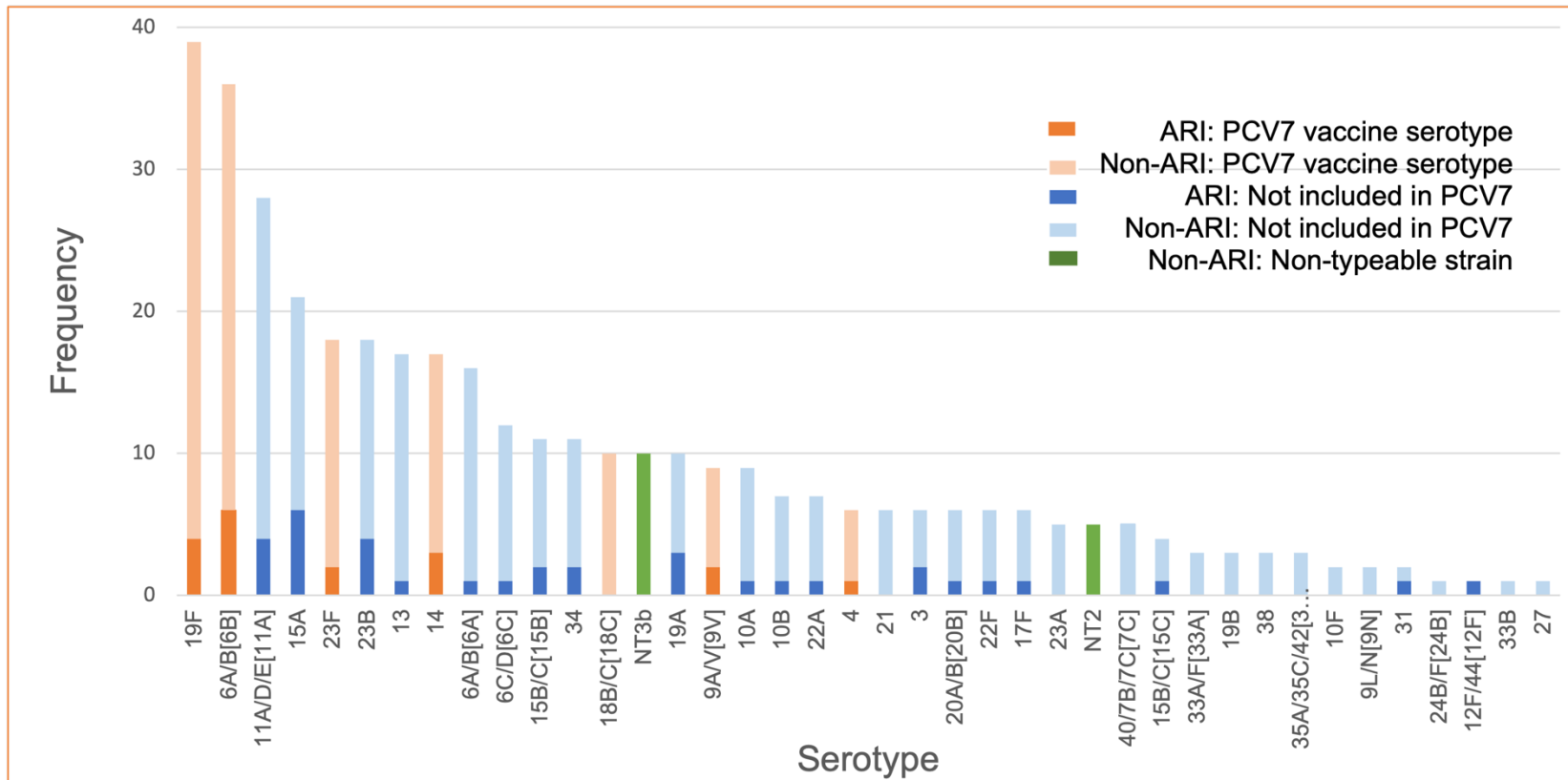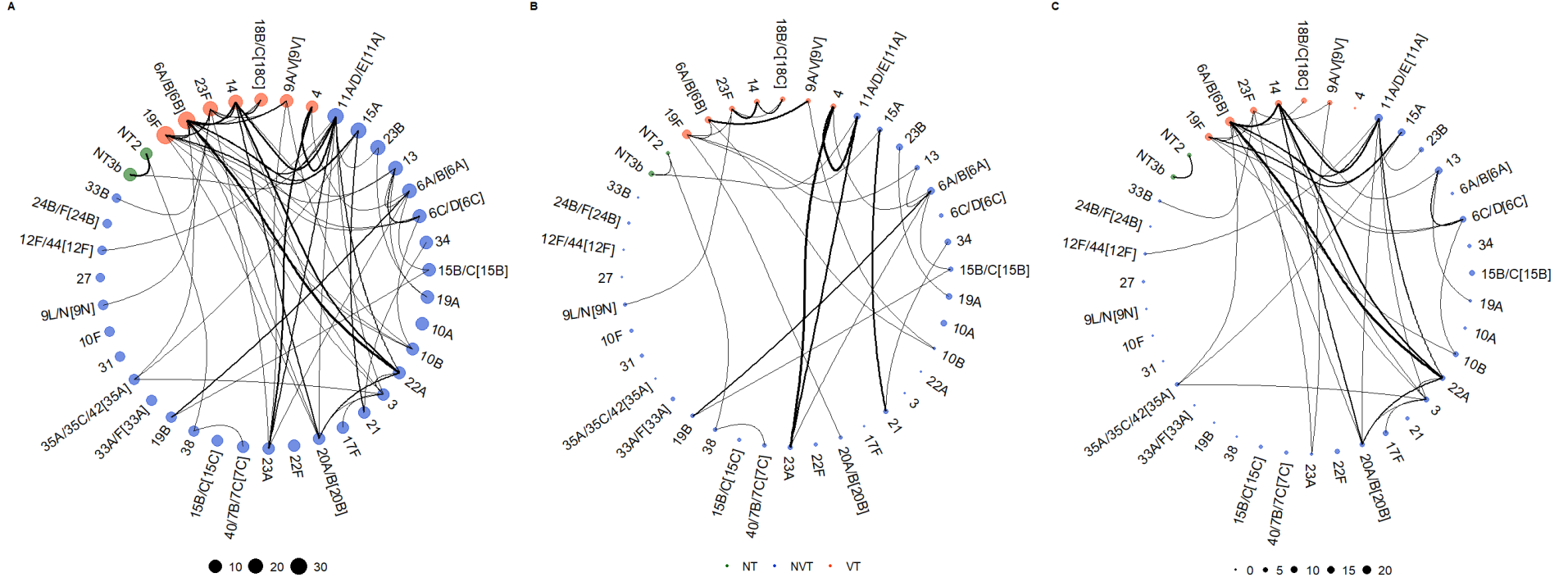Supplementary Figure 1. Frequency of detection of individual pneumococcal serotypes and non-typeable strains among 302 samples from selected subset of 27 RESPIRA-Peru participants, inclusive of single and co-colonization detections.

