

---

# Diploid VCF: Determining sites with only heterozygous calls

Uploading full diploid VCF

```
In[1]:= fullgenomeDIP = Import[
    "/Users/otto/Documents/Students/AnnaBazzicalupo/MetalAdaptation/Genomics/07
    _genomicsDB/full_genome.vcf"];

In[2]:= fullheader = fullgenomeDIP[[1 ;; 58]];

In[3]:= header = fullgenomeDIP[[58]];

In[4]:= fullgenomeDIP = Drop[fullgenomeDIP, 58];

In[5]:= header
Out[5]= {##CHROM, POS, ID, REF, ALT, QUAL, FILTER, INFO, FORMAT, CdBM23_S1, CdBM25_S10,
    CdBM26_S18, CdBM29_S26, CdBM30_S34, CdBM32_S42, CdBM36_S50, CdBM37_S58,
    CdBM39_S2, CdBM42_S11, CdBM43_S19, CdBM44_S27, CdBM45_S35, CdBM46_S43,
    CdBM47_S51, CdBM48_S59, CoBM12_S4, CoBM14_S13, CoBM15_S21, CoBM16_S29,
    CoBM17_S37, CoBM18_S45, CoBM1_S3, CoBM20_S53, CoBM21_S61, CoBM2_S12,
    CoBM3_S20, CoBM4_S28, CoBM5_S36, CoBM6_S44, CoBM7_S52, CoBM8_S60,
    CuBM10_S54, CuBM11_S62, CuBM12_S6, CuBM13_S15, CuBM14_S23, CuBM15_S31,
    CuBM16_S39, CuBM17_S47, CuBM18_S55, CuBM3_S5, CuBM4_S14, CuBM6_S22,
    CuBM7_S30, CuBM8_S38, CuBM9_S46, MnBM12_S63, MnBM13_S7, MnBM14_S16,
    MnBM15_S24, MnBM16_S32, MnBM17_S40, MnBM18_S48, MnBM20_S56, MnBM21_S64,
    MnBM23_S8, MnBM24_S17, MnBM25_S25, MnBM27_S33, MnBM28_S41, MnBM29_S49,
    MnBM31_S57, MnBM32_S65, MnBM34_S66, MnBM38_S72, MnBM39_S78, MnBM42_S84,
    MnBM44_S90, NiBM11_S73, NiBM12_S79, NiBM14_S85, NiBM16_S91, NiBM17_S97,
    NiBM21_S103, NiBM22_S109, NiBM24_S68, NiBM25_S74, NiBM27_S80, NiBM28_S86,
    NiBM29_S92, NiBM30_S98, NiBM4_S96, NiBM6_S102, NiBM8_S108, NiBM9_S67,
    OLY077_S101, ZnBM11_S104, ZnBM12_S110, ZnBM15_S69, ZnBM16_S75, ZnBM17_S81,
    ZnBM19_S87, ZnBM22_S93, ZnBM23_S99, ZnBM25_S105, ZnBM28_S111, ZnBM29_S70,
    ZnBM31_S76, ZnBM34_S82, ZnBM37_S88, ZnBM38_S94, ZnBM39_S100, ZnBM41_S106,
    ZnBM42_S112, ZnBM43_S71, ZnBM44_S77, ZnBM45_S83, ZnBM46_S89, ZnBM47_S95}

In[6]:= Length[fullgenomeDIP]
Out[6]= 19 627
```

Keeps only those sites with depth  $\geq 5$  and that have some “1|1” calls (stripping out heterozygous only calls):

```
In[7]:= droppos = -1 + Position[header, "CdBM23_S1"][[1, 1]];
    (** columns to be dropped before first sample*)
```

```

In[8]:= genomeDIP =
  Table[".|.", {i, 1, Length[fullgenomeDIP]}, {j, 1, Length[header] - droppos}];

In[9]:= For[i = 1, i ≤ Length[fullgenomeDIP], i++,
  For[j = 1 + droppos, j ≤ Length[header], j++,
    temp = StringSplit[fullgenomeDIP[[i, j]], {":"}];
    If[temp[[1]] ≠ "|.", If[Length[temp] ≥ 3,
      If[ToExpression[temp[[3]]] ≥ 5,
        genomeDIP[[i, j - droppos]] = StringReplace[temp[[1]], "/" → "|"]]]];
    (*Strips out difference in phasing information*)
  ]
]

In[10]:= genomeDIP // Length
Out[10]=
19 627

In[11]:= For[i = 1;
  keep = Table[1, {i, 1, Length[genomeDIP]}], i ≤ Length[genomeDIP], i++,
  tally = Tally[genomeDIP[[i]]];
  If[Length[Position[tally, "1|1"]] == 0, keep[[i]] = 0]
]

In[12]:= keeptable = {};
droptableDIP = {};
For[i = 1, i ≤ Length[genomeDIP], i++,
  If[keep[[i]] > 0,
    keeptable = AppendTo[keeptable, fullgenomeDIP[[i, 1 ;; 2]]],
    droptableDIP = AppendTo[droptableDIP, fullgenomeDIP[[i, 1 ;; 2]]];
]

In[15]:= keeptable[[1 ;; 10]]
Out[15]=
{{ref|NC_001133|, 12 690}, {ref|NC_001133|, 15 592},
 {ref|NC_001133|, 19 971}, {ref|NC_001133|, 23 712},
 {ref|NC_001133|, 23 713}, {ref|NC_001133|, 25 340}, {ref|NC_001133|, 25 487},
 {ref|NC_001133|, 25 488}, {ref|NC_001133|, 25 489}, {ref|NC_001133|, 25 497}}

In[16]:= Length[keeptable]
Out[16]=
11 300

In[17]:= Length[droptableDIP]
Out[17]=
8327

In[18]:= Export["sitestokeep.csv", keeptable];

```

# Looking at data from snpEff

## Uploading data

Converting information from snpEff

```
In[19]:= fullgenomeSNPEFF = Import[
    "/Users/otto/Documents/Students/AnnaBazzicalupo/MetalAdaptation/Genomics/
    snpEff_RMheterozygotes_RMmodifiers_4Nov2024.tsv"];

In[20]:= header = fullgenomeSNPEFF[[1]]
Out[20]= {CHROM, chr, POS, REF, ALT, QUAL, FORMAT, gene, effect, mut_type, gene_code,
    base_change, aa_change, ANN, OLY077_S101, CdBM23_S1, CdBM25_S10, CdBM26_S18,
    CdBM29_S26, CdBM30_S34, CdBM32_S42, CdBM36_S50, CdBM37_S58, CdBM39_S2,
    CdBM42_S11, CdBM43_S19, CdBM44_S27, CdBM45_S35, CdBM46_S43, CdBM47_S51,
    CdBM48_S59, CoBM12_S4, CoBM14_S13, CoBM15_S21, CoBM16_S29, CoBM17_S37,
    CoBM18_S45, CoBM1_S3, CoBM20_S53, CoBM21_S61, CoBM2_S12, CoBM3_S20, CoBM4_S28,
    CoBM5_S36, CoBM6_S44, CoBM7_S52, CoBM8_S60, CuBM10_S54, CuBM11_S62, CuBM12_S6,
    CuBM13_S15, CuBM14_S23, CuBM15_S31, CuBM16_S39, CuBM17_S47, CuBM18_S55, CuBM3_S5,
    CuBM4_S14, CuBM6_S22, CuBM7_S30, CuBM8_S38, CuBM9_S46, MnBM12_S63, MnBM13_S7,
    MnBM14_S16, MnBM15_S24, MnBM16_S32, MnBM17_S40, MnBM18_S48, MnBM20_S56,
    MnBM21_S64, MnBM23_S8, MnBM24_S17, MnBM25_S25, MnBM27_S33, MnBM28_S41,
    MnBM29_S49, MnBM31_S57, MnBM32_S65, MnBM34_S66, MnBM38_S72, MnBM39_S78,
    MnBM42_S84, MnBM44_S90, NiBM11_S73, NiBM12_S79, NiBM14_S85, NiBM16_S91,
    NiBM17_S97, NiBM21_S103, NiBM22_S109, NiBM24_S68, NiBM25_S74, NiBM27_S80,
    NiBM28_S86, NiBM29_S92, NiBM30_S98, NiBM4_S96, NiBM6_S102, NiBM8_S108, NiBM9_S67,
    ZnBM11_S104, ZnBM12_S110, ZnBM15_S69, ZnBM16_S75, ZnBM17_S81, ZnBM19_S87,
    ZnBM22_S93, ZnBM23_S99, ZnBM25_S105, ZnBM28_S111, ZnBM29_S70, ZnBM31_S76,
    ZnBM34_S82, ZnBM37_S88, ZnBM38_S94, ZnBM39_S100, ZnBM41_S106, ZnBM42_S112,
    ZnBM43_S71, ZnBM44_S77, ZnBM45_S83, ZnBM46_S89, ZnBM47_S95, AC, AF, AN,
    BaseQRankSum, DP, FS, MLEAC, MLEAF, MQ, MQRankSum, QD, ReadPosRankSum, SOR, LOF}

In[21]:= fullgenomeSNPEFF = Drop[fullgenomeSNPEFF, 1];

Keeps only those sites with depth ≥5 and that have some “1|1” calls (stripping out heterozygous only
calls):

In[22]:= droppos = -1 + Position[header, "OLY077_S101"][[1, 1]];
    (** columns to be dropped before first sample*)

In[23]:= topos = Position[header, "ZnBM47_S95"][[1, 1]]; (** last metal column*)
```

```
In[24]:= genelist = Sort[Union[fullgenomeSNPEFF[All, 8]]]
```

```
Out[24]=
```

```
{ABP1, ACB1, ACC1, ADE6, ADR1, AFT1, AGP1, AHK1, ALD5, ALY2, APC2, ARO3, ASN1,
ATG11, ATG2, BDS1, BIR1, BLM10, BNA6, BNI1, BNI4, BRR2, BSC1, BSD2, BUD19,
BUL1, BUL2, CAJ1, CCR4, CCW12, CDC25, CIC1, CLB3, CLN3, CNE1, COG1, COG3, COQ1,
CPA1, CSM3, CUE3, CWC22, CWH41, CYK3, DAL2, DAN4, DBF20, DBP10, DDR48, DNF1,
DOA4, DOT6, DSC2, DSE4, DUS4, EBS1, ECM14, ECM22, EFR3, ERB1, ERG1, ERG27,
ERG7, ERG9, FAS2, FAU1, FCY2, FET4, FIG2, FIG4, FLC2, FLO1, FLO9, FMP52, FRE6,
FSF1, FYV10, FYV6, FZF1, GAS4, GCD2, GPB1, GPB2, GPH1, GSC2, HAP1, HBT1, HEH2,
HHF2, HIS4, HMF1, HO, HRT3, HSL1, HSP104, HUL5, HXT13, IDP1, IES3, ILV2, IMA1,
INP2, IOC4, IPI3, IRC20, IRC8, IST2, ISU1, ITC1, KAR3, KGD1, KIN1, KIN82, KRE5,
KSP1, KTR3, LAM1, LAM6, LOS1, LRG1, MAM3, MAS2, MCK1, MCM5, MCT1, MDH2, MDL2,
MDM30, MET10, MET30, MEX67, MHP1, MKT1, MLF3, MLH3, MLS1, MMS4, MNN9, MOT1,
MPA43, MRL1, MRPL36, MSC6, MSS11, MSS2, MTR4, MYO2, NAM8, NAR1, NFT1, NGG1,
NIP100, NPL3, NSR1, NUC1, NUG1, OAF1, OCA4, OCA5, OPI1, OSH2, PBP2, PBS2, PCL5,
PDA1, PDR1, PDR10, PDX1, PET111, PET127, PFK26, PHM7, PHO23, PHO81, PHO84,
PIB1, PIR3, PKP1, PLB2, PMA1, POL3, PPQ1, PRC1, PRI1, PRI2, PRP2, PRP8, PTK2,
PYK2, QRI7, RAD16, RAD17, RAD26, RBK1, RCE1, RCK2, RCO1, REC102, RED1, RH01,
RIM11, RIM21, RKM3, RMP1, RNY1, ROG1, RPA135, RPI1, RPL22A, RPL2A, RPS15,
RPS2, RPT5, RRB1, RRG7, RRP46, RRP6, RSC1, RSE1, RTC2, SAK1, SAP4, SBE2, SEC8,
SET2, SFP1, SHP1, SIW14, SKN1, SMC2, SMY2, SNF7, SNT2, SPC105, SP077, SPS100,
SRP40, SSE1, SSK2, SSQ1, SSZ1, STE5, STP3, STT3, SUB2, SUC2, SUM1, SWC5, SWS2,
SWT1, SYF2, SYG1, TAF8, TAH11, TAO3, tC(GCA)B, TC089, tE(UUC)G3, TFB1, TFG1,
TIM54, tK(CUU)E2, TOM1, TOP1, TOP2, TOS3, TPS3, TRK2, TRL1, TRT2, tS(AGA)M,
TUS1, UBC1, UBP5, UBR2, UBX7, UGA3, UGA4, UIP5, ULS1, UME6, URA2, URB1, USA1,
UTP21, UTP8, VBA1, VCX1, VHR2, VID22, VPS13, VPS63, VPS74, VRP1, VTC1, VTC3,
VTC4, VTC5, WAR1, YAP6, YBL109W, YBR134W, YBR242W, YBR292C, YCF1, YCK1,
YCT1, YDL176W, YDL199C, YDR003W-A, YDR157W, YDR269C, YDR381C-A, YDR541C,
YDR544C, YEF1, YER087C-A, YER156C, YFL021C-A, YFR036W-A, YGR126W, YGR130C,
YGR266W, YHC1, YHC3, YHL008C, YHR028W-A, YHR071C-A, YIH1, YIL092W, YIR020W-A,
YJL211C, YKR073C, YLL020C, YLL066W-B, YLR108C, YLR296W, YLR312C, YLR372W,
YML119W, YMR027W, YMR317W, YNL109W, YOR029W, YOR1, YOR296W, YOR343C, YPK1,
YPL025C, YPL114W, YPR078C, YPR089W, YPR117W, YRA1, YRB2, ZDS2, ZRT1, ZRT3}
```

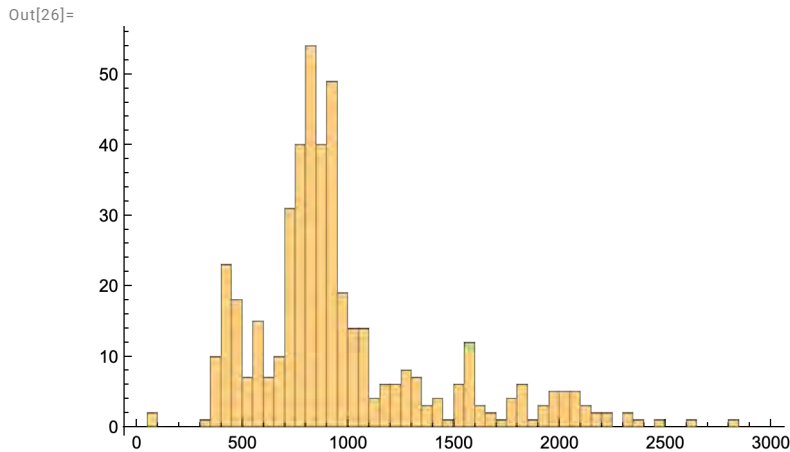
Plotting the depth of coverage at that site:

```
In[25]:= Max[fullgenomeSNPEFF[All, 129]]
```

```
Out[25]=
```

```
17 792
```

```
In[26]:= fullgenedepth =  
Histogram[fullgenomeSNPEFF[All, 129], {50}, PlotRange -> {{0, 3000}, Automatic}]
```



There are two low outliers (BSC1 and HAP1, filtered out below for having too many “.” genotypes):

```
In[27]:= Select[fullgenomeSNPEFF[All, 129], # < 300 &]  
Out[27]=  
{ 91, 84 }
```

There are three high outliers (all FLO1, filtered out below for having too many “.” genotypes):

```
In[28]:= Select[fullgenomeSNPEFF[All, 129], # > 3000 &]  
Out[28]=  
{ 15 599, 15 734, 17 792 }
```

Mean depth:

```
In[29]:= Mean[fullgenomeSNPEFF[All, 129]] // N  
Out[29]=  
1072.34
```

## Dropping tRNAs, checking overlapping coding regions (snpeff), and dropping dubious genes

Dropping tRNAs, which we drop {"tC(GCA)B", "tE(UUC)G3", "tK(CUU)E2", "tS(AGA)M"} and TRT2 (which is tT(CGU)K), but first checking that their annotations from snpeff do not involve other genes (other than upstream or downstream modifiers):

```
In[30]:= dropgenes = {"tC (GCA) B", "tE (UUC) G3", "tK (CUU) E2", "tS (AGA) M", "TRT2"};
```

Depth of coverage for these genes is pretty typical:

```
In[31]:= Select[fullgenomeSNPEFF, MemberQ[dropgenes, #[[8]] &] [[All, {8, 129}]]
Mean[%[[All, 2]]] // N
```

```
Out[31]=
{{tC(GCA)B, 1316}, {tK(CUU)E2, 1111},
 {tE(UUC)G3, 398}, {TRT2, 2091}, {tS(AGA)M, 885}}
```

```
Out[32]=
1160.2
```

Dropping these five tRNAs

```
In[33]:= Length[fullgenomeSNPEFF];
fullgenomeSNPEFF = Select[fullgenomeSNPEFF, MemberQ[dropgenes, #[[8]] == False &];
%% - Length[fullgenomeSNPEFF]
```

```
Out[35]=
5
```

Looking over all genes whose most extreme snpEff calls involve more than one protein-coding gene:

```
In[36]:= catSNPEFF = {"LOW", "MODERATE", "HIGH"}; (*Not "MODIFIER"*)
```

```
In[37]:= Clear[sumFULL]
sumFULL = Table["ERROR", {i, 1, Length[fullgenomeSNPEFF]}];
For[i = 1, i ≤ Length[fullgenomeSNPEFF], i++,
  temp = StringSplit[fullgenomeSNPEFF[[i, 14]], {"|"}];
  temp2 = Tally[temp];
  temp3 = Select[temp2, MemberQ[catSNPEFF, #[[1]] &];
  sumFULL[[i]] = Total[temp3] [[2]]
]
```

```
In[40]:= Position[sumFULL, _? (# > 1 &)]
```

```
Out[40]=
{{84}, {120}, {227}, {229}, {296}, {317}, {356}, {380}, {439}}
```

```
In[41]:= Position[sumFULL, _? (# > 2 &)]
```

```
Out[41]=
{ }
```

**#84: YDR269C is dubious, but CCC2 is verified (SGD) [Updated]**

```
In[42]:= fixme = 84;
```

```
In[43]:= fullgenomeSNPEFF[[fixme, 8]]
```

```
Out[43]=
YDR269C
```

Manually swapping for the second gene:

```
In[44]:= fullgenomeSNPEFF[[fixme]]
```

```
Out[44]=
{chrIV, 4, 1005804, G, T, 283.29, GT:AD:DP:GQ:PL, YDR269C,
 MODERATE, missense_variant, YDR269C, c.185C>A, p.Thr62Asn,
```

```

T|missense_variant|MODERATE|YDR269C|YDR269C|transcript|YDR269C_mRNA|
protein_coding|1/1|c.185C>A|p.Thr62Asn|185/324|185/324|62/107||,T|
missense_variant|MODERATE|CCC2|YDR270W|transcript|YDR270W_mRNA|protein_coding
|1/1|c.130G>T|p.Val44Leu|130/3015|130/3015|44/1004||,T|upstream_gene_variant|
MODIFIER|HEL2|YDR266C|transcript|YDR266C_mRNA|protein_coding||c.-3781C>A||||
3781|,T|upstream_gene_variant|MODIFIER|CIA1|YDR267C|transcript|YDR267C_mRNA|
protein_coding||c.-2302C>A||||2302|,T|upstream_gene_variant|MODIFIER|GL02|
YDR272W|transcript|YDR272W_mRNA|protein_coding||c.-3206G>T||||3206|,T|
upstream_gene_variant|MODIFIER|DON1|YDR273W|transcript|YDR273W_mRNA|
protein_coding||c.-4372G>T||||4372|,T|downstream_gene_variant|MODIFIER|MSW1|
YDR268W|transcript|YDR268W_mRNA|protein_coding||c.*661G>T||||661|,T|
downstream_gene_variant|MODIFIER|YDR271C|YDR271C|transcript|YDR271C_mRNA|
protein_coding||c.*2591C>A||||2591|,0:3,0:3:99:0,109,
0:5,0:5:99:0,135,0:3,0:3:99:0,113,0:4,0:4:99:0,104,0:3,0:3:99:0,100,
0:4,0:4:99:0,115,0:3,0:3:99:0,100,0:3,0:3:99:0,100,0:4,0:4:99:0,107,
0:4,0:4:99:0,100,0:4,0:4:99:0,137,0:3,0:3:99:0,100,0:4,0:4:99:0,109,
0:7,0:7:99:0,125,0:3,0:3:99:0,100,0:4,0:4:99:0,141,0:3,0:3:99:0,105,
0:3,0:3:99:0,103,0:3,0:3:99:0,109,0:4,0:4:99:0,100,0:3,0:3:99:0,100,
0:3,0:3:99:0,114,0:4,0:4:99:0,141,0:3,0:3:99:0,100,0:5,0:5:99:0,128,
0:3,0:3:99:0,122,0:5,0:5:99:0,116,1:0,11:11:99:304,0,
0:3,0:3:99:0,100,0:3,0:3:99:0,100,0:4,0:4:99:0,155,0:3,0:3:99:0,118,
0:3,0:3:99:0,100,0:4,0:4:99:0,135,0:4,0:4:99:0,100,0:3,0:3:99:0,99,
0:4,0:4:99:0,104,0:3,0:3:99:0,100,0:3,0:3:99:0,100,0:8,0:8:99:0,148,
0:3,0:3:99:0,109,0:4,0:4:99:0,154,0:3,0:3:99:0,103,0:3,0:3:99:0,100,
0:3,0:3:99:0,115,0:4,0:4:99:0,132,0:4,0:4:99:0,103,0:4,0:4:99:0,131,
0:3,0:3:99:0,100,0:3,0:3:99:0,122,0:3,0:3:99:0,110,0:3,0:3:99:0,100,
0:3,0:3:99:0,107,0:3,0:3:99:0,100,0:3,0:3:99:0,100,0:4,0:4:99:0,118,
0:3,0:3:99:0,100,0:6,0:6:99:0,131,0:3,0:3:99:0,100,0:3,0:3:99:0,118,
0:5,0:5:99:0,122,0:3,0:3:99:0,100,0:4,0:4:99:0,132,0:4,0:4:99:0,131,
0:3,0:3:99:0,100,0:3,0:3:99:0,100,0:3,0:3:99:0,113,0:3,0:3:99:0,100,
0:3,0:3:99:0,100,0:3,0:3:99:0,109,0:3,0:3:99:0,100,0:3,0:3:99:0,100,
0:3,0:3:99:0,112,0:4,0:4:99:0,137,0:3,0:3:99:0,118,0:3,0:3:99:0,100,
0:5,0:5:99:0,159,0:3,0:3:99:0,122,0:3,0:3:99:0,109,0:4,0:4:99:0,104,
0:3,0:3:99:0,114,0:5,0:5:99:0,170,0:5,0:5:99:0,144,0:4,0:4:99:0,141,
0:3,0:3:99:0,122,0:4,0:4:99:0,155,0:10,0:10:99:0,153,
0:3,0:3:99:0,100,0:3,0:3:99:0,122,0:3,0:3:99:0,100,0:3,0:3:99:0,118,
0:4,0:4:99:0,119,0:4,0:4:99:0,137,0:5,0:5:99:0,141,0:3,0:3:99:0,118,
0:4,0:4:99:0,126,0:3,0:3:99:0,100,0:3,0:3:99:0,100,0:4,0:4:99:0,133,
0:9,0:9:99:0,157,0:7,0:7:99:0,143,0:4,0:4:99:0,100,0:4,0:4:99:0,129,
0:3,0:3:99:0,100,0:6,0:6:99:0,166,0:6,0:6:99:0,180,0:7,0:7:99:0,173,
0:4,0:4:99:0,104,0:4,0:4:99:0,109,0:3,0:3:99:0,114,1,0.009091,
110,NA,426,0.,1,0.009091,60.,NA,25.75,NA,2.494,NA}

```

```

In[45]:= fullgenomeSNPEFF[fixme] = {"chrIV", 4, 1005804, "G", "T", 283.29, "GT:AD:DP:GQ:PL",
    "CCC2", "MODERATE", "missense_variant", "YDR270W", "c.130G>T", "p.Val44Leu",

```

```

"T|missense_variant|MODERATE|YDR269C|YDR269C|transcript|YDR269C_mRNA|
protein_coding|1/1|c.185C>A|p.Thr62Asn|185/324|185/324|62/107||,T|
missense_variant|MODERATE|CCC2|YDR270W|transcript|YDR270W_mRNA|
protein_coding|1/1|c.130G>T|p.Val44Leu|130/3015|130/3015|44/1004||,T|
upstream_gene_variant|MODIFIER|HEL2|YDR266C|transcript|YDR266C_mRNA|
protein_coding||c.-3781C>A||||3781|,T|upstream_gene_variant|MODIFIER|
CIA1|YDR267C|transcript|YDR267C_mRNA|protein_coding||c.-2302C>A||||2302
|,T|upstream_gene_variant|MODIFIER|GL02|YDR272W|transcript|YDR272W_mRNA|
protein_coding||c.-3206G>T||||3206|,T|upstream_gene_variant|MODIFIER|
DON1|YDR273W|transcript|YDR273W_mRNA|protein_coding||c.-4372G>T||||4372
|,T|downstream_gene_variant|MODIFIER|MSW1|YDR268W|transcript|
YDR268W_mRNA|protein_coding||c.*661G>T||||661|,T|downstream_gene
_variant|MODIFIER|YDR271C|YDR271C|transcript|YDR271C_mRNA|protein_coding
||c.*2591C>A||||2591|", "0:3,0:3:99:0,109",
"0:5,0:5:99:0,135", "0:3,0:3:99:0,113", "0:4,0:4:99:0,104", "0:3,0:3:99:0,100",
"0:4,0:4:99:0,115", "0:3,0:3:99:0,100", "0:3,0:3:99:0,100", "0:4,0:4:99:0,107",
"0:4,0:4:99:0,100", "0:4,0:4:99:0,137", "0:3,0:3:99:0,100", "0:4,0:4:99:0,109",
"0:7,0:7:99:0,125", "0:3,0:3:99:0,100", "0:4,0:4:99:0,141", "0:3,0:3:99:0,105",
"0:3,0:3:99:0,103", "0:3,0:3:99:0,109", "0:4,0:4:99:0,100", "0:3,0:3:99:0,100",
"0:3,0:3:99:0,114", "0:4,0:4:99:0,141", "0:3,0:3:99:0,100", "0:5,0:5:99:0,128",
"0:3,0:3:99:0,122", "0:5,0:5:99:0,116", "1:0,11:11:99:304,0",
"0:3,0:3:99:0,100", "0:3,0:3:99:0,100", "0:4,0:4:99:0,155", "0:3,0:3:99:0,118",
"0:3,0:3:99:0,100", "0:4,0:4:99:0,135", "0:4,0:4:99:0,100", "0:3,0:3:99:0,99",
"0:4,0:4:99:0,104", "0:3,0:3:99:0,100", "0:3,0:3:99:0,100", "0:8,0:8:99:0,148",
"0:3,0:3:99:0,109", "0:4,0:4:99:0,154", "0:3,0:3:99:0,103", "0:3,0:3:99:0,100",
"0:3,0:3:99:0,115", "0:4,0:4:99:0,132", "0:4,0:4:99:0,103", "0:4,0:4:99:0,131",
"0:3,0:3:99:0,100", "0:3,0:3:99:0,122", "0:3,0:3:99:0,110", "0:3,0:3:99:0,100",
"0:3,0:3:99:0,107", "0:3,0:3:99:0,100", "0:3,0:3:99:0,100", "0:4,0:4:99:0,118",
"0:3,0:3:99:0,100", "0:6,0:6:99:0,131", "0:3,0:3:99:0,100", "0:3,0:3:99:0,118",
"0:5,0:5:99:0,122", "0:3,0:3:99:0,100", "0:4,0:4:99:0,132", "0:4,0:4:99:0,131",
"0:3,0:3:99:0,100", "0:3,0:3:99:0,100", "0:3,0:3:99:0,113", "0:3,0:3:99:0,100",
"0:3,0:3:99:0,100", "0:3,0:3:99:0,109", "0:3,0:3:99:0,100", "0:3,0:3:99:0,100",
"0:3,0:3:99:0,112", "0:4,0:4:99:0,137", "0:3,0:3:99:0,118", "0:3,0:3:99:0,100",
"0:5,0:5:99:0,159", "0:3,0:3:99:0,122", "0:3,0:3:99:0,109", "0:4,0:4:99:0,104",
"0:3,0:3:99:0,114", "0:5,0:5:99:0,170", "0:5,0:5:99:0,144", "0:4,0:4:99:0,141",
"0:3,0:3:99:0,122", "0:4,0:4:99:0,155", "0:10,0:10:99:0,153",
"0:3,0:3:99:0,100", "0:3,0:3:99:0,122", "0:3,0:3:99:0,100", "0:3,0:3:99:0,118",
"0:4,0:4:99:0,119", "0:4,0:4:99:0,137", "0:5,0:5:99:0,141", "0:3,0:3:99:0,118",
"0:4,0:4:99:0,126", "0:3,0:3:99:0,100", "0:3,0:3:99:0,100", "0:4,0:4:99:0,133",
"0:9,0:9:99:0,157", "0:7,0:7:99:0,143", "0:4,0:4:99:0,100", "0:4,0:4:99:0,129",
"0:3,0:3:99:0,100", "0:6,0:6:99:0,166", "0:6,0:6:99:0,180", "0:7,0:7:99:0,173",
"0:4,0:4:99:0,104", "0:4,0:4:99:0,109", "0:3,0:3:99:0,114", 1, 0.009091`,
110, "NA", 426, 0.`, 1, 0.009091`, 60.`, "NA", 25.75`, "NA", 2.494`, "NA");

