

Supplementary Table 1. Calcium permeability of $\alpha 9\alpha 10$ wild type, mutant and chimeric receptors.

Receptor	% resp. post – BAPTA	pCa/pNa
Heteromeric receptors		
Rat $\alpha 9\alpha 10$	14.8 ± 3.1 (n=12)	7.9 ± 0.6 (n=11)
Chick $\alpha 9\alpha 10$	100.3 ± 14.1 (n=6)**	2.3 ± 0.3 (n=9)**
Homomeric receptors		
Rat $\alpha 9$	14.3 ± 2.9 (n=7)	6.1 ± 1.2 (n=4)
Chick $\alpha 9$	99.5 ± 15.1 (n=4)**	2.6 ± 0.3 (n=12)**
Chick $\alpha 10$	12.7 ± 4.7 (n=10)	6.9 ± 1.0 (n=8)
Hybrid receptors		
Rat $\alpha 9$ /Chick $\alpha 10$	21.8 ± 8.2 (n=5)	9.0 ± 1.0 (n=7)
Chick $\alpha 9$ /Rat $\alpha 10$	103.4 ± 20.0 (n=7)**	N.D.
Rat mutant and chimeric receptors		
Rat $\alpha 9D110N\alpha 10$	59.8 ± 11.9 (n=6)**	5.5 ± 0.3 (n=7)*
Rat $\alpha 9S127F\alpha 10$	49.4 ± 8.4 (n=5)*	5.4 ± 0.4 (n=5)*
Rat $\alpha 9A24'P\alpha 10$	22.1 ± 9.5 (n=3)	8.5 ± 1.2 (n=7)
Rat $\alpha 9I7'V/M11'L\alpha 10$	23.0 ± 2.9 (n=5)	7.0 ± 1.1 (n=5)
Rat $\alpha 9A-4'D\alpha 10$	59.5 ± 5.9 (n=4)**	4.8 ± 0.3 (n=11)**
Rat $\alpha 9(IC-chick \alpha 9)\alpha 10$	N.D.	8.0 ± 1.4 (n=7)
Rat $\alpha 9D110N/S127F/A-4'D\alpha 10$	100.5 ± 13.9 (n=6)**	3.2 ± 0.4 (n=7)**
Chick mutant receptors		
Chick $\alpha 9N110D\alpha 10$	N.D.	2.3 ± 0.2 (n=5)
Chick $\alpha 9F127S\alpha 10$	N.D.	2.3 ± 0.1 (n=6)
Chick $\alpha 9D-4'A\alpha 10$	40.8 ± 6.0 (n=10)##	3.7 ± 0.4 (n=11)#
Chick $\alpha 9N110D/F127S/D-4'A\alpha 10$	63.7 ± 8.2 (n=19)#	2.7 ± 0.3 (n=6)

Values are mean ± S.E.M. n=number of oocytes. *t* test vs rat $\alpha 9\alpha 10$ receptor, * $p < 0.05$, ** $p < 0.001$. *t* test vs chicken $\alpha 9\alpha 10$ receptor, # $p < 0.05$, ## $p < 0.001$. N.D., not determined.

Supplementary Table 2. Accession numbers for extant sequences used in the ancestral sequence reconstruction analysis.

