

Vosaroxin in combination with decitabine in newly diagnosed older patients with acute myeloid leukemia or high-risk myelodysplastic syndrome

Naval Daver,¹ Hagop Kantarjian,¹ Guillermo Garcia-Manero¹, Elias Jabbour,¹ Gautam Borthakur,¹ Mark Brandt,¹ Sherry Pierce,¹ Kenneth Vaughan,¹ Jing Ning,² Graciela M. Nogueras González,² Keyur Patel,³ Jeffery Jorgensen,³ Naveen Pemmaraju,¹ Tapan Kadia,¹ Marina Konopleva,¹ Michael Andreeff,¹ Courtney DiNardo,¹ Jorge Cortes,¹ Renee Ward,⁴ Adam Craig⁴ and Farhad Ravandi¹

¹Department of Leukemia, ²Department of Biostatistics, and ³Department of Hematopathology, The University of Texas M.D. Anderson Cancer Center, Houston, TX, USA and ⁴Sunesis Pharmaceuticals Inc., South San Francisco, CA, USA

©2017 Ferrata Storti Foundation. This is an open-access paper. doi:10.3324/haematol.2017.168732

Received: March 17, 2017.

Accepted: July 12, 2017.

Pre-published: July 20, 2017.

Correspondence: ndaver@mdanderson.org or fravandi@mdanderson.org

SUPPLEMENTAL DATA

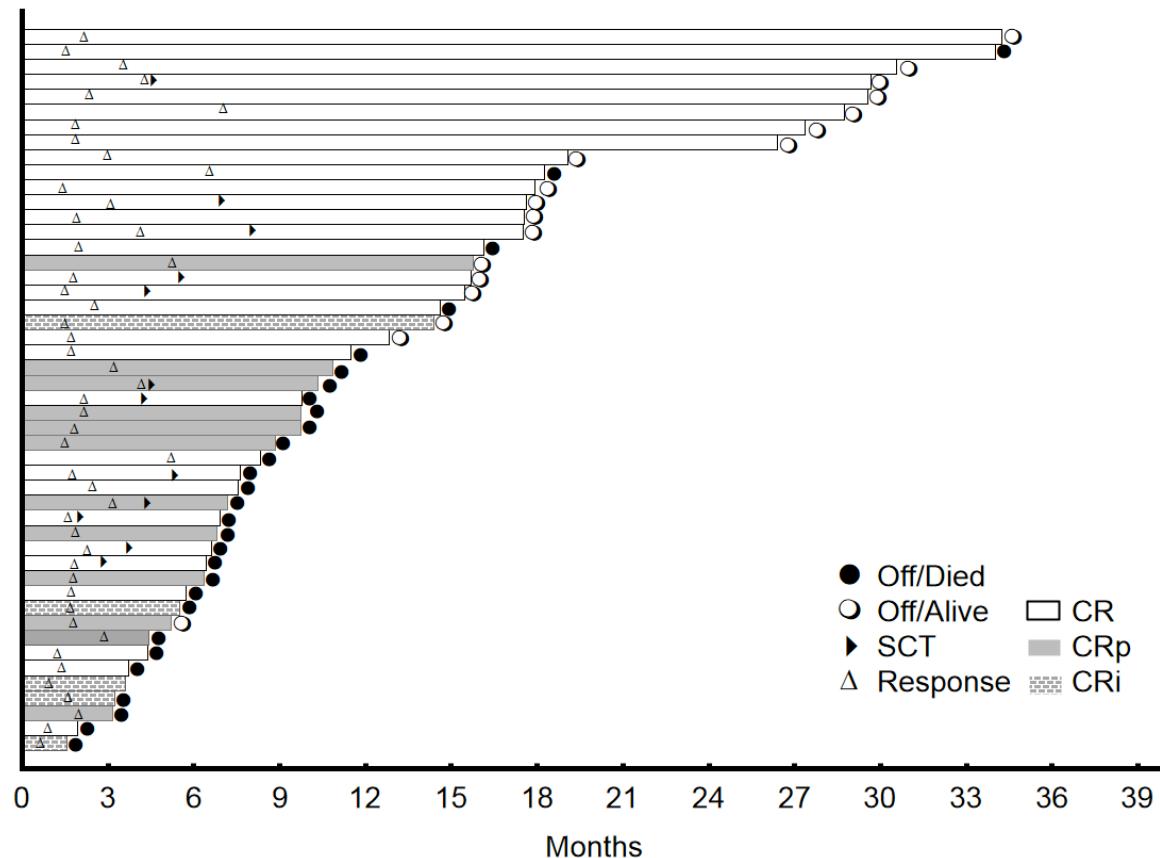
Supplemental Table 1: Coverage by genes and codons tested for adequate amplicons

