

Figure S1. Effects of *Epichloë* endophyte and *Pseudomonas* on germination potential (A), germination percentage (B), germination index (C), root length (D), seeding length (E), fresh weight (F), dry weight (G) of *A. inebrians* seeds. (EI: endophyte-infected, EF: endophyte-free, E was the *Epichloë* endophyte fungi, P was inoculating of *Pseudomonas*. St1-St34 represented inoculating different *Pseudomonas* strains. CK represented inoculating LB fluid nutrient medium on *A. inebrians*. These small letters indicated mean significant difference at $P<0.05$ among different inoculations. The * represented there is a significant difference between EI and EF.)

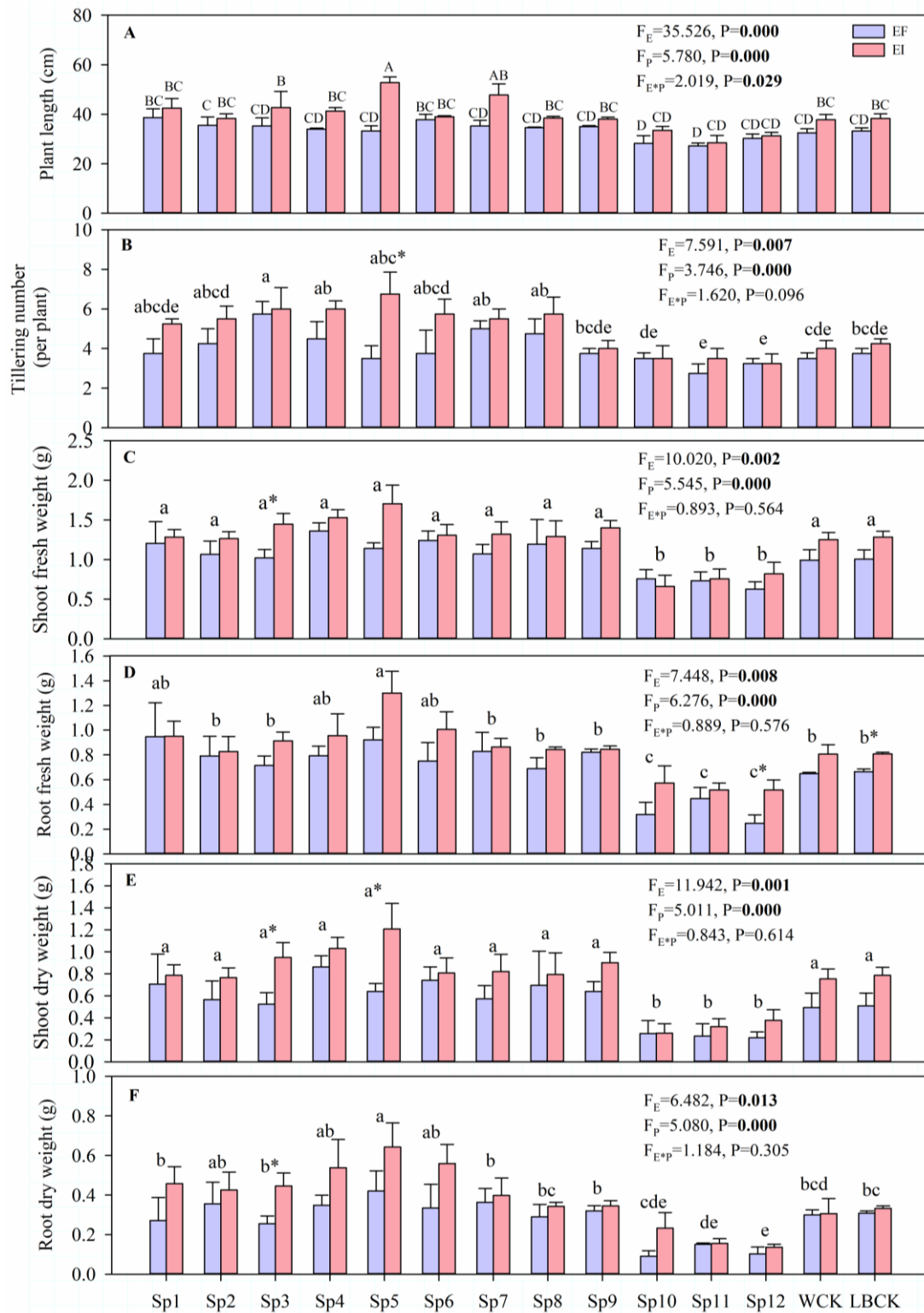


Figure S2. Effects of *Epichloë* endophyte and *Pseudomonas* on plant length (A), tillering number (B), shoot fresh weight (C), root fresh weight (D), shoot dry weight (E) and root dry weight (F) of *A. inebrians* plants. (E was the *Epichloë* endophyte, P was inoculating of *Pseudomonas*. These small letters indicated mean significant difference at $P < 0.05$ among different inoculations of *A. inebrians* plants. The * represented there is a significant difference between EI and EF. Different capital letters indicate significant ($P < 0.05$) difference between all treatments.)

