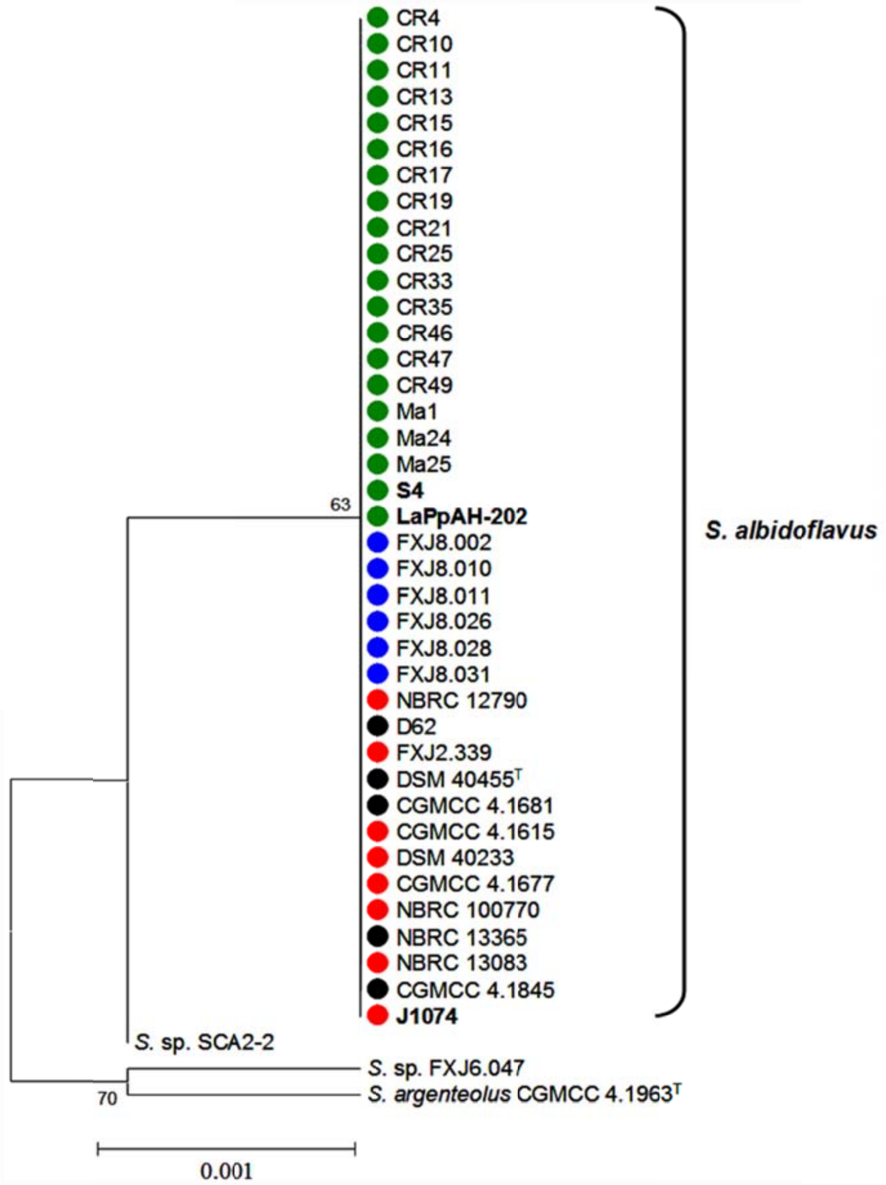

FIG S1 Phylogenetic NJ tree of *S. albidoflavus* strains based on the 16S rRNA gene sequences. Only bootstrap support values above 50% are shown. The bar indicates 0.1% estimated sequence divergence. Discs in green, blue, red and black represent insects, sea, soil and other sources, respectively. The genome strains are shown in bold, and SM8 and CNY228 are not included in this phylogeny for their 16S rRNA gene sequences are unavailable in public databases.