Species	Common name	Accession number	Species	Common name	Accession number
Homo sapiens	Human	ENST00000310169	Macropus eugenii	Kangaroo	ENSMEUT00000010173
Pan troglodytes	Chimp	ENSPTRT00000029845	Monodelphis domestica	Opossum	ENSMODT00000026177
Gorilla gorilla	Gorilla	ENSGGOT00000016585	Sarcophilus harrisii	Tasmanian Devil	ENSSHAT00000021202
Pongo pygmaeus	Orangutan	ENSPPYT00000017774	Ornitorhynchus anatinus	Platypus	ENSOANT00000009111
Nomascus leucogenys	Gibbon	ENSNLET00000021872	Gallus gallus	Chick	NM_204760.1
Macaca mulatta	Rhesus	ENSMMUT00000042318	Meleagris gallopavo	Turkey	ENSMGAT00000013757
Callithrix jacchus	Marmoset	ENSCJAT00000038044	Taeniopygia guttata	Zebrafinch	ENSTGUT00000009067
Otolemur garnettii	Bushbaby	ENSOGAT00000005574	Geospiza fortis	Ground Finch	JH739887:9,834,012-9,840,454
Tupaia belangeri	Treeshrew	ENSBET00000001200	Anolis carolinensis	Lizard	ENSACAT00000011801
Mus musculus	Mouse	ENSMUST00000031108	Trachemys scripta elegans	Red-eared Turtle	AY768813
Rattus norvegicus	Rat	ENSRNOT00000003382	Chrysemys picta bellii	Painted turtle	JH584508:2,534,511-2,540,976
Dipodomys ordii	Kangaroo rat	ENSDORT00000014382	Pelodiscus sinensis	Chinese Turtle	ENSPSIT00000019878
Cavia porcellus	Guinea Pig	ENSCPOT00000008419	Xenopus tropicalis	Frog	ENSXETT00000027968
Spermophilus tridecemlineatus	Squirrel	ENSSTOT00000004710	Latimeria chalumnae	Coelacanth	ENSLACT00000010953
Oryctolagus cuniculus	Rabbit	ENSOCUT00000017103	Tetraodon nigroviridis	Tetraodon	ENSTNIT00000017438
Ochotona princeps	Pika	ENSOPRT00000016494			ENSTNIT00000008010
Bos taurus	Cow	ENSBTAT00000039651	Takifugu rubripes	Fugu	AY299469.1
Sus scrofa	Boar	ENSSSCT00000032423			AY299470.1
Vicugna pacos	Alpaca	ENSVPAT00000000639	Oryzias latipes	Medaka	ENSORLT00000005502
Tursiops truncatus	Dolphin	ENSTTRT00000002840			ENSORLT00000007166
Myotis lucifugus	Microbat	ENSMLUT00000000889	Gasterosteus aculeatus	Stickleback	ENSGACT00000023751
Pteropus vampyrus	Megabat	ENSPVAT00000003813			ENSGACT00000021407
Equus caballus	Horse	ENSECAT00000008299	Xiphophorus maculatus	Platyfish	ENSXMAT00000008427
Felis catus	Cat	ENSFCAT00000012398			ENSXMAT00000009716
Canis familiaris	Dog	ENSCAFT00000025220	Oreochromis niloticus	Tilapia	ENSONIT00000006179
Mustela putorius furo	Ferret	ENSMPUT00000006182			ENSONIT00000011351
Ailuropoda melanoleuca	Panda	ENSAMET00000010609	Oncorhynchus mykiss	Trout	AY611482
Sorex araneus	Shrew	ENSSART00000006640			AY037940
Loxodonta africana	Elephant	ENSLAFT00000000185	Danio rerio	Zebrafish	ENSDART000000081942
Dasybus novemcinctus	Armadillo	ENSNOT00000010472			ENSDART000000077335

Sequences were downloaded from GenBank (www.ncbi.nlm.nih.gov/genbank), Ensembl (www.ensembl.org) and UCSC (<http://genome.ucsc.edu/>) databases. Data for Ground Finch and Painted turtle shows the gene location for the respective UCSC genome browsers.

Supplementary Table 3. Evolutionary history of the 44 sites that show clade-specific non-synonymous substitutions.

