Supplementary Data

Supplementary Table S1. Gene Mutation Frequency in Familial Adenomatous Polyposis and Sporadic Papillary Thyroid Cancer

Gene	*PTC in FAP* (n = *12*)	*TCGA of PTC* (n = *496*)	*AACR GENIE PTC* (n = *560*)
BRAF	17%	60%	65%
RET	8%	7%	4%
APC	58%	1%	3%
CUX1	25%	1%	3%
KMT2C	33%	1%	2%
TTN	50%	3%	0
TG	8%	3%	0
OBSCN	33%	1%	0
MUC5B	25%	1%	0
EVPL	25%	1%	0
PKHD1	25%	1%	0
DYNC1H1	25%	0.7%	0
DNAH10	25%	0.7%	0
VPS13D	25%	0.7%	0
DST	25%	0.5%	0
PLXNB1	25%	0.5%	0
LAMA5	25%	0.5%	0
TRANK1	25%	0.5%	0
PRDM15	25%	0.5%	0
TNRC18	25%	0.5%	0
PCLO	33%	0.2%	0
MKI67	25%	0.2%	0
FLNA	25%	0.2%	0
VCAN	25%	0.2%	0
XRN1	25%	0.2%	0
DSCAM	25%	0.2%	0
RYR3	25%	0.2%	0
KMT2D	58%	0	0
HSPG2	33%	0	0
MEGF8	33%	0	0
MKL1	25%	0	0
ALKBH7	25%	0	0
CACNA1H	25%	0	0
CCDC168	25%	0	0
FOXD4L5	25%	0	0
HECTD1	25%	0	0
PLD1	25%	0	0
SNRPA1	25%	0	0
OTOF	25%	0	0
RAP1GAP2	25%	0	0
SETD1B	25%	0	0
CDC42BPG	25%	0	0
BOD1L1	25%	0	0
IGFN1	25%	0	0

Mutation frequencies of genes mutated in at least 25% of the sequenced PTCs are listed.

AACR-GENIE, American Association for Cancer Research Genomics Evidence Neoplasia Information Exchange; FAP, familial adenomatous polyposis, *n*, number, PTC, papillary thyroid cancer; TCGA, The Cancer Genome Research Atlas.