```



#120: YFL021C-A is dubious, but GAT1 is verified (SGD) [Updated]

In[46]:= **fixme = 120;**

Manually swapping for the second gene:

```
In[47]:= fullgenomeSNPEFF[[fixme]]
```

```
Out[47]=
```

```
{chrVI, 6, 96312, C, T, 839.29, GT:AD:DP:GQ:PL, YFL021C-A,
MODERATE, missense_variant, YFL021C-A, c.304G>A, p.Ala102Thr,
T|missense_variant|MODERATE|YFL021C-A|YFL021C-A|transcript|YFL021C-A_mRNA|
protein_coding|1/1|c.304G>A|p.Ala102Thr|304/855|304/855|102/284|,T|
missense_variant|MODERATE|GAT1|YFL021W|transcript|YFL021W_mRNA|protein_coding
|1/1|c.347C>T|p.Ala116Val|347/1533|347/1533|116/510|,T|upstream_gene_variant
|MODIFIER|FRS2|YFL022C|transcript|YFL022C_mRNA|protein_coding||c.-1302G>A|||
|1302|,T|downstream_gene_variant|MODIFIER|BUD27|YFL023W|transcript|
YFL023W_mRNA|protein_coding||c.*2936C>T|||2936|,T|downstream_gene_variant|
MODIFIER|PAU5|YFL020C|transcript|YFL020C_mRNA|protein_coding||c.*2919G>A|||
2919|,T|downstream_gene_variant|MODIFIER|YFL019C|YFL019C|transcript|
YFL019C_mRNA|protein_coding||c.*3940G>A|||3940|,
0:13,0:13:99:0,393, 0:12,0:12:99:0,329, 0:8,0:8:99:0,236, 0:20,0:20:99:0,484,
0:8,0:8:99:0,200, 0:14,0:14:99:0,452, 0:13,0:13:99:0,239, 0:24,0:24:99:0,545,
0:10,0:10:99:0,330, 0:11,0:11:99:0,348, 0:8,0:8:99:0,220, 0:10,0:10:99:0,267,
0:10,0:10:99:0,297, 0:16,0:16:99:0,469, 0:11,0:11:99:0,292, 0:14,0:14:99:0,399,
0:11,0:11:99:0,306, 0:9,0:9:99:0,278, 0:12,0:12:99:0,314, 0:11,0:11:99:0,401,
0:8,0:8:99:0,232, 0:10,0:10:99:0,294, 0:10,0:10:99:0,313, 0:16,0:16:99:0,464,
0:27,0:27:99:0,714, 0:16,0:16:99:0,423, 0:11,0:11:99:0,288, 0:11,0:11:99:0,251,
0:6,0:6:99:0,172, 0:8,0:8:99:0,270, 0:19,0:19:99:0,514, 0:26,0:26:99:0,827,
0:23,0:23:99:0,744, 0:11,0:11:99:0,358, 0:21,0:21:99:0,582, 0:10,0:10:99:0,278,
0:3,0:3:99:0,109, 0:4,0:4:99:0,116, 0:7,0:7:99:0,121, 0:12,0:12:99:0,367,
0:17,0:17:99:0,344, 0:21,0:21:99:0,495, 0:10,0:10:99:0,270, 0:7,0:7:99:0,101,
0:11,0:11:99:0,279, 0:12,0:12:99:0,331, 0:6,0:6:99:0,178, 0:9,0:9:99:0,274,
0:18,0:18:99:0,587, 0:7,0:7:99:0,221, 0:6,0:6:99:0,146, 0:6,0:6:99:0,124,
0:7,0:7:99:0,244, 0:12,0:12:99:0,384, 0:15,0:15:99:0,474, 0:10,0:10:99:0,129,
0:15,0:15:99:0,326, 0:9,0:9:99:0,214, 0:12,0:12:99:0,363, 0:8,0:8:99:0,200,
0:5,0:5:99:0,140, 0:7,0:7:99:0,200, 0:11,0:11:99:0,377, 0:16,0:16:99:0,323,
1:0,25:25:99:860,0, 0:18,0:18:99:0,529, 0:24,0:24:99:0,702,
0:17,0:17:99:0,510, 0:17,0:17:99:0,492, 0:15,0:15:99:0,504,
0:14,0:14:99:0,451, 0:10,0:10:99:0,308, 0:11,0:11:99:0,276, 0:9,0:9:99:0,247,
0:11,0:11:99:0,329, 0:14,0:14:99:0,421, 0:17,0:17:99:0,458, 0:28,0:28:99:0,800,
0:19,0:19:99:0,562, 0:12,0:12:99:0,359, 0:16,0:16:99:0,517, 0:9,0:9:99:0,266,
0:16,0:16:99:0,368, 0:8,0:8:99:0,268, 0:13,0:13:99:0,358, 0:15,0:15:99:0,285,
0:15,0:15:99:0,445, 0:13,0:13:99:0,452, 0:19,0:19:99:0,638, 0:7,0:7:99:0,203,
0:12,0:12:99:0,306, 0:6,0:6:99:0,100, 0:9,0:9:99:0,296, 0:6,0:6:99:0,200,
0:11,0:11:99:0,236, 0:12,0:12:99:0,364, 0:14,0:14:99:0,396, 0:18,0:18:99:0,550,
0:19,0:19:99:0,485, 0:12,0:12:99:0,247, 0:9,0:9:99:0,306, 0:12,0:12:99:0,416,
0:5,0:5:99:0,100, 0:13,0:13:99:0,408, 0:9,0:9:99:0,306, 0:17,0:17:99:0,364,
0:9,0:9:99:0,180, 0:8,0:8:99:0,274, 0:12,0:12:99:0,302, 0:6,0:6:99:0,186,
1, 0.009091, 110, NA, 1372, 0., 1, 0.009091, 60., NA, 33.57, NA, 2.584, NA}
```

```
In[48]:= fullgenomeSNPEFF[[fixme]] = {"chrVI", 6, 96312, "C", "T", 839.29`, "GT:AD:DP:GQ:PL",
" GAT1", "MODERATE", "missense_variant", "YFL021W", "c.347C>T", "p.Ala116Val",
```

"T|missense\_variant|MODERATE|YFL021C-A|YFL021C-A|transcript|YFL021C-A\_mRNA|  
 protein\_coding|1/1|c.304G>A|p.Ala102Thr|304/855|304/855|102/284|,T|  
 missense\_variant|MODERATE|GAT1|YFL021W|transcript|YFL021W\_mRNA|  
 protein\_coding|1/1|c.347C>T|p.Ala116Val|347/1533|347/1533|116/510|,T|  
 upstream\_gene\_variant|MODIFIER|FRS2|YFL022C|transcript|YFL022C\_mRNA|  
 protein\_coding||c.-1302G>A|1302|,T|downstream\_gene\_variant|MODIFIER|  
 BUD27|YFL023W|transcript|YFL023W\_mRNA|protein\_coding||c.\*2936C>T|2936|,T|downstream\_gene\_variant|MODIFIER|PAU5|YFL020C|transcript|  
 YFL020C\_mRNA|protein\_coding||c.\*2919G>A|2919|,T|downstream\_gene  
 \_variant|MODIFIER|YFL019C|YFL019C|transcript|YFL019C\_mRNA|protein\_coding  
 ||c.\*3940G>A|3940|", "0:13,0:13:99:0,393",  
 "0:12,0:12:99:0,329", "0:8,0:8:99:0,236", "0:20,0:20:99:0,484",  
 "0:8,0:8:99:0,200", "0:14,0:14:99:0,452", "0:13,0:13:99:0,239",  
 "0:24,0:24:99:0,545", "0:10,0:10:99:0,330", "0:11,0:11:99:0,348",  
 "0:8,0:8:99:0,220", "0:10,0:10:99:0,267", "0:10,0:10:99:0,297",  
 "0:16,0:16:99:0,469", "0:11,0:11:99:0,292", "0:14,0:14:99:0,399",  
 "0:11,0:11:99:0,306", "0:9,0:9:99:0,278", "0:12,0:12:99:0,314",  
 "0:11,0:11:99:0,401", "0:8,0:8:99:0,232", "0:10,0:10:99:0,294",  
 "0:10,0:10:99:0,313", "0:16,0:16:99:0,464", "0:27,0:27:99:0,714",  
 "0:16,0:16:99:0,423", "0:11,0:11:99:0,288", "0:11,0:11:99:0,251",  
 "0:6,0:6:99:0,172", "0:8,0:8:99:0,270", "0:19,0:19:99:0,514",  
 "0:26,0:26:99:0,827", "0:23,0:23:99:0,744", "0:11,0:11:99:0,358",  
 "0:21,0:21:99:0,582", "0:10,0:10:99:0,278", "0:3,0:3:99:0,109",  
 "0:4,0:4:99:0,116", "0:7,0:7:99:0,121", "0:12,0:12:99:0,367",  
 "0:17,0:17:99:0,344", "0:21,0:21:99:0,495", "0:10,0:10:99:0,270",  
 "0:7,0:7:99:0,101", "0:11,0:11:99:0,279", "0:12,0:12:99:0,331",  
 "0:6,0:6:99:0,178", "0:9,0:9:99:0,274", "0:18,0:18:99:0,587",  
 "0:7,0:7:99:0,221", "0:6,0:6:99:0,146", "0:6,0:6:99:0,124", "0:7,0:7:99:0,244",  
 "0:12,0:12:99:0,384", "0:15,0:15:99:0,474", "0:10,0:10:99:0,129",  
 "0:15,0:15:99:0,326", "0:9,0:9:99:0,214", "0:12,0:12:99:0,363",  
 "0:8,0:8:99:0,200", "0:5,0:5:99:0,140", "0:7,0:7:99:0,200",  
 "0:11,0:11:99:0,377", "0:16,0:16:99:0,323", "1:0,25:25:99:860,0",  
 "0:18,0:18:99:0,529", "0:24,0:24:99:0,702", "0:17,0:17:99:0,510",  
 "0:17,0:17:99:0,492", "0:15,0:15:99:0,504", "0:14,0:14:99:0,451",  
 "0:10,0:10:99:0,308", "0:11,0:11:99:0,276", "0:9,0:9:99:0,247",  
 "0:11,0:11:99:0,329", "0:14,0:14:99:0,421", "0:17,0:17:99:0,458",  
 "0:28,0:28:99:0,800", "0:19,0:19:99:0,562", "0:12,0:12:99:0,359",  
 "0:16,0:16:99:0,517", "0:9,0:9:99:0,266", "0:16,0:16:99:0,368",  
 "0:8,0:8:99:0,268", "0:13,0:13:99:0,358", "0:15,0:15:99:0,285",  
 "0:15,0:15:99:0,445", "0:13,0:13:99:0,452", "0:19,0:19:99:0,638",  
 "0:7,0:7:99:0,203", "0:12,0:12:99:0,306", "0:6,0:6:99:0,100",  
 "0:9,0:9:99:0,296", "0:6,0:6:99:0,200", "0:11,0:11:99:0,236",  
 "0:12,0:12:99:0,364", "0:14,0:14:99:0,396", "0:18,0:18:99:0,550",  
 "0:19,0:19:99:0,485", "0:12,0:12:99:0,247", "0:9,0:9:99:0,306",

```
"0:12,0:12:99:0,416", "0:5,0:5:99:0,100", "0:13,0:13:99:0,408",
"0:9,0:9:99:0,306", "0:17,0:17:99:0,364", "0:9,0:9:99:0,180",
"0:8,0:8:99:0,274", "0:12,0:12:99:0,302", "0:6,0:6:99:0,186", 1, 0.009091`,
110, "NA", 1372, 0.`, 1, 0.009091`, 60.`, "NA", 33.57`, "NA", 2.584`, "NA"};
```

### #227: YJL211C is dubious, but PEX2 is verified (SGD) [Updated]

```
In[49]:= fixme = 227;
```

Manually swapping for the second gene:

```
In[50]:= fullgenomeSNPEFF[[fixme]]
```

Out[50]=

```
{chrX, 10, 37037, C, T, 1239.29, GT:AD:DP:GQ:PL, YJL211C,
MODERATE, missense_variant, YJL211C, c.164G>A, p.Cys55Tyr,
T|missense_variant|MODERATE|YJL211C|YJL211C|transcript|YJL211C_mRNA|
protein_coding|1/1|c.164G>A|p.Cys55Tyr|164/444|164/444|55/147||,T|
missense_variant|MODERATE|PEX2|YJL210W|transcript|YJL210W_mRNA|protein_coding
|1/1|c.119C>T|p.Ala40Val|119/816|119/816|40/271||,T|upstream_gene_variant|
MODIFIER|OPT1|YJL212C|transcript|YJL212C_mRNA|protein_coding||c.-788G>A||||
788|,T|upstream_gene_variant|MODIFIER|CBP1|YJL209W|transcript|YJL209W_mRNA|
protein_coding||c.-968C>T||||968|,T|downstream_gene_variant|MODIFIER|YJL213W
|YJL213W|transcript|YJL213W_mRNA|protein_coding||c.*3879C>T||||3879|,T|
downstream_gene_variant|MODIFIER|NUC1|YJL208C|transcript|YJL208C_mRNA|
protein_coding||c.*3157G>A||||3157|,T|downstream_gene_variant|MODIFIER|LAA1|
YJL207C|transcript|YJL207C_mRNA|protein_coding||c.*4352G>A||||4352|,
0:3,0:3:99:0,100, 0:8,0:8:99:0,129, 0:7,0:7:99:0,189, 0:3,0:3:99:0,109,
0:4,0:4:99:0,118, 0:3,0:3:99:0,111, 0:4,0:4:99:0,135, 0:3,0:3:99:0,100,
0:4,0:4:99:0,135, 0:3,0:3:99:0,109, 0:3,0:3:99:0,100, 0:4,0:4:99:0,119,
0:3,0:3:99:0,100, 0:4,0:4:99:0,135, 0:3,0:3:99:0,110, 0:3,0:3:99:0,100,
0:6,0:6:99:0,116, 0:3,0:3:99:0,100, 0:3,0:3:99:0,100, 0:3,0:3:99:0,104,
0:3,0:3:99:0,109, 0:4,0:4:99:0,119, 0:3,0:3:99:0,103, 0:4,0:4:99:0,114,
0:4,0:4:99:0,115, 0:4,0:4:99:0,119, 0:4,0:4:99:0,110, 0:4,0:4:99:0,141,
0:3,0:3:99:0,113, 0:3,0:3:99:0,100, 0:4,0:4:99:0,107, 0:3,0:3:99:0,100,
0:4,0:4:99:0,110, 0:4,0:4:99:0,130, 0:3,0:3:99:0,122, 0:3,0:3:99:0,100,
0:4,0:4:99:0,100, 0:4,0:4:99:0,115, 0:4,0:4:99:0,137, 0:3,0:3:99:0,109,
0:3,0:3:99:0,100, 0:3,0:3:99:0,105, 0:3,0:3:99:0,100, 0:4,0:4:99:0,151,
0:3,0:3:99:0,110, 0:3,0:3:99:0,104, 0:8,0:8:99:0,176, 0:6,0:6:99:0,119,
0:3,0:3:99:0,100, 0:3,0:3:99:0,100, 0:3,0:3:99:0,113, 0:3,0:3:99:0,100,
0:3,0:3:99:0,100, 0:4,0:4:99:0,100, 0:3,0:3:99:0,100, 0:3,0:3:99:0,103,
0:3,0:3:99:0,118, 0:3,0:3:99:0,100, 0:3,0:3:99:0,107, 0:3,0:3:99:0,107,
0:3,0:3:99:0,100, 0:7,0:7:99:0,227, 0:3,0:3:99:0,109, 0:3,0:3:99:0,113,
0:3,0:3:99:0,100, 0:4,0:4:99:0,139, 0:4,0:4:99:0,115, 0:4,0:4:99:0,114,
1:0,39:39:99:1260,0, 0:5,0:5:99:0,132, 0:4,0:4:99:0,133,
0:3,0:3:99:0,109, 0:4,0:4:99:0,110, 0:4,0:4:99:0,102, 0:3,0:3:99:0,100,
0:3,0:3:99:0,103, 0:5,0:5:99:0,135, 0:5,0:5:99:0,174, 0:3,0:3:99:0,100,
0:3,0:3:99:0,100, 0:3,0:3:99:0,107, 0:4,0:4:99:0,135, 0:3,0:3:99:0,104,
0:4,0:4:99:0,115, 0:4,0:4:99:0,128, 0:4,0:4:99:0,124, 0:5,0:5:99:0,181,
0:3,0:3:99:0,100, 0:4,0:4:99:0,123, 0:3,0:3:99:0,114, 0:4,0:4:99:0,132,
0:3,0:3:99:0,101, 0:3,0:3:99:0,100, 0:3,0:3:99:0,109, 0:3,0:3:99:0,100,
0:4,0:4:99:0,127, 0:3,0:3:99:0,117, 0:3,0:3:99:0,118, 0:3,0:3:99:0,100,
0:4,0:4:99:0,111, 0:4,0:4:99:0,114, 0:4,0:4:99:0,114, 0:3,0:3:99:0,100,
0:5,0:5:99:0,113, 0:4,0:4:99:0,135, 0:4,0:4:99:0,122, 0:3,0:3:99:0,114,
0:3,0:3:99:0,100, 0:3,0:3:99:0,100, 0:15,0:15:99:0,245, 1,
0.009091, 110, NA, 452, 0., 1, 0.009091, 60., NA, 31.78, NA, 1.096, NA}
```

```

In[51]:= fullgenomeSNPEFF[[fixme]] = {"chrX", 10, 37037, "C", "T", 1239.29, "GT:AD:DP:GQ:PL",
  "PEX2", "MODERATE", "missense_variant", "YJL210W", "c.119C>T", "p.Ala40Val",
  "T|missense_variant|MODERATE|YJL211C|YJL211C|transcript|YJL211C_mRNA|
  protein_coding|1/1|c.164G>A|p.Cys55Tyr|164/444|164/444|55/147||,T|
  missense_variant|MODERATE|PEX2|YJL210W|transcript|YJL210W_mRNA|
  protein_coding|1/1|c.119C>T|p.Ala40Val|119/816|119/816|40/271||,T|
  upstream_gene_variant|MODIFIER|OPT1|YJL212C|transcript|YJL212C_mRNA|
  protein_coding||c.-788G>A||||788|,T|upstream_gene_variant|MODIFIER|CBP1
  |YJL209W|transcript|YJL209W_mRNA|protein_coding||c.-968C>T||||968|,T|
  downstream_gene_variant|MODIFIER|YJL213W|YJL213W|transcript|YJL213W_mRNA
  |protein_coding||c.*3879C>T||||3879|,T|downstream_gene_variant|MODIFIER
  |NUC1|YJL208C|transcript|YJL208C_mRNA|protein_coding||c.*3157G>A||||
  3157|,T|downstream_gene_variant|MODIFIER|LAA1|YJL207C|transcript|
  YJL207C_mRNA|protein_coding||c.*4352G>A||||4352|",
  "0:3,0:3:99:0,100", "0:8,0:8:99:0,129", "0:7,0:7:99:0,189", "0:3,0:3:99:0,109",
  "0:4,0:4:99:0,118", "0:3,0:3:99:0,111", "0:4,0:4:99:0,135", "0:3,0:3:99:0,100",
  "0:4,0:4:99:0,135", "0:3,0:3:99:0,109", "0:3,0:3:99:0,100", "0:4,0:4:99:0,119",
  "0:3,0:3:99:0,100", "0:4,0:4:99:0,135", "0:3,0:3:99:0,110", "0:3,0:3:99:0,100",
  "0:6,0:6:99:0,116", "0:3,0:3:99:0,100", "0:3,0:3:99:0,100", "0:3,0:3:99:0,104",
  "0:3,0:3:99:0,109", "0:4,0:4:99:0,119", "0:3,0:3:99:0,103", "0:4,0:4:99:0,114",
  "0:4,0:4:99:0,115", "0:4,0:4:99:0,119", "0:4,0:4:99:0,110", "0:4,0:4:99:0,141",
  "0:3,0:3:99:0,113", "0:3,0:3:99:0,100", "0:4,0:4:99:0,107", "0:3,0:3:99:0,100",
  "0:4,0:4:99:0,110", "0:4,0:4:99:0,130", "0:3,0:3:99:0,122", "0:3,0:3:99:0,100",
  "0:4,0:4:99:0,100", "0:4,0:4:99:0,115", "0:4,0:4:99:0,137", "0:3,0:3:99:0,109",
  "0:3,0:3:99:0,100", "0:3,0:3:99:0,105", "0:3,0:3:99:0,100", "0:4,0:4:99:0,151",
  "0:3,0:3:99:0,110", "0:3,0:3:99:0,104", "0:8,0:8:99:0,176", "0:6,0:6:99:0,119",
  "0:3,0:3:99:0,100", "0:3,0:3:99:0,100", "0:3,0:3:99:0,113", "0:3,0:3:99:0,100",
  "0:3,0:3:99:0,100", "0:4,0:4:99:0,100", "0:3,0:3:99:0,100", "0:3,0:3:99:0,103",
  "0:3,0:3:99:0,118", "0:3,0:3:99:0,100", "0:3,0:3:99:0,107", "0:3,0:3:99:0,107",
  "0:3,0:3:99:0,100", "0:7,0:7:99:0,227", "0:3,0:3:99:0,109", "0:3,0:3:99:0,113",
  "0:3,0:3:99:0,100", "0:4,0:4:99:0,139", "0:4,0:4:99:0,115", "0:4,0:4:99:0,114",
  "1:0,39:39:99:1260,0", "0:5,0:5:99:0,132", "0:4,0:4:99:0,133",
  "0:3,0:3:99:0,109", "0:4,0:4:99:0,110", "0:4,0:4:99:0,102", "0:3,0:3:99:0,100",
  "0:3,0:3:99:0,103", "0:5,0:5:99:0,135", "0:5,0:5:99:0,174", "0:3,0:3:99:0,100",
  "0:3,0:3:99:0,100", "0:3,0:3:99:0,107", "0:4,0:4:99:0,135", "0:3,0:3:99:0,104",
  "0:4,0:4:99:0,115", "0:4,0:4:99:0,128", "0:4,0:4:99:0,124", "0:5,0:5:99:0,181",
  "0:3,0:3:99:0,100", "0:4,0:4:99:0,123", "0:3,0:3:99:0,114", "0:4,0:4:99:0,132",
  "0:3,0:3:99:0,101", "0:3,0:3:99:0,100", "0:3,0:3:99:0,109", "0:3,0:3:99:0,100",
  "0:4,0:4:99:0,127", "0:3,0:3:99:0,117", "0:3,0:3:99:0,118", "0:3,0:3:99:0,100",
  "0:4,0:4:99:0,111", "0:4,0:4:99:0,114", "0:4,0:4:99:0,114", "0:3,0:3:99:0,100",
  "0:5,0:5:99:0,113", "0:4,0:4:99:0,135", "0:4,0:4:99:0,122", "0:3,0:3:99:0,114",
  "0:3,0:3:99:0,100", "0:3,0:3:99:0,100", "0:15,0:15:99:0,245", 1, 0.009091,
  110, "NA", 452, 0., 1, 0.009091, 60., "NA", 31.78, "NA", 1.096, "NA"};

```

#229: BUD19 is dubious [HIGH], but RPL39 is verified [LOW] (SGD) [Updated]

```
In[52]:= fixme = 229;
```

Manually swapping for the second gene:

```
In[53]:= fullgenomeSNPEFF[[fixme]]
```