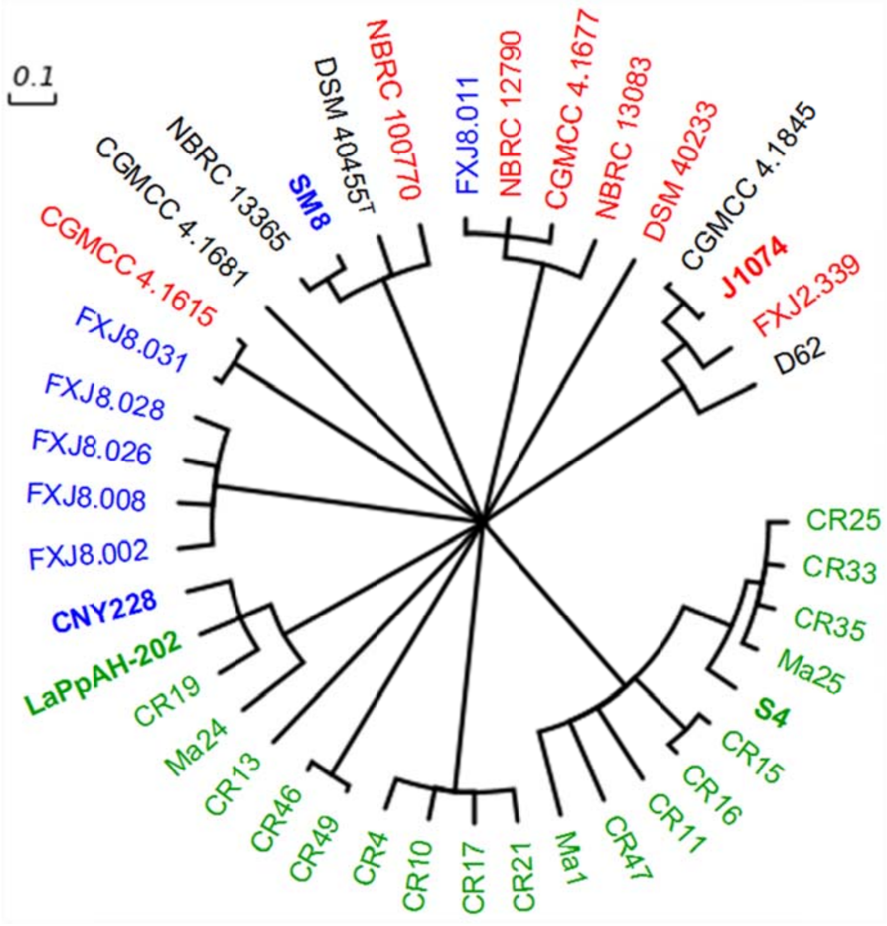

FIG S2 Clonal genealogy inferred by ClonalFrame. Strains from insects, sea, soil and other sources are in green, blue, red and black, respectively. The bar indicates 10% estimated sequence divergence.

