

Dexamethasone promotes durable factor VIII-specific tolerance in hemophilia A mice via thymic mechanisms

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Supplementary Material

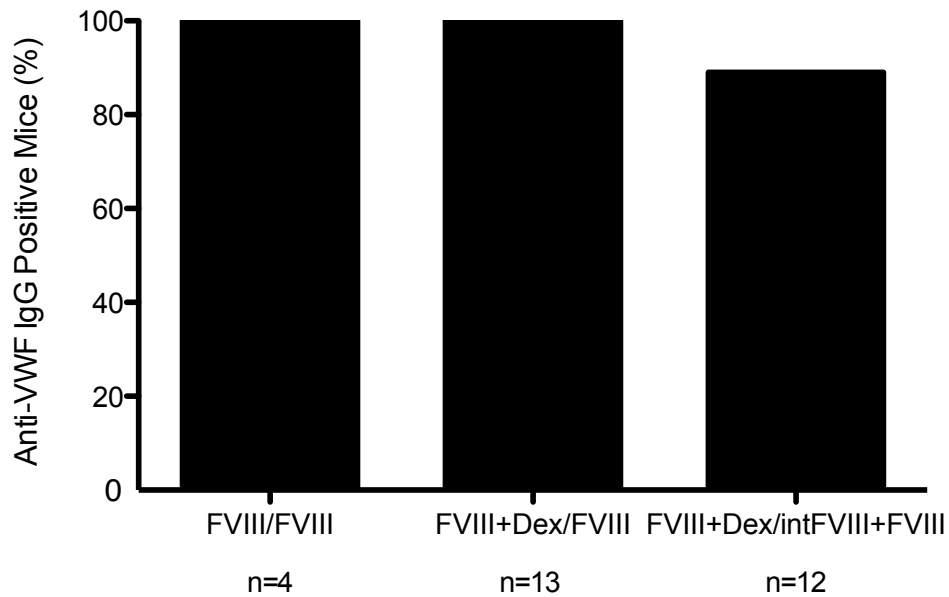


Figure S1. Administration of Dex during initial FVIII exposure does not impair the immune response to VWF. Anti-VWF IgG incidence at week 22, following exposure to VWF (Week 18-21) in mice initially treated with FVIII or FVIII+Dex and with no evidence of anti-FVIII IgG at week 4.

Table S1. Genes down-regulated following FVIII+Dex treatment.

Gene Name	Transcript Count Ratio	
	FVIII+Dex vs FVIII	Dex vs HBSS
<i>Ccr4</i>	-5.82	-14.45
<i>Rag1</i>	-4.18	-16.00
<i>Cd69</i>	-3.51	-4.40
<i>Ccr9</i>	-3.46	-9.90
<i>Slamf1</i>	-3.20	-6.50
<i>Cd8b1</i>	-3.18	-7.77
<i>Cd40lg</i>	-2.99	-2.56
<i>Cxcl1</i>	-2.90	-2.37
<i>Rag2</i>	-2.84	-9.21
<i>Rorc</i>	-2.78	-5.65
<i>Cd8a</i>	-2.67	-7.74
<i>Cd4</i>	-2.66	-5.06
<i>Il9</i>	-2.64	-2.26
<i>Il12b</i>	-2.60	-2.49
<i>Bcl6</i>	-2.59	-3.30
<i>Il27</i>	-2.54	-3.06
<i>Mr1</i>	-2.48	-3.26
<i>Sh2d1a</i>	-2.39	-6.68
<i>Il13</i>	-2.23	-2.38
<i>Ccl22</i>	-2.22	-2.51
<i>Il16</i>	-2.22	-3.05
<i>Socs1</i>	-2.20	-4.55
<i>Card9</i>	-2.12	-3.32
<i>Cxcr4</i>	-2.12	-3.98
<i>Tcf7</i>	-2.12	-5.16
<i>Lck</i>	-2.06	-4.47
<i>Icam2</i>	-2.02	-3.09

Table S2. Genes up-regulated following FVIII+Dex treatment.

