Table S1. Crimson clover accessions trialed from the National Plant Germplasm System (NPGS) collection, including country of origin and years planted in the trial.

Accession #	Country of Origin	Years Planted		
		2012-2013	2013-2014	2014-2015
PI 233279	Israel	X	X	X
PI 233812	Italy	X	X	X
PI 251562	Former Serbia and Montenegro	X	X	X
PI 251563	Former Serbia and Montenegro	X	X	X
PI 298099	Hungary	X		
PI 338674	Morocco	X	X	X
PI 369045	USA (Georgia)	X	X	X
PI 378130	France	X	X	X
PI 418831	Italy	X		
PI 418900	Italy	X	X	X
PI 418901	Italy	X	X	X
PI 422487	Germany	X	X	X
PI 442556	Belgium	X	X	X
PI 499564	China	X	X	X
PI 527691	USA (Florida)	X	X	X
PI 556990	USA (Mississippi)	X	X	X
PI 561569	USA (Mississippi)	X	X	X
PI 561942	USA (Georgia)	X	X	X
PI 561943	USA (Alabama)	X	X	X
PI 561944	USA (Georgia)	X	X	X
PI 603034	USA (Kentucky)	X	X	X
PI 613042	USA (Georgia)	X	X	X
PI 613043	USA (Alaska)	X	X	X
PI 613044	USA (Alabama)	X	X	X
PI 613045	USA (Alabama)	X	X	X
PI 613046	USA (Georgia)	X	X	X
PI 613047	USA (Georgia)	X	X	X
PI 613048	USA (Maryland)	X	X	X
PI 613049	USA (Kentucky)	X	X	X
PI 613050	USA (Texas)	X		
PI 654999	Germany	X		
PI 655002	France	X		
PI 655005	Italy	X		
PI 655006	Portugal	X	X	X
PI 655007	Germany	X	X	X
PI 663842	USA (Maryland)	X		
PI 663850	USA (Mississippi)	X	X	X

