Table S1. Clinical and genetic features and mutations in 42 patients with non-familial adrenal pheochromocytoma.

Case number	Malignancy[a]	Age at diagnosis [years]	Tumor size [mm]	Gender	Biochemical phenotype[b]							Mutation[c] (S/C)
					P-NMN	P-MN	U-NMN	U-MN	U-NE	U-E	U-D	
1	Benign	74	75	F	-	-	-	-	-	-	-	
2	Malignant	52	120	M	-	**1.00**	**173.00**	**-**	**63.50**	**1.49**	-	
3	Benign	61	60	F	-	-	-	-	**18.20**	**80.00**	0.91	*NF1* (S)
4	Benign	59	70	F	-	-	-	-	**28.25**	**1.00**	**1.19**	
5	Benign	66	24	M	-	0.67	**14.00**	**-**	**7.63**	0.35	-	
6[d]	Benign	51	35	F	-	-	-	-	-	-	-	
7	Benign	62	40	F	-	-	-	-	**1.03**	**1.66**	0.53	
9	Benign	53	50	F	-	-	-	-	-	-	-	*NF1* (S)
10	Malignant	80	75	F	-	-	-	-	**21.95**	**2.19**	0.30	*NF1* (S)
11	Benign	54	25	F	-	-	-	-	**3.63**	0.35	0.52	*EPAS1* (-)
13	Benign	60	55	F	-	-	-	-	**3.95**	**43.75**	**1.16**	
15	Benign	59	45	M	-	-	-	-	**9.08**	**42.40**	-	
17	Benign	72	50	M	-	-	-	-	-	-	-	
18	Benign	59	70	M	-	-	-	-	**1.55**	0.67	0.65	
19[e]	Benign	56	50	F	-	-	-	-	**26.75**	**1.20**	0.70	*EPAS1* (C)
20	Benign	19	45	F	-	-	-	-	**50.25**	0.41	**1.76**	
21	Benign	50	70	F	-	-	-	-	-	-	-	
22	Benign[f]	61	120	F	-	**1.67**	**93.33**	-	**6.93**	0.63	0.45	*EPAS1* (-)
23	Benign	68	35	F	-	-	-	-	-	-	-	
24	Benign	71	40	M	-	**2.00**	**7.33**	-	-	-	-	
25	Benign	83	55	F	-	**18.33**	**5.17**	-	-	-	-	*NF1* (S)
32	Benign	39	30	M	**8.67**	0.67	**2.85**	0.56	-	-	-	
33	Benign	76	40	F	**8.17**	**3.33**	**3.35**	**3.50**	-	-	-	
34	Benign	54	17	M	**5.33**	**1.00**	**1.53**	0.81	-	-	-	
35	Benign	75	60	M	-	-	-	-	-	-	-	
36	Benign	71	35	F	**4.83**	**8.33**	**1.84**	**13.38**	-	-	-	
37	Benign	70	30	F	**3.17**	**3.67**	**1.23**	**2.23**	-	-	-	
38	Benign	47	30	M	**10.50**	**1.00**	-	-	**19.49**	-	-	*EPAS1* (S+C)
40	Benign	63	32	F	**2.50**	**24.67**	-	-	-	-	-	
41	Benign	68	20	F	-	-	-	-	-	**3.58**	-	
42	Benign	62	30	F	-	-	**1.47**	**4.06**	-	-	-	*RET* (S)
44	Benign	68	55	F	-	-	-	-	**2.73**	**10.97**	-	*NF1* (S)
45	Benign	58	30	M	-	-	0.75	**4.13**	**2.84**	-	-	
46	Benign	54	50	F	**1.77**	**27.39**	-	-	-	-	-	
47	Benign	42	90	M	**19.61**	**40.11**	-	-	**1.42**	**12.91**	-	*NF1* (S)
48	Benign	59	60	F	**20.09**	**19.85**	-	-	-	-	-	*NF1* (S)
49	Benign	76	25	F	**3.16**	**4.91**	-	-	-	-	-	
50	Benign	80	10	F	**1.98**	**1.54**	-	-	-	-	-	
51	Benign	43	55	M	**4.58**	**22.61**	-	-	-	-	-	*NF1* (S)
52	Benign	43	37	F	**6.63**	0.72	-	-	-	-	-	*EPAS1* (S)
53[g]	Benign	63	80	F	**8.16**	**26.96**	-	-	-	-	-	*NF1* (S)
54	Benign	58	20	M	**13.30**	**2.70**	-	-	**1.00**	**7.87**	-	*NF1* (S)

Table S1. *(Continued)*

Abbreviations: S, somatic; C, constitutional (found in blood or normal tissue DNA); F, female; M, male; P, plasma; U, urine; NMN, normetanephrine; MN, metanephrine; NE, norepinephrine; E, epinephrine; D, dopamine; -, missing data.

[a]Tumors were defined as malignant only in the presence of distant metastases, according to WHO criteria (DeLellis *et al.* 2004).
[b]Urine and plasma levels (when available) have been normalized to the value considered normal for each method of measuring. Levels above the normal reference range (≥ 1.0) are indicated in bold.
[c]Mutation analysis has been performed for the genes *RET*, *VHL*, *SDHB*, *SDHD*, *MAX* and *NF1* (Welander *et al.* 2012) and *TMEM127* (Figure S1).
[d]Carried a non-synonymous *SDHB* polymorphism (rs11203289).
[e]Carried a sequence variant in *TMEM127*, as detailed in Figure S1.
[f]Malignant according to AFIP criteria (Lack 2007), local invasion.
[g]Carried a non-synonymous *SDHD* polymorphism (rs11214077).