

Table S1. The plot characteristics of the four successional stages in a Miyaluo region of Sichuan.

Forest Type	Community Height(m)	Slope	Average Elevation	Dominant Species
Shrub grassland	2.2±1.1	10-18	3582-3643-	<i>Salix cupularis</i> , <i>Koehneana</i>
Broad leaved forest	11±4.3	18-20	3435-3572.9	<i>Betula</i> , <i>Acer</i> , <i>Populus</i>
Coniferous broadleaved forest	13±5.2	17	3551.8-3579	<i>Betula</i> , <i>Abies</i> , <i>Acer</i>
Primary forest	17±3.1	18-25	3579.4-3716.7	<i>Picea</i> , <i>Abies</i>

Table S2. The bacterial communities in the different rehabilitation stages at different Phylum levels.

	SG	BF	MF	PF
Proteobacteria	42.06±4.23a	39.34±4.81a	38.00±3.92a	39.32±4.24a
Acidobacteria	26.39±4.61b	35.03±4.48a	35.82±4.90a	36.74±4.07a
Bacteroidetes	10.29±2.38a	8.83±1.42ab	7.7±0.57b	9.47±1.28a
Actinobacteria	8.22±2.28a	5.66±0.89b	5.3±1.31b	5.78±0.77b
Verrucomicrobia	5.68±2.14ab	5.78±0.99ab	7.12±1.29a	4.85±0.73b
Nitrospirae	2.40±0.77a	1.10±0.72b	1.20±0.46b	0.20±0.14c
Gemmatimonadetes	1.33±0.58a	1.44±0.26a	1.36±0.19a	1.31±0.38a
Candidate_division_WPS-1	1.01±0.43a	1.27±0.67a	1.00±0.15a	1.37±0.14a
Chloroflexi	0.60±0.38b	0.49±0.22b	1.30±0.68a	0.35±0.20b
others	2.02±0.73a	1.05±0.14b	1.19±0.14b	0.60±0.63c

Table S3. The bacterial communities in the different rehabilitation stages at different Class levels.

	SG	BF	MF	PF
Alphaproteobacteria	17.59±2.13a	21.50±3.94a	17.95±7.55a	21.82±2.82a
Betaproteobacteria	13.72±3.38a	8.04±1.40b	7.53±3.57bc	5.27±1.98c
Acidobacteria_Gp3	6.03±2.53b	11.15±1.97a	8.42±3.55b	11.40±1.11a
Acidobacteria_Gp1	3.44±2.72c	8.65±2.17b	7.43±3.26b	13.39±3.41a
Actinobacteria	8.62±2.38a	5.93±0.89b	4.99±2.39b	6.20±0.90b
Gammaproteobacteria	5.71±1.23b	6.73±0.93b	5.46±2.34b	8.52±0.53a
Sphingobacteriia	5.58±1.74bc	6.86±1.33ac	4.83±2.07b	8.27±1.36a
Deltaproteobacteria	6.37±2.16a	3.20±0.78b	2.70±1.14b	2.77±0.98b
Spartobacteria	2.73±1.41a	3.16±0.79a	3.34±1.56a	1.48±0.24b
Subdivision3	2.78±1.00a	2.50±0.57a	2.59±1.09a	3.05±0.59

Table S4. The bacterial communities in the different rehabilitation stages at different Order levels.

	SG	BF	MF	PF
Rhizobiales	8.79±0.77a	9.52±2.31a	9.42±1.74a	7.97±1.35a
Sphingobacteriales	5.44±1.73b	6.74±1.31b	5.36±0.80b	8.13±1.35a
Rhodobacterales	3.09±0.64c	4.78±0.73b	4.40±0.53b	5.58±0.71a
Myxococcales	4.33±1.13a	2.60±0.72b	2.43±0.36b	2.13±0.88b
Actinomycetales	3.15±1.00a	2.23±0.36bc	2.12±0.53c	2.83±0.37ab
Nitrospirales	2.63±0.85a	1.20±0.79b	1.30±0.49b	0.22±0.16c
Xanthomonadales	1.34±0.52b	1.94±0.48a	1.60±0.39ab	1.99±0.19a
Burkholderiales	1.53±0.35a	1.09±0.25b	1.00±0.18b	1.12±0.19b
Cytophagales	1.97±0.78a	0.69±0.41b	0.89±0.25b	0.53±0.34b
Gaiellales	1.37±0.60a	0.87±0.25b	1.01±0.34ab	0.43±0.11c

Table S5. Mantel test showing the effects of rehabilitation stage and soil factors on bacteria community structure.

