Table SI. *Compilation of genotypic and phenotypic data from 112 cases of autosomal recessive congenital ichthyosis (ARCI) in which disease-causing mutations were found[a]. An asterisk (*) after the patient number indicates subjects who belong to the same family Some data are from previous publications (Ref.). For abbreviations see bottom of the Table*

Pat. no.	Diagnosis	Mutations	Consequences of mutations	IS	ES	Co	Ect	Anh	PPK	Ref.
		TGM1 (HGVS: NM_000359.2)								
1*	LI	c.1074C>G/c.1135G>C	p.Ser358Arg/p.Val379Leu	1.9	0.9	Yes	Yes	Yes	Yes	
2*	LI	c.1074C>G/c.1135G>C	p.Ser358Arg/p.Val379Leu	1.8	1	Yes	Yes	Yes	Yes	
3	LI	c.1074C>G/c.1074C>G	p.Ser358Arg/p.Ser358Arg	2.6	0.1	Yes	Yes	Yes	Yes	
4	LI	c.877-2A>G/c.1094A>G	splice site (in 5)/p.Tyr365Cys	0.8	0.3	Yes	No	Yes	Yes	
5	LI	c.877-2A>G/c.1074C>G	splice site (in 5)/p.Ser358Arg	3	0.2	Yes	Yes	Yes	Yes	
6	SICI	c.944G>A/c.944G>A	p.Arg315His/p.Arg315His	0.7	0.4	Yes	No	Yes	No	
7	LI	c.877-2A>G/c.877-2A>G	splice site (in 5)/splice site (in 5)	3.3	1.8	Yes	Yes	Yes	Yes	
8	CIE	c.788G>A/c.2150T>G	p.Trp263Term/p.Leu717Arg	0.2	2.5	(Y)	No	?	Yes	
9	LI	c.877-2A>G/c.1121A>G	splice site (in 5)/p.Tyr374Cys	2.5	0.1	Yes	Yes	Yes	Yes	
10*	LI	c.877-2A>G/c.1187G>T	splice site (in 5)/p.Arg396Leu	1.2	0.2	Yes	Yes	(Y)	Yes	
11*	LI	c.877-2A>G/c.1187G>T	splice site (in 5)/p.Arg396Leu	1.1	0.5	Yes	Yes	(Y)	Yes	
12	LI	c.877-2A>G/c.877-2A>G	splice site (in 5)/splice site (in 5)	2.1	0	Yes	Yes	(Y)	Yes	
13	SICI	c.918C>G/c.1187G>T	p.Asp306Glu/p.Arg396Leu	0.4	0	Yes	No	No	(Y)	
14*	LI	c.1074C>G/c.1163T>C	p.Ser358Arg/p.Leu388Pro	2.4	1	Yes	Yes	Yes	Yes	
15*	LI	c.872G>A/c.1074C>G	p.Gly291Asp/p.Ser358Arg	1.1	0.5	Yes	Yes	(Y)	(Y)	
16	LI	c.877-2A>G/c.877-2A>G	splice site (in 5)/splice site (in 5)	2.7	0	Yes	No	Yes	Yes	
17	LI	c.877-2A>G/c.877-2A>G	splice site (in 5)/splice site (in 5)	3.6	1.3	Yes	No	Yes	Yes	
18*	LI	c.1074C>G/c.1187G>T	p.Ser358Arg/p.Arg396Leu	2.7	0.7	Yes	Yes	Yes	Yes	
19*	LI	c.1074C>G/c.1187G>T	p.Ser358Arg/p.Arg396Leu	3	0.7	Yes	Yes	Yes	Yes	
20	LI	c.1074C>G/c.1074C>G	p.Ser358Arg/p.Ser358Arg	1.7	0.2	(Y)	Yes	Yes	Yes	
21	LI	c.1074C>G/c.1074C>G	p.Ser358Arg/p.Ser358Arg	2	0	Yes	Yes	Yes	Yes	
22	LI	c.1074C>G/c.1438A>T	p.Ser358Arg/p.Ile480Phe	1.5	0.8	Yes	No	(Y)	No	
23	LI	c.877-2A>G/c.1074C>G	splice site (in 5)/p.Ser358Arg	3.9	0.6	(Y)	Yes	Yes	Yes	
24*	LI	c.1074C>G/c.2088+1G>T	p.Ser358Arg/splice site (in 13)	2.6	0.1	Yes	Yes	Yes	Yes	28
25*	LI	c.1074C>G/c.2088+1G>T	p.Ser358Arg/splice site (in 13)	3	0.7	Yes	Yes	Yes	Yes	28
26*	LI	c.1074C>G/c.1135G>C	p.Ser358Arg/p.Val379Leu	1.8	0.7	Yes	Yes	Yes	Yes	28
27	LI	c.1074C>G/c.1094A>G	p.Ser358Arg/p.Tyr365Cys	2.6	0.9	Yes	No	?	Yes	