Gene Name	Transcript Count Ratio	
	FVIII+Dex vs FVIII	Dex vs HBSS
Cd36	7.20	19.89
Cfd	7.17	10.08
Mme	6.10	22.78
Pparg	5.80	20.07
Tlr5	5.53	20.38
H2-Q10	5.08	25.14
C7	4.60	10.55
Il18rap	3.89	3.10
Itga2b	3.75	58.09
C4a	3.71	12.35
Cd209g	3.63	25.37
Il22ra2	3.20	53.55
Ppbp	3.16	11.22
Pdgfrb	2.72	3.28
Tal1	2.41	3.33
Il33	2.27	5.11
Fn1	2.26	3.90
Gzmb	2.21	3.17
Marco	2.19	175.11
Cfh	2.18	4.25
Cxcl13	2.16	19.57
Cdh5	2.15	6.77
Cebpb	2.14	5.60
Cd14	2.08	3.84
Bst1	2.02	2.11
Vtn	2.02	5.02
Serp1g1	2.01	5.53

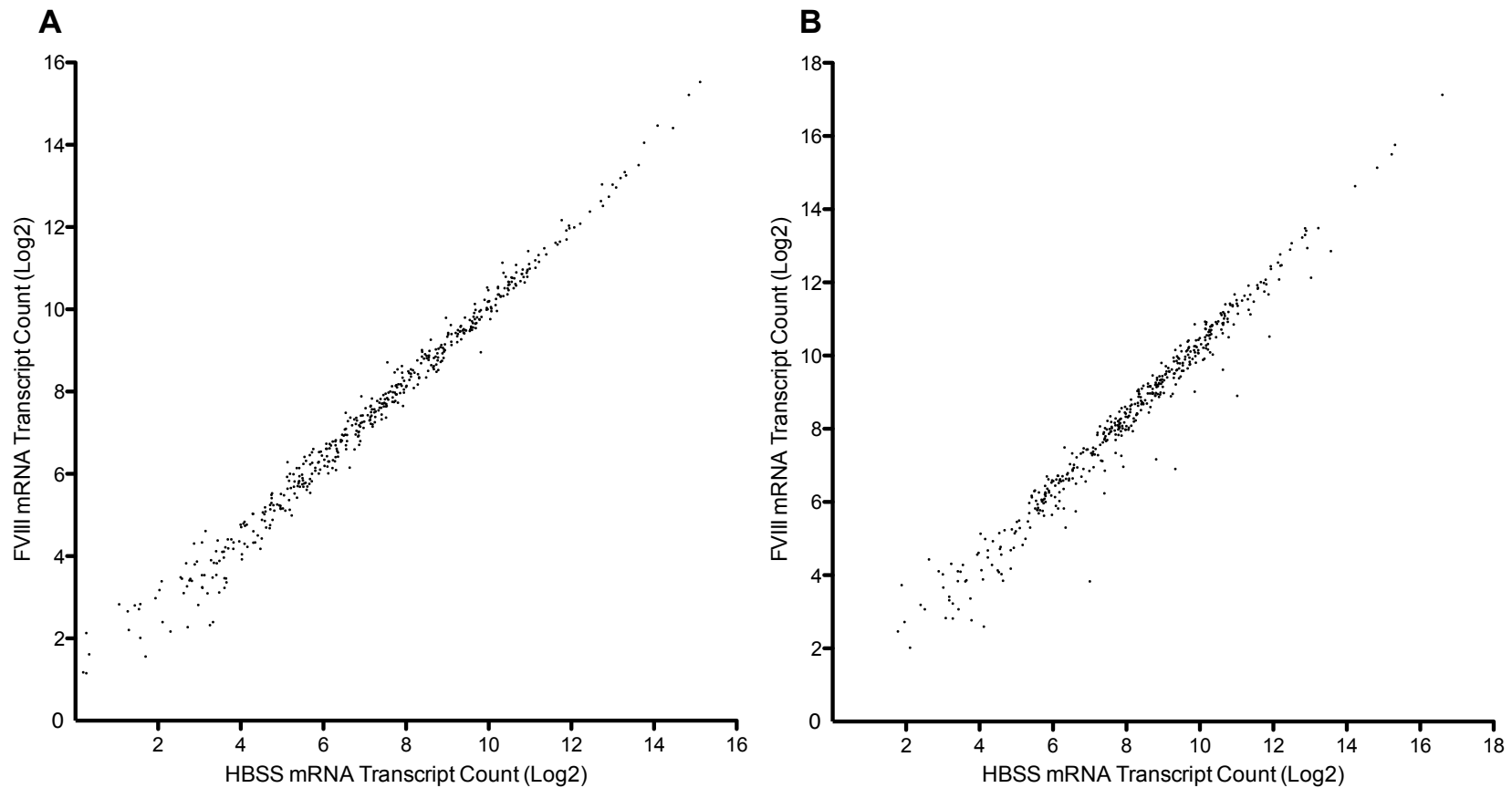


Figure S2. Intense FVIII exposure does not alter the thymic or splenic mRNA transcript profile of E16KO mice. A. Thymic and **B.** Splenic mRNA transcript counts three days after treatment with FVIII (6 IU IV) versus mRNA transcript counts three days after treatment with HBSS alone (250 μ l IV, 100 μ l IP). Each point corresponds with the average mRNA transcript count of 3 different tissue samples. n=3 for each condition.