Site	Eutheria		Metatheria		Theria		Monotreme		Mammalia		Diapsida		Turtles		Sauropsida		Amniota		Amphibia		Tetrapoda		
	Rat	Codon	Post. Prob.	Codon	Post. Prob.	Codon	Post. Prob.	Platypus	Codon	Post. Prob.	Chick	Codon	Post. Prob.	Codon	Post. Prob.	Codon	Post. Prob.	Codon	Post. Prob.	Xenopus	Codon	Post. Prob.	
33	AAA K	AAG K	0.999968 1.0	AAG K	0.947556 0.999976	AAG K	0.980355 0.995121	ATG M	ATG M	0.875919 0.987831	ATG M	ATG M	0.981199 0.999757	ATG M	ATG M	0.984044 0.999994	ATG M	0.912263 0.997952	ATG M	ATG M	0.902249 0.995508		
37	GAT D	GAC D	0.999917 1.0	GAC D	0.998744 0.999996	GAC D	0.986087 0.999918	GAC D	GAC D	0.948283 0.995952	GAA E	GAA E	0.99648 0.998446	GAA E	GAA E	0.999802 0.999857	GAA E	0.993511 0.98991	GAC D	GAC D	0.824915 0.994705		
93	ACG T	AAG K	0.995936 0.999645	AAG K	0.999306 0.999999	AAG K	0.988271 0.999913	CGC R	AAG K	0.933143 0.991434	AAA K	AAA K	0.662802 0.99968	AAG K	AAG K	0.994426 0.999999	AAG K	0.804652 0.999984	AAG K	AAG K	0.906185 0.999879		
96	CGA R	CGA R	0.960023 1.0	AGA R	0.996165 0.999999	AGA R	0.679704 0.999909	CGC R	AGA R	0.674178 0.982	AAG K	AAA K	0.983338 0.999675	AAA K	AAA K	0.97806 0.845044	AAA K	0.986518 0.996901	AAA K	0.590542 0.522337	AGA R	AAA K	0.577899 0.521896
98	CAG Q	CAG Q	0.99992 1.0	CAG Q	0.998737 0.999998	CAG Q	0.966128 0.999764	CAG Q	CAG Q	0.80817 0.967166	AAA K	GAA E	0.531526 0.467214	GAA E	GAA E	0.790863 0.845044	GAA E	0.741545 0.675684	GAA E	GAA E	0.717703 0.972992		
110	GAT D	GAC D	0.999927 1.0	GAC D	0.998841 0.999914	GAC D	0.963557 0.991988	AGC S	AAC N	0.889631 0.731713	AAT N	AAT N	0.592312 0.99998	AAC N	AAC N	0.994375 0.99997	AAC N	0.839908 0.999976	AAC N	AAC N	0.967832 0.999668		
127	TCT S	TCT S	0.999934 1.0	TCT S	0.998728 0.999996	TCT S	0.955586 0.998858	TTC F	TTT F	0.838522 0.994938	TTT F	TTT F	0.957522 0.999997	TTT F	TTT F	0.999253 1.0	TTT F	0.978388 0.999999	TTT F	TTT F	0.862442 0.999991		
142	CTC L	CTG L	0.999643 1.0	CTT L	0.986843 0.999999	CTG L	0.706028 0.999929	CTG L	CTG L	0.620667 0.98995	AAA K	AAA K	0.993216 0.999999	AAA K	AAA K	0.999649 0.999999	AAA K	0.986187 0.999943	AAG K	AAA K	0.399004 0.968596		
188	GCC A	GCC A	0.999398 1.0	GCA A	0.99058 0.999999	GCC A	0.617347 0.99996	GCC A	GCC A	0.549187 0.996605	TCT S	TCT S	0.943237 0.918497	GCT A	GCT A	0.999388 0.999388	GCT A	0.970579 0.929026	GCT A	ACT T	GCT A	0.708181 0.836777	
242	GTC V	GTC V	0.901521 1.0	GTT V	0.992323 0.999843	GTT V	0.704169 0.98894	ATC I	GTT V	0.441771 0.74293	TTT F	TTT F	0.959607 0.999997	TTT F	TTT F	0.999313 1.0	TTT F	0.980779 0.999997	TTT F	TTT F	0.932381 0.999955		
246	ATC I	ATC I	0.999893 1.0	ATC I	0.998325 0.999997	ATC I	0.968441 0.999319	CTC L	CTC L	0.459063 0.768614	CTT L	CTC L	0.719474 0.999824	CTC L	CTC L	0.992953 0.999985	CTC L	0.801886 0.997253	CTC L	ATT I	ATT I	0.26041 0.860318	
