

Supplementary Table 1. Population based comparative analysis on *DBP* genetic variants.

SNP ID (Major/Minor allele)	Allele / Genotype	All control	All probands	OR (95%CI)	χ^2 (P)	Male Control	Male Probands	OR (95%CI)	χ^2 (P)	Female control	Female probands	OR (95%CI)	χ^2 (P)
rs7041(A/C)	A	0.48	0.46	0.94 (0.77-1.15)	0.33 (0.57)	0.44	0.46	1.07 (0.82-1.39)	0.28 (0.59)	0.50	0.47	0.86 (0.58-1.25)	0.65 (0.42)
	C	0.52	0.54	1.06 (0.86-1.29)		0.56	0.54	0.93 (0.71-1.21)		0.50	0.53	1.06 (0.80-1.70)	
	AA	0.19	0.21	1.14 (0.80-1.64)	4.19 (0.12)	0.18	0.22	1.26 (0.80-2.01)	1.23 (0.54)	0.19	0.18	0.88 (0.45-1.73)	1.08 (0.58)
	AC	0.58	0.50	0.75 (0.56-0.99)		0.53	0.48	0.84 (0.58-1.22)		0.62	0.58	0.85 (0.49-1.47)	
	CC	0.23	0.29	1.30 (0.94-1.79)		0.29	0.30	1.01 (0.67-1.52)		0.19	0.24	1.43 (0.73-2.78)	
rs4588(G/T)	G	0.72	0.71	0.94 (0.75-1.18)	0.26 (0.61)	0.73	0.70	0.87 (0.65-1.18)	0.74 (0.39)	0.72	0.74	1.10 (0.72-1.69)	0.22 (0.64)
	T	0.28	0.29	1.06 (0.85-1.33)		0.27	0.30	1.13 (0.84-1.53)		0.28	0.26	0.90 (0.59-1.38)	
	GG	0.50	0.49	0.96 (0.72-1.29)	0.69 (0.70)	0.52	0.48	0.86 (0.58-1.25)	0.83 (0.66)	0.48	0.53	1.19 (0.69-2.05)	0.54 (0.76)
	GT	0.45	0.44	0.98 (0.73-1.30)		0.43	0.45	0.86 (0.58-1.26)		0.47	0.42	0.81 (0.47-1.40)	
	TT	0.05	0.07	1.29 (0.70-2.38)		0.05	0.07	1.28 (0.59-2.78)		0.05	0.05	1.10 (0.33-3.70)	
rs3755967(C/T)	C	0.70	0.70	1.00 (0.80-1.25)	0.00 (0.97)	0.70	0.69	0.95 (0.71-1.26)	0.13 (0.72)	0.69	0.72	1.16 (0.76-1.78)	0.49 (0.48)
	T	0.30	0.30	0.99 (0.79-1.24)		0.30	0.31	1.05 (0.79-1.40)		0.31	0.28	0.86 (0.56-1.31)	
	CC	0.46	0.49	1.10 (0.83-1.47)	2.63 (0.26)	0.48	0.48	0.99 (0.68-1.45)	0.73 (0.69)	0.45	0.54	1.40 (0.81-2.43)	2.51 (0.28)
	CT	0.47	0.42	0.82 (0.61-1.09)		0.45	0.43	0.91 (0.63-1.34)		0.49	0.38	0.65 (0.37-1.11)	
	TT	0.07	0.09	1.38 (0.82)		0.07	0.09	1.32 (0.67-2.59)		0.06	0.08	1.41 (0.48-4.11)	

χ^2 = Chi square; P = p value ($P \leq 0.05$); OR= Odds ratio; 95% CI= 95% Confidence Interval; statistically significant differences are presented in bold.

Supplementary Table 2. Population- based comparative analysis on haplotype frequency

Groups	Variant combinations	Haplotypes	Control	Probands	OR (95%CI)	χ^2 (Pvalue)
All	rs7041-rs4588- rs3755967	A-G-C	0.18	0.15	0.85 (0.64-1.13)	0.90 (0.34)
		A-G-T	0.04	0.03	0.59 (0.33-1.06)	2.78 (0.09)
		A-T-C	0.01	0.02	1.18 (0.53-2.65)	0.002 (0.95)
		A-T-T	0.24	0.26	1.12 (0.87-1.44)	0.77 (0.37)
		C-G-C	0.48	0.51	1.14 (0.92-1.41)	1.13 (0.28)
		C-G-T	0.02	0.02	0.87 (0.37-2.00)	0.14 (0.70)
		C-T-C	0.02	0.01	0.34 (0.14-0.78)	4.06 (0.04)
		C-T-T	0.01	0.01	1.02 (0.24-4.47)	0.003 (0.95)
Male	rs7041-rs4588- rs3755967	A-G-C	0.15	0.15	1.00 (0.68-1.49)	0.001 (0.97)
		A-G-T	0.04	0.03	0.68 (0.28-1.64)	1.01 (0.31)
		A-T-C	0.03	0.02	0.87 (0.30-2.48)	0.09 (0.75)
		A-T-T	0.23	0.26	1.12 (0.70-1.80)	0.91 (0.34)
		C-G-C	0.51	0.51	0.99 (0.64-1.51)	0.01 (0.91)
		C-G-T	0.02	0.01	0.61 (0.19-1.92)	0.87 (0.35)
		C-T-C	0.01	0.01	0.52 (0.10-2.61)	0.65 (0.42)
		C-T-T	0.01	0.01	1.82 (0.13-24.58)	0.20 (0.65)
Female	rs7041-rs4588- rs3755967	A-G-C	0.21	0.18	0.90 (0.55-1.49)	0.27 (0.59)
		A-G-T	0.04	0.01	0.17 (0.004-6.90)	2.49 (0.11)
		A-T-C	0.01	0.00	0.42 (0.002-65.5)	0.64 (0.42)
		A-T-T	0.24	0.25	1.14 (0.61-2.13)	0.03 (0.86)
		C-G-C	0.45	0.52	1.24 (0.69-2.19)	1.78 (0.18)
		C-G-T	0.01	0.02	2.13 (0.34-13.42)	0.10 (0.74)
		C-T-C	0.03	0.01	0.38 (0.04-3.05)	1.54 (0.21)
		C-T-T	0.01	0.01	1.758e-008 (1.758e-008- 1.758e-008)	0.58 (0.44)

