

Supplementary material

Supplementary Figure 1A: Traffic light plot for the risk of bias assessment for the included studies

		Risk of bias domains					
		D1	D2	D3	D4	D5	Overall
Study	Attam 2015	+	+	+	+	+	+
	Bansal 2017	+	+	+	+	+	+
	Weston 2017	+	+	+	+	+	+
	Bang 2018	+	+	+	+	+	+
	Saxena 2018	-	+	+	+	+	-
	Lee 2018	-	+	+	+	+	-
	Cheng 2019	+	+	+	+	+	+
	Di Mitri 2019	+	+	+	+	+	+
	Moreira 2020	+	+	+	+	+	+
	Tong 2020	-	+	+	-	+	-
	Wang 2020	+	+	+	+	+	+
	Bang 2020	+	+	+	+	+	+
	Takasumi 2021	+	+	+	-	+	-
	Ladd 2021	+	+	-	+	+	-
	Zhou 2021	-	+	+	+	+	-
	Paik 2021	+	+	+	+	+	+

Domains:

D1: Bias arising from the randomization process.

D2: Bias due to deviations from intended intervention.

D3: Bias due to missing outcome data.

D4: Bias in measurement of the outcome.

D5: Bias in selection of the reported result.

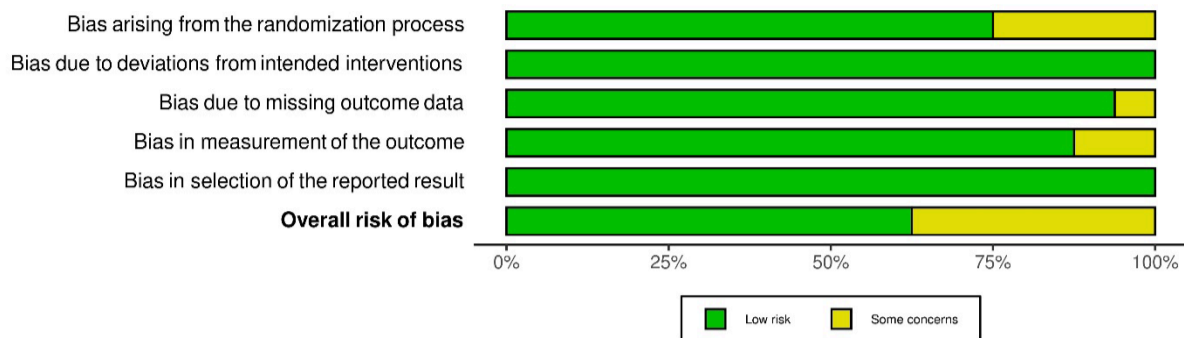
Judgement

- Some concerns

+ Low

Supplementary material

Supplementary Figure 1B: Summary plot for the risk of bias assessment for the included studies



Supplementary table 1: Definition of outcomes used in the included studies

Authors	Adequacy	Cellularity	Bloodiness
Attam 2015 ^[18]	0 = inadequate aspirate for the cytopathologist to make a diagnosis; 1 = adequate aspirate	0 = no cells; 1 = sparsely cellular; 2 = moderately cellular; 3 = highly cellular	0 = free of blood; 1 = contaminated with red blood cells; 2 = blood clots present
Bansal 2017 ^[19]	0 = inadequate aspirate for the cytopathologist to make a diagnosis; 1 = adequate aspirate	0 = no cells; 1 = sparsely cellular; 2 = moderately cellular 3 = highly cellular	0 = no blood; 1 = contaminated with red blood cells; 2 = blood clots present
Weston 2017 ^[20]	Cellularity score < 2 = inadequate; Cellularity score 2 – 3 = adequate	2 = estimated cell count > 500 cells; 3 = estimated cell count > 1000 cells	
Bang 2018 ^[21]	Adequacy defined as FNA sample being of sufficient quality to render a preliminary diagnosis		mild < 33%; moderate 33-66%; severe > 66%
Lee 2018 ^[22]	Adequacy defined as FNA sample being of sufficient quality to render a preliminary diagnosis	fair, <10 cell nests; good, 10 to 20 cell nests; excellent, >20 cell nests	3 or fewer blood clots (<25% of the slide) 4 – 6 blood clots (25–50% of the slide) 7 or more blood clots (> 50% of the slide)
Saxena 2018 ^[23]	Adequacy defined as FNA sample being of sufficient quality to render a preliminary diagnosis		
Cheng 2019 ^[24]		0 (absence or < 10% of cell groups); 1+ (10–50% of cell groups); 2+ (50–70% of cell groups); 3+ (70–90% of cell groups)	1+ (red blood cells 10–50%); 2+ (red blood cells 50–70%); 3+ (red blood cells 70–90%)

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Di Mitri 2019 ^[25]			high-moderate contamination ($\geq 33\%$: interference with the pathological diagnosis); none-mild contamination ($\leq 33\%$: non-interference with the pathological diagnosis)
Moreira 2020 ^[26]	Adequacy defined as sample containing adequate cellular material for a conclusive histological diagnosis	0 = no cells; 1 = sparsely cellular; 2 = moderately cellular 3 = highly cellular	'none', absent blood cells; 'low', a few blood cells without affecting histological diagnosis; 'moderate', partially obscured by blood cells but possible histological diagnosis; 'high', hidden by blood cells leading to inadequate interpretation
Tong 2020 ^[27]	0=no valid specimen; 1=insufficient tissue to diagnose; 2=moderate tissue but still diagnosable; 3=sufficient tissue for diagnosis		0=no blood contamination; 1=slight blood contamination, sparseness of RBCs; 2=moderate blood contamination, monolayer of RBCs; 3=significant blood contamination, cell clustering or stratification
Wang 2020 ^[28]	score 0 = sample with no material; score 1 = samples did not provide histological information; score 2 = limited histological assessment; score 3 = architecturally intact piece of tissue with a length of at least 550 μm Score of 2 or 3 = adequate	Score 2 = moderate Score 3 = high	score 3 = < 25%; score 2 = 25%– 50 %; score 1 = >50%; score 0 = no material
Bang 2020 ^[29]		Low Intermediate High	
Takasumi 2021 ^[30]	Adequacy defined as FNA sample being of sufficient quality to render a preliminary diagnosis	0 = no cells; 1 = sparsely cellular; 2 = moderately cellular; 3 = highly cellular	
Ladd 2021 ^[31]	Adequacy defined as FNA sample being of sufficient quality to render a preliminary diagnosis	0—insufficient material for interpretation; 1—sufficient material for limited cytological	1—blood present; 2—blood clots present