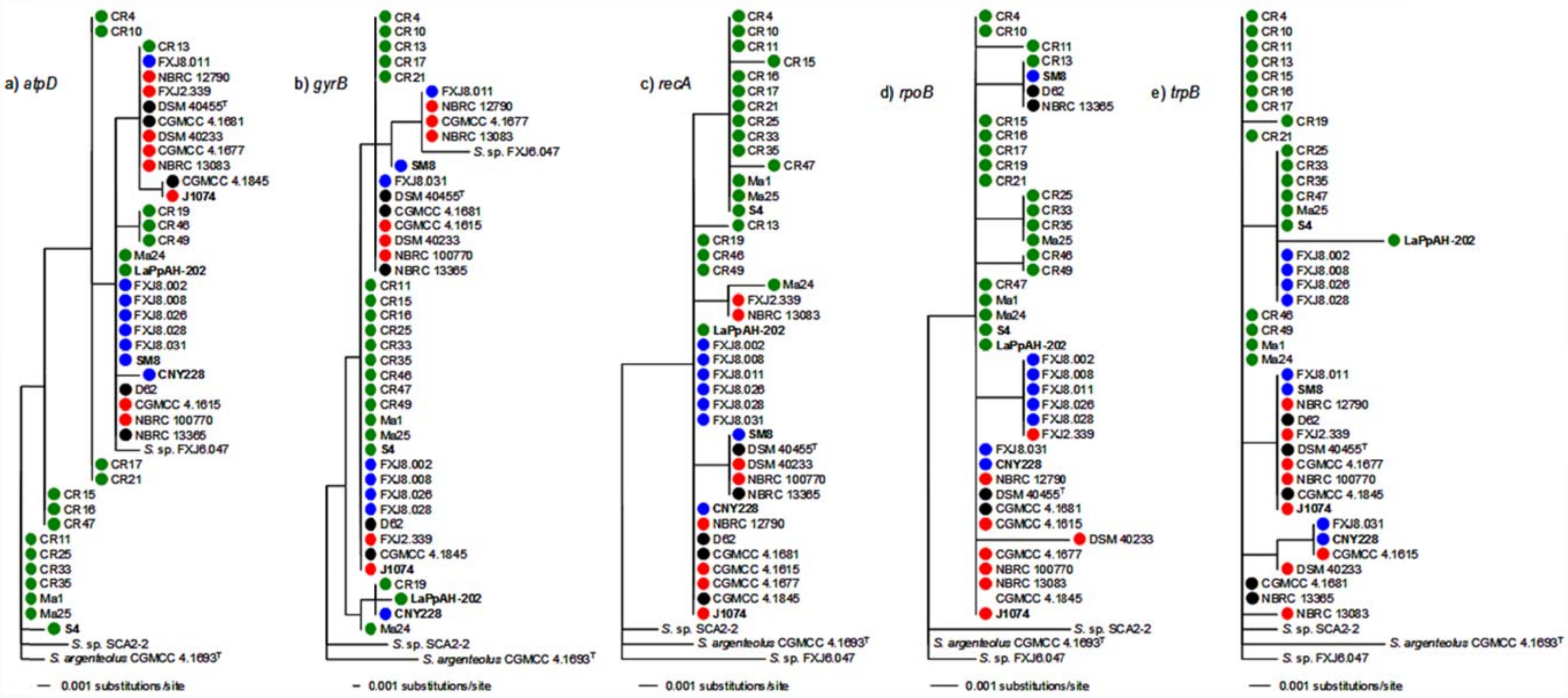

FIG S3 ML phylogenies of *atpD*, *gyrB*, *recA*, *rpoB and trpB* (a-e) based upon 41 strains of *S. albidoflavus*. Discs in green, blue, red and black represent insects, sea, soil and other sources, respectively. The bars indicate 0.1% estimated sequence divergence in respective phylogenies.

TABLE S1 Strains used in this study and GenBank accession numbers of alleles of loci

