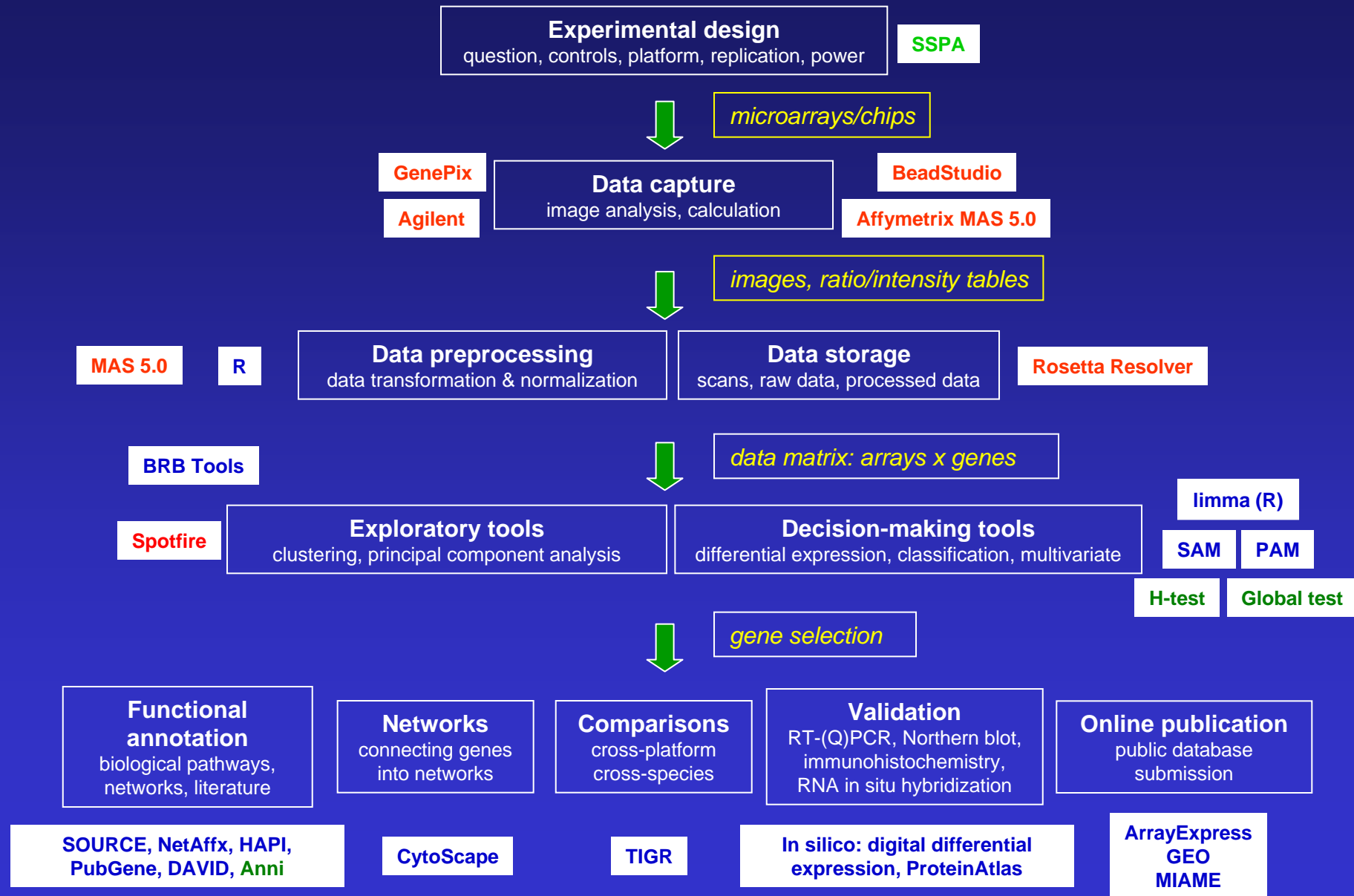
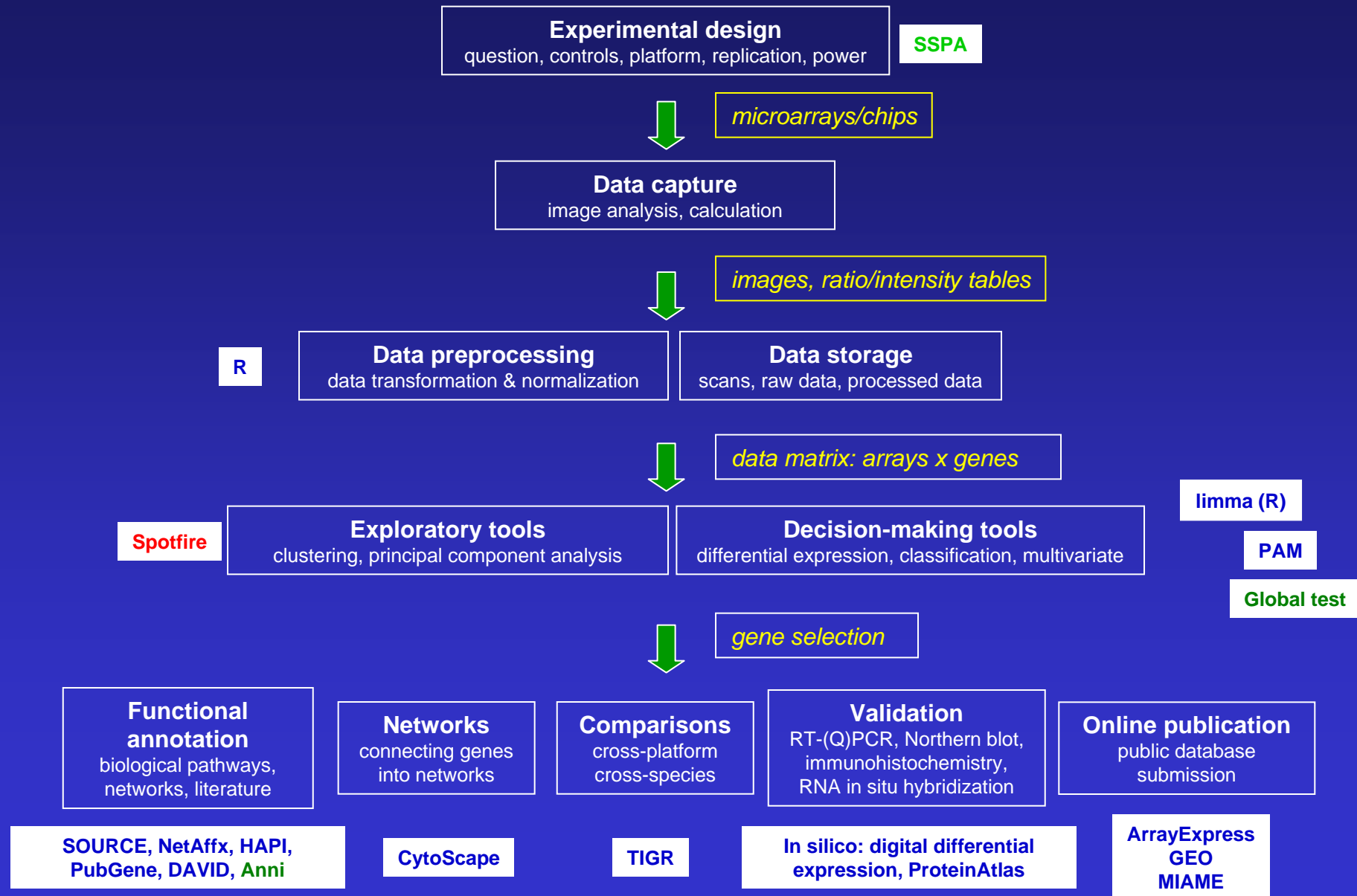


# Expression analysis and interpretation



# Expression analysis and interpretation



# DMD muscle data

- Pescatori et al, FASEB J 2007, 21:1210-26
- muscle samples from 19 young Duchenne muscular dystrophy (DMD) patients and 14 similar age controls
- run on Affymetrix U133A chips (some reruns)
- a selection of genes based on expression difference from the median by at least 1.5 in at least 20% of the arrays (1663 probe sets)
- limma, PAM, clustering, globaltest, power

A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
Probe set	Name	GB acc	Symbol	Cytoband	C_1	C_2	C_3	C_4	C_5	C_6	C_7	C_8	C_9	C_10
200014_s_at	heterogeneous nuclear ribonucleopro	NM_004500	HNRNPC	Chr:14q11.2	7.918846	8.39622	8.066378	7.954816	8.584641	7.390049	8.088675	8.816465	7.212393	8.164675
200021_at	cofilin 1 (non-muscle)	NM_005507	CFL1	Chr:11q13	11.07204	11.61825	11.089855	11.951819	11.654462	10.63493	11.12147	11.66739	10.44762	8.164675
200027_at	asparaginyl-tRNA synthetase	NM_004539	NARS	Chr:18q21.2-q21.3	9.114633	9.687555	9.108984	9.248428	10.05149	8.634838	9.156263	9.590625	10.340398	9.164675
200028_s_at	StAR-related lipid transfer (START) d	NM_020151	STARD7	Chr:2q11.2	10.39944	11.25323	10.58315	10.87135	11.26197	10.547	10.45207	11.19189	10.67277	1.164675
200033_at	DEAD (Asp-Glu-Ala-Asp) box polype	NM_004396	DDX5	Chr:17q21	8.756398	9.725073	9.683109	9.483501	9.674204	8.852589	9.751701	9.686544	8.331187	9.164675
200040_at	KH domain containing, RNA binding,	NM_006559	KHDRBS1	Chr:1p32	8.866123	9.629319	9.351637	9.115745	9.766624	8.788442	9.162154	9.835983	8.252977	9.164675