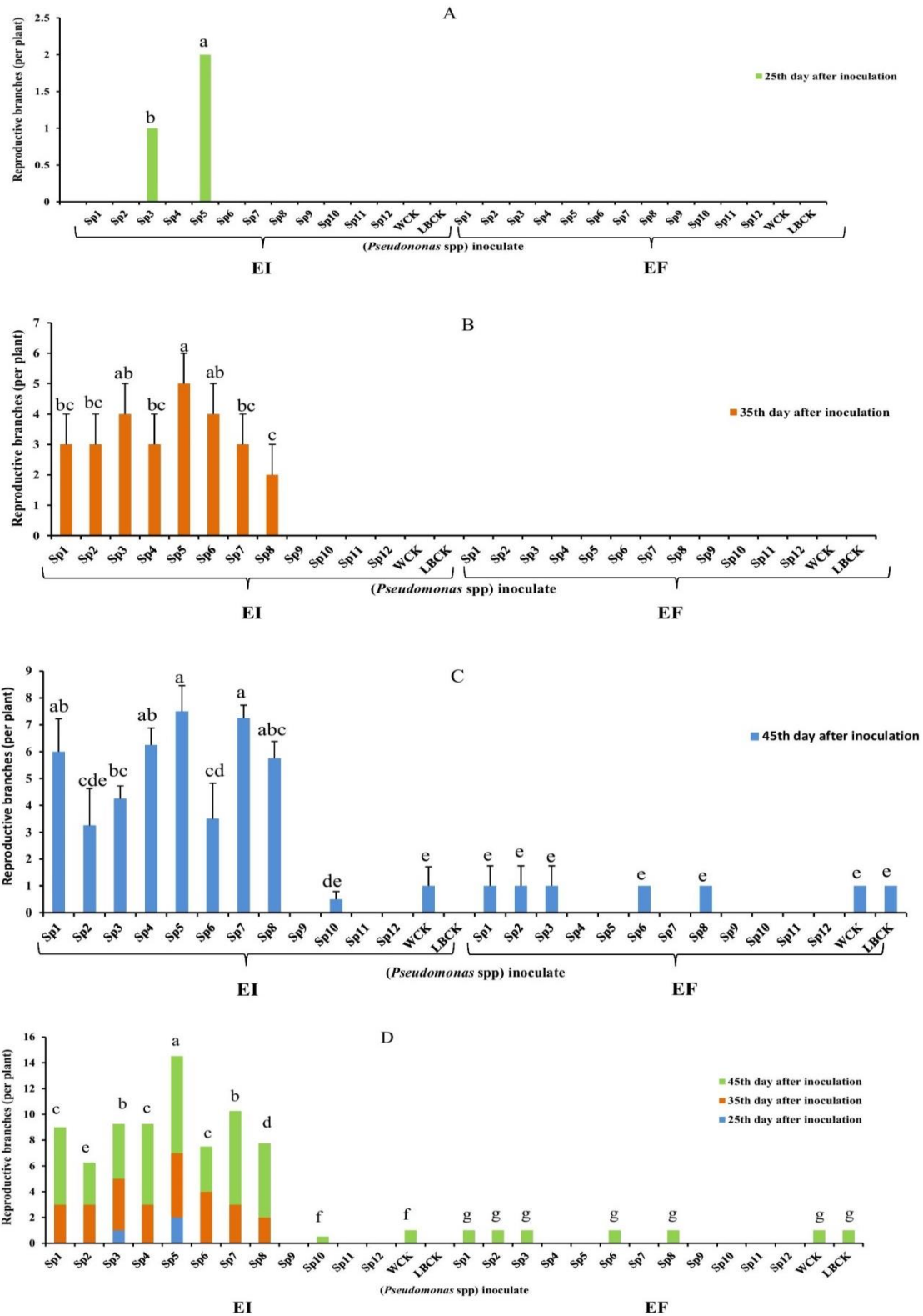


Figure S3. The number of reproductive branches in *A. inebrians* under inoculating *Pseudomonas*. (A) was the number of reproductive branches of *A. inebrians* under inoculating *Pseudomonas* at the 25th day; (B) was the number of reproductive branches of *A. inebrians* under inoculating *Pseudomonas* at the 35th day; (C) was the number of reproductive branches of *A. inebrians* under inoculating *Pseudomonas* at the 45th day; and (D) was the total reproductive branches of *A. inebrians* under inoculating *Pseudomonas*.

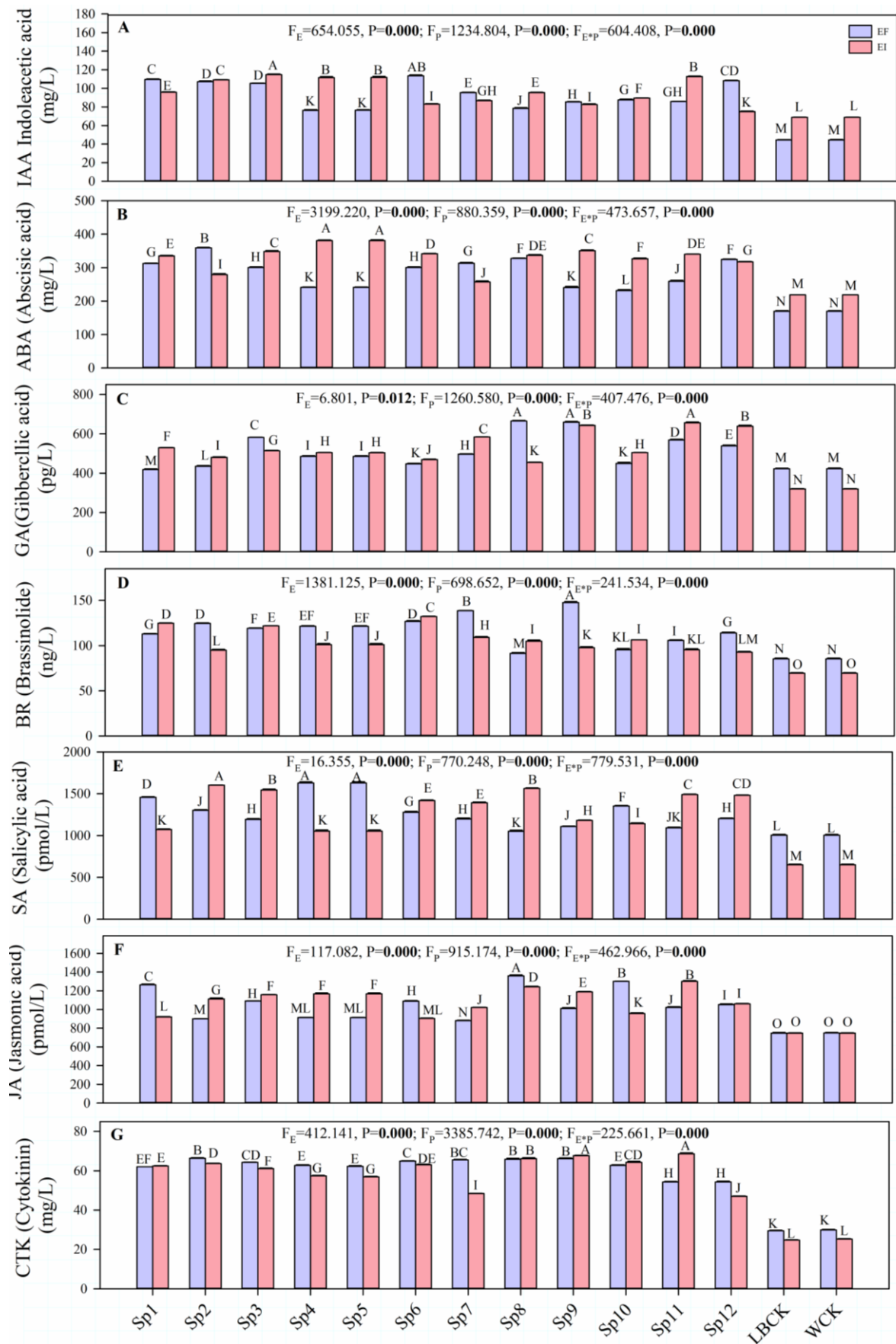


Figure S4. Effects of *Epichloë* endophyte (E) and inoculate *Pseudomonas* strains on IAA (A), ABA (B), GA (C), BR (D), SA (E), JA (F) and BR (G) of *A. inebrians* plants.