PI number	Metagenomic library size (Megabases)	Number of contigs (range 300bp-190kb)	GC content	Taxa recovered based on rRNA operon identity at >99%, fragment length >1kb, gap size 25bp, E-value <0.001 *	Shared protein families, tRNAs, rRNAs, ORFs and transposon genes (orthologous metagenomic regions)																					
					Rhizobium leguminosarum WSM1689	Rhizobium leguminosarum WSM2304	Rhizobium leguminosarum Rt24.2	PI 369045	PI 603034	PI 561943	PI 556990	PI 613043	PI 378130	PI 527691	PI 499564	PI 251563	PI 561942	PI 655007	PI 655006	PI 561569	PI 613042	PI 338674	PI 613044	PI 418900	PI 663850	PI 561944
	6.8 MB Genome	na	60.9	Rhizobium leguminosarum WSM1689 (reference)	9343	7533	7724	4546	6163	6071	3704	4871	4122	6922	4094	10729	8850	13447	11962	11913	9962	14753	12507	14964	14517	15202
	6.9 MB Genome	na	61.1	Rhizobium leguminosarum WSM2304 (reference)	7533	9437	7542	4686	6338	6064	3591	4731	4060	7044	4150	10623	8911	13467	11894	11922	10012	14767	12646	15152	14671	15079
	7.6 MB Genome	na	60.6	Rhizobium leguminosarum Rt24.2 (reference)	7724	7542	9986	5175	6865	6735	4262	5275	4597	7662	4597	12110	9703	14744	13431	12803	10557	16089	13810	16330	16215	16421
PI 369045	20.1	8752	58.2	Rh.leg (BIHB 1217, CB782, Vaf10, Norway), Rh. etli (8C-3, IE4803) Rh. phaseoli (R744), Rh. gallicum (R602), SinoRh. fredii (NXT3), BradyRh. Japonicum (J5)	4546	4686	5175	20729	7754	10459	9630	9626	8785	5874	9107	12585	10856	12100	12309	12301	14462	12015	13017	14292	12636	15138
PI 603034	5.86	11449	55.2	Rh.leg (BIHB 1217, Vaf-108, bv. trifolii WSM1325, N941), Rh. etli (Mim1)	6163	6338	6865	7754	21237	9837	7587	9615	7618	10113	9015	12327	13821	14385	14447	15840	14369	15749	15358	17533	16037	17974
PI 561943	4.64	10117	55.2	Rh.leg (BIHB 1217, WSM1689, viciae)B. mega. (JX285), B. safensis (BRM1), Rh. etli (CIAT 652), Sph sp. (KC8)	6071	6064	6735	10459	9837	21296	9688	10989	9271	8300	9417	13957	13640	14777	14903	16270	16655	15937	15153	17800	16071	18716
PI 556990	6.13	13402	58.8	Rh.leg (BIHB 1217, trifolii,Vaf10), BradyRh. sp. (SK17, ORS285), BradyRh. japonicum (E109)	3704	3591	4262	9630	7587	9688	24045	10235	9079	6616	10710	11298	12234	10146	12142	12922	15188	10638	12591	12748	11231	17402
PI 613043	6.06	12163	61.4	Rh.leg (Rt780_131, Vaf-108), Rh. gallicum (IE4872), Sph sp. (MM-1), SinoRh fredii (NGR234), R. etli (CIAT 652)	4871	4731	5275	9626	9615	10989	10235	24770	9230	9139	11283	12994	14546	12528	14151	15929	16513	13348	14535	15534	14789	17382
PI 378130	7.58	15541	50.4	Rh.leg (trifolii, BIHB 1217, viciae, Vaf10, WSM1689), Aq. balticum (DSM 16537)	4122	4060	4597	8785	7618	9271	9079	9230	25918	7289	9701	10900	11370	10812	11909	12743	12924	12700	12873	13271	11629	15617
PI 527691	6.58	14494	55.4	Rh.leg (BIHB 1217, WSM1689, viciae, Norway), Rh. phaseoli (N161), Sph. sp. (KC8, Cra20)	6922	7044	7662	5874	10113	8300	6616	9139	7289	26007	9894	12351	16744	15637	15306	17038	13318	17738	16745	19478	18475	18889
PI 499564	7.16	15552	61.9	Rh. leg (trifolii, N741) Br. sp. (SK17), Sp. panacis (DCY99), Rh. phaseoli (R611), Shinella sp. (HZN7)	4094	4150	4597	9107	9015	9417	10710	11283	9701	9894	26703	11703	15512	11393	13960	14499	14552	12129	15171	14838	13153	18656
PI 251563	16.5	5693	60.9	Rh.leg (BIHB 1217, Vaf10), Ag. tumefaciens (S33), St. maltophilia (ISMMS2), SinoRh. americanum (CCGM7)	10729	10623	12110	12585	12327	13957	11298	12994	10900	12351	11703	33332	17931	29181	28964	22097	20944	30438	30021	34478	33903	34836
PI 561942	6.81	14450	61.7	Rh.leg (Norway, BIHB 1217, Vaf10), S. japonicum (UT26S), Rh. etli (N561), Rh. phaseoli (Brasil 5)	8850	8911	9703	10856	13821	13640	12234	14546	11370	16744	15512	17931	35484	20167	21353	24492	21635	22587	22824	25332	23228	26930
PI 655007	13.9	13732	61.6	Rh.leg (BIHB 1217, WSM1325, 3841, WSM1689, Vaf-108), Rh. phaseoli (N261), Pae. polymyxa (YC0136), St. maltophilia (OUC_Est10)	13447	13467	14744	12100	14385	14777	10146	12528	10812	15637	11393	29181	20167	40957	31643	26585	22624	36825	33150	41225	39980	38376
PI 655006	17.4	8325	61.6	Rh.leg (BIHB 1217, Norway, WSM2304, Vaf10), BradyRh. sp. (SK17), Rh. phaseoli (R611), Rh. etli (Mimosae), St. maltophilia (OUC_Est10)	11962	11894	13431	12309	14447	14903	12142	14151	11909	15306	13960	28964	21353	31643	41907	25876	22984	33432	33459	37535	37707	41210
PI 561569	7.78	16562	60.8	Rh.leg (BIHB 1217, trifolii, Vaf10,, Norway, WSM1325), Pse. fluorescens strain (Pt14), Rh. etli (phaseoli, IE4803)	11913	11922	12803	12301	15840	16270	12922	15929	12743	17038	14499	22097	24492	26585	25876	44922	25362	29579	27712	32811	30158	36268
PI 613042	8.91	18163	58.1	Rh.leg (WSM2304, viciae, Vaf10, Norway), Rh. gallicum (IE4872), MesoRh. loti (NZP2037), Rh. phaseoli (R744), Rh. etli (CFN 42), BradyRh. japonicum (61A10)	9962	10012	10557	14462	14369	16655	15188	16513	12924	13318	14552	20944	21635	22624	22984	25362	45772	24467	23679	27699	25309	30639
PI 338674	14.8	12810	59.9	Rh.leg (BIHB 1217,Norway, WSM1689, CIAT894,), Rh. etli,St. maltophilia	14753	14767	16089	12015	15749	15937	10638	13348	12700	17738	12129	30438	22587	36825	33432	29579	24467	49889	35165	44180	42882	41096
PI 613044	21.5	13492	62.8	Rh.leg, Rh. etli, MesoRh. ciceri (WSM1284), Xa. campestris, St. maltophilia	12507	12646	13810	13017	15358	15153	12591	14535	12873	16745	15171	30021	22824	33150	33459	27712	23679	35165	52387	40488	39598	42609
PI 418900	11.5	12507	62.4	Rh.leg (BIHB 1217, viciae,Vaf-108, IRBG74, N161) Rh. etli, St. maltophilia (K279a)	14964	15152	16330	14292	17533	17800	12748	15534	13271	19478	14838	34478	25332	41225	37535	32811	27699	44180	40488	60889	50749	46122
PI 663850	15.1	12746	62.1	Rh.leg (BIHB 1217, Norway, viciae, WSM1325), Rh. etli, St. maltophilia s(OUC_Est10), Ag. radiobacter (K84), SinoRh. meliloti GR4	14517	14671	16215	12636	16037	16071	11231	14789	11629	18475	13153	33903	23228	39980	37707	30158	25309	42882	39598	50749	61241	45913
PI 561944	23.7	18765	61.7	Rh.leg (BIHB 1217, Norway, WSM1325, BIHB 1148) Rh. etli, Br. japonicum (J5, sp. SK17), MesoRh. ciceri (WSM1284)	15202	15079	16421	15138	17974	18716	17402	17382	15617	18889	18656	34836	26930	38376	41210	36268	30639	41096	42609	46122	45913	72930

Figure S1. Metagenomic analysis of nodule endophytes cultured from field collected crimson clover accessions in 2015. Identified microbial taxa are followed by respective strains or biovar indication. Color gradient represents shared protein family, tRNA, rRNA, or transposon genes among accessions. Blue indicates a low amount of shared genetic content and yellow represents a high amount of shared genetic content. *** *Rh.= Rhizobium, MesoRh.= Mesorhizobium, Xa.= Xanthomonas, St.= Stenotrophomonas, Aq.= Aquiflexum, SinoRh.= Sinorhizobium, BradyRh.= Bradyrhizobium, Ag.= Agrobacetrium, Pae.= Paenibacillus, Sph.= Sphingomonas, Pse.= Pseudomonas***