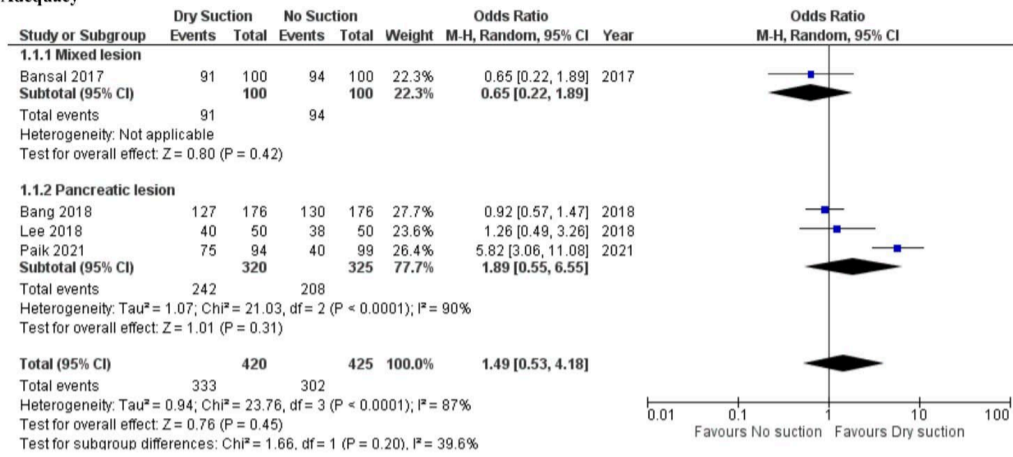
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		interpretation, but may not be representative of the entire lesion; 2—sufficient material for adequate cytological interpretation	
Zhou 2021 ^[32]	Grade A – existing core tissue (defined as an architecturally intact piece of tissue with a long axis measuring at least 550 µm) Grade B – existing core fragments, which does not meet the criteria for architecturally intact histology, but can still yield a diagnosis based on cell morphology; Grade C – no lesion tissue found, and a diagnosis cannot be made based on the sample	Grade A, > 4 clusters, with a minimum of 10 cells in each cluster; Grade B, approximately 2–4 clusters, with a minimum of 10 cells in each cluster; Grade C, < 2 clusters or no cellular smear	
Paik 2021 ^[33]	Poor—no cellular material or inconspicuous whitish core mixed with blood; Fair—presence of whitish core; Good—whitish core with the presence of a wormlike tissue architecture		

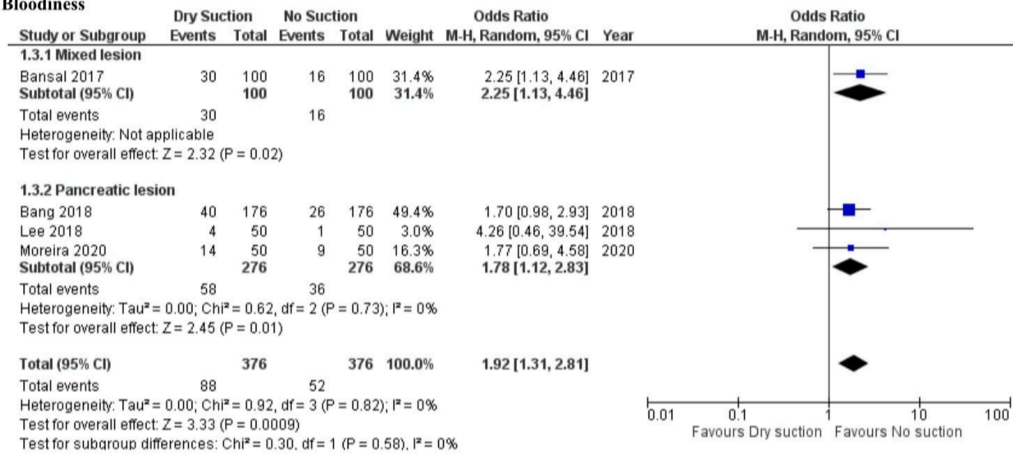
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Supplementary Figure 2A: Pair-wise meta-analysis for dry suction vs. no suction based on lesion type