200047_s_at	YY1 transcription factor	NM_003403	YY1	Chr:14q	7.135867	8.129392	7.794879	7.876145	8.393572	7.405903	8.057751	8.444429	7.325544	9.164675
200059_s_at	ras homolog gene family, member A	BC001360	RHOA	Chr:3p21.3	9.646119	10.61882	10.4419	10.18595	10.83677	9.877575	10.6456	10.88546	9.554924	1.164675
200071_at	survival motor neuron domain contain	BF224259	SMNDC1	Chr:10q23	6.149709	7.038994	6.740277	7.082972	7.242648	6.238686	7.090714	7.456025	6.530901	8.164675
200075_s_at	guanylate kinase 1	BC006249	GUK1	Chr:1q32-q41	7.289037	7.691275	7.572192	7.431634	7.971799	7.336901	7.367908	8.047307	7.127634	7.164675
200082_s_at		A1805587			10.95106	11.22	10.85855	10.78187	11.47665	10.26469	11.05738	10.73368	10.08313	1.164675
200085_s_at	transcription elongation factor B (SIII)	NM_007108	TCEB2	Chr:16p12.3	9.778732	10.47875	9.94952	9.935264	10.01479	9.651977	10.14753	9.532533	8.76163	9.164675
200595_s_at	eukaryotic translation initiation factor	NM_003750	EIF3A	Chr:10q26	7.099211	8.444418	7.363054	7.962637	8.397342	7.012748	8.088542	8.629757	6.869164	8.164675
200599_s_at	heat shock protein 90kDa beta (Grp9	NM_003299	HSP90B1	Chr:12q24.2-q24.3	7.932592	8.062915	8.162834	8.273404	8.633074	7.589984	7.944977	8.162066	7.375766	8.164675
200600_at	moesin	NM_002444	MSN	Chr:Xq11.2-q12	7.27281	8.022614	7.749865	7.04056	8.327102	6.910069	7.351198	8.296714	7.223661	7.164675
200603_at	protein kinase, cAMP-dependent, reg	AL050038	PRKAR1A	Chr:17q23-q24	7.824111	10.0226	8.949175	10.20213	9.689263	8.52597	9.472245	10.09406	8.815134	9.164675
