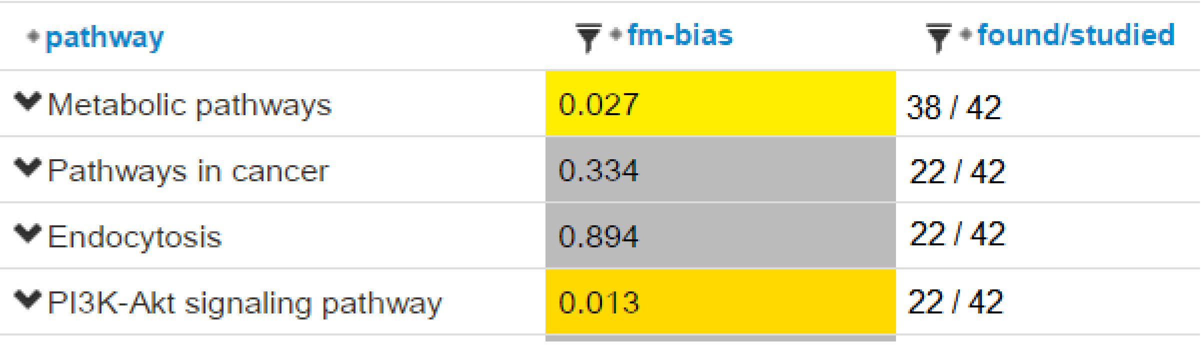
# Supplementary Information

## Supplementary Table 1: Mutations observed in treatment refractory patient:

| CHROM | POS | REF | ALT | Gene | exon | hgvs | class |
|---|---|---|---|---|---|---|---|
| 1 | 70555500 | A | G | LRRC7 | Ex23of25 | c.4429A>Gp.Lys1477Glu | NSC |
| 2 | 44051563 | T | C | ABCG5 | Ex8of13 | c.913A>Gp.Thr305Ala | NSC |
| 2 | 111399042 | C | A | BUB1 | Int21/22 | c.2626-1G>T | ESS |
| 3 | 175165091 | A | G | NAALADL2 | Ex6of14 | c.1165A>Gp.Lys389Glu | NSC |
| 5 | 66461444 | C | A | MAST4 | Ex29of29 | c.6437C>Ap.Pro2146Gln | NSC |
| 7 | 100683053 | A | G | MUC17 | Ex3of13 | c.8356A>Gp.Thr2786Ala | NSC |
| 7 | 100683036 | T | C | MUC17 | Ex3of13 | c.8339T>Cp.Ile2780Thr | NSC |
| 7 | 152373159 | A | C | XRCC2 | Ex1of3 | c.6T>Gp.Cys2Trp | NSC |
| 7 | 100349919 | T | C | ZAN | Ex13of46 | c.2191T>Cp.Ser731Pro | NSC |
| 11 | 71946892 | C | A | INPPL1 | Ex25of28 | c.2741C>Ap.Ser914X | SG |
| 12 | 11461675 | C | G | PRB4 | Ex3of4 | c.242G>Cp.Arg81Pro | NSC |
| 15 | 41192690 | C | A | VPS18 | Ex4of5 | c.1674C>Ap.Tyr558X | SG |
| 18 | 23731828 | C | A | PSMA8 | Ex3of7 | c.254C>Ap.Thr85Asn | NSC |
| 19 | 17392967 | G | T | ANKLE1 | Ex2of9 | c.164G>Tp.Gly55Val | NSC |
| 19 | 4429600 | C | A | CHAF1A | Ex9of15 | c.1770C>Ap.Asp590Glu | NSC |
| 19 | 18547504 | C | G | ISYNA1 | Ex5of11 | c.599G>Cp.Arg200Pro | NSC |
| 19 | 44352666 | G | A | ZNF283 | Ex7of7 | c.1913G>Ap.Cys638Tyr | NSC |
| 19 | 56663216 | A | G | ZNF444:AC024580.1 | Int3/4:Ex1of2 | c.297+4639A>G:c.35T>Cp.Val12Ala | INTR:NSC |

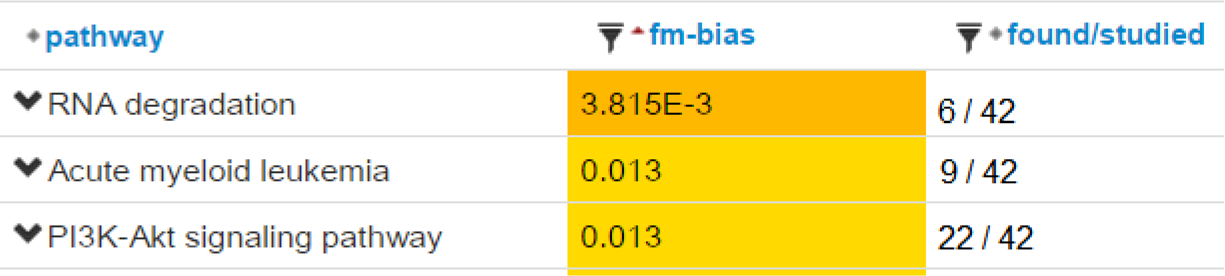
## Supplementary Table 2 – Mutated pathways

2A) Mutated pathways ordered by frequency of observed mutations. Fields as calculated by IntoGen, see URL http://www.intogen.org/ for documentation



| pathway | fm-bias | found/studied |
|---|---|---|
| Metabolic pathways | 0.027 | 38 / 42 |
| Pathways in cancer | 0.334 | 22 / 42 |
| Endocytosis | 0.894 | 22 / 42 |
| PI3K-Akt signaling pathway | 0.013 | 22 / 42 |

2B) Mutated pathways ordered by significance (fm-bias). Fields as calculated by IntoGen, see URL http://www.intogen.org/ for documentation



| pathway | fm-bias | found/studied |
|---|---|---|
| RNA degradation | 3.815E-3 | 6 / 42 |
| Acute myeloid leukemia | 0.013 | 9 / 42 |
| PI3K-Akt signaling pathway | 0.013 | 22 / 42 |

## Supplementary Table 3 – Primer sequences used for validation of known driver mutations in *KIT* and *KRAS*

| Gene_Exon_Direction | Primer sequence (5' to 3') |
|---|---|
| KIT_Ex10-11_F | ATGGGCTGTGAGTTGGGAG |
| KIT_Ex10-11_R | TCAGGTGGAACAAAACAAAGG |
| KIT_Ex17_F | TGTGAACATCATTCAAGGCG |
| KIT_Ex17_R | AAATGTGTGATATCCCTAGACAGG |
| KRAS_Ex2_F | TTTGTATTAAAAGGTACTGGTGGAG |
| KRAS_Ex2_R | TGAAACCCAAGGTACATTTCAG |