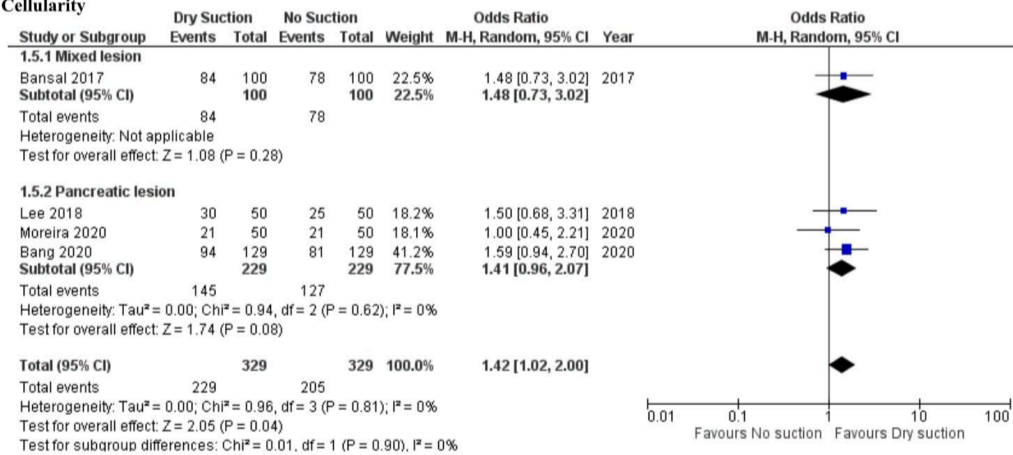
(A) Adequacy



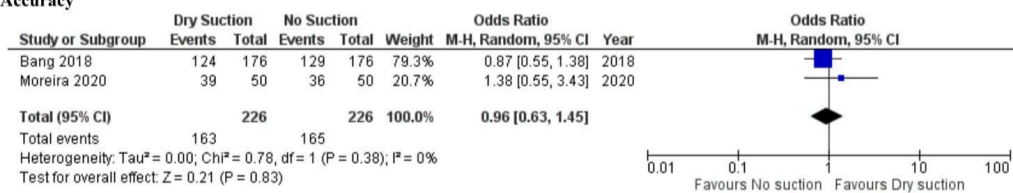
(B) Bloodiness



(C) Cellularity



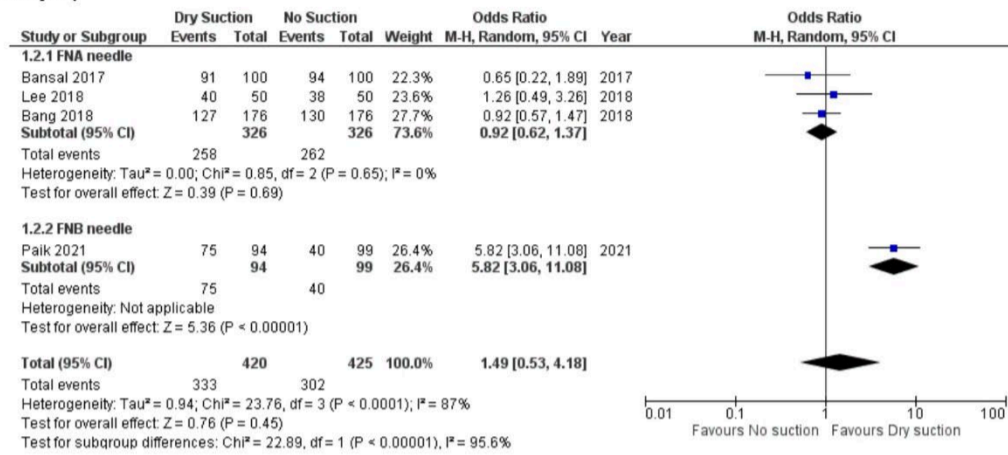
(D) Accuracy



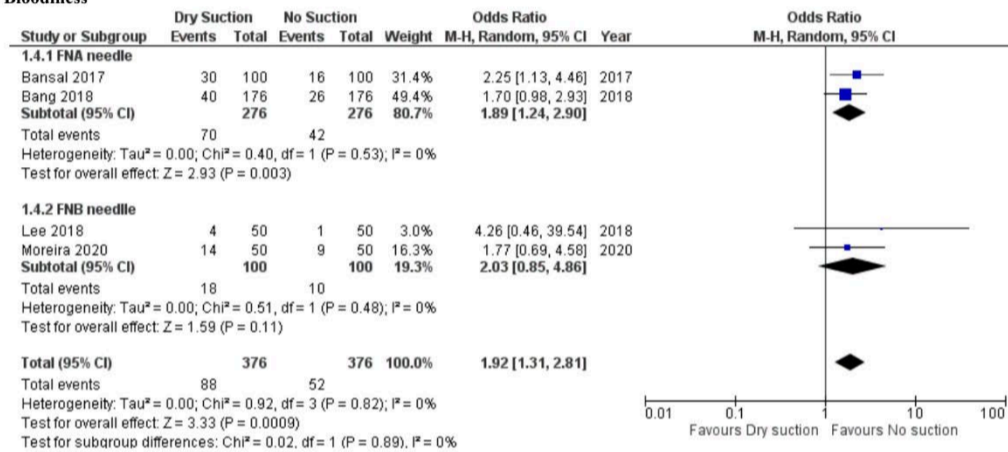
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Supplementary Figure 2B: Pair-wise meta-analysis for dry suction vs. no suction based on needle type