200604_s_at	protein kinase, cAMP-dependent, reg	M18468	PRKAR1A	Chr:17q23-q24	8.642109	7.884982	8.371968	9.741969	8.290226	7.186059	8.371968	8.297832	8.094395	9.164675
200605_s_at	protein kinase, cAMP-dependent, reg	NM_002734	PRKAR1A	Chr:17q23-q24	9.262165	9.773465	9.683404	10.92465	10.12385	8.407957	9.865127	10.17828	9.315651	9.164675
200608_s_at	RAD21 homolog (S. pombe)	NM_006265	RAD21	Chr:8q24	6.608359	7.012721	6.974495	6.374947	7.554621	7.051058	7.379475	7.942491	6.788927	7.164675
200625_s_at	CAP, adenylate cyclase-associated	NM_006367	CAP1	Chr:1p34.2	8.268198	8.60326	8.641089	7.59472	8.716706	7.651726	8.178686	8.398343	8.022471	9.164675
200634_at	profilin 1	NM_005022	PFN1	Chr:17p13.3	8.970029	10.28978	9.651248	9.413157	10.19205	8.489958	9.181246	9.625831	8.188392	9.164675
200638_s_at		BC003623			7.004488	7.021724	7.208632	6.867082	7.856879	7.018365	7.022764	8.047975	6.95408	7.164675
200639_s_at		NM_003406			8.234613	8.654657	8.510732	7.810585	8.99401	7.165201	8.359571	8.921852	7.236809	9.164675
200641_s_at		U28964			7.993665	7.400007	8.063015	7.842273	7.966777	7.430774	7.827732	7.800911	7.488991	7.164675
200647_x_at		NM_003752			10.01083	10.48397	8.914358	10.12769	10.49196	9.67129	10.16078	9.804091	9.15349	1.164675
200648_s_at	glutamate-ammonia ligase (glutamine	NM_002065	GLUL	Chr:1q31	9.752971	10.55965	10.2097	10.04379	10.66623	9.885625	11.56517	9.844597	9.623692	1.164675
200650_s_at	lactate dehydrogenase A	NM_005555	LDHA	Chr:11p15.4	10.52844	10.84853	11.58725	10.24843	10.13564	10.18883	11.73775	11.88888	10.22456	1.164675
200653_s_at			A1	Chr:14q24-q31	8.4									15
200655_s_at			A1	Chr:14q24-q31	8.0									19
200657_at			5A5	Chr:Xq24-q26	8									75
