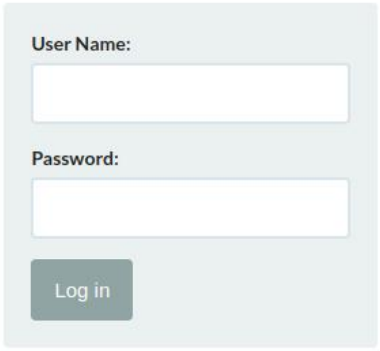
SuGR

Welcome to SuGR (SAFIR02 Upload Gustave Roussy), the Shiny application that allows you to check, edit your files and submit them on Synapse.

1- Enter your Synapse User Name and Password

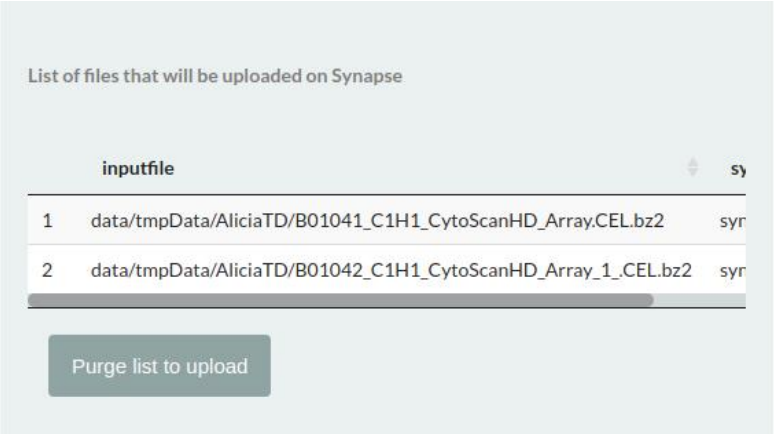


Please contact Alicia TRAN DIEN (alicia.tran-dien@gustaveroussy.fr) from Bioinformatics plateform for any requests.

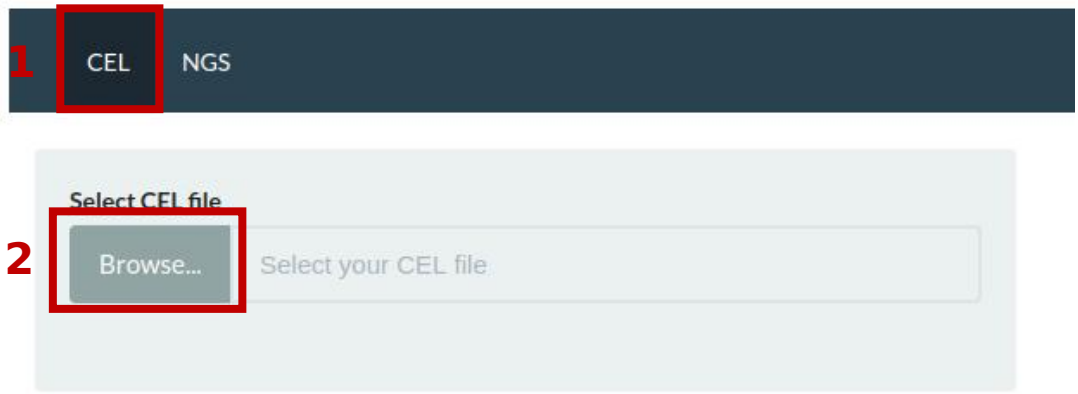
2- Upload your files

- You can select multiple files at the same time.
- If you don’t see your file, it means that the file you are trying to upload was not supported by SuGR. Please ensure that your file has either a .CEL/.CEL.bz2 or a .tsv extension. Otherwise, the warning below will show up.