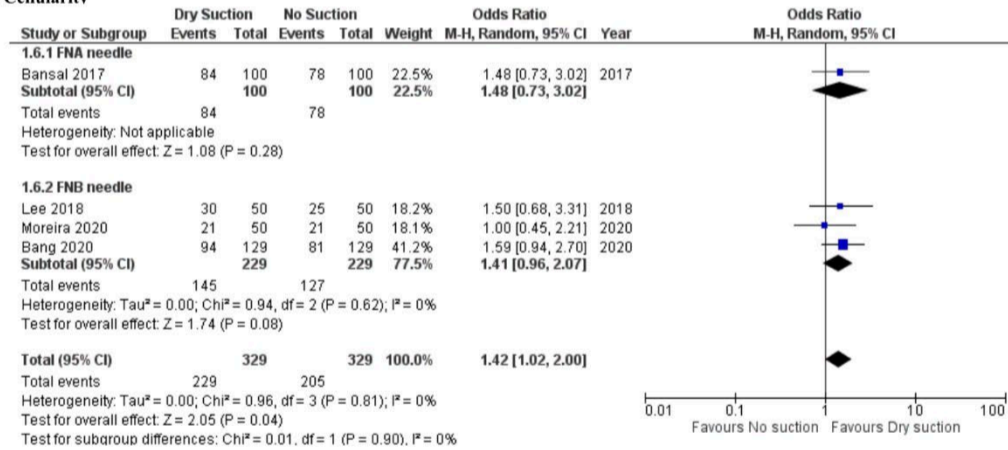
(A) Adequacy



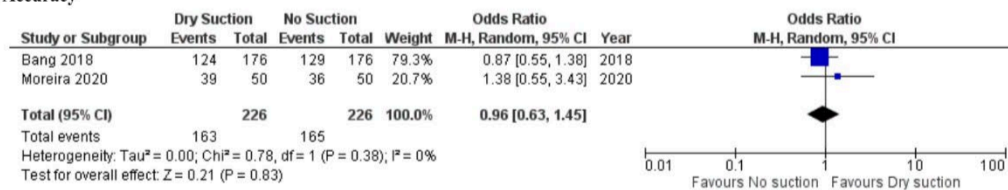
(B) Bloodiness



(C) Cellularity



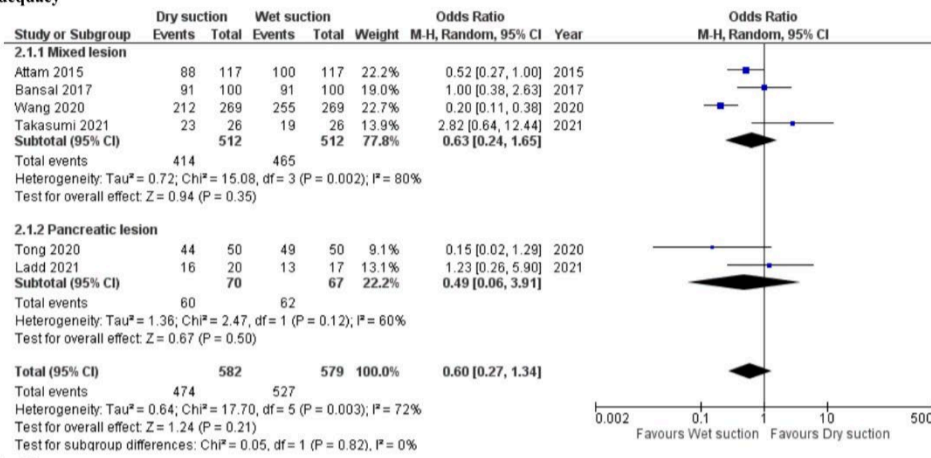
(D) Accuracy



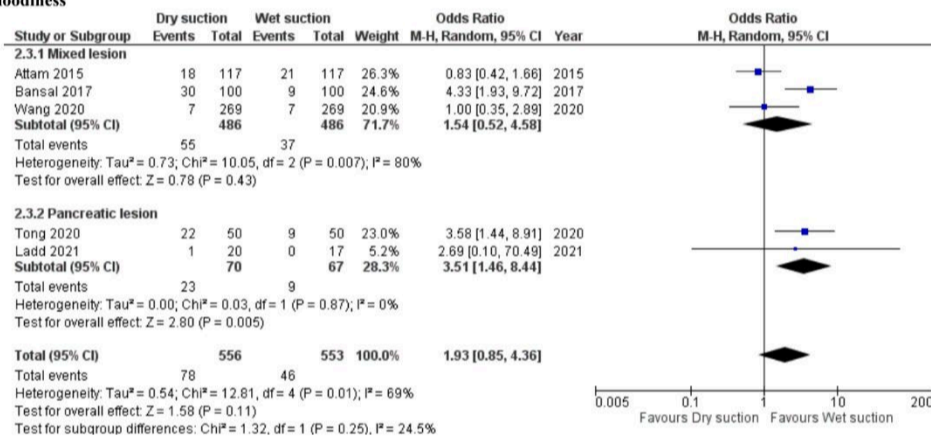
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Supplementary Figure 3A: Pair-wise meta-analysis for dry suction vs. wet suction based on lesion type

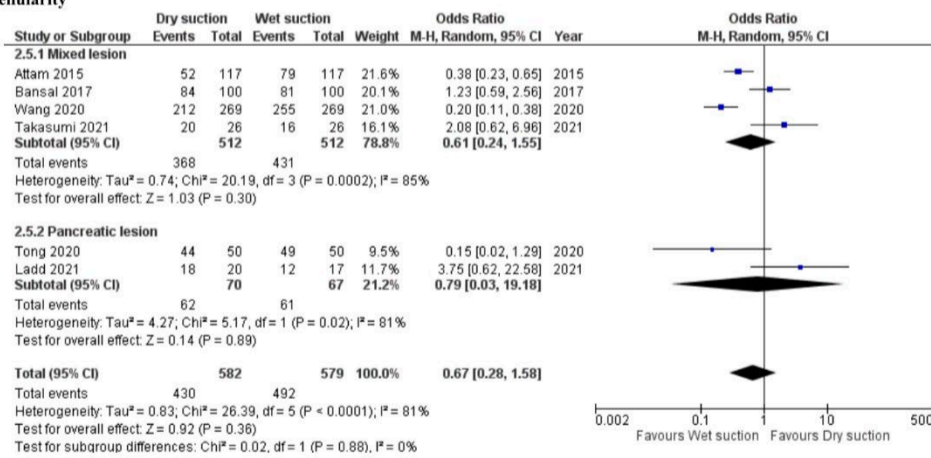
(A) Adequacy



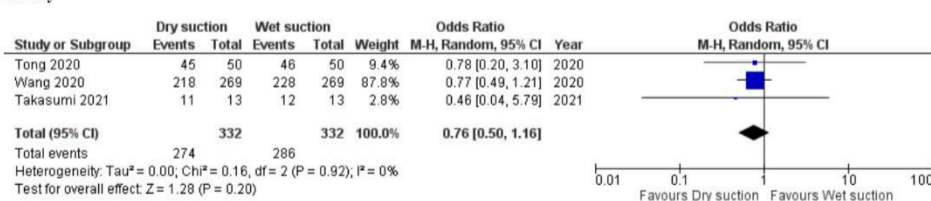
(B) Bloodiness



(C) Cellularity



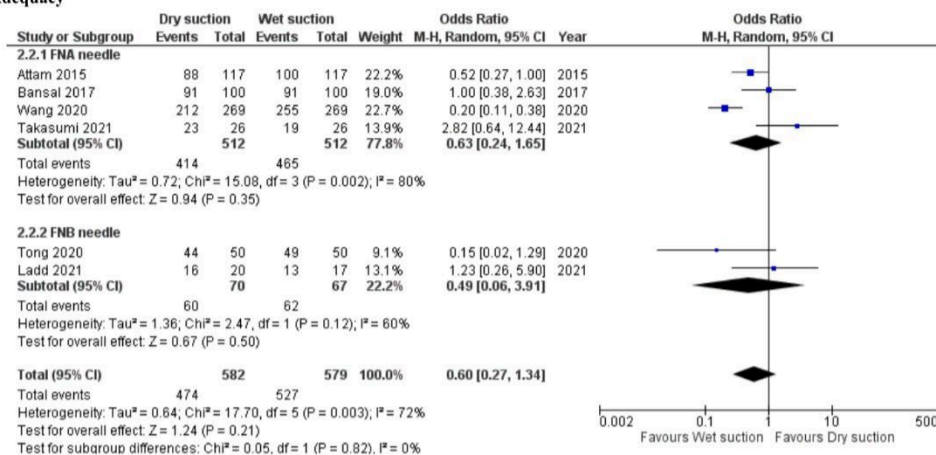
(D) Accuracy



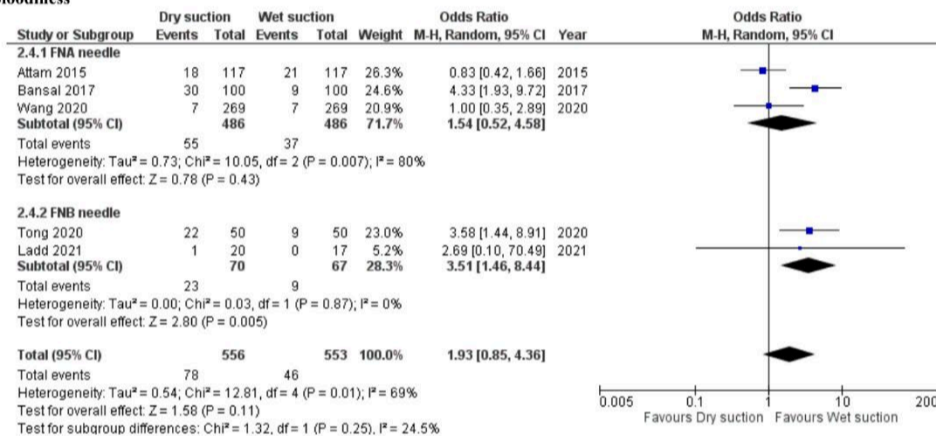
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Supplementary Figure 3B: Pair-wise meta-analysis for dry suction vs. wet suction based on needle type

