

**SUPPLEMENTARY INFORMATION TO
A MATHEMATICAL ALGORITHM FOR DISCOVERING STATES OF
EXPRESSION FROM DIRECT GENETIC COMPARISON BY MICROARRAYS**

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Equation (1.2):

$$f'(x) = \left(\frac{a_1 * a_2}{(x + a_2)^2} + \frac{ns + a_3}{(ns - x + a_3)^2} \right) * a_5 * \left(\frac{1}{1 + \left(\frac{a_7}{x}\right)^{a_6}} + \frac{a_8}{1 + \left(\frac{a_{10}}{x}\right)^{a_9}} - \frac{a_{11}}{x + a_{12}} \right) * \left(1 + \frac{a_{13}}{1 + \left|1 - \frac{a_{15}}{x}\right|^{a_{14}}}\right)$$

+

$$\left(\frac{a_1 * x}{x + a_2} + \frac{x}{ns - x + a_3} - a_4 \right) * a_5 * \left(\frac{\frac{a_6 * \left(\frac{a_7}{x}\right)^{a_6}}{x} + a_8 * \frac{a_9 * \left(\frac{a_{10}}{x}\right)^{a_9}}{x}}{\left(1 + \left(\frac{a_7}{x}\right)^{a_6}\right)^2 + \left(1 + \left(\frac{a_{10}}{x}\right)^{a_9}\right)^2} + \frac{a_{11}}{(x + a_{12})^2} \right) * \left(1 + \frac{a_{13}}{1 + \left|1 - \frac{a_{15}}{x}\right|^{a_{14}}}\right)$$

+

$$\left(\frac{a_1 * x}{x + a_2} + \frac{x}{ns - x + a_3} - a_4 \right) * a_5 * \left(\frac{1}{1 + \left(\frac{a_7}{x}\right)^{a_6}} + \frac{a_8}{1 + \left(\frac{a_{10}}{x}\right)^{a_9}} - \frac{a_{11}}{x + a_{12}} \right) * \left(\frac{a_{13} * a_{14} * \text{sign}(a_{15} - x) * \left(\frac{a_{15}}{x^2}\right) * \left|1 - \frac{a_{15}}{x}\right|^{a_{14}-1}}{\left(1 + \left|1 - \frac{a_{15}}{x}\right|^{a_{14}}\right)^2} \right)$$

+

$$\frac{a_{19} * \left(\frac{a_{16}}{x}\right) * \left(\frac{a_{17}}{x}\right)^{a_{16}}}{\left(1 + \left(\frac{a_{17}}{x}\right)^{a_{16}}\right)^2}$$

Construction of Equation (1.1) and Legend of Web Figure 1.

Construction of equation (1.1). Our goal in constructing equation (1.1) is to generate a flexible formula that has the ability to adapt in fitting the data sets of the heterogeneous curves of this family. Such an equation is expected to contain parameters that vary to fit differences in curvature at various ranks (x -coordinates). The total number of parameters and complexity are not limiting factors because of the speed of current computers and the availability of mathematical software packages. We start with the equation:

$$y = \frac{x}{ns - x + a_3}$$

ns corresponds to the total number of spots; $ns = 3840$ for the 1.7K microarray.

(a) shows the effects of varying a_3 on the curve plot. To replicate the rapid elevation of the segment of the curve of (b) that corresponds to lower ranks, we add:

$$y = \left(\frac{a_1 * x}{x + a_2} + \frac{x}{3840 - x + a_3} - a_4 \right)$$

(b-d) show the effects of variations in a_1 , a_2 , and a_4 . Our next goal is to control the slope of the segment of the curve preceding the point of inflection and the position of the inflection rank. (e) shows the plot of the equation

$$y = \frac{1}{1 + \left(\frac{a_7}{x}\right)^{a_6}}$$

and the effects of varying a_7 and a_6 . (f-g) plot the equation:

$$y = \left(\frac{a_1 * x}{x + a_2} + \frac{x}{3840 - x + a_3} - a_4 \right) * a_5 * \left(\frac{1}{1 + \left(\frac{a_7}{x}\right)^{a_6}} \right)$$

and show the effects of variability in a_5 , a_6 , and a_7 . (f) shows that variations in parameters a_6 and a_7 affect the inflection rank. To gain a fine control on the effects of a_5 , a_6 and a_7 on curvature, we added parameters a_8 - a_{12} .

$$y = \left(\frac{a_1 * x}{x + a_2} + \frac{x}{3840 - x + a_3} - a_4 \right) * a_5 * \left(\frac{1}{1 + \left(\frac{a_7}{x}\right)^{a_6}} + \frac{a_8}{1 + \left(\frac{a_{10}}{x}\right)^{a_9}} - \frac{a_{11}}{x + a_{12}} \right)$$

Next, we recreate the 'step' in curvature that occurs in association with the inflection point of the curves generated by the human 1.7 and 19K microarrays (see Figure 1 and supplementary information on the web address above). (h) shows the plot of the equation:

$$y = 1 + \frac{a_{13}}{1 + \left| 1 - \frac{a_{15}}{x} \right|^{a_{14}}}$$

where $a_{15} = 1000$ and the effects of variations in a_{14} . (i) shows the effects of varying a_{14} and a_{15} on the plot of:

$$y = \left(\frac{a_1 * x}{x + a_2} + \frac{x}{3840 - x + a_3} - a_4 \right) * a_5 * \left(\frac{1}{1 + \left(\frac{a_7}{x} \right)^{a_6}} + \frac{a_8}{1 + \left(\frac{a_{10}}{x} \right)^{a_9}} - \frac{a_{11}}{x + a_{12}} \right) * \left(1 + \frac{a_{13}}{1 + \left| 1 - \frac{a_{15}}{x} \right|^{a_{14}}} \right)$$

(i) also shows that variations in a_{14} and a_{15} also affect the inflection rank. The curves generated by the lymphoma lack a 'step' at the inflection point; there, parameters a_{14} and a_{15} are applied to recreate the rapid rise in slope seen at higher ranks (see supplementary information). Finally, we added parameters a_{16} - a_{19} in:

$$\left(\frac{1}{1 + \left(\frac{a_{17}}{x} \right)^{a_{16}}} - a_{18} \right) * a_{19}$$

to control the slope of its initial rise (a_{16} and a_{17} , (j)) and the vertical position of the curve (a_{18} and a_{19} , (k-l)). Current computers handle Equation (1.1) efficiently.

Legend of Web Figure 2

Equation (1.1) fits the data sets of 60/60 human 1.7K (1.7K), 200/200 human 19K (19KP1 and 19kP2)), and all 266 publicly available curves of the lymphoma study (Alizadeh AA al. *Nature* 2000, 403: 503-511). Negative background-subtracted intensity measurements are transformed to 1 (log = 0). Column *a* shows the log transformation of the background-subtracted intensity measurements in channel 1 (red) and channel 2 (magenta). Column *b* and *d* superimpose the plots of equation 1.1 (black and blue) onto the corresponding data sets in channels 1 and

2 (red and magenta), respectively. Columns *c* and *d* show the plots of equation 1.2 corresponding to the data sets of channels 1 and 2, respectively. The enclosed Excel sheet contains the 266 (a_1, \dots, a_{19}) parameters of equation (1.1) and the norms of residuals of the fits.

Normalization And Spot Ranks

Fitting the sorted data of symmetrical images into equation (1.1) generates 2 intensity curves I_1 and I_2 (Figure 1a), 2 log curves L_1 and L_2 (Figure 1b), and 2 separate Spot Orders (SO1 and SO2). Each spot can thus be represented by its 2 ranks $(r_1(s), r_2(s))$ in SO1 and SO2, respectively. Normalization is applied to annul confounding experimental variations in labeling, laser and probe intensities. It is based on the idea that the expression levels of the predominant majority of genomic spots do not differ between 2 samples. Normalization implies that the products of all the expression measurements of the 2 samples are equal; thus:

$$\prod_{s=1}^{3840} \left(\frac{e^{L_1(r_1(s))}}{e^{L_2(r_2(s))}} \right) = 1 \quad (2.1)$$

Formula (2.1) leads to:

$$\frac{\prod_{p=1}^{3840} e^{L_1(p)}}{\prod_{p=1}^{3840} e^{L_2(p)}} = 1, \text{ and } \sum_{p=1}^{3840} (L_1(p) - L_2(p)) = 0 \quad (2.2)$$

Where p denotes the same rank in SO1 and SO2. Formula (2.2) uncovers a new strategy for normalization (Figure 1e). Specifically, the y-coordinates or expression values of the spots of SO2 are transformed to become equal to the expression values of spots having equal ranks in SO1. For instance, to normalize the

expression data of L_2 , shown in Figure 1d, to model the log curve L_1 , shown in Figure 1b, a normalization function N is applied to the data of L_2 such as:

$$N(p) = I_1(p) \quad \text{and}$$

$$\text{normalized } L_2(p) = \log(N(p)) = L_1(p) \quad \mathbf{(2.3)}$$

Where p denotes the same rank in SO1 and SO2. A specific rank may correspond to 2 different spots in SO2 and SO1. Hence, the normalized $L_2(p)$ satisfies equation (2.2).

Let g be the normalized function, and let a and b be the ranks of a single spots in symmetrical images, then the

$$\text{Normalized ratio} = \frac{e^{g(a)}}{e^{g(b)}} = e^{g(a)-g(b)}$$

RT-PCR Primers/Annealing Temperatures:

G3PDH

Forward primer: 5'-CAAGGTCATCCCTGAGCTGAAC-3'

Reverse primer: 5'-TCGCTGTTGAAGTCAGAGGAGAC-3'

Annealing Temperature: 60°C

SN25

Forward primer: 5'-CAAGTTGGCTGATGAGTCGCTG-3'

Reverse primer: 5'-TGATTTGGTCCATCCCTTCCTC-3'

Annealing Temperature: 60°C

M6A

Forward primer: 5'-AATGCTGTATCAAATGCCTGGG-3'

Reverse primer: 5'-GCCATCTCAAATGTAGGTTTGAG-3'

Annealing Temperature: 60°C

143F

Forward primer: 5'-CCTACAAGAATGTGGTTGGTGCC-3'

Reverse primer: 5'-GCAAAGTGTCTCCAGCTCCTTCTC-3'

Annealing Temperature: 60°C

CHIN

Forward primer: 5'-CCATCCAAAGAGTCTTGGTCAGG-3'

Reverse primer: 5'-GTTGCCAGATTGTCACAGACGAC-3'

Annealing Temperature: 60°C

CALM

Forward primer: 5'-TGGCTGACCAACTGACTGAAGAG-3'

Reverse primer: 5'-GTA ACTCTGCTTCTGTGGGATTCTG-3'

Annealing Temperature: 60°C

MYPR

Forward primer: 5'-CTCAAAGGGTACTTCCACTGATGG-3'

Reverse primer: 5'-CAATAGGCAGATTTGGGCAAAC-3'

Annealing Temperature: 60°C

TBB3

Forward primer: 5'-ATGGGCACGTTGCTCATCAG-3'

Reverse primer: 5'-TCGTTGTCGATGCAGTAGGTCTC-3'

Annealing Temperature: 60°C

HB2J

Forward primer: 5'-TGGTCTGCTCTGTGAGTGGTTTC-3'

Reverse primer: 5'-TGTTTCCAGCATCACCAGGGTC-3'

Annealing Temperature: 60°C

K2C8

Forward primer: 5'-CCATTAAGGATGCCAACGCC-3'

Reverse primer: 5'-GACGTTTCATCAGCTCCTGGTACTC-3'

Annealing Temperature: 60°C

MT2

Forward primer: 5'-GCAAATGCACCTCCTGCAAG-3'

Reverse primer: 5'-CGTTCTTTACATCTGGGAGCGG-3'

Annealing Temperature: 60°C

RLA1

Forward primer: 5'-CATTCTGCACGACGATGAGGTG-3'

Reverse primer: 5'-CAGATGAGGCTCCCAATGTTGAC-3'

Annealing Temperature: 60°C

PTPZ

Forward primer: 5'-AAACCTCGTGGAGAAAGGAAGG-3'

Reverse primer: 5'-GCGTG TAGTGATACTGTGTGACCAC-3'

Annealing Temperature: 60°C

EAT1

Forward primer: 5'-TGTGAGGACAGACAGAAGGCAAAG-3'

Reverse primer: 5'-TGGGCTGGAAGAGACCATGAAGAC-3'

Annealing Temperature: 60°C

TBB5

Forward primer: 5'-GAGTTCCCAGACCGCATCATG-3'

Reverse primer: 5'-GATGTCGTAGAGTGCCTCGTTGTC-3'

Annealing Temperature: 60°C

OSTP

Forward primer: 5'-TGCAGCCTTCTCAGCCAAAC-3'

Reverse primer: 5'-CCACAGCATCTGGGTATTTGTTG-3'

Annealing Temperature: 60°C

AMO2

Forward primer: 5'-TGTGCCAGGACTCTTTTCTTCC-3'

Reverse primer: 5'-AAGGTTCAAGTGTCCCCTGTGTCAG-3'

Annealing Temperature: 60°C

PTRR

Forward primer: 5'-TCAAGGACGCTGTGCTCTACTCTG-3'

Reverse primer: 5'-CCAGGAAGTAAAGGAAGAAGGTCAC-3'

Annealing Temperature: 60°C

SPCO

Forward primer: 5'-TCAGGGTGTTTGGCATGTCC-3'

Reverse primer: 5'-TGTGGGAGGAGATGAAGACCAC-3'

Annealing Temperature: 60°C

ANX5

Forward primer: 5'-CCCTCATCAGAGTCATGGTTTCC-3'

Reverse primer: 5'-TCATCTTCTCCACAGAGCAGCAG-3'

Annealing Temperature: 58°C

RL10

Forward primer: 5'-AATTCGGCATGAGGGACCAC-3'

Reverse primer: 5'-AATCTTGGCATCAGGGACCAC-3',

Annealing Temperature: 56°C

MAPB

Forward primer: 5'-CGCTGAACAATTACCTGCCAAATG-3'

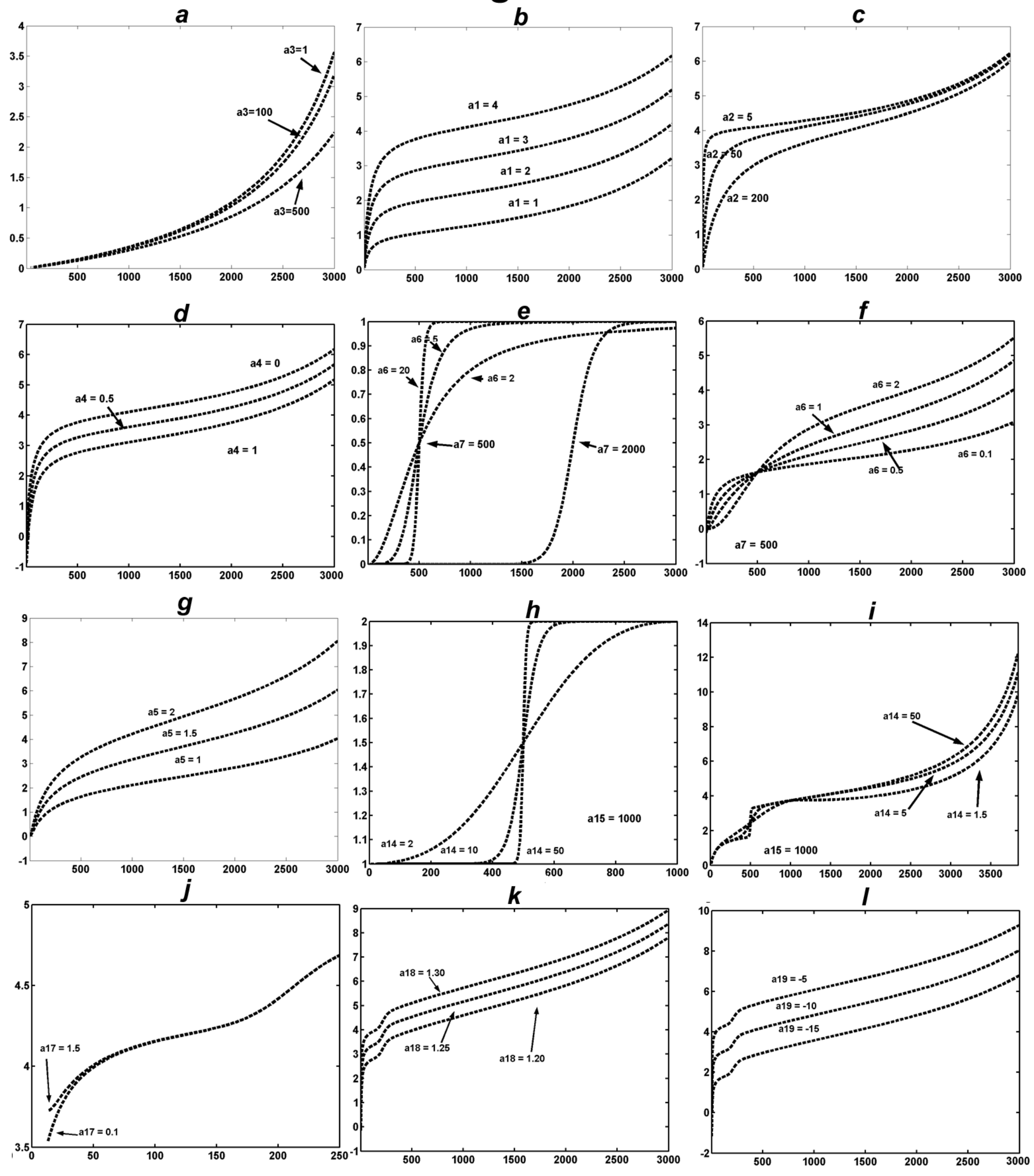
Reverse primer: 5'-CCTAGCAGAAGTCAGTTGTGTTGG-3'

Annealing Temperature: 60°C

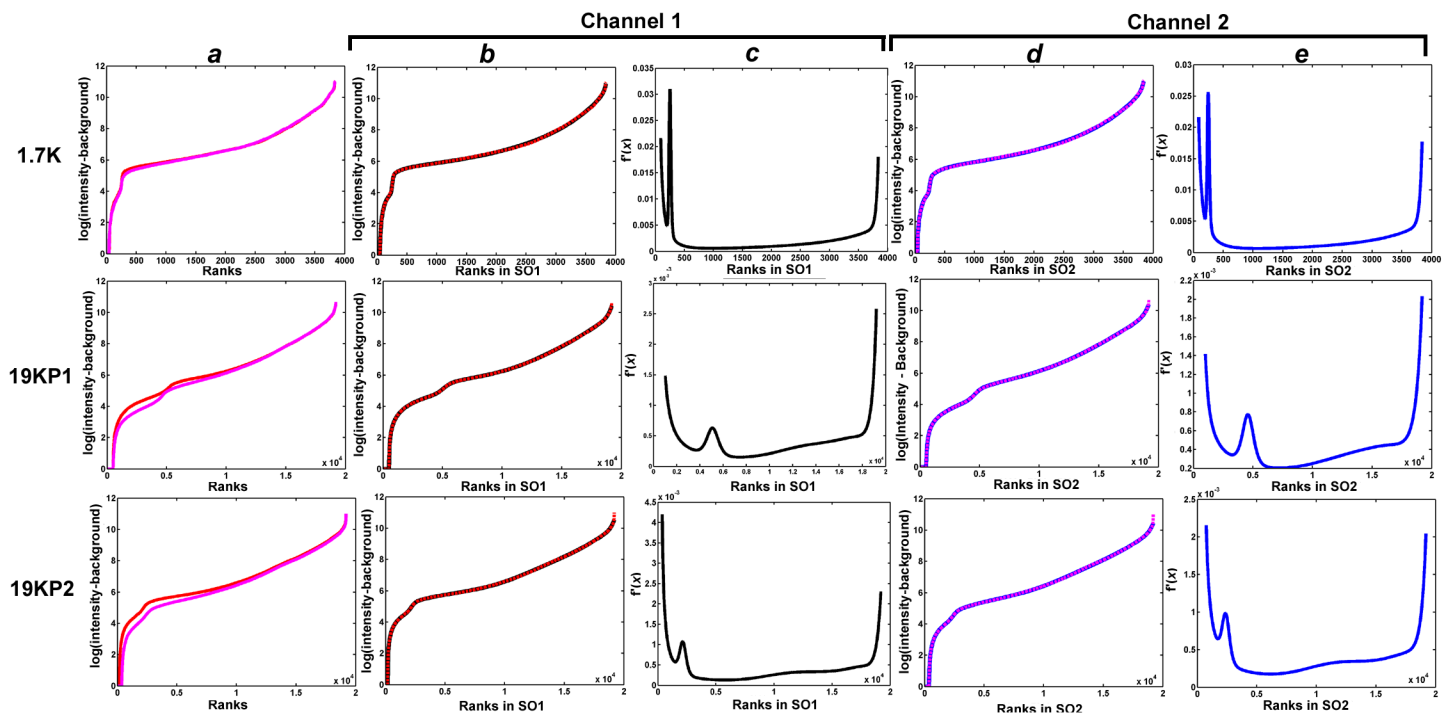
Legend of Web Figure 3

The algorithm is applied to analyze the same-to-same (split-control) data of Rosenzweig et al. (Environmental Health Perspectives 112:480-487, 2004). H001451, H001476, H001488, H001494 are the symmetrical sets (dye swap) of H001452, H001477, H001489 H001495, respectively. The Figure plots the raw data (black and magenta) and curve fits (red and blue) of the Cy3 (black and red) and Cy5 (magenta and blue) images. The green arrows point to the CR.