- On the side panel, you can see the list of files that will be uploaded on Synapse

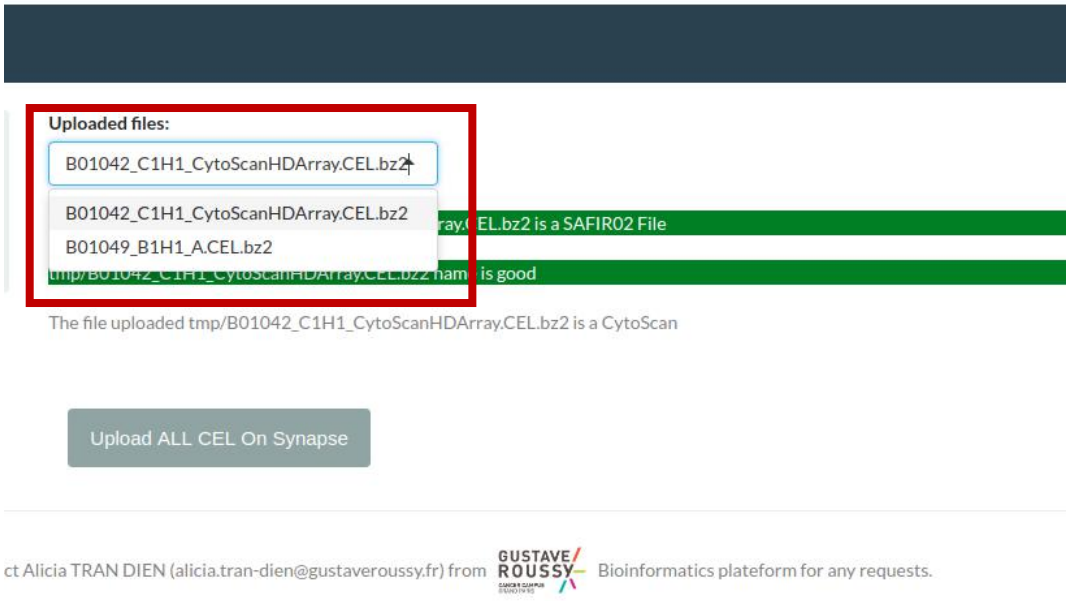


a- *Upload CEL file*



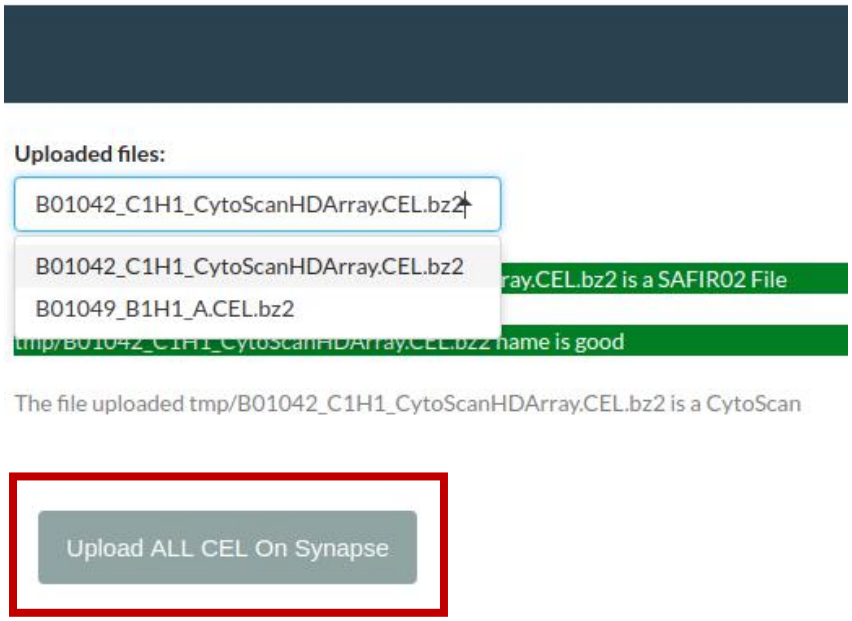
Warning : Everytime you will click on Browse, the previous list of files to upload will be deleted.

- Select your file in the drop down menu



ct Alicia TRAN DIEN (alicia.tran-dien@gustaveroussy.fr) from GUSTAVE ROUSSY Bioinformatics plateform for any requests.