Supplementary Figure 2. Hierarchical edge bundling graph displaying co-detections of individual pneumococcal serotypes or strains **(A)** overall, **(B)** among samples preceded by no PCV7 vaccine doses, and **(C)** samples preceded by at least one dose of PCV7. Size of circle indicates frequency of detection. Thickness of connecting lines indicates the frequency of co-detection of two individual serotypes/strains.

Supplementary Table. Relative abundance of individual pneumococcal serotypes/strains in co-colonization detections according to inclusion in PCV7 and PCV7 vaccination status.

Serotype/strain	Number of co-colonization detections	Non-dominant* N (%)	Dominant* N (%)	Vaccination Yes N (%)	Vaccination No N (%)
PCV7 VT	57	41 (72)	16 (28)	29 (51)	28 (49)
6A/B[6B]	15	11 (73)	4 (27)	11 (73)	4 (27)
14	12	10 (83)	2 (17)	8 (67)	4 (33)
19F	10	5 (50)	5 (50)	5 (50)	5 (50)
23F	8	4 (50)	4 (50)	3 (38)	5 (62)
4	5	5 (100)	0 (0)	0 (0)	5 (100)
9V	4	3 (75)	1 (25)	1 (25)	3 (75)
18C	3	3 (100)	0 (0)	1 (33)	2 (67)
PCV7 NVT	75	49 (65)	26 (35)	40 (53)	35 (47)
11A/D/E[11A]	11	9 (82)	2 (18)	6 (55)	5 (45)
15A	8	6 (75)	2 (25)	4 (50)	4 (50)
22A	7	6 (86)	1 (14)	7 (100)	0 (0)
13	6	3 (50)	3 (50)	4 (67)	2 (33)
23A	5	2 (40)	3 (60)	1 (20)	4 (80)
6A/B[6A]	4	4 (100)	0 (0)	0 (0)	4 (100)
6C/D[6C]	4	0 (0)	4 (100)	4 (100)	0 (0)
20A/B[20B]	4	1 (25)	3 (75)	3 (75)	1 (25)
21	4	2 (50)	2 (50)	0 (0)	4 (100)
3	3	3 (100)	0 (0)	3 (100)	0 (0)
35A/35C/42[35A]	2	1 (50)	1 (50)	2 (100)	0 (0)
19B	2	0 (0)	2 (100)	0 (0)	2 (100)
38	2	2 (100)	0 (0)	0 (0)	2 (100)
19A	2	2 (100)	0 (0)	1 (50)	1 (50)
10B	2	2 (100)	0 (0)	1 (50)	1 (50)
23B	2	1 (50)	1 (50)	1 (50)	1 (50)
17F	1	1 (100)	0 (0)	1 (100)	0 (0)
15B/C[15B]	1	1 (100)	0 (0)	0 (0)	1 (100)
34	1	1 (100)	0 (0)	0 (0)	1 (100)
40/7B/7C[7C]	1	0 (0)	1 (100)	0 (0)	1 (100)
9L/9N[9N]	1	1 (100)	0 (0)	0 (0)	1 (100)
12F/44[12F]	1	0 (0)	1 (100)	1 (100)	0 (0)
33B	1	1 (100)	0 (0)	1 (100)	0 (0)
NT					
NT3B	5	4 (80)	1 (20)	3 (60)	2 (40)
NT2	5	5 (100)	0 (0)	3 (60)	2 (40)

*Serotypes that comprised >=70% of the relative abundance of the sample derived from microarray results were considered 'dominant,' those that comprised <70% of the relative abundance were considered 'non-dominant'