Web Figure 1



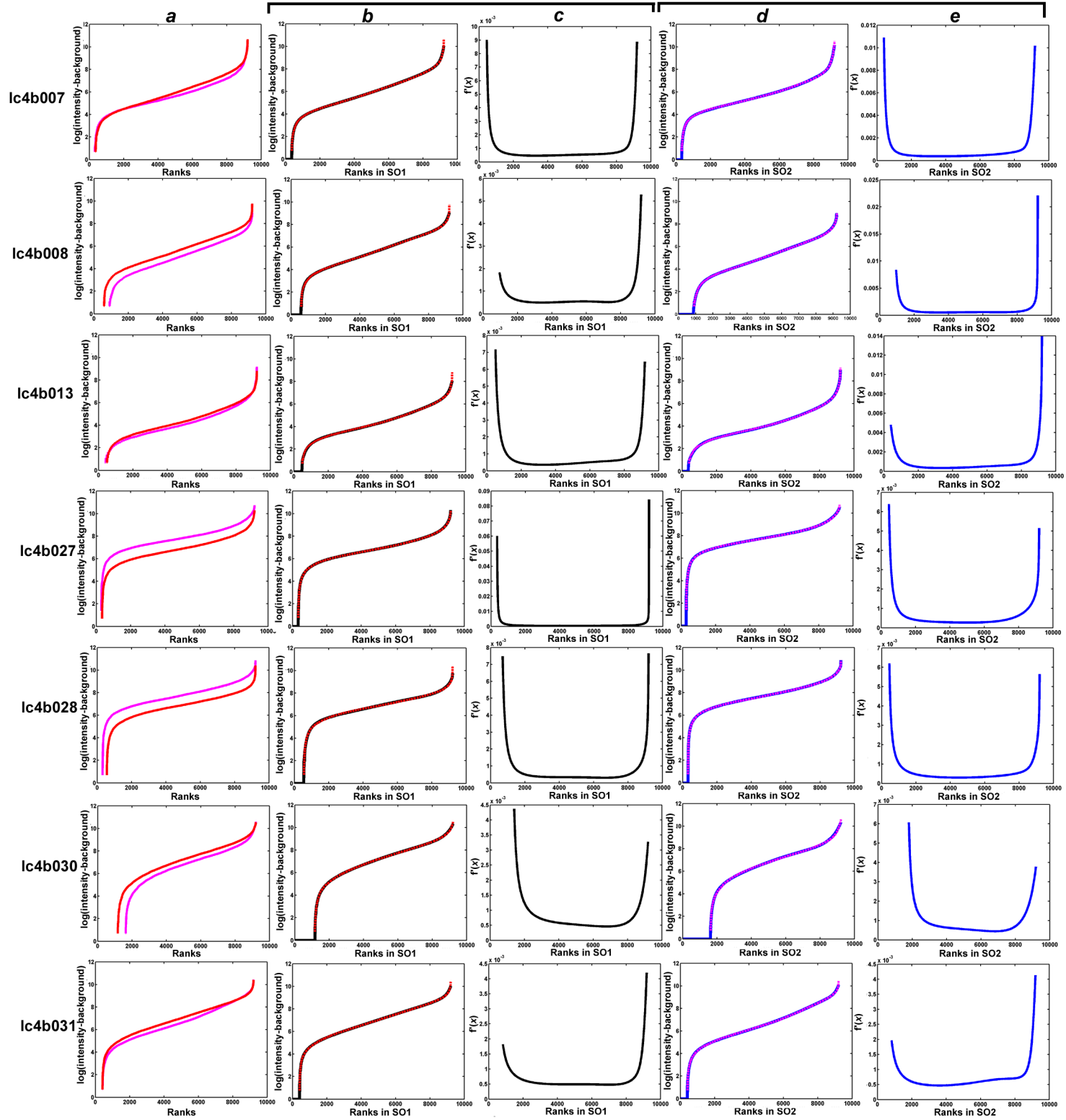
Web Figure 2



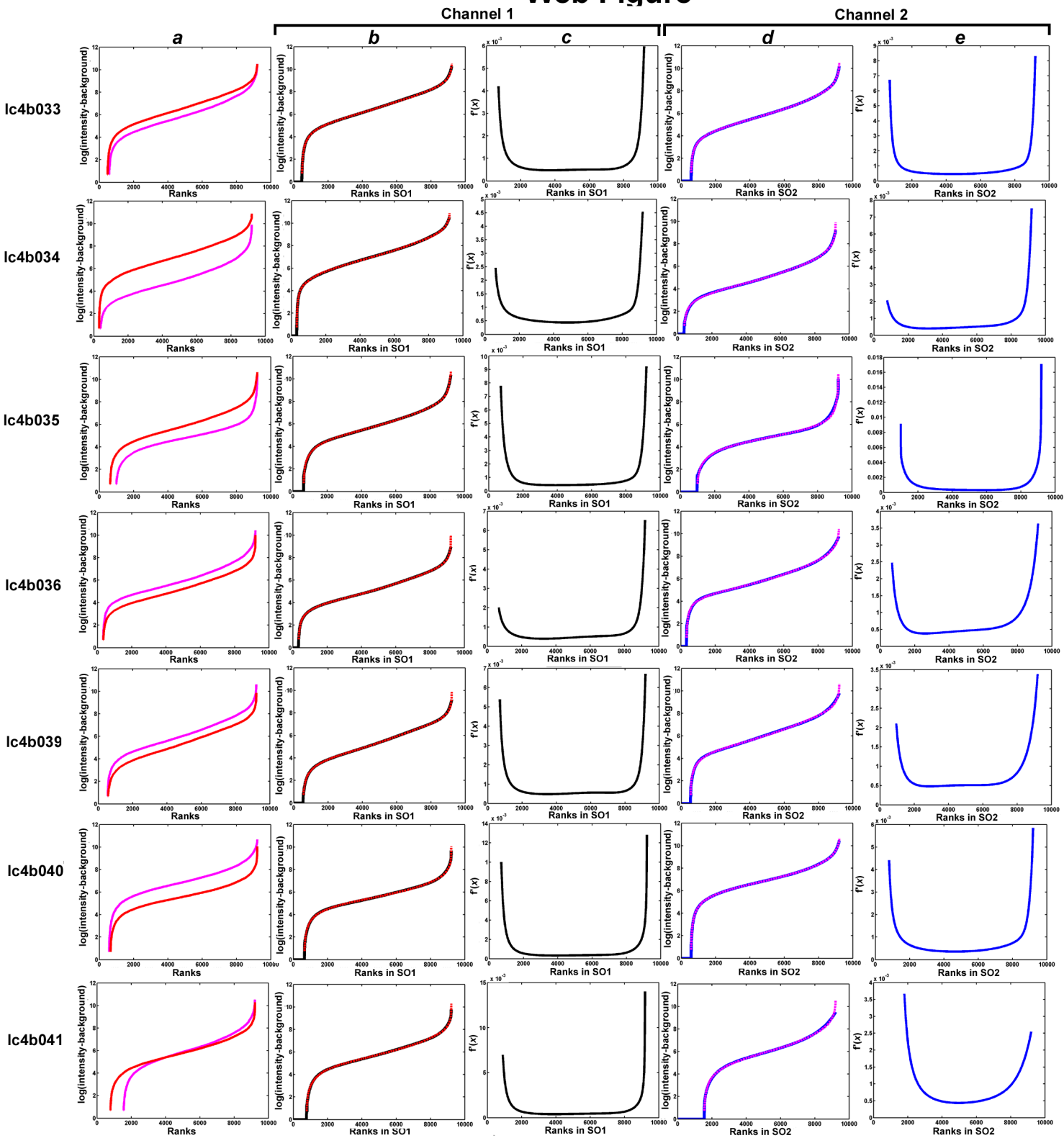
Web Figure

Channel 1

Channel 2



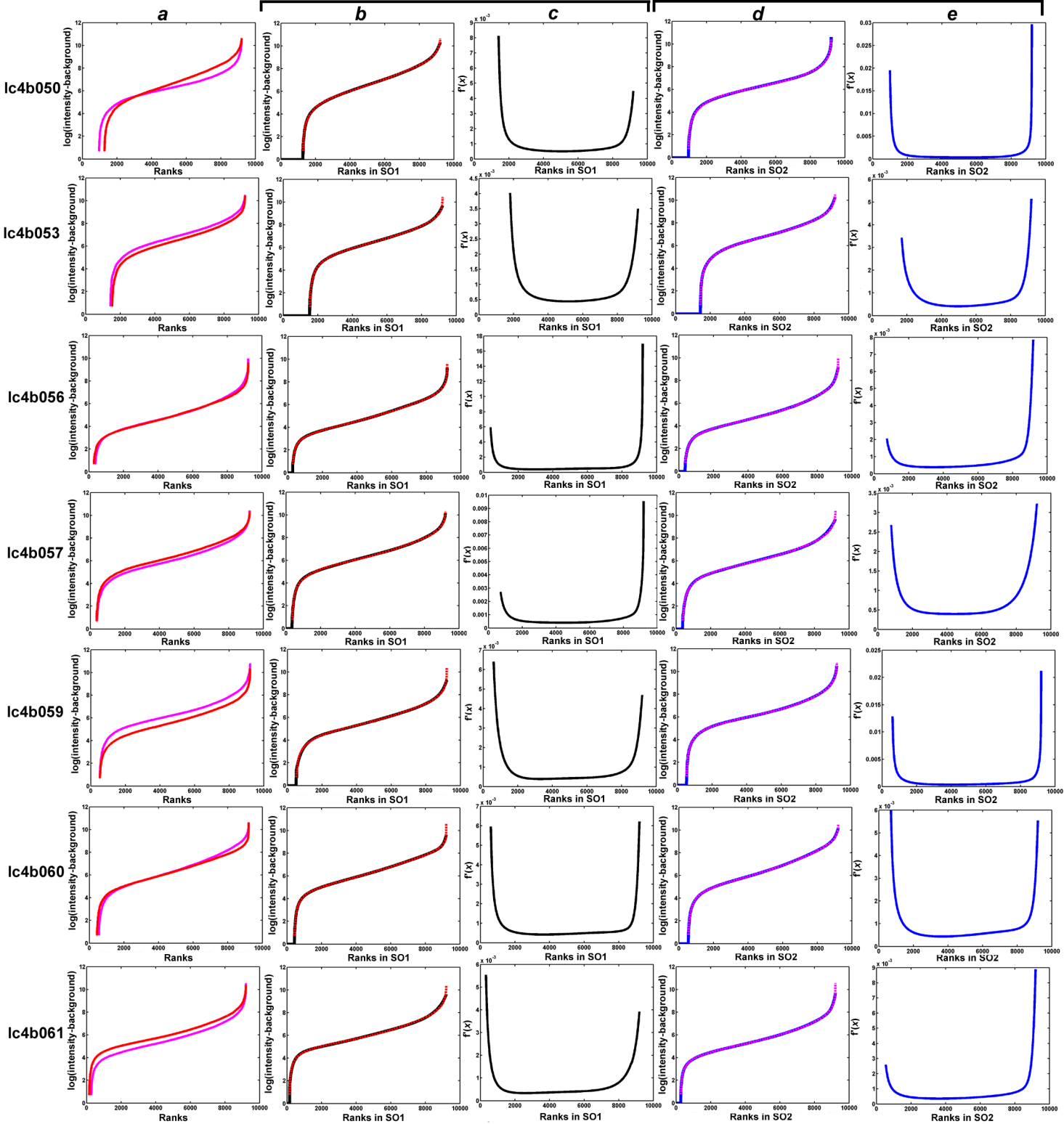
Web Figure



Web Figure

Channel 1

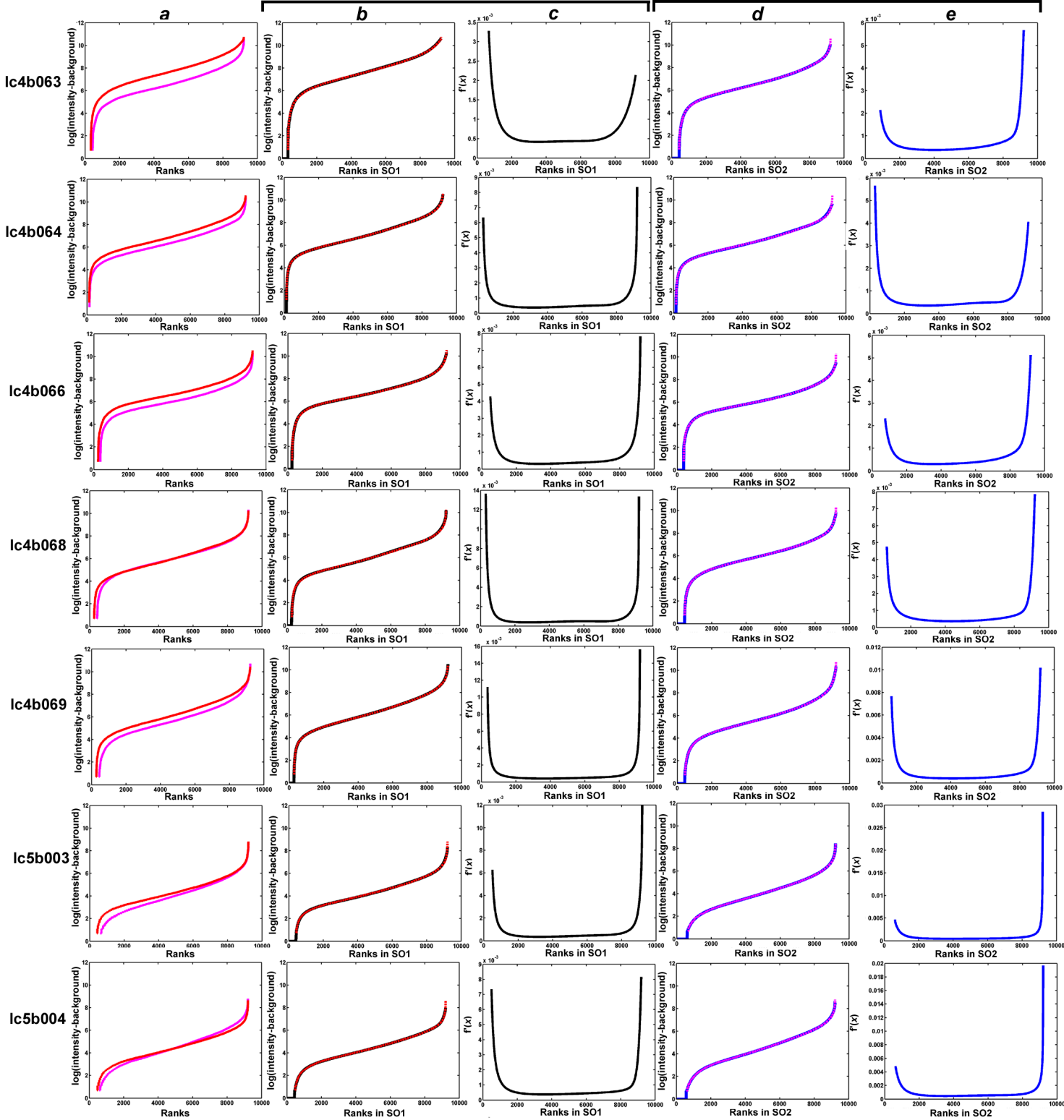
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Web Figure

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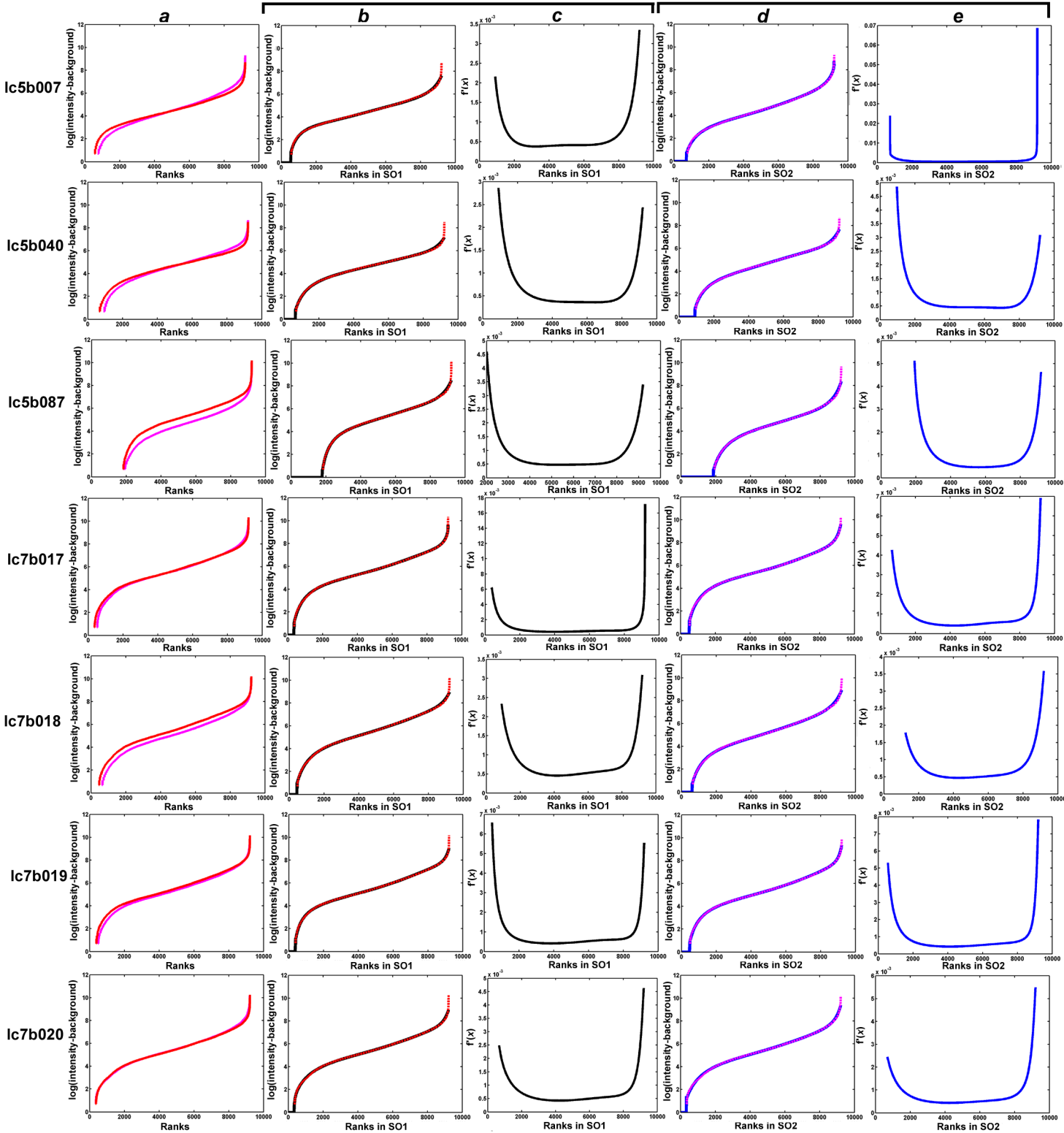
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Web Figure

