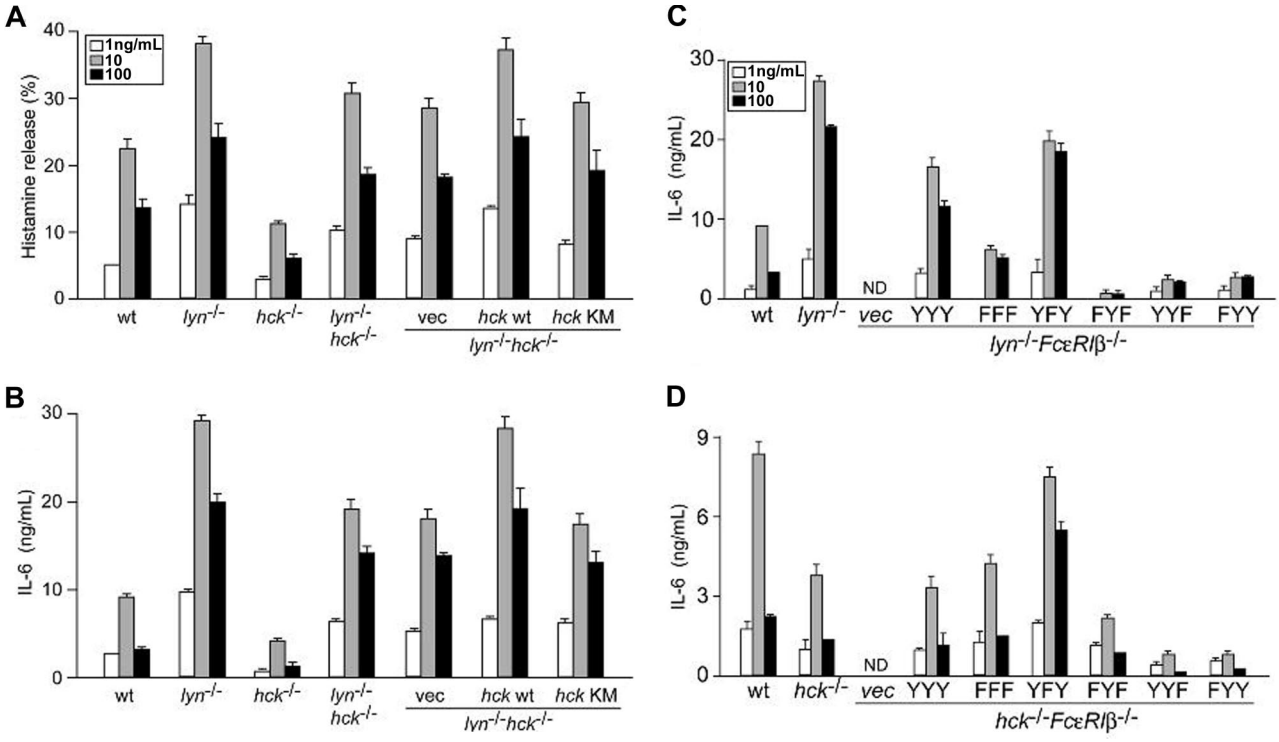
Erratum for Kilmon et al. Macrophages prevent the differentiation of autoreactive B cells by secreting CD40 ligand and interleukin-6. Blood. 2007;110:1595-1602.

In the article by Kilmon et al entitled "Macrophages prevent the differentiation of autoreactive B cells by secreting CD40 ligand and interleukin-6," which appeared in the September 1, 2007, issue of *Blood* (Volume 110:1595-1602), the DOI in the title-page note was incorrect. The correct DOI is 10.1182/blood-2006-12-061648.

The online DOI was corrected in departure from print.

Erratum for Hong et al. The Src family kinase Hck regulates mast cell activation by suppressing an inhibitory Src family kinase Lyn. Blood. 2007;110:2511-2519.

In the article by Hong et al entitled "The Src family kinase Hck regulates mast cell activation by suppressing an inhibitory Src family kinase Lyn," which appeared in the October 1, 2007, issue of *Blood* (Volume 110:2511-2519), panels C and D were mistakenly omitted from Figure 7. The complete figure, displaying panels A-D, should have appeared as shown here. The second sentence of the figure legend should have ended with ". . . or 20 hours (B-D)."