Out[53]=

```
{chrX, 10, 76405, G, A, 839.29, GT:AD:DP:GQ:PL,
BUD19, HIGH, stop_gained, YJL188C, c.106C>T, p.Gln36*,
A|stop_gained|HIGH|BUD19|YJL188C|transcript|YJL188C_mRNA|protein_coding|1/1|c
.106C>T|p.Gln36*|106/309|106/309|36/102||,A|synonymous_variant|LOW|RPL39|
YJL189W|transcript|YJL189W_mRNA|protein_coding|2/2|c.87G>A|p.Leu29Leu|87/156|
87/156|29/51||,A|upstream_gene_variant|MODIFIER|SOP4|YJL192C|transcript|
YJL192C_mRNA|protein_coding|c.-2991C>T||||2991|,A|upstream_gene_variant|
MODIFIER|RPS22A|YJL190C|transcript|YJL190C_mRNA|protein_coding|c.-1103C>T||
||1103|,A|upstream_gene_variant|MODIFIER|MNN5|YJL186W|transcript|
YJL186W_mRNA|protein_coding|c.-3750G>A||||3750|,A|downstream_gene_variant|
MODIFIER|YJL193W|YJL193W|transcript|YJL193W_mRNA|protein_coding|c.*3831G>A|
||3831|,A|downstream_gene_variant|MODIFIER|RPS14B|YJL191W|transcript|
YJL191W_mRNA|protein_coding|c.*1794G>A||||1794|,A|downstream_gene_variant|
MODIFIER|SWE1|YJL187C|transcript|YJL187C_mRNA|protein_coding|c.*398C>T||||
398|, 0:11,0:11:99:0,164, 0:9,0:9:99:0,270, 0:10,0:10:99:0,200,
0:8,0:8:99:0,103, 0:3,0:3:99:0,118, 0:12,0:12:99:0,271, 0:4,0:4:99:0,135,
0:7,0:7:99:0,155, 0:7,0:7:99:0,111, 0:14,0:14:99:0,458, 0:8,0:8:99:0,225,
0:6,0:6:99:0,139, 0:7,0:7:99:0,152, 0:9,0:9:99:0,224, 0:3,0:3:99:0,110,
0:8,0:8:99:0,227, 0:5,0:5:99:0,159, 0:6,0:6:99:0,153, 0:7,0:7:99:0,146,
0:11,0:11:99:0,277, 0:7,0:7:99:0,223, 0:9,0:9:99:0,197, 0:3,0:3:99:0,118,
0:13,0:13:99:0,402, 0:13,0:13:99:0,264, 0:13,0:13:99:0,107,
0:7,0:7:99:0,121, 0:10,0:10:99:0,165, 0:8,0:8:99:0,217, 0:9,0:9:99:0,315,
0:7,0:7:99:0,135, 0:20,0:20:99:0,551, 0:14,0:14:99:0,262, 0:12,0:12:99:0,209,
0:7,0:7:99:0,148, 0:8,0:8:99:0,140, 0:3,0:3:99:0,100, 0:5,0:5:99:0,135,
0:4,0:4:99:0,116, 0:8,0:8:99:0,253, 0:3,0:3:99:0,100, 0:11,0:11:99:0,314,
0:10,0:10:99:0,240, 0:4,0:4:99:0,103, 0:5,0:5:99:0,159, 0:11,0:11:99:0,150,
0:3,0:3:99:0,118, 0:7,0:7:99:0,136, 0:8,0:8:99:0,129, 0:9,0:9:99:0,180,
0:5,0:5:99:0,105, 0:7,0:7:99:0,127, 0:3,0:3:99:0,109, 0:4,0:4:99:0,133,
0:5,0:5:99:0,115, 0:10,0:10:99:0,101, 0:3,0:3:99:0,117, 0:3,0:3:99:0,100,
0:4,0:4:99:0,140, 0:3,0:3:99:0,107, 0:6,0:6:99:0,218, 0:6,0:6:99:0,127,
0:8,0:8:99:0,169, 0:10,0:10:99:0,311, 0:5,0:5:99:0,159, 0:5,0:5:99:0,118,
0:7,0:7:99:0,204, 0:9,0:9:99:0,250, 0:15,0:15:99:0,182, 0:7,0:7:99:0,172,
0:13,0:13:99:0,197, 0:7,0:7:99:0,198, 0:9,0:9:99:0,177, 0:9,0:9:99:0,157,
0:4,0:4:99:0,127, 0:6,0:6:99:0,113, 0:6,0:6:99:0,135, 0:20,0:20:99:0,348,
0:6,0:6:99:0,135, 0:5,0:5:99:0,173, 0:12,0:12:99:0,338, 0:10,0:10:99:0,180,
0:15,0:15:99:0,143, 0:12,0:12:99:0,355, 0:4,0:4:99:0,128, 0:14,0:14:99:0,174,
0:12,0:12:99:0,139, 0:14,0:14:99:0,157, 0:12,0:12:99:0,339, 0:9,0:9:99:0,124,
0:8,0:8:99:0,208, 0:3,0:3:99:0,100, 0:7,0:7:99:0,184, 1:0,24:24:99:860,0,
0:8,0:8:99:0,196, 0:5,0:5:99:0,102, 0:8,0:8:99:0,120, 0:5,0:5:99:0,135,
0:7,0:7:99:0,118, 0:10,0:10:99:0,136, 0:12,0:12:99:0,194, 0:5,0:5:99:0,135,
0:9,0:9:99:0,178, 0:8,0:8:99:0,245, 0:3,0:3:99:0,118, 0:4,0:4:99:0,122,
0:11,0:11:99:0,320, 0:11,0:11:99:0,200, 0:6,0:6:99:0,124, 0:6,0:6:99:0,185,
1, 0.009091, 110, NA, 890, 0., 1, 0.009091, 60., NA, 34.97, NA, 1.519, NA}
```

```
In[54]:= fullgenomeSNPEFF[fixme] = {"chrX", 10, 76405, "G", "A", 839.29, "GT:AD:DP:GQ:PL",
"RPL39", "LOW", "synonymous_variant", "YJL189W", "c.87G>A", "p.Leu29Leu",
```



"A|stop\_gained|HIGH|BUD19|YJL188C|transcript|YJL188C\_mRNA|protein\_coding|1/1|c  
 .106C>T|p.Gln36\*|106/309|106/309|36/102||,A|synonymous\_variant|LOW|RPL39  
 |YJL189W|transcript|YJL189W\_mRNA|protein\_coding|2/2|c.87G>A|p.Leu29Leu|  
 87/156|87/156|29/51||,A|upstream\_gene\_variant|MODIFIER|SOP4|YJL192C|  
 transcript|YJL192C\_mRNA|protein\_coding||c.-2991C>T||||2991|,A|  
 upstream\_gene\_variant|MODIFIER|RPS22A|YJL190C|transcript|YJL190C\_mRNA|  
 protein\_coding||c.-1103C>T||||1103|,A|upstream\_gene\_variant|MODIFIER|  
 MNN5|YJL186W|transcript|YJL186W\_mRNA|protein\_coding||c.-3750G>A||||3750  
 |,A|downstream\_gene\_variant|MODIFIER|YJL193W|YJL193W|transcript|  
 YJL193W\_mRNA|protein\_coding||c.\*3831G>A||||3831|,A|downstream\_gene  
 \_variant|MODIFIER|RPS14B|YJL191W|transcript|YJL191W\_mRNA|protein\_coding  
 ||c.\*1794G>A||||1794|,A|downstream\_gene\_variant|MODIFIER|SWE1|YJL187C|  
 transcript|YJL187C\_mRNA|protein\_coding||c.\*398C>T||||398|",  
 "0:11,0:11:99:0,164", "0:9,0:9:99:0,270", "0:10,0:10:99:0,200",  
 "0:8,0:8:99:0,103", "0:3,0:3:99:0,118", "0:12,0:12:99:0,271",  
 "0:4,0:4:99:0,135", "0:7,0:7:99:0,155", "0:7,0:7:99:0,111",  
 "0:14,0:14:99:0,458", "0:8,0:8:99:0,225", "0:6,0:6:99:0,139",  
 "0:7,0:7:99:0,152", "0:9,0:9:99:0,224", "0:3,0:3:99:0,110",  
 "0:8,0:8:99:0,227", "0:5,0:5:99:0,159", "0:6,0:6:99:0,153",  
 "0:7,0:7:99:0,146", "0:11,0:11:99:0,277", "0:7,0:7:99:0,223",  
 "0:9,0:9:99:0,197", "0:3,0:3:99:0,118", "0:13,0:13:99:0,402",  
 "0:13,0:13:99:0,264", "0:13,0:13:99:0,107", "0:7,0:7:99:0,121",  
 "0:10,0:10:99:0,165", "0:8,0:8:99:0,217", "0:9,0:9:99:0,315",  
 "0:7,0:7:99:0,135", "0:20,0:20:99:0,551", "0:14,0:14:99:0,262",  
 "0:12,0:12:99:0,209", "0:7,0:7:99:0,148", "0:8,0:8:99:0,140",  
 "0:3,0:3:99:0,100", "0:5,0:5:99:0,135", "0:4,0:4:99:0,116", "0:8,0:8:99:0,253",  
 "0:3,0:3:99:0,100", "0:11,0:11:99:0,314", "0:10,0:10:99:0,240",  
 "0:4,0:4:99:0,103", "0:5,0:5:99:0,159", "0:11,0:11:99:0,150",  
 "0:3,0:3:99:0,118", "0:7,0:7:99:0,136", "0:8,0:8:99:0,129", "0:9,0:9:99:0,180",  
 "0:5,0:5:99:0,105", "0:7,0:7:99:0,127", "0:3,0:3:99:0,109", "0:4,0:4:99:0,133",  
 "0:5,0:5:99:0,115", "0:10,0:10:99:0,101", "0:3,0:3:99:0,117",  
 "0:3,0:3:99:0,100", "0:4,0:4:99:0,140", "0:3,0:3:99:0,107", "0:6,0:6:99:0,218",  
 "0:6,0:6:99:0,127", "0:8,0:8:99:0,169", "0:10,0:10:99:0,311",  
 "0:5,0:5:99:0,159", "0:5,0:5:99:0,118", "0:7,0:7:99:0,204",  
 "0:9,0:9:99:0,250", "0:15,0:15:99:0,182", "0:7,0:7:99:0,172",  
 "0:13,0:13:99:0,197", "0:7,0:7:99:0,198", "0:9,0:9:99:0,177",  
 "0:9,0:9:99:0,157", "0:4,0:4:99:0,127", "0:6,0:6:99:0,113",  
 "0:6,0:6:99:0,135", "0:20,0:20:99:0,348", "0:6,0:6:99:0,135",  
 "0:5,0:5:99:0,173", "0:12,0:12:99:0,338", "0:10,0:10:99:0,180",  
 "0:15,0:15:99:0,143", "0:12,0:12:99:0,355", "0:4,0:4:99:0,128",  
 "0:14,0:14:99:0,174", "0:12,0:12:99:0,139", "0:14,0:14:99:0,157",  
 "0:12,0:12:99:0,339", "0:9,0:9:99:0,124", "0:8,0:8:99:0,208",  
 "0:3,0:3:99:0,100", "0:7,0:7:99:0,184", "1:0,24:24:99:860,0",  
 "0:8,0:8:99:0,196", "0:5,0:5:99:0,102", "0:8,0:8:99:0,120", "0:5,0:5:99:0,135",

```
"0:7,0:7:99:0,118", "0:10,0:10:99:0,136", "0:12,0:12:99:0,194",
"0:5,0:5:99:0,135", "0:9,0:9:99:0,178", "0:8,0:8:99:0,245",
"0:3,0:3:99:0,118", "0:4,0:4:99:0,122", "0:11,0:11:99:0,320",
"0:11,0:11:99:0,200", "0:6,0:6:99:0,124", "0:6,0:6:99:0,185", 1, 0.009091`,
110, "NA", 890, 0.`, 1, 0.009091`, 60.`, "NA", 34.97`, "NA", 1.519`, "NA"};
```

### #296: VPS63 is uncharacterized, but YPT6 is verified (SGD) [Updated]

```
In[55]:= fixme = 296;
```

Manually swapping for the second gene :

```
In[56]:= fullgenomeSNPEFF[[fixme]]
```

Out[56]=

```
{chrXII, 12, 668352, C, G, 549.29, GT:AD:DP:GQ:PL, VPS63,
MODERATE, missense_variant, YLR261C, c.212G>C, p.Ser71Thr,
G|missense_variant|MODERATE|VPS63|YLR261C|transcript|YLR261C_mRNA|protein_coding
|1/1|c.212G>C|p.Ser71Thr|212/327|212/327|71/108||,G|missense_variant|MODERATE
|YPT6|YLR262C|transcript|YLR262C_mRNA|protein_coding|1/1|c.540G>C|p.Glu180Asp
|540/648|540/648|180/215||,G|upstream_gene_variant|MODIFIER|HSP60|YLR259C|
transcript|YLR259C_mRNA|protein_coding|c.-3350G>C||||3350|,G|upstream_gene
_variant|MODIFIER|RED1|YLR263W|transcript|YLR263W_mRNA|protein_coding|c.-198
88C>G||||1988|,G|upstream_gene_variant|MODIFIER|RPS28B|YLR264W|transcript|
YLR264W_mRNA|protein_coding|c.-4779C>G||||4779|,G|downstream_gene_variant|
MODIFIER|LCB5|YLR260W|transcript|YLR260W_mRNA|protein_coding|c.*445C>G||||
445|,G|downstream_gene_variant|MODIFIER|TMA7|YLR262C-A|transcript|YLR262C-
A_mRNA|protein_coding|c.*1116G>C||||1116|, 0:15,0:15:99:0,486,
0:33,0:33:99:0,1029, 0:20,0:20:99:0,656, 0:18,0:18:99:0,643,
0:9,0:9:99:0,253, 0:20,0:20:99:0,718, 0:19,0:19:99:0,660, 0:19,0:19:99:0,575,
0:7,0:7:99:0,217, 0:10,0:10:99:0,341, 0:11,0:11:99:0,278, 0:27,0:27:99:0,895,
0:14,0:14:99:0,489, 0:14,0:14:99:0,405, 0:17,0:17:99:0,519,
0:14,0:14:99:0,468, 0:12,0:12:99:0,423, 1:0,15:15:99:570,0,
0:9,0:9:99:0,270, 0:19,0:19:99:0,570, 0:17,0:17:99:0,572, 0:11,0:11:99:0,360,
0:14,0:14:99:0,436, 0:16,0:16:99:0,530, 0:11,0:11:99:0,365, 0:24,0:24:99:0,847,
0:18,0:18:99:0,657, 0:7,0:7:99:0,238, 0:11,0:11:99:0,336, 0:14,0:14:99:0,341,
0:21,0:21:99:0,765, 0:22,0:22:99:0,790, 0:28,0:28:99:0,900, 0:10,0:10:99:0,331,
0:24,0:24:99:0,822, 0:9,0:9:99:0,317, 0:3,0:3:99:0,100, 0:5,0:5:99:0,128,
0:8,0:8:99:0,239, 0:10,0:10:99:0,364, 0:11,0:11:99:0,292, 0:21,0:21:99:0,635,
0:19,0:19:99:0,558, 0:8,0:8:99:0,278, 0:11,0:11:99:0,403, 0:14,0:14:99:0,428,
0:18,0:18:99:0,628, 0:12,0:12:99:0,379, 0:13,0:13:99:0,474, 0:14,0:14:99:0,473,
0:13,0:13:99:0,423, 0:17,0:17:99:0,595, 0:4,0:4:99:0,129, 0:7,0:7:99:0,150,
0:8,0:8:99:0,274, 0:12,0:12:99:0,422, 0:19,0:19:99:0,619, 0:12,0:12:99:0,377,
0:14,0:14:99:0,341, 0:18,0:18:99:0,605, 0:8,0:8:99:0,277, 0:12,0:12:99:0,372,
0:19,0:19:99:0,592, 0:15,0:15:99:0,557, 0:12,0:12:99:0,437, 0:21,0:21:99:0,660,
0:17,0:17:99:0,560, 0:15,0:15:99:0,487, 0:28,0:28:99:0,905, 0:14,0:14:99:0,409,
0:20,0:20:99:0,685, 0:8,0:8:99:0,287, 0:19,0:19:99:0,698, 0:17,0:17:99:0,561,
0:24,0:24:99:0,811, 0:17,0:17:99:0,632, 0:10,0:10:99:0,370, 0:17,0:17:99:0,555,
0:20,0:20:99:0,668, 0:19,0:19:99:0,611, 0:24,0:24:99:0,812, 0:17,0:17:99:0,597,
0:20,0:20:99:0,706, 0:17,0:17:99:0,596, 0:15,0:15:99:0,505, 0:26,0:26:99:0,943,
0:16,0:16:99:0,539, 0:15,0:15:99:0,548, 0:16,0:16:99:0,534, 0:16,0:16:99:0,459,
0:18,0:18:99:0,602, 0:14,0:14:99:0,324, 0:13,0:13:99:0,440, 0:13,0:13:99:0,434,
0:13,0:13:99:0,450, 0:11,0:11:99:0,365, 0:23,0:23:99:0,801, 0:13,0:13:99:0,413,
0:19,0:19:99:0,574, 0:13,0:13:99:0,393, 0:18,0:18:99:0,627, 0:9,0:9:99:0,281,
0:17,0:17:99:0,585, 0:15,0:15:99:0,540, 0:12,0:12:99:0,315, 0:18,0:18:99:0,563,
0:15,0:15:99:0,512, 0:15,0:15:99:0,563, 0:8,0:8:99:0,229, 0:7,0:7:99:0,237,
1, 0.009091, 110, NA, 1668, 0., 1, 0.009091, 60., NA, 33.61, NA, 0.818, NA}
```

```
In[57]:= fullgenomeSNPEFF[fixme] =
{"chrXII", 12, 668352, "C", "G", 549.29, "GT:AD:DP:GQ:PL", "YPT6",
```

"MODERATE", "missense\_variant", "YLR261C", "c.540G>C", "p.Glu180Asp",  
 "G|missense\_variant|MODERATE|VPS63|YLR261C|transcript|YLR261C\_mRNA|  
 protein\_coding|1/1|c.212G>C|p.Ser71Thr|212/327|212/327|71/108||,G|  
 missense\_variant|MODERATE|YPT6|YLR262C|transcript|YLR262C\_mRNA|  
 protein\_coding|1/1|c.540G>C|p.Glu180Asp|540/648|540/648|180/215||,G|  
 upstream\_gene\_variant|MODIFIER|HSP60|YLR259C|transcript|YLR259C\_mRNA|  
 protein\_coding||c.-3350G>C||||3350|,G|upstream\_gene\_variant|MODIFIER|  
 RED1|YLR263W|transcript|YLR263W\_mRNA|protein\_coding||c.-1988C>G||||1988  
 |,G|upstream\_gene\_variant|MODIFIER|RPS28B|YLR264W|transcript|  
 YLR264W\_mRNA|protein\_coding||c.-4779C>G||||4779|,G|downstream\_gene  
 \_variant|MODIFIER|LCB5|YLR260W|transcript|YLR260W\_mRNA|protein\_coding||c  
 .\*445C>G||||445|,G|downstream\_gene\_variant|MODIFIER|TMA7|YLR262C-A|  
 transcript|YLR262C-A\_mRNA|protein\_coding||c.\*1116G>C||||1116|",  
 "0:15,0:15:99:0,486", "0:33,0:33:99:0,1029", "0:20,0:20:99:0,656",  
 "0:18,0:18:99:0,643", "0:9,0:9:99:0,253", "0:20,0:20:99:0,718",  
 "0:19,0:19:99:0,660", "0:19,0:19:99:0,575", "0:7,0:7:99:0,217",  
 "0:10,0:10:99:0,341", "0:11,0:11:99:0,278", "0:27,0:27:99:0,895",  
 "0:14,0:14:99:0,489", "0:14,0:14:99:0,405", "0:17,0:17:99:0,519",  
 "0:14,0:14:99:0,468", "0:12,0:12:99:0,423", "1:0,15:15:99:570,0",  
 "0:9,0:9:99:0,270", "0:19,0:19:99:0,570", "0:17,0:17:99:0,572",  
 "0:11,0:11:99:0,360", "0:14,0:14:99:0,436", "0:16,0:16:99:0,530",  
 "0:11,0:11:99:0,365", "0:24,0:24:99:0,847", "0:18,0:18:99:0,657",  
 "0:7,0:7:99:0,238", "0:11,0:11:99:0,336", "0:14,0:14:99:0,341",  
 "0:21,0:21:99:0,765", "0:22,0:22:99:0,790", "0:28,0:28:99:0,900",  
 "0:10,0:10:99:0,331", "0:24,0:24:99:0,822", "0:9,0:9:99:0,317",  
 "0:3,0:3:99:0,100", "0:5,0:5:99:0,128", "0:8,0:8:99:0,239",  
 "0:10,0:10:99:0,364", "0:11,0:11:99:0,292", "0:21,0:21:99:0,635",  
 "0:19,0:19:99:0,558", "0:8,0:8:99:0,278", "0:11,0:11:99:0,403",  
 "0:14,0:14:99:0,428", "0:18,0:18:99:0,628", "0:12,0:12:99:0,379",  
 "0:13,0:13:99:0,474", "0:14,0:14:99:0,473", "0:13,0:13:99:0,423",  
 "0:17,0:17:99:0,595", "0:4,0:4:99:0,129", "0:7,0:7:99:0,150",  
 "0:8,0:8:99:0,274", "0:12,0:12:99:0,422", "0:19,0:19:99:0,619",  
 "0:12,0:12:99:0,377", "0:14,0:14:99:0,341", "0:18,0:18:99:0,605",  
 "0:8,0:8:99:0,277", "0:12,0:12:99:0,372", "0:19,0:19:99:0,592",  
 "0:15,0:15:99:0,557", "0:12,0:12:99:0,437", "0:21,0:21:99:0,660",  
 "0:17,0:17:99:0,560", "0:15,0:15:99:0,487", "0:28,0:28:99:0,905",  
 "0:14,0:14:99:0,409", "0:20,0:20:99:0,685", "0:8,0:8:99:0,287",  
 "0:19,0:19:99:0,698", "0:17,0:17:99:0,561", "0:24,0:24:99:0,811",  
 "0:17,0:17:99:0,632", "0:10,0:10:99:0,370", "0:17,0:17:99:0,555",  
 "0:20,0:20:99:0,668", "0:19,0:19:99:0,611", "0:24,0:24:99:0,812",  
 "0:17,0:17:99:0,597", "0:20,0:20:99:0,706", "0:17,0:17:99:0,596",  
 "0:15,0:15:99:0,505", "0:26,0:26:99:0,943", "0:16,0:16:99:0,539",  
 "0:15,0:15:99:0,548", "0:16,0:16:99:0,534", "0:16,0:16:99:0,459",  
 "0:18,0:18:99:0,602", "0:14,0:14:99:0,324", "0:13,0:13:99:0,440",

```
"0:13,0:13:99:0,434", "0:13,0:13:99:0,450", "0:11,0:11:99:0,365",
"0:23,0:23:99:0,801", "0:13,0:13:99:0,413", "0:19,0:19:99:0,574",
"0:13,0:13:99:0,393", "0:18,0:18:99:0,627", "0:9,0:9:99:0,281",
"0:17,0:17:99:0,585", "0:15,0:15:99:0,540", "0:12,0:12:99:0,315",
"0:18,0:18:99:0,563", "0:15,0:15:99:0,512", "0:15,0:15:99:0,563",
"0:8,0:8:99:0,229", "0:7,0:7:99:0,237", 1, 0.009091`, 110, "NA",
1668, 0.`, 1, 0.009091`, 60.`, "NA", 33.61`, "NA", 0.818`, "NA"};
```

#317: VRP1 is verified, but OPI9 is dubious (SGD) [Kept as is]

```
In[58]:= fixme = 317;
```

Kept as is:

In[59]:= **fullgenomeSNPEFF[[fixme]]**

Out[59]=

```
{chrXII, 12, 804694, G, A, 355.29, GT:AD:DP:GQ:PL, VRP1,
MODERATE, missense_variant, YLR337C, c.413C>T, p.Ala138Val,
A|missense_variant|MODERATE|VRP1|YLR337C|transcript|YLR337C_mRNA|protein_coding|
1/1|c.413C>T|p.Ala138Val|413/2454|413/2454|138/817||,A|missense_variant|
MODERATE|OPI9|YLR338W|transcript|YLR338W_mRNA|protein_coding|1/1|c.349G>A|p.
Ala117Thr|349/858|349/858|117/285||,A|upstream_gene_variant|MODIFIER|SGD1|
YLR336C|transcript|YLR336C_mRNA|protein_coding||c.-2298C>T||||2298|,A|
upstream_gene_variant|MODIFIER|RPP0|YLR340W|transcript|YLR340W_mRNA|
protein_coding||c.-1193G>A||||1193|,A|upstream_gene_variant|MODIFIER|SP077|
YLR341W|transcript|YLR341W_mRNA|protein_coding||c.-2691G>A||||2691|,A|
downstream_gene_variant|MODIFIER|YLR339C|YLR339C|transcript|YLR339C_mRNA|
protein_coding||c.*1090C>T||||1090|, 0:10,0:10:99:0,224,
0:18,0:18:99:0,224, 0:7,0:7:99:0,228, 0:8,0:8:99:0,201, 0:5,0:5:99:0,118,
0:13,0:13:99:0,378, 0:10,0:10:99:0,180, 0:11,0:11:99:0,244,
0:7,0:7:99:0,228, 0:5,0:5:99:0,150, 0:5,0:5:99:0,135, 0:17,0:17:99:0,371,
0:4,0:4:99:0,128, 0:7,0:7:99:0,187, 0:8,0:8:99:0,246, 0:11,0:11:99:0,295,
0:5,0:5:99:0,115, 0:5,0:5:99:0,122, 0:5,0:5:99:0,132, 0:9,0:9:99:0,251,
0:7,0:7:99:0,159, 0:5,0:5:99:0,180, 0:11,0:11:99:0,338, 0:13,0:13:99:0,357,
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0:4,0:4:99:0,99, 0:6,0:6:99:0,135, 0:14,0:14:99:0,407, 0:12,0:12:99:0,245,
0:16,0:16:99:0,568, 0:6,0:6:99:0,148, 0:12,0:12:99:0,346, 0:5,0:5:99:0,140,
0:3,0:3:99:0,104, 0:5,0:5:99:0,122, 0:4,0:4:99:0,135, 0:4,0:4:99:0,113,
0:8,0:8:99:0,214, 0:12,0:12:99:0,392, 0:6,0:6:99:0,218, 0:8,0:8:99:0,161,
0:4,0:4:99:0,119, 0:10,0:10:99:0,317, 0:4,0:4:99:0,122, 0:8,0:8:99:0,192,
0:10,0:10:99:0,262, 0:10,0:10:99:0,197, 0:4,0:4:99:0,122, 0:6,0:6:99:0,204,
0:4,0:4:99:0,99, 0:4,0:4:99:0,154, 0:5,0:5:99:0,135, 0:8,0:8:99:0,162,
0:8,0:8:99:0,173, 0:7,0:7:99:0,191, 0:8,0:8:99:0,250, 0:6,0:6:99:0,190,
0:7,0:7:99:0,191, 0:7,0:7:99:0,228, 0:4,0:4:99:0,135, 0:10,0:10:99:0,263,
1:0,10:10:99:376,0, 0:9,0:9:99:0,225, 0:13,0:13:99:0,430, 0:9,0:9:99:0,336,
0:18,0:18:99:0,585, 0:11,0:11:99:0,283, 0:11,0:11:99:0,203,
0:8,0:8:99:0,103, 0:9,0:9:99:0,184, 0:9,0:9:99:0,240, 0:11,0:11:99:0,302,
0:10,0:10:99:0,351, 0:8,0:8:99:0,279, 0:16,0:16:99:0,521,
0:12,0:12:99:0,345, 0:8,0:8:99:0,241, 0:14,0:14:99:0,509, 0:8,0:8:99:0,273,
0:12,0:12:99:0,435, 0:13,0:13:99:0,356, 0:7,0:7:99:0,209, 0:11,0:11:99:0,393,
0:7,0:7:99:0,225, 0:8,0:8:99:0,264, 0:9,0:9:99:0,232, 0:7,0:7:99:0,225,
0:9,0:9:99:0,296, 0:4,0:4:99:0,133, 0:7,0:7:99:0,219, 0:9,0:9:99:0,300,
0:8,0:8:99:0,221, 0:7,0:7:99:0,196, 0:10,0:10:99:0,276, 0:7,0:7:99:0,184,
0:12,0:12:99:0,358, 0:6,0:6:99:0,214, 0:10,0:10:99:0,316, 0:9,0:9:99:0,192,
0:6,0:6:99:0,164, 0:12,0:12:99:0,259, 0:5,0:5:99:0,113, 0:9,0:9:99:0,162,
0:7,0:7:99:0,247, 0:9,0:9:99:0,210, 0:5,0:5:99:0,128, 0:4,0:4:99:0,107,
1, 0.009091, 110, NA, 924, 0., 1, 0.009091, 60., NA, 29.03, NA, 1.609, NA}
```

