Table SI. Genotype and allele frequency distribution of the VDR SNPs in PsV cases stratified by BMI status.

A, FokI (rs2228570)

Genotype/allele	BMI ≥25 (n=142), n (%)	BMI <25 (n=61), n (%)
CC	73 (51.41)	23 (37.71)
TC	53 (37.32)	30 (49.18)
TT	16 (11.27)	8 (13.11)
C	199 (70.07)	76 (62.30)
T	85 (29.93)	46 (37.70)

B, BsmI (rs1544410)

Genotype/allele	BMI ≥25 (n=142), n (%)	BMI <25 (n=61), n (%)
GG	43 (30.28)	19 (31.15)
GA	80 (56.34)	27 (44.26)
AA	19 (13.38)	15 (24.59)
G	166 (58.45)	65 (53.28)
A	118 (41.55)	57 (46.72)

C, TaqI (rs731236)

Genotype/allele	BMI ≥25 (n=142), n (%)	BMI <25 (n=61), n (%)
TT	45 (31.69)	20 (32.79)
CT	64 (45.07)	24 (39.34)
CC	33 (23.24)	17 (27.87)
T	154 (54.23)	64 (52.46)
C	130 (45.77)	58 (47.54)

The BMI was calculated as weight in kilograms divided by height in meters squared. PsV, psoriasis vulgaris; SNPs, single nucleotide polymorphisms; VDR, vitamin D receptor.

Table SII. Genetic model analysis of the VDR SNPs in PsV cases stratified by BMI status.

A, FokI (rs2228570)

Genetic model	OR (95% CI)	P-value	Adjusted P-value
Dominant TT + TC vs. CC	0.572 (0.310-1.057)	0.074	0.404
Recessive TT vs. TC + CC	0.841 (0.340-2.085)	0.709	0.874
Overdominant TC vs. TT + CC	0.615 (0.336-1.128)	0.117	0.468
Allelic T vs. C	0.706 (0.452-1.102)	0.124	0.478

B, BsmI (rs1544410)

Genetic model	OR (95% CI)	P-value	Adjusted P-value
Dominant AA + GA vs. GG	1.042 (0.544-1.994)	0.902	0.928
Recessive AA vs. GA + GG	0.474 (0.222-1.010)	0.053	0.364
Overdominant GA vs. GG + AA	1.625 (0.888-2.974)	0.115	0.468
Allelic A vs. G	0.811 (0.518-1.272)	0.335	0.659

C, TaqI (rs731236)

Genetic model	OR (95% CI)	P-value	Adjusted P-value
Dominant CC + CT vs. TT	1.051 (0.554-1.996)	0.878	0.921
Recessive CC vs. CT + TT	0.784 (0.396-1.550)	0.483	0.734
Overdominant CT vs. TT + CC	1.265 (0.687-2.330)	0.451	0.718
Allelic C vs. T	0.931 (0.596-1.458)	0.744	0.893

P-values were adjusted by Benjamini-Hochberg correction. OR, odds ratio; PsV, psoriasis vulgaris; SNPs, single nucleotide polymorphisms; VDR, vitamin D receptor.

Table SIII. Genotype and allele frequency distribution of the VDR SNPs in mild and severe PsV cases.

A, FokI (rs2228570)

Genotype/allele	Severe PsV (n=156), n (%)	Mild PsV (n=47), n (%)
CC	72 (46.15)	24 (51.06)
TC	66 (42.31)	17 (36.17)
TT	18 (11.54)	6 (12.77)
C	210 (67.31)	65 (69.15)
T	102 (32.69)	29 (30.85)

B, BsmI (rs1544410)

Genotype/allele	Severe PsV (n=156), n (%)	Mild PsV (n=47), n (%)
GG	50 (32.05)	12 (25.53)
GA	80 (51.28)	27 (57.45)
AA	26 (16.67)	8 (17.02)
G	180 (57.69)	51 (54.26)
A	132 (42.31)	43 (45.74)

C, TaqI (rs731236)

Genotype/allele	Severe PsV (n=156), n (%)	Mild PsV (n=47), n (%)
TT	53 (33.97)	12 (25.53)
CT	66 (42.31)	22 (46.81)
CC	37 (23.72)	13 (27.66)
T	172 (55.13)	46 (48.94)
C	140 (44.87)	48 (51.06)

PsV, psoriasis vulgaris; SNPs, single nucleotide polymorphisms; VDR, vitamin D receptor.