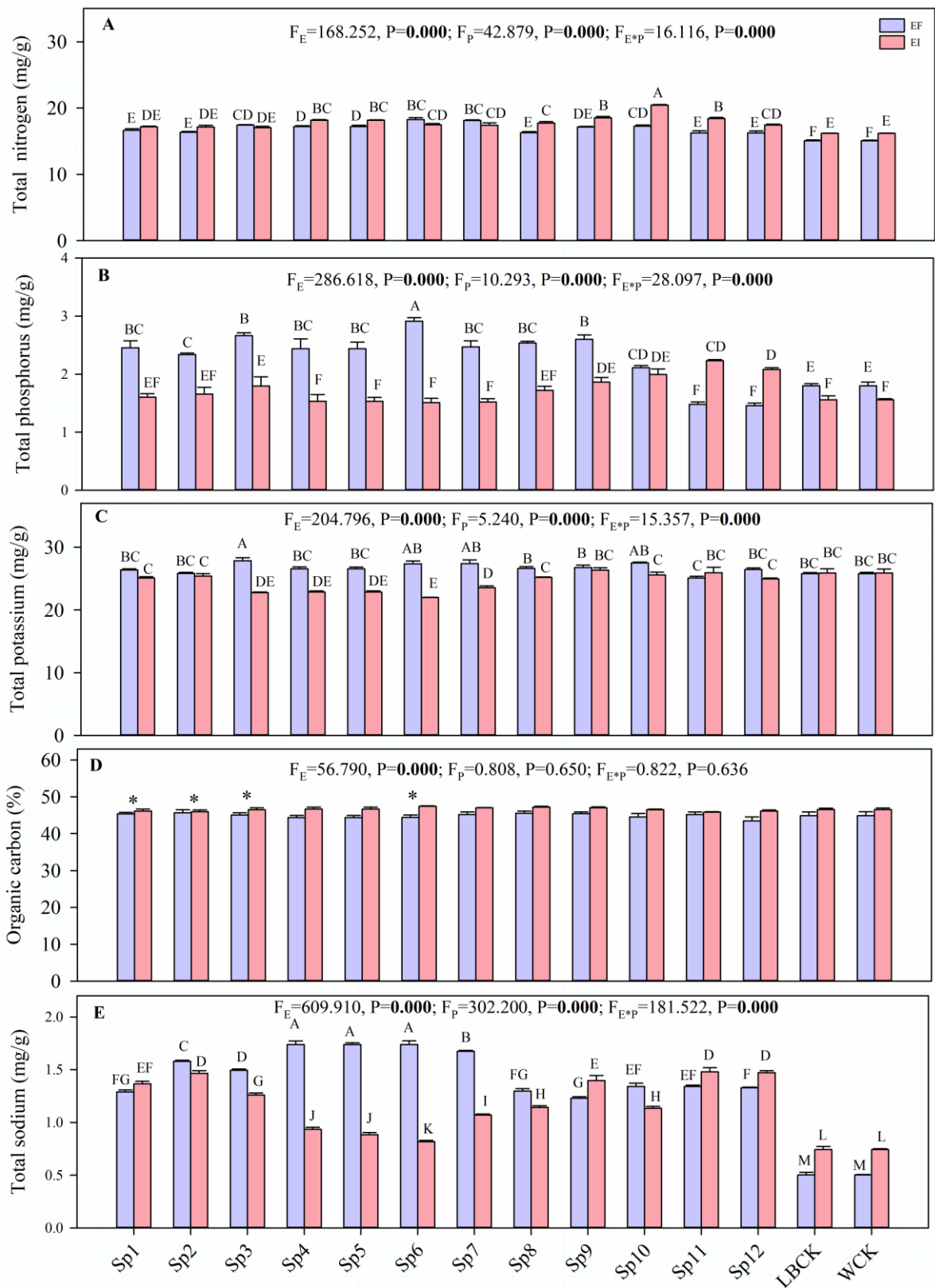
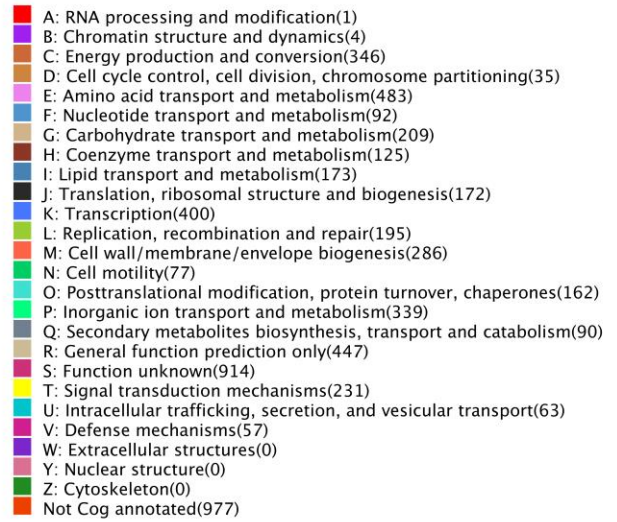
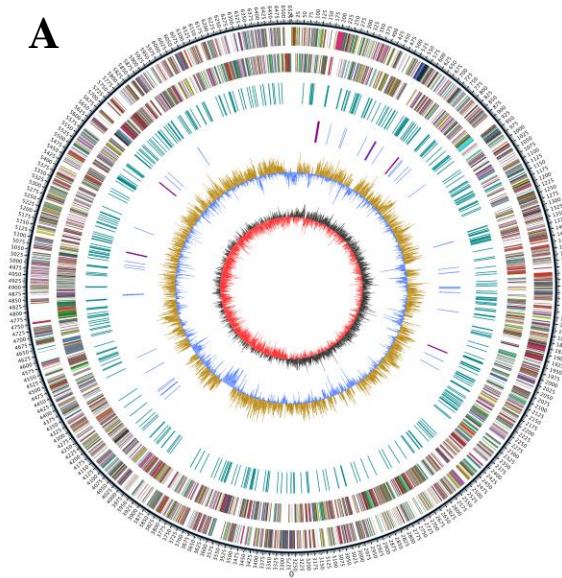
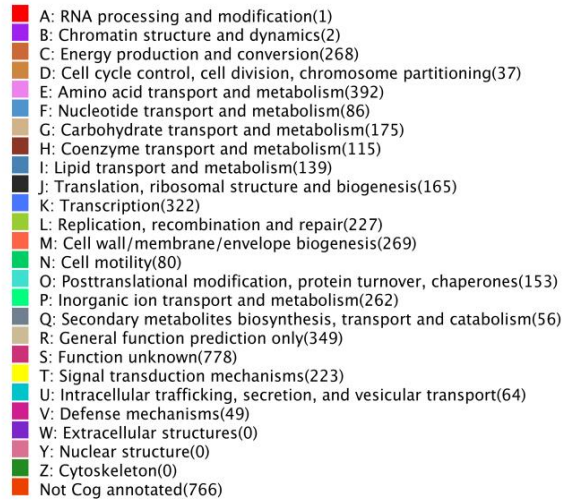
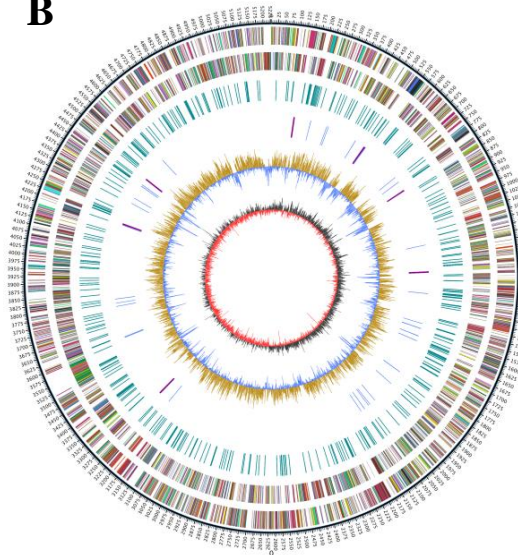
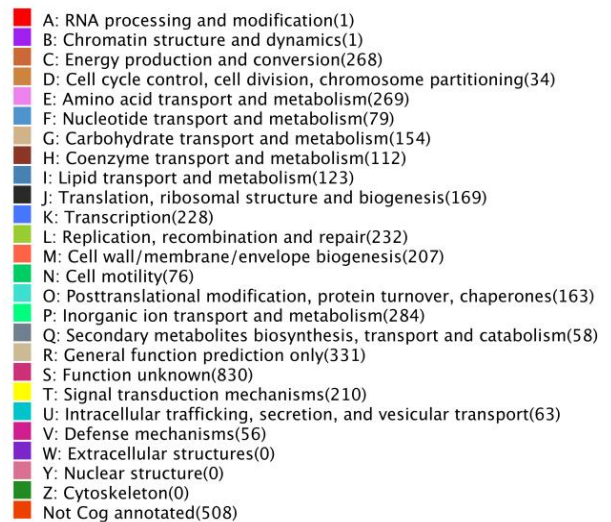
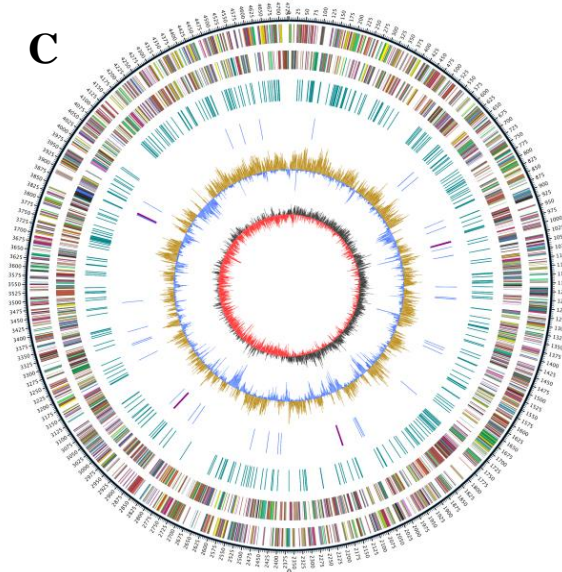
