beta) (Cbx1), mRNA	3.460	2.56E-05
1419735_at	casein kappa	3.425	6.93E-05
1435950_at	hairless	3.390	3.00E-04
1439663_at	Patched homolog 1 (Ptch1), mRNA	3.390	1.22E-04
1420017_at	tetraspanin 8	3.390	6.35E-05
1449559_at	homeo box, msh-like 2	3.289	9.60E-05
1418471_at	placental growth factor	3.257	1.94E-04
1452240_at	bruno-like 4, RNA binding protein (Drosophila)	3.165	8.21E-05
1431166_at	chromodomain helicase DNA binding protein 1	3.058	5.07E-05
1416003_at	claudin 11	2.950	3.31E-06
1425425_a_at	Wnt inhibitory factor 1	2.874	4.74E-05
1422914_at	trans-acting transcription factor 5	2.865	2.56E-04
1449470_at	distal-less homeobox 1	2.857	3.92E-07
1435790_at	olfactomedin 2	2.817	3.11E-04
1449863_a_at	distal-less homeobox 5	2.725	1.43E-04
1437060_at	olfactomedin 4	2.674	5.24E-04
1453131_at	CD300 antigen like family member G	2.591	5.74E-05
1443227_at	basic leucine zipper and W2 domains 2	2.584	7.53E-05
1421677_at	fibroblast growth factor 20	2.558	1.01E-05
1422655_at	patched homolog 2	2.532	5.69E-06
1451629_at	limb-bud and heart	2.494	1.07E-06
1437419_at	BMP2 inducible kinase	2.469	3.54E-04
1423671_at	delta/notch-like EGF-related receptor	2.421	5.97E-05
1441350_at	fibroblast growth factor 3	2.410	1.66E-06
1434559_at	syntaxin 3	2.398	5.66E-05
1450135_at	frizzled homolog 3 (Drosophila)	2.387	3.41E-05
1440274_at	CAMP-GEFII	2.370	9.77E-06
1449049_at	toll-like receptor 1	2.364	1.60E-04
1459720_x_at	Timeless interacting protein (Tipin), mRNA	2.353	2.61E-06
1443087_at	CDC23 (cell division cycle 23, yeast, homolog)	2.304	5.15E-06
1450475_at	distal-less homeobox 3	2.304	6.01E-04
1422985_at	frizzled homolog 1 (Drosophila)	2.273	3.29E-07
1424446_at	armadillo repeat containing 7	2.257	1.73E-04

1435521_at	Musashi homolog 2 (Drosophila)	2.252	3.75E-04
1433471_at	transcription factor 7, T-cell specific	2.252	1.68E-07
1422537_a_at	inhibitor of DNA binding 2	2.227	6.08E-04
1427328_a_at	CLIP associating protein 2	2.217	1.42E-04
1456746_a_at	Cd99 antigen-like 2	2.203	1.91E-05
1428014_at	histone 1, H4h	2.203	1.38E-04
1423259_at	inhibitor of DNA binding 4	2.193	6.03E-05
1431053_at	M-phase phosphoprotein 9	2.169	1.04E-04
1454086_a_at	LIM domain only 2	2.160	1.16E-05
1448886_at	GATA binding protein 3	2.151	8.15E-05
1416552_at	Dppa5a, developmental pluripotency associated 5A, Esg1, ecat2	2.139	1.99E-04
1428424_at	polycomb group ring finger 3	2.137	1.25E-04
1434593_at	eukaryotic translation initiation factor 5A2	2.128	1.26E-04
1456341_a_at	Kruppel-like factor 9	2.128	4.53E-04
1441339_at	chromodomain helicase DNA binding protein 9	2.123	2.81E-06
1421341_at	axin2	2.114	1.81E-05
1425611_a_at	cut-like 1 (Drosophila)	2.105	1.48E-04
1429217_at	zinc finger protein 655	2.075	4.04E-04
1450082_s_at	ets variant gene 5	2.066	1.33E-05
1436218_at	leucine-rich repeat-containing G protein-coupled receptor 6	2.066	4.98E-06
1445315_at	WNK lysine deficient protein kinase 2	2.066	6.16E-04
1430216_at	zinc finger protein 292	2.058	9.40E-05
1449317_at	CASP8 and FADD-like apoptosis regulator	2.053	4.70E-05
1427540_at	ZW10 interactor	2.045	9.09E-06
1448925_at	twist homolog 2 (Drosophila)	2.033	3.61E-04
1419380_at	zinc finger protein 423	2.024	3.69E-06
1441938_x_at	Cdk5 and Abl enzyme substrate 1	2.020	4.31E-05
1455280_at	Fras1 related extracellular matrix protein 1	2.016	2.64E-05
1440086_at	ring finger protein 182	2.000	4.71E-04
1437904_at	developmentally regulated RNA binding protein 1	1.965	4.06E-04
1446259_at	CD180 antigen (Cd180), mRNA	1.961	3.54E-05
1437395_at	zinc finger, CCHC domain containing 11	1.961	1.08E-04
1427526_at	FGFR1 oncogene partner 2	1.949	1.02E-04
1455823_at	Bardet-Biedl syndrome 4 homolog (human)	1.942	2.27E-04
1438815_at	histone 2, H2aa2	1.927	5.80E-04
1419848_x_at	toll-like receptor 7	1.927	3.30E-06
1460725_at	xeroderma pigmentosum, complementation group A	1.927	5.50E-05
1448158_at	syndecan 1	1.923	5.95E-06
1416129_at	ERBB receptor feedback inhibitor 1	1.919	1.82E-05
1448742_at	snail homolog 1 (Drosophila)	1.916	6.53E-05
1443962_at	transcription factor Dp 2	1.916	2.60E-04
1452021_a_at	hairy and enhancer of split 6 (Drosophila)	1.908	4.75E-06
1425895_a_at	inhibitor of DNA binding 1	1.905	5.82E-04
1457276_at	SNF1-like kinase 2	1.894	4.21E-06
1453688_at	CWF19-like 2, cell cycle control (S. pombe)	1.890	1.17E-04
1457586_at	RAS p21 protein activator 2 (Rasa2), mRNA	1.873	5.35E-05
1436469_at	Bromodomain containing 7 (Brd7), mRNA	1.862	4.86E-04
1434196_at	DnaJ (Hsp40) homolog, subfamily A, member 4	1.862	4.81E-05
1455717_s_at	dishevelled associated activator of morphogenesis 2	1.859	1.78E-04
1416451_s_at	taube nuss	1.859	1.94E-05
1437162_at	GPI-anchored membrane protein 1 (Gpiap1), mRNA	1.855	2.13E-05
1445314_at	ets variant gene 1	1.852	2.01E-04
1459910_at	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	1.845	3.65E-05
1416630_at	inhibitor of DNA binding 3	1.825	2.65E-05
1424614_at	FGF receptor activating protein 1	1.818	4.43E-05
1429634_at	zinc finger protein 580	1.815	1.05E-04
1443002_at	zinc finger RNA binding protein	1.805	2.92E-04
1429962_at	CCAAT/enhancer binding protein zeta	1.799	5.56E-05
1457327_at	SNF2 histone linker PHD RING helicase	1.786	7.95E-07
1457038_at	Fras1 related extracellular matrix protein 2	1.783	2.94E-05
1443471_at	zinc finger and BTB domain containing 20	1.783	2.02E-04
1425107_a_at	leukemia inhibitory factor receptor	1.779	2.04E-05