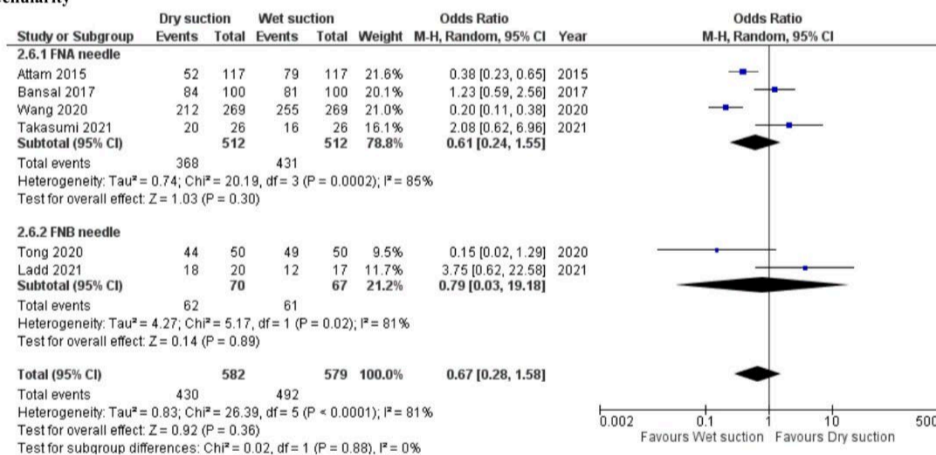
(A) Adequacy



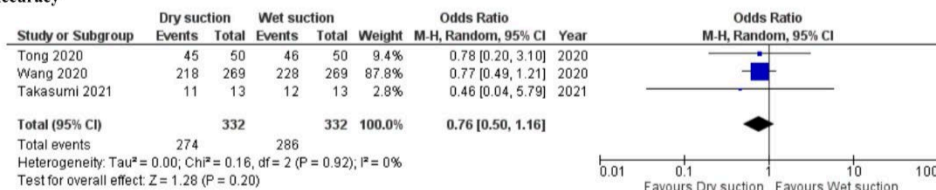
(B) Bloodiness



(C) Cellularity



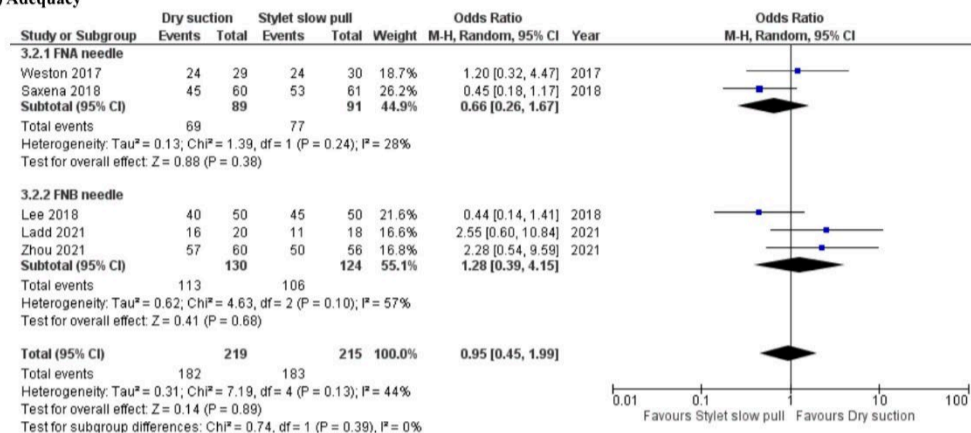
(D) Accuracy



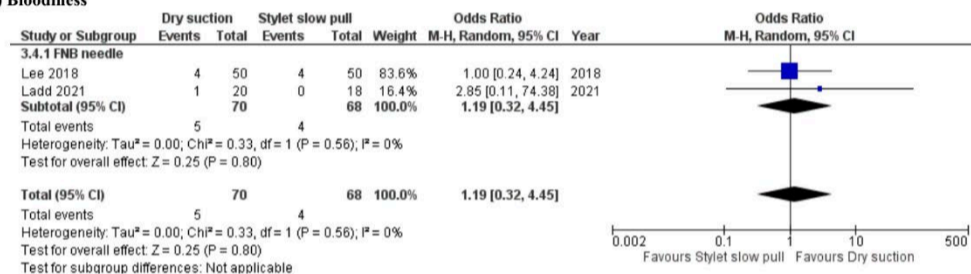
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Supplementary Figure 4: Pair-wise meta-analysis for dry suction vs. stylet slow pull based on needle type