28	LI	c.160C>T/c.1927+1G>A	p.Arg54Term/splice site (in 12)	3.1	1.1	Yes	No	Yes	Yes	
29	CIE	c.1074C>G/c.877-2A>G	p.Ser358Arg/splice site (in 5)	2.1	1.7	Yes	No	Yes	Yes	
30	LI	c.427C>T/c.1135G>C	p.Arg143Cys/p.Val379Leu	3.7	1.3	Yes	Yes	Yes	Yes	
31	LI	c.401A>G/c.566dupG	p.Tyr134Cys/p.Ser190fs	3.9	0.1	Yes	Yes	Yes	Yes	
32	LI	c.1074C>G/c.1074C>G	p.Ser358Arg/p.Ser358Arg	4	1	Yes	Yes	Yes	Yes	
33	LI	c.1135G>C/1166G>A	p.Val379Leu/p.Arg389His	3	0.5	Yes	Yes	Yes	Yes	
34*	LI	c.425G>A/c.1389A>T	p.Arg142His/p.Gln463His	1.7	0	No	No	No	Yes	
35*	LI	c.425G>A/c.1389A>T	p.Arg142His/p.Gln463His	1.1	0.5	(Y)	No	Yes	Yes	
36	LI	c.427C>T/c.427C>T	p.Arg143Cys/p.Arg143Cys	3.5	1	Yes	Yes	?	Yes	
37	CIE	c.790C>T/c.1074C>G	p.Arg264Trp/p.Ser358Arg	1.7	1.8	Yes	No	Yes	(Y)	
38	BSI	c.1094A>G/c.1438A>T	p.Tyr365Cys/p.Ile480Phe	1.5	0	Yes	No	Yes	No	
39	LI	c.427C>T/c.877-2A>G	p.Arg143Cys/splice site (in 5)	3.1	0.8	Yes	No	Yes	Yes	
40	LI/PI	c.919C>G/c.1074C>G	p.Arg307Gly/p.Ser358Arg	0.4	0	(Y)	No	Yes	Yes	
41*	LI	c.877-2A>G/c.1166G>C	splice site (in 5)/p.Arg389Pro	2.8	0.5	Yes	Yes	Yes	Yes	
42*	LI	c.877-2A>G/c.1166G>C	splice site (in 5)/p.Arg389Pro	2.6	0.6	(Y)	(Y)	Yes	Yes	
43	SICI	c.1094A>G/c.1094A>G	p.Tyr365Cys/p.Tyr365Cys	0.1	0.1	Yes	(Y)	?	?	
44	LI	c.877-2A>G/c.1135G>C	splice site (in 5)/p.Val379Leu	2.9	1.9	Yes	Yes	Yes	Yes	
45	LI	c.1135G>C/c.1403-?_2225+?[2]	p.Val379Leu/*nihil*[a]	3.1	0.4	Yes	Yes	Yes	Yes	
46	LI	c.425G>A/c.425G>A	p.Arg142His/p.Arg142His	3.8	1	Yes	Yes	Yes	Yes	
47	LI	c.1094A>G/c.877-2A>G	p.Tyr365Cys/splice site (in 5)	1.5	0	Yes	No	(Y)	Yes	
48	SICI	c.877-2A>G/919C>G	splice site (in 5)/p.Arg307Gly	0.5	0	Yes	(Y)	No	No	24
49	LI	c.401A>G/c.877-2A>G	p.Tyr134Cys/splice site (in 5)	2.6	0.1	Yes	No	Yes	Yes	
50*	LI	c.1187G>A/c.1686_1695delCCACGGCAGC	p.Arg396His/p.His563fs	3.8	1.9	Yes	Yes	Yes	Yes	
51*	LI	c.1187G>A/c.1686_1695delCCACGGCAGC	p.Arg396His/p.His563fs	4	1.1	Yes	Yes	Yes	Yes	
52	LI	c.428G>A/c.428G>A	p.Arg143His/p.Arg143His	3.4	1.1	Yes	Yes	Yes	Yes	
53	LI	c.428G>A/c.428G>A	p.Arg143His/p.Arg143His	4	1	Yes	Yes	Yes	Yes	
54*	LI	c.877-2A/c.877-2A	splice site (in 5)/splice site (in 5)	2.9	1.9	Yes	No	Yes	Yes	
55*	LI	c.877-2A/c.877-2A	splice site (in 5)/splice site (in 5)	2.2	1	Yes	No	Yes	Yes	
56	LI	c.877-2A/c.1226_1227delCA	splice site (in 5)/p.Thr409fs	2.6	1.3	Yes	Yes	Yes	(Y)	
		NIPAL4 (HGVS: NM_001099287.1)								
57	LI	c.527C>A/c.889G>A	p.Ala176Asp/p.Gly297Arg	2.1	0.3	?	Yes	Yes	Yes	
58	LI	c.527C>A/c.527C>A	p.Ala176Asp/p.Ala176Asp	1.8	0	(Y)	No	Yes	No	31
59	LI	c.527C>A/c.527C>A	p.Ala176Asp/p.Ala176Asp	1.9	0.1	No	Yes	Yes	Yes	
60	LI	c.527C>A/c.527C>A	p.Ala176Asp/p.Ala176Asp	1.7	0.3	Yes	No	Yes	Yes	