Table SIV. Genetic model analysis of the VDR SNPs in mild and severe PsV cases.

A, FokI (rs2228570)

Genetic model	OR (95% CI)	P-value	Adjusted P-value
Dominant TT + TC vs. CC	1.217 (0.634-2.339)	0.555	0.789
Recessive TT vs. TC + CC	0.891 (0.332-2.393)	0.819	0.921
Overdominant TC vs. TT + CC	1.294 (0.659-2.540)	0.454	0.718
Allelic T vs. C	1.089 (0.662-1.790)	0.738	0.893

B, BsmI (rs1544410)

Genetic model	OR (95% CI)	P-value	Adjusted P-value
Dominant AA + GA vs. GG	0.727 (0.348-1.519)	0.396	0.691
Recessive AA vs. GA + GG	0.975 (0.409-2.326)	0.954	0.963
Overdominant GA vs. GG + AA	0.780 (0.404-1.506)	0.459	0.718
Allelic A vs. G	0.870 (0.547-1.383)	0.638	0.830

C, TaqI (rs731236)

Genetic model	OR (95% CI)	P-value	Adjusted P-value
Dominant CC + CT vs. TT	0.666 (0.320-1.389)	0.279	0.641
Recessive CC vs. CT + TT	0.813 (0.389-1.701)	0.583	0.810
Overdominant CT vs. TT + CC	0.833 (0.433-1.604)	0.585	0.810
Allelic C vs. T	0.780 (0.492-1.238)	0.291	0.655

P-values were adjusted by Benjamini-Hochberg correction. OR, odds ratio; PsV, psoriasis vulgaris; SNPs, single nucleotide polymorphisms; VDR, vitamin D receptor.

Table SV. Genotype and allele frequency distribution of the VDR SNPs in PsV cases with and without scalp involvement.

A, FokI (rs2228570)

Genotype/allele	**With scalp PsV (n=115), n (%)**	**Without scalp PsV (n=88), n (%)**
CC	51 (44.35)	45 (51.14)
TC	53 (46.09)	30 (34.09)
TT	11 (9.56)	13 (14.77)
C	155 (67.39)	120 (68.18)
T	75 (32.61)	56 (31.82)

B, BsmI (rs1544410)

Genotype/allele	**With scalp PsV (n=115), n (%)**	**Without scalp PsV (n=88), n (%)**
GG	38 (33.05)	24 (27.27)
GA	59 (51.30)	48 (54.55)
AA	18 (15.65)	16 (18.18)
G	135 (58.70)	96 (54.55)
A	95 (41.30)	80 (45.45)

C, TaqI (rs731236)

Genotype/allele	**With scalp PsV (n=115), n (%)**	**Without scalp PsV (n=88), n (%)**
TT	40 (34.78)	25 (28.41)
CT	49 (42.61)	39 (44.32)
CC	26 (22.61)	24 (27.27)
T	129 (56.09)	89 (50.57)
C	101 (43.91)	87 (49.43)

PsV, psoriasis vulgaris; SNPs, single nucleotide polymorphisms; VDR, vitamin D receptor.

Table SVI. Genetic model analysis of the VDR SNPs in PsV cases with and without scalp involvement.