Erratum for Goodeve et al. Phenotype and genotype of a cohort of families historically diagnosed with type 1 von Willebrand disease in the European study, Molecular and Clinical Markers for the Diagnosis and Management of Type 1 von Willebrand Disease (MCMDM-1VWD). Blood. 2007;109:112-121.

The article by Goodeve et al entitled "Phenotype and genotype of a cohort of families historically diagnosed with type 1 von Willebrand disease in the European study, Molecular and Clinical Markers for the Diagnosis and Management of Type 1 vonWillebrand Disease (MCMDM-1VWD)" which appeared in the January 1, 2007, issue of *Blood* (109:112-121) has been found to contain a factual error by the MCMDM-1VWD partners. Family P10F4I:2 was said to have 2 mutations, N1421K plus L881R. The latter mutation now appears to

Table 2. Number of mutations and median phenotype in 150 index cases with type 1 VWD

Multimer pattern	No. of IC per group	No. of mutations per IC	No. of mutations per group	FVIII:C, IU/dL	VWF;RCo IU/dL	VWF:Ag IU/dL	VWF:CB IU/dL	VWF: RCo/VWF: Ag	% blood group O	Bleeding score
NM	51	1or>1	**58**	66	42	45	48	0.93	60	8.0
NM	45	1	**45**	67	**42**	**44**	**48**	**0.98**	**60**	**8.0**
NM	6	>1	**13**	**29**	**41**	47	**49**	**0.92**	**83**	**8.5**

be a DNA sequencing artifact. As a consequence, P10F4I2 should move from Table 6 to Table 5. This reduces the total number of mutations identified from 124 to 123 and alters the article as follows (numbers altered are indicated by bold text):

Page 114, results under Mutation Analysis should read; **88** had 1 mutation, **16** had 2, and 1 had 3. A total of **123** candidate mutations were identified, of which **74** were different and **53** were novel.

Page 115; Table 2, Group 2 data in 3 rows is altered by the change of patient group of this mutation. A corrected version of this table appears above.

Results under Group 2 should read; Of 51 ICs with NMs and a mutation, **45** ICs had 1 candidate mutation identified (Table 5), while **6** had more than 1 mutation (Table 6). **Twenty-three** different single missense changes were identified.

In the bottom line of Figure 1, boxes 3 and 4 from the left hand side should read 1 Mutation n = **45**, > 1 Mutation n = **6**.

Page 116, Table 6; Results under Group 2 should read; **5** group 2 ICs had 2 mutations: **4** had 2 missense changes, while the **fifth** had a missense plus a splice site change. 4 of the **5** were compound heterozygotes, while **1** had allelic changes (Table 6).

Page 118 & 119; Data on P10F4I:2 more properly belongs in Table 5. The titles for these 2 tables should now read:

Table 5. *VWF* mutations and phenotype in **45** group 2 index cases with normal multimers and a single mutation.

Table 6. *VWF* mutations and phenotype in **6** group 2 index cases with normal multimers and more than 1 mutation.

Page 120, paragraph 3; Discussion, should read: Only a few such mutations were identified in this cohort (14 of **123** mutations, 11%).

The following mutations did not correctly follow Human Genome Variation Society guidelines http://www.hgvs.org/mutnomen/ and should be amended as below. Numbering follows the reference sequences for cDNA NM_000552.3, gDNA ENSG00000110799 and protein NP_000543.2.

In Table 3, P3F1II1, D1277-E78delinsL should read D1277_L1278delinsE; P2F16II2, 7239C>T should read 7085G>T.

In Table 4, P2F1II1, 4449delG (L1481fs) should read 4453delG (V1485fs).

In Table 5, Various IC, −2520C>T should read −2522C>T; P3F10II1, S1024fs should read W1025fs; P12F4II12, 3839–3845ins7 (F1280fs) should read 3839_3845dup7 (D1283fs); P5F6II3, 7551G>A should read 7552G>A.

In Table 6, P7F14I1, −3266G>C should read −3268G>C; P7F14I1, −2730C>T should read −2731C>T; P7F14I1, −2326T>C should read −2328T>C.