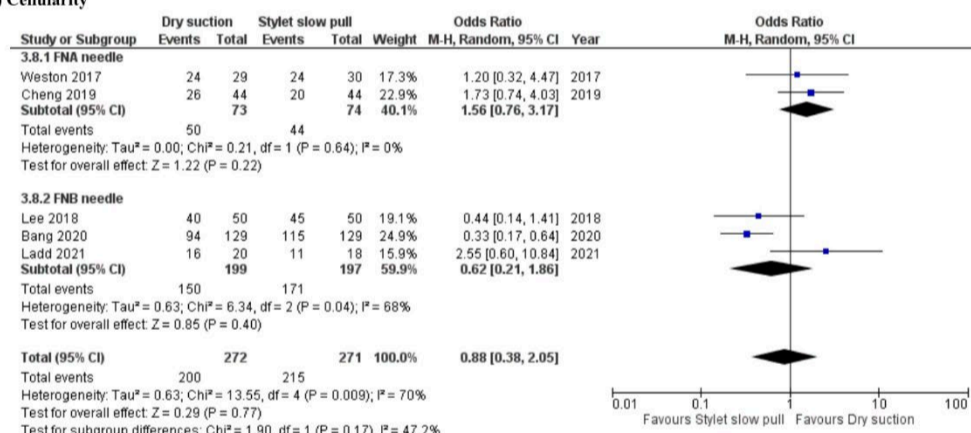
(A) Adequacy



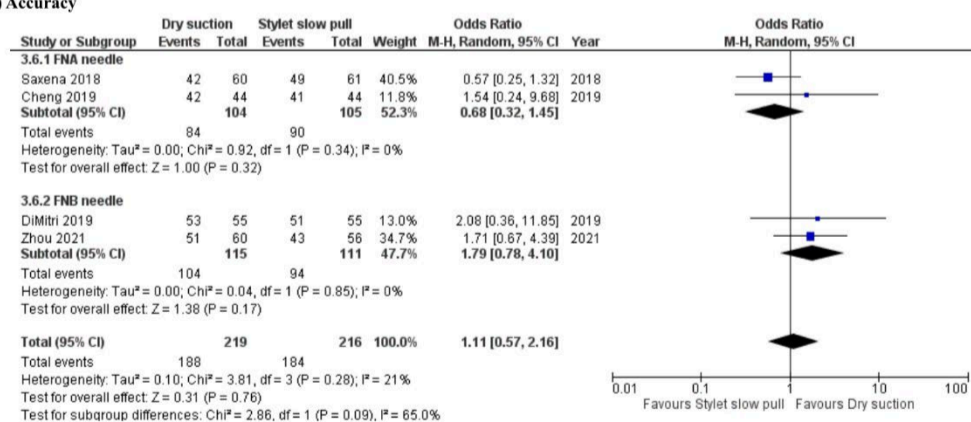
(B) Bloodiness



(C) Cellularity



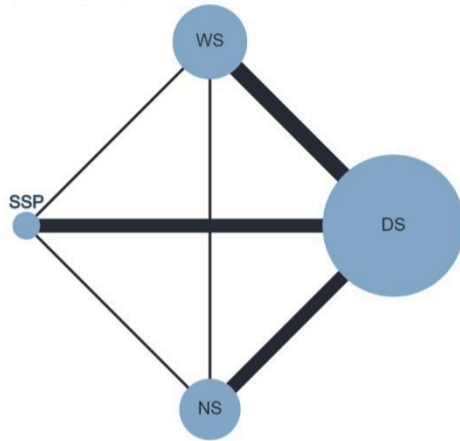
(D) Accuracy



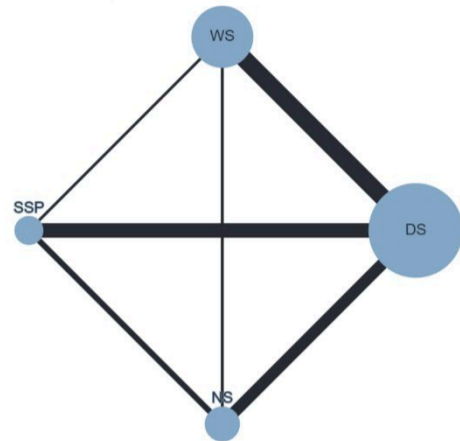
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Supplementary Figure 5: Network plots for the outcomes (5A) Sample adequacy, (5B) Moderate to high cellularity, (5C) Gross bloodiness, (5D) Diagnostic accuracy

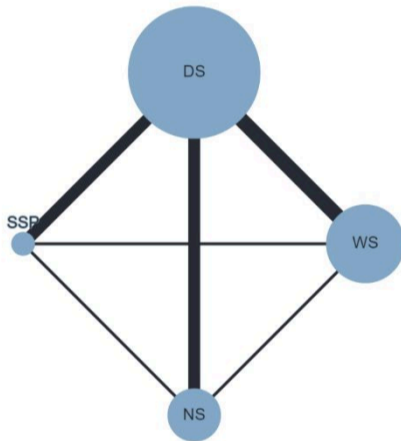
5A: Sample adequacy



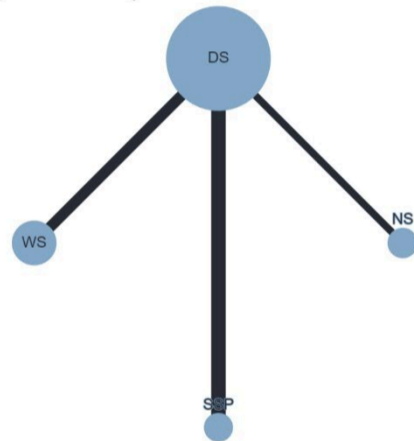
5B: Moderate to high cellularity



5C: Gross bloodiness



5D: Diagnostic accuracy



Supplementary material

Supplementary table 2: League table for the treatment estimates from the Bayesian network meta-analysis for sample adequacy

Dry suction			
1.45 (0.60, 3.49)	No suction		
0.94 (0.36, 2.52)	0.64 (0.19, 2.23)	Stylet slow pull	
0.61 (0.26, 1.49)	0.42 (0.13, 1.38)	0.65 (0.19, 2.24)	Wet suction

Supplementary table 3: League table for the treatment estimates from the Bayesian network meta-analysis for cellularity

Dry suction			
1.47 (0.63, 3.52)	No suction		
0.67 (0.29, 1.60)	0.46 (0.17, 1.31)	Slow stylet pull	
0.65 (0.31, 1.48)	0.45 (0.16, 1.33)	0.97 (0.33, 2.91)	Wet suction

Supplementary table 4: League table for the treatment estimates from the Bayesian network meta-analysis for gross bloodiness

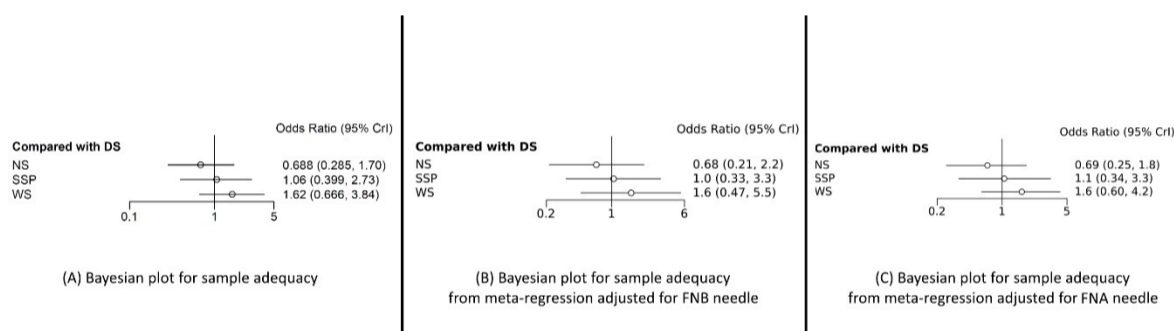
Dry suction			
1.84 (0.94, 3.79)	No suction		
1.00 (0.44, 2.25)	0.54 (0.19, 1.47)	Stylet slow pull	
2.00 (1.03, 4.14)	1.02 (0.41, 2.44)	1.88 (0.68, 5.34)	Wet suction

