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Pediatric Crohn disease patients exhibit specific ileal transcriptome and microbiome signature

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Corrigendum

Original citation: J Clin Invest. 2014;124(8):3617–3633. doi:10.1172/JCI75436. Citation for this corrigendum: J Clin Invest. 2015;125(3):1363. doi:10.1172/JCI79657. The authors recently completed an additional sample quality control process for the RNA-sequencing (RNA-seq) data reported in the manuscript that involved matching base calling from the RNA-seq data to the associated genotyping data and clinical metadata for each subject. This process identified 55 RNA-seq data files that were not linked to the correct clinical metadata. For 41 RNA-seq data files, the relabeling occurred within Crohn disease (CD) cases. For 6 files, the relabeling resulted in a change in diagnosis from ulcerative colitis (UC) to CD, while for 6 files, the relabeling resulted in a change in diagnosis from CD to UC. One file was relabeled within the non–inflammatory bowel diseases (non-IBD) control group, and for 1 file, relabeling resulted in a change from CD to non-IBD control. In addition, the authors identified 13 cases of sample duplication, 7 cases of African American race or IBD-undefined (IBD-U) diagnosis, and 20 cases in which the link between the RNA-seq data, genotype data, and clinical metadata could not be confirmed because of uncertain base calling. This included 26 CD cases, 12 UC cases, and 2 non-IBD control cases that must be excluded from the analysis. The data set for NCBI's Gene Expression Omnibus (GEO GSE57945) has […]

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Correction of the mislabeling did not result in a significant difference in the clinical and demographic features of the cohort (Table 1). Following the correction, 1,159 of 1,281 (90%) genes from the original publication for the core ileal CD (iCD) gene list (Supplemental Table 3) were still determined to be significantly and differentially expressed between 2 independent groups of iCD versus control; 155 of 179 (87%) genes from the publication for the colon-only CD (cCD) versus UC gene list (Supplemental Table 12) were still determined to be significantly and differentially expressed between cCD and UC; and 342 of 345 (99%) genes from the publication for the iCD without deep ulcers (iCD-noDU) versus iCD with deep ulcers (iCD-DU) gene list (Supplemental Table 13) were still determined to be significantly and differentially expressed between iCD-noDU and iCD-DU. This included upregulation of *DUOX2* and suppression of *APOA1* within the top 5 up- and downregulated genes within the core ileal CD gene list and maximal suppression of *APOA1* within the cCD versus UC comparison and the iCD-DU versus iCD-noDU comparison.

The authors regret the errors.

Table 1. RISK RNA-seq cohort clinical and demographic characteristics

	Ctl *n* = 42	UC1 *n* = 38	cCD1 *n* = 33	UC2 *n* = 24	cCD2 *n* = 23	iCD1 *n* = 81	iCD2 *n* = 81	All iCD *n* = 162	iCD-DU *n* = 76	iCD-noDU *n* = 86
Mean (SD) age (yr)	11 (3)	12 (3)	12 (3)	14 (3)	13 (3)	12 (3)	12 (3)	12 (3)	12 (3)	12 (3)
Male sex (%)	62	47	52	71	61	60	57	59	58	60
MED ethnicity (3 of 4 grandparents) (%)	95	88	91	88	83	85	88	86	89	84
Perianal involvement (%)	0	0	18	0	26	20	14	17	17	17
Ileal deep ulcers (%)	0	0	0	0	0	52	42	47	100	0
Body mass index Z<-2 (%)	0	3	18	4	17	20	17	19	23	15
PCDAI at diagnosis										
≤10 (inactive, %)	NA	NA	13	NA	5	11	9	10	13	7
11 to 30 (mild, %)	NA	NA	32	NA	33	35	47	41	32	49[A]
>30 (moderate-severe, %)	NA	NA	55	NA	62	54	44	49	55	

Differences between selected groups were tested by ANOVA for continuous variables and χ^2 for dichotomous variables. Ctl, control; MED, mixed European descent. [A]$P = 0.03$ vs. iCD-DU.