<u>Gene</u>	<u>Exons (codons) tested</u>
<u>Gene</u>	<u>Exons (codons) tested</u>
ABL1 (NM_005157)	1-11 (1-1004), 11 (1079-1150)
ASXL1 (NM_015338)	2-12 (20-1542)
BRAF (NM_004333)	1 (1-23), 1-18 (34-717), 18 (725-767)
DNMT3A (NM_022552)	2-23 (1-913)
EGFR (NM_005228)	1 (1-24), 2-20 (30-786), 20-23 (792-927), 23-26 (935-1043), 26-27 (1047-1061), 27-28 (1067-1211)
EZH2 (NM_004456)	2-5 (3-162), 6-7 (171-217), 8-20 (243-752)
FLT3 (NM_004119)	2-24 (15-994)
GATA1 (NM_002049)	2-5 (1-287), 6 (291-405), 6 (407-414)
GATA2 (NM_032638)	2-6 (1-481)
HRAS (NM_005343)	2-5 (1-190)
IDH1 (NM_005896)	3-10 (1-415)
IDH2 (NM_002168)	1 (1-14), 1-11 (26-453)
IKZF2 (NM_016260)	2-8 (1-527)
JAK2 (NM_004972)	3-18 (1-806), 19-25 (812-1133)
KIT (NM_000222)	1-6 (1-334), 6-21 (367-977)
KRAS (NM_004985)	2-5 (1-189)
MDM2 (NM_002392)	1-11 (1-498)
MLL (NM_005933)	1-5 (103-1190), 6-36 (1207-3970)
MPL (NM_005373)	1-9 (1-488), 10-12 (490-636)
MYD88 (NM_002468)	1 (1-6), 1-5 (15-310)
NOTCH1 (NM_017617)	2-31 (21-1893), 31-34 (1902-2286), 34 (2289-2552)
NPM1 (NM_002520)	1-7 (1-181), 7-11 (187-295)
NRAS (NM_002524)	2-5 (1-190)
PTPN11 (NM_002834)	1-4 (1-157), 5-15 (176-594)
RUNX1 (NM_001754)	2-4 (1-70), 4-9 (73-437)
TET2 (NM_001127208)	3 (1-854), 3-11 (866-2003)
TP53 (NM_000546)	2-11 (1-394)
WT1 (NM_024426)	1 (1-59, 72-105, 122-216), 2-10 (216-518)

*Sequencing coverage of the genes: The above table describes adequacy of coverage in our assay across the full set of covered genes, exons, and codons. Adequately covered amplicons are defined as those having total coverage depth of greater than or equal to 250 reads, or for which an orthogonal mutation analysis testing has been performed. Presence of mutations outside the tested regions listed below cannot be ruled out. Due to space limitations, only certain genes may be listed. A full list of covered genes & codons for the specific test results on this sample is available upon request.

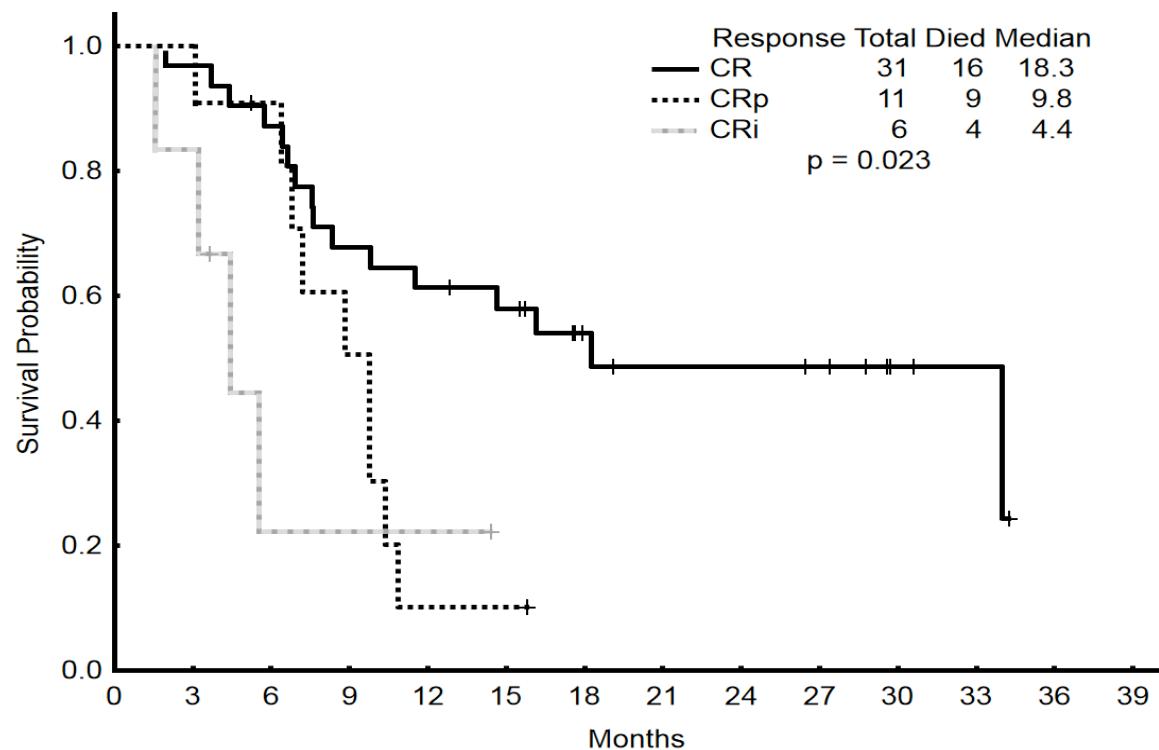
Supplemental Figure 1

Swim-plot of responders highlighting time of response, disposition, and survival to date



Supplemental Figure 2

Survival among patients who achieved a best response of CR versus CRp versus CRI

**Supplemental Figure 3**

Survival among patients who achieved a best response of CR or CRI/CRp by MRD at response (+/- 3 months) by multiplanar flow cytometry

