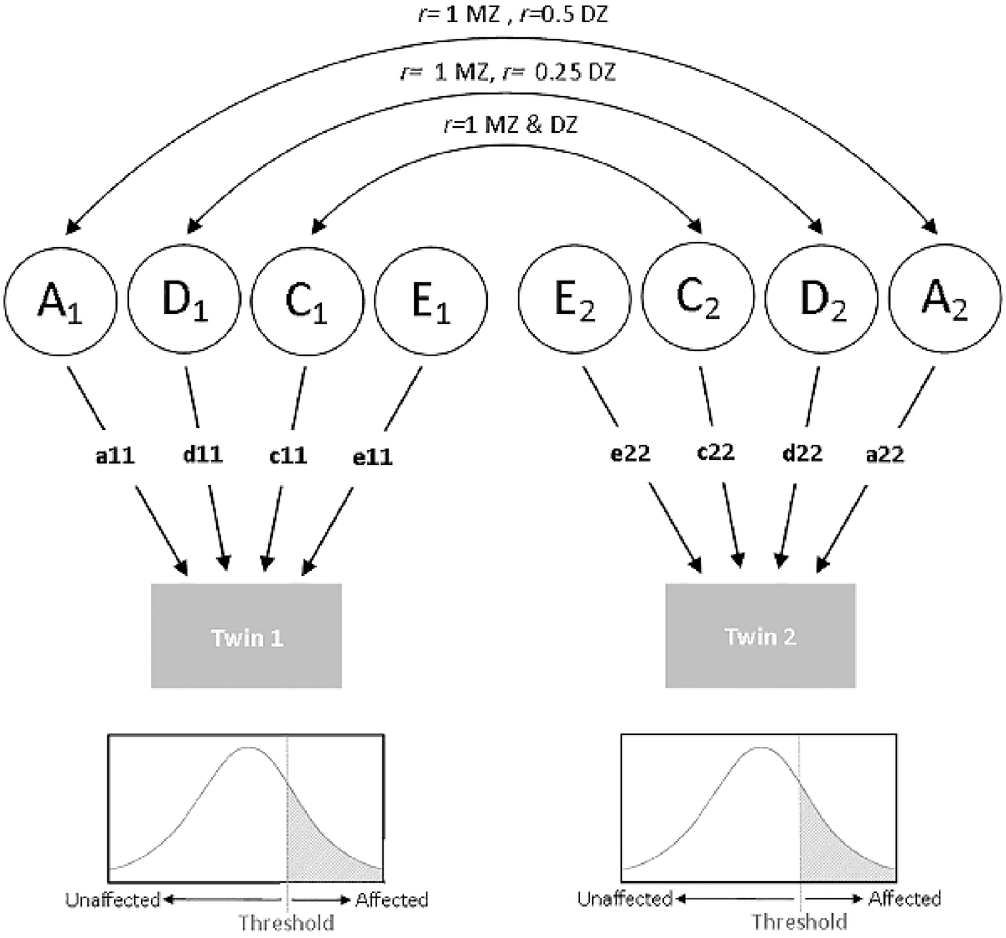
Supplementary Online Content

van Straalen KR, Prens EP, Willemsen G, Boomsma DI, van der Zee HH. Contribution of genetics to the susceptibility to hidradenitis suppurativa in a large, cross-sectional Dutch twin cohort. *JAMA Dermatol.* Published online October 14, 2020. doi:10.1001/jamadermatol.2020.3630

eFigure. Liability Threshold Model
eTable. Standardized Variance Components and Goodness-of-Fit Statistics Worst-Case Scenario

eFigure. Liability Threshold Model



Note that D and C cannot be estimated in one model, so separate ACE and ADE models need to be constructed.

Abbreviations: a path, coefficient for A; A, additive genetic factors; c path, coefficient for C; C, common/shared environmental factors; d path, coefficient for D; D, dominant genetic factors; DZ, dizygotic; e path, coefficient for E; E, unique/unshared environmental factors; MZ, monozygotic twins.

eTable. Standardized Variance Components and Goodness-of-Fit Statistics Worst-Case Scenario

		Standardized Variance Components			**Fit Statistics**						**Heritability**
	Model	A	C / D	E	AIC	ΔAIC	-2LL	Δ-2LL	ep	p-value	h^2 (95% CI)
<u>Hidradenitis suppurativa</u>											
Threshold model fitting	Saturated				-9667.37	-	340.63	-	8	-	
	Covariate Age				-9671.37	-4.00	340.63	0.00	6	1.00	
	Threshold T1 = T2[1]				-9674.98	7.61	341.02	0.39	4	0.98	
	Threshold MZ = DZ				-9673.50	6.31	342.50	1.88	4	0.76	
Genetic model fitting	ACE	0.75	0.00	0.25	-9674.03	0.95[2]	341.97	0.95	5	-	
	ADE	0.00	0.77	0.23	-9674.63	0.35[2]	341.37	0.35	5	-	
	AE[1]	0.75	0.00[3]	0.25	-9676.03	-2.00	341.97	0.00	4	1.00	75% (37-93%)
	CE	0.00[3]	0.59	0.41	-9673.26	0.77	344.74	2.78	4	0.10	
	E	0.00[3]	0.00[3]	1.00	-9664.91	9.12	355.09	13.12	3	<0.01	

A, C, D, and E represent the proportion of the variance explained by respectively addictive genetic, dominant genetic, common environmental, and unique environmental effects. -2LL = minus 2 log likelihood, Δ-2LL = the difference in -2LL between the submodel and the main model, ep = estimated parameters, AIC = Akaike information criterion, ΔAIC = the difference in AIC between the submodel and the main model, h2 represents the narrow sense heritability, defined as the proportion of genetic variance (A+D) to total phenotypic variance. [1] indicates the best fitting model. [2]compared with best threshold model. [3] indicates fixed values