Table S3. Hereditary cases used as controls in gene expression analysis.

Sample	Syndrome	Germline mutation	Age at diagnosis [years]	Gender	Tumor type
8	MEN2A	*RET* (c.1900T>C, p.Cys634Arg)	40	M	Pheochromocytoma
12	NF1	*NF1* (c.5609G>A, loss of splice site)[a]	70	F	Pheochromocytoma
14	MEN2A	*RET* (c.1900T>G, p.Cys634Gly)	52	M	Pheochromocytoma
55	PGL5	*SDHA* (c.223C>T, p.Arg75X)[b]	20	F	Paraganglioma
56	VHL	*VHL* (c.308C>T, p.Pro103Leu)	32	F	Pheochromocytoma

[a]Causing exon skipping as previously described (Welander *et al.* 2012).

[b]Associated with loss of SDHA and SDHB protein expression in the tumor (Welander *et al.* 2013).