C E	3BJ		1		2	3 4≥5	i FG		1		2	3 4≥5
	1,765				405	116 5763			1,071		266	93 35 52
-	3,558 independent 95% CS in 2,406 regions of 79 traits						2,348 independent 95% CS in 1,517 regions of 67 traits					
	1	2–5	6-10	11-20	21–50	>50	1	2-5	6–10	11–20	21-50	>50
	479	773	473	586	668	579	343	534	375	393	440	263
_	2,979 CS of 79 traits fine-mapped to ≤50 variants						2,085 CS of 67 traits fine-mapped to ≤50 variants					
	>90%	50-90%	10-50%		1-10%	≤1%	>90%	50-90%	10-50%		1–10%	≤1%
	471	416	1,407		1,103	161	337	188	936		730	157
	2,294 CS of 79 traits have a variant with PIP >10%						- 1,461 CS of 63 traits have a variant with PIP >10% -					
:	>90%50–90% 10–509			10-50%			>90%50-90	1%		10-50%		
	476 455	5		5,397			342 232			3,774		
_	6,328 variant-trait pairs have PIP >10%								4,348 variant-trait pa	irs have PIP >10%	6 —	
e (JKBB	1		2	3	4 ≥5	Colocaliz	zation >90%		50-90%	10–50%	1–10%
e (JKBB	1 6,640		2,86		4 ≥5 763 1,145	Colocaliz	zation _{>90%}		50–90% 6,033	10–50% 7,054	1–10% 1,441
e լ	JKBB		endent 95% CS	2,86				14,151	nave an eQTL variant	6,033	7,054	
e լ	JKBB 1		endent 95% CS i 6–10	2,86	31 1,450			14,151 27,238 genes I	nave an eQTL variant	6,033	7,054	
e լ		27,276 indepe		2,86 in 12,859 regi	31 1,450 ions of 119 traits	763 1,145		14,151 27,238 genes I 0%	nave an eQTL variant	6,033 with PIP >10% in	7,054	
e (1	27,276 indepe	6–10 3,574	2,86 in 12,859 regi 11–20 4,138	1,450 ions of 119 traits 21–50 5,350	763 1,145	>90% 50–9	14,151 27,238 genes I 0% 71	nave an eQTL variant 5,173 variants have PI	6,033 with PIP >10% in 10–50% 364,054	7,054 ≥1 tissue(s) —	
e (1	27,276 indepe 2–5 5,459	6–10 3,574	2,86 in 12,859 regi 11–20 4,138	1,450 ions of 119 traits 21–50 5,350	763 1,145	>90% 50–9	14,151 27,238 genes I 0% 71		6,033 with PIP >10% in 10–50% 364,054	7,054 ≥1 tissue(s) —	
e (1 3,835	27,276 indepe 2–5 5,459 22,356 CS of 119 t	6-10 3,574 raits fine-mappe	2,86 in 12,859 regi 11–20 4,138	51 1,450 ions of 119 traits 21–50 5,350 annts	763 1,145 >50 4,920	>90% 50–9 29,448 41,6	14,151 27,238 genes I 0% 71 435		6,033 with PIP >10% in 10–50% 364,054 P >10% in ≥1 tiss	7,054 ≥1 tissue(s) —	
	1 3,835 >90% 3,670	27,276 indepe 2–5 5,459 22,356 CS of 119 t 50–90%	6-10 3,574 raits fine-mappe 10-50% 10,667	2,86 in 12,859 regi 11–20 4,138 ed to ≤50 varia	61 1,450 ions of 119 traits 21–50 5,350 ants 1–10%	763 1,145 >50 4,920 ≤1%	>90% 50–9 29,448 41,6 >90% 712	14,151 27,238 genes l 0% 71 438 50–90% 440		6,033 with PIP >10% in 10–50% 364,054 P >10% in ≥1 tiss 10–50% 2,785	7,054 ≥1 tissue(s) ————————————————————————————————————	1,441
	1 3,835 >90% 3,670	27,276 indepe 2–5 5,459 22,356 CS of 119 t 50–90% 2,456 S of 117 traits have a	6-10 3,574 raits fine-mappe 10-50% 10,667	2,86 in 12,859 regi 11–20 4,138 ed to ≤50 varia	61 1,450 ions of 119 traits 21–50 5,350 ants 1–10%	763 1,145 >50 4,920 ≤1%	>90% 50–9 29,448 41,6 >90% 712	14,151 27,238 genes l 0% 71 438 50–90% 440	5,173 variants have PI	6,033 with PIP >10% in 10–50% 364,054 P >10% in ≥1 tiss 10–50% 2,785	7,054 ≥1 tissue(s) ————————————————————————————————————	1,441
!	1 3,835 >90% 3,670 - 16,793 C	27,276 indepe 2–5 5,459 22,356 CS of 119 t 50–90% 2,456 CS of 117 traits have a	6-10 3,574 raits fine-mappe 10-50% 10,667	2,86 in 12,859 regi 11–20 4,138 ed to ≤50 varia	61 1,450 ions of 119 traits 21–50 5,350 ants 1–10%	763 1,145 >50 4,920 ≤1%	>90% 50-9 29,448 41,6 >90% 712 3,93	14,151 27,238 genes I 0% 71	5,173 variants have PI	6,033 with PIP >10% in 10–50% 364,054 P >10% in ≥1 tiss 10–50% 2,785 ant with coloc PIP	7,054 ≥1 tissue(s) ————————————————————————————————————	1,441