**Maternal and child FADS genotype as determinants of cord blood long chain polyunsaturated fatty acid (LCPUFA) concentrations in the Seychelles Child Development Study**

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| **Online Resource 1:** Maternal and child genotype distribution in Seychellois NC2 participants | | | | |
|  |  | ***n* (%)** | | |
| **SNP** | ***n*** | **Homozygous major** | **Heterozygous** | **Homozygous minor** |
| **Maternal FADS** |  |  |  |  |
| ***FADS1* rs174537** | 1062 | 723 (68.1) GG | 303 (28.5) GT | 36 (3.4) TT |
| ***FADS1* rs174561** | 1062 | 762 (71.8) TT | 268 (25.2) TC | 32 (3.0) CC |
| ***FADS2* rs174575** | 1062 | 663 (62.4) CC | 346 (32.6) CG | 53 (5.0) GG |
| ***FADS1-FADS2* rs3834458** | 1062 | 746 (70.2) TT | 285 (26.8) Tdel | 31 (2.9) deldel |
| **Child FADS** |  |  |  |  |
| ***FADS1* rs174537** | 916 | 600 (65.5) GG | 275 (30.0) GT | 41 (4.5) TT |
| ***FADS1* rs174561** | 916 | 627 (68.4) TT | 258 (28.2) TC | 31 (3.4) CC |
| ***FADS2* rs174575** | 916 | 553 (60.4) CC | 320 (34.9) CG | 43 (4.7) GG |
| ***FADS1-FADS2* rs3834458** | 916 | 613 (66.9) TT | 268 (29.3) Tdel | 35 (3.8) deldel |
| *n for maternal FADS according to those participants with both genotype and cord PUFA data; n for child FADS according to those participants with both genotype and cord PUFA data* | | | | |

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| **Online Resource 2:** Minor allele frequency (MAF) of single nucleotide polymorphisms (SNPs) genotyped in Seychellois NC2 participants and other populations | | | | | | | |
|  |  |  | **Population** | | | | |
| **SNP** | **Gene** | **Allele** | **NC2 Mothers** | **NC2 Children** | **European** | **African** | **Global** |
| rs174537 | FADS1 | G/T | 0.177 | 0.195 | 0.349 | 0.025 | 0.303 |
| rs174561 | FADS1 | T/C | 0.156 | 0.175 | 0.303 | 0.02 | 0.28 |
| rs174575 | FADS2 | C/G | 0.213 | 0.222 | 0.255 | 0.21 | 0.209 |
| rs3834458 | FADS1-2 | T/del | 0.163 | 0.185 | 0.346 | 0.021 | 0.296 |
| *MAF according to “1000Genomes” data available from dbSNP at www.ncbi.nlm.nih.gov* | | | | | | | |

**Online Resource 3: Correlations between maternal and cord PUFA status**

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|  | **Cord PUFA** | | | | | | | | | | | |
| **Maternal** | **LA** | **ALA** | **AA** | **EPA** | **DHA** | **n-6:n-3 ratio** | **EPA+DHA** | **AA:LA** | | **EPA:ALA** | | **DHA:ALA** |
| **LA** | 0.100\*\* | -0.015 | -0.047 | 0.001 | -0.058 | 0.051 | -0.055 | | -0.085\*\* | | 0.006 | 0.011 |
| **ALA** | -0.014 | 0.009 | -0.091\*\* | 0.013 | -0.028 | -0.049 | -0.026 | | -0.077\* | | 0.029 | -0.004 |
| **AA** | 0.087\*\* | -0.019 | -0.038 | -0.017 | 0.049 | -0.027 | 0.044 | | -0.066\* | | -0.014 | 0.036 |
| **EPA** | 0.027 | -0.041 | -0.086\*\* | 0.071\* | 0.067\* | -0.096\*\* | 0.075\* | | -0.091\*\* | | 0.090\*\* | 0.077\* |
| **DHA** | 0.069\* | -0.038 | -0.076\* | 0.070\* | 0.108\*\*\* | -0.106\*\* | 0.114\*\*\* | | -0.094\*\* | | 0.091\*\* | 0.098\*\* |
| **n-6:n-3 ratio** | 0.010 | 0.023 | 0.049 | -0.066\* | -0.128\*\*\* | 0.135\*\*\* | -0.133\*\*\* | | 0.038 | | -0.085\*\* | -0.082\*\* |
| **EPA+DHA** | 0.068\* | -0.040 | -0.080\*\* | 0.073\* | 0.109\*\*\* | -0.109\*\*\* | 0.115\*\*\* | | -0.098\*\* | | 0.095\*\* | 0.101\*\* |
| **AA:LA** | 0.028 | -0.007 | 0.004 | -0.018 | 0.087\*\* | -0.052 | 0.081\*\* | | -0.003 | | -0.015 | 0.025 |
| **EPA:ALA** | 0.039 | -0.046 | -0.002 | 0.050 | 0.080\*\* | -0.039 | 0.085\*\* | | -0.017 | | 0.055 | 0.070\* |
| **DHA:ALA** | 0.080\* | -0.039 | -0.052 | 0.062\* | 0.109\*\*\* | -0.088\*\* | 0.113\*\*\* | | -0.077 | | 0.078\*\* | 0.095\*\* |
| *Pearson correlation coefficients; All cord PUFA were logged after adding a constant to all +1; P<0.05 considered statistically significant; \*P<0.05, \*\*P<0.01; \*\*\*P<0.001* | | | | | | | | | | | | |