Channel 1

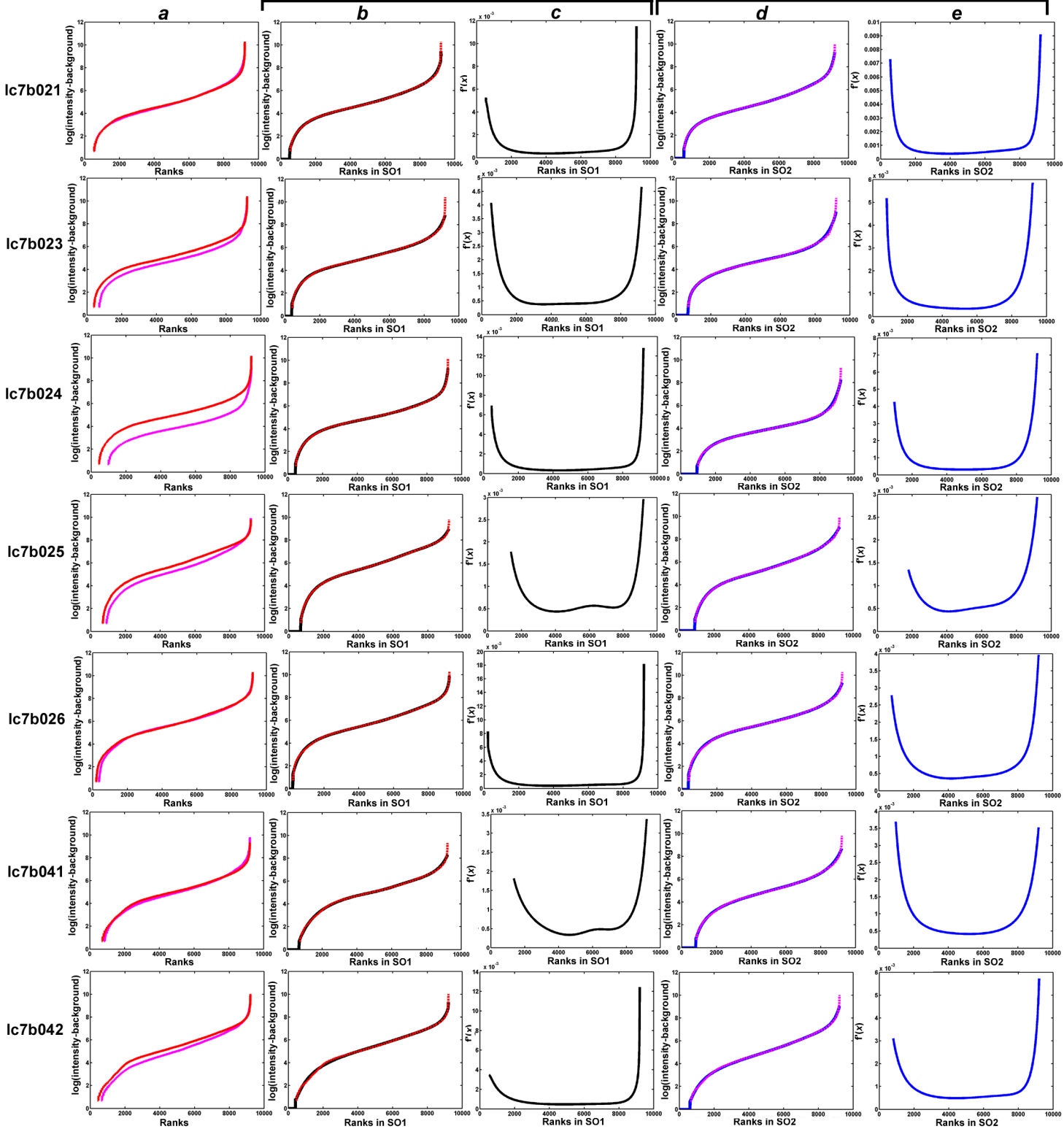
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Web Figure

Channel 1

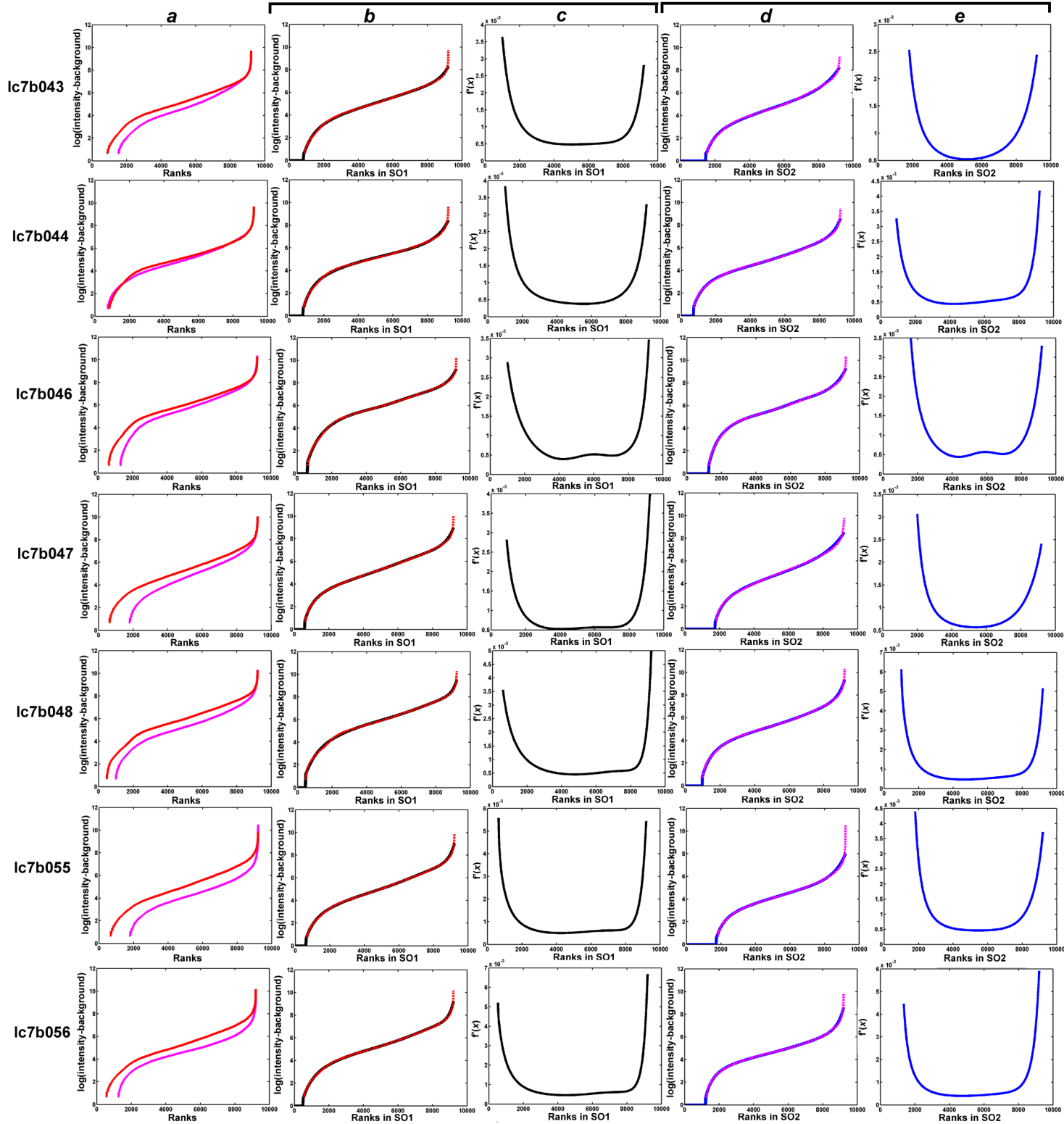
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Web Figure

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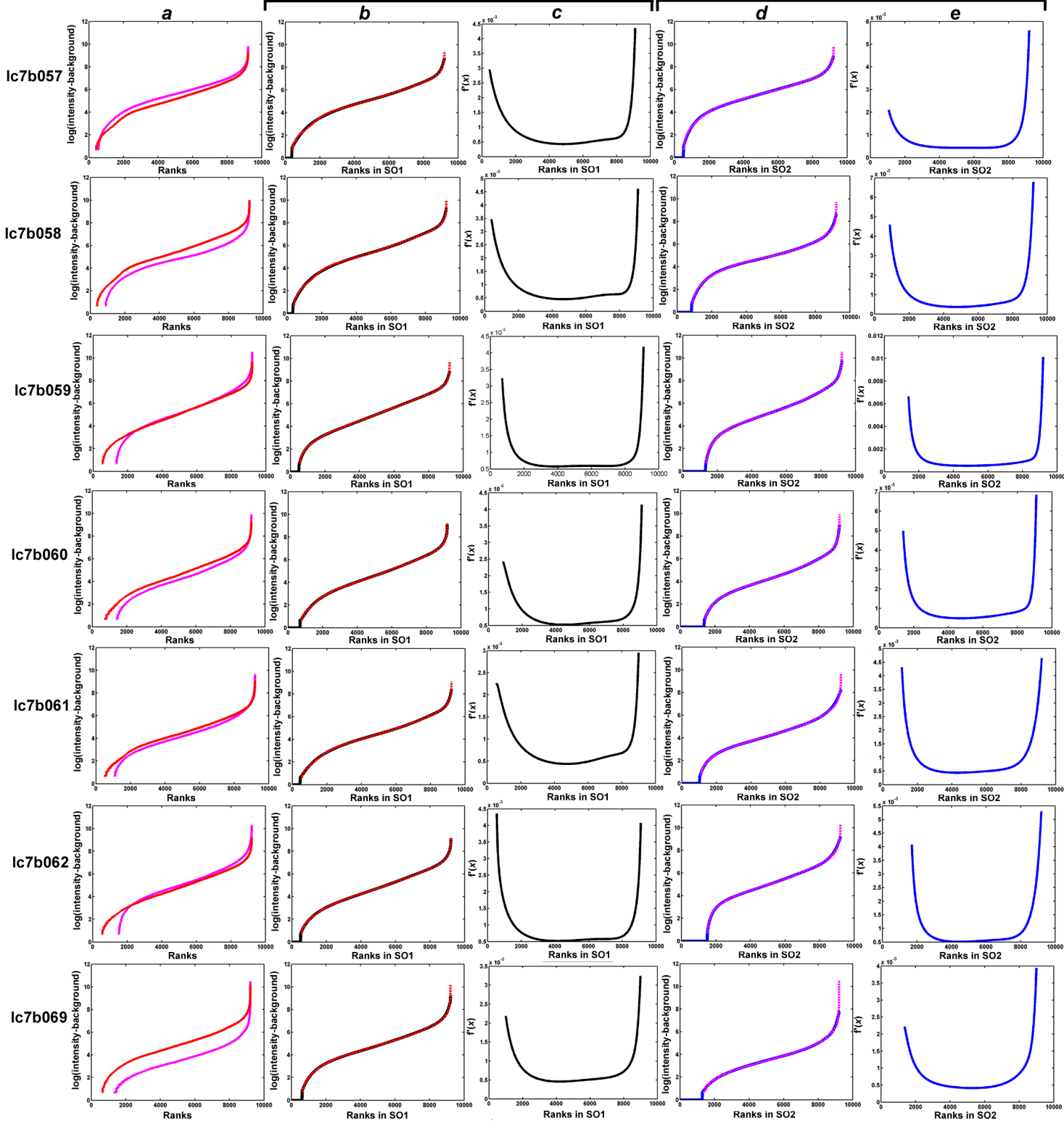
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Web Figure

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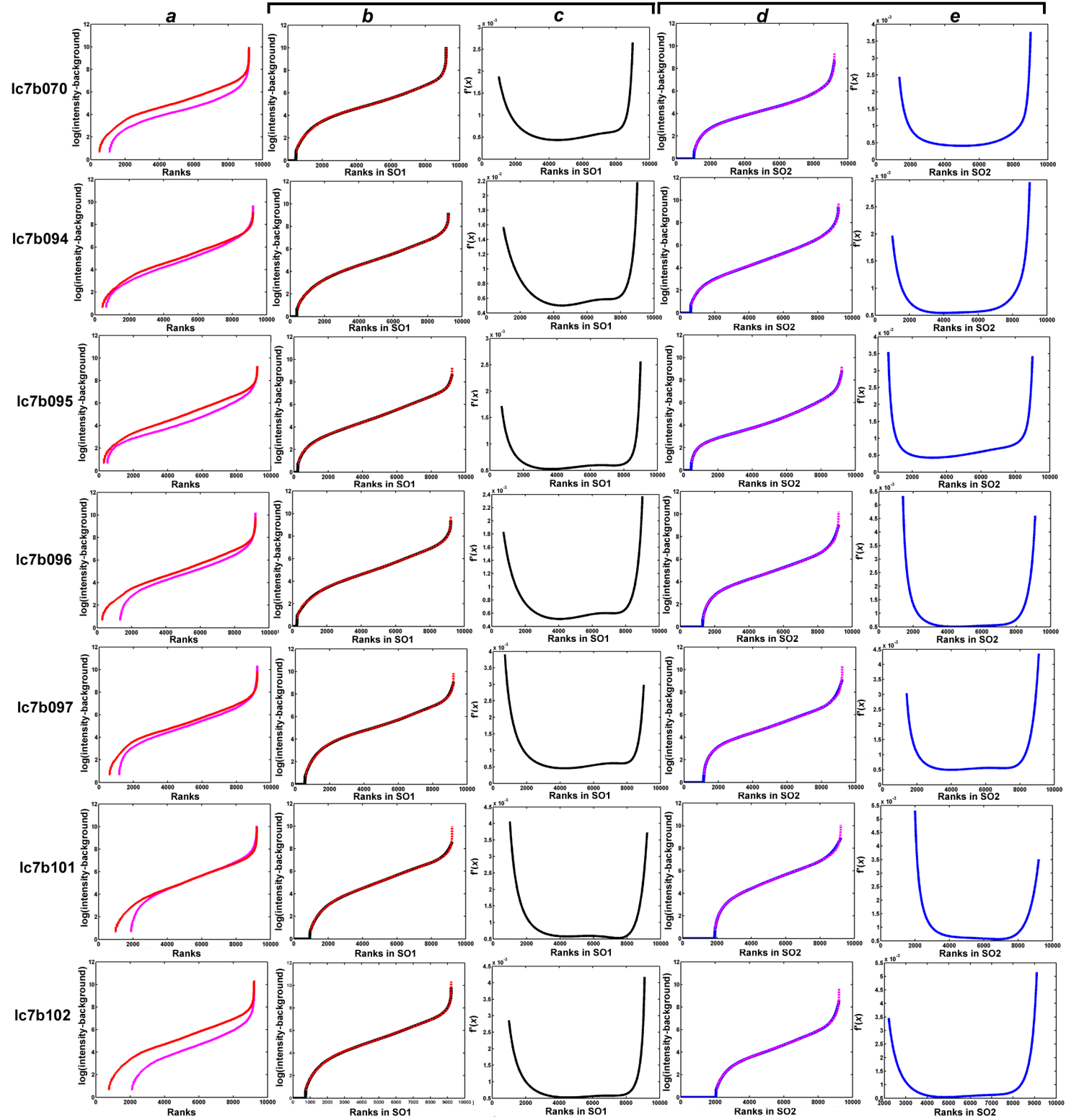
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Web Figure

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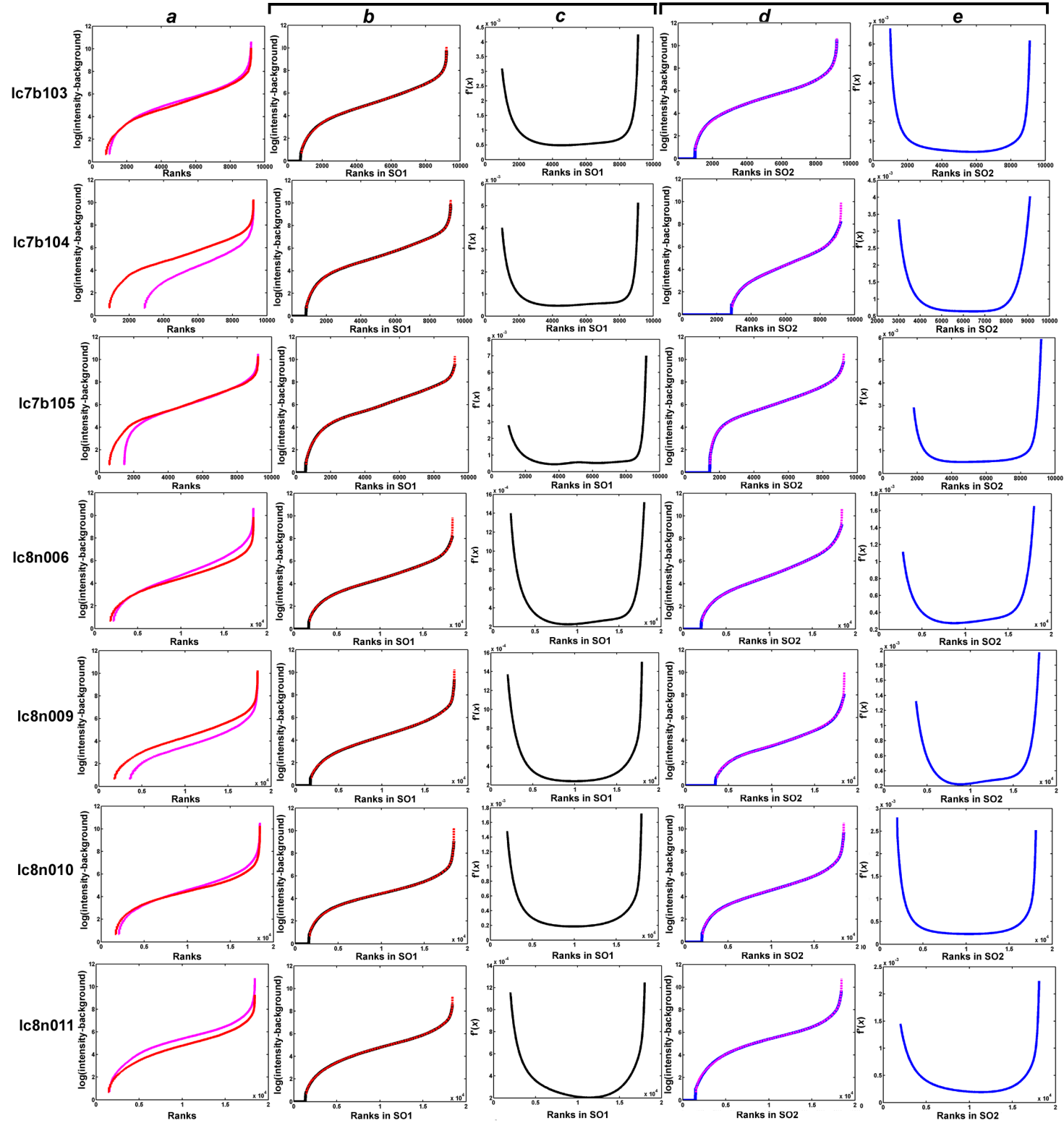
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Web Figure

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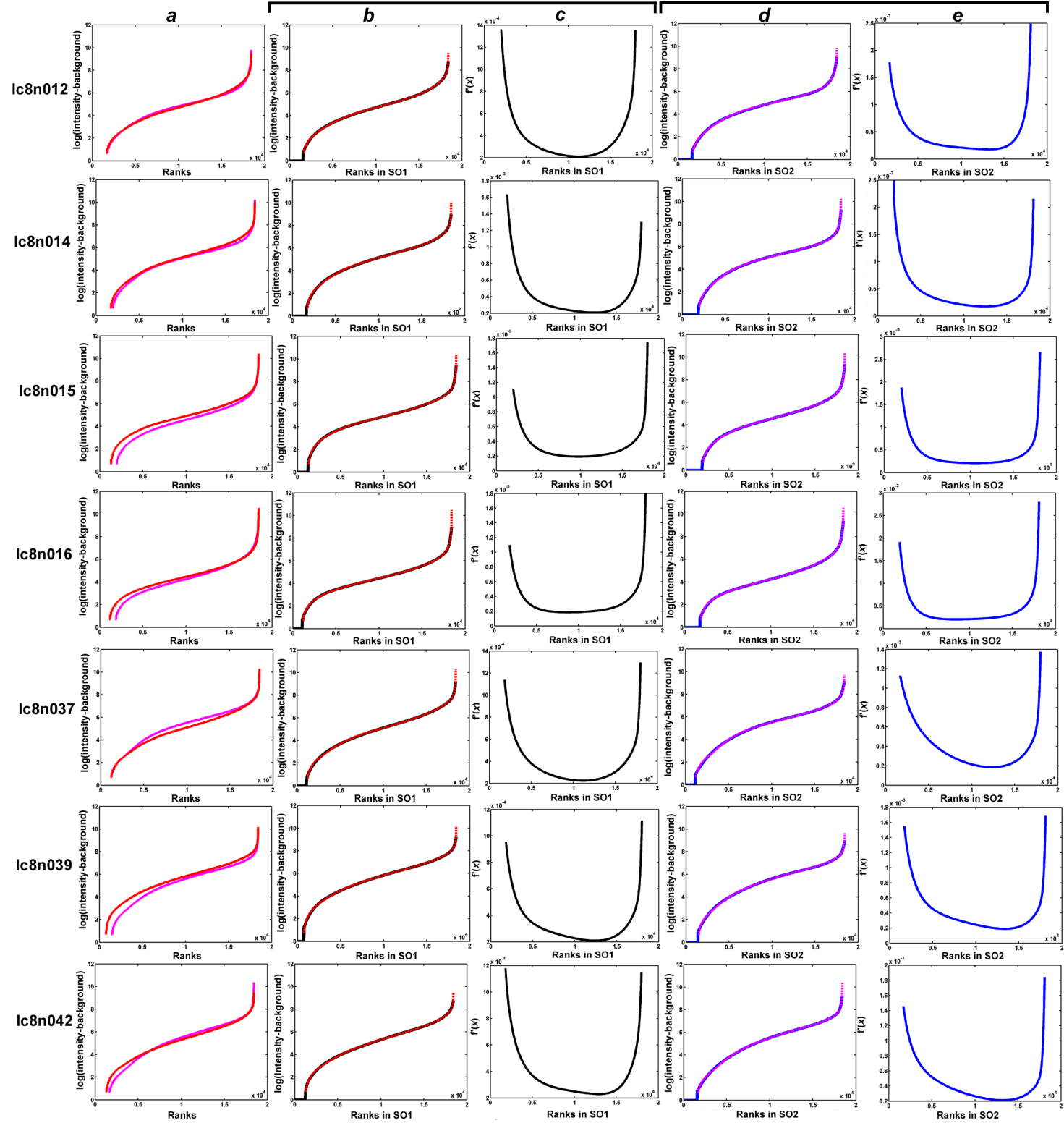
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Web Figure

