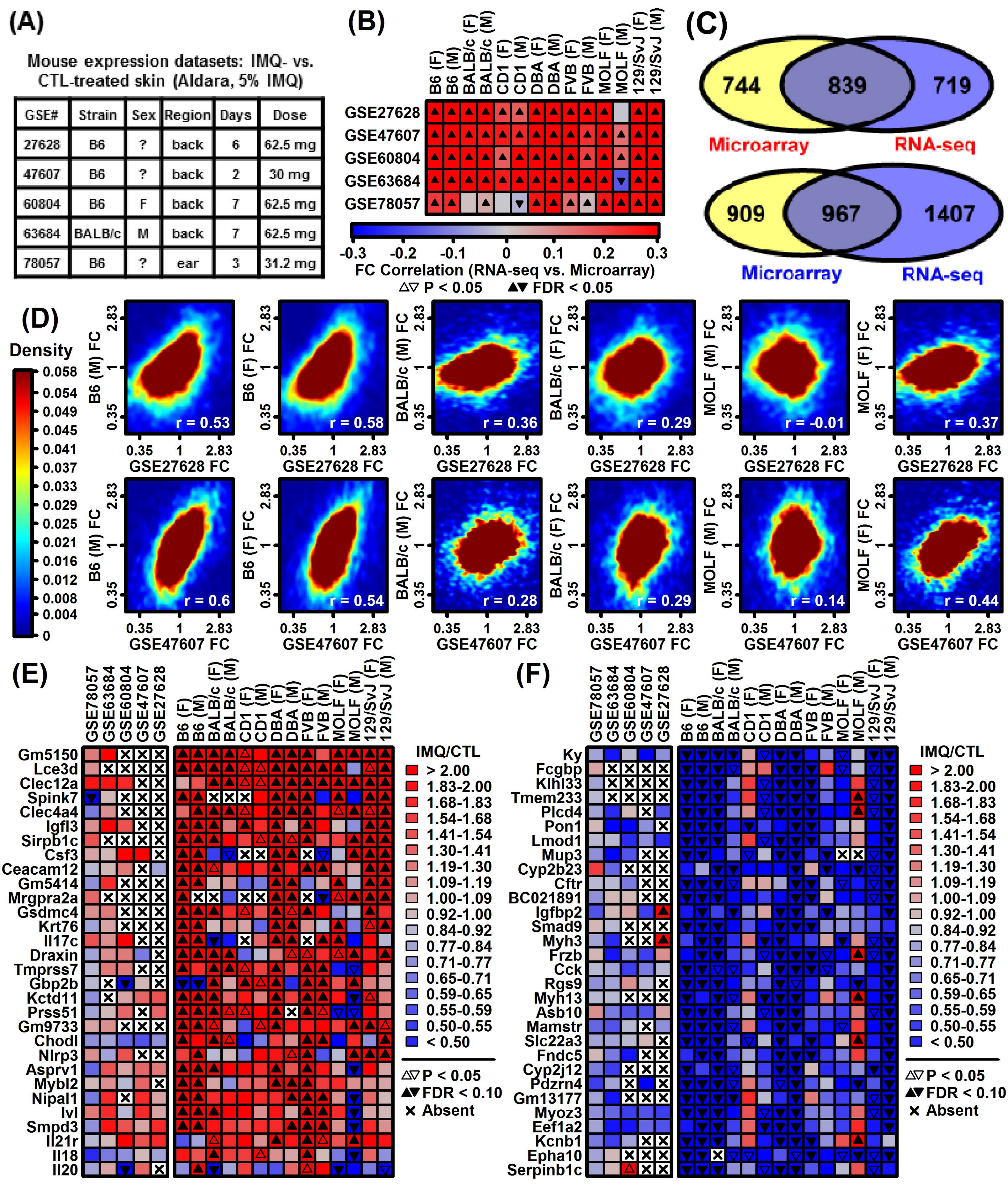
Additional File 7. Microarray dataset comparison. (A) Microarray datasets that have compared IMQ- and CTL-treated mouse skin. (B) RNA-seq vs. microarray correlation of FC estimates (rows: microarray datasets; columns: RNA-seq data from current study). (C) Overlap of genes elevated (top) or repressed (bottom) by IMQ in RNA-seq and microarray experiments (top: FC > 2.0 with FDR < 0.10; bottom: FC < 0.50 with FDR < 0.10). Microarray totals include genes altered in any of the 5 previous experiments. RNA-seq totals include genes altered in either sex of the B6 or BALB/c strains. (D) Gene density scatterplots comparing FC estimates (IMQ/CTL) from previous array studies (GSE27628 or GSE47607; horizontal axes) to RNA-seq estimates from B6, BALB/c or MOLF mice (vertical axes). (E) IMQ-increased DEGs identified by RNA-seq but not previously by microarray (FC > 2.0 with FDR < 0.10). (F) IMQ-decreased DEGs identified by RNA-seq but not previously by microarray (FC < 0.50 with FDR < 0.10).



Mouse expression datasets: IMQ- vs. CTL-treated skin (Aldara, 5% IMQ)

GSE#	Strain	Sex	Region	Days	Dose
27628	B6	?	back	6	62.5 mg
47607	B6	?	back	2	30 mg
60804	B6	F	back	7	62.5 mg
63684	BALB/c	M	back	7	62.5 mg
78057	B6	?	ear	3	31.2 mg