200660_at	S100 calcium binding protein A11	NM_005620	S100A11	Chr:1q21	7.056163	6.851102	7.267336	6.507493	7.571276	6.514735	6.865756	7.252195	6.467524	6.164675
200662_s_at	translocase of outer mitochondrial m	NM_014765	TOMM20	Chr:1q42	7.029009	8.15905	7.800866	8.029042	8.451982	7.092995	7.935571	8.21847	7.026289	8.164675
200663_at	CD63 molecule	NM_001780	CD63	Chr:12q12-q13	10.3555	11.43284	10.57023	11.13447	11.06319	10.59525	10.63627	10.63667	10.12056	8.164675
200665_s_at	secreted protein, acidic, cysteine-ric	NM_003118	SPARC	Chr:5q31.3-q32	11.04891	9.917575	11.85395	10.00113	11.86788	10.49744	11.30159	10.51546	10.41931	1.164675
200678_x_at	granulin	NM_002087	GRN	Chr:17q21.32	8.285004	8.347935	8.427979	8.272118	8.716335	7.772966	8.67811	8.655144	8.005575	8.164675
200691_s_at	heat shock 70kDa protein 9 (mortalin	BC000478	HSPA9	Chr:5q31.1	9.515343	9.672915	8.998402	8.958743	9.827555	9.075354	9.023797	9.940526	8.533631	9.164675
200692_s_at	heat shock 70kDa protein 9 (mortalin	NM_004134	HSPA9	Chr:5q31.1	8.911464	8.691304	8.452133	8.511191	9.098145	8.237518	8.505773	9.078773	8.060418	8.164675
200693_s_at	tyrosine 3-monooxygenase/tryptophan	NM_006826	YWHAQ	Chr:2p25.1	9.05831	8.492015	8.964193	8.406174	9.083662	8.234565	8.781048	9.323832	8.19858	8.164675
200698_at	KDEL (Lys-Asp-Glu-Leu) endoplasmic	AL542253	KDELRL2	Chr:7p22.1	7.419564	7.475148	8.179143	7.661577	8.439573	7.284971	7.63395	7.726742	7.190066	7.164675
200700_s_at	KDEL (Lys-Asp-Glu-Leu) endoplasmic	NM_006854	KDELRL2	Chr:7p22.1	7.933286	8.216821	8.60094	8.508283	8.215828	7.720572	8.414678	8.637277	7.51817	8.164675