## #356: DDR48 is verified, but YMR173W-A is dubious (SGD) [Kept as is]

```
In[60]:= fixme = 356;
```

Kept as is:

```
In[61]:= fullgenomeSNPEFF[[fixme]]
```

```
Out[61]=
```

```
{chrXIII, 13, 609388, A, G, 342.29, GT:AD:DP:GQ:PL, DDR48,
MODERATE, missense_variant, YMR173W, c.700A>G, p.Asn234Asp,
G|missense_variant|MODERATE|DDR48|YMR173W|transcript|YMR173W_mRNA|protein_coding
|1/1|c.700A>G|p.Asn234Asp|700/1293|700/1293|234/430||,G|synonymous_variant|
LOW|YMR173W-A|YMR173W-A|transcript|YMR173W-A_mRNA|protein_coding|1/1|c.492A>G
|p.Leu164Leu|492/1185|492/1185|164/394||,G|upstream_gene_variant|MODIFIER|
EAR1|YMR171C|transcript|YMR171C_mRNA|protein_coding||c.-3868T>C||||3868|,G|
upstream_gene_variant|MODIFIER|YMR172C-A|YMR172C-A|transcript|YMR172C-A_mRNA|
protein_coding||c.-1177T>C||||1177|,G|upstream_gene_variant|MODIFIER|SIP18|
YMR175W|transcript|YMR175W_mRNA|protein_coding||c.-1628A>G||||1628|,G|
upstream_gene_variant|MODIFIER|YMR175W-A|YMR175W-A|transcript|YMR175W-A_mRNA|
protein_coding||c.-1926A>G||||1926|,G|upstream_gene_variant|MODIFIER|ECM5|
YMR176W|transcript|YMR176W_mRNA|protein_coding||c.-2352A>G||||2352|,G|
downstream_gene_variant|MODIFIER|HOT1|YMR172W|transcript|YMR172W_mRNA|
protein_coding||c.*1248A>G||||1248|,G|downstream_gene_variant|MODIFIER|PAI3|
YMR174C|transcript|YMR174C_mRNA|protein_coding||c.*771T>C||||771|,
0:7,0:7:99:0,159, 0:11,0:11:99:0,111, 0:8,0:8:99:0,170, 0:7,0:7:99:0,246,
0:5,0:5:99:0,103, 0:9,0:9:99:0,149, 0:9,0:9:99:0,168, 0:10,0:10:99:0,264,
0:4,0:4:99:0,111, 0:6,0:6:99:0,104, 1:0,11:11:99:363,0, 0:6,0:6:99:0,142,
0:4,0:4:99:0,128, 0:5,0:5:99:0,131, 0:5,0:5:99:0,163, 0:9,0:9:99:0,302,
0:7,0:7:99:0,124, 0:7,0:7:99:0,111, 0:5,0:5:99:0,103, 0:8,0:8:99:0,202,
0:5,0:5:99:0,155, 0:6,0:6:99:0,144, 0:11,0:11:99:0,116, 0:10,0:10:99:0,185,
0:5,0:5:99:0,163, 0:9,0:9:99:0,251, 0:22,0:22:99:0,313, 0:5,0:5:99:0,140,
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0:21,0:21:99:0,596, 0:7,0:7:99:0,123, 0:12,0:12:99:0,188, 0:5,0:5:99:0,166,
0:4,0:4:99:0,109, 0:5,0:5:99:0,134, 0:4,0:4:99:0,104, 0:5,0:5:99:0,163,
0:6,0:6:99:0,101, 0:10,0:10:99:0,187, 0:4,0:4:99:0,101, 0:7,0:7:99:0,146,
0:10,0:10:99:0,136, 0:8,0:8:99:0,270, 0:4,0:4:99:0,135, 0:5,0:5:99:0,125,
0:7,0:7:99:0,110, 0:7,0:7:99:0,225, 0:5,0:5:99:0,103, 0:6,0:6:99:0,137,
0:4,0:4:99:0,100, 0:4,0:4:99:0,107, 0:4,0:4:99:0,104, 0:8,0:8:99:0,235,
0:6,0:6:99:0,159, 0:8,0:8:99:0,203, 0:6,0:6:99:0,139, 0:5,0:5:99:0,155,
0:4,0:4:99:0,141, 0:5,0:5:99:0,111, 0:9,0:9:99:0,183, 0:7,0:7:99:0,113,
0:8,0:8:99:0,122, 0:13,0:13:99:0,399, 0:10,0:10:99:0,160, 0:9,0:9:99:0,183,
0:11,0:11:99:0,342, 0:7,0:7:99:0,174, 0:9,0:9:99:0,202, 0:19,0:19:99:0,297,
0:19,0:19:99:0,632, 0:20,0:20:99:0,585, 0:10,0:10:99:0,157,
0:8,0:8:99:0,194, 0:9,0:9:99:0,224, 0:9,0:9:99:0,105, 0:13,0:13:99:0,234,
```

```
0:8,0:8:99:0,263, 0:14,0:14:99:0,392, 0:19,0:19:99:0,151, 0:12,0:12:99:0,148,
0:10,0:10:99:0,208, 0:9,0:9:99:0,126, 0:25,0:25:99:0,354, 0:8,0:8:99:0,198,
0:7,0:7:99:0,114, 0:7,0:7:99:0,263, 0:6,0:6:99:0,180, 0:10,0:10:99:0,129,
0:3,0:3:99:0,104, 0:6,0:6:99:0,218, 0:7,0:7:99:0,137, 0:7,0:7:99:0,191,
0:8,0:8:99:0,103, 0:11,0:11:99:0,334, 0:21,0:21:99:0,514, 0:12,0:12:99:0,128,
0:11,0:11:99:0,331, 0:9,0:9:99:0,154, 0:10,0:10:99:0,175, 0:9,0:9:99:0,233,
0:25,0:25:99:0,281, 0:5,0:5:99:0,141, 0:22,0:22:99:0,455, 0:7,0:7:99:0,195,
0:11,0:11:99:0,325, 0:3,0:3:99:0,114, 0:13,0:13:99:0,189, 1,
0.009091, 110, NA, 972, 0., 1, 0.009091, 57.68, NA, 31.12, NA, 1.802, NA}
```

### #380: YNL109W is dubious, as is YNL108C (SGD) [To be dropped]

```
In[62]:= fixme = 380;
```

```
In[63]:= fullgenomeSNPEFF[[fixme]]
```

```
Out[63]=
```

```
{chrXIV, 14, 419354, G, A, 446.29, GT:AD:DP:GQ:PL, YNL109W,
MODERATE, missense_variant, YNL109W, c.391G>A, p.Gly131Arg,
A|missense_variant|MODERATE|YNL109W|YNL109W|transcript|YNL109W_mRNA|
protein_coding|1/1|c.391G>A|p.Gly131Arg|391/546|391/546|131/181||,A|
missense_variant|MODERATE|YNL108C|YNL108C|transcript|YNL108C_mRNA|
protein_coding|1/1|c.473C>T|p.Pro158Leu|473/813|473/813|158/270||,A|
upstream_gene_variant|MODIFIER|CYB5|YNL111C|transcript|YNL111C_mRNA|
protein_coding||c.-2052C>T||||2052|,A|upstream_gene_variant|MODIFIER|NOP15|
YNL110C|transcript|YNL110C_mRNA|protein_coding||c.-866C>T||||866|,A|
upstream_gene_variant|MODIFIER|YAF9|YNL107W|transcript|YNL107W_mRNA|
protein_coding||c.-744G>A||||744|,A|upstream_gene_variant|MODIFIER|RRT16|
YNL105W|transcript|YNL105W_mRNA|protein_coding||c.-4801G>A||||4801|,A|
downstream_gene_variant|MODIFIER|DBP2|YNL112W|transcript|YNL112W_mRNA|
protein_coding||c.*3073G>A||||3073|,A|downstream_gene_variant|MODIFIER|INP52
|YNL106C|transcript|YNL106C_mRNA|protein_coding||c.*1590C>T||||1590|,
0:10,0:10:99:0,151, 0:7,0:7:99:0,136, 0:5,0:5:99:0,159, 0:11,0:11:99:0,137,
0:4,0:4:99:0,109, 0:7,0:7:99:0,196, 0:8,0:8:99:0,105, 0:8,0:8:99:0,191,
0:5,0:5:99:0,113, 0:7,0:7:99:0,99, 0:7,0:7:99:0,123, 0:8,0:8:99:0,237,
0:8,0:8:99:0,112, 0:7,0:7:99:0,125, 0:8,0:8:99:0,120, 0:6,0:6:99:0,125,
0:4,0:4:99:0,119, 0:6,0:6:99:0,200, 0:4,0:4:99:0,104, 0:7,0:7:99:0,116,
0:6,0:6:99:0,150, 1:0,12:12:99:467,0, 0:13,0:13:99:0,106, 0:10,0:10:99:0,123,
0:12,0:12:99:0,151, 0:10,0:10:99:0,130, 0:9,0:9:99:0,177, 0:7,0:7:99:0,114,
0:4,0:4:99:0,132, 0:9,0:9:99:0,101, 0:14,0:14:99:0,258, 0:12,0:12:99:0,172,
0:21,0:21:99:0,135, 0:4,0:4:99:0,126, 0:19,0:19:99:0,202, 0:5,0:5:99:0,169,
0:4,0:4:99:0,135, 0:6,0:6:99:0,140, 0:4,0:4:99:0,135, 0:8,0:8:99:0,107,
0:13,0:13:99:0,138, 0:10,0:10:99:0,167, 0:7,0:7:99:0,99, 0:6,0:6:99:0,138,
0:6,0:6:99:0,130, 0:10,0:10:99:0,146, 0:7,0:7:99:0,223, 0:10,0:10:99:0,187,
0:9,0:9:99:0,259, 0:7,0:7:99:0,158, 0:7,0:7:99:0,142, 0:4,0:4:99:0,133,
```



```
0:4,0:4:99:0,113, 0:5,0:5:99:0,125, 0:4,0:4:99:0,103, 0:7,0:7:99:0,208,
0:9,0:9:99:0,103, 0:3,0:3:99:0,100, 0:6,0:6:99:0,138, 0:7,0:7:99:0,123,
0:3,0:3:99:0,109, 0:6,0:6:99:0,105, 0:7,0:7:99:0,225, 0:9,0:9:99:0,283,
0:12,0:12:99:0,165, 0:11,0:11:99:0,164, 0:15,0:15:99:0,122,
0:9,0:9:99:0,166, 0:15,0:15:99:0,204, 0:13,0:13:99:0,184, 0:11,0:11:99:0,268,
0:21,0:21:99:0,130, 0:23,0:23:99:0,142, 0:17,0:17:99:0,198,
0:15,0:15:99:0,147, 0:12,0:12:99:0,178, 0:13,0:13:99:0,121, 0:22,0:22:99:0,125,
0:11,0:11:99:0,342, 0:8,0:8:99:0,166, 0:19,0:19:99:0,102, 0:22,0:22:99:0,211,
0:11,0:11:99:0,249, 0:10,0:10:99:0,147, 0:26,0:26:99:0,186, 0:13,0:13:99:0,260,
0:10,0:10:99:0,156, 0:11,0:11:99:0,237, 0:9,0:9:99:0,233, 0:8,0:8:99:0,109,
0:10,0:10:99:0,203, 0:4,0:4:99:0,114, 0:6,0:6:99:0,207, 0:8,0:8:99:0,137,
0:9,0:9:99:0,114, 0:8,0:8:99:0,177, 0:11,0:11:99:0,101, 0:10,0:10:99:0,173,
0:13,0:13:99:0,109, 0:6,0:6:99:0,138, 0:8,0:8:99:0,139, 0:7,0:7:99:0,119,
0:9,0:9:99:0,148, 0:11,0:11:99:0,138, 0:6,0:6:99:0,112, 0:9,0:9:99:0,101,
0:10,0:10:99:0,114, 0:10,0:10:99:0,107, 0:7,0:7:99:0,144, 0:4,0:4:99:0,127,
1, 0.009091, 110, NA, 1025, 0., 1, 0.009091, 60., NA, 25.41, NA, 1.981, NA}
```

Dropping this (will do in the next folder so it doesn't affect the numbering):

```
fullgenomeSNPEFF=Select[fullgenomeSNPEFF,StringContainsQ#[[8]],"YNL109W"]==False&];
```

### #4439: YPL114W is dubious, but YPL113C is verified (SGD) [Updated]

```
In[64]:= fixme = 439;
```

Manually swapping for the second gene:

```
In[65]:= fullgenomeSNPEFF[[fixme]]
```

```
Out[65]=
```

```
{chrXVI, 16, 336149, G, A, 896.29, GT:AD:DP:GQ:PL, YPL114W,
MODERATE, missense_variant, YPL114W, c.202G>A, p.Ala68Thr,
A|missense_variant|MODERATE|YPL114W|YPL114W|transcript|YPL114W_mRNA|
protein_coding|1/1|c.202G>A|p.Ala68Thr|202/420|202/420|68/139||,A|
missense_variant|MODERATE|YPL113C|YPL113C|transcript|YPL113C_mRNA|
protein_coding|1/1|c.995C>T|p.Ala332Val|995/1191|995/1191|332/396||,A|
upstream_gene_variant|MODIFIER|BEM3|YPL115C|transcript|YPL115C_mRNA|
protein_coding||c.-663C>T||||663|,A|upstream_gene_variant|MODIFIER|CAR1|
YPL111W|transcript|YPL111W_mRNA|protein_coding||c.-3795G>A||||3795|,A|
downstream_gene_variant|MODIFIER|HOS3|YPL116W|transcript|YPL116W_mRNA|
protein_coding||c.*4450G>A||||4450|,A|downstream_gene_variant|MODIFIER|PEX25
|YPL112C|transcript|YPL112C_mRNA|protein_coding||c.*1287C>T||||1287|,A|
downstream_gene_variant|MODIFIER|IMT2|tM(CAU)P|transcript|tM(CAU)P_tRNA|
protein_coding||c.*2699C>T||||2699|WARNING_TRANSCRIPT_NO_START_CODON,A|
downstream_gene_variant|MODIFIER|GDE1|YPL110C|transcript|YPL110C_mRNA|
protein_coding||c.*4919C>T||||4919|, 0:10,0:10:99:0,307,
0:5,0:5:99:0,128, 0:8,0:8:99:0,276, 0:7,0:7:99:0,201, 0:4,0:4:99:0,99,
```

```

0:7,0:7:99:0,185, 0:6,0:6:99:0,214, 0:6,0:6:99:0,194, 0:4,0:4:99:0,110,
0:5,0:5:99:0,163, 0:6,0:6:99:0,169, 0:5,0:5:99:0,174, 0:6,0:6:99:0,180,
0:5,0:5:99:0,150, 0:4,0:4:99:0,123, 0:8,0:8:99:0,241, 0:4,0:4:99:0,112,
0:4,0:4:99:0,119, 0:4,0:4:99:0,100, 0:7,0:7:99:0,178, 0:4,0:4:99:0,130,
0:4,0:4:99:0,132, 0:7,0:7:99:0,185, 0:10,0:10:99:0,162, 0:3,0:3:99:0,100,
0:9,0:9:99:0,275, 0:7,0:7:99:0,182, 1:0,28:28:99:917,0, 0:4,0:4:99:0,110,
0:5,0:5:99:0,169, 0:10,0:10:99:0,321, 0:10,0:10:99:0,360,
0:19,0:19:99:0,577, 0:5,0:5:99:0,181, 0:7,0:7:99:0,259, 0:6,0:6:99:0,200,
0:3,0:3:99:0,100, 0:3,0:3:99:0,100, 0:3,0:3:99:0,100, 0:6,0:6:99:0,176,
0:7,0:7:99:0,180, 0:11,0:11:99:0,341, 0:6,0:6:99:0,176, 0:5,0:5:99:0,159,
0:4,0:4:99:0,113, 0:9,0:9:99:0,244, 0:6,0:6:99:0,126, 0:7,0:7:99:0,137,
0:5,0:5:99:0,159, 0:8,0:8:99:0,258, 0:4,0:4:99:0,135, 0:5,0:5:99:0,150,
0:3,0:3:99:0,100, 0:4,0:4:99:0,100, 0:3,0:3:99:0,114, 0:9,0:9:99:0,280,
0:7,0:7:99:0,203, 0:5,0:5:99:0,173, 0:4,0:4:99:0,137, 0:6,0:6:99:0,204,
0:3,0:3:99:0,113, 0:7,0:7:99:0,190, 0:8,0:8:99:0,254, 0:5,0:5:99:0,144,
0:7,0:7:99:0,229, 0:9,0:9:99:0,270, 0:12,0:12:99:0,380, 0:9,0:9:99:0,260,
0:9,0:9:99:0,256, 0:11,0:11:99:0,263, 0:9,0:9:99:0,278, 0:5,0:5:99:0,138,
0:9,0:9:99:0,146, 0:8,0:8:99:0,255, 0:8,0:8:99:0,270, 0:9,0:9:99:0,295,
0:8,0:8:99:0,260, 0:11,0:11:99:0,325, 0:9,0:9:99:0,294, 0:5,0:5:99:0,169,
0:14,0:14:99:0,303, 0:6,0:6:99:0,222, 0:8,0:8:99:0,269, 0:8,0:8:99:0,249,
0:7,0:7:99:0,215, 0:8,0:8:99:0,219, 0:5,0:5:99:0,172, 0:9,0:9:99:0,273,
0:9,0:9:99:0,293, 0:5,0:5:99:0,159, 0:7,0:7:99:0,218, 0:4,0:4:99:0,113,
0:5,0:5:99:0,135, 0:7,0:7:99:0,198, 0:7,0:7:99:0,199, 0:6,0:6:99:0,173,
0:10,0:10:99:0,278, 0:8,0:8:99:0,257, 0:11,0:11:99:0,364,
0:8,0:8:99:0,214, 0:7,0:7:99:0,144, 0:7,0:7:99:0,113, 0:9,0:9:99:0,270,
0:11,0:11:99:0,360, 0:5,0:5:99:0,135, 0:6,0:6:99:0,132, 0:6,0:6:99:0,180,
0:9,0:9:99:0,246, 0:4,0:4:99:0,100, 0:3,0:3:99:0,100, 1, 0.009091,
110, NA, 766, 0., 1, 0.009091, 60., NA, 32.01, NA, 0.997, NA}

```

```

In[66]:= fullgenomeSNPEFF[fixme] =
{chrXVI", 16, 336149, "G", "A", 896.29`, "GT:AD:DP:GQ:PL", "YPL113C",
"MODERATE", "missense_variant", "YPL113C", "c.995C>T", "p.Ala332Val",
"A|missense_variant|MODERATE|YPL114W|YPL114W|transcript|YPL114W_mRNA|
protein_coding|1/1|c.202G>A|p.Ala68Thr|202/420|202/420|68/139||,A|
missense_variant|MODERATE|YPL113C|YPL113C|transcript|YPL113C_mRNA|
protein_coding|1/1|c.995C>T|p.Ala332Val|995/1191|995/1191|332/396||,A|
upstream_gene_variant|MODIFIER|BEM3|YPL115C|transcript|YPL115C_mRNA|
protein_coding||c.-663C>T||||663|,A|upstream_gene_variant|MODIFIER|CAR1
|YPL111W|transcript|YPL111W_mRNA|protein_coding||c.-3795G>A||||3795|,A|
downstream_gene_variant|MODIFIER|HOS3|YPL116W|transcript|YPL116W_mRNA|
protein_coding||c.*4450G>A||||4450|,A|downstream_gene_variant|MODIFIER|
PEX25|YPL112C|transcript|YPL112C_mRNA|protein_coding||c.*1287C>T||||
1287|,A|downstream_gene_variant|MODIFIER|IMT2|tM(CAU)P|transcript|tM(CAU)
P_tRNA|protein_coding||c.*2699C>T||||2699|WARNING_TRANSCRIPT_NO_START

```

```

_CODON,A|downstream_gene_variant|MODIFIER|GDE1|YPL110C|transcript|
YPL110C_mRNA|protein_coding||c.*4919C>T||||4919|",
"0:10,0:10:99:0,307", "0:5,0:5:99:0,128", "0:8,0:8:99:0,276",
"0:7,0:7:99:0,201", "0:4,0:4:99:0,99", "0:7,0:7:99:0,185", "0:6,0:6:99:0,214",
"0:6,0:6:99:0,194", "0:4,0:4:99:0,110", "0:5,0:5:99:0,163", "0:6,0:6:99:0,169",
"0:5,0:5:99:0,174", "0:6,0:6:99:0,180", "0:5,0:5:99:0,150", "0:4,0:4:99:0,123",
"0:8,0:8:99:0,241", "0:4,0:4:99:0,112", "0:4,0:4:99:0,119", "0:4,0:4:99:0,100",
"0:7,0:7:99:0,178", "0:4,0:4:99:0,130", "0:4,0:4:99:0,132", "0:7,0:7:99:0,185",
"0:10,0:10:99:0,162", "0:3,0:3:99:0,100", "0:9,0:9:99:0,275",
"0:7,0:7:99:0,182", "1:0,28:28:99:917,0", "0:4,0:4:99:0,110",
"0:5,0:5:99:0,169", "0:10,0:10:99:0,321", "0:10,0:10:99:0,360",
"0:19,0:19:99:0,577", "0:5,0:5:99:0,181", "0:7,0:7:99:0,259",
"0:6,0:6:99:0,200", "0:3,0:3:99:0,100", "0:3,0:3:99:0,100", "0:3,0:3:99:0,100",
"0:6,0:6:99:0,176", "0:7,0:7:99:0,180", "0:11,0:11:99:0,341",
"0:6,0:6:99:0,176", "0:5,0:5:99:0,159", "0:4,0:4:99:0,113", "0:9,0:9:99:0,244",
"0:6,0:6:99:0,126", "0:7,0:7:99:0,137", "0:5,0:5:99:0,159", "0:8,0:8:99:0,258",
"0:4,0:4:99:0,135", "0:5,0:5:99:0,150", "0:3,0:3:99:0,100", "0:4,0:4:99:0,100",
"0:3,0:3:99:0,114", "0:9,0:9:99:0,280", "0:7,0:7:99:0,203", "0:5,0:5:99:0,173",
"0:4,0:4:99:0,137", "0:6,0:6:99:0,204", "0:3,0:3:99:0,113", "0:7,0:7:99:0,190",
"0:8,0:8:99:0,254", "0:5,0:5:99:0,144", "0:7,0:7:99:0,229", "0:9,0:9:99:0,270",
"0:12,0:12:99:0,380", "0:9,0:9:99:0,260", "0:9,0:9:99:0,256",
"0:11,0:11:99:0,263", "0:9,0:9:99:0,278", "0:5,0:5:99:0,138",
"0:9,0:9:99:0,146", "0:8,0:8:99:0,255", "0:8,0:8:99:0,270", "0:9,0:9:99:0,295",
"0:8,0:8:99:0,260", "0:11,0:11:99:0,325", "0:9,0:9:99:0,294",
"0:5,0:5:99:0,169", "0:14,0:14:99:0,303", "0:6,0:6:99:0,222",
"0:8,0:8:99:0,269", "0:8,0:8:99:0,249", "0:7,0:7:99:0,215", "0:8,0:8:99:0,219",
"0:5,0:5:99:0,172", "0:9,0:9:99:0,273", "0:9,0:9:99:0,293",
"0:5,0:5:99:0,159", "0:7,0:7:99:0,218", "0:4,0:4:99:0,113",
"0:5,0:5:99:0,135", "0:7,0:7:99:0,198", "0:7,0:7:99:0,199",
"0:6,0:6:99:0,173", "0:10,0:10:99:0,278", "0:8,0:8:99:0,257",
"0:11,0:11:99:0,364", "0:8,0:8:99:0,214", "0:7,0:7:99:0,144",
"0:7,0:7:99:0,113", "0:9,0:9:99:0,270", "0:11,0:11:99:0,360",
"0:5,0:5:99:0,135", "0:6,0:6:99:0,132", "0:6,0:6:99:0,180",
"0:9,0:9:99:0,246", "0:4,0:4:99:0,100", "0:3,0:3:99:0,100", 1, 0.009091`,
110, "NA", 766, 0.`, 1, 0.009091`, 60.`, "NA", 32.01`, "NA", 0.997`, "NA"};

```

## Revised gene list

Dropping dubious YNL109W from above (done now to avoid affecting the numbering):

```

In[67]:= fullgenomeSNPEFF =
Select[fullgenomeSNPEFF, StringContainsQ[#[[8]], "YNL109W"] == False &];

```

```
In[68]:= genelist = Sort[Union[fullgenomeSNPEFF[All, 8]]]
```

```
Out[68]=
```

```
{ABP1, ACB1, ACC1, ADE6, ADR1, AFT1, AGP1, AHK1, ALD5, ALY2, APC2, ARO3, ASN1, ATG11,
ATG2, BDS1, BIR1, BLM10, BNA6, BNI1, BNI4, BRR2, BSC1, BSD2, BUL1, BUL2, CAJ1,
CCC2, CCR4, CCW12, CDC25, CIC1, CLB3, CLN3, CNE1, COG1, COG3, COQ1, CPA1, CSM3,
CUE3, CWC22, CWH41, CYK3, DAL2, DAN4, DBF20, DBP10, DDR48, DNF1, DOA4, DOT6,
DSC2, DSE4, DUS4, EBS1, ECM14, ECM22, EFR3, ERB1, ERG1, ERG27, ERG7, ERG9,
FAS2, FAU1, FCY2, FET4, FIG2, FIG4, FLC2, FLO1, FLO9, FMP52, FRE6, FSF1, FYV10,
FYV6, FZF1, GAS4, GAT1, GCD2, GPB1, GPB2, GPH1, GSC2, HAP1, HBT1, HEH2, HHF2,
HIS4, HMF1, HO, HRT3, HSL1, HSP104, HUL5, HXT13, IDP1, IES3, ILV2, IMA1, INP2,
IOC4, IPI3, IRC20, IRC8, IST2, ISU1, ITC1, KAR3, KGD1, KIN1, KIN82, KRE5, KSP1,
KTR3, LAM1, LAM6, LOS1, LRG1, MAM3, MAS2, MCK1, MCM5, MCT1, MDH2, MDL2, MDM30,
MET10, MET30, MEX67, MHP1, MKT1, MLF3, MLH3, MLS1, MMS4, MNN9, MOT1, MPA43,
MRL1, MRPL36, MSC6, MSS11, MSS2, MTR4, MYO2, NAM8, NAR1, NFT1, NGG1, NIP100,
NPL3, NSR1, NUC1, NUG1, OAF1, OCA4, OCA5, OPI1, OSH2, PBP2, PBS2, PCL5, PDA1,
PDR1, PDR10, PDX1, PET111, PET127, PEX2, PFK26, PHM7, PHO23, PHO81, PHO84,
PIB1, PIR3, PKP1, PLB2, PMA1, POL3, PPQ1, PRC1, PRI1, PRI2, PRP2, PRP8, PTK2,
PYK2, QRI7, RAD16, RAD17, RAD26, RBK1, RCE1, RCK2, RCO1, REC102, RED1, RH01,
RIM11, RIM21, RKM3, RMP1, RNY1, ROG1, RPA135, RPI1, RPL22A, RPL2A, RPL39,
RPS15, RPS2, RPT5, RRB1, RRG7, RRP46, RRP6, RSC1, RSE1, RTC2, SAK1, SAP4, SBE2,
SEC8, SET2, SFP1, SHP1, SIW14, SKN1, SMC2, SMY2, SNF7, SNT2, SPC105, SP077,
SPS100, SRP40, SSE1, SSK2, SSQ1, SSZ1, STE5, STP3, STT3, SUB2, SUC2, SUM1,
SWC5, SWS2, SWT1, SYF2, SYG1, TAF8, TAH11, TA03, TC089, TFB1, TFG1, TIM54,
TOM1, TOP1, TOP2, TOS3, TPS3, TRK2, TRL1, TUS1, UBC1, UBP5, UBR2, UBX7, UGA3,
UGA4, UIP5, ULS1, UME6, URA2, URB1, USA1, UTP21, UTP8, VBA1, VCX1, VHR2, VID22,
VPS13, VPS74, VRP1, VTC1, VTC3, VTC4, VTC5, WAR1, YAP6, YBL109W, YBR134W,
YBR242W, YBR292C, YCF1, YCK1, YCT1, YDL176W, YDL199C, YDR003W-A, YDR157W,
YDR381C-A, YDR541C, YDR544C, YEF1, YER087C-A, YER156C, YFR036W-A, YGR126W,
YGR130C, YGR266W, YHC1, YHC3, YHL008C, YHR028W-A, YHR071C-A, YIH1, YIL092W,
YIR020W-A, YKR073C, YLL020C, YLL066W-B, YLR108C, YLR296W, YLR312C, YLR372W,
YML119W, YMR027W, YMR317W, YOR029W, YOR1, YOR296W, YOR343C, YPK1, YPL025C,
YPL113C, YPR078C, YPR089W, YPR117W, YPT6, YRA1, YRB2, ZDS2, ZRT1, ZRT3}
```

Checking all of the systematic ("Y...") names:

```
In[69]:= checkme = {"YBL109W", "YBR134W", "YBR242W", "YBR292C", "YDL199C",
"YDR003W-A", "YDR157W", "YDR541C", "YDR544C", "YER087C-A", "YFR036W-A",
"YGR126W", "YGR130C", "YGR266W", "YHL008C", "YHR028W-A", "YHR071C-A",
"YIL092W", "YIR020W-A", "YKR073C", "YLL020C", "YLL066W-B", "YLR108C",
"YLR296W", "YML119W", "YMR027W", "YMR317W", "YOR029W", "YOR296W",
"YOR343C", "YPL025C", "YPL113C", "YPL114W", "YPR078C", "YPR089W"};
```