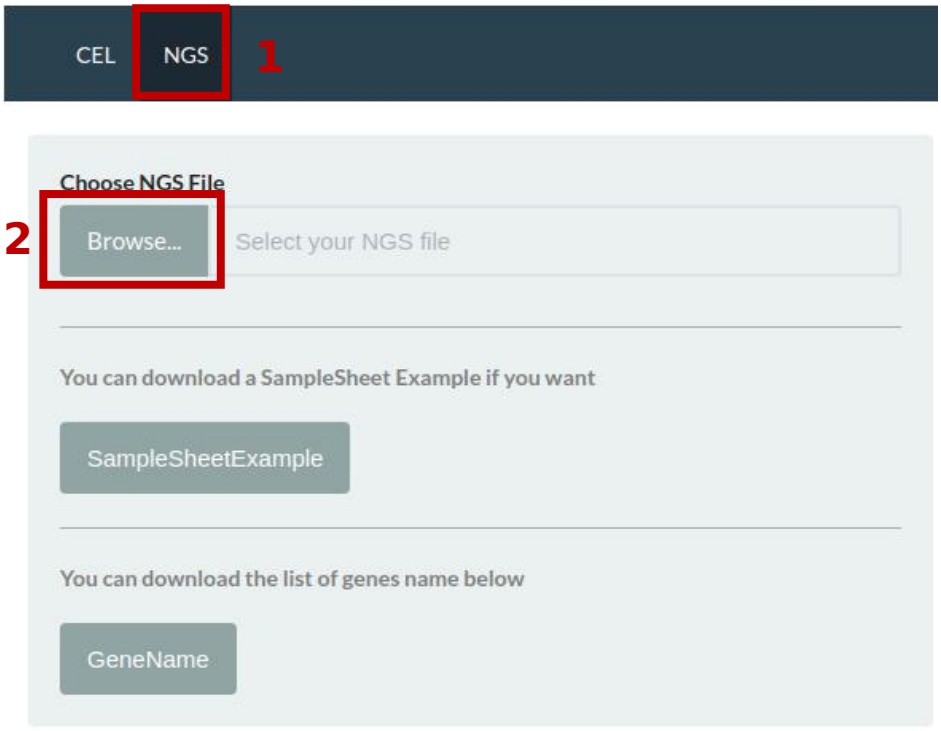
- Upload all the files on Synapse



GUSTAVE ROUSSY CANCER CAMPUS GRAND PARIS

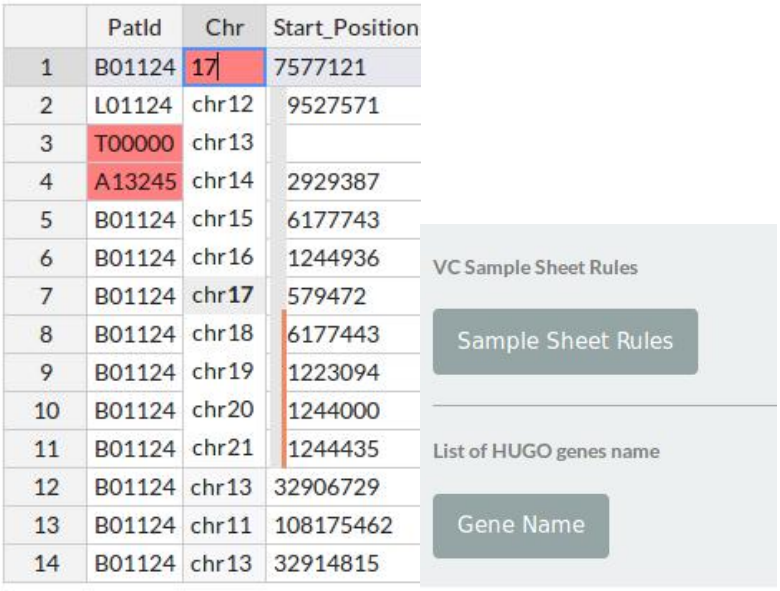
b- Upload NGS file

- You can select multiple files at the same time.