61*	LI	c.527C>A/c.527C>A	p.Ala176Asp/p.Ala176Asp	2.8	0.7	No	Yes	Yes	No	31
62*	LI	c.527C>A/c.527C>A	p.Ala176Asp/p.Ala176Asp	1.8	0.9	No	No	Yes	No	31
63	CIFS	c.527C>A/c.772+1G>A	p.Ala176Asp/splice site (in 5)	1.6	0	No	No	No	Yes	31
64	CIE	c.527C>A/c.527C>A	p.Ala176Asp/p.Ala176Asp	1.2	1.2	No	No	Yes	Yes	
65	CIFS	c.527C>A/c.527C>A	p.Ala176Asp/p.Ala176Asp	1.4	0	?	?	Yes	No	
66	LI	c.527C>A/c.527C>A	p.Ala176Asp/p.Ala176Asp	2.9	1.1	?	Yes	Yes	No	
67	LI	c.527C>A/c.527C>A	p.Ala176Asp/p.Ala176Asp	2.6	1	No	No	Yes	No	
68	LI	c.527C>A/c.527C>A	p.Ala176Asp/p.Ala176Asp	2.8	0.4	No	No	Yes	Yes	

Table SI *contd.*

Pat. no.	Diagnosis	Mutations	Consequences of mutations	IS	ES	Co	Ect	Anh	PPK	Ref.
69	CIE	c.527C>A/c.527C>A	p.Ala176Asp/p.Ala176Asp	2.3	1.6	No	No	Yes	No	
70	LI	c.527C>A/c.527C>A	p.Ala176Asp/p.Ala176Asp	3	0.1	No	No	Yes	No	
71	CIE	c.527C>A/c.527C>A	p.Ala176Asp/p.Ala176Asp	2.4	2	?	Yes	Yes	Yes	
		ALOX12B (HGVS: NM_001139.2)								
72	SICI	c.1562A>G/c.1562A>G	p.Tyr521Cys/p.Tyr521Cys	0.9	0.4	Yes	No	Yes	Yes	
73	CIFS	c.1562A>G/c.1562A>G	p.Tyr521Cys/p.Tyr521Cys	1.5	0.9	?	No	(Y)	(Y)	
74	SICI	c.1385G>A/c.1385G>A	p.Gly462Asp/p.Gly462Asp	1.5	0.1	Yes	No	Yes	Yes	24
75	SICI	c.199A>T/c.1562A>G	p.Ile67Phe/p.Tyr521Cys	1.2	0.4	Yes	No	Yes	Yes	24
76*	LI	c.1562A>G/c.1562A>G	p.Tyr521Cys/p.Tyr521Cys	1.9	0.4	Yes	No	Yes	Yes	
77*	LI	c.1562A>G/c.1562A>G	p.Tyr521Cys/p.Tyr521Cys	1.9	0.5	Yes	No	Yes	Yes	
78	SICI	c.1562A>G/c.1562A>G	p.Tyr521Cys/p.Tyr521Cys	1	0.1	Yes	No	Yes	No	24
79	CIE	c.1562A>G/c.1562A>G	p.Tyr521Cys/p.Tyr521Cys	1.3	1.2	Yes	No	Yes	Yes	
80	SICI	c.1562A>G/c.1562A>G	p.Tyr521Cys/p.Tyr521Cys	1	0.1	Yes	No	Yes	Yes	24
81	SICI	c.1562A>G/c.1562A>G	p.Tyr521Cys/p.Tyr521Cys	1.2	1.7	Yes	No	Yes	(No)	24
82	SICI	c.1654+3A>G/c.1654+3A>G	splice site (in 12)/splice site (in 12)	2.9	1.1	Yes	No	Yes	Yes	24
83	CIE	c.1654+3A>G/c.1654+3A>G	splice site (in 12)/splice site (in 12)	1.4	0.8	Yes	No	Yes	Yes	
84	SICI	c.1579G>A/c.1790C>A	p.Val527Met/p.Ala597Glu	1	0.3	Yes	No	No	(Y)	24
85	LI	c.1265C>T/c.1562A>G	p.Pro422Leu/p.Tyr521Cys	1.6	0	Yes	No	(Y)	Yes	15
86	SICI	c.1562A>G/c.1562A>G	p.Tyr521Cys/p.Tyr521Cys	0.3	0	Yes	No	?	No	24
		ALOXE3 (HGVS: NM_021628.2)								
87	CIFS	c.353-1G>C/c.353-1G>C	splice site (in 3)/splice site (in 3)	1.4	0.4	No	No	(Y)	Yes	
88*	CIFS	c.631C>T/c.1889C>T	p.Arg211Term/p.Pro630Leu	1	0	No	No	Yes	No	15
89*	CIFS	c.631C>T/c.1889C>T	p.Arg211Term/p.Pro630Leu	1	1	No	No	Yes	No	15
90	SICI	c.1280T>C/c.1280T>C	p.Leu427Pro/p.Leu427Pro	1	0.1	Yes	No	Yes	No	24
91	SICI	c.700C>T/c.1889C>T	p.Arg234Term/p.Pro630Leu	0.7	0.1	Yes	No	Yes	No	24
92	SICI	c.1305+1_1305+2delGTinsTA /homozygous	splice site (in 10)/splice site (in 10)	2.2	0.1	Yes	No	Yes	Yes	15
