Amino acid comparison						
Substitution	**P117T**		**D496N**		**Q609K**	
Amino acid change	Proline	Threonine	Aspartic acid	Asparagine	Glutamine	Lysine
Polarity/charge	Non-polar	Polar	Negatively charged	Polar	Polar	Positively charged
pH	Neutral	Neutral	Acidic	Neutral	Neutral	Basic
Residue weight	97	101	115	114	128	128
Hydrophobicity score	-1.6	-0.7	-3.5	-3.5	-3.5	-3.9
Hydrophilicity score	0.0	-0.4	3.0	0.2	0.2	3.0
Secondary structure propensity	Strong α breaker Strong β breaker	α indifferent β former	Weak α former Strong β breaker	α breaker β breaker	α former β former	α former β breaker
Grantham difference*	38		23		53	
SIFT prediction	Tolerated		Damaging		Tolerated	
PolyPhen prediction	Benign		Benign		Benign	
LRT prediction	Neutral		Neutral		Neutral	
MutationTaster prediction	Polymorphism		Disease causing		Polymorphism	
MutationAssessor prediction	Neutral		Medium impact		Neutral	
FATHMM prediction (A score of less than -1.5 predicts damaging)	-1.05		0.39		0.6	
PhyloP conservation score (The larger the score, the more conserved the site, max 2.941)	2.832		2.643		1.324	
GERP conservation score (The larger the score, the more conserved the site, max 6.17)	4.2		5.11		2.63	
Consurf conservation score (The larger the score, the more conserved the site, max 9)	4		6		1	
dbSNP	rs186296463		rs111291437		-	

Supplemental table 1: The physiochemical and functional consequences of autism associated NHE9 substitutions determined as described in the Methods. *The higher the Grantham difference score, the less tolerated the amino acid substitution. Highest score is 215 for Trp-Cys and lowest is 5 for Leu-Ile substitution.