

Additional file 3. Summary of NGS analysis

Sample type	Total reads	Reads mapped to the reference genome	Read length	Number of mapped genes	Mapped %
IR^a	51,519,438	45,416,972	100	28,256	95.61
ID^b	53,444,250	44,573,700	100	33,976	93.01

^a IR, iron-rich.

^b ID, iron-deficient.

This table represents the depth and length of the experimental groups, the accuracy as

well.