1451281_at	zinc finger protein 96	1.779	2.41E-05
1422031_a_at	zinc finger, A20 domain containing 3	1.779	2.10E-04
1422470_at	BCL2/adenovirus E1B 19kDa-interacting protein 1, NIP3	1.776	2.68E-06
1419816_s_at	ERBB receptor feedback inhibitor 1	1.776	1.02E-04
1428574_a_at	chimerin (chimaerin) 2	1.770	3.75E-04
1424074_at	basic transcription factor 3-like 4	1.767	7.20E-08
1419716_a_at	POU domain, class 2, transcription factor 1	1.764	2.12E-04
1456351_at	bromodomain containing 8	1.761	2.27E-04
1448662_at	frizzled homolog 6 (Drosophila)	1.754	3.08E-04
1425464_at	GATA binding protein 6	1.751	2.84E-04
1418176_at	vitamin D receptor	1.748	8.72E-07
1429399_at	ring finger protein 125	1.745	4.02E-05
1441467_at	Tetraspanin 5 (Tspan5), mRNA	1.730	9.28E-05
1417958_at	tetraspan 1	1.727	2.04E-07
1455188_at	Eph receptor B1	1.724	3.03E-05
1443240_at	Glypican 3, mRNA (cDNA clone MGC:35964 IMAGE:4973409)	1.724	3.22E-04
1423040_at	basic leucine zipper and W2 domains 1	1.721	1.81E-04
1428253_at	chromatin modifying protein 2B	1.715	2.73E-05
1419144_at	CD163 antigen	1.712	1.82E-06
1440341_at	Colony stimulating factor 1 receptor (Csf1r), mRNA	1.712	3.25E-04
1434033_at	transducin-like enhancer of split 1, homolog of Drosophila E(spl)	1.712	2.02E-05
1427300_at	LIM homeobox protein 8	1.706	9.39E-06
1427200_at	zinc finger, RAN-binding domain containing 1	1.698	3.45E-06
1449314_at	zinc finger protein, multitype 2	1.678	1.32E-05
1444667_at	bromodomain, testis-specific	1.675	9.94E-05
1448789_at	aldehyde dehydrogenase family 1, subfamily A3	1.667	2.33E-05
1417182_at	DnaJ (Hsp40) homolog, subfamily A, member 2	1.664	3.22E-04
1438239_at	midline 1	1.661	1.63E-05
1448147_at	tumor necrosis factor receptor superfamily, member 19	1.661	6.21E-05
1428396_at	SMAD specific E3 ubiquitin protein ligase 1	1.658	1.14E-04
1447944_at	zinc finger with KRAB and SCAN domains 1	1.658	2.19E-04
1419368_a_at	ring finger protein 138	1.656	1.03E-04
1457441_at	early B-cell factor 1	1.647	3.28E-06
1426152_a_at	kit ligand	1.647	7.29E-07
1451191_at	cellular retinoic acid binding protein II	1.639	1.13E-04
1418147_at	transcription factor AP-2, gamma	1.639	7.92E-08
1426151_a_at	syntaxin 3	1.634	5.37E-05
1448042_s_at	Rnf2, ring finger protein 2 AI326319, AI450156, AU019207, Ring1B	1.626	2.80E-05
1441042_at	fibroblast growth factor 1	1.626	2.01E-04
1421412_at	goosecoid	1.626	6.17E-06
1420615_at	ash2 (absent, small, or homeotic)-like (Drosophila)	1.626	1.07E-05
1458450_at	zinc finger RNA binding protein	1.623	1.21E-05
1423702_at	H1 histone family, member 0	1.621	5.80E-06
1422932_a_at	vav 1 oncogene	1.621	5.27E-07
1418671_at	calpain 5	1.616	4.40E-04
1422021_at	sprouty homolog 4 (Drosophila)	1.613	5.05E-05
1448366_at	syntaxin 1A (brain)	1.613	6.67E-06
1440585_at	syntaxin 6	1.613	1.76E-04
1460441_at	zinc finger, X-linked, duplicated A	1.613	6.27E-06
1434949_at	armadillo repeat containing 8	1.608	6.70E-05
1427956_at	polycomb group ring finger 1	1.608	1.37E-04
1416111_at	CD83 antigen	1.603	6.06E-07
1427941_at	Dicer1, Dcr-1 homolog (Drosophila)	1.603	1.48E-06
1427454_at	homeo box C6	1.603	7.72E-05
1451739_at	Kruppel-like factor 5	1.603	5.55E-08
1417839_at	claudin 5	1.600	3.16E-04
1425555_at	CDC2-related kinase 7	1.597	8.02E-06
1441544_at	Cyclin M3 (Cnnm3), mRNA	1.597	2.81E-07
1421298_a_at	homeodomain interacting protein kinase 1	1.597	1.29E-04
1446349_at	zinc finger protein 78	1.597	4.09E-06
1421943_at	transforming growth factor alpha	1.595	2.78E-06
1446048_at	Cadherin 11 (Cdh11), mRNA	1.592	5.51E-05

1427618_at	cadherin 9	1.592	2.44E-06
1435903_at	CD300A antigen	1.592	1.17E-05
1416895_at	ephrin A1	1.592	7.44E-06
1454880_s_at	Bcl2 modifying factor	1.590	1.52E-04
1451156_s_at	very low density lipoprotein receptor	1.590	2.75E-04
1423528_at	breast carcinoma amplified sequence 3	1.585	4.32E-05
1429086_at	grainyhead-like 2 (Drosophila)	1.585	6.98E-05
1419126_at	homeo box D9	1.585	2.65E-04
1418213_at	keratin complex 1, acidic, gene 23	1.585	2.44E-07
1419356_at	Kruppel-like factor 7 (ubiquitous)	1.582	1.14E-04
1420376_a_at	H3 histone, family 3B	1.580	2.89E-05
1438495_at	topoisomerase (DNA) I	1.580	1.27E-04
1425693_at	Braf transforming gene	1.577	4.40E-06
1442757_at	leucine-rich repeats and calponin homology (CH) domain containing 1	1.577	1.37E-06
1449732_at	zinc finger proliferation 1	1.575	9.62E-05
1434234_at	zinc finger protein 341	1.575	3.62E-06
1444328_at	clathrin, light polypeptide (Lca)	1.572	6.46E-06
1424355_a_at	transcriptional regulator, SIN3B (yeast)	1.570	2.90E-06
1421151_a_at	Eph receptor A2	1.567	2.96E-04
1439638_at	Erbb2 interacting protein	1.567	2.09E-06
1419874_x_at	zinc finger and BTB domain containing 16	1.567	9.97E-05
1426753_at	PHD finger protein 17	1.565	1.66E-06
1453247_at	zinc fingerprotein 618	1.565	9.53E-06
1416511_a_at	CDC42 effector protein (Rho GTPase binding) 4	1.563	2.55E-04
1418285_at	ephrin B1	1.563	2.82E-05
1417394_at	Kruppel-like factor 4 (gut)	1.563	1.25E-05
1455658_at	CGG triplet repeat binding protein 1	1.560	3.24E-05
1452718_at	E3 ubiquitin protein ligase, HECT domain containing, 1	1.560	8.96E-05
1426332_a_at	claudin 3	1.558	6.84E-04
1439079_a_at	Erbb2 interacting protein	1.558	3.88E-06
1448765_at	Fyn proto-oncogene	1.555	1.46E-05
1418478_at	LIM domain only 1	1.555	2.93E-06
1426981_at	proprotein convertase subtilisin/kexin type 6	1.550	4.61E-06
1428034_a_at	tumor necrosis factor receptor superfamily, member 9	1.548	7.45E-06
1424298_at	zinc finger protein 282	1.548	4.77E-06
1419474_a_at	ets homologous factor	1.546	2.94E-07
1424638_at	cyclin-dependent kinase inhibitor 1A (P21)	1.543	4.10E-04
1434370_s_at	Fas-associated factor 1	1.543	4.14E-07
1418581_a_at	LIM motif-containing protein kinase 2	1.543	9.36E-05
1437657_at	zinc finger protein 291	1.543	7.10E-06
1454305_at	chromobox homolog 3 (Drosophila HP1 gamma)	1.541	7.20E-04
1455368_at	zinc finger, DHHC domain containing 3	1.541	4.87E-05
1423805_at	disabled homolog 2 (Drosophila)	1.538	5.69E-07
1453848_s_at	zinc finger, BED domain containing 3	1.538	6.44E-06
1421005_at	centrosomal protein 1	1.536	1.13E-05
1457577_at	Ephrin B2 (Efnb2), mRNA	1.536	7.94E-05
1424127_at	eyes absent 2 homolog (Drosophila)	1.536	2.93E-06
1441635_at	Germ cell nuclear factor protein (Nr6a1)	1.536	2.42E-05
1455725_a_at	H3 histone, family 3B	1.536	5.76E-05
1419654_at	transducin-like enhancer of split 3, homolog of Drosophila E(spl)	1.536	3.29E-05
1428634_at	TWIST neighbor	1.536	1.89E-04
1456639_at	zinc finger protein 398	1.536	1.56E-05
1451696_at	zinc finger protein 64	1.536	2.78E-08
1449126_at	zinc finger protein 90	1.536	1.66E-06
1425092_at	cadherin 10	1.534	3.09E-05
1439019_at	Fraser syndrome 1 homolog (human)	1.531	1.02E-05
1431993_a_at	ring finger protein 38	1.531	1.60E-04
1444246_at	chromodomain helicase DNA binding protein 2	1.527	9.26E-07
1433507_a_at	high mobility group nucleosomal binding domain 2	1.527	2.05E-07
1450267_at	toll-like receptor 8	1.527	2.62E-05
1428378_at	zinc finger CCCH type, antiviral 1	1.527	7.87E-06
1452504_s_at	chitobiase, di-N-acetyl-	1.524	2.97E-05

