**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 instructurally abnormal fetuses with a normal chromosomalmicroarray 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 structuralanomalies 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 fetalstructural anomalies: a prospective cohort study | Sample size included in Mellis et al., 2021 study |

NT: nuchal translucency; SR: systematic review