	Bacteria	
	R ²	<i>p</i>
Rehabilitation stage	0.544	0.001
pH	0.608	0.001
EC	-0.071	0.726
AK	0.175	0.05
AP	0.292	0.002
N	-0.073	0.716
C	0.015	0.384
TP	-0.021	0.49
TK	0.156	0.108
NH4	0.114	0.129
NO3	-0.028	0.578
WCS	0.209	0.023
CN	0.37	0.002

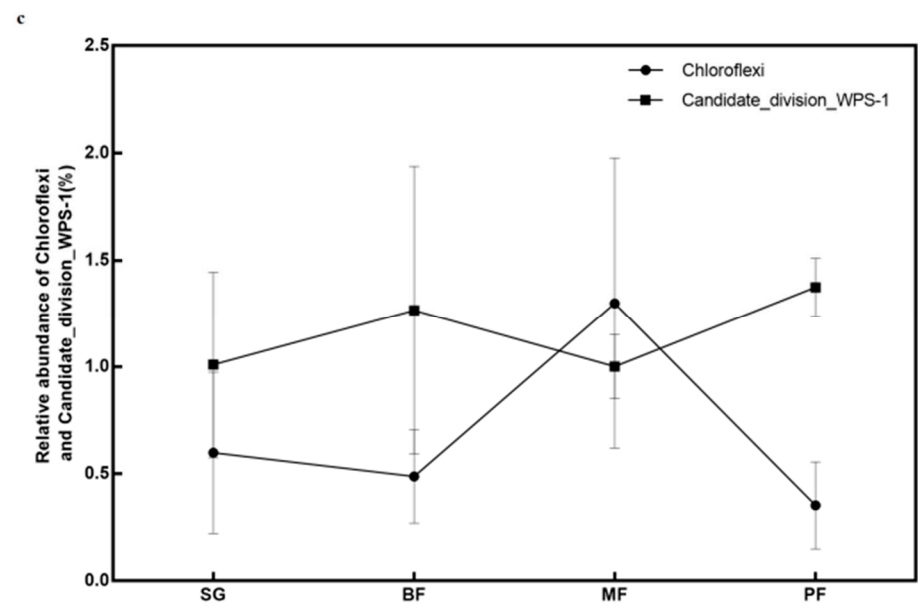
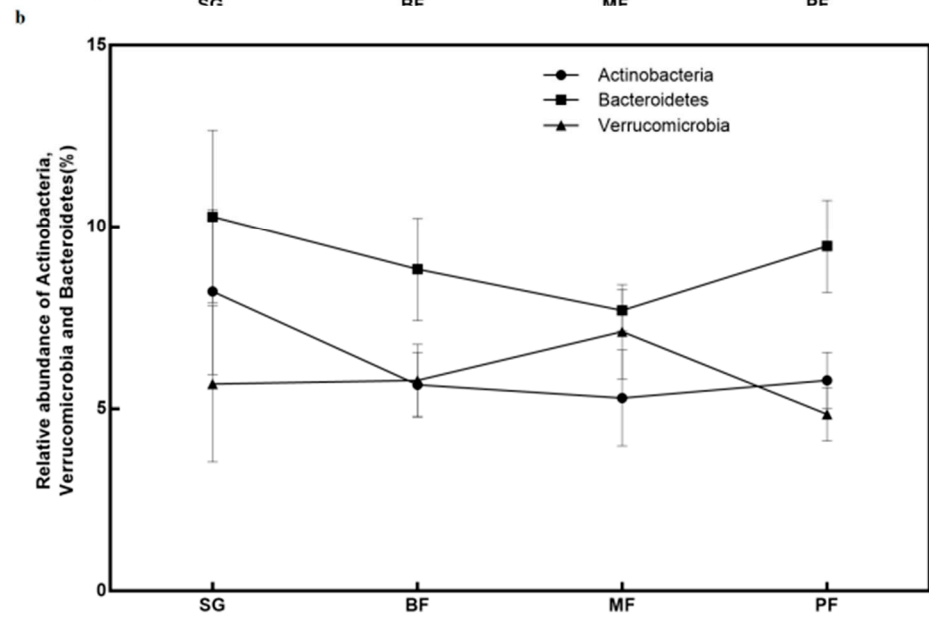
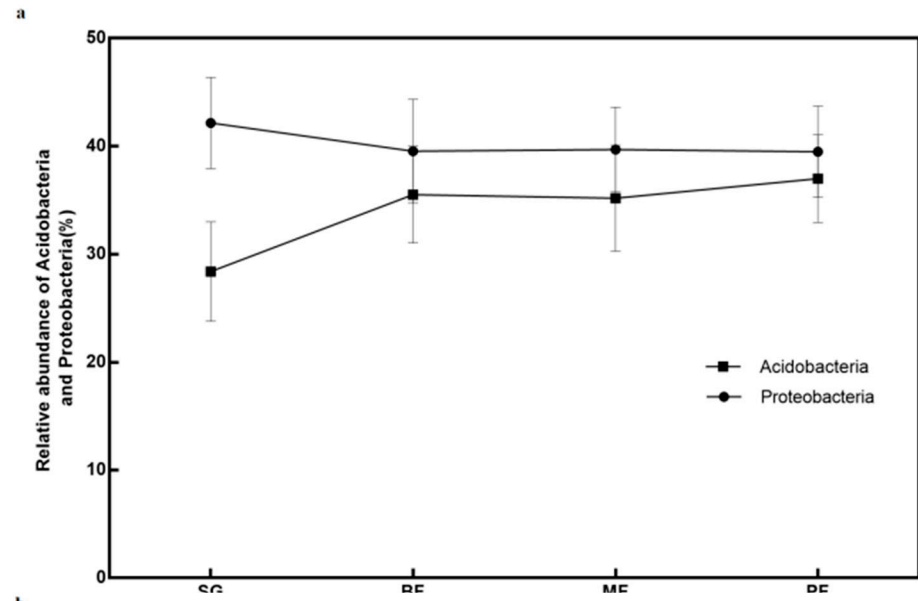
Table S6. Relative importance of the significant independent variables explaining the variance in abundance of the different taxonomic groups.