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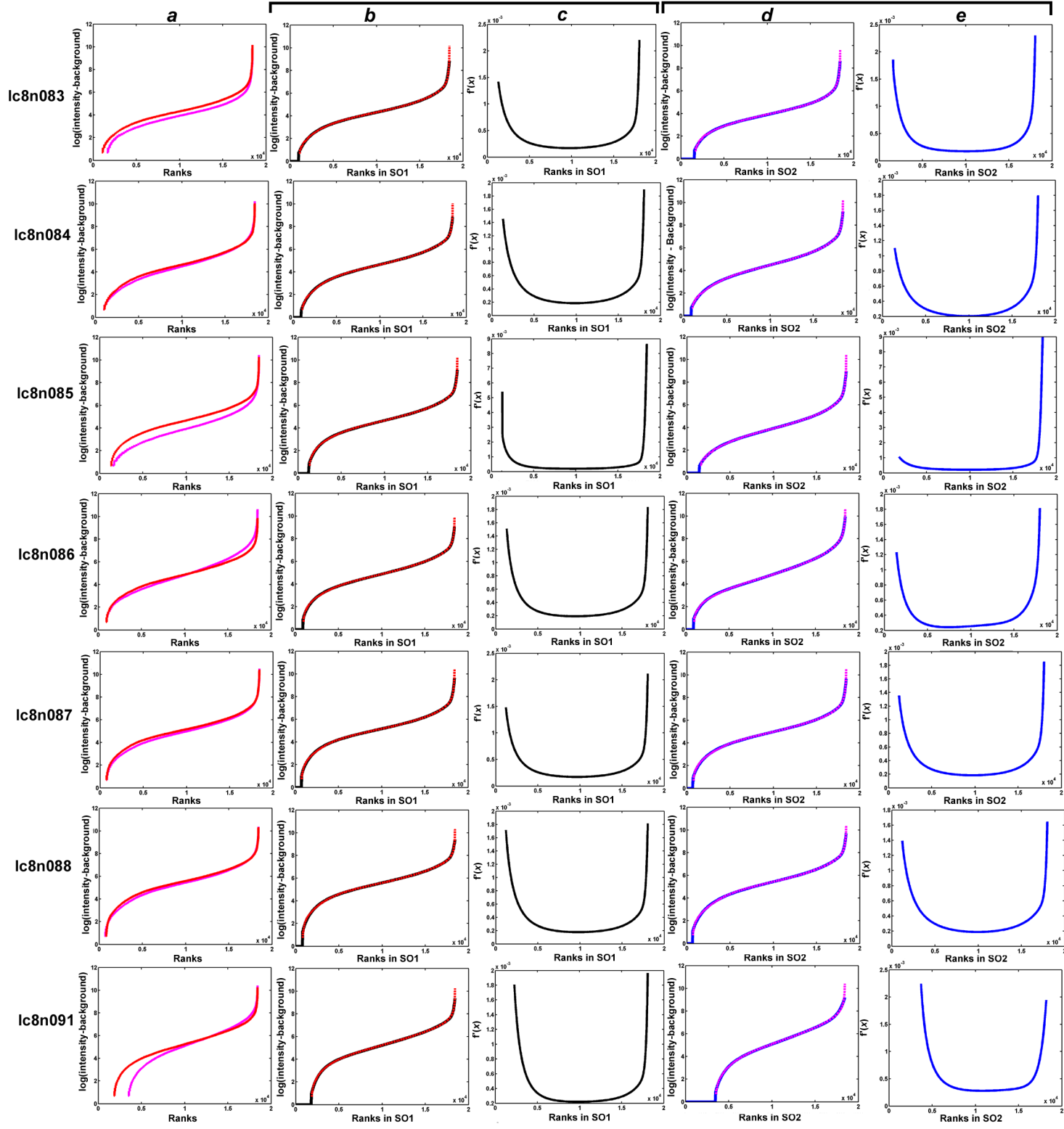
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Web Figure

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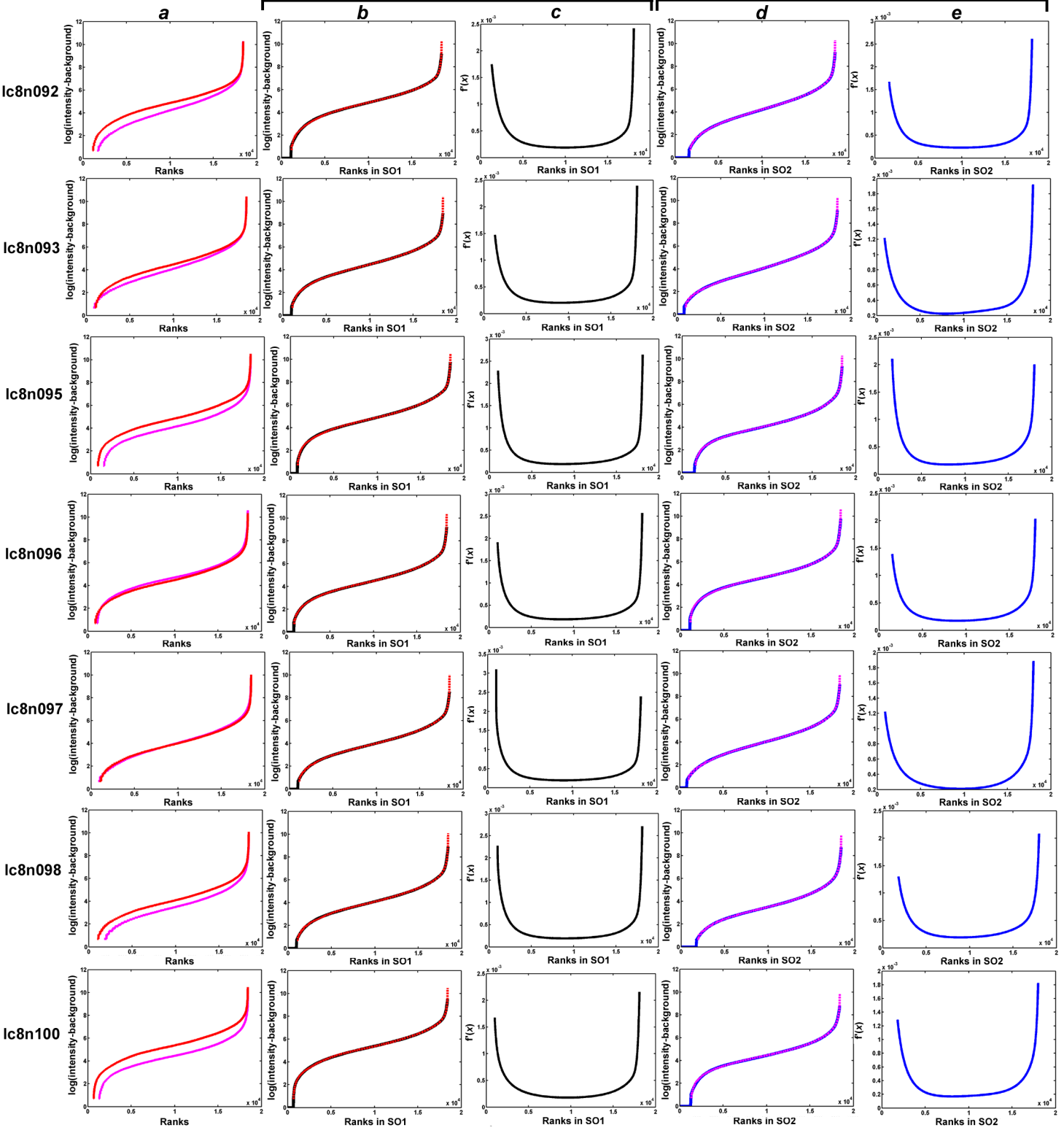
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Web Figure

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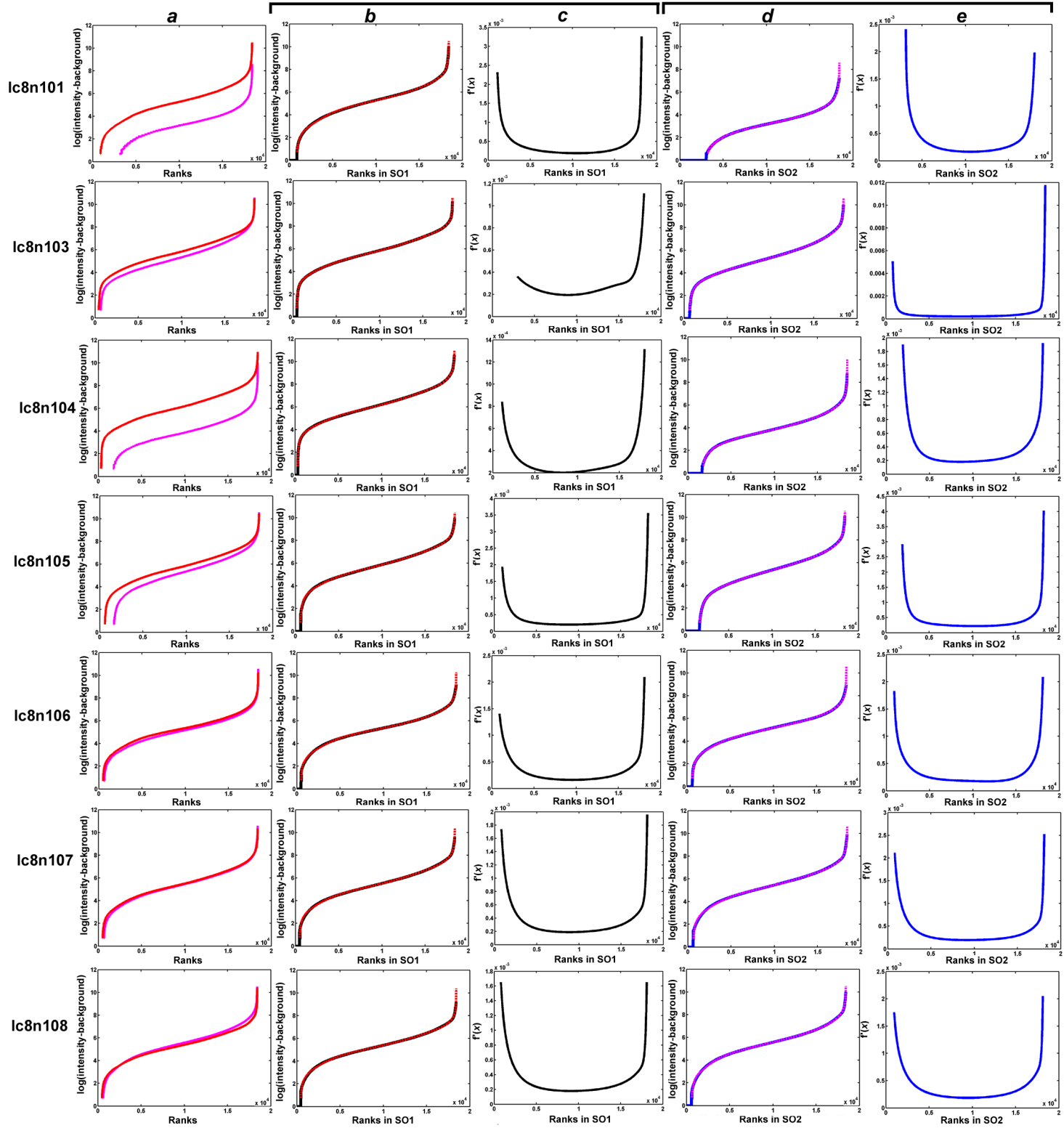
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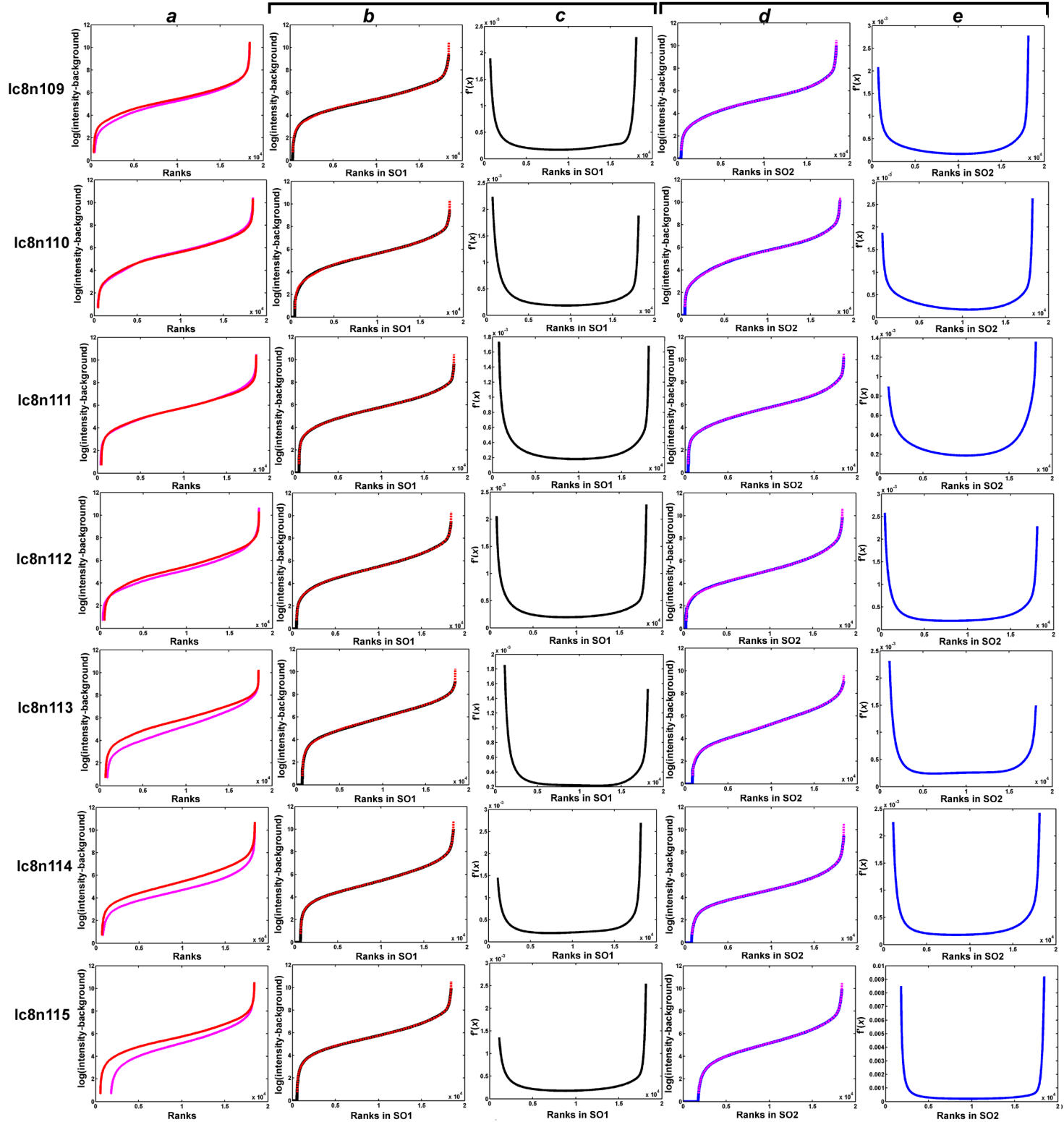
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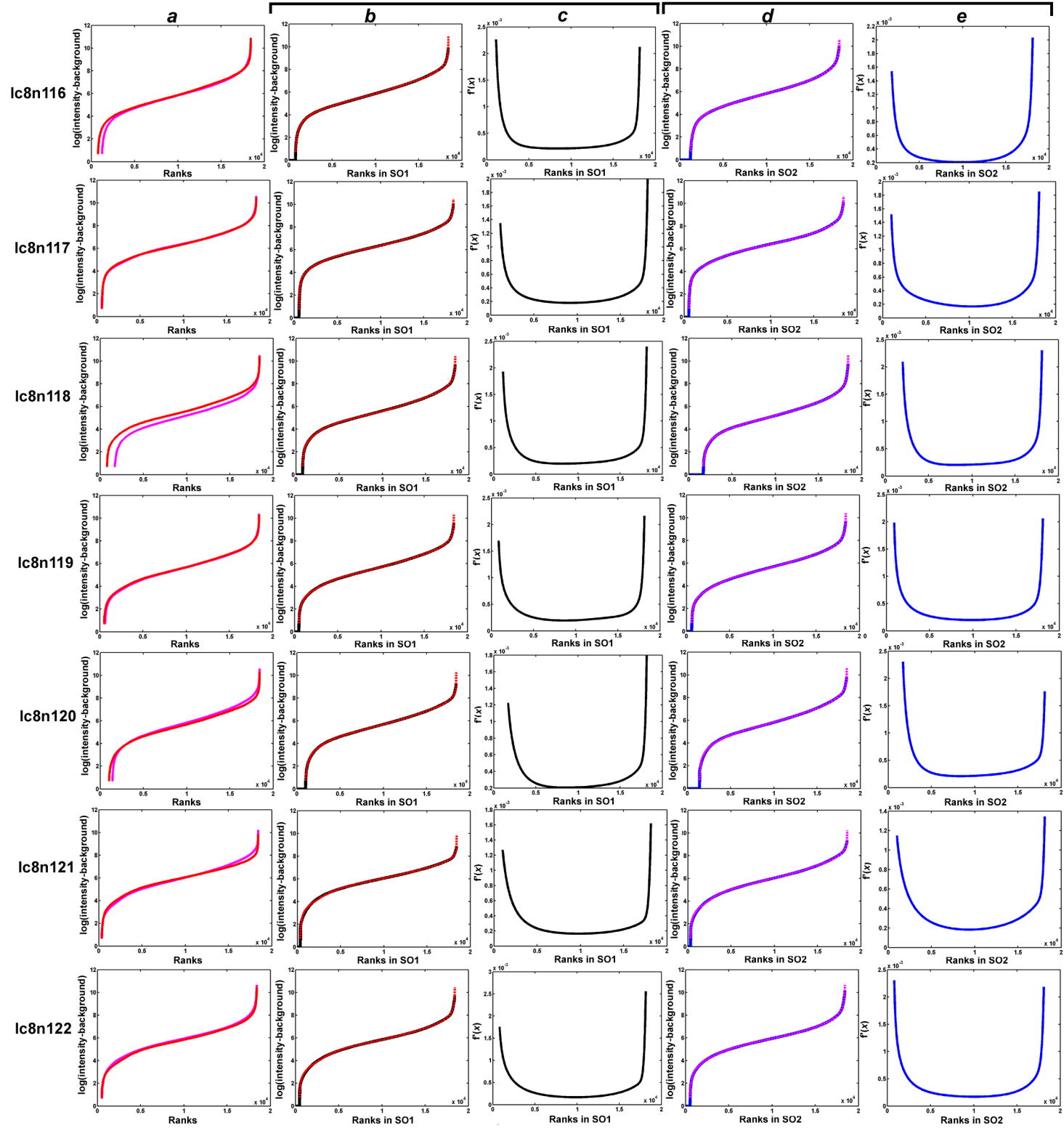
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Web Figure