249	GTC V	GTC V	0.99961 1.0	GTG V	0.98625 0.999999	GTC V	0.747431 0.999983	GTC V	GTC V	0.751173 0.999715	ATT I	GTT V	0.717027 0.59319	GTT V	GTT V	0.997879 0.999781	GTT V	0.918802 0.983768	GTC V	GTC V	0.69103 0.997998		
258	AGT S	AGT S	0.999812 1.0	AGT S	0.880598 0.999998	AGT S	0.879335 0.999792	AGC S	AGT S	0.640856 0.96194	CGA G	GGA G	0.996629 0.999995	GGA G	GGA G	0.999817 0.999999	GCA G	0.99594 0.999979	GCA G	GCA G	0.873924 0.999721		
264 (-4)	GCC A	GCC A	0.999807 1.0	GCC A	0.965065 0.999999	GCC A	0.934727 0.999882	GCT A	GCC A	0.774575 0.972705	GAC D	GAC D	0.987182 0.999952	GAC D	GAC D	0.999121 0.999994	GAC D	0.98158 0.99997	GAC D	GAT D	GAC D	0.595193 0.999652	
275 (7)	ATC I	ATC I	0.999587 0.999988	GTC V	0.98052 0.999847	GTC V	0.842804 0.989284	GTT V	GTT V	0.61047 0.998547	GTT V	GTT V	0.994343 0.999962	GTT V	GTT V	0.996667 0.996153	GTT V	0.995471 0.999887	GTT V	GTT V	0.950968 0.999937		
279 (11)	ATG M	ATG M	1.0 1.0	ATG M	0.999996 1.0	ATG M	0.999671 0.999965	ATG M	ATG M	0.97864 0.984981	CTG L	CTG L	0.624986 0.999984	CTA L	CTG L	0.988652 0.999998	CTG L	0.995471 0.999894	CTG L	CTG L	0.617643 0.998694		
292 (24)	GCC A	GCC A	0.998616 0.999994	CCT P	0.990677 0.999993	CCT P	0.636669 0.997871	CCC P	CCT P	0.658219 0.999929	CCC P	CCT P	0.870725 0.999999	CCT P	CCT P	0.99813 1.0	CTG P	0.534754 1.0	CCT P	CCA P	CCT P	0.818513 0.999997	
308	GCC A	GCC A	0.993274 1.0	GCC A	0.998376 0.999995	GCC A	0.978912 0.999454	GCC A	GCC A	0.888521 0.938851	ACC T	ACA T	0.579751 0.999987	ACA T	ACA T	0.995165 0.999998	ACA T	0.607855 0.999971	ACC T	ACC T	0.794182 0.999604		
309	TTG L	TTG L	0.999343 1.0	CTG L	0.537791 0.999991	CTG L	0.577439 0.999242	CTC L	CTG L	0.549259 0.931341	ATG M	ATG M	0.999983 0.999999	ATG M	ATG M	0.999999 1.0	ATG M	0.999989 0.999997	ATG M	ATG M	0.999842 0.999952		
319	ATG M	ATG M	1.0 1.0	ATG M	0.999996 1.0	ATG M	0.999575 0.999985	ATG M	ATG M	0.976377 0.989684	ATT I	ATT I	0.925374 0.999985	ATT I	ATT I	0.998304 0.999998	ATT I	0.941893 0.999969	ATT I	ATT I	0.651947 0.985645		
320	GTG V	GTG V	0.999863 1.0	GTG V	0.997493 0.999998	GTG V	0.923768 0.998663	GTG V	GTG V	0.592964 0.908957	ATA I	ATA I	0.986353 0.999981	ATA I	ATA I	0.999929 0.999998	ATA I	0.994623 0.99994	ATA I	ATA I	0.924154 0.999196		
323	ATT I	ATC I	0.999927 1.0	ATC I	0.99888 0.999999	ATC I	0.992839 0.999992	ATC I	ATC I	0.983062 0.999924	GTC V	ATC I	0.951222 0.988072	ATC I	ATC I	0.999266 0.999996	ATC I	0.986444 0.999731	ATC I	ATC I	0.973588 0.999966		
325	TTC F	TTC F	0.999933 1.0	TTC F	0.998991 1.0	TTC F	0.993408 0.999991	TTC F	TTC F	0.960456 0.997931	CAC H	CAC H	0.954074 0.989754	CAC H	CAC H	0.999374 0.999991	CAC H	0.976856 0.999081	CTC L	CTC L	0.89598 0.65687		

