Supplementary files for:

**Blood RNA sequencing confirms upregulated BATF2 and FCGR1A expression in children with autism spectrum disorder**

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**Supplementary Table S1:** Primers used for real-time qPCR.

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**Supplementary Table S2:** Real-time qPCR analyses compared PBMC gene expression levels in children with ASD vs. either all neurotypical controls (left); only their neurotypical siblings (middle) or only unrelated neurotypical children (right). N shows numbers for neurotypical controls/ASD for each comparison. Outlier samples were removed. Note that SERPING1 was the only significant gene showing differential expression in PBMCs from the ASD group and their neurotypical siblings (bold fonts).

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<tr>
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<th>ASD vs. sibling controls</th>
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**Supplementary Table S3:** Summary of Spearman correlation test of top 10 RNA-seq genes and serum endocannabinoids in (a) ASD samples only; (b) neurotypical controls; (c) ASD and neurotypical controls combined. Outlier samples were removed. P-value is two-tailed; N, XY pairs. Serum endocannabinoid levels are taken from Aran et al. 2019. Correlations with p<0.05 are shown in bold fonts.

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<th>BATF2</th>
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</table>
**Supplementary Figure. S1:** Real-time qPCR measurements for whole blood RNA expression levels in ASD and control children (Israeli cohort). Box plots show mean ± SEM RNA levels for neurotypical control vs. ASD whole blood samples. Outliers were removed and analysis was done using a non-parametric Mann Whitney test. As shown, p values for gene expression (qPCR measurements) in ASD vs. control blood samples indicated lack of significant differences for the presented genes.
**Supplementary Figure. S2:** RNA expression by real-time qPCR in PBMCs from children with ASD and all neurotypical control children (U.S. cohort). Graphs show mean ± SED for control and ASD samples for each of the top 10 genes found by RNA-seq of whole blood samples from the Israeli cohort. Outliers were removed and analysis was done using a non-parametric Mann Whitney test. No significant differences in gene expression were found between ASD and control PBMCs (p>0.1 for the 10 tested genes).
**Supplementary Figure S3:** Correlations for whole blood \(LY6E\) expression levels with serum palmitoylethanolamide (PEA) levels in children with ASD and neurotypical controls (Israeli cohort). Correlations are shown for (a) neurotypical control children (N=19); (b) ASD children (N=30). The r and p values for each correlation plot (Spearman test) are shown in each panel. PEA levels were taken from Aran et al. 2019. See Methods for further details.
Supplementary Figure S4: Correlations for whole blood mRNA expression levels with serum endocannabinoid levels in children with ASD and neurotypical controls combined (Israeli cohort). Correlations are shown for (a) FCGR1A and palmitoylethanolamide (PEA); (b) LY6E and PEA; (c) FBXO6 and arachidonic acid (AA); (d) ISG15 and AA; (e) LINC00869 and oleoyl serine (OS); (f) LY6E and anandamide (AEA). The r and p values for each correlation plot (Spearman test) are shown in each panel. Open circles indicate control children, while closed circles indicate ASD children; individual findings for whole blood mRNA expression and serum EC levels were combined for controls (open circles) and children with ASD (closed circles) for calculating r and p values for each correlation. Endocannabinoid levels were taken from Aran et al. 2019.