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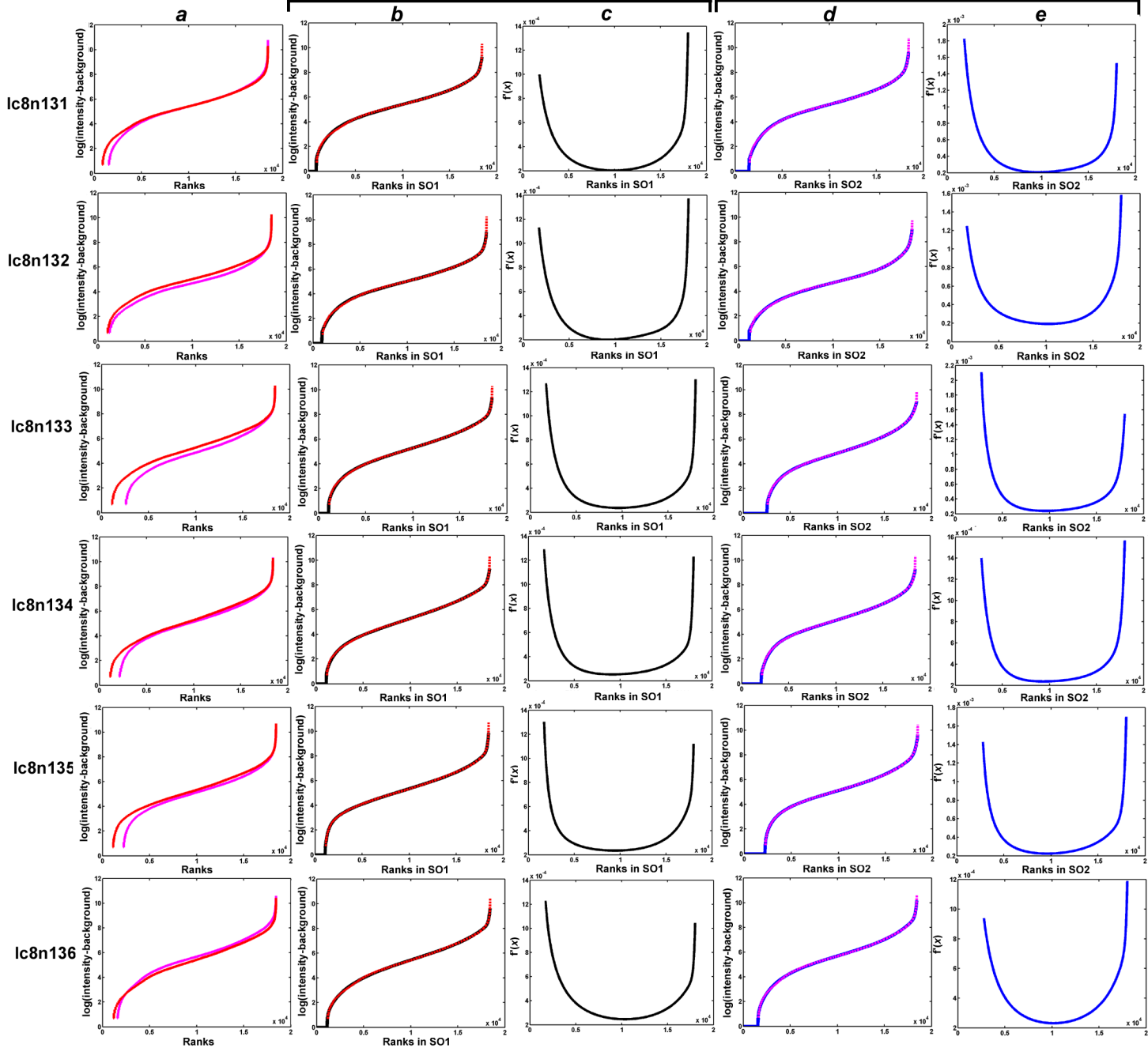
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Web Figure

Channel 1

Channel 2

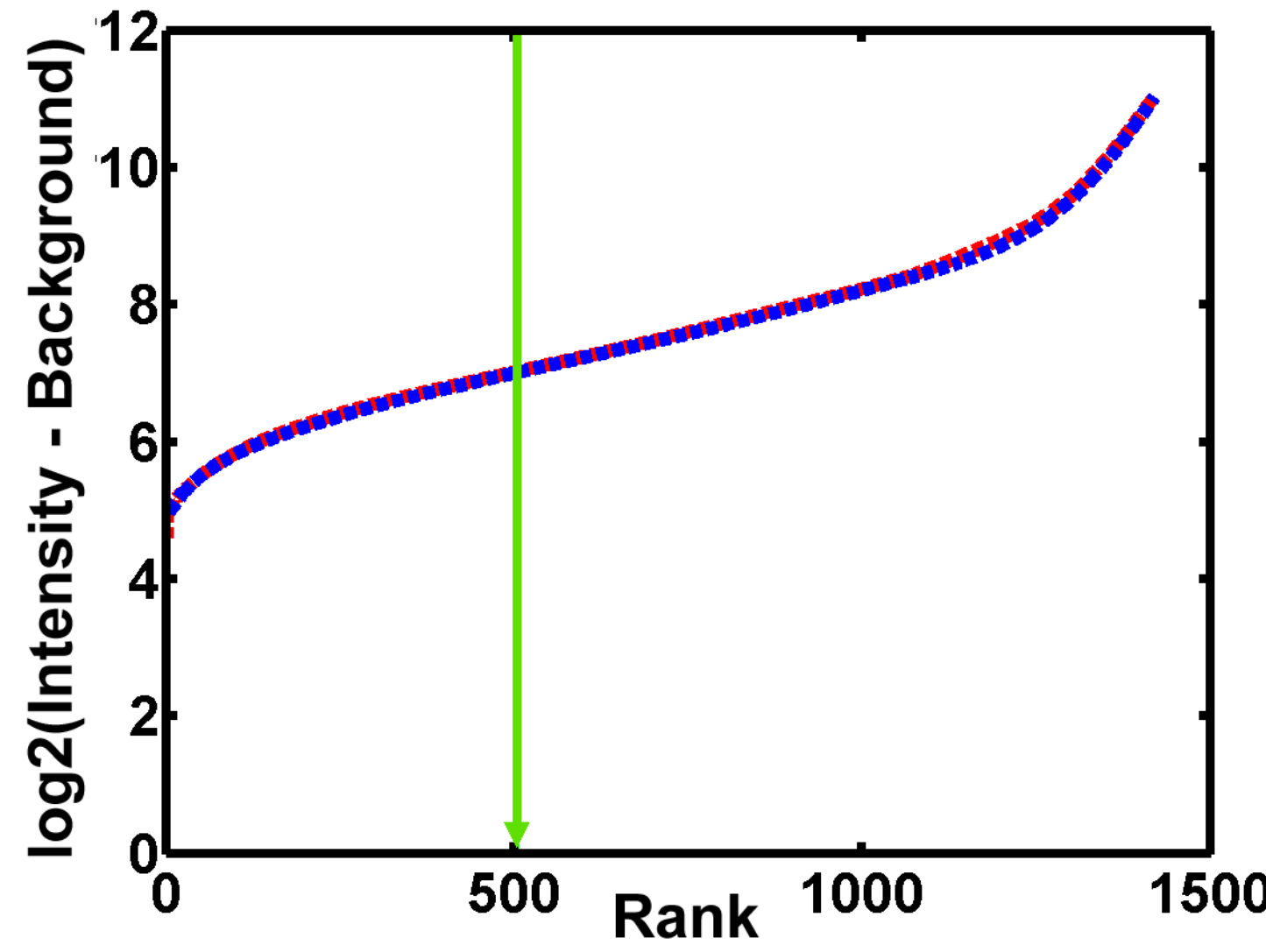
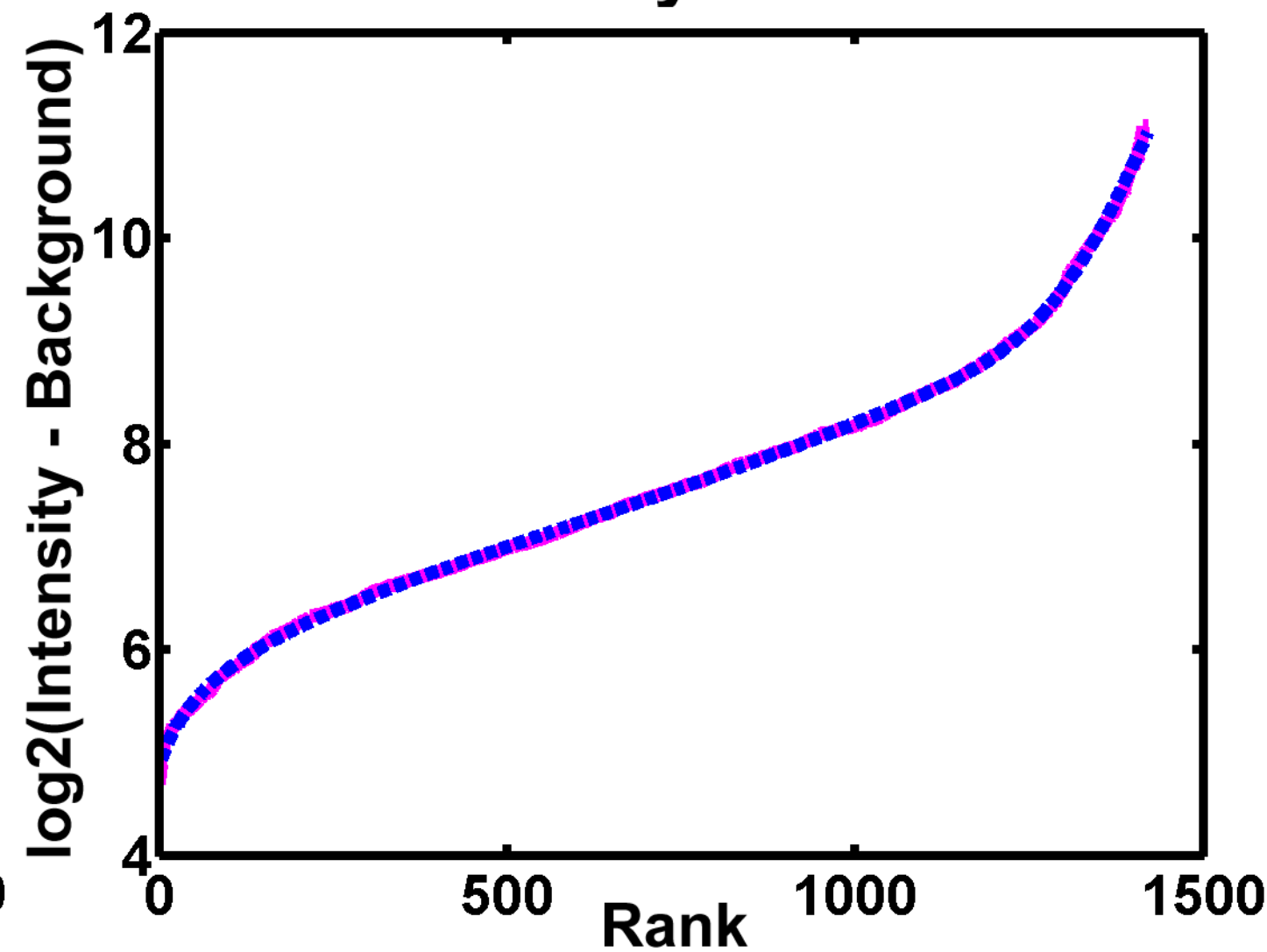
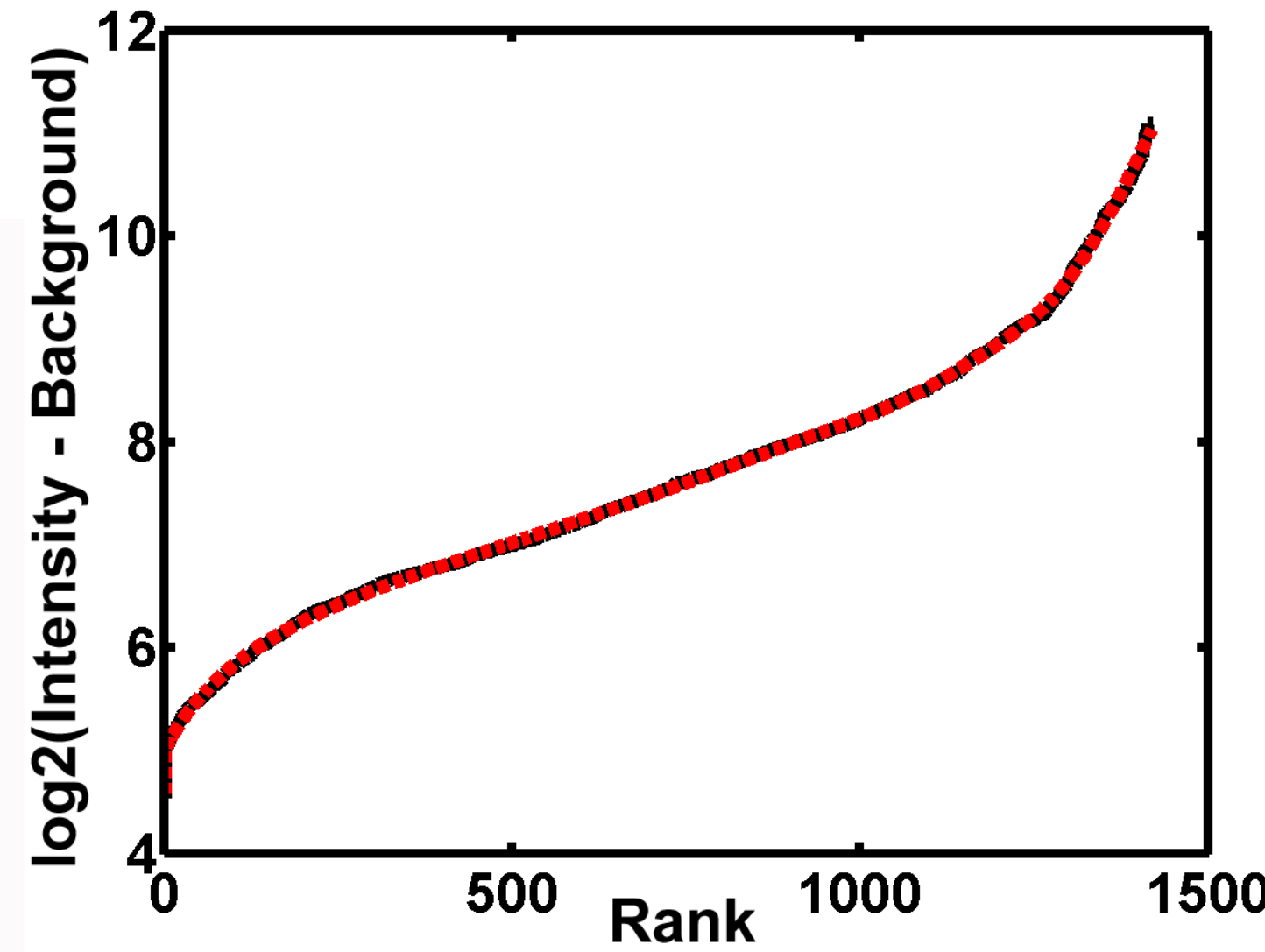


Web Figure 3

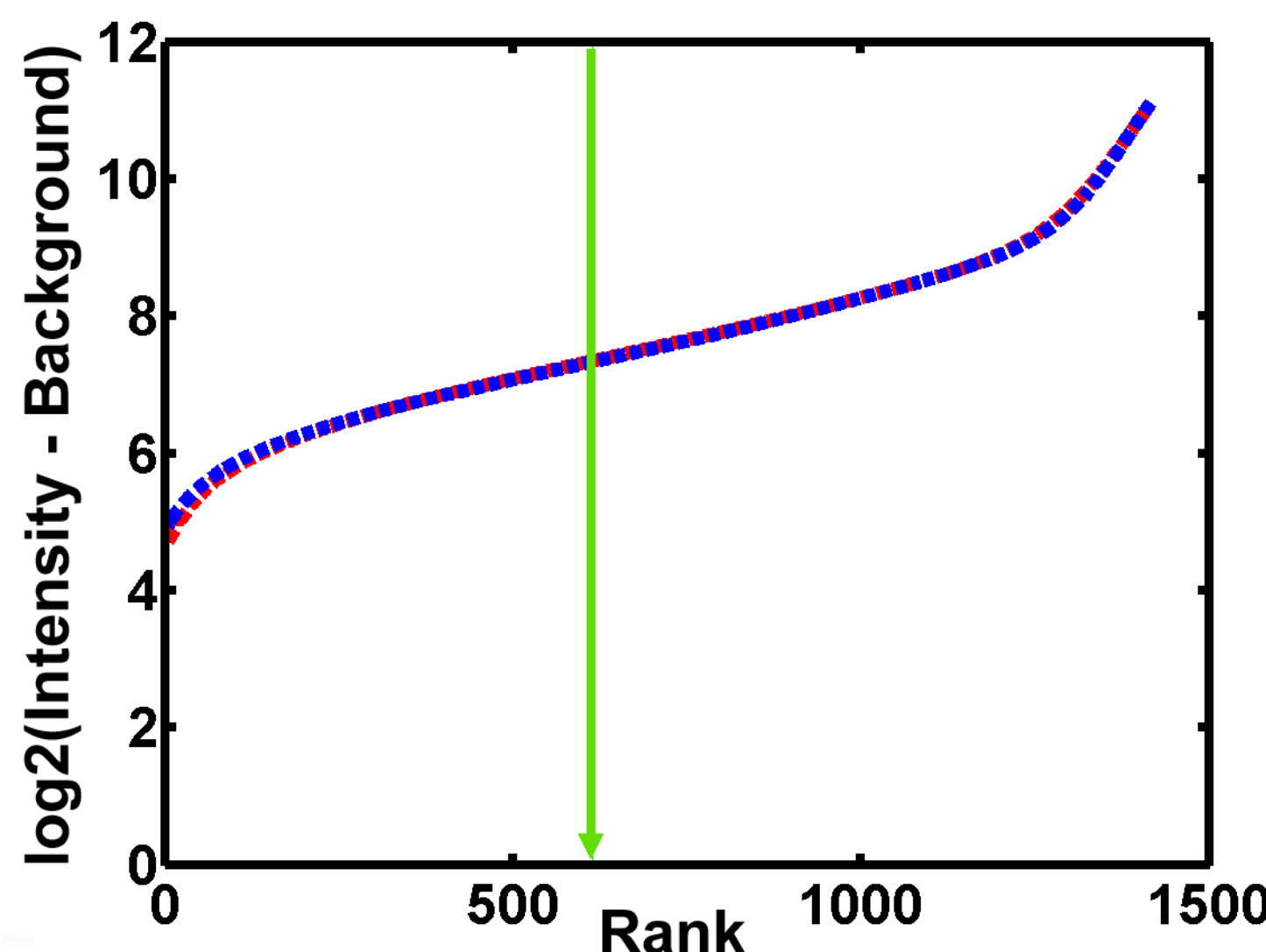
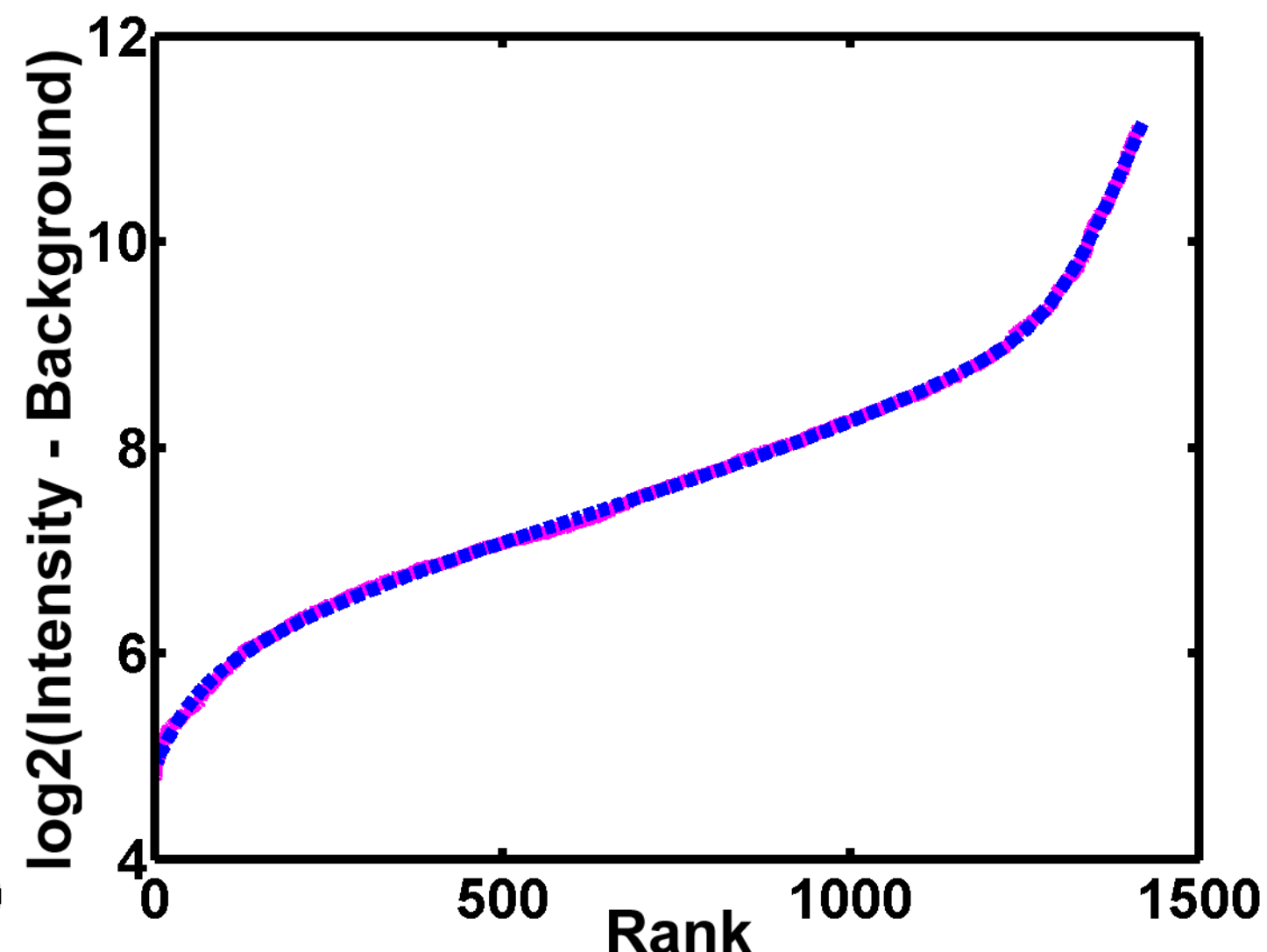
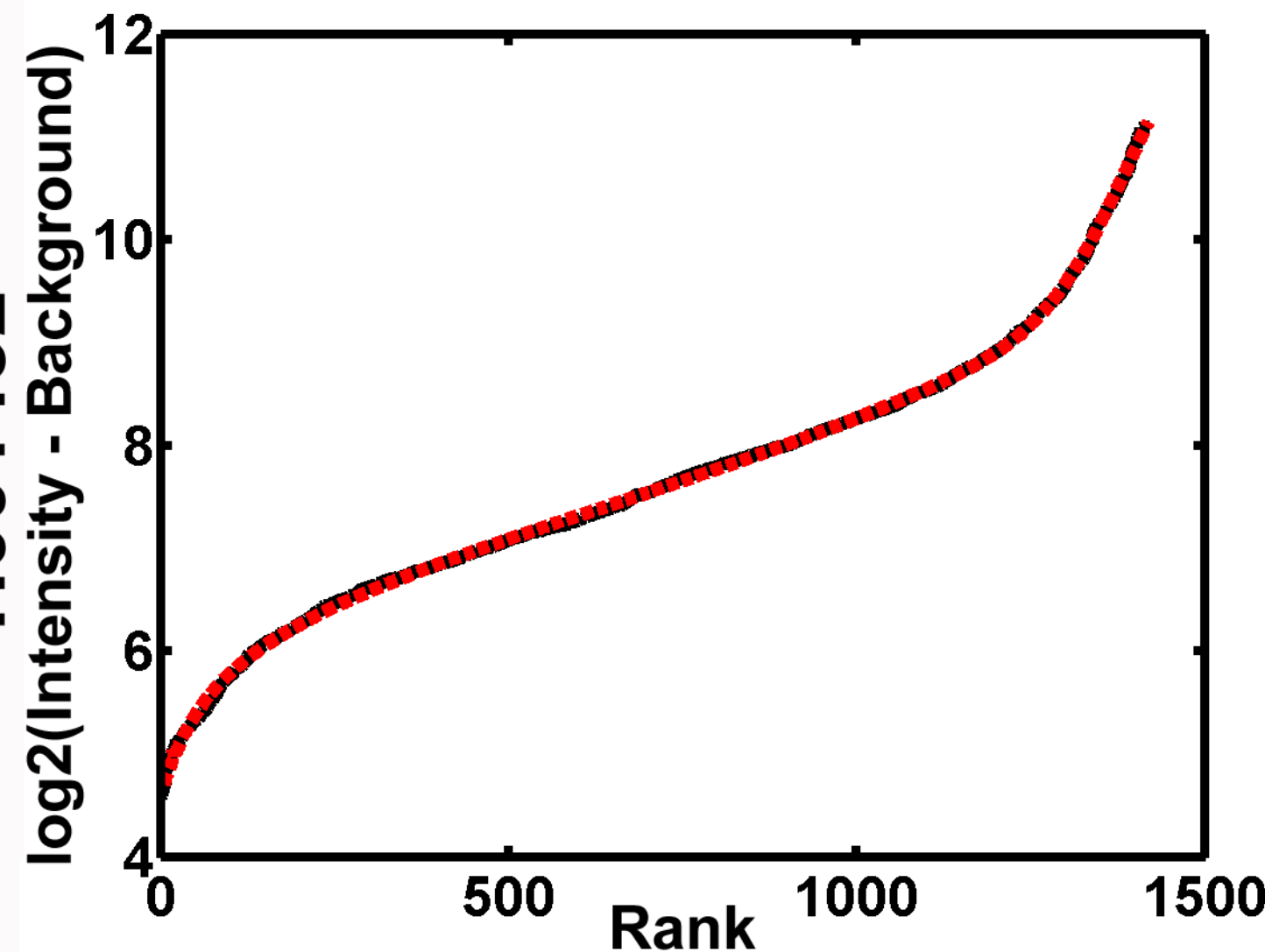
Cy3