328	GCT A	GCT A	0.995196 1.0	GCT A	0.997419 0.999998	GCT A	0.892862 0.999855	GAG E	GCA A	0.493543 0.979798	TCA S	TCA S	0.952928 0.917654	GCA A	0.999746 0.999472	GCA A	0.947117 0.937386	GCA A	0.928055 0.946151	CCA P	GCA A	0.740914 0.533981
331	CGG R	CGG R	0.998102 0.999996	AAA K	0.997557 0.999937	AAA K	0.854535 0.993233	AAA K	AAA K	0.935192 0.999367	AAG K	AAA K	0.90225 0.999783	CAA Q	0.998003 0.998455	AAA K	0.963369 0.994791	AAA K	0.958549 0.999927	AAG K	AAA K	0.937724 0.999978
335	CAC H	CAC H	0.999704 0.999995	CAG Q	0.995117 0.998904	CAG Q	0.548199 0.812583	CAC H	CAG Q	0.462515 0.806577	CAG Q	CAG Q	0.492965 0.972923	CAA Q	0.993318 0.999858	CAG Q	0.644583 0.975235	CAG Q	0.539619 0.902294	CGA R	CAG Q	0.542204 0.888208
343	AAG K	AAA K	0.999811 1.0	AAA K	0.609899 0.999993	AAA K	0.745984 0.997784	GAC D	GAC D	0.783314 0.971695	GAC D	GAC D	0.995155 0.999953	GAC D	0.999627 0.999994	CAG D	0.99666 0.999982	GAC D	0.973365 0.999266	GAC D	GAC D	0.969443 0.997674
347	AGG R	AGG R	0.999923 0.999996	AAG K	0.999466 0.999937	AAG K	0.981713 0.993243	AAG K	AAG K	0.991476 0.999379	AAA K	AAG K	0.889011 0.999993	AAG K	0.999172 0.999999	AAG K	0.97511 0.999998	AAG K	0.993385 0.999985	AAG K	AAG K	0.993093 0.999981
349	TTG L	TTG L	0.999611 1.0	TTG L	0.524789 0.999988	TTG L	0.730763 0.996495	TTC F	TTT F	0.466321 0.983754	TTT F	TTT F	0.989112 0.999997	TTT F	0.999367 1.0	TTT F	0.982892 0.999999	TTT F	0.675471 0.999964	TTC F	TTT F	0.612035 0.999991
359	CTT L	CTT L	0.680673 0.999999	ACC T	0.986025 0.999753	ACC T	0.558892 0.999033	ACA T	ACA T	0.602421 0.999898	ACA T	ACA T	0.996139 0.999988	ACA T	0.999754 0.999215	ACA T	0.99477 0.999993	ACA T	0.799137 0.999988	ACC T	ACA T	0.755072 0.999966
433	AAG K	AAG K	0.999966 1.0	AAG K	0.99942 0.999979	AAG K	0.992556 0.996635	TTG L	AAG N	0.927419 0.536267	AAT N	AAT N	0.923762 0.999982	AAT N	0.998268 0.999998	AAT N	0.939691 0.99999	AAT N	0.718655 0.997755	AAC N	AAT N	0.647508 0.999564
435	CTC L	CTC L	0.999872 1.0	CTC L	0.99794 1.000000	CTC L	0.966429 0.999957	CTG L	CTC L	0.8213 0.990964	GTT V	GTT V	0.90968 0.997935	GTT V	0.991874 0.983105	GTT V	0.905866 0.984785	TTG F	0.504518 0.66944	TAC Y	TTC F	0.831531 0.740009
436	AAG K	AAA K	0.998099 1.0	AAA K	0.999606 0.999994	AAA K	0.992141 0.999393	AAA K	AAA K	0.924666 0.937147	CGA R	AGA R	0.995753 0.999996	AGA R	0.999873 1.0	AGA R	0.999008 0.999982	AGA R	0.990783 0.99441	AGA R	AGA R	0.992435 0.999744
441	ACC T	ACC T	0.995121 0.999997	AAT N	0.980802 0.999984	AAC N	0.782498 0.994709	CAC N	AAC N	0.877683 0.990106	AAC N	AAC N	0.98792 0.999981	AAC N	0.964151 0.999998	AAC N	0.982949 0.99998	AAC N	0.936589 0.99316	ATA I	AAC N	0.642084 0.69386
442	AAC N	AAT N	0.97425 0.999983	AAT N	0.98925 0.999974	AAT N	0.951303 0.9951	AGT S	AGT S	0.923553 0.89845	CGG R	CGT R	0.796367 0.997699	CGT R	0.623181 0.999996	CGT R	0.814856 0.997835	AGT S	0.95114 0.971402	AGT S	AGT S	0.959204 0.99819
443	TCC S	TCC S	0.999447 0.99999	GCC A	0.668732 0.999941	GCC A	0.757464 0.993406	GCC A	GCC A	0.647609 0.999331	GCC A	GCT A	0.539524 0.999983	GCT A	0.993587 0.999998	GCT A	0.75733 0.999996	GCT A	0.71229 0.999976	GCT A	GCT A	0.761969 0.999956
446	AGC S	AGT S	0.584729 0.999996	ATC I	0.848136 0.999967	ATC I	0.35655 0.963449	AGC S	ATC I	0.330706 0.9617	ATT I	ATT I	0.948061 0.996124	ATT I	0.997344 0.999754	ATT I	0.960462 0.999815	ATT I	0.662485 0.995676	ATC I	ATT I	0.609413 0.990927
455	ATA I	ATA I	0.999915 1.0	ATC I	0.701751 0.999987	ATA I	0.57847 0.996463	ATG M	ATG M	0.943437 0.985573	ATG M	ATG M	0.999983 0.999999	ATG M	0.999999 1.0	ATG M	0.999994 1.0	ATG M	0.999647 0.999976	ATG M	ATG M	0.999954 0.999998
469	GTC V	GTG V	0.999429 0.999999	GCT A	0.696203 0.996124	GTC V	0.344397 0.831443	GTC V	GTC V	0.71753 0.82836	TTT F	TTC F	0.840713 0.999997	TTC F	0.99761 1.0	TTC F	0.936443 0.999997	TTC F	0.935329 0.998428	TTC F	TTC F	0.955683 0.999648
471	ACC T	ACT T	0.999859 0.999988	AGT S	0.997929 0.999927	AGT S	0.933768 0.992577	AGC S	AGT S	0.657575 0.999137	AGC S	AGT S	0.527757 0.999977	AGT S	0.690869 0.999997	AGT S	0.576924 0.999994	AGC S	0.503567 0.999967	AGC S	AGC S	0.62493 0.99994
476	GCA A	GCA A	0.965295 1.0	GCT A	0.725488 0.999998	GCC A	0.472878 0.999815	GCC A	GCC A	0.715269 0.971228	GGG G	GCC G	0.867877 0.999923	GCC G	0.998318 0.999993	GCC G	0.944997 0.998758	GCC G	0.608731 0.642489	GCC A	GCC G	0.604591 0.640808
479	GAT D	GAT D	0.999865 0.999996	GTT V	0.369214 0.453305	GTT V	0.515961 0.461885	GTG V	GTT V	0.864457 0.924135	GCT A	GTT V	0.93035 0.450021	ATT I	0.995934 0.995946	GTT V	0.935196 0.502008	GTT V	0.928592 0.913722	GTG V	GTT V	0.875834 0.978764

