

Table S3. Summary of total filtered variants per panel gene in familial and sporadic APS patients subdivided per gastric disease.

PATIENTS	Gastric disease			PANEL GENES												Total	%
	disease	N	Alleles	<i>ATP4A</i>	<i>SLC26A9</i>	<i>SLC9A4</i>	<i>SLC9A2</i>	<i>PTH2R</i>	<i>PTH1R</i>	<i>SLC4A2</i>	<i>SLC26A7</i>	<i>KCNQ1</i>	<i>KCNE2</i>	<i>KCNJ16</i>	<i>CCKBR</i>		
FAMILIAL	gNET*	13	26	5	2	0	0	1	1	2	0	1	0	0	0	12	46.1
	CAG**	38	76	5	9	1	1	3	4	3	6	1	0	0	0	33	43.4
	Non-gastric	6	12	3	3	0	0	0	1	0	2	0	0	0	0	9	75.0
	Total	57	114	13	14	1	1	4	6	5	8	2	0	0	0	54	47.4
SPORADIC	gNET	11	22	0	1	0	0	0	0	0	2	0	0	0	0	3	13.6
	CAG	8	16	1	1	0	0	1	2	1	1	0	0	0	0	7	43.7
	Total	19	38	1	2	0	0	1	2	1	3	0	0	0	0	10	26.3
TOTAL	gNET	24	48	5	3	0	0	1	1	2	2	1	0	0	0	15	31.2
	CAG	46	92	6	10	1	1	4	6	4	7	1	0	0	0	40	43.5
	Non-gastric	6	12	3	3	0	0	0	1	0	2	0	0	0	0	9	75.0
	Total	76	152	14	16	1	1	5	8	6	11	2	0	0	0	64	42.1

* Includes the variants previously described in families F1 and F2 (Calvete et al. 2015 and 2017).

** Includes the variants found in the 5 thyrogastric families from the Discovery WES 1 study.