

Figure S1. Positive expression of the normally maternally expressed p57 excludes the possibility of the presence of complete androgenic tissue in the hydropic villi. (A-B) Both hydropic villi (100X and inset, 400X). C-D) Enlarged villi were positive for p57 (cyclin-dependent kinase inhibitor 1C) staining in the nuclei (200X).

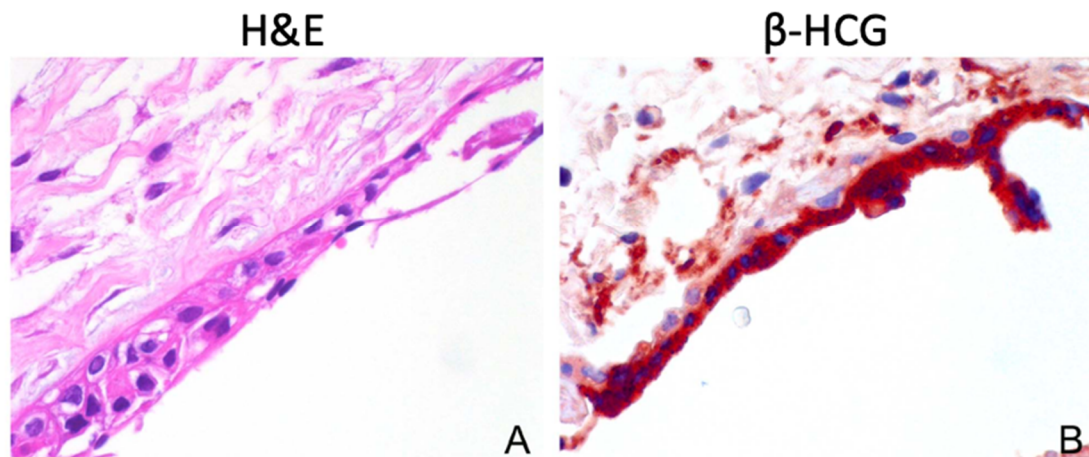


Figure S2. Significant β -HCG expression in hyperplastic cytotrophoblasts.

(A) H&E staining of hyperplastic trophoblasts (most are cytotrophoblasts, 400X). (B)

Hyperplastic trophoblasts are positive for β -HCG (human chorionic gonadotropin β -subunit) (hematoxylin stain, 400X). Microscopic (histological) descriptions: Cytotrophoblasts: small, round mononuclear cells with distinct cell borders, minimal clear or eosinophilic cytoplasm and single vesicular nuclei; Syncytial trophoblasts: multinucleated giant cells with abundant eosinophilic or basophilic cytoplasm, often with multiple intracytoplasmic vacuoles and dense pyknotic nuclei.