The 42 sites that show clade-specific non-synonymous substitutions are enumerated. Numbering is after rat $\alpha 9$ subunit; for sites located at or near the TM2 domain, numbering after Miller *et al.*, 1989 is shown between brackets. Sites analyzed by site-directed mutagenesis are highlighted in light blue. Sites located in the MA α -helix of the intracellular domain, and analyzed by the construction of a chimeric subunit, are highlighted in yellow.

Corresponding codons and aminoacids for the predicted ancestral sequences are shown for the major group nodes: Eutheria (placental mammals), Metatheria (marsupials), Theria, Monotreme, Mammalia, Diapsida (birds, lizards, snakes and crocodiles), Turtles, Sauropsida (birds and reptiles), Amniota, Amphibia and Tetrapoda. For groupings and node locations see the phylogeny of Supplementary figure 3. Between brackets, posterior probabilities of the marginal reconstruction for each character state (see Methods). For the monotreme and amphibian groups codons and aminoacids for extant platypus and frog $\alpha 9$ sequences, respectively, are shown. Codons and aminoacids of extant rat and chick $\alpha 9$ sequences are also depicted. Red, mammalian specific aminoacids; blue, sauropsid specific aminoacids; orange, tetrapod specific aminoacid; white, monotreme specific aminoacids; green, amphibian specific aminoacids. The same color coding was used to highlight these 42 sites in the alignment of Supplementary Figure 1.