Cy5

H001451



H001452

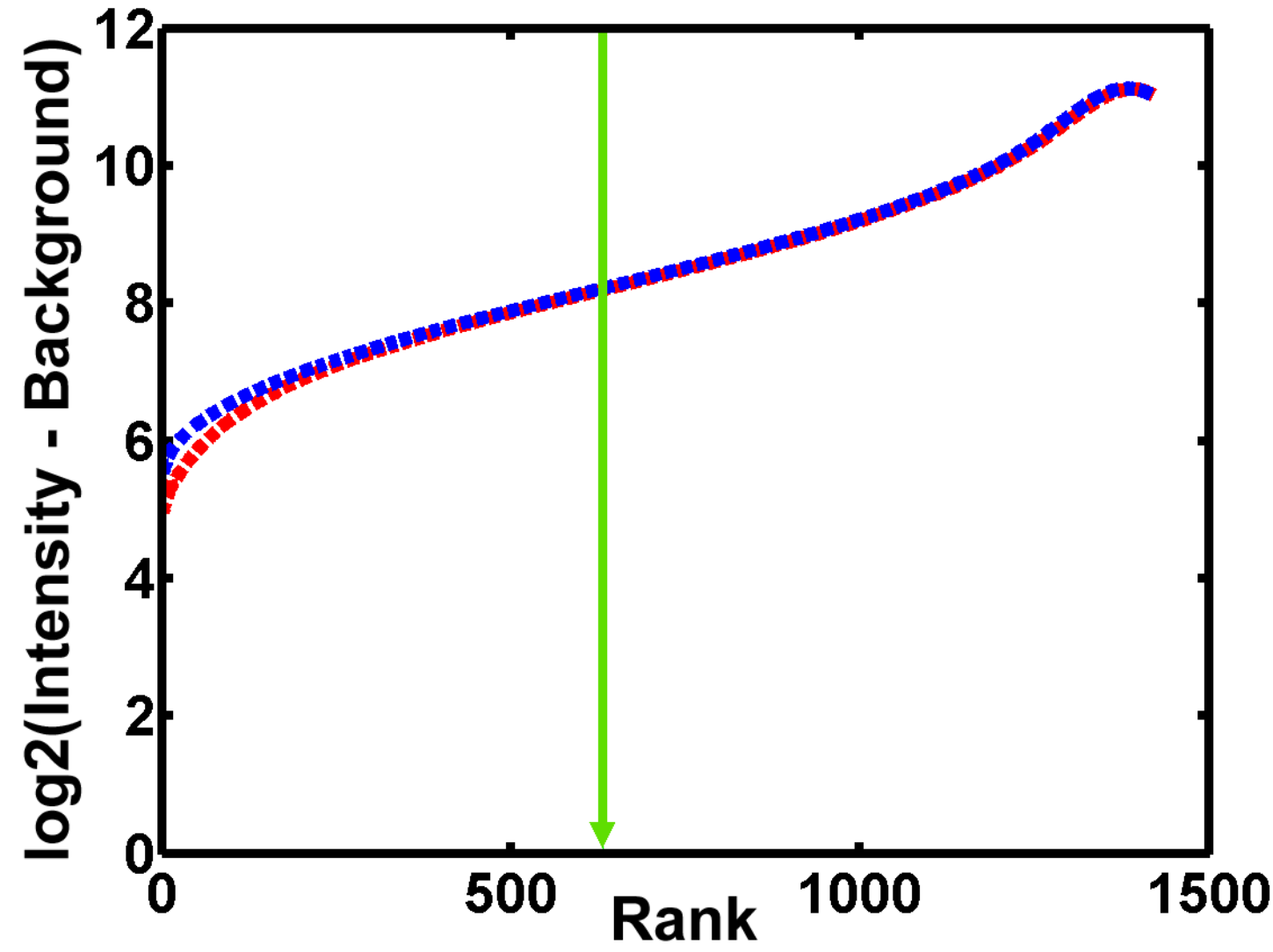
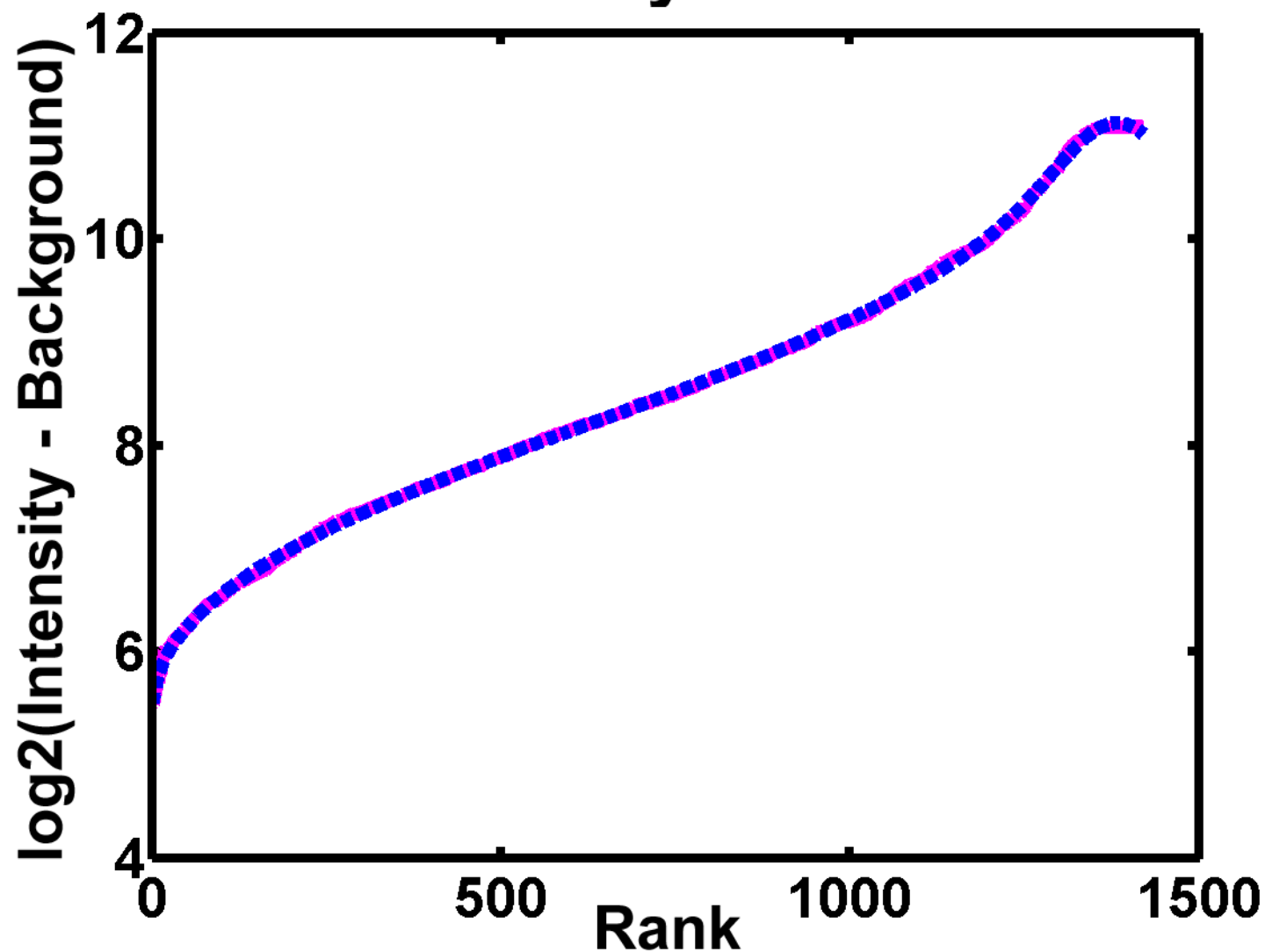
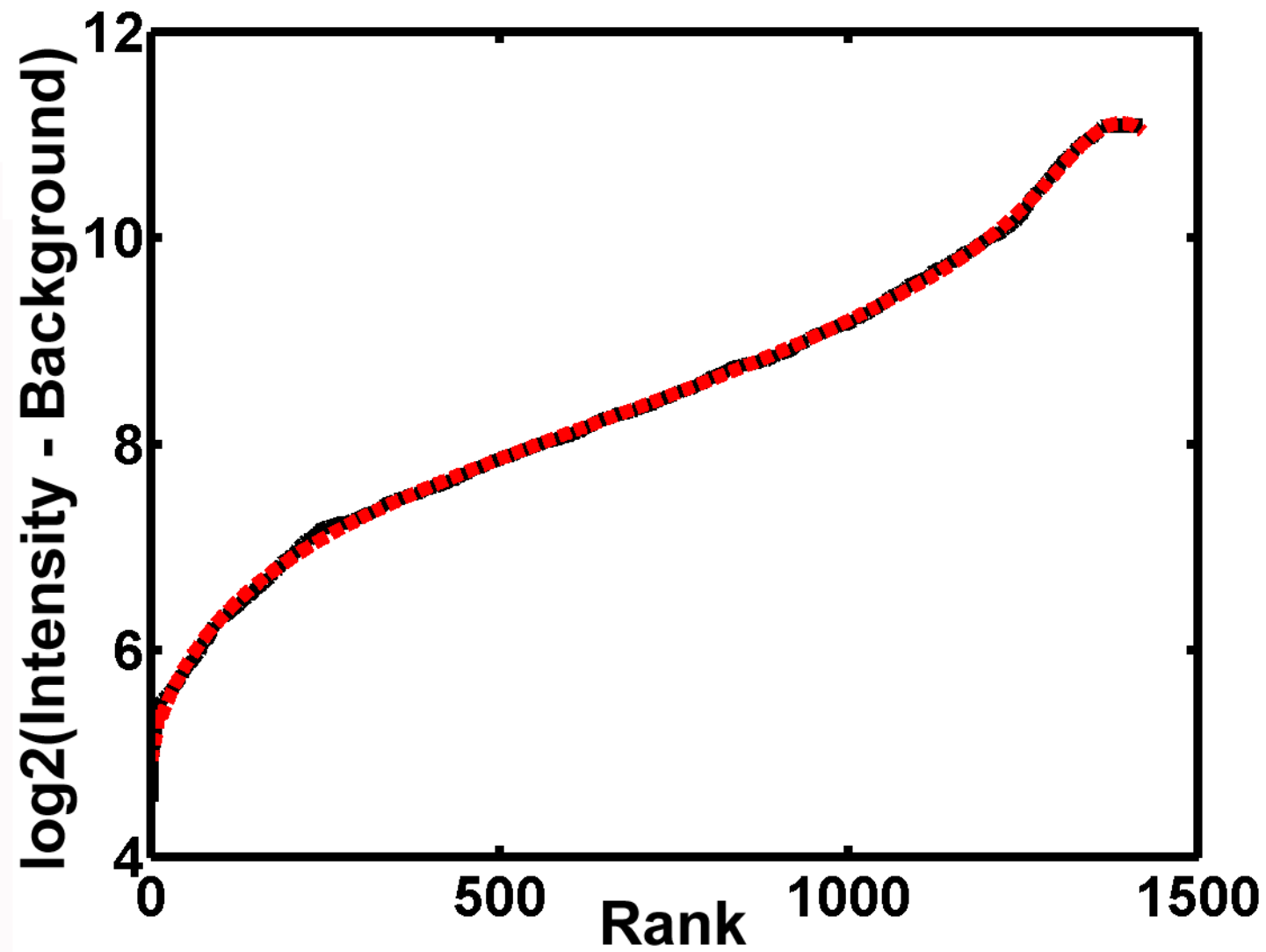


