

#155240 THYROID CARCINOMA, FAMILIAL MEDULLARY; MTC

OMIM Gene ID	HGNC	UniProtAC
164761	RET	P07949
191315	NTRK1	P04629

Table 1: OMIM - UniProtAC mapping

Legend

- N1: #input proteins associated to the significant GO term
- N2: #proteins associated to the significant GO term
- P-value: Bonferroni-corrected p-value of Fisher's exact test
- *red*: go terms not related to the input proteins
- *blue*: go terms related to the input proteins (enriched uniquely by network-based method)
- *green*: go terms ancestors of terms enriched with the standard method (enriched uniquely by network-based method)

1 Standard enrichment

GO Term	N1	N2	P-value	Description
GO:0010976	2	148	0.00618548	positive regulation of neuron projection development
GO:0018108	2	322	0.029387	peptidyl-tyrosine phosphorylation
GO:0018212	2	332	0.0312435	peptidyl-tyrosine modification
GO:0031346	2	335	0.0318116	positive regulation of cell projection organization
GO:0007497	1	2	0.0429215	posterior midgut development

Table 2: Overrepresented GO terms with the standard enrichment

2 Network-based enrichment

GO Term	N1	N2	P-value	Description
GO:0048485	2	36	0.000501794	sympathetic nervous system development
GO:0021675	2	133	0.00699169	nerve development

Table 3: Overrepresented terms with the network-based enrichment. Only terms not detected with the standard method.