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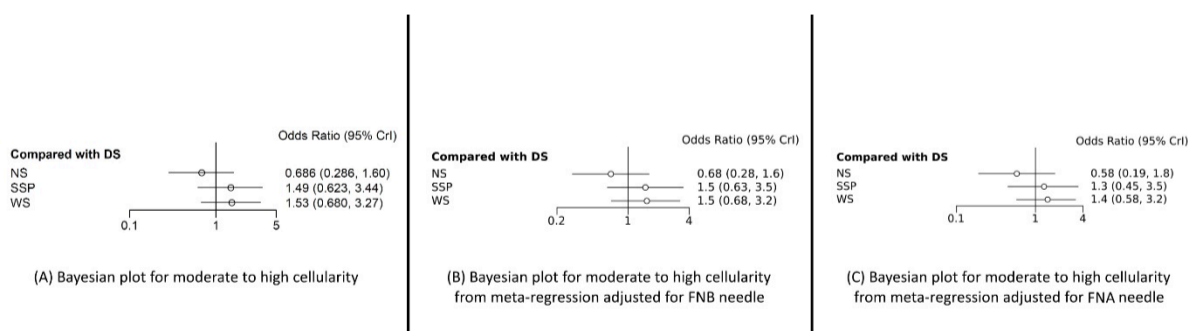
Supplementary table 5: League table for the treatment estimates from the Bayesian network meta-analysis for diagnostic accuracy

Dry suction			
0.99 (0.53, 1.97)	No Suction		
1.08 (0.57, 2.20)	1.10 (0.43, 2.89)	Stylet slow pull	
0.75 (0.37, 1.46)	0.76 (0.28, 1.86)	0.69 (0.25, 1.73)	Wet suction

Supplementary Figure 6: Bayesian Forest plot for adequacy

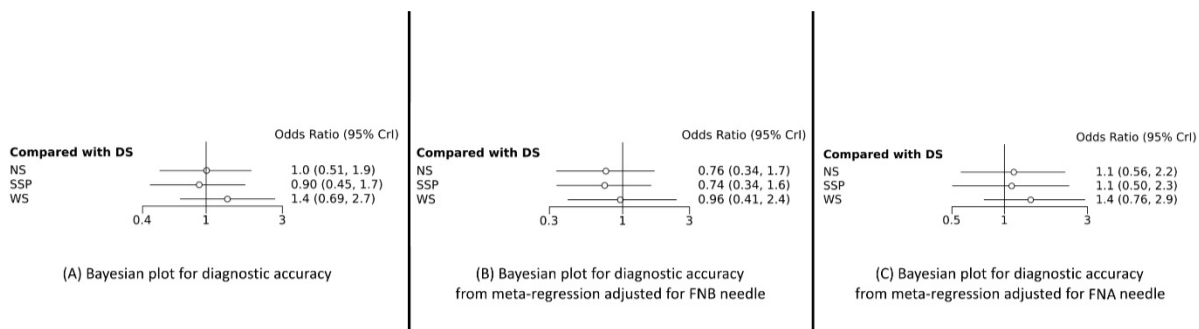


Supplementary Figure 7: Bayesian Forest plot for moderate to high cellularity



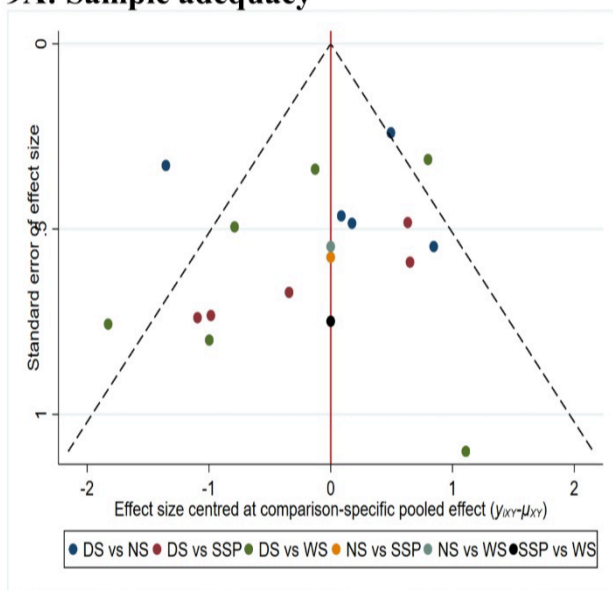
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Supplementary Figure 8: Bayesian Forest plot for diagnostic accuracy

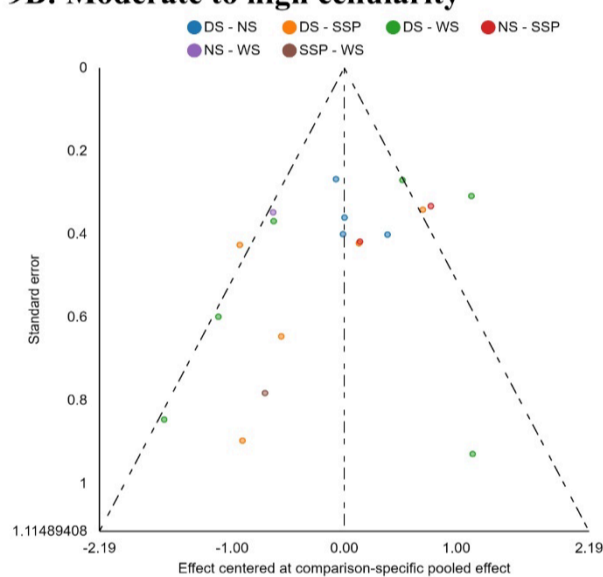


Supplementary Figure 9: Funnel plot for assessment of small study effect for various outcomes (9A) Sample adequacy, (9B) Moderate to high cellularity, (9C) Gross bloodiness, (9D) Diagnostic accuracy

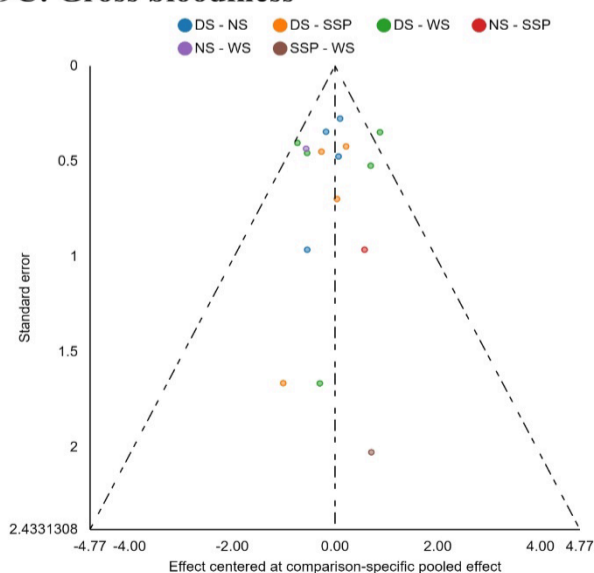
9A: Sample adequacy



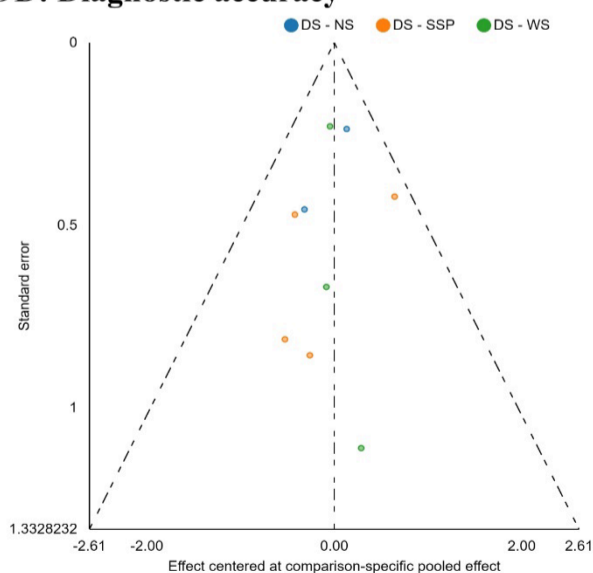
9B: Moderate to high cellularity



9C: Gross bloodiness



9D: Diagnostic accuracy



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Supplementary Table 6: Wald test for estimation of global inconsistency in networks of outcomes