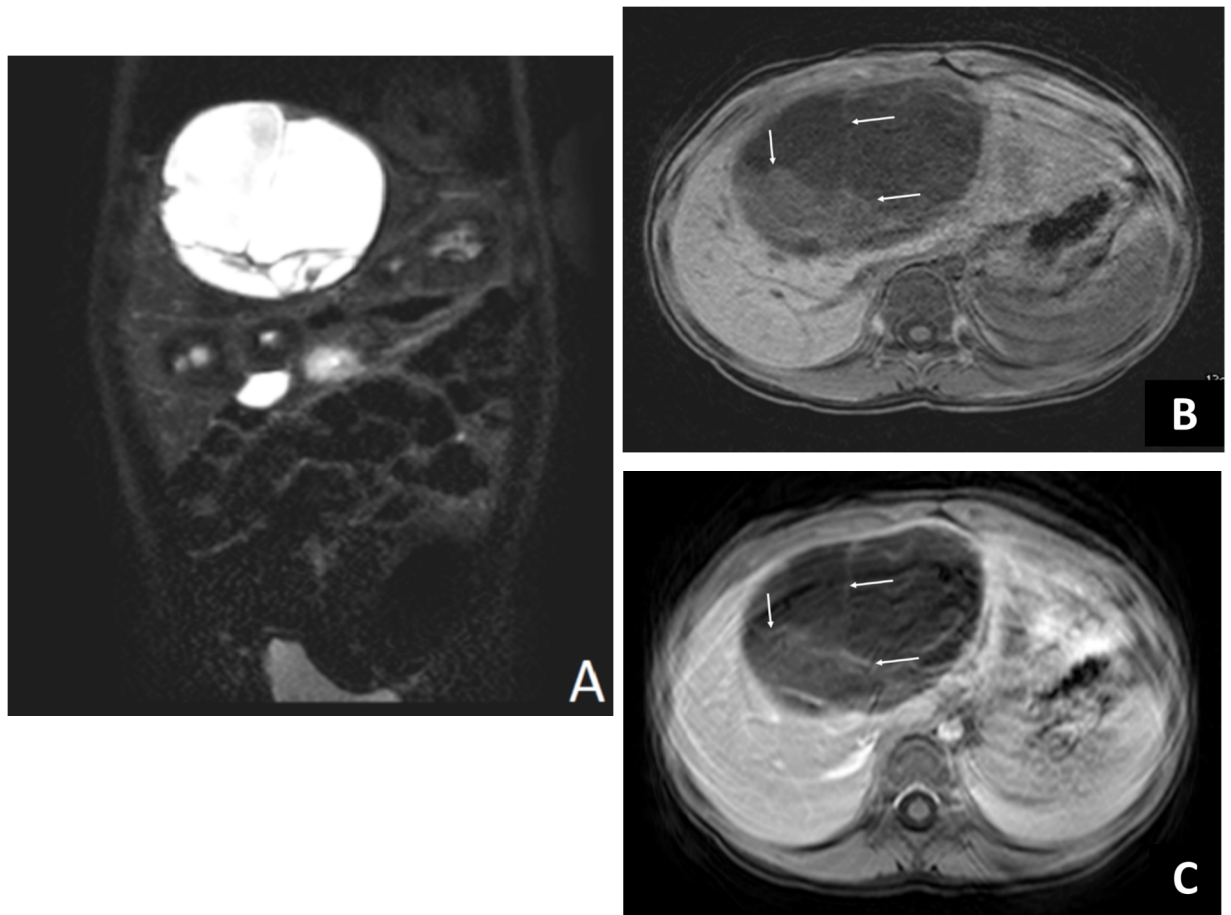


Figure S3. The presence of mesenchymal hamartoma in the living baby.

(A) Abdominal MRI coronal T2WI with fat suppression revealed multiple hepatic cystic nodules and masses compatible with the image pattern of a mesenchymal hamartoma. (B-C) Abdominal MRI axial images, including T1WI and contrast-enhanced T1WI at the level of a large hepatic mass, showed most cystic components and some enhancing inner septae (white arrows).