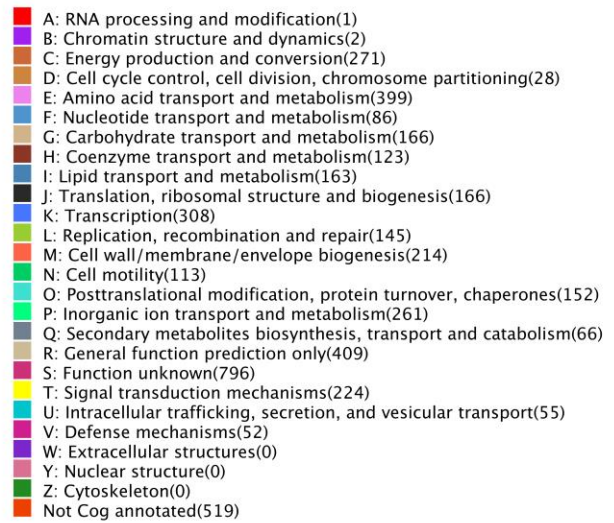
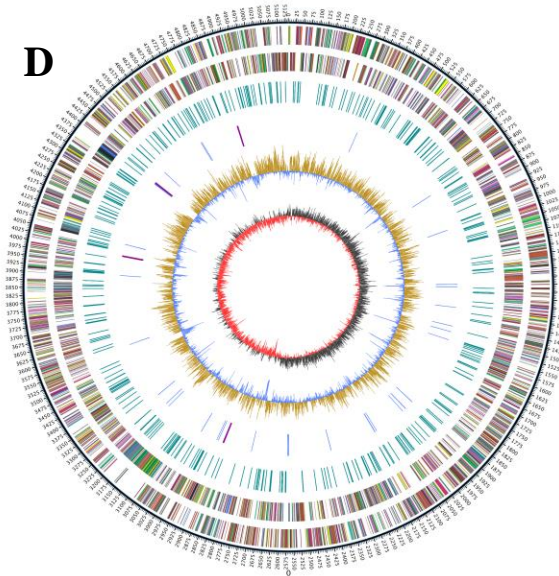
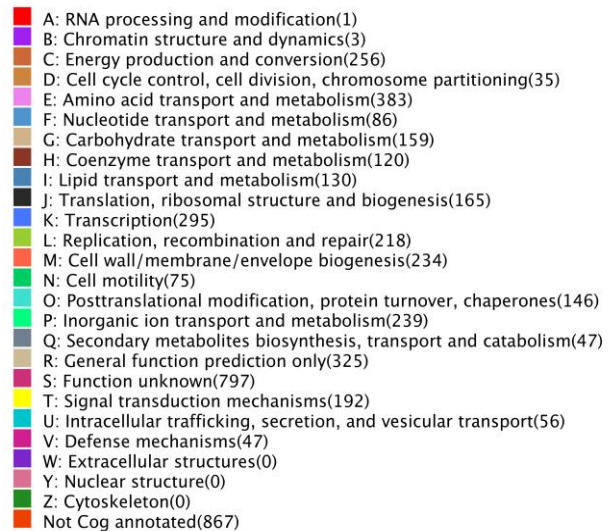
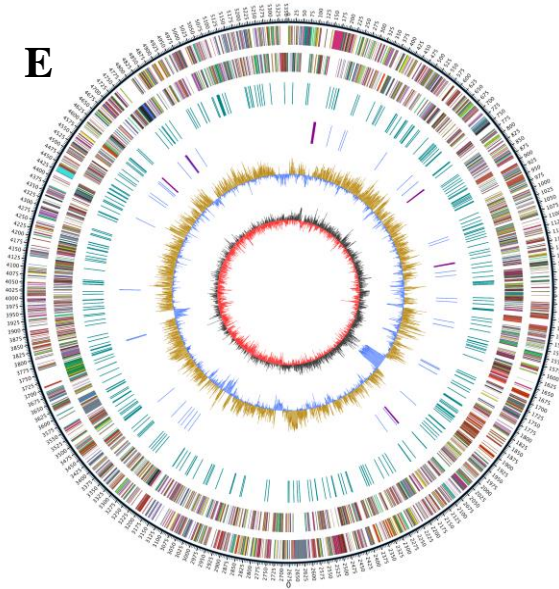
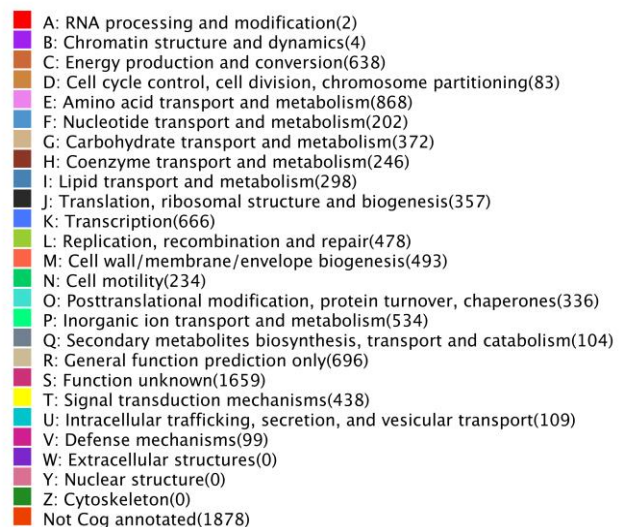
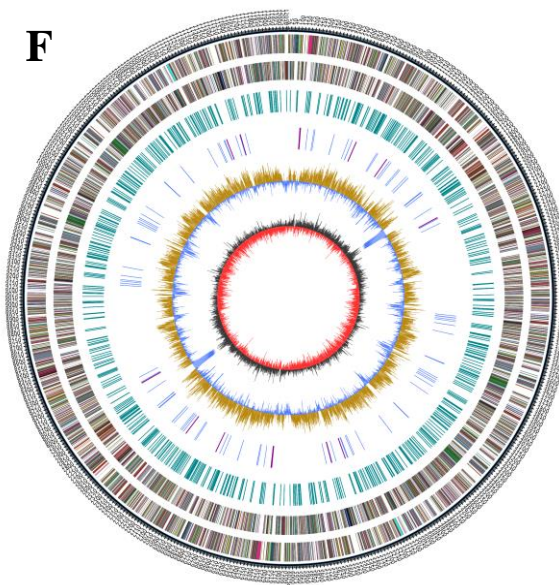