Supplementary Table 4. *pK/pNa of $\alpha 9\alpha 10$ wild type, mutant and chimeric receptors.*

Receptor	E_{rev}	pK/pNa
Heteromeric receptors		
Rat $\alpha 9\alpha 10$	-7.3 ± 1.6 (n=20)	1.1 ± 0.2 (n=6)
Chick $\alpha 9\alpha 10$	-2.7 ± 0.6 (n=27)	0.9 ± 0.1 (n=8)
Homomeric receptors		
Rat $\alpha 9$	-10.8 ± 2.4 (n=5)	1.2 ± 0.1 (n=4)
Chick $\alpha 9$	-2.2 ± 0.7 (n=23)	1.21 ± 0.05 (n=5)
Chick $\alpha 10$	$+0.19 \pm 1.9$ (n=14)	1.26 ± 0.04 (n=4)
Hybrid receptors		
Rat $\alpha 9$ Chick $\alpha 10$	-4.5 ± 1.8 (n=16)	1.2 ± 0.1 (n=7)
Chick $\alpha 9$ Rat $\alpha 10$	-1.9 ± 0.9 (n=7)	N.D.
Rat mutant and chimeric receptors		
Rat $\alpha 9D110N\alpha 10$	-6.3 ± 2.3 (n=12)	1.3 ± 0.1 (n=7)
Rat $\alpha 9S127F\alpha 10$	-4.7 ± 1.1 (n=7)	1.3 ± 0.2 (n=5)
Rat $\alpha 9A24'P\alpha 10$	-4.9 ± 1.8 (n=10)	1.3 ± 0.2 (n=4)
Rat $\alpha 9I7'V/M11'L\alpha 10$	-4.4 ± 1.1 (n=9)	1.3 ± 0.1 (n=6)
Rat $\alpha 9A-4'D\alpha 10$	-3.0 ± 0.8 (n=15)*	0.51 ± 0.05 (n=8)*
Rat $\alpha 9(IC-chick \alpha 9)\alpha 10$	-4.8 ± 1.8 (n=10)	1.0 ± 0.05 (n=3)
Rat $\alpha 9D110N/S127F/A-4'D\alpha 10$	-2.5 ± 0.7 (n=23)*	0.70 ± 0.06 (n=10)*
Chick mutant receptors		
Chick $\alpha 9N110D\alpha 10$	-2.5 ± 1.0 (n=9)	1.15 ± 0.05 (n=6)
Chick $\alpha 9F127S\alpha 10$	-1.8 ± 1.1 (n=9)	1.00 ± 0.05 (n=5)
Chick $\alpha 9D-4'A\alpha 10$	-0.4 ± 1.4 (n=9)	0.8 ± 0.1 (n=7)
Chick $\alpha 9N110D/F127S/D-4'A\alpha 10$	-3.7 ± 0.6 (n=9)	1.1 ± 0.1 (n=4)

Values are mean \pm S.E.M. n=number of oocytes. *t* test vs rat $\alpha 9\alpha 10$ receptor, * $p < 0.05$. N.D., not determined.