1426124_a_at	CDC-like kinase 1	1.522	4.48E-04
1423203_a_at	centrin 1	1.520	3.93E-05
1453415_at	zinc finger CCCH type containing 6	1.520	3.85E-05
1419307_at	tumor necrosis factor receptor superfamily, member 13c	1.517	1.26E-05
1435071_at	zinc finger, FYVE domain containing 1	1.517	5.08E-05
1439080_at	Erbb2 interacting protein	1.515	2.55E-04
1435608_at	zinc and ring finger 3	1.515	7.58E-06
1434236_at	zinc finger, DHHC domain containing 20	1.515	3.33E-06
1437201_at	leucine rich repeat containing 4C	1.513	1.23E-06
1419369_at	ring finger protein 138	1.513	6.77E-05
1456912_at	zinc finger protein 691	1.513	2.30E-05
1420745_a_at	cyclin D-type binding-protein 1	1.511	3.78E-04
1445635_at	Eph receptor A7, mRNA (cDNA clone MGC:14056 IMAGE:3991628)	1.508	4.73E-07
1449295_at	transcriptional regulator protein	1.508	2.84E-05
1434651_a_at	claudin 3	1.506	6.78E-05
1421604_a_at	Kruppel-like factor 3 (basic)	1.506	1.12E-05
1425635_at	tyrosine kinase, non-receptor, 1	1.506	3.03E-04
1420675_at	zinc finger protein 113	0.664	3.65E-04
1429111_at	talin 2	0.663	1.39E-06
1448837_at	villin 1	0.663	8.08E-06
1416757_at	Zwilch, kinetochore associated, homolog (Drosophila)	0.663	1.95E-04
1459009_at	Utrophin	0.662	3.35E-07
1424789_at	GLI-Kruppel family member HKR2	0.661	3.29E-04
1434824_at	bromodomain adjacent to zinc finger domain, 1B	0.661	4.18E-04
1459589_at	crystallin, lamda 1	0.658	4.71E-04
1419979_s_at	cAMP responsive element binding protein 3	0.657	4.54E-04
1433592_at	calmodulin 1	0.657	1.00E-06
1419573_a_at	lectin, galactose binding, soluble 1	0.656	4.00E-05
1445534_at	Filamin, beta, mRNA (cDNA clone IMAGE:3488025)	0.655	8.48E-05
1438861_at	basonuclin 2	0.654	1.49E-07
1420631_a_at	bladder cancer associated protein homolog (human)	0.654	3.66E-05
1449233_at	basic helix-loop-helix domain containing, class B, 8	0.652	3.29E-04
1438498_at	zinc finger, MYND domain containing 15	0.652	3.31E-04
1423505_at	transgelin	0.651	2.61E-05
1451537_at	chitinase 3-like 1	0.651	3.94E-06
1452968_at	collagen triple helix repeat containing 1	0.650	1.38E-04
1448594_at	WNT1 inducible signaling pathway protein 1	0.648	8.58E-06
1417067_s_at	chaperone, ABC1 activity of bc1 complex like (S. pombe)	0.648	7.80E-06
1422748_at	zinc finger homeobox 1b	0.647	2.61E-06
1441198_at	zinc finger protein 39	0.647	2.92E-05
1458141_at	CAMP specific phosphodiesterase 7B (PDE7B gene)	0.646	7.38E-05
1416246_a_at	coronin, actin binding protein 1A	0.646	4.05E-06
1421251_at	zinc finger protein 40	0.646	2.28E-04
1456405_at	death inducer-obliterator 1	0.645	3.87E-05
1450416_at	chromobox homolog 5 (Drosophila HP1a)	0.641	1.26E-04
1452265_at	CLIP associating protein 1	0.641	8.21E-06
1417457_at	CDC28 protein kinase regulatory subunit 2	0.641	8.39E-05
1422308_a_at	lectin, galactose binding, soluble 7	0.641	1.36E-04
1438817_at	DNA2 DNA replication helicase 2-like (yeast)	0.640	3.07E-06
1426808_at	lectin, galactose binding, soluble 3	0.640	3.30E-05
1424698_s_at	grancalcin	0.639	4.38E-04
1438833_at	cancer susceptibility candidate 5	0.638	7.64E-07
1437643_at	centromere protein J	0.638	1.63E-04
1428460_at	synapsin II	0.637	3.34E-05
1416265_at	calpain 10	0.637	1.61E-04
1448289_at	collapsin response mediator protein 1	0.637	6.31E-05
1420863_at	dynactin 4	0.637	4.92E-05
1423691_x_at	keratin complex 2, basic, gene 8	0.637	1.20E-05
1427884_at	procollagen, type III, alpha 1	0.635	6.14E-06
1435781_at	cullin associated and neddylation disassociated 1	0.632	1.20E-06
1456483_at	zinc finger protein 9	0.629	4.69E-04
1424629_at	breast cancer 1	0.627	1.67E-05

1430139_at	helicase, lymphoid specific	0.627	5.52E-06
1439436_x_at	inner centromere protein	0.626	2.64E-05
1439945_at	zinc finger protein 449	0.626	2.08E-05
1418133_at	B-cell leukemia/lymphoma 3	0.626	4.41E-05
1441375_at	Leucine-rich repeats and immunoglobulin-like domains 1 (Lrig1), mRNA	0.623	7.33E-05
1422279_at	Friend virus susceptibility 1	0.622	2.81E-06
1418495_at	zinc finger CCCH type containing 8	0.620	3.50E-06
1433623_at	zinc finger protein 367	0.620	1.09E-04
1422481_at	keratin complex 2, basic, gene 1	0.620	1.36E-07
1454849_x_at	clusterin	0.618	4.51E-05
1427290_at	keratin complex 2, basic, gene 19	0.614	5.50E-05
1434201_at	Chordin-like 1 (Chrdl1), mRNA	0.612	1.76E-07
1450536_s_at	keratin associated protein 12-1	0.612	4.51E-06
1425356_at	zinc finger protein 142	0.612	2.80E-05
1439407_x_at	transgelin 2	0.611	8.05E-07
1437788_at	trans-acting transcription factor 6	0.609	2.49E-04
1439631_at	zinc finger, CCHC domain containing 11	0.608	1.70E-05
1450842_a_at	centromere autoantigen A	0.604	9.42E-05
1439030_at	GDP-mannose pyrophosphorylase B	0.604	1.01E-05
1428503_a_at	NFKB inhibitor interacting Ras-like protein 1	0.598	1.20E-04
1416083_at	zinc finger, A20 domain containing 2	0.597	1.56E-05
1418735_at	keratin complex 2, basic, gene 4	0.597	6.76E-05
1436095_at	chromodomain helicase DNA binding protein 5	0.596	7.68E-05
1428650_at	tensin 1	0.596	1.99E-04
1448467_a_at	tangerin	0.595	8.37E-07
1421460_at	desmocollin 1	0.593	1.00E-04
1427366_at	keratin associated protein 3-1	0.593	1.01E-05
1437355_at	zinc finger, CCHC domain containing 5	0.592	1.31E-04
1451484_a_at	synapsin I	0.585	4.82E-06
1437685_x_at	fibromodulin	0.580	1.25E-06
1451637_a_at	mucin 10, submandibular gland salivary mucin	0.579	1.02E-04
1451997_at	zinc finger protein 426	0.578	3.35E-06
1455187_at	zinc finger and BTB domain containing 40	0.576	8.66E-06
1444043_at	GLI-Kruppel family member GLI3 (Gli3), mRNA	0.569	6.45E-06
1418608_at	calmodulin-like 3	0.567	8.83E-05
1455113_at	armadillo repeat containing 8	0.562	9.25E-07
1427348_at	zinc finger CCCH type containing 12A	0.562	1.07E-04
1417878_at	E2F transcription factor 1	0.561	2.93E-05
1429347_at	Bcl2-like 14 (apoptosis facilitator)	0.558	2.01E-05
1426471_at	zinc finger protein 52	0.557	1.19E-04
1424407_s_at	chromobox homolog 6	0.555	2.19E-05
1417917_at	calponin 1	0.554	9.53E-06
1425705_a_at	ERO1-like beta (S. cerevisiae)	0.554	1.60E-05
1418091_at	transcription factor CP2-like 1	0.553	5.57E-05
1415948_at	cellular repressor of E1A-stimulated genes 1	0.549	1.78E-04
1439040_at	centromere protein E	0.549	3.95E-06
1430669_at	keratin associated protein 4-7	0.547	5.97E-05
1457571_at	zinc finger protein 68	0.546	3.41E-07
1447812_x_at	filamin C, gamma (actin binding protein 280)	0.544	1.82E-05
1423809_at	transcription factor 19	0.542	2.08E-05
1417552_at	fibroblast activation protein	0.540	1.44E-04
1422747_at	CHK2 checkpoint homolog (S. pombe)	0.536	5.71E-07
1448788_at	Cd200 antigen	0.532	4.32E-04
1433862_at	extra spindle poles-like 1 (S. cerevisiae)	0.532	6.56E-08
1427179_at	keratin complex 1, acidic, gene 3	0.528	4.73E-06
1451611_at	HRAS like suppressor 3	0.526	9.14E-07
1422582_at	leptin	0.525	3.82E-04
1452166_a_at	keratin complex 1, acidic, gene 10	0.519	1.51E-04
1455642_a_at	tetraspanin 17	0.519	3.56E-06
1424218_a_at	cAMP responsive element binding protein 3-like 4	0.518	9.73E-06
1419295_at	cAMP responsive element binding protein 3-like 1	0.517	6.05E-06
1418063_at	keratocan	0.515	7.97E-05