Figure S5. Effects of *Epichloë* endophyte (E) and inoculation of *Pseudomonas* strains on total nitrogen (A), total phosphorus (B), total potassium (C), organic carbon (D) and total sodium (E) of *A. inebrians* plants.

A**B****C**

D**E****F**

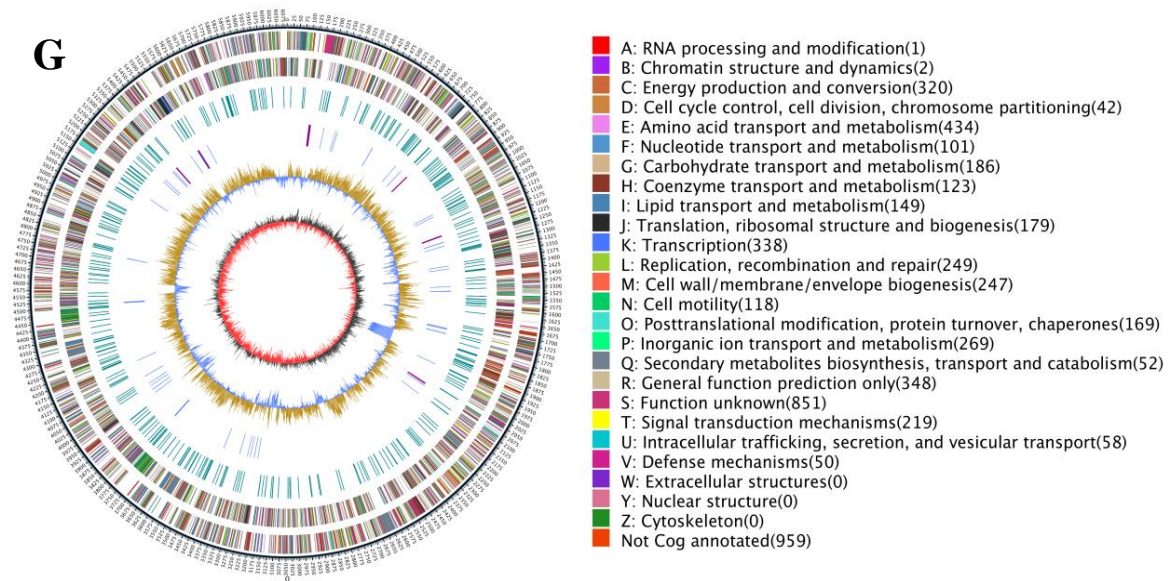


Figure S6. Genomic map of *Pseudomonas*. A: Sp1; B: Sp3; C: Sp5; D: Sp7; E: Sp10; F: Sp11; G: Sp12.

Note: The outermost circle represents the size of the genome, which is 5kb; The second and third circles represent genes on the positive and negative strands of the genome, respectively, with different colors representing different COG functions of genes. The fourth circle is a repeating sequence; the fifth circle has blue tRNA and purple rRNA; The sixth circle represents the GC content. Yellow indicates that the GC content in the region is higher than the average GC content of the genome, while blue indicates that the GC content in the region is lower than the average GC content of the genome. The higher the peak, the greater the difference between the GC content and the average GC content; The innermost circle is GC skew, with red indicating areas where C content is greater than G, and dark gray indicating areas where G content is greater than C.