Some now have standardized names (replacing these names):

```
In[70]:= Position[fullgenomeSNPEFF[All, 8], "YDL176W"][[1, 1]]
```

```
Out[70]=  
50
```

```
In[71]:= fullgenomeSNPEFF[%, 8] = "GID12"
```

```
Out[71]=  
GID12
```

```
In[72]:= Position[fullgenomeSNPEFF[All, 8], "YDR381C-A"][[1, 1]]
```

```
Out[72]=  
91
```

```
In[73]:= fullgenomeSNPEFF[%, 8] = "COI1"
```

```
Out[73]=  
COI1
```

```
In[74]:= Position[fullgenomeSNPEFF[All, 8], "YER156C"][[1, 1]]
```

```
Out[74]=  
113
```

```
In[75]:= fullgenomeSNPEFF[%, 8] = "MYG1"
```

```
Out[75]=  
MYG1
```

```
In[76]:= Position[fullgenomeSNPEFF[All, 8], "YLR312C"][[1, 1]]
```

```
Out[76]=  
315
```

```
In[77]:= fullgenomeSNPEFF[%, 8] = "ATG39"
```

```
Out[77]=  
ATG39
```

```
In[78]:= Position[fullgenomeSNPEFF[All, 8], "YLR372W"][[1, 1]]
```

```
Out[78]=  
321
```

```
In[79]:= fullgenomeSNPEFF[%, 8] = "EL03"
```

```
Out[79]=  
EL03
```

```
In[80]:= Position[fullgenomeSNPEFF[All, 8], "YPR117W"][[1, 1]]
```

```
Out[80]=  
452
```

```
In[81]:= fullgenomeSNPEFF[%, 8] = "HOB2"
```

```
Out[81]=  
HOB2
```

Throwing out the dubious genes according to SGD [6 Nov 2024] (keeping uncharacterized):

```
In[82]:= dropme = {"YBL109W", "YBR134W", "YDR544C", "YER087C-A", "YFR036W-A",
  "YHR028W-A", "YHR071C-A", "YIR020W-A", "YLL020C", "YPL025C"};
```

Depth of coverage for these genes is pretty typical:

```
In[83]:= Select[fullgenomeSNPEFF, MemberQ[dropme, #[[8]]] &] [[All, {8, 129}]]
Mean[%[[All, 2]]] // N
```

```
Out[83]=
{{YBL109W, 410}, {YBR134W, 976}, {YDR544C, 400},
 {YER087C-A, 814}, {YFR036W-A, 823}, {YHR028W-A, 691},
 {YHR071C-A, 968}, {YIR020W-A, 726}, {YLL020C, 1251}, {YPL025C, 846}}
```

```
Out[84]=
790.5
```

Dropping these ten dubious genes:

```
In[85]:= Length[fullgenomeSNPEFF];
fullgenomeSNPEFF = Select[fullgenomeSNPEFF, MemberQ[dropme, #[[8]]] == False &];
%% - Length[fullgenomeSNPEFF]
```

```
Out[87]=
10
```

```
In[88]:= genelist = Sort[Union[fullgenomeSNPEFF[All, 8]]]
Out[88]= {ABP1, ACB1, ACC1, ADE6, ADR1, AFT1, AGP1, AHK1, ALD5, ALY2, APC2, ARO3, ASN1, ATG11,
ATG2, ATG39, BDS1, BIR1, BLM10, BNA6, BNI1, BNI4, BRR2, BSC1, BSD2, BUL1, BUL2,
CAJ1, CCC2, CCR4, CCW12, CDC25, CIC1, CLB3, CLN3, CNE1, COG1, COG3, COI1, COQ1,
CPA1, CSM3, CUE3, CWC22, CWH41, CYK3, DAL2, DAN4, DBF20, DBP10, DDR48, DNF1,
DOA4, DOT6, DSC2, DSE4, DUS4, EBS1, ECM14, ECM22, EFR3, ELO3, ERB1, ERG1, ERG27,
ERG7, ERG9, FAS2, FAU1, FCY2, FET4, FIG2, FIG4, FLC2, FLO1, FLO9, FMP52, FRE6,
FSF1, FYV10, FYV6, FZF1, GAS4, GAT1, GCD2, GID12, GPB1, GPB2, GPH1, GSC2, HAP1,
HBT1, HEH2, HHF2, HIS4, HMF1, HO, HOB2, HRT3, HSL1, HSP104, HUL5, HXT13, IDP1,
IES3, ILV2, IMA1, INP2, IOC4, IPI3, IRC20, IRC8, IST2, ISU1, ITC1, KAR3, KGD1,
KIN1, KIN82, KRE5, KSP1, KTR3, LAM1, LAM6, LOS1, LRG1, MAM3, MAS2, MCK1, MCM5,
MCT1, MDH2, MDL2, MDM30, MET10, MET30, MEX67, MHP1, MKT1, MLF3, MLH3, MLS1,
MMS4, MNN9, MOT1, MPA43, MRL1, MRPL36, MSC6, MSS11, MSS2, MTR4, MYG1, MYO2,
NAM8, NAR1, NFT1, NGG1, NIP100, NPL3, NSR1, NUC1, NUG1, OAF1, OCA4, OCA5, OPI1,
OSH2, PBP2, PBS2, PCL5, PDA1, PDR1, PDR10, PDX1, PET111, PET127, PEX2, PFK26,
PHM7, PHO23, PHO81, PHO84, PIB1, PIR3, PKP1, PLB2, PMA1, POL3, PPQ1, PRC1,
PRI1, PRI2, PRP2, PRP8, PTK2, PYK2, QRI7, RAD16, RAD17, RAD26, RBK1, RCE1,
RCK2, RCO1, REC102, RED1, RH01, RIM11, RIM21, RKM3, RMP1, RNY1, ROG1, RPA135,
RPI1, RPL22A, RPL2A, RPL39, RPS15, RPS2, RPT5, RRB1, RRG7, RRP46, RRP6, RSC1,
RSE1, RTC2, SAK1, SAP4, SBE2, SEC8, SET2, SFP1, SHP1, SIW14, SKN1, SMC2, SMY2,
SNF7, SNT2, SPC105, SP077, SPS100, SRP40, SSE1, SSK2, SSQ1, SSZ1, STE5, STP3,
STT3, SUB2, SUC2, SUM1, SWC5, SWS2, SWT1, SYF2, SYG1, TAF8, TAH11, TA03, TC089,
TFB1, TFG1, TIM54, TOM1, TOP1, TOP2, TOS3, TPS3, TRK2, TRL1, TUS1, UBC1, UBP5,
UBR2, UBX7, UGA3, UGA4, UIP5, ULS1, UME6, URA2, URB1, USA1, UTP21, UTP8, VBA1,
VCX1, VHR2, VID22, VPS13, VPS74, VRP1, VTC1, VTC3, VTC4, VTC5, WAR1, YAP6,
YBR242W, YBR292C, YCF1, YCK1, YCT1, YDL199C, YDR003W-A, YDR157W, YDR541C,
YEF1, YGR126W, YGR130C, YGR266W, YHC1, YHC3, YHL008C, YIH1, YIL092W, YKR073C,
YLL066W-B, YLR108C, YLR296W, YML119W, YMR027W, YMR317W, YOR029W, YOR1, YOR296W,
YOR343C, YPK1, YPL113C, YPR078C, YPR089W, YPT6, YRA1, YRB2, ZDS2, ZRT1, ZRT3}

In[89]:= Length[genelist]
Out[89]= 342
```

## Checking ExcessHet - No further filtering of data needed

```
In[90]:= fullgenomeDIP[1]
Out[90]= {ref|NC_001133|, 136, ., G, A, 15763.5, .,
AC=84;AF=0.382;AN=220;BaseQRankSum=0.030;DP=2265;ExcessHet=126.3747;FS=5.880;
InbreedingCoeff=-0.6296;MLEAC=85;MLEAF=0.386;MQ=58.67;MQRankSum=-1.655e+00;QD
=10.81;ReadPosRankSum=0.754;SOR=0.387, GT:AD:DP:GQ:PGT:PL:PS,
0|0:12,0:15:36:0|1:136_G_A:0,36,540:136, 0|1:9,2:15:57:0|1:136_G_A:57,0,361:136,
```

0|1:23,8:33:99:0|1:136\_G\_A:245,0,879:136,  
 0/0:5,0:5:15:...:0,15,141, 0|1:11,5:18:99:0|1:136\_G\_A:173,0,447:136,  
 0|1:16,4:21:99:0|1:136\_G\_A:120,0,645:136,  
 0|1:17,10:29:99:0|1:136\_G\_A:354,0,675:136,  
 0|1:7,3:11:97:0|1:136\_G\_A:97,0,285:136, 0|1:20,2:25:24:0|1:136\_G\_A:24,0,746:136,  
 0|1:4,1:8:30:0|1:136\_G\_A:30,0,154:136, 0|0:9,0:10:27:0|1:136\_G\_A:0,27,394:136,  
 0|1:5,2:9:69:0|1:136\_G\_A:69,0,167:136, 0|1:18,6:25:99:0|1:136\_G\_A:194,0,738:136,  
 0|1:13,1:18:3:0|1:136\_G\_A:3,0,518:136, 0|1:3,7:12:99:0|1:136\_G\_A:263,0,105:136,  
 0/0:9,0:9:0:...:0,0,107, 0|0:5,0:5:15:0|1:136\_G\_A:0,15,225:136,  
 0/0:5,0:5:0:...:0,0,41, 0|1:9,9:19:99:0|1:136\_G\_A:331,0,351:136,  
 0|1:10,5:16:99:0|1:136\_G\_A:176,0,368:136,  
 0|0:7,0:12:21:0|1:136\_G\_A:0,21,315:136,  
 0|1:22,11:34:99:0|1:136\_G\_A:359,0,857:136,  
 0|1:3,3:13:99:0|1:136\_G\_A:106,0,117:136, 0|1:6,1:11:24:0|1:136\_G\_A:24,0,249:136,  
 0/0:20,1:26:18:...:0,18,829, 0|1:17,10:29:99:0|1:136\_G\_A:335,0,673:136,  
 0|1:6,1:9:13:0|1:136\_G\_A:13,0,249:136, 0|1:6,7:15:99:0|1:136\_G\_A:272,0,231:136,  
 0|0:7,0:7:21:0|1:136\_G\_A:0,21,304:136, 0|1:23,3:29:57:0|1:136\_G\_A:57,0,924:136,  
 0|1:31,8:42:99:0|1:136\_G\_A:202,0,1242:136,  
 0|1:15,8:32:99:0|1:136\_G\_A:291,0,563:136,  
 0|0:19,1:21:15:0|1:136\_G\_A:0,15,795:136, 0/1:12,5:22:99:...:163,0,489,  
 0|1:7,1:12:21:0|1:136\_G\_A:21,0,291:136, 0|1:6,8:15:99:0|1:136\_G\_A:292,0,228:136,  
 0|1:10,1:12:12:0|1:136\_G\_A:12,0,406:136, 0|1:4,2:8:72:0|1:136\_G\_A:72,0,162:136,  
 0|0:17,0:20:51:0|1:136\_G\_A:0,51,718:136, 0/0:12,0:15:36:...:0,36,540,  
 0|1:12,7:21:99:0|1:136\_G\_A:255,0,472:136,  
 0|1:11,6:18:99:0|1:136\_G\_A:219,0,440:136,  
 0|1:9,4:13:99:0|1:136\_G\_A:141,0,366:136,  
 0|1:14,5:19:99:0|1:136\_G\_A:142,0,551:136,  
 0|1:9,3:15:73:0|1:136\_G\_A:73,0,343:136, 0|0:13,0:13:39:0|1:136\_G\_A:0,39,571:136,  
 0|1:9,4:13:99:0|1:136\_G\_A:141,0,366:136,  
 0|1:18,12:32:99:0|1:136\_G\_A:415,0,706:136,  
 0|1:11,1:16:9:0|1:136\_G\_A:9,0,444:136, 0|1:13,6:20:99:0|1:136\_G\_A:213,0,528:136,  
 0|1:17,9:28:99:0|1:136\_G\_A:316,0,665:136,  
 0|1:7,1:10:21:0|1:136\_G\_A:21,0,291:136,  
 0|1:12,8:22:99:0|1:136\_G\_A:296,0,480:136, 0|1:6,1:9:24:0|1:136\_G\_A:24,0,249:136,  
 0|0:8,0:10:24:0|1:136\_G\_A:0,24,360:136, 0|1:9,5:15:99:0|1:136\_G\_A:183,0,319:136,  
 0|1:9,1:11:4:0|1:136\_G\_A:4,0,364:136, 0|0:18,1:20:12:0|1:136\_G\_A:0,12,718:136,  
 0|1:11,10:24:99:0|1:136\_G\_A:387,0,432:136,  
 0|1:3,7:10:99:0|1:136\_G\_A:265,0,105:136,  
 0|1:21,5:26:99:0|1:136\_G\_A:139,0,821:136,  
 0|1:9,6:18:99:0|1:136\_G\_A:220,0,360:136,  
 0|0:19,1:24:15:0|1:136\_G\_A:0,15,800:136,  
 0|1:11,4:17:99:0|1:136\_G\_A:109,0,439:136,  
 0|1:23,3:29:16:0|1:136\_G\_A:16,0,935:136,  
 0|1:18,9:29:99:0|1:136\_G\_A:294,0,721:136,



```

0|0:30,0:30:65:...:0,65,907, 0|1:17,5:25:99:0|1:136_G_A:159,0,699:136,
0|1:13,4:19:88:0|1:136_G_A:88,0,523:136,
0|1:12,4:19:60:0|1:136_G_A:60,0,482:136,
0|1:7,8:16:99:0|1:136_G_A:315,0,270:136,
0|1:8,7:22:99:0|1:136_G_A:205,0,294:136,
0|0:14,1:16:0:0|1:136_G_A:0,0,585:136, 0|1:12,2:18:48:0|1:136_G_A:48,0,498:136,
0|1:10,2:16:43:0|1:136_G_A:43,0,403:136,
0|1:12,12:26:99:0|1:136_G_A:453,0,442:136,
0|1:21,9:37:99:0|1:136_G_A:278,0,844:136, 0|0:17,1:24:9:0|1:136_G_A:0,9,709:136,
0|1:11,11:24:99:0|1:136_G_A:425,0,429:136,
0|1:20,11:35:99:0|1:136_G_A:383,0,777:136,
0|1:10,7:17:99:0|1:136_G_A:264,0,388:136,
0|1:21,12:37:99:0|1:136_G_A:419,0,820:136,
0|1:15,7:26:99:0|1:136_G_A:245,0,577:136,
0|1:12,14:27:99:0|1:136_G_A:531,0,462:136,
0|1:19,8:30:99:0|1:136_G_A:238,0,721:136,
0|1:12,4:21:91:0|1:136_G_A:91,0,455:136,
0|1:10,5:17:99:0|1:136_G_A:176,0,405:136,
0|0:19,2:24:10:0|1:136_G_A:0,10,798:136,
0|1:18,8:29:99:0|1:136_G_A:271,0,695:136,
0|1:18,6:25:99:0|1:136_G_A:198,0,697:136,
0|1:14,3:19:73:0|1:136_G_A:73,0,579:136, 0|1:3,6:9:99:0|1:136_G_A:232,0,108:136,
0|1:15,7:26:99:0|1:136_G_A:212,0,584:136,
0|0:11,0:13:33:0|1:136_G_A:0,33,484:136, 0|1:24,2:28:4:0|1:136_G_A:4,0,913:136,
0|1:16,9:26:99:0|1:136_G_A:330,0,619:136,
0|1:16,11:30:99:0|1:136_G_A:410,0,628:136,
0|0:26,2:34:5:0|1:136_G_A:0,5,1066:136,
0|1:12,5:18:99:0|1:136_G_A:155,0,478:136,
0|1:25,4:33:41:0|1:136_G_A:41,0,1038:136,
0|1:9,3:20:91:0|1:136_G_A:91,0,369:136, 0|0:7,0:11:21:0|1:136_G_A:0,21,315:136,
0|0:25,1:27:33:0|1:136_G_A:0,33,1057:136,
0|1:11,8:22:99:0|1:136_G_A:277,0,413:136,
0|1:13,3:16:87:0|1:136_G_A:87,0,479:136,
0|0:22,1:25:24:0|1:136_G_A:0,24,934:136, 0|0:35,0:35:99:...:0,105,966,
0|1:17,16:34:99:0|1:136_G_A:540,0,655:136,
0|1:10,2:13:54:0|1:136_G_A:54,0,403:136,
0|1:11,2:14:51:0|1:136_G_A:51,0,445:136}

```

```

In[91]:= For[i = 1; highEXHET = {}, i ≤ Length[fullgenomeDIP], i++,
  temp = StringSplit[fullgenomeDIP[[i, 8]], {";" }];
  temp2 = ToExpression[StringSplit[temp[[6]], {"="}]] [[2]];
  highEXHET = Append[highEXHET, {fullgenomeDIP[[i, 1]], fullgenomeDIP[[i, 2]], temp2}]
]

```

```
In[92]:= highEXHET = highEXHET /. {"ref|NC_001133|" → "chrI", "ref|NC_001134|" → "chrII",
  "ref|NC_001135|" → "chrIII", "ref|NC_001136|" → "chrIV",
  "ref|NC_001137|" → "chrV", "ref|NC_001138|" → "chrVI",
  "ref|NC_001139|" → "chrVII",
  "ref|NC_001140|" → "chrVIII", "ref|NC_001141|" → "chrVIX",
  "ref|NC_001142|" → "chrX",
  "ref|NC_001143|" → "chrXI", "ref|NC_001144|" → "chrXII",
  "ref|NC_001145|" → "chrXIII", "ref|NC_001146|" → "chrXIV", "ref|NC_001147|" →
  "chrXV", "ref|NC_001148|" → "chrXVI", "ref|NC_001224|" → "chrmt"};
```

```
In[93]:= highEXHET = Select[highEXHET, #[[3]] ≥ 50 &];
```

Looking at the ExcessHet calls from the diploid lines above 50:

```
In[94]:= {Min[highEXHET[[All, 3]], Max[highEXHET[[All, 3]]]}
Out[94]=
{50.0838, 171.074}
```

The only positions in common are:

```
In[95]:= temppos = Intersection[highEXHET[[All, 2]], fullgenomeSNPEFF[[All, 3]]
Out[95]=
{25178, 889748}
```

But this isn't on the same chromosome (position 25178) or is a site with more than one alternate allele and so filtered out (position 889748):

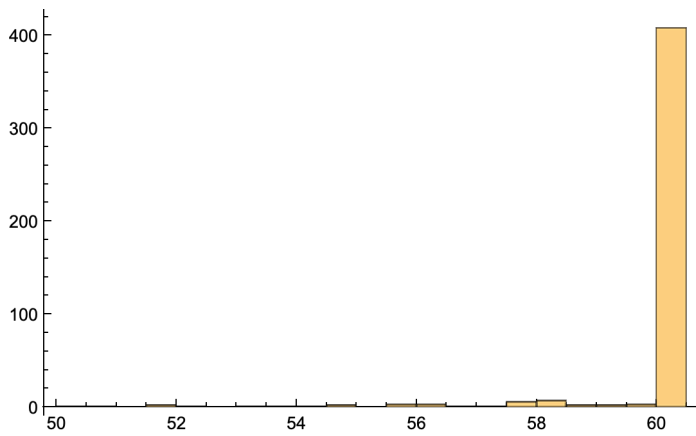
```
In[96]:= Select[highEXHET, MemberQ[temppos, #[[2]]] &]
Out[96]=
{{chrI, 25178, 159.842}, {chrXV, 889748, 54.1748}}

In[97]:= Select[fullgenomeSNPEFF[[All, 1 ;; 3]], MemberQ[temppos, #[[3]]] &]
Out[97]=
{{chrXIII, 13, 25178}, {chrXV, 15, 889748}}
```

## Checking MQ

The mapping quality is almost always 60:

```
In[98]:= Histogram[fullgenomeSNPEFF[All, 133]]  
Out[98]=
```



Many of the ones with lower mapping quality are the ones with missing genotype calls (filtered out below):

```
In[99]:= Select[fullgenomeSNPEFF[All, {1, 3, 8, 133}], #[4] < 60 &] // MatrixForm
```

```
Out[99]//MatrixForm=
```

chrI	25 487	FL09	58.61
chrI	25 489	FL09	57.62
chrI	27 090	FL09	52.4
chrI	204 218	FL01	56.97
chrI	206 360	FL01	54.5
chrI	206 363	FL01	54.41
chrI	206 375	FL01	53.78
chrV	22 913	HXT13	51.91
chrVIII	93 335	YHL008C	58.24
chrVIII	93 350	YHL008C	58.24
chrVIII	93 359	YHL008C	58.13
chrVIII	93 361	YHL008C	58.11
chrVIII	93 370	YHL008C	58.16
chrVIII	93 375	YHL008C	58.16
chrVIII	93 391	YHL008C	58.28
chrVIII	93 577	YHL008C	51.63
chrVIII	93 608	YHL008C	54.81
chrVIII	93 624	YHL008C	56.2
chrVIII	93 898	YHL008C	50.58
chrX	715 087	DAN4	58.93
chrX	715 108	DAN4	57.88
chrX	715 114	DAN4	57.14
chrX	715 117	DAN4	59.04
chrX	715 141	DAN4	55.81
chrX	715 149	DAN4	59.1
chrXI	144 880	PIR3	55.87
chrXI	144 883	PIR3	56.03
chrXI	578 481	YKR073C	53.08
chrXI	578 485	YKR073C	50.17
chrXI	613 636	SRP40	59.9
chrXII	5683	YLL066W-B	57.77
chrXII	650 822	HAP1	59.76
chrXIII	588 588	MSS11	59.85
chrXIII	609 388	DDR48	57.68
chrXIII	908 159	YMR317W	57.88
chrXIII	908 168	YMR317W	57.87
chrXIII	908 215	YMR317W	56.28
chrXIII	908 221	YMR317W	55.95

```
In[100]:=
```

```
Union[%[[All, 3]]]
```

```
Out[100]=
```

```
{DAN4, DDR48, FL01, FL09, HAP1, HXT13, MSS11,
  PIR3, SRP40, YHL008C, YKR073C, YLL066W-B, YMR317W}
```

Mean mapping quality of all genes:

```
In[101]:= Mean[fullgenomeSNPEFF[All, 133]]
```

```
Out[101]= 59.7012
```

Mean mapping quality of the genes dropped below with  $\geq 5$  “.” calls:

```
In[102]:= {"BSC1", "DAN4", "FL01", "FL09", "HAP1", "MSS11", "PIR3", "YHL008C", "YKR073C"};
Select[fullgenomeSNPEFF, MemberQ[%, #[[8]] &];
Mean[%[[All, 133]]]
```

```
Out[104]= 56.6091
```

Of the genes filtered out because of having 5 or more uncalled genotypes, all but BSC1 have  $MQ < 60$

Mean mapping quality of the genes not dropped, but having some “.” calls:

```
In[105]:= {"SRP40", "YGR130C", "YLL066W-B", "YLR296W", "YMR317W"};
Select[fullgenomeSNPEFF, MemberQ[%, #[[8]] &];
Mean[%[[All, 133]]]
```

```
Out[107]= 58.8042
```

Of the genes not filtered out (but of concern), three have  $MQ < 60$  {SRP40,YLL066W-B,YMR317W}.

## Dropping genes with too many uncalled or low depth (<5) genotypes

### Processing and dropping genes with too many poor quality genotypes

Sites that were hard to call (low depth or no genotype call) can indicate duplicated genes and alignment problems. Here we identify these:

```
In[108]:= droppos = -1 + Position[header, "OLY077_S101"][[1, 1]];
(*# columns to be dropped before first sample*)
```

```
In[109]:= topos = Position[header, "ZnBM47_S95"][[1, 1]]; (*# last sample column*)
```

```
In[110]:= genomeSNPEFF = Table[".", {i, 1, Length[fullgenomeSNPEFF]}, {j, 1, topos - droppos}];
```

```
In[111]:= genomeSNPEFF[[1]] // Length
```

```
Out[111]= 110
```

In[112]:=

**fullgenomeSNPEFF[[1]]**

Out[112]=

```
{chrI, 1, 25487, TG, T, 1492.81, GT:AD:DP:GQ:PL, FL09,
HIGH, frameshift_variant, YAL063C, c.2481delC, p.Phe827fs,
T|frameshift_variant|HIGH|FL09|YAL063C|transcript|YAL063C_mRNA|protein_coding|1/
1|c.2481delC|p.Phe827fs|2481/3969|2481/3969|827/1322||,T|upstream_gene
_variant|MODIFIER|YAL063C-A|YAL063C-A|transcript|YAL063C-A_mRNA|
protein_coding||c.-2803delC||||2803|,T|downstream_gene_variant|MODIFIER|
YAL064W|YAL064W|transcript|YAL064W_mRNA|protein_coding||c.*3638delG||||3638|
, 0:12,0:12:99:0,402, 0:20,0:20:99:0,644, 0:18,0:18:99:0,592,
0:24,0:24:99:0,719, 1:0,4:4:99:142,0, 0:15,0:15:99:0,495, 0:12,0:12:99:0,213,
0:24,0:24:99:0,696, 0:7,0:7:99:0,169, 0:16,0:16:99:0,393, 0:14,0:14:99:0,562,
0:18,0:18:99:0,620, 0:14,0:14:99:0,382, 0:21,0:21:99:0,719, 0:14,0:14:99:0,433,
0:16,0:16:99:0,486, 0:17,0:17:99:0,559, 0:9,0:9:99:0,331, 0:3,0:3:99:0,113,
0:25,0:25:99:0,621, 1:0,5:6:99:136,0, 0:19,0:19:99:0,552, 0:20,0:20:99:0,630,
0:20,0:20:99:0,637, 0:9,0:9:99:0,304, 0:18,0:18:99:0,635, 0:11,0:11:99:0,319,
0:12,0:12:99:0,369, 0:17,0:17:99:0,508, 0:19,0:19:99:0,528, 0:27,0:27:99:0,887,
0:19,0:19:99:0,675, 0:22,0:22:99:0,734, 0:18,0:18:99:0,598, 0:27,0:27:99:0,940,
0:18,0:18:99:0,549, 1:0,3:4:99:135,0, 0:15,0:15:99:0,372, 0:8,0:8:99:0,157,
0:16,0:16:99:0,548, 0:12,0:12:99:0,330, 0:25,0:25:99:0,822, 0:1,0:3:45:0,45,
0:15,0:15:99:0,506, 0:15,0:15:99:0,495, 0:15,0:15:99:0,468, 0:12,0:12:99:0,291,
0:14,0:14:99:0,320, 0:8,0:8:99:0,288, 0:25,0:25:99:0,702, 0:14,0:14:99:0,445,
0:13,0:13:99:0,355, 1:0,3:3:99:130,0, 1:0,5:5:99:225,0, 0:5,0:5:99:0,155,
0:18,0:18:99:0,521, 0:9,0:9:99:0,259, 0:1,0:1:32:0,32, 0:19,0:19:99:0,695,
0:14,0:14:99:0,491, 1:0,3:3:99:123,0, 0:14,0:14:99:0,471, 0:17,0:17:99:0,532,
0:23,0:23:99:0,643, 0:11,0:11:99:0,319, 0:22,0:22:99:0,723, 0:28,0:28:99:0,851,
0:39,0:39:99:0,1169, 0:24,0:24:99:0,593, 0:27,0:27:99:0,814, 0:13,0:13:99:0,450,
0:6,0:6:99:0,229, 0:14,0:14:99:0,245, 0:12,0:12:99:0,441, 0:18,0:18:99:0,602,
0:22,0:22:99:0,784, 0:14,0:14:99:0,405, 0:22,0:22:99:0,743, 0:34,0:34:99:0,1106,
0:15,0:15:99:0,495, 0:18,0:18:99:0,450, 0:12,0:12:99:0,398, 0:15,0:15:99:0,495,
0:22,0:22:99:0,653, 0:26,0:26:99:0,902, 0:26,0:26:99:0,969, 1:0,11:14:99:377,0,
0:25,0:25:99:0,682, 0:16,0:16:99:0,430, 1:0,5:7:99:106,0, 0:17,0:17:99:0,495,
0:11,0:11:99:0,385, 0:33,0:33:99:0,936, 0:19,0:19:99:0,617, 0:12,0:12:99:0,307,
0:7,0:7:99:0,263, 0:20,0:20:99:0,608, 0:35,0:35:99:0,1113, 0:25,0:25:99:0,876,
0:17,0:17:99:0,524, 0:12,0:12:99:0,397, 0:13,0:13:99:0,409, 0:16,0:16:99:0,444,
0:16,0:16:99:0,517, 0:13,0:13:99:0,360, 0:15,0:15:99:0,385, 0:35,0:35:99:0,1125,
0:18,0:18:99:0,623, 1:1,5:7:99:217,0, 0:12,0:12:99:0,396, 9, 0.082, 110, 1.47,
1799, 0., 9, 0.082, 58.61, 0., 33.17, 0.792, 0.846, (FL09|YAL063C|1|1.00)}
```

```
In[113]:=
For[i = 1, i ≤ Length[fullgenomeSNPEFF], i++,
  For[j = 1 + droppos, j ≤ topos, j++,
    temp = StringSplit[fullgenomeSNPEFF[[i, j]], {":"}];
    genomeSNPEFF[[i, j - droppos]] = temp[[1]];
  ]
]
```

```
In[114]:=
genomeSNPEFF // Length
```

```
Out[114]=
446
```

```
In[115]:=
Tally[Select[genomeSNPEFF[[1]], # ≠ "." &]]
```

```
Out[115]=
{{0, 101}, {1, 9}}
```