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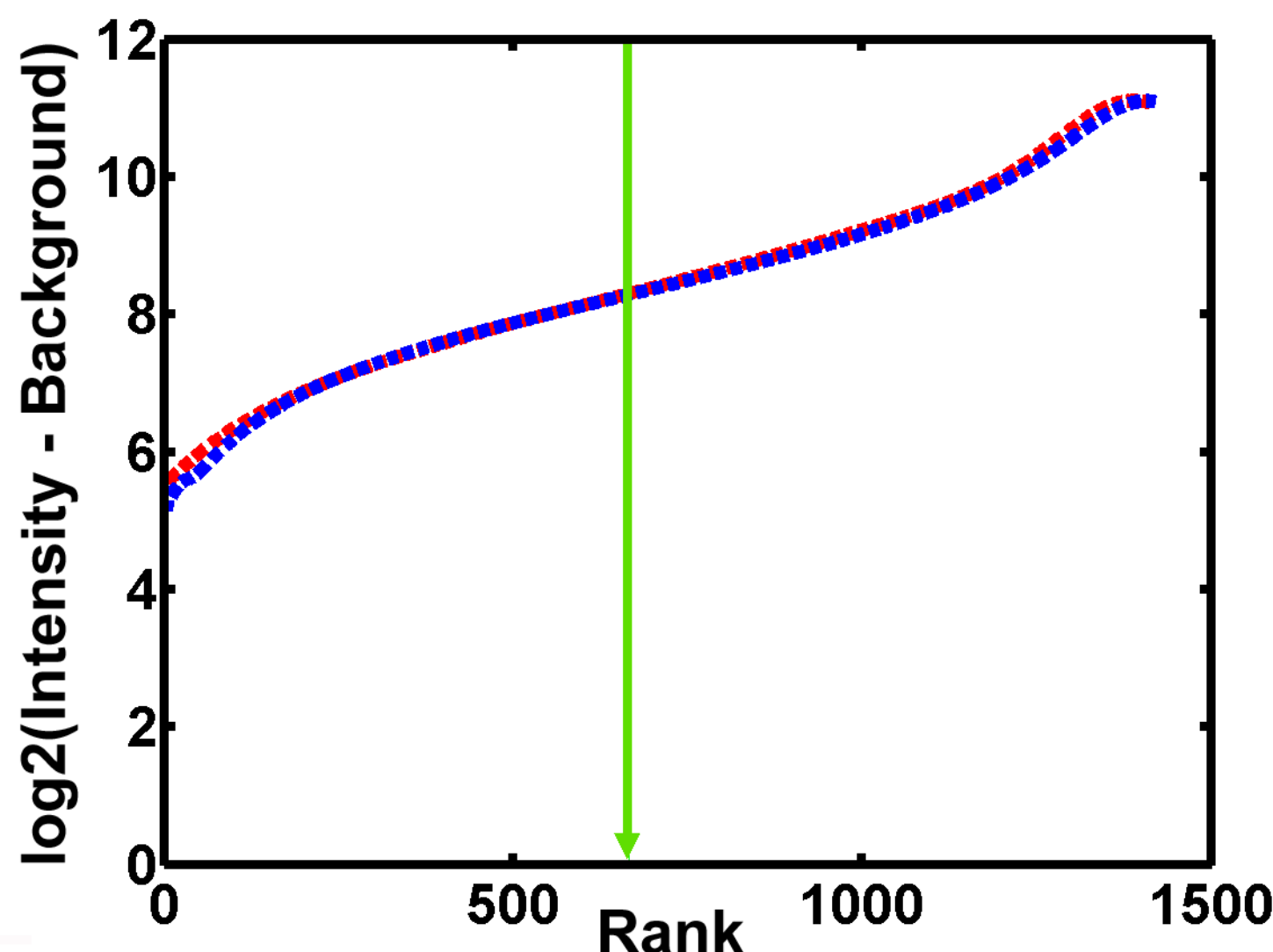
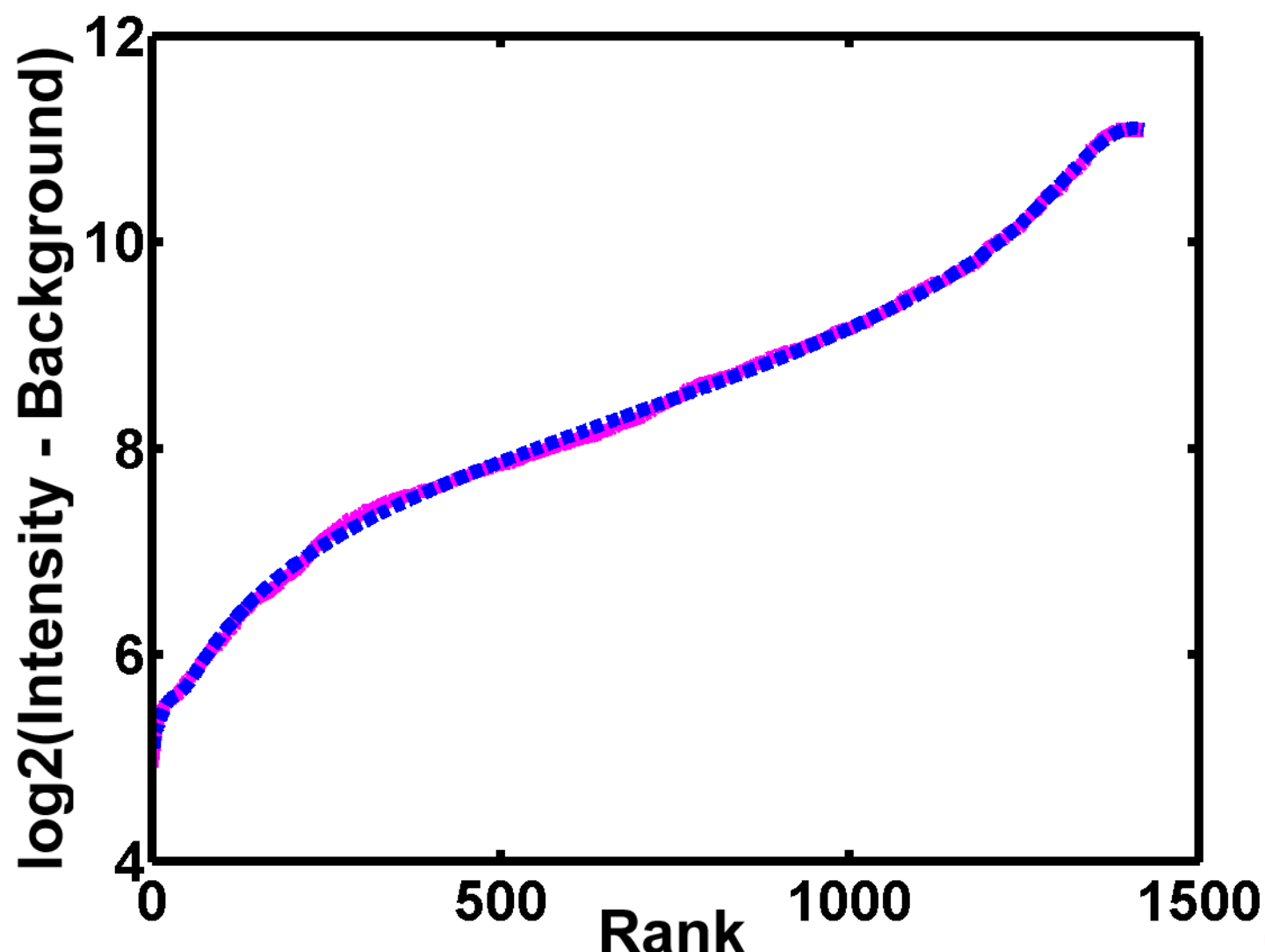
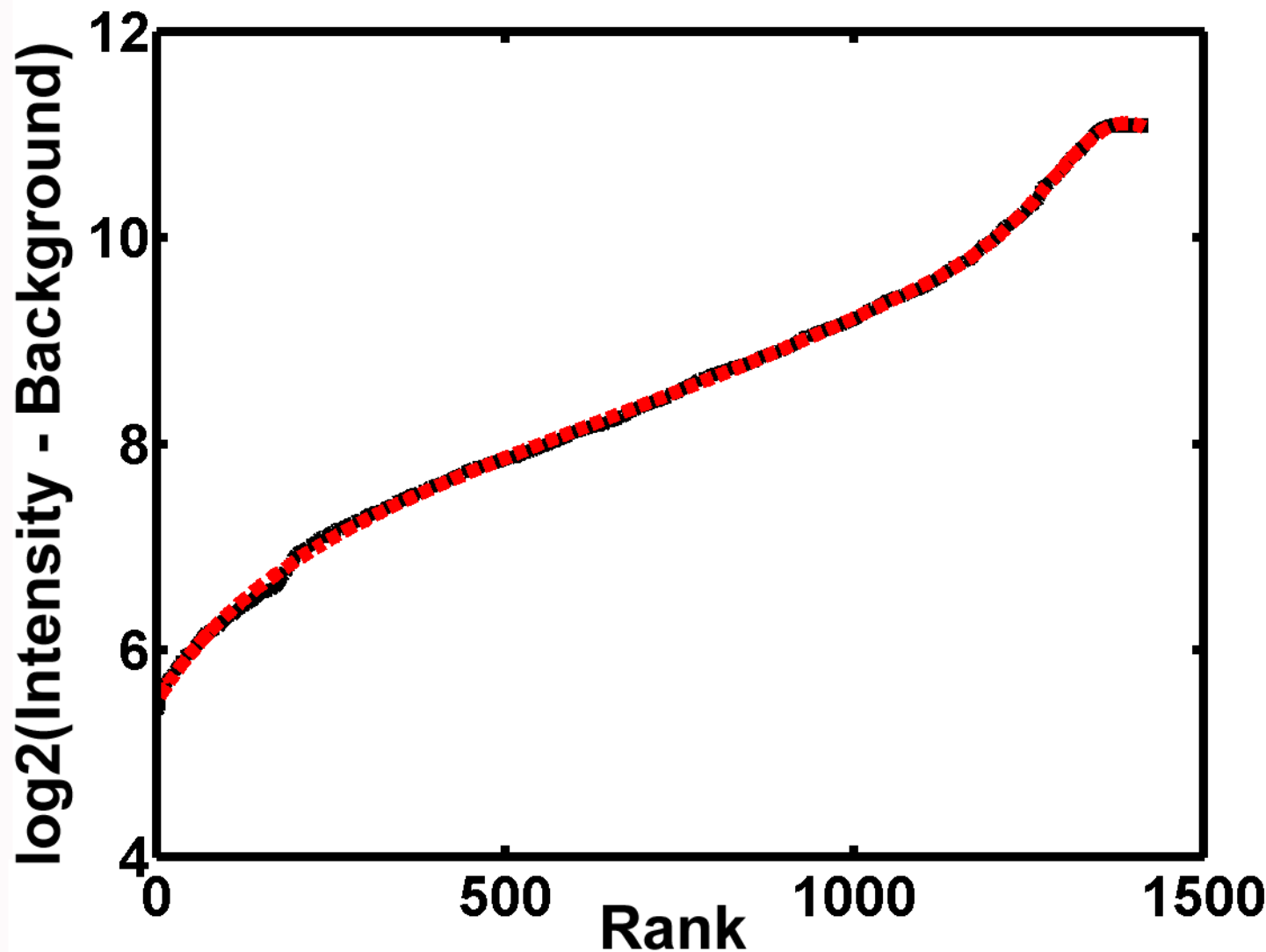
Cy3

Cy5

H001476



H001477

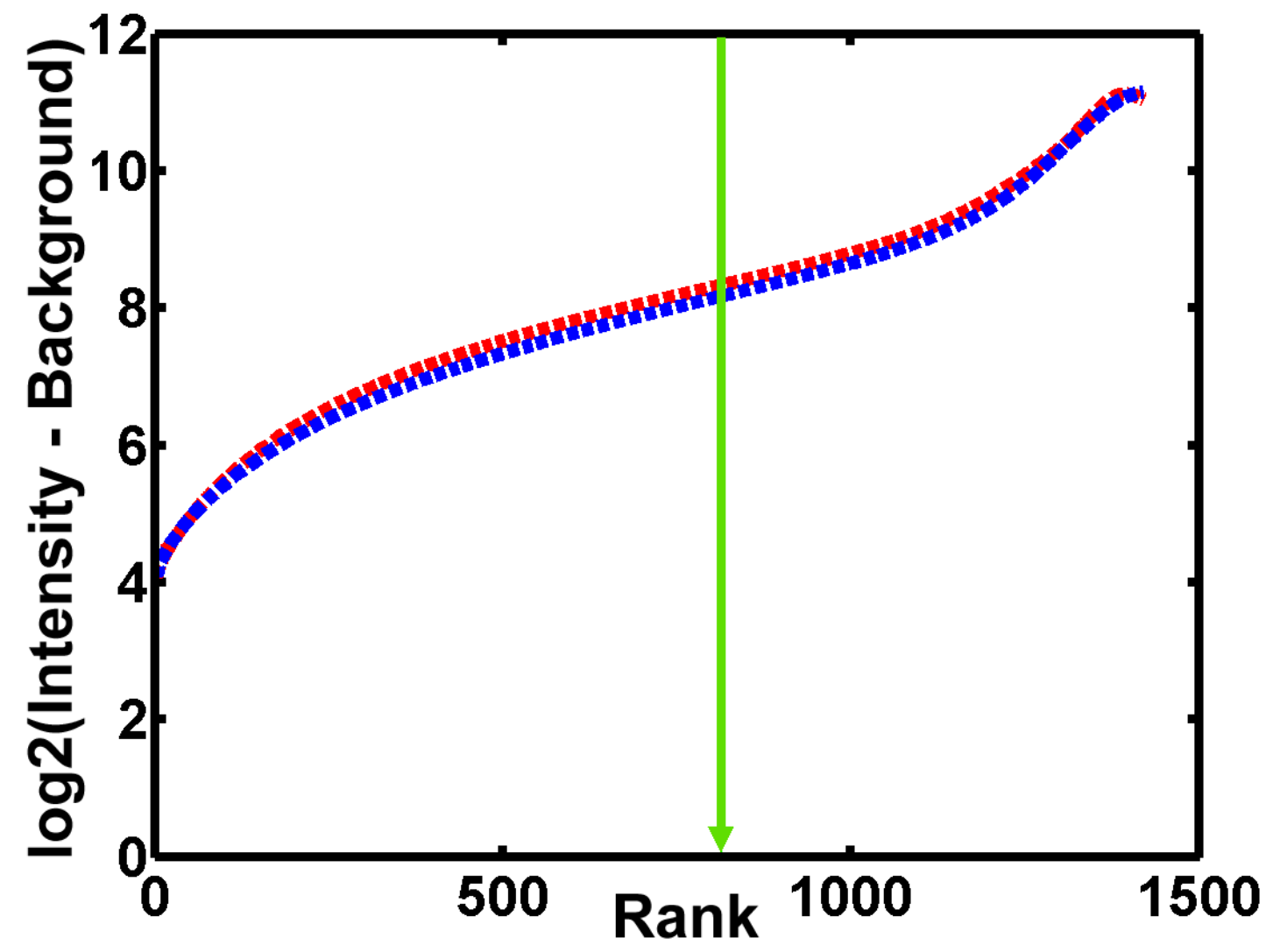
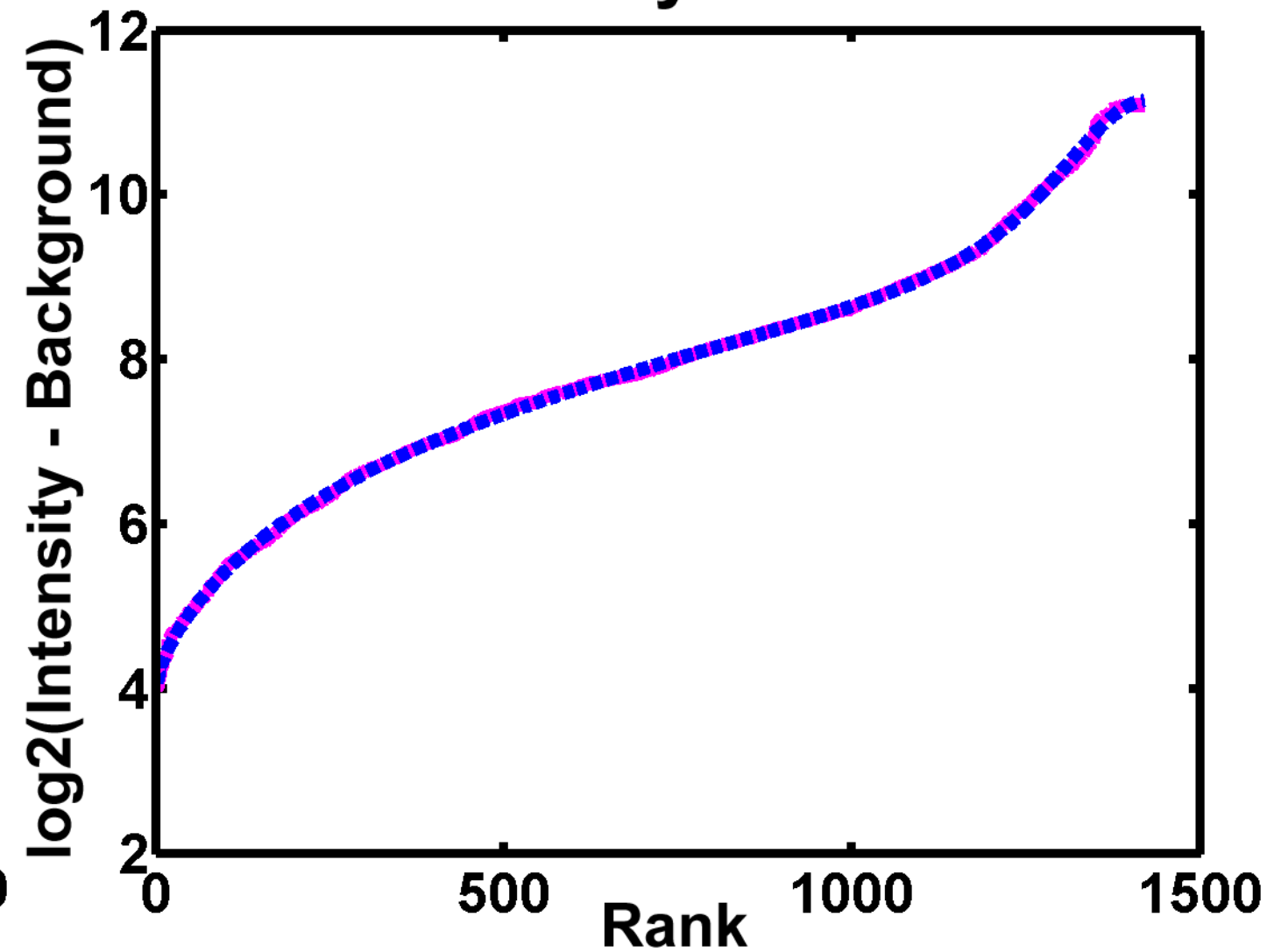
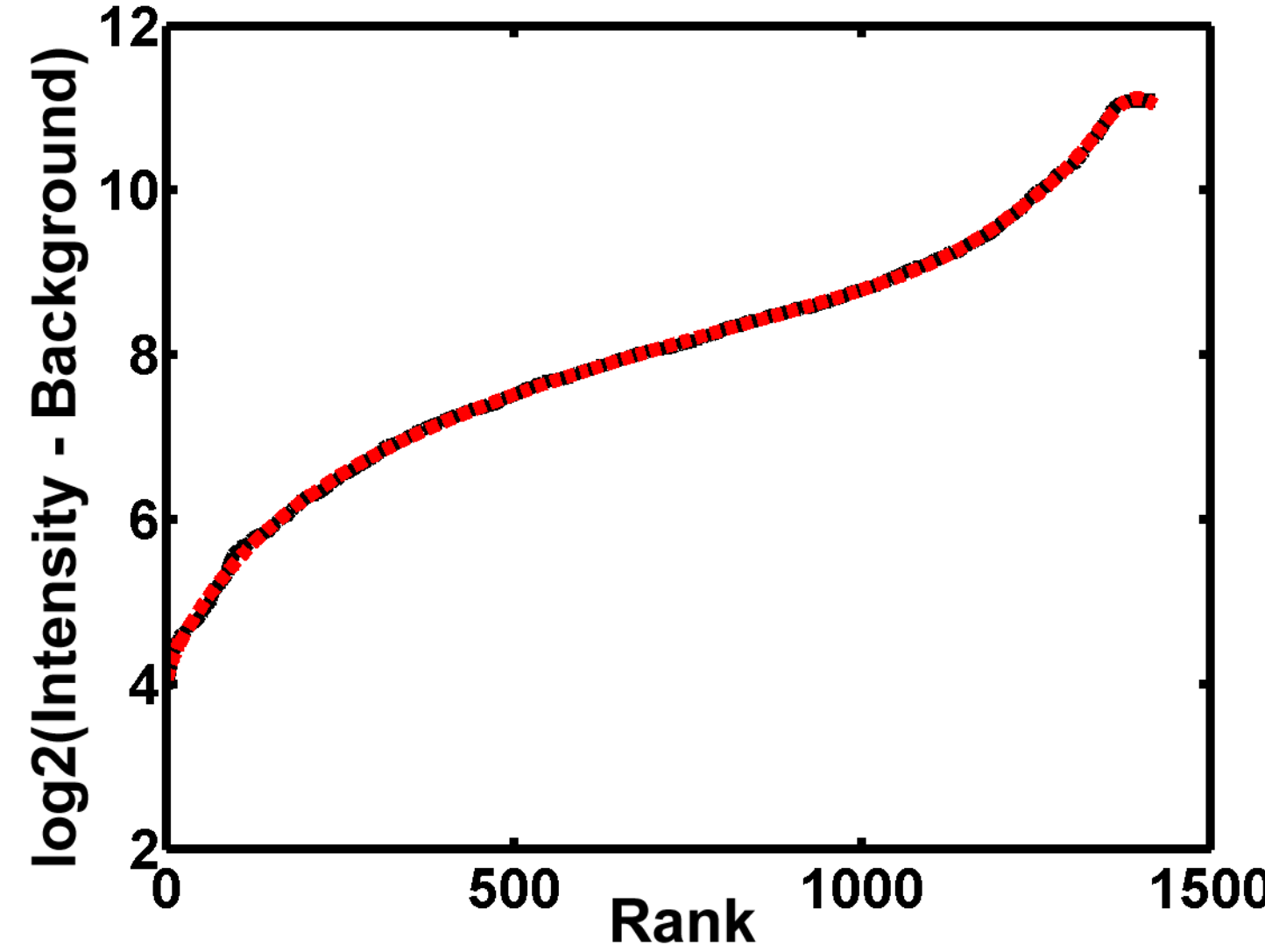