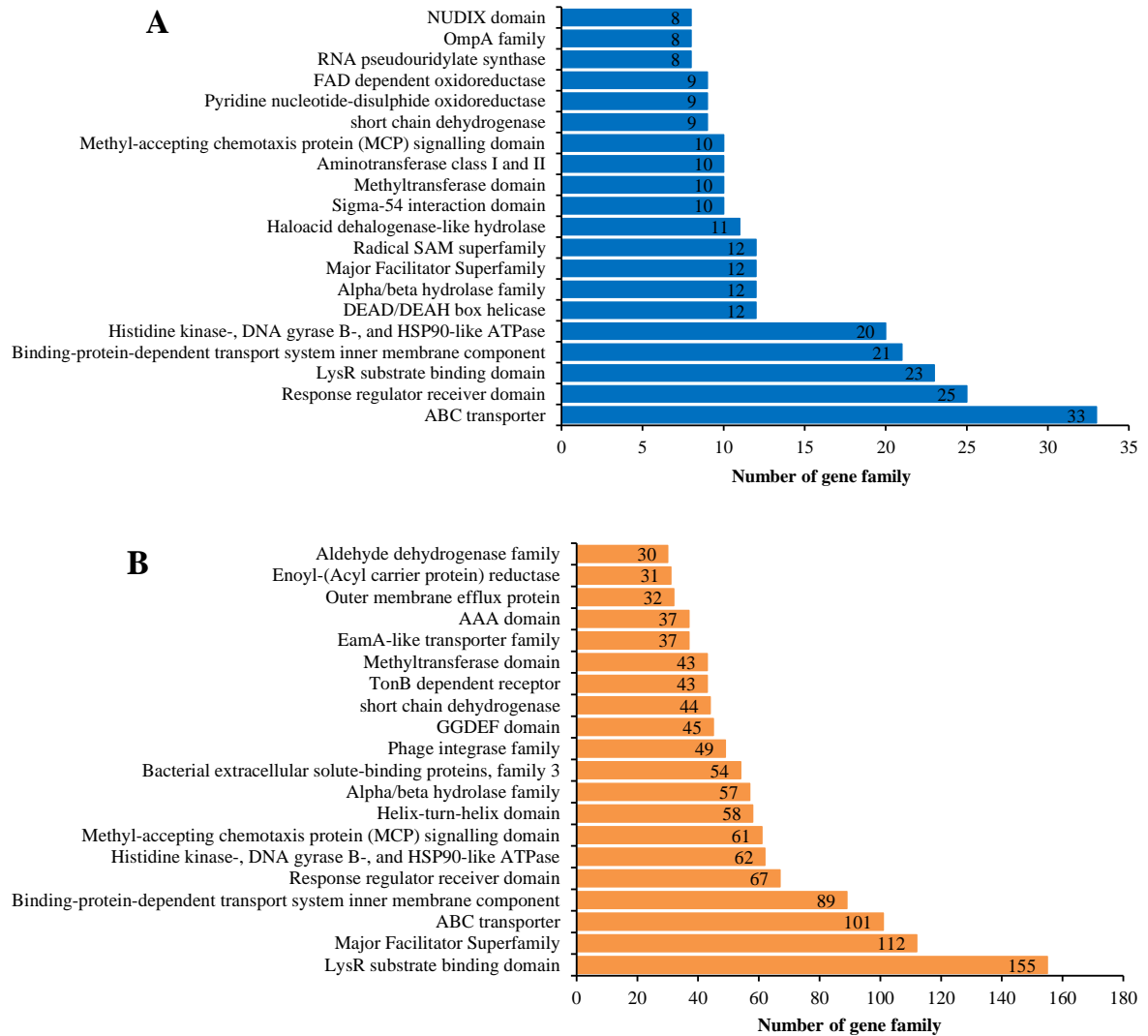
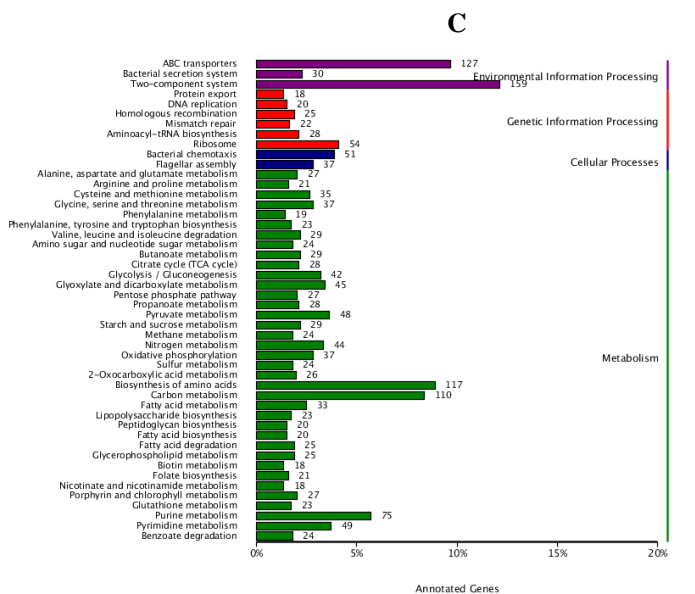
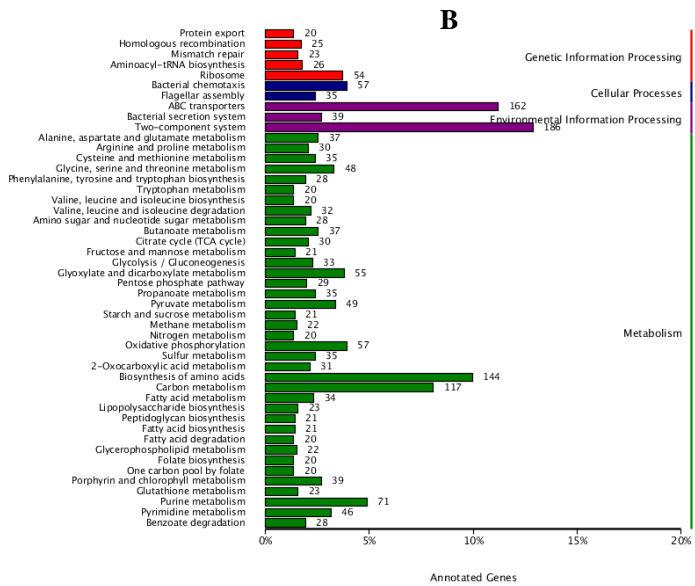
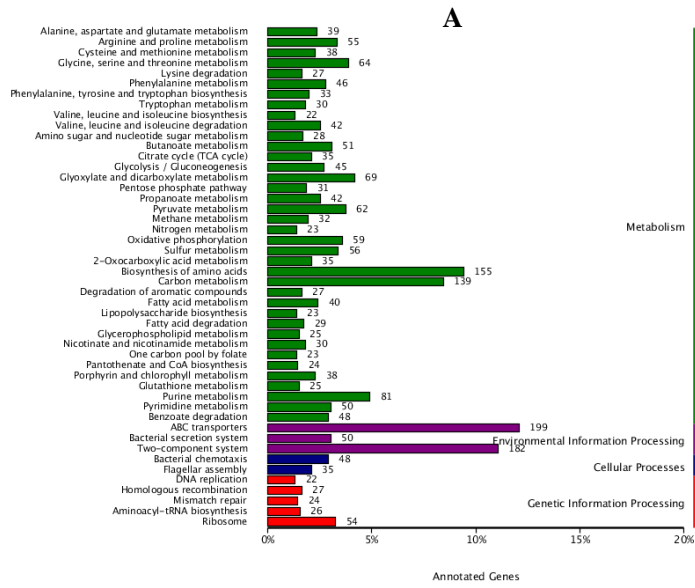
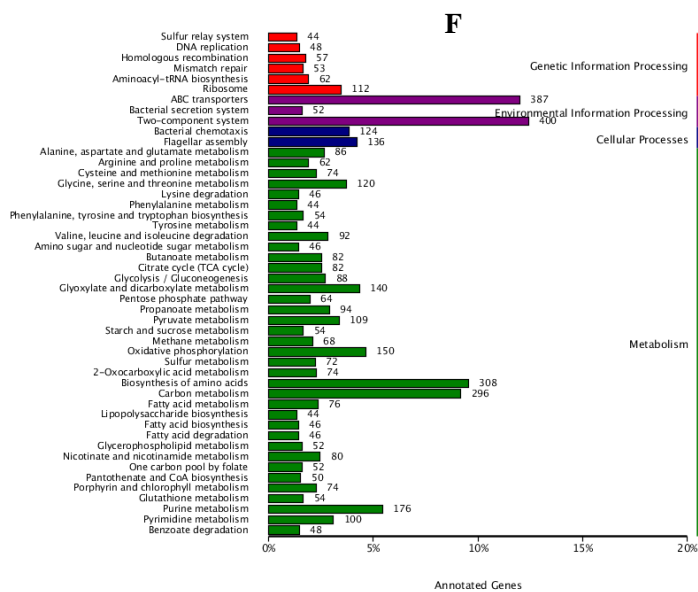
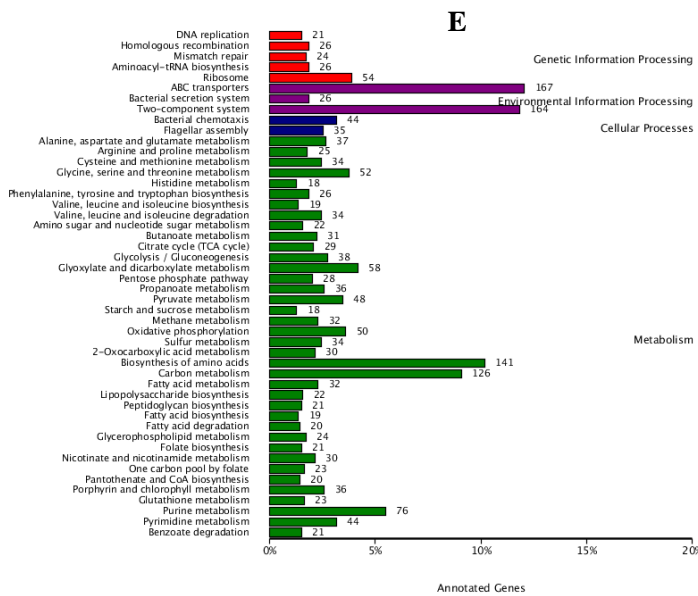
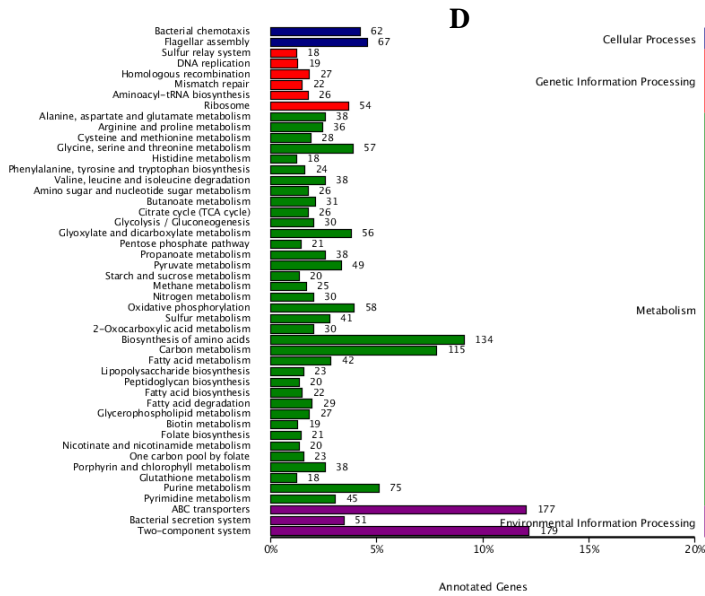