Strain	16S rRNA	*atpD*	*gyrB*	*recA*	*rpoB*	*trpB*
CGMCC 4.1615	DQ026642	FJ406408	FJ406419	FJ406430	FJ406441	FJ406452
CGMCC 4.1677	AB184129	FJ406410	FJ406421	FJ406432	FJ406443	FJ406454
CGMCC 4.1681	Z76684	FJ406407	FJ406418	FJ406429	FJ406440	FJ406451
CGMCC 4.1845	AY999871	EF031314	EF055001	EF055056	EF055111	EF055166
CNY228	-	ARIN01000050	ARIN01000043	ARIN01000026	ARIN01000049	ARIN01000040
CR10	KM189917	KM189938	KM189965	KM189992	KM190019	KM190046
CR11	KM189918	KM189939	KM189966	KM189993	KM190020	KM190047
CR13	KM189919	KM189940	KM189967	KM189994	KM190021	KM190048
CR15	KM189920	KM189941	KM189968	KM189995	KM190022	KM190049
CR16	KM189921	KM189942	KM189969	KM189996	KM190023	KM190050
CR17	KM189922	KM189943	KM189970	KM189997	KM190024	KM190051
CR19	KM189923	KM189944	KM189971	KM189998	KM190025	KM190052
CR21	KM189924	KM189945	KM189972	KM189999	KM190026	KM190053
CR25	KM189925	KM189946	KM189973	KM190000	KM190027	KM190054
CR33	KM189926	KM189947	KM189974	KM190001	KM190028	KM190055
CR35	KM189927	KM189948	KM189975	KM190002	KM190029	KM190056
CR4	KM189916	KM189937	KM189964	KM189991	KM190018	KM190045
CR46	KM189928	KM189949	KM189976	KM190003	KM190030	KM190057
CR47	KM189929	KM189950	KM189977	KM190004	KM190031	KM190058
CR49	KM189930	KM189951	KM189978	KM190005	KM190032	KM190059
D62	KM189935	KM189962	KM189989	KM190016	KM190043	KM190070
DSM 40233	Z76678	FJ406415	FJ406426	FJ406437	FJ406448	FJ406459
DSM 40455^T	Z76676	FJ406416	FJ406427	FJ406438	FJ406449	FJ406460
FXJ2.339	KM189934	KM189961	KM189988	KM190015	KM190042	KM190069
FXJ8.002	HQ622469	KM189955	KM189982	KM190009	KM190036	KM190063
FXJ8.008	HQ622474	KM189956	KM189983	KM190010	KM190037	KM190064
FXJ8.011	HQ622477	KM189957	KM189984	KM190011	KM190038	KM190065
FXJ8.026	HQ622487	KM189958	KM189985	KM190012	KM190039	KM190066

FXJ8.028	HQ622488	KM189959	KM189986	KM190013	KM190040	KM190067
FXJ8.031	HQ622489	KM189960	KM189987	KM190014	KM190041	KM190068
J1074	Gene ID: 5144945	Gene ID: 15145285	Gene ID: 15146834	Gene ID: 15144914	Gene ID: 15147536	Gene ID: 15148665
LaPpAH-202	ARDM01000035	ARDM01000005	ARDM01000003	ARDM01000014	ARDM01000001	ARDM01000004
Ma1	KM189931	KM189952	KM189979	KM190006	KM190033	KM190060
Ma24	KM189932	KM189953	KM189980	KM190007	KM190034	KM190061
Ma25	KM189933	KM189954	KM189981	KM190008	KM190035	KM190062
NBRC 100770	AB249937	FJ406411	FJ406422	FJ406433	FJ406444	FJ406455
NBRC 12790	AB184147	FJ406412	FJ406423	FJ406434	FJ406445	FJ406456
NBRC 13083	AB184299	FJ406414	FJ406425	FJ406436	FJ406447	FJ406458
NBRC 13365	AB184355	FJ406413	FJ406424	FJ406435	FJ406446	FJ406457
S4	CADY01000206	CADY01000160	CADY01000191	CADY01000147	CADY01000075	CADY01000035
SM8	-	AMPN01000168	AMPN01000124	AMPN01000014	AMPN01000123	AMPN01000292
S. argenteolus CGMCC 4.1693^{T}	EU048540	EF031302	EF054989	EF055044	EF055099	EF055154
S. sp. FXJ6.047	GU002076	JQ258968	JQ258989	JQ258947	JQ259010	JQ259031
S. sp. SCA2-2	KM189936	KM189963	KM189990	KM190017	KM190044	KM190071

- Sequences unavailable in public databases.

TABLE S2 Values of I^S_A and recombination rates in the Structure-defined populations when $K = 5$

Population color in Fig. 2	No. of strains	I^S_A	Recombination rate[a]	
			ρ/θ	r/m
Blue	4	-	-	-
Green	10	0.1785 ($P < 0.01$)	0.02 ± 0.004	1.12 ± 0.09
Purple	4	-	-	-
Red	17	0.0153 ($P = 0.360$)	8.71 ± 1.11	1.74 ± 0.22
Yellow	6	0.1470 ($P = 0.060$)	0.01 ± 0.002	0.42 ± 0.04

[a] The mean values of five independent runs of ClonalFrame are shown as average ± standard error of the mean.

- Values unavailable for a lack of polymorphic sites in populations.