Web Figure 3

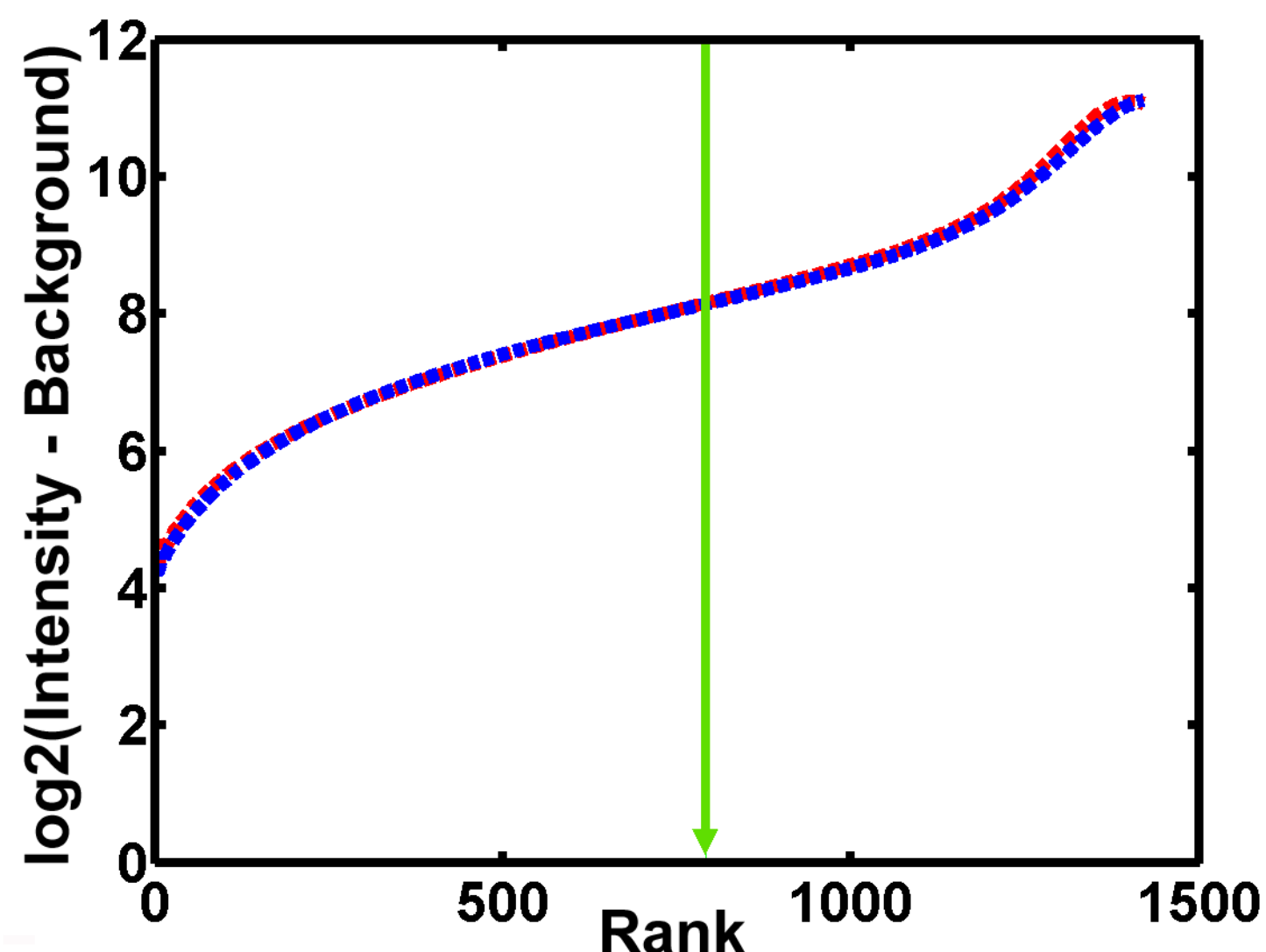
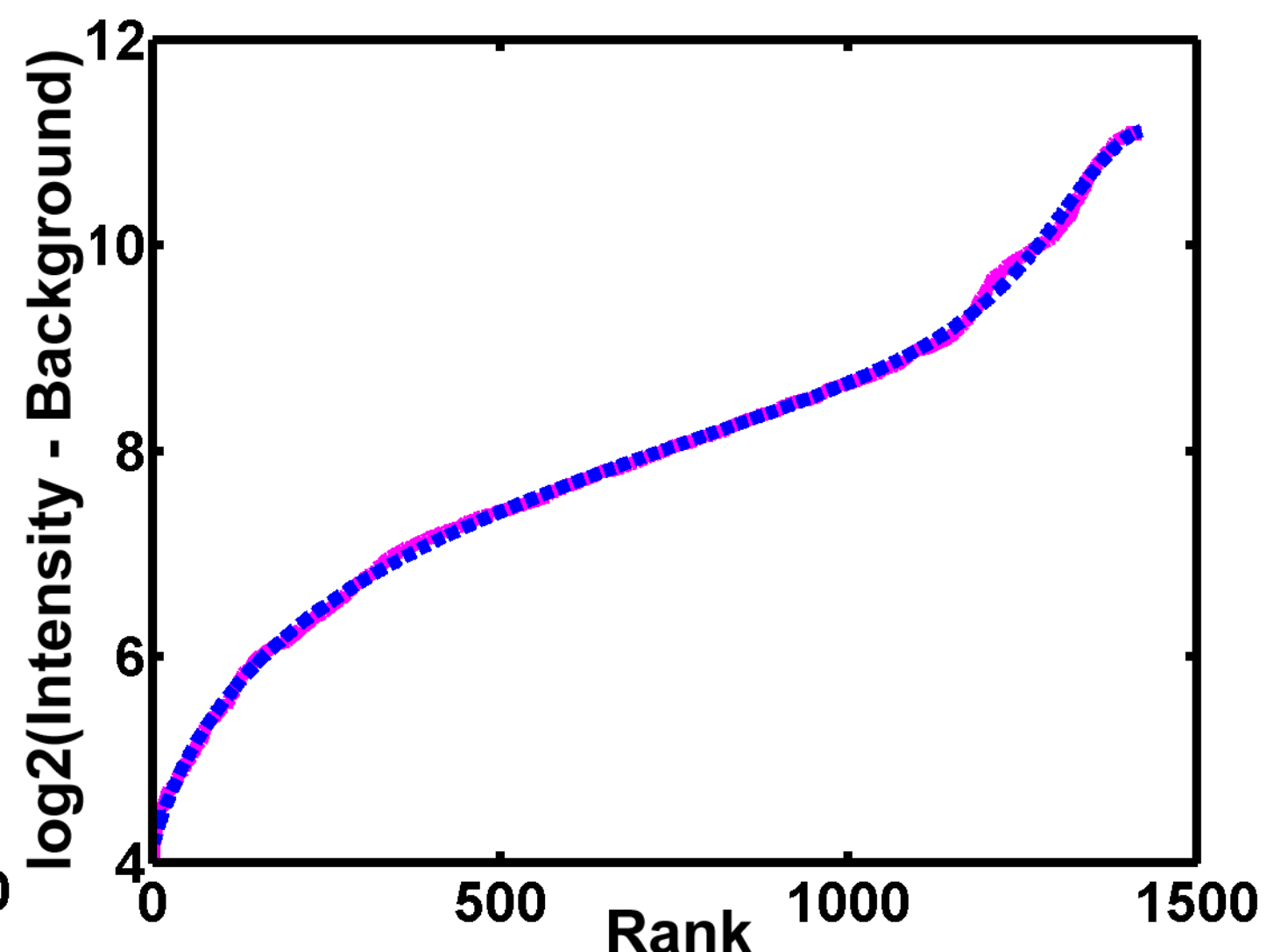
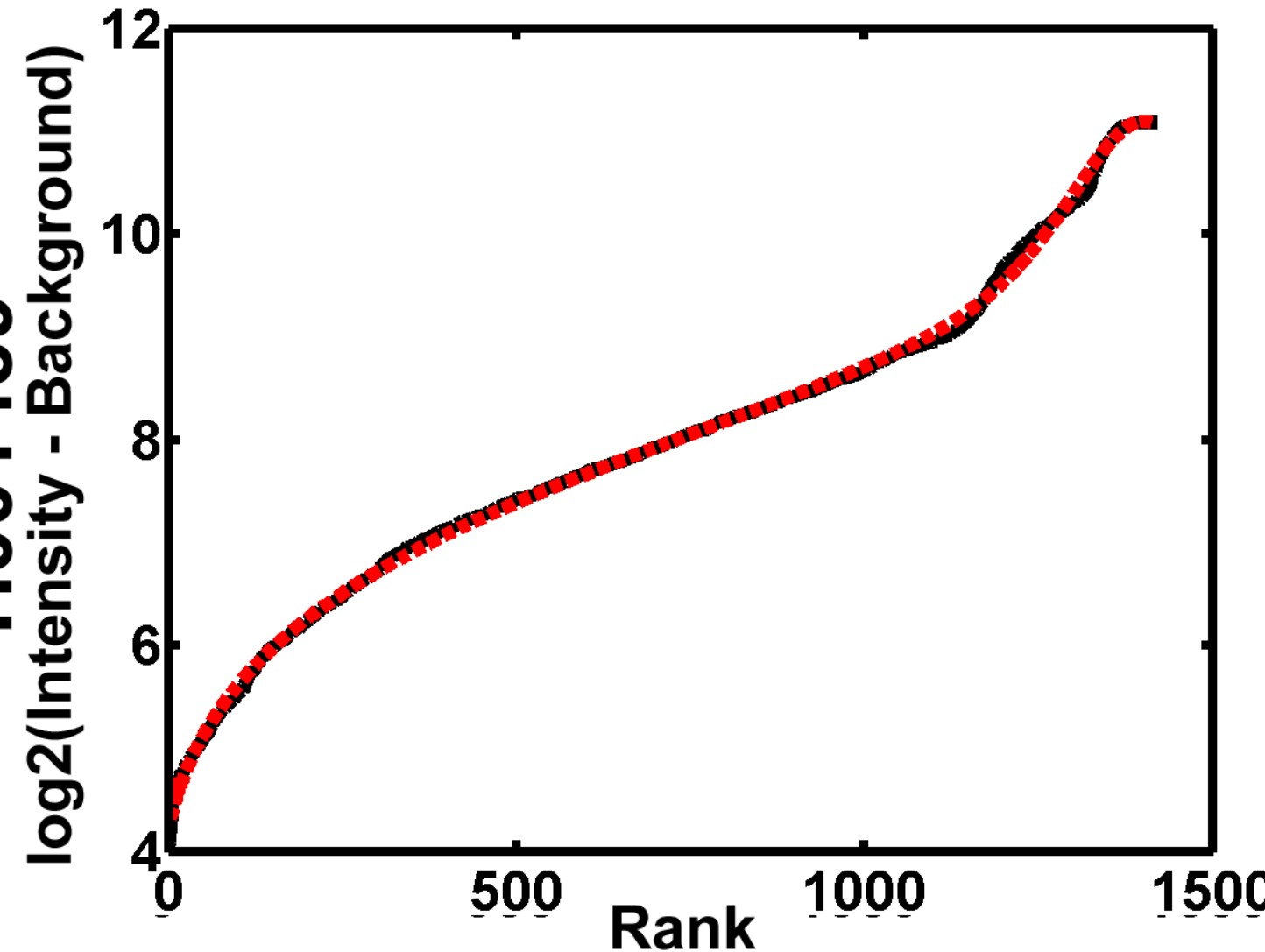
Cy3

Cy5

H001488



H001489

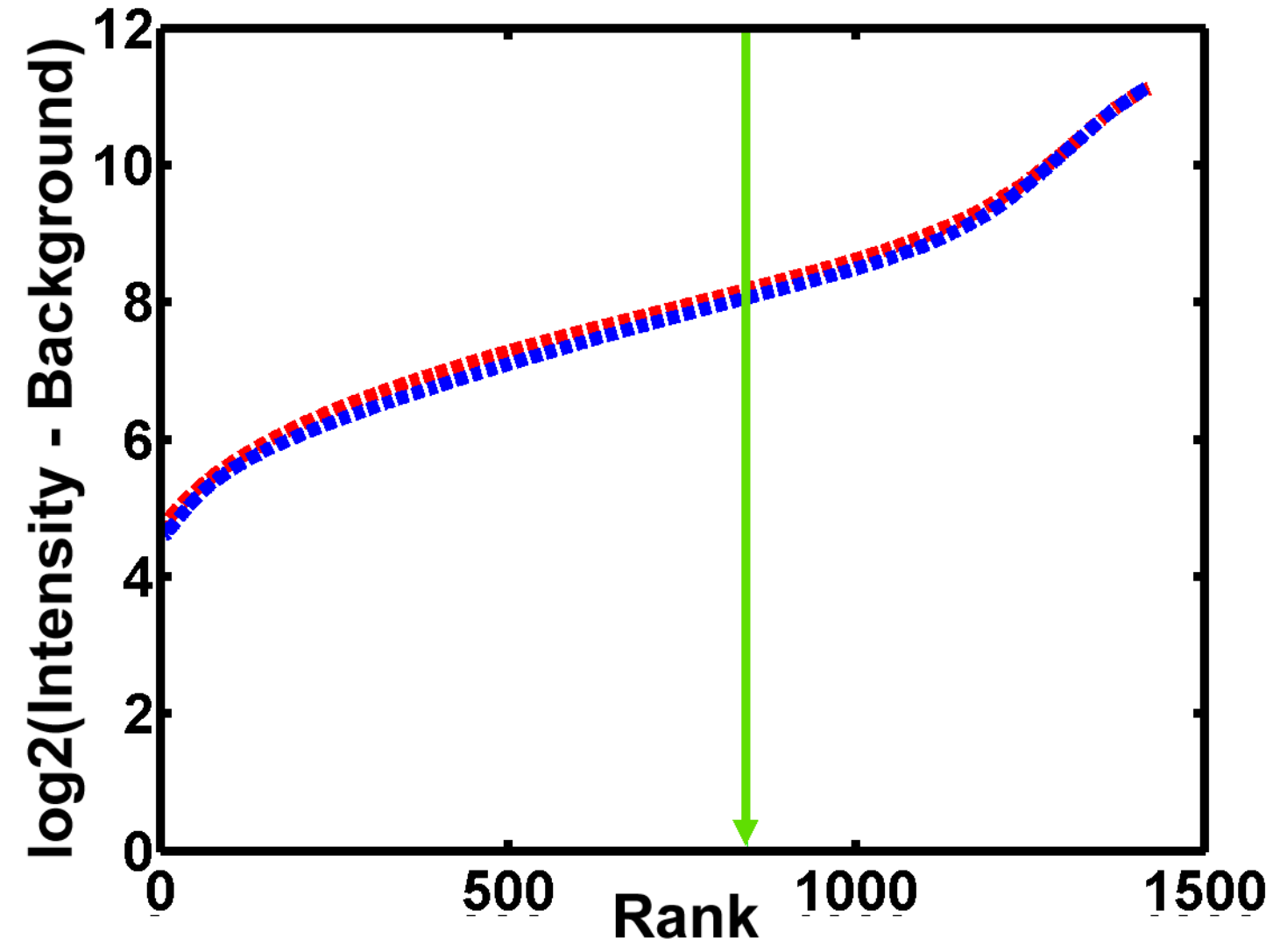
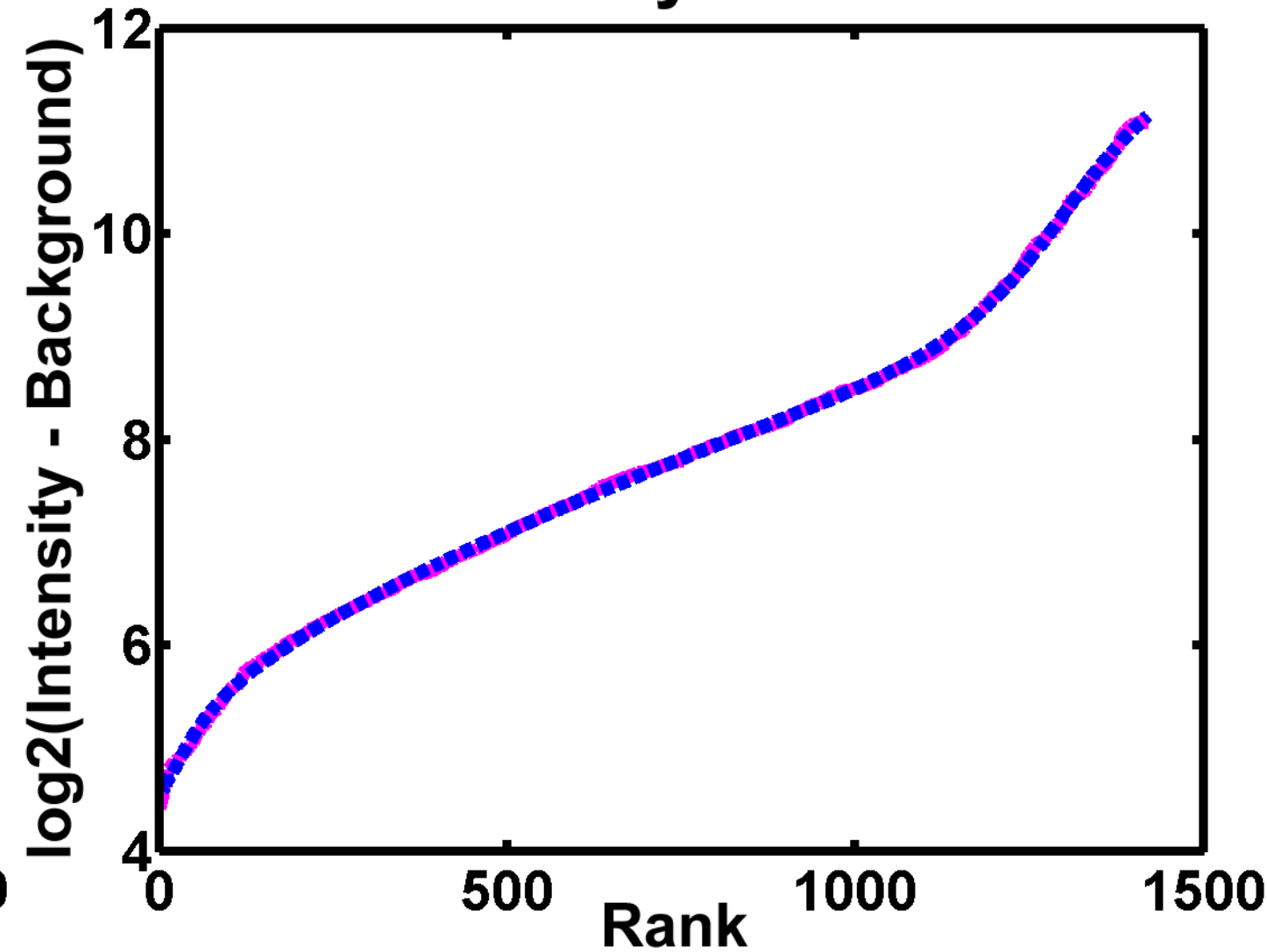
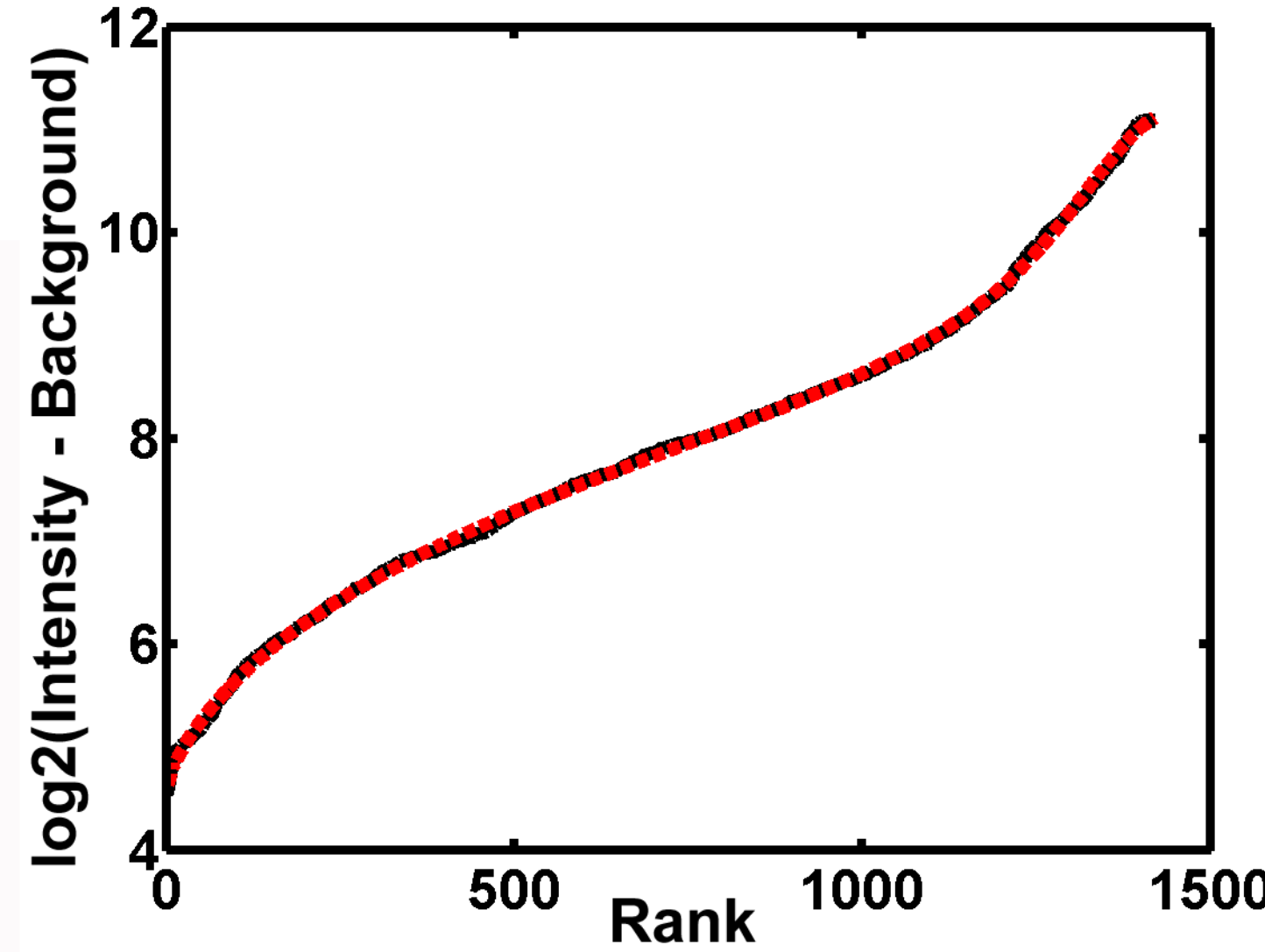


Web Figure 3

Cy3

Cy5

H001494



H001495

