

**Supplementary Table 1. Baseline demographic and clinical characteristics of patients with chronic genotypes 1-6 HCV infection receiving sofosbuvir/velpatasvir in the ASTRAL-1-3 Phase 3 clinical trials, stratified by receipt of opioid substitution therapy**

Characteristic	OST at enrollment (n = 51)	No OST at enrollment (n = 984)
Mean age (SD), years	49 (10)	53 (11)
Male sex, n (%)	39 (76%)	591 (60%)
White race, n (%)	46 (90%)	821 (83%)
Mean BMI (SD)	26 (6)	27 (5)
Methadone, n (%)		
Methadone	34 (67%)	-
Buprenorphine	17 (33%)	-
HCV genotype, n (%)		
1a	12 (24%)	198 (20%)
1b	1 (2%)	117 (12%)
2	8 (16%)	230 (23%)
3	24 (47%)	253 (26%)
4	6 (12%)	110 (11%)
5	-	35 (4%)
6	-	41 (4%)
Mean HCV RNA log <sub>10</sub> IU/mL (SD)	6.3 (0.70)	6.3 (0.70)
F4 (cirrhosis), n (%)	13 (25%)	207 (21%)
Median ALT (Q1, Q3)	68 (40, 119)	58 (36, 107)
Prior HCV treatment experience, n (%)	11 (22%)	280 (28%)
PEG-IFN/ribavirin*	9 (82%)	193 (69%)
PEG-IFN/ribavirin/DAA*	1 (9%)	56 (20%)
Other*	1 (9%)	31 (11%)

\*percentage is among those with prior HCV treatment experience

**Supplementary Table 2. Treatment completion, adherence, efficacy and safety outcomes among patients with chronic genotypes 1-6 HCV infection receiving sofosbuvir/velpatasvir in the ASTRAL-1-3 Phase 3 clinical trials, stratified by receipt of opioid substitution therapy**

Outcome	OST at enrollment (n = 51)	%, 95% CI	No OST at enrollment (n = 984)	%, 95% CI	<i>P</i>
Treatment completion	49	96 (87, >99)	981	99.7 (99, >99)	0.02
Adherence ( $\geq 90\%$ )	46	90 (79, 97)	946	96 (95, 97)	0.06
SVR12	49	96 (87, >99)	966	98 (97, 99)	0.26
Adverse events	44	86 (74, 94)	778	79 (77, 82)	0.29
Serious adverse events	3	6 (1, 16)	20	2 (1, 3)	0.10

**Supplementary Table 3. Efficacy stratified by HCV genotype among patients with chronic genotypes 1-6 HCV infection receiving sofosbuvir/velpatasvir in the ASTRAL-1-3 Phase 3 clinical trials, stratified by receipt of opioid substitution therapy**

Outcome	SVR in those with OST at enrollment (n = 51)	%, 95% CI	SVR in those with no OST at enrollment (n = 984)	%, 95% CI	<i>P</i>
Genotype 1a	12/12	100 (74, 100)	194/198	98 (95, 99)	1.00
Genotype 1b	1/1	100 (3, 100)	116/117	99 (95, 100)	1.00
Genotype 2	7/8	88 (47, >99)	230/230	100 (98, 100)	0.03
Genotype 3	23/24	96 (79, >99)	241/253	95 (92, 98)	1.00
Genotype 4	6/6	100 (54, 100)	110/110	100 (97, 100)	1.00
Genotype 5	-	-	34/35	97 (85, >99)	-
Genotype 6	-	-	41/41	100 (91, 100)	-