1436186_at	E2F transcription factor 8	0.515	2.98E-06
1433681_x_at	calpain 3	0.515	2.94E-05
1460082_at	inhibitor of growth family, member 3	0.512	9.59E-05
1448835_at	E2F transcription factor 6	0.505	1.37E-05
1457275_at	desmuslin	0.501	3.13E-04
1442140_at	tenascin N	0.500	1.10E-05
1418440_at	procollagen, type VIII, alpha 1	0.499	4.76E-07
1422954_at	zinc finger protein 60	0.497	5.33E-06
1440770_at	B-cell leukemia/lymphoma 2	0.494	2.40E-05
1434573_at	TRAF3 interacting protein 3	0.494	1.51E-05
1442542_at	eyes absent 4 homolog (Drosophila)	0.493	2.16E-04
1446636_at	tensin 3	0.492	2.19E-05
1418804_at	succinate receptor 1	0.491	1.27E-06
1424567_at	tetraspan 2	0.490	2.87E-05
1427161_at	centromere autoantigen F	0.480	2.36E-05
1443931_at	Zinc finger protein 617 (Zfp617), mRNA	0.478	8.22E-07
1418093_a_at	epidermal growth factor	0.473	1.73E-04
1425262_at	CCAAT/enhancer binding protein (C/EBP), gamma	0.469	2.45E-04
1417268_at	CD14 antigen	0.469	5.95E-04
1419521_at	zinc finger protein 94	0.464	4.15E-04
1431035_at	dishevelled associated activator of morphogenesis 1	0.464	1.75E-05
1417644_at	sarcospan	0.464	6.85E-05
1457424_at	eyes absent 1 homolog (Drosophila)	0.462	3.80E-05
1426180_a_at	submaxillary gland androgen regulated protein 2	0.462	5.01E-08
1445256_at	Vinculin, mRNA (cDNA clone MGC:6134 IMAGE:3495710)	0.460	6.82E-06
1421355_at	transglutaminase 3, E polypeptide	0.456	5.05E-05
1429067_at	calpain, small subunit 2	0.444	3.33E-04
1428052_a_at	zinc finger, MYM domain containing 1	0.444	4.19E-05
1437095_at	tetraspanin 18	0.442	3.24E-06
1454884_at	BTB (POZ) domain containing 4	0.439	4.01E-04
1435005_at	centromere protein E	0.433	5.74E-06
1425237_at	keratin associated protein 16-8	0.421	2.05E-05
1420358_at	keratin associated protein 13	0.418	2.25E-08
1445032_at	Death associated protein kinase 1 (Dapk1), mRNA	0.418	3.63E-05
1416025_at	fibrinogen, gamma polypeptide	0.416	9.41E-06
1431727_at	submandibular gland protein C	0.411	1.39E-05
1417686_at	lectin, galactose binding, soluble 12	0.407	3.79E-04
1422814_at	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	0.404	2.19E-05
1456228_x_at	myelin basic protein	0.404	7.48E-05
1416658_at	frizzled-related protein	0.401	1.78E-04
1460218_at	CD52 antigen	0.397	3.00E-05
1416342_at	tenascin C	0.391	1.18E-04
1449919_at	keratin associated protein 6-2	0.382	6.36E-06
1455519_at	desmoglein 1 beta	0.375	1.56E-06
1423010_at	sacsin	0.358	2.16E-04
1421691_at	keratin associated protein 16-7	0.357	9.29E-07
1420466_at	salivary protein 2	0.351	1.37E-05
1424528_at	cell growth regulator with EF hand domain 1	0.347	1.28E-05
1421855_at	fibrinogen-like protein 2	0.342	7.62E-05
1450633_at	calmodulin 4	0.342	9.47E-06
1429540_at	cornifelin	0.339	2.71E-06
1430731_at	keratin associated protein 2-4	0.336	5.41E-07
1424531_a_at	transcription elongation factor A (SII), 3	0.331	3.45E-06
1449073_at	filamin C, gamma (actin binding protein 280)	0.317	1.27E-06
1422640_at	protocadherin beta 9	0.315	6.16E-04
1459897_a_at	suprabasin	0.313	2.81E-06
1424529_s_at	cell growth regulator with EF hand domain 1	0.309	1.40E-06
1422837_at	sciellin	0.308	1.19E-04
1455900_x_at	transglutaminase 2, C polypeptide	0.302	3.11E-06
1443745_s_at	dentin matrix protein 1	0.291	8.52E-06
1416455_a_at	crystallin, alpha B	0.287	1.11E-05
1421589_at	keratin complex 1, acidic, gene 1	0.286	7.06E-08

1420183_at	Loricrin (Lor), mRNA	0.273	4.86E-07
1431255_at	calreticulin 3	0.244	5.08E-05
1426043_a_at	calpain 3	0.218	3.23E-07
1418314_a_at	ataxin 2 binding protein 1	0.212	2.01E-04
1417979_at	tenomodulin	0.207	1.70E-04
1435649_at	nexilin	0.203	2.10E-08
1423253_at	myelin protein zero	0.201	1.11E-04
1422588_at	keratin complex 2, basic, gene 6b	0.198	5.57E-05
1458000_at	desmoglein 1 alpha	0.197	6.25E-06
1422654_at	sarcoglycan, alpha (dystrophin-associated glycoprotein)	0.186	2.34E-05
1445824_at	zinc finger protein 458	0.186	8.34E-06
1416776_at	crystallin, mu	0.180	3.79E-05
1420751_at	keratin associated protein 6-1	0.180	2.99E-07
1422529_s_at	calsequestrin 2	0.167	1.99E-05
1448168_a_at	salivary protein 1	0.164	9.03E-05
1427735_a_at	actin, alpha 1, skeletal muscle	0.162	2.09E-07
1418413_at	caveolin 3	0.157	1.55E-06
1459266_at	ARP3 actin-related protein 3 homolog (yeast) (Actr3), mRNA	0.130	1.94E-04
1418951_at	taxilin beta	0.129	9.86E-07
1427211_at	keratin associated protein 8-1	0.128	1.06E-04
1436867_at	sarcalumenin	0.122	7.54E-06
1448745_s_at	loricrin	0.110	1.13E-04
1423238_at	integrin beta 1 binding protein 2	0.109	8.05E-06
1448932_at	keratin complex 1, acidic, gene 16	0.109	4.43E-06
1435191_at	corneodesmosin	0.108	5.84E-04
1460185_at	keratin complex 2, basic, gene 18	0.104	2.37E-06
1418742_at	keratin complex 1, acidic, gene 4	0.104	9.74E-05
1428007_at	keratin associated protein 13-1	0.099	2.53E-06
1422598_at	calsequestrin 1	0.098	2.19E-04
1420409_at	keratin complex 1, acidic, gene 24	0.093	2.35E-08
1420884_at	sarcolipin	0.077	3.79E-06
1448327_at	actinin alpha 2	0.070	3.40E-05
1425382_a_at	aquaporin 4	0.068	2.93E-04
1418677_at	actinin alpha 3	0.067	1.57E-04
1427751_a_at	keratin complex 1, acidic, gene 5	0.054	4.32E-05
1447456_x_at	demilune cell and parotid protein ; cDNA sequence BC005655	0.050	9.98E-06
1435585_at	transcription elongation factor A (SII)-like 7	0.049	4.59E-06
1451551_at	keratin complex 2, basic, gene 16	0.049	4.73E-05
1452957_at	keratin associated protein 3-3	0.041	9.06E-06

[*] List of differentially expressed genes that distinguish between salivary gland tissue from double mutant mice and single mutant β-cat^{GOF} mice according to gene chip analysis. Affymetrix probe set ID (Probe ID), gene description, fold change (fc), and p-value (p) are shown. Grey-marked genes were specifically discussed in the text.

Table S3: Gene set enrichment analysis (GSEA)[1]

Double-mutant salivary glands *vs.* single mutant beta-catenin glands at P1

Gene Set name		Size	ES	NES	FDR (q-val)	Gene Set Description
Wnt target gene sets	WNT_TARGETS	17	-0.79	-2.19	0.0035	Wnt up-regulated genes in Wnt homepage (Nusse lab)
	WNT_Signaling	45	-0.36	-1.99	0.0524	Wnt target genes from literature (curated by GEArray)
	Sansom_APC_LOSS4_UP	115	-0.69	-2.39	0.0013	Up-regulated in the mouse small intestine 4 d after Apc loss
Cell Cycle-related	CELL_Cycle	67	-0.61	-1.77	0.0019	Cell cycle genes (defined by Broad Institute)
	BRENTANI_CELL_CYCLE	73	-0.62	-1.98	0.0278	Cancer-related genes involved in cell cycle
	G1_TO_S_CELL_CYCLE_REACTOME	59	-0.49	-1.82	0.0675	Genes involved in G1 to S progression of cell cycle
Apoptosis	REACTOME_APOPTOSIS	102	0.59	1.62	0.0481	Genes involved in Apoptosis
Differentiation	STRUCTURAL_MOLECULE_ACTIVITY	243	0.36	1.89	0.0512	Structural integrity of a complex or assembly within or outside a cell

Double-mutant tumor-propagating CD24+CD29+ cells *vs.* single mutant beta-catenin CD24+CD29+ cells at P90

Gene Set name	Size	ES	NES	FDR (q-val)	Gene Set Description
MULTICELLULAR_ORGANISM_DEVELOPMENT	78	-0.45	-2.03	0.0751	Early organism development

[1] Table includes gene sets strongly enriched in double-mutant salivary glands at P1 and double-mutant tumor-propagating cells compared to single mutant beta-catenin glands at P90, as determined by gene set enrichment analysis (GSEA).
Gene sets were generated and published in the Molecular Signature Database (MsigDB; Broad Institute, http://www.broad.mit.edu/gsea/msigdb). Size indicates number of genes included in each gene set. Enrichment score (ES) and normalized enrichment score (NES) and FDR were calculated by GSEA. Negative ES, negative NES, and FDR<0.2 indicate significant enrichment of a specific gene set in double-mutant salivary glands compared to single mutant beta-catenin glands.