93	LI	c.1889C>T/c.1889C>T	p.Pro630Leu/p.Pro630Leu	2.4	1	No	No	Yes	No	
94	SICI	c.327C>A/c.1889C>T	p.Cys109Term/p.Pro630Leu	1.4	0.1	?	No	No	No	24
95	CIFS	c.327C>A/c.1889C>T	p.Cys109Term/Pro630Leu	0.9	1	No	No	Yes	(Y)	
		ABCA12 (HGVS: NM_173076.2)								
96	CIE	c.4139A>G/c.4554G>A	p.Asn1380Ser/p.Trp1518Term	2.5	1.4	(Y)	Yes	(Y)	Yes	
97	HI-like	c.4896delG/c.4541G>A	p.Ser1633fs/p.Arg1514His	3.5	1.9	Yes	Yes	Yes	Yes	
98	HI-like	c.7137delG/c.7412G>A	p.Met2380fs/p.Gly2471Glu	2.9	3.9	Yes	Yes	Yes	Yes	
99	HI	c.3270T>G/c.3673C>T	p.Tyr1090Term/p.Arg1225Term	4	4	Yes	Yes	Yes	Yes	32
100	HI	c.3265G>T/c.5128+3A>G	p.Val1089Phe/splice site (in 33)	3.5	3.5	Yes	Yes	Yes	Yes	33
101	HI	c.3829+1G>A/c.3829+1G>A	splice site (in 26)/splice site (in 26)	4	3.5	Yes	Yes	Yes	Yes	33
102	HI-like	c.596G>A/1782G>A	p.Trp199Term/p.Glu594Glu	3.9	3	Yes	Yes	Yes	Yes	
103	CIE	c.1002_1004delAACinsT/c.6263T>C	p.Thr335fs/p.Leu2088Pro	1	0.7	?	No	No	No	
		SLC27A4 (HGVS: NM_005094.3)								
104	IPS	c.504C>A/c.504C>A	p.Cys168Term/p.Cys168Term	1.3	0	(Y)	No	?	No	25
105	IPS	c.504C>A/c.504C>A	p.Cys168Term/p.Cys168Term	0.2	0.1	(Y)	No	No	No	25
106	IPS	c.504C>A/c.988-2A>G	p.Cys168Term/splice site (in 7)	0.1	0.2	?	No	No	No	25
107*	IPS	c.504C>A/c.1511G>A	p.Cys168Term/p.Arg504His	1.1	0	Yes	No	No	No	34
108*	IPS	c.504C>A/c.1511G>A	p.Cys168Term/p.Arg504His	2	0.4	(Y)	No	No	No	34
		CYP4F22 (HGVS: NM_173483.3)								
109	LI	c.59dupG/c.727C>T	p.Ile21fs/p.Arg243Cys	1	1.5	Yes	No	Yes	No	
110	CIE	c.727C>T/c.727C>T	p.Arg243Cys/p.Arg243Cys	1.5	1.9	?	No	Yes	No	
111	LI	c.667C>T/c.667C>T	p.Gln223Term/p.Gln223Term	2.1	0.3	?	No	(Y)	Yes	
		PNPLA1 (HGVS: NM_001145717.1)								
112	LI	c.775+3A>T/c.775+3A>T	splice site (in 5)/splice site (in 5)	1.8	0.9	?	Yes	Yes	Yes	

[a]Discussion of the mutation findings: ***TGM1***: 29 different mutations were revealed in 111 alleles. The splice site mutation c.877-2A>G was identified in 24% of *TGM1* alleles and was found in 21 Swedish and 6 Danish alleles. The p.Ser358Arg substitution was found in 22% of *TGM1* alleles and only in Swedish patients, the other mutations found were less frequent. Most of the mutations have been previously described (4, 5, 28, 35–42), but 8 novel mutations were identified (see Table II). We also found 2 additional sequence variants, resulting in the amino acid substitutions p.Val518Met and p.Glu520Gly, which are indicated as disease-causing in HGMD. However, they were shown to be benign variants by segregation analyses in the families investigated (data not shown). Patient 45 initially revealed only one mutation, but a complementary analysis later