

Table S2. Comparison of *pAtGCSpro*₁₁₇₈-Cas9-*Rj7*, *pUbiquitin*_{pro}-Cas9-*Rj7*, *pYAO*_{pro}-Cas9-*Rj7*, and *p2×35Spro*-Cas9-*Rj7* genome editing efficiency in soybean hairy roots

Cas9 system	no. of H/BM roots/ of roots examined	no. H/BM rate (%)
<i>p2×35Spro</i> -Cas9- <i>Rj7</i>	17/30	56.7 %
<i>pUbiquitin</i> _{pro} -Cas9- <i>Rj7</i>	4/30	13.3 %
<i>pYAO</i> _{pro} -Cas9- <i>Rj7</i>	4/30	13.3 %
<i>pAtGCSpro</i> ₁₁₇₈ -Cas9- <i>Rj7</i>	21/30	70.0 %