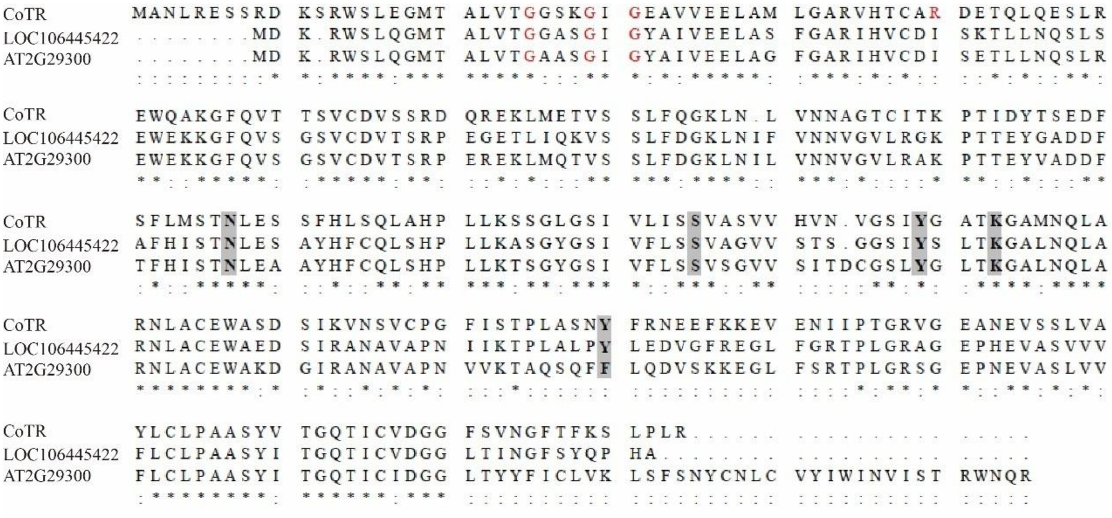
Supplementary Figure S4. Sequence alignment of BnTR1 and SDR proteins. The amino acids in red color represent the typical motifs (Gly-X_3-Gly-X-Gly), and a basic place (R49). The amino acids in grey represent the conserved residues that are responsible for catalytic function (N127, S155, Y168, K172, Y209).



```
CoTR          MANLRESSRD KSRWSLEGMT ALVTGGSKGI GEAVVEELAM LGARVHTCAR DETQLQESLR
LOC106445422  ........MD K.RWSLQGMT ALVTGGASGI GYAIVEELAS FGARIHVCDI SKTLLNQSLS
AT2G29300     ........MD K.RWSLQGMT ALVTGAASGI GYAIVEELAG FGARIHVCDI SETLLNQSLR
              :::::::::* *:****:*** *****:::** *:*:*****: :***:*:*:: ::*:*::**:

CoTR          EWQAKGFQVT TSVCDVSSRD QREKLMETVS SLFQGKLN.L VNNAGTCITK PTIDYTSEDF
LOC106445422  EWEKKGFQVS GSVCDVTSRP EGETLIQKVS SLFDGKLNIF VNNVGVLRGK PTTEYGADDF
AT2G29300     EWEKKGFQVS GSVCDVTSRP EREKLMQTVS SLFDGKLNIL VNNVGVLRAK PTTEYVADDF
              **::*****: :*****:**: ::*:*:::** ***:****:: ***:*::::* **::*:::**

CoTR          SFLMSTNLES SFHLSQLAHP LLKSSGLGSI VLISSVASVV HVN.VGSIYG ATKGAMNQLA
LOC106445422  AFHISTNLES AYHFCQLSHP LLKASGYGSI VFLSSVAGVV STS.GGSIYS LTKGALNQLA
AT2G29300     TFHISTNLEA AYHFCQLSHP LLKTSGYGSI VFLSSVSGVV SITDCGSLYG LTKGALNQLA
              :*::*****: ::*::**:** ***:**:*** *::***::** :::::**:*: :****:****

CoTR          RNLACEWASD SIKVNSVCPG FISTPLASNY FRNEEFKKEV ENIIPTGRVG EANEVSSLVA
LOC106445422  RNLACEWAED SIRANAVAPN IIKTPLALPY LEDVGFREGL FGRTPLGRAG EPHEVASVVV
AT2G29300     RNLACEWAKD GIRANAVAPN VVKTAQSQFF LQDVSKKEGL FSRTPLGRSG EPNEVASLVV
              ********:* :*::*:*:*: :::*:::::: :::::::::: ::::*:**:* *::**:*:*:

CoTR          YLCLPAASYV TGQTICVDGG FSVNGFTFKS LPLR...... .......... .....
LOC106445422  FLCLPAASYI TGQTICVDGG LTINGFSYQP HA........ .......... .....
AT2G29300     FLCLPAASYI TGQTICIDGG LTYYFICLVK LSFSNYCNLC VYIWINVIST RWNQR
              :********: ******:*** :::::::::: :::::::::: :::::::::: :::::
```