

**Table S3.** Enriched Gene Ontology (GO) Terms for Upregulated Genes in the Basal Epidermis of P2.5 *Kit<sup>W-v</sup>/Kit<sup>W-v</sup>* Mice

GO Organizing Principle	Gene Ontology Term <sup>a</sup>	Fold Enrichment	<i>p</i> -Value
Biological Process	embryogenesis and morphogenesis	8.28	5.47E-03
Molecular Function	phosphoric monoester hydrolase activity	4.87	8.88E-03
Molecular Function	catalytic activity	2.15	9.43E-03
Biological Process	morphogenesis	2.19	1.46E-02
Biological Process	RNA processing	2.84	1.79E-02
Molecular Function	signal transducer activity	2.31	2.10E-02
Biological Process	development	2.28	2.32E-02
Molecular Function	cell adhesion molecule activity	3.61	2.42E-02
Cellular Component	extracellular space	2.17	2.59E-02
Molecular Function	enzyme regulator activity	2.52	4.55E-02

<sup>a</sup>Enriched GO terms, that were significantly enriched ( $p \leq 0.05$ ) by  $\geq 2$ -fold, relative to all of the assayed genes on the 35K array (35328 genes), were obtained by Over-Representation Analysis using EASE software (Hosack *et al.*, 2003).