χ^2 = Chi square; P = p value ($P \leq 0.05$); OR= Odds ratio; 95% CI= 95% Confidence Interval; statistically significant differences are presented in bold.

Supplementary Table 3. Vitamin D levels in ASD subjects from different parts of the world

Disorder	Population	No of case/control	Circulating VitD level (Mean $\pm$ SD)		P value	Method used	C.Ref
			Control	Case			
ASD	Italy	54/36	24.62 $\pm$ 13.18 ng/mL	18.61 $\pm$ 8.33 ng/mL	P= 0.014	Chemiluminescence	Petruzzelli, M. G. <i>et al. Dis. Markers.</i> 2020 , 9292560 (2020).
	Turkey	100/100	48.57 $\pm$ 22.36 nmol/L	42.86 $\pm$ 19.84 nmol/L	P = 0.037	enzyme immunoassay method using the LIAISON ^{VR} device	Şengenç, E., Kırkım, E. & Saltık, S. <i>J. Int. Med. Res.</i> 48(7) , 300060520934638 (2020).
	Iran	31/31	15.25 $\pm$ 7.89 ng/mg	9.03 $\pm$ 4.14 ng/mg	P<0.001	ELISA method using Euroimmun kit,	Arastoo, A. A. <i>et al. Ital. J. Pediatr.</i> 44(1) , 150 (2018).
	Turkey	18/25	29.42 $\pm$ 9.07 ng/mL	14.3 $\pm$ 7.23 ng/mL	P<0.001	Chemiluminescence using Architect CI-16200	Garipardic, M. <i>et al. Med. Sci. Monit.</i> 23 , 1378–1384 (2017).
	Egypt	122/100	42.51 $\pm$ 9.48 ng/ml	18.02 $\pm$ 8.75 ng/ml	P $\leq$ 0.0001	ELISA Kit using Immundiagnostik AG,	Saad, K. <i>et al. Nutr. Neurosci.</i> 19(8) , 346–351(2015).

Supplementary Table 4. Details of primer sequences, PCR cycling conditions and reagents used

Variant	Oligonucleotide sequences (5'-3')	Reagents used for PCR reaction	PCR condition	Amplicon size (bp)	Restriction enzyme used for RFLP	Recognition sites	C.Ref.	Fragment sizes (bp)
rs7041 (A/C) and rs4588 (G/T)	F:GCCATGTTAAGTGGAG GGTTAC R:TGGTTTTTCAGACTGG CAGA	20 µl reaction mix containing 75-100ng template DNA, 20 pmoles of each primer, 200 µM dNTP mix, 1X buffer B, 25 mM MgCl ₂ and 1 U Taq polymerase (NEB)	Initial denaturation 95° -5 min; 35 cycles of - denaturation: 95°C-30 s, annealing: 61°C -30s and extension: 72°C - 30s; final extension 72°C - 5 min	rs7041 176	Hae III (CutSmart)	5'...CG▼CC...3' 3'...CC▲GG...5'	41	AA:176 AC:176/130/46 CC:130/46
				rs4588 176	Btg I (CutSmart)	5'...C▼CRYGG ...3' 3'...GGYRC▲C ...5'	NIL	GG:119/577 GT:176/119/57 TT:176
rs3755967 (C/T)	F:AACCCAGGAAGTCAA TGAG R:TGAAGGCCTACCAATG TTCA	20 µl reaction mix containing 75-100 ng genomic DNA, 1X Taq B buffer, 20 pmoles of each primer, 200 µM dNTP mix, , 25 mM MgCl ₂ and 1 U Taq polymerase (NEB)	Initial denaturation 95°C-5mins; 35 cycles of denaturation at 95°C- 30sec, annealing at 59°C-20 sec, extension at 72°C-20 sec; final extension at 72°C for 5 mins	180	EcoRV (NEB 3.1)	5'...GAT▼ATC ...3' 3'...CTA▲TAG ...5'	NIL	CC: 100/80 CT:180/100/80 TT:180