Supplementary Table 1. Exome sequencing coverage.

<u>101-1</u>	<u>102-1</u>	<u>103-1</u>
50x	90x	67x
42x	77x	54x
50M	82M	69M
93%	96%	94%
79%	91%	84%
	101-1 50x 42x 50M 93% 79%	101-1102-150x90x42x77x50M82M93%96%79%91%



Supplementary Figure 1. EKVP due to GJA1 mutation has onset in late infancy.

(a) Subject 102-1 is seen at 6 months of age and does not show evidence of skin disease. (b) Subject 103-1 is seen at 3 months of age and does not show evidence of skin disease. In both cases, skin lesions began to appear later in infancy with darkening, scaling, and erythema worsening over time.



Supplementary Figure 2. Histology of EKVP due to GJA1 mutation.

10X images of tissue sections from less severely affected (**a**-**c**) and more severely affected (**d**,**e**) skin are shown from EKVP affected individuals, except 101-1, from whom only less severely affected skin was available. (**a**) Biopsy of the right thigh of subject 101-1 shows mild papillomatosis, basket weave orthokeratosis, and follicular plugging. (**b**) Biopsy of a compound nevus on the lower back of subject 102-1 shows acanthosis, papillomatosis, orthohyperkeratosis, and follicular plugging as junctional nests of melanocytes. (**c**) Biopsy from the flank of subject 103-1 shows papillomatosis and orthohyperkeratosis. (**d**) More severely affected skin on the upper thigh from subject 102-1 shows acanthosis, and compact orthohyperkeratosis. (**e**) Similarly, more severely affected skin on the back of subject 103-1 shows marked acanthosis, hypergranulosis, and compact orthohyperkeratosis. (**e**) Similarly, more severely affected skin on the back of subject 103-1 shows marked acanthosis, hypergranulosis, and compact orthohyperkeratosis.



Supplementary Figure 3. Facial features of subjects with EKVP due to GJA1 mutation.

Subjects show hyperkeratosis around the eyes and mouth, and periorificial darkening. All subjects have hair with density appropriate to their age. There is no evidence of nasal or eye abnormalities or other craniofacial defects typically seen in ODDD. (a) 101-1. (b) 102-1. (c) 103-1.



Supplementary Figure 4. Enlarged white lunulae in EKVP subjects with *GJA1* mutation. Close-up images of the nails of affected individuals are shown. In subjects 101-1 and 102-1, who bear the same E227D *GJA1* mutation, there are enlarged, porcelain-white lunulae extending from the cuticle to the free edge of the nail (**a**, **b**). In subject 103-1, who has an A44V mutation, enlarged white lunulae are present and extend to within 2mm of the nail free edge (**c**).



Supplementary Figure 5. Identification of GJA1 mutations by exome sequencing.

Screen captures from the Integrative Genomics Viewer (IGV) depict aligned reads (gray arrows) from exome sequencing of three subjects. For each, base position on chromosome 6 is shown at the top (hg19 for 101-1 and 103-1, hg18 for 102-1), wild-type DNA and protein sequence is at the bottom, and mutant bases are in colored letters within the aligned reads. The total number of reads at the mutant position and the base count at that position are shown in the yellow box. Mutations are p.E227D, c.A681T (subjects 101-1 and 102-1) and p.A44V, c.C131T (subject 103-1) (NCBI RefSeg NM 000165).

GJA1_Cx43_human GJA1_Cx43_ocrangutan GJA1_Cx43_dog GJA1_Cx43_elephant GJA1_Cx43_elephant GJA1_Cx43_chicken GJA1_Cx43_chicken GJA1_Cx43_frog GJA1_Cx43_zebrafish	M G D W S A L G K L L D K V Q A Y S T A G G K V W L S V L F I F R I L L L G T A V E S A W G D E Q S A F R C N T Q Q P G M G D W S A L G K L L D K V Q A Y S T A G G K V W L S V L F I F R I L L L G T A V E S A W G D E Q S A F R C N T Q Q P G M G D W S A L G K L L D K V Q A Y S T A G G K V W L S V L F I F R I L L L G T A V E S A W G D E Q S A F R C N T Q Q P G M G D W S A L G K L L D K V Q A Y S T A G G K V W L S V L F I F R I L L L G T A V E S A W G D E Q S A F R C N T Q Q P G M G D W S A L G K L L D K V Q A Y S T A G G K V W L S V L F I F R I L L L G T A V E S A W G D E Q S A F R C N T Q Q P G M G D W S A L G K L L D K V Q A Y S T A G G K V W L S V L F I F R I L L L G T A V E S A W G D E Q S A F R C N T Q Q P G M G D W S A L G K L L D K V Q A Y S T A G G K V W L S V L F I F R I L L L G T A V E S A W G D E Q S A F R C N T Q Q P G M G D W S A L G R L L D K V Q A Y S T A G G K V W L S V L F I F R I L L L G T A V E S A W G D E Q S A F R C N T Q Q P G M G D W S A L G R L L D K V Q A Y S T A G G K V W L S V L F I F R I L L L G T A V E S A W G D E Q S A F R C N T Q Q P G M G D W S A L G R L L D K V Q A Y S T A G G K V W L S V L F I F R I L L L G T A V E S A W G D E Q S A F R C N T Q Q P G	60 60 60 60 60 60 60
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Supplementary Figure 6. Human Cx43 and orthologs.

Transmembrane domains are outlined, and conserved residues are shaded gray. Cx43 mutation sites

A44V and E227D are shaded red.