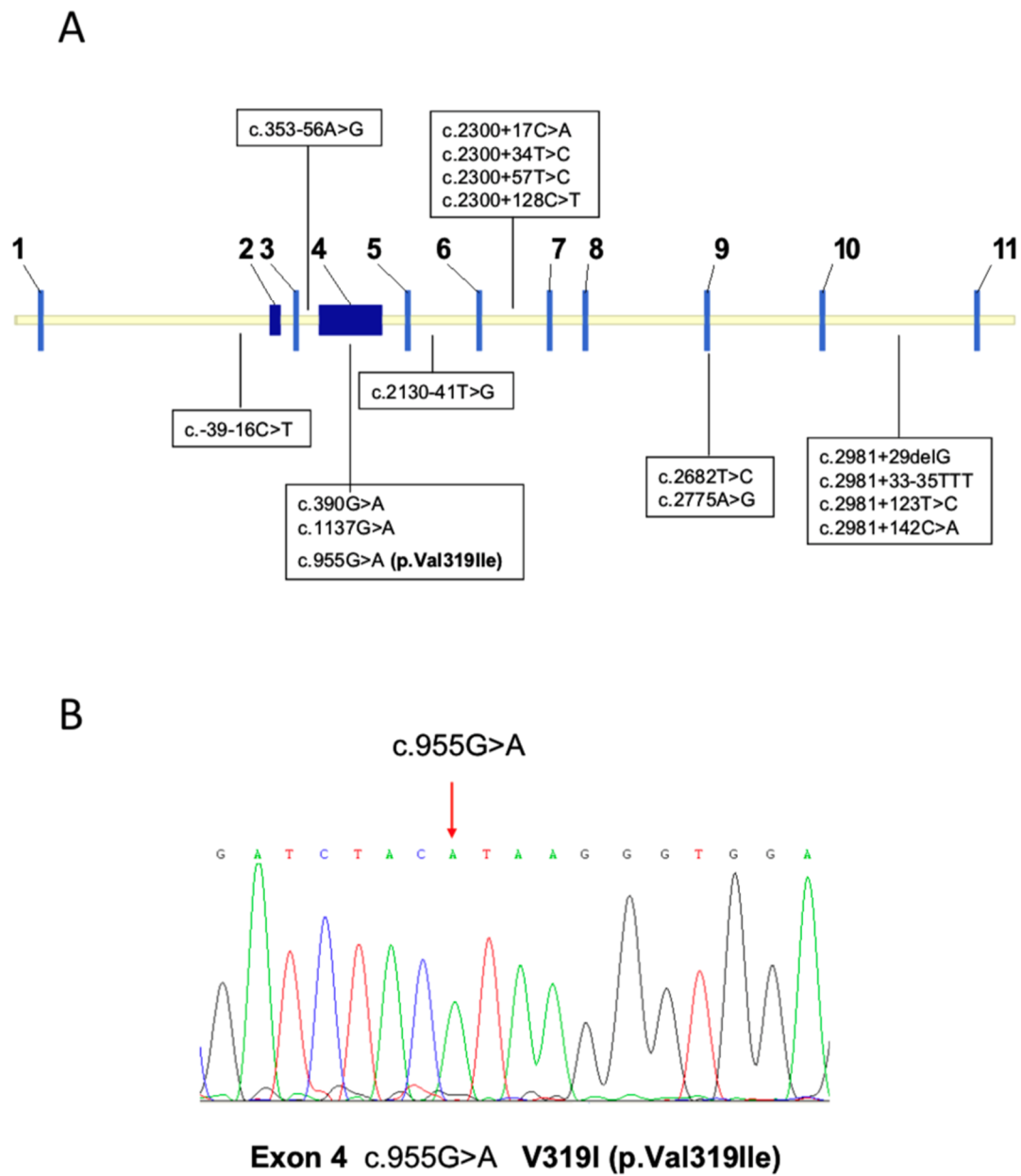


Figure S4. Identification of a nonsynonymous variant in NLRP7.

(A) Schematic representation of NLRP7 (NACHT, LRR and PYD domain-containing protein 7) mutations/variants identified in the patient compared to NC_000019.8. **(B)** Missense mutation c.955G>A in exon 4, resulting in an amino acid change from valine to isoleucine.

Supplemental Table I

Bisulfite sequencing primer list

| Primer name | Accession number | Primer sequence (5'→3') | Band size (bp) | Tm | Reference |
|-------------|------------------|---|----------------|----|-------------|
| KvDMR | AJ006345 | F-TGATGTGTTTATTATTTYGGGG R-CCCTAAAATCCCAAATCCTC | 304 | 55 | [1] |
| ZIM2/PEG3 | AC006115 | F-AAAAGGTATTAATTATTTATAGTTTGGT R-AAAAATATCCACCCTAAACTAATAA | 322 | 53 | [2] |
| SNRPN | AC009696 | F-GGTTTTTTTTTATTGTAATAGTGTTGTGGGG R-CTCCAAAACAAAAAACTTTAAAACCCAAATTC | 409 | 51 | [2] |
| SNRPN | AC009696 | F-AGGTTTTTTTTTATTGTAATAGTGTTGTGGGG R-TCCAAAACAAAAAACTTTAAAACCCAAATTC | 355 | 67 | [3] |
| PEG10 | AC069292 | F- GTGTTATGTTTTATAAATAGATAAG R- AACTCATATACCTCTACAATTC | 375 | 53 | [4] |
| H19 | AF087017 | F-TGTATAGTATATGGGTATTTTTGGAGGTTT R-TCCTATAAATATCCTATTCCCAAATAACC | 231 | 54 | [2] |
| GNAS1-1A | AL121917 | F-TTTTGTTTTTTTTTYGTTTGTTTAT R-ACAACTTCRACAACCACCTCRACAAC | 219 | 55 | [2] |
| GNAS1-AS | AL121917 | F- AATTGTGGTATGAGGAAGAGTGAT R- TCAACCATTAACAAAAATCATACC | 235 | 58 | Self-design |
| GNAS1-XLαs | AL121917 | F-AGGTTTGTAAGGTTGTTTTAGAG R- AAATCTCCATCCAAAACTACTACC | 298 | 51 | Self-design |
| NESP55 | AL12191 | F-TTTTTGTAGAGTTAGAGGGTAGGT | 343 | 55 | [2] |

| | | | | | |
|-------------------|---------------|---|-----|----|-----|
| | 7 | R-AAATAAAACAACCTCAAAATCTACC | | | |
| IGDMR (CG4) | NT_0264 37 | F- TTTTATTATTGAATTGGGTTTGTTAGT R- ACAATTCCTACTACAAAATTTCAACA | 311 | 57 | [5] |
| GTL2-DMR (CG7) | NT_0264 37 | F- TTGTGTTTGAATTTATTTTGTTT R- CCCCAAATTCTATAACAAATTACT | 168 | 55 | [5] |

