```
MMQLLQLLLGLLGPGGYLFLLGDCQEVTTLTVKYQVSEEVPSGTVIGKLSQELGREERRR
QAGAAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPCLVSFDVLATGDLALI
HVEIQVLDINDHQPRFPKGEQELEISESASLRTRIPLDRALDPDTGPNTLHTYTLSPSEHFA
LDVIVGPDETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSNDNSP
AFAESSLALEIQEDAAPGTLLIKLTATDPDQGPNGEVEFFLSKHMPPEVLDTFSIDAKTGQ
VILRRPLDYEKNPAYEVDVQARDLGPNPIPAHCKVLIKVLDVNDNIPSIHVTWASQPSLVS
EALPKDSFIALVMADDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQ
WPKYTLTLLAQDQGLQPLSAKKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKA
HDADLGINGKVSYRIQDSPVAHLVAIDSNTGEVTAQRSLNYEEMAGFEFQVIAEDSGQP
MLASSVSVWVSLLDANDNAPEVVQPVLSDGKASLSVLVNASTGHLLVPIETPNGLGPA
GTDTPPLATHSSRPFLLTTIVARDADSGANGEPLYSIRSGNEAHLFILNPHTGQLFVNVTN
ASSLIGSEWELEIVVEDQGSPPLQTRALLRVMFVTSVDHLRDSARKPGALSMSMLTVICL
AVLLGIFGLILALFMSICRTEKKDNRAYNCREAESTYRQQPKRPQKHIQKADIHLVPVLRG
QAGEPCEVGQSHKDVDKEAMMEAGWDPCLQAPFHLTPTLYRTLRNQGNQGAPAESR
EVLQDTVNLLFNHPRQRNASRENLNLPEPQPATGQPRSRPLKVAGSPTGRLAGDQGSE
EAPQRPPASSATLRRQRHLNGKVSPEKESGPRQILRSLVRLSVAAFAERNPVEELTVDSP
PVQQISQLLSLLHQGQFQPKPNHRGNKYLAKPGGSRSAIPDTDGPSARAGGQTDPEQE
EGPLDPEEDLSVKQLLEEELSSLLDPSTGLALDRLSAPDPAWMARLSLPLTTNYRDNVIS
PDAAATEEPRTFQTFGKAEAPELSPTGTRLASTFVSEMSSLLEMLLEQRSSMPVEAASE
ALRRLSVCGRTLSLDLATSAASGMKVQGDPGGKTGTEGKSRGSSSSSRCL
```

Supplemental Fig. 4: Mass spectrometry analysis of urine: peptide coverage of PCDH12 sequence.

Methods. Urines were collected and pooled from 4 healthy volunteers after informed consent. To enhance the detection of low abundance proteins, samples were first treated with the ProteoMiner kit from BioRad consisting of a highly diverse library of hexapeptides bound to chromatographic supports, thereby decreasing the dynamic concentration range of the protein sample. Briefly, samples were treated according to the manufacturer's protocole and the eluted protein fractions were deposited on a 1D-SDS-PAGE before being subjected to a short separation (pseudo-stacking). After Coomassie staining, proteins were digested in-gel with trypsin. All fractions were analyzed with LC-MS/MS in triplicate, as described previously (Dos Santos A., Court M., Thiers V., Sar S., Guettier C., Samuel D., Brechot C., Garin J., Demaugre F., Masselon CD. (May 31, 2010) Mol Cell Proteomics M110.000026, PMID: 20513801).

Results. Seven peptides (in red) specific of human PCDH12 sequence were detected, with high scores. The transmembrane and cytoplasmic domains are in blue.