Warning : Everytime you will click on Browse, the previous list of files to upload will be deleted.

- A discrepancy will be mark in red. You can edit the table by double clicking on the cell, select your correction in the drop down menu and type Enter after modification. You can also get some help by looking at the Sample Sheet Rules or the list of Gene Name files.



Nom du colonne	Example	NB
PatId	B01002	Lettre B ou L suivie de 5 chiffres. Si T = SAFIR-TOR = Pas accepté
Chr	chr17	chr + numero du chromosome
Start_Position	41223094	
Reference_Seq	T	Si SNV, Ref et Var sont représentés par une seule base.
Variant_Seq	C	
Global_Conclusion	NA	Ne pas mettre l'accent dans les mots ni caractère spéciaux
Manual_Var_Comment	NA	Ne pas mettre l'accent dans les mots ni caractère spéciaux
Manual_Var_Classif	0	0 = polymorphisme : 1000genome ou ESP >=1 % VP = PAS un polymorphisme 1000genome ou ESP <1%) - COSMIC ID present VPI = PAS un polymorphisme 1000genome ou ESP <1%) - PAS de COSMIC ID present - predit deletere par au moins 1 outil VNP = PAS un polymorphisme 1000genome ou ESP <1%) - PAS de COSMIC ID present - PAS predit deletere ==> on retrouve les synonymes dedans
Variant_Freq	51.8	Utilise "point" mais pas "virgule"; un chiffre entre 0 et 100
Position_Cov	396	Utiliser la même qualité de filtres pour cette information et «Variant Cov »
End_Position	41223094	
Strand	-	utilise "-" ou "+" ou NA
Variant_Cov	205	Utiliser la même qualité de filtre pour cette information et « Position Cov »
Quality	2132.79	Utilise "point" mais pas "virgule" – Mettre NA si PGM non utilisé
Strand_Bias	0.5019	Utilise "point" mais pas "virgule" – valeur entre 0 et 1
Amplicon_Ref	AMPL3658889274	
Gene_Symbol	BRCA1	
Protein_Change	p.Ser1634Gly	En suivant les recommandations HGVS, reporter les variant avec les amino acides en code 3 lettres
Exon	16	Mettre juste le numero d'exon mais pas "exonXX" / "exXX"
RefSeq_Id	NM_007300.3	Se limiter à la liste des NM définie pour le projet
cDNA_Change	c.4900A>G	
Codon	1634	Reporter le numéro de l'exon, pas le p.
Type	SNP	Utilise "SNP", "INS" ou "DEL"
MAF_classification	missense_variant	lister tout ce qui est accepter
ESP_Freq	0.326628	Utilise "point" mais pas "virgule", version base de données XX
by1000G_Freq	0.36147757255936674	Utilise "point" mais pas "virgule", version base de données XX
DbSNP_Id	rs1799966	version base de données XX
COSMIC_Id	COSM3755560,COSM3755559	Ne reporter QUE les COSM ID, pas les informations tissus ou autres informations + version base de données XX

Don’t forget to click on Save changes after editing.

Warning : Clicking again on the file in the drop down menu will erase your modifications.

