

Supplemental table I. A complete list of genes identified by haplotype-based computational genetic analysis of the amount of KC in wound tissue.

Supplemental Figure 1. The amount of 14 different cytokines and chemokines within wound tissue obtained 24 hr after incision was measured. Each data point represents the average $\pm$ S.E. of n=10 determinations.

Supplemental Table I (part 1): A complete list of genes identified by haplotype-based computational genetic analysis of the amount of KC in wound tissue.

P-value	Genetic Effect	Haplotype	Chr.	Position	#SNPs	Symbol
1.1e-05	0.73		1	74.669852~74.671336	7	Cyp27a1
1.1e-05	0.73		4	125.207346~125.208721	17	Grik3
1.1e-05	0.73		4	125.211094~125.211119	4	Grik3
1.1e-05	0.73		10	59.576740~59.584831	17	Chst3
1.1e-05	0.73		10	61.093558~61.097728	4	Tysnd1
1.1e-05	0.73		11	78.352599~78.353591	5	lft20
2.4e-05	0.73		8	79.802418~79.803032	11	Nr3c2
2.5e-05	0.73		11	76.601248~76.661990	30	Cpd
3.4e-05	0.75		11	70.939579~70.940226	4	Nalp1
4.1e-05	0.74		17	40.274722~40.292788	10	Rhag
4.4e-05	0.74		11	70.907566~70.908262	8	Nalp1
5.3e-05	0.81		11	88.154834~88.155372	9	Msi2
5.7e-05	0.73		4	125.188454~125.206490	14	Grik3
6.2e-05	0.73		2	90.982568~90.993715	10	Madd
8.4e-05	0.71		6	14.278129~14.278630	9	*
8.5e-05	0.71		11	64.249538~64.251074	10	**
9e-05	0.71		14	117.364492~117.412129	72	Abcc4
9.3e-05	0.71		4	131.022983~131.437859	8	Ptpru
9.4e-05	0.71		11	70.928754~70.928772	4	Nalp1
9.6e-05	0.71		2	73.368808~73.381696	39	Chrna1
9.6e-05	0.71		8	113.858940~114.798753	24	St3gal2
9.6e-05	0.71		11	70.908457~70.908671	8	Nalp1
9.6e-05	0.71		11	88.155476~88.157376	5	Msi2
9.6e-05	0.71		4	125.161365~125.173016	18	Grik3
9.6e-05	0.71		10	128.194437~128.202721	20	Mmp19
9.7e-05	0.71		11	69.806871~69.828197	14	Gabarap
9.7e-05	0.71		11	70.915846~70.929711	9	Nalp1
9.9e-05	0.74		2	80.232804~80.233961	5	Frzb
0.00011	0.73		2	90.993929~91.427751	5	Nr1h3
0.00014	0.8		11	88.893699~88.893787	4	Gm525
0.00018	0.71		14	117.551686~117.552679	14	Abcc4
0.00019	0.73		11	70.516532~70.659647	53	Kif1c
0.00019	0.71		11	94.162635~94.162824	4	Abcc3
0.0002	0.7		2	73.382419~73.382504	4	Chrna1
0.00021	0.73		7	30.201601~30.201691	4	Prodh2
0.00022	0.73		8	127.456231~127.475372	86	Agt
0.00025	0.72		11	70.922707~70.923143	9	Nalp1
0.00028	0.72		8	127.230745~127.443761	14	Galnt2
0.00032	0.99		7	98.502231~98.512397	4	***
0.00036	0.71		11	64.251558~64.338078	8	Hs3st3a1
0.00039	0.71		1	74.665030~74.668728	6	Cyp27a1
0.00041	0.7		11	69.147845~69.148708	4	Kcnab3
0.00041	0.7		2	73.381878~73.382124	7	Chrna1
0.00041	0.7		6	114.443463~115.455651	92	Hrh1
0.00043	0.7		4	125.208723~125.211061	10	Grik3
0.00043	0.69		10	127.961180~128.194192	24	Pa2g4
0.0005	0.69		11	69.611531~69.612034	6	Chrnb1

Supplemental Table I (part 2)

P-value	Genetic Effect	Haplotype	Chr.	Position	#SNPs	Symbol
0.0017	0.69		19	44.033515~44.037965	14	Cpn1
0.0018	0.68		11	53.801899~53.802116	4	Slc22a21
0.0019	0.98		11	41.843879~41.845351	4	Gabrg2
0.0046	0.48		17	23.594630~23.699333	27	Prss21
0.0055	0.47		8	58.954366~59.004937	12	Glra3
0.0081	0.49		4	98.838500~99.680046	4	Ror1

* [ENSMUSG00000061474](#)

** [ENSMUSG00000053481](#)

*** [2210018M11Rik](#)



