Supplemental Figure 1: Selected Cluster Defining Genes in BALB/c, TxA23, and HDT libraries

A

Total Cells Analyzed

	Healthy	HDT	TxA23	Total
Raw Cell Counts	10871	10963	14793	36627
Filtered Cell Counts	7395	9960	11996	29351

B

Gene	Adj P Value	Cluster
Tff1	0	0
Muc5ac	0	0
Il33	0	0
Muc6	2.75E-110	1
Tff1	0	2
Muc5ac	0	2
Pga5	0	3
Muc6	0	3
Pgc	0	3
Clu	0	3
Sox9	0	3
Atp4b	0	4
Atp4a	0	4
Muc6	4.49E-272	5
Pgc	0	6
Gif	0	6
Gif	0	7
Pgc	0	7

Gene	Adj P Value	Cluster
Mki67	0	8
Cdk1	0	8
Pcna	0	8
Tff2	1.88E-07	8
Acta2	0	9
Myl9	0	9
Pecam1	0	10
Ptprc	0	11
Cd3e	0	11
Igkc	6.90E-77	11
Lyz2	0	12
Csf1r	0	12
Cd14	5.29E-273	12
Chga	0	13
Chgb	0	13
Hdc	0	13
Sst	7.45E-27	13
Trbc2	0	14
Cd3d	0	14
Ptprc	0	14
Ighm	0	14

Supplemental Figure 1: Selected Cluster Defining Genes in BALB/c, TxA23, and HDT libraries. **(A)** Raw and post read filtering counts for number of cells sequenced from BALB/c, TxA23, and HDT libraries. **(B)** Selected cluster defining genes used to label t-SNE clusters in Figure 1.

Supplemental Figure 2: Largest significant differences in gene expression between *Gif+* and *Gif-* metaplasia.

A **Numbers of Cells Meeting SPEM Criteria**

Library	Total
Gif-	479
Gif+	125

B **All genes with Log FC >1, P value <.05**

Gene	Avg Log FC	pct.1	pct.2	Adj P Value	Cluster
Gif	4.38	1	0	1.85E-117	*Gif+*
Spp1	2.16	0.228	0.031	3.85E-09	*Gif+*
Gkn3	1.69	0.833	0.585	4.73E-11	*Gif+*
Clps	1.58	1	0.882	3.38E-17	*Gif+*
Pla2g1b	1.32	0.895	0.752	1.39E-07	*Gif+*
Cd177	1.21	0.175	0.018	1.21E-07	*Gif+*
Sprr2a3	1.07	0.9	0.684	5.13E-09	*Gif-*

Supplemental Figure 2. **(A)** Count of cells in the *Tff2+Muc6+Gif-* and *Tff2+Muc6+Gif+* libraries. **(B)** A list of all genes significantly associated with either *Gif+* or *Gif-* metaplasia with log fold change >1 and a p value <0.05.

Supplemental Figure 3: Largest significant differences in gene expression between acute and chronic metaplasia.

A Number of cells meeting SPEM criteria

Library	Total Number
Drug-Induced	184
Inflammation-Induced	604

B All genes with Log FC >1, P value <.05

Gene	Avg Log FC	pct.1	pct.2	Adj P Val	Cluster
Cd74	3.91	0.922	0.012	9.70E-71	Inflammation
H2-Ab1	2.61	0.83	0.006	3.08E-58	Inflammation
Cym	2.49	0.25	0.065	0.00176	Inflammation
H2-Aa	2.35	0.786	0	5.88E-53	Inflammation
Spink4	2.30	0.745	0.393	5.03E-23	Inflammation
H2-Eb1	2.28	0.773	0	1.77E-51	Inflammation
Sprr2a3	2.24	0.851	0.476	1.38E-38	Inflammation
H2-K1	2.22	0.947	0.798	1.26E-61	Inflammation
Bpifb1	2.15	0.834	0.405	6.20E-33	Inflammation
Spp1	2.15	0.643	0.076	2.08E-54	Drug
H2-D1	2.07	0.979	0.929	1.55E-68	Inflammation
AW112010	2.02	0.673	0.143	5.49E-32	Inflammation
B2m	1.83	0.97	0.982	1.01E-57	Inflammation
Pga5	1.71	0.685	0.268	4.51E-21	Inflammation
Muc6	1.67	1	1	1.67E-17	Inflammation
Ly6a	1.41	0.356	0.036	7.44E-12	Inflammation
Cela1	1.41	0.827	0.379	4.10E-32	Drug
Gkn3	1.40	0.81	0.635	1.02E-12	Drug
Psmb8	1.39	0.685	0.161	4.91E-33	Inflammation
Nupr1	1.37	0.223	0.083	0.32407	Inflammation
Rbp1	1.37	0.595	0.131	4.90E-36	Drug
Ttr	1.34	0.75	0.181	5.85E-46	Drug
Tmsb10	1.30	0.972	0.923	1.23E-43	Inflammation
Ubd	1.24	0.312	0	8.12E-12	Inflammation
Chil4	1.24	0.142	0	0.008003	Inflammation
H2-DMa	1.19	0.577	0.018	3.33E-30	Inflammation
Kcne3	1.19	0.613	0.108	2.78E-40	Drug
Psmb9	1.15	0.625	0.173	2.03E-25	Inflammation
Iigp1	1.14	0.324	0.018	3.18E-11	Inflammation
Pigr	1.14	0.952	0.762	2.53E-30	Inflammation
Scgb2b7	1.08	0.274	0.131	0.598698	Inflammation
Gm10260	1.08	0.976	0.591	1.60E-43	Drug
H2-DMb1	1.05	0.533	0	1.81E-27	Inflammation
H2-Q7	1.04	0.575	0.036	1.21E-28	Inflammation
Cgref1	1.02	0.519	0.345	4.07E-05	Inflammation

Supplemental Figure 3. **(A)** Count of cells in the drug-induced and inflammation-induced SPEM libraries. **(B)** A list of all genes significantly associated with either drug-induced or inflammation-induced metaplasia with log fold change >1 and a p value <0.05.