Figure S7. Annotated information of the top 20 core genome (A) and dispensable genome (B).





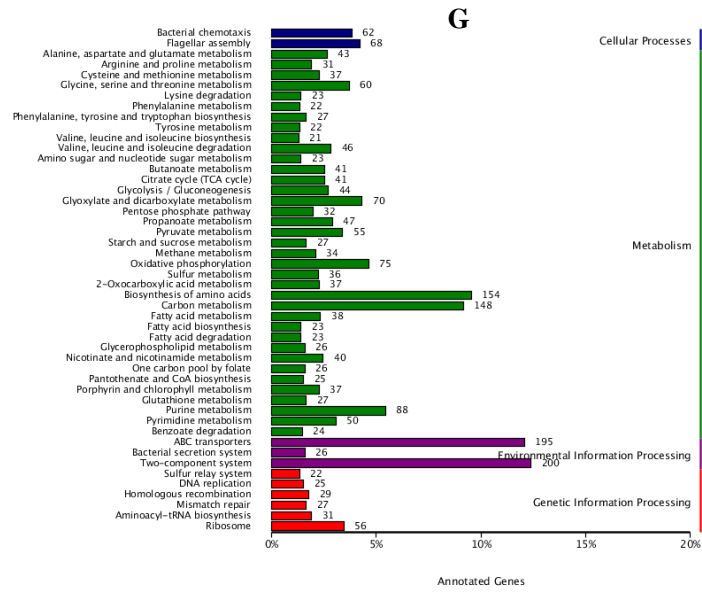


Figure S8. Specific gene family annotation information, A: Strain Sp1; B: Strain Sp3; C: Strain Sp5; D: Strain Sp7; E: Strain Sp10; F: Strain Sp11; G: Strain Sp12.

