

Table S4: Summary of coding and selected non-coding *de novo* indels and non-synonymous SNVs

Gene	Candidate HSCR gene (listed in Table S3)	Mutation (most severe among all isoforms)	Mutation type	Patient ID	Verified by Sanger sequencing	Expressed in enteric neural crest cells <small>nrcourse*</small>	Frequency in internal controls (N=493)	Maximum frequency across all public databases	TP>20 true positive phredscore GATK	Residual Variation Intolerance Score (RVIS)	Sorting Tolerant From Intolerant (SIFT)	Polymorphism Phenotyping (Polyphen2_HDIV)	Combined Annotation Dependent Depletion score (CADD)
<i>De novo</i> coding variants													
<i>CCT2</i>	No	NC_000012.11:g.69993654G>A	missense	HD09C	Yes	Yes	0	0	41	11.05%	D	D	32
<i>VASH1</i>	No	NC_000014.8:g.77242233A>G	splicing	HD09C	Yes	Yes	0	0	39	25.70%	NA	NA	23.9
<i>CYP26A1</i>	No	NG_008067.1:g.7481A>G	missense	HK9C	Yes	Yes	0	0	40	10.02%	T	B	18.47
<i>PKD1L2</i>	No	NG_033236.1:g.84039G>A	synonymous	HD09C	Yes	No	0	0	43	98.71%	NA	NA	9.129
<i>TMEM175</i>	No	NC_000004.11:g.952275C>T	synonymous	HK9C	Yes	Yes	0	8.83E-06	55	98.56%	NA	NA	11.94
<i>CSMD3</i>	No	NC_000008.10:g.113841961T>C	missense	VH105C	Yes	No	0	8.13E-06	58	0.13%	T	B	7.16
<i>CCDC82</i>	No	NC_000011.9:g.96117858A>T	synonymous	VH108C	Yes	Yes	0	0	63	74.54%	NA	NA	0.773
<i>De novo</i> non-coding variants in selected ENS genes													
<i>NRG1</i>	Yes	NG_012005.2:g.667454G>C	SNV	VH106C	Yes	Yes	0	0	49	NA	NA	NA	1.46
<i>NRG1</i>	Yes	NG_012005.2:g.92222G>T	SNV	HK164C	Yes	Yes	0	0	37	NA	NA	NA	0.679
<i>NRG1</i>	Yes	NG_012005.2:g.146124A>G	SNV	VH108C	Yes	Yes	0	0	55	NA	NA	NA	3.126
<i>ERBB4</i>	Yes	NG_011805.1:g.835055_835059delAAACA	indel	VH106C	Yes	Yes	0	0	40	NA	NA	NA	6.129
<i>SEMA3A</i>	Yes	NG_011489.1:g.210732delT	indel	VH106C	Yes	Yes	0	0	32	NA	NA	NA	1.407
<i>ZEB2</i>	Yes	NC_000002.11:g.145137510C>T	SNV	HK164C	Yes	Yes	0	0	55	NA	NA	NA	NA
<i>DCC</i>	Yes	NG_013341.2:g.651331G>A	SNV	HK180C	Yes	Yes	0	0	41	NA	NA	NA	0.668

D: damaging; B: benign; T: tolerated; NA: not applicable; *In-house unpublished data