	Acidobacteria	Actinobacteria	Proteobacteria	Bacteroidetes	Nitrospirae	Verrucomicrobia	Gemmatimonadetes	Chloroflexi	candida_division_WPS-1
pH	0.2774 (-1.918)*	0.1493 (0.978)	0.077 (1.696)	0.1705 (1.472)	0.2651 (1.383)	0.0183 (-1.402)	0.0104 (0.103)	0.0152 (-0.781)	0.1017 (-1.288)
EC	0.0164 (0.843)	0.046 (-1.204)	0.0245 (-0.302)	0.1819 (-2.532)*	0.0503 (0.594)	0.0309 (1.432)	0.0122 (0.462)	0.0191 (0.528)	0.017 (0.665)
AK	0.1049 (0.043)	0.0951 (-0.044)	0.0968 (0.339)	0.0485 (-0.604)	0.0828 (-0.547)	0.0675 (-0.101)	0.0186 (0.524)	0.0336 (-0.176)	0.1126 (0.172)
AP	0.0424 (0.199)	0.0396 (-0.434)	0.0393 (-1.057)	0.1409 (1.938)	0.1874 (-1.4)	0.0359 (1.739)	0.1199 (1.89)	0.2203 (-1.371)	0.4316 (2.4)*
TN	0.0223 (0.559)	0.0265 (0.569)	0.0737 (-0.126)	0.0235 (0.529)	0.0097 (-0.005)	0.0873 (-1.344)	0.0844 (-1.862)	0.1864 (-1.8)	0.0476 (-1.07)
SOC	0.0265 (-0.488)	0.0304 (-0.553)	0.0741 (0.21)	0.027 (-0.681)	0.0128 (0.053)	0.0877 (1.052)	0.0862 (1.827)	0.141 (1.6)	0.0566 (1.063)
TP	0.0071 (-0.396)	0.0107 (-0.587)	0.0283 (-0.999)	0.0321 (1.234)	0.0041 (0.157)	0.1779 (3.024)**	0.0712 (-0.303)	0.1408 (2.359)*	0.0227 (0.038)
TK	0.1783 (2.204)*	0.117 (-1.019)	0.2957 (-2.481)*	0.0209 (-0.193)	0.0133 (-0.284)	0.1518 (1.195)	0.05 (-1.26)	0.0923 (0.707)	0.0227 (0.319)
NH4	0.0039 (0.218)	0.0611 (0.938)	0.008 (0.414)	0.1186 (-2.421)*	0.0064 (-0.022)	0.0109 (-0.694)	0.0478 (-0.63)	0.0313 (-0.889)	0.019 (0.017)
NO3	0.0167 (0.162)	0.0813 (-0.743)	0.0264 (0.921)	0.1281 (-1.723)	0.053 (-1.057)	0.0053 (0.004)	0.0983 (1.202)	0.0061 (-0.324)	0.0075 (-0.025)
WCS	0.0859 (-1.489)	0.1744 (1.653)	0.1215 (1.561)	0.0124 (0.794)	0.0035 (0.409)	0.2008 (-2.897)*	0.1653 (-1.658)	0.0188 (0.225)	0.0063 (0.123)
CN	0.0482 (1.36)	0.0346 (-0.212)	0.1013 (-1.585)	0.0514 (1.06)	0.0299 (-0.307)	0.057 (0.93335)	0.2144 (-2.604)*	0.0691 (-0.299)	0.0587 (-0.693)
AGE	0.1701 (0.209)	0.1339 (-0.132)	0.0332 (1.189)	0.0443 (-0.404)	0.2817 (-1.016)	0.0686 (-2.265)*	0.0215 (-0.644)	0.0261 (-0.287)	0.0958 (-1.475)