200701_at	Niemann-Pick disease, type C2	NM_006432	NPC2	Chr:14q24.3	7.87864	8.727836	8.420007	8.298858	9.071418	8.080662	8.600653	8.476974	7.723253	8.164675
200703_at		NM_003746			7.707872	8.712702	8.019429	6.929005	8.479138	7.23975	7.543361	7.970388	7.978817	8.164675
200709_at	FK506 binding protein 1A, 12kDa	NM_000801	FKBP1A	Chr:20p13	8.793736	9.072511	9.437606	8.868876	9.736249	8.385783	9.048867	9.447632	8.185505	9.164675
200710_at	acyl-Coenzyme A dehydrogenase, ve	NM_000018	ACADVL	Chr:17p13-p11	10.69904	11.83154	10.8157	10.77482	11.52758	11.31217	10.95571	11.66214	10.67952	1.164675
200726_at	protein phosphatase 1, catalytic sub	NM_002710	PPP1CC	Chr:12q24.1-q24.2	8.079618	9.360702	8.652351	9.195271	9.614534	8.905459	8.790406	9.381647	8.293043	9.164675
200728_at	ARP2 actin-related protein 2 homolog	BE566290	ACTR2	Chr:2p14	7.704105	8.042527	8.385408	8.150618	9.039814	7.298198	7.969223	8.753007	7.236025	8.164675
200730_s_at	protein tyrosine phosphatase type IV	BF576710	PTP4A1	Chr:6q12	6.496365	6.641089	6.459622	8.488207	6.588109	7.512454	7.340178	8.809989	6.611811	8.164675
200732_s_at	protein tyrosine phosphatase type IV	AF378248	PTP4A1	Chr:6q12	8.923289	8.734484	8.923289	10.23424	8.289884	8.733027	8.733027	8.482481	8.234484	8.164675

Probe annotation      RMA normalized intensities

# Platform comparison data

- Pedotti et al. BMC Genomics 2008, 9:124
- hippocampus samples from 5 deltaC-doublecortin-like kinase and 5 wildtype mice
- run on 5 different microarray platforms incl.
  - Affymetrix: one-color arrays, probesets
  - Illumina: one-color arrays, probes
  - Agilent: two-color arrays, probes
- Normalization & QC, Finding differentially expressed genes in R (limma)