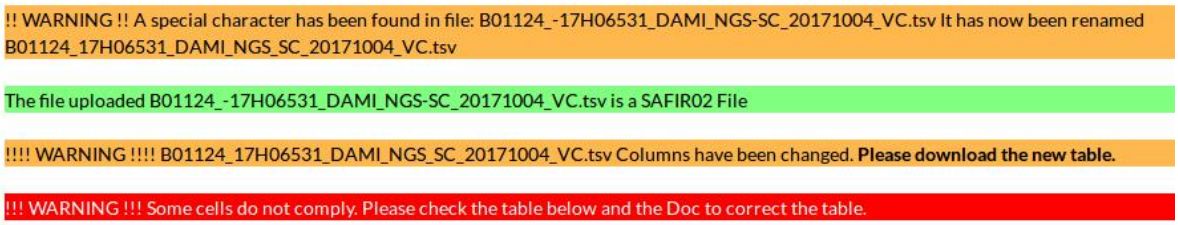
	nd	Variant_Cov	Quality	Strand_Bias	Amplicon_Ref	Gene_Symbol	Protein_Change	Exon	RefSeq_Id	cDNA_Change	Codon	Type	MAF_classification	ESF
1		1308	17020	0.5051	AMPL7153020889	Tp53	p.R273C	8	NM_000546.5	c.817C>T	273	SNP	Missense_Mutation	_
2		846	10628.6	0.5062	AMPL7153093291	NF1	p.Val341Arg	9	NM_001042492.2	c.1020dupT	341	INS	Frame_Shift_Ins	_
3				2										
4		1996	33785.7	-1	AMPL7156564246	BrCA1	p.V2466A	14	NM_000059.3	c.7397T>C	2466	SNP	Missense_Mutation	_
5		1444	24518.4	0.5	AMPL7154537885	MAP3K1	p.V906I	14	NM_005921.1	c.2716G>A	906	SNP	Missense_Mutation	_
6		271	1330.75	0.5555	AMPL7154370157	BRCA1	p.P871L	10	NM_007294.3	c.2612C>T	871	SNP	Missense_Mutation	_
7		884	12891.6	0.5208	AMPL7152996432	TP53	p.P72R	12	NM_000546.5	c.215C>G	72	s	Missense_Mutation	36.
8		1110	18695.5	0.5	AMPL7154537882	MAP3K1	p.D806N	14	NM_005921.1	c.2416G>A	806	SNP	Missense_Mutation	_
9		248	1126	0.5157	AMPL7156567638	BRCA1	p.S1613G	15	NM_007294.3	c.4837A>G	1613	SNP	Missense_Mutation	_
10		99	424.779	0.5336	AMPL7154370149	BRCA1	p.K1183R	10	NM_007294.3	c.3548A>G	1183	SNP	Missense_Mutation	_
11		209	815.407	0.6118	AMPL7154370153	BRCA1	p.E1038G	10	NM_007294.3	c.3113A>G	1038	z	Missense_Mutation	_
12		738	9815.09	0.5081	AMPL7153359848	BRCA2	p.N372H	10	NM_000059.3	c.1114A>C	372	SNP	Missense_Mutation	23.
13		1148	14233.3	0.5033	AMPL7154368713	ATM	p.D1853N	37	NM_000051.3	c.5557G>A	1853	SNP	Missense_Mutation	_
14		174	1216.49	0.5561	AMPL7154368671	BRCA2	p.R2108H	11	NM_000059.3	c.6323G>A	2108	SNP	Missense_Mutation	_

- The new version of your table can be download by clicking on:

3- Warning Color

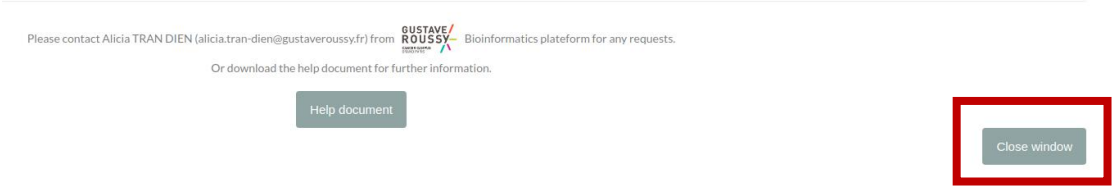
- A green warning indicates that the file is correct and can be uploaded
- An orange warning indicates that the file is incorrect but the problem has been corrected (ex: space found in file name) and the file ready to be uploaded. Note that once the file has been rename, you can not click again on the drop down menu. You will have to upload it again
- A red warning indicates that the file is incorrect and that a new version has to be edited and/or download.

Make sure that there are no red warnings before uploading on synapse.



4- Disconnecting

You can disconnect from Synapse and close the app/window by clicking on the button below. Note that all the temp files will be deleted as well.



5- Contact

If you need any help or requests, please contact Alicia TRAN DIEN (alicia.tran-dien@gustaveroussy.fr) from Gustave Roussy Bioinformatics plateform.