Suppl Table 4: Affymetrix gene profiling of CD24$^+$CD29$^+$ salivary gland cells at P80*

Salivary gland CD24$^+$CD29$^+$ tumor propagating cell-gene signature

[1] = Bmpr1a^{LOF}

[2] = β-cat^{GOF}

[3] =double mutant

Probe ID	Symbol	UniGene	fc [3] / [1]	Regulation [3] / [1]	p [3] / [1]	fc [3] / [2]	Regulation [3] / [2]	p [3] / [2]
1425642_at	Cep290	Mm.229114	3.891	up	8.30E-05	5.098	up	6.83E-04
1420411_a_at	Pi4k2b	Mm.248647	3.571	up	3.82E-04	2.638	up	1.60E-05
1420330_at	Clec4e	Mm.248327	3.369	up	3.82E-06	1.580	up	1.32E-05
1437689_x_at	Clu	Mm.200608	2.663	up	3.27E-04	2.354	up	1.36E-05
1451798_at	Il1rn	Mm.882	2.310	up	3.76E-04	1.584	up	1.73E-06
1447084_at	Nfatc1	Mm.329560	2.216	up	8.39E-04	1.026	up	1.42E-06
1449254_at	Spp1	Mm.288474	2.184	up	2.37E-04	1.306	up	5.46E-05
1421473_at	Il1a	Mm.15534	2.155	up	1.10E-04	1.549	up	2.78E-07
1447669_s_at	Gng4	Mm.215394	2.066	up	9.23E-05	1.533	up	1.68E-04
1449984_at	Cxcl2	Mm.4979	2.050	up	3.79E-04	1.130	up	1.34E-04
1442376_at	Ablim1	Mm.217161	1.967	up	2.93E-06	2.951	up	3.42E-07
1421341_at	Axin2	Mm.71710	1.930	up	3.41E-04	1.898	up	8.07E-05
1436826_at	Tmtc3	Mm.296805	1.824	up	4.05E-04	2.548	up	1.35E-05
1433596_at	Dnajc6	Mm.76494	1.816	up	5.75E-04	2.491	up	2.97E-06
1421492_at	Ptgds2	Mm.442454	1.663	up	9.28E-05	2.135	up	8.43E-06
1433966_x_at	Asns	Mm.2942	1.634	up	3.88E-08	2.939	up	1.37E-05
1428748_at	Zfp826	Mm.100056	1.583	up	4.01E-04	2.229	up	7.11E-05
1420549_at	Gbp1	Mm.457978	1.534	up	5.81E-05	2.697	up	1.51E-06
1448595_a_at	Bex1	Mm.422943	1.513	up	2.37E-06	2.557	up	1.63E-04
1442282_at	Vmn2r84	Mm.359168	1.407	up	1.64E-06	2.165	up	2.75E-04
1433781_a_at	Cldn12	Mm.40132	1.381	up	8.04E-05	2.766	up	3.81E-05
1420410_at	Nr5a2	Mm.16794	1.373	up	7.95E-05	2.409	up	3.09E-05
1425964_x_at	Hspb1	Mm.13849	1.365	up	1.30E-05	2.023	up	4.61E-04
1425454_a_at	Il12a	Mm.103783	1.346	up	7.81E-04	2.685	up	6.30E-07
1460603_at	Samd9l	Mm.196013	1.331	up	1.29E-05	2.187	up	1.12E-04
1433374_at	Supt7l	Mm.164187	1.319	up	1.53E-05	2.698	up	6.33E-05
1423626_at	Dst	Mm.336625	1.296	up	2.29E-04	2.292	up	5.73E-05
1449211_at	Bpnt1	Mm.227549	1.294	up	5.63E-05	2.281	up	4.04E-06
1430744_at	Napsa	Mm.383181	1.290	up	2.75E-04	2.072	up	9.02E-07
1436865_at	Slc26a11	Mm.31869	1.239	up	8.74E-06	2.549	up	3.95E-06
1457769_at	H60a	Mm.387042	1.234	up	1.01E-05	2.969	up	7.54E-06
1422873_at	Prg2	Mm.142727	1.198	up	7.80E-04	2.471	up	1.67E-06
1455521_at	Klf12	Mm.458816	1.163	up	5.93E-07	2.049	up	1.06E-06
1429366_at	Lrrc34	Mm.45373	1.159	up	4.60E-04	2.309	up	1.19E-04
1455164_at	Cdgap	Mm.370848	1.158	up	1.03E-04	9.923	up	9.34E-07
1435203_at	Man2a2	Mm.269245	1.142	up	2.19E-04	2.153	up	5.46E-05
1425521_at	Paip1	Mm.132584	1.125	up	3.54E-05	3.036	up	1.04E-05
1424748_at	Galnt11	Mm.425232	1.121	up	5.39E-05	2.129	up	5.17E-05
1430139_at	Hells	Mm.57223	1.103	up	1.41E-05	1.515	up	6.14E-05
1459253_at	Arrdc3	Mm.423137	1.086	up	8.80E-06	3.616	up	3.11E-05
1452855_at	Ly6k	Mm.273319	1.080	up	2.75E-07	2.204	up	4.84E-05
1418872_at	Abcb1b	Mm.146649	1.075	up	5.07E-04	2.655	up	2.63E-05
1418148_at	Abhd1	Mm.389615	1.060	up	7.17E-05	2.775	up	1.36E-05
1418645_at	Hal	Mm.13000	1.060	up	5.56E-06	2.599	up	8.49E-05
1438239_at	Mid1	Mm.34441	1.049	up	2.41E-04	3.717	up	3.42E-06
1457936_at	Mapk8	Mm.21495	1.016	up	4.56E-05	6.864	up	4.96E-05
1450897_at	Arhgap5	Mm.35059	1.015	up	2.78E-05	2.256	up	2.14E-06
1426753_at	Phf17	Mm.286285	1.008	up	1.68E-04	2.227	up	1.80E-06
1451704_at	Abpd	Mm.389857	17.022	down	2.60E-07	1.026	up	1.35E-05
1427380_at	Klk1b3	Mm.439740	12.599	down	6.00E-07	1.002	up	3.08E-06
1420770_at	Klk1b24	Mm.444308	10.713	down	6.26E-04	1.082	up	9.67E-08
1421587_at	Klk1b27	Mm.445911	9.346	down	7.61E-07	1.019	up	9.93E-05
1419675_at	Ngf	Mm.1259	3.273	down	6.00E-04	1.003	up	7.25E-07
1433769_at	Als2cl	Mm.86338	3.143	down	2.89E-04	1.201	up	6.35E-05
1451637_a_at	Muc10	Mm.200411	2.670	down	1.60E-07	1.658	up	9.91E-06
1448962_at	Myh11	Mm.250705	2.391	down	2.05E-04	1.134	up	6.04E-04
1420700_s_at	Folr4	Mm.86738	2.353	down	4.08E-04	1.097	up	1.39E-04
1453568_at	Dapl1	Mm.275769	2.275	down	1.51E-05	1.351	up	8.10E-07
1449191_at	Wfdc12	Mm.6433	2.190	down	3.29E-04	1.581	up	4.55E-06
1426044_a_at	Prkcq	Mm.329993	2.122	down	2.05E-05	1.038	up	1.17E-05
1418353_at	Cd5	Mm.779	2.116	down	7.78E-05	1.197	up	1.71E-05
1416454_s_at	Acta2	Mm.213025	2.046	down	9.14E-06	1.047	up	2.54E-06
1418612_at	Slfn1	Mm.10948	2.028	down	1.92E-04	1.202	up	2.66E-05
1427532_at	Trat1	Mm.167298	2.023	down	2.63E-04	1.344	up	3.91E-06
1446675_at	Adk	Mm.188734	1.527	down	5.26E-05	2.049	up	1.29E-05
1439843_at	Camk4	Mm.222329	1.455	down	3.83E-05	2.411	up	2.24E-04
1417459_at	Dcpp1	Mm.371556	1.359	down	4.85E-04	3.931	up	7.87E-06
1435462_at	Plcxd2	Mm.380993	1.221	down	2.98E-06	11.585	up	1.09E-08
1425764_a_at	Bcat2	Mm.24210	1.202	down	1.22E-04	2.147	up	5.28E-06
1431708_a_at	Tia1	Mm.423551	1.149	down	1.10E-04	2.069	up	3.77E-05
1452406_x_at	Erdr1	Mm.391385	1.129	down	3.51E-04	2.299	up	1.83E-05

