**Supplementary Table 1.** Excluded studies and reasons

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| **Authors** | **Year** | **Title** | | | **Reasons for the exclusion** |
| Sparks et al. | 2020 | Exome Sequencing for Prenatal Diagnosis in Nonimmune Hydrops Fetalis | | | 15 isolated increased nuchal translucencies. No diagnostic genetic variant could be extracted from this SR |
| ﻿Pauta et al. | 2019 | ﻿Single gene, gene panel and exome sequencing applied in structurally abnormal fetuses with a normal chromosomal microarray analysis | | | No isolated increased NT |
| ﻿Borrell et al. | 2019 | | "﻿Single gene, gene panel and exome sequencing applied in | ﻿ No isolated increased NT, no diagnostic genetic variant could be extracted from this SR | | |
| Lord et al. | 2019 | | ﻿Prenatal exome sequencing analysis in fetal structural  anomalies detected by ultrasonography (PAGE): a cohort study | Sample size included in Mellis et al., 2021 study | | |
| ﻿Petrovski et al. | 2019 | | ﻿Whole-exome sequencing in the evaluation of fetal  structural anomalies: a prospective cohort study | Sample size included in Mellis et al., 2021 study | | |

NT: nuchal translucency; SR: systematic review