All mutant sites and the tally of mutations in them:

```
In[116]:=
summarytable = Table[{fullgenomeSNPEFF[[i, 1]],
  fullgenomeSNPEFF[[i, 3]], fullgenomeSNPEFF[[i, 8]], fullgenomeSNPEFF[[i, 9]],
  Sort[Tally[genomeSNPEFF[[i]]]}], {i, 1, Length[genomeSNPEFF]}};
```

The set of sites where the number of "." calls was ≥5:

```
In[117]:=
dropthese = Select[summarytable, (#[[5, 1, 1]] == ".") && (#[[5, 1, 2]] ≥ 5) &];
dropthese // MatrixForm
```

```
Out[118]//MatrixForm=
{chrI, 27090, FL09, LOW, {{., 83}, {0, 2}, {1, 25}}},
{chrI, 204218, FL01, MODERATE, {{., 71}, {0, 19}, {1, 20}}},
{chrI, 206360, FL01, LOW, {{., 80}, {0, 16}, {1, 14}}},
{chrI, 206363, FL01, LOW, {{., 70}, {0, 26}, {1, 14}}},
{chrI, 206375, FL01, LOW, {{., 95}, {0, 1}, {1, 14}}},
{chrIV, 384924, BSC1, HIGH, {{., 99}, {0, 7}, {1, 4}}},
{chrVIII, 93335, YHL008C, LOW, {{., 41}, {0, 1}, {1, 68}}},
{chrVIII, 93350, YHL008C, LOW, {{., 39}, {0, 3}, {1, 68}}},
{chrVIII, 93359, YHL008C, MODERATE, {{., 29}, {0, 15}, {1, 66}}},
{chrVIII, 93375, YHL008C, HIGH, {{., 30}, {0, 44}, {1, 36}}},
{chrVIII, 93391, YHL008C, MODERATE, {{., 65}, {0, 9}, {1, 36}}},
{chrX, 715087, DAN4, LOW, {{., 6}, {0, 97}, {1, 7}}},
{chrX, 715108, DAN4, LOW, {{., 65}, {0, 2}, {1, 43}}},
{chrX, 715114, DAN4, LOW, {{., 68}, {0, 5}, {1, 37}}},
{chrX, 715141, DAN4, LOW, {{., 61}, {0, 27}, {1, 22}}},
{chrXI, 144880, PIR3, LOW, {{., 76}, {0, 5}, {1, 29}}},
{chrXI, 144883, PIR3, LOW, {{., 52}, {0, 29}, {1, 29}}},
{chrXI, 578481, YKR073C, HIGH, {{., 32}, {0, 77}, {1, 1}}},
{chrXII, 650822, HAP1, HIGH, {{., 90}, {0, 14}, {1, 6}}},
{chrXII, 650830, HAP1, LOW, {{., 98}, {0, 1}, {1, 11}}},
{chrXIII, 588588, MSS11, MODERATE, {{., 8}, {0, 25}, {1, 77}}}
```

```
In[119]:=
dropme = Union[droptheses[All, 3]]
% // Length

Out[119]=
{BSC1, DAN4, FLO1, FLO9, HAP1, MSS11, PIR3, YHL008C, YKR073C}

Out[120]=
9
```

Depth of coverage for these genes is much higher on average, with both the high outliers (FLO1) and the two low outliers (BSC1 and HAP1):

```
In[121]:=
Select[fullgenomeSNPEFF, MemberQ[dropme, #][8]] &][All, {8, 129}]
Mean[%][All, 2]] // N

Out[121]=
{{FLO9, 1799}, {FLO9, 1584}, {FLO9, 2213}, {FLO1, 348},
 {FLO1, 15599}, {FLO1, 15734}, {FLO1, 17792}, {BSC1, 91}, {YHL008C, 2060},
 {YHL008C, 2102}, {YHL008C, 2001}, {YHL008C, 1983}, {YHL008C, 1921},
 {YHL008C, 1941}, {YHL008C, 2062}, {YHL008C, 1441}, {YHL008C, 1946},
 {YHL008C, 1810}, {YHL008C, 2247}, {DAN4, 905}, {DAN4, 1522}, {DAN4, 1559},
 {DAN4, 1583}, {DAN4, 1310}, {DAN4, 628}, {PIR3, 2648}, {PIR3, 2800},
 {YKR073C, 1609}, {YKR073C, 1536}, {HAP1, 509}, {HAP1, 84}, {MSS11, 658}}

Out[122]=
2938.28
```

Mapping quality is also poorer on average (except for BSC1):

```
In[123]:=
Select[fullgenomeSNPEFF, MemberQ[dropme, #][8]] &][All, {8, 133}]
Mean[%][All, 2]] // N

Out[123]=
{{FLO9, 58.61}, {FLO9, 57.62}, {FLO9, 52.4}, {FLO1, 56.97}, {FLO1, 54.5},
 {FLO1, 54.41}, {FLO1, 53.78}, {BSC1, 60.}, {YHL008C, 58.24}, {YHL008C, 58.24},
 {YHL008C, 58.13}, {YHL008C, 58.11}, {YHL008C, 58.16}, {YHL008C, 58.16},
 {YHL008C, 58.28}, {YHL008C, 51.63}, {YHL008C, 54.81}, {YHL008C, 56.2},
 {YHL008C, 50.58}, {DAN4, 58.93}, {DAN4, 57.88}, {DAN4, 57.14},
 {DAN4, 59.04}, {DAN4, 55.81}, {DAN4, 59.1}, {PIR3, 55.87}, {PIR3, 56.03},
 {YKR073C, 53.08}, {YKR073C, 50.17}, {HAP1, 59.76}, {HAP1, 60.}, {MSS11, 59.85}}

Out[124]=
56.6091
```

Dropping all sites (32) in the nine genes with  $\geq 5$  “.” calls:



```
In[125]:=
Length[fullgenomeSNPEFF];
fullgenomeSNPEFF = Select[fullgenomeSNPEFF, MemberQ[dropme, #[[8]] == False &];
%% - Length[fullgenomeSNPEFF]
```

```
Out[127]=
32
```

Considering the others with uncalled genotypes, first recalculating the summary table:

```
In[128]:=
genomeSNPEFF = Table[".", {i, 1, Length[fullgenomeSNPEFF]}, {j, 1, topos - droppos}];
For[i = 1, i ≤ Length[fullgenomeSNPEFF], i++,
  For[j = 1 + droppos, j ≤ topos, j++,
    temp = StringSplit[fullgenomeSNPEFF[[i, j]], {":"}];
    genomeSNPEFF[[i, j - droppos]] = temp[[1]];
  ]
]
summarytable = Table[{fullgenomeSNPEFF[[i, 1]],
  fullgenomeSNPEFF[[i, 3]], fullgenomeSNPEFF[[i, 8]], fullgenomeSNPEFF[[i, 9]],
  Sort[Tally[genomeSNPEFF[[i]]]}], {i, 1, Length[genomeSNPEFF]}}];
```

```
In[130]:=
consider =
  Select[summarytable, (#[[5, 1, 1]] == ".") && (#[[5, 1, 2]] < 5) && (#[[5, 1, 2]] ≥ 1) &];
consider // MatrixForm
```

```
Out[131]//MatrixForm=
( chrVII  753 296  YGR130C  MODERATE  {{., 1}, {0, 23}, {1, 86}}
  chrXI   613 636  SRP40    MODERATE  {{., 1}, {0, 1}, {1, 108}}
  chrXII  5683   YLL066W-B  HIGH     {{., 3}, {0, 99}, {1, 8}}
  chrXII  723 168  YLR296W  HIGH     {{., 2}, {0, 104}, {1, 4}}
  chrXIII 908 215  YMR317W  LOW      {{., 1}, {0, 17}, {1, 92}}
  chrXIII 908 221  YMR317W  LOW      {{., 2}, {0, 9}, {1, 99}} )
```

```
In[132]:=
considergenes = Union[consider[[All, 3]]
% // Length
```

```
Out[132]=
{SRP40, YGR130C, YLL066W-B, YLR296W, YMR317W}
```

```
Out[133]=
5
```

Depth of coverage for these genes is much higher on average, with both the high outliers (FLO1) and the two low outliers (BSC1 and HAP1):

```
In[134]:=
Select[fullgenomeSNPEFF, MemberQ[considergenes, #[[8]] &] [[All, {8, 129}]]
Mean[%[[All, 2]]] // N
```

```
Out[134]=
{{YGR130C, 2020}, {YGR130C, 2020}, {YGR130C, 1799}, {YGR130C, 1809},
{SRP40, 1173}, {YLL066W-B, 607}, {YLR296W, 974}, {YLR296W, 977},
{YMR317W, 1959}, {YMR317W, 1960}, {YMR317W, 1836}, {YMR317W, 1789}}
```

```
Out[135]=
1576.92
```

Mapping quality is also poorer on average:

```
In[136]:=
Select[fullgenomeSNPEFF, MemberQ[considergenes, #[[8]] &] [[All, {8, 133}]]
Mean[%[[All, 2]]] // N
```

```
Out[136]=
{{YGR130C, 60.}, {YGR130C, 60.}, {YGR130C, 60.}, {YGR130C, 60.},
{SRP40, 59.9}, {YLL066W-B, 57.77}, {YLR296W, 60.}, {YLR296W, 60.},
{YMR317W, 57.88}, {YMR317W, 57.87}, {YMR317W, 56.28}, {YMR317W, 55.95}}
```

```
Out[137]=
58.8042
```

This is in the bottom 2% of MQ:

```
In[138]:=
Quantile[fullgenomeSNPEFF[[All, 133]], 0.019]
```

```
Out[138]=
59.9
```

These genes are kept but will be flagged as:

{SRP40,YLL066W-B,YMR317W} have MQ<60

{YGR130C,YMR317W} have depth ~ twice average depth (~1000)

Genes with suggestions of excessive SNP mutations include the above:

```
In[139]:=
consider = Select[summarytable, (#[[5, 1, 2]] ≤ 105) && (#[[5, 2, 2]] ≤ 105) &];
consider // MatrixForm
```

```
Out[140]//MatrixForm=
(
chrIV 815 428 NGG1 MODERATE {{0, 100}, {1, 10}}
chrVII 753 296 YGR130C MODERATE {{., 1}, {0, 23}, {1, 86}}
chrVII 869 872 TFG1 MODERATE {{0, 104}, {1, 6}}
chrXI 613 636 SRP40 MODERATE {{., 1}, {0, 1}, {1, 108}}
chrXII 5683 YLL066W-B HIGH {{., 3}, {0, 99}, {1, 8}}
chrXII 723 168 YLR296W HIGH {{., 2}, {0, 104}, {1, 4}}
chrXIII 908 159 YMR317W HIGH {{0, 8}, {1, 102}}
chrXIII 908 168 YMR317W HIGH {{0, 8}, {1, 102}}
chrXIII 908 215 YMR317W LOW {{., 1}, {0, 17}, {1, 92}}
chrXIII 908 221 YMR317W LOW {{., 2}, {0, 9}, {1, 99}}
)
```

In[141]:=

```
considergenes = Union[consider[All, 3]]
% // Length
```

Out[141]=

```
{NGG1, SRP40, TFG1, YGR130C, YLL066W-B, YLR296W, YMR317W}
```

Out[142]=

```
7
```

Depth of coverage for these genes is much higher on average:

In[143]:=

```
Select[fullgenomeSNPEFF, MemberQ[considergenes, #[[8]] &] [All, {8, 129}]]
Mean[%[All, 2]] // N
```

Out[143]=

```
{{NGG1, 642}, {YGR130C, 2020}, {YGR130C, 2020}, {YGR130C, 1799}, {YGR130C, 1809},
 {TFG1, 798}, {SRP40, 1173}, {YLL066W-B, 607}, {YLR296W, 974}, {YLR296W, 977},
 {YMR317W, 1959}, {YMR317W, 1960}, {YMR317W, 1836}, {YMR317W, 1789}}
```

Out[144]=

```
1454.5
```

Mapping quality is also poorer on average:

In[145]:=

```
Select[fullgenomeSNPEFF, MemberQ[considergenes, #[[8]] &] [All, {8, 133}]]
Mean[%[All, 2]] // N
```

Out[145]=

```
{{NGG1, 60.}, {YGR130C, 60.}, {YGR130C, 60.}, {YGR130C, 60.}, {YGR130C, 60.},
 {TFG1, 60.}, {SRP40, 59.9}, {YLL066W-B, 57.77}, {YLR296W, 60.}, {YLR296W, 60.},
 {YMR317W, 57.88}, {YMR317W, 57.87}, {YMR317W, 56.28}, {YMR317W, 55.95}}
```

Out[146]=

```
58.975
```

## Revised gene list

In[147]:=

```
genelist = Sort[Union[fullgenomeSNPEFF[All, 8]]]
Length[%]
```

Out[147]=

```
{ABP1, ACB1, ACC1, ADE6, ADR1, AFT1, AGP1, AHK1, ALD5, ALY2, APC2, ARO3, ASN1, ATG11,
ATG2, ATG39, BDS1, BIR1, BLM10, BNA6, BNI1, BNI4, BRR2, BSD2, BUL1, BUL2, CAJ1,
CCC2, CCR4, CCW12, CDC25, CIC1, CLB3, CLN3, CNE1, COG1, COG3, COI1, COQ1, CPA1,
CSM3, CUE3, CWC22, CWH41, CYK3, DAL2, DBF20, DBP10, DDR48, DNF1, DOA4, DOT6,
DSC2, DSE4, DUS4, EBS1, ECM14, ECM22, EFR3, EL03, ERB1, ERG1, ERG27, ERG7, ERG9,
FAS2, FAU1, FCY2, FET4, FIG2, FIG4, FLC2, FMP52, FRE6, FSF1, FYV10, FYV6, FZF1,
GAS4, GAT1, GCD2, GID12, GPB1, GPB2, GPH1, GSC2, HBT1, HEH2, HHF2, HIS4, HMF1,
HO, HOB2, HRT3, HSL1, HSP104, HUL5, HXT13, IDP1, IES3, ILV2, IMA1, INP2, IOC4,
IPI3, IRC20, IRC8, IST2, ISU1, ITC1, KAR3, KGD1, KIN1, KIN82, KRE5, KSP1, KTR3,
LAM1, LAM6, LOS1, LRG1, MAM3, MAS2, MCK1, MCM5, MCT1, MDH2, MDL2, MDM30, MET10,
MET30, MEX67, MHP1, MKT1, MLF3, MLH3, MLS1, MMS4, MNN9, MOT1, MPA43, MRL1,
MRPL36, MSC6, MSS2, MTR4, MYG1, MYO2, NAM8, NAR1, NFT1, NGG1, NIP100, NPL3,
NSR1, NUC1, NUG1, OAF1, OCA4, OCA5, OPI1, OSH2, PBP2, PBS2, PCL5, PDA1, PDR1,
PDR10, PDX1, PET111, PET127, PEX2, PFK26, PHM7, PHO23, PHO81, PHO84, PIB1, PKP1,
PLB2, PMA1, POL3, PPQ1, PRC1, PRI1, PRI2, PRP2, PRP8, PTK2, PYK2, QRI7, RAD16,
RAD17, RAD26, RBK1, RCE1, RCK2, RC01, REC102, RED1, RH01, RIM11, RIM21, RKM3,
RMP1, RNY1, ROG1, RPA135, RPI1, RPL22A, RPL2A, RPL39, RPS15, RPS2, RPT5, RRB1,
RRG7, RRP46, RRP6, RSC1, RSE1, RTC2, SAK1, SAP4, SBE2, SEC8, SET2, SFP1, SHP1,
SIW14, SKN1, SMC2, SMY2, SNF7, SNT2, SPC105, SP077, SPS100, SRP40, SSE1, SSK2,
SSQ1, SSZ1, STE5, STP3, STT3, SUB2, SUC2, SUM1, SWC5, SWS2, SWT1, SYF2, SYG1,
TAF8, TAH11, TA03, TC089, TFB1, TFG1, TIM54, TOM1, TOP1, TOP2, TOS3, TPS3, TRK2,
TRL1, TUS1, UBC1, UBP5, UBR2, UBX7, UGA3, UGA4, UIP5, ULS1, UME6, URA2, URB1,
USA1, UTP21, UTP8, VBA1, VCX1, VHR2, VID22, VPS13, VPS74, VRP1, VTC1, VTC3,
VTC4, VTC5, WAR1, YAP6, YBR242W, YBR292C, YCF1, YCK1, YCT1, YDL199C, YDR003W-A,
YDR157W, YDR541C, YEF1, YGR126W, YGR130C, YGR266W, YHC1, YHC3, YIH1, YIL092W,
YLL066W-B, YLR108C, YLR296W, YML119W, YMR027W, YMR317W, YOR029W, YOR1, YOR296W,
YOR343C, YPK1, YPL113C, YPR078C, YPR089W, YPT6, YRA1, YRB2, ZDS2, ZRT1, ZRT3}
```

Out[148]=

333

Plotting the depth of coverage at that site:

In[149]:=

```
Mean[fullgenomeSNPEFF[All, 129]] // N
```

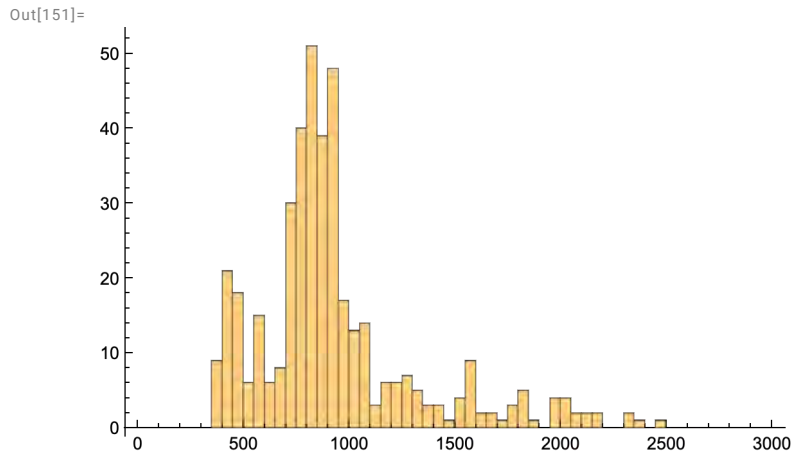
Out[149]=

933.978

```
In[150]:=
Max[fullgenomeSNPEFF[All, 129]]
```

```
Out[150]=
2469
```

```
In[151]:=
Histogram[fullgenomeSNPEFF[All, 129], {50}, PlotRange → {{0, 3000}, Automatic}]
```



## Exporting

For printing, we want a shorter header table:

```
In[152]:=
newheader = Table[StringSplit[header[[i]], "_"][[1], {i, 1, Length[header]}]
```

```
Out[152]=
{CHROM, chr, POS, REF, ALT, QUAL, FORMAT, gene, effect, mut, gene, base, aa,
ANN, OLY077, CdBM23, CdBM25, CdBM26, CdBM29, CdBM30, CdBM32, CdBM36, CdBM37,
CdBM39, CdBM42, CdBM43, CdBM44, CdBM45, CdBM46, CdBM47, CdBM48, CoBM12,
CoBM14, CoBM15, CoBM16, CoBM17, CoBM18, CoBM1, CoBM20, CoBM21, CoBM2,
CoBM3, CoBM4, CoBM5, CoBM6, CoBM7, CoBM8, CuBM10, CuBM11, CuBM12, CuBM13,
CuBM14, CuBM15, CuBM16, CuBM17, CuBM18, CuBM3, CuBM4, CuBM6, CuBM7, CuBM8,
CuBM9, MnBM12, MnBM13, MnBM14, MnBM15, MnBM16, MnBM17, MnBM18, MnBM20,
MnBM21, MnBM23, MnBM24, MnBM25, MnBM27, MnBM28, MnBM29, MnBM31, MnBM32,
MnBM34, MnBM38, MnBM39, MnBM42, MnBM44, NiBM11, NiBM12, NiBM14, NiBM16,
NiBM17, NiBM21, NiBM22, NiBM24, NiBM25, NiBM27, NiBM28, NiBM29, NiBM30,
NiBM4, NiBM6, NiBM8, NiBM9, ZnBM11, ZnBM12, ZnBM15, ZnBM16, ZnBM17, ZnBM19,
ZnBM22, ZnBM23, ZnBM25, ZnBM28, ZnBM29, ZnBM31, ZnBM34, ZnBM37, ZnBM38,
ZnBM39, ZnBM41, ZnBM42, ZnBM43, ZnBM44, ZnBM45, ZnBM46, ZnBM47, AC, AF, AN,
BaseQRankSum, DP, FS, MLEAC, MLEAF, MQ, MQRankSum, QD, ReadPosRankSum, SOR, LOF}
```

First recalculating the summary table:

```
In[153]:=
genomeSNPEFF = Table[-1, {i, 1, Length[fullgenomeSNPEFF]}, {j, 1, topos - droppos}];
For[i = 1, i ≤ Length[fullgenomeSNPEFF], i++,
  For[j = 1 + droppos, j ≤ topos, j++,
    temp = StringSplit[fullgenomeSNPEFF[[i, j]], {":"}];
    temp2 = temp[[1]];
    genomeSNPEFF[[i, j - droppos]] = temp2;
  ]
]
```

The following sites are “1”s in OLY077 and so we swap 1’s for 0’s and call these revertants

```
In[154]:=
Position[genomeSNPEFF, _? (#[[1]] == "1" &) ] [[All, 1]]

Part: Part specification List[[1]] is longer than depth of object. ⓘ
Part: Part specification List[[1]] is longer than depth of object. ⓘ
Part: Part specification 0[[1]] is longer than depth of object. ⓘ
General: Further output of Part::partd will be suppressed during this calculation. ⓘ
```

```
Out[154]:=
{155, 234, 322, 323, 324, 325}
```

Swapping 0<->1 and calling “.” 0 (like OLY077):

```
In[155]:=
For[i = 1, i ≤ Length[%], i++,
  genomeSNPEFF[[%[[i]]] =
    Mod[ToExpression[StringReplace[genomeSNPEFF[[%[[i]]], "." → "1"]] + 1, 2]
]
```

Swapped variants positions:

```
In[156]:=
fullgenomeSNPEFF[[%, {1, 3, 8}]]

Out[156]:=
{{chrVII, 753 296, YGR130C}, {chrXI, 613 636, SRP40},
 {chrXIII, 908 159, YMR317W}, {chrXIII, 908 168, YMR317W},
 {chrXIII, 908 215, YMR317W}, {chrXIII, 908 221, YMR317W}}
```

All remaining “.” are treated as identical to OLY077 (not mutant) and 0/1 treated as numbers (only in genomeSNPEFF, summarytable and fullgenomeSNPEFF remain the same):

```
In[157]:=
genomeSNPEFF = genomeSNPEFF /. "." → "0";
genomeSNPEFF = ToExpression /@ genomeSNPEFF;
```

Number of unique mutations:

```
In[159]:= Length[genomeSNPEFF]
```

```
Out[159]= 414
```

Number of mutational hits:

```
In[160]:= Total[Total[genomeSNPEFF]]
```

```
Out[160]= 523
```

As expected (once revertants were recoded), OLY077 has no mutations

```
In[161]:= Total[genomeSNPEFF[[All, 1]]]
```

```
Out[161]= 0
```

Number of lines per unique mutation:

```
In[162]:= Sort[Tally[Sum[genomeSNPEFF[[All, i]], {i, 1, 110}]]]
```

```
Out[162]= {{1, 384}, {2, 18}, {3, 2}, {4, 2}, {6, 1}, {8, 3}, {9, 1}, {10, 1}, {17, 1}, {23, 1}}
```

Genes with excessive SNP mutations include:

```
In[163]:= toopoly = Position[genomeSNPEFF, _?(Total[#] > 5 &)] [[All, 1]]
```

```
Out[163]= {68, 155, 159, 236, 322, 323, 324, 325}
```

The genotype call for OLY077:

```
In[164]:= fullgenomeSNPEFF[[toopoly, Position[newheader, "OLY077"][[1, 1]]] // MatrixForm
```

```
Out[164]//MatrixForm=
```

$$\begin{pmatrix} 0:3,0:3:99:0,100 \\ 1:0,21:21:99:945,0 \\ 0:8,0:8:99:0,175 \\ 0:13,0:13:99:0,226 \\ 1:0,10:10:99:450,0 \\ 1:0,10:10:99:450,0 \\ 1:0,9:9:99:406,0 \\ 1:0,9:9:99:406,0 \end{pmatrix}$$

In[165]:=

```
consider = summarytable[["toopoly"]];
consider // MatrixForm
```

Out[166]//MatrixForm=

```
( chrIV  815 428    NGG1    MODERATE    {{0, 100}, {1, 10}}
  chrVII 753 296   YGR130C MODERATE {{., 1}, {0, 23}, {1, 86}}
  chrVII 869 872    TFG1    MODERATE    {{0, 104}, {1, 6}}
  chrXII  5683   YLL066W-B  HIGH    {{., 3}, {0, 99}, {1, 8}}
  chrXIII 908 159   YMR317W  HIGH    {{0, 8}, {1, 102}}
  chrXIII 908 168   YMR317W  HIGH    {{0, 8}, {1, 102}}
  chrXIII 908 215   YMR317W  LOW     {{., 1}, {0, 17}, {1, 92}}
  chrXIII 908 221   YMR317W  LOW     {{., 2}, {0, 9}, {1, 99}} )
```

Depth of coverage for these genes is higher on average:

In[167]:=

```
fullgenomeSNPEFF[["toopoly", {8, 129}]]
Mean[%["All", 2]] // N
```

Out[167]=

```
{ {NGG1, 642}, {YGR130C, 1809}, {TFG1, 798}, {YLL066W-B, 607},
  {YMR317W, 1959}, {YMR317W, 1960}, {YMR317W, 1836}, {YMR317W, 1789} }
```

Out[168]=

1425.

