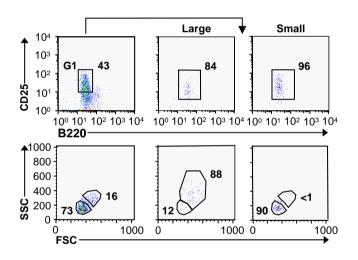
4	Δ
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FISH <sup>a</sup>	pre-BI	<i>ex vivo</i> transitional pre-BI	<i>in vitro</i> transitional pre-BI <sup>b</sup>	pre- BCR <sup>+</sup>	pre-BII	immature B	mature B <sup>c</sup>
RNA	CD19 <sup>+</sup> c-kit <sup>+</sup>	B220 <sup>+</sup> c-kit <sup>+</sup> CD2 <sup>+</sup>	B220+c-kit+ sµHC+	B220+ SL156+ k <sup>-</sup>	B220 <sup>+</sup> CD25 <sup>+</sup>	B220 <sup>+</sup> IgM <sup>+</sup>	B220 <sup>+</sup> IgM <sup>+</sup>
DNA	B220 <sup>+</sup> c-kit <sup>+</sup>				B220 <sup>+</sup> CD25 <sup>+</sup>		CD43 depletion

В



Cell sorting. (A) <sup>a</sup> BM cells were sorted on a FACSVantageSE<sup>TM</sup> or FACSAria (Becton Dickinson) into discrete developmental stages using specific surface markers. Cells were analyzed by RNA or DNA FISH. <sup>b</sup> sµHC<sup>+</sup> cells were sorted using the Alexa Fluor® 488 Signal Amplification Kit (Molecular Probes). <sup>c</sup> Splenic B cells for DNA-FISH were enriched by CD43 depletion using magnetic beads (Miltenyl Biotech). Typically, sort purities were >90%, except large pre-BII cells ~80%. (B) The pre-BII population was gated as B220<sup>+</sup>CD25<sup>+</sup> (G1) and sorted into large and small fractions using forward scatter. The numbers show the percentage of cells within the indicated gates before and after sorting.