1436796_at	Matr3	Mm.215034	1.128	down	2.35E-07	2.333	up	7.21E-05
1447517_at	Skiv2l2	Mm.291029	1.107	down	7.18E-07	23.144	up	2.06E-05
1421628_at	Il18r1	Mm.253664	1.074	down	2.17E-04	2.775	up	1.98E-08
1437308_s_at	F2r	Mm.24816	1.037	down	5.36E-05	3.819	up	1.08E-05
1420505_a_at	Stxbp1	Mm.278865	1.037	down	3.03E-05	2.911	up	8.93E-05
1448712_at	Chm	Mm.257316	1.036	down	1.98E-05	2.772	up	3.83E-05
1450837_at	Prp2	Mm.333439	2.478	up	2.44E-04	1.141	down	9.62E-04
1449153_at	Mmp12	Mm.2055	2.386	up	3.71E-06	1.013	down	1.82E-04
1431035_at	Daam1	Mm.87417	2.128	up	1.46E-04	2.076	down	1.52E-04
1429443_at	Cpne4	Mm.326240	2.047	up	7.83E-05	1.055	down	5.16E-07
1450680_at	Rag1	Mm.828	1.524	up	2.77E-04	3.785	down	2.66E-05
1439426_x_at	Lyz1	Mm.177539	1.265	up	6.09E-04	2.372	down	5.72E-05
1419394_s_at	S100a8	Mm.21567	1.129	up	1.25E-05	3.532	down	8.09E-06
1423547_at	Lyz2	Mm.45436	1.126	up	8.46E-05	2.102	down	1.75E-05
1424339_at	Oasl1	Mm.95479	1.090	up	4.93E-05	2.018	down	9.74E-06
1445305_at	Slc10a7	Mm.334631	1.074	up	5.25E-05	2.014	down	6.07E-05
1448756_at	S100a9	Mm.2128	1.073	up	8.26E-04	2.582	down	5.41E-04
1441228_at	Apold1	Mm.296104	1.011	up	4.04E-06	2.082	down	5.97E-04
1452592_at	Mgst2	Mm.24679	1.011	up	6.31E-05	2.763	down	7.82E-08
1420398_at	Rgs18	Mm.253927	1.006	up	1.31E-06	2.893	down	1.62E-07
1453644_at	Obp1a	Mm.430771	57.487	down	3.72E-05	1.137	down	4.07E-05
1437432_a_at	Trim12	Mm.458309	24.627	down	3.56E-05	1.012	down	8.10E-06
1421803_at	Apbh	Mm.6205	21.606	down	1.19E-04	1.043	down	1.09E-04
1419090_x_at	Klk1b26	Mm.439663	11.300	down	3.47E-06	3.415	down	1.88E-04
1420490_at	Klk1b16	Mm.440887	9.701	down	4.05E-04	1.279	down	2.57E-06
1425144_at	Klk1b11	Mm.443378	9.173	down	2.09E-05	2.075	down	5.38E-05
1418093_a_at	Egf	Mm.252481	8.961	down	7.72E-05	1.401	down	2.55E-04
1420701_at	Klk1b1	Mm.447819	8.958	down	6.41E-05	1.387	down	1.54E-07
1449313_at	Klk1b5	Mm.443373	7.628	down	1.38E-05	2.216	down	1.62E-04
1451607_at	Klk1b21	Mm.443292	7.373	down	1.31E-04	1.387	down	1.86E-04
1421372_at	Klk1b4	Mm.440886	7.294	down	4.40E-05	1.251	down	2.88E-04
1449463_at	Klk1b8	Mm.435488	7.244	down	3.78E-06	1.403	down	4.35E-05
1449838_at	Crisp3	Mm.14138	6.279	down	6.35E-05	1.537	down	1.15E-07
1416325_at	Crisp1	Mm.16781	6.068	down	5.28E-05	2.469	down	5.72E-05
1421490_at	Prpmp5	Mm.441627	5.010	down	3.26E-06	3.225	down	7.50E-05
1424592_a_at	Dnase1	Mm.440565	4.112	down	2.73E-05	1.889	down	1.73E-07
1424857_a_at	Trim34	Mm.326945	4.070	down	8.92E-05	1.371	down	2.05E-05
1449447_at	Cst10	Mm.117117	3.625	down	5.36E-05	1.834	down	2.33E-04
1419595_a_at	Ggh	Mm.20461	3.237	down	2.09E-04	2.913	down	1.56E-04
1416456_a_at	Chia	Mm.46418	3.116	down	8.13E-04	1.284	down	3.00E-05
1420492_s_at	Smr3a	Mm.431303	3.069	down	7.04E-08	1.528	down	2.05E-06
1454608_x_at	Ttr	Mm.2108	2.790	down	4.79E-05	1.348	down	1.78E-04
1453752_at	Rpl17	Mm.276337	2.611	down	9.84E-05	1.210	down	1.98E-05
1448626_at	Cdk5rap1	Mm.289427	2.573	down	1.05E-05	2.330	down	3.05E-06
1417023_a_at	Fabp4	Mm.582	2.559	down	3.43E-04	1.474	down	4.62E-06
1448998_at	Lpo	Mm.41236	2.549	down	5.32E-05	1.173	down	4.46E-05
1428010_at	Timm9	Mm.207767	2.522	down	1.05E-06	1.766	down	8.99E-05
1437614_x_at	Zdhhc14	Mm.476811	2.379	down	6.32E-05	3.162	down	4.49E-06
1425505_at	Mylk	Mm.33360	2.375	down	2.91E-04	1.139	down	4.14E-04
1450136_at	Cd38	Mm.249873	2.358	down	2.88E-07	2.442	down	3.85E-06
1449526_a_at	Gdpd3	Mm.246881	2.284	down	1.95E-04	2.029	down	1.26E-04
1449212_at	Pip	Mm.214755	2.270	down	1.09E-04	1.128	down	6.60E-05
1417765_a_at	Amy1	Mm.439727	2.245	down	2.86E-04	1.252	down	1.30E-04
1430465_at	Raly	Mm.221440	2.219	down	1.58E-04	1.884	down	1.92E-04
1444322_at	Lcn11	Mm.27838	2.211	down	8.38E-07	1.421	down	2.29E-06
1423450_a_at	Hs3st1	Mm.12559	2.128	down	3.87E-05	3.962	down	2.70E-05
1428402_at	Zcchc3	Mm.427626	2.111	down	1.34E-04	2.168	down	2.70E-04
1440582_at	Itch	Mm.208286	2.090	down	2.37E-07	2.001	down	1.45E-07
1423110_at	Col1a2	Mm.277792	2.078	down	2.26E-05	1.570	down	1.02E-04
1415837_at	Klk1	Mm.142722	2.064	down	1.70E-04	2.372	down	1.67E-05
1423608_at	Itm2a	Mm.193	2.029	down	2.39E-04	1.322	down	1.36E-04
1419814_s_at	S100a1	Mm.24662	2.020	down	6.75E-06	1.132	down	1.07E-04
1444416_at	Cenpa	Mm.290563	2.012	down	2.98E-06	11.798	down	4.69E-05
1419764_at	Chi3l3	Mm.387173	1.822	down	2.85E-05	4.038	down	8.12E-06
1426278_at	Ifi27	Mm.271275	1.703	down	7.11E-06	3.049	down	5.01E-06
1418967_a_at	St7	Mm.12051	1.699	down	6.33E-06	4.363	down	1.72E-06
1428820_at	Mapre1	Mm.143877	1.593	down	4.95E-07	2.286	down	3.13E-04
1450753_at	Nkg7	Mm.34613	1.513	down	4.39E-06	2.205	down	4.58E-05
1436107_at	Lsm8	Mm.275158	1.512	down	2.60E-05	5.470	down	5.19E-06
1457458_at	Zc3h4	Mm.333594	1.489	down	5.68E-05	2.534	down	5.98E-04
1450883_a_at	Cd36	Mm.18628	1.485	down	8.83E-05	2.425	down	9.15E-06
1426166_at	Mup5	Mm.445286	1.472	down	2.42E-05	2.399	down	7.27E-06
1460241_a_at	St3gal5	Mm.38248	1.435	down	2.00E-04	2.156	down	1.27E-04
1434572_at	Hdac9	Mm.310551	1.431	down	1.33E-04	2.116	down	5.97E-07
1436485_s_at	Whrn	Mm.300397	1.384	down	1.30E-05	2.210	down	1.98E-06
1449015_at	Retnla	Mm.441868	1.344	down	1.93E-04	3.434	down	3.70E-05
1427306_at	Ryr1	Mm.439745	1.336	down	8.50E-06	2.035	down	1.85E-07
1422824_s_at	Eps8	Mm.235346	1.310	down	4.58E-05	2.085	down	2.20E-04
1449465_at	Reln	Mm.425236	1.300	down	6.19E-05	3.672	down	4.72E-05
1418722_at	Ngp	Mm.236225	1.296	down	3.99E-07	5.603	down	7.82E-08
1432026_a_at	Herc5	Mm.297393	1.293	down	6.54E-04	2.016	down	2.20E-05
1424775_at	Oas1a	Mm.14301	1.279	down	1.17E-07	2.827	down	2.65E-05
1428490_at	C1galt1	Mm.102752	1.264	down	1.88E-04	2.100	down	2.44E-06
1442107_at	Flnb	Mm.475646	1.251	down	2.09E-05	4.390	down	2.60E-04
1429359_s_at	Rbpms	Mm.323997	1.211	down	4.58E-05	2.334	down	1.31E-05
1453196_a_at	Oasl2	Mm.228363	1.205	down	4.08E-06	2.012	down	2.48E-05
1455359_at	Ptpn14	Mm.4498	1.204	down	5.86E-06	2.062	down	1.15E-06
1419691_at	Camp	Mm.3834	1.189	down	7.69E-07	2.971	down	3.10E-05
1437874_s_at	Hexb	Mm.27816	1.133	down	3.19E-04	2.373	down	2.70E-04