Mapping quality is also poorer on average:

In[169]:=

```
fullgenomeSNPEFF[["toopoly", {8, 133}]]
Mean[%["All", 2]] // N
```

Out[169]=

```
{ {NGG1, 60.}, {YGR130C, 60.}, {TFG1, 60.}, {YLL066W-B, 57.77},
  {YMR317W, 57.88}, {YMR317W, 57.87}, {YMR317W, 56.28}, {YMR317W, 55.95} }
```

Out[170]=

58.2188

Ones below 60 are in the bottom 2% of MQ:

In[171]:=

```
Quantile[fullgenomeSNPEFF[["All", 133]], 0.019]
```

Out[171]=

59.9

In[172]:=

```
considergenes = Union[consider[["All", 3]]
% // Length
```

Out[172]=

```
{ NGG1, TFG1, YGR130C, YLL066W-B, YMR317W }
```

Out[173]=

5



In[174]:=

```

toprintmultiple =
  Sort[Table[{fullgenomeSNPEFF[[toopoly[[i]], 8]], fullgenomeSNPEFF[[toopoly[[i]], 11]],
    StringJoin[fullgenomeSNPEFF[[toopoly[[i]], 1]], "."],
    ToString[fullgenomeSNPEFF[[toopoly[[i]], 3]]],
    fullgenomeSNPEFF[[toopoly[[i]], 12]], fullgenomeSNPEFF[[toopoly[[i]], 13]],
    summarytable[[toopoly[[i]], 5]], genomeSNPEFF[[toopoly[[i]]]].
    newheader[[1 + droppos ;; topos]], {i, 1, Length[toopoly]}]]];
MatrixForm[%]

```

Out[175]//MatrixForm=

NGG1	YDR176W	chrIV.815428	c.977G>A	p
TFG1	YGR186W	chrVII.869872	c.2099T>C	p
YGR130C	YGR130C	chrVII.753296	c.543_548delATCGTC	p.Se
YLL066W-B	YLL066W-B	chrXII.5683	c.85_103delCACACCCACACCCACACAC	
YMR317W	YMR317W	chrXIII.908159	c.797_804delCGGCAACG	
YMR317W	YMR317W	chrXIII.908168	c.806_833delCTAGCGTAATTAGTTCAGAAGCTTCATG	
YMR317W	YMR317W	chrXIII.908215	c.852G>A	p
YMR317W	YMR317W	chrXIII.908221	c.858G>A	p

In[176]:=

```

Export[
  "/Users/otto/Documents/Students/AnnaBazzicalupo/MetalAdaptation/Genomics/
  toopolymorphic_8Nov2024.tsv", toprintmultiple];

```

The remaining sites:

In[177]:=

```
rest = Complement[Table[i, {i, 1, Length[fullgenomeSNPEFF]}], toopoly];
```

In[178]:=

```
Length[rest] + Length[toopoly] - Length[fullgenomeSNPEFF]
```

Out[178]=

0

Including NGG1 and TFG1:

In[179]:=

```
fullgenomeSNPEFF[[68, 8]]
```

Out[179]=

NGG1

In[180]:=

```
fullgenomeSNPEFF[[159, 8]]
```

Out[180]=

TFG1

In[181]:=

```
rest = Sort[Join[rest, {68, 159}]]];
```

```
In[182]:=
toprint =
  Table[{fullgenomeSNPEFF[[rest[[i]], 8]], fullgenomeSNPEFF[[rest[[i]], 11]], StringJoin[
    fullgenomeSNPEFF[[rest[[i]], 1]], ".", ToString[fullgenomeSNPEFF[[rest[[i]], 3]]],
    fullgenomeSNPEFF[[rest[[i]], 12]], fullgenomeSNPEFF[[rest[[i]], 13]],
    genomeSNPEFF[[rest[[i]]].newheader[[1 + droppos ;; topos]], {i, 1, Length[rest]]}];
MatrixForm[%[[1 ;; 12]]]
(*The first 12 lines shows the nature of parallel SNPs in different lines*)
```

```
Out[183]//MatrixForm=
( CNE1 YAL058W chrI.37834 c.371C>T p.Thr124Met MnBM14
  CNE1 YAL058W chrI.38041 c.578C>T p.Ser193Leu MnBM14
  GPB2 YAL056W chrI.40593 c.1335A>C p.Leu445Phe CoBM17
  FLC2 YAL053W chrI.48206 c.2308A>G p.Asn770Asp MnBM14
  OAF1 YAL051W chrI.48640 c.77C>T p.Ala26Val MnBM14
  CLN3 YAL040C chrI.66785 c.736T>G p.Leu246Val CoBM3
  CCR4 YAL021C chrI.112637 c.723C>G p.Asp241Glu MnBM42
  CCR4 YAL021C chrI.113278 c.82C>T p.Leu28Leu MnBM42
  SHP1 YBL058W chrII.112395 c.959A>T p.Glu320Val CoBM6
  COQ1 YBR003W chrII.243326 c.518C>A p.Pro173His CuBM15
  RKM3 YBR030W chrII.299270 c.979G>C p.Gly327Arg CoBM4 + NiBM24
  IST2 YBR086C chrII.421076 c.1966G>T p.Ala656Ser NiBM12 )
```

```
In[184]:=
Length[toprint]
```

```
Out[184]=
408
```

For each SNP that occurs multiple times, make a separate row:

```
In[185]:=
For[i = 1; toappend = {}, i ≤ Length[toprint], i++,
  splits = Length[toprint[[i, 6]]];
  If[splits > 1,
    temp = toprint[[i, 6]];
    toprint[[i, 6]] = toprint[[i, 6]][[1]];
    For[j = 2, j ≤ splits, j++,
      toadd = toprint[[i]];
      toadd[[6]] = temp[[j]];
      toappend = Append[toappend, toadd]
    ]
  ]
]
```

Sorting then putting the metal first:

```
In[186]:=
Sort[Join[toprint, toappend]];
mat = Transpose[Join[{Transpose[%[[All, 6]]], Transpose[%[[All, 1 ;; 5]]}]];
MatrixForm[mat]
```

```
Out[188]//MatrixForm=
( CNE1 YAL058W chrI.37834 c.371C>T p.Thr124Met MnBM14
  CNE1 YAL058W chrI.38041 c.578C>T p.Ser193Leu MnBM14
  GPB2 YAL056W chrI.40593 c.1335A>C p.Leu445Phe CoBM17
  FLC2 YAL053W chrI.48206 c.2308A>G p.Asn770Asp MnBM14
  OAF1 YAL051W chrI.48640 c.77C>T p.Ala26Val MnBM14
  CLN3 YAL040C chrI.66785 c.736T>G p.Leu246Val CoBM3
  CCR4 YAL021C chrI.112637 c.723C>G p.Asp241Glu MnBM42
  CCR4 YAL021C chrI.113278 c.82C>T p.Leu28Leu MnBM42
  SHP1 YBL058W chrII.112395 c.959A>T p.Glu320Val CoBM6
  COQ1 YBR003W chrII.243326 c.518C>A p.Pro173His CuBM15
  RKM3 YBR030W chrII.299270 c.979G>C p.Gly327Arg CoBM4 + NiBM24
  IST2 YBR086C chrII.421076 c.1966G>T p.Ala656Ser NiBM12 )
```

CuBM18	ABP1	YCR088W	chrIII.265691	c.624A>C
MnBM42	ACB1	YGR037C	chrVII.559830	c.165G>A
ZnBM12	ACC1	YNR016C	chrXIV.660428	c.947G>T
ZnBM15	ACC1	YNR016C	chrXIV.660428	c.947G>T
ZnBM23	ADE6	YGR061C	chrVII.613265	c.2701G>C
MnBM23	ADR1	YDR216W	chrIV.896208	c.1174C>T
CoBM17	AFT1	YGL071W	chrVII.372520	c.509C>T
MnBM31	AGP1	YCL025C	chrIII.76154	c.1765delA
MnBM31	AGP1	YCL025C	chrIII.76159	c.1761G>T
CdBM25	AHK1	YDL073W	chrIV.329143	c.2531G>A
MnBM18	ALD5	YER073W	chrV.304100	c.71C>A
CoBM16	ALY2	YJL084C	chrX.277922	c.80delT
CoBM2	APC2	YLR127C	chrXII.397423	c.897G>A
MnBM23	ARO3	YDR035W	chrIV.522083	c.268G>A
CoBM18	ASN1	YPR145W	chrXVI.822877	c.258A>C
MnBM42	ATG11	YPR049C	chrXVI.662014	c.2660G>T
CuBM6	ATG2	YNL242W	chrXIV.195289	c.3966A>G
CoBM5	ATG39	YLR312C	chrXII.757873	c.961T>C
MnBM42	BDS1	YOL164W	chrXV.7199	c.1025C>T
MnBM18	BIR1	YJR089W	chrX.588774	c.1057C>T
CuBM7	BLM10	YFL007W	chrVI.127204	c.3726C>T
CdBM44	BNA6	YFR047C	chrVI.245165	c.1delA
CoBM2	BNI1	YNL271C	chrXIV.132973	c.2411C>G
MnBM39	BNI4	YNL233W	chrXIV.214433	c.2512A>T
MnBM42	BRR2	YER172C	chrV.533465	c.2557T>A
NiBM24	BSD2	YBR290W	chrII.783212	c.622C>T
NiBM11	BSD2	YBR290W	chrII.783400	c.810G>T
ZnBM11	BSD2	YBR290W	chrII.783400	c.810G>T
CuBM14	BUL1	YMR275C	chrXIII.817667	c.915G>T
CoBM7	BUL2	YML111W	chrXIII.48465	c.1524T>A
MnBM42	CAJ1	YER048C	chrV.247483	c.675G>A
CoBM3	CCC2	YDR270W	chrIV.1005804	c.130G>T
MnBM42	CCR4	YAL021C	chrI.112637	c.723C>G
MnBM42	CCR4	YAL021C	chrI.113278	c.82C>T
MnBM31	CCW12	YLR110C	chrXII.369713	c.386C>A
MnBM21	CDC25	YLR310C	chrXII.752946	c.4047delA
MnBM25	CDC25	YLR310C	chrXII.753045	c.3949G>T
MnBM18	CDC25	YLR310C	chrXII.753381	c.3589_3612delGTCAACATTATGAGAACATTTTTG
MnBM23	CDC25	YLR310C	chrXII.755637	c.1357T>A
MnBM23	CDC25	YLR310C	chrXII.755641	c.1353T>A
MnBM24	CDC25	YLR310C	chrXII.755784	c.1210A>T
MnBM24	CDC25	YLR310C	chrXII.755785	c.1209T>A
MnBM24	CDC25	YLR310C	chrXII.755790	c.1203delT
MnBM27	CDC25	YLR310C	chrXII.755841	c.1152dupA
MnBM20	CDC25	YLR310C	chrXII.755855	c.1139T>A
MnBM20	CDC25	YLR310C	chrXII.755857	c.1136delG
MnBM15	CDC25	YLR310C	chrXII.755928	c.1065delG
MnBM32	CDC25	YLR310C	chrXII.756549	c.444delG
MnBM14	CIC1	YHR052W	chrVIII.211267	c.420A>G
MnBM14	CLB3	YDL155W	chrIV.178021	c.1249G>A
CoBM3	CLN3	YAL040C	chrI.66785	c.736T>G
MnBM14	CNE1	YAL058W	chrI.37834	c.371C>T
MnRM14	CNF1	YAL058W	chrI.38041	c.578C>T

MnBM17	COG1	YGL223C	chrVII.80104	c.262A>T
MnBM38	COG1	YGL223C	chrVII.80104	c.262A>T
MnBM42	COG3	YER157W	chrV.485939	c.1152G>T
MnBM27	COI1	YDR381C-A	chrIV.1238427	c.230G>T
NiBM6	COI1	YDR381C-A	chrIV.1238427	c.230G>T
CuBM15	COQ1	YBR003W	chrII.243326	c.518C>A
MnBM42	CPA1	YOR303W	chrXV.882919	c.21A>G
CdBM30	CSM3	YMR048W	chrXIII.367082	c.102T>C
MnBM42	CUE3	YGL110C	chrVII.302721	c.691A>T
MnBM42	CWC22	YGR278W	chrVII.1047684	c.954G>A
MnBM42	CWH41	YGL027C	chrVII.444280	c.1864G>C
CdBM23	CYK3	YDL117W	chrIV.249010	c.437delA
CdBM39	CYK3	YDL117W	chrIV.249010	c.437delA
MnBM42	DAL2	YIR029W	chrIX.411668	c.862T>A
CdBM30	DBF20	YPR111W	chrXVI.747862	c.567delA
ZnBM16	DBP10	YDL031W	chrIV.396323	c.2107A>T
CdBM42	DDR48	YMR173W	chrXIII.609388	c.700A>G
CuBM6	DNF1	YER166W	chrV.513891	c.1148G>C
CdBM30	DNF1	YER166W	chrV.516594	c.3860dupT
ZnBM19	DOA4	YDR069C	chrIV.587104	c.616C>T
MnBM42	DOT6	YER088C	chrV.334086	c.1103C>A
MnBM42	DSC2	YOL073C	chrXV.194233	c.568T>C
MnBM12	DSE4	YNR067C	chrXIV.757064	c.2036G>A
CoBM6	DUS4	YLR405W	chrXII.930419	c.631C>T
CoBM8	EBS1	YDR206W	chrIV.864180	c.2127A>T
ZnBM16	ECM14	YHR132C	chrVIII.369079	c.716G>C
MnBM42	ECM22	YLR228C	chrXII.600763	c.1701C>T
CdBM32	EFR3	YMR212C	chrXIII.692578	c.465delT
ZnBM28	EL03	YLR372W	chrXII.868274	c.921C>A
CdBM30	ERB1	YMR049C	chrXIII.369659	c.859C>A
CoBM4	ERG1	YGR175C	chrVII.848366	c.58G>T
MnBM12	ERG27	YLR100W	chrXII.341936	c.127C>A
MnBM14	ERG7	YHR072W	chrVIII.240532	c.1435C>T
MnBM17	ERG9	YHR190W	chrVIII.484871	c.27G>A
MnBM42	FAS2	YPL231W	chrXVI.110829	c.2178T>C
MnBM42	FAU1	YER183C	chrV.553782	c.188T>G
NiBM30	FCY2	YER056C	chrV.266649	c.1465C>T
CdBM32	FET4	YMR319C	chrXIII.912911	c.1628G>C
CdBM42	FET4	YMR319C	chrXIII.914235	c.303delT
MnBM14	FIG2	YCR089W	chrIII.270029	c.2596G>A
CuBM14	FIG4	YNL325C	chrXIV.29337	c.2042G>A
MnBM14	FLC2	YAL053W	chrI.48206	c.2308A>G
MnBM42	FMP52	YER004W	chrV.159636	c.57C>T
MnBM38	FRE6	YLL051C	chrXII.37938	c.1534A>G
CoBM15	FSF1	YOR271C	chrXV.831557	c.486T>C
MnBM13	FYV10	YIL097W	chrIX.181615	c.1189C>T
CoBM3	FYV10	YIL097W	chrIX.181770	c.1344A>C
MnBM14	FYV6	YNL133C	chrXIV.374578	c.115C>T
MnBM29	FZF1	YGL254W	chrVII.22857	c.554T>A
MnBM42	GAS4	YOL132W	chrXV.72169	c.870A>G
MnBM32	GAT1	YFL021W	chrVI.96312	c.347C>T
CoBM17	GCD2	YGR083C	chrVII.644958	c.1858A>T
MnBM42	GID12	YDL176W	chrIV.143605	c.1509T>G

MnBM38	GPB1	YOR371C	chrXV.1033961	c.222A>G
CoBM17	GPB2	YAL056W	chrI.40593	c.1335A>C
MnBM42	GPH1	YPR160W	chrXVI.862883	c.1578C>A
MnBM42	GSC2	YGR032W	chrVII.550683	c.2420G>T
MnBM29	HBT1	YDL223C	chrIV.58214	c.2192C>A
MnBM42	HEH2	YDR458C	chrIV.1381715	c.332A>G
CoBM1	HHF2	YNL030W	chrXIV.577027	c.302_*4delTCGGTGGTTAAACAA
ZnBM38	HHF2	YNL030W	chrXIV.577027	c.302_*4delTCGGTGGTTAAACAA
ZnBM31	HIS4	YCL030C	chrIII.66139	c.2195C>T
CdBM26	HMF1	YER057C	chrV.270774	c.353A>G
CdBM32	HO	YDL227C	chrIV.46589	c.1442delA
MnBM14	HOB2	YPR117W	chrXVI.765419	c.5395A>T
MnBM42	HRT3	YLR097C	chrXII.337183	c.83G>T
CoBM2	HSL1	YKL101W	chrXI.249736	c.817A>C
ZnBM44	HSP104	YLL026W	chrXII.90370	c.1748A>T
MnBM42	HUL5	YGL141W	chrVII.239990	c.1638G>T
CdBM45	HUL5	YGL141W	chrVII.240693	c.2341G>A
CdBM46	HUL5	YGL141W	chrVII.240693	c.2341G>A
CdBM47	HUL5	YGL141W	chrVII.240693	c.2341G>A
CdBM30	HUL5	YGL141W	chrVII.240739	c.2387G>A
MnBM32	HXT13	YEL069C	chrV.22913	c.319C>T
NiBM6	IDP1	YDL066W	chrIV.334907	c.73C>A
MnBM42	IES3	YLR052W	chrXII.247694	c.494T>A
MnBM32	ILV2	YMR108W	chrXIII.484091	c.8G>A
MnBM42	IMA1	YGR287C	chrVII.1068655	c.337T>C
CdBM44	INP2	YMR163C	chrXIII.585173	c.1215delA
CoBM15	IOC4	YMR044W	chrXIII.356311	c.928C>A
MnBM42	IPI3	YNL182C	chrXIV.297316	c.312C>T
MnBM42	IRC20	YLR247C	chrXII.633065	c.290C>T
MnBM42	IRC8	YJL051W	chrX.340621	c.835G>T
NiBM12	IST2	YBR086C	chrII.421076	c.1966G>T
MnBM32	ISU1	YPL135W	chrXVI.297897	c.345G>A
MnBM42	ITC1	YGL133W	chrVII.259225	c.1519A>T
CoBM21	KAR3	YPR141C	chrXVI.815942	c.1982A>T
MnBM42	KGD1	YIL125W	chrIX.124369	c.1681T>G
CdBM29	KIN1	YDR122W	chrIV.694840	c.157_159delCAG
CdBM30	KIN82	YCR091W	chrIII.275091	c.694delC
MnBM38	KRE5	YOR336W	chrXV.952618	c.2846C>G
CoBM12	KSP1	YHR082C	chrVIII.268511	c.3038G>C
CuBM9	KSP1	YHR082C	chrVIII.271417	c.132T>G
CdBM23	KTR3	YBR205W	chrII.634214	c.593G>A
CdBM43	KTR3	YBR205W	chrII.634214	c.593G>A
MnBM14	LAM1	YHR155W	chrVIII.407313	c.211C>T
MnBM14	LAM1	YHR155W	chrVIII.407513	c.411C>T
MnBM42	LAM6	YLR072W	chrXII.279869	c.1008C>A
NiBM24	LOS1	YKL205W	chrXI.53317	c.3267A>G
MnBM17	LRG1	YDL240W	chrIV.23136	c.314T>G
MnBM13	MAM3	YOL060C	chrXV.214417	c.1720delA
MnBM31	MAM3	YOL060C	chrXV.214417	c.1720delA
MnBM16	MAM3	YOL060C	chrXV.214928	c.1209delG
MnBM17	MAM3	YOL060C	chrXV.215066	c.1072G>T
CoBM12	MAM3	YOL060C	chrXV.215342	c.796T>C

CoBM18	MAM3	YOL060C	chrXV.215920	c.218T>G
CoBM16	MAS2	YHR024C	chrVIII.158818	c.375T>A
CoBM18	MCK1	YNL307C	chrXIV.57472	c.102G>A
MnBM42	MCM5	YLR274W	chrXII.693876	c.2322T>C
CoBM6	MCT1	YOR221C	chrXV.756662	c.897C>T
MnBM42	MDH2	YOL126C	chrXV.82001	c.920G>A
CoBM12	MDL2	YPL270W	chrXVI.30675	c.194G>T
MnBM14	MDM30	YLR368W	chrXII.858040	c.501C>T
MnBM16	MET10	YFR030W	chrVI.216146	c.2835C>T
CdBM26	MET30	YIL046W	chrIX.269753	c.1103A>C
MnBM42	MEX67	YPL169C	chrXVI.229047	c.1792C>T
MnBM42	MHP1	YJL042W	chrX.362671	c.1423G>T
MnBM14	MKT1	YNL085W	chrXIV.469502	c.2372G>A
MnBM14	MLF3	YNL074C	chrXIV.487720	c.405A>T
MnBM42	MLH3	YPL164C	chrXVI.241077	c.421A>G
CdBM47	MLS1	YNL117W	chrXIV.407160	c.803A>G
CuBM9	MMS4	YBR098W	chrII.442065	c.551G>C
MnBM42	MNN9	YPL050C	chrXVI.461357	c.610G>T
MnBM42	MOT1	YPL082C	chrXVI.399531	c.4553C>T
MnBM17	MPA43	YNL249C	chrXIV.180823	c.200A>G
MnBM42	MRL1	YPR079W	chrXVI.699233	c.365G>A
MnBM42	MRPL36	YBR122C	chrII.484228	c.276T>C
MnBM27	MSC6	YOR354C	chrXV.1001702	c.1524T>G
MnBM32	MSS2	YDL107W	chrIV.269200	c.280G>A
MnBM14	MSS2	YDL107W	chrIV.269955	c.1035G>A
MnBM42	MTR4	YJL050W	chrX.342637	c.116A>G
CdBM44	MYG1	YER156C	chrV.483851	c.491G>A
CdBM26	MYO2	YOR326W	chrXV.929249	c.3529G>T
NiBM21	NAM8	YHR086W	chrVIII.278622	c.470T>C
MnBM14	NAR1	YNL240C	chrXIV.199110	c.868C>T
CoBM6	NFT1	YKR103W	chrXI.655246	c.2167A>G
CuBM10	NGG1	YDR176W	chrIV.815428	c.977G>A
CuBM11	NGG1	YDR176W	chrIV.815428	c.977G>A
CuBM12	NGG1	YDR176W	chrIV.815428	c.977G>A
CuBM13	NGG1	YDR176W	chrIV.815428	c.977G>A
CuBM14	NGG1	YDR176W	chrIV.815428	c.977G>A
CuBM17	NGG1	YDR176W	chrIV.815428	c.977G>A
CuBM18	NGG1	YDR176W	chrIV.815428	c.977G>A
CuBM4	NGG1	YDR176W	chrIV.815428	c.977G>A
CuBM7	NGG1	YDR176W	chrIV.815428	c.977G>A
CuBM9	NGG1	YDR176W	chrIV.815428	c.977G>A
MnBM42	NIP100	YPL174C	chrXVI.222669	c.105A>C
MnBM23	NPL3	YDR432W	chrIV.1329113	c.331C>A
CoBM8	NSR1	YGR159C	chrVII.806709	c.948C>T
MnBM42	NUC1	YJL208C	chrX.40977	c.207T>A
CoBM12	NUG1	YER006W	chrV.164204	c.1482A>T
MnBM14	OAF1	YAL051W	chrI.48640	c.77C>T
CoBM21	OCA4	YCR095C	chrIII.288718	c.541G>A
CoBM14	OCA5	YHL029C	chrVIII.47582	c.387C>G
MnBM42	OPI1	YHL020C	chrVIII.66824	c.633C>T
MnBM42	OSH2	YDL019C	chrIV.417674	c.3841G>A
CdBM29	PBP2	YBR233W	chrII.683908	c.481G>A
MnBM22	PDS2	YJL120C	chrX.170460	c.1636C>G

ZnBM23	PBS2	YJL128C	chrX.178468	c.1636G>C
ZnBM39	PBS2	YJL128C	chrX.178937	c.1167G>T
MnBM14	PCL5	YHR071W	chrVIII.237545	c.542C>T
MnBM42	PDA1	YER178W	chrV.546977	c.161A>G
CuBM17	PDR1	YGL013C	chrVII.469242	c.3054_3056dupCAA
MnBM39	PDR1	YGL013C	chrVII.470618	c.1681C>T
MnBM12	PDR10	YOR328W	chrXV.932506	c.704T>A
MnBM25	PDR10	YOR328W	chrXV.934229	c.2427T>A
CoBM1	PDX1	YGR193C	chrVII.885051	c.691C>G
MnBM42	PET111	YMR257C	chrXIII.779986	c.2046G>A
MnBM16	PET127	YOR017W	chrXV.361851	c.440G>A
MnBM42	PEX2	YJL210W	chrX.37037	c.119C>T
NiBM6	PFK26	YIL107C	chrIX.165562	c.200G>T
CdBM29	PHM7	YOL084W	chrXV.162510	c.155A>G
ZnBM44	PHO23	YNL097C	chrXIV.441972	c.387A>T
NiBM28	PHO81	YGR233C	chrVII.957826	c.385A>T
NiBM4	PHO84	YML123C	chrXIII.24560	c.1240dupG
NiBM11	PHO84	YML123C	chrXIII.25111	c.690C>A
ZnBM11	PHO84	YML123C	chrXIII.25111	c.690C>A
CoBM1	PHO84	YML123C	chrXIII.25178	c.623G>A
ZnBM38	PHO84	YML123C	chrXIII.25178	c.623G>A
ZnBM42	PHO84	YML123C	chrXIII.25233	c.567delT
NiBM9	PHO84	YML123C	chrXIII.25469	c.331delA
MnBM14	PIB1	YDR313C	chrIV.1089472	c.608C>T
CoBM6	PKP1	YIL042C	chrIX.275280	c.1013C>A
CoBM5	PLB2	YMR006C	chrXIII.278590	c.1092C>G
ZnBM37	PMA1	YGL008C	chrVII.479933	c.2734A>G
ZnBM45	PMA1	YGL008C	chrVII.480320	c.2347G>C
ZnBM46	PMA1	YGL008C	chrVII.480320	c.2347G>C
ZnBM29	PMA1	YGL008C	chrVII.480586	c.2081A>C
CoBM21	PMA1	YGL008C	chrVII.481133	c.1534G>A
ZnBM41	PMA1	YGL008C	chrVII.482054	c.613G>A
CoBM7	PMA1	YGL008C	chrVII.482195	c.472G>C
CuBM3	PMA1	YGL008C	chrVII.482217	c.450G>T
ZnBM17	PMA1	YGL008C	chrVII.482300	c.367C>A
CdBM42	POL3	YDL102W	chrIV.277623	c.752A>G
CdBM39	PPQ1	YPL179W	chrXVI.208936	c.788delA
MnBM42	PPQ1	YPL179W	chrXVI.208977	c.821T>C
MnBM42	PRC1	YMR297W	chrXIII.862525	c.604A>T
MnBM42	PRI1	YIR008C	chrIX.374079	c.228C>T
MnBM24	PRI2	YKL045W	chrXI.354438	c.946G>T
CuBM18	PRP2	YNR011C	chrXIV.644572	c.2379C>T
NiBM6	PRP8	YHR165C	chrVIII.432396	c.4553C>T
NiBM4	PRP8	YHR165C	chrVIII.436626	c.323C>T
ZnBM47	PTK2	YJR059W	chrX.546347	c.561C>G
ZnBM43	PTK2	YJR059W	chrX.546698	c.913delG
ZnBM43	PTK2	YJR059W	chrX.546700	c.914A>T
CoBM8	PTK2	YJR059W	chrX.547433	c.1649_1650delGA
CoBM8	PTK2	YJR059W	chrX.547441	c.1655C>T
CuBM14	PYK2	YOR347C	chrXV.985697	c.766C>T
MnBM14	QRI7	YDL104C	chrIV.273879	c.998G>T
CoBM17	RAD16	YBR114W	chrII.467332	c.85A>T
MnBM42	RAD17	YOR368W	chrXV.1027373	c.531G>T