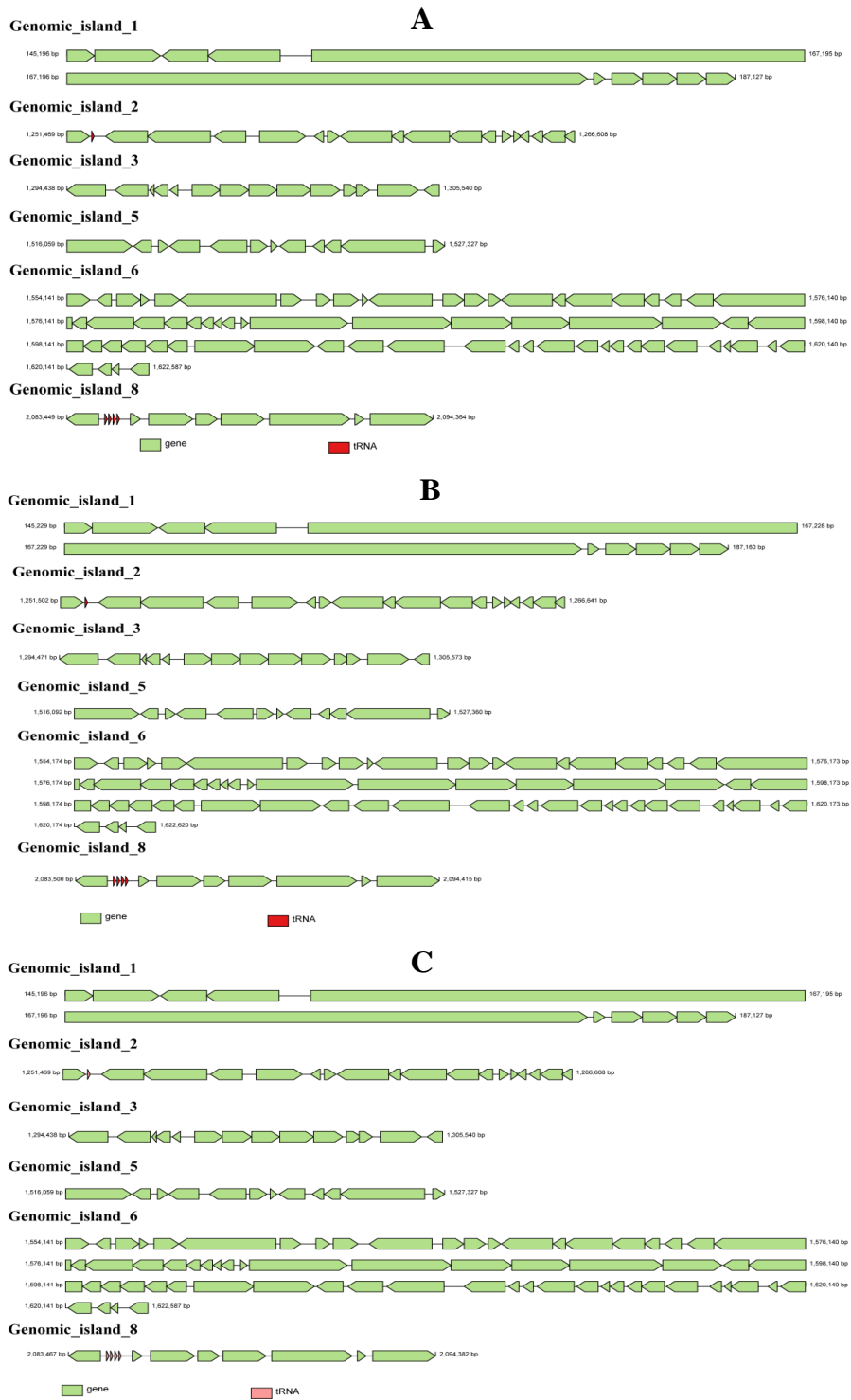


Figure S9. Gene island information shared by three inhibitory strains. (A) represented the gene fragment composition information of the base island in strain Sp10. (B) represented the gene fragment composition information of gene island in strain Sp11. (C) represented the composition information of gene island fragment in strain Sp12.

Table S1. Effects of inoculation of *Pseudomonas* on seed germination and comprehensive evaluation of the growth promotion.

Strains	Mean (U)	comprehensive assessment	Strains	Mean (U)	comprehensive assessment
St1	0.67±0.03ab	P	St18	0.47±0.03c	N
St2	0.65±0.02ab	P	St19	0.45±0.02cd	N
St3	0.68±0.02ab	P	St20	0.39±0.02d	N
St4	0.68±0.02ab	P	St21	0.66±0.02ab	P
St5	0.69±0.03ab	P	St22	0.7±0.02ab	P
St6	0.69±0.03ab	P	St23	0.68±0.01ab	P
St7	0.7±0.04ab	P	St24	0.7±0.03a	P
St8	0.67±0.02ab	P	St25	0.69±0.02ab	P
St9	0.67±0.02ab	P	St26	0.7±0.02ab	P
St10	0.66±0.02ab	P	St27	0.7±0.04a	P
St11	0.66±0.02ab	P	St28	0.69±0.02ab	P
St12	0.66±0.02ab	P	St29	0.7±0.03a	P
St13	0.67±0.02ab	P	St30	0.4±0.01d	N
St14	0.67±0.02ab	P	St31	0.2±0.02e	I
St15	0.62±0.02b	P	St32	0.22±0.02e	I
St16	0.67±0.03ab	P	St33	0.21±0.02e	I
St17	0.4±0.01d	N	St34	0.21±0.01e	I

Note: St1-St34 represented strains of *Pseudomonas*, P was promotion, N was no effect, I was Inhibition.

Values were mean ± standard error (SE), n=4 with bars indicating SE. These different small letters represented that there was a significant difference among the 34 inoculated strains at P<0.05.

Table S2. Information of *Pseudomonas* strains, based on the genome sequencing

Strain	Genome size (bp)	GC content	rRNA genes	tRNA genes	Coding density (%)	Protein coding sequences (CDS)
Sp1	6529891	61.81%	22	80	88.52%	983
Sp3	5483521	61.28%	22	77	89.59%	986
Sp5	4810218	62.43%	12	62	93.34%	962
Sp7	5134834	62.37%	12	67	89.88%	978
Sp10	5388833	60.96%	22	81	88.64%	979
Sp11	6384282	61.88%	22	78	88.63%	989
Sp12	6089740	60.94%	44	179	88.60%	987

Table S3. Information of horizontal gene transfer

Sample	Share number	Total number
Sp1	0	686
Sp3	0	725
Sp5	0	768
Sp7	0	386
Sp10	0	532
Sp11	0	1069
Sp12	0	555

Table S4. Information of SNP (single nucleotide variation), Small InDel and structural variation

Sample	SNP Number	Small InDel Number	structural variation	
			Insertion Number	Deletion Number
Sp3	359094	15591	14	59
Sp5	86323	4143	1	2
Sp7	126108	6228	1	6
Sp10	338213	11336	2	64
Sp11	256	5	6	144
Sp12	292103	9697	3	72

Note: SNP: nucleic acid variation at a single site; Small InDel: Insertion or deletion of a sequence of small fragments at a location in the genome, less than 50 bp in length; SV: Large gene segment insertion, deletion, repetition, inversion and the length is less than 50 bp.

Table S5. The id of gene islands predicted by 7 strains and the information of gene fragments contained in the gene islands were involved in this paper. (Note: Because the attached table is too large, the title part of the chart, such as strain number, gene island number and gene number, has been marked with orange. The 6 key gene islands with high similarity mentioned in the paper, Sp10, Sp11 and Sp12, have been marked with blue background.)

Table S6. Gene function annotation information of gene fragments contained in 6 gene islands with high similarity in Sp10, Sp11 and Sp12. (Note: Only genes annotated to KEGG function are listed; those that have not been annotated are not shown. As the table is too large, the title parts of the chart such as strain number, gene island number and gene number have been marked in orange. “✓” represented a gene is present in strain.