disclosed an exon 10-14 duplication which implicates *TGM1* as culprit. A younger sister with LI has the identical genotype, whereas the mother carries the point mutation (V379L) and the father has a gene duplication. ***NIPAL4***: In total, 15 patients with *NIPAL4* mutations were found in the Scandinavian population when combining data from this study with those of a previous study (31). The previously described missense mutation c.527C>A, p.Ala176Asp (9) was the most common one in the Swedish population. It was found on 16 out of 18 (93%) Swedish alleles, and it was the only mutation found in the Danish population. Also, 2 other previously described *NIPAL4* mutations (9, 31) were found in a heterozygous state in 2 Swedish patients. ***ALOX12B***: The missense mutation c. 1562A>G, p.Tyr521Cys (43) was found to be the most common one. Together with the patients previously reported by us (24), this mutation was found on 20 out of 30 (67%) alleles in our cohort. The other mutations were also previously reported (24, 43–45). ***ALOXE3***: Mutations were found in a total of 18 alleles. Most of these were previously described (8, 24, 43), but one novel mutation was identified (see Table II). ***ABCA12***: Together with 5 mutations previously described in 6 alleles from Swedish patients (32, 33), mutations were found in 10 additional alleles, 7 of the mutations are novel (see Table II). Patient 102 carries a silent mutation affecting the last base of exon 14, which is a potential splice site. The bioinformatic tool Mutation Taster2 predicts this variant to be disease-causing (http://www.nature.com/nmeth/journal/v11/n4/full/nmeth.2890.html). ***SLC27A4***: Mutations were seen in a total of 10 alleles in the Swedish and Danish population; the p.Cys168Term mutation was the most common (70% of alleles). All mutations were previously described as causing IPS (25, 34). ***CYP4F22***: Six alleles were shown to harbour 3 different mutations; none of them has been reported previously (see Table II). ***PNPLA1***: One novel homozygous splice site mutation, c.778+3A>T, was found in a Swedish patient (see Table II). HI: harlequin ichthyosis; LI: lamellar ichthyosis; CIE: congenital ichthyosiform erythroderma; SICI: self-improving collodion ichthyosis; BSI: bathing suit ichthyosis; IPS: ichthyosis prematurity syndrome; CIFS: congenital ichthyosis with fine/focal scaling. The 4 last diagnoses are included in PI (pleomorphic ichthyosis) (18). IS: ichthyosis score; ES: erythema score; Co: collodion membrane at birth; Ect: ectropion; Anh: anhidrosis; PPK; palmoplantar keratoderma.