SUPPLEMENTARIES

Table S1 – Primers for Exons of *UGT1A1* (NM_000463)

Exon	Variant	Primer	Sequences 5' → 3'	Product Size (bp)
1	p.I47=	UGT1A1_1_F	TCTCTGAAAGTGAACTCCCTGC	700
		UGT1A1_1_R	CTCAAATTCCAGGCTGCATGG	
3	p.Arg336Trp p.Arg346Val	UGT1A1_3_F	GCATCCACTTGTTTCATTAAGC	415
		UGT1A1_3_R	ACCTATACATCCAATCCGCCC	
5	p.His487Tyr p.Tyr486Asp	UGT1A1_5_F	TCTGGTAGTCTTCTTAAGCAGCC	446
		UGT1A1_5_R	AGTTTGGAAATGACTAGGGAATGG	

Table S2: Characteristic of Neonates in Cases and Controls Groups

Characteristic	Cases (N=116)	%	Controls (N=115)	%	p-value*
Sex					**0,950**
Male	61	52.6	60	52,2	
Female	55	47.4	55	47,8	
Birth Weight (gram)					**0,772**
Average (SD)	3125 (345,6)		3138 (371,2)		
Range	2.500−4.300		2.500−4.250		
Feeding					**0,483**
Breast milk	94	81,0	98	85,2	
Formula	-	-	-	-	
Mix of both	22	19,0	17	14,3	
Sibling with Jaundice					**0,319**
Yes	26	22,4	19	16,4	
No	90	77,6	96	80,6	
ABO Blood Group	18	15,5	9	7,75	**0,065**
Coombs Test Results					
Negative	116	100	115	100	
Positive	-		-0		

*) Chi–square, except Birth weight

Table S3 - Characteristic of the Mothers

Characteristic	Cases (n=116)	%	Controls (n=115)	%
Age (Years)				
Average (SD)	30 (6,1)	-	30,9 (5,8)	-
Median	30	-	31	-
Range	18–43	-	17–47	-
Parity				
1	54	46.6	41	35.7
2–3	50	43.1	61	53.0
≥ 4	12	10.3	13	11.3
Median	2	1.7	2	1.7
Range	1–7	-	1–7	-
Delivery method				
Cesarean delivery	57	49.1	87	75.7
Normal	53	45.7	28	24.3
Vacuum	3	2.6	0	0
Forceps	3	2.6	0	0
Consanguinity				
Yes	0	0	0	0
No	116	100	115	100

Table S4 –Results of Complete Blood Count (CBC) Test

	Cases (n=116)	Controls (n=115)
Hemoglobin (g/dL)		
Average (SD)	16.52 (2.5)	15.91 (2.0)
Range	9.5–22.90	11.6–21.6
Hematocrit (%)		
Average (SD)	46.04 (7.72)	44.68 (5.67)
Median	46.65	43.65
Range	27.0–63.10	31.7–59.6
Leukocyte (µL)		
Average (SD)	12.83 (3.60)	15.52 (5.20)
Median	12.47	15.22
Range	2.9–24.8	3.7–32.3
Reticulocyte		
Average (SD)	3.55 (2.86)	4.40 (2.44)
Median	2.94	4.65
Range	0.45–14.8	0.52–10.73
Erythrocyte		
Average (SD)	4.87 (1.12)	4.62 (0.59)
Median	4.79	4.56
Range	2.69–13.40	3.49–6.35

Table S5 - Statistic of Deep-Targeted Sequencing Results

	Cases N (%)	**Controls N (%)**
Coverage (Average)		
Variants Identified	521	498
Variants with coverage ≥ 10	481	448
Deletion	37(8)	26(6)
Insertion	21(4)	21(5)
SNP	423(88)	401(89)
* UTRs	344	349
* Intronic	38	31
* Exonic	40	21
* Downstream of the gene	1	0

SNP : Single Nucleotide Polymorphism, UTRs: Untranslated Regions

Table S6 – Risk Analysis of TA repeats in the promoter of *UGT1A1*

Allele	**Cases (n=232)**		**Controls (n=230)**		**OR**	**95%CIs**	**p-value***
	n	**%**	**n**	**%**			
TA_6	149	64.2	157	68.3			
TA_5	58	25.0	51	22.2	1.19	0.77-1.86	0.41
TA_7	25	10.8	22	9.5	1.20	0.65-2.22	0.57

*Chi−Square