MnBM42	RAD26	YJR035W	chrX.498452	c.1098G>T
CoBM6	RBK1	YCR036W	chrIII.193474	c.178C>T
CoBM2	RCE1	YMR274C	chrXIII.814661	c.651C>A
NiBM30	RCK2	YLR248W	chrXII.634675	c.424G>A
MnBM32	RCO1	YMR075W	chrXIII.414724	c.743G>A
MnBM42	REC102	YLR329W	chrXII.787194	c.656T>G
CoBM3	RED1	YLR263W	chrXII.672772	c.2433T>C
CoBM16	RHO1	YPR165W	chrXVI.875682	c.315T>C
CoBM5	RIM11	YMR139W	chrXIII.547166	c.1042G>A
ZnBM45	RIM21	YNL294C	chrXIV.79837	c.412_423delTTAGCCTCGTTG
CoBM4	RKM3	YBR030W	chrII.299270	c.979G>C
NiBM24	RKM3	YBR030W	chrII.299270	c.979G>C
MnBM32	RMP1	YLR145W	chrXII.432455	c.288A>T
MnBM42	RNY1	YPL123C	chrXVI.317909	c.1037A>G
CuBM18	ROG1	YGL144C	chrVII.232669	c.1839A>C
MnBM42	RPA135	YPR010C	chrXVI.580614	c.583A>G
MnBM42	RPI1	YIL119C	chrIX.137759	c.119A>G
MnBM42	RPL22A	YLR061W	chrXII.263199	c.6C>T
MnBM42	RPL2A	YFR031C-A	chrVI.221115	c.157G>A
ZnBM22	RPL39	YJL189W	chrX.76405	c.87G>A
CoBM18	RPS15	YOL040C	chrXV.253378	c.200C>G
ZnBM43	RPS2	YGL123W	chrVII.278292	c.676A>G
CdBM32	RPT5	YOR117W	chrXV.546205	c.1177G>A
MnBM42	RRB1	YMR131C	chrXIII.533259	c.1440G>A
CdBM37	RRG7	YOR305W	chrXV.889748	c.718delA
ZnBM15	RRG7	YOR305W	chrXV.889748	c.718delA
MnBM39	RRP46	YGR095C	chrVII.675732	c.611A>T
ZnBM17	RRP46	YGR095C	chrVII.675732	c.611A>T
CoBM7	RRP6	YOR001W	chrXV.327032	c.201T>C
CuBM4	RSC1	YGR056W	chrVII.602841	c.1181G>T
CuBM10	RSE1	YML049C	chrXIII.176494	c.1812C>T
CuBM12	RSE1	YML049C	chrXIII.176494	c.1812C>T
CuBM13	RSE1	YML049C	chrXIII.176494	c.1812C>T
CuBM4	RSE1	YML049C	chrXIII.176494	c.1812C>T
CdBM29	RTC2	YBR147W	chrII.537159	c.594delA
ZnBM45	SAK1	YER129W	chrV.418015	c.735T>C
ZnBM46	SAK1	YER129W	chrV.418015	c.735T>C
CdBM37	SAP4	YGL229C	chrVII.65388	c.1571delA
MnBM32	SBE2	YDR351W	chrIV.1178933	c.268G>A
MnBM42	SEC8	YPR055W	chrXVI.670433	c.2758G>A
CoBM18	SET2	YJL168C	chrX.103711	c.718C>T
CdBM29	SFP1	YLR403W	chrXII.926537	c.970C>T
CdBM30	SFP1	YLR403W	chrXII.927434	c.1867C>T
CoBM7	SFP1	YLR403W	chrXII.927464	c.1897G>A
CdBM25	SFP1	YLR403W	chrXII.927603	c.2038delC
CoBM6	SHP1	YBL058W	chrII.112395	c.959A>T
CoBM2	SIW14	YNL032W	chrXIV.574713	c.208C>T
CoBM20	SIW14	YNL032W	chrXIV.574928	c.428dupT
CoBM20	SIW14	YNL032W	chrXIV.574936	c.431A>C
CoBM17	SIW14	YNL032W	chrXIV.575008	c.503T>A
CoBM16	SIW14	YNL032W	chrXIV.575167	c.662C>A
CoBM18	SIW14	YNL032W	chrXIV.575229	c.724G>A



MnBM42	SKN1	YGR143W	chrVII.775395	c.203G>T
NiBM4	SMC2	YFR031C	chrVI.217643	c.2464C>A
MnBM13	SMY2	YBR172C	chrII.579318	c.2055C>T
NiBM27	SNF7	YLR025W	chrXII.195133	c.687delA
ZnBM41	SNT2	YGL131C	chrVII.263930	c.1930G>C
MnBM42	SNT2	YGL131C	chrVII.264038	c.1822C>A
MnBM42	SPC105	YGL093W	chrVII.336233	c.1348C>T
CdBM30	SP077	YLR341W	chrXII.807779	c.404delA
CdBM48	SPS100	YHR139C	chrVIII.378250	c.950T>C
CdBM39	SRP40	YKR092C	chrXI.613636	c.244_249dupTCTTCT
MnBM42	SSE1	YPL106C	chrXVI.351134	c.1142C>T
MnBM12	SSK2	YNR031C	chrXIV.681959	c.3475G>T
CoBM15	SSQ1	YLR369W	chrXII.860006	c.455C>T
MnBM14	SSZ1	YHR064C	chrVIII.226595	c.547G>A
ZnBM16	STE5	YDR103W	chrIV.660940	c.2591C>T
CoBM21	STP3	YLR375W	chrXII.871981	c.285T>A
MnBM42	STT3	YGL022W	chrVII.454170	c.1767G>T
MnBM16	SUB2	YDL084W	chrIV.305733	c.497A>G
MnBM42	SUC2	YIL162W	chrIX.38717	c.1333G>A
MnBM14	SUM1	YDR310C	chrIV.1083280	c.1037C>T
MnBM42	SWC5	YBR231C	chrII.682726	c.365G>A
MnBM14	SWS2	YNL081C	chrXIV.476401	c.219A>G
ZnBM16	SWT1	YOR166C	chrXV.648177	c.326T>C
MnBM14	SYF2	YGR129W	chrVII.750554	c.155C>T
CoBM18	SYG1	YIL047C	chrIX.266383	c.1441G>A
CoBM1	TAF8	YML114C	chrXIII.42805	c.771G>T
MnBM42	TAH11	YJR046W	chrX.522532	c.485C>T
MnBM42	TAO3	YIL129C	chrIX.110175	c.3063A>G
NiBM28	TCO89	YPL180W	chrXVI.205993	c.747delG
CoBM7	TFB1	YDR311W	chrIV.1086043	c.979G>T
CuBM11	TFG1	YGR186W	chrVII.869872	c.2099T>C
CuBM14	TFG1	YGR186W	chrVII.869872	c.2099T>C
CuBM17	TFG1	YGR186W	chrVII.869872	c.2099T>C
CuBM18	TFG1	YGR186W	chrVII.869872	c.2099T>C
CuBM7	TFG1	YGR186W	chrVII.869872	c.2099T>C
CuBM9	TFG1	YGR186W	chrVII.869872	c.2099T>C
MnBM42	TIM54	YJL054W	chrX.334668	c.404A>C
MnBM42	TOM1	YDR457W	chrIV.1371088	c.1299T>G
CoBM15	TOM1	YDR457W	chrIV.1375220	c.5433delT
MnBM14	TOP1	YOL006C	chrXV.315291	c.97G>C
MnBM14	TOP2	YNL088W	chrXIV.461419	c.3716G>A
MnBM42	TOS3	YGL179C	chrVII.163625	c.1467G>A
CoBM15	TPS3	YMR261C	chrXIII.792034	c.1336G>C
CoBM3	TRK2	YKR050W	chrXI.529178	c.1364A>C
CoBM16	TRL1	YJL087C	chrX.270084	c.2402C>A
MnBM32	TUS1	YLR425W	chrXII.984340	c.1447T>C
CdBM32	UBC1	YDR177W	chrIV.817301	c.424G>A
MnBM13	UBP5	YER144C	chrV.459312	c.912A>G
CdBM37	UBR2	YLR024C	chrXII.191296	c.1985delT
NiBM4	UBX7	YBR273C	chrII.749280	c.92G>T
MnBM42	UGA3	YDL170W	chrIV.157116	c.799C>A
NiBM17	UGA4	YDL210W	chrIV.85469	c.1200G>T
MnBM42	UTR5	YGR041W	chrVII.500470	c.404G>T

MnBM42	UIP5	YKR044W	chrXI.522478	c.464C>I
MnBM16	ULS1	YOR191W	chrXV.695079	c.2605G>C
CoBM17	UME6	YDR207C	chrIV.867413	c.110A>T
MnBM42	URA2	YJL130C	chrX.170952	c.1416T>C
CoBM6	URB1	YKL014C	chrXI.415085	c.1829A>C
MnBM42	USA1	YML029W	chrXIII.217976	c.615G>T
MnBM42	UTP21	YLR409C	chrXII.936628	c.606A>G
MnBM14	UTP8	YGR128C	chrVII.748798	c.1294G>A
MnBM14	UTP8	YGR128C	chrVII.749839	c.253G>A
MnBM42	VBA1	YMR088C	chrXIII.443426	c.1677T>C
MnBM28	VCX1	YDL128W	chrIV.233157	c.506C>T
MnBM12	VCX1	YDL128W	chrIV.233168	c.517C>G
MnBM29	VCX1	YDL128W	chrIV.233168	c.517C>G
MnBM14	VCX1	YDL128W	chrIV.233180	c.529G>A
CdBM39	VHR2	YER064C	chrV.283415	c.807delA
MnBM42	VID22	YLR373C	chrXII.871029	c.339C>T
MnBM42	VPS13	YLL040C	chrXII.54731	c.8915G>A
MnBM42	VPS13	YLL040C	chrXII.56151	c.7495G>T
MnBM13	VPS74	YDR372C	chrIV.1221843	c.307G>T
MnBM32	VRP1	YLR337C	chrXII.804694	c.413C>T
CoBM8	VTC1	YER072W	chrV.302912	c.107G>A
CoBM5	VTC1	YER072W	chrV.303000	c.196delA
MnBM42	VTC3	YPL019C	chrXVI.515669	c.1349delC
CoBM3	VTC4	YJL012C	chrX.411818	c.1581delC
CoBM3	VTC4	YJL012C	chrX.411821	c.1579C>G
CoBM2	VTC4	YJL012C	chrX.412379	c.1021G>T
CoBM6	VTC4	YJL012C	chrX.413090	c.310G>T
CoBM15	VTC5	YDR089W	chrIV.622165	c.54C>A
CdBM30	VTC5	YDR089W	chrIV.622197	c.93delA
CoBM21	VTC5	YDR089W	chrIV.622611	c.500T>A
CoBM4	VTC5	YDR089W	chrIV.624684	c.2575delA
MnBM42	WAR1	YML076C	chrXIII.112816	c.2532G>A
MnBM42	WAR1	YML076C	chrXIII.114669	c.679C>A
CdBM32	YAP6	YDR259C	chrIV.974680	c.1102delA
CoBM12	YBR242W	YBR242W	chrII.704814	c.145C>G
CdBM26	YBR292C	YBR292C	chrII.784713	c.360delA
CdBM46	YBR292C	YBR292C	chrII.784713	c.360delA
MnBM32	YBR292C	YBR292C	chrII.784713	c.360delA
MnBM42	YCF1	YDR135C	chrIV.726227	c.1325A>G
MnBM42	YCK1	YHR135C	chrVIII.373427	c.883dupA
CoBM5	YCT1	YLL055W	chrXII.30835	c.727C>G
NiBM16	YDL199C	YDL199C	chrIV.102171	c.1183C>T
MnBM42	YDL199C	YDL199C	chrIV.103015	c.339G>A
CdBM23	YDR003W-A	YDR003W-A	chrIV.454818	c.47delA
CdBM43	YDR003W-A	YDR003W-A	chrIV.454818	c.47delA
CdBM26	YDR157W	YDR157W	chrIV.770136	c.217delT
MnBM14	YDR541C	YDR541C	chrIV.1520152	c.547A>G
NiBM21	YEF1	YEL041W	chrV.76333	c.390G>A
MnBM42	YGR126W	YGR126W	chrVII.745887	c.53C>T
MnBM14	YGR130C	YGR130C	chrVII.752033	c.1812G>A
MnBM14	YGR130C	YGR130C	chrVII.752066	c.1779G>A
MnBM14	YGR130C	YGR130C	chrVII.752345	c.1500G>A
MnBM42	YGR266W	YGR266W	chrVII.1023209	c.554A>G

MnBM42	YCR200W	YCR200W	chrVII.1023209	c.557A>G
CoBM5	YHC1	YLR298C	chrXII.724909	c.508A>G
MnBM42	YHC3	YJL059W	chrX.325172	c.209G>T
MnBM42	YIH1	YCR059C	chrIII.223643	c.588A>G
CdBM39	YIL092W	YIL092W	chrIX.190465	c.1409delA
MnBM38	YLR108C	YLR108C	chrXII.367554	c.571G>C
CdBM39	YLR296W	YLR296W	chrXII.723168	c.205delA
CdBM46	YLR296W	YLR296W	chrXII.723168	c.205delA
MnBM39	YLR296W	YLR296W	chrXII.723168	c.205delA
ZnBM17	YLR296W	YLR296W	chrXII.723168	c.205delA
ZnBM19	YLR296W	YLR296W	chrXII.723175	c.198A>T
MnBM42	YML119W	YML119W	chrXIII.31178	c.568A>C
MnBM44	YMR027W	YMR027W	chrXIII.326810	c.934C>A
CdBM37	YOR029W	YOR029W	chrXV.384807	c.220delT
CoBM4	YOR029W	YOR029W	chrXV.384807	c.220delT
MnBM42	YOR1	YGR281W	chrVII.1053072	c.249G>T
CdBM32	YOR1	YGR281W	chrVII.1053612	c.789C>T
MnBM14	YOR1	YGR281W	chrVII.1055438	c.2615C>T
MnBM42	YOR296W	YOR296W	chrXV.872765	c.2564A>G
MnBM32	YOR343C	YOR343C	chrXV.968197	c.278G>A
MnBM14	YPK1	YKL126W	chrXI.206869	c.1163A>T
CoBM3	YPL113C	YPL113C	chrXVI.336149	c.995C>T
MnBM42	YPR078C	YPR078C	chrXVI.697845	c.421C>T
CoBM15	YPR089W	YPR089W	chrXVI.713743	c.469G>T
CoBM15	YPR089W	YPR089W	chrXVI.715738	c.2464G>T
CoBM12	YPT6	YLR261C	chrXII.668352	c.540G>C
MnBM42	YRA1	YDR381W	chrIV.1237754	c.431T>C
CdBM23	YRB2	YIL063C	chrIX.243630	c.114delA
CdBM43	YRB2	YIL063C	chrIX.243630	c.114delA
MnBM42	ZDS2	YML109W	chrXIII.53046	c.1407C>T
MnBM14	ZRT1	YGL255W	chrVII.21582	c.605A>G
MnBM42	ZRT3	YKL175W	chrXI.118899	c.107G>A

The length matches that expected from the tally of multiply hit genes:

In[189]:=

**Length[mat]**

Out[189]=

450

In[190]:=

**Sort[Tally[Sum[genomeSNPEFF[All, i], {i, 1, 110}]]][1 ;; 4]**  
**%[All, 1].%[All, 2] + (6 + 10) (\*Adding NGG1 and TFG1\*)**

Out[190]=

{{1, 384}, {2, 18}, {3, 2}, {4, 2}}

Out[191]=

450

In[192]:=

**Export[**

**"/Users/otto/Documents/Students/AnnaBazzicalupo/MetalAdaptation/Genomics/SNPs\_8**  
**Nov2024.tsv", mat];**

Tally by line:

In[193]:=

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newheader[[16 ;; 124]] // Length
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Out[193]=

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109
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In[194]:=

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bymetal = Tally[Sort[Join[mat[[All, 1]], newheader[[16 ;; 124]]]];
bymetal[[All, 2]] = bymetal[[All, 2]] - 1;
bymetal
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Out[196]=

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  {CdBM36, 0}, {CdBM37, 4}, {CdBM39, 6}, {CdBM42, 3}, {CdBM43, 3}, {CdBM44, 3},
  {CdBM45, 1}, {CdBM46, 3}, {CdBM47, 2}, {CdBM48, 1}, {CoBM1, 4}, {CoBM12, 6},
  {CoBM14, 1}, {CoBM15, 8}, {CoBM16, 5}, {CoBM17, 6}, {CoBM18, 7}, {CoBM2, 6},
  {CoBM20, 2}, {CoBM21, 5}, {CoBM3, 8}, {CoBM4, 4}, {CoBM5, 6}, {CoBM6, 8}, {CoBM7, 5},
  {CoBM8, 5}, {CuBM10, 2}, {CuBM11, 2}, {CuBM12, 2}, {CuBM13, 2}, {CuBM14, 5},
  {CuBM15, 1}, {CuBM16, 0}, {CuBM17, 3}, {CuBM18, 5}, {CuBM3, 1}, {CuBM4, 3},
  {CuBM6, 2}, {CuBM7, 3}, {CuBM8, 0}, {CuBM9, 4}, {MnBM12, 5}, {MnBM13, 5},
  {MnBM14, 36}, {MnBM15, 1}, {MnBM16, 5}, {MnBM17, 4}, {MnBM18, 3}, {MnBM20, 2},
  {MnBM21, 1}, {MnBM23, 5}, {MnBM24, 4}, {MnBM25, 2}, {MnBM27, 3}, {MnBM28, 1},
  {MnBM29, 3}, {MnBM31, 4}, {MnBM32, 13}, {MnBM34, 0}, {MnBM38, 5}, {MnBM39, 4},
  {MnBM42, 102}, {MnBM44, 1}, {NiBM11, 2}, {NiBM12, 1}, {NiBM14, 0}, {NiBM16, 1},
  {NiBM17, 1}, {NiBM21, 2}, {NiBM22, 0}, {NiBM24, 3}, {NiBM25, 0}, {NiBM27, 1},
  {NiBM28, 2}, {NiBM29, 0}, {NiBM30, 2}, {NiBM4, 4}, {NiBM6, 4}, {NiBM8, 0},
  {NiBM9, 1}, {ZnBM11, 2}, {ZnBM12, 1}, {ZnBM15, 2}, {ZnBM16, 4}, {ZnBM17, 3},
  {ZnBM19, 2}, {ZnBM22, 1}, {ZnBM23, 2}, {ZnBM25, 0}, {ZnBM28, 1}, {ZnBM29, 1},
  {ZnBM31, 1}, {ZnBM34, 0}, {ZnBM37, 1}, {ZnBM38, 2}, {ZnBM39, 1}, {ZnBM41, 2},
  {ZnBM42, 1}, {ZnBM43, 3}, {ZnBM44, 2}, {ZnBM45, 3}, {ZnBM46, 2}, {ZnBM47, 1}}
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In[197]:=

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Total[bymetal[[All, 2]]]
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Out[197]=

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450
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In[198]:=

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Sort[Union[mat[All, 2]]]
Length[%]
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Out[198]=

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ATG2, ATG39, BDS1, BIR1, BLM10, BNA6, BNI1, BNI4, BRR2, BSD2, BUL1, BUL2, CAJ1,
CCC2, CCR4, CCW12, CDC25, CIC1, CLB3, CLN3, CNE1, COG1, COG3, COI1, COQ1, CPA1,
CSM3, CUE3, CWC22, CWH41, CYK3, DAL2, DBF20, DBP10, DDR48, DNF1, DOA4, DOT6,
DSC2, DSE4, DUS4, EBS1, ECM14, ECM22, EFR3, ELO3, ERB1, ERG1, ERG27, ERG7, ERG9,
FAS2, FAU1, FCY2, FET4, FIG2, FIG4, FLC2, FMP52, FRE6, FSF1, FYV10, FYV6, FZF1,
GAS4, GAT1, GCD2, GID12, GPB1, GPB2, GPH1, GSC2, HBT1, HEH2, HHF2, HIS4, HMF1,
HO, HOB2, HRT3, HSL1, HSP104, HUL5, HXT13, IDP1, IES3, ILV2, IMA1, INP2, IOC4,
IPI3, IRC20, IRC8, IST2, ISU1, ITC1, KAR3, KGD1, KIN1, KIN82, KRE5, KSP1, KTR3,
LAM1, LAM6, LOS1, LRG1, MAM3, MAS2, MCK1, MCM5, MCT1, MDH2, MDL2, MDM30, MET10,
MET30, MEX67, MHP1, MKT1, MLF3, MLH3, MLS1, MMS4, MNN9, MOT1, MPA43, MRL1,
MRPL36, MSC6, MSS2, MTR4, MYG1, MYO2, NAM8, NAR1, NFT1, NGG1, NIP100, NPL3,
NSR1, NUC1, NUG1, OAF1, OCA4, OCA5, OPI1, OSH2, PBP2, PBS2, PCL5, PDA1, PDR1,
PDR10, PDX1, PET111, PET127, PEX2, PFK26, PHM7, PHO23, PHO81, PHO84, PIB1,
PKP1, PLB2, PMA1, POL3, PPQ1, PRC1, PRI1, PRI2, PRP2, PRP8, PTK2, PYK2, QRI7,
RAD16, RAD17, RAD26, RBK1, RCE1, RCK2, RCO1, REC102, RED1, RH01, RIM11, RIM21,
RKM3, RMP1, RNY1, ROG1, RPA135, RPI1, RPL22A, RPL2A, RPL39, RPS15, RPS2, RPT5,
RRB1, RRG7, RRP46, RRP6, RSC1, RSE1, RTC2, SAK1, SAP4, SBE2, SEC8, SET2, SFP1,
SHP1, SIW14, SKN1, SMC2, SMY2, SNF7, SNT2, SPC105, SPO77, SPS100, SRP40, SSE1,
SSK2, SSQ1, SSZ1, STE5, STP3, STT3, SUB2, SUC2, SUM1, SWC5, SWS2, SWT1, SYF2,
SYG1, TAF8, TAH11, TA03, TC089, TFB1, TFG1, TIM54, TOM1, TOP1, TOP2, TOS3, TPS3,
TRK2, TRL1, TUS1, UBC1, UBP5, UBR2, UBX7, UGA3, UGA4, UIP5, ULS1, UME6, URA2,
URB1, USA1, UTP21, UTP8, VBA1, VCX1, VHR2, VID22, VPS13, VPS74, VRP1, VTC1,
VTC3, VTC4, VTC5, WAR1, YAP6, YBR242W, YBR292C, YCF1, YCK1, YCT1, YDL199C,
YDR003W-A, YDR157W, YDR541C, YEF1, YGR126W, YGR130C, YGR266W, YHC1, YHC3,
YIH1, YIL092W, YLR108C, YLR296W, YML119W, YMR027W, YOR029W, YOR1, YOR296W,
YOR343C, YPK1, YPL113C, YPR078C, YPR089W, YPT6, YRA1, YRB2, ZDS2, ZRT1, ZRT3}
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Out[199]=

331

Gene list with all lines:

In[200]:=

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Sort[Union[mat[[All, 2]]]
Length[%]
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Out[200]=

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{ABP1, ACB1, ACC1, ADE6, ADR1, AFT1, AGP1, AHK1, ALD5, ALY2, APC2, ARO3, ASN1, ATG11,
ATG2, ATG39, BDS1, BIR1, BLM10, BNA6, BNI1, BNI4, BRR2, BSD2, BUL1, BUL2, CAJ1,
CCC2, CCR4, CCW12, CDC25, CIC1, CLB3, CLN3, CNE1, COG1, COG3, COI1, COQ1, CPA1,
CSM3, CUE3, CWC22, CWH41, CYK3, DAL2, DBF20, DBP10, DDR48, DNF1, DOA4, DOT6,
DSC2, DSE4, DUS4, EBS1, ECM14, ECM22, EFR3, ELO3, ERB1, ERG1, ERG27, ERG7, ERG9,
FAS2, FAU1, FCY2, FET4, FIG2, FIG4, FLC2, FMP52, FRE6, FSF1, FYV10, FYV6, FZF1,
GAS4, GAT1, GCD2, GID12, GPB1, GPB2, GPH1, GSC2, HBT1, HEH2, HHF2, HIS4, HMF1,
HO, HOB2, HRT3, HSL1, HSP104, HUL5, HXT13, IDP1, IES3, ILV2, IMA1, INP2, IOC4,
IPI3, IRC20, IRC8, IST2, ISU1, ITC1, KAR3, KGD1, KIN1, KIN82, KRE5, KSP1, KTR3,
LAM1, LAM6, LOS1, LRG1, MAM3, MAS2, MCK1, MCM5, MCT1, MDH2, MDL2, MDM30, MET10,
MET30, MEX67, MHP1, MKT1, MLF3, MLH3, MLS1, MMS4, MNN9, MOT1, MPA43, MRL1,
MRPL36, MSC6, MSS2, MTR4, MYG1, MYO2, NAM8, NAR1, NFT1, NGG1, NIP100, NPL3,
NSR1, NUC1, NUG1, OAF1, OCA4, OCA5, OPI1, OSH2, PBP2, PBS2, PCL5, PDA1, PDR1,
PDR10, PDX1, PET111, PET127, PEX2, PFK26, PHM7, PHO23, PHO81, PHO84, PIB1,
PKP1, PLB2, PMA1, POL3, PPQ1, PRC1, PRI1, PRI2, PRP2, PRP8, PTK2, PYK2, QRI7,
RAD16, RAD17, RAD26, RBK1, RCE1, RCK2, RCO1, REC102, RED1, RH01, RIM11, RIM21,
RKM3, RMP1, RNY1, ROG1, RPA135, RPI1, RPL22A, RPL2A, RPL39, RPS15, RPS2, RPT5,
RRB1, RRG7, RRP46, RRP6, RSC1, RSE1, RTC2, SAK1, SAP4, SBE2, SEC8, SET2, SFP1,
SHP1, SIW14, SKN1, SMC2, SMY2, SNF7, SNT2, SPC105, SPO77, SPS100, SRP40, SSE1,
SSK2, SSQ1, SSZ1, STE5, STP3, STT3, SUB2, SUC2, SUM1, SWC5, SWS2, SWT1, SYF2,
SYG1, TAF8, TAH11, TA03, TC089, TFB1, TFG1, TIM54, TOM1, TOP1, TOP2, TOS3, TPS3,
TRK2, TRL1, TUS1, UBC1, UBP5, UBR2, UBX7, UGA3, UGA4, UIP5, ULS1, UME6, URA2,
URB1, USA1, UTP21, UTP8, VBA1, VCX1, VHR2, VID22, VPS13, VPS74, VRP1, VTC1,
VTC3, VTC4, VTC5, WAR1, YAP6, YBR242W, YBR292C, YCF1, YCK1, YCT1, YDL199C,
YDR003W-A, YDR157W, YDR541C, YEF1, YGR126W, YGR130C, YGR266W, YHC1, YHC3,
YIH1, YIL092W, YLR108C, YLR296W, YML119W, YMR027W, YOR029W, YOR1, YOR296W,
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Out[201]=

331

Gene list without the mutator lines MnBM14 and MnBM42:

In[202]:=

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Union[Sort[Select[mat, MemberQ[{"MnBM14", "MnBM42"}, #[[1]] == False &] [[All, 2]]]
Length[%]
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Out[202]=

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BIR1, BLM10, BNA6, BNI1, BNI4, BSD2, BUL1, BUL2, CCC2, CCW12, CDC25, CLN3, COG1,
COI1, COQ1, CSM3, CYK3, DBF20, DBP10, DDR48, DNF1, DOA4, DSE4, DUS4, EBS1, ECM14,
EFR3, ELO3, ERB1, ERG1, ERG27, ERG9, FCY2, FET4, FIG4, FRE6, FSF1, FYV10, FZF1,
GAT1, GCD2, GPB1, GPB2, HBT1, HHF2, HIS4, HMF1, HO, HSL1, HSP104, HUL5, HXT13,
IDP1, ILV2, INP2, IOC4, IST2, ISU1, KAR3, KIN1, KIN82, KRE5, KSP1, KTR3, LOS1,
LRG1, MAM3, MAS2, MCK1, MCT1, MDL2, MET10, MET30, MLS1, MMS4, MPA43, MSC6, MSS2,
MYG1, MYO2, NAM8, NFT1, NGG1, NPL3, NSR1, NUG1, OCA4, OCA5, PBP2, PBS2, PDR1,
PDR10, PDX1, PET127, PFK26, PHM7, PHO23, PHO81, PHO84, PKP1, PLB2, PMA1, POL3,
PPQ1, PRI2, PRP2, PRP8, PTK2, PYK2, RAD16, RBK1, RCE1, RCK2, RCO1, RED1, RH01,
RIM11, RIM21, RKM3, RMP1, ROG1, RPL39, RPS15, RPS2, RPT5, RRG7, RRP46, RRP6,
RSC1, RSE1, RTC2, SAK1, SAP4, SBE2, SET2, SFP1, SHP1, SIW14, SMC2, SMY2, SNF7,
SNT2, SP077, SPS100, SRP40, SSK2, SSQ1, STE5, STP3, SUB2, SWT1, SYG1, TAF8,
TCO89, TFB1, TFG1, TOM1, TPS3, TRK2, TRL1, TUS1, UBC1, UBP5, UBR2, UBX7, UGA4,
ULS1, UME6, URB1, VCX1, VHR2, VPS74, VRP1, VTC1, VTC4, VTC5, YAP6, YBR242W,
YBR292C, YCT1, YDL199C, YDR003W-A, YDR157W, YEF1, YHC1, YIL092W, YLR108C,
YLR296W, YMR027W, YOR029W, YOR1, YOR343C, YPL113C, YPR089W, YPT6, YRB2}
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Out[203]=

210