A, FokI (rs2228570)			
Genetic model	**OR (95% CI)**	**P-value**	**Adjusted P-value**
Dominant TT + TC vs. CC	1.313 (0.753-2.292)	0.337	0.659
Recessive TT vs. TC + CC	0.610 (0.259-1.436)	0.258	0.641
Overdominant TC vs. TT + CC	1.653 (0.932-2.932)	0.086	0.404
Allelic T vs. C	1.037 (0.667-1.616)	0.866	0.921
B, BsmI (rs1544410)			
Genetic model	**OR (95% CI)**	**P-value**	**Adjusted P-value**
Dominant AA + GA vs. GG	0.760 (0.413-1.397)	0.377	0.690
Recessive AA vs. GA + GG	0.835 (0.399-1.749)	0.633	0.830
Overdominant GA vs. GG + AA	0.878 (0.503-1.532)	0.647	0.832
Allelic A vs. G	0.844 (0.557-1.280)	0.403	0.691
C, TaqI (rs731236)			
Genetic model	**OR (95% CI)**	**P-value**	**Adjusted P-value**
Dominant CC + CT vs. TT	0.744 (0.408-1.358)	0.335	0.659
Recessive CC vs. CT + TT	0.779 (0.410-1.479)	0.445	0.718
Overdominant CT vs. TT + CC	0.933 (0.533-1.633)	0.808	0.919
Allelic C vs. T	0.801 (0.530-1.211)	0.269	0.641

P-values were adjusted by Benjamini-Hochberg correction. OR, odds ratio; PsV, psoriasis vulgaris; SNPs, single nucleotide polymorphisms; VDR, vitamin D receptor.

Table SVII. Genotype and allele frequency distribution of the VDR SNPs in PsV cases with and without genital involvement.

A, FokI (rs2228570)

Genotype/allele	With genital PsV (n=55), n (%)	Without genital PsV (n=148), n (%)
CC	23 (41.82)	73 (49.32)
TC	25 (45.45)	58 (39.19)
TT	7 (12.73)	17 (11.49)
C	71 (64.55)	204 (68.92)
T	39 (35.45)	92 (31.08)

B, BsmI (rs1544410)

Genotype/allele	With genital PsV (n=55), n (%)	Without genital PsV (n=148), n (%)
GG	21 (38.18)	41 (27.70)
GA	26 (47.27)	81 (54.73)
AA	8 (14.55)	26 (17.57)
G	68 (61.82)	163 (55.07)
A	42 (38.18)	133 (44.93)

C, TaqI (rs731236)

Genotype/allele	With genital PsV (n=55), n (%)	Without genital PsV (n=148), n (%)
TT	21 (38.19)	44 (29.73)
CT	25 (45.45)	63 (42.57)
CC	9 (16.36)	41 (27.70)
T	67 (60.91)	151 (51.01)
C	43 (39.09)	145 (48.99)

PsV, psoriasis vulgaris; SNPs, single nucleotide polymorphisms; VDR, vitamin D receptor.

Table SVIII. Genetic model analysis of the VDR SNPs in PsV cases with and without genital involvement.

A, FokI (rs2228570)

Genetic model	**OR (95% CI)**	**P-value**	**Adjusted P-value**
Dominant TT + TC vs. CC	1.354 (0.725-2.531)	0.342	0.659
Recessive TT vs. TC + CC	1.124 (0.439-2.878)	0.808	0.919
Overdominant TC vs. TT + CC	1.293 (0.692-2.416)	0.420	0.709
Allelic T vs. C	1.218 (0.768-1.933)	0.402	0.691

B, BsmI (rs1544410)

Genetic model	**OR (95% CI)**	**P-value**	**Adjusted P-value**
Dominant AA + GA vs. GG	0.620 (0.323-1.191)	0.151	0.544
Recessive AA vs. GA + GG	0.799 (0.338-1.889)	0.609	0.822
Overdominant GA vs. GG + AA	0.742 (0.399-1.379)	0.345	0.659
Allelic A vs. G	0.757 (0.470-1.211)	0.222	0.641

C, TaqI (rs731236)

Genetic model	**OR (95% CI)**	**P-value**	**Adjusted P-value**
Dominant CC + CT vs. TT	0.685 (0.358-1.310)	0.253	0.641
Recessive CC vs. CT + TT	0.511 (0.229-1.136)	0.100	0.432
Overdominant CT vs. TT + CC	1.124 (0.603-2.096)	0.712	0.874
Allelic C vs. T	0.668 (0.416-1.067)	0.076	0.404

P-values were adjusted by Benjamini-Hochberg correction. OR, odds ratio; PsV, psoriasis vulgaris; SNPs, single nucleotide polymorphisms; VDR, vitamin D receptor.