

## **Description of Additional Supplementary Files**

### **Supplementary Data 1**

Genome-wide siRNA screen - viability hit list. Genes below the indicated fold-change (FC) threshold are shown in sheet 1, and the corresponding enrichment analysis (EA) data are shown in sheet 2. EA performed using DAVID (<https://david.ncifcrf.gov/>).

### **Supplementary Data 2**

Genome-wide siRNA screen - glycolysis hit list. Genes below the indicated fold-change (FC) threshold are shown in sheet 1, and the corresponding enrichment analysis (EA) data are shown in sheet 2. EA performed using DAVID (<https://david.ncifcrf.gov/>).

### **Supplementary Data 3**

Genome-wide siRNA screen – enhancers of the BRAF inhibitor response, glycolysis and viability hit list. Genes below the indicated fold-change (FC) threshold are shown in sheet 1, and the corresponding enrichment analysis (EA) data are shown in sheet 2. EA performed using DAVID (<https://david.ncifcrf.gov/>).

### **Supplementary Data 4**

RNA sequencing data for the mRNA binding, transport and translation gene set in melanoma patients on progression after treatment with MAPK pathway inhibitors. Data sourced from <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE65186><sup>24</sup>.

### **Supplementary Data 5**

RNA sequencing data for polysome profiling analysis of A375 melanoma cells, without or without BRAF inhibition. Anota2seq was used to determine transcriptome-wide changes in mRNA abundance, translation and buffering. See methods for details.

### **Supplementary Data 6**

Gene set enrichment analysis (GSEA) of polysome profiling RNA sequencing data. Enrichment data for the Hallmark and KEGG gene sets for the indicated comparisons are shown in separate data sheets (<https://www.gsea-msigdb.org/gsea/index.jsp>; NES = normalised enrichment score; See methods for details).

### **Supplementary Data 7**

Functional annotation enrichment analysis was performed on 579 significantly buffered genes (FDR < 0.1; see Supplementary Data 5) using DAVID (<https://david.ncifcrf.gov/>; GO Biological Process and KEGG; P-value < 0.05).