NOTE:., P<0.01; *, P<0.01; * *, P<0.001.

Table S7. ANOVA analysis (Simple effect) explaining the explanatory value of single factors on the change of soil bacterial community.

	Simple effect
pH	14.31%
Restoration stage	17.88%
AP	9.83%
WCS	0.40%



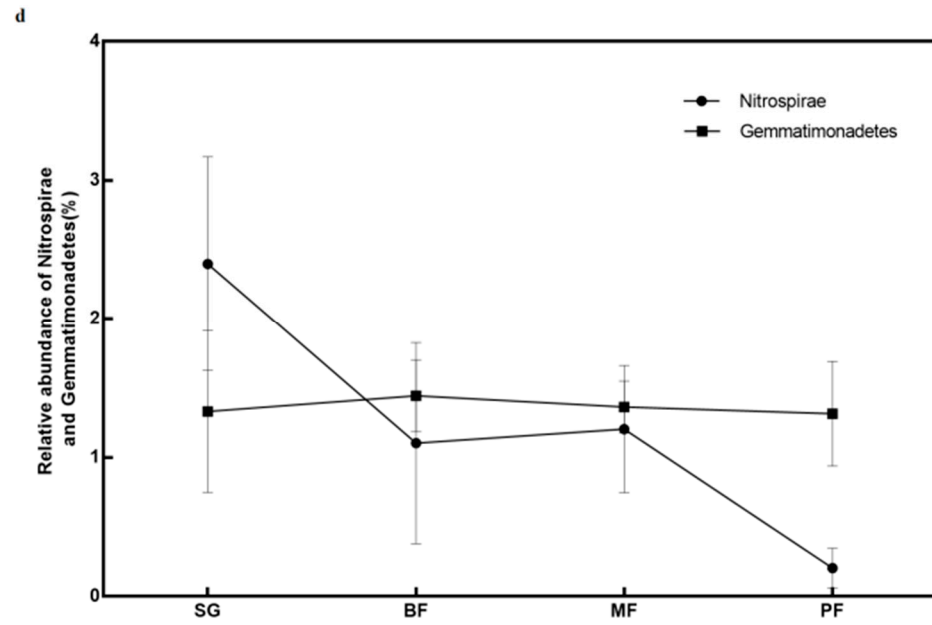


Figure S1. The relative abundance of dominant bacterial (a, b, c and d) at different rehabilitation stages. Error bars denote standard deviation. SG: Shrub-grassland; BF: Broad leaved; MF: Coniferous broadleaved; PF: Primary forest.