PCR program:

95: 5 min--(95: 30 sec--X: 45 sec--72: 1 min) ×40--72: 10 min—4

Supplemental Table II Genomic DNA sequencing primers

| Primer name | Region | Primer sequence (5'→3') | Band size (bp) |
|-------------|--------|--|----------------|
| NLRP2 | Exon1 | CACTGCTAACTTATTTTTCAT TGGCCTTCTGAATTTCTAAA | 556 |
| | Exon2 | GGAGATAAGAGAAAGGAACAA CCAGATCTCACATGAAGAATA | 208 |
| | Exon3 | CTAATCTAGGCTTCACTACT TTCTTCCCTCTATTCTTACG | 352 |
| | Exon4 | CACATTTGTAGCTTATTTGC ATAAATGCTTTGTGTTACATAG | 305 |
| | Exon5A | CTCTCCCTTCCCTCCTCACC GCTTGGGCTAGGATGTGTGG | 406 |
| | Exon5B | AGCTGGTCTTCAGGGACTGG GCAGAGGAAACGCAGGAACA | 524 |
| | Exon5C | CTGCAGATGGAGAAGGGGGA AGCGAGGCCAAAGGAGTAGT | 456 |
| | Exon5D | ACCCTGGAGAAGGAGGAGGA TAAGGGGGCATGGGATGAGG | 544 |
| | Exon6 | CAGCCGTGATGGACACACAT GGACAGGACTCTCTCAATTCCC | 357 |
| | Exon7 | CGAGCCCCTGGTTTCCATTT CTGCATCCTGGGTCATCTGC | 378 |
| Primer | Region | Primer sequence (5'→3') | Band size |

| name | | | (bp) |
|-------|--------|--|------|
| NLRP2 | Exon8 | ACGTGGTCCTATTTCTCCCACA TCAGGCATGACCATTGCTCG | 267 |
| | Exon9 | GCTAGCCGGGAAGGTTGAAG ACCCTACTCAAACCCGGAGG | 306 |
| | Exon10 | ACTCACAGGTTCTGGGTTTGC GGGAAGTCGGCTTCACTGAT | 302 |
| | Exon11 | GCACTGGCTGCATTAACTG CAGTCTCCTACAGCAGGTCCA | 300 |
| | Exon12 | CAGGAAAGGTGACCCATGCC TCTTTTCTCTAACTTGTCAAAGCCCA | 538 |

PCR program: 95: 5 min--(95: 30 sec--55: 45 sec--72: 1 min) ×35--72: 10 min—4

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2. Judson, H.; Hayward, B.E.; Sheridan, E.; Bonthron, D.T. A global disorder of imprinting in the human female germ line. *Nature* **2002**, *416*, 539-542, doi:10.1038/416539a.
3. El-Maarri, O.; Seoud, M.; Coullin, P.; Herbiniaux, U.; Oldenburg, J.; Rouleau, G.; Slim, R. Maternal alleles acquiring paternal methylation patterns in biparental complete hydatidiform moles. *Hum Mol Genet* **2003**, *12*, 1405-1413, doi:10.1093/hmg/ddg152.
4. Monk, D.; Wagschal, A.; Arnaud, P.; Muller, P.S.; Parker-Katiraei, L.; Bourc'h, D.; Scherer, S.W.; Feil, R.; Stanier, P.; Moore, G.E. Comparative analysis of human chromosome 7q21 and mouse proximal chromosome 6 reveals a placental-specific imprinted gene, TFPI2/Tfpi2, which requires EHMT2 and EED for allelic-silencing. *Genome Res* **2008**, *18*, 1270-1281, doi:10.1101/gr.077115.108.

5. Kagami, M.; Sekita, Y.; Nishimura, G.; Irie, M.; Kato, F.; Okada, M.; Yamamori, S.; Kishimoto, H.; Nakayama, M.; Tanaka, Y.; et al. Deletions and epimutations affecting the human 14q32.2 imprinted region in individuals with paternal and maternal upd(14)-like phenotypes. *Nat Genet* **2008**, *40*, 237-242, doi:ng.2007.56 [pii]
10.1038/ng.2007.56.