Outcomes	Chi-square with degrees of freedom	P-value
Sample adequacy	chi ² (6) = 3.48	0.747
Moderate to high cellularity	chi ² (6) = 10.29	0.113
Gross bloodiness	chi ² (6) = 4.01	0.674
Diagnostic accuracy	chi ² (0) = 0.00	-

Supplementary Table 7: Summary of findings table with quality of evidence

	Direct OR	Confidence	Indirect OR	Confidence	NMA OR	Confidence
Sample adequacy						
DS – NS	1.48 (0.66 – 3.29)	Low ^{¶,§}	1.13 (0.07 – 18.91)	Low ^{¶,§}	1.45 (0.67 – 3.13)	Low ^{¶,Δ}
DS – SSP	0.99 (0.40 – 2.44)	Moderate [¶]	0.61 (0.03 – 10.71)	Low ^{¶,§}	0.94 (0.40 – 2.24)	Low ^{¶,Δ}
DS – WS	0.60 (0.27 – 1.35)	Low ^{¶,§}	1.29 (0.07 – 22.50)	Low ^{¶,§}	0.64 (0.29 – 1.39)	Low ^{¶,Δ}
NS – SSP	0.35 (0.05 – 2.48)	Low ^{¶,§}	0.86 (0.23 – 3.16)	Low ^{¶,§}	0.65 (0.22 – 1.93)	Low ^{¶,Δ}
NS – WS	1.55 (0.23 – 10.57)	Low ^{¶,§}	0.26 (0.07 – 0.90)	Low ^{¶,§}	0.44 (0.16 – 1.23)	Low ^{¶,Δ}
SSP – WS	0.48 (0.05 – 4.22)	Low ^{¶,§}	0.76 (0.21 – 7.88)	Low ^{¶,§}	0.67 (0.22 – 2.03)	Low ^{¶,Δ}
Moderate to high cellularity						
DS – NS	1.38 (0.66 – 2.89)	Moderate [¶]	2.10 (0.28 – 15.88)	Low ^{¶,§}	1.45 (0.73 – 2.90)	Low ^{¶,Δ}
DS – SSP	0.82 (0.39 – 1.73)	Low ^{¶,§}	0.11 (0.01 – 1.02)	Low ^{¶,§}	0.67 (0.33 – 1.72)	Low ^{¶,Δ}
DS – WS	0.64 (0.32 – 1.26)	Low ^{¶,§}	1.14 (0.11 – 11.36)	Low ^{¶,§}	0.67 (0.35 – 1.29)	Low ^{¶,Δ}
NS – SSP	0.28 (0.10 – 0.80)	Low ^{¶,§}	1.13 (0.28 – 4.57)	Low ^{¶,§}	0.46 (0.20 – 1.07)	Low ^{¶,Δ}
NS – WS	0.83 (0.19 – 3.60)	Low ^{¶,§}	0.33 (0.11 – 0.98)	Low ^{¶,§}	0.46 (0.19 – 1.03)	Low ^{¶,Δ}
SSP – WS	2.08 (0.26 – 16.56)	Low ^{¶,§}	0.84 (0.30 – 2.30)	Low ^{¶,§}	1.00 (0.40 – 2.47)	Low ^{¶,Δ}
Gross bloodiness						
DS – NS	1.97 (1.15 – 3.38)	Moderate [¶]	0.26 (0.02 – 2.90)	Low ^{¶,§}	1.79 (1.06 – 3.03)	Low ^{¶,§}
DS – SSP	1.09 (0.55 – 2.13)	Moderate [¶]	0.19 (0.00 – 12.98)	Low ^{¶,§}	1.04 (0.53 – 2.03)	Low ^{¶,Δ}
DS – WS	1.88 (1.11 – 3.20)	Low ^{¶,§}	2.12 (0.12 – 37.52)	Low ^{¶,§}	1.89 (1.12 – 3.18)	Low ^{¶,§}
NS – SSP	0.23 (0.02 – 2.39)	Low ^{¶,§}	0.66 (0.27 – 1.62)	Moderate [¶]	0.58 (0.25 – 1.34)	Low ^{¶,Δ}
NS – WS	1.93 (0.65 – 5.70)	Low ^{¶,§}	0.70 (0.29 – 1.71)	Low ^{¶,§}	1.05 (0.53 – 2.10)	Low ^{¶,Δ}
SSP – WS	0.95 (0.02 – 53.06)	Low ^{¶,§}	1.87 (0.79 – 4.41)	Low ^{¶,§}	1.81 (0.78 – 4.20)	Low ^{¶,Δ}
Diagnostic accuracy						
DS – NS	0.96 (0.63 – 1.45)	Moderate [¶]	-	-	0.96 (0.63 – 1.45)	Very low ^{¶,Δ,¥}
DS – SSP	1.06 (0.60 – 1.85)	Moderate [¶]	-	-	1.06 (0.60 – 1.85)	Very low ^{¶,Δ,¥}
DS – WS	0.76 (0.50 – 1.16)	Moderate [¶]	-	-	0.76 (0.50 – 1.16)	Very low ^{¶,Δ,¥}
NS – SSP	-	-	1.11 (0.55 – 2.22)	Moderate [¶]	1.11 (0.55 – 2.22)	Very low ^{¶,Δ,¥}
NS – WS	-	-	0.79 (0.44 – 1.43)	Moderate [¶]	0.79 (0.44 – 1.43)	Very low ^{¶,Δ,¥}
SSP – WS	-	-	0.72 (0.35 – 1.45)	Moderate [¶]	0.72 (0.35 – 1.45)	Very low ^{¶,Δ,¥}

¶ risk of bias; Δ Imprecision; § Heterogeneity; ¥ Incoherence