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| **Supplementary Table 1S**. Overview of alleles that will interfere with interpretation of the prenatal ABO assay | | |
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| O alleles with 796C>A; 803G>C (shown in bold). The 796C>A and 803G>C double substitutions in O alleles will be positive for blood group B in the B primers: | | |
| *ABO\*O.01.24* | 106G>T; 188G>A; 189C>T; 261delG; 297A>G; 526C>G; 657C>T; 703G>A; **796C>A**;**803G>C**; 930G>A | Val36Phe; Arg63His; Thr88Profs\*31 |
| *ABO\*O.01.41* | 261delG; 297A>G; 526C>G; 657C>T; 703G>A; **796C>A**; **803G>C**; 930G>A | Thr88Profs\*31 |
| *ABO\*O.11* | 297A>G; 505\_507delCAG; 526C>G; 657C>T; 703G>A; **796C>A**;**803G>C**; 930G>A | Gln169del; Arg176Gly; Gly235Ser; Leu266Met; Gly268Ala |
| *ABO\*O.12* | 297A>G; 526C>G; 563G>A; 657C>T; 703G>A; **796C>A**; **803G>C;**930G>A | Arg176Gly; Arg188His; Gly235Ser; Leu266Met; Gly268Ala |
|  |  |  |
| O alleles without the characteristic 261delG deletion, excluding the *ABO\*O.02* and *ABO\*O.03* alleles: | | |
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| *ABO\*O.04.01* | 87\_88insG | Val30Glyfs\*27 |
| *ABO\*O.05* | 322C>T | Gln108Ter |
| *ABO\*O.06* | 542G>A | Trp181Ter |
| *ABO\*O.07* | 467C>T; 893C>T | Pro156Leu; Ala298Val |
| *ABO\*O.08* | 927C>A | Tyr309Ter |
| *ABO\*O.09.01* | 646T>A; 681G>A; 771C>T; 829G>A | Phe216Ile; Val277Met |
| *ABO\*O.09.02* | 297A>G; 646T>A; 681G>A; 771C>T; 829G>A | Phe216Ile; Val277Met |
| *ABO\*O.10* | 66\_67insG | Phe23Valfs\*34 |
| *ABO\*O.11* | 297A>G; 505\_507delCAG; 526C>G; 657C>T; 703G>A; 796C>A; 803G>C; 930G>A | Gln169del; Arg176Gly; Gly235Ser; Leu266Met; Gly268Ala |
| *ABO\*O.12* | 297A>G; 526C>G; 563G>A; 657C>T; 703G>A; 796C>A; 803G>C; 930G>A | Arg176Gly; Arg188His; Gly235Ser; Leu266Met; Gly268Ala |
| *ABO\*O.13* | 452T>G | Val151Gly |
| *ABO\*O.14* | 635T>A | Val212Glu |
| *ABO\*O.15* | 793T>C | Tyr265His |
| *ABO\*O.16* | 106G>T; 188G>A; (203+1\_204-1)\_(\*490\_?)del | ? |
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|  |  |  |

Data taken from Erythrogene v0.8 (27 Nov 2017), <http://www.erythrogene.com> [27] and ABO (ISBT 001) blood group alleles v1.1 171023.

Allele frequencies for the *ABO\*O.01.24* have been estimated as follows: 1000 Genomes: 0.82%; Africa: 0.45%; America: 1.44%; East Asia: 0%; Europe: 2.39%; South Asia: 0.1%. Allele frequencies for the *ABO\*O.16* have been estimated as follows: 1000 Genomes: 0.4%; Africa: 1.29%; America: 0.43%; East Asia: 0%; Europe: 0%; South Asia: 0%.