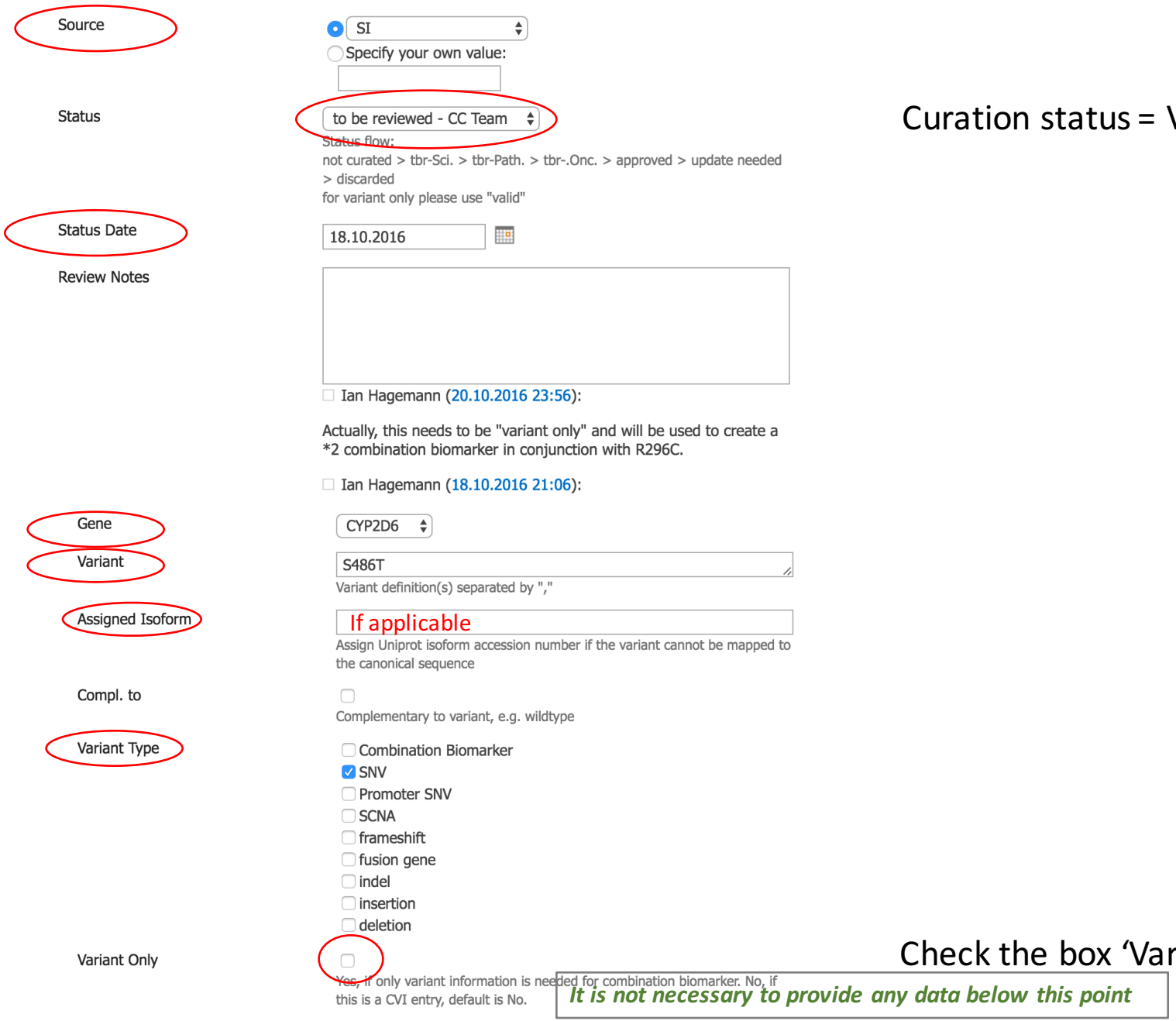
cvi_id = 2080

Variant only CVI

Required field in red



Curation status = Valid

Check the box ‘Variant only’

Combination biomarker

Source: SI
Specify your own value:

Status: to be reviewed - CC Team
Status flow:
not curated > tbr-Sci. > tbr-Path. > tbr-.Onc. > approved > update needed > discarded
for variant only please use "valid"

Status Date: 20.10.2016

Review Notes:
Ian Hagemann (21.10.2016 00:00):
Combination biomarker for *2 allele: R296C S486T

Gene: CYP2D6

Variant: R296C, S486T
Variant definition(s) separated by ","

Assigned Isoform:
Assign Uniprot isoform accession number if the variant cannot be mapped to

Compl. to:
Complementary to variant, e.g. wildtype

Variant Type:
- [x] Combination Biomarker
- [ ] SNV
- [ ] Promoter SNV
- [ ] SCNA
- [ ] frameshift
- [ ] fusion gene
- [ ] indel
- [ ] insertion
- [ ] deletion

Variant Only:
Yes, if only variant information is needed for combination biomarker. No, if this is a CVI entry, default is No.

Combined Variants:
ABCB1 amp (SCNA) - 19
ABCB1 S893A/T (SNV) -
ABL1 A196V (SNV) - 179
ABL1 A344V (SNV) - 174
ABL1 A350V (SNV) - 174
ABL1 A365V (SNV) - 174
ABL1 A366G (SNV) - 174

Add >
< Remove

CYP2D6 R296C (SNV) -
CYP2D6 S486T (SNV) -

Add references of CVIs that are part of the combination biomarker.