1425908_at	Gnb1	Mm.2344	1.122	down	4.27E-06	9.115	down	5.58E-05
1423555_a_at	Ifi44	Mm.30756	1.032	down	2.29E-06	2.300	down	5.93E-05

[*] List of differentially expressed genes that distinguish between $CD24^+CD29^+$ salivary gland tumor propagating cells of double mutant mice and $CD24^+CD29^+$ salivary gland cells of single mutant mice according to gene chip analysis. Affymetrix probe set ID (Probe ID), gene symbol (Symbol), Unigene ID, gene description, fold change (fc) and p-value (p) are shown. Grey-marked genes were specifically discussed in the text.

Supplemental Table 5. Oligo sequences used for quantitative Real-Time PCR.

Gene	**Primer sequence**
m*c-myc* forward	5’-TCCTGAAGCAGATCAGCAACAACC-3’
m*c-myc* reverse	5’-TGCTTGAATGGACAGGATGTAGGC-3’
m*Fas* forward	5’-AGTGCAAACCAGACTTCTACTGCG-3’
m*Fas* reverse	5’-AAGGATGGTCAACAACCATAGGCG-3’
m*CK6* forward	5’-AGAGAGGGGTCGCATGAACT-3’
m*CK6* reverse	5’-TCATCTGTTAGACTGTCTGCCTT-3’
m*Loricrin* forward	5’-TTGTGGAAAGACCTCTGGTGGAGG-3’
m*Loricrin* reverse	5’-AACCACCTCCATAGGAACCACCG-3`;
m*Axin2* forward	5’-AACTGAAACTGGAGCTGGAAAGCC-3’
m*Axin2* reverse	5’-TTTGTGGGTCCTCTTCATAGCTGC-3’
m*Lef-1* forward	5’-TGATGCCCAATATGAACAGCGACC-3’
m*Lef-1* reverse	5’-TTGCTTGGAGTTGACATCTGACGG-3’
m*Bmp4* forward	5’-AGAAGAATAAGAACTGCCGTCGCC-3’
m*Bmp4* reverse	5’-ATGGCATGGTTGGTTGAGTTGAGG-3’
m*Msx2* forward	5'-AAATCTGGTTCCAGAACCGAAGGG-3'
m*Msx2* reverse	5'-CATGGTAGATGCCATATCCAACCG-3'
m*β-actin* forward	5’-TCGTGCGTGACATCAAAGAGAAGC-3’
m*β-actin* reverse	5’-ATGGATGCCACAGGATTCCATACC-3’
m*Dppa5* forward	5’-GAAATATCTGTTTGGCCCACAGGG-3’
m*Dppa5* reverse	5’-GCCATGGACTGAAGCATCCATTTAGC-3’
m*Dkk1* forward	5’-TGTTGTGCAAGACACTTCTGGTCC-3’
m*Dkk1* reverse	5’-TGTGGAGCCTAGAAGAATTGCTGG-3’
m*Nr5a2* forward	5’-ACACAGAAGTCGCGTTCAACAACC-3’
m*Nr5a2* reverse	5’-TAGTTGCAAACCGTGTAGTCCAGC-3’
m*Lrrc34* forward	5’-TCAAGGGAATAAACCTGAACCGGC-3’
m*Lrrc34* reverse	5’-ATTGCAGCTGACATCAAGGTAGCG-3’
m*Dnaja1* forward	5’-TACAGCTGGTTGAAGCATTGTGCG-3’
m*Dnaja1* reverse	5’-TCATATGGCCGACGGTATATTGGC-3’
m*Pdpn* forward	5’-CACAGAGAACACGAGAGTACAACC-3’
m*Pdpn* reverse	5’-ACGCCAACTATGATTCCAACCAGG-3’
m*Cdgap* forward	5’-ATTGCCGGATTGGAAGAGAAAGCC-3’
m*Cdgap* reverse	5’-ACGGTTGCTAAGTTCCAGTTGTGG-3’
m*Abcb1b* forward	5’-TTATGCTGCTTGTTTCCGGTTCGG-3’
m*Abcb1b* reverse	5’-TTTGGCTTTCGCATAGTCAGGAGC-3’
m*Geminin* forward	5’-ATCTCAGACTTCAAGCTGTGGTCC-3’
m*Geminin* reverse	5’-TTTATTCTCCTTTCTCAGGCGGGC-3’
m*Klf5* forward	5’-ACGTCAATGAAACAGTTCCAGGGC-3’
m*Klf5* reverse	5’-TTGGGTTGTGAATCGCCAGTTTGG-3’
m*Fgf5* forward	5’-TCCTTGCTCTTCCTCATCTTCTGC-3’
m*Fgf5* reverse	5’-ACTGGAAACTGCTATGTTCCGAGC-3’
m*Klk1b3* forward	5’-ACCGATTTGTCAGCAAAGCCATCC-3’
m*Klk1b3* reverse	5’-AATTTGGTGGGTGTAATGCTGCCC-3’

m*Dnajc6* forward	5’-TCATTTGCCAGCAAACCTACCACC-3’
m*Dnajc6* reverse	5’-AAGCTCACGTTGTAATTGGGTCGG-3’
m*Klf3* forward	5’-GAA GCC CAA CAA ATA TGG GGT-3’
m*Klf3* reverse	5’-GGA CGG GAA CTT CAG AGA GG-3’
m*Tbx6* forward	5’-GGCAGCTCCATCTGTACCAT-3’
m*Tbx6* reverse	5’-ACCGAGGCTCAGTACATTGG-3’
m*Trim2* forward	5’-TGGACAGTTCAAAAGTCGTTTCG-3’
m*Trim2* reverse	5’-AATGCTAACCCACTTGTTGTCAT-3’
m*Ctnnb1* forward	5´-TGATTCGAAACCTTGCCCTTTGCC-3´
m*Ctnnb1* reverse	5´-TTACAATCCGGTTGTGAACGTCCC-3´
m*Mll1* forward	5´-AACAAGCATGGATCTCCCAATGCC-3´
m*Mll1* reverse	5´-ACATGTAGCAACCAATGCCCTTGC-3´
m*Cbp* forward	5´-ACCACAAGTCCATTTGGACAACCC-3´
m*Cbp* reverse	5´-TTCCCACTGATGTTTGCAACTGGG-3
m*Ash1* forward	5´-AGTTGAAGCTATGCAACGCCAAGC-3´
m*Ash1* reverse	5´-TTCAATTCCGGGCTGACAAACTGG-3´
m*Ash2* forward	5´-AAATGGTGTCAATCAGGGTGTGGC-3´
m*Ash2* reverse	5´-ACATCAGCCAGTGTGTGTTCTACC-3´
m*Hells* forward	5´-TTCGGAAATGTAATGGACAGC-3´
m*Hells* reverse	5´-GGGCCACATACAAGAAAAGG-3´
m*Amy1* forward	5´-ACATGTGGCCTGGAGACATAAAGG-3´
m*Amy1* reverse	5´-ATCCCACTTGCGCATAACTTTGCC-3´
h*NR5A2* forward	5’-TCATGGCCTATTTGCAGCAAGAGC-3’
h*NR5A2* reverse	5’-ACCACTTGTCGGTAAATGTGGTCG-3’
h*ABCB1B* forward	5’-AAGGCCTAATGCCGAACACATTGG-3’
h *ABCB1B* reverse	5’-TTTGCCATCAAGCAGCACTTTCCC-3’
h*LRRC34* forward	5’-TAATGATATTGGGCCCGAAGGTGG-3’
h*LRRC34* reverse	5’-TTGCATTCCCAGATCACAGTCACC-3’
h*HELLS* forward	5’-AAGGCATGGAATGGCTTAGGATGC-3’
h*HELLS* reverse	5’-CCAGTTAGGAAGTGTAGACAAAGGGC-3`
h*DNAJC6* forward	5’-ATCGAACTGCCAAGTTTCACAGCC-3’
h*DNAJC6* reverse	5’-ACCAACCAGAATTGATGATGCCGC-3’
h*MLL1* forward	5’-AGCAAGGTCATGGCAACAATCAGG-3’
h*MLL1* reverse	5’-AGCTGCATTGGAAATCTGAGACGG-3’
h*ASH2* forward	5’-ATGGTTCACGGCTGACACATTTGG-3’
h*ASH2* reverse	5’-TTCGGATGTTCATCCTGTGTTCGG-3’
h*AXIN2* forward	5'-TTCGGATGTTCATCCTGTGTTCGG-3'
h*AXIN2* reverse	5'-TGGTGCAAAGACATAGCCAGAACC-3'
h*β-ACTIN* forward	5’-TGGCACCACACCTTCTACAATGAGC-3’
h*β-ACTIN* reverse	5’-GCACAGCTTCTCCTTAATGTCACGC-3’

Supplemental Table 6. Oligonucleotide sequences used for transient RNAi.

