

## Supplementary figure 2.15

```
$ ffq -l 2 CRX118013 -o metadata.json
```

```
{
  "PRJNA118013": {
    "accession": "PRJNA118013",
    "title": "affy_cinetique_lyon_rose: Flower/Petal initiation and development in roses",
    "description": "affy_cinetique_lyon_rose. The objective is to identify genes involved i
n petal development and senescence. R. chinensis cv Old Blush (OB) was used for the following r
easons: it is a diploid Chinese rose that participated in the generation of modern roses (recur
rent flowering, scent, etc.). The objective here is to identify genes whose expression is assoc
iated with different flower development stages, from floral meristem to senescing flower. These
genes are putative candidates involved in floral initiation, development and senescence. All s
amples were collected at the same time early in the afternoon. Meristems and early flower devel
opment stages were dissected under a microscope. Total RNA was extracted from harvested tissues
using the Plant RNA kit (Macherey Nagel), and then used to hybridize Rosa-Affymetrix microarra
ys. Keywords: time course Overall design: 12 arrays - rose 6 developmental stages, 2 replicates
each.",
    "dbxref": "GSE18342",
    "organism": "Rosa chinensis",
    "target_material": "eTranscriptome"
  }
}
```