Gene	**Oligo No.**	**Target Sequence**
β-catenin	1	5’-GCUGAAACAUGCAGUUGUAUU-3´
	2	5’-GAUAAAGGCUACUGUUGGAUU-3´
	3	5’-CCACUAAUGUCCAGCGUUUUU-3´
	4	5’-ACAAGUAGCUGAUAUUGAUUU-3´
Mll1	1	5’-CGCCAAAUGGAGCGAGUUU-3´
	2	5’-CCACCAAACCCACGAAGAA-3´
	3	5’-AGACAAAGCCCUCGAAGGA-3´
	4	5’-GCACAGUGGUCUCACGAUU-3´
Dppa5a	1	5’-GUUACAUCCUAGCAAGAUA-3´
	2	5’-AGUCGCUGGUGCUGAAAUA-3´
	3	5’-CCACAGGGAUCUCGAAUGU-3´
	4	5’-CGAAGAACUUAUCGAGGUC-3´
Crebbp (CBP)	1	5’-GGACAGCUGUUUACCAUGA-3´
	2	5’-GGAAUGAAGUCAAGGUUUG-3´
	3	5’-GAAAGCAGCUGUGUACAAU-3´
	4	5’-GCACAAGGAGGUAUUCUUU-3´
Ash1l	1	5’-GCGAAACAAUGGACAAUUA-3´
	2	5’-CAAGUAAGCUCGAGUCUGA-3´
	3	5’-GCUUAAGUAUUGAGUGUAA-3´
	4	5’-UAGUUGGACUGGUUAAUAA-3´
Control	1	5’-UGGUUUACAUGUCGACUAA-3´
	2	5’-UGGUUUACAUGUUGUGUGA-3´
	3	5’-UGGUUUACAUGUUUUCUGA-3´
	4	5’-UGGUUUACAUGUUUUCCUA-3´

Supplemental Table 7. Oligo sequences used for quantitative Real-Time PCR of ChIP samples.

Gene	**Primer sequence**	**Amplicon**
m*Mll1* forward_I	5'-ACATTCAATGGGAGAGTGCTTGCC-3'	chr9:44692191+44692323
m*Mll1* reverse_I	5'-AAAGAATCTCTCTCAGTGCCTCCC-3'	
m*Mll1* forward_II	5'-AGCGTCGCCCAATTGATTCTATGC-3'	chr9:44689986+44690098
m*Mll1* reverse_II	5'-AAAGAGCTCCAAGCGTGAAGATGG-3'	
m*Mll1* forward_III	5'-ACTGCCCTAGGAGTAACACATCTGC-3'	chr9:44688508+44688616
m*Mll1* reverse_III	5'-TTCACAGATTACCTCATCCGAGCC-3'	
m*Mll1* forward_IV	5'-AGCACCAACTCCATGCAAGTAACC-3'	chr9:44686793+44686890
m*Mll1* reverse_IV	5'-TAAGCTGACAACACAGATCCCAGG-3'	
m*Hells* forward_I	5'-AGCACCAGAATCAAAGGTGTGTGC-3'	chr19:39003188+39003313
m*Hells* reverse_I	5'-TGTTGGCCTCCAACTCAGAAATCC-3'	
m*Hells* forward_II	5'-ACCTACCGAAAGGACAGGTATTGG-3'	chr19:39005106+39005195
m*Hells* reverse_II	5'-TAATGATGGTCCCGAGTTGTTCGG-3'	
m*Hells* forward_III	5'-ACTTGAATCCCGTTCTGAAAGCCC-3'	chr19:39005840+39005941
m*Hells* reverse_III	5'-AGCATGGCTGGAGTAATCACCG-3'	
m*Hells* forward_IV	5'-TGTGTGTGTGAGTGTGAGATGTCC-3'	chr19:39007011+39007138
m*Hells* reverse_IV	5'-TGCAGAGGTACCAGGTTTGTTTCC-3'	
m*Ash2* forward_I	5'-ATAGCCATCACTTCATGGCACAGG-3'	chr8:26952740+26952888
m*Ash2* reverse_I	5'-ACGCAGAGATTGGTTAACTGTGGG-3'	
m*Ash2* forward_II	5'-AAGCATATGGGTGGGCTCTAAACC-3'	chr8:26951979+26952076
m*Ash2* reverse_II	5'-TACATGCGCACACATCCGTAAAGC-3'	
m*Ash2* forward_III	5'-AAGCAAGACAAATGTGTTCGCGGC-3'	chr8:26950689+26950787
m*Ash2* reverse_III	5'-CTTGCAATGCTTGGTCCTGAAAGC-3'	
m*Ash2* forward_IV	5'-AACAGCAGCATGGAAGTGTAAGCC-3'	chr8:26948631+26948773
m*Ash2* reverse_IV	5'-ACCATAGCTAATGCAAGACCAGGG-3'	
m*Myc* forward	5'-TGCCCAGTCAACATAACTGTACGACC-3'	chr15:61816229+61816317
m*Myc* reverse	5'-AGAGCCACTTAGGGATAAACAGCC-3'	
m*Gapdh* forward	5'-ACGGCGGTTCATTCATTTCCTTCC-3'	chr6:125114819+125114915
m*Gapdh* reverse	5'-TGCATACCTTTGCGCATCATCTCC-3'	
h*MLL1* forward_I	5'-TCTTCCTTCTTTCTGCTGCCTTGC-3'	chr11:118304931+118305068
h*MLL1* reverse_I	5'-TGTGTCAACAGATTTCTTCCCGCC-3'	
h*MLL1* forward_II	5'-TTCGGGCTAACCCATCTTGTATCC-3'	chr11:118306634+118306727
h*MLL1* reverse_II	5'-AGAGCAGCTTCCAGTATAACGCGG-3'	
h*MLL1* forward_III	5'-ACCTCCTTTCCCTCTGAAGATAACGG-3'	chr11:118309754+118309845
h*MLL1* reverse_III	5'-AGAAACTGTAGCCCTGTAAGACGG-3'	
h*MLL1* forward_IV	5'-CCATGTAGTTGGAGAACCAAAGGC-3'	chr11:118309754+118309845
h*MLL1* reverse_IV	5'-CAACTCACATTTAAGCACCAACTCC-3'	
h*HELLS* forward_I	5'-TAACTATCCTGTGAGATTGGGCGAGG-3'	chr10:96304154+96304293
h*HELLS* reverse_I	5'-ATTAGCCTGGAATGGGCTAATGTCCG-3'	
h*HELLS* forward_II	5'-GGCGCCTTGCAAAGTATTAACAGC-3'	chr10:96305252+96305370
h*HELLS* reverse_II	5'-TAACTATCCTGTGAGATTGGGCGAGG-3'	
h*HELLS* forward_III	5'-GGGAGAAAGGCTGTTTCTTGTTGG-3'	chr10:96306052+96306164

h*HELLS* reverse_III	5'-AGTTGTTCAACCATTGCTGGAGCC-3'	
h*HELLS* forward_IV	5'-TTGGGTGCCACAGTTGGTAAATGG-3'	chr10:96307516+96307632
h*HELLS* reverse_IV	5'-ACGGAAGGAGTATTACTGGAGTGG-3'	
h*ASH2* forward_I	5'-TAGAAGCAAGTCACTGAGTCCAGC-3'	chr8:37960686+37960777
h*ASH2* reverse_I	5'-GATTACAGGAGTGAGCCATCATGC-3'	
h*ASH2* forward_II	5'-ACCAGCTACTGTTGATGACTTCCC-3'	chr8:37962357+37962438
h*ASH2* reverse_II	5'-ATGTAGACAAGTTTGGTGCCCAGC-3'	
h*ASH2* forward_III	5'-AAGCTGCAGGAGTATGAAGTTCGG-3'	chr8:37963787+37963923
h*ASH2* reverse_III	5'-ACCGCTTACATCGACCAAGTTTGC-3'	
h*ASH2* forward_IV	5'-AATGGCAGGATCACAGCTTTCTGC-3'	chr8:37965508+37965626
h*ASH2* reverse_IV	5'-ATAAAGGAAAGCTGGGTGTGGTGG-3'	
h*MYC* forward	5'-GCGCCCATTAATACCCTTCTTTCC-3'	chr8:128747818+128747989
h*MYC* reverse	5'-ATAAATCATCGCAGGCGGAACAGC-3'	
h*ACTIN* forward	5'-TGCAGAAAGTGCAAAGAACACGGC-3'	chr7:5568420+5568576
h*ACTIN* reverse	5'-TGTGGGTGTAGGTACTAACACTGG-3'	